

# The helicase HAGE prevents interferon- $\alpha$ -induced PML expression in ABCB5 + malignant melanoma-initiating cells by promoting the expression of SOCS1

MG Mathieu<sup>1,2</sup>, AK Miles<sup>1,2</sup>, M Ahmad<sup>1</sup>, ME Buczek<sup>1</sup>, AG Pockley<sup>1</sup>, RC Rees<sup>1</sup> and T Regad<sup>\*,1</sup>

The tumour suppressor PML (promyelocytic leukaemia protein) regulates several cellular pathways involving cell growth, apoptosis, differentiation and senescence. PML also has an important role in the regulation of stem cell proliferation and differentiation. Here, we show the involvement of the helicase HAGE in the transcriptional repression of PML expression in ABCB5 + malignant melanoma-initiating cells (ABCB5 + MMICs), a population of cancer stem cells which are responsible for melanoma growth, progression and resistance to drug-based therapy. HAGE prevents PML gene expression by inhibiting the activation of the JAK–STAT (janus kinase–signal transducers and activators of transcription) pathway in a mechanism which implicates the suppressor of cytokine signalling 1 (SOCS1). Knockdown of HAGE led to a significant decrease in SOCS1 protein expression, activation of the JAK–STAT signalling cascade and a consequent increase of PML expression. To confirm that the reduction in SOCS1 expression was dependent on the HAGE helicase activity, we showed that SOCS1, effectively silenced by small interfering RNA, could be rescued by re-introduction of HAGE into cells lacking HAGE. Furthermore, we provide a mechanism by which HAGE promotes SOCS1 mRNA unwinding and protein expression *in vitro*. Finally, using a stem cell proliferation assay and tumour xenotransplantation assay in non-obese diabetic/severe combined immunodeficiency mice, we show that HAGE promotes MMICs-dependent tumour initiation and tumour growth by preventing the anti-proliferative effects of interferon- $\alpha$  (IFN $\alpha$ ). Our results suggest that the helicase HAGE has a key role in the resistance of ABCB5 + MMICs to IFN $\alpha$  treatment and that cancer therapies targeting HAGE may have broad implications for the treatment of malignant melanoma.

*Cell Death and Disease* (2014) 5, e1061; doi:10.1038/cddis.2014.29; published online 13 February 2014

**Subject Category:** Cancer

Malignant melanoma-initiating cells (MMICs) are a population of cancer cells that possess the stem cell properties of self-renewal and differentiation.<sup>1</sup> This population of cells express the ATP-binding cassette member 5 (ABCB5), a protein that renders malignant melanoma drug-resistant and refractory to therapy. ABCB5 + MMICs also express HAGE (DDX43), a DEAD-Box RNA helicase expressed specifically by tumour cells, that has been shown to have a key role in promoting the proliferation of ABCB5 + MMICs and their survival by enhancing the expression of the small GTPase NRAS.<sup>2</sup> As a consequence, this population is thought to be responsible for a highly aggressive type of cancer with a poor prognostic outcome.<sup>3,4</sup> Besides drug-based therapy, interferon- $\alpha$  (IFN $\alpha$ ) has also been used for the treatment of patients with malignant melanoma and has been shown to result in a modest improvement of relapse-free survival and overall survival.<sup>5–7</sup> The mechanisms underlying resistance to IFN $\alpha$  treatment and the involvement of MMICs in this process are unknown.

IFN $\alpha$  signals through the JAK–STAT (janus kinase–signal transducers and activators of transcription) pathway and

results in the induction of several genes. This endows IFN $\alpha$  with multiple effects in a variety of malignancies that range from antiangiogenic effects to potent immunoregulatory, differentiation-inducing, pro-apoptotic and anti-proliferative properties.<sup>8,9</sup> The gene encoding promyelocytic leukaemia protein (PML) is a well-known downstream target of IFNs signalling and its induction by IFNs results in a significant increase in the expression of PML and the number of PML nuclear bodies (PML-NBs).<sup>10–12</sup> PML, a member of the Ring-B Box-Coiled Coil family, is a tumour suppressor which was originally identified at the breakpoint of the t (15;17) translocation found in acute promyelocytic leukaemia (APL).<sup>13–15</sup> It is at the heart of many cellular pathways such as cell growth, differentiation, DNA damage, senescence, apoptosis and anti-viral responsiveness.<sup>16–18</sup> PML functions by interacting and recruiting different factors that compose these cellular processes into subnuclear structures known as PML-NBs, of which it is the essential component.<sup>18</sup> Although the role of PML in IFNs-mediated antiviral responses has been well studied, little is known about its role in the

<sup>1</sup>The John van Geest Cancer Research Centre, School of Science and Technology, Nottingham Trent University, Clifton Lane, Nottingham, UK

\*Corresponding author: T Regad, The John van Geest Cancer Research Centre, School of Science and Technology, Nottingham Trent University, Clifton Lane, Nottingham, NG11 8NS, UK. Tel: +44 (0)115 848 3501; Fax: +44 (0)115 848 3384; E-mail: tarik.regad@ntu.ac.uk

<sup>2</sup>These authors contributed equally to this work.

**Keywords:** PML; DDX43; MMIC; SOCS1; melanoma; interferon- $\alpha$

**Abbreviations:** MMIC, malignant melanoma-initiating cell; ABCB5, ATP-binding cassette subfamily B member 5; SOCS1, suppressor of cytokine signalling 1; HAGE, helicase antigen; PML, promyelocytic leukaemia protein; Jak1, janus kinase 1; Jak2, janus kinase 2; STAT1, signal transducer and activator of transcription 1; STAT2, signal transducer and activator of transcription 2; IFN $\alpha$ , interferon  $\alpha$ ; IFNs, interferons

Received 07.1.14; accepted 08.1.14; Edited by G Melino

anti-tumour properties of IFNs.<sup>16,19</sup> On the basis of this background, we hypothesised that the helicase HAGE (DDX43) may endow MMICs with a resistance to the anti-tumour effects of IFN-induced PML. Here, we reveal a previously unknown role of HAGE, namely that it ensures the survival of MMICs in response to the anti-proliferative and pro-apoptotic effects of IFN $\alpha$ . Using a stem cell proliferation assay and tumour xenotransplantation assay in non-obese diabetic/severe combined immunodeficiency (NOD/SCID) mice, we show that HAGE promotes tumour initiation and MMIC-dependent growth by preventing the IFN $\alpha$ -induced inhibition. HAGE expression in malignant melanoma cells prevents the activation of the JAK–STAT signalling pathway which is involved in the induction of PML transcription. Knockdown of HAGE in ABCB5 + MMICs results in increased PML expression at the RNA and protein levels. This event is favoured through an increase in expression of the suppressor of cytokine signalling SOCS1 protein, a known positive regulator of ubiquitination and degradation of JAK proteins.<sup>20</sup> HAGE knockdown in melanoma cell lines expressing ABCB5 decreases SOCS1 protein expression and this is reversed by re-introducing HAGE in these cells. An *in vitro* unwinding assay provides a mechanistic insight by demonstrating the capacity of the helicase HAGE to unwind SOCS1 RNA complexes and thereby promote the expression of SOCS1 protein. Collectively, these findings support the model by which HAGE promotes the initiation of tumours by ABCB5 + MMICs and their resistance to the anti-proliferative effects of IFN $\alpha$  by inactivating the JAK–STAT pathway which is necessary for PML expression via a mechanism which involves the SOCS1.

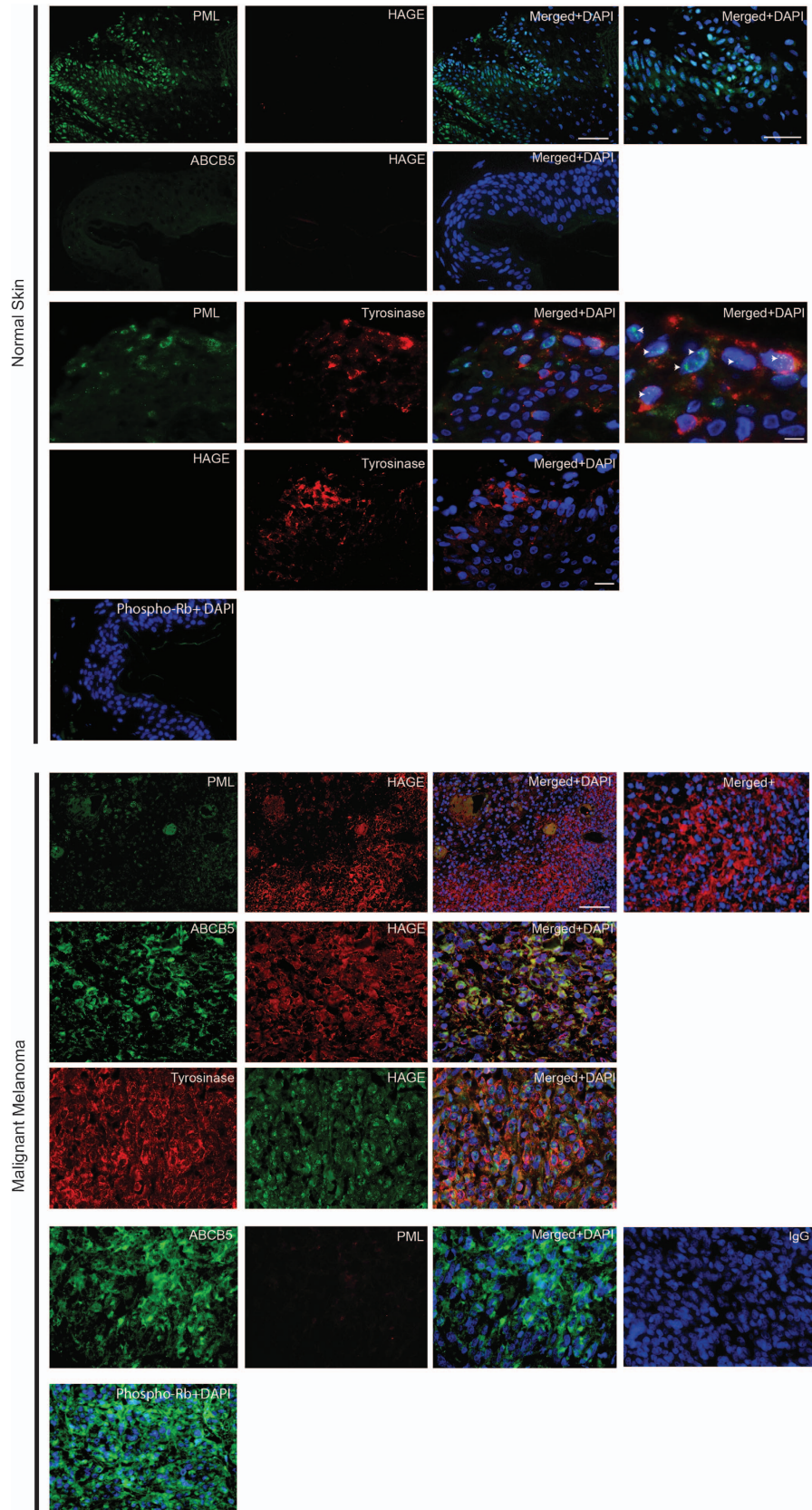
## Results

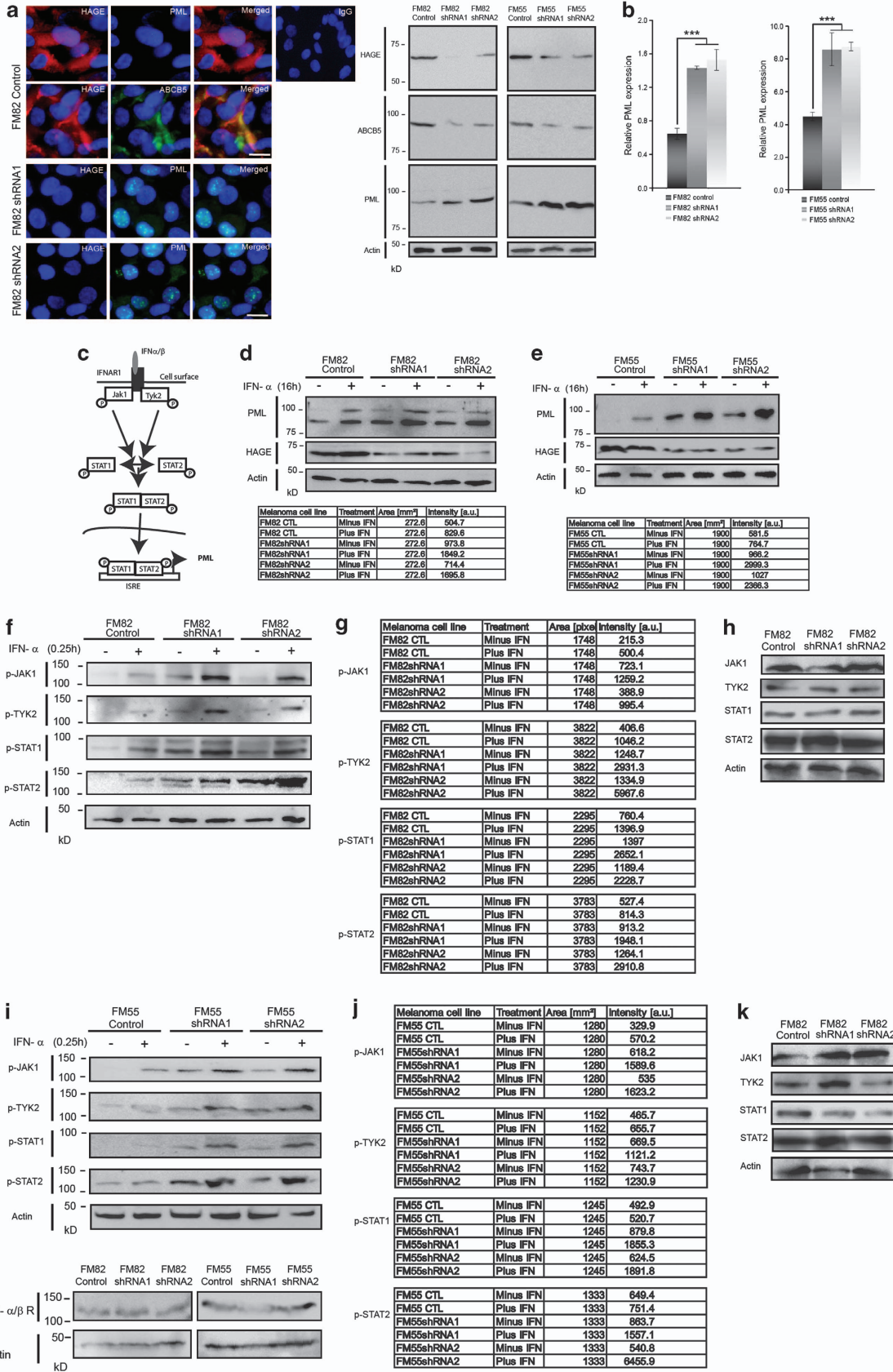
**Decreased PML expression in HAGE + – ABCB5 + MMICs.** The loss of PML expression has been previously reported in several solid tumours from different tissue origins.<sup>21</sup> To investigate the expression status of PML in HAGE + and ABCB5 + MMICs, we performed immunostaining on a malignant melanoma tissue microarray (TMA) using antibodies against PML, HAGE and ABCB5. PML expression was significantly decreased in HAGE + and ABCB5 + tumour cells when compared with the control (normal skin). As a consequence, this decrease correlated with the absence of PML-NBs of which, PML is the essential component. PML has been shown to promote the hypo-phosphorylation of the retinoblastoma protein (Rb), which regulates the cell cycle progression at the G1–S phase by interacting and sequestering the transcription factor E2F.<sup>22</sup> Immunostaining on a malignant melanoma TMA using an antibody against the phosphorylated forms of Rb showed an increased expression of phosphorylated Rb in malignant melanoma when compared with the normal skin control

(Figure 1). Furthermore, PML expression was found in melanocytes of normal skin and in HAGE + – ABCB5 + melanoma cells as shown using an antibody against Tyrosinase, a specific marker of melanin-producing cells. Interestingly, PML was expressed in tissues surrounding ABCB5- and HAGE-expressing cells within the tumours (Figure 1 and Supplementary Figure 1). Similar results were obtained using malignant melanoma cell lines FM82 and FM55, which co-express HAGE and ABCB5.<sup>2</sup> The permanent knockdown of HAGE in these cell lines using small hairpin RNAs (FM82 shRNA 1 and 2, FM55 shRNA 1 and 2) increased PML expression (Figure 2a). The molecular weight of the PML protein (~90 kDa) observed by immunoblotting (IB) suggests that the dominant isoform expressed in these cell lines may corresponds to PML isoforms II, III or both. To further investigate this, we have tested by IB two additional antibodies on whole cell extracts from FM82 control, FM82 shRNA and another melanoma cell line FM6 (Supplementary Figures 2B and C). The first antibody recognises the PML epitope, which maps to a region between 375 and 425 and therefore should recognises all PML isoforms with the exception of isoforms VI and VII. The second antibody recognises the PML epitope, which maps to a region between 575 and 625 and should only recognise PML I and PML IV. The immunoblot using the first antibody showed predominant expression of a band at ~90 kDa, however, the immunoblot with the second antibody showed weak expression of bands at ~80 kDa and ~100 kDa (Supplementary Figures 2B and C). From these results, we concluded that the predominant band at ~90 kDa may represent PML isoforms II or III or both. The decreased expression of PML protein in the presence of HAGE might result from a decrease in PML gene expression. We investigated this possibility by performing a semi-quantitative real-time PCR on mRNAs isolated from FM82 and FM55 controls and FM82 and FM55 shRNAs cell lines. We found that HAGE knockdown resulted in increased PML gene expression when compared with controls (Figure 2b). These results suggest that HAGE negatively regulates the basal expression of PML gene in HAGE + ABCB5 + MMICs.

**HAGE prevents IFN-induced PML expression.** The binding of type I IFNs to the IFN $\alpha$  receptor (IFNAR) triggers the activation of Jak proteins (Jak1 and Tyk2) which become auto-phosphorylated and activate members of the STAT family through tyrosine phosphorylation. Activated STATs form dimers, translocate to the nucleus, bind to specific response elements in promoters of target genes and transcriptionally activate these genes<sup>9</sup> (Figure 2c). The PML gene promoter possesses an IFN-stimulated response element, which is inducible by IFN type I (Figure 2c). To investigate the mechanism by which HAGE regulates PML gene expression, FM82 and FM55 controls and FM82 and

**Figure 1** Expression of PML in HAGE-positive and ABCB5-positive malignant melanoma. Top panel: representative image of immunohistochemistry with antibodies to PML (green) or ABCB5 (green) or Tyrosinase (red) or HAGE (red) or phospho-Rb (green) on normal skin sections. The arrows indicate PML-NBs in Tyrosinase-positive cells. Lower panel: representative image of immunohistochemistry with antibody to PML (green or red), ABCB5 (green), Tyrosinase (red), HAGE (red) or phospho-Rb (green) in malignant melanoma tissue sections. The negative controls used were an IgG isotype from mouse and rabbit. The blue staining (DAPI) corresponds to the nucleus. Scale bars represent 100  $\mu$ m (20  $\times$ ), 50  $\mu$ m (40  $\times$ ), 20  $\mu$ m (40  $\times$ )





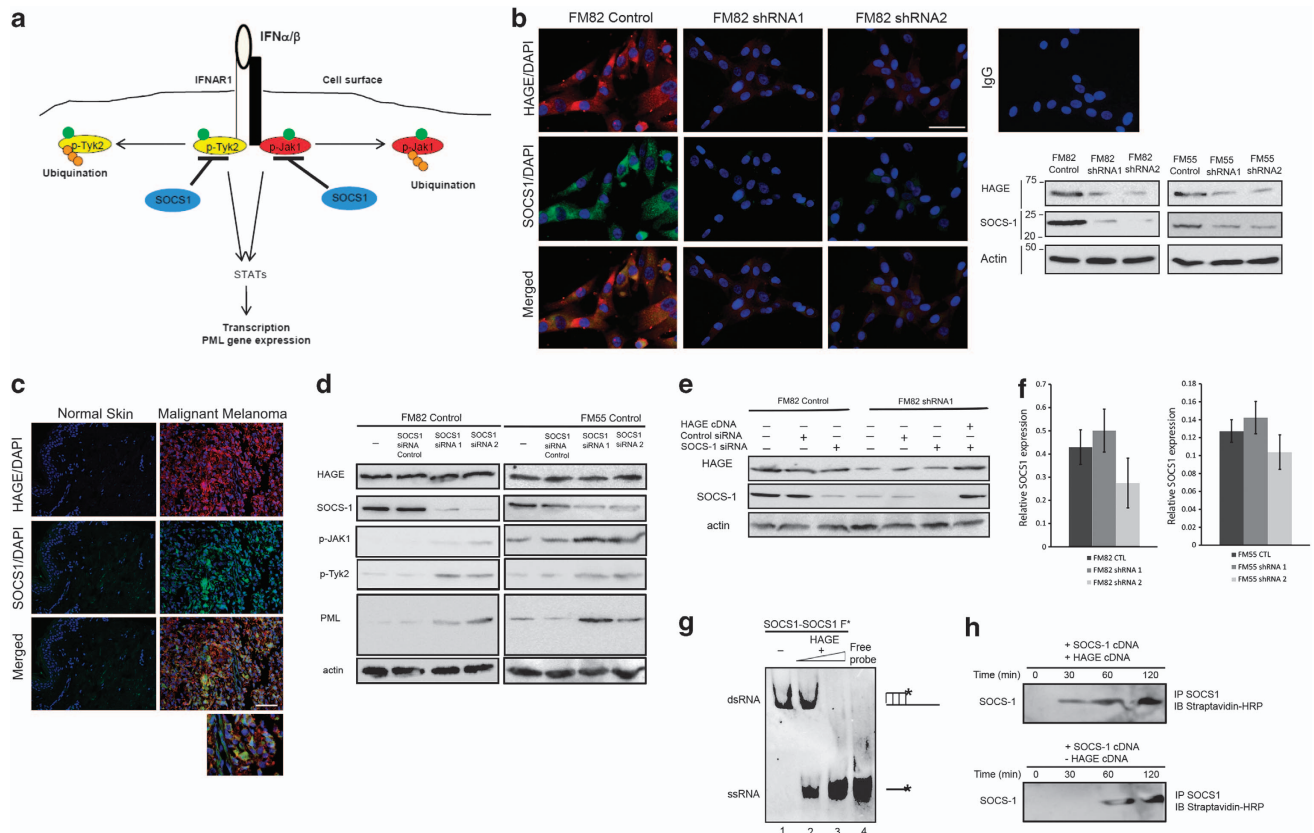
FM55 shRNAs were treated with IFN $\alpha$ . PML protein expression upon IFN $\alpha$  treatment was significantly increased in HAGE knockdown cell lines when compared with FM82 and FM55 control (Figures 2d and e). This result suggests that HAGE prevents IFN $\alpha$ -mediated PML gene expression. Analysis of the JAK–STAT pathway in FM82 and FM55 controls and FM82 and FM55 shRNAs following IFN $\alpha$  treatment showed a decrease in Jak1, Tyk2, STAT1 and STAT2 phosphorylation in the presence of HAGE (Figures 2f, g, i and j). This downregulation of the JAK–STAT pathway might be due to a decrease in IFNAR expression on the surface of FM82 and FM55 control cells, thereby resulting in a reduced ligand binding. IB with a specific antibody to IFNAR and using lysates from FM82 and FM55 controls and FM82 and FM55 shRNAs showed no significant difference in IFNAR expression in the presence of HAGE and when HAGE is knocked down (Figure 2l). Finally, IB using antibodies to total Jak1, Tyk2, Stat1 and Stat2 showed no difference in their expression in FM82 and FM55 controls and FM82 and FM55 shRNAs (Figures 2h and k). As the phosphorylation of STAT1 and STAT2, and the dimerisation, nuclear translocation and activation of target genes are dependent on Jak1 and Tyk2 auto-phosphorylation (p-Jak1 and p-Tyk2). These results suggest that HAGE prevents IFN $\alpha$ -mediated PML gene expression via a negative regulation of Jak1 and Tyk2 phosphorylation.

**HAGE promotes the expression of SOCS1.** The SOCS1 belongs to the SOCS family of negative regulators of the JAK–STAT pathway. SOCS proteins can directly bind to the phosphorylated forms of JAKs via their central domain SH2 and the C-terminal SOCS box region. This binding triggers the ubiquitination and degradation of JAKs through the formation of an E3 ubiquitin ligase complex comprising Cullin2 and the elongin B/C<sup>20</sup> (Figure 3a). To investigate the potential involvement of SOCS1 in the HAGE-mediated downregulation of p-Jak1 and p-Tyk2, we performed an immunostaining with antibodies against HAGE and SOCS1 on FM82 control and FM82 shRNAs cell lines. SOCS1 was co-expressed together with HAGE in FM82 controls and its expression decreased when HAGE was knocked down (FM82 shRNAs) (Figure 3b). These results were confirmed by IB using cell extracts from FM82 and FM55 controls and FM82 and FM55 shRNAs (Figure 3b). Interestingly, SOCS3, another member of the SOCS family of proteins was also

downregulated in FM82 and FM55 shRNAs (Supplementary Figure 2A). However, we were not able to detect SOCS2 another member of this family by IB using a previously described SOCS2 specific antibody (data not shown).<sup>23</sup> Furthermore, SOCS1 expression was increased in HAGE-positive malignant melanoma tissue, thereby confirming the *in vitro* observations above (Figure 3c). To determine the functional relationship between HAGE and SOCS1, we used knockdown experiments using specific small interfering RNAs (siRNAs) for SOCS1 mRNA in FM82 and FM55 controls cell lines which naturally express HAGE. SOCS1 knockdown increased the expression of p-Jak1, p-Tyk2 and PML protein and suggested that SOCS1 has a role in HAGE-mediated downregulation of JAK–STAT–PML pathway (Figure 3d).

RNA helicases of the DEAD-box family unwind RNA duplexes by local strand separation in an ATP-dependent fashion. As a result, RNA helicases are involved in specific processes such as ribosome biogenesis, pre-mRNA splicing and translation.<sup>24–26</sup> HAGE may enhance SOCS1 translation and promote its expression by unwinding and stabilising SOCS1 mRNA. To investigate if HAGE promotes the expression of SOCS1 protein, we knocked down SOCS1 mRNA in FM82 control and in FM82 shRNA1 cell lines. SOCS1 protein level was significantly decreased in FM82 shRNA when compared with FM82 control (Figure 3e). Furthermore, SOCS1 protein expression was significantly restored when HAGE was ectopically expressed in FM82 shRNA1 transfected with a HAGE-expressing plasmid (Figure 3e). The decrease of SOCS1 expression was not due to a decrease of its mRNA expression upon HAGE knockdown as no significant changes in SOCS1 mRNA expression were observed by semi-quantitative real-time PCR on RNAs isolated from FM82 and FM55 controls and FM82 and FM55 shRNAs cell lines (Figure 3f). HAGE may promote SOCS1 protein expression through its unwinding activity towards SOCS1 RNA. To determine if HAGE induces the unwinding of SOCS1 RNA, we performed an *in vitro* RNA unwinding assay in the absence or presence of different concentrations of recombinant HAGE protein and SOCS1 RNA duplexes. Remarkably, HAGE was able to unwind SOCS1 RNA duplexes in a dose-dependent fashion (Figure 3g). Finally, ectopic expression of HAGE promoted the translation of SOCS1 as shown by IB and using a metabolic labelling assay of nascent protein synthesis (Figure 3h).<sup>23,27</sup> Taken together, these results suggest that

**Figure 2** Expression of PML in malignant melanoma cell lines and JAK–STAT pathway analysis in IFN $\alpha$  treated and untreated FM82 and FM55 control and FM82 and FM55 shRNA malignant melanoma cell lines. (a) Left panel: IF with antibodies to PML (green), ABCB5 (green) and HAGE (red) on FM82 control and FM82 shRNA1 and 2 (HAGE knocked down). Right panel: IB with antibodies to HAGE, ABCB5, PML and actin (loading control) using whole lysates from FM82 and FM55 control and FM82 and FM55 shRNA1 and 2. (b) Semi-quantitative real-time PCR of PML mRNAs isolated from FM82 control and FM82 shRNA1. Mann–Whitney *U*-test: \*\*\**P* = <0.001. (c) Schematic representation of JAK–STAT signalling pathway upon induction by IFN type I. (d and e) IB with antibodies to PML, HAGE and actin using whole extracts from IFN $\alpha$  treated (16 h) and untreated FM82 and FM55 control and FM82 and FM55 shRNA1 and 2. Quantification of PML protein expression in plus and minus IFN $\alpha$ -treated cells. (f) IB with antibodies to the phosphorylated forms of Jak1, Tyk2, STAT1 and STAT2 using whole cell extracts from IFN $\alpha$  treated (0.25 h) and untreated FM82 control and FM82 shRNA1 and 2. (g) Quantification of the phosphorylated forms of Jak1, Tyk2, STAT1 and STAT2 using whole cell extracts from IFN $\alpha$  treated (0.25 h) and untreated FM82 control and FM82 shRNA1 and 2. (h) IB with antibodies to total Jak1, Tyk2, STAT1 and STAT2 using whole extracts from FM82 control and FM82 shRNA1 and 2. (i) Values expressed in Arbitrary Units (AU) using Aida Image Analyser (v.3.52) IB with antibodies to the phosphorylated forms of Jak1, Tyk2, STAT1 and STAT2 using whole cell extracts from IFN $\alpha$  treated (0.25 h) and untreated FM55 control and FM55 shRNA1 and 2. (j) Quantification of the phosphorylated forms of Jak1, Tyk2, STAT1 and STAT2 using whole cell extracts from IFN $\alpha$  treated (0.25 h) and untreated FM55 control and FM55 shRNA1 and 2. (k) IB with antibodies to total Jak1, Tyk2, STAT1 and STAT2 using whole extracts from FM55 control and FM55 shRNA1 and 2. (l) IB with antibody to IFN  $\alpha/\beta$  receptor (IFN receptor type I) and actin using whole extracts from untreated FM82 and FM55 control and FM82 and FM55 shRNA1 and 2



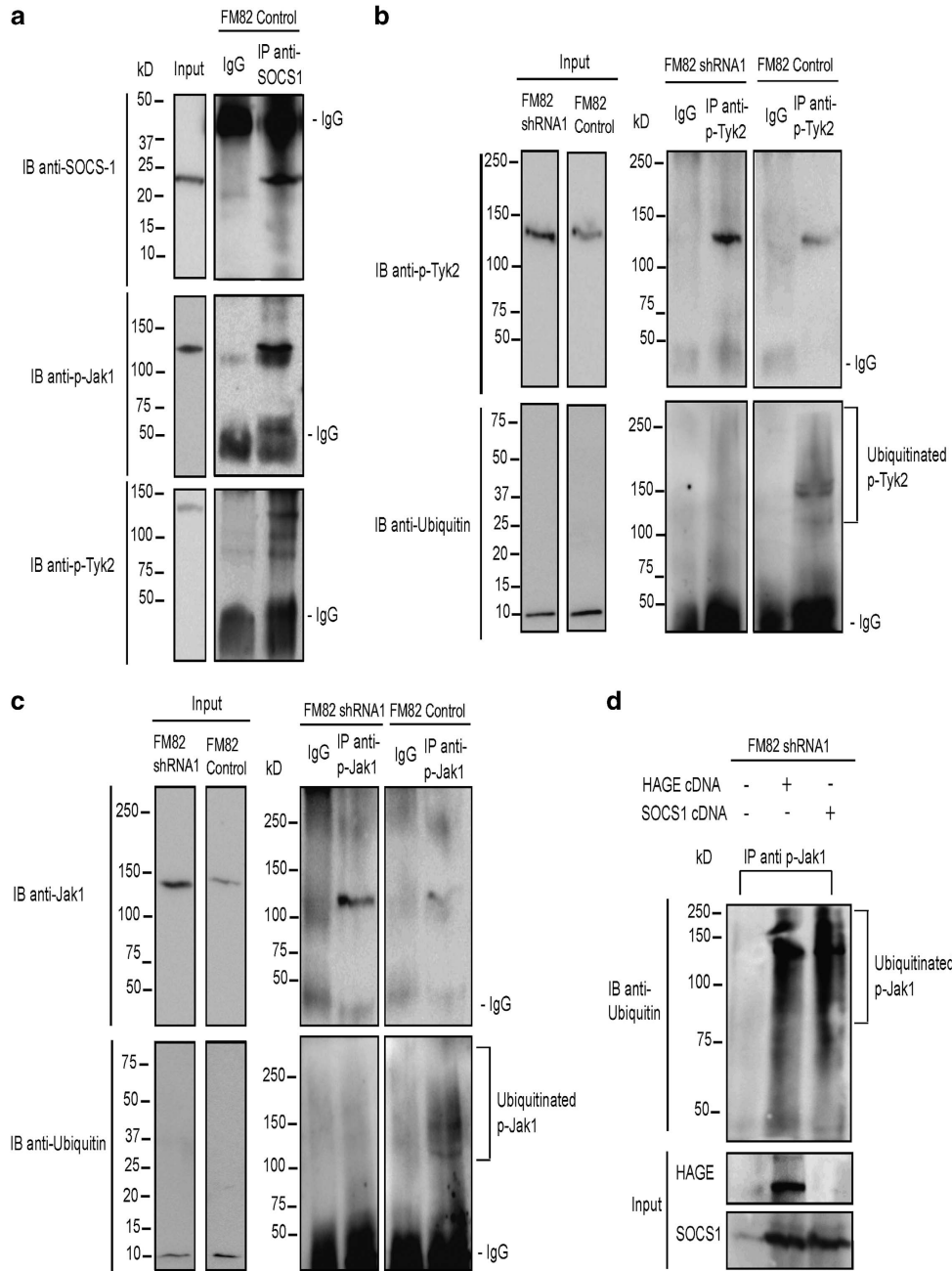
**Figure 3** HAGE enhances SOCS1 RNA unwinding and protein expression. (a) Schematic representation of the mechanism of action of SOCS1. (b) Left panel: IF with antibodies to SOCS1 (green) and HAGE (red) on FM82 control and FM82 shRNA1 and 2 (HAGE knocked down). Right panel: IB with antibodies to HAGE, SOCS1 and actin (loading control) using whole lysates from FM82 and FM55 control and FM82 and FM55 shRNA1 and 2. Scale bar 50  $\mu$ m. (c) Representative image of immunohistochemistry with antibodies to SOCS1 (green) and HAGE (red) on normal skin and malignant melanoma sections. Scale bar 100  $\mu$ m. (d) IB with antibodies to HAGE, SOCS1, p-Jak1, p-Tyk2, PML and actin using whole cell extracts from FM82 and FM55 control and FM82 and FM55 shRNA1 and 2 transfected with siRNA control and siRNA for SOCS1 mRNA. (e) Transient silencing of SOCS1 in HAGE stable knockdown and control FM82 cells followed by rescue of HAGE expression using a HAGE cDNA expression vector. Actin was measured as a loading control. (f) Semi-quantitative real-time PCR of SOCS1 mRNAs isolated from FM82 control and FM82 shRNA1. (g) Unwinding of biotinylated SOCS1 N-terminal complementary RNA sequence-SOCS1 RNA duplexes in the presence of increasing HAGE protein concentrations (lane 1: 0  $\mu$ g, lane 2: 0.6  $\mu$ g, lane 3: 1.2  $\mu$ g). Biotinylated SOCS1 N-terminal complementary RNA sequence was used as a loading control in lane 4. (h) IP with antibody to SOCS1 of biotin alkyl metabolically labelled (30, 60 and 120 min) and unlabelled SOCS1 proteins followed by IB with streptavidin antibody from FM82 control whole cell extracts transfected with SOCS1cDNA and with or without transfected HAGE cDNA

HAGE enhances the expression of SOCS1 protein expression by promoting SOCS1 RNA unwinding.

**SOCS1 promotes p-Jak1 and p-Tyk2 ubiquitination.** SOCS1 has been shown to inhibit the JAK-STAT pathway by interacting with the phosphorylated forms of Janus protein kinases.<sup>28,29</sup> To investigate the potential interaction of SOCS1 with p-Jak1 and p-Tyk2, we performed an immunoprecipitation (IP) of cell extracts from FM82 control using SOCS1 antibody. IB of SOCS1 immunoprecipitates with antibodies against SOCS1, p-Jak1 and p-Tyk2 revealed the presence of SOCS1, p-Jak1 and p-Tyk2 in SOCS1 immunocomplexes (Figure 4a). SOCS1 interactions with p-Jak1 and p-Tyk2 may result in their ubiquitination and therefore their degradation by the ubiquitin proteasome system (Figure 4a). To investigate this possibility, we performed IPs of cell extracts from FM82 control and FM82 shRNA using antibodies against p-Jak1 and p-Tyk2. IB using antibodies against p-Jak1, p-Tyk2 and ubiquitin revealed the presence of p-Jak1 and p-Tyk2 in p-Jak1 and p-Tyk2

immunoprecipitates, respectively. Furthermore, p-Jak1 and p-Tyk2 were highly ubiquitinated in the FM82 control immunoprecipitates when compared with FM82 shRNA immunoprecipitates (Figures 4b and c). Finally, the rescue of HAGE or SOCS1 expression by ectopic expression in FM82 shRNA1 promoted the ubiquitination status of p-Jak1 (Figure 4d). These results demonstrate that SOCS1 interaction with p-Jak1 and p-Tyk2 promotes their ubiquitination and this increases in the presence of HAGE.

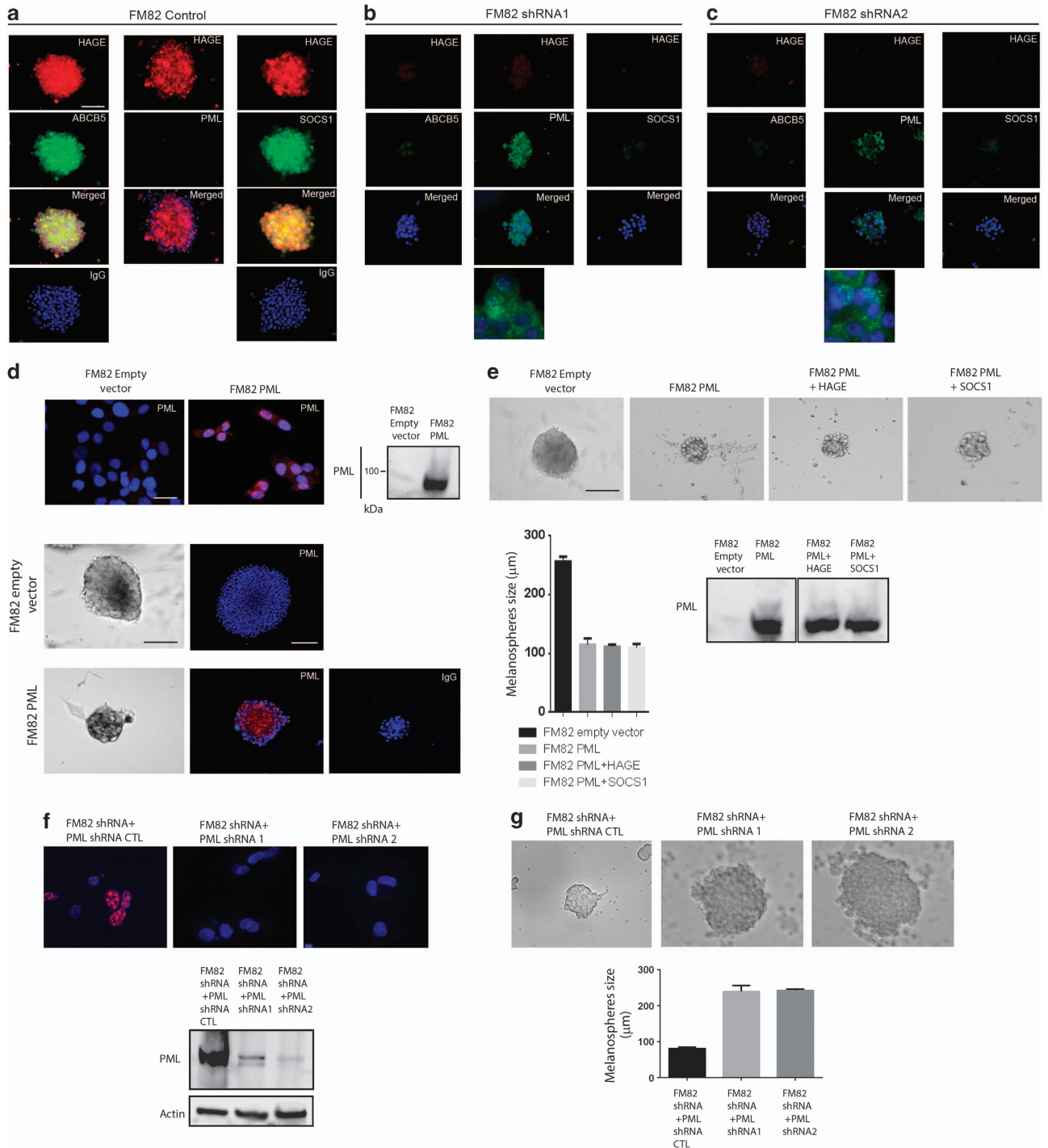
**HAGE provide ABCB5 + MMICs resistance to the anti-proliferative effect IFN $\alpha$  in vivo.** We have previously shown that HAGE is expressed by ABCB5 + MMICs. These cells possess the capacity of self-renewal and differentiation into ABCB5 + or ABCB5 - cells.<sup>2</sup> To investigate if HAGE provides resistance to the anti-proliferative effect of IFN $\alpha$  treatment mediated at least through PML, we performed a self-renewal assay using FM82 control and FM82 shRNA cell lines. These melanoma spheres were stained using antibodies against HAGE, ABCB5, SOCS1 and PML.



**Figure 4** SOCS1 induces ubiquitination of p-Jak1 and p-Tyk2 in FM82 control malignant melanoma cell lines. **(a)** IP with antibody to SOCS1 or rabbit IgG followed by IB with antibodies to SOCS1, p-Jak1 and p-Tyk2 from FM82 control whole cell extracts. **(b and c)** IP with antibody to p-Jak1 or p-Tyk2 and corresponding IgG (rabbit or goat, respectively) followed by IB with antibodies to p-Jak1 or p-Tyk2 and ubiquitin from FM82 control and FM82 shRNA1 whole cell extracts. **(d)** IP with antibody to p-Jak1 followed by whole cell extracts IB with an antibody to ubiquitin from FM82 shRNA1 transfected with HAGE cDNA or SOCS1 cDNA. The protein expression of HAGE and SOCS1 was determined by IB with the corresponding antibodies

Interestingly, SOCS1 was highly expressed in FM82 control when compared with FM82 shRNAs. In contrast, PML expression was higher in FM82 shRNAs when compared with FM82 control (Figures 5a, b and c). Furthermore, melanoma spheres generated from FM82 stably expressing PMLII gave rise to smaller spheres when compared with FM82 stably expressing the empty vector (Figures 5d and e). The ectopic expression of HAGE or SOCS1 in FM82 stably expressing PMLII did not affect the anti-proliferative effect of

PMLII on the spheres growth (Figure 5e). In addition, PML knockdown by lentiviral expression of PML shRNAs in FM82 shRNA resulted in significantly bigger sized spheres when compared with spheres generated from FM82 shRNA infected with control lentiviruses (Figures 5f and g). Finally, IFN $\alpha$  treatment of growing FM82 and FM55 control and FM82 and FM55 shRNA melanoma spheres resulted in significantly smaller FM82 and FM55 shRNA spheres when compared with the FM82 and FM55 control spheres

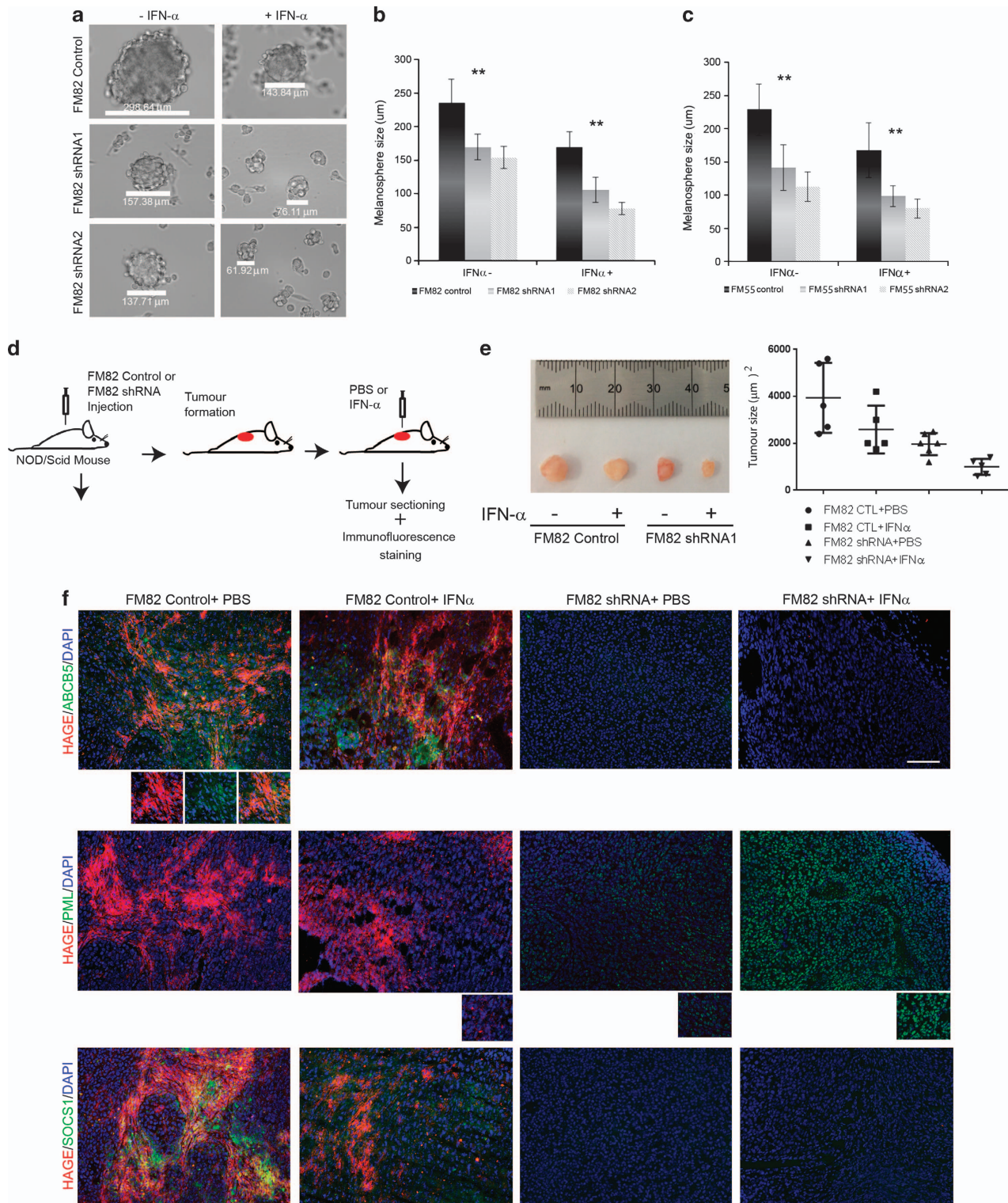


**Figure 5** HAGE counteracts the anti-proliferative effect of IFN $\alpha$  in ABCB5 + MMICs. (a, b and c) IF with antibodies to HAGE (red), ABCB5 (green), SOCS1 (green) and PML (green) on FM82 control, FM82 shRNA1 and 2 melanoma spheres. (d) IF and IB with an antibody to PML (or IgG) on FM82 cell lines and corresponding melanoma spheres stably-expressing PML or the empty vector. (e) FM82 empty vector and stably expressing PML spheres formation in the presence or absence of cDNA transfected HAGE or SOCS1. ANOVA:  $***P = < 0.0001$ . Scale bar 100  $\mu\text{m}$  (for spheres) and 20  $\mu\text{m}$  (for cells). (f) IF and IB with an antibody to PML on FM82 shRNA/PMLshRNA CTL and FM82shRNA/PMLshRNA 1 and 2. (g) Spheres formation assay from FM82shRNA/PMLshRNA CTL and FM82shRNA/PML shRNA 1 and 2. ANOVA:  $***P = < 0.0001$

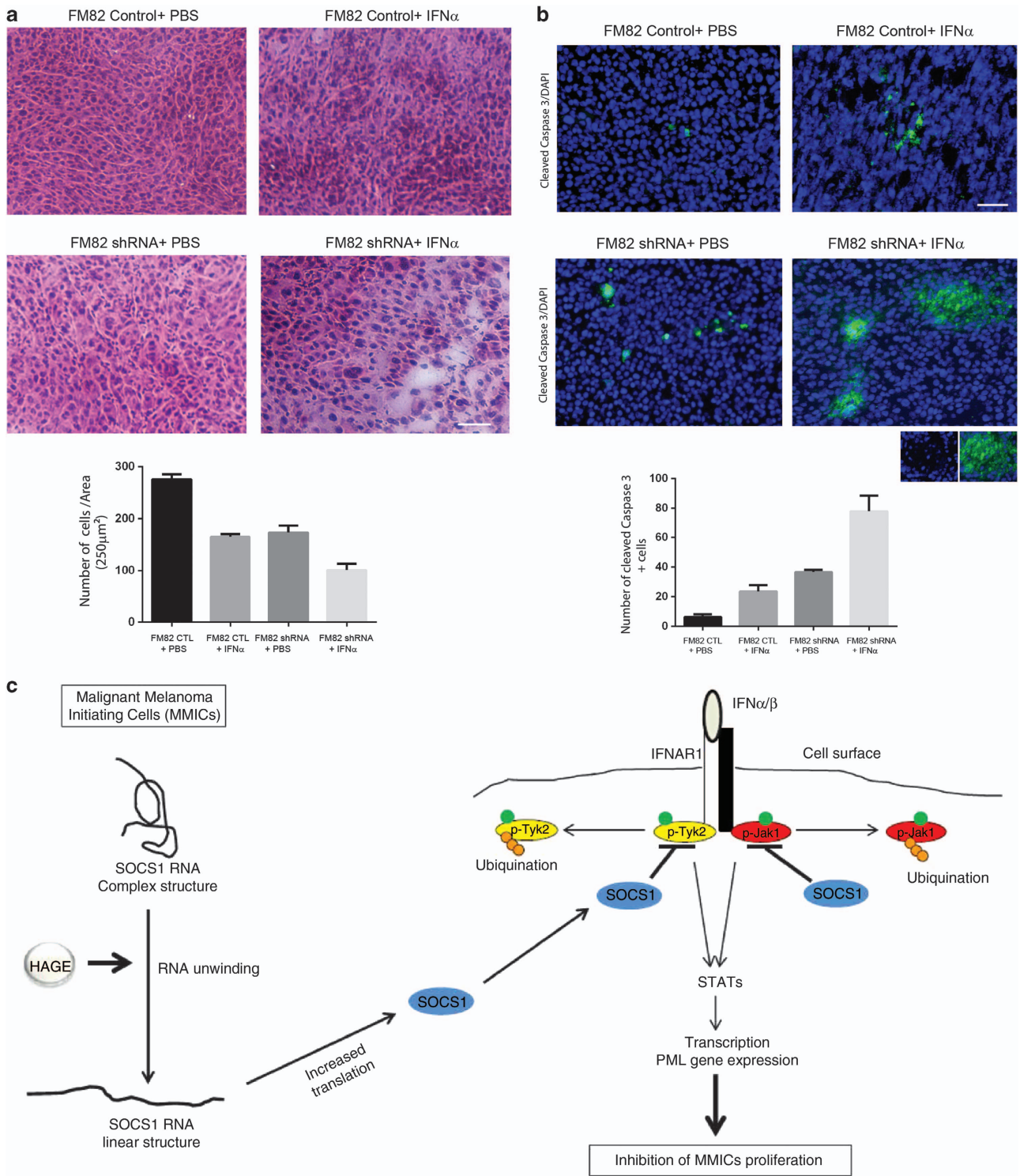
(Figures 6a, b and c). Similar results were observed with tumours derived from FM82 (control) and FM82 shRNA cell lines that had been xenotransplanted into NOD/SCID mice and treated with IFN $\alpha$  (Figures 6d and e). Immunostaining of sections from these tumours using PML antibody revealed an

increased expression of PML in FM82 shRNA tumours treated with IFN $\alpha$  when compared with FM82 control, FM82 control treated with IFN $\alpha$  and IFN $\alpha$  untreated FM82 shRNA-derived tumours (Figure 6f). PML increased expression in IFN $\alpha$ -treated FM82 shRNA-derived tumours correlated with





**Figure 6** HAGE counteracts the anti-proliferative effect of IFN $\alpha$  *in vivo*. (a, b and c) FM82 and FM55 controls and FM82 and FM55 shRNA 1 and 2 melanoma sphere formation in the presence or absence of IFN $\alpha$ . Student *t*-test: \*\**P* = < 0.01. (d) Summary of the *in vivo* experimental procedure. (e) Measurement of tumour growth in mice injected with either FM82 control cells or FM82 shRNA1 cells and treated or untreated with IFN $\alpha$ . ANOVA: \*\**P* = < 0.0028; Mann-Whitney *U*-test: \**P* = < 0.0108 (when comparing FM82 control + PBS and FM82 shRNA + PBS; Mann-Whitney *U*-test: \*\**P* = < 0.0079 (when comparing FM82 control + IFN $\alpha$  and FM82 shRNA + IFN $\alpha$  treated). (f) Immunohistochemistry/fluorescence staining with antibodies to HAGE (red), ABCB5 (green), SOCS1 (green) and on sections from FM82 control and FM82 shRNA1 NOD/SCID xenotransplanted tumours and treated or untreated with IFN $\alpha$ . Scale bar 100  $\mu$ m



**Figure 7** IFN $\alpha$  treatment of HAGE knocked down NOD/Scid xenotransplanted tumours results in a decreased cellularity and increased apoptosis. (a) Hematoxylin and eosin stain on sections from FM82 control and FM82 shRNA1 NOD/SCID xenotransplanted tumours and treated or untreated with IFN $\alpha$ . ANOVA: \*\*\* $P$  = <0.0001 (b) Immunohistochemistry/IF staining with antibody against the apoptotic marker cleaved caspase 3 on sections from FM82 control and FM82 shRNA1 NOD/SCID xenotransplanted tumours and treated or untreated with IFN $\alpha$ . ANOVA: \*\*\* $P$  = <0.0001. (c) Proposed schematic representation of the mechanism by which the helicase HAGE inactivate the anti-proliferative effect of IFN $\alpha$  in ABCB5 + MMICs

an increased apoptosis and a decreased cellularity in these tumours when compared with FM82 control, FM82 control treated with IFN $\alpha$  and IFN $\alpha$ -untreated FM82 shRNA-derived

tumours (Figures 7a and b). Taken together, these results suggest that HAGE expression in ABCB5 + MMICs provides resistance to IFN alpha-PML mediated anti-proliferative and

pro-apoptotic effects by promoting the expression of SOCS1 and the inhibition of PML expression through the inactivation of JAK–STAT pathway (Figure 7c).

## Discussion

Chemotherapy and adjuvant IFN $\alpha$  therapy have been used to prevent recurrence of disease in patients with malignant melanoma. Despite important advances, the fact that many patients develop resistance to these therapies highlights the need to identify and further dissect the cellular and molecular mechanisms that are involved in this resistance.<sup>5</sup> MMICs have been shown to offer such resistance to chemotherapy via their expression of ABCB5. This allows these populations to initiate and perpetuate their malignancy.<sup>1</sup> In this regard, the mechanisms implicating ABCB5 + MMICs in chemo-resistance have been well studied.<sup>3,4,30</sup> However, it is not known if these populations of melanoma cancer stem cells are implicated in the resistance to IFN $\alpha$  therapy. This study focused on investigating those mechanisms with an emphasis on molecules that are involved in the JAK–STAT signalling cascade, a pathway which is activated by IFN $\alpha$ .<sup>9</sup> Indeed, we show here that the helicase HAGE provide MMICs with resistance to the anti-proliferative effects of IFN $\alpha$  by enhancing the expression of SOCS1, a negative regulator of JAK–STAT pathway.<sup>20,31</sup> We have previously shown that HAGE promotes the proliferation and survival of MMICs by promoting the unwinding and the translation of NRAS mRNA.<sup>2</sup> Consistently, a similar mechanism is described here, where we show that HAGE unwinds SOCS1 mRNAs/siRNA duplexes and may therefore promote SOCS1 translation in tumour cells. SOCS1, a ubiquitin E3 ligase, has been shown to bind the phosphorylated forms of JAKs proteins, trigger their ubiquitination and prime them for protein degradation.<sup>28,29,31</sup> We show that HAGE knockdown results in a decreased ubiquitination of p-Jak1 and p-Tyk2, which further demonstrates a functional link between HAGE and SOCS1. Furthermore, SOCS1 was found to be highly expressed in HAGE-expressing tumour cells highlighting the importance of this molecule in melanoma progression. SOCS1 has also been shown to have an important role in melanoma progression and in the downregulation of biological responses by endogenous and/or therapeutically administered cytokines.<sup>32,33</sup> The tumour suppressor PML has an important role in many cellular processes such as cell growth, apoptosis and differentiation. PML exerts its functions by interacting and recruiting different factors into subnuclear structures known as PML-NBs.<sup>17,18</sup> PML localisation is not restricted to PML-NBs and it is observed to be present in other cellular compartments such as the nucleoplasm, the nucleolus, the nuclear envelope and the cytoplasm.<sup>34</sup> The PML gene encodes a variety of isoforms, which are found in all human cell types, with isoform I/II having the highest levels of expression.<sup>35</sup> Expression of PML and its isoforms can be induced at the transcriptional level by the JAK–STAT pathway in response to IFN. Interestingly, PML II, PMLIII or both seem to be predominantly expressed in malignant melanoma cell lines and their level of expression increases following IFN $\alpha$  treatment. Although the localisation of this isoform is mostly nuclear, a cytoplasmic expression can also be observed.

As HAGE prevents the activation of the JAK–STAT pathway in ABCB5 + MMICs, it appears that PML mRNA expression appears to be affected and this leads to the observed decrease in PML protein expression. This is probably the case, as PML expression upon IFN $\alpha$  treatment was also affected by HAGE expression. Moreover, several studies have reported a role for PML in the regulation of stem cell proliferation and differentiation<sup>22,36</sup> and this effect involving HAGE might be one of the mechanisms by which cancer stem cells avoid the anti-proliferative and pro-apoptotic responses mediated by PML. Interestingly, PML expression is found in the cells surrounding HAGE + cells, which suggest that HAGE targets specifically PML to prevent its anti-proliferative and pro-apoptotic functions. Furthermore, FM82 HAGE shRNA tumours treated with IFN $\alpha$  have an increased level of PML expression (and PML-NBs), higher levels of apoptosis and lower cellularity. Finally, PML knock down in FM82 HAGE shRNA resulted in increased size of spheres which pointed out to the specific targeting of PML by HAGE.

Collectively, these findings provide evidence for a previously unknown role of HAGE in ABCB5 + MMIC-dependent resistance to PML-mediated anti-proliferative response of IFN $\alpha$ . We clearly demonstrate that HAGE prevents the activation of JAK–STAT pathway responsible for the induction of the expression of the tumour suppressor PML. Finally, as HAGE is expressed only by tumour cells, these results suggest that cancer therapies targeting HAGE helicase may have broad applications for treating ABCB5 + malignant melanoma and for preventing resistance to IFN $\alpha$  treatment.

## Materials and Methods

**Cell lines and growth conditions.** The human melanoma cell lines, FM82, FM55 and FM6, were a kind gift from Professor D. Schadendorf of the Deutsches Krebsforschungszentrum (Heidelberg, Germany). All cells were cultured as previously described<sup>2</sup> in RPMI 1640 media (Lonza, Basel, Switzerland) supplemented with 10% (v/v) fetal calf serum and 1% (w/v) L-glutamine (Lonza). Cells were incubated at 37 °C in 5% (v/v) CO<sub>2</sub> and 100% humidity. IFN $\alpha$ 2a (IMR-236, Imgenex, San Diego, CA, USA) was used at a concentration of 1000 U/ml.

**Stable and transient transfection of cell lines.** A stable knockdown cell line was created using shRNA-bearing plasmids specific for HAGE (Sure Silencing shRNA Plasmid for Human DDX43, SABiosciences, Crawley, UK). FM82 and FM55 cells were seeded at  $5 \times 10^4$  cells/well into a 24-well plate and grown overnight. About 1.2  $\mu$ g of SureSilencing shRNA were transfected into cells using Lipofectamine 2000 (Invitrogen, Paisley, UK), as described by the manufacturer. Forty-eight hours later, the cells were seeded into a 96-well plate and grown in media treated with 500  $\mu$ g/ml G418 antibiotic to allow selection of plasmid-transfected cells. HAGE expression status was monitored using semi-quantitative real-time PCR, western-blotting and immunofluorescence (IF). The transient knockdown of SOCS1 was carried out using an SOCS1-specific siRNA molecule (Eurogentec, Southampton, UK; sense: 5'-CGACAAUGCAGUCUCCACAdTdT-3'; anti-sense: 5'-UGUGGAGACUGCAUUGUCGdTdT-3') and Interferin transfection reagent (Polyplus, Illkirch, France) following the manufacturer's recommendations. FM82 empty vector (transfected with pcDNA3.1) and FM82 PMLII cell lines (transfected with pcDNA3.1-PMLII, a kind gift from Dr Mounira Chelbi-Alix, University of PARIS 5) were generated using the same procedure as above. HAGE or SOCS1 ectopic expression were carried out using pCMV6-DLX5-HAGE (SC126051, OriGene, Rockville, MD, USA) and pCMV6-XL4-SOCS1 (SC111081, OriGene). Transfection was performed using Lipofectamine 2000 protocol and 12  $\mu$ g of the vector was used to transfect a T25 flask, as described by the manufacturer. Cells were harvested for protein extraction 48 h after transfection. PML lentiviral plasmids shRNA control and PML shRNA1 and 2 were purchased from Sigma (St. Louis, MO, USA) (TRCN0000003866, TRCN0000003869, SHC001). The lentiviral packaging mix was also purchased from Sigma (SHP001).

The lentiviral particules used to infect FM82shRNA were produced corresponding to the manufacturer recommendations.

**Antibodies.** For this study, we used monoclonal antibodies to HAGE (1:250 for IB; 1:50 IF, SAB1400618, Sigma), ABCB5 (1:500 for IB; 1:100 for IF, HPA026975, Sigma), PML (1:500 for IF, sc-5621), PML (1:250 for IF; 1:250 for IB, sc-966, Santa Cruz Biotechnology, Montgomery, TX, USA), PML (1:1000 for WB, A310-390A PML Antibody AbVantage Pack, Bethyl Laboratories, Dallas, TX, USA),  $\beta$ -actin (1:250 for IB, sc-130657, Santa Cruz Biotechnology), SOCS1 (1:300 for IB, 3950, Cell Signaling Technology, Danvers, MA, USA), SOCS1 (1:100 for IP, 1:200 for IB; 1:100 for IF, sc-9021, Santa Cruz Biotechnology), Ubiquitin (1:300 for IB, 3933, Cell Signaling Technology), Phospho-Jak1 (1:300 for IB, 3331, Cell Signaling Technology), Phospho-Jak1 (1:100 for IP; 1:200 for IB, sc-101716, Santa Cruz Biotechnology), Phospho-Stat1 (1:300 for IB, 9171, Cell Signaling Technology), Phospho-Stat1 (1:300 for IB, 9171, Cell Signaling Technology), Phospho-Stat2 (1:500 for IB, 07-224, Millipore, Billerica, MA, USA), Phospho-Tyk2 (1:200 for IB; 1:100 for IP, sc-11763, Santa Cruz Biotechnology), IFN  $\alpha/\beta$  R (1:200 for IB, sc-7391, Santa Cruz Biotechnology), Tyrosinase (1:200 for IF; ab112231, Abcam, Cambridge, UK), SOCS3 (1:200 for IB; sc-51699, Santa Cruz Biotechnology), SOCS2 (1:200 for IB; sc-9022, Santa Cruz Biotechnology), Cleaved caspase 3 (1:200 for IF, 9661; Cell Signaling Technology) and Phospho-Rb (1:200 for IF, 9308; Cell Signaling Technology).

**Immunohistochemistry and IF.** Paraffin-embedded human melanoma TMA's were purchased from US Biomax (Rockville, MD, USA). The sections were de-waxed, re-hydrated in graded alcohols, rinsed in ddH<sub>2</sub>O and antigen retrieval was performed for 10 min (0.01 M citrate phosphate buffer at pH 6.0) in a microwave at 1000W. The tumours excised from NOD/SCID mice were embedded in OCT media, fixed in 2-methyl-butane (Sigma) that had been super-cooled in liquid N<sub>2</sub> and sectioned using a CM1900 cryostat (Leica, Wetzlar, Germany). Melanoma cells were fixed in 4% (w/v) paraformaldehyde and then treated as follows: the sections or cancer cells were washed three times in 1X phosphate-buffered saline (PBS) for 10 min each, blocked and permeabilised in 10% (w/v) bovine serum albumin in 0.1% (v/v) PBS-Tween, incubated overnight with primary antibody (in blocking solution), washed three times for 10 min each with 1X PBS, incubated for one hour with secondary antibody (in blocking solution) and washed three times with 1X PBS. Sections and melanoma cells were counterstained and mounted with DAPI fluorescent medium (Vector Laboratories, Peterborough, UK) for IF microscopy.

**Genetic analysis.** FM82 and FM55 control and FM82 and FM55 shRNAs cells were grown to 80% confluence as described above. Total RNA was extracted from cells using RNA-STAT 60 reagent (AMS Biotechnology, Abingdon, UK) as described by the manufacturer. Extracted RNAs were quantified using a Nanodrop spectrophotometer (Thermo Scientific, Loughborough, UK). Moloney murine leukemia virus reverse transcriptase (Promega, Madison, WI, USA), oligo-dT primers (Promega) and 2  $\mu$ g of total RNA were subsequently used for cDNA synthesis following the manufacturer's protocol. Semi-quantitative real-time PCR was then carried out using primers (all MWG Eurofins, Ebersberg, Germany) specific for PML (forward: 5'-GGAGCAGGATAGTGCCTTTG-3'; reverse: 5'-CTGGCCATCTCCTCGTAGTC-3', and SOCS1 (forward: 5'-CGACAATG CAGTCTCCACAG-3'; reverse 5'-GAGGAGGAGGAAGAGGAGGA-3') and the housekeeping genes TBP1 (forward: 5'-TGCACAGGAGCAAGAGTGAA-3'; reverse: 5'-CACATCACAGCTCCCCACCA-3') and HPRT1 (forward: 5'-TGAC ACTGGCAAAACAATGCA-3'; reverse: 5'-GGTCCTTTTACCAGCAAGCT-3') using a Rotor-Gene 6000 real-time PCR cycler (Qiagen, Venlo, The Netherlands). Forty cycles were performed and melt curves were ratified following each analysis. Expression of the genes of interest was normalised using averaged results for the housekeeping genes and  $2^{-\Delta\Delta C_T}$  calculations were performed.

**IB, IP and protein metabolic labelling.** For IB, cancer cells were collected, washed with 1X PBS, lysed in 1X solution containing 50 mM Tris-HCl (pH 6.8), 100 mM dithiothreitol, 2% (w/v) SDS, 0.1% (w/v) bromophenol blue and 10% (v/v) glycerol, and loaded on Tris/glycine SDS-polyacrylamide gels. Proteins were separated alongside a molecular weight marker (BioRad, Hercules, CA, USA). Protein bands were transferred onto Amersham Hybond-P PVDF membranes (GE Healthcare, Chalfont, UK). Membranes were blocked with 10% (w/v) Marvel milk/tris-buffered saline (TBS) solution with 0.05% (v/v) Tween-20 (TBST). Following washes in TBST, membranes were incubated with primary

antibodies (in blocking solution) overnight at 4 °C followed by washing and incubation with secondary antibodies for 1 h at room temperature, prior to visualisation using Rapid Step ECL reagent (Calbiochem, Billerica, MA, USA) and a CCD camera (Fujifilm, Bedford, UK). For IP, the cells were lysed in IP buffer (0.05 M Tris pH 7.4, 0.15 M NaCl, 0.5% (v/v) Triton X-100, and 0.001 M EDTA). The extracts were pre-cleared for 1 h at 4 °C using Protein G Plus-Agarose beads (IP08, Calbiochem) and corresponding IgGs. For the antibody binding, antibodies to SOCS1, Phospho-Jak1 or Phospho-Tyk2 were incubated with agarose beads for 2 h in IP buffer before adding the pre-cleared extracts for overnight IP. For SOCS1 protein labelling, FM82 control cell line was transfected with SOCS1 cDNA (OriGene, SC111081) and with or without HAGE cDNA. 24 h later the cells were divided into four flasks, each containing  $1 \times 10^6$  cells for each experiment (in the presence or absence of HAGE). Each flask was incubated in a media without methionine for 30 min (RPMI-1640, R7513; Sigma) and 50  $\mu$ M of protein labelling compound (L-azidohomoalanine) was added (for 0, 30, 60 and 120 min) as recommended by the manufacturer (Click-it AHA (L-azidohomoalanine) for nascent protein synthesis, C10102; Invitrogen). The cell extracts from each flask were treated with Biotin alkyne (Click-it Biotin Protein Analysis Detection Kit, C33372, Invitrogen) and subjected to IP with SOCS1 antibody, followed by IB with Streptavidin-HRP.

**In vitro transcription and RNA labelling.** The plasmid pCMV6-XL4 containing SOCS1 was purchased from OriGene (SC111081) and used for *in vitro* transcription using T7 promoter to generate SOCS1 transcript (Ambion, Paisley, UK). SOCS1 N-terminal RNA complementary sequence 5'-ACAACCAGGUGG-CAGCCGACAAUGCAGUCUCCACAGCAGC-3' labelled using Pierce RNA 3' End Biotinylation Kit (Thermo Scientific). The labelling efficiency was determined by dot blotting following the manufacturer's recommendations.

**Native RNA gels and winding/unwinding assay.** Biotinylated N-terminal RNA complementary sequence (2 pmol; labelling efficiency higher than 75%; was placed to wind with unlabelled SOCS1 RNA in a solution containing 3.5 mM equimolar of ATP/MgCl<sub>2</sub> for 5 min at 95 °C, followed by 1 h at 37 °C. Recombinant HAGE protein was added at two different concentrations (0.6  $\mu$ g, 1.2  $\mu$ g) after the RNA winding assay, followed by 1 h incubation at 37 °C. The reactions were stopped by the addition of 50% (v/v) glycerol, 20 mM EDTA, 2% (w/v) SDS and 0.025% (w/v) bromophenol blue. Samples were analysed on 10% (w/v) native acrylamide gels in 1  $\times$  TBE buffer followed by blot transfer and visualisation using a Chemiluminescent Detection Module (Thermo Scientific).

**Melanoma spheroid cell culture.** For the culture of melanoma spheres, cells from FM82 empty vector, FM82 PMLII, FM82 and FM55 controls and FM82 and FM55 shRNAs were cultured at clonal density ( $1 \times 10^4$  cells/ml in 24-well plates) in a DMEM/F12 media (Gibco Invitrogen, Paisley, UK; 32 500) supplemented with N-2 Max Media (R&D Systems, Minneapolis, MN, USA; AR009), and daily addition of 100 ng/ml FGF basic and 100 ng/ml EGF (both from Sigma) for a 10-day culture period.<sup>2</sup> The differentiation of melanoma spheres was induced by the withdrawal of FGF basic and EGF. The cells were stained by IF as described above. For IFN $\alpha$  studies, the melanoma spheres were cultured for 15 days and IFN $\alpha$  (1000 U/ml) was added at day 9 and 12. Sphere diameters were measured using Carl Zeiss AxioVision software.

**Tumour transplantation assay.** NOD/SCID mice were acquired (Harlan Laboratories, Sharnlow, UK) and kept in accordance with the Animals (Scientific Procedures) Act 1986. The mice were used for tumour transplantation Assay (xenotransplantation assay) using FM82 control or FM82 shRNA cells, as previously described.<sup>2</sup> When tumours reached 3 mm<sup>2</sup> in size (monitored using a caliper), PBS or IFN $\alpha$ 2a ( $4 \times 10^6$  IU) (PHP107Z, AbD Serotec, Hercules, CA, USA) were injected locally three times a week for a period of 4 weeks. The tumours were collected and measured using a ruler. The sections were obtained from three different levels within the tumours (10 sections of 10  $\mu$ m separating each level). For determining the tumours cellularity and the counting of the number of cells expressing the cleaved caspase 3, three pictures were taken randomly from each sections and from each level and were used for the counting. The sections were stained by immunohistochemistry/IF as described above.

## Conflict of Interest

The authors declare no conflict of interest.

**Acknowledgements.** This work was funded by The John and Lucille van Geest Foundation. We would like to thank Dr Mounira Chelbi-Alix for the PML plasmids (CNRS FRE3235, Université Paris Descartes, Paris, France), Mr Stephen Reeder and Mrs Anne Schneider for their precious help.

- Schatton T, Murphy GF, Frank NY, Yamaura K, Waaga-Gasser AM, Gasser M, Zhan Q, Jordan S, Duncan LM, Weishaupt C, Fuhlbrigge RC, Kupper TS, Sayegh MH, Frank MH. Identification of cells initiating human melanomas. *Nature* 2008; **451**: 345–349.
- Linley AJ, Mathieu MG, Miles AK, Rees RC, McArdle SEB, Regad T. The Helicase HAGE expressed by malignant melanoma-initiating cells is required for tumor cell proliferation *in vivo*. *J Biol Chem* 2012; **287**: 13633–13643.
- Frank NY, Schatton T, Kim S, Zhan Q, Wilson BJ, Ma J, Saab KR, Osherov V, Widlund HR, Gasser M, Waaga-Gasser AM, Kupper TS, Murphy GF, Frank MH. VEGFR-1 expressed by malignant melanoma initiating cells is required for tumor growth. *Cancer Res* 2011; **71**: 1474–1485.
- Wilson BJ, Schatton T, Zhan Q, Gasser M, Ma J, Saab KR, Schanche R, Waaga-Gasser AM, Gold JS, Huang Q, Murphy GF, Frank MH, Frank NY. ABCB5 identifies a therapy-refractory tumor cell population in colorectal cancer patients. *Cancer Res* 2011; **71**: 5307–5316.
- Hauschild A. Adjuvant interferon alpha for melanoma: new evidence-based treatment recommendations? *Current Oncol* 2009; **16**(3): 3–6.
- Wheatley K, Ives N, Hancock B, Gore M, Eggermont A, Suci S. Does adjuvant interferon-alpha for high-risk melanoma provide a worthwhile benefit? A meta-analysis of the randomised trials. *Cancer Treat Rev* 2003; **29**(4): 241.
- Tarhini AA, Gogas H, Kirkwood JM. IFN- $\alpha$  in the treatment of melanoma. *J Immunol* 2012; **15**(8): 3789–3793.
- Aaronson S, Horvath CM. A road map for those who don't know JAK-STAT. *Science Signal* 2002; **296**(5573): 1653–1655.
- Schindler C, Plumlee C. Interferons pen the JAK–STAT pathway. *Semin Cell Dev Biol* 2008; **19**(4): 311–318.
- Chelbi-Alix MK, Pelicano KL, Quignon F, Koken MH, Venturini L, Stadler M, Pavlovic J, Degos L. Induction of the PML protein by interferons in normal and APL cells. *Leukemia* 1995; **9**(12): 2027–2033.
- Stadler M, Chelbi-Alix MK, Koken MH, Venturini L, Lee C, Saib A, Quignon F, Pelicano L, Guillemain MC, Schindler C *et al*. Transcriptional induction of the PML growth suppressor gene by interferons is mediated through an ISRE and a GAS element. *Oncogene* 1995; **11**(12): 2565–2573.
- Lavau C, Marchio A, Fagioli M, Jansen J, Falini B, Lebon P *et al*. The acute promyelocytic leukaemia-associated PML gene is induced by interferon. *Oncogene* 1995; **11**(5): 871–876.
- de The H, Chomienne C, Lanotte M, Degos L, Dejean A. The t(15;17) translocation of acute promyelocytic leukaemia fuses the retinoic acid receptor alpha gene to a novel transcribed locus. *Nature* 1990; **347**: 558–561.
- Borrow J, Goddard AD, Sheer D, Solomon E. Molecular analysis of acute promyelocytic leukemia breakpoint cluster region on chromosome 17. *Science* 1990; **249**(4976): 1577–1580.
- Kakizuka A, Miller WH Jr., Umesono K, Warrell RP Jr, Frankel SR, Murty VV *et al*. Chromosomal translocation t(15;17) in human acute promyelocytic leukemia fuses RAR alpha with a novel putative transcription factor, PML. *Cell* 1991; **66**(4): 663–674.
- Regad T, Chelbi-Alix MK. Role and fate of PML nuclear bodies in response to interferon and viral infections. *Oncogene* 2001; **20**(49): 7274–7286.
- Salomoni P, Pandolfi PP. The role of PML in tumor suppression. *Cell* 2002; **108**(2): 165–170.
- Lallemant-Breitenbach PML nuclear bodies. *Cold Spring Harb Perspect Biol* 2010; **2**(5): a000661.
- Marie-Claude G, Chelbi-Alix MK. Role of promyelocytic leukemia protein in host antiviral defense. *J Interferon Cytokine Res* 2011; **31**(1): 145–158.
- Kamura T, Sato S, Haque D, Liu L, Kaelin WG Jr, Conaway RC, Conaway JW. The Elongin BC complex interacts with the conserved SOCS-box motif present in members of the SOCS, ras, WD-40 repeat, and ankyrin repeat families. *Genes Dev* 1998; **12**(24): 3872–3881.
- Gurrieri C, Capodici P, Bernardi R, Scaglioni PP, Nafa K, Rush LJ *et al*. Loss of the tumor suppressor PML in human cancers of multiple histologic origins. *J Natl Cancer Inst* 2004; **96**(4): 269–279.
- Regad T, Bellodi C, Nicotera P, Salomoni P. The tumor suppressor PML regulates cell fate in the developing neocortex. *Nat Neurosci* 2009; **12**: 132–140.
- Groskreutz DJ, Babor EC, Monick MM, Varga SM, Hunninghake GW. Respiratory syncytial virus limits  $\alpha$  subunit of eukaryotic translation initiation factor 2 (eIF2 $\alpha$ ) phosphorylation to maintain translation and viral replication. *J Biol Chem* 2010; **285**(31): 24023–24031.
- Cordin O, Banroques J, Tanner NK, Linder P. The DEAD box protein family of RNA helicases. *Gene* 2006; **367**: 17–37.
- Linder P. Dead-box proteins. A family affair—active and passive players in RNP remodeling. *Nucleic Acids Res* **34**: 4168–4180.
- Jankowsky A, Guenther UP, Jankowsky E. The RNA helicase database. *Nucleic Acids Res* 2011; **39**(2006): 338–341.
- Dias WB, Cheung WD, Wang Z, Hart GW. Regulation of calcium/calmodulin-dependent kinase IV by O-GlcNAc modification. *J Biol Chem* 2009; **284**(32): 21327–21337.
- Piganis RAR, De Weerd NA, Gould J, Schindler CW, Mansell A, Nicholson SE, Hertzog PJ. Suppressor of cytokine signaling (SOCS) 1 inhibits type I interferon (IFN) signaling via the interferon  $\alpha$  receptor (IFNAR1) associated tyrosine kinase Tyk2. *J Biol Chem* 2011; **286**(39): 33811–33818.
- Ungureanu D, Saharinen P, Junttila I, Hilton DJ, Silvennoinen O. Regulation of Jak2 through the ubiquitin-proteasome pathway involves phosphorylation of Jak2 on Y1007 and interaction with SOCS-1. *Mol Cell Biol* 2002; **22**(10): 3316–3326.
- Regad T. Molecular and cellular pathogenesis of melanoma initiation and progression. *Cell Mol Life Sci* 2013; **70**(21): 4055–4065.
- Endo TA, Masuhara M, Yokouchi M, Suzuki R, Sakamoto H, Mitsui K, Yoshimura A. A new protein containing an SH2 domain that inhibits JAK kinases. *Nature* 1997; **387**(6636): 921–924.
- Li Z, Metzke D, Nashan D, Müller-Tidow C, Serve HL, Poremba C, Luger TA, Böhm M. Expression of SOCS-1, suppressor of cytokine signalling-1, in human melanoma. *J Invest Dermatol* 2004; **123**(4): 737–745.
- Lesinski GB, Zimmerman JM, Kreiner M, Trefry J, Bill MA, Young GS, Becknel B, Carson WE. Modulation of SOCS protein expression influences the interferon responsiveness of human melanoma cells. *BMC Cancer* 2010; **10**(1): 142.
- Carracedo A, Ito K, Pandolfi PP. The nuclear bodies inside out: PML conquers the cytoplasm. *Curr Opin Cell Biol* 2011; **23**(3): 360–366.
- Condemine W, Takahashi Y, Zhu J, Puvion-Dutilleul F, Guegan S *et al*. Characterization of endogenous human promyelocytic leukemia isoforms. *Cancer Res* 2006; **66**: 6192–6198.
- Ito K, Bernardi R, Morotti A, Matsuoka S, Saglio G, Ikeda Y *et al*. PML targeting eradicates quiescent leukaemia-initiating cells. *Nature* 2008; **453**(7198): 1072–1078.



**Cell Death and Disease** is an open-access journal published by **Nature Publishing Group**. This work is licensed under a **Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported License**. To view a copy of this license, visit <http://creativecommons.org/licenses/by-nc-sa/3.0/>

Supplementary Information accompanies this paper on Cell Death and Disease website (<http://www.nature.com/cddis>)