Table S1. Differentially expressed genes (≥ 2.0 fold-change) in transformed clones for Ingenuity Pathway Analysis.

Symbol*	Name	Geom mean of intensities in AllExp	Geom mean of intensities in Cntl	Fold-change AllExp v Cntl
Ly6a	lymphocyte antigen 6 complex, locus A (Ly6a)	3459.91	241.21	14.344
Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a)	2653.67	283.33	9.366
Anxa8	annexin A8 (Anxa8)	1769.99	201.3	8.793
Anxa8	annexin A8 (Anxa8)	1643.92	201.4	8.162
Ly6e		7597.81	942.86	8.058
LOC100038882	PREDICTED: hypothetical protein LOC100038882 (LOC100038882)	8113.77	1026.19	7.907
Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a)	6350.65	810.62	7.834
Ly6e	lymphocyte antigen 6 complex, locus E (Ly6e)	3308.57	428.16	7.727
Dnali1		847.82	123.07	6.889
Irf7	interferon regulatory factor 7 (Irf7)	1017.71	161.95	6.284
Oas1g	2'-5' oligoadenylate synthetase 1G (Oas1g)	3235.96	549.33	5.891
Oas1g	2'-5' oligoadenylate synthetase 1G (Oas1g)	1525.74	297.97	5.120
Apol9b	apolipoprotein L 9b (Apol9b)	2060.57	403.99	5.101
Ephx1	epoxide hydrolase 1, microsomal (Ephx1)	3226.02	651.91	4.949
6530402F18Rik		562.92	117.51	4.790
LOC223672		4372.4	929.09	4.706
Capg	capping protein (actin filament), gelsolin-like (Capg), transcript variant 1	1175.06	257.51	4.563
Trp53inp1	transformation related protein 53 inducible nuclear protein 1 (Trp53inp1)	1959.4	452.54	4.330
Fam134b	family with sequence similarity 134, member B (Fam134b), transcript variant 2	724.96	173.3	4.183
Bst2	bone marrow stromal cell antigen 2 (Bst2)	2738.66	658.89	4.156
Lgals3	lectin, galactose binding, soluble 3 (Lgals3)	7860.48	1921.47	4.091
Car13	carbonic anhydrase 13 (Car13)	1127.91	300.25	3.757
2210023G05Rik	RIKEN cDNA 2210023G05 gene (2210023G05Rik)	1582.82	423.2	3.740
Ak1	adenylate kinase 1 (Ak1)	961.3	261.58	3.675
Ccng1	cyclin G1 (Ccng1)	6384.15	1808.89	3.529
D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed (D12Ertd647e), transcript variant 4	7607.3	2428.97	3.132
D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed (D12Ertd647e), transcript variant 5	6887.52	2209.86	3.117
Sqrdl	sulfide quinone reductase-like (yeast) (Sqrdl)	510.39	169.95	3.003
Ifitm3	interferon induced transmembrane protein 3 (Ifitm3)	11505.6	3864.62	2.977
A330089M16Rik		345.61	118.59	2.914
Pde3a		312.92	107.45	2.912
H2-T23	histocompatibility 2, T region locus 23 (H2-T23)	820.86	290.26	2.828
Irf9	interferon regulatory factor 9 (Irf9)	1109.91	401.34	2.766
Ifitm1	interferon induced transmembrane protein 1 (Ifitm1)	11647.61	4415.68	2.638
Coro1b	coronin, actin binding protein 1B (Coro1b)	3655.52	1388.93	2.632
Fxyd5	FXYD domain-containing ion transport regulator 5 (Fxyd5)	482.22	187.45	2.573
Lynx1	Ly6/neurotoxin 1 (Lynx1)	333.02	134.73	2.472
Gsdmdc1	gasdermin domain containing 1 (Gsdmdc1)	600.77	247.38	2.429
Gsdmdc1	gasdermin domain containing 1 (Gsdmdc1)	2484.51	1023.12	2.428
LOC100047963	PREDICTED: similar to ADIR1 (LOC100047963)	1338.77	568.37	2.355
scl0001379.1_70		448.96	190.92	2.352

LOC100044430	PREDICTED: similar to Interferon activated gene 205 (LOC100044430)	706.3	301	2.347
Ifi30	interferon gamma inducible protein 30 (Ifi30)	897.22	391.25	2.293
Ggta1	glycoprotein galactosyltransferase alpha 1, 3 (Ggta1)	445.66	194.68	2.289
Dhrs7	dehydrogenase/reductase (SDR family) member 7 (Dhrs7)	1062.82	470.24	2.260
EG433865	PREDICTED: predicted gene, EG433865 (EG433865)	917	408.53	2.245
St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2 (St3gal2), transcript variant 2	713.98	320.45	2.228
Tdrd7	tudor domain containing 7 (Tdrd7)	1442.82	649.42	2.222
Actb	actin, beta, cytoplasmic (Actb)	2099.32	953.95	2.201
Mlkl	mixed lineage kinase domain-like (Mlkl) XM_924589	2327.26	1061.25	2.193
Tspo	translocator protein (Tspo)	3682.07	1685.41	2.185
LOC100047261	PREDICTED: similar to spermidine/spermine N1-acetyltransferase (LOC100047261), misc RNA.	2692.75	1239.31	2.173
Trim47	tripartite motif-containing 47 (Trim47)	532.06	246.19	2.161
Fbxo6	F-box protein 6 (Fbxo6)	2408.36	1118.16	2.154
Actb	actin, beta (Actb)	1935.11	902.48	2.144
Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 (Ddx60)	301.87	141.38	2.135
Arsa	arylsulfatase A (Arsa)	1536.34	720.1	2.134
LOC100046469	PREDICTED: similar to Plec1 protein, transcript variant 1 (LOC100046469)	311.62	146.43	2.128
4732458O05Rik		739.23	349.99	2.112
Klf4	Kruppel-like factor 4 (gut) (Klf4)	511.31	244.53	2.091
Tspo	translocator protein (Tspo)	3653.66	1752.05	2.085
Gsdmdc1	gasdermin domain containing 1 (Gsdmdc1)	989.09	474.6	2.084
Adfp	adipose differentiation related protein (Adfp)	495.37	238.46	2.077
LOC100046469	PREDICTED: similar to Plec1 protein, transcript variant 1 (LOC100046469)	297.84	144.79	2.057
Txnip	thioredoxin interacting protein (Txnip), transcript variant 1	1205.52	588.87	2.047
Ostf1	osteoclast stimulating factor 1 (Ostf1)	2024.89	999.75	2.025
Ifi204	interferon activated gene 204 (Ifi204)	526.61	261.34	2.015
Ifi30	interferon gamma inducible protein 30 (Ifi30)	446.48	221.79	2.013
Txnip	thioredoxin interacting protein (Txnip), transcript variant 2	2023.78	1008.19	2.007
Plec1	plectin 1 (Plec1), transcript variant 11	642.3	320.33	2.005
Avpr1a	arginine vasopressin receptor 1A (Avpr1a)	119.45	239.23	-2.003
Stx11	PREDICTED: syntaxin 11 (Stx11)	476.09	962.23	-2.021
LOC674960	PREDICTED: similar to high-mobility group box 1 (LOC674960), misc RNA.	207.59	423.13	-2.038
Cdh3		236.11	481.91	-2.041
Epha1	Eph receptor A1 (Epha1)	152.84	312.81	-2.047
9030624G23Rik	PREDICTED: RIKEN cDNA 9030624G23 gene (9030624G23Rik)	209.44	429.74	-2.052
Odf2	outer dense fiber of sperm tails 2 (Odf2)	176.63	362.96	-2.055
Gpr23		120.58	248.34	-2.060
Plac1	placental specific protein 1 (Plac1)	144.78	301.93	-2.085
Rhobtb1	Rho-related BTB domain containing 1 (Rhobtb1)	149.14	311.12	-2.086
Dlg3	discs, large homolog 3 (Drosophila) (Dlg3)	184.06	384.19	-2.087
Il16	interleukin 16 (Il16)	119.14	248.84	-2.089
Emb	embigin (Emb)	112.55	235.47	-2.092
Syngr1	synaptogyrin 1 (Syngr1), transcript variant 1b	131.19	274.58	-2.093
Gstm5	glutathione S-transferase, mu 5 (Gstm5)	645.4	1353.64	-2.097
Ttc28	PREDICTED: tetratricopeptide repeat domain 28 (Ttc28)	163.9	344.43	-2.101

OTTMUSG00000004461	predicted gene, OTTMUSG00000004461 (OTTMUSG00000004461)	283.31	596.28	-2.105
scl0002255.1_1		112.54	236.88	-2.105
Ipo5	importin 5 (Ipo5)	734.9	1561.97	-2.125
4932408C11Rik		114.17	243.49	-2.133
Nfib		225.47	486.74	-2.159
0610007N19Rik	PREDICTED: RIKEN cDNA 0610007N19 gene (0610007N19Rik)	193.4	417.94	-2.161
Odz3	odd Oz/ten-m homolog 3 (Drosophila) (Odz3)	201.81	440.42	-2.182
Fez1	fasciculation and elongation protein zeta 1 (zygin I) (Fez1)	148.41	324.42	-2.186
Gpx7	glutathione peroxidase 7 (Gpx7)	113.21	250.59	-2.213
Spnb2	spectrin beta 2 (Spnb2), transcript variant 2	470.32	1045.74	-2.223
Myh10	myosin, heavy polypeptide 10, non-muscle (Myh10)	684.26	1529.88	-2.236
5730525O22Rik		430.32	969.43	-2.253
D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5 (D17H6S56E-5)	186.87	423.51	-2.266
Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1 (Ptprz1)	125.27	284.11	-2.268
Epm2aip1	EPM2A (laforin) interacting protein 1 (Epm2aip1)	264.3	600.86	-2.273
LOC382555		1230.93	2813.45	-2.286
Dmrta2	doublesex and mab-3 related transcription factor like family A2 (Dmrta2)	137.06	313.52	-2.287
AI448196		114.48	263.81	-2.304
Zfp703	PREDICTED: zinc finger protein 703 (Zfp703)	391.4	902.42	-2.306
Serping1		119.48	276.16	-2.311
4931406P16Rik	RIKEN cDNA 4931406P16 gene (4931406P16Rik)	677.59	1572.48	-2.321
scl0002507.1_236		200.88	468.46	-2.332
Gpc2	glypican 2 (cerebroglycan) (Gpc2)	120.71	283.55	-2.349
B3galnt1	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1 (B3galnt1)	116.04	273.84	-2.360
Jam3	junction adhesion molecule 3 (Jam3)	174.99	412.96	-2.360
Trim27		164.85	390.33	-2.368
C130020C13Rik		290.18	688.75	-2.374
Id4	inhibitor of DNA binding 4 (Id4)	137.36	326.52	-2.377
1700007G11Rik	RIKEN cDNA 1700007G11 gene (1700007G11Rik)	135.21	322.38	-2.384
Fez1	fasciculation and elongation protein zeta 1 (zygin I) (Fez1)	139.52	333.3	-2.389
Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like (Hnrpdl)	738.22	1799.3	-2.437
Cd276	CD276 antigen (Cd276)	166.19	406.02	-2.443
Stard10	START domain containing 10 (Stard10)	307.04	757.47	-2.467
6330406I15Rik	RIKEN cDNA 6330406I15 gene (6330406I15Rik)	166.71	412.7	-2.476
6330406I15Rik	RIKEN cDNA 6330406I15 gene (6330406I15Rik)	195.57	495.49	-2.534
Tacstd2	tumor-associated calcium signal transducer 2 (Tacstd2)	153.81	392.36	-2.551
Cirbp	cold inducible RNA binding protein (Cirbp)	409.68	1074.94	-2.624
scl0003131.1_3		153.72	423.07	-2.752
1110003F05Rik		157.63	437.68	-2.777
Gstk1	glutathione S-transferase kappa 1 (Gstk1)	139.38	389.34	-2.793
Wipf1	WAS/WASL interacting protein family, member 1 (Wipf1)	136.35	393.6	-2.887
Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1 (Serping1)	121.56	353.11	-2.905
LOC226017		117.03	345.25	-2.950
Tagln	transgelin (Tagln)	166.59	493.83	-2.964
Capn6	calpain 6 (Capn6)	128.03	383.66	-2.997
Myl9	PREDICTED: myosin, light polypeptide 9, regulatory (Myl9)	129.58	390.16	-3.011
Mex3a	mex3 homolog A (C. elegans) (Mex3a)	213.27	654.17	-3.067

Srpx	sushi-repeat-containing protein (Srpx)	109.82	341.53	-3.110
Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (Ddx25)	148.63	463.87	-3.121
Hal	histidine ammonia lyase (Hal)	137.09	432.99	-3.158
Zfp521	zinc finger protein 521 (Zfp521), transcript variant 2	141.01	447.51	-3.174
Igf2bp3		183.29	607.5	-3.314
Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related) (Runx1t1)	130.59	436.55	-3.343
ORF63	open reading frame 63 (ORF63)	151.84	521.34	-3.433
Nid2	nidogen 2 (Nid2)	172.18	601.87	-3.496
9430052C07Rik		199.83	728.58	-3.646
Mdk	midkine (Mdk), transcript variant 3	129.78	473.63	-3.649
Dlk1	delta-like 1 homolog (Drosophila) (Dlk1)	118.1	439.12	-3.718
Gstk1	glutathione S-transferase kappa 1 (Gstk1)	164.83	617.04	-3.743
Asphd2	aspartate beta-hydroxylase domain containing 2 (Asphd2)	138.1	524.37	-3.797
Igf2	insulin-like growth factor 2 (Igf2)	143.14	552.37	-3.859
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1 (Serpinf1)	178.21	688.69	-3.864
Grb10		1774.18	7351.32	-4.144
Gm22	PREDICTED: gene model 22, (NCBI) (Gm22)	153.24	638.28	-4.165
Fgf5	fibroblast growth factor 5 (Fgf5)	505.61	2138	-4.229
Armcx1	armadillo repeat containing, X-linked 1 (Armcx1)	135.78	578.19	-4.258
Podxl2	podocalyxin-like 2 (Podxl2)	128.65	565.65	-4.397
Limch1	LIM and calponin homology domains 1 (Limch1)	121	575.33	-4.755
6330404C01Rik		140.77	692.04	-4.916
1700048O20Rik		137.09	681.52	-4.971
Prkg1		137.04	725.13	-5.291
Zic1	zinc finger protein of the cerebellum 1 (Zic1)	140	822.89	-5.878
EG433229	PREDICTED: predicted gene, EG433229, transcript variant 7 (EG433229)	165.76	1010.61	-6.097
Mmp2	matrix metallopeptidase 2 (Mmp2)	339.09	2992.32	-8.825
Sfrp2	secreted frizzled-related protein 2 (Sfrp2)	329.33	4098.72	-12.446
Cxcl12	chemokine (C-X-C motif) ligand 12 (Cxcl12), transcript variant 3	138.6	1903.43	-13.733
Cxcl12	chemokine (C-X-C motif) ligand 12 (Cxcl12), transcript variant 1	127.73	3105.6	-24.314
Ptn	pleiotrophin (Ptn)	120.37	5835.39	-48.479
Cxcl12		137.3	9349	-68.092

*Highlighted genes were identified with multiple probes.