Supplementary Table S1

Nanostring nCounter^{TM} profiling of isogenic malignant melanoma cells: Gene expression changes in BRAF^{V600E}/NRAS^{Q61K} relative to BRAF^{V600E}/NRAS^{Q61}

gene	**description**	**fold change**[1]	***p* value**
ITGA1	integrin subunit alpha 1	31.78	0.00001
ITGA7	integrin subunit alpha 7	13.64	0.00046
FN1	fibronectin	10.56	0.00007
PDGFRB	platelet derived growth factor receptor beta	9.38	0.00051
MEOX2	mesenchyme homeobox 2	8.00	0.00013
COL6A2	collagen type VI alpha 2 chain	7.52	0.00025
FHL1	four and a half LIM domains protein 1	6.23	0.00007
TNC	tenascin C	5.94	0.00005
CHRDL1	chordin like 1	5.78	0.00041
COL6A1	collagen type VI alpha 1 chain	5.62	0.00015
GSN	gelsolin	5.46	0.00001
ITGB3	integrin subunit beta 3	5.24	0.00005
RAMP1	receptor activity modifying protein 1	5.13	0.00019
SRPX2	sushi repeat containing protein X-linked 2	5.13	0.00035
LAMA5	laminin subunit alpha 5	5.10	0.00030
TWIST1	twist basic helix-loop-helix transcription factor 1	5.03	0.00026
CLDN4	claudin 4	4.26	0.00060
HEG1	heart development protein with EGF like domains 1	4.23	0.00011
CXCL8	C-X-C motif chemokine ligand 8	4.17	0.00013
GJA5	gap junction protein alpha 5	4.03	0.00120
JUN	Jun proto-oncogene	-4.04	0.00073
AREG	amphiregulin	-7.73	0.00117
HMOX1	heme oxygenase 1	-15.44	0.00001

[1] expression changes (fold change ≥ 4; Benjamini-Yekutieli adjusted *p* value) as displayed by heatmap depiction in Figure 1b