Supplementary Materials:

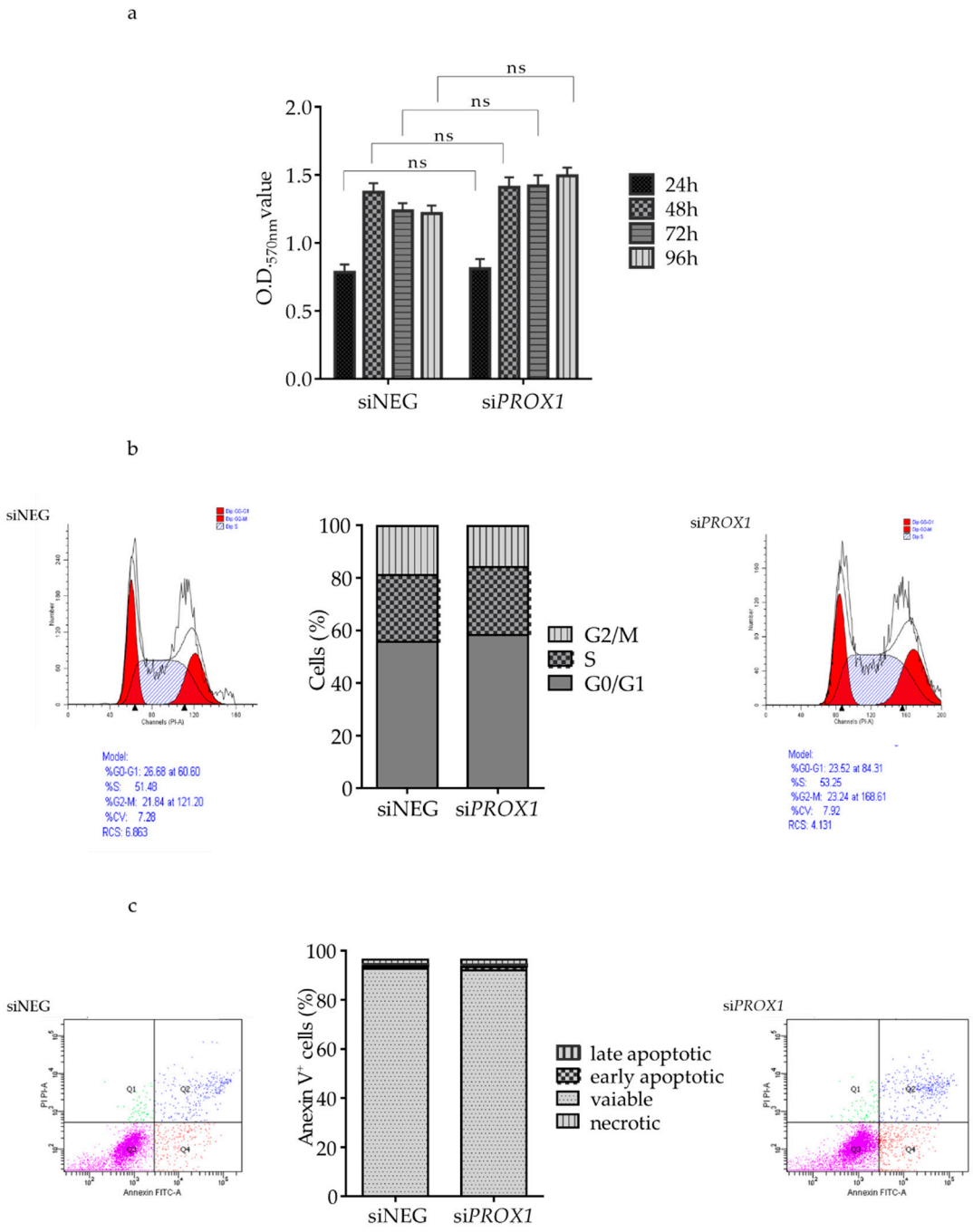

Figure S1. The effect of *PROX1* silencing on the cell cycle, the proliferation and the survival of CGTH-W-1 cells. (**a**) CGTH cell proliferation 24, 48, 72 and 96 h following transfection with *PROX1* siRNA measured by MTT assay. The proliferation of *PROX1*-depleted cells as measured by MTT assay did not differ when compared to the proliferation of control cells transfected with siNEG. Observed small differences were not statistically significant. (**b**) Effect of *PROX1* knock-down on cell cycle and (**c**) apoptosis in CGTH cells. The cell cycle distribution and apoptosis in CGTH cells with silenced *PROX1* and in control cells was measured by flow cytometry 48 h after transfection. The MTT assay was performed in five replicates for each time point. Error bars represent means with standard deviations (SD). A570: absorbance at 570 nm.

Table S1. The primers nucleotide sequences.

prospero homeobox 1 (*PROX1*)	5′–CCAGCTCCAATATGCTGAAGACCTA-3′ 5′–CATCGTTGATGGCTTGACGTG–3′
beta actin (*ACTB*)	5′–FGCCGAGGACTTTGATTGC–3′ 5′–CTGTGTGGACTTGGGAGAG–3′
caldesmon 1 (*CALD1*)	5′–GAGCGTCGCAGAGAACTTAGA–3′ 5′–TCCTCTGGTAGGCGATTCTTT–3′
integrin subunit alpha 2 (*ITGA2*)	5′–GCAAACCTCTGCAAACCCAG–3′ 5′–CGGTTCTCAGGAAAGCCACT–3′
periostin (*POSTN*)	5′–CTGCTTCAGGGAGACACACC–3′ 5′–CACTGAGAACGACCTTCCCTT–3′
hyaluronan synthase 2 (*HAS2*)	5′–TGACAGGCATCTCACGAACC–3′ 5′–CAGCCATTCTCGGAAGTAGG–3′
integrin alpha 11 (*ITGA11*)	5′–GTTGTGCAGTATGGCGAAGA–3′ 5′–TTCTGGAAAGCCTCTGAGCG–3′
caveolin-2 (*CAV2*)	5′–ACGGAGAAGGCGGACGTA–3′ 5′–AAAGGAGTGCGTAGTCACCG–3′
cell migration inducing protein, hyaluronan binding (*CEMIP*)	5′–CCAGGAATGTTGAATGTCT–3′ 5′–ATTGGCTCTTGGTGAATG–3′
TRIO and F-actin binding protein (*TRIOBP*)	5′–CCAGCCAAGGTCTGATGATG–3′ 5′–TGGCTGACCGTCTATGTGAG–3′
tyrosine phosphatase, non-receptor type 14 (*PTPN14*)	5′–AGCCGAATCCGTGAAGTTGT–3′ 5′–GTGGCTTTTGGTTCGTCCAC–3′
FERM domain containing 5 (*FRMD5*)	5′–CAGCATTGAGGAGGAGAAGG–3′ 5′–TCCACCTGGCTAGTTTTTGG–3′
collagen, type XVIII, alpha 1 (*COL18A1*)	5′–AAGGACGAGCTGCTGTTTCC–3′ 5′–TTGCCGTCAAAGGAGAAGATG–3′
activated leukocyte cell adhesion molecule (*ALCAM*)	5′–TGGACAATTACTGGCAGTGG–3′

	5′–TATCTCGTCTGCCTCATCGTG–3′
dedicator of cytokinesis 1 (*DOCK1*)	5′–TGTGTACCACAAGAGCTGGTT-3′ 5′–TGTCCACCAAAATTTTCAGGACTTT-3′
SRY (sex determining region Y)-box 2 (*SOX2*)	5′–AACCAGCGCATGGACAGTTA–3′ 5′–GACTTGACCACCGAACCCAT–3′
EPH receptor A2 (*EPHA2*)	5′–CCATTAAGGACTCGGGGCAG–3′ 5′–TTGCCATACGGGTGTGTGAG–3′
nucleophosmin (*NPM1*)	5′–AGGAGTGGGGTTGAAAAGCG–3′ 5′–AGAACGCTGCTCCAGAGAAC–3′
plexin B2 (*PLXNB2*)	5′–GCAGAAACTGAGCTGGACCAC–3′ 5′–TTCTCGCTGCGGAAGAAGTC–3′
tubulin beta 2A (*TUBB2A*)	5′–GGACGAGATGGAGTTCACCG–3′ 5′–ACCATGCTTGAGGACAACAGA–3′
epidermal growth factor receptor pathway substrate 8 (*EPS8*)	5′–GCCAACTTCTAATCGCCATA–3′ 5′–TCACTGTTGTTCCTTGCTAC–3′
GATA binding protein 3 (*GATA3*)	5′–GCCGTTGAGGGTTTCAGAGA–3′ 5′–TCCGAGCACAACCACCTTAG–3′
sapiens Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (*RAPH1*)	5′–TCTTTGAGTATGGATGAGGCTG–3′ 5′–GTGATGCTGGAATGGGAGG–3′
Rho-associated, coiled-coil containing protein kinase 1 (*ROCK1*)	5′–AGGAAGGCGGACATATTAGTCCCT–3′ 5′–AGACGATAGTTGGGTCCCGGC–3′
dynein, cytoplasmic 1, heavy chain 1 (*DYNC1H1*)	5′–GCCACCGTCAGTTTTGACAC–3′ 5′–AAATTGCCTCCACCAAACGC–3′
SRY-box 9 (*SOX9*)	5′–AGGAAGTCGGTGAAGAACGG–3′ 5′–AAGTCGATAGGGGGCTGTCT–3′
neuropilin 2 (*NRP2*)	5′–TCGGCTTTTGCAGGTGAGAA–3′ 5′–TTTCTTTGTCGGTCGAGGGG–3′
protein tyrosine kinase 2 (*PTK2*)	5′–GGTGCAATGGAGCGAGTATT–3′

	5′–GCCAGTGAACCTCCTCTGA–3′
ADAM metallopeptidase with thrombospondin type 1 motif 3 (*ADAMTS3*)	5′–CGACTCGTGATGGTTCTCCT–3′ 5′–TGCTCAGGGTTGGAAGACAC–3′
dystroglycan 1 (*DAG1*)	5′–GCAGGGACTGGGAGAACCA–3′ 5′–ACAGCCTCGTGAAGGTCTGAA–3′
claudin 12 (*CLND12*)	5′–TCAAAGCATGAAGAAAACGAGGC-3′ 5′–GCTACTGAGGCGATTCCACA–3′
spectrin repeat containing, nuclear envelope 2 (*SYNE2*)	5′–GTGGTCTCTGTCAACGTGAGC–3′ 5′–GAGCGACTGTCGTAAGCCC-3′
pseudopodium-enriched atypical kinase 1 (*PEAK1*)	5′–TGCTGCACCTACCCAACCCC–3′ 5′–GGGAGTCTGTAGTGGCAAAAGCCA–3′
plexin A1 (*PLXNA1*)	5′–CACCATGATGCTCACCCCA–3′ 5′–ATACACCTCGCCTGTCTGCT–3′
septin 6 (*SEPT6*)	5′–AATGGAACCATGAACGCCCA-3′ 5′–GCTTCACAAAGTCGCAGTGG-3′
supervillin (*SVIL*)	5′–TGGTGTTTGATTTTGGTAGTGAA–3′ 5′–TAAGCGGATTGCATTCTCCA–3′
FERM RhoGEF (*ARHGEF*) and pleckstrin domain protein 1 (chondrocyte-derived) (*FARP1*)	5′–GACTTCAGGGACTGCCGAG–3′ 5′–GGACGTCGTTGAACAGGAAG-3′
Wiskott-Aldrich syndrome-like (*WASL*)	5′–CCCTCTTCACTTTCCTCGGC–3′ 5′–CCCACAATAGTTTCCCATCC-3′
phosphatidylinositol-4-phosphate 5-kinase type 1 gamma (*PIP5K1C*)	5′–CACACAGTCGTCTGGACAGG–3′ 5′–AAAGTAGATGTCGGTGGCGG–3′
syndecan 3 (*SDC3*)	5′–AGCGTCACATACCAGAAGCC–3′ 5′–GGCAGACCTTGGGAGAGAG–3′
nucleoporin 50 (*NUP50*)	5′–CGGAAGGAGGTGCTACTGC–3′ 5′–ACTCGAATCTACCCCCAAAAC–3′
profilin 2 (*PFN2*)	5′–GACTGCACAATGGACATCCG–3′

	5′–TTTTGCCATTGAGTATGCCTTC–3′
doublecortin like kinase 1 (*DCLK1*)	5′–AAGTCCATCATGTCCTTCGGC–3′ 5′–CTGGGGAGATGGCATACACA–3′
phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha (*PIK3CA*)	5′–GGGACCCGATGCGGTTAG–3′ 5′–AAGTGGATGCCCCACAGTTC–3′
melanoma cell adhesion molecule (*MCAM*)	5′–CCCTCACACCAGACTCCAAC–3′ 5′–TGATCTCCTGCTTCCCTGAG –3′
death associated protein kinase 3 (*DAPK3*)	5′–AATCTGAGGAGCTGGGTTGC–3′ 5′–TGAACTTGGCTGCGTACTCC–3′
eukaryotic translation initiation factor 6 (*EIF6*)	5′–ACTGTGAGATCGGCTGCTTT–3′ 5′–TCCTGGTCGGTGGTATTGTTG–3′
collagen type VI alpha 1 chain (*COL6A1*)	5′–ATTGCCAAGGACTTCGTCGT–3′ 5′–TCCACTGCAGGCTCTTGATG–3′
major vault protein (*MVP*)	5′–CAGGATGTGTATGTGCTGTCGG–3′ 5′–GCTGGAGGCTCTTAGCTGTGTC–3′
integrin alpha 6 (*ITGA6*)	5′–ATGCACGCGGATCGAGTTT–3′ 5′–TTCCTGCTTCGTATTAACATGCT–3′
ADAM metallopeptidase domain 12 (*ADAM12*)	5′–AAATCCCATGACAATGCGCAG–3′ 5′–CATGACAATTCCCCCAGACTGG–3′
bromodomain and WD repeat domain containing 3 (*BRWD3*)	5′–CTACCCAGATCGAAGCCGAG–3′ 5′–GGAATGTGTGCATTTGCTGC–3′
myosin VI (*MYO6*)	5′–TGGGTTTGGACCAAGATGAT–3′ 5′–CATCACGAGCATTGTTTGCT–3′
CD63 molecule (*CD63*)	5′–GTTACCGCGTCACATGAGGG–3′ 5′–GTTACCGCGTCACATGAGGG-3′
collagen, type XV, alpha 1 (*COL15A1*)	5′–CCTGCTCTGCATTTGGCTGCTCTG–3′ 5′–AACAGTCCTGCAGCTCTGGCCTG–3′
integrin linked kinase (*ILK*)	5′–ATCACTCCACAGTCCTCAGGC–3′

	5′–CGGCACTGAGTGAAAATGTCG–3′
CDC42 effector protein (Rho GTPase binding) 3 (*CDC42EP3*)	5′–TTTGACCCCATCTCATTTCG–3′ 5′–GGTCTTGGCTGGCATTTTGG–3′
microtubule-associated protein 4 (*MAP4*)	5′–ACGTCTCCTACCTCCTCACG–3′ 5′–TGCCTCTAGTGTGGCAATGA–3′
tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (*PTPN13*)	5′–TTGGAATGACACTGTATTGGGG–3′ 5′–CCAAGCAGTATGCTGTTGAGAT–3′
Rho GTPase activating protein 18 (*ARHGAP18*)	5′–ACTAACAGCCTACCACCCCA–3′ 5′–ACTGGCCATATCTGCGACTC–3′

Table S2. Antibodies used for protein detection in PROX-1 deficient CGTH-W-1 cells in Western blot (WB) and immunofluorescent (IF) analyses.

Used antibodies	**WB dilution**	**IF dilution**
Primary antibodies		
Human Prox1 Antibody (Polyclonal Goat IgG) (cat no AF2727, R&D Systems, USA)	1:2000	1:500
Human Caveolin-2 Antibody (cat no ab75865, Abcam, USA)	1:500	1:500
Human Caveolin-2 (Tyr19) Antibody (cat no, ab3417Abcam, USA)	1:500	1:500
Human FAK Antibody (cat no #3285, Cell Signaling, USA)	1:1000	1:500
Phospho FAK (Tyr397) Antibody (cat no #3283b, Cell Signaling, USA)	1:1000	1:500
Phospho-Src Family (Tyr416) Antibody (cat no #2101 Abcam, USA)	1:1000	n/a
Anti-Ezrin / Radixin / Moesin antibody (cat no ab118572, Abcam, USA)	1:1000	1:500
Anti-Ezrin (phospho Thr567)/ Radixin (phospho Thr564)/ Moesin (phospho Thr558) antibody (cat no ab76247, Abcam, USA)	1:1000	1:500
Nesprin 2 (cat no PA5-62155, ThermoFisher Scientific, USA)	1:1000	1:500
Integrin alpha 2/CD49b Antibody (2B6) (cat no H00003673-M01, Novus Biologicals, USA)	1:1000	n/a

Human EphA2 Antibody (cat no AF3035, R&D Systems, USA)	1:2000	n/a
Integrin alpha 11 Antibody (cat no AF4235, Novus Biologicals, USA)	1:1000	n/a
Anti-β-actin (cat no A2228 Sigma-Aldrich, USA)	1:5000	n/a
Secondary antibodies		
HRP Rabbit Anti-Goat IgG (cat no 305-035-046, JacksonImmunoResearch, USA)	1:20000	n/a
HRP Goat Anti-Rabbit Immunoglobulins (cat no P0448, DAKO, Denmark)	1:5000	n/a
Rabbit F(ab')2 polyclonal Secondary Antibody to Goat IgG-H&L DyLight® 594 (cat no ab96885, Abcam, United Kingdom)	n/a	1:500
Goat anti-Rabbit IgG (H+L) Secondary Antibody, Rhodamine Red (cat no 111-025-144, Jackson ImmunoResearch Laboratories, USA)	n/a	1:100

n/a: analysis not performed.

Table S3. The list of genes with number of reads in a given biological replicate (I, II, III) for cells treated with lipofectamine with control siRNA (siNEG) and lipofectamine alone (Lipo). The fold change (FC) and adj. P. values (p.adj) are provided.

Gene	refSeq	Lipo I	Lipo II	Lipo III	siNEG I	siNEG II	siNEG III	log2FoldChange	p.adj	FC
PLAT	NM_000930	52	50	88	284	263	291	-1.066822979	4.64E-06	0.48
GABARAPL1	NM_031412	100	93	83	383	316	438	-1.021792085	1.34E-06	0.49
NUPR1	NM_001042483	340	281	377	1208	1160	1447	-0.989195929	6.66E-08	0.50
NKD2	NM_033120	15	18	25	69	83	125	-0.923903394	0.00345	0.53
LPAR1	NM_001401	128	183	208	577	591	716	-0.920146757	3.31E-06	0.53
SEPT3	NM_145733	115	116	98	415	352	445	-0.905518146	1.68E-05	0.53
NEK11	NM_024800	19	20	15	71	77	103	-0.901080038	0.00465	0.54
AKAP12	NM_005100	48	55	62	196	202	227	-0.90102719	0.00021	0.54
COL15A1	NM_001855	41	55	53	198	166	205	-0.896496725	0.00035	0.54
ARHGDIB	NM_001175	79	76	82	274	255	326	-0.867928859	0.00013	0.55
LGALS3BP	NM_005567	100	125	149	444	323	499	-0.802534722	0.00041	0.57
SNCA	NM_000345	21	20	19	81	74	88	-0.800368935	0.01522	0.57
SLC43A2	NM_152346	23	16	34	112	78	95	-0.764425239	0.02322	0.59
SVIL	NM_021738	38	50	37	164	124	152	-0.763260478	0.01022	0.59
TUBB2B	NM_178012	159	182	175	501	530	602	-0.754837792	0.00018	0.59
ANO1	NM_018043	130	84	102	397	297	372	-0.748731647	0.00513	0.60
RALBP1	NM_006788	93	66	54	325	282	173	-0.747429956	0.02179	0.60
KIAA1211	NM_020722	71	46	65	203	183	233	-0.741523585	0.00922	0.60
STAT2	NM_005419	44	43	46	154	153	143	-0.734565468	0.0123	0.60
SLC16A14	NM_152527	29	21	18	85	73	100	-0.725621586	0.03684	0.60

POU3F4	NM_000307	30	15	18	96	58	98	-0.717383051	0.0489	0.61
NREP	NM_001142476	92	132	117	323	360	381	-0.716553226	0.00279	0.61
NPHP3	NM_153240	18	25	18	76	59	95	-0.711471163	0.0462	0.61
CLEC2B	NM_005127	22	26	29	93	78	101	-0.707206834	0.03623	0.61
ZNF362	NM_152493	123	109	131	400	423	321	-0.704944667	0.00863	0.61
STK32B	NM_018401	36	67	48	136	174	188	-0.69781426	0.02331	0.62
ASNS	NM_001673	332	193	234	828	730	863	-0.686600008	0.01195	0.62
SORT1	NM_002959	62	70	61	171	217	223	-0.684436521	0.01581	0.62
RNF144A	NM_014746	53	53	38	188	147	141	-0.683267919	0.03214	0.62
SPON2	NM_012445	64	66	80	212	206	233	-0.680478974	0.01111	0.62
C1QTNF6	NM_031910	37	60	48	154	122	193	-0.674123552	0.02843	0.63
SLC36A1	NM_078483	140	70	93	441	339	247	-0.672511057	0.0489	0.63
MXD4	NM_006454	53	54	67	206	152	189	-0.670966936	0.02052	0.63
ZEB2	NM_014795	66	73	70	245	218	187	-0.669651874	0.01985	0.63
CADM1	NM_014333	241	379	433	1105	848	1154	-0.660432033	0.00487	0.63
CRISPLD1	NM_031461	53	64	84	208	178	231	-0.658411235	0.01926	0.63
DNASE2	NM_001375	140	162	210	494	484	525	-0.657765228	0.00423	0.63
FAM129A	NM_052966	150	164	187	446	451	572	-0.652533885	0.00332	0.64
DYNC2H1	NM_001080463	53	73	53	169	162	223	-0.647298727	0.02812	0.64
TNFRSF21	NM_014452	176	239	265	669	554	742	-0.641639622	0.00345	0.64
ACP6	NM_016361	126	111	127	324	344	406	-0.638175786	0.0106	0.64
PEAK1	NM_024776	114	116	87	308	303	335	-0.636112139	0.01664	0.64
SPRED2	NM_181784	178	195	189	586	500	534	-0.63582467	0.00454	0.64
CLIP3	NM_015526	110	120	106	365	294	330	-0.635611855	0.012	0.64
TIPARP	NM_001184718	140	181	175	532	524	387	-0.627106864	0.02082	0.65
IL13RA1	NM_001560	80	81	75	243	211	245	-0.626165986	0.02102	0.65
TUBA1A	NM_006009	2721	2898	3917	8375	8006	10082	-0.606568814	0.00203	0.66
EMP1	NM_001423	2930	2995	3802	9099	8541	9138	-0.605105324	0.0011	0.66
TNPO2	NM_001136196	561	504	646	1651	1493	1592	-0.595544086	0.00465	0.66
LDB1	NM_001113407	153	175	235	579	494	504	-0.594497906	0.01803	0.66
TPRG1L	NM_182752	163	164	173	439	439	505	-0.580204894	0.012	0.67
ATP2A2	NM_170665	969	702	630	2482	2057	2067	-0.579971735	0.04033	0.67
SNIP1	NM_024700	115	152	171	418	337	457	-0.573558556	0.02179	0.67
ZC3H7A	NM_014153	126	134	111	333	319	376	-0.563059664	0.03097	0.68
ADAM19	NM_033274	1784	1300	1782	5027	4108	4261	-0.56274257	0.02331	0.68
PPP1R15A	NM_014330	161	168	275	503	504	657	-0.555416743	0.04623	0.68
HMOX1	NM_002133	130	124	185	404	373	423	-0.553921086	0.03725	0.68
USP10	NM_005153	202	226	229	516	534	709	-0.538471518	0.02136	0.69
SLC7A11	NM_014331	393	398	396	1091	964	1072	-0.533071771	0.012	0.69
ITPRIPL2	NM_001034841	173	220	209	479	511	606	-0.532870193	0.02331	0.69
SSH1	NM_018984	284	438	308	775	852	1129	-0.526420087	0.04824	0.69
TM9SF2	NM_004800	351	317	358	932	824	945	-0.524894517	0.01908	0.70
CABIN1	NM_012295	161	167	162	398	362	561	-0.524056877	0.04917	0.70

HN1	NM_001002032	626	646	844	1948	1665	1859	-0.514815951	0.01848	0.70
TRIB2	NM_021643	602	817	986	2140	1862	2208	-0.514649284	0.02277	0.70
ALDH1L2	NM_001034173	191	218	194	509	440	637	-0.508642072	0.04123	0.70
CASP4	NM_001225	381	439	371	991	899	1203	-0.506073362	0.02231	0.70
CCND1	NM_053056	4420	7771	7765	16341	15019	20145	-0.503145861	0.04824	0.71
TCAF1	NM_014719	218	233	216	536	537	657	-0.500756504	0.03637	0.71
FAM134A	NM_024293	201	202	219	538	464	597	-0.489566782	0.04377	0.71
CALM2	NM_001743	1353	1562	1776	3913	3374	4162	-0.448482011	0.02331	0.73
C11orf84	NM_138471	548	592	680	1450	1252	1754	-0.438357954	0.04958	0.74
PSAT1	NM_058179	1133	1189	1153	2968	2443	3015	-0.429791634	0.04472	0.74
HSPA5	NM_005347	2908	3734	3341	4336	3703	4702	0.4104203	0.0489	1.33
CYCS	NM_018947	1672	2209	1892	2249	2258	2623	0.447451367	0.03328	1.36
MBOAT7	NM_024298	772	891	1128	1106	1066	1234	0.452167691	0.0489	1.37
PSMB2	NM_002794	3940	5518	5562	5833	5345	7261	0.453502808	0.03515	1.37
ATP5L	NM_006476	3014	3658	3531	4077	3821	4729	0.454490803	0.01502	1.37
RBX1	NM_014248	1200	1335	1485	1612	1594	1712	0.458966205	0.02216	1.37
ARL4C	NM_005737	458	519	496	522	591	658	0.47483912	0.04033	1.39
HIST1H2AJ	NM_021066	1420	2169	1818	1947	1923	2617	0.475481249	0.04458	1.39
DNER	NM_139072	392	514	496	573	498	613	0.476009276	0.03386	1.39
SNRPA1	NM_003090	923	1159	1256	1313	1246	1429	0.486879645	0.01581	1.40
TMBIM6	NM_001098576	1745	1367	1824	2133	1669	2077	0.487738201	0.04929	1.40
INSIG1	NM_005542	976	1298	1145	1185	1389	1465	0.492884012	0.02537	1.41
GNG5	NM_005274	880	1127	1226	1219	1089	1538	0.494379271	0.02082	1.41
DSN1	NM_024918	356	321	455	452	396	476	0.498561382	0.04946	1.41
ATP6AP2	NM_005765	207	244	259	270	264	295	0.498671749	0.04562	1.41
SEC62	NM_003262	726	1142	1195	1199	1051	1317	0.499327596	0.03725	1.41
MRPL32	NM_031903	717	835	880	1033	828	1024	0.499351722	0.01522	1.41
RFC4	NM_002916	306	364	362	386	392	426	0.508168526	0.02368	1.42
TLN2	NM_015059	289	295	422	374	346	441	0.51000441	0.04859	1.42
PCIF1	NM_022104	234	298	327	320	262	411	0.512532491	0.04859	1.43
AP3D1	NM_003938	480	623	582	661	563	743	0.517956357	0.01458	1.43
DUSP12	NM_007240	222	368	328	339	299	406	0.519987831	0.04928	1.43
PPP6R1	NM_014931	628	918	872	948	816	1029	0.523087116	0.01529	1.44
TYMS	NM_001071	1699	2047	2257	2254	2196	2546	0.524836792	0.0047	1.44
DUSP7	NM_001947	604	1075	903	835	948	1120	0.529756695	0.04115	1.44
POMK	NM_032237	245	259	222	276	256	296	0.53044301	0.03637	1.44
TMEM55A	NM_018710	159	213	198	213	196	235	0.531314181	0.04033	1.45
DHX34	NM_014681	221	272	319	341	268	306	0.531799877	0.03725	1.45
DLC1	NM_182643	354	370	359	412	397	435	0.532035324	0.01748	1.45
WSB2	NM_018639	600	958	941	916	848	1073	0.533530455	0.02082	1.45
ANKRD13A	NM_033121	418	459	446	519	473	529	0.53493096	0.012	1.45
TMX1	NM_030755	626	815	761	827	851	826	0.538116865	0.01198	1.45
CCSAP	NM_145257	180	230	272	268	247	241	0.538545359	0.04472	1.45
MYL12B	NM_033546	1281	1788	1578	1613	1819	1842	0.541678845	0.01075	1.46

MSANTD3	NM_001198805	385	386	429	463	428	476	0.543839018	0.01222	1.46
DCTD	NM_001012732	511	808	761	737	736	868	0.543921435	0.01694	1.46
LGR4	NM_018490	164	213	159	204	167	225	0.545832533	0.0489	1.46
DUSP1	NM_004417	397	568	494	564	485	592	0.554137571	0.01195	1.47
RBM8A	NM_005105	1867	1623	1640	1771	1922	2124	0.556055474	0.01195	1.47
SAPCD2	NM_178448	115	178	151	155	148	178	0.561385337	0.04754	1.48
GALNT1	NM_020474	186	254	249	236	224	302	0.562617356	0.02216	1.48
TTL	NM_153712	234	316	275	284	308	313	0.569035904	0.01773	1.48
MRPL51	NM_016497	573	619	546	621	668	637	0.571007903	0.01075	1.49
DONSON	NM_017613	111	137	108	119	115	147	0.574384579	0.04958	1.49
NKD1	NM_033119	517	875	836	780	620	1026	0.575009236	0.02331	1.49
TWF1	NM_001242397	261	500	321	377	340	438	0.576655711	0.04033	1.49
SEMA3C	NM_006379	186	165	177	199	162	212	0.581777505	0.02683	1.50
CDK2AP2	NM_005851	2312	2707	2934	3433	2261	3084	0.584171958	0.0059	1.50
DNM1	NM_004408	133	154	199	185	163	166	0.584518663	0.03511	1.50
DNAJB6	NM_058246	1498	1493	1697	2157	1313	1623	0.586350956	0.01581	1.50
TFPI2	NM_006528	271	511	342	361	352	480	0.587153696	0.03357	1.50
PCGF3	NM_006315	158	219	229	185	225	234	0.588380739	0.02368	1.50
BAG4	NM_004874	262	581	397	375	402	508	0.592694031	0.04472	1.51
CCDC50	NM_178335	300	454	325	388	349	424	0.594424779	0.01433	1.51
TSPAN13	NM_014399	246	341	291	294	268	388	0.596271348	0.012	1.51
FSTL3	NM_005860	143	115	190	144	156	164	0.597507111	0.04472	1.51
NAA30	NM_001011713	182	256	172	214	206	223	0.598874659	0.02527	1.51
GREM1	NM_013372	465	1047	794	753	748	880	0.602190219	0.03038	1.52
BNC1	NM_001717	129	175	157	145	165	171	0.607949562	0.02182	1.52
NXPE3	NM_145037	139	294	204	187	184	274	0.612911764	0.0447	1.53
CD68	NM_001251	791	979	844	1026	796	1007	0.615873619	0.00194	1.53
HIST1H3J	NM_003535	101	109	164	124	107	149	0.617170601	0.03725	1.53
MAPKAPK2	NM_032960	282	319	279	302	279	360	0.620473654	0.0052	1.54
CPOX	NM_000097	90	95	79	83	73	110	0.621418323	0.04822	1.54
NUP50	NM_007172	759	1259	943	958	901	1274	0.621540282	0.00741	1.54
AREL1	NM_001039479	423	485	618	530	546	529	0.622791718	0.00498	1.54
FLNC	NM_001458	2402	3143	3685	3246	2893	3762	0.623212811	0.0011	1.54
LOXL1	NM_005576	153	132	175	193	119	156	0.623677512	0.0326	1.54
EIF4EBP2	NM_004096	269	519	355	395	369	392	0.635385931	0.01604	1.55
INPP5A	NM_005539	91	182	143	107	146	149	0.639493528	0.04025	1.56
PLOD2	NM_182943	604	1017	572	640	675	911	0.64303359	0.01604	1.56
HAS2	NM_005328	666	888	762	726	769	948	0.645140892	0.00105	1.56
SIRPA	NM_080792	105	163	109	134	106	133	0.645655298	0.02537	1.56
HDAC4	NM_006037	145	176	176	182	145	180	0.65012615	0.00903	1.57
AGPAT9	NM_032717	91	171	149	128	132	141	0.650371156	0.02331	1.57
TENM2	NM_001122679	466	836	575	539	556	809	0.650909561	0.01146	1.57
RASA4	NM_006989	530	539	719	590	571	707	0.651473937	0.00149	1.57

VASN	NM_138440	160	217	269	226	205	217	0.652644162	0.0106	1.57
SSX2IP	NM_001166293	150	178	125	131	134	189	0.652723324	0.01958	1.57
IMPAD1	NM_017813	520	1193	826	816	798	861	0.662947581	0.01462	1.58
ABCB10	NM_012089	62	124	94	84	87	90	0.665497724	0.0355	1.59
WWC1	NM_001161661	215	279	337	269	259	312	0.667794255	0.00345	1.59
PALLD	NM_001166108	71	102	106	85	76	106	0.673309022	0.02147	1.59
AKIRIN1	NM_024595	315	600	443	409	352	577	0.677205342	0.01021	1.60
BACE1	NM_012104	323	543	612	429	462	561	0.681458429	0.00528	1.60
MTSS1L	NM_138383	296	470	422	385	383	418	0.684297401	0.00193	1.61
DCUN1D5	NM_032299	457	629	433	507	511	484	0.689987729	0.00306	1.61
PDGFA	NM_002607	1707	3950	2853	2510	2635	2994	0.691013583	0.0088	1.61
PCDHGC5	NM_018929	103	139	159	124	108	155	0.691220898	0.01021	1.61
WDR62	NM_001083961	191	182	213	203	158	220	0.694886767	0.00345	1.62
ADAMTS14	NM_139155	67	68	56	67	55	45	0.697560707	0.03725	1.62
TMEM64	NM_001008495	96	164	96	101	102	126	0.701193319	0.01803	1.63
TNFRSF19	NM_018647	215	345	241	202	250	318	0.701728881	0.00729	1.63
FBN1	NM_000138	1839	2689	2103	2352	2111	2139	0.703160267	0.00035	1.63
SETD7	NM_030648	227	358	251	259	255	295	0.710619456	0.00302	1.64
PDHX	NM_003477	201	171	186	173	156	210	0.722304201	0.0031	1.65
PLAGL1	NM_001080954	70	122	96	67	91	97	0.726856732	0.01581	1.66
ZC3HAV1L	NM_080660	62	124	64	60	74	77	0.727565965	0.02542	1.66
VPS33A	NM_022916	99	89	91	71	87	96	0.728302176	0.012	1.66
LFNG	NM_001040167	93	101	84	110	53	81	0.730269349	0.01958	1.66
COL8A1	NM_020351	369	365	511	405	391	404	0.731356882	0.00058	1.66
SUV39H1	NM_003173	112	138	154	127	114	137	0.736143382	0.00332	1.67
RAB3B	NM_002867	123	239	155	154	123	192	0.737955576	0.00903	1.67
CACNA2D3	NM_018398	98	99	109	98	90	91	0.739730974	0.00672	1.67
NBN	NM_002485	264	438	344	249	326	399	0.74289834	0.00279	1.67
TWIST1	NM_000474	898	1216	1080	1043	900	1189	0.747560647	1.47E-05	1.68
LCLAT1	NM_001002257	204	371	235	238	190	305	0.764284717	0.00345	1.70
EIF5A2	NM_020390	87	151	127	88	118	106	0.778548471	0.00549	1.72
LAYN	NM_178834	106	141	138	101	121	119	0.78136486	0.00228	1.72
CA13	NM_198584	33	60	58	34	36	45	0.792519686	0.01587	1.73
INIP	NM_021218	206	216	207	201	179	196	0.792786456	0.00024	1.73
IGIP	NM_001007189	41	50	44	29	29	45	0.795114107	0.01604	1.74
RLTPR	NM_001013838	70	84	72	80	51	51	0.799627889	0.00937	1.74
IRS1	NM_005544	308	460	392	366	303	394	0.803345441	6.00E-05	1.75
CACNA2D1	NM_000722	144	185	164	148	125	168	0.807545325	0.00038	1.75
KLF16	NM_031918	67	64	80	62	56	53	0.809029848	0.0065	1.75
ALCAM	NM_001627	1013	1302	1050	979	887	1222	0.831786863	2.17E-06	1.78
ELL2	NM_012081	178	239	240	167	168	241	0.837600357	0.00014	1.79

SDC4	NM_002999	281	502	390	293	321	384	0.860609114	8.84E-05	1.82
FGF2	NM_002006	115	131	144	125	92	94	0.893108889	0.00029	1.86
GREM2	NM_022469	60	91	102	59	62	68	0.90667285	0.00094	1.87
GNPNAT1	NM_198066	769	1398	1000	785	789	1037	0.913639509	8.59E-06	1.88
PMAIP1	NM_021127	115	182	166	105	119	139	0.927163397	7.58E-05	1.90
ARSJ	NM_024590	103	94	84	82	64	62	0.928542513	0.00058	1.90
ENPP1	NM_006208	172	358	200	176	159	214	0.940787974	0.00019	1.92
NIPA1	NM_144599	146	172	183	118	123	153	0.95941304	6.55E-06	1.94
EFHD2	NM_024329	1688	1937	2594	1917	1343	1724	0.970830704	2.19E-07	1.96
GADD45A	NM_001924	149	258	288	186	158	157	1.00213665	1.47E-05	2.00
UBE2V2	NM_003350	1426	2111	1458	1247	1238	1418	1.009614125	4.72E-08	2.01
TMTC3	NM_181783	215	208	207	169	136	170	1.02660053	3.81E-07	2.04
CAV2	NM_001233	800	1400	992	746	747	920	1.027547381	1.50E-07	2.04
SLC9A6	NM_001042537	159	213	242	126	130	179	1.075579012	2.76E-07	2.11
MMP1	NM_002421	1231	1928	1938	939	903	1723	1.09564922	2.19E-07	2.14
TAF9B	NM_015975	403	523	388	292	280	370	1.112067054	4.00E-09	2.16
TULP3	NM_001160408	514	683	569	411	420	440	1.121466442	1.06E-10	2.18
FAM46A	NM_017633	131	243	149	89	104	113	1.210305447	2.19E-07	2.31

Table S4. The list of genes with number of reads in a given biological replicate (I, II, III) for cells treated with lipofectamine with control siRNA (siNEG) and lipofectamine with anti-Prox siRNA (siProx). The fold change (FC) and adj. P. values (p.adj) are provided

Gene	refSeq	siNEG I	siNEG II	siNEG III	siProx_sig I	siProx_sig II	siProx_sig III	log2FoldChange	p.adj	FC
PROX1	NM_002763	62	58	103	9	3	3	-1.94842698	3.30E-09	0.26
BCHE	NM_000055	56	27	41	7	1	5	-1.356975	0.00023	0.39
RASSF2	NM_170774	127	100	126	37	5	27	-1.309931997	1.66E-05	0.40
SOX2	NM_003106	53	58	48	10	7	7	-1.279746525	0.00028	0.41
MXRA5	NM_015419	59	63	81	17	6	13	-1.262999511	0.00015	0.42
FTH1	NM_002032	13694	12408	16689	4735	2522	3501	-1.201940321	2.09E-19	0.43
PNMA2	NM_007257	78	95	91	27	12	18	-1.155317074	0.00022	0.45
FBXO32	NM_058229	80	74	59	30	6	7	-1.152255526	0.00099	0.45
AHRR	NM_001242412	344	330	377	102	66	91	-1.14874647	3.38E-08	0.45
LZTS1	NM_021020	155	106	142	43	22	28	-1.146113924	3.62E-05	0.45
ITGA11	NM_001004439	547	517	535	229	84	112	-1.133746031	1.20E-08	0.46
GPR27	NM_018971	61	44	39	12	7	6	-1.128923066	0.00202	0.46
CEMIP	NM_018689	65	70	94	26	11	12	-1.122742787	0.00057	0.46
PEG10	NM_001172438	2026	1959	2502	889	389	491	-1.112049717	6.16E-13	0.46
SAMD9	NM_001193307	113	111	121	44	17	25	-1.070602811	0.00019	0.48
TESK1	NM_006285	94	47	63	20	10	13	-1.065095072	0.0022	0.48
MBD6	NM_052897	119	100	113	55	14	12	-1.064743602	0.001	0.48
FAM167A	NM_053279	243	271	247	79	49	70	-1.061523987	6.00E-06	0.48
ZNF213	NM_004220	41	53	72	20	4	11	-1.048351057	0.00371	0.48
GRIN2A	NM_001134407	59	49	61	17	9	10	-1.047367797	0.00272	0.48
EBF1	NM_024007	68	67	55	20	10	12	-1.045952801	0.00235	0.48
IGFBP7	NM_001553	75	96	57	33	6	14	-1.04446737	0.00289	0.48
CHST15	NM_015892	56	55	49	21	8	4	-1.042551342	0.0045	0.49

FXYD6	NM_001164836	735	837	985	363	168	194	-1.032197849	1.78E-08	0.49
C1R	NM_001733	108	100	137	61	9	20	-1.016790685	0.0017	0.49
PHACTR2	NM_001100164	213	250	322	93	38	84	-1.011755299	2.79E-05	0.50
ICA1	NM_022307	71	67	69	23	13	13	-1.002394661	0.0027	0.50
FBXW7	NM_033632	152	138	245	63	26	53	-1.000609293	0.00023	0.50
PLSCR4	NM_020353	132	111	157	46	26	33	-0.998122633	0.00028	0.50
ADAMTS3	NM_014243	31	42	33	13	3	4	-0.99073792	0.01073	0.50
DCLK1	NM_004734	49	43	37	11	2	13	-0.988289339	0.00961	0.50
PRSS23	NM_007173	504	454	537	206	117	100	-0.986817172	2.87E-06	0.50
ZNF709	NM_152601	55	54	51	28	4	2	-0.986270618	0.01057	0.50
NR3C2	NM_000901	42	37	57	15	5	9	-0.985328139	0.00804	0.51
KLF9	NM_001206	149	157	183	55	31	47	-0.982315438	0.00014	0.51
TP53I11	NM_006034	65	61	64	29	9	8	-0.976174924	0.00576	0.51
AFF3	NM_001025108	76	62	59	30	9	9	-0.975726766	0.00576	0.51
ADAM12	NM_003474	125	101	112	47	20	26	-0.9503423	0.00114	0.52
AHR	NM_001621	259	253	386	113	53	93	-0.950044281	3.04E-05	0.52
SERTAD2	NM_014755	143	199	215	89	29	44	-0.943255221	0.00047	0.52
ZFP36	NM_003407	173	194	188	55	40	59	-0.934992749	0.00038	0.52
VGLL3	NM_016206	192	171	149	104	17	30	-0.932341349	0.00366	0.52
DOCK11	NM_144658	367	233	347	169	52	64	-0.931164215	0.00032	0.52
ZNF627	NM_145295	151	169	95	78	18	22	-0.924882503	0.00606	0.53
SLC1A4	NM_003038	656	604	750	293	125	209	-0.91529234	1.35E-07	0.53
CDYL2	NM_152342	61	64	83	32	4	19	-0.915137485	0.00988	0.53
SLC38A1	NM_001077484	291	257	301	129	48	84	-0.912771813	3.31E-05	0.53
BOC	NM_033254	36	35	45	16	4	6	-0.911294588	0.01867	0.53
TIMP3	NM_000362	14279	12017	17623	5796	3270	4409	-0.907127547	1.91E-09	0.53
SNED1	NM_001080437	159	145	204	74	35	41	-0.899867175	0.00049	0.54
SDC2	NM_002998	215	235	239	74	59	65	-0.898029189	0.00032	0.54
REPIN1	NM_001099695	80	54	53	27	11	10	-0.897277998	0.01284	0.54
ZBED4	NM_014838	149	130	199	78	26	39	-0.895063382	0.00101	0.54
EGR1	NM_001964	83	80	72	31	18	14	-0.893824626	0.00752	0.54
RSBN1	NM_018364	183	148	179	84	21	52	-0.884013249	0.00117	0.54
PCK2	NM_004563	218	225	257	88	59	62	-0.879072801	0.00023	0.54
CHST1	NM_003654	160	121	179	69	34	33	-0.878876404	0.00137	0.54
RAPH1	NM_213589	139	153	183	71	17	56	-0.878475015	0.00213	0.54
CELSR3	NM_001407	194	152	184	82	36	44	-0.873539768	0.00067	0.55
SPTBN2	NM_006946	141	128	158	65	31	32	-0.870981401	0.00146	0.55
PIK3C2A	NM_002645	111	94	146	58	23	22	-0.86745071	0.00448	0.55
TFG	NM_001195478	282	266	368	177	61	47	-0.865904245	0.00197	0.55
ZNF71	NM_021216	45	36	20	10	5	6	-0.86589755	0.0318	0.55
LCA5	NM_001122769	149	128	188	61	32	46	-0.86507229	0.00107	0.55
FAM155A	NM_001080396	197	144	184	87	31	45	-0.864303014	0.00105	0.55
TCTN2	NM_024809	66	64	77	27	16	13	-0.863273734	0.01154	0.55
BCL6	NM_001706	106	49	113	47	8	20	-0.863039932	0.01591	0.55
PLK2	NM_006622	98	101	128	49	23	24	-0.86284093	0.00392	0.55
MESDC1	NM_022566	28	32	62	8	6	12	-0.858588954	0.03053	0.55

PCDH18	NM_019035	318	322	340	198	53	70	-0.856515744	0.00091	0.55
SCD5	NM_001037582	122	123	162	64	20	41	-0.855342394	0.00238	0.55
H6PD	NM_004285	110	124	149	56	23	37	-0.854479675	0.00246	0.55
ICK	NM_014920	170	211	234	82	39	69	-0.853234499	0.00066	0.55
MYO6	NM_004999	64	79	105	41	11	20	-0.849309417	0.01159	0.56
ZBED3	NM_032367	30	29	41	12	6	4	-0.8492693	0.03425	0.56
GATA3	NM_001002295	165	152	186	65	35	54	-0.848855542	0.00088	0.56
EFHD1	NM_025202	37	29	30	9	5	7	-0.847286217	0.03486	0.56
ARRDC3	NM_020801	104	115	132	58	13	37	-0.846208618	0.00566	0.56
NPTX1	NM_002522	88	84	98	32	28	12	-0.843621614	0.01379	0.56
CALD1	NM_033138	1080	914	1101	455	192	373	-0.842073076	1.73E-06	0.56
APOL6	NM_030641	38	25	33	8	4	9	-0.834241303	0.039	0.56
DPP8	NM_130434	187	206	188	108	42	34	-0.83236461	0.00367	0.56
RCOR2	NM_173587	137	148	154	66	34	36	-0.831796736	0.00229	0.56
ULK1	NM_003565	232	205	264	114	52	59	-0.829366913	0.00045	0.56
SKI	NM_003036	896	920	877	502	209	178	-0.82870438	0.0004	0.56
KLHL24	NM_017644	60	64	62	19	8	24	-0.825507501	0.02198	0.56
PBXIP1	NM_020524	131	112	137	64	20	36	-0.824950487	0.00411	0.56
LHFP	NM_005780	191	168	224	102	25	63	-0.824593509	0.00204	0.56
CREBRF	NM_153607	234	221	288	113	53	74	-0.822057071	0.00028	0.57
POSTN	NM_006475	50	41	53	13	8	16	-0.820651548	0.02994	0.57
ZBTB10	NM_001105539	75	45	99	26	15	19	-0.820596197	0.01944	0.57
PIK3R2	NM_005027	554	698	612	372	108	160	-0.818330389	0.00055	0.57
GSTM2	NM_001142368	201	137	200	88	31	54	-0.816359015	0.00206	0.57
NTF3	NM_001102654	100	118	126	52	23	32	-0.812453442	0.00576	0.57
TFAP2C	NM_003222	690	807	989	410	200	217	-0.805896418	4.38E-05	0.57
STOX2	NM_020225	37	30	31	7	7	8	-0.804165051	0.04721	0.57
TXNIP	NM_006472	593	406	478	201	121	156	-0.803027687	0.00022	0.57
TMEM131	NM_015348	221	188	194	140	24	39	-0.800324365	0.01248	0.57
KLF7	NM_003709	218	223	212	140	31	51	-0.798519684	0.00568	0.57
RAB3D	NM_004283	248	253	236	107	55	80	-0.796140875	0.00068	0.58
PTEN	NM_000314	33	43	42	16	4	11	-0.7934996	0.04507	0.58
AKAP13	NM_006738	109	69	88	42	10	30	-0.793047632	0.01883	0.58
OLFM2	NM_058164	140	120	134	47	39	33	-0.791359751	0.00742	0.58
SLC7A8	NM_012244	87	65	98	41	19	15	-0.790168998	0.01908	0.58
FAM160B1	NM_020940	93	108	159	47	22	42	-0.790159854	0.00937	0.58
TRIQK	NM_001171799	143	127	137	63	25	44	-0.788649173	0.00457	0.58
ST6GAL2	NM_032528	260	196	281	88	64	81	-0.78435973	0.00147	0.58
ODF2L	NM_001007022	96	113	112	47	17	38	-0.783965445	0.01053	0.58
SLC1A1	NM_004170	83	101	97	38	23	25	-0.7826926	0.01354	0.58
TCF20	NM_005650	97	71	84	37	19	21	-0.779789565	0.01742	0.58
FOSL1	NM_005438	6092	4516	6229	2639	1383	1717	-0.778572314	1.01E-06	0.58
LMO4	NM_006769	171	202	109	113	16	32	-0.778445245	0.03072	0.58
KIAA1549	NM_001164665	86	88	114	52	16	24	-0.777641665	0.01482	0.58
DDX52	NM_007010	461	341	435	275	69	90	-0.774483034	0.00432	0.58
ROCK1	NM_005406	616	629	882	394	105	248	-0.774345099	0.00066	0.58

CELSR1	NM_014246	192	153	220	77	41	66	-0.772646685	0.00235	0.59
PRDM8	NM_001099403	52	66	63	26	7	21	-0.770732687	0.03538	0.59
PTGER2	NM_000956	79	99	79	31	23	23	-0.770148052	0.02129	0.59
RPS6KA2	NM_001006932	201	218	238	102	40	80	-0.768800642	0.0016	0.59
IRS2	NM_003749	212	281	298	129	61	76	-0.768252156	0.00142	0.59
VLDLR	NM_003383	130	107	139	51	19	51	-0.767208203	0.01021	0.59
BRWD3	NM_153252	118	101	107	63	14	31	-0.76705928	0.01591	0.59
ZMAT3	NM_022470	163	129	196	59	31	66	-0.76490315	0.00653	0.59
SHROOM3	NM_020859	77	73	90	32	21	20	-0.761048554	0.02145	0.59
PYGO1	NM_015617	199	153	181	79	31	68	-0.760837457	0.00434	0.59
PKN3	NM_013355	79	60	52	37	7	15	-0.75929963	0.04322	0.59
PLXND1	NM_015103	91	96	125	45	20	35	-0.757674525	0.01296	0.59
RASSF3	NM_178169	68	77	85	41	16	15	-0.757636463	0.02783	0.59
MYEF2	NM_016132	48	46	63	22	8	16	-0.755544698	0.04276	0.59
BTBD3	NM_014962	290	268	343	123	88	84	-0.755346346	0.00125	0.59
DCHS1	NM_003737	418	373	554	216	107	138	-0.753643571	0.00021	0.59
LTBP1	NM_206943	104	99	129	52	19	38	-0.751008338	0.01215	0.59
UHRF1BP1	NM_017754	60	84	80	46	8	18	-0.748964727	0.04051	0.60
KCNF1	NM_002236	67	54	70	18	16	21	-0.74880524	0.03793	0.60
PIM1	NM_002648	354	372	405	120	117	121	-0.744376241	0.00333	0.60
RAB30	NM_014488	81	97	93	45	14	30	-0.740489316	0.02295	0.60
RAB6B	NM_016577	133	131	184	55	42	46	-0.740212028	0.00903	0.60
DAAM2	NM_001201427	98	73	100	31	22	31	-0.738861421	0.02296	0.60
SOGA1	NM_080627	377	342	419	197	90	113	-0.738111986	0.00032	0.60
ZNRF3	NM_001206998	206	130	164	95	39	34	-0.737960144	0.01422	0.60
MN1	NM_002430	162	195	143	70	32	66	-0.734650662	0.01112	0.60
COL6A3	NM_004369	186	183	238	94	45	69	-0.731844845	0.00272	0.60
RECQL	NM_032941	387	291	385	244	64	75	-0.731155163	0.00903	0.60
SIX1	NM_005982	204	180	215	101	38	70	-0.730812942	0.00315	0.60
PAG1	NM_018440	171	170	241	95	46	58	-0.726361862	0.00434	0.60
C14orf93	NM_001130708	72	78	76	37	17	19	-0.721351482	0.03453	0.61
RCAN3	NM_013441	389	365	451	199	101	126	-0.720084689	0.00032	0.61
PPP1R13L	NM_006663	72	59	82	25	18	23	-0.711406346	0.04115	0.61
CLIC4	NM_013943	5948	5813	6713	3569	1354	1986	-0.711203772	7.72E-06	0.61
ATRX	NM_000489	781	766	963	481	158	294	-0.707689189	0.00026	0.61
PLEC	NM_201380	2512	2379	2616	1364	656	715	-0.707497666	4.78E-05	0.61
CHAC1	NM_024111	343	275	325	159	94	72	-0.706379641	0.00539	0.61
CYTL1	NM_018659	98	143	149	55	33	42	-0.704683266	0.0191	0.61
COL18A1	NM_030582	121	123	146	60	32	41	-0.704050007	0.01272	0.61
DAB2IP	NM_032552	499	516	644	303	124	180	-0.703041041	0.00027	0.61
SLC48A1	NM_017842	103	104	119	66	18	30	-0.702345542	0.02561	0.61
LTN1	NM_015565	337	311	377	175	66	131	-0.701947612	0.00117	0.61
KIAA1522	NM_020888	174	148	188	87	43	48	-0.700460545	0.00779	0.62
IFNGR2	NM_005534	181	192	244	138	34	53	-0.699924224	0.01492	0.62
MAST4	NM_001164664	88	73	102	37	16	34	-0.698475425	0.03373	0.62
SLC23A2	NM_203327	262	247	274	166	38	87	-0.696578514	0.00889	0.62

ME1	NM_002395	439	441	573	235	99	193	-0.695107409	0.00067	0.62
NUAK1	NM_014840	345	359	427	224	85	107	-0.694360385	0.00182	0.62
HGSNAT	NM_152419	162	194	234	83	38	84	-0.694148697	0.01047	0.62
GNG2	NM_053064	664	566	674	282	148	255	-0.69245161	0.00033	0.62
CD109	NM_133493	1100	1111	1256	654	182	473	-0.690702995	0.00187	0.62
TTBK2	NM_173500	91	87	114	58	13	31	-0.690370422	0.03671	0.62
RERE	NM_001042681	151	142	134	78	33	40	-0.690266115	0.01583	0.62
MSC	NM_005098	210	219	297	149	45	73	-0.685040078	0.0081	0.62
SETBP1	NM_015559	110	110	127	52	29	38	-0.684652872	0.02007	0.62
PROSER1	NM_025138	246	207	305	151	46	82	-0.683715121	0.00651	0.62
DPF3	NM_012074	127	129	123	74	27	34	-0.683363849	0.02261	0.62
TRIOBP	NM_001039141	388	421	525	262	89	148	-0.682085259	0.0016	0.62
SOX9	NM_000346	384	324	466	236	77	125	-0.681880537	0.00245	0.62
TMEM65	NM_194291	320	295	345	188	73	95	-0.679451994	0.00246	0.62
HAGH	NM_005326	81	70	88	31	22	25	-0.677990066	0.04439	0.63
PPAP2B	NM_003713	523	501	621	320	106	196	-0.677096914	0.00087	0.63
COL4A1	NM_001845	291	296	289	197	47	90	-0.674339349	0.01195	0.63
TTC28	NM_001145418	231	213	294	127	53	89	-0.673021959	0.00425	0.63
PREX1	NM_020820	148	184	185	111	26	55	-0.672758875	0.02282	0.63
SLC44A2	NM_020428	191	182	255	114	36	80	-0.671448962	0.01009	0.63
WIPI1	NM_017983	108	124	122	50	26	47	-0.669004512	0.02691	0.63
NACC2	NM_144653	114	104	129	35	39	37	-0.668951942	0.04056	0.63
NIN	NM_020921	242	218	344	134	55	103	-0.667661001	0.00605	0.63
THAP2	NM_031435	124	100	117	62	31	26	-0.665006032	0.03453	0.63
DAG1	NM_001177639	582	544	722	320	141	230	-0.664212613	0.00032	0.63
CCDC88C	NM_001080414	164	130	150	69	47	37	-0.663795879	0.02443	0.63
FBXL20	NM_032875	77	80	121	49	20	27	-0.662562467	0.04477	0.63
REST	NM_001193508	874	901	1260	541	214	389	-0.661811347	0.00047	0.63
RB1CC1	NM_014781	468	437	591	236	96	221	-0.661157277	0.00279	0.63
LRP1	NM_002332	429	320	401	235	82	119	-0.66069144	0.00402	0.63
ZFHX3	NM_006885	613	416	495	269	148	136	-0.660252016	0.00576	0.63
DYNC1H1	NM_001376	710	532	772	377	165	214	-0.658862635	0.00077	0.63
MANEAL	NM_001113482	101	86	127	66	21	25	-0.658641146	0.04462	0.63
GRB10	NM_005311	2688	2246	2655	1746	455	806	-0.658511287	0.00327	0.63
GAB1	NM_207123	96	98	124	42	26	41	-0.657051445	0.03549	0.63
C2orf69	NM_153689	147	143	151	90	25	49	-0.656439181	0.02341	0.63
GOLGB1	NM_004487	310	332	333	210	62	103	-0.656127257	0.00742	0.63
SPG20	NM_015087	246	213	181	149	29	68	-0.651953959	0.03666	0.64
MAML2	NM_032427	258	291	339	151	73	105	-0.651377404	0.00367	0.64
KLF2	NM_016270	133	121	159	52	48	38	-0.651239261	0.03511	0.64
POU2F1	NM_002697	173	147	222	114	29	60	-0.650939869	0.02276	0.64
PIEZO1	NM_001142864	577	545	722	341	165	185	-0.650918967	0.00093	0.64
ELF1	NM_172373	150	121	140	77	37	34	-0.648232049	0.02911	0.64
SYNE3	NM_152592	239	228	288	167	51	70	-0.647752211	0.01305	0.64
MPHOSPH8	NM_017520	162	157	145	112	26	38	-0.647188039	0.04338	0.64
CHSY1	NM_014918	364	405	281	269	54	91	-0.646135684	0.04089	0.64

SLC25A43	NM_145305	220	215	286	116	58	91	-0.644940645	0.00659	0.64
ETV1	NM_001163147	789	598	846	432	187	231	-0.64415407	0.00105	0.64
EIF4E3	NM_001134651	98	99	130	52	32	30	-0.642977686	0.04003	0.64
F3	NM_001993	280	307	387	153	70	139	-0.639053285	0.00624	0.64
PTP4A1	NM_003463	936	1007	945	697	174	291	-0.637582167	0.01046	0.64
RBBP6	NM_006910	105	128	146	68	24	47	-0.637533568	0.03419	0.64
CDKN1B	NM_004064	207	174	176	111	45	53	-0.636489581	0.0197	0.64
CAMTA2	NM_001171167	153	121	176	79	41	43	-0.635431516	0.02453	0.64
PRRC2C	NM_015172	1792	1721	2249	1166	375	735	-0.634397279	0.00088	0.64
CLIP1	NM_002956	231	182	238	115	43	87	-0.633447558	0.01209	0.64
CRAMP1L	NM_020825	146	106	124	72	26	41	-0.632130074	0.03738	0.65
WDR35	NM_001006657	139	136	210	85	29	65	-0.631728775	0.02839	0.65
ADCY9	NM_001116	124	115	137	68	25	46	-0.631546856	0.03128	0.65
RIN2	NM_001242581	132	86	124	63	22	40	-0.629762151	0.04515	0.65
FBLN1	NM_006486	318	253	269	139	71	105	-0.628592472	0.00772	0.65
ARHGAP5	NM_001030055	487	495	758	223	133	272	-0.627049442	0.01195	0.65
BLID	NM_001001786	117	117	158	87	22	39	-0.626658893	0.04531	0.65
UTRN	NM_007124	298	224	335	191	61	79	-0.626013191	0.01729	0.65
MED12	NM_005120	813	706	804	445	166	301	-0.625821386	0.0009	0.65
SMAD1	NM_005900	140	169	173	87	39	54	-0.624617903	0.02289	0.65
MAP4K4	NM_145686	588	536	776	334	187	191	-0.622043978	0.00281	0.65
AHNAK	NM_001620	849	760	746	504	197	226	-0.621568535	0.00458	0.65
HIPK3	NM_005734	221	264	354	170	53	101	-0.619758568	0.01656	0.65
COL6A1	NM_001848	7009	7044	7781	4620	1970	1980	-0.619512009	0.00205	0.65
ZNF827	NM_178835	206	287	435	175	75	96	-0.619112381	0.02445	0.65
CLDND1	NM_001040182	843	833	745	594	147	246	-0.618929133	0.01628	0.65
KLF4	NM_004235	135	124	113	62	30	45	-0.618533751	0.04013	0.65
RSF1	NM_016578	302	309	365	154	82	132	-0.618307659	0.00509	0.65
KIRREL	NM_018240	803	834	957	490	187	345	-0.618021486	0.00082	0.65
KMT2C	NM_170606	115	129	173	84	36	34	-0.617871267	0.04425	0.65
ABCC5	NM_005688	156	166	207	114	23	68	-0.616372176	0.04276	0.65
TMEM87B	NM_032824	164	188	150	105	36	52	-0.615750708	0.03556	0.65
SZT2	NM_015284	224	204	198	153	45	46	-0.615113866	0.04569	0.65
EPS8	NM_004447	167	145	209	84	50	57	-0.615096476	0.02201	0.65
CENPE	NM_001813	261	288	280	134	88	85	-0.613962345	0.01353	0.65
CCNG2	NM_004354	127	147	189	90	25	61	-0.61392389	0.03968	0.65
JMJD1C	NM_032776	292	288	303	173	58	115	-0.613651422	0.00921	0.65
FZD2	NM_001466	259	223	274	134	65	89	-0.613103129	0.00811	0.65
ELMSAN1	NM_001043318	209	175	189	91	50	73	-0.612512965	0.01843	0.65
SEPN1	NM_206926	726	638	934	430	224	220	-0.61230469	0.00367	0.65
DUSP4	NM_001394	189	173	241	108	46	75	-0.610655636	0.01577	0.65
UBN1	NM_001079514	202	252	239	157	47	69	-0.609857094	0.02783	0.66
NR3C1	NM_001018076	440	483	505	297	100	172	-0.609777537	0.00483	0.66
TAOK1	NM_020791	1177	1206	1932	757	335	570	-0.608718648	0.00246	0.66
FAM127B	NM_001078172	300	263	265	136	83	92	-0.608171523	0.01195	0.66
PPP1CC	NM_002710	3397	2682	2708	1996	662	912	-0.607380134	0.00533	0.66

IRF2BP2	NM_001077397	3133	3267	3532	1923	902	1096	-0.606593482	0.00023	0.66
LRFN4	NM_024036	276	207	314	159	48	104	-0.605791146	0.01838	0.66
FN1	NM_212482	4220	3589	5296	2185	1201	1642	-0.604570403	0.00022	0.66
TMEM132B	NM_052907	154	135	161	60	43	60	-0.604368773	0.03556	0.66
CREB3L2	NM_194071	1020	742	1064	475	281	317	-0.60170887	0.00231	0.66
TGIF2	NM_001199514	143	132	168	91	29	51	-0.600600729	0.03628	0.66
IGF2R	NM_000876	725	688	856	380	214	280	-0.600580088	0.00086	0.66
SEC11A	NM_014300	598	515	566	384	115	183	-0.599873655	0.00919	0.66
C9orf91	NM_153045	194	218	248	125	45	87	-0.599393345	0.01829	0.66
GBP5	NM_001134486	210	189	254	111	72	58	-0.59893121	0.027	0.66
PTPN13	NM_080685	300	317	365	199	76	113	-0.598383699	0.0077	0.66
ZNF217	NM_006526	197	179	235	130	42	68	-0.596314322	0.02352	0.66
PCDHB2	NM_018936	122	121	163	65	28	59	-0.594677464	0.04477	0.66
MAP1LC3A	NM_032514	187	146	147	73	53	49	-0.594402126	0.04584	0.66
SLC7A5	NM_003486	1925	1821	1991	898	615	656	-0.593206903	0.00205	0.66
TENM4	NM_001098816	165	122	170	86	27	63	-0.592341089	0.04281	0.66
SH3BGRL	NM_003022	606	616	784	355	172	260	-0.591290816	0.00135	0.66
PPDPF	NM_024299	3494	3504	4172	1876	1159	1253	-0.590042006	0.00082	0.66
ULBP1	NM_025218	153	153	193	70	54	58	-0.589723612	0.03759	0.66
GORASP2	NM_001201428	423	405	435	302	72	146	-0.589134658	0.02284	0.66
TMED5	NM_016040	477	544	493	315	142	143	-0.587383406	0.01269	0.67
MVP	NM_005115	777	516	751	371	192	231	-0.586913759	0.00522	0.67
HIAT1	NM_033055	162	154	154	102	29	55	-0.586784366	0.04474	0.67
ARPIN	NM_182616	165	173	184	98	42	63	-0.584962622	0.02717	0.67
PTPN14	NM_005401	1646	1358	1780	1041	335	591	-0.584558133	0.00271	0.67
KHSRP	NM_003685	1956	2132	2573	1410	477	847	-0.583840609	0.00197	0.67
KLHL11	NM_018143	214	176	289	131	53	80	-0.58239103	0.024	0.67
SNAP23	NM_003825	489	498	631	263	121	249	-0.582047648	0.00714	0.67
PTGS2	NM_000963	221	230	377	132	71	110	-0.581075744	0.02511	0.67
KLHL42	NM_020782	170	151	208	92	46	65	-0.579767083	0.02788	0.67
SFRP1	NM_003012	2101	1686	2592	1104	617	760	-0.579023078	0.00117	0.67
SYNE2	NM_182914	169	165	217	127	40	53	-0.572516713	0.04601	0.67
ECM1	NM_004425	896	701	896	414	224	343	-0.572485771	0.00231	0.67
ZNF638	NM_001014972	594	558	698	382	132	243	-0.571313826	0.0046	0.67
COL27A1	NM_032888	288	292	351	163	77	128	-0.569618147	0.01055	0.67
RNF167	NM_015528	776	570	773	449	169	246	-0.569550032	0.00576	0.67
PLXNA3	NM_017514	290	248	309	122	92	105	-0.569081308	0.02198	0.67
SLC35E2B	NM_001110781	270	243	305	165	89	61	-0.567058483	0.04489	0.67
RAB6A	NM_002869	2447	1907	2782	1322	561	1005	-0.565844816	0.00127	0.68
MARK4	NM_001199867	414	379	415	245	84	165	-0.565621652	0.01073	0.68
SMYD2	NM_020197	235	238	275	180	43	86	-0.564395427	0.04306	0.68
TNRC6A	NM_014494	307	327	605	261	80	154	-0.564002802	0.04231	0.68
TOX2	NM_001098797	379	387	506	251	111	149	-0.563291412	0.00768	0.68
MTHFD2	NM_006636	4715	4661	5621	2764	1368	1938	-0.562519461	0.00011	0.68
SGCB	NM_000232	2080	1918	2370	1376	513	758	-0.562137808	0.00125	0.68
CPSF1	NM_013291	653	419	712	358	131	232	-0.562020816	0.01422	0.68

CNTRL	NM_007018	174	154	214	100	38	76	-0.561615832	0.03799	0.68
MAN1A1	NM_005907	540	465	591	337	104	219	-0.560182729	0.01138	0.68
PIK3CA	NM_006218	344	383	414	247	83	140	-0.560009798	0.0146	0.68
PARP3	NM_001003931	174	176	194	108	44	65	-0.559851487	0.03415	0.68
SGPP1	NM_030791	317	297	403	152	84	159	-0.559137607	0.02017	0.68
ZNF625	NM_145233	253	291	349	167	90	94	-0.559134666	0.02127	0.68
RALGDS	NM_006266	194	149	177	85	53	62	-0.556023177	0.04432	0.68
SGMS1	NM_147156	227	208	281	117	46	119	-0.555923885	0.04115	0.68
DOCK1	NM_001380	385	300	426	232	77	146	-0.555765726	0.01683	0.68
ANP32B	NM_006401	2487	2212	2579	1346	480	1172	-0.555232193	0.0085	0.68
MEGF9	NM_001080497	149	146	164	89	38	55	-0.554639026	0.04558	0.68
CAT	NM_001752	225	227	212	135	58	75	-0.552202067	0.03284	0.68
PMP22	NM_153322	583	635	625	343	157	252	-0.551769148	0.00503	0.68
CHD6	NM_032221	181	190	212	109	48	76	-0.550925198	0.03241	0.68
SARS	NM_006513	1581	1485	1574	1070	306	604	-0.550705722	0.01073	0.68
FBXL7	NM_012304	638	602	669	346	210	198	-0.550685954	0.01063	0.68
PXDN	NM_012293	2837	2010	2946	1762	689	768	-0.550489288	0.01112	0.68
PRKACA	NM_002730	869	616	1134	495	232	321	-0.54806181	0.01063	0.68
ZCCHC14	NM_015144	482	426	546	270	136	181	-0.547692391	0.00547	0.68
THBS1	NM_003246	26436	24762	29712	15425	8736	8130	-0.546891483	0.00504	0.68
OBSL1	NM_015311	182	173	224	113	53	65	-0.545225201	0.03698	0.69
CNOT4	NM_001190850	811	818	799	584	211	224	-0.545118451	0.02445	0.69
MAP4	NM_002375	1514	1302	1648	929	389	538	-0.54465533	0.0014	0.69
PALM2	NM_001037293	571	588	720	351	118	305	-0.543302805	0.02103	0.69
LIN54	NM_194282	224	176	198	111	59	68	-0.538929913	0.04274	0.69
OLFML2B	NM_015441	314	450	426	278	99	119	-0.537778758	0.04401	0.69
EAF1	NM_033083	370	337	463	220	106	149	-0.536847834	0.01105	0.69
MDK	NM_001012334	2607	2439	3072	1256	799	1166	-0.536753827	0.00316	0.69
GPATCH2	NM_018040	242	192	218	133	46	89	-0.536189998	0.04228	0.69
FADS1	NM_013402	1840	1579	1561	1215	349	593	-0.535432742	0.02	0.69
SESN2	NM_031459	339	327	332	193	80	139	-0.533947397	0.01815	0.69
MYADM	NM_001020820	1056	837	1298	729	280	321	-0.533727733	0.01683	0.69
MNT	NM_020310	238	193	227	120	60	85	-0.533305603	0.03376	0.69
CD9	NM_001769	395	337	430	198	101	171	-0.532385982	0.01411	0.69
MOB1B	NM_173468	482	447	618	279	111	245	-0.530577093	0.01832	0.69
SNX12	NM_013346	650	475	472	385	136	152	-0.530246262	0.04833	0.69
NFIX	NM_002501	830	784	1135	541	243	351	-0.529886454	0.00458	0.69
ASAP2	NM_003887	859	735	839	359	278	309	-0.529446421	0.01783	0.69
RIN3	NM_024832	344	291	404	166	110	134	-0.528040035	0.02295	0.69
CXCL12	NM_001178134	3274	2867	3847	1958	902	1304	-0.527656127	0.00055	0.69
BOD1L1	NM_148894	450	426	446	256	117	175	-0.527438149	0.01045	0.69
LTBP2	NM_000428	354	354	408	226	104	131	-0.526811957	0.0148	0.69
SDC3	NM_014654	2134	1968	2507	1057	773	751	-0.526418992	0.01219	0.69
ZNF800	NM_176814	339	303	446	228	81	144	-0.526063974	0.02338	0.69
CAMSAP1	NM_015447	529	451	625	304	172	171	-0.526036714	0.0161	0.69
CTNNBIP1	NM_001012329	776	714	871	378	224	351	-0.524127594	0.00765	0.70

NEFM	NM_005382	256	260	314	127	85	116	-0.524008183	0.03351	0.70
GPX8	NM_001008397	1208	1159	1318	696	311	536	-0.522913065	0.00235	0.70
PIP5K1C	NM_012398	406	391	435	225	116	165	-0.522772531	0.01138	0.70
SH3PXD2B	NM_001017995	2085	1587	2652	1216	642	708	-0.522227358	0.00981	0.70
ANKRD52	NM_173595	313	252	393	180	83	128	-0.521325674	0.02524	0.70
PHKB	NM_000293	265	226	266	136	61	113	-0.521032015	0.03376	0.70
SMS	NM_004595	989	1048	938	703	231	355	-0.520594358	0.01938	0.70
SMURF2	NM_022739	818	782	1048	564	209	352	-0.517552046	0.00716	0.70
RAB14	NM_016322	985	953	1157	586	244	472	-0.516092902	0.00599	0.70
CRTC3	NM_022769	302	281	328	174	85	117	-0.516065652	0.02097	0.70
LRP5	NM_002335	296	272	360	138	111	111	-0.515612465	0.0463	0.70
RSRC2	NM_023012	717	672	791	444	212	257	-0.513923747	0.00654	0.70
CMIP	NM_198390	777	846	1006	589	236	296	-0.509975303	0.01257	0.70
PTBP3	NM_001163790	250	273	345	169	82	107	-0.509546465	0.03208	0.70
ZC3HAV1	NM_020119	573	485	670	261	197	223	-0.509195075	0.02633	0.70
CRMP1	NM_001014809	594	560	593	352	151	239	-0.506137801	0.00984	0.70
MTA1	NM_004689	628	585	710	408	193	208	-0.504222578	0.01521	0.71
EHD3	NM_014600	325	268	383	218	81	115	-0.502099722	0.03663	0.71
JAK1	NM_002227	794	886	1146	719	200	324	-0.501151342	0.04241	0.71
MLLT11	NM_006818	1142	1111	1272	652	322	512	-0.501043051	0.00344	0.71
EIF4G3	NM_001198802	1153	966	1206	623	308	469	-0.500392505	0.00383	0.71
KHDRBS1	NM_006559	2348	2494	3641	1677	686	1236	-0.500001969	0.01046	0.71
H1F0	NM_005318	1369	1374	1227	887	345	494	-0.499950819	0.01392	0.71
EPHX1	NM_001136018	630	569	635	328	187	247	-0.498525786	0.0111	0.71
ANKH	NM_054027	386	391	449	220	124	164	-0.498026614	0.01883	0.71
PCYOX1	NM_016297	216	207	256	135	55	95	-0.497555353	0.0466	0.71
MEX3C	NM_016626	456	491	557	319	143	179	-0.493000225	0.01881	0.71
SRCAP	NM_006662	836	796	1135	623	236	338	-0.489935064	0.01595	0.71
LMNA	NM_170707	8816	8256	9254	5178	2257	3945	-0.489774542	0.00202	0.71
PLXNA1	NM_032242	500	561	643	382	144	213	-0.489269463	0.02172	0.71
FYCO1	NM_024513	597	592	623	316	197	239	-0.486868399	0.01854	0.71
WASL	NM_003941	678	679	796	458	197	274	-0.486335636	0.01006	0.71
SASH1	NM_015278	469	402	631	282	125	227	-0.482930864	0.03053	0.72
LIX1L	NM_153713	2541	2071	2749	1667	718	802	-0.482315591	0.01474	0.72
ZNF598	NM_178167	872	695	847	551	193	318	-0.481928944	0.01965	0.72
ADNP	NM_181442	303	320	439	183	102	155	-0.481666139	0.04166	0.72
CHP1	NM_007236	440	539	752	332	169	223	-0.481600015	0.03779	0.72
PRDM4	NM_012406	325	358	427	227	111	133	-0.480030486	0.03494	0.72
ANKRD11	NM_013275	959	964	1459	638	331	452	-0.479979377	0.01591	0.72
TAB2	NM_015093	831	711	1009	386	209	458	-0.479070192	0.04979	0.72
ZNF532	NM_018181	1207	1148	1496	778	396	468	-0.478391177	0.00811	0.72
KIAA1143	NM_020696	379	320	457	256	105	137	-0.476157654	0.03831	0.72
DDAH1	NM_012137	346	284	340	197	91	127	-0.475282468	0.03738	0.72
ATL3	NM_015459	3340	3160	5045	2237	865	1873	-0.473123566	0.03082	0.72
SURF4	NM_033161	1257	1222	1485	944	260	579	-0.472949743	0.04042	0.72
MFAP4	NM_001198695	1423	1387	1813	952	355	719	-0.472504399	0.01564	0.72

SKAP2	NM_003930	314	281	324	202	73	126	-0.472017338	0.04669	0.72
WIPI2	NM_016003	5251	4833	5370	2754	1722	2012	-0.47095122	0.00836	0.72
NIPBL	NM_133433	1076	924	1303	751	252	461	-0.470704636	0.02158	0.72
PDE12	NM_177966	359	347	496	204	118	179	-0.470009979	0.04228	0.72
ITGA6	NM_001079818	1311	1162	1422	940	310	498	-0.46860925	0.02125	0.72
NOL4L	NM_080616	483	450	507	311	143	171	-0.467166534	0.02818	0.72
SPEN	NM_015001	657	472	705	364	154	274	-0.466745209	0.03038	0.72
WBP2	NM_012478	456	553	488	306	150	191	-0.46641142	0.04042	0.72
GLUL	NM_001033056	716	745	786	457	204	321	-0.465556413	0.01354	0.72
ARID1A	NM_006015	1539	1360	1594	1033	352	631	-0.464841576	0.01668	0.72
FARP1	NM_005766	368	306	450	235	105	145	-0.461819767	0.04115	0.73
PRRC2A	NM_004638	2536	2702	3011	1939	805	916	-0.460975289	0.02158	0.73
PPP6R3	NM_001164160	2717	2426	3106	1521	691	1370	-0.460421957	0.01477	0.73
CHMP1B	NM_020412	678	528	783	365	153	339	-0.459579229	0.04845	0.73
EXOSC10	NM_001001998	1085	1059	1039	684	282	449	-0.458118616	0.0159	0.73
UBQLN2	NM_013444	2099	2004	2241	1243	668	836	-0.457695337	0.00628	0.73
SBF1	NM_002972	602	577	708	447	180	208	-0.456734843	0.04013	0.73
POFUT1	NM_015352	459	423	516	325	125	170	-0.455765018	0.03857	0.73
GPD2	NM_000408	531	504	665	367	161	217	-0.455137009	0.02483	0.73
PLXNB2	NM_012401	463	363	525	249	142	184	-0.451947536	0.04058	0.73
UBR7	NM_175748	1442	1360	1286	924	355	564	-0.450795235	0.02345	0.73
SH3BP4	NM_014521	1207	1255	1609	743	398	614	-0.450596774	0.01472	0.73
JAM3	NM_032801	591	483	703	394	140	257	-0.448957996	0.04042	0.73
MAPK1	NM_002745	1032	1091	1298	750	317	461	-0.44384902	0.01482	0.74
SRRM2	NM_016333	7707	5819	7377	4465	2010	2831	-0.443274593	0.00887	0.74
PCNXL2	NM_014801	505	514	578	364	164	179	-0.442851859	0.04838	0.74
PTPN23	NM_015466	460	445	586	316	152	185	-0.442657704	0.03775	0.74
SLTM	NM_024755	881	938	1090	639	250	418	-0.442398691	0.02007	0.74
STK24	NM_001032296	771	826	903	527	270	301	-0.440523684	0.02949	0.74
ARL6IP5	NM_006407	872	782	1012	577	251	362	-0.437500348	0.01692	0.74
RBM25	NM_021239	1669	1492	1962	1108	441	757	-0.437408486	0.01315	0.74
XPO1	NM_003400	1587	1486	2021	1278	408	654	-0.437117255	0.04166	0.74
YWHAQ	NM_006826	6988	5348	6437	3893	1530	3041	-0.435656668	0.02599	0.74
LOXL2	NM_002318	1579	1407	1981	1051	499	651	-0.434109215	0.0144	0.74
CYR61	NM_001554	948	871	806	499	252	411	-0.430738177	0.04217	0.74
HMGA1	NM_145901	14955	15317	15991	10860	4913	5061	-0.430481408	0.03735	0.74
WIPF1	NM_003387	671	660	781	489	214	245	-0.430202001	0.04274	0.74
CBFB	NM_022845	1035	712	1014	553	288	369	-0.429903437	0.03831	0.74
PHGDH	NM_006623	3087	2981	3956	1827	1166	1322	-0.423387341	0.02781	0.75
ARFGEF2	NM_006420	845	757	849	571	213	341	-0.422223047	0.03549	0.75
ACSL4	NM_022977	708	705	724	421	191	348	-0.420648544	0.04176	0.75
SEC22B	NM_004892	793	650	923	545	223	304	-0.420038636	0.04068	0.75
HIVEP3	NM_001127714	1051	1006	1023	631	342	400	-0.41627452	0.03511	0.75
NRP2	NM_201266	2829	2399	2814	1758	921	914	-0.412018462	0.04601	0.75
G3BP2	NM_203505	2749	2256	2970	1550	833	1168	-0.411802804	0.01497	0.75
MAP1B	NM_005909	3890	3621	3895	2515	1217	1447	-0.411272039	0.0203	0.75

ATN1	NM_001007026	1483	1478	1762	978	481	673	-0.41092578	0.0144	0.75
CDCA7L	NM_018719	837	708	829	532	248	298	-0.408604231	0.04365	0.75
NUMA1	NM_006185	4668	3918	5821	3059	1275	2250	-0.404503417	0.02639	0.76
LARP1	NM_015315	7912	6567	10125	5391	2245	3639	-0.402250869	0.02561	0.76
RALGAPB	NM_020336	769	674	843	430	225	370	-0.400706047	0.04477	0.76
PDZD8	NM_173791	642	671	782	424	193	337	-0.398916729	0.0485	0.76
MGEA5	NM_012215	1152	1175	1388	784	387	522	-0.396779242	0.02476	0.76
ETV5	NM_004454	1182	1203	1390	739	401	563	-0.395724177	0.02788	0.76
BNIP3L	NM_004331	1512	1614	1971	1117	524	695	-0.394964556	0.02811	0.76
CDC42EP3	NM_006449	2654	2722	3228	1465	956	1362	-0.39442127	0.04766	0.76
NAV1	NM_020443	2138	2187	2413	1580	707	850	-0.386984114	0.04042	0.76
DLG5	NM_004747	1574	1528	1942	1099	503	733	-0.384098425	0.02453	0.77
NLN	NM_020726	1041	1053	1173	738	291	506	-0.383287065	0.04519	0.77
CTNND1	NM_001085458	1117	1057	1415	774	385	485	-0.383028966	0.04077	0.77
ABL1	NM_005157	1035	918	1171	639	328	466	-0.378329808	0.03759	0.77
PFN2	NM_053024	2550	2551	3219	1705	826	1324	-0.372013377	0.03045	0.77
TIMP2	NM_003255	1654	1663	1866	1139	491	813	-0.370484201	0.03567	0.77
CTNNA1	NM_001903	5816	5234	7218	4145	1978	2540	-0.343778342	0.04802	0.79
RPS6	NM_001010	13602	12416	13972	14428	6469	10206	0.322938165	0.04615	1.25
SLC25A5	NM_001152	10122	10704	12050	11771	5467	8519	0.339522557	0.03738	1.27
RPS2	NM_002952	22474	17852	22275	21310	10457	17183	0.347530816	0.0469	1.27
EEF1B2	NM_001037663	3682	3111	3519	3586	1768	2742	0.349271986	0.04314	1.27
CTTN	NM_001184740	1878	1986	2501	2269	1148	1582	0.357898553	0.04164	1.28
ERGIC3	NM_198398	950	916	1109	1013	536	791	0.364090294	0.04295	1.29
SEMA7A	NM_003612	2002	1908	2319	2332	1050	1598	0.364457769	0.02481	1.29
AIFM1	NM_004208	1133	1101	1169	1289	602	838	0.364557696	0.04068	1.29
H2AFZ	NM_002106	8703	8558	10364	9614	5180	6855	0.365662515	0.02261	1.29
GET4	NM_015949	2318	1973	2264	2267	1275	1604	0.367017192	0.04164	1.29
RPS15	NM_001018	11288	9587	11103	11533	6070	7692	0.369440203	0.02719	1.29
NSUN2	NM_017755	821	820	998	903	454	741	0.371449612	0.04801	1.29
DHCR24	NM_014762	1675	1633	1882	1809	966	1327	0.371588837	0.02719	1.29
RPL18A	NM_000980	11017	10106	11238	10515	6109	8725	0.371852268	0.03271	1.29
YIF1A	NM_020470	856	892	974	953	483	738	0.374150379	0.04157	1.30
PSMD2	NM_002808	2758	2410	2884	3241	1215	2193	0.377023181	0.04057	1.30
HIST1H3I	NM_003533	7794	6757	9195	8796	3729	6702	0.37730191	0.03112	1.30
CD81	NM_004356	886	790	928	1011	436	676	0.380103001	0.03486	1.30
MGST3	NM_004528	3994	4073	4239	4429	2418	2964	0.380911878	0.02934	1.30
RPF1	NM_025065	858	729	870	861	431	680	0.381141125	0.04068	1.30
ID1	NM_002165	2963	2588	3657	3687	1615	2176	0.381728089	0.03015	1.30
IARS2	NM_018060	803	775	791	914	399	635	0.387056439	0.04069	1.31
CFL1	NM_005507	17927	16402	17780	16876	10930	13125	0.38847322	0.04075	1.31
POLD2	NM_006230	2586	2308	2686	2866	1399	1868	0.389191172	0.01595	1.31
BSG	NM_001728	3697	3211	3701	3297	2214	2803	0.391106092	0.04729	1.31
PSMB4	NM_002796	2307	2132	2485	2297	1377	1823	0.394869612	0.0253	1.31
C19orf53	NM_014047	1519	1341	1654	1390	845	1349	0.39537197	0.0483	1.32
UFD1L	NM_005659	646	614	702	764	353	495	0.397704911	0.0297	1.32

OSTC	NM_021227	873	873	1044	979	545	726	0.403575218	0.02484	1.32
KARS	NM_001130089	995	984	1072	1121	581	785	0.404259583	0.02027	1.32
MAGOH	NM_002370	710	815	811	783	449	662	0.404354556	0.04723	1.32
RBM17	NM_032905	844	845	976	1012	531	630	0.404810003	0.02911	1.32
HJURP	NM_018410	2046	1893	2476	2054	1244	1817	0.406273422	0.02861	1.33
RPS4X	NM_001007	29975	27513	31022	29198	15424	27257	0.406393257	0.02604	1.33
ERF	NM_006494	897	803	961	1049	476	678	0.408591498	0.01854	1.33
RNF115	NM_014455	1130	907	1029	1074	603	814	0.409290006	0.03233	1.33
EIF3B	NM_001037283	1871	1416	1903	1829	1057	1296	0.40987859	0.02945	1.33
C7orf50	NM_001134396	3163	3125	3601	3102	1965	2831	0.410188681	0.02936	1.33
APLP2	NM_001642	652	598	716	776	347	510	0.410422488	0.02295	1.33
PLAUR	NM_002659	2093	1929	2408	1970	1355	1769	0.411756659	0.03968	1.33
FMNL3	NM_175736	389	349	413	424	196	336	0.412284474	0.04654	1.33
MYBBP1A	NM_001105538	1340	1285	1519	1601	758	1060	0.412413672	0.01121	1.33
PSMB7	NM_002799	1408	1359	1749	1415	999	1159	0.413001566	0.04769	1.33
NCAPD2	NM_014865	4487	3650	4740	4406	2646	3292	0.414686542	0.01949	1.33
BRK1	NM_018462	1298	1098	1323	1238	811	931	0.415339031	0.03799	1.33
TBL3	NM_006453	545	432	547	557	314	375	0.415967687	0.04276	1.33
ATP13A3	NM_024524	868	932	1122	1004	507	891	0.416140071	0.03422	1.33
HDGF	NM_004494	6379	5665	7179	7124	3887	4617	0.416302832	0.01248	1.33
NOP14	NM_003703	721	597	612	691	398	495	0.416736632	0.04723	1.33
CRCP	NM_001142414	494	378	512	494	282	355	0.418965454	0.04492	1.34
MRPL37	NM_016491	2379	1997	2575	2406	1393	1825	0.419077588	0.01508	1.34
MRPL20	NM_017971	1448	1364	1565	1581	734	1322	0.419171504	0.01942	1.34
ABRACL	NM_021243	360	308	370	378	205	273	0.41939484	0.0452	1.34
DAD1	NM_001344	2952	2612	3210	3253	1555	2437	0.419700218	0.00727	1.34
SYPL1	NM_006754	531	537	711	611	338	504	0.42030165	0.03549	1.34
SHCBP1	NM_024745	550	509	468	634	266	405	0.42098154	0.04993	1.34
FAM96B	NM_016062	532	468	565	553	279	463	0.421770575	0.03237	1.34
GNG12	NM_018841	3641	3144	4800	4137	2310	2945	0.421978578	0.02024	1.34
HSPD1	NM_002156	5694	5436	6633	5237	3728	5172	0.422160937	0.04011	1.34
MCM6	NM_005915	1742	1515	1959	1613	1167	1367	0.422729888	0.04312	1.34
EEF1A1	NM_001402	48806	46126	53371	55375	23922	45128	0.423086466	0.01379	1.34
LAMB1	NM_002291	1073	1060	1217	1198	716	817	0.424722034	0.02398	1.34
EXOSC2	NM_014285	464	483	633	552	323	417	0.426365636	0.03799	1.34
GADD45GIP1	NM_052850	5760	5470	6484	6085	3402	4976	0.427013582	0.00828	1.34
SSR1	NM_003144	1132	1178	1304	1295	624	1094	0.427048667	0.01949	1.34
NPLOC4	NM_017921	768	752	893	884	508	588	0.427439659	0.02376	1.34
FUT8	NM_178156	4251	4055	4726	4133	2878	3431	0.427893978	0.02874	1.35
ABHD2	NM_152924	1934	1646	2250	2237	1191	1372	0.427989106	0.01742	1.35
MFN2	NM_001127660	1338	1148	1556	1438	780	1095	0.428477504	0.01272	1.35
POLR2F	NM_021974	356	337	406	412	179	339	0.429814034	0.0449	1.35
EIF3D	NM_003753	2123	2074	2167	2360	1225	1702	0.431175704	0.00887	1.35
FAM129B	NM_022833	2725	2444	2976	2825	1847	1924	0.431941819	0.02874	1.35
EIF2S2	NM_003908	571	453	621	576	321	459	0.432392033	0.02904	1.35
SUMO3	NM_006936	1045	994	1127	1289	529	879	0.432679564	0.01295	1.35

NUDC	NM_006600	1441	1311	1459	1518	752	1245	0.433124648	0.01285	1.35
PTK2	NM_005607	1079	994	1162	1235	549	944	0.433428812	0.01256	1.35
DEPDC1	NM_001114120	584	588	572	568	368	497	0.433535232	0.04453	1.35
SOD2	NM_001024465	787	668	834	799	469	611	0.433660507	0.02047	1.35
VKORC1	NM_024006	726	821	858	840	501	641	0.433941459	0.02708	1.35
PRPF6	NM_012469	455	365	460	474	230	371	0.434835745	0.03167	1.35
EIF4A1	NM_001204510	12713	11503	14065	14092	6440	11599	0.435241644	0.00865	1.35
DNAJB1	NM_006145	746	612	823	792	502	493	0.436719458	0.04519	1.35
R3HDM1	NM_015361	702	552	934	767	464	558	0.437234488	0.04494	1.35
ZNF330	NM_014487	394	321	429	387	238	317	0.437611609	0.04228	1.35
USP14	NM_005151	668	565	754	778	308	615	0.438017519	0.03214	1.35
GINS2	NM_016095	357	335	477	433	211	337	0.438432405	0.036	1.36
MRPL9	NM_031420	762	737	788	762	502	610	0.439396304	0.03082	1.36
TCEB2	NM_207013	2073	1671	2068	2167	1105	1578	0.440353339	0.00779	1.36
UBE2K	NM_005339	697	723	842	713	473	663	0.440593461	0.03453	1.36
DDX23	NM_004818	502	479	551	613	296	387	0.44085253	0.01889	1.36
CENPN	NM_001100624	984	1133	1164	1238	769	719	0.442291062	0.04817	1.36
BDKRB1	NM_000710	465	385	434	556	256	292	0.442395638	0.04288	1.36
ZWINT	NM_032997	1220	1053	1460	1291	698	1103	0.442516565	0.01483	1.36
ASPSCR1	NM_024083	280	262	351	336	172	244	0.443377204	0.03759	1.36
COPS8	NM_006710	2041	1786	2293	2309	1232	1547	0.443422895	0.00707	1.36
KCNQ5	NM_001160133	272	267	344	359	165	229	0.443440111	0.03808	1.36
PPAN	NM_020230	532	525	703	556	374	509	0.44502434	0.04044	1.36
RPL32	NM_001007074	5288	5575	5529	6041	3721	3828	0.445118242	0.0253	1.36
RNASEH2A	NM_006397	3085	2872	2706	3794	1588	2158	0.446471817	0.01817	1.36
UBE2N	NM_003348	471	415	499	479	235	460	0.446736425	0.04101	1.36
CPSF4	NM_006693	321	255	362	376	156	275	0.446793642	0.04206	1.36
MCM7	NM_005916	1413	1318	1248	1438	673	1298	0.447152655	0.03163	1.36
EXOC7	NM_001145299	401	397	407	460	233	332	0.449354423	0.02441	1.37
COPS6	NM_006833	3015	2893	2856	3602	1619	2313	0.450314744	0.0077	1.37
PAK1IP1	NM_017906	465	395	525	530	251	395	0.450448824	0.01883	1.37
CKB	NM_001823	293	297	346	342	200	245	0.452224459	0.03567	1.37
ILF2	NM_004515	1541	1430	1801	1816	828	1413	0.4527704	0.00657	1.37
ATP5C1	NM_001001973	875	945	1081	1088	582	770	0.453135493	0.01025	1.37
C11orf73	NM_016401	381	345	528	466	256	330	0.453136023	0.03345	1.37
CD63	NM_001780	1352	1186	1303	1564	719	1008	0.453474593	0.00743	1.37
HIST1H2AL	NM_003511	2167	2018	2135	2702	1162	1606	0.454006437	0.00744	1.37
USP39	NM_006590	593	727	771	913	381	530	0.454190623	0.02437	1.37
POLR2E	NM_002695	1068	806	846	1059	546	719	0.455526569	0.02468	1.37
MRPS16	NM_016065	847	887	932	951	531	761	0.455978912	0.01216	1.37
TCP1	NM_030752	2558	2118	2713	2897	1228	2229	0.456047232	0.00831	1.37
CIRH1A	NM_032830	1045	945	1149	1308	547	862	0.459613502	0.00648	1.38
CDC20	NM_001255	1630	1596	1270	1567	999	1237	0.460156113	0.04115	1.38
RPL37	NM_000997	828	964	886	1132	550	641	0.460542778	0.02384	1.38
SFT2D1	NM_145169	541	493	614	620	364	402	0.460553647	0.02098	1.38
SNX17	NM_014748	799	579	693	824	420	531	0.462180545	0.02127	1.38

TSR1	NM_018128	769	686	727	812	471	563	0.463388373	0.01628	1.38
SUPT4H1	NM_003168	556	564	617	564	389	493	0.464727826	0.02839	1.38
TMA7	NM_015933	591	496	540	793	257	427	0.46474927	0.03779	1.38
NT5DC2	NM_001134231	1731	1485	1971	1557	1245	1417	0.464883323	0.03738	1.38
CCDC34	NM_030771	229	215	283	245	144	228	0.465209693	0.04814	1.38
DDX50	NM_024045	306	324	401	343	219	304	0.465346024	0.03738	1.38
TSTA3	NM_003313	372	344	426	368	252	333	0.466128819	0.03567	1.38
NOC2L	NM_015658	1625	1124	1577	1842	860	1040	0.466590948	0.01782	1.38
BIRC5	NM_001012271	1934	1859	1936	1872	1440	1408	0.466714408	0.03831	1.38
FABP5	NM_001444	1816	1787	1923	2042	1346	1245	0.468713857	0.02861	1.38
ABCE1	NM_002940	2415	2217	2586	2855	1424	1890	0.468992529	0.00235	1.38
LIN7C	NM_018362	648	576	787	646	415	618	0.469085818	0.02395	1.38
ANGPT1	NM_001146	221	206	260	293	107	212	0.470422184	0.04629	1.39
SRSF7	NM_001031684	1661	1556	2143	1699	1158	1575	0.470565574	0.01883	1.39
FXYD5	NM_014164	2897	2555	3642	3235	2030	2302	0.470619024	0.01216	1.39
UBE2J1	NM_016021	267	306	372	363	191	260	0.472908539	0.02809	1.39
EARS2	NM_001083614	272	268	330	351	164	242	0.473228193	0.02221	1.39
SLC5A6	NM_021095	1294	1196	1425	1445	910	937	0.473364992	0.01571	1.39
MRPL23	NM_021134	678	660	714	665	417	653	0.473936898	0.02198	1.39
MRFAP1	NM_033296	3007	2904	3273	3488	2046	2239	0.474285711	0.00799	1.39
WDHD1	NM_007086	283	258	320	351	159	242	0.474514993	0.02161	1.39
COPE	NM_007263	787	634	729	871	406	596	0.477119419	0.00871	1.39
FTSJ2	NM_013393	499	470	554	580	253	501	0.477563833	0.01908	1.39
MDFIC	NM_001166345	230	230	300	288	145	226	0.477773096	0.03006	1.39
CCDC124	NM_001136203	1203	969	1257	1303	741	871	0.477874836	0.00855	1.39
PREB	NM_013388	465	379	473	509	267	359	0.478561586	0.01305	1.39
SRPRB	NM_021203	364	445	435	500	222	377	0.479551536	0.02295	1.39
TMEM147	NM_032635	797	686	778	902	457	597	0.479626579	0.00686	1.39
RNF14	NM_183400	311	276	369	326	174	325	0.479929179	0.03681	1.39
RING1	NM_002931	422	339	373	393	251	324	0.480429928	0.03013	1.40
HIST1H3C	NM_003531	10059	8643	9492	11451	5320	7775	0.48048821	0.00194	1.40
HIGD2A	NM_138820	1954	1575	1887	1903	1211	1452	0.481219973	0.01051	1.40
UQCRQ	NM_014402	1165	1050	1050	1391	702	766	0.481708735	0.01552	1.40
DNAJA3	NM_005147	407	326	455	423	244	348	0.481724411	0.01931	1.40
SFXN1	NM_022754	2201	2200	2177	2523	948	2464	0.482476545	0.04111	1.40
LMLN	NM_001136049	159	146	201	206	105	133	0.482925041	0.0485	1.40
ARMC8	NM_015396	413	349	427	362	245	404	0.484218342	0.04159	1.40
RCE1	NM_005133	414	379	466	480	240	373	0.485000476	0.01073	1.40
C3orf14	NM_020685	249	264	310	314	163	240	0.485604173	0.02242	1.40
BCS1L	NM_001079866	354	348	397	419	217	319	0.485938283	0.01296	1.40
EEF1D	NM_001130053	5841	5403	5201	6953	2867	4855	0.486395951	0.00598	1.40
PAFAH1B3	NM_001145940	257	232	241	329	141	186	0.487153541	0.03276	1.40
EDF1	NM_003792	1300	1075	1207	1196	854	966	0.487959374	0.01997	1.40
NCLN	NM_020170	628	574	675	651	432	508	0.488019021	0.01497	1.40
EIF1AX	NM_001412	805	763	970	1113	423	731	0.488248999	0.00725	1.40
ITGA2	NM_002203	828	742	884	1017	463	673	0.48886016	0.00347	1.40

RPL29	NM_000992	7532	7631	9495	9110	4772	7303	0.490010856	0.00175	1.40
SOD1	NM_000454	3264	2773	3126	3153	1970	2664	0.49016268	0.00657	1.40
MRPS6	NM_032476	1033	1092	1168	1109	728	959	0.490165916	0.01146	1.40
TXN	NM_003329	1921	1599	2235	1967	1275	1614	0.492806311	0.00835	1.41
TMEM258	NM_014206	558	425	532	607	309	410	0.494232425	0.01047	1.41
PDLIM7	NM_005451	985	891	1180	1171	638	824	0.494589313	0.00367	1.41
RPS11	NM_001015	18229	16287	15618	18740	10968	13621	0.494907071	0.00685	1.41
RHOC	NM_001042679	2373	2407	3020	2839	1608	2240	0.496365693	0.00262	1.41
HIST1H2AH	NM_080596	3229	3409	4207	3683	2568	2885	0.496742502	0.01175	1.41
NUP54	NM_017426	301	382	438	393	240	338	0.496766906	0.02783	1.41
PHPT1	NM_014172	839	579	756	775	366	786	0.497020674	0.03256	1.41
RPLP1	NM_001003	7079	5397	5615	7574	2870	6031	0.497123522	0.0186	1.41
UBA52	NM_003333	2900	2415	3155	3226	1752	2319	0.497213505	0.00177	1.41
YTHDF2	NM_001173128	400	366	455	395	279	366	0.497765503	0.02367	1.41
XRCC6	NM_001469	7180	6126	6879	7467	4060	5937	0.497884166	0.00201	1.41
SRP72	NM_006947	4293	4067	3905	4389	2080	4442	0.498206995	0.01921	1.41
LAS1L	NM_031206	1780	1357	1540	2008	981	1152	0.498410366	0.00902	1.41
COPS3	NM_003653	675	612	836	777	450	600	0.499680663	0.00657	1.41
CLIC1	NM_001288	9498	8862	10479	10958	5569	8536	0.500002289	0.00066	1.41
LAMTOR1	NM_017907	1576	1287	1558	1633	827	1404	0.50052982	0.00466	1.41
NUDCD3	NM_015332	1183	1130	1243	1217	915	883	0.502409985	0.02227	1.42
OAZ1	NM_004152	3392	3129	3492	3661	2216	2728	0.502569422	0.00302	1.42
WBSCR22	NM_017528	843	801	837	893	482	798	0.503754648	0.00751	1.42
ARRB2	NM_004313	429	352	432	399	291	347	0.503871248	0.0253	1.42
ATXN7L3	NM_020218	329	309	375	341	242	286	0.503960517	0.02441	1.42
BANF1	NM_001143985	462	392	563	551	253	450	0.504207156	0.01117	1.42
COX6C	NM_004374	780	632	739	1059	355	583	0.505134036	0.0146	1.42
RNH1	NM_203384	916	729	788	1053	425	728	0.505553204	0.00875	1.42
SRA1	NM_001035235	668	562	588	826	321	513	0.505571557	0.01045	1.42
CCNB1	NM_031966	635	592	710	739	395	559	0.506189751	0.00369	1.42
INHBA	NM_002192	507	435	487	613	248	432	0.506659136	0.00917	1.42
HIST1H2BH	NM_003524	2374	1897	2015	3024	1130	1640	0.506842744	0.00939	1.42
C1QBP	NM_001212	2014	1749	2454	2131	1351	1830	0.508020739	0.00562	1.42
STRAP	NM_007178	276	284	350	354	189	260	0.509113364	0.01295	1.42
GALNT14	NM_024572	194	174	218	240	98	195	0.509385611	0.03284	1.42
RPS18	NM_022551	2661	2414	2189	2820	1250	2512	0.510337544	0.01411	1.42
C6orf48	NM_001040438	295	298	334	394	153	299	0.510839387	0.01742	1.42
RPS23	NM_001025	6840	5691	7661	7408	4423	5550	0.511321421	0.00218	1.43
C12orf43	NM_022895	177	158	209	230	93	173	0.511340088	0.03267	1.43
CENPO	NM_024322	360	316	368	427	171	352	0.512169268	0.01776	1.43
AIMP2	NM_006303	1560	1334	2036	1846	1141	1258	0.512724467	0.00865	1.43
CMC2	NM_020188	618	585	712	768	362	572	0.513260223	0.00287	1.43
TTF2	NM_003594	357	281	431	363	273	281	0.514591016	0.03376	1.43
EMC3	NM_018447	327	293	348	419	169	293	0.514623904	0.01132	1.43
DCXR	NM_016286	287	284	322	371	154	287	0.515589509	0.01448	1.43
PURB	NM_033224	194	234	328	289	172	207	0.516042551	0.03556	1.43

VEGFC	NM_005429	531	526	635	587	365	520	0.516483457	0.0083	1.43
UBIAD1	NM_013319	360	322	377	411	208	325	0.517636792	0.00826	1.43
WDR70	NM_018034	169	185	161	200	109	158	0.517985367	0.03836	1.43
CECR5	NM_033070	429	333	428	448	238	369	0.518128821	0.00987	1.43
CDK4	NM_000075	594	505	593	635	334	530	0.518554335	0.00544	1.43
TACO1	NM_016360	269	219	247	233	161	253	0.519227373	0.03886	1.43
MPI	NM_002435	180	140	169	173	119	141	0.520122482	0.04408	1.43
TSEN34	NM_001077446	290	175	276	317	160	193	0.520444585	0.03376	1.43
WDR12	NM_018256	384	386	422	363	331	325	0.521558887	0.04278	1.44
MRPS28	NM_014018	351	266	366	398	199	283	0.521894264	0.01045	1.44
EIF3K	NM_013234	2303	2172	2543	2722	1485	1962	0.522424842	0.00071	1.44
HIST1H2AG	NM_021064	5051	4296	5967	6543	3074	4036	0.522567918	0.00083	1.44
EBNA1BP2	NM_001159936	3440	3235	3651	4322	1982	2959	0.523619484	0.00035	1.44
CACYBP	NM_014412	634	542	444	768	299	460	0.524167927	0.02318	1.44
TGFBI	NM_000358	14805	14618	18872	18153	10467	13484	0.524762648	0.001	1.44
U2AF1	NM_006758	1091	1143	1027	1372	554	1089	0.525564355	0.00897	1.44
FADD	NM_003824	919	747	983	1194	563	637	0.525711681	0.00553	1.44
ORC1	NM_001190818	166	129	176	186	96	145	0.526415051	0.03158	1.44
RPL27A	NM_000990	6433	5759	7609	7729	4556	5018	0.526458368	0.00235	1.44
MRPS18B	NM_014046	1038	947	1210	1271	660	902	0.527534803	0.00104	1.44
ACAD9	NM_014049	224	239	306	286	165	234	0.528004695	0.01671	1.44
RNF26	NM_032015	1134	894	868	1169	617	826	0.5286025	0.00805	1.44
SWI5	NM_001040011	186	168	181	177	136	160	0.529278509	0.04217	1.44
AP2M1	NM_001025205	6538	6148	6594	7500	3856	5822	0.529873898	0.00049	1.44
SAP18	NM_005870	1041	937	1132	1194	676	875	0.529986861	0.00154	1.44
NEU1	NM_000434	165	150	207	191	138	133	0.530229828	0.04274	1.44
SNRPE	NM_003094	1637	1680	2105	2056	839	2090	0.530814365	0.01803	1.44
NDUFA3	NM_004542	415	319	382	498	192	346	0.531078675	0.01121	1.45
LSM2	NM_021177	772	796	824	858	507	755	0.531629965	0.00457	1.45
RPS6KA4	NM_003942	529	459	551	596	380	383	0.531660425	0.01099	1.45
COL7A1	NM_000094	189	159	200	208	140	141	0.532232822	0.03364	1.45
TMEM205	NM_001145416	548	431	440	545	297	438	0.532883392	0.01057	1.45
BABAM1	NM_001033549	698	601	671	721	429	596	0.533233188	0.00456	1.45
FOXRED1	NM_017547	199	159	214	235	108	181	0.533291728	0.02034	1.45
SCAMP3	NM_005698	368	322	545	464	294	329	0.533333809	0.01955	1.45
ACLY	NM_001096	2101	1968	2419	2579	1310	1892	0.533808802	0.00035	1.45
RNF149	NM_173647	160	147	157	187	95	144	0.534556805	0.02701	1.45
AATF	NM_012138	1469	1460	1712	1881	931	1347	0.534647384	0.00046	1.45
SFXN4	NM_213649	145	113	122	167	75	114	0.534772826	0.04252	1.45
RPL26L1	NM_016093	1563	1454	1803	1921	985	1391	0.534883593	0.00045	1.45
CSE1L	NM_001316	1740	1373	1755	2009	873	1550	0.535809239	0.00183	1.45
HIST1H2AE	NM_021052	1227	997	1146	1478	660	940	0.536003834	0.0016	1.45
MEMO1	NM_015955	579	523	589	612	344	555	0.53636443	0.00539	1.45
POLRMT	NM_005035	204	255	243	266	177	188	0.536365476	0.0291	1.45
EXOSC5	NM_020158	257	208	273	336	134	216	0.537084048	0.01296	1.45
MRPS23	NM_016070	307	226	300	328	166	262	0.537354758	0.01244	1.45

EXOSC7	NM_015004	248	222	247	324	137	205	0.537992293	0.01199	1.45
POLA2	NM_002689	307	274	346	367	200	267	0.538525856	0.00689	1.45
NDUFB8	NM_005004	1361	1240	1540	1583	812	1310	0.538879636	0.00094	1.45
DDX39A	NM_005804	886	678	953	883	653	653	0.538950903	0.0146	1.45
SLC35B1	NM_005827	354	373	417	473	206	373	0.539406366	0.00663	1.45
ABCD3	NM_002858	221	220	316	265	185	220	0.54108573	0.02345	1.46
MIIP	NM_021933	272	285	306	322	226	221	0.541623286	0.02119	1.46
UAP1	NM_003115	591	619	685	792	383	548	0.542366867	0.00161	1.46
NDUFAF6	NM_152416	150	156	171	184	87	172	0.5425298	0.03181	1.46
DGCR6L	NM_033257	382	344	374	497	211	313	0.54256851	0.00545	1.46
ANKRD13C	NM_030816	362	329	457	469	216	362	0.543058826	0.00551	1.46
TRAP1	NM_016292	1099	951	1201	1206	743	923	0.543101966	0.00217	1.46
UHMK1	NM_175866	665	573	654	752	407	544	0.543123779	0.00218	1.46
NAA20	NM_016100	622	469	615	735	323	509	0.543737687	0.00326	1.46
HDAC3	NM_003883	419	359	349	466	238	331	0.545299886	0.00813	1.46
OSGEP	NM_017807	199	174	191	184	146	173	0.545419814	0.03562	1.46
CDKN3	NM_005192	1782	1800	1937	1920	964	2167	0.546201139	0.01285	1.46
COX4I1	NM_001861	1677	1859	2196	2018	1333	1695	0.546409099	0.00367	1.46
TMEM237	NM_001044385	196	195	280	285	103	247	0.546555347	0.03174	1.46
POLR2H	NM_006232	312	318	347	328	192	367	0.546943083	0.01982	1.46
HMBS	NM_000190	244	201	194	286	120	198	0.547033504	0.0203	1.46
CDC45	NM_003504	525	454	605	620	346	455	0.547169794	0.00267	1.46
NSFL1C	NM_016143	828	787	887	907	593	716	0.547265944	0.00367	1.46
DDX55	NM_020936	618	633	672	638	515	531	0.547475751	0.01649	1.46
RPL7A	NM_000972	4019	3701	4040	4412	2017	4402	0.547735492	0.00649	1.46
CHPT1	NM_020244	152	127	248	209	131	138	0.548294858	0.04654	1.46
RFT1	NM_052859	804	846	786	1055	572	604	0.548640394	0.00653	1.46
ARHGAP18	NM_033515	442	352	410	468	302	311	0.548884693	0.01195	1.46
HAUS7	NM_017518	264	243	258	334	153	224	0.549555174	0.00831	1.46
SMARCE1	NM_003079	1201	667	1313	1106	789	907	0.549759466	0.02582	1.46
CISD2	NM_001008388	406	428	431	479	307	352	0.551169567	0.00799	1.47
ASB1	NM_001040445	580	523	583	604	356	558	0.551398583	0.00467	1.47
GMPR2	NM_001002002	236	243	292	311	155	242	0.551562779	0.00805	1.47
PPP1CA	NM_002708	4672	3683	4813	5076	2924	3743	0.551702356	0.00078	1.47
C12orf57	NM_138425	1191	898	1265	1181	767	1022	0.553057959	0.0043	1.47
ORMDL2	NM_014182	116	86	139	149	64	110	0.553156142	0.04231	1.47
GFER	NM_005262	200	205	191	216	142	186	0.553682786	0.02229	1.47
UBXN2A	NM_181713	107	134	142	155	104	95	0.553805397	0.04943	1.47
NOLC1	NM_004741	1561	1477	1692	1903	968	1420	0.554635688	0.00029	1.47
TRIAP1	NM_016399	285	300	362	389	188	295	0.555175706	0.00522	1.47
C8orf76	NM_032847	263	228	279	324	166	219	0.556094365	0.00683	1.47
PET100	NM_001171155	125	146	144	193	70	139	0.556470323	0.0337	1.47
PSMB6	NM_002798	1857	1478	1728	1629	1274	1545	0.556647808	0.00978	1.47
MRPS5	NM_031902	280	225	286	318	147	270	0.557469582	0.0101	1.47
AKAP8	NM_005858	683	702	739	819	523	568	0.557665283	0.00451	1.47
BAG6	NM_001098534	740	642	721	754	556	558	0.558203299	0.01009	1.47

SNRPD2	NM_004597	1531	1401	1579	1740	925	1426	0.558216487	0.00056	1.47
SDHD	NM_003002	640	686	731	844	449	587	0.560031583	0.00136	1.47
MTMR14	NM_001077525	159	121	162	178	76	166	0.56041823	0.03373	1.47
THOC6	NM_024339	438	392	439	534	329	297	0.561639209	0.01202	1.48
TXNDC17	NM_032731	271	190	241	296	138	224	0.562242192	0.01248	1.48
COA1	NM_018224	743	684	826	868	557	601	0.565024131	0.00317	1.48
RANGAP1	NM_002883	718	561	671	637	631	445	0.565058667	0.04389	1.48
AMDHD2	NM_001145815	94	85	108	128	68	77	0.565162105	0.04217	1.48
HIST2H2BE	NM_003528	5979	4803	5804	6689	3324	5176	0.565167848	0.00028	1.48
RPL23A	NM_000984	356	328	259	438	209	255	0.565269436	0.01713	1.48
TSN	NM_004622	512	405	512	561	337	400	0.565975824	0.00383	1.48
SLC35A5	NM_017945	165	179	186	247	72	209	0.566228681	0.04179	1.48
TAGLN2	NM_003564	5732	5250	6773	6766	3760	5490	0.566834125	0.00023	1.48
OIP5	NM_007280	214	191	231	277	103	231	0.567736717	0.01688	1.48
ARL16	NM_001040025	124	137	138	188	72	128	0.568613167	0.02561	1.48
MED10	NM_032286	211	230	327	258	182	255	0.568641033	0.02064	1.48
POLDIP2	NM_015584	700	691	870	721	603	670	0.56923616	0.01202	1.48
EMP3	NM_001425	2841	2495	3074	2689	2205	2498	0.569421338	0.00764	1.48
UBE2D3	NM_181891	3008	3065	3402	3263	2482	2651	0.569469707	0.00521	1.48
POLD4	NM_021173	434	336	479	417	293	413	0.570337508	0.01023	1.48
NRAS	NM_002524	1101	1129	1540	1362	844	1184	0.570409585	0.00229	1.48
DKC1	NM_001363	857	752	991	997	574	786	0.570931262	0.00087	1.49
RPL27	NM_000988	13162	12429	15143	16840	7972	12716	0.571486601	5.62E-05	1.49
LRRC14	NM_014665	239	200	227	215	207	175	0.571623554	0.04228	1.49
HSPA8	NM_006597	10810	10776	12559	12215	7306	11317	0.571948625	0.00072	1.49
BYSL	NM_004053	255	212	314	369	181	186	0.57219353	0.01298	1.49
ATPIF1	NM_016311	234	241	203	361	108	215	0.574007933	0.02445	1.49
MMS19	NM_022362	343	260	350	384	228	264	0.574126965	0.00652	1.49
IMPDH2	NM_000884	1712	1455	2041	1883	1370	1381	0.574595346	0.00539	1.49
EFR3A	NM_015137	345	342	452	343	280	398	0.574943659	0.01883	1.49
ADAMTS1	NM_006988	143	132	211	189	94	175	0.575145864	0.02476	1.49
ATP5G2	NM_005176	2241	1600	2056	2199	1448	1679	0.57677837	0.00321	1.49
TUBA3C	NM_006001	1332	1163	1332	1613	757	1196	0.577193288	0.00027	1.49
DNPEP	NM_012100	140	137	158	195	91	130	0.578919977	0.01459	1.49
CCT5	NM_012073	4716	4195	5560	5611	3607	3820	0.578978987	0.00142	1.49
CCT2	NM_006431	749	693	705	978	370	723	0.579349684	0.0027	1.49
WBSCR16	NM_030798	233	180	225	279	119	212	0.57938616	0.00951	1.49
SMAD5	NM_001001420	273	242	266	390	132	245	0.580199124	0.00897	1.50
ARFIP1	NM_001025595	101	85	93	108	64	95	0.580600677	0.04013	1.50
GTF2A2	NM_004492	411	402	539	606	244	437	0.582146699	0.00239	1.50
PHB	NM_002634	989	888	970	1118	732	749	0.582326199	0.0032	1.50
SCP2	NM_002979	384	416	466	414	299	440	0.582409739	0.00963	1.50
PPP4C	NM_002720	1039	939	1113	1194	677	965	0.583185905	0.00043	1.50
CEP97	NM_024548	138	123	196	186	102	142	0.583257743	0.01849	1.50
PLIN3	NM_005817	116	116	126	167	93	85	0.583276395	0.03259	1.50
PDXK	NM_003681	382	351	355	448	260	307	0.58462833	0.00402	1.50

DRG1	NM_004147	846	765	893	967	594	733	0.587330784	0.0009	1.50
HSPBP1	NM_001130106	684	492	651	745	441	503	0.58762412	0.00298	1.50
DLG4	NM_001128827	127	125	131	140	119	98	0.587798717	0.04274	1.50
LDLR	NM_000527	1063	1046	1170	1306	754	960	0.588040488	0.00041	1.50
HNRNPA1	NM_031157	924	1096	922	1038	718	960	0.589450459	0.00648	1.50
ERCC2	NM_000400	257	200	271	305	187	188	0.589484968	0.01018	1.50
APOOL	NM_198450	135	108	171	150	126	107	0.591665856	0.04068	1.51
H2AFV	NM_012412	5131	3997	5323	5582	3457	4156	0.593005583	0.00059	1.51
C6orf1	NM_001008704	242	263	259	294	204	214	0.594068814	0.01053	1.51
JMJD6	NM_001081461	135	141	195	176	107	161	0.594631386	0.01695	1.51
PDXP	NM_020315	318	257	380	322	271	273	0.595454165	0.01591	1.51
HIST1H3A	NM_003529	2578	1953	2206	3081	1161	2337	0.595965429	0.0021	1.51
NCAPH	NM_015341	272	287	345	376	227	243	0.596200283	0.00508	1.51
ATAD3A	NM_001170535	574	463	399	474	344	529	0.597013534	0.01782	1.51
TIA1	NM_022173	302	271	399	297	217	385	0.597470724	0.01893	1.51
DPH1	NM_001383	209	260	235	275	182	207	0.597654519	0.01186	1.51
ILK	NM_004517	407	443	487	482	324	430	0.598956099	0.00355	1.51
NRG1	NM_013956	207	186	155	284	107	162	0.598985556	0.0175	1.51
RAB32	NM_006834	162	177	183	187	133	170	0.599015689	0.01508	1.51
BCAR3	NM_003567	314	278	380	397	208	310	0.599043558	0.00207	1.51
RPL7	NM_000971	10683	10982	13068	12536	8402	10697	0.599394674	0.00066	1.52
FAM207A	NM_058190	639	584	780	866	406	622	0.599982502	0.00033	1.52
FKBP4	NM_002014	2383	2304	2609	2976	1732	2056	0.600627852	0.00023	1.52
SLC39A3	NM_144564	253	206	254	317	152	215	0.600918617	0.00364	1.52
MCAM	NM_006500	640	601	585	950	385	468	0.601642749	0.0031	1.52
SLC25A32	NM_030780	997	964	927	1096	824	744	0.601821407	0.00775	1.52
ATG4B	NM_013325	426	340	428	433	300	370	0.602336022	0.0043	1.52
EIF3L	NM_016091	2926	2395	2616	3094	2107	2119	0.602432078	0.00266	1.52
NPM1	NM_002520	19436	19075	21165	21319	14068	19352	0.603631518	0.00053	1.52
COG4	NM_015386	603	600	751	812	399	637	0.604758545	0.0004	1.52
RPLP0	NM_001002	14216	11861	13185	16483	7790	13075	0.60538772	0.00014	1.52
ANAPC15	NM_014042	460	490	394	700	295	348	0.606327557	0.00712	1.52
RPL11	NM_000975	36792	37344	39995	42126	32388	29679	0.606688192	0.00422	1.52
SAFB2	NM_014649	166	163	174	253	72	193	0.607172979	0.02261	1.52
LY6K	NM_017527	369	250	269	366	224	259	0.608998488	0.00995	1.53
RHBDD3	NM_012265	148	113	122	147	113	106	0.609130817	0.02994	1.53
MRPL27	NM_016504	129	110	139	185	88	100	0.609307285	0.01591	1.53
RPL39L	NM_052969	181	100	134	179	64	185	0.612227189	0.04627	1.53
NUPL1	NM_014089	388	424	530	567	326	375	0.61241904	0.00178	1.53
NAA38	NM_032356	687	759	823	974	554	619	0.612696556	0.00087	1.53
STX4	NM_004604	445	426	460	510	388	341	0.612969177	0.00832	1.53
OGFOD3	NM_024648	191	188	321	254	226	169	0.613275796	0.03549	1.53
MRPL33	NM_004891	138	134	159	185	70	178	0.613287413	0.02118	1.53
HIST1H1D	NM_005320	4507	3671	4555	6041	2290	4157	0.614031404	0.00024	1.53
MRPL21	NM_181514	1320	1180	1357	1604	846	1195	0.614097647	7.89E-05	1.53
QTRT1	NM_031209	104	94	109	118	84	94	0.614101778	0.02501	1.53

CASP3	NM_032991	279	269	393	310	267	288	0.614981961	0.01353	1.53
HRAS	NM_001130442	85	60	79	97	57	69	0.616888386	0.03778	1.53
BAIAP2	NM_017451	785	541	715	861	525	546	0.618449044	0.00288	1.54
BCL7C	NM_004765	441	462	425	544	289	447	0.61860916	0.00155	1.54
OGG1	NM_016820	255	197	258	236	234	187	0.619147685	0.02737	1.54
DDX3X	NM_001356	1730	2044	1944	2688	1150	1774	0.620465161	0.00028	1.54
FRMD5	NM_032892	136	138	157	209	91	129	0.620628845	0.00831	1.54
ADSL	NM_000026	1585	1565	1660	2204	1177	1234	0.620813069	0.00056	1.54
SUPT3H	NM_003599	150	162	153	157	136	149	0.621377768	0.02226	1.54
EIF4H	NM_022170	5855	4732	6592	6371	5045	4341	0.621454528	0.00542	1.54
MTOR	NM_004958	369	298	378	466	205	348	0.621535954	0.00117	1.54
TRIM23	NM_001656	59	62	88	99	54	58	0.621897628	0.04144	1.54
HSPA14	NM_016299	143	147	164	220	108	122	0.623724324	0.00888	1.54
SNRPG	NM_003096	158	140	169	196	102	158	0.623840528	0.00663	1.54
ZNF593	NM_015871	372	351	353	366	319	319	0.624412127	0.01084	1.54
MRPL2	NM_015950	411	299	301	396	255	321	0.625492691	0.00654	1.54
PPP1R14B	NM_138689	3536	3027	3263	4311	2298	2796	0.625889001	0.00013	1.54
WDR77	NM_024102	638	541	700	699	491	563	0.626084169	0.00163	1.54
IRF3	NM_001571	425	313	387	418	323	315	0.626098102	0.00785	1.54
RRP9	NM_004704	282	216	201	293	174	216	0.626338286	0.00867	1.54
NANS	NM_018946	624	548	621	746	451	507	0.626844517	0.00077	1.54
SIVA1	NM_006427	533	502	461	642	386	414	0.62717135	0.00252	1.54
DHPS	NM_001930	628	468	552	631	464	455	0.627323023	0.00522	1.54
RPS28	NM_001031	3965	3037	3968	5150	2627	2814	0.628992873	0.00045	1.55
ATG101	NM_001098673	135	115	103	153	110	87	0.629576024	0.03246	1.55
PSMG4	NM_001128592	337	173	267	322	211	220	0.629853527	0.01628	1.55
EIF4A3	NM_014740	344	300	387	420	287	271	0.630046566	0.00436	1.55
UBA3	NM_003968	534	547	425	570	330	575	0.630103438	0.00628	1.55
NAA10	NM_003491	346	276	305	368	253	264	0.630653278	0.00504	1.55
ZNF511	NM_145806	292	255	351	280	275	276	0.630820544	0.01591	1.55
PFDN5	NM_002624	719	590	475	757	339	705	0.631901271	0.00828	1.55
CUTA	NM_001014433	425	362	448	531	297	359	0.632656567	0.00066	1.55
PLEKHA2	NM_021623	1024	900	1203	1049	936	889	0.632701154	0.00654	1.55
ORC6	NM_014321	311	278	368	423	212	294	0.633279713	0.00075	1.55
PRMT1	NM_001536	2908	2329	2653	3230	1878	2402	0.633382582	0.00017	1.55
TRAPPC2L	NM_016209	735	599	800	911	470	669	0.633539625	0.00015	1.55
SSRP1	NM_003146	1668	1571	1983	1695	1555	1540	0.634454239	0.00598	1.55
WDR34	NM_052844	479	467	498	501	430	419	0.634503868	0.00694	1.55
TAF1A	NM_001201536	98	88	122	128	82	93	0.635317111	0.0175	1.55
FARSA	NM_004461	2939	2533	3318	3441	2246	2556	0.635839509	0.0003	1.55
PTPRN	NM_002846	56	74	78	103	48	65	0.636030884	0.03421	1.55
MRPL14	NM_032111	363	357	353	420	270	342	0.638275247	0.00183	1.56
PARP2	NM_005484	124	100	78	160	61	100	0.639075289	0.02809	1.56
METTL13	NM_015935	123	98	166	144	105	126	0.640624777	0.01722	1.56
CDC6	NM_001254	431	359	326	470	283	339	0.640934177	0.00332	1.56
UQCC2	NM_032340	661	542	671	818	369	655	0.641305834	0.0003	1.56

ZNF576	NM_001145347	145	104	152	182	115	100	0.641667867	0.01683	1.56
UNC45A	NM_018671	436	335	581	571	330	400	0.643128139	0.00195	1.56
GEMIN6	NM_024775	175	184	183	216	130	187	0.644888238	0.00487	1.56
C7orf55	NM_197964	396	347	372	454	293	329	0.644985679	0.00163	1.56
JMJD4	NM_023007	104	72	91	118	69	83	0.645058114	0.02102	1.56
FDX1L	NM_001031734	256	182	223	259	195	185	0.646170192	0.00995	1.57
HYPK	NM_016400	328	307	370	427	198	370	0.647365922	0.00101	1.57
SART3	NM_014706	498	429	608	594	425	437	0.647903466	0.00214	1.57
MANF	NM_006010	1710	1365	1531	1917	1019	1546	0.649159645	0.00012	1.57
PRKCDBP	NM_145040	854	735	858	1092	631	653	0.64927885	0.00049	1.57
GEMIN2	NM_003616	431	402	405	510	297	400	0.649305507	0.00068	1.57
FBL	NM_001436	1376	946	1133	1631	760	1044	0.649548271	0.00043	1.57
FIS1	NM_016068	334	268	260	433	182	265	0.649689858	0.00256	1.57
SLC16A3	NM_001206950	129	128	142	178	83	143	0.651134451	0.00652	1.57
WDR61	NM_025234	158	133	137	190	107	132	0.651145209	0.00692	1.57
WDR83OS	NM_016145	1838	1525	1731	2035	1351	1480	0.651154742	0.00047	1.57
EP300	NM_001429	176	176	72	238	85	158	0.651315769	0.04946	1.57
CCDC51	NM_024661	109	109	165	142	114	117	0.651995382	0.0181	1.57
NIP7	NM_016101	1282	997	1053	1391	749	1126	0.652265448	0.00035	1.57
DCTPP1	NM_024096	1151	1108	1170	1422	718	1226	0.653219888	0.00012	1.57
HSD17B7	NM_016371	78	78	81	103	54	87	0.653293314	0.01997	1.57
AURKA	NM_003600	101	87	143	147	90	94	0.653493411	0.01539	1.57
DNPH1	NM_006443	81	81	152	106	91	112	0.654414892	0.03421	1.57
ATOX1	NM_004045	725	631	781	946	537	595	0.654482297	0.00025	1.57
LMAN2	NM_006816	1717	1685	2020	2163	1350	1673	0.655083666	8.66E-05	1.57
EIF3J	NM_003758	290	244	243	380	168	243	0.65787056	0.00168	1.58
MRPL4	NM_015956	182	154	187	192	143	175	0.658082426	0.00657	1.58
CSTF2	NM_001325	312	271	310	304	304	242	0.658308926	0.01486	1.58
ADORA2B	NM_000676	96	70	73	128	58	68	0.658327143	0.02445	1.58
CD151	NM_001039490	2112	1632	2075	2088	1829	1562	0.658541269	0.00515	1.58
FAM175B	NM_032182	127	141	81	200	72	114	0.660903238	0.02633	1.58
RABAC1	NM_006423	1124	895	1317	1133	925	1088	0.661311251	0.00229	1.58
GIPC1	NM_202470	798	883	977	883	750	889	0.661398346	0.00295	1.58
PMVK	NM_006556	181	194	208	284	137	170	0.66200068	0.00218	1.58
LAMTOR4	NM_001008395	126	76	111	150	75	98	0.662052577	0.01433	1.58
PSMG1	NM_003720	800	623	907	819	595	812	0.663284078	0.00135	1.58
CHST11	NM_018413	83	65	80	109	54	75	0.664039358	0.01829	1.58
FKBP2	NM_004470	619	694	739	762	562	650	0.664758755	0.0012	1.59
NDUFB9	NM_005005	1196	985	1166	1408	790	1072	0.665575019	5.03E-05	1.59
SSR4	NM_001204527	720	628	581	974	419	584	0.665769573	0.00051	1.59
EGLN2	NM_053046	351	359	383	351	360	331	0.667022675	0.01073	1.59
SNF8	NM_007241	467	414	481	575	283	500	0.66716359	0.00032	1.59
S100A16	NM_080388	4148	3398	3712	4424	3003	3436	0.667512195	0.00035	1.59
CLDN12	NM_012129	43	56	77	80	37	72	0.667965067	0.03775	1.59
PALB2	NM_024675	110	95	138	133	81	132	0.669048067	0.01055	1.59
NRIP3	NM_020645	279	214	242	354	153	246	0.669238032	0.00138	1.59

NHP2	NM_017838	758	717	691	931	562	643	0.66934496	0.0004	1.59
NUDT6	NM_007083	75	49	67	90	45	68	0.671689211	0.02623	1.59
DHX16	NM_003587	353	330	439	507	251	361	0.672150686	0.0002	1.59
HEXB	NM_000521	158	134	150	213	92	153	0.67422924	0.00343	1.60
DCAF15	NM_138353	466	400	597	543	443	418	0.674319268	0.00364	1.60
DHX35	NM_021931	210	219	172	269	165	179	0.675393353	0.00547	1.60
CDK14	NM_012395	165	156	243	219	141	201	0.678573044	0.0043	1.60
IFRD2	NM_006764	537	481	574	714	351	529	0.678893543	4.58E-05	1.60
RPS3	NM_001005	12583	11172	11059	14610	6937	13758	0.678898113	0.00028	1.60
RUFY1	NM_025158	365	316	193	356	279	262	0.67959341	0.01854	1.60
ABCF3	NM_018358	331	321	239	426	206	296	0.679674743	0.00275	1.60
HNRNPD	NM_031370	696	684	892	929	525	784	0.680133105	8.05E-05	1.60
NTMT1	NM_014064	159	115	99	167	88	138	0.680472361	0.0125	1.60
C1orf52	NM_198077	114	110	116	150	88	111	0.681193028	0.00628	1.60
PCNA	NM_182649	859	804	947	1122	582	892	0.681733834	1.70E-05	1.60
ALG5	NM_013338	140	171	109	227	86	148	0.682500462	0.01223	1.60
RANBP17	NM_022897	168	164	193	247	74	254	0.683993573	0.01533	1.61
LRRC58	NM_001099678	279	283	374	395	216	326	0.68461272	0.00046	1.61
OXLD1	NM_001039842	52	48	67	78	61	39	0.684879116	0.04274	1.61
RPL18	NM_000979	10241	10226	11569	12783	7777	10809	0.685620127	1.34E-05	1.61
RPL37A	NM_000998	6435	4907	5594	7624	4179	5093	0.685723046	4.86E-05	1.61
PAGR1	NM_024516	388	314	367	493	277	307	0.685924049	0.00051	1.61
HIST1H2BG	NM_003518	703	615	680	896	488	615	0.685989371	5.72E-05	1.61
BAP1	NM_004656	1163	935	1205	1483	750	1069	0.687054144	1.09E-05	1.61
DUSP3	NM_004090	130	136	208	192	142	141	0.689227058	0.00804	1.61
POLR2G	NM_002696	305	261	328	360	242	285	0.690438171	0.00082	1.61
FAM118A	NM_017911	61	42	56	51	52	65	0.692014714	0.04274	1.62
FAH	NM_000137	38	46	34	68	22	50	0.692022876	0.04923	1.62
UQCRH	NM_006004	796	661	747	1010	550	658	0.692161312	7.10E-05	1.62
CCT7	NM_006429	1419	987	1309	1511	940	1228	0.693265686	0.00021	1.62
RUVBL2	NM_006666	662	531	681	848	441	597	0.694012655	3.51E-05	1.62
TJP2	NM_001170416	242	234	303	288	230	250	0.694033637	0.00272	1.62
NME3	NM_002513	87	62	71	100	73	60	0.695579501	0.02345	1.62
MED27	NM_004269	175	154	162	221	133	150	0.695868447	0.00247	1.62
SKA3	NM_145061	197	235	247	251	142	311	0.696842861	0.00598	1.62
TK1	NM_003258	1661	1326	1731	1709	1395	1472	0.697298437	0.00091	1.62
PARL	NM_018622	182	147	166	199	158	143	0.697681391	0.00677	1.62
RPS16	NM_001020	12417	11577	13750	15583	10220	11276	0.697992633	4.27E-05	1.62
PHB2	NM_001144831	1998	1827	1828	2232	1438	1955	0.69930037	0.00011	1.62
PTTG1	NM_004219	313	280	332	405	203	338	0.69997388	0.00024	1.62
R3HCC1	NM_001136108	146	133	141	209	88	149	0.70015882	0.00246	1.62
HIST3H2A	NM_033445	408	322	415	559	247	377	0.700548338	0.00012	1.63
POLR1E	NM_022490	637	569	540	797	372	641	0.700987158	0.00021	1.63
CKS1B	NM_001826	1327	1061	976	1810	597	1261	0.701138671	0.00118	1.63
SNRPB	NM_198216	3846	4167	4090	5620	3194	3424	0.701350476	6.56E-05	1.63
C4orf22	NM_001206997	81	91	101	124	63	103	0.701567399	0.00792	1.63

DGKH	NM_178009	45	35	42	53	36	46	0.701587941	0.03828	1.63
FAM98C	NM_174905	73	65	64	86	52	79	0.70220062	0.01703	1.63
EIF3G	NM_003755	842	608	728	860	641	662	0.704424187	0.00107	1.63
ESRRA	NM_004451	252	290	295	391	206	268	0.708256655	0.00033	1.63
LYSMD1	NM_212551	75	81	93	102	88	70	0.708459507	0.01849	1.63
FDPS	NM_002004	60	53	78	63	43	103	0.70880359	0.03453	1.63
HIST1H2BN	NM_003520	2024	1928	1864	2389	1509	1948	0.709641635	6.40E-05	1.64
HSP90B1	NM_003299	8464	8158	8300	10195	5579	9548	0.710062312	3.00E-05	1.64
FAU	NM_001997	1821	1682	1882	2010	1581	1709	0.710582139	0.0004	1.64
HSPE1	NM_002157	1342	1099	1231	1735	829	1214	0.710648713	7.31E-06	1.64
HYAL2	NM_003773	134	152	141	193	108	148	0.71277396	0.00238	1.64
GLIPR2	NM_022343	170	158	160	227	123	161	0.712986733	0.0013	1.64
PSMD13	NM_002817	350	311	380	453	220	406	0.714822441	0.00023	1.64
GADD45B	NM_015675	232	198	300	313	208	220	0.71520904	0.00125	1.64
NUP37	NM_024057	113	105	129	198	67	118	0.71523042	0.00425	1.64
DYNLL2	NM_080677	268	233	296	325	214	269	0.715627648	0.0005	1.64
HIST1H3B	NM_003537	8499	7233	9260	12784	5333	7910	0.715972234	6.85E-07	1.64
TSSC4	NM_005706	175	141	190	239	116	176	0.71638295	0.0009	1.64
RNF181	NM_016494	205	168	155	214	124	220	0.716998021	0.00385	1.64
PSMC4	NM_006503	1676	1433	2024	1980	1287	1849	0.717261207	6.77E-05	1.64
ABT1	NM_013375	208	160	215	276	146	186	0.718781827	0.00068	1.65
RPS5	NM_001009	3627	2868	3429	4114	2580	3274	0.719125358	2.31E-05	1.65
RUVBL1	NM_003707	854	662	847	948	692	721	0.719186643	0.0004	1.65
FRA10AC1	NM_145246	82	68	63	103	43	94	0.720812181	0.01533	1.65
CHCHD6	NM_032343	63	50	42	71	45	58	0.721196714	0.0251	1.65
MRPL48	NM_016055	89	96	92	146	69	88	0.721503751	0.00576	1.65
TATDN1	NM_032026	98	100	117	133	89	109	0.723122409	0.00468	1.65
KRT18	NM_000224	91	87	102	150	67	89	0.723790699	0.00474	1.65
PPAPDC1A	NM_001030059	34	29	40	56	32	32	0.724556197	0.03799	1.65
EIF2D	NM_006893	66	72	79	87	66	79	0.725148892	0.01255	1.65
AUP1	NM_181575	359	282	348	511	237	297	0.7258816	0.00016	1.65
BAG1	NM_001172415	73	71	71	111	50	78	0.726230396	0.00903	1.65
NDUFB4	NM_004547	1907	1702	1883	2402	1312	1903	0.726397301	2.15E-06	1.65
HSP90AB1	NM_007355	3846	3106	4914	5335	2621	4234	0.727383091	9.71E-06	1.66
SUPT16H	NM_007192	512	470	595	557	481	534	0.728177575	0.00107	1.66
PRMT5	NM_006109	1166	1219	1386	1571	1001	1242	0.728579021	2.15E-05	1.66
FKBP11	NM_016594	70	82	83	118	57	85	0.734206138	0.00675	1.66
HIST2H2AB	NM_175065	1315	1203	1435	1897	915	1295	0.73421241	3.68E-07	1.66
PRELID1	NM_013237	1593	1429	1707	2133	938	1927	0.735458552	3.42E-05	1.66
CTNNBL1	NM_030877	476	401	399	521	307	506	0.735699904	0.00035	1.67
CAMTA1	NM_015215	57	48	57	67	45	68	0.737572936	0.01731	1.67
LUC7L3	NM_016424	428	347	386	453	281	477	0.74016029	0.00046	1.67
SRPX	NM_006307	300	365	394	442	324	325	0.740522425	0.00082	1.67
PSMA7	NM_002792	3544	2987	3344	3649	2753	3597	0.743274573	0.00015	1.67
MRPL54	NM_172251	129	93	128	188	89	107	0.743692095	0.00249	1.67
RPS19	NM_001022	11878	11182	11040	16521	7749	11805	0.745209212	6.26E-07	1.68

DUS3L	NM_020175	144	120	122	162	108	143	0.747288611	0.00252	1.68
PTGES2	NM_025072	257	213	331	340	220	271	0.747385217	0.0004	1.68
RECK	NM_021111	41	26	47	49	39	43	0.748817042	0.03079	1.68
C14orf2	NM_004894	1806	1514	2003	2132	1524	1742	0.749101043	5.17E-05	1.68
KIAA0101	NM_014736	968	1089	1070	1395	848	1014	0.75116234	2.17E-05	1.68
TMEM160	NM_017854	265	217	286	324	216	260	0.751625794	0.00031	1.68
KRTCAP2	NM_173852	855	593	882	1034	658	718	0.751645582	0.00012	1.68
PAPD5	NM_001040284	113	108	153	173	110	117	0.751732644	0.00222	1.68
GRB14	NM_004490	39	33	37	53	36	39	0.755764508	0.02558	1.69
UROD	NM_000374	735	631	807	1051	483	777	0.757309969	1.54E-06	1.69
AP2A1	NM_014203	663	621	554	856	669	432	0.758725142	0.00373	1.69
TIMM10	NM_012456	539	521	449	731	349	563	0.761418787	7.91E-05	1.70
EPHA2	NM_004431	939	873	1088	1011	985	940	0.761725132	0.00113	1.70
LSP1	NM_001013253	28	27	25	43	24	33	0.761974141	0.03549	1.70
CKS2	NM_001827	326	297	395	462	206	437	0.762591465	0.00022	1.70
GSTO1	NM_004832	157	117	140	184	121	141	0.762992639	0.00149	1.70
CHCHD10	NM_213720	331	281	412	492	246	354	0.763290532	3.21E-05	1.70
EMC8	NM_006067	323	276	260	363	271	277	0.765739164	0.0009	1.70
ROMO1	NM_080748	1046	780	934	1393	565	1074	0.769191801	2.30E-05	1.70
C14orf80	NM_001134875	101	95	108	150	62	133	0.769332427	0.00266	1.70
PITRM1	NM_001242307	164	137	154	233	104	168	0.770065415	0.00045	1.71
LZIC	NM_032368	113	128	108	171	81	142	0.771136551	0.00194	1.71
SF3B5	NM_031287	825	725	758	1037	502	966	0.772973274	3.42E-05	1.71
RPS14	NM_001025070	476	361	295	722	201	441	0.773197379	0.00235	1.71
TMED9	NM_017510	1620	1272	1665	2014	1255	1495	0.773580421	5.50E-06	1.71
ATXN10	NM_013236	584	654	663	1095	352	730	0.777689854	9.22E-05	1.71
PSMD3	NM_002809	870	631	842	968	704	778	0.779339743	0.00011	1.72
OTUD3	NM_015207	78	67	59	93	59	82	0.780920296	0.00698	1.72
RPP21	NM_001199120	97	90	128	176	80	101	0.781352876	0.00151	1.72
HIST1H2AK	NM_003510	244	245	220	338	193	245	0.781770228	0.00018	1.72
SCO1	NM_004589	110	103	122	152	87	132	0.782758189	0.00109	1.72
CENPH	NM_022909	63	74	66	95	57	81	0.782769884	0.00588	1.72
DIO2	NM_013989	18	16	31	36	22	27	0.78441187	0.03886	1.72
CRLS1	NM_019095	192	186	232	254	142	272	0.78456814	0.00049	1.72
COX5B	NM_001862	899	752	993	1194	748	850	0.784965011	6.77E-06	1.72
MRPL24	NM_145729	1034	660	695	1252	562	870	0.787008893	0.00016	1.73
ATP5E	NM_006886	536	622	727	831	382	884	0.789929414	0.00024	1.73
MAGOHB	NM_018048	2065	1739	1545	2073	1485	2192	0.790734163	0.00023	1.73
MKKS	NM_170784	68	58	76	92	48	94	0.790800588	0.00576	1.73
DAPK3	NM_001348	353	295	360	394	377	294	0.791630643	0.00184	1.73
KIAA2013	NM_138346	128	157	170	210	148	142	0.792949879	0.00118	1.73
RPL35	NM_007209	7332	6658	7466	8884	5308	8742	0.794649284	2.53E-06	1.73
EMG1	NM_006331	677	579	732	834	551	726	0.795455007	1.03E-05	1.74
IGFBP6	NM_002178	239	179	188	291	180	199	0.795621733	0.00042	1.74
RPS21	NM_001024	5098	5400	5295	6550	5007	5156	0.798862329	5.17E-05	1.74
NDUFA13	NM_015965	1514	1326	1454	1868	1250	1475	0.805498165	4.96E-06	1.75

DACT3	NM_145056	17	35	40	45	36	36	0.805898031	0.02672	1.75
EIF6	NM_181468	1948	1618	2309	2559	1947	1721	0.806627037	0.00012	1.75
HIST1H2AB	NM_003513	898	860	853	1355	675	861	0.807158499	8.03E-07	1.75
COX6B1	NM_001863	2294	1955	2000	2757	1710	2291	0.80796762	2.77E-06	1.75
EBP	NM_006579	293	248	298	349	192	396	0.808913199	0.00028	1.75
CRABP2	NM_001878	337	310	305	374	312	344	0.809837203	0.0004	1.75
SSNA1	NM_003731	278	253	291	438	189	301	0.810680225	1.03E-05	1.75
OTOGL	NM_173591	10	15	23	26	17	26	0.811194851	0.04042	1.75
NTHL1	NM_002528	103	79	83	147	75	89	0.813405589	0.00181	1.76
PAAF1	NM_025155	260	140	137	304	119	229	0.813410326	0.00277	1.76
URM1	NM_001135947	157	146	178	304	100	167	0.814017072	0.00032	1.76
HIST1H3G	NM_003534	4515	3985	4223	6057	3117	4802	0.81437107	5.44E-08	1.76
RAB34	NM_001144943	754	763	777	923	690	856	0.81462959	3.61E-05	1.76
BOP1	NM_015201	371	298	311	487	308	295	0.815359079	0.00016	1.76
DKK1	NM_012242	61	59	71	114	40	80	0.817166105	0.00384	1.76
RPS3A	NM_001006	4770	4791	4482	7541	2791	5963	0.818644042	9.17E-06	1.76
UBE2S	NM_014501	3379	2654	3119	4455	2160	3533	0.819192372	1.27E-07	1.76
BRMS1	NM_001024957	607	612	361	794	427	629	0.822048797	0.00064	1.77
BCL2L12	NM_138639	822	686	730	895	766	754	0.823555043	0.00021	1.77
DPH5	NM_001077394	101	88	93	140	80	107	0.825299382	0.0009	1.77
CHCHD2	NM_016139	2954	2586	2879	3745	2233	3214	0.826412471	2.00E-07	1.77
NEDD8	NM_006156	381	334	622	484	634	616	0.826704349	0.03373	1.77
PSMD14	NM_005805	746	930	1071	1342	630	1126	0.826770307	4.56E-06	1.77
COL17A1	NM_000494	25	34	48	42	40	51	0.828156057	0.018	1.78
HIST1H4C	NM_003542	7431	7443	7468	11272	6082	7404	0.828346998	5.33E-08	1.78
MRTO4	NM_016183	715	601	660	813	654	677	0.828836324	8.77E-05	1.78
HIST1H2BD	NM_021063	6673	6072	6892	8357	5627	7264	0.830442618	6.84E-07	1.78
NDUFS5	NM_001184979	844	671	622	945	464	1076	0.830986458	0.00031	1.78
COMMD8	NM_017845	90	68	102	137	53	124	0.831259345	0.00208	1.78
PRDX4	NM_006406	88	67	67	128	55	88	0.833063423	0.00218	1.78
NDUFV1	NM_007103	2142	1865	2419	2807	1892	2265	0.835362404	9.08E-07	1.78
PSMC1	NM_002802	969	972	1434	1486	1088	1090	0.835735318	4.27E-05	1.78
TEX264	NM_001129884	132	113	101	191	96	123	0.836118153	0.00057	1.79
LAMTOR2	NM_014017	364	350	378	475	346	383	0.836727683	3.80E-05	1.79
ATP5G1	NM_001002027	297	374	408	556	276	397	0.837976976	6.80E-06	1.79
RPS12	NM_001016	7912	6938	8511	10403	6657	8498	0.845342868	8.76E-08	1.80
LGALS1	NM_002305	7757	5374	6310	9631	6338	5790	0.845364453	3.97E-05	1.80
HIST1H1A	NM_005325	447	353	255	688	251	381	0.852054834	0.00043	1.81
CEBPZ	NM_005760	138	140	91	209	71	197	0.856100911	0.00268	1.81
PCOLCE	NM_002593	384	431	347	561	357	417	0.857100607	3.64E-05	1.81
AUH	NM_001698	45	40	47	73	39	55	0.860307497	0.00457	1.82
IMP4	NM_033416	554	501	558	727	510	567	0.861021327	5.86E-06	1.82
GEM	NM_005261	345	370	449	536	315	468	0.861099345	2.53E-06	1.82
HIST1H4F	NM_003540	1743	1324	1374	2546	916	1914	0.865574033	8.64E-06	1.82
POLR2L	NM_021128	2731	2277	2538	3538	2324	2600	0.867633832	6.26E-07	1.82
TBRG4	NM_004749	532	419	407	641	406	519	0.872348822	1.34E-05	1.83

C3orf52	NM_024616	36	16	36	51	26	44	0.873543724	0.0125	1.83
PSMD4	NM_002810	42	23	31	34	67	29	0.877095978	0.02253	1.84
HIST1H2BE	NM_003523	1210	848	1004	1584	750	1279	0.885275068	6.54E-07	1.85
TRPV2	NM_016113	83	85	78	148	53	115	0.886077604	0.00078	1.85
COX7B	NM_001866	2462	2019	2343	3215	1631	3123	0.886358846	4.04E-07	1.85
AP2S1	NM_004069	1261	1064	1356	1987	865	1471	0.887320208	3.30E-09	1.85
NDUFA1	NM_004541	1205	976	1072	1805	846	1185	0.889709316	1.72E-08	1.85
SPHK1	NM_182965	829	700	885	1052	776	902	0.89051798	2.15E-06	1.85
CCT3	NM_005998	1651	2053	1616	2721	1424	2213	0.897654326	1.17E-06	1.86
HIST1H4B	NM_003544	2112	1736	1745	2756	1431	2419	0.897803276	2.52E-07	1.86
HIST3H2BB	NM_175055	632	707	676	975	600	771	0.898665456	3.79E-07	1.86
MYDGF	NM_019107	343	299	400	436	332	432	0.902947462	1.31E-05	1.87
IFI27L2	NM_032036	56	45	95	66	90	87	0.907095874	0.00635	1.88
ARMC10	NM_001161009	104	76	94	150	88	101	0.907592323	0.00028	1.88
RNF121	NM_018320	267	195	270	384	270	217	0.908033029	0.00011	1.88
NDUFS6	NM_004553	532	395	413	691	395	513	0.910341982	1.87E-06	1.88
METTL1	NM_005371	91	90	98	186	73	101	0.916284385	0.00018	1.89
EIF4E2	NM_004846	149	105	117	215	88	172	0.923109028	0.00011	1.90
UQCC3	NM_001085372	207	202	253	375	167	269	0.923255909	8.21E-07	1.90
ANO3	NM_031418	17	8	10	30	15	18	0.925132836	0.01791	1.90
KRTAP2-3	NM_001165252	11	9	20	32	16	20	0.925886516	0.01628	1.90
ATP5G3	NM_001002258	1530	1156	1467	2089	1254	1545	0.926903335	1.96E-08	1.90
C12orf73	NM_001135570	29	31	27	51	34	38	0.931108262	0.00544	1.91
UTP18	NM_016001	235	218	247	384	173	307	0.931549035	8.21E-07	1.91
HIST1H2BI	NM_003525	2080	1622	1767	3054	1324	2348	0.932283848	1.96E-08	1.91
MTFP1	NM_016498	189	118	151	240	147	179	0.932594882	5.62E-05	1.91
PARK7	NM_007262	3058	2492	2624	3841	2668	3120	0.933700321	3.08E-07	1.91
MCTS1	NM_014060	17	10	13	27	12	32	0.947140725	0.01379	1.93
PDIA6	NM_005742	2194	2184	2240	3207	1825	2953	0.949416632	4.64E-09	1.93
WDR46	NM_005452	141	122	190	151	155	257	0.950743281	0.00074	1.93
SYTL3	NM_001242384	142	122	109	265	95	142	0.953084363	6.94E-05	1.94
HIST1H4E	NM_003545	2510	1737	2150	3628	1849	2375	0.953907633	9.98E-09	1.94
LSM7	NM_016199	750	529	611	953	524	848	0.953959751	3.30E-07	1.94
IL24	NM_001185156	17	32	30	57	18	51	0.958041274	0.00653	1.94
TMEM208	NM_014187	145	125	131	239	106	176	0.969062364	6.77E-06	1.96
ATP5I	NM_007100	426	225	242	473	276	411	0.971822471	6.89E-05	1.96
EED	NM_003797	155	113	150	203	108	233	0.975965773	5.92E-05	1.97
CCDC47	NM_020198	488	363	312	578	348	586	0.99345379	9.71E-06	1.99
NDUFA8	NM_014222	404	399	432	642	349	566	0.994316681	9.17E-09	1.99
SLC50A1	NM_018845	176	196	234	306	202	259	0.99955655	1.04E-06	2.00
PSMC3	NM_002804	2092	1625	2286	2628	2296	2377	1.001605124	1.33E-06	2.00
RRP15	NM_016052	114	90	105	174	96	139	1.004497455	1.19E-05	2.01
DYNLT1	NM_006519	420	318	401	595	319	554	1.016280392	4.37E-08	2.02
HIST1H4H	NM_003543	5539	5078	3899	8708	3478	7757	1.021391999	1.01E-06	2.03
MMP3	NM_002422	43	42	42	61	50	72	1.028198627	0.00074	2.04
TMEM203	NM_053045	49	51	38	89	52	64	1.04749031	0.00032	2.07

CYC1	NM_001916	548	407	528	900	500	603	1.092430801	1.23E-10	2.13
POLR3K	NM_016310	273	247	279	435	271	376	1.096122651	2.86E-09	2.14
NOSIP	NM_015953	310	191	301	396	323	373	1.106828322	9.71E-07	2.15
SLCO4A1	NM_016354	42	28	29	57	42	63	1.124202852	0.00035	2.18
CARNMT1	NM_152420	24	23	23	47	31	45	1.149888996	0.00043	2.22
HIST1H4A	NM_003538	1941	1582	1666	2885	2214	2146	1.158358159	3.30E-09	2.23
TSEN54	NM_207346	35	34	47	82	54	59	1.211235891	2.38E-05	2.32
NDUFA2	NM_002488	399	332	210	676	359	487	1.224791363	1.11E-07	2.34
ZBED2	NM_024508	55	65	43	191	61	126	1.541948147	2.84E-09	2.91

Table S5. Gene Ontology terms overrepresented among the differentiating genes (q.value <0.05) in PROX1 depleted cells. ID–GO identifier, GeneRatio – the ratio of number of differentiating genes in a given term to the number of differentiating genes with GO identifier ; BgRatio—the ratio of number of not differentiating genes in a given term to the number of expressed genes with GO identifier; p-value-p-value in hypergeometric test; q-value-p-value after FDR correction; Count—number of differentiating genes contributing to a given term; BP—biological processes BP, MF—molecular function; CC—cellular component.

Biological Process - upregulated							
ID	**Description**	**GeneRatio**	**BgRatio**	**pvalue**	**p.adjust**	**qvalue**	**Count**
GO:0022613	ribonucleoprotein complex biogenesis	98/675	410/8624	4.2E-25	1.5E-21	1.37E-21	98
GO:0006413	translational initiation	54/675	166/8624	1.17E-20	1.73E-17	1.58E-17	54
GO:0006364	rRNA processing	64/675	230/8624	3.07E-20	2.74E-17	2.5E-17	64
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	35/675	82/8624	4.26E-18	2.53E-15	2.31E-15	35
GO:0019080	viral gene expression	48/675	160/8624	7.23E-17	2.86E-14	2.61E-14	48
GO:0072599	establishment of protein localization to endoplasmic reticulum	35/675	90/8624	1.48E-16	5.29E-14	4.83E-14	35
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	37/675	107/8624	1.76E-15	5.21E-13	4.76E-13	37
GO:0019083	viral transcription	44/675	149/8624	2.82E-15	7.72E-13	7.05E-13	44
GO:0044033	multi-organism metabolic process	48/675	177/8624	5.96E-15	1.42E-12	1.29E-12	48
GO:0022618	ribonucleoprotein complex assembly	43/675	176/8624	7.68E-12	1.3E-09	1.19E-09	43
GO:1901361	organic cyclic compound catabolic process	58/675	296/8624	3.22E-11	4.99E-09	4.56E-09	58
GO:0071826	ribonucleoprotein complex subunit organization	43/675	185/8624	4.48E-11	6.65E-09	6.07E-09	43
GO:0019439	aromatic compound catabolic process	57/675	292/8624	5.63E-11	8.03E-09	7.33E-09	57
GO:0006323	DNA packaging	36/675	139/8624	6.84E-11	9.38E-09	8.56E-09	36
GO:0046700	heterocycle catabolic process	56/675	289/8624	1.13E-10	1.49E-08	1.36E-08	56
GO:0044270	cellular nitrogen compound catabolic process	56/675	292/8624	1.71E-10	2.18E-08	1.99E-08	56
GO:0051290	protein heterotetramerization	15/675	28/8624	3.12E-10	3.7E-08	3.38E-08	15
GO:0006334	nucleosome assembly	29/675	101/8624	3.55E-10	4.09E-08	3.73E-08	29
GO:0034728	nucleosome organization	32/675	122/8624	5.62E-10	6.26E-08	5.71E-08	32

GO:0065004	protein-DNA complex assembly	38/675	165/8624	8.23E-10	8.62E-08	7.87E-08	38
GO:0019058	viral life cycle	59/675	329/8624	8.61E-10	8.76E-08	8E-08	59
GO:0006119	oxidative phosphorylation	25/675	83/8624	1.97E-09	1.85E-07	1.69E-07	25
GO:0045815	positive regulation of gene expression, epigenetic	20/675	63/8624	3.06E-08	2.47E-06	2.26E-06	20
GO:0006342	chromatin silencing	22/675	76/8624	4.14E-08	3.14E-06	2.86E-06	22
GO:0022900	electron transport chain	22/675	81/8624	1.45E-07	9.97E-06	9.1E-06	22
GO:0022904	respiratory electron transport chain	22/675	81/8624	1.45E-07	9.97E-06	9.1E-06	22
GO:0009126	purine nucleoside monophosphate metabolic process	38/675	198/8624	1.59E-07	1.05E-05	9.58E-06	38
GO:0009167	purine ribonucleoside monophosphate metabolic process	38/675	198/8624	1.59E-07	1.05E-05	9.58E-06	38
GO:1904872	regulation of telomerase RNA localization to Cajal body	9/675	15/8624	3.41E-07	2.06E-05	1.88E-05	9
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	9/675	15/8624	3.41E-07	2.06E-05	1.88E-05	9
GO:0031145	anaphase-promoting complex-dependent catabolic process	19/675	70/8624	1.04E-06	5.25E-05	4.79E-05	19
GO:0097031	mitochondrial respiratory chain complex I biogenesis	16/675	52/8624	1.19E-06	5.37E-05	4.91E-05	16
GO:0045653	negative regulation of megakaryocyte differentiation	7/675	11/8624	4.36E-06	0.000183	0.000167	7
GO:0006457	protein folding	30/675	164/8624	8.89E-06	0.000333	0.000304	30
GO:0033238	regulation of cellular amine metabolic process	14/675	49/8624	1.45E-05	0.000506	0.000462	14
GO:0051444	negative regulation of ubiquitin-protein transferase activity	17/675	70/8624	1.95E-05	0.000648	0.000592	17
GO:1904668	positive regulation of ubiquitin protein ligase activity	17/675	70/8624	1.95E-05	0.000648	0.000592	17
GO:0006091	generation of precursor metabolites and energy	38/675	240/8624	2.02E-05	0.000653	0.000596	38
GO:1901657	glycosyl compound metabolic process	42/675	278/8624	2.39E-05	0.000761	0.000695	42
GO:0000387	spliceosomal snRNP assembly	11/675	35/8624	4.54E-05	0.001363	0.001244	11
GO:0030162	regulation of proteolysis	53/675	394/8624	5.9E-05	0.001722	0.001572	53
GO:0002220	innate immune response activating cell surface receptor signaling pathway	17/675	78/8624	8.56E-05	0.002365	0.002159	17
GO:0002223	stimulatory C-type lectin receptor signaling pathway	17/675	78/8624	8.56E-05	0.002365	0.002159	17
GO:0042176	regulation of protein catabolic process	40/675	275/8624	8.89E-05	0.002435	0.002223	40
GO:0002479	antigen processing and presentation of exogenous	12/675	44/8624	9.77E-05	0.002618	0.00239	12

	peptide antigen via MHC class I, TAP-dependent						
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	12/675	44/8624	9.77E-05	0.002618	0.00239	12
GO:0022411	cellular component disassembly	50/675	380/8624	0.000167	0.004153	0.003791	50
GO:0042776	mitochondrial ATP synthesis coupled proton transport	7/675	17/8624	0.000169	0.004183	0.003819	7
GO:0006289	nucleotide-excision repair	19/675	98/8624	0.000177	0.004317	0.003941	19
GO:0038061	NIK/NF-kappaB signaling	17/675	84/8624	0.000224	0.00526	0.004801	17
GO:0009894	regulation of catabolic process	47/675	355/8624	0.000226	0.00526	0.004801	47
GO:0030219	megakaryocyte differentiation	9/675	29/8624	0.000251	0.005658	0.005165	9
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	17/675	86/8624	0.000301	0.006742	0.006155	17
GO:0007339	binding of sperm to zona pellucida	6/675	14/8624	0.000391	0.008393	0.007662	6
GO:0035036	sperm-egg recognition	6/675	14/8624	0.000391	0.008393	0.007662	6
GO:0031349	positive regulation of defense response	30/675	202/8624	0.000464	0.009724	0.008877	30
GO:0045727	positive regulation of translation	14/675	66/8624	0.000477	0.009889	0.009027	14
GO:0070203	regulation of establishment of protein localization to telomere	5/675	10/8624	0.000523	0.010702	0.00977	5
GO:0015985	energy coupled proton transport, down electrochemical gradient	7/675	20/8624	0.000547	0.010824	0.009882	7
GO:0019693	ribose phosphate metabolic process	40/675	307/8624	0.000899	0.016513	0.015075	40
GO:0001736	establishment of planar polarity	17/675	95/8624	0.000999	0.017971	0.016405	17
GO:0007164	establishment of tissue polarity	17/675	95/8624	0.000999	0.017971	0.016405	17
GO:0051897	positive regulation of protein kinase B signaling	10/675	42/8624	0.001189	0.020877	0.019058	10
GO:0033209	tumor necrosis factor-mediated signaling pathway	16/675	91/8624	0.001686	0.027943	0.025508	16
GO:0051169	nuclear transport	41/675	334/8624	0.002463	0.03883	0.035448	41
GO:0009988	cell-cell recognition	6/675	19/8624	0.002517	0.038994	0.035597	6
GO:0060765	regulation of androgen receptor signaling pathway	6/675	19/8624	0.002517	0.038994	0.035597	6
GO:0032481	positive regulation of type I interferon production	11/675	54/8624	0.002657	0.040625	0.037086	11
GO:0031329	regulation of cellular catabolic process	34/675	267/8624	0.003113	0.046208	0.042183	34
GO:0006940	regulation of smooth muscle contraction	6/675	20/8624	0.003361	0.048685	0.044444	6
GO:1905330	regulation of morphogenesis of an epithelium	18/675	115/8624	0.003424	0.049388	0.045086	18
Molecular Function - upregulated							
GO:0003735	structural constituent of ribosome	53/661	169/8488	1.37E-19	8.22E-17	7.55E-17	53

GO:0019843	rRNA binding	18/661	56/8488	1.12E-07	2.24E-05	2.06E-05	18
GO:0046982	protein heterodimerization activity	42/661	257/8488	2.84E-06	0.000425	0.000391	42
GO:0051082	unfolded protein binding	19/661	79/8488	6.88E-06	0.000687	0.000631	19
GO:0003954	NADH dehydrogenase activity	11/661	35/8488	4.33E-05	0.002838	0.002608	11
GO:0008137	NADH dehydrogenase (ubiquinone) activity	11/661	35/8488	4.33E-05	0.002838	0.002608	11
GO:0050136	NADH dehydrogenase (quinone) activity	11/661	35/8488	4.33E-05	0.002838	0.002608	11
GO:0043021	ribonucleoprotein complex binding	19/661	93/8488	7.94E-05	0.004322	0.003972	19
GO:0045296	cadherin binding	36/661	260/8488	0.000473	0.018892	0.017363	36
GO:0098631	protein binding involved in cell adhesion	36/661	260/8488	0.000473	0.018892	0.017363	36
GO:0070628	proteasome binding	5/661	10/8488	0.000511	0.019122	0.017575	5
GO:0015078	hydrogen ion transmembrane transporter activity	13/661	60/8488	0.000579	0.019559	0.017976	13
GO:0008026	ATP-dependent helicase activity	16/661	84/8488	0.000653	0.019559	0.017976	16
GO:0070035	purine NTP-dependent helicase activity	16/661	84/8488	0.000653	0.019559	0.017976	16
GO:0001054	RNA polymerase I activity	5/661	12/8488	0.001407	0.035474	0.032603	5
GO:0016779	nucleotidyltransferase activity	18/661	107/8488	0.001421	0.035474	0.032603	18
GO:0046933	proton-transporting ATP synthase activity, rotational mechanism	5/661	13/8488	0.002141	0.047503	0.043659	5
Cellular Component - upregulated							
GO:0005840	ribosome	60/693	189/9021	1.27E-22	6.16E-20	5.18E-20	60
GO:0044445	cytosolic part	54/693	166/9021	5.19E-21	1.26E-18	1.06E-18	54
GO:0044815	DNA packaging complex	33/693	67/9021	9.35E-20	1.13E-17	9.52E-18	33
GO:0000786	nucleosome	31/693	61/9021	3.79E-19	3.06E-17	2.57E-17	31
GO:0005743	mitochondrial inner membrane	76/693	363/9021	1.85E-16	1.28E-14	1.08E-14	76
GO:0032993	protein-DNA complex	38/693	117/9021	4.25E-15	2.58E-13	2.16E-13	38
GO:0070469	respiratory chain	23/693	67/9021	3.38E-10	1.17E-08	9.84E-09	23
GO:0098803	respiratory chain complex	19/693	56/9021	1.48E-08	3.98E-07	3.34E-07	19
GO:0005852	eukaryotic translation initiation factor 3 complex	8/693	15/9021	4.61E-06	7.46E-05	6.26E-05	8
GO:0031012	extracellular matrix	35/693	224/9021	3.89E-05	0.000553	0.000464	35
GO:1905369	endopeptidase complex	14/693	59/9021	0.000112	0.00133	0.001117	14
GO:1905368	peptidase complex	16/693	75/9021	0.000145	0.001597	0.001341	16
GO:0005682	U5 snRNP	6/693	14/9021	0.000353	0.003296	0.002768	6
GO:0005913	cell-cell adherens junction	35/693	270/9021	0.001478	0.012355	0.010378	35
GO:0070069	cytochrome complex	5/693	16/9021	0.005638	0.039063	0.032811	5
Biological Process - downregulated							
GO:0051270	regulation of cellular component movement	51/422	405/8624	2.79E-10	5.27E-07	4.54E-07	51
GO:0040012	regulation of locomotion	50/422	395/8624	3.53E-10	5.27E-07	4.54E-07	50
GO:2000145	regulation of cell motility	49/422	387/8624	5.35E-10	5.27E-07	4.54E-07	49

GO:0031175	neuron projection development	53/422	440/8624	6.26E-10	5.27E-07	4.54E-07	53
GO:0060284	regulation of cell development	48/422	418/8624	2.08E-08	9.99E-06	8.6E-06	48
GO:0048589	developmental growth	37/422	309/8624	3.4E-07	8.79E-05	7.56E-05	37
GO:0030198	extracellular matrix organization	24/422	155/8624	4.42E-07	9.28E-05	7.99E-05	24
GO:0043062	extracellular structure organization	24/422	155/8624	4.42E-07	9.28E-05	7.99E-05	24
GO:0008285	negative regulation of cell proliferation	40/422	354/8624	5.23E-07	0.000104	8.92E-05	40
GO:0051493	regulation of cytoskeleton organization	30/422	249/8624	4.03E-06	0.000589	0.000507	30
GO:0051384	response to glucocorticoid	13/422	63/8624	8.55E-06	0.00115	0.00099	13
GO:0009743	response to carbohydrate	18/422	115/8624	1.06E-05	0.001319	0.001136	18
GO:0014065	phosphatidylinositol 3-kinase signaling	13/422	73/8624	4.51E-05	0.003608	0.003107	13
GO:0032970	regulation of actin filament-based process	21/422	170/8624	7.97E-05	0.005253	0.004523	21
GO:0032535	regulation of cellular component size	22/422	191/8624	0.000154	0.00823	0.007087	22
GO:0030278	regulation of ossification	14/422	95/8624	0.000196	0.009986	0.008599	14
GO:0010810	regulation of cell-substrate adhesion	15/422	107/8624	0.000207	0.010218	0.008798	15
GO:0010463	mesenchymal cell proliferation	7/422	27/8624	0.000242	0.01129	0.009722	7
GO:0071385	cellular response to glucocorticoid stimulus	7/422	27/8624	0.000242	0.01129	0.009722	7
GO:0050673	epithelial cell proliferation	21/422	185/8624	0.000266	0.012075	0.010397	21
GO:0006935	chemotaxis	23/422	213/8624	0.000288	0.012915	0.01112	23
GO:0090066	regulation of anatomical structure size	24/422	229/8624	0.000335	0.014434	0.012429	24
GO:0043068	positive regulation of programmed cell death	32/422	346/8624	0.000368	0.015085	0.012989	32
GO:0050900	leukocyte migration	16/422	125/8624	0.000372	0.015085	0.012989	16
GO:0015804	neutral amino acid transport	5/422	14/8624	0.00038	0.015085	0.012989	5
GO:1905276	regulation of epithelial tube formation	5/422	14/8624	0.00038	0.015085	0.012989	5
GO:0010631	epithelial cell migration	17/422	138/8624	0.000389	0.015085	0.012989	17
GO:0090132	epithelium migration	17/422	138/8624	0.000389	0.015085	0.012989	17
GO:0032271	regulation of protein polymerization	14/422	102/8624	0.000417	0.015941	0.013727	14
GO:0007610	behavior	24/422	233/8624	0.000433	0.016163	0.013918	24
GO:1903825	organic acid transmembrane transport	7/422	31/8624	0.000604	0.020519	0.017668	7
GO:1905039	carboxylic acid transmembrane transport	7/422	31/8624	0.000604	0.020519	0.017668	7
GO:0071417	cellular response to organonitrogen compound	26/422	268/8624	0.000637	0.02143	0.018453	26
GO:0031589	cell-substrate adhesion	20/422	184/8624	0.000651	0.02143	0.018453	20
GO:0010001	glial cell differentiation	13/422	96/8624	0.000758	0.023592	0.020315	13
GO:1901699	cellular response to nitrogen compound	29/422	316/8624	0.000782	0.02391	0.020588	29

GO:0061448	connective tissue development	15/422	121/8624	0.000791	0.023964	0.020635	15
GO:0061387	regulation of extent of cell growth	9/422	53/8624	0.00096	0.027585	0.023753	9
GO:1901698	response to nitrogen compound	38/422	461/8624	0.001023	0.028663	0.024681	38
GO:0044087	regulation of cellular component biogenesis	38/422	462/8624	0.001065	0.029593	0.025482	38
GO:0090288	negative regulation of cellular response to growth factor stimulus	11/422	76/8624	0.00109	0.03005	0.025876	11
GO:0014070	response to organic cyclic compound	38/422	464/8624	0.001153	0.031027	0.026716	38
GO:0070373	negative regulation of ERK1 and ERK2 cascade	7/422	35/8624	0.001304	0.034266	0.029505	7
GO:1901655	cellular response to ketone	8/422	45/8624	0.001343	0.035	0.030138	8
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	10/422	67/8624	0.001432	0.036478	0.03141	10
GO:0051093	negative regulation of developmental process	33/422	393/8624	0.001607	0.04043	0.034813	33
GO:0043269	regulation of ion transport	19/422	184/8624	0.001628	0.04043	0.034813	19
GO:0009611	response to wounding	28/422	316/8624	0.001635	0.04043	0.034813	28
GO:0030203	glycosaminoglycan metabolic process	11/422	81/8624	0.001854	0.043291	0.037276	11
GO:0090342	regulation of cell aging	6/422	28/8624	0.00199	0.04584	0.039471	6
GO:0010563	negative regulation of phosphorus metabolic process	27/422	306/8624	0.002092	0.046598	0.040124	27
GO:0045936	negative regulation of phosphate metabolic process	27/422	306/8624	0.002092	0.046598	0.040124	27
GO:0003013	circulatory system process	18/422	178/8624	0.002694	0.053748	0.046281	18
GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	4/422	13/8624	0.002839	0.055729	0.047986	4
GO:0198738	cell-cell signaling by wnt	27/422	314/8624	0.003013	0.057246	0.049293	27
Molecular Function - downregulated							
GO:0035591	signaling adaptor activity	9/413	36/8488	4.08E-05	0.014981	0.013383	9
GO:0005070	SH3/SH2 adaptor activity	7/413	23/8488	7.63E-05	0.014981	0.013383	7
GO:0017022	myosin binding	8/413	31/8488	8.61E-05	0.014981	0.013383	8
GO:0019838	growth factor binding	12/413	72/8488	0.000162	0.016891	0.015089	12
GO:0004871	signal transducer activity	38/413	437/8488	0.000326	0.028337	0.025314	38
GO:0015175	neutral amino acid transmembrane transporter activity	5/413	15/8488	0.000533	0.039726	0.035488	5
GO:0008201	heparin binding	9/413	52/8488	0.000798	0.047426	0.042367	9
GO:0000982	transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	20/413	189/8488	0.00085	0.047426	0.042367	20
GO:0001077	transcriptional activator activity, RNA polymerase II core promoter proximal	15/413	124/8488	0.000963	0.047426	0.042367	15

	region sequence-specific binding						
GO:0001228	transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	18/413	164/8488	0.000999	0.047426	0.042367	18
GO:0019904	protein domain specific binding	33/413	387/8488	0.001126	0.048963	0.04374	33
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	6/413	26/8488	0.001283	0.050206	0.044851	6
GO:0016303	1-phosphatidylinositol-3-kinase activity	5/413	18/8488	0.001347	0.050206	0.044851	5
GO:0005539	glycosaminoglycan binding	10/413	68/8488	0.001539	0.053564	0.04785	10
Cellular Component - downregulated							
GO:0005578	proteinaceous extracellular matrix	22/439	115/9021	2.62E-08	9.82E-06	9.17E-06	22
GO:0044420	extracellular matrix component	14/439	57/9021	3.82E-07	7.15E-05	6.69E-05	14
GO:0005615	extracellular space	34/439	393/9021	0.000752	0.049225	0.046013	34
GO:0043235	receptor complex	15/439	122/9021	0.000819	0.049225	0.046013	15
GO:0098644	complex of collagen trimers	4/439	10/9021	0.000919	0.049225	0.046013	4