

Supplemental Tables 2 to 9. Summary Tables indicate genes with > 2 fold differential expression on pairwise comparison among the cells transduced with GFP or SHP adenovirus. 3T3-L1 cells were transduced with GFP control or SHP adenovirus for three days, treated with differentiation cocktail to induce differentiation for two days, and gene expression was analyzed using Affymetrix GeneChip® Mouse Genome 430A 2.0 Array platform. Genes involved in regulation of cell adhesion (Table 2), cytoskeleton organization and biogenesis (Table 3), extracellular space (Table 4), cell cycle (Table 5), cell growth (Table 6), gene transcription (Table 7), signaling transduction (Table 8) and transport (Table 9) were presented. Day 0 (G0 and S0) represents unstimulated cells, whereas day 2 (G2 and S2) represents cells after hormonal stimulation for two days.

Supplemental Table 2 Cell adhesion

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
Col11a1	NM_00772	2.01	-2.27	-1.12	-5.12	505.8	1017.7	450.9	198.7
Col5a1	AW744319	2.17	-2.48	1.06	-5.08	419.4	908.4	442.9	178.7
Pvrl3	BG070704	2.28	1.02	1.01	-2.22	283.6	646.1	286.3	291.2
Pvrl3	NM_02149	3.38	-1.53	1.9	-2.73	39.1	132.3	74.4	48.5
Ceacam1	NM_01192	3.5	-3.36	1.24	-9.47	39.5	138.2	49.1	14.6
Dpt	NM_01975	3.84	-1.52	1.23	-4.73	2373.4	9124.3	2926.4	1928.6
Rom1	NM_00907	3.93	-2	3.73	-2.1	16.5	64.8	61.6	30.8
Itga6	BM935811	4.12	1.18	1.64	-2.14	142.3	586.7	232.8	273.7
Col5a3	NM_01691	4.67	1.8	1.09	-2.38	415.7	1940.5	452.9	815.2
	BB377340	4.79	-1.05	1.64	-3.07	412.9	1976.8	676.5	643.7
Edil3	AF031524	4.81	1.25	1.45	-2.65	146.5	704.6	213.1	265.4
Cd33	NM_02129	6.23	10.85	-7.24	-4.16	56.5	352.2	7.8	84.6
Dsg2	C79957	8.94	1.71	1.76	-2.96	6.3	56.3	11.1	19
Cspg2	BM251152	10.4	2.33	1.6	-2.79	668.3	6950.9	1069.1	2492.6
Icam2	NM_01049	14.24	-1.58	1.39	-16.22	4.1	58.4	5.7	3.6
1110007F2	BC022666	14.33	-1.87	1.17	-22.93	4.8	68.8	5.6	3
Col15a1	AF011450	14.46	1.1	3.02	-4.37	13.5	195.2	40.8	44.7
Ceacam1	BC016891	19.27	-1.14	5.14	-4.3	3.7	71.3	19	16.6
Ceacam1	X67278	23.12	6.86	1.02	-3.29	4.2	97.1	4.3	29.5
Ceacam1	M77196	35.82	3.08	2.24	-5.21	1.7	60.9	3.8	11.7
170005111	BE945716	-2.35	5.61	-3.16	4.18	30.3	12.9	9.6	53.9
Zyx	BB759260	-3.29	-1.31	1.11	2.79	163.3	49.6	181.7	138.3
Thbs1	AI385532	-4.89	-1.86	-1.3	2.02	4146.1	847.2	3181.4	1710.7
Arvcf	BE947943	-5.06	1.95	1.29	12.74	32.9	6.5	42.4	82.8
Thbs1	AI385532	-5.24	-1.69	-1.27	2.44	5558.1	1061.6	4370.8	2586
Pcdhb13	NM_05313	-9.73	-2.77	-1.59	2.21	64.2	6.6	40.4	14.6
Col8a1	NM_00773	-12.56	-5.78	1.2	2.6	56.5	4.5	67.6	11.7
Gpnmb	NM_05311	-19.18	-9.38	1.93	3.94	118.9	6.2	228.9	24.4

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

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Supplemental Table 3 Cytoskeleton organization and biogenesis

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
Pclo	NM_01199	2.56	-3.81	-1.01	-9.81	184.5	471.9	183.4	48.1
Krt1-13	NM_01066	46.87	-1.89	3.47	-25.47	11.9	557.7	41.3	21.9
Krt1-15	NM_00846	106.89	-1.35	3.26	-44.4	2.7	288.6	8.8	6.5
AV006891	NM_02305	-2.15	1.95	-1.87	2.24	102.6	47.7	55	107
Spnb1	NM_01367	-2.96	2.32	-1.47	4.67	41.2	13.9	28	64.9
Myl4	NM_01085	-4.52	-1.5	-1.22	2.48	56	12.4	46	30.7
Tagln	BB114067	-5.87	-2.77	1.06	2.25	109.1	18.6	115.6	41.8
Actl7a	NM_00961	-10.71	6.47	-18.59	3.73	63.2	5.9	3.4	22
	AW259435	-29.06	-1.81	-1.01	15.94	52.3	1.8	51.9	28.7
Acta2	NM_00739	-35.37	-17.4	1.08	2.2	8216.2	232.3	8894.5	511.2

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

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Supplemental Table 4 Extracellular space

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
1110018M03Rik	BC027250	2.27	-1.63	1.52	-2.44	35.5	80.6	53.8	33.1
2810038K19Rik	NM_02368	2.69	-4.23	1.49	-7.64	37.8	101.6	56.3	13.3
Lrp5	BC011374	3.14	2.11	-1.73	-2.56	105.6	331.1	61.2	129.1
Cldn15	NM_02171	3.31	-1.32	-1.56	-6.85	142.4	471	91	68.8
1300007F04Rik	AI467583	7.36	2.22	1.36	-2.44	14.2	104.5	19.3	42.8
Egfl9	NM_13412	10.07	-11.11	25.79	-4.34	2.8	28.2	72.2	6.5
Dio2	AF177197	10.98	-1.28	2.27	-6.2	4.8	52.7	10.9	8.5
Spon2	NM_13390	18.07	-2.55	1.37	-33.75	289.1	5224.9	395.3	154.8
Pip	NM_00884	74.14	101.33	-3.22	-2.36	2.9	215	0.9	91.2
Ear1	AF306665	106.19	28.4	-2.21	-8.26	37.8	4014	17.1	485.7
Serpini1	NM_00925	-2.01	3.05	-1.01	6.08	74	36.9	73.5	224.4
2010109H09Rik	NM_02562	-2.07	2.61	-2.07	2.61	79.8	38.6	38.6	100.7
Efna1	D38146	-2.09	1.47	-1.31	2.35	332.7	158.9	254.3	373.3
Lox	M65143	-2.12	1.63	-1.34	2.59	14146.1	6668.6	10584.5	17290.6
	BG244279	-2.16	1.37	1.13	3.34	771.2	356.8	872.6	1193.4
4432405B04Rik	AK012720	-2.16	-1.27	1.57	2.66	75.3	34.9	118.4	93
Jam2; JAM-2; Jc	AK010826	-2.29	1.02	1.03	2.41	48.3	21.1	49.7	50.9
	BG244279	-2.45	1.43	1.39	4.86	471.4	192.6	655.3	935.2
2010011I20Rik	AK008190	-2.49	1.65	-1.74	2.36	100.3	40.3	57.5	95.1
Pvrl2	BC009088	-2.6	-1.34	1.29	2.5	300.5	115.8	388.4	289.1
Angptl2; Arp2	AK011976	-3.22	1.53	-1.09	4.52	46.7	14.5	43	65.6
Thsd1	AW121720	-3.32	-1.09	-1.12	2.72	52.5	15.8	47	43
Itih2	NM_01058	-3.64	-1.07	-1.07	3.17	66.7	18.3	62.3	58
Prdc	NM_01182	-3.71	-1.04	-1.1	3.23	358.5	96.6	325.5	312.4
Tnc	NM_01160	-3.85	-2.39	1.27	2.04	593.5	154.2	751.1	314.9
Rarres2	BI328146	-4.18	1.81	-1.34	5.66	589.2	141	440.8	797.8
Rarres2	AV012073	-4.21	1.52	-1.27	5.04	756	179.4	594.2	904.5
Cldn2	NM_01667	-4.8	1.01	-1.84	2.64	68.6	14.3	37.3	37.8
Slpi	NM_01141	-5.03	-1.94	1.14	2.96	10359.5	2057.9	11794.1	6083.5
Serpine2	NM_00925	-5.23	-2.28	1.16	2.68	2762.9	528	3216.5	1412.5
Aig1	NM_02544	-5.74	-1.22	-1.13	4.15	259	45.1	228.5	187.3
Galgt2	NM_00808	-7.67	28.59	-16.73	13.1	36.8	4.8	2.2	62.9
1110035L05Rik	AW050002	-7.99	1.56	-1.72	7.22	54.3	6.8	31.5	49.1
Lgals3bp	NM_01115	-9.27	-2.85	-1.25	2.61	4165.3	449.5	3337.4	1172.4
D930038M13Rik	BC026627	-10.24	-6.03	1.2	2.05	1119.2	109.3	1348.4	223.6
Tslp	NM_02136	-17.08	-2.03	-1.18	7.16	104.2	6.1	88.5	43.7
Phxr4	NM_00883	-29.3	1.54	-10.15	4.43	128.9	4.4	12.7	19.5
2510004L01Rik	BB132493	-69.18	-8.15	-1.4	6.06	2725.8	39.4	1944	238.6
2510004L01Rik	BB741897	-81.8	-4.1	-1.39	14.31	531.7	6.5	381.5	93
Ces1	NM_02145	-131.67	-16.8	-1.53	5.13	592.5	4.5	388	23.1

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

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Supplemental Table 5 Regulation of cell cycle

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
	AV259620	2.36	-1.68	1.49	-2.66	118.3	279.2	176	105
Tacc3	NM_01152	2.49	-1.33	1.33	-2.49	128.6	320.6	171	128.6
1190002H2	NM_02542	2.73	-2.04	-1.07	-5.97	31.5	86	29.4	14.4
Ccnb1	NM_00762	2.75	-2.7	1.36	-5.47	423.7	1163.8	574.9	212.8
Ccnb2	AK013312	3.35	-1.55	1.63	-3.19	306.5	1028	499.4	322.5
Elk1	AI385733	3.36	-1.37	2.1	-2.19	41.6	139.8	87.5	63.9
Ccnb1	AU015121	3.71	-1.87	2.18	-3.17	284.5	1054.3	621.3	332.3
Plagl1	AF147785	3.85	-2.43	1.16	-8.07	295.2	1136.9	342.8	140.8
Ccnb1	NM_00762	3.95	-1.34	2.06	-2.58	493.5	1951.3	1016	756
	AV216875	4.15	-7.11	7.64	-3.86	8.1	33.6	61.9	8.7
G0s2	NM_00805	7.18	10.42	-14.89	-10.27	28.3	203.3	1.9	19.8
	BB408123	9.92	1.84	2.2	-2.45	20	198.4	44	80.9
E2f3	BI989566	-2.09	-1.15	1.2	2.18	95.6	45.7	114.4	99.5
Egfr	AK014017	-2.12	1.47	-1.27	2.45	56.2	26.5	44.1	65
Mafk	NM_01075	-2.33	1.87	-1.97	2.22	426.4	183	216.7	405.7
Gadd45b	AK010420	-2.51	1.28	-1.59	2.01	1442.9	574.2	904.9	1156.9
Cdkn1a	AK007630	-2.58	-1.09	1.12	2.64	4546.9	1765.8	5072.6	4656.4
Csnk2a2	BG070990	-2.82	-1.2	1.46	3.43	52.8	18.7	77.2	64.1
Il1b	BC011437	-4.04	1.56	-1.53	4.13	52.9	13.1	34.6	54.1
Erbb3	BF140685	-4.32	8.72	-12.49	3.01	58.7	13.6	4.7	41
Mpl	AF360122	-4.58	-1.7	1.32	3.56	46.3	10.1	61.1	36
Figf	NM_01021	-4.84	-2.25	1.02	2.2	2135.4	441.5	2184	972.6
Cdkn1a	NM_00766	-5.13	-1.43	1.48	5.32	404.9	79	599.4	420.1
Map3k8	NM_00774	-5.5	1.99	1.03	11.29	253.5	46.1	261.9	520.6
Figf	BB359521	-5.53	-3.27	1.34	2.26	3310.7	598.2	4428	1353.3
Gadd45g	AK007410	-6.06	1.09	-1.98	3.35	2224.9	367.1	1125.5	1229.4
Figf	BB359521	-7.02	-3.89	1.17	2.11	4529.9	645	5284	1358.8
Dst	NM_01008	-7.04	-1.44	1.68	8.27	31.7	4.5	53.4	37.2
Il1a	BC003727	-26.68	-4.77	-2.19	2.56	66.7	2.5	30.5	6.4

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

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Supplemental Table 6 Regulation of cell growth

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
	BB074430	3.04	-1.06	-1.19	-3.84	111.3	338.8	93.2	88.3
Igfbp4	BC019836	4.19	1.67	1.22	-2.05	3337	13984.8	4082.6	6821.4
Ndn	AW743020	4.88	1.16	1.07	-3.94	123.1	601.3	132	152.5
Ndn	NM_01088	5.58	1.08	1.34	-3.87	64.7	361	86.8	93.4
Igfbp4	BC019836	6.46	1.5	1.37	-3.15	2079.1	13437.5	2848.8	4271.5
Ndn	AV124445	6.74	1.28	1.05	-5.02	63.1	425.3	66	84.8
Igfbp4	NM_01051	9.22	1.47	1.62	-3.86	1123.5	10358.9	1819.7	2683.9
Igfbp5	BF225802	27.1	-4.41	2.83	-42.15	4.2	113.8	11.9	2.7
Wisp2	NM_01687	-2.44	-1.07	-1	2.28	398.3	163.3	397.6	372.7
Igfbp3	AV175389	-2.44	7.93	1.16	22.42	73	29.9	84.6	670.5
Wisp1	NM_01886	-2.5	1.32	1.08	3.54	404.8	162.2	435.2	574.5
9530081K	NM_03012	-5.67	-2.69	1.03	2.17	172.8	30.5	178	66.1
Prss11	NM_01956	-6.37	-3.89	1.38	2.26	125.5	19.7	173.6	44.6
	BB559067	-13.88	-9.71	1.79	2.55	77.7	5.6	138.9	14.3

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

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Supplemental Table 7A Regulation of transcription

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
Hnrapab	NM_01044	2.08	1.07	-1.36	-2.64	208.8	434.4	153.4	164.7
Dlx4	NM_00786	2.12	-2.15	2.19	-2.07	45.8	97	100.4	46.8
Srebf2	BM123132	2.12	1.23	-1.54	-2.65	385.7	817.1	250.4	308.9
Tle4	AU045006	2.16	-1.23	1.08	-2.46	92.7	200.3	99.9	81.5
Ebf3	AK014058	2.17	1.03	-2.04	-4.29	346.1	751.7	169.9	175.3
Mycbp	BB046347	2.27	1.13	-1.02	-2.04	190.6	432.7	186.8	211.6
Notch1	NM_00871	2.3	1	1.02	-2.23	64.2	147.4	65.8	66.1
Srebf2	BM123132	2.35	-1.33	-1.01	-3.16	288.1	676.8	284.1	214.3
Mrps25	AK004037	2.47	-2.28	-1.13	-6.36	28.1	69.3	24.9	10.9
Tcf3	BE994269	2.69	1.35	-1.07	-2.12	549.4	1477.1	515.8	695.3
Trps1	NM_03200	2.69	-1.06	1.11	-2.58	566.2	1525.2	626.2	590.9
Hira	AW537496	2.98	-5.69	5.53	-3.07	10.4	31	57.5	10.1
Ash2l	BM207355	3.55	3.67	-2.23	-2.16	23.9	84.9	10.7	39.3
Hoxd3	NM_01046	4.29	-3.02	4.81	-2.7	19.1	82	91.9	30.4
Al481750	BC016109	5.67	-4.89	1.89	-14.7	9.6	54.4	18.1	3.7
Zfp146	NM_01198	6.58	-5.19	16.24	-2.1	20	131.6	324.8	62.6
Gtf2i; SPINAK	AK006796	7.83	-2.38	6.44	-2.9	7.8	61.1	50.2	21.1
Rorb	BC024842	12.18	3.33	-1.31	-4.79	5.5	67	4.2	14
Cebpa	BC011118	12.39	17.19	-3.97	-2.86	12.7	157.4	3.2	55
Hoxb7	X06762	12.88	1.97	1.25	-5.24	4.8	61.8	6	11.8
Ebf2	U71189	27.32	-1.89	2.38	-21.66	9.2	251.3	21.9	11.6
Ebf2	U71189	55.74	1.13	10.19	-4.82	2.7	150.5	27.5	31.2

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

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Supplemental Table 7B Regulation of transcription

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
Rora	BI660199	-2.01	1.3	-1.15	2.26	207.8	103.6	180.2	234.2
Runx1	NM_00982	-2.02	4.21	-1.69	5.01	195	96.6	115.1	484
Bteb1	NM_01063	-2.03	1.22	-1.04	2.38	374.5	184.6	359.9	439.8
Ahr	BE989096	-2.05	1.62	1.36	4.52	727.4	354.3	988.7	1602.1
Runx1	NM_00982	-2.1	2.37	-1.24	4.02	141.6	67.4	114.3	271.1
Zfp99; 231	AK009842	-2.19	1.36	-1.31	2.28	100.6	45.9	77	104.8
Ddef1	BE943736	-2.2	1.26	-1.25	2.22	124.2	56.5	99.6	125.2
Nr3c1	NM_00817	-2.22	-1.21	1.09	2.01	1716.7	773.9	1874.1	1555
Bteb1	BE995545	-2.31	2.05	-1.4	3.38	128	55.5	91.4	187.6
Rora	NM_01364	-2.43	1.08	1.19	3.13	122.2	50.3	145.9	157.5
Bteb1	AW488885	-2.52	1.84	-1.95	2.39	3800.5	1506.4	1952.2	3594.1
C330013J2	AA139561	-2.58	3.1	-3.61	2.22	92.3	35.8	25.6	79.4
Klf7	BB524597	-2.63	1.41	-1.66	2.25	268	101.8	161.9	228.7
Pou6f1	AK009674	-2.8	-1.84	1.39	2.12	329.3	117.6	459	249.2
Tbx3	AA543734	-2.87	1.61	-1.8	2.57	222.4	77.4	123.8	199
Tgif	NM_00937	-2.95	1.69	-1.71	2.92	1387.3	470	811	1371.9
Rbpsuh	NM_00903	-2.97	-1.09	-1.09	2.5	518.5	174.6	474.7	435.7
Nr3c1	NM_00817	-3.18	-1.04	-1.03	2.97	2264.7	711.2	2196.2	2112.1
Sfp1	NM_01135	-3.19	1.11	-1.71	2.08	58.4	18.3	34.2	38
Neud4	AW553317	-3.3	18.15	-7.32	8.18	30	9.1	4.1	74.4
Nr1d2	NM_01158	-3.42	1	-1.22	2.82	112.7	33	92.6	93
Ddit3	NM_00783	-3.65	-1.64	1.02	2.27	2121.5	580.7	2158.2	1317.3
Nr0b2	BC019540	-3.66	1.19	99.12	432.09	213.3	58.3	21141.6	25190.8
Per3	NM_01106	-3.92	-1.23	-1.56	2.04	62.4	15.9	39.9	32.4
Nr1d2	NM_01158	-4.14	-1.24	-1.55	2.15	1615	390.2	1042	840.6
Klf7	BB524597	-4.81	4.22	-5.8	3.5	138.6	28.8	23.9	100.9
Stat2	AF088862	-5.01	-2.1	-1.06	2.26	369.1	73.6	349.3	166.6
Madh7	BF226166	-5.27	2.22	-2.61	4.5	621.2	117.8	238.2	529.7
Mnt	NM_01081	-5.48	-1.89	-1.04	2.78	478.3	87.3	459.1	242.6
Sox15	AF182945	-7.17	1.5	1.26	13.55	33.7	4.7	42.5	63.7
Utf1	NM_00948	-7.85	1.65	-2.09	6.19	87.9	11.2	42	69.3
C330003B	AU019881	-8.08	-1	1.13	9.13	71.9	8.9	81.3	81.3
Mef2b	D87833	-8.25	2.83	-2.52	9.25	75.9	9.2	30.1	85.1
Egr4	NM_02059	-8.25	2.3	-7.53	2.52	60.2	7.3	8	18.4
lsgf3g	NM_00839	-8.89	-3.18	-1.2	2.34	1279.4	143.9	1068.7	336.6
Nfatc2	AF289078	-10.69	2.06	-2.06	10.69	52.4	4.9	25.4	52.4
Ankrd1	AK009959	-11.27	-4.45	1.27	3.2	206.3	18.3	261	58.6
	BB550183	-11.38	-3.64	-1.16	2.7	1081	95	935.6	256.8
Dbp	BC018323	-11.47	-1.84	-1.57	3.98	493.4	43	315.1	171.3
Og9x	NM_00875	-19.52	1.72	-1.75	19.22	52.7	2.7	30.1	51.9
Ankrd1	AK009959	-221.41	-5.48	-1.28	31.71	376.4	1.7	295.1	53.9

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

Song G et al/SHP in Adipogenesis

Supplemental Table 8 Signal transduction

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
Pde10a	BQ180352	3.17	1.33	-1.59	-3.77	162	513.7	102.1	136.2
Gpsm2	BE457924	4.36	1.83	-1.24	-2.95	13.4	58.4	10.8	19.8
Wnt4	NM_00952	13.65	-1.73	6.6	-3.58	8.4	114.7	55.4	32
Lrba	NM_03069	-2.48	1.31	-1.34	2.42	359.8	144.8	268.4	351
Pwp2h	AB041855	-2.69	-1.41	1.23	2.34	86.2	32.1	105.7	75.2
Lrdd	NM_02265	-2.87	1.13	-1.22	2.66	101.2	35.3	82.9	93.8
Pilra	BB775785	-3.02	-1.94	1.88	2.93	29.3	9.7	55	28.4
Grb14	NM_01671	-5.21	-1.98	1.13	2.99	1093.1	209.9	1239.9	627
Wnt7b	W29605	-9.21	1.73	-2.9	5.49	105	11.4	36.2	62.6
	BB100249	-37.81	-2.24	-1.52	11.09	336.5	8.9	220.9	98.7
Rgs16	U72881	-95.66	-2.67	-2.81	12.77	334.8	3.5	119.2	44.7
Rgs16	U94828	-340	-5.53	-1.69	36.33	408	1.2	241.3	43.6

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)

Song G et al/SHP in Adipogenesis

Supplemental Table 9 Transport

Common	GenBank	G2/G0	S2/S0	S0/G0	S2/G2	G0	G2	S0	S2
Ralgds	NM_00905	2.35	1.29	-1.22	-2.21	440.6	1034	362.3	467.8
Lman2	AK004952	2.43	-1.21	1.3	-2.25	286.6	696.1	373.3	309.7
Slc25a20	AV008091	2.44	-1.08	1.02	-2.59	233.6	568.9	237.8	219.4
Fabp5	BC002008	3.09	-1.1	1.6	-2.12	2401.7	7425.2	3841.2	3496.5
	AK011116	3.22	-2.26	2.46	-2.96	25.4	81.7	62.4	27.6
Ucp2	BC012697	3.31	1.38	-1.48	-3.56	682.6	2257.4	459.9	634.6
Pctp	AF114437	4.69	1.23	1.14	-3.35	28.6	134.2	32.6	40.1
Syt13	BE648447	4.82	1.3	-1.82	-6.72	27.6	133.1	15.2	19.8
Cd36	BB534670	4.9	-1.46	-1.06	-7.56	10.5	51.4	9.9	6.8
Slc2a4	AB008453	5.22	-4.86	4.29	-5.91	10.3	53.8	44.2	9.1
Grin2b	NM_00817	6.66	1.19	-1.25	-7.01	8	53.3	6.4	7.6
Kcnk4	NM_00843	9.57	-1.45	1.74	-8.01	7.2	68.9	12.5	8.6
Syt12	NM_13416	10.01	1.44	2.15	-3.24	10.2	102.1	21.9	31.5
Slc31a2	NM_02528	-2.11	-1.89	1.89	2.11	278.3	131.7	524.8	278.1
Snx10	AK010399	-2.17	1.15	1.17	2.93	707.3	325.6	828.9	953.6
Ap2a2; L2f	AK009735	-2.36	3.51	-2.64	3.14	187.1	79.2	71	249
Kcnk2	NM_01060	-2.5	-1.16	1.11	2.38	147.1	58.8	162.8	140.2
Psmb9	AW048052	-2.64	1.05	-1.06	2.59	445.7	169	418.9	438
Abca8b	AF213393	-2.78	1.35	-1.05	3.58	97.5	35.1	93	125.5
Srcasm	BC004710	-3.56	4.04	-7.17	2.01	64.5	18.1	9	36.4
Aqp3	AF104416	-4.26	-1.6	1.6	4.25	90.7	21.3	144.8	90.6
Kif17	AW492270	-4.29	-1.27	-1.17	2.9	50.6	11.8	43.4	34.2
Lcn2	X14607	-4.5	2.09	-1.12	8.37	12179.3	2705.5	10862.2	22650
Slc20a1	BB465699	-4.82	15.37	-24.87	2.98	728.6	151.1	29.3	450.4
Apoa2	NM_01347	-5.05	-1.18	-1.11	3.86	51.5	10.2	46.5	39.4
P2rx4	AJ251462	-5.93	-2.34	-1.04	2.43	1484.1	250.3	1422	607.9
Slc20a1	NM_01574	-6.09	-1.3	-1.72	2.73	1175.9	193	682.7	526.2
Syng1	NM_00930	-7.39	-1.92	-1.22	3.16	58.4	7.9	47.9	25
P2rx3	BC023089	-8.57	-1.9	-1.09	4.15	264.9	30.9	244	128.1
	BB332449	-13.81	1.63	-1.42	15.83	12395.7	897.8	8710.9	14210.2
Cp	BB009037	-19.51	1.3	1.05	26.65	3979	203.9	4171.4	5433.9
Slc15a2	BC018335	-32.55	-9.28	1.01	3.53	179	5.5	180	19.4
Abcb1a	AY029778	-129.18	-21.31	1.24	7.49	710.5	5.5	878	41.2
Abcb1a	NM_05409	-374.95	-16.47	1.23	27.93	1499.8	4	1839.9	111.7

(top: G2/G0>2, S2/G2<2; bottom: G2/G0<2, S2/G2>2)