

Table SI. Results from mouse tumor metastasis RT2 Profiler™ PCR array.

Gene	Description	Average Cq		Fold change (HP vs. CON)
		CON group	HP group	
Apc	Adenomatosis polyposis coli	25.91	26.04	-1.0392
Brms1	Breast cancer metastasis-suppressor 1	26.35	26.42	1.0032
Ccl7	Chemokine (C-C motif) ligand 7	21.98	22.73	-1.5971
Cd44	CD44 antigen	20.78	21.12	-1.2020
Cd82	CD82 antigen	24.26	24.54	-1.1530
Cdh1	Cadherin 1	33.41	33.08	1.3237 ^b
Cdh11	Cadherin 11	35.00	33.71	2.5750 ^b
Cdh6	Cadherin 6	35.00	35.00	1.0530 ^c
Cdh8	Cadherin 8	35.00	35.00	1.0530 ^c
Cdkn2a	Cyclin-dependent kinase inhibitor 2A	32.94	33.51	-1.4097 ^b
Chd4	Chromodomain helicase DNA binding protein 4	21.81	22.11	-1.1691
Col4a2	Collagen, type IV, α 2	22.86	22.81	1.0902
Csf1	Colony stimulating factor 1 (macrophage)	23.22	23.51	-1.1611
Ctbp1	C-terminal binding protein 1	23.76	24.02	-1.1372
Ctnna1	Catenin (cadherin associated protein), α 1	22.36	22.49	-1.0392
Ctsk	Cathepsin K	27.51	28.60	-2.0215
Ctsl	Cathepsin L	19.72	19.76	1.0242
Cxcl12	Chemokine (C-X-C motif) ligand 12	29.42	29.09	1.3237
Cxcr2	Chemokine (C-X-C motif) receptor 2	35.00	35.00	1.0530 ^c
Cxcr4	Chemokine (C-X-C motif) receptor 4	35.00	35.00	1.0530 ^c
Denr	Density-regulated protein	21.88	22.06	-1.0758
Elane	Elastase, neutrophil expressed	28.99	31.52	-5.4848 ^a
Ephb2	Eph receptor B2	33.33	31.77	3.1049 ^b
Etv4	Ets variant gene 4 (E1A enhancer binding protein, E1AF)	22.85	23.16	-1.1773
Ewsr1	Ewing sarcoma breakpoint region 1	21.67	22.07	-1.2530
Fat1	FAT tumor suppressor homolog 1 (Drosophila)	24.76	24.84	-1.0038
Fgfr4	Fibroblast growth factor receptor 4	27.43	27.99	-1.4000
Flt4	FMS-like tyrosine kinase 4	28.64	29.19	-1.3903
Fn1	Fibronectin 1	19.28	19.13	1.1684
Fxyd5	FXFD domain-containing ion transport regulator 5	23.67	23.88	-1.0984
Gpnmb	Glycoprotein (transmembrane) nmb	21.74	21.56	1.1930
Hgf	Hepatocyte growth factor	33.34	32.20	2.3207 ^b
Hpse	Heparanase	24.85	24.95	-1.0178
Hras	Harvey rat sarcoma virus oncogene 1	23.91	24.06	-1.0537
Htatip2	HIV-1 tat interactive protein 2, homolog (human)	23.71	24.75	-1.9527
Igf1	Insulin-like growth factor 1	32.39	32.17	1.2265 ^b
Il18	Interleukin 18	26.38	26.72	-1.2020
Il1b	Interleukin 1 β	31.94	32.20	-1.1372 ^b
Itga7	Integrin α 7	27.93	28.28	-1.2104
Itgb3	Integrin β 3	29.20	29.60	-1.2530
Kiss1	KISS-1 metastasis-suppressor	31.69	32.65	-1.8473 ^b
Kiss1r	KISS1 receptor	29.77	30.79	-1.9258 ^a
Kras	V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	22.67	22.90	-1.1138
Lpar6	Lysophosphatidic acid receptor 6	24.43	24.94	-1.3523
Mcam	Melanoma cell adhesion molecule	27.39	27.93	-1.3807
Mdm2	Transformed mouse 3T3 cell double minute 2	21.40	21.69	-1.1611
Met	Met proto-oncogene	23.66	23.92	-1.1372
Mmp10	Matrix metalloproteinase 10	28.49	28.95	-1.3063
Mmp11	Matrix metalloproteinase 11	23.99	24.44	-1.2972
Mmp13	Matrix metalloproteinase 13	27.51	27.94	-1.2794
Mmp2	Matrix metalloproteinase 2	31.29	32.13	-1.6999 ^b
Mmp3	Matrix metalloproteinase 3	25.65	25.44	1.2180
Mmp7	Matrix metalloproteinase 7	35.00	35.00	1.0530 ^c
Mmp9	Matrix metalloproteinase 9	27.70	27.85	-1.0537
Mta1	Metastasis associated 1	21.92	21.98	1.0101
Mtss1	Metastasis suppressor 1	23.57	23.95	-1.2358
Myc	Myelocytomatosis oncogene	19.30	19.14	1.1766

Table SI. Continued.

Gene	Description	Average Cq		Fold change (HP vs. CON)
		CON group	HP group	
Mycl	V-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	30.37	30.64	-1.1451 ^b
Nf2	Neurofibromatosis 2	23.73	24.17	-1.2883
Nme1	Non-metastatic cells 1, protein (NM23A) expressed in	21.70	21.70	1.0530
Nme2	Non-metastatic cells 2, protein (NM23B) expressed in	19.62	19.60	1.0677
Nme4	Non-metastatic cells 4, protein expressed in	24.34	24.56	-1.1061
Nr4a3	Nuclear receptor subfamily 4, group A, member 3	29.33	29.45	-1.0320
Plaur	Plasminogen activator, urokinase receptor	23.63	23.96	-1.1937
Pnn	Pinin	22.32	22.81	-1.3337
Pten	Phosphatase and tensin homolog	22.36	22.50	-1.0464
Rb1	Retinoblastoma 1	25.34	25.71	-1.2273
Rorb	RAR-related orphan receptor β	32.45	32.82	-1.2273 ^b
Rpsa	Ribosomal protein SA	17.30	17.25	1.0902
Set	SET nuclear oncogene	23.56	24.00	-1.2883
Smad2	MAD homolog 2 (Drosophila)	24.22	24.55	-1.1937
Smad4	MAD homolog 4 (Drosophila)	21.91	22.45	-1.3807
Src	Rous sarcoma oncogene	24.80	25.41	-1.4494
Sstr2	Somatostatin receptor 2	29.48	30.84	-2.4376 ^a
Syk	Spleen tyrosine kinase	33.12	33.99	-1.7356 ^b
Tcf20	Transcription factor 20	21.57	21.79	-1.1061
Tgfb1	Transforming growth factor, β 1	23.39	23.48	-1.0108
Timp2	Tissue inhibitor of metalloproteinase 2	21.56	21.74	-1.0758
Timp3	Tissue inhibitor of metalloproteinase 3	28.64	28.67	1.0314
Timp4	Tissue inhibitor of metalloproteinase 4	30.26	30.16	1.1286 ^b
Tnfsf10	Tumor necrosis factor (ligand) superfamily, member 10	31.57	32.16	-1.4294 ^b
Trp53	Transformation related protein 53	23.00	23.08	-1.0038
Tshr	Thyroid stimulating hormone receptor	27.81	28.94	-2.0783
Vegfa	Vascular endothelial growth factor A	21.30	21.7	-1.2530

^aThe gene's average threshold cycle was relatively high (>30) in either the control or the test sample and was reasonably low in the other sample (<30), indicating that the expression level of the gene was low in 1 sample and detected in another, and that the fold change was as big as the calculated fold change. ^bThe gene's average threshold cycle was relatively high (>30), indicating that its relative expression level was low, in both the control and experimental samples, and the P-value for the fold-change was either unavailable or high (P>0.05). ^cThe gene's average threshold cycle was either not determined or greater than the defined cut-off (default 35), in both samples indicating that its relative expression level was undetected, and the fold-change result was erroneous and un-interpretable. HP, hydrostatic pressure; CON, control.