Table SI. Melanoma cell lines used in the present study.

Cell line	Tumor type	Source
Hbl	Malignant melanoma	Dr. G. Ghanem-Free University of Brussels
Malme-3M	Malignant melanoma	American Type Culture Collection
MeWo	Malignant melanoma	American Type Culture Collection
SK-MEL-2	Malignant melanoma	American Type Culture Collection
SK-MEL-3	Malignant melanoma	American Type Culture Collection
SK-MEL-5	Malignant melanoma	American Type Culture Collection
SK-MEL-28	Malignant melanoma	American Type Culture Collection
501mel	Malignant melanoma	Dr. R. Halaban-Yale University

Table SII. Mutational status of cell lines.

Cell line	Mutation	Reference
Hbl	wt	Herraiz C et al.: Int. J. Biochem. Cell. Biol.2012, 44:2244-2252.
Malme-3M	V600Eamplified	Wajapeyee N et al.: Cell 2008, 132:363-364.
MeWo	wt	Domenzain-Reyna C et al.: J. Biol. Chem. 2009, 284:12306-12317.
SK-MEL-2	NRASQ61R	Singh S et al.: Mol. Cancer Ther. 2010, 9:3330-3341. Wajapeyee N et al.: Cell 2008, 132:363-364.
SK-MEL-3	BRAFV600E	Mazzio EA and Soliman KFA: Cancer Genomics & Proteomics 2018, 15:349-364.
SK-MEL-5	BRAFV600E heterozyg.	Singh S et al.: Mol. Cancer Ther. 2010, 9:3330-3341.
SK-MEL-28	BRAFV600E homozyg.	Smalley et al.: Mol. Cancer Ther. 2008, 7:2876-2883. Singh S et al.: Mol. Cancer Ther. 2010, 9:3330-3341. Wajapeyee N et al.: Cell 2008, 132:363-364.
501mel	BRAFV600E amplified	Packer LM et al.: Pigment Cell & Melanoma Res. 2009, 22:785-798.

wt, wild type (no BRAF or NRAS mutations).

Table SIII.31 GLI -binding sites in the proximal (-2092+112) SLUG promoter. Mismatched oligonucleotides are shown in bold andtwo mismatches are marked in green. All other sites contain three mismatches.

Positionof GLI binding sites in SLUGpromoter	Sequence	Positionof GLI binding sites in SLUGpromoter	Sequence
+102 to +110	GACCGCCGT	-1091 to -1099	GACCATACA
-15 to -23	ACCCTCCCA	-1119 to -1127	AACCACCTG
-64 to -72	AACCTCTCA	-1235 to -1243	AGGGTGATC
-119 to -127	GACAACAGA	-1325 to -1333	GACAATGCA
-152 to -160	AACAGCCCA	-1379 to -1387	AAACACACA
-223 to -231	GCTCACCGA	-1387 to -1395	CACCCTCCA
-254 to -262	TAGCTCCCA	-1401 to -1409	TGAGTGCCC
-363 to -371	AGGGCGGCC	-1561 to -1569	TGTGTGGAG
-373 to -381	GGTGTGGTG	-1702 to -1710	TGTGTGTTT
-383 to -391	AGGCTGGCC	-1738 to -1746	TGTGTTTTC
-452 to -460	TATTTGGTC	-1833 to -1841	TACCAGCAA
-788 to -796	CCGGTGGTT	-1869 to -1877	GAATACACA
-871 to -879	TACAACCCT	-1937 to -1945	TCTGTGATC
-880 to -888	AAAGACCCA	-1982 to -1990	GTGCACCCT
-927 to -935	CACCACATA	-2016 to -2024	GGTGTGGCC
-1051 to -1059	TGGGTTCTT		

GLIconsensus binding sites: GACCACCCA and TGGGTGGTC

Table SIV. Quantification of ChIP PCR bands (Fig. 4). The numbers are arbitrary units corresponding to the strength of each band. GLI1-3 were immunoprecipitated by a specific antibody for each protein (see Materials and methods). The quantification was performed by the ImageJ software.

Segment A	Input	IgG	GLI	H3
GLI1	13753	0	19068	20330
GLI2	12286	0	16124	19302
GLI3	11033	0	5866	6389
Segment B	Input	IgG	GLI	H3
GLI1	11814	0	0	28113
GLI2	21000	0	0	21956
GLI3	25998	0	15803	29607
Segment C	Input	IgG	GLI	H3
GLI1	29550	0	20561	23168
GLI2	19341	0	6356	4519
GLI3	16739	0	16613	11995
Segment D	Input	IgG	GLI	H3
GLI1	20843	0	11166	30365
GLI2	29220	0	16356	32008
GLI3	16984	0	0	23562