

Table S1

List of melanoma patient specimens used in this study and frequency of ALDH⁺ subpopulations in the original and xenografted patient tumors

Patients	Gender	Age	Type	Origin	Percentage of ALDH⁺ population in patient tumors	Percentage of ALDH⁺ population in Xenografted tumors
MF347	Female	55	Primary	Skin	0.13%	0.13%
MF348	Female	86	Primary	Skin	ND	0.08%
111308	Male	69	Primary	Skin	0.1%	0.1%
MB947p	Female	65	Primary	Skin	0.2%	0.1%
MB947m	Female	65	Metastasis	Lymph node	0.7%	1.15%
MB952	Female	77	Metastasis	Lymph node	shift	shift
MB1009	Male	63	Metastasis	Lymph node	ND	shift
MB1047	Female	28	Metastasis	Lymph node	ND	0.55%
MB1374	Male	51	Metastasis	Lymph node	0.34%	ND
82909	Male	56	Metastasis	Adrenal gland	0.36%	0.36%
MB929	Female	68	Metastasis	Skin	0.16%	0.16%
MB1375	Male	42	Metastasis	Spleen	0.44%	ND

Nine tumors from melanoma patients and 10 xenografted tumors derived from direct *in vivo* xenograft were analyzed.
ND: not determined.

Table S2

PCR primers used in qRT-PCR in this study

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>ADAR</i>	GCTCTCCGTGTCTTGATTGGG	GAGGAGGAGCATAGTTCTTCTGA
<i>ALDH1A1</i>	ACTGCTCTCCACGTGGCATCTTTA	TGCCAACCTCTGTTGATCCTGTGA
<i>ALDH1A2</i>	AGGGCAGTTCTTGCAACCATGGAA	CACACACTCCAATGGGTTTCATGTC
<i>ALDH1A3</i>	ACCTGGAGGTCAAGTTCACCAAGA	ACGTCGGGCTTATCTCCTTCTTCC
<i>ALDH1B1</i>	TGCTGCAGAGTGTGAGCAT	GGTGGTAGGGTTGACCGTCG
<i>ALDH3A1</i>	TGTGTCAAAGGCGCCATGAGCAAG	GGCGTTCCATTCACTTGTGCAG
<i>ALDH3B1</i>	ACAAGTCAGCCTTCGAGTCGG	AGCACCACACAGTTCCTGC
<i>ALDH4A1</i>	TGCAGTACCAAGTGTGCGCTTT	AATCTCCGCTTGGATCACGGTCTT
<i>CDC42</i>	CTTGCTTGTGGGACTCAAATTG	GGCTCTTCTTCGGTTCGGAG
<i>GAPDH</i>	TGCACCACCAACTGCTTAGC	GGCATGGACTGTGGTCATGAG
<i>MLANA</i>	GGCTGTTGGTATTGTAGAAGACG	TTGAAGAGACACTTTGCTGTCC
<i>TYRP1</i>	TCTCTGGGCTGTATCTTCTTCC	GTCTGGGCAACACATACCACT
<i>USH1C</i>	GCTCCTACGCATCAAGAAGG	CCGCTCATACACAGCAGAAA

Table S3

List of predicted RARE elements between upstream (-10 kb) to downstream (+1 kb) of TSS

Genes	Strand	RARE Sequence	dTSS	Genes	Strand	RARE Sequence	dTSS
<i>ACVR1B</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-4503	<i>ITPKA</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-4080
<i>ACHE</i>	(+)	<u>AGGTCAGGAGTTCA</u>	+183	<i>ITPKA</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-7798
<i>ACHE</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-286	<i>KRT18</i>	(-)	<u>AGTTCAGAAGTTCA</u>	-78996
<i>ACHE</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-1511	<i>LRRC48</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-6566
<i>ACHE</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-3276	<i>LRRC48</i>	(-)	<u>AGTTCAGGAGTTCA</u>	+821
<i>AMT</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-7513	<i>PCDH11X</i>	(+)	<u>GGGTCAGGGGTCA</u>	+670
<i>APOL1</i>	(+)	<u>AGTTCAGAGGTCA</u>	-9599	<i>PIAS2</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-4152
<i>CDC42</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-2719	<i>PIGH</i>	(-)	<u>GGGTCAGGAGTTCA</u>	-1405
<i>CDC42</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-8170	<i>PPP1R3C</i>	(-)	<u>AGGTCAGCAGTTCA</u>	-4284
<i>CDC42</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-8483	<i>PRKCZ</i>	(+)	<u>AGGTCAGCAGTTCA</u>	-3923
<i>CDYL</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-7797	<i>PTGS2</i>	(+)	<u>AGGTCAAGAGTTCA</u>	-803
<i>CNTFR</i>	(+)	<u>GGGTCAAGGGTCA</u>	-7811	<i>RAB15</i>	(-)	<u>AGGTCATGAGGTCA</u>	-5372
<i>CPNE6</i>	(-)	<u>AGGTCAGAGTTCA</u>	-9694	<i>RAD17</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-8867
<i>DONSON</i>	(-)	<u>AGGTCAGAAGTTCA</u>	-7715	<i>REG1A</i>	(+)	<u>GGGTCAGGGGTCA</u>	+451
<i>DPP3</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-8303	<i>RNASE1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-9000
<i>EPB41</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-3372	<i>RTEL1</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-8112
<i>FAM128B</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-3273	<i>RTEL1</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-7440
<i>FAM128B</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-2706	<i>RTEL1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-7750
<i>FERMT3</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-1269	<i>SCARF1</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-2277
<i>FERMT3</i>	(-)	<u>AGTTCAGGAGTTCA</u>	-8136	<i>SETD7</i>	(+)	<u>AGGTCAGGAGTTCA</u>	+989
<i>GAGE5</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-1832	<i>SETD7</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-4853
<i>GFAP</i>	(+)	<u>AGGTCAGAGGTCA</u>	-8455	<i>SLC2A11</i>	(+)	<u>AGGTCAGTAGTTCA</u>	+124
<i>GGA1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-4690	<i>SPSB4</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-4284
<i>GGA1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-8078	<i>TAGAP</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-2485
<i>GLUL</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-5706	<i>THRSP</i>	(+)	<u>AGTTCAGGAGTTCA</u>	-1843
<i>GLUL</i>	(+)	<u>AGTTCATGGGTTCA</u>	-6245	<i>TMEM174</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-9283
<i>GNB5</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-6749	<i>TLL3</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-4129
<i>GPR37L1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-4279	<i>UBTD2</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-7173
<i>GPR37L1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-7949	<i>UBTD2</i>	(+)	<u>AGTTCAGGGTTCA</u>	+650
<i>GPR37L1</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-2044	<i>UBTD2</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-5007
<i>HIF3A</i>	(-)	<u>AGGTCAGGAGTTCA</u>	-3169	<i>UBXD5</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-4263
<i>HIF3A</i>	(+)	<u>AGTTCAGGTTCA</u>	-6674	<i>ZNF75A</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-603
<i>IL28RA</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-1444				
<i>IL28RA</i>	(+)	<u>AGGTCAGGAGTTCA</u>	-7344				
<i>IL28RA</i>	(-)	<u>AGGTCAGAAGTTCA</u>	-5041				