# Genome sequence of the hyperinvasive *Campylobacter jejuni* strains

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A thesis submitted in partial fulfilment of the
requirements of Nottingham Trent University
for the degree of Doctor of Philosophy

**November 2012**

# ABSTRACT

*Campylobacter jejuni* is the world's major cause of gastroenteritis in humans. Although motility, toxin production, adhesion and invasion are some of the key factors associated with *C. jejuni* pathogenesis, their mechanism in the disease process remains unclear. The key aim of this project is to study the genetic basis of hyperinvasiveness in a group of six *C. jejuni* strains which have been reported as hyperinvasive into human intestinal cell lines.

Here, genomotyping of the hyperinvasive *C. jejuni* was performed by comparative genomic hybridization (CGH) against four low invasive *C. jejuni* strains. A group of 67 genes were identified as being present or highly divergent/absent in the hyperinvasive versus low invasive *C. jejuni* strains. Of these, nine genes were present and six genes were highly divergent/absent in all hyperinvasive *C. jejuni*. The PCR screening of these 15 genes in nine additional low invasive *C. jejuni* strains showed a significant association with the hyperinvasive phenotype. The majority of identified genes encoded proteins with essential cellular and metabolic functions along with some genes with known virulence related roles. Thus, the hyperinvasive phenotype is characterised by different functional networks rather than a single gene or gene cluster. All strains showed an overall genetic variability and the capsule, lipooligosaccharide, flagellar biosynthesis and restriction modification regions were the most diverse. The hierarchical clustering based on comparative genomic hybridization (CGH) did not group together the hyperinvasive *C. jejuni* as a single group and these strains possessed different MLST profiles.

The hyperinvasive *C. jejuni* strains were shown to contain additional genetic content by pooled suppressive subtractive hybridization (PSSH). Eleven inserts were identified in total which were variably distributed in the hyperinvasive *C. jejuni* strains. Of these four sequences were specific to the hyperinvasive *C. jejuni* as these were absent from all thirteen low invasive *C. jejuni* strains tested. The majority of sequences matched with genes in *Campylobacter* and other bacteria and one sequence had no homology with anything in the databases today. Since, there is no insert identified as present in all the hyperinvasive *C. jejuni* strains it can be suggested that each strain might have evolved a different mechanism for hyperinvasiveness and that this phenotype is a multifactorial process.

*C. jejuni* 01/10 and 01/51 whole genome sequences identified no unique genetic content in either strain except for a prophage in *C. jejuni* 01/51. *C. jejuni* 01/10 was found to contain two prophages. *C. jejuni* 01/51 has a highly mosaic capsule locus with genes similar to *C. jejuni* subsp. *doylei* and *C. lari* capsular polysaccharide genes. Some genes with homology to the *C. jejuni* subsp. *doylei* capsule genes were also identified in *C. jejuni* 01/10 capsule region. This is evidence of genetic recombination with capsule genes from other pathogenic *Campylobacter* species which is not reported in the capsule region of other *Campylobacter* strains sequenced to date. This suggests that the highly diverse capsule in *C. jejuni* 01/10 and 01/51 is required for the hyperinvasive phenotype in these strains.

This study has provided detailed insight into the genomic structure of the hyperinvasive *C. jejuni* strains and has highlighted genetic factors involved in their hyperinvasive phenotype.

# DECLARATIONS

**Section 1**: This is an original piece of research work carried out by the author in the School of Science and Technology at Nottingham Trent University. The adhesion and invasion profiling of hyperinvasive and low invasive *C. jejuni* strains used in this study was originally reported by Fearnley *et al* (2008) and later re-confirmed by my predecessor post-graduate researcher, Dr Afzal Javed at NTU (Javed., 2009). The phylogeny of hyperinvasive *C. jejuni* 01/51 and 01/10 strains (chapter 6) was performed by Dr Alan McNally at NTU. There is no material contained within this thesis that has been submitted for any other degree, or at any other institution.

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# ACKNOWLEDGEMENTS

I would like to thank Almighty Allah for giving me the strength and courage to lead this project to completion. My very many special thanks and highest regards are for my most worthy director of studies, Dr Georgina Manning. She has not only been a great mentor throughout my studies but has also been a fantasic listener. Dr Manning has always been on forefront to provide continuous guidance, encouragement and support during this project. This research work would have not possible without her support and guidance. I would like to thank Dr Alan McNally for being a supportive supervisor and for his generous help with a lot of complex data analysis involved in this project. Dr McNally has always extended his most useful ideas for the progression of this research work. My sincere regards are for Professor Steve Forsythe for being an actively participating supervisor and many interesting discussions in this research.

I am thankful to Professor Ian Connerton of the University of Nottingham for preliminary discussions in the CGH study and Mr Colin Nicholson, the University of Nottingham post-genomics facitlity at the QMC for performing DNA microarray hybridization and for allowing me to work in parallel with him during the experiment. I am grateful to Professor Nadia Chuzhanova, NTU, for performing the statistical analysis of CGH data and overall statistics help in different parts of this study. I would like to thank Dr Chrystala Constantinidou and Mrs Mala Patel (University of Birmingham) for performing genome sequening on my strains and for giving me a chance to experience the next generation sequencing technique in the their genomics lab.

Thanks to my lovely colleagues in the microbiology laboratory and in postgraduate research office for providing a co-operative, comfortable and most enjoyable environment for work. I am thankful to the microbiology preparation room team members for always being supporting and helpful to me.

I would also like to thank my family; Ani, Neena, Nadia and Maman for their patience and support throughout this time demanding research period. I also owe my thanks to Misbah, Umair and Ahmed, and Miquette for their support and for organising most wanted relaxing breaks during my thesis write up period.

This project is funded by the NTU Vice chancellor’s sponsorship.

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# LIST OF ABBREVIATIONS

| | |
|---|---|
| ATCC | American Type Culture Collection |
| AFLP | Amplified fragment length polymorphism |
| ATP | Adenosine triphosphate |
| BA | Butzler agar |
| BB | Bolton broth |
| BMDCs | Bone marrow derived murine dendritic cells |
| bp | Base pair |
| CAPs | Cationic antimicrobial peptides/proteins |
| CDS | Coding sequence |
| CDT | Cytolethal distending toxin |
| CEB | *Campylobacter* Enrichment Broth |
| cfu | Colony forming unit |
| CGH | Comparative genomic hybridization |
| Cia | *Campylobacter* invasion antigen |
| CJIE | *Campylobacter jejuni* integrated element |
| CMLP | *Campylobacter* Mu like prophage |
| CPS/CAP | Capsular polysaccharides |
| cy-dCTP | Cyanine 2’-deoxycytidine 5’-triphosphate |
| DCs | Dendritic cells |
| DNA | Deoxyribonucleic acid |
| dNTP | 2’-deoxynucleoside 5’-triphosphate |
| EDTA | Ethylenediamine tetra-acetic acid |
| ERK | Extracellular signal regulated kinase |
| *feds* | Flagellar coexpressed determinants |
| FISH | Fluorescence *In situ* Hybridization |
| *fla*-SVR | *fla*-amplified short variable regions |
| FM | Flagellar modification |

| | |
|---|---|
| GBS | Guillain Barré syndrome |
| G + C | Guanine and cytosine |
| HMW | High molecular weight |
| HS | Heat stable |
| Ig | Immunoglobulin |
| IL | Interleukin |
| IPEC | Intestinal pig epithelial cells |
| kbp | Kilobase pair |
| LB | Luria-Bertani broth |
| LegAm | Legionaminic acid |
| LOS | Lipooligosaccharide |
| LPS | Lipopolysaccharides |
| MAP | Mitogen activated protein |
| (m)CCDA | (modified) charcoal cefoperazone deoxycholate |
| MCP | Methyl-accepting chemotaxis protein |
| MeOPN | O-methyl phosphoramidate |
| MFS | Miller Fisher syndrome |
| MHA | Muller Hinton agar |
| MHB | Muller Hinton broth |
| MLST | Multi-locus sequence typing |
| MOMP | Major outer membrane protein |
| NCTC | National Collection of Type Cultures |
| NF-kB | Nuclear factor-kappa-enhancer of activated B cells |
| OD | Optical density |
| ORF | Open reading frame |
| *p* value | Probability value |
| PAMPs | Pathogen associated molecular patterns |
| PB | Preston broth |
| PBS | Phosphate buffered saline solution |

| | |
|---|---|
| PCR | Polymerase chain reaction |
| PFGE | Pulsed-field gel electrophoresis |
| PseAc | Pseudaminic acid |
| PSSH | Pooled suppressive subtractive hybridization |
| RAPD | Random amplification polymorphic DNA |
| RFLP | Restriction fragment length polymorphism |
| RM | Restriction modification |
| ROS | Reactive oxygen species |
| rpm | Revolutions per minute |
| rRNA | Ribosomal ribonucleic acid |
| TAE | Tris/acetate/EDTA |
| TLRs | Toll-like receptors |
| sIg | Secretory immunoglobulin |
| σ28 | Sigma factor 28 or fliA (promoter) |
| σ54 | Sigma factor 54 or rpoN (promoter) |
| SSH | Suppressive subtractive hybridization |
| Tm | Melting temperature |
| v/v | Volume per volume |
| w/v | Weight per volume |

## *Chapter One*

# INTRODUCTION

# INTRODUCTION

## 1.1 *Campylobacter* species in general

*Campylobacter* species are small Gram negative (0.5-5.0 µm long and 0.2-0.8 µm wide), spiral shaped, non-spore forming fermentative bacteria. These bacteria exhibit darting motility due to the presence of unipolar or dipolar flagella. *Campylobacter* species grow under microaerobic conditions in an atmosphere containing 3-15% $CO_2$ and 3-5% $O_2$. *Campylobacter* species have a growth temperature range of maximum ~46 °C and minimum 30 °C (Davis and DiRita., 2008). Levin *et al* (2007) proposed that *Campylobacter* species should be referred to as “thermotolerant” as they do not represent characteristics of a classic thermophile with a growth temperature of 55 °C. *Campylobacter* species are known to lack the glycolytic enzyme 6-phosphofructokinase, hence are unable to metabolize carbohydrates. Recently Stahl *et al* (2011) showed that *C. jejuni* is able to utilize L-fucose released by intestinal mucin glycoproteins. *Campylobacter* species use amino acids, mainly serine (Velayudhan *et al*., 2004), and some organic acids including pyruvate and lactate (Thomas *et al*., 2011) as carbon sources for energy production.

## 1.2 History of *Campylobacter* species

*Campylobacter* species were described as “Vibrio” like organisms in 1913, causing disease in bovines and ovines (McFadyean and Stockman., 1913, Vandamme *et al*., 2010). Later Smith and Taylor (1919), isolated spiral shaped bacteria from bovine abortions. These bacteria had similar morphology as described before by McFadyean and Stockman and were named “*Vibrio fetus*” (Smith and Taylor., 1919). These *Vibrio* like bacteria from human infections were studied in detail by King (1957). She noticed that although these bacteria were “*Vibrio* like” they showed growth at much higher temperatures hence they were later called “*Vibrio jejuni*”. *Vibrio* like organisms were also found in the faeces of pigs suffering from diarrhoea and were known as *Vibrio coli* (Doyle., 1944).

The first microscopic evidence of *Campylobacter* species came from Escherich (1886) who observed spiral bacteria, simply named “*Cholera infantum*”, in the samples taken from colon of infants who died of cholera like disease as well as from stools of infants suffering from diarrhoea (Escherich., 1886). These bacteria were considered unculturable. It was not until 1963, when Sebald and Veron classified *Campylobacter* as a separate genus based mainly on the small genome size, anaerobic growth and fermentative metabolism. *Campylobacter* were first isolated from stool samples of patients with enteritis by a filtration method (Dekeyser *et al.*, 1972). Later on, *Campylobacter jejuni* and *Campylobacter coli* were also differentiated from each other (Skirrow., 1977). Now, *C. jejuni* and *C. coli* are considered as the major enteric pathogens of humans causing disease in the developing (Coker *et al.*, 2002) and developed world (Altekruse *et al.*, 1998).

## 1.3 Taxonomy of *Campylobacter* species

Since the first taxonomical classification of the *Campylobacter* genus by Sebald and Veron in 1963, the genus has undergone considerable changes (On., 2001, Debruyne *et al.*, 2005). The very early classification described four species in the *Campylobacter* genus including *C. jejuni*, *C. coli*, *C. fetus* and *C. sputorum*. The diversity in the *Campylobacter* genus was first defined by studying the 16S rRNA gene sequence in these bacteria. The 16S rRNA gene is highly conserved in bacteria and is of considerable length (~1500 bp) that makes it a useful tool for phylogenomic classification (Man *et al.*, 2010). The study of 16S rRNA gene sequences, fatty acid profiles and flagellar structure defined a genus called *Helicobacter* that included the formely named *C. pylori* and *C. mustelae* (Goodwin *et al.*, 1989). The 16S rRNA sequence divergence also classified the oral anaerobes *Wolinella curva* and *W. recta* into the *Campylobacter* genus (Vandamme *et al.*, 1991). These techniques together with other immunotyping data and whole cell protein profile classified the aero-tolerant campylobacters *A. nitrofigilis* and *A. cryoaerophilus* into another genus called *Arcobacter* (Vandamme *et al.*, 1991 and 1992). Later on, a new bacterial family called *Campylobacteraceae* was defined that included genera *Arcobacter*, *Campylobacter*, *Sulfurospirillum* and *Bacteroides ureolyticus* (Vandamme., 2000). Recently, Vandamme *et al* (2010) studied 26 *Bacteroides ureolyticus* strains using 16S rRNA and *cpn*60 gene sequences, amplified fragment length polymorphism and protein profiling. Vandamme *et al* (2010) reclassified *B. ureolyticus* as a species in the *Campylobacter* genus, *Campylobacer ureolyticus*. The bacterial families Camplobacteraceae and Helicobacteraceae are included in the rRNA super-family VI and form a part of the Epsilobacteria or Proteobacteria (Cavalier-Smith., 2002).

The *Campylobacter* genus consists of 20 species and sub-species (Fernández *et al*., 2008). In the same year, Debruyne *et al* (2008) reported 17 species and 6 sub-species in the *Campylobacter* genus with the number of species in this genus continuously increasing.

*C. jejuni*, *C. coli*, *C. lari*, *C. fetus*, *C. hyointestinalis*, *C. upsaliensis*, *C. gracilis*, *C. showae* are some well-known species included in the *Campylobacter* genus (Debruyne *et al*., 2005). *C. jejuni* contains two sub-species, *C. jejuni* subsp. *jejuni* and *C. jejuni* subsp. *doylei*. *C. jejuni* subsp. *jejuni* is present as commensal bacteria in the intestinal tract of domestic and commercial animals and it is also the most common cause of gastroenteritis in humans (Miller *et al*., 2007) whereas *C. jejuni* subsp. *doylei* has only been isolated from human cases of septicaemia and bacteraemia (Lastovica., 2006). Other phenotypic and biochemical characteristics that distinguish *C. jejuni* subsp. *doylei* from *C. jejuni* subsp. *jejuni* include the inability of *C. jejuni* subsp. *doylei* to reduce nitrate, variable growth rate at 42 °C, absence of γ-glutamyl transferase (GGT) and L-arginine arylamidase enzymatic activity and susceptibility to cephalothin (Miller *et al*., 2007). The two sub-species show significant sequence divergence at the genome level (Parker *et al*., 2007). The sequence variation at the *nap* gene locus has been used to develop a multiplex PCR assay for *Campylobacter* diagnosis at the sub-species level (Miller *et al*., 2007). Using the readily available genome sequence data for *C. jejuni* strains, Taboada *et al* (2012) has reported a highly sensitive comparative genomic fingerprinting method for *C. jejuni* sub-speciation. This method relies on identifying variability at muliple alleles widely distributed in the assessory gene pool across the whole genome (Taboada *et al*., 2012).

### 1.4 Isolation and further classification of *Campylobacter* species

The first step in detection of *Campylobacter* species is their isolation from samples. Further classification is carried out by phenotyping or genotyping. Some of these methods are discussed below briefly.

#### *1.4.1 Isolation and phenotyping*

All *Campylobacter* species except for *C. gracilis* show oxidase activity. This phenotype has been used for the development of selective media containing one or more oxygen scavengers (*i.e*. blood, ferrous ions) with selective antibiotics (Corry *et al*., 1995). A number of selective broths including Bolton Broth (BB), *Campylobacter* Enrichment Broth (CEB) and Preston Broth (PB) with oxygen limiting enzyme oxyrase have been successfully used for the isolation of *Campylobacter* species (Abeyta *et al*., 1997, Baylis *et al*., 2000). The selective agars *i.e.* Preston, charcoal cefoperazone deoxycholate (CCDA) and Butzler Agar (BA) have been used efficiently for the isolation of *Campylobacter* species. The standard method used at present for the detection of *Campylobacter* species is by plating and enumeration directly on mCCDA. The Bolton Broth (BB) and Muller Hinton Broth (MHB) are used for growth in liquid culture or as an enrichment step (ISO 2006a and 2006b).

Other phenotypes differentiating *Campylobacter* species include catalase activity, growth at 25 °C or 42 °C and resistance to antibiotics including naladixic acid, cephalothin and fluoroquinolones. *C. jejuni* can hydrolyse sodium hippurate, indoxyle acetate and reduces nitrate. *C. coli* are unable to hydrolyse hippurate and it is the lack of this activity that differentiates *C. jejuni* from *C. coli*. Still there are some hippurate negative *C. jejuni* isolates which are deficient of hippurate activity (Koenraad *et al*., 1995). *C. fetus* is the only member of *Campylobacter* species that can survive in the presence of glycine and can produce hydrogen sulphide (On., 1996). A series of biochemical tests are commercially available as rapid identification kits (e.g. Campy API kits) that can differentiate all *Campylobacter* species (Hoosain and Lastovica., 2009, Reina *et al*., 1995). Other rapid methods that can detect and confirm *Campylobacter* species include Fluorescence *In situ* Hybridization (FISH) (Lehtola *et al*., 2006) and latex autoagglutination (Wilma *et al*., 1992).

Another phenotypic method used to discriminate between *Campylobacter* species is serotyping. The Penner serotyping scheme is the most acceptable and widely used phenotypic scheme for typing of *Campylobacter* species. It differentiates strains based on the soluble heat stable (HS) antigen. In Penner serotyping, a passive haemagglutination reaction is observed by mixing the bacterial cell suspension with different antisera (Penner and Hennessy., 1980). The *C. jejuni* capsular polysaccharides (Karlyshev *et al*., 2000, Wren *et al*., 2001) have been shown as the serodeterminant of Penner serotyping. The Penner serotyping scheme contains 48 antisera for *C. jejuni* and 15 antisera for *C. coli* and recognizes 63 serotypes (Penner *et al*., 1983). The main drawbacks of Penner serotyping are non-typeability of a large number of *Campylobacter* strains compared to modern day genotyping methods and cross reactivity with more than one antiserum (Cornelius *et al*., 2010). Another method used for *Campylobacter* species serotyping is called Lior serotyping. It is based on heat labile antigens. It can differentiate between 150 serotypes of *C. jejuni*, *C. coli* and *C. lari* (Lior *et al*., 1982).

Penner serotyping is generally combined with another typing technique called phage typing for diagnosis of *Campylobacter* species. In phage typing, the phage pattern of an isolate is compared to the profile of other virulent bacteriophage. Two or more strains with identical bacteriophage patterns form a phage type (Frost *et al*., 1999). Serotyping and phage typing have poor resolution. These techniques have to be combined with advanced molecular typing for epidemiological and surveillance studies (Hopkins *et al*., 2004).

### *1.4.2 Genotyping*

Molecular typing methods are used for bacterial identification and speciation in both pure and mixed cultures. These techniques are sensitive, rapid and highly discriminatory compared to the conventional phenotypic methods. A number of genotypic methods have been developed for typing of *Campylobacter* species. The advantages and drawbacks of these techniques for *Campylobacter* species typing have been recently reviewed (Ahmed *et al*., 2012). The pulsed-field gel electrophoresis (PFGE), ribotyping and flagellin gene typing, restricted and amplified chromosomal fragment length polymorphism (RFLP and AFLP) are a few examples of the genotyping techniques (Nielsen *et al*., 2000).

PFGE is based on digesting the chromosomal DNA with different restriction enzymes *e.g*. *Sma*I, *Kpn*I and *Sal*I. This digestion generates DNA fragments of variable length. The variation in length of resulting fragments is compared to generate a PFGE profile for the isolate (O’Leary *et al*., 2011, Gilpin *et al*., 2006, Peters., 2009). The electrophoresis profiles generated for a large number of strains can be analysed by computerized software (*e.g*. BioNumerics by Applied Maths, Ghent, Belgium). PFGE is a useful technique which successfully discriminates closely related strains but it requires technical expertise (Peters., 2009, Pittenger *et al*., 2009).

Restricted Fragment Length Polymorphism (RFLP) is a technique that detects variation in a selected locus in the genome e.g. *fla*, *porA*. The flagellin and MOMP are stable but highly genetically diverse regions in *Campylobacter* species (Cody *et al*., 2009). For example, in *fla*-typing, the *fla* gene is PCR amplified and digested with one or more restriction enzymes (*fla*-RFLP) or the PCR product is sequenced using the gene specific primers *fla*-amplified short variable regions (*fla*-SVR) (On *et al*., 2008). Amplified fragment length polymorphism (AFLP) like RFLP involves digesting the genomic DNA with two or more restriction enzymes which are ligated to specific adaptors. These labelled fragments are then PCR amplified using fluorescent labelled primers (On *et al*., 2008). AFLP has been used as a highly discriminatory and reproducible molecular typing technique used in epidemiological studies (Johnsen *et al*., 2007, Siemer *et al*., 2005). Another technique used for typing of *Campylobacter* species is Random Amplification of Polymorphic DNA (RAPD). This method involves PCR amplification of genomic regions by using one 10-15 bp primer that will produce several fragments of variable lengths in different strains as a result of primer binding at different sites (On *et al*., 2008). Ribotyping detects variations in the ribosomal DNA genes. The genomic DNA is digested with two enzymes followed by hybridization with probed rRNA specific primers. The characteristic ribosomal pattern of each isolate is then visualised (On *et al*., 2008). A fully automated ribotyping method is also developed now that has further improved the speed and reproducibility of this method (Pavlic and Griffiths., 2009). However, ribotyping lacks discriminatory ability for *Campylobacter* species (Pavlic and Griffiths., 2009, Ge *et al*., 2006).

Currently, Multi-locus Sequence Typing (MLST) is frequently used as a genotyping technique to study *Campylobacter* species. MLST is based on studying the DNA sequence variation in *Campylobacter* housekeeping (usually seven) genes. Each sequenced gene is given an arbitrary allele number. The allele number for all the genes are combined to assign a unique sequence type number to each strain. *C. jejuni* has been shown to be diverse and have a weakly clonal structure (Dingle *et al*., 2002, Manning *et al*., 2003).

With an increasing number of genome sequences of *Campylobacter* species becoming available, a number of high-throughput genome based typing techniques have been designed. These techniques are based on studying differences between *Campylobacter* strains at the whole genome level. DNA microarray technology is also being developed as a diagnostic tool for use in epidemiological and phylogenetic studies (Marotta *et al*., 2012, Pittenger *et al*., 2012, Taboada *et al*., 2012).

## 1.5 Campylobacteriosis: a disease burden on public health

*Campylobacter* species has been identified as a major zoonotic pathogen causing gastroenteritis in humans worldwide. According to the European Centre of Disease Control (ECDC) and European Foods Safety Agency (EFSA) *Campylobacter* species caused gastroenteritis was most common in the European Union (EU) followed by salmonellosis and yersiniosis in a five years period (EFSA., 2007, 2010a). There were just around 200,000 human cases of campylobacteriosis recorded in 2009 and 2010 (EFSA., 2009 and 2010a). This number represented a 14.2% rise from 2006 which is a significant burden on the economy.

The Foodborne Diseases Active Surveillance Network (FoodNet) of the Centres for Disease Control and Prevention (CDC) estimated that *Campylobacter* species cause approximately 845,000 cases of illness in the USA each year. This number is still an underestimate as a lot of cases remain unreported and undiagnosed (Anonymous., 2010).

Similarly, the number of human cases of campylobacteriosis in the EU is not an actual representation of true disease burden implicated by *Campylobacter* species. It is estimated that in EU approximately 2 to 20 million people may get campylobacteriosis per year (EFSA., 2010b). *Campylobacter* species are the most common cause of foodborne outbreaks in the UK. There were approximately 321,000 human cases of *Campylobacter* food poisoning, over 15,000 hospitalizations and 76 deaths in England and Wales in 2008. The food poisoning caused by *Campylobacter* species costs £583 million which represents one third of the cost of foodborne illness in England and Wales in 2008 (http://www.food.gov.uk/multimedia/pdfs/campylobacterstrategy.pdf). In 2010, 62,684 human cases of enteric and non-enteric *Campylobacter* species caused infections were reported in England and Wales. This figure was six times higher than human food poisoning cases of *Salmonella* (9133 cases) reported in 2010 (http://www.hpa.org.uk/Topics/InfectiousDiseases/). Chicken and related products are the major reservoir in most cases (50-80% of cases) with broiler chickens accounting for 20-30% of these cases (EFSA., 2010b).

Based on the significance of disease burden of *Campylobacter* caused infections in the UK, the government has introduced an “Innovation Strategy for *Campylobacter*” from 2010 through to 2015. The program aims to research ways to control *Campylobacter* species at all levels in the food chain from farms to consumers, (http://www.food.gov.uk/multimedia/pdfs/campylobacterstrategy.pdf). The European Food Standards Agency has also advised on conducting an active surveillance of campylobacteriosis in all European member states with an emphasis on detecting unreported cases of campylobacteriosis. This surveillance strategy also aims to identify the unknown reservoirs of *Campylobacter* caused infections by advanced molecular techniques.

Huge costs are incured with *Campylobacter* associated infections mainly due to medical costs, long absences of employees from work, expenses incurred as a result of product recalls, legal charges etc. It is estimated that the total costs linked to campylobacteriosis is $1billion per annum in USA (CAST., 1994). In a surveillance conducted in Netherlands recently, it has been reported that the costs associated with campylobacteriosis is 21 million euros per annum (Havelaar *et al*., 2005).

### 1.6 *Campylobacter* species sources and transmission of infection

*Campylobacter* species form part of normal flora of wildlife and domestic birds. This may be because of the higher body temperature of avian hosts favours their survival (Skirrow, 1977) and chicken is responsible for harbouring *Campylobacter* species (Corry and Atabay, 2001). Most cases of campylobacteriosis are related to the consumption of raw or undercooked poultry products or by cross contamination of raw or undercooked foods. Chicken is a rich source of essential proteins and minerals, and requires shorter preparation time compared to cooking pork and beef. These factors influence their popularity and enhance the chances of *Campylobacter* species related outbreaks (Corry and Atabay, 2001). Among *Campylobacter* species, *C. coli* and *C. jejuni* are the most prevalent in outbreaks. *C. jejuni* is responsible for 12 times the human cases compared to *C. coli* in England and Wales (Friedman *et al*., 2000). *C. coli* is dominant in free range and organic chickens whereas *C. jejuni* is mainly isolated from caged chicken breeds (El-Shibiny *et al*., 2005).

*Campylobacter* species are present in the intestine of chicken and mainly located in the cecum and colon (Berrang *et al*., 2001). During slaughter and processing of chicken, the intestine may rupture and bacteria spread all over on the skin and get trapped in skin pores and cracks. *Campylobacter* species can persist on the carcass under frozen conditions and at 4 °C. Under favourable conditions these bacteria can grow on the skin and can be spread by cross contamination (Chantarapanont *et al*., 2003). Even under controlled packaging conditions *Campylobacter* species can persist on chicken skin and can spread by improper handling and storage at the consumer end (Scherer *et al*., 2006).

Other processed animal meats have been shown to harbour *Campylobacter* species and these include cattle, sheep, pigs, turkey and ducks (Humphrey *et al*., 2007). The highest prevalence of *Campylobacter* species is on pig carcasses, compared to sheep and beef (Nesbakken *et al*., 2003). This may be because the skin remains on pig carcass during most of the slaughter and processing of meat (Moore *et al*., 2005). *Campylobacter* species are present in the digestive tract of healthy cattle (Atabay and Corry., 1998) whereas the lowest prevalence of *Campylobacter* species is in sheep (Zweifel and Stephan., 2004). Shellfish obtained from water systems contaminated with *Campylobacter* species is also a major source of dissemination of infection (Wilson and Moore., 1996). The transmission of *Campylobacter* species to the human hosts is also attributed to the consumption of unpasteurised milk and milk products. The cross contamination with animal faeces is the likely cause of transmission of *Campylobacter* species in milk especially during the milking process (Zilbauer *et al*., 2008, Hänninen *et al*., 2000, Shane., 2000). Consumption of untreated water and direct contact with domestic and farm animals are high risk factors for *Campylobacter* species transmission to humans (Gilpin *et al*., 2008, Coker *et al*., 2002, Shane., 2000). Environmental contamination with animal faeces is also a major factor contributing to the transmission of *Campylobacter* species infection to humans (Ridley *et al*., 2008). Wills and Murray (1997) reported that *Campylobacter* species were present in large numbers in chicken intestines during summer months (May through to October) and a significant reduction in number was observed in winter months. A similar trend was noticed when chickens were sampled in summer months showing 87-97% of samples tested positive for *C. jejuni*. In December and in January only 7% and 33% of chickens sampled were positive for *C. jejuni* respectively. This may also correlate with the number of *Campylobacter* species associated outbreaks in humans and the outbreaks in humans are thought to be seasonal too (Wills and Murray., 1997).

## 1.7 Enteric *C. jejuni* infection and clinical symptoms

The most common symptoms of *C. jejuni* infections are typical of gastroenteritis. Variability in the clinical symptoms of *C. jejuni* have been reported ranging from watery diarrhoea with no inflammation to mucous containing bloody diarrhoea. The severe diarrhoeal attack is characterised by abdominal cramps and fever within 48 hours of the initial attack (Zilbauer *et al*., 2008). The illness is self-limiting and the duration of illness is less than 7 days. Recurrence of illness can be observed in patients with low immune responses (Wassenaar and Blaser., 1999). The incidence of *C. jejuni* infections is very high in immunocompromised people e.g. AIDS patients (Coker *et al*., 2002). In developing countries, children in early childhood are found to be most susceptible to *C. jejuni* infections because of their undeveloped immune system with the incidence of infection decreases in late childhood (Wassenaar and Blaser., 1999). Asymptomatic *C. jejuni* infections are also more frequently reported in the developing countries where individuals are in close contact with animals and are exposed to bad sanitation conditions (Coker *et al*., 2002). In contrast, in developed countries only farm and slaughter house workers and consumers of raw milk etc represented asymptomatic carriers of *C. jejuni* (Wassenaar and Blaser., 1999).

### *1.7.1 Complex disease*

A prolonged and life-threatening consequence of *C. jejuni* infection is the development of a neurological disease which is characterized by the ascending paralysis of peripheral and cranial nerves. This disease is called Guillain Barré syndrome. The first case of *C. jejuni* caused GBS was reported in 1982 as a post infection complication of *C. jejuni* enteritis (Rhodes and Tattersfield., 1982). Later research showed that *C. jejuni* produces lipooligosaccharides (LOS) that mimic the gangliosides of the nervous system initiating a host inflammatory immune response against the pathogen that causes nerve damage (Hadden and Gregson., 2001, Moran and Prendergast., 2001, Aspinall *et al*., 1994). In addition to the nervous system damage other body organs can also get affected and even death occurs in severe cases (Korinthenberg and Monting., 1996). The global GBS incidence rate is between 0.4-4.0 per 100,000 cases annually with more cases reported in infants and elderly patients (McGrogan *et al*., 2009, Hadden and Gregson., 2001, Asbury and Cornblath., 1990). A recent review of GBS reported cases in the literature associated *Campylobacter* species with 31% of GBS incidents arising from gastrointestinal infections (Poropatich *et al*., 2010). The development of GBS is dependent on strain type and fitness of host cells. In some cases, *C. jejuni* causes Miller Fisher Syndrome (MFS) which is a less severe subtype of GBS. The typical symptoms of MFS include weakness of gait (ataxia), dysfunction of reflexes and defects in eye movement. Around 5% of GBS cases are of MFS (Hughes and Cornblath., 2005, Govoni and Granieri., 2001).

Recently, *C. jejuni* has been reported to cause endocarditis in patients with artificial heart valve transplants (Dinant *et al*., 2011) and reactive arthritis (Hannu *et al*., 2004).

## 1.8 Treatment

The disease caused by the *Campylobacter* species is generally self-limiting. In case of systemic infections, macrolides (*e.g.* erythromycin), fluoroquinolones (*e.g.* ciprofloxacin) and tetracyclines are used for treatment. The antimicrobial resistance is recognized as a major factor in persistence of *Campylobacter* species caused infections in public health (EFSA., 2012, Moore *et al*., 2006, McDermott *et al*., 2005). The antibiotic susceptibility testing methods and the interpretation of test results for *Campylobacter* species vary considerably in different countries which makes it difficult to establish a list of effective antibiotics for treating infections caused by this bacteria (EFSA., 2012).

The most recent EFSA (2012) report indicated that the human clinical *C. jejuni* isolates showed highest frequency of resistance against ciprofloxacin (51.6%) followed by resistance to nalidixic acid (49.8%). Among the human *C. coli* strains, the highest resistance was observed against nalidixic acid (69%) whereas the second highest resistance was reported against ciprofloxacin (66%) (EFSA., 2012).

## 1.9 Host immune response to *C. jejuni* infections

*C. jejuni* is a communal organism in chicken gut but causes disease when inside the human intestinal tract. To establish infection in humans *C. jejuni* has to overcome several host defence mechanisms. These bacteria have to pass through the acidic stomach environment, and when inside the intestinal tract they have to withstand high bile salt concentrations (Dasti *et al*., 2010). Indeed, the mucin rich mucosal lining acts as a physical barrier for the underlying epithelium against foreign intrusion (Hugdahl *et al*., 1988). *C. jejuni* has developed a number of factors to survive these hostile host gut conditions and initiate infection. *C. jejuni* peptidoglycan cell envelope that maintains the helical corkscrew shape of the bacterial cell contributes to overcoming the mucosal cell lining (Frirdich *et al*., 2012). A transcriptional study of *C. jejuni* strains has reported upregulation of flagella, LOS and capsule related genes when in contact with the intestinal mucosa suggesting a role of these surface structures in penetrating mucus (Tu *et al*., 2008). The majority of *C. jejuni* strains have developed resistance to the potent effects of bile salts in intestine (Van Deun *et al*., 2007).

The human body has a specialised immune defence system to provide protection against microbial infection. The human immune system can be broadly divided into the innate immune response and adaptive immune response. The factors and mechanisms of these immune systems in response to the *C. jejuni* infection will be briefly discussed here;

### *1.9.1 Innate immune system*

The innate immune response is the first line of defence that bacteria encounter after entering the human body. When bacteria invade the intestinal mucosa the underlying epithelial cells respond to the bacterial invasion by releasing cytokines, chemokines and antimicrobial peptides. These elements of the innate immune system initiate an inflammatory response by recruiting macrophages and dendritic cells (DCs). *C. jejuni* strains have shown to initiate a pro-inflammatory response in cultured human epithelial cells by the production of cytokines interleukin 8 (IL-8) (Hickey *et al*., 1999, Mellits *et al*., 2002, Zheng *et al*., 2008).

*C. jejuni* infection leads to the activation of transcription factor NF-kB. The release of NF-kB is coordinated with IL-8 production (Zheng *et al*., 2008). The NF-kB/rel family of transcription factors forms part of the early immune response to microbial infection and controls transcription of genes encoding for cytokines and chemokines (Silverman and Maniatis., 2001). Using a gnotobiotic IL-10; NF-kB mouse infection model Lippert *et al* (2009) showed that *C. jejuni* infection triggered NF-kB transcriptional activity that resulted in rapid recruitment of cytokines in the infected mouse colon. This immune response resulted in rapid and severe inflammatory colitis in the infected animal. In addition, *C. jejuni* infection promoted NF-kB production initiating cytokine gene expression in bone marrow derived DCs (Lippert *et al*., 2009). The vertebrates recognise products of microbial infection by specific membrane receptors called TLRs (Toll-like receptors) activating an immune response (Dunne and O’Neill., 2005). There are 10 protein receptors in the TLR family that interact with “pathogen associated molecular patterns” (PAMPs) (Medzhitov., 2001, Schnare *et al*., 2001). The TLRs work individually or in combination to recognize microbial patterns. The expression of TLRs is tightly regulated to prevent an inappropriate activation of pro-inflammatory response.

When required host cells block TLR activity through expression of TLR-inhibitory protein Tollip (Melmed *et al*., 2003). The microbial triggers for TLRs include surface polysaccharides such as LOS, capsule, flagellin and DNA (de Zoete *et al*., 2010). Recently, the sialylated flagellin of *C. jejuni* has been shown as a molecular trigger for activating TLR-4 (Kuijf *et al*., 2010). Al-Sayeqh *et al* (2010) has reported that the transcription factor NF-kB can directly detect *C. jejuni* infection and does not require other surface proteins including TLRs.

Different types of proinflammatory (IL-1α, IL-6, IL-8, TNFα) and anti-inflammatory (TGF-ß1, TGF-ß2, TGF-ß3, IL-4, IL-10) cytokines are recruited as an innate immune response to *C. jejuni* infection (Bahrami *et al*., 2011, Hu *et al*., 2006a). The trigger of *C. jejuni* invading epithelial cells results in a rapid proinflammatory response as the first line of defence. Once released these cytokines are transported to T-cells where they act as a stimulus for adaptive immunity bridging with innate immunity (Hu *et al*., 2006b). *C. jejuni* surface structures, mainly LOS, interact with the TLR-2 receptors present on epithelial cells to activate IL-6 production. IL-8 is released when *C. jejuni* is recognised by extracellular signal regulated kinase (ERK) and p38 mitogen activated protein (MAP) kinase pathways (Borrmann *et al*., 2007). More recently Zheng *et al* (2008) have reported that cytolethal distending toxin was important in IL-8 production. The interaction with host epithelial cells also contributed to IL-8 release (MacCallum *et al*., 2006, Hickey *et al*., 1999). MacCallum *et al* (2006) also showed that the type of infected cell line and *C. jejuni* strain played a critical role in adhesion/invasion mediated IL-8 response. A recent study showed a *C. jejuni* mutant in *pgp1* (peptidoglycan peptidase 1) was unable to maintain the helical cell shape, was deficient in chick colonization and promoted chemokine IL-8 production in epithelial cells. This suggests that *C. jejuni* helical shape morphology also contributes to the innate immune response against *C. jejuni* infection (Frirdich *et al*., 2012). *C. jejuni* infection acts as a stimulus for the release of anti-inflammatory IL-4 and IL-10 cytokines. IL-4 and IL-10 have immunoregulatory effects as they prevent tissue damage by terminating the production of the proinflammatory host response. IL-4 has been reported to down regulate the proinflammatory effects by IL-1α, IL-1 ß and TNFα chemokines (Bogdan *et al*., 1993). IL-10 has been shown to provide resistance against infection to the host and plays a critical role in clearing out infection by immunostimulatory activities (Asadullah *et al*., 2003, Lindsay and Hodgson., 2001) . More recently, *C. jejuni* infection of IL-4 preinfused intestinal pig epithelial cells (IPEC-1) has been shown to change their physiology allowing increased invasion and damaging the paracellular junctions which suggests a link between invasion and IL-4 production (Parthasarathy and Mansfield., 2009). In another study, an IL-10 deficient mouse was orally inoculated with *C. jejuni* 11168 that showed enhanced colonization of colon and development of severe enteritis within 2-35 days of infection. This showed IL-10 to be important in *C. jejuni* gastroenteritis (Mansfield *et al*., 2007).

The inflammatory response to microbial infection in humans is characterised by the production of neutrophils in the intestine. In cases of severe colitis, neutrophils damage the mucosal structure, migrate across epithelial cells and cause complete dynfunction of the intestine (Anderson *et al*., 1986). In *C. jejuni* infected human epithelial cells increased amounts of neutrophils were recruited that move from the basolateral to apical side of the epithelium concentrating in intestinal crypts (Murphy *et al*., 2011). The cationic antimicrobial peptides/proteins (CAPs) are produced by the host innate immune system in response to the microbial infection (Eckmann., 2004). Defensins and cathelicidins are two example of CAPs frequently recruited in an innate immune response to bacterial infection (Lehrer., 2004). Cathelicidins are secreted by neutrophils targeting at the infected tissue (Iimura *et al*., 2005). Another cationic antimicrobial peptide, Bactericidal/Permeability Increasing Protein (BPI) is produced in response to neutrophil recruitment and is accumulated in neutrophil vacuoles. BPI mediates killing by interacting with the lipid A structure of LOS in Gram negative bacteria (Weiss., 2003, Eckmann., 2004). An *in vitro* study with *C. jejuni* strain 11168 reported enhanced ß- defensin production. The bactericidal activity of ß-defensins killed bacteria by damaging their cell wall suggesting an important role of defensins in innate immune response (Zilbauer *et al*., 2005). Recently, a *C. jejuni* mutant in the *waaF* gene was deficient in ß-defensin production showing that *C. jejuni* lipooligosaccharides contribute to mediating innate immune protection in human body (Keo *et al*., 2011). The innate complement system in humans also has an inhibitory and antibacterial response to *Campylobacter* species infection (Fernández *et al*., 1995). Capsule polysaccharides in *C. jejuni* have stimulatory effects on complement based immunity in the human host (Guerry *et al*., 2012).

### *1.9.2 Adapted antibody immunity*

Adapted or acquired immunity is an essential defence strategy developed by vertebrates against microbial infection. The primary response of adapted immunity to *Campylobacter* species infection is the secretion of sIgA (immunoglobulin A) in the human gastrointestinal tract. This antibody immune response is dependent on age and geographical location of subjects. The epidemiological evidence of acquired immunity mediated by *C. jejuni* infection in developing countries showed that campylobacteriosis cases decreased with an increasing age accompanied with milder symptoms to illness. This is because in the developing world infants are frequently exposed to food borne pathogens including *Campylobacter* species due to the lack of hygiene standards which results in early development of an anti-*Campylobacter* antibody mediated immune response in early childhood (2-5 years of age). The increasing level of IgA in adults is accompanied by milder and self-limiting *C. jejuni* disease profile with an overall decrease in the number of *C. jejuni* mediated illnesses (Tribble *et al*., 2008). In comparison, in industrialized nations general health conditions and public awareness of food borne infections is better which results in more incidents of *Campylobacter* enteritis reported in the adult population (Tribble *et al*., 2007). The epidemiological data obtained from individuals in contact with dairy farms and frequently consuming raw milk showed a lower incidence of *C. jejuni* mediated diarrhoea compared to people not exposed to raw milk on daily basis (Blaser, *et al*., 1987). Both a symptomatic and an asymptomatic *Campylobacter* infection mounted an equally intense *Campylobacter*-specific IgA antibody response (Tribble *et al*., 2007). In *Campylobacter* disease, the adaptive immunity is stimulated by bacterial surface structures including flagellin (Baqar *et al*., 2008), LOS and capsule polysaccharides (Moran and Prendergast., 2001).

The *C. jejuni* colonization of the chicken gut also mediates an adaptive antibody response that varies with the age of the chicken. In 1-2 week old birds, the levels of maternal derived IgY (Immunoglobulin Y) antibodies are high and this amount levels out just after 3 weeks making chicken flocks more susceptible to colonization by *C. jejuni* (Cawthraw and Newell., 2010). *C. jejuni* surface polysaccharides mainly flagella and the surface expressed CadF adhesin are major stimulants for antibody production in chicken within first three weeks (Shoaf-Sweeney *et al*., 2008, Cawthraw *et al*., 2000).

## 1.10 Pathogenesis mechanisms of *C. jejuni* infection

*C. jejuni* is a versatile organism. It has developed specialized mechanisms to survive in the environment and to cause pathogenesis in the host. For mediating an enteric or blood infection *C. jejuni* has to pass through a number of physical and chemical barriers in the host gastrointestinal tract. *C. jejuni* has to penetrate the mucosal protective layer of the gut, adhere to or/and invade intestinal epithelial cells, survive and multiply inside the cells and in some severe cases migrate into the blood. A brief description of the key virulence associated factors studied in *C. jejuni* is stated below.

### *1.10.1 Flagella*

*Campylobacter* species possess one or two polar flagella that make them motile. This motility is essential for colonization of the avian gut and invasion of the mucous layer of the intestine in humans during diarrhoeal infection (Jagannathan and Penn., 2005, Grant *et al*., 1993, Nachamkin *et al*., 1993, Morooka *et al*., 1985). The *Campylobacter* flagellum is composed of two main homologous units, flagellin A (FlaA) and flagellin B (FlaB). The gene *flaA* is regulated by σ28 (sigma factor 28) and *flaB* is regulated by σ54 (sigma factor 54) (Jagannathan and Penn., 2005). *In vitro*, the role of FlaA in colonization, adherence and invasion of *C. jejuni* in human intestinal cells has been reported (Wassenaar *et al*., 1991, Jain *et al*., 2008). However, the *flaB C. jejuni* mutant formed flagella with a normal structure and had no influence on virulence (Wassenaar *et al*., 1991, Guerry., 2007). *C. jejuni* produces eight different types of proteins when it comes in contact with the host surface (Konkel *et al*., 2004).

Due to the lack of type III secretion system in *C. jejuni*, the secretion and transport of flagellated and non-flagellated proteins in the host cells is controlled by flagella. The secretion of the key proteins called *Campylobacter* invasion antigen (Cia) that allows the growth of *C. jejuni* in INT-407 cells in serum free medium or in the presence of bile salts was found to be under the control of flagellin signals (Christensen *et al*., 2009, Ko and Park., 2000). CiaB is an important virulence protein secreted during initial *C. jejuni* infection and is translocated through the intestinal cells. However, the mechanism of this translocation is still unknown (Guerry., 2007, Poly and Guerry., 2008). Recently, a set of four genes called flagellar coexpressed determinants (*feds*) have been identified as a part of the flagellar regulatory system in *C. jejuni*. The transcription of *feds* and *cia*I are coregulated that in turn is dependent on the expression of *flaA* (Barrero-Tobon and

Hendrixon., 2012). *C. jejuni* flagella are unique structures. Even though these are highly motile, they are not recognised by the Toll-like receptor sites (TLR-5) on human epithelial cells, thereby avoiding the innate host immunity and invade epithelial cells (Andersen-Nissen *et al*., 2005). Glycosylation of flagella is an essential phenomenon adopted by *C. jejuni* which will be discussed in a later section (Guerry., 2007).

### *1.10.2 Chemotaxis*

Motile bacteria contain a chemosensory system which they use to move towards favourable conditions and away from harmful environments (Lux and Shi., 2004). As a pathogen inside the living host, *C. jejuni* is attracted towards the glycoprotein mucin of the mucosal lining of epithelial cells, amino acids (e.g. aspartate, serine, cysteine) and other organic salts (citrate, fumarate, malate) (Hugdahl *et al*., 1988, Baserisalehi and Bahador., 2011). Methyl accepting chemotaxis proteins (MCP) are recognized to sense these chemicals in *C. jejuni* (Vegge *et al*., 2009). A mutagenesis study by Hendrixson and DiRita (2004) identified the role of *C. jejuni* methyl accepting chemotaxis receptors (Cj0019c and Cj0262c) in chicken gut colonization. A *C. jejuni* mutant in *cheY*, a chemotaxis regulatory gene that controls flagellar rotation, was deficient in chick colonization (Hendrixson and DiRita., 2004) but displayed a hyperinvasive phenotype (Golden and Acheson., 2002). On the contrary, *C. jejuni* strains with two copies of the *cheY* gene were unable to cause disease in ferret infection model but successfully colonized the mouse intestine (Yao *et al*., 1997). In a recent study, the elevated expression of a chemotaxis related gene *cheW* reduced the subcellular translocation of *C. jejuni* (van Alphen *et al*., 2008).

It can be proposed that chemotaxis facilitates *C. jejuni* migration to the mucin in intestine but has no role in invasion through the mucosal lining (Konkel *et al*., 2001). Similarly, mutation in an autoinducer-2 (AI-2) production gene (*luxS*) abolished *in vitro* adherence and colonization of chick hepatoma (LMH) cells (Quinones *et al*., 2009). In *C. jejuni*, LuxS is an important enzyme of the methyl recycling pathway and produces AI-2 as its meabolic byproduct (Plummer., 2012). Inactivation of chemoreceptor, CetB (Cj1189) in *C. jejuni* completely eliminated their ability to invade cultured human epithelial cell lines (Golden and Acheson., 2002). A transposon mutagenesis study has reported a transposon inserted in a chemoreceptor gene, Cj0952c that together with an adjacent chemotaxis related gene Cj0951c was important in host cell invasion, motility and chemotaxis response toward formic acid (Tareen *et al*., 2010). Recently, a tissue culture study using INT-407 cells showed that a *C. jejuni* 81-176 mutant in a chemoreceptor gene *cheR*, resulted in a hyperadherent and hyperinvasive phenotype whereas deletion of another chemoreceptor gene *cheB* was responsible for a non-adherent and non-invasive profile (Kanungpean *et al*., 2011). The same study reported that a *cheRB* mutant was unable to colonize the chick cecum. Therefore, the research in *Campylobacter* chemotaxis system shows that it not only allows survival of bacteria under environmental stresses but it also has an important role in virulence particularly in host cell interaction.

### *1.10.3 Adhesion and Invasion*

*C. jejuni* interaction with host cells has been studied as a critical process in the mediation of disease in human hosts (Hu and Kopecko., 2008). However, the mechanism that *C. jejuni* uses for adhesion and invasion is not understood fully. It was suggested that *C. jejuni* adheres to the epithelial cells before internalization. It was observed that when the bacteria were present in high cell density, the cell shape and flagellar orientation changes which allows bacteria to penetrate the mucus that protects the intestinal epithelium. This process was considered related to the adhesion of *C. jejuni* to the host cells (Ferrero and Lee., 1988). Everest *et al* (1992) showed that *C. jejuni* and *C. coli* strains were able to adhere to the epithelial cells without invading them afterwards. During binding to the host cells, *C. jejuni* preferentially associated with the intercellular junctions that would allow bacteria to tanscytose the cell monolayers (Konkel *et al*., 1992a, Oelschlaeger *et al*., 1993) and this attachment to the host cell membrane was promoted by centrifugation (DeMelo *et al*., 1989; Konkel *et al*., 1992b). However, the colonization studies showed the adhesion of host cells is not an essential step as *C. jejuni* was successfully able to stay in the intestine after colonizing the mucus suggesting that *C. jejuni* might invade the epithelial cells directly (Lee *et al*., 1986).

Early research proposed different mechanisms which *C. jejuni* uses to invade host cells but there is no consensus on these mechanisms. Like other invasive pathogens including *Listeria*, *Shigella* and *Salmonella*, *C. jejuni* may invade the host cells in a microfilament dependant manner (DeMelo *et al*., 1989, Konkel and Joens, 1989; Konkel *et al*., 1992b) while the other studies found that the invasion remained unaffected in the presence of microfilament inhibitors (Oelschlaeger *et al*., 1993). This suggested that the entry into host cells was via a microtubule dependant pathway (Oelschlaeger *et al*., 1993). During the *C. jejuni* 81-176 invasion process into INT-407 cells, actin filament depolymerisation and polymerisation of microtubule bundles took place in response to the signal transduction from bacterial cells bound to the cell surface. This resulted in the formation of finger like protrusions by the cell surface which engulf bacteria. *C. jejuni* survives within these membrane-bound endosomes which are then transported along the microtubules to the perinuclear region of the cell (Hu *et al*., 2008). A novel host signal transduction pathway has also been proposed for *C. jejuni* invasion into the differentiated enterocyte like cells (Wooldridge *et al*., 1996). Wooldridge *et al* (1996) showed that *Campylobacter* species stimulate a receptor on host cell membrane that interacts with molecules associated with caveolae. This interaction results in a signal transduction event that causes ruffling across the membrane and subsequent actin filament dependent endocytosis of *C. jejuni* (Figure 1.1).

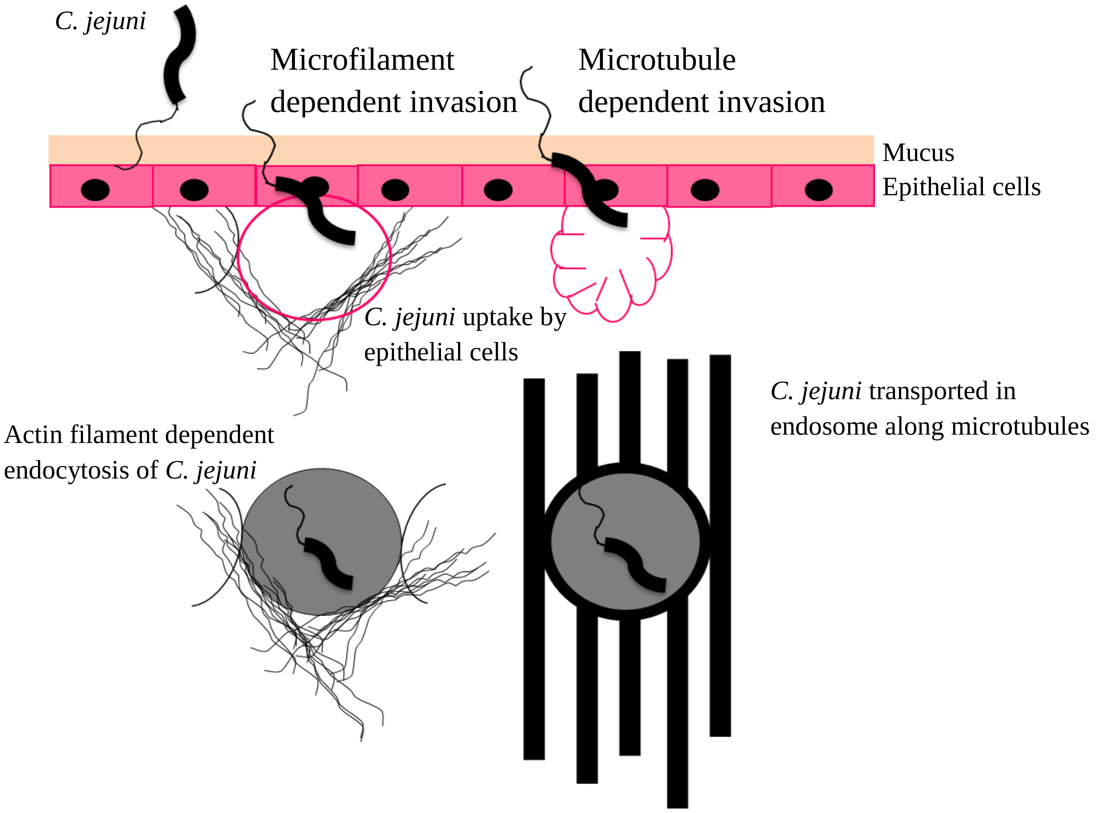


Figure 1.1: A diagrammatic representation of the proposed mechanisms of *C. jejuni* invasion into the epithelial cell lining.

The ability of *C. jejuni* to attach to and invade epithelial cells is generally strongly correlated with severity of clinical symptoms presented (Fauchere *et al*., 1986). Several studies have used *in vitro* cultured cell lines of human and non-human origin to investigate *C. jejuni* interaction with host cells (Konkel *et al*., 2001, Ketley., 1997, Prasad *et al*., 1996, Konkel and Joens., 1989). In addition, *in vivo* animal infection models including primates have been used to study the role of invasion and adhesion in *C. jejuni* pathogenesis (Senior *et al*., 2011, Yao *et al*., 1997, Babakhani and Joens., 1993, Russell *et al*., 1993). All these studies have reported adhesion and invasion as important factors contributing to *C. jejuni* pathogenesis. *C. jejuni*'s ability to adhere to and invade epithelial cells very strongly depends on strain type and the infection model used (for example type of intestinal cell line used) (Prasad *et al*., 1996, Konkel and Joens., 1989, Newell *et al*., 1985).

Research has also suggested that clinical human isolates of *C. jejuni* are generally more adherent and invasive than non-clinical isolates. Prasad *et al* (1996) demonstrated that human isolates are more pathogenic than chicken isolates for their invasion, adhesion and cytotoxin production phenotypes using the human cell lines HeLa and HEp-2 cells as *in vitro* models. Similar results were reported by Konkel and Joens (1989) for nine clinical and four nonclinical strains of *C. jejuni* tested for their adherence and invasion to cultured HEp-2 cells. Newell *et al* (1985) compared two main phenotypes (*i.e.* adherence and invasion) of *C. jejuni* environmental isolates and strains obtained from diarrhoea patients to HeLa cells using electron microscopy and immunofluorescence. The authors concluded that the clinical isolates were more invasive than the nonclinical strains. This difference in the invasion potential between the human and animal isolates was also reported by Biswas *et al*., 2000. A detailed study classified *C. jejuni* strains isolated from clinical, poultry and environmental sources as hyper, high and low invasive using an *in vitro* invasion assay. It was reported that the hyperinvasive category had a greater proportion of clinical isolates compared to strains from other sources (Fearnley *et al*., 2008). Based on the above studies it can be suggested that adhesion and invasion are important phenotypes contributing to *C. jejuni* pathogenesis. In contrast, another research group (van Deun *et al*., 2007) did not find any difference in the invasion potential among the set of human and poultry isolates investigated. However, *C. jejuni* adhesion and invasion is a multifactorial process and other bacterial factors that contribute to this phenotype still need investigation.

### *1.10.3.1 Factors influencing adhesion and invasion in C. jejuni*

*Campylobacter* species do not possess a Type III secretion system and other structures including fimbriae or pilli as in other Gram negative bacteria such as *Salmonella* and *E. coli*. Instead adherence and invasion of intestinal epithelial cells is mediated by several other bacterial structures. Some of these factors directly influence adhesion and invasion of *C. jejuni* to the host surface receptors while others play an indirect role in host cell interaction. The role of these host cell interaction factors in *C. jejuni* pathogenesis has only started to be understood (Hu and Kopecko., 2008, Dasti *et al*., 2010).

A functional *C. jejuni* flagellar export apparatus is required for delivery of effector proteins into host epithelial cells. A flagellin protein, FlaC which is structurally homologous to FlaA and FlaB has been shown to support the flagellar export apparatus. FlaC has also been found to have a role in *in vitro* invasion of host epithelial cells (Song *et al*., 2004). Two *Campylobacter* invasion antigen (Cia) effector proteins, CiaB with limited homology to SipB of *Salmonella* species and CiaC with no known similarity to any other proteins that have been characterised (Christensen *et al*., 2009). An insertion mutation into gene, Cj1242 which was annotated as CiaC in *C. jejuni* clinical strain F38011 showed defects in motility, adherence and internalization of INT-407 cells (Christensen *et al*., 2009). In contrast, mutation in *ciaB* had no effect on the invasion potential of *C. jejuni* 81-176 in T84 cells (Novik *et al*., 2010) suggesting that the role of CiaB in invasion is strain and cell line dependant. Another Cia protein called CiaI (Cj1450) has been recently identified in *C. jejuni*. CiaI contains an amino terminal type III secretion sequence and is transported via the flagellar type III secretion system into host epithelial cells. A *C. jejuni ciaI* mutant was attenuated for survival in cultured INT-407 and HeLa epithelial cells which suggests CiaI might have a role in intracellular survival (Buelow *et al*., 2011). Not all Cia proteins are known yet nor their exact mechanism in *C. jejuni* host interaction is fully understood however a *C. jejuni* strain lacking CiaB secretion ability inhibited secretion of other Cia proteins into the epithelial cells (Ko and Park., 2000).

In bacteria, the main role of σ28 genes is in the functioning of flagella (Carrillo *et al*., 2004, Goon *et al*., 2006, Poly *et al*., 2007a). However, *C. jejuni* expresses some σ28 genes that are not important in motility but have been involved in invasion and damage to epithelial cells (Goon *et al*., 2006, Poly *et al*., 2007a). A σ28 dependent gene *fspA* is expressed as two alleles *fspA1* and *fspA2* in some *C. jejuni* strains. FspA1 and FspA2 proteins are not directly involved in *C. jejuni* invasion however FspA2 has been implicated in apoptosis of INT-407 cells (Poly *et al.*, 2007a). Another flagella dependent gene with a role in invasion of intestinal epithelial cells is *cj0977* (Goon *et al.*, 2006). At first the Cj0977 protein was shown to be secreted in the cytoplasm. Its secretion was independent of the flagellar export apparatus and had no effect on motility (Goon *et al.*, 2006). A later study contradicted the initial research and showed a *cj0977* mutant to be deficient in motility in a liquid culture and was unable to invade epithelial cells (Novik *et al.*, 2010). Inactivation of *fliS* (σ28) and *rpoN* (σ54) resulted in reduced motility and defects in invasion of HeLa cells (Fernando *et al.*, 2007). A flagellar coexpressed determinant, FedA, together with CiaI has been reported recently to be involved in the invasion of human epithelial cells (Barrero-Tobon and Hendrixson., 2012). Chemotaxis and the glycosylation systems (O and N-linked) also have an important role in influencing the adhesion and invasion phenotypes in *C. jejuni* and these have been discussed in detail in sections 1.10.2 and 1.10.9 respectively.

Other surface polysaccharides including LOS and capsule have been implicated in adherence and invasion of epithelial cells and *in vitro* ferret model of infection (Karlyshev *et al.*, 2000, Bacon *et al.*, 2001, Kanpies *et al.*, 2004, Bachtiar *et al.*, 2007, Louwen *et al.*, 2008). An initial study investigated the role of *C. jejuni* LOS in host cell interaction and internalization. This study showed that the purified extract of LOS promoted adhesion to epithelial cells and this interaction was eliminated with the oxidation of LOS (McSweegan and Walker., 1986). Kanpies *et al* (2004) reported that a mutant in *C. jejuni* 81-176 LOS locus lost its ability to invade cultures human epithelial cell lines. Bacon *et al* (2001) demonstrated the role of *C. jejuni* 81-176 LOS in invasion and serum resistance using INT-407 cell lines in an *in vitro* model. Sialylated LOS exposed on the outer surface of *C. jejuni* has been shown to influence invasion (Louwen *et al.*, 2008, Habib *et al.*, 2009). Louwen *et al* (2008) showed that the mutation in *cst-II* gene encoding for sialyltranferase in GBS associated *C. jejuni* strains made them defective in invasion of intestinal epithelial cells. To further investigate the role of LOS in *C. jejuni* pathogenesis, Marsden *et al* (2009) showed that a *C. jejuni* mutant lacking a functional LOS locus was unable to invade Caco-2 cells. Mutations in one aminotransferase encoding gene *wlaRG* and two glycosyltranferase encoding genes *wlaTB* and *wlaTC* in LOS core in *C. jejuni* 81116 deprived the mutants in their ability to invade *in vitro* human epithelial cell lines. Moreover, mutants in these three genes showed reduced immunogenicity and invasion into chick embryonic fibroblasts (Holden *et al*., 2012). Recently, Javed *et al* (2012) showed that a transposon inserted in a LOS gene, *cj1136*, which encodes for a putative galactosyltransferase in *C. jejuni* NCTC11168 significantly reduced the ability of the mutant *C. jejuni* 01/51 strain to invade into cultured INT-407 and Caco-2 cells. All the above studies strongly support the role of LOS in *C. jejuni* interaction to the human cells.

*Campylobacter* species contain adhesins or binding factors that are required to adhere and internalize the host epithelium. The CadF (*Campylobacter* adhesion to fibronectin) is an outer membrane protein present in all *C. jejuni* and *C. coli* strains and establishes bacterial interaction with the host extracellular fibronectin receptors (Konkel *et al*., 1997). The *cadF* gene sequence in *C. jejuni* has a 39 bp insertion compared to the *cadF* in *C. coli*. This sequence difference in the *cadF* gene resulted in *C. jejuni* being more adherent and invasive to the INT-407 epithelial cells compared to *C. coli* strains. Furthermore, isogenic *cadF* mutant strains showed significantly impaired host cell interaction ability confirming its role in *C. jejuni* pathogenesis (Krause-Gruszczynska *et al*., 2007). A recent study reported that *C. jejuni* fibronectin binding proteins, CadF and FlaA, mediate invasion of host epithelial cells via an epidermal growth factor (EGF) pathway. This process involves activation of *C. jejuni* cytoskeleton related proteins mainly, P13 kinase, c-Src and focal adhesion kinase (FAK) (Eucker and Konkel., 2012). Two surface exposed lipoprotein adhesins, CapA and JlpA, have been shown to mediate *C. jejuni in vitro* adhesion to the human epithelial cell lines and in vivo colonization of chicken gut (Ashgar *et al*., 2007, Jin *et al*., 2001, Pei and Blaser., 1993).

*Campylobacter* species contain different periplasmic proteins PEB 1-4 that serve as adhesins (Pei *et al*., 1991). PEB 1 is a 28-kDa protein and is conserved in *C. jejuni* and *C. coli* strains (Pei and Blaser., 1993, Pei *et al*., 1991). PEB 1 has immunogenic and immunoprotective properties (Du *et al*., 2008) and is required for *C. jejuni* binding to HeLa cells (Pei *et al*., 1998). It is functionally homologous to periplasmic binding proteins from other Gram negative bacteria with a role in glutamate/aspartate transport (Leon-Kempis Mdel *et al*., 2006, Pei and Blaser., 1993). PEB 1 was detected in culture supernatants by cell fractionation and immunoblotting techniques confirming that PEB1 in *C. jejuni* is a periplasmic associated protein and not an inner or outer membrane protein (Leon-Kempis Mdel *et al*., 2006). PEB 3 has antigenic properties similar to PEB 1 and shares homology with class 1 pili in *Neisseria meningitidis* and heat-labile enterotoxin B subunit in *E. coli,* and is required for interaction with intestinal epithelial cells (Pei *et al*., 1991). PEB 4 is another periplasmic chaperone in *C. jejuni* as antigenic in nature as PEB 1. It is involved in adhesion to INT-407 cells, biofilm formation and mice colonization (Asakura *et al*., 2007) as well as invasion of cultured human epithelial cells (Kervela *et al*., 1993). Recently, another periplasmic-binding protein encoding gene, Cj1289, has been identified in *C. jejuni*. This protein is structurally similar to PEB 4 in *C. jejuni* and may have a role in virulence (Kale *et al*., 2011). HtrA is a periplasmic protein in *C. jejuni* with dual functionality: a chaperone and a protease. HtrA chaperone activity is required for interaction with host epithelial cells and binding to macrophages (Baek *et al*., 2011a).

Other bacterial factors recently identified that influence adhesion and invasion phenotypes include a *C. jejuni* 11168 antigen encoding gene, *cj0034c*, with a role in invasion of INT-407 epithelial cell lines. Furthermore, mutants in *cj0034c, cj0404, cj0525c* were reduced in invasion of spleen and liver (Nielsen *et al*., 2012). Oxidoreductase encoding genes *cj0004c* and *cj0005c* involved in sulphite metabolism in cytoplasm (Tareen *et al*., 2011), polyphosphate kinase 2 encoding gene (*ppk2*) required for inorganic polyphosphate (poly P) synthesis as an alternate energy source in stress conditions (Gangaiah *et al*., 2010) are important *C. jejuni* metabolic pathways that influence *C. jejuni* attachment and internalization in *in vitro* tissue culture assays. A formate metabolism related operon (fdhTU) expressed as two alleles *fdhT* and *fdhU* has been recently identified in *C. jejuni* to have a role in internalization of bacterial cells in an *in vitro* colony based assay and by using fluorescence microscopy (Pryjma *et al*., 2012).

The bacterial factors reported as influencing the adhesion and invasion phenotypes of *C. jejuni* strains are summarized in table 1.1.

Table 1.1: Summary of the bacterial factors influencing adhesion and invasion of *C. jejuni*.

| | | Phenotype | | |
|---|---|---|---|---|
| **Bacterial factor** | **Function** | **Adhesion** | **Invasion** | **Reference** |
| **Flagella** | | | | |
| FlaA | Flagellin A | | √ | Wassenaar *et al*., 1991, Jain *et al*., 2008, Eucker and Konkel., 2012 |
| FlaC | Flagellar export apparatus | | √ | Song *et al*., 2004 |
| *cj0977* | Flagellum | | √ | Goon *et al*., 2006 |
| **Sigma factors** | | | | |
| σ28 (*fliS*) | Transcription of flagellar genes | | √ | Carrillo *et al*., 2004, Fernando *et al*., 2007 |
| σ54 (*rpoN*) | | | √ | Fernando *et al*., 2007 |
| **Chemotaxis** | | | | |
| *luxS* | Autoinducer-2 (AI-2) producing gene (methyl recycling pathway) | √ | | Quinones *et al*., 2009 |
| CetB | Chemoreceptor | | √ | Golden and Acheson., 2002 |
| *cj0952c* | Formic acid chemoreceptor | | √ | Tareen *et al*., 2010 |
| CheR, CheB | Chemoreceptor | √ | √ | Kanungpean *et al*., 2011 |
| **LOS** | | | | |
| Cst-II | Sialyltranferase | | √ | Louwen *et al*., 2008 |
| WlaRG | Aminotransferase | | √ | Holden *et al*., 2012 |
| WlaTB, WlaTC | Glycosyltranferase | | √ | |
| *cj1136* | Putative galactosyltransferase | | √ | Javed *et al.,* 2012 |
| **Periplasmic adhesins** | | | | |
| CadF | *Campylobacter* adhesion to fibronectin | √ | √ | Krause-Gruszczynska *et al*., 2007, Eucker and Konkel., 2012 |
| CapA, JlpA | Lipoprotein adhesins | | √ | Asghar *et al*., 2007 |
| PEB1 | Periplasmic adhesins | √ | | Pei *et al*., 1998 |
| PEB 3 | | √ | | Pei *et al*., 1991 |
| PEB4 | Periplasmic chaperone | √ | √ | Asakura *et al*., 2007, Kervela *et al*., 1993 |
| HtrA | Periplasmic protein | √ | | Baek *et al*., 2011a |
| **Toxin** | | | | |
| CdtA,CdtC | Cytolethal distending toxin (CDT) subunits | √ | | Lee *et al*., 2003 |
| **Capsule** | | | | |
| KpsE | Capsular polysaccharide ABC transporter | √ | √ | Bachtiar *et al*.,2007 |
| JJD26997_1801 | Capsular polysaccharide biosynthesis | | √ | Javed *et al*., 2010 |
| **O-linked glycosylation system** | | | | |
| PseAc | Pseudaminic acid | √ | √ | Ewing *et al*., 2009 |
| **N-linked glycosylation system** | | | | |
| PglH | General glycosylation pathway protein | √ | √ | Karlyshev *et al*., 2004 |
| PglB | Oligosaccharide transferase | √ | √ | Szymanski *et al*., 2002 |
| PglE | Putative aminotransferase | √ | √ | |
| *cj1121c* | Aminotransferase | √ | | Vijayakumar *et al*., 2006 |
| **Other** | | | | |
| FedA | Flagellar coexpressed determinant | | √ | Barrero-Tobon and Hendrixson., 2012 |
| CiaC | *Campylobacter* invasion antigen (Cia) | √ | | Christensen *et al*., 2009 |
| CiaI | | | √ | Barrero-Tobon and Hendrixson., 2012 |
| *cj0034c*, *cj0404*, *cj0525c* | Antigen encoding genes | | √ | Nielsen *et al*., 2012 |
| *cj0004c* | Oxidoreductase | √ | √ | Tareen *et al*., 2011 |
| *cj0005c* | Sulphite metabolism | √ | √ | |
| *ppk2* | Polyphosphate kinase 2 in inorganic polyphosphate (poly P) synthesis | √ | √ | Gangaiah *et al*., 2010 |
| FdhTU | Formate metabolism | | √ | Pryjma *et al*., 2012 |
| *feoB* | Ferrous iron uptake | | √ | Raphael and Joens., 2003 |

### *1.10.4 Translocation*

*Campylobacter* infections are initiated by interaction of bacteria with the intestinal mucus lining followed by invasion of epithelial cells. *Campylobacter* strains are also isolated from cases of bacteraemia which suggests the ability of bacteria to cross epithelium into the extra-intestinal locations. *C. jejuni* are able to translocate through the otherwise impermeable epithelial cell layer by using three reported systems. *Campylobacter* strains have been observed to translocate by paracellular pathway or paracytosis in which bacteria move through the epithelial cells without invading them via tight junctions between them (Everest *et al*., 1992, Konkel *et al*., 1992a, Grant *et al*., 1993). In the second system, *C. jejuni* are observed to use specialized intestinal epithelial cells called M-cells to translocate through the epithelial cell layer into the underlying lymphoid tissue (Walker *et al*., 1988). Finally, the third translocation mechanism called transcellular translocation or transcytosis involves bacterial invasion into the epithelial cells from where they travel through the cytoplasm appearing at the other side (Hu *et al*., 2008, Brás and Ketley., 1999). Within 60 minutes of post-infection, *C. jejuni* 81-176 was internalised into endosomes. These bacteria containing endosomes travelled for 8-10 hours from the apical surface to the basolateral surface where they were released by exocytosis (*i.e.* endosome fusion to the basolateral surface) Hu *et al*., 2008. The transcellular movement of *C. jejuni* 81-176 (Hu *et al*., 2008a) and more recently of *C. fetus* 11686 (Baker and Graham., 2010) carried on without compromising the integrity of polarized Caco-2 cells monolayer. By contract, a study that infected polarized human colonic HCA-7 cells with *C. jejuni* (Beltinger *et al*., 2008) observed complete loss of colonic cells integrity and disruption of cellular tight junctions within 6 hours of infection. A modification of transcellular transport called subvasion has been reported in *C. jejuni* recently where bacteria travel for a few hours at the cell basal layer of infected cells before finally invading the epithelial cells (van Alphen *et al*., 2008, Pogacar *et al*., 2010).

### *1.10.5 Toxin production*

*Campylobacter* species are known to produce several toxins but the cytolethal distending toxin (CDT) is the only one studied in detail (Wassenaar and Blaser., 1999). CDT is composed of three subunits Cdt A, B and C. The presence of these protein subunits is necessary for the function of CDT (Pickett *et al*., 1996). CdtB acts as a nuclease (Lee *et* *al*., 2003) and has shown structural similarity to the DNAase I of the mammalian eukaryotic cells (Lara-Tejero and Galan., 2000). Lee *et al* (2003) demonstrated that only CdtA and CdtC but not CdtB show close affinity and bind to the HeLa cell surface. This might suggest that CdtB might be transported to the nucleus to digest DNA and kill the cell. CDT causes HeLa and Caco-2 cells to be blocked in the G2 phase during the mitotic cell cycle thus resulting in eventual cell death (Whitehouse *et al*., 1998). It has been recently reported that *C. jejuni* survives and multiplies in human monocytes and utilizes CDT to initiate an apoptotic state in cells that leads to the cell death (Hickey *et al*., 2005). *C. jejuni* CDT induces the release of the cytokine Interleukin-8 (IL-8) from the intestinal epithelial cells by two mechanisms (Hickey *et al*., 2000). In the first mechanism, the live *C. jejuni* cells are needed to adhere and invade the epithelial cells and then induce IL-8 production which is responsible for the proinflammatory response seen in diarrhoeal disease (Hickey *et al*., 1999). The other mechanism for IL-8 production requires the production of CDT itself and requires the presence of all the three CDT subunits (*i.e.* CdtA, B and C) (Hickey *et al*., 2000). This mechanism of CDT activity has been demonstrated by the Hickey group (Hickey *et al*., 1999, Hickey *et al*., 2000) *in vitro* studies using human epithelial cell lines. However, there is no *in vivo* confirmation of the pathogenicity of CDT inside the human host.

### *1.10.6 Iron homeostasis*

Iron is an essential nutrient of bacteria required for the survival in diverse environments. It is also required for electron transport, oxidative stress responses and expression of pathogenic genes (Johnson *et al*., 2005, McHugh *et al*., 2003, Bou-Abdallah *et al*., 2002, Escolar *et al*., 1999, Mason and Cammack., 1992, Hantke., 1981).

*Campylobacter* species have evolved an efficient iron uptake, transport and storage system. *C. jejuni* acquires iron in different ways. The *C. jejuni* genome sequence contains only one ferrous iron uptake gene *feoB* (Raphael and Joens., 2003). *C. jejuni* 81-176 with an inactivated *feoB* gene showed reduced invasion of INT-407 human epithelial cells and porcine IPEC-1 small intestine cells. *C. jejuni* NCTC11168 *feoB* mutants were unable to colonize and persist in the rabbit ileum. Mutants in the *feoB* gene of *C. jejuni* NCTC11168, 81-176 and ACTC 43431 were also deficient in colonization of the chick cecum and showed reduced infection in piglet virulence models (Naikare *et al*., 2006). An outer surface receptor, CfrB has been recently identified in many *C. jejuni* strains. The CfrB receptor has ~34% similarity with CfrA. The synthesis of the CfrB receptor is essential for ferric iron uptake. A *C. jejuni* mutant in the *cfrB* gene was defective in colonization of the chick intestinal tract (Xu *et al*., 2010).

When *C. jejuni* is present inside the human or avian host it has to obtain iron from complex molecules including heme, haemoglobin, transferrin and lactoferrin (Palyada *et al*., 2004). The genes responsible for iron uptake from these compounds are present in two transcriptional sets and are located together upstream of the *ctuA* gene that encodes for an outer membrane receptor (Holmes *et al*., 2005). The protein, CtuA has a role in promoting chick colonization (Palyada *et al*., 2004). The loss of the *ctuA* gene does not abolish ferri-lactoferrin transport that suggests alternate processes used by *C. jejuni* for iron uptake inside the host (Miller *et al*., 2008a).

*C. jejuni* produces many exogenous siderophores (Guerry *et al*., 1997, Richardson and Park., 1995, Baig *et al*., 1986). Among these siderophores, a ferri-enterochelin transport system in *C. jejuni* consists of a number of outer membrane associated proteins. A periplasmic receptor protein (CfrA), an outer membrane binding protein (CeuE), and an iron transport complex (CeuBCD) (Richardson and Park., 1995). This iron associated transport system is conserved in many *C. jejuni* and *C. coli* strains.

*C. jejuni* contains a ferritin like protein, Cft that has a role in excessive iron storage and survival under oxidative stress conditions (Palyada *et al*., 2004). In addition to Cft, a single putative bacterioferritin protein (Dps) is present in *C. jejuni* (Wai *et al*., 1995). The Dps protein has ~40 iron and oxygen binding sites and has a role in iron storage and protection against hydrogen peroxide damage. Dps expression is observed under both iron excess and depleted conditions (Ishikawa *et al*., 2003). The piglets inoculated with wild type *C. jejuni* strains showed upregulation of *dps* gene with symptoms similar to human campylobacterosis (Theoret *et al*., 2011). Another gene, Cj0241c, encoding for a probable iron binding protein, has been identified in sequenced *C. jejuni* strains with putative role in iron storage which also reflects the importance to safeguard bacteria under potent amount of metals including iron (van Vliet *et al*., 2002).

Iron homeostasis in bacteria is a well observed process which is regulated at the transcriptional level. The transcriptional factor Fur regulates the amount of iron available to bacteria in the form of ferrous ions. *C. jejuni* encodes for two homologous transcriptional regulators (Fur and PerR). PerR, regulates the expression of the enzymes catalase (KatA) and alkyl hydroperoxidase (AhpC) that have a role in the oxidative stress response (van Vliet *et al.*, 1999). Mutation of the *perR* gene in *C. jejuni* resulted in defects of colonization in the chick intestinal tract (Palyada *et al.*, 2009). Iron metabolism and storage is an essential phenomenon in *C. jejuni* which involves several genes from multiple cellular processes particularly energy metabolism and oxidative stress response systems. The specific role of these genes in iron homeostasis and *C. jejuni* pathogenesis still need characterization.

### *1.10.7 Lipopolysaccharide*

*C. jejuni* like many other Gram negative bacteria, has diverse surface polysaccharide materials of variable length and density that form lipooligosaccharide (LOS) and capsule (Wassenaar and Blaser., 1999, Moran., 1997). These surface structures have a key role in serological identification of *C. jejuni* and also contribute to its pathogenesis (Zilbauer *et al.*, 2008). LPS are high molecular weight units with an outer core composed of 10-15 repeating oligosaccharide residues. LOS, in contrast, has a low molecular weight and lacks repeating oligosaccharide units in the outer core. Both LOS and LPS are anchored to lipid A on the surface. The lipid A of *C. jejuni* is an endotoxin (Moran., 1997) which induces an immune response in human hosts (Bax *et al.*, 2011, Heikema *et al.*, 2010, Kuijf *et al.*, 2010). The electron microscopic characterization of *C. jejuni* lipopolysaccharides (LPS) by Karlyshev *et al* (2001) demonstrated, for the first time, that the high molecular weight lipopolysaccharides (HMWs) in *C. jejuni* are capsular polysaccharides (CPS). The outer core of LOS is a highly variable in different *C. jejuni* strains (Dorrell *et al.*, 2001, Parker *et al.*, 2008). The LOS outer core mimics the human gangliosides as it coated with the sialic acid residues. The structural similarity of LOS to human brain ganglosides develops into the neuropathies called GBS and MFS (Yu *et al.*, 2011, Guerry and Szymanski., 2008, Yuki *et al.*, 1995, Aspinall *et al.*, 1994). The role of bacterial LOS in causing neurological disorders in humans has recently been reviewed (Yuki., 2010). The sialylation of LOS in *C. jejuni* is responsible for serum resistance by the pathogen against host antigens (Keo *et al.*, 2011, Guerry *et al.*, 2000). Also, sialylated LOS triggers a variety of immune response systems in *in vitro* studies and in mice infection model which showed sialylation to be a complex but essential phenomenon in *C. jejuni* mediated neurological complications (Huizinga *et al.*, 2012). Recently, Naito *et al* (2010) showed the importance of the LOS outer core genes (*waaF* and *lgtF*) in stress response, intraepithelial survival and pathogenesis of *C. jejuni*. By generating mutants in the LOS outer core genes these authors were able to show that a fully functional outer core was required to initiate immune response and biofilm formation (Naito *et al*., 2010). The role of LOS in biofilm formation has also been studied earlier by Corcoran and Moran (2007). Marsden *et al* (2009) showed that deletion of LOS biosynthesis genes (*cj1132c* and *cj1152c*) in *C. jejuni* NCTC11168 resulted in loss of growth and natural transformation of mutants.

### *1.10.8 Capsule biosynthesis locus*

Capsule is the high molecular weight polysaccharide surface structure in *C. jejuni* (Karlyshev *et al*., 2000). The synthesis of capsule polysaccharides is independent of the low molecular weight polysaccharides, LOS and is attached to the bacterial cell surface via phospholipid linkage (Oldfield *et al*., 2002). The capsular region in *C. jejuni* is composed of conserved *kps* genes which border the central variable region (Figure 1.2).

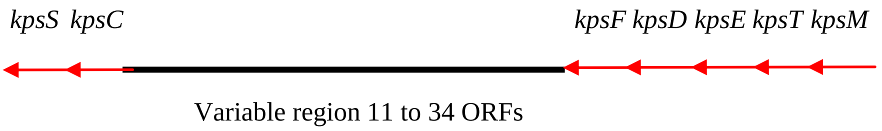


Figure 1.2: Schematic representation of the capsule region of *C. jejuni*.

The capsule region varies in size between 15 to 34 kbp as the central variable region consists of 11 to 34 ORFs. This variability in the capsule region is reflected in diverse capsular structures in different *C. jejuni* strains (Guerry *et al*., 2012).

Capsule has antigenic properties and it is the major serodeterminant in the Penner serotyping scheme (Karlyshev *et al*., 2000). Capsule is a complex and phase variable structure in different *C. jejuni* strains. The *C. jejuni* switches on/off the expression of its capsule which is due to the slip strand mismatching in one or more of the conserved *kps* genes (Guerry and Szymanski., 2008, Karlyshev *et al*., 2005 a and b, Bacon *et al*., 2001). *C. jejuni* capsules show variability in sugar molecules and possess other structural extensions that are responsible for different serotypes of *C. jejuni* strains. The structural variability of capsule is associated with the expression of heptoses of unusual configuration (*i.e. altro, ido, gulo, talo*) and O-methyl phosphoramidate (MeOPN) modifications (McNally *et al*., 2006b and 2007). The capsular structure gets more complicated by the introduction of a deoxy modification at C-6 position of a polysaccharide chain in addition to a normal heptose sugar (Guerry *et al*., 2012). For example, the *C. jejuni* strains of serotype complex HS23/36 contain both the *glycero*-D-*altro*-heptose and its complementary 6-deoxy-*altro*-heptose (Aspinall *et al*., 1993, Kanipes *et al*., 2006). Similarly, MeOPN can be located on different sugar residues in different CPS structures (Guerry *et al*., 2012).

Capsule has a role in serum resistance, survival to phagocytic activity and complement mediated immunity (Keo *et al*., 2011, Guerry and Szymanski., 2008). *C. jejuni* mutants in the capsule polysaccharide transport protein encoding gene (*kpsM*) were more susceptible to the host complement immune system whereas LOS mutant showed sensitivity to the cationic antimicrobial drugs including polymixin B (Keo *et al*., 2011). A previous study showed that the capsulated *C. jejuni* strains were resistant to killing to by ß-defensins 1 and lysozyme activity (Zilbauer *et al*., 2008). A further study showed that the CPS loci in *C. jejuni* provide resistance to the innate host immunity. Recently, Rose *et al* (2012) showed that only a slight variation in the capsule composition of *C. jejuni* NCTC11168, for example the lack of MeOPN modification, increased cytokine production by bone marrow derived murine dendritic cells (BMDCs). This confirms the role of *C. jejuni* capsule in survival against the host innate immunity.

The capsule has a role in virulence mechanisms including adhesion and invasion of *C. jejuni* (Bachtiar *et al*., 2007, Bacon *et al*., 2001). *C. jejuni* mutant in *kpsE* capsule gene in *C. jejuni* 81116 resulted in reduced adhesion and invasion of the mutant however, colonization of the chicken intestine remained unaffected (Bachtiar *et al*., 2007). The capsular gene mutants in *C. jejuni* also resulted in impaired virulence profile in the ferret disease model (Bacon *et al*., 2001). A recent study showed that surface related structures, primarily capsular polysaccharides, are subjected to genetic variation in the chicken intestine which is the main reservoir of *C. jejuni* strains (Wilson *et al*., 2010). These changes may increase the virulence of some *C. jejuni* strains by improving their ability to invade the human intestine (Pope *et al*., 2007). This provides an interesting link between *C. jejuni* surface polysaccharide, invasion and virulence mechanism.

### *1.10.9 Protein glycosylation systems in Campylobacter* species

Glycosylation is a well-known phenomenon in eukaryotes. The study of surface structures for their role in bacterial virulence has also identified glycosylation as a prominent mechanism in prokaryotes. There are two glycosylation systems studied in *Campylobacter* species. The O-linked glycosylation system that glycosylates the flagella (Guerry *et al*., 2006, McNally *et al*., 2006a, Goon *et al*., 2003, Thibault *et al*., 2001, Doig *et al*., 1996) and the N-linked glycosylation system that decorates other periplasmic proteins (Linton *et al*., 2002, Young *et al*., 2002, Szymanski *et al*., 1999). The O-linked glycosylation system links the glycans to the hydroxyl oxygen of serine or threonine amino acids in the target flagellin protein. The N-linked glycosylation system modifies asparagine residues on many outer membrane proteins (Szymanski *et al*., 1999, Szymanski *et al*., 2003, Szymanski and Wren., 2005).

In *Campylobacter* species, O-glycan modification is an essential process for flagella synthesis and motility. This post translational modification of flagellins was first identified in *C. coli* and then this process was studied in *C. jejuni* and *C. coli* (Alm *et al*., 1992, Logan *et al*., 1989). There are two major O-glycans that modify flagellins in *Campylobacter* species, both having a similar structure and each composed of similar 9-carbon sugars. These saccharides are pseudaminic acid (PseAc) and legionaminic acid (LegAm) (McNally *et al*., 2007, Schirm *et al*., 2003, Thibault *et al*., 2001). The major glycan coating *C. jejuni* flagellins is PseAc whereas LegAm modifies *C. coli* flagellins (Young *et al*., 2007). In *C. jejuni* the PseAc glycans are synthesized by proteins encoded by several *pse* genes. It has been reported recently that the PseAc in *C. jejuni* have a variety of substitutions including an acetamidino, O-acetyl or N-acetylglutamine attachments (Schirm *et al*., 2005, Thibault *et al*., 2001). Genome sequence analysis of *C. jejuni* 81-176 revealed a group of genes encoding for the O-glycosylation system located adjacent to the flagellin synthesis genes and this region was highly variable (Guerry and Szymanski., 2008). The glycosylation at seven specific serine or threonine residues is important for the motility and autoagglutination phenotypes in *C. jejuni* (Ewing *et al*., 2009). Since O-glycan coated flagellins are surface exposed they may play a role in promoting interaction between flagella of neighbouring bacteria and facilitate autoagglutination. The two processes; flagellin glycosylation and autoagglutination together may also allow survival of bacteria inside the host. *C. jejuni* 81-176 mutants in PseAc glycans resulted in defects in motility and autoagglutination.

*In vitro* adhesion and invasion of cultured epithelial cells and virulence in the ferret disease model was decreased (Ewing *et al*., 2009, Guerry *et al*., 2006). Another study showed that *C. jejuni* mutants in LegAm had defects in colonization of chicks (Howard *et al*., 2009). The glycan coated flagella showed antigenic properties which suggests that the O-linked glycosylation system may have a role in survival in host cells by escaping the host immune responses (Thibault *et al*., 2001, Guerry., 2007, Young *et al*., 2007).

The N –linked glycosylation system in *Campylobacter* species is encoded by *pgl* genes. The *pgl* genes are conserved in *C. jejuni* and *C. coli*. The translational products of pgl system are multi-sugar molecules (usually 7 sugars) (Jervis *et al*., 2012). A number of studies have suggested that the N-linked glycosylation system in *C. jejuni* is required to mediate host interactions. Mutants in *pgl* genes were unable to adhere to and invade human epithelial cells and were unsuccessful in colonizing the avian intestinal tract (Kelly *et al*., 2006, Hendrixson and DiRita., 2004, Karlyshev *et al*., 2004, Szymanski *et al*., 2002). Kakuda and DiRita (2006) showed that glycosylation of the periplasmic protein Cj1496c was required for the adherence and invasion of INT-407 cells and colonization of the chicken intestinal tract. Karlyshev *et al* (2004) reported a *pglH C. jejuni* mutant with reduced adherence and invasion to Caco-2 cells. Similarly, mutational inactivation of the glycosylation system genes, oligosaccharide transferase (*pglB*) and putative aminotransferase (*pglE*) in *C. jejuni* 81-176 impaired its ability to adhere and invade INT-407 cells (Szymanski *et al*., 2002). Another aminotransferase encoding gene, *cj1121c* which is a glycoprotein of N-linked glycosylation system was reported to be involved in motility and *in vitro* host cell interaction (Vijayakumar *et al*., 2006).

Currently, over 70 N-linked glycosylation proteins have been identified in *C. jejuni* (Kowarik *et al*., 2006, Young *et al*., 2002). The N-linked glycosylation system modifies the VirB10 protein which is encoded on the pVir plasmid in some *C. jejuni* strains (Larsen *et al*., 2004). VirB10 is homologous to the proteins of T4SS and is involved in DNA transformation (Bacon *et al*., 2000). The N-linked glycans modify VirB10 at two asparagine residues providing stability to the protein. However, the glycosylation of only one asparagine residue of VirB10 is required for the expression of this protein (Larsen *et al*., 2004). A recent study suggested that the Pgl system releases free oligosaccharides (fOS) in the periplasmic space. The amount of these fOS produced is influenced by the salt concentration. This suggests that fOS may provide protection under osmotic stress conditions (Nothaft *et al*., 2009).

The *C. jejuni* N-linked glycosylation system also influences the host immune system by recognizing specific lectins present on macrophages and some dendritic cells. A *C. jejuni* mutant of *pglA* promoted excessive release of IL-6 (interleukin-6) from human dendritic cells which suggests that the N-linked glycosylation system may function to enable the organism to evade the immune response during infection in human hosts (van Sorge *et al*., 2009).

## 1.11 Project background and key aims of research

The ability to attach to and internalize the human epithelial cells is an essential phenomenon used by *C. jejuni* to cause an asymptomatic or diarrhoeal disease (Young *et al*., 2007).

In a recent development to differentiate the adhesion and invasion virulence traits of clinical and non-clinical *C. jejuni* strains, Fearnley *et al* (2008) studied 74 strains of poultry origin and 39 clinical strains isolated from patients with enteritis and bacteraemia. This study categorised the *C. jejuni* strains into three classes; low invasive, highly invasive and hyperinvasive strains using INT407 cell lines, Caco-2 and HT29-Cl.16E mucous secreting cell lines. The invasion potential for these *C. jejuni* strains into INT-407 cells is presented in Figure 1.3.

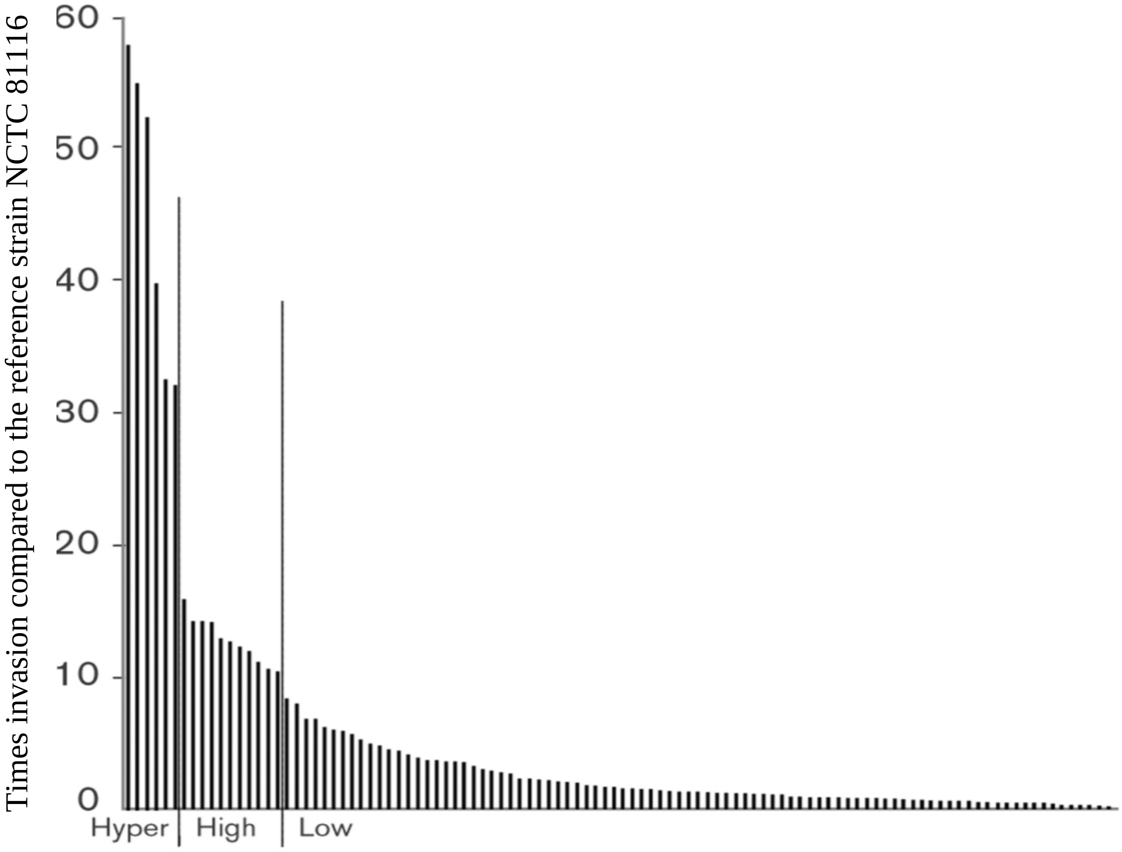


Figure 1.3: Distribution of 113 *C. jejuni* isolates tested for their ability to invade into INT-407 cells compared to the low invasive reference *C. jejuni* strain NCTC 81116. © 2012 Crown copyright.

The hyperinvasive strains were >25 times more invasive compared to the reference strain. The high invasive strains were at least 10 times as invasive and the low invasive *C. jejuni* strains were less than 10 times as invasive as the reference strain (Fearnley *et al.,* 2008).

Six clinical hyperinvasive *C. jejuni* isolates (01/10, 01/35, 01/04, 01/41, 01/51, EX114) were identified in this study which showed significantly higher levels of invasion (>25-fold) into the human intestinal cell lines INT-407 and Caco-2 compared to the low invasive reference *C. jejuni* 81116 (Fearnley *et al*., 2008).

A hyperinvasive *C. jejuni* strain 01/51 has been characterised in detail by transposon mutagenesis (Javed *et al*, 2010). A transposon mutant library composed of 800 mutants was screened. An initial study identified 26 mutants with high motility and reduced invasiveness which were selected for further investigation. Six genes (*cipA*, *cj0690c*, *cj1136*, *cj1245c*, *cj1305c* amd *cj1539c*) were identified with potential roles in invasiveness and this was confirmed by targeted mutagenesis, complementation and phenotype studies. These genes with a role in invasiveness were also studied for colonization of the chick gut (Javed *et al*, 2010).

In this PhD project, all six hyperinvasive *C. jejuni* strains identified by Fearnley *et al* (2008) were studied. The initial hypothesis was that this group of stains possesses extra genetic material to make them hyperinvasive. Therefore, this study was designed to investigate the genomic basis of invasiveness in these hyperinvasive *C. jejuni* strains using advanced molecular techniques such as Comparative Genomic Hybridization (CGH), Suppressive Subtractive Hybridization (SSH) and genome sequencing.

The main aims of this project are;

- To determine differences between selected *C. jejuni* hyperinvasive strains compared with low invasive strains at the genomic level.
- To establish the function of genes of interest identified in the hyperinvasive *C. jejuni* strains.
- To relate any genomic variations identified by using the molecular techniques to the phenotypic characteristics of the strains.
- To understand more about how this major human pathogen has evolved based on the knowledge acquired in this study.

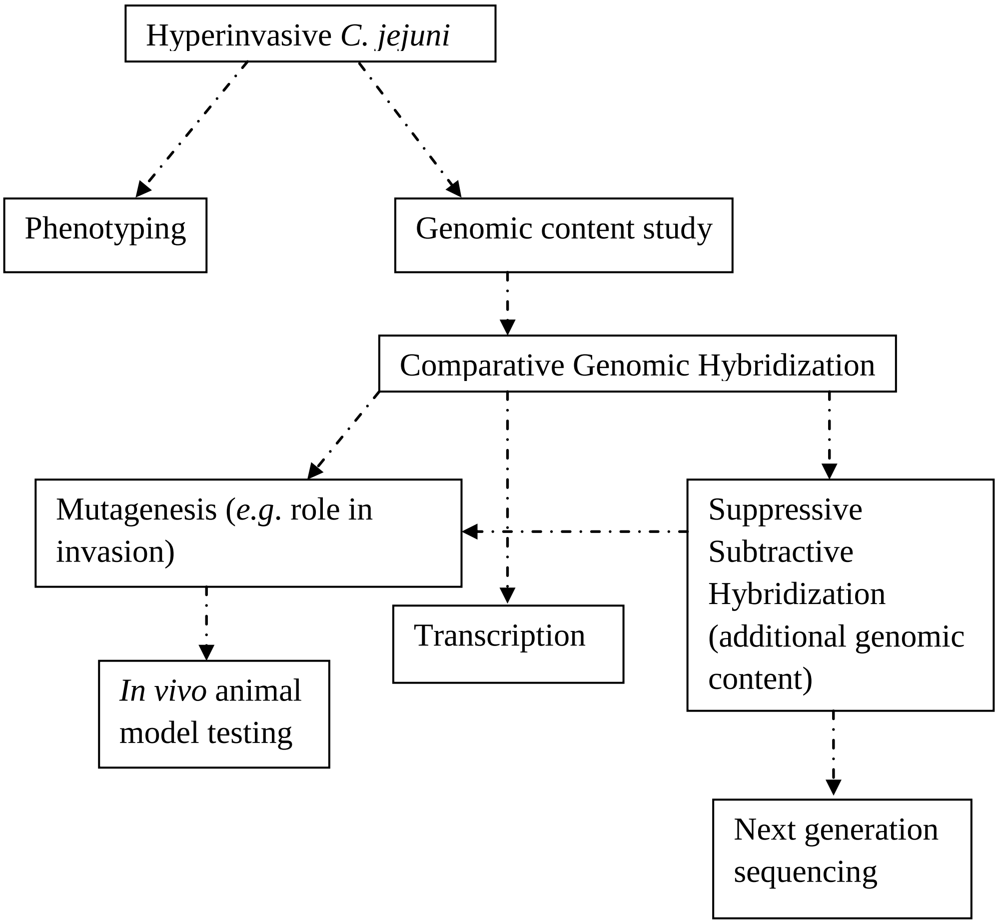


Figure 1.4: The proprosed research plan for this project.

## *Chapter Two*

# MATERIALS AND METHODS

# MATERIALS AND METHODS

## 2.1 Bacterial strains

This study employed 24 *Campylobacter jejuni* strains and *Campylobacter coli* RM2228. All *Campylobacter jejuni* isolates used in this study were obtained from the Veterinary Laboratory Agency, Weybridge, UK. *Campylobacter coli* RM2228 was provided by Prof Ian Connerton, University of Nottingham, UK (Table 2.1).

Table 2.1: The bacterial strains used in this study.

| **Bacterial strain** | **Source** | **Isolated from** | **Invasion profile*** | **MLST** | | **Reference** |
|---|---|---|---|---|---|---|
| | | | | **Clonal complex** | **ST complex** | |
| 01/10 | Human clinical | Blood | Hyperinvasive | 21 | 21 | Fearnley *et al*., 2008 |
| 01/35 | | Faecal | Hyperinvasive | 21 | 22 | |
| 01/04 | | Blood | Hyperinvasive | 677 | 677 | |
| 01/41 | | Faecal | Hyperinvasive | 21 | 916 | |
| 01/51 | | Faecal | Hyperinvasive | 21 | 21 | |
| EX114 | | Environment (Puddle isolate from outside a boiler house in South East of England) | Hyperinvasive | 682 | 914 | |
| 01/30 | | | Low invasive | 45 | 45 | |
| 01/32 | | | Low invasive | 22 | 22 | |
| 01/46 | | | Low invasive | 21 | 21 | |
| 01/39 | | | Low invasive | 21 | 53 | |
| 01/44 | | | Low invasive | 21 | 21 | |
| 01/05 | | | Low invasive | 508 | 508 | |
| 01/08 | | | Low invasive | 61 | 61 | |
| 01/11 | | | Low invasive | 45 | 137 | |
| 01/36 | | | Low invasive | 354 | 324 | |
| C2/3 | | | Low invasive | 21 | 21 | |
| 01/46 | | | Low invasive | 21 | 21 | Fearnley *et al*., 2008 MLST-this study |
| 01/44 | | | Low invasive | 21 | 21 | Fearnley *et al*., 2008 MLST-this study |
| C12/11 | Poultry | | Low invasive | 658 | 908 | Fearnley *et al*., 2008 |
| C27/14 | | | Low invasive | 257 | 257 | |
| C69/2 | | | Low invasive | 443 | 393 | |
| C110/4 | | | Low invasive | 433 | 433 | |
| 81116 | Human | | Low invasive | 283 | 267 | Isolated from patient suffering with diarrhoea from a water-borne outbreak in 1981(Palmer *et al*., 1983) |
| RM1221 | Poultry | Chicken carcass | Not known | 354 | 354 | This is a fully genome sequenced *C. jejuni* strain (Fouts *et al*., 2005) |
| *C. coli* RM2228 | Poultry | Chicken | Not known | 828 | 1063 | This is the first genome sequenced *C. coli* (Fouts *et al*., 2005) |
| *E. coli* TOP10F'** | Not applicable | Invitrogen, UK | Not known | Not applicatble | | FL {lacIq Tn10 (TetR)} mcrA ƒ¢(mrr-hsdRMS-mcrBC) ƒ$^3$80lacZƒ¢M15 ƒ¢lacƒ′74 recA1araD139 ƒ¢(ara-leu)7697 galU galK rpsL (StrR) endA1 nupG |

*Invasive phenotype is based on the *in vitro* invasion potential of isolates tested using INT-407 cells. Hyperinvasive *C. jejuni* strains showed 25X invasiveness whereas the low invasive *C. jejuni* corresponded to 10X invasion potential compared to the reference *C. jejuni* 81116. ** The *E. coli* competent cells for cloning used in the pooled suppressive subtractive hybridization study.

## 2.2 Primers used in this study

All primers used in this study were purchased from Eurofins (MWG operon, UK) and are shown in the tables 2.2.1, 2.2.2 and 2.2.3.

Table 2.2.1: Oligonucleotides used in the Comparative Genomic Hybridization (CGH) study.

| Oligonucleotide | Gene | Tm*(°C) | Sequence (5' to 3') | Expected product size (bp) |
|---|---|---|---|---|
| modA F | *modA* | 52 | TTAAAAGAATTTGAAGAAAAATT | 750 |
| modA R | | 52 | TTCAAAGGCTAATTTTTTATC | |
| metF F | *metF* | 52 | GAGCAAATTTGGATCAATC | 1005 |
| metF R | | 52 | TTAGCTTTAATGCTTTTTGG | |
| CJ_10000868 F | CJE0669 | 58 | CACTTCCCCCTTGACTGG | 490 |
| CJ_10000868 R | | 58 | GGAGAAGTCCACACAGAAG | |
| CJ_10000908 F | CJE0838 | 60 | GTATAGTAGGGCAAAATATTGC | 369 |
| CJ_10000908 R | | 62 | CCAATAACTTTTCCAGCTTGTG | |
| his S F | *hisS* | 48 | GTAGGAGAAAGT TCTGA | 1120 |
| his S R | | 48 | ACAAACTTTACCATTTTTG | |
| Pro C F | *proC* | 40 | ATTAATCTTGATAATAAT | 575 |
| Pro C R | | 44 | CAGCATTAGCAATGC | |
| CJ_10001541 F | CJE0320 | 52 | CTTTTAAATCAAGATGGGG | 507 |
| CJ_10001541 R | | 50 | CACAAGATCTTTTTACATC | |
| aat F | *aat* | 52 | GGAGAAAAA ATCAGTGATG | 535 |
| aat R | | 48 | CCCATAAATTCTAAATGTT | |
| CCOA0033 F | CCOA0033 | 54 | GCTAAACTTGTATAGATTGG | 390 |
| CCOA0033 R | | 52 | CTAGCCCATGCA AGTTC | |
| opCcV F | CJE1112 | 60 | GCAGGATCTTTTATTGATACAC | 760 |
| opCcV R | | 62 | CCTATATATAAACCATCTTCCATG | |
| CJ_10001535 F | CJE0801 | 48 | CGGAGTGTTTTTAATGC | 490 |
| CJ_10001535 R | | 49 | GGTGTGATAAAATTCAGG | |
| opCcV609 F | CJE0315 | 50 | GAAGCT TTTGTGCATGG | 750 |
| opCcV609 R | | 54 | CATAATCACTCTTGCTTCC | |
| tgt F | *tgt* | 52 | GCCTTTTTCAAAACAAAGC | 950 |
| tgt R | | 50 | CATGATCGTTGATAAATTC | |
| CJE1128 F | CJE1128 | 56 | CATGCTACCTACACATTTAG | 230 |
| CJE1128 R | | 58 | GGAGTCTTTCCA ACACCAC | |
| CJE0731 F | CJE0731 | 56 | GCGACTTGTGATGGAGTG | 1700 |
| CJE0731 R | | 58 | GTTGCCATATTAAACATTAAATG | |

Tm*(°C) is the melting temperature of oligonucleotides. These genes were selected for PCR screening as they were found as present (Table 4.1a) or absent/highly divergent (Table 4.1b) in the hyperinvasive *C. jejuni* strains (Chapter 4). The PCR primers were designed based on the conserved sequence of genes in all sequenced *Campylobacter* species strains publically available of Campybd (http://www.xbase.ac.uk/campydb/) and NCBI (http://www.ncbi.nlm.nih.gov/genome/campylobacter/) unless otherwise stated.

Table 2.2.2: The primer and adaptor sequences used in Pooled Suppressive Subtractive Hybridization (PSSH) study.

| **Oligonucleotide** | **Insert/gene** | **Sequence (5' to 3')** | **Tm*(°C)** | **Expected product size (bp)** |
|---|---|---|---|---|
| C1-bioF-2F | *bioF-2* (8-amino-7-oxononanoate synthase) | GGGGAATGATTATTTAAATTTAAGC | 64 | 941 |
| C1 bioF-2 R |  | GCACAGTAGGTTCTTTTATAGC | 62 |  |
| C2 Res mod F | Restriction modification system | GACGCAGCAGAGTATAAAC | 56 | 1400 |
| C2 Res mod R |  | CACTTAGCTCTTGCTCAG | 54 |  |
| C5-ThiG F | *thiG* (thiazole synthase) | GGCAAATACGAGTTTGATTCAAG | 64 | 700 |
| C5-ThiG R |  | GTTAATGGAGAACTGCTTTAGC | 62 |  |
| C6-P kinase F | Polyphosphate kinase | CGCGAACTTTCTTGGCTTCGC | 66 | 1450 |
| C6-P kinase R |  | GAAGCTAAGTGCGTTGCACGAC | 68 |  |
| C8-lysC F | *lysC* (aspartokinase) | GTGGAACAAGCGTTGGAACAC | 64 | 950 |
| C8-lysC R |  | GCTCTAACTGCAAGTTCTCCG | 64 |  |
| C9-mem lipo F | Membrane-associated lipoprotein | CATTAGAGGTATCCCAAGATG | 60 | 735 |
| C9-mem lipo R |  | GGTGCGGGCCTCTTCGC | 60 |  |
| C10-Ferredox F | Ferredoxin | CTATTGCTTGTGGTTCTTGTATTG | 64 | 225 |
| C10-Ferredox R |  | CAAAAACTGGAGTGTCCCCAC | 64 |  |
| C11-Tri ester F | Tributyrin esterase | CAAACTTCTAGTGTTGTTACACG | 64 | 235 |
| C11-Tri ester R |  | GATCGTTTCAGTATCATCGGG | 62 |  |
| C13-Put reg F | Putative two component regulator | GCCTATTATGGATGGACTGG | 60 | 445 |
| C13-Put reg R |  | CTTCACCCACTTTATCTCTTAC | 62 |  |
| C14-MuSo1 F | Prophage MuSo1 | GAATAGCAAAAGCCCAAGCGG | 64 | 760 |
| C14-MuSo1 R |  | CACTTCTACTTTTCCTAATGTAAC | 64 |  |
| C15-GDP dehyd F | Putative GDP-mannose 4,6 dehydratase | CAGGATTTACAGGGCAAGTTG | 62 | 750 |
| C15-GDP dehyd R |  | CTTCAGGAAGTTTAAAAGGCTTC | 62 |  |
| C20-CJE1142 F | Hypothetical protein CJE1142 | GATGATGATATAGATAAACCTTATG | 64 | 740 |
| C20-CJE1142 R |  | CCACCTGCTTTAATGATAACAC | 64 |  |
| C21-flaA F | *flaA* (Flagellin subunit A) | CACCAATGTTGCAGCTTTAAATGC | 68 | 1620 |
| C21-flaA R |  | CTGAACAGAATTAGCCTGTGCC | 66 |  |
| C22-fkbM F | FkbM family methyltransferase | GACCTTTACCTTTTATACTTGC | 60 | 740 |
| C22-fkbM R |  | CAGGATCTGCTTTGTAAATAGC | 62 |  |
| C23-Esterase F | Esterase (*Clostridium lentocellum* DSM 5427) | CAATATCCAAAAGCGTATGCGC | 64 | 445 |
| C23-Esterase R |  | CACCAAACACATCTTGATAATAG | 62 |  |
| C25-C8J 1243 F | Hypothetical protein (C8J_1243) | CGATTCTTGTGATGATGTAGAAC | 64 | 1100 |
| C25-C8J 1243 R |  | GATCCCTACAAGGATAAGAGATG | 66 |  |
| C27-Dom prot F | Conserved domain protein | GCTTTAAACCTTAGCCTCTTTG | 62 | 645 |
| C27- Dom prot R |  | GATTAATCAAAGCATCATAATACC | 62 |  |
| C28-Phage pro F | Phage uncharacterized protein | CAAATGAACAAAAGCACGAAAACAC | 68 | 1680 |
| C28-Phage pro R |  | CTTATTCTTGAAACAGAGTTAAAATG | 66 |  |
| C29-unknown 1F | Unknown 1 | CCTATAGGTATCCATAGAAAAG | 60 | 235 |
| C29-unknown 1R |  | GGTCTACTGGTATTTATTTCAC | 60 |  |
| C32-DNA dom F | Restriction modification system DNA specificity domain-containing | GCAGGTCTGGAGAGAAAGAAC | 64 | 690 |
| C32-DNA dom R |  | CTAATACTTTCAGTTTTCTGCTTTC | 66 |  |
| C33-S trans F | Putative sugar transferase (*Campylobacter jejuni* subsp. *jejuni* IA3902) | GTTATGATTGACTTTAGTCATCAAAG | 66 | 1690 |
| C33-S trans R |  | GAAGCTACTATATCTGGACGATG | 66 |  |

Continuous

Table 2.2.2: The primer and adaptor sequences used in Pooled Suppressive Subtractive Hybridization (PSSH) study.

| **Oligonucleotide** | **Insert/gene name** | **Sequence (5' to 3')** | **Tm*(°C)** | **Expected product size (bp)** |
|---|---|---|---|---|
| C34-Thi syn F | Thiazole synthase *thiG* (*C. jejuni* subsp. *doylei* 269.97) | GGCAAATACGAGTTTGATTCAAGA | 66 | 741 |
| C34-Thi syn R | | GGAGAACTTGCTTTAGCCTCG | 64 | |
| C37-50S F | 50S ribosomal protein | CGCAAAATGATGAAAGGGCG | 60 | 375 |
| C37-50S R | | CAGTATATTTCATTTTGGCTCTC | 62 | |
| C38-Unknown 2F | Unknown 2 | CCTATAGGTATCCATAGAAGAG | 62 | 229 |
| C38-Unknown 2R | | GAGAATTAAAATGAATTATGGAAC | 60 | |
| C39-Put mem F | Putative membrane protein | GAACAAAGACAAATCATAGAAGAAG | 66 | 1699 |
| C39-Put mem R | | GTATGGTATATAGTATGTTTAGCAC | 66 | |
| C40- S kinase F | Sensor histidine kinase | CTTAGAAAGTCTTATAGAACAAAC | 62 | 763 |
| C40- S kinase R | | CACTTTGAAAACTTAACTCTCC | 60 | |
| C41-Hypo pro F | Conserved hypothetical protein | GGAAGGGATGATGGATTTGG | 60 | 1678 |
| C41-Hypo pro R | | CAAACCACAACATAATATATCC | 58 | |
| C42-Nic Tran F | Nicotinate phosphoribosyltransferase | CTT CTT TAG CCT TGC TTT GTG | 60 | 1374 |
| C42-Nic Tran R | | GTT TAG GCG AGA GTT TTA CTT C | 62 | |
| C43-ISHa1675 F | ISHa1675 transposase B | GTG CAG TAA AAT ATA GAA TTT ATC C | 64 | 574 |
| C43-ISHa1675 R | | CTT CTT GCT TCA ACG ATA GAT AG | 64 | |
| C44-Cj8486 F | Hypothetical protein Cj8486_0894c and CJE0961 | CAT CTT TCA CAT ACA GAT CTT G | 60 | 890 |
| C44-cj8486 R | | GCT TTT AAT TAA ATC AAT AAT TTG AG | 62 | |
| C45-CCO0105 F | Hypothetical protein CCO0105 | GAT GCT TGA AAA TCT AAT AGC AC | 62 | 144 |
| C45-CCO0105 R | | CAC AAA TAC CCA TAA AGA TGA G | 60 | |
| C50-flaB F | *flaB* (Flagellin subunit B) | GGA TAA ACA CCA ACA TCG GTG | 62 | 1610 |
| C50-flaB R | | CAT TTT GCT GCA CTG CAT TAG C | 64 | |
| C51-C8J0142 F | Hypothetical protein C8J_0142 | CAT CTT TGT TTG CTT TAG TAG | 56 | 625 |
| C51-C8J0142 R | | CAA AGA AAT AGG CTC TAT CAC | 58 | |
| C52-murD F | *murD* (UDP-N-acetylmuramoylalanine--D-glutamate ligase) | CAC TTT TTG GAT ACG GAA AAA CC | 64 | 1180 |
| C52-murD R | | CTT TAA AGA CTT TTC CAC GCT C | 62 | |
| C54-tet F | *tet* (tetracycline) | CGATCTTGTTGATAAAGATAACG | 62 | 730 |
| C54-tet R | | GTTAAGGAATATAATTAGATTCAG | 60 | |
| C56-Met chem F | Methyl- accepting chemotaxis protein | CAAAGACTTGATAAACATAGTTC | 60 | 1710 |
| C56-Met chem R | | GAGTTTAGAGGCACCATTTAG | 60 | |
| C57-Phage tail F | Phage tail fibre protein | GTCTTAATAGGAGGATTGGGAG | 64 | 250 |
| C57-Phage tail R | | GGGCAGGTCTAAATACATATTTG | 64 | |

Continuous

Table 2.2.2: The primer and adaptor sequences used in Pooled Suppressive Subtractive Hybridization (PSSH) study.

| **Oligonucleotide** | **Insert/gene name** | **Sequence (5' to 3')** | **Tm*(°C)** | **Expected product size (bp)** |
|---|---|---|---|---|
| C62-Put S tran F | Putative sugar transferase (*Campylobacter jejuni* subsp. *jejuni* CG8486) | CGTAGTTATCCCAATCTATAATG | 62 | 1210 |
| C62-Put S tran R | | CGAGTAAGAACATAACCTATTC | 60 | |
| M13 F(−20) | Sequencing primers for PCR ® 2.1 TOPO cloning vector (Invitrogen UK) | 5′-GTAAAACGACGGCCAG-3′ | Not applicable | Dependent on cloned sequence size |
| M13 R | | 5′-CAGGAAACAGCTATGAC-3′ | | |
| 16S rRNA F | *C. jejuni* (MWG, Eurofins, UK) | 5'-AATCTAATGGCTTAACCATTA-3' | 54 | 852 |
| 16S rRNA R | | 5'-GTAACTAGTTTAGTATTCCGG-3' | 58 | |
| Adaptor 1 | CLONE-TECH PCR™-Select Bacterial Genome Subtraction kit (Clonetech, UK) | 5'-CTAATACGACTCACTATAGGGC tcgagcggccgcccgggcaggt-3'<br>3'-GGCCCGTCCA-5' | Not applicable | |
| Adaptor 2R | | 5'-CTAATACGACTCACTATAGGGC agcgtggtcgcggccgaggt-3'<br>3'-GCCGGCTCCA-5' | | |
| PCR primer 1 | | 5'-CTAATACGACTCACTATAGGGC-3' | 66 | Not applicable |
| Nested primer 1 | | 5'-tcgagcggccgcccgggcaggt-3' | 68 | Not applicable |
| Nested primer 2R | | 5'-agcgtggtcgcggccgaggt-3' | 68 | |

*Tm (°C) represents the melting temperature. Where the gene was present in more than one *Campylobacter* species strain with sequences publically available on Campydb (http://www.xbase.ac.uk/campydb/) and NCBI (http://www.ncbi.nlm.nih.gov/genome/campylobacter/), the PCR primers were designed based on conserved sequence of the gene in these strains. In case of gene present in other bacteria the PCR primer pair was designed based on the sequence in respective strain only. For the unknown inserts 1 and 2, the primers were designed from the insert sequence.

Table 2.2.3: MLST PCR and sequencing primers used in this study.

| **Gene** | **PCR primers** | **Sequencing primers** |
|---|---|---|
| | **Sequence (5' to 3')** | |
| *aspA F* | A1 AAAGCTGCAGCTATGGC | S3 CCAACTGCAAGATGCTGTACC |
| aspartate | A3 ATGAGGTTTATTATGGAGTGC | |
| | A9 AGTACTAATGATGCTTATCC* | |
| *aspA R* | A2 AAGCGCAATATCAGCCACTC | S6 TTCATTTGCGGTAATACCATC |
| | A4 CCTCTTTGGCTATAGAAGCTG | |
| | A10 ATTTCATCAATTTGTTCTTTGC* | |
| *glnA F* | A1 TAGGAACTTGGCATCATATTACC | S1 GCTCAATTCATGGATGGC |
| glutamine synthetase | | S3 CATGCAATCAATGAAGAAAC* |
| *glnA R* | A2 TTGGACGAGCTTCTACTGGC | S4 GCATACCATTGCCATTATCTCCG |
| | | S6 TTCCATAAGCTCATATGAAC* |
| *gltA F* | A1 GGGCTTGACTTCTACAGCTACTTG | S1 GTGGCTATCCTATAGAGTGGC |
| citrate synthase | | S3 CTTATATTGATGGAGAAAATGG* |
| *gltA R* | A2 CCAAATAAAGTTGTCTTGGACGG | S6 CCAAAGCGCACCAATACCTG* |
| | | S8 TGCTATACAGGCATAAGGATG |
| *glyA F* | A1GAGTTAGAGCGTCAATGTGAAGG | S3 AGCTAATCAAGGTGTTTATGCGG |
| serine hydroxy methyl transferase | | S5 GCTAATCAAGGTGTTTATAT** |
| | | S7 AGCCTAATTCAGGTTCTCAA** |
| *glyA R* | A2 AAACCTCTGGCAGTAAGGGC | S4 AGGTGATTATCCGTTCCATCGC |
| *tkt F* | A1 TTTAAGTGCTGATATGGTGC | S1 TGCACCTTTGGGCTTAGC |
| transketolase | A3 GCAAACTCAGGACACCCAGG* | S5 GCTTAGCAGATATTTTAAGTG |
| *tkt R* | A4 CATAGCGTGTTCTCTGATACC | S4 ACTTCTTCACCCAAAGGTGCG |
| | A6 AAAGCATTGTTAATGGCTGC* | S6 AAGCCTGCTTGTTCTTTGGC |
| *pgm F* | A1 TTGGAACTGATGGAGTTCG | S3 GCTTATAAGGTAGCACCTACTG |
| phospho glucomutase | A3 TCAGGGCTTACTTCTATAGG | S5 GGTTTTAGATGTGGCTCATG* |
| | A7 TACTAATAATATCTTAGTAGG* | |
| *pgm R* | A2AAGAGCTTAATATCTCTGGCTTCTAG | S2 TCCAGAATAGCGAAATAAGG* |
| | A4 AGCTTAATATCTCTGGCTTC | |
| | A8 CACAACATTTTTCATTTCTTTTTC* | |
| *uncA F* | A3 AAAGCTGATGAGATCACTTC | S3 AAAGTACAGTGGCACAAGTGG* |
| ATP synthase alpha subunit | A7 ATGGACTTAAGAATATTATGGC* | S5 TGTTGCAATTGGTCAAAAGC |
| *uncA R* | A2 GCTAAGCGGAGAATAAGGTGG | S4 TGCCTCATCTAAATCACTAGC* |
| | A4 ATTCTTTGTCCACGTTCAAG | |
| | A8 ATAAATTCCATCTTCAAATTCC* | |

The *C. jejuni* MLST primers were sourced from pubmlst.org/campylobacter/. PCR primer pairs amplify ~1kb internal region of each gene. Sequencing primers are nested inside the PCR primers and sequence ~600 bases region. Alternate primers are provided for some genes. * represent preferred primers with best results. ** are primers designed by Jonas Waldenström (Lund University, Sweden) and work best for the wild bird isolates. The melting temperature Tm (°C) for the MLST PCR primers was 50 °C.

## 2.3 Culture media

All culture media were obtained from Oxoid (Basingstoke, Hampshire, UK). The media were prepared in distilled water and sterilised by autoclaving at 121 °C, 15 psi for 15 minutes. The media plates were stored at 4 °C and were used within two weeks of preparation.

- mCCDA (modified *Campylobacter* Blood free selective agar base)

mCCDA was prepared in Duran bottles by weighing out 22.75 g of mCCDA agar powder dissolved in 500 ml of deionised distilled water.

Composition: nutrient broth no. 2 (25 g), amphotericin B (10 mg), bacteriological charcoal (4 g), cefoperazone (33 mg), casein hydrolysate (3 g), sodium deoxycholate (1 g), ferrous sulfate (250 mg), sodium pyruvate (250 mg), agar (12 g) added to deionized water (1 L).

- Mueller Hinton Broth* (MHB)

MHB was prepared in Duran bottles by weighing out 21 g of MHB dissolved in 1 L of deionized distilled water.

- Mueller-Hinton Agar* (MHA)

Thirty eight grammes of MHA was dissolved in 1 L of distilled water.

*composed of beef, dehydrated infusion from 300 g, starch 1.5 g, casein hydrolysate 17.5 g and agar 17.0 g per litre.

## 2.4 Bacterial culture maintenance and growth

All *Campylobacter* stocks were maintained at -80 ºC as 1ml aliquots in 20% glycerol MHB.

The *Campylobacter* stocks from the -80 ºC freezer were routinely sub-cultured on mCCDA (modified *Campylobacter* Blood free selective agar base) grown for 48 hours at 37 ºC in microaerobic atmosphere (10% $CO_2$, 5% $O_2$, 85% $N_2$ by vol) in anaerobic jars containing a CampyGen® pack to generate an anaerobic atmosphere or in an anaerobic workstation (Don Whitley scientific, UK).

The *E. coli* TOP10F’ competent cells were grown on Luria Bertani (LB) agar plates incubated at 37 ºC for 16-20 hours.

## 2.5 General buffers

- 0.1 M Phosphate buffered saline (PBS) and 1 M Tris-Chloride buffer (Sigma-Aldrich UK)

PBS and 10 mM Tris-Cl buffer were purchased as a sterile ready to use product. The 1 M Tris-Cl buffer was diluted to 10 mM concentration in distilled water for use in genomic DNA extraction procedure.

- 50X Tris-acetate-EDTA buffer (TAE)

50X TAE buffer was purchased from National Diagnostics, England. It was diluted in distilled water to obtain 1X TAE buffer.

## 2.6 DNA extraction procedures

### *2.6.1 Genomic DNA extraction*

The Qiagen genomic DNA extraction kit (Midi) and Qiagen genomic kit 100/G, (Qiagen, Crawley, UK) were used for the genomic DNA preparation following the manufacturer's instructions. It was critical to have high quality DNA for all molecular procedures used in this study. The following main steps were amended in the Qiagen genomic extraction procedure;

- To ensure the complete degradation of proteins and nucleases, proteinase K (3-15 units/mg) (Sigma-Aldrich, UK) was used at a concentration of 20 mg/ml and the duration of incubation was extended to 120 minutes at 37 °C.
- It was also important that the DNA was washed three times with 500 µl of 70% (v/v) ethanol to ensure complete removal of buffer salts.
- After the wash with 70% (v/v) ethanol the genomic DNA pellet was dried for 15 minutes. It was important not to over dry the DNA pellet to ensure complete solubilisation in the rehydration buffer (*i.e*, 10 mM Tris-Cl buffer/distilled sterile water). For CGH and Illumina genome sequencing the genomic DNA was eluted in 10 mM Tris-Cl buffer whereas for the PSSH plasmid DNA sequencing and genome sequencing by pyrosequencing/454 the genomic DNA was dissolved in distilled sterile water.

### *2.6.2 Plasmid DNA extraction*

Plasmid DNA extraction was carried out using QIAprep spin miniprep kit (Qiagen, Crawley, UK) as instructed by the manufacturer. Briefly, a single *E. coli* colony containing plasmid was picked and grown in 5ml LB broth supplemented with antibiotics (50 µg/ml kanamycin or ampicillin) for 16-18 hours with shaking at 37 °C. The bacterial pellet was re-suspended in 250 µl of buffer P1 followed by the cell lysis by addition of 250 µl of buffer P2. Buffer N3 (350 µl) was added and mixed to allow precipitation of genomic DNA and cell proteins. The suspension was applied to the silica column provided with the kit and centrifuged at 14,000×g to allow the genomic DNA to bind to the column and any precipitated proteins were removed. The column was washed with wash buffer PE and the plasmid DNA was eluted in 50 µl of water.

### *2.6.3 Determination of DNA concentration*

The concentration and purity of plasmid and genomic DNA was determined by a NanoDrop® ND-1000 UV-Vis spectrophotometer (NanoDrop Technologies, USA) prior to use in molecular techniques. For double stranded DNA, one microliter of the sample was used to record the concentration at a wavelength of 260 nm. For purified DNA, the desired 260:280 ratio reflecting protein contamination was 1.8-1.9 and 260:230 ratio (hydrocarbon contamination) was 2.0. Both the plasmid and genomic DNA were kept frozen at -20 °C.

## 2.7 Polymerase Chain Reaction

### *2.7.1 Standard PCR*

Each PCR reaction was carried out in either 50 µl, 30 µl or 25 µl volumes. Each PCR reaction mix contained 5X Green GoTaq® flexi PCR buffer (1X final concentration), $MgCl_2$ (25 mM) (1.0-4.0 mM final concentration), GoTaq® DNA polymerase 5 u/µl (1.25 u final concentration) (Promega, Southampton, UK), 0.7 mM dNTPs (Sigma-Aldrich, UK), 5 µM of each forward and reverse primer (Eurofins, MWG) and 15-25 ng of DNA template. Initial DNA denaturation was carried out at 94 °C for 5 minutes, followed by 30 cycles of denaturation at 94 °C for 45 sec, annealing for 45 sec based on the melting temperature (Tm°C) of the primers and extension was carried out for 1-2 minutes at 72 °C. A final extension step was performed at 72 °C for 5-10 minutes. The PCR product was visualised by agarose gel electrophoresis as stated later (section 2.7.3).

### *2.7.2 Colony PCR*

A loopful of freshly grown bacteria was suspended in 300 µl of sterile distilled water. The suspension was boiled to 100 °C for 10 minutes to lyse the cells. The suspension was centrifuged at 15,500 rpm for 5 minutes and 1 µl of the supernatant was used in the PCR procedure as explained in section 2.7.1.

### *2.7.3 Agarose gel electrophoresis*

DNA fragments were analysed on 1-1.5% w/v agarose gels containing SYBR® Safe DNA gel stain (10,000X) (1× final concentration) (Invitrogen, UK) prepared in 1×TAE buffer. The sample (10 µl) was mixed with 2 µl of 6×loading buffer (Promega, Southampton, UK) before loading on the gel. A 1 kbp or 100 bp DNA ladder (Promega, UK) was used as the DNA marker and 250 ng of the marker was loaded on the gel. The agarose gel was electrophoresed in a Mini Sub® Cell GT tank submerged in 1×TAE and at 90-100 V. The DNA bands were visualised under ultra-violet light using InGenius® gel documentation system (Syngene, UK).

### *2.7.4 Cloning into pCR 2.1-TOPO® vector*

The pCR 2.1-TOPO® vector was used for cloning PSSH secondary PCR products which comes a part of TOPO TA Cloning® kit (Invitrogen, UK). This vector contains single 3´-thymidine (T) overhangs that bind with a single deoxyadenosine (A) residues added to the 3’ ends of PCR products by *Taq* polymerase activity. It contains ampicillin and kanamycin resistance genes for antibiotics screening. It has M13 forward and reverse primers binding sites for sequencing and contains several restriction sites including *Eco*R I, *Hind* III and *Bam*H I with endonuclease activity that can be used to determine the size of cloned PCR product.

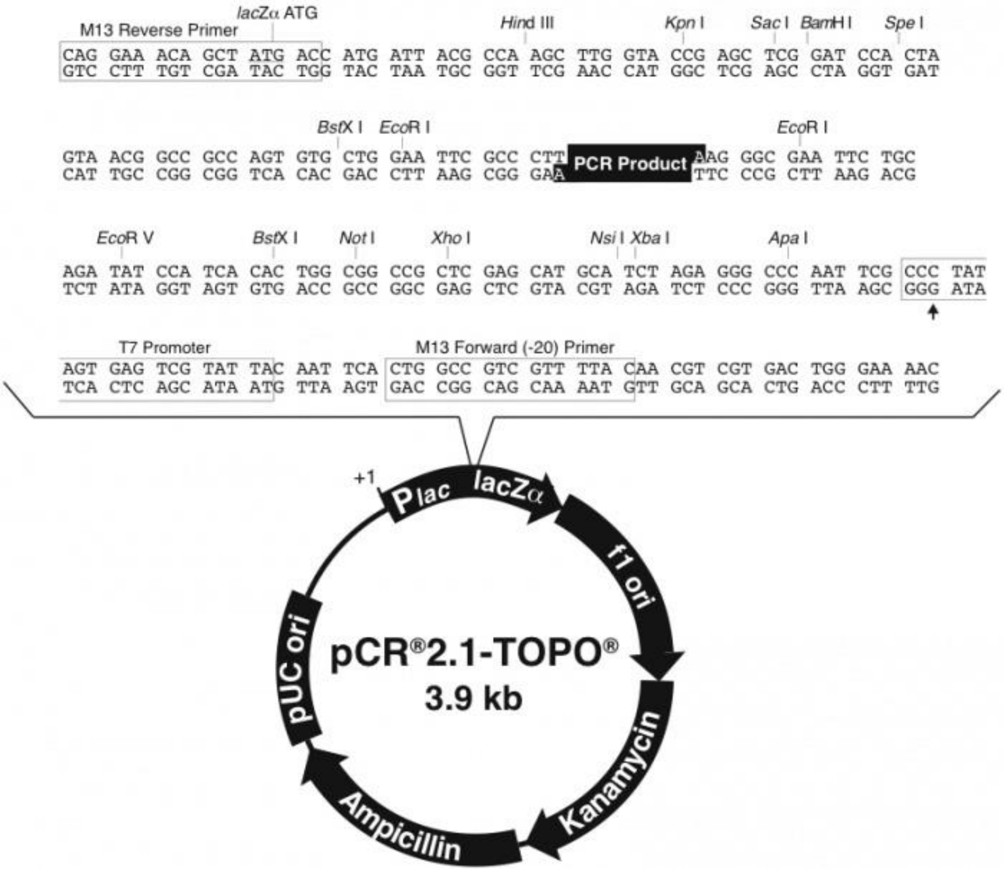


Figure 2.1: The map of pCR 2.1-TOPO® cloning vector (Invitrogen, UK).

Cloning was performed as described in the manufacturer's manual. Briefly, a reaction mixture was prepared containing 0.5–4 µl of fresh PCR product, 1 µl of salt solution made upto a total volume of 5 µl of sterile distilled water. To this 1 µl of pCR 2.1-TOPO® vector was added making up the total reaction mixture volume to 6 µl. After gently mixing the reaction mixture, it was incubated for 30 minutes at the room temperature (22–23 °C). The ligation mixture was used to transform 10F' *E. coli* chemically competent cells. The clones with inserts were selected by blue white screening using 40 mg/ml X-gal, 100 mM IPTG (isopropyl-beta-D-thiogalactopyranoside) (Invitrogen, UK) and antibiotics 50 µg/ml kanamycin (Sigma-Aldrich, UK) or 50 µg/ml ampicillin (Sigma-Aldrich, UK) in LB agar plates which were incubated for 16-18 hours at 37 °C. After incubation, the light blue or white colonies were picked up and sub-cultured onto the fresh LB plates supplemented with 50 µg/ml ampicillin or 50 µg/ml kanamycin.

### *2.7.5 Heat shock transformation of 10F' E. coli cells*

Two microliters of the ligation reaction mix was added to one 50 µl vial of One Shot® TOPO 10F'chemically competent *E. coli* cells (Invitrogen, UK) and incubated on ice for 30 minutes. The cells were heat shocked for 30 seconds at 42 °C followed by recovery in 250 µl of S.O.C medium (provided with the kit) with shaking (200 rpm) for one hour at 37 °C. The cells were plated onto antibiotic (ampicillin or kanamycin) supplemented LB plates. These plates were incubated overnight and transformed *E. coli* cells were selected.

### *2.7.6 Purification of PCR products*

The PCR products were purified using QIAquick PCR purification kit (Qiagen, Crawley, UK) to get rid of excess nucleotides, primers and DNA polymerase and salts. The cleanup was carried out as per the manufacturer's instructions. Briefly, the PCR product was mixed with a loading buffer PB and applied to a silica spin column provided with the kit. The column was centrifuged at 14,000×g followed by two washes with wash buffer PE and the purified product was eluted in 50 µl of distilled water.

## *2.8 Multi locus sequence typing (MLST)*

MLST was carried out as described previously by Dingle *et al*., 2001. Briefly, seven *C. jejuni* housekeeping genes *aspA*, *glnA*, *gltA*, *glyA*, *pgm*, *tkt*, *uncA* were amplified by PCR (2.7.1) using the gene specific PCR primer listed in the table 2.2.3. Each PCR product was purified as stated in section 2.7.6. A 400-500 bp fragment of each gene was sequenced (Source Bioscience, UK) using a separate set of sequencing primers (Table 2.2.3). Based on the sequencing data each strain was assigned an allele number, sequence type (ST) and clonal complex (CC) from the *Campylobacter* MLST database (http://pubmlst.org/campylobacter/).

## *2.9 Serotyping*

Six hyperinvasive and four low invasive *C. jejuni* strains were serotyped by using soluble heat-stable (HS) antigenic Penner serotyping scheme with a panel of 66 O antisera (Penner *et al*., 1983). The serotyping was performed by Dr Judith Richardson at the *Campylobacter* reference unit, Health Protection Agency (HPA), Colindale, UK.

## *Chapter* ***Three***

# PHENOTYPIC CHARACTERIZATION OF THE HYPERINVASIVE *C. JEJUNI* STRAINS

# PHENOTYPIC CHARACTERIZATION OF THE HYPERINVASIVE *C. JEJUNI* STRAINS

## 3.1 INTRODUCTION

Enteric pathogens that cause disease in humans including *C. jejuni* often have to survive in the environment as well as inside the human host. *C. jejuni* have evolved mechanisms that allow survival under both conditions.

### *3.1.1 C. jejuni virulence factors inside the host*

*C. jejuni* have a wide host range and are present in cattle, wild birds, poultry, pigs, cattle, dogs, cats, mink, rabbit and insects (Fitzgerald and Nachamkin., 2007, Humphrey *et al*., 2007). These bacteria are commensal in chicken and the contaminated chicken carcasses during slaughtering process are the major source of transmission of *C. jejuni* inside humans. *C. jejuni* prefer to grow under microaerobic conditions. The optimum human body temperature (37°C) and reduced oxygen conditions inside human gut offer suitable conditions for *C. jejuni* growth (Humphrey *et al*., 2007).

During the infection process inside the human host, *C. jejuni* encounters the host immune system which provides defence against any pathogen attacks (Wooldridge and Ketley., 1997). The innate immune response to *C. jejuni* infection recruits macrophages and dendritic cells (DCs) initiating an inflammatory response at the site of infection (Hickey *et al*., 1999, Mellits *et al*., 2002, Zheng *et al*., 2008). Inside the macrophages, other defence mechanisms are also active such as oxidative products, nutrient limitation and acidic pH which have detrimental effects on *C. jejuni* survival (De Melo *et al*., 1989, Day *et al*., 2000). These reactive oxygen molecules including hydrogen peroxide, superoxides and halogenated oxygen molecules target ribosomal RNA, nucleic acid and protein structures resulting in prompt death of bacteria (Baillon *et al*., 1999). Research has suggested that *Campylobacters* are generally killed within 24 to 48 hours of entering the human phagocytes (Wassenaar *et al*., 1997). On the contrary, the increasing number of enteric infections by *C. jejuni* indicates that they have developed mechanisms for survival under unfavourable environmental conditions (Mihaljevic *et al.*, 2007, Day *et al*., 2000, Baillon *et al*., 1999). Some of these survival mechanisms reported include transition from a viable to a viable-nonculturable state and transformation from spiral to coccal form in which bacteria are present in a dormant state (Kelly *et al*., 2001, Harvey and Leach., 1998). A number of stress related response systems have been related to pathogenesis in *C. jejuni*. These include global stress responses under *spoT* dependent stringent response that play a role in aerotolerance and survival in the stationary phase. The stringent response system has also been found to control some key pathogenesis mechanisms in *C. jejuni* including adhesion, invasion and intracellular survival (Gaynor *et al*., 2005)

### *3.1.2 C. jejuni survival in environment*

*C. jejuni* are widely dispersed in a variety of environments. *C. jejuni* are frequently isolated from food and exist as planktonic form in rivers, lakes, streams and soil (Luechtefeld *et al*., 1982, Harvey and Leach., 1998, Baillon *et al*., 1999, Kelly *et al*., 2001, Martinez-Rodriguez *et al*., 2004, Mihaljevic *et al*., 2007, Kaakoush *et al*., 2007). Poultry farms and slaughter houses are the major sources of *Campylobacter* species contamination (Humphrey *et al*., 2007, Havelaar *et al*., 2007). Also, campylobacters are frequently isolated from domestic kitchens and catering environments where they appear to stick to the work surfaces (Humphrey *et al*., 2007). In these environments, *C. jejuni* has to withstand stresses such as atmospheric oxygen pressure, temperature and nutrition variations (Day *et al*., 2000, Mihaljevic *et al*., 2007). *C. jejuni* has shown to form biofilm on insert surfaces including food products (Sulaeman *et al*., 2010). The aerobic conditions have been found to enhance biofilm formation ability of some *C. jejuni* isolates which may suggest biofilm formation as a useful adaptation for the environmental survival of these bacteria (Reuter *et al*., 2010).

### *3.1.3 In vitro invasion assay related stresses*

Adhesion to host epithelial cells is a critical step in *C. jejuni* pathogenesis that involves several adhesins present on the bacterial surface (e.g. flagella, lipooligosaccharides and capsule). These adherent bacteria may invade the host epithelial cells and develop an infection. Adhesion and invasion have been studied as important events in *C. jejuni* enteritis in a number of *in vitro* assays using human and non-human epithelial cell lines (Konkel *et al*., 2001). These studies have used human intestinal cells (INT407) and human colon cells (Caco-2) to study adhesion and invasion of *C. jejuni* and *C. coli* (Everest *et al*., 1992, Konkel *et al*., 1997, Fearnley *et al*., 2008). A clear relationship exists between the intensity of the *Campylobacter* disease severity and the adhesion and invasion potential of strains to the epithelial cells (Russell *et al*., 1993). *In vitro*, gentamicin protection invasion assays have been used to determine the bacterial invasion potential using these intestinal cell lines (Elsinghorst, 1994). During this assay, cells are exposed to different environmental stresses that affect the survival of bacteria while invading epithelial cells. Reactive oxygen molecules are released as the product of oxidative metabolism in eukaryotic cells that may affect the survival of invading bacteria.

In this study, the hyperinvasive and low invasive *C. jejuni* strains were tested for their growth rate, stresses encountered during the invasion assays (normal air pressure, hydrogen peroxide ($H_2O_2$) stress and motility) and other virulence related phenotypes such as autoagglutination activity, the ability to survive under sodium deoxycholic acid stress and biofilm formation. The aims of this study were;

- To determine if there were any other phenotypic characteristics that distinguished the hyperinvasive *C. jejuni* from the low invasive *C. jejuni* strains.
- To investigate the effects of a number of stresses that the organism would experience during *in vitro* invasion assays and to confirm that the differences seen were due to the hyperinvasion rather than the stresses.

## 3.2 METHODS

### *3.2.1 Growth curve using viable count method*

The growth rate of the hyperinvasive and low invasive *C. jejuni* strains was determined. For this study, bacteria were grown on modified *Campylobacter* Blood free selective agar base (mCCDA) plates (Oxoid, UK) for 48 hours under microaerobic conditions at 37 ºC. The growth from the plate was harvested using a cotton swab in 2.5 ml of sterile Phosphate Buffered Saline (PBS). A two ml volume of this suspension was used to inoculate 200 ml of pre-warmed MH broth (Oxoid, UK). A 2 ml sample was carefully removed from the above broth at time zero for viable count. The bacterial broth was then sealed in a gas jar containing a CampyGen gas pack (Oxoid, UK) and incubated with shaking (180 rpm) at 37 ºC. The growth rate readings were taken during the late log phase, stationary and death phase. At time intervals 16, 20, 24, 28, 48 hours, 2 ml samples were carefully removed from the broth, serially diluted, and plated onto predried mCCDA plates. The plates were microaerobically incubated at 37 ºC for 24-48 hours. After incubation *C. jejuni* colonies were identified and counted to determine the viable count.

### *3.2.2 Resistance to aeration stress*

During the invasion assay, the bacterial cells are exposed to a variety of atmospheric air stress conditions. For this assay, the bacterial strain grown as stated above was resuspended in 2.5 ml of sterile PBS. The pre-warmed MH broth (200 ml) was inoculated with 2 ml of the bacterial suspension. The broth was microaerobically incubated at 37 ºC in gas jars with a CampyGen pack with constant agitation at 180 rpm for 24 hours. After overnight incubation when the cell density would be in the order of approx $10^8$-$10^9$ cfu/ml, the gas pack was removed and a time zero reading was taken and the bacterial culture was exposed to atmospheric oxygen stress by gentle shaking at 180 rpm at 37 ºC. Samples were removed at hourly intervals for 6 hours. The samples were serially diluted and plated onto mCCDA plates for viable counts.

### *3.2.3 Sensitivity to hydrogen peroxide*

The bacterial cells are exposed to the toxic effects of free oxygen radicals released by the eukaryotic cells during an invasion assay. For the assay, the bacterial growth from mCCDA plate grown under microaerobic conditions at 37 °C for 48 hours was used to prepare bacterial cell suspension in 2.5 ml of sterile PBS. The pre-warmed MH broth (200 ml) was inoculated with 2 ml of this bacterial suspension. The bacterial broth was incubated in anaerobic gas jars containing CampyGen pack with shaking at 180rpm at 37 ºC for 24 hours. After overnight incubation (approx $10^8$-$10^9$ cfu/ml), a time zero reading was taken for viable count after which 0.36 µl of 30% $H_2O_2$ was added to the broth to give a final concentration of 0.5 mM (calculation given below). After the addition of $H_2O_2$, samples were taken out at time intervals 20, 40, 60, 80, 100, 120 minutes of exposure which were serially diluted and cfu/ml calculated.

Calculation of $H_2O_2$ concentration

The formula used for calculating molarity of 30% $H_2O_2$ for use in hydrogen peroxide sensitivity assay is given below;

$$\text{Molarity} = \frac{\text{percentage} \times \text{density} \times 1000}{100 \times \text{Mol. weight}}$$

The molarity calculated for 30% $H_2O_2$ was 9.7 M.
For use in the hydrogen peroxide assay, a fresh stock solution of 9.7 mM $H_2O_2$ was prepared each time by diluting 30% $H_2O_2$ 1000 folds in sterile distilled water (10 µl of 30% $H_2O_2$ added to 10 ml of sterile distilled water). Required concentration of 0.5 mM was made by diluting 52 µl of 9.7 mM $H_2O_2$ stock solution in 950 µl of MH broth.

### *3.2.4 Motility assay*

The *C. jejuni* cell suspension was prepared by harvesting bacterial growth from mCCDA plates grown for 48 hours under microaerobic conditions at 37 °C in sterile PBS. The optical density at 600 nm was adjusted to approximately 1.0 for each bacterial suspension. An aliquot of 0.1 µl of this bacterial cell suspension was used to inoculate 0.4% (w/v) MH agar plates. The plates were incubated microaerobically at 37 ºC for 24 to 48 hours. After incubation the diameter of the zone of growth was measured in millimetres.

### *3.2.5 Autoagglutination assay*

The autoagglutination assay was followed as described by Golden and Acheson (2002). The autoagglutination ability of the hyperinvasive and low invasive *C. jejuni* strains was measured by harvesting the bacterial growth from 48 hours grown mCCDA plates in sterile PBS. The absorbance at 600 nm of this bacterial suspension was adjusted to approximately 1.0. Two millilitres of this bacterial suspension was transferred to sterile glass test tubes (10 x 75 mm) and incubated undisturbed at 37 ºC for 24 hours under microaerobic conditions. After incubation, 1ml of the supernatant was carefully pipetted out from the test tubes and the absorbance at 600 nm was recorded again. Autoagglutination ability was calculated as the difference between the absorbance (600 nm) measured after 24 hours and the absorbance taken at the start of incubation.

### *3.2.6 Resistance to sodium deoxycholic acid stress*

The survival ability of hyperinvasive and low invasive *C. jejuni* strains under sodium deoxycholic acid stress was measured. A stock solution (50 mg/ml) of sodium deoxycholic acid (≥ 98% purity) (Sigma-Aldrich, USA) was prepared in sterile distilled water. This stock solution was used to prepare a series of concentrations of sodium deoxycholic acid in mCCDA from 1-16 mg/ml. The *C. jejuni* suspension was prepared by harvesting growth from a 48 hour grown mCCDA plate into 2.5 ml of sterile PBS. This bacterial suspension was diluted 1000 folds in sterile PBS. Five microlitres of the diluted suspension was spotted onto mCCDA plates containing different concentrations of sodium deoxycholic acid. Plates were incubated for 48 hours at 37 ºC under microaerobic conditions. After incubation, the presence or absence of *C. jejuni* growth on each tested concentration was observed and the Minimum Inhibitory Concentration (MIC) of sodium deoxycholic acid was recorded.

### *3.2.7 Biofilm study*

*C. jejuni* grown on mCCDA plate for 48 hours under microaerobic conditions at 37 °C was used to inoculate 2.5 ml of sterile PBS. This bacterial suspension was diluted 1000 fold in MH broth. Aliquots of 150 µl of 1000 fold diluted bacterial stock suspension and MH broth only (control) were added in the allocated columns of a 96 well micro-titre plate. The plate was placed in a plastic box containing a CampyGen pack sealed with a lid and autoclave tape to ensure microaerobic conditions. The plate was incubated without shaking at 37 ºC for 2, 5 and 7 days to allow the biofilm to grow. After incubation at specified time intervals, the contents of the micro-titre plate were emptied and each well was washed twice with 200 µl of deionised water.

All inoculated wells of the micro-titre plate were stained with 200 µl of 0.01% (v/v) crystal violet dye (Biomérieux, Marcy I´Etoile, France) and left at room temperature for 15 minutes. The crystal violet dye was discarded and the plate was washed twice with deionised sterile water to remove excess dye. One hundred and fifty microliters of 70% ethanol was added to each well for 15 minutes at room temperature to solubilise the stain. The optical density of each well was read at 540 nm using a micro-titre plate reader.

Calculation of biofilm formed

The optical density reading for each well of 96 well plate was used to calculate the average $OD_{540\ nm}$ and amount of biofilm formed by it as follows, Biofilm formed = OD $_{(540\ \mathrm{nm})}$ of strain investigated (test) – OD $_{(540\ \mathrm{nm})}$ of MH broth only (control)

## 3.3 RESULTS AND DISCUSSION

The growth profile of six hyperinvasive (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and six low invasive *C. jejuni* strains (01/30, 01/32, 01/46, 01/39, 01/44, 81116) was performed. All *C. jejuni* strains were also tested for the invasion assays related stresses (atmospheric oxygen, hydrogen peroxide, motility) and other virulence related phenotypes (autoagglutination, survival in sodium deoxycholic acid stress and biofilm formation). It was determined if the hyperinvasive *C. jejuni* strains could be distinguished from the low invasive strains based on these phenotypes. Also, to find if the invasion phenotype observed for these *C. jejuni* strains was not due to the stresses encountered by them during the invasion assays.

### *3.3.1 Growth rate study of the hyperinvasive and low invasive C. jejuni strains*

The ability of *C. jejuni* strains to grow in nutrient broth (MH broth) was compared to determine if the differences observed in their invasion profile was not due to any variation in their growth rate. To achieve this, the growth profile of the hyperinvasive *C. jejuni* strains was compared with low invasive strains in MH broth overtime. A representative graph of triplicate growth experiments is shown (Figure 3.1). The readings were taken during the log phase because in invasion assays *C. jejuni* inoculums are taken from the exponential growth phase. Hu and Kopecko (1999) showed that *C. jejuni* in exponential growth phase showed maximum invasion of INT 407 cells.

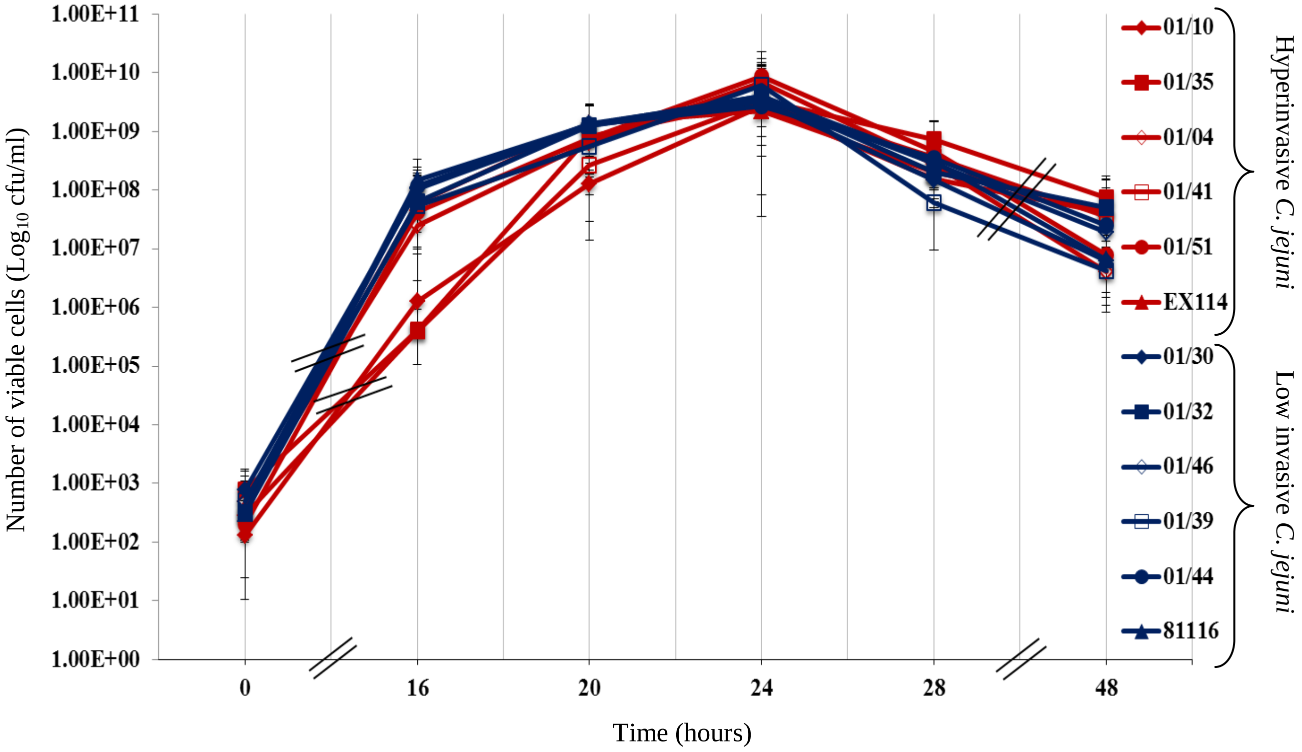


Figure 3.1: The growth curve of the hyperinvasive and the low invasive *C. jejuni* strains.

The growth rate of the hyperinvasive *C. jejuni* (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* strains (01/30, 01/32, 01/46, 01/39, 01/44, 81116) was determined in MH broth and readings were taken at different time intervals up to 48 hours and the viable count determined. The error bars represent 95% +/- CI in triplicate experiments.

It was observed from figure 3.1 that all the *C. jejuni* strains exhibited normal growth in late exponential phase under microaerobic conditions at 37 °C. The majority of *C. jejuni* strains reached $10^7$-$10^8$ cfu/ml after 16 hours of growth. Interestingly, after the same growth time the hyperinvasive *C. jejuni* 01/10, 01/35 and 01/41 showed $10^5$-$10^6$ cfu/ml. This suggests that these strains might be slow in adjusting to the growth medium compared to the other strains. This growth rate variation in early log phase is not an influencing factor to invasion as all the strains showed progressive growth up to 24 hours (~$10^9$ cfu/ml). This was followed by a rapid decline in growth up to 48 hours. Generally, the growth profile of bacteria is divided into four phases. During the initial lag phase bacteria adjust to the new environment of the growth medium which is followed by the exponential growth or log phase. The bacteria then enter into a prolonged stationary phase and finally the death phase. The *C. jejuni* strains studied here did not show a classic stationary phase. The lack of a stationary phase in *C. jejuni* strains has been reported in previous studies (Kelly *et al*., 2001).

Ideally the growth study should be performed in MHA/MHB biphasic medium as it has been used as a preferred medium in invasion assays in previous studies (Hu and Kopecko., 1999, Gaynor *et al*., 2004, Kakuda and DiRita., 2006). Recently, Javed *et al* (2010) reported that the hyperinvasive *C. jejuni* 01/51 showed same growth rate in both the MH broth and Mueller-Hinton agar/Mueller Hinton broth (MHA/MHB) biphasic medium. This suggests that the MH broth can also be used to find growth phases over time for *C. jejuni* strains for use in the invasion assay. This experiment showed that the inoculum taken from 24 hours grown *C. jejuni* cultures were suitable for use in invasion assays. Javed *et al* (2010) selected a 22 hours grown *C. jejuni* 01/51 culture in (MHA/MHB) biphasic medium for use in the invasion assay.

There was no distinct grouping of the hyperinvasive *C. jejuni* strains separate from the low invasive strains in this experiment.

### *3.3.2 Survival of the hyperinvasive and low invasive C. jejuni strains under atmospheric stress*

*C. jejuni* are microaerobic bacteria that cannot survive under normal atmospheric pressure (Luechtefeld *et al*., 1982, Ketley., 1997, Mihaljevic *et al*., 2007). Recently, Kaakoush *et al* (2007) defined *C. jejuni* as an obligate microaerophile. Cold temperature treatment and exposure to aeration are considered as the control measures for eliminating *C. jejuni* from poultry (Kelana and Griffiths., 2003). Also, during *in vitro* assays *C. jejuni* are exposed to a number of stresses. For example, during gentamicin protection invasion assay after the epithelial cell monolayers are infected with bacteria they are incubated under 5% (v/v) $CO_2$ to allow bacteria to invade cells. *C. jejuni* are exposed to the atmospheric oxygen when cell monolayers are washed with PBS and later treated with gentamicin to remove any external bacteria that have not invaded the cells. Finally, the epithelial cells are treated with a detergent, Triton-X100 to lyse the cells. All these stresses could introduce bias in invasion assays. In this study, the hyperinvasive and the low invasive *C. jejuni* strains were exposed to the atmospheric air stress for a period of upto 6 hours in MH broth with constant shaking at 180 rpm at 37

°C. A representative graph of triplicate experiments showing survival of strains under atmospheric air stress is presented in figure 3.2.

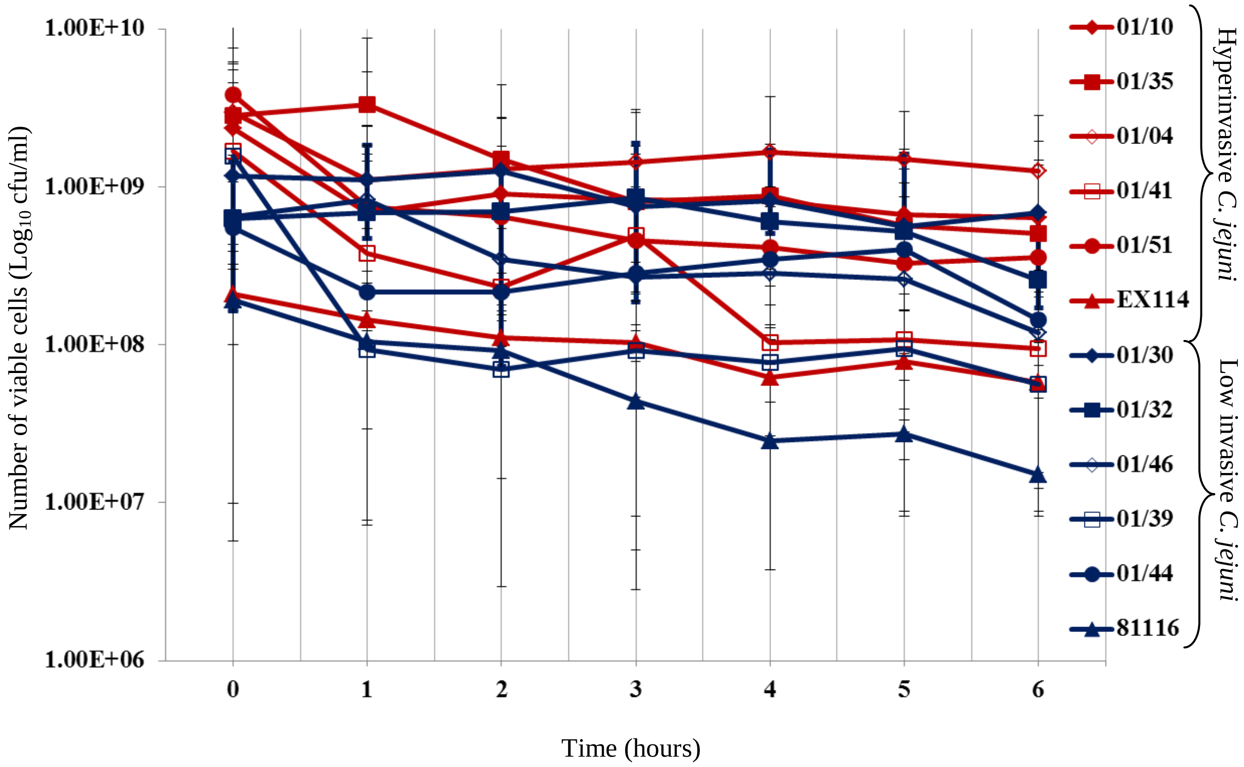


Figure 3.2: The resistance to atmospheric air stress study of hyperinvasive and low invasive *C. jejuni*.

Response of the hyperinvasive *C. jejuni* (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* strains (01/30, 01/32, 01/46, 01/39, 01/44, 81116) to aeration stress was performed by exposing the *C. jejuni*, grown cultures in MH broth, to atmospheric air and samples were taken at hourly intervals up to 6 hours and the viable cell count determined. The error bars represent 95% +/-CI in triplicate assays.

Ideally, this experiment should be performed in the tissue culture medium and 5% (v/v) $CO_2$ rather than full atmospheric to evaluate the actual effects of these conditions on bacteria during gentamicin protection assay but the aim of this study was not to use *C. jejuni* strains in invasion assays as the invasion phenotype of these strains was already characterized by Fearnley *et al* (2008). It would be interesting to assess if the hyperinvasive *C. jejuni* would behave differently from the low invasive *C. jejuni* strains in response to the normal atmospheric air. Figure 3.2 showed that both the hyperinvasive and the low invasive *C. jejuni* strains survived upto 6 hours of air exposure but showed variability in their response to air stress. However, no grouping of the hyperinvasive *C. jejuni* separate from the low invasive strains was observed based on their response pattern to atmospheric stress. After one hour of atmospheric exposure there was an initial drop in the viable cell number observed for the hyperinvasive *C. jejuni* 01/10, 01/51, 01/41 and the low invasive *C. jejuni* strain 01/39. This reduction was most prominent for *C. jejuni* 01/39 where the number of viable cells decreased by one log. This initial drop in the viable cell numbers may be the time required by these strains to adjust to the air stress and turn on their atmospheric response system. The other *C. jejuni* strains where this reduction in viable cell counts was not seen may reflect that they are more stable strains and adapt better to the atmospheric stress. The *C. jejuni* cultures grown for upto 6 hours but under microaerobic conditions would be a useful control for the aeration stress study but it was not performed.

The survival of all *C. jejuni* isolates in this study under the normal atmospheric air suggests the aerobic adaptation of *C. jejuni* strains. In a previous study, *C. jejuni* were exposed to air for 2-3 days on blood agar. After this prolonged air exposure the bacteria were sub-cultured and grew normally under air. This aerobic adaptation of *C. jejuni* was accompanied by the change in cell morphology to coccid shape and changes in the expression pattern of some outer membrane proteins suggesting that *C. jejuni* adapts to aerobic metabolism when outside the host body such as in food and farm environments (Jones *et al*., 1993). Later, Harvey and Leach (1998) also reported that *C. jejuni* avoids oxidative damage by cell surface changes as reflected in the coccal cell morphology. Another study investigated the use of aeration stress as a control measure for reducing the number of *C. jejuni* in poultry semen (Cole *et al*., 2004b). Cole *et al* (2004b) reported that aeration was unable to reduce *C. jejuni* from poultry semen samples suggesting that they survived in air. *C. jejuni* cultures grown in MH broth for 24 hours with the maximum cell density of $10^{8-}10^{9}$ cfu/ml were selected for this aeration stress study. The high bacterial cell density might facilitate microaerophilic bacteria to withstand the aeration stress. In addition, in the liquid bacteriological media the solubility of oxygen is relatively low with nutrient rich conditions that might provide favourable conditions for the bacteria to survive. *C. jejuni* strains have been reported previously to show marked resistance when exposed to air in high cell densities (Kelly., 2005, Mohammad *et al*., 2005, Kaakoush *et al*., 2007) and in liquid growth media (Mohammad *et al*., 2005).

### *3.3.3 Sensitivity to hydrogen peroxide ($H_2O_2$) of hyperinvasive and low invasive C. jejuni strains*

Inside the eukaryotic cells, *C. jejuni* are exposed to the reactive oxygen species released as bi-products of aerobic respiration such as superoxides and hydrogen peroxide. Hydrogen peroxide acts as a bactericidal agent reacting with reduced iron, products of the nitric oxide synthase activity, to form toxic intermediates including hypochlorous ions, hydroxyl radicals, hydroxide anions and nitrogen dioxide (Day *et al*., 2000).

The hyperinvasive and the low invasive *C. jejuni* strains were tested to determine if the two groups of strains showed same level of response to hydrogen peroxide stress. *C. jejuni* strains were exposed to 0.5 mM hydrogen peroxide solution in MH broth and the number of surviving bacteria was determined every 20 minutes for up to 120 minutes. All the *C. jejuni* strains survived exposure to 0.5 mM hydrogen peroxide with viable cells recovered after 120 minutes exposure. A representative graph of triplicate experiments showing response of each strain to 0.5 mM hydrogen peroxide is plotted (Figure 3.3). The low invasive *C. jejuni* 01/39, however, showed a 6 log reduction in viable cell count after 120 minutes which suggest that this strain was relatively sensitive to 0.5 mM $H_2O_2$ stress. There was no grouping of the hyperinvasive separating them from the low invasive *C. jejuni* strains based on their response to 0.5 mM $H_2O_2$.

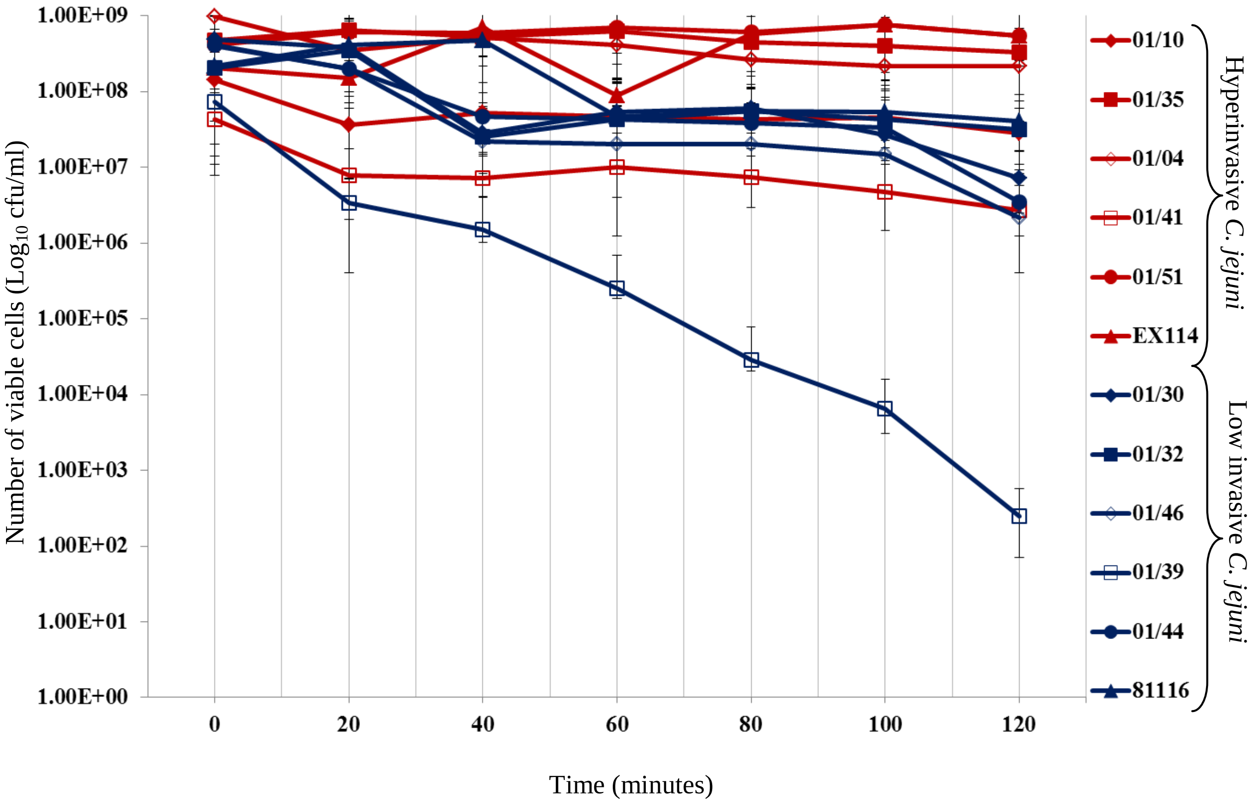


Figure 3.3: The sensitivity to hydrogen peroxide study of the hyperinvasive and the low invasive *C. jejuni* strains.

The hyperinvasive (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* (01/30, 01/32, 01/46, 01/39, 01/44, 81116) strains were grown for 24 hours in MH broth and exposed to 0.5 mM $H_2O_2$. The samples were taken at different time intervals up to 120 minutes for viable counts and the response of hyperinvasive and low invasive *C. jejuni* strains to 0.5 mM hydrogen peroxide was studied. The error bars represent 95% +/-CI in triplicate assays.

In a previous report, the *C. jejuni* strains were reported as resistant to 1 mM hydrogen peroxide over a sixty minutes exposure period which is in agreement with our results (Day *et al.*, 2000). This resistance was attributed to the protective activity of catalase which is encoded by the *katA* gene (van Vliet *et al.*, 1999, Day *et al.*, 2000). The *C. jejuni* strains with catalase activity degraded $H_2O_2$ allowing them to survive the oxygen burst inside macrophages (Day *et al.*, 2000). An ankyrin containing protein, Cj1386 (Flint *et al.*, 2012) located downstream to KatA regulon allows intracellular survival of *C. jejuni* by trafflicking heme to catalase. All the hyperinvasive and low invasive *C. jejuni* strains used in this study were tested for the catalase activity. Catalase test was performed by dipping a small bacterial colony on a plastic loop into 30% $H_2O_2$

solution and the release of bubbles showed catalase activity. All the *C. jejuni* strains were positive for catalase activity including *C. jejuni* 01/39 which showed a dramatic reduction in viable cells when exposed to 0.5 mM $H_2O_2$ for 120 minutes. This suggests that the relative sensitivity of *C. jejuni* 01/39 to $H_2O_2$ may be related to the oxygen stress response systems in *C. jejuni* other than catalase. Iron dismutase reductases (SodB*)* in *C. jejuni* have been reported to provide oxygen resistance (Pesci *et al*., 1994) that allowed intracellular survival of *C. jejuni* in INT407 cell lines. Baillon *et al* (1999) reported an iron containing hydroperoxide reductase (AhpC) that provides aerotolerance and resistance to oxidative stress in *C. jejuni*. Studies by Ishikawa *et al* (2003) demonstrated the activity of an iron based protein (Dps) that confers resistance to *C. jejuni* against the toxic effects of hydrogen peroxide by scavenging free iron particles present inside cells. In contrast, Velayudhan *et al* (2004) and Wainwright *et al* (2005) have attributed the strict microaerophilic nature of *C. jejuni* to the presence of active oxygen sensitive enzymes in *C. jejuni* such as L-serine dehydratase and rubredoxin oxidoreductase.

### *3.3.4 Motility profile of hyperinvasive and low invasive C. jejuni strains*

The flagellar motility in *C. jejuni* has been proved as a key virulence factor involved *in vivo* invasion of the human intestinal cell line models (Morooka *et al*., 1985, Grant *et al*., 1993, Guerry., 2007). Motility is responsible for the invasion and internalisation of *C. jejuni* (Grant *et al*., 1993) but not the only factor required for *C. jejuni* pathogenesis (Wassenaar *et al*., 1991). The motility profile of the hyperinvasive and low invasive *C. jejuni* strains was tested to determine if the reduced invasion potential of the low invasive *C. jejuni* strains (Fearnley *et al*., 2008) was due to the reduced motility of these strains. The *C. jejuni* strains showed a lot of variability in motility profile when observed after 48 hours of microaerobic incubation at 37 °C (Figure 3.4).

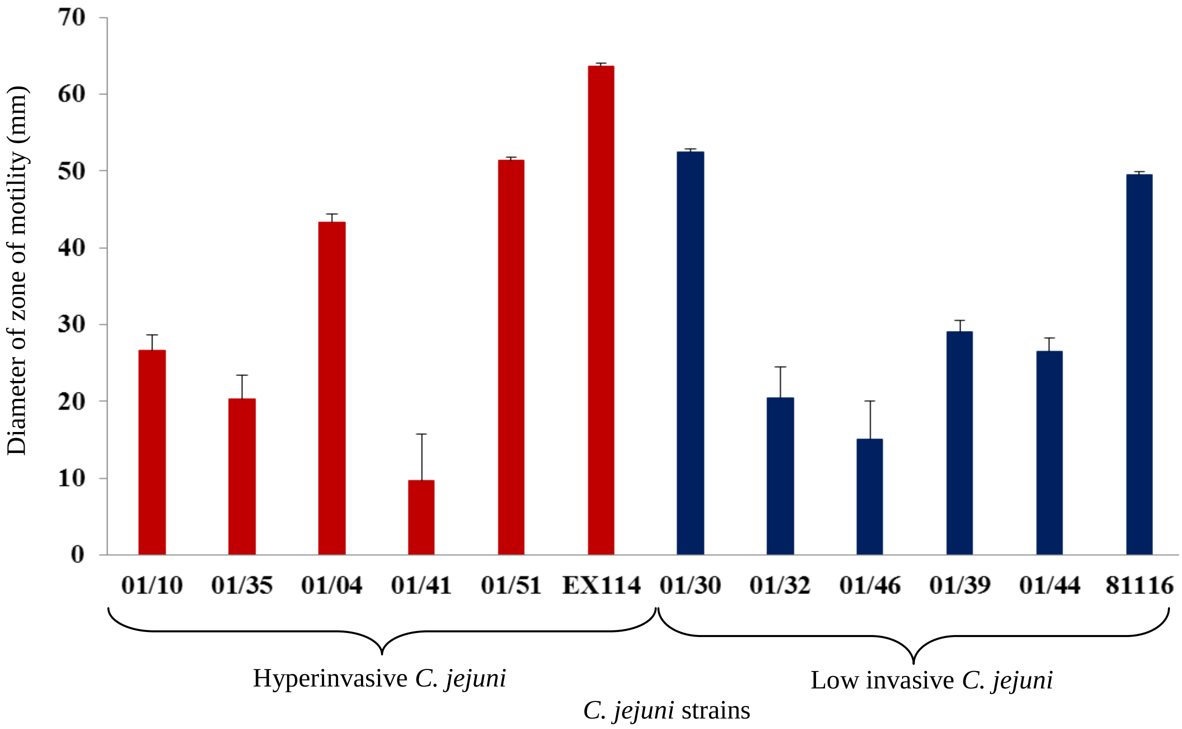


Figure 3.4: The comparison of motility zones (millimeters) for the hyperinvasive and low invasive *C. jejuni* strains measured after 48 hours of microaerobic incubation at 37°C.

The motility profile of the hyperinvasive *C. jejuni* (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* (01/30, 01/32, 01/46, 01/39, 01/44, 81116) was measured as the growth zone diameters in millimetres after 48 hours of microaerobic incubation. The error bars indicate 95% CI in triplicate experiments.

Among the hyperinvasive *C. jejuni* strains, EX114 was most motile followed by *C. jejuni* 01/51 and 01/04 whereas 01/41 showed lowest motility. Within the low invasive *C. jejuni* strains, 01/30 and 81116 displayed highest motility while 01/46 had reduced motility. In addition, there was no clear grouping of the hyperinvasive *C. jejuni* strains as a distinct group based on the motility phenotype. Fearnley *et al*., 2008 tested motility for the hyperinvasive *C. jejuni* EX114 and the low invasive 81116 using semi-solid media. Both strains showed a diameter of growth zones varying between 50-58 mm and were classed as fully motile. The average diameter of growth zones recorded in our study for *C. jejuni* EX114 and 81116 was 64 mm and 50 mm respectively which is very similar to those reported by Fearnley *et al* (2008).

### *3.3.5 Autoagglutination activity of hyperinvasive and low invasive C. jejuni strains*

The autoagglutination (AAG) activity has been recognised as a key virulence factor responsible for the host cell interaction in many Gram negative pathogenic bacteria (Misawa and Blaser., 2000) particularly in the *C. jejuni* closely related bacteria *Helicobacter pylori* (Cole *et al*., 2004a). Autoagglutination activity in *C. jejuni* has also been reported in the literature (Golden and Acheson., 2002, Misawa and Blaser., 2000, Guerry *et al*., 2006). In this study, most of the *C. jejuni* strains autoagglutinated (AAG) after undisturbed microaerobic incubation at 37 °C for 24 hours except for the low the invasive *C. jejuni* strains 01/39 and 81116 (Figure 3.5). The AAG activity of the low invasive *C. jejuni* 01/39 and 81116 was significantly lower ($p$=0.000384 and 0.000689 respectively) when compared against the low invasive *C. jejuni* 01/46 which showed highest autoagglutination activity in this study. However, there was no grouping of the hyperinvasive *C. jejuni* strains based on AAG phenotype.

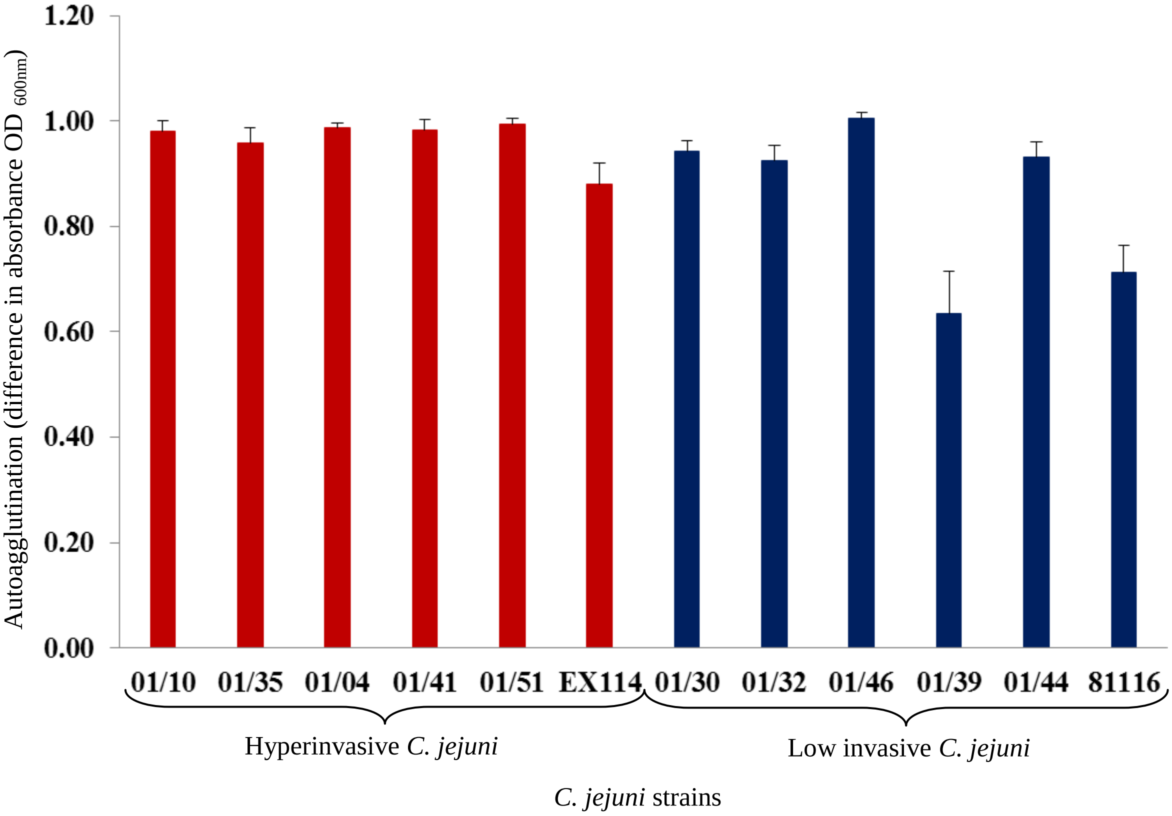


Figure 3.5: The autoagglutination ability of the hyperinvasive and the low invasive *C. jejuni* strains.

The ability to autoagglutinate in the hyperinvasive *C. jejuni* (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* strains (01/30, 01/32, 01/46, 01/39, 01/44, 81116) was determined by measuring the difference in absorbance at $OD_{600nm}$ of *C. jejuni* cultures incubated overnight at 37 °C. The error bars show 95% CI in triplicate experiments. The statistical significance was calculated by using the Student's T-test ($p$=0.001) (Microsoft$^{®}$ Excel 2010).

The autoagglutination (AAG) characteristic of *C. jejuni* strains has been found to have an essential role in bacterial adherence to INT407 cell lines, hence linked to *C. jejuni* virulence (Misawa and Blaser., 2000). Misawa and Blaser (2000) and Guerry (2007) also reported that intact flagella were required for autoagglutination in *C. jejuni* and the aflagellate mutants of *C. jejuni* lack autoagglutination ability. In this study, the hyperinvasive *C. jejuni* 01/41 showed reduced motility (Figure 3.4) but retained high levels of autoagglutination (Figure 3.5). A similar trend was observed for the hyperinvasive *C. jejuni* 01/35, and the low invasive *C. jejuni* strains 01/32 and 01/46. By contrast, the hyperinvasive *C. jejuni* (01/51 and EX114) and the low invasive *C. jejuni* strain 01/30 showed high motility profile (figure 3.4) and high AAG activity.

The low invasive *C. jejuni* strain 81116 was fully motile but displayed lower level of AAG activity. This suggests that the findings of Misawa and Blaser (2000) and Guerry (2007) could not be truly compared with the autoagglutination and motility experiment results recorded in this study.

### *3.3.6 Survival of the hyperinvasive and the low invasive C. jejuni strains under sodium deoxycholic acid stress*

Enteric pathogens are exposed to a number of antimicrobial agents in the intestine including bile salts and gastric acid. *C. jejuni* have been found to be resistant against the damaging effects of bile salts (Raphael *et al*., 2005). The sensitivity of the hyperinvasive and low invasive *C. jejuni* strains to bile salts was tested at a range of concentrations from 16 mg/ml to 1 mg/ml of sodium deoxycholic acid. All the hyperinvasive and low invasive *C. jejuni* isolates studied exhibited similar levels of resistance to sodium deoxycholic acid with all strains showing Minimum Inhibitory Concentration (MIC) at 7.5 mg/ml except for the hyperinvasive *C. jejuni* 01/04 that showed inhibition at a lower concentration of 2 mg/ml (Table 3.1). There was no grouping of the hyperinvasive *C. jejuni* separate from the low invasive *C. jejuni* strains based on their response to sodium deoxycholic acid stress.

| ***C. jejuni* strain** | **Invasion profile** | **Threshold inhibitory sodium deoxycholic acid concentration (mg/ml) n=3** |
|---|---|---|
| 01_10 | Hyperinvasive | 7.5 |
| 01_35 | | 7.5 |
| 01_04 | | 2 |
| 01_41 | | 7.5 |
| 01_51 | | 7.5 |
| EX114 | | 7.5 |
| 01_30 | Low invasive | 7.5 |
| 01_32 | | 7.5 |
| 01_46 | | 7.5 |
| 01_39 | | 7.5 |
| 01_44 | | 7.5 |
| 81116 | | 7.5 |

Table 3.1: The Minimum Inhibitory Concentration (MIC) of sodium deoxycholic acid for *C. jejuni* isolates.

The response of hyperinvasive (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* (01/30, 01/32, 01/46, 01/39, 01/44, 81116) strains to the sodium deoxycholic acid stress was investigated. The concentrations of sodium deoxycholic acid tested ranged between 16 mg/ml to 1 mg/ml. The assay was performed in triplicate.

All the *C. jejuni* strains used in our study were human clinical isolates except the hyperinvasive *C. jejuni* EX114 (Table 2.1) which is an environmental isolate. A previous study reported that the clinical *C. jejuni* isolates were more resistant to sodium deoxycholate stress than the poultry isolates. The clinical *C. jejuni* isolates survived under a much higher concentration (16 mg/ml) of sodium deoxycholate (Van Deun *et al*., 2007). In contract, our study showed that the human clinical *C. jejuni* isolates were more sensitive at a much lower concentration of sodium deoxyxholic acid. This suggests that the response of *C. jejuni* strains to bile salts in the human intestine is not dependant on source of strain isolation. Also, the growth of majority of *C. jejuni* strains was inhibited at the same sodium deoxycholic acid concentration showing that this phenotype does not influence invasion.

### *3.3.7 Biofilm formation in the hyperinvasive and low invasive C. jejuni*

A bacterial biofilm is a stable and complex structure formed on a living or non-living surface with different cohesive forces strengthened by exopolysaccharides (EPS) (Shirtliff *et al*., 2002, Dunne., 2002). The first step in biofilm formation is the "primary adhesion" of bacteria to any surface (biotic or abiotic). The primary adhesion is a reversible attachment of bacteria to a surface that requires the surface to be suitable for bacterial attachment and growth termed "surface conditioning". The final step in biofilm formation called "secondary adhesion" which is the anchoring or irreversible locking phase of bacterial attachment to the surface. As the stage of secondary adhesion progresses, other planktonic microorganisms and materials in the surrounding environment can also stick to surface bound bacteria forming an aggregate on the substratum. Once the process of irreversible attachment of bacteria completes the overall density and complexity of the bacterial community may start to increase forming mature biofilm. At some point, when the biofilm reaches a critical mass, a dynamic equilibrium is reached at which the cells in closest contact with the surface closest to the substratum begin to die due to the lack of nutrients or perfusion, pH changes, oxygen or an accumulation of a toxic by-product (Shirtliff *et al*., 2002).

The biofilm formation in *C. jejuni* has been reported (Joshua *et al*., 2006, Kalmokoff *et al*., 2006, Reeser *et al*., 2007). Joshua *et al* (2006) reported three forms of biofilm formed by *C. jejuni* in liquid media *i.e.* attachment to the glass surfaces, unattached clumps (flocs) formation, pellicle formation at the liquid gas interface. *C. jejuni* biofilm formation on a variety of other abiotic surfaces such as polyvinyl chloride plastic, acrylonitrile butadiene etc has also been shown (Resser *et al*., 2007). The biofilm mode of life provides resistance to bacteria under stress conditions such as the antimicrobial agents, oxygen and nutritional pressures (Joshua *et al*., 2006, Kalmokoff *et al*., 2006). Motility (Joshua *et al*., 2006, Kalmokoff *et al*., 2006, Reeser *et al*., 2007) and quorum sensing (Reeser *et al*., 2007) influenced biofilm phenotype in *C. jejuni*. The molecular analysis of *C. jejuni* biofilm revealed upregulation of genes responsible for stress control, protein synthesis, catabolism and energy generation (Kalmokoff *et al*., 2006).

In this study, the hyperinvasive and low invasive *C. jejuni* strains were allowed to form biofilm in 96 well plastic tissue culture plates undisturbed under microaerobic conditions at 37 °C and the amount of biofilm formed was studied at different time intervals (Figure 3.6). The biofilm formation potential of the hyperinvasive and the low invasive *C. jejuni* strains was very variable with no grouping of the hyperinvasive *C. jejuni* strains separate from the low invasive *C. jejuni* strains.

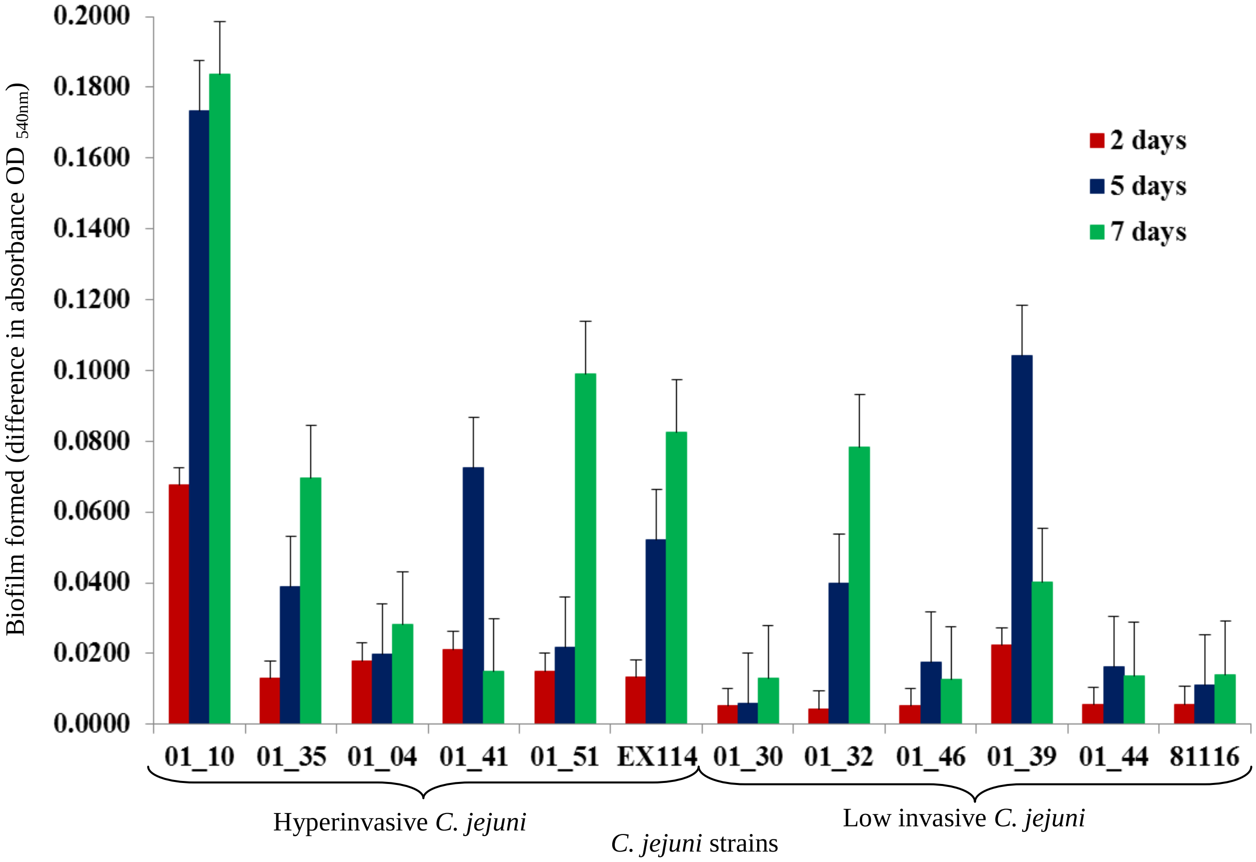


Figure 3.6: The percentage (%) mean biofilm formation of hyperinvasive and low invasive *C. jejuni* isolates at different time intervals.

The biofilm formation ability of the hyperinvasive (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and low invasive *C. jejuni* strains (01/30, 01/32, 01/46, 01/39, 01/44, 81116) was investigated. The error bars indicate 95% CI in triplicate experiments.

After 2 days of static microaerobic incubation at 37 °C the hyperinvasive *C. jejuni* 01/10 was the only strain which formed a lot of biofilm while the other strains showed only very low levels of biofilm formation. This suggests that the majority of *C. jejuni* strains were in early stages of biofilm development after 2 days. The biofilm formation progressed for all *C. jejuni* strains to 5 days of undisturbed microaerobic incubation. The low invasive *C. jejuni* 01/39 showed the highest increase in the amount of biofilm formed followed by *C. jejuni* 01/10 and *C. jejuni* 01/41 compared to other strains after 5 days period.

There was no link between the motility phenotype (Joshua *et al*., 2006, Kalmokoff *et al*., 2006, Reeser *et al*., 2007) and the amount of biofilm formed in our study as *C. jejuni* 01/41 showed remarkably reduced motility (Figure 3.4) but still formed biofilm.

Similarly, *C. jejuni* 01/10 and *C. jejuni* 01/39 were only moderately motile but showed high amount of biofilm formed. After 7 days of microaerobic incubation, 4 out of 12 *C. jejuni* strains (01/41, 01/46, 01/39, 01/44) showed a decrease in the amount of biofilm whereas the rest of strains continued to form biofilm. This might suggest that the bacterial cells reached dynamic equilibrium in the mature biofilm (Shirtliff *et al*., 2002) and began to die and detached themselves which was evident by the decrease in the amount of biofilm formed for some *C. jejuni* strains. Also, this experiment suggested that the *C. jejuni* strains achieved biofilm maturity at different times.

## 3.4 CONCLUSIONS AND FUTURE WORK

The hyperinvasive and the selected low invasive *C. jejuni* strains were tested in the invasion assays related stress factors (response to atmospheric air, $H_2O_2$ and motility) and the other virulence related phenotypes (autoagglutination, sodium deoxycholic acid stress and biofilm formation). All the *C. jejuni* investigated survived the atmospheric air and $H_2O_2$ stress. All the *C. jejuni* strains showed high level of variability in their motility and there was no distinct grouping of the hyperinvasive *C. jejuni* separate from the low invasive *C. jejuni* strains based on these phenotypes. All the *C. jejuni* strains showed variable autoagglutination activity, sodium deoxycholic acid stress response and biofilm formation ability. In addition, the hyperinvasive *C. jejuni* could not be distinguished from the low invasive group of *C. jejuni* strains based on any of the virulence phenotypes tested.

It seems therefore that this group of strains share only the hyperinvasive phenotype and it was hypothesised that the difference in invasion potential between the hyperinvasive and the low invasive *C. jejuni* strains reported by Fearnley *et al* (2008) might be due to the differences at their genome level. Therefore, as the next step in this project the six hyperinvasive *C. jejuni* strains were compared with a selected group of the low invasive *C. jejuni* strains using comparative genomic hybridization (CGH). Some future work may also involve actually investigating the mechanism of *C. jejuni* uptake and survival within the host cells.

## *Chapter Four*

# GENOTYPING OF THE HYPERINVASIVE *C. JEJUNI* STRAINS BY COMPARATIVE GENOMIC HYBRIDIZATION (CGH)

# GENOTYPING OF THE HYPERINVASIVE *C. JEJUNI* STRAINS BY COMPARATIVE GENOMIC HYBRIDIZATION (CGH)

## 4.1 INTRODUCTION

The previously defined group of six clinical hyperinvasive *C. jejuni* strains with the hyperinvasive phenotype were compared at the genome level using DNA microarray with four low invasive clinical *C. jejuni*. This comparative phylogenomics study was performed to find whether the hyperinvasive *C. jejuni* strains form a cluster separate from the low invasive strains based on their genomic content as well as to identify any genomic regions conserved or variable between the two groups.

### *4.1.1 Comparative Genomic Hybridization as a tool to study phylogeny and diversity*

Comparative Genomic Hybridization (CGH) is a DNA microarray based technique used to compare a test genome with a control genome, affixed on a microscopic slide-sized glass support, to find genomic content present or absent in the test genome. Comparative genomics using DNA microarrays have been used to study relatedness and differences between different bacterial populations and some examples are discussed below. CGH has been used to study genomic content differences between 42 isolates of *Helicobacter pylori* causing a number of chronic conditions in humans including peptic ulcer, gastric cancer or gastritis and other complex diseases that are linked to virulence gene clusters including the cag pathogenicity island (PAI). This study identified genes uniquely associated with gastroduodenal diseases. One thousand and nineteen genes were found to be present in all isolates, with 341 genes being variable. The most variable genes linked with gastritis, duodenal ulcer, or gastric cancers were present in Pathogenicity Zones (PZs) and the cag PAI. (Romo-Gonzalez *et al*., 2009).

In another study, CGH was used to find genomic diversity amongst *Cronobacter* species including *C. sakazakii, C. malonaticus* and *C. turicensis*. This study identified *Cronobacter* species specific genes and genes related to *Cronobacter* isolates from outbreaks in neonatal intensive care units. Genes associated with copper and silver resistance, those encoding for multidrug efflux pumps and many adhesins were reported

(Kucerova *et al*., 2010). This study used the GACK algorithm, trinary cut off for determining present and divergent genes (Kim *et al*., 2002) and phylogenomic analysis was performed by using "Cluster" software (Eisen *et al*., 1998). Interstrain genomic polymorphisms associated with *P. gingivalis* were investigated by comparing the known invasive *P. gingivalis* strain to the non-invasive *P. gingivalis* strain by DNA microarray. Several accessory genes with functions encoding for lipoproteins, capsular biosynthesis, regulatory and immunoreactive proteins, and transport of metabolites were divergent in the non-invasive strain suggesting that gene loss was indicative of the *P. gingivalis* non-invasive phenotype (Dolgilevich *et al*., 2011).

DNA microarrays have been used to study phylogeny and genetic diversity of *C. jejuni* strains based on host association, disease profile and virulence related phenotypes (Quiñones *et al*., 2008, Parker *et al*., 2006, Champion *et al*., 2005, Pearson *et al*., 2003, Dorrell *et al*., 2001). *C. jejuni* strains with a variety of Penner serotypes were studied using CGH to define the structure of the *C. jejuni* genome and to find genomic similarities between them (Dorrell *et al*., 2001). DNA microarrays separated the functional core comprising essential genes from the dispensable genes that make up the accessory genome. This study found 1,300 out of 1,654 genes were part of the core genome and at least 21% of the genes were dispensable as they were missing in one or more of the strains studied. The conserved genes mainly encoded for metabolism, cellular, regulatory and biosynthetic processes. The accessory genome was dominated by virulence related genes including flagellar modification genes, lipo-oligosaccharide and capsule encoding genes. CGH data did not cluster strains based on the Penner serotypes suggesting that the genome similarity between strains from the same serotype may not be enough to cluster them together (Dorrell *et al*., 2001).

Another study, investigated the genomic diversity in 18 *C. jejuni* strains isolated from a variety of sources (Pearson *et al*., 2003). This study identified 7 regions of immense variability between the strains studied which were called the plasticity regions (PRs). PR1 to PR7 made up 50% of the variable genome content of the strains. PR1 consisted of genes required for using alternative electron acceptors for respiration that may provide a selective advantage to strains in oxygen depleted conditions. PR2, PR3, and PR7 were dominated by genes encoding outer membrane and periplasmic proteins and many hypothetical genes with putative functions that may explain the phenotypic variation and survival of strains in different environments. PR4, PR5, and PR6 contained genes involved in the synthesis part of the flagellin glycosylation locus. Pearson *et al* (2003) defined a dynamic cut off algorithm similar to the GACK matrix (Kim *et al*., 2002) to determine present or divergent genes.

Due to the highly diverse nature of the *C. jejuni* genome and the advantage of CGH in the absence of genome sequencing the use of CGH as a genomotyping tool did expand. A large scale CGH study exploited a collection of CGH data from three previous small scale *C. jejuni* microarray studies (Leonard *et al*., 2004, Pearson *et al*.,2003, Dorrell *et al*., 2001) and integrated it with additional DNA microarray analysis performed on 51 *C. jejuni* strains isolated from food and clinical sources (Taboada *et al*., 2004). This CGH meta-analysis of 97 *C. jejuni* strains showed that the newly investigated *C. jejuni* strains contain the majority of the genes which were reported as part of the accessory gene pool in previous studies, suggesting that the *C. jejuni* core genome was expanding (Taboada *et al*., 2004).

Another study used DNA microarrays to investigate the GBS and enteritis associated *C. jejuni* isolates with an aim to identify genetic markers of GBS. However, this study could not identify any GBS specific genetic markers (Leonard *et al*., 2004). A shot gun DNA microarray technique comparing sequenced *C. jejuni* NCTC11168 with the, at that time unsequenced *C. jejuni* 81-176 genome, identified several *C. jejuni* 81-176 specific genes that were dispersed in conserved and accessory parts of the genome (Poly *et al*., 2005).

A comparative phylogenomics study combined with Bayesian-based statistical analysis was used to study phylogeny of *C. jejuni* strains from humans, chicken, bovines, ovines and the environment. Out of 111 *C. jejuni* isolates studied, 70 strains were isolated form patients with gastroenteritis, septicaemia, GBS and from asymptomatic carriers. The aim of this study was to find if strains clustered together based on host sources and disease severity in human hosts. The Bayesian analysis revealed two distinct clades a “livestock” clade and a “nonlivestock” clade with further clusters of environmental isolates (Champion *et al*., 2005). Interestingly, the majority of the human isolates were part of the nonlivestock clade proposing that most *C. jejuni* infections came from nonlivestock sources. Several genes (Cj1321 to Cj1326) within the flagellin glycosylation locus were associated with strains in the livestock cluster (Champion *et al*., 2005).

The genomic diversity in a collection of *C. jejuni* and *C. coli* strains from clinical and veterinary sources was investigated using a *C. jejuni* RM1221 and *C. jejuni* NCTC11168 pan array (Parker *et al*., 2006). The *C. jejuni* and *C. coli* populations investigated showed genomic diversity in four *C. jejuni* RM1221 integrated mobile genomic islands (CJIEs). An additional 18 regions of diversity were also identified containing lipooligosaccharide and capsule biosynthesis genes (Parker *et al*., 2006). Later, Parker *et al*., (2007) used CGH to study genomic diversity at the *C. jejuni* subspecies level. The *C. jejuni* subsp. *jejuni* and *C. jejuni* subsp. *doylei* formed separate clusters and showed immense genomic diversity between them based on the two techniques used. *C. jejuni* subsp. *doylei* unique gene clusters mainly related to metabolism, transport and pathogenesis were identified that were absent from *C. jejuni* subsp. *jejuni* (Parker *et al*., 2007).

A 70-mer oligonucleotide array was used to find similarities and differences between closely related (based on similar PFGE profile) chicken and human clinical isolates. CGH grouped isolates in the same way as defined by PFGE. Also, the chicken and human clinical C. *jejuni* isolates did not cluster according to source by CGH (Rodin *et al*., 2008).

*C. jejuni* clinical strains with different disease severities were compared using DNA microarrays to see if gene markers associated with different disease outcomes could be identified. It was shown that *C. jejuni* strains from patients with neurological disorders like Guillain Barré syndrome and Miller Fisher syndromes clustered separately from enteritis associated *C. jejuni* isolates (Quinones *et al*., 2008). Large mobile genetic islands mainly characterized by prophage genes were dominant in strains causing neuropathies (Quinones *et al*., 2008). Recently, DNA microarray analysis was used to study the role of genetic diversity in the disease profile of three *C. jejuni* human disease isolates (11168, 33292 and 81-176) and genetically marked variants of these strains. The data showed immense genetic variability in three gene clusters associated with the synthesis and modification of capsule, flagella and lipooligosaccharide (Wilson *et al*., 2010).

CGH was used to study population dynamics of *C. coli* strains from poultry, environment and human clinical cases. *C. coli* isolated from diverse sources clustered based on the host species and CGH identified host associated genes showing host adaptation. The clustering of *C. coli* strains from diverse sources was attributed to origin from a common ancestor and molecular events like lateral gene transfer (Lang *et al*., 2010).

Another CGH study was performed on 80 *C. jejuni* isolates from diverse sources representing a variety of clonal complexes to show the association of clonal complexes with isolation source. This study identified a clade of water/wildlife associated *C. jejuni* strains separate from the human food chain isolates. Nine regions of divergence were found unique to this clade of strains suggesting a trend towards niche adaptation. These gene clusters were part of the accessory genome and included the virulence related cytolethal distending toxin (*cdt*) genes (Hepworth *et al*., 2011).

All above studies signify the importance of DNA microarray as a powerful molecular tool to study phylogeny and diversity between *C. jejuni* strains. The strains have been distinguished based on disease profile and transmission source at the sub-species level. Most studies reported that the flagellar modification genes, capsule biosynthesis loci, and LOS were the most variable regions. Here, we have used CGH to compare six hyperinvasive *C. jejuni* strains with four low invasive *C. jejuni* identified by Fearnley *et al* (2008).

The aim of this study was to:

(i) Determine the phylogenomic relationship between hyperinvasive and low invasive *C. jejuni* strains at the whole genome level using hierarchical clustering of CGH data.

(ii) Identify gene/gene clusters specific to the hyperinvasive *C. jejuni* that may distinguish them from low invasive *C. jejuni* and explain the hyperinvasive phenotype of this unique group of hyperinvasive *C. jejuni*.

## 4.2 METHODS

### *4.2.1 Microarray design and construction*

The *C. jejuni/C. coli* pan array used here was designed based on 1884 annotated coding sequences (CDSs) from the fully genome sequenced *C. jejuni* RM1221, additional CDSs from *C. jejuni* NCTC11168 and *C. jejuni* 81-176. Genes unique to *C. coli* RM2228, ORFs from the *C. jejuni* 81-176 pTet plasmid and *C. coli* pCC31 plasmid were also represented on the array. This represented a total of 2,628 annotated CDSs on the pan array. The pan array was constructed as described elsewhere (John *et al*., 2011).

### *4.2.2 Enzymatic labelling of genomic DNA with Cy3 dCTP and Cy5 dCTP and hybridization*

Three micrograms of the control (*C. jejuni* RM1221) and test genomic DNA (Hyperinvasive/low invasive *C. jejuni*) was prepared as described in section 2.6.1. The reference and test genomic DNA was enzymatically labelled with fluorescent dyes Cy5-dCTP and Cy3-dCTP (Amersham, GE healthcare) respectively by following the protocol described in detail by Dorrell *et al* (2001). A brief protocol is given below;

- One microgram of the genomic DNA from test *C. jejuni* strain was mixed with the random primers (Promega, UK) at a concentration of 3 µg/µl and volume was made up to 41.5 µl with sterile distilled water in a PCR tube.
- The reaction mix was heated at 95 °C in thermocycler for 5 minutes and then snap cooled on ice.
- Five microliters of 10X buffer (part of random primers, Promega, UK), 5 µl of dNTP mix (5 mM each dATP, dGTP And dTTP, 2 nm dCTP, Sigma-Aldrich, UK), 1.5 µl of Cy3-dCTP (25 nmol) (Amersham, GE healthcare; catalogue number PA55021) and 1 µl of DNA polymerase I large klenow fragment, exonuclease minus (Promega, UK; catalogue no; M2181) were added to the above reaction mix.
- The labelling reaction mix was incubated at 37 °C for 90 minutes.
- The above procedure was carried out for the labelling of reference *C. jejuni* genomic DNA (section 2.5) replacing Cy3-dCTP with Cy5-dCTP (25 nmol) (Amersham, GE healthcare; catalogue number PA53021).

#### *4.2.2.1 Hybridization*

Each enzymatic labelling reaction was purified using MinElute PCR purification kit (Qiagen, Crawley, UK) as stated in the kit's instruction manual. Each labelled test and control genomic DNA was mixed together in a maximum reaction volume of 4.5 µl (0.5 µg of genomic DNA concentration). The hybridization was carried out at the University of Nottingham, post genomics facility at the Queen's Medical Centre (Nottingham, UK). The hybridization procedure was followed as detail in detail previously (John *et al*., 2011). Each array image was obtained as a .gps file and the layout of oligonucleotides on the array was presented as .gal file.

### *4.2.3 Tools for CGH data analysis and hierarchical clustering*

Each microarray image was analysed using Gene pix pro 6 software (Molecular Devices Corporation, Sunnyvale, CA). Any anomalous spots with low signal intensities or too high or low background noise on the array were identified. Gene pix pro 6 computed several ratio quantities each of which contained different information for each spot on the array. Among these, an important parameter called the "$\log_2$ratio" for each spot was calculated. $\mathrm{Log}_2$ratio is the base two logarithm of ratio of median intensities *i.e.* $\log_2$ratio of median intensity at 532 nm (Cy3-test strain)/ ratio of median intensity at 635 nm (Cy5-reference strain). The ratio of medians is the ratio of the background subtracted median pixel intensity at the second wavelength (532 nm) to the background subtracted median pixel intensity at the first wavelength (635 nm). The log base two transform is a simple and quicker way of presenting differences between two conditions (for example, present and absent/divergent genes in this study). The data for each spot on the array was corrected by normalization by using the global normalization method in which the image and result were normalized together. By default, the mean of the ratio of medians used for normalization was set to 1.0. This deleted any ratio values less than 0.1 or greater than 10 as well as any spots that were flagged as bad spots. The results for each complete image were generated as Gene pix results (.gpr) file. This file contained general information about the image acquisition and analysis as well as the numerical data generated from each spot on the array (Molecular Devices Corporation, Sunnyvale, CA). The numerical data in .gps file was converted into text delimited (.dat) file and imported into the statistical software, SPSS 17.0 (IBM SPSS Statistics, IBM

Corporation). This program was used for further data rearrangement and to check the smoothness of the array data by plotting histograms. All the unnormalized bad spots were removed from data. Furthermore, any control spots on the array were checked to confirm the successful hybridization and image analysis. Finally, a file (.SPSS) which only contained unique oligo IDs, gene name and $\log_2$ratios for all the normalized and perfect spots was generated. This file was converted into a text delimited file (.dat) for use in “GACK” software (Kim *et al*., 2002) which assigned genes into present and absent/divergent categories. The GACK analysis program selected a dynamic cut off value based on shape of the signal strength for each spot to be classified as present or divergent (Kim *et al*., 2002). This was done by calculating the Estimated Probability of Presence (EPP) value for each spot on the array based on its $\log_2$ratio. GACK calculated EPP by dividing the normal (expected) distribution curve $\log_2$ratio values where all the spots on the array have worked against the actual (observed) $\log_2$ratio distribution values for all spots on the array.

$$\%\text{EPP}=100\text{x (normal expected value/observed value)}$$

The trinary cut off method was used at a %EPP cut off 1 set to 0 and %EPP cut off 2 set to100. Under these parameters, the genes with 0% or 100% EPP were assigned into highly divergent/absent and present categories respectively. Any genes with EPP between 0% and 100% were classed into an uncertain category. These uncertain genes represent the class of genes that could not be assigned into present or highly divergent/absent categories with high confidence therefore they were called slightly divergent genes. Trinary output (.cdt) file containing the cut off values for all genes as binary numbers was generated with present genes designated as 1, slightly divergent genes designated as 0 and highly divergent/absent genes designated as -1 (Kim *et al*., 2002). Phylogenomic analysis was performed by “Cluster” software (Eisen *et al*., 1998). The GACK trinary file was converted to text delimited (.dat) format by using SPSS statistical software and imported to Cluster. Using “Cluster” software, the Pearson Correlation coefficient was applied with correlation centered selected as the similarity metrics to establish relationship between strains. The Pearson Correlation between any two series of numbers $x= (x_{1,} x_2\ldots..x_n)$ and $y = (y_{1,} y_2\ldots..y_n)$ is defined by the equation below;

$$r = \frac{1}{n} \sum_{i=1}^{n} \left( \frac{x_i - \overline{x}}{\sigma_x} \right) \left( \frac{y_i - \overline{y}}{\sigma_y} \right)$$

where $\overline{x}$ represents the average values in x and $\sigma_x$ is the standard deviation of these values. If x and y values were plotted as curves then r shows how similar the shapes of the two curves are.

The Pearson correlation is always between 1 and -1 where 1 represents that that the two series are identical, 0 indicates that they are completely uncorrelated and -1 means that they are perfectly opposite (Eisen *et al*., 1998).

For hierarchical clustering, an agglomerative clustering method was used based on the average linkage clustering algorithm by Sokal and Michener (1958). This process performed repeated clustering cycles joining the true items (genes) or pseudo-items (groups of genes) with the smallest distance between them by a branch/node of a tree whereby the length of the branch represented the distance between them. The whole process was repeated for whole dataset replacing items with computed distances by new items until one item remained. The average distance between joining nodes is generated as (.atr) output file (Appendix: supplementary table 1). The clustering along with the average linkage distance between clusters was visualised by “Tree view” software (Eisen *et al*., 1998) (Figure 4.3).

### *4.2.4 Classification of loci specific to the hyperinvasive C. jejuni and further analysis*

Further mining of CGH data was performed by Professor Nadia Chuzhanova (Physics and Maths department, NTU) through personal communication. This analysis was carried out by using the Delphi 7 object-oriented programming language. The analysis run is included in appendix, supplementary file 1. The aim was to find genes present or absent/highly divergent in all *C. jejuni* strains in one group compared against the other group (*e.g.* genes present in all the six hyperinvasive *C. jejuni* strains and absent/highly divergent from the four low invasive *C. jejuni* strains studied by CGH and vice versa). If there were n number of *C. jejuni* strains in the hyperinvasive group and k number of *C. jejuni* strains in the low invasive group then the criteria was defined as follow:

- If a gene was present in all n strains and absent/highly divergent from all k strains.

Various other criteria were tried with the following being successful:

(1) if a gene was present in all n strains and absent/highly divergent in k-1 strains.

(2) if a gene was absent/highly divergent in all n strains and present in k-1 strains.

(3) if a gene was present in all k strains and absent/highly divergent in n-1 strains.

(4) if a gene was absent/highly divergent in all k strains and present in n-1 strains.

(5) if a gene was present in n-1 strains and absent/highly divergent from k-1 strains.

(6) if a gene was absent/highly divergent in n-1 strains and present in k-1 strains.

Artemis software from http://www.sanger.ac.uk/resources/software/artemis/ (Rutherford *et al*., 2000) was used to produce circular diagrams of the pan array to compare the variability between strains based on the CGH data.

## 4.3 RESULTS AND DISCUSSION

### *4.3.1 Genomotyping of hyperinvasive C. jejuni using Comparative Genomic Hybridization*

The six hyperinvasive *C. jejuni* (01/10, 01/35, 01/04, 01/41, 01/51, EX114) and four selected low invasive *C. jejuni* (01/30, 01/32, 01/46, 01/39) strains (Fearnley *et al*., 2008) were studied by using comparative genomic hybridization (CGH). Each of the test *C. jejuni* strain and the control strain, *C. jejuni* RM1221, was hybridized on the *C. jejuni /C. coli* pan DNA microarray. Each hybridization was performed in triplicate. Each gene was represented by duplicate synthetic oligonucleotides on the array.

#### *4.3.1.1 Robustness of genomotyping using DNA microarray*

After data processing and thorough filtration using Gene pix pro 6 software (Molecular Devices Corporation, Sunnyvale, CA) and SPSS 17.0 (IBM SPSS Statistics, IBM Corporation) the normalized $\log_2$ratio values (base two logarithm of ratio of median intensities) were also used to generate histograms to check the quality of each array. A histogram comparing the $\log_2$ratio values for all the normalized spots for one array experiment of *C. jejuni* 01/41 has been presented as an example to demonstrate the robustness of our DNA microarray data (Figure 4.1). Using SPSS 17.0 (IBM SPSS Statistics, IBM Corporation), the $\log_2$ratio values for each strain from three independent array experiments was averaged (Appendix: supplementary table 2) for calculating the GACK trinary cutoffs.

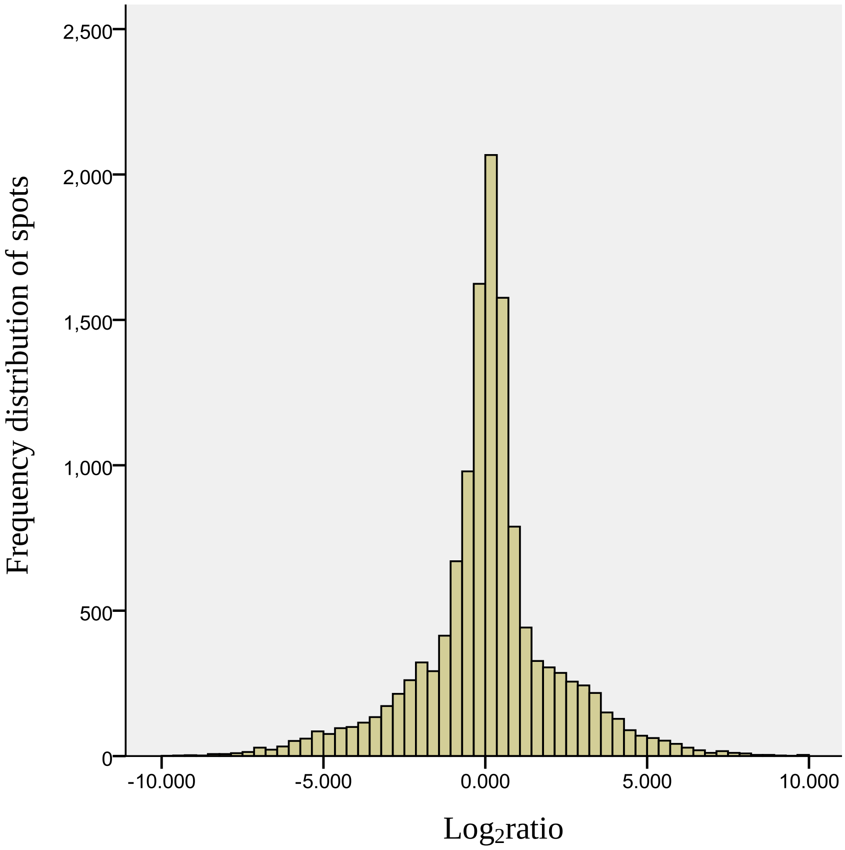


Figure 4.1: A histogram comparing the frequency distribution of spots based on their $\log_2$ratios.

The data showed a smooth and tight peak representing miminal technical error associated with the microarray experiment that could occur due to inefficient samples labelling and failure of proper hybridisation. It is important to note that a histogram is only an indicative of overall array quality based on the ratios but doesnot provide information about the individual genes. The associated detailed information of signal strength for each spot is analysed to have complete confidence in data quality.

### *4.3.1.2 Preliminary microarray data analysis*

For phylogenomic comparisons, the normalized $\log_2$ratios for each spot on the array were applied to the most strict values of the trinary cut off matrix in GACK software (available at http://falkow.stanford.edu/) to classify genes as present or absent/highly divergent (Kim *et al.*, 2002). The GACK cut off algorithm has been developed as an improved analytical method for determining the presence or divergence of genes applied to *C. jejuni* and *H. pylori* genomotyping data (Kim *et al*., 2002). GACK assigns a gene into present or divergent category irrespective of any normalization. Unlike constant cut off values used in empirical methods, GACK generates an independent cut off for each experimental dataset. Thus GACK provides more confidence in gene category assignment. Since each gene is represented twice on the array, SPSS 17.0 (IBM SPSS Statistics, IBM Corporation) was used to determine an average presence/absence category for each gene (Appendix: supplementary table 3). The dataset from one *C. jejuni* 01/41 array experiment has been presented as an example to demonstrate trinary cut off as the best method for identification of divergent genes using “Estimated Probability of Present genes (EPP)” values (Figure 4.2).

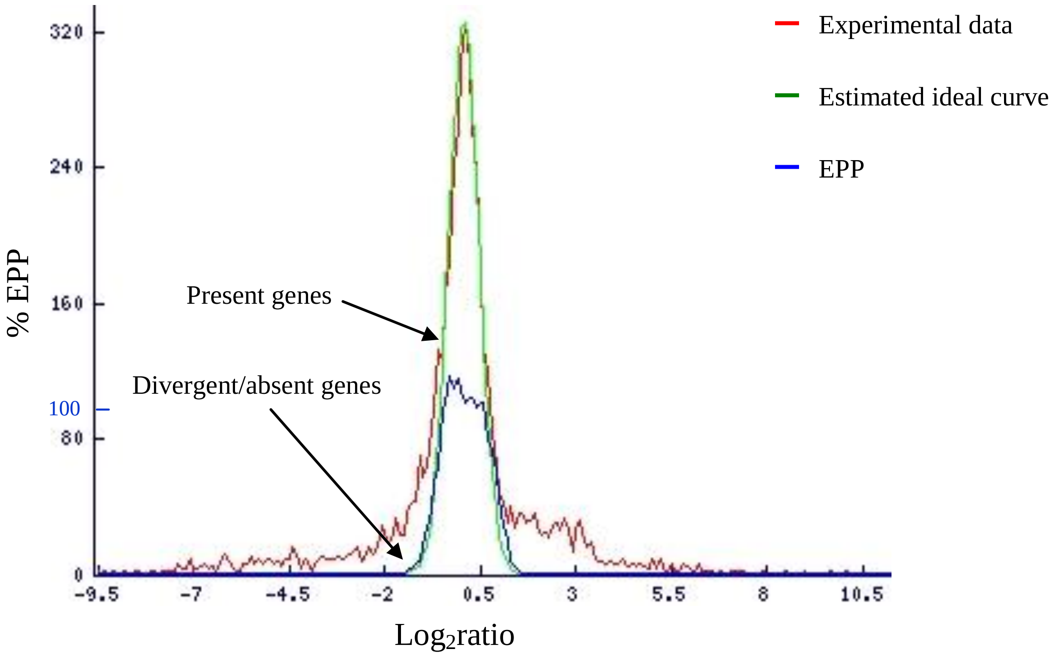


Figure 4.2: GACK trinary cut off algorithm for gene category assignment for an experimental dataset (*C. jejuni* 01/04).

The observed $\log_2$ ratio values from one *C. jejuni* 01/41 array experiment compared against the ideal curve $\log_2$ ratio values and EPP for each gene determined by GACK trinary cut-off. The EPP is 0% at $\log_2$ ratio of ~ -1.5 and 100% at ~ -1.4.

The majority of the distribution of observed normalized hybridization data overlapped the normal distribution of data as expected. The observed distribution tailed off to 0% EPP ($\log_2$ ratio ~ -1.5) where highly divergent genes existed. The increase of EPP to 100% ($\log_2$ratio ~ -1.4) subsequently increased the expected probability towards present genes. The transition region between 0% EPP and 100% EPP (*i.e.* $\log_2$ratio of ~ -1.5 and ~ -1.4) contained slightly divergent genes. Other studies phylogenomically comparing the human clinical *C. jejuni* isolates derived from different sources and their disease profile have successfully validated GACK software for classifying genes into present or divergent categories (Champion *et al.*, 2005, Poly *et al.*, 2004, Pearson *et al.*, 2003). For example in the study by Champion *et al* (2005) the classification of genes into present and divergent categories was validated by an empirical cut off determination that produced a very similar list of present and divergent genes. Based on the successful application of GACK analysis, only GACK cut offs were used for assigning genes present or divergent status in this study.

Using the CGH data, the core genome was determined by calculating the total number of genes present in all test *C. jejuni* strains studied by CGH. This was calculated as follows;

$$\text{Core genome (\%)} = \frac{\text{Number of CDSs present in all test } \textit{C. jejuni} \text{ strains}}{\text{Total number of functional reference CDSs on array}} \times 100$$

There were 623 (23.7%) functional CDSs in the core genome that mainly consisted of genes involved in essential regulatory, cellular and metabolic functions. The remaining genes formed the accessory genome as they were variable between the strains. The accessory genome mainly comprised of CDSs associated with capsule, LOS, flagellar and restriction modification systems. For selection of genes specific to the hyperinvasive *C. jejuni* strains only present and highly divergent genes were considered to have absolute confidence in selection.

### *4.3.2 Phylogenomic clustering of hyperinvasive and low invasive C. jejuni by CGH*

Based on CGH data, the phylogenomic relationship was established between the hyperinvasive and low invasive *C. jejuni* strains by using "Cluster" software that performed a Pearson correlation average linkage clustering by comparing the present and highly divergent/absent genes. The hyperinvasive and low invasive *C. jejuni* strains were also compared based on their MLST profiles (Figure 4.3).

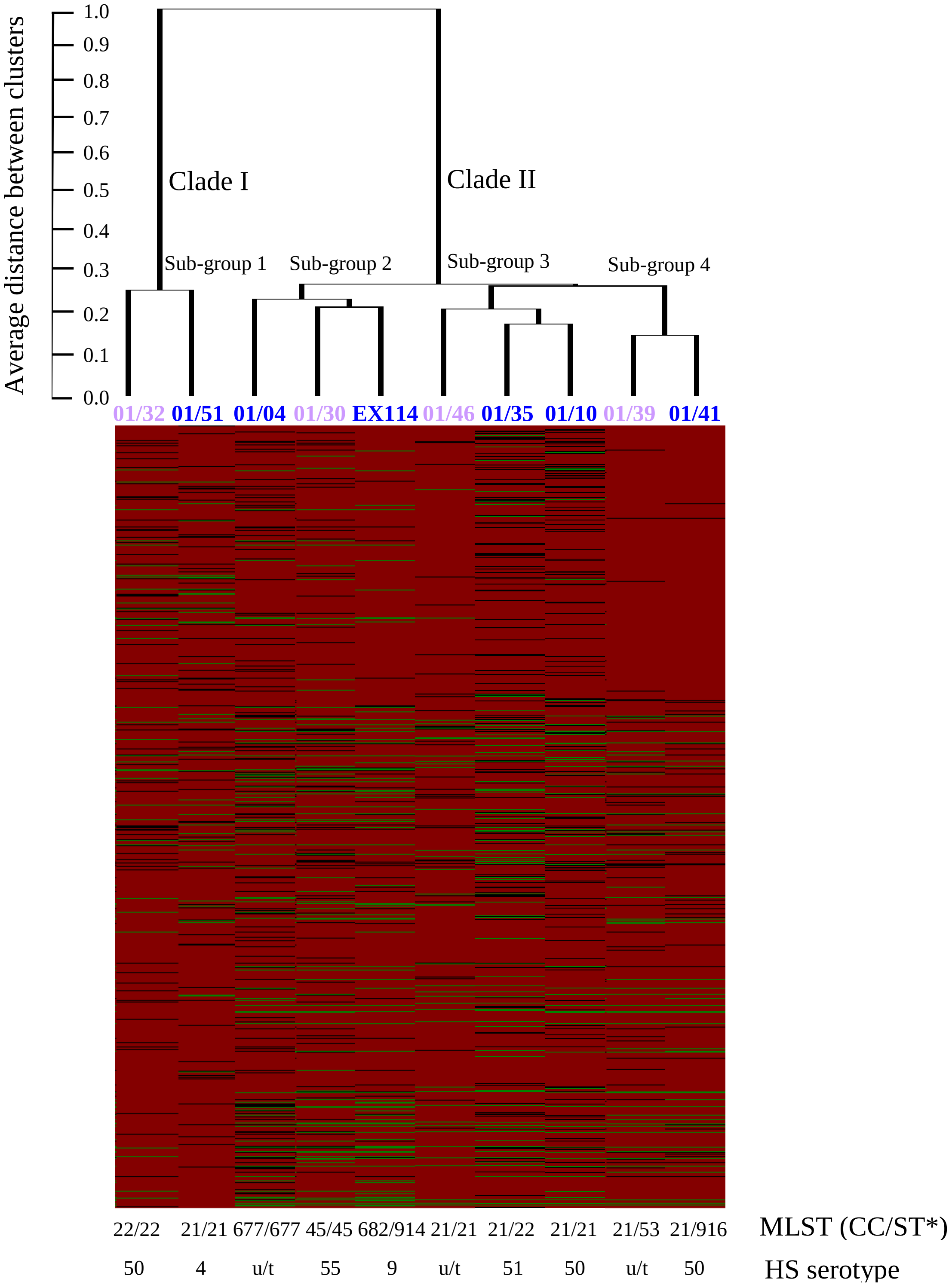


Figure 4.3: The hierarchical clustering of hyperinvasive *C. jejuni* and low invasive *C. jejuni* based on CGH along with the MLST profile and Penner (HS) serotype. The heat map respresenting present and highly divergent/absent genes in all *C. jejuni* isolates across the whole genome with genes arranged in ascending order.
*CC = Clonal Complex and ST = Sequence Type; u/t = untypeable
Hyperinvasive *C. jejuni* = blue; Low invasive *C. jejuni* = purple; Genes present = red; Genes highly divergent/absent = green and Genes slightly divergent = black

The phylogenomic clustering of six hyperinvasive and four low invasive *C. jejuni* strains examined in CGH study was performed using "Cluster" software (Eisen *et al*., 1998). *C. jejuni* isolates formed two distinct clades (I and II) based on the genome similarity between them and there was no distinct grouping of the hyperinvasive *C. jejuni* isolates as a separate cluster from the low invasive *C. jejuni*. Clade I had only one subgroup 1 and Clade II was subdivided into three sub groups 2, 3 and 4. Clade I clustered two strains in sub group 1; low invasive *C. jejuni* 01/32 and a hyperinvasive *C. jejuni* 01/51. Clade II clustered eight strains which were sub divided into three sub groups. The sub-group 2 showed the hyperinvasive *C. jejuni* EX114 linked to the low invasive *C. jejuni* 01/30 and both of these strains were related to the hyperinvasive *C. jejuni* 01/04. The third sub-group represented two hyperinvasive *C. jejuni* 01/10 and 01/35 that clustered together and were very closely related to a low invasive *C. jejuni* 01/46. Finally, the sub-group 4 was composed of the low invasive *C. jejuni* isolate 01/39 and the hyperinvasive *C. jejuni* 01/41.

All the hyperinvasive *C. jejuni* strains showed different MLST profiles. The *C. jejuni* strains in subgroups 3 and 4 in Clade II belonged to the clonal complex 21 but there was no grouping based on sequence type. All the other subgroups possessed mixed MLST types. The clonal complex 21 is one of the largest *C. jejuni* clonal complexes containing strains from human, animal and environmental sources (Manning *et al*., 2003, Dingle *et al*., 2001, Best *et al*., 2004). *C. jejuni* 01/51 was the only strain in clade I which belonged to ST 21 complex therefore the association between clade II and ST 21 complex is not absolute. Similarly, there was no common Penner (HS) serotype amongst all the hyperinvasive *C. jejuni* strains. Indeed HS50 was shared between the hyperinvasive and low invasive *C. jejuni* strains. Three strains were not successfully serotyped which may be due to the age of bacterial culture or antisera (Mckay *et al*., 2001).

Taboada *et al* (2007) investigated the relationship between neuropathogenic and enteritis causing *C. jejuni* strains using CGH. In agreement with our findings, Taboada *et al* (2007) also could not identify distinct clustering associated with different disease profiles and reported great levels of genomic similarity between them. In a later investigation, Taboada *et al* (2008) compared 32 South African *C. jejuni* strains associated with enteritis, Guillain-Barré or Miller Fisher syndromes using CGH and MLST. This study argued that MLST is a useful but limited technique as it considers variation in few housekeeping genes and does not account for variation across the whole genome as represented by DNA microarray (Taboada *et al*., 2008). In a phylogenomics study, Champion *et al* (2005) reported results similar to our CGH study with no clustering of the 111 clinical isolates based on the disease symptom. In contrast, the same study identified distinct clusters based on the source of transmission. A partial grouping was observed based on MLST profiles of *C. jejuni* strains studied. The phylogenetic analysis of *C. jejuni* strains from a variety of disease profiles showed that strains with asymptomatic carriage, diarrhoea, bloody diarrhoea, vomiting, septicaemia, and GBS did not cluster as distinct clonal groups. However, six environmental *C. jejuni* isolates clustered as a separate clonal group (Champion *et al*., 2005). In another study, *C. jejuni* strains selected based on Penner serotypes were compared by CGH. The *C. jejuni* strains with similar Penner serotypes could not be clustered together by CGH suggesting that the *C. jejuni* strains with the same serotype were otherwise variable based on the whole genome content (Dorrell *et al*., 2001).

It is also important to note here that the *C. jejuni* strains studied in this project were not selected based on MLST or HS serotype but on the invasion phenotype hence, complete association of strains based on MLST type or Penner HS serotype was not expected. The fact that only four low invasive *C. jejuni* strains have been selected for phylogenomic comparison which could be a limiting factor to emphasize on the genetic similarities and differences identified in the hyperinvasive group of *C. jejuni*.

The failure of hyperinvasive *C. jejuni* to form a distinct clade by CGH might reflect the characteristic invasion profile of these strains to be associated with subtle changes in number of genes at the nucleotide level that would not be detected using DNA microarrays (Malik-Kale *et al*., 2007). It can be argued that the variation in a phenotype may not necessarily be reflected in the genome content of *C. jejuni*. It may be stimulated by the expression of gene (s) belonging to one or more functional pathways (Konkel *et al*., 1990). In addition, the host factors may also significantly contribute to the *C. jejuni* virulence phenotypes (Taboada *et al*., 2007).

### *4.3.3 Identification of loci specific to hyperinvasive C. jejuni and PCR validation of CGH results*

The CGH data was further analysed to identify gene/s present in all six hyperinvasive *C. jejuni* strains and absent/highly divergent form the low invasive group of *C. jejuni* strains, and vice versa that might explain the hyperinvasive phenotype of these strains. The analysis performed is described in section 4.2.4. There was no such combination of conserved or variable genes found in all the hyperinvasive *C. jejuni* compared to the low invasive *C. jejuni* strains.

The selection was extended to find present or divergent genes in the majority of hyperinvasive *C. jejuni* strains (section 4.2.4), which identified 67 genes. These genes were classified into six groups based on their presence or divergence in the hyperinvasive *C. jejuni* strains. Only Groups 1 and 2 are presented here in tables 4.1a and 4.1b. The presence or variability of genes in these two groups was further validated by PCR (Figures 4.4a and 4.4b). The primers and expected amplicon sizes are listed in table 2.2.1. The rest of genes arranged in four groups (3, 4, 5 and 6) are provided in the supplementary table 4 in the appendix.

Table 4.1a: Genes selected from CGH data as present in all hyperinvasive *C. jejuni*.

| **Gene name/number** | | | **Hyperinvasive *C. jejuni*** | | | | | | **Low-invasive *C. jejuni*** | | | | **Role/function** | | | **COG functional grouping** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **GROUP 1: Genes present in all hyperinvasive *C.jejuni* and** | | | **01_10** | **01_35** | **01_04** | **01_41** | **01_51** | **EX114** | **01_30** | **01_32** | **01_46** | **01_39** | ***C. jejuni* NCTC11168** | ***C. jejuni* RM1221** | ***C. coli* RM2228** | Fouts *et al*., 2005 |
| ***C. jejuni* NCTC 111** | ***C. jejuni* RM1221** | ***C. coli* RM2228** | | | | | | | | | | | | | | |
| Cj0738 | CJE0838 | ..... | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | hypothetical protein | hypothetical protein | .... | Hypothetical |
| *hisS* (Cj0765c) | *hisS* (CJE0856 ) | *hisS* (CCO0821) | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | histidyl-tRNA synthetase | histidyl-tRNA synthetase | histidyl-tRNA synthetase | Translation |
| *aat* (Cj1109) | *aat* (CJE1252) | *aat* (CCO1187) | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | putative leucyl/phenylalanyl-tRNA--protein | leucyl/phenylalanyl-tRNA--protein transferase | leucyl/phenylalanyl-tRNA--protein transferase | Posttranslational modification, protein turnover, chaperones |
| *proC* (Cj1076) | *proC* (CJE1219) | *proC* (CCO1150) | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative pyrroline-5-carboxylate reductase | pyrroline-5-carboxylate reductase | pyrroline-5-carboxylate reductase | Amino acid transport and metabolism |
| *metF* (Cj1202) | *metF* (CJE1336) | *metF* (CCO1273) | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 5,10-methylenetetrahydrofolate reductase | 5,10-methylenetetrahydrofolate reductase | 5,10-methylenetetrahydrofolate reductase | Amino acid transport and metabolism |
| ......... | ........ | CCOA0033 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | ….. | ….. | hypothetical protein | Hypothetical |
| Cj0564 | CJE0669 | ......... | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | putative integral membrane protein | hypothetical protein | …. | Hypothetical |
| *modA* (Cj0303c) | *modA* (CJE0348) | *modA* (CCO0388) | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | putative molybdate-binding lipoprotein | molybdenum ABC transporter, periplasmic | molybdenum ABC transporter, periplasmic | Transport and metabolism |
| Cj0271 | CJE0320 | CCO0340 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | bacterioferritin comigratory protein homolog | antioxidant, AhpC/Tsa family | bacterioferritin comigratory protein homolog | Posttranslational modification, protein turnover, chaperones |

1=present;-1=absent/highly divergent

Group 1 contains 9 genes present in all hyperinvasive *C. jejuni* and absent/highly divergent from three of four of low invasive *C. jejuni*.

Table 4.1b: Genes selected from CGH data as absent/highly divergent in all hyperinvasive *C. jejuni*.

| **Gene name/number** | | | **Hyperinvasive *C. jejuni*** | | | | | | **Low-invasive *C. jejuni*** | | | | **Role/function** | | | **COG functional grouping** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **GROUP 2: Genes highly divergent/absent in all hyperinvasive *C.jejuni* and present in three of four low invasive *C. jejuni*** | | | **01_10** | **01_35** | **01_04** | **01_41** | **01_51** | **EX114** | **01_30** | **01_32** | **01_46** | **01_39** | ***C. jejuni* NCTC11168** | ***C. jejuni* RM1221** | ***C. coli* RM2228** | Fouts *et al* ., 2005 |
| ........ | CJE1112 | CCOA0144 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | ..... | hypothetical protein | hypothetical protein | Hypothetical |
| Cj0266c | CJE0315 | CCO0335 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0266c | Probable cell wall/membrane biogenesis |
| Cj0701 | CJE0801 | CCO0767 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | putative protease | peptidase, U32 family | probable proteinase Cj0701 | Posttranslational modification, protein turnover, chaperones |
| *tgt* (Cj1010) | *tgt* (CJE1090) | *tgt* (CCO1072) | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | queuine tRNA-ribosyltransferase | queuine tRNA-ribosyltransferase | queuine tRNA-ribosyltransferase | Translation |
| ......... | CJE1128 | ......... | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | ..... | hypothetical protein | hypothetical protein | Hypothetical |
| .......... | CJE0731 | ......... | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | ..... | type III restriction/modification enzyme, | ..... | Replication,recombination and repair |

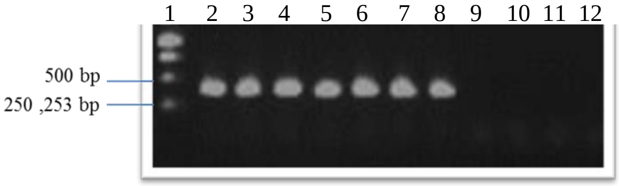
1=present;-1=absent/highly divergent

Group 2 consists of 6 genes highly divergent/absent in all hyperinvasive *C. jejuni* and present in three of four low invasive *C. jejuni*.

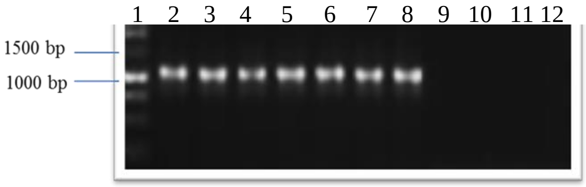
PCR screening of genes listed in group 1 and 2 (Table 4.1a and 4.1b) further validated their presence and absence in the hyperinvasive and low invasive *C. jejuni* isolates.

(a)

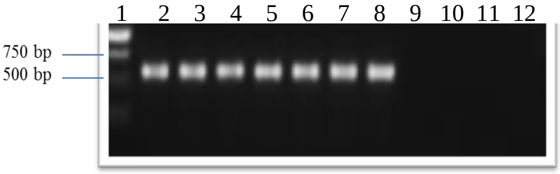
(i) CJE0838



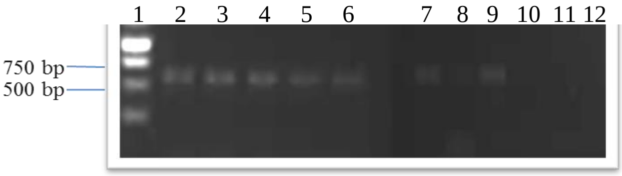
(ii) *hisS*



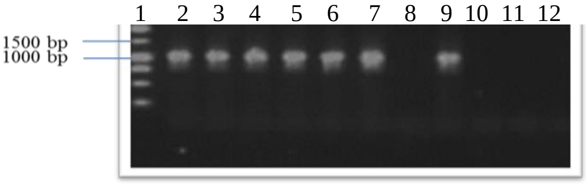
(iii) *aat*



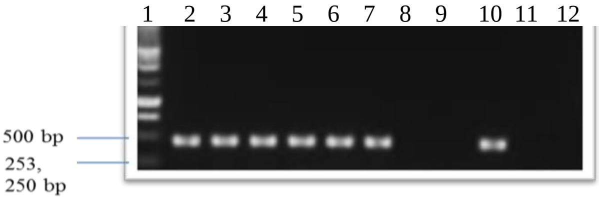
(iv) *proC*



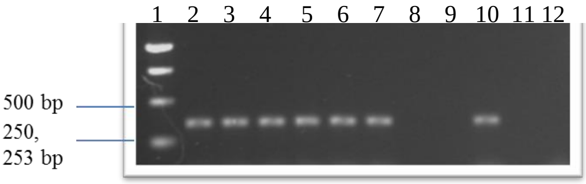
(v) *metF*



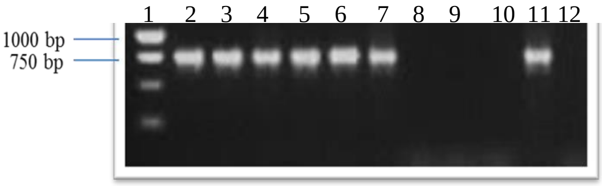
(vi) CJE0669



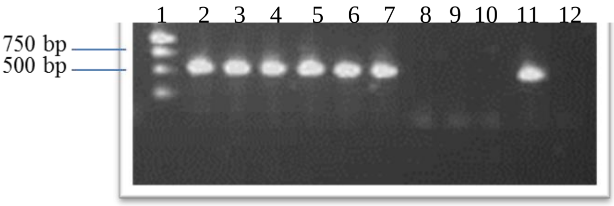
(vii) CCOA0033



(viii) *modA*

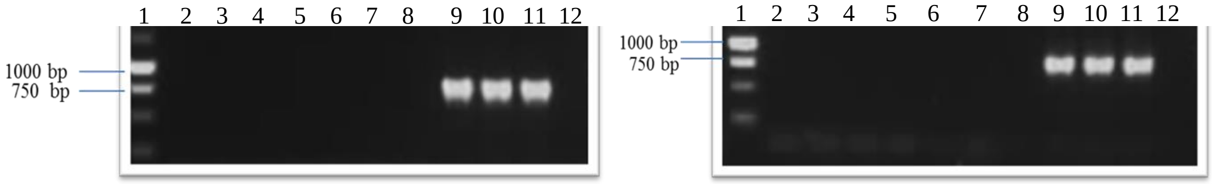


(ix) CJE0320

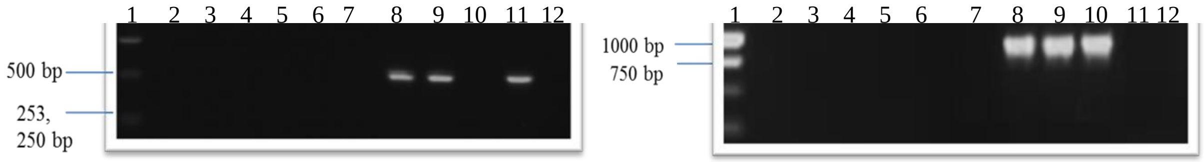


Continouous

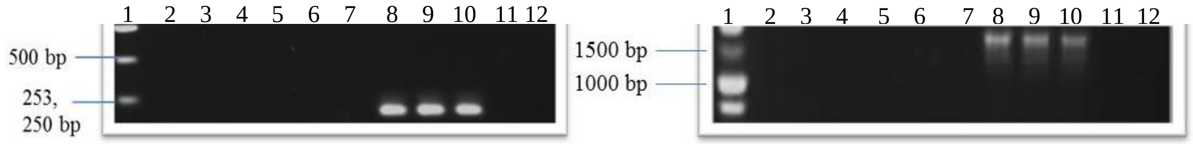
(b)


(x) CJE1112

(xi) CJE0315


(xii) CJE0801

(xiii) *tgt*


(xiv) CJE1128

(xv) CJE0731

Figure: 4.4: PCR validation of CGH data.

(a) PCR verification of genes present in all hyperinvasive *C. jejuni* and highly divergent from three of four low invasive *C. jejuni* (Group 1, table 4.1a). (i) CJE0838 (ii) *hisS* (iii) *aat* (iv) *proC* (v) *metF* (vi) CJE0669 (vii) CCOA0033 (viii) *modA* (ix) CJE0320. (b) Six genes included in group 2 (Table 4.1b) were found as highly divergent in all hyperinvasive and low invasive *C. jejuni* with an exception of one low invasive *C. jejuni* strain in each case. (x) CJE1112 (xi) CJE0315 (xii) CJE0801 (xiii) *tgt* (xiv) CJE1128 (xv) CJE0731.

Each gel was loaded: Lane 1; 1 kbp DNA marker (Promega, UK); (lanes 2-7); hyperinvasive *C. jejuni* strains 01/10, 01/35, 01/04, 01/41, 01/51, EX114. Lanes (8-11); low invasive *C. jejuni* strains 01/30, 01/32, 01/46, 01/39. Lane 12; negative control.

### *4.3.4 Presence of hyperinvasive-associated loci in an additional group of low invasive C. jejuni isolates*

To investigate the presence of the identified genes amongst a wider group of strains PCR screening on additional 9 low invasive *C. jejuni* strains was conducted (Table 4.2).

Table 4.2: Summary of PCR screening for the identified genes (Table 4.1a and 4.1b) in the hyperinvasive and low invasive *C. jejuni* strains.

| Gene name/number in *C. jejuni* RM1221 | PCR profile of hyperinvasive and low invasive *C. jejuni* | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Hyperinvasive *C. jejuni* | | | | | | Low invasive *C. jejuni* | | | | | | | | | | | | | |
| **GROUP 1: Genes present in all hyperinvasive *C. jejuni*** | **01_10** | **01_35** | **01_04** | **01_41** | **01_51** | **EX114** | **01_30** | **01_32** | **01_46** | **01_39** | **01_05** | **01_08** | **01_11** | **01_36** | **C2/3** | **C12/11** | **C27/14** | **C69/2** | **C110/4** | ***p*-value*** |
| CJE0838 | + | + | + | + | + | + | + | - | - | - | - | - | - | - | - | - | - | - | - | 0.000 |
| *hisS* (CJE0856) | + | + | + | + | + | + | + | - | - | - | - | - | - | - | - | - | - | - | - | 0.000 |
| *aat* (CJE1252) | + | + | + | + | + | + | + | - | - | - | + | - | - | - | - | - | - | - | - | 0.001 |
| *proC* (CJE1219) | + | + | + | + | + | + | - | + | - | - | - | - | - | - | - | - | - | - | - | 0.000 |
| *metF* (CJE1336) | + | + | + | + | + | + | - | + | - | - | + | - | - | - | - | - | - | - | - | 0.001 |
| CCOA0033 | + | + | + | + | + | + | - | - | + | - | - | - | - | - | - | - | - | - | - | 0.000 |
| CJE0669 | + | + | + | + | + | + | - | - | + | - | - | - | - | - | - | - | - | - | - | 0.000 |
| *modA* (CJE0348) | + | + | + | + | + | + | - | - | - | + | + | + | - | - | - | - | - | - | - | 0.003 |
| CJE0320 | + | + | + | + | + | + | - | - | - | + | - | - | - | - | - | - | - | - | - | 0.000 |
| **GROUP 2: Genes highly divergent/absent in all hyperinvasive *C. jejuni*** | | | | | | | | | | | | | | | | | | | | |
| CJE1112 | - | - | - | - | - | - | - | + | + | + | + | + | + | + | + | + | + | + | + | 0.000 |
| CJE0315 | - | - | - | - | - | - | - | + | + | + | + | + | + | + | + | + | + | + | + | 0.000 |
| CJE0801 | - | - | - | - | - | - | + | + | - | + | + | + | + | + | + | + | + | + | + | 0.000 |
| *tgt* (CJE1090) | - | - | - | - | - | - | + | + | + | - | + | + | + | + | + | + | + | + | + | 0.000 |
| CJE1128 | - | - | - | - | - | - | + | + | + | - | + | + | + | + | + | + | - | - | - | 0.011 |
| CJE0731 | - | - | - | - | - | - | + | + | + | - | - | - | - | - | - | - | - | - | - | 0.517 |

+=present, - =absent

*Chi-square, Fisher's exact test was performed to determine if the presence or absence of identified genes in the hyperinvasive group of *C. jejuni* strains was statistically significant. Significance level =1% (*p*=0.01).

Table 4.2 (group 1) showed that most of the additional low invasive *C. jejuni* isolates were negative for genes present in all hyperinvasive *C. jejuni*. In group 1, six genes (CJE0838, *hisS*, *proC*, CCOA0033, CJE0669 and CJE0320) were highly divergent in 1/13 low invasive *C. jejuni* isolates. Among the additional *C. jejuni* strains PCR screened, *C. jejuni* 01/05 was the only isolate positive for three genes *i.e*. *aat*, *metF* and *modA* followed by *C. jejuni* 01/08 that was positive for *modA* only.

For the genes in group 2, the majority of the additional low invasive *C. jejuni* strains possessed these genes. PCR analysis showed that four genes (CJE1112, CJE0315, CJE0801 and *tgt*) were present in a total of 12/13 low invasive *C. jejuni*. Additionally, all the 9 additional low invasive *C. jejuni* strains were negative by PCR for CJE0731 whereas, three low invasive *C. jejuni* (C27/14, C69/2, C110/4) strains showed negative results for CJE1128 in this group.

PCR screening of 9 additional low invasive *C. jejuni* isolates for genes present or highly divergent in all hyperinvasive *C. jejuni* (group 1 and group 2, Table 4.1a and 4.1b) showed a strong statistical correlation (p=0.01 at 1% significance level) between the presence and absence of these genes in the hyperinvasive *C. jejuni* for 13/15 genes. CJE1128 (hypothetical protein) (p=0.011) and CJE0731 (type III restriction modification enzyme) (0.517) were the two exceptions. This result suggests that although the genes in group 1 and 2 are not part of the same functional group or pathway these genes could be considered as genetic markers for the hyperinvasive phenotype. Previously, a cluster of six genes (*cj1321*-*cj1326*) in the O-linked glycosylation locus were identified, using parsimony based algorithm, as characteristic of chicken/livestock campylobacters. This gene cluster present in 16/17 isolates, was identified in an additional six chicken isolates that were not tested in the original study confirming that these genes: *cj1321* to *cj1326*, were genetic markers for livestock/chicken isolates (Champion *et al*., 2005).

### *4.3.5 Functional importance of hyperinvasive linked loci identified by CGH*

The phylogenomics study identified 67 genes which belonged to different functional categories. The functional significance of the presence or absence of these genes in the hyperinvasive *C. jejuni* strains, particularly for the genes listed in group 1 and 2 (Table 4.1a and 4.1b) is discussed below;

#### *4.3.5.1 Group 1: Genes present in the all hyperinvasive C. jejuni*

Group 1 had nine genes present in all hyperinvasive *C. jejuni* strains but highly divergent in the majority of the low invasive *C. jejuni* (Table 4.2). Important metabolic genes including carboxylate reductase and methyltetrahydrofolate reductase, tRNA synthesis genes *i.e*. histidyl-tRNA synthase and leucyl/phenylalanyl tRNA synthase formed this group. Metabolic and biosynthetic and DNA and RNA processing genes have been reported as an integral part of the *C. jejuni* core genome (Parker *et al*., 2006, Pearson *et al*., 2003, Dorrell *et al*., 2001). The conservation of these genes may confer increased survival chances for bacteria especially in the hostile environment inside the human host. A histidyl tRNA synthetase encoding gene (*hisS*-CJE0856) was present in all hyperinvasive *C. jejuni* strains. In *C. jejuni* RM1221, *hisS* is a 1,227 bp (408 amino acids) long gene. Histidyl tRNA synthetase (HisRS) is an enzyme which is composed of a small peptide chain of about 420-550 amino acids. HisRS has important catalytic properties in several regulatory mechanisms of cell metabolism. HisRS is responsible for synthesizing histidyl-transfer RNA, which is important for inserting histidine into protein structures. HisRS has been found to act as an antigen responsible for causing autoimmune diseases in humans such as rheumatic arthritis or myositis (Freist *et al*., 1999). Using comparative phylogenomics Aklujkar and Lovely (2010) showed that the attenuation of *hisS* resulted in physiological changes in *Pelobacter carbinolicus* by altering its iron III reduction pathway.

Another gene in Group 1, which was found to be present in all the hyperinvasive *C. jejuni*, is *aat* (CJE1252 in *C. jejuni* RM1221). It is a 648 bp long gene. It encodes for a Leucyl/phenylalanyl-tRNA protein transferase and contains 415 amino acids. The role of *aat* is to transfer a Leucine or Phenylalanine to the N terminal of Arginine or Lysine containing proteins to allow their breakdown (Shrader *et al*., 1993). The function of *aat* in *C. jejuni* pathogenesis is not yet characterised.

A metabolic gene present in all hyperinvasive *C. jejuni* strains and highly divergent in the majority of low invasive *C. jejuni* is *proC* (CJE1219 in *C. jejuni* RM1221), encoding for pyrroline-5-carboxylate synthase. CJE1219 is 732 bp (199 amino acids) in size in *C. jejuni* RM1221. This is a key enzyme of proline metabolism involved in the synthesis of L-proline and ornithine. Proline has a well-studied function related to maintaining redox balance under osmotic stress in several bacteria (Perez-Arellano *et al*., 2010). Previously, in a transposon mutagenesis study of hyperinvasive *C. jejuni* 01/51, a transposon was inserted in a metabolic gene *putA* (Cj1503c in *C. jejuni* NCTC11168) encoding for a putative proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase, an enzyme involved in the oxidation of proline into glutamate. The transposon inserted in *putA* reduced invasion of the *C. jejuni* 01/51 mutant into INT-407 and Caco2 cells (Javed *et al*., 2010). Another metabolic gene in Group 1, is *metF* (CJE1336 in *C. jejuni* RM1221). CJE1336 is a 849 bp long gene and encodes 282 amino acids. In *C. jejuni* RM1221, *metF* encodes for a metabolic enzyme 5, 10-methylenetetrahydrofolate reductase. This protein is a flavoprotein that catalyses the conversion of 5-methyltetrahydrofolate to 5, 10-methylenetetrahydrofolate.

The presence of genes related to metabolic and regulatory pathways in hyperinvasive *C. jejuni* might reflect that the hyperinvasive *C. jejuni* do not have well characterised pathogenicity factors as in other enteric pathogens like *E. coli* and *Salmonella enterica* but are opportunistic pathogens. In 1988, Stanley Falkow devised the molecular version of Koch’s postulates by defining the “virulence factor” in a pathogen and stated that a virulence factor must be present in a pathogenic strain and absent from the non-pathogenic strain. Pallen and Wren (2007) argued that the definition of virulence factors cannot be strict as many bacteria adapt to different functions in different conditions. For example, the uropathogenic *E. coli* lives in the human intestine but acts as a pathogen in the human bladder. Similarly, the enterohaemorrhagic *E. coli* is commensal in bovine intestine but causes disease when inside the human gut (Pallen and Wren., 2007). Likewise, *C. jejuni* is commensal in chickens and a pathogen in humans. Thus, the *C. jejuni* infection in humans is a multifactorial mechanism that results from the requirement of bacteria to survive inside the human host. In a recent study, Hofreuter *et al* (2008) reported that the subtle genomic changes in *C. jejuni* metabolic pathways significantly influenced their ability to utilize nutrients and colonize specific host tissues. This suggests that the metabolic diversity is an important factor in this organism in defining host specificity.

A molybdenum ABC transporter gene, *modA* (CJE0348 in *C. jejuni* RM1221) was present in all hyperinvasive *C. jejuni* strains but highly divergent in 10/13 of the low invasive *C. jejuni* isolates studied. CJE0348 is a 750 bp (249 amino acids) in size in *C. jejuni* RM1221. The putative molybdenum ABC transporter binding protein (*modA)* is a part of molybdenum transport apparatus *modC* CJE0345 (Cj0300c), *B* CJE0346 (Cj0301c) and *A* CJE0348 (Cj0302) and it is present in the hypervariable Plasticity Region (PR) 1 (Pearson *et al*., 2003) and Plasticity Region (PR) 2 (Dorrell *et al*., 2001) in *C. jejuni* strains identified in comparative phylogenomics studies (Pearson *et al*., 2003, Dorrell *et al*., 2001). Molybdenum has been shown to have a role in nitrate metabolism by the catalytic activity of a flavoprotein enzyme, nitrate reductase, enabling nitrate to act as a terminal electron acceptor in place of oxygen under oxygen deficient conditions in *Campylobacter* (Sellars *et al*., 2002, Pearson *et al*., 2003). DNA microarray studies based on NCTC11168 as the reference strain (Parker *et al*., 2006) showed that the *C. jejuni* RM1221 and other investigated *C. jejuni* strains were diverse in the molybdenum ABC transport region. However, in the current study this region was present in all hyperinvasive *C. jejuni* strains which may reflect the increased fitness of these strains compared to the low invasive *C. jejuni* to allow survival in diverse ecological niches and utilize a variety of metabolic resources.

Another gene, CJE0320 (in *C. jejuni* RM1221) is present in all hyperinvasive *C. jejuni* and highly divergent in the majority of low invasive *C. jejuni*. The size of this gene is 456 bp (151 amino acids). In *C. jejuni* RM1221, CJE0320 is annotated as peroxiredoxin enzyme in the antioxidant/AhpCTCA family. Cj0271 and CCO0340 are the homologues of this gene in *C. jejuni* NCTC11168 and *C. coli* RM2228 respectively. In *C. jejuni* NCTC11168, Cj0271 has been shown to have a role in reducing hydrogen and organic peroxides, thus conferring resistance under oxidative stress conditions (Atack *et al*., 2008).

Interestingly, *modA* and CJE0320 have related functions and their presence in the hyperinvasive *C. jejuni* strains in this study may provide advantage under oxidative stress conditions.

In group 1, three genes (CCOA0033 in *C. coli* RM2228, CJE0838 and CJE0669 in *C. jejuni* RM1221) with a putative role were present in all the hyperinvasive *C. jejuni* strains. CCOA0033 is a 213 bp gene encoding 70 amino acids. CJE0838 and CJE0669 are 957 bp (318 amino acids) and 207 bp (68 amino acids) in size respectively. Fouts *et* *al* (2005) identified several hypothetical genes in the genome sequences of different *Campylobacter* strains. These genes add to the genomic diversity of this organism.

A periplasmic membrane encoding gene *lolA* (CJE1021 in RM1221) (Group 5; supplementary table 4) was present in five hyperinvasive *C. jejuni* and three low invasive *C. jejuni* strains except and highly divergent in *C. jejuni* 01/04 and the low invasive *C. jejuni* strain 01/32. Two other genes (Cj0544, Cj0151c in NCTC11168) with a predicted role as a periplasmic protein were also included in group 5. The homologues of these genes in *C. jejuni* RM1221 (*i.e.* CJE0648 and CJE0147) have no function characterized. In *C. jejuni*, outer membrane proteins have been found to play a role in virulence in particular in the adherence and invasion of intestinal epithelial cells. The role of surface exposed proteins including, major outer membrane proteins (MOMP-PorA), JlpA, PEB1a, *Campylobacter* adhesion to fibronectin (CadF) and FlpA in adherence and internalization of cultured epithelial cells in known in *C. jejuni* (Jin *et al*., 2001, Pei *et al*., 1998, Monteville *et al*., 2003, Krause-Gruszczynska *et al*., 2007, Flanagan *et al*., 2009). The function of these genes is not characterised yet in the *C. jejuni* strains studied here but taking into account the importance of outer membrane proteins in host cell interaction, these genes may have a potential role in virulence in particular invasion of hyperinvasive *C. jejuni* strains.

#### *4.3.5.2 Group 2: Genes highly divergent/absent in all hyperinvasive C. jejuni*

Based on CGH data, a second group of six genes were identified as divergent in all hyperinvasive *C. jejuni* but present in most of the low invasive *C. jejuni* strains studied (Table 4.2). It can be argued that in the case of this group the presence of genes in the low invasive *C. jejuni* strains may be responsible in reducing the invasion potential of these strains. The process of gene loss or genome decay is evident in some bacterial pathogens. The best examples where the pathogens have lost genes to acquire smaller genomes in order to adapt to the specialised host niches are *Yersinia pestis* and *S. enterica* servar Typhi (Pallen and Wren., 2007).

A hypothetical protein (CJE0315) was found to be highly divergent in all hyperinvasive *C. jejuni* and present in 12/13 low invasive *C. jejuni* (01/32, 01/46, 01/39) but highly divergent in low invasive *C. jejuni* 01/30. In *C. jejuni* RM1221, this gene is a 510bp long and the translated protein contains 169 amino acids. In NCTC11168 and *C. coli* RM2228, this gene is annotated as a putative integral membrane protein (*i.e.* Cj0266c and CCO0335 respectively). There are other membrane associated protein encoding genes found to be absent from the majority of the hyperinvasive *C. jejuni* strains. For example, a membrane protein encoding gene (CJE0989) annotated as SCO1/SenC family protein in *C. jejuni* RM1221 (Group 3; supplementary table 4) and a porin domain protein CJE1165 in *C. jejuni* RM1221 (Group 6; supplementary table 4) characterised as a probable periplasmic protein were highly divergent from the majority of the hyperinvasive *C. jejuni* strains but present in the most of the low invasive *C. jejuni*. This may suggest that these genes may not have a role in invasion phenotype of the hyperinvasive group of *C. jejuni* strains.

Another gene highly divergent in all hyperinvasive *C. jejuni* strains is CJE0801. This gene is a 1,254 bp (417 amino acids) long and has similarity to peptidase U32, in RM1221. The role of this peptidase in *C. jejuni* pathogenesis is not known. Periplasmic proteases are an important part of the cell envelope of Gram negative bacteria as they provide resistance against extracellular stresses including oxygen and temperature fluctuations. CJE0801 belongs to the functional category of post-translational modification, protein turn over, chaperone. In *C. jejuni*, a periplasmic protease HtrA, has been shown to provide protection against heat and oxidative stress conditions in *C. jejuni* (Baek *et al*., 2011b). Recently, the role of a peptidoglycan peptidase (*pgp1*) in *C. jejuni* virulence has been characterised using *C. jejuni* 81-176 as the model organism (Frirdich *et al*., 2012). In *C. jejuni* 81-176, has been shown to be involved in maintaining the helical cell shape and in other virulence phenotypes mainly altered innate immune response, motility and biofilm formation (Frirdich *et al*., 2012). Since, CJE0801 was missing from all the hyperinvasive *C. jejuni* strains; this may suggest that this gene may be involved in supressing invasion in the low invasive *C. jejuni* strains.

A tRNA processing and modification gene, queuine tRNA ribosyltransferase (*tgt*) (CJE1090 in *C. jejuni* RM1221) was highly divergent/absent from all hyperinvasive *C. jejuni* but present in all low invasive strains except *C. jejuni* 01/39. In *C. jejuni* RM1221, CJE1090 is 1,122 bp in size and encodes a 373 amino acids polypeptides. The function of *tgt* in the bacterial translational process is to catalyse the incorporation of queuine which is a hyper-modified base in the wobble position of the anticodon of tRNAs by an exchange reaction with guanine (Fouts *et al*., 2005).

A type III restriction/modification enzyme encoding gene CJE0731 in *C. jejuni* RM1221 was found to be highly divergent in all hyperinvasive *C. jejuni* strains and present in only three low invasive *C. jejuni* (01/30, 01/32, 01/46). CJE0731 in *C. jejuni* RM1221 is 2,028 bp (675 amino /acids) in size. In contrast, a type I restriction enzyme M protein (Cj1553c-*hsdM*) was found to be present in majority of hyperinvasive *C. jejuni* strains except in *C. jejuni* 01/51 and highly divergent from three low invasive *C. jejuni* strains but present in low invasive *C. jejuni* 01/30 (Group 5, supplementary table 4). Restriction modification regions (RM) are variable regions in the *C. jejuni* genome. There are different types of RM systems characterised in *C. jejuni* strains referred to as type I, II and III. *C. jejuni* strains have characteristic RM regions that show strain to strain variation. The diversity seen in the RM systems in *C. jejuni* might reflect it as hotspot for horizontal gene transfer like within other variable regions in the *C. jejuni* genome including CAP, LOS and FM regions (Miller *et al*., 2005). For example, *C. jejuni* 81-176 has its unique type I restriction modification system which is absent from *C. jejuni* RM1221 and NCTC11168 (Hofreuter *et al*., 2006). Another *C. jejuni* strain, ATCC43431, has all restriction modification systems as present in *C. jejuni* NCTC11168 and also contains additional complements of RM systems (Poly *et al*., 2004). Previously, RM regions have been reported as highly divergent in NCTC11168 (Cj0625–Cj0629) and RM1221 (CJE0731 and CJE0732) in a number of *C. jejuni* strains studied by DNA microarray (Parker *et al*., 2006, Dorrell *et al*., 2001). This reflects that RM systems are dispensable in *C. jejuni* and may not necessarily influence virulence but are required to generate diversity in genomes.

#### *4.3.5.3 Important loci present or variable in other groups*

Flagellar biosynthesis loci have been well studied virulence determinants in *C. jejuni* (Duong and Konkel., 2009, Rodin *et al*., 2008, Parker *et al*., 2006, Champion *et al*., 2005, Pearson *et al*., 2003, Dorrell *et al*., 2001). In our study, the flagellar basal-hook body protein (*fliE*) was present in five hyperinvasive *C. jejuni* but highly divergent in the hyperinvasive *C. jejuni* 01/51 (Group 5; supplementary table 4). This flagella gene, *fliE* was highly divergent in three of four low invasive *C. jejuni*. However, *C. jejuni* 01/51 exhibited fully motile profile in our study (section 3.4.5). Based on the importance of flagella in *C. jejuni* virulence and survival inside the human host and its fully motile phenotype (Grant *et al*., 1993, Nachamkin *et al*., 1993, Morooka *et al*., 1985) it may be argued that the divergence of *fliE* in *C. jejuni* 01/51 might only be the sequence variation rather than the absence of gene. It would be interesting to re-confirm the absence of *fliE* in *C. jejuni* 01/51 by PCR or to be more precise by Southern blotting.

Two genes (*cfrA*; CJE0847 and *ceuB*; CJE1541) encoding for ferric receptor and iron transport permease proteins respectively were also identified in this study (Group 5; supplementary table 4). These genes were present in five of six hyperinvasive *C. jejuni* strains and highly divergent from three of four low invasive *C. jejuni*. The iron receptor, CfrA and CeuB are important components of the ferric enterobactin transport system in many *C. jejuni* strains. These receptors have a high affinity for iron and scavenge iron molecules from inside the gastrointestinal tract by forming ferric enterobactin complex which are transported through the bacterial periplasmic membrane (Zeng *et al*., 2009). The role of *cfrA* and *ceuB* genes in iron uptake system and in chicken colonization has been well investigated in *C. jejuni* (Stintzi *et al*., 2008, Palyada *et al*., 2004. A mutant in the *cfrA* gene, completely abolished enterobactin mediated transport and chicken colonization potential compared to the parent strain where the colonization was recorded to $10^7$cfu/ml of caecal content (Palyada *et al*., 2004). Recently, another ferric enterobactin receptor, CfrB was identified in *Campylobacter* with a role in iron acquisition and chicken colonization. This study showed that inactivation of the *cfrB* gene greatly reduced colonization of the chicken intestine (Xu *et al*., 2010).

Another important gene CCO0783 (*arsC*) in *C. coli* RM2228 encoding for arsenic resistance has been found as present in the majority of hyperinvasive *C. jejuni* and absent/highly divergent from the majority of low invasive *C. jejuni* strain (Group 5; supplementary table 4). Arsenic is a naturally present toxic metalloid which is an additive in poultry feed. Poultry being the main reservoir of *Campylobacter* species the isolates have developed marked arsenic resistance. A well characterised arsenic resistance gene *arsC* in *C. jejuni* encodes for an arsenate reductase that converts arsenate into arsenite (Wang *et al*., 2009). A previous study used Suppressive Subtractive Hybridization to show the presence of *arsC* in *C. jejuni* NCTC11168 and absence from *C. jejuni* 81116 (Ahmed *et al*., 2002). In the recently sequenced *C. jejuni* RM1221 four genes with three of them similar to *ars* genes have been identified (Fouts *et al*., 2005). These *ars* genes have homologues in other sequenced *C. jejuni* strains including *C. jejuni* NCTC11168 (Parkhill *et al*., 2000) and *C. jejuni* 81-176 (Hofreuter *et al*., 2006). Wang *et al* (2009) has characterised *ars* operon in *C. jejuni* RM1221 and found a number of clinical *C. jejuni* isolates to show very high levels of arsenic resistance. The presence of *arsC* in most of the hyperinvasive *C. jejuni* and absence in majority of low invasive might signify increased fitness of hyperinvasive *C. jejuni* in the environment compared to the low invasive *C. jejuni*.

Another gene CJE1310 in *C. jejuni* RM1221 encoding for twin-arginine translocation protein (TatA/E) was found to be present in 5 hyperinvasive *C. jejuni* except in *C. jejuni* 01/35. This gene was found as absent/highly divergent in 3 low invasive *C. jejuni* but present in low invasive *C. jejuni* 01/30 (Group 5, supplementary table 4). In bacteria, the twin-arginine translocase (TAT) secretion system has a role in identifying partially or fully folded proteins and transports them across the cytoplasmic membrane. With an increasing number of *C. jejuni* genome sequences becoming available a number of TAT related genes are being identified (Rajashekara *et al*., 2009). A knockout mutant in *tatC* was found to be deficient in virulence related phenotypes including biofilm formation, motility, flagella synthesis, increased antimicrobial resistance and survival under environmental stresses (Rajashekara *et al*., 2009). Rajashekara *et al* (2009) also showed the importance of *tatC* in chicken colonization. The presence of a twin-arginine related gene in the majority of hyperinvasive *C. jejuni* and absence in most of the low invasive *C. jejuni* might contribute to the improved stress responses and virulence related traits in the hyperinvasive *C. jejuni*. It would be interesting to characterize the role of this gene in all hyperinvasive *C. jejuni*.

A DNA methyltransferase encoding gene CJE1077 (*gidB*) was identified as highly divergent/absent in 5 hyperinvasive *C. jejuni* but present in hyperinvasive *C. jejuni* EX114. This gene was highly divergent in 3/4 low invasive *C. jejuni* (Group 6, supplementary table 4). In a recent study, a gene Cj1461 encoding for a putative DNA methyltranferase was found to have a role in the regulation of virulence in *C. jejuni* (Kim *et al*, 2008). In that study, a mutant in Cj1461 showed reduced adhesion and motility, but increased invasion. CJE1077 (*gidB*) may have a potential role in *C. jejuni* virulence but it has not been characterised as yet.

It is important to analyse the sequence of genes which are identified as being present in the majority of hyperinvasive *C. jejuni* and in one low invasive *C. jejuni* strain or vice versa to account for any gene sequence variation which cannot be detected by the DNA microarray or PCR.

In summary, CGH identified genes of diverse functions. The majority of genes have functions related to the essential cellular and metabolic pathways. Some other genes with role in virulence are also identified. The genes identified as being present and highly divergent/absent in all the hyperinvasive *C. jejuni* strains are the markers of hyperinvasion phenotype as being statistically associated with this group of strains.

### *4.3.6 Distribution of hyperinvasive loci in the pan genome*

The 67 genes identified as present or highly divergent in the hyperinvasive *C. jejuni* strains compared against the low invasive *C. jejuni* and vice versa were classified into six groups (Table 4.1a and 4.1b, and supplementary table 4 in appendix). The distribution of these 67 loci was plotted on the pan genome to see whether any of the selected genes were present in the same operon or functionally identical clusters (Figure 4.5).

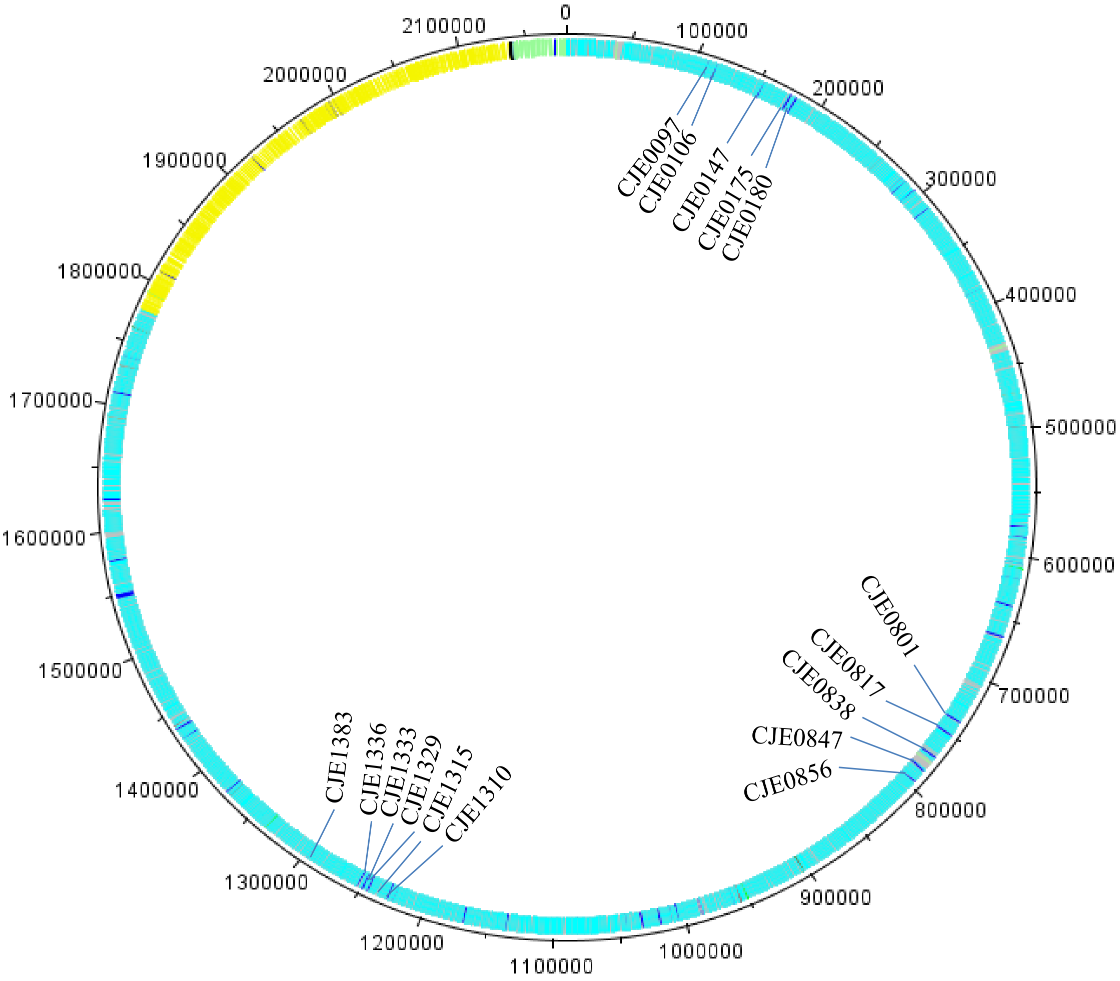


Figure 4.5: Circular diagram of the *C. jejuni*/*C. coli* pan genome showing the distribution of 67 hyperinvasive-associated loci. The region on the pan genome starting from mark ‘0’ and coloured sky blue represents the *C. jejuni* RM1221 genome. The yellow region shows additional genes present in *C. coli* RM2228. The light green and black regions are the loci unique to *C. jejuni* 81-176 and *C. jejuni* 11168 respectively. The selected 67 CDSs (Table 4.1a and 4.1b, and supplementary table 4 in appendix) that were conserved or highly divergent in the hyperinvasive compared to the low invasive *C. jejuni* in this phylogenomics study are highlighted in a dark blue colour. This diagram was generated using the Artemis genome viewing tool (Rutherford *et al.*, 2000). The representative position of some loci which are present close to each other on the pan genome is also shown.

Overall, the majority of 67 genes were randomly distributed across the pan genome. None of the genes belonged to the same operon. The figure 4.5 showed that the genes, CJE0097, CJE0106, CJE0147, CJE0175, *purN* (CJE0180), are present close together between 100,000 bp and 200,000 bp positions on the pan genome but these genes are not adjacent or functionally identical. Similarly, a group of five genes (CJE0801, CJE0817, CJE0838, *cfrA* (CJE0847) and *hisS* (CJE0856) are present between 700,000 bp and 800,000 bp locations and 6 genes (CJE1310, *tsf* (CJE1315), CJE1329, CJE1333, *metF* (CJE1336) and CJE1383) are located between 120,0000 bp and130,0000 bp positions on the pan genome. All the genes within these clusters are not part of the same functional category. The phylogenomic analysis of hyperinvasive *C. jejuni* strains indicates that the hyperinvasive phenotype may not be defined by the presence or absence of gene clusters of one particular functional group. This unique phenotype may be a function of genes of different cellular pathways.

### ***4.3.7 Variability in the hyperinvasive C. jejuni at the whole genome level based on CGH data***

Given that no obvious clusters of the previously identified 67 loci were found it was decided to see the overall diversity in the hyperinvasive and low invasive *C. jejuni* strains and to identify genomic regions that were hotspots for diversity (Figure 4.6).

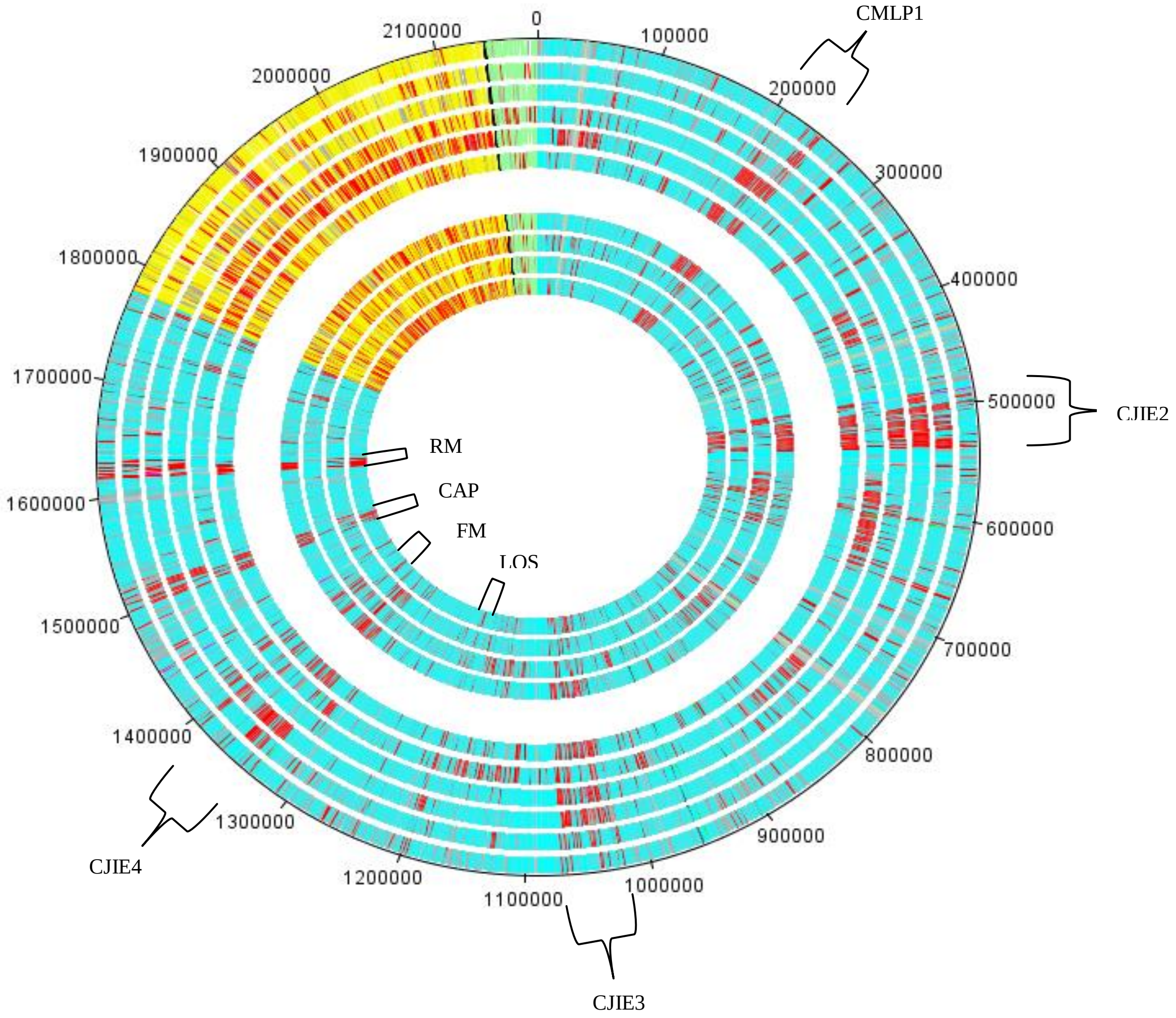


Figure 4.6: The colour coded diagrammatic representation of the CGH pan genome showing genes slightly or highly divergent/absent in the six hyperinvasive and four low invasive *C. jejuni*. The *C. jejuni* RM1221genome on the pan array is coded sky blue. The genes unique to other *C. jejuni* sequenced strains and *C. coli* RM2228 are added to the end of *C. jejuni* RM1221 sequence and include the unique *C. coli* RM2228 CDS (Yellow), unique *C. jejuni* 11168 CDS (Black) and *C. jejuni* 81-176 CDS (Green). The outer six circles (outwards to inwards) represent hyperinvasive *C. jejuni* strains in the order of *C. jejuni* 01/10, 01/35, 01/04, 01/41, 01/51, EX114 followed by four low invasive *C. jejuni* strains, 01/30, 01/32, 01/46, 01/39. Slightly divergent genes are coloured grey and highly divergent genes are red as identified by CGH for each *C. jejuni* strain. CMLP (*Campylobacter* Mu like prophage), CJIE 2, 3, 4 (*Campylobacter jejuni* integrated element), LOS (Lipooligosacccharide), FM (Flagellar modification), CAP (Capsule polysaccharide), RM (Restriction modification) regions in *C. jejuni* RM1221 are labelled.

Our results showed that both groups of *C. jejuni* strains were very diverse irrespective of their invasion phenotype. In the majority of *C. jejuni* strains investigated by CGH, the most variability appeared in the *C. jejuni* RM1221 specific prophages and other mobile genetic integrated regions including CMLP1, CJIE2, CJIE3, CJIE4 (Fouts *et al*., 2005). Virulence related surface structures in *C. jejuni* including capsular polysaccharides (CAP) and lipo-oligosaccharides (LOS), Restriction Modification (RM) and Flagellar Modification (FM) regions were also variable amongst most strains (Figure 4.6). The result is not surprising as these regions showed a great degree of variation in other *C. jejuni* strains with different phenotypes, originating from a variety of sources and disease profiles (Parker *et al*., 2006, Pearson *et al*., 2003, Dorrell *et al*., 2001). Pearson *et al* (2003) studied genomic diversity in 18 *C. jejuni* isolates from a variety of sources using a NCTC11168 DNA microarray. This study identified seven hypervariable genomic regions called Plasticity Regions (PR). Most *C. jejuni* strains were highly divergent in PR5 and 6 which included capsule, LOS biosynthesis and flagella modification genes (Pearson *et al*., 2003). In the other phylogenomics study by Parker *et al* (2006) a collection of 67 *C. jejuni* and 12 *C. coli* strains were studied using a *C. jejuni* NCTC11168 and RM1221 combined array. This study showed that the majority of the strains investigated were lacking/highly divergent in the unique *C. jejuni* RM1221 CJIEs. These tested strains were also highly variable in the capsule and LOS regions (Parker *et al*., 2006).

*C. jejuni* and *C. coli* are closely related species with the majority of genes common in the core and dispensable part of their pan genome. Still the two species contain unique sets of genes that define them as separate species (Lefebure *et al*., 2010). This variation was clearly shown in all *C. jejuni* strains (Figure 4.6) whereby there are many of the *C. coli* specific genes (yellow) that are highly divergent in the *C. jejuni* strains tested here. This also shows a clear advantage of a *C. jejuni* and *C. coli* pan array used in the comparative study over a single genome based arrays used in previous DNA microarray studies (Dorrell *et al*., 2001, Pearson *et al*., 2003) as it covers diversity across the *Campylobacter* genus.

The diversity seen in figure 4.6 agrees with the phylogenomic clustering of the six hyperinvasive and four low invasive *C. jejuni* strains (Figure 4.3). The hyperinvasive *C. jejuni* 01/10 and *C. jejuni* 01/35 were most similar to the reference strains on the pan array with the least number of divergent genes *i.e.* (522 and 550 respectively). The most diverse across the *C. jejuni*/ *C. coli* pan genome was *C. jejuni* 01/51 with 859 divergent genes. The hyperinvasive *C. jejuni* 01/10 possessed some of the loci in CMLP1 and the genes in other *C. jejuni* RM1221 characteristic genomic islands also appeared to be present in this strain. Similarly, most genes in the LOS and FM regions were found to be similar to those present in the reference *C. jejuni* RM1221, whereas, some genes in the CPS region and the RM locus were highly divergent from *C. jejuni* RM1221 (Figure 4.6).

Interestingly, unlike the majority of other *C. jejuni* strains investigated in this phylogenomics study it appears that the *C. jejuni* RM1221 integrated genetic elements CMLP1, CJIE2 and RM region were present in the hyperinvasive *C. jejuni* 01/51. The LOS and FM loci appeared to be highly divergent from those found in *C. jejuni* RM1221. Some genes, including the *kps* genes, in the capsule region of *C. jejuni* RM1221 were also found to be present in *C. jejuni* 01/51. In a previous study, using a *C. jejuni* NCTC11168 based DNA microarray the capsule locus of *C. jejuni* 01/51 was reported as absent (Dr Georgina Manning; personal communication).

## 4.4 SUMMARY AND CONCLUSIONS

The comparative phylogenomics study of six hyperinvasive compared against four low invasive *C. jejuni* strains showed that the hyperinvasive *C. jejuni* did not form a distinct cluster separate from the low invasive *C. jejuni*. There was no gene or gene cluster present or highly divergent/absent in all hyperinvasive *C. jejuni*. However, a number of genes were found to be statistically associated with the hyperinvasion phenotype either by being present or absent from the majority of these strains. These represented genes from a variety of functional categories including genes involved in cellular and metabolic functions, some pathogenesis loci and several genes encoding for hypothetical proteins. Among these, nine genes were present and six genes were absent/highly divergent in all six hyperinvasive *C. jejuni*. PCR screening showed the distribution of these 15 genes in an additional population of 9 low invasive *C. jejuni* strains. This confirmed that the presence or absence of these 15 genes as a genetic marker for the hyperinvasive *C. jejuni*. This DNA microarray study showed that all 10 *C. jejuni* strains showed great diversity at the whole genome level irrespective of their invasion phenotype. The most variable regions in the majority of *C. jejuni* strains were CMLP1, CJIE 2, 3, 4 characteristic of *C. jejuni* RM1221 and *C. jejuni* virulence associated regions like flagellar modification, restriction modification, lipooligosaccharide and capsule. Based on this comparative phylogenomics study it is possible to conclude that the hyperinvasive phenotype is a multifactorial function involving genes from a variety of pathways. Genes involved in essential cellular process that form a part of the core genome may have key a role in the hyperinvasive phenotype in addition to the known *C. jejuni* pathogenesis related loci. Additionally, each of the hyperinvasive *C. jejuni* may use different mechanisms resulting in the hyperinvasive phenotype rather than same gene/gene clusters or pathways.

## 4.5 LIMITATIONS OF DNA MICROARRAY AND NEXT STEP

A major drawback of CGH is that the array is based on the genomic content of already sequenced genomes limiting the information generated to the variation of genes compared to the reference genomes for the phylogenomic comparisons. In addition, DNA microarray does not take into account point mutations, deletions and genomic rearrangements. Also, lack of representation of promoter regions and non-translated RNAs are some other limitations to this approach (Champion *et al*., 2005, Pearson *et al*., 2003). This suggests that the *C. jejuni* strains investigated might contain additional genomic content that could not be picked up in DNA microarray. A quantitative bias is introduced by using all genes on the array for analysis. A number of false positive or negative genes can be detected. To eliminate these will require further validation by alternate screening methods like PCR.

To address the drawbacks of CGH and inverstigate the additional genomic content present in the hyperinvasive *C. jejuni* a Pooled Suppressive Subtractive Hybridization (PSSH) technique was performed (Gerrish *et al*., 2010). The aim of PSSH was to identify any genomic regions that were unique to the pool of six hyperinvasive *C. jejuni* strains compared against the four low invasive *C. jejuni*. This approach will be discussed in the next chapter.

## *Chapter Five*

# SUPPRESSIVE SUBTRACTIVE HYBRIDIZATION STUDY OF THE HYPERINVASIVE *C. JEJUNI* STRAINS

# SUPPRESSIVE SUBTRACTIVE HYBRIDIZATION STUDY OF THE HYPERINVASIVE *C. JEJUNI* STRAINS

## 5.1 INTRODUCTION

After the phylogenomic comparison performed using CGH discussed in the previous chapter, the hyperinvasive *C. jejuni* strains were further investigated at the genome content level by using a technique called Suppressive Subtractive Hybridization (SSH). The main objective of this study was to find genomic regions unique to the hyperinvasive *C. jejuni* strains that were absent from the low invasive *C. jejuni*. It was assumed that these genomic regions are common in all the hyperinvasive *C. jejuni* strains and would be linked to their hyperinvasive phenotype.

### *5.1.1 Suppressive Subtractive Hybridization as a genomotyping technique*

Suppressive Subtractive hybridization is a method to identify unique genomic regions present in one strain (the tester) but absent from the reference strain (the driver) (Agron *et al*., 2002, Ahmed *et al*., 2002). SSH complements the DNA microarray by providing additional information about the genomic structure of the test organism. Whole genome sequencing projects of a large number of strains can be costly and very time consuming. In the absence of genome sequences, SSH can be a good technique to a study closely related strains at the genome level. SSH can easily identify unique genomic regions of about 10-50kb in size and any false positive sequences can be deleted by PCR analysis. SSH has identified genomic variability in *C. jejuni* strains with different colonisation potentials (Ahmed *et al*., 2002). In that study, *C. jejuni* strain 81116, with relatively good chicken colonization potential was compared with *C. jejuni* NCTC11168 by subtractive hybridization to find unique genomic regions in *C. jejuni* 81116 that would account for the difference in colonization potential seen between the two strains. Two hybridization cycles identified 24 clones containing sequences present in 81116 and absent from NCTC11168. Some sequences had similarities with other *C. jejuni* strains while the majority were orthologous to other bacteria. The majority of sequences were found to have functions related to the restriction modification enzymes, arsenic resistance genes, cytochrome c oxidase III, dTDP glucose 4, 6 dehydratase, gamma glutamyl transpeptidase and abortive phage resistance genes (Ahmed *et al*., 2002). In another study, SSH has been used to identify the virulence markers in clinical *H. pylori* isolates from children with peptic ulcers (Oleastro *et al*., 2006). That study identified two genes with putative roles as an outer membrane protein and in lipooligosaccharide biosynthesis to be associated with peptic ulcer disease in children. Another study used SSH to explore the genomic diversity between *C. jejuni* strains from diverse sources including rabbit, cattle and wild birds representing different MLST clonal complexes (Hepworth *et al*., 2007). Here the majority (97%) of SSH inserts identified had similarities with other *C. jejuni*. These inserts mainly encoded for metabolic genes and they were variably distributed among different clonal complexes. However there was no correlation found with the source of strain isolation suggesting that horizontal gene transfer was a rare event between the MLST types studied (Hepworth *et al*., 2007). Using suppressive subtractive hybridization, a number of virulence associated genomic regions have been found in *Escherichia coli* (Dai *et al*., 2010). This study compared an avian associated pathogenic *E. coli* (APEC) with the human uropathogenic *E. coli* to identify genomic regions that would differentiate the two pathotypes. Twenty eight genes were identified that were present in the APEC but absent from the UPEC strain. A genetic marker for adhesion unique to the APEC strain was found. This gene encoded for a putative autotransporter that lead to a 124 kDa adhesive protein that showed high levels of adhesion *in vitro* in chicken fibroblast cell lines (Dai *et al*., 2010). In a recent study, enterohaemorrhagic *E. coli* (EHEC) strains of serotype O26 from a young calf and a human diarrheal patient were investigated by SSH with an aim to identify genomic markers for host preference. The genomic markers associated with host specificity were not found but a number of pathogenicity islands not associated with the EHEC strains were present in the EHEC bovine strain (Bardiau *et al*., 2012). In all above studies, SSH was used to compare one strain with another strain in a single experiment.

### *5.1.2 Pooled Suppressive Subtractive Hybridization to study hyperinvasive C. jejuni*

A new SSH technique called Pooled Suppressive Subtractive Hybridization (PSSH) has been developed and validated recently (Gerrish *et al*., 2010). This method involves genomic DNA comparisons of sets of phenotypically related strains with a reference strain in a single experiment. The inserts identified can be related to the specific strains by PCR screening. Gerrish *et al* (2010) have successfully used PSSH to screen multiple clinical *Staphylococcus aureus* isolates with different levels of disease severity identifying unique genes specific to strains in each pool creating a signature profile for the strains. In this study, the six hyperinvasive *C. jejuni* strains were pooled together as the tester and hybridized against a pool of four low invasive *C. jejuni* (driver) that were previously investigated in the comparative phylogenomic study.

## 5.2 METHODS

### *5.2.1 Pooled Suppressive Subtractive Hybridization*

Suppressive Subtractive Hybridization was carried out by using the CLONE-TECH PCR™-Select Bacterial Genome Subtraction kit (Clonetech, UK) according to manufacturer's instructions. Briefly, the genomic DNA from *C. jejuni* strains was prepared as stated in the genomic DNA extraction procedure in section 2.6.1. The genomic DNA (2 µg) of all six hyperinvasive *C. jejuni* strains (01/10, 01/35, 01/04, 01/41, 01/51, EX114) was mixed together as a "tester" and the genomic DNA (2 µg) of the four low invasive *C. jejuni* strains (01/30, 01/32, 01/46, 01/39) was pooled together as a "driver". Both tester and driver genomic DNA was enzymatically fragmented with *Alu*I and *Dra*I to create blunt ended fragments of size 0.1 to 2.0 kbp. The fragmented tester DNA was divided into two aliquots each ligated to a different adaptor (1 or 2R). The adaptor was ligated to the 5'end of each strand of the double stranded DNA. The first hybridization was carried out by denaturing each aliquot of the adaptor ligated tester DNA and mixing separately with an excess of heat-denatured driver DNA. This hybridization step was carried out at 63 ˚C for 1.5 hours. In the second hybridization, the two adaptor-ligated aliquots were mixed with more freshly denatured driver DNA and incubated overnight at 63 ˚C. The two sets of hybridizations allowed tester DNA to hybridize with the driver DNA or if tester specific, to itself. The tester specific DNA was amplified by primary and secondary PCR cycles. The first set of subtractive hybridization was carried out at 63 ˚C as recommended by the manufacturer. For *C. jejuni* SSH, Ahmed *et al* (2002) repeated the second subtractive hybridization step once by using 10µl of secondary PCR product with a hybridization temperature of 61 ˚C. It ensured efficient subtraction by reducing the number of driver specific sequences. In this study, the secondary hybridization step was carried out twice as recommended by Ahmed *et al* (2002) since a pooled *C. jejuni* sample was used in SSH here. A flow diagram illustrates the PSSH procedure followed (Figure 5.1).

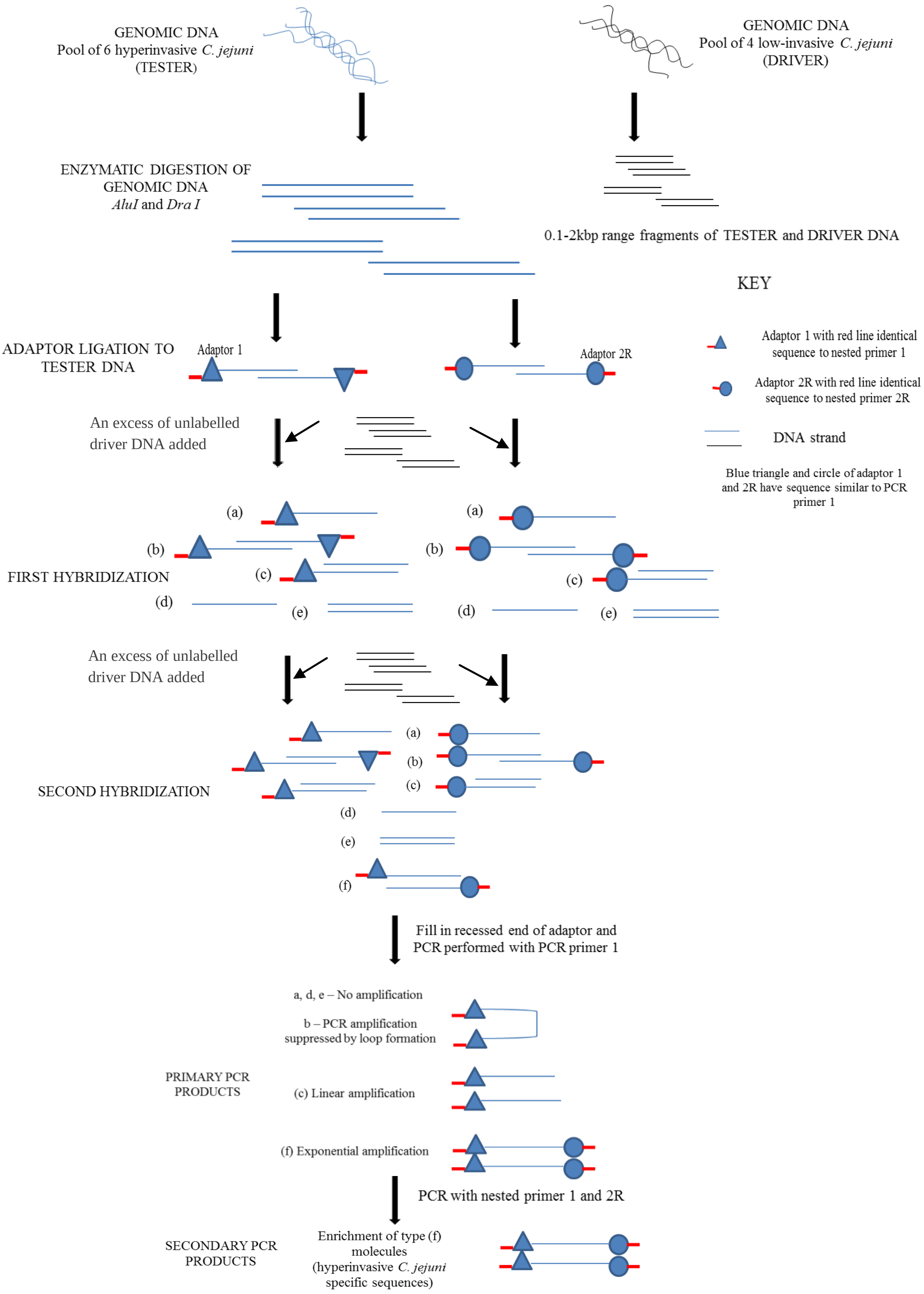


Figure 5.1: A diagram illustrating the methodology used for the pooled suppressive subtractive hybridization.

]

The enzymatically digested tester DNA of pool of 6 hyperinvasive *C. jejuni* strains was subdivided into two sections. Each aliquot was ligated to separate adaptor. During the first hybridization each aliquot was mixed with an excess of freshly denatured drive DNA (pool of 4 low invasive *C. jejuni*). The two aliquots were mixed in the second hybridization with the addition of more denatured driver DNA. During primer PCR, primer 1 amplified the DNA sequences specific to the tester DNA and absent from driver DNA (f molecules). The type f molecules were further enriched in the secondary PCR reaction using nested primers 1 and 2R.

The regions common between the diver and tester genomic DNA hybridized to produce type c molecules. Tester specific DNA fragments formed hybrids with the complementary tester specific DNA (molecules b & f). Similarly, homologous driver specific DNA fragments annealed with complementary driver specific DNA fragments (molecule e). In addition, single stranded tester and driver molecules were also produced (molecules a & d). Two sets of suppression PCR reactions were carried out to amplify and select tester specific sequences. During primary PCR, the adaptors (1 and 2R) at the 5’ end of the dsDNA were duplicated onto the 3’ end of the opposite strand. Primer 1 was used to exponentially amplify dsDNA fragments with both adaptors, 1 and 2R, at either end (molecule f). The dsDNA with adaptor attached at one end only (type c molecules) underwent linear amplification. The dsDNA molecules with only one type of adaptor (molecules b) at both ends were not amplified due to binding of complementary adaptor sequence. The driver specific sequences were not amplified as there was no adaptor attached to them (molecules a, d & e). Secondary PCR was performed using nested primers 1 and 2. These primers were specific to the adaptors 1 and 2R sequences and therefore exponentially amplified the type f molecules. The secondary PCR product was rich with the tester specific sequences.

### *5.2.2 Cloning of PSSH inserts*

The secondary PCR amplicons were ligated into the pCR ® 2.1 TOPO vector using TOPO TA Cloning® kit (Invitrogen, UK). The pCR ® 2.1 TOPO vector with the insert was cloned in 10F’ *E. coli* chemically competent cells as recommended by the manufacturer. The successfully transformed bacteria were selected by using antibiotic(s) and blue white screening. The procedures for cloning and transformation of 10F’ *E. coli* cells (Table 2.1) are briefly discussed in section 2.7.4. The plasmid DNA was extracted from each clone containing the insert by using QIAprep spin miniprep kit (Qiagen, Crawley, UK) (2.6.2). The plasmid DNA was sequenced by single read sequencing using M13 reverse primers (Eurofins, MWG, UK). The similarity of the sequences to the known bacterial genome sequences was performed by using BLASTn and BLASTx searches at the National Centre of Biotechnology Information (NCBI) website. PCR screening was carried out by standard PCR protocol (section 2.7.1) to determine the distribution of these hyperinvasive specific sequences in all six hyperinvasive *C. jejuni* strains. An additional population of 9 low invasive *C. jejuni* strains was also analysed by PCR for the presence or absence of these hyperinvasive *C. jejuni* specific sequences. Details of all primers used in the PCR screen are listed in Table 2.2.2.

## 5.3 RESULTS AND DISCUSSION

### *5.3.1 Preparation of the driver and tester genomic DNA fragments*

Genomic DNA of all 6 hyperinvasive *C. jejuni* strains as a pooled sample “tester” and 4 low invasive *C. jejuni* strains mixed together as “driver” was partially digested with *Alu*I and *Dra*I enzymes. This enzymatic digestion successfully generated small DNA fragments in the size range of 0.1-2 kbp (Figure 5.2).

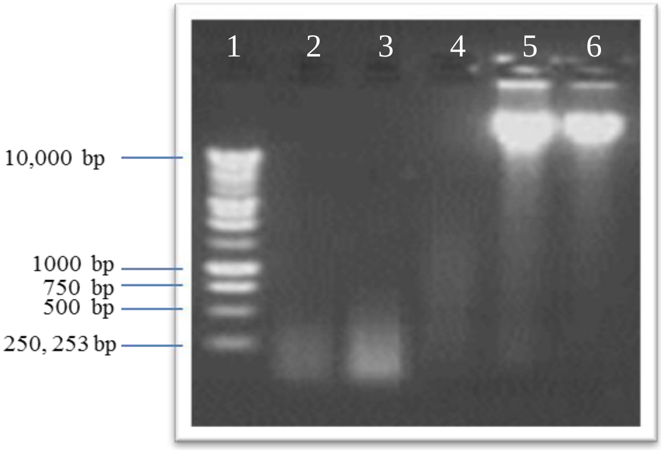


Figure 5.2: The enzymatically digested genomic DNA of the pool of hyperinvasive *C. jejuni* (tester), low invasive *C. jejuni* (driver) and *E. coli* (control) compared to the undigested genomic DNA of the hyperinvasive and low invasive *C. jejuni*.
Lane 1: 1 kbp DNA marker (Promega, UK). The *Alu*I and *Dra*I digested genomic DNA of "tester" *C. jejuni* (lane 2) and "driver" *C. jejuni* (lane 3). The control *E. coli* genomic DNA was digested with *Rsa*I (lane 4). The undigested genomic DNA of "tester" *C. jejuni* (lane 5) and "driver" *C. jejuni* (lane 6) was run as a control to determine the success of enzymatic digestion. The PCR products are analysed on a 2% (w/v) agarose gel.

### *5.3.2 Ligation of adaptors 1 and 2R to the fragmented tester genomic DNA*

After the enzymatic digestion of the genomic DNA, the relevant adaptor (1 or 2R) was then ligated to blunt tester fragments via a blunt ended reaction (section 5.2.1) which occurs between two ds DNA fragments. Therefore, because the 5'ends of the adaptor are unphosphorylated, the adaptor can only ligate via its 3'end to the 5'end of the tester DNA fragment and so only one strand of the adaptor anneals to generate the tester fragments below;

Figure 5.3: The diagram of the adaptor (1 or 2R) ligation to the tester genomic DNA fragment and the primers annealing in PCR reaction for adaptor efficiency testing.

The efficiency of ligation of adaptors to the genomic DNA was tested by PCR amplification (Figure 5.4).

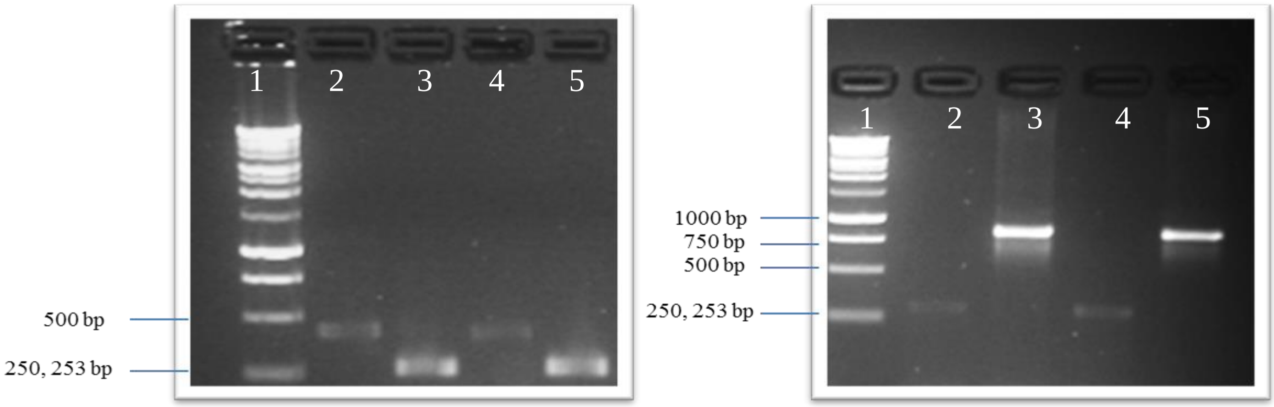

(a) (b)

Figure 5.4 (a): The ligation efficiency testing of *E. coli* (control) and (b) the tester hyperinvasive *C. jejuni*.

(a) Lanes 2 and 4 contain the control *E. coli* (tester) genomic DNA PCR products amplified by using 23S RNA forward and reverse primers. The partially digested genomic DNA of the control *E. coli* (tester) ligated to adaptor 1 (lane 3) and 2R (lane 5) was amplified by using PCR 1 and 23S RNA forward primers. (b) Adaptor 1 and 2R ligated to the partially digested *C. jejuni* “tester” genomic DNA was amplified using PCR 1 and 16S rRNA forward primers (lanes 2 and 4 respectively). The tester genomic DNA of *C. jejuni* was amplified by using 16S rRNA forward and reverse primers (lanes 3 and 5 respectively). Lane 1: 1 kbp DNA marker (Promega, UK). The PCR products were analysed on a 1% (w/v) agarose gel.

PCR amplification using PCR primer 1 specific to the sequence of adaptor 1 and 2R, and 16S rRNA forward primer for the tester *C. jejuni* as a template generated an ~ 290 bp PCR product. A similar size PCR product was produced when amplification was performed for the adaptor ligated control *E. coli* (tester) using PCR 1 and 23S RNA forward primers. This suggests that the enzymatic digestion (5.3.1) produced the DNA fragments of the expected size range of 0.1-2 kbp however, a larger proportion of smaller sized DNA fragment were generated compared to the larger fragments. An expected band of 852 bp was produced by using 16S rRNA forward and reverse primers for the undigested *C. jejuni* tester genomic DNA and 374 bp for the control *E. coli* tester genomic DNA with 23S RNA forward and reverse primers.

The brightness of the adaptor ligated DNA fragment band was very similar to the 16S rRNA product band (Figure 5.4b). This suggests that a high proportion of the adaptor ligated DNA fragments was generated that would ensure efficient hybridization.

### *5.3.3 Subtractive Hybridization I and II*

The suppressive subtractive hybridization procedure was followed as previously described in detail (Ahmed *et al*., 2002). Briefly, 1 and 2R adaptor ligated tester DNA aliquots and the driver DNA (without adaptors) were heat denatured. Two sets of hybridization reactions were carried out at 63 °C. During the first hybridization step, each aliquot of the adaptor ligated tester DNA was mixed separately with an excess of the freshly denatured driver DNA. This step allowed homologous tester and driver DNA fragments to form hybrids. During the second hybridization the 1 and 2R adaptor ligated aliquots were mixed together with an addition of fresh driver DNA. This allowed annealing of any leftover homologous tester and driver DNA fragments. In this step, adaptor 1 ligated tester specific DNA fragments formed homologues with the adaptor 2R ligated tester specific DNA fragments. During hybridization, a range of other molecules were also produced that are shown in figure 5.1.

### *5.3.4 Two second sets of subtractive hybridization steps for the selection of tester specific C. jejuni sequences*

The subtractive hybridization was repeated twice at a lower temperature of 61 °C to enhance the efficiency of subtraction as recommended by Ahmed *et al* (2002). This ensured selection of sequences unique to the hyperinvasive *C. jejuni*. During this step, 10 µl of the secondary PCR product was used as a tester which was heat denatured and mixed with an excess of freshly denatured driver DNA. Two hybridizations were performed as before followed by primary and secondary PCRs. The products of primary and secondary PCR were checked by gel electrophoresis. The primary PCR product showed a smear whereas the secondary PCR product had more distinct bands (Figure 5.5). This showed that secondary PCR product was enriched with tester specific sequences containing products of different sizes.

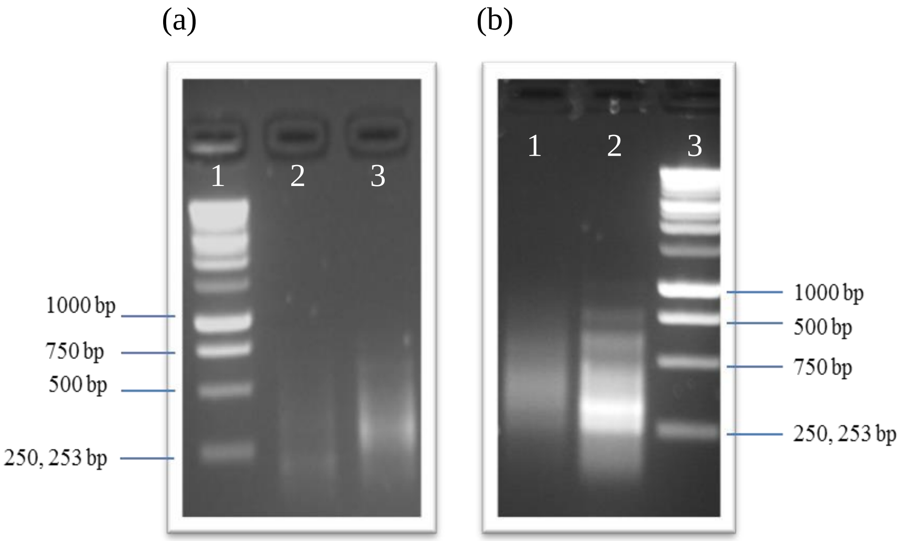


Figure 5.5: The primary and secondary PCR products (a) Control *E. coli* and (b) *C. jejuni*.

(a) Lane 1: 1 kbp DNA marker (Promega, UK), lane 2: primary PCR product of subtracted sample, lane 3: secondary PCR product of subtracted sample. (b) Lane 1: primary and lane 2 secondary PCR product of subtracted sample, lane 3: 1 kbp DNA marker (Promega, UK). The PCR products are analysed on a 2% (w/v) agarose gel.

### *5.3.5 Analysis of successful subtraction of the secondary PCR product*

To further show that the secondary PCR product is enriched with tester *C. jejuni* sequences a validation PCR was performed comparing the loss of a housekeeping gene in the subtracted sample and conservation of this gene in the unsubtracted sample. The PCR analysis was performed with the subtracted control *E. coli* sample after subtractive hybridizations performed at 63 °C compared with the unsubtracted sample using the 23S RNA forward and reverse primers (Figure 5.6 a and b). The PCR screening of the subtracted test *C. jejuni* sample after two sets of subtractive hybridization at 61 °C was carried out using 16S rRNA primers which was compared against the unsubtracted sample (Figure 5.6 c and d).

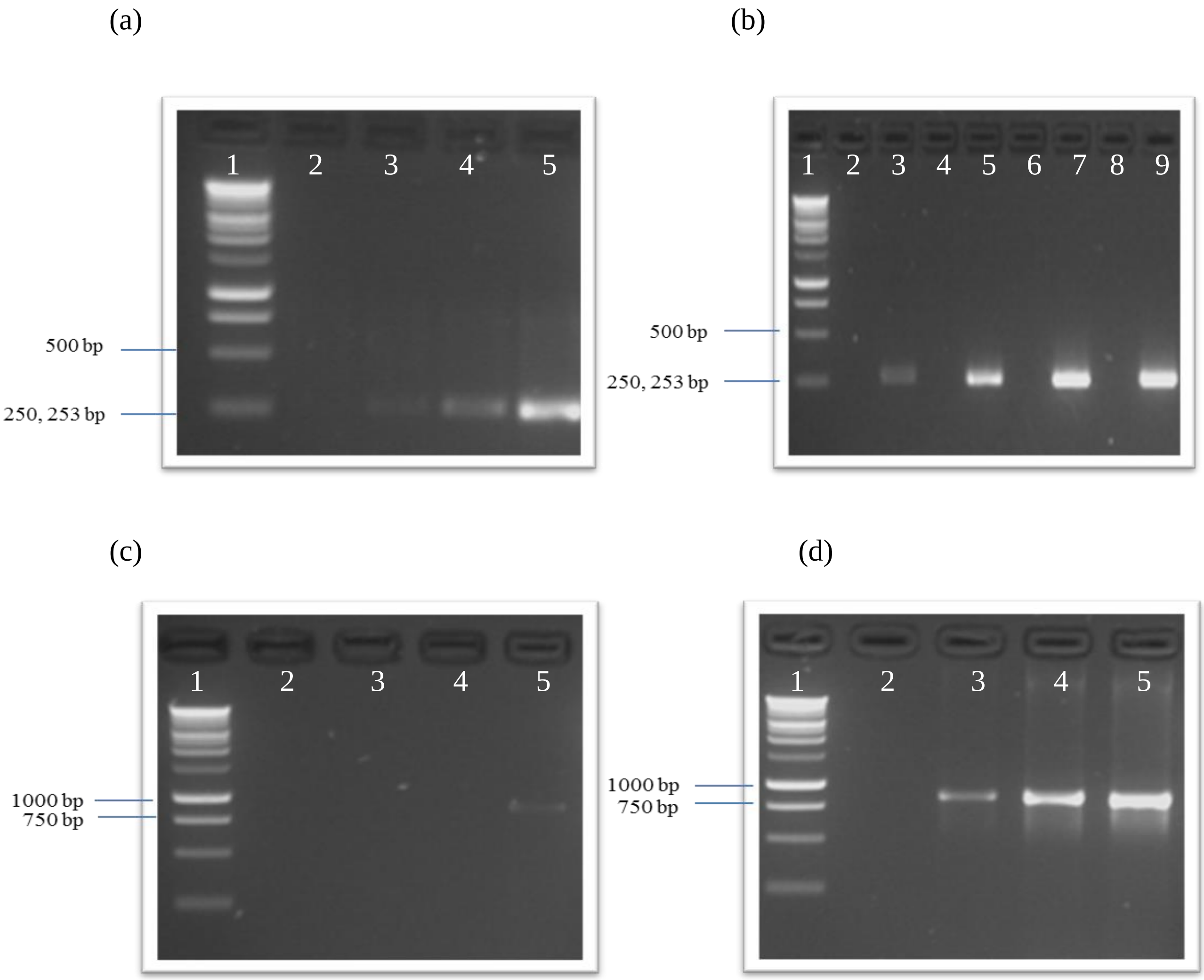


Figure 5.6: The subtraction efficiency of (a) subtracted control *E. coli* (b) unsubtracted control *E. coli* (c) subtracted test hyperinvasive *C. jejuni* and (d) unsubtracted test hyperinvasive *C. jejuni*.
Each gel was loaded: Lane 1; 1 kbp DNA marker (Promega, UK); (a) (lanes 2, 3, 4, 5); subtracted sample after 18, 21, 24, 27 PCR amplification cycles respectively; (b) (lanes 3, 5, 7 and 9); unsubtracted sample after 18, 21, 24, 27 cycles respectively; (lanes 2, 4, 6, 8); Blank; (c) (Lanes 2, 3, 4, 5); PCR products after 18, 21, 24 and 27 amplification cycles respectively (d) (Lanes 2, 3, 4, 5); PCR products after 18, 21, 24 and 27 amplification cycles respectively. The PCR products were analysed on a 2% (w/v) agarose gel.

For the subtracted test *C. jejuni* sample, there was no product seen after 18, 21 and 24 cycles for the subtracted sample whereas a faint band was seen after 27 cycles. For the unsubtracted *C. jejuni* sample on the other hand, no band was observed after 18 cycles with a faint band observed after 21 cycles that got brighter after 24 and 27 cycles. This result showed that two cycles of subtractive hybridization at a lower annealing temperature proved to be a successful step when studying groups of strains as “tester” in a single subtractive hybridization experiment. This reduced the number of tester and driver homologous sequences thus improving the efficiency of subtractive hybridization.

### *5.3.6 Preparation of subtractive hybridization library*

The secondary PCR products were ligated into pCR ® 2.1 TOPO vector using TOPO TA Cloning® kit (Invitrogen, UK) and transformed into 10F’ *E. coli* chemically competent cells. This technique produced 102 colonies of which 62 colonies had inserts. The size of inserts was determined by colony PCR using M13 forward and reverse primers followed by analysis on a 1% (w/v) agarose gel. An example gel picture is shown here (Figure 5.7).

Figure 5.7: The colony PCR screening of clones to determine the size of sequences inserted into pCR ® 2.1 TOPO vector.

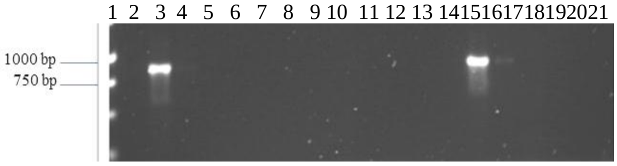
The clones 1-29 (lanes 2-30) showed insert sizes in the range of 300-1000 bp. Lane 1:1 kbp DNA marker (Promega, UK). Lane 31: negative control.

Each clone generated a PCR product more than 200 bp in size. Therefore, all inserts were sequenced.

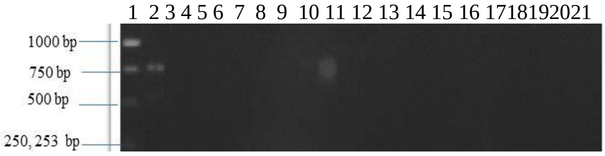
### *5.3.7 Selection of the hyperinvasive C. jejuni specific sequences from subtractive hybridization library*

Sequence similarity carried out using *Campylobacter* specific database (www.campydb) and BLAST searches at NCBI genome bank (www.blast.ncbi.nlm.nih.gov/Blast.cgi) identified 38 out of 62 inserts as duplicates. This showed a limitation of the subtractive hybridization technique where inserts that are in more abundance get amplified (Gerrish *et al*., 2010). Only one representative of the duplicate insert was further analysed. PCR analysis of the remaining 24 inserts identified 11/24 inserts as specific to one or more hyperinvasive *C. jejuni* strains and absent from all low invasive *C. jejuni* strains used as driver. The rest of the 13 inserts were false positives (*i.e*. inserts present in one or more of the low invasive *C. jejuni* strains used as driver). PCR screening also showed the distribution of inserts in an additional 9 low invasive *C. jejuni* strains that was not used in PSSH (Figure 5.8). The PCR analysis results are summarized in table 5.1.

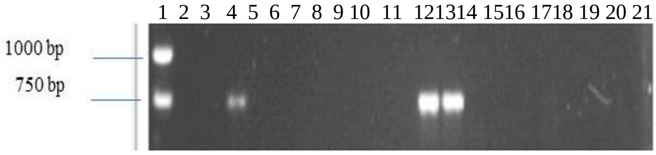
Insert 1



Insert 14

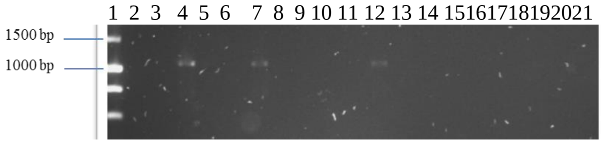


Insert 15



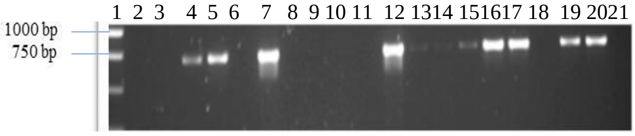
Insert 22

Insert 25

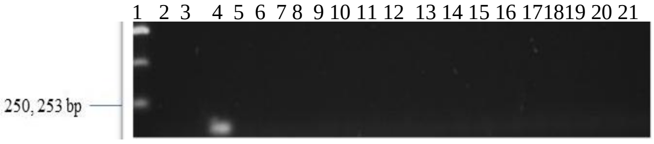


Insert 32

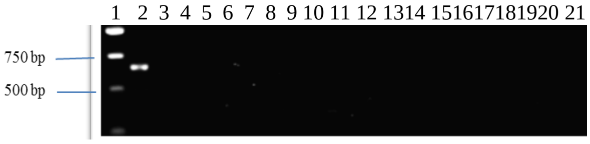
Insert 34



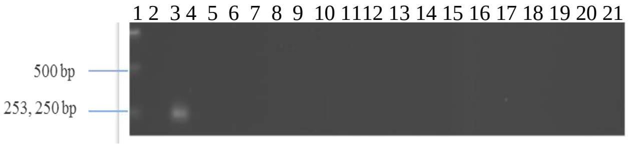
Insert 38



Insert 54



Insert 57

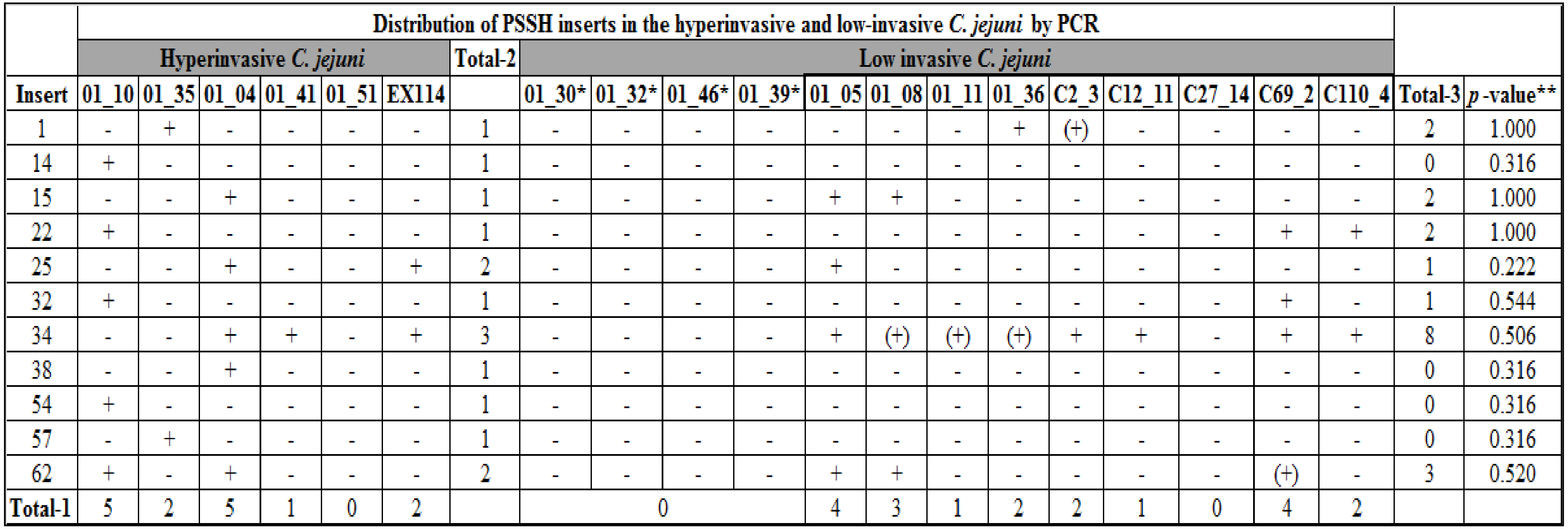


Insert 62

Figure 5.8: PCR screening on a 1% (w/v) agarose gel to show the distribution of 11 inserts in the hyperinvasive and low invasive *C. jejuni* strains.

Lane 1:1 kbp DNA marker (Promega, UK). Lane 2-7; hyperinvasive *C. jejuni* strains 01/10, 01/35, 01/04, 01/41, 01/51, EX114. Lanes 8-20; low invasive *C. jejuni* strains 01/30, 01/32, 01/46, 01/39, 01/05, 01/08, 01/11, 01/36, C2/3, C12/11, C27/14, C69/2, C110/4. Lane 21:negative control. The primers used in PCR screening and the expected product band size are listed in table 2.2.2.

Table 5.1: The distribution of inserts identified by PSSH in the hyperinvasive and low invasive *C. jejuni* strains by PCR analysis.



| | Distribution of PSSH inserts in the hyperinvasive and low-invasive *C. jejuni* by PCR | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Hyperinvasive *C. jejuni* | | | | | | Total-2 | Low invasive *C. jejuni* | | | | | | | | | | | | | | |
| **Insert** | **01_10** | **01_35** | **01_04** | **01_41** | **01_51** | **EX114** | | **01_30*** | **01_32*** | **01_46*** | **01_39*** | **01_05** | **01_08** | **01_11** | **01_36** | **C2_3** | **C12_11** | **C27_14** | **C69_2** | **C110_4** | **Total-3** | ***p*-value**** |
| 1 | - | + | - | - | - | - | 1 | - | - | - | - | - | - | - | + | (+) | - | - | - | - | 2 | 1.000 |
| 14 | + | - | - | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 0.316 |
| 15 | - | - | + | - | - | - | 1 | - | - | - | - | + | + | - | - | - | - | - | - | - | 2 | 1.000 |
| 22 | + | - | - | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | + | + | 2 | 1.000 |
| 25 | - | - | + | - | - | + | 2 | - | - | - | - | + | - | - | - | - | - | - | - | - | 1 | 0.222 |
| 32 | + | - | - | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | + | - | 1 | 0.544 |
| 34 | - | - | + | + | - | + | 3 | - | - | - | - | + | (+) | (+) | (+) | + | + | - | + | + | 8 | 0.506 |
| 38 | - | - | + | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 0.316 |
| 54 | + | - | - | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 0.316 |
| 57 | - | + | - | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 0.316 |
| 62 | + | - | + | - | - | - | 2 | - | - | - | - | + | + | - | - | - | - | - | (+) | - | 3 | 0.520 |
| **Total-1** | 5 | 2 | 5 | 1 | 0 | 2 | | 0 | | | | 4 | 3 | 1 | 2 | 2 | 1 | 0 | 4 | 2 | | |

+=present, - =absent; (+) =partially present (a feint band seen on the gel).

*=The low invasive *C. jejuni* strains used as "driver" in PSSH experiment.

Total-1=Total number inserts present in each hyperinvasive/low invasive *C. jejuni* strain. Total-2: Total number of hyperinvasive *C. jejuni* strains positive for each insert. Total-3: Total number of low invasive *C. jejuni* strains positive for each insert.

**Chi-square, Fisher's exact test was performed to determine if the genes detected in the hyperinvasive group of *C. jejuni* strains was statistically significant. Significance level =1% ($p$=0.01).

The presence of inserts in the hyperinvasive *C. jejuni* strains and their absence from the 13 low invasive *C. jejuni* strains was not statistically significant (Table 5.1). There was no sequence present in all hyperinvasive *C. jejuni*. Eight inserts were specific to only one hyperinvasive *C. jejuni* strain (inserts; 1, 4, 15, 22, 32, 38, 54, 57). Inserts 25 and 62 were present in two hyperinvasive *C. jejuni* whereas insert 34 was found in 3/6 hyperinvasive *C. jejuni* strains. All the inserts were absent from the low invasive *C. jejuni* strains used in the PSSH. This suggests that the pooled suppressive subtractive hybridization technique can successfully detect the sequences specific to strains studied together as a group rather than one to one strain comparison as in a DNA microarray and single SSH experiments. In addition, PSSH can even detect sequences specific to a single strain in a tester pool of several strains. These sequences might be small in size or present in small quantities. Thus, PSSH is sensitive, cost effective and time efficient modification of subtractive hybridization (Gerrish *et al*., 2010).

To complement the CGH data; the prevalence of these 11 inserts was screened by PCR in an additional 9 low invasive *C. jejuni* strains which were not a part of PSSH experiment (Table 5.1). The PCR screening showed that 4 inserts (14, 38, 54, and 57) were absent from all additional low-invasive strains tested, hence specific to the hyperinvasive *C. jejuni*. Six inserts were present in up to three of the low invasive *C. jejuni* strains. Insert 34 was most widely prevalent in the additionally screened low invasive *C. jejuni* strains as it was present in 8/9 of the strains. After the identification of tester specific inserts by PSSH, a standard PCR reaction or Southern hybridization (Ahmed *et al*., 2002) can be used to determine the distribution of inserts in a larger population of strains. This prevents the need of repeating individual subtractions thus reducing chances of error due to multiple sets of experiments and more confidence of dataset.

Interestingly, 5/11 inserts were present in the hyperinvasive *C. jejuni* 01/04 and *C. jejuni* 01/10 with no insert detected in *C. jejuni* 01/51. The PCR profile of the non-PSSH tested low invasive *C. jejuni* population showed that *C. jejuni* 01/05 and C69/2 were positive for greatest number of inserts (4/11) and *C. jejuni* C27/14 did not show presence of any of the 11 inserts (Table 5.1).

### *5.3.8 Homology of the hyperinvasive C. jejuni specific sequences*

The predicted amino acid similarity based on BLAST searches was between 89-100 % for all the inserts (Table 5.2).

Table 5.2: The inserts identified by PSSH as specifically present in hyperinvasive *C. jejuni* strains "tester" and absent from low invasive *C. jejuni* "driver".

| **Insert/Clone** | **Size (bp)** | **Predicted protein similarity** | **Closest match** | **Query coverage (%)** | **Predicted amino acids similarity (%)** |
|---|---|---|---|---|---|
| 1 | 154 | 8-amino-7-oxononanoate | *bioF-2* (*C. coli* RM2228) | 72 | 98 |
| 14 | 191 | Prophage MuSo1, F protein, putative | *C. jejuni* subsp. *jejuni* 260.94/ ICDCCJ07001_672 (*C. jejuni* subsp. *jejuni* ICDCCJ07001) | 76 | 100 |
| 15 | 238 | GDP mannose 4,6 dehydratase | *C. jejuni* subsp. *jejuni* 260.94/ ICDCCJ07001_1357 (*C. jejuni* subsp. *jejuni* ICDCCJ07001) | 86 | 93 |
| 22 | 312 | FkbM family methyltranferase | JJD26997_1251 *C. jejuni* subsp. *doylei* 269.97 | 86 | 96 |
| 25 | 214 | Hypothetical protein | C8J_1243(*C. jejuni* subsp. *jejuni* 81116) | 82 | 95 |
| 32 | 756 | Restriction modification system DNA specificity domain containing protein | *Helicobacter canadensis* MIT 98-5491 | 81 | 89 |
| 34 | 213 | Thiazole synthase | *thiG* (*C. jejuni* subsp. *doylei* 269.97) | 80 | 100 |
| 38 | 229 | No similarity found | ..... | ..... | ..... |
| 54 | 791 | Putative tetracycline resistance protein | *tet* (O/W/32/O) *Streptococcus gallolyticus* subsp. *gallolyticus* ATCC BAA-2069 plasmid pSGG1 | 56 | 97 |
| 57 | 282 | Phage tail fibre protein | BAV0033 (*Bordetella avium* 197N) | 63 | 35 |
| 62 | 235 | Putative sugar transferase | (*C. jejuni* subsp. *jejuni* CG8486) | 84 | 97 |

Predicted protein similarity and closest match show the function/role of the best match for the insert in publically available microbial genome sequences.

Query coverage percentage is the length of each insert used by BLASTx search to find similarity in the sequence database.

The percentage predicted amino acid similarity between the query sequence (insert) and its best protein match in the genome sequence database.

Out of 11 inserts, 4 inserts (14, 38, 54 and 57) were only present in the hyperinvasive *C. jejuni* and absent from the low invasive *C. jejuni* strains. Seven inserts had sequence similarities within the *Campylobacter* genus. Four of 11 inserts (14, 15, 25, and 62) were similar to other *C. jejuni* subsp. *jejuni* strains and 2 inserts (22, 34) were similar to the *C. jejuni* subsp. *doylei* whilst one insert (insert 1) was similar in the *C. coli* genome. Three inserts (32, 54 and 57) were similar to other bacteria. One insert (insert 38) had no sequence similarity to the available sequences in the genome databases searched.

### *5.3.9 Genotyping based on PSSH reveals hyperinvasive C. jejuni specific genes*

Using a pool of six hyperinvasive *C. jejuni* as tester and a group of four low invasive *C. jejuni* a suppressive hybridization study was performed. A variety of genes were identified in this study as specifically present in one or more of the six hyperinvasive *C. jejuni* in the pooled SSH study compared to the low invasive *C. jejuni*. The majority of inserts have homologues found in the *Campylobacter* genus. This may be because the number of *Campylobacter* strains that have been sequenced has rapidly increased providing more information about the genomic structure and diversity exhibited by this pathogen (Fouts *et al*., 2005).

The genes identified in the PSSH study will be discussed below.

Insert 1

Genomic subtractive hybridization identified insert 1 to have similarity to a gene, *bioF*-2 encoding for 8-amino-7-oxononanoate synthase in *C. coli* RM2228 (Table 5.2).

PCR screening showed that insert 1 was present in only one hyperinvasive *C. jejuni* 01/35 and two non-PSSH low invasive *C. jejuni* (*i.e*. 01/36, C2/3) (summary Table 5.1). The PCR product was seen as a bright band in the low invasive *C. jejuni* 01/36 after 30 amplification cycles whereas only a faint band was observed for *C. jejuni* C2/3 after the same number of cycles (Figure 5.8). This might suggest that *bio-F2* may have a variable sequence in this strain. By contrast, our CGH study (chapter 4) showed that *bioF-2* gene was present in 4/6 hyperinvasive (*C. jejuni* 01/35, 01/04, 01/41 and EX114) whilst slightly divergent in the hyperinvasive *C. jejuni* 01/10 and highly divergent/absent in the hyperinvasive *C. jejuni* 01/51. CGH data also showed that *bioF-2* was present in the low invasive *C. jejuni* 01/30 and 01/46 but highly divergent in the low invasive *C. jejuni* 01/32 and 01/39. Unlike for PSSH, where the distribution of each insert in *C. jejuni* strains was determined by PCR the CGH result for this gene was not validated by PCR.
BioF-2 is an enzyme involved in biotin biosynthesis. It catalyses the decarboxylation of amino acids by condensation between amino acid and acetyl-coA producing 8-amino-7-

oxononanoate as an important subtrate in biotin production (Alexeev *et al*., 1998). BioF-2 is an important metabolic enzyme in *C. jejuni* (Fouts *et al*., 2005). The detection of metabolic gene as a genetic marker by the genomic subtractive hybridization in a hyperinvasive *C. jejuni* may suggest the role of metabolic pathways in the hyperinvasive phenotype. The metabolic core of *C. jejuni* is generally considered stable. The horizontal transfer of metabolism related genes showed that these genes are under selective pressure and confer advantage to pathogenic bacteria in disease process inside the host cells. The similarity of insert 1 to the gene *bioF-2* in *C. jejuni* sister species, *C. coli* validates recent research findings that *C. jejuni* and *C. coli* are more closely related species to each other than to other member of the *Campylobacter* genus (Fouts *et al*., 2005). Still there is enough genomic variation in two species allowing the transfer of genomic material between them. There is also emerging scientific evidence of convergence of *C. jejuni* and *C. coli* genomes resulting in the evolution of conserved core genomes which is attributed to several epidemiological and ecological factors including human activity (Sheppard *et al*., 2008) which further supports our findings.

Insert 14

Insert 14, showed similarity to the prophage MuSo1, F protein, with putative similarity in *C. jejuni subsp. jejuni* ICDCCJ07001 and 260.94 (Table 5.2). This insert was present in the hyperinvasive *C. jejuni* 01/10 and absent from the PSSH and PCR screened low invasive *C. jejuni* strains (Figure 5.8 and Table 5.1).

Bacteriophage are the vehicle of horizontal gene transfer that contribute to diversity in the bacterial genome and may carry genes that contribute to the virulence in bacterial pathogens. Examples include emergence of bacterial pathogens including *E. coli* O157 and *V. cholerae* (Canchaya *et al*., 2004). *E. coli* O157, an important human pathogen contains two lambdoid prophages that encode for Shiga-like toxins (Stx) which is a major virulence factor for this strain (Wagner *et al*., 2002). There is an evidence of presence of prophages and insertion elements (IS) in *Campylobacter* species (Fouts *et al*., 2005). A *Campylobacter* Mu-like phage (CMLP1) in *C. jejuni* RM1221 genome is located upstream of *argC* locus and encodes for proteins with resemblance to the bacteriophage Mu and other Mu-like prophage proteins. CMLP1 in *C. jejuni* does not contain any virulence determinants but may contribute towards pathogenicity by changing the function of other virulence related genes. Other mobile genetic elements in

*C. jejuni* RM1221 include *Campylobacter* Integrated Elements (CJIEs 2, 3 and 4) scattered along the genome. These integrated elements are absent from the first genome sequenced *C. jejuni* NCTC11168. *C. jejuni* RM1221 like genetic elements are conserved in several other *C. jejuni* and *C. coli* strains but show a high level of diversity (Parker *et al.*, 2006, Clark and Ng., 2008). The prophages showed high levels of recombination resulting in mosaic pattern of distribution of these prophages in *C. jejuni* strains. The detailed sequence analyses of CMLP 1 from different *C. jejuni* strains showed homology to the bacteriophage characteristic of enteric pathogens that are known to be responsible for a number of virulence phenotypes including host specificity (Clark and Ng., 2008). *C. jejuni* ICDCCJ07001 is a GBS associated strain isolated from a GBS outbreak in North China in 2007. This strain contains *C. jejuni* RM1221 characteristic CMLP1 but in the reverse orientation. The CMLP1 in *C. jejuni* ICDCCJ07001 is inducible but is not known to contain any virulence related genes (Zhang *et al.*, 2010). To date, there is no biological evidence to prove the role of these prophage genes in virulence of the hyperinvasive *C. jejuni* strains.

Insert 57

A phage tail fibre protein I (insert 57) in *Bordetella avium* 197N (Table 5.2) has been identified only in the hyperinvasive *C. jejuni* 01/35 and absent from all low invasive *C. jejuni* strains (Table 5.1 and Figure 5.8). *Bordetella avium* is a pathogenic bacteria of wild and domesticated birds mainly commercially raised turkeys. It is the causative agent of bordetellosis, a respiratory illness in avian species (Sebaihia *et al.*, 2006). *B. avium* 197N is a well-studied sequenced strain of this avian pathogen. *B. avium* 197N contains three prophages namely prophage A (BAV0391-BAV0433), prophage B (BAV1280-BAV1342) and the third prophage (BAV1423-BAV1482). Prophage A has genes encoding for a well-known phenomenon in *Bordetella* species known as switching tropism (Sebaihia *et al.*, 2006). Tropism switching activity determines the specificity of bacterial receptors to the host surface. However, in *B. avium* 197N most of the internal region responsible for tropism (BAV0416-BAV0430) is missing and the transcriptase responsible for tropism switch over is also absent (Sebaihia *et al.*, 2006). The insert found in the hyperinvasive *C. jejuni* 01/35 with similarity to the phage tail fibre protein, (BAV0033) in *B. avium* 197N is a part of prophage A. Since, poultry is the common host for *B. avium* and *C. jejuni*, the transfer of genes encoded on mobile genetic elements is expected which may contribute to the diversity in genome.

Insert 15 and 62

A sequence (insert 15) identified by PSSH was only found in the hyperinvasive *C. jejuni* 01/04. In the non-PSSH low invasive *C. jejuni* strains analysed by PCR, insert 15 was detected in *C. jejuni* 01/05 and 01/08 (Figure 5.8 and Table 5.1). This insert showed similarity to GDP mannose 4, 6 dehydratase in *C. jejuni* 260.94 and ICDCCJ07001 (Table 5.2). The gene ICDCCJ07001_1357 is the part of *C. jejuni* ICDCCJ07001 capsule locus.
The product of gene *dmhA* (GDP mannose 4, 6 dehydratase) is an enzyme responsible for the conversion of heptose to deoxyheptose. It is located in the variable region of CPS loci of many *C. jejuni* strains (Karlyshev *et al*., 2005a, Poly *et al*., 2011). Karlyshev *et al* (2005a) found *dmhA* in the caspule locus of many *C. jejuni* strains, fully functional in some strains but variable in other *C. jejuni* strains. *C. jejuni* ICDCCJ07001 is a GBS associated clinical isolate. It is very similar to another sequenced GBS causing *C. jejuni* strain 260.94. Both strains have the Penner serotype (HS41) and share sequence similarity in their capsule region (Zhang *et al*., 2010).

Another insert 62, showed similarity to a putative sugar transferase in *C. jejuni* 8486 (Table 5.2). PCR analysis showed that this insert was present in two hyperinvasive *C. jejuni* 01/10 and 01/04. Among the additional low invasive *C. jejuni* strains screened by PCR, this insert was present in *C. jejuni* 01/05 and 01/08. A faint band was also seen in low invasive *C. jejuni* C69/2 (Figure 5.8 and Table 5.1). Putative sugar transferase is a sugar biosynthesis gene present in the *C. jejuni* CPS region (Poly *et al*., 2011). *C. jejuni* CG8486 is a human clinical isolate from a soldier presenting symptoms of bloody diarrhoea. The CAP locus in *C. jejuni* GC8486 is a 26kbp region and belongs to the Penner serotype (HS4). The CAP locus in *C. jejuni* CG8486 is similar in size to the CAP region in *C. jejuni* 81-176 but smaller than in *C. jejuni* NCTC11168. The *C. jejuni* CG8486 CAP locus encodes for sugar transferases already known in the capsule locus of *C. jejuni* strains (Poly *et al*., 2007b).

The capsule locus in *C. jejuni* is composed of a highly variable central region enclosed by the conserved *kps* genes on either side. Due to the variabiliy in middle capsular region it is responsible for the generation of diverse polysaccharide structures in different *C. jejuni* strains. These diverse capsule structures assigns strains to different

Penner serotypes (Dorrell *et al*., 2001, Pearson *et al*., 2003, Karlyshev *et al*., 2005a and b, Poly *et al*., 2011). The strains within the same Penner serotype complexes are found to have similar CPS region (Karlyshev *et al*., 2005a and b, Poly *et al*., 2011). In contrast to the reports of above authors the Penner serotype of the hyperinvasive *C. jejuni* 01/10 is HS50 whereas *C. jejuni* 01/04 is not known (data discussed in chapter 4). The capsule biosynthesis genes in the hyperinvasive *C. jejuni* strains identified here with the best match to other *C. jejuni* CPS genes may suggest a mosaic pattern of distribution of the variable capsular genes in *C. jejuni* (Poly *et al*., 2011). As the CPS regions are known to be variable amongst strains which is likely the reason that by using SSH approach these kinds of strain-specific genes are detected. The surface capsular structures in *C. jejuni* are known to contribute to pathogenesis mainly, adhesion and invasion of host cells and serum resistance (Bacon *et al*., 2001, Guerry *et al*., 2002). Hence, the role of capsule in the hyperinvasive phenotype of *C. jejuni* strains studied here cannot be neglected.

### Inserts 22 and 34

Inserts 22 and insert 34 showed maximum similarity to the FkbM family methyltransferase and thiazole synthase (*thiG*) in *C. jejuni* subsp. *doylei* respectively (Table 5.2). Insert 22 was present the hyperinvasive *C. jejuni* 01/10. The low invasive *C. jejuni* C69/2 and C110/4 were also positive for insert 22. Insert 34, was found to be present in the hyperinvasive *C. jejuni* 01/04, 01/41 and EX114 (Table 5.1). Among the additional low invasive *C. jejuni* strains insert 34 was present in *C. jejuni* 01/05, C2/3, C12/11, C69/2, C110/4 seen as bright bands on the agarose gel (Figure 5.8). There were feint bands detected in the low invasive *C. jejuni* 01/08, 01/11, 01/36 that may represent polymorphic gene in these strains.

The similarity of inserts 22 and 34 in *C. jejuni* subsp. *doylei* suggests that the two species (*i.e*. *C. jejuni* subsp. *jejuni* and *C. jejuni* subsp. *doylei*) frequently exchange genetic material. This is in contrast to the findings by Parker *et al* (2007) who reported these two subspecies of *C. jejuni* as highly divergent from each other using MLST and a DNA microarray based comparative genomics based indexing (CGI).

DNA methyltransferases are diversely present in bacteria and usually form a part of R-M systems in bacteria (Dale and Park., 2004). They are responsible for the methylation of $N^6$ position in adenine and $N^4$ and $C^5$ position in cytosine in bacteria (Wion and

Casadesús., 2006. Like the variable CPS genes, DNA methyltransferases encoding genes are likely to be identified in SSH screening as they are variably distributed among the *C. jejuni* strains. Recently, the role of a DNA methyltransferase encoded by the gene Cj1461 in *C. jejuni* virulence has been demonstrated. This DNA methyltransferase influenced adherence, invasion and motility in *C. jejuni* 81-176 (Kim *et al*., 2008). Having known the role of DNA methyltransferase in virulence it would be interesting to study the role of FkbM family methyltransferase in invasion and other virulence traits in the hyperinvasive *C. jejuni* 01/10.

Thiazole synthase is an important enzyme of thiazole biosynthesis. In *E. coli* and other anaerobic bacteria the components of this enzyme; ThiH, ThiG, ThiS and ThiF are essential for thiamine biosynthesis process. During this process an intermediate product, dehydroglycine is produced which is taken up by ThiG to be used for thiazole cyclization process (Kriek *et al*., 2007).

Insert 32

Insert 32 was similar to the Restriction modification system DNA specificity domain-containing protein in *H. canadensis* MIT 98-5491 (Table 5.2). PCR screening showed the presence of this insert in the hyperinvasive *C. jejuni* 01/10. Among the low invasive *C. jejuni* strains not a part of PSSH experiment, insert 32 was only present in the low invasive *C. jejuni* C69/2 (Figure 5.8 and Table 5.1). The restriction modification systems in bacteria are defence systems against the foreign DNA especially introduced by the lytic and lysogenic bacteriophage. Different types of RM systems are present in bacteria called type I, II, II and IV. The type I RM system in a number of *C. jejuni* strains has been studied in detail (Miller *et al*., 2005). There are few type II and III RM systems in sequenced genomes of *C. jejuni* NCTC11168, *C. jejuni* RM1221, *C. coli* RM2228 and *C. lari* RM2100 (Fouts *et al*., 2005). *H. hepaticus* ATCC 51449 is like other *Campylobacter* species strains in RM systems with only few RM system genes. In contrast, *C. upsaliensis* RM3195 genome has DNA sequences encoding for adenosine and cytosine DNA-methyltransferases in addition to a putative type II and III RM systems (Fouts *et al*., 2005) hence, similar to *H. pylori* that has three to four type I R-M systems (Miller *et al*., 2005). The restriction modification systems have shown extensive diversity based on the origin of strains (Parker *et al*., 2007, Ahmed *et al*., 2002, Dorrell *et al*., 2001). A putative RM DNA sequence in the hyperinvasive *C. jejuni* from *Helicobacter* species may contribute to enhanced resistance against the foreign DNA making this strain more stable inside the host and in outside environment.

### 5.3.9.7 Insert 54

Insert 54, showed match with a putative tetracycline resistance gene *tet* (O/W/32/O) in *Streptococcus gallolyticus* subsp. *gallolyticus* ATCC BAA-2069 plasmid pSGG1 (Table 5.2). This insert was only present in the hyperinvasive *C. jejuni* 01/10 (Figure 5.8 and Table 5.1). Antibiotic resistance among *C. jejuni* strains is highly prevalent and is a major threat to human health (Pratt and Korolik., 2005). There are a number of tetracycline resistance genes that are either chromosomally encoded or located on a plasmid (Roberts., 2005). In *Campylobacter* species *tetO* gene is mainly responsible for tetracycline resistance (Pratt and Korolik., 2005). This gene encodes for a Tet(O) protein that protects the ribosome from the damaging effects of tetracycline (Roberts., 2005). Natural transformation allows transfer of antibiotics resistance between *Campylobacter* species in a mixed population (Jeon *et al*., 2008). A self-transmissible plasmid pIP1433 in *C. coli* BM2509 carries *tetO* gene and transfer of this gene is evident in the streptococcus and enterococcus species causing high levels of tetracycline resistance in these organisms (Zilhao *et al*., 1988). A recent study has shown the transfer of antibiotic resistance between *C. jejuni* and *H. pylori* strains by conjugation (Oyarzabal *et al*., 2007). This suggests that *C. jejuni* is capable of uptaking antibiotics resistance genes from other organisms. The identification of insert in the hyperinvasive *C. jejuni* 01/10 with similarity to *tetO* from *S. gallolyticus* subsp. *gallolyticus* ATCC BAA-2069 plasmid pSGG1 may suggest it to be a stable strain with added tetracycline resistance. The increased antibiotic resistance would allow improved survival inside the human host. It would be interesting to know how antibiotic resistance would influence the invasion phenotype in this hyperinvasive *C. jejuni* strain.

### Insert 25

Insert 25 was found in the hyperinvasive *C. jejuni* 01/04 and EX114. PCR analysis showed that this insert was present in the low invasive *C. jejuni* 01/05 (Figure 5.8 and Table 5.1). The similarity of insert 25 to the hypothetical gene in the *C. jejuni* 81116

(Table 5.2) highlights the fact that a large proportion of *C. jejuni* genome is functionally uncharacterized and these regions of unknown function add to the genome diversity.

Insert 38

One sequence detected in only *C. jejuni* 01/04 (Figure 5.8 and Table 5.1) has no similarity found in the genome databases searches (Table 5.2). The identification of such functionally uncharacterised sequences may suggest that the hyperinvasive *C. jejuni* strains have sufficient variation in their genome.

Such broad range of inserts recovered from PSSH with similarity to within and between species genomic regions and to other organisms suggests that hyperinvasive *C. jejuni* strains have a striking ability to diversify by accepting genomic materials from other sources to evolve as versatile human pathogens.

## 5.4 CONCLUSIONS AND NEXT STEP

The pooled suppressive subtracted hybridization study compared 6 hyperinvasive *C. jejuni* as a tester with a group of 4 low invasive *C. jejuni* strains as a driver. This technique identified 11 sequences specific to the hyperinvasive *C. jejuni* that were absent from the low invasive *C. jejuni* strains. There was no insert common in all the hyperinvasive *C. jejuni* strains. All inserts were present in one or more hyperinvasive *C. jejuni* strains and were variably distributed in the additional low invasive *C. jejuni* strains only screened by PCR. This suggests that the sequences identified may just represent the strain specific genes rather than the hyperinvasive *C. jejuni* specific genes. The detected sequences had a range of functions with inter and intra species homology and similarity with other bacteria. This proved that the hyperinvasive *C. jejuni* are a diverse group of strains. Both the DNA microarray and subtractive hybridization showed that the hyperinvasive *C. jejuni* 01/10 was the most diverse strain and *C. jejuni* 01/51 was least variable. These two hyperinvasive strains were selected for further analysis by the next generation genome sequencing.

## *Chapter Six*

# WHOLE GENOME SEQUENCING OF *C. JEJUNI* 01/10 AND 01/51

# WHOLE GENOME SEQUENCING OF *C. JEJUNI* 01/10 AND 01/51

## 6.1 INTRODUCTION

Genome sequencing has become a tool in providing detailed insight into the genomic diversity and evolution of bacteria. The genomic structure of two hyperinvasive *C. jejuni* strains (01/10 and 01/51) was studied in greater depth by using whole genome sequencing.

### *6.1.1 Campylobacter genome*

The first *Campylobacter* genome to be sequenced was *C. jejuni* NCTC11168 was sequenced in 2000. The sequencing data revealed that *C. jejuni* 11168 has a 1.6 Mb genome containing 1,641,481 base pairs with 30.6% G+C content and represented an AT rich genome. The genes in the genome encoded for 1,654 proteins and 54 stable types of RNA (Parkhill *et al*., 2000). Later, re-annotation and reanalysis of NCTC11168 genome sequencing data reduced the predicted protein sequences from 1,654 to 1,643. The functional categories were revised and new information for several coding sequences was added which was not reported before (Gundogdu *et al*., 2007). The *C. jejuni* 11168 genome is unique as it does not contain large inserts or prophage sequences and very few sequence repeats. There are hypervariable regions present marked by homopolymeric repeats and low G+C content compared to the whole genome (Parkhill *et al*., 2000). Most of the hypervariable sequences encode for surface structures such as LOS, capsule, flagellar biosynthesis and the glycosylation locus (Miller, 2008). Later another *C. jejuni* isolate was sequenced and compared with non-*C. jejuni* isolates. *C. jejuni* RM1221 has a large size genome (1.8 Mb) compared to *C. jejuni* 11168. It contains one *Campylobacter* Mu-like prophage (CMLP1) and three insertion elements and some additional capsule biosynthesis genes that are absent from *C. jejuni* NCTC11168. *C. jejuni* NCTC11168 and *C. jejuni* RM1221 were more closely related to *C. coli* than to *C. lari* and *C. upsaliensis* (Fouts *et al*., 2005). Other *C. jejuni* strains fully genome sequenced and characterised include *C. jejuni* 81-176 (Hofreuter *et al*., 2006), 81116 (Pearson *et al*., 2007), CG8486 (Poly *et al*., 2007b), M1 (Friis *et al*., 2010), ICDCCJ07001 (Zhang *et al*., 2010) and S3 (Cooper *et al*., 2011). The genome of *C. jejuni* subsp. *doylei* has been sequenced and contains 2,037 genes with 251 pseudogenes (Parker *et al*., 2007). Strain to strain variation is observed based on the genome sequence data. The genome sequence of human clinical isolates NCTC11168, 81-176 and CG8486 have 1,474 conserved genes. *C. jejuni* 81-176 contains 35 unique genes, CG8486 shows 38 unique genes and *C. jejuni* NCTC11168 has 8 unique genes (Champion *et al*., 2008). A DNA microarray comparison showed that several *C. jejuni* strains were highly variable compared to the reference strain NCTC11168. Seven hypervariable plasticity (PR1-PR7) regions were identified in the genome of *C. jejuni* strains examined that consisted of 50% of the variable gene pool (Pearson *et al*., 2003). Some *Campylobacter* strains contain plasmids. For example, pVir and pTet plasmids are present in *C. jejuni* 81-176 (Batchelor *et al*., 2004, Bacon *et al*., 2000) and the pVir plasmid has a role in pathogenesis (Champion *et al*., 2008). The number of *Campylobacter* strains sequenced is ever increasing. To date, 15 *Campylobacter* strains have been full genome sequenced consisting of 11 *C. jejuni* strains (including *C. jejuni* subsp. *doylei* 269.97) and 4 non-*C. jejuni* strains. There are also a number of on-going *Campylobacter* genome projects. Whole genome sequencing has become a crucial technique providing useful information about the differences in their virulence potential and host specificity of campylobacters.

### *6.1.2 Study aims*

The CGH study of the hyperinvasive *C. jejuni* showed that *C. jejuni* 01/10 and *C. jejuni* 01/51 were the most variable strains when compared to the reference strains. Similarly, the PSSH comparison of the hyperinvasive *C. jejuni* strains identified most additional sequences in *C. jejuni* 01/10 whereas none of the inserts were present in *C. jejuni* 01/51. Additionally, *C. jejuni* 01/51 has been studied in detail by insertional mutagenesis which identified several genes with potential roles in hyperinvasion of this strain (Javed *et al*., 2010). It was observed using DNA microarray technology that *C. jejuni* 01/51 lacked some capsule biosynthesis genes which are present in many other *C. jejuni* strains (Dr Georgina Manning; personal communication) and the CGH data in this project showed that this strain possesses the *kps* and some other capsule genes similar to those present in *C. jejuni* RM1221. Based on these studies and available resources *C. jejuni* 01/10 and *C. jejuni* 01/51 were selected for sequencing using next generation sequencing techniques. *C. jejuni* 01/51 was genome sequenced using two methods; pyrosequencing/454 and Illumina sequencing. *C. jejuni* 01/10 was genome sequenced only by Illumina sequencing. The genome sequence data mining was performed with the following key aims;

- Identify additional genomic content unique to the hyperinvasive *C. jejuni* 01/51 and *C. jejuni* 01/10
- Annotate potential CDS to classify gene function and associate any relationship to the hyperinvasive phenotype exhibited by these strains.
- Phylogenomic comparison of the hyperinvasive *C. jejuni* compared with other available genome sequenced *C. jejuni* strains.

## 6.2 METHODS

The genomic DNA of *C. jejuni* 01/51 and 01/10 was prepared by using the Qiagen genomic DNA extraction kit. The method followed is discussed in material and methods chapter 2 (section 2.6.1).

### *6.2.1 Illumina sequencing*

The Illumina sequencing was performed by the genome sequence facility at the University of Exeter, Exeter, UK (Figure 6.1).

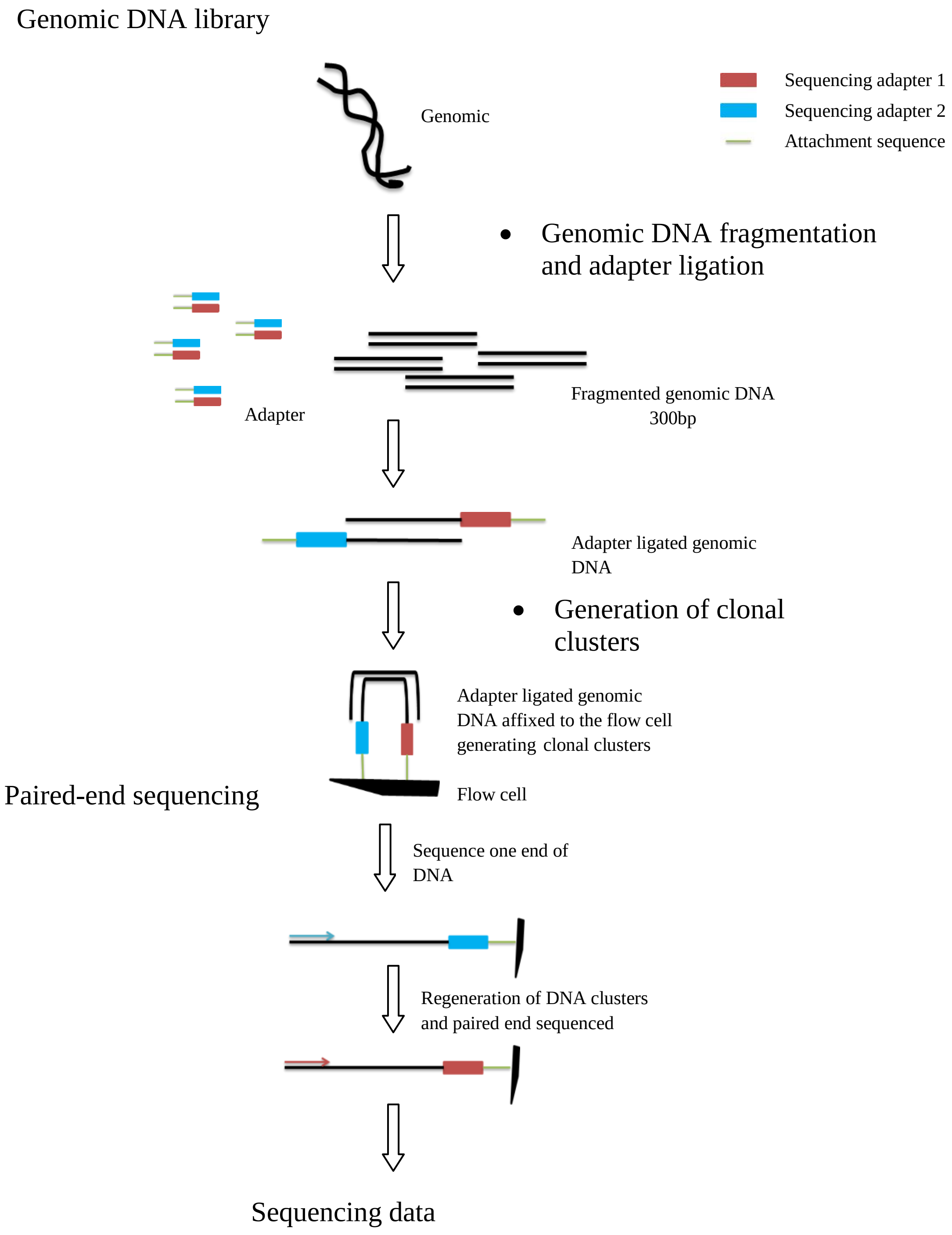


Figure 6.1: A diagrammatic representation of Illumina sequencing technique.

In this sequencing method, the genomic DNA was fragmented by shearing generating 300bp size fragments using the Tru-Seq Genomic library preparation kit. Multiplex PCR was than performed using 6 bp index sequences into a single lane. The genomic DNA fragments were sequenced using paired end 72 bp read lengths on an Illumina GAIIx sequencer using SCS software (v 2.8) (Figure 6.1).

The raw sequence data for *C. jejuni* 01/51 and 01/10 was provided in 72 and 75 contigs respectively. *De novo* assembly was performed using the velvet assembly program (v 1.0.18) (Zerbino and Birney., 2008). The annotation of the reference strain *C. jejuni* RM1221 was transferred onto the un-annotated query sequence using the Rapid Annotation Transfer Tool (RATT) (Otto *et al*., 2011). GLIMMER (v 3.02) (Salzberg *et al*., 1998) prediction was used to identify ORFs which were unique to the sequenced genome. These ORFs were annotated by Campydb and the NCBI BLASTx tools.

### *6.2.2 Pyrosequencing/454*

Pyrosequencing of *C. jejuni* 01/51 and genome assembly was performed by Dr Chrystala Constantinidou in the genome sequence facility at the University of Birmingham (Figure 6.2).

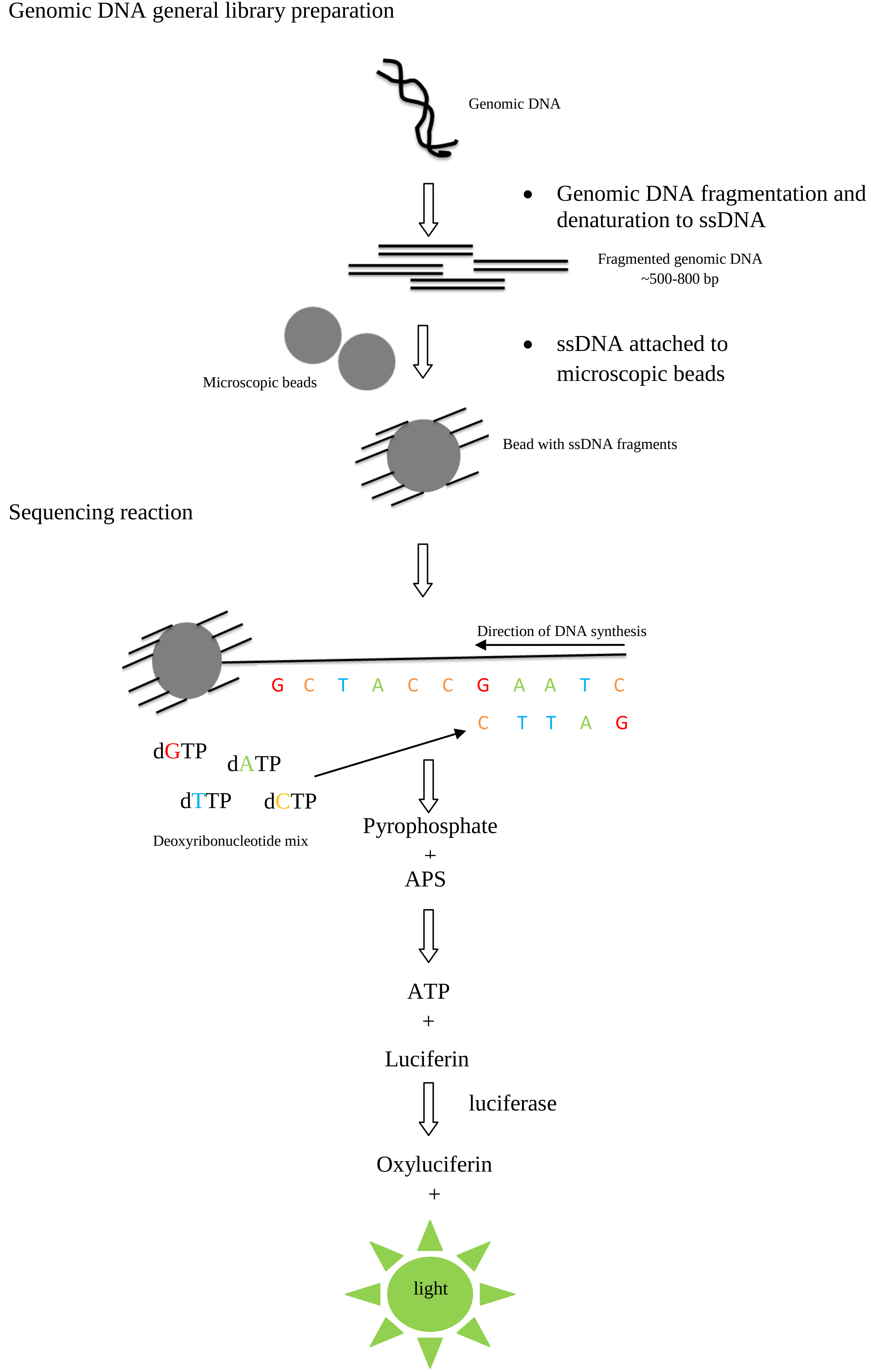


Figure 6.2: A schematic illustration of 454/pyrosequencing method.

*C. jejuni* 01/51 genomic DNA was sheared into single stranded DNA fragments of 500-800 bp in length. A single end DNA library was prepared following the general library preparation method. The GS FLX Titanium general DNA library kit was used to generate DNA template with amplification and sequencing adaptors. Emulsion PCR was performed for the enrichment of DNA template and the resulting library was sequenced by using the GS FLX Titanium platform (Figure 6.2).

The 454 sequencing performed 12x coverage of the *C. jejuni* 01/51 genome. The contigs were assembled using Newbler (v 2.5) (http://454.com/products/analysis-software/index.asp) mapped against the reference *C. jejuni* RM1221. The assembled genome sequence (.embl) of *C. jejuni* 01/51 was provided. An ACT (Carver *et al*., 2005) comparison sequence file of *C. jejuni* 01/51 and RM1221 was also provided.

The Illumina and 454 sequence data for *C. jejuni* 01/51 was combined using MIRA (v 3.4) (Chevreux *et al*., 1999). Any un-annotated genomic regions identified at this stage were annotated using Campydb and NCBI BLASTx searches. Features of the sequenced data were analysed using Artemis (Rutherford *et al*., 2000). The combined *C. jejuni* 01/51 assembly was compared with *C. jejuni* 01/10 Illumina sequence using the Annotation Comparison Tool (ACT) (Carver *et al*., 2005).

Dr Alan McNally (NTU) assembled *C. jejuni* 01/10 Illumina sequencing data, and performed the combined assembly on *C. jejuni* 01/51 and 01/10 sequences.

### *6.2.3 Phylogeny*

Whole genome phylogeny was performed using the assembled 01/51 and 01/10 genomes and 11 publicly available *C. jejuni* genome sequences (including *C. jejuni* subsp. *doylei* 269.97). Whole genome alignments were performed using Mugsy (Angiuoli., 2011), and the core genome extracted from the resulting alignment using a pipeline developed by Jason Sahl (Sahl., 2012) and adapted by Alan McNally. The concatenated core genome alignment was used to create a maximum likelihood phylogeny with RaxML (Stamatakis., 2005) implementing 100 bootstraps. The resulting tree was visualised and edited using Figtree.

## 6.3 RESULTS AND DISCUSSION

Two hyperinvasive *C. jejuni* strains (*C. jejuni* 01/10 and 01/51) were genome sequenced and analysed to determine if the two strains contain any additional genomic content that may be the signature for their hyperinvasive phenotype.

### *6.3.1 Genome sequence facts*

The combined assembly of pryosequencing and Illumina sequencing data for *C. jejuni* 01/51 showed that the genome of *C. jejuni* 01/51 is a single circular chromosome of 1,617,079 bp in length with an average G+C content of 30.45% (Table 6.1). Illumina sequencing of *C. jejuni* 01/10 genome identified it as a single circular chromosome with a genome size of 1,677,053 bp and G+C ratio of 30.49%. Other key characteristics of genomes are in table 6.1 below;

Table 6.1: The genome features of *C. jejuni* 01/51 and 01/10.

| **Genome features of two *C. jejuni* genomes** | ***C. jejuni* 01/51*** | ***C. jejuni* 01/10**** |
|---|---|---|
| Chromosome size (bp) | 1,617,079 | 1,677,053 |
| Number of contigs | 72 | 75 |
| N50 contig length | 103,524 | 120,479 |
| G+C content | 30.45% | 30.49% |
| Number of genes (without pseudo) | 1,739 | 1,724 |
| Genes with function | 1,378 | 1,385 |
| Hypothetical genes (including conserved) | 361 | 339 |
| Genes with unknown function | 0 | 0 |
| Phage/genomic islands | 1 | 2 |
| Plasmids | 0 | 0 |
| Restriction/Modification system | 8 | 8 |
| Virulence related genes | | |
| *cadF* | 1 | 1 |
| *jlpA* | 1 | 1 |
| 43-kDa MOMP | 1 | 1 |
| Fibronectin binding proteins | 3 | 3 |
| Two component regulator systems | 19 | 17 |
| Response regulator | 11 | 10 |
| Sensor histidine kinase | 8 | 7 |
| Membrane associated proteins | 77 | 72 |

*features based on Illumina/454 combined assembly
** features based on Illumina sequencing

### *6.3.2 Phylogeny*

A phylogenetic comparison of the whole genome sequence of the hyperinvasive *C. jejuni* 01/51 and 01/10 was made with other published complete *C. jejuni* and *C. jejuni* subsp. *doylei* 269.97 genome sequences (Figure 6.3).

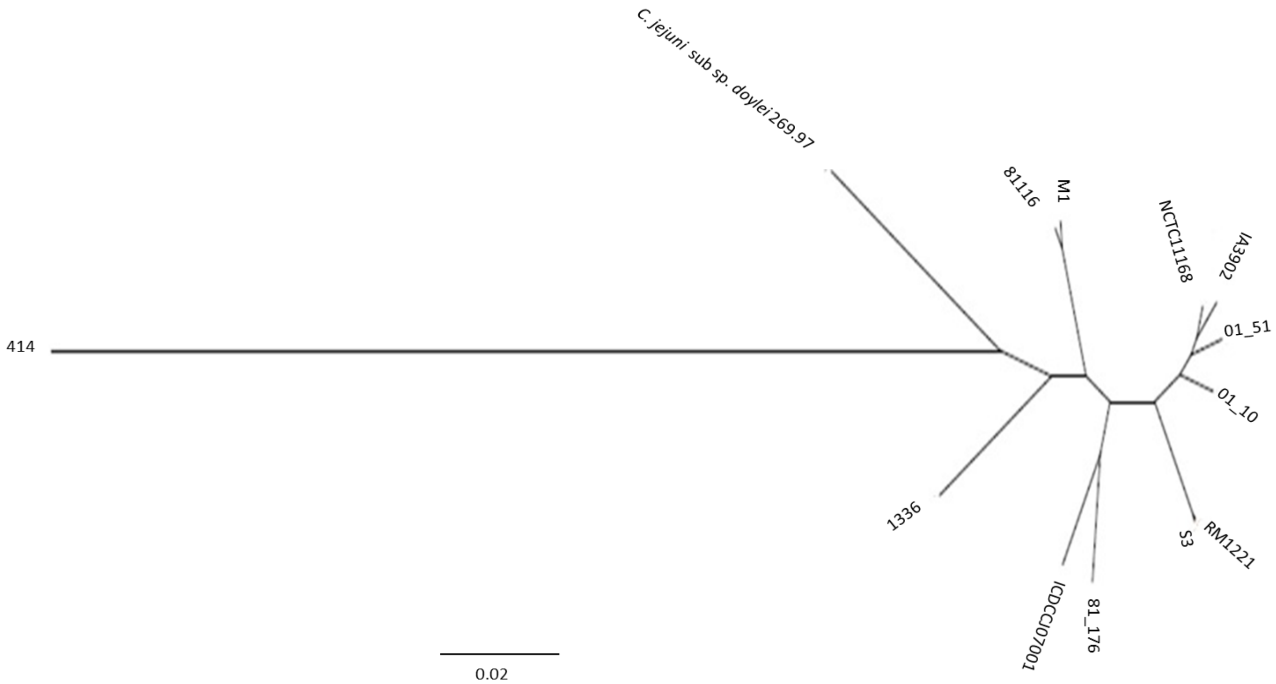


Figure 6.3: Phylogeny of *C. jejuni* 01/10 and 01/51 compared with other *C. jejuni* strains and *C. jejuni* subsp. *doylei* 269.97 based on genome sequence data.
The bar scale at the bottom represents the number of nucleotide substitutions.

Based on the genome sequence data, *C. jejuni* 01/10 and *C. jejuni* 01/51 formed a cluster with *C. jejuni* NCTC11168 and *C. jejuni* IA3902 suggesting that the genome composition of these strains is very similar. The human clinical isolate *C. jejuni* NCTC11168 has a chromosome size of 1,641,481 bp (Parkhill *et al.*, 2000) which is smaller in size compared to the *C. jejuni* chicken isolate RM1221 which is interrupted by four prophages/insertion sequences and some additional capsule loci in its genome (Fouts *et al.*, 2005). *C. jejuni* IA3902 is a pathogenic strain responsible for causing ovine abortion cases in sheep in USA with a chromosome size of 1,672,219 bp (Burrough *et al.*, 2009). The chromosome size of these strains is comparable to that of *C. jejuni* 01/51 and 01/10 respectively. The phylogenomic clustering of *C. jejuni* 01/10 and 01/51 close together reflected that these two hyperinvasive *C. jejuni* strains have a similar genomic content.

### *6.3.3 Prophages/Genomic regions*

When compared against the reference *C. jejuni* RM1221 genome both hyperinvasive *C. jejuni* strains lacked the four *C. jejuni* RM1221 characteristic prophages /genomic islands. Prophages are the vehicle of horizontal or lateral gene transfer. These may carry genes that provide a selective advantage to bacteria for survival in diverse environments and may have a role in virulence (Fouts *et al*., 2005). *C. jejuni* 01/51 contains only one small prophage of 5,031 bp containing 6 ORFs with similarity to a replication domain protein in *Vibrio chloreae* species and genes with hypothetical function in *Halomonas* strain GFAJ-1 (Phung *et al*., 2012) (Appendix: supplementary table 5).

In *C. jejuni* 01/10, two prophages were inserted in the genome (Appendix: supplementary table 6). Prophage 1 is 10,297 bp in size containing 7 ORFs with functional homology to phage related integrases and nucleases. Prophage 2 is large 28,602 bp in size and it is composed of 33 ORFs. The majority of these ORFs shared identity with phage structural proteins including prophage basal plate and tail assembly proteins. Additionally, ORFs with homology to nucleases and several hypothetical proteins were also present within this prophage. A few ORFs showed similarity to the genes from *C. jejuni* RM1221 Mu-like prophage (CMLP1) which may suggest that the role of these prophages in these strains is similar. The role of *C. jejuni* RM1221 prophage in *C. jejuni* pathogenesis is not known (Fouts *et al*., 2005) however recently it was showed that the presence of *dns* (extracellular deoxyribonuclease) in the *C. jejuni* RM1221 Mu-like prophage inhibits natural transformation in *C. jejuni* strains (Gaasbeek *et al*., 2010). The activation of these prophages and their role in the hyperinvasive virulence trait of these strains cannot be demonstrated at this stage.

*C. jejuni* 01/51 and 01/10 genomes do not contain any unique genes that are not present in other campylobacters. Some ORFs which showed best matches to members of the *Campylobacter* genus other than *C. jejuni* RM1221 mainly *C. jejuni* subspecies are listed in the supplementary tables 4 (*C. jejuni* 01/51) and 5 (*C. jejuni* 01/10) in the appendix. The LOS biosynthesis region for *C. jejuni* 01/51 and 01/10 are also listed (Appendix: supplementary tables 4 and 5 respectively). Other genes with membrane associated functions, restriction modification systems and hypothetical roles were mainly identified.

### *6.3.3.1 Validation of CGH and PSSH study results in C. jejuni 01/51 and 01/10 whole genome sequences*

Based on the results of CGH study, 522 and 859 divergent genes were identified in *C. jejuni* 01/10 and 01/51 respectively compared with the reference *C. jejuni*/*C.coli* genes on the pan array. This indicated that *C. jejuni* 01/10 was most similar and *C. jejuni* 01/51 was most divergent from the reference genes on the array compared with other *C. jejuni* strains investigated in the CGH study (section 4.3.7). The whole genome sequencing showed 337 genes to be absent from *C. jejuni* 01/10 and 313 genes were indicated as absent from *C. jejuni* 01/51 when mapped against the reference *C. jejuni* RM1221.

In agreement with the CGH findings, the whole genome sequence of *C. jejuni* 01/10 validated that some capsule and LOS genes homologous to those present in *C. jejuni* RM1221 were identified in the capsule and LOS regions of this strain. The capsule region of *C. jejuni* 01/10 is discussed later (Table 6.3; section 6.3.4) and the LOS region is listed in the supplementary table 6 in appendix. Unlike CGH data, however, the whole genome sequencing showed that *C. jejuni* RM1221 characteristic CJIE 2, 3 and 4 were absent from *C. jejuni* 01/10.

Both the CGH and whole genome sequencing showed that CJIE3 and 4 which are present in *C. jejuni* RM1221 were absent from *C. jejuni* 01/51 genome. In contrast to CGH data, the whole genome sequencing showed that *C. jejuni* RM1221 characteristic CMLP1, CJIE2 were missing from *C. jejuni* 01/51 genome. Interestingly, the whole genome sequencing did not identify any *C. jejuni* RM1221 homologous capsular genes in this strain. The capsule region of *C. jejuni* 01/51 (Table 6.2) is discussed in detail in section 6.3.4. The genome sequence of *C. jejuni* 01/51 showed that the LOS region possessed several LOS genes similar to those present in the LOS locus of *C. jejuni* RM1221 (Appendix: supplementary table 5). Based on the whole genome sequencing, mainly the hypothetical genes present in *C. jejuni* RM1221 were absent from *C. jejuni* 01/10 and 01/51.

The PSSH study identified five sequences (14, 22, 32, 54 and 62) to be present in the hyperinvasive *C. jejuni* strain 01/10 (Table 5.1; section 5.3.7). The whole genome sequencing verified 3/5 of these sequences (14, 22 and 54) in *C. jejuni* 01/10 (Appendix: supplementary table 6). It can be argued that the two sequences (32 and 62) which could not be detected in the genome sequence may not be sequenced as the Illumina sequence represents the draft genome sequence of this strain. In *C. jejuni* 01/51, none of the PSSH identified sequences were present (Table 5.1; section 5.3.7).

### *6.3.4 C. jejuni capsule region*

Capsule polysaccharides regions are known to be hypervariable in *Campylobacter* species (Fouts *et al*., 2005, Dorrell *et al*., 2001) and so the CPS regions of both 01/10 and 01/51 were studied in some detail.

#### *6.3.4.1 C. jejuni 01/51 capsule*

Based on 454 and Illumina genome sequencing, *C. jejuni* 01/51 was found to have a diverse capsule region (Figure 6.4).

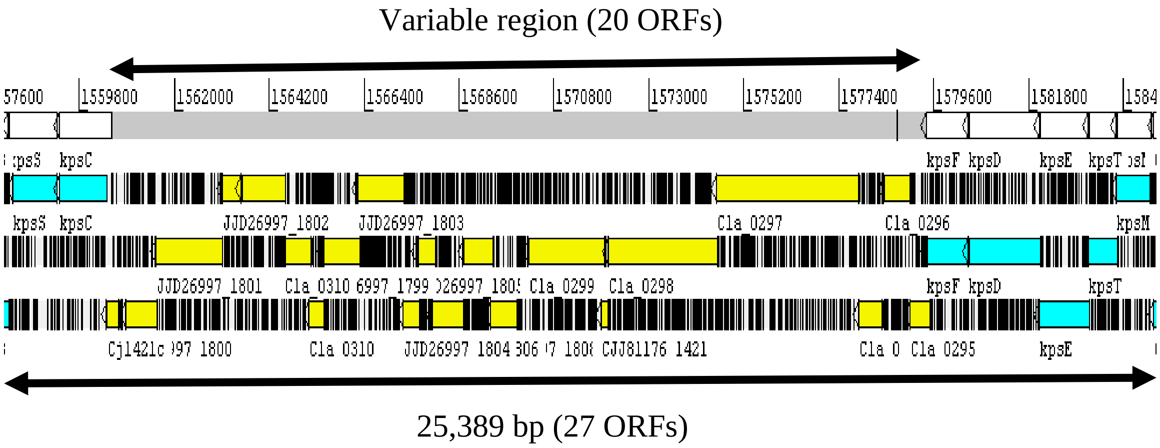


Figure 6.4: The capsule region in *C. jejuni* 01/51.
The ORFs in the capsular central variable region are yellow and the bordering *kps* genes are skyblue.

The capsule in *C. jejuni* 01/51 is a 25,389 bp region containing 27 ORFs. It is composed of a unique central variable region (20 genes) bordered by conserved *kps* genes encoding for the capsule polysaccharide export proteins.

The majority of genes in the variable region share similarity with *C. jejuni* subsp. *doylei* (9/27) and *C. lari* (9/27) capsule genes (Table 6.2) annotated here as JJD26997 and Cla respectively.

Table 6.2: CDS in the capsule region of *C. jejuni* 01/51.

| **Locus tag** | **Gene homolog/ortholog** | **Function** |
|---|---|---|
| *kpsS* | CJE1600 | capsule polysaccharide export protein KpsS [*Campylobacter jejuni* RM1221] |
| *kpsC* | CJE1601 | capsule polysaccharide export protein KpsC [*Campylobacter jejuni* RM1221] |
| | CJ1421c | capsular polysaccharide biosynthesis heptosyltransferase [*Campylobacter jejuni* subsp. *jejuni* NCTC11168] |
| | JJD26997_1800 | nucleoside-diphosphate-sugar pyrophosphorylase [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1801 | capsular polysaccharide biosynthesis protein [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1802 | capsular polysaccharide biosynthesis protein, putative [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | Cla_0310 | capsular polysaccharide biosynthesis protein, putative [*Campylobacter lari* RM2100] |
| | Cla_0310 | capsular polysaccharide biosynthesis protein, putative [*Campylobacter lari* RM2100] |
| | Cla_0310 | capsular polysaccharide biosynthesis protein, putative [*Campylobacter lari* RM2100] |
| | JJD26997_1799 | hypothetical protein [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1803 | hypothetical protein [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1804 | conserved domain protein [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1806 | conserved hypothetical protein [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1807 | HAD-superfamily hydrolase [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | JJD26997_1808 | hypothetical protein [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | Cla_0299 | putative sugar transferase [*Campylobacter lari* RM2100] |
| | CJJ81176_1421 | putative sugar transferase [*Campylobacter jejuni* subsp. *jejuni* 81-176] |
| | Cla_0298 | hypothetical protein [*Campylobacter lari* RM2100] |
| | Cla_0297 | putative glycosyltransferase [*Campylobacter lari* RM2100] |
| | Cla_0296 | conserved hypothetical protein [*Campylobacter lari* RM2100] |
| | Cla_0296 | conserved hypothetical protein [*Campylobacter lari* RM2100] |
| | Cla_0295 | putative glycerol-3-phosphate cytidyltransferase [*Campylobacter lari* RM2100] |
| *kpsF* | CJE1617 | rabinose-5-phosphate isomerase [*Campylobacter jejuni* RM1221] |
| *kpsD* | CJE1618 | capsular polysaccharide ABC transporter, periplasmic polysaccharide-binding protein [*Campylobacter jejuni* RM1221] |
| *kpsE* | CJE1619 | capsular polysaccharide ABC transporter [*Campylobacter jejuni* RM1221] |
| *kpsT* | CJE1620 | capsular polysaccharide ABC transporter, ATP-binding protein [*Campylobacter jejuni* RM1221] |
| *kpsM* | CJE1621 | capsular polysaccharide ABC transporter, permease protein [*Campylobacter jejuni* RM1221] |

### *6.3.4.2 C. jejuni 01/10 capsule*

The complete capsule region in *C. jejuni* 01/10 is 35,448 bp in size and contains 29 ORFs (Figure 6.5). Of these 29 ORFs, seven are conserved *kps* genes enclosing the central variable region consisting of 22 ORFs.

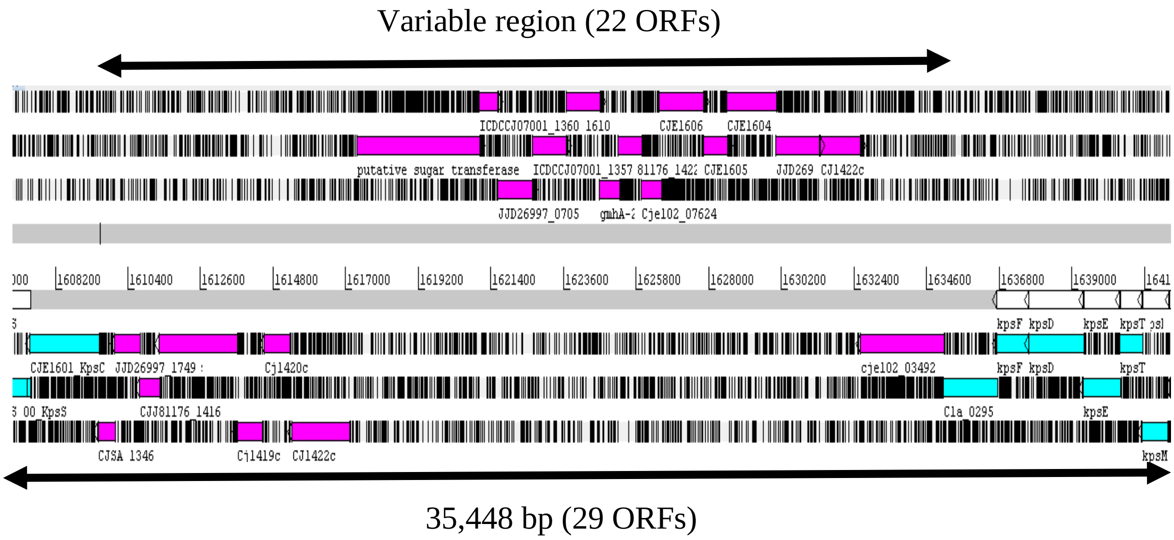


Figure 6.5: The capsule locus in *C. jejuni* 01/10.

The CDS in the central variable capsular region are pink and the surrounding *kps* genes are skyblue.

The CDS in the capsule region of *C. jejuni* 01/10 are listed in table 6.3.

Table 6.3: Genes in the capsule region of *C. jejuni* 01/10.

| Locus tag | Gene homolog/ortholog | Function |
|---|---|---|
| *kpsS* | CJE1600 | capsule polysaccharide export protein KpsS [*Campylobacter jejuni* RM1221] |
| *kpsC* | CJE1601 | capsule polysaccharide export protein KpsC [*Campylobacter jejuni* RM1221] |
| | CJSA_1346 | cysC adenylylsulfate kinase [*Campylobacter jejuni* subsp. *jejuni* IA3902] |
| | JJD26997_1749 | putative sugar-1-phosphate nucleotidyltransferase [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | CJJ81176_1416 | class I glutamine amidotransferase, putative [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| | CJ1418c | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* NCTC11168] |
| | CJ1419c | methyltransferase [*Campylobacter jejuni* subsp. *jejuni* NCTC11168] |
| | CJ1420c | methyltransferase [*Campylobacter jejuni* subsp. *jejuni* NCTC11168] |
| | CJ1422c | sugar transferase [*Campylobacter jejuni* subsp. *jejuni* NCTC11168] |
| | putative sugar transferase | *Campylobacter jejuni* subsp. *jejuni* LMG 23218 |
| | ICDCCJ07001_1360 | dTDP-6-deoxy-D-xylo-4-hexulose-3,5-epimerase [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| | JJD26997_0705 | GDP-fucose synthetase [ *Campylobacter jejuni* subsp. *doylei* 269.97] |
| | ICDCCJ07001_1357 | GDP-mannose 4,6-dehydratase [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| | CJE1610 | capsular biosynthesis sugar kinase [*Campylobacter jejuni* RM1221] |
| | *gmhA-2* | phosphoheptose isomerase [*Campylobacter jejuni* RM1221] |
| | CJJ81176_1422 | capsular biosynthesis nucleotidyltransferase, putative [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| | Cje102_07624 | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| | CJE1606 | haloacid dehalogenase-like hydrolase [*Campylobacter jejuni* RM1221] |
| | CJE1605 | capsular polysaccharide biosynthesis protein [*Campylobacter jejuni* RM1221] |
| | CJE1604 | capsular polysaccharide biosynthesis protein [*Campylobacter jejuni* RM1221] |
| | JJD26997_1797 | alpha-2,3-sialyltransferase [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| | CJ1422c | sugar transferase [*Campylobacter jejuni* subsp. *jejuni* NCTC11168] |
| | Cje102_03492 | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| | Cla_0295 | putative glycerol-3-phosphate cytidyltransferase [*Campylobacter lari* RM2100] |
| *kpsF* | CJE1617 | rabinose-5-phosphate isomerase [*Campylobacter jejuni* RM1221] |
| *kpsD* | CJE1618 | capsular polysaccharide ABC transporter, periplasmic polysaccharide-binding protein [*Campylobacter jejuni* RM1221] |
| *kpsE* | CJE1619 | capsular polysaccharide ABC transporter [*Campylobacter jejuni* RM1221] |
| *kpsT* | CJE1620 | capsular polysaccharide ABC transporter, ATP-binding protein [*Campylobacter jejuni* RM1221] |
| *kpsM* | CJE1621 | capsular polysaccharide ABC transporter, permease protein [*Campylobacter jejuni* RM1221] |

The majority of genes (25/29) in the capsule region were homologous to other *C. jejuni* capsule genes however, the CPS region in *C. jejuni* 01/10 was also found to contain three genes with similarity to *C. jejuni* subsp. *doylei* capsule genes (JJD26997_1749, JJD26997_0705 and JJD26997_1797) and one gene showed homology to *C. lari* CPS gene (Cla_0295). This *C. lari* homologous capsule gene was also present in the *C. jejuni* 01/51 capsule region. However, the level of interspecies similarity of genes in *C. jejuni* 01/10 CPS region was not as seen in the case of *C. jejuni* 01/51.

*C. lari* is found in wild birds, particularly seagulls (Glunder and Petermann., 1989). It is frequently isolated from freshwater, seawater and shellfish (Rosef *et al*., 2008). Unlike *C. jejuni* and *C. coli* which are isolated from human gastroenteritis cases only a limited number of *C. lari* isolates are associated with human illness (Miller *et al*., 2008b), however there are reports of *C. lari* causing severe bacteraemia in humans (Werno *et al*., 2002, Godreuil *et al*., 2000). *C. lari* RM2100 is a human clinical isolate (Fouts *et al*., 2005, Miller *et al*., 2008b). Based on its genome sequence, ~ 90% of the genome content of this strain is similar to other *Campylobacter* species (Fouts *et al*., 2005, Miller *et al*., 2008b). Similarly, *C. jejuni* subsp. *doylei* is more frequently isolated from blood cultures than stool samples (Parker *et al*., 2007).

The homology of genes within the capsule region of the hyperinvasive *C. jejuni* 01/51 and *C. jejuni* 01/10 to *C. lari* and *C. jejuni* subsp. *doylei* capsule genes makes it a novel region as this interspecies mosaicism in the capsule locus has not been reported in other sequenced *C. jejuni* strains. This mosaic pattern of genes in the capsule region suggests that homologous recombination is an active phenomenon in this region which has resulted in these two hyperinvasive *C. jejuni* strains acquiring genes from other pathogenic *Campylobacter* subspecies. The presence of capsule genes from *C. lari* and *C. jejuni* subsp. *doyeli* in hyperinvasive *C. jejuni* 01/10 and 01/51 strains is a common genetic signature of these two CPS regions which has not been observed in other campylobacters and perhaps this trait is the determinant of hyperinvasivess in these strains. Furthermore, JJD26997_1801 in the *C. jejuni* 01/51 CPS region with similarity to the *C. jejuni* subsp. *doylei* capsule gene (Table 6.2) was also previously identified by transposon mutagenesis study of *C. jejuni* 01/51 and a mutant in this gene resulted in reduced invasion in INT-407 and Caco-2 epithelial cells (Javed *et al*., 2010) confirming the role of capsule in the hyperinvasive phenotype of *C. jejuni* 01/51.

It is important to validate the role of capsule in the hyperinvasive profile of *C. jejuni* 01/10 by mutagenesis. The Cla_0295 homologous gene encoding for a putative glycerol-3-phosphate cytidyltransferase in *C. lari* RM2100 is the best candidate for mutagenesis study as a homologue of this gene was also identified in *C. jejuni* 01/51 CPS region.

Interestingly, some genes were identified in multiple copies. For example, three copies of the Cla_0310 orthologous genes encoding for a putative polysaccharide biosynthesis protein and two copies of genes encoding for the conserved hypothetical proteins (Cla_0296) were identified in the CPS region of *C. jejuni* 01/51. Similarly, the capsule locus in *C. jejuni* 01/10 possesses two copies of a sugar transferase encoding gene, Cj1422c. Previous studies on *C. jejuni* capsule regions have reported that gene duplication is commonly observed in the CPS region of *C. jejuni* strains which adds to the variability in this region (Karlyshev *et al*., 2005a, Guerry *et al*., 2012, Parker and

Huynh., 2012). These multiple copies of genes may provide selective advantage to bacteria in survival inside the host and disease profile (Fouts *et al*., 2005). An additional 11 capsule polysaccharide genes were identified in *C. jejuni* 01/51 which were not a part of the capsule region but were randomly distributed in the chromosome (supplementary table 5). Of these eight genes (*kpsS*, *kpsC*, CJSA_1346, JJD26997_1749, CJJ81176_1416, Cj1418c, Cj1419c, Cj1420c) were present clustered together. This also shows that *C. jejuni* 01/51 has two copies of some of the *kps* gene homologues. The other three genes (CJSA_1363 and CJSA_1352) and CJSA_1357 were located separately. This random distribution of capsule genes has also been observed in CPS regions for *C. jejuni* strains of different Penner serotypes (Parker and Huynh., 2012) and was reported in the *C. upsaliensis* capsule locus (Fouts *et al*., 2005). Unlike in *C. jejuni* 01/51, no additional CPS genes outside the capsule region could be identified in *C. jejuni* 01/10.

It have been reported that despite the variability in the central CPS region some capsular genes are conserved in many *C. jejuni* strains. These include the heptose biosynthesis genes (*hddC*, *gmhA*, *hddA*) and the genes encoding for O-methyl phosphoramidate (MeOPN) capsular modifications (Guerry *et al*., 2012). In *C. jejuni* NCTC11168, four genes (Cj1415c-Cj1418c) have been reported to be involved in MeOPN synthesis and these genes are highly conserved in other *C. jejuni* strains. Also, two genes Cj1419c and Cj1420c with a role in methyl transferases were always found adjacent to the MeOPN synthesis genes (McNally *et al*., 2007). Two transferases encoding genes Cj1421c and Cj1422c present in *C. jejuni* NCTC11168 are responsible for adding MeOPN to two different sugars in a HS2 serotype CPS (McNally *et al*., 2007) (Figure 6.6).

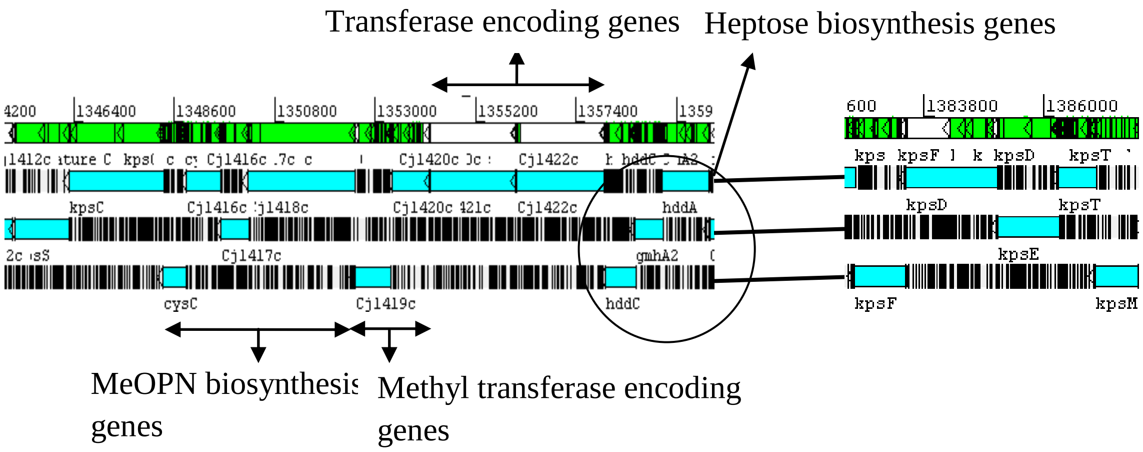


Figure 6.6: A representation of the partial capsule locus in *C. jejuni* NCTC111168 showing heptose and MeOPN biosynthesis genes and transferase encoding genes.

In *C. jejuni* 01/51 CPS region, the *hddC*, *gmhA*, *hddA* homologous gene cluster was not identified. *C. jejuni* 01/10 contains a *gmhA-2* homologous gene in its CPS locus. Parker and Huynh (2012) have also observed that these heptose synthesis genes were missing from *C. jejuni* subsp. *jejuni* IA3902. Additionally, one MeOPN synthesis gene homolog (Cj1418c) was identified within the *C. jejuni* 01/10 CPS region and as a part of the *C. jejuni* 01/51 additional capsule genes with the methyl transferases encoding genes (Cj1419c-Cj1420c) present adjacent to it. In *C. jejuni* 01/51, the ORFs with similarity to the two transferases (Cj1421c and Cj1422c) were not present and *C. jejuni* 01/10 contains two copies of Cj1422c homologous gene.

Further analysis of the capsule locus does need to be done.

### *6.3.5 Is capsule or LOS the serodeterminant in C. jejuni 01/51?*

Capsule is considered as the serodeterminant in Penner HS serotyping of *C. jejuni* strains (Karlyshev *et al*., 2000) and in this study *C. jejuni* 01/51 was identified as serotype HS4 (section 4.3.2 and Figure 4.3 in chapter 4).

The nucleotide sequence of the capsule locus of other HS4 serotype *C. jejuni* strains (Poly *et al*., 2011) was compared with the capsule sequence of *C. jejuni* 01/51 but no similarity was observed. Interestingly a mutant in capsule gene, JJD26997_1801 (Javed *et al*., 2010) and a mutant in a LOS gene (*cj1136*) (Javed *et al*., 2012) in *C. jejuni* 01/51 were also serotyped as part of this study. The capsule gene (JJD26997_1801) mutant retained the serotype of the wild type strain whereas the mutant in the LOS gene (*cj1136*) gene altered the serotype of the mutant to HS50. This may suggest that LOS and not the capsule is responsible for serotype specificity in this strain.

It would be useful to confirm the above observation in *C. jejuni* 01/10 generating mutants in LOS and capsule genes.

## 6.4 SUMMARY

In summary, the phylogeny based on the whole genome sequence of the hyperinvasive *C. jejuni* 01/10 and 01/51 grouped them together. There was no unique genomic content present in these strains except for a prophage in *C. jejuni* 01/51. Two prophages were found in *C. jejuni* 01/10. The capsule region was the most diverse region but was different between the two strains. The capsule loci in *C. jejuni* 01/51 and 01/10 CPS region showed homology with the *C. jejuni* subsp. *doylei* and *C. lari* capsule genes. This mosaicism in the capsule region containing genes with homology to other *Campylobacter* species has not been reported in other *C. jejuni* strains. This shows that the capsule region in hyperinvasive *C. jejuni* 01/51 and 01/10 is a hotspot for homologous recombination and that this mosaicism in the capsule region may be a marker for hyperinvasion in *C. jejuni*. Some capsular genes were present in multiple copies in the capsule region of *C. jejuni* 01/51 and 01/10 with a few capsule genes also identified outside the CPS region in *C. jejuni* 01/51. *C. jejuni* 01/51 is serotype HS4 but its capsule sequence is different from other HS4 serotype *C. jejuni* strains. A capsule gene, JJD26997_1801, mutant in *C. jejuni* 01/51 did not change the serotype whereas a LOS gene, *cj1136*, mutant changed the serotype of the mutant suggesting that LOS is the serodeterminant in *C. jejuni* 01/51.

## *Chapter Seven*

# THESIS DISCUSSION AND FUTURE WORK

# THESIS DISCUSSION AND FUTURE WORK

*C. jejuni* is an enteric pathogen and it is the major cause of campylobacteriosis worldwide. The molecular mechanisms underlying *C. jejuni* pathogenesis are still being investigated. Some key factors that have been studied to be associated with the *C. jejuni* pathogenesis include motility, chemotaxis, toxin production and invasion (Young *et al*., 2007, Dasti *et al*., 2010). *C. jejuni* has been shown to successfully invade the epithelial cells in *in vitro* assays in several studies (Fauchere *et al*., 1986, Konkel and Joens., 1989, DeMelo *et al*., 1989, Everest *et al*., 1992). Usually the severity of clinical symptoms is related to the ability of *C. jejuni* isolates to invade the intestinal epithelial cells (Konkel *et al*., 2001). Recently, an invasion study of *C. jejuni* isolated from different sources grouped together six strains based on their hyperinvasive phenotype (Fearnley *et al*., 2008). One of these hyperinvasive *C. jejuni* strains, 01/51, was investigated further by transposon mutagenesis and a number of genes were identified with potential roles in invasion (Javed *et al*., 2010). In this research project, all the hyperinvasive *C. jejuni* strains identified by Fearnley *et al* (2008) were studied at the genome content level to identify any common basis of hyperinvasiveness in this group of strains. For the genome based study, CGH, PSSH and next generation genome sequencing methods have been used.

In the preliminary part of this research project all the hyperinvasive *C. jejuni* strains were tested in *in vitro* assays of environmental stress that the bacteria are exposed to during invasion assays (*i.e.* growth rate, survival in atmospheric air and hydrogen peroxide stress, and motility) and a few other virulence related factors (*i.e.* autoagglutination, sodium deoxycholic acid stress and biofilm formation). Motility is an important virulence phenotype in *C. jejuni* and loss of flagella has been shown to result in reduced invasion of intestinal epithelial cells in several studies (Grant *et al*., 1993, Wassenaar *et al*., 1991). Reactive oxygen species (ROS) are produced as toxic molecules inside macrophages to kill intracellular pathogens by damaging the essential cellular components including nucleic acids, lipids and proteins (Jamieson, 1998). To circumvent the harmful effects of ROS, *C. jejuni* has evolved several protective enzymes *e.g.* catalase and superoxide dismutase (De Melo *et al*., 1989, Day *et al*., 2000). During the invasion assays, bacteria are exposed to a number of stress factors including 5% (v/v) $CO_2$, atmospheric air and Triton X-100. Also, the radical oxygen molecules are produced as a byproduct of oxidative metabolism in the actively growing tissue culture cells. In this study, all the *C. jejuni* strains showed a similar pattern of growth in the exponential phase (section 3.3.1). In addition, all the *C. jejuni* strains survived the atmospheric air and hydrogen peroxide stresses and displayed high levels of variation in motility (sections 3.3.2 to 3.3.4). For the other virulence related phenotypes studied, strain to strain variation was evident with no grouping of the hyperinvasive *C. jejuni* strains (sections 3.3.5 to 3.3.7) and so at this point it seemed that the only phenotype relating these strains to each other was their hyperinvasiveness.

Since the six hyperinvasive strains appeared to be significantly more invasive than the other strains tested at the time (Fearnley *et al.*, 2008) it was hypothesized that they possessed extra/novel DNA that was related to this phenotype. Several studies have successfully used DNA microarrays to highlight similarities and differences at the gene content level that may account for the observed phenotypic variation between *C. jejuni* strains (Quiñones *et al.*, 2008, Parker *et al.*, 2006, Champion *et al.*, 2005, Pearson *et al.*, 2003, Dorrell *et al.*, 2001). In this study, the hyperinvasive *C. jejuni* strains were compared with a group of four low invasive *C. jejuni* strains by using CGH. The objective was to determine if the hyperinvasive *C. jejuni* strains would group together as a distinct group based on their genomic content and also to identify similar regions of variability between these strains. The hierarchical clustering based on CGH did not group the hyperinvasive *C. jejuni* strains together. The hyperinvasive *C. jejuni* strains exhibited different MLST and HS serotype profiles (section 4.3.2). Further analysis of the CGH data identified 67 genes which were present or variable in the majority of the hyperinvasive *C. jejuni* compared with the low invasive *C. jejuni* strains (section 4.3.3 and appendix: supplementary table 4). Group 1 consisted of 9 genes that were present in all the hyperinvasive *C. jejuni* strains and highly divergent/absent from the majority of low invasive strains. Similarly, group 2 possessed 6 genes that were highly divergent/absent from the all the hyperinvasive *C. jejuni* and present in most of the low invasive *C. jejuni* strains (section 4.3.3). Since only 4 low invasive *C. jejuni* strains were studied by using CGH an additional 9 low invasive *C. jejuni* strains were screened by PCR for the genes identified in groups 1 and 2 (section 4.3.4). The PCR analysis further validated the CGH data and showed a statistically significant association between presence or absence of 13/15 genes (except for CJE1128 and CJE0731) in the hyperinvasion phenotype. Hence, these genes may be considered as putative markers of hyperinvasiveness.

Further characterisation of these genes is required.

The majority of genes identified in the CGH study belonged to different functional categories (section 4.3.5). These genes were not located in the same operon and were randomly distributed in the pan genome (section 4.3.6). Group 1 was dominated by the metabolic genes (*proC* and *metF* and *modA*) as well as posttranslational modification, protein turnover, and chaperone encoding genes (*aat* and CJE0320). In group 2, genes encoding for proteins involved in translation and posttranslational functions (*tgt* and CJE0801), cell membrane biogenesis (CJE0315) and nucleic acid replication and repair (CJE0731) were identified. In addition both groups (1 and 2) contained genes with hypothetical roles. Overall the other groups (Appendix: supplementary table 4) also represented functional groups including the iron transport system (CfrA; CJE0347 and CeuB; CJE1541), arsenic resistance encoding gene (*arsC*) and the twin-arginine translocase (TAT) secretion system (CJE1310). This suggests that the genes involved in essential cellular and metabolic functions are important in defining the hyperinvasive phenotype. Additionally, this unique phenotype is characterised by genes from different cellular networks rather than by gene(s) belonging to a single functional category. Subtle genetic changes in the nucleotide sequence of a gene introduced by point mutation, addition/deletion or substitution of a single nucleotide may account for the observed variation in phenotype (Malik-Kale *et al*., 2007). These changes cannot be identified by DNA microarrays and whole genome sequencing will be required to observe them. However, genome sequencing for a large number of strains can be expensive; hence, the importance of DNA microarrays cannot be neglected. It is also important to consider the host factors that contribute to an infection process which further complicates the strain to strain phenotype variations (Taboada *et al*., 2007). The increased invasiveness observed in *in vitro* cultured cell lines may not be due to differences in genetic content but due to expression or regulation differences in single or multiple genes (Konkel *et al*., 1990). Therefore, it would be interesting to compare the full sequences of genes identified in the CGH study as present in both hyperinvasive and low invasive strains (Appendix: supplementary table 4) to identify more subtle differences contributed by single nucleotide changes in the gene sequence. Also, it is possible that those genes identified as being present in all the hyperinvasive *C. jejuni* and only one of the low invasive *C. jejuni* strains (Group 1: section 4.3.3) are not expressed in that low invasive *C. jejuni* strain which can be tested by transcriptional analysis of these genes and this work is currently being undertaken by others in the laboratory.

The majority of *C. jejuni* strains showed genomic diversity, mainly in surface related structures, including the LOS, CPS and flagella biosynthesis loci as well as in the restriction modification (RM) systems (section 4.3.7). This strain to strain variation has been observed in other studies (Dorrell *et al*., 2001, Pearson *et al*., 2003, Parker *et al*., 2006). It was also interesting to note that *C. jejuni* 01/10 was most similar to the reference genes on the array whereas *C. jejuni* 01/51 was the most diverse hyperinvasive *C. jejuni* strain.

Since DNA microarray analysis only provides comparison with the reference genes on the array, the hyperinvasive *C. jejuni* strains were also studied by using pooled suppressive subtractive hybridization (PSSH) (Gerrish *et al*., 2010) to identify any additional genomic content that the hyperinvasive *C. jejuni* strains commonly share which may account for their hyperinvasive phenotype. In this technique, the genomic DNA of all the hyperinvasive *C. jejuni* strains was pooled together as “tester” and hybridized against a pool of four low invasive *C. jejuni* strains “driver”. Eleven sequences were identified in total and validated by PCR analysis as being absent from all the four low invasive driver *C. jejuni* strains (section 5.3.7). PCR screening also showed the distribution of the 11 identified sequences in the hyperinvasive *C. jejuni* strains and in an additional 9 low invasive *C. jejuni* strains that were not used in the PSSH experiment. Each sequence was found to be present in one or more hyperinvasive *C. jejuni* strains but none of them were present in all hyperinvasive strains. These sequences were variably distributed in the non-PSSH tested low invasive strains. Four sequences (14, 38, 54, and 57) were only identified in the hyperinvasive *C. jejuni* strains as these sequences were also absent from the PCR analysed 9 low invasive *C. jejuni* strains. However, these sequences cannot be associated with the hyperinvasive phenotype and likely only represent strain specific sequences. None of the identified sequences were present in *C. jejuni* 01/51 whereas *C. jejuni* 01/10 was positive for most (5/11) inserts.

The 11 identified inserts showed homology with genes in other *Campylobacter* strains and from other bacteria (section 5.3.8). Insert 14 showed similarity to a prophage

MuSo1, F protein in *C. jejuni subsp. jejuni* ICDCCJ07001 and 260.94. Inserts 54 and 57 were homologous to a putative tetracycline resistance gene *tet* (O/W/32/O) in *Streptococcus gallolyticus* subsp. *gallolyticus* ATCC BAA-2069 plasmid pSGG1 and the phage tail fibre protein I in *Bordetella avium* 197N respectively. Most genome sequenced *Campylobacter* strains contain characteristic prophages which contribute to the genetic diversity and stability of bacterial genomes (Fouts *et al*., 2005). Insert 38 had no known sequence match in the genome sequence databases searched and many represent strain specific DNA. Therefore, the identification of prophage-related sequences is expected in the hyperinvasive *C. jejuni* strains.

The role of these genes in invasiveness can be studied by mutagenesis. The PSSH method can successfully identify additional genomic content in the tester strains but it is a complicated and time-consuming method (Ahmed *et al*., 2002, Hepworth *et al*., 2007).

Based on the results of CGH and PSSH studies, the genomic structure of two hyperinvasive *C. jejuni* strains was studied further by whole genome sequencing. High through-put genome sequencing is the most reliable method to study genetic content variations and to identify pathogenesis associated in *C. jejuni* strains (Fouts *et al*., 2005, Hofreuter *et al*., 2006, Pearson *et al*., 2007, Poly *et al*., 2007b, Friis *et al*., 2010, Zhang *et al*., 2010). The hyperinvasive *C. jejuni* 01/51 strain was sequenced by using 454/pyrosequencing and Illumina sequencing methods and the genome sequences by the two methods were combined whereas for the hyperinvasive *C. jejuni* 01/10 the sequencing was performed just by using the Illumina sequencing. The genomes of *C. jejuni* 01/51 and *C. jejuni* 01/10 are 1,617,079 bp and 1,677,053 bp in sizes respectively (section 6.3.1). The phylogenomic clustering compared with all eleven published complete *C. jejuni* and *C. jejuni* subsp. *doylei* 269.97 genome sequences clustered the two hyperinvasive *C. jejuni* strains together suggesting that their genomic content is more similar to each other than to the other strains in the database (section 6.3.2). Genome sequencing of the other 4 hyperinvasive *C. jejuni* strains (Fearnley *et al*., 2008) would be helpful in studying the genomic diversity and evolution of these strains. The genome sequences of both strains identified strain specific sequences with gene similarities within the *Campylobacter* genus suggesting that these strains do not contain unique sequences. The only exception was of a prophage identified in the *C. jejuni* 01/51 that showed similarity with genes from *V. chloreae* and *Halomonas* species. Two prophages were identified in *C. jejuni* 01/10 which showed similarity with the other *Campylobacter* prophage related genes (section 6.3.3). The capsule region of the two genome sequenced hyperinvasive *C. jejuni* strains was highly diverse (section 6.3.4). In the hyperinvasive *C. jejuni* strain 01/51, the CPS region was found to be 25,389 bp in size and the hyperinvasive *C. jejuni* 01/10 possessed a larger (35,448 bp) CPS region. The majority of genes in *C. jejuni* 01/51 capsule region showed similarity with the *C. lari* and *C. jejuni* subsp. *doylei* capsule genes. The capsule region in *C. jejuni* 01/10 contains most genes showing homology with other *C. jejuni* strains, however three genes with similarity to the *C. jejuni* subsp. *doylei* capsule genes and one *C. lari* capsule gene homologue were also identified in the *C. jejuni* 01/10 CPS region. This mosaic pattern of gene distribution in the capsule region sharing homology with other *Campylobacter* species capsule genes has not been reported previously in *C. jejuni*. It can be suggested that the capsule region in the two genome sequenced hyperinvasive *C. jejuni* strains is highly recombinagenic and may be the signature for the hyperinvasive phenotype in these strains. Furthermore, a mutant in a capsule gene (JJD26997_1801) in *C. jejuni* 01/51 resulted in reduced invasion in INT-407 and Caco-2 (Javed *et al*., 2010) proposing the role of this gene in the hyperinvasive phenotype of *C. jejuni* 01/51. The homologue of the Cla_0295 capsule gene in *C. lari* RM2100 was present in both the *C. jejuni* 01/10 and 01/51 CPS regions and mutants in this gene should be tested in invasion studies to confirm the role of capsule in hyperinvasiveness. The structural analysis of the *C. jejuni* 01/51 and 01/10 capsules will further support the genome sequence data.

There were additional capsule genes identified as randomly scattered in the genome of *C. jejuni* 01/51 that were not a part of the capsular region. This was also observed by Parker and Huynh (2012) in capsules of *C. jejuni* strains of different Penner serotypes. Also, gene duplication was noted in the capsule region of *C. jejuni* 01/51 and 01/10 which has been reported in other *Campylobacter* strains (Karlyshev *et al*., 2005a, Fouts *et al*., 2005, Parker and Huynh., 2012).

The capsule has been considered as the serodeterminant in the Penner serotyping scheme (Karlyshev *et al*., 2000). *C. jejuni* 01/51 and 01/10 were serotyped as HS4 and HS50 respectively (section 4.3.2 and Figure 4.3; chapter 4). Poly *et al* (2011) recently suggested that the capsule region of *C. jejuni* strains within the same serotype is conserved. Contrary to this, a sequence comparison of the *C. jejuni* 01/51 CPS region with a HS4 *C. jejuni* strain did not show any homology between them. This suggests that in *C. jejuni* 01/51 other outer surface structures (LOS or flagella) are being recognised in HS serotyping instead of the capsule. It would also be useful to compare the capsule sequence of *C. jejuni* 01/10 with other HS50 *C. jejuni* strains to validate the association between serotype and the capsule in this hyperinvasive strain.

To further investigate if the LOS is responsible for Penner serotype specificity mutants in a LOS gene (*cj1136*) and a capsule gene (JJD26997_1801) in *C. jejuni* 01/51 (Javed *et al.*, 2012) were serotyped (section 6.3.5). The LOS gene (*cj1136*) mutant changed the serotype to HS50 whereas the mutant in the capsule gene, with homology to JJD26997_1801, in *C. jejuni* 01/51 (Javed *et al.*, 2010) remained the same as the wild type strain which supports the fact that the capsule is not being recognised in serotyping and the LOS is the serodeterminant instead.

In summary, the phenotypic characterization of the *C. jejuni* strains in virulence related assays showed variation among strains with no grouping of the hyperinvasive *C. jejuni* as a distinct group. It therefore indicates that these strains share only the hyperinvasive phenotype which strengthens the approach to look for the underlying genetic components responsible for this uniquely shared phenotype. It also confirmed that the differences in the invasion potential of the *C. jejuni* strains was not due to the reduced growth and motility or inability to survive under atmospheric air and reactive oxygen stresses. The phylogenomic clustering based on the CGH data could not cluster the hyperinvasive *C. jejuni* strains as a separate group away from low invasive strains. In total, 67 genes were identified as present or missing from the hyperinvasive *C. jejuni* strains. Genes related to essential cellular functions were mainly identified along with some characterized virulence related loci. All the *C. jejuni* strains showed genome diversity in the LOS, capsule, RM and flagella biosynthesis regions. Two groups of genes were identified; with group 1 containing 9 genes present in all the hyperinvasive *C. jejuni* strains and group 2 with 6 genes which were highly divergent/absent from all the hyperinvasive *C. jejuni* strains. The genes were markers for hyperinvasion as a strong association was seen between their presence and absence and the hyperinvasive phenotype. The PSSH, identified 11 sequences which were variably distributed in the hyperinvasive *C. jejuni* and 9 non-PSSH tested low invasive *C. jejuni* strains. From these, 4/11 inserts were hyperinvasive *C. jejuni* specific but these were not present in all the hyperinvasive strains. The pyrosequencing/Illumina genome sequences of the hyperinvasive *C. jejuni* 01/10 and 01/51 did not identify any sequences unique to these strains that were not present in the other sequenced *Campylobacter* strains except for a prophage in *C. jejuni* 01/51. A novel CPS region was characterised in *C. jejuni* 01/51 and 01/10 possessing loci with similarity to the *C. jejuni* subsp. *doylei* and *C. lari* capsule genes which is evident of interspecies homologous gene transfer in the capsule confirming the role of capsule in the hyperinvasive phenotype of these strains. It would be interesting to characterize the CPS regions in other four hyperinvasive *C. jejuni* strains to further validate the association between capsule and hyperinvasiveness. *C. jejuni* 01/51 was serotyped as HS4 but its capsule sequence was different from HS4 serotyped *C. jejuni* strains and the capsule gene mutant in *C. jejuni* 01/51 did not change its serotype suggesting that the capsule is not recognised during serotyping. However, the changed serotype of a LOS mutant in *C. jejuni* 01/51 suggests that LOS is the serodeterminant. This study represents a complex analysis of the genome of a phenotypically identical group of *C. jejuni* strains and has provided insight into the genetic basis for hyperinvasion.

### What next in this project?

The transcriptional study of genes identified by CGH as present in all hyperinvasive *C. jejuni* and highly divergent from the majority of low invasive *C. jejuni* strains will show whether these genes are only expressed in the hyperinvasive group of strains and may account for the hyperinvasive phenotype of these strains. Since genes of different functional categories have been identified in the CGH and PSSH studies, it would be interesting to study the link/communication between different cellular networks and their role in hyperinvasion. The CGH and PSSH identified loci should be investigated further by mutagenesis and *in vitro* invasion assays. These genes are also the potential markers for studying the mechanism of *C. jejuni* uptake and survival into host cells.

The whole genome sequences of the hyperinvasive *C. jejuni* 01/10 and 01/51 should be compared in more detail with the sequenced *C. jejuni* strains other than *C. jejuni* RM1221. The remaining four hyperinvasive *C. jejuni* strains (01/35, 01/04, 01/41 and EX114) should be whole genome sequenced and the genome sequences of all six hyperinvasive *C. jejuni* strains should be compared. It would be interesting to observe if all the hyperinvasive *C. jejuni* strains share the mosaic pattern of interspecies gene distribution in their CPS regions. The comparison with CPS regions of some of the low invasive *C. jejuni* stains would also be a useful control as this will validate the role of capsule in hyperinvasiveness. The invasion profile of the majority of sequenced

*C. jejuni* strains is unknown.  It would be useful to screen these strains in invasion assays to see if more strains possess the hyperinvasive phenotype.

## *Chapter Eight*

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# APPENDIX

# APPENDIX

Supplementary table 1: The average linkage distance between clusters as determined by the "Cluster" software.

| | | | |
|---|---|---|---|
| NODE1X | ARRY7X | ARRY3X | 0.95513916015625 |
| NODE2X | ARRY6X | NODE1X | 0.90911865234375 |
| NODE3X | ARRY0X | NODE2X | 0.8590087890625 |
| NODE4X | ARRY1X | NODE3X | 0.8590087890625 |
| NODE5X | ARRY8X | ARRY5X | 0.8580322265625 |
| NODE6X | NODE4X | NODE5X | 0.8580322265625 |
| NODE7X | ARRY2X | NODE6X | 0.85394287109375 |
| NODE8X | ARRY9X | ARRY4X | 0.836669921875 |
| NODE9X | NODE7X | NODE8X | 0.836669921875 |

Note: The Pearson correlation (centered) was used as the similarity metrics for performing clustering (Eisen *et al*., 1998).

Supplementary table 2: The log 2 ratios *for all genes on the array for six hyperinvasive and four low invasive *C. jejuni* strains.

| | **Hyperinvaisve *C. jejuni*** | | | | | | **Low invasive *C. jejuni*** | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Oligo_ID | *C. jejuni* 01_10 | *C. jejuni* 01_35 | *C. jejuni* 01/04 | *C. jejuni* 01/41 | *C. jejuni* 01/51 | *C. jejuni* EX114 | *C. jejuni* 01/30 | *C. jejuni* 01/32 | *C. jejuni* 01/46 | *C. jejuni* 01/39 |
| CJ_10000002 | -0.1 | 0.3 | 0.5 | -0.1 | 0 | 0 | 0 | -0.1 | 0.1 | 0 |
| CJ_10000005 | -1.1 | 1.2 | 0.2 | 0.3 | -0.2 | 0.1 | 0.1 | -0.4 | 0.3 | 0.2 |
| CJ_10000007 | -0.3 | 0.2 | 0 | 0.1 | 0.2 | 0 | 0 | -0.1 | -0.3 | 0 |
| CJ_10000008 | -0.1 | -0.2 | 0.6 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | -0.2 | 0 |
| CJ_10000009 | -0.2 | -0.6 | -0.8 | 0.1 | -0.1 | -2 | -0.1 | 0.1 | 0.9 | -0.9 |
| CJ_10000010 | -0.2 | -0.1 | 0.4 | 0.2 | 0 | 0.1 | 0.2 | -0.2 | -0.2 | 0.2 |
| CJ_10000011 | -0.5 | -0.1 | -0.2 | 0 | 0 | -1.6 | -0.1 | 0 | 0.2 | 0 |
| CJ_10000013 | -0.4 | 0 | 0.4 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| CJ_10000014 | 0.1 | 0.5 | -0.2 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0.2 | 0.1 |
| CJ_10000015 | 2.2 | 2.5 | 3.1 | 0.8 | -1.9 | 1.4 | 2.4 | -0.5 | 1.1 | 1 |
| CJ_10000016 | 0.2 | 0.2 | 0.7 | 0.4 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000017 | 2.8 | 3.8 | 0.5 | 1.1 | -1.8 | 0.3 | 1 | -1 | 1.5 | 1.8 |
| CJ_10000018 | -1.6 | -0.4 | -0.9 | -0.2 | -0.4 | -0.1 | -0.1 | 0.1 | 0.1 | 0.2 |

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|---|---|---|---|---|---|---|---|---|---|---|
| CJ_10000020 | 3.3 | 4.3 | 1.9 | 1.1 | -1.6 | 5.6 | 1.6 | -1.8 | 1.2 | 2 |
| CJ_10000022 | -0.6 | 0 | -0.1 | 0.1 | 0 | 0 | -0.1 | 0 | -0.1 | 0 |
| CJ_10000023 | 0.6 | -0.4 | 0 | 0.1 | -1 | 0 | 1.5 | 0.8 | 0.2 | 0 |
| CJ_10000024 | -0.7 | 1.6 | 1.6 | 0 | -0.1 | 0.1 | -0.2 | 0 | -0.8 | -0.1 |
| CJ_10000026 | 0.1 | 0.2 | 1 | 0.1 | 0.3 | 0.1 | 0.1 | -0.1 | -0.4 | -0.1 |
| CJ_10000028 | -0.3 | -2 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | -0.4 | -0.2 | -0.3 |
| CJ_10000031 | 0.3 | -0.2 | 0.7 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000033 | -2.2 | -2.3 | 0.6 | -0.1 | -0.3 | 0.2 | -0.1 | -0.1 | 0.8 | 0 |
| CJ_10000035 | 2.4 | 3 | 1.2 | 0.7 | -1.1 | 1.1 | 0.8 | -0.8 | 1 | 1 |
| CJ_10000036 | 1.2 | 0.7 | -0.2 | 0.5 | -0.8 | 0.5 | 0.5 | 0.1 | 0.1 | 0.3 |
| CJ_10000043 | -0.5 | -0.1 | 0.4 | 0 | -0.1 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000044 | 2.2 | 2.1 | 1.4 | 0.6 | -0.7 | 0.2 | -0.1 | -1.3 | 0.3 | 0.7 |
| CJ_10000045 | 0.1 | -1.1 | 0.5 | 0.3 | 0.1 | 0.1 | 0.2 | 0.2 | 0 | 0 |
| CJ_10000046 | -0.2 | -0.1 | 0.7 | 0.2 | 0 | 0.1 | 0.2 | 0.1 | -0.3 | 0 |
| CJ_10000047 | -1.7 | -0.1 | -0.1 | 0.2 | -0.3 | 0.5 | 0.1 | 0 | 0.1 | 0.3 |
| CJ_10000050 | -0.7 | -0.5 | 0.3 | 0.1 | 0 | 0.3 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000052 | -1.4 | -0.8 | -0.9 | 0 | 0 | 0.3 | 0 | -0.2 | -0.3 | 0 |

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| CJ_10000053 | -2 | -0.1 | -0.9 | 0 | 0 | 0.2 | -0.2 | 0 | -0.1 | 0 |
| CJ_10000054 | -0.5 | -0.4 | 0.7 | 0 | -0.1 | 0.3 | 0 | 0 | -1.2 | 0.1 |
| CJ_10000055 | -0.5 | -0.3 | -1.2 | 0 | 0.1 | 0 | -0.1 | -0.2 | -0.1 | 0.1 |
| CJ_10000056 | -2 | 1.1 | 0 | 0.5 | -0.3 | 0 | 0.2 | -0.2 | -0.3 | 0.3 |
| CJ_10000058 | -0.5 | 0 | -0.2 | 0.2 | 0.1 | -0.1 | -0.1 | -0.2 | -0.2 | 0.1 |
| CJ_10000059 | -0.6 | 0.5 | 0.5 | 0.1 | -0.1 | 0.4 | 0.1 | -0.2 | 0.4 | 0.2 |
| CJ_10000061 | -1.1 | 1.6 | 0.6 | 0.2 | -0.3 | 0.4 | -0.1 | -0.4 | 0.1 | 0.3 |
| CJ_10000062 | -1.1 | -0.3 | 0.6 | 0.2 | 0 | 0.2 | 0 | -0.2 | 0.2 | 0.1 |
| CJ_10000063 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0.3 | 0.5 | 0 |
| CJ_10000064 | 0.5 | 0.4 | 0.5 | 0.1 | -0.3 | 0.4 | 0 | -0.3 | 0 | 0.2 |
| CJ_10000065 | 0.1 | 0.2 | 0.3 | 0.2 | 0.1 | 0.2 | -0.2 | -0.1 | -0.1 | 0.1 |
| CJ_10000066 | -0.6 | -0.4 | -0.2 | 0.2 | -0.2 | 0.1 | 0 | 0 | 0 | 0 |
| CJ_10000067 | 0 | 0 | 0.2 | 0.2 | -0.1 | 0.3 | 0 | -0.1 | 0 | 0.2 |
| CJ_10000068 | 0.5 | 1.1 | -0.8 | 0.3 | -0.5 | -0.4 | -0.4 | -0.3 | 0.4 | 0.4 |
| CJ_10000069 | -0.8 | -0.3 | 0.4 | 0.2 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000070 | 2.6 | 1.1 | 0.9 | 0.4 | -0.9 | 0.4 | 0.4 | -0.2 | 0.3 | 0.6 |
| CJ_10000071 | 0.1 | 0.2 | 0.5 | 0.2 | 0.3 | 0 | 0.1 | 0 | -0.1 | -0.1 |

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| CJ_10000073 | -1.3 | -1.3 | -0.2 | 0.2 | 0.3 | 0.1 | 0.1 | 0.1 | -0.8 | -0.2 |
| CJ_10000074 | -0.2 | 0.1 | 0.4 | 0.2 | 0.3 | 0.1 | 0 | 0 | 0 | -0.1 |
| CJ_10000075 | 0.2 | -0.9 | 0.5 | 0.1 | 0.3 | -0.1 | 0.1 | 0.2 | -0.5 | -0.2 |
| CJ_10000077 | -0.3 | -0.2 | 0.6 | 0.2 | 0.1 | 0.2 | 0.2 | -0.1 | -0.1 | 0.1 |
| CJ_10000078 | -0.2 | -1.4 | 1.3 | 0.1 | 0.1 | -0.1 | 0.2 | 0 | -0.1 | -0.1 |
| CJ_10000080 | 0.3 | 0.3 | 0.8 | 0.2 | 0.2 | 0.1 | 0.2 | 0 | -0.1 | 0.1 |
| CJ_10000082 | 0.6 | 0.3 | 0.3 | 0.3 | 0.2 | 0.2 | 0.2 | -0.1 | 0 | 0.1 |
| CJ_10000083 | 0 | 0 | 0.5 | 0.2 | 0.1 | 0.1 | 0 | -0.1 | -0.1 | 0 |
| CJ_10000084 | 0.4 | -0.6 | 0.4 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | 0.2 | -0.1 |
| CJ_10000085 | -0.1 | 0.2 | 0.7 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 |
| CJ_10000086 | -0.5 | -0.1 | 0.4 | 0.3 | 0.1 | 0.3 | 0.2 | 0.1 | 0.1 | 0.1 |
| CJ_10000087 | -0.9 | -1.4 | 1 | 0.2 | -0.1 | 0 | 0.2 | 0 | 0 | 0 |
| CJ_10000088 | 0.1 | 0 | 0.8 | 0.2 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000089 | 0.1 | 0 | 0.4 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | -0.2 | 0 |
| CJ_10000091 | -0.4 | -0.7 | 0.5 | 0.2 | 0.1 | 0.2 | 0.2 | 0.1 | -0.1 | 0 |
| CJ_10000092 | -0.2 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | 0 | 0.1 | -0.1 | 0 |
| CJ_10000095 | 0.1 | 0.2 | -1 | 0.2 | 0 | -0.7 | -0.9 | -1.2 | -0.1 | 0.1 |

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| CJ_10000100 | -0.9 | 0.1 | -4.4 | 0.1 | -0.9 | -3.2 | -3.4 | -1.8 | -0.2 | 0 |
| CJ_10000102 | 0.5 | 0.3 | -0.3 | 0.2 | -0.3 | 0.2 | 0.1 | -0.7 | 0.3 | 0.4 |
| CJ_10000103 | -0.3 | 0.2 | 0.4 | 0.2 | -1.4 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000104 | 0.2 | -0.2 | 0.6 | 0.1 | 0 | 0.3 | 0.1 | -0.1 | 0.5 | 0 |
| CJ_10000105 | 0.4 | -0.3 | 1.3 | 0.2 | 0.2 | 0.3 | 0.3 | 0 | -0.2 | 0 |
| CJ_10000106 | -0.7 | -0.3 | 0.3 | 0.2 | 0.1 | 0.2 | -0.1 | 0.2 | -0.3 | 0 |
| CJ_10000107 | 0.4 | -0.3 | 0.4 | 0.1 | -0.1 | 0.2 | 0.2 | -0.1 | 0.3 | -0.1 |
| CJ_10000110 | -1.9 | -1.2 | -1.1 | 0 | 0 | 0 | -0.4 | -0.4 | 0.1 | -0.1 |
| CJ_10000112 | 0.9 | 0.5 | 0.7 | 0.3 | 0 | 0.4 | 0.3 | 0 | 0.2 | 0.3 |
| CJ_10000113 | -0.1 | -0.3 | 0.5 | 0.1 | -0.1 | 0.1 | 0.2 | 0.1 | 0 | 0 |
| CJ_10000114 | 0.1 | 0.2 | 0 | 0.2 | -0.1 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10000115 | 0.2 | 0.4 | 0.7 | 0.4 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 |
| CJ_10000116 | 0 | -0.1 | 0.6 | 0.2 | 0 | 0.1 | 0.3 | 0.1 | 0 | 0 |
| CJ_10000117 | 1 | 1 | 0.2 | 0.3 | -0.3 | 0.3 | 0.4 | -0.1 | 0.1 | 0.4 |
| CJ_10000118 | -0.7 | -0.4 | 0.1 | 0.1 | 0.1 | 0.2 | 0.3 | 0.2 | -0.3 | 0 |
| CJ_10000120 | -0.4 | -0.9 | 0.7 | 0.2 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| CJ_10000121 | 0.2 | 0.2 | 0.7 | 0.2 | -0.1 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 |

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| CJ_10000123 | -0.5 | -1.6 | -0.1 | 0.1 | 0 | -0.2 | 0.2 | 0 | -0.3 | 0.1 |
| CJ_10000125 | 0.8 | -0.4 | 1.3 | 0.2 | 0.1 | 0.1 | 0.2 | 0.2 | -0.1 | 0.2 |
| CJ_10000126 | -0.2 | 0.2 | 0.3 | 0.1 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0.1 |
| CJ_10000128 | 0.3 | -1 | 0.9 | 0.2 | 0.1 | -0.4 | 0.1 | 0.1 | 0 | 0.1 |
| CJ_10000129 | -0.1 | 0 | 0.1 | 0.2 | 0.2 | 0 | -0.2 | -0.3 | -0.1 | 0 |
| CJ_10000131 | 0.1 | -0.1 | 0.2 | 0.1 | -0.2 | 0.1 | 0.1 | -0.1 | 0.1 | -0.1 |
| CJ_10000132 | -0.6 | -0.3 | 0.4 | 0.1 | 0 | 0.2 | -0.4 | -0.1 | -0.2 | 0 |
| CJ_10000135 | 1.2 | 1.2 | 0.5 | 0.1 | -0.4 | 0.4 | 0.3 | -0.1 | 0.3 | 0.5 |
| CJ_10000136 | -0.9 | 0 | 0 | 0.2 | -0.1 | 0.3 | 0.1 | 0 | 0.1 | 0.2 |
| CJ_10000137 | -0.9 | 0.1 | -0.3 | 0 | -0.3 | 0 | 0 | -0.1 | 0.2 | 0.1 |
| CJ_10000138 | -0.4 | 0.1 | 0 | 0.3 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0.1 |
| CJ_10000139 | -0.8 | -0.1 | 0.5 | 0.2 | 0 | 0.4 | 0.2 | 0 | 0 | 0.2 |
| CJ_10000140 | -0.1 | 0 | 0.5 | 0.2 | 0 | 0.1 | 0.1 | 0 | -0.2 | -0.1 |
| CJ_10000141 | 0.4 | 0.3 | 0.6 | 0.1 | 0.2 | 0 | 0.2 | 0.1 | -0.1 | 0 |
| CJ_10000142 | 0.6 | 0.2 | 0.5 | 0.1 | 0.1 | 0.3 | 0.2 | 0 | -0.1 | 0.1 |
| CJ_10000143 | -0.4 | -0.6 | 0 | 0 | 0 | 0.3 | 0 | 0.1 | 0.3 | 0 |
| CJ_10000144 | -2.5 | -1.7 | -2.5 | 0 | 0 | 0.1 | -0.1 | -0.2 | -0.1 | 0.1 |

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| CJ_10000145 | 0.4 | 0.8 | -1.4 | 0.1 | 0.9 | 0.5 | 0.1 | 0 | 0.2 | 0.1 |
| CJ_10000146 | -0.4 | -1.3 | -2.4 | -0.1 | -0.3 | 0.2 | 0.1 | 0 | 0.5 | 0 |
| CJ_10000147 | -1 | 0.4 | -0.1 | 0.2 | -0.1 | 0.4 | -0.3 | -0.1 | 0 | 0.2 |
| CJ_10000148 | -1.1 | -0.5 | -0.3 | 0.1 | 1.2 | 0.1 | -0.2 | 0.1 | -0.3 | -0.1 |
| CJ_10000149 | -2 | -0.2 | 0.7 | 0.1 | 0.1 | 0.1 | 0.1 | -0.2 | 0.1 | 0 |
| CJ_10000150 | -0.4 | -0.2 | 0.4 | 0 | 0 | 0.2 | 0 | -0.2 | 0 | 0 |
| CJ_10000151 | 0.2 | 0.3 | 0.6 | 0.2 | -0.4 | 0.1 | 0 | -0.2 | -0.1 | 0.1 |
| CJ_10000152 | -0.5 | -0.3 | 0.3 | 0 | 0 | 0 | 0 | -0.1 | 0.2 | 0 |
| CJ_10000153 | -0.3 | -0.1 | 0.4 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | -0.1 |
| CJ_10000154 | -0.2 | 0.1 | 0.4 | 0.2 | 0.5 | 0.3 | -0.1 | 0 | 0.5 | 0.1 |
| CJ_10000155 | 0 | -0.7 | 0.8 | 0.1 | -0.1 | 0.2 | 0.2 | 0.2 | 0 | 0 |
| CJ_10000156 | -0.2 | -0.6 | 0.2 | 0.1 | -0.4 | 0.3 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000157 | -0.5 | -0.2 | 0.7 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0.2 | 0 |
| CJ_10000158 | -2.1 | -0.4 | 0 | 0.1 | -0.1 | 0.1 | -0.1 | -0.3 | -0.1 | 0 |
| CJ_10000159 | 0 | -0.1 | 0.4 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10000160 | -0.2 | 0.2 | 0.6 | 0.3 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0.2 |
| CJ_10000162 | -0.2 | -0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.1 | 0 | 0 | 0 |

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| CJ_10000163 | -0.2 | -0.1 | 0.2 | 0.2 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000164 | 1.5 | 1.3 | 1.1 | 0.2 | -0.2 | 0 | 0.3 | 0.2 | 0.2 | 0 |
| CJ_10000165 | -0.1 | -0.4 | 0.6 | 0.2 | 0 | 0.3 | 0 | 0.2 | 0 | 0.1 |
| CJ_10000166 | -0.2 | 0.2 | 0.5 | 0.2 | 0.2 | 0.1 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000168 | 0.7 | 0.7 | 0.5 | 0.3 | 0.1 | 0.3 | 0.2 | 0 | 0.1 | 0 |
| CJ_10000169 | 0.1 | 0.6 | 0 | 0.2 | 0.4 | 0.2 | 0 | -0.1 | 0.2 | 0.1 |
| CJ_10000170 | 1.4 | 0.1 | 1.3 | 0.5 | -0.3 | 0.4 | 0.3 | -0.3 | 0.7 | 0.6 |
| CJ_10000171 | -0.6 | 0.3 | 0.1 | 0.1 | 0 | 0.4 | 0 | -0.1 | -0.1 | 0.1 |
| CJ_10000172 | -0.9 | 0.1 | -0.2 | 0.1 | -0.5 | 0.2 | 0 | -0.1 | 0.1 | 0 |
| CJ_10000173 | -0.5 | -0.9 | 0.1 | 0 | -0.2 | 0.2 | 0 | -0.3 | -0.1 | 0.1 |
| CJ_10000174 | -0.5 | -0.5 | 0 | 0.1 | 0.1 | 0.2 | -0.1 | 0 | -0.1 | 0 |
| CJ_10000175 | -0.7 | -0.6 | 0.4 | 0.2 | 0.5 | 0.3 | 0 | -0.1 | 0 | 0.1 |
| CJ_10000176 | -0.6 | -0.1 | -0.1 | -0.1 | -0.3 | -0.1 | -0.1 | 0 | 0.3 | 0.1 |
| CJ_10000177 | 0.1 | -0.3 | -0.2 | 0.1 | 0 | -0.2 | -0.5 | -0.2 | 0.1 | 0.1 |
| CJ_10000179 | -0.9 | -0.5 | 0 | 0.1 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0 |
| CJ_10000180 | 0.6 | 0.1 | -0.1 | 0.1 | -0.4 | 0.4 | 0.1 | -0.1 | -0.2 | 0.1 |
| CJ_10000181 | -0.6 | -0.1 | -0.4 | 0.1 | 0 | 0.2 | -0.1 | -0.1 | 0 | 0.1 |

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| CJ_10000183 | 1 | 0.4 | 0.6 | 0.2 | -0.3 | 0.4 | 0.5 | 0 | 0.2 | 0.4 |
| CJ_10000184 | -0.2 | -0.1 | 0.3 | 0.3 | 0.1 | 0.1 | 0.1 | -0.2 | -0.3 | 0.2 |
| CJ_10000185 | -1.6 | -0.7 | -1 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 |
| CJ_10000186 | 0 | -1.5 | -0.9 | -0.3 | 0 | -0.2 | -0.5 | -0.1 | -0.3 | -0.4 |
| CJ_10000187 | 0.1 | 0.1 | 0.4 | 0.2 | 0.2 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000188 | 0.3 | 0.1 | -5.8 | 0.2 | -0.4 | -1.5 | -0.2 | -1.2 | 0.4 | 0.1 |
| CJ_10000189 | 0 | 0 | -0.2 | 0.1 | -0.1 | -0.1 | -0.5 | -0.6 | 0 | 0.1 |
| CJ_10000190 | -0.6 | -0.1 | -0.2 | 0.2 | 0.1 | 0 | -0.2 | 0.1 | 0 | 0 |
| CJ_10000191 | 0 | -0.3 | 0.8 | 0.2 | 0.1 | 0 | 0 | 0.1 | 0 | 0 |
| CJ_10000193 | -0.8 | -1.2 | 1 | 0.2 | -0.2 | 0.4 | 0.3 | 0.1 | 0.3 | 0.1 |
| CJ_10000196 | 0.1 | -0.4 | 0.3 | 0 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | -0.2 |
| CJ_10000200 | 0.4 | 0.1 | 0.7 | 0.1 | 0 | 0.1 | 0.1 | -0.2 | 0 | 0.1 |
| CJ_10000204 | 0.2 | 0 | -0.9 | 0 | -0.2 | 0 | -0.3 | 0.1 | 0.1 | 0.1 |
| CJ_10000210 | 0 | 0.1 | 0.3 | 0.1 | 0.2 | 0.2 | 0.1 | 0.2 | -0.1 | 0 |
| CJ_10000213 | 0.7 | 0.2 | 0.8 | 0.3 | 0.1 | 0.2 | 0.3 | 0.2 | -0.2 | 0 |
| CJ_10000214 | 0.5 | -0.6 | 0.6 | 0.1 | -0.1 | 0.1 | 0 | -0.5 | 0.2 | -0.1 |
| CJ_10000215 | -0.1 | 0 | 0.9 | 0.1 | 0 | 0.3 | 0 | 0 | 0 | 0 |

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| CJ_10000216 | -0.6 | -0.2 | 0.1 | 0.2 | 0.1 | 0.2 | -0.2 | 0 | -0.1 | 0.1 |
| CJ_10000217 | -1.1 | -0.3 | -0.1 | 0 | 0 | 0.3 | 0 | 0 | 0.4 | -0.1 |
| CJ_10000218 | -1 | -0.2 | -0.4 | 0.1 | -0.1 | 0.2 | -0.1 | -0.2 | 0 | 0.1 |
| CJ_10000219 | -0.4 | 0 | 0.3 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| CJ_10000220 | -0.2 | -0.6 | 0.2 | 0.1 | -0.1 | 0 | 0 | -0.2 | 0 | 0 |
| CJ_10000221 | -0.1 | 0.1 | 0.5 | 0.1 | 0 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000222 | -1.8 | 0 | -0.1 | 0.1 | 0 | 0.3 | -0.1 | 0 | 0 | 0.1 |
| CJ_10000223 | 0 | 0.3 | 0 | 0 | -0.2 | 0.2 | 0 | 0 | 0.2 | 0.1 |
| CJ_10000224 | -0.4 | -0.1 | 0.4 | 0.1 | 0.1 | 0.2 | 0 | -0.1 | 0 | 0 |
| CJ_10000225 | -1.1 | 0.9 | -0.3 | 0.3 | -0.1 | 0.4 | 0.2 | -0.1 | -0.1 | 0.2 |
| CJ_10000228 | -0.4 | -0.1 | -0.7 | 0.1 | 0 | 0.3 | 0 | 0.1 | 0.1 | 0.1 |
| CJ_10000230 | -0.2 | 0.1 | 0.2 | 0.8 | -0.2 | -0.1 | 0 | 0.5 | 0.1 | 0.9 |
| CJ_10000231 | -1.1 | -0.2 | 0 | 0.2 | 0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| CJ_10000232 | -0.1 | 0.1 | 0.5 | 0.3 | 0.1 | 0 | -0.3 | 0.2 | -0.4 | -0.3 |
| CJ_10000234 | 0.2 | 0.2 | 0.3 | 0.2 | 0 | 0.1 | 0 | 0 | 0.2 | 0.1 |
| CJ_10000235 | 0 | -0.1 | 0 | 0.2 | 0 | 0 | -0.2 | 0.1 | 0 | 0 |
| CJ_10000236 | 0.2 | 0 | -0.3 | 0.2 | 0.1 | -1.7 | -0.2 | 0.1 | -0.3 | -0.1 |

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|---|---|---|---|---|---|---|---|---|---|---|
| CJ_10000237 | -0.8 | -0.4 | -0.3 | 0.1 | 0 | 0.2 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000238 | -0.7 | -1.3 | -0.2 | 0 | -0.2 | 0.4 | 0 | -0.1 | 0.3 | 0.2 |
| CJ_10000239 | -1.3 | -1 | -0.4 | 0.2 | -0.1 | 0.3 | -0.1 | -0.2 | -0.1 | 0.1 |
| CJ_10000240 | -1.3 | -0.3 | -0.7 | 0.1 | 0 | 0.3 | -0.2 | 0 | 0.3 | 0.2 |
| CJ_10000241 | -0.2 | -0.1 | 0.6 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 |
| CJ_10000242 | -2.9 | -0.2 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.3 | -0.1 | 0.1 |
| CJ_10000243 | -1 | -0.2 | -0.2 | 0.1 | 0 | 0.2 | 0 | -0.1 | 0 | 0.1 |
| CJ_10000244 | -0.3 | -0.1 | 0.4 | 0 | -0.1 | 0.2 | 0 | 0 | -0.2 | 0.1 |
| CJ_10000245 | -0.7 | 0.3 | 0 | 0.1 | 0.2 | 0.1 | -0.2 | 0 | 0.2 | 0.1 |
| CJ_10000246 | -0.6 | -0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000247 | 0.4 | 0.4 | 0.5 | 0.1 | 0 | 0 | 0.2 | 0 | 0 | 0.1 |
| CJ_10000248 | 0.3 | 0.2 | 0.6 | 0.2 | -0.1 | 0.1 | 0.2 | 0 | 0 | 0.1 |
| CJ_10000249 | -0.6 | -0.2 | -0.2 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0 | 0 |
| CJ_10000252 | -0.6 | -0.2 | 0.3 | 0 | 0 | 0.3 | 0.1 | 0.1 | -0.2 | 0 |
| CJ_10000254 | 0.4 | -1 | 0.5 | 0.4 | 0.1 | 0 | -0.1 | -0.2 | -0.1 | 0.1 |
| CJ_10000255 | 0.2 | 0.3 | 0.3 | 0.2 | 0 | 0.1 | 0.2 | 0 | 0.1 | 0 |
| CJ_10000256 | 0.3 | -0.2 | 0.3 | 0.2 | 0.3 | 0 | 0 | 0.2 | -0.3 | -0.1 |

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| CJ_10000257 | 0 | 0.2 | 0.2 | 0.1 | -0.1 | 0 | -0.7 | 0 | 0.1 | 0 |
| CJ_10000258 | -0.1 | 0 | 0.1 | 0.2 | 0 | 0.3 | 0 | 0 | -0.3 | 0 |
| CJ_10000259 | 0.8 | 0.3 | 0.8 | 0 | 0.1 | 0 | 0.3 | 0.1 | 0.1 | 0 |
| CJ_10000260 | 0.6 | -0.2 | -0.2 | 0.2 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| CJ_10000261 | -0.4 | 0.2 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 |
| CJ_10000262 | 0.1 | -0.7 | 0.9 | -0.2 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | -0.2 |
| CJ_10000263 | 0 | 0.2 | 0.3 | 0.1 | -0.1 | 0.3 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000264 | 0.7 | 0.2 | 0.5 | 0.3 | 0.2 | 0 | 0 | -0.1 | -0.2 | 0.1 |
| CJ_10000265 | -0.1 | 0.4 | 1 | 0.1 | -0.2 | 0.1 | 0.2 | -0.1 | 0 | 0.2 |
| CJ_10000267 | -0.1 | 0.1 | 0.5 | 0.2 | 0.1 | 0.1 | 0 | -0.2 | 0 | 0 |
| CJ_10000268 | 0.7 | 0.8 | 0.2 | 0.1 | -0.2 | 0.1 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10000269 | 0 | 0 | 0.7 | 0.2 | 0.1 | 0.2 | 0.1 | -0.3 | 0 | 0.1 |
| CJ_10000270 | 0.7 | 0.3 | 0.9 | 0.2 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000271 | -0.8 | -0.2 | 0.4 | 0.3 | -0.1 | 0.1 | 0.2 | 0.1 | 0.1 | 0 |
| CJ_10000272 | -0.1 | -0.2 | 0.5 | 0.2 | 0.1 | 0.1 | 0.2 | -0.3 | -0.1 | 0.1 |
| CJ_10000273 | 0.5 | 0.2 | 0.6 | 0.1 | 0 | 0.2 | 0.2 | 0 | -0.1 | -0.1 |
| CJ_10000276 | -0.5 | -0.2 | -0.2 | 0 | 0 | 0.3 | 0.1 | 0 | 0 | 0.1 |

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| CJ_10000278 | -0.1 | 0.4 | 0 | 1 | 0.2 | 0.1 | 0.2 | -0.1 | 0 | -0.1 |
| CJ_10000279 | -0.2 | -0.1 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | -0.1 | 0 |
| CJ_10000280 | -1 | -0.7 | 0.1 | 0.2 | 0.2 | -0.1 | -0.3 | 0.3 | -0.6 | -0.1 |
| CJ_10000281 | 5.6 | 1.3 | -0.1 | 1.2 | 0.1 | -0.9 | 1.9 | 1.7 | 2.7 | -1.3 |
| CJ_10000282 | -0.2 | -0.8 | 0.4 | 0.1 | 0.4 | 0.2 | 0 | 0.3 | 0 | 0 |
| CJ_10000284 | 0.5 | -0.6 | 0 | 0.1 | 0.4 | -0.4 | 0 | 0.1 | -0.2 | -0.1 |
| CJ_10000285 | -0.6 | -0.1 | -0.2 | 0 | 0 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| CJ_10000286 | -0.3 | 0.6 | 0.9 | 0.2 | 0.1 | 0.1 | 0.1 | -0.1 | -0.2 | 0 |
| CJ_10000287 | -0.5 | -0.2 | 0.1 | 0.1 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0 |
| CJ_10000288 | 0.2 | -0.6 | 1.4 | 0.1 | 0 | 0 | 0 | 0.1 | 0.2 | -0.1 |
| CJ_10000289 | -0.1 | 0.1 | 0.7 | 0.3 | 0.2 | 0.1 | 0 | 0 | 0 | 0.1 |
| CJ_10000290 | 1 | 0.5 | 0.5 | 0.4 | -0.1 | 0.3 | 0.2 | -0.2 | 0 | 0.2 |
| CJ_10000291 | -0.4 | -0.7 | 0.6 | 0.2 | -0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.1 |
| CJ_10000292 | -1.7 | -0.9 | -0.5 | 0.1 | -0.1 | 0.5 | 0.1 | 0.1 | 0.4 | 0.1 |
| CJ_10000293 | 3 | 2.4 | 3.1 | 0.9 | -0.7 | 0.8 | 1.3 | -0.4 | 0.7 | 0.8 |
| CJ_10000294 | -0.7 | -0.6 | 0.2 | 0.1 | -0.1 | -0.1 | 0 | 0.1 | -0.4 | 0.1 |
| CJ_10000295 | 0.1 | -0.1 | 0.6 | 0.1 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0 |

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| CJ_10000296 | -2.1 | -1.2 | -0.1 | 0.1 | 0.2 | 0.3 | 0 | 0.1 | -0.2 | 0 |
| CJ_10000297 | -0.7 | -0.5 | 0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| CJ_10000298 | -0.6 | 0.2 | 0.2 | -0.2 | -0.3 | 0.2 | 0.1 | 0 | 0.3 | 0 |
| CJ_10000299 | 0.5 | -0.1 | -0.8 | 0 | -0.2 | 0.1 | -0.2 | 0 | 0.4 | 0.1 |
| CJ_10000302 | -0.8 | -0.2 | -0.8 | -1.7 | 0 | 0.1 | -0.4 | 1.2 | -0.1 | -1.5 |
| CJ_10000304 | 0.4 | 0.5 | -0.1 | 0.2 | 0.1 | 0.2 | -0.1 | -0.2 | -0.1 | 0 |
| CJ_10000305 | -0.6 | 0 | -0.6 | -1.3 | 0 | 0.1 | -0.1 | 1.4 | 0 | -1.3 |
| CJ_10000307 | 0.3 | -0.3 | 0.4 | 0.2 | 0.2 | 0.1 | 0.2 | 0.3 | -0.3 | -0.1 |
| CJ_10000308 | -0.8 | -0.6 | -0.1 | 0.1 | 0.2 | 0 | -0.7 | -0.1 | -0.2 | 0 |
| CJ_10000310 | -0.2 | -0.2 | 1.2 | 0.2 | 0.1 | 0.2 | -0.1 | -0.2 | -0.2 | 0.1 |
| CJ_10000311 | -0.4 | -0.3 | 0 | 0.2 | 0.1 | 0.3 | -0.2 | 0 | 0 | 0.1 |
| CJ_10000312 | -0.1 | -0.3 | 1 | 0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| CJ_10000313 | -3.9 | -2.5 | 0.3 | 0.1 | -0.1 | 0.2 | 0.1 | -0.2 | -0.1 | 0 |
| CJ_10000314 | 0.1 | 0.1 | 0.3 | 0.2 | -0.1 | 0.2 | 0 | -0.2 | -0.1 | 0.1 |
| CJ_10000316 | -0.1 | -0.1 | 0.6 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | -0.2 | -0.1 |
| CJ_10000317 | -0.7 | 0.5 | 0.3 | 0.3 | -0.2 | 0.1 | 0 | -0.6 | -0.1 | 0.1 |
| CJ_10000318 | 1.2 | 0.4 | 1.2 | 0.2 | -0.2 | 0.2 | 0.3 | -0.1 | 0.2 | 0.1 |

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| CJ_10000319 | 0.1 | 0.3 | 0.2 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0.1 | 0 |
| CJ_10000320 | -0.6 | 0.1 | -2 | 0 | -0.2 | -1.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000322 | -0.4 | -0.2 | 0.1 | 0.1 | -0.1 | 0.1 | -0.1 | -0.4 | 0 | 0 |
| CJ_10000323 | -1.8 | -0.7 | 0.2 | 0 | -0.1 | 0.2 | -0.2 | 0.2 | -0.4 | 0 |
| CJ_10000325 | -0.1 | 0 | 0.3 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | 0 |
| CJ_10000326 | -1.6 | -0.3 | -0.2 | 0 | -0.1 | 0.2 | 0 | 0 | 0.1 | 0.1 |
| CJ_10000328 | 0.4 | 0.6 | -0.2 | 0.1 | -0.1 | 0.2 | 0.1 | 0.3 | -0.1 | -0.1 |
| CJ_10000329 | -0.3 | 0.3 | 0.5 | 0.2 | 0.2 | 0.1 | 0.1 | 0.2 | -0.3 | 0 |
| CJ_10000331 | 0.9 | -0.1 | -0.2 | 0.2 | 0 | -0.9 | -0.1 | 0.1 | -0.3 | -0.1 |
| CJ_10000332 | -0.2 | -0.3 | -0.2 | 0.1 | 0 | 0.5 | -0.1 | -0.1 | 0.2 | 0.1 |
| CJ_10000334 | -0.8 | -0.4 | 0.9 | 0 | -0.2 | 0.2 | 0.1 | 0 | -0.2 | 0 |
| CJ_10000335 | -1.3 | -0.4 | -0.7 | 0.2 | 0.1 | 0.3 | -0.2 | 0 | 0.4 | 0.1 |
| CJ_10000336 | -0.1 | -1.9 | 1 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0.3 | -0.1 |
| CJ_10000337 | -0.1 | -0.2 | 0.6 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000340 | -3.2 | -0.1 | 0.1 | 0.1 | -0.3 | 0.2 | -0.1 | 0 | 0.1 | 0.1 |
| CJ_10000341 | 0 | -0.2 | 0.6 | 0.1 | 0 | 0.2 | 0.1 | 0 | 0 | 0 |
| CJ_10000342 | -0.7 | -0.5 | -0.1 | 0 | -0.2 | 0.2 | 0 | 0 | 0 | 0 |

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| CJ_10000343 | -0.2 | -0.2 | 0.4 | 0.2 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0.1 |
| CJ_10000344 | -0.2 | -0.1 | 0.3 | 0.1 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000347 | -0.4 | -0.2 | 0.3 | 0.1 | 0 | 0.2 | 0.1 | 0.1 | -0.2 | 0 |
| CJ_10000349 | -0.8 | -0.3 | 0.4 | 0.1 | 0 | 0.2 | 0.1 | 0.1 | 0.1 | 0 |
| CJ_10000350 | -1.6 | -1 | -0.7 | 0.1 | 0 | 0.1 | -0.2 | -0.8 | 0.1 | 0.1 |
| CJ_10000352 | -0.7 | 0.1 | 0.6 | 0.1 | 0.1 | 0.2 | 0.3 | 0.2 | -0.2 | 0 |
| CJ_10000353 | -0.4 | -0.1 | -0.3 | 0.1 | -0.1 | 0.2 | 0 | 0.1 | 0.1 | 0.1 |
| CJ_10000354 | -0.7 | -0.1 | 0.2 | 0.3 | 0.1 | 0.1 | 0 | 0.2 | -0.3 | -0.1 |
| CJ_10000355 | 0.3 | -0.4 | 0.4 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | -0.1 |
| CJ_10000356 | 0.1 | 0 | -0.2 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | -0.1 | -0.1 |
| CJ_10000357 | -0.4 | -0.9 | 0.4 | -0.1 | 0.1 | -0.2 | 0 | 0 | -0.1 | -0.2 |
| CJ_10000358 | -1.6 | -0.2 | 0.3 | 0.1 | 0.4 | 0.1 | -0.3 | 0 | -0.2 | 0 |
| CJ_10000359 | -0.1 | -0.1 | 0.3 | 0.1 | 0 | 0.3 | 0.1 | 0 | 0 | 0.2 |
| CJ_10000361 | -0.4 | 0.1 | 0.6 | 0.2 | 0 | 0.2 | 0 | -0.1 | -0.1 | 0 |
| CJ_10000362 | -0.4 | 0 | -0.8 | 0.2 | 0.1 | 0.2 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10000364 | -0.1 | 0.2 | -0.2 | 0.1 | -0.4 | 0.4 | 0.2 | -0.1 | 0.1 | 0.2 |
| CJ_10000365 | 0.5 | 0 | 0.5 | 0.3 | 0.1 | 0.2 | 0.2 | 0 | 0 | 0 |

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| CJ_10000367 | 0.2 | 0.3 | 0.3 | 0.2 | -0.1 | 0.2 | 0.2 | 0 | -0.1 | 0.1 |
| CJ_10000368 | 0.7 | 0.1 | 0.4 | 0.1 | 0 | 0.1 | 0.2 | -0.2 | 0.1 | 0 |
| CJ_10000370 | 0 | -0.3 | 0.3 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10000373 | 0.3 | 0.3 | 0 | 0.2 | 1 | -0.5 | -0.2 | 0.1 | -0.1 | -0.1 |
| CJ_10000374 | 2.3 | 1.6 | 0.9 | 0.4 | -0.4 | 0.4 | 0.5 | -0.1 | 0.2 | 0.2 |
| CJ_10000376 | -0.9 | -0.4 | -0.3 | 0.2 | 0.1 | 0.2 | 0 | 0.3 | -0.1 | 0 |
| CJ_10000377 | 2 | 2.5 | 2.5 | 0.7 | -1 | 1.7 | 1.6 | -0.6 | 0.7 | 0.9 |
| CJ_10000379 | -0.5 | -1.3 | 0.3 | 0.1 | 0.1 | 0.2 | 0 | 0.2 | -0.3 | 0 |
| CJ_10000381 | -1 | -1 | -0.1 | 0.2 | 0 | 0.3 | -0.2 | -0.2 | 0 | 0 |
| CJ_10000382 | -0.5 | 0.3 | 0.2 | 0.1 | -0.2 | 0.3 | 0.2 | 0 | 0 | 0.2 |
| CJ_10000383 | -0.3 | -0.2 | 0.1 | -0.1 | -0.1 | 0.2 | 0 | -0.3 | -0.2 | -0.1 |
| CJ_10000384 | -1.2 | 0.7 | -0.1 | 0.1 | -0.3 | 0.2 | 0.1 | -0.3 | 0.1 | 0.1 |
| CJ_10000385 | -0.2 | 0 | 0.4 | 0.2 | 0 | 0.1 | -0.2 | -0.3 | 0 | 0 |
| CJ_10000386 | -0.7 | -0.7 | 0.5 | 0.1 | 0 | 0.1 | 0 | 0 | -1.5 | 0 |
| CJ_10000387 | 1 | 1.8 | 0.7 | 0.3 | -1 | 0.5 | 0.6 | -0.1 | 0.3 | 0.3 |
| CJ_10000388 | -0.3 | 0 | 0.1 | 0.2 | 0.1 | 0.3 | -0.1 | -0.1 | -0.1 | 0 |
| CJ_10000389 | -0.4 | -1.6 | 0 | 0 | 0.2 | 0.1 | -0.1 | 0.2 | 0.4 | 0 |

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| CJ_10000390 | 0.1 | 0.2 | 1.9 | -0.1 | 0 | 0.1 | -0.1 | -0.2 | -0.3 | 0.4 |
| CJ_10000391 | 0 | 0 | 0.6 | 0 | 0 | 0.2 | 0 | -0.1 | -0.1 | 0.1 |
| CJ_10000393 | -0.5 | -0.1 | 0.2 | 0.2 | -0.2 | 0.2 | 0 | 0 | 0 | 0 |
| CJ_10000394 | -0.6 | 0 | -0.2 | 0.1 | -0.1 | 0.3 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000395 | -1.4 | 0 | -0.4 | -0.2 | -0.3 | 0.3 | -0.1 | 0.1 | 0.4 | 0 |
| CJ_10000396 | -0.5 | 0 | 0.3 | 0.1 | -0.3 | 0.3 | 0.2 | 0 | 0 | 0.2 |
| CJ_10000397 | -0.1 | 0.1 | 0.4 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000398 | -0.9 | -0.3 | -0.2 | -0.1 | -0.1 | 0.1 | -0.2 | 0.1 | 0.1 | -0.1 |
| CJ_10000399 | 0 | 0.1 | 0.8 | 0 | -0.2 | 0 | 0 | -0.1 | 0.3 | 0.1 |
| CJ_10000400 | -0.8 | -0.6 | -1.8 | 0.2 | -0.2 | 0.3 | -1.1 | -0.6 | 0 | 0.2 |
| CJ_10000401 | 0.2 | 0.2 | 0.7 | 0.1 | -0.2 | 0.1 | 0.1 | 0.1 | -0.1 | 0 |
| CJ_10000402 | 0 | 0.7 | -0.1 | 0.1 | -0.2 | 0.3 | 0.1 | 0 | 0.2 | 0.2 |
| CJ_10000403 | -0.3 | 0.4 | -0.1 | 0.2 | -0.1 | 0.3 | 0 | 0 | 0.1 | 0 |
| CJ_10000404 | 0.2 | -0.1 | -0.6 | 0 | -0.4 | 0.3 | 0 | 0.2 | -0.1 | 0 |
| CJ_10000405 | 0.3 | 0.5 | 0.3 | 0.2 | 0.6 | 0 | 0.1 | 0 | -0.2 | 0.1 |
| CJ_10000406 | -0.9 | -0.3 | -0.6 | 0 | 0 | 0.2 | 0 | 0.1 | 0 | 0.1 |
| CJ_10000407 | -0.2 | -0.3 | 0.2 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.1 | -0.1 |

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| CJ_10000408 | -0.7 | 0.3 | 1 | 0.1 | 0.2 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| CJ_10000409 | 0.2 | 0.5 | 0.4 | 0.2 | 0.3 | 0 | -0.1 | -0.1 | 0.1 | -0.1 |
| CJ_10000410 | 0 | 0.6 | 0.4 | 0.1 | 0 | 0.2 | 0 | 0 | 0.1 | 0 |
| CJ_10000411 | 0.3 | -0.1 | 0.5 | 0 | -0.1 | 0 | 0.1 | 0 | -0.2 | 0 |
| CJ_10000412 | -0.1 | -0.1 | 0.4 | 0.1 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 |
| CJ_10000413 | -0.1 | -0.5 | -0.2 | 0 | 0 | 0.1 | 0 | 0.1 | 0.5 | 0.1 |
| CJ_10000414 | -0.8 | 0 | -0.5 | -0.1 | 0 | 0.3 | 0 | 0 | 0.1 | 0 |
| CJ_10000415 | -0.7 | 0 | 0.1 | 0.2 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0.2 |
| CJ_10000417 | -1.1 | -0.5 | 0 | 0.2 | -0.2 | 0.4 | 0 | 0.1 | -0.2 | 0.2 |
| CJ_10000418 | -0.5 | -0.4 | -0.5 | 0.1 | 0 | 0.2 | 0 | -0.1 | -0.2 | 0.1 |
| CJ_10000419 | -1 | -0.6 | -2 | 0.1 | -0.4 | -0.3 | -0.3 | -1.2 | -0.1 | 0.1 |
| CJ_10000420 | -0.3 | -0.1 | 0.1 | 0.2 | -0.2 | 0.1 | 0 | 0 | 0 | 0 |
| CJ_10000421 | -0.4 | -0.2 | 0 | 0.2 | 0.1 | 0.2 | 0.2 | 0 | -0.1 | 0.1 |
| CJ_10000422 | -0.3 | 0.1 | -0.1 | 0 | -0.3 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| CJ_10000423 | -0.1 | 0.3 | 0.1 | 0.1 | -0.1 | 0.3 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10000424 | -0.4 | -0.1 | -0.4 | 0 | -0.1 | 0.1 | -0.1 | 0 | 0 | 0 |
| CJ_10000425 | -0.9 | 0.1 | 0.1 | 0.2 | -0.3 | 0 | 0 | -0.1 | 0.6 | 0.3 |

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| CJ_10000426 | 0 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000427 | -0.3 | 0.2 | -0.4 | 0 | -0.2 | 0.3 | -0.2 | -0.1 | 0 | 0.1 |
| CJ_10000428 | 0 | -2 | 0.4 | 0.1 | 0.1 | 0.2 | 0 | 0 | -0.9 | 0 |
| CJ_10000429 | -0.1 | -0.7 | -0.2 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | -0.3 | 0.1 |
| CJ_10000430 | -0.4 | -0.1 | 0.2 | 0.1 | -0.1 | 0.3 | 0 | -0.1 | 0.2 | 0.2 |
| CJ_10000433 | -0.2 | 0.1 | 0.2 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| CJ_10000434 | 0.6 | -0.5 | 0.8 | 0.2 | 0.2 | 0 | 0 | 0 | 0.3 | 0 |
| CJ_10000435 | -0.3 | -0.1 | -0.1 | 0.1 | 0.1 | 0.2 | -0.2 | -0.2 | 0 | 0 |
| CJ_10000436 | -0.1 | 0.7 | 0.9 | 0.1 | 0 | 0 | 0.1 | -0.1 | 0 | 0.2 |
| CJ_10000437 | 0.5 | 0.9 | 1.1 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | 0.2 | -0.1 |
| CJ_10000438 | -0.8 | 0.2 | -1.2 | 0 | 0.1 | -0.1 | -0.1 | -0.3 | -0.9 | -0.2 |
| CJ_10000439 | 0.1 | 0.5 | 0.8 | 0.2 | 0 | 0.2 | 0.1 | 0 | 0.2 | 0.2 |
| CJ_10000441 | 0.2 | 0.6 | 0.6 | 0.3 | -0.4 | 0.3 | 0.3 | 0 | 0.2 | 0.1 |
| CJ_10000442 | -0.5 | 0 | -0.1 | 0.1 | 0 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000444 | 0 | 0.6 | 0.7 | 0.2 | -0.3 | 0.2 | 0.3 | -0.2 | 0.1 | 0.1 |
| CJ_10000445 | -0.1 | 0 | -0.2 | 0.1 | 0 | 0.2 | -0.1 | -0.2 | 0.1 | 0.1 |
| CJ_10000446 | -2.6 | -1.2 | 0.2 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0.5 | 0 |

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| CJ_10000447 | 0.1 | 0.8 | 0.6 | 0.3 | -0.1 | 0.1 | 0.2 | -0.1 | 0 | 0 |
| CJ_10000448 | 0.7 | 0.8 | 0.6 | 0.3 | -0.1 | 0.1 | 0.1 | 0 | 0.2 | 0 |
| CJ_10000450 | -0.1 | 1.1 | 1.2 | 0.4 | -0.3 | 0.3 | 0.3 | 0 | 0.1 | 0.2 |
| CJ_10000451 | -0.3 | 0.1 | -0.1 | 0 | 0 | 0.1 | -0.2 | -0.3 | 0.1 | 0.1 |
| CJ_10000452 | 0.2 | -0.2 | -0.1 | 0.1 | 0 | 0.1 | 0.1 | 0.1 | -2.3 | -0.1 |
| CJ_10000453 | -0.4 | -0.2 | -0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 | 0 | 0 |
| CJ_10000454 | -0.5 | 0.1 | 0.3 | 0.2 | 0.1 | 0.2 | 0.1 | 0 | -0.4 | 0 |
| CJ_10000455 | -0.4 | -0.6 | 0.4 | -0.1 | -0.2 | 0.2 | -0.1 | 0 | -0.2 | 0 |
| CJ_10000456 | -1.2 | -0.3 | -0.7 | 0.1 | 0 | 0.3 | 0 | 0 | 0.2 | 0 |
| CJ_10000457 | 0 | -0.1 | 0.2 | 0.2 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| CJ_10000458 | 0.7 | 0.5 | 1.3 | 0.3 | 0 | 0.3 | 0 | -0.1 | -0.1 | 0.1 |
| CJ_10000459 | 0.1 | 0.3 | 0 | 0.1 | 0.1 | 0.2 | -0.1 | 0.1 | 0 | 0 |
| CJ_10000465 | 3.2 | 4.2 | 0.7 | -0.1 | -0.8 | 0.9 | 1.5 | -1.9 | 1.1 | -0.2 |
| CJ_10000466 | -0.4 | -0.3 | -0.1 | 0.2 | 0.1 | 0.2 | -0.1 | -0.2 | 0 | 0 |
| CJ_10000467 | 3.9 | 3 | 0.1 | -0.2 | -1.4 | 1.2 | 3.7 | 0.5 | 0.2 | -0.1 |
| CJ_10000468 | 0.4 | 0.3 | 0.3 | 0.2 | -0.2 | 0.2 | 0.3 | 0 | 0 | 0.2 |
| CJ_10000470 | -0.5 | -0.1 | 0.2 | 0.2 | -0.2 | 0.1 | 0.2 | 0 | 0.2 | 0.1 |

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| CJ_10000471 | -0.1 | 0.2 | 0.4 | 0.2 | 0 | 0.1 | 0.1 | 0 | 0 | 0 |
| CJ_10000472 | -0.8 | -0.1 | 0 | 0 | -0.3 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000473 | 1.1 | 0.4 | 0.5 | 0.4 | 0.1 | -0.4 | 0 | 0.1 | 0 | -0.1 |
| CJ_10000474 | 0.7 | -0.9 | -0.7 | 0.2 | 0.1 | -0.7 | 0 | 0.1 | 0.1 | 0 |
| CJ_10000475 | 0.2 | 0 | 0.3 | 0.2 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0.2 |
| CJ_10000476 | -0.6 | -1.4 | 0.8 | 0.1 | 0 | 0.2 | 0.4 | 0 | 0 | 0.1 |
| CJ_10000477 | 0.3 | 0.3 | 0.6 | 0.2 | 1.2 | 0.1 | 0 | 0.1 | 0 | 0 |
| CJ_10000478 | 0 | -0.7 | -0.2 | -0.1 | 0 | 0.1 | -0.2 | -0.1 | -0.3 | 0 |
| CJ_10000479 | -0.5 | -0.3 | -0.4 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0 |
| CJ_10000480 | -1.2 | -0.5 | -0.7 | 0.1 | 0.5 | 0.3 | -0.1 | 0 | 0 | 0 |
| CJ_10000481 | 0.2 | -0.4 | 0.6 | 0.1 | 0.2 | 0.1 | 0.1 | 0.1 | -0.1 | 0 |
| CJ_10000482 | 1.4 | 1.2 | 0 | 0.2 | 0 | 0.1 | 1.7 | 1.5 | 1.5 | 0 |
| CJ_10000484 | -0.1 | -0.7 | 0.1 | 0 | 0.2 | 0.3 | 0.1 | 0 | -0.2 | 0 |
| CJ_10000485 | 0.1 | -0.1 | 0.5 | 0 | 0.3 | 0.1 | 0 | 0.1 | -0.1 | 0 |
| CJ_10000486 | -0.2 | -0.3 | 0.2 | 0.2 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000487 | -0.2 | -1 | 0.5 | 0.3 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10000488 | 0.7 | -0.3 | 1.1 | 0.2 | 0 | 0.2 | 0.1 | 0 | -0.2 | 0.2 |

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| CJ_10000489 | -0.4 | -0.2 | -0.2 | 0.2 | 0 | 0.2 | 0 | -0.1 | -0.1 | 0 |
| CJ_10000490 | -0.5 | -0.4 | -4.2 | 0.1 | 0.1 | -1.3 | -1.7 | -1.1 | 0 | 0 |
| CJ_10000491 | 0.1 | -0.1 | 0.5 | 0.1 | 0 | 0.2 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000492 | -0.5 | -0.3 | 0.5 | 0 | -0.1 | 0.3 | -0.1 | -0.2 | 0 | 0.1 |
| CJ_10000494 | -0.8 | -0.3 | -0.5 | 0 | -0.2 | 0.3 | 0 | -0.1 | 0 | 0.2 |
| CJ_10000495 | -0.2 | -0.1 | 0.1 | 0.1 | 0 | 0.2 | 0 | 0 | -0.2 | 0.1 |
| CJ_10000496 | -0.1 | 0.1 | 0 | -0.1 | -0.2 | 0.3 | 0 | -0.1 | 0.3 | 0.1 |
| CJ_10000497 | -0.4 | 0 | 0.1 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.2 |
| CJ_10000498 | 0.1 | -0.1 | 0.1 | 0.1 | 0.2 | 0.1 | -0.1 | 0 | 0.1 | 0.1 |
| CJ_10000507 | -0.2 | -0.5 | -0.1 | 0.1 | -1.7 | 0.2 | -0.1 | 0 | -0.2 | 0 |
| CJ_10000508 | 0 | -1.1 | 0.4 | 0 | 0 | 0.3 | 0 | -0.1 | -0.1 | 0 |
| CJ_10000509 | -0.1 | 0 | 0.4 | 0.1 | 0.2 | 0 | 0.1 | -0.2 | -0.1 | 0 |
| CJ_10000510 | 0.2 | 0 | 0.3 | 0.2 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | 0.2 |
| CJ_10000511 | -0.5 | -0.1 | 0.3 | 0.2 | -0.2 | 0.3 | 0.2 | -0.1 | -0.2 | 0 |
| CJ_10000512 | -0.4 | -0.1 | -0.1 | 0.2 | 0 | 0.2 | 0.1 | 0.1 | -0.2 | 0.1 |
| CJ_10000513 | 0.1 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0 |
| CJ_10000514 | 0 | -0.1 | 0.2 | 0.3 | 0.1 | 0 | 0.2 | 0 | 0 | -0.1 |

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| CJ_10000515 | -2.5 | 0.2 | 0.2 | 0.2 | 0 | 0.2 | 0.1 | -0.2 | 0 | -0.1 |
| CJ_10000516 | 0.1 | 0 | 0.4 | 0.1 | 0.1 | 0.1 | -0.4 | -0.1 | -0.1 | 0 |
| CJ_10000517 | 0.2 | 0 | 0.8 | 0.3 | 0.2 | 0 | 0.2 | 0 | -0.2 | 0 |
| CJ_10000518 | 0.9 | 0.4 | 0.2 | 0.2 | -0.2 | 0.2 | 0.1 | 0 | 0 | 0 |
| CJ_10000519 | -1 | -0.1 | -0.4 | 0.2 | 0 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000520 | -0.7 | 0.1 | 0.5 | 0 | 0 | 0.3 | 0.2 | 0.2 | -0.1 | -0.1 |
| CJ_10000522 | -0.4 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | -0.1 | -0.2 | 0 | 0.1 |
| CJ_10000526 | -0.4 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | -0.1 | 0 | -0.1 |
| CJ_10000528 | -0.5 | 0 | -0.1 | 0.2 | 0.8 | 0.2 | -0.2 | 0 | -0.1 | -0.1 |
| CJ_10000534 | 2.6 | 2.9 | 1.4 | 2 | 0.6 | -0.8 | -1.4 | -1.4 | 2.9 | 4.1 |
| CJ_10000538 | -0.8 | -0.6 | 0.1 | 0.1 | 0 | 0.2 | -0.1 | -0.1 | -0.1 | -0.1 |
| CJ_10000539 | -0.5 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0.1 |
| CJ_10000540 | 2.5 | -2.2 | 2 | 0.5 | 0 | 0.6 | 0.6 | -0.1 | 0.4 | 0.5 |
| CJ_10000541 | 0.1 | -0.2 | -0.1 | 0 | -0.1 | 0 | -0.1 | 0 | 0 | 0.2 |
| CJ_10000543 | 0 | 0.2 | -0.3 | -0.4 | 1 | 0.3 | 0.1 | 1.2 | 0.2 | -0.5 |
| CJ_10000544 | -2.1 | -1 | -1.2 | 0.1 | 0 | -1 | 0.2 | -0.2 | 0 | 0 |
| CJ_10000545 | 0.3 | 0 | 0.1 | 0.1 | -0.1 | 0.2 | -0.1 | 0 | 0 | 0.2 |

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| CJ_10000546 | -0.1 | 0 | -0.3 | 0.2 | 0.2 | 0.2 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10000547 | -0.6 | -0.7 | -0.5 | 0.1 | 0.2 | 0.2 | 0.2 | -0.1 | -0.4 | 0.1 |
| CJ_10000548 | -0.4 | 0 | 0.4 | 0.2 | 0.1 | 0.2 | 0 | -0.3 | 0.2 | 0.1 |
| CJ_10000549 | -0.6 | -0.1 | -0.1 | 0.2 | -0.3 | 0.1 | -0.3 | -0.4 | 0.1 | -0.2 |
| CJ_10000550 | 0 | 0 | 0.3 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0.1 | 0 |
| CJ_10000551 | -0.6 | -0.3 | -0.1 | 0.1 | -0.1 | 0.3 | -0.1 | -0.1 | 0.3 | 0.1 |
| CJ_10000552 | 1.7 | 0 | 0.4 | 0.1 | 0.9 | 0 | -0.7 | 0.1 | 0 | -0.1 |
| CJ_10000555 | 0.2 | 1.3 | 0.2 | 0.4 | -0.6 | 0 | 0.1 | 1.1 | 1.9 | 0 |
| CJ_10000557 | -1.1 | 0.2 | -0.5 | 0.7 | -0.1 | 0.2 | -0.1 | -0.8 | 0.8 | 0.7 |
| CJ_10000564 | 0.2 | -0.3 | -0.1 | 0.1 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10000565 | 0.3 | 0 | -0.1 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0.3 | 0.1 |
| CJ_10000566 | -0.2 | 0 | 0.2 | 0.2 | 0 | 0.1 | 0.1 | -0.1 | 0 | 0.2 |
| CJ_10000567 | -0.2 | -0.2 | -0.4 | 0.1 | 0.1 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 |
| CJ_10000568 | -0.1 | -0.2 | 0.3 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000569 | 0 | 0.3 | 0.4 | -0.1 | -0.2 | 0.2 | 0 | -0.2 | 0.2 | 0.2 |
| CJ_10000570 | -0.2 | 0.1 | 0.2 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.2 |
| CJ_10000571 | -0.5 | -0.3 | 0.1 | 0 | 0 | 0 | 0 | -0.2 | -0.1 | 0 |

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| CJ_10000572 | -0.1 | 0 | 0 | 0.1 | 0 | 0.3 | 0 | 0.1 | -0.1 | 0 |
| CJ_10000573 | 0.2 | 0.2 | 0.2 | 0.1 | -0.2 | 0 | -0.3 | -0.1 | 0 | 0 |
| CJ_10000574 | -1.5 | -2.5 | -0.2 | 0 | 0 | 0.1 | -0.1 | 0 | 0 | 0.1 |
| CJ_10000575 | 0.2 | 0.2 | 0 | 0.3 | 0 | 0 | -0.2 | -0.1 | -0.1 | 0.1 |
| CJ_10000576 | 0.1 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | 0.1 | 0.2 | 0.1 | 0.1 |
| CJ_10000578 | 0.2 | 0.2 | 0.2 | 0.1 | 0.2 | 0.1 | -0.2 | 0 | -0.1 | 0.1 |
| CJ_10000579 | -0.1 | 0.1 | 0.7 | 0.2 | 0.1 | 0.2 | 0 | -0.1 | -0.1 | 0.1 |
| CJ_10000580 | 0.1 | 0.2 | 0.6 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.2 | 0.1 |
| CJ_10000581 | -0.4 | 0.3 | 0.2 | 0.1 | 0 | 0.2 | -0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10000582 | -0.4 | -0.4 | 0.3 | 0.1 | 0.4 | -0.2 | 0.2 | 0.3 | -0.9 | 0 |
| CJ_10000583 | -0.7 | -0.4 | -0.2 | 0 | 0.1 | -0.1 | 0.1 | 0.4 | -0.6 | 0 |
| CJ_10000584 | -0.1 | -0.1 | -0.8 | 0.1 | 0.1 | -0.5 | -0.5 | -0.3 | -0.2 | 0 |
| CJ_10000586 | 0.4 | -0.2 | 0.4 | 0.3 | 0.3 | -0.1 | 0 | -0.4 | -0.4 | 0 |
| CJ_10000587 | 0.9 | -0.2 | 0.2 | 0.4 | 0 | 0.3 | 0.2 | 0.1 | 0 | 0.1 |
| CJ_10000589 | 0.5 | -0.1 | -1.3 | -0.1 | -0.2 | 0.1 | -0.1 | 0.5 | -0.1 | 0 |
| CJ_10000590 | -0.6 | -0.1 | -0.5 | 0.1 | 0 | 0.1 | -0.1 | -0.1 | 0.2 | 0 |
| CJ_10000591 | -0.1 | -0.5 | -0.1 | 0.2 | -0.4 | 0.1 | 0 | -0.8 | -0.4 | 0 |

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| CJ_10000592 | -0.1 | 0 | -0.2 | 0.2 | -0.1 | 0.4 | 1.3 | 0.4 | 0.7 | 0.5 |
| CJ_10000593 | -0.1 | 0 | -0.3 | 0 | 0.1 | 0.3 | 0.1 | -0.1 | 0 | 0.1 |
| CJ_10000594 | -0.3 | -0.2 | 0.3 | 0.1 | 0 | 0.2 | 0.1 | 0 | -0.2 | 0 |
| CJ_10000595 | -1 | -0.5 | 0.2 | 0 | 0 | 0.2 | 0 | -0.3 | 0.1 | 0 |
| CJ_10000596 | -0.4 | -0.2 | 0.2 | 0.1 | 0 | 0.2 | 0.1 | 0 | 0 | 0.2 |
| CJ_10000597 | 0.3 | 0.4 | 0.7 | 0.1 | 0 | 0 | 0 | 0 | 0.1 | 0 |
| CJ_10000598 | -0.6 | -0.2 | -0.6 | 0.2 | -0.1 | 0.2 | -0.2 | -0.3 | 0.2 | 0 |
| CJ_10000599 | -0.4 | -0.1 | -0.4 | 0.1 | 0.1 | 0.2 | 0 | 0 | -0.2 | 0.2 |
| CJ_10000600 | -0.2 | -0.3 | -0.1 | 0.1 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0 |
| CJ_10000601 | -0.7 | -0.3 | -0.3 | 0 | 0 | 0.3 | 0 | -0.1 | 0.1 | 0.1 |
| CJ_10000602 | 0.1 | 0 | 0 | 0.2 | 0 | 0 | -0.1 | -0.1 | 0 | 0.1 |
| CJ_10000603 | -0.1 | 0.1 | -0.8 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.2 | 0.1 |
| CJ_10000604 | -0.3 | -0.1 | -0.2 | 0 | -0.1 | 0.2 | -0.1 | -0.1 | 0.2 | 0.1 |
| CJ_10000605 | -0.2 | 0.1 | -0.2 | 0.1 | 0 | 0.1 | -0.1 | -0.1 | 0 | 0.1 |
| CJ_10000606 | 0.1 | -0.4 | -0.3 | 0.2 | 0 | 0.1 | -1 | -0.2 | -0.4 | 0 |
| CJ_10000607 | -0.2 | -0.1 | 0.4 | 0.3 | 0.1 | 0.1 | -0.1 | 0.2 | 0 | 0 |
| CJ_10000608 | -0.4 | -0.2 | -0.2 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | -0.1 | 0.1 |

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| CJ_10000609 | -0.2 | 0 | -0.4 | 0 | -0.1 | 0 | 0 | -0.1 | 0 | 0 |
| CJ_10000610 | 0.1 | -0.3 | 0.4 | 0.2 | 0.2 | 0.1 | 0 | -0.1 | -0.2 | 0 |
| CJ_10000611 | 0.1 | -0.1 | 0.1 | 0.2 | 0.1 | 0.1 | 0 | 0.2 | -0.4 | 0 |
| CJ_10000614 | 0 | 5.2 | -0.2 | 0.2 | 0 | 0.1 | 0 | 0.2 | 0.1 | 0 |
| CJ_10000615 | -0.2 | -0.3 | 0.2 | 0 | -0.3 | 0.3 | 0 | 0.1 | -0.1 | 0.1 |
| CJ_10000616 | 0.3 | -0.3 | 0 | 0.3 | -0.3 | 0.5 | 0.4 | 0.2 | 0.4 | 0 |
| CJ_10000617 | 0 | 0.1 | 0.2 | 0.1 | 0 | 0.2 | 0.1 | 0.1 | 0 | 0.1 |
| CJ_10000618 | -0.2 | -0.2 | -0.5 | 0.2 | -0.2 | -0.1 | 0.1 | -0.2 | -0.3 | 0.1 |
| CJ_10000619 | -0.1 | 0.2 | -0.2 | 0.2 | 0.1 | 0.1 | 0.2 | -0.1 | 0.2 | 0.1 |
| CJ_10000620 | -0.1 | 0 | 0 | 0.1 | 0 | 0.3 | 0 | 0.1 | -0.2 | 0 |
| CJ_10000621 | -0.4 | -0.2 | -0.3 | 0 | -0.3 | 0.4 | 0.1 | 0.1 | 0.3 | 0.2 |
| CJ_10000622 | 0.1 | 0.2 | 0 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000625 | 3.4 | 3.8 | 0.8 | 1.2 | -1.6 | 1.3 | -0.1 | -0.9 | 1.1 | 1.4 |
| CJ_10000626 | 1.9 | 2.4 | 0.3 | 0.8 | -0.6 | 0.8 | 0.1 | -0.5 | 0.8 | 0.7 |
| CJ_10000627 | -0.4 | -0.3 | 0.2 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | 0 |
| CJ_10000628 | -0.1 | -0.2 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0 | 0 | 0.1 |
| CJ_10000629 | 0.2 | 0.4 | 0.4 | 0.1 | 0.1 | 0.2 | 0.1 | -0.2 | -0.1 | 0.1 |

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| CJ_10000630 | 0 | 0.3 | 1.2 | 0.3 | 0.4 | -0.2 | 0 | 0.3 | -0.3 | 0.2 |
| CJ_10000631 | 0.1 | 0.1 | 0.3 | 0.2 | 0.2 | -0.1 | 0.1 | 0.1 | -0.3 | -0.1 |
| CJ_10000632 | 0.5 | 0.1 | 0.1 | 0 | 0 | 0.2 | -0.3 | 0 | -0.2 | 0.1 |
| CJ_10000633 | -1.1 | -0.2 | -2.2 | 0.4 | 0.1 | 0 | -0.2 | -0.3 | 0.1 | -0.2 |
| CJ_10000634 | -0.5 | -0.3 | -0.8 | 0.1 | 0 | -0.1 | -0.2 | 0.2 | 0.1 | 0 |
| CJ_10000635 | 0.1 | -0.2 | -0.3 | 0.2 | 0.1 | 0.2 | -0.1 | 0.1 | -0.2 | 0 |
| CJ_10000637 | 0.1 | -0.4 | 0.2 | 0 | 0.1 | 0.3 | 0.3 | 0 | 0 | 0.1 |
| CJ_10000639 | -0.3 | -0.5 | -1.1 | 0 | -0.2 | -0.2 | -0.1 | 0.3 | -0.7 | 0.1 |
| CJ_10000640 | 0.1 | 0.2 | -2.2 | 0.5 | 0.1 | -0.3 | -1.2 | -2.2 | 0.1 | 0 |
| CJ_10000641 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000642 | -0.2 | 0 | 0.2 | 0.2 | 0.1 | 0.3 | 0.2 | 0 | 0 | 0.3 |
| CJ_10000643 | 0.4 | 0.3 | -0.4 | 0.3 | -0.2 | 0.5 | 0.2 | -0.2 | 0 | 0.3 |
| CJ_10000644 | -0.4 | -0.1 | -0.7 | 0.1 | 0 | 0.2 | -0.3 | 0 | -0.1 | 0 |
| CJ_10000645 | 0.2 | 0.4 | 0.2 | 0 | -0.3 | 0.2 | 0 | 0.2 | 0.3 | 0.2 |
| CJ_10000646 | 0.1 | 0.2 | -0.3 | 0.3 | -0.2 | 0.3 | 0 | -0.3 | 0 | 0.3 |
| CJ_10000647 | -0.4 | 0.5 | -0.8 | 0.2 | -0.1 | 0.2 | -0.1 | -0.3 | 0.2 | 0.2 |
| CJ_10000648 | 0.4 | 0.2 | 0.7 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |

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| CJ_10000649 | -0.4 | 0.3 | -0.1 | 0.2 | -0.2 | 0.3 | 0.1 | 0 | 0 | 0.3 |
| CJ_10000650 | -0.7 | 0.3 | 0 | 0.2 | 0.2 | 0 | -0.2 | -0.2 | 0 | 0 |
| CJ_10000651 | -0.3 | -0.3 | -0.2 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0.2 | 0 |
| CJ_10000652 | -0.4 | 0.3 | -0.2 | 0.1 | -0.2 | 0.2 | 0 | -0.2 | 0.3 | 0.1 |
| CJ_10000653 | 0 | 0.2 | 0.2 | 0.1 | 0 | 0.2 | 0.1 | -0.1 | 0.1 | 0.1 |
| CJ_10000655 | -0.1 | -0.4 | -0.7 | 0 | 0.1 | 0.3 | 0.1 | -0.2 | 0 | -0.1 |
| CJ_10000656 | -0.1 | -0.2 | -2.9 | 0.2 | 0.2 | -1.4 | -1.2 | -1.1 | -0.2 | -0.1 |
| CJ_10000657 | 0.2 | -0.2 | 0.5 | 0.1 | 0.1 | -0.3 | -1.2 | 0.4 | -2 | -0.5 |
| CJ_10000658 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | 0 | 0 | -0.6 | -0.2 | -0.2 |
| CJ_10000659 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0.2 | 0 | 0.1 | 0 | 0 |
| CJ_10000660 | 0.7 | -1.3 | -0.5 | -0.3 | -0.1 | 0 | 0.8 | 0.3 | -0.7 | -0.4 |
| CJ_10000661 | -0.2 | 0.2 | 0 | 0.2 | 0 | 0.3 | 0.6 | 0.5 | -0.1 | 0 |
| CJ_10000662 | 1 | 0.8 | 0.2 | 0.3 | -0.2 | 0.1 | 0.1 | -0.3 | 0.1 | 0.2 |
| CJ_10000663 | -0.3 | 0.5 | 0 | 0.1 | -0.3 | 0 | 0.2 | 0.2 | 0 | 0 |
| CJ_10000664 | 0.1 | 0.4 | 0.4 | 0.3 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000665 | -0.2 | -0.3 | 0 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000666 | 0.1 | -0.1 | 0.5 | 0.3 | 0 | 0.2 | 0.2 | 0 | -0.1 | 0.1 |

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| CJ_10000667 | -0.4 | -0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0.2 |
| CJ_10000668 | -1.1 | -0.5 | 0.4 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| CJ_10000669 | -0.1 | -0.1 | 0.3 | 0.1 | -0.1 | 0.3 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10000670 | -0.4 | -0.2 | -0.2 | 0.2 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0.1 |
| CJ_10000671 | -2.3 | -1.3 | -0.8 | 0.1 | -0.2 | 0.3 | -0.1 | 0.1 | 0.3 | 0 |
| CJ_10000672 | -0.8 | -0.1 | -0.7 | 0.1 | -0.1 | 0.2 | -0.1 | 0 | 0.3 | 0.1 |
| CJ_10000673 | -0.1 | 0 | 0 | 0.1 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0.2 |
| CJ_10000675 | -0.2 | 0.3 | -0.2 | 0.1 | -0.2 | 0.5 | 0 | -0.1 | 0.1 | 0.2 |
| CJ_10000676 | 0 | 0 | 0.4 | 0 | 0.2 | 0.1 | 0.1 | 0.2 | -0.1 | 0 |
| CJ_10000677 | 0.2 | 0 | 0.5 | 0.2 | 0.2 | 0 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000678 | -0.5 | -0.5 | -0.1 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0 |
| CJ_10000679 | -0.5 | -0.6 | 0.1 | 0.1 | 0.2 | 0.2 | 0.1 | 0.4 | -0.1 | 0 |
| CJ_10000680 | -1.1 | -0.4 | 0.3 | 0.1 | 0.2 | 0.1 | 0.2 | 0.2 | -0.3 | -0.1 |
| CJ_10000681 | 0 | -0.1 | 0.4 | 0 | 0 | 0.1 | 0.1 | 0.1 | -0.3 | 0 |
| CJ_10000682 | 0.3 | -0.5 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | 0.2 | -0.1 | 0 |
| CJ_10000683 | -0.5 | 0 | -0.2 | 0.1 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000684 | -0.2 | -0.1 | -0.2 | 0 | -0.2 | 0.2 | 0 | 0.1 | 0 | 0 |

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| CJ_10000685 | -0.1 | 0.1 | -0.1 | 0 | -0.1 | 0.2 | -0.1 | 0.1 | -0.1 | 0 |
| CJ_10000686 | -0.7 | -0.4 | 0.2 | 0 | 0 | 0.2 | 0.1 | 0.1 | -0.1 | 0.1 |
| CJ_10000687 | 0.2 | -0.1 | 0.3 | 0.1 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000688 | -0.3 | -0.3 | -0.1 | 0 | -0.1 | 0.2 | -0.1 | 0 | 0 | 0.1 |
| CJ_10000689 | 0.3 | 0 | 0 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 | 0 |
| CJ_10000690 | 1.9 | 1.1 | 1.3 | 0.4 | -0.4 | 0.3 | 0.3 | -0.2 | 0.2 | 0.4 |
| CJ_10000691 | 0.9 | 0.5 | 0.1 | 0.2 | 0 | -0.1 | 0.1 | -0.3 | 0.1 | 0.2 |
| CJ_10000692 | -0.8 | -0.9 | 0.2 | 0.1 | 0.1 | 0.1 | -0.1 | 0.2 | -0.3 | -0.1 |
| CJ_10000693 | 0.3 | 0.1 | 0.5 | 0.3 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000694 | 0.3 | 0.4 | 0.1 | 0.3 | 0.1 | 0.2 | 0.1 | -0.1 | 0.2 | 0.1 |
| CJ_10000695 | 0.1 | 0.1 | 0.3 | 0.2 | 0 | 0 | -0.2 | 0.1 | 0.1 | 0 |
| CJ_10000696 | 0.3 | 0.3 | 0.6 | 0.2 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0 |
| CJ_10000697 | -0.3 | 0 | -0.2 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000698 | 0 | -0.6 | 0.3 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0 | 0 |
| CJ_10000699 | 1.1 | 1.2 | 0.2 | 0.3 | -0.7 | 0.5 | 0.4 | -0.7 | 0.6 | 0.5 |
| CJ_10000700 | -0.4 | 0.1 | -0.1 | 0.2 | -0.1 | 0.4 | 0.2 | -0.2 | 0.2 | 0.4 |
| CJ_10000701 | -1.2 | -0.5 | -0.4 | 0.1 | -0.1 | 0.2 | -0.1 | 0.1 | -0.2 | 0.1 |

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| CJ_10000702 | 0 | 0 | 0.5 | 0.3 | 0.1 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| CJ_10000703 | -0.4 | 0.1 | 0.4 | 0.1 | 0.2 | 0.2 | 0 | 0 | -0.1 | 0 |
| CJ_10000704 | -1.4 | -0.4 | -0.3 | 0.2 | -0.1 | 0.1 | 0 | 0 | 0 | 0 |
| CJ_10000705 | -1.4 | -0.4 | -0.1 | -0.1 | 0 | 0.1 | 0 | 0 | -0.1 | 0 |
| CJ_10000706 | -1.6 | 0 | -0.6 | 0.2 | 0.1 | -0.1 | -0.1 | 0 | 0 | 0.1 |
| CJ_10000708 | 0.3 | -0.2 | 0 | 0.2 | 0.3 | 0.2 | 0.2 | -0.2 | -0.1 | -0.1 |
| CJ_10000709 | -0.9 | -0.1 | -0.4 | 0.3 | 0.2 | 0 | -0.2 | 0 | -0.1 | -0.1 |
| CJ_10000710 | -0.4 | -0.2 | -0.2 | 0.2 | 0 | 0.2 | -0.2 | -0.2 | 0 | 0.2 |
| CJ_10000711 | -0.4 | 0 | -0.1 | 0.2 | -0.2 | 0.2 | 0 | -0.1 | 0 | 0.2 |
| CJ_10000712 | -0.1 | 0.1 | -0.8 | 0.1 | -0.1 | -0.1 | -0.2 | -0.5 | 0.1 | 0.1 |
| CJ_10000713 | -1.6 | -0.4 | -4.2 | 0.1 | -0.1 | -1 | 0 | 0.1 | 0.4 | 0.1 |
| CJ_10000714 | -0.8 | -0.1 | -0.5 | 0.1 | -0.2 | 0.4 | 0 | 0 | 0.1 | 0.3 |
| CJ_10000715 | -0.3 | 0 | -2.9 | 0.1 | -0.2 | -1 | 0.1 | -0.2 | 0.1 | 0.2 |
| CJ_10000716 | -0.4 | -0.4 | 0.5 | 0.3 | -0.2 | 0.2 | 0.2 | 0 | 0 | 0 |
| CJ_10000717 | -0.5 | 0 | 0 | 0.1 | 0.1 | 0 | 0 | 0.1 | 0 | 0 |
| CJ_10000718 | -0.1 | 0.5 | 0.3 | 0.1 | -0.1 | 0.2 | 0.2 | -0.1 | 0.2 | 0.2 |
| CJ_10000719 | 0.1 | -0.8 | 0.9 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | -0.1 |

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| CJ_10000720 | -0.1 | 0.2 | 0 | 0 | -0.1 | 0.3 | -0.1 | -0.1 | -0.1 | 0.2 |
| CJ_10000721 | 0.4 | 0.5 | 0.7 | 0.3 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | 0.1 |
| CJ_10000722 | -0.2 | 0.5 | 0.3 | 0.1 | -0.2 | 0.2 | -0.1 | 0 | 0.5 | 0.1 |
| CJ_10000723 | 0.3 | -2 | 0.5 | 0 | 0 | 0.1 | 0 | 0 | -0.1 | 0.1 |
| CJ_10000724 | 0.1 | -0.1 | 0.7 | 0.1 | 0.3 | 0.1 | -0.1 | 0.1 | -0.2 | 0 |
| CJ_10000725 | 1.7 | 2 | 2.3 | 0.2 | -0.5 | 0.5 | 1.1 | -0.5 | 0.7 | 0.6 |
| CJ_10000726 | -0.1 | -0.1 | -0.3 | 0.1 | -0.1 | 0.2 | 0 | 0.1 | -0.2 | 0 |
| CJ_10000727 | 0.8 | 0.2 | -1.8 | 0.2 | 0 | -2.9 | -0.4 | -0.2 | -0.2 | 0.2 |
| CJ_10000729 | -0.5 | -0.3 | -0.3 | -0.1 | 0.1 | 0.1 | -0.1 | 0.1 | -0.2 | -0.1 |
| CJ_10000730 | -0.8 | -0.3 | 0 | 0.2 | 0.3 | 0.1 | -0.1 | 0.1 | -0.2 | 0 |
| CJ_10000731 | 0.4 | 0.4 | 0.6 | 0.4 | -0.3 | 0.2 | 0.2 | 0.1 | 0 | 0.1 |
| CJ_10000732 | -0.1 | 0.2 | -0.1 | 0.2 | 0 | -0.2 | -0.9 | -0.7 | 0.1 | 0 |
| CJ_10000733 | -0.9 | 0.1 | -0.2 | 0.1 | 0 | 0.3 | 0 | -0.2 | -0.1 | 0.1 |
| CJ_10000734 | -1 | -1 | -0.1 | 0 | -0.1 | 0.2 | 0.1 | 0.1 | -0.1 | 0 |
| CJ_10000735 | -0.2 | 0.1 | 0.6 | 0.3 | 0.1 | 0.2 | 0.1 | 0.1 | -0.1 | 0.1 |
| CJ_10000736 | -0.1 | -0.2 | 0.1 | 0.3 | 0.1 | 0.2 | 0 | 0 | -0.1 | 0 |
| CJ_10000737 | 0.2 | -0.2 | 0.7 | 0.2 | 0 | 0.1 | 0.2 | 0.1 | 0.8 | 0.1 |

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| CJ_10000738 | 0.1 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.1 | 0.1 | 0 | 0.1 |
| CJ_10000739 | -0.6 | -0.1 | 0 | 0.1 | 0 | 0.3 | 0.2 | -0.1 | 0 | 0.2 |
| CJ_10000740 | -0.3 | 0.1 | 0.8 | 0.1 | -0.1 | 0.3 | 0.2 | 0 | 0 | 0.1 |
| CJ_10000741 | -0.1 | 0.6 | 0.2 | 0.1 | -0.2 | 0 | 0.2 | -0.1 | 0.2 | 0.2 |
| CJ_10000742 | -0.8 | 0.3 | 0.4 | 0 | 0 | -0.5 | -0.8 | -0.9 | 0 | 0.2 |
| CJ_10000743 | -0.3 | 0.2 | 0.1 | 0 | 0.1 | 0 | -0.3 | -0.2 | -0.3 | 0 |
| CJ_10000744 | 0.4 | 0.8 | 0.5 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| CJ_10000745 | -0.1 | -0.1 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | -0.3 | 0.1 |
| CJ_10000746 | 0 | -0.1 | 0.2 | 0.1 | 0 | 0.1 | -0.1 | -0.1 | 0 | 0 |
| CJ_10000747 | -0.2 | -0.1 | -0.3 | 0.1 | -0.1 | 0.2 | -0.2 | -0.2 | 0.1 | 0.1 |
| CJ_10000748 | 0.2 | 0.4 | 0 | 0.2 | -0.1 | 0.3 | 0.1 | -0.1 | 0.1 | 0.2 |
| CJ_10000749 | 0 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | -0.2 | -0.1 | -0.2 | 0.1 |
| CJ_10000750 | -0.6 | -0.2 | -0.3 | 0 | 0 | 0.1 | 0 | 0.2 | -0.1 | 0 |
| CJ_10000751 | -0.2 | -0.2 | -0.2 | 0.1 | 0 | 0.2 | 0 | 0.1 | 0 | 0.1 |
| CJ_10000753 | 2.1 | 1.4 | 0 | -0.1 | -0.1 | 1.1 | 0.3 | -1.4 | 1.1 | -0.4 |
| CJ_10000757 | 0.4 | 0.6 | -0.4 | 0.2 | -0.4 | 0.3 | -0.1 | -0.1 | 0.2 | 0.3 |
| CJ_10000758 | -1 | -0.8 | 0.3 | 0.2 | 0 | 0.2 | 0.1 | 0.1 | -0.1 | 0.1 |

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| CJ_10000759 | -0.1 | 0 | 0.1 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10000760 | 0 | 0.1 | 0.2 | 0.2 | -0.1 | 0.3 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10000765 | -0.8 | -0.1 | 0.1 | 0.4 | 0.3 | 0.5 | -0.1 | 0.1 | 0.1 | 0.2 |
| CJ_10000786 | -0.1 | -5.2 | -0.4 | 0.3 | 1 | -0.2 | -0.5 | 0.4 | -0.3 | 0.1 |
| CJ_10000790 | 0 | 0.2 | 0.1 | 0.3 | 0.1 | 0 | -0.5 | -0.1 | -0.2 | 0.2 |
| CJ_10000791 | 0.6 | -0.4 | 0.4 | 0.2 | 0.1 | 0.1 | -0.3 | 0.2 | 0 | 0 |
| CJ_10000794 | -0.2 | 0.6 | 0.8 | 0.4 | -0.1 | 0.3 | 0.3 | 0 | -0.1 | 0.2 |
| CJ_10000806 | -0.1 | -0.1 | 0 | 0.1 | -0.1 | 0.4 | 0.1 | 0.1 | 0.2 | 0 |
| CJ_10000816 | -0.7 | 1.3 | 1.5 | 0.5 | -0.1 | 0.1 | 0.1 | 0.8 | 0 | 0.4 |
| CJ_10000819 | 1.5 | 1 | 2 | 0.5 | 0 | 0.3 | 0 | 1.1 | -0.2 | 0.1 |
| CJ_10000822 | 0.3 | 0.3 | 0 | 0.2 | 0 | 0.3 | -0.1 | 0 | 0 | 0.1 |
| CJ_10000825 | 2.8 | 2.5 | 1.6 | 0.8 | -0.8 | 0.1 | 0.7 | -0.7 | 0.6 | 0.8 |
| CJ_10000826 | 3 | 2.7 | 0.8 | 0.1 | -1.5 | -0.2 | 0.5 | 0.6 | 0.9 | 0 |
| CJ_10000828 | -0.1 | 1.2 | 1.1 | 0.1 | 0.2 | 0.1 | 0 | 0.7 | 0.2 | -0.1 |
| CJ_10000842 | 0 | -0.4 | 0 | 0.2 | 0.3 | 0.2 | -0.2 | 0 | -0.2 | 0.1 |
| CJ_10000846 | 1.2 | 0.7 | 1.6 | 1 | 0.5 | 0.7 | 0.1 | 0.4 | 1.2 | -0.1 |
| CJ_10000847 | 2.8 | 0.3 | -0.9 | 0.1 | 0 | -1.1 | -0.3 | 1.5 | 1.8 | -1.5 |

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| CJ_10000875 | 3.3 | 4 | 2.9 | 0.9 | -1.5 | 1.1 | 1.3 | -0.9 | 1 | 1.4 |
| CJ_10000880 | 1.4 | 1.3 | 3.4 | 1.6 | -3 | 2.8 | 1.5 | 0.5 | 2.2 | 0.9 |
| CJ_10000885 | -0.7 | 0.1 | 0 | 0.3 | -0.2 | -0.1 | -0.5 | -0.8 | 0.7 | 0.5 |
| CJ_10000897 | -0.6 | 0.9 | 2.6 | 0.5 | -1 | 0.1 | 0.3 | 0.2 | 1.5 | 1 |
| CJ_10000914 | 0.1 | 0.1 | -0.8 | 0.2 | 0.2 | -0.2 | -0.3 | 0.3 | 0.1 | 0.1 |
| CJ_10000933 | 0 | -1.8 | 1.4 | 0.3 | -0.3 | 0.2 | 0 | 0 | 0.5 | 0.3 |
| CJ_10000937 | 0.5 | 1.1 | 0.9 | 0.4 | -0.3 | 0.2 | 0 | -0.5 | 0.3 | 0.4 |
| CJ_10000938 | 0.3 | 0.2 | 0.2 | 0.2 | -1.5 | 0.3 | 0 | -0.1 | -0.1 | 0.1 |
| CJ_10000960 | -0.1 | 0.2 | -0.1 | 0.1 | -0.2 | 0.4 | 0.1 | 0 | 0.1 | 0.2 |
| CJ_10000970 | -2.5 | -0.6 | -1.1 | 0.2 | 0.1 | -0.2 | -0.6 | 0.2 | 0.2 | 0.2 |
| CJ_10000981 | 0.5 | 0.2 | 0.6 | 0.4 | 0.1 | 0.2 | 0 | 0 | 0 | 0 |
| CJ_10000982 | 0.3 | 0 | -0.2 | 0.1 | 0.1 | -0.1 | -0.3 | -0.3 | 0 | 0 |
| CJ_10000983 | 1.5 | -0.1 | 1.1 | 0.5 | 0 | 0.2 | 0.7 | 0.2 | 0.3 | 0.3 |
| CJ_10000991 | -0.3 | -0.2 | 0.3 | 0.4 | 0.3 | 0.2 | 0 | 0.6 | 0 | -0.1 |
| CJ_10000992 | -0.2 | 0.3 | 0.3 | 0.2 | 0.2 | 0 | 0.1 | 0 | -0.2 | -0.1 |
| CJ_10000995 | 0.6 | 0.3 | 0.7 | 0.1 | 0.2 | -0.1 | 0.3 | 0.1 | -0.2 | -0.2 |
| CJ_10000996 | 0.3 | 0.2 | 0.4 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | -0.1 | -0.1 |

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| CJ_10000997 | 0.3 | 0.5 | 0.2 | 0.3 | 0 | 0.1 | -0.1 | 0.3 | 0 | 0.2 |
| CJ_10001000 | -0.1 | -0.1 | -0.1 | 0.2 | 0 | 0.1 | 0 | -0.1 | 0.2 | 0.1 |
| CJ_10001006 | -0.2 | 0.3 | -0.3 | 0.3 | 0.1 | 0.1 | -0.1 | -0.4 | -0.1 | 0.1 |
| CJ_10001008 | 0.4 | 0.3 | 0.5 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001009 | 1.1 | 1.4 | 1.7 | 0.4 | -0.3 | 0.4 | 0.3 | 0.5 | 0.3 | 0.6 |
| CJ_10001011 | 0.4 | 0.7 | 0.3 | 0.4 | 0 | 0.2 | -0.2 | 0 | 0.1 | 0.3 |
| CJ_10001014 | 0.2 | 0.5 | 0.8 | 0.2 | 0.1 | 0.2 | 0.1 | 0.5 | 0 | 0.1 |
| CJ_10001017 | -1.2 | -0.7 | 0.4 | 0.2 | 0.3 | 0.2 | -0.1 | 0.4 | -0.3 | 0 |
| CJ_10001018 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0.2 | 0 | 0.1 | -0.1 | 0.1 |
| CJ_10001019 | -0.2 | -0.4 | -0.8 | 0.2 | -0.1 | 0.1 | 0 | 0.6 | 0 | 0.3 |
| CJ_10001029 | -0.7 | 0 | 0.6 | 0.3 | 0 | 0.2 | 0.1 | 0.3 | 0.1 | 0 |
| CJ_10001030 | 0.5 | 0.5 | 0.2 | 0 | 0 | 0 | 0 | 0 | -0.1 | 0 |
| CJ_10001032 | 0 | -0.1 | 0.1 | 0.2 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | 0.2 |
| CJ_10001033 | 0.1 | -0.4 | 0.4 | 0.1 | 0 | 0.2 | 0 | -0.1 | 0 | 0 |
| CJ_10001045 | -0.6 | -0.5 | 0 | 0.2 | 0.2 | 0.1 | -0.2 | 0.6 | -0.1 | 0.1 |
| CJ_10001047 | -1.3 | -0.3 | 0.1 | 0.1 | 0.1 | 0.3 | 0 | 0.1 | -0.3 | 0.1 |
| CJ_10001055 | -0.4 | -0.1 | -0.2 | 0.2 | -0.1 | 0.4 | -0.1 | -0.2 | 0.2 | 0.1 |

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| CJ_10001061 | -0.7 | -0.1 | -0.5 | 0.3 | 0.1 | 0.3 | 0 | 0.1 | 0.1 | -0.1 |
| CJ_10001062 | 1.7 | 1.2 | 1.1 | 0.6 | 0 | 0.4 | 0.4 | 0 | 0 | 0.2 |
| CJ_10001066 | 3.9 | 0.9 | 0.8 | 0 | -0.1 | 0.4 | 0.6 | 0.6 | 0.1 | -0.1 |
| CJ_10001074 | 0.5 | 0.5 | 0.1 | 0.2 | 0.2 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| CJ_10001075 | 0.2 | 0.2 | 0.8 | 0.2 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | 0 |
| CJ_10001082 | -0.1 | 0.5 | 0.7 | 0.5 | 0 | 0.1 | -0.1 | 0.3 | 0.3 | 0.1 |
| CJ_10001101 | -0.2 | 0.4 | 0 | 0.3 | -0.1 | 0.3 | 0.1 | -0.1 | 0.1 | 0.1 |
| CJ_10001104 | 2.4 | 1.6 | 1.3 | 0.2 | -0.3 | 0.9 | 1.3 | 1 | 0.7 | 0.9 |
| CJ_10001107 | 2.7 | 2.4 | 1.7 | 1 | -1.3 | 1 | 0.9 | -0.8 | 0.8 | 1 |
| CJ_10001109 | 0.2 | 0 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.2 | -0.1 |
| CJ_10001112 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 | 0.2 | -0.1 | -0.2 |
| CJ_10001122 | 2.1 | 1.4 | 0.8 | 0.3 | -0.4 | -0.7 | 0 | 0.3 | 0.2 | 0.2 |
| CJ_10001128 | -0.5 | -0.2 | -0.9 | 0.1 | 0 | 0 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001136 | -0.9 | -0.1 | 0.3 | 0.1 | 0 | 0.1 | 0.4 | 0.1 | 0.1 | -0.1 |
| CJ_10001141 | -0.4 | -0.5 | -0.2 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.1 | 0.1 |
| CJ_10001142 | 0.5 | 0.4 | 0.7 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.1 |
| CJ_10001144 | 0 | -0.1 | 0.5 | 0 | 0.2 | 0.1 | 0.1 | -0.1 | -0.2 | 0.1 |

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| CJ_10001145 | -0.1 | 0.1 | 0.2 | 0.1 | 0.2 | 0.2 | 0 | -0.1 | 0 | 0 |
| CJ_10001146 | -0.2 | 0.1 | 0 | -0.1 | -0.1 | 0.1 | -0.2 | 0 | 0.4 | -0.1 |
| CJ_10001148 | 0.2 | 0.3 | 0.4 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 | -0.2 | -0.1 |
| CJ_10001149 | 0.5 | 0.4 | 0.6 | 0.2 | 0.1 | 0 | 0.1 | -0.2 | 1.5 | 0 |
| CJ_10001150 | 0.1 | 0.1 | 0.4 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0 |
| CJ_10001151 | 0.2 | 0.2 | 0.5 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 | 0 |
| CJ_10001152 | 1.5 | 1.8 | 0 | 0.2 | -0.8 | 0.3 | 0.2 | -0.2 | 0.5 | 0.2 |
| CJ_10001153 | -0.5 | 0.1 | -0.4 | 0.1 | 0 | 0.1 | 0 | 0 | 0.1 | 0 |
| CJ_10001154 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | 0 | -0.1 | 0 | -0.1 |
| CJ_10001155 | 1.9 | 2.1 | 1.2 | 0.3 | -0.7 | 0.3 | 0.4 | -0.3 | 0.6 | 0.2 |
| CJ_10001157 | -0.3 | 0.2 | -0.1 | 0 | -0.1 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001158 | 0.6 | 0.9 | -2 | 0.1 | -0.4 | -1.8 | -2.9 | -0.4 | -0.5 | 0 |
| CJ_10001161 | -0.2 | 0.2 | 0 | 0.1 | 0 | 0.3 | -0.1 | -0.3 | 0 | 0 |
| CJ_10001162 | 0.3 | 0 | 0.4 | 0 | -0.1 | 0.2 | 0 | 0 | 0 | 0.1 |
| CJ_10001164 | -0.3 | 0 | -0.2 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0.2 | 0.1 |
| CJ_10001166 | -0.2 | 0.1 | -0.4 | 0.1 | 0 | 0.1 | -0.3 | -0.4 | 0 | 0 |
| CJ_10001168 | -0.4 | -0.6 | -0.5 | -0.1 | 0.1 | 0.2 | -0.1 | 0 | 0.2 | 0.2 |

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| CJ_10001169 | -0.3 | 0.6 | -0.1 | 0.1 | -0.2 | 0.3 | 0 | -0.2 | 0.3 | 0.1 |
| CJ_10001170 | -0.4 | -0.7 | 0.4 | 0.2 | -0.2 | 0.5 | -0.1 | -0.1 | 0.7 | 0.3 |
| CJ_10001171 | -0.5 | 0.5 | 0.3 | 0 | 0 | -0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10001172 | 0.1 | -0.2 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0 | -0.1 | 0.1 |
| CJ_10001173 | -0.3 | -0.3 | -0.2 | 0 | 0.1 | -0.2 | -0.2 | -0.2 | 1.7 | 0 |
| CJ_10001174 | 0.2 | 0.2 | 0.7 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001175 | 0 | 0.2 | 0.4 | 0.1 | 0 | 0.2 | 0 | 0 | 0 | 0 |
| CJ_10001176 | 0.4 | 0 | -0.2 | 0.1 | 0.1 | -1.4 | 1.4 | 1.5 | 0.8 | 0 |
| CJ_10001177 | 0 | 0.1 | 0.2 | 0.1 | -0.2 | 0.2 | 0.1 | 0 | 0 | 0 |
| CJ_10001178 | 0.3 | -0.1 | 0.5 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0.1 | 0 |
| CJ_10001179 | -0.5 | 0 | -0.7 | 0.1 | 0 | 0.1 | -0.1 | 0.1 | -0.1 | 0 |
| CJ_10001180 | -0.1 | -0.1 | -0.4 | 0.1 | 0 | 0.1 | 0 | 0 | -0.1 | 0 |
| CJ_10001181 | -0.2 | 0.2 | -0.1 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001182 | -0.3 | 0.4 | 0.6 | 0.1 | -0.2 | 0.2 | 0.1 | 0 | 0.1 | 0 |
| CJ_10001183 | 0 | -0.2 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0 | 0.1 |
| CJ_10001186 | 0 | 0 | 0.1 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0 | 0 |
| CJ_10001188 | -0.7 | -0.9 | -0.1 | 0 | -0.1 | 0.2 | 0 | 0 | 0.2 | 0.1 |

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| CJ_10001189 | 0.3 | 0.1 | 0.1 | -0.1 | -0.2 | 0.2 | 0.1 | -0.1 | 0 | 0.2 |
| CJ_10001191 | -0.1 | 0.2 | -1.2 | 0 | -0.1 | 0.2 | 0 | -0.2 | 0 | -0.1 |
| CJ_10001192 | -1.5 | -0.2 | 0.5 | 0 | 0 | 0.3 | 0 | 0.1 | 0 | 0.1 |
| CJ_10001193 | -0.7 | -0.3 | 0.4 | 0.1 | 0 | 0.3 | 0 | 0 | 0 | 0 |
| CJ_10001195 | -0.5 | -0.1 | 0.1 | -0.1 | -0.1 | 0.2 | -0.2 | -0.1 | 0.2 | 0 |
| CJ_10001196 | -0.5 | 0.4 | -0.5 | 0.3 | -0.2 | -0.5 | 0.2 | -0.2 | 0.3 | 0.2 |
| CJ_10001198 | -0.9 | 2.8 | 0.3 | 0.8 | -1.1 | 0.1 | 0 | -1.7 | -0.2 | 0.8 |
| CJ_10001199 | 0 | -0.2 | 0.5 | 0.3 | 0.2 | 0.2 | -0.1 | 0.2 | 0 | 0.2 |
| CJ_10001201 | -0.7 | -0.2 | 0 | 0.1 | -0.5 | 0.3 | 0 | 0.1 | 0.2 | 0.1 |
| CJ_10001206 | 0.1 | 0.2 | 0 | 0.1 | -0.1 | -0.1 | -0.1 | 0.2 | 0.1 | -0.1 |
| CJ_10001207 | -0.7 | 0.4 | -0.8 | 0 | -0.3 | 0.2 | 0 | -0.3 | 0.2 | 0.1 |
| CJ_10001208 | 2.9 | 2.6 | 1.5 | 0.8 | -0.8 | 0.8 | 1 | -0.6 | 0.6 | 0.9 |
| CJ_10001210 | 0.3 | 0.2 | 0.4 | 0.1 | -0.2 | 0.2 | 0 | -0.2 | 0.1 | 0.1 |
| CJ_10001211 | -0.4 | 1.1 | 3.6 | 0.3 | -0.7 | 0.5 | 1.1 | 0.5 | 0 | 0.4 |
| CJ_10001213 | 0.2 | 0.5 | 0.4 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10001214 | -0.4 | 0.1 | 0.3 | 0.1 | 0 | 0.3 | 0.1 | -0.2 | 0 | 0 |
| CJ_10001216 | 0.2 | 0 | 0.3 | 0.1 | 0.3 | 0.1 | 0.1 | 0 | -0.1 | 0.1 |

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| CJ_10001217 | 0.4 | 0.4 | 0.5 | 0.2 | 0.3 | 0 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001218 | -0.3 | 0.2 | 0.4 | 0 | 0 | 0.2 | 0 | 0 | 1.3 | 0 |
| CJ_10001220 | -0.7 | -0.3 | 0.1 | 0.2 | 0.2 | 0.4 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001222 | 0.3 | 0 | 0.6 | 0 | 0 | 0.2 | -0.1 | -0.2 | 0 | 0 |
| CJ_10001223 | -0.5 | -0.5 | 0.1 | -0.1 | 0 | 0.2 | 0.2 | -0.1 | 0.1 | 0.1 |
| CJ_10001224 | 0 | -0.3 | 0.1 | 0.2 | 0 | 0.1 | 0.1 | 0 | 0.2 | 0.1 |
| CJ_10001225 | -0.4 | -0.2 | -0.3 | 0.4 | 0.3 | 0.1 | 0 | 0.1 | 0 | 0.1 |
| CJ_10001226 | 0 | 1 | 0.2 | 0.3 | -0.6 | 0.2 | 0.1 | -0.5 | 0.4 | 0.3 |
| CJ_10001227 | 0 | -0.2 | -1.7 | 0.2 | -0.1 | 0 | 0.1 | -0.1 | 0.1 | 0 |
| CJ_10001228 | 0.1 | 0.1 | 0.3 | 0.1 | -0.1 | 0.2 | 0 | 0.1 | 0 | 0 |
| CJ_10001229 | 1.6 | 1.4 | 0.6 | 0.3 | -0.8 | 0.4 | -0.2 | -0.7 | 0.2 | 0.3 |
| CJ_10001230 | 1.1 | 0.6 | 0 | 0 | -0.3 | 0.2 | 0.1 | 0 | 0.3 | 0.1 |
| CJ_10001231 | -0.2 | 0.1 | -0.1 | 0.1 | -0.1 | -0.1 | 0 | 0 | 0.1 | 0 |
| CJ_10001232 | 0.4 | 0.3 | 0.3 | 0.1 | 0 | 0.1 | 0.2 | -0.1 | 0 | 0.1 |
| CJ_10001233 | 1.3 | 1.3 | 0.2 | 0.2 | -0.5 | 0.3 | 0.3 | -0.3 | 0.3 | 0.1 |
| CJ_10001234 | 0 | -0.3 | 0.8 | 0.3 | 0.1 | 0.1 | -0.1 | 0.7 | 0 | 0.1 |
| CJ_10001235 | 0 | 0.1 | -0.3 | 0.1 | 0 | 0 | -0.1 | -0.1 | 0.1 | 0 |

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| CJ_10001236 | 0.5 | 0.5 | -1.2 | 0 | -0.3 | -0.2 | 0.2 | 0 | 0.1 | 0 |
| CJ_10001239 | -0.3 | -0.2 | 0.4 | 0 | 0 | 0.2 | 0.1 | -0.3 | 0.2 | 0.1 |
| CJ_10001241 | 0.1 | 0.9 | 0.1 | 0.3 | 0 | -0.1 | -0.1 | -0.3 | -0.4 | 0.1 |
| CJ_10001243 | 3.1 | 2.9 | 3.1 | 1 | 0.2 | 1.5 | 0.8 | -0.7 | 1.1 | 1.1 |
| CJ_10001244 | -2.4 | 0 | -0.9 | 0 | 0 | -0.8 | -0.2 | -0.1 | 0 | 0.1 |
| CJ_10001246 | -0.1 | -0.2 | 0.4 | 0 | -0.9 | 0 | -0.1 | 0.1 | -0.2 | 0 |
| CJ_10001249 | -0.5 | -0.1 | -0.5 | 0 | -0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| CJ_10001250 | -0.1 | 0 | -0.2 | 0 | -0.1 | 0.1 | 0 | 0.1 | -0.2 | -0.1 |
| CJ_10001251 | -1.4 | 0.2 | -0.9 | 0.1 | -0.1 | 0.1 | -0.2 | -0.1 | 0 | 0 |
| CJ_10001252 | -0.3 | 0.3 | -0.5 | 0.1 | -0.1 | 0.1 | -0.1 | -0.2 | 0.1 | 0.1 |
| CJ_10001254 | -0.1 | 0.2 | -1.4 | -1.1 | 0 | -0.6 | 0 | 1.2 | 0 | -1.4 |
| CJ_10001256 | 0.3 | 0.3 | 0.4 | 0 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0 |
| CJ_10001257 | -0.8 | 0 | -0.8 | -0.2 | -0.1 | 0.2 | 0 | -0.1 | 0.4 | -0.1 |
| CJ_10001258 | 0.8 | 0.6 | -0.2 | -0.2 | 0.4 | -0.3 | -0.5 | 0.7 | -0.1 | -0.5 |
| CJ_10001259 | -0.2 | -0.1 | -0.8 | -0.1 | 0 | 0.2 | -0.1 | 0 | 0.1 | 0 |
| CJ_10001260 | 0 | 0.1 | 0.5 | 0 | -0.2 | 0.4 | 0.1 | -0.1 | 0 | 0.2 |
| CJ_10001265 | -0.6 | -0.1 | -1.2 | -0.4 | 0 | 0 | -0.5 | 0 | 0.4 | -0.2 |

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| CJ_10001266 | -0.5 | -0.2 | -0.2 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 | 0.2 | 0.1 |
| CJ_10001268 | 0.3 | -0.3 | 0.8 | 0.1 | 0.2 | 0.1 | 0.1 | -0.1 | 0 | -0.1 |
| CJ_10001269 | 0.9 | 0.7 | 0.3 | 0.4 | -0.1 | 0.2 | 0.1 | -0.5 | 0.2 | 0.2 |
| CJ_10001271 | 0.9 | 0.1 | 0.4 | -0.1 | -0.1 | 0.1 | 0 | 0.3 | 0 | 0 |
| CJ_10001272 | 0.2 | 0 | -0.1 | 0.1 | -0.2 | 0.3 | 0.2 | -0.2 | 0 | 0.2 |
| CJ_10001273 | 0 | 0.1 | 0.2 | 0 | -0.1 | 0.2 | 0.2 | 0 | -0.2 | 0.1 |
| CJ_10001274 | 0.1 | 0.3 | -5.1 | 0.1 | -0.2 | -1.7 | 0.1 | -0.1 | 0.2 | 0 |
| CJ_10001275 | -0.1 | 0 | -0.4 | 0.1 | 0 | 0.1 | -0.1 | -0.2 | 0 | 0.1 |
| CJ_10001279 | 2.5 | 2.2 | 0.9 | 0.7 | -1 | 0.7 | 0.9 | -0.6 | 1 | 0.8 |
| CJ_10001280 | 0.1 | 0.3 | -4.1 | 0.1 | -0.1 | -0.9 | -1.7 | -1.1 | 0.1 | 0 |
| CJ_10001281 | -0.5 | -0.1 | -0.7 | 0 | -0.1 | 0.2 | -2.4 | -0.1 | 0.1 | -0.1 |
| CJ_10001283 | 4.7 | 4.5 | -0.8 | 1.6 | -1.5 | 1.7 | 0.2 | -1.2 | 2.3 | 1.5 |
| CJ_10001284 | 0.2 | 0.8 | 0.7 | 0.1 | -0.1 | 0.3 | 0.1 | -0.3 | 0.2 | 0.1 |
| CJ_10001285 | 0.4 | 0.2 | 0.4 | 0.1 | 0.2 | 0.2 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001286 | -0.1 | 0 | 0.1 | -0.1 | 0.1 | 0.2 | 0.1 | -0.2 | 0.2 | 0 |
| CJ_10001287 | -0.3 | -0.1 | 0.4 | 0 | 0.1 | 0.1 | 0 | -0.2 | 0 | 0.1 |
| CJ_10001288 | -0.4 | 0 | -0.6 | -0.1 | 0.2 | 0.1 | 0 | 0.2 | 0.3 | 0.1 |

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| CJ_10001289 | -0.6 | 0.6 | 0.4 | -0.1 | -0.2 | 0.3 | 0.2 | 0.1 | 0.5 | 0.1 |
| CJ_10001290 | 0.3 | 0.3 | 0.3 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10001292 | -0.7 | 0.4 | 0.2 | 0.1 | -0.1 | 0.2 | 0.1 | -0.3 | 0.2 | 0.1 |
| CJ_10001293 | 0.2 | 0.2 | 0.4 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| CJ_10001294 | -0.1 | -0.2 | 0.1 | 0 | -0.8 | -1.3 | 0 | 0 | -0.1 | 0 |
| CJ_10001295 | 0.9 | 0.1 | 0.5 | 0.1 | 0 | 0.3 | 0.2 | 0 | -0.2 | 0 |
| CJ_10001296 | 0 | 0.1 | -0.1 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0 |
| CJ_10001297 | 2.9 | 2.8 | 1.2 | 0.9 | -1.2 | 1.1 | 1.4 | -0.1 | 0.9 | 1.2 |
| CJ_10001298 | 0.8 | 0.6 | 0.8 | 0.2 | 0 | 0 | 0.2 | 0 | 0 | -0.1 |
| CJ_10001299 | 0.4 | 0.2 | 0.4 | 0.1 | -0.1 | 0.1 | 0.2 | 0 | 0 | 0 |
| CJ_10001300 | 0.4 | 0.4 | 0.4 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0.1 | -0.1 |
| CJ_10001301 | 0.3 | 0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 | 0.1 | 0 |
| CJ_10001302 | 1.6 | 1.3 | 1 | 0.1 | -0.6 | 0.3 | 0.5 | -0.3 | 0 | 0.4 |
| CJ_10001303 | 0 | 0 | -0.3 | 0 | -0.1 | -0.1 | 0 | -0.1 | 0.1 | 0.1 |
| CJ_10001304 | -0.7 | -0.1 | -0.8 | 0 | -0.3 | 0.1 | -0.9 | 0 | -1.2 | 0 |
| CJ_10001305 | 0.3 | 0.5 | -0.4 | -0.1 | -0.2 | 0.2 | -0.1 | -0.1 | 0.1 | -0.1 |
| CJ_10001308 | -0.1 | -0.2 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0.1 | 0 |

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| CJ_10001309 | 0.1 | 0.2 | -5.2 | 0.2 | 0.2 | 0.1 | 0 | -1.6 | 0 | 0.1 |
| CJ_10001310 | -0.2 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | 0 |
| CJ_10001311 | 0.3 | 0.3 | 0.5 | 0.2 | 0.1 | 0.2 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10001312 | 0 | -0.4 | 0 | 0 | 0.2 | 0 | -0.1 | 0 | -0.1 | -0.1 |
| CJ_10001314 | 0.8 | 1.5 | 0.5 | 0.5 | -0.5 | 0.4 | 0.3 | -0.8 | 0.4 | 0.6 |
| CJ_10001315 | 0 | 0.3 | 0.4 | 0.2 | -1 | 0.2 | -0.1 | -0.3 | 0.1 | 0.1 |
| CJ_10001316 | 0.2 | -0.1 | 0.9 | 0 | 0.2 | 0.1 | -0.3 | -0.2 | -0.1 | 0 |
| CJ_10001317 | 0 | -0.1 | 0 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0.1 | 0.1 |
| CJ_10001318 | 0.1 | 0.1 | 0.2 | 0.1 | -0.4 | 0 | -0.1 | 0 | 0 | 0 |
| CJ_10001319 | 0.3 | 0.1 | 0.3 | 0.1 | 0 | 0.1 | 0.1 | -0.2 | 0 | 0 |
| CJ_10001320 | -0.8 | -0.1 | -0.7 | -0.1 | -0.4 | 0.2 | -0.1 | 0 | 0.3 | 0.1 |
| CJ_10001322 | -0.7 | -0.4 | 0.1 | 0.1 | 0 | 0 | 0 | 0.1 | 0 | 0.1 |
| CJ_10001323 | -0.2 | 0 | -0.2 | 0 | -0.1 | 0.1 | -0.1 | -0.2 | -0.1 | 0 |
| CJ_10001324 | 0.6 | 0.5 | 0.3 | 0.2 | -0.1 | 0.2 | 0.2 | -0.1 | 0.1 | 0.1 |
| CJ_10001325 | -0.1 | 0.1 | -1.8 | 0.1 | -0.3 | 0.2 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001327 | 0.5 | 0 | 0.2 | 0.1 | 0 | 0.1 | 0.2 | -0.1 | -0.1 | 0.1 |
| CJ_10001328 | 0 | -0.1 | 0.2 | 0.1 | 0 | 0.2 | -0.1 | 0 | -0.2 | -0.1 |

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| CJ_10001329 | 0.5 | 0.1 | 0.4 | 0 | 0 | 0 | 0 | 0 | 0 | -0.1 |
| CJ_10001330 | -0.2 | -0.1 | -0.1 | 0 | 0 | 0 | 0.1 | -0.2 | -0.1 | -0.1 |
| CJ_10001332 | -0.4 | -0.1 | -6.7 | 0 | -0.1 | 0 | 0 | -2.1 | -0.1 | 0.1 |
| CJ_10001333 | 1.2 | 1 | 1.1 | 0.2 | -0.2 | 0.2 | 0.3 | -0.1 | 0.1 | 0.1 |
| CJ_10001334 | 0.2 | 0.2 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0 |
| CJ_10001335 | 0.3 | 0.1 | 0.5 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| CJ_10001336 | 6 | 7.2 | -0.1 | 1.3 | -2.6 | -0.4 | 1.9 | 1.1 | 7.1 | 0.4 |
| CJ_10001337 | 0 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0 | 0 | 0 |
| CJ_10001338 | 0.1 | 0 | 0.4 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| CJ_10001340 | 0.4 | 0.1 | 0.4 | 0.2 | 0.2 | -0.1 | 0.1 | 0 | -0.2 | 0 |
| CJ_10001341 | -0.1 | 0.2 | 0.1 | 0.1 | 0 | 0.2 | 0 | 0 | 0.1 | 0 |
| CJ_10001347 | -0.2 | 0 | -7.1 | 0.1 | 0 | 0.2 | 0 | -2.3 | 0 | 0 |
| CJ_10001350 | 0.8 | 0.5 | 0.5 | 0.1 | 0.1 | 0 | 0.2 | 0 | 0 | 0 |
| CJ_10001352 | 0.2 | -0.3 | 0 | 0 | 0.1 | 0.1 | 0.2 | 0.2 | -0.2 | 0 |
| CJ_10001353 | 0 | 0 | -0.1 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0.1 | 0 |
| CJ_10001354 | 0.6 | 0.4 | 0.6 | 0.2 | 0 | 0.1 | 0.2 | 0.1 | 0 | 0 |
| CJ_10001355 | 0 | 0 | 0.2 | 0.2 | 0.1 | 0.2 | 0 | 0.1 | 0 | 0.1 |

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| CJ_10001356 | -0.5 | -0.3 | -0.2 | 0.1 | 0 | 0.2 | -0.1 | -0.1 | 0.1 | 0 |
| CJ_10001357 | 0.3 | 0.3 | 0.2 | 0 | -0.1 | 0 | -0.1 | -0.1 | 0.1 | 0 |
| CJ_10001358 | -0.3 | 0 | -0.2 | 0 | -0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| CJ_10001359 | 0.3 | 0.1 | 0.2 | 0.2 | 0.2 | 0 | 0.1 | 0 | -0.2 | 0 |
| CJ_10001360 | 0 | 0.1 | 0.3 | -0.1 | -0.2 | 0.2 | 0 | 0 | 0.3 | 0 |
| CJ_10001361 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0 |
| CJ_10001362 | 0.3 | 0.3 | 0.5 | 0.1 | 0 | 0.2 | 0.1 | 0 | 0 | 0 |
| CJ_10001363 | 0.2 | 0.1 | 0.4 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | 0 |
| CJ_10001365 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0 | 0 | -0.1 |
| CJ_10001367 | -0.1 | -0.1 | 0 | 0 | 0 | 0.2 | -0.1 | 0 | 0 | 0.1 |
| CJ_10001370 | 0.1 | -0.5 | 0.1 | -0.1 | -0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 |
| CJ_10001371 | -1.1 | 1.2 | -0.4 | 0.6 | -0.5 | 0.7 | -0.2 | -1 | 0.5 | 0.6 |
| CJ_10001372 | 0.2 | -0.1 | 0.2 | 0.1 | 0.1 | -0.1 | -0.1 | 0.4 | -0.2 | -0.2 |
| CJ_10001374 | -0.1 | 0.1 | -3.4 | 0.1 | -0.2 | 0.1 | 0 | -1.3 | 0 | 0.1 |
| CJ_10001375 | 0.4 | 0.2 | 0.3 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10001376 | 0.3 | 0.3 | 0.4 | 0 | 0 | 0.2 | 0 | 0.1 | -0.1 | -0.1 |
| CJ_10001377 | -0.2 | 0.1 | -0.4 | 0.2 | -0.2 | 0.1 | 0 | 0 | 0.2 | 0.2 |

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| CJ_10001378 | 0.2 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | -0.1 |
| CJ_10001379 | -0.1 | 0.1 | 0.2 | 0.1 | 0 | 0.1 | 0.1 | -0.5 | 0.1 | 0 |
| CJ_10001380 | 0 | 0.2 | 0.1 | 0.1 | 0.1 | -1.4 | 0 | -0.1 | 0.1 | 0 |
| CJ_10001381 | -0.2 | 0 | -0.2 | 0 | 0 | 0 | -0.1 | 0 | 0.1 | -0.1 |
| CJ_10001382 | 0.2 | 0.3 | 0.3 | 0.2 | 0 | -1.4 | 0 | -0.1 | 0 | 0 |
| CJ_10001383 | -0.4 | -0.2 | -0.2 | 0.2 | 0 | 0.2 | -0.1 | -0.2 | 0.2 | 0.2 |
| CJ_10001384 | 0.5 | 0.3 | 0.6 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 |
| CJ_10001385 | 0.4 | 0.3 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CJ_10001386 | 0.6 | 0.5 | 0.6 | 0.2 | 0 | 0.3 | 0.2 | -0.1 | 0 | 0 |
| CJ_10001389 | 0 | 0 | -0.2 | 0.2 | 0.2 | 0 | -0.2 | -0.1 | -0.1 | -0.1 |
| CJ_10001390 | -0.3 | 0.2 | 0.3 | 0.1 | 0.1 | 0.3 | 0.1 | 0.9 | -0.1 | -0.1 |
| CJ_10001391 | -1.9 | 0.5 | -0.7 | 0.8 | 0.2 | 0.8 | -0.1 | 0.5 | 0.6 | 0.7 |
| CJ_10001393 | 0.3 | -0.1 | -0.3 | 0.4 | 0.1 | 0 | 0.2 | 0.3 | 0 | 0 |
| CJ_10001395 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 | -0.2 | 0 |
| CJ_10001396 | 0.4 | 0.4 | 0.4 | 0 | 0 | -0.2 | 0.2 | -0.1 | 0 | -0.2 |
| CJ_10001398 | 0.3 | 0.4 | -0.4 | 0.2 | -0.1 | -0.1 | -0.1 | -0.2 | 0.1 | -0.1 |
| CJ_10001399 | 0.3 | 0.1 | 0.5 | 0.1 | 0.1 | -0.6 | -0.1 | 0.1 | -0.3 | -0.1 |

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| CJ_10001401 | -0.4 | 0.2 | 0.3 | 0.1 | 0.2 | 0 | -0.1 | 0.2 | -0.1 | -0.2 |
| CJ_10001402 | -0.2 | 0.2 | 0.2 | 0.1 | 0 | 0.1 | 0.1 | -0.2 | 0 | -0.1 |
| CJ_10001403 | 0.1 | 0.1 | 0.2 | 0.2 | -0.1 | 0.1 | 0.1 | 0.3 | 0 | 0.2 |
| CJ_10001404 | -0.4 | -0.4 | -0.5 | 0 | 0.1 | -0.1 | 0 | -0.2 | 0 | 0 |
| CJ_10001405 | 0 | -0.4 | 0.3 | 0 | 0 | 0.1 | 0.1 | 0 | -0.2 | 0 |
| CJ_10001406 | 0.1 | 0 | 0.2 | 0.1 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0 |
| CJ_10001407 | 0 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 |
| CJ_10001409 | 0.2 | 0.3 | 0.5 | 0.1 | -0.1 | 0.1 | 0.2 | -0.1 | -0.1 | 0.1 |
| CJ_10001411 | 0.1 | 0.1 | -0.1 | 0 | -0.1 | 0 | 0 | 0 | -0.1 | 0 |
| CJ_10001412 | -1.1 | 0.2 | 0.1 | 0.1 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0.1 |
| CJ_10001413 | 0.4 | 0.2 | 0.3 | 0.1 | 0.1 | -0.2 | 0 | -0.1 | -0.1 | 0 |
| CJ_10001415 | -0.1 | -0.2 | 0 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | -0.1 | 0 |
| CJ_10001416 | -0.3 | -0.1 | 0.2 | 0.2 | 0 | 0.1 | -0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10001417 | -0.4 | -0.1 | -0.1 | 0.1 | 0.1 | 0.1 | -0.2 | 0.2 | -0.2 | 0 |
| CJ_10001418 | 0.4 | 0.2 | 0.5 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 |
| CJ_10001420 | -0.3 | 0 | 0 | 0 | 0.1 | 0.1 | 0.2 | 0.2 | -0.2 | 0 |
| CJ_10001421 | 0.3 | 0 | 0.2 | 0.1 | 0.1 | 0 | 0.2 | 0.2 | -0.2 | -0.1 |

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| CJ_10001423 | 1.2 | 0.7 | 0.3 | 0.1 | -0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10001424 | 3.3 | 2.8 | 2.4 | 0.9 | -1.3 | 0.5 | 1.5 | -0.4 | 0.8 | 0.8 |
| CJ_10001425 | 0.9 | 0.6 | 0.3 | 0.1 | -0.2 | -0.2 | -0.1 | -0.2 | 0.1 | 0.1 |
| CJ_10001426 | 0 | 0.1 | 0.2 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10001427 | 0.5 | 0.3 | 0.2 | 0.1 | 0 | 0.1 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001428 | -1 | -0.7 | -0.2 | -0.1 | -0.1 | 0.1 | -0.2 | 0 | -0.3 | -0.2 |
| CJ_10001429 | -0.2 | 0.1 | -0.2 | 0.1 | 0 | 0.1 | 0 | 0 | 0.1 | -0.1 |
| CJ_10001430 | -0.1 | -0.2 | -0.1 | 0 | 0 | 0 | -0.1 | -0.1 | -0.1 | 0 |
| CJ_10001431 | 0.5 | -0.1 | -0.1 | 0 | 0.1 | 0.1 | -0.3 | 0 | 0 | -0.2 |
| CJ_10001432 | -0.1 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | 0.1 |
| CJ_10001433 | -0.2 | -0.1 | -0.3 | 0.1 | 0 | 0.3 | -0.1 | -0.1 | 0.2 | 0.1 |
| CJ_10001434 | 0.1 | 0.3 | 0.3 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0.2 | 0 |
| CJ_10001435 | -0.2 | 0 | -0.3 | 0.3 | 0.1 | 0.3 | -0.1 | -0.1 | 0 | 0.1 |
| CJ_10001436 | 0.1 | 0.3 | 0.3 | 0.1 | 0 | 0.2 | 0.2 | -0.1 | 0 | 0.1 |
| CJ_10001438 | 0.2 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 |
| CJ_10001439 | 0.2 | 0 | 0.4 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 |
| CJ_10001440 | 0 | -0.1 | 0.5 | 0.2 | 0 | 0 | 0.1 | 0.1 | 0 | -0.1 |

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| CJ_10001441 | 0.6 | 0.3 | 0.5 | 0.3 | 0 | 0 | 0.3 | 0.1 | -0.2 | 0 |
| CJ_10001442 | 0.3 | 0.1 | 0.2 | 0.2 | 0.2 | -0.1 | 0 | 0.1 | -0.1 | -0.1 |
| CJ_10001443 | -0.1 | -0.4 | 0.6 | 0.2 | 0.1 | 0 | 0.1 | 0 | -0.2 | -0.1 |
| CJ_10001444 | 0.5 | 0.3 | 0.3 | 0.1 | 0 | 0 | 0.1 | 0 | 0 | -0.1 |
| CJ_10001445 | 0.6 | 0.5 | 0.5 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10001446 | 0.5 | 0.1 | 0.5 | 0.2 | 0 | 0 | 0.2 | 0.1 | -0.3 | 0 |
| CJ_10001448 | 0.7 | 0.3 | 0.6 | 0.3 | -0.1 | 0.4 | 0.2 | -0.3 | 0.1 | 0.2 |
| CJ_10001449 | -0.6 | -0.1 | 0 | 0 | -0.3 | 0.1 | 0.1 | 0.1 | -0.1 | 0 |
| CJ_10001450 | -0.4 | 0.1 | -0.2 | 0.1 | -0.3 | 0.3 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001451 | -0.4 | 0 | -0.1 | 0.2 | 0 | 0.3 | 0.2 | 0 | 0.3 | 0.2 |
| CJ_10001452 | 0.6 | 0.4 | 0.7 | 0.1 | 0.1 | -0.1 | 0.1 | 0 | -0.2 | -0.1 |
| CJ_10001453 | 0 | 0.1 | 0.3 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10001454 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | 0.1 |
| CJ_10001455 | 0.4 | 0.1 | 0.7 | -0.1 | 0 | 0.1 | 0 | 0 | 0.1 | 0 |
| CJ_10001456 | -1.2 | 0 | -0.1 | -0.1 | -0.1 | 0.1 | 0 | 0 | 0.2 | 0 |
| CJ_10001457 | -1.1 | 0.1 | -0.9 | 0.1 | -0.1 | 0.3 | -0.3 | 0 | 0.2 | 0.1 |
| CJ_10001458 | -0.3 | 0 | 0.1 | 0 | -0.2 | 0.2 | 0 | 0 | 0.3 | 0.1 |

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| CJ_10001459 | -1.2 | 0.1 | -0.2 | 0.1 | 0.2 | 0 | -0.5 | 0.4 | 0 | 0.1 |
| CJ_10001460 | -0.4 | 0.3 | 0 | 0 | 0 | 0.1 | -0.1 | 0 | -0.1 | 0 |
| CJ_10001461 | -0.1 | 0 | 0.4 | 0.1 | 0 | 0 | -0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10001462 | -1.2 | -0.1 | -1.8 | -0.3 | -0.1 | 0.4 | -0.4 | 0.6 | -0.7 | 0.5 |
| CJ_10001463 | 0 | 0 | 0.1 | 0 | 0 | 0.2 | 0 | 0.1 | -0.1 | 0 |
| CJ_10001464 | 0.3 | -0.6 | -1.3 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | -0.3 | -0.1 |
| CJ_10001465 | -0.9 | -0.3 | -1 | 0 | -0.1 | 0.1 | -0.3 | 0.1 | -0.1 | -0.1 |
| CJ_10001466 | 0 | -0.1 | -0.1 | 0 | 0 | 0.1 | -0.1 | 0 | 0 | 0 |
| CJ_10001467 | -1.5 | -0.5 | 0.1 | 0 | 0.1 | 0.2 | 0.1 | 0.2 | 0.1 | 0 |
| CJ_10001469 | 0.2 | -0.1 | 0 | 0.1 | 0 | 0.4 | 0.2 | 0 | -0.1 | 0 |
| CJ_10001471 | -1 | 0 | -1.2 | 0.2 | 0 | 0 | -0.6 | 0 | 0.2 | -0.2 |
| CJ_10001472 | -0.3 | -0.1 | -0.3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CJ_10001473 | -0.2 | 0.1 | 0.2 | 0 | -0.1 | 0 | 0 | 0 | 0.3 | 0 |
| CJ_10001474 | -0.1 | 0.2 | -0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001475 | 1.9 | 0 | 0.6 | 0 | -0.7 | 0.3 | -0.2 | -0.3 | 0.6 | 0.1 |
| CJ_10001476 | -0.6 | -0.6 | -1.2 | 0 | 0 | 0 | -0.3 | -0.2 | 0.2 | 0 |
| CJ_10001477 | -0.2 | 0.9 | 0.9 | 0.4 | -0.3 | 0.5 | 0.4 | -0.2 | 0.3 | 0.2 |

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| CJ_10001479 | 0.1 | 0.2 | -0.1 | 0 | -0.1 | -0.1 | -0.3 | -0.2 | 0.3 | -0.1 |
| CJ_10001480 | 0 | 0 | 0.6 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| CJ_10001481 | 3.8 | 3.6 | 1.5 | 0.1 | -1.2 | 1.1 | 1.1 | -0.8 | 0.9 | 0.2 |
| CJ_10001482 | -0.1 | 0 | 0.1 | 0 | -0.1 | 0 | -0.1 | -0.2 | 0.3 | 0 |
| CJ_10001483 | 1 | 0.7 | 0.3 | 0.3 | -0.6 | 0.5 | 0.3 | 0.2 | 0.3 | 0.3 |
| CJ_10001484 | 0 | 0.2 | 0.1 | 0.2 | 0.1 | 0.1 | -0.1 | -0.1 | 0 | 0 |
| CJ_10001486 | -0.6 | -0.1 | -0.5 | 0.2 | 0 | 0.3 | 0.1 | 0 | 0 | 0 |
| CJ_10001487 | -0.2 | -0.1 | -0.2 | 0.1 | 0.1 | 0.1 | -0.3 | 0 | -0.1 | -0.1 |
| CJ_10001488 | -0.4 | -0.6 | 0.1 | 0 | 0 | 0.3 | 0.1 | 0.1 | -0.3 | 0.1 |
| CJ_10001489 | -0.2 | -0.3 | -0.3 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 | 0 |
| CJ_10001490 | -0.3 | -1.5 | -0.7 | 0.2 | 0.5 | 0.2 | -0.6 | 0.3 | 0 | 0.1 |
| CJ_10001491 | -0.1 | 0.1 | 0.3 | 0 | -0.1 | 0.1 | -0.1 | 0.2 | -0.1 | -0.1 |
| CJ_10001492 | 0 | 0.1 | 0 | 0.1 | 0 | 0.2 | -0.1 | 0 | 0 | 0 |
| CJ_10001493 | 0.2 | 0.3 | 0 | 0.2 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0.1 |
| CJ_10001494 | 0.6 | 0.3 | 0.5 | 0.3 | 0.2 | -0.1 | 0.2 | 0.2 | -0.1 | -0.1 |
| CJ_10001495 | 0.4 | 0.2 | 0 | 0.1 | -0.1 | 0 | 0 | -0.2 | 0.1 | 0 |
| CJ_10001496 | 0.2 | 0.2 | -0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 | 0 | 0.1 |

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| CJ_10001497 | 0.4 | 0.1 | 0.2 | 0.1 | -0.2 | 0 | 0 | 0.1 | 0.1 | 0 |
| CJ_10001498 | -0.4 | -0.1 | -0.5 | 0.1 | 0 | 0.3 | 0 | -0.1 | 0.1 | 0.1 |
| CJ_10001499 | 0 | 0.1 | 0.1 | 0.1 | -0.2 | 0.3 | 0.1 | -0.2 | 0 | 0 |
| CJ_10001500 | -2.1 | 0 | -0.2 | 0 | 0 | 0 | 0 | -0.3 | -0.2 | 0.1 |
| CJ_10001501 | 0.5 | 0.9 | 0.3 | 0.2 | -0.4 | 0.3 | 0.3 | -0.2 | 0.3 | 0.3 |
| CJ_10001502 | 0.7 | 0 | -0.1 | 0.2 | 0.1 | -0.3 | 0.3 | 0.1 | 0.1 | 0 |
| CJ_10001505 | -0.6 | -0.2 | -0.4 | 0 | 0 | 0.3 | 0 | 0 | 0.2 | 0 |
| CJ_10001506 | -0.1 | 0 | -0.4 | -0.1 | -0.2 | -0.1 | 0.2 | 0 | 0.1 | 0.1 |
| CJ_10001507 | 0 | 0.1 | -0.6 | 0.1 | -0.1 | 0.1 | -0.2 | -0.2 | 0 | 0.1 |
| CJ_10001508 | 2.8 | -0.4 | 0.8 | 0.1 | 0.2 | 0.1 | 1.1 | 0 | 0.7 | 0 |
| CJ_10001509 | -0.8 | -0.2 | -0.1 | 0.2 | 0.1 | 0.1 | -0.1 | 0 | -0.1 | -0.2 |
| CJ_10001510 | 0.9 | 0.4 | -0.1 | 0.2 | -0.2 | 0.1 | 0.2 | -0.3 | 0.1 | -1.3 |
| CJ_10001512 | 0.3 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | -0.3 | -0.1 | -0.1 |
| CJ_10001513 | -0.3 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 |
| CJ_10001514 | 0.3 | 0 | 0.1 | 0.2 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| CJ_10001515 | -0.8 | -0.3 | -0.5 | 0.1 | 0 | 0.1 | -0.2 | 0.1 | 0.1 | -0.1 |
| CJ_10001516 | 0.4 | 0.1 | 0.2 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 |

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| CJ_10001517 | -0.3 | -0.6 | -0.3 | 0.1 | 0.2 | 0.1 | -0.2 | 0.1 | -0.2 | 0 |
| CJ_10001518 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 | -0.1 | -0.1 |
| CJ_10001519 | -0.5 | -0.2 | 0.7 | 0.1 | 0.1 | 0 | 0.1 | 0.4 | -0.1 | -0.2 |
| CJ_10001520 | 0.5 | 0.5 | -0.1 | 0.2 | -0.2 | -0.9 | -0.1 | 0 | 0.2 | 0.2 |
| CJ_10001521 | -3.8 | 0 | 0.5 | 0.1 | 0.1 | 0.3 | 0 | 0 | 0.1 | 0.1 |
| CJ_10001522 | -1.4 | -0.2 | -0.2 | 0.1 | 0.1 | 0.2 | -0.2 | -0.6 | -0.1 | 0 |
| CJ_10001523 | 3.3 | 5.5 | -0.5 | 1.9 | -1.4 | 5.4 | -0.1 | -1.3 | 1.1 | 1.8 |
| CJ_10001524 | -0.8 | -0.3 | -0.6 | 0 | 0 | 0.2 | -0.1 | -0.2 | 0.2 | 0.1 |
| CJ_10001526 | -0.6 | -0.3 | 0 | -0.1 | 0 | 0.1 | 0.1 | 0.1 | 1.7 | 0.1 |
| CJ_10001527 | -0.5 | -0.6 | -0.1 | 0 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0.1 |
| CJ_10001528 | -0.7 | -0.4 | -0.9 | 0.1 | 0 | 0.3 | -0.1 | 0 | 0.1 | 0 |
| CJ_10001529 | 0.2 | 0.1 | 0.5 | 0.1 | 0.1 | -0.1 | 0 | -0.1 | -0.3 | 0 |
| CJ_10001530 | -0.2 | 0 | 0.2 | 0 | 0 | 0.1 | 0 | -0.1 | 0.1 | 0 |
| CJ_10001531 | 0.3 | -0.1 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0 | 0 |
| CJ_10001533 | 0.9 | 0.4 | 0.6 | 0.3 | 0.2 | 0 | 0.1 | 0 | 0 | 0 |
| CJ_10001535 | -0.2 | 0 | -1.3 | 0.1 | -0.3 | -0.2 | 0.1 | 0.1 | 0.3 | 0 |
| CJ_10001536 | -0.5 | 0 | -0.5 | 0 | -0.6 | 0.2 | 0 | 0 | 0.2 | 0.2 |

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| CJ_10001537 | 0.3 | 0.3 | 0 | 0.1 | -0.1 | 0.1 | 0.2 | 0 | 0.2 | 0.1 |
| CJ_10001538 | 0.2 | 0 | -0.1 | 0 | -0.2 | 0.2 | 0.1 | 0.1 | -0.1 | 0.1 |
| CJ_10001539 | 1.7 | 1.2 | 0.6 | 0.1 | -0.4 | 0.3 | 0.5 | 0.2 | 0.1 | -0.1 |
| CJ_10001540 | 0.3 | 0 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | -0.1 | -0.1 |
| CJ_10001541 | -0.1 | -0.2 | 0.2 | 0.1 | 0.1 | 0.1 | -1 | -0.5 | -0.3 | -0.1 |
| CJ_10001542 | 0.5 | 0 | 0.3 | 0.1 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| CJ_10001543 | -0.9 | 0 | 0.1 | 0 | -0.1 | 0 | 0 | -0.1 | -0.1 | -0.1 |
| CJ_10001544 | 0 | -0.5 | 0.5 | -0.1 | 0 | 0 | 0 | 0 | 1.2 | -0.1 |
| CJ_10001545 | -0.4 | 0.3 | 0.1 | 0.1 | 0.1 | 0.3 | 0.1 | -0.1 | -0.3 | 0.1 |
| CJ_10001546 | 0.1 | 0 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | 0 |
| CJ_10001547 | 1.4 | 1.1 | 0.6 | 0.2 | 0 | 0.1 | 0.3 | -0.3 | 2.4 | 0 |
| CJ_10001548 | 0.4 | 0.2 | 0.3 | 0 | 0 | 0 | -0.1 | -0.3 | 0 | 0 |
| CJ_10001550 | 0.2 | 0 | 0.5 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | 1.3 | -0.2 |
| CJ_10001552 | 0 | 0.1 | 0 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 | -0.2 |
| CJ_10001553 | -0.4 | -0.2 | -0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0.6 | -0.1 |
| CJ_10001555 | -3.8 | 0.6 | 0.4 | 0.3 | -0.2 | -1.2 | -1.2 | -1.6 | 0.2 | 0.2 |
| CJ_10001556 | 0 | 0.1 | -0.1 | 0.1 | -0.1 | 0.1 | -0.1 | -0.2 | -0.1 | 0 |

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| CJ_10001558 | -2.3 | 0 | -0.4 | 0.1 | -0.1 | -0.1 | -0.3 | -0.3 | 0.1 | -0.1 |
| CJ_10001560 | -6.6 | 0.3 | 0.3 | 0.1 | -0.4 | 0.2 | -0.1 | -0.2 | -0.1 | 0.1 |
| CJ_10001562 | -0.3 | 0.5 | 0 | -0.1 | -0.5 | 0.3 | 0.1 | 0 | -0.2 | 0 |
| CJ_10001563 | 0.8 | 0.4 | 0.7 | 0.2 | 0.1 | 0 | 0.2 | 0.1 | -0.1 | -0.1 |
| CJ_10001564 | 0.4 | 0.3 | 0.2 | 0.2 | -0.1 | 0.1 | 0.2 | -0.1 | -0.1 | -0.1 |
| CJ_10001565 | -0.1 | -0.2 | 0.1 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| CJ_10001566 | 0.3 | 0 | 0 | 0 | 0.1 | -0.1 | 0 | 0.1 | -0.1 | -0.2 |
| CJ_10001567 | -0.4 | -0.8 | -0.7 | 0 | 0 | 0.1 | -0.1 | 0 | 0.1 | 0 |
| CJ_10001568 | 0 | -0.2 | 0.3 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 1.4 | 0 |
| CJ_10001569 | -0.6 | -0.1 | -0.2 | -0.1 | -0.1 | 0.2 | 0 | -0.1 | -0.1 | 0 |
| CJ_10001570 | -0.1 | 0 | 0 | 0.2 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0 |
| CJ_10001571 | -0.3 | 0 | -0.4 | 0 | 0 | 0.2 | -0.1 | 0 | 1.9 | 0.1 |
| CJ_10001572 | -0.1 | -0.3 | -0.4 | 0 | 0 | 0.3 | 0.1 | 0 | -0.1 | 0.2 |
| CJ_10001573 | 0.2 | -0.3 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 |
| CJ_10001574 | 0.4 | 0.3 | 0.6 | 0.1 | 0 | 0 | 0 | -0.2 | 0.9 | 0 |
| CJ_10001575 | 0.3 | 0.3 | 0.5 | 0.1 | 0.1 | 0.1 | 0.1 | -0.2 | 0 | 0 |
| CJ_10001576 | 0.4 | 0.2 | 0.5 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | 0 |

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| CJ_10001577 | -0.3 | -0.3 | 0 | -0.1 | 0 | 0 | -0.1 | -0.2 | 1.3 | 0 |
| CJ_10001578 | -0.7 | -0.3 | -0.6 | 0.2 | -0.2 | -1 | -0.1 | -0.6 | 0.1 | 0 |
| CJ_10001579 | 0.2 | -0.2 | -0.1 | 0.1 | 0.2 | 0.2 | -0.1 | -0.2 | -0.2 | 0.1 |
| CJ_10001580 | -0.2 | -0.3 | -0.2 | 0 | -0.3 | 0.3 | 0.2 | 0 | 0.1 | 0.1 |
| CJ_10001581 | 0 | 0.1 | 0 | 0 | -0.2 | 0 | 0 | -0.2 | -0.2 | 0.1 |
| CJ_10001582 | -0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 |
| CJ_10001583 | 0.3 | 0.4 | 0.1 | 0.2 | -0.3 | 0.1 | -1.8 | 0 | 0.2 | 0 |
| CJ_10001584 | -0.7 | -0.3 | -0.1 | 0 | -0.1 | 0 | -0.3 | 0.1 | -0.1 | -0.2 |
| CJ_10001585 | -0.2 | 0 | -0.3 | -0.1 | 0 | 0.2 | -0.1 | -0.1 | 0.2 | 0 |
| CJ_10001586 | -0.5 | 0 | -0.5 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0.2 | -0.2 |
| CJ_10001587 | 0.3 | 0.5 | -0.2 | 0.1 | 0 | -0.1 | -0.4 | -0.6 | 0.2 | -0.1 |
| CJ_10001588 | 0.3 | 0.4 | 0.3 | 0.1 | 0 | -0.1 | -0.4 | -0.1 | 0 | -0.2 |
| CJ_10001590 | 0 | 0.2 | 0.4 | 0.2 | 0.1 | -0.1 | -0.1 | -0.1 | 0 | -0.1 |
| CJ_10001591 | -0.2 | 0.2 | 0.3 | 0.1 | 0.2 | 0 | -0.1 | -0.1 | -0.2 | -0.2 |
| CJ_10001593 | -0.3 | -0.1 | -0.5 | 0.1 | 0 | 0.2 | -0.1 | -0.3 | 0 | 0.1 |
| CJ_10001596 | 0.7 | 0.1 | 0.4 | 0 | -0.1 | 0.3 | 0.1 | -0.1 | 0.1 | 0.1 |
| CJ_10001597 | 0 | 0.1 | -0.1 | -0.1 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0 |

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| CJ_10001598 | -0.1 | 0 | 0 | -0.1 | 0 | 0.1 | 0 | -0.3 | 0.2 | 0 |
| CJ_10001599 | 0 | -0.1 | -0.1 | 0 | 0 | 0.1 | 0 | 0 | 0.2 | 0 |
| CJ_10001600 | -0.2 | 0 | -0.1 | 0.1 | 0 | 0 | 0 | 0 | 0 | -0.1 |
| CJ_10001601 | 0.5 | 0.4 | 0.5 | 0 | -0.1 | 0.2 | 0.1 | -0.1 | 0.8 | 0 |
| opCcV0100000001 | -0.1 | -0.2 | 0.5 | -0.2 | 0.2 | 0.1 | 0 | 0.1 | -0.2 | -0.1 |
| opCcV0100000002 | 0 | 0.1 | 0.1 | -0.1 | 0 | 0 | -0.2 | -0.1 | 0.2 | -0.2 |
| opCcV0100000004 | -0.4 | -0.4 | 0 | -0.1 | 0.1 | 0.1 | -0.1 | -0.2 | -0.2 | 0 |
| opCcV0100000008 | -0.1 | -0.2 | -0.1 | 0.1 | 0 | 0 | 0 | -0.1 | 0.1 | -0.2 |
| opCcV0100000009 | 0.6 | 0.6 | 0.4 | 0.1 | 0.2 | -0.1 | -0.2 | 0 | -0.6 | -0.1 |
| opCcV0100000014 | 0.5 | 0.2 | 0.2 | -0.1 | 0 | 0 | 0.2 | 0.1 | 0 | -0.2 |
| opCcV0100000017 | 0.7 | -0.7 | 0.7 | -0.1 | 0 | 0.3 | 0.4 | 0 | -0.1 | 0 |
| opCcV0100000019 | -0.1 | 0.1 | 0 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | 0.1 |
| opCcV0100000023 | -2.2 | -1.8 | 0 | -0.5 | 0.8 | 0 | -0.8 | 1.2 | -0.6 | -0.7 |
| opCcV0100000025 | 0.1 | 0 | 0.3 | -0.2 | 0.1 | 0.2 | 0 | 0 | -0.1 | 0 |
| opCcV0100000033 | -1.1 | -1.5 | -0.3 | -0.1 | 0 | -0.3 | 0.3 | 0.4 | -0.4 | -0.1 |
| opCcV0100000035 | -0.6 | -0.2 | -0.9 | -0.1 | -0.1 | -0.1 | 0 | 0.1 | 0 | 0 |
| opCcV0100000036 | 0.6 | 0.4 | 0.2 | -0.1 | -0.2 | 0.2 | -0.2 | 0 | 0.1 | 0 |

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| opCcV0100000037 | 0.1 | -0.1 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 | -0.1 |
| opCcV0100000038 | -0.6 | -0.4 | -0.5 | -0.1 | -0.3 | 0.2 | -0.2 | -0.9 | 0.2 | 0.1 |
| opCcV0100000039 | -0.9 | -0.2 | 0.3 | 0 | 0 | 0.1 | 0.2 | -0.1 | 0.1 | 0 |
| opCcV0100000040 | -0.5 | -0.7 | -2.1 | -0.3 | 0.2 | -1.4 | -1.5 | -0.3 | -0.1 | -0.1 |
| opCcV0100000041 | -0.9 | 1.3 | -1.9 | -0.1 | 0.1 | -1.9 | -1.3 | -0.1 | 0 | -0.2 |
| opCcV0100000046 | -1.4 | -0.9 | 1 | -0.1 | 0.6 | 0 | 0.2 | 0.5 | -0.5 | -0.4 |
| opCcV0100000047 | -1 | -0.2 | -1 | -0.2 | 0 | 0.1 | -0.2 | -0.1 | 0.3 | 0 |
| opCcV0100000049 | -1.6 | -1.9 | -0.8 | 0 | 0.4 | -0.3 | -0.2 | 0.9 | -1 | -0.2 |
| opCcV0100000050 | -1.9 | -1.4 | 0 | -0.2 | -0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.4 |
| opCcV0100000053 | 0.2 | -0.2 | 0.7 | 0 | 0 | 0.2 | 0.1 | -0.2 | 0.6 | 0 |
| opCcV0100000055 | 0.1 | 0.2 | 0 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | -0.1 |
| opCcV0100000057 | 1.1 | -0.6 | 0.6 | 0 | 0 | 0.2 | 0.5 | 0.1 | 0.1 | 0 |
| opCcV0100000060 | 1.6 | 0.4 | -0.1 | 0.1 | -0.1 | 0.3 | 0.1 | -0.1 | 0.1 | -0.1 |
| opCcV0100000068 | 0 | 0.2 | 0.2 | -0.1 | -0.1 | 0 | -0.2 | 0 | -0.1 | 0 |
| opCcV0100000069 | 2.5 | 1.4 | 1.8 | 0.6 | -0.7 | 0.5 | 0.5 | -0.6 | 0.7 | 0.6 |
| opCcV0100000072 | -0.9 | -1.9 | 0.1 | -0.3 | -0.1 | 0.3 | 0.2 | 0.4 | -0.3 | 0.1 |
| opCcV0100000075 | 0.2 | 0.3 | 0.4 | 0 | 0 | 0 | 0 | -0.2 | 0 | -0.1 |

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| opCcV0100000078 | 0.4 | 0.3 | 0 | 0 | 0 | 0.3 | 0 | 0 | 0.2 | 0 |
| opCcV0100000079 | 0.3 | 0 | 0.2 | 0 | 0 | 0 | -0.2 | 0.1 | 0.2 | 0.1 |
| opCcV0100000085 | -0.3 | 0 | -0.2 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0 | -0.2 |
| opCcV0100000087 | 0.2 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | 0 | -0.1 |
| opCcV0100000091 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCcV0100000095 | 0 | -0.1 | -0.3 | 0.1 | 0.3 | -1.7 | -2.4 | 0.1 | 0 | 0 |
| opCcV0100000098 | 1.8 | 1.3 | 1.4 | 0.5 | -0.4 | 0.6 | 0.4 | -0.6 | 0.2 | 0.6 |
| opCcV0100000101 | 0.4 | 0.1 | 0.3 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0.1 | 0.1 |
| opCcV0100000104 | 0.6 | 0.3 | 0.6 | 0.1 | 0.1 | 0 | -0.1 | -0.1 | 0 | 0 |
| opCcV0100000105 | 0.9 | 0.7 | 0.4 | 0.1 | -0.2 | 0.2 | -0.3 | -0.5 | 0.3 | 0.2 |
| opCcV0100000109 | -0.9 | 0.1 | 0.4 | -0.1 | -0.2 | -0.4 | -0.2 | 0.2 | -0.2 | 0 |
| opCcV0100000111 | -0.2 | -0.3 | 0.7 | 0.1 | 0.2 | 0.3 | 0.5 | 0 | -0.2 | 0 |
| opCcV0100000118 | 0.2 | 0.1 | 0.3 | 0 | 0.1 | -0.1 | -0.3 | -0.1 | -0.1 | 0 |
| opCcV0100000123 | -1.1 | -0.9 | -0.6 | 0 | 0.2 | -0.6 | -0.2 | -0.2 | 0 | -0.1 |
| opCcV0100000126 | 0.2 | -0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0 |
| opCcV0100000129 | -0.6 | -0.2 | -0.6 | 0 | -0.1 | 0.2 | -0.5 | -0.1 | -0.1 | 0 |
| opCcV0100000132 | 0.7 | 0.4 | -1.8 | 0.1 | 0.1 | -1.6 | -1.9 | -1.7 | -0.1 | 0 |

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| opCcV0100000135 | -0.3 | 1 | 1.3 | 0.1 | -0.3 | 0.5 | 0.4 | -0.4 | -0.3 | -0.1 |
| opCcV0100000137 | 0 | 0 | -4.6 | -0.2 | -0.2 | -1.4 | -3 | -1.4 | 0 | 0.1 |
| opCcV0100000143 | 1.2 | 0.9 | 0.2 | 0.3 | 0 | 0 | 0.7 | -0.1 | 0.3 | 0.2 |
| opCcV0100000148 | 0.3 | -0.2 | 0.1 | 0 | 0 | -0.1 | -0.1 | 0 | 0 | -0.1 |
| opCcV0100000149 | 0.4 | 0.6 | 1 | 0.3 | 0 | 0.5 | 0.2 | 0.1 | -0.1 | 0.4 |
| opCcV0100000151 | 0.4 | 0.5 | 0.3 | 0 | 0 | 0 | -0.1 | 0 | 0.1 | -0.1 |
| opCcV0100000153 | 0.1 | 0.1 | 0.6 | 0.2 | 0 | 0.3 | 0 | -0.1 | 0 | 0 |
| opCcV0100000155 | 0.8 | 1.1 | -0.5 | 0.4 | -0.4 | -0.2 | 0.3 | -0.6 | 0.1 | 0.4 |
| opCcV0100000158 | 0 | 0.2 | 0.2 | 0 | 0 | 0.2 | 0 | 0 | -0.1 | -0.1 |
| opCcV0100000161 | 0.7 | 1.1 | 0.7 | 0.1 | -0.2 | -0.1 | 0.4 | -0.1 | 0.1 | -0.1 |
| opCcV0100000162 | 0.2 | 0.1 | -4.6 | 0 | 0.1 | -0.1 | 0.2 | -1.6 | 0 | 0 |
| opCcV0100000164 | -0.2 | -0.1 | -0.1 | -0.2 | -0.1 | 0.3 | -0.1 | 0 | 0 | -0.1 |
| opCcV0100000167 | -1.2 | -0.5 | -1 | -0.1 | 0 | 0.2 | -0.2 | 0 | 0.1 | 0 |
| opCcV0100000169 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | 0.1 | 0 | -0.1 |
| opCcV0100000171 | -0.1 | -0.2 | 0.1 | 0 | 0.1 | -0.7 | 0 | 0 | 0.2 | 0.1 |
| opCcV0100000172 | -0.5 | -0.2 | 1.3 | -0.4 | 0 | -0.1 | -0.2 | 0.2 | -0.3 | -0.2 |
| opCcV0100000174 | 0.2 | 0 | 0.6 | 0.2 | 0.1 | 0.3 | 0.2 | -0.1 | 0.1 | -0.1 |

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| opCcV0100000182 | -0.4 | 0 | -0.6 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 |
| opCcV0100000184 | 0 | -0.3 | -0.8 | 0 | 0.1 | -0.2 | 0.2 | 0.2 | -0.1 | 0.1 |
| opCcV0100000186 | 0.2 | -0.6 | 0.6 | -0.1 | 0.4 | 0 | -0.1 | 0.2 | -0.1 | -0.1 |
| opCcV0100000192 | 0.2 | 0.1 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCcV0100000195 | -0.4 | -0.1 | -0.3 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0 |
| opCcV0100000198 | 1.8 | 0 | 0.9 | 0.4 | -0.2 | 0.1 | 0.4 | -0.4 | 0.3 | 0.3 |
| opCcV0100000200 | 1.5 | 1.2 | 0.7 | -0.5 | -0.7 | 0.9 | 0.7 | 0.4 | 0.8 | 0.1 |
| opCcV0100000201 | -0.6 | 2.2 | 2.2 | 0.8 | -0.9 | 0.6 | 0.8 | -0.5 | 0.5 | 0.5 |
| opCcV0100000205 | 0.1 | -0.2 | 0.1 | -0.2 | -0.1 | 0.2 | -0.1 | 0 | -0.1 | -0.1 |
| opCcV0100000216 | 0.2 | 0 | -0.4 | 0.1 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| opCcV0100000220 | -0.1 | -0.7 | 1.2 | 0.4 | -0.2 | 0.4 | 0.6 | -0.2 | 0.3 | 0.5 |
| opCcV0100000222 | -0.4 | 0 | -0.3 | -0.1 | -0.3 | 0.2 | 0 | -0.1 | 0.1 | 0.1 |
| opCcV0100000225 | -2 | -1.5 | -0.9 | -0.8 | 0.4 | 0 | -0.4 | 0.9 | -0.4 | -0.6 |
| opCcV0100000232 | 0.3 | 0 | 0 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100000236 | -3.2 | -1.4 | 0.3 | 0 | -0.1 | -0.3 | 0.1 | 0.9 | 0.5 | 0.1 |
| opCcV0100000237 | -0.3 | 0 | -0.5 | 0 | 0.1 | 0 | -0.1 | 0 | 0.1 | -0.2 |
| opCcV0100000239 | -2.6 | -1.3 | 0.8 | -0.2 | -0.2 | -0.2 | 0 | 0.2 | 0.1 | 0.1 |

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| opCcV0100000240 | 1.4 | 0.1 | 0.8 | 0 | -0.1 | 0.2 | 0 | 0.1 | -0.1 | 0 |
| opCcV0100000241 | -0.1 | 0.3 | 0.6 | 0 | 0 | 0.4 | 0.2 | 0 | 0 | 0 |
| opCcV0100000242 | -1.2 | -1.1 | 0 | -0.2 | 0.1 | -0.2 | 0.3 | 0.4 | 0.1 | 0 |
| opCcV0100000243.80 | 3.7 | 1.7 | 0.4 | -0.7 | -1.7 | -0.2 | 0.6 | 1.9 | 1.8 | -0.9 |
| opCcV0100000243.90 | 6 | 1.2 | -0.2 | 0.2 | -2.7 | -0.2 | -1.9 | 1.1 | 2.8 | -1.9 |
| opCcV0100000243.C | 1.5 | 1.2 | -0.2 | -1.8 | -0.5 | 0.8 | -0.7 | -1 | 1.9 | -0.6 |
| opCcV0100000244 | 0.8 | 0 | 0.2 | 0 | -0.1 | 0 | 0.3 | -0.3 | 0 | 0.1 |
| opCcV0100000245 | -0.1 | 0.1 | -6.1 | 0 | 0 | -2.4 | -2.1 | 0.1 | 0.1 | 0 |
| opCcV0100000250 | 0.1 | -0.9 | -0.5 | -0.1 | 0.2 | -0.5 | 0.1 | -0.6 | -0.1 | -0.1 |
| opCcV0100000256 | 0.5 | 0 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | 0.1 | -0.1 | 0 |
| opCcV0100000260 | 1.3 | -0.4 | 0.6 | -0.2 | -0.1 | 0.3 | -0.1 | 0.5 | -0.1 | 0 |
| opCcV0100000264 | 0.1 | -0.3 | -0.1 | -0.1 | 0 | 0 | -0.1 | 0 | 0.1 | 0 |
| opCcV0100000268 | 0.7 | 0 | 0.5 | 0 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| opCcV0100000274 | 0.6 | 0.3 | 0.1 | 0 | 0 | 0.1 | 0.2 | 0 | -0.2 | -0.2 |
| opCcV0100000278 | -0.4 | -1 | -0.1 | -0.1 | 0.1 | -0.3 | -0.2 | 0.1 | -0.2 | -0.1 |
| opCcV0100000279 | -0.5 | -1.7 | -0.1 | -0.6 | 0.5 | 0.1 | -0.1 | 1.3 | -0.4 | -0.4 |
| opCcV0100000280 | 4 | 0.5 | 1.1 | -0.3 | -1.9 | -0.1 | 0.6 | -1.9 | 1 | -0.4 |

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| opCcV0100000281 | 0.7 | -0.1 | 0.2 | 0 | -0.1 | 0.2 | -0.6 | -0.1 | 0.3 | 0 |
| opCcV0100000282 | 1.5 | 0.1 | 0.5 | 0.2 | 0.1 | 0.1 | 0.3 | 0.1 | -0.2 | 0 |
| opCcV0100000286 | 0 | -0.3 | 0.5 | 0.1 | 0 | 0.1 | -0.1 | 0 | -0.1 | 0 |
| opCcV0100000291 | -0.1 | 0.2 | -0.3 | 0 | -0.2 | 0 | 0 | -0.4 | 0.4 | 0 |
| opCcV0100000293 | 0.3 | 0.3 | 0.1 | 0 | 0 | -2.4 | -2.3 | 0.1 | 0 | -0.1 |
| opCcV0100000299 | 0.6 | 0.2 | 0.9 | 0 | 0.1 | 0 | 0.2 | 0 | -0.1 | -0.2 |
| opCcV0100000300 | 0.8 | 0.4 | 0.7 | 0 | 0 | -0.1 | 0.1 | 0.1 | 0 | -0.2 |
| opCcV0100000304 | 0.6 | 0.4 | -2 | 0 | -0.1 | -2 | -1.7 | -1.6 | 0 | -0.1 |
| opCcV0100000307 | -1.9 | -0.6 | -0.2 | 0 | 0.1 | -0.7 | -1 | -0.3 | 0 | 0 |
| opCcV0100000311 | 0.6 | 0.2 | 0.5 | 0.2 | 0 | -0.1 | 0.1 | 0 | 0 | -0.1 |
| opCcV0100000312 | 5.1 | 4.5 | -1 | 0.9 | -2.1 | -1.2 | -0.1 | -1.1 | 2.4 | 1.6 |
| opCcV0100000315 | -1.1 | -1.2 | -0.2 | 0.1 | 0.1 | 0.6 | -0.1 | 0.5 | -0.7 | 0 |
| opCcV0100000317 | 0.2 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0.2 | 0.1 | -0.1 | -0.1 |
| opCcV0100000320 | 0.5 | 0.1 | 0.4 | -0.1 | 0 | 0.1 | 0 | 0 | -0.2 | -0.1 |
| opCcV0100000321 | -0.1 | -0.2 | -0.1 | 0 | 0 | -0.1 | -0.1 | -0.1 | -0.2 | -0.1 |
| opCcV0100000324 | 0.3 | -0.1 | 0.2 | 0 | -0.1 | 0.2 | -0.1 | 0.1 | -0.2 | 0 |
| opCcV0100000326 | -0.5 | -0.3 | -0.1 | 0 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.2 |

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| opCcV0100000327 | -0.1 | -0.2 | 0.2 | 0 | -0.1 | 0.2 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100000330 | -0.8 | -0.4 | 0.6 | -0.2 | -0.1 | -0.2 | 0.2 | 0.9 | -0.5 | -0.2 |
| opCcV0100000333 | -0.2 | 0 | -0.2 | 0 | -0.2 | 0 | -0.2 | -0.4 | 0 | 0 |
| opCcV0100000336 | 0 | -0.1 | 0.1 | -0.1 | -0.2 | 0.1 | 0 | -0.1 | 0 | 0.1 |
| opCcV0100000337 | 0.5 | 0.2 | -3.1 | 0.1 | 0.1 | -1.2 | 0 | -0.1 | -0.1 | -0.1 |
| opCcV0100000338 | 0.4 | -0.4 | -1.4 | 0.2 | 0.1 | -0.5 | -0.9 | 0.1 | -0.1 | -0.1 |
| opCcV0100000339 | 0.8 | -0.9 | 0.8 | 0.1 | -0.3 | 0.6 | 0.5 | 0.2 | 0.5 | 0.3 |
| opCcV0100000340 | 0.7 | -0.5 | 0.3 | 0.1 | -0.4 | 0.3 | -0.3 | 0.1 | -0.8 | -0.2 |
| opCcV0100000343 | 1.7 | 1.2 | 0.8 | 0.3 | -0.7 | 0.5 | 0.5 | -0.2 | 0.4 | 0.4 |
| opCcV0100000344 | -3.1 | -0.5 | 0.3 | -0.1 | 0 | -0.5 | 0.3 | 0 | -0.5 | -0.1 |
| opCcV0100000348 | 1.5 | 1.2 | -0.2 | 0.1 | -0.6 | -0.1 | -0.4 | -0.6 | 0.1 | 0.2 |
| opCcV0100000349 | 0 | 0 | -0.1 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | 0.1 | 0 |
| opCcV0100000351 | -0.4 | 0 | -0.5 | -0.1 | -0.3 | -0.2 | -0.8 | 0.1 | 0.1 | 0 |
| opCcV0100000355 | -1.8 | -1.4 | -0.5 | -0.2 | 0.3 | -0.1 | -0.4 | 0.4 | -0.2 | -0.3 |
| opCcV0100000358 | -0.7 | -0.7 | 0.5 | -0.1 | 0.2 | 0.2 | 0.2 | 0.2 | -0.2 | -0.2 |
| opCcV0100000360 | -0.1 | -1.2 | -0.6 | 0 | 0.1 | -0.2 | -0.2 | -0.1 | -0.2 | -0.1 |
| opCcV0100000361 | -5.5 | 0.3 | -4.3 | -0.7 | 1.3 | -1.3 | -2 | 0.9 | -0.6 | -1 |

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| opCcV0100000364 | -1.4 | -2.1 | -0.5 | -0.4 | 0.4 | -0.1 | -0.3 | 0.5 | -0.5 | -0.4 |
| opCcV0100000367 | -1.5 | -0.4 | 1.4 | -0.2 | -0.3 | 0.4 | 0.5 | 0.2 | 0 | -0.1 |
| opCcV0100000368 | -0.9 | -0.2 | 0.4 | 0.1 | 0.1 | 0.3 | 0.2 | 0.3 | -0.6 | -0.1 |
| opCcV0100000370 | 0.3 | -0.2 | -0.2 | -0.1 | 0 | 0.1 | 0 | 0 | -0.1 | 0.1 |
| opCcV0100000376 | 1.8 | 1.6 | 1.9 | 1.3 | -1.3 | 0.3 | 1.1 | 0.2 | 1.4 | -0.5 |
| opCcV0100000377 | -0.7 | 0.1 | 0.6 | -0.1 | 0.1 | 0.1 | 0 | 0.3 | -0.9 | -0.1 |
| opCcV0100000384 | 0.2 | 0.1 | 0.2 | 0.1 | 0.1 | -0.1 | -0.1 | 0 | 0 | -0.1 |
| opCcV0100000385 | -0.4 | -0.9 | 0 | -0.1 | 0 | -0.1 | -0.4 | 0 | -0.1 | 0 |
| opCcV0100000387 | -2 | -1.1 | -0.2 | 0 | 0.3 | 0.1 | -0.2 | 0.7 | -0.6 | 0 |
| opCcV0100000391 | -0.4 | -0.3 | 0.3 | 0 | -0.4 | 0.3 | 0.1 | 0.2 | 0.1 | 0.1 |
| opCcV0100000396 | -0.2 | 0.3 | 0.1 | -0.3 | -0.2 | 0.3 | 0.1 | 0.2 | 0.1 | 0.1 |
| opCcV0100000397 | 0.4 | -0.8 | 0.1 | -0.1 | 0.2 | 0 | 0.1 | -0.2 | 0.1 | -0.1 |
| opCcV0100000400 | 0.2 | -1 | -0.2 | 0 | 0 | -0.3 | -0.2 | -0.1 | 0 | -0.1 |
| opCcV0100000408 | -3.2 | -1.1 | -1.4 | -0.2 | 0 | -0.9 | 0 | 0.2 | -0.3 | 0.1 |
| opCcV0100000411 | -0.4 | -0.1 | -0.1 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 | 0 |
| opCcV0100000412 | 0.8 | -0.2 | 0.1 | 0 | 0.1 | -0.1 | 0.1 | 0.2 | -0.2 | -0.1 |
| opCcV0100000414 | -0.6 | -0.1 | -0.5 | 0.1 | -0.2 | 0.2 | 0.1 | -0.2 | 0.2 | 0.1 |

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| opCcV0100000416 | 0.9 | -0.6 | -0.3 | 0.3 | 0.5 | 0 | -0.1 | 0 | 0 | 0.3 |
| opCcV0100000422 | 0.3 | 0.2 | -2.3 | 0 | 0 | -1.7 | -1.7 | -0.8 | 0.2 | -0.1 |
| opCcV0100000425 | 1 | 0.7 | 0.8 | 0.2 | 0.1 | -0.2 | 0.2 | -0.1 | 0 | 0 |
| opCcV0100000427 | 0.8 | 0.5 | 0.7 | 0.3 | 0.2 | -0.1 | 0.2 | 0.1 | -0.1 | -0.1 |
| opCcV0100000428 | 0.1 | 0.6 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0 | 1 | 0.2 |
| opCcV0100000429 | 0 | 0 | -0.2 | -0.1 | 0.1 | 0.2 | -0.1 | -0.1 | 0.1 | 0.1 |
| opCcV0100000434 | 0.3 | -0.2 | 0 | 0.1 | 0.1 | -0.1 | -0.2 | -0.1 | 1.1 | 0 |
| opCcV0100000437 | -0.3 | -0.6 | 0.3 | 0 | -0.1 | 0.2 | 0.1 | -0.3 | -0.2 | 0 |
| opCcV0100000443 | -0.1 | 0.4 | 0 | -0.1 | -0.2 | 0.1 | -0.1 | 0.1 | 0.2 | -0.1 |
| opCcV0100000444 | 0 | 0 | -1.6 | -0.1 | -0.2 | -0.8 | -1.1 | -1.1 | 0 | 0.1 |
| opCcV0100000446 | -0.1 | -0.5 | 0 | 0 | 0.1 | 0.2 | 0.2 | 0 | -0.1 | -0.1 |
| opCcV0100000447 | 0.4 | -0.2 | 0.4 | 0 | -0.1 | -0.1 | 0.2 | 0.1 | -0.2 | 0 |
| opCcV0100000448 | 0.2 | -1.6 | -0.2 | -0.1 | 0 | 0.1 | -0.2 | -0.1 | 0.2 | -0.1 |
| opCcV0100000451 | 0.9 | 1 | 0.8 | 0.2 | 0.1 | 0.2 | 0.3 | -0.1 | -0.1 | 0.2 |
| opCcV0100000452 | -1.4 | -0.1 | -0.4 | -0.1 | 0 | 0.2 | -0.2 | -0.2 | 0 | 0.1 |
| opCcV0100000455 | 1.3 | 1.2 | 0.8 | 0 | 0 | 0.2 | 0.2 | -0.1 | 0.3 | 0 |
| opCcV0100000458 | 0.1 | 0.2 | 0.4 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | 0 |

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| opCcV0100000463 | 0.1 | 0.1 | -0.2 | -0.1 | -0.1 | 0 | -0.2 | -0.1 | 0.1 | 0 |
| opCcV0100000467 | 0.9 | 0 | 0.2 | 0.1 | -0.3 | 0 | 0.3 | 0.3 | -0.2 | -0.1 |
| opCcV0100000469 | -1.5 | -1.6 | -0.5 | -0.1 | 0.3 | -0.1 | -0.2 | 0.3 | -0.4 | -0.3 |
| opCcV0100000470 | 1.1 | -1.6 | 0.2 | 0.6 | 0 | 0.5 | 1 | 0.5 | -0.9 | -0.4 |
| opCcV0100000472 | -3.4 | -3.5 | -6.1 | -1.1 | 1.3 | -1.7 | -1.5 | 1.3 | -1.5 | -1.4 |
| opCcV0100000476 | 0.9 | -0.3 | 0.2 | 0.1 | 0 | -0.3 | -0.5 | -0.1 | -0.1 | 0 |
| opCcV0100000478 | 0.8 | 0.7 | 0.8 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0.1 |
| opCcV0100000479 | -2.1 | -1.3 | -0.8 | -0.4 | 0.7 | -0.6 | -0.3 | 0 | -1.8 | 0 |
| opCcV0100000481 | -0.4 | 0.2 | 0.5 | 0.1 | 0 | 0.3 | -0.1 | 0 | 0.2 | 0.1 |
| opCcV0100000484 | 0.2 | 0.1 | 0.4 | 0.3 | -0.1 | 0.4 | 0.5 | -0.3 | 0.4 | 0.2 |
| opCcV0100000492 | 0.3 | 0.4 | 0.3 | -0.1 | -0.2 | 0 | -0.1 | 0.1 | 0.1 | -0.1 |
| opCcV0100000495 | -1.8 | -0.7 | 0.1 | 0 | 0.8 | -0.1 | -0.1 | 0.6 | -1.3 | -0.1 |
| opCcV0100000497 | 0 | -0.2 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0 | 0 |
| opCcV0100000498 | 0.4 | 0.6 | 0.2 | 0 | 0.2 | 0 | 0 | -0.1 | -0.2 | -0.1 |
| opCcV0100000503 | 3.2 | 0.5 | -0.5 | 0 | 1.2 | 1.1 | -1.9 | 1.2 | 1.3 | 0.2 |
| opCcV0100000504 | 0.2 | 0 | 0.5 | -0.1 | 0.1 | 0.2 | -0.1 | 0 | 0.1 | -0.1 |
| opCcV0100000505 | -1.2 | 0 | -0.7 | 0 | 0.4 | -0.2 | -0.4 | -0.1 | -0.5 | 0 |

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| opCcV0100000506 | 3 | 3.1 | 3.2 | 0.9 | -0.8 | 1 | 1.2 | -0.9 | 1.3 | 1 |
| opCcV0100000510 | 0.4 | -0.3 | 0.5 | 0 | -0.1 | 0 | 0.1 | 0.3 | -0.4 | -0.3 |
| opCcV0100000512 | -0.2 | -0.2 | -0.6 | 0 | -0.3 | 0.2 | 0.1 | -0.1 | 0 | 0.1 |
| opCcV0100000513 | -1.4 | -0.6 | -0.2 | -0.2 | 0 | -0.1 | 0.2 | 0.3 | -0.3 | 0 |
| opCcV0100000517 | -0.9 | -0.8 | 0 | 0 | 0.1 | -0.1 | 0 | 0.2 | -0.3 | -0.1 |
| opCcV0100000520 | -0.3 | -0.2 | -0.4 | -0.1 | 0 | 0.2 | -0.1 | -0.1 | 0.2 | 0 |
| opCcV0100000521 | 1.2 | 0.6 | 0.6 | 0.1 | -0.2 | 0.3 | 0.1 | 0 | 0.1 | 0 |
| opCcV0100000530 | -0.1 | 0.1 | -0.1 | -0.1 | -0.1 | 0.4 | 0 | -0.1 | 0.2 | 0.2 |
| opCcV0100000532 | -0.4 | -0.2 | 0.5 | -0.2 | -0.4 | 0.5 | 0.1 | -0.3 | 0.1 | 0 |
| opCcV0100000534 | -0.1 | -0.2 | -0.1 | -0.1 | -0.1 | 0.1 | 0 | -0.2 | 0 | 0 |
| opCcV0100000540 | 0.5 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCcV0100000548 | -1.3 | 0.6 | 0 | 0 | 0.2 | -0.1 | -0.2 | 0.2 | -0.3 | -0.1 |
| opCcV0100000549 | -1.5 | -2.1 | -0.9 | -0.1 | 0 | -0.3 | 0.3 | 1.7 | -2.8 | -0.3 |
| opCcV0100000551 | 0.9 | 0 | 0.7 | 0.4 | 0.7 | -0.9 | 0.2 | 0.7 | 0.5 | 0 |
| opCcV0100000555 | -2.7 | -2.1 | -0.7 | 0 | 0.2 | 0.1 | -0.3 | 0.4 | -0.2 | -0.1 |
| opCcV0100000557 | -0.3 | -0.1 | 0 | 0 | -0.1 | 0.2 | 0 | 0.1 | 0 | -0.1 |
| opCcV0100000559 | 0 | 0 | 0.2 | -0.1 | -0.3 | 0.2 | 0.1 | 0 | 0.1 | 0 |

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| opCcV0100000560.60 | 2.2 | 0.8 | -0.3 | 0.1 | -1.3 | -0.1 | 0.1 | 1.6 | 1.4 | -0.8 |
| opCcV0100000560.80 | 2.1 | -0.1 | -2.1 | -0.5 | 0.4 | -0.6 | -1 | 1.7 | 0 | -2.6 |
| opCcV0100000560.90 | 0.1 | 1.2 | -0.4 | -1.2 | -1 | -0.4 | -1.4 | 0 | -0.3 | -0.3 |
| opCcV0100000561 | -0.4 | 0.2 | -0.3 | -0.1 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0 |
| opCcV0100000562 | -0.2 | -0.2 | -0.2 | -0.3 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | -0.1 |
| opCcV0100000563 | 0.3 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0 | -0.3 | -0.1 | -0.1 |
| opCcV0100000564 | 0.5 | 0.2 | 0.3 | 0.1 | 0.1 | 0 | 0.1 | 0 | -0.1 | -0.2 |
| opCcV0100000567 | 1.1 | 0.7 | 0.8 | 0.3 | -0.2 | 0.4 | 0.2 | -0.2 | 0.3 | 0.2 |
| opCcV0100000568 | 0.2 | -0.1 | 0.2 | -0.1 | 0 | 0.1 | 0 | 0 | -0.1 | 0 |
| opCcV0100000570 | -0.8 | -0.3 | -0.1 | 0.2 | 0.3 | 0 | -0.1 | 0.6 | -0.1 | -0.2 |
| opCcV0100000573 | 0.1 | 0.1 | 0.1 | -0.1 | 0.2 | -0.1 | -0.1 | 0 | -0.1 | -0.2 |
| opCcV0100000574 | 0.8 | 0.9 | -0.6 | 0.2 | -0.5 | 0.1 | 0 | -0.6 | -0.2 | 0.2 |
| opCcV0100000578 | -0.1 | -0.5 | -0.2 | -0.1 | 0 | 0 | -0.1 | 0.2 | -0.1 | -0.2 |
| opCcV0100000581 | 4.4 | 1.4 | 1.3 | -0.5 | -0.6 | -0.2 | 0.4 | -0.5 | 1.1 | -0.8 |
| opCcV0100000583 | 0.4 | -0.1 | -4.6 | 0 | 0.2 | -2 | -2.1 | -1.8 | -0.1 | -0.1 |
| opCcV0100000584 | 1.6 | 2.1 | -2.1 | 0.9 | -1.8 | -0.8 | -1 | -0.2 | 0.9 | -2 |
| opCcV0100000585 | 0 | 0 | -5.4 | 0 | -0.2 | -1.7 | -1.9 | -1.8 | -0.1 | 0 |

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| opCcV0100000588 | 0.2 | -0.2 | 0.5 | 0.1 | -0.1 | 0.1 | 0.3 | -0.1 | -0.1 | 0.1 |
| opCcV0100000589 | -0.4 | 0 | -5.1 | 0 | -0.1 | 0.2 | 0.1 | -1.7 | 0.1 | 0 |
| opCcV0100000590 | -0.4 | -0.1 | -0.1 | 0 | 0 | 0.2 | 0.1 | 0 | 0 | 0 |
| opCcV0100000593 | -1.2 | -0.7 | 0.4 | -0.2 | 0.2 | 0.5 | -0.1 | 0.6 | -0.3 | -0.3 |
| opCcV0100000595 | -0.2 | 0.1 | 0.2 | -0.1 | 0.1 | 0.1 | 0 | -0.2 | 0.1 | 0.1 |
| opCcV0100000596 | -2.7 | -1.1 | 1.2 | -0.1 | 0 | 0.8 | 0.4 | 0.2 | -0.1 | 0.1 |
| opCcV0100000602 | -0.8 | -0.4 | -0.2 | -0.3 | -0.1 | 0.1 | 0 | 0.2 | 0 | 0 |
| opCcV0100000606 | 0.7 | 0.7 | 0.5 | 0.1 | -0.5 | 0.5 | 0.3 | -0.3 | -0.2 | 0.4 |
| opCcV0100000615 | 0.7 | 0.3 | -0.7 | -0.1 | -0.2 | 0.1 | 0.2 | 0 | 0.3 | 0.2 |
| opCcV0100000623 | -4.8 | -4.8 | 0.5 | -1.3 | 1.9 | -1.2 | -1.5 | 1.7 | -1.6 | -1.5 |
| opCcV0100000625 | 0.2 | 0.1 | -1 | 0.1 | 0.1 | -0.7 | -0.9 | -0.6 | -0.1 | -0.1 |
| opCcV0100000627 | -2.4 | 0.9 | -0.9 | 0.2 | -0.3 | 0.3 | 0.5 | -0.2 | 0.1 | 0.2 |
| opCcV0100000628 | 0.3 | 0 | 0.3 | 0 | 0 | 0.1 | 0 | 0.2 | 0 | 0 |
| opCcV0100000630 | 0.1 | -0.2 | 0.4 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.2 | 0 |
| opCcV0100000631 | 0.1 | -0.1 | 0.3 | 0.1 | 0 | 0.1 | -0.1 | 0.2 | 0.1 | 0 |
| opCcV0100000633 | 2.4 | 2.1 | -1.2 | -0.3 | -2.2 | 2.6 | 0.6 | 0.4 | 1.3 | 0.1 |
| opCcV0100000637 | -0.3 | 0 | 0 | 0 | -0.1 | 0.2 | -0.1 | 0 | 0 | 0 |

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| opCcV0100000640 | -4.5 | -3.6 | 0.2 | -0.6 | 1.6 | 0.1 | 0 | 1.6 | -1.3 | -1.5 |
| opCcV0100000643 | 0.1 | 0.1 | -0.1 | -0.1 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| opCcV0100000645 | -1.8 | -0.8 | -0.3 | 0.1 | 0.2 | 0.3 | 0 | 0 | 0.1 | -0.1 |
| opCcV0100000651 | 1.3 | 2 | 1.6 | 0.1 | 0.3 | 0.9 | 0.6 | -1.1 | 1.4 | -0.4 |
| opCcV0100000654 | 0.6 | 0.3 | 0.4 | -0.1 | 0.1 | 0 | 0 | 0.2 | 0 | -0.2 |
| opCcV0100000655 | 0.5 | -0.1 | 0.3 | 0.2 | 0.2 | -0.7 | 0.1 | -0.1 | 0.2 | -0.1 |
| opCcV0100000657 | 0.8 | 0.3 | 0.4 | 0.2 | 0.1 | -1.4 | 0.4 | 0 | -0.1 | 0.1 |
| opCcV0100000658 | -0.3 | -0.4 | -0.2 | -0.1 | 0.1 | 0.2 | -0.1 | 0.1 | 0 | -0.1 |
| opCcV0100000661 | -0.2 | 0 | -0.3 | -0.1 | -0.2 | 0 | 0 | 0 | 0.1 | -0.1 |
| opCcV0100000662 | 0.5 | 0.3 | 0.9 | -0.1 | -0.1 | 0 | 0.1 | -0.2 | -0.1 | -0.1 |
| opCcV0100000664 | 0.5 | -0.3 | -0.1 | 0 | 0 | 0.2 | 0.1 | 0 | 0 | 0 |
| opCcV0100000666 | 0 | -0.2 | -0.1 | -0.1 | 0.2 | -0.2 | 0.1 | -0.1 | -0.1 | -0.2 |
| opCcV0100000672 | 0.9 | 0.6 | 0.7 | 0.2 | 0 | 0 | 0 | -0.3 | 0.3 | 0.1 |
| opCcV0100000674 | -3.4 | -0.7 | -0.3 | -0.2 | 0.1 | 0.1 | -0.2 | 0.6 | -0.2 | -0.3 |
| opCcV0100000681 | 0 | -0.1 | -0.8 | 0 | 0 | -0.1 | -2.4 | 0 | 0.1 | 0 |
| opCcV0100000683 | -0.2 | -0.3 | -0.2 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.3 | -0.1 |
| opCcV0100000684 | 0 | 0 | 1 | -0.1 | -0.1 | 0.2 | 0 | 0.1 | -0.1 | -0.1 |

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| opCcV0100000685 | -0.8 | -1.9 | 2.8 | 0.2 | -0.1 | -0.2 | 0.3 | 0.1 | -0.3 | 0 |
| opCcV0100000691 | -3.3 | -3.5 | 0 | -0.9 | 1 | 0 | -0.6 | 1 | -1.4 | -0.9 |
| opCcV0100000693 | 0.8 | 0.3 | 0.2 | 0.1 | 0.3 | -0.1 | 0 | -0.1 | -0.1 | -0.2 |
| opCcV0100000696 | 2.7 | 1.6 | 1 | 0.3 | -0.8 | 0.4 | 0.7 | 0 | 0.5 | 0.3 |
| opCcV0100000698 | -0.4 | -0.4 | 1.2 | -0.2 | 0 | 0.4 | 0.5 | 0.1 | -0.1 | -0.3 |
| opCcV0100000699 | 0.6 | 0.2 | 0.4 | 0 | -0.2 | 0.3 | 0.2 | 0 | 0.3 | 0 |
| opCcV0100000700 | 0 | -0.5 | -2 | -0.1 | 0 | 0.2 | -0.1 | -0.5 | -0.1 | -0.1 |
| opCcV0100000702 | 0.3 | -0.3 | -0.3 | 0 | 0.1 | -0.4 | -0.5 | 0 | 0.1 | -0.1 |
| opCcV0100000703 | -0.1 | 0 | 0.4 | 0 | 0 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| opCcV0100000704 | -0.8 | -0.7 | -0.5 | -0.1 | 0.3 | -0.2 | -0.1 | 0.1 | -0.1 | -0.2 |
| opCcV0100000707 | 5.1 | 0.5 | -0.3 | -0.3 | 1.9 | -0.6 | -1.4 | 1.8 | -0.8 | -0.2 |
| opCcV0100000708 | 0.7 | -0.2 | 0.4 | 0.1 | 0.2 | 0.2 | 0.1 | 0.3 | -0.3 | -0.1 |
| opCcV0100000710 | -0.7 | -0.5 | 0.2 | -0.1 | 0.4 | -0.3 | 0 | 0.5 | -0.3 | -0.4 |
| opCcV0100000711 | 0.1 | 0 | -3.6 | -0.1 | 0.1 | -1.9 | -2 | -1 | 0.1 | -0.1 |
| opCcV0100000714 | 0 | 0.2 | 0.2 | -0.2 | 0 | 0 | -0.1 | -0.1 | 0.2 | -0.1 |
| opCcV0100000717 | 0.1 | -0.1 | -5.3 | 0 | 0 | -2.2 | -2.4 | -1.7 | 0.3 | 0 |
| opCcV0100000718 | 3.5 | 3.1 | -0.2 | 0.9 | -1.2 | -0.6 | -0.5 | -0.7 | 1.2 | 1 |

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| opCcV0100000719 | 0.6 | 0.4 | -0.5 | 0 | -0.3 | -0.1 | 0 | -0.4 | 0.3 | 0.1 |
| opCcV0100000721 | 4.9 | 3.9 | -0.7 | 1 | -1.9 | 0.5 | 0.9 | -0.7 | 1.2 | 1.1 |
| opCcV0100000723 | -0.8 | -0.2 | -0.2 | 0 | -0.3 | 0.2 | -0.1 | 0.2 | 0.3 | 0 |
| opCcV0100000724 | 0.5 | -0.5 | 1.8 | 0 | -0.1 | 0.1 | 0.1 | 0.3 | 0.1 | 0 |
| opCcV0100000725 | 0.1 | 0.1 | 0.6 | 0 | -0.1 | 0.3 | 0.1 | 0.2 | 0.2 | 0.1 |
| opCcV0100000727 | 1.7 | 1.6 | -0.8 | -0.1 | 0.2 | 0 | -0.1 | 0.6 | -0.8 | -0.3 |
| opCcV0100000730 | 0 | 0.2 | -0.2 | 0 | -0.1 | -0.3 | -0.2 | -0.4 | 0 | -0.1 |
| opCcV0100000733 | 0.2 | 0 | -0.1 | 0 | -0.1 | 0 | 0 | -0.2 | 0 | -0.1 |
| opCcV0100000734 | 0 | 0.1 | 0 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 0 |
| opCcV0100000736 | 0.2 | 0.2 | -0.3 | -0.1 | -0.1 | -0.1 | 0 | 0 | -0.1 | 0 |
| opCcV0100000737 | -1.2 | -0.7 | -0.6 | -0.2 | 0.2 | 0 | -0.3 | 0 | -0.1 | -0.2 |
| opCcV0100000739 | -3.2 | -0.6 | -2 | -0.5 | -0.1 | -0.4 | -1 | 0.3 | 0 | -0.7 |
| opCcV0100000743 | 0.3 | 0 | 0 | 0.1 | 0 | 0.1 | 0 | 0 | 0 | 0 |
| opCcV0100000750 | 0 | -0.4 | 0.1 | 0.1 | 0 | 0.3 | 0.1 | 0.4 | -0.4 | 0 |
| opCcV0100000751 | -0.1 | 0.2 | -1.2 | 0 | -0.2 | 0.2 | -0.1 | -0.1 | 0.2 | 0 |
| opCcV0100000756 | 2.5 | 1.6 | 1.2 | 0.2 | -1.3 | 0.8 | 0.8 | -0.2 | 1.4 | -1.5 |
| opCcV0100000757 | -0.6 | -0.5 | -0.6 | -0.2 | -0.1 | -0.1 | 0 | 0.2 | 0 | -0.1 |

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| opCcV0100000765 | -0.7 | 0.1 | -1.8 | -0.1 | -0.1 | 0.1 | -0.1 | -0.1 | -0.1 | 0.1 |
| opCcV0100000767 | -0.6 | 0.2 | -0.6 | -0.2 | -0.3 | 0.2 | -0.1 | 0 | 0.3 | -0.1 |
| opCcV0100000769 | 0.4 | 0.7 | -0.3 | 0 | -0.3 | 0.4 | 0.1 | -0.1 | 0.2 | 0.1 |
| opCcV0100000770 | -0.4 | -0.4 | 0 | -0.1 | -0.2 | 0.1 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100000778 | 2.7 | 2.2 | 2.5 | 0.6 | -1.3 | 0.9 | 1 | -0.5 | 1 | 0.8 |
| opCcV0100000779 | 1.7 | 1.2 | 1.8 | 0.3 | -0.6 | 0.7 | 0.7 | -0.5 | 0.2 | 0.6 |
| opCcV0100000786 | -0.5 | -0.4 | -0.4 | 0 | 0 | 0.1 | -0.3 | -0.1 | 0 | 0 |
| opCcV0100000787 | 0.4 | 0.5 | 0.4 | 0.1 | -0.1 | 0 | -0.1 | 0 | 0.3 | 0 |
| opCcV0100000788 | 0.5 | -0.1 | 0.7 | 0 | -0.1 | 0.1 | 0.2 | -0.1 | 0 | 0 |
| opCcV0100000795 | -0.2 | -0.1 | -4.3 | 0 | 0 | -1.4 | -1.6 | -1.4 | 0 | 0 |
| opCcV0100000797 | 0.5 | 0.5 | 0.3 | 0.3 | -0.1 | 0.1 | 0.2 | 0 | 0 | -0.1 |
| opCcV0100000801 | -1.5 | -1.4 | -0.4 | 1.6 | 0.7 | -0.5 | -1.2 | 0.8 | -0.4 | -0.5 |
| opCcV0100000806 | 0 | 0.1 | 0 | -0.1 | -0.2 | 0.3 | 0 | -0.1 | 0.2 | 0 |
| opCcV0100000813 | 0.3 | 0.1 | 0.2 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 | -0.1 |
| opCcV0100000814 | -0.9 | -1.4 | 0.5 | 0.1 | 0 | -0.1 | 0 | 0.3 | -0.3 | -0.1 |
| opCcV0100000816 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0.2 | 0.1 |
| opCcV0100000821 | 1.2 | 0.8 | 0.4 | 0 | -0.6 | 0.3 | 0.2 | -0.2 | 0.3 | 0.2 |

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| opCcV0100000826 | -0.4 | -0.7 | 0.5 | -0.1 | 0.3 | 0.1 | 0 | 0.2 | 0.5 | -0.1 |
| opCcV0100000828 | -2.7 | -2.9 | -0.2 | -0.2 | 0.1 | -0.2 | -0.3 | 0.3 | -0.6 | -0.4 |
| opCcV0100000829 | 0.4 | 0.8 | 0.7 | 0 | -0.1 | 0.1 | 0 | -0.2 | 0 | 0 |
| opCcV0100000830 | -0.9 | -0.2 | -3.9 | -0.1 | 0.1 | -1 | -1.3 | -1.4 | 0 | 0 |
| opCcV0100000834 | -0.1 | 0 | -0.4 | 0 | 0 | -0.4 | -0.1 | -0.1 | 0 | -0.1 |
| opCcV0100000835 | 0.8 | 0.6 | -5.4 | 0 | -0.2 | -2.1 | -2.3 | 0 | -0.5 | 0.1 |
| opCcV0100000840 | -0.9 | -0.7 | -0.4 | 0 | 0.3 | 0.2 | 0 | 0 | -0.1 | 0 |
| opCcV0100000845 | -2.1 | -1.3 | -0.6 | -0.2 | 0.2 | 0 | -0.3 | 0.4 | -0.3 | 0.1 |
| opCcV0100000852 | -0.1 | -0.2 | 0 | 0 | 0.1 | 0.2 | 0 | -0.3 | 0 | 0 |
| opCcV0100000853 | 0.1 | -1.2 | -0.3 | -0.4 | 0.6 | 0 | 0.1 | 0.5 | -0.2 | -0.1 |
| opCcV0100000856 | -0.6 | -0.4 | 0.4 | -0.1 | -0.1 | 0.1 | -0.7 | 0 | 0 | 0.1 |
| opCcV0100000857 | 0.5 | 0.2 | 0.3 | 0.1 | 0 | 0.2 | 0.1 | 0 | 0.1 | -0.1 |
| opCcV0100000860 | 1.1 | -0.6 | 0.8 | 0.1 | -0.4 | 0.5 | 0.5 | 0.4 | 0.1 | 0 |
| opCcV0100000861 | 0.4 | 0.3 | -0.4 | 0.2 | -0.3 | -0.2 | 0.1 | -0.3 | 0.2 | 0.1 |
| opCcV0100000864 | 0.2 | 0.2 | 0 | 0.1 | -0.1 | -0.1 | 0 | 0 | 0.1 | -0.1 |
| opCcV0100000865 | 0.2 | 0.1 | -4 | 0 | -0.2 | -1.3 | -1.9 | 0.1 | 0.1 | 0 |
| opCcV0100000867 | -1.6 | 0.2 | 0.2 | -0.1 | 0.4 | 0.2 | 0.4 | 0.4 | -0.9 | -0.3 |

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| opCcV0100000868 | 0 | 0.1 | 0.7 | 0.1 | 0.6 | 0.2 | 0.3 | 0.5 | 0 | 0.1 |
| opCcV0100000873 | 0.3 | 0.1 | 0.5 | 0 | 0.2 | 0 | -0.1 | -0.1 | 0.1 | 0 |
| opCcV0100000875 | -0.7 | -0.7 | -0.4 | -0.1 | -0.1 | 0.1 | -0.3 | -0.1 | -0.2 | -0.2 |
| opCcV0100000877 | -2.2 | -2 | -0.5 | 0 | 0 | 0 | -0.5 | 0.4 | -0.1 | -0.1 |
| opCcV0100000878 | 0.6 | 0.3 | 0.8 | 0.1 | 0.1 | 0.1 | 0.2 | -0.2 | 0 | 0 |
| opCcV0100000879 | -0.8 | -0.6 | -0.4 | -0.1 | 0.1 | -0.4 | -0.7 | 0.3 | -0.7 | -0.2 |
| opCcV0100000882 | -1 | -0.3 | -1.5 | -0.5 | 0 | 0.2 | -0.4 | 0 | 0 | -0.3 |
| opCcV0100000884 | 0 | -0.1 | -0.1 | 0.1 | -1.6 | -0.1 | -0.1 | -0.1 | 0.1 | -0.2 |
| opCcV0100000885 | 0.3 | 0.1 | 0.2 | 0.2 | 0.1 | 0.1 | 0.1 | -0.5 | 0 | 0 |
| opCcV0100000887 | 0.3 | -0.6 | 0.2 | 0.3 | 0.3 | -0.6 | 0 | 0 | -0.1 | -0.2 |
| opCcV0100000888 | 0.3 | 0 | -0.2 | 0 | -0.2 | -1.5 | 0.1 | 0 | 0 | -0.9 |
| opCcV0100000890 | -0.1 | -4.4 | 0.1 | -1.1 | 2.5 | 0.2 | -1 | 1.8 | -1.5 | -2 |
| opCcV0100000894 | 0.3 | 0 | 0.2 | -0.1 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| opCcV0100000895 | 0.4 | 0 | 0.2 | 0.1 | 0.2 | 0 | 0 | 0 | -0.3 | -0.1 |
| opCcV0100000896 | 0.3 | -0.2 | 0.5 | 0 | 0.1 | 0.2 | 0.5 | 0 | -0.3 | 0 |
| opCcV0100000898 | 1.6 | 1.4 | 1.6 | 0.3 | -0.6 | 0.4 | 0.4 | 0 | 0.3 | 0.1 |
| opCcV0100000900 | 0.4 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 0 | 0 |

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| opCcV0100000903 | 0.2 | 0.6 | 0.2 | 0.2 | 0 | -0.1 | 0 | -0.2 | 0 | 0 |
| opCcV0100000904 | 0 | 0.2 | -0.1 | 0 | 0.9 | -2.1 | -2.7 | 0 | 0.2 | -0.1 |
| opCcV0100000905 | -0.5 | -0.3 | 0.1 | -0.1 | -0.3 | 0.3 | 0.1 | -0.1 | 0.1 | 0.1 |
| opCcV0100000908 | 0.2 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0.1 | -0.1 | 0 | -0.1 |
| opCcV0100000909 | 0.5 | 0.1 | -0.7 | 0.1 | 0 | -0.7 | -0.6 | -0.4 | -0.1 | -0.1 |
| opCcV0100000910 | -0.6 | -0.7 | -1 | -0.2 | -0.1 | 0.1 | -0.3 | 0.1 | 0.3 | -0.1 |
| opCcV0100000911 | -0.3 | -0.2 | 0 | 0.1 | 0.2 | 0 | 0.1 | 0.2 | -0.2 | -0.2 |
| opCcV0100000912 | 0.2 | 0 | 0.2 | -0.1 | -0.1 | 0.2 | 0.1 | 0 | 0 | 0 |
| opCcV0100000915 | 0.2 | 0.1 | -4.3 | -0.1 | -0.1 | -1.4 | -2.2 | 0.1 | 0 | 0 |
| opCcV0100000917 | 0.7 | 0.2 | 0.3 | 0 | 0 | 0.3 | 0.4 | 0.2 | -0.2 | -0.2 |
| opCcV0100000918 | 0 | 0 | 0.1 | 0 | -0.1 | 0.2 | 0.1 | 0.1 | -0.1 | 0 |
| opCcV0100000921 | -1 | -0.5 | -3.2 | -0.3 | 0.2 | -2.9 | -3.2 | -0.9 | 0.3 | 0 |
| opCcV0100000922 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0.1 | -0.4 | 0 | 0 | 0.1 |
| opCcV0100000923 | -2.8 | -3.3 | -3.7 | -1.1 | 0.6 | -1 | -1.3 | 0.4 | -0.4 | -1.1 |
| opCcV0100000924 | 0.4 | 0 | 0.3 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0.1 | -0.1 |
| opCcV0100000928 | 0.2 | -0.8 | -1.7 | 0.1 | -0.5 | 0.1 | -0.6 | 0.5 | 0.4 | -0.1 |
| opCcV0100000931 | -1.4 | -1.3 | -0.1 | -0.4 | 2.3 | 0 | 0 | 0.6 | -0.2 | -0.4 |

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| opCcV0100000932 | 0.5 | 0.3 | -0.3 | 0 | -0.4 | 0.1 | 0.2 | -0.2 | 0.1 | 0.1 |
| opCcV0100000934 | -0.3 | -0.3 | -0.3 | 0 | 0 | 0.2 | 0 | -0.1 | -0.1 | -0.1 |
| opCcV0100000937 | 0.3 | 0 | 0.1 | 0 | 0 | 0.1 | 0 | 0 | -0.1 | 0 |
| opCcV0100000943 | 0.5 | 0.2 | 0.2 | 0 | -0.1 | 0 | 0.1 | 0 | 0 | -0.1 |
| opCcV0100000951 | 0.2 | -0.3 | 0.2 | -0.1 | -0.1 | 0.1 | -0.5 | 0.4 | 0 | 0 |
| opCcV0100000954 | -0.1 | -1.4 | 0 | -0.3 | 0 | 0.1 | 0 | 0 | -0.3 | -0.4 |
| opCcV0100000958 | -0.6 | 0.1 | 0 | -0.1 | 0 | 0.1 | -0.1 | -0.3 | 0.4 | 0 |
| opCcV0100000962 | 0.7 | 0.1 | 0.6 | 0 | 0.2 | 0 | 0.2 | 0 | -0.2 | -0.1 |
| opCcV0100000965 | -2.4 | 0.2 | -2 | 0.9 | 0.7 | -1 | 1.6 | 0.7 | -0.2 | 0.1 |
| opCcV0100000966 | -0.9 | -0.7 | -1.2 | -0.1 | 0.3 | -0.4 | -0.7 | 0 | -0.3 | 0.1 |
| opCcV0100000970 | -2.3 | -1.9 | -1.1 | -0.5 | 0.5 | -0.1 | -0.6 | 1 | -0.4 | -0.5 |
| opCcV0100000973 | -0.3 | 0.4 | 0.6 | 0 | 0 | 0.1 | 0 | -0.1 | 0.3 | 0 |
| opCcV0100000975 | 0.3 | 0.1 | -4.3 | -0.1 | -0.2 | -1.3 | 0.1 | 0 | 0.3 | 0 |
| opCcV0100000976 | -0.3 | 0.2 | -0.1 | 0 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0.2 |
| opCcV0100000981 | 0.6 | -0.2 | 0.6 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | -0.3 | -0.1 |
| opCcV0100000987 | -0.9 | -0.4 | 0.1 | 0.2 | 0.6 | -0.4 | 0 | 0.7 | -0.5 | -0.3 |
| opCcV0100000989 | -1.2 | -0.8 | -0.3 | -0.2 | 0.1 | -0.2 | -0.1 | 1 | -0.3 | -0.1 |

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| opCcV0100000996 | -0.1 | 0.4 | 0.8 | 0.4 | -0.7 | 0.3 | 0 | -0.2 | -0.2 | 0.6 |
| opCcV0100000998 | -0.2 | -0.2 | -0.2 | 0.1 | 0 | 0.3 | 0 | -0.1 | 0 | 0.1 |
| opCcV0100000999 | -0.5 | -0.4 | 0.2 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0 |
| opCcV0100001000 | 0.3 | 0.1 | 0.4 | 0 | -0.2 | -0.1 | 0 | 0.2 | -0.3 | 0 |
| opCcV0100001001 | 1 | 0.5 | 0.3 | 0.2 | -0.2 | 0.2 | 0.2 | -0.3 | 0 | 0.1 |
| opCcV0100001004 | 0.2 | 0 | 0.5 | 0 | -0.1 | 0.3 | 0.3 | -0.1 | 0 | -0.1 |
| opCcV0100001007 | -0.2 | -0.3 | -2.5 | -0.1 | 0 | -0.6 | -0.1 | 0 | 0 | 0 |
| opCcV0100001009 | -0.1 | -0.3 | -2.8 | -0.1 | 0.1 | -1.5 | -0.1 | 0.1 | 0.1 | -0.1 |
| opCcV0100001010 | 0 | -0.2 | 0 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCcV0100001011 | 0.3 | -0.2 | 0.1 | 0.2 | 0.2 | -0.1 | 0 | 0.3 | -0.4 | -0.3 |
| opCcV0100001012 | -0.1 | -0.1 | 0.1 | 0 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| opCcV0100001013 | -5.7 | -3.8 | -0.9 | -2.7 | 3.9 | -1.9 | -1.9 | 1 | -3.7 | -1.8 |
| opCcV0100001015 | -0.1 | 0.1 | 0.8 | 0 | 0 | 0.3 | 0.2 | -0.2 | -0.1 | 0.1 |
| opCcV0100001017 | 1.3 | -0.9 | 0.8 | 0.1 | 0.2 | 0.3 | 0.6 | 0.6 | -0.7 | 0 |
| opCcV0100001019 | -0.1 | -0.1 | 0 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0.2 | 0.1 |
| opCcV0100001021 | -0.5 | 0.3 | -0.4 | 0 | -0.1 | -0.1 | -0.1 | 0.2 | 0 | -0.1 |
| opCcV0100001023 | 0 | -1.9 | -0.6 | -0.3 | 0.5 | -0.3 | -0.3 | 0.2 | -0.5 | -0.4 |

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| opCcV0100001025 | -0.1 | -0.5 | 0.1 | 0 | 0.3 | -0.2 | 0 | 0.1 | -0.2 | -0.1 |
| opCcV0100001026 | 1.6 | 0.6 | 0.8 | -0.1 | -1.2 | 0.3 | 0.6 | -1.1 | 1 | -0.4 |
| opCcV0100001029 | -0.5 | -0.8 | -0.5 | -0.1 | 0 | 0.2 | 0 | -0.1 | -0.2 | -0.1 |
| opCcV0100001030 | 0.8 | 0 | 0.4 | 0.1 | 0.1 | 0.2 | 0.3 | 0.1 | -0.2 | -0.1 |
| opCcV0100001032 | 0.4 | 0 | 0.7 | -0.1 | 0.2 | -0.1 | 0 | -1 | -0.2 | -0.2 |
| opCcV0100001034 | -0.1 | 0.1 | -0.5 | -0.2 | -0.1 | -0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCcV0100001037 | -0.8 | -0.3 | -1.7 | -0.2 | 0 | 0.1 | -0.2 | 0.7 | 0 | -0.5 |
| opCcV0100001038 | 0.2 | 0 | 0.2 | 0.1 | 0.1 | 0 | 0.1 | 0.1 | -0.2 | -0.1 |
| opCcV0100001047 | 0.4 | 0.3 | -5.3 | 0.1 | -0.2 | -1.8 | -1.9 | -0.1 | 0.2 | 0.1 |
| opCcV0100001049 | -2.3 | -1.8 | -0.2 | -0.1 | 0.3 | -0.2 | -0.2 | 0.4 | -0.3 | 0.1 |
| opCcV0100001051 | 0.3 | 0 | -0.1 | 0 | 0 | 0 | 0 | 0 | 0 | -0.1 |
| opCcV0100001058 | 0.9 | 0 | -0.1 | 0 | 0.1 | -0.1 | 0.1 | 0.2 | -0.2 | -0.1 |
| opCcV0100001061 | -0.8 | -0.5 | -0.4 | -0.1 | -0.1 | 0.1 | -0.1 | 0 | 0 | -0.1 |
| opCcV0100001062 | 0.2 | -0.1 | 0 | 0.1 | 0.3 | -0.1 | 0 | 0.1 | -0.2 | -0.2 |
| opCcV0100001064 | -0.1 | -0.2 | 0 | -0.1 | 0 | 0.2 | 0 | 0 | 0.2 | 0 |
| opCcV0100001066 | -3.1 | -2.6 | -0.5 | -0.1 | 0 | -0.1 | -0.3 | 0.3 | 1 | -0.1 |
| opCcV0100001071 | -2.6 | -1 | -1.6 | -0.2 | 0 | -0.5 | -1.3 | 0.2 | -0.3 | -0.1 |

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| opCcV0100001072 | 1 | 0.9 | 0.5 | 0.2 | -0.2 | 0.1 | 0.2 | -0.1 | 0.5 | -0.1 |
| opCcV0100001073 | 0.7 | 0.6 | 0.4 | 0.1 | -0.2 | 0.1 | 0.1 | -0.2 | 0.1 | 0 |
| opCcV0100001075 | 0 | 0.1 | 0.2 | -0.1 | -0.1 | 0.2 | 0 | 0.1 | 0.1 | 0 |
| opCcV0100001078 | 0.3 | 0 | 0.1 | -0.1 | 0 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| opCcV0100001079 | 0.3 | 0.1 | 0.3 | 0.1 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100001080 | -0.4 | -0.4 | -0.6 | 0 | 0 | 0.1 | 0 | 0.1 | 0 | -0.1 |
| opCcV0100001081 | 1.2 | -0.1 | 0.1 | 0 | -0.2 | 0 | -0.1 | 0.3 | 0.3 | 0 |
| opCcV0100001082 | 2.8 | 2.6 | 1.8 | 0.7 | -0.7 | 0.2 | 0.4 | -0.4 | 0.4 | 0.4 |
| opCcV0100001086 | 0.1 | 0.1 | -2.7 | -0.2 | 0 | -1 | -1.2 | 0.2 | 0 | -0.1 |
| opCcV0100001089 | 0.7 | 0.3 | 0.6 | 0.1 | 0.1 | -0.1 | 0 | -0.1 | 0.1 | 0 |
| opCcV0100001090 | -3.1 | -0.5 | 1.1 | -0.6 | -0.1 | 0.5 | 0.3 | 1.1 | 0 | -0.5 |
| opCcV0100001098 | 1.4 | 1 | -1.2 | -0.1 | -0.1 | -1.6 | -2.2 | -1.8 | 0.1 | -0.3 |
| opCcV0100001100 | -0.3 | -0.1 | -0.1 | 0 | 0 | 0 | -0.2 | 0.1 | -0.1 | 0 |
| opCcV0100001102 | -0.7 | 0.2 | -0.1 | -0.2 | -0.4 | 0.3 | 0.1 | -0.1 | 0.3 | 0.1 |
| opCcV0100001107 | 0.5 | 0.5 | 0.9 | 0.2 | 0.2 | -0.2 | 0.5 | 0.2 | 0.1 | 0.1 |
| opCcV0100001110 | -4.7 | -3.4 | -0.7 | -1.3 | 1.1 | -1.1 | -1 | 0.8 | -1.3 | -1.2 |
| opCcV0100001111.50 | 2.1 | -0.5 | -0.3 | -1.7 | -0.7 | -1.3 | 0.3 | 0.3 | 1.9 | 0 |

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| opCcV0100001111.70 | 1.6 | 0.7 | -1.2 | 0 | -1.1 | -0.1 | 1.8 | 0.4 | 1.9 | -0.5 |
| opCcV0100001111.90 | 1.3 | 0.5 | -0.6 | 0.2 | -1 | -0.3 | -0.2 | 0 | 1.6 | -0.3 |
| opCcV0100001111.A | -0.5 | 0.1 | -0.7 | -0.2 | 0.5 | 0.2 | -0.1 | 0 | 0.3 | 0 |
| opCcV0100001111 | 0.7 | 0.5 | 0.7 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | 0.3 | -0.1 |
| opCcV0100001112 | 0.2 | 0.2 | 0.3 | 0 | 0.1 | 0 | 0 | 0 | 0 | -0.1 |
| opCcV0100001113 | -0.4 | -0.4 | -0.1 | 0 | 0.1 | 0.1 | -0.6 | 0 | -0.1 | 0 |
| opCcV0100001117 | 0.5 | 0.4 | 0.5 | 0 | 0 | -1.4 | 0 | 0 | 0.1 | -0.1 |
| opCcV0100001120 | -0.1 | -0.1 | -0.3 | 0 | -0.1 | 0.2 | 0.1 | -0.1 | 0.2 | 0 |
| opCcV0100001125 | 0 | -0.3 | -0.1 | -0.3 | -0.1 | 0.1 | -0.1 | 0 | 0.1 | -0.3 |
| opCcV0100001126 | -0.4 | -1 | -1 | 0.2 | 0.1 | 0 | -0.1 | 0.2 | -0.4 | 0.1 |
| opCcV0100001127 | -0.9 | -0.6 | -0.9 | -0.1 | 0 | 0.5 | 0.1 | 0.1 | 0.2 | 0 |
| opCcV0100001129 | -1.9 | -0.3 | -0.5 | -0.2 | 0.3 | -0.2 | -0.4 | 0.1 | -0.4 | -0.4 |
| opCcV0100001135 | -0.8 | -2.3 | 0 | 0 | 0.3 | -1.5 | 0.4 | 0.3 | -1.2 | 0.1 |
| opCcV0100001137 | -1.3 | -1.3 | 0.3 | -0.2 | 0.1 | 0.1 | 0 | 0 | -0.2 | 0 |
| opCcV0100001138 | -1.6 | -0.5 | -0.2 | 0 | -0.1 | 0 | -0.8 | -0.2 | -0.2 | -0.1 |
| opCcV0100001143 | -1.2 | -2.6 | -0.2 | -0.2 | 0.2 | -0.1 | -0.2 | 0.1 | -0.4 | -0.2 |
| opCcV0100001146 | -0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0 |

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| opCcV0100001149 | -0.8 | -0.8 | 0.6 | 0 | 0.2 | 0.1 | 0.2 | 0 | -0.3 | 0 |
| opCcV0100001150 | 0.2 | 0 | -0.2 | -0.1 | 0 | 0 | 0.1 | 0 | 0 | -0.1 |
| opCcV0100001151 | 0 | 0.2 | -4.3 | -0.1 | -0.1 | -1.3 | -1.5 | -1.1 | 0.1 | -0.1 |
| opCcV0100001159 | -0.1 | -0.1 | 0.1 | -0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| opCcV0100001161 | 0.7 | 0.2 | 0.6 | -0.1 | 0 | 0 | 0.1 | -0.1 | 0.1 | 0 |
| opCcV0100001164 | -0.5 | -0.4 | -0.3 | -0.1 | 0.1 | 0 | -0.1 | -0.1 | 0 | 0 |
| opCcV0100001167 | 1.8 | 1.4 | -0.4 | -1.4 | 0.5 | 0 | 0.8 | 0.6 | 1 | -1.3 |
| opCcV0100001169 | 0.3 | -0.2 | 0.2 | 0 | -0.2 | -0.1 | 0.2 | 0.1 | -0.3 | -0.1 |
| opCcV0100001170 | 0.6 | 0.3 | -2.4 | -0.1 | -0.3 | -1.6 | -2.1 | 0 | 0.3 | 0.1 |
| opCcV0100001173 | 1 | 0.5 | 0.6 | 0.1 | -0.1 | 0 | 0.1 | 0.1 | 0 | 0 |
| opCcV0100001174 | -0.9 | -0.7 | -0.7 | -0.1 | 0.2 | 0.1 | 0 | 0.2 | -0.1 | -0.1 |
| opCcV0100001175 | 1.3 | -1.2 | 1.3 | -0.3 | -0.4 | 1 | 0 | 0.5 | -0.2 | 0.3 |
| opCcV0100001190 | 2.1 | -1.2 | 1.8 | -0.2 | 0.5 | 0 | 0.4 | 0.5 | -0.4 | -0.4 |
| opCcV0100001191 | 0.6 | -0.3 | 1.1 | -0.2 | -0.1 | 0.3 | 0.2 | 0.3 | 0.6 | 0 |
| opCcV0100001194 | 0.9 | 0.4 | 0.5 | 0 | 0.1 | -0.2 | 0.1 | 0 | -0.2 | -0.2 |
| opCcV0100001196 | 0.7 | 0.2 | 0.3 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.1 | 0.1 |
| opCcV0100001198 | -1.4 | -0.3 | -0.9 | -0.1 | -0.1 | -0.3 | -0.1 | 0.7 | -0.3 | 0 |

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| opCcV0100001199 | 0.4 | 0.7 | 0.2 | 0 | -0.2 | 0.1 | 0 | 0.1 | 0.1 | 0 |
| opCcV0100001200.70 | 2 | 1.5 | -0.4 | -0.9 | -2.5 | -1.1 | 0.1 | 0.7 | 1.6 | 0.5 |
| opCcV0100001200.A | 0.9 | 1.3 | 0.2 | 0 | -0.8 | 0.4 | 0.5 | 0 | 1 | 0.4 |
| opCcV0100001200.C | 3.5 | 0.5 | -0.2 | -0.6 | -1.3 | -0.5 | -0.5 | 0.5 | 2 | -0.9 |
| opCcV0100001200 | 2.2 | 0.3 | 1 | -0.2 | -0.3 | -0.1 | 0.3 | 0.3 | 0.2 | -0.1 |
| opCcV0100001203 | -1.8 | -0.2 | -0.3 | -0.1 | -0.2 | 0.1 | 0 | 0.3 | 0.1 | 0.3 |
| opCcV0100001204 | -0.8 | 0.1 | -0.2 | 0 | 0 | 0.1 | 0 | -0.3 | 0 | 0 |
| opCcV0100001205 | 0 | 0.1 | 0 | 0 | 0 | 0.2 | 0.1 | 0 | 0.1 | -0.1 |
| opCcV0100001210 | -0.4 | -0.1 | -0.4 | -0.1 | 0 | -0.2 | -0.1 | 0 | 0.2 | 0.1 |
| opCcV0100001212 | -0.3 | -0.2 | 0.4 | -0.1 | 0.1 | -0.2 | 0 | -0.3 | 0.5 | 0 |
| opCcV0100001213 | 0.3 | 0.3 | 0.2 | 0 | 0.3 | 0 | 0 | 0 | 0 | -0.2 |
| opCcV0100001214 | -0.6 | -0.3 | 1.5 | -0.1 | 0.1 | -0.3 | -0.2 | 0.2 | -0.1 | -0.1 |
| opCcV0100001216 | -0.6 | -1 | -1.1 | 0 | 0.2 | -0.7 | -0.4 | -0.3 | 0 | -0.1 |
| opCcV0100001219 | -0.5 | -0.2 | -0.3 | -0.1 | 0 | 0.3 | -0.1 | 0.1 | 0 | 0 |
| opCcV0100001221 | -2.5 | -1.8 | -0.9 | -0.3 | 0.4 | 0.3 | 0 | 0.8 | -0.2 | -0.4 |
| opCcV0100001222 | 0.7 | 0.3 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | 0 | 0 | -0.1 |
| opCcV0100001223 | 0.2 | -0.1 | 0.7 | -0.1 | -0.2 | 0 | 0 | 0 | -0.1 | 0 |

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| opCcV0100001225 | -0.7 | 0.1 | -1.2 | 0 | -0.4 | 0.2 | -0.1 | -0.1 | 0.3 | 0.1 |
| opCcV0100001231 | -2 | 0.4 | -0.5 | 0 | 0 | -0.3 | -0.5 | -0.5 | 0.1 | 0.1 |
| opCcV0100001232 | -5.2 | -5 | -1.1 | -0.8 | 1.6 | -1.3 | -1.5 | 0.5 | -1.7 | -0.8 |
| opCcV0100001233 | -0.7 | -0.7 | -0.3 | 0.1 | 0.3 | -0.2 | -0.1 | -0.3 | 0 | 0.1 |
| opCcV0100001236 | -0.8 | -0.8 | -3.4 | -0.4 | 0.2 | 0.2 | -0.2 | -0.5 | -0.5 | -0.3 |
| opCcV0100001238 | 0.8 | 0.9 | 0.9 | 0 | -0.3 | 0.2 | 0.2 | -0.2 | 0.4 | 0 |
| opCcV0100001240 | 0.4 | 0.9 | 0.4 | 0.3 | -0.1 | 0.2 | 0.3 | -0.1 | 0 | 0.2 |
| opCcV0100001242 | 0.3 | 0.2 | 0 | 0 | -0.1 | 0 | 0.2 | 0 | 0 | 0 |
| opCcV0100001244 | 0.2 | 0.1 | 0.4 | -0.1 | -0.1 | 0.2 | 0.1 | -0.1 | -0.2 | 0 |
| opCcV0100001246 | 0.6 | 0.4 | 0.2 | 0 | 0.1 | -0.1 | 0 | -0.1 | -0.2 | -0.1 |
| opCcV0100001248 | -2.6 | -1.9 | -1.5 | -0.6 | 0.9 | -0.1 | -0.2 | 0.2 | -0.5 | -0.6 |
| opCcV0100001251 | -0.8 | -0.7 | 0.3 | -0.4 | 0.4 | -0.2 | 0 | 0.4 | -0.2 | -0.3 |
| opCcV0100001252 | 0.3 | 0.1 | -0.1 | 0 | 0 | 0 | 0.1 | 0.1 | 0 | -0.1 |
| opCcV0100001255 | -0.2 | 0 | -3.5 | -0.1 | 0.1 | -0.9 | 0 | -0.1 | 0.2 | 0.1 |
| opCcV0100001260 | 1 | 0 | 1.3 | 0.2 | 0.7 | 0.4 | 0.3 | -0.1 | 0 | 0.1 |
| opCcV0100001261 | -0.7 | -0.6 | 0.1 | -0.3 | 0.2 | 0.2 | -0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100001263 | 1.1 | -0.8 | 0.7 | 0.4 | 0 | 0.3 | 0.3 | 0.4 | 0.4 | 0.2 |

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| opCcV0100001264.60 | 3.3 | 1.7 | 0.6 | 0.4 | -1.7 | 0.1 | 0.4 | 0.9 | 0.9 | -0.4 |
| opCcV0100001264.70 | 1.9 | 1.2 | -0.9 | -0.9 | -1.6 | 0.2 | 0.5 | 1.6 | 2.5 | -1.2 |
| opCcV0100001264.80 | 2.3 | 6.5 | -1 | 0.8 | -0.4 | -0.8 | 4 | 0.6 | 0.1 | 0.6 |
| opCcV0100001264.90 | -1 | -1.2 | -1.3 | -0.1 | 0.3 | 0.1 | 0.3 | -0.2 | -0.3 | -0.3 |
| opCcV0100001264.A | -2.7 | -2.2 | -4.5 | -0.5 | 1 | 0.2 | 0.2 | 0.2 | -0.1 | -0.4 |
| opCcV0100001264 | -1.5 | -2.2 | -3.2 | -0.2 | 0.9 | -0.1 | 0.5 | 0 | -0.4 | -0.2 |
| opCcV0100001265 | 1 | -3 | 0 | -0.7 | 1 | 0.2 | -0.1 | 1.9 | 0.2 | -0.9 |
| opCcV0100001266 | 0.3 | 0.2 | 0.9 | 0 | 0.1 | 0.3 | 0.4 | 0.2 | -0.1 | -0.1 |
| opCcV0100001268 | 1.1 | 0.7 | 0.6 | 0.1 | -0.2 | 0.2 | 0.3 | -0.1 | 0.1 | 0.1 |
| opCcV0100001270 | -1.9 | -0.8 | -0.3 | -0.1 | -0.1 | 0.1 | -0.1 | 0.1 | -0.1 | 0 |
| opCcV0100001271 | -0.5 | 0 | 0.3 | -0.1 | -0.1 | 0 | 0.1 | 0.1 | 0.2 | 0 |
| opCcV0100001272 | -1.2 | -0.7 | -0.2 | 0.2 | 0.4 | -0.3 | 0.2 | 0.4 | -0.7 | 0 |
| opCcV0100001273 | -0.1 | 0.2 | 0.1 | -0.1 | -0.4 | 0.2 | 0 | -0.1 | 0.1 | 0.1 |
| opCcV0100001275 | 0.7 | 1.4 | 0.5 | -0.1 | 0.7 | 0.7 | -0.4 | 1.4 | -0.6 | 0.3 |
| opCcV0100001276 | 0.3 | 0 | 0.1 | -0.1 | 0 | 0.2 | 0 | 0 | 0 | 0 |
| opCcV0100001278 | 1.5 | -0.3 | 1.8 | 0.1 | 0.2 | 0.7 | 0.2 | 0.5 | 0.8 | 0.3 |
| opCcV0100001279 | -1 | -0.6 | -2.7 | 0 | 0.1 | 0 | 0 | -1.2 | 0 | -0.1 |

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| opCcV0100001281 | -1.9 | -2.1 | -1 | 0 | 1.2 | -0.1 | -0.3 | 0.3 | -0.6 | -0.2 |
| opCcV0100001286 | 0.2 | 0 | 0.3 | 0.1 | 0.1 | 0.1 | -0.1 | 0.2 | 0.1 | 0 |
| opCcV0100001288 | -0.1 | 0.2 | -0.2 | -0.1 | -0.2 | 0.2 | -0.2 | 0 | 0.1 | 0.2 |
| opCcV0100001290 | 1.5 | -0.5 | -0.1 | 0.3 | 0.1 | 0 | 0 | 0 | -0.3 | 0.3 |
| opCcV0100001291 | 2.8 | 1.5 | 1.5 | 0.2 | -0.9 | 0.5 | 0.6 | -0.2 | 0.6 | 0.3 |
| opCcV0100001292.50 | 3.1 | 1.3 | -0.9 | -2.1 | 0.2 | -0.1 | 0.5 | 0.7 | -0.4 | -1.4 |
| opCcV0100001292.90 | 0 | -0.1 | -0.1 | -0.2 | 0.1 | -0.3 | -0.9 | -1 | 0.1 | -0.1 |
| opCcV0100001292.A | -0.1 | 0 | -0.1 | -0.1 | 0 | 0.1 | 0 | -0.8 | 0.1 | 0 |
| opCcV0100001292.C | 3.1 | 1.1 | 0 | -0.7 | 0.4 | 0.1 | 0.4 | 1.2 | 2.2 | -1.9 |
| opCcV0100001292 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0 | -0.1 | -0.6 | 0 | -0.1 |
| opCcV0100001294 | 0.6 | 0.7 | 0.2 | 0.1 | -0.4 | 0.2 | 0.1 | -0.1 | 0.1 | 0.1 |
| opCcV0100001295 | -0.9 | -0.5 | -0.3 | -0.2 | 0.1 | 0.1 | -0.1 | 0 | -0.2 | -0.1 |
| opCcV0100001297 | 0.4 | -0.5 | 0.2 | 0.1 | 0.2 | -0.1 | -0.1 | 0.2 | -0.2 | -0.1 |
| opCcV0100001299 | 0.4 | 0.1 | 0.4 | 0.3 | -0.1 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| opCcV0100001302 | -0.2 | -0.3 | -0.1 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | 0 |
| opCcV0100001305 | -0.7 | -0.9 | -0.7 | 0.2 | -0.2 | -0.2 | -0.2 | 0.7 | -1.2 | -0.1 |
| opCcV0100001307 | -0.2 | -0.2 | 0.2 | 0 | 0 | 0.2 | -0.1 | -0.1 | 0.2 | 0.1 |

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| opCcV0100001308 | -0.1 | -0.3 | 0.1 | 0 | 0.3 | 0 | 0 | 0 | -0.1 | -0.1 |
| opCcV0100001309 | -3.1 | -3.3 | -1.1 | -1.2 | 1.1 | -0.6 | -1 | 1.7 | -1.5 | -1.3 |
| opCcV0100001310 | -0.1 | -0.3 | 0.3 | -0.1 | 0.1 | 0 | 0 | 0.1 | -0.2 | -0.1 |
| opCcV0100001311 | -0.4 | -0.2 | -0.7 | -0.1 | -0.2 | -0.2 | -0.2 | 0 | 0.2 | -0.1 |
| opCcV0100001316 | 0.5 | 0.3 | -2.9 | 0.1 | -0.2 | -1 | -1.3 | -0.1 | 0 | 0 |
| opCcV0100001319 | -4.3 | -1.7 | -4.5 | -0.3 | 0.5 | -0.6 | -1.1 | -0.9 | -0.3 | -0.4 |
| opCcV0100001320 | 0.2 | -0.2 | 0.5 | 0 | 0.2 | 0.3 | 0.3 | 0.1 | 0.1 | -0.1 |
| opCcV0100001322 | 1.8 | 0.7 | 1.8 | 0.3 | -1 | 0.7 | 0.8 | -0.4 | 0.7 | 0.6 |
| opCcV0100001324 | 1.7 | 1.3 | 1.4 | 0.3 | -0.6 | 0.5 | 0.6 | -0.4 | 0.7 | 0.5 |
| opCcV0100001325 | -0.1 | -0.3 | 0.2 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | -0.2 | -0.2 |
| opCcV0100001326 | 0.1 | 0.4 | 0.2 | -0.2 | -0.4 | 0.3 | 0 | 0 | -0.1 | -0.1 |
| opCcV0100001327 | 0.5 | -0.2 | 0.5 | 0.1 | 0 | -0.1 | -0.1 | 0 | 0 | -0.1 |
| opCcV0100001332 | -0.6 | -0.4 | 0.2 | -0.1 | 0 | -0.1 | 0.3 | 0.1 | -0.1 | 0 |
| opCcV0100001340 | -0.1 | 0 | 0.1 | -0.1 | -0.1 | -0.1 | -0.1 | 0.1 | -0.3 | -0.1 |
| opCcV0100001341 | -0.4 | -0.8 | 2.5 | 0.2 | 1.2 | 1 | 1.4 | 0.3 | -0.2 | 0.2 |
| opCcV0100001344 | -0.2 | -0.6 | 0.5 | 0.1 | 0.3 | 0.1 | 0.3 | 0.3 | -0.3 | -0.1 |
| opCcV0100001345 | -0.3 | 0.3 | 0.1 | 0 | -0.3 | 0 | -0.4 | 0.2 | -0.2 | 0 |

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| opCcV0100001347 | 0.7 | 0.3 | 0.1 | 0 | -0.1 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCcV0100001353 | 0 | 0 | -6.5 | 0 | 0 | 0.1 | -0.1 | -1.9 | 0.1 | 0 |
| opCcV0100001356 | 0.1 | -1.3 | -0.5 | 0.1 | 0.3 | -0.1 | -0.1 | 0.4 | -0.7 | -0.1 |
| opCcV0100001357 | 0.4 | 0.4 | 0.1 | 0 | 0 | 0 | -0.1 | 0 | 0.1 | 0 |
| opCcV0100001358 | 0.4 | 0.4 | 0.5 | 0.1 | -0.2 | -0.3 | 0.2 | -0.1 | -0.1 | -0.1 |
| opCcV0100001361 | 0.7 | -0.9 | 0.3 | 0 | 0.2 | -0.1 | 0.2 | 0.7 | -0.3 | -0.2 |
| opCcV0100001367 | 1.7 | 1.6 | 0.4 | -2 | -1 | 0.2 | -0.5 | 0.1 | 1.2 | -1.6 |
| opCcV0100001370 | 0.5 | 0.3 | 0.5 | 0 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100001371 | -0.2 | -0.4 | 0.2 | 0.1 | 0.2 | -0.2 | 0.2 | -0.1 | -0.2 | -0.1 |
| opCcV0100001377 | 0.2 | 0.1 | 0.4 | 0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100001378 | 0.5 | 0.1 | 0.3 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCcV0100001381 | 0.7 | 0.4 | 0.4 | 0.2 | 0 | 0 | 0 | -0.1 | 0 | 0.1 |
| opCcV0100001383 | -0.5 | -0.2 | 0.5 | -0.1 | 0.2 | 0 | 0 | 0.2 | -0.1 | -0.1 |
| opCcV0100001389 | 0 | 0.1 | 0.3 | 0 | 0.1 | 0.2 | 0 | 0.2 | -0.1 | 0 |
| opCcV0100001390 | -0.6 | -0.5 | -0.5 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCcV0100001394 | -0.2 | -0.3 | 0.1 | -0.2 | -0.1 | 0.2 | -0.2 | 0.1 | 0 | -0.1 |
| opCcV0100001395 | -0.5 | -0.2 | -7.4 | -0.1 | -0.1 | 0.2 | 0 | -1.7 | 0.1 | 0 |

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| opCcV0100001399 | -1.1 | 0 | 0.6 | 0.1 | 0.1 | 0.3 | 0.2 | 0.2 | -0.6 | 0 |
| opCcV0100001402 | 0.3 | -0.1 | 0.3 | 0 | 0.2 | 0.1 | -0.4 | -0.4 | 0.1 | 0 |
| opCcV0100001404 | -0.2 | -0.5 | 0.7 | 0 | 0.2 | -0.1 | 0.1 | 0.2 | -0.2 | -0.2 |
| opCcV0100001406 | 0.9 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 | 0 |
| opCcV0100001411 | -5.4 | -4.1 | -4.3 | -0.3 | 2.7 | -1.4 | -2.1 | 2 | -1.5 | -1.6 |
| opCcV0100001414 | -0.1 | -0.4 | 0.5 | 0.1 | 0.3 | 0.3 | 0.3 | 0.7 | -0.1 | -0.2 |
| opCcV0100001415.80 | -0.8 | -0.5 | 0.2 | -0.1 | -0.3 | -1 | -1.1 | 0.2 | -0.4 | -0.1 |
| opCcV0100001415.90 | 0.1 | -0.2 | -0.2 | -0.1 | -0.1 | -0.2 | -0.2 | 0 | -0.1 | -0.1 |
| opCcV0100001415.A | -0.8 | -0.4 | -0.8 | -0.1 | 0 | 0 | -0.3 | 0.1 | 0.1 | -0.1 |
| opCcV0100001415.C | 1.3 | 1 | -0.2 | 0 | -1.1 | -0.7 | -0.2 | -0.3 | 1 | -0.1 |
| opCcV0100001415 | 0.3 | 0 | 0 | 0 | 0 | -0.1 | -0.1 | 0 | -0.1 | -0.2 |
| opCcV0100001418 | 0.2 | 0 | 0.4 | 0 | -0.1 | 0.2 | 0 | -0.1 | -0.1 | 0 |
| opCcV0100001421 | -0.8 | 0 | 0 | -0.1 | -0.1 | 0 | -0.3 | -0.1 | 0.1 | 0 |
| opCcV0100001423 | 0.3 | 0.2 | 0.3 | 0.2 | 0 | 0.1 | 0 | 0 | 0.1 | -0.1 |
| opCcV0100001424 | 1.5 | 0.5 | 2.5 | 0.5 | -0.7 | 0.2 | 0.6 | -0.4 | 0.5 | 0.5 |
| opCcV0100001425 | -0.3 | -0.2 | 0.9 | -0.1 | -0.1 | 0.3 | 0.3 | 0.4 | 0 | -0.1 |
| opCcV0100001431 | 2.1 | -1.5 | 1.3 | -0.1 | 0.2 | 0.5 | 0.1 | 0.6 | 0.3 | 0 |

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| opCcV0100001432 | -5.2 | 0.4 | -2.6 | -0.8 | 0.7 | -1.2 | -1.1 | 0.6 | -1.2 | -0.5 |
| opCcV0100001435 | 0.6 | 0.4 | 0.3 | 0 | -0.3 | 0.3 | 0.2 | -0.1 | 0.2 | 0 |
| opCcV0100001437 | -0.6 | -0.5 | -1.2 | -0.2 | 0.2 | -0.1 | 0 | 0.1 | -0.2 | -0.2 |
| opCcV0100001440 | 0.3 | 0 | 0 | 0 | 0.2 | -0.1 | 0 | 0.1 | -0.2 | -0.2 |
| opCcV0100001442 | 1.1 | -1.2 | 0.5 | -0.1 | 0.2 | -0.2 | -0.5 | -0.2 | -0.9 | -0.2 |
| opCcV0100001444 | -0.8 | -0.8 | -0.2 | -0.2 | 0.1 | 0.1 | -0.4 | 0.6 | -0.1 | -0.2 |
| opCcV0100001446 | 0.5 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | -0.1 | -0.2 | 0 | -0.1 |
| opCcV0100001448 | -1.1 | 0.4 | 0.5 | 0 | 0.1 | 0 | 0 | 0.1 | 0.2 | 0 |
| opCcV0100001449 | 0.3 | 0.1 | 0.5 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.1 |
| opCcV0100001451 | 2.2 | -0.2 | 0.4 | 0.4 | 0.3 | 0 | -0.5 | 0.9 | -1.5 | -0.2 |
| opCcV0100001452 | 0 | -0.2 | -0.6 | -0.1 | 0.1 | -0.5 | 0.2 | -0.3 | -0.1 | 0 |
| opCcV0100001453 | 0.2 | 0 | 0.3 | 0 | 0.1 | 0.2 | 0.2 | 0 | -0.1 | 0 |
| opCcV0100001454 | -0.6 | -1.3 | -0.1 | -0.1 | 0.3 | 0.1 | -0.3 | -0.2 | 0.2 | 0 |
| opCcV0100001455 | 0.5 | 0.3 | 0.2 | 0.1 | 0 | -0.1 | 0.2 | -0.1 | 0 | -0.1 |
| opCcV0100001456 | 0 | -0.1 | 0 | -0.1 | -0.1 | 0 | 0 | 0 | 0 | -0.2 |
| opCcV0100001459 | 2.2 | 0.9 | -0.1 | 0.2 | -0.4 | -0.4 | -0.5 | -0.2 | 0.2 | 0.4 |
| opCcV0100001461 | -4.1 | -0.4 | -0.3 | 0 | 0.2 | -0.2 | -0.3 | 0.5 | -0.3 | -0.2 |

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| opCcV0100001462 | -0.1 | -0.7 | -0.3 | -0.2 | 0.1 | 0 | -0.5 | 0.3 | -0.2 | -0.2 |
| opCcV0100001465 | -0.2 | -0.1 | 0.1 | -0.1 | 0 | -0.1 | 0 | -0.5 | 1 | -0.1 |
| opCcV0100001466 | -0.8 | -0.5 | -1.8 | 0 | 0 | 0.1 | -0.1 | 0.1 | 0 | -0.1 |
| opCcV0100001467 | 0.2 | 0 | 0.1 | 0 | -0.1 | 0 | 0 | -0.1 | 0 | -0.1 |
| opCcV0100001471 | -1.8 | -1.3 | 0.2 | -0.3 | 0.1 | -0.2 | 0.4 | 0.3 | -0.6 | -0.4 |
| opCcV0100001476 | -0.9 | -0.6 | 0.3 | -0.1 | 0 | -0.2 | 0 | 0.3 | -0.1 | -0.1 |
| opCcV0100001479 | -0.8 | -0.3 | 0.1 | 0 | 0 | 0 | 0.1 | 0.1 | -0.2 | -0.2 |
| opCcV0100001480 | -2.3 | -0.2 | -0.1 | -0.4 | -0.1 | 0.1 | -0.1 | 0.6 | -0.5 | -0.4 |
| opCcV0100001482 | -0.6 | -0.3 | 0.5 | 0 | 0.1 | 0.2 | 0 | -0.4 | 0.1 | 0 |
| opCcV0100001483 | 0.3 | 0 | 0.2 | 0 | 0 | 0 | 0.1 | -0.1 | 0 | -0.1 |
| opCcV0100001488 | -0.8 | -1.5 | -0.8 | -0.2 | 0.6 | -0.3 | -0.5 | 0.6 | -0.3 | -0.2 |
| opCcV0100001489 | 0.9 | -0.2 | 1.9 | 0.5 | 0 | 0.2 | 0.8 | -0.1 | 0.2 | 0.5 |
| opCcV0100001493 | -0.6 | -1.6 | -0.3 | 0 | 0 | 0 | 0 | 0.1 | 0.1 | 0.1 |
| opCcV0100001498 | 2.1 | 1.7 | 0.2 | 0.6 | -0.8 | 0 | -0.1 | -0.5 | 0.7 | 0.5 |
| opCcV0100001501 | -0.7 | -0.3 | -1 | -0.1 | 0 | -0.6 | -0.3 | 0 | 0.1 | -0.1 |
| opCcV0100001504 | -0.2 | 0 | -0.5 | -0.1 | 0 | -0.9 | -0.3 | -0.5 | -0.3 | 0.2 |
| opCcV0100001513 | -1.3 | -1.1 | 0.9 | 0 | 0.4 | 0.1 | -0.2 | 0.1 | -0.5 | -0.3 |

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| opCcV0100001515 | -1.4 | -0.9 | -0.5 | 0 | 0.3 | 0.1 | -0.6 | 0.5 | -1.4 | -0.1 |
| opCcV0100001519 | -1.7 | -1.5 | -1 | -0.4 | 0.3 | -0.1 | -0.2 | 0 | -0.4 | -0.1 |
| opCcV0100001521 | -0.4 | -0.9 | -2.3 | -0.2 | -0.4 | -0.2 | -0.4 | -0.1 | -0.3 | -0.1 |
| opCcV0100001522 | -0.1 | -0.6 | 0 | -0.3 | -0.1 | 0.2 | -0.1 | 0.3 | -0.2 | -0.3 |
| opCcV0100001526 | 0.7 | -0.4 | 0.6 | 0 | -0.3 | 0.2 | -1 | 0.1 | 0.1 | 0 |
| opCcV0100001528 | -0.8 | 0.2 | 0 | 0 | 0 | -0.1 | -0.1 | 0 | -0.1 | -0.1 |
| opCcV0100001535 | 0.1 | -1.1 | -1.1 | 0 | 0.3 | 0 | -0.4 | 0.2 | -0.3 | 0 |
| opCcV0100001536 | 0 | -1.2 | 0 | 0 | 0.3 | 0 | 0 | 0.3 | -1.3 | 0 |
| opCcV0100001537 | 1.2 | 1.1 | -0.1 | 0.2 | -0.2 | -0.1 | 0.1 | -0.4 | 0.3 | 0.2 |
| opCcV0100001538 | 0 | -0.2 | -0.3 | -0.1 | -0.1 | 0.2 | -0.1 | -0.1 | -0.2 | -0.1 |
| opCcV0100001540 | -0.7 | -0.7 | -0.3 | 0 | 0.2 | -0.1 | -0.4 | -0.3 | -0.1 | 0 |
| opCcV0100001541 | -1.4 | 1.5 | 0.9 | 0.1 | 0 | 0 | 0.3 | 0.6 | -0.3 | 0 |
| opCcV0100001543 | 0 | 0.3 | 0 | 0.1 | -0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0.1 |
| opCcV0100001549 | -0.5 | -0.5 | -0.3 | 0 | 0.4 | -0.2 | -0.3 | 0.3 | 0.8 | -0.1 |
| opCcV0100001553 | 0.6 | 0.2 | 0.4 | 0.1 | -0.1 | 0 | 0 | 0 | 0 | 0 |
| opCcV0100001554 | 0.5 | 0.2 | 0.2 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | 0 |
| opCcV0100001559 | -1.6 | -3.3 | -0.3 | 0.1 | 0.3 | 0.4 | 0.1 | 0.1 | 0.2 | -0.1 |

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| opCcV0100001561 | 0.5 | 0 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0.1 | 0 | -0.1 |
| opCcV0100001563 | -0.2 | 0 | -0.5 | 0 | 0 | 0 | -0.1 | 0 | 0.1 | -0.3 |
| opCcV0100001566 | 0.2 | -0.6 | 1.3 | 0.4 | 0.4 | 0.1 | -1 | 0.2 | -0.2 | -0.1 |
| opCcV0100001567 | 0.1 | -0.2 | -0.2 | -0.1 | -0.1 | 0.1 | -0.1 | -0.2 | -0.7 | 0 |
| opCcV0100001569 | -1.7 | -0.1 | -0.4 | -0.2 | -0.1 | -0.4 | -0.2 | 0.1 | -0.3 | 0 |
| opCcV0100001570 | 0.1 | 0 | 0 | -0.1 | 0 | 0.1 | -0.2 | -0.3 | 1.2 | 0 |
| opCcV0100001572 | 0 | 0 | 0.2 | 0 | 0.2 | 0.1 | -0.1 | 0 | -0.1 | -0.1 |
| opCcV0100001578 | 0.1 | 0.2 | 0.1 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 | 0 |
| opCcV0100001583 | -0.3 | -0.4 | 0 | -0.2 | -0.2 | 0.1 | -0.1 | 0.2 | 0 | -0.1 |
| opCcV0100001584 | 0.3 | -0.1 | 0 | 0 | 0 | 0 | 0.1 | 0 | 0 | 0 |
| opCcV0100001587 | -0.5 | -0.9 | -0.3 | 0 | 0.1 | 0.3 | -0.2 | 0.2 | -0.1 | 0 |
| opCcV0100001592 | 0.1 | -0.2 | 0.8 | 0 | 0.1 | -0.1 | 0.1 | 0.1 | 0.3 | -0.1 |
| opCcV0100001594 | 0.7 | 0.2 | 0.4 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 | -0.1 |
| opCcV0100001598 | -0.8 | 0.2 | 0.4 | -0.2 | -0.1 | 0.2 | 0 | 0.2 | 0.4 | 0.1 |
| opCcV0100001599 | -0.3 | -0.3 | -0.4 | 0.2 | 0.1 | -0.1 | -0.2 | 0 | 0.1 | -0.1 |
| opCcV0100001602 | 0.4 | 0 | -0.4 | -0.1 | -0.2 | -0.1 | 0.1 | 0.1 | 0 | 0 |
| opCcV0100001606 | 1.7 | 0.9 | 0.4 | 0.2 | 0.4 | 0.1 | -0.1 | -0.1 | 0.1 | 0.1 |

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| opCcV0100001607 | -2.9 | -3.6 | -0.2 | 0 | 0.3 | -0.5 | 0 | 0.8 | -1 | -0.2 |
| opCcV0100001610 | 0.2 | -0.6 | -0.9 | 0.1 | 0.2 | -0.4 | -0.9 | 0.3 | -0.1 | -0.2 |
| opCcV0100001611 | 0.4 | 0 | -0.2 | 0 | 0 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| opCcV0100001614 | 0.2 | -0.5 | 0 | -0.2 | 0.2 | 0 | -0.2 | 0.1 | -0.2 | -0.2 |
| opCcV0100001619 | 0.1 | 0.1 | 0 | -0.1 | 0.7 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| opCcV0100001620 | 0.2 | 0 | 1.2 | 0 | 0.1 | 0.2 | 0.1 | -0.1 | 0 | 0 |
| opCcV0100001622 | -2.8 | -2.8 | -2 | -0.4 | 0.3 | -0.2 | -0.7 | 1 | -1.3 | -0.5 |
| opCcV0100001623 | 0.7 | 0.4 | 0.9 | 0.2 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 |
| opCcV0100001624 | -0.8 | -1.3 | 0.5 | 0.1 | -0.5 | 0.1 | -0.2 | 0.2 | -0.4 | 0 |
| opCcV0100001625 | -0.4 | -0.1 | 0.6 | 0 | 0 | -0.2 | -0.3 | -0.1 | -0.2 | -0.1 |
| opCcV0100001629 | -0.3 | -0.4 | -0.1 | -0.2 | -0.2 | 0.1 | -0.2 | 0.2 | 0.2 | 0.1 |
| opCcV0100001630 | 0.4 | 0 | 0.2 | -0.1 | 0 | -0.1 | -0.1 | 0.2 | 0.1 | 0.1 |
| opCcV0100001631 | 0.2 | 0.5 | 0.8 | 0 | -0.6 | 0.2 | 0.2 | -0.2 | 0.2 | 0.2 |
| opCcV0100001634 | -0.8 | -1.6 | 2 | 0.2 | 0.3 | 0.3 | 0.2 | 0.4 | 0.2 | 0.6 |
| opCcV0100001635 | 0.3 | 0.2 | 0.3 | 0 | 0 | 0 | -0.1 | -0.2 | 0.1 | 0.1 |
| opCcV0100001636 | -0.2 | 0 | -0.2 | 0 | -0.1 | 0.2 | -0.1 | -0.1 | 0.1 | 0 |
| opCcV0100001639 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 | 0 | -0.2 | -0.1 |

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| opCcV0100001640 | -0.5 | -1.9 | 0 | 0 | 0.2 | -0.1 | -0.5 | 0.8 | 0.2 | 0 |
| opCcV0100001641 | 0.1 | -0.2 | 0.6 | 0 | 0 | -0.7 | 0 | 0 | 0 | -0.1 |
| opCcV0100001644 | -1.8 | -1.4 | -1.4 | -0.1 | -0.2 | 0.2 | 0.1 | 0.1 | -0.3 | 0 |
| opCcV0100001647 | 0.1 | 0.1 | -0.1 | 0 | -0.2 | 0.1 | 0 | 0.1 | 0.1 | 0 |
| opCcV0100001649 | -0.9 | -0.4 | -0.3 | -0.2 | -0.1 | 0.1 | -0.1 | 0 | 0 | 0 |
| opCcV0100001653 | 0.4 | 0.3 | 0.7 | 0 | -0.2 | 0.1 | 0 | 0.2 | -0.1 | 0 |
| opCcV0100001654 | 0.5 | 0 | 0.5 | -0.1 | -0.2 | 0.2 | 0.3 | 0 | -0.2 | 0 |
| opCcV0100001655 | 1.4 | -1.2 | -0.1 | 0.1 | -0.2 | 0.1 | 0.6 | -0.1 | 0.6 | 0.5 |
| opCcV0100001656 | 0.4 | -0.1 | 0.5 | 0 | 0 | -0.1 | 0.1 | 0 | 0.1 | -0.1 |
| opCcV0100001657 | -0.3 | 0 | 0.4 | 0 | -0.1 | 0 | -0.1 | 0.1 | -0.2 | -0.2 |
| opCcV0100001658 | 0 | 0 | 0 | 0.1 | 0 | 0 | -0.2 | -0.2 | 0.2 | -0.1 |
| opCcV0100001659 | 0.7 | 0.4 | 1.2 | 0 | 0 | 0.5 | 0.6 | 0.6 | -0.2 | 0 |
| opCcV0100001660 | 0.2 | 0 | 0 | 0.1 | 0.1 | -1.6 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100001664 | -0.3 | -0.3 | 0 | -0.1 | 0.1 | 0.5 | -0.2 | 0.3 | -0.1 | -0.1 |
| opCcV0100001676 | 0.5 | 0.4 | 0.1 | -0.1 | -0.1 | 0 | 0 | 0.1 | 0.2 | 0 |
| opCcV0100001678 | -0.5 | -0.4 | 0.7 | 0 | 0 | 0.5 | 0.4 | 0.1 | 0 | 0 |
| opCcV0100001679.70 | 2.4 | 1.5 | 0.7 | 0 | -0.3 | 0.5 | -0.7 | 0.3 | 0.2 | -0.2 |

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| opCcV0100001679.80 | 1.5 | 0.8 | 0.2 | 0 | 0.1 | 0.9 | 0.4 | 0.6 | 1 | 0 |
| opCcV0100001679.90 | 2.7 | 0.5 | -0.2 | 0.9 | 0.6 | -0.6 | 0.5 | 1.1 | 0 | -0.9 |
| opCcV0100001679.A | -0.1 | 0.3 | -0.6 | 0 | -0.1 | 0 | 0 | -0.2 | 0.2 | 0.1 |
| opCcV0100001679 | 0.9 | 0.6 | 0 | 0.2 | 0.1 | -0.5 | -0.3 | -0.5 | -0.2 | 0 |
| opCcV0100001680 | 0.4 | 0.3 | 0.7 | 0 | -0.2 | -0.1 | 0.2 | 0.1 | 0.1 | -0.1 |
| opCcV0100001682 | 0 | -0.3 | -0.6 | 0 | 0.1 | -0.3 | -0.3 | 0 | 0.2 | 0 |
| opCcV0100001684 | -1.7 | -1.8 | -0.2 | 0 | 0 | -0.1 | -0.3 | 0.5 | -0.8 | -0.2 |
| opCcV0100001686 | 0.5 | 0.3 | 0.5 | -0.1 | 0 | 0 | -0.2 | 0 | 0.3 | 0.1 |
| opCcV0100001688 | 0.8 | 0.5 | 0.6 | 0.2 | 0 | 0.4 | 0.3 | -0.1 | 0 | 0 |
| opCcV0100001689 | 0 | -0.1 | -0.6 | 0 | 0 | -0.2 | -0.7 | 0 | 0.1 | 0.1 |
| opCcV0100001691 | 0 | 0 | 0.3 | -0.1 | 0 | 0.1 | -0.1 | -0.1 | -0.2 | 0 |
| opCcV0100001692 | 0.3 | -0.1 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0.1 | 0.1 | 0 |
| opCcV0100001694 | 1.7 | -0.6 | 0.2 | -1.2 | 0.6 | -0.5 | 0.9 | 1 | 0.2 | 0 |
| opCcV0100001695 | -0.5 | -0.4 | -0.2 | 0 | 0 | 0 | -0.1 | 0 | -0.1 | -0.1 |
| opCcV0100001698 | -0.1 | 0 | -0.1 | 0 | -0.1 | 0.2 | 0.2 | 0 | 0 | 0 |
| opCcV0100001702 | 0.1 | -0.3 | 0 | 0 | 0 | 0 | -0.2 | -0.1 | -0.1 | -0.1 |
| opCcV0100001703 | -0.5 | -0.9 | -1 | -0.1 | -0.1 | -0.4 | -0.6 | -0.1 | 0 | -0.1 |

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| opCcV0100001709 | -1 | 0 | -0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0.2 | 0.1 | -0.1 |
| opCcV0100001710 | 1.3 | 1 | -2.3 | 0.4 | -0.4 | 0.2 | 0 | -1 | 0.5 | 0.3 |
| opCcV0100001711 | 0.1 | 0 | 0.2 | -0.1 | -0.1 | -0.1 | -0.1 | 0 | -0.1 | 0 |
| opCcV0100001712 | -0.7 | -1.2 | 0 | 0 | 0.3 | -0.1 | -0.1 | -0.1 | -0.4 | -0.2 |
| opCcV0100001724 | -0.2 | -0.2 | 0 | -0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.2 |
| opCcV0100001727 | 0.7 | -0.2 | 0.1 | 0 | 0.1 | -0.2 | 0.1 | 0.7 | -0.1 | -0.2 |
| opCcV0100001728 | 0.1 | -0.1 | -0.2 | 0 | -0.1 | 0.2 | 0 | 0 | 0.2 | 0 |
| opCcV0100001729 | 0 | 0 | -0.3 | 0 | -0.2 | 0.1 | 0 | -0.1 | -0.1 | -0.1 |
| opCcV0100001730 | 0.3 | 0.1 | 0.1 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0.1 |
| opCcV0100001733 | 1.4 | 0.3 | 0.4 | 0.1 | -0.3 | 0 | 0.1 | -0.3 | 0.3 | 0.1 |
| opCcV0100001737 | 0 | -0.1 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0 | -0.1 | 0 |
| opCcV0100001738 | 0 | 0 | 0 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 |
| opCcV0100001739 | -0.4 | 0 | -0.4 | 0 | -0.1 | 0 | -0.3 | 0 | 0.3 | 0 |
| opCcV0100001741 | 0.2 | 0.3 | -4.4 | 0 | -0.1 | -1.8 | -2.1 | 0 | 0.2 | 0 |
| opCcV0100001742 | -0.2 | -0.6 | 0 | -0.3 | 0 | 0.2 | -0.5 | 0.4 | -0.2 | 0 |
| opCcV0100001743 | -0.6 | -0.3 | -0.8 | -0.1 | 1.9 | 0.2 | -0.1 | -0.1 | 0.1 | -0.1 |
| opCcV0100001745 | -4.7 | -3.7 | -3.6 | -1 | 1.5 | -1.1 | -1.3 | 1.2 | -1 | -1.3 |

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| opCcV0100001748 | -0.3 | -0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 | 0.2 | -0.1 | -0.1 |
| opCcV0100001750 | 0.2 | -0.1 | 0.3 | 0 | 0.1 | 0 | -0.1 | -0.2 | 0 | -0.1 |
| opCcV0100001753 | 0.1 | -0.1 | 0 | -0.1 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100001754 | -0.4 | -4 | -3.9 | -1.4 | 1.8 | 0.2 | -0.2 | 1.2 | -1.6 | -1.5 |
| opCcV0100001758 | -1.5 | -1.8 | -0.3 | 0 | 0.4 | -0.1 | -0.8 | -0.2 | -2 | 0.2 |
| opCcV0100001762 | -0.2 | 0 | -0.5 | 0 | 0.1 | 0 | -0.1 | 0 | 0.1 | -0.2 |
| opCcV0100001763 | -0.9 | -0.7 | -4.9 | -0.1 | 0.1 | 0.1 | -0.2 | -1.2 | 0.3 | -0.2 |
| opCcV0100001764 | -0.5 | -0.2 | -1.1 | 0.1 | -0.1 | -0.3 | -0.5 | 0.2 | -0.7 | -0.1 |
| opCcV0100001765 | -1.5 | 0 | 0.2 | -0.1 | 0.5 | 0.1 | -0.5 | 0.4 | -0.2 | 0 |
| opCcV0100001767 | 0.1 | -0.4 | 1.5 | 0.2 | 0.3 | 0.3 | 0.7 | 0.4 | -0.4 | -0.1 |
| opCcV0100001768 | -1 | -0.8 | -1.1 | -0.1 | 0.2 | 0 | -0.1 | 0.2 | 0 | -0.2 |
| opCcV0100001769 | -1.1 | -0.6 | -1.1 | -0.1 | 0.2 | -0.1 | -1.1 | 0.1 | -0.3 | -0.3 |
| opCcV0100001770 | -0.4 | -0.4 | 0.1 | -0.3 | -0.1 | 0.3 | 0.1 | 0.2 | -0.2 | 0 |
| opCcV0100001771 | 0.4 | -0.3 | -0.1 | 0.1 | 0 | 0 | 0 | 0.3 | -0.1 | -0.1 |
| opCcV0100001774 | -2.8 | 4.4 | 2.7 | -0.1 | -1.3 | -0.3 | 0.7 | 0.5 | 1.2 | -0.5 |
| opCcV0100001776 | 0 | 1.4 | 1.2 | -0.1 | -0.7 | 0 | 0.5 | 0.1 | -0.2 | -0.1 |
| opCcV0100001778 | 0.4 | -3.3 | -3.3 | 0.1 | 1.5 | -0.1 | -1.2 | 0.1 | 0 | -0.2 |

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| opCcV0100001780 | 0.1 | 0.2 | 0.2 | 0 | 0 | -0.3 | -0.1 | 0 | 0.1 | 0.1 |
| opCcV0100001781 | 0.1 | 0 | -3.7 | 0 | 0 | 0 | -1.7 | 0 | 0.2 | 0 |
| opCcV0100001782 | 0.8 | 0.4 | 0.6 | 0.4 | 0 | -0.3 | 0.1 | 0.7 | -0.5 | 0 |
| opCcV0100001783 | -0.6 | -0.2 | -0.1 | -0.2 | -0.1 | 0.1 | 0 | 0 | 0.2 | 0 |
| opCcV0100001784 | 0.7 | 0.5 | 0.9 | 0 | 0 | 0.1 | 0.3 | 0 | -0.1 | 0 |
| opCcV0100001786 | -0.1 | -0.2 | -0.2 | 0.1 | 0 | -0.1 | -0.1 | -0.1 | 0 | -0.2 |
| opCcV0100001787 | -5.4 | -4.9 | -3.9 | -1.4 | 1.6 | -1.2 | -1.7 | 1.4 | -1.8 | -1.4 |
| opCcV0100001788 | 0.2 | -0.1 | -0.1 | 0 | 0 | -1.6 | -1.6 | -0.1 | 0 | 0 |
| opCcV0100001793 | -0.6 | -0.6 | -1.7 | 0 | 0.1 | -0.2 | -0.5 | -0.3 | -0.1 | -0.1 |
| opCcV0100001795 | -0.3 | -0.4 | 0 | -0.1 | 0.2 | -0.5 | -0.1 | 0.3 | -0.3 | -0.1 |
| opCcV0100001796 | 0.4 | 0.4 | 0.3 | -0.4 | -0.3 | -0.8 | 0.2 | 0.3 | -0.3 | -0.2 |
| opCcV0100001797 | 1 | 1 | 0.2 | -0.4 | -0.6 | 1 | 0.8 | -0.4 | 0.9 | 0.1 |
| opCcV0100001800 | -0.3 | -0.1 | -0.3 | -0.2 | -0.2 | 0.1 | 0 | 0 | -0.1 | -0.2 |
| opCcV0100001801 | -1.5 | -1.1 | 0.1 | 0.1 | 0.3 | -0.1 | -0.1 | -0.1 | -0.4 | -0.5 |
| opCcV0100001802 | -0.5 | -0.5 | -0.4 | -0.2 | -0.1 | 0.1 | -0.4 | 0.1 | 0.2 | -0.1 |
| opCcV0100001806.50 | 4.1 | 1 | -0.6 | -1.3 | -0.1 | 0.1 | -0.9 | 0.6 | 0.8 | 1 |
| opCcV0100001806.60 | 1.7 | 1.8 | -0.3 | 0.5 | -1.7 | -1 | 0.8 | 0 | 0 | 0.4 |

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| opCcV0100001806.90 | 0.3 | -0.1 | 0.5 | 0 | 0 | -0.1 | 0.3 | 0.1 | 0.3 | -0.2 |
| opCcV0100001806.A | -0.4 | 0.1 | -0.6 | -0.1 | 0 | 0 | 0 | 0.1 | 0.2 | -0.2 |
| opCcV0100001806 | 0.6 | 0.1 | 0.4 | 0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100001808 | -2.4 | -0.9 | -1.1 | -0.5 | 0 | 0.4 | -0.1 | 0.6 | -0.3 | 0 |
| opCcV0100001809 | 0.5 | 0.2 | 0.2 | -0.1 | -0.2 | 0.2 | 0 | -0.2 | -0.1 | 0 |
| opCcV0100001810 | -1.7 | 1.5 | -0.1 | -0.1 | -0.2 | 0 | 0.1 | 0.5 | -1 | 0.3 |
| opCcV0100001812 | 0.7 | 0.2 | 0.4 | 0.1 | 0 | 0.2 | 0 | -0.1 | 0 | -0.1 |
| opCcV0100001813 | -0.8 | -0.1 | 0.7 | -0.3 | 0 | 0.2 | 0.3 | 0.6 | 0.2 | -0.1 |
| opCcV0100001815 | 2.8 | 0.5 | -0.9 | -0.3 | 2 | -0.4 | -0.9 | 0.9 | -0.8 | -0.1 |
| opCcV0100001822 | -0.1 | 0 | -0.1 | 0 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 |
| opCcV0100001823 | -0.7 | -0.5 | 0 | 0 | -0.1 | 0 | -0.2 | -0.1 | -0.1 | -0.1 |
| opCcV0100001824 | 0.7 | 0.2 | 0.7 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCcV0100001825 | -0.3 | -0.6 | -1.5 | -0.3 | -0.1 | 0.1 | 0 | 0.1 | 0 | 0 |
| opCcV0100001830 | -0.7 | -0.6 | -0.4 | -0.1 | 0.1 | 0.2 | -0.2 | 0 | -0.2 | -0.2 |
| opCcV0100001833 | 1.2 | -0.8 | -2.5 | 0.1 | 0.7 | -0.4 | -0.1 | 0.8 | -1.4 | 0.3 |
| opCcV0100001835 | 0 | -0.1 | -0.6 | 0 | 0.2 | 0.1 | -0.2 | -0.2 | -0.1 | -0.1 |
| opCcV0100001836 | -0.3 | -0.2 | 1 | 0.2 | 0.1 | 0.4 | 0.2 | 0.1 | -0.1 | 0.3 |

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| opCcV0100001837 | 0.4 | 0.5 | 0.5 | 0.1 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | -0.2 |
| opCcV0100001838 | -0.2 | -0.1 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100001839 | -0.6 | -0.6 | -0.7 | -0.1 | 0 | 0.1 | -0.2 | 0.1 | -0.1 | -0.1 |
| opCcV0100001840 | 1.4 | 2.1 | 0.3 | 0.2 | -0.9 | 0.5 | 0.7 | -0.3 | 0.3 | 0.2 |
| opCcV0100001842 | 0 | -0.2 | -5.8 | -0.1 | 0.1 | -0.1 | -0.1 | -1.9 | -0.2 | -0.1 |
| opCcV0100001843 | 0.9 | -1.4 | -0.1 | -0.2 | -0.2 | 0 | -0.2 | 0.4 | -0.3 | 0 |
| opCcV0100001847 | -0.9 | -0.6 | 0 | -0.1 | -0.1 | 0.3 | -0.1 | 0 | 0 | -0.1 |
| opCcV0100001848 | 0.1 | 0 | -0.4 | -0.1 | 0.1 | -0.2 | -0.3 | 0.1 | -0.1 | -0.1 |
| opCcV0100001850 | 0.5 | 0.4 | 0.1 | 0 | -0.1 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCcV0100001857 | -1 | -1 | -4.3 | 0.4 | 0.4 | -0.4 | -1.3 | -1.4 | 0.3 | 0.1 |
| opCcV0100001858 | -0.7 | -0.1 | -0.8 | -0.3 | -0.2 | 0.1 | -0.2 | 0 | 0.3 | -0.1 |
| opCcV0100001859 | 0.4 | 0.8 | 0.6 | -0.2 | -0.2 | 0.1 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100001862 | -1.1 | 0 | -0.1 | 0 | -0.1 | 0.1 | 0 | 0.1 | 0 | 0 |
| opCcV0100001863 | 0.3 | 0.2 | -0.4 | 0 | 0 | -1.7 | -2.4 | 0.1 | 0.1 | -0.1 |
| opCcV0100001865 | -0.1 | -0.1 | -0.5 | 0 | 0.1 | 0 | -0.3 | -0.1 | -0.1 | -0.1 |
| opCcV0100001868 | 1.1 | 0.4 | 1.1 | 0.1 | 0.3 | -0.2 | 0 | 0.1 | -0.1 | -0.1 |
| opCcV0100001871 | 0.9 | 0.3 | 0.6 | -0.2 | -0.2 | 0.2 | 0.1 | 0 | 0 | 0 |

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| opCcV0100001874 | 0.4 | -0.2 | -1 | -0.3 | 0.1 | -0.3 | -0.4 | 0.5 | 0.2 | -0.3 |
| opCcV0100001875 | 0.5 | -0.1 | 0.5 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0 | -0.2 |
| opCcV0100001877 | 1.3 | 0.6 | 0.9 | 0 | -0.1 | 0.3 | 0.3 | -0.1 | 0 | 0 |
| opCcV0100001879 | 1.1 | 1.3 | 0.7 | 0.2 | -0.5 | -0.1 | 0 | -0.8 | 0.7 | 0.2 |
| opCcV0100001883 | 2 | 0.6 | 4.5 | -0.4 | -1 | 0.2 | 0.2 | -1.1 | 1.1 | 0.2 |
| opCcV0100001885 | -0.7 | -0.2 | -0.1 | -0.3 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | -0.1 |
| opCcV0100001886 | 0 | -0.1 | -0.5 | -0.1 | 0 | 0 | 0 | 0.1 | -0.1 | -0.2 |
| opCcV0100001889 | 0.3 | 0 | 0.2 | 0 | 0.2 | 0 | 0 | 0.2 | -0.2 | -0.2 |
| opCcV0100001890 | -0.3 | -0.2 | -3.6 | -0.1 | -0.1 | -0.9 | -1.6 | 0 | 0 | -0.1 |
| opCcV0100001891 | 0.1 | -0.1 | 0 | -0.3 | -0.3 | -0.3 | 0 | 0 | 0 | 0 |
| opCcV0100001893 | 1.2 | 0.7 | 0.7 | 0 | -0.3 | 0.1 | 0.2 | 0.2 | 0 | -0.1 |
| opCcV0100001939 | 0.7 | -2.6 | 0.1 | -0.8 | 0.9 | -0.7 | -1 | 3.8 | 1.5 | -1 |
| opCcV0100001985 | 0.1 | -0.1 | -0.2 | -0.1 | -0.1 | 0.1 | -0.8 | -0.1 | 0.1 | -0.1 |
| opCcV0100001986 | 0.4 | -0.4 | 0.4 | 0 | -0.1 | 0.1 | 0.3 | 0 | -0.1 | 0.1 |
| opCcV0100001989 | 1.1 | -0.4 | 1.4 | -0.2 | -0.4 | 0.2 | 0.2 | 0.3 | 0 | 0 |
| opCcV0100001990 | -1 | -0.8 | -0.6 | 0 | 0.6 | -0.1 | 0.4 | 0 | -0.6 | 0 |
| opCcV0100002002 | 0.2 | -0.3 | 0.4 | 0.1 | 0.2 | 0.3 | 0.3 | 0.1 | -0.1 | 0 |

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| opCcV0100002009 | 0.7 | -1.4 | 1.1 | -0.1 | -1 | -0.1 | 0.2 | 1.6 | 1.2 | -1.3 |
| opCcV0100002077 | 0.1 | -1.1 | 0.2 | -0.8 | -1.1 | -0.2 | -1.6 | -0.2 | 0 | -3.1 |
| opCcV0100002088 | 0 | -0.1 | -0.2 | 0.1 | 0 | -0.6 | 0 | 0.1 | 0.1 | -0.1 |
| opCcV0100002089 | 0.3 | 0.2 | 0 | 0 | 0 | 0 | 0 | 0.2 | 0 | -0.2 |
| opCcV0100002090 | -0.9 | -0.9 | -0.6 | -0.2 | 0 | 0 | -0.4 | 0.3 | -0.3 | -0.1 |
| opCcV0100002091 | -0.3 | 0 | -4.6 | -0.1 | -0.1 | -0.1 | -0.1 | -1.4 | 0.2 | 0 |
| opCcV0100002092.50 | 1.1 | -0.7 | 0 | -1.9 | -1.4 | 0.3 | -0.4 | 0.1 | 1.9 | -1.5 |
| opCcV0100002092.70 | 7.6 | 1.3 | -0.1 | -0.7 | -1.5 | 0.1 | 0.3 | 0.5 | 0.1 | -0.1 |
| opCcV0100002092.80 | 2.4 | 1.6 | -0.5 | -1.1 | -2 | 0.3 | -0.4 | 0.6 | 0.6 | -0.5 |
| opCcV0100002092 | 2.1 | 0.5 | -0.4 | 1.1 | 0.2 | -0.3 | 0.3 | 1.2 | 0.3 | -1.4 |
| opCjjV010000001 | 0.4 | 0.3 | 0 | 0.1 | 0 | 0 | -0.2 | -0.1 | 0.1 | 0 |
| opCjjV010000003 | 0.1 | 0.2 | 0.4 | 0 | 0.2 | 0.1 | -0.2 | -0.2 | -0.1 | -0.1 |
| opCjjV010000004 | 0.4 | 0.2 | 0.5 | 0.2 | 0.2 | 0 | -0.1 | 0 | 0.1 | -0.1 |
| opCjjV010000005 | -0.3 | 0.2 | 0.2 | 0.1 | -0.2 | 0.1 | 0.1 | 0 | 0.1 | 0.1 |
| opCjjV010000006 | 0.2 | 0.1 | 0.2 | 0 | 0 | 0 | 0 | 0.2 | -0.1 | -0.1 |
| opCjjV010000007 | 0.3 | 0.1 | 0.4 | 0 | 0 | 0.2 | 0.2 | -0.1 | -0.1 | 0 |
| opCjjV010000008 | 0.2 | 0.1 | 0.1 | 0.1 | -0.2 | -0.1 | 0 | -0.1 | 0.1 | -0.2 |

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| opCjjV010000009 | 0.5 | 0.2 | 0.4 | 0.2 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjjV010000010 | 0.3 | 0 | 0.2 | 0 | 0 | 0 | -0.1 | -0.1 | 0 | 0 |
| opCjjV010000011 | 0 | 0.1 | 0.3 | 0.2 | 0.2 | -0.2 | -0.1 | 0 | -0.1 | -0.1 |
| opCjjV010000013 | 0 | -0.1 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCjjV010000014 | -1.5 | 0 | -0.4 | -0.1 | -0.2 | -0.1 | -0.2 | 0.1 | 0.1 | 0.1 |
| opCjjV010000016 | 0.4 | 0.4 | 0.3 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjjV010000017 | 0.4 | 0.6 | 0.4 | 0 | -0.1 | 0 | -0.1 | 0 | 0 | 0 |
| opCjjV010000021 | 0.1 | 0.1 | 0.4 | -0.1 | 0 | 0.1 | 0.1 | -0.1 | 0.1 | 0 |
| opCjjV010000022 | -0.4 | 0 | -0.2 | -0.1 | -0.2 | 0.2 | -0.1 | 0 | 0.1 | 0 |
| opCjjV010000023 | 0.3 | -0.4 | 0.7 | 0 | 0 | -0.1 | -0.2 | 0.2 | -0.5 | 0 |
| opCjjV010000024 | 0.2 | 0.2 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | 0.1 | 0.1 |
| opCjjV010000025 | 0.5 | 0.2 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCjjV010000026 | 0.4 | 0.6 | 0.5 | 0 | 0.1 | -0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjjV010000027 | 0.4 | 0.3 | 0.4 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0.1 |
| opCjjV010000028 | -0.3 | -0.3 | -3.1 | 0 | 0.1 | 0.4 | -0.1 | -1.4 | 0.2 | 0 |
| opCjjV010000030 | 0 | 0.1 | -0.2 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0 |
| opCjjV010000031 | -0.5 | 0.1 | 0.2 | -0.1 | -0.2 | 0.2 | 0 | -0.1 | 0 | 0 |

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| opCjjV010000032 | 0.7 | 0.5 | 0.7 | 0.2 | 0 | -0.1 | 0 | 0 | 0 | 0 |
| opCjjV010000034 | -0.1 | 0.1 | -1.3 | 0 | 0 | -0.6 | -0.5 | -0.5 | 0 | 0.1 |
| opCjjV010000035 | 0.1 | -0.2 | -0.1 | 0.1 | 0.1 | 0.2 | 0 | 0 | -0.3 | 0 |
| opCjjV010000036 | 0 | 0.1 | 0.1 | -0.1 | -0.2 | 0 | 0 | 0 | -0.1 | 0.1 |
| opCjjV010000038 | -0.2 | 0.3 | -0.3 | 0.1 | -0.1 | 0 | -0.2 | 0 | 0.3 | 0 |
| opCjjV010000039 | -0.4 | -0.1 | -1.2 | 0.4 | 0.2 | -0.7 | 0 | -0.6 | 0.6 | -0.3 |
| opCjjV010000041 | -0.8 | -0.5 | 0.1 | 0.1 | 0 | 0.3 | 0.1 | 0.1 | 0 | 0.1 |
| opCjjV010000046 | 0.3 | 0.3 | 0.5 | 0 | 0.1 | -0.2 | -0.1 | 0 | 0.1 | -0.1 |
| opCjjV010000047 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 | 0 | -0.1 | 0 |
| opCjjV010000049 | 0.5 | 0.3 | 0.6 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 1.2 | 0 |
| opCjjV010000050 | -0.6 | -0.2 | -0.5 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0.1 | 0 |
| opCjjV010000051 | 0.2 | 0.3 | 0.3 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0 | 0 |
| opCjjV010000052 | 0.7 | 0.6 | 0.8 | 0.1 | 0.1 | -0.1 | 0.1 | 0.1 | 0.1 | 0 |
| opCjjV010000055 | -0.1 | 0 | -0.2 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0 | 0.1 |
| opCjjV010000058 | 1.1 | 1.1 | 1 | 0.1 | -0.4 | 0.2 | 0.2 | -0.1 | 0.2 | 0 |
| opCjjV010000060 | 0.8 | 0.4 | 0.5 | 0.2 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 |
| opCjjV010000061 | 0.2 | 0.1 | 0.2 | 0 | -0.1 | -0.1 | 0 | 0.2 | 0.2 | -0.1 |

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| opCjjV010000062 | 0.1 | 0 | 0 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 0 |
| opCjjV010000064 | 0.8 | 0.3 | 0.5 | 0.2 | -0.1 | 0 | 0.1 | 0 | 0.1 | 0.2 |
| opCjjV010000065 | -0.5 | 0.1 | -0.2 | -0.1 | -0.3 | 0.3 | 0 | 0 | 0.2 | 0.1 |
| opCjjV010000066 | 0.4 | 0.4 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | 0 | -0.1 |
| opCjjV010000067 | 0.9 | 1.4 | 0.9 | 0.1 | 0 | -0.2 | 0 | 0 | 0.2 | 0 |
| opCjjV010000068 | 0.5 | 0.2 | 0.5 | 0 | 0.1 | 0 | 0 | -0.1 | -0.2 | -0.1 |
| opCjjV010000070 | 0.1 | 0.4 | 0.2 | 0.1 | -0.1 | 0 | 0 | 0 | 0.3 | 0.1 |
| opCjjV010000071 | -0.3 | 0 | -0.4 | -0.1 | -0.1 | 0.2 | -0.1 | -0.1 | -0.1 | -0.1 |
| opCjjV010000073 | 1 | 1.1 | 0.7 | 0.3 | 0 | 0 | 0.1 | -0.2 | 0.1 | 0.1 |
| opCjjV010000074 | -0.4 | -0.1 | 0.2 | 0 | 0 | 0.2 | 0 | -0.1 | 0 | 0.2 |
| opCjjV010000075 | -0.1 | -0.2 | -0.3 | -0.1 | 0 | 0 | -0.3 | 0.1 | 0 | -0.2 |
| opCjjV010000076 | 0.4 | -0.1 | 0.4 | 0 | 0 | 0.3 | 0 | -0.1 | -0.1 | 0.1 |
| opCjjV010000078 | 0.2 | 0.2 | 0.5 | 0 | 0.1 | 0 | 0.1 | -0.1 | 0.1 | -0.1 |
| opCjjV010000080 | 0.6 | 0.4 | 0.5 | 0 | -0.2 | 0.1 | -0.2 | 0 | 0.3 | 0.1 |
| opCjjV010000081 | -0.1 | 0.1 | -0.1 | -0.1 | -0.1 | 0.2 | 0 | 0 | 0.2 | 0 |
| opCjjV010000082 | 5.1 | 4.8 | 3 | 1.4 | -2.1 | 0 | 1.7 | -0.3 | 1.3 | 1.4 |
| opCjjV010000083 | 0.5 | 0.4 | 0.1 | 0.1 | -0.1 | -0.1 | 0 | 0 | 0 | -0.1 |

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| opCjjV010000084 | 0.3 | 0 | 0.1 | 0 | 0 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCjjV010000085 | 0.7 | 0.3 | 0.4 | 0.1 | 0.1 | -0.1 | 0 | 0 | -0.1 | -0.2 |
| opCjjV010000087 | -0.6 | -0.2 | -0.8 | -0.2 | 0 | 0.3 | -0.1 | 0 | 0.2 | -0.1 |
| opCjjV010000088 | 0.4 | 0.6 | 0.3 | 0.1 | -0.3 | 0 | 0.1 | 0.1 | 0.2 | -0.1 |
| opCjjV010000089 | 1.1 | 0.8 | 0.9 | 0 | -0.2 | 0.1 | 0.2 | 0.1 | 0 | 0 |
| opCjjV010000091 | 0 | -1.6 | 0.5 | 0 | 0.7 | 0.1 | 0.1 | 0.2 | 0 | 0 |
| opCjjV010000092 | 0.3 | 0.3 | 0.4 | 0.1 | 0 | 0 | 0.1 | -0.1 | 0.2 | 0 |
| opCjjV010000093 | -0.1 | 0.3 | -0.7 | -0.1 | -0.2 | 0 | -0.1 | -0.1 | 0.2 | 0.1 |
| opCjjV010000094 | 0.7 | 0.4 | 0.6 | 0.1 | 0.2 | 0 | 0.1 | 0 | 0.1 | -0.1 |
| opCjjV010000095 | 0.2 | 0.3 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | -0.1 |
| opCjjV010000098 | 0.3 | 0.3 | 0.3 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 | -0.1 |
| opCjjV010000099 | 0.3 | 0.3 | 0.3 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 | 0.1 | 0 |
| opCjjV010000100 | 0.9 | 0.4 | -2.9 | 0.2 | 0 | 0.1 | 0.1 | -1.1 | 0.2 | 0.1 |
| opCjjV010000101 | -0.2 | 0 | 0.1 | 0 | 0.2 | 0.2 | -0.1 | 0 | 0.2 | 0.1 |
| opCjjV010000102 | 0.1 | 0.1 | 0.2 | -0.1 | -0.3 | 0.2 | 0.1 | -0.1 | 0.2 | 0.1 |
| opCjjV010000103 | -0.1 | 0.2 | -0.1 | 0 | -0.2 | 0.2 | 0 | -0.1 | 0.1 | 0.1 |
| opCjjV010000104 | 0 | -0.1 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | -0.3 | 0 | -0.1 |

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| opCjjV010000105 | -0.1 | 0.2 | -0.2 | -0.2 | -0.3 | 0.2 | -0.1 | 0.2 | 0.3 | 0.1 |
| opCjjV010000108 | 0.3 | 0.6 | 0.1 | -0.1 | -0.3 | 0.2 | 0.1 | -0.1 | 0.1 | 0 |
| opCjjV010000109 | -0.3 | 0 | -0.4 | -0.2 | -0.4 | 0 | -0.1 | 0 | 0 | -0.1 |
| opCjjV010000110 | 0 | 0.3 | 0 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | 0.2 | -0.2 |
| opCjjV010000115 | 0.2 | 0.1 | 0.4 | -0.1 | -0.1 | 0.1 | 0 | 0 | 0 | 0 |
| opCjjV010000117 | -0.3 | 0 | -0.2 | -0.1 | -0.1 | 0.3 | -0.1 | -0.1 | 0.1 | 0.1 |
| opCjjV010000119 | 0 | 0 | -0.5 | 0 | 0.1 | -0.1 | -0.1 | -0.1 | 0.1 | -0.3 |
| opCjjV010000120 | -0.2 | 0 | -0.2 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | 0 |
| opCjjV010000121 | 0 | -0.1 | 0 | -0.1 | 0 | 0 | 0 | 0 | 0.1 | -0.1 |
| opCjjV010000122 | 0.2 | -0.2 | 0.3 | 0 | 2.5 | 0.1 | 0.1 | 0 | 0 | -0.1 |
| opCjjV010000123 | 0.5 | 0.4 | 0.6 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0 |
| opCjjV010000124 | -0.1 | -0.1 | 0 | -0.1 | -0.1 | 0.3 | 0 | -0.2 | 0.2 | 0.2 |
| opCjjV010000125 | 0.4 | 0.2 | 0.4 | 0.1 | 0 | 0 | 0 | -0.1 | 0.2 | 0.1 |
| opCjjV010000126 | 1.1 | 0.6 | 1 | 0 | -0.1 | -0.1 | 0.2 | -0.2 | 0 | 0 |
| opCjjV010000127 | 0.2 | 0.2 | 0.1 | -0.1 | -0.2 | 0 | 0.2 | 0.1 | 0 | 0 |
| opCjjV010000128 | -0.5 | 0.2 | 0.3 | 0 | 0 | 0 | 0.1 | -0.1 | 0 | 0 |
| opCjjV010000130 | 0.2 | 0.2 | -0.1 | -0.1 | -0.2 | -0.1 | 0 | 0 | 0.1 | -0.1 |

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| opCjjV010000131 | 0 | 0.1 | -0.1 | 0 | 0 | 0 | 0 | -0.1 | 0.2 | 0 |
| opCjjV010000132 | 0.1 | 0 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0.2 | 0 | -0.3 |
| opCjjV010000133 | -0.7 | -0.8 | -1 | -0.1 | 0 | -0.8 | -0.1 | -1.2 | 0 | -0.1 |
| opCjjV010000134 | 0.7 | 0.3 | 0.2 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | -0.1 | -0.1 |
| opCjjV010000137 | 0.5 | 0.3 | 0.4 | 0 | 0 | 0.1 | 0.2 | 0 | -0.1 | 0 |
| opCjjV010000138 | 0.3 | 0.3 | 0.2 | 0.2 | 0.2 | -0.1 | 0.1 | -0.1 | -0.1 | -0.1 |
| opCjjV010000141 | 0.3 | 0.4 | 0.2 | 0.1 | 0 | 0 | -0.1 | 0 | 0.2 | -0.1 |
| opCjjV010000143 | 0.5 | 0.2 | 0.5 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCjjV010000144 | 0.6 | 0.3 | 0.6 | 0.1 | 0.1 | -1.2 | 0.1 | 0 | 0 | 0 |
| opCjjV010000146 | 0.6 | 0.2 | 0.6 | 0 | 0 | 0.1 | 0.1 | -0.1 | 0.1 | 0 |
| opCjjV010000147 | 0.4 | 0.4 | 0.5 | 0.1 | 2.9 | 0.1 | 0.1 | 0 | 0 | 0 |
| opCjjV010000151 | 0.4 | 0.1 | 0.5 | 0 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.2 |
| opCjjV010000152 | 0.5 | 0.3 | 0.4 | 0.1 | -0.1 | 0.1 | 0.1 | -0.1 | 0 | -0.1 |
| opCjjV010000154 | 0.2 | -0.1 | 0 | 0 | -0.1 | 0 | 0 | 0 | -0.1 | -0.1 |
| opCjjV010000155 | 0.5 | 0.3 | 0.2 | 0.1 | -0.1 | 0 | 0.2 | -0.1 | 0 | 0.1 |
| opCjjV010000156 | -0.5 | 0 | -0.1 | 0 | -0.1 | 0.3 | -0.3 | 0 | 0.2 | 0 |
| opCjjV010000157 | 0 | -0.2 | 0.2 | -0.1 | -0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 |

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| opCjjV010000158 | -0.8 | -0.5 | -0.3 | -0.3 | -0.1 | 0.2 | 0.1 | 0 | 0.2 | 0 |
| opCjjV010000159 | 0 | -0.1 | -0.1 | -0.1 | 0 | 0.1 | 0.1 | 0 | 0 | -0.1 |
| opCjjV010000160 | 0.7 | 0.2 | 0.6 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0 |
| opCjjV010000161 | 0.1 | 0 | 0.2 | 0 | -0.2 | 0.3 | 0 | 0 | 0.1 | 0 |
| opCjjV010000163 | -0.4 | 0 | -7.7 | -0.1 | -0.1 | -2 | -2.3 | -2.2 | 0.2 | 0 |
| opCjjV010000164 | -0.3 | 0.1 | -0.5 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0.1 | -0.2 |
| opCjjV010000165 | 0.1 | 0.1 | 0 | 0 | 0 | 0.1 | -0.1 | 0 | 0.1 | 0 |
| opCjjV010000166 | 0.2 | 0 | -0.2 | 0 | 3.7 | 0 | -0.2 | 0 | 0 | 0 |
| opCjjV010000167 | 0.3 | 0.2 | 0.2 | 0.1 | -0.2 | 0.1 | -0.1 | 0.1 | 0.3 | 0.1 |
| opCjjV010000169 | 0 | -0.2 | 0.4 | -0.1 | 0.1 | 0.1 | -0.1 | 0 | -0.1 | -0.1 |
| opCjjV010000170 | 0.4 | -0.4 | -0.2 | 0.1 | 0.3 | -0.1 | -0.3 | -0.1 | -0.2 | 0 |
| opCjjV010000171 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0 | -0.3 | 0 | 0.2 | 0.1 |
| opCjjV010000172 | 3.6 | -0.1 | 3.2 | 0.9 | 0.1 | 0.8 | 1 | -0.1 | -0.5 | 0.8 |
| opCjjV010000174 | 0.2 | 0.1 | 0.6 | 0.1 | 0.2 | 0 | -0.3 | 0 | 0 | -0.1 |
| opCjjV010000175 | -0.6 | -0.1 | -0.2 | -0.1 | 0.1 | 0.2 | 0 | 0.1 | 0.2 | 0.3 |
| opCjjV010000176 | 0.3 | 0 | 0.1 | 0 | -0.3 | 0 | -0.4 | -0.1 | 0.2 | 0.1 |
| opCjjV010000177 | 0.1 | 0.2 | -0.1 | 0 | -0.1 | 0.1 | -0.3 | -0.1 | 0.1 | -0.1 |

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| opCjjV010000179 | 0.2 | 0.4 | 0.2 | 0 | 0 | -0.1 | 0.1 | -0.1 | 0 | -0.1 |
| opCjjV010000180 | -0.2 | 0.1 | -0.5 | 0.1 | 0 | 0 | 0 | 0 | 0.1 | -0.2 |
| opCjjV010000181 | 1.3 | 1 | 0.8 | 0.1 | -0.2 | 0.2 | 0.2 | -0.2 | 0.2 | 0.2 |
| opCjjV010000182 | 0.5 | 0.2 | 0.3 | 0.1 | 0 | -0.1 | 0.1 | 0 | -0.1 | -0.1 |
| opCjjV010000184 | 0.2 | 0 | 0.6 | 0.1 | -0.1 | 0.3 | 0.2 | -0.2 | 0 | 0 |
| opCjjV010000187 | 0.4 | 0.2 | 0.6 | 0 | 0 | 0.1 | 0.1 | -0.1 | 0 | -0.3 |
| opCjjV010000188 | 0.5 | 0.4 | 0.5 | 0 | -0.2 | 0 | -0.1 | -0.1 | 0.1 | 0 |
| opCjjV010000189 | 0.5 | 0.4 | 0.7 | 0.1 | 0 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCjjV010000192 | -0.1 | -0.1 | -0.1 | 0 | 0.1 | 0 | -0.4 | -0.2 | -0.1 | -0.2 |
| opCjjV010000193 | -0.5 | -0.2 | -0.6 | 0 | -0.1 | 0.2 | -0.3 | -0.1 | 0.2 | 0 |
| opCjjV010000195 | 0.8 | 0.3 | 0.9 | 0.1 | 0 | 0.1 | 0.3 | 0 | -0.1 | 0.1 |
| opCjjV010000196 | 0.6 | 0.3 | 0.4 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjjV010000197 | -0.1 | -0.2 | 0 | 0 | 0 | 0 | 0 | 0.2 | 0.1 | 0 |
| opCjjV010000198 | -0.5 | -0.1 | -1 | 0 | 0 | 0.1 | -0.3 | -0.2 | 0.4 | 0 |
| opCjjV010000201 | 0.7 | 0.3 | 0.3 | 0.1 | 0.2 | -0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjjV010000205 | -1.4 | -0.2 | -0.7 | -0.1 | 0.2 | -0.1 | -0.4 | 0.2 | -0.2 | -0.1 |
| opCjjV010000206 | -0.3 | -0.2 | -0.3 | -0.1 | -0.1 | 0 | 0 | 0.2 | 0 | 0 |

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| opCjjV010000207 | -0.5 | -0.1 | 0.3 | -0.1 | 0.2 | 0 | 0 | 0.1 | -0.1 | -0.2 |
| opCjjV010000208 | 0.7 | 0.2 | 0.3 | 0.2 | 0.2 | -0.2 | 0 | -0.2 | -0.1 | -0.1 |
| opCjV0100000001 | 0 | 0 | 0.3 | -0.1 | 0 | 0.2 | 0.1 | -0.2 | -0.1 | 0.1 |
| opCjV0100000002 | 0.2 | -0.1 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000005 | -0.7 | -0.2 | -4 | 0 | 0 | -2.2 | -1.1 | 0.1 | 0.4 | 0 |
| opCjV0100000006 | -0.2 | -0.4 | 0.6 | -0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.3 | -0.1 |
| opCjV0100000007 | -0.7 | -0.3 | -0.2 | -0.2 | 0.1 | 0.2 | 0 | 0.2 | 0.1 | 0.3 |
| opCjV0100000010 | -0.2 | -0.2 | -0.3 | 0 | 0.1 | 0.2 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000011 | -7.1 | -6.3 | -2.8 | -0.3 | 2.8 | -1 | -2.3 | 0.5 | -3 | -0.3 |
| opCjV0100000012 | 0.5 | 0.3 | 0.8 | 0.1 | 0.1 | -0.1 | 0.1 | 0.2 | -0.2 | -0.1 |
| opCjV0100000013 | 0.2 | 0 | 0.3 | -0.1 | 0 | 0.1 | -0.1 | 0 | 0.1 | 0 |
| opCjV0100000014 | -0.6 | -0.1 | -0.5 | 0 | -0.1 | 0 | -0.1 | 0 | 0.3 | 0 |
| opCjV0100000015 | 0.2 | 0.2 | 0.5 | 0 | -0.1 | 0 | -0.1 | 0.1 | 0.1 | -0.1 |
| opCjV0100000017 | -1.6 | 0 | 0.2 | -0.3 | -0.2 | 0 | -0.2 | 0 | -0.2 | -0.2 |
| opCjV0100000020 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | 0.2 | 0.1 | -0.1 | 0 | 0.1 |
| opCjV0100000021 | -0.4 | 0 | 0 | -0.2 | -0.2 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000022 | -2 | -0.2 | -1.4 | -0.5 | -0.1 | -1.2 | -0.9 | -0.2 | 0 | -0.5 |

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| opCjV0100000023 | 0.3 | 0.3 | 0.2 | 0 | -0.1 | 0.2 | 0.2 | 0.1 | 0 | 0 |
| opCjV0100000025 | 0.2 | 0 | -0.1 | 0.1 | 0.1 | 0.2 | 0 | -0.2 | 0 | 0 |
| opCjV0100000026 | -6.7 | -5.3 | -4.2 | -1.8 | 2 | -1.3 | -1.9 | 2.2 | -2.1 | -1.7 |
| opCjV0100000027 | -0.8 | -0.3 | -6.2 | 0 | 0.1 | -1.8 | -2 | -0.2 | 0.4 | 0 |
| opCjV0100000028 | 0.2 | 0.5 | 0.8 | 0.1 | 0.1 | 0.3 | 0.1 | -0.1 | 0 | 0.1 |
| opCjV0100000029 | -5.2 | -4.2 | -4.9 | -1.4 | 1.6 | -1.2 | -2 | 1.6 | -1.6 | -1.5 |
| opCjV0100000030 | 0 | 0 | 0.2 | -0.1 | 0.1 | 0 | -0.2 | 0 | 0.1 | 0 |
| opCjV0100000036 | 1 | 0.5 | 0.8 | 0.3 | 0 | -0.1 | 0.1 | 0 | 0.2 | -0.1 |
| opCjV0100000039 | -0.1 | -0.3 | 0.6 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | -0.2 | 0 |
| opCjV0100000040 | -0.2 | 0 | -0.1 | -0.1 | -0.2 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| opCjV0100000041 | -1.4 | -0.2 | 0.9 | 0 | 0.2 | 0.1 | 0.3 | 0.3 | -0.1 | -0.2 |
| opCjV0100000042 | -0.2 | 0 | 0.1 | 0 | -0.2 | 0.2 | -0.1 | -0.2 | 0.2 | 0 |
| opCjV0100000043 | -0.1 | 0.1 | 0 | -0.1 | -0.1 | 0.2 | 0 | -0.2 | 0 | 0.1 |
| opCjV0100000044 | 0.1 | 0.1 | 0.3 | 0 | 0 | -0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000045 | -0.3 | 0 | 0 | -0.2 | -0.3 | 0.2 | 0 | 0.1 | 0.3 | -0.1 |
| opCjV0100000047 | 0.4 | -0.1 | 0.2 | 0 | 0 | 0.1 | -0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000048 | -0.4 | 0.2 | -1 | -0.1 | -0.2 | 0.2 | -0.1 | -0.2 | 0.4 | 0.1 |

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| opCjV0100000049 | -0.1 | 0 | 0 | 0 | -0.1 | 0.3 | -0.1 | 0 | 0.1 | 0.1 |
| opCjV0100000050 | 0.1 | -0.1 | -0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 | -0.2 | 0 |
| opCjV0100000051 | 0 | 0.2 | 0.3 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0.3 | 0 |
| opCjV0100000052 | -0.3 | -0.4 | -1.6 | 0 | 0.2 | 0.1 | -0.1 | 0 | 0 | 0 |
| opCjV0100000053 | -0.4 | -0.1 | -0.2 | -0.1 | -0.2 | 0.2 | -0.1 | -0.2 | 0.2 | 0 |
| opCjV0100000055 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | 0 | 0 | 0 | 0.1 | 0 |
| opCjV0100000056 | -0.2 | -0.2 | 0 | -0.1 | 0 | 0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100000058 | 0.4 | 0.1 | 0.5 | 0 | 0.1 | 0 | 0 | 0 | 0.1 | 0.1 |
| opCjV0100000059 | -5.3 | -0.2 | -4.1 | 0 | 1.7 | -1.4 | -1.7 | 0.3 | -2.3 | 0 |
| opCjV0100000060 | 0.4 | 0.2 | 0.5 | 0 | -0.1 | 0.1 | -0.2 | 0 | 0.1 | 0 |
| opCjV0100000061 | 1 | 0.6 | 0.9 | 0.2 | -0.1 | 0 | 0.2 | 0 | 0 | -0.1 |
| opCjV0100000062 | -0.1 | 0.1 | -0.1 | 0 | 0 | -1.8 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000064 | -5.7 | -0.9 | -4.2 | -0.2 | 1.9 | -1.3 | -1.9 | 0.2 | -1.7 | -0.2 |
| opCjV0100000065 | 0.9 | 0.4 | 0.5 | 0.1 | 0 | 0 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100000066 | 0.1 | 0.1 | 0.5 | -0.1 | -0.1 | 0.2 | 0.1 | 0 | 0.1 | 0.1 |
| opCjV0100000067 | 0.4 | 0.4 | 0.2 | 0.1 | -0.1 | 0 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000068 | 0.2 | -0.1 | 0 | 0 | 0.2 | -0.1 | 0 | 0.1 | 0 | -0.1 |

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| opCjV0100000069 | 0 | 0.1 | 0.3 | 0 | -0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 |
| opCjV0100000070 | -0.3 | 0 | 0 | -0.1 | -0.1 | 0.3 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000071 | 0 | -1.2 | -1.2 | -2.2 | 4 | -2.2 | -2.9 | 2.8 | -0.4 | -2.3 |
| opCjV0100000072 | -0.4 | 0.1 | -0.2 | -0.1 | -0.1 | 0.2 | -0.1 | 0.1 | 0.2 | 0 |
| opCjV0100000073 | 1 | 0.8 | 0.8 | 0.2 | -0.1 | 0.1 | 0.2 | -0.2 | 0.1 | 0.1 |
| opCjV0100000074 | -0.1 | 0.1 | 0 | 0 | 0 | 0.2 | -0.1 | -0.1 | 0 | 0 |
| opCjV0100000075 | 0.5 | 0.6 | 0.7 | -0.1 | 0 | 0 | 0.2 | 0 | -0.2 | -0.1 |
| opCjV0100000077 | -0.2 | 0.1 | -0.1 | 0 | -0.2 | 0.2 | -0.1 | 0 | 0 | 0.1 |
| opCjV0100000078 | 0 | 0.2 | 0.7 | 0 | 0.2 | -0.1 | -0.1 | 0 | -0.4 | -0.1 |
| opCjV0100000080 | 0.2 | 0.2 | 0.4 | 0.1 | 0.2 | 0.1 | -0.2 | 0 | 0.1 | 0 |
| opCjV0100000082 | -0.5 | 0 | 0.2 | -0.1 | 0 | 0.2 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000084 | 0.3 | 0.1 | 0.7 | 0.1 | 0.1 | 0 | -0.4 | 0.1 | 0 | -0.1 |
| opCjV0100000085 | 0.6 | 0.3 | 0.5 | 0.1 | -0.1 | 0 | 0 | 0.1 | 0 | -0.1 |
| opCjV0100000087 | -0.4 | 0.2 | -0.2 | -0.1 | -0.1 | 0 | 0 | 0.1 | 0.1 | -0.1 |
| opCjV0100000088 | 0.2 | 0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 | -0.3 | -0.1 | -0.1 |
| opCjV0100000089 | 0.3 | 0 | 0.1 | 0 | -0.1 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000092 | -0.3 | 0.2 | -2 | -0.1 | -0.3 | -1.3 | -1.8 | -1.1 | 0.1 | 0.1 |

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| opCjV0100000093 | 0.7 | 0.5 | 0.2 | 0.2 | 0 | 0.1 | 0 | 0 | 0 | -0.1 |
| opCjV0100000094 | -0.1 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 0 | -0.2 | 0 |
| opCjV0100000095 | 0.3 | 0.2 | 1 | 0 | 0.2 | 0 | 0 | -1 | -0.1 | -0.1 |
| opCjV0100000096 | 0.1 | -0.1 | 0.3 | 0.2 | 0.2 | 0 | -0.2 | -0.2 | 0 | 0 |
| opCjV0100000098 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0.2 | 0.2 | -0.2 | 0.1 | 0.1 |
| opCjV0100000099 | -0.1 | 0.1 | 0.2 | 0 | -2.4 | 0.2 | 0 | 0 | 0 | 0.1 |
| opCjV0100000100 | 0.1 | 0.1 | 0.4 | -0.1 | 0.1 | 0.3 | 0.1 | 0 | 0 | 0.1 |
| opCjV0100000101 | 0.2 | 0.3 | 0.5 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0.1 | 0.1 |
| opCjV0100000102 | 0.3 | 0.3 | 0.5 | 0.1 | -1.3 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000103 | 1.1 | 0.6 | 1.4 | 0.2 | 0.3 | -0.2 | -0.1 | -0.1 | 0 | 0.1 |
| opCjV0100000106 | -0.5 | -0.3 | -0.5 | -0.1 | -0.3 | 0.2 | -0.2 | -0.1 | 0.1 | -0.1 |
| opCjV0100000108 | 0.2 | 0.2 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | -0.1 | -0.1 |
| opCjV0100000109 | -0.1 | 0.1 | -0.3 | -0.2 | -0.3 | 0.2 | 0 | 0.1 | 0.1 | 0 |
| opCjV0100000110 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0.1 | 0 | -0.1 | 0.2 | 0 |
| opCjV0100000111 | 0.8 | 0.3 | 0.5 | 0.1 | 0.1 | 0.2 | 0.3 | 0 | 0 | 0.1 |
| opCjV0100000112 | 0.6 | 0.5 | -0.1 | 0.1 | -0.1 | 0 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000114 | -5.3 | -4.1 | -3.7 | -1.3 | 1.9 | -1.4 | -0.1 | 1.6 | -1.3 | -1.3 |

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| opCjV0100000115 | 0.1 | 0.2 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0.2 | 0 |
| opCjV0100000116 | 0.1 | 0.4 | 0 | 0 | -0.1 | 0.1 | -0.1 | 0 | 0.3 | 0 |
| opCjV0100000117 | -0.2 | 0.1 | -0.5 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0.1 | -0.2 |
| opCjV0100000118 | 0.4 | 0.1 | 0.4 | 0.1 | 0.2 | 0 | -0.1 | -0.1 | 0.1 | -0.1 |
| opCjV0100000120 | 0 | -0.1 | -0.5 | 0 | -1.6 | 0.2 | -0.2 | -0.2 | 0 | 0 |
| opCjV0100000121 | 0.1 | 0.4 | 0.3 | 0 | 0 | -0.1 | 0 | 0 | 0 | -0.1 |
| opCjV0100000122 | 0.3 | 0.2 | 0.2 | 0.1 | 0 | 0 | -0.3 | 0 | 0 | 0.1 |
| opCjV0100000124 | 0.4 | 0.2 | 0.6 | 0 | 0.3 | -0.1 | 0 | -0.1 | -0.2 | -0.1 |
| opCjV0100000125 | 0.7 | 0.4 | 0.8 | 0.2 | 0.2 | -0.1 | -0.2 | -0.3 | 0 | 0.2 |
| opCjV0100000126 | 0.2 | 0.3 | 0.2 | 0.2 | -0.7 | 0.3 | 0 | -0.2 | 0.3 | 0.3 |
| opCjV0100000127 | 0.5 | 0.3 | 0.7 | 0 | 0.2 | 0 | 0 | -0.1 | -0.2 | 0 |
| opCjV0100000130 | 0.6 | 0.2 | 0.7 | -0.1 | -0.1 | 0.3 | 0.1 | 0 | 0.2 | -0.1 |
| opCjV0100000131 | -0.2 | 0.1 | -0.1 | 0 | -0.2 | 0.2 | 0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000132 | 0.3 | 0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000133 | 0.2 | 0 | 0.2 | 0 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000134 | 0.2 | 0.2 | 0.2 | 0 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000135 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 | 0.2 | 0 | 0 | 0 | 0 |

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| opCjV0100000136 | 0.2 | 0.2 | 0 | 0 | -0.2 | 0.1 | 0.1 | 0 | 0.1 | 0.1 |
| opCjV0100000137 | -0.4 | 0.1 | -0.1 | -0.1 | 0 | 0 | -0.4 | 0.2 | -0.1 | -0.1 |
| opCjV0100000138 | -0.5 | 0.2 | -0.3 | 0 | -0.1 | 0 | 0.1 | -0.3 | -0.1 | 0 |
| opCjV0100000140 | -1.9 | -4.4 | -0.3 | -1.3 | 1.9 | 0 | -0.9 | 1.6 | -1.5 | -1.5 |
| opCjV0100000141 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0.1 |
| opCjV0100000142 | 0.6 | 0.2 | 0.7 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | 0.1 |
| opCjV0100000143 | 0.1 | -0.1 | 0 | 0.1 | -0.9 | 0 | -0.3 | -0.1 | 0.2 | 0 |
| opCjV0100000144 | 0.7 | -0.1 | 1 | 0 | 0 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000145 | -0.1 | -0.2 | 0.1 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100000146 | 0 | 0 | 0 | 0 | -1.2 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000147 | 0.2 | 0.2 | 0.5 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 |
| opCjV0100000150 | -0.4 | -0.2 | -0.6 | 0.1 | 0.1 | 0.1 | 0 | -0.2 | 0.2 | 0.1 |
| opCjV0100000151 | -0.2 | 0.1 | 0 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | 0.2 | 0.1 |
| opCjV0100000152 | 0.1 | 0.3 | 0.5 | 0.2 | -0.8 | 0 | 0 | 0 | 0 | -0.1 |
| opCjV0100000153 | -0.4 | -0.8 | -0.4 | 0 | 0.1 | 0 | -0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000154 | 0.4 | 0.1 | 0.2 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000155 | -0.2 | 0.1 | -0.1 | -0.1 | -0.2 | 0.1 | 0 | -0.1 | 0.2 | 0.1 |

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| opCjV0100000156 | -0.2 | 0 | -0.4 | -0.1 | -0.3 | 0.2 | -0.1 | 0 | 0 | -0.1 |
| opCjV0100000158 | -0.6 | -2.2 | -2.1 | -0.7 | 1.2 | -0.5 | -0.1 | 1.1 | -0.7 | -0.1 |
| opCjV0100000159 | -0.1 | 0.1 | 0.1 | -0.1 | -0.4 | 0.3 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000160 | 0 | 0.3 | 0.3 | -0.1 | -0.1 | 0.2 | 0.1 | 0.1 | 0.3 | 0 |
| opCjV0100000161 | 0.8 | 0 | 0 | 0.2 | 0.1 | -0.1 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000164 | -2.1 | -1.5 | -0.9 | -0.4 | 0.6 | -0.8 | -1.1 | -0.1 | -0.5 | -0.4 |
| opCjV0100000165 | -0.2 | -4.7 | -2.1 | -1.5 | 1.3 | -1.2 | -0.1 | 5.5 | -2 | -1.4 |
| opCjV0100000166 | -1 | -0.4 | -2.7 | 0.1 | -0.3 | 0.4 | 0.1 | -0.3 | 0.1 | 0.3 |
| opCjV0100000169 | 0 | 0 | -1.6 | 0 | -0.1 | -0.9 | -2.7 | -0.1 | 0.1 | 0.1 |
| opCjV0100000170 | 0.6 | 0.4 | -0.1 | 0.3 | -1.8 | -0.1 | 0 | -0.4 | 0 | 0 |
| opCjV0100000172 | 0.4 | 0.2 | 0.4 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000173 | 0.3 | 0.3 | 0 | -1.4 | -0.4 | -1.4 | -1.7 | 0.9 | 0 | -1.5 |
| opCjV0100000174 | -1.3 | -0.8 | 0.1 | -0.3 | 0.2 | 0 | -0.1 | 0.2 | -0.1 | -0.3 |
| opCjV0100000175 | 0.6 | 0.5 | 0.1 | 0.1 | 0.2 | 0 | -0.2 | -0.4 | 0 | 0 |
| opCjV0100000176 | 0.3 | 0.4 | 0.3 | 0.1 | 0.2 | 0 | -0.1 | 0 | 0.1 | 0 |
| opCjV0100000178 | 0.3 | 0 | 0.3 | -0.1 | -0.1 | 0 | 0.2 | 0 | -0.1 | 0 |
| opCjV0100000179 | 0.7 | 0.3 | 0.5 | 0.1 | 0.2 | 0 | 0 | 0 | -0.1 | -0.1 |

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| opCjV0100000180 | 0 | 0.1 | -4.5 | 0 | -0.1 | -1.3 | -1.4 | 0.2 | 0 | -0.1 |
| opCjV0100000181 | -0.6 | -0.5 | 0 | -0.1 | 0.2 | 0 | 0.1 | 0.1 | -0.2 | -0.2 |
| opCjV0100000183 | 0.4 | 0.3 | 0.6 | 0 | -0.1 | 0.1 | 0.2 | 0 | 0.1 | 0 |
| opCjV0100000187 | -0.4 | 0 | -0.4 | 0 | -0.2 | 0.3 | 0 | -0.1 | 0.2 | 0 |
| opCjV0100000188 | -4.8 | -4 | -3.7 | -1.3 | 2.2 | -1.5 | -1.6 | 1.5 | -1.6 | -1.7 |
| opCjV0100000189 | 0.4 | 0.1 | 0.5 | 0.2 | 0.1 | 0.1 | 0.1 | -0.2 | 0 | 0 |
| opCjV0100000190 | -2.5 | -2.2 | -0.1 | -1.7 | 2.3 | -2.5 | -0.2 | 2.8 | 0 | -1.8 |
| opCjV0100000191 | 0.4 | 0.4 | 0.4 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0 |
| opCjV0100000192 | -4 | -3.5 | -3.7 | -1 | 1.6 | -1.2 | -1.3 | 1.3 | -1.3 | -1.2 |
| opCjV0100000193 | 0.3 | 0.1 | -0.1 | 0.1 | 0.1 | -1.8 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000194 | 0.6 | 0.5 | 0.5 | 0.1 | -0.1 | 0 | 0 | 0 | 0 | -0.1 |
| opCjV0100000195 | 0.1 | 0.2 | 0.4 | 0.2 | 0 | 0.3 | 0.1 | -0.2 | 0 | 0.2 |
| opCjV0100000196 | -0.1 | -0.2 | -2 | 0.1 | 0.1 | -1.5 | -1.8 | -1 | 0.2 | 0 |
| opCjV0100000197 | 0 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | 0 |
| opCjV0100000198 | 0.4 | 0.5 | 0.4 | 0 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000199 | 0.3 | 0.5 | 0.4 | 0 | 0 | -0.1 | 0.2 | -0.2 | 0 | 0 |
| opCjV0100000200 | 0 | -0.1 | 0.2 | 0 | 0 | 0 | 0.2 | 0.1 | -0.2 | -0.1 |

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| opCjV0100000201 | 0.1 | 0 | 0.3 | 0 | 0.2 | -0.1 | 0.2 | 0.2 | 0 | -0.1 |
| opCjV0100000202 | 0.1 | -0.1 | 0 | 0 | 0.1 | 0.1 | 0 | 0 | 0 | -0.2 |
| opCjV0100000203 | -0.7 | -0.1 | -0.2 | -0.3 | -0.3 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000205 | -0.3 | -0.5 | -0.3 | 0.1 | 0.1 | 0.1 | -0.2 | 0.1 | -0.1 | -0.1 |
| opCjV0100000206 | 0 | 0.2 | 0.5 | -0.1 | -0.2 | 0.2 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000207 | -0.9 | -0.3 | -2.2 | -0.1 | -0.2 | -0.7 | -1.3 | 0 | 0.3 | 0 |
| opCjV0100000208 | -1.2 | -0.6 | -0.2 | -0.1 | -0.2 | 0.3 | -0.1 | 0 | 0.2 | 0.1 |
| opCjV0100000211 | -0.3 | -0.2 | -0.8 | -2.4 | 2.9 | -2.4 | -2.9 | 2.1 | 0.2 | -1.9 |
| opCjV0100000212 | 0.8 | 0.6 | 0.9 | 0 | -0.1 | -0.1 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100000213 | 0.2 | 0.2 | 0.5 | -0.1 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0 |
| opCjV0100000214 | 0.5 | 0.3 | 0.5 | 0 | -0.1 | 0 | 0.1 | -0.2 | 0 | 0 |
| opCjV0100000215 | 0.4 | 0.4 | -5.4 | -1.8 | 5.3 | -2.7 | -2.9 | 5.5 | 0.1 | -1.7 |
| opCjV0100000216 | -3.7 | -3 | -3.1 | -0.9 | 1.3 | -0.9 | -1.5 | 2.4 | -1.1 | -1.3 |
| opCjV0100000218 | -0.1 | 0.1 | 0.2 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0 |
| opCjV0100000219 | -0.1 | 0.1 | 0 | 0 | -0.1 | 0.2 | 0 | 0 | 0.1 | 0 |
| opCjV0100000220 | -3.9 | -3.5 | -1.7 | -1 | 1.5 | 0 | -1.2 | 1.5 | -0.1 | -1.2 |
| opCjV0100000222 | 0.1 | 0.4 | 0.2 | 0 | -0.2 | 0.1 | 0 | -0.2 | -0.1 | 0 |

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| opCjV0100000223 | 0.2 | 0.1 | -0.3 | 0.1 | 0.1 | -1.5 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000224 | 0.3 | 0.2 | 0.5 | 0.2 | 0 | 0.1 | 0.3 | 0.1 | -0.3 | -0.1 |
| opCjV0100000225 | 0.4 | 0 | 0 | 0.1 | 0.2 | -0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000228 | 0.6 | 0.3 | -0.1 | 0.3 | 0.3 | -0.1 | -0.3 | 0.1 | -0.2 | -0.1 |
| opCjV0100000232 | -0.7 | -0.4 | -0.7 | -0.1 | -0.1 | 0.3 | -0.1 | 0.1 | 0.1 | 0 |
| opCjV0100000233 | -0.1 | 0 | 0.2 | 0 | -0.2 | 0.1 | -0.1 | 0.1 | -0.1 | 0 |
| opCjV0100000235 | -0.5 | -2.4 | -4.8 | -1.7 | 2.2 | 0.1 | -0.1 | 1.8 | -3.1 | -1.5 |
| opCjV0100000238 | -0.1 | -0.1 | 0 | 0 | -0.2 | 0.4 | -0.1 | 0 | 0.2 | 0 |
| opCjV0100000239 | -0.5 | -0.3 | 0 | -0.1 | 0 | 0.1 | -0.1 | 0 | 0.1 | 0 |
| opCjV0100000240 | -0.7 | -0.4 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | -0.2 | -0.1 |
| opCjV0100000241 | 0.1 | 0.3 | 0.2 | -0.1 | 0 | 0 | 0 | 0 | -0.1 | 0 |
| opCjV0100000242 | -0.1 | 0 | 0 | -0.1 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000243 | -0.8 | -0.2 | -0.5 | 0 | -0.1 | 0.3 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000244 | 0.3 | 0.3 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000245 | -0.1 | 0.1 | 0.1 | 0 | -0.1 | 0.2 | -0.1 | 0 | 0.2 | 0.1 |
| opCjV0100000246 | 0.5 | 0.5 | 0.3 | 0.2 | 0 | 0.2 | 0.1 | -0.2 | -0.1 | 0.1 |
| opCjV0100000250 | 0.1 | 0 | 0.2 | 0 | -0.1 | 0.1 | 0.2 | 0.1 | 0.2 | -0.1 |

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| opCjV0100000252 | 0.1 | 0 | -1.4 | 0 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0 |
| opCjV0100000253 | 0.7 | 0.5 | 0.6 | 0.1 | 0.1 | 0 | 0.2 | 0.2 | 0 | -0.1 |
| opCjV0100000255 | 0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | 0 | -0.2 | -0.2 |
| opCjV0100000256 | -0.1 | 0.1 | 0.4 | 0 | 0 | 0.1 | 0.2 | 0 | 0 | -0.1 |
| opCjV0100000257 | -0.3 | -0.1 | -2.1 | 0 | -0.2 | -1 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000259 | 0.1 | 0 | 0.2 | 0 | 0.1 | -0.1 | 0.1 | 0.1 | -0.2 | -0.1 |
| opCjV0100000260 | 0.5 | 0.2 | 0.4 | 0.1 | -0.1 | 0 | 0.1 | -0.5 | 0 | 0 |
| opCjV0100000262 | 0.5 | 0.5 | 0.3 | 0 | -0.1 | 0 | -0.1 | 0.1 | 0.2 | 0.1 |
| opCjV0100000263 | 0.2 | 0.4 | 0.2 | 0 | -0.2 | 0.1 | -0.2 | -0.1 | 0.1 | 0.1 |
| opCjV0100000264 | 0.2 | 0.3 | 0.4 | 0.1 | 0 | 0.2 | 0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000265 | 0.2 | 0.5 | 0.1 | 0 | -0.1 | -2.1 | -1.7 | -0.1 | 0.1 | 0 |
| opCjV0100000266 | 0.4 | 0.3 | 0.5 | 0.1 | 0.1 | 0.2 | 0.2 | 0 | 0.1 | 0 |
| opCjV0100000267 | 0.5 | 0.2 | 0.5 | 0 | 0.1 | -0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000268 | 0.4 | 0.2 | 0.5 | 0 | 0.1 | 0 | 0 | -0.1 | 0 | 0 |
| opCjV0100000269 | 0.4 | -1 | -0.7 | -1.9 | 3.3 | -0.7 | -2.8 | 2.8 | -0.1 | -2.1 |
| opCjV0100000270 | -0.5 | 0 | -0.4 | 0 | -0.2 | 0.2 | 0 | 0 | 0.2 | 0.1 |
| opCjV0100000271 | -0.4 | -0.1 | 0.6 | 0 | 0 | 0.2 | 0.2 | 0.2 | -0.2 | 0 |

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| opCjV0100000272 | -0.2 | -0.1 | -0.2 | 0 | -0.1 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000273 | 0.2 | 0.3 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0.1 | 0 | -0.1 |
| opCjV0100000274 | 0.6 | 0.2 | 0.4 | 0 | 0 | 0 | 0.2 | 0 | -0.1 | -0.1 |
| opCjV0100000276 | -0.4 | -0.2 | -0.4 | 0.1 | -0.1 | 0.1 | -0.2 | 0.2 | 0.2 | 0 |
| opCjV0100000279 | -5.3 | -4.4 | -6.1 | -1.7 | 2.4 | -2.2 | -1.8 | 1.7 | -1.6 | -1.6 |
| opCjV0100000280 | 0.3 | 0.6 | 0.5 | 0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.2 |
| opCjV0100000281 | 0.3 | 0.2 | 0.3 | -0.1 | -0.1 | -0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000282 | -0.2 | 0 | 0.1 | 0 | 0 | 0.2 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000283 | 0.3 | 0.1 | 0.5 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000284 | 0.2 | 0.1 | 0.5 | -0.1 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0.1 |
| opCjV0100000285 | -0.8 | 0 | -0.3 | 0 | -0.2 | 0.2 | 0.1 | 0 | 0.2 | 0.1 |
| opCjV0100000286 | -0.2 | 0.1 | -0.4 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0.2 | -0.1 |
| opCjV0100000287 | -0.1 | -0.1 | -0.3 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0 | 0 |
| opCjV0100000288 | 0.2 | 0.4 | 0.2 | 0.1 | 0 | 0 | 0.1 | -0.1 | 0.1 | -0.1 |
| opCjV0100000290 | -0.3 | -0.2 | 0.1 | 0 | 0 | 0.2 | 0 | -0.1 | 0 | 0 |
| opCjV0100000292 | 0.6 | 0.2 | 0.3 | 0.2 | 0.3 | 0 | -0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000293 | 0.1 | 0.2 | 0.2 | -0.3 | 0 | 0 | 0 | 0.1 | -0.1 | -0.2 |

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| opCjV0100000295 | 0.6 | 0.1 | 0.4 | 0 | -0.1 | 0.2 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100000296 | 0.8 | 0.3 | 0.4 | 0.2 | 0 | 0 | 0.2 | 0 | -0.1 | -0.1 |
| opCjV0100000298 | 0.2 | 0 | 0.2 | 0 | 0 | 0 | 0 | 0 | 0 | -0.1 |
| opCjV0100000299 | -1.2 | -0.6 | -1.4 | -0.1 | 1.3 | -0.6 | -0.4 | 0.6 | -0.3 | -0.2 |
| opCjV0100000300 | -0.1 | -0.2 | -5 | 0 | 0 | -1.6 | -0.1 | 0.1 | 0.2 | 0 |
| opCjV0100000304 | -1.5 | -1.2 | -0.9 | -0.2 | 0.3 | 0 | -0.4 | 0.1 | -0.1 | -0.2 |
| opCjV0100000305 | -0.7 | -0.1 | -5 | -0.2 | -0.3 | -1.5 | -1.1 | -1.5 | 0.3 | 0.1 |
| opCjV0100000306 | 0.1 | -0.1 | 0.6 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0.1 | 0 |
| opCjV0100000307 | 0 | 0.4 | 0.1 | 0 | -0.2 | 0.1 | 0 | 0 | 0.2 | 0.1 |
| opCjV0100000308 | -0.6 | 0.2 | -0.2 | 0.1 | -0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.1 |
| opCjV0100000309 | 0.5 | 0.6 | 0.5 | 0 | -0.1 | -0.1 | 0.1 | 0.1 | 0.1 | -0.2 |
| opCjV0100000310 | 0.3 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100000311 | 0.2 | 0 | 0.3 | 0 | -0.1 | 0 | 0.1 | -0.2 | 0 | 0.1 |
| opCjV0100000312 | 0.4 | 0.5 | 0.4 | -0.2 | -0.1 | 0 | -0.1 | 0.1 | 0.3 | 0 |
| opCjV0100000313 | 0.5 | -0.1 | 0.4 | 0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000317 | 0.4 | 0.3 | 0.4 | 0 | 0 | 0.1 | 0.2 | 0 | -0.1 | 0 |
| opCjV0100000320 | -0.6 | 0.2 | 0 | 0 | 0 | 0 | -0.1 | 0.1 | 0 | -0.2 |

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| opCjV0100000321 | -0.4 | 0 | -0.1 | -0.1 | -0.2 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000322 | 1 | 0.5 | 0.9 | 0 | 0 | -0.1 | 0.2 | -0.1 | -0.1 | -0.1 |
| opCjV0100000323 | 0.7 | 0.2 | 0.3 | 0 | 0 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000324 | 0.4 | 0 | 0.5 | 0 | -0.1 | -0.1 | -0.1 | 0 | 0 | 0 |
| opCjV0100000326 | -0.4 | -0.2 | -0.4 | 0.1 | -0.1 | 0.1 | -0.2 | -0.1 | 0 | -0.1 |
| opCjV0100000329 | 0.2 | 0.1 | -3.9 | 0 | -0.1 | -1.4 | -1.5 | -1.5 | 0 | 0 |
| opCjV0100000330 | 0.2 | 0.4 | 0.4 | 0 | -0.1 | 0.2 | 0.1 | -0.1 | 0.3 | -0.1 |
| opCjV0100000331 | 0.2 | 0 | -0.2 | 0 | 0 | -0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000332 | -1.9 | -1.1 | -4.7 | -0.3 | 0.3 | -0.7 | -0.2 | -1.1 | 0.1 | -0.3 |
| opCjV0100000336 | -0.7 | -0.4 | -0.3 | -0.2 | -0.1 | 0.2 | 0 | -0.1 | 0.2 | 0.1 |
| opCjV0100000337 | 0.1 | 0.2 | -0.4 | -0.2 | -0.1 | 0.1 | -0.1 | 0 | -0.4 | -0.1 |
| opCjV0100000338 | -0.8 | -0.1 | 0 | -0.1 | -0.2 | 0.2 | -0.2 | 0 | 0.4 | 0 |
| opCjV0100000339 | -0.5 | -0.1 | -0.3 | -0.1 | -0.1 | 0 | -0.3 | 0 | 0.1 | -0.1 |
| opCjV0100000340 | 0 | 0.2 | 0 | -0.1 | -0.1 | 0 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000341 | -0.1 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000342 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0 | -0.2 | -0.2 |
| opCjV0100000345 | -2.1 | -1.1 | -0.2 | 0.1 | 0.1 | 0 | -0.3 | -0.1 | -0.2 | -0.2 |

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| opCjV0100000346 | 0.2 | 0.1 | 0.2 | 0 | 0.1 | 0 | 0 | 0 | 0 | -0.1 |
| opCjV0100000348 | 0.2 | 0.1 | 0 | 0.2 | 0 | 0 | 0 | 0.1 | 0.2 | -0.1 |
| opCjV0100000349 | -0.5 | -0.1 | -0.4 | -0.4 | -0.1 | 0.1 | -0.1 | 0 | -0.1 | -0.2 |
| opCjV0100000350 | -0.5 | 0 | 0 | -0.1 | -0.2 | 0.1 | 0 | 0.1 | 0.1 | -0.1 |
| opCjV0100000351 | -1.3 | -0.1 | -0.6 | 0.1 | 0.2 | -0.3 | -0.3 | -0.2 | -0.1 | -0.2 |
| opCjV0100000354 | 0.8 | 0.6 | 0.7 | 0.1 | 0 | 0 | 0.2 | 0.1 | 0 | -0.1 |
| opCjV0100000355 | -1.4 | -0.1 | -0.7 | -0.2 | 0 | 0.2 | -0.3 | 0 | 0.1 | -0.1 |
| opCjV0100000356 | 0.6 | 0.8 | 1 | 0.1 | -0.1 | -0.2 | 0.2 | -0.1 | 0.2 | -0.1 |
| opCjV0100000357 | -5 | -4.6 | -1.6 | -1.3 | 2.2 | 0 | -0.8 | 3.2 | -2 | -1.8 |
| opCjV0100000358 | 0.1 | 0.2 | 0.3 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0 | -0.1 |
| opCjV0100000361 | -0.5 | 0 | -1.1 | -0.1 | -0.1 | 0.2 | -0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100000363 | 0 | 0.1 | -0.1 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | -0.1 |
| opCjV0100000364 | 0.8 | -0.6 | 0.2 | -2.3 | 2.8 | -2.6 | -2.7 | 2.2 | -0.2 | -2.2 |
| opCjV0100000365 | -0.6 | -1 | -1.9 | 0 | 0.2 | -1.9 | -0.8 | 0.2 | -0.1 | -0.1 |
| opCjV0100000366 | 0.6 | 0.2 | 0.1 | 0 | -0.1 | -0.2 | 0 | 0.2 | 0 | -0.2 |
| opCjV0100000367 | 0.3 | 0.2 | 0.8 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 | -0.1 |
| opCjV0100000370 | 0.2 | 0.1 | 0.4 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | -0.1 |

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| opCjV0100000371 | 1 | 0.4 | 0.8 | 0.1 | 0 | -0.2 | 0.2 | 0.2 | -0.1 | -0.1 |
| opCjV0100000372 | 0.7 | 0.7 | 0.6 | 0.3 | 0 | 0.1 | 0.1 | -0.1 | 0.1 | -0.1 |
| opCjV0100000373 | 0.3 | 0.1 | -5.4 | 0 | 0 | -2.1 | -1.4 | -0.2 | 0 | -0.1 |
| opCjV0100000378 | 0.2 | 0 | 0.2 | 0 | 0.1 | 0.2 | 0.1 | -0.3 | 0.2 | 0.1 |
| opCjV0100000381 | 0.3 | 0.1 | 0.2 | 0.1 | 0.1 | -0.2 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000382 | 1.1 | 0.5 | 1 | 0 | -0.2 | 0 | 0.2 | 0 | -0.7 | 0.1 |
| opCjV0100000383 | -0.1 | 0.3 | 0.3 | -0.1 | 0 | 0.1 | -0.4 | -0.1 | 0.2 | 0 |
| opCjV0100000384 | -0.6 | -0.5 | -2.8 | -0.1 | 0.1 | -1.4 | -1.8 | 0 | 0.2 | 0 |
| opCjV0100000385 | -0.2 | 0.1 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0.2 | 0 |
| opCjV0100000386 | -0.1 | 0.1 | 0 | -0.1 | -0.1 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000390 | 0.1 | 0.5 | 0.4 | 0.1 | 0 | -0.1 | -0.1 | -0.1 | 0 | -0.1 |
| opCjV0100000391 | -0.2 | 0.3 | -1.1 | -0.6 | -0.1 | -0.8 | -1.2 | -0.4 | -0.8 | 0 |
| opCjV0100000392 | -0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 | -0.1 | -0.1 | 0 | -0.1 |
| opCjV0100000393 | -0.2 | 0.2 | -0.3 | 0.1 | 0 | 0.1 | 0 | -0.2 | 0.2 | 0 |
| opCjV0100000394 | 0.5 | 0.3 | 0.4 | 0.1 | 0 | 0 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100000395 | -0.4 | 0 | 0.7 | 0 | 0.1 | 0.2 | 0 | 0 | -0.3 | 0 |
| opCjV0100000396 | -4.9 | -4.1 | -3.3 | -1.2 | 1.8 | -0.9 | -2.5 | 1.5 | -1.5 | -1.4 |

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| opCjV0100000397 | -0.7 | 0 | -0.2 | -0.1 | -0.4 | 0.2 | -0.1 | 0 | 0.2 | 0 |
| opCjV0100000398 | -1.3 | -0.2 | -0.5 | -0.1 | -0.2 | 0 | 0 | -0.3 | 0.1 | 0.1 |
| opCjV0100000399 | -3.2 | -2.6 | -2.2 | -0.9 | 1.6 | -0.8 | -1 | 1.1 | -1 | -1 |
| opCjV0100000401 | 0 | -0.2 | 0.4 | -0.2 | 0.1 | 0.1 | 0 | -0.2 | 0.1 | 0 |
| opCjV0100000402 | 0.7 | 0.5 | 0.5 | 0.2 | 0.1 | 0 | 0.1 | 0 | 0 | 0 |
| opCjV0100000403 | -0.1 | 0.2 | 0.3 | -0.2 | -0.1 | 0 | -0.1 | -0.1 | -0.6 | 0 |
| opCjV0100000404 | -0.3 | 0 | -1 | 0 | 0 | 0.1 | -1 | -0.6 | 0.3 | 0.1 |
| opCjV0100000406 | -0.3 | -0.6 | -0.5 | -1.1 | 0.1 | 0 | -0.1 | 0.4 | 0.2 | -2 |
| opCjV0100000407 | 0.3 | 0.1 | 0.4 | 0 | 0 | 0.1 | 0 | -0.4 | -0.1 | -0.1 |
| opCjV0100000408 | -0.5 | 0 | -0.5 | -0.1 | -0.1 | 0.2 | -0.1 | -0.1 | 0.2 | 0.1 |
| opCjV0100000409 | -0.1 | 0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.5 | 0 | 0.1 |
| opCjV0100000410 | 0.3 | 0.2 | 0 | 0 | 0.1 | 0 | -0.1 | -0.2 | 0 | 0 |
| opCjV0100000412 | 0.2 | 0.3 | 0.4 | -0.1 | -0.2 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000413 | 0.6 | 0.3 | 0.5 | 0.1 | -0.1 | 0 | 0 | 0 | 0.1 | 0.1 |
| opCjV0100000414 | -4.1 | -3.2 | -6.5 | -1 | 1.6 | -1.2 | -1.3 | 0.8 | -1.3 | -1.3 |
| opCjV0100000416 | -0.6 | 0 | 0.3 | 0 | 0 | -0.2 | 0.4 | 0.3 | 0.2 | 0 |
| opCjV0100000417 | 0.2 | -0.1 | -0.4 | -2 | 3.3 | -2 | -2.5 | 3.2 | -0.2 | -0.1 |

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| opCjV0100000418 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000419 | 0.2 | 0 | 0.4 | 0 | -0.2 | 0.2 | 0 | -0.1 | 0 | 0 |
| opCjV0100000423 | -4 | -2.7 | -0.3 | -0.7 | 1.2 | 0 | -0.2 | 1.1 | -0.7 | -0.8 |
| opCjV0100000425 | 0.3 | 0.3 | 0.5 | 0.1 | 0.3 | 0 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000426 | -0.1 | -0.5 | 0 | -1.6 | 3.3 | -1.6 | -1.2 | 3.2 | 0 | -3.2 |
| opCjV0100000428 | 0.1 | -0.1 | 0.3 | 0 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000430 | 0.6 | 0.4 | 0.7 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000433 | 0.3 | 0.1 | 0.4 | 0 | 0 | 0 | -0.1 | -0.1 | 0 | 0 |
| opCjV0100000434 | 0.5 | 0.2 | 0.4 | 0.3 | 0.3 | 0 | -0.1 | 0.1 | -0.3 | 0 |
| opCjV0100000435 | 0.5 | 0.6 | 0.4 | 0 | -0.3 | -0.1 | 0.1 | -0.1 | 0 | -0.1 |
| opCjV0100000436 | 0.6 | 0.3 | 0.5 | -0.1 | -0.2 | 0 | -0.1 | 0 | 0.1 | 0 |
| opCjV0100000437 | 0.8 | 0.6 | 0.9 | 0 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0 |
| opCjV0100000438 | 0.6 | 0.1 | 0.6 | 0 | -0.1 | 0 | 0.1 | 0.2 | 0.1 | 0 |
| opCjV0100000439 | -0.4 | 0.2 | -0.2 | -0.1 | -0.3 | 0.2 | 0 | 0 | 0.2 | 0.1 |
| opCjV0100000442 | 0.1 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | -0.1 | -0.1 | 0 | 0 |
| opCjV0100000444 | -0.3 | -0.1 | -0.5 | -0.1 | -0.4 | -0.8 | -1.3 | 0.1 | 0.3 | 0 |
| opCjV0100000445 | 0.5 | 0.3 | 0.3 | 0.1 | 0 | 0 | -0.1 | 0 | 0 | -0.1 |

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| opCjV0100000448 | -0.1 | -0.2 | 0.2 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0.1 | 0.1 |
| opCjV0100000449 | -0.2 | 0 | 0 | 0 | 0.2 | 0.1 | -0.1 | 0 | 0 | 0 |
| opCjV0100000450 | -0.2 | 0 | 0.5 | -0.3 | 0 | -0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100000451 | 0.3 | 0.5 | 0.3 | 0 | -0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCjV0100000454 | 0.3 | 0.1 | 0.6 | 0.1 | 0.2 | 0 | 0.1 | 0 | -0.2 | 0 |
| opCjV0100000455 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | 0 | -0.1 | 0.1 | 0.1 |
| opCjV0100000456 | -0.2 | -1.5 | 0.3 | -0.4 | 0.5 | -0.1 | -0.1 | 0.2 | 0 | -0.4 |
| opCjV0100000457 | 0.9 | 0.8 | 0.6 | 0.2 | 0.1 | 0 | 0.3 | -0.1 | -0.1 | 0 |
| opCjV0100000458 | 0.4 | -0.3 | 0.3 | 0 | 0.1 | 0.2 | -0.1 | 0 | -0.2 | 0 |
| opCjV0100000459 | 0.4 | 0.4 | 0.3 | 0.1 | -0.1 | 0 | 0.2 | 0 | 0.1 | 0 |
| opCjV0100000460 | -0.2 | 0.1 | -0.4 | 0 | -0.2 | 0.1 | -0.2 | -0.1 | 0.1 | 0 |
| opCjV0100000461 | -0.5 | 0 | -0.4 | -0.1 | 0 | 0.2 | 0 | 0.2 | 0.1 | 0.1 |
| opCjV0100000462 | 0.3 | 0.4 | 0.5 | 0 | -0.2 | 0 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000464 | 0.6 | 0.2 | -0.1 | 0.1 | 0 | 0.1 | -0.2 | -0.1 | 0 | 0 |
| opCjV0100000467 | -5.2 | -3.7 | -3.7 | -1.4 | 2.1 | -1.5 | -1.4 | 1.7 | -1.5 | -1.4 |
| opCjV0100000468 | 0.2 | 0.1 | 0.4 | 0 | -0.1 | 0 | -0.2 | 0.1 | 0 | -0.1 |
| opCjV0100000470 | -0.5 | -0.2 | -0.5 | 0 | -0.1 | 0.2 | -0.2 | 0 | 0.2 | 0 |

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| opCjV0100000471 | -0.4 | 0 | 0 | 0 | 0 | 0 | -0.2 | 0 | 0.1 | 0.1 |
| opCjV0100000472 | 0.3 | 0.2 | 0.3 | 0.1 | -0.3 | 0 | 0 | 0 | 0 | 0 |
| opCjV0100000474 | 0.5 | 0.4 | 0.8 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 | 0 |
| opCjV0100000475 | 0.1 | 0 | 0.2 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 | -0.1 |
| opCjV0100000476 | -0.2 | 0.1 | -0.1 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 |
| opCjV0100000478 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 | 0.2 | 0 |
| opCjV0100000479 | 0.8 | 0.4 | 1.1 | 0.1 | 0 | 0.1 | 0.2 | -0.1 | 0 | 0 |
| opCjV0100000480 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 | 0 | 0.1 |
| opCjV0100000481 | -0.1 | 0.2 | 0 | 0.1 | 0 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000483 | -0.3 | -5.2 | -0.3 | -1.4 | 3 | 0 | -0.1 | 2 | -1.9 | -1.7 |
| opCjV0100000484 | -0.1 | -0.2 | 0 | 0 | 0.2 | -0.1 | 0 | -0.2 | -0.1 | 0 |
| opCjV0100000485 | -0.2 | 0.2 | -0.1 | 0 | -0.2 | 0.2 | -0.1 | 0 | 0.3 | 0 |
| opCjV0100000486 | 0.7 | 0.3 | 0.5 | 0 | 0 | 0.1 | 0.2 | 0 | -0.1 | -0.1 |
| opCjV0100000487 | 0 | -0.1 | 0.4 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | -0.1 |
| opCjV0100000488 | 0.2 | 0 | -0.4 | -0.1 | 0.1 | -0.2 | -0.5 | 0.2 | 0.1 | 0 |
| opCjV0100000489 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.1 | 0 | -0.1 | 0.1 | -0.1 |
| opCjV0100000490 | 0.2 | 0.1 | 0.5 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 |

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| opCjV0100000492 | 0 | 0 | -0.2 | -0.1 | -0.2 | 0.1 | -0.2 | -0.2 | 0.1 | 0.1 |
| opCjV0100000493 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000494 | -0.9 | -0.5 | -1.1 | 0 | 0 | 0.4 | -0.1 | -0.1 | 0.5 | 0.1 |
| opCjV0100000495 | -0.1 | -0.2 | -0.1 | -0.1 | 0.1 | 0.2 | -0.1 | 0 | 0 | -0.1 |
| opCjV0100000496 | 0.1 | 0.1 | 0.2 | 0 | 0.4 | 0.2 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000497 | 0.1 | 0 | 0.8 | -0.1 | -0.1 | 0.3 | 0 | 0 | 0.1 | 0 |
| opCjV0100000500 | 0.3 | 0.1 | 0.3 | 0 | 0.3 | -0.1 | -0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000504 | -0.6 | -0.5 | -0.3 | -0.1 | 0.2 | -0.4 | -0.3 | 0.1 | -0.2 | -0.4 |
| opCjV0100000505 | -0.1 | -0.3 | 0.3 | 0.1 | 2.9 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000507 | 0.3 | 0.3 | 0.3 | 0 | -0.2 | 0.2 | -0.1 | -0.2 | 0 | 0.1 |
| opCjV0100000509 | -0.8 | 0.4 | 0.2 | -0.1 | -0.1 | -0.1 | 0 | 0.2 | 0 | -0.1 |
| opCjV0100000510 | -5.3 | -4.7 | -4.8 | -1.5 | 2.6 | -1.4 | -2.1 | 2 | -1.6 | -1.5 |
| opCjV0100000512 | 1 | 1 | 0.6 | 0.2 | 0.1 | -0.1 | 0.1 | -0.1 | -0.2 | -0.2 |
| opCjV0100000513 | 0.4 | 0.3 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0 | 0 |
| opCjV0100000514 | 1 | 0.5 | 0.7 | 0.1 | 0 | 0 | 0.3 | 0.1 | -0.1 | 0 |
| opCjV0100000517 | 0.3 | 0.2 | -1.3 | -0.1 | -0.1 | -0.3 | -0.8 | 0 | 0 | 0 |
| opCjV0100000519 | 0.1 | -0.1 | 0.2 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.1 | 0 |

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| opCjV0100000520 | 0.3 | 0.2 | 0.3 | 0.2 | 0.2 | 0.1 | 0.1 | -0.1 | 0 | 0.1 |
| opCjV0100000521 | -0.1 | 0 | -0.1 | 0.2 | -0.4 | 0.1 | -0.1 | 0.1 | 0.1 | -0.1 |
| opCjV0100000522 | 0.9 | 0.5 | 1.3 | 0.1 | 0.1 | -0.1 | 0.2 | 0.1 | -0.2 | -0.1 |
| opCjV0100000523 | -0.2 | -0.1 | -0.3 | 0.1 | 0 | 0 | -0.1 | -0.2 | 0.2 | 0.1 |
| opCjV0100000524 | -0.3 | 0.1 | 0.1 | 0 | -1 | 0.3 | 0.2 | -0.1 | 0.2 | 0 |
| opCjV0100000525 | -0.2 | 0.1 | -0.3 | -0.1 | -0.1 | 0 | -0.1 | -0.1 | 0.3 | 0 |
| opCjV0100000527 | 0.2 | 0.2 | 0.2 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000528 | -0.5 | -0.1 | -0.6 | 0 | -0.2 | 0.3 | -0.1 | 0 | 0.3 | 0.2 |
| opCjV0100000529 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.1 | -0.1 | -0.2 | 0.1 | 0 |
| opCjV0100000530 | 0 | 0 | -3.5 | 0.1 | 0 | 0.1 | -1.3 | -0.1 | 0.1 | 0 |
| opCjV0100000532 | 0.2 | 0 | 0.3 | 0 | 0 | 0.1 | 0.1 | 0 | -0.2 | -0.1 |
| opCjV0100000533 | -0.6 | 0 | -0.7 | 0 | 0 | 0 | 0 | -0.1 | 0 | 0 |
| opCjV0100000534 | 0.5 | 0.5 | 0.4 | 0.1 | -0.2 | 0.1 | 0.2 | 0 | 0 | 0.1 |
| opCjV0100000535 | 0.5 | 0.3 | 0.5 | 0 | -0.1 | 0.2 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100000536 | 1.1 | 1 | 0.6 | 0.3 | -0.2 | 0.1 | 0.3 | -0.1 | 0.1 | 0.1 |
| opCjV0100000538 | 0.1 | 0.1 | -0.3 | -0.2 | -0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000539 | 0.3 | 0.4 | 0.4 | 0 | -0.2 | 0.1 | 0.1 | 0 | 0 | 0 |

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| opCjV0100000540 | 0.7 | 0.4 | 0.2 | 0.1 | -0.1 | 0 | 0 | 0.1 | 0.1 | 0.2 |
| opCjV0100000542 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000543 | 0.8 | 0.4 | 0.3 | 0.2 | 0.2 | -0.1 | 0 | -0.1 | 0 | 0 |
| opCjV0100000545 | -0.1 | -0.2 | -0.6 | 0 | 0.1 | 0.1 | -0.2 | -0.1 | 0.1 | 0 |
| opCjV0100000546 | 0.8 | 0.6 | 0.7 | 0 | 0.3 | -0.1 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000547 | 0.2 | 0.1 | 0.3 | 0.1 | -0.3 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCjV0100000549 | -4.4 | -4.3 | -2.5 | -1.5 | 1.7 | -0.9 | -1.2 | 1.4 | -1.5 | -1.6 |
| opCjV0100000550 | 0.1 | 0 | 0.2 | 0.2 | 0 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000552 | -0.1 | 0.3 | 0 | -0.1 | -0.1 | 0.1 | -0.1 | 0 | 0.2 | -0.1 |
| opCjV0100000553 | -8.6 | -5.7 | -2.9 | -1.7 | 3.6 | -1.8 | -2.5 | 2.6 | -2.9 | -1.9 |
| opCjV0100000555 | -0.6 | -0.4 | -1.5 | 0.1 | 0.4 | -1.2 | -1.9 | -1.4 | -0.2 | -0.1 |
| opCjV0100000557 | 0.3 | 0.4 | 0.1 | 0.1 | -0.2 | 0.1 | 0 | -0.2 | 0 | -0.1 |
| opCjV0100000558 | 0 | 0.3 | 0.3 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100000559 | 0.4 | 0.2 | 0.5 | 0 | 0 | 0.1 | 0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000560 | 0.9 | 0.5 | 0.9 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 | -0.1 |
| opCjV0100000562 | -3.9 | -3.2 | -5.3 | -1.1 | 1.5 | -1.8 | -1.3 | 1.1 | -1 | -1.2 |
| opCjV0100000563 | 0.8 | 0.3 | 0.3 | -0.1 | -0.1 | 0.2 | 0.2 | -0.1 | 0.1 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| opCjV0100000564 | 0.5 | 0.4 | 0 | 0.1 | -0.1 | 0 | -0.1 | 0 | 0 | 0 |
| opCjV0100000565 | -1.5 | -1.3 | -1.7 | 0 | 0.5 | 0 | -0.4 | 0.2 | -0.4 | 0.1 |
| opCjV0100000566 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0 | 0 |
| opCjV0100000567 | 0.2 | 0.3 | 0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0 | -0.2 |
| opCjV0100000568 | 0.3 | 0.4 | 0.4 | 0 | -0.1 | 0 | 0.1 | 0 | 0 | 0 |
| opCjV0100000569 | 0.6 | 0.3 | 0.3 | 0.1 | -0.1 | 0.2 | 0 | -0.5 | -0.1 | 0 |
| opCjV0100000570 | 0.6 | 0.1 | 0.6 | 0.1 | 0.1 | 0 | 0.2 | 0 | -0.2 | -0.2 |
| opCjV0100000571 | -0.7 | -0.1 | -0.6 | 0 | -0.1 | 0.3 | -0.2 | 0 | 0.3 | -0.1 |
| opCjV0100000572 | 0.4 | 0.3 | 0.1 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000573 | 0 | 0.4 | 0.2 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000574 | 0.3 | 0.1 | 0.2 | -0.1 | -0.1 | 0 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000576 | -1.4 | 0 | -0.5 | 0 | 0.2 | -0.1 | -0.4 | 0 | -0.1 | 0 |
| opCjV0100000577 | -0.4 | 0 | -0.1 | 0 | 0.1 | 0.1 | 0 | 0.2 | 0.1 | 0 |
| opCjV0100000578 | 0.8 | 0.5 | 0.4 | 0.3 | 0.3 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000579 | 0.3 | 0 | 0 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 | 0 |
| opCjV0100000581 | -0.2 | -0.5 | -0.3 | -0.2 | 0.3 | -0.3 | 0 | 0.4 | -0.2 | -0.3 |
| opCjV0100000582 | -0.1 | -0.2 | -0.1 | 0 | 0 | 0.2 | 0.1 | 0.1 | -0.1 | 0 |

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| opCjV0100000587 | -0.2 | -0.2 | 0 | -0.1 | -0.1 | 0.3 | 0 | 0.2 | 0 | 0 |
| opCjV0100000588 | 0.4 | 0.2 | 0.4 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000589 | 0.6 | -0.4 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0.3 | -0.4 | -0.2 |
| opCjV0100000590 | 0.7 | 0.2 | 0.9 | 0.1 | 0.2 | -0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000591 | -1 | -0.8 | 0.5 | -0.2 | 0.5 | 0.1 | -0.3 | 0.5 | -0.2 | -0.2 |
| opCjV0100000594 | 0.7 | 0.1 | 0.6 | 0.1 | 0.1 | 0 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000595 | -2.9 | 0.1 | -0.9 | 0 | 0 | -0.4 | -0.7 | -0.1 | -0.1 | -0.1 |
| opCjV0100000596 | -0.8 | 0 | 0.2 | 0 | 0 | 0 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000598 | -2.7 | -2.2 | -2.4 | -2.3 | 2.8 | -1.9 | -2.2 | 2.5 | -0.6 | -1.9 |
| opCjV0100000600 | 0.3 | 0.4 | -0.1 | 0.1 | 0 | -2.2 | -3 | 0 | 0.1 | 0 |
| opCjV0100000601 | -2.5 | 0 | 0 | 0.2 | 0.3 | 0.2 | 0.3 | 0.9 | -1.1 | 0.2 |
| opCjV0100000604 | -2 | -1 | -0.9 | -1.9 | 1.7 | -2 | -1.9 | 1 | -0.1 | -1.7 |
| opCjV0100000605 | -1 | -0.3 | -0.6 | -0.1 | -0.1 | 0.3 | -0.2 | -1.7 | 0.2 | 0.1 |
| opCjV0100000606 | -0.4 | -0.1 | 0 | 0 | 0 | 0.2 | 0 | -0.1 | -0.2 | -0.1 |
| opCjV0100000609 | 0.3 | -0.2 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0 | 0 |
| opCjV0100000611 | -1.9 | -0.1 | -1.4 | 0 | 0.1 | -1.6 | -0.3 | 0.2 | -0.2 | -0.1 |
| opCjV0100000612 | -0.4 | -0.1 | 0.1 | 0.1 | -0.1 | 0.3 | 0 | 0.2 | 0.2 | 0 |

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| opCjV0100000613 | 0.1 | 0.4 | -0.9 | 0.1 | 0 | 0 | 0.2 | -0.1 | -0.1 | 0 |
| opCjV0100000614 | -0.5 | -0.3 | -2.7 | 0 | 0 | 0.2 | 0 | 0.1 | 0.2 | 0.1 |
| opCjV0100000615 | -1.4 | 0.1 | -0.1 | -0.1 | 0.5 | 0 | -1.1 | 0.2 | -0.3 | -0.1 |
| opCjV0100000616 | 0.5 | 0.4 | 0.6 | 0.1 | -0.1 | 0.2 | 0.2 | 0 | 0 | -0.1 |
| opCjV0100000617 | 0.4 | -0.2 | 0.4 | 0 | 0.2 | 0.1 | -0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100000618 | 0.2 | 0.2 | -0.1 | 0 | 0 | 0 | -0.2 | -0.2 | 0 | -0.1 |
| opCjV0100000620 | 0.2 | -3.4 | 0.1 | -0.7 | 1.4 | -0.3 | -0.5 | 1.7 | -0.1 | -1.1 |
| opCjV0100000622 | -0.1 | -0.2 | 0.7 | -0.1 | -0.1 | 0.2 | 0.1 | 0 | 0 | 0 |
| opCjV0100000623 | 0 | 0.2 | 0.1 | 0.1 | 0.2 | 0.1 | 0 | 0 | -0.2 | 0 |
| opCjV0100000624 | -3.8 | -2.2 | -1.9 | -0.7 | 0.9 | -1.1 | -1.7 | -0.1 | -1.3 | -0.7 |
| opCjV0100000625 | 0.1 | 0.3 | 0.2 | 0.1 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 |
| opCjV0100000626 | -5.6 | -5.5 | 0.2 | -1.5 | 2.4 | 0.3 | 0.1 | 2.9 | -1.6 | -1.6 |
| opCjV0100000627 | 0.3 | -0.1 | 0.2 | 0 | 0.2 | 0.2 | -0.1 | 0 | 0.2 | 0 |
| opCjV0100000628 | 0.3 | 0.1 | 0.5 | 0 | 0 | 0 | 0.3 | 0.3 | -0.1 | -0.1 |
| opCjV0100000629 | -0.3 | -0.1 | -0.3 | 0 | 0 | 0.2 | 0.1 | 0.1 | 0.1 | 0 |
| opCjV0100000630 | -0.2 | -0.1 | -0.3 | -0.2 | 0 | 0 | -0.2 | 0.1 | 0 | -0.1 |
| opCjV0100000631 | -0.3 | -0.2 | -0.4 | -0.1 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | 0 |

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| opCjV0100000634 | 0.1 | 0 | -0.1 | 0 | 0.1 | 0.2 | 0.1 | 0.1 | 0 | -0.1 |
| opCjV0100000635 | 0.5 | 0 | 0.3 | 0 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000636 | -1.1 | -0.4 | -0.5 | 0 | 0 | 0.3 | 0.1 | 0.2 | 0.5 | 0.1 |
| opCjV0100000637 | 0.2 | 0 | 0 | 0 | -0.1 | 0.2 | 0.2 | -0.1 | 0 | 0 |
| opCjV0100000638 | -0.1 | -0.3 | -0.2 | 0 | 0 | -0.5 | 0.1 | 0 | 0 | 0.1 |
| opCjV0100000639 | -0.1 | 0.2 | -0.7 | 0 | -0.2 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000640 | 0.4 | 0.2 | -0.4 | 0.1 | 0 | -2.7 | 0 | 0 | -0.1 | 0 |
| opCjV0100000642 | 0.1 | -0.1 | 0.2 | 0 | 0 | 0.1 | -0.1 | 0 | -0.1 | 0 |
| opCjV0100000644 | -0.2 | -1.6 | -0.8 | 0 | 0.1 | 0 | -1.3 | -1.3 | 0 | 0 |
| opCjV0100000645 | -6 | -4.7 | -1.5 | -1.3 | 2.2 | -1.7 | -1.8 | 1.8 | -1.6 | -1.6 |
| opCjV0100000646 | -0.3 | 0.1 | -0.3 | -0.1 | -0.2 | 0.2 | -0.5 | -0.2 | 0.2 | 0 |
| opCjV0100000647 | -0.2 | 0 | -0.4 | 0 | -0.2 | 0.3 | 0 | -0.2 | 0.1 | 0.2 |
| opCjV0100000649 | 0.1 | -0.3 | 0.4 | 0 | 0.1 | 0.1 | 0 | 0.2 | -0.2 | 0 |
| opCjV0100000650 | 0.4 | 0.2 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000651 | 0.4 | 0.1 | 0.1 | 0.2 | 0.2 | 0.2 | 0.1 | 0.1 | -0.1 | 0.1 |
| opCjV0100000652 | -0.7 | -0.3 | -0.9 | -0.1 | 0 | 0 | -0.1 | 0.1 | 0.2 | 0 |
| opCjV0100000654 | -1.3 | -0.3 | -0.7 | -2.1 | 3.1 | -2.6 | -2.7 | 3.3 | 0 | -0.4 |

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| opCjV0100000656 | -0.2 | -0.2 | -2.7 | 0 | 0 | -0.6 | 0 | 0 | 0 | 0 |
| opCjV0100000658 | 0.3 | 0 | 0 | 0 | 0 | 0.1 | 0.1 | 0.2 | -0.3 | -0.1 |
| opCjV0100000659 | 0.4 | -0.1 | 0.4 | 0 | 0 | 0 | 0.1 | 0.1 | -0.2 | -0.2 |
| opCjV0100000660 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0.2 | 0.1 | 0 | -0.1 |
| opCjV0100000663 | 0.3 | 0.2 | 0.5 | 0 | 0 | 0.2 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000664 | 0.1 | -0.2 | 0.7 | -0.1 | 0 | 0 | 0 | 0.2 | -0.3 | -0.1 |
| opCjV0100000665 | -0.8 | -0.6 | -0.6 | 0 | -0.1 | 0.2 | 0 | 0.1 | 0.1 | 0.1 |
| opCjV0100000667 | 0 | 0.1 | 0.8 | -1.9 | 2.9 | -2.7 | -2.5 | 3 | -0.1 | -1.5 |
| opCjV0100000668 | 0.4 | 0.3 | -4.7 | 0 | -0.1 | -2 | 0.1 | 0 | 0 | 0 |
| opCjV0100000669 | 0 | 0 | -0.1 | -0.1 | -0.1 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100000670 | -0.8 | 0 | -1.6 | -0.3 | -0.4 | -0.1 | -0.1 | -0.3 | 0.5 | 0.1 |
| opCjV0100000671 | 0.4 | 0.3 | -0.1 | 0 | -0.1 | -1.6 | 0 | -0.1 | 0.3 | 0 |
| opCjV0100000672 | 0 | 0 | 0.2 | 0 | 0 | 0.1 | 0.1 | 0 | -0.3 | -0.1 |
| opCjV0100000673 | 0.3 | 0 | 0.3 | 0 | 0.1 | 0 | 0.1 | 0.2 | 0 | -0.1 |
| opCjV0100000674 | -0.6 | 0 | -0.6 | 0 | -0.2 | 0.1 | 0 | 0.1 | 0.2 | 0 |
| opCjV0100000676 | 0.3 | 0.1 | 0.8 | -0.1 | -0.1 | 0.1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100000677 | 0.7 | 0.5 | 0.5 | 0.1 | -0.2 | 0.2 | 0.1 | 0 | 0.2 | -0.1 |

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| opCjV0100000678 | -0.6 | -0.3 | -0.6 | -0.1 | 0 | 0.2 | 0 | 0.2 | 0.1 | 0.1 |
| opCjV0100000679 | -0.2 | -0.2 | 0.1 | -0.1 | 0.1 | -0.1 | -0.1 | 0.4 | -0.1 | -0.3 |
| opCjV0100000680 | 0.9 | 0.8 | 0.9 | 0.1 | -0.3 | 0.2 | 0.1 | -0.1 | 0.2 | -0.1 |
| opCjV0100000681 | -0.5 | 0 | -0.6 | -0.1 | -0.2 | 0.2 | 0 | 0 | 0.2 | -0.1 |
| opCjV0100000683 | 0.4 | 0.3 | 0.3 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0 | -0.1 |
| opCjV0100000684 | 0.2 | 0.1 | 0.6 | -0.1 | -0.1 | 0 | 0 | 0 | 0.1 | -0.1 |
| opCjV0100000685 | -5.2 | -5.9 | -0.5 | -1.8 | 2.1 | -1.6 | -2.1 | 2.1 | -3.2 | -1.8 |
| opCjV0100000687 | -0.3 | -0.2 | 0.1 | -0.1 | 0 | 0.1 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000688 | 0.2 | 0 | 0.2 | 0 | 0 | 0 | 0 | 0 | -0.1 | 0 |
| opCjV0100000689 | 0 | 0 | -2.4 | 0 | 0.1 | -2.4 | -1 | 0 | -0.1 | 0 |
| opCjV0100000690 | -0.1 | -2.1 | 0.6 | -0.1 | 0.7 | -0.1 | 0.2 | 0.2 | 0.1 | 0 |
| opCjV0100000691 | 0.6 | 0.4 | 0.8 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | -0.1 |
| opCjV0100000692 | 0 | 0.3 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | -0.1 | 0 | -0.1 |
| opCjV0100000693 | 0.6 | 0.5 | 0.7 | -0.1 | -0.2 | 0 | -0.1 | -0.2 | 0.4 | -0.1 |
| opCjV0100000695 | 0.2 | -0.7 | -0.6 | 0 | 0.3 | 0 | 0 | 0.1 | 0 | 0 |
| opCjV0100000696 | 0.7 | 0.4 | 0.6 | 0.1 | 0 | -0.1 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100000697 | -0.4 | -0.2 | -0.2 | 0 | -0.1 | 0 | -0.2 | 0.1 | 0.1 | 0 |

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| opCjV0100000698 | -0.3 | -0.1 | -7.7 | -0.1 | -0.2 | -2.4 | 0 | 0 | 0.1 | 0 |
| opCjV0100000699 | 0 | 0.1 | -5.1 | -0.1 | -0.2 | 1.7 | 0 | 0.1 | 0.2 | 0 |
| opCjV0100000700 | 0.5 | 0.1 | 0.5 | 0.1 | 0 | 0 | 0.2 | 0.1 | -0.2 | -0.1 |
| opCjV0100000701 | -0.8 | -0.8 | 0.2 | -0.2 | 0 | 0.2 | 0.1 | 0.5 | 0 | -0.2 |
| opCjV0100000702 | -0.1 | 0 | -0.8 | 0 | 0 | -2.3 | 0.1 | 0.1 | -0.1 | -0.2 |
| opCjV0100000703 | 0.3 | 0.1 | 0.2 | 0.1 | -0.1 | 0.1 | 0 | 0.1 | 0 | 0 |
| opCjV0100000704 | 0.3 | -0.1 | 0.3 | -0.1 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | -0.1 |
| opCjV0100000705 | 0.3 | 0 | 0.5 | 0 | 0.1 | 0.1 | 0 | 0.2 | -0.1 | -0.2 |
| opCjV0100000706 | 0.7 | 0 | 0.5 | 0.1 | 0 | 0 | 0.1 | 0.2 | -0.1 | -0.1 |
| opCjV0100000707 | 0.6 | 0.4 | 0.6 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0 | -0.1 |
| opCjV0100000709 | 0.6 | 0.4 | 0.8 | 0 | 0 | 0.1 | 0.3 | -0.1 | 0 | 0 |
| opCjV0100000712 | 0.3 | 0 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0 | -0.1 | 0 |
| opCjV0100000713 | -0.5 | -0.1 | -0.4 | 0 | -0.1 | 0.2 | -0.1 | -0.1 | 0.2 | 0 |
| opCjV0100000714 | -0.5 | -0.5 | -0.4 | -0.1 | -0.2 | 0 | -0.1 | -0.4 | 0.2 | 0 |
| opCjV0100000715 | 0.3 | 0.3 | 0.4 | 0.1 | -0.1 | 0.3 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000716 | 0.4 | 0.2 | 0.4 | 0 | 0 | 0.2 | 0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100000717 | 1.1 | 0.8 | 0.7 | 0.2 | 0.2 | -0.3 | 0.2 | -0.1 | 0.1 | -0.1 |

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| opCjV0100000718 | -1.7 | 0 | 0.2 | 0 | -0.1 | 0.1 | -0.1 | -0.1 | 0 | 0 |
| opCjV0100000720 | 0 | 0 | 0 | 0 | 0.1 | -0.1 | -0.3 | -0.1 | -0.1 | -0.2 |
| opCjV0100000722 | -1.5 | -0.8 | -1.6 | -1.7 | 2 | -3 | -0.1 | 2 | -0.1 | -1.6 |
| opCjV0100000723 | -0.2 | 0.1 | -0.1 | -0.1 | -0.2 | 0.1 | 0 | 0.1 | 0.2 | -0.1 |
| opCjV0100000725 | 0.1 | -0.1 | -0.2 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| opCjV0100000726 | -0.1 | -0.3 | -0.2 | -0.1 | 0 | -0.1 | 0.2 | 0.4 | -0.1 | -0.2 |
| opCjV0100000727 | -0.2 | -0.1 | 0 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | -0.1 | -0.1 |
| opCjV0100000728 | 0.2 | -0.1 | 0.1 | 0 | 0.2 | 0 | 0.1 | 0 | -0.2 | -0.1 |
| opCjV0100000729 | -0.7 | -0.4 | -0.4 | -0.2 | 0 | 0 | -0.1 | 0.3 | 0.1 | -0.1 |
| opCjV0100000733 | -0.5 | -0.1 | -0.6 | 0 | -0.1 | 0.1 | 0 | -0.1 | 0.2 | 0 |
| opCjV0100000734 | 0.4 | 0.3 | -5.9 | 0 | 0 | -2 | 0.1 | 0 | 0 | 0 |
| opCjV0100000735 | 0.3 | 0.2 | 0 | -0.1 | -0.1 | -0.2 | -0.2 | 0 | 0.1 | 0 |
| opCjV0100000736 | 0.7 | 0.4 | 0.7 | 0.1 | 0 | 0.2 | 0.2 | 0 | 0.1 | 0 |
| opCjV0100000737 | 0.7 | 0.5 | 0.7 | 0.2 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000738 | 0.6 | -0.2 | -0.1 | 0 | -0.1 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 |
| opCjV0100000739 | 0.1 | -0.3 | 0 | 0 | 0 | 0.1 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000740 | 0.8 | 0.5 | 0.6 | 0.1 | 0 | 0 | 0.2 | 0 | 0 | -0.1 |

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| opCjV0100000741 | 0 | 0.1 | 0.2 | -0.1 | -0.1 | 0.1 | 0.1 | 0 | 0.2 | 0 |
| opCjV0100000743 | -0.8 | -0.3 | -0.8 | -1.7 | 2.9 | -2.1 | -0.3 | 3.7 | -0.3 | -1.8 |
| opCjV0100000744 | -0.6 | -0.1 | -0.8 | 0 | 0 | -0.1 | 0 | 0.1 | 0.1 | 0 |
| opCjV0100000747 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | -0.1 | 0.1 | 0 | -0.1 |
| opCjV0100000748 | 0.2 | 0.3 | 0.2 | 0.1 | -0.1 | 0.2 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000749 | 0.4 | 0.2 | -0.2 | 0 | 0.1 | -0.2 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000750 | 0.1 | 0 | 0.2 | -0.1 | 0 | 0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000751 | 0.6 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | 0 | -0.1 | -0.2 |
| opCjV0100000752 | -0.9 | -0.6 | 0.4 | -0.1 | 0.4 | 0 | 0 | 0.3 | -0.2 | -0.4 |
| opCjV0100000753 | -0.1 | -0.2 | 0.1 | 0 | 0 | 0 | 0 | 0.1 | -0.1 | -0.3 |
| opCjV0100000754 | -0.2 | -0.1 | -0.2 | 0.1 | 0.1 | 0.1 | 0 | 0.2 | -0.1 | -0.1 |
| opCjV0100000755 | 0.7 | 0.6 | 0.2 | 0 | 0 | 0.2 | 0.2 | 0.1 | 0.1 | -0.1 |
| opCjV0100000759 | 0.1 | -0.3 | 0.4 | -0.1 | 0.3 | -0.1 | -0.1 | 0 | -0.2 | -0.1 |
| opCjV0100000760 | -7.3 | -4.7 | -2.2 | -0.1 | 2.3 | -1.8 | -2 | 0.1 | -2.5 | -0.2 |
| opCjV0100000761 | -0.5 | -0.4 | -0.3 | 0 | 0 | 0.3 | -0.2 | -0.3 | 0.1 | 0 |
| opCjV0100000762 | 0.2 | 0.2 | 0.2 | 0 | 0.1 | 0.2 | 0.1 | -0.2 | 0 | -0.1 |
| opCjV0100000765 | 0.2 | 0.3 | -0.2 | -2.3 | 2.3 | -2.2 | -2.7 | 2.3 | 0.1 | -2 |

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| opCjV0100000766 | -0.7 | -0.2 | -0.5 | -0.1 | -0.2 | 0.2 | -0.1 | 0 | 0 | 0.1 |
| opCjV0100000767 | 0.9 | 0.5 | 0.5 | 0.1 | -0.1 | 0 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000768 | -0.5 | 0.2 | -0.5 | -0.2 | -0.4 | 0.2 | 0 | -0.1 | 0.3 | 0.1 |
| opCjV0100000769 | -0.5 | 0.1 | -0.7 | -0.1 | -0.3 | -0.1 | -0.4 | -0.4 | 0.1 | 0 |
| opCjV0100000770 | 0.6 | 0.4 | 0.5 | 0 | -0.1 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000771 | 0.6 | 0 | 0.6 | 0.1 | 0.1 | 0.1 | 0.2 | 0 | -0.1 | 0 |
| opCjV0100000774 | 0 | 0.1 | 0 | 0 | 0.1 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000775 | -1.8 | -1.5 | -6.1 | -0.3 | 0.6 | -2.2 | -2.1 | 0.4 | -0.4 | -0.6 |
| opCjV0100000777 | -5 | -3.8 | -3 | -1.1 | 1.8 | -1.5 | -2.3 | 1.8 | -1.8 | -1.6 |
| opCjV0100000778 | 0.3 | 0.3 | 0.4 | 0 | -0.1 | -0.2 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000779 | -0.2 | -0.1 | -0.1 | 0 | 0 | 0 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000780 | 0.4 | 0.2 | 0.1 | 0 | 0.1 | -0.1 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000781 | -0.3 | 0 | 0.1 | -0.1 | -0.1 | 0.2 | -0.4 | -0.2 | 0.2 | 0.1 |
| opCjV0100000782 | 0.3 | 0.4 | 0.5 | -0.1 | 0.1 | 0.1 | 0 | -0.2 | -0.1 | 0 |
| opCjV0100000783 | 0.1 | 0.2 | 0.2 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0 | 0 |
| opCjV0100000786 | 0.7 | 0.7 | 0.8 | 0.1 | 0 | -0.2 | 0 | 0 | 0.2 | 0 |
| opCjV0100000787 | -1.1 | -1.5 | -0.8 | -0.3 | 0.3 | -0.1 | -0.2 | 0.1 | 0.3 | -0.2 |

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| opCjV0100000788 | -0.2 | -1.5 | 0.4 | -0.4 | 0.1 | 0.1 | 0.1 | 0.2 | -0.3 | -0.1 |
| opCjV0100000789 | 0.5 | 0.4 | 0.3 | 0.2 | 0 | 0.1 | 0.1 | -0.3 | 0.1 | 0.2 |
| opCjV0100000792 | 0.5 | 0.3 | 0.3 | 0.2 | 0 | 0 | 0 | 0 | 0.1 | -0.1 |
| opCjV0100000793 | -1 | -0.5 | -0.2 | 0 | -0.1 | 0.2 | -0.1 | 0.1 | 0.1 | -0.1 |
| opCjV0100000794 | -3.2 | -2.6 | -3 | -0.6 | 1.2 | -0.7 | -1.3 | 2 | -0.9 | -1 |
| opCjV0100000795 | 0.1 | 0.1 | 0.3 | -0.1 | -0.1 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000796 | 0.2 | 0.4 | 0.4 | 0.1 | 0 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100000797 | -0.2 | 0.2 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | 0.1 | 0.1 | 0 |
| opCjV0100000798 | 0.6 | 0.2 | 0.1 | -1.2 | 3 | -2.2 | -2.1 | 2.3 | 0.1 | -2.1 |
| opCjV0100000799 | -0.2 | 0.4 | -0.7 | 0 | -0.1 | 0 | -0.4 | 0 | 0 | 0 |
| opCjV0100000800 | 0.5 | 0.2 | 0.3 | 0 | 0 | 0.2 | 0 | 0 | 0 | -0.1 |
| opCjV0100000802 | 0.9 | 1 | 1.2 | 0.3 | 0.1 | 0 | 0.1 | -0.1 | -0.3 | 0 |
| opCjV0100000804 | -4.3 | -3.1 | -1 | -1.1 | 1.2 | -1.2 | -1.2 | 1 | -1.2 | -1.3 |
| opCjV0100000807 | -0.1 | -0.1 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 0 | 0.1 | 0 |
| opCjV0100000809 | 0.5 | 0.2 | 0.7 | 0 | 0.3 | -0.1 | 0.1 | -0.1 | -0.4 | 0 |
| opCjV0100000810 | 0.5 | 0.5 | 1 | 0 | 0 | 0.1 | 0.5 | 0.2 | 0 | 0.1 |
| opCjV0100000812 | 0 | 0 | -0.1 | 0.1 | 0.1 | 0.1 | 0 | -0.2 | 0.2 | 0 |

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| opCjV0100000813 | -0.2 | -0.2 | -0.3 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 |
| opCjV0100000815 | 0.5 | 0.4 | -0.5 | 0.2 | 0.1 | -0.1 | -0.5 | -0.4 | 0 | 0 |
| opCjV0100000816 | 0.3 | 0 | -0.2 | 0 | -0.1 | 0 | 0.1 | -0.3 | 0 | 0 |
| opCjV0100000817 | -0.1 | 0.2 | -1.6 | 0 | -0.4 | 0.3 | -0.1 | 0 | 0.1 | 0.1 |
| opCjV0100000818 | 0 | 0.1 | 0.1 | 0 | -0.1 | 0.1 | 0.1 | 0 | 0.1 | 0.1 |
| opCjV0100000819 | -0.2 | 0.1 | 0.4 | 0 | 0.2 | 0 | 0 | 0 | -0.1 | 0 |
| opCjV0100000820 | 0.2 | 0 | 0.3 | 0.1 | -0.4 | 0.3 | 0.2 | 0.1 | 0.4 | 0.1 |
| opCjV0100000821 | 0.3 | 0.3 | 0.3 | 0.1 | 0 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000822 | 0 | 0 | -0.4 | 0 | 0 | -0.1 | -0.1 | -0.3 | 0.1 | 0 |
| opCjV0100000823 | -0.1 | 0 | -0.3 | -0.1 | -0.3 | 0.2 | 0 | 0 | 0.2 | 0.1 |
| opCjV0100000824 | 0.2 | 0.3 | 0.1 | -0.1 | -0.3 | 0 | -0.1 | -0.1 | 0.1 | 0.1 |
| opCjV0100000828 | -3.4 | -2.9 | -3.4 | -1 | 1.1 | -0.8 | -1 | 1 | -1.5 | 0.1 |
| opCjV0100000829 | 0 | 0.1 | 0.3 | 0.1 | 0.2 | -0.1 | 0 | -0.1 | 0.2 | 0 |
| opCjV0100000830 | 0.5 | 0.3 | 0.6 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0.1 |
| opCjV0100000832 | -5.8 | -0.2 | -2.1 | -1.4 | 1.9 | -1.8 | -0.1 | 1.7 | -2.4 | -1.4 |
| opCjV0100000834 | 0.8 | 0.5 | 1.1 | 0.1 | 0.3 | 0 | 0.1 | 0 | 0 | 0 |
| opCjV0100000835 | -0.7 | -0.2 | -0.8 | -0.2 | 0.1 | 0.3 | -0.2 | -0.1 | 0.3 | 0 |

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| opCjV0100000836 | 0.4 | 0.3 | 0.8 | -0.1 | 0 | 0 | 0 | 0 | 0.2 | -0.1 |
| opCjV0100000837 | -0.2 | -0.3 | -0.3 | -0.1 | 0 | 0.3 | -0.1 | -0.1 | 0.2 | 0 |
| opCjV0100000839 | 0.8 | 0.5 | 0.3 | 0.2 | 0.1 | -2 | 0 | 0.2 | 0.1 | -0.1 |
| opCjV0100000840 | -0.4 | 0.2 | 0.2 | 0 | -0.1 | 0.1 | 0 | 0 | 0 | 0 |
| opCjV0100000841 | -0.6 | -0.1 | -0.5 | -0.2 | -0.2 | 0.1 | -0.1 | -0.1 | 0.1 | 0.1 |
| opCjV0100000842 | 0.4 | 0.4 | 0.3 | 0.1 | -0.1 | 0 | -0.1 | 0 | 0.2 | 0 |
| opCjV0100000843 | -0.9 | -1 | 0 | -0.2 | 0.5 | 0 | 0.1 | 0.7 | -0.4 | -0.4 |
| opCjV0100000844 | -2.2 | 0.1 | -1.2 | 0 | 0 | -1 | -0.2 | 0 | 0 | -0.1 |
| opCjV0100000845 | -1.8 | -1 | -3 | 0 | -0.1 | -0.5 | -1 | -0.2 | 0 | -0.1 |
| opCjV0100000846 | 0.7 | 0.4 | 0.5 | 0.1 | 0 | 0.1 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000847 | -0.3 | 0 | -0.2 | -0.1 | -0.2 | 0.2 | 0 | 0 | 0.1 | 0 |
| opCjV0100000849 | 0.2 | 0.2 | 0.3 | 0 | 0 | 0.1 | -0.1 | 0 | -0.2 | -0.1 |
| opCjV0100000851 | 0.1 | 0 | 0.3 | 0 | 0.1 | 0 | -0.2 | -0.1 | 0 | -0.1 |
| opCjV0100000853 | 0.1 | 0.1 | 0.2 | 0 | 0.1 | 0.1 | 0 | 0 | 0.2 | 0 |
| opCjV0100000855 | 0.1 | 0.1 | 0.2 | 0.1 | 2.5 | 0.2 | 0 | -0.1 | 0.2 | 0.1 |
| opCjV0100000856 | -0.6 | -0.6 | -0.1 | 0 | 0.2 | 0.2 | -0.2 | -0.1 | -0.1 | 0 |
| opCjV0100000857 | -0.1 | -0.7 | 0.8 | -0.1 | 0.3 | 0.1 | 0.1 | 0.5 | -0.3 | -0.2 |

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| opCjV0100000858 | -0.7 | -0.7 | -0.2 | -0.1 | 0 | 0.2 | 0 | -0.2 | 0.2 | 0.1 |
| opCjV0100000859 | -0.2 | 0.2 | 0.5 | 0.1 | 0.3 | 0 | 0 | 0 | 0 | 0 |
| opCjV0100000860 | -0.4 | -0.5 | -0.2 | -0.1 | 0.3 | -0.2 | -0.3 | 0 | -0.1 | -0.1 |
| opCjV0100000861 | -6.2 | -0.1 | -6.2 | 0 | 0.1 | -1.8 | -2 | -0.3 | -1.2 | 0 |
| opCjV0100000862 | 0.5 | 0.3 | 0.5 | 0 | -0.2 | 0.1 | 0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000863 | 0.5 | 0.1 | 0.4 | 0.2 | -0.1 | 0.1 | 0.3 | -0.2 | 0.1 | -0.1 |
| opCjV0100000864 | 0.3 | 0.3 | 0 | 0 | -0.2 | 0 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100000865 | 0.4 | 0.1 | 0.2 | 0.1 | 0 | 0 | -0.1 | 0.1 | 0.1 | 0 |
| opCjV0100000866 | -0.8 | 0 | -0.1 | -0.1 | -0.2 | 0.1 | -0.2 | -0.1 | 0 | 0.1 |
| opCjV0100000867 | 0 | -1.7 | -0.7 | -0.2 | 2.2 | -0.4 | -2.2 | 0.1 | 0 | -0.2 |
| opCjV0100000868 | -0.5 | -0.2 | -0.7 | -0.1 | 0 | -1.4 | -0.3 | 0.1 | -0.1 | -0.1 |
| opCjV0100000869 | -0.3 | 0 | -0.2 | -0.1 | -0.1 | 0 | -0.1 | -0.1 | 0 | 0 |
| opCjV0100000870 | 0.1 | 0.2 | -0.1 | 0 | 0 | 0 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100000872 | -5.4 | -4.5 | -5.5 | -1.1 | 1.8 | -1.6 | -1.6 | 1.7 | -1.4 | -1.4 |
| opCjV0100000873 | 0.2 | -0.1 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | -0.1 | -0.2 |
| opCjV0100000874 | -0.1 | -0.4 | -0.8 | -0.2 | 0.1 | -0.2 | -0.2 | -0.1 | -0.3 | -0.2 |
| opCjV0100000875 | -0.7 | -0.4 | -0.9 | -0.1 | 0 | -0.8 | -0.3 | -0.9 | 0.1 | -0.1 |

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| opCjV0100000876 | 0.1 | -0.2 | 0.3 | 0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 | 0 |
| opCjV0100000877 | 0.2 | -0.2 | -1.8 | 0.1 | 0.3 | 0 | 0 | -0.2 | 0.1 | 0.1 |
| opCjV0100000878 | -0.4 | -0.5 | 0.2 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000879 | 0.1 | 0 | 0.1 | 0.1 | 1.3 | 0.1 | 0 | 0 | 0 | 0 |
| opCjV0100000880 | -0.2 | -0.1 | 0 | -0.1 | 0 | 0.2 | -0.1 | 0 | 0.4 | 0.1 |
| opCjV0100000881 | -0.6 | 0.1 | -0.1 | 0.1 | 0.2 | 0.1 | -0.2 | 0.1 | 0 | 0 |
| opCjV0100000883 | -0.6 | 0 | -1 | -0.2 | 0 | -1.3 | -0.3 | -1.1 | 0.4 | 0 |
| opCjV0100000884 | -0.4 | 0 | -0.1 | 0.1 | 0.2 | 0 | -0.2 | 0.1 | 0.1 | -0.1 |
| opCjV0100000887 | 0.5 | 0.2 | 0.3 | 0 | -0.2 | 0.2 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000888 | -0.4 | -0.2 | -0.2 | -0.1 | 0 | 0.1 | -0.1 | -0.1 | 0 | -0.1 |
| opCjV0100000890 | 0 | 0.1 | -0.1 | 0 | 0 | 0.2 | -0.4 | -0.1 | 0.1 | -0.2 |
| opCjV0100000891 | 0.3 | 0 | -1.7 | -1.6 | 1.9 | -2.1 | -2.1 | 1.6 | -0.1 | -1.8 |
| opCjV0100000892 | -0.1 | -0.3 | 0.3 | -0.3 | 0.2 | -0.1 | -0.1 | 0.3 | -0.3 | -0.3 |
| opCjV0100000894 | -0.4 | -0.1 | -0.6 | 0.1 | 0 | 0.2 | -0.1 | 0 | 0 | 0 |
| opCjV0100000895 | -2.8 | -1.4 | -0.8 | -0.3 | 0.4 | -1.4 | -1.1 | 0 | -0.3 | -0.5 |
| opCjV0100000896 | -7 | -0.2 | -1.7 | 0 | 2.2 | -1.6 | -2.3 | -0.1 | -1.4 | -0.1 |
| opCjV0100000897 | -2.5 | -1.9 | -1.6 | -0.6 | 0.6 | -0.7 | -0.9 | 0.2 | -0.6 | -0.6 |

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| opCjV0100000898 | -0.2 | -0.3 | -0.2 | -0.2 | 0 | 0.3 | -0.2 | -0.2 | -0.1 | 0.1 |
| opCjV0100000899 | 0.2 | 0.1 | 0.4 | 0.2 | 0.3 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000900 | -0.5 | -0.5 | -0.3 | -0.1 | 0.2 | 0.1 | -0.2 | 0 | -0.2 | -0.1 |
| opCjV0100000901 | -0.4 | 0 | -0.3 | -0.4 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0.1 |
| opCjV0100000902 | -7.4 | -0.2 | -3.4 | 0 | 0.6 | -1.1 | -0.7 | -0.1 | -0.4 | 0.1 |
| opCjV0100000904 | -0.2 | -0.1 | -0.6 | 0 | 0 | 0 | 0 | -0.1 | 0 | 0.1 |
| opCjV0100000905 | -0.3 | -0.1 | -0.1 | -0.1 | -0.1 | 0.2 | 0 | -0.2 | 0.2 | 0.2 |
| opCjV0100000906 | -0.1 | -0.1 | -0.1 | 0 | 0 | 0 | -0.1 | -0.2 | -0.1 | 0 |
| opCjV0100000907 | 0 | 0.1 | 0.4 | -0.1 | 0 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| opCjV0100000908 | -0.1 | -0.2 | 0.3 | 0 | 0 | 0.1 | 0 | -0.1 | 0.1 | 0.1 |
| opCjV0100000909 | 0.3 | 0 | -0.1 | -0.5 | 0.3 | -0.5 | -0.6 | 0.2 | -0.1 | -0.7 |
| opCjV0100000910 | -3 | -2.6 | -1.4 | -0.5 | 0.5 | -0.3 | -0.7 | 0.4 | -0.6 | -0.5 |
| opCjV0100000911 | -0.4 | -0.2 | -3 | -0.2 | -0.1 | -1.2 | -1.7 | -1.1 | -0.1 | 0 |
| opCjV0100000912 | -0.7 | -0.3 | -1.1 | -0.2 | -0.2 | 0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100000913 | -0.2 | 0.3 | 0.2 | 0 | -0.2 | 0.2 | 0 | 0 | 0.2 | 0.1 |
| opCjV0100000914 | 0.5 | 0.2 | -0.7 | 0.1 | 0 | -0.2 | 0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000915 | 0 | -1.6 | -0.4 | -0.5 | 0.6 | -1.6 | -0.7 | 0.5 | -0.1 | -0.6 |

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| opCjV0100000916 | -0.1 | 0.4 | 0.5 | 0.1 | -0.1 | 0 | 0 | -0.1 | 0.1 | -0.1 |
| opCjV0100000917 | -3.6 | -3 | -1.4 | -0.8 | 1.3 | -1 | -1.3 | 1.1 | -0.9 | -0.9 |
| opCjV0100000918 | 0.4 | 0.2 | 0.3 | 0 | 0 | 0 | -0.1 | 0 | 0 | 0 |
| opCjV0100000919 | -0.8 | -0.2 | -0.7 | -0.2 | -0.2 | 0.2 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100000920 | -0.2 | -0.3 | 0.2 | -0.1 | 0.6 | -0.1 | -0.6 | -0.1 | -0.2 | -0.3 |
| opCjV0100000921 | -3.9 | -2.5 | -1.3 | -0.8 | 0.8 | -0.4 | -0.8 | 0.6 | -0.6 | -0.6 |
| opCjV0100000922 | -0.3 | -0.3 | -2.2 | -0.1 | 0.1 | 0.2 | -0.4 | 0 | 0 | 0 |
| opCjV0100000923 | 0.5 | 0.2 | 0.8 | 0.1 | 0.4 | 0.1 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100000924 | -2.5 | -0.3 | -1 | 0 | 0 | 0.2 | -0.6 | -0.1 | -0.6 | 0.1 |
| opCjV0100000925 | 0.4 | 0.2 | -0.8 | 0 | 0 | -0.8 | -0.6 | -0.6 | 0.1 | 0 |
| opCjV0100000927 | 0.4 | 0.2 | 0.7 | 0.1 | 0.2 | 0.1 | 0 | -0.2 | 0.1 | 0.1 |
| opCjV0100000929 | 0 | -0.2 | 0.1 | 0 | 0.1 | -0.1 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100000930 | -0.4 | -0.1 | -0.1 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100000931 | -0.3 | -0.3 | 0 | -0.1 | 0 | 0 | 0 | 0.1 | 0.1 | 0 |
| opCjV0100000933 | 0.3 | 0.1 | 0.5 | 0.1 | 0.2 | -0.2 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000935 | 0.6 | 0.5 | 0.1 | 0.1 | -0.1 | 0 | 0 | -0.2 | 0.1 | 0 |
| opCjV0100000936 | -1.3 | -1.3 | -0.6 | -0.4 | 0.3 | -0.2 | -0.6 | 0.4 | -0.3 | -0.2 |

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| opCjV0100000937 | 0.2 | 0.2 | 0.2 | -0.1 | -0.1 | 0 | 0 | -0.2 | 0.1 | 0 |
| opCjV0100000938 | 0.1 | 0.2 | -0.4 | 0 | -0.2 | -0.1 | 0.1 | 0 | 0.2 | 0.1 |
| opCjV0100000940 | 0.2 | 0.3 | 0.2 | 0 | -0.2 | 0 | 0 | -0.1 | 0 | -0.1 |
| opCjV0100000941 | -0.1 | -0.2 | 0.1 | -0.1 | 0 | 0.2 | 0 | 0.2 | -0.1 | 0 |
| opCjV0100000942 | 0 | 0 | 0.1 | 0.1 | 0.1 | -0.1 | 0 | 0 | -0.1 | -0.2 |
| opCjV0100000943 | -0.1 | -0.1 | 0.1 | -0.1 | -0.2 | 0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100000944 | -2.6 | -2.4 | -2.7 | -0.8 | 1.3 | -2 | -1.3 | 1.9 | -0.6 | -1 |
| opCjV0100000945 | -1 | -0.4 | -0.3 | -0.1 | 0 | 0.2 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000946 | 0.4 | 0.2 | 0.4 | 0 | -0.1 | 0.2 | 0.1 | 0 | -0.2 | 0.1 |
| opCjV0100000947 | -0.2 | -0.1 | -0.6 | -0.2 | 0 | 0 | -0.3 | -0.1 | -0.1 | -0.1 |
| opCjV0100000948 | 0.4 | -0.2 | 0.5 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 |
| opCjV0100000951 | -5.3 | -5.6 | -4.7 | -1.6 | 1.7 | -1.3 | -1.9 | 2 | -2 | -1.6 |
| opCjV0100000952 | 0.1 | 0.2 | -0.2 | 0 | -0.1 | -0.1 | -0.1 | -0.1 | 0.1 | -0.1 |
| opCjV0100000953 | 0.5 | 0.1 | 0.5 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0 |
| opCjV0100000954 | -1.2 | 0 | -0.6 | -0.1 | -0.3 | 0.2 | -0.1 | 0 | 0.3 | 0 |
| opCjV0100000956 | 0.4 | 0.2 | 0.3 | 0.1 | -0.1 | 0.2 | 0 | -0.2 | 0.1 | 0 |
| opCjV0100000958 | 0.4 | 0.1 | 0.3 | 0 | 0.1 | -0.1 | 0.1 | 0.2 | -0.1 | -0.2 |

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| opCjV0100000960 | -0.2 | 0.1 | -0.4 | 0.1 | 0 | 0 | 0 | 0 | 0.1 | -0.3 |
| opCjV0100000962 | -0.7 | -0.3 | -0.9 | -0.1 | -0.2 | 0.3 | 0 | 0 | 0.3 | 0.2 |
| opCjV0100000963 | 0.8 | 0.5 | 0.8 | 0 | 0 | 0.1 | -0.9 | -0.5 | 0 | 0 |
| opCjV0100000965 | 0.1 | -0.2 | -0.5 | 0 | 0.1 | 0.1 | 0 | 0.2 | 0 | -0.1 |
| opCjV0100000966 | -0.5 | -0.1 | -0.6 | -0.1 | -0.2 | 0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100000967 | -0.2 | -0.1 | -0.1 | -0.1 | -0.1 | 0.2 | 0 | -0.2 | 0.1 | 0 |
| opCjV0100000969 | 0.1 | 0.1 | 0.2 | 0 | -0.1 | 0.2 | 0.1 | 0.1 | 0.1 | 0 |
| opCjV0100000970 | -0.1 | 0 | -0.2 | 0 | -0.1 | 0.3 | 0.1 | -0.1 | 0 | 0.1 |
| opCjV0100000971 | -1.1 | 0.2 | -0.5 | -0.1 | 0 | -0.1 | -0.2 | 0 | 0 | 0.1 |
| opCjV0100000972 | 0.7 | 0.6 | 0.5 | 0 | 0.1 | -0.1 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000974 | 0.2 | 0.1 | 0.2 | 0 | -0.1 | -0.1 | -0.1 | 0 | 0.1 | 0 |
| opCjV0100000975 | 0.6 | 0.2 | 0.6 | 0 | 0 | 0 | 0 | 0 | -0.1 | 0 |
| opCjV0100000977 | 0.3 | 0.3 | 0.4 | 0 | -0.1 | 0 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100000979 | 0.7 | 0.3 | 1 | 0 | 0 | 0.3 | 0.3 | 0.2 | 0 | 0 |
| opCjV0100000981 | 0 | -0.1 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | -0.2 | -0.1 |
| opCjV0100000982 | -0.4 | -0.8 | -0.3 | -0.1 | 0.2 | 0.1 | -0.1 | 0.1 | -0.2 | -0.1 |
| opCjV0100000983 | -0.8 | -0.6 | -0.8 | -1.3 | 1.8 | 0 | -0.4 | 2.2 | 0.1 | -1.2 |

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|---|---|---|---|---|---|---|---|---|---|---|
| opCjV0100000984 | -0.1 | -0.1 | -0.1 | -0.1 | -0.3 | 0.2 | 0 | 0 | 0.2 | 0 |
| opCjV0100000986 | -0.3 | -0.1 | -0.5 | 0.1 | 0 | 0.2 | 0 | 0.1 | 0.3 | 0 |
| opCjV0100000988 | 0.2 | 0 | 0.1 | 0 | 0.1 | 0.1 | 0.2 | 0.1 | -0.1 | -0.1 |
| opCjV0100000989 | 0.2 | 0 | -5.6 | 0.1 | 0 | 0.3 | 0 | -1.9 | -0.2 | 0 |
| opCjV0100000991 | -0.6 | -0.3 | -0.8 | -0.1 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100000992 | 0.7 | 0.5 | 0.2 | 0.2 | 0.1 | -0.1 | 0.1 | -0.1 | -0.3 | 0 |
| opCjV0100000993 | -0.5 | -0.4 | -5 | -0.1 | 0 | 0.1 | -0.2 | -1.4 | -0.1 | -0.1 |
| opCjV0100000994 | 0.3 | -0.1 | 0.3 | 0 | 0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100000995 | 0.2 | 0 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100000996 | 0 | 0.2 | 0 | -0.1 | -0.2 | 0.1 | -0.1 | -0.2 | 0.4 | 0 |
| opCjV0100000997 | 0.4 | 0.1 | 0.3 | 0.1 | 0.1 | 0 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100000998 | 0.2 | 0.1 | 0.3 | 0.1 | 0.2 | 0.1 | -0.1 | 0 | -0.1 | 0 |
| opCjV0100000999 | -5.7 | -5.9 | -4.9 | -1.5 | 1.9 | -1.2 | -1.8 | 1.8 | -2 | -1.6 |
| opCjV0100001000 | 0.4 | 0.3 | 0.4 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0 |
| opCjV0100001001 | -3.8 | -1.2 | -2.1 | -0.4 | 0.5 | -0.5 | -0.1 | -0.4 | -0.1 | -0.4 |
| opCjV0100001002 | 0.7 | 0.6 | 0.8 | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0 |
| opCjV0100001003 | 0.2 | 0.4 | 0.2 | 0.1 | 0 | 0.1 | -0.2 | -0.1 | 0.1 | 0 |

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| opCjV0100001004 | -0.1 | 0 | 0.1 | 0 | 0.1 | 0.1 | -0.2 | -0.2 | 0 | -0.1 |
| opCjV0100001005 | 0 | 0 | 0.4 | 0 | 0 | 0.2 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100001006 | -0.6 | -0.5 | -3.6 | -0.1 | 0 | 0.3 | -0.3 | -1.3 | 0.3 | -0.1 |
| opCjV0100001007 | 0.4 | 0.4 | 0.4 | 0 | -0.1 | -0.1 | -0.1 | 0.1 | 0.1 | -0.1 |
| opCjV0100001008 | -0.3 | 0.1 | -0.9 | -0.1 | -0.3 | 0.1 | -0.3 | -0.2 | 0.3 | 0.1 |
| opCjV0100001010 | 0 | 0.1 | 0.2 | -0.1 | -0.2 | 0.3 | 0.2 | 0 | 0 | 0 |
| opCjV0100001011 | 0.4 | 0 | 0.2 | -0.1 | 0 | 0 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100001012 | 0.4 | 0.1 | -0.4 | 0 | 0 | 0 | -0.1 | 0.2 | 0 | -0.2 |
| opCjV0100001013 | 0.2 | 0.1 | 0.1 | -0.1 | 0 | 0.1 | 0.1 | 0.2 | 0 | -0.1 |
| opCjV0100001014 | 0.3 | -0.2 | 0.3 | 0.1 | 0 | 0.1 | 0.1 | 0 | -0.1 | -0.1 |
| opCjV0100001016 | -0.1 | 0 | -0.2 | -0.1 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | -0.1 |
| opCjV0100001017 | 1.3 | 1 | 0.7 | 0.1 | -0.1 | 0.2 | 0.2 | -0.2 | 0.2 | 0.1 |
| opCjV0100001018 | 0.4 | 0.2 | -4.2 | 0 | 0 | -1.4 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100001019 | 0.3 | 0.1 | 0.4 | 0.1 | 0 | 0.3 | 0 | -0.2 | 0 | 0.1 |
| opCjV0100001020 | 0 | -0.3 | -0.8 | -1.7 | 3.2 | -2.5 | -2.5 | 3.9 | -0.3 | -1.8 |
| opCjV0100001021 | 0.4 | 0.4 | 0.4 | -0.1 | -0.2 | 0.1 | 0.1 | 0 | 0.2 | 0 |
| opCjV0100001022 | 0.2 | 0 | 0 | 0 | 0 | 0 | -0.2 | -0.1 | 0 | 0 |

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| opCjV0100001023 | 0.1 | 0.3 | 0.1 | 0.1 | 0 | 0.2 | -0.2 | -0.2 | 0 | 0 |
| opCjV0100001024 | -0.3 | 0.2 | -1.1 | -0.1 | -0.1 | -2.1 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100001025 | -6.5 | -6 | -3 | -0.2 | 3 | -2.4 | -2.6 | 0.6 | -2.2 | -0.3 |
| opCjV0100001026 | -5.3 | -4.4 | -6.7 | -1.2 | 1.6 | -2.2 | -0.2 | 2.9 | -1.2 | -1.4 |
| opCjV0100001028 | -0.3 | 0 | -0.1 | 0 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0 |
| opCjV0100001029 | 0.2 | -0.4 | 0.3 | -0.1 | 0.1 | 0.2 | 0 | -0.9 | 0 | 0 |
| opCjV0100001030 | -0.2 | -0.1 | -0.4 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0 | 0 |
| opCjV0100001031 | 0.2 | 0.1 | 0.2 | 0 | 0 | 0 | 0.1 | 0.3 | -0.1 | -0.1 |
| opCjV0100001032 | 0.2 | 0.1 | 0.3 | 0 | -0.1 | 0.1 | -0.1 | -0.2 | -0.1 | -0.1 |
| opCjV0100001034 | 0.4 | 0.3 | 0.2 | 0 | 0 | 0 | 0 | 0.2 | -0.3 | -0.1 |
| opCjV0100001035 | 0.3 | 0.2 | 0.1 | 0 | 0 | 0 | -0.1 | 0.2 | 0 | -0.1 |
| opCjV0100001036 | 0.3 | 0.3 | 0.3 | 0 | 0 | 0.2 | 0.1 | 0.1 | -0.1 | 0 |
| opCjV0100001038 | 0.5 | 0.2 | 0.3 | 0 | 0.1 | -0.1 | 0.1 | 0.1 | -0.1 | -0.2 |
| opCjV0100001039 | 0.8 | 0.2 | 0.3 | 0.2 | 0.2 | 0 | 0.1 | 0.1 | -0.1 | -0.1 |
| opCjV0100001040 | -0.4 | -0.1 | 0.3 | 0 | 0.2 | 0.2 | 0.2 | 0.5 | -0.4 | -0.2 |
| opCjV0100001041 | 0.4 | 0.2 | -0.2 | 0 | 0.1 | -1.4 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100001042 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | 0.1 | -0.1 | -0.2 |

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| opCjV0100001044 | -3 | 0.5 | 0.3 | -0.2 | -0.2 | 0.2 | 0.4 | 0.3 | 0.2 | -1.2 |
| opCjV0100001045 | -0.5 | -0.1 | -0.3 | 0 | 0 | 0.2 | -0.1 | 0 | 0.3 | 0 |
| opCjV0100001046 | 0.3 | 0.5 | 0.6 | 0 | -0.1 | 0.1 | 0.2 | 0 | 0 | 0 |
| opCjV0100001047 | -0.1 | 0.2 | -0.2 | 0 | -0.1 | 0.2 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100001048 | 0 | 0.2 | 0 | 0.1 | -0.2 | 0.3 | 0 | 0 | 0.3 | 0 |
| opCjV0100001049 | 0.4 | 0.3 | 0.2 | 0.2 | 0 | 0 | 0.1 | -0.1 | 0 | 0 |
| opCjV0100001050 | -0.3 | 0 | 0.4 | 0 | -0.1 | 0.3 | 0 | 0 | 0 | -0.1 |
| opCjV0100001051 | 0.2 | 0.1 | 0 | 0 | 0 | 0 | -0.1 | -0.1 | 0.1 | 0 |
| opCjV0100001052 | -0.5 | -0.2 | -0.8 | -0.1 | -0.1 | 0.1 | -0.1 | 0.1 | 0.1 | 0 |
| opCjV0100001054 | -0.2 | -0.3 | -0.1 | 0 | 0 | 0.1 | 0 | 0.1 | -0.1 | 0 |
| opCjV0100001055 | 0 | 0 | -0.2 | 0 | 0 | 0 | 0 | 0.1 | 0 | 0 |
| opCjV0100001056 | 0.2 | 0.1 | 0.1 | 0.1 | -0.1 | 0.1 | 0.1 | 0.2 | -0.1 | -0.1 |
| opCjV0100001057 | -4.5 | -0.7 | -0.6 | -0.1 | 0 | -1.1 | -1.8 | -0.1 | -0.1 | -0.1 |
| opCjV0100001058 | -3.8 | -3.2 | -3.4 | -1.2 | 2 | -1.3 | -1.5 | 1.3 | -1.2 | -1.4 |
| opCjV0100001061 | -4.5 | 0.1 | -2.6 | 0 | -0.2 | -0.9 | -0.8 | -0.9 | 0.1 | 0 |
| opCjV0100001063 | -0.8 | -0.4 | -0.8 | -0.1 | -0.1 | 0.3 | -0.1 | 0.1 | 0.4 | 0 |
| opCjV0100001066 | -0.3 | 0.1 | -0.4 | 0 | -0.1 | -0.3 | -0.2 | -0.2 | 0.1 | 0 |

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| opCjV0100001067 | 0.3 | 0.1 | 0.5 | 0.1 | 0.2 | 0 | 0.1 | 0 | -0.2 | 0 |
| opCjV0100001068 | -0.5 | -0.4 | -2 | -0.1 | 0.1 | 0.2 | -0.1 | -1 | 0.2 | 0 |
| opCjV0100001069 | 0.3 | 0.2 | 0.3 | 0 | 0 | -0.1 | -0.2 | 0.1 | 0.2 | 0 |
| opCjV0100001070 | -0.5 | -0.1 | -0.4 | 0 | 0 | 0.2 | -0.1 | 0.1 | 0.1 | 0 |
| opCjV0100001071 | -0.7 | -0.2 | -0.5 | -0.1 | -0.1 | 0.1 | -0.1 | 0 | 0.1 | -0.1 |
| opCjV0100001072 | -0.3 | -0.1 | -0.1 | 0 | 0 | 0.2 | 0 | 0 | -0.1 | -0.1 |
| opCjV0100001073 | -0.4 | -0.2 | -0.8 | 0 | 0 | -1 | 0 | -0.1 | 0.1 | 0 |
| opCjV0100001074 | -3 | -0.7 | -2.7 | 0 | -0.2 | -0.7 | -0.8 | 0.4 | 0.9 | 0 |
| opCjV0100001075 | 0.6 | 0.4 | 0.5 | 0 | 0 | 0 | 0 | -0.1 | 0 | 0 |
| opCjV0100001076 | -0.1 | -0.1 | -0.1 | -0.2 | 0.2 | -0.2 | -0.1 | 0.2 | 0 | -0.2 |
| opCjV0100001077 | 0.1 | 0.1 | 0.2 | 0 | 0 | 0 | 0.1 | 0.2 | -0.1 | -0.1 |
| opCjV0100001078 | 0.2 | 0.1 | 0.1 | 0 | 0 | -0.1 | -0.1 | 0.2 | 0.1 | 0 |
| opCjV0100001079 | -0.5 | -0.5 | -0.9 | 0 | 0.2 | 0.1 | -0.1 | 0 | -0.1 | -0.1 |
| opCjV0100001081 | 0.5 | -0.5 | 0.4 | 0.1 | 0 | 0.1 | 0.2 | 0 | 0 | -0.1 |
| opCjV0100001085 | -6.4 | -4.1 | -3.5 | 0 | 1.3 | -2 | -1.8 | -1 | -0.8 | -1.3 |
| opCjV0100001087 | -5.1 | -3.7 | -0.1 | -0.9 | 1.8 | -1.1 | -1.5 | 1.7 | -1.2 | -1.2 |
| opCjV0100001088 | 0.2 | 0 | 0 | -0.1 | -0.2 | 0 | 0 | -0.1 | 0 | 0 |

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| opCjV0100001089 | 0.1 | 0.3 | 0.2 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0.1 | 0 |
| opCjV0100001090 | 0 | 0 | -0.1 | 0 | 0.1 | 0.1 | 0 | -0.2 | 0 | 0 |
| opCjV0100001093 | -4.1 | 0 | -2.8 | 0 | 0 | -1 | 0.1 | 0.1 | 0 | 0 |
| opCjV0100001094 | -0.8 | 0.1 | 0.3 | 0 | 0 | 0.2 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100001095 | 0.4 | 0.3 | 0.6 | 0 | 0 | 0 | -0.2 | 0.1 | 1.3 | 0.1 |
| opCjV0100001096 | 0.7 | 0.4 | -3.6 | 0 | 0 | -1.5 | -1.8 | -1.6 | 0 | -0.1 |
| opCjV0100001097 | 0.1 | -0.1 | 0.1 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.1 | 0.1 |
| opCjV0100001098 | -1.5 | -0.7 | 0.9 | -1 | 1.2 | -0.1 | -0.7 | 1.7 | -0.8 | -0.9 |
| opCjV0100001099 | -0.3 | 0 | -0.3 | 0 | -0.1 | 0.2 | 0 | 0 | 0.1 | 0.1 |
| opCjV0100001100 | 0.6 | 0.4 | 0.4 | 0 | 0 | 0 | 0.2 | 0 | 0 | -0.1 |
| opCjV0100001101 | -0.4 | 0 | -0.3 | 0.1 | -0.2 | 0.2 | 0 | 0 | 0.1 | -0.1 |
| opCjV0100001102 | -3.4 | -3 | -0.9 | -0.9 | 2 | -0.7 | -1.4 | 1.6 | -1 | -1.1 |
| opCjV0100001103 | 0.5 | 0.3 | 0.3 | -0.1 | -0.1 | 0.1 | 0 | 0 | 0.1 | -0.1 |
| opCjV0100001104 | 0.1 | 0.2 | 0.4 | 0 | -0.2 | 0.1 | 0 | -0.1 | 0.1 | -0.1 |
| opCjV0100001105 | -0.3 | -0.1 | -4.7 | 0.1 | -0.1 | -1.4 | 0 | -0.1 | 0.3 | 0 |
| opCjV0100001106 | 0.2 | 0 | 0.3 | -0.1 | 0 | -1 | 0 | 0.1 | -0.1 | -0.1 |
| opCjV0100001107 | -0.3 | 0.2 | 0.7 | 0.1 | -0.1 | 0 | -0.1 | 0 | 0 | -0.1 |

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|---|---|---|---|---|---|---|---|---|---|---|
| opCjV0100001108 | 0.7 | 0.3 | 1 | 0.1 | 0 | 0 | 0.1 | 0.1 | 0 | -0.1 |
| opCjV0100001109 | 0.6 | 0.1 | 0.4 | 0.1 | 0.2 | 0 | 0 | -0.1 | -0.2 | -0.2 |
| opCjV0100001110 | -0.9 | -0.5 | -0.6 | 0 | -0.1 | 0.2 | -0.2 | 0.1 | -0.3 | -0.1 |
| opCjV0100001111 | 0.7 | 0.3 | 0.6 | 0.2 | 0.1 | -0.1 | 0.3 | 0 | -0.1 | -0.2 |
| opCjV0100001112 | -1.4 | -0.3 | -0.9 | -0.1 | 0 | 0.1 | -0.1 | 0.3 | 0 | 0 |
| opCjV0100001113 | 0.2 | 0.2 | 0.4 | -0.1 | 0 | 0.1 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100001114 | -6 | -6.7 | -2.1 | -1.1 | 3.3 | -0.9 | -3.5 | 2.9 | -2.6 | -1.2 |
| opCjV0100001115 | 0.2 | 0.1 | 0.3 | 0 | 0 | 0 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100001116 | 1 | 0.7 | 0.7 | 0.1 | 0.1 | -0.1 | 0.1 | 0 | 0.1 | 0 |
| opCjV0100001117 | 0.3 | 0.1 | 0.4 | 0.1 | 0.1 | 0.1 | 0 | -0.1 | -0.1 | 0 |
| opCjV0100001118 | 0.6 | 0 | -0.1 | 0.1 | 0 | 0.2 | 0 | 0 | 0.1 | 0 |
| opCjV0100001120 | 0.6 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0.1 | -0.1 | 0.1 | 0 |
| opCjV0100001121 | -3.3 | -3.1 | -3.1 | -2 | 2.9 | -1.7 | -1.7 | 1.7 | -1.1 | -2.1 |
| opCjV0100001122 | -0.3 | 0.1 | -0.1 | -0.1 | -0.2 | 0.2 | 0 | 0 | 0.1 | -0.1 |
| opCjV0100001123 | 0.4 | 0.2 | 0.4 | 0 | -0.1 | 0 | 0.1 | 0 | 0 | -0.1 |
| opCjV0100001124 | -0.5 | -0.1 | -2.1 | 0 | -0.1 | -1 | 0 | 0 | 0.1 | 0 |
| opCjV0100001125 | -0.2 | -0.2 | -2.7 | 0.1 | 0 | 0.1 | -0.1 | -0.6 | 0 | 0 |

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| opCjV0100001126 | 0.7 | 0.4 | 0.5 | 0 | -0.2 | 0.2 | 0 | 0.1 | 0 | 0 |
| opCjV0100001127 | 0 | 0.1 | 0.1 | -0.1 | -0.2 | 0 | -0.1 | -0.3 | 0 | -0.1 |
| opCjV0100001128 | 0.5 | 0.7 | 0.6 | 0 | -0.2 | 0.2 | 0.1 | 0.1 | 0.3 | 0.2 |
| opCjV0100001129 | 0.1 | -0.2 | 0.1 | 0 | -0.1 | 0.1 | 0 | 0.1 | -0.1 | 0 |
| opCjV0100001130 | 0 | -0.3 | -0.1 | 0 | 0.1 | 0.2 | 0.1 | 0 | -0.1 | 0 |
| opCjV0100001131 | 0.8 | 0.4 | 0.5 | 0.2 | 0 | 0 | 0.1 | 0.1 | -0.1 | -0.2 |

*The log 2 ratio values for each strain is calculated by taking average of the log 2 ratios for three independent array experiments.

Supplementary table 3: GACK trinary cutoffs for all genes on the array for six hyperinvasive and four low invasive *C. jejuni* strains.

| | Gene | | | | | | Hyperinvasive *C. jejuni* | | | | | | Low invasive *C. jejuni* | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Oligo_ID | Number_RM1221 | Name_RM1221 | Number_11168 | Name_11168 | Number_RM2228 | Name_RM2228 | 01_10 | 01_35 | 01_04 | 01_41 | 01_51 | EX114 | 01_30 | 01_32 | 01_46 | 01_39 | Role_11168 | Role_RM1221 | Role_RM2228 |
| "CJ_10001524" | CJE0001 | dnaA | Cj0001 | dnaA | CCO0032 | DnaA | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chromosomal replication initiator protein | chromosomal replication initiation protein | chromosomal replication initiator protein DnaA |
| "CJ_10001526" | CJE0002 | dnaN | Cj0002 | dnaN | CCO0033 | DnaN | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA polymerase III, beta chain | DNA polymerase III subunit beta | DNA polymerase III, beta subunit |
| "CJ_10001527" | CJE0003 | gyrB | Cj0003 | gyrB | CCO0034 | GyrB | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA gyrase subunit B | DNA gyrase subunit B | DNA gyrase, B subunit |
| "CJ_10001528" | CJE0004 | - | Cj0004c | - | - | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10001529" | CJE0005 | - | Cj0005c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative molybdenum containing oxidoreductase | molybdopterin oxidoreductase family protein | - |
| "CJ_10001530" | CJE0006 | - | Cj0006 | - | CCO0041 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | Na+/H+ antiporter family protein | probable integral membrane protein Cj0006 |
| "CJ_10001531" | CJE0007 | gltB | Cj0007 | gltB | CCO0042 | gltB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glutamate synthase (NADPH) large subunit | glutamate synthase, large subunit | glutamate synthase, large subunit |
| "CJ_10001533" | CJE0008 | gltD | Cj0009 | gltD | CCO0043 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glutamate synthase (NADPH) small subunit | glutamate synthase, small subunit | glutamate synthase (NADPH) small chain Cj0009 |
| "CJ_10001023" | CJE0009 | rnhB | Cj0010c | rnhB | CCO0044 | rnhB | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | ribonuclease HII | ribonuclease HII | ribonuclease HII |
| "CJ_10001024" | CJE0010 | comEA | Cj0011c | - | - | - | 1 | 1 | 1 | 1 | 1 | 0 | -1 | -1 | 1 | 1 | putative non-specific DNA binding protein | competence protein ComEA | - |
| "CJ_10001025" | CJE0011 | rbr | Cj0012c | - | CCO0045 | rr2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | non-haem iron protein | rubrerythrin | rubrerythrin |
| "CJ_10001026" | CJE0012 | ilvD | Cj0013 | ilvD | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | 1 | dihydroxy-acid dehydratase | dihydroxy-acid dehydratase | - |
| "CJ_10001028" | CJE0013 | - | Cj0014c | - | - | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | putative integral membrane protein | pseudogene | - |
| "CJ_10001030" | CJE0015 | - | Cj0015c | - | CCO0047 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001032" | CJE0016 | - | Cj0016 | - | CCO0049 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transcriptional regulatory protein | ExsB | exsB protein |
| "opCcV0100001629" | CJE0017 | - | Cj0017c | - | CCO0050 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP /GTP binding protein | disulfide bond formation protein, DsbB family | probable ATP /GTP binding protein Cj0017c |
| "CJ_10001036" | CJE0018 | - | Cj0018c | - | CCO0051 | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 0 | 1 | small hydrophobic protein | hypothetical protein | small hydrophobic protein Cj0018c -related |
| "CJ_10001038" | CJE0019 | - | Cj0019c | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | -1 | MCP-domain signal transduction protein | methyl-accepting chemotaxis protein | - |
| "CJ_10001051" | CJE0020 | - | Cj0020c | - | - | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | 1 | cytochrome C551 peroxidase | cytochrome c551 peroxidase | - |
| "CJ_10001052" | CJE0021 | - | Cj0021c | - | CCO0052 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | fumarylacetoacetate hydrolase family protein | fumarylacetoacetate hydrolase family protein |
| "CJ_10001053" | CJE0022 | - | Cj0022c | - | CCO0053 | - | 1 | 1 | 1 | 0 | -1 | 1 | 0 | -1 | 1 | -1 | putative ribosomal pseudouridine synthase | RNA pseudouridylate synthase family protein | RNA pseudouridylate synthase family |
| "CJ_10001054" | CJE0023 | - | Cj0023 | purB | CCO0054 | purB | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | adenylosuccinate lyase | adenylosuccinate lyase | adenylosuccinate lyase |
| "CJ_10001056" | CJE0024 | nrdA | Cj0024 | nrdA | CCO0055 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | ribonucleoside-diphosphate reductase alpha | ribonucleotide-diphosphate reductase alpha | ribonucleoside reductase, alpha subunit |
| "CJ_10001058" | CJE0025 | - | Cj0025c | - | CCO0056 | gltP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane symporter | sodium/dicarboxylate symporter | sodium/dicarboxylate symporter family protein |
| "CJ_10001060" | CJE0026 | thyX | Cj0026c | - | CCO0057 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | thymidylate synthase | Thymidylate synthase complementing protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001063" | CJE0027 | pyrG | Cj0027 | pyrG | CCO0058 | pyrG | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | CTP synthase | CTP synthetase | CTP synthase |
| "CJ_10001065" | CJE0028 | recJ | Cj0028 | recJ | CCO0059 | recJ | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | | 1 | putative single-stranded-DNA-specific | single-stranded-DNA-specific exonuclease RecJ | single-stranded-DNA-specific exonuclease RecJ |
| "CJ_10001067" | CJE0029 | ansA | Cj0029 | ansA | CCO0060 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | cytoplasmic L-asparaginase | L-asparaginase | L-asparaginase II |
| "CJ_10001084" | CJE0030 | - | Cj0030 | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10001086" | CJE0031 | - | Cj0031 | - | CCO0070 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 1 | putative type IIS restriction /modification | type II restriction-modification enzyme | type II restriction-modification enzyme |
| "CJ_10001089" | CJE0032 | - | Cj0033 | - | CCO0073 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | -1 | Putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0033 |
| "CJ_10001092" | CJE0033 | - | Cj0034c | - | CCO0075 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0034c |
| "CJ_10001095" | CJE0034 | - | Cj0035c | - | CCO0076 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 0 | putative efflux protein | drug resistance transporter, Bcr/CflA family | probable efflux protein Cj0035c |
| "CJ_10001100" | CJE0035 | - | Cj0036 | - | CCO0077 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001103" | CJE0036 | - | Cj0037c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cytochrome c | cytochrome c family protein | - |
| "CJ_10001106" | CJE0037 | - | Cj0038c | - | CCO0078 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0038c |
| "CJ_10001109" | CJE0038 | typA | Cj0039c | typA | CCO0079 | typA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | GTP-binding protein typA homolog | GTP-binding protein TypA | GTP-binding protein TypA |
| "CJ_10001119" | CJE0039 | - | Cj0040 | - | CCO0080 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001121" | CJE0040 | - | Cj0041 | - | CCO0081 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001123" | CJE0041 | flgD | Cj0042 | flgD | CCO0082 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative flagellar hook assembly protein | flagellar hook assembly protein | probable flagellar hook assembly protein Cj0042 |
| "CJ_10001125" | CJE0042 | - | Cj0043 | flgE | CCO0083 | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | -1 | 0 | flagellar hook protein flgE | flagellar hook protein | flagellar hook protein flgE Cj0043 |
| "CJ_10001128" | CJE0043 | - | Cj0044c | - | CCO0084 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001134" | CJE0044 | - | Cj0045c | - | CCO0085 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | putative iron-binding protein | hypothetical protein | conserved hypothetical protein |
| "opCjV0100001066" | CJE0045 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001138" | CJE0046 | - | Cj0046 | - | CCO0087 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 0 | pseudogene | pseudogene | C4-dicarboxylate transporter |
| "CJ_10001141" | CJE0048 | trmU | Cj0053c | trmU | CCO0088 | trmU | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA | tRNA | tRNA |
| "CJ_10001144" | CJE0049 | - | Cj0054c | - | CCO0089 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | lysine decarboxylase family protein | Predicted Rossmann fold nucleotide-binding |
| "opCjV0100000022" | CJE0050 | - | - | - | - | - | -1 | 1 | 0 | 0 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000192" | CJE0051 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100001058" | CJE0052 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000772" | CJE0053 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10001165" | CJE0054 | - | Cj0057 | - | CCO0113 | - | 1 | 1 | -1 | 1 | 1 | | 1 | 1 | 1 | 1 | putative periplasmic protein | hmcD domain protein | probable periplasmic protein Cj0057 |
| "CJ_10001167" | CJE0055 | - | Cj0058 | - | CCO0114 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 0 | putative periplasmic protein | peptidase family protein | probable periplasmic protein Cj0058 |
| "CJ_10001168" | CJE0056 | fliY | Cj0059c | fliY | CCO0115 | fliY | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellar motor switch protein | flagellar motor switch protein | fliY protein (fliY) |
| "CJ_10001172" | CJE0057 | fliM | Cj0060c | fliM | CCO0116 | fliM | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar motor switch protein | flagellar motor switch protein | flagellar motor switch protein FliM |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001176" | CJE0058 | fliA | Cj0061c | fliA | CCO0117 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative RNA polymerase sigma factor for | flagellar biosynthesis sigma factor FliA | probable RNA polymerase sigma factor for |
| "CJ_10001180" | CJE0059 | - | Cj0062c | - | CCO0118 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0062c |
| "CJ_10001183" | CJE0060 | - | Cj0063c | - | CCO0119 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP-binding protein | ATPase, ParA family | ATP-binding protein (ylxH) |
| "CJ_10001186" | CJE0061 | flhF | Cj0064c | flhF | CCO0120 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar biosynthesis protein | flagellar biosynthesis protein | flagellar biosynthetic protein FlhF, putative |
| "CJ_10001188" | CJE0062 | folK | Cj0065c | folK | CCO0121 | folK | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative | 2-amino-4-hydroxy-6- | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase |
| "CJ_10001210" | CJE0063 | aroQ | Cj0066c | aroQ | CCO0122 | aroQ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3-dehydroquinate dehydratase | 3-dehydroquinate dehydratase | 3-dehydroquinate dehydratase, type II |
| "opCcV0100000682" | CJE0064 | - | Cj0067 | - | CCO0123 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | chlorohydrolase | chlorohydrolase |
| "opCcV0100000642" | CJE0065 | sppA | Cj0068 | pspA | CCO0124 | sppA | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | protease | signal peptide peptidase SppA, 36K type | protease IV (PspA) |
| "CJ_10001216" | CJE0066 | - | Cj0069 | - | CCO0125 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001219" | CJE0067 | - | Cj0070c | - | CCO0126 | - | -1 | 1 | 1 | 1 | -1 | | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001223" | CJE0068 | - | Cj0072c | - | - | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | pseudogene | - |
| "CJ_10001227" | CJE0069 | - | Cj0073c | - | CCO0129 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001230" | CJE0070 | - | Cj0074c | - | CCO0130 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative iron-sulfur protein | iron-sulfur cluster binding protein | iron-sulfur cluster binding protein |
| "CJ_10001232" | CJE0071 | - | Cj0075c | - | CCO0131 | glcF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative oxidoreductase iron-sulfur subunit | cysteine-rich domain protein | conserved hypothetical secreted protein |
| "CJ_10001235" | CJE0072 | lctP | Cj0076c | lctP | CCO0132 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | L-lactate permease | L-lactate permease | L-lactate permease (lctP) |
| "CJ_10001257" | CJE0073 | cdtC | Cj0077c | cdtC | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | cytolethal distending toxin | cytolethal distending toxin, subunit C | - |
| "CJ_10001259" | CJE0074 | cdtB | Cj0078c | cdtB | CCO0369 | cdtB | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cytolethal distending toxin | cytolethal distending toxin, subunit B | cytolethal distending toxin A |
| "CJ_10001261" | CJE0075 | cdtA | Cj0079c | cdtA | CCO0370 | cdtA | 0 | 1 | 1 | -1 | 0 | 1 | 1 | -1 | | 1 | cytolethal distending toxin | cytolethal distending toxin, subunit A | cytolethal distending toxin A |
| "CJ_10001264" | CJE0076 | - | Cj0080 | - | CCO0133 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0080 |
| "CJ_10001266" | CJE0077 | cydA | Cj0081 | cydA | CCO0134 | cydA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cytochrome bd oxidase subunit I | cytochrome d ubiquinol oxidase, subunit I | cytochrome d ubiquinol oxidase, subunit I |
| "CJ_10001269" | CJE0078 | cydB | Cj0082 | cydB | CCO0135 | cydB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | cytochrome bd oxidase subunit II | cytochrome d ubiquinol oxidase, subunit II | cytochrome d ubiquinol oxidase, subunit II |
| "opCjV0100000945" | CJE0079 | - | - | - | - | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001272" | CJE0080 | - | Cj0085c | - | CCO0139 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative amino acid recemase | aspartate racemase, putative | aspartate racemase |
| "CJ_10001273" | CJE0081 | ung | Cj0086c | ung | CCO0140 | ung | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | uracil-DNA glycosylase | uracil-DNA glycosylase | uracil-DNA glycosylase |
| "CJ_10001275" | CJE0082 | aspA | Cj0087 | aspA | CCO0141 | aspA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | aspartate ammonia-lyase | aspartate ammonia-lyase | aspartate ammonia-lyase |
| "CJ_10001277" | CJE0083 | dcuA | Cj0088 | dcuA | CCO0142 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | putative anaerobic C4-dicarboxylate transporter | anaerobic C4-dicarboxylate transporter | Dcu family anaerobic dicarboxylate transport |
| "CJ_10001287" | CJE0084 | - | Cj0089 | - | CCO0143 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0089 |
| "CJ_10001290" | CJE0085 | - | Cj0090 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | - |
| "CJ_10001292" | CJE0086 | - | Cj0091 | - | CCO0144 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0091 |
| "CJ_10001294" | CJE0087 | - | Cj0092 | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10001296" | CJE0088 | - | Cj0093 | - | CCO0145 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0093 , putative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001299" | CJE0089 | rplU | Cj0094 | rplU | CCO0146 | rplU | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L21 | 50S ribosomal protein L21 | ribosomal protein L21 |
| "CJ_10001301" | CJE0090 | rpmA | Cj0095 | rpmA | CCO0147 | rpmA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L27 | 50S ribosomal protein L27 | ribosomal protein L27 |
| "CJ_10001303" | CJE0091 | - | Cj0096 | - | CCO0148 | obg | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative GTP-binding protein | GTP-binding protein, GTP1/Obg family | GTP-binding protein Obg |
| "CJ_10001305" | CJE0092 | proB | Cj0097 | proB | CCO1787 | proB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative glutamate 5-kinase | gamma-glutamyl kinase | glutamate 5-kinase |
| "CJ_10001307" | CJE0093 | fmt | Cj0098 | fmt | CCO1783 | fmt | 1 | -1 | | | -1 | -1 | 1 | -1 | -1 | -1 | methionyl-tRNA formyltransferase | methionyl-tRNA formyltransferase | methionyl-tRNA formyltransferase |
| "CJ_10001316" | CJE0094 | - | Cj0099 | birA | CCO1782 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative biotin--[acetyl-CoA-carboxylase] | biotin--protein ligase | biotin--acetyl-CoA-carboxylase ligase |
| "CJ_10001319" | CJE0095 | - | Cj0100 | - | CCO1781 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | parA family protein | chromosome partitioning protein, ParA family | parA family protein Cj0100 |
| "CJ_10001322" | CJE0096 | - | Cj0101 | - | CCO1780 | spo0J | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | parB family protein | chromosome partitioning protein, ParB family | chromosome partioning protein, ParB family |
| "CJ_10001324" | CJE0097 | - | Cj0102 | - | CCO1779 | - | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | ATP synthase F0 sector B' subunit | ATP synthase subunit B | ATP synthase F0, subunit b' (atpF'), putative |
| "CJ_10001327" | CJE0098 | - | Cj0103 | atpF | CCO1778 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP synthase F0 sector B subunit | ATP synthase subunit B | ATP synthase B/B' CF(0) superfamily |
| "CJ_10001330" | CJE0099 | atpH | Cj0104 | atpH | CCO1777 | atpH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP synthase F1 sector delta subunit | ATP synthase subunit D | ATP synthase F1, delta subunit |
| "CJ_10001334" | CJE0100 | atpA | Cj0105 | atpA | CCO1776 | atpA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP synthase F1 sector alpha subunit | ATP synthase subunit A | ATP synthase F1, alpha subunit |
| "CJ_10001337" | CJE0101 | atpG | Cj0106 | atpG | CCO1775 | atpG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP synthase F1 sector gamma subunit | ATP synthase subunit C | ATP synthase F1, gamma subunit |
| "CJ_10001340" | CJE0102 | atpD | Cj0107 | atpD | CCO1774 | atpD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP synthase F1 sector beta subunit | ATP synthase subunit B | ATP synthase F1, beta subunit |
| "CJ_10001343" | CJE0103 | atpC | Cj0108 | atpC | CCO1773 | atpC | 1 | 1 | | 1 | -1 | 1 | -1 | -1 | 1 | -1 | ATP synthase F1 sector epsilon subunit | ATP synthase subunit epsilon | ATP synthase F1, epsilon subunit |
| "CJ_10000466" | CJE0104 | - | Cj0109 | exbB3 | CCO1772 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | exbB\tolQ family transport protein | MotA/TolQ/ExbB proton channel family protein | exbB/tolQ family transport protein Cj0109 |
| "CJ_10000468" | CJE0105 | - | Cj0110 | exbD3 | CCO1771 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | exbD\tolR family transport protein | TonB system transport protein ExbD, putative | exbD/tolR family transport protein Cj0110 |
| "CJ_10000470" | CJE0106 | - | Cj0111 | - | CCO1770 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | periplasmic protein | TonB domain protein | periplasmic protein Cj0111 |
| "CJ_10000471" | CJE0107 | tolB | Cj0112 | - | CCO1769 | tolB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | periplasmic protein | translocation protein TolB precursor | colicin tolerance-like protein (tolB) |
| "opCcV0100001578" | CJE0108 | - | Cj0113 | pal | CCO1768 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | peptidoglycan associated lipoprotein (omp18) | peptidoglycan-associated lipoprotein Omp18 | omp18 |
| "CJ_10000472" | CJE0109 | - | Cj0114 | - | CCO1767 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0114 |
| "CJ_10000473" | CJE0110 | slyD | Cj0115 | slyD | CCO1766 | slyD | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | peptidyl-prolyl cis-trans isomerase | FKBP-type peptidyl-prolyl cis-trans isomerase | FKBP-type peptidyl prolyl cis-trans isomerase; |
| "CJ_10000474" | CJE0111 | fabD | Cj0116 | fabD | CCO1765 | fabD | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | malonyl CoA-acyl carrier protein transacylase | acyl-carrier-protein S-malonyltransferase | malonyl CoA-acyl carrier protein transacylase |
| "CJ_10000475" | CJE0112 | mtnA | Cj0117 | pfs | CCO1764 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 5'-methylthioadenosine\S-adenosylhomocysteine | 5'-methylthioadenosine/S-adenosylhomocysteine | MTA/SAH nucleosidase |
| "CJ_10000476" | CJE0113 | - | Cj0118 | - | CCO1763 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | PP-loop family protein | conserved hypothetical protein |
| "CJ_10000487" | CJE0114 | - | Cj0119 | - | CCO1762 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | pyrazinamidase/nicotinamidase, putative | conserved hypothetical protein |
| "CJ_10000488" | CJE0115 | - | Cj0120 | - | CCO1761 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000489" | CJE0116 | - | Cj0121 | - | CCO1760 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR00043 |
| "CJ_10000490" | CJE0117 | - | Cj0122 | - | CCO1759 | - | 0 | 0 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000491" | CJE0118 | dusB | Cj0123c | - | CCO1756 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transcriptional | tRNA-dihydrouridine | probable transcription |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | regulator | synthase B | regulator Cj0123c |
| "CJ_10000492" | CJE0119 | - | Cj0124c | - | CCO1755 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0124c |
| "CJ_10000493" | CJE0120 | - | Cj0125c | - | CCO1754 | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | dksA-like protein | dnaK suppressor protein, putative | dnaK suppressor, putative |
| "CJ_10000494" | CJE0121 | - | Cj0126c | - | CCO1753 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical secreted protein |
| "CJ_10000495" | CJE0122 | accD | Cj0127c | accD | CCO1752 | accD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | acetyl-coenzyme A carboxylase carboxyl | acetyl-CoA carboxylase beta subunit | acetyl-CoA carboxylase, carboxyl transferase, |
| "CJ_10000496" | CJE0123 | - | Cj0128c | - | CCO1751 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | suhB-like protein | Inositol monophosphatase family protein | conserved hypothetical protein |
| "CJ_10000507" | CJE0124 | - | Cj0129c | - | CCO1750 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | outer membrane protein | outer membrane protein, OMP85 family | outer membrane protein Cj0129c |
| "CJ_10000508" | CJE0125 | tyrA | Cj0130 | tyrA | CCO1749 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative prephenate dehydrogenase | prephenate dehydrogenase | Prephenate dehydrogenase |
| "CJ_10000509" | CJE0126 | - | Cj0131 | - | CCO1748 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | peptidase, M23/M37 family | probable periplasmic protein Cj0131 |
| "CJ_10000510" | CJE0127 | lpxC | Cj0132 | lpxC | CCO1747 | lpxC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UDP-3-O-[3-hydroxymyristoyl] n-acetylglucosamine | UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine | UDP-3-0-acyl N-acetylglucosamine deacetylase |
| "CJ_10000512" | CJE0128 | - | Cj0133 | - | CCO1746 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000514" | CJE0129 | thrB | Cj0134 | thrB | CCO1745 | thrB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | homoserine kinase | homoserine kinase | homoserine kinase |
| "CJ_10000516" | CJE0130 | - | Cj0135 | - | CCO1744 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF448) |
| "CJ_10000517" | CJE0131 | infB | Cj0136 | infB | CCO1743 | infB | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | -1 | translation initiation factor IF-2 | translation initiation factor IF-2 | translation initiation factor IF-2 |
| "CJ_10000519" | CJE0132 | rbfA | Cj0137 | - | CCO1742 | rbfA | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | ribosome-binding factor A | ribosome-binding factor A |
| "CJ_10000520" | CJE0133 | - | Cj0138 | - | CCO1741 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000536" | CJE0134 | - | Cj0139 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | putative endonuclease | McrBC restriction endonuclease system, McrB | - |
| "CJ_10000537" | CJE0135 | - | Cj0140 | - | - | - | 0 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000538" | CJE0136 | - | Cj0141c | - | CCO1737 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ABC transporter integral membrane protein | cation ABC transporter, permease protein | ABC transporter integral membrane protein |
| "CJ_10000539" | CJE0137 | - | Cj0142c | - | CCO1736 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ABC transporter ATP-binding protein | cation ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "CJ_10000541" | CJE0138 | - | Cj0143c | - | CCO1735 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | periplasmic solute binding protein for ABC | cation ABC transporter, periplasmic | adhesion protein, putative |
| "opCjV0100000828" | CJE0139 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "CJ_10001578" | CJE0140 | - | Cj1564 | - | CCO1678 | - | 0 | 0 | 0 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | putative methyl-accepting chemotaxis signal | methyl-accepting chemotaxis protein | methyl-accepting chemotaxis protein (tlpA) |
| "CJ_10000544" | CJE0141 | - | Cj0145 | - | CCO1732 | - | -1 | 0 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Tat (twin-arginine translocation) pathway signal |
| "CJ_10000546" | CJE0142 | trxB | Cj0146c | trxB | CCO1731 | trxB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | thioredoxin reductase | thioredoxin-disulfide reductase | thioredoxin reductase |
| "CJ_10000548" | CJE0143 | trx | Cj0147c | trxA | CCO1730 | trx | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | thioredoxin | thioredoxin | thioredoxin |
| "CJ_10000550" | CJE0144 | - | Cj0148c | - | CCO1729 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Endonuclease |
| "CJ_10000564" | CJE0145 | hom | Cj0149c | hom | CCO1728 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | homoserine dehydrogenase | homoserine dehydrogenase | homoserine dehydrogenase |
| "CJ_10000565" | CJE0146 | - | Cj0150c | - | CCO1727 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | aminotransferase | aspartate aminotransferase | aspartate aminotransferase |
| "CJ_10000566" | CJE0147 | - | Cj0151c | - | CCO1726 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0151c |
| "CJ_10000567" | CJE0148 | - | Cj0152c | - | CCO1725 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | Cj0152c |
| "CJ_10000569" | CJE0149 | - | Cj0153c | - | CCO1724 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative rRNA methylase | RNA methyltransferase, TrmH family | RNA methyltransferase, TrmH family, group 3 |
| "CJ_10000570" | CJE0150 | - | Cj0154c | - | CCO1723 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative methylase | tetrapyrrole methylase family protein | conserved hypothetical protein TIGR00096 |
| "CJ_10000572" | CJE0151 | rpmE | Cj0155c | rpmE | CCO1722 | rpmE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L31 | ribosomal protein L31 | ribosomal protein L31 |
| "CJ_10000574" | CJE0152 | - | Cj0156c | - | CCO1721 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | conserved hypothetical protein TIGR00046 | conserved hypothetical protein TIGR00046 |
| "CJ_10000576" | CJE0153 | - | Cj0157c | - | CCO1720 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0157c |
| "CJ_10000578" | CJE0154 | - | Cj0158c | - | CCO1719 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative haem-binding lipoprotein | cytochrome c family protein | conserved hypothetical protein |
| "CJ_10000592" | CJE0155 | - | Cj0159c | - | CCO1718 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | 6-pyruvoyl tetrahydrobiopterin synthase, | 6-pyruvoyl tetrahydrobiopterin synthase, |
| "CJ_10000593" | CJE0156 | - | Cj0160c | - | CCO1717 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | radical SAM domain protein | radical SAM domain protein, putative |
| "CJ_10000594" | CJE0157 | - | Cj0161c | moaA | CCO1716 | moaA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | molybdenum cofactor biosynthesis protein A | molybdenum cofactor biosynthesis protein A | molybdopterin cofactor biosynthesis protein A |
| "CJ_10000595" | CJE0158 | - | Cj0162c | - | CCO1715 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0162c |
| "CJ_10000596" | CJE0159 | - | Cj0163c | - | CCO1714 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000597" | CJE0160 | - | Cj0164c | ubiA | CCO1713 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative 4-hydroxybenzoate | 4-hydroxybenzoate octaprenyltransferase | 4-hydroxybenzoate polyprenyltransferase, |
| "CJ_10000599" | CJE0161 | miaA | Cj0166 | miaA | CCO1712 | miaA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA delta(2)-isopentenylpyrophosphate | tRNA delta(2)-isopentenylpyrophosphate | tRNA delta(2)-isopentenylpyrophosphate |
| "CJ_10000601" | CJE0162 | - | Cj0167c | - | CCO1711 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | hypothetical protein | membrane protein, putative |
| "opCjjV010000101" | CJE0163 | - | Cj0168c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "opCcV0100001164" | CJE0164 | sodB | Cj0169 | sodB | CCO1706 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | superoxide dismutase (Fe) | superoxide dismutase, Fe | superoxide dismutase (fe) |
| "CJ_10000628" | CJE0165 | - | Cj0172c | - | CCO1705 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | saccharopine dehydrogenase | saccharopine dehydrogenase |
| "CJ_10000630" | CJE0166 | - | Cj0173c | - | CCO1704 | potA | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | putative iron-uptake ABC transport system | iron ABC transporter, ATP binding subunit | spermidine/putrescine ABC transporter, |
| "CJ_10000631" | CJE0167 | - | Cj0174c | - | CCO1703 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative iron-uptake ABC transport system | iron ABC transporter, permease protein | iron compound ABC transporter, permease protein, |
| "CJ_10000632" | CJE0168 | - | Cj0175c | - | CCO1702 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative iron-uptake ABC transport system | iron ABC transporter, periplasmic iron-binding | iron transport protein |
| "CJ_10000634" | CJE0169 | - | Cj0176c | - | CCO1701 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | hypothetical protein | probable lipoprotein Cj0176c -related protein |
| "CJ_10000636" | CJE0170 | - | Cj0177 | - | CCO1700 | - | 1 | 1 | 0 | 1 | 0 | 1 | -1 | -1 | 1 | 1 | putative lipoprotein | TonB-dependent colicin lipoprotein, putative | lipoprotein, putative |
| "CJ_10000638" | CJE0171 | - | Cj0178 | - | CCO1699 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative outer membrane siderophore receptor | TonB-dependent colicin receptor protein, | TonB-dependent receptor |
| "CJ_10000640" | CJE0172 | - | Cj0179 | exbB1 | CCO1698 | - | 1 | 1 | -1 | 1 | 1 | 0 | -1 | -1 | 1 | 1 | biopolymer transport protein | TonB system transport protein ExbB | biopolymer transport protein Cj0179 |
| "CJ_10000654" | CJE0173 | - | Cj0180 | exbD1 | CCO1697 | - | 0 | 0 | | 1 | 1 | | | 1 | -1 | 1 | biopolymer transport protein | biopolymer transport protein, ExbD/TolR family | biopolymer transport protein Cj0180 |
| "CJ_10000656" | CJE0174 | - | Cj0181 | tonB1 | CCO1696 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | possible tonB transport protein | TonB-dependent colicin receptor protein, | probable tonB transport protein Cj0181 |
| "CJ_10000657" | CJE0175 | - | Cj0182 | - | CCO1695 | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | transmembrane transport | antibiotic transport protein, | transmembrane transport |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | protein | putative | protein Cj0182 |
| "CJ_10000659" | CJE0176 | - | Cj0183 | - | CCO1693 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein with | transporter, putative | transporter, putative |
| "CJ_10000660" | CJE0177 | - | Cj0184c | - | CCO1692 | - | 1 | -1 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | possible serine\threonine protein phosphatase | Ser/Thr protein phosphatase family protein | probable serine/threonine protein phosphatase |
| "CJ_10000661" | CJE0178 | - | Cj0185c | - | CCO1691 | phnA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phnA-like protein | PhnA domain protein | phnA protein |
| "CJ_10000663" | CJE0179 | - | Cj0186c | - | CCO1690 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | integral membrane protein, TerC family | membrane protein, TerC family |
| "CJ_10000665" | CJE0180 | purN | Cj0187c | purN | CCO1687 | purN | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | phosphoribosylglycinamide formyltransferase | phosphoribosylglycinamide formyltransferase | phosphoribosylglycinamide formyltransferase |
| "CJ_10000667" | CJE0181 | - | Cj0188c | - | CCO1686 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | YjeF-related protein N-terminus family |
| "CJ_10000669" | CJE0182 | - | Cj0189c | - | CCO1685 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000683" | CJE0183 | - | Cj0190c | - | CCO1684 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | Mg chelatase-related protein | Mg chelatase-related protein |
| "CJ_10000685" | CJE0184 | def | Cj0191c | def | CCO1683 | def | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | polypeptide deformylase | peptide deformylase | polypeptide deformylase |
| "CJ_10000687" | CJE0185 | clpP | Cj0192c | clpP | CCO1682 | clpP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP-dependent clp protease proteolytic subunit | ATP-dependent Clp protease proteolytic subunit | ATP-dependent Clp protease, proteolytic subunit |
| "CJ_10000689" | CJE0186 | tig | Cj0193c | tig | CCO1681 | tig | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | trigger factor (peptidyl-prolyl cis /trans | trigger factor | trigger factor |
| "CJ_10000690" | CJE0187 | folE | Cj0194 | folE | CCO1680 | folE | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | GTP cyclohydrolase I | GTP cyclohydrolase I | GTP cyclohydrolase I |
| "CJ_10000691" | CJE0188 | fliI | Cj0195 | fliI | CCO1679 | fliI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | flagellum-specific ATP synthase | flagellum-specific ATP synthase | flagellum-specific ATP synthase |
| "CJ_10000693" | CJE0189 | purF | Cj0196c | purF | CCO0286 | purF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | amidophosphoribosyltransferase | amidophosphoribosyltransferase | amidophosphoribosyltransferase |
| "CJ_10000695" | CJE0190 | dapB | Cj0197c | dapB | CCO0287 | dapB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | dihydrodipicolinate reductase | dihydrodipicolinate reductase | dihydrodipicolinate reductase |
| "CJ_10000697" | CJE0191 | - | Cj0198c | - | CCO0288 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | helicase-like protein | ATPase, AAA family protein | ATPase, AAA family |
| "CJ_10000699" | CJE0192 | - | Cj0199c | - | CCO0289 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0199c |
| "CJ_10000711" | CJE0193 | - | Cj0200c | - | CCO0290 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0200c |
| "CJ_10000713" | CJE0194 | - | Cj0201c | - | CCO0290 | - | 0 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable periplasmic protein Cj0200c |
| "CJ_10000715" | CJE0195 | - | Cj0202c | - | - | - | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000716" | CJE0196 | - | Cj0203 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane transport protein | pseudogene | - |
| "CJ_10000717" | CJE0197 | - | Cj0204 | - | CCO0294 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | oligopeptide transporter, OPT family | oligopeptide transporter, OPT family |
| "CJ_10000719" | CJE0198 | - | Cj0205 | bacA | CCO0295 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative undecaprenol kinase (bacitracin | undecaprenol kinase, putative | undecaprenol kinase, putative |
| "CJ_10000721" | CJE0199 | thrS | Cj0206 | thrS | CCO0296 | thrS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | threonyl-tRNA synthetase | threonyl-tRNA synthetase | threonyl-tRNA synthetase |
| "CJ_10000723" | CJE0200 | infC | Cj0207 | infC | CCO0297 | infC | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | translation initiation factor IF-3 | translation initiation factor IF-3 | translation initiation factor IF-3 |
| "CJ_10000725" | CJE0201 | - | Cj0208 | - | CCO0298 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | DNA modification methylase (adenine-specific | D12 class N6 adenine-specific DNA | ulcer associated adenine specific DNA |
| "opCjV0100001041" | CJE0202 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100000895" | CJE0203 | - | - | - | - | - | -1 | -1 | 0 | 0 | 1 | -1 | -1 | 1 | 1 | 0 | - | hypothetical protein | - |
| "opCjV0100000671" | CJE0204 | - | Cj0223 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |
| "opCjV010000 | CJE0205 | - | Cj0223 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0223" | | | | | | | | | | | | | | | | | | | |
| "opCjV010000 0062" | CJE0206 | - | Cj0223 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |
| "opCjV010000 0934" | CJE0207 | - | Cj0223 | - | - | - | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |
| "opCjV010000 0204" | CJE0208 | - | Cj0223 | - | - | - | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |
| "opCjV010000 0005" | CJE0209 | - | - | - | - | - | 0 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0365" | CJE0210 | - | Cj0223 | - | - | - | 0 | 0 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |
| "CJ_10000727" | CJE0211 | - | Cj0223 | - | - | - | 1 | 1 | -1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | pseudogene | pathogenicity domain protein | - |
| "opCjV010000 0640" | CJE0212 | - | Cj0223 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | pseudogene | pathogenicity protein, homolog | - |
| "opCjV010000 0722" | CJE0213 | - | - | - | - | - | 0 | 0 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0482" | CJE0214 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0190" | CJE0215 | - | - | - | - | - | -1 | -1 | 1 | -1 | 1 | -1 | 0 | 1 | 1 | -1 | - | phage repressor protein, putative | - |
| "opCjV010000 0686" | CJE0216 | - | - | - | - | - | 0 | -1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0915" | CJE0217 | - | - | - | - | - | 1 | -1 | 1 | 0 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0231" | CJE0218 | - | - | - | - | - | 0 | -1 | 0 | -1 | 1 | 0 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0743" | CJE0219 | - | - | - | - | - | 0 | 1 | 0 | -1 | 1 | -1 | 0 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0516" | CJE0220 | dam | - | - | - | - | 1 | 0 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | DNA adenine methylase | - |
| "opCjV010000 0891" | CJE0221 | - | - | - | - | - | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | phage virion morphogenesis protein, putative | - |
| "opCjV010000 0215" | CJE0222 | - | - | - | - | - | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | tail tape measure protein, TP901 family | - |
| "opCjV010000 0032" | CJE0223 | - | - | - | - | - | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0440" | CJE0224 | - | - | - | - | - | 1 | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0893" | CJE0225 | - | - | - | - | - | 1 | 0 | -1 | -1 | 1 | -1 | 0 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0592" | CJE0226 | - | - | - | - | - | 1 | 0 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | -1 | - | phage major tail tube protein, putative | - |
| "opCjV010000 0364" | CJE0227 | - | - | - | - | - | 1 | 0 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | major tail sheath protein | - |
| "opCjV010000 1020" | CJE0228 | - | - | - | - | - | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV010000 0959" | CJE0229 | - | - | - | - | - | 1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0217" | CJE0230 | - | - | - | - | - | 0 | 1 | 0 | -1 | | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0593" | CJE0231 | - | - | - | - | - | 1 | 0 | 0 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | tail fiber protein H, putative | - |
| "opCjV010000 0426" | CJE0232 | - | - | - | - | - | 1 | 0 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | phage tail protein, putative | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV0100000427" | CJE0233 | - | - | - | - | - | 0 | 0 | 0 | | | | | -1 | 1 | | - | baseplate assembly protein J, putative | - |
| "opCjV0100000033" | CJE0234 | - | - | - | - | - | 1 | 0 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | baseplate assembly protein W, putative | - |
| "opCjV0100000643" | CJE0235 | - | - | - | - | - | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000541" | CJE0236 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | baseplate assembly protein V, putative | - |
| "opCjV0100000173" | CJE0237 | - | - | - | - | - | 1 | 1 | 1 | -1 | 0 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000210" | CJE0238 | - | - | - | - | - | 1 | 1 | 0 | | | | | | 1 | | - | hypothetical protein | - |
| "opCjV0100000765" | CJE0239 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | lipoprotein, putative | - |
| "opCjV0100000950" | CJE0240 | - | - | - | - | - | 1 | 1 | 1 | | -1 | 1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000655" | CJE0241 | - | - | - | - | - | 1 | 1 | 1 | | | | | -1 | 1 | | - | hypothetical protein | - |
| "opCjV0100000798" | CJE0242 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000724" | CJE0243 | - | - | - | - | - | 1 | 1 | 1 | | | 1 | 1 | -1 | 1 | | - | hypothetical protein | - |
| "opCjV0100000443" | CJE0244 | - | - | - | - | - | 1 | 1 | 1 | | -1 | 1 | -1 | 1 | 1 | -1 | - | Mu-like prophage I protein, putative | - |
| "opCjV0100000269" | CJE0245 | - | - | - | - | - | 1 | 0 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000177" | CJE0246 | - | - | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000328" | CJE0247 | - | - | - | - | - | 1 | 1 | 0 | -1 | | 1 | 1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100001082" | CJE0248 | - | - | - | - | - | 1 | 1 | 0 | 0 | 1 | 0 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000909" | CJE0249 | - | - | - | - | - | 1 | 1 | 1 | 0 | 1 | 0 | -1 | 1 | 1 | -1 | - | phage uncharacterized protein | - |
| "opCjV0100000353" | CJE0250 | - | - | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100000297" | CJE0251 | - | - | - | - | - | -1 | 1 | 0 | -1 | | 1 | 1 | -1 | 1 | 0 | - | prophage MuSo1, F protein, putative | - |
| "opCjV0100000585" | CJE0252 | - | - | - | - | - | 1 | 1 | 1 | | 1 | 1 | -1 | 1 | 1 | -1 | - | phage tail protein, putative | - |
| "opCjV0100000667" | CJE0253 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | tail protein X, putative | - |
| "opCjV0100000604" | CJE0254 | - | - | - | - | - | -1 | 0 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | tail protein D, putative | - |
| "opCjV0100000932" | CJE0255 | - | - | - | - | - | 0 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | DNA-binding protein, putative | - |
| "opCjV0100000957" | CJE0256 | dns | - | - | - | - | 1 | 1 | 0 | | | | -1 | -1 | 1 | | - | extracellular deoxyribonuclease | - |
| "opCjV0100000211" | CJE0257 | - | - | - | - | - | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000654" | CJE0258 | - | - | - | - | - | 0 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | 0 | - | hypothetical protein | - |
| "opCjV0100000071" | CJE0259 | - | - | - | - | - | 1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV010000 | CJE0260 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0417" | | | | | | | | | | | | | | | | | | | |
| "opCjV010000 0431" | CJE0261 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0185" | CJE0262 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | conserved hypothetical protein TIGR01671 | - |
| "opCjV010000 0791" | CJE0263 | - | - | - | - | - | -1 | -1 | -1 | -1 | -1 | 0 | -1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 1084" | CJE0264 | - | - | - | - | - | 1 | -1 | -1 | -1 | -1 | 1 | 0 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0344" | CJE0265 | - | - | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | 1 | -1 | - | host-nuclease inhibitor protein Gam, putative | - |
| "opCjV010000 0376" | CJE0266 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV010000 0598" | CJE0267 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV010000 0580" | CJE0268 | - | - | - | - | - | -1 | -1 | -1 | | | | | | -1 | | - | hypothetical protein | - |
| "opCjV010000 0034" | CJE0269 | - | - | - | - | - | 1 | 1 | 1 | | | | | -1 | 1 | | - | bacteriophage DNA transposition protein B, | - |
| "opCjV010000 0708" | CJE0270 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | bacteriophage DNA transposition protein A, | - |
| "opCjV010000 1121" | CJE0271 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0076" | CJE0272 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | transcriptional regulator, putative | - |
| "opCjV010000 0632" | CJE0273 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCcV010000 0484" | CJE0275 | argC | Cj0224 | argC | CCO0299 | argC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | N-acetyl-gamma-glutamyl-phosphate reductase | N-acetyl-gamma-glutamyl-phosphate reductase | N-acetyl-gamma-glutamyl-phosphate reductase |
| "opCcV010000 1416" | CJE0276 | - | Cj0225 | - | CCO0300 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | putative acetyltransferase | acetyltransferase, GNAT family | probable acetyltransferase Cj0225 |
| "opCcV010000 0716" | CJE0277 | argB | Cj0226 | argB | CCO0301 | argB | 1 | -1 | 0 | 0 | 1 | 0 | -1 | 1 | -1 | 1 | acetylglutamate kinase | acetylglutamate kinase | acetylglutamate kinase |
| "opCcV010000 1452" | CJE0278 | argD | Cj0227 | argD | CCO0302 | - | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | acetylornithine aminotransferase | acetylornithine aminotransferase | acetylornithine transaminase Cj0227 |
| "CJ_10001433" | CJE0279 | pcm | Cj0228c | pcm | CCO0303 | pcm | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | protein-L-isoaspartate O-methyltransferase | protein-L-isoaspartate O-methyltransferase | protein-L-isoaspartate O-methyltransferase |
| "CJ_10001434" | CJE0280 | - | Cj0229 | - | CCO0304 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative acetyltransferase | transferase, hexapeptide repeat family | carbonic anhydrase, family 3 VC0058 |
| "CJ_10001435" | CJE0281 | - | Cj0230c | - | CCO0305 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | nicotinate phosphoribosyltransferase | nicotinate phosphoribosyltransferase, putative |
| "CJ_10001436" | CJE0282 | nrdB | Cj0231c | nrdB | CCO0306 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ribonucleoside-diphosphate reductase beta chain | ribonucleotide-diphosphate reductase beta | ribonucleoside-diphosphate reductase, beta |
| "CJ_10001437" | CJE0283 | - | Cj0232c | - | CCO0307 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0232c |
| "CJ_10001438" | CJE0284 | pyrE | Cj0233c | pyrE | CCO0308 | pyrE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative orotate phosphoribosyltransferase | orotate phosphoribosyltransferase | orotate phosphoribosyltransferase |
| "CJ_10001449" | CJE0285 | frr | Cj0234c | frr | CCO0309 | frr | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | ribosome recycling factor | ribosome releasing factor | ribosome recycling factor |
| "CJ_10001450" | CJE0286 | secG | Cj0235c | secG | CCO0310 | secG | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative protein-export membrane protein | protein-export membrane protein | protein translocation protein, low temperature |
| "CJ_10001451" | CJE0287 | - | Cj0236c | - | CCO0311 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0236c |
| "CJ_10001452" | CJE0288 | cynT | Cj0237 | cynT | CCO0312 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | carbonic anyhydrase | carbonic anhydrase | Carbonic anhydrase |
| "CJ_10001453" | CJE0289 | - | Cj0238 | - | CCO0313 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane | mechanosensitive ion | probable integral membrane |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | protein | channel family protein | protein Cj0238 |
| "CJ_10001454" | CJE0290 | - | Cj0239c | - | CCO0314 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | nifU protein homolog | NifU family protein | nifU protein homolog Cj0239c |
| "CJ_10001455" | CJE0291 | - | Cj0240c | - | CCO0315 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative aminotransferase (nifS protein | cysteine desulfurase | cysteine desulfurase |
| "CJ_10001456" | CJE0292 | - | Cj0241c | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative iron-binding protein | pseudogene | - |
| "CJ_10001457" | CJE0293 | - | Cj0243c | - | CCO0316 | - | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001458" | CJE0294 | rpmI | Cj0244 | rpmI | CCO0317 | rpmI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50s ribosomal protein L35 | 50S ribosomal protein L35 | ribosomal protein L35 |
| "CJ_10001469" | CJE0295 | rplT | Cj0245 | rplT | CCO0318 | rplT | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L20 | 50S ribosomal protein L20 | ribosomal protein L20 |
| "CJ_10001470" | CJE0296 | - | Cj0246c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative MCP-domain signal transduction protein | hypothetical protein | - |
| "CJ_10001471" | CJE0297 | - | Cj0247c | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | hypothetical protein | pseudogene | - |
| "CJ_10001472" | CJE0298 | - | Cj0248 | - | CCO0319 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001474" | CJE0299 | - | Cj0249 | - | CCO0320 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001476" | CJE0300 | - | Cj0250c | - | CCO0255 | proP | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | putative transmembrane transport protein | major facilitator superfamily protein | proline/betaine transporter (proP) |
| "CJ_10001477" | CJE0301 | - | Cj0251c | - | CCO0323 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | Highly acidic protein | hypothetical protein | hypothetical protein |
| "CJ_10001479" | CJE0302 | moaC | Cj0252 | moaC | CCO0324 | moaC | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | molybdenum cofactor biosynthesis protein C | molybdenum cofactor biosynthesis protein C | molybdenum cofactor biosynthesis protein C |
| "CJ_10001480" | CJE0303 | - | Cj0253 | - | CCO0325 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001482" | CJE0304 | - | Cj0254 | - | CCO0326 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001498" | CJE0305 | xth | Cj0255c | - | CCO0327 | xth | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | exodeoxyribonuclease | exodeoxyribonuclease III | exodeoxyribonuclease III |
| "CJ_10001499" | CJE0306 | - | Cj0256 | - | CCO0328 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | sulfatase, putative | membrane protein, putative |
| "CJ_10001500" | CJE0307 | dgkA | Cj0257 | dgkA | CCO0329 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | diacylglycerol kinase | diacylglycerol kinase | diacylglycerol kinase Cj0257 |
| "CJ_10001501" | CJE0308 | - | Cj0258 | - | CCO0330 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | Putative helix turn helix motif protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001503" | CJE0309 | pyrC | Cj0259 | pyrC | CCO0331 | pyrC | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | dihydroorotase | dihydroorotase | dihydroorotase, homodimeric type |
| "opCjV0100000803" | CJE0310 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | - | D12 class N6 adenine-specific DNA | - |
| "CJ_10001506" | CJE0311 | - | Cj0261c | - | CCO0333 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001510" | CJE0313 | - | Cj0263 | - | CCO0282 | bisZ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | putative integral membrane protein | zinc transporter ZupT | biotin sulfoxide reductase VC1950 |
| "CJ_10000543" | CJE0314 | - | Cj0144 | - | CCO1733 | - | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | methyl-accepting chemotaxis signal transduction | methyl-accepting chemotaxis protein | methyl-accepting chemotaxis protein (tlpA) |
| "CJ_10001535" | CJE0315 | - | Cj0266c | - | CCO0335 | - | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0266c |
| "CJ_10001536" | CJE0316 | - | Cj0267c | - | CCO0336 | - | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0267c |
| "CJ_10001537" | CJE0317 | - | Cj0268c | - | CCO0337 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane protein | SPFH domain / Band 7 family protein | probable transmembrane protein Cj0268c |
| "CJ_10001538" | CJE0318 | ilvE | Cj0269c | ilvE | CCO0338 | ilvE | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | branched-chain amino acid aminotransferase | branched-chain amino acid aminotransferase | branched-chain amino acid aminotransferase |
| "CJ_10001539" | CJE0319 | - | Cj0270 | - | CCO0339 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | Possible isomerase | 4-oxalocrotonate tautomerase family protein | 4-oxalocrotonate tautomerase (dmpI)-related |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001541" | CJE0320 | - | Cj0271 | - | CCO0340 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | bacterioferritin comigratory protein homolog | antioxidant, AhpC/Tsa family | bacterioferritin comigratory protein homolog |
| "CJ_10001543" | CJE0321 | - | Cj0272 | - | CCO0341 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001545" | CJE0322 | fabZ | Cj0273 | fabZ | CCO0342 | fabZ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | (3R)-hydroxymyristoyl-[acyl carrier protein] | (3R)-hydroxymyristoyl ACP dehydratase | beta-hydroxyacyl-(acyl-carrier-protein) |
| "CJ_10001547" | CJE0323 | lpxA | Cj0274 | lpxA | CCO0343 | lpxA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | acyl-[acyl-carrier-protein]--UDP-N- | UDP-N-acetylglucosamine acyltransferase | acyl-[acyl-carrier-protein]--UDP-N- |
| "CJ_10001563" | CJE0324 | clpX | Cj0275 | clpX | CCO0344 | clpX | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP-dependent clp protease ATP-binding subunit | ATP-dependent protease ATP-binding subunit | ATP-dependent Clp protease, ATP-binding subunit |
| "CJ_10001564" | CJE0325 | mreB | Cj0276 | mreB | CCO0345 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | homolog of E. coli rod shape-determining | cell shape-determining protein MreB | rod shape-determining protein (mreB) |
| "CJ_10001565" | CJE0326 | - | Cj0277 | - | CCO0346 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | rod shape-determining protein MreC | rod shape-determining protein (mreC), putative |
| "CJ_10001566" | CJE0327 | carB | Cj0279 | carB | CCO0357 | carB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | carbamoyl-phosphate synthase large chain | carbamoyl-phosphate synthase large subunit | carbamoyl-phosphate synthase, large subunit |
| "CJ_10001567" | CJE0328 | - | Cj0280 | - | CCO0358 | - | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001569" | CJE0329 | tal | Cj0281c | tal | CCO0359 | tal | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transaldolase | transaldolase | transaldolase |
| "CJ_10001571" | CJE0330 | serB | Cj0282c | serB | CCO0360 | serB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phosphoserine phosphatase | phosphoserine phosphatase SerB | phosphoserine phosphatase SerB |
| "CJ_10001572" | CJE0331 | cheW | Cj0283c | cheW | CCO0361 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chemotaxis protein | purine-binding chemotaxis protein CheW | chemotaxis protein Cj0283c |
| "CJ_10001574" | CJE0332 | cheA | Cj0284c | cheA | CCO0362 | cheA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chemotaxis histidine kinase | chemotaxis protein CheA | histidine kinase (cheA) |
| "CJ_10001576" | CJE0333 | cheV | Cj0285c | cheV | CCO0363 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chemotaxis protein | chemotaxis protein CheV | chemotaxis protein (cheV) |
| "CJ_10000002" | CJE0334 | - | Cj0286c | - | CCO0364 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000004" | CJE0335 | greA | Cj0287c | greA | CCO0365 | - | -1 | -1 | 0 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | transcription elongation factor | transcription elongation factor GreA | transcription elongation factor Cj0287c |
| "CJ_10000006" | CJE0336 | lpxB | Cj0288c | lpxB | CCO0366 | lpxB | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | -1 | 1 | lipid-A-disaccharide synthase | lipid-A-disaccharide synthase | lipid-A-disaccharide synthase |
| "CJ_10000008" | CJE0337 | - | Cj0289c | peb3 | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | major antigenic peptide PEB3 | major antigenic peptide PEB3 | - |
| "CJ_10000009" | CJE0338 | - | Cj0291c | - | CCO0371 | - | 1 | 0 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | glycerol-3-phosphate transporter (possible | pseudogene | phosphoglycerate transporter protein pgtP |
| "CJ_10000010" | CJE0339 | - | Cj0291c | - | CCO0372 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | glycerol-3-phosphate transporter (possible | pseudogene | phosphoglycerate transporter protein pgtP |
| "CJ_10000011" | CJE0340 | - | Cj0291c | - | CCO0373 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | glycerol-3-phosphate transporter (possible | pseudogene | phosphoglycerate transporter protein pgtP |
| "CJ_10000012" | CJE0341 | - | Cj0291c | - | CCO0374 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glycerol-3-phosphate transporter (possible | pseudogene | phosphoglycerate transporter protein pgtP |
| "CJ_10000030" | CJE0342 | panC | Cj0297c | panC | CCO0380 | panC | 0 | 0 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | pantoate--beta-alanine ligase | pantoate--beta-alanine ligase | pantoate--beta-alanine ligase |
| "CJ_10000032" | CJE0343 | panB | Cj0298c | panB | CCO0381 | panB | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 3-methyl-2-oxobutanoate | 3-methyl-2-oxobutanoate | 3-methyl-2-oxobutanoate |
| "CJ_10000034" | CJE0344 | - | Cj0299 | - | - | - | 1 | 1 | | 1 | 1 | -1 | | 1 | 1 | 1 | putative periplasmic beta-lactamase | beta-lactamase | - |
| "CJ_10000035" | CJE0345 | modC | Cj0300c | modC | CCO0385 | modC | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative molybdenum transport ATP-binding | molybdenum ABC transporter, ATP-binding protein | molybdenum ABC transporter, ATP-binding protein |
| "CJ_10000036" | CJE0346 | modB | Cj0301c | modB | CCO0386 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative molybdenum transport system permease | molybdenum ABC transporter, permease protein | molybdenum ABC transporter, permease protein |
| "CJ_10000038" | CJE0347 | - | Cj0302c | - | CCO0387 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | TOBE domain protein | molybdenum-pterin binding domain protein, |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000039" | CJE0348 | modA | Cj0303c | modA | CCO0388 | modA | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | putative molybdate-binding lipoprotein | molybdenum ABC transporter, periplasmic | molybdenum ABC transporter, periplasmic |
| "CJ_10000040" | CJE0349 | - | Cj0304c | bioC | CCO0389 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative biotin synthesis protein | biotin biosynthesis protein BioC | biotin synthesis protein BioC, putative |
| "CJ_10000042" | CJE0350 | - | Cj0305c | - | CCO0390 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF452) |
| "CJ_10000049" | CJE0351 | bioF | Cj0306c | bioF | CCO0391 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | 8-amino-7-oxononanoate synthase | 8-amino-7-oxononanoate synthase | 8-amino-7-oxononanoate synthase |
| "CJ_10000051" | CJE0352 | bioA | Cj0307 | bioA | CCO0393 | bioA | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | adenosylmethionine-8-amino-7-oxononanoate | adenosylmethionine--8-amino-7-oxononanoate | adenosylmethionine--8-amino-7-oxononanoate |
| "CJ_10000053" | CJE0353 | bioD | Cj0308c | bioD | CCO0394 | - | -1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative dethiobiotin synthetase | dethiobiotin synthetase | probable dethiobiotin synthase Cj0308c |
| "CJ_10000055" | CJE0354 | - | Cj0309c | - | CCO0395 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative efflux protein | multidrug resistance protein, SMR family | probable efflux protein Cj0309c |
| "CJ_10000056" | CJE0355 | - | Cj0310c | - | CCO0396 | - | -1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative efflux protein | multidrug resistance protein, SMR family | probable efflux protein Cj0310c |
| "CJ_10000057" | CJE0356 | rplY | Cj0311 | - | CCO0397 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ctc protein homolog | 50S ribosomal protein L25 | ribosomal 5S rRNA E-loop binding protein |
| "CJ_10000058" | CJE0357 | pth | Cj0312 | pth | CCO0398 | pth | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | peptidyl-tRNA hydrolase | peptidyl-tRNA hydrolase | peptidyl-tRNA hydrolase |
| "CJ_10000059" | CJE0358 | - | Cj0313 | - | CCO0399 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0313 |
| "CJ_10000060" | CJE0359 | lysA | Cj0314 | lysA | CCO0400 | lysA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | diaminopimelate decarboxylase | diaminopimelate decarboxylase | diaminopimelate decarboxylase |
| "CJ_10000061" | CJE0360 | - | Cj0315 | - | CCO0401 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | HAD-superfamily hydrolase, subfamily IIA | HAD-superfamily hydrolase, subfamily IIA |
| "CJ_10000069" | CJE0361 | pheA | Cj0316 | pheA | CCO0402 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chorismate mutase\prephenate dehydratase | chorismate mutase/prephenate dehydratase | chorismate mutase / prephenate dehydratase |
| "CJ_10000071" | CJE0362 | hisC | Cj0317 | hisC | CCO0403 | hisC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | probable histidinol-phosphate aminotransferase | histidinol-phosphate aminotransferase | histidinol-phosphate aminotransferase |
| "CJ_10000073" | CJE0363 | fliF | Cj0318 | fliF | CCO0404 | fliF | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | flagellar M-ring protein | flagellar M-ring protein | flagellar M-ring protein FliF |
| "CJ_10000075" | CJE0364 | fliG | Cj0319 | fliG | CCO0405 | fliG | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | flagellar motor switch protein | flagellar motor protein | flagellar motor switch protein FliG |
| "CJ_10000076" | CJE0365 | - | Cj0320 | fliH | CCO0406 | fliH | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | putative flagellar assembly protein | flagellar assembly protein | flagellar export protein (fliH) |
| "CJ_10000077" | CJE0366 | dxs | Cj0321 | dxs | CCO0407 | dxs | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1-deoxyxylulose-5-phosphate synthase | 1-deoxy-D-xylulose-5-phosphate synthase | deoxyxylulose-5-phosphate synthase |
| "CJ_10000078" | CJE0367 | - | Cj0322 | perR | CCO0408 | furR1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | peroxide stress regulator | transcriptional regulator, Fur family | transcriptional regulator, Fur family |
| "CJ_10000079" | CJE0368 | - | Cj0323 | - | CCO0409 | - | 0 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000080" | CJE0369 | ubiE | Cj0324 | ubiE | CCO0410 | ubiE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ubiquinone\menaquinone biosynthesis | ubiquinone/menaquinone biosynthesis | gerC2 protein (gerC2) |
| "CJ_10000081" | CJE0370 | xseA | Cj0325 | xseA | CCO0414 | xseA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | exodeoxyribonuclease VII large subunit | exodeoxyribonuclease VII, large subunit | exodeoxyribonuclease VII, large subunit |
| "CJ_10000619" | CJE0371 | serC | Cj0326 | serC | CCO0415 | serC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphoserine aminotransferase | phosphoserine aminotransferase | phosphoserine aminotransferase |
| "CJ_10000620" | CJE0372 | - | Cj0327 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | endoribonuclease L-PSP family protein | - |
| "CJ_10000621" | CJE0373 | fabH | Cj0328c | fabH | CCO0416 | fabH | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 3-oxoacyl-[acyl-carrier-protein] synthase | 3-oxoacyl-(acyl carrier protein) synthase | beta-ketoacyl-acp synthase III |
| "CJ_10000622" | CJE0374 | plsX | Cj0329c | plsX | CCO0417 | plsX | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative fatty acid\phospholipid synthesis | fatty acid/phospholipid synthesis protein | fatty acid/phospholipid synthesis protein PlsX |
| "opCcV0100001244" | CJE0375 | rpmF | Cj0330c | rpmF | CCO0418 | rpmF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L32 | 50S ribosomal protein L32 | ribosomal protein L32 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000623" | CJE0376 | - | Cj0331c | - | CCO0419 | - | 1 | 1 | | 1 | 1 | | 0 | | 1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000624" | CJE0377 | ndk | Cj0332c | ndk | CCO0420 | - | 1 | 1 | -1 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | nucleoside diphosphate kinase | nucleoside diphosphate kinase | nucleoside diphosphate kinase Cj0332c |
| "opCcV0100000143" | CJE0378 | - | Cj0333c | fdxA | CCO0421 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ferredoxin | ferredoxin, 4Fe-4S | ferredoxin |
| "CJ_10000627" | CJE0379 | - | Cj0334 | ahpC | CCO0422 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | alkyl hydroperoxide reductase | antioxidant, AhpC/Tsa family | antioxidant, AhpC/Tsa family VC0731 |
| "CJ_10000629" | CJE0380 | flhB | Cj0335 | flhB | CCO0423 | flhB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar biosynthetic protein | flagellar biosynthetic protein FlhB | flagellar biosynthetic protein FlhB |
| "CJ_10000647" | CJE0381 | - | Cj0336c | motB | CCO0424 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative flagellar motor protein | flagellar motor protein | chemotaxis motB protein, putative |
| "CJ_10000648" | CJE0382 | - | Cj0337c | motA | CCO0425 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellar motor proton channel | flagellar motor protein | probable flagellar motor proton channel Cj0337c |
| "CJ_10000649" | CJE0383 | polA | Cj0338c | polA | CCO0426 | polA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA polymerase I | DNA polymerase I | DNA polymerase I (polA) |
| "CJ_10000650" | CJE0384 | - | Cj0339 | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative transmembrane transport protein | major facilitator family transporter | - |
| "CJ_10000651" | CJE0385 | - | Cj0340 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative nucleoside hydrolase | inosine-uridine preferring nucleoside hydrolase | - |
| "CJ_10000652" | CJE0386 | - | Cj0341c | - | CCO0427 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | membrane protein, putative |
| "opCjV0100000999" | CJE0387 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000510" | CJE0388 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000162" | CJE0389 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10000653" | CJE0390 | uvrA | Cj0342c | uvrA | CCO0431 | uvrA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | excinuclease ABC subunit A | excinuclease ABC subunit A | excinuclease ABC, A subunit |
| "CJ_10000655" | CJE0391 | - | Cj0343c | - | CCO0432 | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical integral membrane |
| "opCjjV010000041" | CJE0392 | - | Cj0344 | - | - | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "opCjV0100000687" | CJE0393 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10000658" | CJE0394 | trpE | Cj0345 | trpE | CCO0433 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative anthranilate synthase component I | anthranilate synthase component I | anthranilate synthase component I |
| "CJ_10000676" | CJE0395 | trpD | Cj0346 | trpD | CCO0434 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | anthranilate synthase component II | anthranilate synthase component II | anthranilate phosphoribosyltransferase, |
| "CJ_10000677" | CJE0396 | trpF | Cj0347 | trpF | CCO0435 | trpF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | N-(5'-phosphoribosyl)anthranilate isomerase | N-(5'phosphoribosyl)anthranilate isomerase | N-(5'phosphoribosyl)anthranilate isomerase |
| "CJ_10000678" | CJE0397 | trpB | Cj0348 | trpB | CCO0436 | trpB | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tryptophan synthase beta chain | tryptophan synthase subunit beta | tryptophan synthase, beta subunit |
| "CJ_10000679" | CJE0398 | trpA | Cj0349 | trpA | CCO0437 | trpA | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tryptophan synthase alpha chain | tryptophan synthase, alpha subunit | tryptophan synthase, alpha subunit |
| "CJ_10000680" | CJE0399 | - | Cj0350 | - | CCO0438 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000681" | CJE0400 | fliN | Cj0351 | fliN | CCO0439 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar motor switch protein | flagellar motor switch protein | flagellar switch protein |
| "CJ_10000682" | CJE0401 | - | Cj0352 | - | CCO0440 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane protein | hypothetical protein | probable transmembrane protein Cj0352 |
| "CJ_10000684" | CJE0402 | - | Cj0353c | - | CCO0441 | gppA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphatase | phosphatase, Ppx/GppA family | guanosine pentaphosphate phosphohydrolase |
| "CJ_10000686" | CJE0403 | - | Cj0354c | fdxB | CCO0442 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ferredoxin | ferredoxin, 4Fe-4S | ferredoxin |

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| "CJ_10000688" | CJE0404 | - | Cj0355c | - | CCO0443 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | two-component regulator | DNA-binding response regulator | response regulator |
| "CJ_10000705" | CJE0405 | - | Cj0356c | - | CCO0444 | folB | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | folB domain protein | dihydroneopterin aldolase |
| "CJ_10000706" | CJE0406 | - | Cj0357c | - | CCO0445 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical protein TIGR00023 |
| "CJ_10000707" | CJE0407 | - | Cj0358 | - | CCO0446 | mauG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cytochrome C551 peroxidase | cytochrome c551 peroxidase | cytochrome c551 peroxidase |
| "opCcV010000 1679.60" | CJE0408 | - | - | - | - | - | 1 | 1 | 0 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "CJ_10000708" | CJE0409 | glmM | Cj0360 | - | CCO0447 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phospho-sugar mutase | phosphoglucosamine mutase | phosphoglucosamine mutase |
| "CJ_10000709" | CJE0410 | glmM | Cj0361 | - | CCO0448 | mrsA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phospho-sugar mutase | phosphoglucosamine mutase | PUTATIVE PHOSPHOSUGAR ISOMERASE PROTEIN |
| "CJ_10000710" | CJE0411 | glmM | Cj0362 | - | CCO0449 | mrsA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative phospho-sugar mutase | phosphoglucosamine mutase | phosphoglucosamine mutase |
| "CJ_10000712" | CJE0412 | - | Cj0363c | - | CCO0452 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative oxidoreductase | coproporphyrinogen III oxidase | oxygen-independent coproporphyrinogen III |
| "CJ_10000714" | CJE0413 | - | Cj0364 | - | CCO0453 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCcV010000 1459" | CJE0414 | cmeC | Cj0365c | - | CCO0454 | - | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | putative outer membrane channel protein | RND efflux system, outer membrane lipoprotein | multidrug efflux pump channel protein, putative |
| "opCcV010000 0610" | CJE0415 | cmeB | Cj0366c | - | CCO0455 | - | | | 0 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | transmembrane efflux protein | RND efflux system, inner membrane transporter | transmembrane efflux protein Cj0366c |
| "opCcV010000 1785" | CJE0416 | cmeA | Cj0367c | - | CCO0456 | - | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | putative membrane fusion component of efflux | RND efflux system, membrane fusion protein CmeA | HlyD family secretion protein, putative |
| "CJ_10000733" | CJE0417 | - | Cj0368c | - | CCO0457 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | transcriptional regulatory protein | transcriptional regulator, TetR family | transcriptional regulator, tetR family, |
| "CJ_10000734" | CJE0418 | - | Cj0369c | - | CCO0458 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ferredoxin domain-containing integral membrane | iron-sulfur cluster-binding domain protein | ferrodoxin-like protein |
| "CJ_10000735" | CJE0419 | rpsU | Cj0370 | rpsU | CCO0459 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S21 | 30S ribosomal protein S21 | ribosomal protein S21 |
| "CJ_10000736" | CJE0420 | - | Cj0371 | - | CCO0460 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellar motility protein | hypothetical protein | probable flagellar motility protein Cj0371 |
| "CJ_10000737" | CJE0421 | - | Cj0372 | - | CCO0461 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | glutathionylspermidine synthase family protein | glutathionylspermidine synthase family protein |
| "CJ_10000738" | CJE0422 | - | Cj0373 | - | CCO0462 | hprA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative D-2-hydroxyacid dehydrogenase | 2-hydroxyacid dehydrogenase | phosphoglycerate dehydrogenase |
| "CJ_10000739" | CJE0423 | - | Cj0374 | - | CCO0463 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF520) |
| "CJ_10000740" | CJE0424 | - | Cj0375 | - | CCO0464 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0375 |
| "CJ_10000741" | CJE0425 | - | Cj0376 | - | CCO0465 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0376 |
| "CJ_10000755" | CJE0426 | - | Cj0377 | - | CCO0466 | - | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | probable AAA family ATPase | ATPase, AAA family protein | probable AAA family ATPase Cj0377 |
| "CJ_10000757" | CJE0427 | - | Cj0378c | - | CCO0467 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0378c |
| "CJ_10000759" | CJE0428 | - | Cj0379c | - | CCO0468 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000761" | CJE0429 | - | Cj0380c | - | CCO0469 | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 0 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000763" | CJE0430 | pyrF | Cj0381c | pyrF | CCO0470 | pyrF | | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | orotidine 5'-phosphate decarboxylase | orotidine 5'-phosphate decarboxylase | orotidine 5`-phosphate decarboxylase |
| "CJ_10000765" | CJE0431 | nusB | Cj0382c | nusB | CCO0471 | nusB | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | transcription termination | transcription | transcription antitermination |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | protein | antitermination protein NusB | factor NusB |
| "CJ_10000767" | CJE0432 | ribH | Cj0383c | ribH | CCO0472 | ribH | 0 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | | 1 | 6,7-dimethyl-8-ribityllumazine synthase | riboflavin synthase subunit beta | 6,7-dimethyl-8-ribityllumazine synthase |
| "CJ_10000768" | CJE0433 | kdsA | Cj0384c | kdsA | CCO0473 | kdsA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 2-dehydro-3-deoxyphosphooctonate aldolase | 2-dehydro-3-deoxyphosphooctonate aldolase | 2-dehydro-3-deoxyphosphooctonate aldolase |
| "CJ_10000769" | CJE0434 | - | Cj0385c | - | CCO0474 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 0 | -1 | 1 | putative integral membrane protein | integral membrane protein | probable integral membrane protein Cj0385c |
| "CJ_10000770" | CJE0435 | - | Cj0386 | - | CCO0475 | - | -1 | 1 | | 1 | -1 | 1 | 1 | 1 | 1 | -1 | putative GTP-binding protein | GTP-binding protein EngA | GTPase |
| "CJ_10000790" | CJE0436 | aroK | Cj0387 | aroK | CCO0476 | aroK | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | shikimate kinase | shikimate kinase | shikimate kinase |
| "CJ_10000793" | CJE0437 | trpS | Cj0388 | trpS | CCO0477 | trpS | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | tryptophanyl-tRNA synthetase | tryptophanyl-tRNA synthetase | tryptophanyl-tRNA synthetase |
| "CJ_10000796" | CJE0438 | serS | Cj0389 | serS | CCO0478 | serS | 1 | 1 | 1 | 1 | 0 | 1 | -1 | -1 | 1 | 1 | seryl-tRNA synthetase | seryl-tRNA synthetase | seryl-tRNA synthetase |
| "CJ_10000798" | CJE0439 | - | Cj0390 | - | CCO0479 | - | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | putative transmembrane protein | TPR domain protein | probable transmembrane protein Cj0390 |
| "CJ_10000800" | CJE0440 | - | Cj0391c | - | CCO0480 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000802" | CJE0441 | pyk | Cj0392c | pyk | CCO0481 | pyk | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | pyruvate kinase | pyruvate kinase | pyruvate kinase |
| "CJ_10000804" | CJE0442 | - | Cj0393c | - | CCO0482 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | putative oxidoreductase | malate:quinone oxidoreductase, putative | probable oxidoreductase Cj0393c |
| "CJ_10000806" | CJE0443 | - | Cj0394c | - | CCO0483 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | transcriptional activator, putative, Baf family | transcriptional activator, putative, Baf family |
| "CJ_10000807" | CJE0444 | - | Cj0395c | - | CCO0484 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | tram-like protein | conserved hypothetical protein |
| "CJ_10000808" | CJE0445 | - | Cj0396c | - | CCO0485 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0396c |
| "CJ_10000819" | CJE0446 | - | Cj0397c | - | CCO0486 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000822" | CJE0447 | gatC | Cj0398 | gatC | CCO0487 | gatC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative Glu-tRNAGln amidotransferase subunit C | aspartyl/glutamyl-tRNA amidotransferase subunit | glutamyl-tRNA(Gln) amidotransferase, C subunit |
| "CJ_10000825" | CJE0448 | - | Cj0399 | - | CCO0488 | cvpA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative integral membrane protein | cvpA family protein | CvpA family protein |
| "CJ_10000828" | CJE0449 | fur | Cj0400 | fur | CCO0489 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ferric uptake regulator | ferric uptake regulation protein | ferric uptake regulator Cj0400 |
| "opCcV0100001338" | CJE0450 | lysS | Cj0401 | lysS | CCO0490 | lysS | 1 | 1 | 1 | 0 | 1 | -1 | -1 | 1 | -1 | -1 | lysyl-tRNA synthetase | lysyl-tRNA synthetase | lysyl-tRNA synthetase |
| "opCcV0100000067" | CJE0451 | glyA | Cj0402 | glyA | CCO0491 | glyA | -1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | -1 | 1 | serine hydroxymethyltransferase | serine hydroxymethyltransferase | serine hydroxymethyltransferase |
| "opCcV0100001753" | CJE0452 | - | Cj0403 | - | CCO0492 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000833" | CJE0453 | - | Cj0404 | - | CCO0493 | - | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | putative transmembrane protein | hypothetical protein | probable transmembrane protein Cj0404 |
| "CJ_10000834" | CJE0454 | aroE | Cj0405 | aroE | CCO0494 | aroE | 0 | 0 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | shikimate 5-dehydrogenase | shikimate 5-dehydrogenase | shikimate 5-dehydrogenase |
| "CJ_10000835" | CJE0455 | - | Cj0406c | - | CCO0495 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0406c |
| "CJ_10000846" | CJE0456 | lgt | Cj0407 | lgt | CCO0496 | lgt | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | prolipoprotein diacylglyceryl transferase | prolipoprotein diacylglyceryl transferase | prolipoprotein diacylglyceryl transferase |
| "CJ_10000849" | CJE0457 | frdC | Cj0408 | frdC | CCO0497 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | fumarate reductase cytochrome B subunit | fumarate reductase, cytochrome b subunit | Fumarate reductase respiratory complex, |
| "CJ_10000852" | CJE0458 | frdA | Cj0409 | frdA | CCO0498 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | fumarate reductase flavoprotein subunit | fumarate reductase | succinate dehydrogenase flavoprotein Cj0409 |
| "CJ_10000855" | CJE0459 | frdB | Cj0410 | frdB | CCO0499 | sdhB | 0 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | fumarate reductase iron-sulfur protein | succinate dehydrogenase | fumarate reductase iron-sulfur protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000857" | CJE0460 | - | Cj0411 | - | CCO0500 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 0 | putative ATP /GTP binding protein | GTP-binding protein | probable ATP /GTP binding protein Cj0411 |
| "CJ_10000859" | CJE0461 | - | Cj0412 | - | CCO0501 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative ATP /GTP binding protein | GTP-binding protein | probable ATP /GTP binding protein Cj0412 |
| "CJ_10000861" | CJE0462 | - | Cj0413 | - | CCO0502 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | conserved hypothetical secreted protein, |
| "CJ_10000862" | CJE0463 | - | Cj0414 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | putative oxidoreductase subunit | hypothetical protein | - |
| "CJ_10000864" | CJE0464 | - | Cj0415 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative oxidoreductase subunit | oxidoreductase, putative | - |
| "opCjV0100000636" | CJE0465 | - | - | - | - | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100001087" | CJE0466 | - | - | - | - | - | -1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10000878" | CJE0467 | - | Cj0418c | - | CCO0503 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | hypothetical protein | srpA-related protein |
| "CJ_10000881" | CJE0468 | - | Cj0419 | - | CCO0504 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | HIT family protein | HIT domain protein |
| "CJ_10000883" | CJE0469 | - | Cj0420 | - | CCO0505 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 0 | 1 | putative periplasmic protein | hypothetical protein | conserved hypothetical secreted protein |
| "CJ_10000884" | CJE0470 | - | Cj0421c | - | CCO0506 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0421c |
| "CJ_10000885" | CJE0471 | - | Cj0422c | - | CCO0507 | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | putative H-T-H containing protein | hypothetical protein | conserved hypothetical protein |
| "opCjV0100000549" | CJE0472 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000188" | CJE0473 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000961" | CJE0474 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | lipoprotein, putative | - |
| "opCcV0100001299" | CJE0475 | - | Cj0426 | - | CCO0512 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ABC transporter ATP-binding protein | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein (yheS) |
| "CJ_10001596" | CJE0476 | - | Cj0427 | - | CCO0513 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001597" | CJE0477 | - | Cj0428 | - | CCO0514 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001598" | CJE0478 | - | Cj0429c | - | CCO0515 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCjV0100001079" | CJE0479 | - | - | - | - | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001599" | CJE0480 | - | Cj0430 | - | CCO0516 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical integral membrane |
| "CJ_10001600" | CJE0481 | - | Cj0431 | - | CCO0517 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic ATP /GTP-binding protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001601" | CJE0482 | murD | Cj0432c | murD | CCO0524 | murD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UDP-N-acetylmuramoylalanine--D-glutamate ligase | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate | UDP-N-acetylmuramoylalanine--D-glutamate ligase |
| "CJ_10000001" | CJE0483 | mraY | Cj0433c | mraY | CCO0525 | mraY | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | phospho-N-acetylmuramoyl-pentapeptide- | phospho-N-acetylmuramoyl-pentapeptide- | phospho-N-acetylmuramoyl-pentapeptide- |
| "CJ_10000003" | CJE0484 | pgm | Cj0434 | pgm | CCO0526 | gpmA | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphoglycerate mutase | phosphoglyceromutase | phosphoglycerate mutase, |
| "CJ_10000005" | CJE0485 | fabG | Cj0435 | fabG | CCO0527 | fabG | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 3-oxoacyl-[acyl-carrier protein] reductase | 3-ketoacyl-(acyl-carrier-protein) reductase | 3-oxoacyl-(acyl-carrier-protein) reductase |
| "CJ_10000007" | CJE0486 | - | Cj0436 | - | CCO0528 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCjV0100001038" | CJE0487 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | - | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000022" | CJE0488 | sdhA | Cj0437 | sdhA | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | succinate dehydrogenase flavoprotein subunit | succinate dehydrogenase, flavoprotein subunit | - |
| "CJ_10000023" | CJE0489 | sdhB | Cj0438 | sdhB | - | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative succinate dehydrogenase iron-sulfur | succinate dehydrogenase, iron-sulfur protein | - |
| "CJ_10000024" | CJE0490 | sdhC | Cj0439 | sdhC | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | putative succinate dehydrogenase subunit C | succinate dehydrogenase, C subunit | - |
| "CJ_10000025" | CJE0491 | - | Cj0440c | - | CCO0529 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative transcriptional regulator | TenA/Thi-4 family protein | transcriptional regulator TenA, putative |
| "opCjV0100000088" | CJE0492 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10000026" | CJE0493 | acpP | Cj0441 | acpP | CCO0530 | acpP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | acyl carrier protein | acyl carrier protein | acyl carrier protein |
| "CJ_10000027" | CJE0494 | fabF | Cj0442 | fabF | CCO0531 | fabB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3-oxoacyl-[acyl-carrier-protein] synthase | 3-oxoacyl-(acyl carrier protein) synthase | beta ketoacyl-acyl carrier protein synthase II |
| "CJ_10000028" | CJE0495 | accA | Cj0443 | accA | CCO0532 | accA | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | acetyl-coenzyme A carboxylase carboxyl | acetyl-CoA carboxylase alpha subunit | acetyl-CoA carboxylase, carboxyl transferase, |
| "opCcV0100001291" | CJE0496 | - | Cj0444 | - | CCO0537 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | pseudogene | pseudogene | iron-regulated outer membrane virulence protein, |
| "CJ_10000031" | CJE0497 | - | Cj0447 | - | CCO0538 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | NUDIX domain protein | conserved hypothetical protein TIGR00052 |
| "CJ_10000033" | CJE0498 | - | Cj0448c | - | CCO0539 | - | -1 | -1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative MCP-type signal transduction protein | methyl-accepting chemotaxis protein | methyl-accepting chemotaxis transducer (tlpC) |
| "CJ_10000043" | CJE0499 | - | Cj0449c | - | CCO0540 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF465) family |
| "opCcV0100000349" | CJE0500 | rpmB | Cj0450c | rpmB | CCO0541 | rpmB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L28 | 50S ribosomal protein L28 | ribosomal protein L28 |
| "CJ_10000044" | CJE0501 | rpe | Cj0451 | rep | CCO0542 | rpe | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | ribulose-phosphate 3-epimerase | ribulose-phosphate 3-epimerase | ribulose-phosphate 3-epimerase |
| "CJ_10000045" | CJE0502 | - | Cj0452 | dnaQ | CCO0543 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | exonuclease, possibly dna polymerase III epsilon | DNA polymerase III subunit epsilon | DNA polymerase III epsilon subunit (dnaQ) |
| "CJ_10000046" | CJE0503 | thiC | Cj0453 | thiC | CCO0544 | thiC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | thiamin biosynthesis protein ThiC | thiamine biosynthesis protein ThiC | thiamine biosynthesis protein ThiC |
| "CJ_10000047" | CJE0504 | - | Cj0454c | - | CCO0545 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0454c |
| "CJ_10000048" | CJE0505 | - | Cj0455c | - | CCO0546 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0455c |
| "CJ_10000050" | CJE0506 | - | Cj0456c | - | CCO0547 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000052" | CJE0507 | - | Cj0457c | - | CCO0548 | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative lipoprotein | hypothetical protein | probable lipoprotein Cj0457c |
| "CJ_10000054" | CJE0508 | miaB | Cj0458c | - | CCO0549 | miaB | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | tRNA-i(6)A37 thiotransferase enzyme MiaB | tRNA-i(6)A37 thiotransferase enzyme MiaB |
| "CJ_10000062" | CJE0509 | - | Cj0459c | - | CCO0550 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000063" | CJE0510 | nusA | Cj0460 | nusA | CCO0551 | nusA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | transcription termination factor | transcription elongation factor NusA | transcription termination factor NusA |
| "CJ_10000064" | CJE0511 | - | Cj0461c | - | CCO0552 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | transporter, putative | permease, putative |
| "CJ_10000065" | CJE0512 | - | Cj0462 | - | CCO0553 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR00423 |
| "CJ_10000066" | CJE0513 | - | Cj0463 | - | CCO0554 | - | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | zinc protease-like protein | peptidase, putative | processing protease (ymxG) |
| "CJ_10000067" | CJE0514 | recG | Cj0464 | recG | CCO0555 | recG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | ATP-dependent DNA helicase | ATP-dependent DNA helicase RecG | ATP-dependent DNA helicase RecG |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000068" | CJE0515 | - | Cj0465c | - | CCO0556 | - | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000070" | CJE0516 | - | Cj0466 | - | CCO0557 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative transcriptional regulator | transcriptional regulator, putative | probable transcription regulator Cj0466 |
| "CJ_10000072" | CJE0517 | - | Cj0467 | - | CCO0559 | glnP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | amino-acid ABC transporter integral membrane | amino acid ABC transporter, permease protein, | glutamine ABC transporter, permease protein |
| "CJ_10000074" | CJE0518 | - | Cj0468 | - | CCO0560 | glnP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | amino-acid ABC transporter integral membrane | amino acid ABC transporter, permease protein, | glutamine ABC transporter, permease protein |
| "CJ_10000082" | CJE0519 | - | Cj0469 | - | CCO0562 | glnQ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | amino-acid ABC transporter ATP-binding protein | amino acid ABC transporter, ATP-binding protein | glutamine/glutamate ABC transporter, ATP-binding |
| "CJ_10000083" | CJE0520 | tuf | Cj0470 | tuf | CCO0566 | tuf | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | elongation factor TU | elongation factor Tu | translation elongation factor Tu |
| "CJ_10000084" | CJE0521 | rpmG | Cj0471 | rpmG | CCO0567 | rpmG | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L33 | 50S ribosomal protein L33 | ribosomal protein L33 |
| "CJ_10000085" | CJE0522 | secE | Cj0472 | secE | CCO0569 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | preprotein translocase SecE subunit | translocase | preprotein translocase SecE chain Cj0472 |
| "CJ_10000086" | CJE0523 | nusG | Cj0473 | nusG | CCO0570 | nusG | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transcription antitermination protein | transcription antitermination protein NusG | transcription termination/antitermination factor |
| "CJ_10000087" | CJE0524 | rplK | Cj0474 | rplK | CCO0571 | rplK | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L11 | 50S ribosomal protein L11 | ribosomal protein L11 |
| "CJ_10000088" | CJE0525 | rplA | Cj0475 | rplA | CCO0572 | rplA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L1 | 50S ribosomal protein L1 | ribosomal protein L1 |
| "CJ_10000089" | CJE0526 | rplJ | Cj0476 | rplJ | CCO0573 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L10 | 50S ribosomal protein L10 | 50S ribosomal protein L10 Cj0476 |
| "CJ_10000090" | CJE0527 | rplL | Cj0477 | rplL | CCO0574 | rplL | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L7 /L12 | 50S ribosomal protein L7/L12 | ribosomal protein L7/L12 |
| "CJ_10000091" | CJE0528 | rpoB | Cj0478 | rpoB | CCO0575 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA-directed RNA polymerase beta chain | DNA-directed RNA polymerase, beta subunit | DNA-directed RNA polymerase, beta subunit |
| "CJ_10000092" | CJE0529 | rpoB | Cj0479 | rpoB | CCO0576 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA-directed RNA polymerase beta chain | DNA-directed RNA polymerase, beta subunit | DNA-directed RNA polymerase beta chain , |
| "CJ_10000093" | CJE0530 | - | Cj0480c | - | CCO0578 | - | 0 | -1 | -1 | 1 | 0 | -1 | -1 | -1 | 1 | 1 | putative transcriptional regulator | transcriptional regulator, IclR family | probable transcription regulator Cj0480c |
| "opCcV010000 0230" | CJE0531 | - | - | - | CCO0579 | - | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | - | hypothetical protein | probable lyase Cj0481 |
| "CJ_10000094" | CJE0532 | - | Cj0481 | - | CCO0580 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | putative lyase | dihydrodipicolinate synthase, putative | altronate hydrolase |
| "CJ_10000095" | CJE0533 | uxaA | - | - | - | - | 1 | 1 | 0 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | - | pseudogene | - |
| "CJ_10000097" | CJE0534 | - | Cj0484 | - | CCO0582 | - | 0 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | transmembrane transport protein | tartrate transporter, putative | transmembrane transport protein Cj0484 |
| "CJ_10000098" | CJE0535 | - | Cj0485 | - | CCO0583 | - | 1 | 0 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative oxidoreductase | short chain dehydrogenase | probable oxidoreductase Cj0485 |
| "CJ_10000099" | CJE0536 | fucP | Cj0486 | - | CCO0584 | fucP | 1 | 1 | -1 | 1 | 1 | | 1 | -1 | 1 | 1 | putative sugar transporter | L-fucose permease | L-fucose permease |
| "CJ_10000100" | CJE0537 | - | Cj0487 | - | CCO0585 | - | 0 | 1 | -1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000101" | CJE0538 | - | Cj0488 | - | CCO0586 | - | -1 | 0 | -1 | 1 | 1 | | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF718) |
| "CJ_10000109" | CJE0539 | aldA | Cj0490 | - | CCO0587 | - | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | pseudogene | aldehyde dehydrogenase | probable lactaldehyde dehydrogenase truncated |
| "CJ_10000113" | CJE0540 | rpsL | Cj0491 | rpsL | CCO0588 | rpsL | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S12 | 30S ribosomal protein S12 | ribosomal protein S12 |
| "CJ_10000115" | CJE0541 | rpsG | Cj0492 | rpsG | CCO0589 | rpsG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S7 | 30S ribosomal protein S7 | ribosomal protein S7 |
| "CJ_10000116" | CJE0542 | fusA | Cj0493 | fusA | CCO0590 | fusA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | elongation factor G | elongation factor EF-2 | translation elongation factor G |
| "opCjV010000 0897" | CJE0544 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | site-specific recombinase, phage integrase | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV010000 0168" | CJE0545 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | DNA binding domain, excisionase family | - |
| "opCjV010000 0553" | CJE0546 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | pentapeptide repeat family protein | - |
| "opCjV010000 0167" | CJE0547 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0090" | CJE0548 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | phage anti-repressor protein, putative | - |
| "opCjV010000 0446" | CJE0549 | - | - | - | - | - | | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0163" | CJE0550 | - | - | - | - | - | -1 | -1 | -1 | 0 | 1 | -1 | -1 | 1 | -1 | 1 | - | site-specific DNA-methyltransferase, putative | - |
| "opCjV010000 0554" | CJE0551 | - | - | - | - | - | | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 1062" | CJE0552 | - | - | - | - | - | | -1 | -1 | -1 | 1 | 0 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0291" | CJE0554 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0756" | CJE0555 | - | - | - | - | - | | | | | | | -1 | -1 | | | - | hypothetical protein | - |
| "opCjV010000 0790" | CJE0556 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0463" | CJE0557 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0608" | CJE0558 | - | - | - | - | - | | | -1 | | | | 1 | -1 | | | - | hypothetical protein | - |
| "opCjV010000 0149" | CJE0559 | - | - | - | - | - | | | -1 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0254" | CJE0560 | - | - | - | - | - | | | -1 | | | -1 | | -1 | | | - | hypothetical protein | - |
| "opCjV010000 0597" | CJE0561 | - | - | - | - | - | | | -1 | -1 | -1 | -1 | 1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0602" | CJE0562 | - | - | - | - | - | | | | | | | | | | -1 | - | hypothetical protein | - |
| "opCjV010000 0387" | CJE0563 | - | - | - | - | - | | | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0421" | CJE0564 | - | - | - | - | - | | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0004" | CJE0565 | - | - | - | - | - | | | | | | | | -1 | | | - | hypothetical protein | - |
| "opCjV010000 0955" | CJE0566 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | DNA/RNA non-specific endonuclease | - |
| "opCjV010000 0508" | CJE0567 | - | - | - | - | - | | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 0 | - | hypothetical protein | - |
| "opCjV010000 0171" | CJE0568 | - | - | - | - | - | | | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0325" | CJE0569 | - | - | - | - | - | | | -1 | -1 | | | | -1 | 1 | -1 | - | phage repressor protein, putative | - |
| "opCjV010000 0973" | CJE0570 | - | - | - | - | - | | | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0113" | CJE0571 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0018" | CJE0572 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | lipoprotein, putative | - |
| "opCjV010000 | CJE0573 | - | - | - | - | - | | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | 0 | - | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0063" | | | | | | | | | | | | | | | | | | | |
| "opCjV010000 0415" | CJE0574 | - | - | - | - | - | | -1 | -1 | -1 | | 1 | -1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0316" | CJE0575 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0315" | CJE0576 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0129" | CJE0577 | - | - | - | - | - | | | -1 | | -1 | -1 | -1 | -1 | 1 | -1 | - | terminase B protein, putative | - |
| "opCjV010000 0083" | CJE0578 | - | - | - | - | - | | | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0745" | CJE0579 | - | - | - | - | - | | -1 | -1 | -1 | | | 1 | 1 | | -1 | - | hypothetical protein | - |
| "opCjV010000 0037" | CJE0580 | - | - | - | - | - | | | -1 | | -1 | 1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0400" | CJE0581 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0694" | CJE0582 | - | - | - | - | - | | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV010000 1059" | CJE0583 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0732" | CJE0584 | - | - | - | - | - | | | -1 | -1 | 1 | -1 | -1 | 1 | 0 | 1 | - | hypothetical protein | - |
| "opCjV010000 0491" | CJE0585 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0666" | CJE0586 | - | - | - | - | - | | | -1 | 1 | 1 | | | 1 | | 1 | - | hypothetical protein | - |
| "opCjV010000 0583" | CJE0587 | - | - | - | - | - | | | -1 | | | | -1 | -1 | | | - | hypothetical protein | - |
| "opCjV010000 0249" | CJE0588 | - | - | - | - | - | | | -1 | -1 | -1 | -1 | 1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0236" | CJE0589 | - | - | - | - | - | | | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0976" | CJE0590 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0760" | CJE0591 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0011" | CJE0592 | - | - | - | - | - | -1 | -1 | -1 | 0 | 1 | -1 | -1 | 1 | -1 | 0 | - | hypothetical protein | - |
| "opCjV010000 0466" | CJE0593 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 1114" | CJE0594 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0157" | CJE0595 | - | - | - | - | - | | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0319" | CJE0596 | - | - | - | - | - | | -1 | -1 | 0 | | 1 | 1 | 1 | -1 | 0 | - | hypothetical protein | - |
| "opCjV010000 0852" | CJE0597 | - | - | - | - | - | -1 | -1 | -1 | 0 | 1 | -1 | -1 | 1 | -1 | 0 | - | hypothetical protein | - |
| "opCjV010000 0009" | CJE0598 | - | - | - | - | - | | | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0123" | CJE0599 | - | - | - | - | - | -1 | -1 | -1 | 0 | -1 | -1 | -1 | 1 | -1 | 0 | - | hypothetical protein | - |
| "opCjV010000 0091" | CJE0600 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV010000 0645" | CJE0601 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0787" | CJE0602 | - | - | - | - | - | 0 | -1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10000118" | CJE0603 | - | Cj0495 | - | CCO0593 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000119" | CJE0604 | - | Cj0496 | - | CCO0594 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000120" | CJE0605 | - | Cj0497 | - | CCO0595 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | ATP-dependent nuclease (addB), putative |
| "CJ_10000121" | CJE0606 | trpC | Cj0498 | trpC | CCO0596 | trpC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | indole-3-glycerol phosphate synthase | indole-3-glycerol phosphate synthase | indole-3-glycerol phosphate synthase |
| "CJ_10000129" | CJE0607 | - | Cj0499 | - | CCO0597 | hit | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | HIT-like protein | Hit family protein | hit family protein |
| "CJ_10000131" | CJE0608 | - | Cj0500 | - | CCO0598 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP /GTP binding protein | GTP-binding protein | rhodanese-like domain protein, putative |
| "CJ_10000133" | CJE0609 | - | Cj0501 | - | CCO0599 | amt | | -1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | pseudogene | pseudogene | ammonium transporter |
| "CJ_10000135" | CJE0610 | hemH | Cj0503c | hemH | CCO0600 | hemH | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative ferrochelatase | ferrochelatase | ferrochelatase |
| "CJ_10000136" | CJE0611 | - | Cj0504c | - | CCO0602 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | oxidoreductase, Gfo/Idh/MocA family | oxidoreductase, Gfo/Idh/MocA family, putative |
| "CJ_10000137" | CJE0612 | - | Cj0505c | - | CCO0604 | degT | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative aminotransferase (degT family) | DegT/DnrJ/EryC1/StrS aminotransferase family | A porR mutant of Pophyromonas gingivalis shows |
| "CJ_10000138" | CJE0613 | alaS | Cj0506 | alaS | CCO0605 | alaS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | alanyl-tRNA synthetase | alanyl-tRNA synthetase | alanyl-tRNA synthetase |
| "CJ_10000139" | CJE0614 | maf | Cj0507 | maf | CCO0606 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | MAF homolog | Maf-like protein | Maf protein, putative |
| "CJ_10000140" | CJE0615 | pbpA | Cj0508 | pbpA | CCO0607 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | penicillin-binding protein | penicillin-binding protein 1A | penicillin-binding protein 1A (PBP-1A) |
| "opCcV010000 0257" | CJE0616 | clpB | Cj0509c | clpB | CCO0608 | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 0 | ATP-dependent CLP protease ATP-binding subunit | ATP-dependent chaperone protein ClpB | ATP-dependent Clp protease, ATP-binding subunit |
| "opCcV010000 0188" | CJE0617 | - | Cj0510c | - | CCO0609 | - | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000149" | CJE0618 | ctpA | Cj0511 | - | CCO0611 | prc | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative secreted protease | carboxyl-terminal protease | protease |
| "CJ_10000151" | CJE0619 | purC | Cj0512 | purC | CCO0612 | purC | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | phosphoribosylaminoimidazole-succinocarboxamide | phosphoribosylaminoimidazole-succinocarboxamide | phosphoribosylaminoimidazole-succinocarboxamide |
| "CJ_10000153" | CJE0620 | purS | Cj0513 | - | CCO0613 | purS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | phosphoribosylformylglycinamidine synthase, purS | phosphoribosylformylglycinamidine synthase, PurS |
| "CJ_10000154" | CJE0621 | purQ | Cj0514 | purQ | CCO0614 | purQ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphoribosylformylglycinamidine synthase I | phosphoribosylformylglycinamidine synthase | phosphoribosylformylglycinamidine synthase I |
| "CJ_10000155" | CJE0622 | - | Cj0515 | - | CCO0615 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0515 |
| "CJ_10000156" | CJE0623 | - | Cj0516 | plsC | CCO0616 | - | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative 1-acyl-SN-glycerol-3-phosphate | 1-acyl-sn-glycerol-3-phosphate acyltransferase, | 1-acyl-sn-glycerol-3-phosphate acyltransferase, |
| "CJ_10000157" | CJE0624 | - | Cj0517 | crcB | CCO0617 | crcB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | CRCB protein homolog | CrcB | crcB protein |
| "CJ_10000158" | CJE0625 | htpG | Cj0518 | htpG | CCO0618 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hsp90 family heat shock protein | heat shock protein 90 | hsp90 family heat shock protein Cj0518 |
| "CJ_10000159" | CJE0626 | - | Cj0519 | - | CCO0619 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000165" | CJE0627 | - | Cj0520 | - | CCO0620 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0520 |
| "CJ_10000169" | CJE0628 | - | Cj0523 | - | CCO0621 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | Na/Pi-cotransporter, putative | Na/Pi cotransporter, putative |
| "CJ_10000172" | CJE0629 | - | Cj0525c | pbpB | CCO0622 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative penicillin-binding protein | penicillin-binding protein | cell division protein (ftsI) |
| "CJ_10000173" | CJE0630 | fliE | Cj0526c | fliE | CCO0623 | fliE | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | putative flagellar hook-basal | flagellar basal body protein | flagellar hook-basal body |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | body complex | | complex protein |
| "CJ_10000174" | CJE0631 | flgC | Cj0527c | flgC | CCO0624 | flgC | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar basal-body rod protein | flagellar basal body rod protein | flagellar basal-body rod protein FlgC |
| "CJ_10000175" | CJE0632 | flgB | Cj0528c | flgB | CCO0625 | flgB | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellar basal-body rod protein | flagellar basal body rod protein | flagellar basal-body rod protein FlgB |
| "CJ_10000176" | CJE0633 | - | Cj0529c | - | CCO0626 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Uncharacterized BCR, YceG family COG1559 |
| "CJ_10000177" | CJE0634 | - | Cj0530 | - | CCO0627 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0530 |
| "CJ_10000781" | CJE0635 | icd | Cj0531 | icd | CCO0628 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | isocitrate dehydrogenase | isocitrate dehydrogenase, NADP-dependent | isocitrate dehydrogenase, NADP-dependent |
| "CJ_10000782" | CJE0636 | mdh | Cj0532 | mdh | CCO0629 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | malate dehydrogenase | malate dehydrogenase | malate dehydrogenase Cj0532 |
| "CJ_10000783" | CJE0637 | sucC | Cj0533 | sucC | CCO0630 | sucC | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | succinyl-coA synthetase beta chain | succinyl-CoA synthase, beta subunit | succinyl-CoA synthase, beta subunit |
| "CJ_10000784" | CJE0638 | sucD | Cj0534 | sucD | CCO0631 | sucD | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | succinyl-coA synthetase alpha chain | succinyl-CoA synthase, alpha subunit | SucD |
| "opCcV010000 1932" | CJE0639 | oorD | Cj0535 | oorD | CCO0632 | korD | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 0 | OORD subunit of 2-oxoglutarate:acceptor | 2-oxoglutarate:acceptor oxidoreductase, delta | ferrodoxin-like protein |
| "CJ_10000786" | CJE0640 | oorA | Cj0536 | oorA | CCO0633 | vorB | 1 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | OORA subunit of 2-oxoglutarate:acceptor | 2-oxoglutarate ferredoxin oxidoreductase | ferredoxin oxidoreductase, alpha subunit |
| "CJ_10000788" | CJE0641 | oorB | Cj0537 | oorB | CCO0634 | oorB | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | OORB subunit of 2-oxoglutarate:acceptor | ferrodoxin oxidoreductase beta subunit | ferredoxin oxidoreductase, beta subunit |
| "CJ_10000791" | CJE0642 | oorC | Cj0538 | oorC | CCO0635 | - | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | OORC subunit of 2-oxoglutarate:acceptor | indolepyruvate ferredoxin oxidoreductase | ferredoxin oxidoreductase, gamma subunit |
| "CJ_10000794" | CJE0643 | - | Cj0539 | - | CCO0636 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000797" | CJE0644 | - | Cj0540 | - | CCO0637 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000809" | CJE0645 | - | Cj0541 | - | CCO0638 | ispB | 1 | 0 | 1 | | -1 | 1 | -1 | 1 | 1 | -1 | polyprenyl synthetase | polyprenyl synthetase family protein | octaprenyl-diphosphate synthase (ispB) |
| "CJ_10000810" | CJE0646 | hemA | Cj0542 | hemA | CCO0639 | hemA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glutamyl-tRNA reductase | glutamyl-tRNA reductase | glutamyl-tRNA reductase |
| "CJ_10000811" | CJE0647 | proS | Cj0543 | proS | CCO0640 | proS | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | prolyl-tRNA synthetase | prolyl-tRNA synthetase | prolyl-tRNA synthetase |
| "CJ_10000812" | CJE0648 | - | Cj0544 | - | CCO0641 | - | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative integral memnbrane protein | hypothetical protein | probable integral memnbrane protein Cj0544 |
| "CJ_10000813" | CJE0649 | hemC | Cj0545 | hemC | CCO0642 | hemC | 1 | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | porphobilinogen deaminase | porphobilinogen deaminase | porphobilinogen deaminase |
| "CJ_10000815" | CJE0650 | - | Cj0546 | - | CCO0643 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase, | conserved hypothetical protein TIGR00148, |
| "CJ_10000817" | CJE0651 | flaG | Cj0547 | flaG | CCO0644 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | possible flagellar protein | flagellar protein FlaG | probable flagellar protein Cj0547 |
| "CJ_10000820" | CJE0652 | fliD | Cj0548 | fliD | CCO0645 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative flagellar hook-associated protein | flagellar hook-associated protein | flagellar hook-associated protein 2 (fliD), |
| "CJ_10000823" | CJE0653 | fliS | Cj0549 | fliS | CCO0646 | fliS | 1 | 1 | 1 | | -1 | 1 | 1 | -1 | 1 | 1 | flagellar protein | flagellar protein FliS | flagellar protein FliS |
| "CJ_10000826" | CJE0654 | - | Cj0550 | - | CCO0647 | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000836" | CJE0655 | efp | Cj0551 | efp | CCO0649 | efp | 1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | elongation factor P | elongation factor P | translation elongation factor P |
| "CJ_10000837" | CJE0656 | - | Cj0552 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hydrophobic protein | hypothetical protein | - |
| "CJ_10000838" | CJE0657 | - | Cj0553 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | putative integral membrane protein | hypothetical protein | - |
| "CJ_10000839" | CJE0658 | - | Cj0554 | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 0 | 1 | 1 | -1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000840" | CJE0659 | - | Cj0555 | - | - | - | -1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | putative integral membrane protein | hypothetical protein | - |
| "CJ_10000842" | CJE0660 | - | Cj0556 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000844" | CJE0661 | - | Cj0557c | - | CCO0650 | - | 1 | 1 | 1 | -1 | -1 | 1 | | -1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0557c |
| "CJ_10000845" | CJE0662 | - | Cj0557c | - | CCO0651 | - | 1 | 1 | 1 | 0 | 1 | 1 | 1 | -1 | 0 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0557c |
| "CJ_10000850" | CJE0663 | - | Cj0559 | - | CCO0653 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | oxidoreductase | pyridine nucleotide-disulphide oxidoreductase | oxidoreductase Cj0559 |
| "CJ_10000853" | CJE0665 | - | Cj0560 | - | CCO0655 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | putative integral membrane protein | pseudogene | MATE efflux family protein, putative |
| "CJ_10000865" | CJE0666 | - | Cj0561c | - | CCO0656 | - | 1 | 0 | 1 | 1 | -1 | -1 | -1 | 0 | 1 | 1 | possible periplasmic protein | hypothetical protein | probable periplasmic protein Cj0561c |
| "CJ_10000866" | CJE0667 | dnaB | Cj0562 | dnaB | CCO0657 | dnaB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | replicative DNA helicase | replicative DNA helicase | replicative DNA helicase |
| "CJ_10000867" | CJE0668 | - | Cj0563 | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000868" | CJE0669 | - | Cj0564 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | putative integral membrane protein | hypothetical protein | - |
| "opCjV010000 0279" | CJE0670 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | GTP-binding protein | - |
| "opCjV010000 0872" | CJE0671 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 1026" | CJE0672 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10000882" | CJE0673 | - | Cj0570 | - | CCO0247 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative ATP /GTP binding protein | pseudogene | probable ATP /GTP binding protein Cj0570 |
| "CJ_10000889" | CJE0674 | - | Cj0571 | - | CCO0245 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative transcriptional regulator | transcriptional regulator, putative | probable transcription regulator Cj0571 |
| "CJ_10000890" | CJE0675 | ribB | Cj0572 | ribA | CCO1384 | ribBA | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone | bifunctional 3,4-dihydroxy-2-butanone | 3,4-dihydroxy-2-butanone 4-phosphate |
| "CJ_10000891" | CJE0676 | - | Cj0573 | - | CCO1383 | - | 1 | - | 1 | 0 | -1 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | GatB/Yqey family protein | YqeY family protein |
| "CJ_10000892" | CJE0677 | ilvB | Cj0574 | ilvI | CCO1382 | ilvB | 1 | 1 | | 1 | -1 | 0 | -1 | 1 | 1 | -1 | acetolactate synthase large subunit | acetolactate synthase III large subunit | acetolactate synthase, large subunit, |
| "CJ_10000893" | CJE0678 | ilvH | Cj0575 | ilvH | CCO1381 | ilvN | 1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | acetolactate synthase small subunit | acetolactate synthase III small subunit | acetolactate synthase, small subunit |
| "CJ_10000894" | CJE0679 | lpxD | Cj0576 | lpxD | CCO1380 | lpxD | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | UDP-3-O-[3-hydroxymyristoyl] glucosamine | UDP-3-O-[3-hydroxymyristoyl] glucosamine | UDP-3-O-[3-hydroxymyristoyl] glucosamine |
| "CJ_10000895" | CJE0680 | queA | Cj0577c | queA | CCO1379 | queA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | S-adenosylmethionine:tRNA | S-adenosylmethionine:tRNA | S-adenosylmethionine:tRNA |
| "CJ_10000896" | CJE0681 | tatC | Cj0578c | mttB | CCO1378 | tatC | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | sec-independant protein translocase | Sec-independent protein translocase TatC | Sec-independent protein translocase TatC |
| "CJ_10000897" | CJE0682 | tatB | Cj0579c | - | CCO1377 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | sec-independent translocase | Sec-independent protein translocase protein |
| "CJ_10000898" | CJE0683 | - | Cj0580c | - | CCO1376 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | putative oxidoreductase | coproporphyrinogen III oxidase | oxygen-independent coproporphyrinogen III |
| "CJ_10000899" | CJE0684 | nidH | Cj0581 | - | CCO1375 | mutT | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | putative NTPase | dinucleoside polyphosphate hydrolase | (di)nucleoside polyphosphate hydrolase |
| "CJ_10000900" | CJE0685 | - | Cj0582 | lysC | CCO1374 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | aspartokinase, alpha and beta subunits | aspartate kinase | aspartate kinase, monofunctional class |
| "CJ_10000901" | CJE0686 | - | Cj0583 | - | CCO1373 | - | 1 | 1 | 1 | 1 | -1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000902" | CJE0687 | - | Cj0584 | - | CCO1372 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | DNA polymerase III subunit delta | DNA polymerase III delta prime subunit (holB) |
| "opCcV010000 0841" | CJE0688 | folP | Cj0585 | folP | CCO1371 | folP | 1 | 1 | 1 | 1 | -1 | 0 | -1 | 1 | 0 | 1 | putative dihydropteroate synthase | dihydropteroate synthase | dihydropteroate synthase (folP) |
| "CJ_10000903" | CJE0689 | ligA | Cj0586 | ligA | CCO1368 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | DNA ligase | DNA ligase | DNA ligase (NAD) Cj0586 |
| "CJ_10000904" | CJE0690 | - | Cj0587 | - | CCO1366 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0587 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000905" | CJE0691 | tlyA | Cj0588 | tlyA | CCO1365 | tly | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | putative haemolysin | hemolysin A | hemolysin (tly) |
| "CJ_10000906" | CJE0692 | - | Cj0589 | ribF | CCO1364 | ribF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative riboflavin kinase /FMN | hypothetical protein | riboflavin biosynthesis protein RibF |
| "CJ_10000907" | CJE0693 | - | Cj0590 | - | CCO1363 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | hypothetical protein | methyltransferase, putative | methyltransferase, putative |
| "CJ_10000915" | CJE0694 | - | Cj0591c | - | CCO1362 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0591c -related protein |
| "CJ_10000917" | CJE0695 | - | Cj0592c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000920" | CJE0696 | - | Cj0593c | - | CCO1361 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0593c |
| "CJ_10000923" | CJE0697 | - | Cj0594c | - | CCO1360 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | DNA/RNA non-specific endonuclease | DNA/RNA non-specific endonuclease |
| "CJ_10000925" | CJE0698 | nth | Cj0595c | nth | CCO1359 | nth | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | endonuclease III | endonuclease III | endonuclease III |
| "CJ_10000926" | CJE0699 | - | Cj0596 | - | CCO1358 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | peptidyl-prolyl cis-trans isomerase | major antigenic peptide PEB4 | peptidyl-prolyl cis-trans isomerase |
| "CJ_10000927" | CJE0700 | fbaA | Cj0597 | fba | CCO1357 | fba | 1 | 1 | 1 | -1 | -1 | 1 | 0 | -1 | 1 | -1 | fructose-bisphosphate aldolase | fructose-bisphosphate aldolase | fructose-bisphosphate aldolase, class II |
| "CJ_10000929" | CJE0701 | - | Cj0598 | - | CCO1356 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | -1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0598 |
| "CJ_10000931" | CJE0702 | - | Cj0599 | - | CCO1355 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative periplasmic protein | chemotaxis protein MotB, putative | probable periplasmic protein Cj0599 |
| "CJ_10000932" | CJE0703 | - | Cj0600 | - | CCO1354 | - | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000942" | CJE0704 | - | Cj0601c | - | CCO0684 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative sodium-dependent transmembrane | sodium-dependent transporter, putative | sodium- and chloride-dependent transporter |
| "CJ_10000944" | CJE0705 | - | Cj0602c | - | CCO0685 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | | 1 | hypothetical protein | MOSC domain protein | MOSC domain protein |
| "CJ_10000947" | CJE0706 | dsbD | Cj0603c | dsbD | CCO0686 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative thiol:disulfide interchange protein | thiol:disulfide interchange protein DsbD | thiol:disulfide interchange protein DsbD |
| "CJ_10000950" | CJE0707 | - | Cj0604 | - | CCO0687 | - | 1 | 1 | 1 | 1 | -1 | 0 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | Domain of unknown function (DUF344) family |
| "CJ_10000952" | CJE0708 | - | Cj0605 | - | CCO0688 | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | putative amidohydrolase | carboxypeptidase | peptidase, M20/M25/M40 family |
| "CJ_10000954" | CJE0709 | - | Cj0606 | - | CCO0689 | - | 1 | 1 | 1 | -1 | -1 | 0 | 0 | -1 | 1 | 1 | putative periplasmic protein | macrolide-specific efflux protein macA | probable periplasmic protein Cj0606 |
| "CJ_10000956" | CJE0710 | - | Cj0607 | - | CCO0690 | ybjZ | -1 | 0 | 1 | 1 | | 1 | -1 | -1 | 1 | 1 | ABC-type transmembrane transport protein | macrolide-specific efflux protein macB | ABC transporter, ATP-binding protein |
| "CJ_10000958" | CJE0711 | - | Cj0608 | - | CCO0691 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative outer membrane protein | outer membrane efflux protein | outer membrane efflux family protein, putative |
| "CJ_10000960" | CJE0712 | - | Cj0609c | - | CCO0692 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible periplasmic protein | hypothetical protein | probable periplasmic protein Cj0609c |
| "CJ_10000961" | CJE0713 | - | Cj0610c | - | CCO0693 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0610c |
| "CJ_10000972" | CJE0714 | algI | Cj0611c | - | CCO0694 | - | 1 | 1 | | 1 | -1 | 1 | -1 | -1 | 1 | -1 | putative transmembrane transport protein | alginate O-acetyltransferase AlgI | probable transmembrane transport protein |
| "opCcV0100000246" | CJE0715 | ftn | Cj0612c | cft | CCO0695 | pfr | -1 | -1 | 1 | 0 | 1 | 1 | -1 | 1 | -1 | 1 | ferritin | nonheme iron-containing ferritin | ferritin |
| "CJ_10000976" | CJE0716 | - | Cj0613 | pstS | CCO0696 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | possible periplasmic phosphate binding protein | phosphate ABC transporter, periplasmic | probable periplasmic phosphate binding protein |
| "CJ_10000979" | CJE0717 | - | Cj0614 | pstC | CCO0697 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | putative phosphate transport system permease | phosphate ABC transporter, permease protein | probable phosphate transport system permease |
| "CJ_10000981" | CJE0718 | - | Cj0615 | pstA | CCO0698 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phosphate transport system permease | phosphate ABC transporter, permease protein | probable phosphate transport system permease |
| "CJ_10000983" | CJE0719 | pstB | Cj0616 | pstB | CCO0699 | pstB | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phosphate transport ATP-binding | phosphate ABC transporter, ATP-binding protein | phosphate ABC transporter, ATP-binding protein |
| "CJ_10000987" | CJE0720 | - | Cj0618 | - | CCO0700 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | hypothetical protein | pseudogene | conserved hypothetical protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV0100001074" | CJE0721 | - | - | - | - | - | -1 | 0 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10000988" | CJE0722 | - | Cj0619 | - | CCO0701 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | putative integral membrane protein | MATE efflux family protein | probable integral membrane protein Cj0619 |
| "CJ_10000990" | CJE0723 | - | Cj0620 | - | CCO0702 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001001" | CJE0724 | - | Cj0621 | - | CCO0703 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001003" | CJE0725 | hypF | Cj0622 | hypF | CCO0704 | hypF | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | transcriptional regulatory protein hypF | [NiFe] hydrogenase maturation protein HypF | [NiFe] hydrogenase maturation protein HypF |
| "CJ_10001006" | CJE0726 | hypB | Cj0623 | hypB | CCO0705 | hypB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hydrogenase isoenzymes formation protein | hydrogenase accessory protein HypB | hydrogenase accessory protein HypB |
| "CJ_10001009" | CJE0727 | hypC | Cj0624 | hypC | CCO0706 | hypC | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hydrogenase isoenzymes formation protein | hydrogenase assembly chaperone HypC/HupF | hydrogenase assembly chaperone hypC/hupF |
| "CJ_10001011" | CJE0728 | hypD | Cj0625 | hypD | CCO0707 | hypD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hydrogenase isoenzymes formation protein | hydrogenase expression/formation protein HypD | hydrogenase expression/formation protein HypD |
| "CJ_10001013" | CJE0729 | hypE | Cj0626 | hypE | CCO0708 | - | 1 | 1 | 1 | 1 | -1 | | 1 | -1 | -1 | -1 | hydrogenase isoenzymes formation protein | hydrogenase expression/formation protein HypE | hydrogenase isoenzymes formation protein Cj0626 |
| "CJ_10001015" | CJE0730 | hypA | Cj0627 | hypA | CCO0709 | hypA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | | 1 | hydrogenase expression /formation protein | hydrogenase nickel insertion protein HypA | hydrogenase nickel insertion protein HypA |
| "opCjV0100000653" | CJE0731 | - | - | - | - | - | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | - | type III restriction/modification enzyme, | - |
| "opCjV0100000114" | CJE0732 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | type III restriction-modification enzyme | - |
| "CJ_10001019" | CJE0733 | - | Cj0630c | - | CCO0710 | - | 1 | 0 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000102" | CJE0734 | - | Cj0631c | - | CCO0711 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | putative ribonuclease | RNB-like protein | probable ribonuclease Cj0631c |
| "CJ_10000103" | CJE0735 | ilvC | Cj0632 | ilvC | CCO0712 | ilvC | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | ketol-acid reductoisomerase | ketol-acid reductoisomerase | ketol-acid reductoisomerase |
| "CJ_10000104" | CJE0736 | - | Cj0633 | - | CCO0713 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0633 |
| "CJ_10000105" | CJE0737 | dprA | Cj0634 | - | CCO0714 | dprA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | SMF family protein | DNA processing protein A | DNA processing chain A (dprA) |
| "CJ_10000106" | CJE0738 | - | Cj0635 | - | CCO0715 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | Holliday junction resolvase-like protein | conserved hypothetical protein TIGR00250 |
| "CJ_10000107" | CJE0739 | - | Cj0636 | - | CCO0716 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NOL1\NOP2\sun family protein | NOL1/NOP2/sun family protein | Sun/nucleolar protein family protein VC1502 |
| "CJ_10000108" | CJE0740 | msrA | Cj0637c | mrsA | CCO0717 | msrA | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative peptide methionine sulfoxide reductase | peptide methionine sulfoxide reductase | peptide methionine sulfoxide reductase |
| "CJ_10000110" | CJE0741 | ppa | Cj0638c | ppa | CCO0718 | ppa | -1 | -1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | inorganic pyrophosphatase | inorganic pyrophosphatase | inorganic pyrophosphatase |
| "CJ_10000112" | CJE0742 | adk | Cj0639c | adk | CCO0719 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | adenylate kinase | adenylate kinase | adenylate kinase Cj0639c |
| "CJ_10000114" | CJE0743 | aspS | Cj0640c | aspS | CCO0720 | aspS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | aspartyl-tRNA synthetase | aspartyl-tRNA synthetase | aspartyl-tRNA synthetase |
| "CJ_10000122" | CJE0744 | - | Cj0641 | - | CCO0721 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | ATP-NAD kinase, putative | inorganic polyphosphate/ATP-NAD kinase |
| "CJ_10000123" | CJE0745 | recN | Cj0642 | recN | CCO0722 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative DNA repair protein | DNA repair protein RecN | DNA repair protein RecN, putative |
| "CJ_10000124" | CJE0746 | - | Cj0643 | - | CCO0723 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative two-component response regulator | response regulator/GGDEF domain protein | response regulator/GGDEF domain protein, |
| "CJ_10000125" | CJE0747 | - | Cj0644 | - | CCO0724 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hydrolase, TatD family | hydrolase, TatD family |
| "CJ_10000126" | CJE0748 | - | Cj0645 | - | CCO0725 | dniR | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative secreted transglycosylase | membrane-bound lytic murein transglycosylase D, | regulatory protein DniR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000127" | CJE0749 | rlpA | Cj0646 | - | CCO0726 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | rare lipoprotein A | lipoprotein, rare lipoprotein A family |
| "CJ_10000128" | CJE0750 | - | Cj0647 | - | CCO0727 | - | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | hypothetical protein | phosphatase, YrbI family | phosphatase, YrbI family |
| "CJ_10000130" | CJE0751 | - | Cj0648 | - | CCO0728 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000132" | CJE0752 | - | Cj0649 | - | CCO0729 | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | OstA family protein | ostA family protein |
| "CJ_10000134" | CJE0753 | - | Cj0650 | - | CCO0730 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP /GTP binding protein | GTP-binding protein | GTP-binding protein EngB |
| "CJ_10000141" | CJE0754 | - | Cj0651 | - | CCO0731 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0651 |
| "CJ_10000142" | CJE0755 | pbpC | Cj0652 | pbpC | CCO0732 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | penicillin-binding protein | penicillin-binding protein 2 | penicillin-binding protein 2 (pbp2) |
| "CJ_10000143" | CJE0756 | - | Cj0653c | - | CCO0733 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative aminopeptidase | peptidase, M24 family | peptidase, M24 family protein |
| "opCjV0100000750" | CJE0757 | - | Cj0654c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | di-/tripeptide transporter | - |
| "CJ_10000144" | CJE0758 | - | Cj0654c | - | - | - | -1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | pseudogene | - |
| "opCjV0100000166" | CJE0759 | - | Cj0654c | - | - | - | 0 | 0 | -1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | pseudogene | hypothetical protein | - |
| "CJ_10000145" | CJE0761 | - | Cj0659c | - | CCO0734 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0659c , putative |
| "CJ_10000146" | CJE0762 | - | Cj0660c | - | CCO0735 | - | 1 | 0 | -1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative transmembrane protein | hypothetical protein | probable transmembrane protein Cj0660c |
| "CJ_10000147" | CJE0763 | era | Cj0661c | era | CCO0736 | era | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | GTP-binding protein ERA homolog | GTP-binding protein Era | GTP-binding protein Era |
| "CJ_10000148" | CJE0764 | hslU | Cj0662c | hslU | CCO0737 | hslU | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative heat shock protein | ATP-dependent protease ATP-binding subunit | heat shock protein HslVU, ATPase subunit HslU |
| "CJ_10000150" | CJE0765 | hslV | Cj0663c | hslV | CCO0738 | hslV | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative heat shock protein | ATP-dependent protease peptidase subunit | heat shock protein |
| "CJ_10000152" | CJE0766 | rplI | Cj0664c | rplI | CCO0739 | rplI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L9 | 50S ribosomal protein L9 | ribosomal protein L9 |
| "CJ_10000160" | CJE0767 | argG | Cj0665c | argG | CCO0740 | argG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | argininosuccinate synthase | argininosuccinate synthase | argininosuccinate synthase |
| "CJ_10000161" | CJE0768 | - | Cj0667 | - | CCO0741 | - | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | S4 domain protein | S4 domain protein |
| "CJ_10000162" | CJE0769 | - | Cj0668 | - | CCO0742 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP /GTP-binding protein | conserved hypothetical protein TIGR00150 | conserved hypothetical protein TIGR00150 |
| "opCcV0100000267" | CJE0770 | - | Cj0669 | - | CCO0743 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | ABC-transporter ATP-binding protein | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "opCcV0100002014" | CJE0771 | rpoN | Cj0670 | rpoN | CCO0744 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | RNA polymerase sigma-54 factor | DNA-directed RNA polymerase subunit N | RNA polymerase sigma-54 factor, putative |
| "CJ_10000163" | CJE0772 | dcuB | Cj0671 | dcuB | CCO0745 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative anaerobic C4-dicarboxylate transporter | anaerobic C4-dicarboxylate transporter | anaerobic C4-dicarboxylate membrane transporter |
| "CJ_10000164" | CJE0773 | - | Cj0672 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | Putative periplasmic protein | hypothetical protein | - |
| "CJ_10000166" | CJE0774 | - | Cj0676 | kdpA | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | pseudogene | - |
| "CJ_10000168" | CJE0775 | - | Cj0677 | kdpB | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | potassium-transporting ATPase B chain | pseudogene | - |
| "CJ_10000170" | CJE0776 | - | Cj0678 | kdpC | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | pseudogene | potassium-transporting ATPase, C subunit, | - |
| "CJ_10000178" | CJE0777 | - | Cj0679 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | truncated KdpD protein | pseudogene | - |
| "CJ_10000179" | CJE0778 | uvrB | Cj0680c | uvrB | CCO0746 | uvrB | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | excinuclease ABC subunit B | excinuclease ABC subunit B | excinuclease ABC, B subunit |
| "CJ_10000180" | CJE0779 | - | Cj0681 | - | CCO0747 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000181" | CJE0780 | - | Cj0682 | - | CCO0748 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000182" | CJE0781 | - | Cj0683 | - | CCO0749 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | prepilin-like protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000183" | CJE0782 | priA | Cj0684 | priA | CCO0750 | priA | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative primosomal protein N' | primosome assembly protein PriA | primosomal protein N` |
| "opCjjV010000198" | CJE0783 | - | Cj0685c | - | - | - | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | possible sugar transferase | invasion phenotype protein | - |
| "CJ_10000184" | CJE0785 | ispG | Cj0686 | gcpE | CCO0752 | ispG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | gcpE protein homolog | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate | 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate |
| "CJ_10000185" | CJE0786 | flgH | Cj0687c | flgH | CCO0753 | flgH | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellar L-ring protein precursor | flagellar L-ring protein precursor | flagellar L-ring protein FlgH |
| "CJ_10000186" | CJE0787 | pta | Cj0688 | pta | CCO0754 | carB | 1 | -1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | putative phosphate acetyltransferase | phosphate acetyltransferase | carbamoyl-phosphate synthase, large subunit |
| "CJ_10000187" | CJE0788 | ackA | Cj0689 | ackA | CCO0755 | ackA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | acetate kinase | acetate kinase | acetate kinase |
| "CJ_10000188" | CJE0789 | - | Cj0690c | - | - | - | 1 | 1 | -1 | 1 | 0 | -1 | 1 | -1 | 1 | 1 | possible restriction /modification enzyme | hypothetical protein | - |
| "CJ_10000189" | CJE0790 | - | Cj0691 | - | CCO0756 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0691 |
| "CJ_10000190" | CJE0791 | - | Cj0692c | - | CCO0757 | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0692c |
| "CJ_10000191" | CJE0792 | mraW | Cj0693c | - | CCO0758 | mraW | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | S-adenosyl-methyltransferase | S-adenosyl-methyltransferase MraW |
| "CJ_10000192" | CJE0793 | - | Cj0694 | - | CCO0759 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | putative periplasmic protein | peptidyl-prolyl cis-trans isomerase D, homolog | conserved hypothetical secreted protein, |
| "CJ_10000193" | CJE0794 | ftsA | Cj0695 | ftsA | CCO0760 | ftsA | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cell division protein ftsA | cell division protein FtsA | cell division protein FtsA |
| "CJ_10000194" | CJE0795 | ftsZ | Cj0696 | ftsZ | CCO0761 | ftsZ | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | cell division protein ftsZ | cell division protein FtsZ | cell division protein FtsZ |
| "CJ_10000195" | CJE0796 | - | Cj0697 | flgG2 | CCO0762 | flgG_1 | 1 | 1 | 1 | | | 1 | | 1 | | -1 | putative flagellar basal-body rod protein | flagellar basal-body rod protein | flagellar basal-body rod protein (flgG) |
| "CJ_10000196" | CJE0797 | flgG | Cj0698 | flgG | CCO0763 | flgG | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar basal-body rod protein | flagellar basal-body rod protein FlgG | flagellar basal-body rod protein (flgG) |
| "CJ_10000204" | CJE0798 | glnA | Cj0699c | glnA | CCO0765 | glnA | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | glutamine synthetase | glutamine synthetase, type I | glutamine synthetase, type I |
| "opCcV0100001719" | CJE0799 | - | - | - | CCO0766 | - | -1 | 0 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | -1 | - | hypothetical protein | conserved hypothetical protein |
| "CJ_10000206" | CJE0800 | - | Cj0700 | - | CCO0766 | - | 0 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000209" | CJE0801 | - | Cj0701 | - | CCO0767 | - | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | putative protease | peptidase, U32 family | probable proteinase Cj0701 |
| "CJ_10000212" | CJE0802 | purE | Cj0702 | purE | CCO0768 | purE | 1 | 1 | -1 | -1 | -1 | 1 | 0 | 1 | 1 | -1 | phosphoribosylaminoimidazole carboxylase | phosphoribosylaminoimidazole carboxylase | phosphoribosylaminoimidazole carboxylase, |
| "CJ_10000214" | CJE0803 | - | Cj0703 | - | CCO0769 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | pseudogene | conserved hypothetical protein |
| "CJ_10000216" | CJE0804 | glyQ | Cj0704 | glyQ | CCO0770 | glyQ | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | glycyl-tRNA synthetase alpha chain | glycyl-tRNA synthetase alpha subunit | glycyl-tRNA synthetase, alpha subunit |
| "CJ_10000218" | CJE0805 | - | Cj0705 | - | CCO0771 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | conserved hypothetical protein TIGR00486 | conserved hypothetical protein TIGR00486 |
| "CJ_10000220" | CJE0806 | - | Cj0706 | - | CCO0772 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000222" | CJE0807 | waaA | Cj0707 | kdtA | CCO0773 | waaA | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3-deoxy-D-manno-octulosonic-acid transferase | 3-deoxy-D-manno-octulosonic-acid transferase | 3-deoxy-d-manno-octulosonic-acid transferase |
| "CJ_10000223" | CJE0808 | - | Cj0708 | - | CCO0774 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ribosomal pseudouridine synthase | RNA pseudouridylate synthase family protein | ribosomal large subunit pseudouridine synthase |
| "CJ_10000234" | CJE0809 | ffh | Cj0709 | ffh | CCO0775 | ffh | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | signal recognition particle protein | signal recognition particle protein | signal recognition particle protein |
| "opCcV0100000480" | CJE0810 | rpsP | Cj0710 | rpsP | CCO0776 | rpsP | | 0 | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 30S ribosomal protein S16 | 30S ribosomal protein S16 | ribosomal protein S16 |
| "CJ_10000235" | CJE0811 | - | Cj0711 | - | CCO0777 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000238" | CJE0812 | rimM | Cj0712 | rimM | CCO0778 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative 16S rRNA processing protein | 16S rRNA processing protein RimM | 16S rRNA processing protein RimM, putative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000240" | CJE0813 | trmD | Cj0713 | trmD | CCO0779 | trmD | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA (guanine-N1)-methyltransferase | tRNA (guanine-N(1)-)-methyltransferase | tRNA (guanine-N1)-methyltransferase |
| "CJ_10000242" | CJE0814 | rplS | Cj0714 | rplS | CCO0780 | rplS | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L19 | 50S ribosomal protein L19 | ribosomal protein L19 |
| "CJ_10000244" | CJE0815 | - | Cj0715 | - | CCO0781 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | transthyretin-like periplasmic protein | transthyretin-like protein | transthyretin family protein |
| "CJ_10000246" | CJE0816 | - | Cj0716 | - | CCO0782 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phospho-2-dehydro-3-deoxyheptonate | 3-deoxy-7-phosphoheptulonate synthase | phospho-2-dehydro-3-deoxyheptonate aldolase |
| "CJ_10000247" | CJE0817 | - | Cj0717 | - | CCO0783 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | hypothetical protein | arsC family protein |
| "CJ_10000249" | CJE0818 | dnaE | Cj0718 | dnaE | CCO0784 | dnaE | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA polymerase III, alpha chain | DNA polymerase III subunit alpha | DNA polymerase III, alpha subunit |
| "CJ_10000258" | CJE0819 | - | Cj0719c | - | CCO0785 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | conserved hypothetical protein TIGR00044 | conserved hypothetical protein TIGR00044 |
| "CJ_10000260" | CJE0820 | flaC | Cj0720c | flaC | CCO0786 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellin | flagellin subunit protein FlaC | flagellin |
| "CJ_10000262" | CJE0821 | - | Cj0721c | - | CCO0787 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0721c |
| "CJ_10000265" | CJE0822 | - | Cj0722c | - | CCO0788 | hemG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative DNA methylase | modification methylase, HemK family | protoporphyrinogen oxidase (hemK) |
| "CJ_10000267" | CJE0823 | - | Cj0723c | - | CCO0789 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane zinc-metalloprotease | peptidase, M48 family | zinc-metallo protease (YJR117W) |
| "CJ_10000269" | CJE0824 | - | Cj0724 | - | CCO0790 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000271" | CJE0825 | mogA | Cj0725c | mog | CCO0791 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | molybdopterin biosynthesis protein | molybdenum cofactor biosynthesis protein | molybdopterin biosynthesis protein Cj0725c |
| "CJ_10000272" | CJE0826 | corA | Cj0726c | corA | CCO0792 | corA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | magnesium and cobalt transport protein | magnesium and cobalt transport protein CorA | magnesium and cobalt transport protein CorA |
| "CJ_10000274" | CJE0827 | - | Cj0727 | - | CCO0793 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | putative periplasmic solute-binding protein | ABC transporter, periplasmic substrate-binding | ABC transporter, periplasmic binding protein |
| "CJ_10000276" | CJE0828 | - | Cj0728 | - | CCO0794 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0728 |
| "CJ_10000287" | CJE0829 | - | Cj0729 | - | CCO0795 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000289" | CJE0830 | - | Cj0730 | - | CCO0796 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transport system permease | ABC transporter, permease protein | probable ABC transport system permease Cj0730 |
| "CJ_10000292" | CJE0831 | - | Cj0731 | - | CCO0797 | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transport system permease | ABC transporter, permease protein | permease protein |
| "CJ_10000295" | CJE0832 | - | Cj0732 | - | CCO0798 | potA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ABC transport system ATP-binding protein | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "CJ_10000297" | CJE0833 | - | Cj0733 | - | CCO0799 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | HAD-superfamily subfamily IB hydrolase | HAD-superfamily subfamily IB hydrolase, |
| "CJ_10000299" | CJE0834 | cjaC | Cj0734c | hisJ | CCO0800 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | histidine-binding protein precursor | CjaC | histidine-binding protein precursor |
| "CJ_10000300" | CJE0835 | - | Cj0735 | - | - | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000302" | CJE0836 | - | Cj0736 | - | - | - | 0 | 1 | 0 | -1 | 1 | 1 | 0 | 1 | 1 | -1 | hypothetical protein | pseudogene | - |
| "CJ_10000304" | CJE0837 | - | Cj0737 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | haemagglutination domain protein | - |
| "CJ_10000306" | CJE0838 | - | Cj0738 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | hypothetical protein | hypothetical protein | - |
| "opCjV0100001024" | CJE0839 | - | Cj0741 | - | - | - | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000910" | CJE0840 | - | Cj0741 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "opCjV0100000193" | CJE0841 | - | Cj0742 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |
| "opCjV010000 | CJE0842 | - | Cj0742 | - | - | - | -1 | 1 | 0 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | pseudogene | hypothetical protein | - |

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| 0611" | | | | | | | | | | | | | | | | | | | |
| "CJ_10000911" | CJE0843 | - | Cj0742 | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | pseudogene | hypothetical protein | - |
| "CJ_10000914" | CJE0844 | - | Cj0752 | - | - | - | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | pseudogene | pseudogene | - |
| "CJ_10000916" | CJE0845 | tonB | Cj0753c | tonB3 | CCO0809 | - | 1 | - | 1 | -1 | 0 | -1 | 1 | -1 | 1 | 1 | tonB transport protein | TonB | TonB |
| "opCjV010000 0226" | CJE0846 | - | - | - | - | - | 0 | 1 | -1 | 1 | 1 | | | 1 | 1 | 0 | - | hypothetical protein | - |
| "CJ_10000919" | CJE0847 | cfrA | Cj0755 | cfrA | CCO0810 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | putative iron uptake protein | ferric receptor CfrA | ferric receptor CfrA |
| "CJ_10000922" | CJE0848 | hrcA | Cj0757 | hrcA | CCO0811 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | putative heat shock regulator | heat-inducible transcription repressor | probable heat shock regulator Cj0757 |
| "CJ_10000935" | CJE0849 | grpE | Cj0758 | grpE | CCO0812 | grpE | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | heat shock protein grpE | co-chaperone protein GrpE | co-chaperone GrpE |
| "CJ_10000936" | CJE0850 | dnaK | Cj0759 | dnaK | CCO0813 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | heat shock protein dnaK | molecular chaperone DnaK | heat shock protein dnaK Cj0759 |
| "CJ_10000937" | CJE0851 | - | Cj0760 | - | CCO0816 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000938" | CJE0852 | - | Cj0761 | - | CCO0817 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000939" | CJE0853 | aspC | Cj0762c | aspB | CCO0818 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | aspartate aminotransferase | aspartate aminotransferase | probable aspartate transaminase Cj0762c |
| "CJ_10000940" | CJE0854 | cysE | Cj0763c | cysE | CCO0819 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | serine acetyltransferase | serine acetyltransferase | serine O-acetyltransferase |
| "CJ_10000941" | CJE0855 | speA | Cj0764c | speA | CCO0820 | speA | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | biosynthetic arginine decarboxylase | arginine decarboxylase | arginine decarboxylase |
| "CJ_10000943" | CJE0856 | hisS | Cj0765c | hisS | CCO0821 | hisS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | histidyl-tRNA synthetase | histidyl-tRNA synthetase | histidyl-tRNA synthetase |
| "CJ_10000946" | CJE0857 | tmk | Cj0766c | tmk | CCO0822 | tmk | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | 1 | putative thymidylate kinase | thymidylate kinase | thymidylate kinase |
| "CJ_10000949" | CJE0858 | coaD | Cj0767c | kdtB | CCO0823 | coaD | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3-deoxy-D-manno-octulosonic-acid transferase | phosphopantetheine adenylyltransferase | pantetheine-phosphate adenylyltransferase |
| "CJ_10000965" | CJE0859 | - | Cj0768c | - | CCO0824 | ubiX | 1 | 1 | 1 | | -1 | | -1 | | | -1 | putative decarboxylase | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase | phenylacrylic acid decarboxylase, |
| "CJ_10000966" | CJE0860 | - | Cj0769c | - | CCO0825 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | putative periplasmic protein | flagellar basal body P-ring biosynthesis | probable periplasmic protein Cj0769c |
| "CJ_10000967" | CJE0861 | - | Cj0770c | - | CCO0826 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 0 | 1 | 1 | putative periplasmic protein | lipoprotein, NLPA family | D-methionine-binding lipoprotein MetQ |
| "CJ_10000968" | CJE0862 | - | Cj0771c | - | CCO0827 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | putative periplasmic protein | lipoprotein, NLPA family | D-methionine-binding lipoprotein MetQ |
| "CJ_10000969" | CJE0863 | - | Cj0772c | - | CCO0828 | - | -1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | putative periplasmic protein | lipoprotein, NLPA family | D-methionine-binding lipoprotein MetQ |
| "CJ_10000970" | CJE0864 | - | Cj0773c | - | CCO0829 | - | -1 | 0 | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | binding-protein dependent transport system | ABC transporter, permease protein | ABC transporter, permease component CAC0985 |
| "CJ_10000971" | CJE0865 | - | Cj0774c | - | CCO0830 | - | 1 | 1 | 1 | -1 | -1 | | 1 | -1 | 1 | -1 | ABC transport system ATP-binding protein | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "CJ_10000973" | CJE0866 | valS | Cj0775c | valS | CCO0831 | valS | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | valyl-tRNA synthetase | valyl-tRNA synthetase | valyl-tRNA synthetase |
| "CJ_10000975" | CJE0867 | - | Cj0776c | - | CCO0832 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0776c |
| "CJ_10000978" | CJE0868 | - | Cj0777 | - | CCO0833 | rep | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative ATP-dependent DNA helicase | ATP-dependent DNA helicase, putative | rep helicase, single-stranded DNA-dependent |
| "CJ_10000994" | CJE0869 | - | Cj0778 | peb2 | CCO0834 | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | major antigenic peptide PEB2 | major antigenic peptide PEB2 | accessory colonization factor AcfC VC0841 , |
| "CJ_10000995" | CJE0870 | tpx | Cj0779 | tpx | CCO0837 | tpx | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | probable thiol peroxidase | thiol peroxidase | thiol peroxidase |
| "CJ_10000996" | CJE0871 | napA | Cj0780 | napA | CCO0838 | napA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | periplasmic nitrate reductase | periplasmic nitrate reductase, large subunit | periplasmic nitrate reductase, large subunit |
| "CJ_10000997" | CJE0872 | napG | Cj0781 | napG | CCO0839 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ferredoxin | quinol dehydrogenase periplasmic component | probable ferredoxin Cj0781 |
| "CJ_10000998" | CJE0873 | napH | Cj0782 | napH | CCO0840 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | putative ferredoxin | quinol dehydrogenase membrane component | iron-sulfur cluster-binding protein napH |

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| "CJ_10000999" | CJE0874 | napB | Cj0783 | napB | CCO0841 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | periplasmic nitrate reductase small subunit | periplasmic nitrate reductase, small subunit | NapB periplasmic nitrate reductase |
| "CJ_10001000" | CJE0875 | napL | Cj0784 | - | CCO0842 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | NapL | probable periplasmic protein Cj0784 |
| "CJ_10001002" | CJE0876 | napD | Cj0785 | napD | CCO0843 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 0 | 1 | 1 | possible napD protein homolog | NapD | probable napD protein homolog Cj0785 |
| "CJ_10001005" | CJE0877 | - | Cj0786 | - | CCO0844 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | small hydrophobic protein | hypothetical protein | small hydrophobic protein Cj0786 -related |
| "CJ_10001008" | CJE0878 | - | Cj0787 | - | CCO0848 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001027" | CJE0879 | - | Cj0788 | - | CCO0849 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001029" | CJE0880 | - | Cj0789 | - | CCO0850 | cca | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative RNA nucleotidyltransferase | polyA polymerase family protein | tRNA nucleotidyltransferase |
| "CJ_10001031" | CJE0881 | purU | Cj0790 | purU | CCO0851 | purU | 0 | 1 | -1 | 0 | 1 | 0 | -1 | 0 | 1 | -1 | formyltetrahydrofolate deformylase | formyltetrahydrofolate deformylase | formyltetrahydrofolate deformylase |
| "CJ_10001033" | CJE0882 | - | Cj0791c | - | CCO0965 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative aminotransferase | aminotransferase, putative | nifS-like protein |
| "CJ_10001034" | CJE0883 | - | Cj0792 | - | CCO0966 | - | 1 | 1 | 1 | -1 | 1 | -1 | 0 | -1 | -1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001035" | CJE0884 | - | Cj0793 | - | CCO0967 | - | 0 | 1 | 0 | 0 | 1 | 1 | 1 | 0 | -1 | -1 | signal transduction histidine kinase | sensor histidine kinase | signal-transducing protein, histidine kinase |
| "CJ_10001037" | CJE0885 | - | Cj0794 | - | CCO0873 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001039" | CJE0886 | - | Cj0795c | murF | CCO0854 | murF | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | -1 | 1 | putative | Mur ligase family protein | UDP-MurNac-pentapeptide presynthetase (murF) |
| "CJ_10001041" | CJE0887 | - | Cj0796c | - | CCO0855 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase |
| "CJ_10001043" | CJE0888 | - | Cj0797c | - | CCO0856 | - | 1 | 1 | | | -1 | 1 | 1 | -1 | 1 | | hypothetical protein | prevent-host-death family protein | prevent-host-death family protein |
| "CJ_10001055" | CJE0889 | ddl | Cj0798c | ddlA | CCO0857 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative D-alanine--D-alanine ligase | D-alanylalanine synthetase | D-alanine--D-alanine ligase |
| "CJ_10001057" | CJE0890 | ruvA | Cj0799c | ruvA | CCO0858 | ruvA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | putative Holliday junction DNA helicase | Holliday junction DNA helicase RuvA | Holliday junction DNA helicase RuvA |
| "CJ_10001059" | CJE0891 | - | Cj0800c | - | CCO0859 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001061" | CJE0892 | mviN | Cj0801 | - | CCO0860 | mviN | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | integral membrane protein (MVIN homolog) | integral membrane protein MviN | integral membrane protein MviN |
| "CJ_10001062" | CJE0893 | cysS | Cj0802 | cysS | CCO0861 | cysS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cysteinyl-tRNA synthetase | cysteinyl-tRNA synthetase | cysteinyl-tRNA synthetase |
| "CJ_10001064" | CJE0894 | - | Cj0803 | msbA | CCO0862 | msbA | 1 | 1 | 1 | 0 | 1 | 1 | 1 | -1 | 1 | 1 | lipid export ABC transport protein | ABC transporter, ATP-binding protein/permease | multidrug resistance protein (msbA) |
| "CJ_10001066" | CJE0895 | pyrD | Cj0804 | pyrD | CCO0863 | pyrD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | dihydroorotate dehydrogenase | dihydroorotate dehydrogenase | dihydroorotate dehydrogenase |
| "CJ_10001068" | CJE0896 | - | Cj0805 | - | CCO0864 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative zinc protease | peptidase, M16 family | protease (pqqE) |
| "CJ_10001070" | CJE0897 | dapA | Cj0806 | dapA | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | dihydrodipicolinate synthase | dihydrodipicolinate synthase | - |
| "CJ_10001072" | CJE0898 | - | Cj0807 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative oxidoreductase | 7-alpha-hydroxysteroid dehydrogenase | - |
| "CJ_10001091" | CJE0899 | - | Cj0808c | - | - | - | 1 | -1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | 0 | small hydrophobic protein | hypothetical protein | - |
| "CJ_10001094" | CJE0900 | - | Cj0809c | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | putative hydrolase | metallo-beta-lactamase family protein | - |
| "CJ_10001097" | CJE0901 | nadE | Cj0810 | nadE | - | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative NH(3)-dependent NAD(+) synthetase | NAD+ synthetase | - |
| "CJ_10001099" | CJE0902 | lpxK | Cj0811 | lpxK | - | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | -1 | 1 | 1 | putative tetraacyldisaccharide 4'-kinase | tetraacyldisaccharide 4'-kinase | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001101" | CJE0903 | thrC | Cj0812 | thrC | CCO0871 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | threonine synthase | threonine synthase | threonine synthase |
| "CJ_10001104" | CJE0904 | kdsB | Cj0813 | kdsB | CCO0872 | kdsB | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 3-deoxy-manno-octulosonate cytidylyltransferase | 3-deoxy-manno-octulosonate cytidylyltransferase | 3-deoxy-D-manno-octulosonate |
| "CJ_10001107" | CJE0905 | - | Cj0814 | - | CCO0873 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001112" | CJE0906 | - | Cj0817 | glnH | CCO0876 | glnH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glutamine-binding periplasmic protein | amino acid-binding protein | glutamine ABC transporter, periplasmic |
| "CJ_10001133" | CJE0907 | fliP | Cj0820c | fliP | CCO0880 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | flagellar biosynthesis protein | flagellar biosynthesis protein | flagellar biosynthesis protein Cj0820c |
| "CJ_10001137" | CJE0908 | glmU | Cj0821 | glmU | CCO0881 | glmU | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UDP-N-acetylglucosamine pyrophosphorylase | UDP-N-acetylglucosamine pyrophosphorylase | UDP-N-acetylglucosamine pyrophosphorylase |
| "CJ_10001140" | CJE0909 | coaBC | Cj0822 | dfp | CCO0882 | coaBC | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 0 | 1 | DNA /pantothenate metabolism flavoprotein | phosphopantothenoylcysteine | phosphopantothenoylcysteine |
| "CJ_10001143" | CJE0910 | - | Cj0823 | - | CCO0883 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001146" | CJE0911 | uppS | Cj0824 | uppS | CCO0884 | uppS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative undecaprenyl diphosphate synthase | undecaprenyl diphosphate synthase | undecaprenyl diphosphate synthase |
| "CJ_10001148" | CJE0912 | - | Cj0825 | - | CCO0885 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative processing peptidase | peptidase, A24 family | type IV prepilin peptidase, probable , putative |
| "CJ_10001150" | CJE0913 | - | Cj0826 | - | CCO0886 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical integral membrane |
| "CJ_10001152" | CJE0914 | truA | Cj0827 | truA | CCO0887 | truA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative tRNA pseudouridine synthase | tRNA pseudouridine synthase A | tRNA pseudouridine synthase A |
| "CJ_10001169" | CJE0915 | ilvA | Cj0828c | ilvA | CCO0888 | ilvA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | threonine dehydratase biosynthetic | threonine dehydratase | threonine dehydratase |
| "CJ_10001171" | CJE0916 | - | Cj0829c | - | CCO0889 | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | hypothetical protein | CoA-binding domain protein | CoA-binding domain protein |
| "CJ_10001175" | CJE0917 | - | Cj0830 | - | CCO0890 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0830 |
| "CJ_10001179" | CJE0918 | trmA | Cj0831c | trmA | CCO0891 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA (uracil-5-)-methyltransferase | tRNA (uracil-5-)-methyltransferase | tRNA (uracil-5-)-methyltransferase |
| "CJ_10001182" | CJE0919 | - | Cj0832c | - | CCO0892 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | Na+/H+ antiporter family protein | probable integral membrane protein Cj0832c |
| "CJ_10001185" | CJE0920 | - | Cj0833c | - | CCO0893 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | oxidoreductase | oxidoreductase, short chain | oxidoreductase, short chain |
| "CJ_10001187" | CJE0921 | - | Cj0834c | - | CCO0894 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | ankyrin repeat-containing possible periplasmic | ankyrin repeat protein | conserved hypothetical protein |
| "CJ_10001190" | CJE0922 | acnB | Cj0835c | acnB | CCO0895 | acnB | 0 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | -1 | 1 | aconitate hydratase | aconitate hydratase | aconitate hydratase 2 |
| "CJ_10001192" | CJE0923 | ogt | Cj0836 | ogt | CCO0896 | ogt | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | methylated-DNA--protein-cysteine | methylated-DNA--protein-cysteine | methylated-DNA--protein-cysteine |
| "CJ_10001195" | CJE0924 | - | Cj0837c | - | CCO0897 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001215" | CJE0925 | metG | Cj0838c | metS | CCO0898 | metS | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | methionyl-tRNA synthetase | methionine--tRNA ligase | methionyl-tRNA synthetase |
| "CJ_10001218" | CJE0926 | - | Cj0839c | - | CCO0899 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001222" | CJE0927 | fbp | Cj0840c | fbp | CCO0900 | fbp | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative fructose-1,6-bisphosphatase | fructose-1,6-bisphosphatase | fructose-1,6-bisphosphatase |
| "CJ_10001226" | CJE0928 | mobB | Cj0841c | - | CCO0901 | mobB | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | putative ATP/GTP binding protein | molybdopterin-guanine dinucleotide biosynthesis | molybdopterin-guanine dinucleotide biosynthesis |
| "CJ_10001229" | CJE0929 | - | Cj0842 | - | CCO0902 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | lipoprotein, putative |
| "CJ_10001231" | CJE0930 | - | Cj0843c | - | CCO0903 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative secreted transglycosylase | soluble lytic murein transglycosylase, putative | soluble lytic murein transglycosylase (slt), |
| "CJ_10001234" | CJE0931 | - | Cj0844c | - | CCO0904 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | YGGT family protein | probable integral membrane protein Cj0844c |
| "CJ_10001237" | CJE0932 | gltX | Cj0845c | gltX | CCO0905 | gltX | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | glutamyl-tRNA synthetase | glutamyl-tRNA synthetase | glutamyl-tRNA synthetase |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001239" | CJE0933 | - | Cj0846 | - | CCO0906 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | Ser/Thr protein phosphatase family protein | Predicted DNA repair exonuclease |
| "CJ_10001244" | CJE0934 | psd | Cj0847 | psd | CCO0907 | psd | -1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative phosphatidylserine decarboxylase | phosphatidylserine decarboxylase | phosphatidylserine decarboxylase |
| "CJ_10000197" | CJE0935 | - | Cj0848c | - | CCO0908 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | hypothetical protein | FlhB domain protein | FlhB domain protein |
| "CJ_10000198" | CJE0936 | - | Cj0849c | - | CCO0909 | - | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000199" | CJE0937 | - | Cj0850c | - | CCO0910 | - | 1 | 1 | 1 | | 1 | | 0 | -1 | 1 | -1 | transmembrane transport protein | major facilitator family protein | major facilitator family transporter, putative |
| "CJ_10000200" | CJE0938 | - | Cj0851c | - | CCO0911 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0851c |
| "CJ_10000201" | CJE0939 | - | Cj0852c | - | CCO0912 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0852c |
| "CJ_10000202" | CJE0940 | hemL | Cj0853c | hemL | CCO0913 | hemL | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | glutamate-1-semialdehyde 2,1-aminomutase | glutamate-1-semialdehyde aminotransferase | glutamate-1-semialdehyde-2,1-aminomutase |
| "CJ_10000203" | CJE0941 | - | Cj0854c | - | CCO0914 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0854c |
| "CJ_10000205" | CJE0942 | folD | Cj0855 | folD | CCO0915 | folD | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar biosynthesis protein | folD bifunctional protein | methylene-tetrahydrofolate dehydrogenase (folD) |
| "CJ_10000208" | CJE0943 | lepB | Cj0856 | lepP | CCO0916 | - | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | signal peptidase I | signal peptidase I | Signal peptidase I |
| "CJ_10000211" | CJE0944 | - | Cj0857c | moeA | CCO0987 | - | 1 | 1 | 0 | 1 | 1 | | | 1 | 1 | 1 | putative molybdopterin biosynthesis protein | molybdopterin biosynthesis MoeA protein, | molybdopterin biosynthesis protein (moeA) |
| "CJ_10000227" | CJE0945 | murA | Cj0858c | murA | CCO0986 | murA | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | -1 | -1 | UDP-N-acetylglucosamine | UDP-N-acetylglucosamine | UDP-N-acetylglucosamine |
| "CJ_10000228" | CJE0946 | - | Cj0859c | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000229" | CJE0947 | - | Cj0860 | - | CCO0985 | - | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | probable integral membrane protein | integral membrane protein | membrane protein |
| "CJ_10000230" | CJE0948 | pabA | Cj0861c | pabA | CCO0984 | pabA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | para-aminobenzoate synthase glutamine | para-aminobenzoate synthase glutamine | para-aminobenzoate synthase glutamine |
| "CJ_10000231" | CJE0949 | pabB | Cj0862c | pabB | CCO0983 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | para-aminobenzoate synthase component I | para-aminobenzoate synthase glutamine | para-aminobenzoate synthetase (pabB) |
| "CJ_10000232" | CJE0950 | - | Cj0863c | xerD | CCO0982 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | DNA recombinase | site-specific recombinase, phage integrase | DNA recombinase Cj0863c |
| "CJ_10000233" | CJE0951 | dsbA | Cj0864 | - | CCO0980 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative periplasmic protein | thiol:disulfide interchange protein DsbA | thiol:disulfide interchange protein, DsbA |
| "opCcV0100000804" | CJE0952 | dsbB | Cj0865 | dsbB | CCO0981 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | -1 | putative disulfide oxidoreductase | putative disulfide oxidoreductase | disulfide bond formation protein |
| "opCjjV010000091" | CJE0953 | - | Cj0866 | ast | - | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | pseudogene | - |
| "CJ_10000237" | CJE0954 | - | Cj0872 | dsbA | CCO0980 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative protein disulphide isomerase | thiol:disulfide interchange protein DsbA, | thiol:disulfide interchange protein, DsbA |
| "CJ_10000253" | CJE0955 | - | Cj0874c | - | - | - | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | cytochrome C | pseudogene | - |
| "CJ_10000255" | CJE0958 | - | Cj0878 | - | CCO0979 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000256" | CJE0959 | - | Cj0879c | - | CCO0978 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0879c |
| "CJ_10000257" | CJE0960 | - | Cj0880c | - | CCO0977 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000259" | CJE0961 | - | Cj0881c | - | CCO0976 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCcV0100001566" | CJE0962 | flhA | Cj0882c | flhA | CCO0975 | flhA | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | flagellar biosynthesis protein | flagellar biosynthesis protein | flagellar biosynthesis protein FlhA |
| "CJ_10000264" | CJE0963 | - | Cj0883c | - | CCO0974 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | RrF2 family protein, putative | rrf2 family protein (putative transcriptional |
| "CJ_10000280" | CJE0964 | rpsO | Cj0884 | rpsO | CCO0973 | rpsO | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 30S ribosomal protein S15 | 30S ribosomal protein S15 | ribosomal protein S15 |
| "CJ_10000281" | CJE0965 | - | Cj0886c | ftsK | CCO0972 | ftsK | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | putative cell division protein | cell division protein FtsK, | cell division protein (ftsK) |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | putative | |
| "CJ_10000282" | CJE0966 | - | Cj0887c | flaD | CCO0971 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellin | flagellar hook-associated protein | probable flagellin Cj0887c |
| "CJ_10000283" | CJE0967 | - | Cj0888c | - | CCO0989 | - | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | ABC transport system ATP-binding protein | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "CJ_10000284" | CJE0968 | - | Cj0889c | - | CCO0990 | - | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | putative sensory trasnduction histidine kinase | sensor histidine kinase | histidine protein kinase PhoR VC0720 , putative |
| "CJ_10000285" | CJE0969 | - | Cj0890c | - | CCO0991 | drrA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative sensory transduction transcriptional | DNA-binding response regulator | response regulator DrrA |
| "CJ_10000286" | CJE0970 | serA | Cj0891c | serA | CCO0992 | serA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | D-3-phosphoglycerate dehydrogenase | D-3-phosphoglycerate dehydrogenase | D-3-phosphoglycerate dehydrogenase |
| "CJ_10000288" | CJE0971 | - | Cj0892c | - | CCO0993 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0892c |
| "CJ_10000291" | CJE0972 | rpsA | Cj0893c | rpsA | CCO0994 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S1 | 30S ribosomal protein S1 | ribosomal protein S1 VC1915 , putative |
| "CJ_10000294" | CJE0973 | ispH | Cj0894c | lytB | CCO0995 | ispH | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | lytB homolog | 4-hydroxy-3-methylbut-2-enyl diphosphate | hydroxymethylbutenyl pyrophosphate reductase |
| "CJ_10000310" | CJE0974 | aroA | Cj0895c | aroA | CCO0996 | aroA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 3-phosphoshikimate 1-carboxyvinyltransferase | 3-phosphoshikimate 1-carboxyvinyltransferase | 3-phosphoshikimate 1-carboxyvinyltransferase |
| "CJ_10000311" | CJE0975 | pheT | Cj0896c | pheT | CCO0997 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phenylalanyl-tRNA synthetase beta chain | phenylalanyl-tRNA synthetase beta subunit | phenylalanyl-tRNA synthetase, beta subunit, |
| "CJ_10000312" | CJE0976 | pheS | Cj0897c | pheS | CCO0998 | pheS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phenylalanyl-tRNA synthetase alpha chain | phenylalanyl-tRNA synthetase alpha subunit | phenylalanyl-tRNA synthetase, alpha subunit |
| "CJ_10000313" | CJE0977 | - | Cj0898 | - | CCO0999 | - | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | HIT-family protein | HIT family protein | HIT family protein |
| "CJ_10000314" | CJE0978 | thiJ | Cj0899c | thiJ | CCO1000 | thiJ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 4-methyl-5(beta-hydroxyethyl)-thiazole | 4-methyl-5(B-hydroxyethyl)-thiazole | ThiJ/PfpI family protein |
| "CJ_10000315" | CJE0979 | - | Cj0900c | - | CCO1001 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | -1 | small hydrophobic protein | hypothetical protein | small hydrophobic protein Cj0900c -related |
| "CJ_10000316" | CJE0980 | - | Cj0901 | - | CCO1002 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative amino acid ABC tansporter permease | amino acid ABC tansporter, permease protein, | amino acid ABC tansporter, permease protein |
| "CJ_10000317" | CJE0981 | - | Cj0902 | glnQ | CCO1003 | glnQ | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative glutamine transport ATP-binding | amino acid ABC transporter, ATP-binding protein | amino acid ABC transporter, ATP-binding protein |
| "CJ_10000319" | CJE0982 | - | Cj0903c | - | CCO1004 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative amino-acid transport protein | amino acid carrier protein | sodium:alanine symporter family protein |
| "CJ_10000321" | CJE0983 | - | Cj0904c | - | CCO1006 | - | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative RNA methylase | RNA methyltransferase, TrmH family | rRNA methylase |
| "CJ_10000330" | CJE0984 | alr | Cj0905c | alr | CCO1007 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | alanine racemase | alanine racemase | alanine racemase, putative |
| "CJ_10000331" | CJE0985 | - | Cj0906c | - | CCO1008 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | conserved hypothetical secreted protein |
| "CJ_10000332" | CJE0986 | - | Cj0908 | - | CCO1009 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0908 |
| "CJ_10000333" | CJE0987 | - | Cj0909 | - | CCO1010 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0909 |
| "CJ_10000334" | CJE0988 | - | Cj0910 | - | CCO1011 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0910 |
| "CJ_10000335" | CJE0989 | - | Cj0911 | - | CCO1012 | - | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic protein | SCO1/SenC family protein | probable periplasmic protein Cj0911 |
| "opCcV0100000950" | CJE0990 | cysK | Cj0912c | cysM | CCO1013 | cysK | -1 | -1 | 0 | 0 | 1 | -1 | 0 | 1 | -1 | -1 | cysteine synthase | cysteine synthase A | cysteine synthase A |
| "CJ_10000336" | CJE0991 | hup | Cj0913c | hupB | CCO1014 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA-binding protein HU homolog | DNA-binding protein HU | DNA-binding protein HU |
| "opCcV0100001041" | CJE0992 | ciaB | Cj0914c | - | CCO1015 | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | CiaB protein | invasion antigen B | CiaB protein Cj0914c |
| "CJ_10000339" | CJE0993 | - | Cj0915 | - | CCO1016 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative hydrolase | thioesterase family protein | probable hydrolase Cj0915 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000348" | CJE0994 | - | Cj0916c | - | CCO1017 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF466) |
| "CJ_10000349" | CJE0995 | cstA | Cj0917c | cstA | CCO1018 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | carbon starvation protein A homolog | carbon starvation protein A | carbon starvation protein A homolog Cj0917c |
| "CJ_10000350" | CJE0996 | prsA | Cj0918c | prsA | CCO1019 | prsA | 0 | 0 | 0 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | ribose-phosphate pyrophosphokinase | ribose-phosphate pyrophosphokinase | ribose-phosphate pyrophosphokinase |
| "CJ_10000352" | CJE0997 | - | Cj0919c | - | CCO1020 | glnP | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC-type amino-acid transporter | amino acid ABC transporter, permease protein | amino acid ABC transporter, permease protein |
| "CJ_10000354" | CJE0998 | - | Cj0920c | - | CCO1021 | glnP | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC-type amino-acid transporter | amino acid ABC transporter, permease protein | amino acid ABC transporter, permease protein |
| "CJ_10000356" | CJE0999 | pebA | Cj0921c | peb1A | CCO1022 | glnH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | probable ABC-type amino-acid transporter | amino acid ABC transporter, periplasmic amino | amino acid ABC transporter, amino acid-binding |
| "CJ_10000358" | CJE1000 | pebC | Cj0922c | pebC | CCO1003 | glnQ | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | ABC-type amino-acid transporter ATP-binding | amino acid ABC transporter, ATP-binding protein | amino acid ABC transporter, ATP-binding protein |
| "CJ_10000359" | CJE1001 | cheR | Cj0923c | cheR | CCO1024 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative MCP protein methyltransferase | chemotaxis protein methyltransferase CheR | chemotaxis protein methyltransferase CheR, |
| "CJ_10000362" | CJE1002 | cheB | Cj0924c | - | CCO1025 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative MCP protein-glutamate methylesterase | protein-glutamate methylesterase CheB | protein-glutamate methylesterase CheB |
| "CJ_10000365" | CJE1003 | rpiB | Cj0925 | rpiB | CCO1026 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ribose 5-phosphate isomerase | ribose 5-phosphate isomerase B | sugar-phosphate isomerase |
| "CJ_10000376" | CJE1004 | - | Cj0926 | - | CCO1027 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj0926 |
| "CJ_10000377" | CJE1005 | apt | Cj0927 | apt | CCO1028 | apt | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | adenine phosphoribosyltransferase | adenine phosphoribosyltransferase | adenine phosphoribosyltransferase |
| "CJ_10000379" | CJE1006 | - | Cj0928 | - | CCO1029 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein (dedA | DedA family protein | conserved hypothetical integral membrane |
| "CJ_10000381" | CJE1007 | - | Cj0929 | pepA | CCO1030 | pepA | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | aminopeptidase | leucyl aminopeptidase | cytosol aminopeptidase |
| "CJ_10000383" | CJE1008 | - | Cj0930 | - | CCO1031 | ychF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative GTP-binding protein | GTP-binding protein YchF | GTP-binding protein YchF |
| "opCcV0100000857" | CJE1009 | argH | Cj0931c | argH | CCO1032 | argH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | argininosuccinate lyase | argininosuccinate lyase | argininosuccinate lyase |
| "CJ_10000385" | CJE1010 | pckA | Cj0932c | pckA | CCO1033 | pckA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | phosphoenolpyruvate carboxykinase (ATP) | phosphoenolpyruvate carboxykinase | phosphoenolpyruvate carboxykinase (ATP) |
| "CJ_10000387" | CJE1011 | - | Cj0933c | pycB | CCO1034 | oadA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative pyruvate carboxylase B subunit | oxaloacetate decarboxylase, alpha subunit, | oxaloacetate decarboxylase, alpha subunit |
| "CJ_10000388" | CJE1012 | - | Cj0934c | - | CCO1036 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane transport protein | sodium transporter, putative | sodium- and chloride-dependent transporter |
| "CJ_10000390" | CJE1013 | - | Cj0935c | - | CCO1037 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | putative transmembrane transport protein | sodium transporter, putative | sodium- and chloride-dependent transporter |
| "opCcV0100001238" | CJE1014 | atpE | Cj0936 | atpE | CCO1038 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | ATP synthase F0 sector C subunit | ATP synthase subunit C | ATP synthase F0, C subunit, putative |
| "CJ_10000403" | CJE1015 | - | Cj0937 | - | CCO0852 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj0937 |
| "CJ_10000405" | CJE1016 | aas | Cj0938c | aas | CCO0853 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative 2-acylglycerophosphoethanolamine | 2-acyl-glycerophospho-ethanolamine | 2-acylglycerophosphoethanolamine |
| "CJ_10000407" | CJE1017 | - | Cj0939c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000409" | CJE1018 | - | Cj0940c | glnP | CCO0957 | glnP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glutamine transport system permease | amino acid ABC transporter, permease protein, | amino acid ABC transporter, permease protein |
| "CJ_10000410" | CJE1019 | - | Cj0941c | - | CCO0954 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane | permease, putative | probable integral membrane |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | protein | | protein Cj0941c |
| "CJ_10000412" | CJE1020 | secA | Cj0942c | secA | CCO0953 | secA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | preprotein translocase SECA subunit | translocase | preprotein translocase, SecA subunit |
| "CJ_10000414" | CJE1021 | lolA | Cj0943 | - | CCO0952 | - | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative periplasmic protein | outer-membrane lipoprotein carrier protein | probable periplasmic protein Cj0943 |
| "CJ_10000416" | CJE1022 | - | Cj0944c | - | CCO0951 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0944c |
| "CJ_10000421" | CJE1023 | - | Cj0945c | - | CCO0950 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative helicase | hypothetical protein | TPR domain protein, putative |
| "CJ_10000432" | CJE1024 | - | Cj0946 | - | CCO0949 | - | 1 | 1 | 1 | -1 | -1 | | | | | -1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj0946 |
| "CJ_10000433" | CJE1025 | - | Cj0947c | - | CCO0947 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative hydrolase | hydrolase, carbon-nitrogen family | probable hydrolase Cj0947c |
| "CJ_10000434" | CJE1026 | - | Cj0948c | - | CCO0946 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane transport protein | cation efflux family protein | probable transmembrane transport protein |
| "CJ_10000436" | CJE1027 | - | Cj0949c | - | CCO0945 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | peptidyl-arginine deiminase family protein | peptidyl-arginine deiminase family protein |
| "CJ_10000437" | CJE1028 | - | Cj0950c | - | CCO0944 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | Putative lipoprotein | heat shock protein HslJ, putative | secreted protein involved in flagellar motility |
| "opCjV010000 1011" | CJE1029 | - | Cj0951c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative MCP-domain signal transduction protein | hypothetical protein | - |
| "CJ_10000439" | CJE1030 | - | Cj0951c | - | CCO0943 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative MCP-domain signal transduction protein | methyl-accepting chemotaxis protein | probable membrane protein Cj0952c |
| "CJ_10000441" | CJE1032 | - | Cj0952c | - | CCO0943 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | pseudogene | probable membrane protein Cj0952c |
| "CJ_10000443" | CJE1033 | purH | Cj0953c | purH | CCO0942 | purH | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | phosphoribosylaminoimidaz olecarboxamide | bifunctional | phosphoribosylaminoimidaz olecarboxamide |
| "CJ_10000447" | CJE1034 | - | Cj0954c | - | CCO0941 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative dnaJ-like protein | DnaJ domain protein | DnaJ domain protein |
| "CJ_10000450" | CJE1035 | purL | Cj0955c | purL | CCO0940 | purL | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | phosphoribosylformylglycin amidine synthase | phosphoribosylformylglycin amidine synthase | phosphoribosylformylglycin amidine synthase II |
| "CJ_10001081" | CJE1036 | trmE | Cj0956c | thdF | CCO0939 | trmE | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative thiophene and furan oxidation protein | tRNA modification GTPase | tRNA modification GTPase TrmE |
| "CJ_10001082" | CJE1037 | - | Cj0957c | - | CCO0938 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001083" | CJE1038 | - | Cj0958c | - | CCO0937 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative membrane protein | putative inner membrane protein translocase | 60 kDa inner-membrane protein |
| "CJ_10001085" | CJE1039 | - | Cj0959c | - | CCO0936 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR00278, |
| "CJ_10001087" | CJE1040 | rnpA | Cj0960c | rnpA | CCO0935 | rnpA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative ribonuclease P protein component | ribonuclease P protein component | ribonuclease P protein component |
| "opCcV010000 1871" | CJE1041 | rpmH | Cj0961c | rpmH | CCO0934 | rpmH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | 50S ribosomal protein L34 | ribosomal protein L34 |
| "CJ_10001090" | CJE1042 | - | Cj0962 | - | CCO0933 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative acetyltransferase | acetyltransferase, GNAT family | acetyltransferase, GNAT family |
| "CJ_10001093" | CJE1043 | - | Cj0963 | - | CCO0932 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | phage SPO1 DNA polymerase-related protein |
| "CJ_10001096" | CJE1044 | - | Cj0964 | - | CCO0931 | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0964 |
| "CJ_10001098" | CJE1045 | - | Cj0965c | - | CCO0930 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | thioesterase family protein | thioesterase family protein, putative |
| "opCjV010000 0416" | CJE1046 | - | - | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001117" | CJE1047 | - | Cj0967 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | pseudogene | - |
| "opCjV010000 0857" | CJE1048 | - | - | - | - | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001118" | CJE1049 | - | Cj0968 | - | - | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | Putative periplasmic protein | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV010000 0581" | CJE1050 | - | Cj0971 | - | - | - | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | pseudogene | hypothetical protein | - |
| "CJ_10001120" | CJE1051 | - | Cj0970 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10001122" | CJE1052 | - | Cj0971 | - | - | - | 1 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10001124" | CJE1053 | - | Cj0972 | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10001126" | CJE1054 | - | Cj0973 | - | - | - | | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10001129" | CJE1055 | - | Cj0974 | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10001132" | CJE1056 | - | Cj0975 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative outer-membrane protein | pseudogene | - |
| "CJ_10001136" | CJE1058 | - | Cj0976 | - | CCO1042 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | methyltransferase, putative | conserved hypothetical protein |
| "opCcV010000 1219" | CJE1059 | - | Cj0977 | - | CCO1043 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | probable lipoprotein Cj0978c -related protein |
| "CJ_10001161" | CJE1060 | - | Cj0978c | - | CCO1044 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | thermonuclease family protein |
| "CJ_10001162" | CJE1061 | - | Cj0979c | - | CCO1045 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative secreted nuclease | thermonuclease family protein | probable peptidase Cj0980 |
| "CJ_10001164" | CJE1062 | pepD | Cj0980 | - | CCO1046 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative peptidase | aminoacyl-histidine dipeptidase | major facilitator family transporter |
| "CJ_10001166" | CJE1063 | cjaB | Cj0981c | - | CCO0255 | proP | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | transmembrane transport protein | transport protein CjaB | proline/betaine transporter (proP) |
| "opCcV010000 0748" | CJE1064 | - | Cj0982c | - | CCO1048 | - | 1 | 1 | 0 | -1 | 0 | -1 | 0 | 1 | | -1 | putative amino-acid transporter periplasmic | surface antigen, CjaA | ABC transporter, periplasmic substrate-binding |
| "opCjjV010000 156" | CJE1065 | jlpA | Cj0983 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative lipoprotein | surface-exposed lipoprotein | - |
| "CJ_10001170" | CJE1066 | - | Cj0984 | - | CCO1050 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF328) |
| "CJ_10001174" | CJE1067 | hipO | Cj0985c | hipO | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hippurate hydrolase | hippurate hydrolase | - |
| "CJ_10001178" | CJE1068 | - | Cj0986c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | - |
| "CJ_10001209" | CJE1069 | - | Cj0989 | - | CCO1051 | - | 0 | 0 | 1 | 0 | 1 | -1 | -1 | 1 | -1 | 1 | putative membrane protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001211" | CJE1070 | - | Cj0990c | - | CCO1052 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001212" | CJE1071 | - | Cj0991c | - | CCO1053 | glpC | 0 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | 0 | -1 | putative oxidoreductase ferredoxin-type electron | iron-sulfur cluster-binding domain protein | anaerobic glycerol-3-phosphate dehydrogenase, |
| "CJ_10001213" | CJE1072 | hemN | Cj0992c | hemN | CCO1054 | hemN | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | oxygen-independent coproporphyrinogen III | coproporphyrinogen III oxidase | oxygen-independent coproporphyrinogen III |
| "CJ_10001214" | CJE1073 | - | Cj0993c | - | CCO1055 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001217" | CJE1074 | argF | Cj0994c | argF | CCO1056 | argF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ornithine carbamoyltransferase | ornithine carbamoyltransferase | ornithine carbamoyltransferase |
| "CJ_10001221" | CJE1075 | hemB | Cj0995c | hemB | CCO1057 | hemB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | delta-aminolevulinic acid dehydratase | delta-aminolevulinic acid dehydratase | porphobilinogen synthase |
| "CJ_10001225" | CJE1076 | ribA | Cj0996 | ribA | CCO1058 | ribA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | GTP cyclohydrolase II | GTP cyclohydrolase II protein | GTP cyclohydrolase II |
| "CJ_10001255" | CJE1077 | gidB | Cj0997 | - | CCO1059 | gidB | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | gidB homolog | methyltransferase GidB | methyltransferase GidB |
| "CJ_10001256" | CJE1078 | - | Cj0998c | - | CCO1060 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0998c |
| "CJ_10001258" | CJE1079 | - | Cj0999c | - | CCO1061 | - | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | -1 | putative integral membrane protein | hypothetical protein | membrane protein, putative |
| "CJ_10001260" | CJE1080 | - | Cj1000 | - | CCO1062 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transcriptional regulator (lysR | transcriptional regulator, LysR family | transcription regulator LysR family VCA0542 , |
| "opCcV010000 | CJE1081 | rpoD | Cj1001 | rpoD | CCO1063 | rpoD | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | RNA polymerase sigma | RNA polymerase sigma | RNA polymerase sigma |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1743" | | | | | | | | | | | | | | | | | factor (sigma-70) | factor | factor RpoD |
| "opCcV0100001596" | CJE1082 | sixA | Cj1002c | - | CCO1064 | - | -1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | phosphohistidine phosphatase SixA | phosphohistidine phosphatase SixA, putative |
| "CJ_10001263" | CJE1083 | - | Cj1003c | - | CCO1065 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | rhomboid family protein | glp regulon protein (glpG) isolog |
| "CJ_10001265" | CJE1084 | - | Cj1004 | - | CCO1066 | - | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1004 |
| "CJ_10001268" | CJE1085 | - | Cj1005c | - | CCO1067 | ftsH_1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane bound ATPase | cell division protein FtsH, putative | cell division protein (ftsH) |
| "CJ_10001271" | CJE1086 | - | Cj1006c | - | CCO1068 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical proteinCj1006c | MiaB-like tRNA modifying enzyme | MiaB-like tRNA modifying enzyme |
| "CJ_10001284" | CJE1087 | - | Cj1007c | - | CCO1069 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative membrane protein | mechanosensitive ion channel family protein | conserved hypothetical integral membrane |
| "CJ_10001285" | CJE1088 | aroB | Cj1008c | aroB | CCO1070 | aroB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3-dehydroquinate synthase | 3-dehydroquinate synthase | 3-dehydroquinate synthase |
| "CJ_10001286" | CJE1089 | - | Cj1009c | - | CCO1071 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | trkA domain protein | TrkA domain protein |
| "CJ_10001288" | CJE1090 | tgt | Cj1010 | tgt | CCO1072 | tgt | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | queuine tRNA-ribosyltransferase | queuine tRNA-ribosyltransferase | queuine tRNA-ribosyltransferase |
| "CJ_10001289" | CJE1091 | - | Cj1011 | - | CCO1073 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1011 |
| "opCjV0100000026" | CJE1092 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCcV0100001013" | CJE1093 | - | - | - | CCOA0089 | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCcV0100000010" | CJE1094 | - | - | - | CCOA0088 | - | | | 0 | | | -1 | -1 | -1 | 1 | | - | site-specific recombinase, phage integrase | site-specific recombinase XerC, putative |
| "opCjV0100000710" | CJE1095 | - | - | - | - | - | | -1 | 0 | -1 | -1 | 1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCcV0100001390" | CJE1096 | - | - | - | CCOA0087 | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | erythrocyte membrane-associated antigen |
| "opCjV0100001060" | CJE1097 | - | - | - | - | - | | -1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCcV0100000501" | CJE1098 | - | - | - | CCOA0086 | - | | -1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCcV0100000426" | CJE1099 | - | - | - | CCOA0085 | - | | | 1 | | | | | -1 | | -1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100001086" | CJE1100 | - | - | - | - | - | | | 0 | | | | 0 | -1 | 1 | -1 | - | death-on-curing family protein | - |
| "opCcV0100000781" | CJE1101 | - | - | - | CCOA0056 | - | | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000105" | CJE1102 | - | - | - | - | - | | | 0 | | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCcV0100000147" | CJE1103 | - | - | - | CCOA0047 | - | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | 0 | 1 | - | hypothetical protein | Domain of unknown function (DUF332) superfamily |
| "opCjV0100000362" | CJE1104 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCcV0100002089" | CJE1105 | - | - | - | CCOA0045 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | TraG protein, putative |
| "opCjV0100000980" | CJE1106 | - | - | - | CCOA0045 | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | TraG protein, putative |
| "opCjV0100000731" | CJE1107 | - | - | - | CCOA0045 | - | | | 1 | | | 1 | 1 | 1 | | | - | TraG-like protein | TraG protein, putative |
| "opCjV0100000054" | CJE1108 | - | - | - | - | - | | | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 | CJE1109 | - | - | - | - | - | | | -1 | -1 | 1 | -1 | -1 | 1 | 0 | 1 | - | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0503" | | | | | | | | | | | | | | | | | | | |
| "opCcV0100001931" | CJE1110 | - | - | - | CCOA0143 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000107" | CJE1111 | - | - | - | CCOA0143 | - | | | -1 | -1 | -1 | -1 | 1 | -1 | 1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCcV0100000005" | CJE1112 | - | - | - | CCOA0144 | - | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000544" | CJE1113 | - | - | - | - | - | | | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCcV0100000110" | CJE1114 | - | - | - | CCOA0038 | - | 1 | 1 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | -1 | - | hypothetical protein | Phage lysozyme, putative |
| "opCcV0100001232" | CJE1115 | - | - | - | CCOA0037 | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000182" | CJE1116 | - | - | - | - | - | | | -1 | | | | 1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000742" | CJE1117 | - | - | - | - | - | -1 | | 0 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000502" | CJE1118 | - | - | - | - | - | | | -1 | -1 | -1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000186" | CJE1119 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000289" | CJE1120 | - | - | - | - | - | | | 0 | -1 | 1 | -1 | -1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000377" | CJE1121 | - | - | - | - | - | | -1 | 0 | | | | | -1 | | | - | pseudogene | - |
| "opCjV0100001091" | CJE1122 | - | - | - | - | - | | | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000343" | CJE1123 | - | - | - | - | - | | | 1 | | | 1 | | -1 | | | - | hypothetical protein | - |
| "opCjV0100000335" | CJE1124 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000556" | CJE1125 | - | - | - | - | - | | | 0 | | | | 1 | -1 | | | - | hypothetical protein | - |
| "opCcV0100000144" | CJE1126 | - | - | - | CCOA0009 | - | | | 0 | | 1 | -1 | | 1 | 1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000380" | CJE1127 | - | pTet_43 | - | - | - | | 0 | 1 | | | | | -1 | | | hypothetical protein | hypothetical protein | - |
| "opCjV0100000139" | CJE1128 | - | - | - | - | - | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000785" | CJE1130 | - | - | - | - | - | | -1 | -1 | | | | | -1 | | | - | hypothetical protein | - |
| "opCjV0100001092" | CJE1131 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV0100000277" | CJE1132 | - | - | - | - | - | | | -1 | | | | | 1 | 1 | | - | hypothetical protein | - |
| "opCjV0100000420" | CJE1133 | - | - | - | - | - | | | -1 | | -1 | -1 | | -1 | 1 | | - | hypothetical protein | - |
| "opCjV0100000318" | CJE1134 | - | - | - | - | - | | | -1 | | | | | -1 | | | - | hypothetical protein | - |
| "opCjV0100000949" | CJE1135 | - | - | - | CCOA0038 | - | | | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | Phage lysozyme, putative |
| "opCjV0100000854" | CJE1136 | - | - | - | - | - | | | -1 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCcV0100001378" | CJE1137 | - | - | - | CCOA0040 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | conserved hypothetical protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100000863" | CJE1138 | - | - | - | CCOA0041 | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCcV0100001069" | CJE1139 | - | - | - | CCOA0141 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | - | hypothetical protein | conserved hypothetical protein |
| "opCjV0100000936" | CJE1140 | - | - | - | - | - | 0 | -1 | 0 | 0 | 1 | 1 | -1 | 1 | 1 | 0 | - | pseudogene | - |
| "opCcV0100001183" | CJE1141 | - | - | - | CCOA0129 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | hypothetical protein | vgrG protein VCA0018 , putative |
| "opCcV0100000261" | CJE1142 | - | - | - | CCOA0099 | - | | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | vgrG protein VCA0123 , putative |
| "opCjV0100000008" | CJE1143 | - | - | - | - | - | | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000334" | CJE1144 | - | - | - | - | - | | -1 | -1 | -1 | 1 | 0 | -1 | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000499" | CJE1145 | - | - | - | - | - | | | -1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCcV0100000277" | CJE1146 | - | - | - | CCOA0095 | - | | | -1 | | | | | -1 | | | - | hypothetical protein | hypothetical protein |
| "opCcV0100001147" | CJE1147 | - | - | - | CCOA0094 | - | -1 | | -1 | | | | 1 | -1 | 1 | | - | hypothetical protein | conserved hypothetical protein |
| "opCjV0100000648" | CJE1148 | - | - | - | - | - | | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000917" | CJE1149 | - | - | - | - | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCcV0100000669" | CJE1150 | - | - | - | CCOA0098 | - | | | -1 | | | -1 | -1 | 1 | | | - | hypothetical protein | conserved hypothetical protein |
| "opCcV0100001445" | CJE1151 | - | - | - | CCOA0096 | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000097" | CJE1152 | - | - | - | - | - | | | -1 | -1 | -1 | 0 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCcV0100002028" | CJE1153 | - | - | - | CCOA0091 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCcV0100000319" | CJE1154 | - | - | - | CCOA0090 | - | -1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | hypothetical protein |
| "opCjV0100000357" | CJE1155 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10001291" | CJE1156 | - | Cj1012c | - | CCO1079 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | 0 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1012c |
| "CJ_10001293" | CJE1157 | - | Cj1013c | - | CCO1080 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | cytochrome c biogenesis protein, CcmF/CycK/CcsA | cytochrome c biogenesis protein (ycf5) |
| "CJ_10001295" | CJE1158 | livF | Cj1014c | livF | CCO1081 | livF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | branched-chain amino-acid ABC transport system | high affinity branched-chain amino acid ABC | branched chain amino acid ABC transporter, |
| "CJ_10001298" | CJE1159 | livG | Cj1015c | livG | CCO1082 | livG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | branched-chain amino-acid ABC transport system | high affinity branched-chain amino acid ABC | branched chain amino acid ABC transporter, |
| "CJ_10001300" | CJE1160 | livM | Cj1016c | livM | CCO1083 | livM | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative branched-chain amino-acid ABC transport | high affinity branched-chain amino acid ABC | branched chain amino acid ABC transporter, |
| "CJ_10001310" | CJE1161 | livH | Cj1017c | livH | CCO1084 | livH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | branched-chain amino-acid ABC transport system | high affinity branched-chain amino acid ABC | branched chain amino acid ABC transporter, |
| "CJ_10001311" | CJE1162 | - | Cj1018c | livK | CCO1085 | livJ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | branched-chain amino-acid ABC transport system | high affinity branched-chain amino acid ABC | branched chain amino acid ABC transporter, |
| "CJ_10001313" | CJE1163 | - | Cj1019c | livJ | CCO1086 | livJ | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | branched-chain amino-acid ABC transport system | high affinity branched-chain amino acid ABC | branched chain amino acid ABC transporter, |
| "CJ_10001315" | CJE1164 | - | Cj1020c | - | CCO1087 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative cytochrome C | cytochrome c family protein | probable cytochrome C Cj1020c |
| "CJ_10001318" | CJE1165 | - | Cj1021c | - | CCO1088 | - | 1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | putative periplasmic protein | porin domain protein | probable periplasmic |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | protein Cj1021c -related |
| "CJ_10001321" | CJE1166 | - | Cj1022c | - | CCO1089 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1022c |
| "CJ_10001323" | CJE1167 | asd | Cj1023c | asd | CCO1090 | asd | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | aspartate-semialdehyde dehydrogenase | aspartate-semialdehyde dehydrogenase | aspartate-semialdehyde dehydrogenase |
| "CJ_10001326" | CJE1168 | - | Cj1024c | - | CCO1091 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | signal-transduction regulatory protein | sigma-54 dependent DNA-binding response | response regulator |
| "CJ_10001329" | CJE1169 | - | Cj1025c | - | CCO1092 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001333" | CJE1170 | - | Cj1026c | - | CCO1093 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj1026c |
| "CJ_10001350" | CJE1171 | gyrA | Cj1027c | gyrA | CCO1094 | gyrA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA gyrase subunit A | DNA gyrase subunit A | DNA gyrase, A subunit |
| "CJ_10001351" | CJE1172 | ctsW | Cj1028c | - | CCO1095 | ctsW | 1 | 1 | 1 | | -1 | 0 | -1 | | 1 | | possible purine/pyrimidine | transformation system protein | transformation system protein |
| "CJ_10001353" | CJE1173 | mapA | Cj1029c | mapA | CCO1096 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | outer membrane liproprotein MapA | outer membrane liproprotein MapA |
| "CJ_10001355" | CJE1174 | lepA | Cj1030c | lepA | CCO1097 | lepA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | lepA GTP-binding protein homolog | GTP-binding protein LepA | GTP-binding protein LepA |
| "CJ_10001357" | CJE1175 | - | Cj1031 | - | CCO1098 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative outer membrane component of efflux | pseudogene | probable outer membrane component of efflux |
| "CJ_10001358" | CJE1176 | - | Cj1032 | - | CCO1099 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane fusion component of efflux | hypothetical protein | probable membrane fusion component of efflux |
| "CJ_10001360" | CJE1177 | - | Cj1033 | - | CCO1100 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane component of efflux | AcrB/AcrD/AcrF family protein | probable integral membrane component of efflux |
| "CJ_10001361" | CJE1178 | - | Cj1034c | - | CCO1101 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible dnaJ-like protein | DnaJ domain protein | DnaJ domain protein |
| "CJ_10001363" | CJE1179 | - | Cj1035c | - | CCO1102 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible transferase | arginyl-tRNA-protein transferase | probable transferase Cj1035c |
| "CJ_10001368" | CJE1180 | - | Cj1036c | - | CCO1103 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001375" | CJE1181 | - | Cj1037c | pycA | CCO1104 | carB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative pyruvate carboxylase A subunit | acetyl-CoA carboxylase | carbamoyl-phosphate synthase, large subunit |
| "CJ_10001376" | CJE1182 | - | Cj1038 | - | CCO1105 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | probable cell division/peptidoglycan | cell division protein, FtsW/RodA/SpoVE family | cell cycle protein, FtsW/RodA/SpoVE family |
| "CJ_10001377" | CJE1183 | murG | Cj1039 | murG | CCO1106 | murG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative | N-acetylglucosaminyl transferase | UDP-N-acetylglucosamine--N-acetylmuramyl- |
| "CJ_10001379" | CJE1184 | - | Cj1040c | - | CCO1107 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative transmembrane transport protein | hypothetical protein | cyanate MFS transporter, putative |
| "CJ_10001380" | CJE1185 | - | Cj1041c | - | CCO1108 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic ATP/GTP-binding protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001382" | CJE1186 | - | Cj1042c | - | CCO1109 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative transcriptional regulatory protein | transcriptional regulator, AraC family | probable transcription regulatory protein |
| "CJ_10001384" | CJE1187 | - | Cj1043c | - | CCO1110 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible transferase | thiamine-phosphate pyrophosphorylase, putative | thiamine-phosphate pyrophosphorylase, putative |
| "CJ_10001386" | CJE1188 | thiH | Cj1044c | thiH | CCO1111 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | thiH protein | thiamine biosynthesis protein ThiH | thiH protein Cj1044c |
| "CJ_10001390" | CJE1189 | thiG | Cj1045c | thiG | CCO1112 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | thiG protein | thiazole synthase | thiamin biosynthesis protein thiG Cj1045c |
| "CJ_10001393" | CJE1190 | thiF | Cj1046c | moeB | CCO1113 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative molybdopterin biosynthesis protein | thiamine biosynthesis protein ThiF | HesA/MoeB/ThiF family protein |
| "CJ_10001404" | CJE1191 | thiS | Cj1047c | - | CCO1114 | thiS | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | thiamine biosynthesis protein ThiS | thiamine biosynthesis protein ThiS |
| "CJ_10001405" | CJE1192 | dapE | Cj1048c | dapE | CCO1116 | dapE | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | succinyl-diaminopimelate desuccinylase | succinyl-diaminopimelate desuccinylase | succinyl-diaminopimelate desuccinylase |
| "CJ_10001407" | CJE1193 | - | Cj1049c | - | CCO1117 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | transporter, LysE family | probable integral membrane protein Cj1049c |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001408" | CJE1194 | - | Cj1050c | - | CCO1118 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | putative transferase | NAD-dependent deacetylase | probable transferase Cj1050c |
| "CJ_10001410" | CJE1195 | - | Cj1051c | - | CCO1119 | - | | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | 1 | restriction modification enzyme | type II restriction-modification enzyme | type I restriction modification enzyme |
| "CJ_10001412" | CJE1196 | mutS | Cj1052c | mutS | CCO1120 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative mismatch repair protein | recombination and DNA strand exchange inhibitor | probable mismatch repair protein Cj1052c |
| "CJ_10001414" | CJE1197 | - | Cj1053c | - | CCO1121 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1053c |
| "CJ_10001416" | CJE1198 | murC | Cj1054c | murC | CCO1122 | murC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UDP-N-acetylmuramate--alanine ligase | UDP-N-acetylmuramate--L-alanine ligase | UDP-N-acetylmuramate--alanine ligase |
| "CJ_10001422" | CJE1199 | - | Cj1056c | - | CCO1127 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 0 | 1 | hypothetical protein | hydrolase, carbon-nitrogen family | hydrolase, carbon-nitrogen family |
| "CJ_10000918" | CJE1200 | - | Cj1057c | - | CCO1128 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative coiled-coil protein | exodeoxyribonuclease VII, small subunit, | exodeoxyribonuclease VII, small subunit, |
| "CJ_10000921" | CJE1201 | guaB | Cj1058c | guaB | CCO1129 | guaB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | inosine-5'-monophosphate dehydrogenase | inositol-5-monophosphate dehydrogenase | inosine-5'-monophosphate dehydrogenase |
| "CJ_10000924" | CJE1202 | gatA | Cj1059c | gatA | CCO1130 | gatA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | Glu-tRNAGln amidotransferase subunit A | glutamyl-tRNA amidotransferase subunit A | glutamyl-tRNA(Gln) amidotransferase, A subunit |
| "opCcV0100001814" | CJE1203 | - | Cj1060c | - | CCO1131 | - | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | - | hypothetical protein | hypothetical protein |
| "opCcV0100000011" | CJE1204 | ileS | Cj1061c | ileS | CCO1132 | ileS | 1 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 0 | isoleucyl-tRNA synthetase | isoleucyl-tRNA synthetase | isoleucyl-tRNA synthetase |
| "CJ_10000928" | CJE1205 | - | Cj1062 | - | CCO1133 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | hypothetical protein | competence/damage-inducible domain protein | conserved hypothetical integral membrane |
| "CJ_10000930" | CJE1206 | - | Cj1063 | - | CCO1134 | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | possible acetyltransferase | acetyltransferase, GNAT family | probable acetyltransferase Cj1063 |
| "opCcV0100001454" | CJE1208 | - | Cj1064 | - | CCO1135 | - | 0 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | pseudogene | pseudogene | nitroreductase family protein |
| "CJ_10000933" | CJE1209 | - | Cj1066 | rdxA | CCO1137 | - | 1 | -1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | nitroreductase | nitroreductase family protein | nitroreductase Cj1066 |
| "CJ_10000934" | CJE1210 | pgsA | Cj1067 | pgsA | CCO1138 | pgsA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | CDP-diacylglycerol--glycerol-3-phosphate | CDP-diacylglycerol--glycerol-3-phosphate | CDP-diacylglycerol--glycerol-3-phosphate |
| "CJ_10000945" | CJE1211 | - | Cj1068 | - | CCO1139 | - | 1 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative integral membrane protein | membrane-associated zinc metalloprotease, | membrane-associated zinc metalloprotease, |
| "CJ_10000948" | CJE1212 | - | Cj1069 | - | CCO1140 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | LapB |
| "CJ_10000951" | CJE1213 | rpsF | Cj1070 | rpsF | CCO1144 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | 1 | 1 | 1 | 30S ribosomal protein S6 | 30S ribosomal protein S6 | 30S ribosomal protein S6 Cj1070 |
| "CJ_10000953" | CJE1214 | ssb | Cj1071 | ssb | CCO1145 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | single-strand DNA binding protein | single-strand DNA-binding protein | single strand DNA binding protein |
| "CJ_10000955" | CJE1215 | rpsR | Cj1072 | rpsR | CCO1146 | rpsR | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 30S ribosomal protein S18 | 30S ribosomal protein S18 | ribosomal protein S18 |
| "CJ_10000957" | CJE1216 | lon | Cj1073c | lon | CCO1147 | lon | 1 | 1 | 1 | 1 | -1 | | -1 | -1 | 1 | -1 | ATP-dependent protease La | ATP-dependent protease La | ATP-dependent protease La |
| "CJ_10000959" | CJE1217 | - | Cj1074c | - | CCO1148 | - | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj1074c |
| "CJ_10000962" | CJE1218 | - | Cj1075 | - | CCO1149 | - | 0 | 1 | -1 | -1 | 1 | 0 | 1 | -1 | -1 | -1 | hypothetical protein | hypothetical protein | Uncharacterized BCR, COG1699 subfamily |
| "CJ_10000963" | CJE1219 | proC | Cj1076 | proC | CCO1150 | proC | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative pyrroline-5-carboxylate reductase | pyrroline-5-carboxylate reductase | pyrroline-5-carboxylate reductase |
| "CJ_10000964" | CJE1220 | ctsT | Cj1077 | - | CCO1151 | ctsT | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | putative periplasmic protein | transformation system protein | transformation system protein |
| "CJ_10000974" | CJE1221 | - | Cj1078 | - | CCO1152 | - | 1 | 1 | | 1 | -1 | 1 | -1 | 1 | 1 | -1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1078 |
| "CJ_10000977" | CJE1222 | - | Cj1079 | - | CCO1153 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1079 |
| "CJ_10000980" | CJE1223 | hemD | Cj1080c | - | CCO1154 | hemD | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | uroporphyrinogen-III synthetase | uroporphyrinogen-III synthase |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000982" | CJE1224 | thiE | Cj1081c | thiE | CCO1155 | thiE | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | thiamin-phosphate pyrophosphorylase | thiamine-phosphate pyrophosphorylase | thiamine-phosphate pyrophosphorylase |
| "CJ_10000984" | CJE1225 | thiD | Cj1082c | thiD | CCO1156 | thiD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphomethylpyrimidine kinase | phosphomethylpyrimidine kinase | phosphomethylpyrimidine kinase |
| "CJ_10000986" | CJE1226 | - | Cj1083c | - | CCO1157 | nth | 0 | 1 | 1 | 1 | 0 | -1 | -1 | -1 | -1 | -1 | possible nuclease | endonuclease III, putative | endonuclease III |
| "CJ_10000989" | CJE1227 | - | Cj1084c | - | CCO1158 | - | 1 | 1 | 1 | | -1 | | 1 | -1 | 1 | | putative ATP/GTP-binding protein | hypothetical protein | Protein of unknown function (DUF815) |
| "CJ_10000991" | CJE1228 | mfd | Cj1085c | mfd | CCO1159 | mfd | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | transcription-repair coupling factor | transcription-repair coupling factor | transcription-repair coupling factor |
| "CJ_10000992" | CJE1229 | - | Cj1086c | - | CCO1160 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function, DUF583 superfamily |
| "CJ_10000993" | CJE1230 | - | Cj1087c | - | CCO1161 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic protein | peptidase, M23/M37 family | probable periplasmic protein Cj1087c |
| "CJ_10001004" | CJE1231 | folC | Cj1088c | folC | CCO1162 | folC | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | folylpolyglutamate synthase/dihydrofolate | folC bifunctional protein | folylpolyglutamate synthase (folC) |
| "CJ_10001007" | CJE1232 | - | Cj1089c | - | CCO1163 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001010" | CJE1233 | - | Cj1090c | - | CCO1164 | - | 1 | 1 | 1 | 0 | 1 | -1 | -1 | 1 | 0 | 0 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj1090c |
| "CJ_10001012" | CJE1234 | leuS | Cj1091c | leuS | CCO1165 | leuS | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | -1 | leucyl-tRNA synthetase | leucyl-tRNA synthetase | leucyl-tRNA synthetase |
| "CJ_10001014" | CJE1235 | secF | Cj1092c | secF | CCO1166 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | protein-export membrane protein | protein export protein SecF | protein-export membrane protein SecF |
| "CJ_10001017" | CJE1236 | secD | Cj1093c | secD | CCO1167 | secD | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | protein-export membrane protein | protein export protein SecD | protein-export membrane protein SecD |
| "CJ_10001018" | CJE1237 | yajC | Cj1094c | - | CCO1168 | yajC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | preprotein translocase subunit YajC | preprotein translocase, YajC subunit |
| "CJ_10001020" | CJE1238 | cutE | Cj1095 | - | CCO1169 | - | | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | putative integral membrane protein | apolipoprotein N-acyltransferase | apolipoprotein N-acyltransferase (cute), |
| "CJ_10001021" | CJE1239 | metK | Cj1096c | metK | CCO1174 | metK | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | S-adenosylmethionine synthetase | S-adenosylmethionine synthetase | S-adenosylmethionine synthetase |
| "CJ_10001022" | CJE1240 | - | Cj1097 | - | CCO1175 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | putative transmembrane transport protein | sodium/dicarboxylate symporter | probable transmembrane transport protein Cj1097 |
| "CJ_10001040" | CJE1241 | pyrB | Cj1098 | pyrB | CCO1176 | pyrB | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | aspartate carbamoyltransferase | aspartate carbamoyltransferase catalytic | aspartate carbamoyltransferase |
| "CJ_10001042" | CJE1242 | pepF | Cj1099 | - | CCO1177 | pepF | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | peptidase (M3 family) | oligoendopeptidase F | oligoendopeptidase F |
| "CJ_10001044" | CJE1243 | - | Cj1100 | - | CCO1178 | - | 1 | 1 | 1 | 0 | 0 | -1 | 1 | -1 | 1 | -1 | hypothteical protein Cj1100 | hypothetical protein | conserved hypothetical protein |
| "CJ_10001045" | CJE1244 | - | Cj1101 | - | CCO1179 | rep | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP-dependent DNA helicase | ATP-dependent DNA helicase, UvrD/REP family | DNA helicase II (uvrD) |
| "CJ_10001046" | CJE1245 | truB | Cj1102 | truB | CCO1180 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | | tRNA pseudouridine synthase B | tRNA pseudouridine synthase B | tRNA pseudouridine synthase B, putative |
| "CJ_10001047" | CJE1246 | csrA | Cj1103 | csrA | CCO1181 | csrA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | carbon storage regulator homolog | carbon storage regulator | carbon storage regulator |
| "CJ_10001048" | CJE1247 | ispE | Cj1104 | - | CCO1182 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical proteinCj1104 | 4-diphosphocytidyl-2-C-methyl-D-erythritol | GHMP kinases putative ATP-binding protein domain |
| "CJ_10001049" | CJE1248 | smpB | Cj1105 | smpB | CCO1183 | smpB | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | -1 | small protein B homolog | SsrA-binding protein | SsrA-binding protein |
| "opCcV0100000735" | CJE1249 | - | Cj1106 | - | CCO1184 | - | -1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | possible periplasmic thioredoxin | thioredoxin domain protein | thioredoxin, putative |
| "CJ_10001050" | CJE1250 | - | Cj1107 | - | CCO1185 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | hypothetical protein | hypothetical protein | Uncharacterized ACR, COG2127 |
| "CJ_10001069" | CJE1251 | clpA | Cj1108 | clpA | CCO1186 | clpA | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | ATP-dependent CLP protease ATP-binding | ATP-dependent Clp protease, ATP-binding | ATP-dependent Clp protease, ATP-binding |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | subunit | subunit | subunit |
| "CJ_10001071" | CJE1252 | aat | Cj1109 | aat | CCO1187 | aat | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | putative leucyl/phenylalanyl-tRNA--protein | leucyl/phenylalanyl-tRNA--protein transferase | leucyl/phenylalanyl-tRNA--protein transferase |
| "CJ_10001073" | CJE1253 | - | Cj1110c | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative MCP-type signal transduction protein | methyl-accepting chemotaxis protein | - |
| "CJ_10001074" | CJE1254 | - | Cj1111c | - | CCO1188 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | integral membrane protein, MarC family | probable integral membrane protein Cj1111c |
| "CJ_10001075" | CJE1255 | msrB | Cj1112c | - | CCO1189 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | methionine sulfoxide reductase B | PilB-related protein |
| "CJ_10001076" | CJE1256 | - | Cj1113 | - | CCO1190 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF455) |
| "CJ_10001077" | CJE1257 | pssA | Cj1114c | pssA | CCO1191 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | CDP-diacylglycerol--serine | CDP-diacylglycerol--serine | CDP-diacylglycerol--serine |
| "CJ_10001078" | CJE1258 | - | Cj1115c | - | CCO1192 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | 1 | putative membrane protein | phosphatidylserine decarboxylase-related | phosphatidylserine decarboxylase-related |
| "CJ_10001079" | CJE1259 | ftsH | Cj1116c | ftsH | CCO1193 | ftsH | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | -1 | 1 | membrane bound zinc metallopeptidase | cell division protein FtsH | cell division protein FtsH |
| "CJ_10001080" | CJE1260 | - | Cj1117c | prmA | CCO1194 | prmA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | possible ribosomal protein methyltransferase | ribosomal protein L11 methyltransferase | ribosomal protein L11 methyltransferase VC0293 |
| "opCcV0100001838" | CJE1261 | cheY | Cj1118c | cheY | CCO1195 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chemotaxis regulatory protein | chemotaxis protein CheY | chemotaxis regulatory protein Cj1118c |
| "opCjjV010000092" | CJE1262 | pglG | Cj1119c | wlaM | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | general glycosylation pathway protein | - |
| "opCcV0100001169" | CJE1263 | pglF | Cj1120c | wlaL | CCO1196 | pglF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative sugar epimerase/dehydratase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100001599" | CJE1264 | pglE | Cj1121c | wlaK | CCO1197 | pglE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative aminotransferase (degT family) | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100000909" | CJE1265 | pglD | Cj1123c | wlaI | CCO1198 | pglD | 1 | 1 | 0 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | putative transferase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100000601" | CJE1266 | pglC | Cj1124c | wlaH | CCO1199 | pglC | 1 | -1 | 0 | | 1 | 1 | -1 | 1 | -1 | 1 | putative galactosyltransferase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100001943" | CJE1267 | pglA | Cj1125c | wlaG | CCO1200 | pglA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative galactosyltransferase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100001680" | CJE1268 | pglB | Cj1126c | wlaF | CCO1201 | pglB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative integral membrane protein (possible | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100000963" | CJE1269 | pglJ | Cj1127c | wlaE | CCO1202 | pglJ | 1 | -1 | -1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | putative glycosyltransferase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100001010" | CJE1270 | pglI | Cj1128c | wlaD | CCO1203 | pglI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glycosyltransferase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100000192" | CJE1271 | pglH | Cj1129c | wlaC | CCO1204 | pglH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glycosyltransferase | general glycosylation pathway protein | general glycosylation pathway protein |
| "opCcV0100000153" | CJE1272 | wlaB | Cj1130c | wlaB | CCO1205 | wlaB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ABC-type transport protein | ABC transporter, ATP-binding/permease protein | ABC transporter, ATP-binding/permease protein |
| "opCcV0100001263" | CJE1273 | galE | Cj1131c | galE | CCO1206 | galE | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UDP-glucose 4-epimerase | UDP-glucose 4-epimerase | UDP-glucose 4-epimerase |
| "CJ_10001156" | CJE1274 | wlaX | Cj1132c | - | CCO1207 | wlaX | 1 | 1 | 1 | 1 | 0 | 0 | 1 | -1 | 1 | 1 | hypothetical protein | polysaccharide biosynthesis protein | polysaccharide biosynthesis protein |
| "opCcV0100001916" | CJE1275 | waaC | Cj1133 | waaC | CCO1208 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative lipopolysaccharide heptosyltransferase | lipopolysaccharide heptosyltransferase I | lipopolysaccharide heptosyltransferase-1 (rfaC) |
| "CJ_10001157" | CJE1276 | waaM | Cj1134 | htrB | CCO1209 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipid A biosynthesis lauroyl | lipid A biosynthesis lauroyl acyltransferase | heat shock protein B (ibpB), putative |
| "CJ_10001158" | CJE1277 | - | Cj1135 | - | CCO1210 | - | 1 | 1 | -1 | 1 | 0 | -1 | -1 | -1 | 1 | 1 | putative two-domain glycosyltransferase | lipooligosaccharide biosynthesis | glycosyl transferase, group 2 family protein |
| "opCjV0100000275" | CJE1278 | - | - | - | - | - | -1 | -1 | -1 | | -1 | 1 | | 1 | -1 | -1 | - | lipooligosaccharide biosynthesis | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV0100000610" | CJE1279 | - | - | - | - | - | | | -1 | | -1 | -1 | 1 | -1 | | -1 | - | lipooligosaccharide biosynthesis | - |
| "CJ_10001197" | CJE1280 | - | Cj1139c | - | CCO1213 | - | 1 | 1 | 1 | 0 | -1 | -1 | | 1 | 1 | -1 | putative galactosyltransferase | lipooligosaccharide biosynthesis | glycosyl transferase, group 2 family protein, |
| "opCjV0100000624" | CJE1281 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10001206" | CJE1282 | waaV | Cj1146c | waaV | CCO1219 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glucosyltransferase | lipooligosaccharide biosynthesis | glycosyl transferase, putative |
| "CJ_10001207" | CJE1283 | waaF | Cj1148 | waaF | CCO1220 | rfaF | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | ADP-heptose--LPS heptosyltransferase | ADP-heptose--LPS heptosyltransferase II | ADP-heptose-lps heptosyltransferase II (rfaF) |
| "opCjV0100000220" | CJE1284 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | - | lipooligosaccharide biosynthesis | - |
| "CJ_10001241" | CJE1285 | - | Cj1149c | gmhA | CCO1222 | gmhA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | Phosphoheptose isomerase | phosphoheptose isomerase | phosphoheptose isomerase |
| "CJ_10001243" | CJE1286 | hldE | Cj1150c | waaE | CCO1223 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative ADP-heptose synthase | D,D-heptose 1-phosphate | rfaE protein |
| "CJ_10001246" | CJE1287 | waaD | Cj1151c | waaD | CCO1224 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | ADP-L-glycero-D-manno-heptose-6-epimerase | ADP-L-glycero-D-mannoheptose-6-epimerase | ADP-L-glycero-D-mannoheptose-6-epimerase (rfaD) |
| "CJ_10001248" | CJE1288 | - | Cj1152c | - | CCO1225 | - | | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | putative phosphatase | hydrolase, putative | histidinol phosphatase domain protein |
| "CJ_10001249" | CJE1289 | cyf | Cj1153 | - | CCO1226 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic cytochrome C | cytochrome c553 | probable periplasmic cytochrome C Cj1153 |
| "CJ_10001250" | CJE1290 | - | Cj1154c | - | CCO1227 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | small hydrophobic protein | cytochrome oxidase maturation protein, | small hydrophobic protein Cj1154c -related |
| "CJ_10001251" | CJE1291 | - | Cj1155c | - | CCO1228 | fixI | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cation-transporting ATPase | heavy metal translocating P-type ATPase | cation-transporting ATPase, P-type (copA) |
| "CJ_10001252" | CJE1292 | rho | Cj1156 | rho | CCO1229 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | transcription termination factor | transcription termination factor Rho | transcription termination factor Cj1156 |
| "CJ_10001253" | CJE1293 | dnaX | Cj1157 | dnaX | CCO1231 | dnaZX | -1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | putative DNA polymerase III subunit gamma | DNA polymerase III subunits gamma and tau | DNA polymerase III gamma and tau subunits |
| "CJ_10000207" | CJE1294 | - | Cj1159c | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | small hydrophobic protein | pseudogene | - |
| "CJ_10000213" | CJE1295 | - | Cj1161c | - | CCO1232 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cation-transporting ATPase | copper-translocating P-type ATPase | copper-translocating P-type ATPase |
| "CJ_10000215" | CJE1296 | - | Cj1162c | - | CCO1233 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | heavy-metal-associated domain, putative |
| "CJ_10000217" | CJE1297 | - | Cj1163c | - | CCO1234 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cation transport protein | cation efflux family protein | cation efflux family protein |
| "CJ_10000219" | CJE1298 | - | Cj1164c | - | CCO1235 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000221" | CJE1299 | - | Cj1165c | - | CCO1236 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1165c |
| "CJ_10000224" | CJE1300 | - | Cj1166c | - | CCO1237 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1166c |
| "CJ_10000225" | CJE1301 | ldh | Cj1167 | ldh | CCO1238 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative L-lactate dehydrogenase | L-lactate dehydrogenase | L-lactate dehydrogenase |
| "CJ_10000226" | CJE1302 | - | Cj1168c | - | CCO1239 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | putative integral membrane protein (dedA | DedA family protein | probable integral membrane protein (dedA |
| "opCjjV010000049" | CJE1303 | - | Cj1169c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000236" | CJE1304 | - | Cj1170c | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | outer membrane protein | hypothetical protein | - |
| "CJ_10000239" | CJE1305 | ppiB | Cj1171c | ppi | CCO1240 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | peptidyl-prolyl cis-trans isomerase | peptidyl-prolyl cis-trans isomerase B | peptidyl-prolyl cis-trans isomerase, |
| "CJ_10000241" | CJE1306 | - | Cj1172c | - | CCO1241 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR01033 |
| "CJ_10000243" | CJE1307 | - | Cj1173 | - | CCO1242 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative efflux protein | multidrug resistance | probable efflux protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | protein, SMR family | Cj1173 |
| "CJ_10000245" | CJE1308 | - | Cj1174 | - | CCO1243 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative efflux protein | multidrug resistance protein, SMR family | probable efflux protein Cj1174 |
| "CJ_10000248" | CJE1309 | argS | Cj1175c | argS | CCO1244 | argS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | arginyl-tRNA synthetase | arginyl-tRNA synthetase | arginyl-tRNA synthetase |
| "CJ_10000250" | CJE1310 | - | Cj1176c | - | CCO1245 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | hypothetical protein | twin-arginine translocation protein, TatA/E | Sec-independent protein translocase protein |
| "CJ_10000251" | CJE1311 | - | Cj1177c | gmk | CCO1246 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | guanylate kinase | guanylate kinase | guanylate kinase Cj1177c |
| "CJ_10000252" | CJE1312 | - | Cj1178c | - | CCO1247 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | highly acidic protein | hypothetical protein | highly acidic protein Cj1178c |
| "CJ_10000261" | CJE1313 | fliR | Cj1179c | fliR | CCO1248 | fliR | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar biosynthetic protein | flagellar biosynthesis protein | flagellar biosynthetic protein FliR |
| "CJ_10000263" | CJE1314 | - | Cj1180c | - | CCO1249 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transporter ATP binding protein | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "CJ_10000266" | CJE1315 | tsf | Cj1181c | tsf | CCO1250 | tsf | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | elongation factor TS | elongation factor Ts | translation elongation factor Ts |
| "CJ_10000268" | CJE1316 | rpsB | Cj1182c | rpsB | CCO1251 | rpsB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S2 | 30S ribosomal protein S2 | ribosomal protein S2 |
| "CJ_10000270" | CJE1317 | - | Cj1183c | cfa | CCO1252 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cyclopropane-fatty-acyl-phospholipid | cyclopropane-fatty-acyl-phospholipid synthase, | cyclopropane fatty acid synthase (cfa) |
| "CJ_10000273" | CJE1318 | petC | Cj1184c | petC | CCO1253 | petC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ubiquinol-cytochrome C reductase | ubiquinol--cytochrome c reductase, cytochrome c1 | ubiquinol cytochrome c oxidoreductase, |
| "CJ_10000275" | CJE1319 | petB | Cj1185c | petB | CCO1254 | petB | 0 | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative ubiquinol-cytochrome C reductase | ubiquinol--cytochrome c reductase, cytochrome b | ubiquinol cytochrome c oxidoreductase, |
| "CJ_10000277" | CJE1320 | petA | Cj1186c | petA | CCO1256 | - | 1 | 0 | -1 | 0 | 1 | 1 | 0 | 0 | 1 | 1 | putative ubiquinol-cytochrome C reductase | ubiquinol--cytochrome c reductase, iron-sulfur | ubiquinol cytochrome c oxidoreductase, Rieske |
| "CJ_10000278" | CJE1321 | arsB | Cj1187c | arsB | CCO1257 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative arsenical pump membrane protein | arsenical pump membrane protein | arsenic efflux pump arsB |
| "CJ_10000279" | CJE1322 | gidA | Cj1188c | gidA | CCO1258 | gidA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glucose inhibited division protein A homolog | glucose-inhibited division protein A | glucose inhibited division protein A |
| "CJ_10000290" | CJE1323 | - | Cj1189c | - | CCO1259 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative signal-transduction sensor protein | methyl-accepting chemotaxis protein | methyl-accepting chemotaxis protein |
| "CJ_10000293" | CJE1324 | - | Cj1190c | - | CCO1260 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative MCP-domain signal transduction protein | methyl-accepting chemotaxis protein | methyl-accepting chemotaxis protein (tlpA) |
| "CJ_10000296" | CJE1325 | - | Cj1191c | - | CCO1261 | - | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative signal-transduction sensor protein | methyl-accepting chemotaxis protein | methyl-accepting chemotaxis protein |
| "CJ_10000298" | CJE1326 | dctA | Cj1192 | dctA | CCO1262 | dctA | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative C4-dicarboxylate transport protein | C4-dicarboxylate transport protein | C4-dicarboxylate transport protein |
| "CJ_10000301" | CJE1327 | - | Cj1193c | - | CCO1263 | - | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1193c |
| "CJ_10000303" | CJE1328 | - | Cj1194 | - | CCO1264 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible phosphate permease | phosphate transporter family protein | probable phosphate permease Cj1194 |
| "CJ_10000305" | CJE1329 | - | Cj1195c | pyrC2 | CCO1265 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | putative dihydroorotase | dihydroorotase | dihydroorotase, putative |
| "CJ_10000307" | CJE1330 | gpsA | Cj1196c | gpsA | CCO1266 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | glycerol-3-phosphate dehydrogenase [NAD(P)+] | NAD(P)H-dependent glycerol-3-phosphate | glycerol-3-phosphate dehydrogenase (NAD |
| "CJ_10000308" | CJE1331 | gatB | Cj1197c | gatB | CCO1267 | gatB | 0 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | Glu-tRNAGln amidotransferase subunit B | aspartyl/glutamyl-tRNA amidotransferase subunit | glutamyl-tRNA(Gln) amidotransferase, B subunit |
| "CJ_10000309" | CJE1332 | luxS | Cj1198 | - | CCO1268 | luxS | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | S-ribosylhomocysteinase | autoinducer-2 production protein LuxS |
| "CJ_10000318" | CJE1333 | - | Cj1199 | - | CCO1269 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | putative iron/ascorbate-dependent | oxidoreductase, 2OG-Fe(II) oxygenase family | oxidoreductase, 2OG-Fe(II) oxygenase family |
| "CJ_10000320" | CJE1334 | - | Cj1200 | - | CCO1271 | - | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic protein | lipoprotein, NLPA family | D-methionine-binding lipoprotein MetQ |
| "CJ_10000322" | CJE1335 | metE | Cj1201 | metE | CCO1272 | metE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 5-methyltetrahydropteroyltriglutamate-- | 5-methyltetrahydropteroyltriglutamate-- | 5-methyltetrahydropteroyltriglutamate-- |
| "CJ_10000323" | CJE1336 | metF | Cj1202 | metF | CCO1273 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 5,10- | 5,10- | 5,10- |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | methylenetetrahydrofolate reductase | methylenetetrahydrofolate reductase | methylenetetrahydrofolate reductase |
| "CJ_10000324" | CJE1337 | - | Cj1203c | - | CCO1274 | - | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | -1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1203c |
| "CJ_10000325" | CJE1338 | atpB | Cj1204c | atpB | CCO1275 | atpB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP synthase F0 sector A subunit | ATP synthase subunit A | ATP synthase F0, A subunit |
| "CJ_10000326" | CJE1339 | radA | Cj1205c | radA | CCO1276 | radA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative DNA repair protein RadA (ATP-dependant | DNA repair protein RadA | DNA repair protein RadA |
| "CJ_10000327" | CJE1340 | ftsY | Cj1206c | ftsY | CCO1282 | ftsY | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative signal recognition particle protein | signal recognition particle-docking protein | signal recognition particle-docking protein |
| "CJ_10000328" | CJE1341 | - | Cj1207c | - | CCO1283 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein thiredoxin | lipoprotein, putative | thiol:disulfide interchange protein DsbE, |
| "CJ_10000329" | CJE1342 | - | Cj1208 | - | CCO1284 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000337" | CJE1343 | - | Cj1209 | - | CCO1285 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | HDIG/HD/KH domain protein |
| "CJ_10000338" | CJE1344 | - | Cj1210 | - | CCO1286 | dedA | -1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | DedA family protein | conserved hypothetical integral membrane |
| "CJ_10000340" | CJE1345 | - | Cj1211 | - | CCO1287 | - | -1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | ComEC/Rec2 family protein | competence locus E (comE3), putative |
| "CJ_10000341" | CJE1346 | rbn | Cj1212c | rbn | CCO1288 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ribonuclease BN | ribonuclease BN | ribonuclease BN, putative |
| "CJ_10000342" | CJE1347 | glcD | Cj1213c | glcD | CCO1289 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glycolate oxidase subunit D | glycolate oxidase, subunit GlcD | probable glycolate oxidase chain D Cj1213c |
| "CJ_10000343" | CJE1348 | - | Cj1214c | - | CCO1290 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCjV010000 0308" | CJE1349 | - | - | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10000344" | CJE1350 | - | Cj1215 | - | CCO1291 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | peptidase, M23/M37 family | probable periplasmic protein Cj1215 |
| "CJ_10000345" | CJE1351 | - | Cj1216c | - | CCO1292 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000346" | CJE1352 | - | Cj1217c | - | CCO1293 | - | 1 | 1 | | 1 | -1 | 1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000347" | CJE1353 | ribE | Cj1218c | ribA | CCO1294 | ribE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative riboflavin synthase alpha chain | riboflavin synthase subunit alpha | riboflavin synthase, alpha subunit |
| "CJ_10000360" | CJE1354 | - | Cj1219c | - | CCO1295 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1219c |
| "CJ_10000364" | CJE1355 | groES | Cj1220 | groES | CCO1296 | groES | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 10 kD chaperonin (cpn10) | co-chaperonin GroES | chaperonin, 10 kDa |
| "opCcV010000 0358" | CJE1356 | groEL | Cj1221 | groEL | CCO1297 | groEL | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 60 kD chaperonin (cpn60) | chaperonin GroEL | chaperonin, 60 kDa |
| "CJ_10000368" | CJE1357 | - | Cj1222c | - | CCO1300 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative two-component sensor | sensor histidine kinase | signal-transducing protein, histidine kinase, |
| "CJ_10000370" | CJE1358 | - | Cj1223c | - | CCO1301 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative two-component regulator | DNA-binding response regulator | response regulator |
| "CJ_10000371" | CJE1359 | - | Cj1224 | - | CCO1302 | - | 0 | 1 | 1 | 1 | 1 | 1 | | 1 | 1 | 1 | putative iron-binding protein | non-heme iron protein, hemerythrin family | methyl-accepting chemotaxis protein, putative |
| "CJ_10000372" | CJE1360 | - | Cj1225 | - | - | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | - |
| "CJ_10000373" | CJE1361 | - | Cj1226c | - | CCO1314 | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | putative two-component sensor | sensor histidine kinase | signal-transducing protein, histidine kinase |
| "CJ_10000374" | CJE1362 | - | Cj1227c | - | CCO1315 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative two-component regulator | DNA-binding response regulator | outer membrane protein R (ompR) |
| "CJ_10000375" | CJE1363 | htrA | Cj1228c | htrA | CCO1316 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | serine protease (protease DO) | protease DO | serine protease (htrA) |
| "CJ_10000389" | CJE1364 | - | Cj1229 | cbpA | CCO1317 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative curved-DNA binding protein | co-chaperone protein DnaJ | co-chaperone-curved DNA binding protein A |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000391" | CJE1365 | - | Cj1230 | hspR | CCO1318 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative heat shock transcriptional regulator | transcriptional regulator, MerR family | probable heat shock transcription regulator |
| "CJ_10000393" | CJE1366 | - | Cj1231 | kefB | CCO1319 | kefB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glutathione-regulated potassium-efflux | sodium/hydrogen exchanger family protein | glutathione-regulated potassium-efflux system |
| "CJ_10000395" | CJE1367 | - | Cj1232 | - | CCO1320 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000397" | CJE1368 | - | Cj1233 | - | CCO1321 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative hydrolase | HAD-superfamily hydrolase, subfamily IA, variant | probable hydrolase Cj1233 |
| "CJ_10000398" | CJE1369 | glyS | Cj1234 | glyS | CCO1322 | glyS | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glycyl-tRNA synthetase beta chain | glycyl-tRNA synthetase beta subunit | glycyl-tRNA synthetase, beta subunit |
| "CJ_10000399" | CJE1370 | - | Cj1235 | - | CCO1323 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | peptidase, M23/M37 family | peptidase, M23/M37 family |
| "CJ_10000400" | CJE1371 | - | Cj1236 | - | CCO1324 | - | 0 | 0 | -1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000401" | CJE1372 | - | Cj1237c | - | CCO1327 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible phosphatase | phosphatase, Ppx/GppA family | phosphatase, Ppx/GppA family, putative |
| "CJ_10000402" | CJE1373 | pdxJ | Cj1238 | pdxJ | CCO1328 | pdxJ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative pyridoxal phosphate biosynthetic | pyridoxal phosphate biosynthetic protein | pyridoxal phosphate biosynthetic protein PdxJ |
| "CJ_10000417" | CJE1374 | pdxA | Cj1239 | pdxA | CCO1329 | pdxA | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative pyridoxal phosphate biosynthetic | 4-hydroxythreonine-4-phosphate dehydrogenase | 4-hydroxythreonine-4-phosphate dehydrogenase |
| "opCcV0100000600" | CJE1375 | - | Cj1240c | - | CCO1330 | - | 1 | 1 | 0 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1240c |
| "CJ_10000419" | CJE1376 | - | Cj1240c | - | - | - | 0 | 0 | -1 | 1 | 0 | 0 | 0 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000422" | CJE1377 | - | Cj1241 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative transmembrane transport protein | transporter, putative | - |
| "CJ_10000424" | CJE1378 | - | Cj1242 | - | CCO1332 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000426" | CJE1379 | hemE | Cj1243 | hemE | CCO1333 | hemE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | uroporphyrinogen decarboxylase | uroporphyrinogen decarboxylase | uroporphyrinogen decarboxylase |
| "CJ_10000427" | CJE1380 | - | Cj1244 | - | CCO1334 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | radical SAM domain protein | MoaA/NifB/PqqE family protein, putative |
| "CJ_10000428" | CJE1381 | - | Cj1245c | - | CCO1335 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1245c |
| "CJ_10000429" | CJE1382 | uvrC | Cj1246c | uvrC | CCO1336 | uvrC | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | excinuclease ABC subunit C | excinuclease ABC subunit C | excinuclease ABC, C subunit |
| "CJ_10000430" | CJE1383 | - | Cj1247c | - | CCO1337 | - | -1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCjV0100000727" | CJE1384 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10000431" | CJE1385 | guaA | Cj1248 | guaA | CCO1338 | guaA | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | GMP synthase (glutamine-hydrolyzing) | bifunctional GMP synthase/glutamine | GMP synthase |
| "CJ_10000445" | CJE1386 | - | Cj1249 | - | CCO1343 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000448" | CJE1387 | purD | Cj1250 | purD | CCO1344 | purD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphoribosylamine--glycine ligase | phosphoribosylamine--glycine ligase | phosphoribosylamine--glycine ligase |
| "CJ_10000451" | CJE1388 | - | Cj1251 | - | CCO1345 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000453" | CJE1389 | - | Cj1252 | - | CCO1346 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | organic solvent tolerance protein, putative | conserved hypothetical secreted protein, |
| "CJ_10000455" | CJE1390 | pnp | Cj1253 | pnp | CCO1347 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | polyribonucleotide nucleotidyltransferase | polyribonucleotide nucleotidyltransferase | polyribonucleotide nucleotidyltransferase |
| "CJ_10000456" | CJE1391 | - | Cj1254 | - | CCO1348 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000457" | CJE1392 | - | Cj1256c | - | CCO1351 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1256c |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000458" | CJE1393 | - | Cj1257c | - | CCO1352 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative efflux pump | pseudogene | multi-drug resistance protein |
| "CJ_10000459" | CJE1394 | - | Cj1258 | - | CCO1353 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible phosphotyrosine protein phosphatase | low molecular weight phosphotyrosine protein | low molecular weight protein |
| "opCcV010000 1939" | CJE1395 | porA | Cj1259 | porA | CCO0683 | - | 1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | major outer membrane protein | major outer membrane protein | major outer membrane protein |
| "opCcV010000 1977" | CJE1396 | - | Cj1260c | dnaJ | CCO0682 | dnaJ | -1 | -1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | chaperone DnaJ | co-chaperone protein DnaJ | heat shock protein |
| "opCcV010000 0324" | CJE1397 | racR | Cj1261 | racR | CCO0681 | drrA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | two-component regulator | DNA-binding response regulator | response regulator (ompR) |
| "CJ_10001102" | CJE1398 | racS | Cj1262 | racS | CCO0680 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | two-component sensor (histidine kinase) | sensor histidine kinase | signal-transducing protein, histidine kinase |
| "CJ_10001105" | CJE1399 | recR | Cj1263 | recR | CCO0679 | recR | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | -1 | recombination protein | recombination protein RecR | recombination protein RecR |
| "CJ_10001108" | CJE1400 | hydD | Cj1264c | hydD | CCO0678 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | putative hydrogenase maturation protease | hydrogenase maturation protease HydD | hydrogenase expression/formation protein |
| "CJ_10001111" | CJE1401 | hydC | Cj1265c | hydC | CCO0677 | hyaC | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | Ni/Fe-hydrogenase B-type cytochrome subunit | quinone-reactive Ni/Fe hydrogenase, cytochrome b | quinone-reactive Ni/Fe hydrogenase, cytochrome b |
| "CJ_10001113" | CJE1402 | hydB | Cj1266c | hydB | CCO0676 | - | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | Ni/Fe-hydrogenase large subunit | quinone-reactive Ni/Fe-hydrogenase, large | hydrogenase (NiFe) large chain Cj1266c |
| "CJ_10001114" | CJE1403 | hydA | Cj1267c | hydA | CCO0675 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | Ni/Fe-hydrogenase small chain | quinone-reactive Ni/Fe-hydrogenase, small | quinone-reactive Ni/Fe hydrogenase, small |
| "CJ_10001115" | CJE1404 | - | Cj1268c | - | CCO0674 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | oxidoreductase, FAD-dependent | oxidoreductase, FAD-binding, putative |
| "CJ_10001131" | CJE1405 | - | Cj1269c | amiA | CCO0673 | amiA | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | putative N-acetylmuramoyl-L-alanine amidase | N-acetylmuramoyl-L-alanine amidase | N-acetylmuramoyl-L-alanine amidase (amiA) |
| "CJ_10001135" | CJE1406 | - | Cj1270c | - | CCO0672 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | oxidoreductase, 2-nitropropane dioxygenase | oxidoreductase, 2-nitropropane dioxygenase |
| "CJ_10001139" | CJE1407 | tyrS | Cj1271c | tyrS | CCO0671 | tyrS | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | tyrosyl-tRNA synthetase | tyrosyl-tRNA synthetase | tyrosyl-tRNA synthetase |
| "CJ_10001142" | CJE1408 | - | Cj1272c | spoT | CCO0670 | spoT | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative guanosine-3',5'-bis(diphosphate) | RelA/SpoT family protein | penta-phosphate |
| "CJ_10001145" | CJE1409 | rpoZ | Cj1273c | rpoZ | CCO0669 | rpoZ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative DNA-directed RNA polymerase omega | DNA-directed RNA polymerase omega subunit | DNA-directed RNA polymerase, omega subunit |
| "CJ_10001149" | CJE1410 | pyrH | Cj1274c | pyrH | CCO0668 | pyrH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | uridylate kinase | uridylate kinase | uridylate kinase |
| "CJ_10001151" | CJE1411 | - | Cj1275c | - | CCO0667 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | peptidase, M23/M37 family | probable periplasmic protein Cj1275c |
| "CJ_10001153" | CJE1412 | - | Cj1276c | - | CCO0665 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | cell division protein FtsX, putative | cell division membrane protein (ftsX) |
| "CJ_10001154" | CJE1413 | lolD | Cj1277c | - | CCO0664 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transporter ATP-binding protein | lipoprotein releasing system ATP-binding protein | cell division protein (ftsE) |
| "CJ_10001155" | CJE1414 | trmB | Cj1278c | - | CCO0663 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | tRNA (guanine-N(7)-)-methyltransferase | methyltransferase, putative, putative |
| "CJ_10001173" | CJE1415 | - | Cj1279c | - | CCO0662 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative fibronectin domain-containing | fibronectin type III domain protein | Fibronectin type III domain protein |
| "CJ_10001177" | CJE1416 | - | Cj1280c | - | CCO0661 | rluD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ribosomal pseudouridine synthase | ribosomal large subunit pseudouridine synthase, | ribosomal large subunit pseudouridine synthase, |
| "CJ_10001181" | CJE1417 | - | Cj1282 | mrdB | CCO0660 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | RodA protein homolog | rod shape-determining protein RodA, putative | RodA protein homolog Cj1282 |
| "opCjV010000 0721" | CJE1418 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | - | site-specific recombinase, phage integrase | - |
| "opCjV010000 0575" | CJE1419 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | DNA binding protein, putative | - |
| "opCjV010000 0641" | CJE1420 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 | CJE1421 | - | - | - | - | - | -1 | -1 | -1 | 0 | 1 | -1 | -1 | 1 | -1 | 0 | - | site-specific DNA- | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0968" | | | | | | | | | | | | | | | | | | methyltransferase | |
| "opCjV0100000601" | CJE1422 | - | - | - | - | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | - | emm-like protein | - |
| "opCjV0100000882" | CJE1423 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000896" | CJE1424 | - | - | - | - | - | -1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000764" | CJE1425 | - | - | - | - | - | | 1 | -1 | 1 | | | | -1 | | 1 | - | hypothetical protein | - |
| "opCjV0100000038" | CJE1426 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000024" | CJE1427 | - | - | - | - | - | | 1 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100000303" | CJE1428 | - | - | - | - | - | | 1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100000019" | CJE1429 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100000825" | CJE1430 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | RloG protein, putative | - |
| "opCjV0100000964" | CJE1431 | - | - | - | - | - | | 1 | -1 | 1 | | | | 1 | | 1 | - | hypothetical protein | - |
| "opCjV0100000453" | CJE1432 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000230" | CJE1433 | - | - | - | - | - | | 1 | | 1 | | | | -1 | | 1 | - | hypothetical protein | - |
| "opCjV0100000258" | CJE1434 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000086" | CJE1435 | - | - | - | - | - | | 1 | -1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | - | DNA-binding protein Roi | - |
| "opCjV0100000850" | CJE1436 | - | - | - | - | - | | 1 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV0100000261" | CJE1437 | - | - | - | - | - | | 0 | -1 | 1 | -1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000511" | CJE1438 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000359" | CJE1439 | - | - | - | - | - | | -1 | -1 | 0 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV0100000561" | CJE1440 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | - | signal peptidase I, putative | - |
| "opCjV0100000910" | CJE1441 | - | - | - | - | - | -1 | -1 | 0 | 0 | 1 | 0 | -1 | 1 | 0 | -1 | - | DNA/RNA non-specific endonuclease | - |
| "opCjV0100001085" | CJE1442 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | -1 | -1 | -1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000221" | CJE1444 | - | - | - | - | - | | -1 | -1 | 0 | 1 | -1 | -1 | 1 | 1 | 0 | - | hypothetical protein | - |
| "opCjV0100000498" | CJE1445 | - | - | - | - | - | | -1 | -1 | 0 | 1 | -1 | 1 | -1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000808" | CJE1447 | - | - | - | - | - | | | -1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | - | hypothetical protein | - |
| "opCjV0100000711" | CJE1448 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000548" | CJE1452 | - | - | - | - | - | | | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV0100000031" | CJE1453 | - | - | - | - | - | | | | 1 | | | | -1 | | 1 | - | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV010000 0719" | CJE1454 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | phage head-tail adaptor, putative | - |
| "opCjV010000 0405" | CJE1455 | - | - | - | - | - | | -1 | -1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0757" | CJE1456 | - | - | - | - | - | -1 | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0469" | CJE1457 | - | - | - | - | - | | -1 | -1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | - | hypothetical protein | - |
| "opCjV010000 0506" | CJE1458 | - | - | - | - | - | | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | major capsid protein, HK97 family | - |
| "opCjV010000 0621" | CJE1459 | - | - | - | - | - | | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0657" | CJE1460 | - | - | - | - | - | | -1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0148" | CJE1461 | - | - | - | - | - | | -1 | -1 | 1 | 0 | | -1 | -1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0902" | CJE1462 | - | - | - | - | - | -1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | - | hypothetical protein | - |
| "opCjV010000 0773" | CJE1463 | - | - | - | - | - | | 1 | -1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0301" | CJE1464 | - | - | - | - | - | | 1 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0369" | CJE1465 | - | - | - | - | - | | 1 | | 1 | 1 | 1 | 1 | -1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0730" | CJE1466 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0128" | CJE1467 | - | - | - | - | - | | 1 | -1 | 1 | | 1 | | -1 | 1 | 1 | - | hypothetical protein | - |
| "opCjV010000 0675" | CJE1468 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | phage protein, HK97 gp10 family | - |
| "opCjV010000 0861" | CJE1469 | - | - | - | - | - | -1 | 1 | -1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | - | portal protein, HK97 family | - |
| "opCjV010000 1119" | CJE1470 | - | - | - | - | - | | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | toxin-antitoxin protein, putative | - |
| "opCjV010000 0368" | CJE1471 | - | - | - | - | - | 1 | 1 | | 1 | | | 1 | -1 | 1 | 1 | - | phage terminase, large subunit, putative | - |
| "opCcV010000 0560.80" | CJE1472 | - | - | - | - | - | 1 | 1 | -1 | 0 | 1 | -1 | -1 | 1 | 1 | -1 | - | "phage terminase, small subunit, putative" | - |
| "opCjV010000 0064" | CJE1473 | - | - | - | - | - | -1 | 0 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | HNH endonuclease domain protein | - |
| "opCjV010000 0059" | CJE1474 | - | - | - | - | - | -1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | hypothetical protein | - |
| "CJ_10001184" | CJE1475 | - | Cj1283 | ktrB | CCO1388 | - | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | putative K+ uptake protein | potassium uptake protein, TrkH family | probable K+ uptake protein Cj1283 |
| "CJ_10001189" | CJE1476 | - | Cj1284 | ktrA | CCO1389 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative K+ uptake protein | potassium uptake protein TrkA, putative | probable K+ uptake protein Cj1284 |
| "CJ_10001191" | CJE1477 | - | Cj1285c | - | CCO1390 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | Uncharacterized ACR, COG1427 |
| "CJ_10001193" | CJE1478 | upp | Cj1286c | upp | CCO1391 | upp | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | uracil phosphoribosyltransferase | uracil phosphoribosyltransferase | uracil phosphoribosyltransferase |
| "CJ_10001196" | CJE1479 | - | Cj1287c | - | CCO1392 | maeB | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | malate oxidoreductase | NADP-dependent malic enzyme, truncation | malic enzyme |
| "CJ_10001199" | CJE1480 | gltX | Cj1288c | gltX2 | CCO1393 | gltX | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glutamyl-tRNA synthetase | glutamyl-tRNA synthetase | glutamyl-tRNA synthetase |
| "CJ_10001201" | CJE1481 | - | Cj1289 | - | CCO1394 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | possible periplasmic protein | hypothetical protein | probable periplasmic protein Cj1289 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001220" | CJE1482 | - | Cj1290c | accC | CCO1395 | accC | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | biotin carboxylase | acetyl-CoA carboxylase | acetyl-CoA carboxylase, biotin carboxylase |
| "CJ_10001224" | CJE1483 | accB | Cj1291c | accB | CCO1396 | accB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative biotin carboxyl carrier protein of | acetyl-CoA carboxylase, biotin carboxyl carrier | acetyl-CoA carboxylase, biotin carboxyl carrier |
| "CJ_10001228" | CJE1484 | - | Cj1292 | dcd | CCO1397 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible deoxycytidine triphosphate deaminase | deoxycytidine triphosphate deaminase | probable dCTP deaminase Cj1292 |
| "CJ_10001233" | CJE1485 | flmA | Cj1293 | - | CCO1398 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | possible sugar nucleotide epimerase/dehydratase | polysaccharide biosynthesis protein | polysaccharide biosynthesis protein |
| "CJ_10001236" | CJE1486 | - | Cj1294 | - | CCO1399 | - | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative aminotransferase (degT family) | aminotransferase, DegT/DnrJ/EryC1/StrS family | probable aminotransferase (degT family) Cj1294 |
| "CJ_10001238" | CJE1487 | - | Cj1295 | - | CCO1400 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001245" | CJE1488 | - | Cj1298 | - | CCO1402 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001247" | CJE1489 | - | Cj1299 | acpP2 | CCO1403 | - | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 0 | 1 | 1 | putative acyl carrier protein | acyl carrier protein, putative | probable acyl carrier protein Cj1299 -related |
| "CJ_10001267" | CJE1490 | - | Cj1300 | - | CCO1404 | - | 1 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001274" | CJE1491 | - | Cj1302 | - | CCO1405 | - | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | HAD-superfamily phosphatase, subfamily IIIC | HAD-superfamily phosphatase, subfamily IIIC |
| "CJ_10001276" | CJE1492 | - | Cj1303 | fabH2 | CCO1406 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative 3-oxoacyl-[acyl-carrier-protein] | 3-oxoacyl-(acyl carrier protein) synthase | 3-oxoacyl-(acyl-carrier-protein) synthase III, |
| "CJ_10001278" | CJE1493 | - | Cj1304 | acpP3 | CCO1407 | - | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | -1 | putative acyl carrier protein | acyl carrier protein, putative | probable acyl carrier protein Cj1304 -related |
| "opCjV0100000925" | CJE1494 | - | Cj1306c | - | CCO1408 | - | 1 | 1 | 0 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001280" | CJE1495 | - | Cj1306c | - | CCO1410 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001281" | CJE1496 | - | Cj1307 | - | CCO1411 | - | 1 | 1 | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | putative amino acid activating enzyme | amino acid adenylation domain protein | amino acid adenylation domain protein |
| "opCjV0100001065" | CJE1497 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | acetyltransferase, GNAT family | - |
| "opCjV0100000777" | CJE1498 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | formyl transferase domain protein | - |
| "CJ_10001282" | CJE1499 | - | Cj1308 | acpP4 | CCO1414 | - | 1 | 1 | 0 | 1 | -1 | 1 | -1 | 0 | 1 | 1 | putative acyl carrier protein | acyl carrier protein, putative | probable acyl carrier protein Cj1308 -related |
| "opCjV0100000515" | CJE1500 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | polysaccharide deacetylase family protein | - |
| "opCjV0100000278" | CJE1501 | - | - | - | - | - | | -1 | -1 | | -1 | -1 | | 1 | 1 | -1 | - | hypothetical protein | - |
| "opCjV0100000441" | CJE1502 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | aminoglycoside N3-acetyltransferase domain | - |
| "opCjV0100000035" | CJE1503 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10001297" | CJE1504 | - | Cj1310c | - | CCO1419 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001302" | CJE1506 | neuA | Cj1311 | neuA2 | CCO1421 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | acylneuraminate cytidylyltransferase | CMP-N-acetylneuraminic acid synthetase | CMP-N-acetylneuraminic acid synthetase (neuA) |
| "CJ_10001304" | CJE1507 | - | Cj1312 | - | CCO1422 | - | 0 | 1 | 0 | 1 | 0 | 1 | -1 | 1 | -1 | 1 | possible flagellar protein | flagellar protein, putative | probable flagellar protein Cj1312 |
| "CJ_10001306" | CJE1508 | - | Cj1313 | - | CCO1423 | - | -1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible flagellar protein | acetyltransferase, GNAT family | probable flagellar protein Cj1313 |
| "opCcV0100000429" | CJE1509 | - | Cj1314c | - | CCO1424 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cyclase | imidazoleglycerol phosphate synthase, cyclase | probable cyclase Cj1314c |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100000900" | CJE1510 | - | Cj1315c | - | CCO1425 | hisH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | amidotransferase | imidazole glycerol phosphate synthase, glutamine | imidazole glycerol phosphate synthase, glutamine |
| "opCcV0100000878" | CJE1511 | - | Cj1316c | - | CCO1426 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | flagellin modification protein, PseA | PseA protein |
| "CJ_10001308" | CJE1512 | neuB | Cj1317 | neuB3 | CCO1427 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | N-acetylneuraminic acid synthetase | N-acetylneuraminic acid synthetase | spore coat polysaccharide biosynthesis protein |
| "CJ_10001309" | CJE1513 | - | Cj1319 | - | CCO1430 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative nucleotide sugar dehydratase | NAD-dependent epimerase/dehydratase family | probable nucleotide sugar dehydratase Cj1319 |
| "CJ_10001332" | CJE1514 | - | Cj1320 | - | CCO1431 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative aminotransferase (degT family) | aminotransferase, DegT family | probable aminotransferase (degT family) Cj1320 |
| "opCjV0100000414" | CJE1515 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | formyltransferase, putative | - |
| "CJ_10001347" | CJE1516 | ptmC | Cj1327 | neuB2 | CCO1433 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | N-acetylneuraminic acid synthetase | N-acetylneuraminic acid synthetase | capsular polysaccharide biosynthesis protein |
| "CJ_10001348" | CJE1517 | neuC | Cj1328 | neuC2 | CCO1434 | - | 0 | 1 | | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative N-acetylglucosamine-6-phosphate | UDP-N-acetylglucosamine 2-epimerase | UDP-N-acetylglucosamine 2-epimerase |
| "CJ_10001349" | CJE1518 | - | Cj1329 | - | CCO1435 | mpg | 1 | 1 | | 1 | 1 | -1 | 1 | 1 | 1 | 1 | putative sugar-phosphate nucleotide transferase | nucleotidyltransferase family protein | Mannose-1-phosphate guanyltransferase |
| "CJ_10001364" | CJE1519 | - | Cj1330 | - | CCO1436 | - | -1 | 0 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001366" | CJE1520 | ptmB | Cj1331 | ptmB | CCO1437 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | acylneuraminate cytidylyltransferase (flagellin | posttranslational flagellin modification protein | acylneuraminate cytidylyltransferase, putative |
| "CJ_10001369" | CJE1521 | ptmA | Cj1332 | ptmA | CCO1438 | - | 1 | 1 | | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative oxidoreductase (flagellin | flagellin modification protein A | probable oxidoreductase (flagellin modification) |
| "opCcV0100001710" | CJE1522 | - | Cj1318 | - | CCO1428 | - | 1 | 1 | -1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | motility accessory factor | conserved hypothetical protein |
| "CJ_10001373" | CJE1523 | - | Cj1334 | - | CCO1440 | - | 0 | 1 | | 0 | -1 | -1 | -1 | -1 | | 1 | hypothetical prootein Cj1334 (1318 family) | motility accessory factor | hypothetical prootein Cj1334 (1318 family) |
| "opCcV0100000701" | CJE1524 | - | Cj1318 | - | CCO1429 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | hypothetical protein | motility accessory factor | conserved hypothetical protein |
| "CJ_10001374" | CJE1525 | - | Cj1337 | - | CCO1442 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | motility accessory factor | conserved hypothetical protein |
| "opCjjV010000192" | CJE1526 | flaB | Cj1338c | flaB | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | flagellin | flagellin | - |
| "opCjV0100000504" | CJE1527 | - | - | - | - | - | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | - | hypothetical protein | - |
| "opCjjV010000104" | CJE1528 | flaA | Cj1339c | flaA | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | flagellin | flagellin | - |
| "CJ_10001388" | CJE1529 | - | Cj1340c | - | CCO1445 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | motility accessory factor | conserved hypothetical protein |
| "CJ_10001394" | CJE1531 | - | Cj1342c | - | CCO1448 | - | 1 | -1 | -1 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001396" | CJE1532 | ctsG | Cj1343c | - | CCO1449 | ctsG | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative periplasmic protein | transformation system protein | transformation system protein |
| "CJ_10001398" | CJE1533 | gcp | Cj1344c | - | CCO1450 | gcp | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative glycoprotease | O-sialoglycoprotein endopeptidase | O-sialoglycoprotein endopeptidase |
| "CJ_10001399" | CJE1534 | - | Cj1345c | - | CCO1451 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1345c |
| "CJ_10001400" | CJE1535 | dxr | Cj1346c | dxr | CCO1452 | dxr | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative 1-deoxy-D-xylulose 5-phosphate | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | 1-deoxy-D-xylulose 5-phosphate reductoisomerase |
| "CJ_10001401" | CJE1536 | cdsA | Cj1347c | cdsA | CCO1453 | cdsA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphatidate | phosphatidate | phosphatidate |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | cytidylyltransferase | cytidylyltransferase | cytidylyltransferase |
| "CJ_10001402" | CJE1537 | - | Cj1348c | - | CCO1454 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative coiled-coil protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001403" | CJE1538 | - | Cj1349c | - | CCO1455 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible fibronectin/fibrinogen-binding protein | fibronectin/fibrinogen binding protein, | fibronectin/fibrinogen-binding protein, |
| "CJ_10001417" | CJE1539 | - | Cj1350 | mobA | CCO1456 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative molybdopterin-guanine dinucleotide | molybdopterin-guanine dinucleotide biosynthesis | molybdopterin-guanine dinucleotide biosynthesis |
| "CJ_10001420" | CJE1540 | pldA | Cj1351 | pldA | CCO1457 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phospholipase A | phospholipase A | phospholipase A |
| "CJ_10001423" | CJE1541 | ceuB | Cj1352 | ceuB | CCO1458 | ceuB | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | enterochelin uptake permease | enterochelin ABC transporter, permease protein | enterochelin ABC transporter, permease protein |
| "CJ_10001425" | CJE1542 | ceuC | Cj1353 | ceuC | CCO1459 | ceuC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | enterochelin uptake permease | enterochelin ABC transporter, permease protein | enterochelin ABC transporter, permease protein |
| "CJ_10001427" | CJE1543 | ceuD | Cj1354 | ceuD | CCO1460 | ceuD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | enterochelin uptake ATP-binding protein | enterochelin ABC transporter, ATP-binding | enterochelin ABC transporter, ATP-binding |
| "CJ_10001428" | CJE1544 | - | Cj1355 | ceuE | CCO1461 | ceuE | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | enterochelin uptake periplasmic binding protein | pseudogene | enterochelin ABC transporter, periplasmic |
| "CJ_10001429" | CJE1545 | - | Cj1356c | - | CCO1462 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001430" | CJE1546 | nrfA | Cj1357c | - | CCO1464 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic cytochrome C | cytochrome c552 | probable periplasmic cytochrome C Cj1357c |
| "CJ_10001431" | CJE1547 | nrfH | Cj1358c | - | CCO1465 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative periplasmic cytochrome C | cytochrome c-type protein nrfH | probable periplasmic cytochrome C Cj1358c |
| "CJ_10001432" | CJE1548 | ppk | Cj1359 | ppk | CCO1466 | ppk | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | polyphosphate kinase | polyphosphate kinase | polyphosphate kinase |
| "opCjV0100000483" | CJE1549 | - | - | - | - | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | pseudogene | - |
| "opCjV0100000871" | CJE1550 | - | - | - | - | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000227" | CJE1551 | - | - | - | - | - | 1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV0100000140" | CJE1552 | - | - | - | - | - | -1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10000351" | CJE1553 | - | Cj1361c | - | CCO1471 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000353" | CJE1554 | ruvB | Cj1362 | ruvB | CCO1472 | ruvB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | holliday junction DNA helicase | Holliday junction DNA helicase RuvB | Holliday junction DNA helicase RuvB |
| "CJ_10000355" | CJE1555 | - | Cj1363 | amaA | CCO1473 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | acid membrane antigen A | hypothetical protein | acid membrane antigen A Cj1363 |
| "CJ_10000357" | CJE1556 | fumC | Cj1364c | fumC | CCO1474 | fumC | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | fumarate hydratase | fumarate hydratase, class II | fumarate hydratase, class II |
| "CJ_10000361" | CJE1557 | - | Cj1365c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative secreted serine protease | serine protease, subtilase family | - |
| "CJ_10000363" | CJE1558 | glmS | Cj1366c | glmS | CCO1475 | glmS | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glucosamine--fructose-6-phosphate | D-fructose-6-phosphate amidotransferase | glucosamine--fructose-6-phosphate |
| "CJ_10000366" | CJE1559 | - | Cj1367c | - | CCO1476 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible nucleotidyltransferase | GlnD family protein | probable nucleotidyltransferase Cj1367c |
| "CJ_10000367" | CJE1560 | - | Cj1368 | - | CCO1477 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR00423 |
| "CJ_10000369" | CJE1561 | - | Cj1369 | - | CCO1478 | - | 0 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | putative transmembrane transport protein | xanthine/uracil permease family protein | probable transmembrane transport protein Cj1369 |
| "CJ_10000378" | CJE1562 | - | Cj1370 | - | CCO1479 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | putative nucleotide phosphoribosyltransferase | nucleotide phosphoribosyltransferase, putative | probable nucleotide phosphoribosyltransferase |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000380" | CJE1563 | - | Cj1371 | - | CCO1480 | - | 1 | 1 | | 1 | 1 | 1 | 1 | 1 | -1 | 1 | putative periplasmic protein (vacJ homolog) | lipoprotein, VacJ family | probable periplasmic protein (vacJ homolog) |
| "CJ_10000382" | CJE1564 | - | Cj1372 | - | CCO1481 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | toluene tolerance protein, putative | probable periplasmic protein Cj1372 |
| "CJ_10000384" | CJE1565 | - | Cj1373 | - | CCO1482 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical integral membrane |
| "CJ_10000386" | CJE1566 | - | Cj1374c | - | CCO1483 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | non-canonical purine NTP pyrophosphatase, | Ham1 family |
| "opCjjV010000 122" | CJE1567 | - | Cj1375 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative efflux protein | multidrug resistance efflux transporter, | - |
| "CJ_10000392" | CJE1568 | - | Cj1377c | - | CCO1490 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | putative ferredoxin | iron-sulfur cluster-binding domain protein | iron-sulfur cluster-binding protein, putative |
| "CJ_10000394" | CJE1569 | selA | Cj1378 | selA | CCO1489 | selA | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | L-seryl-tRNA(SeC) selenium transferase | selenocysteine synthase | L-seryl-tRNA selenium transferase |
| "CJ_10000396" | CJE1570 | selB | Cj1379 | selB | CCO1488 | selB | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative selenocysteine-specific elongation | selenocysteine-specific elongation factor | selenocysteine-specific translation elongation |
| "CJ_10000404" | CJE1571 | - | Cj1380 | - | CCO1487 | dsbC | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1380 |
| "CJ_10000406" | CJE1572 | - | Cj1381 | - | CCO1486 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj1381 |
| "CJ_10000408" | CJE1573 | fldA | Cj1382c | fldA | CCO1492 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flavodoxin | flavodoxin | flavodoxin |
| "CJ_10000411" | CJE1574 | - | Cj1383c | - | CCO1493 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000413" | CJE1575 | - | Cj1384c | - | CCO1494 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000415" | CJE1576 | katA | Cj1385 | katA | CCO1495 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | catalase | catalase | catalase |
| "CJ_10000418" | CJE1577 | - | Cj1386 | - | CCO1496 | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ankyrin-repeat containing protein | ankyrin repeat protein | ankyrin domain protein |
| "CJ_10000420" | CJE1578 | - | Cj1387c | - | CCO1497 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | helix-turn-helix containing protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000423" | CJE1579 | - | Cj1388 | - | CCO1499 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | endoribonuclease L-PSP, putative | endoribonuclease L-PSP, putative |
| "CJ_10000425" | CJE1580 | - | Cj1389 | - | CCO1500 | - | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | pseudogene | pseudogene | C4-dicarboxylate anaerobic carrier, putative |
| "CJ_10000435" | CJE1581 | metC | Cj1393 | - | CCO1502 | metC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | cystathionine beta-lyase | rhodanese domain protein/cystathionine |
| "CJ_10000438" | CJE1582 | - | Cj1394 | - | CCO1503 | purB | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | -1 | 1 | putative fumarate lyase | adenylosuccinate lyase | adenylosuccinate lyase |
| "CJ_10000440" | CJE1583 | - | Cj1395 | - | CCO1504 | - | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | pseudogene | MmgE/PrpD family protein | MmgE/PrpD family protein, putative |
| "CJ_10000442" | CJE1584 | - | Cj1397 | - | CCO1505 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | feoA family protein | ferrous iron transport protein A, putative |
| "CJ_10000444" | CJE1585 | - | Cj1398 | feoB | CCO1506 | feoB | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | ferrous iron transport protein | pseudogene | ferrous iron transport protein B |
| "CJ_10000446" | CJE1586 | - | Cj1399c | hydA2 | CCO1507 | - | -1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative Ni/Fe-hydrogenase small subunit | hydrogenase, (NiFe)/(NiFeSe) small subunit | quinone-reactive Ni/Fe hydrogenase, small |
| "CJ_10000449" | CJE1587 | fabI | Cj1400c | fabI | CCO1508 | fabI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative enoyl-[acyl-carrier-protein] reductase | enoyl-(acyl carrier protein) reductase | enoyl-(acyl-carrier-protein) reductase |
| "CJ_10000452" | CJE1588 | tpiA | Cj1401c | tpiA | CCO1509 | tpiA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | putative triosephosphate isomerase | triosephosphate isomerase | triosephosphate isomerase |
| "CJ_10000454" | CJE1589 | pgk | Cj1402c | pgk | CCO1510 | pgk | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | phosphoglycerate kinase | phosphoglycerate kinase | phosphoglycerate kinase |
| "CJ_10000477" | CJE1590 | gapA | Cj1403c | gapA | CCO1511 | gap | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | glyceraldehyde 3-phosphate dehydrogenase | glyceraldehyde 3-phosphate dehydrogenase A | glyceraldehyde-3-phosphate dehydrogenase, type |
| "CJ_10000478" | CJE1591 | nadD | Cj1404 | - | CCO1512 | nadD | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | nicotinate (nicotinamide) nucleotide | nicotinate (nicotinamide) nucleotide |
| "CJ_10000479" | CJE1592 | - | Cj1405 | - | CCO1513 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | iojap-related protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000480" | CJE1593 | - | Cj1406c | - | - | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000481" | CJE1594 | algC | Cj1407c | - | CCO1515 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative phospho-sugar mutase | phosphomannomutase/phosphoglucomutase | phosphomannomutase (algC){Pseudomonas |
| "CJ_10000482" | CJE1595 | fliL | Cj1408 | fliL | CCO1516 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible flagellar protein | flagellar basal body-associated protein | probable flagellar protein Cj1408 |
| "CJ_10000483" | CJE1596 | acpS | Cj1409 | acpS | CCO1517 | acpS | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative holo-[acyl-carrier protein] synthase | 4'-phosphopantetheinyl transferase | holo-(acyl-carrier-protein) synthase |
| "CJ_10000484" | CJE1597 | - | Cj1410c | - | CCO1518 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1410c |
| "CJ_10000485" | CJE1598 | - | Cj1411c | - | CCO1519 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative cytochrome P450 | cytochrome P450 family protein | probable cytochrome P450 Cj1411c |
| "CJ_10000486" | CJE1599 | - | Cj1412c | - | CCO1520 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1412c |
| "CJ_10000497" | CJE1600 | kpsS | Cj1413c | - | CCO1521 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible polysaccharide modification protein | capsule polysaccharide export protein KpsS | capsule polysaccharide biosynthesis protein |
| "CJ_10000498" | CJE1601 | kpsC | Cj1414c | - | CCO1522 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible polysaccharide modification protein | capsule polysaccharide export protein KpsC | capsule polysaccharide biosynthesis protein |
| "opCjV0100000467" | CJE1602 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | capsular polysaccharide biosynthesis protein, | - |
| "opCjV0100000584" | CJE1603 | - | - | - | - | - | | -1 | -1 | | -1 | -1 | -1 | 1 | | | - | capsular polysaccharide biosynthesis protein, | - |
| "opCjV0100000374" | CJE1604 | - | - | - | - | - | | | -1 | | | -1 | -1 | 1 | 1 | -1 | - | capsular polysaccharide biosynthesis protein, | - |
| "opCjV0100000251" | CJE1605 | - | - | - | - | - | | -1 | -1 | | | 1 | | | | | - | capsular polysaccharide biosynthesis protein, | - |
| "opCjV0100000333" | CJE1606 | - | - | - | - | - | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | -1 | -1 | - | haloacid dehalogenase-like hydrolase | - |
| "opCjV0100000661" | CJE1607 | - | - | - | - | - | -1 | -1 | -1 | -1 | | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "CJ_10000523" | CJE1608 | - | Cj1423c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | putative sugar-phosphate nucleotidyltransferase | capsular biosynthesis nucleotidyltransferase, | - |
| "CJ_10000525" | CJE1609 | - | Cj1424c | gmhA2 | - | - | 1 | 1 | 0 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | putative phosphoheptose isomerase | phosphoheptose isomerase | - |
| "CJ_10000527" | CJE1610 | - | Cj1425c | - | - | - | 0 | 0 | 1 | 1 | | 1 | 1 | -1 | 1 | 1 | putative sugar kinase | capsular biosynthesis sugar kinase, putative | - |
| "opCjV0100001098" | CJE1611 | wcbK | - | - | - | - | 0 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | GDP-mannose 4,6-dehydratase | - |
| "opCjV0100000619" | CJE1612 | fcl | Cj1428c | fcl | - | - | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | GDP-L-fucose synthetase | - |
| "opCjV0100000987" | CJE1613 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | | 1 | 1 | -1 | - | capsular polysaccharide biosynthesis protein, | - |
| "opCjV0100000978" | CJE1614 | - | - | - | - | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | hypothetical protein | - |
| "opCjV0100001043" | CJE1615 | - | - | - | - | - | | | -1 | -1 | | -1 | -1 | 1 | 0 | -1 | - | capsular polysaccharide biosynthesis | - |
| "opCjV0100000633" | CJE1616 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | capsular polysaccharide biosynthesis protein, | - |
| "CJ_10000581" | CJE1617 | kpsF | Cj1443c | kpsF | CCO1550 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | KpsF protein | arabinose-5-phosphate isomerase | KpsF protein Cj1443c |
| "CJ_10000583" | CJE1618 | kpsD | Cj1444c | kpsD | CCO1551 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative capsule polysaccharide export system | capsular polysaccharide ABC transporter, | polysaccharide biosynthesis protein, putative |
| "CJ_10000585" | CJE1619 | kpsE | Cj1445c | kpsE | CCO1552 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative capsule polysaccharide export system | capsular polysaccharide ABC transporter | probable capsule polysaccharide export system |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100000731" | CJE1620 | kpsT | Cj1447c | kpsT | CCO1553 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative capsule polysaccharide export | capsular polysaccharide ABC transporter, | lipopolysaccharide ABC export system, |
| "opCcV0100001067" | CJE1621 | kpsM | Cj1448c | kpsM | CCO1554 | abcT3 | -1 | -1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | - | capsular polysaccharide ABC transporter, | KpsM |
| "CJ_10000587" | CJE1622 | - | Cj1449c | - | CCO1555 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000588" | CJE1623 | - | Cj1450 | - | CCO1556 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | putative ATP/GTP-binding protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000589" | CJE1624 | - | Cj1451 | dut | CCO1557 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative dUTPase | deoxyuridine triphosphatase domain protein | probable dUTP diphosphatase Cj1451 |
| "CJ_10000590" | CJE1625 | - | Cj1452 | - | CCO1558 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1452 |
| "CJ_10000591" | CJE1626 | - | Cj1453c | - | CCO1559 | - | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | hypothetical protein | PP-loop family protein | conserved hypothetical protein |
| "CJ_10000607" | CJE1627 | yliG | Cj1454c | - | CCO1560 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | MiaB-like tRNA modifying enzyme YliG, TIGR01125 | MiaB-like tRNA modifying enzyme YliG, TIGR01125 |
| "CJ_10000609" | CJE1628 | prfB | Cj1455 | prfB | CCO1561 | prfB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | peptide chain release factor 2 | peptide chain release factor 2 | peptide chain release factor 2 |
| "opCcV0100000633" | CJE1629 | - | Cj1456c | - | CCO1562 | - | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | hypothetical protein |
| "opCcV0100000250" | CJE1630 | - | - | - | CCO1563 | - | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | - | hypothetical protein | lipoprotein, putative |
| "CJ_10000612" | CJE1631 | - | Cj1457c | - | CCO1564 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | tRNA pseudouridine synthase D | tRNA pseudouridine synthase D, putative |
| "CJ_10000613" | CJE1632 | - | Cj1458c | thiL | CCO1565 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative thiamin-monophosphate kinase | thiamine monophosphate kinase | thiamin-monophosphate kinase, putative |
| "CJ_10000614" | CJE1633 | - | Cj1459 | - | CCO1566 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000615" | CJE1634 | - | Cj1460 | - | CCO1567 | - | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000616" | CJE1635 | - | Cj1461 | - | CCO1568 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | possible DNA methylase | site-specific DNA methyltransferase, putative | probable DNA methylase Cj1461 |
| "CJ_10000617" | CJE1636 | flgI | Cj1462 | flgI | CCO1569 | flgI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar P-ring protein | flagellar P-ring protein precursor | flagellar P-ring protein FlgI |
| "CJ_10000618" | CJE1637 | - | Cj1463 | - | CCO1570 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001312" | CJE1638 | - | Cj1464 | - | CCO1571 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001314" | CJE1639 | - | Cj1465 | - | CCO1572 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001317" | CJE1640 | - | Cj1466 | flgK | CCO1573 | flgK | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative flagellar hook-associated protein | flagellar hook-associated protein | flagellar hook-associated protein 1 (HAP1) |
| "CJ_10001320" | CJE1641 | - | Cj1467 | - | CCO1574 | - | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001325" | CJE1642 | - | Cj1468 | - | CCO1575 | - | 1 | 1 | -1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | membrane protein, putative |
| "CJ_10001328" | CJE1643 | ctsF | Cj1470c | - | CCO1576 | ctsF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | general secretory pathway protein F | general secretory pathway protein F |
| "CJ_10001331" | CJE1644 | ctsE | Cj1471c | - | CCO1577 | ctsE | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative type II protein secretion system E | general secretory pathway protein E | general secretory pathway protein E |
| "CJ_10001335" | CJE1645 | ctsX | Cj1472c | - | CCO1578 | ctsX | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | transformation system protein | transformation system protein |
| "CJ_10001338" | CJE1646 | ctsP | Cj1473c | - | CCO1579 | ctsP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP/GTP-binding protein | transformation system protein | transformation system protein |
| "CJ_10001341" | CJE1647 | ctsD | Cj1474c | - | CCO1580 | ctsD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative type II protein | general secretory pathway | general secretory pathway |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | secretion system D | protein D | protein D |
| "CJ_10001352" | CJE1648 | ctsR | Cj1475c | - | CCO1581 | ctsR | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | transformation system protein | transformation system protein |
| "CJ_10001354" | CJE1649 | - | Cj1476c | - | CCO1582 | - | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | pyruvate-flavodoxin oxidoreductase | pyruvate ferredoxin/flavodoxin oxidoreductase | pyruvate ferredoxin/flavodoxin oxidoreductase |
| "CJ_10001356" | CJE1650 | - | Cj1477c | - | CCO1583 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative hydrolase | HAD-superfamily hydrolase, subfamily IA, variant | phosphoglycolate phosphatase |
| "CJ_10001359" | CJE1651 | cadF | Cj1478c | cadF | CCO1584 | cadF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | outer membrane fibronectin-binding protein | fibronectin-binding protein | fibronectin-binding protein |
| "opCcV0100000256" | CJE1652 | rpsI | Cj1479c | rpsI | CCO1585 | rpsI | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S9 | 30S ribosomal protein S9 | ribosomal protein S9 |
| "CJ_10001362" | CJE1653 | rplM | Cj1480c | rplM | CCO1586 | rplM | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L13 | 50S ribosomal protein L13 | ribosomal protein L13 |
| "CJ_10001365" | CJE1654 | - | Cj1481c | - | CCO1589 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative helicase | ATP-dependent DNA helicase, UvrD/REP family | helicase, putative |
| "CJ_10001367" | CJE1655 | - | Cj1482c | - | CCO1590 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001370" | CJE1656 | - | Cj1483c | - | CCO1591 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj1483c |
| "CJ_10001372" | CJE1657 | - | Cj1484c | - | CCO1592 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1484c |
| "opCcV0100000330" | CJE1658 | - | Cj1485c | - | CCO1593 | - | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1485c -related |
| "CJ_10001378" | CJE1659 | - | Cj1486c | - | CCO1594 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1486c -related |
| "CJ_10001381" | CJE1660 | ccoP | Cj1487c | ccoP | CCO1595 | ccoP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cb-type cytochrome C oxidase subunit III | cytochrome c oxidase, cbb3-type, subunit III | cytochrome c oxidase, cbb3-type, subunit III |
| "CJ_10001383" | CJE1661 | ccoQ | Cj1488c | ccoQ | CCO1596 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cb-type cytochrome C oxidase subunit IV | cytochrome c oxidase, cbb3-type, subunit IV | conserved hypothetical protein |
| "CJ_10001385" | CJE1662 | ccoO | Cj1489c | ccoO | CCO1597 | ccoO | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | cb-type cytochrome C oxidase subunit II | cytochrome c oxidase, cbb3-type, subunit II | cytochrome c oxidase, cbb3-type, subunit II |
| "CJ_10001387" | CJE1663 | ccoN | Cj1490c | ccoN | CCO1598 | ccoN | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 1 | cb-type cytochrome C oxidase subunit I | cytochrome c oxidase, cbb3-type, subunit I | cytochrome c oxidase, cbb3-type, subunit I |
| "CJ_10001389" | CJE1664 | - | Cj1491c | - | CCO1599 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative two-component regulator | DNA-binding response regulator | transcriptional regulatory protein KdpE, |
| "CJ_10001392" | CJE1665 | - | Cj1492c | - | CCO1600 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | putative two-component sensor | sensory box sensor histidine kinase, putative | signal-transducing histidine kinase, putative |
| "CJ_10001395" | CJE1666 | - | Cj1493c | - | CCO1601 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1493c |
| "CJ_10001397" | CJE1667 | carA | Cj1494c | carA | CCO1602 | carA | 0 | 1 | 1 | 1 | | 1 | -1 | | 1 | 1 | carbamoyl-phosphate synthase small chain | carbamoyl-phosphate synthase small subunit | carbamoyl-phosphate synthase, small subunit |
| "CJ_10001406" | CJE1668 | - | Cj1495c | - | CCO1603 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001409" | CJE1669 | - | Cj1496c | - | CCO1604 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1496c |
| "CJ_10001411" | CJE1670 | - | Cj1497c | - | CCO1605 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001413" | CJE1671 | purA | Cj1498c | purA | CCO1606 | purA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | adenylosuccinate synthetase | adenylosuccinate synthetase | adenylosuccinate synthetase |
| "opCcV0100000651" | CJE1672 | - | - | - | CCO1608 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 0 | - | hypothetical protein | probable integral membrane protein Cj1500 |
| "CJ_10001415" | CJE1673 | - | Cj1500 | - | CCO1609 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | hypothetical protein | conserved hypothetical protein |
| "opCjjV010000193" | CJE1674 | - | Cj1501 | - | - | - | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001418" | CJE1675 | putP | Cj1502c | putP | CCO1611 | putP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | sodium/proline symporter | sodium/proline permease | proline permease (putP) |
| "CJ_10001421" | CJE1676 | - | Cj1503c | putA | CCO1612 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative proline | bifunctional putA protein, putative | proline dehydrogenase |
| "CJ_10001424" | CJE1677 | selD | Cj1504c | selD | CCO1613 | selD | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | putative selenide,water dikinase | selenide, water dikinase | selenide, water dikinase |
| "CJ_10001426" | CJE1678 | - | Cj1505c | - | CCO1614 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | predicted Transcriptional regulator |
| "CJ_10001439" | CJE1679 | - | Cj1506c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative MCP-type signal transduction protein | methyl-accepting chemotaxis protein | - |
| "CJ_10001440" | CJE1680 | - | Cj1507c | - | CCO1615 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | ModE repressor domain protein | N-terminal HTH domain of molybdenum-binding |
| "CJ_10001441" | CJE1681 | fdhD | Cj1508c | fdhD | CCO1616 | fdhD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | FdhD protein | formate dehydrogenase accessory protein | formate dehydrogenase family accessory protein |
| "CJ_10001442" | CJE1682 | fdhC | Cj1509c | fdhC | CCO1617 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative formate dehydrogenase, cytochrome B | formate dehydrogenase, cytochrome b subunit | formate dehydrogenase cytochrome B chain |
| "CJ_10001443" | CJE1683 | fdhB | Cj1510c | fdhB | CCO1618 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative formate dehydrogenase iron-sulfur | formate dehydrogenase, iron-sulfur subunit | formate dehydrogenase, iron-sulfur subunit |
| "CJ_10001444" | CJE1684 | fdhA | Cj1511c | fdhA | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative formate dehydrogenase large subunit | formate dehydrogenase, alpha subunit, | - |
| "CJ_10001445" | CJE1685 | - | Cj1513c | - | CCO1620 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible periplasmic protein | tat domain protein | probable periplasmic protein Cj1513c -related |
| "CJ_10001446" | CJE1686 | - | Cj1514c | - | CCO1621 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "opCjV0100000299" | CJE1687 | - | - | - | - | - | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | - | hypothetical protein | - |
| "CJ_10001447" | CJE1688 | nspC | Cj1515c | - | CCO1622 | nspC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative decarboxylase | carboxynorspermidine decarboxylase | carboxynorspermidine decarboxylase |
| "CJ_10001448" | CJE1689 | - | Cj1516 | - | CCO1623 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative periplasmic oxidoreductase | oxidoreductase, putative | probable periplasmic oxidoreductase Cj1516 |
| "CJ_10001459" | CJE1690 | - | Cj1517 | moaD | CCO1624 | - | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | possible molybdopterin converting factor, | thiS family protein | probable molybdopterin converting factor, chain |
| "CJ_10001460" | CJE1691 | - | Cj1518 | moaE | CCO1625 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible molybdopterin converting factor, | molybdopterin converting factor, subunit 2 | molybdopterin biosynthesis protein E chain |
| "opCcV0100001980" | CJE1692 | - | - | - | CCO1626 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | probable molybdopterin biosynthesis protein |
| "CJ_10001461" | CJE1693 | - | Cj1519 | moeA2 | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative molybdopterin biosynthesis protein | molybdopterin biosynthesis MoeA protein, | - |
| "CJ_10001463" | CJE1694 | cas2 | Cj1521c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | CRISPR-associated protein Cas2 | - |
| "CJ_10001464" | CJE1695 | cas1 | Cj1522c | - | - | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | CRISPR-associated protein Cas1 | - |
| "CJ_10001465" | CJE1697 | - | Cj1523c | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hyopthetical protein Cj1523c | pseudogene | - |
| "opCjV0100000404" | CJE1698 | - | - | - | - | - | 1 | 1 | 0 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001466" | CJE1699 | - | Cj1528 | - | CCO1630 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | pseudogene | pseudogene | C4-dicarboxylate anaerobic carrier, putative |
| "CJ_10001467" | CJE1700 | purM | Cj1529c | purM | CCO1632 | purM | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | phosphoribosylformylglycinamidine cyclo-ligase | phosphoribosylaminoimidazole synthetase | phosphoribosylformylglycinamidine cyclo-ligase |
| "CJ_10001468" | CJE1701 | - | Cj1530 | - | CCO1633 | - | 0 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative ATP/GTP-binding protein | dephospho-CoA kinase | dephospho-CoA kinase |
| "CJ_10001484" | CJE1702 | dapF | Cj1531 | dapF | CCO1634 | dapF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative diaminopimelate epimerase | diaminopimelate epimerase | diaminopimelate epimerase |
| "CJ_10001486" | CJE1703 | - | Cj1532 | - | CCO1635 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible periplasmic protein | mannosyl-glycoprotein | bax protein, putative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10001488" | CJE1704 | - | Cj1533c | - | CCO1636 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative helix-turn-helix containsing protein | hypothetical protein | conserved hypothetical ATP-binding protein, |
| "CJ_10001490" | CJE1705 | - | Cj1534c | - | CCO1641 | - | 1 | -1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | possible bacterioferritin | bacterioferritin, putative | bacterioferrin, putative |
| "CJ_10001492" | CJE1706 | pgi | Cj1535c | pgi | CCO1642 | pgi | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative glucose-6-phosphate isomerase | glucose-6-phosphate isomerase | glucose-6-phosphate isomerase |
| "CJ_10001493" | CJE1707 | galU | Cj1536c | galU | CCO1643 | galU | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UTP--glucose-1-phosphate uridylyltransferase | UTP-glucose-1-phosphate uridylyltransferase | UTP-glucose-1-phosphate uridylyltransferase |
| "CJ_10001494" | CJE1708 | acs | Cj1537c | acs | CCO1644 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | acetyl-coenzyme A synthetase | acetyl-coenzyme A synthetase | acetyl-CoA synthetase |
| "CJ_10001495" | CJE1709 | - | Cj1538c | - | CCO1645 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative anion-uptake ABC-transport system | tungsten ABC transporter, ATP-binding protein, | glutamine ABC transporter, ATP-binding protein |
| "CJ_10001496" | CJE1710 | - | Cj1539c | - | CCO1646 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative anion-uptake ABC-transport system | tungstate ABC transporter, permease protein, | ABC transporter, permease protein |
| "CJ_10001497" | CJE1711 | - | Cj1540 | - | CCO1647 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | tungstate ABC transporter, periplasmic | probable periplasmic protein Cj1540 |
| "CJ_10001513" | CJE1712 | - | Cj1541 | - | CCO1648 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | tungstate ABC transporter, periplasmic | hypothetical protein |
| "CJ_10001515" | CJE1713 | - | Cj1542 | - | CCO1652 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR00370 |
| "CJ_10001517" | CJE1714 | - | Cj1543 | - | CCO1653 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | urea amidolyase-related protein |
| "CJ_10001518" | CJE1715 | - | Cj1544c | - | CCO1655 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | integral membrane protein | probable integral membrane protein Cj1544c |
| "CJ_10001520" | CJE1716 | - | Cj1545c | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | MdaB protein homolog | flavodoxin-like fold domain protein | - |
| "CJ_10001521" | CJE1717 | - | Cj1546 | - | - | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | transcriptional regulator, putative | - |
| "CJ_10001522" | CJE1718 | - | Cj1547 | - | CCO1659 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | homolog of BLC protein | pseudogene | outer membrane lipoprotein Blc, putative |
| "opCcV010000 1745" | CJE1719 | - | Cj1548c | - | CCO1660 | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | putative NADP-dependent alcohol dehydrogenase | oxidoreductase, zinc-binding dehydrogenase | probable alcohol dehydrogenase (NADP) Cj1548c |
| "opCjV010000 0360" | CJE1720 | - | - | - | - | - | -1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | pseudogene | - |
| "opCjV010000 0526" | CJE1721 | - | - | - | - | - | -1 | | -1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | - | RloC protein, putative | - |
| "opCjV010000 0237" | CJE1722 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | pseudogene | - |
| "opCjV010000 0763" | CJE1723 | - | - | - | - | - | 1 | - | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | MloA protein, putative | - |
| "opCjV010000 0327" | CJE1724 | hsdM | - | - | - | - | -1 | | -1 | -1 | | -1 | -1 | 1 | 1 | -1 | - | type I restriction-modification system, M | - |
| "opCjV010000 0827" | CJE1725 | - | - | - | - | - | 1 | -1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | - | 4-carboxymuconolactone decarboxylase, putative | - |
| "opCjV010000 0389" | CJE1726 | - | - | - | - | - | 0 | -1 | 0 | -1 | 1 | 1 | 0 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0776" | CJE1727 | - | - | - | - | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "opCjV010000 0501" | CJE1728 | - | - | - | - | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | -1 | - | transporter, putative | - |
| "CJ_10001555" | CJE1729 | - | Cj1555c | - | - | - | -1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | pseudogene | - |
| "CJ_10001558" | CJE1730 | - | Cj1558 | - | - | - | -1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | putative membrane protein | permease, putative | - |
| "CJ_10001560" | CJE1731 | arsR | Cj1561 | - | CCO1673 | - | -1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | putative transcriptional regulator | arsenical resistance operon repressor | transcriptional regulator, ArsR family |
| "opCjV010000 | CJE1732 | arsC | - | - | - | - | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | - | arsenate reductase | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0248" | | | | | | | | | | | | | | | | | | | |
| "opCjV010000 0235" | CJE1733 | - | - | - | - | - | 1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | arsenical-resistance protein, putative | - |
| "CJ_10001562" | CJE1734 | - | Cj1563c | - | CCO1677 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative transcriptional regulator | pseudogene | probable transcription regulator Cj1563c |
| "CJ_10001580" | CJE1736 | pflA | Cj1565c | pflA | CCO0279 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | paralysed flagellum protein | paralyzed flagella protein PflA | paralysed flagella protein (pflA), putative |
| "CJ_10001582" | CJE1737 | nuoN | Cj1566c | nuoN | CCO0278 | nuoN | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain N | NADH-quinone oxidoreductase, N subunit | NADH-ubiquinone oxidoreductase, NQO14 subunit |
| "CJ_10001584" | CJE1738 | nuoM | Cj1567c | nuoM | CCO0277 | nuoM | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | NADH dehydrogenase I chain M | NADH-quinone oxidoreductase, M subunit | NADH-ubiquinone oxidoreductase, NQO13 subunit |
| "CJ_10001586" | CJE1739 | nuoL | Cj1568c | nuoL | CCO0276 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | NADH dehydrogenase I chain L | NADH dehydrogenase subunit L | NADH2 dehydrogenase (ubiquinone) I chain L |
| "CJ_10001587" | CJE1740 | nuoK | Cj1569c | nuoK | CCO0275 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | NADH dehydrogenase I chain K | NADH-quinone oxidoreductase, K subunit | NADH2 dehydrogenase (ubiquinone) I chain K |
| "CJ_10001588" | CJE1741 | nuoJ | Cj1570c | nuoJ | CCO0274 | nuoJ | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | NADH dehydrogenase I chain J | NADH dehydrogenase subunit J | NADH-ubiquinone oxidoreductase, NQO10 subunit |
| "CJ_10001590" | CJE1742 | nuoI | Cj1571c | nuoI | CCO0273 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain I | NADH dehydrogenase subunit I | NADH2 dehydrogenase (ubiquinone) I chain I |
| "CJ_10001591" | CJE1743 | nuoH | Cj1572c | nuoH | CCO0272 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain H | NADH dehydrogenase subunit H | NADH2 dehydrogenase (ubiquinone) chain 1 |
| "CJ_10001593" | CJE1744 | nuoG | Cj1573c | nuoG | CCO0271 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | probable NADH dehydrogenase I chain G | NADH dehydrogenase gamma subunit | probable NADH2 dehydrogenase (ubiquinone) I |
| "CJ_10000511" | CJE1745 | - | Cj1574c | - | CCO0270 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000513" | CJE1746 | - | Cj1575c | - | CCO0269 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000515" | CJE1747 | nuoD | Cj1576c | nuoD | CCO0268 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain D | NADH dehydrogenase delta subunit | NADH2 dehydrogenase (ubiquinone) I chain D |
| "CJ_10000518" | CJE1748 | nuoC | Cj1577c | nuoC | CCO0267 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain C | NADH dehydrogenase subunit C | NADH2 dehydrogenase (ubiquinone) I chain C |
| "opCcV010000 0039" | CJE1749 | nuoB | Cj1578c | nuoB | CCO0266 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain B | NADH dehydrogenase beta subunit | NADH2 dehydrogenase (ubiquinone) I chain B |
| "CJ_10000521" | CJE1750 | nuoA | Cj1579c | nuoA | CCO0265 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | NADH dehydrogenase I chain A | NADH dehydrogenase alpha subunit | NADH2 dehydrogenase (ubiquinone) I chain A |
| "CJ_10000522" | CJE1751 | - | Cj1580c | - | CCO0264 | abcT11 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative peptide ABC-transport system | peptide ABC transporter, ATP-binding protein | oligopeptide ABC transporter, ATP-binding |
| "CJ_10000524" | CJE1752 | - | Cj1581c | - | CCO0263 | dppD | | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative peptide ABC-transport system | peptide ABC transporter, ATP-binding protein | peptide ABC transporter, ATP-binding protein |
| "CJ_10000526" | CJE1753 | - | Cj1582c | - | CCO0262 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative peptide ABC-transport system permease | peptide ABC transporter, permease protein | peptide ABC transporter, permease protein |
| "CJ_10000528" | CJE1754 | - | Cj1583c | - | CCO0261 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative peptide ABC-transport system permease | peptide ABC transporter, permease protein | peptide ABC transporter, permease protein, |
| "CJ_10000540" | CJE1755 | - | Cj1584c | - | CCO0260 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative peptide ABC-transport system | peptide ABC transporter, periplasmic | peptide ABC transporter, peptide-binding |
| "CJ_10000542" | CJE1756 | - | Cj1585c | - | CCO0259 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | putative oxidoreductase | oxidoreductase, FAD-binding, iron-sulfur | probable oxidoreductase Cj1585c |
| "CJ_10000545" | CJE1757 | - | Cj1586 | - | CCO0258 | hmpA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative bacterial haemoglobin | flavohemoprotein, truncation | flavohemoprotein |
| "CJ_10000547" | CJE1758 | - | Cj1587c | - | CCO0256 | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | putative ABC transporter | cyclic peptide ABC transporter, ATP-binding | pyoverdine ABC export system, |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000549" | CJE1759 | - | Cj1588c | - | - | - | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | putative transmembrane transport protein | pseudogene | - |
| "opCjV0100001112" | CJE1760 | - | - | - | CCO0255 | proP | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | proline/betaine transporter (proP) |
| "CJ_10000551" | CJE1761 | - | Cj1589 | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | metallo-beta-lactamase domain protein | - |
| "CJ_10000552" | CJE1762 | infA | Cj1590 | infA | CCO0244 | infA | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | translation initiation factor IF-1 | translation initiation factor IF-1 | translation initiation factor IF-1 |
| "opCjjV010000151" | CJE1763 | rpmJ | Cj1591 | rpmJ | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L36 | ribosomal protein L36 | - |
| "CJ_10000555" | CJE1764 | rpsM | Cj1592 | rpsM | CCO0243 | rpsM | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S13 | 30S ribosomal protein S13 | ribosomal protein S13p/S18e |
| "opCcV0100001449" | CJE1765 | rpsK | Cj1593 | rpsK | CCO0242 | rpsK | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S11 | 30S ribosomal protein S11 | ribosomal protein S11 |
| "CJ_10000568" | CJE1766 | rpsD | Cj1594 | rpsD | CCO0241 | rpsD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S4 | 30S ribosomal protein S4 | ribosomal protein S4 |
| "CJ_10000571" | CJE1767 | rpoA | Cj1595 | rpoA | CCO0240 | rpoA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA-directed RNA polymerase alpha chain | DNA-directed RNA polymerase alpha subunit | DNA-directed RNA polymerase, alpha subunit |
| "CJ_10000573" | CJE1768 | rplQ | Cj1596 | rplQ | CCO0239 | rplQ | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 50S ribosomal protein L17 | 50S ribosomal protein L17 | ribosomal protein L17 |
| "CJ_10000575" | CJE1769 | hisG | Cj1597 | hisG | CCO0238 | hisG | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ATP phosphoribosyltransferase | ATP phosphoribosyltransferase | ATP phosphoribosyltransferase |
| "CJ_10000577" | CJE1770 | hisD | Cj1598 | hisD | CCO0237 | hisD | -1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | histidinol dehydrogenase | histidinol dehydrogenase | histidinol dehydrogenase |
| "CJ_10000579" | CJE1771 | hisB | Cj1599 | hisB | CCO0236 | hisB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | imidazoleglycerol-phosphate | imidazole glycerol-phosphate | imidazoleglycerol-phosphate |
| "CJ_10000580" | CJE1772 | - | Cj1600 | hisH | CCO0235 | hisH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | amidotransferase HisH | imidazole glycerol phosphate synthase, glutamine | imidazole glycerol phosphate synthase, glutamine |
| "CJ_10000582" | CJE1773 | hisA | Cj1601 | hisA | CCO0234 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | phosphoribosylformimino-5-aminoimidazole | phosphoribosylformimino-5-aminoimidazole | phosphoribosylformimino-5-aminoimidazole |
| "CJ_10000584" | CJE1774 | - | Cj1602 | - | - | - | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | hypothetical protein | HrgA protein | - |
| "CJ_10000586" | CJE1775 | - | Cj1603 | hisF | CCO0233 | hisF | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | cyclase | imidazole glycerol phosphate synthase subunit | imidazoleglycerol phosphate synthase, cyclase |
| "CJ_10000598" | CJE1776 | hisI | Cj1604 | hisI | CCO0232 | - | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | phosphoribosyl-AMP cyclohydrolase/ | phosphoribosyl-ATP | phosphoribosyl-ATP |
| "CJ_10000600" | CJE1777 | - | Cj1605c | dapD | CCO0230 | dapD | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | possible | 2,3,4,5-tetrahydropyridine-2-carboxylate | tetrahydrodipicolinate N-succinyltransferase |
| "CJ_10000602" | CJE1778 | mrp | Cj1606c | mrp | CCO0229 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ATP/GTP-binding protein (mrp protein | ATP/GTP-binding protein | ATP-binding protein (mpr) |
| "CJ_10000603" | CJE1779 | ispDF | Cj1607 | - | CCO0228 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | bifunctional 2-C-methyl-D-erythritol 4-phosphate | ispD/ispF bifunctional enzyme |
| "CJ_10000604" | CJE1780 | - | Cj1608 | - | CCO0227 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible two-component regulator | DNA-binding response regulator, putative | response regulator, putative |
| "CJ_10000605" | CJE1781 | - | Cj1609 | - | CCO0226 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible sulfate adenylyltransferase | ATP-sulfurylase family protein | sulfate adenylyltransferase, putative |
| "CJ_10000606" | CJE1782 | pgpA | Cj1610 | pgpA | CCO0225 | pgpA | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | 0 | 1 | putative phosphatidylglycerophosphatase | phosphatidylglycerophosphatase A | phosphatidylglycerophosphatase A |
| "CJ_10000608" | CJE1783 | rpsT | Cj1611 | rpsT | CCO0224 | rpsT | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S20 | 30S ribosomal protein S20 | ribosomal protein S20 |
| "CJ_10000610" | CJE1784 | prfA | Cj1612 | prfA | CCO0223 | prfA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | peptide chain release factor 1 | peptide chain release factor 1 | peptide chain release factor 1 |
| "CJ_10000611" | CJE1785 | - | Cj1613c | - | CCO0222 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | hypothetical protein | Protein of unknown function (DUF319) family |
| "CJ_10000633" | CJE1786 | chuA | Cj1614 | chuA | CCO0221 | - | 0 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | haemin uptake system outer membrane receptor | TonB-dependent heme receptor | iron-regulated outer membrane virulence protein, |
| "CJ_10000635" | CJE1787 | - | Cj1615 | chuB | CCO0220 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative haemin uptake | hemin ABC transporter, | probable hemein uptake |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | system permease protein | permease protein, | system permease protein |
| "CJ_10000637" | CJE1788 | - | Cj1616 | chuC | CCO0219 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative haemin uptake system ATP-binding | hemin ABC transporter, ATP-binding protein, | iron (III) ABC transporter, ATP-binding protein |
| "CJ_10000639" | CJE1789 | - | Cj1617 | chuD | CCO0218 | - | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | putative haemin uptake system periplasmic | hemin ABC transporter, periplasmic hemin-binding | iron ABC transporter, periplasmic |
| "CJ_10000641" | CJE1790 | - | Cj1618c | - | CCO0217 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | pseudogene | conserved hypothetical protein |
| "CJ_10000642" | CJE1791 | kgtP | Cj1619 | kgtP | CCO0215 | kgtP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | alpha-ketoglutarate permease | alpha-ketoglutarate permease | dicarboxylic acid transport protein |
| "CJ_10000643" | CJE1792 | mutY | Cj1620c | mutY | CCO0214 | mutY | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | A/G-specific adenine glycosylase | A/G-specific adenine glycosylase | A/G-specific adenine glycosylase |
| "CJ_10000644" | CJE1793 | - | Cj1621 | - | CCO0209 | - | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1621 |
| "CJ_10000645" | CJE1794 | - | Cj1622 | ribD | CCO0202 | ribD | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative riboflavin-specific deaminase | riboflavin biosynthesis protein RibD, putative | riboflavin biosynthesis protein (ribG) |
| "CJ_10000646" | CJE1795 | - | Cj1623 | - | CCO0201 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative membrane protein | hypothetical protein | probable membrane protein Cj1623 |
| "CJ_10000662" | CJE1796 | sdaA | Cj1624c | sdaA | CCO0200 | sdaA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | L-serine dehydratase | L-serine ammonia-lyase | L-serine dehydratase 1 |
| "CJ_10000664" | CJE1797 | sdaC | Cj1625c | sdaC | CCO0199 | sdaC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | serine transporter | serine transporter | serine transporter (sdaC) |
| "CJ_10000666" | CJE1798 | - | Cj1626c | - | CCO0198 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1626c |
| "CJ_10000668" | CJE1799 | - | Cj1627c | - | CCO0197 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000670" | CJE1800 | - | Cj1628 | exbB2 | CCO0195 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative exbB/tolQ family transport protein | TonB system transport protein ExbB | probable exbB/tolQ family transport protein |
| "CJ_10000671" | CJE1801 | exbD | Cj1629 | exbD2 | CCO0194 | - | -1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative exbD/tolR family transport protein | biopolymer transport exbD protein | tolR protein, putative |
| "CJ_10000672" | CJE1802 | - | Cj1630 | tonB2 | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative tonB transport protein | pseudogene | - |
| "CJ_10000673" | CJE1803 | - | Cj1631c | - | CCO0193 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000674" | CJE1804 | - | Cj1632c | - | CCO0192 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1632c -related |
| "CJ_10000675" | CJE1805 | - | Cj1633 | - | CCO0191 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000692" | CJE1806 | aroC | Cj1634c | aroC | CCO0180 | aroC | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | chorismate synthase | chorismate synthase | chorismate synthase |
| "CJ_10000694" | CJE1807 | rncS | Cj1635c | rnc | CCO0179 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ribonuclease III | ribonuclease III | ribonuclease III Cj1635c |
| "CJ_10000696" | CJE1808 | rnhA | Cj1636c | rnhA | CCO0178 | rnhA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ribonuclease HI | ribonuclease H | RNase H |
| "CJ_10000698" | CJE1809 | - | Cj1637c | - | CCO0177 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1637c |
| "CJ_10000700" | CJE1810 | dnaG | Cj1638 | dnaG | CCO0176 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | DNA primase | DNA primase | DNA primase, probable CP0919 , putative |
| "opCcV0100001481" | CJE1811 | - | Cj1639 | - | CCO0175 | - | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | -1 | 1 | nifU protein homolog | NifU family protein | nifU protein homolog Cj1639 |
| "CJ_10000701" | CJE1812 | - | Cj1640 | - | CCO0174 | - | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000702" | CJE1813 | murE | Cj1641 | murE | CCO0173 | murE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | UDP-N-acetylmuramoylalanyl-D-glutamate--2, | UDP-N-acetylmuramoylalanyl-D-glutamate--2, | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, |
| "CJ_10000703" | CJE1814 | - | Cj1642 | - | CCO0172 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein TIGR00103 |
| "CJ_10000704" | CJE1815 | - | Cj1643 | - | CCO0171 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | PDZ domain protein | probable periplasmic protein Cj1643 |
| "CJ_10000718" | CJE1816 | ispA | Cj1644 | ispA | CCO0170 | ispA | 1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | geranyltranstransferase | geranyltranstransferase | geranyltranstransferase (ispA) |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000720" | CJE1817 | tkt | Cj1645 | tkt | CCO0169 | tkt | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | transketolase | transketolase | transketolase |
| "CJ_10000722" | CJE1818 | - | Cj1646 | iamB | CCO0168 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transport system permease protein | ABC transporter, permease protein, putative | conserved hypothetical integral membrane |
| "CJ_10000724" | CJE1819 | - | Cj1647 | iamA | CCO0167 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transport system ATP-binding | ABC transporter, ATP-binding protein | ABC transporter |
| "CJ_10000726" | CJE1820 | - | Cj1648 | - | CCO0166 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible ABC transport system periplasmic | ABC transporter, periplasmic substrate-binding | conserved hypothetical protein |
| "CJ_10000728" | CJE1821 | - | Cj1649 | - | CCO0165 | - | -1 | 0 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | putative lipoprotein | lipoprotein, putative | probable lipoprotein Cj1649 |
| "CJ_10000729" | CJE1822 | - | Cj1650 | - | CCO0164 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000730" | CJE1823 | map | Cj1651c | map | CCO0163 | map | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | methionine aminopeptidase | methionine aminopeptidase | methionine aminopeptidase, type I |
| "CJ_10000731" | CJE1824 | murI | Cj1652c | murI | CCO0162 | murI | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | glutamate racemase | glutamate racemase | glutamate racemase |
| "CJ_10000732" | CJE1825 | nlpC | Cj1653c | - | CCO0161 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | probable lipoprotein | lipoprotein NlpC | lipoprotein, NLP/P60 family |
| "CJ_10000742" | CJE1826 | - | Cj1654c | nhaA2 | CCO0158 | nhaA | 0 | 1 | 1 | 1 | 1 | 0 | -1 | -1 | 1 | 1 | Na(+)/H(+) antiporter | Na+/H+ antiporter NhaA | Na+/H+ antiporter NhaA |
| "CJ_10000743" | CJE1827 | - | Cj1654c | nhaA3 | CCO0159 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | Na(+)/H(+) antiporter | Na+/H+ antiporter NhaA | Na+/H+ antiporter Cj1654c |
| "CJ_10000744" | CJE1828 | - | Cj1654c | nhaA4 | CCO0160 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | Na(+)/H(+) antiporter | Na+/H+ antiporter NhaA | Na+/H+ antiporter Cj1654c |
| "opCjV0100000794" | CJE1829 | - | - | - | - | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | hypothetical protein | - |
| "CJ_10000745" | CJE1830 | - | Cj1658 | - | CCO0156 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | iron permease, FTR1 family | probable integral membrane protein Cj1658 |
| "CJ_10000746" | CJE1831 | - | Cj1659 | p19 | CCO0155 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | periplasmic protein p19 | hypothetical protein | periplasmic protein p19 Cj1659 |
| "CJ_10000747" | CJE1832 | - | Cj1660 | - | CCO0154 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative integral membrane protein | hypothetical protein | probable integral membrane protein Cj1660 |
| "CJ_10000748" | CJE1833 | - | Cj1661 | - | CCO0153 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible ABC transport system permease protein | ABC transporter, permease protein | ABC transporter, ATP-binding protein, putative |
| "CJ_10000749" | CJE1834 | - | Cj1662 | - | CCO0152 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative integral membrane protein | ABC transporter, permease protein | permease protein, putative |
| "CJ_10000750" | CJE1835 | - | Cj1663 | - | CCO0151 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ABC transport system ATP-binding | ABC transporter, ATP-binding protein | ABC transporter, ATP-binding protein |
| "CJ_10000751" | CJE1836 | - | Cj1664 | - | CCO0150 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | possible periplasmic thiredoxin | thiredoxin, homolog | probable periplasmic thiredoxin Cj1664 |
| "CJ_10000771" | CJE1837 | - | Cj1665 | - | CCO0149 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 0 | 1 | possible lipoprotein thiredoxin | thioredoxin family protein | thioredoxin, putative |
| "CJ_10000772" | CJE1838 | - | Cj1666c | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | -1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000773" | CJE1839 | - | Cj1667c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | repA protein homolog | hypothetical protein | - |
| "CJ_10000774" | CJE1840 | - | Cj1668c | - | - | - | 1 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 1 | putative periplasmic protein | hypothetical protein | - |
| "CJ_10000775" | CJE1841 | - | Cj1669c | - | CCO1793 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative ATP-dependent DNA ligase | DNA ligase | DNA ligase |
| "CJ_10000776" | CJE1842 | - | Cj1670c | - | CCO1794 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1670c |
| "CJ_10000777" | CJE1843 | - | Cj1671c | - | CCO1795 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000778" | CJE1844 | eno | Cj1672c | eno | CCO1796 | eno | 1 | - | 1 | -1 | 1 | -1 | 1 | -1 | 1 | 0 | enolase | phosphopyruvate hydratase | enolase |
| "CJ_10000779" | CJE1845 | recA | Cj1673c | recA | CCO1797 | recA | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | recA protein | recombinase A | recA protein |
| "CJ_10000780" | CJE1846 | - | Cj1674 | - | CCO1798 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10001473" | CJE1847 | fliQ | Cj1675 | fliQ | CCO1799 | fliQ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | flagellar biosynthetic protein | flagellar biosynthesis protein | flagellar biosynthetic protein FliQ |
| "CJ_10001475" | CJE1848 | murB | Cj1676 | murB | CCO1800 | murB2 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | putative UDP-N-acetylenolpyruvoylglucosa | UDP-N-acetylenolpyruvoylglucosa | UDP-N-acetoenolpyruvoylglucosam |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | mine | mine reductase | ine reductase |
| "CJ_10001483" | CJE1849 | - | Cj1680c | - | CCO1802 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1680c |
| "CJ_10001485" | CJE1850 | cysQ | Cj1681c | cysQ | CCO1803 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | cysQ protein homolog | CysQ | 3'(2'),5'-bisphosphate nucleotidase, putative |
| "CJ_10001487" | CJE1851 | gltA | Cj1682c | gltA | CCO1804 | gltA | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | citrate synthase | citrate synthase | citrate synthase I |
| "CJ_10001489" | CJE1852 | - | Cj1684c | - | CCO1805 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative transmembrane transport protein | sodium/hydrogen exchanger family protein | probable transmembrane transport protein |
| "CJ_10001491" | CJE1853 | bioB | Cj1685c | bioB | CCO1806 | bioB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative biotin synthase | biotin synthase | biotin synthase |
| "CJ_10001502" | CJE1854 | topA | Cj1686c | topA | CCO1807 | topA | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | DNA topoisomerase I | DNA topoisomerase I | DNA topoisomerase I |
| "CJ_10001505" | CJE1855 | - | Cj1687 | - | CCO1808 | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative efflux protein | major facilitator superfamily protein | probable efflux protein Cj1687 |
| "CJ_10001507" | CJE1856 | secY | Cj1688c | secY | CCO1809 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | preprotein translocase subunit | preprotein translocase SecY | preprotein translocase, SecY subunit |
| "CJ_10001509" | CJE1857 | rplO | Cj1689c | rplO | CCO1810 | rplO | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L15 | 50S ribosomal protein L15 | ribosomal protein L15 |
| "opCcV0100000232" | CJE1858 | rpsE | Cj1690c | rpsE | CCO1811 | rpsE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S5 | 30S ribosomal protein S5 | ribosomal protein S5 |
| "CJ_10001512" | CJE1859 | rplR | Cj1691c | rplR | CCO1812 | rplR | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L18 | 50S ribosomal protein L18 | ribosomal protein L18 |
| "CJ_10001514" | CJE1860 | rplF | Cj1692c | rplF | CCO1813 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L6 | 50S ribosomal protein L6 | 50S ribosomal protein L6 Cj1692c |
| "CJ_10001516" | CJE1861 | rpsH | Cj1693c | rpsH | CCO1814 | rpsH | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S8 | 30S ribosomal protein S8 | ribosomal protein S8 |
| "opCcV0100000311" | CJE1862 | rpsN | Cj1694c | rpsN | CCO1815 | rpsN | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S14 | ribosomal protein S14 | ribosomal protein S14p/S29e |
| "CJ_10001519" | CJE1863 | rplE | Cj1695c | rplE | CCO1816 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 50S ribosomal protein L5 | 50S ribosomal protein L5 | 50S ribosomal protein L5 Cj1695c |
| "opCcV0100001194" | CJE1864 | rplN | Cj1696c | rplN | CCO1818 | rplN | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L24 | 50S ribosomal protein L24 | ribosomal protein L14 |
| "CJ_10001540" | CJE1865 | rplX | Cj1697c | rplX | CCO1817 | rplX | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L14 | 50S ribosomal protein L14 | ribosomal protein L24 |
| "CJ_10001542" | CJE1866 | rpsQ | Cj1698c | rpsQ | CCO1819 | rpsQ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S17 | 30S ribosomal protein S17 | ribosomal protein S17 |
| "CJ_10001544" | CJE1867 | rpmC | Cj1699c | rpmC | CCO1820 | rpmC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L29 | 50S ribosomal protein L29 | ribosomal protein L29 |
| "CJ_10001546" | CJE1868 | rplP | Cj1700c | rplP | CCO1821 | rplP | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L16 | 50S ribosomal protein L16 | ribosomal protein L16 |
| "CJ_10001548" | CJE1869 | rpsC | Cj1701c | rpsC | CCO1822 | rpsC | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 30S ribosomal protein S3 | 30S ribosomal protein S3 | ribosomal protein S3 |
| "CJ_10001550" | CJE1870 | rplV | Cj1702c | rplV | CCO1823 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L22 | 50S ribosomal protein L22 | 50S ribosomal protein L22 Cj1702c |
| "CJ_10001552" | CJE1871 | rpsS | Cj1703c | rpsS | CCO1824 | rpsS | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S19 | 30S ribosomal protein S19 | ribosomal protein S19 |
| "CJ_10001553" | CJE1872 | rplB | Cj1704c | rplB | CCO1825 | rplB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L2 | 50S ribosomal protein L2 | ribosomal protein L2 |
| "CJ_10001556" | CJE1873 | rplW | Cj1705c | rplW | CCO1826 | rplW | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 50S ribosomal protein L23 | 50S ribosomal protein L23 | ribosomal protein L23 |
| "CJ_10001568" | CJE1874 | rplD | Cj1706c | rplD | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L4 | 50S ribosomal protein L4 | - |
| "CJ_10001570" | CJE1875 | rplC | Cj1707c | rplC | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 50S ribosomal protein L3 | 50S ribosomal protein L3 | - |
| "opCcV0100000037" | CJE1876 | rpsJ | Cj1708c | rpsJ | CCO0002 | rpsJ | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 30S ribosomal protein S10 | 30S ribosomal protein S10 | ribosomal protein S10 |
| "opCjV0100000962" | CJE1877 | - | - | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | hypothetical protein | - |
| "CJ_10001573" | CJE1878 | - | Cj1709c | - | CCO0003 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative ribosomal pseudouridine synthase | RNA pseudouridylate synthase family protein | RNA pseudouridine synthase, RsuA family |
| "CJ_10001575" | CJE1879 | - | Cj1710c | - | CCO0004 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | metallo-beta-lactamase family protein | conserved hypothetical protein subfamily |
| "CJ_10001577" | CJE1880 | ksgA | Cj1711c | ksgA | CCO0005 | ksgA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | putative dimethyladenosine transferase (16S rRNA | dimethyladenosine transferase | dimethyladenosine transferase |
| "CJ_10001579" | CJE1881 | - | Cj1712 | - | CCO0006 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | purine nucleoside phosphorylase (punB) |
| "CJ_10001581" | CJE1882 | - | Cj1713 | - | CCO0007 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | radical SAM enzyme, Cfr family | radical SAM enzyme, Cfr family |
| "CJ_10001583" | CJE1883 | - | Cj1714 | - | CCO0008 | - | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | 1 | 1 | small hydrophobic protein | hypothetical protein | hypothetical protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjV0100000081" | CJE1884 | - | - | - | - | - | -1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | - | lipopolysaccharide core biosynthesis protien, | - |
| "CJ_10001585" | CJE1885 | - | Cj1715 | - | CCO0014 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative acetyltransferase | acetyltransferase, GNAT family | acetyltransferase, GNAT family, putative |
| "opCcV0100001061" | CJE1886 | leuD | Cj1716c | leuD | CCO0015 | leuD | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative 3-isopropylmalate dehydratase small | 3-isopropylmalate dehydratase, small subunit | 3-isopropylmalate dehydratase, small subunit |
| "opCcV0100000744" | CJE1887 | leuC | Cj1717c | leuC | CCO0016 | leuC | 1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | 3-isopropylmalate dehydratase large subunit | isopropylmalate isomerase large subunit | 3-isopropylmalate dehydratase, large subunit |
| "CJ_10000014" | CJE1888 | leuB | Cj1718c | leuB | CCO0017 | leuB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 3-isopropylmalate dehydrogenase | 3-isopropylmalate dehydrogenase | 3-isopropylmalate dehydrogenase |
| "CJ_10000016" | CJE1889 | leuA | Cj1719c | leuA | CCO0018 | leuA | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 2-isopropylmalate synthase | 2-isopropylmalate synthase | 2-isopropylmalate synthase |
| "CJ_10000018" | CJE1890 | - | Cj1720 | - | CCO0019 | - | -1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein |
| "CJ_10000019" | CJE1891 | - | Cj1721c | - | CCO0020 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | possible outer membrane protein | hypothetical protein | probable outer membrane protein Cj1721c |
| "CJ_10000021" | CJE1892 | - | Cj1724c | - | CCO0022 | - | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | GTP cyclohydrolase I family protein | GTP cyclohydrolase I subfamily, putative |
| "opCcV0100000585" | CJE1893 | - | Cj1725 | - | CCO0023 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj1725 |
| "CJ_10000037" | CJE1894 | metA | Cj1726c | metA | CCO0024 | metA | 0 | 0 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative homoserine O-succinyltransferase | homoserine O-succinyltransferase | homoserine O-succinyltransferase |
| "opCcV0100001193" | CJE1895 | metX | Cj1727c | metY | CCO0027 | metC | 0 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | putative O-acetylhomoserine (thiol)-lyase | homoserine O-acetyltransferase | O-acetylhomoserine sulfhydrylase |
| "CJ_10000041" | CJE1896 | - | Cj1729c | flgE2 | CCO0029 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | flagellar hook subunit protein | flagellar hook protein | flagellar hook protein FlgE |
| "opCcV0100001311" | CJE1897 | ruvC | Cj1731c | ruvC | CCO0031 | ruvC | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | crossover junction endodeoxyribonuclease | Holliday junction resolvase | crossover junction endodeoxyribonuclease RuvC |
| "CJ_10000460" | - | - | - | virB8 | - | - | 1 | -1 | 1 | 0 | 1 | -1 | 1 | 1 | 0 | 0 | VirB8 | - | - |
| "CJ_10000461" | - | - | - | virB9 | - | - | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | VirB9 | - | - |
| "CJ_10000462" | - | - | - | virB10 | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | VirB10 | - | - |
| "CJ_10000464" | - | - | - | virB11 | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | VirB11 | - | - |
| "CJ_10000465" | - | - | - | virD4 | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | VirD4 | - | - |
| "CJ_10000753" | - | - | - | topA | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 0 | TopA | - | - |
| "CJ_10000756" | - | - | - | ssb | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | Ssb | - | - |
| "CJ_10000803" | - | - | - | repA | - | - | -1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 0 | -1 | pseudogene | - | - |
| "CJ_10000877" | - | - | - | virB4 | - | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | VirB4 | - | - |
| "CJ_10001589" | - | - | - | repA | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 1 | putative replication protein A | - | - |
| "CJ_10001592" | - | - | - | repB | - | - | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | replication protein B | - | - |
| "CJ_10001594" | - | - | - | orf4 | - | - | 1 | 1 | 0 | -1 | -1 | | -1 | 1 | 1 | 1 | unknown | - | - |
| "CJ_10001595" | - | - | - | orf3 | - | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | unknown | - | - |
| "CJ_10001532" | - | - | Cj0008 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000625" | - | - | Cj0170 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000626" | - | - | Cj0171 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001504" | - | - | Cj0260c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | small hydrophobic protein | - | - |
| "CJ_10001534" | - | - | Cj0265c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | putative cytochrome C-type haem-binding | - | - |
| "opCjjV010000018" | - | - | Cj0416 | - | - | - | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000875" | - | - | Cj0417 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000886" | - | - | Cj0423 | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | putative integral membrane protein | - | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000887" | - | - | Cj0424 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | putative acidic periplasmic protein | - | - |
| "CJ_10000888" | - | - | Cj0425 | - | - | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | - | - |
| "CJ_10000869" | - | - | Cj0565 | - | - | - | 1 | 1 | 1 | -1 | -1 | 0 | -1 | -1 | -1 | -1 | pseudogene | - | - |
| "CJ_10000871" | - | - | Cj0566 | - | - | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | -1 | 1 | hypothetical protein | - | - |
| "CJ_10000873" | - | - | Cj0567 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000876" | - | - | Cj0568 | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000880" | - | - | Cj0569 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001016" | - | - | Cj0628 | - | - | - | 1 | 1 | 1 | 1 | 0 | -1 | 1 | -1 | -1 | -1 | putative lipoprotein | - | - |
| "opCjjV010000 135" | - | - | Cj0629 | - | - | - | 1 | 1 | 0 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | putative lipoprotein | - | - |
| "CJ_10000912" | - | - | Cj0747 | - | - | - | 0 | -1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000913" | - | - | Cj0748 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 102" | - | - | Cj0873c | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000254" | - | - | Cj0876c | - | - | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | putative periplasmic protein | - | - |
| "opCjjV010000 034" | - | - | Cj0877c | - | - | - | 1 | 1 | 0 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 204" | - | - | Cj0969 | - | - | - | | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | pseudogene | - | - |
| "CJ_10001208" | - | - | Cj0987c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative integral membrane protein | - | - |
| "opCjjV010000 207" | - | - | Cj0988c | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | - | - | - |
| "CJ_10001419" | - | - | Cj1055c | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | putative integral membrane protein | - | - |
| "CJ_10001116" | - | - | Cj1122c | wlaJ | - | - | 0 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | putative integral membrane protein | - | - |
| "CJ_10001159" | - | - | Cj1136 | - | - | - | -1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | putative galactosyltransferase | - | - |
| "CJ_10001160" | - | - | Cj1137c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | hypothetcal protein Cj1137c | - | - |
| "CJ_10001194" | - | - | Cj1138 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative galactosyltransferase | - | - |
| "CJ_10001198" | - | - | Cj1140 | - | - | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001200" | - | - | Cj1141 | neuB1 | - | - | 1 | 1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | N-acetylneuraminic acid synthetase | - | - |
| "CJ_10001202" | - | - | Cj1142 | neuC1 | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | putative N-acetylglucosamine-6-phosphate | - | - |
| "CJ_10001203" | - | - | Cj1143 | neuA1 | - | - | 1 | 1 | -1 | 1 | -1 | -1 | 0 | -1 | 1 | -1 | acylneuraminate cytidylyltransferase | - | - |
| "CJ_10001204" | - | - | Cj1144c | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10001205" | - | - | Cj1145c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10001270" | - | - | Cj1301 | - | - | - | 1 | -1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001336" | - | - | Cj1321 | - | - | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | putative transferase | - | - |
| "CJ_10001339" | - | - | Cj1322 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001342" | - | - | Cj1323 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10001344" | - | - | Cj1324 | - | - | - | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001345" | - | - | Cj1325 | - | - | - | | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001346" | - | - | Cj1326 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000499" | - | - | Cj1415c | cysC | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 0 | -1 | 1 | 1 | possible adenylylsulfate kinase | - | - |
| "CJ_10000500" | - | - | Cj1416c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative sugar nucleotidyltransferase | - | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000501" | - | - | Cj1417c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000502" | - | - | Cj1418c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | hypothtical protein Cj1418c | - | - |
| "CJ_10000503" | - | - | Cj1419c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | possible methyltransferase | - | - |
| "CJ_10000504" | - | - | Cj1420c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000505" | - | - | Cj1421c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | | -1 | -1 | possible sugar transferase | - | - |
| "CJ_10000506" | - | - | Cj1422c | - | - | - | 1 | 1 | 1 | 1 | | 1 | 1 | -1 | 1 | 1 | possible sugar transferase | - | - |
| "CJ_10000529" | - | - | Cj1426c | - | - | - | | 1 | 0 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000530" | - | - | Cj1427c | - | - | - | | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | putative sugar-nucleotide | - | - |
| "CJ_10000531" | - | - | Cj1428c | fcl | - | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | 1 | putative fucose synthetase | - | - |
| "CJ_10000532" | - | - | Cj1429c | - | - | - | -1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000533" | - | - | Cj1430c | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | putative nucleotide-sugar epimerase/dehydratase | - | - |
| "CJ_10000534" | - | - | Cj1431c | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000535" | - | - | Cj1432c | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | putative sugar transferase | - | - |
| "CJ_10000553" | - | - | Cj1433c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10000554" | - | - | Cj1434c | - | - | - | | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | putative sugar transferase | - | - |
| "CJ_10000556" | - | - | Cj1435c | - | - | - | 1 | 1 | 0 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10000557" | - | - | Cj1436c | - | - | - | 0 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative aminotransferase | - | - |
| "CJ_10000558" | - | - | Cj1437c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative aminotransferase | - | - |
| "CJ_10000559" | - | - | Cj1438c | - | - | - | 1 | 1 | 1 | | -1 | -1 | 1 | 1 | | | putative sugar transferase | - | - |
| "CJ_10000560" | - | - | Cj1439c | glf | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | -1 | | UDP-galactopyranose mutase | - | - |
| "CJ_10000561" | - | - | Cj1440c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | putative sugar transferase | - | - |
| "CJ_10000562" | - | - | Cj1441c | kfiD | - | - | 1 | 1 | 1 | | -1 | 1 | 1 | 1 | -1 | 1 | putative UDP-glucose 6-dehydrogenase | - | - |
| "CJ_10000563" | - | - | Cj1442c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001462" | - | - | Cj1520 | - | - | - | 0 | 1 | -1 | 0 | 1 | 1 | 0 | 1 | -1 | 1 | hypotetical protein Cj1520 | - | - |
| "CJ_10001523" | - | - | Cj1549c | - | - | - | 1 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative type I restriction enzyme R protein | - | - |
| "CJ_10001525" | - | - | Cj1550c | - | - | - | 1 | 1 | 0 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | putative ATP/GTP-binding protein | - | - |
| "CJ_10001549" | - | - | Cj1551c | - | - | - | 1 | 1 | 0 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | putative type I restriction enzyme S protein | - | - |
| "CJ_10001551" | - | - | Cj1552c | - | - | - | 1 | - | 0 | | | 1 | 1 | | | -1 | hypothetical protein | - | - |
| "CJ_10001554" | - | - | Cj1553c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | putative type I restriction enzyme M protein | - | - |
| "CJ_10001557" | - | - | Cj1556 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10001478" | - | - | Cj1677 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | putative lipoprotein | - | - |
| "opCjjV010000086" | - | - | Cj1678 | - | - | - | 1 | 1 | 0 | -1 | -1 | 0 | -1 | -1 | 1 | -1 | - | - | - |
| "CJ_10001481" | - | - | Cj1679 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000072" | - | - | Cj1723c | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | putative periplasmic protein | - | - |
| "opCjjV010000036" | - | - | Cjp03 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000463" | - | - | Cjp04 | - | - | - | -1 | -1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000083" | - | - | Cjp04 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000099" | - | - | Cjp04 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000008" | - | - | Cjp05 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000046" | - | - | Cjp06 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCjjV010000 040" | - | - | Cjp07 | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 0 | 1 | hypothetical protein | - | - |
| "opCjjV010000 067" | - | - | Cjp07 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000467" | - | - | Cjp08 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 024" | - | - | Cjp08 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000469" | - | - | Cjp09 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 004" | - | - | Cjp09 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000752" | - | - | Cjp10 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 073" | - | - | Cjp10 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 103" | - | - | Cjp11 | rnpB | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | ribonuclease P, RNA component | - | - |
| "CJ_10000754" | - | - | Cjp12 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 022" | - | - | Cjp13 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000758" | - | - | Cjp14 | - | - | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000760" | - | - | Cjp15 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000762" | - | - | Cjp16 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | - | - |
| "CJ_10000764" | - | - | Cjp17 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10000766" | - | - | Cjp18 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 110" | - | - | Cjp19 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 113" | - | - | Cjp19 | - | - | - | 1 | 1 | 1 | 0 | 1 | | -1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10000785" | - | - | Cjp20 | - | - | - | 1 | 1 | 1 | 1 | -1 | | | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 141" | - | - | Cjp20 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000787" | - | - | Cjp21 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | -1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 005" | - | - | Cjp21 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000789" | - | - | Cjp22 | - | - | - | 1 | 0 | 0 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 206" | - | - | Cjp22 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000792" | - | - | Cjp23 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 205" | - | - | Cjp23 | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000795" | - | - | Cjp24 | - | - | - | 0 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 014" | - | - | Cjp24 | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 006" | - | - | Cjp25 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 079" | - | - | Cjp25 | - | - | - | 1 | 1 | 0 | -1 | -1 | 1 | 0 | 1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10000799" | - | - | Cjp26 | - | - | - | 1 | 1 | 1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 179" | - | - | Cjp26 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000801" | - | - | Cjp27 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 070" | - | - | Cjp27 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 080" | - | - | Cjp28 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "CJ_10000805" | - | - | Cjp29 | - | - | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000023" | - | - | Cjp29 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | hypothetical protein | - | - |
| "CJ_10000814" | - | - | Cjp30 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000064" | - | - | Cjp30 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000816" | - | - | Cjp31 | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000818" | - | - | Cjp32 | - | - | - | 0 | 1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000052" | - | - | Cjp32 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000821" | - | - | Cjp33 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000051" | - | - | Cjp33 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000824" | - | - | Cjp34 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000050" | - | - | Cjp34 | - | - | - | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000827" | - | - | Cjp35 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000197" | - | - | Cjp35 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000829" | - | - | Cjp36 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000175" | - | - | Cjp36 | - | - | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000830" | - | - | Cjp37 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000831" | - | - | Cjp38 | - | - | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | -1 | -1 | 1 | hypothetical protein | - | - |
| "CJ_10000832" | - | - | Cjp39 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | 1 | hypothetical protein | - | - |
| "CJ_10000841" | - | - | Cjp40 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000843" | - | - | Cjp41 | - | - | - | | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | hypothetical protein | - | - |
| "CJ_10000848" | - | - | Cjp43 | - | - | - | 1 | 1 | 1 | 1 | -1 | | -1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "CJ_10000851" | - | - | Cjp44 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000854" | - | - | Cjp45 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | hypothetical protein | - | - |
| "CJ_10000856" | - | - | Cjp46 | - | - | - | 1 | 0 | 1 | -1 | -1 | 1 | 1 | 0 | -1 | -1 | hypothetical protein | - | - |
| "CJ_10000858" | - | - | Cjp47 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000860" | - | - | Cjp48 | - | - | - | 0 | 1 | 1 | 1 | 0 | 1 | 0 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000863" | - | - | Cjp49 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | hypothetical protein | - | - |
| "CJ_10000870" | - | - | Cjp50 | - | - | - | 1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000872" | - | - | Cjp51 | - | - | - | -1 | 1 | 1 | | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000874" | - | - | Cjp52 | - | - | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "CJ_10000879" | - | - | Cjp54 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | VirB7 | - | - |
| "opCjjV010000109" | - | - | Cjr03 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000127" | - | - | Cjr06 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000130" | - | - | Cjr09 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000105" | - | - | Cjt02 | - | - | - | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCcV0100000317" | - | - | - | - | CCO0001 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | similar to 50S ribosomal protein L3 |
| "opCcV0100000640" | - | - | - | - | CCO0011 | - | -1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | pseudogene |
| "opCcV0100001650" | - | - | - | - | CCO0025 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001876" | - | - | - | - | CCO0026 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | - | - | YeeE/YedE family protein family |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100002071" | - | - | - | - | CCO0035 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | Tat (twin-arginine translocation) pathway signal |
| "opCcV0100002054" | - | - | - | - | CCO0036 | - | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | Chain B, Stru |
| "opCcV0100001228" | - | - | - | - | CCO0037 | - | 1 | 1 | 1 | 0 | -1 | | 1 | -1 | 1 | 0 | - | - | Chain B, Stru |
| "opCcV0100001744" | - | - | - | - | CCO0038 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001285" | - | - | - | - | CCO0039 | - | -1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 0 | 0 | - | - | sodium:solute symporter family protein |
| "opCcV0100000410" | - | - | - | - | CCO0040 | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | - | - | Protein of unknown function, DUF485 superfamily |
| "opCcV0100000937" | - | - | - | - | CCO0048 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000276" | - | - | - | - | CCO0067 | - | 1 | 1 | 0 | 1 | -1 | -1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100000178" | - | - | - | - | CCO0068 | - | 1 | 1 | 0 | 1 | -1 | -1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001696" | - | - | - | - | CCO0069 | - | 1 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000483" | - | - | - | - | CCO0072 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | probable integral membrane protein Cj0033 |
| "opCcV0100001621" | - | - | - | - | CCO0074 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | - | - | conserved hypothetical protein |
| "opCcV0100001498" | - | - | - | - | CCO0092 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000901" | - | - | - | - | CCO0093 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | probable periplasmic protein Cj0057 |
| "opCcV0100001086" | - | - | - | - | CCO0094 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000235" | - | - | - | - | CCO0095 | - | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | -1 | 1 | - | - | probable periplasmic protein Cj0057 |
| "opCcV0100000045" | - | - | - | - | CCO0096 | - | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000580" | - | - | - | - | CCO0097 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000649" | - | - | - | - | CCO0098 | - | 1 | 1 | -1 | 1 | -1 | 1 | 0 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000634" | - | - | - | - | CCO0099 | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | -1 | - | - | probable periplasmic protein Cj0057 |
| "opCcV0100000623" | - | - | - | - | CCO0100 | - | -1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100000499" | - | - | - | - | CCO0101 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 0 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001681" | - | - | - | - | CCO0102 | - | 1 | 1 | 0 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000103" | - | - | - | - | CCO0104 | - | 1 | 1 | 0 | -1 | 1 | 0 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001477" | - | - | - | - | CCO0105 | - | 1 | 1 | 0 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001918" | - | - | - | - | CCO0106 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 | - | - | - | - | CCO0107 | - | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 0 | - | - | conserved hypothetical |

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| 1220" | | | | | | | | | | | | | | | | | | | protein |
| "opCcV010000 0418" | - | - | - | - | CCO0108 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0721" | - | - | - | - | CCO0109 | - | 1 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1335" | - | - | - | - | CCO0110 | - | 1 | 1 | 0 | | -1 | 1 | 1 | 1 | 1 | 1 | - | - | probable periplasmic protein Cj0057 |
| "opCcV010000 0581" | - | - | - | - | CCO0111 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 1091" | - | - | - | - | CCO0112 | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0775" | - | - | - | - | CCO0127 | - | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | - | - | methyl-accepting chemotaxis protein, putative |
| "opCcV010000 0715" | - | - | - | - | CCO0128 | - | 1 | 1 | 0 | 1 | -1 | 1 | -1 | 0 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1622" | - | - | - | - | CCO0136 | - | -1 | -1 | -1 | 0 | 1 | 1 | -1 | 1 | -1 | 0 | - | - | hypothetical protein |
| "opCcV010000 1293" | - | - | - | - | CCO0137 | - | 1 | -1 | 0 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | - | - | transcriptional regulator, Crp family, putative |
| "opCcV010000 0793" | - | - | - | - | CCO0138 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0316" | - | - | - | - | CCO0181 | - | 1 | 1 | 0 | -1 | -1 | 1 | 0 | 1 | 1 | 1 | - | - | filamentous hemagglutinin, intein-containing, |
| "opCcV010000 1392" | - | - | - | - | CCO0182 | - | | -1 | 0 | | | 1 | | -1 | | | - | - | hemagglutinin/hemolysin-related protein |
| "opCcV010000 1501" | - | - | - | - | CCO0183 | - | 0 | 0 | 0 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | - | - | Hemolysin, putative |
| "opCcV010000 1076" | - | - | - | - | CCO0184 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | Hemolysin, putative |
| "opCcV010000 1872" | - | - | - | - | CCO0185 | - | | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 1181" | - | - | - | - | CCO0186 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0939" | - | - | - | - | CCO0187 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | - | - | filamentous hemagglutinin 1, putative |
| "opCcV010000 2052" | - | - | - | - | CCO0188 | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0029" | - | - | - | - | CCO0189 | - | | | -1 | | | -1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1039" | - | - | - | - | CCO0190 | - | 1 | 1 | 1 | 1 | 0 | 0 | 0 | -1 | 1 | 1 | - | - | hemolysin activation protein HecB, putative |
| "opCcV010000 1254" | - | - | - | - | CCO0203 | - | 1 | 1 | 1 | | 1 | 0 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0013" | - | - | - | - | CCO0204 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | 1 | 0 | -1 | - | - | hypothetical protein |
| "opCcV010000 0114" | - | - | - | - | CCO0210 | - | 1 | -1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1920" | - | - | - | - | CCO0212 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 1217" | - | - | - | - | CCO0213 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | methyl-accepting chemotaxis protein, putative |
| "opCcV010000 0117" | - | - | - | - | CCO0231 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0991" | - | - | - | - | CCO0246 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |

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| "opCcV0100000193" | - | - | - | - | CCO0248 | - | 1 | 1 | 1 | 0 | -1 | 0 | 0 | -1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100000024" | - | - | - | - | CCO0249 | - | 1 | 1 | 1 | 0 | 1 | -1 | 1 | -1 | 0 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100000266" | - | - | - | - | CCO0250 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV0100000545" | - | - | - | - | CCO0251 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | lipoprotein, putative |
| "opCcV0100000645" | - | - | - | - | CCO0252 | - | -1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | probable integral membrane protein Cj0564 |
| "opCcV0100001358" | - | - | - | - | CCO0253 | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000876" | - | - | - | - | CCO0254 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000630" | - | - | - | - | CCO0257 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | glcG protein |
| "opCcV0100000875" | - | - | - | - | CCO0280 | - | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | - | - | methyl-accepting chemotaxis protein (tlpA) |
| "opCcV0100000323" | - | - | - | - | CCO0281 | - | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100000310" | - | - | - | - | CCO0284 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000982" | - | - | - | - | CCO0285 | - | 1 | 1 | 1 | 1 | | 1 | 1 | | | 1 | - | - | CAAX amino terminal protease family protein |
| "opCcV0100001967" | - | - | - | - | CCO0291 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | -1 | -1 | - | - | Hypothetical cytosolic protein, putative |
| "opCcV0100000695" | - | - | - | - | CCO0292 | - | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100000694" | - | - | - | - | CCO0293 | - | 1 | 1 | 1 | -1 | -1 | -1 | 0 | 1 | -1 | -1 | - | - | penicillin-binding protein, putative |
| "opCcV0100001345" | - | - | - | - | CCO0332 | - | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | - | - | TM2 domain protein, putative |
| "opCcV0100000810" | - | - | - | - | CCO0347 | - | 1 | 1 | 0 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100001609" | - | - | - | - | CCO0349 | - | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 0 | 1 | 1 | - | - | carboxyphosphonoenolpyruvate phosphonomutase |
| "opCcV0100000265" | - | - | - | - | CCO0350 | citZ | 1 | 1 | 1 | -1 | -1 | 1 | 0 | -1 | 1 | 0 | - | - | 2-methylcitrate synthase |
| "opCcV0100000345" | - | - | - | - | CCO0351 | b0334 | 1 | 1 | 0 | -1 | 1 | 1 | 0 | 1 | -1 | -1 | - | - | pseudogene |
| "opCcV0100001597" | - | - | - | - | CCO0352 | - | 1 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | 1 | - | - | ID867 |
| "opCcV0100001722" | - | - | - | - | CCO0353 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | - | - | membrane protein , putative |
| "opCcV0100001475" | - | - | - | - | CCO0354 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV0100001552" | - | - | - | - | CCO0355 | - | 1 | -1 | 0 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | probable periplasmic protein Cj0413 , putative |
| "opCcV0100001845" | - | - | - | - | CCO0356 | - | 1 | 1 | -1 | -1 | 1 | | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001068" | - | - | - | - | CCO0368 | cdtC | 1 | -1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | cytolethal distending toxin C |
| "opCcV0100001565" | - | - | - | - | CCO0382 | - | 1 | 1 | 0 | -1 | -1 | 1 | 0 | -1 | 1 | -1 | - | - | lipoprotein, putative |
| "opCcV010000 | - | - | - | - | CCO0383 | - | 1 | 1 | 1 | 0 | -1 | -1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0043" | | | | | | | | | | | | | | | | | | | protein |
| "opCcV0100000228" | - | - | - | - | CCO0384 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | Helix-turn-helix domain protein |
| "opCcV0100001055" | - | - | - | - | CCO0411 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | - | - | tricarboxylate transport protein TctA, putative |
| "opCcV0100000706" | - | - | - | - | CCO0412 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | tricarboxylate transport protein TctB, putative |
| "opCcV0100000550" | - | - | - | - | CCO0413 | - | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | tricarboxylate transport protein TctC, putative |
| "opCcV0100000263" | - | - | - | - | CCO0428 | - | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | - | - | membrane protein, putative |
| "opCcV0100000869" | - | - | - | - | CCO0429 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | membrane protein, putative |
| "opCcV0100000673" | - | - | - | - | CCO0430 | - | -1 | -1 | 0 | 0 | 1 | -1 | 0 | 1 | -1 | -1 | - | - | membrane protein, putative |
| "opCcV0100001556" | - | - | - | - | CCO0508 | - | | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | -1 | - | - | integral membrane protein |
| "opCcV0100000214" | - | - | - | - | CCO0509 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | lipoprotein, putative |
| "opCcV0100001612" | - | - | - | - | CCO0510 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | - | - | integral membrane protein |
| "opCcV0100001340" | - | - | - | - | CCO0511 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | integral membrane protein |
| "opCcV0100001167" | - | - | - | - | CCO0518 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | methyl-accepting chemotaxis protein, putative |
| "opCcV0100000166" | - | - | - | - | CCO0533 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | membrane protein , putative |
| "opCcV0100000566" | - | - | - | - | CCO0534 | - | | | 0 | 1 | 0 | -1 | -1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001168" | - | - | - | - | CCO0535 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | L-carnitine dehydratase |
| "opCcV0100000692" | - | - | - | - | CCO0536 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | citE, putative |
| "opCcV0100000378" | - | - | - | - | CCO0601 | - | 1 | 1 | 0 | -1 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001123" | - | - | - | - | CCO0603 | - | 1 | 1 | 0 | -1 | -1 | 1 | 0 | 1 | 1 | -1 | - | - | B. subtilis YxjH and YxjG proteins homolog |
| "opCcV0100000398" | - | - | - | - | CCO0610 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001104" | - | - | - | - | CCO0654 | - | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV0100001383" | - | - | - | - | CCO0658 | - | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001296" | - | - | - | - | CCO0751 | - | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001853" | - | - | - | - | CCO0764 | - | 1 | 1 | 1 | 1 | -1 | 1 | 0 | 0 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000207" | - | - | - | - | CCO0804 | - | 1 | 1 | 0 | 1 | -1 | | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100001158" | - | - | - | - | CCO0807 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000865" | - | - | - | - | CCO0808 | - | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | pseudogene |
| "opCcV0100001674" | - | - | - | - | CCO0814 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 0 | -1 | - | - | hypothetical protein |

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| "opCcV010000 1532" | - | - | - | - | CCO0815 | - | 1 | 1 | 0 | -1 | 0 | -1 | 0 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0380" | - | - | - | - | CCO0845 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | azlC protein, putative |
| "opCcV010000 0914" | - | - | - | - | CCO0846 | - | 1 | 0 | 0 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | - | - | Branched-chain amino acid transport protein, |
| "opCcV010000 1559" | - | - | - | - | CCO0847 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | transporter, LysE family |
| "opCcV010000 1442" | - | - | - | - | CCO0865 | dapA | 1 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | - | - | dihydrodipicolinate synthase |
| "opCcV010000 2024" | - | - | - | - | CCO0866 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | 1 | - | - | probable oxidoreductase Cj0807 |
| "opCcV010000 0315" | - | - | - | - | CCO0867 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | small hydrophobic protein Cj0808c |
| "opCcV010000 0086" | - | - | - | - | CCO0868 | - | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | - | - | probable hydrolase Cj0809c |
| "opCcV010000 1659" | - | - | - | - | CCO0869 | nadE | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | NAD+ synthetase |
| "opCcV010000 1955" | - | - | - | - | CCO0870 | lpxK | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | tetraacyldisaccharide-1-P 4'-kinase |
| "opCcV010000 1395" | - | - | - | - | CCO0917 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | ferric uptake regulation protein, putative |
| "opCcV010000 1593" | - | - | - | - | CCO0918 | - | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1708" | - | - | - | - | CCO0919 | fimA | 1 | 1 | 1 | 0 | -1 | -1 | 0 | -1 | 0 | 1 | - | - | periplasmic solute binding protein for ABC |
| "opCcV010000 0916" | - | - | - | - | CCO0921 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | membrane protein, putative |
| "opCcV010000 1855" | - | - | - | - | CCO0922 | - | 1 | 1 | | 1 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 1245" | - | - | - | - | CCO0923 | - | 0 | -1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 0808" | - | - | - | - | CCO0924 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0122" | - | - | - | - | CCO0925 | - | | -1 | -1 | -1 | | -1 | -1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1262" | - | - | - | - | CCO0926 | - | 1 | 1 | 1 | 0 | 1 | -1 | -1 | 1 | 1 | 0 | - | - | hypothetical protein |
| "opCcV010000 0529" | - | - | - | - | CCO0927 | - | | 1 | -1 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1870" | - | - | - | - | CCO0928 | - | -1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1938" | - | - | - | - | CCO0929 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0722" | - | - | - | - | CCO0955 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | inner membrane protein, putative |
| "opCcV010000 1617" | - | - | - | - | CCO0956 | - | | 1 | 1 | 1 | 0 | 0 | 0 | 1 | -1 | 0 | - | - | conserved hypothetical protein |
| "opCcV010000 1038" | - | - | - | - | CCO0968 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1944" | - | - | - | - | CCO0970 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0061" | - | - | - | - | CCO1005 | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | -1 | - | - | sodium/alanine symporter VC2356 |
| "opCcV010000 | - | - | - | - | CCO1040 | - | 1 | 1 | 0 | -1 | -1 | 1 | 0 | -1 | 1 | 0 | - | - | conserved hypothetical |

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| 1105" | | | | | | | | | | | | | | | | | | | protein |
| "opCcV010000 0131" | - | - | - | - | CCO1041 | - | 1 | 1 | 0 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1819" | - | - | - | - | CCO1049 | - | 1 | -1 | 0 | -1 | 1 | 0 | -1 | 1 | 0 | 1 | - | - | surface-exposed lipoprotein |
| "opCcV010000 1438" | - | - | - | - | CCO1075 | - | 1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 1590" | - | - | - | - | CCO1076 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1714" | - | - | - | - | CCO1077 | - | 1 | 1 | -1 | 1 | 0 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0376" | - | - | - | - | CCO1078 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | - | - | hypothetical protein |
| "opCcV010000 0365" | - | - | - | - | CCO1115 | - | 1 | 1 | 0 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | - | - | adenine specific DNA methyltransferase |
| "opCcV010000 1628" | - | - | - | - | CCO1123 | - | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0022" | - | - | - | - | CCO1124 | - | 1 | 1 | 1 | 1 | -1 | 1 | 0 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1229" | - | - | - | - | CCO1125 | - | 1 | -1 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | - | - | VgrG protein, putative |
| "opCcV010000 0141" | - | - | - | - | CCO1126 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | pseudogene |
| "opCcV010000 0525" | - | - | - | - | CCO1142 | - | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1697" | - | - | - | - | CCO1143 | - | 1 | 1 | 0 | | 1 | -1 | 1 | 1 | 1 | 1 | - | - | transporter, MFS superfamily |
| "opCcV010000 1165" | - | - | - | - | CCO1170 | - | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | oxidoreductase, short-chain |
| "opCcV010000 2057" | - | - | - | - | CCO1171 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0357" | - | - | - | - | CCO1172 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0331" | - | - | - | - | CCO1173 | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0771" | - | - | - | - | CCO1211 | - | 1 | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | -1 | - | - | glycosyl transferase, group 1 family protein |
| "opCcV010000 1761" | - | - | - | - | CCO1212 | - | 1 | 0 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | general stress protein A, putative |
| "opCcV010000 1473" | - | - | - | - | CCO1214 | - | 1 | 1 | -1 | 0 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0308" | - | - | - | - | CCO1215 | - | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | -1 | - | - | bifunctional alpha-2,3/-2,8-sialyltransferase |
| "opCcV010000 0837" | - | - | - | - | CCO1216 | - | -1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 0 | 0 | - | - | hypothetical protein |
| "opCcV010000 0084" | - | - | - | - | CCO1217 | - | 1 | 1 | 0 | 0 | -1 | 1 | -1 | 1 | 1 | 0 | - | - | sialyl transferase |
| "opCcV010000 1797" | - | - | - | - | CCO1218 | - | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1035" | - | - | - | - | CCO1221 | - | -1 | | | | 1 | 1 | 1 | | | | - | - | lipooligosaccharide 5G8 epitope |
| "opCcV010000 0093" | - | - | - | - | CCO1277 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0726" | - | - | - | - | CCO1278 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | 1 | - | - | hydrolase, carbon-nitrogen family |

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| "opCcV0100000994" | - | - | - | - | CCO1279 | - | 1 | 1 | 1 | 1 | -1 | 1 | 0 | -1 | 1 | 1 | - | - | polysaccharide deacetylase family protein |
| "opCcV0100001233" | - | - | - | - | CCO1280 | - | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001155" | - | - | - | - | CCO1281 | - | 1 | 1 | 0 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | cobalamin synthesis protein/P47K family protein |
| "opCcV0100000977" | - | - | - | - | CCO1298 | - | 1 | 1 | 0 | -1 | 1 | 0 | 0 | 1 | -1 | 1 | - | - | sodium/pantothenate symporter , putative |
| "opCcV0100000688" | - | - | - | - | CCO1299 | - | 1 | 1 | 0 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100000196" | - | - | - | - | CCO1303 | - | 1 | 1 | -1 | -1 | | 1 | 1 | 1 | 1 | -1 | - | - | Ribbon-helix-helix protein, copG family domain |
| "opCcV0100000897" | - | - | - | - | CCO1304 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100002006" | - | - | - | - | CCO1305 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000805" | - | - | - | - | CCO1306 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | cytochrome c family protein |
| "opCcV0100001726" | - | - | - | - | CCO1307 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001573" | - | - | - | - | CCO1308 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | putative periplasmic protein |
| "opCcV0100001188" | - | - | - | - | CCO1309 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | putative periplasmic protein |
| "opCcV0100000386" | - | - | - | - | CCO1310 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | putative periplasmic protein |
| "opCcV0100000226" | - | - | - | - | CCO1311 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100001368" | - | - | - | - | CCO1312 | - | 1 | - | 0 | | 1 | 1 | -1 | 1 | | -1 | - | - | filamentous haemagglutinin domain protein |
| "opCcV0100000823" | - | - | - | - | CCO1325 | - | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000145" | - | - | - | - | CCO1326 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV0100000048" | - | - | - | - | CCO1331 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001666" | - | - | - | - | CCO1339 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | ISCco1, transposase |
| "opCcV0100000302" | - | - | - | - | CCO1340 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | methyltransferase Atu0936 , putative |
| "opCcV0100001923" | - | - | - | - | CCO1341 | - | 1 | -1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | phospholipid N-methyltransferase, putative |
| "opCcV0100000839" | - | - | - | - | CCO1342 | - | 1 | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000125" | - | - | - | - | CCO1349 | - | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | membrane protein, putative |
| "opCcV0100000978" | - | - | - | - | CCO1369 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved domain protein |
| "opCcV0100000088" | - | - | - | - | CCO1370 | - | 1 | 1 | 1 | 1 | | 1 | 0 | 1 | 1 | -1 | - | - | ABC transporter ATP-binding protein |
| "opCcV0100002007" | - | - | - | - | CCO1409 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001457" | - | - | - | - | CCO1412 | - | | -1 | -1 | -1 | 0 | -1 | -1 | 1 | 0 | -1 | - | - | acetyltransferase, GNAT family family |
| "opCcV010000 | - | - | - | - | CCO1413 | - | 0 | -1 | 0 | 1 | 1 | 0 | 1 | 1 | -1 | 0 | - | - | formyltransferase, putative |

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| 1412" | | | | | | | | | | | | | | | | | | | |
| "opCcV010000 0663" | - | - | - | - | CCO1416 | - | 1 | 1 | 0 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0913" | - | - | - | - | CCO1417 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0752" | - | - | - | - | CCO1418 | - | 1 | 1 | 1 | 1 | | 1 | | 1 | 1 | 1 | - | - | 3-oxoacyl-(acyl-carrier-protein) synthase III, |
| "opCcV010000 0923" | - | - | - | - | CCO1432 | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | - | hypothetical protein |
| "opCcV010000 1279" | - | - | - | - | CCO1443 | - | 0 | 0 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | flagellin Cj1338c |
| "opCcV010000 1264" | - | - | - | - | CCO1444 | - | -1 | -1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | - | - | flagellin (flaA) |
| "opCcV010000 1857" | - | - | - | - | CCO1446 | - | 0 | 0 | -1 | 1 | 1 | 0 | -1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 2050" | - | - | - | - | CCO1447 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0979" | - | - | - | - | CCO1467 | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | toxin-like outer membrane protein, putative |
| "opCcV010000 0464" | - | - | - | - | CCO1468 | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | vacuolating cytotoxin precursor, putative |
| "opCcV010000 0890" | - | - | - | - | CCO1469 | - | 1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1571" | - | - | - | - | CCO1484 | - | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | integral membrane protein, putative |
| "opCcV010000 0355" | - | - | - | - | CCO1485 | - | -1 | -1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | - | - | probable efflux protein Cj1375 |
| "opCcV010000 1484" | - | - | - | - | CCO1514 | - | 1 | 1 | -1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 0262" | - | - | - | - | CCO1523 | - | | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | Nucleotidyl transferase family |
| "opCcV010000 1218" | - | - | - | - | CCO1524 | - | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 0 | -1 | - | - | hypothetical protein |
| "opCcV010000 0342" | - | - | - | - | CCO1525 | - | | -1 | -1 | -1 | | -1 | 1 | -1 | -1 | -1 | - | - | Phosphoribulokinase / Uridine kinase family |
| "opCcV010000 1239" | - | - | - | - | CCO1526 | - | 1 | 1 | 1 | | | | | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1514" | - | - | - | - | CCO1527 | - | 1 | 1 | 0 | 0 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | alpha-2,3-sialyltransferase |
| "opCcV010000 1172" | - | - | - | - | CCO1528 | - | 1 | 1 | | 0 | 1 | -1 | 1 | 1 | 0 | 1 | - | - | haloacid dehalogenase-like hydrolase, putative |
| "opCcV010000 0209" | - | - | - | - | CCO1529 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | -1 | - | - | Domain of unknown function (DUF386) superfamily |
| "opCcV010000 1274" | - | - | - | - | CCO1530 | - | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | -1 | - | - | Putative cyclase superfamily |
| "opCcV010000 0032" | - | - | - | - | CCO1531 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | - | - | UDP-glucose 4-epimerase, putative |
| "opCcV010000 1588" | - | - | - | - | CCO1532 | serA | 1 | 1 | -1 | -1 | 1 | 1 | 0 | 1 | 0 | 0 | - | - | D-3-phosphoglycerate dehydrogenase |
| "opCcV010000 0872" | - | - | - | - | CCO1533 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase, |
| "opCcV010000 1550" | - | - | - | - | CCO1534 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | - | - | acylneuraminate cytidylyltransferase, putative |

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| "opCcV0100000382" | - | - | - | - | CCO1535 | - | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | -1 | 1 | - | - | glycosyl transferase, group 2 family protein |
| "opCcV0100001735" | - | - | - | - | CCO1536 | - | 1 | 1 | 1 | 1 | -1 | 1 | 0 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000112" | - | - | - | - | CCO1537 | - | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 0 | -1 | - | - | DcbE, putative |
| "opCcV0100000971" | - | - | - | - | CCO1538 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | alpha-2,3-sialyltransferase |
| "opCcV0100000350" | - | - | - | - | CCO1539 | cysC | 1 | -1 | 0 | 1 | 1 | 1 | 0 | 1 | -1 | 0 | - | - | adenylylsulfate kinase |
| "opCcV0100001905" | - | - | - | - | CCO1540 | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | - | - | transporter, sodium/sulfate symporter family, |
| "opCcV0100000496" | - | - | - | - | CCO1541 | - | 1 | 1 | -1 | -1 | 1 | 0 | 0 | 1 | 1 | 0 | - | - | sulfate adenylyltransferase, subunit |
| "opCcV0100001898" | - | - | - | - | CCO1542 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 0 | - | - | sulfate adenylyltransferase, subunit 2 |
| "opCcV0100000677" | - | - | - | - | CCO1543 | cysQ | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | - | - | 3'(2'),5'-bisphosphate nucleotidase |
| "opCcV0100001820" | - | - | - | - | CCO1544 | - | 1 | 1 | 0 | 1 | -1 | 0 | 1 | -1 | 1 | -1 | - | - | alpha-2,3-sialyltransferase |
| "opCcV0100000849" | - | - | - | - | CCO1546 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 0 | 1 | -1 | - | - | Glycosyl transferase family 8 family |
| "opCcV0100000616" | - | - | - | - | CCO1547 | ggaB | 1 | 1 | 1 | 0 | -1 | 0 | -1 | 1 | 1 | -1 | - | - | capsular polysaccharide synthesis-C |
| "opCcV0100000636" | - | - | - | - | CCO1548 | ggaB | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | minor teichoic acids biosynthesis protein ggab |
| "opCcV0100002058" | - | - | - | - | CCO1549 | - | -1 | 1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 | 1 | - | - | capsule biosynthesis protein, putative |
| "opCcV0100001140" | - | - | - | - | CCO1587 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | DnaJ-related protein |
| "opCcV0100000059" | - | - | - | - | CCO1588 | - | 1 | -1 | 0 | -1 | 1 | -1 | 1 | 1 | -1 | 0 | - | - | conserved hypothetical protein |
| "opCcV0100002045" | - | - | - | - | CCO1610 | - | 0 | 1 | 1 | 1 | -1 | 0 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000233" | - | - | - | - | CCO1627 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | AgrC, putative |
| "opCcV0100000893" | - | - | - | - | CCO1628 | - | 1 | 1 | 0 | -1 | -1 | 1 | 1 | -1 | 1 | 0 | - | - | hypothetical protein |
| "opCcV0100001511" | - | - | - | - | CCO1629 | - | 1 | -1 | 1 | | 0 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000974" | - | - | - | - | CCO1631 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000632" | - | - | - | - | CCO1637 | - | 1 | 1 | 0 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000523" | - | - | - | - | CCO1638 | - | 1 | 0 | 1 | 1 | -1 | -1 | 0 | 1 | 1 | 0 | - | - | ISCco1, transposase orfB |
| "opCcV0100001018" | - | - | - | - | CCO1639 | - | 1 | 1 | 0 | -1 | 1 | 1 | 0 | 1 | 1 | -1 | - | - | ISCco1, transposase orfA |
| "opCcV0100000802" | - | - | - | - | CCO1651 | - | 1 | 1 | 1 | -1 | 0 | -1 | 1 | 1 | 1 | 1 | - | - | pseudogene |
| "opCcV0100000373" | - | - | - | - | CCO1654 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001856" | - | - | - | - | CCO1656 | mdaB | 1 | -1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 0 | - | - | modulator of drug activity (mda66) |
| "opCcV010000 | - | - | - | - | CCO1657 | mdaB | 0 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | modulator of drug activity |

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| 1037" | | | | | | | | | | | | | | | | | | | (mda66) |
| "opCcV010000 1139" | - | - | - | - | CCO1658 | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | 0 | - | - | major facilitator family transporter, putative |
| "opCcV010000 1384" | - | - | - | - | CCO1661 | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | HsdR |
| "opCcV010000 0533" | - | - | - | - | CCO1662 | - | 1 | 1 | 0 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1548" | - | - | - | - | CCO1663 | - | 1 | 1 | 1 | 1 | | 1 | | 1 | 1 | 0 | - | - | Helicase conserved C-terminal domain protein |
| "opCcV010000 0565" | - | - | - | - | CCO1664 | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | HsdS |
| "opCcV010000 1895" | - | - | - | - | CCO1665 | - | 1 | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | MloA |
| "opCcV010000 0986" | - | - | - | - | CCO1666 | - | 1 | - | 0 | -1 | 1 | 0 | 1 | 1 | 1 | -1 | - | - | HsdM |
| "opCcV010000 1132" | - | - | - | - | CCO1667 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0572" | - | - | - | - | CCO1668 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | sarcosine oxidase, putative |
| "opCcV010000 1564" | - | - | - | - | CCO1669 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | NADP(H) oxidoreductase CC0205 |
| "opCcV010000 1197" | - | - | - | - | CCO1670 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 1574" | - | - | - | - | CCO1671 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | catalase-like protein |
| "opCcV010000 0460" | - | - | - | - | CCO1674 | arsC | 1 | -1 | -1 | -1 | 0 | 1 | 1 | 1 | -1 | -1 | - | - | arsC |
| "opCcV010000 2074" | - | - | - | - | CCO1675 | arsC | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | arsenite efflux transporter |
| "opCcV010000 1754" | - | - | - | - | CCO1676 | arsC | 1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | arsenite efflux transporter |
| "opCcV010000 0794" | - | - | - | - | CCO1688 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1259" | - | - | - | - | CCO1689 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0936" | - | - | - | - | CCO1694 | - | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | 1 | -1 | - | - | major facilitator family transporter, putative |
| "opCcV010000 1518" | - | - | - | - | CCO1707 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | integral membrane protein, putative |
| "opCcV010000 2061" | - | - | - | - | CCO1708 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | integral membrane protein, putative |
| "opCcV010000 2049" | - | - | - | - | CCO1710 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 2027" | - | - | - | - | CCO1734 | - | 0 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 1016" | - | - | - | - | CCO1738 | - | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | - | - | Protein of unknown function DUF262 family |
| "opCcV010000 1826" | - | - | - | - | CCO1739 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1409" | - | - | - | - | CCO1740 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0462" | - | - | - | - | CCO1758 | - | 1 | -1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 1365" | - | - | - | - | CCO1784 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | | 1 | 1 | - | - | hypothetical protein |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100001864" | - | - | - | - | CCO1785 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100002070" | - | - | - | - | CCO1786 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000420" | - | - | - | - | CCO1801 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000124" | - | - | - | - | CCOA_CcrnpB2 | - | | -1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | sRNA |
| "opCcV0100001087" | - | - | - | - | CCOA_CcrnpB3 | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | 0 | - | - | sRNA |
| "opCcV0100001665" | - | - | - | - | CCOA_CctmRNA2 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | - | - | sRNA |
| "opCcV0100001861" | - | - | - | - | CCOA0001 | - | 1 | 1 | 0 | -1 | 1 | 1 | 0 | 1 | -1 | 1 | - | - | replication protein |
| "opCcV0100000083" | - | - | - | - | CCOA0002 | - | 1 | 1 | 0 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000854" | - | - | - | - | CCOA0003 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001773" | - | - | - | - | CCOA0004 | - | 1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV0100001736" | - | - | - | - | CCOA0005 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV0100000493" | - | - | - | - | CCOA0006 | - | 1 | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | | - | - | conserved hypothetical protein |
| "opCcV0100000042" | - | - | - | - | CCOA0007 | - | | | 0 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000980" | - | - | - | - | CCOA0010 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | helicase, Snf2 family |
| "opCcV0100000134" | - | - | - | - | CCOA0011 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000200" | - | - | - | - | CCOA0012 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000902" | - | - | - | - | CCOA0013 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001913" | - | - | - | - | CCOA0016 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | 1 | - | - | TraH protein |
| "opCcV0100001144" | - | - | - | - | CCOA0017 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV0100000842" | - | - | - | - | CCOA0018 | - | 1 | 1 | 1 | 0 | -1 | 1 | 0 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100002059" | - | - | - | - | CCOA0019 | - | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001136" | - | - | - | - | CCOA0020 | - | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | - | - | 882aa long hypothetical purine NTPase, putative |
| "opCcV0100001603" | - | - | - | - | CCOA0021 | - | | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | DNA primase TraC |
| "opCcV0100000729" | - | - | - | - | CCOA0022 | - | | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | DNA primase, putative |
| "opCcV0100001108" | - | - | - | - | CCOA0023 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100001673" | - | - | - | - | CCOA0024 | - | | -1 | 0 | | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000619" | - | - | - | - | CCOA0025 | - | | | 1 | -1 | -1 | -1 | 1 | -1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 | - | - | - | - | CCOA0026 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | - | - | conserved hypothetical |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1721" | | | | | | | | | | | | | | | | | | | protein |
| "opCcV010000 1306" | - | - | - | - | CCOA0027 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 1844" | - | - | - | - | CCOA0028 | - | -1 | -1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0173" | - | - | - | - | CCOA0029 | - | | | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1116" | - | - | - | - | CCOA0030 | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 2023" | - | - | - | - | CCOA0031 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1560" | - | - | - | - | CCOA0032 | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 2082" | - | - | - | - | CCOA0033 | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0028" | - | - | - | - | CCOA0034 | - | | | 0 | | | | | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1968" | - | - | - | - | CCOA0035 | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1381" | - | - | - | - | CCOA0036 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0052" | - | - | - | - | CCOA0039 | - | | 1 | 1 | 1 | 1 | -1 | | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0466" | - | - | - | - | CCOA0046 | - | -1 | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0891" | - | - | - | - | CCOA0048 | - | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0012" | - | - | - | - | CCOA0049 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0224" | - | - | - | - | CCOA0050 | - | 1 | -1 | 1 | | -1 | 0 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0332" | - | - | - | - | CCOA0051 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 0 | - | - | conserved hypothetical protein |
| "opCcV010000 1725" | - | - | - | - | CCOA0052 | - | 1 | 1 | 1 | -1 | 1 | 0 | -1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV010000 1608" | - | - | - | - | CCOA0053 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0456" | - | - | - | - | CCOA0054 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0146" | - | - | - | - | CCOA0055 | - | 1 | 1 | 0 | 0 | | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 2055" | - | - | - | - | CCOA0057 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | DNA repair protein RAD50, putative |
| "opCcV010000 1777" | - | - | - | - | CCOA0058 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0712" | - | - | - | - | CCOA0059 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 2018" | - | - | - | - | CCOA0060 | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 0 | -1 | - | - | hypothetical protein |
| "opCcV010000 0880" | - | - | - | - | CCOA0061 | - | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 0 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1073" | - | - | - | - | CCOA0062 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0740" | - | - | - | - | CCOA0063 | - | 1 | -1 | 0 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | - | - | TnpY |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100001142" | - | - | - | - | CCOA0064 | - | 1 | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 0 | -1 | - | - | hypothetical protein |
| "opCcV0100001700" | - | - | - | - | CCOA0065 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | - | - | mobilization/transfer protein |
| "opCcV0100001662" | - | - | - | - | CCOA0066 | - | 1 | 0 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000366" | - | - | - | - | CCOA0067 | - | 1 | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | - | - | aminoglycoside 3'-phosphotransferase |
| "opCcV0100001497" | - | - | - | - | CCOA0068 | - | 1 | 1 | 0 | -1 | 1 | -1 | 0 | 1 | 0 | 1 | - | - | aminoglycoside 3'-phosphotransferase, |
| "opCcV0100000812" | - | - | - | - | CCOA0069 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | pyrrolidone-carboxylate peptidase |
| "opCcV0100001534" | - | - | - | - | CCOA0070 | - | 1 | 1 | -1 | -1 | -1 | 1 | 0 | 1 | 1 | -1 | - | - | hygromycin-B-phosphotransferase |
| "opCcV0100000960" | - | - | - | - | CCOA0071 | - | 1 | 1 | 1 | -1 | | -1 | -1 | -1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001317" | - | - | - | - | CCOA0072 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | -1 | 1 | - | - | TnpV |
| "opCcV0100001506" | - | - | - | - | CCOA0073 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | - | - | site-specific recombinase, resolvase family, |
| "opCcV0100001341" | - | - | - | - | CCOA0074 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000522" | - | - | - | - | CCOA0075 | - | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | 1 | 1 | - | - | transcriptional regulator, Cro/CI family |
| "opCcV0100000944" | - | - | - | - | CCOA0076 | - | 1 | 1 | 1 | -1 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000407" | - | - | - | - | CCOA0077 | - | 1 | 1 | 1 | 1 | -1 | 0 | -1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000685" | - | - | - | - | CCOA0078 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000016" | - | - | - | - | CCOA0079 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000543" | - | - | - | - | CCOA0080 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001312" | - | - | - | - | CCOA0081 | - | 1 | 0 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100001690" | - | - | - | - | CCOA0083 | - | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100001250" | - | - | - | - | CCOA0084 | - | 1 | 1 | 1 | -1 | -1 | 0 | 1 | 1 | -1 | 1 | - | - | Domain of unknown function (DUF332) superfamily |
| "opCcV0100000139" | - | - | - | - | CCOA0101 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100002042" | - | - | - | - | CCOA0102 | - | 0 | -1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | - | - | conserved hypothetical protein |
| "opCcV0100001766" | - | - | - | - | CCOA0103 | - | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | - | - | conserved hypothetical protein |
| "opCcV0100000705" | - | - | - | - | CCOA0104 | - | 1 | 1 | 1 | -1 | -1 | 0 | -1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100001289" | - | - | - | - | CCOA0105 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100002072" | - | - | - | - | CCOA0106 | - | 0 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000094" | - | - | - | - | CCOA0107 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |

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| "opCcV0100001675" | - | - | - | - | CCOA0108 | - | 1 | 1 | 0 | 1 | -1 | 0 | 1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100001626" | - | - | - | - | CCOA0109 | - | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000453" | - | - | - | - | CCOA0110 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001929" | - | - | - | - | CCOA0111 | - | 1 | 1 | 1 | -1 | 0 | -1 | 1 | -1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV0100002037" | - | - | - | - | CCOA0112 | - | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000811" | - | - | - | - | CCOA0113 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100000556" | - | - | - | - | CCOA0114 | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000251" | - | - | - | - | CCOA0115 | - | 1 | 1 | 1 | | -1 | 1 | 0 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100001717" | - | - | - | - | CCOA0116 | - | 1 | 1 | 1 | | -1 | 1 | -1 | 1 | 0 | -1 | - | - | hypothetical protein |
| "opCcV0100001258" | - | - | - | - | CCOA0117 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 0 | 0 | - | - | hypothetical protein |
| "opCcV0100001028" | - | - | - | - | CCOA0118 | - | 1 | 1 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000289" | - | - | - | - | CCOA0119 | - | 1 | 1 | 0 | 1 | -1 | 1 | 0 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001894" | - | - | - | - | CCOA0120 | - | 1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | - | - | hypothetical protein |
| "opCcV0100000073" | - | - | - | - | CCOA0121 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000906" | - | - | - | - | CCOA0122 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000799" | - | - | - | - | CCOA0123 | - | 1 | 1 | 1 | 1 | 0 | 1 | -1 | 1 | | 1 | - | - | hypothetical protein |
| "opCcV0100000283" | - | - | - | - | CCOA0124 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100001464" | - | - | - | - | CCOA0125 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV0100000189" | - | - | - | - | CCOA0126 | - | 1 | 1 | 0 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV0100000285" | - | - | - | - | CCOA0127 | - | 1 | 1 | -1 | -1 | 0 | -1 | 0 | -1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000270" | - | - | - | - | CCOA0128 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV0100001759" | - | - | - | - | CCOA0130 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100000641" | - | - | - | - | CCOA0131 | - | 1 | 0 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV0100001107" | - | - | - | - | CCOA0132 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001807" | - | - | - | - | CCOA0133 | - | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100001253" | - | - | - | - | CCOA0134 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV0100000724" | - | - | - | - | CCOA0135 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 | - | - | - | - | CCOA0136 | - | | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | lipoprotein, putative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0477" | | | | | | | | | | | | | | | | | | | |
| "opCcV010000 0468" | - | - | - | - | CCOA0137 | - | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0670" | - | - | - | - | CCOA0138 | - | 1 | 1 | 1 | 1 | -1 | -1 | 0 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0044" | - | - | - | - | CCOA0139 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | hcp protein |
| "opCcV010000 1716" | - | - | - | - | CCOA0140 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1906" | - | - | - | - | CCOA0142 | - | -1 | 1 | 1 | 1 | -1 | 0 | 1 | 1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0920" | - | - | - | - | CCOA0145 | - | 1 | 1 | 1 | 1 | | 0 | -1 | 1 | 1 | 1 | - | - | pseudogene |
| "opCcV010000 0347" | - | - | - | - | CCOA0146 | - | 1 | 1 | 1 | 1 | 0 | | -1 | 1 | 1 | 1 | - | - | ISCco1, transposase orfB |
| "opCcV010000 0938" | - | - | - | - | CCOA0147 | - | 1 | 1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | - | - | Fic family protein, putative |
| "opCcV010000 1282" | - | - | - | - | CCOA0148 | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | 0 | - | - | pseudogene |
| "opCcV010000 0502" | - | - | - | - | CCOA0149 | - | 1 | 1 | 0 | 1 | 1 | | -1 | 1 | 1 | 1 | - | - | ISCco1, transposase orfB |
| "opCcV010000 0442" | - | - | - | - | CCOA0151 | - | | | 0 | 1 | -1 | -1 | -1 | 1 | 1 | -1 | - | - | lipase family protein |
| "opCcV010000 0253" | - | - | - | - | CCOA0152 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0500" | - | - | - | - | CCOA0153 | - | 1 | 1 | 1 | 0 | -1 | -1 | 1 | 1 | 1 | 0 | - | - | hypothetical protein |
| "opCcV010000 1883" | - | - | - | - | CCOA0154 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0306" | - | - | - | - | CCOA0155 | - | 1 | 1 | 1 | 1 | -1 | 0 | -1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0892" | - | - | - | - | CCOA0156 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 0 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1354" | - | - | - | - | CCOA0157 | - | 1 | -1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 0 | - | - | conserved hypothetical protein |
| "opCcV010000 1811" | - | - | - | - | CCOA0158 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0322" | - | - | - | - | CCOA0159 | - | | -1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | - | - | DNA primase, putative |
| "opCcV010000 1892" | - | - | - | - | CCOA0160 | - | -1 | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | hypothetical protein |
| "opCcV010000 0646" | - | - | - | - | CCOA0161 | - | | | 0 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | - | - | DNA primase, putative |
| "opCcV010000 0935" | - | - | - | - | CCOA0162 | - | | -1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | DNA primase trac |
| "opCcV010000 0552" | - | - | - | - | CCOA0163 | - | | -1 | 1 | -1 | 0 | -1 | -1 | 1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1496" | - | - | - | - | CCOA0164 | - | | -1 | -1 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0772" | - | - | - | - | CCOA0165 | - | | | 1 | | -1 | 1 | -1 | 1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1485" | - | - | - | - | CCOA0167 | - | | | 1 | | | 1 | -1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 2017" | - | - | - | - | CCOA0168 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |

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| "opCcV010000 2056" | - | - | - | - | CCOA0169 | - | 1 | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1829" | - | - | - | - | CCOA0170 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 0 | - | - | hypothetical protein |
| "opCcV010000 1579" | - | - | - | - | CCOA0171 | - | 1 | 0 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0325" | - | - | - | - | CCOA0172 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | 1 | - | - | hypothetical protein |
| "opCcV010000 0449" | - | - | - | - | CCOA0173 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 1185" | - | - | - | - | CCOA0174 | - | 1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0097" | - | - | - | - | CCOA0175 | - | 1 | 0 | 0 | -1 | -1 | -1 | 0 | -1 | 1 | 0 | - | - | VapD-related protein |
| "opCcV010000 2075" | - | - | - | - | CCOA0176 | - | -1 | -1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | - | - | plasmid replication protein, putative |
| "opCcV010000 0102" | - | - | - | - | CCOA0177 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | - | - | site-specific recombinase, resolvase family |
| "opCcV010000 1361" | - | - | - | - | CCOA0178 | - | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | virulence-associated protein 2 |
| "opCcV010000 0271" | - | - | - | - | CCOA0179 | - | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | | -1 | - | - | hypothetical protein |
| "opCcV010000 1182" | - | - | - | - | CCOA0180 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | - | - | TraC protein |
| "opCcV010000 0528" | - | - | - | - | CCOA0181 | - | 1 | -1 | 1 | 1 | 0 | 0 | 0 | 1 | -1 | 0 | - | - | type IV secretion system protein VirB4 |
| "opCcV010000 1249" | - | - | - | - | CCOA0182 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | - | - | antirepressor, putative |
| "opCcV010000 0515" | - | - | - | - | CCOA0184 | - | | 1 | 0 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | single-strand binding protein, putative |
| "opCcV010000 0773" | - | - | - | - | CCOA0185 | - | 1 | 1 | 0 | -1 | 1 | -1 | -1 | 1 | 0 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 2012" | - | - | - | - | CCOA0186 | - | 0 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | type IV secretion system protein, putative |
| "opCcV010000 1201" | - | - | - | - | CCOA0187 | - | 1 | 1 | 0 | 0 | -1 | -1 | -1 | 1 | 1 | -1 | - | - | TrbL/VirB6 plasmid conjugal transfer protein |
| "opCcV010000 1056" | - | - | - | - | CCOA0188 | - | 1 | 1 | 0 | -1 | -1 | 1 | 0 | -1 | 1 | -1 | - | - | lipoprotein, putative |
| "opCcV010000 0925" | - | - | - | - | CCOA0189 | - | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | 1 | - | - | type IV secretion system protein VirB8, |
| "opCcV010000 2034" | - | - | - | - | CCOA0190 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 0 | - | - | type IV secretion system protein VirB9 |
| "opCcV010000 1206" | - | - | - | - | CCOA0191 | - | 1 | 1 | 1 | -1 | 1 | -1 | 0 | 1 | -1 | 1 | - | - | type IV secretion system protein VirB10, |
| "opCcV010000 1020" | - | - | - | - | CCOA0192 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | - | - | type IV secretion system protein VirB11 |
| "opCcV010000 1962" | - | - | - | - | CCOA0193 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | 1 | - | - | cag pathogenicity island protein (cag5), |
| "opCcV010000 0388" | - | - | - | - | CCOA0194 | - | 1 | 1 | -1 | -1 | 1 | 0 | 1 | 1 | 1 | 1 | - | - | cag island protein, putative |
| "opCcV010000 0537" | - | - | - | - | CCOA0195 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | YggA-like protein |
| "opCcV010000 1638" | - | - | - | - | CCOA0196 | - | 1 | 1 | 1 | 1 | 0 | -1 | 0 | 1 | -1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 | - | - | - | - | CCOA0197 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | hypothetical protein |

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| 0099" | | | | | | | | | | | | | | | | | | | |
| "opCcV010000 1852" | - | - | - | - | CCOA0198 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | - | - | hypothetical protein |
| "opCcV010000 1613" | - | - | - | - | CCOA0199 | - | 1 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | DNA topoisomerase III |
| "opCcV010000 0185" | - | - | - | - | CCOA0200 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | hypothetical protein |
| "opCcV010000 1723" | - | - | - | - | CCOA0201 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 0 | 0 | - | - | conserved hypothetical protein |
| "opCcV010000 0363" | - | - | - | - | CCOA0203 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | - | - | ISCco1, transposase orfA |
| "opCcV010000 0605" | - | - | - | - | CCOA0204 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0119" | - | - | - | - | CCOA0205 | - | | 1 | 0 | 0 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | conserved hypothetical protein |
| "opCcV010000 0667" | - | - | - | - | CCOA0206 | tetO | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 0 | -1 | - | - | tetracycline resistance protein |
| "opCcV010000 0942" | - | - | - | - | CCOA0207 | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | - | - | conserved hypothetical protein |
| "opCcV010000 0952" | - | - | - | - | CCOA0208 | - | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 1706" | - | - | - | - | p3384_01 | mob | 1 | 1 | 1 | | -1 | | -1 | 1 | 1 | -1 | - | - | mob |
| "opCcV010000 1047" | - | - | - | - | p3384_02 | repA | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | - | - | repA |
| "opCcV010000 0254" | - | - | - | - | p3384_03 | repB | 1 | 1 | 0 | 1 | -1 | 1 | 0 | -1 | 1 | -1 | - | - | repB |
| "opCcV010000 1624" | - | - | - | - | p3386_01 | - | 0 | -1 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | - | - | hypothetical protein |
| "opCcV010000 1751" | - | - | - | - | p3386_02 | - | 1 | 0 | 0 | 1 | -1 | 1 | 0 | 1 | 1 | 1 | - | - | putative Rep |
| "opCcV010000 1221" | - | - | - | - | p3386_03 | - | -1 | -1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | - | - | hypothetical protein |
| "opCcV010000 0229" | - | - | - | - | pCC31p01 | - | 1 | 0 | 1 | -1 | -1 | -1 | 1 | 1 | -1 | -1 | - | - | teto |
| "opCcV010000 1062" | - | - | - | - | pCC31p02 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | cpp2 |
| "opCcV010000 1209" | - | - | - | - | pCC31p03 | - | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | - | - | cpp3 |
| "opCcV010000 1902" | - | - | - | - | pCC31p04 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | 0 | - | - | cpp4 |
| "opCcV010000 2004" | - | - | - | - | pCC31p05 | - | 0 | -1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | - | - | repa |
| "opCcV010000 0353" | - | - | - | - | pCC31p06 | - | 1 | 0 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | cpp6 |
| "opCcV010000 1022" | - | - | - | - | pCC31p07 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | cpp7 |
| "opCcV010000 1878" | - | - | - | - | pCC31p08 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | - | - | cpp8 |
| "opCcV010000 0179" | - | - | - | - | pCC31p09 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | - | - | cpp9 |
| "opCcV010000 0034" | - | - | - | - | pCC31p10 | - | | -1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | - | - | cpp10 |
| "opCcV010000 2067" | - | - | - | - | pCC31p12 | - | -1 | 1 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | - | - | cpp12 |

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| "opCcV0100001321" | - | - | - | - | pCC31p13 | - | -1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | - | - | cpp13 |
| "opCcV0100002080" | - | - | - | - | pCC31p14 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | cpp14 |
| "opCcV0100001336" | - | - | - | - | pCC31p15 | - | 1 | 0 | 0 | -1 | -1 | 0 | -1 | 1 | 0 | 1 | - | - | cpp15 |
| "opCcV0100000825" | - | - | - | - | pCC31p16 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | -1 | - | - | cpp16 |
| "opCcV0100001960" | - | - | - | - | pCC31p17 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | cpp17 |
| "opCcV0100001732" | - | - | - | - | pCC31p18 | - | 1 | 1 | 1 | 1 | -1 | | | 0 | 1 | -1 | - | - | cpp18 |
| "opCcV0100001909" | - | - | - | - | pCC31p19 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | cpp19 |
| "opCcV0100002068" | - | - | - | - | pCC31p21 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | - | - | cpp22 |
| "opCcV0100000675" | - | - | - | - | pCC31p22 | - | | | 0 | | | 1 | 1 | 1 | | -1 | - | - | cpp23 |
| "opCcV0100001373" | - | - | - | - | pCC31p23 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | cpp24 |
| "opCcV0100001757" | - | - | - | - | pCC31p24 | - | | 0 | 1 | | -1 | | -1 | 1 | -1 | -1 | - | - | cpp25 |
| "opCcV0100000985" | - | - | - | - | pCC31p25 | - | 1 | 1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | 0 | - | - | cpp26 |
| "opCcV0100002035" | - | - | - | - | pCC31p26 | - | 1 | 0 | 1 | 1 | -1 | 1 | -1 | 0 | 1 | 1 | - | - | cpp27 |
| "opCcV0100001362" | - | - | - | - | pCC31p27 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | vapd |
| "opCcV0100001318" | - | - | - | - | pCC31p28 | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 0 | - | - | cpp29 |
| "opCcV0100001969" | - | - | - | - | pCC31p29 | - | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | - | cmgb2 |
| "opCcV0100001153" | - | - | - | - | pCC31p30 | - | 1 | 1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | cmgb3/4 |
| "opCcV0100001760" | - | - | - | - | pCC31p31 | - | 1 | 1 | 0 | -1 | 0 | 1 | -1 | 1 | 1 | 1 | - | - | cpp32 |
| "opCcV0100000972" | - | - | - | - | pCC31p32 | - | 1 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | 1 | -1 | - | - | cpp33 |
| "opCcV0100000194" | - | - | - | - | pCC31p33 | - | 1 | 1 | 1 | | 0 | -1 | 1 | 1 | 1 | 1 | - | - | ssb1 |
| "opCcV0100001287" | - | - | - | - | pCC31p34 | - | 1 | 1 | 0 | -1 | -1 | 1 | 1 | | 1 | -1 | - | - | cpp35 |
| "opCcV0100001463" | - | - | - | - | pCC31p35 | - | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | -1 | 1 | - | - | cmgb5 |
| "opCcV0100001487" | - | - | - | - | pCC31p36 | - | 1 | 1 | 0 | 1 | | 0 | -1 | 1 | 1 | 1 | - | - | cmgb6 |
| "opCcV0100000790" | - | - | - | - | pCC31p38 | - | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | -1 | 1 | - | - | cmgb8 |
| "opCcV0100002021" | - | - | - | - | pCC31p39 | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 0 | 1 | 1 | - | - | cmgb9 |
| "opCcV0100002005" | - | - | - | - | pCC31p40 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | cmgb10 |
| "opCcV0100000177" | - | - | - | - | pCC31p41 | - | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | cmgb11 |
| "opCcV010000 | - | - | - | - | pCC31p42 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | cmgd4 |

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| "opCcV0100000524" | - | - | - | - | pCC31p43 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | 1 | 1 | - | - | cpp44 |
| "opCcV0100000026" | - | - | - | - | pCC31p44 | - | 1 | 1 | 1 | -1 | -1 | 0 | -1 | 1 | 1 | 1 | - | - | cpp45 |
| "opCcV0100000421" | - | - | - | - | pCC31p45 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | - | cpp46 |
| "opCcV0100000761" | - | - | - | - | pCC31p46 | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | -1 | 0 | - | - | cpp47 |
| "opCcV0100001366" | - | - | - | - | pCC31p47 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | - | - | cpp48 |
| "opCcV0100001779" | - | - | - | - | pCC31p48 | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | 1 | - | - | cpp49 |
| "opCcV0100000546" | - | - | - | - | pCC31p49 | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | - | - | cpp50 |
| "opCcV0100001347" | - | - | - | - | pCC31p50 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | - | cpp51 |
| "opCjjV010000019" | - | - | pTet_02 | - | - | - | 1 | 1 | -1 | 1 | -1 | 1 | 0 | 0 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000037" | - | - | pTet_03 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000112" | - | - | pTet_04 | - | - | - | 1 | 1 | 1 | 0 | -1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000194" | - | - | pTet_05 | - | - | - | 1 | 1 | 0 | | -1 | 1 | -1 | 1 | -1 | -1 | hypothetical protein | - | - |
| "opCjjV010000183" | - | - | pTet_06 | - | - | - | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000090" | - | - | pTet_07 | - | - | - | | | 1 | | -1 | 1 | | -1 | | -1 | hypothetical protein | - | - |
| "opCjjV010000199" | - | - | pTet_08 | - | - | - | | -1 | 0 | -1 | 1 | -1 | -1 | 1 | -1 | -1 | hypothetical protein | - | - |
| "opCjjV010000096" | - | - | pTet_09 | - | - | - | | | 0 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000054" | - | - | pTet_10 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000139" | - | - | pTet_11 | - | - | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000107" | - | - | pTet_12 | - | - | - | 1 | 1 | 1 | -1 | -1 | 1 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000116" | - | - | pTet_13 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | 0 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000048" | - | - | pTet_14 | - | - | - | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000173" | - | - | pTet_15 | - | - | - | 1 | 1 | 1 | 1 | -1 | 0 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000148" | - | - | pTet_16 | - | - | - | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000150" | - | - | pTet_17 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000114" | - | - | pTet_18 | - | - | - | 1 | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000002" | - | - | pTet_19 | - | - | - | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000059" | - | - | pTet_20 | - | - | - | 1 | 1 | -1 | -1 | 0 | 1 | 1 | 1 | 1 | -1 | hypothetical protein | - | - |

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| "opCjjV010000 053" | - | - | pTet_21 | - | - | - | | | 1 | -1 | | | -1 | 1 | | | hypothetical protein | - | - |
| "opCjjV010000 043" | - | - | pTet_22 | - | - | - | 1 | 1 | 1 | -1 | 0 | 1 | -1 | -1 | 0 | -1 | hypothetical protein | - | - |
| "opCjjV010000 069" | - | - | pTet_23 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 029" | - | - | pTet_24 | - | - | - | 1 | 1 | 0 | -1 | 1 | 1 | -1 | 1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 202" | - | - | pTet_25 | - | - | - | 1 | - | 0 | 1 | 1 | -1 | 0 | 1 | 1 | 0 | hypothetical protein | - | - |
| "opCjjV010000 063" | - | - | pTet_26 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | | 0 | hypothetical protein | - | - |
| "opCjjV010000 178" | - | - | pTet_27 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 129" | - | - | pTet_28 | - | - | - | 1 | 1 | 0 | | -1 | 0 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 153" | - | - | pTet_29 | - | - | - | 1 | 1 | | 1 | -1 | 0 | 1 | -1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 111" | - | - | pTet_30 | - | - | - | 1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 056" | - | - | pTet_31 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 106" | - | - | pTet_32 | - | - | - | 1 | -1 | 1 | 0 | 1 | -1 | -1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 190" | - | - | pTet_33 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 140" | - | - | pTet_34 | - | - | - | 0 | -1 | 1 | -1 | 1 | 1 | 0 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 042" | - | - | pTet_35 | - | - | - | 1 | 1 | 1 | 0 | -1 | 1 | 0 | 1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 145" | - | - | pTet_36 | - | - | - | 1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 185" | - | - | pTet_37 | - | - | - | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 015" | - | - | pTet_38 | - | - | - | 1 | 1 | 1 | 1 | 1 | 0 | -1 | 1 | -1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 149" | - | - | pTet_39 | - | - | - | 1 | 1 | 1 | -1 | 1 | 1 | 0 | 1 | 1 | 1 | hypothetical protein | - | - |
| "opCjjV010000 077" | - | - | pTet_40 | - | - | - | 1 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 118" | - | - | pTet_41 | - | - | - | 1 | 0 | 1 | -1 | 1 | -1 | -1 | 1 | | 1 | hypothetical protein | - | - |
| "opCjjV010000 057" | - | - | pTet_42 | - | - | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | -1 | 1 | -1 | hypothetical protein | - | - |
| "opCjjV010000 012" | - | - | pTet_43 | - | - | - | | | 1 | -1 | | 1 | 1 | 1 | 1 | | hypothetical protein | - | - |
| "opCjjV010000 097" | - | - | pTet_44 | - | - | - | | | 1 | | -1 | | | 1 | 1 | | hypothetical protein | - | - |
| "opCcV010000 0864" | CJE_Cj16S A | rrsA | Cjr01 | - | CCO_Cc16 SB | rrsB | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 16S ribosomal RNA | 16S ribosomal RNA | 16S ribosomal RNA |
| "opCcV010000 0237" | CJE_Cj23S A | rrlA | Cjr05 | - | CCO_Cc23 SB | rrlB | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 23S ribosomal RNA | 23S ribosomal RNA | 23S ribosomal RNA |
| "opCjV010000 1047" | CJE_Cjrnp B1 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | sRNA | - |
| "opCjjV010000 | CJE_Cjtm | - | Cjs01 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tmRNA | sRNA | - |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 026" | RNA1 | | | | | | | | | | | | | | | | | | |
| "opCcV0100000497" | CJE_tRNA-Ala-1 | - | - | - | CCO_tRNA-Ala-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Ala | tRNA-Ala |
| "opCjV0100000055" | CJE_tRNA-Ala-4 | - | - | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Ala | - |
| "opCcV0100001071" | CJE_tRNA-Arg-1 | - | - | - | CCO_tRNA-Arg-1 | - | -1 | 0 | -1 | 1 | 1 | 0 | -1 | 1 | 0 | 1 | - | tRNA-Arg | tRNA-Arg |
| "opCcV0100000019" | CJE_tRNA-Arg-3 | - | - | - | CCO_tRNA-Arg-3 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Arg | tRNA-Arg |
| "opCcV0100000101" | CJE_tRNA-Arg-4 | - | Cjt3 | - | CCO_tRNA-Arg-4 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA-Arg | tRNA-Arg | tRNA-Arg |
| "opCcV0100001196" | CJE_tRNA-Arg-5 | - | Cjt4 | - | CCO_tRNA-Arg-5 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA-Arg | tRNA-Arg | tRNA-Arg |
| "opCcV0100000195" | CJE_tRNA-Asn-1 | - | - | - | CCO_tRNA-Asn-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Asn | tRNA-Asn |
| "opCcV0100001356" | CJE_tRNA-Asp-1 | - | Cjt2 | - | CCO_tRNA-Asp-1 | - | 1 | -1 | 0 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | tRNA-Asp | tRNA-Asp | tRNA-Asp |
| "opCcV0100000079" | CJE_tRNA-Cys-1 | - | - | - | CCO_tRNA-Cys-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Cys | tRNA-Cys |
| "opCcV0100000222" | CJE_tRNA-Gln-1 | - | - | - | CCO_tRNA-Gln-1 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Gln | tRNA-Gln |
| "opCcV0100000336" | CJE_tRNA-Glu-1 | - | - | - | CCO_tRNA-Glu-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Glu | tRNA-Glu |
| "opCcV0100001543" | CJE_tRNA-Gly-1 | - | - | - | CCO_tRNA-Gly-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Gly | tRNA-Gly |
| "opCcV0100000428" | CJE_tRNA-Gly-3 | - | - | - | CCO_tRNA-Gly-3 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Gly | tRNA-Gly |
| "opCcV0100001173" | CJE_tRNA-His-1 | - | - | - | CCO_tRNA-His-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-His | tRNA-His |
| "opCcV0100001786" | CJE_tRNA-Ile-1 | - | - | - | CCO_tRNA-Ile-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Ile | tRNA-Ile |
| "opCcV0100001686" | CJE_tRNA-Leu-1 | - | - | - | CCO_tRNA-Leu-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Leu | tRNA-Leu |
| "opCcV0100001080" | CJE_tRNA-Leu-2 | - | Cjt01 | - | CCO_tRNA-Leu-2 | - | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA-Leu | tRNA-Leu | tRNA-Leu |
| "opCcV0100001893" | CJE_tRNA-Leu-3 | - | - | - | CCO_tRNA-Leu-3 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Leu | tRNA-Leu |
| "opCcV0100000918" | CJE_tRNA-Leu-4 | - | Cjt05 | - | CCO_tRNA-Leu-4 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA-Leu | tRNA-Leu | tRNA-Leu |
| "opCcV0100000151" | CJE_tRNA-Lys-1 | - | - | - | CCO_tRNA-Lys-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Lys | tRNA-Lys |
| "opCcV0100001079" | CJE_tRNA-Met-1 | - | - | - | CCO_tRNA-Met-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Met | tRNA-Met |
| "opCcV0100001981" | CJE_tRNA-Met-2 | - | - | - | CCO_tRNA-Met-2 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | - | tRNA-Met | tRNA-Met |
| "opCcV0100000391" | CJE_tRNA-Met-3 | - | - | - | CCO_tRNA-Met-3 | - | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Met | tRNA-Met |
| "opCcV0100000776" | CJE_tRNA-Phe-1 | - | - | - | CCO_tRNA-Phe-1 | - | 0 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Phe | tRNA-Phe |
| "opCcV0100000458" | CJE_tRNA-Pro-1 | - | - | - | CCO_tRNA-Pro-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Pro | tRNA-Pro |
| "opCcV0100000055" | CJE_tRNA-SeC-1 | - | - | - | CCO_tRNA-SeC-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-SeC | tRNA-SeC |
| "opCcV0100000787" | CJE_tRNA-Ser-1 | - | - | - | CCO_tRNA-Ser-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Ser | tRNA-Ser |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| "opCcV0100001380" | CJE_tRNA-Ser-2 | - | - | - | CCO_tRNA-Ser-2 | - | | 0 | 0 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | - | tRNA-Ser | tRNA-Ser |
| "opCcV0100001987" | CJE_tRNA-Ser-3 | - | Cjt06 | - | CCO_tRNA-Ser-3 | - | | -1 | -1 | | -1 | -1 | -1 | 1 | 1 | -1 | tRNA-Ser | tRNA-Ser | tRNA-Ser |
| "opCcV0100001276" | CJE_tRNA-Thr-1 | - | - | - | CCO_tRNA-Thr-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Thr | tRNA-Thr |
| "opCjjV010000157" | CJE_tRNA-Thr-2 | - | Cjt1 | - | - | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | tRNA-Thr | tRNA-Thr | - |
| "opCcV0100001423" | CJE_tRNA-Trp-1 | - | - | - | CCO_tRNA-Trp-1 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Trp | tRNA-Trp |
| "opCcV0100001928" | CJE_tRNA-Tyr-1 | - | - | - | CCO_tRNA-Tyr-1 | - | 1 | 0 | 1 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | - | tRNA-Tyr | tRNA-Tyr |
| "opCcV0100001203" | CJE_tRNA-Val-1 | - | - | - | CCO_tRNA-Val-1 | - | -1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Val | tRNA-Val |
| "opCcV0100000443" | CJE_tRNA-Val-3 | - | - | - | CCO_tRNA-Val-3 | - | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | - | tRNA-Val | tRNA-Val |

1=present; -1=absent/highly divergent; 0=slightly divergent

| | |
|---|---|
| 🟩 | Lipooligosaccharide region |
| 🟥 | Flagellar modification region |
| 🟧 | Capsule region in *C. jejuni* RM1221 |
| ⬜ | *C. jejuni* NCTC11168 specific capsule genes |

Supplementary table 4: Genes present and highly divergent/absent in the hyperinvasive and low invasive *C. jejuni*.

| **Gene name/number** | | | **Hyperinvasive *C. jejuni*** | | | | | | **Low-invasive *C. jejuni*** | | | | **Role/function** | | | **COG functional grouping** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **GROUP 3: Genes present in all low-invasive *C. jejuni* and absent/highly divergent form five of six hyperinvasive *C. jejuni*** | | | **01_10** | **01_35** | **01_04** | **01_41** | **01_51** | **EX114** | **01_30** | **01_32** | **01_46** | **01_39** | ***C. jejuni* NCTC11168** | ***C. jejuni* RM1221** | ***C. coli* RM2228** | Fouts *et al*., 2005 |
| ***C. jejuni* NCTC 11168** | ***C. jejuni* RM1221** | ***C. coli* RM2228** | | | | | | | | | | | | | | |
| *accA*(Cj0443) | *accA*(CJE0495) | *accA*(CCO0532) | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | acetyl-coenzyme A carboxylase carboxyl | acetyl-CoA carboxylase alpha subunit | acetyl-CoA carboxylase, carboxyl transferase, | Lipid transport and metabolism |
| Cj0911 | CJE0989 | CCO1012 | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | putative periplasmic protein | SCO1/SenC family protein | probable periplasmic protein Cj0911 | General function prediction only |
| …….. | ……. | CCOA0043 | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | 1 | ….. | hypothetical protein | hypothetical protein | Hypothetical |
| Cj1720 | CJE1890 | CCO0019 | -1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | hypothetical protein | hypothetical protein | conserved hypothetical protein | Hypothetical |
| **GROUP 4: Genes absent/highly divergent in all low-invasive *C. jejuni* and present in five of six hypeinvasive *C. jejuni*** | | | | | | | | | | | | | | | | |
| *infB*(Cj0136) | *infB*(CJE0131) | *infB*(CCO1743) | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | -1 | translation initiation factor IF-2 | translation initiation factor IF-2 | translation initiation factor IF-2 | Translation |
| Cj0380c | ….. | ….. | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | -1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein | Hypothetical |
| Cjp21 | ….. | ….. | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | -1 | -1 | hypothetical protein | …… | ….. | Hypothetical |
| **GROUP 5: Genes present in five of six hyperinvasive *C. jejuni* and absent/highly divergent in three of four low invasive *C. jejuni*** | | | | | | | | | | | | | | | | |
| Cj1002c | *sixA*(CJE1082) | *sixA*(CCO1064) | -1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | conserved hypothetical protein | phosphohistidine phosphatase SixA | phosphohistidine phosphatase SixA, putative | Signal transduction mechanism |
| Cj1176c | CJE1310 | CCO1245 | 1 | -1 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | -1 | hypothetical protein | twin-arginine translocation protein, TatA/E | Sec-independent protein translocase protein | Intracellular trafficking and secretion |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cj1343c | *ctsG*(CJE1532 ) | *ctsG*(CCO1449) | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative periplasmic protein | transformation system protein | transformation system protein | Cell wall/membrane biogenesis |
| Cj1287c | CJE1479 | *maeB* (CCO1392) | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | malate oxidoreductase | NADP-dependent malic enzyme, truncation | malic enzyme | Energy production and conversion |
| Cj1476c | CJE1649 | CCO1582 | 1 | -1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | pyruvate-flavodoxin oxidoreductase | pyruvate ferredoxin/flavodoxin oxidoreductase | pyruvate ferredoxin/flavodoxin oxidoreductase | Energy production and conversion |
| Cj0544 | CJE0648 | CCO0641 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative integral membrane protein | hypothetical protein | probable integral memnbrane protein Cj0544 | Cell wall/membrane biogenesis |
| Cj0943 | *lolA*(CJE1021) | CCO0952 | 1 | 1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | putative periplasmic protein | outer-membrane lipoprotein carrier protein | probable periplasmic protein Cj0943 | Cell wall/membrane biogenesis |
| …….. | …….. | CCO1326 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | …… | ….. | hypothetical protein | Hypothetical |
| Cj0717 | CJE0817 | CCO0783 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | hypothetical protein | *arsC* family protein | Arsenic resistance |
| ….. | ….. | CCOA0113 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | 1 | ….. | ….. | hypothetical protein | Hypothetical |
| Cj0151c | CJE0147 | CCO1726 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | putative periplasmic protein | hypothetical protein | probable periplasmic protein Cj0151c | Hypothetical |
| *pyrC2*(Cj1195c ) | CJE1329 | CCO1265 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | 1 | -1 | -1 | putative dihydroorotase | dihydroorotase | dihydroorotase, putative | Nucleotide transport and metabolism |
| Cjp17 | ….. | ….. | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | ….. | ….. | Hypothetical |
| *sucD*(Cj0534) | *sucD*(CJE0638) | *sucD*(CCO0631) | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | succinyl-coA synthetase alpha chain | succinyl-CoA synthase, alpha subunit | SucD | Energy production and conversion |
| Cjp30 | ….. | ….. | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | hypothetical protein | ….. | ….. | Hypothetical |
| Cjp39 | ….. | ….. | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | 1 | hypothetical protein | ….. | ….. | Hypothetical |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cj0581 | *nidH* (CJE0684) | *mutT* (CCO1375) | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | putative NTPase | dinucleoside polyphosphate hydrolase | (di)nucleoside polyphosphate hydrolase | General function prediction only |
| *cfrA*(Cj0755) | *cfrA*(CJE0847) | CCO0810 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | putative iron uptake protein | ferric receptor CfrA | ferric receptor CfrA | Inorganic iron transport and metabolism |
| Cj1553c*"hsdM "* | ….. | ….. | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | putative type I restriction enzyme M protein | ….. | ….. | Defense mechanisms |
| ….. | ….. | CCO1531 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | …… | ….. | UDP-glucose 4-epimerase, putative | Amino acid transport and metabolism |
| ….. | ….. | CCO0231 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | …… | ….. | hypothetical protein | Hypothetical |
| ….. | ….. | *cysQ* in RM2228 only | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | 1 | -1 | …… | ….. | 3'(2'),5'-bisphosphate nucleotidase | …… |
| ….. | ….. | CCO1688 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | ….. | ….. | hypothetical protein | Hypothetical |
| ….. | ….. | CCOA0017 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | ….. | ….. | hypothetical protein | Hypothetical |
| ….. | ….. | CCOA0026 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | ….. | ….. | conserved hypothetical protein | Hypothetical |
| ….. | ….. | CCO1269 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | 1 | ….. | ….. | TraH protein, Conjugative relaxosome accessory transposon protein | …… |
| *fliE*(Cj0526c) | *fliE*(CJE0630) | *fliE*(CCO0623) | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | putative flagellar hook-basal body complex | flagellar basal body protein | flagellar hook-basal body complex protein | Cell motility/Intracellular trafficking and secretion |
| | CJE1333 | CCO1269 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | -1 | -1 | -1 | putative iron/ascorbate-dependent | oxidoreductase, 2OG-Fe(II) oxygenase family | oxidoreductase, 2OG-Fe(II) oxygenase family | General function prediction only |
| pTet_33 | | | 1 | 1 | 1 | 1 | -1 | 1 | -1 | 1 | -1 | -1 | hypothetical protein | ….. | ….. | Hypothetical |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *tsf*(Cj1181c) | *tsf*(CJE1315) | *tsf* (CCO1250) | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | elongation factor TS | elongation factor Ts | translation elongation factor Ts | Translation |
| Cj0182 | CJE0175 | CCO1695 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | transmembrane transport protein | antibiotic transport protein, putative | transmembrane transport protein Cj0182 | Lipid transport and metabolism |
| Cj0605 | CJE0708 | CCO0688 | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | putative amidohydrolase | carboxypeptidase | peptidase, M20/M25/M40 family | General function prediction only |
| Cj0111 | CJE0106 | CCO1770 | 1 | 1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 | -1 | periplasmic protein | TonB domain protein | periplasmic protein Cj0111 | Transport and binding protein |
| *nusB*(Cj0382c) | *nusB*(CJE0431) | *nusB*(CCO0471) | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | transcription termination protein | transcription antitermination protein NusB | transcription antitermination factor NusB | Transcription |
| *selD*(Cj1504c) | *selD*(CJE1677) | *selD*(CCO1613) | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | putative selenide,water dikinase | selenide, water dikinase | selenide, water dikinase | Translation |
| *ceuB*(Cj1352) | *ceuB*(CJE1541) | *ceuB*(CCO1458) | 1 | 1 | 1 | 1 | 1 | -1 | -1 | 1 | -1 | -1 | enterochelin uptake permease | enterochelin ABC transporter, permease protein | enterochelin ABC transporter, permease protein | Inorganic iron transport and metabolism |
| **GROUP 6: Genes absent/highly divergent in five of six hyperinvasive *C. jejuni* and present in three of four low invasive *C. jejuni*** | | | | | | | | | | | | | | | | |
| Cj1021c | CJE1165 | CCO1088 | 1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | putative periplasmic protein | porin domain protein | probable periplasmic protein Cj1021c-related | Cell wall/membrane biogenesis |
| Cj0102 | CJE0097 | CCO1779 | 1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | -1 | 1 | ATP synthase F0 sector B' subunit | ATP synthase subunit B | ATP synthase F0, subunit b' (atpF'), putative | Energy production and conversion |
| *ispA*(Cj1644) | *ispA*(CJE1816) | *ispA*(CCO0170) | 1 | -1 | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | geranyltranstransferase | geranyltranstransferase | geranyltranstransferase (*ispA*) | Coenzyme transport and metabolism |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cj1247c | CJE1383 | CCO1337 | -1 | 1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein | Hypothetical |
| …….. | ………. | CCOA0028 | -1 | -1 | 1 | -1 | -1 | -1 | 1 | 1 | 1 | -1 | ….. | ….. | hypothetical protein | Hypothetical |
| Cj0208 | CJE0328 | CCO0358 | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | 1 | -1 | hypothetical protein | hypothetical protein | conserved hypothetical protein | Hypothetical |
| *purN*(Cj0187c) | *purN*(CJE0180) | *purN*(CCO1687) | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | phosphoribosyl glycinamide formyltransferase | phosphoribosylglycinamide formyltransferase | phosphoribosyl glycinamide formyltransferase | Nucleotide transport and metabolism |
| Cj0974 | CJE1055 | ….. | -1 | -1 | -1 | -1 | 1 | -1 | 1 | 1 | -1 | 1 | hypothetical protein | hypothetical protein | …… | Hypothetical |
| Cj0997 | *gidB*(CJE1077) | *gidB*(CCO1059) | -1 | -1 | -1 | -1 | -1 | 1 | 1 | 1 | 1 | -1 | *gidB* homolog | methyltransferase GidB | methyltransferase GidB | Cell wall/membrane biogenesis |

1=present;-1=absent/highly divergent

Supplementary table 5: *C. jejuni* 01/10 prophage 1 and 2 genes, ORFs with best match in campylobacters other than *C. jejuni* RM1221 and LOS biosynthesis loci identified by BLASTx annotation tool.

| **Gene homolog/ortholog** | **Annotated function** |
|---|---|
| **Prophage** | |
| CJJ81176_1532 | putative homolog of BLC protein [*Campylobacter jejuni* subsp. *jejuni* 81-176] |
| | replication-associated A domain protein [*Vibrio cholerae* HE39] |
| MOY_16467 | hypothetical protein [*Halomonas* strain GFAJ-1] |
| MOY_16472 | hypothetical protein [*Halomonas* strain GFAJ-1] |
| MOY_16477 | hypothetical protein [*Halomonas* strain GFAJ-1] |
| MOY_16482 | hypothetical protein, partial [*Halomonas* strain GFAJ-1] |
| CJJ81176_1534 | type I restriction-modification enzyme, R subunit [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| **Other genes** | |
| conserved hypothetical protein | *Campylobacter jejuni* subsp. *jejuni* CF93-6 |
| conserved hypothetical protein | *Campylobacter jejuni* subsp. *jejuni* CF93-6 |
| CJSA_0241 | molybdopterin containing oxidoreductase in [ *Campylobacter jejuni* subsp. *jejuni* IA3902] |
| Cj0264c | molybdopterin containing oxidoreductase [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cj1679 | hypothetical protein in *C. jejuni* NCTC 11168 |
| ICDCCJ07001_615 | K+-transporting ATPase, B subunit [ *Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001]. Two component system |

| | |
|---|---|
| Cj0736 | hypothetical protein [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| CJ1055c | sulfatase family protein [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| CJSA_1363 | putative sugar transferase [ *Campylobacter jejuni* subsp. *jejuni* IA3902] |
| CJSA_1352 | putative sugar transferase [ *Campylobacter jejuni* subsp. *jejuni* IA3902] |
| ICDCCJ07001_1325 | cryptic C4-dicarboxylate transporter DcuD [ *Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| Cj0628 | lipoprotein [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cj1137c | glycosyltransferase [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cj1136 | Cj1136 in *C. jejuni* NCTC1168 except 2 nucleotide bases mismatch in the beginning atgaaaaccgt in 01/51 and atgaaaaaagt in NCTC11168 |
| Cj1324 | hypothetical protein [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cj1323 | hypothetical protein [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cj1321 | transferase [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| | putative glysosyltransferase *Campylobacter jejuni* subsp. *jejuni* 87330 |
| CJJ81176_1534 | type I restriction-modification enzyme, R subunit [ *Campylobacter jejuni* subsp. *jejuni* 81-176] |
| CJJ81176_1534 | type I restriction-modification enzyme, R subunit [ *Campylobacter jejuni* subsp. *jejuni* 81-176] |
| CJJ81176_1536 | hypothetical protein in  [ *Campylobacter jejuni* subsp. *jejuni* 81-176] |
| Cj1552c | *mloB* hypothetical protein [ *Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| CJJ81176_1539 | type I restriction-modification system, M subunit [ *Campylobacter jejuni* subsp. *jejuni* 81-176] |

<table>
<tr><td>CJE1600_KpsS</td><td colspan="2"><i>kpsS</i> capsule polysaccharide export protein KpsS [ <i>Campylobacter jejuni</i> RM1221]</td></tr>
<tr><td>CJE1601_KpsC</td><td colspan="2"><i>kpsC</i> capsule polysaccharide export protein KpsC [ <i>Campylobacter jejuni</i> RM1221]</td></tr>
<tr><td>CJSA_1346</td><td colspan="2"><i>cysC</i> adenylylsulfate kinase [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> IA3902]</td></tr>
<tr><td>JJD26997_1749</td><td colspan="2">putative sugar-1-phosphate nucleotidyltransferase [ <i>Campylobacter jejuni</i> subsp. <i>doylei</i> 269.97]</td></tr>
<tr><td>CJJ81176_1416</td><td colspan="2">class I glutamine amidotransferase, putative [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 81-176]</td></tr>
<tr><td>Cj1418c</td><td colspan="2">hypothetical protein [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168]</td></tr>
<tr><td>Cj1419c</td><td colspan="2">methyltransferase [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168]</td></tr>
<tr><td>Cj1420c</td><td colspan="2">methyltransferase [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168]</td></tr>
<tr><td>CJSA_1247</td><td colspan="2">hypothetical protein [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> IA3902]</td></tr>
<tr><td>CJ0628</td><td colspan="2">lipoprotein [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168]</td></tr>
<tr><td>CJ1305c</td><td colspan="2">hypothetical protein [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168]</td></tr>
<tr><td>CJS3_0200</td><td colspan="2">putative integral membrane protein [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> S3]</td></tr>
<tr><td>CJSA_1357</td><td colspan="2">putative sugar nucleotidyltransferase [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> IA3902]</td></tr>
<tr><td>Cj0055c</td><td colspan="2">hypothetical protein [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168]</td></tr>
<tr><td>CJJ81176_0291</td><td colspan="2">biotin sulfoxide reductase [ <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 81-176]</td></tr>
<tr><th colspan="3">LOS region <i>C. jejuni</i> 01/51</th></tr>
<tr><th>Gene name</th><th>Gene homolog</th><th>Annotated function</th></tr>
</table>

| | | |
|---|---|---|
| *wlaB* | CJE1272 | ABC transporter, ATP-binding/permease protein [*Campylobacter jejuni* RM1221] |
| *galE* | CJE1273 | UDP-glucose 4-epimerase [*Campylobacter jejuni* RM1221] |
| *wlaX* | CJE1274 | polysaccharide biosynthesis protein [*Campylobacter jejuni* RM1221] |
| *waaC* | CJE1275 | lipopolysaccharide heptosyltransferase I [*Campylobacter jejuni* RM1221] |
| *waaM* | CJE1276 | lipid A biosynthesis lauroyl acyltransferase [*Campylobacter jejuni* RM1221] |
| | CJE1277 | lipooligosaccharide biosynthesis glycosyltransferase, putative [*Campylobacter jejuni* RM1221] |
| | CJE1278 | lipooligosaccharide biosynthesis galactosyltransferase, putative [*Campylobacter jejuni* RM1221] |
| | CJ1138 | galactosyltransferase in NCTC11168 and putative galactosyltransferase in 84-25 |
| *wlaN* | | beta-1,3 galactosyltransferase [*Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| *cgtB* | | glycosyltransferase [*Campylobacter jejuni* DFVF1099] |
| *cstIII* | | alpha-2,3-/2,8-sialyltransferase [*Campylobacter jejuni* subsp. *jejuni* 84-25] |
| *neuB1* | | N-acetylneuraminic acid synthetase [*Campylobacter jejuni* subsp. *jejuni* 84-25] |
| *neuC1* | | UDP-N-acetylglucosamine 2-epimerase [*Campylobacter jejuni* subsp. *jejuni* 84-25] |
| *neuA1* | | two-domain bifunctional protein [beta-1,4-N-acetylgalactosaminyltransferase/CMP-Neu5Acsynthase [*Campylobacter* |

| | | |
|---|---|---|
| | | *jejuni* subsp. *jejuni* NCTC 11168] |
| | CJE1281 | conserved hypothetical protein [*Campylobacter jejuni* RM1221] |
| *waaV* | CJE1282 | lipooligosaccharide biosynthesis glycosyltransferase [*Campylobacter jejuni* RM1221] |
| *waaF* | CJE1283 | ADP-heptose--LPS heptosyltransferase II [*Campylobacter jejuni* RM1221] |
| *gmhA-1* | CJE1285 | phosphoheptose isomerase [*Campylobacter jejuni* RM1221] |
| *hldE* | CJE1286 | D,D-heptose 1-phosphate adenosyltransferase/7-phosphate kinase [*Campylobacter jejuni* RM1221] |
| *waaD* | CJE1287 | ADP-L-glycero-D-mannoheptose-6-epimerase [*Campylobacter jejuni* RM1221] |
| | CJE1288 | hydrolase, putative [*Campylobacter jejuni* RM1221] |

Supplementary table 6: *C. jejuni* 01/10 prophage 1 and 2 genes, ORFs with best match in campylobacters other than *C. jejuni* RM1221 and LOS biosynthesis loci identified by BLASTx annotation tool.

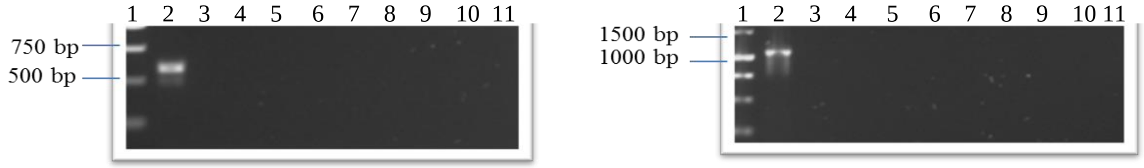
| **Gene homolog/ortholog** | | **Annotated function** |
|---|---|---|
| **Prophage 1** | | |
| JJD26997_0292 | | phage integrase family site specific recombinase [*Campylobacter jejuni* subsp. *doylei* 269.97] |
| Cje102_04044 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| Cje102_04054 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| Type I RM system | | type I restriction-modification system, M subunit [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| Anticodon nuclease | | anticodon nuclease [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| RM system | | restriction modification system DNA specificity subunit [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| HsdR | | type I site-specific deoxyribonuclease, HsdR family protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| **Prophage 2** | | |
| CJS3_0736 | | phage repressor protein, putative [*Campylobacter jejuni* subsp. *jejuni* S3] |
| *dam* | | DNA adenine methylase [*Campylobacter jejuni* RM1221] |
| CJE0221 | | phage virion morphogenesis protein, putative [*Campylobacter jejuni* RM1221] |
| CJE0221 | | phage virion morphogenesis protein, putative [*Campylobacter jejuni* RM1221] |
| CJE0225 | | hypothetical protein [*Campylobacter jejuni* RM1221 ] |
| CJE0226 | | phage major tail tube protein [*Campylobacter jejuni* RM1221 ] |
| CJE0227 | | major tail sheath protein [*Campylobacter jejuni* RM1221 ] |
| Cje140_03187 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 9217] |
| CJJ26094_0481 | | hypothetical protein [*Campylobacter jejuni* subsp.*jejuni* 260.94] |
| ICDCCJ07001_687 | | tail fiber protein H [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |

| | | |
|---|---|---|
| ICDCCJ07001_686 | | phage tail protein [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| CJS3_0717 | | baseplate assembly protein J, putative [*Campylobacter jejuni* subsp. *jejuni* S3] |
| ICDCCJ07001_684 | | baseplate assembly protein V [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| Cje120_04436 | | hypothetical protein cje120_04436 [*Campylobacter jejuni* subsp. *jejuni* LMG 9879] |
| CJE0244 | | Mu-like prophage I protein [*Campylobacter jejuni* RM1221] |
| Cje104_04971 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23223] |
| Cje109_07168 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23263] |
| ICDCCJ07001_676 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| CJE0248 | | hypothetical protein [*Campylobacter jejuni* RM1221] |
| Cje160_04023 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 2008-979] |
| Cje34_01110 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 87459] |
| ICDCCJ07001_672 | | prophage MuSo1, F protein [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| CJE0252 | | phage tail protein [*Campylobacter jejuni* RM1221] |
| ICDCCJ07001_670 | | tail protein D [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| Cje145_09019 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 2008-1025] |
| *dns* | | extracellular deoxyribonuclease [*Campylobacter jejuni* RM1221] |
| Cco16_02733 | | hypothetical protein [*Campylobacter coli* 86119] |
| CSS_0559 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 305] |
| Cje160_04285 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 2008-979] |
| ICDCCJ07001_665 | | host-nuclease inhibitor protein Gam [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| ICDCCJ07001_663 | | bacteriophage DNA transposition protein B [ *Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| CJE0269 | | bacteriophage DNA transposition protein B [ *Campylobacter jejuni* RM1221] |
| CJE0270 | | bacteriophage DNA transposition protein A [ *Campylobacter jejuni* RM1221] |
| **Other genes** | | |
| C8J_0013 | | putative integral membrane protein [*Campylobacter jejuni* subsp. *jejuni* 81116] |

| | | |
|---|---|---|
| *cipA* | | invasion protein CipA [*Campylobacter jejuni subsp. jejuni* NCTC 11168] |
| Cje102_08266 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| Cje52_03044 | | conserved domain protein [*Campylobacter jejuni* subsp. *jejuni* CF93-6] |
| CJ81176_0764 | | putative outer membrane protein [*Campylobacter jejuni* subsp. jejuni 81-176] |
| Cje11_06363 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 60004] |
| Cje102_01575 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| Cj1055c | | sulfatase family protein [*Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cje135_06326 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* ATCC 33560] |
| ICDCCJ07001_1244 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| Cje14_08577 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 53161] |
| Cj1324 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| Cj1355 | | *ceuE* enterochelin uptake periplasmic binding protein [*Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| C8J_1278 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 81116 ] |
| Cje160_07455 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* 2008-979] |
| Cje102_05088 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| ICDCCJ07001_660 | | signal peptidase I [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| ICDCCJ07001_659 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* ICDCCJ07001] |
| Cco19_02101 | | hypothetical protein [*Campylobacter coli* 1091] |
| Cje135_02178 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* ATCC 33560] |
| Cco76_02321 | | hypothetical protein [*Campylobacter coli* LMG 23336] |
| type I RM system | | type I restriction-modification system, S subunit, putative [*Campylobacter coli* 317/04] |
| *mloA* | | MloA protein, putative [*Campylobacter jejuni* subsp. *jejuni* 1336] |
| *hsdM* | | type I restriction-modification system, M subunit [*Campylobacter jejuni* subsp. *jejuni* 1997-4] |
| Cje102_06884 | | hypothetical protein [*Campylobacter jejuni* subsp. *jejuni* LMG 23218] |
| C8J_1455 | | transporter, putative [ *Campylobacter jejuni* subsp. *jejuni* 81116] |
| *fkbM* | | JJD26997_1251_FkbM family methyltransferase [*Campylobacter jejuni* subsp. *doylei* 269.97] |

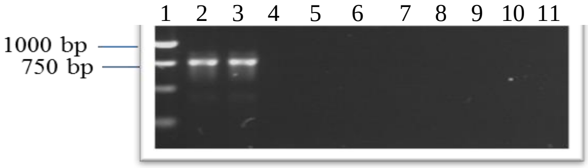
| *tet* | | tetracycline gene [*Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
|---|---|---|
| **LOS region 01/10** | | |
| **Gene name** | **Gene homolog** | **Annotated function** |
| *wlaB* | CJE1272 | ABC transporter, ATP-binding/permease protein [*Campylobacter jejuni* RM1221] |
| *galE* | CJE1273 | UDP-glucose 4-epimerase [*Campylobacter jejuni* RM1221] |
| *wlaX* | CJE1274 | polysaccharide biosynthesis protein [*Campylobacter jejuni* RM1221] |
| *waaC* | CJE1275 | lipopolysaccharide heptosyltransferase I [*Campylobacter jejuni* RM1221] |
| *waaM* | CJE1276 | lipid A biosynthesis lauroyl acyltransferase [*Campylobacter jejuni* RM1221] |
| | CJE1277 | lipooligosaccharide biosynthesis glycosyltransferase, putative [*Campylobacter jejuni* RM1221] |
| | CJ1138 | galactosyltransferase in *C. jejuni* NCTC11168 and putative galactosyltransferase in *C. jejuni* 84-25 |
| *cgtA* | | beta-1,4-N-acetylgalactosaminyltransferase (CgtA) [*Campylobacter jejuni* subsp. *jejuni* M1] |
| *wlaN* | | beta-1,3 galactosyltransferase [*Campylobacter jejuni* subsp. *jejuni* NCTC 11168] |
| CJJ81176_1157 | | alpha-2,3-sialyltransferase [*Campylobacter jejuni* subsp. *jejuni* 81-176] |
| ICDCCJ07001_1099 | | sialic acid synthase [*Campylobacter jejuni* ICDCCJ07001] |
| CJ81176_1159 | | UDP-N-acetylglucosamine 2-epimerase [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| CJ81176_1160 | | beta-1,4-N-acetylgalactosaminyltransferase [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| CJ81176_1161 | | CMP-Neu5Ac synthetase [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| CJ81176_1162 | | acetyltransferase [*Campylobacter jejuni* subsp. *jejuni* 81-176 ] |
| *waaV* | CJE1282 | lipooligosaccharide biosynthesis glycosyltransferase [*Campylobacter jejuni* RM1221] |
| *waaF* | CJE1283 | ADP-heptose--LPS heptosyltransferase II [*Campylobacter jejuni* RM1221] |
| *gmhA-1* | CJE1285 | phosphoheptose isomerase [*Campylobacter jejuni* RM1221] |
| *hldE* | CJE1286 | D,D-heptose 1-phosphate adenosyltransferase/7-phosphate kinase [*Campylobacter jejuni* RM1221] |
| *waaD* | CJE1287 | ADP-L-glycero-D-mannoheptose-6-epimerase [*Campylobacter jejuni* RM1221] |
| | CJE1288 | hydrolase, putative [*Campylobacter jejuni* RM1221] |

(a)



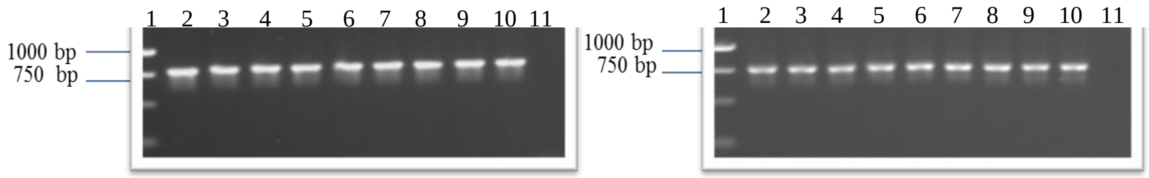
(i) *aat*

(ii) *metF*



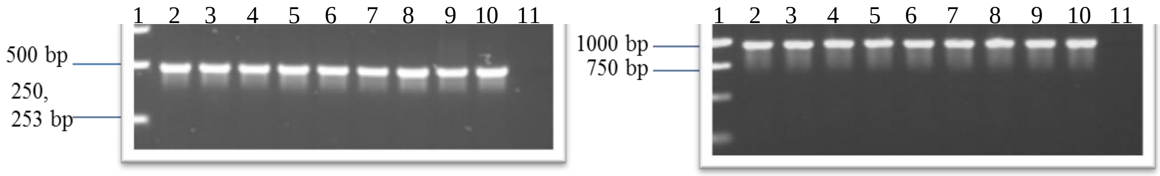
(iii) *modA*

(b)



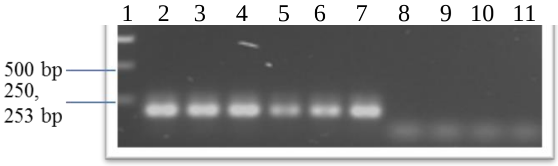
(iv) CJE1112

(v) CJE0315



(vi) CJE0801

(vii) *tgt*



(viii) CJE1128

Supplementary figure 1: Detection of 15 genes by PCR analysis identified by CGH.

(a) Genes present in all hyperinvasive *C. jejuni* (Group 1; table 4.1a); (i) *aat* (ii) *metF* (iii) *modA*. Other six genes (*i.e. hisS*, *proC*, CJE0838, CJE0669, CCOA0033 and CJE0320) were not detected in any of nine low invasive *C. jejuni* strains therefore no gel images are shown. (b) Genes highly divergent/absent from all the hyperinvasive *C. jejuni* strains (Group 2; table 4.1b); (iv) CJE1112 (v) CJE0315 (vi) CJE0801 (vii) *tgt* (viii) CJE1128. One gene, CJE0731 yielded no PCR product for any of the nine low invasive *C. jejuni* hence the gel image is now presented. The PCR primers and expected product sizes are listed in table 2.2.1.

Each gel was loaded: Lane 1; 1kbp DNA marker (Promega, UK); lanes 2-10; *C. jejuni* 01/05**,** 01/08, 01/11, 01/36, C2/3, C12/11, C27/14, C69/2, C110/4; Lane 11; negative control.

Supplementary file 1: The analysis run to identify loci specific to the hyperinvasive *C. jejuni* strains.

```
program data_preproc;
uses windows;
{$R+}
{$X+}
label mm1,mm2;
const
      n_seq=10;
      tab=#09;
var
    inf,inf1,inf2:text;
    tt1:string[1];
    name:string;
    name1:string;
    tt2:string;
    i,j,k,current,al,kk,tab_name:integer;
    name_tab:array[1..45000] of string;
    tab_tab:array[1..45000] of string;
    name_name:array[1..10] of string;
    high:array[1..45000,1..10] of integer;
    status:integer;
    high1,high0,low1,low0:integer;
begin
  Writeln('Start');
  readln;
name_name[1]:='01_10';
name_name[2]:='01_35';
name_name[3]:='01_04';
name_name[4]:='01_41';
```

```
name_name[5]:='01_51';
name_name[6]:='EX114';
name_name[7]:='01_30';
name_name[8]:='01_32';
name_name[9]:='01_46';
name_name[10]:='01_39';

tab_name:=0;
current:=0;
assignfile(inf1,'c:\Alan\all_data');rewrite(inf1);{append(inf1);  }
for al:=1 to n_seq do
begin
name:='c:\ALAN\data\'+copy(name_name[al],1,length(name_name[al]))+'.dat';
writeln(name);

assignfile(inf,name);reset(inf);
readln(inf,tt2);
repeat
name:='';
repeat
read(inf,tt1);
name:=name+tt1;
until tt1=tab;
{writeln(name,'#');  }

if tab_name=0 then begin tab_name:=1;name_tab[tab_name]:=name;current:=1;goto mm1;end else
        begin
        for k:=1 to tab_name do
        begin
```

```
    if (copy(name,1,length(name))=copy(name_tab[k],1,length(name))) then begin current:=k;goto mm1;end;
    end;
    tab_name:=tab_name+1;
    name_tab[tab_name]:=name;current:=tab_name;
    end;
mm1:

name1:='';
repeat
read(inf,tt1);
name1:=name1+tt1;
until tt1=tab;
tab_tab[current]:=name1;

tt2:='';
repeat
read(inf,tt1);
tt2:=tt2+tt1;
until ((tt1=tab) or (EOLN=TRUE));
status:=2;
if copy(tt2,1,1)='1' then status:=1;
if copy(tt2,1,1)='-' then status:=0;
{val(tt2,status,kk);
writeln(tt2); }
readln(inf,tt2);

high[current,al]:=status;
until EOF(inf)=TRUE;
closefile(inf);
```

```
end;

for i:=1 to current do
begin
name:=name_tab[i]+tab+tab_tab[i]+tab;
for j:=1 to 10 do
begin
str(high[i,j]:1,name1);
if high[i,j]<>2 then name:=name+name1+tab else goto mm2;
end;
writeln(inf1,name);
mm2:
end;
closefile(inf1);
assignfile(inf2,'c:\Alan\res.txt');{rewrite(inf2);}append(inf2);
for i:=1 to current do
begin
name:=name_tab[i]+tab+tab_tab[i]+tab;
high1:=0;high0:=0;
low1:=0;low0:=0;

for j:=1 to 6 do
begin
if high[i,j]=1 then high1:=high1+1;
if high[i,j]=0 then high0:=high0+1;
end;

for j:=7 to 10 do
begin
if high[i,j]=1 then low1:=low1+1;
```

```
if high[i,j]=0 then low0:=low0+1;
end;
if (((high1=5) and (low0=3)) or ((high0=5) and (low1=3))) then begin
                                        write(inf2,name);
                                        for k:=1 to 10 do
                                        begin
                                        str(high[i,k]:1,name1);
                                        write(inf2,name1,tab);
                                        end;
                                        writeln(inf2);
                                        end;
end;

closefile(inf2);

writeln('OK');
readln;
end.
```