npg

ORIGINAL ARTICLE

SOX2 regulates self-renewal and tumorigenicity of human melanoma-initiating cells

R Santini[1,4], S Pietrobono[1,4], S Pandolfi[1,4], V Montagnani[1], M D'Amico[2], JY Penachioni[1], MC Vinci[1,5], L Borgognoni[3] and B Stecca[1]

Melanoma is one of the most aggressive types of human cancer, characterized by enhanced heterogeneity and resistance to conventional therapy at advanced stages. We and others have previously shown that HEDGEHOG-GLI (HH-GLI) signaling is required for melanoma growth and for survival and expansion of melanoma-initiating cells (MICs). Recent reports indicate that HH-GLI signaling regulates a set of genes typically expressed in embryonic stem cells, including *SOX2* (sex-determining region Y (SRY)-Box2). Here we address the function of SOX2 in human melanomas and MICs and its interaction with HH-GLI signaling. We find that SOX2 is highly expressed in melanoma stem cells. Knockdown of SOX2 sharply decreases self-renewal in melanoma spheres and in putative melanoma stem cells with high aldehyde dehydrogenase activity (ALDH^{high}). Conversely, ectopic expression of SOX2 in melanoma cells enhances their self-renewal *in vitro*. SOX2 silencing also inhibits cell growth and induces apoptosis in melanoma cells. In addition, depletion of SOX2 progressively abrogates tumor growth and leads to a significant decrease in tumor-initiating capability of ALDH^{high} MICs upon xenotransplantation, suggesting that SOX2 is required for tumor initiation and for continuous tumor growth. We show that SOX2 is regulated by HH signaling and that the transcription factors GLI1 and GLI2, the downstream effectors of HH-GLI signaling, bind to the proximal promoter region of *SOX2* in primary melanoma cells. In functional studies, we find that SOX2 function is required for HH-induced melanoma cell growth and MIC self-renewal *in vitro*. Thus SOX2 is a critical factor for self-renewal and tumorigenicity of MICs and an important mediator of HH-GLI signaling in melanoma. These findings could provide the basis for novel therapeutic strategies based on the inhibition of SOX2 for the treatment of a subset of human melanomas.

Oncogene (2014) **33**, 4697–4708; doi:10.1038/onc.2014.71; published online 31 March 2014

INTRODUCTION

Melanoma is a dynamic and heterogeneous skin cancer, with adverse prognosis in advanced stages. A large body of evidence suggests that within the heterogeneous population that constitutes a melanoma certain cell types exhibit molecular and functional features similar to stem cells. These putative melanoma-initiating cells (MICs) have unlimited self-renewal and multilineage differentiation abilities and the potential to initiate and maintain tumor growth.[1–9] Furthermore, MICs are believed to be resistant to both conventional chemotherapeutic agents and newly developed targeted drugs.[10,11] Although recent studies have began to explore ways to target MICs,[12–14] the molecular players involved in maintenance of MICs have not yet been identified.

We and others have previously shown that HEDGEHOG-GLI (HH-GLI) signaling is required for melanoma growth and stemness.[7,15–18] In physiological conditions, Sonic hedgehog promotes the development of multipotent neural crest progenitors,[19] from which melanocytes originate; it also modulates the proliferation of human melanocytes.[15] Similarly, it regulates brain stem cell lineages[20,21] and skin stem cells.[22,23] Furthermore, HH-GLI signaling has been shown to regulate the transcription factor SOX2 (sex-determining region Y (SRY)-Box2) in several contexts.[24–27]

SOX2 is a member of the high mobility group domain family that plays a critical role in embryonic development and in maintaining pluripotency and self-renewal in embryonic stem cells[28,29] and several cell lineages such as neural cells,[30] osteoblasts[31] and neural crest melanocytes.[32] In adult mice, Sox2 is expressed in different epithelial compartments, in which it marks cells with self-renewal properties, and its targeted ablation lethally disrupts epithelial tissue homeostasis.[33] Moreover, SOX2 is one of the key transcription factors capable of reprogramming differentiated somatic cells into induced pluripotent stem (iPS) cells.[34–36]

Recent studies have pointed to an important role of SOX2 in cancer. *SOX2* is amplified in esophageal, oral and lung squamous cell carcinomas and in small-cell lung cancer.[37–39] SOX2 is involved in several types of cancer, such as glioblastoma and osteosarcoma, and lung, breast, ovarian, pancreatic, prostate and gastric cancers[40–48] and promotes tamoxifen resistance in breast cancer cells.[49] SOX2 is expressed in about 50% of melanomas and only in a minority of nevi.[50–52] Silencing of SOX2 has been shown to decrease A2058 melanoma cell growth *in vivo* but not *in vitro*[50] and to reduce melanoma cell invasion.[53] However, it is currently unknown whether SOX2 is critical in regulating MICs.

Here we have thoroughly investigated the role of SOX2 in melanoma cell proliferation, stemness and tumorigenicity in a

[1]Laboratory of Tumor Cell Biology, Core Research Laboratory—Istituto Toscano Tumori (CRL-ITT), Florence, Italy; [2]Department of Experimental and Clinical Medicine, University of Florence, Florence, Italy and [3]Plastic Surgery Unit, S.M. Annunziata Hospital—Regional Melanoma Referral Center, Istituto Toscano Tumori, Florence, Italy. Correspondence: Dr B Stecca, Laboratory of Tumor Cell Biology, Core Research Laboratory—Istituto Toscano Tumori (CRL-ITT), Viale Pieraccini 6, Florence 50139, Italy.
E-mail: barbara.stecca@ittumori.it
[4]These authors contributed equally to this work.
[5]Current address: Centro Cardiologico Monzino, Milano, Italy.
Received 1 August 2013; revised 13 February 2014; accepted 17 February 2014; published online 31 March 2014

panel of patient-derived MICs and its interaction with HH signaling. We show that silencing of SOX2 leads to a remarkable growth suppression and apoptosis in melanoma cells. Importantly, SOX2 abrogation impairs the ability of MICs to self-renew *in vitro* and to initiate and to maintain tumor growth *in vivo*. Furthermore, we find that SOX2 is directly regulated by HH-GLI signaling and acts as a mediator of HH in melanoma cells.

RESULTS

SOX2 silencing inhibits growth and induces apoptosis in primary melanoma cells

SOX2 expression was investigated in 19 patient-derived primary melanoma cells, in A375 melanoma cell line and in normal human epidermal melanocytes (Supplementary Table S1). Quantitative real-time PCR (qPCR) revealed variable expression of *SOX2*; approximately half of the primary melanoma cultures showed high/intermediate levels and half no/very low expression (Figure 1a), in line with previous immunohistochemistry studies.[50–52] *SOX2* expression was documented at low levels in normal human epidermal melanocytes. Immunofluorescence analysis revealed SOX2 expression in the nuclei of primary melanoma cells (Supplementary Figure S1). No significant correlation was found between *SOX2* expression and tumor grade or other clinical features.

SOX2 silencing has been shown to decrease A2058 melanoma cell growth *in vivo* but not *in vitro*.[50] To clarify its function in melanoma, we knocked down SOX2 in patient-derived melanoma cells with high (SSM2c and M26c) and intermediate (M5 and the A375 melanoma cell line) *SOX2* levels using two independent SOX2 shRNAs (LV-shSOX2-1 and LV-shSOX2-2). SOX2 silencing led to a near complete loss of SOX2 protein (Figure 1b) and resulted in a drastic reduction in the number of viable cells in SSM2c, M26c (Figure 1c), M5 and A375 cells (Supplementary Figure S2). Analysis of the proliferation index, determined by carboxyfluorescein succinimidyl ester (CFSE) staining, indicated that SSM2c and M26c SOX2-depleted cells grew slower than control cells (Figure 1d). Cell cycle analysis confirmed a slight reduction of cells in S phase, but no changes in the fraction of cells in G0/G1 upon SOX2 knockdown ($P < 0.05$ in both cell types; Supplementary Figures S3a and b). SOX2 silencing significantly increased both early and late apoptosis, as shown by Annexin V/7-aminoactino-mycin D (7-AAD) staining (Figures 1e and f). Consistently, SOX2 knockdown induced the expression of the apoptotic markers *TP73* and *NOXA* and concomitant downregulation of the anti-apoptotic factor *BCL-2* (Figure 1g). Transient silencing of SOX2 induced phosphorylation of γH2AX and promoted poly ADP-ribose polymerase (PARP) cleavage, confirming signs of DNA damage and apoptosis as soon as 48 h after transfection (Figure 1h). Altogether, these results indicate that interference with SOX2 function inhibits melanoma cell growth by promoting apoptosis and, partially, by reducing proliferation.

SOX2 expression is enhanced in melanoma cells with stem cell features

Because tumor sphere assay allows the enrichment of potential MICs,[1,7,54–56] we compared *SOX2* expression in melanoma spheres and in adherent cells by qPCR. We found that melanoma spheres obtained from SSM2c and M26c cells were greatly enriched in the expression of *SOX2* when compared with the corresponding adherent cells (Figure 2a). Confocal microscopy in spheres showed SOX2 protein expression in the nucleus of SSM2c and M26c sphere-forming cells, with higher levels in a fraction of them (Figure 2b).

As an alternative approach to analyze SOX2 expression in MICs, we sorted melanoma cells with high aldehyde dehydrogenase activity (ALDH^high), which has been shown to mark a population

enriched for melanoma stem cells.[6,7,57] SOX2 protein level was 2–3-fold higher in ALDH^high cells compared with the ALDH^low population in both SSM2c and M26c cells (Figure 2c). Consistently, expression of *SOX2* mRNA in ALDH^high cells was 2.7- and 3.6-fold higher than in the ALDH^low population, respectively, in SSM2c and M26c cells (Figures 2d and e). In addition, increased expression of *KLF4, NANOG* and, to a lesser extent, *OCT4*, which have a role in the maintenance of cancer stem cells (CSCs), was observed in the ALDH^high population (Figures 2d and e). Altogether, these data indicate that SOX2 is highly expressed in melanoma cells with stem cell-like features.

SOX2 regulates self-renewal of melanoma stem cells

Because SOX2 is highly expressed in the ALDH^high population (Figure 2), which is enriched in CSCs, we evaluated whether SOX2 was involved in the maintenance of putative ALDH^high MICs. To test this possibility, we measured the number of ALDH^high melanoma cells after SOX2 silencing. Cytometric analysis revealed a drastic reduction in the fraction of ALDH^high cells in SSM2c, M26c, M5 and A375 melanoma cells transduced with two different SOX2 shRNAs (Figure 3a and Supplementary Figure S4). Importantly, SOX2 silencing reduced self-renewal of ALDH^high but not that of ALDH^low spheres (Figure 3b), consistent with lower levels of SOX2 expression in ALDH^low cells (Figure 2). Knockdown of SOX2 significantly decreased the size of ALDH^high and, to a lesser extent, of ALDH^low spheres in both SSM2c and M26c cells (Figure 3c), suggesting an effect on proliferation and/or death of sphere-forming progenitor cells. Indeed, analysis of bromodeoxy-yuridine (BrdU) and Annexin V/7-AAD staining indicated that SOX2 silencing diminishes ALDH^high sphere size by reducing prolifera-tion and by increasing apoptosis (early and late). On the other hand, the slight decrease of ALDH^low sphere size upon SOX2 knockdown appeared to depend mostly on reduced proliferation (Figures 3d and e).

As an alternative approach to test the role of SOX2 in MICs, we evaluated whether the modulation of SOX2 could affect the behavior of melanoma spheres, which are enriched in CSCs and are able to self-renew. Interestingly, SOX2 expression correlated with their ability to form primary spheres in limiting dilution assays (Supplementary Figures S5a–c). All melanoma spheres used in this study could form tumors with high penetrance when injected into nude mice (data not shown) and express variable levels of melanoma stem cell markers, including *ABCB5, JARID1B* and *CD271* (Supplementary Figure S5d). To test SOX2 function in melanoma spheres, we first silenced it. In both SSM2c and M26c spheres, LV-shSOX2-1 and LV-shSOX2-2 reduced SOX2 protein levels by 90–95% compared with LV-c control (Figure 4a). SOX2 silencing inhibited self-renewal of SSM2c, M26c, M5 and A375 spheres (Figure 4b). Moreover, SOX2-depleted melanoma spheres were significantly smaller than controls (Figures 4c and d). Knockdown of SOX2 in SSM2c and M26c melanoma spheres slightly reduced cell proliferation, as determined by BrdU incorporation and CFSE analysis (Figure 4e and Supplementary Figure S6a), and increased apoptosis (Figure 4f and Supplementary Figure S6b). To further confirm the effect of SOX2 in melanoma spheres, we overexpressed it in M33c cells, which show low levels of *SOX2* (Figure 1a), and in SSM2c cells. SOX2 overexpression significantly increased the number of secondary spheres (Figures 5a and b) and slightly increased melanoma sphere size (Figures 5c and d). Moreover, SOX2 marginally increased cell proliferation, as determined by CFSE analysis (Supplementary Figure S7a), and decreased apoptosis (Supplementary Figure S7b) of SSM2c and M33c melanoma spheres. qPCR analysis showed that SOX2 induced the expression of *NANOG* and *OCT4* in both sphere types and of *KLF4* only in SSM2c spheres (Figures 5e and f). SOX2 overexpression induced the expression of *BCL-2* and, to a lesser extent,
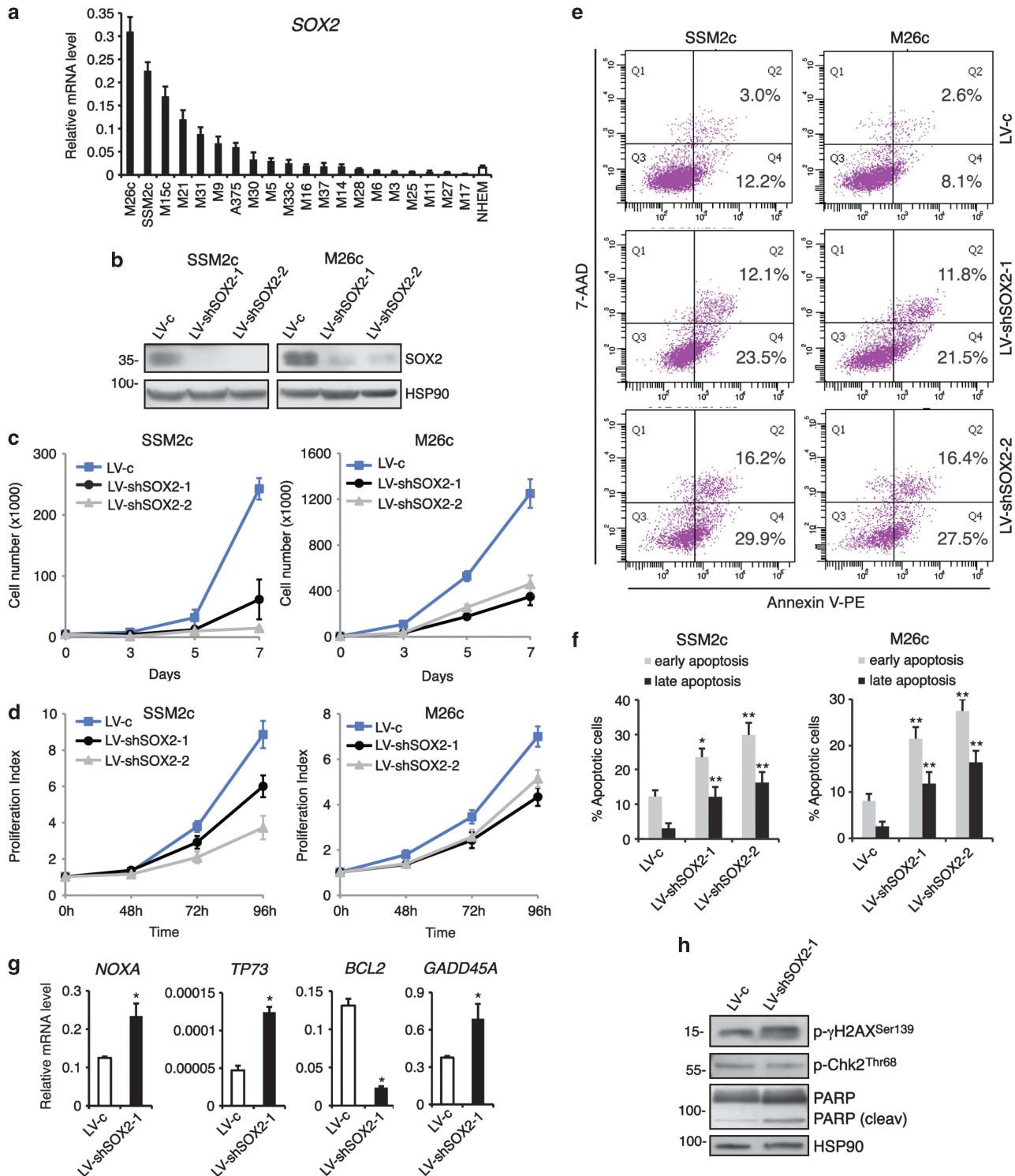
Figure 1. SOX2 silencing suppresses cell growth and induces apoptosis in primary melanoma cells. (**a**) qPCR analysis of *SOX2* in a panel of 19 patient-derived melanoma cells, A375 melanoma cells and normal human epidermal melanocytes. qPCR values reflect C_t values after normalization with two housekeeping genes (*GAPDH* and *β-ACTIN*). (**b**) Western blotting analysis of SSM2c and M26c adherent cells stably transduced with LV-c, LV-shSOX2-1 and LV-shSOX2-2. HSP90 was used as a loading control. (**c**) Growth curves of SSM2c and M26c melanoma cells stably transduced with LV-c, LV-shSOX2-1 or LV-shSOX2-2. Three to five thousands transduced cells/well were plated in 12-well plates, and cells were counted on days 3, 5 and 7. (**d**) Proliferation index measured by CFSE staining in SSM2c and M26c melanoma cells stably transduced with LV-c, LV-shSOX2-1 or LV-shSOX2-2. (**e**, **f**) SSM2c and M26c cells transduced with LV-c, LV-shSOX2-1 or LV-shSOX2-2 were analyzed by flow cytometry for Annexin V$^+$/7-AAD$^-$ (early apoptosis) and Annexin V$^+$/7-AAD$^+$ cells (late apoptosis). (**g**) qPCR analysis of *NOXA*, *TP73*, *BCL-2* and *GADD45A* in M26c cells transduced with LV-c and LV-shSOX2-1. qPCR values reflect C_t values after normalization with two housekeeping genes (*GAPDH* and *β-ACTIN*). (**h**) Western blotting analysis of p-γH2AX, p-Chk2 and poly ADP-ribose polymerase (PARP) in M26c cells, showing increased phosphorylation of γH2AX at Ser139 and PARP cleavage in cells transfected with shSOX2 for 48 h. HSP90 was used as loading control. Data shown are the mean ± s.e.m. of at least three independent experiments. *$P \leqslant 0.05$; **$P \leqslant 0.01$ vs LV-c.
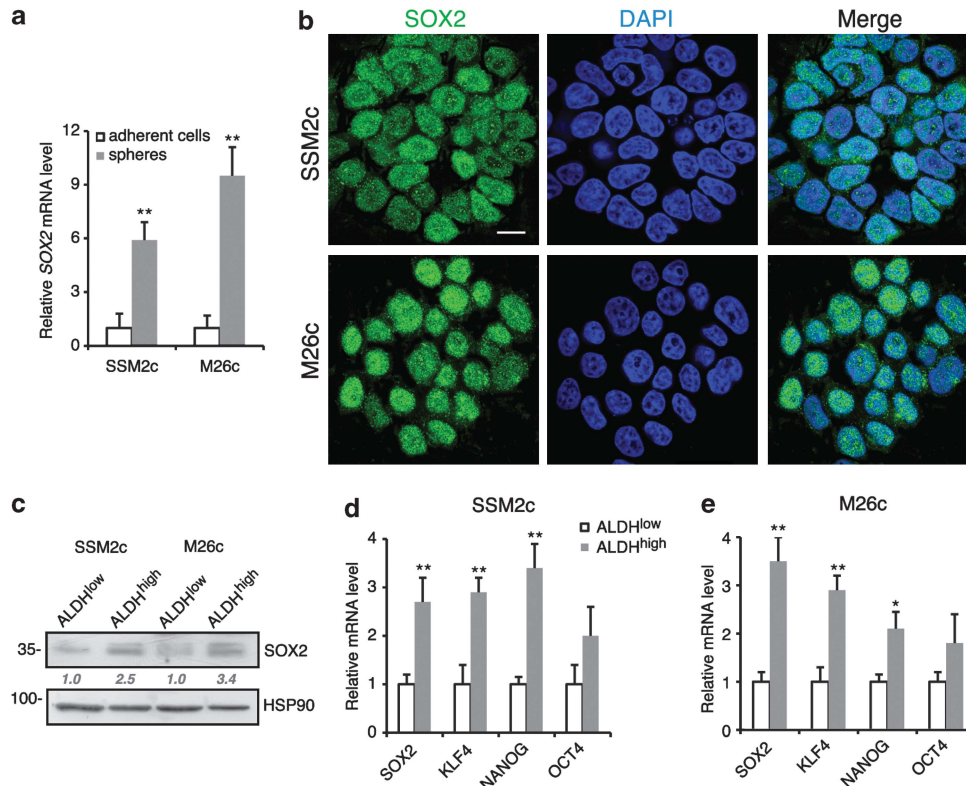
Figure 2. SOX2 expression is enhanced in melanoma cells with stem cell features. (**a**) *SOX2* mRNA expression analysis in adherent cells and spheres of SSM2c and M26c melanoma cells measured by qPCR. C_t values were normalized with two housekeeping genes, with the values in adherent cells equated to 1. (**b**) Confocal images of M26c and SSM2c melanoma spheres after immunolabeling with anti-SOX2 antibody. Nuclei were counterstained with DAPI. Scale bar = 10 μm. (**c**) Western blotting analysis of FACS-sorted ALDH^{low} and ALDH^{high} SSM2c and M26c cells showing the level of SOX2 protein. HSP90 was used as loading control. Quantification of the ratio SOX2/HSP90 is shown in blue. (**d, e**) qPCR analysis of *SOX2*, *KLF4*, *NANOG* and *OCT4* expression in FACS-sorted ALDH^{low} and ALDH^{high} SSM2c and M26c cells. C_t values were normalized with two housekeeping genes, with values in ALDH^{low} cells equated to 1. *$P \leqslant 0.05$; **$P \leqslant 0.01$.

of *BCL-XL* (Figures 5g and h). Altogether, these results indicate that SOX2 regulates self-renewal and promotes survival of MICs.

SOX2 silencing reduces tumor-initiating capability of ALDH^{high} melanoma cells

To address whether SOX2 silencing affects the ability of ALDH^{high} putative MICs to maintain tumor growth, we performed serial transplantation assays using 10 000 ALDH^{high} SSM2c and M26c cells transduced with LV-c, LV-shSOX2-1 or LV-shSOX2-2. In the first passage, SOX2 knockdown significantly reduced tumor growth in SSM2c and M26c xenografts compared with LV-c (Figures 6a–c). In the subsequent *in vivo* passage, SOX2-depleted cells lost their potential to grow (Figures 6a and b). Western blotting analysis confirmed the efficacy of SOX2 downregulation in LV-shSOX2-1 xenografts compared with control tumors (Figure 6d). Consistently, immunocytochemistry of sections obtained from tumors dissected 40 days after injection showed a reduction of SOX2 protein expression in LV-shSOX2-1 tumors compared with control sections (LV-c) (Figure 6e, left panels). SOX2-depleted tumors showed an increase in the number of apoptotic cells, as revealed by activated caspase-3 immunostaining (Figure 6e, right panels), consistent with *in vitro* data (Figures 3 and 4). However, no changes were observed in the number of Ki-67-positive cells (data not shown). To further assess whether SOX2 knockdown could impact on tumor-initiation ability, we performed limiting dilution experiments by subcutaneous injection of 1000, 100 or 10 cells from ALDH^{high} SSM2c and M26c cells transduced with LV-c or LV-shSOX2-1. SOX2-depleted cells at limiting dilution showed greatly reduced tumor take rates

compared with control cells in both SSM2c and M26c xenografts (Figures 6f and g). Calculation of tumor-initiation frequency revealed 100- to 20-fold reduction in the fraction of tumor-initiating cells, respectively, in M26c and SSM2c xenografts upon SOX2 silencing (Figure 6h). Altogether, these data suggest that SOX2 is required to initiate and maintain tumor growth.

SOX2 expression is regulated by HH-GLI signaling in melanoma cells

HH-GLI signaling has been shown to modulate SOX2 expression in several contexts.[24–27] Yet, it is not known whether HH can regulate SOX2 in melanoma cells. qPCR analysis in 19 patient-derived primary melanoma cells revealed a positive correlation between the expression of SOX2 and of the two HH targets *GLI1* and *PATCHED1* (*PTCH1*), the best read-out of an active HH pathway[58] (Figure 7a). To investigate whether HH might regulate SOX2 in melanoma cells, we modulated HH signaling and tested SOX2 expression. Inhibition of HH pathway by silencing the transmembrane receptor SMOOTHENED (SMO) or the downstream transcription factor GLI1 nearly abolished SOX2 protein expression in SSM2c cells and reduced *SOX2* mRNA in melanoma cells (Figures 7b and c), suggesting a regulation of SOX2 at transcriptional level. Consistently, activation of HH signaling by silencing the negative regulator PTCH1 increased *SOX2* mRNA levels, with a stronger induction in cells with higher endogenous *SOX2* expression (Supplementary Figures S8a and b).

To investigate whether the transcriptional regulation of SOX2 by HH-GLI was direct or indirect, we applied a web-based bioinformatic approach to identify putative GLI-binding sites in
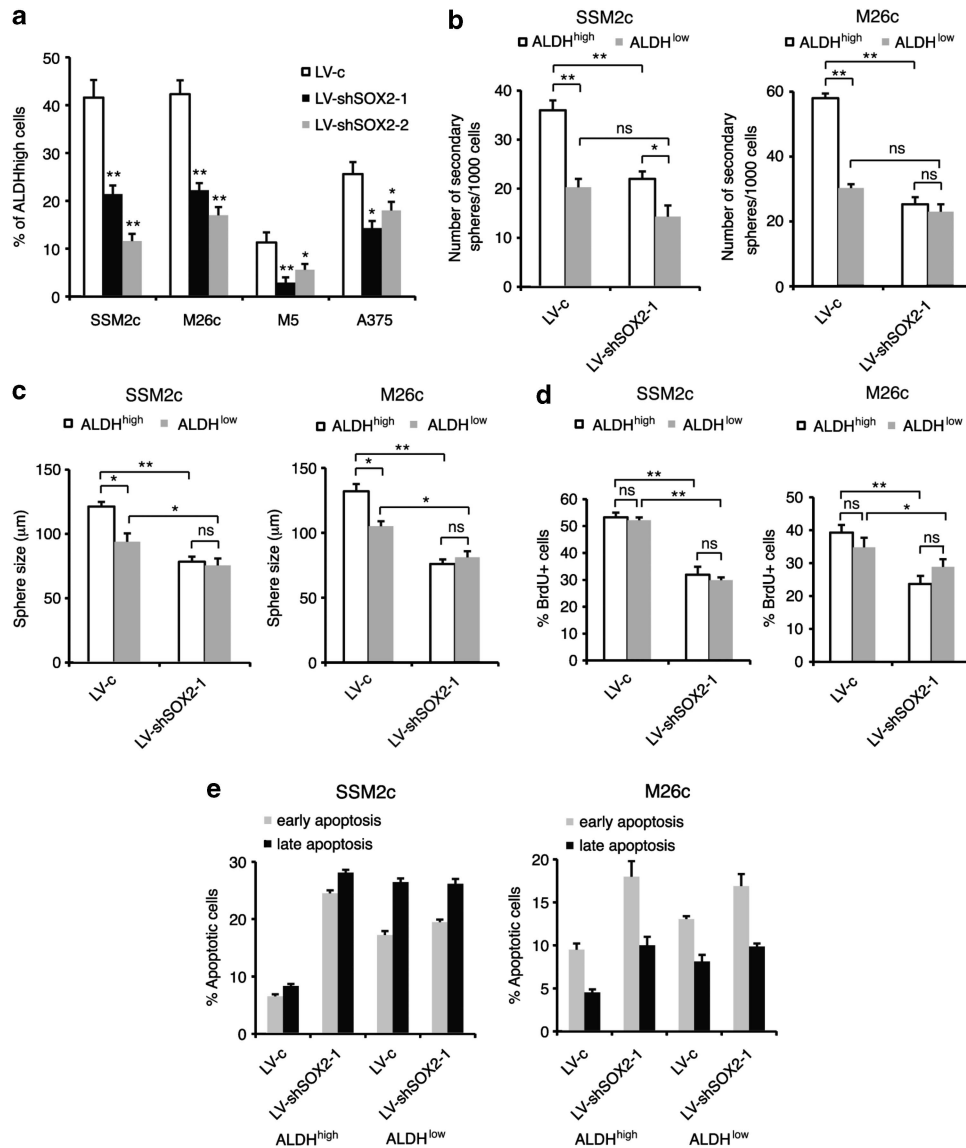
Figure 3. Knockdown of SOX2 reduces number and self-renewal of ALDH[high] melanoma stem cells. (**a**) Quantification of the fraction of ALDH^{high} cells, determined by Aldefluor assay in SSM2c, M26c, M5 and A375 melanoma cells transduced with LV-c, LV-shSOX2-1 or LV-shSOX2-2. Significant reduction in the number of ALDH^{high} cells after silencing of SOX2 in all the four cell types is shown. (**b**, **c**) Number (**b**) and size (**c**) of secondary spheres in ALDH[high] and ALDH[low] SSM2c and M26c cells after silencing of SOX2 with shSOX2-1. (**d**, **e**) Quantification of BrdU incorporation (**d**) and of the fraction of early (Annexin V[+]/7-AAD[−]) and late (Annexin V[+]/7-AAD^{+}) apoptotic cells (**e**) in ALDH[high] and ALDH[low] SSM2c and M26c secondary spheres transduced with LV-c and LV-shSOX2-1. Data shown are the mean ± s.e.m. of at least three independent experiments. *$P \leqslant 0.05$; **$P \leqslant 0.01$.

SOX2 promoter. We detected a possible site with the consensus GLI-binding sites at about 300 bp upstream to SOX2 transcription start site (TSS), within the core proximal promoter region of SOX2 (−528 and +238 from the TSS).[59] Chromatin immunoprecipitation (ChIP) in M26c melanoma cells showed that both endogenous GLI1 and GLI2 transcription factors bound to SOX2 promoter at about 300 bp upstream of the TSS (Figures 7d and e).

SOX2 acts as a mediator of HH-GLI signaling in regulating melanoma cell proliferation and MIC self-renewal

Our findings suggest that HH-GLI signaling directly regulates SOX2 expression in melanoma cells. To investigate whether SOX2 acts as a downstream mediator of HH signaling in regulating melanoma cell growth, we activated HH pathway by silencing PTCH1 and knocked down SOX2 in melanoma cells. We transduced SSM2c

and M26c cells with LV-shPTCH1,[60,61] alone or in combination with LV-shSOX2, and we assessed proliferation. In both the cell types, shPTCH1 increased cell number compared with LV-c, as already reported.[61] Silencing of SOX2 drastically reduced the number of cells compared with LV-c, and it suppressed the increase of cell proliferation induced by HH pathway activation (Figure 7f). These results support the hypothesis that endogenous SOX2 might mediate the effect of HH pathway activation in regulating melanoma cell proliferation.

We next tested for a possible role of SOX2 in controlling HH-mediated MIC self-renewal, using SSM2c and M26c melanoma spheres transduced with LV-shPTCH1 and/or LV-shSOX2. Silencing of PTCH1 increased by two-fold the number of melanoma spheres compared with LV-c (Figures 7g and h), as expected.[61] Silencing of SOX2 decreased the number and size of melanoma spheres, and more importantly, it reverted the increase in self-renewal and
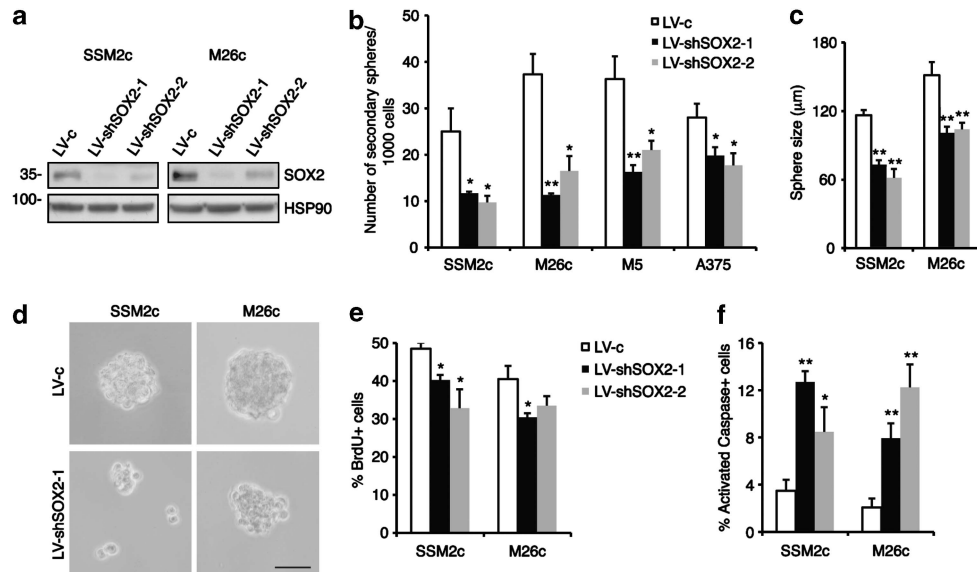
Figure 4. Silencing of SOX2 reduces melanoma sphere self-renewal. (a) Western blotting analysis of SSM2c and M26c spheres transduced with LV-c control, LV-shSOX2-1 and LV-shSOX2-2, showing the near complete loss of SOX2 protein with both shRNAs. HSP90 was used as loading control. (b) Reduction in the number of secondary melanoma spheres after silencing of SOX2. (c) Measurement of the size of SSM2c and M26c secondary melanoma spheres after transduction with in LV-c, LV-shSOX2-1 and LV-shSOX2-2. (d) Representative images of secondary spheres as indicated in panel (c). Scale bar = 150 μm. (e, f) Quantification of BrdU incorporation (e) and of activated Caspase-3+ cells (f) in SSM2c and M26c melanoma spheres after transduction with LV-c, LV-shSOX2-1 and LV-shSOX2-2. At least 10 independent fields of BrdU/DAPI and cleaved Caspase-3/DAPI-labeled cells were counted per condition. Data shown are the mean ± s.e.m. of at least three independent experiments. *$P \leqslant 0.05$; **$P \leqslant 0.01$ vs LV-c.

size induced by shPTCH1 (Figures 7g and h, Supplementary Figure S9a). SOX2 silencing slightly decreased sphere proliferation and abolished the effect of HH pathway activation, as shown by proliferation index analysis (Figure 7i and Supplementary Figure S9b). Analysis of Annexin V/7-AAD staining indicated that SOX2 knockdown increased early and late apoptosis, whereas shPTCH1 increased only early apoptosis in one line (Figure 7j and Supplementary Figure S9c), suggesting sign of proliferative stress. These data suggest that SOX2 mediates, at least in part, the effect of HH pathway activation on the regulation of MIC self-renewal.

DISCUSSION

In this study, we describe for the first time an important role for SOX2 in MICs. We show that depletion of SOX2 reduces MIC self-renewal in vitro and progressively abrogates tumor growth, leading to significant decrease in tumor-initiating capability in vivo. Our study strongly suggests that in melanoma SOX2 is essential for tumor initiation and for tumor maintenance. Furthermore, we provide evidence that SOX2 is directly regulated by the transcription factors GLI1 and GLI2 and that SOX2 functionally acts as a mediator of HH signaling in controlling melanoma cell growth and MIC self-renewal.

The major finding of our investigation is the essential role of SOX2 in the maintenance of melanoma stem cells. This result is in line with the previously described role of SOX2 in other types of cancer.[40-48] Our data suggest that SOX2 expression is not only restricted to melanoma stem cells but is also relevant in non-stem cancer cells, where it is required to sustain the proliferative rate of melanoma cells that constitute the tumor bulk. However, not all melanomas are SOX2-positive; indeed, we find that SOX2 is expressed in about half of melanomas, consistently with previous immunohistochemical studies.[50-52] In addition, we show that the expression of SOX2 correlates with activation of the HH pathway, which is required for melanoma cell proliferation and melanoma stem cell self-renewal.[7,15] Together, our findings suggest that in this subset of melanomas a HH–SOX2 axis is

crucial for the maintenance and survival of both tumor bulk and CSC compartments.

The molecular mechanisms underlying SOX2-mediated stemness remain largely unknown. In this study, we observe induction of NANOG, OCT4 and partly KLF4 upon SOX2 expression. This could be a direct transcriptional effect induced by SOX2 or mediated by the fact that SOX2 induces a stem cell state characterized by expression of these factors. The latter hypothesis is consistent with the findings that SOX2 can reprogram differentiated somatic cells to become iPS cells[34-36] and that SOX2 is required in several types of CSCs.[40-48] Moreover, Sox2 posttranslational modifications have been shown to affect its transcriptional activity and to cooperate in reprogramming embryonic fibroblasts to iPS cells.[62,63] Melanocytes and melanoma cells can also be reprogrammed to iPS by combination of Oct4, Klf4 and c-Myc but in the absence of ectopic Sox2, which is already expressed at high levels in these cells.[64] In addition to SOX2, other stemness-related factors might be critical for melanomas. For instance, OCT4 can induce epithelial dysplasia in mice[65] and promote dedifferentiation of melanoma cells.[66] The regulation of SOX2 by HH signaling, which is often activated in melanomas,[15] raises the challenging possibility that SOX2, together with other GLI targets and stemness factors, might have a critical role in determining the stem-like characteristics of MICs, contributing to the acquisition of a more undifferentiated and aggressive state through a process similar to reprogramming.

Our data indicate that silencing of SOX2 induces apoptosis and signs of DNA damage in melanoma cells and MICs. These data suggest that SOX2 modulates the balance between survival and pro-apoptotic factors. Further studies are needed to explore in detail the mechanisms of apoptosis induced by loss of SOX2 and to investigate whether BCL-2, NOXA or GADD45A are direct transcriptional targets of SOX2 in melanoma. In support of our data, a recent study identified SOX2-binding regions in BCL-2, NOXA/PMAIP1 and GADD45A genes using a ChIP-sequencing approach in glioblastoma cells.[67] In previous experiments, it was found that SOX2 knockdown decreases tumorigenicity of A2058 melanoma cells.[50] Our xenotransplantation experiments using
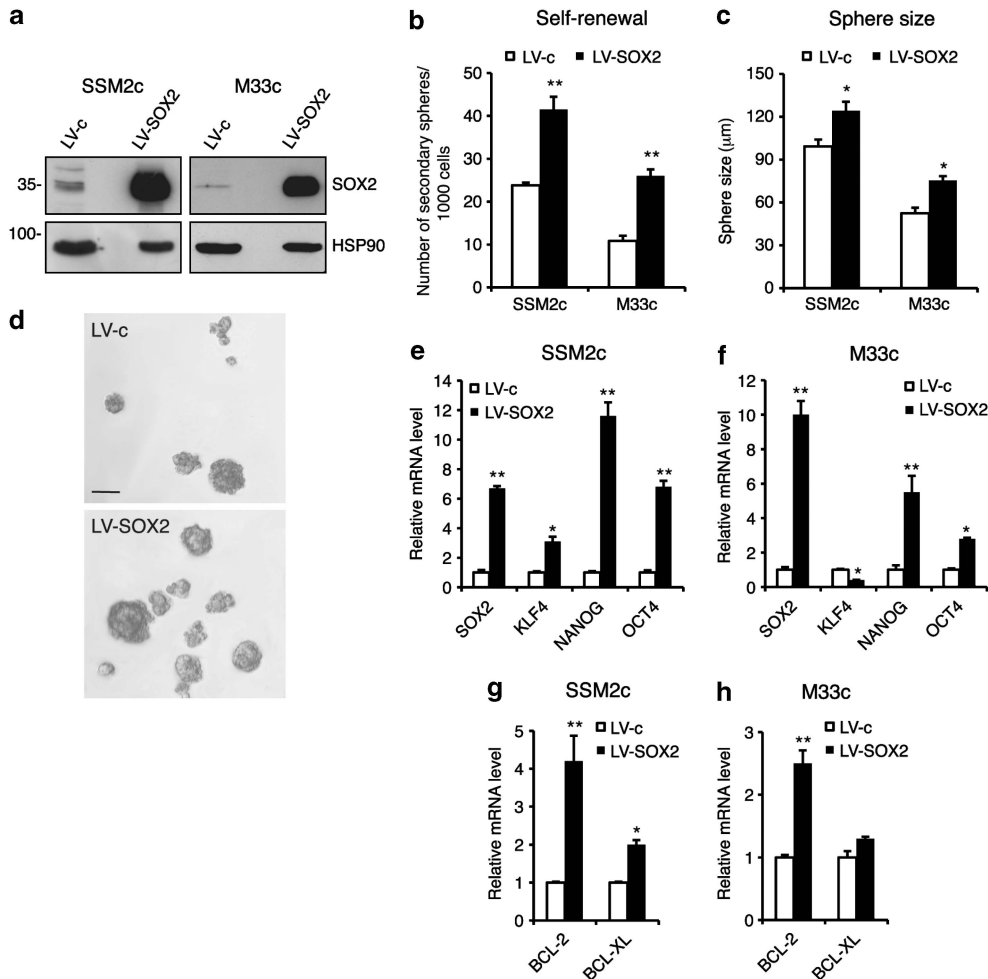
Figure 5. Enhanced SOX2 function increases stemness in melanoma cells. (a) Western blotting analysis shows SOX2 expression levels in control (LV-c) and SOX2-stably transfected (LV-SOX2) SSM2c and M33c melanoma cells. HSP90 was used as loading control. (b) Increase in the number of secondary spheres upon SOX2 expression. (c) Measurement of the size of secondary melanoma spheres in LV-c and LV-SOX2 transfected SSM2c and M33c spheres. (d) Representative images of secondary melanoma spheres as indicated in panel (c). Scale bar = 100 μm. (e–h) Gene expression analysis of SOX2, KLF4, NANOG, OCT4 (e, f) and BCL-2 and BCL-XL (g, h) in LV-c and LV-SOX2 stably transfected melanoma spheres, as measured by qPCR. C_t values were normalized with two housekeeping genes, with the values in control spheres equated to 1. Data shown are the mean ± s.e.m. of at least three independent experiments. *$P \leqslant 0.05$; **$P \leqslant 0.01$ vs LV-c.

patient-derived primary melanoma cells fully confirm this finding. In addition, in our hands SOX2 knockdown also inhibits in vitro growth of primary melanoma cells and of A375 cell line.

HH-GLI pathway has been shown to regulate stemness in several contexts. For instance, ectopic expression of GLI1 in mouse Nestin+ progenitors drives neural stem cell self-renewal and induces the expression of several stemness genes, including Sox2.[60] Nanog, which has been identified as a direct Hh target in neural stem cells,[68] is also a mediator of HH in glioblastoma cells.[69] Here we present evidence that HH signaling regulates SOX2 expression at transcriptional level and that this regulation might be direct, as suggested by the binding of GLI1 and GLI2 to SOX2 promoter. Interestingly, our results indicate that SOX2 function is required for the maintenance of melanoma cell proliferation and MIC self-renewal induced by the activation of HH signaling, suggesting that SOX2 acts as downstream mediator of HH in melanoma cells. In line with our results, SOX2 has recently been shown to be required in Sonic Hedgehog-associated medulloblastomas.[27] In basal cell carcinoma and tumor-initiating pancreatic cancer cells, HH-GLI and epidermal growth factor receptor signaling integration synergistically activates a number of cooperation response genes, including SOX2 and SOX9.[25]

In addition to being controlled by HH, SOX2 might also directly regulate HH signaling, contributing to create a HH-GLI-SOX2 regulatory loop, as suggested by the binding of Sox2 to the promoter of Shh in mouse developing brain[70] and of GLI2, GLI3 and SHH in glioblastoma[67] and neural stem cells.[71]

Although the possibility to selectively target SOX2 or other oncogenic transcription factors remains a challenge, recent studies began to evaluate new strategies to inhibit SOX2. For instance, a zinc finger-based artificial transcription factor approach has been used in breast cancer cells to selectively suppress SOX2 function[72] and a novel inhibitor of Sox2 DNA binding has been identified.[73] However, these strategies have yet limited use in vivo, and further studies are needed to explore novel approaches to effectively and safely target SOX2 in patients. Our study provides several pieces of evidence for the relevance of SOX2 as a therapeutic target in a subset of melanomas. First, we show that SOX2 silencing reduces proliferation and induces apoptosis in melanoma cells (Figure 1). Second, we demonstrate that SOX2 knockdown inhibits self-renewal and tumorigenicity of MICs (Figures 3, 4 and 6). Third, the HH-GLI signaling, which is active in melanomas and MICs,[7,15] induces SOX2 expression (Figure 7 and Supplementary Figure S8).
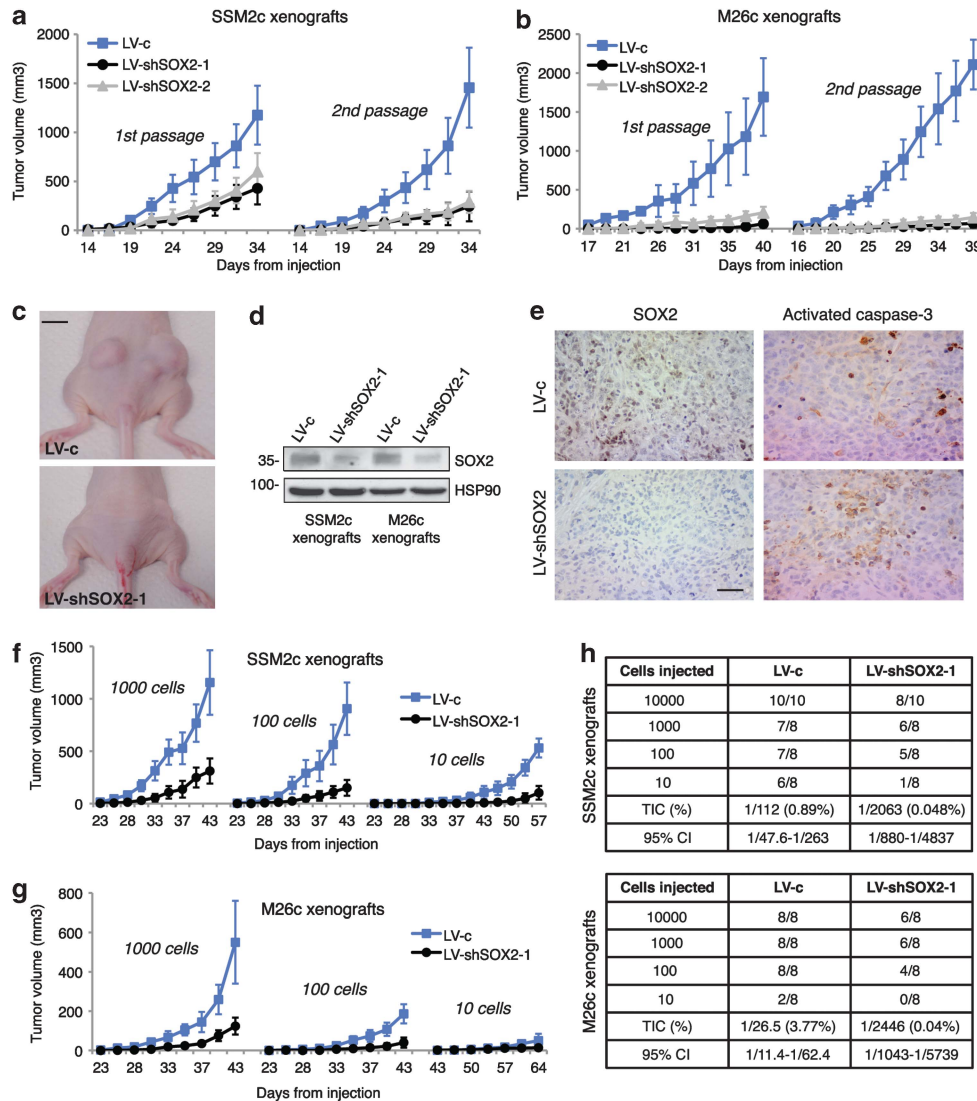
Figure 6. Silencing of SOX2 impairs *in vivo* tumor initiation and growth of ALDH[high] melanoma stem cells. (**a**, **b**) *In vivo* tumor growth after two passages of serial xenotransplantation of FACS-sorted ALDH[high] SSM2c (**a**) and M26c (**b**) cells transduced with LV-c, LV-shSOX2-1 and LV-shSOX2-2. For each group, 10 tumors were analyzed. (**c**) Representative images of subcutaneous xenografts in athymic nude mice taken at the same time for each group. (**d**) Western blotting for SOX2 in SSM2c and M26c xenografts. Note the decrease in SOX2 immunoreactivity in LV-shSOX2 xenografts compared with control LV-c, confirming the efficacy of SOX2 knockdown. HSP90 was used as loading control. (**e**) Expression of SOX2 protein and activated Caspase-3 in paraffin sections of M26c xenografts analyzed by immunocytochemistry. Sections were counterstained with hematoxylin (blue nuclei). (**f**, **g**) *In vivo* tumor growth after subcutaneous injection of 1000, 100 and 10 FACS-sorted ALDH[high] SSM2c and M26c cells transduced with LV-c and LV-shSOX2-1. (**h**) Estimated tumor-initiation frequency after four independent serial dilution (10 000, 1000, 100 and 10 cells) transplantation experiments of FACS-sorted ALDH[high] SSM2c and M26c cells transduced with LV-c and LV-shSOX2-1. Scale bar = 10 mm (**c**) and 80 μm (**e**). Data shown are mean ± s.e.m.

MATERIALS AND METHODS

Patient samples and cell lines

A375 melanoma cells (CRL-1619) were obtained from ATCC (Manassas, VA, USA) and normal human epidermal melanocytes from PromoCell (Heidelberg, Germany). Human melanoma samples (Supplementary Table S1) were obtained after approved protocols by the Ethics Committee. Fresh tissue samples were digested enzymatically using 1 mg/ml collagenase A and 20 μg/ml DNase I (Roche Applied Science, Basel, Switzerland) in Dulbecco's modified Eagle's medium (DMEM)/F12 (Euroclone, Milan, Italy) and filtered, and cells were grown in DMEM/F12 with 10% fetal bovine serum and epidermal growth factor (5 ng/ml) (Life Technologies, Paisley, UK). The identity of melanoma cells was verified by immunocytochemistry using anti-Melan A, anti-S100 and anti-Vimentin antibodies.[7] For melanoma sphere cultures, SSM2c, M5, M26c, M33c and A375 cells were seeded at a concentration of 5000 cells/ml either in DMEM/F12 serum-free medium with N2 supplement, 20 μg/ml insulin,

10 ng/ml epidermal growth factor and 10 ng/ml basic fibroblast growth factor (Life Technologies) or in human embryonic stem cell medium, as previously described.[1,7] Puromycin (Sigma, St Louis, MO, USA) was used at 2 μg/ml.

RNA interference and lentivectors

Lentiviruses were produced in HEK-293T cells as previously reported.[60] Lentiviral vectors were pLKO.1-puro (LV-c) (Open Biosystems, Lafayette, CO, USA), pLKO.1-puro-shSOX2-1 (LV-shSOX2-1) targeting the 3′ untranslated region of SOX2 (targeting sequence 5′-CTGCCGAGAATCCATGTA TAT-3′), pLKO.1-puro-shSOX2-2 (LV-shSOX2-2) targeting the coding region of SOX2 (targeting sequence 5′-CAGCTCGCAGACCTACATGAA-3′) and pSin-EF2-Sox2-Pur (LV-SOX2) (plasmid 16577, Addgene, Cambridge, MA, USA). pLKO.1-puro-shGLI1 (LV-shGLI1), pLKO.1-puro-shSMO (LV-shSMO)[7] and pLV-CTH-shPTCH1 (LV-shPTCH1)[60,61] were previously described.
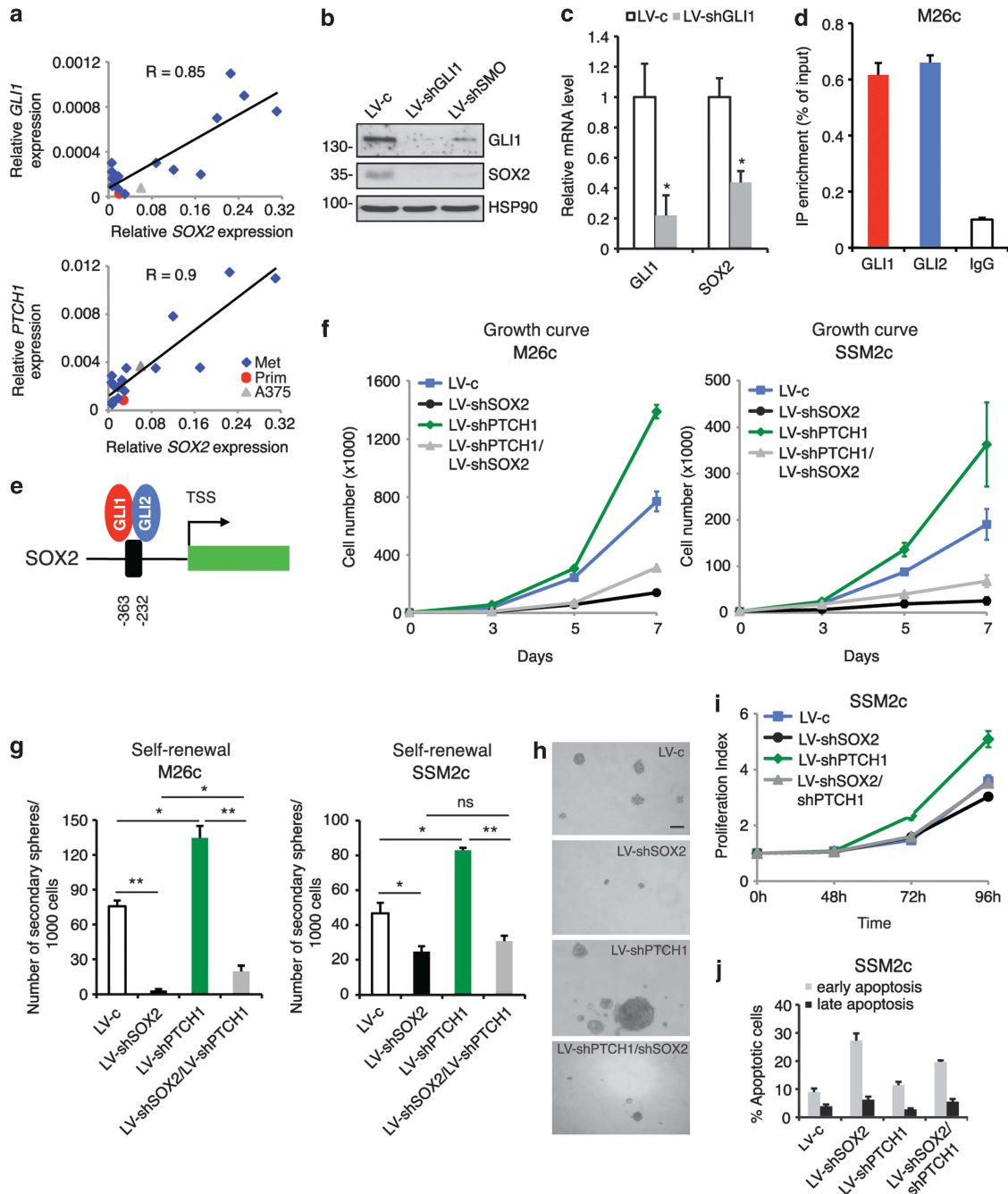
Figure 7. SOX2 is regulated by HH signaling and is required for melanoma cell growth and MIC self-renewal induced by HH activation. (**a**) Linear correlation analysis of *SOX2* with *GLI1* and *PTCH1* expression, as measured by qPCR, in the melanoma cell line A375 and in 19 patient-derived melanoma cultures, 1 of which is from a primary melanoma (Prim) and 18 are from metastases (Met). Each sample is represented by a dot. Axes in each graph represent expression ratio of gene/(GAPDH and β-ACTIN). The extent of the correlation is indicated by R coefficient. (**b**) Western blotting analysis of SSM2c cells transduced with LV-c, LV-shGLI1 and LV-shSMO shows the dramatic reduction of GLI1 and complete loss of SOX2 protein upon inhibition of HH signaling. HSP90 was used as loading control. (**c**) qPCR analysis of SSM2c cells transduced with LV-c and LV-shGLI1, showing the drastic reduction of *GLI1* and *SOX2* mRNA. qPCR values reflect C_t values after normalization with two housekeeping genes, with the values in control equated to 1. (**d**) qPCR analysis of ChIP experiments shows binding of GLI1 and GLI2 at *SOX2* promoter (-363 bp to -232 bp) in M26c melanoma cells. (**e**) Location of the putative GLI-binding site on SOX2 promoter. Numbers indicate the position of the binding site relative to the TSS. (**f**) Growth assay in M26c and SSM2c cells transduced with LV-c, shSOX2-1, shPTCH1 or shPTCH1/shSOX2-1, showing that SOX2 silencing reduces the increase in melanoma cell proliferation induced by shPTCH1. (**g**) Self-renewal assay showing that SOX2 ablation prevents the increase in self-renewal induced by shPTCH1 in M26c and SSM2c melanoma spheres. (**h**) Representative images of panel (**g**). (**i**) Proliferation index measured by CellTrace Violet staining in SSM2c spheres stably transduced with LV-c, LV-shSOX2-1, LV-shPTCH1 or LV-shSOX2-1/LV-shPTCH1. (**j**) Quantification of the fraction of early (Annexin V$^+$/7-AAD$^-$) and late (Annexin V$^+$/7-AAD$^+$) apoptotic cells in SSM2c spheres stably transduced with LV-c, LV-shSOX2-1, LV-shPTCH1 or LV-shSOX2-1/LV-shPTCH1. Scale bar = 100 μm (**h**). Data represent mean ± s.e.m. values. At least three independent experiments were performed. *$P \leqslant 0.05$; **$P \leqslant 0.01$.

Self-renewal assay

For self-renewal assay, cells were transduced with LV-c, LV-shSOX2-1, LV-shSOX2-2 and LV-shPTCH1 lentiviruses or stably transfected with LV-SOX2 and let to form spheres. Primary melanoma spheres were dissociated and plated either in 96-well plates at 1 cell/well or in 12-well plates at 1 cell/μl dilutions. After 1 or 2 weeks, secondary spheres were counted.[7,61] All the experiments were performed in triplicate and repeated at least three times.

Aldefluor assay, proliferation index and apoptosis

The separation of cells with high and low ALDH activity (ALDH[high] and ALDH[low]) was performed using the Aldefluor kit (Stem Cell Technologies, Vancouver, BC, Canada) as already described.[7]

For proliferation index experiments, cells were labeled with 10 μM CFSE or CellTrace Violet (Life Technologies), seeded and allowed to proliferate for 48, 72 and 96 h and analyzed using flow cytometry. Data were normalized to controls arrested at the parent generation with 1ug/ml mitomycin C ($t = 0$ h), and proliferation index was calculated using the ModFit LT software (Verity Software House, Topsham, ME, USA). For apoptosis analysis, cells were exposed to serum-deprived conditions, and apoptosis was measured after 48 h using an Annexin V–phycoerythrin/7-AAD apoptosis kit (BD Biosciences, San Diego, CA, USA).

BrdU incorporation assay and immunostaining

BrdU pulses in melanoma spheres were performed for 8 h (4 μg/ml). Spheres were plated on DMEM/Matrigel (1:40) (BD Biosciences) to allow attachment, fixed with 4% paraformaldehyde and processed as previously described.[60] For apoptosis, spheres were immunolabeled with a rabbit anti-cleaved Caspase3 (Cell Signaling Technologies, Danvers, MA, USA), followed by an anti-rabbit fluorescein isothiocyanate-conjugated secondary antibody. For SOX2 immunofluorescence, spheres were immunolabeled with a rabbit anti-SOX2 antibody (AB5603; Millipore, Billerica, MA, USA) and with an anti-rabbit fluorescein isothiocyanate-conjugated secondary antibody. Formalin-fixed paraffin-embedded sections were subjected to antigen retrieval (with citrate buffer pH 6.0), incubated with rabbit anti-SOX2 antibody (AB5603; Millipore) and rabbit anti-cleaved Caspase3 (Cell Signaling Technologies) and visualized using UltraVision Detection System (Lab Vision, Fremont, CA, USA) and diaminobenzidine (Dako, Carpinteria, CA, USA).

qPCR

Total RNA was isolated as already described.[61] Reverse transcription was performed with High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Carlsbad, CA, USA). QPCR amplifications were carried out at 60 °C using Power SYBR Green PCR Master Mix (Applied Biosystems) on a 7500 Fast Real-Time PCR System (Applied Biosystems) and analyzed by delta-C_t method using GAPDH and β-ACTIN as housekeeping genes. Primer sequences are listed in Supplementary Table S2.

Western blotting

Cells were lysed as previously described.[61] The following antibodies were used: rabbit polyclonal anti-SOX2 (AB5603) (Millipore), rabbit polyclonal anti-GLI1 (Ab49314) (Abcam, Cambridge, MA, USA), mouse anti-HSP90 (Heat Shock Protein 90) (Santa Cruz Biotechnology, Santa Cruz, CA, USA), rabbit anti-phospho-γH2AX (Ser139), rabbit anti-phospho-Chk2 (Thr68), and rabbit anti-poly ADP-ribose polymerase (Cell Signaling Technologies). Chemiluminescent detection was used.

ChIP

M26c cells were fixed with 1% formaldehyde and lysed. DNA was sonicated and diluted with ChIP Dilution Buffer, and Input Material (IM) (5%) was collected. Chromatin was incubated overnight at 4 °C with Dynabeads Protein G (Life Technologies) pre-conjugated with anti-GLI1 antibody (N-16) (Santa Cruz Biotechnology), anti-GLI2 (R&D Systems, Minneapolis, MN, USA) or a non-specific IgG control. DNA was purified, and qPCRs was carried out at 60 °C using Power SYBR Green PCR Master Mix (Life Technologies). ChIP primers are displayed in Supplementary Table S2.

Mouse xenograft assays

Six- to 8-week-old female athymic-nude mice (Foxn1 nu/nu) (Harlan Laboratories, Udine, Italy) were injected subcutaneously in lateral flanks with 10 000, 1000, 100 and 10 FACS (fluorescent-activated cell sorter)-sorted ALDH[high] patient-derived SSM2c and M26c melanoma cells transduced with LV-c, LV-shSOX2-1 or LV-shSOX2-2. For serial transplantation, primary tumors were dissected, dissociated and FACS-sorted ALDH^{high} cells were re-injected. Cells were suspended in Matrigel (BD Biosciences)/DMEM (1/1) before inoculation. Animals were monitored daily, subcutaneous tumor size was measured every 2–3 days by a caliper (2Biological Instruments, Varese, Italy), and tumor volumes were calculated using the formula $V = W^2 \times L \times 0.5$, where W and L are, respectively, tumor width and length. Statistical analysis of tumor take was performed using the ELDA Web-based tool (http://bioinf.wehi.edu.au/software/elda/).[74]

Statistical analysis

Data are presented as mean ± s.e.m. for at least three independent experiments, unless otherwise stated. Statistical analysis of the data was performed by a two-tailed Student's t-test. *$P \leqslant 0.05$; **$P \leqslant 0.01$.

REFERENCES

1 Fang D, Nguyen TK, Leishear K, Finko R, Kulp AN, Hotz S et al. A tumorigenic subpopulation with stem cell properties in melanomas. Cancer Res 2005; 65: 9328–9337.

2 Schatton T, Murphy GF, Frank NY, Yamaura K, Waaga-Gasser AM, Gasser M et al. Identification of cells initiating human melanomas. Nature 2008; 451: 345–349.

3 Boiko AD, Razorenova OV, van de Rijn M, Swetter SM, Johnson DL, Ly DP et al. Human melanoma-initiating cells express neural crest nerve growth factor receptor CD271. Nature 2010; 466: 133–137.

4 Schmidt P, Kopecky C, Hombach A, Zigrino P, Mauch C, Abken H. Eradication of melanomas by targeted elimination of a minor subset of tumor cells. Proc Natl Acad Sci USA 2011; 108: 2474–2479.

5 Civenni G, Walter A, Kobert N, Mihic-Probst D, Zipser M, Belloni B et al. Human CD271-positive melanoma stem cells associated with metastasis establish tumor heterogeneity and long-term growth. Cancer Res 2011; 71: 3098–3109.

6 Boonyaratanakornkit JB, Yue L, Strachan LR, Scalapino KJ, LeBoit PE, Lu Y et al. Selection of tumorigenic melanoma cells using ALDH. J Invest Dermatol 2010; 130: 2799–2808.

7 Santini R, Vinci MC, Pandolfi S, Penachioni JY, Montagnani V, Olivito B et al. Hedgehog-GLI signaling drives self-renewal and tumorigenicity of human melanoma-initiating cells. Stem Cells 2012; 30: 1808–1818.

8 Girouard SD, Murphy GF. Melanoma stem cells: not rare, but well done. Lab Invest 2011; 91: 647–664.

9 Murphy GF, Wilson BJ, Girouard SD, Frank NY, Frank MH. Stem cells and targeted approaches to melanoma cure. Mol Aspects Med (e-pub ahead of print 19 October 2013; doi:10.1016/j.mam.2013.10.003).

10 Chartrain M, Riond J, Stennevin A, Vandenberghe I, Gomes B, Lamant L et al. Melanoma chemotherapy leads to the selection of ABCB5-expressing cells. PLoS One 2012; 7: e36762–e36774.

11 Frank NY, Margaryan A, Huang Y, Schatton T, Waaga-Gasser AM, Gasser M et al. ABCB5-mediated doxorubicin transport and chemoresistance in human malignant melanoma. Cancer Res 2005; 65: 4320–4333.

12 Schlaak M, Schmidt P, Bangard C, Kurschat P, Mauch C, Abken H. Regression of metastatic melanoma in a patient by antibody targeting of cancer stem cells. Oncotarget 2012; 3: 22–30.

13 Pinc A, Somasundaram R, Wagner C, Hörmann M, Karanikas G, Jalili A et al. Targeting CD20 in melanoma patients at high risk of disease recurrence. Mol Ther 2012; 20: 1056–1062.

14 Hu Y, Fu L. Targeting cancer stem cells: a new therapy to cure cancer patients. Am J Cancer Res 2012; 2: 340–356.

15 Stecca B, Mas C, Clement V, Zbinden M, Correa R, Piguet V et al. Melanomas require HEDGEHOG-GLI signaling regulated by interactions between GLI1 and the RAS-MEK/AKT pathways. Proc Natl Acad Sci USA 2007; 104: 5895–5900.

16 Alexaki VI, Javelaud D, Van Kempen LC, Mohammad KS, Dennler S, Luciani F et al. GLI2-mediated melanoma invasion and metastasis. J Natl Cancer Inst 2010; 102: 1148–1159.

17 Jalili A, Mertz KD, Romanov J, Wagner C, Kalthoff F, Stuetz A et al. NVP-LDE225, a potent and selective SMOOTHENED antagonist reduces melanoma growth in vitro and in vivo. PLoS One 2013; 8: e69064.

18 O'Reilly KE, de Miera EV, Segura MF, Friedman E, Poliseno L, Han SW et al. Hedgehog pathway blockade inhibits melanoma cell growth in vitro and in vivo. Pharmaceuticals (Basel) 2013; 6: 1429–1450.

19 Calloni GW, Glavieux-Pardanaud C, Le Douarin NM, Dupin E. Sonic Hedgehog promotes the development of multipotent neural crest progenitors endowed with both mesenchymal and neural potentials. Proc Natl Acad Sci USA 2007; 104: 19879–19884.

20 Lai K, Kaspar BK, Gage FH, Schaffer DV. Sonic hedgehog regulates adult neural progenitor proliferation in vitro and in vivo. Nat Neurosci 2003; 6: 21–27.

21 Machold R, Hayashi S, Rutlin M, Muzumdar MD, Nery S, Corbin JG et al. Sonic hedgehog is required for progenitor cell maintenance in telencephalic stem cell niches. Neuron 2003; 39: 937–950.

22 Hutchin ME, Kariapper MS, Grachtchouk M, Wang A, Wei L, Cummings D et al. Sustained Hedgehog signaling is required for basal cell carcinoma proliferation and survival: conditional skin tumorigenesis recapitulates the hair growth cycle. Genes Dev 2005; 19: 214–223.

23 Brownell I, Guevara E, Bai CB, Loomis CA, Joyner AL. Nerve-derived sonic hedgehog defines a niche for hair follicle stem cells capable of becoming epidermal stem cells. Cell Stem Cell 2011; 8: 552–565.

24 Takanaga H, Tsuchida-Straeten N, Nishide K, Watanabe A, Aburatani H, Kondo T. Gli2 is a novel regulator of sox2 expression in telencephalic neuroepithelial cells. Stem Cells 2009; 27: 165–174.

25 Eberl M, Klingler S, Mangelberger D, Loipetzberger A, Damhofer H, Zoidl K et al. Hedgehog-EGFR cooperation response genes determine the oncogenic phenotype of basal cell carcinoma and tumour-initiating pancreatic cancer cells. EMBO Mol Med 2012; 4: 218–233.

26 Gopinath S, Malla R, Alapati K, Gorantla B, Gujrati M, Dinh DH et al. Cathepsin B and uPAR regulate self-renewal of glioma-initiating cells through GLI-regulated Sox2 and Bmi1 expression. Carcinogenesis 2013; 34: 550–559.

27 Ahlfeld J, Favaro R, Pagella P, Kretzschmar HA, Nicolis S, Schüller U. Sox2 requirement in Sonic hedgehog-associated medulloblastoma. Cancer Res 2013; 73: 3796–3807.

28 Avilion AA, Nicolis SK, Pevny LH, Perez L, Vivian N, Lovell-Badge R. Multipotent cell lineages in early mouse development depend on SOX2 function. Genes Dev 2003; 17: 126–140.

29 Masui S, Nakatake Y, Toyooka Y, Shimosato D, Yagi R, Takahashi K et al. Pluripotency governed by Sox2 via regulation of Oct3/4 expression in mouse embryonic stem cells. Nat Cell Biol 2007; 9: 625–635.

30 Graham V, Khudyakov J, Ellis P, Pevny L. SOX2 functions to maintain neural progenitor identity. Neuron 2003; 39: 749–765.

31 Basu-Roy U, Ambrosetti D, Favaro R, Nicolis SK, Mansukhani A, Basilico C. The transcription factor Sox2 is required for osteoblast self-renewal. Cell Death Differ 2010; 17: 1345–1353.

32 Adameyko I, Lallemend F, Furlan A, Zinin N, Aranda S, Kitambi SS et al. Sox2 and Mitf cross-regulatory interactions consolidate progenitor and melanocyte lineages in the cranial neural crest. Development 2012; 139: 397–410.

33 Arnold K, Sarkar A, Yram MA, Polo JM, Bronson R, Sengupta S et al. Sox2(+) adult stem and progenitor cells are important for tissue regeneration and survival of mice. Cell Stem Cell 2011; 9: 317–329.

34 Takahashi K, Yamanaka S. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. Cell 2006; 126: 663–676.

35 Takahashi K, Tanabe K, Ohnuki M, Narita M, Ichisaka T, Tomoda K et al. Induction of pluripotent stem cells from adult human fibroblasts by defined factors. Cell 2007; 131: 861–872.

36 Yu J, Vodyanik MA, Smuga-Otto K, Antosiewicz-Bourget J, Frane JL, Tian S et al. Induced pluripotent stem cell lines derived from human somatic cells. Science 2007; 318: 1917–1920.

37 Bass AJ, Watanabe H, Mermel CH, Yu S, Perner S, Verhaak RG et al. SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. Nat Genet 2009; 41: 1238–1242.

38 Freier K, Knoepfle K, Flechtenmacher C, Pungs S, Devens F, Toedt G et al. Recurrent copy number gain of transcription factor SOX2 and corresponding high protein expression in oral squamous cell carcinoma. Genes Chromosomes Cancer 2010; 49: 9–16.

39 Rudin CM, Durinck S, Stawiski EW, Poirier JT, Modrusan Z, Shames DS et al. Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. Nat Genet 2012; 44: 1111–1116.

40 Gangemi RM, Griffero F, Marubbi D, Perera M, Capra MC, Malatesta P et al. SOX2 silencing in glioblastoma tumor-initiating cells causes stop of proliferation and loss of tumorigenicity. Stem Cells 2009; 27: 40–48.

41 Basu-Roy U, Seo E, Ramanathapuram L, Rapp TB, Perry JA, Orkin SH et al. Sox2 maintains self renewal of tumor-initiating cells in osteosarcomas. Oncogene 2012; 31: 2270–2282.

42 Nakatsugawa M, Takahashi A, Hirohashi Y, Torigoe T, Inoda S, Murase M et al. SOX2 is overexpressed in stem-like cells of human lung adenocarcinoma and augments the tumorigenicity. Lab Invest 2011; 91: 1796–1804.

43 Chou YT, Lee CC, Hsiao SH, Lin SE, Lin SC, Chung CH et al. The emerging role of SOX2 in cell proliferation and survival and its crosstalk with oncogenic signaling in lung cancer. Stem Cells 2013; 31: 2607–2619.

44 Leis O, Eguiara A, Lopez-Arribillaga E, Alberdi MJ, Hernandez-Garcia S, Elorriaga K et al. Sox2 expression in breast tumours and activation in breast cancer stem cells. Oncogene 2012; 31: 1354–1365.

45 Bareiss PM, Paczulla A, Wang H, Schairer R, Wiehr S, Kohlhofer U et al. SOX2 expression associates with stem cell state in human ovarian carcinoma. Cancer Res 2013; 73: 5544–5555.

46 Herreros-Villanueva M, Zhang JS, Koenig A, Abel EV, Smyrk TC, Bamlet WR et al. SOX2 promotes dedifferentiation and imparts stem cell-like features to pancreatic cancer cells. Oncogenesis 2013; 2: e61.

47 Rybak AP, Tang D. SOX2 plays a critical role in EGFR-mediated self-renewal of human prostate cancer stem-like cells. Cell Signal 2013; 25: 2734–2742.

48 Hütz K, Mejías-Luque R, Farkasova K, Ogris M, Krebs S, Anton M et al. The stem cell factor SOX2 regulates the tumorigenic potential in human gastric cancer cells. Carcinogenesis (e-pub ahead of print 9 December 2013; doi:10.1093/carcin/bgt410).

49 Piva M, Domenici G, Iriondo O, Rábano M, Simões BM, Comaills V et al. Sox2 promotes tamoxifen resistance in breast cancer cells. EMBO Mol Med 2014; 6: 66–79.

50 Laga AC, Lai CY, Zhan Q, Huang SJ, Velazquez EF, Yang Q et al. Expression of the embryonic stem cell transcription factor SOX2 in human skin: relevance to melanocyte and merkel cell biology. Am J Pathol 2010; 176: 903–913.

51 Laga AC, Zhan Q, Weishaupt C, Schairer R, Wiehr S, Kohlhofer U et al. SOX2 and nestin expression in human melanoma: an immunohistochemical and experimental study. Exp Dermatol 2011; 20: 339–345.

52 Chen PL, Chen WS, Li J, Lind AC, Lu D. Diagnostic utility of neural stem and progenitor cell markers nestin and SOX2 in distinguishing nodal melanocytic nevi from metastatic melanomas. Mod Pathol 2013; 26: 44–53.

53 Girouard SD, Laga AC, Mihm MC, Scolyer RA, Thompson JF, Zhan Q et al. SOX2 contributes to melanoma cell invasion. Lab Invest 2012; 92: 362–370.

54 Monzani E, Facchetti F, Galmozzi E, Corsini E, Benetti A, Cavazzin C et al. Melanoma contains CD133 and ABCG2 positive cells with enhanced tumorigenic potential. Eur J Cancer 2007; 43: 935–946.

55 Perego M, Tortoreto M, Tragni G, Mariani L, Deho P, Carbone A et al. Heterogeneous phenotype of human cells with in vitro and in vivo features of tumor-initiating cells. J Invest Dermatol 2010; 130: 1877–1886.

56 Ramgolam K, Lauriol J, Lalou C, Lauden L, Michel L, de la Grange P et al. Melanoma spheroids grown under neural crest cell conditions are highly plastic migratory/invasive tumor cells endowed with immunomodulator function. PLoS One 2011; 6: e18784.

57 Luo Y, Dallaglio K, Chen Y, Robinson WA, Robinson SE, McCarter MD et al. ALDH1A isozymes are markers of human melanoma stem cells and potential therapeutic targets. Stem Cells 2012; 30: 2100–2113.

58 Lee J, Platt KA, Censullo P, Ruiz i Altaba A. Gli1 is a target of Sonic hedgehog that induces ventral neural tube development. Development 1997; 124: 2537–2552.

59 Miyagi S, Nishimoto M, Saito T, Ninomiya M, Sawamoto K, Okano H et al. The Sox2 regulatory region 2 functions as a neural stem cell-specific enhancer in the telencephalon. J Biol Chem 2006; 281: 13374–13381.

60 Stecca B, Ruiz i Altaba A. A GLI1-p53 inhibitory loop controls neural stem cell and tumour cell numbers. EMBO J 2009; 28: 663–676.

61 Pandolfi S, Montagnani V, Penachioni JY, Vinci MC, Olivito B, Borgognoni L et al. WIP1 phosphatase modulates the Hedgehog signaling by enhancing GLI1 function. Oncogene 2013; 32: 4737–4747.

62 Baltus GA, Kowalski MP, Zhai H, Tutter AV, Quinn D, Wall D et al. Acetylation of sox2 induces its nuclear export in embryonic stem cells. Stem Cells 2009; 27: 2175–2184.

63 Jeong CH, Cho YY, Kim MO, Kim SH, Cho EJ, Lee SY et al. Phosphorylation of Sox2 cooperates in reprogramming to pluripotent stem cells. *Stem Cells* 2010; **28**: 2141–2150.

64 Utikal J, Maherali N, Kulalert W, Hochedlinger K. Sox2 is dispensable for the reprogramming of melanocytes and melanoma cells into induced pluripotent stem cells. *J Cell Sci* 2009; **122**: 3502–3510.

65 Hochedlinger K, Yamada Y, Beard C, Jaenisch R. Ectopic expression of Oct-4 blocks progenitor-cell differentiation and causes dysplasia in epithelial tissues. *Cell* 2005; **121**: 465–477.

66 Kumar SM, Liu S, Lu H, Zhang H, Zhang PJ, Gimotty PA et al. Acquired cancer stem cell phenotypes through Oct4-mediated dedifferentiation. *Oncogene* 2012; **31**: 4898–4911.

67 Fang X, Yoon JG, Li L, Yu W, Shao J, Hua D et al. The SOX2 response program in glioblastoma multiforme: an integrated ChIP-seq, expression microarray, and microRNA analysis. *BMC Genomics* 2011; **12**: 11–28.

68 Po A, Ferretti E, Miele E, De Smaele E, Paganelli A, Canettieri G et al. Hedgehog controls neural stem cells through p53-independent regulation of Nanog. *EMBO J* 2010; **29**: 2646–2658.

69 Zbinden M, Duquet A, Lorente-Trigos A, Ngwabyt SN, Borges I, Ruiz i Altaba A. NANOG regulates glioma stem cells and is essential in vivo acting in a cross-functional network with GLI1 and p53. *EMBO J* 2010; **29**: 2659–2674.

70 Favaro R, Valotta M, Ferri AL, Latorre E, Mariani J, Giachino C et al. Hippocampal development and neural stem cell maintenance require Sox2-dependent regulation of Shh. *Nat Neurosci* 2009; **12**: 1248–1256.

71 Engelen E, Akinci U, Bryne JC, Hou J, Gontan C, Moen M et al. Sox2 cooperates with Chd7 to regulate genes that are mutated in human syndromes. *Nat Genet* 2011; **43**: 607–611.

72 Stolzenburg S, Rots MG, Beltran AS, Rivenbark AG, Yuan X, Qian H et al. Targeted silencing of the oncogenic transcription factor SOX2 in breast cancer. *Nucleic Acids Res* 2012; **40**: 6725–6740.

73 Narasimhan K, Pillay S, Bin Ahmad NR, Bikadi Z, Hazai E, Yan L et al. Identification of a polyoxometalate inhibitor of the DNA binding activity of Sox2. *ACS Chem Biol* 2011; **6**: 573–581.

74 Hu Y, Smyth GK. ELDA: extreme limiting dilution analysis for comparing depleted and enriched populations in stem cell and other assays. *J Immunol Methods* 2009; **347**: 70–78.

Supplementary Information accompanies this paper on the Oncogene website (http://www.nature.com/onc)