Supplement Information

Supplementary Figure 1. The smooth muscle phenotype of cultured cells was confirmed (>97% purity) by immunohistochemistry with antibodies against smooth muscle α-actin.

Supplementary Figure 2. Box plot of RMA normalized data

Supplementary Table 1. **All differentially expression genes in HPAH (A) and IPAH (B) compared with Control HPASMC.** The selection procedure was describe in the material and methods. The table was generated by R program. The table shows the entrez gene ID, gene symbol, gene description, the absolute expression level of all nine samples, the fold change of the HPAH and IPAH expression compared with CONTROL, and p-values of the expression changes.

Supplementary Table 2. The 227 genes that expressed differently in HPAH and IPAH HPASMC compared with Normal cells. The table showed the entrez gene ID, gene symbol, the fold change of mRNA expression in HPAH and IPAH samples compared with normal HPASMC, and the normalized expression value of control, HPAH and IPAH samples.

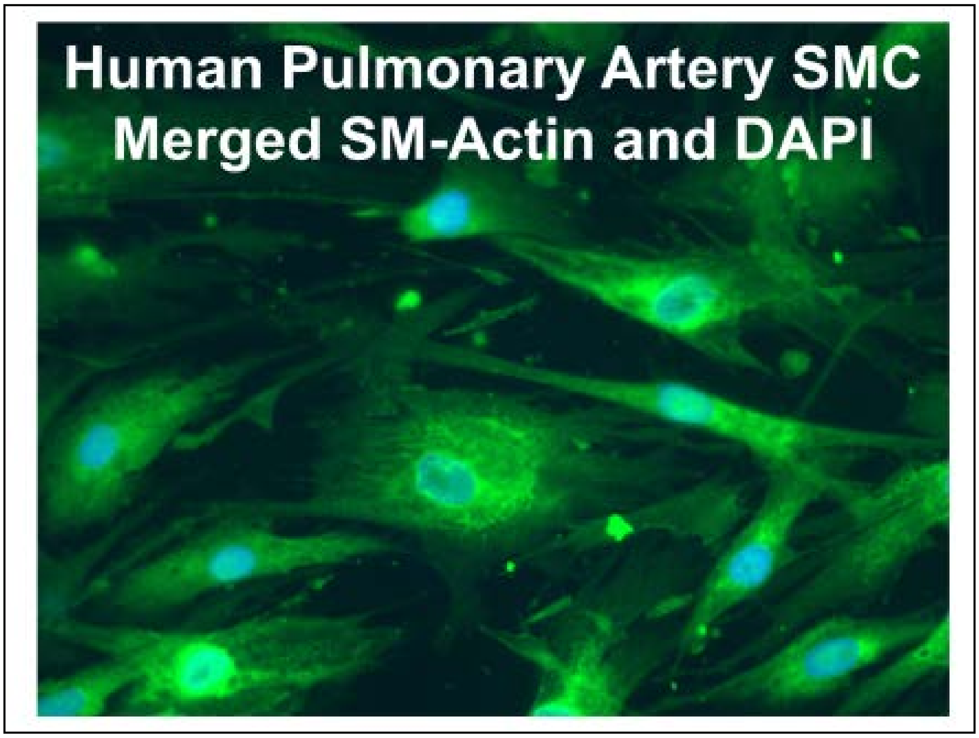
Supplementary Table 3. Biological functions and diseases predicted by Ingenuity Pathway Analysis based on the differentially expressed genes in HPAH and IPAH vs control. The Biological Functional Analysis™ identified the biological functions and/or diseases that were most significant to the data set. The 227 selected genes in table 1 were associated with a biological function in the Ingenuity knowledge base were considered for analysis. Fischer's exact test was used to calculate a p-value determining the probability that each biological function and/or disease assigned to that data set is due to chance alone. The molecules involved in those biological functions were also listed in the table. The molecules involved in those biological functions were also listed in the table. The identity of those molecules can be retrieved from **Supplementary Table 2**.

Supplementary Table 4. **Canonical signal transduction pathways predicted by Ingenuity Pathway Analysis based on the differentially expressed genes in HPAH and IPAH vs control.** Canonical pathways analysis identified the pathways from the Ingenuity Pathways Analysis™ library of canonical pathways that were most significant to the dataset. The 227 selected genes in table 1 were associated with a canonical pathway in the Ingenuity knowledge base were considered for analysis. The significance of the association between the dataset and the canonical pathway was determined as a p-value calculated by Fisher's exact test, a measure of the probability that the association between the proteins in the dataset and the canonical pathway is taking place by chance alone. The ratio is calculated as follows: number of genes in a given pathway that meet the cutoff criteria, divided by the total number of genes that make up that pathway and that are in the reference gene set. The molecules involved in those biological pathways were also listed in the table. The identity of those molecules can be retrieved from **Supplementary Table 2**.

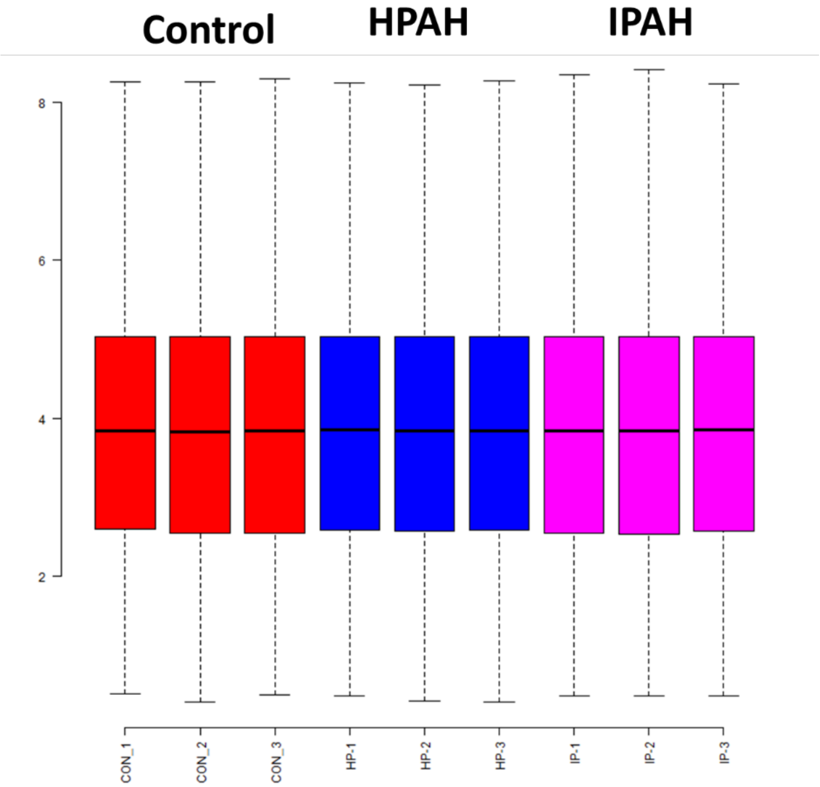
Supplementary Table 5. The list of genes predicted by Ingenuity Pathway Analysis that increase or affect cell proliferation. The identity of those molecules can be retrieved from **Supplementary Table 2**.

Supplementary Table 6. The downstream genes regulated by p53, Rb, FoxM1 and Myc which displayed differentiated expressional changes in HPAH and IPAH samples.

Supplementary Figure 1. The smooth muscle phenotype of cultured cells was confirmed (>97% purity) by immunohistochemistry with antibodies against smooth muscle α-actin.



Supplementary Figure 2. Box plot of RMA normalized data



Supplementary Table 1. **All differentially expression genes in HPAH (A) and IPAH (B) compared with Control HPASMC.** The selection procedure was describe in the material and methods. The table was generated by R program. The table shows the entrez gene ID, gene symbol, gene description, the absolute expression level of all nine samples, the fold change of the HPAH and IPAH expression compared with CONTROL, and p-values of the expression changes.

Supplementary Table 1A.

Entrez ID	symbol	Fold Change	p value	CONTROL-1	CONTROL-2	CONTROL-3	HPAH-1	HPAH-2	HPAH-3
2	A2M	-2.01	1.10E-03	879.90	707.98	886.20	416.93	431.41	380.11
55	ACPP	-2.54	1.16E-03	25.03	33.67	24.71	12.01	10.36	10.52
114	ADCY8	-2.04	2.00E-03	33.19	39.72	37.66	15.71	17.49	20.99
154	ADRB2	2.09	2.18E-04	34.34	35.59	40.81	80.80	74.54	76.00
196	AHR	-1.59	2.01E-04	1377.36	1230.13	1351.21	818.73	838.87	829.20
230	ALDOC	-1.55	7.34E-03	107.46	143.62	122.99	82.42	81.31	76.91
306	ANXA3	2.04	2.31E-04	17.70	17.66	14.89	34.37	34.25	34.11
395	ARHGAP6	-1.68	5.76E-03	108.73	86.26	118.08	62.10	63.53	60.52
414	ARSD	-1.58	1.16E-03	101.00	119.45	111.34	71.78	71.61	66.32
490	ATP2B1	-1.86	4.03E-04	562.04	636.91	627.81	301.05	340.30	340.74
534	ATP6V1G2	-2.35	2.20E-04	92.60	75.32	82.74	36.34	33.53	36.96
624	BDKRB2	-1.61	9.36E-03	237.39	269.06	191.80	143.78	147.05	143.57
627	BDNF	-2.08	1.29E-03	90.29	114.72	101.85	43.64	51.99	52.06
652	BMP4	2.40	3.17E-05	99.53	101.53	88.93	236.87	230.11	230.41
659	BMPR2	-1.75	6.48E-04	757.34	636.74	721.71	381.63	414.56	411.16
684	BST2	1.81	8.07E-03	11.63	13.47	9.43	20.94	23.20	18.45
701	BUB1B	2.01	3.45E-04	28.03	24.33	29.91	56.43	54.28	54.95
920	CD4	-3.18	7.77E-05	59.54	49.91	51.98	15.41	17.62	17.66
978	CDA	-1.54	7.66E-03	52.43	40.75	51.78	32.09	32.25	30.02
983	CDK1	1.98	3.75E-03	25.25	18.50	26.35	48.67	45.73	44.47
991	CDC20	2.72	4.02E-03	81.44	47.78	76.25	200.27	182.50	175.48
1062	CENPE	2.01	1.30E-03	29.50	23.72	31.70	57.00	57.21	56.08
1124	CHN2	1.60	1.52E-03	11.34	12.11	13.68	19.10	19.47	20.89
1138	CHRNA5	1.98	5.26E-03	4.95	6.54	6.25	13.71	11.22	10.15
1240	CMKLR1	2.36	5.74E-03	42.21	28.79	49.58	92.06	101.05	92.02
1306	COL15A1	-3.05	1.63E-03	77.85	54.77	85.92	25.90	23.96	21.88
1364	CLDN4	1.58	6.63E-03	17.45	13.43	17.24	24.36	25.00	26.79
1382	CRABP2	-2.32	5.62E-04	244.75	289.15	243.99	125.73	101.87	107.97
1429	CRYZ	-2.15	1.54E-03	384.26	439.39	342.73	159.61	179.97	202.71
1469	CST1	-4.77	2.44E-04	183.07	125.14	173.28	36.03	31.40	33.48
1512	CTSH	3.57	1.48E-04	23.16	23.51	30.52	94.11	92.30	89.15
1612	DAPK1	3.13	1.55E-04	21.15	19.47	24.19	70.85	71.04	60.65
1734	DIO2	1.73	3.35E-03	30.34	27.65	32.98	49.78	60.23	47.75
1829	DSG2	-5.66	3.97E-06	19.77	22.37	19.10	3.57	3.69	3.56
1831	TSC22D3	1.72	3.38E-04	64.82	69.83	62.66	120.51	106.55	113.22
1832	DSP	1.68	4.59E-03	76.30	63.63	79.87	120.84	135.96	111.46
1903	S1PR3	-1.76	8.36E-04	655.80	566.30	585.29	356.01	359.36	313.69
1910	EDNRB	-7.62	4.90E-04	513.75	796.40	483.84	62.12	81.96	91.48
2047	EPHB1	1.69	2.95E-05	30.46	31.27	31.79	51.72	51.32	54.92
2069	EREG	-6.88	6.81E-04	177.62	133.60	236.07	21.22	26.60	31.71
2078	ERG	8.53	3.40E-03	37.06	12.53	36.89	233.87	262.48	241.19

2123	EVI2A	2.99	1.44E-04	16.17	17.16	16.24	56.93	44.61	46.80
2151	F2RL2	-1.93	8.46E-04	1226.97	980.01	1174.37	558.76	607.44	582.01
2167	FABP4	-4.56	7.90E-03	35.44	14.11	29.28	6.64	4.82	5.81
2304	FOXE1	-2.69	2.54E-03	95.74	60.16	88.12	30.39	29.13	31.10
2487	FRZB	-1.59	9.18E-03	25.32	24.16	30.61	17.26	14.66	18.34
2539	G6PD	-1.51	6.64E-03	572.08	732.76	587.06	419.05	417.25	415.75
2596	GAP43	-1.54	5.93E-04	45.62	50.10	49.37	32.72	29.42	32.10
2635	GBP3	-1.84	1.25E-03	164.63	130.03	149.86	78.61	85.40	77.99
2662	GDF10	1.53	6.03E-03	53.50	42.03	52.91	78.19	75.80	73.08
2791	GNG11	-1.72	8.59E-04	776.26	893.35	752.65	472.84	443.05	490.29
2846	LPAR4	2.01	1.35E-03	21.48	17.83	22.54	44.48	42.35	37.44
2852	GPER	1.55	6.16E-03	76.29	99.86	91.24	145.71	135.96	132.69
2898	GRIK2	-1.87	1.28E-03	140.39	172.19	134.58	81.48	78.81	78.55
2919	CXCL1	-2.48	6.66E-03	129.09	210.43	171.91	56.56	79.77	70.09
2920	CXCL2	-1.69	1.90E-03	29.92	25.87	24.90	14.52	16.25	16.91
2925	GRPR	2.86	3.23E-03	29.34	20.55	34.55	84.02	87.65	69.46
2944	GSTM1	-8.90	7.25E-04	290.76	284.42	288.87	21.01	28.39	47.73
2949	GSTM5	-1.84	4.36E-03	188.17	252.94	188.73	120.79	107.69	113.51
2983	GUCY1B3	-1.96	8.58E-03	92.03	100.65	84.29	50.56	55.14	35.64
3018	HIST1H2BB	1.52	5.05E-03	18.57	16.12	20.80	27.60	28.94	27.55
3082	HGF	-3.80	1.01E-03	512.35	819.97	528.70	159.46	168.61	161.80
3107	HLA-C	-1.59	4.48E-04	1119.40	1256.62	1100.38	738.10	739.96	712.90
3108	HLA-DMA	-1.81	4.73E-05	166.84	176.63	178.90	100.72	94.70	93.43
3113	HLA-DPA1	-6.72	5.71E-05	108.87	121.69	103.19	18.08	13.56	17.99
3161	HMMR	2.54	3.22E-03	11.97	9.11	15.38	30.90	30.80	30.84
3224	HOXC8	1.52	9.28E-05	33.59	32.98	31.01	49.94	48.37	49.94
3357	HTR2B	1.94	9.61E-04	27.50	22.55	27.07	50.04	53.25	46.06
3384	ICAM2	2.00	5.15E-05	24.61	22.81	24.13	45.01	47.99	49.88
3397	ID1	2.67	3.54E-03	147.20	91.89	147.63	367.64	317.50	348.66
3398	ID2	2.76	2.73E-05	297.83	322.10	291.86	901.45	801.93	817.21
3399	ID3	3.34	8.84E-04	58.31	92.13	73.61	260.31	230.92	256.90
3455	IFNAR2	-1.69	1.14E-03	73.27	85.65	72.27	47.55	42.74	46.18
3484	IGFBP1	1.55	2.36E-03	41.55	35.62	36.89	53.97	60.44	62.30
3554	IL1R1	-1.50	3.48E-04	651.19	634.32	658.40	406.25	428.06	457.64
3566	IL4R	-1.72	1.85E-03	217.78	268.08	247.86	130.10	147.77	147.96
3627	CXCL10	-2.28	6.46E-05	6.39	7.38	7.21	3.12	2.97	3.12
3671	ISLR	2.57	5.16E-06	215.15	221.33	208.23	577.31	534.54	547.05
3672	ITGA1	-2.91	1.12E-05	169.36	172.77	176.12	58.74	63.51	55.71
3775	KCNK1	1.55	8.82E-04	34.22	36.97	39.03	54.07	56.93	60.35
3778	KCNMA1	2.08	4.58E-04	145.88	180.85	149.67	332.31	319.33	337.16
3832	KIF11	2.02	5.95E-03	50.41	33.77	50.68	92.54	90.63	89.10
3880	KRT19	2.65	9.07E-03	84.90	45.81	89.27	198.04	192.51	192.39
3897	L1CAM	-1.56	7.30E-05	19.37	18.04	19.59	11.98	12.23	12.22
3918	LAMC2	2.74	1.11E-04	15.14	17.46	14.49	46.23	41.64	41.38
3949	LDLR	-1.54	5.09E-03	520.54	445.23	552.10	302.83	348.19	336.59
3959	LGALS3BP	-1.58	3.39E-04	337.88	368.35	340.87	232.85	219.35	210.44
3976	LIF	-1.63	8.44E-03	86.14	87.97	107.49	49.73	61.64	61.72
4064	CD180	10.04	1.53E-05	3.74	5.14	4.59	44.99	45.14	45.19
4065	LY75	2.04	3.56E-04	4.05	3.73	4.41	8.11	8.95	7.80
4155	MBP	-1.58	7.41E-03	25.15	20.12	20.11	14.90	12.53	14.04
4217	MAP3K5	-1.55	1.54E-03	194.64	226.09	208.12	135.98	142.90	125.60
4239	MFAP4	-2.30	3.96E-03	478.62	693.82	449.87	242.32	234.68	228.71
4241	MFI2	4.10	8.41E-06	38.67	39.45	35.56	147.88	166.78	151.45

4605	MYBL2	1.64	1.12E-03	46.39	42.81	52.22	79.40	75.88	76.40
4629	MYH11	2.20	8.65E-03	27.62	17.91	27.03	55.65	59.44	44.38
4675	NAP1L3	1.77	1.89E-04	32.13	35.19	34.94	59.59	57.33	63.90
4751	NEK2	1.80	7.97E-04	33.47	26.99	31.27	56.02	53.94	54.70
4756	NEO1	-1.62	1.07E-04	320.55	331.98	310.51	198.04	206.84	189.72
4826	NNAT	1.53	1.44E-03	36.33	32.69	39.34	55.94	54.17	55.47
4857	NOVA1	-1.59	7.47E-04	58.11	52.84	56.32	37.33	35.29	32.34
4884	NPTX1	-2.43	4.35E-03	392.77	292.83	441.67	155.59	130.57	177.85
4897	NRCAM	3.54	3.31E-03	19.72	11.95	21.82	58.30	74.50	56.53
4920	ROR2	1.83	1.60E-04	76.84	68.25	75.23	140.35	134.14	128.96
4923	NTSR1	-3.41	5.01E-04	55.41	44.07	56.70	14.88	13.12	17.77
4940	OAS3	1.82	4.34E-04	21.89	18.39	19.90	38.32	36.21	35.17
4958	OMD	5.69	2.47E-04	7.33	4.94	7.49	34.43	39.91	38.04
5026	P2RX5	2.24	9.13E-04	54.50	44.34	58.36	127.07	114.36	111.06
5064	PALM	2.28	4.59E-04	68.16	52.93	62.93	133.06	141.48	144.42
5080	PAX6	1.60	2.05E-03	12.14	10.68	11.55	16.44	19.34	19.37
5126	PCSK2	-8.09	1.71E-04	168.02	119.13	151.97	20.26	14.17	19.82
5154	PDGFA	1.81	1.27E-03	40.12	33.66	38.59	63.65	74.88	65.18
5163	PDK1	-1.51	8.28E-04	545.56	479.09	519.52	339.47	326.74	356.42
5179	PENK	2.66	3.07E-05	142.31	125.74	139.77	363.04	377.09	344.37
5265	SERPINA1	1.73	2.06E-03	9.35	10.84	8.68	15.65	17.97	16.24
5318	PKP2	3.58	1.00E-05	13.47	11.65	12.82	46.02	43.69	45.99
5347	PLK1	2.52	5.73E-03	77.47	47.32	81.89	182.76	169.70	167.76
5352	PLOD2	-1.58	1.83E-03	462.52	378.35	443.15	268.93	267.08	276.08
5383	PMS2L5	1.82	2.54E-04	98.19	103.25	110.73	196.61	176.95	195.82
5519	PPP2R1B	-1.68	4.67E-04	444.20	397.53	426.82	234.43	257.55	265.02
5602	MAPK10	-1.58	3.09E-03	173.51	190.61	173.27	112.56	126.13	100.59
5603	MAPK13	1.84	1.40E-05	30.12	28.32	28.93	53.28	52.30	55.17
5669	PSG1	7.48	2.76E-03	71.01	24.10	50.81	375.16	357.74	358.12
5738	PTGFRN	-1.80	1.75E-03	102.38	81.68	99.08	53.81	54.57	48.82
5764	PTN	-2.09	2.81E-03	118.55	86.88	121.00	49.20	53.32	53.76
5798	PTPRN	-1.51	2.16E-03	44.56	45.14	53.31	31.67	31.85	31.45
5874	RAB27B	-2.01	8.08E-03	40.45	61.01	40.94	24.01	22.15	24.71
5924	RASGRF2	-1.55	3.93E-03	123.62	153.79	125.06	86.31	88.90	84.43
5999	RGS4	1.74	7.49E-03	368.05	264.75	365.26	596.71	597.13	543.69
6000	RGS7	-2.53	1.79E-04	16.90	13.80	16.40	6.42	6.35	5.87
6091	ROBO1	-1.82	3.79E-03	303.49	405.28	308.31	186.21	195.04	177.39
6092	ROBO2	-2.15	7.63E-05	37.15	33.60	35.61	16.60	17.45	15.44
6275	S100A4	-1.50	4.28E-04	384.75	397.71	434.77	274.89	265.36	269.35
6354	CCL7	-1.56	3.98E-03	32.73	31.59	29.90	19.66	22.79	17.86
6364	CCL20	-2.53	9.66E-04	10.75	10.20	13.67	4.40	5.08	4.23
6387	CXCL12	-1.65	5.42E-03	181.42	133.32	161.93	97.04	96.52	95.15
6423	SFRP2	6.82	4.99E-06	11.28	13.15	11.42	81.67	77.12	85.80
6474	SHOX2	-1.89	2.11E-03	38.98	30.01	37.80	19.35	17.62	19.59
6480	ST6GAL1	2.16	4.47E-04	55.77	46.77	55.02	120.83	115.41	103.64
6513	SLC2A1	-1.65	2.49E-05	646.52	642.79	636.43	405.55	382.75	376.89
6542	SLC7A2	2.77	3.15E-03	15.11	19.60	18.56	40.64	63.31	43.70
6649	SOD3	-1.77	4.10E-03	262.53	205.82	250.90	151.23	132.77	123.02
6712	SPTBN2	1.54	3.52E-04	26.07	23.82	23.81	38.76	38.68	36.07
6751	SSTR1	-1.75	6.64E-03	162.38	224.68	188.84	99.39	111.49	118.35
6857	SYT1	-2.03	3.14E-03	99.22	77.09	111.31	47.47	45.63	48.41
6907	TBL1X	-1.62	6.63E-04	136.12	139.52	143.60	78.53	91.61	89.41
6941	TCF19	1.57	3.56E-03	36.24	42.89	44.06	69.87	61.15	62.44

6943	TCF21	-1.56	7.68E-03	1028.50	1364.56	1119.79	710.64	783.75	755.49
7042	TGFB2	1.71	1.26E-04	121.98	136.09	128.15	216.73	215.08	228.02
7043	TGFB3	1.95	8.70E-04	70.27	64.33	82.99	139.08	144.69	141.07
7049	TGFBR3	-1.56	2.01E-04	596.95	547.89	555.80	349.66	366.33	376.04
7100	TLR5	1.59	9.22E-03	10.50	9.85	8.53	17.69	14.31	13.90
7127	TNFAIP2	-1.69	8.06E-03	76.19	106.23	79.98	53.19	50.34	51.81
7130	TNFAIP6	-2.08	6.10E-04	507.88	590.67	469.50	236.23	263.28	253.82
7223	TRPC4	-3.56	6.01E-04	60.41	86.01	69.63	20.46	22.82	17.47
7272	TTK	1.91	9.84E-04	20.00	17.58	22.63	37.06	38.31	39.47
7292	TNFSF4	-1.60	1.95E-03	20.09	20.32	19.55	14.02	12.26	11.23
7357	UGCG	-1.78	1.90E-04	224.49	250.47	226.61	133.46	135.89	124.74
7421	VDR	1.84	1.21E-03	78.87	63.61	77.96	138.92	138.00	127.93
7422	VEGFA	-1.51	2.38E-03	292.27	320.72	274.03	180.92	197.98	207.04
7447	VSNL1	1.70	2.90E-03	9.34	7.96	8.12	13.03	16.25	14.04
7472	WNT2	2.29	2.25E-03	11.50	13.91	11.41	33.37	23.70	27.31
7543	ZFX	-1.57	1.07E-03	171.27	202.36	175.93	115.07	116.71	119.15
7980	TFPI2	-3.40	7.02E-04	682.46	894.80	715.96	186.85	223.03	263.94
8029	CUBN	-1.76	4.66E-05	18.58	19.99	18.50	10.53	10.76	11.14
8226	HDHD1	-1.82	1.55E-04	236.72	234.14	252.33	125.09	131.40	141.62
8228	PNPLA4	-1.54	5.16E-04	130.13	124.14	119.93	79.28	77.05	86.59
8233	ZRSR2	-1.54	6.81E-03	77.84	69.30	65.58	50.82	46.87	40.31
8332	HIST1H2AL	1.71	4.51E-04	47.14	41.99	48.23	82.03	74.69	78.01
8344	HIST1H2BE	1.51	1.62E-03	45.35	47.69	50.01	76.85	65.75	73.11
8345	HIST1H2BH	1.87	5.79E-04	186.34	163.43	185.42	355.25	304.36	340.26
8354	HIST1H3I	1.67	1.88E-04	443.54	435.00	477.52	793.36	731.14	736.08
8357	HIST1H3H	1.77	2.53E-03	167.02	134.93	178.97	287.54	276.60	288.72
8359	HIST1H4A	1.53	5.61E-03	24.38	18.66	21.94	33.47	33.92	32.06
8364	HIST1H4C	1.81	8.69E-04	349.05	412.81	432.48	706.68	746.03	714.47
8406	SRPX	-1.92	7.52E-04	1163.92	941.95	1078.88	588.04	526.41	546.26
8418	CMAH	1.74	1.29E-03	20.42	17.67	22.15	36.27	35.03	33.70
8507	ENC1	-2.23	2.14E-04	84.10	80.74	88.57	33.77	39.67	40.35
8532	CPZ	2.09	1.88E-05	43.17	44.91	47.82	93.30	94.76	96.26
8544	PIR	-3.99	5.05E-05	66.79	81.29	66.58	16.78	18.09	18.92
8612	PPAP2C	-1.84	5.59E-03	207.65	286.03	209.71	125.51	135.81	121.88
8641	PCDHGB4	-1.76	2.72E-04	385.26	440.45	404.77	245.12	225.31	229.35
8673	VAMP8	-1.97	1.01E-03	54.12	51.84	62.14	31.81	26.86	26.82
8788	DLK1	6.97	1.03E-06	32.41	30.37	28.40	211.33	208.35	215.94
8825	LIN7A	-1.64	1.40E-03	53.69	52.32	59.84	31.61	36.90	32.49
8838	WISP3	2.66	8.05E-05	12.00	12.82	10.61	32.86	31.00	30.52
8844	KSR1	-1.59	6.41E-04	121.31	108.34	126.86	74.42	73.29	75.92
8969	HIST1H2AG	1.84	2.68E-03	340.10	277.08	371.17	646.96	585.18	585.92
8988	HSPB3	-1.74	4.15E-03	15.74	18.42	17.61	8.38	10.95	10.45
9021	SOCS3	-1.60	1.59E-03	67.64	76.98	62.49	43.30	42.52	43.56
9079	LDB2	-1.78	4.75E-04	399.61	346.11	398.53	215.04	224.17	203.52
9096	TBX18	-1.60	4.83E-04	196.60	214.89	198.47	134.51	127.91	119.12
9122	SLC16A4	-1.60	9.15E-04	193.86	176.54	194.57	121.69	123.52	107.86
9133	CCNB2	1.99	9.20E-03	63.26	42.65	68.96	121.44	113.15	112.78
9134	CCNE2	1.68	4.13E-03	48.59	59.23	61.13	91.38	88.15	104.43
9194	SLC16A7	-1.64	2.80E-04	244.26	270.88	269.38	159.27	166.40	153.19
9227	LRAT	2.76	4.88E-03	7.32	5.48	6.72	13.33	17.80	22.82
9368	SLC9A3R1	1.58	1.32E-03	212.89	174.85	198.17	308.21	307.18	310.57
9455	HOMER2	1.55	7.13E-04	16.26	16.74	18.42	25.86	28.06	25.81
9493	KIF23	1.58	4.07E-04	106.26	102.36	117.28	168.01	171.23	174.47

9518	GDF15	-1.98	3.31E-04	246.09	285.31	282.49	133.82	130.33	146.61
9536	PTGES	-1.62	4.81E-03	161.05	160.48	128.01	87.70	91.54	99.10
9568	GABBR2	2.12	5.06E-03	321.87	220.13	341.05	611.76	637.30	622.60
9585	KIF20B	1.85	5.39E-03	18.16	14.23	20.89	32.47	34.20	31.83
9674	KIAA0040	4.59	1.51E-04	10.26	13.49	11.71	46.82	55.57	60.38
9732	DOCK4	-1.72	6.22E-04	181.63	172.41	197.45	99.41	113.81	107.47
9770	RASSF2	1.61	1.10E-03	105.74	118.75	97.65	170.87	173.48	174.74
9829	DNAJC6	-1.58	6.09E-03	37.94	50.65	42.52	27.08	28.44	27.31
9837	GINS1	1.59	4.14E-03	43.43	38.83	50.11	68.77	67.25	73.79
9890	LPPR4	-6.70	3.04E-03	193.72	83.52	190.48	24.90	24.85	20.09
9906	SLC35E2	-1.99	2.96E-03	237.62	288.39	241.54	151.49	120.13	113.92
9934	P2RY14	2.24	3.27E-03	8.77	8.76	11.56	18.58	21.34	25.35
9953	HS3ST3B1	-2.53	5.08E-03	172.52	285.83	188.29	79.13	84.36	92.46
10076	PTPRU	2.38	8.33E-04	32.87	39.85	28.60	80.12	82.71	78.77
10216	PRG4	2.06	1.64E-07	9.25	9.32	9.28	18.80	19.25	19.37
10324	KBTBD10	2.17	7.67E-03	15.84	25.29	21.63	38.57	48.80	49.10
10350	ABCA9	-1.53	1.98E-04	28.24	30.01	30.03	20.25	18.78	18.77
10403	NDC80	1.87	6.13E-03	28.07	19.75	28.71	47.82	47.66	47.72
10439	OLFM1	1.70	5.20E-04	67.20	60.09	68.25	103.71	115.87	111.93
10460	TACC3	1.72	1.25E-03	25.71	23.47	28.63	47.35	41.92	44.91
10630	PDPN	2.78	4.19E-04	132.67	97.17	119.57	340.53	320.91	310.26
10635	RAD51AP1	1.58	2.04E-04	19.72	20.54	21.54	33.47	30.95	33.02
10733	PLK4	1.61	5.01E-04	29.70	28.04	32.59	49.24	47.00	49.14
10982	MAPRE2	1.59	5.54E-05	436.68	419.21	417.27	678.66	699.23	649.67
11033	ADAP1	1.64	7.38E-03	21.81	16.68	21.98	35.46	30.66	33.12
11075	STMN2	-5.10	6.27E-04	1572.29	929.85	1464.56	253.31	263.28	261.40
11080	DNAJB4	1.58	6.09E-03	409.15	521.82	459.86	661.23	781.72	751.08
11096	ADAMTS5	-1.68	3.55E-04	181.73	201.49	185.75	118.51	114.03	105.57
11112	HIBADH	-1.54	4.57E-03	424.21	333.64	382.07	256.73	233.34	248.42
11118	BTN3A2	-2.08	2.18E-03	58.93	47.24	50.85	29.31	23.78	22.29
11170	FAM107A	1.59	4.07E-04	58.32	53.11	54.16	86.92	83.24	92.80
11185	INMT	-1.70	6.52E-04	150.73	179.41	175.79	99.22	98.89	99.01
11199	ANXA10	2.90	7.84E-03	8.15	16.45	9.55	35.44	28.51	35.01
11320	MGAT4A	1.72	4.31E-03	4.85	5.79	5.30	9.58	10.05	7.81
22795	NID2	-1.63	2.10E-04	522.06	512.69	478.97	320.14	314.95	292.68
22837	COBLL1	2.08	4.47E-04	94.76	82.66	101.82	181.41	202.06	196.15
22854	NTNG1	2.17	7.41E-05	63.38	61.49	71.36	143.74	139.65	141.59
22875	ENPP4	1.50	2.79E-03	27.94	23.87	26.90	36.84	39.09	42.30
22881	ANKRD6	1.58	4.39E-03	45.36	40.32	49.38	63.87	75.68	73.36
23017	FAIM2	-2.57	3.65E-04	92.05	115.61	104.37	44.25	40.13	36.86
23043	TNIK	1.54	2.86E-03	113.76	97.46	120.27	175.78	170.22	163.31
23136	EPB41L3	-3.78	5.72E-04	178.20	131.28	197.09	45.33	40.44	48.16
23150	FRMD4B	2.84	2.77E-03	21.03	13.72	22.83	55.20	50.77	57.81
23231	SEL1L3	-2.14	4.24E-03	186.18	269.36	182.78	101.51	99.40	98.03
23255	KIAA0802	-1.62	1.47E-05	79.37	82.62	79.88	50.91	49.86	48.41
23397	NCAPH	1.98	3.62E-05	33.69	34.38	32.84	70.54	65.45	63.52
23446	SLC44A1	-1.55	1.88E-03	326.76	377.39	311.23	214.61	224.54	216.62
23460	ABCA6	-2.09	9.09E-03	71.77	111.22	70.56	41.27	41.58	38.62
23554	TSPAN12	-2.79	3.87E-03	23.01	37.26	22.54	10.35	9.87	9.44
23566	LPAR3	-2.49	6.73E-03	32.69	48.29	30.10	16.84	12.25	15.56
23596	OPN3	-1.59	1.08E-04	80.13	83.86	80.61	50.05	53.94	49.47
23671	TMEFF2	-1.83	5.02E-03	21.06	19.20	22.57	10.58	13.76	9.96
23705	CADM1	1.84	6.46E-04	72.81	59.67	70.04	128.50	120.71	123.55

23743	BHMT2	-1.52	5.16E-03	70.07	70.61	68.55	52.86	44.01	41.01
23767	FLRT3	-4.03	4.75E-03	504.32	240.85	428.22	83.25	97.55	110.31
23768	FLRT2	-2.57	6.22E-05	384.61	340.92	392.32	136.64	152.16	145.71
25758	C11orf41	2.81	3.39E-03	23.39	17.47	30.95	73.01	64.53	64.52
25791	NGEF	1.62	7.55E-05	23.60	21.97	22.44	37.43	35.36	37.61
25878	MXRA5	-1.81	2.07E-03	194.87	232.52	180.14	114.24	116.52	104.00
25903	OLFML2B	1.76	2.10E-03	57.20	71.46	60.01	120.42	104.34	107.74
25924	MYRIP	1.90	5.44E-03	20.42	14.07	18.63	30.96	34.48	35.26
25945	PVRL3	-1.54	5.41E-03	435.63	545.64	456.11	289.23	322.21	323.58
25984	KRT23	1.65	1.55E-03	15.04	13.09	15.32	22.15	23.89	25.66
26011	ODZ4	-1.60	1.96E-04	60.01	67.21	63.05	40.67	38.69	39.32
26018	LRIG1	-1.67	8.98E-03	200.13	267.05	200.09	123.65	144.81	130.42
26025	PCDHGA12	-2.39	1.48E-04	106.54	117.74	103.14	49.98	44.46	42.67
27063	ANKRD1	3.49	2.69E-03	28.19	16.51	29.99	90.42	89.69	80.29
27254	CSDC2	-1.54	6.91E-04	103.60	106.43	96.47	68.50	68.80	61.84
27286	SRPX2	-1.66	2.03E-03	281.22	293.75	276.85	195.86	158.87	159.57
28638	TRBC2	3.51	1.27E-03	16.66	10.92	13.52	56.04	40.09	48.01
28755	TRAC	1.53	3.19E-03	8.45	7.49	9.38	13.16	12.41	13.05
29089	UBE2T	1.52	2.49E-03	61.95	65.53	75.21	106.08	97.99	104.29
29128	UHRF1	1.59	1.58E-03	70.42	78.35	85.72	128.41	119.11	124.76
29798	C2orf27A	-2.32	5.63E-04	71.00	76.62	76.82	34.31	35.09	27.25
29906	ST8SIA5	1.59	3.40E-04	40.57	38.67	42.64	64.15	61.51	68.06
29922	NME7	-1.55	1.15E-03	33.38	37.46	36.70	21.80	24.89	22.84
29941	PKN3	1.56	1.65E-04	28.82	30.45	29.91	48.91	44.65	45.41
29953	TRHDE	-2.83	1.40E-04	122.28	101.23	123.13	40.45	43.36	38.49
51200	CPA4	2.57	5.88E-03	165.89	97.27	169.34	365.04	377.40	367.26
51299	NRN1	1.74	6.52E-04	11.81	12.36	13.65	20.79	23.58	21.36
51384	WNT16	-2.72	3.22E-04	137.75	134.17	169.91	50.34	58.43	53.91
51514	DTL	1.59	5.52E-03	92.88	115.84	98.41	177.84	147.89	161.27
51703	ACSL5	1.77	4.11E-03	29.48	23.70	32.32	47.86	53.64	49.86
51752	ERAP1	-1.54	4.14E-03	138.10	116.91	138.82	89.80	88.18	77.38
51816	CECR1	2.02	3.20E-03	13.52	16.77	11.35	27.77	27.86	28.37
54443	ANLN	2.36	8.74E-03	148.25	94.52	176.18	333.89	322.44	330.74
54541	DDIT4	-2.02	4.54E-03	69.82	47.12	55.14	30.32	28.17	26.51
54674	LRRN3	-2.71	5.06E-05	544.23	606.03	548.79	198.36	226.77	202.80
54733	SLC35F2	2.10	1.06E-03	22.20	29.47	28.18	55.81	56.92	54.99
54757	FAM20A	-2.79	1.09E-03	86.61	129.68	99.96	38.75	38.55	36.23
54852	PAQR5	-1.60	8.57E-03	239.60	196.20	268.33	138.23	154.16	146.31
54861	SNRK	1.64	6.75E-03	222.93	216.18	216.45	295.49	382.12	400.25
54874	FNBP1L	1.82	5.87E-03	66.12	58.20	83.43	125.40	136.21	117.25
54960	GEMIN8	-1.61	3.85E-04	101.07	95.65	89.92	61.00	60.60	56.05
54970	TTC12	-1.55	2.94E-03	38.15	46.30	38.57	26.12	25.61	27.72
54986	ULK4	1.89	7.25E-05	23.58	24.30	24.65	44.20	44.10	49.11
55022	PID1	-1.81	6.55E-04	200.52	233.89	209.07	114.19	113.40	128.61
55062	WIPI1	-1.54	6.81E-04	1083.18	1207.44	1039.34	713.90	722.64	727.99
55117	SLC6A15	-6.96	1.91E-03	84.43	185.91	90.02	17.02	15.84	18.90
55166	CENPQ	1.95	3.05E-03	27.15	37.40	30.43	58.67	58.58	67.53
55215	FANCI	1.52	3.42E-04	65.67	59.36	66.79	98.16	96.99	96.77
55240	STEAP3	-1.51	2.21E-03	234.39	265.73	223.12	162.65	150.46	164.53
55258	THNSL2	-2.08	2.12E-04	62.74	71.10	70.01	31.00	31.69	35.42
55276	PGM2	1.90	2.25E-03	218.01	164.48	215.10	365.69	390.23	381.77
55351	STK32B	-1.60	2.14E-03	49.10	43.51	53.63	28.95	31.30	31.34
55355	HJURP	1.53	5.00E-03	66.56	52.10	63.98	96.12	91.22	92.92

55388	MCM10	1.56	3.84E-03	33.32	40.43	39.04	61.52	53.63	61.16
55504	TNFRSF19	-1.73	3.17E-05	152.61	142.28	153.33	87.26	87.25	84.56
55540	IL17RB	1.83	2.87E-03	27.41	37.39	33.71	58.88	63.12	58.65
55691	FRMD4A	-1.53	5.71E-03	58.76	72.63	60.82	38.23	44.10	42.91
55723	ASF1B	1.58	3.70E-03	97.43	97.01	113.59	178.12	148.00	159.31
55790	CSGALNACT1	-1.67	2.67E-04	73.31	81.42	73.78	43.56	45.45	47.59
55816	DOK5	1.91	6.10E-03	179.31	123.40	176.94	300.97	295.36	321.72
55859	BEX1	-3.92	5.96E-05	70.38	58.10	68.22	18.22	16.52	15.38
55930	MYO5C	1.69	4.42E-03	8.53	8.39	6.86	12.52	15.04	12.73
55959	SULF2	2.24	3.45E-04	44.53	44.40	37.33	90.61	102.12	90.00
55971	BAIAP2L1	1.54	7.97E-04	120.71	123.92	121.75	200.54	192.44	171.67
56062	KLHL4	2.05	2.05E-04	4.39	4.80	4.59	9.27	10.30	8.71
56109	PCDHGA6	-1.60	5.13E-03	15.08	19.93	16.34	10.91	10.46	10.66
56112	PCDHGA3	-2.64	2.05E-04	47.22	38.82	46.71	17.42	17.37	15.46
56113	PCDHGA2	-1.53	6.74E-03	43.26	39.75	41.66	25.80	31.54	24.19
56125	PCDHB11	1.55	2.81E-03	17.38	17.40	17.17	29.95	23.81	26.80
56265	CPXM1	1.66	6.20E-03	19.06	21.55	16.05	34.09	29.19	30.69
56477	CCL28	1.63	4.05E-04	57.19	53.37	62.21	95.56	94.00	92.54
56947	MFF	-1.77	3.94E-04	977.73	821.42	888.98	518.29	505.34	497.54
56992	KIF15	1.56	1.00E-02	14.22	10.97	12.97	20.50	17.58	21.44
57057	TBX20	3.70	2.24E-05	8.41	8.78	7.86	32.23	32.35	27.98
57088	PLSCR4	-1.64	2.05E-04	246.37	256.11	248.67	150.72	163.06	143.90
57094	CPA6	-2.34	7.13E-03	41.03	25.47	41.46	16.25	14.92	14.95
57125	PLXDC1	2.77	2.04E-05	44.52	43.70	40.91	128.06	115.01	115.16
57181	SLC39A10	-1.51	7.78E-04	301.46	328.78	327.54	198.83	224.07	212.53
57381	RHOJ	1.72	1.16E-03	125.58	104.48	115.50	213.49	190.33	190.26
57405	SPC25	1.66	3.48E-04	19.05	17.52	20.47	31.50	31.53	31.57
57412	AS3MT	-1.66	5.39E-03	80.82	91.58	70.09	53.43	45.16	47.15
57480	PLEKHG1	-1.69	2.62E-03	19.14	24.63	20.89	13.09	13.08	12.21
57484	RNF150	-2.20	2.84E-04	128.65	131.95	120.21	53.64	64.90	54.83
57575	PCDH10	-1.60	2.75E-04	89.27	87.66	92.08	55.59	59.75	52.67
57580	PREX1	1.84	1.02E-04	24.20	23.57	24.81	47.71	43.77	42.18
57631	LRCH2	-1.68	8.85E-05	80.32	83.41	89.35	49.77	51.10	50.12
57643	ZSWIM5	-1.87	2.72E-03	100.32	85.89	117.06	51.09	56.00	55.06
57648	KIAA1522	1.65	2.01E-04	50.91	57.45	52.17	90.31	86.95	87.78
57717	PCDHB16	-1.95	5.45E-03	119.35	159.84	109.59	70.44	66.85	62.16
60598	KCNK15	1.78	9.74E-04	93.51	85.21	93.80	167.84	174.02	143.83
64093	SMOC1	3.17	2.09E-03	56.25	31.77	44.90	137.50	141.14	142.97
64151	NCAPG	1.87	4.65E-04	65.54	63.02	76.66	129.26	127.34	127.50
64288	ZNF323	-1.63	2.40E-03	16.04	19.06	16.09	10.77	11.02	9.60
64798	DEPDC6	2.07	5.52E-03	17.52	14.91	13.47	33.80	36.02	25.31
64866	CDCP1	1.67	1.69E-03	196.13	238.85	242.89	378.24	373.89	377.47
79056	PRRG4	1.79	2.70E-03	24.82	20.55	27.67	43.50	42.12	44.84
79603	LASS4	1.57	2.28E-04	33.94	32.09	33.40	54.68	49.05	52.03
79682	MLF1IP	1.55	1.87E-03	83.45	68.98	80.29	123.87	117.30	119.21
79772	MCTP1	-1.98	6.21E-04	46.38	54.91	46.12	23.14	24.67	26.60
79781	IQCA1	2.46	5.01E-06	11.64	11.80	11.45	30.00	28.22	27.51
79905	TMC7	1.98	2.04E-04	59.59	54.26	64.88	116.80	120.91	116.56
79966	SCD5	1.60	3.51E-04	121.80	107.19	119.07	189.09	180.74	188.55
79974	C7orf58	-2.15	6.58E-04	405.27	338.39	437.01	178.31	191.45	179.79
80227	PAAF1	-1.55	4.26E-03	61.26	69.89	59.23	44.13	36.72	42.13
80323	CCDC68	-4.00	4.26E-04	116.34	104.55	138.89	24.36	32.10	33.41
80339	PNPLA3	-1.87	3.34E-03	87.09	63.10	79.53	38.90	41.21	42.42

80704	SLC19A3	-1.78	1.02E-03	21.79	18.28	22.40	11.78	12.09	11.27
81493	SYNC	1.58	4.95E-04	189.30	215.03	198.65	316.09	331.83	305.15
81832	NETO1	-3.37	1.71E-03	17.89	26.83	16.93	5.31	6.40	6.59
81849	ST6GALNAC5	-2.10	9.86E-03	34.39	20.85	31.47	14.26	13.82	13.17
83540	NUF2	2.43	2.71E-04	19.72	15.59	19.15	44.10	43.96	44.01
83992	CTTNBP2	-2.26	7.00E-04	50.95	53.64	56.74	26.66	20.24	24.41
84189	SLITRK6	-3.05	6.62E-04	25.59	20.99	19.42	8.44	6.69	6.52
84443	FRMPD3	1.80	6.14E-03	13.34	10.90	15.74	25.94	22.91	23.22
84680	ACCS	-1.50	7.33E-03	36.47	44.24	36.71	28.55	24.06	25.43
84795	PYROXD2	-2.75	3.43E-03	72.15	88.96	58.76	32.27	22.09	25.51
84856	LOC84856	1.60	5.60E-03	64.42	51.15	48.62	89.75	86.38	86.03
84913	ATOH8	2.36	1.90E-04	41.33	35.59	42.66	93.17	99.67	88.88
84952	CGNL1	2.63	4.02E-04	9.29	8.53	8.29	24.66	24.73	19.34
84969	TOX2	1.72	2.54E-03	38.64	38.76	34.37	73.27	58.97	60.02
84978	FRMD5	1.56	5.70E-04	71.54	65.47	72.95	113.85	102.99	110.34
85463	ZC3H12C	-1.52	5.12E-03	145.36	170.77	161.40	93.14	112.18	109.54
85477	SCIN	2.29	2.96E-03	11.67	11.25	12.31	22.01	25.16	33.40
90417	C15orf23	1.51	9.43E-03	135.72	110.12	149.28	199.46	198.52	199.05
91752	ZNF804A	-2.14	4.22E-03	62.72	89.79	75.99	30.45	38.25	38.27
92126	DSEL	-1.71	3.39E-04	919.30	985.23	889.77	571.98	556.10	507.28
92737	DNER	-2.76	3.24E-05	59.29	54.09	60.26	20.36	20.01	22.46
93145	OLFM2	1.57	3.73E-05	324.25	322.89	326.91	528.64	510.81	489.45
114134	SLC2A13	-2.18	3.17E-03	207.37	165.23	239.11	85.95	104.03	90.18
114795	TMEM132B	-2.12	2.23E-04	34.58	33.41	33.89	16.46	14.22	17.30
114899	C1QTNF3	2.94	1.97E-05	9.48	9.91	10.02	29.66	30.26	26.40
114907	FBXO32	2.06	2.15E-03	195.21	224.65	161.81	417.82	415.14	367.19
116093	DIRC1	-2.18	3.33E-03	14.36	18.98	13.85	8.19	6.35	7.09
116159	CYYR1	-2.05	8.73E-05	18.19	18.82	19.04	8.74	8.66	9.89
116496	FAM129A	1.50	3.46E-04	217.33	197.36	210.55	325.40	310.95	301.76
120892	LRRK2	-1.85	1.38E-03	50.74	43.42	55.25	26.60	28.56	25.71
121601	ANO4	-1.96	8.81E-04	135.28	115.75	106.72	61.68	63.25	57.49
122970	ACOT4	1.60	8.79E-03	17.98	14.96	17.45	29.72	22.87	28.06
126820	WDR63	-1.88	3.91E-03	57.04	42.86	56.85	26.51	30.25	26.48
128102	LOC128102	1.82	1.35E-03	9.16	11.23	9.29	18.28	16.73	18.98
128239	IQGAP3	2.09	2.24E-03	32.46	23.89	33.03	64.91	62.02	60.09
129293	C2orf89	-2.19	3.03E-03	84.19	83.22	86.98	47.80	31.19	37.06
130574	LYPD6	-1.53	8.00E-03	17.48	20.41	21.74	11.83	12.59	14.42
130576	LYPD6B	-2.04	3.11E-05	26.69	24.10	24.17	12.18	12.40	12.17
133383	C5orf35	2.04	1.53E-03	12.31	14.42	11.21	25.45	23.40	28.41
137872	ADHFE1	-1.70	6.43E-04	43.58	38.88	40.93	25.82	22.26	24.64
143570	XRRA1	-1.75	1.13E-03	78.66	65.21	76.08	44.37	42.00	39.53
144455	E2F7	1.51	2.10E-03	50.36	53.06	58.34	87.48	77.21	78.82
145781	GCOM1	1.61	8.28E-03	10.30	7.71	10.09	15.69	14.06	15.49
150468	CKAP2L	2.00	5.87E-03	38.28	31.97	50.47	81.85	78.95	81.15
151651	EFHB	-1.74	9.69E-03	8.48	5.97	7.69	4.70	4.07	3.96
157570	ESCO2	2.18	3.35E-03	55.47	36.84	50.68	106.66	98.46	106.02
158866	ZDHHC15	1.77	2.77E-03	12.05	9.01	10.50	19.44	18.44	17.84
161291	TMEM30B	1.86	3.73E-04	63.91	62.50	73.07	122.94	129.48	117.88
200916	RPL22L1	-1.81	2.88E-04	36.62	33.15	33.21	20.10	19.18	17.67
201799	TMEM154	1.56	8.20E-03	69.80	53.41	69.79	100.69	104.48	95.83
219970	GLYATL2	1.63	2.60E-03	29.40	34.45	30.12	51.30	46.11	55.43
220108	FAM124A	1.90	4.95E-04	60.81	73.69	67.95	132.88	121.22	130.07
220134	SKA1	1.80	6.56E-03	25.15	18.96	27.05	44.20	39.44	44.11

220963	SLC16A9	1.64	6.76E-03	8.13	6.10	7.83	12.26	12.70	11.24
221687	RNF182	-1.63	7.72E-04	57.78	64.08	57.06	39.09	36.70	34.29
221955	DAGLB	1.81	3.54E-03	84.01	117.67	98.35	185.39	176.47	182.67
246777	SPESP1	-1.87	1.28E-04	12.61	13.94	12.40	7.11	7.08	6.64
255231	MCOLN2	3.41	3.75E-05	16.74	13.98	16.53	51.73	55.56	53.65
259266	ASPM	2.31	9.73E-03	32.11	19.43	35.62	66.80	67.86	66.52
261729	STEAP2	-1.51	8.44E-05	361.20	345.28	370.13	240.72	241.82	230.58
283120	H19	2.09	1.33E-03	56.97	41.99	52.21	110.45	103.15	103.06
284217	LAMA1	-1.98	4.07E-03	59.87	48.68	67.15	29.45	32.96	26.28
284802	FRG1B	1.65	1.43E-04	155.18	152.80	153.31	238.58	269.21	253.17
286097	EFHA2	-1.52	1.25E-04	59.99	60.11	61.84	37.81	40.94	41.00
286827	TRIM59	1.55	4.32E-03	50.27	46.24	53.84	84.14	80.06	68.79
317772	HIST2H2AB	1.63	7.19E-04	130.25	145.36	152.47	239.91	221.97	234.34
347735	SERINC2	1.53	9.05E-04	713.49	823.45	726.97	1157.16	1119.01	1190.53
348093	RBPMS2	1.71	9.93E-04	45.77	38.71	39.03	74.19	66.78	70.22
353139	LCE2A	3.94	7.08E-04	189.54	249.05	181.43	925.80	653.42	863.59
359821	MRPL42P5	1.98	4.50E-03	25.37	28.43	19.22	47.08	51.18	46.17
374393	FAM111B	2.36	2.25E-04	33.03	37.01	39.89	93.15	84.43	81.50
374969	CCDC23	1.59	4.02E-03	50.12	62.01	48.77	86.50	81.69	88.09
387496	RASL11A	1.50	4.02E-03	50.13	45.45	54.79	80.33	69.46	76.01
389432	SAMD5	-1.55	2.46E-03	21.32	25.54	26.06	15.78	15.46	15.75
392255	GDF6	3.72	1.29E-03	39.35	23.47	37.40	129.80	121.07	121.45
401233	LOC401233	-1.91	4.85E-03	44.72	62.78	58.02	28.93	31.28	26.51
401884	MGC57346	1.86	1.71E-04	160.06	143.78	155.84	303.95	272.36	280.72
440993	LOC440993	-2.05	4.30E-04	42.11	40.32	41.99	19.80	22.80	18.19
619279	ZNF704	1.73	2.92E-03	8.39	7.36	8.37	15.53	13.97	12.13
641371	ACOT1	-1.56	1.44E-03	164.20	176.01	146.16	104.82	101.20	106.44
654342	LOC654342	-1.98	4.07E-04	455.32	393.66	465.67	232.64	207.73	225.21
654433	LOC654433	-1.78	5.36E-04	147.31	138.55	124.81	81.37	73.77	75.04
692087	SNORD49B	-2.50	2.15E-03	12.41	11.65	12.06	4.05	6.14	4.23
100132406	NBPF10	-1.53	9.05E-03	232.20	186.19	246.84	148.79	147.29	139.63
120	ADD3	-1.49	1.81E-03	326.94	273.79	300.80	204.09	205.34	194.36
571	BACH1	-1.24	1.23E-01	84.13	110.90	80.55	76.94	75.74	70.10
694	BTG1	-1.38	1.38E-03	845.74	923.48	821.04	603.33	636.46	641.99
1026	CDKN1A	-1.19	2.57E-03	526.83	552.66	524.95	435.39	441.65	466.02
1033	CDKN3	2.13	2.51E-02	47.83	26.11	55.70	92.84	92.53	91.27
1654	DDX3X	-1.32	2.65E-03	486.23	493.11	492.82	344.43	397.73	373.72
1806	DPYD	-1.32	2.66E-02	299.52	252.44	295.41	223.71	228.14	188.25
2028	ENPEP	-1.66	4.75E-02	10.24	17.57	13.57	8.07	9.50	7.34
2057	EPOR	-1.06	2.48E-02	39.14	38.09	38.40	37.12	35.25	36.50
2104	ESRRG	-1.15	1.63E-01	3.76	4.79	3.85	3.51	3.75	3.50
2700	GJA3	-1.33	3.62E-02	46.96	58.59	43.40	37.33	37.21	37.25
2934	GSN	-1.30	2.13E-03	619.98	595.14	573.47	487.05	443.49	450.16
3575	IL7R	-1.45	4.71E-02	151.98	101.88	136.58	83.95	95.82	90.42
3756	KCNH1	-1.12	4.73E-02	5.89	6.04	6.73	5.50	5.55	5.55
4093	SMAD9	1.64	2.31E-02	108.20	69.70	105.36	152.86	159.13	152.14
4211	MEIS1	-1.45	1.74E-03	311.21	345.45	293.10	214.18	214.76	223.88
4354	MPP1	-1.27	3.96E-02	446.90	364.36	377.91	335.79	286.88	316.39
4741	NEFM	1.59	2.99E-02	16.24	11.02	17.80	23.96	23.40	24.46
5379	PMS2L1	-1.14	2.36E-04	178.92	184.50	180.58	158.45	157.06	160.19
5927	KDM5A	-1.15	3.93E-02	97.20	109.45	103.60	87.23	95.58	86.63
6495	SIX1	1.50	2.68E-02	175.68	248.13	168.49	291.18	299.83	297.01

7779	SLC30A1	-1.25	2.80E-03	244.99	239.77	244.26	181.86	202.03	199.86
8218	CLTCL1	-1.18	1.18E-01	59.07	77.68	65.57	57.19	58.75	54.94
9319	TRIP13	1.50	2.42E-02	83.87	60.29	87.61	117.03	113.29	117.21
9653	HS2ST1	-1.13	4.21E-02	245.23	220.02	240.91	218.06	202.48	206.09
9878	TOX4	-1.07	1.63E-01	506.61	551.55	498.74	494.94	498.08	464.27
10152	ABI2	-1.06	3.36E-02	271.29	261.56	277.74	257.49	253.75	253.72
10395	DLC1	-1.31	1.30E-01	70.96	110.23	80.69	64.54	68.51	67.22
10693	CCT6B	-1.32	2.71E-02	16.25	14.28	18.17	13.04	12.53	11.44
10769	PLK2	-1.66	4.17E-02	417.87	641.30	379.58	285.56	300.35	280.92
10817	FRS3	-1.12	3.57E-02	45.30	50.07	45.01	42.28	40.92	42.14
11009	IL24	-1.63	3.78E-02	10.57	17.48	12.17	7.80	8.62	8.25
22902	RUFY3	-1.22	1.62E-02	75.02	88.95	83.14	67.30	67.90	66.85
23013	SPEN	-1.19	2.77E-02	124.34	140.41	132.76	107.84	119.69	105.55
23102	TBC1D2B	-1.40	1.15E-04	223.85	215.72	214.58	160.00	157.64	150.77
23210	JMJD6	-1.14	1.93E-01	73.05	92.61	74.37	71.66	71.42	68.26
25800	SLC39A6	-1.07	3.05E-03	461.33	471.55	456.66	431.83	435.46	436.19
26039	SS18L1	-1.06	1.30E-01	33.26	32.70	36.19	31.43	32.24	32.28
26061	HACL1	-1.16	2.25E-01	98.47	134.48	103.50	97.46	96.60	96.05
26239	LCE2B	1.62	1.94E-02	119.75	152.10	159.92	255.10	192.81	250.34
28513	CDH19	-1.16	2.38E-02	3.84	4.31	4.07	3.35	3.56	3.64
50651	SLC45A1	-1.17	3.19E-02	37.96	36.65	34.19	28.85	31.99	32.40
51765	MST4	1.78	2.64E-02	79.63	50.03	86.31	117.55	134.35	132.42
53358	SHC3	-1.29	1.26E-01	263.56	381.83	262.73	236.53	233.24	233.54
54916	C14orf101	-1.23	5.23E-02	176.89	137.74	164.86	130.72	130.29	127.67
55006	TRMT61B	-1.25	3.04E-02	81.70	102.06	87.71	72.81	69.80	73.83
55070	DET1	-1.14	1.70E-02	55.09	57.78	53.72	51.30	47.57	47.89
55103	RALGPS2	-1.27	2.51E-03	231.80	231.25	235.14	171.24	191.86	187.79
55157	DARS2	-1.29	1.33E-03	85.35	92.45	88.30	71.70	66.79	67.48
55250	ELP2	-1.18	1.96E-03	153.40	153.09	148.58	133.92	125.90	125.98
55754	TMEM30A	-1.10	5.18E-02	693.51	749.61	685.33	624.66	651.85	664.31
55784	MCTP2	-1.31	2.53E-02	151.60	148.61	176.94	108.47	126.54	128.93
55860	ACTR10	-1.21	1.93E-02	430.30	388.06	376.09	340.23	311.86	337.84
55863	TMEM126B	-1.13	2.79E-03	238.10	233.91	236.90	205.20	205.64	216.72
56967	C14orf132	-1.08	1.83E-02	98.87	97.49	96.32	92.66	87.10	91.23
57639	CCDC146	-1.27	4.77E-02	23.78	26.57	29.11	18.59	21.38	22.77
59353	TMEM35	-1.25	4.86E-02	53.72	67.63	58.85	50.49	44.67	49.58
60489	APOBEC3G	-1.33	3.82E-03	39.80	38.52	42.33	31.37	31.27	27.86
64582	GPR135	-1.07	1.27E-01	84.50	90.32	83.46	82.90	82.11	76.90
64784	CRTC3	-1.15	1.51E-01	271.83	342.96	275.17	254.50	262.74	255.93
79465	ULBP3	-1.09	4.61E-02	121.81	115.36	125.76	114.33	109.25	110.76
79602	ADIPOR2	-1.12	2.74E-02	157.97	165.53	174.42	149.27	144.51	152.13
79670	ZCCHC6	-1.19	2.22E-02	148.29	166.08	154.36	123.02	136.51	135.48
79870	BAALC	-1.07	1.81E-02	379.04	380.76	382.95	366.84	355.06	345.21
80224	NUBPL	-1.23	3.72E-03	51.45	55.49	56.93	44.47	45.57	43.22
80742	PRR3	-1.12	4.38E-02	80.25	87.68	78.12	74.14	74.65	70.41
80830	APOL6	-1.16	1.31E-01	45.52	49.03	42.92	42.12	42.25	34.25
81609	SNX27	-1.15	1.64E-02	189.12	179.17	193.26	167.50	167.04	154.46
84243	ZDHHC18	-1.08	3.52E-02	142.96	150.47	149.41	136.57	133.64	141.58
84250	ANKRD32	-1.26	1.65E-02	13.30	13.92	14.88	10.34	12.18	10.99
85450	ITPRIP	-1.14	1.20E-01	227.05	209.06	230.62	171.79	206.25	206.42
89890	KBTBD6	-1.19	3.66E-02	92.02	76.81	87.10	70.35	70.41	73.98
92017	SNX29	-1.11	1.43E-01	166.08	193.99	163.47	154.94	159.90	157.14
113451	ADC	-1.25	1.62E-02	53.76	62.72	52.90	45.69	45.59	43.73

114879	OSBPL5	-1.15	2.29E-02	78.97	86.87	84.13	74.20	74.55	68.58
114897	C1QTNF1	-1.35	3.68E-04	196.01	203.58	186.98	146.53	146.05	141.56
136306	SVOPL	-1.05	1.35E-01	5.03	5.15	5.47	4.84	5.01	5.01
158219	TTC39B	-1.28	5.49E-02	32.15	38.35	41.77	27.21	31.99	28.42
192670	EIF2C4	-1.13	4.75E-02	58.72	62.79	60.41	53.05	57.75	50.87
199704	ZNF585A	-1.16	1.68E-02	68.77	67.23	75.71	61.41	61.21	59.88
219654	ZCCHC24	-1.14	2.05E-02	270.17	246.61	276.63	232.19	233.51	228.19
221981	THSD7A	-1.37	4.93E-02	11.25	13.13	9.81	8.92	7.14	8.90
256051	ZNF549	-1.17	2.09E-02	45.64	40.20	42.14	37.64	36.71	35.26
259290	TAS2R31	-1.39	2.09E-01	5.22	9.26	5.44	4.08	5.08	5.17
284273	ZADH2	-1.37	3.36E-02	162.40	118.24	149.61	105.65	106.02	103.22
284459	HKR1	-1.08	2.69E-02	32.98	33.48	34.63	30.72	32.30	30.70
319139	SNORD56B	-1.16	2.19E-02	2.84	3.00	2.67	2.49	2.51	2.33
345757	FAM174A	-1.30	1.68E-03	64.86	64.20	67.54	52.07	47.45	52.08
389812	LCN15	-1.10	2.17E-01	19.84	18.60	18.85	18.59	15.28	18.32
439921	MXRA7	-1.13	2.08E-02	721.05	654.58	711.93	624.95	601.03	621.82
677792	SNORA1	-1.31	1.21E-01	12.13	17.88	14.15	11.95	12.07	9.63
729668	LOC729668	-1.05	4.68E-02	23.93	23.77	23.28	21.72	22.81	22.84
100133106	LOC100133106	-1.51	2.27E-02	12.47	17.50	14.92	8.79	10.26	10.58
100287879	LOC100287879	-1.13	1.93E-01	3.69	4.57	3.65	3.42	3.62	3.48

Supplementary Table 1B.

Entrez ID	**Symbol**	**Fold Change**	**p value**	**CONTROL-1**	**CONTROL-2**	**CONTROL-3**	**IPAH-1**	**IPAH-2**	**IPAH-3**
2	A2M	-1.81	1.44E-03	879.90	707.98	886.20	442.80	462.58	462.03
21	ABCA3	2.33	6.68E-04	40.32	33.08	44.61	94.14	89.95	90.29
104	ADARB1	-1.78	6.58E-03	84.15	61.00	73.75	36.97	40.85	45.24
114	ADCY8	2.33	2.40E-04	33.19	39.72	37.66	90.41	87.99	78.77
125	ADH1B	-4.33	2.26E-03	102.73	169.10	89.25	31.73	26.44	25.18
133	ADM	-1.53	3.93E-04	843.26	781.94	876.29	522.88	548.97	558.97
141	ADPRH	1.51	6.33E-03	13.18	11.66	12.12	16.72	21.18	18.07
154	ADRB2	2.19	1.48E-04	34.34	35.59	40.81	77.83	82.46	82.34
157	ADRBK2	2.08	2.44E-04	11.34	9.76	11.74	22.42	23.65	22.34
182	JAG1	-2.54	1.31E-04	111.85	136.37	117.62	48.05	45.89	49.83
196	AHR	-1.84	7.09E-05	1377.36	1230.13	1351.21	728.62	709.89	718.58
202	AIM1	3.64	3.72E-05	25.61	31.37	26.78	105.25	98.05	101.46
216	ALDH1A1	-2.34	7.86E-05	84.74	79.46	73.88	33.47	36.03	32.21
218	ALDH3A1	2.91	5.23E-04	49.25	36.55	49.94	135.87	124.23	134.31
220	ALDH1A3	1.92	1.25E-04	54.58	63.04	58.47	109.58	115.75	112.84
224	ALDH3A2	1.91	8.10E-04	146.36	115.19	132.75	259.51	246.37	246.83
286	ANK1	-1.72	3.88E-03	38.06	32.35	43.20	23.00	20.61	22.27
302	ANXA2	1.55	1.26E-05	1251.78	1212.91	1220.39	1853.59	1935.09	1927.06
306	ANXA3	4.14	7.40E-05	17.70	17.66	14.89	73.46	73.49	60.93
332	BIRC5	3.30	9.11E-04	44.30	29.36	43.81	124.40	134.43	128.52
347	APOD	-1.81	1.83E-04	183.00	159.08	170.30	91.95	97.75	93.99
409	ARRB2	1.52	4.62E-03	73.26	64.12	80.15	103.04	116.42	112.26
490	ATP2B1	-1.65	3.89E-04	562.04	636.91	627.81	364.65	356.64	384.91
534	ATP6V1G2	-1.80	6.28E-04	92.60	75.32	82.74	46.30	46.97	46.33
580	BARD1	2.33	3.18E-03	38.33	33.96	53.43	95.52	100.14	96.77
593	BCKDHA	2.01	1.40E-03	106.77	143.82	119.47	258.09	246.56	239.42
597	BCL2A1	2.13	1.12E-03	17.18	21.69	21.19	38.40	45.70	44.01
624	BDKRB2	-1.87	5.29E-03	237.39	269.06	191.80	138.07	116.81	118.26
627	BDNF	-2.56	2.20E-04	90.29	114.72	101.85	38.41	41.85	39.56
641	BLM	2.45	3.14E-03	25.88	18.43	28.63	65.61	54.99	57.99
652	BMP4	3.32	1.20E-05	99.53	101.53	88.93	332.47	319.55	311.77
653	BMP5	1.83	8.91E-04	4.08	4.02	4.12	6.48	7.91	7.95
669	BPGM	-1.72	1.13E-05	212.41	202.96	204.13	116.98	122.02	121.99
672	BRCA1	1.95	1.91E-03	23.33	23.29	30.66	52.13	49.73	48.96
675	BRCA2	2.33	2.15E-04	21.67	24.60	27.09	58.62	56.45	55.71
699	BUB1	6.37	9.54E-04	42.74	25.96	54.04	269.17	263.65	248.91
701	BUB1B	4.95	1.29E-05	28.03	24.33	29.91	134.01	137.93	135.33
715	C1R	-1.55	3.34E-05	858.71	905.01	866.48	553.71	579.82	558.58

716	C1S	-1.54	2.82E-03	1067.01	1253.23	1006.90	712.78	721.10	722.72
775	CACNA1C	-1.95	1.44E-03	120.08	97.02	123.46	61.62	54.22	58.77
828	CAPS	1.62	1.41E-03	82.96	70.75	71.87	114.31	122.65	129.01
860	RUNX2	1.53	2.84E-03	61.17	73.83	62.47	104.51	103.20	95.36
886	CCKAR	-1.96	7.67E-03	49.36	34.33	51.07	21.28	23.80	23.78
890	CCNA2	2.54	2.44E-04	110.27	90.33	113.06	278.00	262.71	254.70
891	CCNB1	4.25	4.19E-04	46.69	33.29	51.06	199.57	177.08	180.01
899	CCNF	1.98	4.83E-03	26.74	19.15	28.33	50.96	47.69	48.65
920	CD4	-2.00	2.27E-04	59.54	49.91	51.98	26.20	27.04	27.35
978	CDA	2.33	6.93E-04	52.43	40.75	51.78	105.62	119.91	112.14
983	CDK1	4.63	1.86E-04	25.25	18.50	26.35	112.45	111.02	101.34
991	CDC20	7.06	3.05E-04	81.44	47.78	76.25	482.41	501.57	466.35
995	CDC25C	4.13	1.75E-04	15.10	11.34	15.12	60.88	58.31	52.40
1008	CDH10	-4.59	5.22E-03	43.84	18.91	38.45	7.20	6.91	7.95
1012	CDH13	2.30	1.86E-04	98.11	82.46	99.41	213.86	208.02	221.46
1021	CDK6	-1.92	2.77E-04	293.10	261.43	291.12	145.47	137.32	157.57
1031	CDKN2C	2.16	7.05E-03	28.94	17.99	25.28	57.79	51.06	46.81
1033	CDKN3	5.99	1.50E-03	47.83	26.11	55.70	271.99	271.53	232.61
1047	CLGN	1.93	6.97E-05	141.24	129.16	142.62	276.70	264.43	256.21
1058	CENPA	4.19	2.22E-05	50.78	43.89	50.88	187.56	209.38	212.93
1062	CENPE	3.87	1.23E-04	29.50	23.72	31.70	115.22	109.04	103.95
1063	CENPF	4.35	7.60E-04	53.93	36.47	60.86	228.12	199.66	229.59
1111	CHEK1	1.62	2.12E-05	143.22	133.91	137.36	226.22	225.34	220.66
1129	CHRM2	-2.78	1.03E-04	437.24	407.11	411.79	142.33	170.22	139.93
1130	LYST	-1.69	2.06E-03	77.93	94.09	81.70	49.08	46.54	54.60
1163	CKS1B	1.81	1.77E-03	74.38	63.03	69.25	110.77	138.09	124.91
1164	CKS2	1.82	9.91E-04	502.24	417.89	496.17	878.05	902.72	799.74
1277	COL1A1	-1.69	1.67E-03	1225.61	999.83	1190.55	686.55	637.17	696.77
1282	COL4A1	-2.63	5.01E-05	90.65	107.34	97.89	38.49	36.18	37.74
1284	COL4A2	-1.77	1.53E-03	116.59	144.17	115.18	70.74	69.25	71.94
1295	COL8A1	-2.55	9.06E-03	216.00	122.47	214.84	70.85	76.69	69.83
1301	COL11A1	-1.83	9.81E-03	40.39	27.63	40.36	19.88	19.46	20.02
1363	CPE	-1.52	1.15E-04	273.16	254.46	259.38	172.22	166.63	177.62
1466	CSRP2	-1.73	6.37E-03	209.42	206.48	197.31	100.15	111.62	142.90
1468	SLC25A10	1.70	6.41E-04	44.48	51.50	44.91	84.18	77.16	77.78
1469	CST1	-7.23	1.12E-04	183.07	125.14	173.28	21.52	20.52	24.57
1512	CTSH	2.25	7.90E-04	23.16	23.51	30.52	57.68	58.10	58.06
1545	CYP1B1	-1.89	6.80E-03	706.01	467.76	604.58	320.02	303.03	317.58
1556	CYP2B7P1	-1.58	5.18E-03	6.71	5.32	6.63	4.18	3.86	3.77
1612	DAPK1	1.53	2.49E-03	21.15	19.47	24.19	33.57	32.70	33.04
1634	DCN	-1.51	1.57E-04	2448.75	2267.27	2402.30	1570.42	1620.48	1518.41

1734	DIO2	-1.65	6.95E-03	30.34	27.65	32.98	15.47	20.13	19.68
1763	DNA2	1.90	1.94E-03	10.49	12.53	11.46	24.21	18.96	22.38
1767	DNAH5	-1.94	4.85E-03	18.89	27.59	22.94	11.76	11.33	12.79
1829	DSG2	-6.51	7.42E-06	19.77	22.37	19.10	2.95	3.07	3.38
1841	DTYMK	1.94	6.07E-04	94.07	82.56	99.63	183.50	186.38	164.95
1869	E2F1	1.56	4.73E-04	83.84	83.51	73.80	126.69	126.12	123.34
1894	ECT2	2.06	1.84E-04	193.56	214.77	177.90	400.92	403.11	403.86
1903	S1PR3	-1.96	1.35E-04	655.80	566.30	585.29	314.08	299.39	308.56
1910	EDNRB	-2.32	6.53E-03	513.75	796.40	483.84	258.36	257.12	257.39
1946	EFNA5	-1.83	4.85E-03	201.99	259.41	199.49	110.40	135.78	115.12
1956	EGFR	-1.51	3.20E-03	323.41	382.47	344.55	225.73	217.11	251.15
2026	ENO2	1.87	6.30E-05	127.32	120.55	130.06	225.31	247.82	233.49
2044	EPHA5	-2.38	1.37E-03	56.53	76.25	61.31	23.90	28.32	29.23
2047	EPHB1	1.75	6.92E-05	30.46	31.27	31.79	51.73	57.43	54.28
2069	EREG	-6.29	4.23E-04	177.62	133.60	236.07	29.21	27.03	30.74
2078	ERG	6.28	5.79E-03	37.06	12.53	36.89	173.54	193.51	175.84
2123	EVI2A	4.06	1.03E-04	16.17	17.16	16.24	67.85	76.84	56.67
2124	EVI2B	2.99	2.64E-04	38.45	51.05	39.74	127.00	132.49	126.41
2146	EZH2	2.20	1.26E-04	60.29	59.64	69.91	143.17	139.04	135.06
2159	F10	-1.80	3.03E-04	115.12	119.24	104.77	59.04	65.88	63.31
2167	FABP4	-5.13	5.25E-03	35.44	14.11	29.28	4.75	5.16	5.45
2175	FANCA	1.62	9.04E-04	29.31	30.63	28.37	43.15	49.24	50.70
2177	FANCD2	2.66	3.61E-04	23.81	21.42	28.83	66.75	63.91	66.22
2187	FANCB	1.53	3.52E-03	10.94	11.28	13.64	18.45	18.27	18.03
2189	FANCG	1.87	3.49E-05	44.62	44.71	43.85	86.81	84.43	78.42
2192	FBLN1	-1.56	8.63E-03	973.11	730.48	929.90	569.03	577.26	537.37
2195	FAT1	-1.53	8.78E-03	471.29	442.15	509.00	290.95	279.78	361.43
2199	FBLN2	-2.57	4.62E-05	347.53	294.89	331.43	124.93	125.04	128.85
2254	FGF9	1.55	9.50E-04	4.57	3.95	4.52	6.85	6.81	6.48
2304	FOXE1	-2.79	2.76E-03	95.74	60.16	88.12	26.16	31.44	29.92
2305	FOXM1	4.45	1.13E-03	93.95	59.84	110.01	386.13	400.07	387.79
2321	FLT1	-2.33	1.25E-03	17.60	21.11	18.70	7.92	7.08	9.64
2444	FRK	-1.51	3.11E-03	18.70	16.40	20.13	12.34	11.67	12.59
2491	CENPI	3.04	1.67E-03	57.33	41.79	68.30	163.69	160.61	184.27
2534	FYN	-1.57	4.75E-03	268.43	206.34	244.99	155.54	154.34	150.01
2562	GABRB3	2.27	4.52E-04	35.81	28.61	34.82	80.09	72.95	72.24
2564	GABRE	-1.75	9.08E-03	35.00	42.54	29.48	18.52	20.62	21.91
2650	GCNT1	1.64	1.10E-03	139.08	118.77	130.68	197.68	214.75	224.11
2846	LPAR4	1.76	3.20E-03	21.48	17.83	22.54	40.30	35.02	33.67
2892	GRIA3	-1.52	1.57E-03	205.65	170.83	184.62	120.87	124.36	123.64
2898	GRIK2	-3.61	1.21E-04	140.39	172.19	134.58	39.44	39.63	44.72

2952	GSTT1	-7.77	2.98E-05	160.17	134.10	173.33	19.27	18.40	22.48
2983	GUCY1B3	1.99	1.77E-04	92.03	100.65	84.29	183.19	185.43	182.84
3006	HIST1H1C	1.74	2.14E-03	162.66	201.34	191.14	351.45	310.12	303.68
3007	HIST1H1D	2.29	1.01E-03	36.20	26.88	35.36	74.37	73.00	77.64
3008	HIST1H1E	1.74	2.37E-03	1000.61	1300.99	1048.12	1903.65	1985.53	1940.26
3009	HIST1H1B	4.54	7.29E-04	53.24	37.73	66.34	239.63	232.76	242.35
3012	HIST1H2AE	2.42	2.06E-04	10.62	9.86	12.04	27.71	24.50	26.35
3014	H2AFX	1.84	6.58E-04	124.45	104.53	125.37	216.40	227.12	209.32
3015	H2AFZ	2.02	1.80E-04	528.53	620.44	576.62	1201.31	1106.89	1183.86
3018	HIST1H2BB	3.57	1.03E-04	18.57	16.12	20.80	70.66	62.10	65.16
3024	HIST1H1A	3.02	5.76E-06	55.58	54.66	59.61	173.03	163.79	176.46
3096	HIVEP1	-1.91	4.14E-03	98.21	139.06	106.62	59.22	58.12	62.98
3113	HLA-DPA1	-2.13	1.01E-04	108.87	121.69	103.19	52.12	51.87	52.47
3148	HMGB2	2.92	7.33E-04	75.36	55.29	79.38	211.86	208.41	193.79
3161	HMMR	6.80	2.25E-04	11.97	9.11	15.38	86.76	80.41	80.53
3187	HNRNPH1	1.50	2.16E-03	349.02	301.70	359.37	525.52	504.02	487.67
3218	HOXB8	3.15	6.73E-04	45.19	30.90	41.35	118.55	133.26	118.19
3222	HOXC5	-1.85	4.06E-03	19.90	19.28	19.55	12.09	11.06	8.51
3224	HOXC8	-1.58	4.59E-03	33.59	32.98	31.01	23.74	19.50	18.36
3248	HPGD	2.64	1.68E-03	3.59	3.57	3.57	11.94	8.20	8.12
3290	HSD11B1	-2.20	4.65E-04	55.27	62.01	48.68	23.80	25.80	25.75
3357	HTR2B	-1.90	2.67E-03	27.50	22.55	27.07	12.44	15.59	12.63
3384	ICAM2	2.12	1.24E-05	24.61	22.81	24.13	52.20	49.73	49.43
3480	IGF1R	-1.93	1.02E-04	432.83	476.62	438.83	227.61	224.92	247.34
3490	IGFBP7	-1.80	1.91E-05	860.33	860.26	913.24	498.06	473.61	491.03
3554	IL1R1	-2.10	2.75E-06	651.19	634.32	658.40	317.83	301.50	305.33
3566	IL4R	-1.85	6.41E-04	217.78	268.08	247.86	127.88	134.29	135.22
3569	IL6	-1.99	9.83E-03	488.00	743.99	628.19	263.65	337.15	334.64
3598	IL13RA2	2.20	1.91E-04	448.90	390.84	405.54	974.35	929.34	841.05
3624	INHBA	-1.66	5.00E-03	1095.24	1452.69	1189.11	715.31	795.25	740.05
3627	CXCL10	-2.07	3.17E-04	6.39	7.38	7.21	3.68	3.29	3.18
3638	INSIG1	-1.61	7.05E-03	138.28	187.52	149.63	99.43	98.85	97.88
3655	ITGA6	1.90	6.92E-03	224.00	153.99	219.59	402.87	351.75	380.46
3671	ISLR	2.12	4.52E-05	215.15	221.33	208.23	444.54	487.39	434.07
3673	ITGA2	-1.58	3.75E-03	578.99	729.32	641.39	410.26	386.23	435.53
3696	ITGB8	-1.86	9.56E-03	186.66	126.84	170.31	76.89	88.68	94.25
3738	KCNA3	1.53	4.89E-03	19.42	21.69	23.46	29.72	33.79	35.39
3751	KCND2	-3.88	1.88E-04	48.60	51.66	39.96	10.68	13.47	12.02
3775	KCNK1	1.66	2.49E-04	34.22	36.97	39.03	62.59	61.29	59.28
3778	KCNMA1	1.83	8.60E-04	145.88	180.85	149.67	290.93	287.48	293.90

3832	KIF11	4.05	5.74E-04	50.41	33.77	50.68	188.95	165.77	191.64
3833	KIFC1	2.18	5.10E-03	38.11	28.28	45.88	77.46	84.41	82.89
3835	KIF22	2.05	1.02E-04	77.62	67.23	72.82	154.33	143.38	149.49
3838	KPNA2	1.61	5.93E-04	1102.57	964.05	1055.16	1691.97	1744.01	1587.08
3880	KRT19	3.12	5.43E-03	84.90	45.81	89.27	234.63	219.38	231.66
3887	KRT81	1.52	6.42E-03	25.03	20.47	22.13	31.17	34.02	37.74
3897	L1CAM	-1.53	4.18E-04	19.37	18.04	19.59	12.07	12.07	13.19
3908	LAMA2	-1.65	1.59E-03	160.41	144.37	164.34	90.61	89.24	105.08
3912	LAMB1	-1.71	3.40E-03	909.38	1150.78	883.83	576.92	553.17	587.56
3925	STMN1	1.73	2.49E-04	40.34	43.18	39.78	66.14	74.75	72.11
3976	LIF	-2.04	8.82E-03	86.14	87.97	107.49	35.15	55.50	47.61
3978	LIG1	1.66	2.65E-06	57.36	59.71	57.83	97.63	96.55	96.14
4001	LMNB1	2.28	4.08E-05	24.50	22.86	24.07	58.01	54.14	51.06
4060	LUM	-2.40	1.22E-05	1046.68	935.74	1001.49	413.27	412.62	419.84
4064	CD180	35.07	2.77E-06	3.74	5.14	4.59	157.27	155.98	159.24
4126	MANBA	-1.71	9.12E-03	83.95	116.48	83.23	54.36	56.49	54.68
4129	MAOB	1.51	1.78E-03	49.47	41.56	47.73	71.13	71.16	67.35
4133	MAP2	-2.12	7.94E-03	157.20	101.73	160.01	64.66	65.26	67.60
4171	MCM2	1.81	9.03E-05	60.12	64.83	62.07	109.53	119.76	109.33
4172	MCM3	1.77	7.53E-05	102.18	110.73	101.34	188.03	190.30	178.64
4173	MCM4	1.92	1.03E-04	75.90	85.90	76.66	156.88	149.24	151.56
4174	MCM5	2.05	3.04E-05	91.15	89.22	99.43	193.78	188.21	192.87
4176	MCM7	2.12	1.53E-04	123.94	146.20	137.77	302.44	278.50	285.66
4239	MFAP4	-2.59	2.51E-03	478.62	693.82	449.87	200.52	220.34	205.64
4254	KITLG	-1.54	6.00E-04	171.32	157.37	177.84	114.68	105.28	108.48
4281	MID1	-1.83	6.85E-04	600.13	491.80	582.10	298.30	309.59	308.56
4288	MKI67	3.94	5.13E-03	57.29	30.56	70.02	208.85	185.87	227.15
4330	MN1	-1.58	2.38E-03	178.89	175.41	208.96	110.08	120.50	124.93
4363	ABCC1	-1.59	2.59E-03	658.68	571.68	701.64	399.51	385.51	430.76
4436	MSH2	1.50	1.54E-03	46.12	54.65	51.00	76.92	72.95	77.47
4489	MT1A	1.74	7.74E-04	164.29	148.07	154.77	257.82	299.43	255.03
4494	MT1F	1.60	4.11E-03	455.45	430.84	369.61	641.58	737.78	630.57
4495	MT1G	2.38	5.36E-04	75.94	57.30	64.51	165.31	154.20	150.79
4499	MT1M	1.64	3.77E-04	247.84	224.18	244.77	385.08	373.86	415.49
4501	MT1X	1.53	1.39E-03	756.84	631.55	704.82	1055.64	1049.78	1088.82
4600	MX2	1.60	2.31E-03	11.23	12.64	10.75	19.17	16.71	19.36
4605	MYBL2	2.50	2.29E-04	46.39	42.81	52.22	116.18	128.03	109.88
4642	MYO1D	-1.53	4.00E-03	727.34	576.74	689.62	434.06	440.59	429.03
4651	MYO10	-1.69	2.19E-03	630.83	538.02	687.34	366.86	351.83	377.29
4684	NCAM1	4.49	1.08E-04	8.72	6.76	8.93	35.58	34.33	39.68

4685	NCAM2	-2.95	3.76E-03	62.57	36.29	57.90	16.38	18.31	18.45
4741	NEFM	4.81	4.90E-04	16.24	11.02	17.80	69.00	68.87	78.73
4747	NEFL	1.92	3.62E-04	30.31	25.15	26.89	53.93	50.56	53.93
4751	NEK2	4.81	3.05E-05	33.47	26.99	31.27	155.00	135.88	150.34
4756	NEO1	-1.74	1.04E-05	320.55	331.98	310.51	186.08	183.54	182.28
4811	NID1	-1.57	5.47E-05	332.51	350.52	339.60	215.60	210.82	225.37
4826	NNAT	1.76	1.02E-03	36.33	32.69	39.34	64.70	67.44	59.04
4835	NQO2	-1.91	7.61E-06	220.95	222.70	213.80	110.74	117.17	116.40
4854	NOTCH3	-1.72	3.59E-03	157.03	124.90	161.42	82.53	83.12	91.59
4923	NTSR1	2.08	1.12E-03	55.41	44.07	56.70	106.81	115.49	102.19
4940	OAS3	2.19	1.52E-04	21.89	18.39	19.90	45.80	42.03	43.92
4973	OLR1	-3.53	7.34E-03	153.95	74.57	148.20	32.02	37.03	37.72
4982	TNFRSF11B	-1.59	1.36E-04	1119.85	1152.94	1095.88	665.40	732.55	715.75
4998	ORC1L	2.06	1.25E-03	20.33	16.71	21.44	41.56	42.31	36.45
5010	CLDN11	1.92	1.44E-03	853.72	653.94	819.13	1513.18	1498.28	1446.21
5026	P2RX5	1.85	1.78E-03	54.50	44.34	58.36	98.79	93.98	98.12
5067	CNTN3	-1.62	2.27E-03	36.28	42.44	38.34	24.28	26.09	21.76
5080	PAX6	3.48	4.98E-06	12.14	10.68	11.55	39.92	40.04	39.53
5111	PCNA	1.74	2.12E-03	176.48	207.89	159.32	312.34	308.10	324.88
5126	PCSK2	-1.80	4.86E-03	168.02	119.13	151.97	81.31	81.15	81.86
5159	PDGFRB	-2.80	8.59E-04	535.85	735.85	516.04	211.55	218.85	207.31
5165	PDK3	1.65	1.97E-04	49.96	45.79	46.07	75.31	82.18	76.98
5270	SERPINE2	-1.52	2.12E-05	2605.30	2583.93	2471.43	1665.77	1706.72	1667.39
5272	SERPINB9	-2.72	6.83E-03	51.05	94.97	58.98	24.91	25.83	24.51
5324	PLAG1	-1.59	1.70E-03	119.40	98.56	105.35	64.52	67.81	70.55
5327	PLAT	-1.84	4.31E-04	648.86	754.93	775.32	394.38	403.31	387.86
5328	PLAU	1.74	9.92E-04	199.27	248.45	224.14	385.31	397.99	385.42
5332	PLCB4	-1.84	5.54E-05	191.56	209.52	192.70	103.95	109.20	109.74
5334	PLCL1	-1.66	4.90E-03	13.05	12.97	12.98	6.56	7.89	9.00
5347	PLK1	6.44	4.78E-04	77.47	47.32	81.89	475.35	453.51	402.66
5366	PMAIP1	2.18	1.94E-03	157.05	215.23	218.83	419.71	445.60	425.15
5427	POLE2	2.05	3.19E-05	32.66	31.24	34.88	66.30	69.33	67.07
5493	PPL	2.42	2.66E-04	29.61	32.34	35.37	70.67	81.21	83.56
5507	PPP1R3C	-1.86	3.74E-03	789.65	565.64	722.90	371.86	381.73	364.11
5519	PPP2R1B	-1.75	1.45E-04	444.20	397.53	426.82	235.40	252.83	237.82
5557	PRIM1	2.68	3.55E-04	34.33	42.58	33.09	101.05	102.71	90.62
5577	PRKAR2B	-2.06	6.07E-03	109.82	161.90	108.05	60.02	61.11	63.11
5602	MAPK10	-2.11	5.38E-05	173.51	190.61	173.27	89.27	84.29	81.66
5603	MAPK13	1.86	1.16E-05	30.12	28.32	28.93	52.52	55.05	54.55
5698	PSMB9	1.71	3.08E-05	77.02	70.70	73.64	125.67	127.50	124.65

5754	PTK7	-1.87	3.38E-03	124.98	172.72	141.35	83.12	76.41	75.69
5764	PTN	-2.95	6.16E-04	118.55	86.88	121.00	37.55	37.90	35.17
5789	PTPRD	1.80	6.09E-03	15.30	11.64	15.09	23.31	23.66	28.75
5793	PTPRG	-1.79	7.13E-04	250.14	214.18	244.01	130.13	124.46	141.89
5827	PXMP2	1.60	3.63E-04	211.10	194.93	224.73	336.24	331.29	341.78
5874	RAB27B	-2.01	8.36E-03	40.45	61.01	40.94	25.29	22.01	23.40
5888	RAD51	2.21	2.70E-04	33.53	41.90	35.99	82.56	81.13	82.45
5903	RANBP2	-1.53	5.81E-03	208.86	178.57	223.83	128.93	126.78	144.47
5915	RARB	1.97	1.04E-03	10.54	9.64	11.45	22.04	18.27	21.93
5933	RBL1	1.79	6.97E-05	42.78	46.23	47.77	80.12	82.05	83.00
5959	RDH5	3.17	9.71E-04	79.58	52.61	77.71	220.09	217.44	226.84
5982	RFC2	1.69	2.95E-05	121.50	128.83	124.73	203.88	216.90	211.33
5983	RFC3	1.83	3.13E-04	85.56	101.10	88.16	170.67	168.47	164.83
5984	RFC4	1.95	5.21E-04	179.39	223.20	211.46	395.88	405.63	398.58
5985	RFC5	1.92	1.12E-03	39.45	49.72	40.16	86.31	82.26	79.18
6000	RGS7	-3.07	2.07E-04	16.90	13.80	16.40	5.62	4.58	5.16
6091	ROBO1	-1.64	7.86E-03	303.49	405.28	308.31	207.07	197.24	217.56
6092	ROBO2	-2.64	1.75E-04	37.15	33.60	35.61	12.73	15.25	12.33
6201	RPS7	1.50	1.38E-03	52.39	53.68	61.26	81.08	84.25	86.16
6240	RRM1	1.62	1.09E-04	265.85	245.09	249.20	424.86	404.77	398.23
6241	RRM2	3.71	1.02E-03	80.22	51.09	82.30	271.85	256.67	263.63
6331	SCN5A	-1.96	3.12E-05	55.94	60.93	59.49	30.84	28.87	30.32
6335	SCN9A	-2.82	6.91E-04	184.85	141.40	189.04	64.55	54.36	63.98
6347	CCL2	-1.70	5.77E-03	1713.22	1544.60	1778.04	829.19	1132.94	998.00
6364	CCL20	-2.36	1.16E-03	10.75	10.20	13.67	4.65	4.65	5.40
6382	SDC1	1.74	1.53E-03	121.85	137.76	135.79	252.25	232.21	204.80
6387	CXCL12	-2.24	9.22E-04	181.42	133.32	161.93	72.07	71.57	69.37
6414	SEPP1	-1.71	3.62E-03	1263.46	989.09	1233.63	718.92	690.83	631.85
6470	SHMT1	1.66	1.35E-04	31.89	33.72	29.93	52.84	53.64	52.21
6482	ST3GAL1	-2.00	1.93E-03	367.05	272.49	355.71	165.61	167.23	164.62
6491	STIL	2.39	2.75E-03	66.08	45.55	69.22	137.17	146.10	149.34
6515	SLC2A3	-1.76	3.56E-04	623.22	558.80	656.17	350.36	357.43	338.67
6615	SNAI1	-1.56	6.56E-04	59.82	60.65	52.49	36.94	37.00	36.97
6622	SNCA	-3.07	9.15E-03	304.63	593.85	305.39	124.41	124.29	143.23
6638	SNRPN	-2.20	3.17E-03	16.31	11.91	14.96	7.12	5.51	6.96
6649	SOD3	-1.63	3.30E-03	262.53	205.82	250.90	149.43	150.36	142.06
6695	SPOCK1	-1.66	1.26E-03	582.78	700.92	604.41	388.56	358.35	388.13
6751	SSTR1	-2.31	1.36E-03	162.38	224.68	188.84	75.97	83.91	89.11
6775	STAT4	-1.88	4.56E-03	17.93	13.00	14.02	8.77	7.60	7.56
6781	STC1	-1.85	4.63E-04	1093.51	1253.90	1249.47	626.40	697.03	620.43
6839	SUV39H1	1.88	9.90E-05	41.28	38.98	38.34	73.63	79.12	70.45

6907	TBL1X	-1.53	1.84E-04	136.12	139.52	143.60	92.29	86.21	94.78
6941	TCF19	2.51	1.48E-04	36.24	42.89	44.06	98.24	104.61	106.19
7058	THBS2	-2.20	2.96E-05	1126.56	1017.72	1108.04	501.04	472.71	502.91
7083	TK1	3.55	8.35E-04	129.42	93.42	146.51	477.74	419.15	412.88
7100	TLR5	1.55	4.06E-03	10.50	9.85	8.53	15.46	15.51	13.70
7107	GPR137B	-1.63	2.49E-03	355.26	408.50	326.91	233.74	224.44	210.39
7112	TMPO	2.40	3.19E-04	88.58	114.55	101.99	238.14	242.96	252.64
7128	TNFAIP3	-1.82	4.45E-03	245.03	297.23	238.59	122.38	158.92	147.23
7130	TNFAIP6	-1.61	3.28E-03	507.88	590.67	469.50	344.88	320.81	306.64
7153	TOP2A	3.46	3.67E-03	170.78	92.43	174.31	534.32	484.45	495.66
7223	TRPC4	-3.28	5.75E-04	60.41	86.01	69.63	19.50	23.82	22.55
7272	TTK	5.25	3.01E-05	20.00	17.58	22.63	109.37	107.36	99.15
7298	TYMS	2.86	4.96E-05	234.01	199.05	237.15	642.38	629.32	643.62
7403	KDM6A	-1.53	1.40E-03	151.23	178.62	154.48	107.92	103.64	104.78
7422	VEGFA	-1.73	3.27E-04	292.27	320.72	274.03	166.09	172.51	173.41
7443	VRK1	1.81	3.19E-04	60.84	58.44	67.60	118.92	108.64	110.74
7447	VSNL1	1.61	1.99E-03	9.34	7.96	8.12	14.83	12.81	13.34
7458	EIF4H	1.66	2.08E-04	679.58	648.41	695.37	1184.11	1056.31	1108.34
7468	WHSC1	1.82	5.24E-05	66.77	61.27	65.61	113.22	121.00	118.63
7516	XRCC2	2.08	1.64E-04	28.54	34.29	31.69	65.27	64.97	66.65
7772	ZNF229	-1.62	6.79E-03	44.69	59.41	55.20	31.19	31.78	35.17
7813	EVI5	-1.80	4.01E-03	148.81	116.26	145.32	81.15	67.31	79.49
7857	SCG2	-3.18	8.51E-04	48.34	69.00	46.58	17.86	17.09	16.60
7980	TFPI2	-2.03	1.17E-03	682.46	894.80	715.96	382.27	381.57	363.61
7991	TUSC3	-2.13	5.78E-04	424.99	506.90	403.06	222.17	203.35	202.68
8089	YEATS4	1.59	2.27E-03	89.80	109.62	90.82	148.20	154.70	157.30
8208	CHAF1B	1.91	2.40E-05	66.91	61.23	65.25	120.79	125.84	122.46
8226	HDHD1	-1.61	1.31E-04	236.72	234.14	252.33	146.28	156.69	146.10
8233	ZRSR2	-1.50	3.03E-03	77.84	69.30	65.58	43.71	49.73	47.98
8242	KDM5C	-1.77	6.94E-04	225.78	263.69	235.60	126.39	142.31	141.28
8294	HIST1H4I	2.03	3.16E-04	66.35	59.12	58.27	135.40	121.01	116.51
8317	CDC7	2.14	4.96E-04	8.78	8.38	10.53	18.98	20.77	19.61
8318	CDC45	2.27	6.59E-06	56.33	61.47	57.93	134.59	132.25	131.72
8329	HIST1H2AI	4.36	2.77E-03	34.58	23.67	52.27	155.95	172.36	153.48
8330	HIST1H2AK	2.92	1.29E-03	46.79	65.68	45.81	164.87	134.42	163.63
8332	HIST1H2AL	2.80	8.17E-05	47.14	41.99	48.23	135.89	131.60	116.84
8335	HIST1H2AB	2.82	2.18E-04	20.70	17.48	21.02	60.38	49.92	56.78
8336	HIST1H2AM	2.75	4.17E-04	7.87	7.21	9.87	22.35	23.34	22.84
8338	HIST2H2AC	1.52	6.21E-03	412.12	536.18	448.73	735.75	683.71	702.88
8339	HIST1H2BG	2.38	1.43E-05	49.39	52.05	51.35	128.37	119.76	115.81
8341	HIST1H2BN	2.29	4.79E-05	138.27	126.40	139.70	327.90	298.56	299.40

8342	HIST1H2BM	4.44	1.27E-03	271.57	177.91	338.39	1165.92	1158.07	1177.56
8343	HIST1H2BF	4.27	1.95E-03	105.99	55.69	99.22	384.88	378.54	351.02
8344	HIST1H2BE	2.37	7.45E-05	45.35	47.69	50.01	119.76	103.80	115.66
8345	HIST1H2BH	3.00	1.98E-05	186.34	163.43	185.42	553.36	517.67	534.17
8346	HIST1H2BI	2.24	5.64E-03	7.98	6.26	8.67	18.23	13.56	19.53
8347	HIST1H2BC	1.98	4.94E-04	56.01	66.33	54.30	118.96	120.06	111.35
8348	HIST1H2BO	2.17	5.19E-03	17.13	16.62	22.40	44.58	32.72	44.29
8350	HIST1H3A	2.89	1.68E-04	55.95	55.47	68.98	169.35	184.88	166.73
8351	HIST1H3D	2.79	2.16E-03	321.65	254.00	421.35	940.92	876.43	961.04
8352	HIST1H3C	1.96	1.61E-03	34.55	32.80	41.23	71.18	77.84	64.15
8353	HIST1H3E	1.60	4.72E-04	6.33	5.76	6.29	10.06	10.21	9.19
8354	HIST1H3I	2.56	8.83E-06	443.54	435.00	477.52	1184.78	1169.10	1121.51
8355	HIST1H3G	4.56	1.28E-03	231.08	146.66	280.20	977.33	1004.47	1015.20
8356	HIST1H3J	3.17	6.39E-04	25.55	22.54	32.91	85.38	92.44	78.91
8357	HIST1H3H	4.02	8.59E-05	167.02	134.93	178.97	661.40	647.94	625.23
8358	HIST1H3B	3.33	2.30E-03	180.44	139.45	257.30	656.82	646.82	617.58
8359	HIST1H4A	2.16	1.55E-03	24.38	18.66	21.94	50.77	41.12	48.20
8360	HIST1H4D	2.33	2.25E-04	31.52	31.34	37.17	83.47	74.58	74.89
8361	HIST1H4F	2.18	1.43E-03	88.45	92.67	118.10	237.50	211.52	204.52
8364	HIST1H4C	2.88	1.40E-04	349.05	412.81	432.48	1205.17	1163.92	1068.49
8366	HIST1H4B	2.07	1.74E-04	59.59	50.31	58.67	116.60	116.76	115.60
8368	HIST1H4L	2.18	3.47E-03	170.69	139.93	216.92	396.34	371.93	379.21
8418	CMAH	3.54	9.43E-05	20.42	17.67	22.15	72.60	75.58	64.93
8438	RAD54L	1.80	1.51E-04	16.90	19.43	18.02	32.36	33.44	32.12
8507	ENC1	-2.17	3.98E-05	84.10	80.74	88.57	37.05	38.94	40.96
8516	ITGA8	-4.03	2.95E-03	23.13	12.36	22.89	4.67	4.66	5.14
8544	PIR	-2.80	1.03E-04	66.79	81.29	66.58	25.93	25.31	25.44
8555	CDC14B	-1.57	7.60E-03	154.96	201.81	160.35	107.30	105.59	117.14
8601	RGS20	1.57	6.61E-04	27.58	25.69	28.78	44.03	40.07	44.42
8613	PPAP2B	-1.51	3.07E-04	1978.01	1770.34	1812.56	1247.71	1209.62	1235.27
8630	HSD17B6	-1.66	9.24E-03	13.10	9.39	12.65	7.14	7.06	6.91
8633	UNC5C	1.59	6.50E-03	12.42	10.99	14.45	18.96	19.39	21.70
8654	PDE5A	-1.75	1.38E-03	1033.49	824.14	976.69	558.51	525.72	532.91
8742	TNFSF12	1.56	4.32E-03	104.69	107.13	110.89	150.48	191.76	159.62
8743	TNFSF10	4.21	4.66E-05	43.54	39.19	37.94	190.97	154.91	161.83
8771	TNFRSF6B	3.01	1.02E-04	67.11	67.77	71.02	183.23	232.33	203.88
8777	MPDZ	-1.62	5.95E-04	167.97	151.91	179.58	101.73	103.23	103.00
8792	TNFRSF11A	1.55	7.76E-04	29.37	26.47	29.97	45.67	41.84	45.34
8836	GGH	2.20	4.32E-03	50.40	75.83	50.93	132.03	121.84	135.78

8838	WISP3	2.66	2.04E-04	12.00	12.82	10.61	30.14	29.40	34.65
8844	KSR1	-2.45	1.23E-04	121.31	108.34	126.86	44.82	50.64	49.91
8847	DLEU2	2.82	7.87E-03	37.09	19.44	37.75	87.87	91.83	86.19
8900	CCNA1	1.85	5.80E-03	19.54	16.18	18.48	37.60	35.59	27.28
8925	HERC1	-1.52	8.28E-03	101.59	98.12	113.35	65.34	61.90	79.19
8968	HIST1H3F	2.95	2.00E-03	79.16	52.93	86.30	219.63	202.16	221.54
8969	HIST1H2AG	3.16	1.83E-04	340.10	277.08	371.17	1051.40	1048.97	1026.69
8970	HIST1H2BJ	2.01	2.08E-03	6.28	5.30	7.28	13.64	12.11	12.20
9037	SEMA5A	-3.42	1.21E-04	448.27	377.59	468.52	123.58	116.74	138.50
9055	PRC1	4.75	8.98E-04	98.73	58.76	102.26	411.82	415.40	405.96
9066	SYT7	1.82	2.90E-03	64.62	78.96	73.36	143.18	137.78	113.85
9088	PKMYT1	2.32	2.18E-05	28.75	32.09	29.76	68.31	72.34	69.16
9120	SLC16A6	-3.04	4.10E-03	373.96	640.99	392.03	168.35	135.86	158.17
9124	PDLIM1	-1.74	6.89E-03	329.22	440.90	324.99	202.67	225.84	200.66
9127	P2RX6	1.55	7.89E-03	22.01	17.18	19.22	33.33	27.81	29.42
9133	CCNB2	5.42	4.72E-04	63.26	42.65	68.96	329.60	343.46	274.55
9134	CCNE2	2.07	6.67E-04	48.59	59.23	61.13	112.99	122.44	113.66
9156	EXO1	2.38	1.69E-04	27.06	30.25	33.43	72.91	69.27	73.56
9162	DGKI	-1.55	8.79E-04	41.46	37.74	37.85	26.63	25.41	23.33
9184	BUB3	1.64	2.36E-04	278.61	298.38	278.72	476.98	488.26	438.84
9185	REPS2	1.64	1.29E-03	25.01	21.06	24.70	40.67	37.77	37.37
9194	SLC16A7	-1.78	2.23E-04	244.26	270.88	269.38	152.20	138.41	150.97
9212	AURKB	2.92	3.72E-05	63.72	61.93	59.22	181.05	194.35	164.05
9232	PTTG1	4.34	4.21E-04	46.76	32.47	50.62	181.87	188.46	193.74
9244	CRLF1	-1.94	2.79E-04	347.87	385.44	356.65	171.31	200.58	189.56
9252	RPS6KA5	1.80	5.04E-03	24.79	18.33	24.06	44.12	38.45	38.38
9289	GPR56	2.26	3.92E-03	49.39	76.29	51.20	131.56	133.36	134.41
9303	SNORD25	1.66	6.87E-03	3.65	3.49	3.47	5.93	4.88	6.78
9319	TRIP13	3.12	6.20E-04	83.87	60.29	87.61	240.04	243.54	239.51
9368	SLC9A3R1	2.26	1.56E-04	212.89	174.85	198.17	454.32	436.85	435.52
9404	LPXN	1.80	4.61E-03	208.09	289.42	218.05	430.10	438.19	416.48
9424	KCNK6	-1.57	3.75E-03	144.38	119.01	150.84	88.59	89.22	85.92
9451	EIF2AK3	-1.64	2.73E-03	127.92	163.99	138.84	85.85	89.61	87.22
9455	HOMER2	1.84	4.28E-04	16.26	16.74	18.42	34.16	29.86	30.39
9493	KIF23	2.32	3.79E-05	106.26	102.36	117.28	253.05	245.96	256.32
9497	SLC4A7	-1.51	9.99E-04	250.63	228.85	267.47	168.67	159.86	165.25
9518	GDF15	-1.93	5.68E-04	246.09	285.31	282.49	128.39	142.64	149.94
9536	PTGES	-1.75	2.02E-03	161.05	160.48	128.01	85.57	83.84	87.98
9563	H6PD	-1.52	7.32E-04	311.21	283.01	323.65	205.11	192.44	204.68
9582	APOBEC3B	5.23	2.16E-03	62.51	32.14	69.36	303.89	278.38	275.75
9585	KIF20B	4.04	2.87E-04	18.16	14.23	20.89	77.28	69.93	68.30

9603	NFE2L3	1.54	2.46E-03	111.87	95.18	114.98	167.28	157.45	171.27
9700	ESPL1	1.72	3.84E-03	31.37	24.67	32.94	51.89	52.34	49.08
9723	SEMA3E	-2.12	2.69E-04	35.17	32.08	38.25	16.74	15.47	17.48
9728	SECISBP2L	-1.64	3.39E-04	370.18	342.94	386.50	216.29	234.93	218.89
9732	DOCK4	-1.77	3.65E-04	181.63	172.41	197.45	99.26	102.21	110.55
9735	KNTC1	2.06	8.32E-04	29.69	25.26	33.05	62.17	58.12	61.12
9760	TOX	-2.61	3.25E-04	64.68	81.00	64.95	24.96	28.02	27.71
9766	KIAA0247	-1.67	1.38E-03	159.66	197.61	186.56	106.51	110.15	108.72
9768	KIAA0101	3.37	8.07E-04	70.22	52.73	83.65	234.62	237.26	225.15
9787	DLGAP5	7.56	1.32E-03	28.17	14.02	32.42	196.76	184.92	182.72
9824	ARHGAP11A	2.24	3.63E-03	73.85	50.74	77.26	156.55	147.18	148.40
9829	DNAJC6	-1.77	3.77E-03	37.94	50.65	42.52	26.50	24.58	22.99
9833	MELK	2.55	1.34E-04	62.80	56.91	68.88	158.49	170.71	151.73
9837	GINS1	2.18	4.80E-04	43.43	38.83	50.11	97.82	98.00	93.34
9890	LPPR4	-4.41	7.10E-03	193.72	83.52	190.48	33.83	35.73	36.60
9918	NCAPD2	2.05	4.10E-06	162.80	163.42	159.16	332.78	321.08	342.91
9928	KIF14	3.98	5.79E-04	14.89	12.53	19.98	67.42	61.04	60.03
9962	SLC23A2	-1.58	1.85E-04	108.15	106.63	118.66	69.10	71.17	70.12
10024	TROAP	2.72	2.96E-04	25.58	24.73	25.31	59.62	79.42	66.47
10046	MAMLD1	-1.51	1.25E-03	191.99	184.84	192.43	114.87	136.25	125.83
10051	SMC4	2.28	2.65E-03	129.01	87.06	116.70	274.36	238.18	245.71
10112	KIF20A	8.84	2.08E-03	45.71	18.27	48.98	344.17	341.44	312.71
10149	GPR64	2.64	5.49E-04	14.17	10.82	12.04	29.03	34.74	33.99
10212	DDX39	1.79	1.06E-05	62.33	62.77	64.50	117.24	110.36	111.69
10231	RCAN2	-2.61	2.44E-04	203.85	164.92	209.30	73.01	76.15	72.53
10234	LRRC17	1.72	5.33E-05	62.60	63.06	58.57	108.41	101.89	105.82
10272	FSTL3	-1.52	2.45E-03	189.46	157.40	181.98	118.74	119.06	110.92
10293	TRAIP	1.73	9.68E-04	16.79	19.80	18.02	31.87	33.33	29.02
10301	DLEU1	1.99	1.31E-03	52.94	42.48	45.68	97.19	100.34	83.54
10324	KBTBD10	2.63	2.16E-03	15.84	25.29	21.63	55.01	57.50	52.51
10350	ABCA9	-2.04	2.87E-04	28.24	30.01	30.03	16.04	13.31	13.83
10391	CORO2B	1.91	4.18E-05	201.16	190.11	200.46	374.15	396.95	360.57
10403	NDC80	4.86	2.19E-04	28.07	19.75	28.71	132.04	119.11	121.04
10437	IFI30	2.48	7.02E-04	130.54	170.62	127.55	347.93	374.61	342.79
10460	TACC3	2.99	6.22E-05	25.71	23.47	28.63	80.98	74.16	77.85
10465	PPIH	1.51	6.92E-03	46.66	53.45	51.58	66.67	84.25	78.61
10512	SEMA3C	1.58	1.52E-03	378.31	315.55	365.26	584.09	552.15	541.50
10529	NEBL	1.55	6.03E-05	15.33	14.91	14.54	23.72	22.27	23.53
10535	RNASEH2A	2.15	7.19E-05	58.27	53.55	62.57	126.16	124.39	123.83
10584	COLEC10	-3.09	9.75E-03	27.36	54.96	28.09	11.06	12.61	12.09

10610	ST6GALNAC2	2.98	2.74E-03	58.05	37.06	63.87	164.91	155.39	153.03
10615	SPAG5	3.83	8.67E-04	39.32	24.55	38.13	127.77	133.05	129.57
10630	PDPN	3.00	2.77E-04	132.67	97.17	119.57	354.45	341.63	351.63
10635	RAD51AP1	3.26	3.67E-06	19.72	20.54	21.54	69.58	64.70	66.92
10687	PNMA2	-2.04	9.80E-03	28.94	20.68	31.06	11.06	14.66	13.85
10721	POLQ	2.27	1.38E-04	10.86	9.42	9.35	22.92	21.06	23.16
10733	PLK4	3.55	1.27E-05	29.70	28.04	32.59	102.51	108.73	109.45
10783	NEK6	-1.61	1.66E-05	350.72	336.30	348.48	216.26	218.86	208.63
10794	ZNF460	-1.71	7.77E-03	175.14	230.32	192.41	114.13	103.67	132.63
10856	RUVBL2	1.69	1.51E-05	146.70	149.23	151.97	261.54	248.30	246.94
10866	HCP5	1.61	8.17E-03	21.13	20.19	21.61	35.85	37.48	27.77
10867	TSPAN9	-1.50	9.92E-03	52.00	64.24	55.36	35.75	35.52	42.93
10875	FGL2	-1.71	8.53E-05	740.79	792.91	809.93	446.43	474.57	449.53
10891	PPARGC1A	-3.18	1.80E-04	93.91	106.23	88.14	34.16	29.44	27.19
11004	KIF2C	3.76	3.81E-04	15.13	12.12	18.42	57.52	58.10	56.20
11065	UBE2C	2.66	7.10E-04	35.19	26.67	37.11	84.07	88.33	91.22
11067	C10orf10	1.96	2.46E-04	112.50	125.05	126.09	256.70	231.36	224.93
11075	STMN2	-2.73	4.09E-03	1572.29	929.85	1464.56	499.27	474.24	481.33
11095	ADAMTS8	-1.67	1.44E-04	98.07	107.49	95.56	59.73	60.77	59.72
11096	ADAMTS5	-2.55	1.02E-04	181.73	201.49	185.75	70.30	70.32	82.18
11113	CIT	3.45	4.30E-03	71.90	36.45	68.44	205.85	195.17	208.33
11130	ZWINT	2.34	1.09E-06	55.09	55.41	56.74	134.33	127.50	130.31
11144	DMC1	1.69	2.72E-03	6.29	5.52	5.93	11.36	9.71	8.96
11185	INMT	-3.09	1.13E-04	150.73	179.41	175.79	54.18	49.87	59.49
11226	GALNT6	1.54	7.57E-05	159.55	164.76	170.16	248.56	251.50	263.88
11270	NRM	2.09	6.08E-05	107.50	107.61	115.13	228.70	243.86	216.10
11339	OIP5	2.25	5.48E-04	23.40	19.94	25.29	55.52	48.33	50.67
11340	EXOSC8	1.57	7.03E-04	93.18	93.86	94.68	142.73	160.90	137.68
22795	NID2	-2.47	1.52E-05	522.06	512.69	478.97	197.65	201.67	214.64
22801	ITGA11	-2.41	3.14E-03	305.60	205.84	312.25	115.95	113.72	111.67
22854	NTNG1	1.95	1.70E-04	63.38	61.49	71.36	132.16	125.07	124.74
22866	CNKSR2	1.92	3.18E-03	13.44	10.02	10.16	21.41	23.14	20.04
22874	PLEKHA6	-1.71	5.86E-03	133.69	102.98	138.31	77.98	70.32	70.65
22925	PLA2R1	-2.53	3.94E-04	178.37	135.19	167.28	63.48	62.75	64.06
22941	SHANK2	-2.00	2.52E-03	82.51	72.44	85.92	41.22	33.62	45.63
22974	TPX2	3.53	9.14E-04	102.54	67.93	106.21	337.27	328.71	311.71
22995	CEP152	1.52	9.82E-04	12.00	10.50	12.13	17.17	17.35	17.95
23017	FAIM2	2.72	1.48E-04	92.05	115.61	104.37	271.03	297.41	279.71
23022	PALLD	-1.54	5.05E-03	263.36	221.71	284.84	161.28	172.31	166.39
23025	UNC13A	-1.66	2.01E-03	15.80	19.17	18.88	10.23	11.47	10.74
23086	EXPH5	-1.73	1.51E-03	90.64	110.27	94.99	58.91	52.81	59.56

23089	PEG10	2.40	9.89E-03	443.02	242.35	434.09	889.42	903.71	898.78
23102	TBC1D2B	-1.53	7.98E-06	223.85	215.72	214.58	142.44	140.91	143.75
23150	FRMD4B	2.90	2.47E-03	21.03	13.72	22.83	58.72	55.22	53.16
23204	ARL6IP1	1.85	1.21E-04	1094.79	1209.07	1065.47	2138.85	2077.20	2022.96
23213	SULF1	-2.65	3.88E-08	729.50	716.36	720.48	275.52	272.83	269.04
23235	SIK2	-1.60	2.12E-06	585.30	569.30	573.53	356.25	366.04	360.93
23239	PHLPP1	1.78	1.66E-03	44.88	55.05	45.95	79.47	89.48	90.51
23255	KIAA0802	-1.73	1.34E-05	79.37	82.62	79.88	47.97	45.19	46.44
23310	NCAPD3	1.51	2.39E-05	74.68	77.25	77.11	113.05	118.85	114.56
23397	NCAPH	3.82	8.40E-08	33.69	34.38	32.84	130.21	127.66	128.06
23421	ITGB3BP	1.51	5.25E-03	110.21	137.58	111.87	185.88	182.94	172.73
23428	SLC7A8	-1.67	7.23E-03	684.38	517.64	707.37	377.14	391.58	371.42
23460	ABCA6	-2.81	2.66E-03	71.77	111.22	70.56	28.31	30.32	31.55
23461	ABCA5	-1.67	1.79E-03	25.41	31.58	26.87	16.30	16.35	17.49
23554	TSPAN12	-2.34	8.23E-03	23.01	37.26	22.54	12.58	10.99	11.86
23555	TSPAN15	5.35	9.50E-06	16.04	13.83	16.17	83.43	77.16	85.64
23556	PIGN	-1.57	1.37E-03	139.38	122.92	142.96	91.24	85.59	81.72
23594	ORC6L	1.77	1.54E-05	20.57	20.01	21.46	36.58	36.01	37.37
23705	CADM1	1.90	8.00E-04	72.81	59.67	70.04	135.51	129.97	119.87
23710	GABARAPL1	-1.67	2.94E-03	1299.86	1031.63	1286.66	738.76	738.46	694.65
23768	FLRT2	-1.82	2.28E-04	384.61	340.92	392.32	200.82	212.11	201.19
24137	KIF4A	5.23	9.22E-04	30.40	20.44	39.44	158.65	161.29	151.80
25788	RAD54B	2.24	4.07E-04	36.26	29.16	36.63	76.85	75.53	75.73
25797	QPCT	1.53	2.90E-03	85.01	73.97	71.30	111.10	114.69	125.96
25854	FAM149A	2.10	7.76E-03	20.08	12.53	19.53	38.00	36.21	35.30
25878	MXRA5	-7.21	4.11E-05	194.87	232.52	180.14	24.43	29.67	30.18
25886	POC1A	1.94	2.56E-03	26.91	21.43	27.99	47.20	54.75	46.08
25891	PAMR1	-2.45	1.68E-03	591.41	822.76	570.86	277.44	262.96	270.38
25903	OLFML2B	4.82	2.02E-05	57.20	71.46	60.01	300.51	305.59	303.70
25924	MYRIP	1.99	3.34E-03	20.42	14.07	18.63	35.34	34.72	35.79
25984	KRT23	1.53	1.24E-03	15.04	13.09	15.32	22.28	21.50	22.88
26025	PCDHGA12	-1.73	1.82E-03	106.54	117.74	103.14	65.01	68.77	55.67
26147	PHF19	1.66	5.42E-03	66.90	51.09	68.46	102.62	103.41	103.22
26191	PTPN22	2.67	1.65E-03	14.25	21.75	17.13	47.62	50.98	43.15
26271	FBXO5	2.49	3.82E-06	101.69	94.99	93.95	244.74	241.19	238.50
26503	SLC17A5	-1.69	1.95E-03	578.62	722.42	591.50	366.72	374.21	381.87
26585	GREM1	-1.52	1.35E-05	2833.23	2869.71	2787.10	1850.62	1917.34	1832.39
26586	CKAP2	2.56	1.70E-03	165.16	115.59	171.61	399.57	374.16	382.70
27085	MTBP	1.51	5.66E-03	18.19	20.41	16.76	30.77	26.28	26.58
27133	KCNH5	2.20	8.51E-06	6.42	5.84	6.10	13.53	13.41	13.44

27141	CIDEB	1.56	3.05E-03	22.60	19.80	24.38	32.98	34.12	36.98
27166	PRELID1	1.51	3.29E-03	939.51	885.13	765.43	1244.93	1357.92	1300.07
27198	GPR81	1.70	3.18E-04	7.43	6.90	8.06	12.54	12.57	13.01
27295	PDLIM3	2.82	7.12E-04	21.19	15.21	21.19	55.37	53.57	53.17
27316	RBMX	1.52	4.05E-03	132.93	117.21	120.89	168.07	188.83	205.86
27347	STK39	1.56	2.44E-03	383.09	312.42	373.28	557.49	573.60	540.56
28951	TRIB2	-1.58	4.37E-04	53.51	55.14	60.23	34.72	37.40	35.03
29015	SLC43A3	1.77	1.24E-04	553.02	610.28	542.97	992.12	1038.27	996.73
29028	ATAD2	1.95	4.50E-03	63.70	48.79	72.31	122.91	114.71	123.34
29089	UBE2T	2.56	1.35E-04	61.95	65.53	75.21	163.71	182.41	173.13
29091	STXBP6	1.67	3.58E-03	32.85	42.71	36.49	63.31	58.15	65.69
29094	HSPC159	1.51	6.56E-03	109.94	89.98	96.44	135.40	163.15	149.32
29127	RACGAP1	2.66	2.13E-04	158.69	128.51	163.92	403.74	400.76	393.85
29128	UHRF1	2.16	2.48E-04	70.42	78.35	85.72	171.34	159.99	174.20
29798	C2orf27A	-1.55	1.57E-03	71.00	76.62	76.82	50.25	43.57	51.26
29893	PSMC3IP	1.91	3.23E-03	20.64	16.96	23.46	38.14	41.97	36.35
29941	PKN3	1.67	8.21E-06	28.82	30.45	29.91	50.21	49.07	49.53
29953	TRHDE	-2.09	3.39E-04	122.28	101.23	123.13	55.35	55.09	55.72
30061	SLC40A1	-2.81	1.97E-04	559.93	444.43	555.53	183.58	192.36	179.21
50515	CHST11	1.64	3.66E-03	176.82	138.55	166.50	245.46	277.12	267.25
51016	FAM158A	1.60	1.86E-04	34.42	31.87	35.34	53.38	55.87	52.96
51053	GMNN	1.85	4.68E-04	43.72	52.19	47.96	85.40	94.05	87.15
51106	TFB1M	1.49	4.33E-03	54.83	67.44	55.21	88.49	90.77	85.93
51129	ANGPTL4	-2.42	4.37E-05	201.97	225.45	195.36	87.80	83.20	86.16
51155	HN1	1.67	1.86E-03	278.90	227.71	263.77	419.78	457.28	406.04
51171	HSD17B14	-1.64	8.52E-03	32.98	44.85	34.68	21.59	22.49	24.34
51200	CPA4	2.40	7.65E-03	165.89	97.27	169.34	348.49	335.12	354.15
51203	NUSAP1	4.47	1.56E-03	83.21	49.68	93.23	355.26	349.49	305.39
51363	CHST15	-2.08	2.98E-03	310.89	230.70	299.56	121.22	150.48	132.62
51384	WNT16	-1.59	3.59E-03	137.75	134.17	169.91	92.53	92.09	93.15
51512	GTSE1	2.42	6.68E-05	35.67	37.20	41.47	89.71	89.88	96.77
51514	DTL	2.37	2.35E-04	92.88	115.84	98.41	249.02	244.67	232.75
51533	PHF7	1.64	1.04E-03	27.51	30.38	24.84	46.03	45.22	44.73
51555	PEX5L	2.74	2.76E-03	55.36	36.19	59.14	138.77	130.42	143.13
51659	GINS2	2.20	9.78E-05	155.43	144.79	166.47	347.05	355.85	321.80
51704	GPRC5B	-2.41	1.47E-03	170.98	236.06	172.79	74.62	82.59	83.39
51765	MST4	2.14	9.92E-03	79.63	50.03	86.31	159.07	152.96	150.29
51816	CECR1	2.25	3.17E-03	13.52	16.77	11.35	30.08	28.49	35.18
54069	C21orf45	1.60	1.79E-04	39.08	40.28	40.02	63.57	67.65	60.17
54329	GPR85	1.84	6.87E-04	12.57	11.91	14.59	23.67	24.92	23.18

54443	ANLN	5.83	6.49E-04	148.25	94.52	176.18	830.09	823.18	788.08
54478	FAM64A	3.21	5.00E-04	31.05	24.88	35.75	97.85	105.53	90.81
54674	LRRN3	-2.09	7.35E-05	544.23	606.03	548.79	269.54	284.00	258.63
54700	RRN3	-1.53	2.79E-04	147.53	135.21	141.59	94.05	88.30	95.80
54733	SLC35F2	2.73	3.68E-04	22.20	29.47	28.18	75.27	69.69	73.19
54757	FAM20A	-3.53	5.12E-04	86.61	129.68	99.96	28.13	30.68	30.80
54821	ERCC6L	2.55	1.65E-04	5.19	4.35	5.40	12.82	12.28	12.91
54852	PAQR5	-2.61	5.00E-04	239.60	196.20	268.33	87.95	91.54	90.30
54879	ST7L	-1.90	5.93E-04	76.19	85.68	75.66	42.67	44.65	37.62
54892	NCAPG2	2.87	2.14E-04	44.97	44.57	56.51	135.52	135.98	147.95
54941	RNF125	1.66	4.90E-04	10.08	9.90	9.28	17.62	15.42	15.66
55008	HERC6	1.56	1.58E-03	43.22	50.07	43.48	75.50	67.18	71.26
55061	SUSD4	1.61	1.43E-03	14.46	12.67	15.27	21.68	22.97	23.68
55088	C10orf118	-1.71	1.27E-03	120.80	146.94	122.65	73.82	75.23	78.99
55089	SLC38A4	-2.13	6.10E-06	34.47	32.36	33.13	16.07	15.64	15.23
55143	CDCA8	4.04	6.92E-05	36.82	27.77	32.65	131.36	132.57	128.61
55165	CEP55	5.37	1.10E-03	53.26	32.56	64.69	273.78	270.14	264.01
55166	CENPQ	2.21	2.15E-03	27.15	37.40	30.43	77.54	70.30	62.17
55214	LEPREL1	-1.79	1.90E-03	211.76	173.29	225.46	112.81	114.33	113.30
55215	FANCI	2.49	2.69E-05	65.67	59.36	66.79	158.40	153.89	165.16
55224	ETNK2	-2.59	3.48E-04	102.17	134.58	109.48	45.25	44.79	43.46
55228	PNMAL1	1.98	5.12E-04	17.72	20.54	18.23	41.01	35.24	35.62
55243	KIRREL	-1.52	2.16E-04	396.15	441.23	416.94	271.39	280.38	272.17
55244	SLC47A1	2.20	1.52E-03	23.21	18.44	25.30	51.95	50.31	45.21
55247	NEIL3	3.39	5.47E-04	29.72	25.60	38.30	103.03	101.09	112.84
55248	TMEM206	1.66	3.77E-04	31.70	32.90	30.89	48.53	53.97	55.68
55320	C14orf106	1.67	3.56E-03	57.34	47.98	60.10	98.97	84.01	92.62
55351	STK32B	-2.68	1.06E-04	49.10	43.51	53.63	17.44	18.57	18.59
55355	HJURP	4.01	7.13E-05	66.56	52.10	63.98	247.74	254.61	229.19
55388	MCM10	2.25	3.75E-04	33.32	40.43	39.04	80.12	81.57	91.73
55536	CDCA7L	1.69	5.39E-03	64.06	85.62	67.52	115.26	131.71	121.08
55612	FERMT1	1.61	8.50E-03	46.39	35.91	50.07	72.17	72.16	69.41
55635	DEPDC1	5.18	7.47E-04	17.40	11.54	21.25	88.53	86.82	84.41
55706	TMEM48	1.68	6.83E-04	97.79	115.42	99.27	170.23	178.96	176.76
55711	FAR2	-1.62	9.10E-05	188.83	193.01	187.13	122.56	117.56	110.92
55714	ODZ3	-2.09	5.39E-05	196.08	201.97	206.09	96.73	90.10	102.72
55723	ASF1B	2.97	4.00E-05	97.43	97.01	113.59	302.24	317.34	296.34
55732	C1orf112	1.60	1.31E-04	18.98	21.12	20.15	32.81	31.85	31.86
55771	PRR11	3.71	1.98E-03	107.63	62.81	111.51	349.20	337.16	358.29
55789	DEPDC1B	1.93	4.37E-03	13.23	9.82	13.72	23.39	21.98	25.52
55790	CSGALNACT1	-2.15	2.73E-04	73.31	81.42	73.78	33.21	33.77	39.34

55839	CENPN	1.87	5.97E-03	201.67	138.74	195.84	335.54	332.42	335.26
55859	BEX1	-2.98	1.03E-04	70.38	58.10	68.22	22.85	20.34	22.78
55872	PBK	5.28	6.47E-04	36.18	22.25	38.89	173.25	171.56	168.78
56062	KLHL4	2.16	2.41E-05	4.39	4.80	4.59	9.49	10.17	10.15
56106	PCDHGA10	-2.31	5.90E-03	177.14	286.42	187.58	92.52	92.59	96.66
56108	PCDHGA7	-1.87	1.09E-03	21.66	23.84	23.71	13.75	12.33	10.85
56109	PCDHGA6	-1.82	8.64E-03	15.08	19.93	16.34	10.05	7.76	10.44
56111	PCDHGA4	-2.11	7.03E-03	24.02	18.24	28.27	10.01	10.87	12.58
56112	PCDHGA3	-3.34	6.09E-05	47.22	38.82	46.71	13.17	12.69	13.84
56113	PCDHGA2	-1.51	1.71E-04	43.26	39.75	41.66	28.05	28.06	26.60
56114	PCDHGA1	-1.52	1.30E-03	40.71	39.59	43.82	27.24	25.24	29.23
56122	PCDHB14	-3.69	1.18E-03	102.82	157.39	100.14	30.36	31.16	36.12
56123	PCDHB13	-2.39	5.79E-04	18.32	24.35	22.66	9.09	8.86	9.39
56124	PCDHB12	-1.50	8.41E-03	9.98	11.20	9.77	5.93	7.34	7.41
56125	PCDHB11	-1.92	2.36E-07	17.38	17.40	17.17	9.04	8.86	9.10
56126	PCDHB10	-2.38	1.60E-03	20.66	30.35	23.81	10.46	10.43	10.53
56127	PCDHB9	-2.72	1.21E-03	61.17	87.42	63.55	28.21	24.86	24.84
56128	PCDHB8	-1.69	8.40E-03	6.57	7.44	7.36	4.86	3.42	4.35
56133	PCDHB2	-2.08	1.97E-03	58.63	81.94	67.95	35.07	31.90	33.05
56180	MOSPD1	-1.62	2.64E-03	261.93	217.83	230.14	155.61	149.89	133.10
56271	BEX4	-1.95	9.21E-05	307.84	295.83	302.30	144.02	155.95	165.60
56477	CCL28	2.57	3.06E-05	57.19	53.37	62.21	145.85	148.53	150.50
56675	NRIP3	1.63	1.93E-04	159.15	142.80	157.07	247.45	256.87	244.41
56947	MFF	-1.63	6.67E-04	977.73	821.42	888.98	552.59	544.16	554.42
56992	KIF15	3.21	1.26E-04	14.22	10.97	12.97	42.13	38.91	41.61
56999	ADAMTS9	-2.04	3.08E-03	45.89	33.99	47.91	21.66	20.25	20.82
57082	CASC5	4.41	1.36E-03	45.01	28.96	54.60	192.28	176.37	198.06
57125	PLXDC1	3.71	1.69E-06	44.52	43.70	40.91	158.55	164.68	156.02
57194	ATP10A	-2.07	4.48E-03	66.01	49.08	74.45	30.52	30.44	30.44
57205	ATP10D	-1.70	1.02E-05	300.86	295.00	306.22	182.57	173.85	174.33
57211	GPR126	1.78	6.99E-03	40.75	60.44	49.30	90.38	85.76	91.92
57214	KIAA1199	-1.77	9.95E-03	1425.26	1003.11	1449.65	734.49	712.74	745.33
57405	SPC25	4.43	7.68E-06	19.05	17.52	20.47	80.68	87.03	85.23
57480	PLEKHG1	-2.21	6.35E-04	19.14	24.63	20.89	10.41	9.28	9.60
57520	HECW2	-2.57	7.22E-03	78.11	45.58	78.30	25.42	25.87	27.23
57522	SRGAP1	-1.54	2.59E-03	294.53	321.23	322.69	194.69	188.17	226.92
57542	KLHDC5	-1.59	8.68E-04	70.81	84.21	76.89	49.80	48.29	47.67
57546	PDP2	-1.52	1.29E-04	88.50	85.75	89.93	55.13	57.98	60.18
57556	SEMA6A	-2.24	6.73E-04	50.19	44.60	53.97	19.82	21.87	24.71
57580	PREX1	1.64	7.03E-06	24.20	23.57	24.81	40.07	39.21	40.06
57639	CCDC146	-1.54	2.28E-03	23.78	26.57	29.11	16.89	16.67	17.89

57643	ZSWIM5	-2.02	1.71E-03	100.32	85.89	117.06	49.47	48.33	52.56
57650	KIAA1524	2.90	2.30E-05	53.65	54.47	61.99	160.62	166.92	165.24
57717	PCDHB16	-5.14	1.83E-04	119.35	159.84	109.59	26.14	26.36	23.13
58189	WFDC1	-1.76	1.43E-03	249.19	301.39	242.67	153.48	143.16	152.94
58538	MPP4	1.85	5.83E-05	18.77	19.26	19.64	35.30	33.67	37.59
59084	ENPP5	-1.51	4.12E-04	86.89	78.46	86.56	57.04	53.58	55.88
59277	NTN4	-2.16	5.47E-06	136.24	145.23	135.32	63.31	64.61	64.96
60312	AFAP1	-1.72	3.21E-03	275.09	212.85	267.47	141.95	143.04	153.73
60489	APOBEC3G	-1.69	2.02E-04	39.80	38.52	42.33	24.28	24.68	22.43
63901	FAM111A	1.60	5.68E-04	76.56	86.65	78.53	127.61	136.16	123.56
63967	CLSPN	2.44	5.93E-03	29.32	18.96	33.51	66.61	67.20	65.51
64093	SMOC1	3.30	1.94E-03	56.25	31.77	44.90	147.63	138.13	153.38
64105	CENPK	2.14	1.01E-04	62.18	71.45	71.67	142.11	149.44	147.57
64151	NCAPG	3.99	3.26E-05	65.54	63.02	76.66	283.24	256.78	279.23
64288	ZNF323	-1.51	2.31E-03	16.04	19.06	16.09	10.95	11.35	11.58
64641	EBF2	1.73	7.96E-03	6.60	8.03	7.71	14.77	13.23	10.74
64759	TNS3	-1.73	5.26E-03	477.55	357.47	479.94	257.32	246.98	253.84
64785	GINS3	1.81	5.81E-04	29.61	27.28	30.83	56.57	54.31	48.21
64847	SPATA20	-2.92	2.82E-05	317.03	336.17	308.03	106.30	119.28	103.77
64866	CDCP1	2.34	2.56E-04	196.13	238.85	242.89	542.19	518.20	527.04
64901	RANBP17	1.78	2.13E-04	11.00	11.77	11.27	21.64	18.83	20.10
64943	NT5DC2	1.51	3.78E-05	553.68	576.26	586.36	882.12	857.73	847.82
64946	CENPH	2.33	9.32E-04	17.04	12.99	13.16	31.62	32.73	36.16
65997	RASL11B	-2.08	2.89E-03	49.87	66.44	46.91	24.73	26.28	27.36
78995	C17orf53	1.72	1.45E-03	36.81	42.58	46.26	69.59	74.52	71.59
79019	CENPM	1.88	3.98E-03	39.51	28.95	36.14	59.23	71.09	65.95
79056	PRRG4	2.11	1.49E-03	24.82	20.55	27.67	50.91	55.27	47.67
79153	GDPD3	1.63	5.19E-03	15.29	12.11	13.82	21.30	25.12	20.96
79154	DHRS11	1.52	2.69E-03	80.48	71.90	89.57	121.33	123.37	122.78
79172	CENPO	1.84	4.34E-04	69.70	62.24	74.42	122.96	132.56	124.25
79365	BHLHE41	1.51	7.91E-05	74.94	79.13	74.31	115.28	117.25	111.38
79603	LASS4	1.99	1.25E-04	33.94	32.09	33.40	62.34	63.58	71.67
79633	FAT4	-1.67	4.70E-03	225.47	253.46	244.27	137.65	126.97	168.56
79652	TMEM204	-1.63	8.85E-04	300.84	313.66	313.46	175.83	210.09	184.04
79659	DYNC2H1	-1.83	3.34E-03	48.28	49.71	56.61	30.00	23.67	30.86
79674	VEPH1	1.82	1.45E-03	56.02	43.30	51.32	94.77	89.61	90.29
79682	MLF1IP	3.17	5.69E-05	83.45	68.98	80.29	259.95	240.72	237.58
79686	C14orf139	-1.55	2.78E-03	117.61	104.26	125.87	80.18	70.81	74.00
79733	E2F8	3.01	2.01E-07	15.87	15.67	15.26	47.62	46.07	46.97
79750	ZNF385D	2.09	2.16E-04	83.18	100.96	88.66	186.66	193.75	190.60
79789	CLMN	1.57	8.12E-04	7.48	6.99	7.96	11.03	11.81	12.33

79801	SHCBP1	3.66	1.40E-04	63.04	50.03	67.29	226.62	214.55	218.41
79822	ARHGAP28	1.75	2.07E-03	37.02	30.44	31.11	61.57	52.23	58.56
79834	SGK269	-1.57	4.28E-04	374.43	413.53	369.80	237.38	241.71	256.28
79866	C13orf34	1.73	5.19E-05	19.08	20.92	20.14	35.49	33.97	34.39
79905	TMC7	2.37	1.06E-04	59.59	54.26	64.88	136.86	139.15	147.53
79968	WDR76	2.14	1.58E-04	88.27	92.14	80.26	191.86	194.24	172.82
79974	C7orf58	-1.51	5.85E-03	405.27	338.39	437.01	260.34	259.09	262.09
79980	DSN1	1.80	1.13E-04	102.80	112.39	107.30	192.01	203.43	183.99
80010	RMI1	1.92	6.09E-06	27.83	28.65	27.71	55.19	54.18	51.96
80071	CCDC15	1.77	6.06E-03	7.76	10.95	10.23	17.32	17.82	16.12
80176	SPSB1	-1.50	2.61E-03	167.01	172.30	145.45	104.63	114.27	103.41
80210	ARMC9	-1.52	1.25E-05	313.08	300.64	302.37	199.96	204.74	198.21
80310	PDGFD	-1.99	2.36E-03	34.79	44.31	35.63	17.06	19.45	21.22
80315	CPEB4	-2.17	2.02E-03	115.73	159.13	129.70	57.60	60.35	68.80
80323	CCDC68	-2.72	3.03E-04	116.34	104.55	138.89	45.18	42.63	44.67
80339	PNPLA3	-2.19	1.42E-03	87.09	63.10	79.53	36.60	33.95	34.51
80704	SLC19A3	-1.70	2.02E-03	21.79	18.28	22.40	12.74	11.40	12.70
81031	SLC2A10	-1.66	8.00E-03	222.15	306.12	234.43	153.75	148.67	158.21
81610	FAM83D	2.94	1.15E-03	61.62	43.09	65.56	164.38	163.46	172.70
81624	DIAPH3	2.84	3.07E-03	61.95	39.98	68.67	155.86	166.64	161.29
81691	LOC81691	2.10	3.65E-03	42.59	31.43	47.19	81.79	84.61	88.60
81831	NETO2	2.88	3.65E-03	121.43	73.58	128.09	321.47	298.84	308.67
81832	NETO1	-3.34	1.35E-03	17.89	26.83	16.93	5.91	6.01	6.57
81851	KRTAP1-1	2.64	5.38E-03	225.56	130.00	222.78	503.90	524.57	496.75
83461	CDCA3	3.30	2.48E-04	30.24	22.17	28.67	92.18	88.61	86.75
83463	MXD3	1.54	1.53E-03	46.44	40.05	47.46	70.90	69.34	66.42
83540	NUF2	6.10	2.17E-05	19.72	15.59	19.15	117.06	108.27	106.77
83543	AIF1L	3.40	2.62E-04	20.15	15.78	21.52	60.97	65.23	69.22
83716	CRISPLD2	-2.73	1.24E-03	471.21	320.01	442.02	144.77	153.88	153.87
83857	TMTC1	-1.61	9.87E-04	832.11	707.27	780.82	468.84	466.35	507.99
83872	HMCN1	-2.48	4.68E-04	39.48	35.45	40.74	16.28	13.33	17.08
83879	CDCA7	2.17	1.87E-04	13.03	12.53	10.92	27.11	25.15	26.94
83895	KRTAP1-5	3.31	5.74E-04	296.31	444.82	337.33	1185.64	1238.11	1147.63
83903	GSG2	1.66	1.43E-03	30.97	26.46	28.05	43.17	48.83	50.06
83935	TMEM133	1.92	1.93E-03	88.29	113.56	116.47	195.02	206.70	210.00
83956	RACGAP1P	1.83	3.86E-03	6.76	6.52	7.74	14.01	13.64	10.73
83987	CCDC8	1.55	2.48E-03	26.16	23.76	24.83	42.76	35.08	37.80
83990	BRIP1	1.77	2.09E-03	33.09	42.08	35.91	61.62	64.51	70.64
84002	B3GNT5	1.71	7.66E-03	44.25	33.29	41.69	67.81	75.56	60.30
84057	MND1	3.11	2.51E-04	10.36	11.60	13.65	36.10	40.35	34.48
84058	WDR54	1.61	1.09E-03	128.98	155.07	133.84	223.84	226.29	221.10

84197	SGK196	-1.55	2.90E-03	212.99	260.11	237.52	146.68	148.13	163.39
84216	TMEM117	-1.64	8.47E-04	112.72	129.08	113.81	74.46	75.04	67.72
84251	SGIP1	-2.30	5.77E-04	276.20	346.66	279.31	132.24	138.68	121.58
84288	EFCAB2	-1.56	9.04E-04	39.39	39.86	34.78	25.43	23.33	24.34
84293	C10orf58	2.20	1.46E-03	7.14	9.76	7.92	19.43	18.52	16.74
84296	GINS4	1.94	4.43E-03	57.58	44.59	62.87	113.76	110.35	95.90
84441	MAML2	-1.65	5.18E-05	392.88	366.76	389.35	228.31	240.39	229.43
84456	L3MBTL3	-1.56	3.92E-04	60.07	53.43	58.41	35.95	38.19	36.05
84515	MCM8	1.86	4.32E-03	109.81	82.99	117.99	195.54	187.54	194.10
84649	DGAT2	1.94	1.61E-03	53.54	43.25	51.13	106.60	87.93	92.01
84675	TRIM55	2.62	2.40E-04	17.09	15.43	16.70	39.60	40.15	49.26
84681	HINT2	1.50	4.12E-03	258.08	285.32	226.52	397.55	376.59	378.34
84795	PYROXD2	-1.89	6.70E-03	72.15	88.96	58.76	37.88	39.07	39.52
84870	RSPO3	1.90	1.44E-03	96.42	121.94	108.36	189.58	222.58	207.78
84898	PLXDC2	-2.46	7.32E-04	350.25	455.37	336.51	157.91	152.93	153.45
84900	RNFT2	2.01	2.36E-04	42.07	50.09	43.48	89.92	93.85	88.77
84930	MASTL	1.55	2.82E-03	160.61	137.21	172.23	247.56	242.00	240.06
84952	CGNL1	2.42	2.08E-04	9.29	8.53	8.29	18.97	20.89	23.28
84969	TOX2	1.59	4.21E-04	38.64	38.76	34.37	57.24	59.56	60.59
85004	RERG	1.76	6.77E-03	8.06	9.60	11.81	16.65	17.37	17.78
85235	HIST1H2AH	2.76	6.60E-04	8.25	8.44	8.87	20.71	28.55	21.31
85444	LRRCC1	1.78	2.81E-03	52.15	42.46	50.61	92.91	88.93	76.22
85461	TANC1	-1.68	1.42E-03	130.31	159.36	136.07	81.39	84.17	88.18
85463	ZC3H12C	-1.91	2.25E-04	145.36	170.77	161.40	82.86	80.40	86.12
89891	WDR34	1.51	9.68E-05	153.35	159.20	155.49	237.83	242.60	224.20
90102	PHLDB2	-1.84	5.91E-03	137.59	96.48	130.76	67.61	64.21	66.53
90381	C15orf42	2.60	3.95E-03	27.80	18.68	31.89	66.91	64.49	72.64
90417	C15orf23	2.06	1.37E-03	135.72	110.12	149.28	278.23	260.62	275.46
90865	IL33	-2.66	4.42E-03	210.08	129.15	209.07	73.30	67.51	65.08
91057	CCDC34	1.61	1.13E-03	43.50	36.24	37.82	63.57	64.33	61.10
91368	CDKN2AIPNL	1.51	5.58E-03	250.69	193.30	216.83	342.28	326.31	328.16
91526	ANKRD44	-1.59	9.18E-04	46.77	46.54	48.10	31.84	26.75	30.34
91687	CENPL	1.54	2.72E-03	28.42	25.03	24.27	39.77	36.98	43.14
91752	ZNF804A	-1.79	5.35E-03	62.72	89.79	75.99	42.61	42.38	42.89
92126	DSEL	-1.50	8.96E-04	919.30	985.23	889.77	630.37	579.86	651.46
92667	C20orf72	1.82	2.52E-04	51.25	57.45	49.78	95.52	100.27	93.02
92737	DNER	-1.58	3.20E-04	59.29	54.09	60.26	37.38	37.48	35.20
93100	NAPRT1	-1.52	1.96E-03	117.52	111.44	106.41	80.99	68.34	71.89
93166	PRDM6	1.89	2.64E-04	33.49	28.48	28.82	57.65	57.72	56.39
93323	HAUS8	1.62	3.59E-04	17.31	15.00	16.44	26.63	25.78	26.45
93517	SDR42E1	2.10	2.48E-03	18.54	16.42	21.43	39.94	34.05	44.55

112574	SNX18	-1.62	3.41E-05	103.58	112.22	108.42	66.47	66.77	67.35
113115	FAM54A	2.42	3.60E-04	14.88	13.95	15.19	35.56	30.91	39.92
113130	CDCA5	2.39	1.11E-03	28.07	24.15	34.25	72.49	68.22	65.73
113835	ZNF257	1.73	9.18E-03	3.46	2.73	3.99	5.49	6.29	5.81
114134	SLC2A13	-1.74	7.71E-03	207.37	165.23	239.11	118.94	112.88	120.02
114795	TMEM132B	1.58	1.09E-03	34.58	33.41	33.89	55.45	57.25	48.18
114804	RNF157	2.41	9.17E-03	43.18	77.49	44.41	132.67	140.41	124.02
114897	C1QTNF1	-1.66	5.13E-05	196.01	203.58	186.98	116.16	120.86	117.17
114898	C1QTNF2	2.38	7.41E-05	69.06	71.72	80.77	176.09	169.24	182.28
114899	C1QTNF3	1.51	9.11E-04	9.48	9.91	10.02	15.03	15.70	13.58
115701	ALPK2	-1.83	1.74E-05	31.98	33.59	30.86	17.59	17.73	17.49
115752	DIS3L	1.58	4.70E-03	46.32	51.25	40.13	76.70	73.58	67.24
116093	DIRC1	-2.02	2.46E-03	14.36	18.98	13.85	7.47	8.02	7.92
116496	FAM129A	1.89	3.29E-05	217.33	197.36	210.55	387.15	390.62	403.20
116832	RPL39L	2.12	1.11E-04	22.17	22.55	20.46	43.10	49.37	45.62
117854	TRIM6	1.81	3.36E-03	40.76	36.13	31.21	60.14	62.76	72.30
120892	LRRK2	-1.61	2.98E-03	50.74	43.42	55.25	30.00	30.79	32.06
121601	ANO4	-2.17	4.73E-04	135.28	115.75	106.72	52.95	57.49	54.59
122402	TDRD9	1.63	2.18E-03	3.17	3.71	3.85	5.94	5.42	6.09
122704	MRPL52	1.52	4.47E-05	57.86	53.96	54.56	85.32	84.39	83.96
122769	PPIL5	2.07	1.65E-04	26.93	31.17	31.89	62.94	62.48	61.29
126820	WDR63	-1.79	4.50E-03	57.04	42.86	56.85	30.92	27.88	28.84
127435	PODN	-2.38	4.16E-04	994.83	785.02	991.31	398.94	379.57	385.52
128239	IQGAP3	4.86	1.30E-04	32.46	23.89	33.03	149.70	148.46	136.24
128553	TSHZ2	2.10	1.68E-03	19.37	17.56	21.60	44.89	34.90	43.24
130271	PLEKHH2	-1.82	1.41E-04	102.89	95.03	99.52	50.77	56.46	56.37
130576	LYPD6B	-2.25	9.34E-04	26.69	24.10	24.17	9.89	10.33	13.09
131578	LRRC15	-1.99	2.82E-05	245.32	267.47	255.72	129.60	133.11	124.22
131873	COL6A6	-1.65	1.20E-03	46.34	46.50	44.11	28.62	24.50	29.73
132299	OCIAD2	1.86	3.74E-03	40.72	54.88	40.31	86.15	85.83	80.33
133383	C5orf35	1.60	3.25E-03	12.31	14.42	11.21	20.87	19.89	19.89
134492	NUDCD2	1.53	3.05E-03	28.54	22.75	24.98	38.09	39.75	38.76
137835	TMEM71	3.05	8.82E-04	12.07	15.46	13.81	38.54	51.01	36.74
140862	ISM1	-2.91	9.21E-03	170.89	92.74	174.25	43.37	51.50	55.45
143872	ARHGAP42	1.90	2.05E-03	183.20	222.87	249.44	406.45	414.19	422.26
144455	E2F7	1.58	5.89E-04	50.36	53.06	58.34	86.11	82.42	87.53
144535	C12orf55	2.34	1.06E-04	20.25	19.82	18.23	41.98	49.08	45.17
144811	C13orf31	-1.66	2.02E-04	52.67	49.38	46.75	29.53	30.86	28.99
146434	ZNF597	-1.71	2.60E-03	69.43	89.19	79.69	46.10	49.32	44.08
146909	KIF18B	2.19	4.32E-04	24.62	20.77	26.38	54.64	51.30	51.56
146956	EME1	2.38	3.99E-04	14.06	13.29	16.84	32.78	36.98	35.38

147495	APCDD1	1.95	3.37E-03	97.41	133.12	94.83	214.78	211.86	208.42
148206	ZNF714	1.56	2.73E-03	35.40	29.55	34.96	55.47	49.56	50.73
148523	C1orf51	1.63	9.87E-04	40.55	35.89	43.19	63.35	67.33	64.82
150468	CKAP2L	4.40	3.98E-04	38.28	31.97	50.47	188.08	167.13	175.98
151246	SGOL2	2.40	6.24E-03	57.20	36.47	63.53	124.39	122.19	130.70
151648	SGOL1	4.24	4.89E-04	17.32	13.82	22.22	79.37	70.98	75.69
153769	SH3RF2	2.60	5.22E-03	53.19	32.86	57.35	120.82	133.14	119.34
155368	WBSCR27	1.84	2.32E-04	56.84	56.59	55.10	94.59	103.36	111.38
157313	CDCA2	2.26	7.21E-03	56.99	39.62	69.94	126.48	125.62	123.81
157570	ESCO2	3.41	5.81E-04	55.47	36.84	50.68	168.46	159.23	160.52
158158	RASEF	1.51	5.93E-04	11.02	11.74	11.45	16.97	18.37	16.18
160857	CCDC122	-1.67	1.66E-03	36.15	43.46	37.90	21.79	24.87	23.84
161176	C14orf49	-1.54	6.87E-04	80.86	80.95	82.03	50.03	50.54	57.63
161198	CLEC14A	-2.73	3.67E-03	41.68	68.84	46.07	21.03	17.83	18.49
161291	TMEM30B	1.55	1.00E-03	63.91	62.50	73.07	100.82	105.97	102.02
161357	MDGA2	-2.49	1.68E-03	13.95	11.60	17.05	5.78	6.11	5.25
162681	C18orf54	2.30	4.64E-03	21.76	16.21	26.91	51.79	47.14	50.60
163786	SASS6	1.94	5.12E-04	23.89	27.71	29.62	54.23	51.59	52.07
167359	MGC42105	1.91	5.08E-04	16.12	15.79	17.70	34.73	29.18	30.62
167681	PRSS35	-2.08	8.56E-04	66.13	56.79	62.80	32.15	31.41	25.90
169792	GLIS3	-2.05	5.20E-05	175.98	184.25	188.51	85.30	87.37	95.25
192683	SCAMP5	-2.18	2.35E-04	97.98	96.22	101.67	45.74	40.46	49.80
195828	ZNF367	2.18	6.53E-03	56.59	94.72	66.99	163.01	149.52	163.91
196051	PPAPDC1A	-3.67	4.23E-06	130.91	120.05	127.12	33.20	33.52	36.26
199777	ZNF626	-1.50	1.68E-03	177.78	170.23	153.30	118.15	106.52	109.08
219621	C10orf107	-3.78	3.97E-05	30.39	24.29	26.82	6.99	7.10	7.45
219844	HYLS1	2.05	6.93E-03	18.52	12.44	16.54	36.16	33.58	27.77
220042	C11orf82	2.01	2.58E-04	26.65	25.85	30.91	54.86	54.96	57.43
220134	SKA1	3.89	3.33E-04	25.15	18.96	27.05	97.07	96.49	83.17
220441	RNF152	-2.39	7.74E-04	188.28	189.89	236.34	76.07	89.00	91.82
220963	SLC16A9	1.73	4.10E-03	8.13	6.10	7.83	13.33	12.67	12.19
220965	FAM13C	1.72	5.44E-03	25.75	33.20	24.17	49.37	45.10	48.58
221079	ARL5B	-1.58	3.37E-03	210.45	270.42	236.67	148.64	153.11	151.20
221150	SKA3	3.75	5.55E-04	35.05	29.56	46.11	144.13	141.38	129.93
221184	CPNE2	1.57	6.72E-03	136.72	183.07	148.46	249.18	250.25	235.90
221662	RBM24	-1.57	5.42E-03	32.12	39.57	38.37	21.17	24.74	24.33
221756	MGC39372	2.14	4.78E-04	13.17	15.62	15.51	32.80	28.67	33.19
221935	SDK1	2.04	1.36E-03	19.54	15.17	17.88	33.19	34.77	39.45
246777	SPESP1	-2.70	2.57E-05	12.61	13.94	12.40	4.74	5.07	4.64
259266	ASPM	5.43	7.92E-04	32.11	19.43	35.62	157.56	151.91	164.21
283209	PGM2L1	-1.74	1.22E-03	150.81	130.73	158.24	81.04	80.97	90.27

283383	GPR133	-2.10	2.95E-03	55.80	39.57	54.11	22.79	23.63	24.89
283431	GAS2L3	2.22	3.29E-05	91.08	85.83	92.39	211.70	191.24	194.50
284371	ZNF841	-1.60	9.05E-05	63.17	67.12	67.38	40.85	39.77	42.73
284403	WDR62	1.88	5.08E-04	27.64	24.89	27.80	51.56	53.90	45.63
284612	SYPL2	-1.62	2.72E-03	66.03	80.54	65.90	41.19	45.60	44.02
285025	CCDC141	1.55	9.14E-03	5.26	4.15	4.69	8.15	6.60	7.09
285440	CYP4V2	1.73	7.00E-05	222.96	216.08	221.89	404.17	372.28	366.04
285643	KIF4B	2.07	2.28E-04	11.61	11.24	12.77	23.66	26.74	23.36
286097	EFHA2	-1.68	5.57E-06	59.99	60.11	61.84	36.75	35.19	36.27
286826	LIN9	1.77	3.73E-03	14.31	19.23	18.28	31.56	28.93	31.04
286827	TRIM59	2.60	8.34E-05	50.27	46.24	53.84	138.27	131.19	121.01
317772	HIST2H2AB	2.81	2.95E-05	130.25	145.36	152.47	405.15	407.91	389.16
337875	HIST2H2BA	2.04	2.90E-03	493.24	347.98	452.16	938.79	877.91	824.56
339834	CCDC36	1.62	5.97E-03	16.73	14.05	15.57	25.15	28.14	21.77
343099	CCDC18	1.51	6.40E-03	13.92	15.90	12.18	20.53	22.17	20.90
344887	LOC344887	-1.76	2.78E-03	39.99	41.74	34.68	24.98	20.59	20.40
345557	PLCXD3	3.36	1.05E-03	16.94	11.25	17.46	54.02	50.85	48.72
346171	ZFP57	2.17	9.72E-04	12.31	10.24	9.64	23.65	25.04	21.05
347240	KIF24	1.64	4.98E-03	11.57	10.69	13.76	17.87	20.20	20.99
348093	RBPMS2	1.70	6.56E-04	45.77	38.71	39.03	68.75	71.01	69.81
348654	GEN1	1.71	1.15E-04	52.33	55.29	50.40	91.29	86.03	93.05
353139	LCE2A	3.17	6.75E-04	189.54	249.05	181.43	597.07	749.43	619.86
374393	FAM111B	3.37	3.69E-05	33.03	37.01	39.89	129.05	123.90	117.80
374467	C12orf63	4.26	3.69E-04	4.64	3.81	5.54	22.80	17.78	19.08
375444	C5orf34	1.51	6.36E-03	20.15	16.87	17.72	30.30	24.81	27.41
386618	KCTD4	3.05	6.79E-04	13.65	11.14	10.00	35.73	30.68	39.53
387103	CENPW	2.55	1.69E-04	14.15	12.60	15.97	36.75	35.64	36.37
387496	RASL11A	1.54	1.94E-03	50.13	45.45	54.79	81.33	74.79	75.56
388272	C16orf87	-1.77	2.65E-03	90.10	101.26	115.99	52.80	60.49	60.19
388566	ZNF470	-1.58	4.15E-04	37.94	40.87	41.18	26.56	25.51	23.68
389432	SAMD5	-2.03	4.55E-04	21.32	25.54	26.06	11.72	12.45	11.82
390980	ZNF805	-1.64	1.14E-03	81.66	75.79	87.92	49.74	46.42	53.51
399694	SHC4	-2.94	5.83E-03	56.27	109.60	75.30	26.47	27.04	28.49
400451	FAM174B	1.89	3.98E-03	33.29	32.95	34.16	50.80	70.94	67.55
401207	FLJ44606	1.52	6.70E-03	22.75	27.24	22.48	34.34	35.27	40.73
401233	LOC401233	-3.17	4.47E-04	44.72	62.78	58.02	16.56	17.04	18.55
414149	ACBD7	1.52	2.79E-03	6.45	5.44	6.71	9.44	9.34	9.47
440993	LOC440993	-1.53	5.00E-05	42.11	40.32	41.99	27.58	27.72	26.19
441631	TSPAN11	-2.85	7.20E-03	86.37	157.81	88.69	36.53	41.04	39.12
442213	C6orf138	-2.30	4.01E-04	56.71	67.67	55.84	27.83	26.69	23.98
574449	MIR492	1.55	9.05E-03	7.33	5.63	5.83	10.49	9.67	9.00

643853	TMPPE	-1.50	3.11E-03	44.60	47.46	43.61	29.59	33.49	27.36
644128	RPL23AP53	-1.81	8.15E-04	8.85	10.24	9.46	5.33	5.65	4.76
654342	LOC654342	-1.67	1.29E-03	455.32	393.66	465.67	255.25	280.89	250.14
654433	LOC654433	-1.81	1.88E-03	147.31	138.55	124.81	74.04	84.88	67.63
677837	SNORA60	-1.55	2.38E-03	45.41	52.75	47.98	34.03	28.95	31.34
727936	GXYLT2	-1.52	2.59E-04	183.57	171.38	175.98	122.51	115.51	111.31
728392	LOC728392	-3.33	1.34E-03	373.16	239.45	358.23	88.49	100.36	102.57
767582	SNORD114-6	-3.57	1.80E-03	12.25	12.06	18.52	3.30	4.11	4.60
1E+08	TSTD1	2.71	8.50E-04	30.94	42.97	30.61	92.48	93.51	96.76
1E+08	LOC100132288	2.61	3.96E-05	58.54	52.29	61.45	151.35	146.72	151.42
1E+08	LOC100133106	-1.85	4.06E-03	12.47	17.50	14.92	8.54	8.01	7.77
1E+08	CD24	30.08	2.58E-03	28.59	4.96	21.25	590.29	551.33	506.88
25	ABL1	-1.14	4.14E-02	493.67	427.63	479.74	408.72	407.97	410.92
92	ACVR2A	-1.23	3.00E-03	34.33	33.10	33.79	26.20	27.36	29.05
473	RERE	-1.18	1.94E-02	262.23	244.40	277.84	216.21	219.41	231.58
613	BCR	-1.12	4.97E-02	190.89	179.06	199.29	159.66	171.13	175.52
767	CA8	-1.07	3.77E-02	3.59	3.46	3.38	3.30	3.18	3.29
919	CD247	-1.09	2.17E-01	9.91	8.56	8.61	8.55	8.51	7.86
923	CD6	-1.04	1.23E-01	17.49	17.07	17.17	17.06	16.75	16.14
953	ENTPD1	-2.85	2.93E-02	24.89	57.41	24.24	13.91	11.07	12.43
1107	CHD3	-1.20	1.89E-02	166.71	144.71	165.28	131.68	128.55	135.60
1352	COX10	-1.11	4.75E-03	115.38	110.74	113.55	103.88	103.02	99.30
1439	CSF2RB	-1.21	2.41E-02	20.04	17.40	17.50	14.64	15.92	15.01
1871	E2F3	-1.11	1.72E-01	37.15	44.90	39.10	37.13	35.35	37.06
2297	FOXD1	-1.13	3.07E-02	150.03	160.66	170.07	142.02	141.37	142.85
2348	FOLR1	-1.32	2.91E-02	21.33	18.87	20.91	17.06	13.28	16.01
2803	GOLGA4	-1.12	5.15E-02	257.58	225.61	251.50	218.22	213.94	221.47
3064	HTT	-1.16	2.67E-02	139.76	134.98	145.56	118.06	114.19	129.69
3075	CFH	1.52	2.33E-02	287.97	197.26	277.14	393.30	380.52	383.68
3223	HOXC6	-1.37	3.94E-02	58.23	51.51	60.26	49.61	37.30	37.17
3460	IFNGR2	-1.13	3.88E-03	223.34	217.19	225.44	190.62	197.66	201.88
3651	PDX1	-1.09	1.43E-01	24.02	21.12	20.86	20.63	19.36	20.29
3675	ITGA3	1.87	2.31E-02	405.49	241.40	427.01	679.22	648.21	676.16
3920	LAMP2	-1.08	2.01E-02	625.38	602.82	600.75	579.50	562.50	546.02
4035	LRP1	-1.48	4.12E-02	1285.04	953.33	1345.54	804.33	703.46	908.54
4054	LTBP3	-1.35	4.99E-03	232.61	214.85	257.29	171.53	173.83	177.07
4088	SMAD3	-1.17	2.70E-03	464.80	466.06	485.20	390.60	417.54	401.49
4240	MFGE8	-1.34	2.16E-02	2097.67	1621.71	1983.73	1399.92	1449.85	1394.47
4609	MYC	-1.44	2.51E-02	165.49	230.93	181.86	127.72	139.58	133.41

4803	NGF	-1.06	1.70E-01	35.17	32.09	31.50	31.38	30.06	31.34
4837	NNMT	-1.21	3.23E-04	745.27	739.43	736.06	598.39	612.08	631.89
4908	NTF3	-1.21	1.60E-01	27.99	36.01	28.08	21.97	27.77	26.32
6041	RNASEL	-1.28	1.98E-02	23.91	24.09	27.42	18.44	19.05	21.56
6514	SLC2A2	-1.06	2.32E-01	3.27	3.65	3.23	3.21	3.17	3.22
6830	SUPT6H	-1.07	4.10E-02	518.99	510.73	515.91	473.61	473.43	504.07
6909	TBX2	-1.38	5.79E-03	157.81	191.66	165.16	126.47	122.80	123.53
7102	TSPAN7	-1.09	1.87E-01	5.43	6.41	5.54	5.34	5.15	5.42
7150	TOP1	-1.13	3.97E-02	685.84	600.19	653.64	573.14	570.96	577.57
7249	TSC2	-1.19	5.84E-03	239.69	266.00	247.10	213.71	211.68	206.96
7430	EZR	1.78	1.79E-02	321.29	197.99	307.92	500.58	490.94	484.45
7574	ZNF26	-1.10	1.84E-02	27.27	28.50	27.75	26.04	25.71	24.35
7837	PXDN	-1.23	3.25E-04	931.17	931.46	916.10	758.74	730.29	773.80
8237	USP11	-1.10	4.06E-02	286.29	276.61	308.81	263.45	262.94	263.83
8450	CUL4B	-1.33	4.22E-02	252.43	187.99	243.70	173.38	170.47	171.95
8521	GCM1	-1.05	4.90E-02	4.13	4.22	4.19	3.88	4.03	4.08
8707	B3GALT2	-2.20	4.34E-02	12.35	26.69	15.35	7.50	7.08	10.18
8729	GBF1	-1.19	2.88E-02	451.23	399.25	451.57	354.84	352.90	388.34
8871	SYNJ2	-1.44	2.09E-03	162.78	147.32	171.90	111.64	106.93	116.23
8908	GYG2	-1.31	4.80E-02	31.76	42.62	33.54	28.02	26.51	28.03
9074	CLDN6	-1.17	5.32E-02	3.96	4.04	4.67	3.72	3.68	3.47
9635	CLCA2	-4.65	1.81E-02	98.26	30.88	86.04	16.62	15.40	14.23
9871	SEC24D	-1.20	1.80E-02	729.35	803.74	701.74	615.92	648.10	595.94
10014	HDAC5	-1.14	4.52E-02	199.87	220.76	218.45	175.95	194.27	192.13
10577	NPC2	-1.18	4.16E-02	1210.12	1375.61	1154.97	1072.53	1077.34	1011.54
22808	MRAS	-1.28	4.55E-02	240.76	183.79	230.73	168.51	174.03	168.13
22954	TRIM32	-1.15	3.68E-02	164.22	184.53	166.87	145.89	157.36	146.99
23041	MON2	-1.27	2.22E-02	163.53	194.68	170.62	134.67	132.42	149.80
23160	WDR43	-1.22	2.50E-03	281.85	257.03	278.85	225.36	221.71	221.84
23345	SYNE1	-1.27	2.67E-02	47.49	45.99	52.20	38.26	34.51	42.24
23352	UBR4	-1.29	2.83E-02	423.73	431.14	454.94	336.10	294.74	382.18
23389	MED13L	-1.17	4.49E-02	287.92	335.44	291.66	252.79	258.10	271.87
23411	SIRT1	-1.05	2.72E-03	144.32	140.91	143.39	136.57	135.91	135.75
23429	RYBP	-1.31	1.79E-03	142.20	154.63	146.68	108.41	118.74	110.54
23654	PLXNB2	-1.20	2.48E-03	638.65	678.38	629.14	528.73	551.42	546.95
23741	EID1	-1.14	2.31E-02	468.29	485.33	515.35	445.72	408.89	429.48
26092	TOR1AIP1	-1.18	2.90E-02	701.36	765.43	660.84	630.64	589.27	579.95
26813	SNORD36C	-1.30	1.67E-02	101.63	97.81	101.36	74.15	87.49	70.40
27063	ANKRD1	-1.80	4.41E-02	28.19	16.51	29.99	14.63	13.19	13.63
27079	RPUSD2	-1.08	1.44E-01	43.99	44.78	49.21	40.82	43.14	43.97
29035	C16orf72	-1.17	4.94E-02	240.56	282.42	244.01	212.87	225.88	219.37

51310	SLC22A17	-1.45	1.24E-01	156.45	262.72	154.51	126.79	132.84	135.44
51566	ARMCX3	-1.28	3.37E-02	121.47	101.93	125.49	94.97	83.91	94.41
53373	TPCN1	-1.36	2.97E-03	172.68	200.51	180.61	132.79	135.32	140.13
54850	FBXL12	-1.06	5.14E-02	114.25	118.69	113.72	111.68	110.14	106.28
55285	RBM41	-1.12	5.12E-03	27.74	28.99	28.04	24.84	24.76	26.00
55356	SLC22A15	-1.38	1.23E-01	23.57	38.31	25.36	20.53	21.20	21.62
55701	ARHGEF40	-1.21	3.87E-02	80.55	96.71	87.76	75.98	68.88	74.94
55761	TTC17	-1.29	2.18E-01	170.17	271.17	169.24	161.71	154.88	157.03
55779	WDR52	-1.13	5.62E-02	7.40	6.83	6.57	5.99	6.49	5.87
56160	NDNL2	-1.07	2.56E-02	90.89	95.18	89.77	87.37	84.77	84.47
56776	FMN2	-1.44	2.84E-02	205.81	149.90	201.75	127.63	135.28	124.85
57181	SLC39A10	-1.47	2.55E-04	301.46	328.78	327.54	214.97	222.63	212.46
57393	TMEM27	-1.27	5.59E-02	7.49	6.15	7.97	5.41	6.12	5.54
57573	ZNF471	-1.17	1.42E-01	19.48	18.87	19.49	18.61	17.11	13.83
57633	LRRN1	1.97	4.35E-02	31.23	15.36	34.14	52.57	54.08	52.54
58476	TP53INP2	-1.15	1.82E-03	178.03	182.86	184.13	158.09	152.56	161.50
79174	CRELD2	-1.08	1.20E-01	79.64	85.73	75.00	72.92	74.84	74.30
80781	COL18A1	-1.10	4.56E-02	61.93	59.21	56.53	52.40	52.82	56.02
81539	SLC38A1	-1.38	1.43E-04	839.17	864.08	817.70	611.60	588.53	622.03
81622	UNC93B1	-1.31	3.35E-02	100.11	125.54	102.94	91.08	80.54	80.11
84074	QRICH2	-1.30	4.02E-02	26.25	29.72	23.82	22.95	19.07	19.40
84078	KBTBD7	-1.37	5.51E-03	55.40	63.93	56.84	46.03	40.71	41.72
84129	ACAD11	-1.15	5.40E-02	82.59	93.63	97.65	77.83	81.07	78.67
84181	CHD6	-1.19	2.61E-02	97.99	109.45	98.38	84.70	81.67	91.53
85365	ALG2	-1.18	2.22E-01	139.66	192.03	137.94	133.13	130.98	132.63
113235	SLC46A1	-1.10	1.27E-01	65.46	64.98	65.35	54.64	64.64	59.49
128025	WDR64	-1.08	4.64E-02	2.85	2.77	2.68	2.66	2.54	2.49
128312	HIST3H2BB	1.70	1.88E-02	32.77	24.60	23.61	52.69	46.87	38.17
133308	NHEDC2	-1.24	4.31E-02	305.24	245.99	304.21	228.13	230.43	232.01
135656	DPCR1	-1.01	4.17E-02	10.70	10.63	10.69	10.63	10.57	10.57
136242	PRSS37	-1.12	1.18E-01	4.37	4.33	5.01	3.97	3.98	4.31
145389	SLC38A6	-1.31	1.58E-01	202.34	301.95	191.78	184.51	175.62	169.86
147837	ZNF563	-1.08	2.29E-01	13.64	13.97	13.55	13.43	13.37	11.40
151651	EFHB	-1.51	1.98E-02	8.48	5.97	7.69	4.83	4.70	5.10
151790	WDR49	-1.05	2.19E-01	4.04	4.02	4.46	3.97	3.95	3.99
153443	SRFBP1	-1.23	4.13E-02	136.18	162.28	136.35	126.18	111.78	116.37
162394	SLFN5	-1.19	1.29E-04	843.61	865.88	834.91	718.36	707.26	706.07
202374	STK32A	-1.34	2.04E-02	11.59	9.07	11.13	8.08	7.79	7.89
245812	CNPY4	-1.19	1.62E-01	47.39	62.15	47.03	45.83	41.05	44.60
266727	MDGA1	-1.47	4.13E-02	92.13	63.95	93.33	55.38	58.57	55.62
284307	ZIK1	-1.18	4.36E-02	42.41	49.05	41.15	36.71	38.29	37.48

285761	DCBLD1	-1.22	2.65E-02	116.96	132.37	128.28	95.08	109.98	105.54
286148	DPY19L4	-1.15	2.04E-03	188.81	179.14	178.11	159.71	158.28	156.01
337880	KRTAP11-1	-1.06	2.44E-01	9.94	9.76	9.82	9.76	8.58	9.62
339669	C22orf33	-1.11	1.76E-01	6.75	5.64	5.67	5.64	5.39	5.20
345895	RSPH4A	-1.13	1.89E-02	4.87	4.42	4.61	3.99	4.21	4.09
348487	FAM131C	-1.13	3.77E-03	58.16	60.04	58.77	52.82	50.72	53.74
360030	NANOGNB	-1.06	2.14E-01	2.87	2.84	3.17	2.83	2.82	2.74
375061	FAM89A	-1.23	3.80E-04	66.75	66.62	68.57	55.50	52.97	55.73
400713	ZNF880	-1.41	1.17E-05	131.70	136.54	132.10	93.81	95.57	94.07
407024	MIR29B1	-1.05	4.47E-02	1.95	2.02	2.05	1.92	1.91	1.93
440026	TMEM41B	-1.12	2.66E-03	114.59	117.62	111.20	101.83	103.22	102.23
492311	C5orf53	-1.22	4.52E-02	26.14	20.89	23.65	18.54	19.13	20.09

Supplementary Table 2. The 227 genes that expressed differently in HPAH and IPAH HPASMC compared with Normal cells. The table showed the entrez gene ID, gene symbol, the fold change of mRNA expression in HPAH and IPAH samples compared with normal HPASMC, and the normalized expression value of control, HPAH and IPAH samples.

Symbol	**Entrez Gene Name**	**Entrez Gene ID**	**Fold Change (HPAH)**	p-value (HPAH)	**Fold Change (IPAH)**	p-value (IPAH)
A2M	alpha-2-macroglobulin	2	-2.014	1.10E-03	-1.809	1.44E-03
ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	23460	-2.087	9.09E-03	-2.812	2.66E-03
ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	10350	-1.528	1.98E-04	-2.045	2.87E-04
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	11096	-1.683	3.55E-04	-2.554	1.02E-04
ADRB2	adrenoceptor beta 2, surface	154	2.089	2.18E-04	2.191	1.48E-04
AHR	aryl hydrocarbon receptor	196	-1.592	2.01E-04	-1.835	7.09E-05
ANLN	anillin, actin binding protein	54443	2.356	8.74E-03	5.827	6.49E-04
ANO4	anoctamin 4	121601	-1.961	8.81E-04	-2.168	4.73E-04
ANXA3	annexin A3	306	2.044	2.31E-04	4.137	7.40E-05
APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	60489	-1.333	3.82E-03	-1.690	2.02E-04
ASF1B	anti-silencing function 1B histone chaperone	55723	1.576	3.70E-03	2.973	4.00E-05
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	259266	2.308	9.73E-03	5.434	7.92E-04
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	490	-1.860	4.03E-04	-1.651	3.89E-04
ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	534	-2.346	2.20E-04	-1.796	6.28E-04
BDKRB2	bradykinin receptor B2	624	-1.607	9.36E-03	-1.871	5.29E-03
BDNF	brain-derived neurotrophic factor	627	-2.078	1.29E-03	-2.561	2.20E-04
BEX1	brain expressed, X-linked 1	55859	-3.925	5.96E-05	-2.982	1.03E-04
BMP4	bone morphogenetic protein 4	652	2.405	3.17E-05	3.323	1.20E-05
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	2.013	3.45E-04	4.950	1.29E-05
C1QTNF1	C1q and tumor necrosis factor related protein 1	114897	-1.351	3.68E-04	-1.656	5.13E-05
C1QTNF3	C1q and tumor necrosis factor related protein 3	114899	2.935	1.97E-05	1.506	9.11E-04
C2orf27A/ C2orf27B	chromosome 2 open reading frame 27A	29798	-2.322	5.63E-04	-1.547	1.57E-03
CADM1	cell adhesion molecule 1	23705	1.841	6.46E-04	1.903	8.00E-04
CCDC146	coiled-coil domain containing 146	57639	-1.266	4.77E-02	-1.545	2.28E-03
CCDC68	coiled-coil domain containing 68	80323	-4.003	4.26E-04	-2.716	3.03E-04
CCL20	chemokine (C-C motif) ligand 20	6364	-2.526	9.66E-04	-2.356	1.16E-03
CCL28	chemokine (C-C motif) ligand 28	56477	1.633	4.05E-04	2.575	3.06E-05

CCNB2	cyclin B2	9133	1.986	9.20E-03	5.419	4.72E-04
CCNE2	cyclin E2	9134	1.681	4.13E-03	2.066	6.67E-04
CD180	CD180 molecule	4064	10.042	1.53E-05	35.065	2.77E-06
CD4	CD4 molecule	920	-3.185	7.77E-05	-2.003	2.27E-04
CDC20	cell division cycle 20	991	2.717	4.02E-03	7.059	3.05E-04
CDCP1	CUB domain containing protein 1	64866	1.666	1.69E-03	2.342	2.56E-04
CDK1	cyclin-dependent kinase 1	983	1.981	3.75E-03	4.634	1.86E-04
CDKN3	cyclin-dependent kinase inhibitor 3	1033	2.134	2.51E-02	5.987	1.50E-03
CECR1	cat eye syndrome chromosome region, candidate 1	51816	2.017	3.20E-03	2.252	3.17E-03
CENPE	centromere protein E, 312kDa	1062	2.005	1.30E-03	3.865	1.23E-04
CENPQ	centromere protein Q	55166	1.946	3.05E-03	2.211	2.15E-03
CERS4	ceramide synthase 4	79603	1.566	2.28E-04	1.987	1.25E-04
CGNL1	cingulin-like 1	84952	2.631	4.02E-04	2.418	2.08E-04
CKAP2L	cytoskeleton associated protein 2-like	150468	2.004	5.87E-03	4.400	3.98E-04
CMAHP	cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene	8418	1.743	1.29E-03	3.538	9.43E-05
CPA4	carboxypeptidase A4	51200	2.566	5.88E-03	2.399	7.65E-03
CPED1	cadherin-like and PC-esterase domain containing 1	79974	-2.148	6.58E-04	-1.511	5.85E-03
CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	55790	-1.673	2.67E-04	-2.149	2.73E-04
CST1	cystatin SN	1469	-4.771	2.44E-04	-7.229	1.12E-04
CTSH	cathepsin H	1512	3.570	1.48E-04	2.252	7.90E-04
CXCL10	chemokine (C-X-C motif) ligand 10	3627	-2.279	6.46E-05	-2.067	3.17E-04
CXCL12	chemokine (C-X-C motif) ligand 12	6387	-1.651	5.42E-03	-2.238	9.22E-04
DAPK1	death-associated protein kinase 1	1612	3.125	1.55E-04	1.532	2.49E-03
DIRC1	disrupted in renal carcinoma 1	116093	-2.181	3.33E-03	-2.015	2.46E-03
DNAH5	dynein, axonemal, heavy chain 5	1767	-1.455	2.99E-02	-1.935	4.85E-03
DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	9829	-1.583	6.09E-03	-1.770	3.77E-03
DNER	delta/notch-like EGF repeat containing	92737	-2.764	3.24E-05	-1.578	3.20E-04
DOCK4	dedicator of cytokinesis 4	9732	-1.720	6.22E-04	-1.767	3.65E-04
DSEL	dermatan sulfate epimerase-like	92126	-1.709	3.39E-04	-1.501	8.96E-04
DSG2	desmoglein 2	1829	-5.663	3.97E-06	-6.511	7.42E-06
DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	51514	1.586	5.52E-03	2.365	2.35E-04
E2F7	E2F transcription factor 7	144455	1.505	2.10E-03	1.583	5.89E-04
EDNRB	endothelin receptor type B	1910	-7.616	4.90E-04	-2.321	6.53E-03
EFHB	EF-hand domain family, member B	151651	-1.740	9.69E-03	-1.513	1.98E-02
ENC1	ectodermal-neural cortex 1 (with BTB domain)	8507	-2.227	2.14E-04	-2.167	3.98E-05
EPHB1	EPH receptor B1	2047	1.689	2.95E-05	1.748	6.92E-05
EREG	epiregulin	2069	-6.881	6.81E-04	-6.292	4.23E-04
ERG	v-ets avian erythroblastosis virus E26 oncogene homolog	2078	8.529	3.40E-03	6.278	5.79E-03
ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	157570	2.176	3.35E-03	3.414	5.81E-04
EVI2A	ecotropic viral integration site 2A	2123	2.992	1.44E-04	4.062	1.03E-04

FABP4	fatty acid binding protein 4, adipocyte	2167	-4.565	7.90E-03	-5.134	5.25E-03
FAM111B	family with sequence similarity 111, member B	374393	2.357	2.25E-04	3.373	3.69E-05
FAM129A	family with sequence similarity 129, member A	116496	1.500	3.46E-04	1.889	3.29E-05
FAM20A	family with sequence similarity 20, member A	54757	-2.786	1.09E-03	-3.529	5.12E-04
FANCI	Fanconi anemia, complementation group I	55215	1.522	3.42E-04	2.489	2.69E-05
FLRT2	fibronectin leucine rich transmembrane protein 2	23768	-2.573	6.22E-05	-1.820	2.28E-04
FOXE1	forkhead box E1 (thyroid transcription factor 2)	2304	-2.693	2.54E-03	-2.788	2.76E-03
FRMD4B	FERM domain containing 4B	23150	2.845	2.77E-03	2.902	2.47E-03
GDF15	growth differentiation factor 15	9518	-1.981	3.31E-04	-1.933	5.68E-04
GINS1	GINS complex subunit 1 (Psf1 homolog)	9837	1.585	4.14E-03	2.185	4.80E-04
GRIK2	glutamate receptor, ionotropic, kainate 2	2898	-1.872	1.28E-03	-3.612	1.21E-04
HDHD1	haloacid dehalogenase-like hydrolase domain containing 1	8226	-1.817	1.55E-04	-1.610	1.31E-04
HIST1H2AG (includes others)	histone cluster 1, H2ag	8332	1.709	4.51E-04	2.798	8.17E-05
HIST1H2AG (includes others)	histone cluster 1, H2ag	8969	1.840	2.68E-03	3.164	1.83E-04
HIST1H2BB	histone cluster 1, H2bb	3018	1.515	5.05E-03	3.567	1.03E-04
HIST1H2BH/HIST1H2BO	histone cluster 1, H2bo	8345	1.868	5.79E-04	2.999	1.98E-05
HIST1H3A (includes others)	histone cluster 1, H3a	8354	1.667	1.88E-04	2.563	8.83E-06
HIST1H3A (includes others)	histone cluster 1, H3a	8357	1.773	2.53E-03	4.023	8.59E-05
HIST1H4A (includes others)	histone cluster 1, H4a	8359	1.530	5.61E-03	2.156	1.55E-03
HIST1H4A (includes others)	histone cluster 1, H4a	8364	1.815	8.69E-04	2.878	1.40E-04
HIST2H2AB	histone cluster 2, H2ab	317772	1.626	7.19E-04	2.808	2.95E-05
HIST2H2BE (includes others)	histone cluster 2, H2be	8344	1.508	1.62E-03	2.372	7.45E-05
HJURP	Holliday junction recognition protein	55355	1.534	5.00E-03	4.005	7.13E-05
HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	3113	-6.723	5.71E-05	-2.133	1.01E-04

HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	2.538	3.22E-03	6.795	2.25E-04
HOMER2	homer homolog 2 (Drosophila)	9455	1.550	7.13E-04	1.836	4.28E-04
HTATSF1P2	HIV-1 Tat specific factor 1 pseudogene 2	401233	-1.909	4.85E-03	-3.174	4.47E-04
ICAM2	intercellular adhesion molecule 2	3384	1.997	5.15E-05	2.116	1.24E-05
IL1R1	interleukin 1 receptor, type I	3554	-1.505	3.48E-04	-2.102	2.75E-06
IL4R	interleukin 4 receptor	3566	-1.723	1.85E-03	-1.846	6.41E-04
INMT	indolethylamine N-methyltransferase	11185	-1.703	6.52E-04	-3.094	1.13E-04
IQGAP3	IQ motif containing GTPase activating protein 3	128239	2.092	2.24E-03	4.860	1.30E-04
ISLR	immunoglobulin superfamily containing leucine-rich repeat	3671	2.573	5.16E-06	2.119	4.52E-05
KCNK1	potassium channel, subfamily K, member 1	3775	1.555	8.82E-04	1.662	2.49E-04
KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	3778	2.076	4.58E-04	1.831	8.60E-04
KDM5C	lysine (K)-specific demethylase 5C	8242	-1.477	2.28E-03	-1.769	6.94E-04
KIF11	kinesin family member 11	3832	2.019	5.95E-03	4.051	5.74E-04
KIF15	kinesin family member 15	56992	1.560	1.00E-02	3.215	1.26E-04
KIF20B	kinesin family member 20B	9585	1.849	5.39E-03	4.044	2.87E-04
KIF23	kinesin family member 23	9493	1.576	4.07E-04	2.318	3.79E-05
KLHL4	kelch-like family member 4	56062	2.052	2.05E-04	2.163	2.41E-05
KLHL41	kelch-like family member 41	10324	2.174	7.67E-03	2.629	2.16E-03
KNSTRN	kinetochore-localized astrin/SPAG5 binding protein	90417	1.511	9.43E-03	2.061	1.37E-03
KRT19	keratin 19	3880	2.650	9.07E-03	3.117	5.43E-03
KRT23	keratin 23 (histone deacetylase inducible)	25984	1.650	1.55E-03	1.534	1.24E-03
KSR1	kinase suppressor of ras 1	8844	-1.594	6.41E-04	-2.452	1.23E-04
L1CAM	L1 cell adhesion molecule	3897	-1.564	7.30E-05	-1.527	4.18E-04
LCE2A	late cornified envelope 2A	353139	3.940	7.08E-04	3.171	6.75E-04
LIF	leukemia inhibitory factor	3976	-1.627	8.44E-03	-2.037	8.82E-03
LINC00969	long intergenic non-protein coding RNA 969	440993	-2.047	4.30E-04	-1.527	5.00E-05
LOC344887	NmrA-like family domain containing 1 pseudogene	344887	-1.327	3.03E-02	-1.764	2.78E-03
LOC654342	lymphocyte-specific protein 1 pseudogene	654342	-1.975	4.07E-04	-1.672	1.29E-03
LOC654433	uncharacterized LOC654433	654433	-1.784	5.36E-04	-1.813	1.88E-03
LPAR4	lysophosphatidic acid receptor 4	2846	2.009	1.35E-03	1.762	3.20E-03
LPPR4	lipid phosphate phosphatase-related protein type 4	9890	-6.696	3.04E-03	-4.406	7.10E-03
LRRK2	leucine-rich repeat kinase 2	120892	-1.847	1.38E-03	-1.609	2.98E-03
LRRN3	leucine rich repeat neuronal 3	54674	-2.706	5.06E-05	-2.092	7.35E-05
LYPD6B	LY6/PLAUR domain containing 6B	130576	-2.040	3.11E-05	-2.251	9.34E-04
MAPK10	mitogen-activated protein kinase 10	5602	-1.584	3.09E-03	-2.106	5.38E-05
MAPK13	mitogen-activated protein kinase 13	5603	1.840	1.40E-05	1.855	1.16E-05
MCM10	minichromosome maintenance complex component 10	55388	1.563	3.84E-03	2.247	3.75E-04

MFAP4	microfibrillar-associated protein 4	4239	-2.299	3.96E-03	-2.589	2.51E-03
MFF	mitochondrial fission factor	56947	-1.767	3.94E-04	-1.628	6.67E-04
MICU3	mitochondrial calcium uptake family, member 3	286097	-1.519	1.25E-04	-1.681	5.57E-06
MLF1IP	MLF1 interacting protein	79682	1.549	1.87E-03	3.172	5.69E-05
MST4	serine/threonine protein kinase MST4	51765	1.780	2.64E-02	2.141	9.92E-03
MXRA5	matrix-remodelling associated 5	25878	-1.815	2.07E-03	-7.209	4.11E-05
MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	4605	1.638	1.12E-03	2.504	2.29E-04
MYRIP	myosin VIIA and Rab interacting protein	25924	1.896	5.44E-03	1.993	3.34E-03
NCAPG	non-SMC condensin I complex, subunit G	64151	1.872	4.65E-04	3.992	3.26E-05
NCAPH	non-SMC condensin I complex, subunit H	23397	1.977	3.62E-05	3.825	8.40E-08
NDC80	NDC80 kinetochore complex component	10403	1.871	6.13E-03	4.864	2.19E-04
NEFM	neurofilament, medium polypeptide	4741	1.594	2.99E-02	4.807	4.90E-04
NEK2	NIMA-related kinase 2	4751	1.795	7.97E-04	4.810	3.05E-05
NEO1	neogenin 1	4756	-1.620	1.07E-04	-1.745	1.04E-05
NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	81832	-3.369	1.71E-03	-3.335	1.35E-03
NID2	nidogen 2 (osteonidogen)	22795	-1.632	2.10E-04	-2.465	1.52E-05
NNAT	neuronatin	4826	1.528	1.44E-03	1.764	1.02E-03
NTNG1	netrin G1	22854	2.166	7.41E-05	1.946	1.70E-04
NUF2	NUF2, NDC80 kinetochore complex component	83540	2.425	2.71E-04	6.099	2.17E-05
OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	4940	1.823	4.34E-04	2.189	1.52E-04
OLFML2B	olfactomedin-like 2B	25903	1.762	2.10E-03	4.822	2.02E-05
P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	5026	2.242	9.13E-04	1.850	1.78E-03
PAQR5	progestin and adipoQ receptor family member V	54852	-1.605	8.57E-03	-2.610	5.00E-04
PAX6	paired box 6	5080	1.604	2.05E-03	3.476	4.98E-06
PCDHB16	protocadherin beta 16	57717	-1.949	5.45E-03	-5.140	1.83E-04
PCDHGA12	protocadherin gamma subfamily A, 12	26025	-2.388	1.48E-04	-1.728	1.82E-03
PCDHGA2	protocadherin gamma subfamily A, 2	56113	-1.529	6.74E-03	-1.508	1.71E-04
PCDHGA3	protocadherin gamma subfamily A, 3	56112	-2.642	2.05E-04	-3.344	6.09E-05
PCDHGA6	protocadherin gamma subfamily A, 6	56109	-1.603	5.13E-03	-1.818	8.64E-03
PCSK2	proprotein convertase subtilisin/kexin type 2	5126	-8.094	1.71E-04	-1.797	4.86E-03
PDPN	podoplanin	10630	2.781	4.19E-04	2.998	2.77E-04
PIR	pirin (iron-binding nuclear protein)	8544	-3.990	5.05E-05	-2.800	1.03E-04
PKN3	protein kinase N3	29941	1.558	1.65E-04	1.669	8.21E-06
PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	57480	-1.685	2.62E-03	-2.208	6.35E-04
PLK1	polo-like kinase 1	5347	2.517	5.73E-03	6.442	4.78E-04
PLK4	polo-like kinase 4	10733	1.610	5.01E-04	3.550	1.27E-05

PLXDC1	plexin domain containing 1	57125	2.774	2.04E-05	3.712	1.69E-06
PNPLA3	patatin-like phospholipase domain containing 3	80339	-1.875	3.34E-03	-2.186	1.42E-03
PPP2R1B	protein phosphatase 2, regulatory subunit A, beta	5519	-1.676	4.67E-04	-1.747	1.45E-04
PREX1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	57580	1.842	1.02E-04	1.644	7.03E-06
PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	79056	1.786	2.70E-03	2.106	1.49E-03
PTGES	prostaglandin E synthase	9536	-1.615	4.81E-03	-1.747	2.02E-03
PTN	pleiotrophin	5764	-2.089	2.81E-03	-2.951	6.16E-04
PYROXD2	pyridine nucleotide-disulphide oxidoreductase domain 2	84795	-2.753	3.43E-03	-1.888	6.70E-03
RAB27B	RAB27B, member RAS oncogene family	5874	-2.010	8.08E-03	-2.014	8.36E-03
RAD51AP1	RAD51 associated protein 1	10635	1.577	2.04E-04	3.256	3.67E-06
RASL11A	RAS-like, family 11, member A	387496	1.502	4.02E-03	1.541	1.94E-03
RBPMS2	RNA binding protein with multiple splicing 2	348093	1.710	9.93E-04	1.697	6.56E-04
RGS7	regulator of G-protein signaling 7	6000	-2.527	1.79E-04	-3.068	2.07E-04
ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	6091	-1.821	3.79E-03	-1.635	7.86E-03
ROBO2	roundabout, axon guidance receptor, homolog 2 (Drosophila)	6092	-2.149	7.63E-05	-2.638	1.75E-04
S1PR3	sphingosine-1-phosphate receptor 3	1903	-1.756	8.36E-04	-1.960	1.35E-04
SAMD5	sterile alpha motif domain containing 5	389432	-1.552	2.46E-03	-2.026	4.55E-04
SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	23231	-2.135	4.24E-03	-1.636	1.97E-02
SETD9	SET domain containing 9	133383	2.036	1.53E-03	1.599	3.25E-03
SKA1	spindle and kinetochore associated complex subunit 1	220134	1.795	6.56E-03	3.889	3.33E-04
SLC16A7	solute carrier family 16 (monocarboxylate transporter), member 7	9194	-1.638	2.80E-04	-1.777	2.23E-04
SLC16A9	solute carrier family 16, member 9	220963	1.640	6.76E-03	1.731	4.10E-03
SLC19A3	solute carrier family 19 (thiamine transporter), member 3	80704	-1.778	1.02E-03	-1.696	2.02E-03
SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	114134	-2.183	3.17E-03	-1.739	7.71E-03
SLC35F2	solute carrier family 35, member F2	54733	2.100	1.06E-03	2.732	3.68E-04
SLC39A6	solute carrier family 39 (zinc transporter), member 6	25800	-1.066	3.05E-03	-1.251	1.19E-04
SLC9A3R1	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1	9368	1.580	1.32E-03	2.264	1.56E-04
SMOC1	SPARC related modular calcium binding 1	64093	3.172	2.09E-03	3.304	1.94E-03
SOD3	superoxide dismutase 3, extracellular	6649	-1.767	4.10E-03	-1.628	3.30E-03
SOGA2	SOGA family member 2	23255	-1.621	1.47E-05	-1.733	1.34E-05

SPC25	SPC25, NDC80 kinetochore complex component	57405	1.658	3.48E-04	4.434	7.68E-06
SPESP1	sperm equatorial segment protein 1	246777	-1.870	1.28E-04	-2.696	2.57E-05
SSTR1	somatostatin receptor 1	6751	-1.749	6.64E-03	-2.313	1.36E-03
STK32B	serine/threonine kinase 32B	55351	-1.597	2.14E-03	-2.679	1.06E-04
STMN2	stathmin-like 2	11075	-5.099	6.27E-04	-2.727	4.09E-03
TACC3	transforming, acidic coiled-coil containing protein 3	10460	1.725	1.25E-03	2.994	6.22E-05
TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	85461	-1.260	3.25E-02	-1.678	1.42E-03
TBL1X	transducin (beta)-like 1X-linked	6907	-1.615	6.63E-04	-1.534	1.84E-04
TCF19	transcription factor 19	6941	1.570	3.56E-03	2.509	1.48E-04
TFPI2	tissue factor pathway inhibitor 2	7980	-3.403	7.02E-04	-2.034	1.17E-03
TLR5	toll-like receptor 5	7100	1.589	9.22E-03	1.547	4.06E-03
TMC7	transmembrane channel-like 7	79905	1.982	2.04E-04	2.370	1.06E-04
TMEM30B	transmembrane protein 30B	161291	1.856	3.73E-04	1.548	1.00E-03
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	7130	-2.081	6.10E-04	-1.613	3.28E-03
TOX2	TOX high mobility group box family member 2	84969	1.720	2.54E-03	1.587	4.21E-04
TRHDE	thyrotropin-releasing hormone degrading enzyme	29953	-2.834	1.40E-04	-2.086	3.39E-04
TRIM59	tripartite motif containing 59	286827	1.550	4.32E-03	2.597	8.34E-05
TRPC4	transient receptor potential cation channel, subfamily C, member 4	7223	-3.557	6.01E-04	-3.280	5.75E-04
TSPAN12	tetraspanin 12	23554	-2.791	3.87E-03	-2.336	8.23E-03
TTK	TTK protein kinase	7272	1.908	9.84E-04	5.246	3.01E-05
UBE2T	ubiquitin-conjugating enzyme E2T (putative)	29089	1.521	2.49E-03	2.562	1.35E-04
UHRF1	ubiquitin-like with PHD and ring finger domains 1	29128	1.588	1.58E-03	2.156	2.48E-04
VEGFA	vascular endothelial growth factor A	7422	-1.514	2.38E-03	-1.732	3.27E-04
VSNL1	visinin-like 1	7447	1.705	2.90E-03	1.612	1.99E-03
WDR63	WD repeat domain 63	126820	-1.883	3.91E-03	-1.789	4.50E-03
WISP3	WNT1 inducible signaling pathway protein 3	8838	2.664	8.05E-05	2.659	2.04E-04
WNT16	wingless-type MMTV integration site family, member 16	51384	-2.716	3.22E-04	-1.591	3.59E-03
ZC3H12C	zinc finger CCCH-type containing 12C	85463	-1.517	5.12E-03	-1.915	2.25E-04
ZNF780B	zinc finger protein 780B	163131	-1.207	5.51E-02	-1.333	3.02E-02
ZNF804A	zinc finger protein 804A	91752	-2.136	4.22E-03	-1.787	5.35E-03
ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	8233	-1.541	6.81E-03	-1.504	3.03E-03
ZSCAN31	zinc finger and SCAN domain containing 31	64288	-1.631	2.40E-03	-1.511	2.31E-03
ZSWIM5	zinc finger, SWIM-type containing 5	57643	-1.870	2.72E-03	-2.017	1.71E-03

Supplementary Table 3. Biological functions and diseases predicted by Ingenuity Pathway Analysis based on the differentially expressed genes in HPAH and IPAH vs control. The Biological Functional Analysis™ identified the biological functions and/or diseases that were most significant to the data set. The 227 selected genes in table 1 were associated with a biological function in the Ingenuity knowledge base were considered for analysis. Fischer's exact test was used to calculate a p-value determining the probability that each biological function and/or disease assigned to that data set is due to chance alone. The molecules involved in those biological functions were also listed in the table. The molecules involved in those biological functions were also listed in the table. The identity of those molecules can be retrieved from **Supplementary Table 2**.

Category	p-value	Molecules
Cancer	3.08E-17-8.72E-03	BMP4,HMMR,NCAPG,DOCK4,STK32B,CCNB2,CCL20,SEL1L3,MAPK13,VEGFA,CXCL10,CECR1,PLK4,EPHB1,ZC3H12C,MYRIP,CENPE,CTSH,KCNK1,EFHB,NEFM,ZNF780B,KNSTRN,ABCA6,AHR,ASF1B,IL4R,CCNE2,DAPK1,NETO1,TSPAN12,KRT23,SSTR1,EVI2A,L1CAM,TFPI2,CERS4,TANC1,ISLR,LRRN3,KRT19,HIST1H3A (includes others), FOXE1,VSNL1,ENC1,HDHD1,NID2,BDNF,PTN,BEX1,GDF15,ZNF804A,NUF2,TTK,HLA-DPA1,SOD3,ABCA9,KSR1,CGNL1, CDKN3, BDKRB2,ZRSR2,TRHDE,CCL28,DNAH5,MFF,FABP4,MCM10,GRIK2,ROBO2,SOGA2,DNER,SPC25,KLHL41,SLC39A6,MLF1IP,C2orf27A/C2orf27B,PLK1,MFAP4,CSGALNACT1,DSEL,OAS3,SLC16A9,CDK1,PLEKHG1,PTGES,KIF15,PCSK2,KIF20B,ANXA3,WISP3,WDR63,PAX6,ANO4,HIST1H2AG,PLXDC1,MXRA5,RAD51AP1,KIF23,LPAR4,LIF,ATP2B1,CDCP1,CD4,DNAJC6,LPPR4,CXCL12,WNT16,PCDHGA3,SLC16A7,ZSWIM5,FAM111B,NEO1,MYBL2,KDM5C,ADAMTS5,ESCO2,PCDHGA6,TNFAIP6,HIST1H4A,ANLN,INMT,BUB1B,TBL1X,FAM20A,APOBEC3G,KLHL4,MICU3,PREX1,GINS1,CST1,CD180,MAPK10,NDC80,CENPQ,HIST2H2AB,EREG,HIST1H2BH/HIST1H2BO,KIF11,CCDC146,PDPN,PCDHGA12,CDC20,STMN2,FLRT2,RAB27B,ROBO1,NTNG1,NEK2,ICAM2,PRRG4,TMC7,ASPM,KCNMA1,PNPLA3,TOX2,ADRB2,PAQR5,PCDHB16,TACC3,UHRF1,EDNRB,SLC9A3R1,SMOC1,RGS7,CPED1,ZSCAN31,LRRK2,PCDHGA2,IL1R1,CPA4,UBE2T,MST4,HIST2H2BE,ERG,CADM1,TLR5,OLFML2B,E2F7,A2M,DSG2,PPP2R1B,TRIM59
Organismal Injury and Abnormalities	4.75E-13-8.29E-03	BMP4,LIF,CDCP1,CD4,HMMR,CXCL12,WNT16,CCNB2,SEL1L3,MAPK13,CXCL10,VEGFA,SLC16A7,EPHB1,CTSH,KCNK1,NEFM,MYBL2,ADAMTS5,AHR,ASF1B,CCNE2,IL4R,TNFAIP6,KRT23,SSTR1,L1CAM,BUB1B,TFPI2,TBL1X,APOBEC3G,S1PR3,GINS1,KRT19,MAPK10,KIF11,PDPN,CDC20,BDNF,FLRT2,GDF15,PTN,BEX1,TTK,ROBO1,SOD3,BDKRB2,ZRSR2,NEK2,KCNMA1,DNAH5,FABP4,MCM10,ROBO2,GRIK2,ADRB2,PCDHB16,SLC9A3R1,UHRF1,EDNRB,SPC25,SLC39A6,LRRK2,PLK1,MFAP4,C2orf27A/C2orf27B,IL1R1,CDK1,CADM1,HIST2H2BE,ERG,PTGES,TLR5,WISP3,ANXA3,MXRA5,PPP2R1B
Cell Cycle	9.67E-09-8.72E-03	PDPN,KIF23,LIF,BMP4,CDC20,NCAPG,CD4,GDF15,PTN,CXCL12,CCNB2,NUF2,TTK,SKA1,CDKN3,VEGFA,CXCL10,PLK4,NEK2,CENPE,NCAPH,MCM10,HJURP,MYBL2,AHR,IQGAP3,DTL,ESCO2,TACC3,CCNE2,IL4R,UHRF1,ANLN,SPC25,SSTR1,PLK1,BUB1B,CDK1,MST4,KIF15,CD180,KRT19,KIF20B,E2F7,PAX6,NDC80,EREG,KIF11
Cellular Assembly and Organization	9.67E-09-8.09E-03	KIF23,LPAR4,LIF,BMP4,ATP2B1,NCAPG,CXCL12,LPPR4,CCNB2,PCDHGA3,SKA1,CXCL10,VEGFA,EPHB1,PLK4,CENPE,NCAPH,NEFM,NEO1,AHR,DAPK1,PCDHGA6,ANLN,L1CAM,BUB1B,S1PR3,PR

		EX1,MAPK10,NDC80,ENC1,KIF11,PDPN,PCDHGA12,CDC20,STMN2,BDNF,RAB27B,GDF15,PTN,NUF2,TTK,ROBO1,NTNG1,NEK2,ICAM2,MFF,HJURP,ROBO2,ADRB2,TACC3,SLC9A3R1,DNER,KLHL41,SPC25,LRRK2,PCDHGA2,PLK1,IL1R1,CDK1,ERG,PCSK2,KIF20B,PAX6,A2M
DNA Replication, Recombination, and Repair	9.67E-09-8.51E-03	KIF23,LIF,BMP4,CDC20,BDNF,NCAPG,CD4,PTN,CXCL12,CCNB2,TTK,NUF2,SKA1,KSR1,CXCL10,VEGFA,NEK2,CENPE,NCAPH,MYBL2,HJURP,CCNE2,UHRF1,SPC25,PLK1,BUB1B,TFPI2,CDK1,CD180,NDC80,EREG,A2M,KIF11
Cell Death and Survival	3.28E-08-7.9E-03	BMP4,LIF,ATP2B1,CDCP1,CD4,HMMR,CXCL12,WNT16,MAPK13,PCDHGA3,SKA1,VEGFA,CXCL10,PLK4,NEFM,MYBL2,AHR,IL4R,DAPK1,PCDHGA6,ANLN,SSTR1,L1CAM,BUB1B,TFPI2,S1PR3,GINS1,KRT19,MAPK10,NDC80,VSNL1,ENC1,KIF11,HIST1H2BH/HIST1H2BO,PCDHGA12,CDC20,BDNF,GDF15,PTN,TTK,NUF2,SOD3,KSR1,BDKRB2,CDKN3,ICAM2,NEK2,KCNMA1,FABP4,MCM10,GRIK2,ATP6V1G2,ADRB2,DTL,TACC3,UHRF1,EDNRB,SPC25,LRRK2,PLK1,PCDHGA2,IL1R1,OAS3,CDK1,MST4,ERG,CADM1,PTGES,PCSK2,E2F7,PAX6,A2M,DSG2,PPP2R1B
Cellular Function and Maintenance	1.39E-07-8.09E-03	KIF23,LIF,BMP4,ATP2B1,CD4,LPPR4,CXCL12,CCL20,CXCL10,VEGFA,EPHB1,PLK4,CENPE,KCNK1,NEFM,NEO1,AHR,DAPK1,L1CAM,S1PR3,PREX1,MAPK10,NDC80,ENC1,KIF11,PDPN,CDC20,STMN2,BDNF,PTN,TTK,ROBO1,BDKRB2,NTNG1,NEK2,KCNMA1,CCL28,MFF,GRIK2,ROBO2,ADRB2,TACC3,EDNRB,SLC9A3R1,DNER,SPC25,KLHL41,SLC39A6,TRPC4,PLK1,IL1R1,ERG,TLR5,KIF20B,PAX6,A2M,DSG2
Cellular Movement	1.61E-06-8.76E-03	KIF23,LIF,BMP4,CDCP1,CD4,HMMR,CXCL12,CCL20,CCNB2,DOCK4,CXCL10,VEGFA,EPHB1,CTSH,NEO1,AHR,IL4R,ANLN,L1CAM,TFPI2,S1PR3,PREX1,KRT19,MAPK10,VSNL1,EREG,PDPN,CDC20,BDNF,FLRT2,GDF15,PTN,ROBO1,SOD3,BDKRB2,NEK2,ICAM2,KCNMA1,ASPM,DNAH5,CCL28,FABP4,ROBO2,DTL,ADRB2,SLC9A3R1,EDNRB,LRRK2,PLK1,IL1R1,CDK1,CADM1,ERG,PTGES,TLR5,KIF20B,ANXA3,PAX6,A2M
Cell Morphology	1.8E-06-8.09E-03	KIF23,LPAR4,BMP4,LIF,CDCP1,NCAPG,CD4,LPPR4,CXCL12,VEGFA,CXCL10,PLK4,EPHB1,NEFM,NEO1,MYBL2,AHR,IQGAP3,IL4R,SSTR1,L1CAM,FAM20A,S1PR3,PREX1,CD180,FOXE1,ENC1,PDPN,CDC20,STMN2,BDNF,PTN,GDF15,ROBO1,KSR1,SPESP1,BDKRB2,NTNG1,ICAM2,KCNMA1,ROBO2,ADRB2,TACC3,EDNRB,SLC9A3R1,DNER,KLHL41,RGS7,LRRK2,PLK1,TRPC4,IL1R1,CDK1,CADM1,ERG,KIF15,PCSK2,TLR5,PAX6,A2M
Cellular Growth and Proliferation	2.78E-06-8.99E-03	LIF,BMP4,CDCP1,CD4,NCAPG,HMMR,CXCL12,DOCK4,CCL20,CCNB2,WNT16,MAPK13,VEGFA,CXCL10,PLK4,EPHB1,NEO1,MYBL2,ADAMTS5,AHR,IL4R,DAPK1,CCNE2,TNFAIP6,KRT23,SSTR1,L1CAM,BUB1B,TFPI2,S1PR3,CD180,KRT19,MAPK10,EREG,ENC1,HIST1H2BH/HIST1H2BO,KIF11,PDPN,CDC20,NID2,BDNF,GDF15,PTN,TTK,ROBO1,KSR1,BDKRB2,CDKN3,C1QTNF3,NEK2,KCNMA1,FABP4,MCM10,GRIK2,ATP6V1G2,DTL,ADRB2,TACC3,EDNRB,UHRF1,SLC9A3R1,DNER,SLC39A6,LRRK2,TRPC4,PLK1,IL1R1,OAS3,CDK1,ERG,MST4,CADM1,PTGES,KIF15,PCSK2,TLR5,KIF20B,E2F7,TCF19,PAX6,A2M,DSG2,PPP2R1B
Cell-To-Cell Signaling and Interaction	5.06E-06-8.31E-03	BMP4,LIF,PCDHGA12,CDCP1,BDNF,HMMR,CD4,GDF15,PTN,CXCL12,CCL20,PCDHGA3,SOD3,CXCL10,VEGFA,EPHB1,ICAM2,KCNMA1,CCL28,MYBL2,AHR,ADRB2,IL4R,PCDHGA6,PCDHGA2,L1CAM,IL1R1,TFPI2,ERG,CADM1,PTGES,PREX1,TLR5,VSNL1,A2M,DSG2

Cardiovascular System Development and Function	7.91E-06-7.9E-03	PDPN,BMP4,LIF,BDNF,FLRT2,HMMR,PTN,CXCL12,ROBO1,SOD3,VEGFA,CXCL10,BDKRB2,EPHB1,KCNMA1,CCL28,FABP4,AHR,ADRB2,IL4R,CCNE2,EDNRB,TSPAN12,LRRK2,TRPC4,L1CAM,IL1R1,ERG,S1PR3,PTGES,PCSK2,TLR5,E2F7,ANXA3,PAX6,EREG
Cellular Development	8.47E-06-8.99E-03	KIF23,BMP4,LIF,CDCP1,HMMR,CD4,NCAPG,LPPR4,CXCL12,DOCK4,WNT16,CCNB2,CCL20,MAPK13,VEGFA,CXCL10,EPHB1,NEFM,NEO1,MYBL2,ADAMTS5,AHR,IL4R,CCNE2,DAPK1,TNFAIP6,HIST1H4A (includes others),SSTR1,L1CAM,TBL1X,TFPI2,S1PR3,PREX1,KRT19,ENC1,EREG,PDPN,STMN2,CDC20,NID2,BDNF,PTN,GDF15,ROBO1,KSR1,BDKRB2,NTNG1,C1QTNF3,ICAM2,NEK2,ASPM,KCNMA1,FABP4,ROBO2,ADRB2,DTL,TACC3,SLC9A3R1,UHRF1,EDNRB,DNER,KLHL41,SLC39A6,LRRK2,PLK1,TRPC4,IL1R1,OAS3,CDK1,CADM1,MST4,ERG,PTGES,PCSK2,TLR5,E2F7,PAX6,A2M
Metabolic Disease	1.05E-05-7.9E-03	BDNF,CD4,GDF15,HLA-DPA1,VEGFA,CXCL10,KCNK1, FABP4,ROBO2,ADRB2,SLC9A3R1,EDNRB,HIST1H4A,ZSCAN31,CMAHP,EVI2A,SSTR1,FRMD4B,L1CAM,IL1R1,HIST2H2BE (includes others),PCSK2,TLR5,CD180,HIST1H3A,MAPK10,PAX6,TCF19,A2M,CCDC68,HIST1H2BH/HIST1H2BO,KIF11
Organismal Development	1.74E-05-7.93E-03	PDPN,LIF,BMP4,BDNF,FLRT2,PTN,CXCL12,ROBO1,VEGFA,BDKRB2,CXCL10,EPHB1,KCNMA1,CCL28,FABP4,ROBO2,AHR,ADRB2,CCNE2,IL4R,EDNRB,TSPAN12,DNER,LRRK2,L1CAM,TRPC4,CADM1,ERG,S1PR3,PTGES,KRT19,E2F7,ANXA3,PAX6,EREG
Tissue Development	1.74E-05-8.09E-03	KIF23,LPAR4,BMP4,LIF,CDCP1,HMMR,CD4,LPPR4,CXCL12,CCL20,PCDHGA3,CXCL10,VEGFA,EPHB1,NEFM,AHR,IL4R,PCDHGA6,L1CAM,BUB1B,TFPI2,S1PR3,PREX1,KRT19,VSNL1,ENC1,EREG,PDPN,PCDHGA12,CDC20,BDNF,RAB27B,GDF15,PTN,ROBO1,BDKRB2,NTNG1,ICAM2,KCNMA1,CCL28,FABP4,MCM10,ROBO2,ADRB2,EDNRB,DNER,LRRK2,PCDHGA2,TRPC4,PLK1,IL1R1,ERG,CADM1,PTGES,PAX6,A2M,DSG2
Tissue Morphology	1.23E-04-8.75E-03	KIF23,LIF,BMP4,CD4,CXCL12,CCNB2,CCL20,MAPK13,CXCL10,VEGFA,EPHB1,PLK4,CTSH,NEFM,NEO1,MYBL2,AHR,IL4R,SSTR1,L1CAM,FAM20A,S1PR3,PREX1,CD180,KRT19,MAPK10,PDPN,CDC20,BDNF,FLRT2,GDF15,PTN,ROBO1,SOD3,KSR1,BDKRB2,CCL28,ROBO2,ADRB2,TACC3,EDNRB,SLC9A3R1,UHRF1,DNER,RGS7,LRRK2,IL1R1,CADM1,PTGES,KIF15,PCSK2,TLR5,KIF20B,E2F7,PAX6
Embryonic Development	1.29E-04-7.93E-03	PDPN,BMP4,LIF,BDNF,PTN,CXCL12,DOCK4,CCL20,ROBO1,KSR1,CXCL10,VEGFA,BDKRB2,C1QTNF3,EPHB1,MYBL2,ROBO2,AHR,ADRB2,DAPK1,EDNRB,DNER,LRRK2,PLK1,L1CAM,MST4,CADM1,PTGES,KRT19,PAX6,A2M,ENC1,EREG
Inflammatory Response	1.33E-04-8.75E-03	PDPN,LIF,CD4,GDF15,PTN,CXCL12,CCL20,SOD3,VEGFA,CXCL10,C1QTNF3,ICAM2,CCL28,FABP4,NEO1,AHR,ADRB2,IL4R,EDNRB,TNFAIP6,LRRK2,IL1R1,S1PR3,PTGES,PREX1,TLR5,ANXA3,A2M
Cellular Compromise	1.57E-04-6.09E-03	BDKRB2,LPAR4,EPHB1,LIF,BDNF,CXCL12,NEO1,LRRK2,L1CAM
Immune Cell Trafficking	2.17E-04-7.9E-03	PDPN,IL4R,LIF,EDNRB,CD4,PTN,CXCL12,CCL20,LRRK2,L1CAM,IL1R1,SOD3,ERG,VEGFA,S1PR3,CXCL10,PTGES,PREX1,ICAM2,TLR5,CCL28,MAPK10,FABP4,NEO1,A2M,AHR,ADRB2
Post-Translational Modification	2.73E-04-2.73E-04	DAPK1,BMP4,EDNRB,CD4,PTN,LRRK2,PLK1,MAPK13,CDK1,MST4,ERG,VEGFA,PLK4,EPHB1,LRRN3,NEK2,FAM129A,MAPK10,PKN3,EREG,AHR,IQGAP3
Cell Signaling	5.12E-04-8.09E-03	NNAT,LPAR4,BMP4,LIF,ATP2B1,BDNF,CD4,C1QTNF1,CXCL12,CCL20,MAPK13,KSR1,BDKRB2,VEGFA,CXCL10,CCL28,FABP4,AH

		R,ADRB2,DAPK1,SLC9A3R1,EDNRB,RGS7,LRRK2,TRPC4,L1CAM,S1PR3,CD180,A2M
Respiratory System Development and Function	8.03E-04-1.19E-03	PDPN,VEGFA,BMP4,LIF,ROBO1
Lipid Metabolism	9.43E-04-6.35E-03	PDPN,IL4R,BMP4,HOMER2,LIF,EDNRB,BDNF,CD4,C1QTNF1,GDF15,CXCL12,IL1R1,CERS4,CADM1,BDKRB2,CXCL10,VEGFA,S1PR3,C1QTNF3,PTGES,MAPK10,FABP4,PNPLA3,AHR,ADRB2
Small Molecule Biochemistry	9.43E-04-8.09E-03	PDPN,LPAR4,LIF,BMP4,HOMER2,BDNF,CD4,C1QTNF1,GDF15,CXCL12,BDKRB2,CXCL10,VEGFA,C1QTNF3,FABP4,PNPLA3,AHR,ADRB2,IL4R,TNFAIP6,EDNRB,IL1R1,CERS4,CADM1,S1PR3,PTGES,PCSK2,MAPK10,PAX6,FOXE1
Connective Tissue Development and Function	1.26E-03-7.9E-03	VEGFA,PDPN,PTGES,IL4R,LIF,FLRT2,GDF15,IL1R1,ADRB2
Connective Tissue Disorders	1.26E-03-6.58E-03	BMP4,BDNF,CD4,HMMR,CXCL12,CCL20,ROBO1,HLA-DPA1,SOD3,KSR1,VEGFA,CXCL10,FABP4,ADAMTS5,AHR,ADRB2,IL4R,TNFAIP6,EDNRB,ZSCAN31,LRRK2,L1CAM,IL1R1,CSGALNACT1,TFPI2,ERG,CD180
Hypersensitivity Response	1.26E-03-7.88E-03	VEGFA,CXCL10,IL4R,ICAM2,CCL28,CD4,CXCL12,FABP4
Molecular Transport	1.35E-03-8.5E-03	NNAT,DAPK1,LPAR4,EDNRB,SLC9A3R1,ATP2B1,BDNF,CD4,RGS7,CXCL12,CCL20,L1CAM,TRPC4,IL1R1,CERS4,CXCL10,VEGFA,S1PR3,BDKRB2,PTGES,CD180,CCL28,FABP4,A2M,AHR,ADRB2
Carbohydrate Metabolism	1.66E-03-4.56E-03	VEGFA,CXCL10,TNFAIP6,CD4
Cardiovascular Disease	1.88E-03-4.41E-03	VEGFA,TNFAIP6,AHR,ADRB2
Respiratory Disease	2.13E-03-7.89E-03	LIF,CDC20,NID2,CD4,CXCL12,CCNB2,ROBO1,VEGFA,ICAM2,TRHDE,CCL28,NEO1,AHR,IL4R,EDNRB,TNFAIP6,RGS7,PCDHGA2,L1CAM,PLK1,IL1R1,BUB1B,CDK1,CERS4,HIST2H2BE (includes others),PTGES,PCSK2,TLR5,KRT19,ANXA3,MXRA5,PPP2R1B,KIF11
Cell-mediated Immune Response	2.61E-03-7.93E-03	CXCL10,LIF,TLR5,CD4,CCL28,CXCL12,CCL20,IL1R1,AHR
Inflammatory Disease	2.97E-03-7.89E-03	BMP4,BDNF,CD4,HMMR,CXCL12,CCL20,ROBO1,HLA-DPA1,SOD3,KSR1,VEGFA,CXCL10,CCL28,FABP4,ADAMTS5,AHR,ADRB2,IL4R,TNFAIP6,EDNRB,ZSCAN31,LRRK2,L1CAM,IL1R1,CSGALNACT1,TFPI2,ERG,CD180
Skeletal and Muscular Disorders	2.97E-03-6.58E-03	BMP4,BDNF,CD4,HMMR,CXCL12,CCL20,ROBO1,HLA-DPA1,SOD3,KSR1,VEGFA,CXCL10,NEFM,FABP4,ADAMTS5,AHR,ADRB2,IL4R,TNFAIP6,EDNRB,ZSCAN31,LRRK2,L1CAM,IL1R1,CSGALNACT1,TFPI2,ERG,CD180
Hereditary Disorder	3.12E-03-7.9E-03	IL4R,SLC9A3R1,KCNK1,KRT19,SSTR1

Supplementary Table 4. **Canonical signal transduction pathways predicted by Ingenuity Pathway Analysis based on the differentially expressed genes in HPAH and IPAH vs control.** Canonical pathways analysis identified the pathways from the Ingenuity Pathways Analysis™ library of canonical pathways that were most significant to the dataset. The 227 selected genes in table 1 were associated with a canonical pathway in the Ingenuity knowledge base were considered for analysis. The significance of the association between the dataset and the canonical pathway was determined as a p-value calculated by Fisher's exact test, a measure of the probability that the association between the proteins in the dataset and the canonical pathway is taking place by chance alone. The ratio is calculated as follows: number of genes in a given pathway that meet the cutoff criteria, divided by the total number of genes that make up that pathway and that are in the reference gene set. The molecules involved in those biological pathways were also listed in the table. The identity of those molecules can be retrieved from **Supplementary Table 2**.

Ingenuity Canonical Pathways	-log (p-value)	Ratio	Molecules
Mitotic Roles of Polo-Like Kinase	6.04E00	1.08E-01	KIF23,PLK4,CDC20,CCNB2,PLK1,PPP2R1B,CDK1,KIF11
Salvage Pathways of Pyrimidine Ribonucleotides	3.12E00	5.31E-02	DAPK1,NEK2,PLK1,TTK,CDK1,APOBEC3G
DNA damage-induced 14-3-3σ Signaling	2.91E00	1.36E-01	CCNE2,CCNB2,CDK1
IL-6 Signaling	2.67E00	4.84E-02	VEGFA,TNFAIP6,MAPK10,MAPK13,IL1R1,A2M
ATM Signaling	2.32E00	6.06E-02	MAPK10,CCNB2,MAPK13,CDK1
Inhibition of Angiogenesis by TSP1	2.17E00	7.14E-02	VEGFA,MAPK10,MAPK13
Cyclins and Cell Cycle Regulation	1.88E00	4.17E-02	CCNE2,CCNB2,PPP2R1B,CDK1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.86E00	6.12E-02	CCNB2,PLK1,CDK1
GADD45 Signaling	1.67E00	8.33E-02	CCNE2,CDK1
Role of CHK Proteins in Cell Cycle Checkpoint Control	1.61E00	5.08E-02	PLK1,PPP2R1B,CDK1
IL-22 Signaling	1.52E00	8E-02	MAPK10,MAPK13
Estrogen-mediated S-phase Entry	1.52E00	7.14E-02	CCNE2,CDK1
Role of JAK family kinases in IL-6-type Cytokine Signaling	1.49E00	7.14E-02	MAPK10,MAPK13
IL-17A Signaling in Airway Cells	1.44E00	3.95E-02	MAPK10,CCL20,MAPK13
IL-10 Signaling	1.37E00	3.85E-02	IL4R,MAPK13,IL1R1
IL-17 Signaling	1.31E00	4E-02	CXCL10,MAPK10,MAPK13
BMP signaling pathway	1.25E00	3.49E-02	BMP4,MAPK10,MAPK13
Coagulation System	1.22E00	5.26E-02	BDKRB2,A2M
Cell Cycle Regulation by BTG Family Proteins	1.22E00	5.13E-02	CCNE2,PPP2R1B
Ceramide Signaling	1.2E00	3.3E-02	S1PR3,PPP2R1B,KSR1
Superoxide Radicals Degradation	1.18E00	1.25E-01	SOD3

Inhibition of Matrix Metalloproteases	1.14E00	5E-02	A2M,TFPI2
ErbB Signaling	1.14E00	3.33E-02	MAPK10,MAPK13,EREG
HMGB1 Signaling	1.05E00	2.75E-02	MAPK10,MAPK13,IL1R1
IL-1 Signaling	1.05E00	2.75E-02	MAPK10,MAPK13,IL1R1
Prostanoid Biosynthesis	1.01E00	6.67E-02	PTGES
Calcium Transport I	9.66E-01	7.14E-02	ATP2B1
Cdc42 Signaling	9.5E-01	2.15E-02	MAPK10,MAPK13,HLA-DPA1,IQGAP3
HIF1α Signaling	9.46E-01	2.68E-02	VEGFA,MAPK10,MAPK13
Type I Diabetes Mellitus Signaling	9.01E-01	2.48E-02	MAPK10,MAPK13,IL1R1
Endothelin-1 Signaling	8.74E-01	2.08E-02	EDNRB,MAPK10,PNPLA3,MAPK13
Toll-like Receptor Signaling	8.74E-01	3.12E-02	TLR5,MAPK13
Corticotropin Releasing Hormone Signaling	8.59E-01	2.07E-02	VEGFA,BDNF,MAPK13
Glutamate Receptor Signaling	8.38E-01	2.78E-02	HOMER2,GRIK2
CD40 Signaling	7.93E-01	2.82E-02	MAPK10,MAPK13
Eicosanoid Signaling	7.93E-01	2.33E-02	PTGES,PNPLA3
Adenosine Nucleotides Degradation II	7.52E-01	3.57E-02	CECR1
Chemokine Signaling	7.32E-01	2.67E-02	CXCL12,MAPK13
eNOS Signaling	7.26E-01	1.94E-02	VEGFA,BDKRB2,LPAR4
PEDF Signaling	7.13E-01	2.53E-02	BDNF,MAPK13
Cardiomyocyte Differentiation via BMP Receptors	7.09E-01	4.55E-02	BMP4
AMPK Signaling	7E-01	1.66E-02	MAPK13,PPP2R1B,ADRB2
LPS-stimulated MAPK Signaling	6.95E-01	2.41E-02	MAPK10,MAPK13
Basal Cell Carcinoma Signaling	6.95E-01	2.56E-02	BMP4,WNT16
STAT3 Pathway	6.95E-01	2.5E-02	MAPK10,MAPK13
Purine Nucleotides Degradation II (Aerobic)	6.89E-01	2.7E-02	CECR1
Ephrin B Signaling	6.86E-01	2.44E-02	EPHB1,CXCL12
CXCR4 Signaling	5.97E-01	1.72E-02	CD4,CXCL12,MAPK10
RANK Signaling in Osteoclasts	5.84E-01	2.06E-02	MAPK10,MAPK13
TGF-β Signaling	5.84E-01	2.13E-02	BMP4,MAPK13
CDK5 Signaling	5.77E-01	2.06E-02	BDNF,PPP2R1B
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	5.72E-01	1.46E-02	VEGFA,TLR5,CXCL12,WNT16,IL1R1
Factors Promoting Cardiogenesis in Vertebrates	5.7E-01	2.02E-02	CCNE2,BMP4
Bladder Cancer Signaling	5.7E-01	2.06E-02	VEGFA,DAPK1
Acute Phase Response Signaling	5.19E-01	1.66E-02	MAPK13,IL1R1,A2M
NF-κB Signaling	5.02E-01	1.66E-02	BMP4,TLR5,IL1R1
Paxillin Signaling	4.95E-01	1.71E-02	MAPK10,MAPK13
Nitric Oxide Signaling in the Cardiovascular System	4.95E-01	1.6E-02	VEGFA,BDKRB2

Ephrin Receptor Signaling	4.93E-01	1.43E-02	VEGFA,EPHB1,CXCL12
RAR Activation	4.85E-01	1.54E-02	VEGFA,MAPK10,MAPK13
Sertoli Cell-Sertoli Cell Junction Signaling	4.85E-01	1.52E-02	MAPK10,MAPK13,A2M
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	4.77E-01	1.42E-02	MAPK10,MAPK13,PPP2R1B
NRF2-mediated Oxidative Stress Response	4.73E-01	1.54E-02	DNAJC6,ENC1,SOD3
Role of NFAT in Cardiac Hypertrophy	4.65E-01	1.44E-02	LIF,MAPK10,MAPK13
Glucocorticoid Receptor Signaling	4.6E-01	1.34E-02	MAPK10,MAPK13,A2M,ADRB2
Fc Epsilon RI Signaling	4.52E-01	1.71E-02	MAPK10,MAPK13
Renin-Angiotensin Signaling	4.52E-01	1.59E-02	MAPK10,MAPK13
ILK Signaling	4.45E-01	1.46E-02	VEGFA,MAPK10,PPP2R1B
Role of Tissue Factor in Cancer	4.42E-01	1.54E-02	VEGFA,MAPK13
Xenobiotic Metabolism Signaling	4.29E-01	1.39E-02	MAPK13,PPP2R1B,AHR,SOD3
Breast Cancer Regulation by Stathmin1	4.23E-01	1.4E-02	CCNE2,PPP2R1B,CDK1
Gα12/13 Signaling	4.09E-01	1.57E-02	LPAR4,MAPK10
RhoA Signaling	4.09E-01	1.63E-02	LPAR4,ANLN
p38 MAPK Signaling	4.09E-01	1.67E-02	MAPK13,IL1R1
Leukocyte Extravasation Signaling	4.06E-01	1.43E-02	CXCL12,MAPK10,MAPK13

Supplementary Table 5. The list of genes predicted by Ingenuity Pathway Analysis that increase or affect cell proliferation. The identity of those molecules can be retrieved from **Supplementary Table 2**.

	Prediction (based on expression direction)	**Fold Change (HPAH)**	**Fold Change (IPAH)**	**Findings**
ADAMTS5	Increased	-1.695	-2.536	Decreases (1)
ATP2B1	Increased	-1.874	-1.640	Decreases (1)
B4GALT6	Increased	1.705	2.149	Increases (1)
BUB1	Increased	2.360	6.424	Increases (3)
CCNB1	Increased	1.704	4.284	Increases (1)
CCNE2	Increased	1.668	2.081	Increases (1)
CDC20	Increased	2.702	7.124	Increases (1)
CDK1	Increased	1.969	4.674	Increases (6)
CENPF	Increased	1.829	4.382	Increases (1)
CXCL10	Increased	-2.297	-2.052	Decreases (11)
DLGAP5	Increased	2.786	7.634	Increases (6)
DOCK4	Increased	-1.731	-1.754	Decreases (1)
DTL	Increased	1.574	2.382	Increases (1)
EPHB1	Increased	1.677	1.761	Increases (1)
ERG	Increased	8.491	6.342	Increases (3)
FOXM1	Increased	1.673	4.489	Increases (35)
GDF15	Increased	-1.996	-1.920	Decreases (14)
ITGB8	Increased	-1.551	-1.846	Decreases (8)
KCNMA1	Increased	2.060	1.844	Increases (1)
KIAA0101	Increased	1.675	3.402	Increases (3)
KIF11	Increased	2.007	4.085	Increases (1)
KIF20A	Increased	3.060	8.925	Increases (1)
KIF20B	Increased	1.837	4.078	Increases (1)
KIF2C	Increased	1.510	3.792	Increases (2)
KSR1	Increased	-1.605	-2.433	Decreases (13)
MAPK13	Increased	1.827	1.870	Increases (1)
MCM10	Increased	1.551	2.262	Increases (1)
MET	Increased	1.523	1.969	Increases (84)
MKI67	Increased	2.042	3.972	Increases (9)
MST4	Increased	1.769	2.160	Increases (10)
MYBL2	Increased	1.627	2.524	Increases (12)
NCAPG	Increased	1.859	4.022	Increases (4)
NEK2	Increased	1.784	4.850	Increases (3)
NRCAM	Increased	3.520	1.617	Increases (1)
PBK	Increased	2.008	5.324	Increases (1)
PCSK2	Increased	-8.144	-1.782	Decreases (1)
PEG10	Increased	1.701	2.427	Increases (3)
PLK1	Increased	2.502	6.501	Increases (17)
PPP2R1B	Increased	-1.687	-1.733	Decreases (11)
PRKAR2B	Increased	-1.803	-2.048	Decreases (19)
ROBO1	Increased	-1.835	-1.625	Decreases (1)
RRM2	Increased	2.032	3.741	Increases (14)

SPRY1	Increased	-1.828	-1.643	Decreases (3)
SSTR1	Increased	-1.763	-2.298	Decreases (3)
STC1	Increased	-1.768	-1.837	Decreases (1)
TFPI2	Increased	-3.429	-2.020	Decreases (5)
TLR5	Increased	1.579	1.560	Increases (4)
TOP2A	Increased	1.570	3.493	Increases (2)
TPX2	Increased	1.664	3.565	Increases (5)
TTK	Increased	1.895	5.289	Increases (1)
UHRF1	Increased	1.576	2.171	Increases (4)
ADRB2	Affected	2.074	2.208	Affects (2)
BDKRB2	Affected	-1.619	-1.857	Affects (3)
BUB1B	Affected	2.000	4.990	Affects (1)
CADM1	Affected	1.829	1.919	Affects (1)
CD4	Affected	-3.205	-1.987	Affects (16)
CDC25C	Affected	1.618	4.164	Affects (1)
CDCP1	Affected	1.654	2.358	Affects (4)
DAPK1	Affected	3.104	1.544	Affects (1)
DNER	Affected	-2.782	-1.565	Affects (1)
ENC1	Affected	-2.242	-2.150	Affects (5)
HIST1H2BH	Affected	1.856	3.023	Affects (1)
IL1R1	Affected	-1.515	-2.086	Affects (9)
KIF15	Affected	1.550	3.242	Affects (1)
KRT19	Affected	2.635	3.145	Affects (2)
PDPN	Affected	2.764	3.024	Affects (1)
PLK4	Affected	1.599	3.578	Affects (2)
TACC3	Affected	1.713	3.018	Affects (2)
TCF19	Affected	1.559	2.527	Affects (1)
WNT16	Affected	-2.735	-1.579	Affects (1)

Supplementary Table 6. The downstream genes regulated by p53, Rb, FoxM1 and Myc which displayed differentiated expressional changes in HPAH and IPAH samples

Downstream genes regulated by p53

Symbol	**Entrez Gene Name**	**Entrez Gene ID**	**Fold Change (HPAH)**	p-value (HPAH)	**Fold Change (IPAH)**	p-value (IPAH)
A2M	alpha-2-macroglobulin	2	-2.014	1.10E-03	-1.809	1.44E-03
ADRB2	adrenoceptor beta 2, surface	154	2.089	2.18E-04	2.191	1.48E-04
ANLN	anillin, actin binding protein	54443	2.356	8.74E-03	5.827	6.49E-04
ANXA3	annexin A3	306	2.044	2.31E-04	4.137	7.40E-05
ASF1B	anti-silencing function 1B histone chaperone	55723	1.576	3.70E-03	2.973	4.00E-05
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	259266	2.308	9.73E-03	5.434	7.92E-04
BDKRB2	bradykinin receptor B2	624	-1.607	9.36E-03	-1.871	5.29E-03
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	2.013	3.45E-04	4.950	1.29E-05
CCNB2	cyclin B2	9133	1.986	9.20E-03	5.419	4.72E-04
CCNE2	cyclin E2	9134	1.681	4.13E-03	2.066	6.67E-04
CDC20	cell division cycle 20	991	2.717	4.02E-03	7.059	3.05E-04
CDK1	cyclin-dependent kinase 1	983	1.981	3.75E-03	4.634	1.86E-04
CDKN3	cyclin-dependent kinase inhibitor 3	1033	2.134	2.51E-02	5.987	1.50E-03
CTSH	cathepsin H	1512	3.570	1.48E-04	2.252	7.90E-04
DAPK1	death-associated protein kinase 1	1612	3.125	1.55E-04	1.532	2.49E-03
FABP4	fatty acid binding protein 4, adipocyte	2167	-4.565	7.90E-03	-5.134	5.25E-03
FANCI	Fanconi anemia, complementation group I	55215	1.522	3.42E-04	2.489	2.69E-05
FLRT2	fibronectin leucine rich transmembrane protein 2	23768	-2.573	6.22E-05	-1.820	2.28E-04
GDF15	growth differentiation factor 15	9518	-1.981	3.31E-04	-1.933	5.68E-04
HJURP	Holliday junction recognition protein	55355	1.534	5.00E-03	4.005	7.13E-05
HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	2.538	3.22E-03	6.795	2.25E-04
IL4R	interleukin 4 receptor	3566	-1.723	1.85E-03	-1.846	6.41E-04
KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	3778	2.076	4.58E-04	1.831	8.60E-04
KIF23	kinesin family member 23	9493	1.576	4.07E-04	2.318	3.79E-05
KSR1	kinase suppressor of ras 1	8844	-1.594	6.41E-04	-2.452	1.23E-04
LIF	leukemia inhibitory factor	3976	-1.627	8.44E-03	-2.037	8.82E-03
MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	4605	1.638	1.12E-03	2.504	2.29E-04

NCAPG	non-SMC condensin I complex, subunit G	64151	1.872	4.65E-04	3.992	3.26E-05
NCAPH	non-SMC condensin I complex, subunit H	23397	1.977	3.62E-05	3.825	8.40E-08
NDC80	NDC80 kinetochore complex component	10403	1.871	6.13E-03	4.864	2.19E-04
NEK2	NIMA-related kinase 2	4751	1.795	7.97E-04	4.810	3.05E-05
NEO1	neogenin 1	4756	-1.620	1.07E-04	-1.745	1.04E-05
NID2	nidogen 2 (osteonidogen)	22795	-1.632	2.10E-04	-2.465	1.52E-05
PLK1	polo-like kinase 1	5347	2.517	5.73E-03	6.442	4.78E-04
RAD51AP1	RAD51 associated protein 1	10635	1.577	2.04E-04	3.256	3.67E-06
ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	6091	-1.821	3.79E-03	-1.635	7.86E-03
SPC25	SPC25, NDC80 kinetochore complex component	57405	1.658	3.48E-04	4.434	7.68E-06
TBL1X	transducin (beta)-like 1X-linked	6907	-1.615	6.63E-04	-1.534	1.84E-04
TFPI2	tissue factor pathway inhibitor 2	7980	-3.403	7.02E-04	-2.034	1.17E-03
TP53	tumor protein p53	--				
TTK	TTK protein kinase	7272	1.908	9.84E-04	5.246	3.01E-05
UBE2T	ubiquitin-conjugating enzyme E2T (putative)	29089	1.521	2.49E-03	2.562	1.35E-04
UHRF1	ubiquitin-like with PHD and ring finger domains 1	29128	1.588	1.58E-03	2.156	2.48E-04
VEGFA	vascular endothelial growth factor A	7422	-1.514	2.38E-03	-1.732	3.27E-04

Downstream genes regulated by Rb

Symbol	**Entrez Gene Name**	Entrez Gene ID	**Fold Change (HPAH)**	p-value (HPAH)	**Fold Change (IPAH)**	p-value (IPAH)
ASF1B	anti-silencing function 1B histone chaperone	55723	1.576	3.70E-03	2.973	4.00E-05
CCNE2	cyclin E2	9134	1.681	4.13E-03	2.066	6.67E-04
CDK1	cyclin-dependent kinase 1	983	1.981	3.75E-03	4.634	1.86E-04
CPA4	carboxypeptidase A4	51200	2.566	5.88E-03	2.399	7.65E-03
FABP4	fatty acid binding protein 4, adipocyte	2167	-4.565	7.90E-03	-5.134	5.25E-03
HIST1H4A	histone cluster 1, H4a	8364	1.815	8.69E-04	2.878	1.40E-04
HIST2H2BE	histone cluster 2, H2be	8344	1.508	1.62E-03	2.372	7.45E-05
KCNK1	potassium channel, subfamily K, member 1	3775	1.555	8.82E-04	1.662	2.49E-04
MCM10	minichromosome maintenance complex component 10	55388	1.563	3.84E-03	2.247	3.75E-04

MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	4605	1.638	1.12E-03	2.504	2.29E-04
NEFM	neurofilament, medium polypeptide	4741	1.594	2.99E-02	4.807	4.90E-04
PLK1	polo-like kinase 1	5347	2.517	5.73E-03	6.442	4.78E-04
RAD51AP1	RAD51 associated protein 1	10635	1.577	2.04E-04	3.256	3.67E-06
TCF19	transcription factor 19	6941	1.570	3.56E-03	2.509	1.48E-04
VEGFA	vascular endothelial growth factor A	7422	-1.514	2.38E-03	-1.732	3.27E-04

Downstream molecules regulated by Myc

Symbol	**Entrez Gene Name**	Entrez Gene ID	**Fold Change (HPAH)**	p-value (HPAH)	**Fold Change (IPAH)**	p-value (IPAH)
BDNF	brain-derived neurotrophic factor	627	-2.078	1.29E-03	-2.561	2.20E-04
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	2.013	3.45E-04	4.950	1.29E-05
CCNB2	cyclin B2	9133	1.986	9.20E-03	5.419	4.72E-04
CCNE2	cyclin E2	9134	1.681	4.13E-03	2.066	6.67E-04
CDC20	cell division cycle 20	991	2.717	4.02E-03	7.059	3.05E-04
CDK1	cyclin-dependent kinase 1	983	1.981	3.75E-03	4.634	1.86E-04
CXCL10	chemokine (C-X-C motif) ligand 10	3627	-2.279	6.46E-05	-2.067	3.17E-04
FABP4	fatty acid binding protein 4, adipocyte	2167	-4.565	7.90E-03	-5.134	5.25E-03
FAM129A	family with sequence similarity 129, member A	116496	1.500	3.46E-04	1.889	3.29E-05
HIST1H4A (includes others)	--	8364	1.815	8.69E-04	2.878	1.40E-04
PLK1	polo-like kinase 1	5347	2.517	5.73E-03	6.442	4.78E-04
PTN	pleiotrophin	5764	-2.089	2.81E-03	-2.951	6.16E-04
VEGFA	vascular endothelial growth factor A	7422	-1.514	2.38E-03	-1.732	3.27E-04

Downstream molecules regulated by FoxM1

Symbol	**Entrez Gene Name**	Entrez Gene ID	**Fold Change (HPAH)**	p-value (HPAH)	**Fold Change (IPAH)**	p-value (IPAH)
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	2.013	3.45E-04	4.950	1.29E-05
CCNB2	cyclin B2	9133	1.986	9.20E-03	5.419	4.72E-04
CCNE2	cyclin E2	9134	1.681	4.13E-03	2.066	6.67E-04
CDC20	cell division cycle 20	991	2.717	4.02E-03	7.059	3.05E-04

CDK1	cyclin-dependent kinase 1	983	1.981	3.75E-03	4.634	1.86E-04
CDKN3	cyclin-dependent kinase inhibitor 3	1033	2.134	2.51E-02	5.987	1.50E-03
NEK2	--	4751	1.795	7.97E-04	4.810	3.05E-05
PLK1	polo-like kinase 1	5347	2.517	5.73E-03	6.442	4.78E-04
PLK4	polo-like kinase 4	10733	1.610	5.01E-04	3.550	1.27E-05
VEGFA	vascular endothelial growth factor A	7422	-1.514	2.38E-03	-1.732	3.27E-04