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## **BRN2 is a non-canonical melanoma tumor-suppressor**

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► **To cite this version:**

Michael Hamm, Pierre Sohier, Valérie Petit, Jérémy H Raymond, Véronique Delmas, et al.. BRN2 is a non-canonical melanoma tumor-suppressor. *Nature Communications*, 2021, 12 (1), pp.3707. 10.1038/s41467-021-23973-5 . hal-03437816v2

**HAL Id: hal-03437816**

**<https://hal.science/hal-03437816v2>**

Submitted on 26 Nov 2021

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1 BRN2 is a non-canonical melanoma tumor-suppressor

2

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40 The authors declare no potential conflicts of interest.

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43 Running title: BRN2 is a tumor-suppressor

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47 KEYWORDS

48 Melanoma; phenotypic switch; mouse molecular genetics; Haplo-insufficiency;  
49 human; Mitf; Cre-LoxP; tamoxifen; POU3F2

50

51 ABSTRACT (150 words)

52 While the major drivers of melanoma initiation, including activation of NRAS/BRAF  
53 and loss of *PTEN* or *CDKN2A*, have been identified, the role of key transcription  
54 factors that impose altered transcriptional states in response to deregulated signaling  
55 is not well understood. The POU domain transcription factor BRN2 is a key regulator  
56 of melanoma invasion, yet its role in melanoma initiation remains unknown. Here, in  
57 a *Braf*<sup>V600E</sup> *Pten*<sup>F/+</sup> context, we show that *BRN2* haplo-insufficiency promotes  
58 melanoma initiation and metastasis. However, metastatic colonization is less efficient  
59 in the absence of Brn2. Mechanistically, BRN2 directly induces *PTEN* expression and  
60 in consequence represses PI3K signaling. Moreover, MITF, a BRN2 target,  
61 represses *PTEN* transcription. Collectively, our results suggest that on a *PTEN*  
62 heterozygous background somatic deletion of one *BRN2* allele and temporal  
63 regulation of the other allele elicits melanoma initiation and progression.

64

65

66 INTRODUCTION

67 Cancer initiation is triggered by the activation of oncogenic signaling combined with  
68 senescence bypass. Yet while many typical oncogenes and tumor suppressors that  
69 affect cancer initiation have been identified, cancer initiation is likely to be modulated  
70 by additional genetic events. Understanding how non-classical driver mutations may  
71 impact cancer initiation is a key issue that has been relatively underexplored.  
72 Melanoma, a highly aggressive skin cancer, arises through the acquisition of well-  
73 defined genetic and epigenetic modifications in oncogenes and tumor suppressors  
74 and represents an excellent model system to address this key question.

75 As a highly genetically unstable cancer type, the initiation of melanoma  
76 requires the induction of melanocyte proliferation, which is mediated by several major  
77 founder mutations, the most common of which are *BRAF*<sup>V600E</sup> and *NRAS*<sup>Q61K/R</sup> 1,2.  
78 However, activation of BRAF or NRAS is insufficient to promote melanoma initiation  
79 without senescence bypass mediated by additional founder mutations or expression  
80 changes of several genes including *p16*<sup>INK4A</sup>, *CTNNB1*, *PTEN*, or *MDM4* 3-7.

81 The transcription factor BRN2, also known as POU3F2 and N-OCT3, plays a  
82 critical role in neurogenesis and drives proliferation in a range of cancer types with  
83 neural or neuroendocrine origins, including glioblastoma, neuroblastoma, small cell  
84 lung cancer, and neuroendocrine prostate cancer 8-10. In the melanocyte lineage,  
85 BRN2 is not detected in melanoblasts *in vivo* but is heterogeneously expressed in  
86 naevi and melanoma 11-14. *In vitro* studies have shown that BRN2 expression is  
87 induced by a range of melanoma-associated signaling pathways including activation  
88 of the mitogen-activated protein kinase (MAPK) pathway downstream from BRAF,  
89 the PI3K pathway, the LEF- $\beta$ -catenin axis, as well as FGF, TNF- $\alpha$ , EDN3 and SCF

90 signaling <sup>14-17</sup>. Consistent with BRN2 being expressed in a predominantly mutually  
91 exclusive pattern with the Microphthalmia-associated transcription factor (MITF) <sup>13</sup>  
92 that plays a crucial role in melanoma proliferation <sup>18</sup>, BRN2 is repressed by MITF via  
93 miR-211 <sup>19</sup>. However, the relationship between MITF and BRN2 is complex. For  
94 example, BRN2 was recently found to be regulated by E2F1, a cell cycle-regulated  
95 transcription factor that is also a target for MITF, and both BRN2 and MITF are  
96 regulated by PAX3 and WNT/ $\beta$ -catenin <sup>15,16,20-24</sup>. Indeed, both BRN2 and MITF can  
97 regulate expression of AXL <sup>21,25</sup>, with BRN2 repressing AXL expression, thus  
98 enabling some cells in human melanoma to adopt an AXL<sup>High</sup>, MITF<sup>Low</sup> and BRN2<sup>Low</sup>  
99 state <sup>25</sup>. The activation of BRN2 expression in a specific subset of melanoma cells in  
100 response to all three major signaling pathways (MAPK, PI3K/PTEN, and  $\beta$ -catenin)  
101 linked to melanoma initiation (early proliferation and bypass/escape senescence) and  
102 progression (including late proliferation and metastatic dissemination) suggests that  
103 Brn2 is likely to have a critical role in disease progression <sup>26</sup>. Most notably, BRN2 has  
104 been associated with MITF<sup>Low</sup> senescent or slow-cycling cells <sup>11</sup>, and identified as a  
105 key regulator of melanoma invasion and anoikis *in vitro* <sup>13,27,28</sup> and in *in vivo*  
106 xenograft experiments <sup>20,29,30</sup>. Mechanistically, the ability of BRN2 to promote  
107 invasion has been linked to its ability to control expression of PDE5A-mediated cell  
108 contractility, phosphorylation of myosin light chain 2, repression of MITF and PAX3,  
109 and cooperation with bi-allelic loss of CDKN2A <sup>13,20,27,30</sup>. However, despite abundant  
110 information linking BRN2 to melanoma proliferation and invasiveness *in vitro* and in  
111 xenograft experiments, the impact of BRN2 on melanoma initiation and progression  
112 *in vivo* has never been assessed.

113            In this work, we show that BRN2 acts as a tumor suppressor during melanoma  
114 initiation and progression in a *BRAF-PTEN* context since BRN2 and MITF regulate  
115 positively and negatively the transcription of *PTEN*, respectively.

116

117 RESULTS

118

119 BRN2 loss or low expression correlates with reduced survival and worse prognosis.

120 Although BRN2 has been implicated in melanoma invasiveness, and its expression is  
121 highly regulated, whether and how it may contribute to melanoma initiation or  
122 incidence is not understood. To evaluate the prevalence of *BRN2* loss in human skin  
123 cutaneous melanoma (SKCM), we retrieved copy-number alteration (CNA) data for  
124 *BRN2* in SKCM metastases (stage IV) from the Cancer Genome Atlas (TCGA,  
125 <https://cancergenome.nih.gov/>). The *BRN2* locus showed mono-allelic loss in 53%  
126 and bi-allelic loss in 2.7% of all patient samples (n = 367, Figure 1A). Only a minority  
127 (n = 29 of 367, corresponding to 7.9%) of SKCM samples showed a copy-number  
128 gain (n = 27)/amplification (n = 2) for *BRN2*. We did not further analyze these  
129 samples since the expression of BRN2 was slightly increased but not statistically  
130 different (p=0.26, test of Kruskal-Wallis with a Dunn correction) between tumors that  
131 gained and/or amplified this locus compared to the normal situation. We screened a  
132 panel of human melanoma cell lines available in our laboratory (n = 23) for deletions  
133 that affect the *BRN2* locus by comparative genomic hybridization. The *BRN2* locus  
134 showed mono-allelic loss in 48% (11 out 23) of the human melanoma cell lines and  
135 no bi-allelic loss, comparable to the TCGA-data (Supplementary Fig. 1A,  
136 Supplementary Data 1). Notably, BRN2 mRNA levels were significantly lower in  
137 SKCM metastases with bi-allelic BRN2 loss (Supplementary Fig. 1B). The mono- and  
138 bi-allelic loss of *BRN2* was frequently associated with a large segmental deletion of  
139 the long arm of chromosome 6 (Chr.6q) in SKCM metastases and in our cell line  
140 panel (Figure 1B, Supplementary Fig. 1C, Supplementary Data 2). From the TCGA,

141 patients carrying the monoallelic loss of *BRN2* in metastases displayed a trend to  
142 have a shorter overall survival than those with diploid status (Figure 1C). These  
143 results were validated using an independent cohort of 118 regional metastases  
144 previously described <sup>31</sup> (Figure 1D). Moreover, we evaluated the number of *BRN2*  
145 alleles in nevi and melanoma that arose from these nevi using publically available  
146 data <sup>32</sup>. It appears that 28% (5 out of 18) or 22% (4 out of 18) of melanomas  
147 presented either a mono-allelic loss or a gain of *BRN2* respectively compared to nevi  
148 (Supplementary Fig. 1D). The situation is clearly complex, but we may conclude that  
149 *BRN2* mono-allelic loss can occur during the early steps of melanomagenesis.

150 We next assessed the correlation between *BRN2* mRNA levels and overall  
151 patient survival to evaluate the effect of *BRN2* mono-allelic loss on melanoma  
152 progression. We established “*BRN2*-high” and “*BRN2*-low” patient groups based on  
153 RNA-seq data available from the TCGA (*BRN2* subgroups defined as *BRN2*-low ( $\leq 1$   
154 transcript per million reads [TPM]) and *BRN2* expressed/high [ $> 1$  TPM]). Patients in  
155 the “*BRN2*-low” group displayed significantly shorter overall survival than those of the  
156 “*BRN2*-high” group (Figure 1E). Overall, the *BRN2* locus, frequently associated with  
157 a large segmental deletion, is lost (mono- and bi-allelic) in  $\approx 60\%$  of human SKCM  
158 metastases and correlates with significantly reduced overall survival. Since *CCNC*,  
159 *ROS1* and *ARID1B* loci are distal to *BRN2* on chromosome 6, and are known to be  
160 involved in melanomagenesis, we evaluated the overall survival of these patients  
161 according to the presence and the level of mRNA expression of the corresponding  
162 genes. We observed no significant difference between the presence or absence of  
163 these three genes or their expression (Supplementary Fig. 1E-L). Finally, we  
164 compared the loss of 6q with the mono-allelic loss (MAL) of *BRN2* (Supplementary

165 Fig. 1M) and found that 6q loss is associated with a worse prognostic than *BRN2*  
166 mono-allelic loss. This result indicates, as suspected, that other gene(s) located on  
167 6q are of importance in melanomagenesis. Taken together, these data indicate that  
168 in human melanoma *BRN2* loss/low expression is associated with an adverse  
169 outcome for the patient.

170

171 Co-occurrence of *BRN2* loss with mono-allelic loss of *PTEN*

172 We next determined whether *BRN2* loss co-occurs with melanoma driver mutations  
173 by examining the TCGA CNA-data set and human melanoma cell-line panel. There  
174 was no significant correlation between *BRAF* or *NRAS* mutation and *BRN2* loss  
175 (mono- or bi-allelic), neither in human melanoma samples nor the human cell-line  
176 panel (Supplementary Fig. 2A,B). We then searched for co-occurring CNAs of other  
177 known melanoma-associated genes and found that mono-allelic loss of *BRN2* co-  
178 occurred with mono-allelic loss of *PTEN* in approximately 40% of the human  
179 melanoma samples in TCGA and in the human cell-line panel (Supplementary Fig.  
180 2C,D). We next evaluated the concomitant *BRN2* locus alterations, *BRAF/NRAS*  
181 mutations, and *CDKN2A/PTEN* alterations and found the most frequent genetic  
182 constellation that co-occurs with *BRN2* loss in melanoma to be *BRAF<sup>V600X</sup>* mutation  
183 together with mono-allelic *PTEN* loss (Supplementary Fig. 2E). Finally, we compared  
184 the overall survival of human patients with a loss of one allele of *PTEN* who also had  
185 a loss of *BRN2* (monoallelic loss = MAL) with a loss of one allele of *PTEN* and no  
186 loss of *BRN2* (*BRN2*-normal). In this context, patients with loss of *BRN2* showed  
187 significantly lower overall survival than *BRN2*-normal patients (Supplementary Fig.  
188 1N).

189

190 In conclusion, in human melanoma, the loss of *BRN2* is preferentially associated with  
191 *BRAF* mutation together with *PTEN* loss.

192

193 Loss of *BRN2* drives melanomagenesis *in vivo*.

194 These data suggesting that the loss of *BRN2* might be of importance in melanoma  
195 prompted us to evaluate the potential causal role of *BRN2* in melanomagenesis *in*  
196 *vivo* by examining whether heterozygous (het) or homozygous (hom) loss of *Brn2*  
197 affects melanoma initiation and/or progression in a mouse model. Note however, that  
198 while genetic loss of *BRN2* might be important, the complex regulation of *BRN2*  
199 expression driven by melanoma-associated signaling pathways might also play a  
200 major role, especially given that melanoma cells within a single tumor can exhibit  
201 both high and very low *BRN2* expression<sup>13,20</sup>. We therefore developed an inducible  
202 genetically engineered mouse model system for generating *Brn2*-deficient melanoma  
203 driven by the most common alterations in human SKCM (*Braf*<sup>V600E</sup> and *Pten* loss).  
204 Specifically, we used *Tyr::Cre*<sup>ERT2<sup>fl</sup>-Lar</sup>; *Braf*<sup>V600E/+</sup> (called *Braf* from hereon) and  
205 *Tyr::Cre*<sup>ERT2<sup>fl</sup>-Lar</sup>; *Braf*<sup>V600E/+</sup>; *Pten*<sup>F/+</sup> (called *Braf-Pten* from hereon) mice carrying a  
206 tamoxifen-inducible *Cre*-recombinase under the control of the tyrosinase promoter<sup>33-</sup>  
207 <sup>35</sup>. This model system allows melanocyte lineage-specific induction of a *BRAF*<sup>V600E</sup>  
208 mutation and mono-allelic deletion of *Pten* for *Braf-Pten* mice. *Cre*-mediated  
209 defloxing leads to activation of the *Braf*<sup>V600E</sup> oncogene, inducing nevus and  
210 spontaneous melanoma formation in *Braf* mice, reproducing many of the cardinal  
211 histological and molecular features of human melanoma<sup>36</sup>. Bi-allelic and mono-allelic

212 loss of *PTEN* reduces tumor latency in *Braf*<sup>V600E</sup>- and *NRAS*<sup>Q61K</sup>-driven mouse  
213 melanoma models<sup>3,37</sup>.

214 Using these models, we studied the effect of *Brn2* insufficiency (het and hom)  
215 on *in vivo* melanomagenesis by introducing the floxed *Brn2* locus into the genome by  
216 appropriate crossings (Supplementary Fig. 3A)<sup>38</sup>. Specifically, we generated the  
217 mouse lines *Tyr::Cre*<sup>ERT2<sup>o</sup></sup>; *Braf*<sup>V600E/+</sup>; *Brn2*<sup>+/+</sup> (Braf-Brn2-WT), *Tyr::Cre*<sup>ERT2<sup>o</sup></sup>;  
218 *Braf*<sup>V600E/+</sup>; *Brn2*<sup>F/+</sup> (Braf-Brn2-het), *Tyr::Cre*<sup>ERT2<sup>o</sup></sup>; *Braf*<sup>V600E/+</sup>; *Brn2*<sup>F/F</sup> (Braf-Brn2-hom),  
219 *Tyr::Cre*<sup>ERT2<sup>o</sup></sup>; *Braf*<sup>V600E/+</sup>; *Pten*<sup>F/+</sup>; *Brn2*<sup>+/+</sup> (Braf-Pten-Brn2-WT), *Tyr::Cre*<sup>ERT2<sup>o</sup></sup>;  
220 *Braf*<sup>V600E/+</sup>; *Pten*<sup>F/+</sup>; *Brn2*<sup>F/+</sup> (Braf-Pten-Brn2-het) and *Tyr::Cre*<sup>ERT2<sup>o</sup></sup>; *Braf*<sup>V600E/+</sup>; *Pten*<sup>F/+</sup>;  
221 *Brn2*<sup>F/F</sup> (Braf-Pten-Brn2-hom). Cre-mediated defloxing of *Braf*, *Pten*, and *Brn2* loci  
222 was induced by topical application of tamoxifen during the first three days after birth  
223 (Supplementary Fig. 3B). All mice were monitored for the appearance and growth  
224 rate of the first tumor, as well as for the number of tumors/mouse. Note that the  
225 ability to generate either homo- or heterozygous *Brn2* KOs will mimic not only mono  
226 or biallelic loss in humans, but also reflect the variable levels of BRN2 observed  
227 within human tumors<sup>13,20</sup>. In the absence of PTEN (*Pten*<sup>F/F</sup>) on a *Braf*<sup>V600E</sup>  
228 background, the appearance of the tumors was too rapid to observe any difference  
229 between *Brn2* +/+, *Brn2* F/+ or *Brn2* F/F mice.

230 *Braf*-*Brn2*-WT/het/hom mice showed no differences in the appearance of the  
231 first tumor, number of tumors/mouse or the tumor growth rate from those of *Braf*-WT  
232 mice (Figure 2, Supplementary Fig. 3C). However, compared to *Braf*-*Pten*-*Brn2*-WT,  
233 *Braf*-*Pten*-*Brn2*-het/hom mice significantly increased the number of tumors/mouse  
234 and the tumor growth rate, but not the timing of the appearance of the first tumor  
235 (Figure 2, Supplementary Fig. 3D). We verified that *Brn2*, *Braf*, and *Pten* were

236 correctly defloxed in the resulting melanomas (Supplementary Fig. 3E,F). In  
237 summary, our data show that Brn2 acts as a tumor suppressor *in vivo*. As it has been  
238 shown in humans and mice, induction of early proliferation induced by the presence  
239 of the BRAF<sup>V600E</sup> mutation leads to senescence, but it can be bypassed when the  
240 level of Pten is reduced <sup>3,37,39,40</sup>. It is important to note that in the absence of Pten in  
241 the physiological context, proliferation of melanoblasts and melanocytes is not  
242 induced as the reduction/lack of Pten promotes proliferation once the cells are  
243 transformed <sup>3,41</sup>. On a Braf-Pten context the loss/reduction of Brn2 appears to induce  
244 melanoma initiation after promoting proliferation and bypass/escape of senescence,  
245 and then allows the tumor growth as was previously showed *in vivo* <sup>3,37</sup>.

246

247 Reduction of BRN2 levels increases proliferation *in vivo* and *in vitro*.

248 The effect of *Brn2* loss on tumor growth prompted us to investigate whether *Brn2*  
249 loss increases intra-tumor proliferation. Staining sections for Ki-67, a marker of  
250 cycling cells, revealed that melanomas from Braf-Pten-Brn2-het/hom mice displayed  
251 a significantly higher number of Ki-67<sup>+</sup> cells than Braf-Pten-Brn2-WT melanomas  
252 (Figure 3A,B). To confirm this result, we injected Braf-Pten-Brn2 mice with  
253 bromodeoxyuridine (BrdU) two hours prior to euthanization, to determine whether  
254 melanoma cells were slow or fast-dividing. Braf-Pten-Brn2 melanomas had a  
255 significantly higher number of BrdU<sup>+</sup> cells when Brn2 was heterozygous or  
256 homozygous (Figure 3C,D). These results indicated that heterozygous loss of *Pten*  
257 combined with heterozygous/homozygous loss of *Brn2* promotes melanoma  
258 proliferation *in vivo*.

259 We next assessed whether Brn2 knockdown favors proliferation *in vitro* and  
260 whether this mechanism is conserved (i) between human and mouse and (ii)  
261 between transformed and non-transformed cells using Dauv-1 human melanoma cell  
262 line, and the Melan-a mouse melanocyte cell line. These cell lines express both Pten  
263 and Brn2 mRNA and protein (Supplementary Table 1). Dauv-1 cells carry a  
264 BRAF<sup>V600E/+</sup> mutation identical to that used in the mouse melanoma model system,  
265 and Melan-a cells are WT for Braf. siRNA-mediated knockdown of Brn2 significantly  
266 increased cell number 72 h after transfection of both cell lines (Figure 3E-G). Brn2  
267 knockdown, assessed by western blot, led to an increase in cyclin D1 protein levels  
268 in both cell lines, but did not alter cyclin D1 mRNA levels, suggesting a regulation of  
269 cyclin D1 at the protein level (Figure 3F-H). Overall, the reduction of the Brn2 protein  
270 induces cell proliferation of the melanocytic lineage *in vivo* and *in vitro*.

271 Colony formation assays *in vitro* are classically used to show the importance  
272 of a gene in tumorigenesis, and indicate that a single cell may survive *in vitro* and  
273 proliferate to form a colony. Previous work has demonstrated that a reduction in Brn2  
274 levels in melanoma cells has no effect on colony formation<sup>42,43</sup>. However, to test this  
275 in our model, mouse melanoma cell lines were established and characterized from  
276 the different independent Braf-Pten-Brn2 C57BL/6J mouse melanoma; the m50 and  
277 m6 cell lines were Brn2-WT, m59 and m36 were Brn2-het, and m82 and m8 were  
278 Brn2-hom (Supplementary Fig. 4A-F). The presence or absence of Brn2 did not  
279 decrease the ability of these melanoma cell lines to grow in syngeneic mice  
280 (Supplementary Table 2). In other words, it appears that the absence of Brn2 in  
281 these melanoma cells does not affect the implantation of the cells on the body wall,  
282 the proliferation after their transformation or the induction of angiogenesis in an

283 immunocompetent environment. We evaluated the capacity of the m50 (Brn2 WT),  
284 m59 (het), and m82 (hom) cells to generate colonies and observed, in agreement  
285 with previous observations obtained using BRN2 depletion, that the three cell lines  
286 have similar abilities to form colonies (Supplementary Fig. 4G). Moreover, re-  
287 expression of Brn2 using lentivirus infection in two independent m8 and m82 Braf-  
288 Pten-Brn2-hom mouse melanoma cell lines, also indicated that BRN2 does not affect  
289 their capacity to form colonies under these conditions (Supplementary Fig. 4H,I). In  
290 conclusion, as shown in human cell lines, the number of colony forming units is  
291 independent of the presence or absence of Brn2 and consequently this assay is  
292 uninformative regarding the role of Brn2 in melanomagenesis.

293 We also evaluated the activity of BRAF<sup>V600</sup> (PLX4720), MEK (Binimetinib), and  
294 PI3K (LY294002) inhibitors on the capacities of m50, m59 and m82 mouse  
295 melanoma cell lines to form CFU and determined the IC50 of these drugs  
296 (Supplementary Fig. 4J-O). Consistent with observations suggesting that BRN2 may  
297 suppress cell death<sup>43</sup>, Brn2-het/hom cells are more sensitive than WT cells to these  
298 three drugs. We also evaluated the cooperativity of PLX4720 and LY294002 using  
299 various concentrations of each drug, but we did not observe any cooperation/synergy  
300 of these two drugs.

301

302 Mono-allelic loss of Brn2 induces melanoma metastasis.

303 We next evaluated the effects of Brn2 on metastasis formation *in vivo*. Since human  
304 SKCM is known to spread to proximal lymph nodes (LNs), we assessed the presence  
305 of pigmented cells in the inguinal LNs of tumor-bearing Braf-Pten-Brn2 mice.  
306 Specifically, we estimated the volume of the various metastases present in LNs and

307 the number of pigmented areas after haematoxylin & eosin (HE) staining of LN  
308 sections (Figure 4A-C). All Braf-Pten-Brn2 mice, irrespective of BRN2 status, showed  
309 the presence of pigmented cells in both inguinal LNs. However, the LN volume of  
310 Braf-Pten-Brn2-het mice was significantly higher than that of Braf-Pten-Brn2-WT and  
311 Braf-Pten-Brn2-hom (Figure 4A,B). Similarly, Braf-Pten-Brn2-het LNs showed a  
312 higher number of pigmented areas per mm<sup>2</sup> than Braf-Pten-Brn2-WT/hom mice  
313 (Figure 4C).

314 To verify that the pigmented cells in the lymph nodes did not arise from cells in  
315 which the Cre recombinase had not worked efficiently, we tested whether these  
316 pigmented cells were properly defloxed for Brn2. The targeted Brn2-flox allele, used  
317 in our mouse model, has an eGFP-cassette inserted downstream of the floxed *Brn2*  
318 locus (Figure 4D). Thus the production of eGFP occurs once the upstream *Brn2*  
319 is defloxed. Consistent with correct defloxing of *Brn2*, pigmented areas of LNs  
320 expressed GFP in Braf-Pten-Brn2-het/hom mice, but not Braf-Pten-Brn2-WT mice  
321 (Figure 4E). The pigmented cells present in Braf-Pten-Brn2-WT and Braf-Pten-Brn2-  
322 het LNs also expressed Sox10, a melanocytic marker (Figure 4E), that co-localized  
323 with eGFP-expression in Braf-Pten-Brn2-het mice confirming the melanocytic origin  
324 of the pigmented cells observed.

325 To get a better understanding of melanomagenesis in the various Brn2-  
326 WT/het/hom situations, we performed a transcriptomic analysis of the various Brn2  
327 tumors and cell lines (Supplementary Data 3 and 4). The ontology enrichment  
328 analysis indicated that the Braf-Pten-Brn2-het tumors were more inflamed than the  
329 Braf-Pten-Brn2-WT tumors with increased neutrophil-associated gene expression  
330 (Supplementary Fig. 5A). It also suggests that the extracellular-matrix was actively

331 remodeled and that these Braf-Pten-Brn2-het tumors were more subject to  
332 angiogenesis (Supplementary Fig. 5A). Pathway enrichment analysis supported  
333 these results as inflammatory gene expression signatures are enriched from both the  
334 WikiPathways and KEGG databases (Supplementary Fig. 5B,C). Significantly, the  
335 PI3K/AKT pathway was enriched in the Braf-Pten-Brn2-het tumors compared to the  
336 Braf-Pten-Brn2-WT in both WikiPathways and KEGG databases (Supplementary Fig.  
337 5B,C), suggesting that AKT could be more phosphorylated in the Braf-Pten-Brn2-het  
338 tumors. This assumption was verified by Western-blot analysis where  
339 phosphorylation of AKT on S473, a surrogate of the AKT activity, and the  
340 phosphorylation of S6 on S235/236 were significantly increased in Braf-Pten-Brn2-  
341 het/hom tumors compared to Braf-Pten-Brn2-WT tumors (Supplementary Fig. 5D).

342 Gene Set Enrichment Analysis (GSEA) using the melanoma invasive  
343 signature from Verfaillie <sup>44</sup> indicated that Braf-Pten-Brn2-het tumors and cell lines  
344 were more invasive than Braf-Pten-Brn2-hom tumors and cell lines (Figure 4F).  
345 Moreover, from the GO, WikiPathways and KEGG 2019 analyses of the mouse  
346 melanoma tumors, the immune system (cytokine, neutrophil, macrophage) and  
347 angiogenesis are induced in Braf-Pten-Brn2-het tumors compared to Braf-Pten-Brn2-  
348 WT tumors (Supplementary Fig. 5A-C). This information suggests that Braf-Pten-  
349 Brn2-het cells have more potential to metastasize than Braf-Pten-Brn2-WT and Braf-  
350 Pten-Brn2-hom cells. In this respect, we tested the capacity of Braf-Pten-Brn2-hom  
351 (m82) mouse melanoma cell lines re-expressing or not Brn2 (m82 and m82+Brn2) to  
352 invade matrigel in 3D. In the presence of ectopic Brn2, the m82 Brn2 KO melanoma  
353 cell lines have more ability to invade (Figure 4G and S4I). Since AXL, a receptor  
354 tyrosine kinase (RTK), is associated with melanoma metastasis <sup>45</sup>, we also evaluated

355 the level of Axl in mouse melanoma tumors and cells. Braf-Pten-Brn2-het cells  
356 produce slightly more Axl mRNA than Brn2-WT/hom (Figure 4H). This upregulation  
357 does not affect genes that are in *Cis* of Axl suggesting a specific regulation of Axl in a  
358 Braf-Pten-Brn2-het context (Supplementary Fig. 5E-G). Moreover, when the levels of  
359 both BRN2 and MITF are reduced in human melanoma cell lines, the level of AXL  
360 mRNA is induced (Supplementary Fig. 6D,H,L,P,T). More precisely the level of AXL  
361 is slightly, but significantly, higher in Gerlach and DAUV-1 cell lines in which the level  
362 of AXL is already very high, and is higher in SK28 and 501Mel cell lines in which the  
363 level of AXL is much lower than in Gerlach and DAUV-1 cell lines.

364 In conclusion, compared with Braf-Pten-Brn2-WT mice, melanoma initiation is  
365 promoted in both Braf-Pten-Brn2-het/hom mice, but metastasis is promoted only in  
366 Braf-Pten-Brn2-het mice. These observations are consistent with the fact that on a  
367 Brn2-het/hom background melanoma initiation (proliferation and bypass/escape of  
368 senescence) is induced and melanoma invasion and/or survival is inhibited on a  
369 Brn2-hom background.

370

371 BRN2 binds to the *PTEN* promoter and BRN2 loss leads to the reduction of *PTEN*  
372 transcription.

373 The PI3K-AKT pathway is induced in melanoma and its induction abrogates  
374 BRAF<sup>V600E</sup>-induced senescence<sup>46,47</sup>. The loss of *Pten*, a suppressor of the PI3K  
375 pathway, induces melanoma initiation and proliferation *in vivo*<sup>3,37</sup>. Since our Braf-  
376 Pten mouse melanoma model retained one functional allele of *Pten*, we hypothesized  
377 that *Brn2* loss would induce less expression from the WT *Pten* allele, leading to the  
378 increased PI3K-AKT signaling observed (Supplementary Fig. 5D) and consequent

379 melanoma initiation and proliferation. We therefore evaluated the number of Pten  
380 positive cells in the various Braf-Pten tumors by immunohistochemistry and found  
381 that Braf-Pten-Brn2-het/hom tumors showed fewer Pten-pos cells than Braf-Pten-  
382 Brn2-WT tumors (Figure 5A). This result was verified by western blotting of Braf-Pten  
383 tumor samples. The reduction of Brn2 correlates with the reduction of Pten in Braf-  
384 Pten-Brn2-het tumors compared to the Braf-Pten-Brn2-WT tumors (Figure 5B). In  
385 accordance with the reduced protein levels, the mRNA levels of Brn2 and Pten were  
386 significantly lower in Braf-Pten-Brn2-het/hom tumors than in Braf-Pten-Brn2-WT  
387 tumors, suggesting regulation of Pten at the transcriptional level (Figure 5C).

388         Next, we evaluated the mechanism of Pten repression mediated by reduced  
389 levels of Brn2 in the human Dauv-1, Gerlach, SK28, and 501Mel melanoma cell lines  
390 and in the non-transformed mouse Melan-a cell line. siRNA-mediated BRN2  
391 knockdown led to significantly reduced PTEN protein and mRNA levels in cell lines  
392 having high BRN2 expression (Figure 5D,E and Supplementary Fig. 6). In cells with  
393 lower level of BRN2 (501Mel), the reduction of PTEN was not observed.

394         We examined the *PTEN* promoter for BRN2 binding sites conserved between  
395 humans and mice to determine whether BRN2 acts directly on *PTEN* and detected  
396 two potential Brn2 binding sites (BS1 and BS2) at the positions - 2,049 and +761  
397 (numbering relative to TSS). Chromatin-immunoprecipitation (ChIP) for BRN2,  
398 performed on Dauv-1 melanoma cell extracts, followed by qPCR, revealed  
399 quantitative BRN2 binding to both binding sites, comparable to BRN2 binding on the  
400 PAX3 promoter (Figure 5F-H). IgG was used as a negative control.

401         To evaluate Pten promoter activity in response to BRN2, we cloned a 3.2-kb-  
402 human Pten promoter fragment containing the two BRN2 binding sites upstream the

403 luciferase gene to generate the hsPten::Luciferase reporter construct (Figure 5H).  
404 The analysis of human PTEN promoter activity showed an intrinsic activity of  
405 hsPten::Luciferase in human melanoma cells (Supplementary Fig. 7A,B). A  
406 consistent repression of PTEN transcription was observed when a smart-pool of  
407 siBRN2 was added. In contrast, PTEN transcription was activated following co-  
408 transfection of a BRN2 expression vector compared to empty vector in Dauv-1 and  
409 SK28 cell lines in luciferase assay (Figure 5I-L). We performed similar experiments  
410 with the mouse PTEN promoter, which was cloned upstream of the luciferase  
411 construct (Supplementary Fig. 7C-F); Brn2 activated Pten transcription in three  
412 mouse melanoma cell lines (m82, m59 and m50) (Figure 5M,N). In conclusion, BRN2  
413 directly induces PTEN transcription.

414

415 MITF binds the *PTEN* locus and represses *PTEN* transcription.

416 The *MITF* gene encodes a key transcription factor that plays a major role in  
417 melanocyte and melanoma biology <sup>18</sup>. Several studies have reported that *MITF*  
418 transcription is directly repressed by BRN2 whereas a reduction in BRN2 levels leads  
419 to increased MITF levels <sup>13,27,48</sup>, while another study showed that BRN2 induces  
420 MITF <sup>49</sup>. Likely both results are correct due to the versatile role of BRN2 as a  
421 transcription regulator whose activity may be dependent on context including genetic  
422 status and/or the environment <sup>21,26,27</sup>.

423         Knowing the importance of MITF in the melanocyte lineage, we analyzed the  
424 consequences of modulation of MITF expression on PTEN. Using siRNA-mediated  
425 *MITF* knockdown in three human melanoma cell lines expressing high levels of MITF  
426 (501mel, SK28, HBL) led to a significant increase of PTEN protein and mRNA levels

427 (Figure 6A,B). In cells expressing lower levels of MITF, such as Gerlach and Dauv-1,  
428 we did not observe an increase of PTEN (Supplementary Fig. 6C,G). Next, to  
429 determine if MITF directly regulates PTEN expression through proximal enhancers  
430 we performed Cleavage Under Targets and Release Using Nuclease (CUT&RUN)  
431 with antibodies to MITF, as previously described,<sup>50</sup> and to H3K27Ac, revealing active  
432 chromatin, and against H3K4me3, revealing active and poised promoters, in SK28  
433 cell lines that were wild type for *MITF* (MITF-WT) or had loss of function mutations in  
434 all alleles of it ( $\Delta$ MITF) (Figure 6C) <sup>50</sup>. An MITF peak is present within the gene body  
435 of *PTEN* (intron 4), and a second one is 114kb downstream of the *PTEN*  
436 transcriptional start site (TSS) (i.e., +114kb). Both MITF peaks were centered on an  
437 M-box motif (5'-TCATGTG-3'). At both intron-4 and +114kb MITF peaks, the  
438 H3K27Ac signal was unchanged in  $\Delta$ MITF mutant cell lines. However, six distal  
439 enhancers (painted light blue) exhibited a 2-fold greater H3K27ac signal in MITF  
440 mutant cell lines compared to wild-type cell lines (+140kb, +210kb, +230kb, +253kb,  
441 +301kb and +317kb), suggesting increased transcription of *PTEN* in the former. We  
442 confirmed the +140kb MITF peak after performing a quantitative ChIP experiments  
443 on 501Mel cells expressing MITF-HA (Figure 6D,E), using Tyrosinase (TYR) and  
444 PRM1 as positive and negative controls respectively. Overall, reduction of MITF  
445 results in an increase in PTEN mRNA expression. As such, it is plausible that Brn2  
446 induces *Pten* transcription through two different, but concurrent mechanisms: (i)  
447 directly through BRN2 binding to the *PTEN* promoter to induce its transcription and  
448 (ii) indirectly via BRN2 modulating (repressing/inducing depending of the situation)  
449 MITF expression, with MITF binding to the 3' end of *PTEN* to inhibit its transcription.  
450 In the absence of BRN2, these mechanisms are disrupted and *PTEN* transcription is

451 downregulated in our conditions. In conclusion, MITF represses directly *PTEN*  
452 transcription.

453 Overall, our results are consistent with a model in which reduction of BRN2  
454 reduces PTEN transcription *in vitro* and *in vivo*, thus ramping up PI3K signaling and  
455 inducing both the initiation of melanoma and the formation of metastases.

456

## 457 DISCUSSION

458 A well-established principle of cancer biology is that tumors are initiated by a  
459 combination of oncogene activation together with loss of tumor suppressor  
460 expression or activity. In melanoma, key oncogenic drivers, such as BRAF and  
461 NRAS, have been well defined. Loss of P16 or PTEN tumor suppressor activity is  
462 required to bypass oncogene-induced senescence and permit melanoma initiation.  
463 However, while inactivation of tumor suppressors by mutation has been extensively  
464 studied, it is less well understood how their activity may be modulated by changes in  
465 their mRNA expression mediated by key melanoma-associated transcription factors.  
466 At this point, it is important to note that factors involved in melanoma initiation will not  
467 automatically reflect/translate into overall survival. Here, we identify BRN2, a key  
468 transcription factor lying downstream of three melanoma-associated signaling  
469 pathways (WNT/ $\beta$ -catenin, MAPK, and PI3K), as a tumor suppressor that functions  
470 to regulate PTEN expression. Thus, monoallelic loss of *Brn2* promotes melanoma  
471 initiation in a *Braf*<sup>V600E</sup>/*Pten*<sup>F/+</sup> background where mono-allelic loss of *Pten* sensitizes  
472 cells to loss of *Brn2*.

473 Previous work has primarily linked BRN2 to melanoma migration and invasion  
474 *in vitro* and in xenograft experiments<sup>13,20,42,51</sup>, but its role during melanoma initiation

475 and proliferation *in vivo* and in normal melanocytes had not been determined. We  
476 report that, consistent with *BRN2* playing a key role as a tumor suppressor in  
477 melanomagenesis, its locus is frequently lost in human skin cutaneous melanoma  
478 (SKCM) metastases, independently of their *NRAS* or *BRAF* status, and that *BRN2*  
479 status contributes to overall patient survival. Significantly, the overall survival of  
480 patients with a mono-allelic loss of PTEN is higher when the *BRN2* locus is intact.

481         Although these observations are consistent with *BRN2* affecting human  
482 melanoma initiation and progression, loss of the *BRN2* locus is frequently associated  
483 with large segmental deletions that affect the long arm of chromosome 6 (6q) as it  
484 was observed in 14 out of 53, and 9 out of 32 out of primary melanoma and in 17 out  
485 of 21 melanoma cell lines <sup>52-54</sup>, and confirmed in this study on a total of 205 out of  
486 338 melanomas, and 11 out of 25 melanoma cell lines. It has already been shown  
487 that the loss of 6q was associated with a worse prognosis <sup>52</sup>. According to our  
488 observations, the loss of 6q is more detrimental for the overall survival than the focal  
489 loss of the *BRN2* locus (Fig. 1 and Fig. S1). Moreover, *in vitro* studies have shown  
490 that several genes are linked to melanomagenesis in the co-deleted region, including  
491 *ARID1B*, *CCNC*, and *ROS1*, although none have yet been shown to be functionally  
492 important in melanoma *in vivo* <sup>48,55-61</sup>. Similarly, we analysed the SKCM TCGA study  
493 to evaluate the overall survival comparing the mono allelic loss and the diploid state  
494 for *CCNC*, *ROS1* and *ARID1B* (Fig. S1). There is no statistical significance for *CCNC*  
495 ( $p = 0.086$ ), *ROS1* ( $p = 0.27$ ) or *ARID1B* ( $p = 0.66$ ).

496         Thus, it might be argued that any of the genes located in this frequently  
497 deleted region may be acting to modulate melanoma initiation or progression.  
498 However, our functional mouse molecular genetics models show conclusively that

499 the heterozygous or homozygous loss of Brn2 promotes melanoma initiation and  
500 initial growth. Similarly, our transcriptomic analysis showed that the mRNA levels of  
501 the seven genes in the region co-deleted in humans (*Arid1b*, *Mchr2*, *Ccnc*, *Cdk19*,  
502 *Dll1*, *Ros1*, and *Crybg1/Aim1*) were not affected in the mouse tumors (Braf-Pten-  
503 Brn2-WT, Braf-Pten-Brn2-het and Braf-Pten-Brn2-hom). Collectively, these results  
504 strongly suggest that the reduction/loss of Brn2 levels is a critical event that  
505 cooperates with heterozygous Pten to promote the initiation and growth of  
506 melanoma, independently of the co-deleted genes in melanoma. Finally, independent  
507 initiation events are promoted when the level of Brn2 is lower than normal -  
508 heterozygous or homozygous- since the number of independent melanoma is higher  
509 in Braf-Pten-Brn2-het/hom mice than in Braf-Pten-Brn2-WT mice (Figure 2B). Our  
510 observations are therefore consistent with BRN2 acting as a tumor suppressor in  
511 melanoma, and are in full agreement with the predominantly mutually exclusive  
512 pattern of BRN2 and Ki-67 *in situ* staining of invasive melanoma <sup>20</sup>.

513         The presence of Braf<sup>V600E</sup> promotes proliferation prior to inducing senescence  
514 and the loss of Pten results in senescence bypass <sup>3,34,37</sup>. As such, we believe that the  
515 increased proliferation and tumor-initiation frequency observed in our  
516 *Braf<sup>V600E</sup>/Pten<sup>F/+</sup>* model arising as a consequence of the reduction of Brn2, is likely to  
517 occur as a consequence of the ability of Brn2 to activate Pten expression and  
518 suppress PI3K signaling either directly or potentially indirectly via Mitf repression  
519 during early melanomagenesis. In other words, inactivation of Brn2 or a reduction in  
520 its expression would lead to low expression of the remaining Pten allele and as a  
521 consequence increase the probability of senescence bypass. This explanation fits  
522 with the fact that in the absence of Pten on a Braf<sup>V600E</sup> background, the appearance

523 of the tumors is too rapid to observe any difference between Brn2 +/+, Brn2 F/+ or  
524 Brn2 F/F. According to our model the transcription regulation by Brn2 and Mitf would  
525 not affect the level of Pten since it is already lost. Moreover, in a context in which  
526 *Pten* is diploid (WT) and Brn2 is reduced (het or hom), the downregulation of Pten  
527 would be limited and not sufficient to act efficiently as a tumor-suppressor.

528         Although it might be argued that the increase in visible tumor number in a  
529 Braf-Pten-Brn2-het and -hom might be a consequence of the increased proliferation  
530 caused by reduction/loss of Brn2, as evidenced by the increased proportion of Ki-67  
531 positive cells within tumours, we feel this is unlikely. For welfare reasons the Braf-  
532 Pten-Brn2-WT mice were euthanized with tumours (total volume 2 cm<sup>3</sup>) after 4 weeks  
533 with about 8 tumours per mouse; by contrast the Braf-Pten-Brn2-het/hom mice were  
534 euthanized after 1.3 weeks with about 17 tumours per mouse of a similar size to the  
535 WT. Since tumour size is similar in the WT and Brn2 mutants, this indicates that the  
536 total number of cells in the WT and mutant tumours is similar and have undergone a  
537 similar number of cell divisions (though this occurred in a shorter time in the mutant).  
538 Since the WT and mutants have undergone a similar number of cell divisions, if  
539 proliferation were responsible for any increase in number of visible tumours then at 4  
540 weeks the numbers of tumours in the WT should be the same as in the mutant at 1.3  
541 weeks, whereas in fact, the tumour numbers in the WT were around 50% of those in  
542 the Brn2 mutants. Although we do not want to rule out a contribution of proliferation,  
543 the more likely explanation is that the reduction of BRN2 promotes the bypass of  
544 senescence (by reducing the level of Pten) or/and promotes survival of proliferating  
545 melanoma cells at the early stages of initiation.

546 Our *in vivo* data therefore reveal that melanocyte-specific Brn2 reduction in  
547 Braf-Pten mice promotes the initiation and progression of melanoma. Melanoma  
548 initiation is promoted after proliferation is induced through various proteins including  
549 Mitf and senescence bypassed in this case through reduction of the level of Pten.  
550 Melanoma progression is induced by promoting invasion when the level of Brn2 is  
551 intermediate after inducing Axl and modulating the immune system. In the future, we  
552 will have to evaluate the kinase activity of Axl in this context, and the consequences  
553 of its inhibition *in cellulo* and *in vivo* to understand the Mitf/Brn2/Axl *ménage à trois*.  
554 Altogether, we establish Brn2 as a central tumor suppressor, acting at different steps  
555 of melanomagenesis, and complement numerous other studies showing the effect of  
556 Brn2 on invasion <sup>13-15,20,29,51</sup>.

557 *Brn2* heterozygous mice were more prone to form LN metastases efficiently  
558 than mice that were *Brn2* WT when Pten was already heterozygous. The efficiency of  
559 the metastasis process depends on the status of *Brn2* as the number and size of  
560 each micro-metastasis was greater in Brn2 heterozygous than Brn2 wild-type  
561 melanoma. This is important as mono-allelic loss of *BRN2* in human, corresponding  
562 to *BRN2* heterozygous melanoma, occurs in 53% of human melanoma. In *Brn2* wild-  
563 type melanoma, the change of the level/activity of Brn2 is possible but the amount of  
564 protein found in Brn2 wild-type melanoma absorbs better transient Brn2 depletion  
565 than in *Brn2* heterozygous melanoma.

566 Some residual Brn2 activity might be required for efficient melanoma  
567 progression. On one hand, Braf-Pten-Brn2-het and Braf-Pten-Brn2-hom melanomas  
568 proliferate faster, and on the other hand, according to our results (Figure 4F,G) Braf-  
569 Pten-Brn2-hom melanomas have a reduced ability to invade compared to Braf-Pten-

570 Brn2-het melanomas. Moreover, the lack of BRN2 reduces migration and increases  
571 the rate of apoptosis and/or anoikis <sup>20,28,43</sup>. In a more speculative way, one may think  
572 that optimal melanoma progression may be associated with a series of proliferative  
573 and invasive phases. In the absence of BRN2, cells are “fixed” in one stage and  
574 cannot switch from “proliferative” to “invasive” states. These cells are mainly  
575 proliferative and poorly invasive as we observed in Braf-Pten-Brn2-hom situation. In  
576 the presence of Brn2 (as WT [two alleles] or heterozygous [one allele], the  
577 corresponding mRNA and protein concentrations can be positively and negatively  
578 modulated by external/internal factors. The modulation of the level of Brn2 is more  
579 sensitive on a heterozygous background than on a WT background.

580         Altogether, one may understand that melanoma grows faster and forms  
581 melanoma when Brn2 expression is not too high (proliferation handicap) but at the  
582 same time not too low (migration/invasion/survival handicap). Indeed, on the one  
583 hand, Brn2-het and Brn2-hom melanomas proliferate faster, and on the other hand,  
584 Brn2-hom melanomas are handicapped to invade (Figure 4F,G), to migrate <sup>20</sup> and to  
585 die by anoikis <sup>28</sup>.

586         The formation of metastases is a multistep process in which cells proliferating  
587 in the primary tumor, and surviving the metastatic process, must undergo a switch to  
588 an invasive phenotype prior to a switch to a proliferative phenotype on site. Since the  
589 switch from proliferation to invasion, and back, has been associated with the activity  
590 of MITF, it is possible that for efficient metastatic colonization cells must be able to  
591 modulate MITF expression via BRN2. In this respect, it is especially important to note  
592 that BRN2 has been identified as a key regulator of MITF <sup>13,49</sup>. Consistent with the  
593 observation that MITF and BRN2 are frequently observed in mutually exclusive

594 populations in melanoma, and that BRN2 may act *in vivo* as an MITF repressor <sup>13</sup>,  
595 we have observed that in a non-tumoral context, the specific knock-out of Brn2 *in*  
596 *vivo* in melanocytes increases the level of Mitf (publication in preparation).  
597 Importantly, during progression of mouse Braf-Pten melanoma Mitf levels are  
598 modulated. During the initial phase of growth, melanoma cells are pigmented,  
599 indicative of Mitf activity, but later *in situ* they lose pigmentation and ability to produce  
600 Mitf (<sup>62</sup> and not shown). Although the reduction of Brn2 in Braf-Pten-Brn2 primary  
601 melanoma is not sufficient to re-induce Mitf mRNA and pigmentation in all cells of  
602 these primary melanomas, the Braf-Pten melanoma cells that formed LN metastases  
603 were pigmented and re-expressed Sox10, a key transcription activator of Mitf. Thus,  
604 during progression of Braf-Pten melanomas Mitf is produced during initial growth and  
605 subsequently repressed during the second phase, before being re-expressed in LN  
606 metastases. It seems therefore likely that one role of the residual BRN2 in the  
607 heterozygotes may be to facilitate the modulation of MITF expression during  
608 metastatic spread.

609         It has been shown that BRAF and PI3K induce BRN2 <sup>15,16</sup>. In consequence, it  
610 was expected that the level of BRN2 would decrease in the presence of such  
611 inhibitors. In addition, in the presence or absence of BRN2, melanoma cells are  
612 either more resistant or more sensitive to BRAF inhibitors, respectively <sup>28,43</sup>. This  
613 sensitivity would be associated with the function of BRN2 in DNA repair <sup>43</sup>.

614         Although here we have focused on the role of BRN2 in melanoma, BRN2 is  
615 also expressed in a number of other cancer types including small cell lung cancer,  
616 neuroblastoma, glioblastoma and neuroendocrine prostate cancer <sup>8-10</sup>. While BRN2-  
617 mediated regulation of MITF is not likely to be important for non-melanoma cancers

618 that do not express MITF, the ability of BRN2 to modulate PTEN expression  
619 uncovered here may play an equally important role in promoting the initiation and  
620 progression of these cancer types. In this respect the inducible knockout mice  
621 described here may represent an important tool to examine the role of BRN2 in non-  
622 melanoma cancers.

623 In conclusion, our results identify Brn2 as a key tumor suppressor through its  
624 ability to modulate Pten expression that, given the high prevalence of monoallelic  
625 mutations, is likely to play a key role in initiation of human melanoma and likely other  
626 BRN2-expressing cancer types. Since BRN2 expression is activated by PI3K  
627 signaling via PAX3<sup>16</sup>, its ability to suppress PI3K signaling by increasing PTEN  
628 expression may also provide cells with a negative feedback loop to control the PI3K  
629 pathway. Moreover activation of BRN2 by MAPK signaling downstream BRAF<sup>15</sup> as  
630 well as WNT/ $\beta$ -catenin signaling<sup>14</sup>, may also permit coordination between these  
631 pathways and the PTEN/PI3K axis. Finally, given the importance of BRN2 in  
632 melanomagenesis identified here as well as its frequent heterozygosity, it may be  
633 important to further explore whether tumors with low BRN2 expression may be more  
634 susceptible to PI3K pathway inhibition, as it was shown for MAPK inhibitors. In this  
635 respect, this mouse model of BRN2-deficient melanoma could be useful for the pre-  
636 clinical testing of inhibitors for clinical development especially since it has been  
637 shown that BRN2 is involved in DNA repair<sup>43</sup>.

638

639 Figure legends

640

641 Figure 1. One *BRN2* allele is frequently lost in human melanoma and reduced *BRN2*  
642 mRNA level correlates with reduced overall survival.

643 (A) Bar graph showing the status of the *BRN2* locus in human skin cutaneous  
644 melanoma (SKCM) metastases (stage IV). Copy-number alterations (CNAs) were  
645 estimated using the GISTIC algorithm. Two alleles (2a in black), one allele (1a in  
646 red), no allele (0a in orange), and gain and/or amplification (G/Aa in blue) of the  
647 *BRN2* locus are given.

648 (B) Pictogram showing the extent of segmental deletions (red or orange vertical lines)  
649 that affect the *BRN2* locus on Chr.6q16 (dashed blue horizontal line) in SKCM  
650 metastases.

651 (C) Kaplan-Meier curves comparing 10-year overall survival of SKCM patients diploid  
652 for *BRN2* (black line, n = 106) or those with mono-allelic (red n = 156). The TCGA  
653 CNA-data set was analyzed (n = 309). Diploid vs. Mono-allelic loss: log-rank (Mantel-  
654 cox) test (p = 0.067). Data were retrieved from TCGA on August 8, 2019.

655 (D) Kaplan Meier curves comparing melanoma patients with diploid status or mono-  
656 allelic loss of *BRN2* in 118 regional metastatic melanoma patients (p = 0.003, log-  
657 rank test)<sup>31</sup> and unpublished data.

658 (E) Kaplan-Meier curves comparing 30-year overall survival of SKCM patients to  
659 *BRN2* mRNA levels. Log-rank (Mantel-Cox) test (p = 0.03). Data were retrieved from  
660 TCGA on August 8, 2019. Significance was defined as \* (p < 0.05) and \*\*\* (p ≤ 0.001).

661

662 Figure 2. *Brn2* loss potentiates melanomagenesis in *Braf*-*Pten* mice.

663 (A) Macroscopic pictures of the dorsal view of mice with cutaneous melanomas  
664 carrying mutations in the melanocyte lineage for Braf, Pten, and Brn2 after tamoxifen  
665 induction at birth (p1, p2, and p3 – see Supplementary Fig. 3). *Tyr::CreER<sup>T2</sup>*;  
666 *Braf<sup>V600E/+</sup>*; *Pten<sup>+/+</sup>* (= Braf), *Pten<sup>F/+</sup>* (= Pten), *Brn2<sup>+/+</sup>* (=Brn2-WT), *Brn2<sup>F/+</sup>* (= Brn2-het),  
667 and *Brn2<sup>F/F</sup>* (= Brn2-hom). Tumors are highlighted with arrows and the sizes of the  
668 first growing tumors to appear are proportional to the diameters of the circles. F  
669 means floxed allele.

670 (B) All Braf (n = 9), Braf-Brn2-het (n = 8), and Braf-Brn2-hom (n = 4) mice produced  
671 cutaneous melanomas and their number was similar (1 to 2 tumors/mouse). All Braf-  
672 Pten-Brn2-WT (n = 7), Braf-Pten-Brn2-het (n = 21), and Braf-Pten-Brn2-hom (n = 11)  
673 mice produced cutaneous melanomas. Note that in the absence of Pten (*Pten<sup>F/F</sup>*), the  
674 appearance of the melanoma was too rapid to observe any difference between Brn2-  
675 WT, Brn2-het, and Brn2-hom mice. Each dot corresponds to an individual mouse. As  
676 control, mice of different genetic backgrounds were produced and not induced with  
677 tamoxifen (Braf [n = 12], Braf-Brn2-het [n = 25], Braf-Brn2-hom [n = 11], Braf-Pten [n  
678 = 7], Braf-Pten-Brn2-het [n = 13], and Braf-Pten-Brn2-hom [n = 6]; none of them  
679 developed melanoma after 18 months, except one Braf-Pten-Brn2-het mouse that  
680 developed one melanoma after 12 months. None of the mice that were wild-type for  
681 *Braf* displayed any obvious phenotype, irrespective of the status of *Pten* or *Brn2*,  
682 including melanomagenesis and hyperpigmentation.

683 (C) Growth rates of the first tumor appearing in each mouse for Braf-Brn2-WT, Braf-  
684 Brn2-het, Braf-Brn2-hom, Braf-Pten-Brn2-WT, Braf-Pten-Brn2-het, and Braf-Pten-  
685 het-Brn2-hom mice. The number of tumors is determined all along the life of the  
686 mouse by checking the mice a minimum of twice a week. Statistical analysis was

687 performed using the two-tailed unpaired t-test. ns = non-significant, \*p < 0.05, \*\*p <  
688 0.01, and \*\*\* p<0.001. Data are presented as mean values +/- SEM. Braf-Pten-Brn2-  
689 het mice were euthanized in average 1.3 weeks after appearance of the first tumors  
690 with an average of 16 tumors/mouse. Similar results were obtained with Braf-Pten-  
691 Brn2-hom mice. Braf-Pten-Brn2-WT mice were euthanized at 4 weeks with an  
692 average of 8 tumors even though they did not reach a total volume of 2cm<sup>3</sup> except for  
693 one mouse that was euthanized earlier (three weeks).

694

695 Figure 3. BRN2-het/hom induces proliferation *in vitro* and *in vivo*.

696 (A-D) Representative photomicrographs of Ki-67 (A) and BrdU (C) stainings of Braf-  
697 Pten-Brn2-WT/het/hom tumors. Ki-67<sup>+</sup> cells are stained in red. Nuclei are stained in  
698 blue. Scale bar = 40 μm. Three independent tumors for each genotype were used for  
699 these experiments and three independent sections were used for each tumor. A 2-  
700 way ANOVA with Dunnett's multiple comparisons tests were performed. Ki-67<sup>+</sup> (B)  
701 and BrdU (D) stainings of (A) and (C), respectively. Scale bar = 40 μm. Each dot  
702 represents the result for one tumor.

703 (E) Growth rate is induced in Dauv-1 and Melan-a cell lines after reduction of Brn2  
704 using siBRN2 and siScr as control (Scr = scramble). Three independent biological  
705 and technical experiments were performed for each cell line and for each condition.

706 (F-H) Brn2 knock down induces Cyclin D1 protein but not its mRNA in melanocytes.

707 (F) Western blot analysis for Brn2, Cyclin D1, and actin after reduction of Brn2 in  
708 Dauv-1 and Melan-a cells. Experiments were performed independently three times.

709 One representative western blot is shown (raw data are presented in Supplementary

710 Fig. 8). (G,H) Quantification of protein (G) and mRNA (H) levels for Dauv-1 cells after

711 siRNA-mediated knockdown (n = 3, independent experiments). For the proteins, all  
712 values were normalized against the background and corresponding actin loading  
713 control for each sample. Quantification was performed using *Image-J* software. For  
714 mRNA, all values were normalized against those of TBP. au = arbitrary units.  
715 Statistical analysis was performed using the two-tailed unpaired (B,D,E,H) and paired  
716 (G) t-tests. ns = non-significant, \*p < 0.05, \*\*p < 0.01, and \*\*\*p < 0.001. Data are  
717 presented as mean values +/- SEM.

718

719 Figure 4. Mono-allelic loss of *Brn2* induces melanoma metastasis.

720 (A) Upper panel: Representative photomicrographs of *in situ* inguinal lymph nodes  
721 (LN) of Braf-Pten-Brn2-WT/het/hom mice. Scale bar = 1 mm. The pigmented volume  
722 (mm<sup>3</sup>) was estimated for each LN. Lower panel: Representative photomicrographs of  
723 haematoxylin & eosin (H&E) staining of LNs containing pigmented cells. Scale bar =  
724 20 μm.

725 (B) Quantification of the pigmented volume of inguinal LNs in the upper panel of  
726 Figure (A). n = 3, 5, and 5 for WT, het, and hom.

727 (C) Quantification of the pigmented areas per mm<sup>2</sup> of inguinal LNs in the lower panel  
728 of Figure (A). Pigmented areas > 50 μm<sup>2</sup> were considered. n = 3, 5, and 3 for WT,  
729 het, and hom.

730 (D) Scheme showing the defloxing strategy of Brn2 in melanocytes of the primary  
731 tumor that releases eGFP expression upon the defloxing of *Brn2*.

732 (E) Representative photomicrographs, from four independent experiments, of serial  
733 LN sections of Braf-Pten-Brn2-WT and Braf-Pten-Brn2-het mice stained with H&E  
734 and the melanocyte marker Sox10. H&E staining was evaluated for one section and

735 GFP (green channel) and Sox10 staining (red channel) evaluated for an adjacent  
736 section. Scale bar = 20  $\mu$ m.

737 (F) A melanoma invasive signature was significantly enriched in the Braf-Pten-Brn2-  
738 het tumors (left) and in the Braf-Pten-Brn2-het melanoma cell lines (right) compared  
739 to their Braf-Pten-Brn2-hom counterparts.

740 (G) Left: photomicrographs of m82 and m82-BRN2 mouse melanoma cells  
741 embedded as spheroids in 600  $\mu$ g/mL matrigel at t0 (H0) and 18 hrs after (H18).  
742 Right: Boxes and plots represent the area of invasion (red lines on  
743 photomicrographs) quantified with *ImageJ* (n=54 for m82 cells and n=56 for m82-  
744 BRN2 cells). P-value<0.0001. au = arbitrary unit.

745 (H) Axl mRNA is significantly overexpressed in Braf-Pten-Brn2-het melanoma and  
746 melanoma cell lines (n = 10 and 2, respectively) compared to the Braf-Pten-Brn2-WT  
747 (n = 5 and 4, respectively) and Braf-Pten-Brn2-hom (n = 10 and 3, respectively)  
748 tumors.

749 Statistical analysis was performed using the two-tailed unpaired t-test for B, C, G and  
750 H (tumors) and an Anova test for H (cell lines). Data are presented as mean values  
751 +/- SEM for B and C, sd for H, and Box and whiskers (median, min to max) for G. ns  
752 = non-significant, \*p < 0.05, \*\*\*p < 0.001, \*\*\*\* p < 0.0001.

753

754 Figure 5. Brn2 binds to the *Pten* promoter and Brn2 loss leads to Pten transcription  
755 reduction.

756 (A) Representative photomicrographs of immunohistochemistry staining of Pten (red)  
757 in Braf-Pten-Brn2-WT and Braf-Pten-Brn2 mouse melanomas are shown. Scale bar =  
758 40  $\mu$ m. Three independent tumors for each genotype were used for these

759 experiments and three independent sections were used for each tumor. A 2-way  
760 ANOVA with Dunnett's multiple comparisons tests were performed. The percentage  
761 of Pten<sup>+</sup> cells in WT and mutant tumors is shown.

762 (B) Western blot analysis of Brn2, Pten and actin for Braf-Pten-WT and Braf-Pten-  
763 Brn2 from at least three tumors of each genotype. One representative example is  
764 presented, raw data are presented in Supplementary Fig. 8. The relative intensities of  
765 the band were estimated with *ImageJ*.

766 (C) RT-qPCR of Brn2 and Pten from Braf-Pten-WT and Braf-Pten-Brn2 melanomas.  
767 Three independent mouse melanomas per genotype were analyzed. Data were  
768 normalized against the values of Gapdh. au = arbitrary unit.

769 (D) Western blot analysis of BRN2, PTEN and ACTIN from Dauv-1 human melanoma  
770 cells and Melan-a mouse melanocytes after siRNA mediated knockdown. A  
771 representative western blot is shown, raw data are presented in Supplementary Fig.  
772 8. Scr = Scramble.

773 (E) RT-qPCR of BRN2 and PTEN from human melanoma cells (Dauv-1) and mouse  
774 melanocytes (Melan-a) after siRNA-mediated knockdown. Specific primers were  
775 used for human and mouse samples. Dauv-1 (n = 6), Melan-a (n = 4), independent  
776 experiments. Data were normalized against the values for TBP (Dauv-1) or Gapdh  
777 (Melan-a).

778 (F) ChIP assays of BRN2 binding to the *PTEN* promoter in Dauv-1 melanoma cells.  
779 All data shown are representative of at least three independent assays.

780 (G) Quantification of the ChIP-qPCR, plotted and normalized against IgG as the  
781 reference. au = arbitrary unit. n=6, 3, 4 and 3 for BRN2 CDS, PAX3 prom, BS1 and  
782 BS2, respectively.

783 (H) Scheme of the human *PTEN* promoter containing two BRN2 binding sites (BS)  
784 represented as colored circles. Note that BS are conserved between humans and  
785 mice. TSS = transcription start site. Exons (X) 1 and 2 are shown as horizontal  
786 rectangles. The translation start site (ATG) and the end of exon 1 are indicated. All  
787 numbering is relative to the TSS (+1). Representation of the reporter luciferase (luc)  
788 construct with or without *PTEN* promoter.

789 (I-N) Human and mouse *PTEN* promoter activities were evaluated in human Dauv-1  
790 (I,K), SK28 (J,L), and in mouse m82 [Brn2-hom], m59 [Brn2-het], and m50 [Brn2-WT]  
791 (M,N) melanoma cell lines either in the presence of siScr (scramble) or siBrn2  
792 (smart-pool) (I,J,M) or in the presence of expression vector of BRN2 (CMV::BRN2)  
793 (L,N). The experiments were independently performed four (I,J,K) and three (L)  
794 times. They were performed three independent times for m82 and m50, seven for  
795 m59 (M), and seven times for m82, six for m59 and four for m50 (N).

796 Statistical analysis was performed using the two-tailed unpaired t-test for C, E, G and  
797 paired t-test for I-N. Data are presented as mean values +/- SEM for C, E, G, I-M.  
798 Box and whiskers (median, min to max) for N. ns = non-significant, \*p < 0.05, \*\*\*p <  
799 0.001, and \*\*\*\*p < 0.0001.

800

801 Figure 6. MITF binds downstream of *PTEN* gene, MITF loss induces its transcription,  
802 and enhancers flanking *PTEN* are activated in MITF-depleted cells.

803 (A) Western blot analysis of MITF and PTEN from human melanoma cells (501mel,  
804 SK28, and HBL) after siRNA-mediated knockdown. Actin was used as a loading  
805 control. A representative western blot out of three is shown, raw data are presented  
806 in Supplementary Fig. 8. The molecular weight is indicated in kDa. Scr = Scrambled.

807 (B) RT-qPCR of MITF and PTEN from human melanoma cells (501mel and SK28)  
808 after siRNA-MITF and Scr knockdown. All values were normalized against TBP. The  
809 analysis was performed on three independent experiments with technical triplicates,  
810 au = arbitrary unit.

811 (C) Screenshot of IGV genome browser (GRCH37/hg19) visualization of MITF,  
812 H3K27Ac and H3K4me3 binding to the *PTEN* locus in SkMel28 cell lines that are  
813 MITF-WT or mutant (i.e., MITF- $\Delta$ X6 =  $\Delta$ MITF). Blue boxes below MITF and  
814 H3K27Ac tracks: signal above IgG background (i.e., peaks) called by MACS2. *PTEN*  
815 and downstream regions are shown, blue arrows indicate strand orientation and  
816 horizontal rectangles the exons. Y-axes are scaled per antibody sample. Anti-MITF  
817 CUT&RUN peaks present in WT cells that harbor an M-Box binding motif are painted  
818 grey. Six distal enhancers (painted light blue) exhibited a 2-fold greater H3K27ac  
819 signal in MITF mutant cell lines compared to wild-type cell lines. At least two  
820 CUT&RUN biological replicates were performed for MITF, H3K27ac and H3K4me3.

821 (D) ChIP assays of MITF binding downstream of *PTEN* in 501mel human melanoma  
822 cells stably expressing HA-Tagged MITF (location +140kb). ChIP assays are  
823 performed using an antibody against HA and analyzed after a 30-cycle PCR  
824 (exponential phase). The tyrosinase promoter (*TYR*) and *PRM1* were used as  
825 positive and negative controls, respectively. Input represents approximately 3% of  
826 the input used for the ChIP assay. H3 (histone H3) and IgG (Immunoglobulin G) were  
827 used as positive and negative technical controls for each region of interest,  
828 respectively. The oligonucleotides, their positions on the genome, and sizes of the  
829 amplified fragments are shown in Supplementary Tables 3 and 4. All data shown are

830 representative of three independent assays. \* corresponds to the remaining  
831 oligonucleotides.

832 (E) Quantification of the ChIP–qPCR presented in (D) is plotted and normalized  
833 against IgG as a reference. au = arbitrary unit. PRM1 (-): PRM1 (negative control),  
834 TYR (+): tyrosinase promoter (positive control).

835 Statistical analysis was performed using the two-tailed unpaired t-test.

836 Data are presented as mean values +/- SD. ns = non-significant, \*p < 0.05, \*\*p <  
837 0.01, and \*\*\*p < 0.001.

838

839 METHODS

840 Detailed materials and methods are given in the supplemental information.

841

842 *TCGA data*

843 All TCGA data for somatic mutations, copy number alterations (CNAs), RNA-seq  
844 gene expression, and clinical data for skin cutaneous melanoma were retrieved from  
845 the National Cancer Institute (NCI) Genomic Data Commons (GDC) through its  
846 GDC Application Programming Interface (API) using the TCGAbiolinks package or  
847 the CGDS-R package to query the Cancer Genomic Data Server (CGDS) from  
848 cBioPortal.

849

850 *Copy number analysis (CNA)*

851 Preprocessed copy number data was obtained from cBioportal. Copy number data  
852 sets generated by the GISTIC 2.0 algorithms, specifically the  
853 allthresholded.bygenes.txt of the GISTIC output were used. Samples with GISTIC  
854 copy-number values of “-1” were considered as mono-allelic loss (red) and samples  
855 with GISTIC copy-number values of “-2” as bi-allelic loss (orange). TCGA dataset  
856 CNA-data set (n = 367). BRN2 CNA classified as gain/amplification (GISTIC > “+1” or  
857 “+2”) are not shown (n = 29, 7.9%).

858

859 *Level of expression of BRN2 mRNA in melanoma patients*

860 BRN2 mRNA levels were obtained from RNA sequencing data analyzed using the  
861 RNA Seq V2 RSEM pipeline as transcripts per million reads (TPM).

862

863 *Mouse Models*

864 Mice were bred and maintained in the specific pathogen-free mouse colony of the  
865 Institut Curie, in accordance with the institute's regulations and French and European  
866 Union laws. Experimental procedures were specifically approved by the ethics  
867 committee of the Institut Curie CEEA-IC #118 (CEEA-IC 2016-001) in compliance  
868 with the international guidelines. The transgenic *Tyr::Cre<sup>ERT2-Lar</sup>* (also called  
869 *Tyr::Cre<sup>ERT2</sup>*), *Braf<sup>V600E/+</sup>*, *Pten*, and *Brn2* mice have been described, characterized,  
870 and backcrossed onto a C57BL/6 background for more than ten generations <sup>33-</sup>  
871 <sup>35,38,63</sup>. Genotyping were performed accordingly (Supplementary Tables 3 and 4).

872

873 *In vivo gene activation/deletion and melanoma monitoring*

874 Newborn mice were treated dorsally with 0.4 µg/day/ouse tamoxifen from P1 to P3.  
875 Non-tamoxifen-induced mice of the same genotype were used as controls.  
876 Developing skin excrescences > 3 mm diameter were considered to be melanomas,  
877 and validated after growth. Mice were checked two-three times a week to estimate  
878 the volume of the tumors. They were euthanized and autopsied four weeks after  
879 tumor appearance or once the tumors reached 2 cm<sup>3</sup>. Mouse melanomas were  
880 excised, rinsed in cold PBS snap-frozen in liquid nitrogen for subsequent  
881 transcriptomic and western blot analysis and fixed in 4% PFA and embedded in  
882 paraffin or OCT for histological analysis and immunostaining.

883

884 *Immunohistochemistry of mouse melanoma and inguinal lymph nodes*

885 Paraffin-embedded mouse melanomas were sectioned into 7-µm-thick transverse  
886 sections and stained with hematoxylin/eosin (H&E), as previously described <sup>64</sup>.

887 Antibodies are from Nova-Costra for Ki-67, BD Biosciences for BrdU, from Abcam for  
888 SOX10 and Cell signaling for PTEN. Images were captured using a ZEISS Axio  
889 Imager 2 with Axiocam 506 color cameras. Image analysis was performed using  
890 ZEISS ZEN, Adobe Photoshop, and *ImageJ* software. Quantifications of Ki-67 and  
891 BrdU stainings were determined as a percentage. The percentage of Ki-67<sup>+</sup> and  
892 BrdU<sup>+</sup> cells from three fields (1,000-2,000 cells/field) from three independent tumors  
893 per genotype was determined and normalized.

894

#### 895 *Protein extraction from tumors*

896 All steps were performed at 4°C. Tissues were transferred to a tube containing 2.8-  
897 mm stainless steel beads and 1mL RIPA buffer supplemented with sodium  
898 orthovanadate prior adding complete protease inhibitor and PhosSTOP (Roche).  
899 Tissues were homogenized followed by centrifugation at 17,949 g for 1 min.  
900 Supernatants were transferred and centrifuged for 20 min at 15,294 g. Supernatants  
901 were collected and incubated with 200 $\mu$ L previously PBS-washed G-Sepharose  
902 beads for 2h. Samples were centrifuged at 15,294 g for 5 min and quantified using  
903 the Bradford assay.

904

#### 905 *Microarray analysis*

906 Only one tumor per mouse was considered and corresponding to the biggest one.  
907 Tumors had the same size since we harvested tumors for transcriptomic analyses  
908 when they reached a size of 1cm<sup>3</sup>. RNA from mouse melanomas (5 Braf-Pten-Brn2-  
909 WT, 10 Braf-Pten-Brn2-het, and 10 Braf-Pten-Brn2-hom) and mouse melanoma cell  
910 lines (4 Braf-Pten-Brn2-WT, 2 Braf-Pten-Brn2-het, and 3 Braf-Pten-Brn2-hom)

911 established from the mouse melanoma tumors was extracted using the miRNeasy Kit  
912 (Qiagen, #217004). Complete protocol can be found in the supplementary  
913 information.

914 In brief, 11 µg cRNA hybridized to mouse MOE430 gene expression Affymetrix  
915 microarrays (Affymetrix, #900443). The microarray data were normalized using the  
916 RMA (Robust Multichip Average) function of the edgeR package <sup>65</sup>. Differentially  
917 expressed gene analysis was performed with R, for the cell lines and the tumors  
918 using the limma package <sup>66</sup> available from Bioconductor  
919 (<http://www.bioconductor.org>). An enriched gene-ontology (Gene-Ontology  
920 Biological-Process, 2018) and pathway (WikiPathways human, 2019 & KEGG  
921 human, 2019) analysis was performed on the 296 genes found overexpressed in the  
922 Braf-Pten-Brn2-het compared to the Braf-Pten-Brn2-WT using Enrichr <sup>67</sup>. Gene-set  
923 enrichment analysis (GSEA) was performed using the “Verfaillie” signature <sup>44</sup>.

924

#### 925 *Cell lines*

926 Melan-a and C57BL/6 9v cells were grown as previously described <sup>4,68</sup>. 501mel,  
927 501mel-MITF-HA, HBL, SK-Mel-28 (SK28), Gerlach and Dauv-1 cells were grown in  
928 RPMI 1640 media supplemented with 10% FCS and 1% Penicillin-Streptomycin <sup>69-71</sup>.  
929 SK28Δex6 melanoma cells lacking Mitf was previously produced <sup>50</sup>. Cells are  
930 routinely tested for the absence of mycoplasmas using MycoAlert (Lonza). The origin  
931 and the main genetic characteristics of the cell lines are given in the supplemental  
932 information. Mouse melanoma cell lines were established as previously described <sup>72</sup>.

933

#### 934 *Genomic DNA extraction and genotyping from cell culture*

935 Genomic DNA was extracted from melanoma cell lines and column-purified with the  
936 QIAamp Kit (QIAGEN). See Supplementary Tables 3 and 4.

937

#### 938 *siRNA-mediated knock-down*

939 siRNA targeting human BRN2 and MITF was purchased from Dharmacon as a  
940 SMART-pool mix of four sequences. siRNA targeting PTEN from Santa Cruz Biotech.  
941 Si Scramble (siSCR), with no known human or mouse targets, was purchased from  
942 Eurofins Genomics (Supplementary Table 5). Briefly, cells were transfected with  
943 Lipofectamine 2000 with 25-200 pmol siRNA or siSCR (according to the types of  
944 experiments) and assayed for mRNA expression, protein content or luciferase activity  
945 48 or 72 h post-transfection.

946

#### 947 *Clonogenic assays*

948 For clonogenic assays, six-well tissue culture plates were seeded with 500 cells in  
949 complete medium. The medium was changed 24 h after cell seeding and replaced  
950 with complete medium containing the indicated concentrations of Binimetinib  
951 (Selleck), MK-2206 2HCl (Selleck), LY294002 (Calbiochem) or PLX4720 (Axon  
952 Medchem). After 9 days of incubation, colonies were fixed with 4% PFA  
953 (paraformaldehyde), stained with Crystal violet in 10% ethanol, and counted on  
954 images. IC50 were determined for each pharmacological agent and for each cell line  
955 using the number of colonies in mock treated condition as the top response. Cell  
956 lines have been treated with Binimetinib from  $10^{-3}$  to 100  $\mu$ M, with PLX4720 from  $10^{-3}$   
957 to 100  $\mu$ M, with LY294002 from  $5 \cdot 10^{-3}$  to 50  $\mu$ M and with MK-2206 from  $10^{-3}$  to 10  
958  $\mu$ M. We used the resulted sigmoidal curves to calculate the IC50 with Graphpad  
959 Prism. Experiments were performed at least in triplicate.

960

961 *Western blotting and detection*

962 Whole-cell lysate was prepared from cell lines using RIPA buffer supplemented with  
963 sodium orthovanadate, complete inhibitor, and PhosSTOP. SDS-PAGE was carried  
964 out on 10% polyacrylamide protein gels. Following the transfer of the proteins, the  
965 nitrocellulose membranes were blocked in TBST with 5% non-fat dry milk for 1.5h at  
966 RT and then probed with various antibodies. BRN2, Cyclin D1, PTEN, phospho-S6,  
967 S6, phospho-AKT, and AKT antibodies were from Cell signaling, MITF from Abcam,  
968  $\beta$ -actin and vinculin from Sigma. Secondary antibodies were either HRP-conjugated  
969 goat anti-rabbit or anti-mouse IgG. Blots were incubated in ECL (Pierce) and  
970 revealed using ECL hyperfilm (GE Healthcare). All primary antibodies were used at a  
971 dilution of 1/1,000, except  $\beta$ -actin and vinculin (1/5,000). All secondary antibodies  
972 were used at a dilution of 1/20,000. Quantification of the western blots was  
973 performed using *ImageJ* software. See table key resources

974

975 *Chromatin immunoprecipitation*

976 ChIP experiments were performed as previously described <sup>4</sup>, and see Supplementary  
977 Table 6. ChIP assays of BRN2 binding to the *PTEN* promoter. ChIP assays were  
978 performed using an antibody against BRN2 and analyzed after 30-cycle PCR in  
979 exponentially growing phase of Dauv-1 melanoma cells. *PAX3* promoter (prom.) and  
980 Brn2 coding sequences (CDS) were used as positive and negative controls,  
981 respectively. Input represents approximately 0.4% of the input used for the ChIP  
982 assay. H3 (histone H3) and IgG (Immunoglobulin G) were used as positive and  
983 negative controls for each region of interest, respectively. The oligonucleotides, their

984 position on the genome, and the sizes of the amplified fragments are given in  
985 Supplementary Tables 3 and 4.

986

#### 987 *RNA extraction and (ChIP) RT-qPCR*

988 Tissues were crushed with a mortar and pestle, and stainless steel beads. Qiazol  
989 was used to homogenize the samples prior extracting RNA using the miRNeasy Kit.  
990 Purified RNA was reversed transcribed using M-MLV Reverse Transcriptase. Real-  
991 time quantitative PCR (qPCR) was performed using iTaq™ Universal SYBR Green  
992 Supermix. Each sample was run in technical triplicates and the quantified RNA  
993 normalized against TBP (human) or Gapdh (mouse) as housekeeping transcripts  
994 (Supplementary Tables 3 and 4).

995

#### 996 *Software*

997 GraphPad PRISM, R version 3.6.3 (R Foundation for Statistical Computing, Vienna,  
998 Austria), Adobe Illustrator, Adobe Photoshop, and Microsoft Power Point software  
999 were used to analyze data and generate all graphs and figures.

1000

#### 1001 *Quantification and statistical analysis*

1002 Cell culture-based experiments were performed in at least biological triplicate and  
1003 validated three times as technical triplicates. P-values for the comparison of two  
1004 groups were calculated using the unpaired Student t-test or Mann-Whitney test. P-  
1005 values for the comparison of multiple groups were calculated using the analysis of  
1006 variance (ANOVA) and Fisher's least significant difference tests. P-values for  
1007 categorical data were calculated using the Chi-square test. P-values for the

1008 comparison of Kaplan–Meier curves were calculated using the log-rank (Mantel–Cox)  
1009 or Gehan-Breslow-Wilcoxon test giving weight to the early events. P-values were  
1010 reported as computed by Prism 6.

1011

#### 1012 *Data availability*

1013 Microarray gene expression data that support the findings of this study have been  
1014 deposited in Gene Expression Omnibus (GEO) with the accession codes  
1015 GSE126524 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE126524>) and  
1016 GSE163085 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE163085>).

1017 The TCGA Skin Cutaneous Melanoma data referenced during the study are available  
1018 in a public repository from the National Cancer Institute (NCI) Genomic Data  
1019 Commons (GDC) website (<https://portal.gdc.cancer.gov>). Cut&Run assay data that  
1020 support the findings of this study have been deposited in Gene Expression Omnibus  
1021 (GEO) with the accession codes GSE153020  
1022 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE153020>). All the other data  
1023 supporting the findings of this study are available within the article and its  
1024 supplementary information files and from the corresponding author upon reasonable  
1025 request. A reporting summary for this article is available as a Supplementary  
1026 Information file. The data that support the findings of this study are available from the  
1027 corresponding author upon reasonable request.

1028

#### 1029 Acknowledgements

1030 We are grateful to Dorothy C Bennett, Ghanem Ghanem, Florence Faure, and Meenhard  
1031 Herlyn for providing cell lines. Hong Wu for providing Pten flox mice. We thank the Institut  
1032 Curie staff responsible for the animal colony (especially P. Dubreuil), and the histology (S.

1033 Leboucher), FACS (C. Lasgi), and PICT-IBiSA imaging (C. Lovo) facilities. This work was  
1034 supported by the Ligue nationale contre le cancer, INCa, ITMO Cancer, Fondation ARC  
1035 (PGA), and is under the program «Investissements d’Avenir» launched by the French  
1036 Government and implemented by ANR Labex CeITisPhyBio (ANR-11-LBX-0038 and ANR-  
1037 10-IDEX-0001-02 PSL). MH had a fellowship from PSL and FRM, PS had a fellowship from  
1038 INSERM, and MLC had a fellowship from FRM. CRG was supported by the Ludwig Institute  
1039 for Cancer Research. RC was supported in part by a grant from the National Institutes of  
1040 Health (AR062547, RAC) and a postdoctoral fellowship from the American Association for  
1041 Anatomy (CK). ES was supported from the Research Fund of Iceland (184861-053). LL and  
1042 ES are supported by a Jules Verne grant.

1043

1044 Author contributions

1045

1046 M.H., P.S., V.P., J.R., V.D., M.L.C., C.P.K., M.P., F.R., N.C., A.S., L.S.C., L.M., M.L., and  
1047 G.B.J. conducted the experiments

1048 M.H., P.S., R.A.C, C.R.G. and L.L. designed the experiments

1049 M.H., P.S., V.P., F.G., V.D., Z.A., A.S., A.B., I.D., C.R.G., and L.L. wrote and reviewed the  
1050 manuscript

1051 C.R.G., and L.L. secured the funding

1052 D.M. and E.S. provided reagents

1053 I.D., A.S., C.R.G. provided expertise and feedback

1054

1055 Declaration of Interests

1056 The authors declare no competing interests.

1057

1058 Ethical rules

1059 Animal care, use, and experimental procedures were conducted in accordance with

1060 recommendations of the European Community (86/609/EEC) and Union (2010/63/UE) and

1061 the French National Committee (87/848). Animal care and use were approved by the ethics  
1062 committee of the Curie Institute in compliance with the institutional guidelines.

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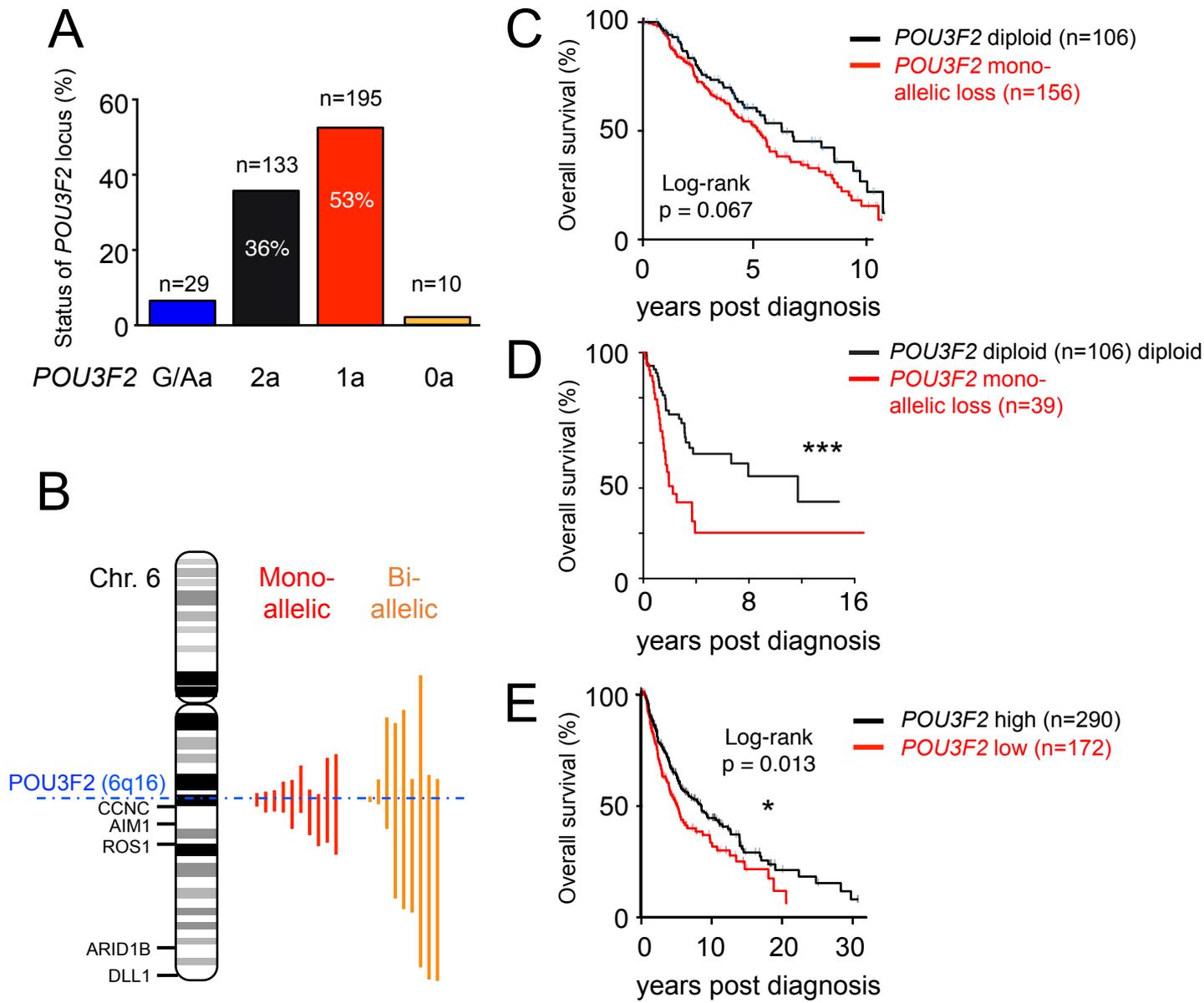


Figure 1

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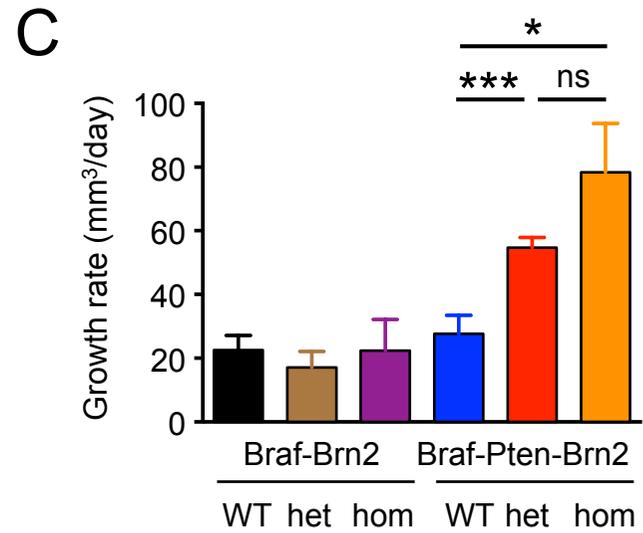
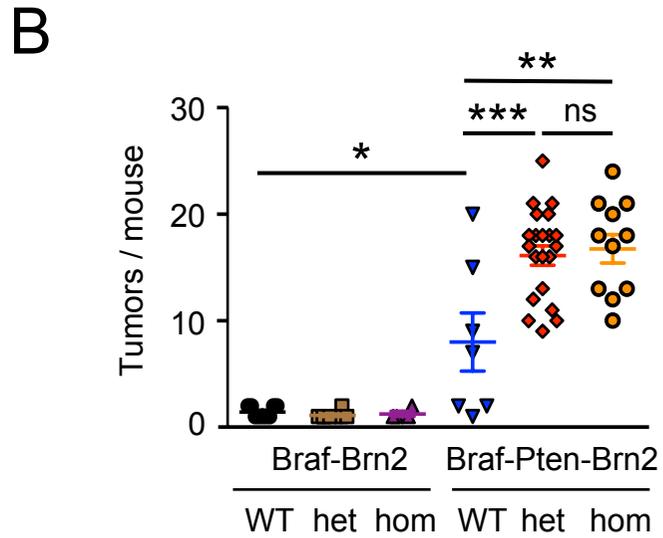
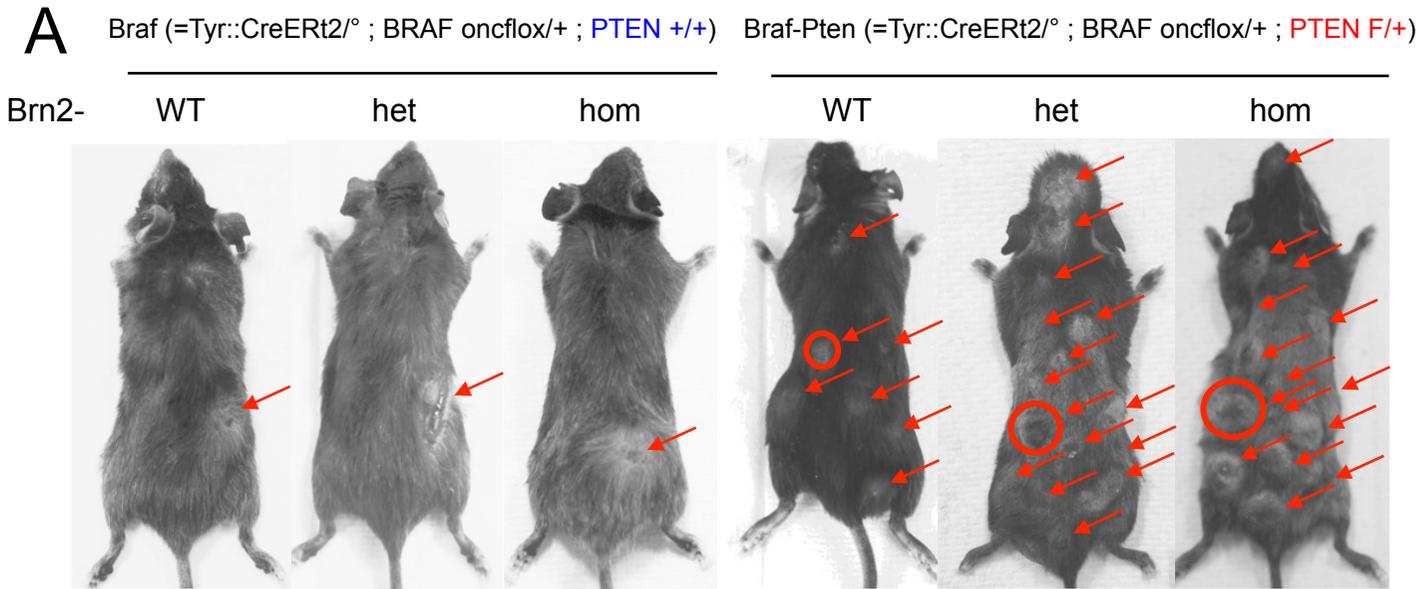


Figure 2

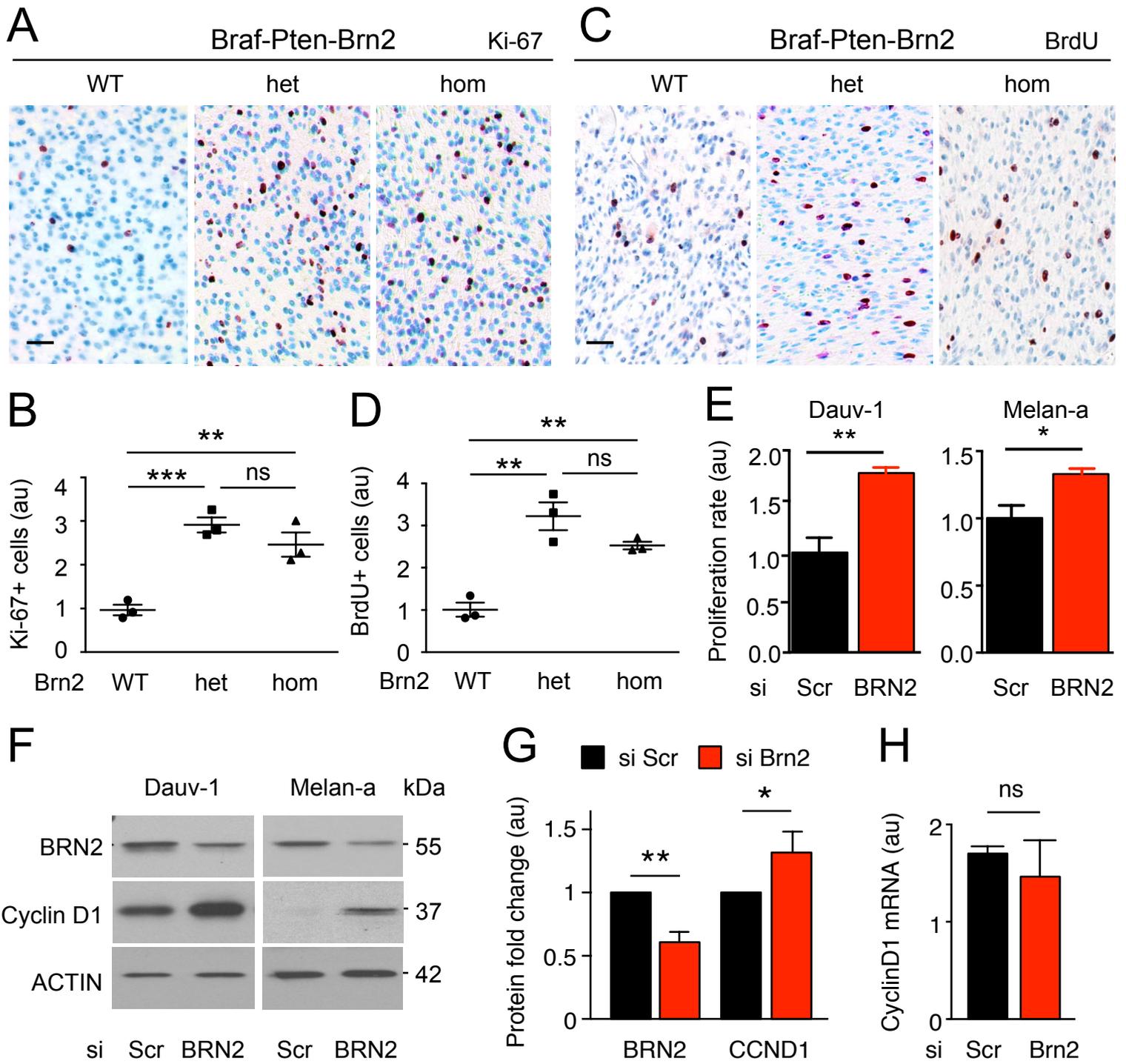


Figure 3

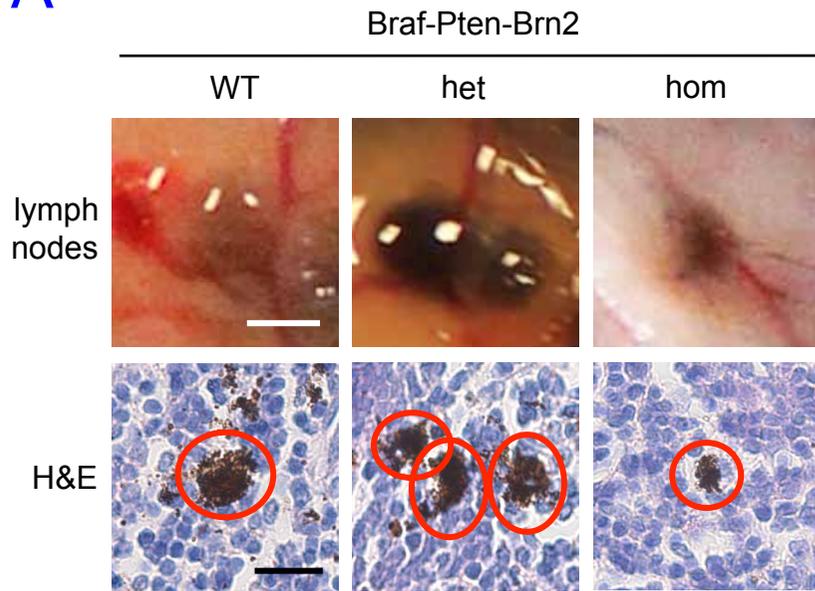
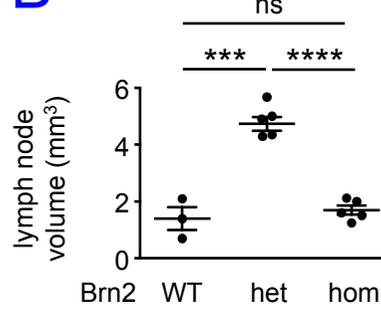
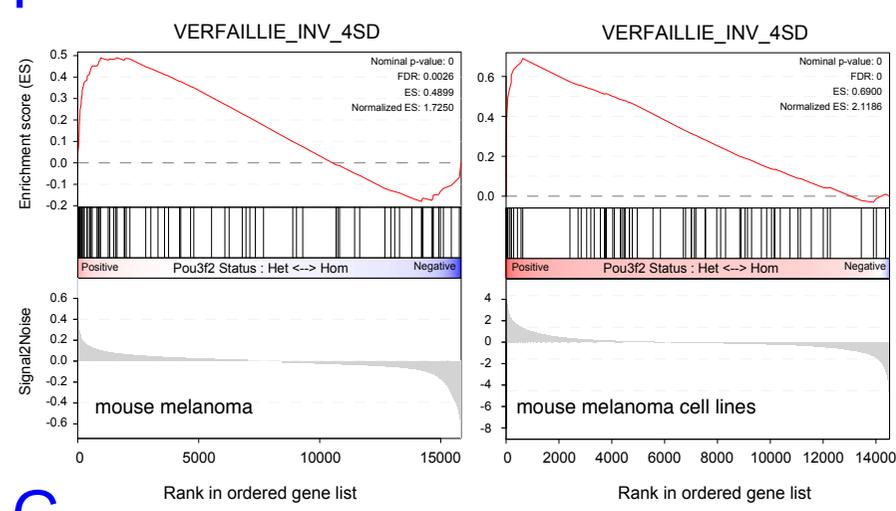
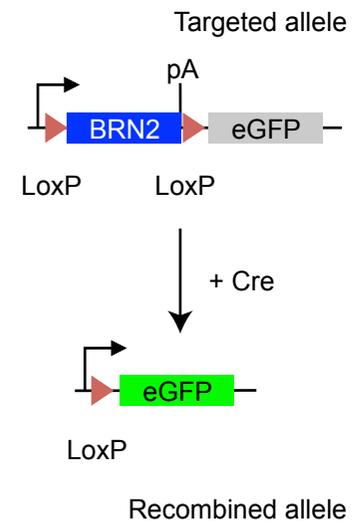
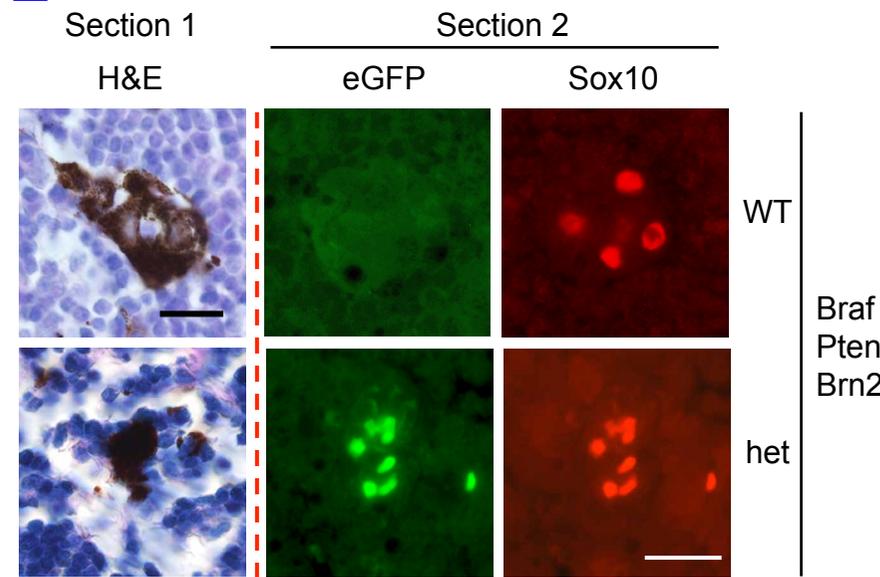
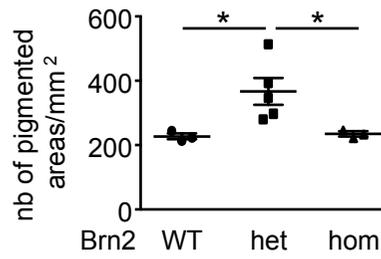
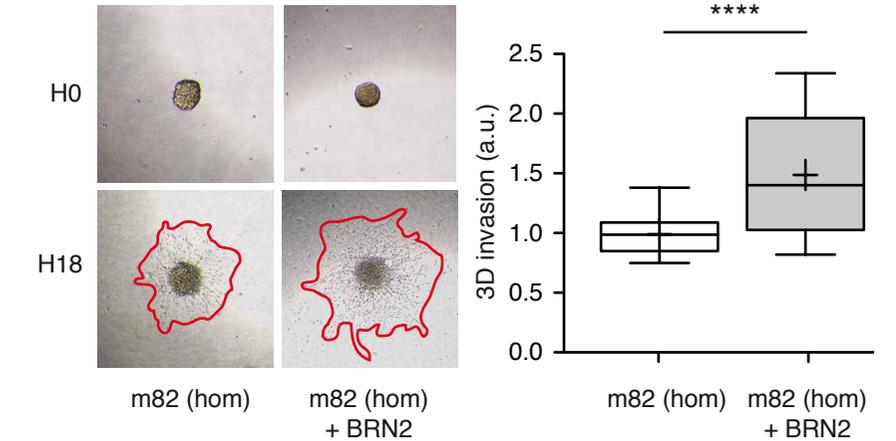
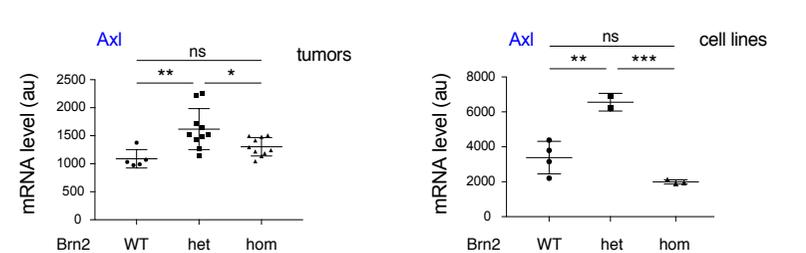
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Figure 4

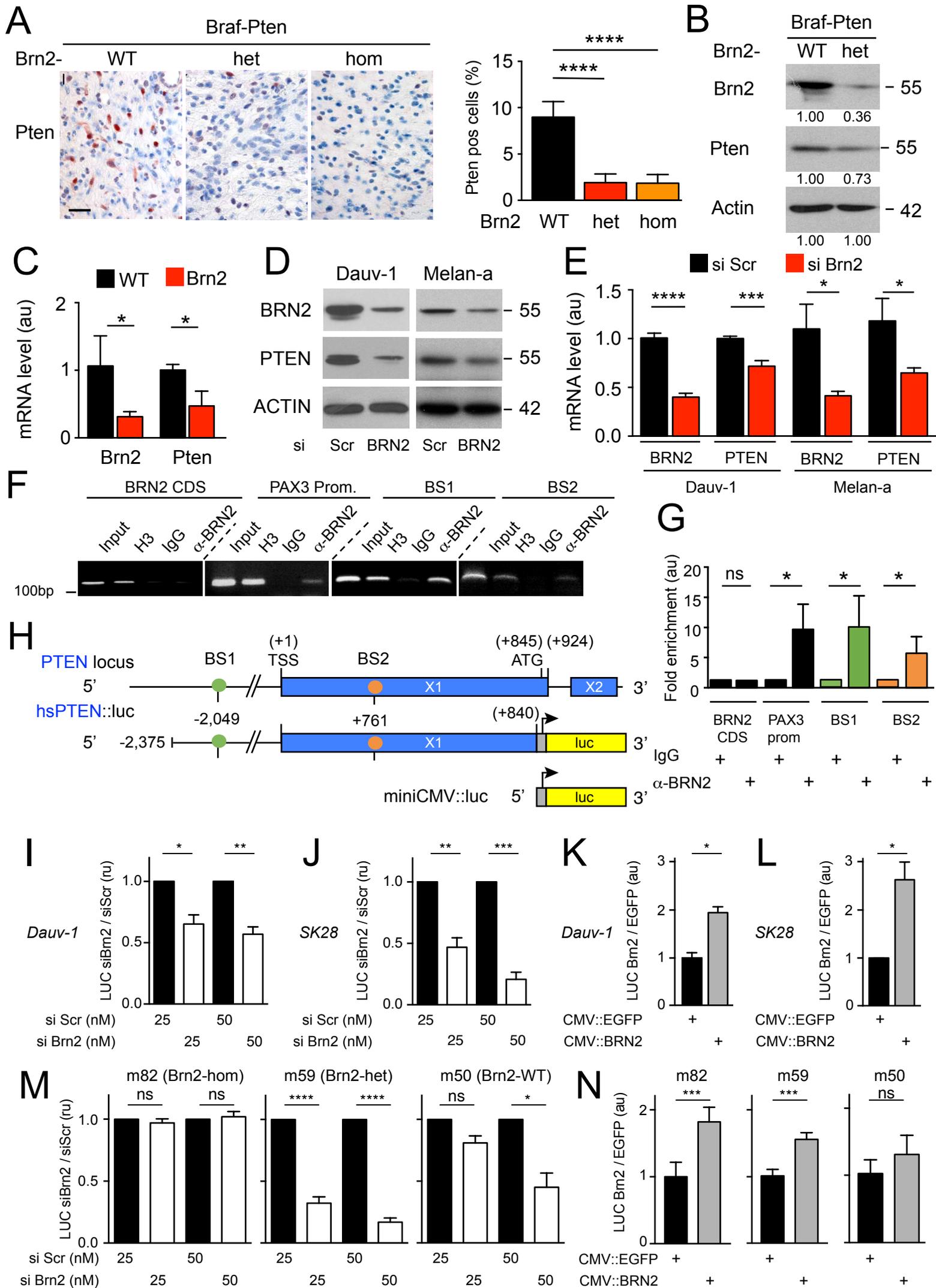


Figure 5

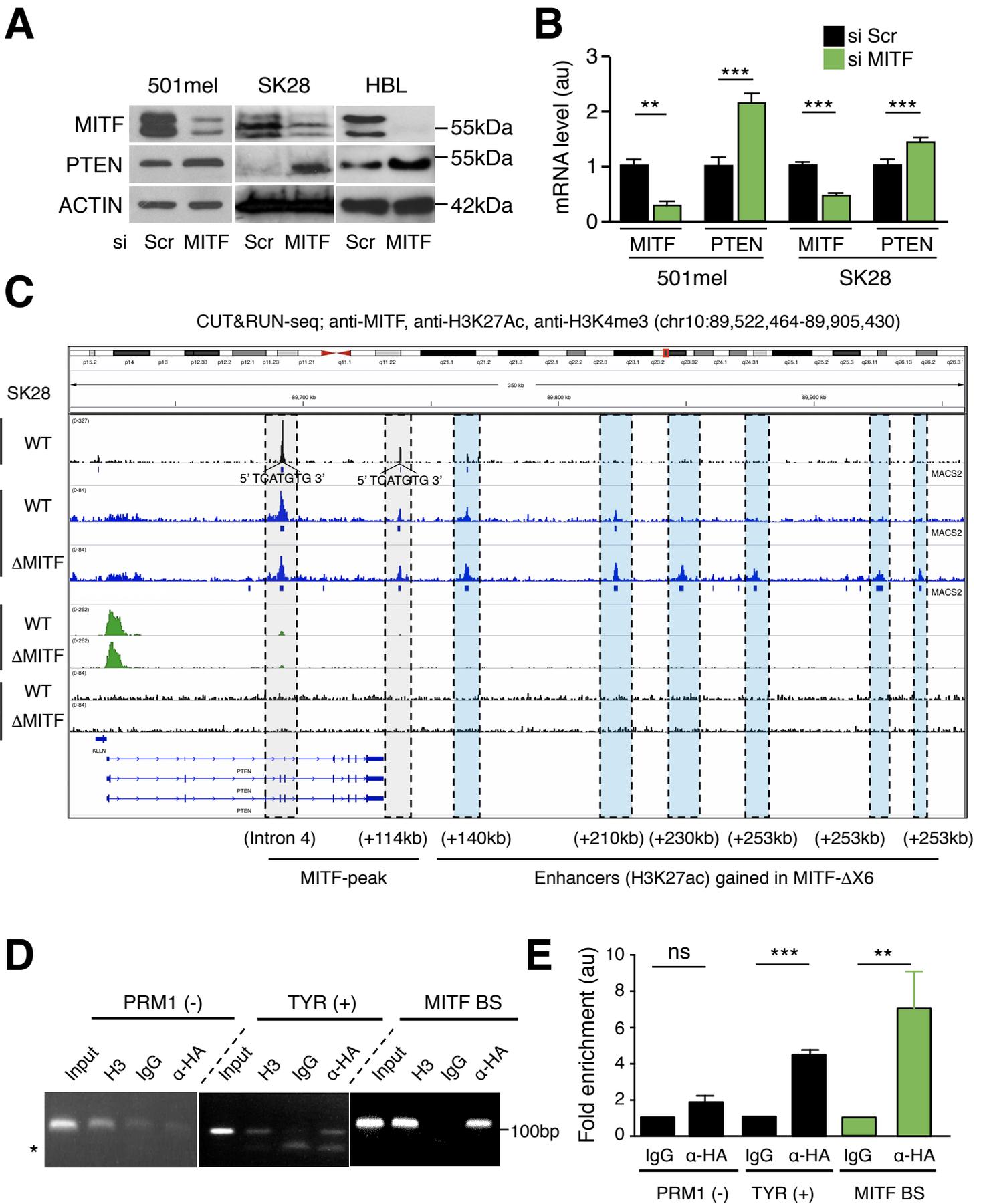


Figure 6