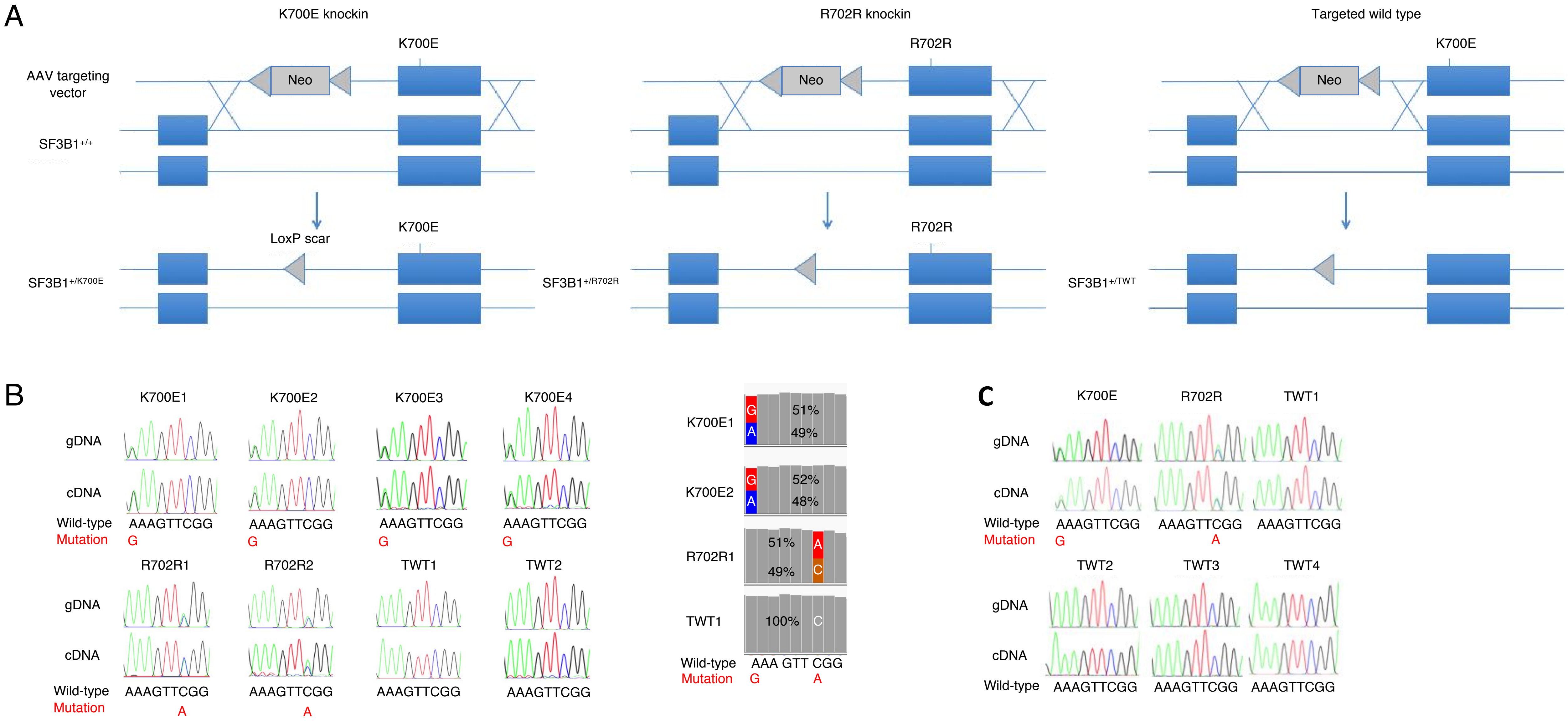
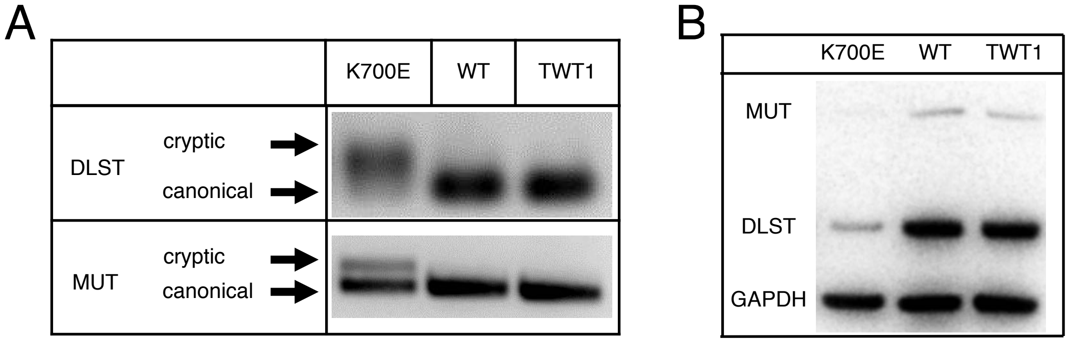
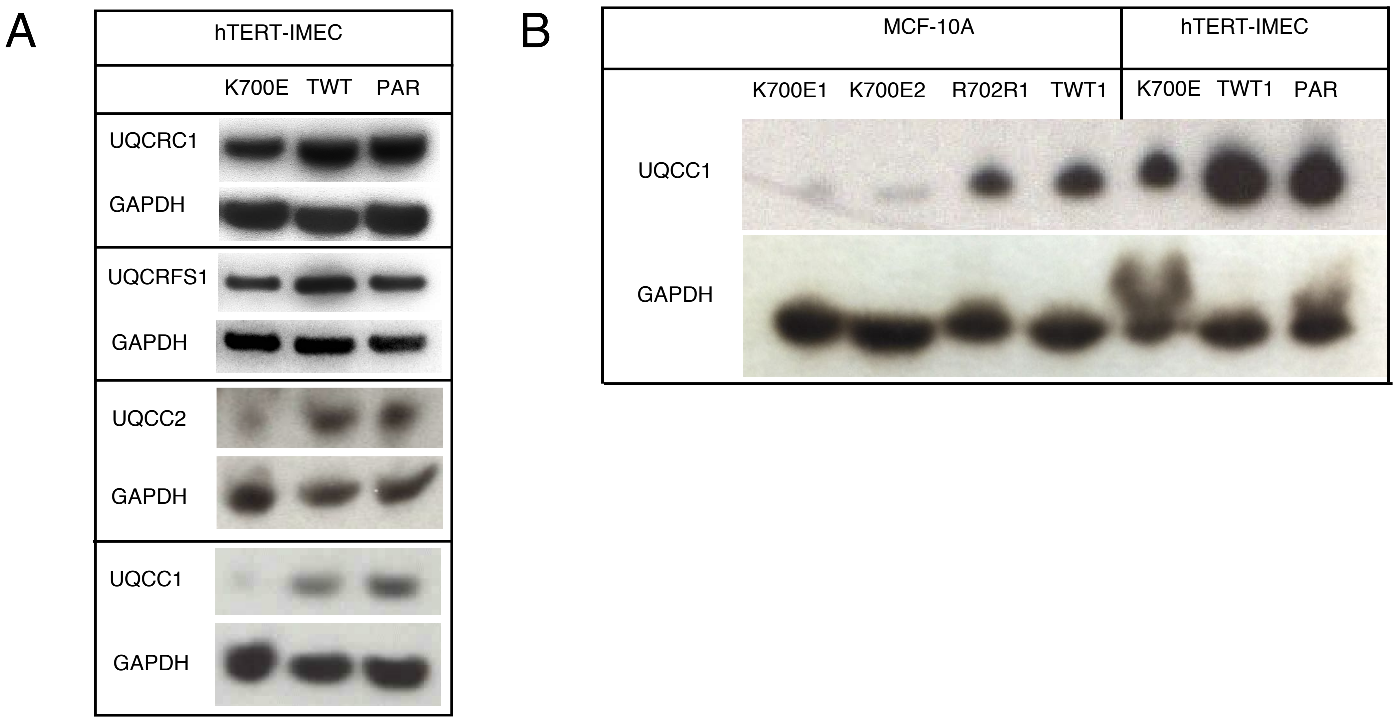


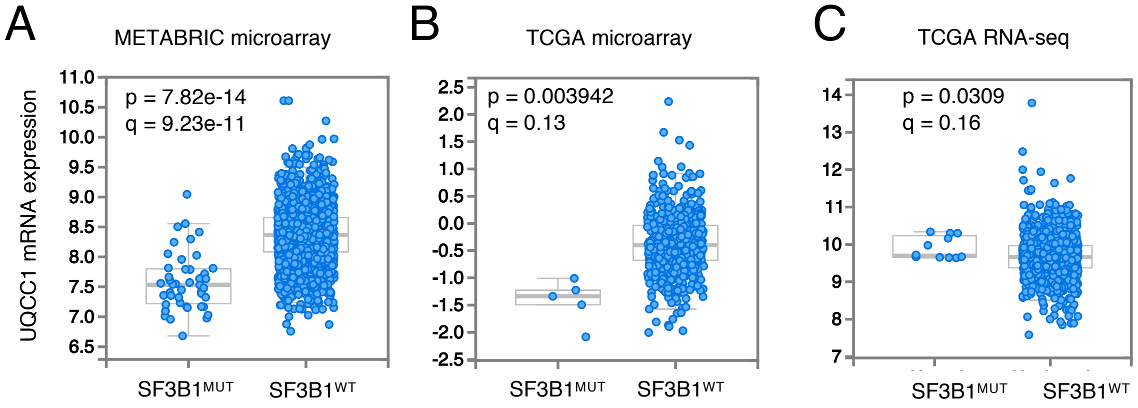
Supplementary Figure S1. Creation of isogenic $SF3B1^{MUT}$ breast epithelial cells. A) Mutant or control adeno-associated virus was used to create heterozygous knockin of K700E, R702R, or targeted wild type (TWT) in MCF-10A cells. B) Clone genotype was confirmed at gDNA and mRNA levels by Sanger sequencing (left), and mRNA expression was quantified in 4 clones by RNA-seq (right). C) For gene targeting of hTERT-IMEC cells, only one K700E clone was isolated (out of 80 postCre clones screened), in contrast to five control clones (out of only 36 screened). This already suggested a deleterious effect of SF3B1 mutation in these cells, and indeed the one K700E knockin did grow slower than control clones (Figure S4B).



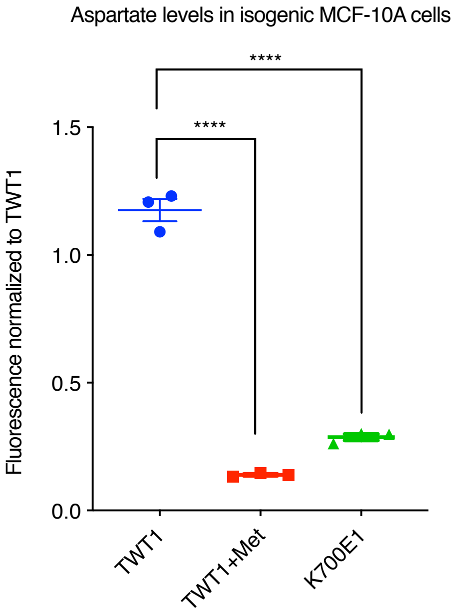
Supplementary Figure S2. Validation of transcriptional and proteomic alterations in hTERT-IMEC SF3B1^{K700E} knockin cells. A) Cryptic splicing of the MUT and DLST genes in isogenic hTERT-IMEC cells. TWT1 = targeted wild type clone 1, WT = wild type, parental hTERT-IMEC cells. B) Western blots showing downregulation of MUT and DLST protein in isogenic hTERT-IMEC cells. Data are representative from two independent experiments.



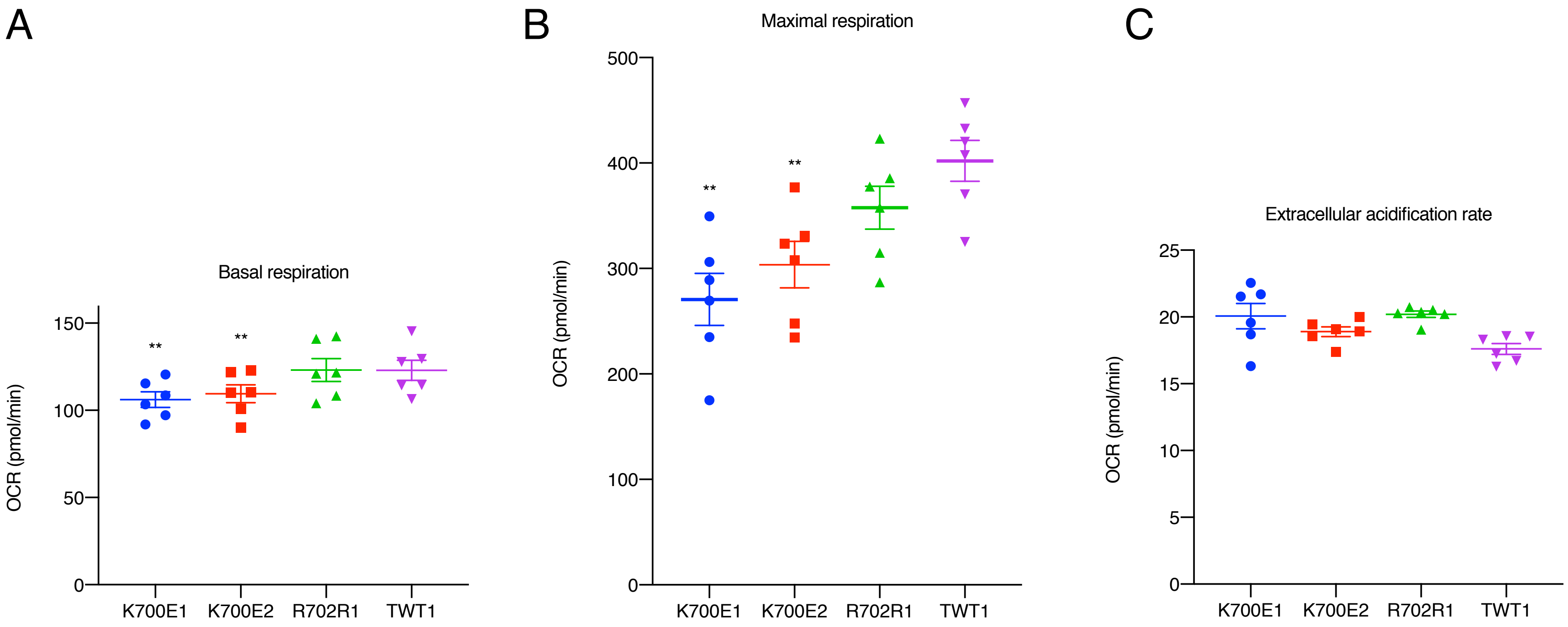
Supplementary Figure S3. Mitochondrial complex III levels in SF3B1^{MUT} hTERT-IMEC cells. A) Western blots of mitochondrial complex III proteins in isogenic hTERT-IMECs, showing significant downregulation of UQCC1 and UQCC2 but more modest downregulation of mature complex III proteins. B) Direct comparison of UQCC1 levels between MCF-10A and hTERT-IMEC cells, demonstrating higher baseline UQCC1 levels in the latter cell line. Data are representative from two independent experiments.



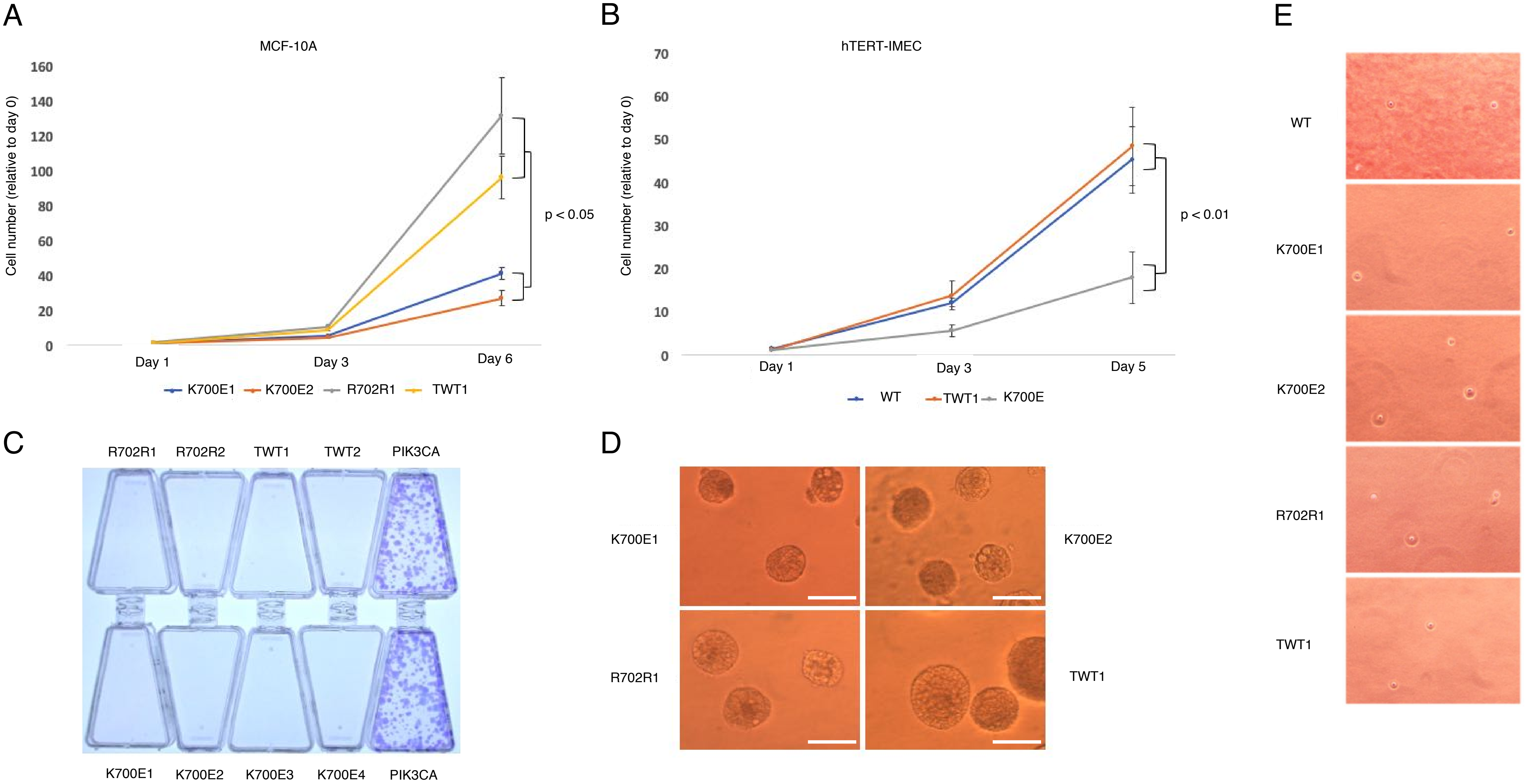
Supplementary Figure S4. UQCC1 mRNA expression in SF3B1^{MUT} breast tumors. UQCC1 mRNA is downregulated in SF3B1^{MUT} breast tumors by microarray analysis in A) METABRIC and B) TCGA, but not in C) RNA-seq analysis in TCGA.



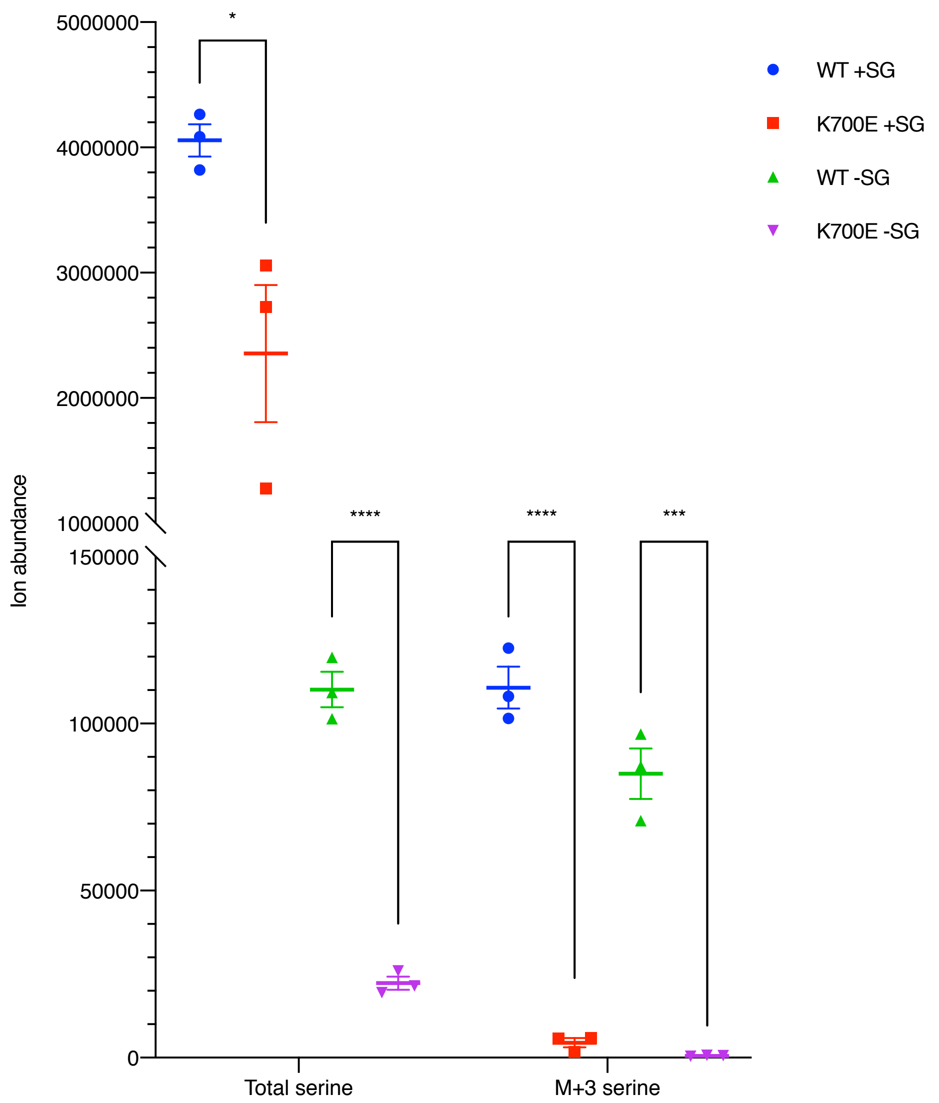
Supplementary Figure S5. Orthogonal validation of reduced aspartate in SF3B1^{MUT} MCF-10A cells. Targeted wild type (TWT1) and SF3B1^{K700E} cells were subjected to fluorometric quantification of aspartate levels. TWT1 exposed to 5mM metformin was used as a control for aspartate suppression. Means are from three biologic replicates. Data are representative of two independent experiments. ***p<0.001, ****p<0.0001 for t-tests.



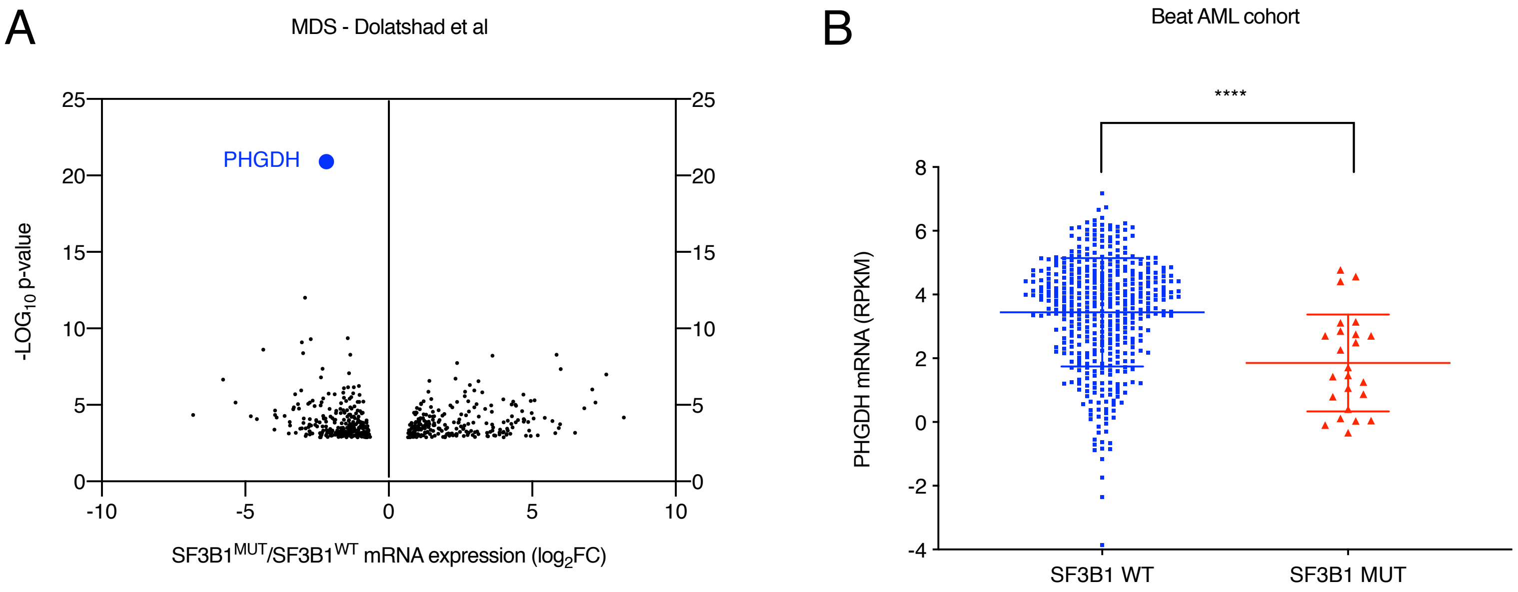
Supplementary Figure S6. Quantification of cellular respiration in isogenic MCF-10A cells. Six biologic replicates from each SF3B1^{MUT} and SF3B1^{WT} clone were processed on a Seahorse XF Analyzer to measure A) baseline oxygen consumption rate (OCR) before addition of inhibitors, B) maximum OCR after addition of FCCP, and C) baseline extracellular acidification rate. T-tests were performed on means from all mutant samples versus all wild type samples, but data for individual clones are also included. ** = $p<0.01$ and *** = $p<0.001$. Data are representative of two independent experiments.



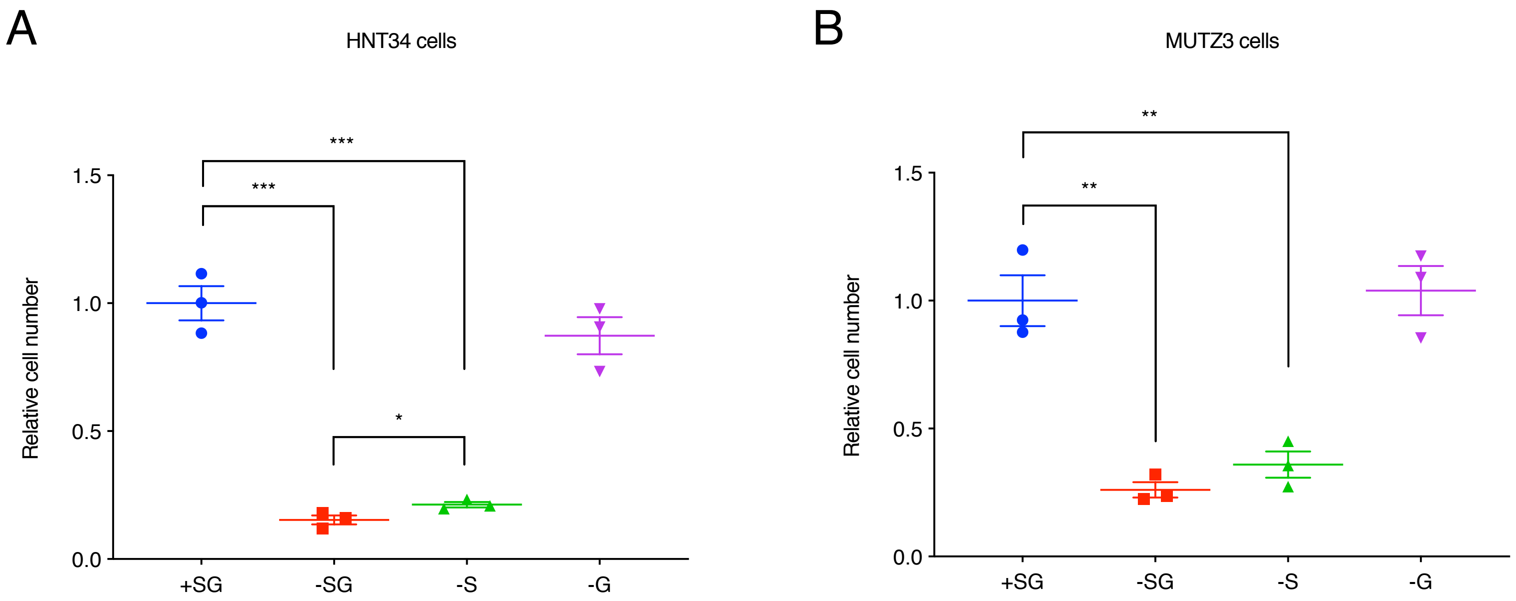
Supplementary Figure S7. Mutant SF3B1 slows, rather than transforms, the growth of breast epithelial cells. Proliferation of $SF3B1^{K700E}$ cells was slower than controls in both A) MCF-10A and B) hTERT-IMEC model systems. Cell number means are from three biologic replicates and data are representative of three independent experiments. All mutant samples were compared with all control samples for t-tests, but growth of individual clones are also shown. C) Isogenic MCF-10A cells still require exogenous EGF, compared with $PIK3CA^{E545K}$ knockin cells. Pictures of crystal violet-stained flasks are representative of two independent experiments. D) Normal mammosphere morphology was seen in all isogenic MCF-10A cells grown in Matrigel. Representative images from one experiment are shown. E) Isogenic MCF-10A cells did not form colonies when grown in soft agar. Representative images from one experiment are shown.



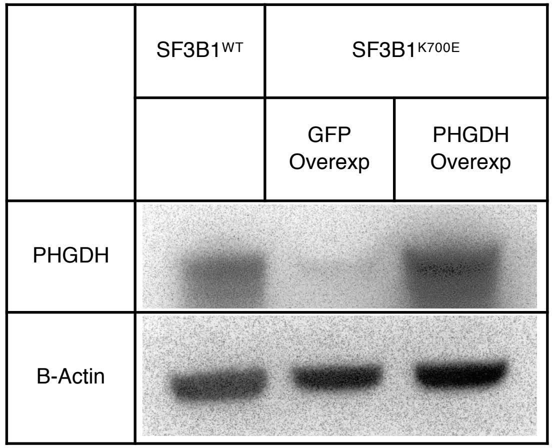
Supplementary Figure S8. Absolute serine levels in isogenic hTERT-IMEC cells. Isotope tracing of ^{13}C-glucose was performed as described in Figure 4F, but here absolute ion abundance levels of total and M+3 serine are shown for comparison**.** Data are from one experiment, three biologic replicates per condition were used. * = p<0.05, *** = p<0.001, and **** = p<0.0001 for t-test comparing mutant to wild type.



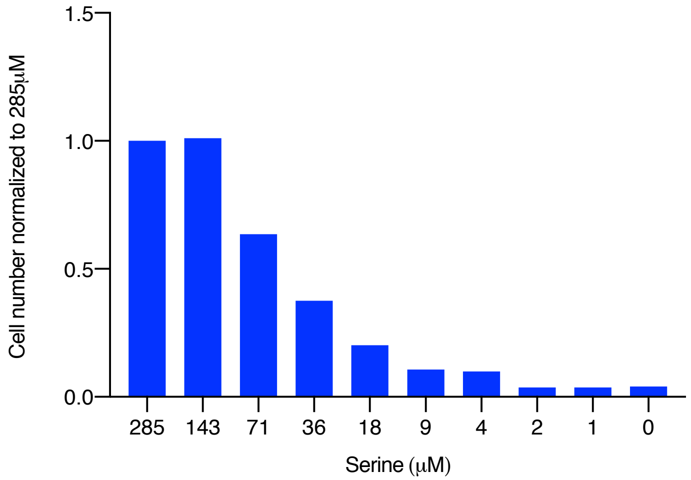
Supplementary Figure S9. Whole gene PHGDH mRNA expression is decreased in SF3B1^{MUT} MDS and AML. A) Gene expression differences between SF3B1^{MUT} to SF3B1^{WT} cases of MDS from Dolatshad et al were graphed as a volcano plot, showing a highly significant downregulation of PHGDH in mutant samples (fold change = 0.22). B) PHGDH expression in SF3B1^{MUT} and SF3B1^{WT} AML samples from Tyner et al are shown, with means and SD. **** = $p<0.0001$ for t-test comparing mutant and wild type.



Supplementary Figure S10. Growth suppression by SG starvation is driven primarily by serine. SF3B1^{MUT} leukemia cell lines HNT34 and MUTZ3 were cultured for 2 days in media with all amino acids, without glycine (G), without serine (S), or without serine and glycine (SG), and cell counts were performed. Data are from one experiment, with three biologic replicates per condition. * = p<0.05, **p<0.01, and ***p<0.001 for t-tests comparing conditions.



Supplementary Figure S11. PHGDH protein levels in rescued SF3B1^{MUT} versus SF3B1^{WT} MCF-10A cells. The K700E1 cells with lentiviral overexpression of GFP or PHGDH were harvested along with TWT1 gene targeting control cells, and Western blotting of PHGDH was performed. Data are from one experiment.



Supplementary Figure S12 . HNT34 cells show partial growth arrest in low serine. SF3B1^{K700E} HNT34 cells were grown in RPMI with the indicated concentrations of serine for 4 days, and cells were counted. Data are from one experiment.

Table S1. Aberrant junctions upregulated in SF3B1-mutant MCF-10A cells. Junction coordinates are from the GRCh38/hg38 version of the human genome. Known refers to junctions already annotated in transcriptional databases of normal human tissue, and novel refers to junctions that are not. Overlap indicates the junction was also upregulated in SF3B1-mutant breast cancers as analyzed by Darman et al. PSI = percent spliced in. dPSI = difference in PSI between mutant and wild type cells. A3SS = alternate 3' splice acceptor site. A5SS = alternate 5' splice donor site. EXE = exon exclusion. EXI = exon inclusion. TCGA = The Cancer Genome Atlas.

Junction	Gene Info	Gene symbol	Strand	annotation	avg PSI mut cells	avg PSI wt cells	dPSI	pvalue	padj	type	TCGA overlap
chr12:120496216-120496401	NM_003746	DYNLL1	+	known	0.620992481	0.077382662	0.54361	1.534E-09	2.01E-05	A3SS	TRUE
chr11:62881447-62881880	NM_001013251	SLC3A2	+	novel	0.113470735	0.003330508	0.11014	5.887E-09	3.86E-05	A3SS	TRUE
chr1:155308965-155310042	NM_001135821	FDPS	+	known	0.723154606	0.435164404	0.28799	6.619E-09	2.89E-05	A3SS/EXE	TRUE
chr1:67424977-67425082	NM_015640	SERBP1	-	known	0.799065288	0.435601523	0.36346	7.113E-09	2.33E-05	A3SS	TRUE
chr20:38002793-38006196	NM_014657	TTI1	-	novel	0.444574142	0.013572878	0.431	9.703E-09	2.55E-05	A3SS	FALSE
chr3:101682509-101682770	NM_000986	RPL24	-	novel	0.115503123	0.000477391	0.11503	1.044E-08	2.28E-05	A3SS	TRUE
chr1:156816112-156816674	NM_003975	SH2D2A	-	novel	0.534467375	0.016659456	0.51781	1.569E-08	2.94E-05	A3SS	FALSE
chr6:10723241-10724555	NM_016462	TMEM14C	+	known	0.691919838	0.038107455	0.65381	2.528E-08	4.15E-05	A3SS	TRUE
chr1:179865869-179877238	NM_145034	TOR1AIP2	-	novel	0.332761454	0.006298083	0.32646	3.016E-08	4.40E-05	A3SS	TRUE
chr20:35556271-35556954	NM_198398	ERGIC3	+	novel	0.25994799	0.007071334	0.25288	4.807E-08	6.31E-05	A3SS	TRUE
chr1:52414647-52414740	NM_032864	PRPF38A	+	novel	0.330470852	0.037561698	0.29291	6.451E-08	7.69E-05	A3SS	TRUE
chr2:23984831-23999654	NM_181713	UBXN2A	+	novel	0.177819061	0.001	0.17682	6.532E-08	7.14E-05	A3SS	FALSE
chr15:24962209-24967028	NM_022804	SNURF	+	novel	0.256046037	0.029602926	0.22644	8.211E-08	8.29E-05	EXI	TRUE
chr3:48634590-48635370	NM_134426	SLC26A6	-	novel	0.306671879	0	0.30667	1.039E-07	9.73E-05	EXI	FALSE
chr12:106985215-106986968	NM_025198	MTERF2	-	known	0.978769841	0.182448108	0.79632	1.551E-07	0.000135656	A3SS	TRUE
chr17:77093347-77094067	NM_001204410	SEC14L1	+	novel	0.482142857	0	0.48214	1.705E-07	0.000139826	EXI	FALSE
chr5:128288578-128289126	NM_001999	FBN2	-	novel	0.375779071	0.004431897	0.37135	1.804E-07	0.000139215	A3SS	FALSE
chrX:47199614-47200409	NM_003334	UBA1	+	novel	0.270630527	0	0.27063	2.222E-07	0.000161988	EXI	TRUE
chr3:136040962-136049243	NM_181897	PPP2R3A	+	novel	0.550744048	0.015625	0.53512	2.231E-07	0.000154027	A3SS	FALSE
chr9:122261498-122264714	NR_027126	RBM18	-	novel	0.441267803	0.082818747	0.35845	2.391E-07	0.00015688	A3SS	TRUE
chr2:196732152-196732425	NM_001080539	CCDC150	+	novel	0.179901961	0	0.1799	2.461E-07	0.000153778	A3SS	FALSE
chr2:68047336-68062957	NM_173177	C1D	-	novel	0.201608252	0.005597344	0.19601	3.003E-07	0.000179105	A3SS/EXE	FALSE
chr4:151179416-151187422	NM_001128923	SH3D19	-	novel	0.633106672	0.01557971	0.61753	3.273E-07	0.000186722	A3SS	FALSE
chr2:17754345-17759911	NM_001130009	GEN1	+	novel	0.968244609	0.071260662	0.89698	3.303E-07	0.000180554	A3SS	FALSE
chr3:172755575-172756982	NM_018098	ECT2	+	known	0.902571829	0.493251283	0.40932	3.435E-07	0.000180289	EXI	FALSE
chr3:172761683-172762397	NM_018098	ECT2	+	novel	0.546545815	0.008964184	0.53758	4.216E-07	0.000212764	A3SS	FALSE
chr10:7799683-7799771	NM_005174	ATP5C1	+	novel	0.111717268	0.008164941	0.10355	5.107E-07	0.000248183	EXI	FALSE
chr3:172755374-172755468	NM_018098	ECT2	+	novel	0.120068139	0.002248661	0.11782	5.783E-07	0.000270965	A3SS	FALSE
chr16:54920327-54923584	NR_110454	CRNDE	-	known	0.703556537	0.139919527	0.56364	7.618E-07	0.000344645	A3SS	TRUE
chrX:47200544-47200893	NM_003334	UBA1	+	novel	0.313643852	0.014285714	0.29936	8.134E-07	0.000355726	EXI	TRUE
chr18:224200-224923	NM_005131	THOC1	-	novel	0.388955634	0.030182432	0.35877	8.201E-07	0.000347088	A3SS	TRUE
chr10:97454799-97455638	NR_109895	ZDHHC16	+	novel	0.61647462	0.03540083	0.58107	9.1E-07	0.000373106	A3SS	TRUE
chr9:99129100-99132496	NM_004612	TGFBR1	+	known	0.476387461	0.117691143	0.3587	9.348E-07	0.00037167	A3SS	FALSE
chr1:100992754-100995109	NM_015958	DPH5	-	novel	0.380007961	0.011064003	0.36894	9.673E-07	0.000373283	A3SS	TRUE
chr3:48633635-48634515	NM_134426	SLC26A6	-	novel	0.435182885	0.030654335	0.40453	1.108E-06	0.000415409	A5SS	FALSE
chr8:100948732-100953268	NM_001135701	YWHAZ	-	novel	0.262905059	0	0.26291	1.124E-06	0.000409606	EXE	FALSE
chr22:50527732-50528511	NM_001953	TYMP	-	novel	0.263941557	0	0.26394	1.138E-06	0.000403628	A3SS	TRUE
chr8:100948732-100953268	NM_001135701	YWHAZ	-	novel	0.082046816	0	0.08205	1.355E-06	0.00046799	A3SS/EXE	FALSE
chr11:66285597-66285700	NM_020470	YIF1A	-	novel	0.090075684	0	0.09008	1.448E-06	0.000487119	A3SS	TRUE
chr13:110237279-110242674	NM_001845	COL4A1	-	novel	0.237681799	0.00248779	0.23519	1.48E-06	0.000485394	EXI	FALSE
chr2:119223888-119230739	NM_182915	STEAP3	+	novel	0.247645177	0.012470291	0.23517	1.551E-06	0.000496317	A3SS	FALSE
chr15:24968082-24974386	NM_005678	SNURF	+	novel	0.207278219	0.024652997	0.18263	1.78E-06	0.000555904	A3SS	TRUE
chr5:43476507-43479889	NM_022483	TMEM267	-	novel	0.08717847	0	0.08718	1.818E-06	0.000554851	A3SS	FALSE
chr12:95266632-95270038	NR_038242	VEZT	+	known	0.756621176	0.46572181	0.2909	2.023E-06	0.000603362	A3SS	TRUE
chr10:5455118-5456064	NR_073040	NET1	+	novel	0.161421242	0.000387597	0.16103	2.141E-06	0.000624218	A3SS	TRUE
chr11:57333071-57333434	NM_003146	SSRP1	-	novel	0.181265105	0.000694444	0.18057	2.207E-06	0.000629389	A3SS	TRUE
chr5:1879845-1880724	NM_016358	IRX4	-	novel	0.43382792	0.036225747	0.3976	2.289E-06	0.00063898	A3SS	FALSE
chr1:3632317-3633397	NM_017818	WRAP73	-	novel	0.401968821	0.023818804	0.37815	2.528E-06	0.00069088	A3SS	TRUE
chr19:45069248-45069985	NR_103529	CLASRP	+	novel	0.066248286	0	0.06625	2.58E-06	0.000690819	A3SS	FALSE
chr4:78554488-78573166	NM_005139	ANXA3	+	novel	0.053007323	0.001213204	0.05179	2.582E-06	0.000677462	A3SS	FALSE
chr2:27037892-27038145	NM_017727	TMEM214	+	novel	0.373380565	0.04541155	0.32797	2.789E-06	0.000717492	EXI	TRUE
chr1:228147699-228148357	NM_001159391	GUK1	+	novel	0.066352156	0.000159337	0.06619	2.946E-06	0.000743268	A3SS	TRUE
chr2:108485908-108486498	NR_028063	GCC2	+	novel	0.722991317	0.022058824	0.70093	3.27E-06	0.000809578	A3SS	TRUE
chr1:3842067-3844906	NM_014704	CEP104	-	novel	0.233477364	0.03153599	0.20194	3.344E-06	0.000812585	A3SS	FALSE
chr17:59001741-59012327	NM_015294	TRIM37	-	novel	0.366638158	0.070416777	0.29622	3.355E-06	0.000800284	A3SS	FALSE
chr11:75479318-75490236	NM_030792	GDPD5	-	novel	0.201716543	0.007653061	0.19406	3.464E-06	0.000811509	A3SS	FALSE
chr2:105097324-105099648	NR_110227	UTAT33	-	novel	0.070422416	0.001689189	0.06873	3.836E-06	0.000883057	A5SS	FALSE
chr10:131969332-131970637	NM_004052	BNIP3	-	novel	0.057985366	0.001082251	0.0569	3.911E-06	0.000884611	A3SS	FALSE
chr10:97743164-97744711	NM_001002261	ZFYVE27	+	novel	0.28254529	0	0.28255	3.963E-06	0.000881362	A3SS	FALSE
chr13:98475002-98475249	NM_003576	STK24	-	novel	0.066016917	0.000588235	0.06543	4.009E-06	0.000876558	A3SS	FALSE
chr2:96619776-96631311	NR_047658	KANSL3	-	novel	0.372742943	0	0.37274	4.11E-06	0.000884058	A3SS	TRUE
chr1:155309076-155310042	NM_001135821	FDPS	+	known	0.6147208	0.268346024	0.34637	4.143E-06	0.000876625	A3SS/EXE	TRUE
chr6:90560234-90561621	NM_145333	MAP3K7	-	novel	0.688653484	0.068346894	0.62031	4.259E-06	0.000886949	A3SS	TRUE
chrX:154779353-154781238	NM_002436	MPP1	-	known	1	0.927565362	0.07243	4.37E-06	0.000895795	A3SS	FALSE
chr2:190683827-190685478	NM_001321315	NAB1	+	known	0.175226001	0.122840282	0.05239	4.462E-06	0.000900613	A3SS	FALSE
chr4:2341615-2353932	NM_001172660	ZFYVE28	-	known	1	0.090277778	0.90972	4.863E-06	0.000966705	EXE	FALSE
chr3:172755374-172755482	NM_018098	ECT2	+	known	0.789015036	0.507178582	0.28184	4.901E-06	0.00095964	A3SS	FALSE
chr20:36653723-36656359	NR_038370	NDRG3	-	novel	0.4121098	0.017112993	0.395	4.97E-06	0.000958823	A3SS	TRUE
chr2:229793130-229795178	NM_001284215	TRIP12	-	novel	0.435183864	0.147023482	0.28816	4.988E-06	0.000948382	A3SS	TRUE
chr9:6241785-6242467	NM_001314045	IL33	+	novel	0.524121668	0.020128824	0.50399	5.001E-06	0.000937379	EXI	FALSE
chr2:229262893-229271013	NM_017933	PID1	-	known	0.510661512	0.157690052	0.35297	5.326E-06	0.000984261	EXI	FALSE
chr18:683395-685920	NM_202758	ENOSF1	-	novel	0.686614112	0.015718451	0.6709	5.404E-06	0.000984705	A3SS	TRUE
chr2:102732426-102736645	NR_136174	MFSD9	-	known	0.840178571	0.028954082	0.81122	6.681E-06	0.001200667	A3SS	FALSE
chr15:40046069-40056673	NR_040062	SRP14-AS1	+	novel	0.707510965	0	0.70751	6.899E-06	0.001223208	A3SS	FALSE
chr19:55146466-55146680	NM_003283	TNNT1	-	known	0.598295151	0.508418738	0.08988	6.98E-06	0.001221064	EXI	FALSE
chr10:7799194-7799590	NM_005174	ATP5C1	+	novel	0.124464714	0.009349244	0.11512	7.126E-06	0.001230254	EXI	FALSE
chr6:109446412-109446678	NM_022765	MICAL1	-	novel	0.32739431	0.040914974	0.28648	7.15E-06	0.001218298	A5SS	FALSE
chr2:26214576-26215052	NM_000182	HADHA	-	novel	0.057860956	0.004313117	0.05355	7.191E-06	0.001209602	A3SS	TRUE
chr14:51725870-51727717	NM_001267047	FRMD6	+	novel	0.089321869	0.000980392	0.08834	7.627E-06	0.001266718	A3SS	FALSE
chr5:1882081-1882602	NM_016358	IRX4	-	novel	0.163596363	0.011417982	0.15218	7.862E-06	0.001289325	A3SS	FALSE
chr21:32453508-32457599	NR_104472	EVA1C	+	novel	0.114177603	0.041058097	0.07312	8.078E-06	0.001308464	A3SS	FALSE
chr8:119793451-119794779	NM_003184	TAF2	-	novel	0.232669721	0.02965135	0.20302	8.71E-06	0.001393523	A5SS	FALSE
chr1:6546390-6549570	NM_024654	NOL9	-	novel	0.159997565	0.002941176	0.15706	9.014E-06	0.001424826	EXI	FALSE
chr11:93154216-93162705	NM_001286139	SLC36A4	-	novel	0.290454011	0.004212562	0.28624	9.124E-06	0.001425138	A3SS	FALSE
chr6:53516240-53520777	NM_001498	GCLC	-	novel	0.132141852	0	0.13214	9.394E-06	0.001450024	A3SS	FALSE

chr14:74882016-74885585	NR_045209	DLST	+	known	0.393703709	0.058761509	0.33494	1.007E-05	0.001536138	EXE	TRUE
chr8:28768376-28769888	NM_001172562	INTS9	-	novel	0.172207207	0.007894737	0.16431	1.064E-05	0.001604199	A3SS	FALSE
chr14:74882016-74885585	NR_045209	DLST	+	known	0.390536382	0.047965499	0.34257	1.084E-05	0.001616056	EXE	TRUE
chr2:231331897-231344948	NM_001271466	ARMC9	+	novel	0.575204123	0	0.5752	1.09E-05	0.001606389	A3SS	TRUE
chr17:58005617-58005800	NR_034041	SRSF1	-	novel	0.070061498	0.002734822	0.06733	1.133E-05	0.001651837	A3SS	FALSE
chr8:130361788-130401884	NM_018482	ASAP1	-	novel	0.297918817	0.01993714	0.27798	1.153E-05	0.001662318	A3SS	FALSE
chr12:105208047-105208157	NM_001251905	APPL2	-	known	0.419645325	0.030952381	0.38869	1.209E-05	0.001724168	A3SS	TRUE
chr1:93154888-93156035	NM_030761	TMED5	-	known	0.117580241	0.052307848	0.06527	1.252E-05	0.001765783	EXI	FALSE
chr1:156562674-156563133	NM_178229	IQGAP3	-	novel	0.370402597	0.010577458	0.35983	1.267E-05	0.001768087	A3SS	FALSE
chr8:9198991-9202391	NR_125431	LOC101929128	+	novel	0.829510543	0.102625483	0.72689	1.362E-05	0.001881159	A3SS	FALSE
chr8:98108768-98117031	NM_005836	RIDA	-	novel	0.106229592	0.001396648	0.10483	1.419E-05	0.001938644	A3SS	FALSE
chr22:19057186-19063201	NR_033674	DGCR2	-	novel	0.204324045	0.003675637	0.20065	1.494E-05	0.002020264	A3SS	TRUE
chr14:74889349-74889877	NR_045209	DLST	+	novel	0.424121033	0.006323913	0.4178	1.495E-05	0.002001362	A3SS	TRUE
chr11:12674834-12675408	NM_021961	TEAD1	+	known	0.696310145	0.589105903	0.1072	1.664E-05	0.002204756	EXI	FALSE
chr17:7932800-7933092	NM_053051	CNTROB	+	novel	0.825721154	0	0.82572	1.668E-05	0.002188232	A3SS	FALSE
chr5:171405403-171406396	NM_199185	NPM1	+	known	0.283893029	0.232465554	0.05143	1.693E-05	0.002199795	EXI	FALSE
chr7:22314745-22315369	NM_012294	RAPGEF5	-	novel	0.170372473	0.005681818	0.16469	1.703E-05	0.002189985	EXI	FALSE
chr3:184869528-184870699	NM_015303	VPS8	+	novel	0.279761905	0.014520202	0.26524	1.708E-05	0.002176251	A3SS	FALSE
chr4:183655974-183658928	NM_152682	RWDD4	-	novel	0.255772687	0.009882909	0.24589	1.709E-05	0.002156272	A3SS	TRUE
chr7:56073111-56074585	NM_015411	SUMF2	+	known	0.132939136	0.066268732	0.06667	1.77E-05	0.00221172	EXE	FALSE
chr1:52904833-52905033	NM_018281	ECHDC2	-	known	0.899810795	0.691247932	0.20856	1.799E-05	0.002226538	EXI	FALSE
chr15:39943485-39945334	NM_001013703	EIF2AK4	+	novel	0.092759114	0.011166851	0.08159	1.887E-05	0.002313326	EXI	FALSE
chr14:21093304-21093585	NM_016423	ZNF219	-	novel	0.440797277	0.048924658	0.39187	1.93E-05	0.002344532	A3SS	FALSE
chr17:64578594-64580788	NM_022739	SMURF2	-	novel	0.246634378	0.002248884	0.24439	1.975E-05	0.002377055	A3SS	TRUE
chr2:106164799-106166055	NR_045607	UXS1	-	known	0.627345715	0.212183657	0.41516	2.135E-05	0.002546807	A3SS	TRUE
chr11:47173915-47175014	NM_032389	ARFGAP2	-	novel	0.097559324	0.006369549	0.09119	2.147E-05	0.002537302	A3SS	TRUE
chr1:209622680-209623504	NM_001017402	LAMB3	-	known	0.111240838	0.051124804	0.06012	2.181E-05	0.002555143	EXE	FALSE
chr10:121974100-121974389	NM_017615	NSMCE4A	-	novel	0.881944444	0.096974206	0.78497	2.215E-05	0.00257145	A3SS	FALSE
chr10:94545907-94546360	NM_018063	HELLS	+	novel	0.327316452	0	0.32732	2.223E-05	0.0025584	A3SS	FALSE
chr1:1308972-1309085	NR_144369	PUSL1	+	known	0.848025567	0.711083411	0.13694	2.25E-05	0.002567322	EXI	FALSE
chr7:36420314-36420611	NM_018685	ANLN	+	novel	0.142264825	0.06513861	0.07713	2.303E-05	0.002605146	A3SS	FALSE
chr15:42830078-42839857	NM_173500	TTBK2	-	novel	0.27750169	0	0.2775	2.31E-05	0.002590449	EXI	FALSE
chr7:74716950-74718860	NR_110044	LOC101926943	-	novel	0.10611623	0.010132198	0.09598	2.313E-05	0.002571342	A5SS	FALSE
chr16:29820510-29830473	NM_017458	MVP	+	known	0.416478043	0.207795799	0.20868	2.335E-05	0.002574817	A3SS	FALSE
chr3:149041680-149042165	NM_139048	HLTF	-	novel	0.341389781	0.079713369	0.26168	2.674E-05	0.002923267	A3SS	TRUE
chr10:97459475-97459658	NM_022362	MMS19	-	novel	0.116608119	0.016744104	0.09986	2.772E-05	0.003005163	A3SS	FALSE
chr5:151032394-151033607	NM_001258456	TNIP1	-	novel	0.107532729	0.011593513	0.09594	2.816E-05	0.003028408	A3SS	TRUE
chr2:27037702-27037814	NM_017727	TMEM214	+	novel	0.395842312	0.035063528	0.36078	2.866E-05	0.003057429	EXI	TRUE
chr16:89587102-89588674	NM_153636	CPNE7	+	known	0.777808691	0.442464181	0.33534	2.877E-05	0.003044411	EXE	FALSE
chr1:38866999-38873017	NR_037632	MYCBP	-	known	0.249582181	0.062452503	0.18713	2.887E-05	0.003029933	A3SS/EXE	TRUE
chr6:128235604-128240034	NM_002844	PTPRK	-	novel	0.062043724	0.002673797	0.05937	2.954E-05	0.003076223	EXI	FALSE
chr6:31644414-31644524	NM_001098534	BAG6	-	novel	0.881224348	0.685793302	0.19543	2.98E-05	0.003078097	EXI	TRUE
chr11:125572569-125575250	NR_110770	EI24	+	novel	0.129617165	0.017126256	0.11249	2.989E-05	0.00306354	A3SS	TRUE
chr11:3676389-3676508	NM_139132	NUP98	-	novel	0.089036639	0	0.08904	3.105E-05	0.003157689	A3SS	TRUE
chr12:120064879-120069263	NM_207311	BICDL1	+	novel	0.301354895	0	0.30135	3.264E-05	0.003294392	EXI	FALSE
chr5:38822873-38845667	NR_109951	OSMR-AS1	-	novel	0.749599359	0	0.7496	3.331E-05	0.003336556	EXI	FALSE
chr1:209622680-209623504	NM_001017402	LAMB3	-	known	0.153696095	0.070759755	0.08294	3.335E-05	0.003315066	EXE	FALSE
chr3:48634590-48634730	NM_134426	SLC26A6	-	novel	0.611111111	0	0.61111	3.355E-05	0.003309959	EXI	FALSE
chr7:74189918-74194740	NM_031992	EIF4H	+	known	0.602329522	0.531560718	0.07077	3.461E-05	0.003388397	EXE	FALSE
chr10:104031609-104032203	NM_000494	COL17A1	-	novel	0.093017568	0	0.09302	3.536E-05	0.003436138	A3SS	FALSE
chr20:31722348-31723863	NM_001322240	BCL2L1	-	known	0.918859649	0.19047619	0.72838	3.536E-05	0.003411229	A3SS	FALSE
chr2:17753967-17759911	NM_001130009	GEN1	+	novel	0.983333333	0.098039216	0.88529	3.575E-05	0.003423353	A3SS	FALSE
chr7:56073111-56074585	NM_015411	SUMF2	+	known	0.14359588	0.076348254	0.06725	3.61E-05	0.003432021	EXE	FALSE
chr3:127695190-127721052	NM_007283	MGLL	-	known	0.199397298	0.096909515	0.10249	3.633E-05	0.003429587	EXE	FALSE
chr17:19283714-19309884	NR_048576	EPN2-AS1	-	known	0.988619855	0.916390964	0.07223	3.812E-05	0.003571939	EXI	FALSE
chr1:46643316-46645160	NM_001256418	ATPAF1	-	novel	0.107840171	0	0.10784	4.006E-05	0.003727736	A3SS	TRUE
chr4:170025842-170026233	NM_021647	MFAP3L	-	novel	0.670409621	0.011904762	0.6585	4.025E-05	0.003718522	EXI	FALSE
chr11:9431003-9433782	NM_006391	IPO7	+	novel	0.095441259	0.002024291	0.09342	4.047E-05	0.003712676	A3SS	FALSE
chr17:74771844-74771959	NR_130954	NAT9	-	novel	0.065658562	0	0.06566	4.069E-05	0.00370763	A3SS	FALSE
chr7:77840300-77893591	NM_020432	PHTF2	+	novel	0.10639468	0.006858427	0.09954	4.12E-05	0.003727736	A3SS	FALSE
chr1:212342280-212345789	NM_001199756	PPP2R5A	+	novel	0.25971243	0.008474576	0.25124	4.168E-05	0.003745068	A3SS	TRUE
chr2:229155964-229262682	NM_001330156	PID1	-	known	0.482902713	0.168479437	0.31442	4.406E-05	0.003932064	EXI	FALSE
chr3:194648795-194651114	NM_018385	LSG1	-	novel	0.101414123	0.011147089	0.09027	4.582E-05	0.004061562	EXE	FALSE
chr19:57397174-57398412	NM_152909	ZNF548	+	novel	0.733901515	0	0.7339	4.629E-05	0.004076005	A3SS	TRUE
chr5:163473557-163474059	NM_012485	HMMR	+	novel	0.087885306	0.004945055	0.08294	4.864E-05	0.004254204	A3SS	FALSE
chr1:93754346-93767235	NM_001261408	BCAR3	-	novel	0.110814452	0.060145202	0.05067	4.972E-05	0.004320034	EXI	FALSE
chr15:24967152-24967931	NM_022804	SNURF	+	novel	0.260538272	0.02791393	0.23262	5.003E-05	0.004318491	EXI	TRUE
chr18:36025678-36026899	NM_018170	RPRD1A	-	known	0.206277261	0.003862725	0.20241	5.004E-05	0.004290977	EXI	TRUE
chrX:48476396-48478009	NM_177439	FTSJ1	+	novel	0.063564708	0	0.06356	5.036E-05	0.004290402	A3SS	FALSE
chr4:39910356-39913610	NM_001100400	PDS5A	-	novel	0.075272601	0.002782917	0.07249	5.048E-05	0.004273142	A3SS	FALSE
chr5:132760013-132760801	NM_015146	SEPT8	-	novel	0.103033551	0.000668449	0.10237	5.442E-05	0.00457703	EXI	FALSE
chr4:17804771-17810446	NR_144310	DCAF16	-	known	0.606715005	0.171036967	0.43568	5.616E-05	0.004693024	EXE	FALSE
chr2:169812524-169815476	NM_014168	METTL5	-	novel	0.124332735	0.016164466	0.10817	5.675E-05	0.004712372	A3SS	TRUE
chr5:79312498-79314379	NM_152405	JMY	+	novel	0.680033937	0.051463117	0.62857	5.686E-05	0.004691588	A3SS	FALSE
chr22:44808438-44814671	NM_181335	ARHGAP8	+	known	0.965334885	0.877059846	0.08828	5.705E-05	0.004678043	EXE	FALSE
chr17:4891124-4891515	NM_170663	MINK1	+	known	0.247161355	0.088792292	0.15837	5.737E-05	0.004674835	A3SS	FALSE
chr11:47496052-47499452	NM_001172639	CELF1	-	novel	0.130749128	0.008775946	0.12197	5.751E-05	0.004657535	EXI	FALSE
chr2:177232030-177232391	NM_001313904	NFE2L2	-	novel	0.11716301	0.02026318	0.0969	5.844E-05	0.004703842	A3SS	TRUE
chr12:117158084-117165484	NM_033624	FBXO21	-	novel	0.5855164	0.299149569	0.28637	5.845E-05	0.004675976	A3SS	TRUE
chr6:31644194-31644306	NM_001098534	BAG6	-	novel	0.872226417	0.681276267	0.19095	5.865E-05	0.004663572	EXI	TRUE
chr6:28281918-28283755	NM_032507	PGBD1	+	known	0.977272727	0.315216115	0.66206	5.921E-05	0.004680078	A3SS	FALSE
chr7:94528250-94533188	NM_022900	CASD1	+	novel	0.38555767	0.003623188	0.38193	5.965E-05	0.004686142	A3SS	TRUE
chr4:39081239-39082024	NM_199039	KLHL5	+	novel	0.105523338	0.006451613	0.09907	5.997E-05	0.004683465	A3SS	FALSE
chr1:203801628-203802568	NM_014827	ZC3H11A	+	novel	0.688509317	0.124440583	0.56407	6.154E-05	0.004777543	A3SS	FALSE
chr17:47138906-47141852	NM_001293091	CDC27	-	novel	0.109985777	0.000976563	0.10901	6.445E-05	0.004974101	A3SS	FALSE
chr22:19961289-19962658	NM_001135162	COMT	+	novel	0.154464501	0.001020408	0.15344	6.477E-05	0.00496981	A3SS	FALSE
chr15:60396427-60397257	NM_004039	ANXA2	-	novel	0.115010106	0.044281413	0.07073	6.603E-05	0.005036844	EXI	FALSE
chr12:109999784-110011990	NM_033121	ANKRD13A	+	novel	0.213019481	0.024751829	0.18827	6.892E-05	0.005226811	A3SS	FALSE
chr22:38295447-38298785	NM_152221	CSNK1E	-	novel	0.359385924	0.204193132	0.15519	7.187E-05	0.005419261	EXI	FALSE
chr16:658344-658509	NM_145294	WDR90	+	novel	0.480263158	0.00862069	0.47164	7.335E-05	0.005499049	A3SS	TRUE
chr16:793274-794033	NM_022092	CHTF18	+	novel	0.402782258	0.00462963	0.39815	7.403E-05	0.005518846	A3SS	FALSE

chr19:6731054-6731198	NM_001080452	GPR108	-	novel	0.354297786	0.076288878	0.27801	7.407E-05	0.005490372	A3SS	TRUE
chr2:232735238-232735762	NR_103492	GIGYF2	+	known	0.221252147	0.010972806	0.21028	7.429E-05	0.005475544	A3SS	TRUE
chr6:41073084-41079004	NM_021705	NFYA	+	novel	0.300673389	0	0.30067	7.497E-05	0.00549481	A3SS	FALSE
chr15:58917020-58932355	NR_135043	SLTM	-	novel	0.25122844	0.016870502	0.23436	7.743E-05	0.005643466	A3SS	TRUE
chr4:22448664-22454865	NM_145290	ADGRA3	-	novel	0.062165611	0.005790494	0.05638	7.829E-05	0.005674755	EXI	FALSE
chr8:38237627-38238106	NM_001164232	DDHD2	+	novel	0.191917264	0.032216559	0.1597	7.892E-05	0.005689228	A3SS	TRUE
chr7:100345968-100349716	NR_036570	STAG3L5P-PVRIG	+	novel	0.954151222	0.590025396	0.36413	8.153E-05	0.005845548	A3SS	TRUE
chr12:50427909-50428916	NR_033200	LARP4	+	novel	0.260263419	0.071657666	0.18861	8.455E-05	0.00602889	A3SS	FALSE
chr3:169093120-169095075	NM_005241	MECOM	-	novel	0.250561669	0	0.25056	8.719E-05	0.006183456	A3SS	FALSE
chr2:206145026-206146902	NM_001199984	NDUFS1	-	known	0.991592405	0.933796843	0.0578	9.107E-05	0.006423771	A3SS	FALSE
chr16:635022-635280	NR_109979	METTL26	-	novel	0.0520326	0	0.05203	9.305E-05	0.006528758	A3SS	TRUE
chr13:110214015-110236890	NM_001845	COL4A1	-	novel	0.085817299	0.001623377	0.08419	9.44E-05	0.006588027	EXI	FALSE
chrX:130637404-130656580	NM_182314	ENOX2	-	novel	0.836512933	0.334707904	0.50181	9.454E-05	0.006562444	A3SS	TRUE
chr8:132798860-132799082	NM_198513	PHF20L1	+	novel	0.228442291	0.037584389	0.19086	9.496E-05	0.006557452	A3SS	FALSE
chr15:40200980-40202389	NM_001211	BUB1B	+	novel	0.307337372	0.050902554	0.25643	9.636E-05	0.006619246	A3SS	FALSE
chr17:80415250-80415649	NM_173627	ENDOV	+	known	1	0.905753927	0.09425	9.712E-05	0.006636608	EXI	FALSE
chr5:140436257-140438493	NM_024668	ANKHD1	+	known	0.51915659	0.061473412	0.45768	9.825E-05	0.006679093	A3SS	TRUE
chr19:9618166-9619431	NM_152289	ZNF561	-	novel	0.553229239	0.116523846	0.43671	9.989E-05	0.006755542	A3SS	TRUE
chr1:23072197-23073273	NM_015013	KDM1A	+	novel	0.111056607	0.017536726	0.09352	0.0001008	0.00678452	A3SS	TRUE
chr2:32388943-32392023	NM_016252	BIRC6	+	novel	0.178528485	0.00528169	0.17325	0.0001009	0.006752047	A3SS	FALSE
chr9:136942997-136943348	NM_018998	FBXW5	-	novel	0.179154012	0.01742919	0.16172	0.0001017	0.006775781	A3SS	TRUE
chr9:121300126-121301962	NM_000177	GSN	+	known	0.253686447	0.007281553	0.2464	0.0001018	0.00674315	EXI	FALSE
chr12:53442733-53443486	NM_018457	PRR13	+	novel	0.225630066	0.035898829	0.18973	0.000104	0.006858859	A3SS	TRUE
chr1:220581118-220593903	NM_018650	MARK1	+	novel	0.17594697	0	0.17595	0.0001041	0.006832109	EXI	FALSE
chr16:57440959-57447341	NM_020313	CIAPIN1	-	novel	0.155000341	0.011627907	0.14337	0.0001048	0.006843483	A3SS	FALSE
chr7:100155181-100155261	NM_018275	C7orf43	-	novel	0.135921745	0	0.13592	0.0001051	0.006827206	A3SS	FALSE
chr4:83456958-83458324	NM_016067	MRPS18C	+	novel	0.059167308	0.004197405	0.05497	0.0001066	0.006888129	A3SS	FALSE
chr1:35746977-35747906	NM_022111	CLSPN	-	novel	0.130142394	0.009054639	0.12109	0.0001071	0.006890187	A3SS	FALSE
chr1:93156084-93156299	NR_030761	TMED5	-	known	0.103164091	0.042962664	0.0602	0.0001178	0.007540736	EXI	FALSE
chr17:18583523-18587665	NR_036647	CCDC144B	-	known	1	0.806547619	0.19345	0.0001181	0.007521008	EXI	FALSE
chr9:35813156-35813265	NM_032593	HINT2	-	novel	0.307101051	0.017114011	0.28999	0.0001183	0.007498555	A3SS	TRUE
chr13:50083194-50104703	NR_109974	DLEU1	+	known	0.995098039	0.93394519	0.06115	0.0001187	0.007486915	A3SS	FALSE
chr11:130122513-130126699	NM_001243299	APLP2	+	known	0.517678868	0.453499382	0.06418	0.0001187	0.007452725	EXE	FALSE
chr2:215379317-215382211	NM_212482	FN1	-	known	0.256608086	0.199914603	0.05669	0.0001193	0.00745141	EXE	FALSE
chr1:213072986-213077695	NM_012424	RPS6KC1	+	known	0.081081331	0	0.08108	0.000121	0.007522424	EXI	FALSE
chr14:50341286-50342131	NM_004196	CDKL1	-	novel	0.156923056	0	0.15692	0.0001227	0.007594747	A3SS	FALSE
chr2:219633457-219633865	NR_048551	SLC4A3	+	novel	0.9	0.098399504	0.8016	0.0001258	0.007749793	A3SS	FALSE
chr7:56032054-56033960	NM_004577	PSPH	-	known	0.893964816	0.713875844	0.18009	0.0001276	0.007822769	EXE	FALSE
chr14:70593009-70593295	NM_005466	MED6	-	known	0.250435496	0.016114449	0.23432	0.00013	0.007934915	A3SS	TRUE
chr8:22604842-22605735	NM_021174	CCAR2	+	known	0.881507108	0.804211137	0.0773	0.0001303	0.007914944	EXE	FALSE
chr2:86171345-86173649	NM_006839	IMMT	-	known	0.579679312	0.395559351	0.18412	0.0001307	0.007900356	A3SS	TRUE
chr6:31634557-31634797	NM_080686	PRRC2A	+	novel	0.116267943	0.010052473	0.10622	0.0001344	0.008089503	A3SS	TRUE
chr16:89291799-89305205	NR_045839	ANKRD11	-	novel	0.180803358	0.016758242	0.16405	0.0001357	0.008127271	A3SS	FALSE
chr10:91484655-91485164	NR_104291	HECTD2	+	novel	0.549938725	0.062030075	0.48791	0.0001364	0.008133684	A3SS	FALSE
chr1:155061489-155061575	NR_040773	DCST1-AS1	-	novel	0.166707832	0	0.16671	0.0001389	0.008244347	EXI	FALSE
chr11:33059095-33061514	NM_001145541	TCP11L1	+	novel	0.339750892	0.025292398	0.31446	0.0001413	0.008353067	A3SS	FALSE
chr15:49239367-49281971	NM_002044	GALK2	+	novel	0.115529799	0.00203252	0.1135	0.0001416	0.008333789	A3SS	FALSE
chr19:32966466-32971835	NM_032816	CEP89	-	known	0.723003082	0.576197648	0.14681	0.0001421	0.00832054	EXE	FALSE
chr7:105536749-105542491	NR_144478	RINT1	+	novel	0.061644924	0	0.06164	0.0001471	0.008576865	A3SS	FALSE
chr3:56615272-56615903	NR_024460	CCDC66	+	novel	0.700897436	0.113431689	0.58747	0.0001492	0.008662045	A3SS	FALSE
chrX:134602122-134733434	NM_001316888	PLAC1	-	known	0.551948052	0.05	0.50195	0.0001556	0.008993384	EXI	FALSE
chr2:169531508-169537226	NR_104020	FASTKD1	-	novel	0.099459474	0	0.09946	0.0001599	0.009198846	A3SS	FALSE
chr22:31754979-31758526	NM_014662	DEPDC5	+	novel	0.078666853	0	0.07867	0.00016	0.009164922	A3SS	FALSE
chr10:87246236-87288441	NR_024397	NUTM2A-AS1	-	novel	0.053025207	0	0.05303	0.0001612	0.009197576	A3SS	FALSE
chr12:2877282-2885262	NR_046432	RHNO1	+	known	0.115458209	0	0.11546	0.000162	0.009202061	A3SS	FALSE
chr21:25735070-25741560	NM_002040	GABPA	+	novel	0.144952167	0.011040707	0.13391	0.0001622	0.009169975	A3SS/EXE	FALSE
chr18:12408007-12421521	NM_006553	PRELID3A	+	novel	0.307946336	0	0.30795	0.0001626	0.009153255	A3SS	FALSE
chr14:50794525-50806736	NM_182946	NIN	-	novel	0.304648616	0.15561169	0.14904	0.0001641	0.009203175	EXI	FALSE
chr11:114446087-114447777	NM_015523	REXO2	+	novel	0.064561929	0.003836472	0.06073	0.0001674	0.009345292	A3SS	FALSE
chr6:109445875-109446135	NM_022765	MICAL1	-	novel	0.287432153	0.008064516	0.27937	0.0001679	0.009335769	A3SS	FALSE
chr8:144468406-144468586	NM_145754	KIFC2	+	novel	0.221366324	0	0.22137	0.0001685	0.009325607	A3SS	FALSE
chr1:21089213-21111322	NM_003760	EIF4G3	-	known	0.214117974	0.108613727	0.1055	0.0001702	0.009383997	EXI	FALSE
chr20:31722348-31723734	NM_138578	BCL2L1	-	known	0.939285714	0.31547619	0.62381	0.0001714	0.009408028	A3SS	FALSE
chr14:73892208-73893775	NR_040251	ZNF410	+	novel	0.23035901	0.004213814	0.22615	0.0001767	0.00965796	A3SS	TRUE
chr15:40364953-40365128	NM_033510	DISP2	+	novel	0.951388889	0.1	0.85139	0.0001792	0.009754911	A3SS	FALSE
chr7:77569794-77571077	NM_001131009	PTPN12	+	novel	0.072869126	0.006944444	0.06592	0.0001847	0.010013976	EXI	FALSE
chr10:116886566-116889093	NM_018330	SHTN1	-	novel	0.182945479	0.038720063	0.14423	0.0001849	0.009983834	EXI	FALSE
chr7:129005176-129014978	NR_034053	TNPO3	-	novel	0.065862916	0	0.06586	0.0001861	0.010007495	A3SS	FALSE
chr3:186787264-186787478	NR_002586	SNORA63	+	novel	0.125221089	0.044166492	0.08105	0.0001865	0.00998914	A3SS	FALSE
chr7:152025884-152027610	NM_022087	GALNT11	+	novel	0.101479313	0.014776698	0.0867	0.0001874	0.009997333	A3SS	FALSE
chr1:43975107-43976089	NM_004047	ATP6V0B	+	known	0.138117244	0.077894221	0.06022	0.0001882	0.009994412	EXE	FALSE
chr12:57716193-57716381	NM_006812	OS9	+	novel	0.063348199	0.000659631	0.06269	0.0001892	0.010008232	A3SS	TRUE
chr7:99561973-99562348	NM_001085368	ZNF655	+	novel	0.095514037	0.021866492	0.07365	0.0001906	0.010043913	A3SS	FALSE
chrX:19645475-19674121	NM_001184960	SH3KBP1	-	novel	0.067793858	0.015138465	0.05266	0.0001912	0.010034019	A5SS	FALSE
chr17:73201900-73203023	NM_018714	COG1	+	novel	0.271378521	0	0.27138	0.0001912	0.009994565	A3SS	TRUE
chr3:48416469-48417910	NM_002673	PLXNB1	-	novel	0.152336988	0.016452251	0.13588	0.0001915	0.009969378	A3SS	FALSE
chr11:125102351-125102733	NR_047592	TMEM218	-	known	0.580288283	0.048917749	0.53137	0.0001918	0.009944753	A3SS	FALSE
chr5:869404-870472	NR_134296	BRD9	-	novel	0.577309192	0.061315122	0.51599	0.0001959	0.010118206	EXI	TRUE
chr7:74189918-74194740	NM_031992	EIF4H	+	known	0.668350544	0.593790551	0.07456	0.0001973	0.010149375	EXE	FALSE
chr5:157488513-157489101	NM_033274	ADAM19	-	novel	0.094005828	0	0.09401	0.0001994	0.01021679	A3SS	FALSE
chr17:7227711-7227976	NM_004422	DVL2	-	novel	0.370427136	0.072336816	0.29809	0.0002014	0.010279852	A3SS	TRUE
chr2:127289519-127289688	NM_001303418	ERCC3	-	novel	0.209268016	0.059714954	0.14955	0.0002042	0.010385141	A3SS	FALSE
chr18:49785372-49787290	NM_006111	ACAA2	-	novel	0.090733829	0	0.09073	0.0002062	0.010446306	A3SS	FALSE
chr7:140041839-140054661	NR_130117	PARP12	-	known	0.052412827	0	0.05241	0.0002175	0.010976545	EXE	FALSE
chr11:46821248-46846219	NM_014756	CKAP5	-	novel	0.168674926	0.111273164	0.0574	0.000218	0.010957311	A3SS	FALSE
chr13:41372830-41373767	NM_024561	NAA16	+	novel	0.403147575	0.021428571	0.38172	0.0002196	0.010998917	A3SS	FALSE
chr16:1683592-1685438	NM_144570	HN1L	+	novel	0.277956044	0.152861598	0.12509	0.0002264	0.011295223	EXI	FALSE
chr1:6545180-6546309	NM_024654	NOL9	-	novel	0.242737143	0.007080528	0.23566	0.0002316	0.011507632	EXI	FALSE
chr9:128325239-128325765	NM_016035	COQ4	+	novel	0.06773585	0	0.06774	0.0002343	0.011602387	A3SS	FALSE
chr1:52905090-52907867	NM_018281	ECHDC2	-	known	0.706460702	0.400365403	0.3061	0.000236	0.011642175	EXE	TRUE
chr17:7944248-7944475	NM_053051	CNTROB	+	known	1	0.893417778	0.10658	0.0002377	0.011681419	EXI	FALSE

chr9:128185776-128190328	NM_001257976	CIZ1	-	known	0.120617937	0.056797225	0.06382	0.0002471	0.012095514	EXE	FALSE
chr15:43473132-43474672	NM_001141980	TP53BP1	-	novel	0.136683783	0.02892325	0.10776	0.0002476	0.012076204	EXI	FALSE
chr12:105120597-105121088	NM_015275	WASHC4	+	novel	0.197945014	0.032051421	0.16589	0.0002494	0.012120159	A3SS	FALSE
chr19:38946605-38948566	NM_148169	FBXO17	-	known	0.398565121	0.017857143	0.38071	0.0002517	0.012185575	A3SS	FALSE
chr1:207785682-207793518	NM_172361	CD46	+	known	0.694068632	0.636798166	0.05727	0.0002521	0.012159298	EXE	FALSE
chr5:109846006-109847627	NM_002372	MAN2A1	+	novel	0.178652878	0	0.17865	0.0002522	0.012119035	A3SS	FALSE
chr1:108937418-108938165	NM_001278203	CLCC1	-	novel	0.101498474	0.011859239	0.08964	0.0002537	0.012149982	EXI	FALSE
chr4:99559361-99563912	NM_152292	TRMT10A	-	known	0.756646277	0.65827838	0.09837	0.0002541	0.012122451	A3SS	FALSE
chr4:83456958-83459739	NM_016067	MRPS18C	+	known	0.212297002	0.0950177	0.11728	0.0002605	0.012382333	EXE	FALSE
chr14:23090101-23090521	NM_014977	ACIN1	-	known	0.334647337	0.160029675	0.17462	0.0002676	0.012674015	EXI	FALSE
chr11:110257927-110258105	NM_002906	RDX	-	novel	0.102945292	0.001022629	0.10192	0.0002706	0.012768875	A3SS	FALSE
chr3:45001608-45005275	NR_023353	EXOSC7	+	novel	0.085246021	0.002024291	0.08322	0.0002731	0.012841282	A3SS	FALSE
chr14:23081836-23089981	NM_014977	ACIN1	-	known	0.334754217	0.128119473	0.20663	0.0002734	0.012810883	EXI	FALSE
chr3:9390497-9391426	NR_132781	THUMPD3-AS1	-	novel	0.205617193	0.068154019	0.13746	0.0002784	0.012996551	A5SS	FALSE
chr11:77672191-77675035	NM_016578	RSF1	-	novel	0.079084066	0	0.07908	0.0002798	0.013018529	A3SS	FALSE
chr2:233414714-233434379	NM_003648	DGKD	+	novel	0.054120711	0.004098361	0.05002	0.0002903	0.013458802	A5SS	FALSE
chr17:76089320-76094413	NM_001282313	EXOC7	-	known	0.795985473	0.700818193	0.09517	0.0002911	0.013448046	EXE	FALSE
chrX:124090764-124090853	NM_006603	STAG2	+	known	0.32169957	0.175239776	0.14646	0.0003014	0.013876633	EXI	TRUE
chr22:38294534-38295386	NM_152221	CSNK1E	-	novel	0.521124428	0.30598802	0.21514	0.0003063	0.014049364	EXI	FALSE
chrX:150985144-150985594	NM_001301228	HMGB3	+	novel	0.054894305	0.002873563	0.05202	0.0003068	0.014023406	EXI	FALSE
chr5:133006920-133026496	NR_131767	ZCCHC10	-	known	0.609514119	0.47014578	0.13937	0.0003088	0.014067829	EXE	FALSE
chr12:54257692-54280007	NM_012117	CBX5	-	known	0.940977377	0.809563208	0.13141	0.0003095	0.014050022	EXE	FALSE
chr2:43577261-43578512	NM_001271643	THADA	-	novel	0.138728918	0	0.13873	0.0003109	0.014064866	A3SS	FALSE
chr1:40481854-40489087	NM_198494	ZFP69	+	known	1	0.924342105	0.07566	0.0003184	0.01435346	EXI	FALSE
chr2:112652798-112652888	NM_005415	SLC20A1	+	novel	0.076505847	0.025199958	0.05131	0.0003205	0.014401626	EXI	FALSE
chr1:179348942-179350276	NR_045530	SOAT1	+	novel	0.085605744	0	0.08561	0.0003228	0.014452553	A3SS	FALSE
chr10:34696440-34814875	NM_019619	PARD3	-	novel	0.11898138	0	0.11898	0.0003256	0.014530355	A3SS	FALSE
chr12:115975349-115975514	NM_015335	MED13L	-	novel	0.326879151	0.021728185	0.30515	0.0003297	0.014662556	A3SS	TRUE
chr12:50780238-50795897	NM_005171	ATF1	+	novel	0.096405276	0.024804867	0.0716	0.0003338	0.014793819	A3SS	FALSE
chr16:47122784-47122888	NM_018092	NETO2	-	known	0.274245855	0.218725548	0.05552	0.0003389	0.01497151	A5SS	FALSE
chr17:59070968-59075646	NM_015294	TRIM37	-	novel	0.263195761	0.002747253	0.26045	0.0003454	0.015205067	A3SS	TRUE
chr2:11767858-11771351	NM_145693	LPIN1	+	novel	0.110876609	0	0.11088	0.0003462	0.015192653	A3SS	FALSE
chr7:23187146-23192976	NM_007342	NUPL2	+	novel	0.111675379	0.022302534	0.08937	0.0003494	0.015281651	EXI	FALSE
chr19:55265378-55265885	NM_001297600	HSPBP1	-	novel	0.37541953	0.072116924	0.3033	0.0003581	0.015607482	A3SS	TRUE
chr10:124972118-124973626	NM_017580	ZRANB1	+	novel	0.081574178	0	0.08157	0.0003631	0.01577428	A3SS	FALSE
chr22:42599793-42602769	NR_103820	POLDIP3	-	known	0.211041673	0.123419363	0.08762	0.0003632	0.015726896	EXE	FALSE
chr16:30407664-30408031	NM_016643	ZNF771	+	known	0.556986532	0.088022675	0.46896	0.0003635	0.015689535	A3SS	FALSE
chr12:52491736-52492648	NM_005554	KRT6A	-	known	0.67289695	0.604688106	0.06821	0.000367	0.015785081	A5SS	FALSE
chr7:128754455-128758870	NR_074086	CALU	+	known	0.867987643	0.782738299	0.08525	0.0003686	0.015801925	EXE	FALSE
chr13:102770100-102773681	NR_104590	TEX30	-	novel	0.109083088	0.002747253	0.10634	0.0003743	0.015995844	A3SS	FALSE
chr19:1609599-1611703	NM_001136139	TCF3	-	novel	0.160730813	0.053441621	0.10729	0.0003754	0.015989105	EXE	FALSE
chr7:30771556-30778417	NM_032222	FAM188B	+	novel	0.512639553	0.053030303	0.45961	0.0003764	0.015983514	A3SS	FALSE
chr1:86376418-86382930	NM_020729	ODF2L	-	known	0.303778225	0.201930746	0.10185	0.0003777	0.01598545	EXE	FALSE
chr8:132799172-132803818	NM_198513	PHF20L1	+	known	0.46378156	0.264328936	0.19945	0.0003881	0.016373338	EXI	FALSE
chr20:35556271-35556990	NM_198398	ERGIC3	+	novel	0.067838324	0.013317238	0.05452	0.0003893	0.016371615	A3SS	TRUE
chr4:25256674-25259051	NR_144633	PI4K2B	+	novel	0.147694546	0.047225491	0.10047	0.0003952	0.016565111	A3SS	FALSE
chr9:136012013-136013198	NM_144653	NACC2	-	novel	0.277421502	0.002427184	0.27499	0.0004001	0.016717387	A3SS	FALSE
chr4:83456958-83459739	NM_016067	MRPS18C	+	known	0.252045907	0.12941834	0.12263	0.0004042	0.01683725	EXE	FALSE
chr15:42840018-42840359	NM_173500	TTBK2	-	novel	0.397275641	0	0.39728	0.0004079	0.016937629	EXI	FALSE
chr2:43774146-43774402	NM_016008	DYNC2LI1	+	novel	0.204124	0	0.20412	0.0004162	0.017227139	EXI	FALSE
chr11:46889591-46889943	NM_002334	LRP4	-	novel	0.5004095	0	0.50041	0.0004178	0.017235513	A3SS	FALSE
chr9:128185776-128190328	NM_001257976	CIZ1	-	known	0.13737516	0.05838929	0.07899	0.0004189	0.017228041	EXE	FALSE
chrX:153454508-153455541	NM_017518	HAUS7	-	known	0.793928186	0.540380078	0.25355	0.0004228	0.017335497	EXE	FALSE
chr14:64113200-64113340	NM_182914	SYNE2	+	novel	0.760731986	0.457897466	0.30283	0.0004232	0.01729592	A5SS	FALSE
chr16:56192616-56275930	NM_138736	GNAO1	+	known	1	0.825	0.175	0.0004235	0.01725496	A5SS	FALSE
chr17:78202751-78204655	NM_001145526	AFMID	+	known	0.15713778	0.076383494	0.08075	0.0004256	0.017288423	EXI	FALSE
chr1:219179246-219210514	NM_001300772	LYPLAL1	+	known	0.083602841	0.006117889	0.07748	0.0004312	0.017462194	A3SS/EXE	FALSE
chr2:97091712-97094700	NM_199336	FAHD2B	-	known	0.457739415	0.109053326	0.34869	0.0004341	0.017522991	EXE	TRUE
chrX:107715950-107716689	NM_001015881	TSC22D3	-	known	0.897758152	0.709599276	0.18816	0.0004412	0.017755063	EXE	FALSE
chr19:30012531-30015535	NR_045557	URI1	+	known	0.153576009	0.080177465	0.0734	0.0004433	0.017784381	A3SS	FALSE
chr3:93927407-93928701	NM_001314077	PROS1	-	known	0.586731128	0.081135531	0.5056	0.0004458	0.01783	EXI	FALSE
chr5:177489841-177490869	NR_103804	PDLIM7	-	novel	0.106137381	0.005030433	0.10111	0.0004496	0.0179285	A3SS/EXE	FALSE
chr3:100709721-100713653	NM_001195478	TFG	+	novel	0.078207571	0.017389876	0.06082	0.0004538	0.018042704	A3SS	FALSE
chr15:55389433-55408220	NM_004748	CCPG1	-	known	0.960455888	0.846923231	0.11353	0.0004543	0.018006982	A5SS	FALSE
chr14:74553076-74555502	NM_000428	LTBP2	-	novel	0.252079115	0.043432086	0.20865	0.0004558	0.018013286	A3SS	FALSE
chr17:47151936-47154671	NM_001293091	CDC27	-	known	0.202704009	0.085964138	0.11674	0.000456	0.017967505	A3SS	TRUE
chr1:45606591-45613168	NM_152298	NASP	+	known	0.751213146	0.63601933	0.11519	0.00046	0.018070954	EXE	FALSE
chr11:120325368-120327451	NM_174926	TMEM136	+	known	0.590433184	0.066666667	0.52377	0.0004608	0.018046423	A3SS	FALSE
chr1:185087640-185091564	NM_007212	RNF2	+	novel	0.224499866	0.04488056	0.17962	0.0004625	0.01805925	A3SS	TRUE
chr4:118278792-118278933	NR_034011	SNHG8	+	novel	0.068210236	0.01096745	0.05724	0.0004635	0.018043153	A3SS	FALSE
chr4:17804771-17810446	NR_144310	DCAF16	-	known	0.424712978	0.157224239	0.26749	0.0004673	0.01813743	EXE	FALSE
chr6:47710886-47711692	NM_153838	ADGRF4	+	novel	0.077212128	0	0.07721	0.0004679	0.018108851	EXI	FALSE
chr7:102433661-102436201	NM_032831	ORAI2	+	known	0.814285714	0.033333333	0.78095	0.0004746	0.018314362	A3SS	FALSE
chr21:46649739-46652844	NM_206962	PRMT2	+	novel	0.246742105	0.074344215	0.1724	0.0004773	0.018364114	EXI	FALSE
chr8:38404506-38407347	NM_001199660	LETM2	+	novel	0.079897008	0.004587156	0.07531	0.0004807	0.018439968	A3SS	FALSE
chr1:6232119-6234885	NM_012405	ICMT	-	known	0.140137227	0.075715639	0.06442	0.0004825	0.018455747	EXE	FALSE
chr22:40404664-40405648	NM_015705	SGSM3	+	known	0.133016588	0.042563491	0.09045	0.0004865	0.018556638	EXE	FALSE
chr17:59940943-59945384	NM_003161	RPS6KB1	+	novel	0.090629989	0	0.09063	0.0004918	0.018703073	A3SS	FALSE
chr1:205811087-205812807	NM_173854	SLC41A1	-	known	0.71154733	0.549825228	0.16172	0.0004985	0.018903834	A5SS	FALSE
chr1:155268197-155268292	NM_003993	CLK2	-	novel	0.092880282	0.001879699	0.091	0.0005005	0.018922745	A3SS	FALSE
chr11:65620966-65622223	NM_032223	PCNX3	+	novel	0.311808579	0.076119842	0.23569	0.0005049	0.019033463	A3SS	FALSE
chr19:40578212-40578447	NM_138392	SHKBP1	+	novel	0.09582403	0.007452981	0.08837	0.0005075	0.019077269	A3SS	TRUE
chr21:37198025-37200213	NM_003316	TTC3	+	novel	0.064443766	0	0.06444	0.0005078	0.019034046	A3SS	TRUE
chr2:86489437-86489519	NM_001146688	KDM3A	+	known	1	0.922906441	0.07709	0.0005134	0.019188991	A3SS	FALSE
chr9:35608509-35608845	NM_006285	TESK1	+	novel	0.157251082	0	0.15725	0.0005167	0.019259303	A3SS	FALSE
chrX:101348401-101348532	NM_001145951	TIMM8A	-	known	0.147092371	0.093019613	0.05407	0.0005221	0.019406487	EXI	FALSE
chr1:74740239-74748750	NR_027962	TYW3	+	novel	0.052664443	0.00127551	0.05139	0.0005236	0.019406222	A5SS	FALSE
chr12:121968169-121971503	NM_144668	WDR66	+	novel	0.073106953	0.002525253	0.07058	0.0005283	0.019524851	EXE	FALSE
chr2:215947113-215996305	NM_018000	MREG	-	known	0.952139475	0.892664158	0.05948	0.0005323	0.01961709	EXE	FALSE
chr16:69121184-69121435	NM_001040146	CHTF8	-	novel	0.052518115	0	0.05252	0.0005344	0.019638655	A3SS	FALSE
chr5:72228383-72232442	NM_015084	MRPS27	-	novel	0.071782926	0.000659631	0.07112	0.0005355	0.019626421	A3SS	FALSE

chr2:200507091-200510010	NM_152387	KCTD18	-	known	0.489176169	0.224150609	0.26503	0.0005372	0.019630773	A5SS	FALSE
chr17:42562219-42562355	NM_025233	COASY	+	known	0.917708895	0.277472527	0.64024	0.0005404	0.019693448	A3SS	FALSE
chr3:149966264-149968357	NM_053024	PFN2	-	known	0.882514715	0.793160128	0.08935	0.000552	0.020060335	A3SS	FALSE
chr1:35405468-35407986	NM_005095	ZMYM4	+	novel	0.175371455	0	0.17537	0.000563	0.020404644	A3SS	TRUE
chrX:124090964-124094017	NM_006603	STAG2	+	known	0.325833227	0.182218948	0.14361	0.000567	0.02049203	EXI	TRUE
chr22:23867899-23868480	NM_001024939	SLC2A11	+	novel	0.320466298	0	0.32047	0.0005689	0.020506308	EXI	FALSE
chr10:45962994-45965788	NR_029388	PARGP1	-	novel	0.354861111	0	0.35486	0.0005709	0.020522592	EXE	FALSE
chr1:11070988-11072086	NM_002685	EXOSC10	-	novel	0.112756503	0.043100646	0.06966	0.0005832	0.020906254	A3SS	TRUE
chr1:31740034-31740109	NM_001294336	ADGRB2	-	known	1	0.877544466	0.12246	0.0005903	0.021104181	EXI	FALSE
chr13:41373880-41374741	NM_024561	NAA16	+	novel	0.463636364	0.048898567	0.41474	0.0005907	0.021060773	A5SS	FALSE
chr16:88586684-88598177	NM_144604	ZC3H18	+	known	0.770087477	0.653971392	0.11612	0.0005982	0.021268942	EXE	FALSE
chr11:72228498-72228646	NM_001567	INPPL1	+	novel	0.396452084	0.022301409	0.37415	0.0005983	0.021214366	A3SS	TRUE
chr17:6895503-6896315	NR_120453	ALOX12P2	+	known	0.895833333	0.588068182	0.30777	0.0006017	0.021279296	EXI	FALSE
chr2:55225313-55232235	NM_152385	CLHC1	-	novel	0.708333333	0	0.70833	0.0006116	0.021571079	EXI	FALSE
chr20:43667303-43673707	NM_002466	MYBL2	+	novel	0.060530797	0.001666667	0.05886	0.0006173	0.021713881	A3SS	FALSE
chr2:55922447-55923710	NM_001039349	EFEMP1	-	known	0.79117902	0.726553168	0.06463	0.0006223	0.021830066	EXE	FALSE
chr5:141680503-141682172	NM_022481	ARAP3	-	known	0.635542929	0.53215723	0.10339	0.0006243	0.021843296	A3SS	FALSE
chr1:43975107-43976089	NM_004047	ATP6V0B	+	known	0.139750454	0.081522545	0.05823	0.0006248	0.021803242	EXE	FALSE
chr10:73824084-73837467	NM_172173	CAMK2G	-	known	0.184274231	0.066304669	0.11797	0.0006345	0.022081517	EXE	FALSE
chr2:169812524-169819560	NM_014168	METTL5	-	novel	0.051221096	0	0.05122	0.0006426	0.022304555	EXE	FALSE
chr14:22768171-22769776	NM_005015	OXA1L	+	novel	0.116639891	0	0.11664	0.0006448	0.02232027	A3SS	TRUE
chr4:39867015-39869393	NM_001100399	PDS5A	-	novel	0.100406681	0.002142968	0.09826	0.0006461	0.022306072	A3SS	FALSE
chr10:79692056-79766270	NR_120613	NUTM2B-AS1	-	known	0.50527027	0.276011738	0.22926	0.0006488	0.022340536	EXE	FALSE
chr2:73266682-73268725	NM_001080410	FBXO41	-	known	1	0.888549331	0.11145	0.0006516	0.022378324	A3SS	FALSE
chr13:32480637-32517856	NM_001320836	N4BP2L2	-	novel	0.859722222	0.236862745	0.62286	0.0006552	0.022443216	EXI	FALSE
chr17:79083955-79084537	NM_001042573	ENGASE	+	known	0.134747518	0.0125	0.12225	0.0006618	0.022612935	A5SS	FALSE
chr7:849603-849831	NM_001130965	SUN1	+	novel	0.148599042	0.009377579	0.13922	0.0006676	0.022749467	A3SS	FALSE
chr3:41239354-41239659	NM_001904	CTNNB1	+	known	0.414551998	0.349502116	0.06505	0.0006698	0.022766905	A3SS	FALSE
chr1:229271370-229286467	NR_073545	RAB4A	+	novel	0.129990417	0.001851852	0.12814	0.000681	0.023088183	A3SS	FALSE
chr9:96943154-96949554	NR_002894	MFSD14C	-	novel	0.651689617	0.378913425	0.27278	0.0006942	0.023474757	EXI	FALSE
chr4:6824684-6842066	NM_014743	KIAA0232	+	known	0.99609375	0.943062191	0.05303	0.0006992	0.02358089	EXE	FALSE
chr1:186331596-186332194	NM_003292	TPR	-	novel	0.081191476	0.002394703	0.0788	0.0007139	0.024016227	A3SS	FALSE
chr10:91264520-91271637	NM_032373	PCGF5	+	known	0.651254804	0.542350667	0.1089	0.0007222	0.024233076	EXI	FALSE
chr6:143333445-143339638	NM_016108	AIG1	+	known	0.891445024	0.808709964	0.08274	0.0007329	0.024528275	EXI	FALSE
chr4:962613-962771	NM_001347	DGKQ	-	known	1	0.941452127	0.05855	0.0007334	0.024482855	EXI	FALSE
chr3:179347810-179348847	NM_033540	MFN1	+	novel	0.281340974	0.156835064	0.12451	0.0007351	0.024477591	A3SS	FALSE
chr22:40404664-40405648	NM_015705	SGSM3	+	known	0.075862429	0.025759618	0.0501	0.0007372	0.024487168	EXE	FALSE
chr1:210233011-210237943	NM_019605	SERTAD4	+	known	1	0.73452381	0.26548	0.0007394	0.024495935	A5SS/EXE	FALSE
chr2:191400468-191408114	NM_012223	MYO1B	+	known	0.850294887	0.79537933	0.05492	0.000742	0.024522073	EXE	FALSE
chr11:65540153-65540244	NM_021070	LTBP3	-	known	0.107824569	0	0.10782	0.0007491	0.024694181	EXI	FALSE
chr9:125484583-125506309	NM_024117	MAPKAP1	-	known	0.616994957	0.555649966	0.06134	0.0007598	0.024982979	EXE	FALSE
chr10:97446353-97451670	NR_109895	ZDHHC16	+	known	0.943885258	0.865423314	0.07846	0.0007655	0.02510735	EXE	FALSE
chr3:159886324-159887707	NM_001197109	SCHIP1	+	known	0.994047619	0.910932873	0.08311	0.0007656	0.025049614	EXI	FALSE
chr14:24296588-24298956	NM_138452	DHRS1	-	known	0.050217405	0	0.05022	0.0007756	0.025313506	EXE	FALSE
chr3:4362254-4410864	NM_182760	SUMF1	-	known	0.096509724	0.023343681	0.07317	0.0007763	0.02527358	EXE	FALSE
chr9:137555648-137564433	NM_001346389	DPH7	-	known	0.994117647	0.915113304	0.079	0.0007897	0.025646677	A3SS	FALSE
chr22:45158185-45163517	NR_038956	NUP50-AS1	-	novel	0.352941176	0.142857143	0.21008	0.00079	0.025591483	EXI	FALSE
chr15:69160757-69196414	NM_015554	GLCE	+	known	0.284891293	0.119953618	0.16494	0.0007912	0.025566582	EXI	FALSE
chr6:99435846-99439768	NM_001346029	USP45	-	known	0.256445869	0.047557604	0.20889	0.0007943	0.025605147	EXE	FALSE
chr13:36335832-36336286	NM_015087	SPG20	-	known	0.298325601	0.195555027	0.10277	0.0007968	0.025621752	EXI	FALSE
chr1:16582758-16585488	NM_017940	NBPF1	-	known	0.118805704	0.006410256	0.1124	0.0007971	0.025569629	EXE	FALSE
chr1:10536297-10599237	NM_004565	PEX14	+	known	0.856960955	0.728951341	0.12801	0.0007973	0.025513664	EXI	FALSE
chr7:149252795-149253558	NM_012256	ZNF212	+	known	1	0.937362758	0.06264	0.0008043	0.025673765	EXI	FALSE
chr3:39100454-39101015	NR_103867	GORASP1	-	known	0.253613506	0.01222421	0.24139	0.0008323	0.026504757	A3SS/EXE	FALSE
chrX:41660582-41665276	NM_003688	CASK	-	novel	0.062230712	0	0.06223	0.0008347	0.026516092	A3SS	FALSE
chr4:82448021-82454721	NR_120457	ENOPH1	+	known	0.279506194	0.191215134	0.08829	0.0008686	0.027527915	EXE	FALSE
chr18:50285247-50285748	NM_014593	CXXC1	-	known	0.204485462	0.021251341	0.18323	0.0008707	0.027528036	EXE	FALSE
chr1:235489255-235494680	NM_152490	B3GALNT2	-	novel	0.06536904	0	0.06537	0.000873	0.027532194	A3SS	FALSE
chr1:52912951-52913894	NM_018281	ECHDC2	-	novel	0.063658779	0	0.06366	0.0008762	0.02756921	EXI	FALSE
chr16:58010112-58012303	NM_024598	USB1	+	novel	0.18578166	0	0.18578	0.0008766	0.027512922	A3SS	FALSE
chr2:85621579-85623605	NM_006590	USP39	+	novel	0.074474788	0.000816993	0.07366	0.0008784	0.027505282	A3SS	FALSE
chr4:20724888-20727284	NR_047661	PACRGL	+	known	0.504001123	0.321802631	0.1822	0.0008813	0.027530133	EXI	FALSE
chr11:4082982-4083241	NM_003156	STIM1	+	novel	0.207144539	0	0.20714	0.0008832	0.027522799	A3SS	TRUE
chr1:153627598-153631010	NM_006271	S100A1	+	known	0.615244055	0.35078869	0.26446	0.0008842	0.027490162	A5SS	FALSE
chr2:218650526-218656149	NR_073600	ZNF142	-	known	0.754913818	0.482352782	0.27256	0.0009015	0.027961263	EXE	FALSE
chr2:171785475-171787570	NR_047549	SLC25A12	-	known	0.981812632	0.926824463	0.05499	0.0009038	0.027965497	EXI	FALSE
chrX:119618786-119625334	NM_145802	SEPT6	-	known	0.198025987	0.025574713	0.17245	0.0009097	0.028082388	EXI	FALSE
chr1:23338608-23344210	NM_005826	HNRNPR	-	known	0.654486479	0.580119489	0.07437	0.0009102	0.028033036	EXE	FALSE
chr1:200586281-200589216	NM_001305792	KIF14	-	novel	0.071732651	0	0.07173	0.0009122	0.028027393	A3SS	FALSE
chr8:125038976-125039794	NM_014846	WASHC5	-	novel	0.117205968	0.004164437	0.11304	0.0009122	0.027963257	A3SS	FALSE
chr6:166366062-166366794	NR_073093	MPC1	-	novel	0.084261344	0.017351974	0.06691	0.0009183	0.028084752	A3SS	FALSE
chr21:46235446-46236828	NR_110567	MCM3AP-AS1	+	novel	0.057490611	0.004919465	0.05257	0.0009186	0.028027249	A5SS	FALSE
chr16:89291183-89291680	NR_045839	ANKRD11	-	known	0.398237179	0.1265921	0.27165	0.0009353	0.028469943	EXI	FALSE
chr18:59155807-59157607	NM_033280	SEC11C	+	known	0.942238718	0.891463394	0.05078	0.0009354	0.028409902	EXI	FALSE
chr5:136132962-136147831	NM_005903	SMAD5	+	known	0.983969636	0.908570347	0.0754	0.0009366	0.028379136	EXE	FALSE
chr9:27029104-27036449	NM_025103	IFT74	+	known	0.141085828	0.015233934	0.12585	0.0009407	0.028437872	EXI	FALSE
chr9:128325881-128332165	NM_016035	COQ4	+	novel	0.058496113	0	0.0585	0.0009461	0.028536211	A3SS	FALSE
chr10:69195265-69196977	NR_136627	SUPV3L1	+	novel	0.053579784	0	0.05358	0.0009462	0.028471874	A3SS	FALSE
chr1:26177580-26180452	NM_006314	CNKSR1	+	known	0.212824485	0.065365909	0.14746	0.0009567	0.028723793	A5SS	FALSE
chr16:55545817-55549255	NM_017839	LPCAT2	+	novel	0.105752341	0	0.10575	0.0009644	0.028888353	A3SS	FALSE
chr7:128748804-128754261	NR_074086	CALU	+	known	0.892511218	0.83233338	0.06018	0.0009915	0.02963273	EXI	FALSE
chr3:15247457-15250974	NM_014296	CAPN7	+	novel	0.091923487	0.020238677	0.07168	0.0010013	0.029855812	A3SS	FALSE
chr10:1072293-1077893	NM_014023	WDR37	+	novel	0.084203526	0	0.0842	0.0010029	0.029836873	A3SS	FALSE
chrX:119625396-119629317	NM_145802	SEPT6	-	novel	0.112733015	0.008064516	0.10467	0.0010054	0.029843904	A3SS	FALSE
chr6:85538864-85541984	NM_153816	SNX14	-	known	0.243643255	0.130142818	0.1135	0.0010082	0.029857773	EXI	FALSE
chr2:97091712-97094700	NM_199336	FAHD2B	-	known	0.431154888	0.069954662	0.3612	0.0010171	0.030055615	EXE	TRUE
chr3:186787882-186789124	NM_001967	EIF4A2	+	known	0.278516894	0.168331514	0.11019	0.001029	0.030339278	EXE	FALSE
chr20:38532859-38535073	NM_020336	RALGAPB	+	known	0.831311923	0.673854046	0.15746	0.0010301	0.030302199	A3SS	FALSE
chr11:47161190-47161445	NR_103472	C11orf49	+	known	0.303109262	0.076430417	0.22668	0.0010409	0.030551784	A3SS	FALSE
chr1:5905483-5905631	NR_111987	NPHP4	-	known	1	0.942880153	0.05712	0.0010455	0.030618566	A3SS	FALSE
chr1:45606591-45613168	NM_152298	NASP	+	known	0.847191604	0.727935324	0.11926	0.0010478	0.03061609	EXE	FALSE

chr7:8227851-8228600	NM_022307	ICA1	-	novel	0.198110998	0.02443609	0.17367	0.001053	0.030701733	EXI	TRUE
chr1:108938216-108939635	NM_001278203	CLCC1	-	novel	0.101098539	0.009353741	0.09174	0.0010613	0.030873658	EXI	FALSE
chr15:90969120-90969523	NR_051984	PRC1-AS1	+	known	0.202939289	0.114682091	0.08826	0.0010679	0.0309978	A3SS	FALSE
chr6:25420164-25426467	NM_017640	CARMIL1	+	novel	0.072768547	0.004237288	0.06853	0.0010716	0.031036591	A3SS	FALSE
chr12:42442741-42445945	NM_016488	PPHLN1	+	novel	0.150228347	0.009341033	0.14089	0.0010735	0.031023598	A3SS	FALSE
chr19:41906025-41906702	NM_199002	ARHGEF1	+	known	0.252162354	0.19162713	0.06054	0.0010753	0.031005818	EXE	FALSE
chrX:85971586-85978766	NM_001320959	CHM	-	known	0.231611313	0.040673077	0.19094	0.0010758	0.030953187	EXI	FALSE
chr15:82475637-82476785	NR_102748	LOC727751	-	novel	0.622977941	0.059150327	0.56383	0.0010771	0.030921916	A3SS	FALSE
chr9:122997361-122998575	NM_012197	RABGAP1	+	novel	0.191036368	0.003731343	0.18731	0.0010809	0.030962713	A3SS	TRUE
chr3:47852938-47853162	NM_002375	MAP4	-	known	0.182993141	0.084039998	0.09895	0.0010814	0.03091132	A3SS	FALSE
chr1:226297832-226301172	NM_173083	LIN9	-	novel	0.085832281	0	0.08583	0.0010973	0.031296876	A3SS	FALSE
chr6:35287845-35290252	NM_003427	ZNF76	+	novel	0.090319191	0	0.09032	0.0010991	0.03127956	A3SS	FALSE
chr11:113815382-113823604	NM_020886	USP28	-	known	0.108160685	0.047943248	0.06022	0.0010994	0.031220403	EXE	FALSE
chr1:234448576-234450427	NM_005646	TARBP1	-	novel	0.588495669	0.427815369	0.16068	0.0011023	0.031236056	A3SS	FALSE
chr3:10118970-10125611	NM_018462	BRK1	+	novel	0.205555867	0.01744186	0.18811	0.0011049	0.031241039	A3SS	FALSE
chr3:186787882-186789124	NM_001967	EIF4A2	+	known	0.200059088	0.133936967	0.06612	0.0011093	0.031299044	EXE	FALSE
chr2:175993223-175994133	NM_030650	LNPK	-	known	0.148064437	0.087358725	0.06071	0.0011129	0.031334023	EXI	FALSE
chr5:90475020-90485524	NM_006467	POLR3G	+	known	0.759223906	0.631022545	0.1282	0.0011321	0.031805521	A3SS	FALSE
chr15:82859168-82864166	NM_199330	HOMER2	-	known	0.279374093	0.182838035	0.09654	0.0011327	0.031754213	A3SS	FALSE
chr18:62107103-62109833	NM_176787	PIGN	-	novel	0.07948505	0	0.07949	0.0011344	0.031733196	A3SS	FALSE
chr6:25974930-25983163	NM_006355	TRIM38	+	novel	0.109438535	0.004237288	0.1052	0.0011441	0.031936174	A5SS	FALSE
chr16:1537753-1557934	NM_024600	TMEM204	+	novel	0.373511905	0.035714286	0.3378	0.001146	0.031923133	A5SS	FALSE
chr11:2972279-2976023	NM_005969	NAP1L4	-	novel	0.171923066	0.080077934	0.09185	0.0011496	0.031955261	A3SS	TRUE
chr13:102638315-102640298	NM_003291	TPP2	+	novel	0.086190763	0.001602564	0.08459	0.0011516	0.031941819	A3SS	FALSE
chr4:9835008-9887566	NM_020041	SLC2A9	-	known	0.911704713	0.798667015	0.11304	0.001158	0.03205299	EXI	FALSE
chr4:9920572-9941912	NM_020041	SLC2A9	-	known	0.981457982	0.913586148	0.06787	0.001161	0.03206807	EXI	FALSE
chr1:93201988-93207106	NM_206886	CCDC18	+	known	0.141965752	0.022660819	0.1193	0.0011676	0.032183195	EXE	FALSE
chr1:179865869-179877692	NM_145034	TOR1AIP2	-	novel	0.07410332	0.003503559	0.0706	0.0011853	0.032602705	A3SS/EXE	FALSE
chr13:102645009-102646279	NM_003291	TPP2	+	novel	0.168415319	0	0.16842	0.0011866	0.03256911	A3SS	FALSE
chr20:62197518-62197851	NM_015666	MTG2	+	novel	0.421428571	0.041666667	0.37976	0.0011874	0.032523302	A5SS	FALSE
chr22:42577962-42578539	NR_002184	RRP7BP	-	novel	0.076670917	0	0.07667	0.0011886	0.032489466	A5SS	FALSE
chr14:64926080-65004248	NM_198686	RAB15	-	known	0.064169071	0	0.06417	0.0011956	0.032610974	EXE	FALSE
chr5:133993018-134004894	NR_036625	VDAC1	-	known	0.861021062	0.700073675	0.16095	0.0011987	0.032627698	A3SS/EXE	FALSE
chr1:6255122-6260824	NM_207370	GPR153	-	novel	0.939285714	0.298869048	0.64042	0.0012007	0.032614609	A3SS	FALSE
chr13:26396354-26397138	NM_001346501	CDK8	+	novel	0.160969817	0	0.16097	0.001209	0.032773055	A3SS	FALSE
chr5:132758824-132759936	NM_015146	SEPT8	-	novel	0.120618156	0.04532482	0.07529	0.0012204	0.033014979	EXI	FALSE
chr14:80906081-80914321	NM_152446	CEP128	-	known	0.988095238	0.916126374	0.07197	0.0012271	0.033125462	EXE	FALSE
chr22:31784875-31784979	NM_014662	DEPDC5	+	novel	0.139978735	0	0.13998	0.0012279	0.033079615	EXI	FALSE
chr1:61686921-61694696	NR_135162	TM2D1	-	known	0.198014747	0.062632755	0.13538	0.0012303	0.033076891	EXI	FALSE
chrX:48893831-48893899	NM_005834	TIMM17B	-	novel	0.059610483	0.001131222	0.05848	0.0012457	0.033423321	A3SS	TRUE
chr20:35472151-35472756	NM_001318219	CEP250	+	novel	0.135250394	0	0.13525	0.0012546	0.033593117	A3SS	FALSE
chr11:46370009-46371312	NM_001105540	DGKZ	+	known	0.989708571	0.919401744	0.07031	0.0012618	0.033715541	EXI	FALSE
chr19:43608107-43611988	NM_182498	ZNF428	-	novel	0.061232978	0.006818182	0.05441	0.0012642	0.033711013	EXI/EXE	FALSE
chr1:19312358-19312728	NR_109848	PQLC2	+	known	0.983314794	0.883900544	0.09941	0.0012668	0.033711507	EXI	FALSE
chr1:161157693-161158411	NM_016406	UFC1	+	known	0.111192812	0.059945599	0.05125	0.0012702	0.033736008	EXE	FALSE
chr22:23791867-23793558	NM_003073	SMARCB1	+	known	0.6614152	0.538379029	0.12304	0.0012732	0.033746946	A5SS	FALSE
chr1:161157693-161158411	NM_016406	UFC1	+	known	0.110313689	0.059531815	0.05078	0.0012773	0.033786698	EXE	FALSE
chrX:111681299-111682235	NM_001324294	ALG13	+	known	0.160086405	0.032377806	0.12771	0.0012824	0.033854193	A3SS	FALSE
chr15:89327079-89327166	NM_002693	POLG	-	novel	0.083526809	0.009180223	0.07435	0.0012825	0.033787109	A3SS	FALSE
chr13:110615647-110622215	NM_018210	NAXD	+	known	0.952582608	0.876101014	0.07648	0.0012934	0.034006724	A5SS	FALSE
chr1:116406148-116418458	NR_024126	ATP1A1-AS1	-	known	0.45297619	0.083333333	0.36964	0.0012937	0.033945848	EXE	FALSE
chr22:31626016-31628002	NM_014338	PISD	-	known	1	0.901852559	0.09815	0.0013003	0.0340508	EXI	FALSE
chr10:38094490-38095357	NM_003421	ZNF37A	+	known	0.308008718	0.088345865	0.21966	0.0013021	0.034031921	EXE	FALSE
chr20:35346461-35347163	NM_199487	UQCC1	-	novel	0.226652017	0	0.22665	0.0013048	0.034033306	EXI	FALSE
chr5:134744052-134750758	NM_001745	CAMLG	+	known	0.879082554	0.796094422	0.08299	0.0013185	0.034322519	EXI	FALSE
chr2:99406106-99408028	NR_135653	REV1	-	known	0.120131707	0	0.12013	0.0013256	0.034438649	EXE	FALSE
chr13:114282127-114286518	NM_080687	UPF3A	+	known	0.269253247	0.072193369	0.19706	0.0013323	0.034544027	EXE	FALSE
chr1:37795846-37799566	NM_152496	MANEAL	+	known	0.197296475	0.096157461	0.10114	0.0013355	0.034559762	EXE	FALSE
chr15:44499813-44501961	NM_016396	CTDSPL2	+	novel	0.075152055	0.004204353	0.07095	0.0013472	0.034794266	EXI	FALSE
chr14:39265421-39276933	NM_203355	MIA2	+	known	0.557461163	0.295196324	0.26226	0.0013474	0.034731372	EXE	TRUE
chr6:158625754-158631322	NM_020823	TMEM181	+	known	0.086652277	0.020108233	0.06654	0.0013514	0.034764193	EXE	FALSE
chr7:2222754-2229983	NM_003550	MAD1L1	-	known	0.064602065	0.006841817	0.05776	0.0013644	0.035029989	EXE	FALSE
chr21:38291747-38296925	NM_170737	KCNJ15	+	known	0.6655228	0.575976389	0.08955	0.0013688	0.03507509	EXI	FALSE
chr13:112875941-112881812	NM_032189	ATP11A	+	novel	1	0.805988368	0.19401	0.0013705	0.035050783	EXE	FALSE
chr15:57063823-57072652	NM_001322165	TCF12	+	known	0.103324436	0.045394131	0.05793	0.0013783	0.035181765	EXI	FALSE
chr4:26742599-26748410	NM_018317	TBC1D19	+	known	1	0.893859649	0.10614	0.0013819	0.035204094	EXI	FALSE
chr10:127008804-127012294	NM_001380	DOCK1	+	known	0.801762504	0.705731848	0.09603	0.0013917	0.035385682	A3SS	FALSE
chr11:64305736-64307167	NM_001282450	ESRRA	+	known	0.820115811	0.72108639	0.09903	0.0013928	0.035345914	EXE	FALSE
chr8:21971968-21974669	NM_015024	XPO7	+	novel	0.06060963	0.003816413	0.05679	0.0013938	0.035302425	A5SS	FALSE
chr1:20779911-20787194	NM_016287	HP1BP3	-	novel	0.665341197	0.505947437	0.15939	0.0013949	0.035261125	EXE	FALSE
chr6:80040703-80042097	NM_003318	TTK	+	novel	0.076190308	0.005296551	0.07089	0.0013992	0.035303851	A3SS	FALSE
chr20:49174269-49188115	NM_017454	STAU1	-	known	0.849736893	0.735576426	0.11416	0.0013994	0.035238985	EXE	FALSE
chr18:12420493-12421521	NM_001142406	PRELID3A	+	novel	0.348076923	0	0.34808	0.0014025	0.03525065	A3SS	FALSE
chr2:164722522-164727968	NM_014900	COBLL1	-	known	1	0.926909323	0.07309	0.0014099	0.035368234	EXE	FALSE
chr1:228140363-228145510	NM_001242840	GUK1	+	known	0.792915971	0.712247503	0.08067	0.0014279	0.035751599	EXE	FALSE
chr20:32161365-32165294	NM_014742	TM9SF4	+	known	0.98580653	0.890494148	0.09531	0.0014352	0.035866606	EXI	FALSE
chr7:195732-208897	NM_020223	FAM20C	+	known	0.902218678	0.779807813	0.12241	0.0014376	0.035857434	EXE	FALSE
chr11:59144896-59145826	NM_198847	FAM111A	+	known	0.692341897	0.609513652	0.08283	0.001439	0.035825567	EXE	FALSE
chr10:93389154-93396141	NM_133337	MYOF	-	known	0.451307632	0.30739086	0.14392	0.0014407	0.035799312	EXE	FALSE
chr12:122855612-122855815	NM_003959	HIP1R	+	novel	0.068133021	0.007042254	0.06109	0.0014444	0.03582266	A3SS	FALSE
chr17:79950578-79951449	NM_019020	TBC1D16	-	known	0.803200747	0.614397453	0.1888	0.0014484	0.035855475	A3SS	FALSE
chr17:4892768-4892945	NM_170663	MINK1	+	novel	0.11234337	0.006578947	0.10576	0.0014485	0.035788988	A3SS	FALSE
chr3:112993124-112996891	NM_138485	GTPBP8	+	known	0.133942382	0.064843884	0.0691	0.0014525	0.03582199	EXE	FALSE
chr11:122155632-122156928	NR_137194	MIR100HG	-	known	0.2545627	0.0437113	0.21085	0.0014581	0.035892849	A5SS	FALSE
chr3:196886694-196899665	NM_152699	SENP5	+	known	0.908879274	0.814401985	0.09448	0.0014592	0.035851358	EXE	FALSE
chr2:55573777-55574368	NM_020463	PPP4R3B	-	novel	0.09109985	0.040123506	0.05098	0.0014644	0.035912677	EXI	FALSE
chrX:49923482-49925170	NM_001272102	CLCN5	+	known	0.936647727	0.703571429	0.23308	0.0014648	0.035854512	A5SS	FALSE
chr2:43774546-43776781	NM_016008	DYNC2LI1	+	novel	0.098761257	0	0.09876	0.0014655	0.035805921	EXI	FALSE
chr9:137728529-137743370	NM_024757	EHMT1	+	known	0.597163766	0.407242308	0.18992	0.0014713	0.035879981	EXI	TRUE
chr19:49048372-49048724	NM_033183	CGB8	-	known	1	0.720907382	0.27909	0.0014746	0.035894275	EXI	FALSE
chr12:51049185-51053811	NR_045017	LETMD1	+	novel	0.263925755	0.082634653	0.18129	0.0014755	0.035849817	A3SS/EXE	FALSE

chr16:16318079-16318513	NR_036447	PKD1P1	+	novel	0.950769231	0.722587719	0.22818	0.0014762	0.035800648	EXI	FALSE
chr12:109483981-109485996	NM_183415	UBE3B	+	novel	0.067392903	0	0.06739	0.001492	0.036117012	A3SS	FALSE
chr13:26671989-26680034	NM_006646	WASF3	+	known	0.25064703	0.104922212	0.14572	0.0014983	0.036200907	EXE	FALSE
chr14:53093444-53103682	NM_030637	DDHD1	-	known	0.788191057	0.541492875	0.2467	0.0015214	0.036692926	EXI	FALSE
chr1:168023047-168038370	NM_018442	DCAF6	+	known	0.250960696	0.188629915	0.06233	0.0015223	0.03664806	EXI	FALSE
chr19:49646202-49646504	NM_021228	SCAF1	+	novel	0.058396533	0	0.0584	0.0015226	0.036587379	A3SS	FALSE
chr17:35670898-35671753	NM_001282	AP2B1	+	known	0.376504845	0.308785466	0.06772	0.001531	0.03672252	EXI	FALSE
chr17:18333288-18335558	NM_148918	SHMT1	-	known	0.732127353	0.628718672	0.10341	0.0015338	0.036721132	EXI	FALSE
chr11:130122513-130126699	NM_001243299	APLP2	+	known	0.517162576	0.457842446	0.05932	0.0015416	0.036842035	EXE	FALSE
chr11:62787527-62789009	NM_199337	TMEM179B	+	novel	0.091861326	0	0.09186	0.0015424	0.036792511	A3SS	FALSE
chr19:1254082-1254166	NM_177401	MIDN	+	novel	0.26094625	0.113424947	0.14752	0.0015449	0.03678667	EXI	FALSE
chr7:23193051-23195838	NM_007342	NUPL2	+	novel	0.15839314	0.033601504	0.12479	0.0015491	0.036818309	A5SS	FALSE
chr1:40531787-40533142	NM_152373	ZNF684	+	known	0.781261141	0.513876748	0.26738	0.0015659	0.037150431	EXI	FALSE
chr11:46821248-46846219	NM_014756	CKAP5	-	novel	0.993055556	0.773002553	0.22005	0.0015781	0.037373741	A5SS	FALSE
chr17:28575544-28575964	NM_005165	ALDOC	-	novel	0.210803111	0.104649976	0.10615	0.0015801	0.03735238	EXI	FALSE
chr8:144255705-144259239	NM_001288814	MROH1	+	known	0.115690228	0	0.11569	0.0015847	0.037393628	EXE	FALSE
chr17:78204900-78205092	NM_001145526	AFMID	+	known	0.246909041	0.056472149	0.19044	0.0015903	0.037458613	EXI	FALSE
chr3:185698347-185823152	NM_001291875	IGF2BP2	-	known	0.787899453	0.659728155	0.12817	0.0016157	0.037990347	EXE	FALSE
chr6:125248383-125253716	NM_001318907	TPD52L1	+	known	0.532797015	0.374124458	0.15867	0.0016263	0.038169812	EXI	FALSE
chrX:63697304-63703169	NM_015185	ARHGEF9	-	novel	0.077571471	0.00625	0.07132	0.00163	0.038188173	EXI	FALSE
chr1:225002927-225007420	NM_001373	DNAH14	+	novel	0.514381271	0.034090909	0.48029	0.0016383	0.038314539	A3SS	FALSE
chr14:75056560-75063953	NR_126395	ACYP1	-	novel	0.251406926	0.019230769	0.23218	0.0016416	0.038322399	EXE	FALSE
chr1:41028726-41037361	NR_037868	SLFNL1-AS1	+	known	0.592328371	0.355880393	0.23645	0.0016434	0.038298399	EXE	FALSE
chr5:141973742-141978302	NM_183401	RNF14	+	known	0.256700064	0.186405791	0.07029	0.0016492	0.03836409	EXE	FALSE
chr20:46355241-46356573	NM_173179	SLC35C2	-	known	0.212607742	0.057539663	0.15507	0.0016513	0.038346207	EXE	FALSE
chr18:50285247-50285748	NM_014593	CXXC1	-	known	0.181551143	0.017937105	0.16361	0.0016644	0.038580519	EXE	FALSE
chr17:75693482-75699758	NR_126037	SAP30BP	+	novel	0.088651853	0	0.08865	0.0016777	0.038820622	A3SS	FALSE
chr17:37489958-37510676	NM_007026	DUSP14	+	known	0.705063177	0.489561765	0.2155	0.001698	0.039221547	A5SS	FALSE
chr1:155061489-155061903	NR_040773	DCST1-AS1	-	known	0.382180561	0.295814363	0.08637	0.0016998	0.039194421	EXE	FALSE
chr11:870499-883147	NM_023947	CHID1	-	known	0.898423169	0.7821754	0.11625	0.0017047	0.039237409	EXE	FALSE
chr15:89317536-89318540	NM_002693	POLG	-	known	0.935989307	0.865231671	0.07076	0.0017072	0.039225721	EXE	FALSE
chr7:140041839-140054661	NR_130117	PARP12	-	known	0.06684976	0	0.06685	0.0017074	0.039162787	EXE	FALSE
chr7:30020304-30022664	NR_046479	FKBP14	-	known	0.100755776	0.044742108	0.05601	0.0017163	0.039297354	EXI	FALSE
chr9:72363631-72364695	NM_001278245	ZFAND5	-	novel	0.058596457	0.001582278	0.05701	0.0017213	0.039343703	A3SS/EXE	FALSE
chr7:56074218-56074585	NM_015411	SUMF2	+	known	0.944447466	0.887004033	0.05744	0.0017396	0.039693522	EXI	FALSE
chr17:39178079-39183712	NM_199248	CACNB1	-	known	0.711309524	0.429629488	0.28168	0.001742	0.039677955	EXE	FALSE
chr8:85113099-85115099	NM_033402	LRRCC1	+	known	0.937258687	0.703296166	0.23396	0.001745	0.039678495	EXE	FALSE
chr22:21629187-21629307	NM_001017964	YDJC	-	known	0.859966435	0.723477908	0.13649	0.0017599	0.039948902	EXI	FALSE
chr8:119794944-119795531	NM_003184	TAF2	-	novel	0.270552397	0.007378265	0.26317	0.0017619	0.039923503	EXI	FALSE
chr11:64800826-64800899	NM_004579	MAP4K2	-	known	0.88693555	0.62429735	0.26264	0.0017715	0.040072235	EXI	FALSE
chr1:235829039-235830225	NM_000081	LYST	-	novel	0.587269622	0.342094017	0.24518	0.0017771	0.040129609	A3SS	FALSE
chr8:85217502-85220305	NR_120681	C8orf59	-	known	0.416878676	0.347308687	0.06957	0.0017818	0.040167489	EXE	FALSE
chr12:32602317-32607937	NM_001304480	FGD4	+	known	0.1772741	0.023008242	0.15427	0.0017889	0.040258394	A3SS	FALSE
chr3:46992555-46993936	NM_015175	NBEAL2	+	known	0.271170946	0.111486526	0.15968	0.0017991	0.040418204	EXI	FALSE
chr20:32114920-32133012	NM_014742	TM9SF4	+	novel	0.12686695	0	0.12687	0.0018215	0.04085254	EXI	FALSE
chr5:43068217-43099019	NR_102752	LOC100506639	+	novel	0.241141457	0.045833333	0.19531	0.0018243	0.040843657	EXE	FALSE
chr22:37641168-37641373	NM_018957	SH3BP1	+	known	0.914942505	0.791197562	0.12374	0.0018404	0.041134217	EXI	FALSE
chr3:23911446-23916783	NM_020345	NKIRAS1	-	novel	0.386760462	0	0.38676	0.0018565	0.041424057	A5SS	FALSE
chr2:91618154-91655367	NR_027238	LOC654342	-	novel	1	0.829623879	0.17038	0.0018568	0.041359631	EXE	FALSE
chr15:68199681-68205244	NR_104583	CALML4	-	known	0.187896825	0	0.1879	0.0018653	0.041478813	EXE	FALSE
chr8:1843436-1857959	NM_014629	ARHGEF10	+	known	0.987794613	0.90443217	0.08336	0.0018668	0.041442262	EXI	FALSE
chr2:159712661-159715680	NM_022826	MARCH7	+	novel	0.478125	0.0625	0.41563	0.0018739	0.04152921	A5SS	FALSE
chr3:10046723-10047883	NM_001319984	FANCD2	+	novel	0.190402173	0.004032258	0.18637	0.0018772	0.04153157	A3SS	FALSE
chr16:1678356-1683508	NM_144570	HN1L	+	novel	0.152358381	0.098503787	0.05385	0.0018778	0.041475788	EXI	TRUE
chr9:123403490-123411775	NM_024820	DENND1A	-	novel	0.224962795	0.122867855	0.10209	0.0018896	0.04166751	EXI	FALSE
chr3:37251484-37281957	NM_002078	GOLGA4	+	known	0.175773592	0.113876219	0.0619	0.0018927	0.041665554	EXE	FALSE
chr1:37795846-37799566	NM_152496	MANEAL	+	known	0.130203542	0.062508184	0.0677	0.0018958	0.041664153	EXE	FALSE
chr10:38096632-38114761	NM_003421	ZNF37A	+	novel	0.110187761	0.003333333	0.10685	0.001897	0.041618724	A3SS	FALSE
chr18:36145034-36145933	NR_137173	ELP2	+	novel	0.111166218	0.001037344	0.11013	0.0019034	0.041691527	A3SS	FALSE
chr11:64925028-64925662	NM_006244	PPP2R5B	+	novel	0.186994949	0	0.18699	0.0019212	0.04201059	A3SS	FALSE
chr17:78187433-78190969	NR_027083	AFMID	+	known	0.924383488	0.823322606	0.10106	0.0019223	0.041963567	A5SS	FALSE
chr9:14088326-14102421	NM_001282787	NFIB	-	known	0.626951538	0.444428694	0.18252	0.0019408	0.042298531	EXI	FALSE
chr4:128946164-128948495	NM_144643	SCLT1	-	novel	0.114044303	0.034315978	0.07973	0.001941	0.042232997	A3SS	FALSE
chr11:10855118-10856143	NM_021211	ZBED5	-	known	0.513043981	0.124006359	0.38904	0.0019515	0.042390112	A3SS	FALSE
chr10:73824084-73837467	NM_172173	CAMK2G	-	known	0.149706885	0.053105522	0.0966	0.0019612	0.042530247	EXE	FALSE
chr17:80214783-80215032	NM_000199	SGSH	-	novel	0.131935295	0.011904762	0.12003	0.0019697	0.04264433	A3SS	TRUE
chr2:55177781-55181569	NM_152385	CLHC1	-	known	0.678571429	0.148601399	0.52997	0.0019704	0.042589011	EXE	FALSE
chr15:41736698-41740052	NM_001164273	MGA	+	known	0.613049451	0.332415277	0.28063	0.001973	0.04257563	A3SS	FALSE
chr11:124625903-124626459	NR_016021	TBRG1	+	novel	0.051420198	0	0.05142	0.0019771	0.042593121	A3SS	FALSE
chr5:154218149-154294815	NM_198321	GALNT10	+	novel	0.109638278	0.01805601	0.09158	0.0019784	0.042551214	A5SS	FALSE
chr3:4362254-4410864	NM_182760	SUMF1	-	known	0.071319253	0.017815687	0.0535	0.0019829	0.042578609	EXE	FALSE
chr14:64924126-64925990	NM_145165	CHURC1	+	novel	0.072180059	0.005521049	0.06666	0.0019855	0.042564517	A3SS	FALSE
chr2:218659130-218659368	NR_073600	ZNF142	-	known	0.969030809	0.757981911	0.21105	0.0020096	0.043011833	A3SS	FALSE
chr19:35000486-35009118	NM_020895	GRAMD1A	+	known	0.966760692	0.846518053	0.12024	0.0020143	0.043042746	EXE	FALSE
chr11:65109923-65110462	NR_073519	VPS51	+	novel	0.107985341	0	0.10799	0.0020165	0.043019712	A3SS	TRUE
chr4:128176907-128178430	NM_018078	LARP1B	+	known	0.487096237	0.052564103	0.43453	0.0020215	0.043055644	EXI	FALSE
chr4:17804771-17805106	NR_144310	DCAF16	-	known	0.935661904	0.733397448	0.20226	0.0020222	0.042999514	A3SS	FALSE
chr16:89972765-89977714	NR_003228	AFG3L1P	+	novel	0.389186211	0.070140797	0.31905	0.0020395	0.043298866	A3SS	FALSE
chr19:53091720-53103264	NM_198893	ZNF160	-	known	1	0.884599673	0.1154	0.0020405	0.043248374	A5SS	FALSE
chr11:18239969-18245909	NM_001199744	SAA2-SAA4	-	known	0.149456686	0.00297619	0.14648	0.002041	0.043190659	EXE	FALSE
chr16:15599024-15600427	NM_014647	KIAA0430	-	known	0.9921875	0.934320887	0.05787	0.00205	0.043311423	A3SS	FALSE
chr16:88809706-88810069	NM_001030018	APRT	-	known	0.382743656	0.318744166	0.064	0.0020549	0.04334443	A3SS	FALSE
chr16:721436-721800	NM_023933	FAM173A	+	known	0.113929998	0.007142857	0.10679	0.002055	0.043277341	EXE	FALSE
chr2:74363628-74365074	NM_023019	DCTN1	-	known	0.055933059	0.004418072	0.05151	0.0020652	0.043422679	EXI	FALSE
chr11:47565986-47571470	NM_175732	PTPMT1	+	known	0.458411651	0.392967614	0.06544	0.0020781	0.043623202	EXE	FALSE
chr3:9911597-9913955	NR_104198	IL17RE	+	known	0.928612479	0.736560722	0.19205	0.0020785	0.043562717	EXE	FALSE
chr6:109159102-109159217	NM_173830	CEP57L1	+	novel	0.087459389	0.004716981	0.08274	0.0020819	0.043563192	A3SS	FALSE
chr7:98981960-98983239	NM_003496	TRRAP	+	novel	0.153986191	0.036393955	0.11759	0.002087	0.04360127	A3SS	FALSE
chr3:46991946-46992474	NM_015175	NBEAL2	+	known	0.317905561	0.127028219	0.19088	0.0020923	0.043642293	EXI	FALSE
chr19:49865279-49866398	NM_007254	PNKP	-	novel	0.102406153	0	0.10241	0.0020993	0.043719609	A3SS	FALSE
chr16:489000-496823	NM_001142272	RAB11FIP3	+	known	0.634732124	0.380620819	0.25411	0.0021066	0.043801754	EXE	FALSE

chr6:158625754-158631322	NM_020823	TMEM181	+	known	0.110006387	0.028383353	0.08162	0.0021087	0.043776063	EXE	FALSE
chr4:39232272-39234765	NM_025132	WDR19	+	known	1	0.926496888	0.0735	0.0021244	0.044031114	A3SS	FALSE
chr11:72822961-72823543	NM_033388	ATG16L2	+	novel	0.141025641	0	0.14103	0.0021522	0.044538365	EXI	FALSE
chr12:4536219-4538408	NR_144382	C12orf4	-	known	0.956101345	0.880092593	0.07601	0.0021564	0.04455457	EXI	FALSE
chr6:85513895-85514069	NM_153816	SNX14	-	known	0.9427077	0.868126814	0.07458	0.0021834	0.04504193	EXI	FALSE
chr10:127257429-127272010	NM_001380	DOCK1	+	novel	0.168368895	0.07327511	0.09509	0.0021879	0.045063863	EXI	FALSE
chr14:24301722-24302003	NM_174913	NOP9	+	novel	0.064341185	0	0.06434	0.0022106	0.045459114	A3SS	FALSE
chr7:100356938-100358226	NR_036570	STAG3L5P-PVRIG	+	novel	0.648809524	0	0.64881	0.002224	0.045663575	A3SS	FALSE
chr9:131643417-131650809	NM_198679	RAPGEF1	-	known	0.559279727	0.385538982	0.17374	0.0022241	0.045593435	EXE	FALSE
chr16:635340-636093	NR_109979	METTL26	-	known	0.394144404	0.313512397	0.08063	0.0022363	0.045772446	EXE	FALSE
chr12:10884275-10973654	NM_001291315	PRH1	-	known	0.357575758	0.078282828	0.27929	0.0022459	0.045897847	EXE	FALSE
chr2:87049790-87052813	NR_026846	LOC285074	-	novel	0.073611306	0.00255102	0.07106	0.0022472	0.045851747	A3SS	FALSE
chr4:140379192-140379568	NM_001153663	SCOC	+	known	0.779682654	0.701882085	0.0778	0.0022477	0.045792345	EXI	FALSE
chr16:721436-721800	NM_023933	FAM173A	+	known	0.057785889	0.002941176	0.05484	0.002248	0.045727451	EXE	FALSE
chr3:68988395-68988505	NR_103826	EOGT	-	novel	0.104145877	0	0.10415	0.0022627	0.045953755	A3SS	FALSE
chr2:160200023-160200185	NM_001282390	ITGB6	-	novel	0.75801021	0.574603175	0.18341	0.0022638	0.045906373	A5SS	FALSE
chr15:68199681-68205244	NR_104583	CALML4	-	known	0.232503608	0	0.2325	0.0022833	0.04622917	EXE	FALSE
chr22:37639846-37641125	NM_018957	SH3BP1	+	known	0.889192233	0.731919225	0.15727	0.002286	0.046212845	EXI	FALSE
chr1:155668777-155670319	NM_001198899	YY1AP1	-	known	0.600403769	0.4344576	0.16595	0.00229	0.04622287	A3SS	FALSE
chr5:79988666-79989151	NM_001167741	MTX3	-	novel	0.179471587	0	0.17947	0.002299	0.046333451	A3SS	FALSE
chr2:218656463-218658979	NR_073600	ZNF142	-	known	0.319378721	0.137475329	0.1819	0.0023068	0.046418359	EXE	FALSE
chr19:17175741-17183828	NM_004145	MYO9B	+	known	0.145404353	0.049382067	0.09602	0.002311	0.046432464	EXE	FALSE
chr3:10918453-10926003	NM_014229	SLC6A11	+	known	0.676041667	0.424393105	0.25165	0.0023155	0.0464515	EXE	FALSE
chr11:123619224-123622477	NM_001286564	GRAMD1B	+	novel	0.060969066	0	0.06097	0.0023169	0.046408024	A3SS	FALSE
chr15:75339344-75339964	NM_001321848	COMMD4	+	known	0.132297211	0.051827641	0.08047	0.0023183	0.04636654	EXE	TRUE
chr1:52912021-52913894	NM_018281	ECHDC2	-	known	0.791047074	0.48902742	0.30202	0.0023207	0.046343914	A3SS	FALSE
chr6:125292909-125300537	NM_016063	HDDC2	-	known	0.506756321	0.447002281	0.05975	0.0023296	0.046450782	EXE	FALSE
chr5:177169559-177191883	NM_022455	NSD1	+	novel	0.078124435	0.015486717	0.06264	0.0023407	0.04660011	EXI	FALSE
chr6:41637273-41638738	NM_001300804	MDFI	+	known	0.214075116	0.082905007	0.13117	0.0023735	0.047182701	EXE	FALSE
chr4:155800074-155802314	NM_001291955	GUCY1B3	+	novel	0.284970238	0	0.28497	0.0023754	0.047149171	A3SS	FALSE
chr9:137453180-137454390	NM_015537	NSMF	-	known	0.204683922	0.108185009	0.0965	0.002386	0.047286977	EXE	FALSE
chr1:61683546-61686791	NR_135162	TM2D1	-	known	0.342195095	0.187429297	0.15477	0.0023937	0.047369255	EXI	FALSE
chr12:77056147-77064542	NM_203394	E2F7	-	novel	0.179903396	0.002083333	0.17782	0.0023963	0.047348657	A3SS	FALSE
chr16:1352306-1361685	NM_032520	GNPTG	+	novel	0.133221348	0	0.13322	0.0024042	0.047434107	A3SS	TRUE
chr2:214792445-214797060	NR_104216	BARD1	-	known	0.979659874	0.902272083	0.07739	0.0024143	0.047560867	EXI	FALSE
chr1:19153954-19154917	NM_020765	UBR4	-	novel	0.384748719	0.088329301	0.29642	0.0024226	0.047653374	A3SS	TRUE
chr15:74448587-74449185	NM_201265	UBL7	-	novel	0.097978316	0.015770893	0.08221	0.0024296	0.047718638	A3SS	FALSE
chr22:45138916-45158059	NR_038957	NUP50-AS1	-	novel	0.445833333	0.078336466	0.3675	0.002444	0.047930262	EXI	FALSE
chr2:74529912-74530271	NR_135772	HTRA2	+	novel	0.441666667	0	0.44167	0.0024509	0.047993606	A3SS	FALSE
chr10:96132670-96133555	NM_001330734	ZNF518A	+	known	0.364331984	0.087121212	0.27721	0.0024811	0.048513048	A3SS	FALSE
chr14:50792881-50794435	NM_182946	NIN	-	novel	0.376128456	0.206229414	0.1699	0.0024868	0.048551087	EXI	FALSE
chr7:100356883-100358226	NR_036570	STAG3L5P-PVRIG	+	novel	0.330454137	0.004032258	0.32642	0.0024868	0.048479141	A3SS	TRUE
chr15:28655420-28655795	NR_036443	HERC2P9	+	known	0.959722222	0.753090659	0.20663	0.0024889	0.04844815	EXE	FALSE
chr3:134195182-134200352	NM_002958	RYK	-	novel	0.062672494	0.000621891	0.06205	0.0024938	0.048472744	EXI	FALSE
chr1:43653799-43655590	NM_014663	KDM4A	+	novel	0.081375867	0.030931308	0.05044	0.0025372	0.049242368	EXI	FALSE
chr12:45893721-45904933	NM_152641	ARID2	+	known	0.983946078	0.922871954	0.06107	0.0025389	0.049203779	EXE	FALSE
chr16:30095434-30096096	NM_031477	YPEL3	-	known	0.892227564	0.6925	0.19973	0.002547	0.049286615	A3SS	FALSE
chr10:35071339-35090429	NM_003591	CUL2	-	known	0.728284897	0.627863899	0.10042	0.0025526	0.049322196	EXE	FALSE
chr19:51581517-51581786	NM_007147	ZNF175	+	known	1	0.818939394	0.18106	0.0025645	0.049480266	A5SS	FALSE
chr1:39463686-39465094	NM_012090	MACF1	+	novel	0.589064823	0.449755374	0.13931	0.0025646	0.049408514	EXI	FALSE
chr16:78115154-78118954	NR_120436	WWOX	+	novel	0.163585165	0	0.16359	0.0025689	0.049419173	EXI	FALSE
chr10:125088319-125110989	NM_001321014	CTBP2	-	novel	0.162850086	0.070874327	0.09198	0.0025778	0.049518338	EXI	FALSE
chr4:119291261-119292337	NM_019050	USP53	+	known	0.874939423	0.794264835	0.08067	0.0025886	0.04965312	EXI	FALSE
chr14:74674111-74675698	NM_001039479	AREL1	-	known	1	0.948350231	0.05165	0.0025998	0.049794595	A5SS	FALSE

Table S2. Genes downregulated in SF3B1-mutant MCF-10A cells. Whole gene mRNA expression ratios for SF3B1-MUT/SF3B1-WT clones were generated from RNA-seq data and those with log2FC less than -0.5 are shown.

GeneID	**Gene symbol**	**baseMean**	**log2FoldChange**	**lfcSE**	**stat**	**pvalue**	**padj**
ENSG00000138028.14	CGREF1	218.6794796	-3.780373937	0.148434	-25.4684	4.41E-143	8.52E-140
ENSG00000130598.15	TNNI2	132.65841	-1.967659757	0.158654	-12.4022	2.54E-35	4.24E-33
ENSG00000134215.15	VAV3	111.9465489	-1.946416459	0.139992	-13.9038	6.01E-44	1.42E-41
ENSG00000149043.16	SYT8	566.6555633	-1.748134523	0.111611	-15.6627	2.72E-55	8.55E-53
ENSG00000137975.7	CLCA2	3759.087379	-1.69829214	0.129518	-13.1124	2.80E-39	5.40E-37
ENSG00000092621.11	PHGDH	827.9149846	-1.647210171	0.141576	-11.6348	2.74E-31	4.07E-29
ENSG00000164961.15	KIAA0196	2534.510992	-1.577438728	0.038313	-41.1724	0	0
ENSG00000154556.17	SORBS2	19.69094735	-1.571586398	0.172912	-9.08893	1.00E-19	7.51E-18
ENSG00000137710.14	RDX	5549.729489	-1.522204625	0.036358	-41.8675	0	0
ENSG00000131269.15	ABCB7	927.2666257	-1.498197537	0.069686	-21.4994	1.58E-102	1.42E-99
ENSG00000107159.12	CA9	81.29717976	-1.483555623	0.162984	-9.10246	8.83E-20	6.74E-18
ENSG00000134900.11	TPP2	2464.458271	-1.44165674	0.045677	-31.5618	1.23E-218	4.17E-215
ENSG00000144045.13	DQX1	38.42176525	-1.391438787	0.165527	-8.4061	4.24E-17	2.59E-15
ENSG00000101407.12	TTI1	1265.844047	-1.381994859	0.065364	-21.1429	3.20E-99	2.55E-96
ENSG00000146085.7	MUT	682.18003	-1.355882455	0.069015	-19.6461	6.24E-86	4.02E-83
ENSG00000105290.11	APLP1	22.28271621	-1.308392795	0.169389	-7.72418	1.13E-14	5.40E-13
ENSG00000150556.16	LYPD6B	20.04537292	-1.28980391	0.174682	-7.38371	1.54E-13	6.67E-12
ENSG00000146094.13	DOK3	39.34971133	-1.284034244	0.166731	-7.70125	1.35E-14	6.41E-13
ENSG00000198919.12	DZIP3	322.8789804	-1.242783832	0.127082	-9.77939	1.38E-22	1.32E-20
ENSG00000179826.6	MRGPRX3	72.17444623	-1.23974557	0.174304	-7.11256	1.14E-12	4.44E-11
ENSG00000197417.7	SHPK	103.7975757	-1.239139334	0.141619	-8.74982	2.14E-18	1.46E-16
ENSG00000137440.4	FGFBP1	576.1582818	-1.230088237	0.088907	-13.8357	1.55E-43	3.56E-41
ENSG00000102580.14	DNAJC3	5866.394177	-1.229340163	0.075322	-16.321	6.99E-60	2.56E-57
ENSG00000198093.10	ZNF649	142.3453925	-1.225578004	0.116031	-10.5625	4.45E-26	5.14E-24
ENSG00000144452.14	ABCA12	2006.358759	-1.213918966	0.090448	-13.4212	4.54E-41	9.16E-39
ENSG00000075711.20	DLG1	2641.17807	-1.210188385	0.061616	-19.641	6.91E-86	4.25E-83
ENSG00000163359.15	COL6A3	1169.513838	-1.208426392	0.076851	-15.7243	1.03E-55	3.40E-53
ENSG00000106804.7	C5	118.7680693	-1.171479239	0.157083	-7.45773	8.80E-14	3.91E-12
ENSG00000174799.10	CEP135	789.5793247	-1.150101603	0.059493	-19.3317	2.91E-83	1.64E-80
ENSG00000135341.17	MAP3K7	2173.927696	-1.147732556	0.050633	-22.6675	9.39E-114	1.15E-110
ENSG00000066027.11	PPP2R5A	1387.346691	-1.138526388	0.082955	-13.7247	7.22E-43	1.57E-40
ENSG00000137075.17	RNF38	485.0381215	-1.131703159	0.076801	-14.7356	3.81E-49	1.03E-46
ENSG00000189001.10	SBSN	57.98445269	-1.125869732	0.153398	-7.33952	2.14E-13	9.14E-12
ENSG00000164828.17	SUN1	3063.865352	-1.115339271	0.047376	-23.5422	1.51E-122	2.27E-119
ENSG00000149294.16	NCAM1	75.65591203	-1.109058598	0.163282	-6.7923	1.10E-11	3.80E-10
ENSG00000115355.15	CCDC88A	1568.027859	-1.105430497	0.06438	-17.1704	4.42E-66	1.99E-63
ENSG00000162545.5	CAMK2N1	732.9859863	-1.104073632	0.093456	-11.8139	3.31E-32	5.14E-30
ENSG00000180998.11	GPR137C	38.53980769	-1.096726247	0.170851	-6.4192	1.37E-10	3.93E-09
ENSG00000119326.14	CTNNAL1	2638.629317	-1.074464384	0.10452	-10.28	8.67E-25	9.31E-23
ENSG00000188042.7	ARL4C	996.0444425	-1.070249772	0.101496	-10.5447	5.37E-26	6.15E-24
ENSG00000139211.6	AMIGO2	1903.969473	-1.0639582	0.070071	-15.184	4.52E-52	1.27E-49
ENSG00000129636.12	ITFG1	975.5886205	-1.063910387	0.077003	-13.8165	2.03E-43	4.57E-41
ENSG00000108947.4	EFNB3	134.6447104	-1.063242662	0.136077	-7.81354	5.56E-15	2.77E-13
ENSG00000119333.11	WDR34	1713.817278	-1.057431976	0.076711	-13.7846	3.15E-43	6.99E-41
ENSG00000009950.15	MLXIPL	16.45129722	-1.053747518	0.173753	-6.06462	1.32E-09	3.29E-08
ENSG00000100341.11	PNPLA5	21.58791168	-1.041971811	0.172431	-6.04284	1.51E-09	3.72E-08
ENSG00000107672.14	NSMCE4A	715.6101165	-1.038204815	0.093238	-11.135	8.48E-29	1.15E-26
ENSG00000137815.14	RTF1	1656.300648	-1.006759289	0.05479	-18.3749	2.09E-75	1.08E-72
ENSG00000047410.13	TPR	11737.89303	-1.003591137	0.022682	-44.2456	0	0
ENSG00000101680.13	LAMA1	955.9136844	-1.000784531	0.059644	-16.7793	3.46E-63	1.38E-60
ENSG00000166033.11	HTRA1	1978.334389	-0.994709047	0.11936	-8.33368	7.84E-17	4.65E-15
ENSG00000064313.11	TAF2	2905.826751	-0.986777803	0.043613	-22.6256	2.43E-113	2.73E-110
ENSG00000005156.11	LIG3	1297.531305	-0.975552435	0.068476	-14.2465	4.71E-46	1.14E-43
ENSG00000046653.14	GPM6B	313.8179098	-0.96990343	0.165971	-5.84381	5.10E-09	1.15E-07
ENSG00000114030.12	KPNA1	1606.818384	-0.95804655	0.042544	-22.5192	2.69E-112	2.80E-109
ENSG00000119285.10	HEATR1	7863.88955	-0.949350106	0.04762	-19.936	1.98E-88	1.41E-85
ENSG00000137941.16	TTLL7	358.0365333	-0.948124537	0.143084	-6.62635	3.44E-11	1.09E-09

ENSG00000102977.13	ACD	921.9741653	-0.942375521	0.053989	-17.455	3.15E-68	1.47E-65
ENSG00000022267.16	FHL1	139.3446082	-0.937063965	0.170194	-5.50587	3.67E-08	7.10E-07
ENSG00000135318.11	NT5E	16831.55838	-0.920062014	0.043743	-21.0333	3.25E-98	2.44E-95
ENSG00000072422.16	RHOBTB1	22.54998514	-0.914593483	0.158389	-5.77434	7.73E-09	1.67E-07
ENSG00000137411.16	VARS2	615.85899	-0.909584934	0.066898	-13.5966	4.19E-42	8.86E-40
ENSG00000137821.11	LRRC49	193.3592879	-0.895440882	0.106339	-8.42066	3.74E-17	2.30E-15
ENSG00000004700.15	RECQL	2732.628448	-0.890884657	0.044978	-19.8071	2.58E-87	1.75E-84
ENSG00000005073.5	HOXA11	66.1252587	-0.889760641	0.14723	-6.04335	1.51E-09	3.71E-08
ENSG00000132964.11	CDK8	990.8299166	-0.886373466	0.058699	-15.1004	1.61E-51	4.44E-49
ENSG00000118523.5	CTGF	272.8085359	-0.884312609	0.096378	-9.17548	4.50E-20	3.53E-18
ENSG00000121892.14	PDS5A	9761.616961	-0.881160766	0.038526	-22.8717	8.89E-116	1.20E-112
ENSG00000132164.9	SLC6A11	560.6294633	-0.865751283	0.138007	-6.27322	3.54E-10	9.52E-09
ENSG00000203668.2	CHML	2344.174068	-0.860245181	0.056335	-15.2703	1.21E-52	3.55E-50
ENSG00000127415.12	IDUA	78.75642847	-0.847581289	0.160675	-5.27512	1.33E-07	2.30E-06
ENSG00000173085.13	COQ2	699.8652582	-0.846971322	0.110975	-7.63211	2.31E-14	1.08E-12
ENSG00000169047.5	IRS1	156.4880631	-0.841394779	0.156713	-5.36903	7.92E-08	1.42E-06
ENSG00000099250.17	NRP1	1700.844799	-0.839365045	0.049361	-17.0047	7.58E-65	3.30E-62
ENSG00000118777.10	ABCG2	89.0215885	-0.832228514	0.171252	-4.85966	1.18E-06	1.68E-05
ENSG00000028310.17	BRD9	1326.365739	-0.827205063	0.141463	-5.84751	4.99E-09	1.13E-07
ENSG00000156103.15	MMP16	115.5843827	-0.826651367	0.139849	-5.91101	3.40E-09	7.91E-08
ENSG00000152527.13	PLEKHH2	112.4596464	-0.823169785	0.127478	-6.45735	1.07E-10	3.12E-09
ENSG00000170903.10	MSANTD4	781.7940976	-0.811656641	0.059751	-13.5839	4.99E-42	1.04E-39
ENSG00000151779.12	NBAS	2454.7205	-0.810729756	0.038071	-21.2953	1.25E-100	1.06E-97
ENSG00000130751.9	NPAS1	20.33150677	-0.808889652	0.174524	-4.63483	3.57E-06	4.50E-05
ENSG00000152495.10	CAMK4	203.7928883	-0.806332942	0.137791	-5.85186	4.86E-09	1.11E-07
ENSG00000138336.8	TET1	47.470735	-0.794111695	0.158647	-5.00552	5.57E-07	8.54E-06
ENSG00000172766.18	NAA16	736.0564765	-0.792069974	0.060233	-13.15	1.70E-39	3.33E-37
ENSG00000134759.13	ELP2	2505.456978	-0.789574488	0.097443	-8.10292	5.37E-16	2.97E-14
ENSG00000117543.20	DPH5	639.4865863	-0.785562596	0.100185	-7.84111	4.47E-15	2.25E-13
ENSG00000197608.11	ZNF841	218.0842187	-0.784295408	0.130626	-6.00411	1.92E-09	4.64E-08
ENSG00000165548.10	TMEM63C	150.2668203	-0.780553416	0.127187	-6.13704	8.41E-10	2.17E-08
ENSG00000138138.13	ATAD1	3421.596145	-0.779893962	0.041145	-18.9547	4.04E-80	2.18E-77
ENSG00000138378.17	STAT4	144.063795	-0.779719581	0.153843	-5.06829	4.01E-07	6.33E-06
ENSG00000087494.15	PTHLH	265.2132949	-0.776460498	0.174818	-4.44154	8.93E-06	0.0001
ENSG00000181104.6	F2R	121.942761	-0.776300015	0.174645	-4.44501	8.79E-06	9.88E-05
ENSG00000186272.12	ZNF17	153.7983741	-0.773718529	0.128346	-6.02838	1.66E-09	4.03E-08
ENSG00000162004.16	CCDC78	76.78639103	-0.770200587	0.144402	-5.33374	9.62E-08	1.70E-06
ENSG00000101230.5	ISM1	157.5740997	-0.764774727	0.113279	-6.75124	1.47E-11	4.95E-10
ENSG00000163378.13	EOGT	3089.12849	-0.761732464	0.046927	-16.2324	2.97E-59	1.03E-56
ENSG00000069122.18	ADGRF5	12.49130872	-0.761549585	0.166448	-4.5753	4.76E-06	5.75E-05
ENSG00000112893.9	MAN2A1	3845.008158	-0.754565795	0.044668	-16.8926	5.10E-64	2.16E-61
ENSG00000141013.15	GAS8	77.50827896	-0.742476506	0.140034	-5.30212	1.14E-07	2.00E-06
ENSG00000143851.15	PTPN7	13.20672353	-0.738992871	0.171169	-4.31733	1.58E-05	0.000163
ENSG00000143315.6	PIGM	678.7899479	-0.738926668	0.057399	-12.8735	6.35E-38	1.14E-35
ENSG00000075702.16	WDR62	777.5485004	-0.738714746	0.093548	-7.89665	2.87E-15	1.47E-13
ENSG00000128510.10	CPA4	201.6302021	-0.738046968	0.172719	-4.27311	1.93E-05	0.000194
ENSG00000095970.16	TREM2	41.95447224	-0.737079147	0.174477	-4.2245	2.39E-05	0.000233
ENSG00000023902.13	PLEKHO1	250.9234025	-0.736865917	0.14583	-5.05293	4.35E-07	6.79E-06
ENSG00000144026.11	ZNF514	77.27800455	-0.736078578	0.156744	-4.69606	2.65E-06	3.46E-05
ENSG00000169715.14	MT1E	6056.247713	-0.73500044	0.115459	-6.36591	1.94E-10	5.46E-09
ENSG00000168243.10	GNG4	1010.480304	-0.73278538	0.076472	-9.58239	9.48E-22	8.60E-20
ENSG00000100505.13	TRIM9	39.3929128	-0.731729658	0.17482	-4.18563	2.84E-05	0.000271
ENSG00000157833.12	GAREM2	226.8282735	-0.730156298	0.132778	-5.49908	3.82E-08	7.35E-07
ENSG00000099822.2	HCN2	151.6437722	-0.728537471	0.169922	-4.28748	1.81E-05	0.000183
ENSG00000142619.4	PADI3	49.77337754	-0.72430776	0.174594	-4.14852	3.35E-05	0.000315
ENSG00000065717.14	TLE2	100.8144699	-0.72201626	0.152497	-4.73462	2.19E-06	2.91E-05
ENSG00000106003.12	LFNG	306.926105	-0.72048832	0.128568	-5.60393	2.10E-08	4.18E-07
ENSG00000067840.12	PDZD4	380.6993988	-0.720482025	0.108109	-6.66443	2.66E-11	8.59E-10
ENSG00000004864.13	SLC25A13	2029.853482	-0.719915632	0.053983	-13.3361	1.43E-40	2.84E-38
ENSG00000161551.13	ZNF577	18.17533569	-0.715056761	0.173211	-4.12824	3.66E-05	0.000338
ENSG00000110075.14	PPP6R3	7006.395951	-0.713784044	0.039307	-18.1592	1.09E-73	5.24E-71

ENSG00000273802.2	HIST1H2BG	6455.516091	-0.710494935	0.169489	-4.19197	2.77E-05	0.000265
ENSG00000135919.12	SERPINE2	1811.051942	-0.709627625	0.107919	-6.57559	4.85E-11	1.50E-09
ENSG00000141404.15	GNAL	644.5758446	-0.701395788	0.072678	-9.65075	4.88E-22	4.46E-20
ENSG00000168385.17	SEPT2	11465.29774	-0.700766727	0.023867	-29.3617	1.69E-189	4.58E-186
ENSG00000111816.7	FRK	330.1252216	-0.699116296	0.085316	-8.19448	2.52E-16	1.42E-14
ENSG00000128739.21	SNRPN	84.23447099	-0.695047983	0.145764	-4.7683	1.86E-06	2.53E-05
ENSG00000102854.15	MSLN	638.5498469	-0.694218016	0.157912	-4.39624	1.10E-05	0.00012
ENSG00000137040.9	RANBP6	2154.481994	-0.694156808	0.061689	-11.2526	2.25E-29	3.20E-27
ENSG00000142173.14	COL6A2	669.839565	-0.692698386	0.154272	-4.49012	7.12E-06	8.23E-05
ENSG00000169896.16	ITGAM	9.677224511	-0.687631361	0.158732	-4.33204	1.48E-05	0.000155
ENSG00000177494.5	ZBED2	1542.782047	-0.687463871	0.116004	-5.9262	3.10E-09	7.24E-08
ENSG00000166394.14	CYB5R2	33.86842973	-0.687397307	0.174708	-3.93455	8.34E-05	0.000697
ENSG00000168615.11	ADAM9	8934.118935	-0.685946508	0.053147	-12.9066	4.13E-38	7.65E-36
ENSG00000138399.17	FASTKD1	1914.37716	-0.683067987	0.07331	-9.31751	1.19E-20	9.76E-19
ENSG00000184305.14	CCSER1	5.973755583	-0.681475132	0.142651	-4.77721	1.78E-06	2.44E-05
ENSG00000119139.17	TJP2	1356.882571	-0.679781119	0.056221	-12.0913	1.17E-33	1.87E-31
ENSG00000057252.12	SOAT1	3929.27557	-0.679183919	0.049047	-13.8477	1.31E-43	3.06E-41
ENSG00000163485.15	ADORA1	129.0726378	-0.675455674	0.136093	-4.96319	6.93E-07	1.05E-05
ENSG00000070601.9	FRMPD1	26.59565875	-0.675038617	0.174171	-3.87572	0.000106	0.000863
ENSG00000112367.10	FIG4	316.1561479	-0.674432556	0.108195	-6.23349	4.56E-10	1.21E-08
ENSG00000143443.9	C1orf56	53.52908105	-0.670767199	0.152641	-4.39442	1.11E-05	0.000121
ENSG00000164120.13	HPGD	5.688981896	-0.669578042	0.142007	-4.7151	2.42E-06	3.18E-05
ENSG00000156931.15	VPS8	739.4665714	-0.669295372	0.072819	-9.19121	3.88E-20	3.07E-18
ENSG00000169750.8	RAC3	733.8227554	-0.668707117	0.086144	-7.76271	8.31E-15	4.03E-13
ENSG00000049323.15	LTBP1	7803.958328	-0.66741442	0.104723	-6.37317	1.85E-10	5.23E-09
ENSG00000136235.15	GPNMB	17.04448395	-0.667362645	0.174198	-3.83106	0.000128	0.001014
ENSG00000265972.5	TXNIP	4865.834501	-0.664383817	0.149579	-4.44168	8.93E-06	0.0001
ENSG00000167676.4	PLIN4	135.3398045	-0.661084675	0.140958	-4.68993	2.73E-06	3.56E-05
ENSG00000148835.10	TAF5	597.6923023	-0.660459293	0.114591	-5.76362	8.23E-09	1.77E-07
ENSG00000011028.13	MRC2	1874.245828	-0.654931832	0.108871	-6.01566	1.79E-09	4.34E-08
ENSG00000187372.11	PCDHB13	19.65363184	-0.648082668	0.174758	-3.70846	0.000209	0.001553
ENSG00000130254.11	SAFB2	1319.120922	-0.647749183	0.093299	-6.94276	3.85E-12	1.39E-10
ENSG00000198814.12	GK	150.3900951	-0.647288223	0.145068	-4.46195	8.12E-06	9.19E-05
ENSG00000143674.10	RP5-862P8.2	2295.476051	-0.645196197	0.041161	-15.6751	2.24E-55	7.21E-53
ENSG00000110031.12	LPXN	126.7323708	-0.641731811	0.168701	-3.80395	0.000142	0.001118
ENSG00000134072.10	CAMK1	26.571896	-0.641205292	0.172597	-3.71505	0.000203	0.001523
ENSG00000124444.15	ZNF576	220.3187079	-0.640447555	0.099495	-6.43696	1.22E-10	3.54E-09
ENSG00000168785.7	TSPAN5	1011.708623	-0.637552512	0.077193	-8.25918	1.47E-16	8.44E-15
ENSG00000145632.14	PLK2	1272.532748	-0.635143098	0.070359	-9.02712	1.76E-19	1.27E-17
ENSG00000197472.14	ZNF695	167.9889221	-0.633699404	0.114605	-5.52942	3.21E-08	6.25E-07
ENSG00000132535.18	DLG4	178.6826609	-0.631863976	0.1158	-5.4565	4.86E-08	9.14E-07
ENSG00000105429.12	MEGF8	1338.382037	-0.631687568	0.066122	-9.55335	1.26E-21	1.13E-19
ENSG00000197249.13	SERPINA1	2447.774467	-0.630335671	0.173591	-3.63116	0.000282	0.002006
ENSG00000064419.13	TNPO3	4051.635119	-0.626413906	0.028205	-22.209	2.81E-109	2.71E-106
ENSG00000166913.12	YWHAB	9219.942017	-0.625620753	0.038524	-16.2398	2.64E-59	9.38E-57
ENSG00000144136.10	SLC20A1	18888.84635	-0.624909399	0.081518	-7.66589	1.78E-14	8.39E-13
ENSG00000213694.3	S1PR3	718.2235734	-0.619631559	0.101164	-6.12503	9.07E-10	2.33E-08
ENSG00000164099.3	PRSS12	937.4255336	-0.618678047	0.050401	-12.2752	1.23E-34	2.00E-32
ENSG00000169851.15	PCDH7	1503.077894	-0.617340053	0.139843	-4.41451	1.01E-05	0.000111
ENSG00000095303.14	PTGS1	155.6421358	-0.614703778	0.106297	-5.78291	7.34E-09	1.60E-07
ENSG00000175066.15	GK5	1261.086681	-0.613726187	0.060761	-10.1007	5.48E-24	5.70E-22
ENSG00000081181.7	ARG2	359.1746329	-0.60951554	0.167451	-3.63996	0.000273	0.001954
ENSG00000204351.11	SKIV2L	1377.988498	-0.607954589	0.054156	-11.226	3.04E-29	4.23E-27
ENSG00000185090.14	MANEAL	865.8403193	-0.607423864	0.131146	-4.63167	3.63E-06	4.55E-05
ENSG00000112237.12	CCNC	4945.984726	-0.606219177	0.057857	-10.4779	1.09E-25	1.23E-23
ENSG00000002726.20	AOC1	88.71220931	-0.60618086	0.174819	-3.46748	0.000525	0.003437
ENSG00000176692.5	FOXC2	96.59551054	-0.60403228	0.133797	-4.51455	6.35E-06	7.43E-05
ENSG00000082497.11	SERTAD4	326.3121677	-0.603474225	0.114583	-5.26669	1.39E-07	2.40E-06
ENSG00000100234.11	TIMP3	434.9281198	-0.603017035	0.162928	-3.70112	0.000215	0.00159
ENSG00000149548.14	CCDC15	187.9077935	-0.602962341	0.125056	-4.82153	1.42E-06	2.00E-05
ENSG00000138356.13	AOX1	629.8363496	-0.602903627	0.128148	-4.70475	2.54E-06	3.33E-05

ENSG00000137642.12	SORL1	643.332815	-0.599756497	0.093472	-6.41642	1.40E-10	4.00E-09
ENSG00000083720.12	OXCT1	2681.13449	-0.598850493	0.093571	-6.39997	1.55E-10	4.40E-09
ENSG00000100603.13	SNW1	2149.238248	-0.598268181	0.053725	-11.1358	8.40E-29	1.15E-26
ENSG00000186088.15	GSAP	269.4732488	-0.597823621	0.13117	-4.55762	5.17E-06	6.23E-05
ENSG00000187189.10	TSPYL4	204.2970348	-0.597481352	0.129536	-4.61246	3.98E-06	4.92E-05
ENSG00000180730.4	SHISA2	60.78761492	-0.596379057	0.152165	-3.91928	8.88E-05	0.000737
ENSG00000197084.5	LCE1C	20.94111575	-0.59589953	0.174425	-3.41636	0.000635	0.004037
ENSG00000215375.6	MYL5	81.30975638	-0.594717795	0.137762	-4.31699	1.58E-05	0.000164
ENSG00000136531.14	SCN2A	22.00197365	-0.593688085	0.167364	-3.54728	0.000389	0.002644
ENSG00000131080.14	EDA2R	306.2207216	-0.592752216	0.104578	-5.66804	1.44E-08	2.96E-07
ENSG00000196730.12	DAPK1	381.3632971	-0.592121345	0.132409	-4.4719	7.75E-06	8.84E-05
ENSG00000125966.9	MMP24	38.99576795	-0.591986139	0.168918	-3.50458	0.000457	0.003048
ENSG00000189164.14	ZNF527	113.7386534	-0.591876619	0.120288	-4.92049	8.63E-07	1.27E-05
ENSG00000182986.12	ZNF320	126.8190582	-0.591453413	0.131611	-4.49395	6.99E-06	8.09E-05
ENSG00000099284.13	H2AFY2	806.0967267	-0.588101013	0.091007	-6.46216	1.03E-10	3.05E-09
ENSG00000142494.13	SLC47A1	465.3594585	-0.586213273	0.073747	-7.94895	1.88E-15	9.82E-14
ENSG00000089057.14	SLC23A2	2245.180915	-0.584927923	0.066338	-8.81732	1.17E-18	8.09E-17
ENSG00000125089.16	SH3TC1	989.1194649	-0.584379249	0.139876	-4.17785	2.94E-05	0.000279
ENSG00000174851.14	YIF1A	1485.290931	-0.584301031	0.042587	-13.7203	7.67E-43	1.65E-40
ENSG00000154310.16	TNIK	206.6693396	-0.582593513	0.107656	-5.4116	6.25E-08	1.14E-06
ENSG00000156502.13	SUPV3L1	1663.142511	-0.581808184	0.063247	-9.19905	3.61E-20	2.87E-18
ENSG00000160305.17	DIP2A	1160.730769	-0.581218473	0.06645	-8.7467	2.20E-18	1.49E-16
ENSG00000176697.18	BDNF	80.48030173	-0.580240284	0.171681	-3.37976	0.000725	0.004528
ENSG00000185697.16	MYBL1	315.7824616	-0.578788228	0.113647	-5.09287	3.53E-07	5.61E-06
ENSG00000198053.11	SIRPA	769.2514276	-0.57681451	0.066414	-8.68513	3.78E-18	2.54E-16
ENSG00000034693.14	PEX3	922.2270474	-0.576773059	0.053996	-10.6817	1.24E-26	1.51E-24
ENSG00000173546.7	CSPG4	50.70822081	-0.575362972	0.171173	-3.3613	0.000776	0.004784
ENSG00000170175.10	CHRNB1	196.0802149	-0.575080878	0.123018	-4.67478	2.94E-06	3.78E-05
ENSG00000183840.6	GPR39	135.4747354	-0.574414095	0.132188	-4.34544	1.39E-05	0.000147
ENSG00000167996.15	FTH1	2094.450858	-0.574250505	0.107825	-5.32579	1.01E-07	1.77E-06
ENSG00000124279.11	FASTKD3	762.2450337	-0.573898213	0.066128	-8.67863	4.01E-18	2.68E-16
ENSG00000049283.17	EPN3	533.4189368	-0.573122764	0.070774	-8.09796	5.59E-16	3.05E-14
ENSG00000158125.9	XDH	4211.742152	-0.570863048	0.093494	-6.10585	1.02E-09	2.60E-08
ENSG00000175130.6	MARCKSL1	1590.607961	-0.570491923	0.0874	-6.52737	6.69E-11	2.03E-09
ENSG00000106565.17	TMEM176B	66.77608971	-0.569697113	0.163429	-3.48591	0.00049	0.003246
ENSG00000114923.16	SLC4A3	363.1218926	-0.568284388	0.099307	-5.72247	1.05E-08	2.21E-07
ENSG00000134962.6	KLB	74.99892151	-0.567716449	0.138488	-4.09939	4.14E-05	0.000379
ENSG00000134802.17	SLC43A3	2224.960698	-0.567530339	0.08854	-6.40988	1.46E-10	4.15E-09
ENSG00000277161.1	PIGW	756.6031984	-0.567104439	0.067798	-8.36463	6.03E-17	3.61E-15
ENSG00000152049.6	KCNE4	16.23302623	-0.565975176	0.170425	-3.32095	0.000897	0.005373
ENSG00000004897.11	CDC27	5674.044551	-0.565945156	0.034568	-16.3722	3.02E-60	1.17E-57
ENSG00000106278.11	PTPRZ1	197.180808	-0.563192013	0.141013	-3.99391	6.50E-05	0.000564
ENSG00000265190.6	ANXA8	3442.083485	-0.563084111	0.100121	-5.62403	1.87E-08	3.75E-07
ENSG00000164406.7	LEAP2	47.26343619	-0.561990974	0.154129	-3.64623	0.000266	0.001912
ENSG00000039650.10	PNKP	718.2052771	-0.561458221	0.057421	-9.77793	1.40E-22	1.33E-20
ENSG00000183873.15	SCN5A	29.84214492	-0.561382153	0.172357	-3.25709	0.001126	0.006522
ENSG00000101977.19	MCF2	220.794249	-0.560122953	0.17476	-3.2051	0.00135	0.007589
ENSG00000111863.12	ADTRP	625.3177559	-0.559516694	0.067479	-8.29166	1.12E-16	6.56E-15
ENSG00000204852.15	TCTN1	462.4654953	-0.556235727	0.080282	-6.9285	4.25E-12	1.53E-10
ENSG00000127586.16	CHTF18	809.0924013	-0.555722984	0.068405	-8.12398	4.51E-16	2.53E-14
ENSG00000110693.16	SOX6	32.79226667	-0.553504546	0.167316	-3.30813	0.000939	0.005578
ENSG00000197713.14	RPE	2490.798981	-0.553107983	0.040975	-13.4988	1.59E-41	3.25E-39
ENSG00000149328.14	GLB1L2	667.7773732	-0.552144068	0.081275	-6.79354	1.09E-11	3.78E-10
ENSG00000170100.13	ZNF778	401.3732727	-0.551894186	0.090827	-6.07632	1.23E-09	3.08E-08
ENSG00000153012.11	LGI2	20.01783214	-0.551443084	0.129431	-4.26051	2.04E-05	0.000203
ENSG00000203780.10	FANK1	21.61849564	-0.551262578	0.174759	-3.15442	0.001608	0.008837
ENSG00000167767.13	KRT80	41.25932281	-0.550799372	0.169962	-3.24072	0.001192	0.006855
ENSG00000121753.12	ADGRB2	395.5268558	-0.548462568	0.133708	-4.10194	4.10E-05	0.000375
ENSG00000169217.8	CD2BP2	2589.633724	-0.547083794	0.061245	-8.93275	4.16E-19	2.94E-17
ENSG00000115970.18	THADA	1496.390694	-0.545501409	0.051433	-10.606	2.79E-26	3.29E-24
ENSG00000186529.14	CYP4F3	25.42279624	-0.545114154	0.171865	-3.17177	0.001515	0.008415

ENSG00000125351.11	UPF3B	267.3404422	-0.544469678	0.115554	-4.71181	2.46E-06	3.22E-05
ENSG00000169252.5	ADRB2	1099.085612	-0.544402463	0.059713	-9.11697	7.73E-20	5.97E-18
ENSG00000137266.14	SLC22A23	254.1216859	-0.540921358	0.125178	-4.32122	1.55E-05	0.000161
ENSG00000086570.12	FAT2	3747.982752	-0.540514466	0.037379	-14.4603	2.16E-47	5.61E-45
ENSG00000151466.11	SCLT1	879.7504116	-0.539873559	0.063166	-8.54686	1.26E-17	8.03E-16
ENSG00000131373.14	HACL1	444.4229284	-0.539415683	0.080667	-6.68697	2.28E-11	7.44E-10
ENSG00000173692.12	PSMD1	9278.466222	-0.538809645	0.041114	-13.1053	3.07E-39	5.84E-37
ENSG00000186017.14	ZNF566	130.8054211	-0.538676071	0.159836	-3.37018	0.000751	0.00466
ENSG00000166479.9	TMX3	4681.254189	-0.537173903	0.043704	-12.2913	1.01E-34	1.66E-32
ENSG00000189280.3	GJB5	1661.843903	-0.537170406	0.069825	-7.69312	1.44E-14	6.81E-13
ENSG00000221821.3	C6orf226	31.37394339	-0.536322808	0.17286	-3.10265	0.001918	0.01022
ENSG00000277075.2	HIST1H2AE	6145.406659	-0.536161435	0.169352	-3.16595	0.001546	0.008546
ENSG00000255346.9	NOX5	55.23690984	-0.535913708	0.157101	-3.41128	0.000647	0.004109
ENSG00000142396.10	ERVK3-1	69.62479994	-0.53564202	0.155009	-3.45555	0.000549	0.003574
ENSG00000165102.14	HGSNAT	1423.374893	-0.535152811	0.077343	-6.91918	4.54E-12	1.63E-10
ENSG00000185838.13	GNB1L	168.35425	-0.533361008	0.110103	-4.84421	1.27E-06	1.80E-05
ENSG00000276256.1	AC011043.1	450.4435355	-0.531246588	0.086952	-6.10967	9.98E-10	2.54E-08
ENSG00000176406.21	RIMS2	22.61133195	-0.529626094	0.174746	-3.03084	0.002439	0.012488
ENSG00000162946.20	DISC1	47.16840546	-0.528228355	0.170396	-3.1	0.001935	0.010293
ENSG00000187498.14	COL4A1	12468.07769	-0.528164529	0.090722	-5.8218	5.82E-09	1.30E-07
ENSG00000175265.17	GOLGA8A	553.2125159	-0.526326971	0.122007	-4.31389	1.60E-05	0.000166
ENSG00000144821.9	MYH15	167.5751233	-0.525223131	0.163859	-3.20533	0.001349	0.007589
ENSG00000133808.4	MICALCL	508.528331	-0.524844903	0.08002	-6.55888	5.42E-11	1.66E-09
ENSG00000103064.13	SLC7A6	1071.042398	-0.52479638	0.055231	-9.50192	2.06E-21	1.82E-19
ENSG00000101040.19	ZMYND8	1628.698803	-0.52457552	0.098219	-5.34089	9.25E-08	1.64E-06
ENSG00000264230.7	ANXA8L1	1555.282842	-0.524180297	0.109317	-4.79503	1.63E-06	2.25E-05
ENSG00000170385.9	SLC30A1	2933.006288	-0.524127345	0.05568	-9.41326	4.81E-21	4.01E-19
ENSG00000119707.13	RBM25	4665.240209	-0.523668719	0.036509	-14.3434	1.17E-46	2.88E-44
ENSG00000155903.11	RASA2	886.642789	-0.522370187	0.05777	-9.04228	1.53E-19	1.13E-17
ENSG00000143353.11	LYPLAL1	443.0396578	-0.522068053	0.080215	-6.50839	7.60E-11	2.27E-09
ENSG00000083817.8	ZNF416	120.1604254	-0.521178953	0.114817	-4.53922	5.65E-06	6.72E-05
ENSG00000113460.12	BRIX1	3149.179223	-0.518826067	0.070079	-7.40348	1.33E-13	5.78E-12
ENSG00000122547.10	EEPD1	86.30016111	-0.518815568	0.132722	-3.90903	9.27E-05	0.000767
ENSG00000143507.17	DUSP10	486.0309905	-0.518686631	0.124517	-4.1656	3.11E-05	0.000294
ENSG00000166833.19	NAV2	562.5545761	-0.517610919	0.114345	-4.52676	5.99E-06	7.09E-05
ENSG00000057019.15	DCBLD2	14028.02692	-0.5173653	0.05024	-10.2978	7.21E-25	7.80E-23
ENSG00000198133.8	TMEM229B	27.69166114	-0.517299513	0.170405	-3.0357	0.0024	0.012344
ENSG00000148200.16	NR6A1	54.9439126	-0.51711885	0.155013	-3.33596	0.00085	0.005148
ENSG00000139344.7	AMDHD1	44.47460665	-0.516604957	0.161176	-3.20522	0.00135	0.007589
ENSG00000196507.10	TCEAL3	171.7867396	-0.515212884	0.109708	-4.6962	2.65E-06	3.46E-05
ENSG00000130054.4	FAM155B	334.7714506	-0.514835069	0.087863	-5.85949	4.64E-09	1.06E-07
ENSG00000163131.10	CTSS	53.53487776	-0.514503472	0.170956	-3.00957	0.002616	0.013216
ENSG00000205269.5	TMEM170B	206.404252	-0.51362925	0.100731	-5.09904	3.41E-07	5.45E-06
ENSG00000158292.6	GPR153	838.389321	-0.512233296	0.077282	-6.62814	3.40E-11	1.08E-09
ENSG00000203811.1	HIST2H3C	174.9125094	-0.511728113	0.172559	-2.96553	0.003022	0.014918
ENSG00000138623.9	SEMA7A	531.6373402	-0.511338251	0.107142	-4.77255	1.82E-06	2.49E-05
ENSG00000077380.15	DYNC1I2	5436.675055	-0.508922328	0.044291	-11.4903	1.48E-30	2.17E-28
ENSG00000169083.15	AR	47.29909455	-0.50888881	0.150156	-3.38908	0.000701	0.004405
ENSG00000136999.4	NOV	87.43910765	-0.508102418	0.134959	-3.76485	0.000167	0.001279
ENSG00000161267.11	BDH1	7.563514215	-0.506848503	0.162192	-3.125	0.001778	0.009614
ENSG00000119689.14	DLST	2597.897651	-0.504446794	0.042746	-11.801	3.86E-32	5.93E-30
ENSG00000095321.16	CRAT	274.8205441	-0.504403924	0.124763	-4.0429	5.28E-05	0.000466
ENSG00000179295.16	PTPN11	12007.70923	-0.504372789	0.029883	-16.8784	6.49E-64	2.66E-61
ENSG00000198768.10	APCDD1L	140.0162509	-0.503607648	0.157009	-3.20752	0.001339	0.007544
ENSG00000175785.12	PRIMA1	14.29374131	-0.503519976	0.168892	-2.98131	0.00287	0.01427
ENSG00000170425.3	ADORA2B	887.1136317	-0.503404058	0.05506	-9.14284	6.08E-20	4.73E-18
ENSG00000256043.2	CTSO	166.0175536	-0.503251927	0.161098	-3.12389	0.001785	0.009643
ENSG00000237190.3	CDKN2AIPNL	857.3237349	-0.502265712	0.089395	-5.61849	1.93E-08	3.86E-07
ENSG00000126777.17	KTN1	13429.95538	-0.500567232	0.034707	-14.4228	3.72E-47	9.49E-45
ENSG00000187240.13	DYNC2H1	2247.209077	-0.500415856	0.07134	-7.01456	2.31E-12	8.61E-11
ENSG00000226887.7	ERVMER34-1	3765.914392	-0.500415655	0.045733	-10.9422	7.24E-28	9.42E-26

Table S3. Genes upregulated in SF3B1-mutant MCF-10A cells. Whole gene mRNA expression ratios for SF3B1-MUT/SF3B1-WT clones were generated from RNA-seq data and those with log2FC greater than 0.5 are shown.

GeneID	Gene symbol	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000130818.11	ZNF426	329.6524616	3.950756024	0.154893	25.50631	1.68E-143	3.78E-140
ENSG00000197020.10	ZNF100	119.6355201	3.874733851	0.16283	23.79617	3.66E-125	6.18E-122
ENSG00000115232.13	ITGA4	175.9992082	3.161915497	0.172986	18.27847	1.23E-74	6.15E-72
ENSG00000047597.5	XK	234.0834229	3.00120594	0.153009	19.61462	1.16E-85	6.82E-83
ENSG00000130829.17	DUSP9	61.52685777	2.55883539	0.167483	15.27822	1.07E-52	3.21E-50
ENSG00000163093.11	BBS5	45.4549652	2.476969263	0.172367	14.37031	7.95E-47	1.99E-44
ENSG00000065621.14	GSTO2	298.6326175	2.255428429	0.139895	16.12231	1.78E-58	6.01E-56
ENSG00000181885.18	CLDN7	875.5541008	2.049222192	0.167708	12.21901	2.46E-34	3.96E-32
ENSG00000079257.7	LXN	169.6214239	1.562062034	0.145356	10.74647	6.16E-27	7.64E-25
ENSG00000184489.11	PTP4A3	139.7800906	1.540492941	0.140213	10.98682	4.42E-28	5.86E-26
ENSG00000023839.10	ABCC2	373.3160399	1.351042061	0.168936	7.997351	1.27E-15	6.74E-14
ENSG00000196502.11	SULT1A1	154.2537007	1.303846225	0.173211	7.527491	5.17E-14	2.35E-12
ENSG00000163898.9	LIPH	22.99788225	1.239383336	0.174237	7.1132	1.13E-12	4.43E-11
ENSG00000204228.3	HSD17B8	95.1843618	1.228257757	0.134829	9.109719	8.26E-20	6.34E-18
ENSG00000188452.13	CERKL	33.93324934	1.149381259	0.171578	6.698868	2.10E-11	6.94E-10
ENSG00000175315.2	CST6	90.89836795	1.139669305	0.150573	7.568861	3.77E-14	1.72E-12
ENSG00000164638.10	SLC29A4	25.58467229	1.107004075	0.17468	6.337318	2.34E-10	6.52E-09
ENSG00000146802.12	TMEM168	924.1688895	1.083569938	0.092185	11.75432	6.71E-32	1.01E-29
ENSG00000165168.7	CYBB	11.58825791	1.080815411	0.167357	6.458131	1.06E-10	3.12E-09
ENSG00000178567.7	EPM2AIP1	182.3130789	1.079947765	0.146908	7.351187	1.96E-13	8.46E-12
ENSG00000143248.12	RGS5	88.0457732	1.063530174	0.134706	7.895177	2.90E-15	1.48E-13
ENSG00000087842.10	PIR	497.0784124	1.061444414	0.099845	10.63095	2.14E-26	2.56E-24
ENSG00000121104.7	FAM117A	68.61453126	1.060306202	0.154187	6.876757	6.12E-12	2.17E-10
ENSG00000166387.11	PPFIBP2	158.3010158	1.018954483	0.118238	8.617862	6.82E-18	4.52E-16
ENSG00000155962.12	CLIC2	27.65363235	1.002111323	0.171985	5.826728	5.65E-09	1.27E-07
ENSG00000162366.7	PDZK1IP1	97.53297919	0.998979783	0.174633	5.72045	1.06E-08	2.23E-07
ENSG00000001561.6	ENPP4	347.5721265	0.995751224	0.10316	9.652466	4.80E-22	4.41E-20
ENSG00000165948.10	IFI27L1	235.7114779	0.993448223	0.095192	10.43621	1.69E-25	1.89E-23
ENSG00000197043.13	ANXA6	1217.437058	0.973392574	0.11769	8.270803	1.33E-16	7.72E-15
ENSG00000102886.14	GDPD3	35.66345318	0.964096944	0.169657	5.682632	1.33E-08	2.73E-07
ENSG00000146411.5	SLC2A12	36.17871637	0.956612705	0.164947	5.799532	6.65E-09	1.46E-07
ENSG00000146477.5	SLC22A3	14.56649731	0.944651065	0.158889	5.945364	2.76E-09	6.50E-08
ENSG00000134070.4	IRAK2	40.38724431	0.937870043	0.171191	5.478495	4.29E-08	8.18E-07
ENSG00000198331.10	HYLS1	344.725221	0.927679389	0.093263	9.946874	2.60E-23	2.59E-21
ENSG00000136155.16	SCEL	149.5167729	0.926795971	0.160221	5.784488	7.27E-09	1.59E-07
ENSG00000226763.4	SRRM5	18.76729467	0.893004437	0.171176	5.216888	1.82E-07	3.05E-06
ENSG00000120915.13	EPHX2	274.2365206	0.891070204	0.088787	10.03601	1.06E-23	1.08E-21
ENSG00000145911.5	N4BP3	58.91551901	0.8827612	0.174462	5.059915	4.19E-07	6.59E-06
ENSG00000163257.10	DCAF16	2331.694825	0.881479587	0.057748	15.26432	1.32E-52	3.80E-50
ENSG00000185507.19	IRF7	203.3012674	0.872576635	0.105055	8.305887	9.91E-17	5.85E-15
ENSG00000145362.17	ANK2	566.4950753	0.865911971	0.128947	6.715254	1.88E-11	6.25E-10
ENSG00000002746.14	HECW1	118.0480945	0.863740383	0.172863	4.996686	5.83E-07	8.92E-06
ENSG00000198848.12	CES1	2195.563385	0.862679559	0.168239	5.127703	2.93E-07	4.74E-06
ENSG00000114841.17	DNAH1	87.71160294	0.851257135	0.149195	5.705654	1.16E-08	2.42E-07
ENSG00000204262.11	COL5A2	285.6266983	0.844436838	0.093534	9.028149	1.75E-19	1.27E-17
ENSG00000168016.13	TRANK1	278.7791868	0.841905081	0.088366	9.527454	1.61E-21	1.43E-19
ENSG00000151240.16	DIP2C	79.53650008	0.827923558	0.137383	6.026382	1.68E-09	4.08E-08
ENSG00000075651.15	PLD1	255.4943119	0.827806948	0.111473	7.426088	1.12E-13	4.94E-12
ENSG00000175352.10	NRIP3	558.8282997	0.826235293	0.17138	4.821074	1.43E-06	2.00E-05
ENSG00000136010.13	ALDH1L2	1661.059835	0.816471585	0.102572	7.959967	1.72E-15	9.05E-14
ENSG00000073331.17	ALPK1	607.8498883	0.814585588	0.086331	9.435655	3.89E-21	3.30E-19
ENSG00000119899.12	SLC17A5	498.7645075	0.811150704	0.072102	11.25009	2.31E-29	3.26E-27
ENSG00000125968.8	ID1	3092.988212	0.806657057	0.063657	12.67185	8.47E-37	1.45E-34
ENSG00000196312.12	MFSD14C	354.2291895	0.804966272	0.09541	8.436928	3.26E-17	2.02E-15
ENSG00000143369.14	ECM1	487.4793287	0.804697299	0.108427	7.421591	1.16E-13	5.10E-12

ENSG00000052344.15	PRSS8	327.8458201	0.804464302	0.17258	4.661386	3.14E-06	4.00E-05
ENSG00000114796.15	KLHL24	849.9569043	0.804060912	0.089794	8.954535	3.41E-19	2.43E-17
ENSG00000061918.12	GUCY1B3	196.6304426	0.802350938	0.162977	4.9231	8.52E-07	1.26E-05
ENSG00000135116.9	HRK	13.20501463	0.801299522	0.172175	4.653993	3.26E-06	4.14E-05
ENSG00000108342.12	CSF3	9372.229358	0.788378392	0.139299	5.659609	1.52E-08	3.09E-07
ENSG00000120696.8	KBTBD7	110.749683	0.785774416	0.173605	4.526219	6.00E-06	7.10E-05
ENSG00000078081.7	LAMP3	134.0504976	0.784946999	0.155748	5.039861	4.66E-07	7.21E-06
ENSG00000157502.13	MUM1L1	238.5753541	0.781588848	0.163539	4.779209	1.76E-06	2.42E-05
ENSG00000183150.7	GPR19	15.3734433	0.776621543	0.168592	4.606521	4.09E-06	5.05E-05
ENSG00000172159.15	FRMD3	81.63208113	0.774692229	0.142977	5.418299	6.02E-08	1.10E-06
ENSG00000105705.15	SUGP1	1467.047036	0.772475377	0.059023	13.08762	3.88E-39	7.28E-37
ENSG00000196371.3	FUT4	25.81665929	0.768955117	0.17411	4.416486	1.00E-05	0.00011
ENSG00000003400.14	CASP10	302.814618	0.768937001	0.117758	6.529827	6.58E-11	2.00E-09
ENSG00000253958.1	CLDN23	52.67134224	0.765742728	0.169725	4.511664	6.43E-06	7.51E-05
ENSG00000185000.10	DGAT1	1100.368454	0.763196196	0.077152	9.892146	4.50E-23	4.44E-21
ENSG00000257446.3	ZNF878	6.880064087	0.762584992	0.14541	5.244375	1.57E-07	2.67E-06
ENSG00000167562.11	ZNF701	162.0796137	0.756487912	0.131375	5.758243	8.50E-09	1.82E-07
ENSG00000119632.3	IFI27L2	651.6361133	0.755697833	0.125795	6.007356	1.89E-09	4.56E-08
ENSG00000172992.11	DCAKD	447.0966796	0.750286421	0.082436	9.101386	8.92E-20	6.77E-18
ENSG00000073150.13	PANX2	130.9973959	0.7401333	0.167196	4.42674	9.57E-06	0.000106
ENSG00000139410.14	SDSL	80.35934452	0.733906147	0.139788	5.250137	1.52E-07	2.59E-06
ENSG00000153982.10	GDPD1	52.79169829	0.725583127	0.152085	4.770893	1.83E-06	2.50E-05
ENSG00000123612.15	ACVR1C	30.88047052	0.718935542	0.169029	4.253339	2.11E-05	0.000209
ENSG00000176532.3	PRR15	48.26012036	0.717824794	0.166472	4.31198	1.62E-05	0.000167
ENSG00000148516.21	ZEB1	56.17163056	0.715630469	0.148749	4.811009	1.50E-06	2.09E-05
ENSG00000197712.11	FAM114A1	2484.624681	0.715391448	0.126438	5.658043	1.53E-08	3.11E-07
ENSG00000105223.19	PLD3	1916.045987	0.715109634	0.048866	14.63399	1.70E-48	4.52E-46
ENSG00000189195.10	BTBD8	51.01726972	0.714135265	0.162825	4.385915	1.15E-05	0.000125
ENSG00000205426.10	KRT81	24429.64861	0.711192135	0.062055	11.46061	2.08E-30	3.02E-28
ENSG00000171295.12	ZNF440	139.0330961	0.710689017	0.1725	4.119939	3.79E-05	0.000349
ENSG00000164749.11	HNF4G	31.63198473	0.709187146	0.17482	4.056681	4.98E-05	0.000441
ENSG00000138798.11	EGF	19.51447684	0.708730167	0.174225	4.067904	4.74E-05	0.000423
ENSG00000123977.9	DAW1	291.8583976	0.700448613	0.174806	4.006999	6.15E-05	0.000536
ENSG00000197619.13	ZNF615	11.86632231	0.699614491	0.144066	4.856208	1.20E-06	1.70E-05
ENSG00000198417.6	MT1F	153.5109599	0.699103761	0.157949	4.426136	9.59E-06	0.000106
ENSG00000125730.16	C3	2615.954605	0.69757977	0.146151	4.772994	1.82E-06	2.48E-05
ENSG00000109738.10	GLRB	133.2203433	0.697353144	0.124205	5.614544	1.97E-08	3.94E-07
ENSG00000145349.16	CAMK2D	785.2455686	0.695367556	0.146216	4.755766	1.98E-06	2.66E-05
ENSG00000133138.19	TBC1D8B	583.4820969	0.693345821	0.074963	9.249143	2.26E-20	1.83E-18
ENSG00000185187.12	SIGIRR	255.3950015	0.686511164	0.10659	6.440673	1.19E-10	3.46E-09
ENSG00000162600.11	OMA1	380.2830357	0.685133231	0.08786	7.797994	6.29E-15	3.11E-13
ENSG00000133135.13	RNF128	25.7688601	0.684241408	0.156014	4.385761	1.16E-05	0.000125
ENSG00000006534.15	ALDH3B1	140.3229543	0.682290629	0.132664	5.143006	2.70E-07	4.39E-06
ENSG00000135119.14	RNFT2	134.0592993	0.68013821	0.133747	5.085267	3.67E-07	5.82E-06
ENSG00000101079.20	NDRG3	1967.382627	0.672955298	0.043862	15.34267	3.97E-53	1.22E-50
ENSG00000119943.11	PYROXD2	69.48747752	0.672185852	0.146058	4.602174	4.18E-06	5.14E-05
ENSG00000116663.10	FBXO6	137.4469682	0.671971906	0.170462	3.942057	8.08E-05	0.000677
ENSG00000121851.12	POLR3GL	251.7049625	0.667783287	0.086108	7.755171	8.82E-15	4.26E-13
ENSG00000196689.11	TRPV1	59.60885705	0.66775787	0.164067	4.070028	4.70E-05	0.00042
ENSG00000169583.12	CLIC3	129.6645374	0.666866914	0.1732	3.850264	0.000118	0.000947
ENSG00000205078.5	SYCE1L	31.23676902	0.665598566	0.168747	3.944351	8.00E-05	0.000673
ENSG00000151490.13	PTPRO	25.82686268	0.664116929	0.174763	3.8001	0.000145	0.001133
ENSG00000069424.14	KCNAB2	553.3251999	0.662523089	0.079287	8.356042	6.49E-17	3.86E-15
ENSG00000213967.10	ZNF726	14.85529327	0.655947691	0.146347	4.48214	7.39E-06	8.47E-05
ENSG00000119411.10	BSPRY	64.68749116	0.653336156	0.162567	4.018875	5.85E-05	0.000512
ENSG00000211584.13	SLC48A1	326.9407977	0.652557785	0.131306	4.96974	6.70E-07	1.01E-05
ENSG00000119227.7	PIGZ	29.0189107	0.649700304	0.170284	3.815382	0.000136	0.001074
ENSG00000123146.19	ADGRE5	876.4230183	0.64623496	0.053759	12.02087	2.76E-33	4.34E-31
ENSG00000071909.18	MYO3B	14.77377663	0.643675023	0.173084	3.718853	0.0002	0.001503

ENSG00000121440.14	PDZRN3	7.596744542	0.64364195	0.150178	4.285857	1.82E-05	0.000184
ENSG00000170965.9	PLAC1	29.98225034	0.64110326	0.174791	3.667837	0.000245	0.001779
ENSG00000099377.13	HSD3B7	81.36423627	0.640083534	0.165522	3.867058	0.00011	0.000891
ENSG00000178852.15	EFCAB13	12.99868185	0.636662483	0.17224	3.696367	0.000219	0.001616
ENSG00000134830.5	C5AR2	48.78104875	0.633479933	0.173753	3.645861	0.000266	0.001914
ENSG00000114779.19	ABHD14B	526.2327533	0.63327064	0.071687	8.833813	1.01E-18	7.01E-17
ENSG00000158560.14	DYNC1I1	235.4455751	0.631835166	0.132172	4.780415	1.75E-06	2.41E-05
ENSG00000141441.15	GAREM1	637.6487605	0.628023767	0.071346	8.802476	1.34E-18	9.18E-17
ENSG00000170915.8	PAQR8	106.796724	0.62707263	0.125433	4.999275	5.75E-07	8.81E-06
ENSG00000089847.12	ANKRD24	10.19244776	0.626069591	0.166835	3.752638	0.000175	0.001333
ENSG00000115226.9	FNDC4	90.8172823	0.624780065	0.156624	3.989052	6.63E-05	0.000574
ENSG00000141971.12	MVB12A	625.7512407	0.623630656	0.067557	9.231129	2.68E-20	2.14E-18
ENSG00000177000.10	MTHFR	465.0560109	0.623611501	0.085851	7.263892	3.76E-13	1.55E-11
ENSG00000185753.12	CXorf38	1234.137026	0.621258728	0.063464	9.789117	1.25E-22	1.21E-20
ENSG00000204389.9	HSPA1A	2786.229167	0.619379459	0.091178	6.793057	1.10E-11	3.79E-10
ENSG00000118960.12	HS1BP3	607.5573036	0.618470247	0.083535	7.403723	1.32E-13	5.78E-12
ENSG00000143252.14	SDHC	1468.842982	0.613958885	0.069439	8.841746	9.42E-19	6.57E-17
ENSG00000130775.15	THEMIS2	145.4017779	0.613920739	0.166943	3.67742	0.000236	0.001723
ENSG00000162817.6	C1orf115	397.4149596	0.613315018	0.173013	3.544917	0.000393	0.002665
ENSG00000119922.9	IFIT2	85.31636059	0.612073535	0.149535	4.093177	4.26E-05	0.000386
ENSG00000248383.4	PCDHAC1	77.56393287	0.610041219	0.174803	3.489878	0.000483	0.003208
ENSG00000165474.5	GJB2	968.1870663	0.610027247	0.11375	5.362894	8.19E-08	1.47E-06
ENSG00000139112.10	GABARAPL1	600.1546182	0.603101149	0.12686	4.754051	1.99E-06	2.67E-05
ENSG00000151023.16	ENKUR	67.89952223	0.601166063	0.141721	4.241898	2.22E-05	0.000218
ENSG00000183111.11	ARHGEF37	140.112	0.59560024	0.164673	3.616858	0.000298	0.002105
ENSG00000179913.10	B3GNT3	816.603796	0.594222446	0.09712	6.118426	9.45E-10	2.41E-08
ENSG00000214140.10	PRCD	30.47762304	0.59298358	0.169855	3.491116	0.000481	0.003197
ENSG00000183287.13	CCBE1	532.8439737	0.592808842	0.074553	7.951529	1.84E-15	9.65E-14
ENSG00000158691.14	ZSCAN12	129.3937141	0.589697033	0.173928	3.390467	0.000698	0.004385
ENSG00000130590.13	SAMD10	79.26473339	0.584952106	0.14229	4.110986	3.94E-05	0.000362
ENSG00000067836.12	ROGDI	319.7126221	0.584414541	0.081195	7.197629	6.13E-13	2.46E-11
ENSG00000204839.8	MROH6	873.2918754	0.582399007	0.067877	8.580186	9.47E-18	6.07E-16
ENSG00000115738.9	ID2	42.62097581	0.581604116	0.162237	3.584913	0.000337	0.002329
ENSG00000176595.3	KBTBD11	206.2751024	0.581441171	0.122911	4.730587	2.24E-06	2.96E-05
ENSG00000003436.14	TFPI	2557.520747	0.5811979	0.146649	3.963186	7.40E-05	0.000629
ENSG00000026652.13	AGPAT4	524.5508554	0.579046768	0.142308	4.068956	4.72E-05	0.000421
ENSG00000163874.9	ZC3H12A	2455.882345	0.577072194	0.055404	10.41566	2.10E-25	2.33E-23
ENSG00000168461.12	RAB31	857.4990819	0.576593135	0.099359	5.803127	6.51E-09	1.44E-07
ENSG00000136828.18	RALGPS1	70.57539294	0.57572486	0.144558	3.982668	6.81E-05	0.000587
ENSG00000102699.5	PARP4	4881.430755	0.575258468	0.035217	16.33479	5.58E-60	2.10E-57
ENSG00000102890.14	ELMO3	1033.288077	0.57437564	0.063146	9.095971	9.37E-20	7.08E-18
ENSG00000158528.11	PPP1R9A	333.0924106	0.574270314	0.144296	3.979813	6.90E-05	0.000592
ENSG00000163536.12	SERPINI1	339.0520394	0.572430758	0.101072	5.663579	1.48E-08	3.03E-07
ENSG00000169403.11	PTAFR	987.9003067	0.57135078	0.124778	4.57892	4.67E-06	5.66E-05
ENSG00000167700.8	MFSD3	1094.345476	0.56840006	0.053204	10.6835	1.22E-26	1.49E-24
ENSG00000013588.6	GPRC5A	4411.176807	0.568319128	0.130171	4.365934	1.27E-05	0.000135
ENSG00000102897.9	LYRM1	528.0008415	0.566834095	0.085777	6.608237	3.89E-11	1.23E-09
ENSG00000026559.13	KCNG1	213.5446036	0.565997019	0.099169	5.707392	1.15E-08	2.40E-07
ENSG00000164442.9	CITED2	287.3213491	0.565806472	0.084014	6.734652	1.64E-11	5.54E-10
ENSG00000171160.17	MORN4	145.7494515	0.563407718	0.122401	4.602985	4.16E-06	5.13E-05
ENSG00000153029.14	MR1	1329.304314	0.563156144	0.094678	5.948107	2.71E-09	6.40E-08
ENSG00000152763.16	WDR78	50.67883104	0.562530034	0.151647	3.70948	0.000208	0.001548
ENSG00000169554.17	ZEB2	26.98241295	0.561485277	0.174805	3.212061	0.001318	0.007451
ENSG00000177854.7	TMEM187	163.1835863	0.560212672	0.127686	4.387431	1.15E-05	0.000124
ENSG00000174567.7	GOLT1A	26.83377916	0.558796785	0.174809	3.196605	0.001391	0.007782
ENSG00000103024.7	NME3	506.2706793	0.557982451	0.082878	6.73255	1.67E-11	5.61E-10
ENSG00000136425.12	CIB2	45.96206631	0.556063501	0.174608	3.184646	0.001449	0.008079
ENSG00000073910.19	FRY	81.49983749	0.555747381	0.138269	4.019333	5.84E-05	0.000511
ENSG00000205464.11	ATP6AP1L	57.56265794	0.553725135	0.162421	3.409202	0.000652	0.004135

ENSG00000076864.19	RAP1GAP	58.89461975	0.551512049	0.161703	3.410649	0.000648	0.004115
ENSG00000074181.8	NOTCH3	200.5527976	0.550965545	0.14423	3.820055	0.000133	0.001057
ENSG00000008382.15	MPND	91.10835656	0.549555581	0.146683	3.74654	0.000179	0.001361
ENSG00000146856.14	AGBL3	71.54104545	0.548308002	0.14378	3.813526	0.000137	0.00108
ENSG00000175318.11	GRAMD2	6.771538752	0.547319137	0.157581	3.473259	0.000514	0.003372
ENSG00000161860.7	SYCE2	17.64575881	0.54731903	0.17356	3.153492	0.001613	0.008858
ENSG00000050426.15	LETMD1	782.9362591	0.546619078	0.074817	7.306054	2.75E-13	1.15E-11
ENSG00000095585.16	BLNK	12.11365462	0.546230829	0.161294	3.386557	0.000708	0.004438
ENSG00000198832.10	SELM	105.5081281	0.54188179	0.170926	3.170267	0.001523	0.008441
ENSG00000149485.17	FADS1	3024.279618	0.54038028	0.174705	3.093094	0.001981	0.010509
ENSG00000141449.14	GREB1L	285.000818	0.540112453	0.104313	5.177802	2.25E-07	3.71E-06
ENSG00000094631.18	HDAC6	903.7573124	0.539502447	0.063975	8.433042	3.37E-17	2.08E-15
ENSG00000124429.17	POF1B	47.76245147	0.538941689	0.147468	3.654637	0.000258	0.00186
ENSG00000163638.13	ADAMTS9	97.08889298	0.538570917	0.137923	3.904877	9.43E-05	0.000779
ENSG00000173137.11	ADCK5	375.6635302	0.538263056	0.081588	6.597361	4.19E-11	1.31E-09
ENSG00000167508.11	MVD	3962.915177	0.538138329	0.050005	10.76169	5.22E-27	6.53E-25
ENSG00000021355.12	SERPINB1	1562.029004	0.535817947	0.124888	4.290401	1.78E-05	0.000181
ENSG00000157353.16	FUK	492.6884038	0.535347879	0.075751	7.067182	1.58E-12	6.05E-11
ENSG00000183208.12	GDPGP1	148.1156533	0.53518644	0.123405	4.336828	1.45E-05	0.000152
ENSG00000107020.9	PLGRKT	676.6478607	0.533065033	0.067333	7.916863	2.44E-15	1.26E-13
ENSG00000196139.13	AKR1C3	844.7482635	0.532392093	0.075614	7.040909	1.91E-12	7.23E-11
ENSG00000187609.15	EXD3	124.9939905	0.530753505	0.143351	3.702469	0.000214	0.001583
ENSG00000143375.14	CGN	436.0310316	0.530674172	0.109173	4.860849	1.17E-06	1.67E-05
ENSG00000175155.8	YPEL2	144.4725157	0.530471443	0.115315	4.600214	4.22E-06	5.18E-05
ENSG00000172318.5	B3GALT1	45.11831227	0.53041202	0.16013	3.312386	0.000925	0.005509
ENSG00000075240.16	GRAMD4	530.9133605	0.529436777	0.072958	7.256728	3.97E-13	1.62E-11
ENSG00000078399.16	HOXA9	126.9842843	0.528748513	0.156807	3.371966	0.000746	0.004636
ENSG00000188001.9	TPRG1	186.6587041	0.528592475	0.172041	3.072482	0.002123	0.011131
ENSG00000184254.16	ALDH1A3	960.1934259	0.527076061	0.142024	3.71117	0.000206	0.001541
ENSG00000143603.18	KCNN3	13.27719451	0.524712154	0.173819	3.018728	0.002538	0.012881
ENSG00000107902.13	LHPP	36.28597008	0.524390306	0.174542	3.004383	0.002661	0.013407
ENSG00000157111.12	TMEM171	35.8322268	0.523022971	0.170308	3.071038	0.002133	0.011172
ENSG00000138185.17	ENTPD1	369.3381568	0.522298745	0.114505	4.561379	5.08E-06	6.12E-05
ENSG00000162496.8	DHRS3	357.8867529	0.519776448	0.16724	3.10797	0.001884	0.010065
ENSG00000125124.11	BBS2	913.4786305	0.519095191	0.064029	8.107228	5.18E-16	2.88E-14
ENSG00000108479.11	GALK1	215.9839396	0.518185291	0.094671	5.473529	4.41E-08	8.39E-07
ENSG00000122378.13	FAM213A	707.3578038	0.518174682	0.140463	3.689044	0.000225	0.001658
ENSG00000072954.6	TMEM38A	151.04764	0.516986348	0.169323	3.053261	0.002264	0.011747
ENSG00000182919.14	C11orf54	219.4263532	0.516357423	0.117784	4.383951	1.17E-05	0.000126
ENSG00000196353.11	CPNE4	20.95944176	0.51549214	0.173695	2.967809	0.002999	0.014838
ENSG00000115966.16	ATF2	2078.87823	0.514966753	0.041053	12.54382	4.30E-36	7.26E-34
ENSG00000007944.14	MYLIP	179.8600216	0.513600291	0.119694	4.290949	1.78E-05	0.000181
ENSG00000138639.17	ARHGAP24	73.79815617	0.512345192	0.145875	3.512218	0.000444	0.002974
ENSG00000155093.17	PTPRN2	15.6031584	0.510345613	0.169529	3.010374	0.002609	0.013191
ENSG00000167711.13	SERPINF2	59.59649911	0.508609935	0.14883	3.417385	0.000632	0.004024
ENSG00000129219.13	PLD2	1513.061488	0.508004306	0.049871	10.18628	2.28E-24	2.41E-22
ENSG00000260001.6	TGFBR3L	14.88598352	0.507910377	0.172994	2.936007	0.003325	0.016167
ENSG00000078967.12	UBE2D4	137.4301304	0.507509333	0.109772	4.623313	3.78E-06	4.71E-05
ENSG00000182325.10	FBXL6	1092.634326	0.505360049	0.055648	9.081288	1.07E-19	8.01E-18
ENSG00000166750.9	SLFN5	2868.021712	0.504483027	0.174806	2.885957	0.003902	0.018329
ENSG00000144331.18	ZNF385B	42.23383693	0.504211226	0.174649	2.886999	0.003889	0.018281
ENSG00000189433.5	GJB4	23.06789135	0.504044742	0.164057	3.072372	0.002124	0.011131
ENSG00000186026.6	ZNF284	21.52719752	0.503561411	0.171583	2.934799	0.003338	0.016218
ENSG00000186591.11	UBE2H	3613.923984	0.502168147	0.101294	4.957508	7.14E-07	1.07E-05
ENSG00000143622.10	RIT1	1103.423018	0.501151478	0.101455	4.93965	7.83E-07	1.17E-05
ENSG00000112294.12	ALDH5A1	801.3161759	0.500718552	0.166216	3.012462	0.002591	0.013115
ENSG00000037757.13	MRI1	547.3592386	0.500481627	0.077904	6.424377	1.32E-10	3.82E-09
ENSG00000187824.8	TMEM220	12.31257896	0.500206322	0.171984	2.908442	0.003632	0.017314

Table S4. Genes downregulated in SF3B1-mutant MCF-10A and also downregulated in SF3B1-mutant METABRIC and/or TCGA. Aber junc = number of aberrant junctions in that gene upregulated in SF3B1-mutant MCF-10A cells. A dash indicates the gene was not downregulated at the cutoffs specified in the methods in the respective datasets.

MCF-10A								METABRIC								TCGA							
Gene symbol	**baseMean**	**log2FC**	**lfcSE**	**stat**	**pvalue**	**padj**	**Aber junc**	**Gene symbol**	**mRNA MUT**	**mRNA WT**	**StDev MUT**	**StDev WT**	**p-Value**	**q-Value**	**Z**	**Gene symbol**	**mRNA MUT**	**mRNA WT**	**StDev MUT**	**StDev WT**	**p-Value**	**q-Value**	**Z**
CLCA2	3759	-1.70	0.13	-13.1	2.8E-39	5.4E-37		CLCA2	5.68	6.2	0.67	1.45	9.7E-06	4.9E-04	-0.36	-							
PHGDH	828	-1.65	0.14	-11.6	2.7E-31	4.1E-29		PHGDH	8.63	9.82	0.7	1.3	8.3E-15	1.3E-11	-0.92	PHGDH	8.21	9.76	0.84	1.77	4.3E-05	5.7E-03	-0.88
KIAA0196	2535	-1.58	0.04	-41.2	0.0E+00	0.0E+00		KIAA0196	8.5	9.07	0.44	0.61	9.1E-11	4.4E-08	-0.93	KIAA0196	9.76	10.93	0.43	0.78	8.6E-07	8.4E-04	-1.50
RDX	5550	-1.52	0.04	-41.9	0.0E+00	0.0E+00	1	RDX	6.66	7.19	0.37	0.51	3.4E-12	2.1E-09	-1.04	RDX	9.31	10.1	0.57	0.83	5.0E-04	2.1E-02	-0.95
ABCB7	927	-1.50	0.07	-21.5	1.6E-102	1.4E-99		ABCB7	7.09	7.67	0.39	0.39	1.0E-12	9.7E-10	-1.49	ABCB7	7.9	8.77	0.37	0.44	4.6E-06	1.6E-03	-1.98
CA9	81	-1.48	0.16	-9.1	8.8E-20	6.7E-18		CA9	5.66	5.88	0.45	0.81	2.8E-03	3.3E-02	-0.27	-							
TPP2	2464	-1.44	0.05	-31.6	1.2E-218	4.2E-215	2	TPP2	6.15	6.31	0.22	0.31	3.1E-05	1.2E-03	-0.52	TPP2	9.43	10.03	0.59	0.57	4.8E-03	6.2E-02	-1.05
DQX1	38	-1.39	0.17	-8.4	4.2E-17	2.6E-15		DQX1	5.43	5.52	0.2	0.28	2.7E-03	3.2E-02	-0.32	-							
TTI1	1266	-1.38	0.07	-21.1	3.2E-99	2.5E-96	1	TTI1	6.13	6.5	0.29	0.32	7.8E-11	3.8E-08	-1.16	TTI1	8.37	9.47	0.28	0.56	1.7E-08	1.1E-04	-1.96
MUT	682	-1.36	0.07	-19.6	6.2E-86	4.0E-83		MUT	7.91	8.41	0.35	0.37	3.0E-12	2.0E-09	-1.35	MUT	9.07	9.8	0.51	0.59	4.0E-04	1.9E-02	-1.24
APLP1	22	-1.31	0.17	-7.7	1.1E-14	5.4E-13		APLP1	5.68	6.02	0.38	0.89	9.1E-07	8.2E-05	-0.38	-							
DZIP3	323	-1.24	0.13	-9.8	1.4E-22	1.3E-20		-								DZIP3	7.95	8.75	0.57	0.74	4.6E-04	2.0E-02	-1.08
SHPK	104	-1.24	0.14	-8.7	2.1E-18	1.5E-16		-								SHPK	7.88	8.54	0.54	0.64	1.5E-03	3.6E-02	-1.03
FGFBP1	576	-1.23	0.09	-13.8	1.6E-43	3.6E-41		FGFBP1	5.38	5.51	0.24	0.65	1.9E-03	2.5E-02	-0.20	-							
DNAJC3	5866	-1.23	0.08	-16.3	7.0E-60	2.6E-57		DNAJC3	5.99	6.37	0.27	0.42	3.3E-12	2.1E-09	-0.90	DNAJC3	10.6	11.09	0.48	0.65	4.6E-03	6.1E-02	-0.75
DLG1	2641	-1.21	0.06	-19.6	6.9E-86	4.2E-83		-								DLG1	9.81	10.44	0.42	0.53	2.9E-04	1.6E-02	-1.19
C5	119	-1.17	0.16	-7.5	8.8E-14	3.9E-12		-								C5	6.47	6.94	0.52	1.09	1.0E-02	9.2E-02	-0.43
CEP135	790	-1.15	0.06	-19.3	2.9E-83	1.6E-80		-								CEP135	7.41	7.81	0.33	0.69	1.4E-03	3.4E-02	-0.58
MAP3K7	2174	-1.15	0.05	-22.7	9.4E-114	1.2E-110	1	MAP3K7	7.84	8.15	0.34	0.41	7.4E-07	6.8E-05	-0.76	MAP3K7	8.94	9.45	0.44	0.58	2.0E-03	4.0E-02	-0.88
PPP2R5A	1387	-1.14	0.08	-13.7	7.2E-43	1.6E-40	1	PPP2R5A	8.08	8.83	0.38	0.57	7.1E-17	4.3E-13	-1.32	PPP2R5A	10.12	11.01	0.35	0.66	1.9E-06	1.2E-03	-1.35
RNF38	485	-1.13	0.08	-14.7	3.8E-49	1.0E-46		RNF38	7.81	8.16	0.35	0.4	3.6E-08	6.6E-06	-0.88	RNF38	9.56	9.97	0.47	0.58	1.2E-02	9.7E-02	-0.71
SBSN	58	-1.13	0.15	-7.3	2.1E-13	9.1E-12		SBSN	5.35	5.45	0.11	0.47	6.6E-06	3.7E-04	-0.21	-							
SUN1	3064	-1.12	0.05	-23.5	1.5E-122	2.3E-119	1	SUN1	7.96	8.43	0.46	0.46	1.8E-08	3.7E-06	-1.02	SUN1	10.34	11.1	0.43	0.47	7.1E-05	7.5E-03	-1.62
NCAM1	76	-1.11	0.16	-6.8	1.1E-11	3.8E-10		NCAM1	5.76	5.86	0.19	0.37	1.9E-03	2.5E-02	-0.27	-							
GPR137C	39	-1.10	0.17	-6.4	1.4E-10	3.9E-09		GPR137C	5.83	5.96	0.23	0.36	6.7E-04	1.2E-02	-0.36	-							
CTNNAL1	2639	-1.07	0.10	-10.3	8.7E-25	9.3E-23		CTNNAL1	6.43	6.76	0.41	0.53	4.8E-06	2.9E-04	-0.62	-							
ITFG1	976	-1.06	0.08	-13.8	2.0E-43	4.6E-41		ITFG1	8.03	8.58	0.49	0.67	4.1E-09	1.0E-06	-0.82	ITFG1	9.19	9.81	0.47	0.64	7.9E-04	2.6E-02	-0.97
WDR34	1714	-1.06	0.08	-13.8	3.2E-43	7.0E-41		WDR34	7.48	8.13	0.37	0.53	2.4E-15	6.3E-12	-1.23	WDR34	9.65	10.71	0.62	0.74	9.7E-05	8.7E-03	-1.43
NSMCE4A	716	-1.04	0.09	-11.1	8.5E-29	1.1E-26	1	NSMCE4A	8.87	9.28	0.42	0.46	7.1E-08	1.1E-05	-0.89	NSMCE4A	8.07	8.97	0.48	0.61	3.8E-05	5.4E-03	-1.48
RTF1	1656	-1.01	0.05	-18.4	2.1E-75	1.1E-72		RTF1	5.83	6.03	0.16	0.25	1.0E-10	4.8E-08	-0.80	RTF1	10.29	10.88	0.29	0.44	2.0E-05	3.7E-03	-1.34
TPR	11738	-1.00	0.02	-44.2	0.0E+00	0.0E+00	1	TPR	8.02	8.61	0.34	0.45	5.4E-15	9.4E-12	-1.31	TPR	11.31	11.91	0.68	0.58	1.2E-02	9.9E-02	-1.03
TAF2	2906	-0.99	0.04	-22.6	2.4E-113	2.7E-110	2	TAF2	7.02	7.35	0.37	0.5	5.8E-07	5.7E-05	-0.66	TAF2	9	9.87	0.51	0.81	9.4E-05	8.6E-03	-1.07
LIG3	1298	-0.98	0.07	-14.2	4.7E-46	1.1E-43		LIG3	6.78	7.25	0.36	0.44	1.1E-10	5.1E-08	-1.07	LIG3	8.77	9.77	0.34	0.62	4.1E-07	5.2E-04	-1.61
KPNA1	1607	-0.96	0.04	-22.5	2.7E-112	2.8E-109		KPNA1	7.21	7.63	0.35	0.38	4.9E-10	1.8E-07	-1.11	KPNA1	10.29	10.83	0.34	0.43	1.6E-04	1.2E-02	-1.26
HEATR1	7864	-0.95	0.05	-19.9	2.0E-88	1.4E-85		HEATR1	7.71	8.15	0.38	0.5	1.5E-09	4.6E-07	-0.88	-							
TTLL7	358	-0.95	0.14	-6.6	3.4E-11	1.1E-09		TTLL7	5.66	5.82	0.17	0.33	2.6E-07	3.2E-05	-0.48	-							
ACD	922	-0.94	0.05	-17.5	3.2E-68	1.5E-65		ACD	7.15	7.5	0.36	0.38	8.9E-08	1.3E-05	-0.92	ACD	7.59	8.33	0.61	0.62	1.6E-03	3.6E-02	-1.19
VARS2	616	-0.91	0.07	-13.6	4.2E-42	8.9E-40		VARS2	8.28	8.62	0.5	0.47	5.4E-05	1.8E-03	-0.72	VARS2	8.97	9.54	0.37	0.54	2.3E-04	1.4E-02	-1.06
RECQL	2733	-0.89	0.04	-19.8	2.6E-87	1.7E-84		RECQL	7.1	7.35	0.33	0.43	1.8E-05	7.9E-04	-0.58	-							
CDK8	991	-0.89	0.06	-15.1	1.6E-51	4.4E-49	1	CDK8	5.8	6	0.16	0.28	1.7E-10	7.5E-08	-0.71	-							
PDS5A	9762	-0.88	0.04	-22.9	8.9E-116	1.2E-112	2	PDS5A	7.29	7.6	0.33	0.39	1.6E-07	2.2E-05	-0.79	PDS5A	11.28	11.58	0.28	0.52	4.1E-03	5.8E-02	-0.58
IDUA	79	-0.85	0.16	-5.3	1.3E-07	2.3E-06		IDUA	6.9	7.39	0.46	0.59	1.4E-08	2.9E-06	-0.83	IDUA	6.73	7.68	0.63	1.06	2.5E-04	1.5E-02	-0.90
COQ2	700	-0.85	0.11	-7.6	2.3E-14	1.1E-12		COQ2	7.64	8.06	0.42	0.48	4.1E-08	6.9E-06	-0.88	COQ2	7.13	7.67	0.3	0.61	4.6E-05	5.9E-03	-0.89
BRD9	1326	-0.83	0.14	-5.8	5.0E-09	1.1E-07	1	BRD9	8.86	9.28	0.4	0.45	1.7E-08	3.4E-06	-0.93	BRD9	9.02	9.47	0.25	0.48	5.7E-05	6.6E-03	-0.94
NBAS	2455	-0.81	0.04	-21.3	1.3E-100	1.1E-97		NBAS	6.85	7.1	0.3	0.3	1.2E-06	1.1E-04	-0.83	-							
ELP2	2505	-0.79	0.10	-8.1	5.4E-16	3.0E-14	1	-								ELP2	10.18	11.15	0.63	1.11	2.5E-04	1.5E-02	-0.87
DPH5	639	-0.79	0.10	-7.8	4.5E-15	2.3E-13	1	DPH5	7.74	7.96	0.36	0.38	2.1E-04	5.0E-03	-0.58	DPH5	8	8.72	0.29	0.48	2.8E-06	1.4E-03	-1.50
ATAD1	3422	-0.78	0.04	-19.0	4.0E-80	2.2E-77		ATAD1	7.56	7.85	0.45	0.51	1.3E-04	3.6E-03	-0.57	ATAD1	9.33	9.96	0.45	0.63	4.8E-04	2.1E-02	-1.00
CCDC78	77	-0.77	0.14	-5.3	9.6E-08	1.7E-06		CCDC78	5.46	5.54	0.14	0.26	2.1E-03	2.7E-02	-0.31	-							
EOGT	3089	-0.76	0.05	-16.2	3.0E-59	1.0E-56	1	EOGT	6.41	6.56	0.27	0.37	8.1E-04	1.4E-02	-0.41	-							
GAS8	78	-0.74	0.14	-5.3	1.1E-07	2.0E-06		GAS8	7.23	7.61	0.41	0.52	3.8E-07	4.2E-05	-0.73	GAS8	8.42	8.88	0.47	0.68	6.0E-03	7.0E-02	-0.68
WDR62	778	-0.74	0.09	-7.9	2.9E-15	1.5E-13		WDR62	5.62	5.78	0.27	0.33	3.2E-04	6.9E-03	-0.48	-							
CPA4	202	-0.74	0.17	-4.3	1.9E-05	1.9E-04		CPA4	5.57	5.93	0.21	0.83	4.3E-15	9.4E-12	-0.43	-							
GNG4	1010	-0.73	0.08	-9.6	9.5E-22	8.6E-20		GNG4	5.53	5.83	0.35	0.83	1.5E-06	1.2E-04	-0.36	-							
PADI3	50	-0.72	0.17	-4.1	3.3E-05	3.1E-04		PADI3	5.37	5.49	0.14	0.45	6.2E-06	3.5E-04	-0.27	-							
SLC25A13	2030	-0.72	0.05	-13.3	1.4E-40	2.8E-38		SLC25A13	6.86	7.3	0.39	0.54	3.1E-09	8.2E-07	-0.81	SLC25A13	8.53	9.06	0.34	0.64	1.7E-04	1.2E-02	-0.83
PPP6R3	7006	-0.71	0.04	-18.2	1.1E-73	5.2E-71		PPP6R3	7.65	7.88	0.44	0.47	1.6E-03	2.3E-02	-0.49	PPP6R3	10.61	11.2	0.2	0.54	3.8E-07	5.2E-04	-1.09
HIST1H2BG	6456	-0.71	0.17	-4.2	2.8E-05	2.6E-04		HIST1H2BG	6.23	6.72	0.72	0.96	5.7E-05	1.9E-03	-0.51	-							
SEPT2	11465	-0.70	0.02	-29.4	1.7E-189	4.6E-186		SEPT2	11.29	11.51	0.31	0.35	3.6E-05	1.3E-03	-0.63	-							
MSLN	639	-0.69	0.16	-4.4	1.1E-05	1.2E-04		MSLN	5.59	6.15	0.44	1.44	2.1E-10	8.3E-08	-0.39	-							

ADAM9	8934	-0.69	0.05	-12.9	4.1E-38	7.7E-36		ADAM9	6.4	6.62	0.45	0.58	2.5E-03	3.0E-02	-0.38	-							
FASTKD1	1914	-0.68	0.07	-9.3	1.2E-20	9.8E-19	1	FASTKD1	6.41	6.64	0.26	0.31	5.5E-07	5.4E-05	-0.74	FASTKD1	7.71	8.22	0.35	0.54	3.5E-04	1.8E-02	-0.94
FIG4	316	-0.67	0.11	-6.2	4.6E-10	1.2E-08		FIG4	7.54	8.05	0.36	0.53	2.7E-12	1.9E-09	-0.96	FIG4	8.44	9.17	0.38	0.68	3.0E-05	4.9E-03	-1.07
C1ORF56	54	-0.67	0.15	-4.4	1.1E-05	1.2E-04		C1ORF56	6.32	6.49	0.31	0.42	1.1E-03	1.7E-02	-0.40	-							
VPS8	739	-0.67	0.07	-9.2	3.9E-20	3.1E-18	1	VPS8	7.77	7.99	0.41	0.33	8.9E-04	1.5E-02	-0.67	VPS8	9.39	9.7	0.28	0.46	2.9E-03	4.9E-02	-0.67
RAC3	734	-0.67	0.09	-7.8	8.3E-15	4.0E-13		-								RAC3	7.52	8.25	0.7	1.07	4.0E-03	5.8E-02	-0.68
TAF5	598	-0.66	0.11	-5.8	8.2E-09	1.8E-07		TAF5	6.2	6.33	0.2	0.27	1.3E-04	3.5E-03	-0.48	TAF5	6.18	6.8	0.46	0.62	7.3E-04	2.5E-02	-1.00
SAFB2	1319	-0.65	0.09	-6.9	3.8E-12	1.4E-10		SAFB2	8.02	8.31	0.38	0.34	1.0E-05	5.1E-04	-0.85	SAFB2	9.99	10.24	0.2	0.45	1.1E-03	3.0E-02	-0.56
GK	150	-0.65	0.15	-4.5	8.1E-06	9.2E-05		GK	6.22	6.41	0.34	0.46	6.1E-04	1.1E-02	-0.41	-							
ZNF576	220	-0.64	0.10	-6.4	1.2E-10	3.5E-09		ZNF576	6.19	6.4	0.24	0.27	4.0E-07	4.3E-05	-0.78	ZNF576	7.4	7.89	0.31	0.49	2.1E-04	1.4E-02	-1.00
TNPO3	4052	-0.63	0.03	-22.2	2.8E-109	2.7E-106	1	TNPO3	8.02	8.34	0.46	0.56	3.1E-05	1.2E-03	-0.57	TNPO3	9.64	10.11	0.37	0.61	9.8E-04	2.9E-02	-0.77
YWHAB	9220	-0.63	0.04	-16.2	2.6E-59	9.4E-57		-								YWHAB	12.75	13.05	0.22	0.44	5.1E-04	2.1E-02	-0.68
GK5	1261	-0.61	0.06	-10.1	5.5E-24	5.7E-22		GK5	6.48	6.74	0.38	0.44	5.9E-05	2.0E-03	-0.59	GK5	8.69	9.28	0.49	0.65	1.6E-03	3.7E-02	-0.91
SKIV2L	1378	-0.61	0.05	-11.2	3.0E-29	4.2E-27		SKIV2L	8.2	8.58	0.46	0.42	2.5E-06	1.8E-04	-0.90	SKIV2L	9.35	10.04	0.3	0.47	4.6E-06	1.6E-03	-1.47
CCNC	4946	-0.61	0.06	-10.5	1.1E-25	1.2E-23		-								CCNC	9.52	10.18	0.41	0.63	1.5E-04	1.1E-02	-1.05
AOC1	89	-0.61	0.17	-3.5	5.3E-04	3.4E-03		AOC1	5.5	5.68	0.16	0.51	3.8E-09	9.6E-07	-0.35	-							
FOXC2	97	-0.60	0.13	-4.5	6.3E-06	7.4E-05		FOXC2	5.8	5.89	0.18	0.28	2.3E-03	2.8E-02	-0.32	-							
SNW1	2149	-0.60	0.05	-11.1	8.4E-29	1.1E-26		SNW1	6.11	6.3	0.27	0.3	4.0E-05	1.5E-03	-0.63	SNW1	9.97	10.56	0.28	0.35	1.5E-05	3.1E-03	-1.69
SLC23A2	2245	-0.58	0.07	-8.8	1.2E-18	8.1E-17		SLC23A2	6.22	6.35	0.25	0.28	1.9E-03	2.5E-02	-0.46	-							
YIF1A	1485	-0.58	0.04	-13.7	7.7E-43	1.6E-40	1	YIF1A	8.64	9	0.36	0.45	4.0E-08	6.8E-06	-0.80	YIF1A	9.69	10.23	0.39	0.65	4.5E-04	2.0E-02	-0.83
SUPV3L1	1663	-0.58	0.06	-9.2	3.6E-20	2.9E-18	1	SUPV3L1	7.21	7.44	0.34	0.37	5.6E-05	1.9E-03	-0.62	SUPV3L1	8.45	9.15	0.46	0.48	2.4E-04	1.4E-02	-1.46
DIP2A	1161	-0.58	0.07	-8.7	2.2E-18	1.5E-16		DIP2A	6.18	6.32	0.25	0.37	1.4E-03	2.0E-02	-0.38	DIP2A	8.97	9.57	0.35	0.5	7.4E-05	7.5E-03	-1.20
BDNF	80	-0.58	0.17	-3.4	7.3E-04	4.5E-03		BDNF	5.56	5.67	0.23	0.26	4.9E-03	4.8E-02	-0.42	-							
XDH	4212	-0.57	0.09	-6.1	1.0E-09	2.6E-08		XDH	5.55	5.72	0.26	0.53	1.9E-04	4.6E-03	-0.32	-							
TMEM176B	67	-0.57	0.16	-3.5	4.9E-04	3.2E-03		TMEM176B	6.21	6.41	0.43	0.53	3.8E-03	4.0E-02	-0.38	-							
SLC4A3	363	-0.57	0.10	-5.7	1.0E-08	2.2E-07	1	SLC4A3	5.76	6.08	0.29	0.48	3.7E-09	9.5E-07	-0.67	-							
CDC27	5674	-0.57	0.03	-16.4	3.0E-60	1.2E-57	2	-								CDC27	10.26	10.51	0.27	0.53	9.2E-03	8.6E-02	-0.47
PTPRZ1	197	-0.56	0.14	-4.0	6.5E-05	5.6E-04		PTPRZ1	5.41	5.49	0.16	0.3	2.7E-03	3.2E-02	-0.27	-							
PNKP	718	-0.56	0.06	-9.8	1.4E-22	1.3E-20	1	PNKP	8.41	8.83	0.39	0.46	7.8E-09	1.8E-06	-0.91	PNKP	8.18	8.88	0.54	0.71	8.6E-04	2.7E-02	-0.99
GLB1L2	668	-0.55	0.08	-6.8	1.1E-11	3.8E-10		GLB1L2	5.86	6.2	0.38	0.65	5.2E-07	5.3E-05	-0.52	-							
FANK1	22	-0.55	0.17	-3.2	1.6E-03	8.8E-03		FANK1	5.55	5.66	0.12	0.17	3.8E-07	4.2E-05	-0.65	-							
CD2BP2	2590	-0.55	0.06	-8.9	4.2E-19	2.9E-17		CD2BP2	9.98	10.21	0.27	0.43	1.5E-06	1.2E-04	-0.53	CD2BP2	10.42	10.77	0.39	0.57	1.0E-02	9.0E-02	-0.61
THADA	1496	-0.55	0.05	-10.6	2.8E-26	3.3E-24	1	THADA	7.02	7.29	0.33	0.33	2.8E-06	2.0E-04	-0.82	THADA	9.6	10.01	0.25	0.4	1.1E-04	9.4E-03	-1.03
UPF3B	267	-0.54	0.12	-4.7	2.5E-06	3.2E-05		UPF3B	7.51	7.78	0.27	0.38	3.9E-08	6.7E-06	-0.71	UPF3B	7.73	8.15	0.45	0.63	8.3E-03	8.2E-02	-0.67
HACL1	444	-0.54	0.08	-6.7	2.3E-11	7.4E-10		HACL1	8.16	8.45	0.36	0.45	5.2E-06	3.0E-04	-0.64	HACL1	7.97	8.39	0.32	0.54	8.2E-04	2.6E-02	-0.78
PSMD1	9278	-0.54	0.04	-13.1	3.1E-39	5.8E-37		PSMD1	9.43	9.64	0.26	0.39	4.9E-06	2.9E-04	-0.54	-							
HIST1H2AE	6145	-0.54	0.17	-3.2	1.5E-03	8.5E-03		HIST1H2AE	5.89	6.27	0.58	0.78	1.1E-04	3.0E-03	-0.49	-							
GNB1L	168	-0.53	0.11	-4.8	1.3E-06	1.8E-05		-								GNB1L	5.65	6.32	0.64	1.01	3.6E-03	5.5E-02	-0.66
RIMS2	23	-0.53	0.17	-3.0	2.4E-03	1.2E-02		RIMS2	5.51	5.69	0.3	0.56	3.3E-04	7.0E-03	-0.32	-							
SLC7A6	1071	-0.52	0.06	-9.5	2.1E-21	1.8E-19		SLC7A6	6.77	6.99	0.38	0.45	3.4E-04	7.0E-03	-0.49	-							
RBM25	4665	-0.52	0.04	-14.3	1.2E-46	2.9E-44		RBM25	8.6	8.78	0.36	0.42	2.4E-03	3.0E-02	-0.43	-							
RASA2	887	-0.52	0.06	-9.0	1.5E-19	1.1E-17		RASA2	5.86	5.99	0.16	0.24	5.3E-06	3.1E-04	-0.54	-							
BRIX1	3149	-0.52	0.07	-7.4	1.3E-13	5.8E-12		-								BRIX1	9.24	9.58	0.3	0.56	2.2E-03	4.3E-02	-0.61
DUSP10	486	-0.52	0.12	-4.2	3.1E-05	2.9E-04		DUSP10	6.73	7.02	0.37	0.58	8.5E-06	4.4E-04	-0.50	-							
DYNC1I2	5437	-0.51	0.04	-11.5	1.5E-30	2.2E-28		DYNC1I2	9.01	9.32	0.3	0.48	2.7E-08	5.0E-06	-0.65	-							
BDH1	8	-0.51	0.16	-3.1	1.8E-03	9.6E-03		BDH1	6.09	6.3	0.38	0.44	1.1E-03	1.7E-02	-0.48	-							
DLST	2598	-0.50	0.04	-11.8	3.9E-32	5.9E-30	3	DLST	6.8	7.15	0.25	0.32	1.8E-11	1.1E-08	-1.09	DLST	10.24	10.85	0.41	0.38	2.8E-04	1.6E-02	-1.61
PTPN11	12008	-0.50	0.03	-16.9	6.5E-64	2.7E-61		PTPN11	8.87	9.16	0.31	0.36	1.9E-07	2.4E-05	-0.81	PTPN11	11.21	11.44	0.26	0.61	1.2E-02	1.0E-01	-0.38

Table S5. Genes upregulated in SF3B1-mutant MCF-10A that were also upregulated in SF3B1-mutant METABRIC and/or TCGA. Aber junc = number of aberrant junctions in that gene upregulated in SF3B1-mutant MCF-10A cells. A dash indicates the gene was not upregulated at the cutoffs specified in the methods in the respective datasets.

MCF-10A								**METABRIC**								**TCGA**							
Gene symbol	**baseMean**	**log2FC**	**lfcSE**	**stat**	**pvalue**	**padj**	**Aber junc**	**Gene symbol**	**mRNA MUT**	**mRNA WT**	**StDev MUT**	**StDev WT**	**p-Value**	**q-Value**	**Z**	**Gene symbol**	**mRNA MUT**	**mRNA WT**	**StDev MUT**	**StDev WT**	**p-Value**	**q-Value**	**Z**
ALPK1	608	0.81	0.09	9.44	3.9E-21	3.3E-19		-								ALPK1	9.3	8.83	0.42	0.71	2.5E-03	4.6E-02	0.66
ANXA6	1217	0.97	0.12	8.27	1.3E-16	7.7E-15		-								ANXA6	12.94	12.33	0.32	0.7	3.2E-05	4.9E-03	0.87
BBS2	913	0.52	0.06	8.11	5.2E-16	2.9E-14		BBS2	8.86	8.58	0.43	0.47	1.4E-04	3.7E-03	0.60	BBS2	10.02	9.39	0.59	0.57	3.6E-03	5.5E-02	1.11
BBS5	45	2.48	0.17	14.37	7.9E-47	2.0E-44		-								BBS5	7.98	7.62	0.34	0.71	4.1E-03	5.8E-02	0.51
COL5A2	286	0.84	0.09	9.03	1.7E-19	1.3E-17		-								COL5A2	13.68	12.86	0.9	1.39	9.2E-03	8.6E-02	0.59
CXorf38	1234	0.62	0.06	9.79	1.3E-22	1.2E-20		CXORF38	7.39	7.2	0.35	0.4	1.1E-03	1.7E-02	0.47	CXORF38	8.22	7.58	0.51	0.59	1.2E-03	3.2E-02	1.08
DCAF16	2332	0.88	0.06	15.26	1.3E-52	3.8E-50	3	DCAF16	7.7	7.35	0.38	0.39	1.8E-07	2.4E-05	0.90	DCAF16	10.44	9.64	0.58	0.7	5.9E-04	2.2E-02	1.14
ENPP4	348	1.00	0.10	9.65	4.8E-22	4.4E-20		-								ENPP4	9.82	8.88	0.44	1.15	8.0E-06	2.3E-03	0.82
FAM114A1	2485	0.72	0.13	5.66	1.5E-08	3.1E-07		-								FAM114A1	10.11	9.44	0.56	0.88	1.6E-03	3.6E-02	0.76
FRY	81	0.56	0.14	4.02	5.8E-05	5.1E-04		-								FRY	10.12	9.19	0.67	1.16	5.4E-04	2.2E-02	0.80
GSTO2	299	2.26	0.14	16.12	1.8E-58	6.0E-56		GSTO2	9.47	9.1	0.72	1.1	1.8E-03	2.4E-02	0.34	-							
HSD17B8	95	1.23	0.13	9.11	8.3E-20	6.3E-18		HSD17B8	7.94	7.5	0.42	0.6	1.7E-08	3.4E-06	0.73	-							
HSD3B7	81	0.64	0.17	3.87	1.1E-04	8.9E-04		-								HSD3B7	10.04	9.59	0.43	0.83	4.0E-03	5.8E-02	0.54
LETMD1	783	0.55	0.07	7.31	2.8E-13	1.1E-11	1	LETMD1	6.65	6.38	0.42	0.42	1.1E-04	3.2E-03	0.64	-							
LXN	170	1.56	0.15	10.75	6.2E-27	7.6E-25		LXN	8.81	8.27	0.96	0.73	5.7E-04	1.1E-02	0.74	-							
LYRM1	528	0.57	0.09	6.61	3.9E-11	1.2E-09		LYRM1	9.53	9.27	0.5	0.49	1.2E-03	1.8E-02	0.53	-							
MRI1	547	0.50	0.08	6.42	1.3E-10	3.8E-09		-								MRI1	9.04	8.82	0.23	0.71	5.4E-03	6.6E-02	0.31
MYLIP	180	0.51	0.12	4.29	1.8E-05	1.8E-04		-								MYLIP	10.18	9.77	0.44	0.77	8.3E-03	8.2E-02	0.53
NME3	506	0.56	0.08	6.73	1.7E-11	5.6E-10		NME3	10.67	10.42	0.51	0.71	1.9E-03	2.5E-02	0.35	-							
OMA1	380	0.69	0.09	7.80	6.3E-15	3.1E-13		OMA1	8.34	8.05	0.4	0.44	2.7E-05	1.1E-03	0.66	OMA1	8.89	8.64	0.25	0.56	5.4E-03	6.6E-02	0.45
PLGRKT	677	0.53	0.07	7.92	2.4E-15	1.3E-13		PLGRKT	10.1	9.72	0.63	0.76	3.3E-04	7.0E-03	0.50	-							
POLR3GL	252	0.67	0.09	7.76	8.8E-15	4.3E-13		POLR3GL	9.4	9.15	0.44	0.48	4.6E-04	8.9E-03	0.52	POLR3GL	9.19	8.76	0.34	0.61	1.2E-03	3.1E-02	0.70
PRR15	48	0.72	0.17	4.31	1.6E-05	1.7E-04		-								PRR15	9.35	8.37	0.78	2.38	1.1E-03	3.1E-02	0.41
PYROXD2	69	0.67	0.15	4.60	4.2E-06	5.1E-05		PYROXD2	7.42	7.06	0.6	0.64	2.9E-04	6.4E-03	0.56	-							
RAB31	857	0.58	0.10	5.80	6.5E-09	1.4E-07		RAB31	11.5	10.92	0.7	0.89	2.7E-06	1.9E-04	0.65	-							
RALGPS1	71	0.58	0.14	3.98	6.8E-05	5.9E-04		RALGPS1	7.53	7.28	0.47	0.56	1.0E-03	1.6E-02	0.45	RALGPS1	8.88	8.27	0.28	0.85	4.7E-06	1.6E-03	0.72
SERPINB1	1562	0.54	0.12	4.29	1.8E-05	1.8E-04		-								SERPINB1	10.25	9.88	0.28	0.63	6.5E-04	2.3E-02	0.59
SRRM5	19	0.89	0.17	5.22	1.8E-07	3.0E-06		-								SRRM5	6.58	4.82	0.69	0.74	2.0E-06	1.2E-03	2.38
SUGP1	1467	0.77	0.06	13.09	3.9E-39	7.3E-37		SUGP1	8.64	8.3	0.28	0.33	4.4E-10	1.7E-07	1.03	SUGP1	9.75	9.14	0.32	0.5	3.1E-05	4.9E-03	1.22
TBC1D8B	583	0.69	0.07	9.25	2.3E-20	1.8E-18		-								TBC1D8B	8.52	7.87	0.47	0.92	5.5E-04	2.2E-02	0.71
TPRG1	187	0.53	0.17	3.07	2.1E-03	1.1E-02		-								TPRG1	9.94	7.53	1.53	2.83	1.8E-04	1.3E-02	0.85
WDR78	51	0.56	0.15	3.71	2.1E-04	1.5E-03		-								WDR78	7.39	6.75	0.41	1.18	1.5E-04	1.2E-02	0.54
ZEB1	56	0.72	0.15	4.81	1.5E-06	2.1E-05		ZEB1	5.68	5.59	0.2	0.22	3.5E-03	3.9E-02	0.41	-							

Table S6. Proteins downregulated in SF3B1-mutant MCF-10A cells. Protein abundance derived from peptide counts is shown for the TWT1, K700E1, and K700E2 MCF-10A clones in this 3-way SILAC experiment. Proteins with SF3B1-mutant/SF3B1-wild type log2 ratios < -0.5 are included. If the corresponding mRNA was misspliced by mutant SF3B1 in our RNA-seq analysis, the predicted effect of the missplicing event on nonsense-mediated decay (NMD) is shown, along with the mutant/wild type whole gene

Accession	Gene name	Avg log2	Log2 K700E1/TWT1	Log2 K700E2/TWT1	Abun TWT1	Abun K700E1	Abun K700E2	Misspliced	NMD predict	log2FC mRNA
NP_065755	STRIP2	-5.38	-5.18	-5.58	195748401	5389655	4086000	FALSE		
NP_001265199	TADA3	-4.51	-5.00	-4.02	649248679	20291785	39930000	FALSE		
NP_000288	PKD2	-3.74	-3.58	-3.90	193694298	16246507	12980000	FALSE		
NP_003116	SPRR1B	-3.61	-3.78	-3.44	56967121	4157387	5263000	FALSE		
NP_005979	SPRR2A	-3.50	-3.49	-3.51	36000056	3210997	3152000	FALSE		
NP_115716	UQCC2	-3.31	-3.51	-3.11	187227677	16395986	21650000	FALSE		
NP_006694	NUDT3	-2.92	-2.56	-3.28	412950765	70040290	42450000	FALSE		
XP_006724040	DYRK1A	-2.77	-2.54	-3.00	81251182	13929582	10190000	FALSE		
NP_060085	NSMCE4A	-2.46	-3.40	-1.52	19483547	1847001	6807000	TRUE	sensitive	-1.038204815
NP_009185	PNKP	-2.43	-2.72	-2.15	78740612	11977011	17730000	TRUE	sensitive	-0.561458221
NP_057260	SDF4	-2.39	-2.14	-2.64	566323783	128458582	90600000	FALSE		
NP_775866	ANKRD52	-2.32	-3.20	-1.45	37430320	4074239	13740000	FALSE		
NP_078837	NAA16	-2.29	-2.41	-2.16	24215591	4553506	5406000	TRUE	sensitive	-0.792069974
NP_076971	ERI3	-2.27	-1.84	-2.70	63867385	17853407	9835000	FALSE		
NP_001449	FLNC	-2.26	-1.92	-2.60	25387191	6697597	4183000	FALSE		
NP_037408	SHPK	-2.22	-2.01	-2.42	34166579	8462384	6369000	FALSE		
NP_775924	SLC9A9	-2.20	-2.11	-2.30	8703310	2017968	1767000	FALSE		
NP_000358	TPMT	-2.18	-2.22	-2.14	416069958	89276379	94090000	FALSE		
XP_006711341	GLUL	-2.13	-2.71	-1.55	294117107	45095969	100200000	FALSE		
NP_001275727	FAM195B	-2.13	-1.71	-2.54	33238428	10136550	5698000	FALSE		
NP_663304	MAP3K7	-2.09	-1.99	-2.19	9441266	2373915	2070000	TRUE	sensitive	-1.147732556
NP_078930	NOL9	-2.05	-1.99	-2.12	110617246	27933903	25530000	TRUE	sensitive	-0.02103464
NP_001124437	SUN1	-1.94	-1.86	-2.02	71437135	19712553	17600000	TRUE	sensitive	-1.115339271
XP_005254128	TPP2	-1.92	-1.98	-1.86	291834771	73870692	80240000	TRUE	sensitive	-1.44165674
NP_036394	HS2ST1	-1.91	-1.74	-2.09	56000932	16750999	13180000	FALSE		
NP_001247422	RDX	-1.91	-1.78	-2.04	786645341	229543809	191100000	TRUE	sensitive	-1.522204625
NP_055217	UQCRQ	-1.88	-1.66	-2.11	332156050	104915628	77130000	FALSE		
XP_011527598	KIZ	-1.86	-2.35	-1.37	48377928	9473237	18760000	FALSE		
XP_011531460	COX7A2L	-1.83	-1.53	-2.12	51238456	17778668	11760000	FALSE		
XP_006721985	NF1	-1.82	-2.37	-1.26	23568929	4558178	9838000	FALSE		
NP_001001522	TAGLN	-1.80	-3.10	-0.50	177109318	20693510	124900000	FALSE		
XP_005249200	MUT	-1.79	-1.71	-1.88	152231850	46497336	41400000	FALSE		
NP_060790	RNF121	-1.79	-2.13	-1.45	64278206	14667635	23480000	FALSE		
NP_056448	FGFR1OP2	-1.77	-1.84	-1.70	65434590	18227105	20160000	FALSE		
XP_011539528	PHGDH	-1.77	-1.85	-1.69	1745226704	485339880	542000000	FALSE		
XP_006724806	FHL1	-1.75	-1.31	-2.19	25828442	10435508	5675000	FALSE		
XP_011523086	KRT15	-1.74	-1.77	-1.70	2201694019	644441674	675800000	FALSE		
NP_060516	AGGF1	-1.73	-1.83	-1.64	10392239	2932593	3332000	FALSE		
NP_005994	UQCRFS1	-1.73	-1.75	-1.70	1695015299	502716823	520700000	FALSE		
NP_006285	UQCRB	-1.72	-1.76	-1.67	1168556328	344922972	366000000	FALSE		
NP_006463	TXNIP	-1.68	-1.64	-1.73	284759527	91275662	86060000	FALSE		
NP_003356	UQCRC1	-1.68	-1.68	-1.68	1916401947	598383433	596800000	FALSE		
NP_055661	KIAA0196	-1.66	-1.69	-1.63	147591099	45684543	47740000	FALSE		
NP_002791	PSMB9	-1.65	-1.86	-1.44	35277316	9734825	13010000	FALSE		
XP_011520823	PDPK1	-1.65	-1.71	-1.58	175359527	53522852	58710000	FALSE		
NP_003357	UQCRC2	-1.64	-1.64	-1.64	1946072323	623701452	623800000	FALSE		
XP_005251332	JPH1	-1.62	-1.41	-1.84	43995841	16582835	12310000	FALSE		
NP_006821	UQCR11	-1.61	-1.70	-1.52	38875800	11958326	13540000	FALSE		
NP_060933	ITFG2	-1.60	-2.42	-0.79	11480153	2145959	6661000	FALSE		
NP_055129	DDX58	-1.58	-1.24	-1.92	27053296	11453834	7153000	FALSE		
NP_109590	RAI1	-1.55	-1.28	-1.83	18083713	7472085	5091000	FALSE		
NP_000682	ALDH3A1	-1.53	-2.19	-0.88	172392490	37696755	93970000	FALSE		
XP_006720172	SIPA1L1	-1.46	-2.16	-0.77	19658526	4390014	11560000	FALSE		
XP_011526362	PIAS4	-1.46	-2.21	-0.71	19552017	4229324	11960000	FALSE		
NP_006107	TAB1	-1.45	-1.28	-1.62	62315396	25645004	20210000	FALSE		
XP_011523099	LIG3	-1.43	-1.40	-1.47	47411739	18012229	17150000	FALSE		
XP_011539009	DRAM2	-1.40	-1.45	-1.36	24223199	8879057	9452000	FALSE		
NP_004087	EIF4EBP2	-1.40	-0.98	-1.82	87717803	44470026	24840000	FALSE		
NP_443183	DNTTIP1	-1.39	-2.10	-0.69	11845327	2771903	7352000	FALSE		
NP_009049	TRIO	-1.37	-1.36	-1.38	85511544	33249752	32840000	FALSE		
XP_011512434	LPCAT1	-1.36	-1.23	-1.49	271065508	115192314	96190000	FALSE		
XP_011532137	PLXNB1	-1.36	-1.61	-1.11	21956078	7186207	10150000	TRUE	sensitive	-0.22420803
NP_851320	GPR180	-1.35	-0.98	-1.71	28415090	14387361	8674000	FALSE		
XP_011524701	KPTN	-1.34	-1.45	-1.23	13176690	4821635	5603000	FALSE		
XP_005262425	DOCK11	-1.34	-1.05	-1.63	2168220	1045419	700300	FALSE		
NP_078846	RNASEH2B	-1.34	-1.65	-1.03	43843686	13976294	21530000	FALSE		
NP_001924	DLST	-1.33	-1.37	-1.29	694743255	269062340	283700000	TRUE	sensitive	-0.504446794
NP_078986	ISOC2	-1.32	-1.36	-1.28	195520167	76103535	80620000	FALSE		
XP_011541279	FAM118B	-1.32	-1.86	-0.77	22123449	6083798	12940000	FALSE		
NP_001034702	IAH1	-1.31	-2.02	-0.61	81631572	20086251	53630000	FALSE		
NP_004385	DAP	-1.31	-1.02	-1.59	72547872	35660102	24120000	FALSE		
XP_005254727	PEAK1	-1.30	-1.50	-1.10	5469239	1936688	2552000	FALSE		
XP_006715163	NQO2	-1.30	-1.94	-0.65	35520765	9277045	22560000	FALSE		

NP_002363	MAN2A1	-1.29	-1.56	-1.03	97303616	33090931	47530000	TRUE	sensitive	-0.754565795
XP_011539405	SZT2	-1.29	-1.53	-1.06	24428609	8482003	11730000	FALSE		
XP_005269346	DLG1	-1.26	-1.22	-1.30	82620584	35510623	33540000	FALSE		
NP_001432	FAAH	-1.26	-1.11	-1.41	24976370	11603313	9418000	FALSE		
NP_001234935	TRIM3	-1.26	-2.02	-0.49	15040598	3696804	10730000	FALSE		
NP_001675	ATP2B4	-1.25	-1.25	-1.26	47906245	20189018	19980000	FALSE		
NP_001164261	MFSD5	-1.25	-1.55	-0.95	24375355	8302629	12640000	FALSE		
NP_000427	OXCT1	-1.23	-1.59	-0.87	303702921	100711529	165800000	FALSE		
XP_011540075	PRKCZ	-1.23	-1.02	-1.43	26467497	13032707	9815000	FALSE		
NP_005580	ALDH6A1	-1.22	-0.93	-1.52	124235188	65341042	43390000	FALSE		
NP_079119	CYBRD1	-1.21	-1.64	-0.79	38951878	12528215	22580000	FALSE		
NP_001193725	PKM	-1.21	-0.87	-1.55	23317872	12752434	7988000	FALSE		
NP_055029	IMPA2	-1.18	-1.40	-0.95	9106523	3446427	4715000	FALSE		
NP_001001503	NDUFV3	-1.17	-0.95	-1.40	80186092	41592553	30420000	FALSE		
NP_060062	MED29	-1.16	-0.96	-1.36	195900556	100431255	76190000	FALSE		
XP_006716943	HINT2	-1.16	-1.38	-0.95	86120167	33146985	44680000	TRUE	sensitive	0.074391935
XP_011519406	DNAJC3	-1.16	-1.22	-1.10	231124618	99123313	107900000	FALSE		
XP_011509985	POTEJ	-1.14	-1.09	-1.19	38206314	17890777	16720000	FALSE		
XP_011520272	THBS1	-1.14	-1.31	-0.96	538479277	216838087	276700000	FALSE		
XP_006719196	RECQL	-1.13	-1.11	-1.15	415080946	192174039	187200000	FALSE		
NP_001132	ALOX15B	-1.12	-0.72	-1.53	32721099	19871375	11330000	FALSE		
NP_002063	GNAQ	-1.12	-1.02	-1.23	460803755	227208198	196600000	FALSE		
NP_001264890	STIM1	-1.12	-1.23	-1.01	48788748	20768249	24250000	TRUE	sensitive	-0.169432302
NP_057137	CCDC53	-1.11	-1.20	-1.03	104378860	45469667	51190000	FALSE		
NP_077306	SLC27A3	-1.11	-1.13	-1.08	56411752	25738429	26680000	FALSE		
XP_005264438	TMEM214	-1.11	-1.18	-1.03	99585953	43806712	48890000	TRUE	sensitive	-0.144761343
NP_006308	BASP1	-1.10	-1.10	-1.11	3200596662	1489185312	1487000000	FALSE		
NP_000843	GSTP1	-1.10	-1.20	-0.99	490398053	213194535	247100000	FALSE		
XP_006710656	IGSF3	-1.09	-1.42	-0.77	37658554	14107088	22060000	FALSE		
NP_078898	FASTKD1	-1.09	-1.48	-0.71	24885076	8944454	15220000	TRUE	sensitive	-0.683067987
NP_001127694	IRX2	-1.09	-1.32	-0.86	8140334	3251170	4487000	FALSE		
XP_011518723	DGKZ	-1.09	-1.25	-0.93	30697427	12911255	16070000	TRUE	sensitive	-0.262177009
XP_006719769	KNTC1	-1.09	-1.18	-1.01	38434548	17003245	19130000	FALSE		
NP_004290	ABCB7	-1.09	-1.59	-0.59	27486940	9124763	18320000	FALSE		
XP_006714556	BRD9	-1.08	-1.36	-0.79	26338164	10286029	15190000	TRUE	sensitive	-0.827205063
NP_001258980	C16orf91	-1.07	-1.20	-0.94	71148039	31054278	37150000	FALSE		
NP_001805	CTSC	-1.06	-1.25	-0.88	1526883171	640611272	831500000	FALSE		
NP_001103132	HECTD4	-1.06	-1.05	-1.07	4499246	2170249	2138000	FALSE		
NP_060504	WDR70	-1.06	-0.88	-1.23	85359388	46226405	36310000	FALSE		
NP_000627	SOD2	-1.06	-1.05	-1.06	1237026426	598383433	591800000	FALSE		
XP_005271687	USP28	-1.05	-1.15	-0.96	40404965	18227105	20840000	TRUE	sensitive	0.024059481
XP_006724688	DLG3	-1.05	-1.34	-0.76	119898748	47254073	70990000	FALSE		
XP_011532334	SLC6A11	-1.05	-1.11	-0.99	29662768	13761418	14930000	TRUE	sensitive	-0.865751283
XP_011510188	MZT2B	-1.05	-1.33	-0.77	19650918	7825230	11530000	FALSE		
NP_006725	HIVEP2	-1.05	-0.86	-1.24	2871179	1584478	1218000	FALSE		
NP_001163	ARG2	-1.04	-1.55	-0.54	71170862	24346405	48880000	FALSE		
XP_011524921	AKT2	-1.04	-1.24	-0.85	42306912	17965517	23460000	FALSE		
XP_005268509	PCDH1	-1.04	-1.17	-0.91	27981446	12434791	14840000	FALSE		
NP_002406	MIF	-1.04	-1.25	-0.83	8429429764	3549193851	4727000000	FALSE		
NP_066957	MRPL23	-1.04	-0.91	-1.17	41104882	21814603	18310000	FALSE		
NP_036595	ATP6V0A2	-1.04	-0.64	-1.44	67618025	43470384	24910000	FALSE		
NP_001186652	CRABP2	-1.04	-1.12	-0.95	24497079	11276328	12640000	FALSE		
NP_056062	CYLD	-1.03	-1.06	-1.00	8665271	4166729	4325000	FALSE		
NP_001191732	ANO6	-1.03	-0.88	-1.18	130473574	71049274	57520000	FALSE		
XP_006714818	SYNPO	-1.03	-1.40	-0.65	22876620	8641759	14620000	FALSE		
NP_001229536	NCAM1	-1.02	-0.90	-1.15	115638387	62183296	52180000	FALSE		
NP_001074002	UNC119B	-1.02	-0.91	-1.14	57202962	30540444	26030000	FALSE		
XP_005249588	RBM33	-1.01	-0.72	-1.30	17573992	10641042	7153000	FALSE		
NP_001273399	C14orf159	-1.01	-1.01	-1.01	46202100	22982408	22910000	FALSE		
XP_005275604	HLA-F	-1.00	-0.69	-1.32	171479555	106410418	68880000	FALSE		
NP_065726	SPC25	-1.00	-0.84	-1.16	92586787	51710418	41340000	FALSE		
NP_001093869	PDS5A	-1.00	-1.01	-0.99	220549791	109493424	111000000	TRUE	sensitive	-0.881160766
NP_057490	UFC1	-1.00	-1.09	-0.90	75218206	35230350	40180000	TRUE	sensitive	0.101440379
XP_011531902	EOGT	-1.00	-1.07	-0.92	164252156	78028079	86660000	TRUE	sensitive	-0.761732464
XP_011537498	CHUK	-1.00	-1.51	-0.48	24854645	8714630	17770000	FALSE		
NP_002044	GBP1	-0.99	-0.97	-1.02	146526008	74879675	72200000	FALSE		
NP_004724	SLC33A1	-0.99	-1.12	-0.86	35627274	16424014	19580000	FALSE		
XP_006716583	EEF1D	-0.98	-1.11	-0.85	154438108	71479026	85390000	FALSE		
XP_005275378	MDC1	-0.98	-1.13	-0.83	86272323	39462477	48420000	FALSE		
NP_001280569	KIAA1033	-0.98	-0.90	-1.05	92130320	49215986	44560000	FALSE		
XP_006716295	TDRP	-0.97	-0.83	-1.12	93423644	52691375	42920000	FALSE		
XP_006713084	FANCD2	-0.97	-1.08	-0.86	21948470	10351426	12090000	TRUE	sensitive	-0.348065338
NP_683710	ABHD11	-0.97	-1.12	-0.82	105291794	48431221	59470000	FALSE		
XP_011542759	KIF13B	-0.97	-1.09	-0.85	14675424	6902196	8135000	FALSE		
XP_011527896	PCNT	-0.97	-1.03	-0.90	25098095	12285312	13410000	FALSE		
NP_006101	CD2BP2	-0.96	-0.91	-1.02	70394868	37519249	34750000	FALSE		
NP_689968	CNPY4	-0.96	-1.18	-0.73	19650918	8644562	11810000	FALSE		
NP_660308	CCDC127	-0.96	-0.83	-1.08	39606147	22235013	18720000	FALSE		

XP_006718553	EML3	-0.96	-0.72	-1.19	46483588	28130094	20390000	FALSE		
NP_001123917	SSFA2	-0.96	-0.90	-1.02	81707650	43928164	40400000	FALSE		
NP_891993	PRKACB	-0.95	-0.50	-1.40	24991586	17694586	9493000	FALSE		
NP_005460	ACOT8	-0.94	-0.95	-0.93	46590097	24084816	24420000	FALSE		
XP_011521076	TELO2	-0.93	-0.97	-0.90	98216551	50299710	52740000	FALSE		
NP_005219	EGFR	-0.93	-0.86	-1.00	303474687	167416567	151700000	FALSE		
XP_011532557	SLC4A7	-0.93	-1.29	-0.57	63935855	26196208	43060000	FALSE		
NP_001032584	DYNLL1	-0.93	-0.92	-0.94	1679799722	888839966	877900000	TRUE	insensitive	-0.089318355
NP_000415	KRT5	-0.92	-1.04	-0.81	16333922114	7960695132	9304000000	FALSE		
XP_011522591	SLC38A10	-0.92	-0.68	-1.17	39149680	24458514	17430000	FALSE		
NP_060024	PARP14	-0.92	-0.85	-1.00	23386342	12985995	11720000	FALSE		
NP_060458	SCYL2	-0.92	-0.77	-1.07	71543644	42078360	33960000	FALSE		
NP_065104	AVEN	-0.92	-0.97	-0.86	53003463	27027686	29150000	FALSE		
NP_115732	NAA38	-0.92	-0.92	-0.91	16775174	8887465	8899000	FALSE		
NP_057240	MTMR2	-0.91	-1.06	-0.77	15816592	7603814	9278000	FALSE		
XP_011533426	MPHOSPH8	-0.91	-1.02	-0.81	44368623	21945397	25350000	FALSE		
XP_011537935	MYOF	-0.91	-0.91	-0.91	81099026	43124714	43160000	TRUE	insensitive	0.217510221
NP_055454	TTC37	-0.91	-1.01	-0.81	65670431	32717233	37350000	FALSE		
XP_005269183	TMBIM6	-0.91	-0.72	-1.10	179391655	108932878	83910000	FALSE		
NP_001269598	DFFB	-0.91	-0.84	-0.97	22481015	12528215	11460000	FALSE		
NP_060937	USE1	-0.91	-0.84	-0.97	36958637	20628113	18820000	FALSE		
XP_006720628	CTDSPL2	-0.91	-1.12	-0.70	17748971	8193322	10940000	TRUE	insensitive	-0.245684397
NP_001531	HSPB1	-0.90	-1.08	-0.73	7057745480	3339923143	4262000000	FALSE		
NP_001107563	CDC27	-0.90	-1.03	-0.78	87413491	42807071	51060000	TRUE	insensitive	-0.565945156
XP_005245566	SNX27	-0.90	-0.78	-1.01	199856606	116033134	99380000	FALSE		
NP_932342	COX20	-0.89	-0.89	-0.89	800339360	432368232	432500000	FALSE		
NP_037431	SAC3D1	-0.89	-0.57	-1.20	28339013	19058582	12340000	FALSE		
NP_001037	SLC12A2	-0.88	-0.97	-0.79	74784562	38079795	43190000	FALSE		
NP_689753	SCFD2	-0.88	-0.91	-0.84	30925661	16470726	17230000	FALSE		
NP_066951	POLR2L	-0.88	-0.90	-0.85	156872601	84147378	86840000	FALSE		
XP_011512359	MTMR12	-0.88	-1.08	-0.67	23043992	10921315	14440000	FALSE		
NP_068749	RINT1	-0.87	-0.61	-1.13	46719430	30512417	21280000	TRUE	insensitive	-0.032690025
XP_005248611	ERBB2IP	-0.87	-0.89	-0.86	31298442	16853766	17300000	FALSE		
NP_001123514	CRYZ	-0.87	-0.97	-0.78	463922949	237391460	270100000	FALSE		
NP_001163887	TJP2	-0.87	-0.90	-0.84	383052156	205066610	214000000	FALSE		
XP_011509246	TRAF3IP1	-0.87	-0.84	-0.90	26695730	14919880	14320000	FALSE		
XP_011531123	GEN1	-0.87	-0.71	-1.02	7767552	4733816	3830000	TRUE	insensitive	-0.103840673
XP_011531857	CAPN7	-0.87	-1.11	-0.62	16227413	7504784	10570000	TRUE	insensitive	-0.09435195
NP_003739	ALDH4A1	-0.86	-0.87	-0.86	70379652	38574944	38710000	FALSE		
XP_005248552	MTX3	-0.86	-1.17	-0.56	55605327	24729445	37820000	TRUE	insensitive	0.039859438
NP_002255	KPNA1	-0.86	-0.66	-1.07	267946314	170032451	127800000	FALSE		
NP_005827	HRSP12	-0.86	-1.00	-0.72	204040890	102019471	124200000	FALSE		
NP_998766	TMED8	-0.86	-0.75	-0.96	32439611	19292143	16670000	FALSE		
NP_001177636	ALS2CL	-0.85	-0.83	-0.87	25136134	14181827	13720000	FALSE		
NP_001005751	FAM21A	-0.85	-0.83	-0.86	153296940	85997182	84590000	FALSE		
XP_011517307	MAPKAP1	-0.84	-0.73	-0.96	15497065	9337771	7982000	TRUE	insensitive	-0.009080879
XP_005261260	MCM3AP	-0.84	-0.84	-0.85	47084604	26364372	26160000	FALSE		
XP_011539538	AGO1	-0.84	-0.74	-0.93	30598526	18329872	16010000	FALSE		
XP_011512599	TAF8	-0.84	-1.03	-0.64	4980058	2437443	3191000	FALSE		
NP_060549	SRBD1	-0.83	-0.89	-0.77	11624701	6265042	6801000	FALSE		
NP_775878	FAM177A1	-0.83	-0.48	-1.18	37559652	26850179	16570000	FALSE		
NP_004228	TRIP13	-0.83	-0.76	-0.91	208225174	123226815	111100000	FALSE		
NP_001001410	TSR3	-0.83	-1.04	-0.62	38655174	18787652	25220000	FALSE		
XP_006721602	DERL2	-0.83	-0.59	-1.06	363576217	240754740	174200000	FALSE		
XP_011526331	MYO9B	-0.82	-1.01	-0.63	286052851	141631426	184800000	TRUE	insensitive	0.031751693
NP_071413	GOLPH3	-0.82	-0.81	-0.83	490930598	279339026	276500000	FALSE		
XP_011522657	ENTHD2	-0.82	-0.46	-1.18	5542274	4037804	2441000	FALSE		
NP_001127910	PHLDB2	-0.82	-0.91	-0.72	80946871	42965892	49090000	FALSE		
XP_011510816	ECT2	-0.81	-0.81	-0.81	10765021	6128642	6143000	TRUE	insensitive	-0.082788029
NP_055953	RTF1	-0.81	-0.80	-0.81	134962170	77308711	77070000	FALSE		
XP_005252630	SVIL	-0.80	-0.86	-0.75	87641725	48328454	52140000	FALSE		
XP_011534877	SYNE2	-0.80	-0.83	-0.78	337101113	189838429	196600000	TRUE	insensitive	0.174629267
XP_011521015	C16orf13	-0.80	-0.82	-0.78	84294298	47646456	49240000	FALSE		
NP_848642	ZBTB8OS	-0.80	-1.03	-0.57	62711001	30755320	42350000	FALSE		
NP_057436	CPA4	-0.79	-0.47	-1.12	3652499	2637371	1681000	FALSE		
NP_852664	PIK3R1	-0.79	-0.89	-0.70	86652712	46908403	53230000	FALSE		
XP_011541292	ALG9	-0.79	-0.62	-0.96	75819221	49253356	38850000	FALSE		
NP_006030	MRC2	-0.79	-0.90	-0.68	6611929	3539851	4126000	FALSE		
NP_036602	TNPO3	-0.79	-0.84	-0.75	154590264	86641810	92150000	TRUE	insensitive	-0.626413906
XP_011535589	SLC25A21	-0.79	-0.52	-1.06	43394826	30213459	20860000	FALSE		
NP_612426	KTI12	-0.79	-0.48	-1.10	24816606	17788010	11610000	FALSE		
XP_005256746	PER1	-0.79	-0.82	-0.76	39065994	22160273	23110000	FALSE		
NP_115753	ELOF1	-0.79	-0.62	-0.96	10978039	7154442	5658000	FALSE		
NP_060309	LPCAT2	-0.78	-0.66	-0.91	113888595	72161025	60690000	TRUE	insensitive	-0.242443309
NP_066409	HIST1H2AD	-0.78	-0.90	-0.66	4209389430	2260871050	2656000000	FALSE		
NP_689794	MOSPD2	-0.78	-1.08	-0.47	129408484	61174313	93160000	FALSE		
XP_006721723	RNF157	-0.78	-0.80	-0.75	8353352	4789870	4975000	FALSE		
NP_112577	SF3B5	-0.77	-0.99	-0.56	139983310	70656892	95040000	FALSE		

NP_996892	FAM45A	-0.77	-0.55	-0.99	179315577	122479419	90250000	FALSE		
XP_011513776	BLVRA	-0.77	-1.02	-0.52	254708762	125936123	177600000	FALSE		
NP_443730	GNB1L	-0.77	-0.99	-0.54	22062587	11089479	15150000	FALSE		
NP_001073936	MYO5B	-0.76	-0.67	-0.86	16090473	10145892	8842000	FALSE		
NP_001229476	ANAPC16	-0.76	-0.76	-0.77	104454937	61818941	61320000	FALSE		
NP_002881	RASA1	-0.76	-0.73	-0.80	69892754	42237182	40210000	FALSE		
NP_001275543	CST3	-0.76	-1.01	-0.51	72601127	35996430	51020000	FALSE		
NP_001157632	PPP6R3	-0.76	-0.76	-0.76	154590264	91163553	91340000	FALSE		
XP_006723661	RALGAPA2	-0.75	-0.83	-0.68	20997497	11818190	13100000	FALSE		
XP_011544063	NSMCE1	-0.75	-0.56	-0.94	35475118	23991392	18510000	FALSE		
NP_008860	SKIV2L	-0.75	-0.92	-0.58	67032225	35379829	44840000	FALSE		
XP_011542112	LOC102723897	-0.75	-0.60	-0.90	70760042	46618787	37930000	FALSE		
NP_057327	CYB5R1	-0.75	-0.74	-0.76	360380946	215343296	213100000	FALSE		
NP_003162	SUPV3L1	-0.75	-0.72	-0.77	118301113	71619163	69460000	TRUE	insensitive	-0.581808184
XP_005273766	TCIRG1	-0.75	-1.04	-0.45	8117510	3959327	5922000	FALSE		
NP_003609	MAP4K3	-0.74	-0.51	-0.97	22153880	15508454	11290000	FALSE		
XP_011517818	FAM208B	-0.74	-0.75	-0.73	16896898	10043126	10160000	FALSE		
XP_011521258	TCF25	-0.74	-0.86	-0.62	36327191	20002169	23610000	FALSE		
NP_000098	DDB2	-0.74	-0.46	-1.02	27661919	20067566	13670000	FALSE		
NP_001887	CSNK2A2	-0.74	-0.67	-0.81	425351460	266820154	243300000	FALSE		
NP_612431	ADAT3	-0.74	-0.91	-0.56	25341544	13471802	17180000	FALSE		
XP_005254082	ABCC4	-0.73	-0.68	-0.79	32759138	20422579	18970000	FALSE		
NP_543012	OVCA2	-0.73	-0.71	-0.76	214083171	131167891	126700000	FALSE		
XP_005245774	SRRM1	-0.73	-0.72	-0.73	5271437	3191378	3181000	FALSE		
XP_005268633	PTGES3	-0.73	-0.89	-0.56	1793155772	967877028	1214000000	FALSE		
NP_689613	C4orf32	-0.72	-0.74	-0.70	173533658	103887959	106600000	FALSE		
NP_003132	TRIM21	-0.72	-0.64	-0.79	103922392	66620956	60100000	FALSE		
NP_001474	GBAS	-0.71	-0.61	-0.82	368521280	241875833	208900000	FALSE		
XP_011511782	STX18	-0.71	-0.63	-0.79	55506426	35818924	32030000	FALSE		
NP_005264	GNB2	-0.71	-0.76	-0.66	536881641	316895645	339200000	FALSE		
NP_115976	CARD6	-0.71	-0.90	-0.52	26018637	13929582	18140000	FALSE		
NP_061903	DHX29	-0.71	-0.64	-0.78	156796523	100431255	91540000	FALSE		
XP_011520970	NPRL3	-0.71	-0.55	-0.87	14743894	10080495	8072000	FALSE		
NP_689407	CSNK1E	-0.70	-0.49	-0.92	20236718	14434073	10680000	TRUE	insensitive	-0.208623849
NP_005139	UNC119	-0.70	-0.86	-0.55	70508985	38883245	48150000	FALSE		
NP_002862	RABIF	-0.70	-0.52	-0.88	135799026	95012639	73600000	FALSE		
NP_060701	SLC38A7	-0.69	-0.65	-0.74	59500515	37892946	35700000	FALSE		
NP_061895	TMX3	-0.69	-0.67	-0.71	364717385	228889838	222400000	FALSE		
NP_955450	PRCP	-0.69	-0.82	-0.56	64065188	36164594	43440000	FALSE		
XP_011514525	MET	-0.69	-0.88	-0.51	43410042	23617694	30560000	FALSE		
NP_001186103	MLST8	-0.69	-0.73	-0.65	90684840	54821452	57690000	FALSE		
NP_001072113	CDC16	-0.69	-0.61	-0.76	60063491	39247600	35370000	FALSE		
NP_004330	PTTG1IP	-0.69	-0.74	-0.64	228994437	137333903	147300000	FALSE		
XP_011538398	ANXA8	-0.69	-0.77	-0.60	1439393602	842968574	950600000	FALSE		
NP_009077	VEZF1	-0.68	-0.56	-0.81	2275490	1544306	1298000	FALSE		
NP_001244110	SLC20A2	-0.68	-0.63	-0.73	42200403	27186507	25460000	FALSE		
NP_002068	GOLGA1	-0.68	-0.77	-0.58	17277288	10117865	11570000	FALSE		
NP_001116827	PPP6C	-0.67	-0.47	-0.87	410288039	295221178	223800000	FALSE		
NP_000812	GGCX	-0.67	-0.83	-0.51	92206398	51775816	64820000	FALSE		
NP_000370	XDH	-0.67	-0.52	-0.81	61524186	42825756	35030000	FALSE		
NP_004795	CIAO1	-0.67	-0.69	-0.65	215680807	134064048	137600000	FALSE		
NP_057293	TRAPPC2L	-0.66	-0.76	-0.57	47731266	28102067	32250000	FALSE		
XP_006722122	UBTF	-0.66	-0.80	-0.53	326982754	187969940	227200000	FALSE		
NP_061326	NDUFA12	-0.66	-0.76	-0.56	154362031	91135525	104600000	FALSE		
NP_001129419	URM1	-0.66	-0.74	-0.58	511699861	307086080	341500000	FALSE		
NP_001034437	EFEMP1	-0.66	-0.56	-0.76	21522434	14630265	12710000	TRUE	insensitive	-0.084219587
XP_005249346	KIF13A	-0.66	-0.75	-0.56	4585214	2721453	3108000	FALSE		
XP_011507484	LYPLAL1	-0.65	-0.66	-0.64	72220737	45656516	46220000	TRUE	insensitive	-0.522068053
NP_001248370	EXTL2	-0.65	-0.70	-0.61	45547830	28120751	29900000	FALSE		
NP_115646	LRRC8C	-0.65	-0.50	-0.80	70067733	49430863	40360000	FALSE		
XP_005254606	B2M	-0.65	-0.67	-0.62	187151599	117341076	121900000	FALSE		
NP_003152	RPS6KB1	-0.64	-0.63	-0.65	42542754	27410726	27160000	TRUE	insensitive	-0.120174549
NP_001598	ACAA1	-0.64	-0.67	-0.60	311767177	195630743	205000000	FALSE		
NP_055690	KIF14	-0.64	-0.62	-0.65	93804033	61136943	59680000	TRUE	insensitive	0.016657955
NP_001271336	TMEM40	-0.63	-0.73	-0.54	49549527	29923843	34110000	FALSE		
NP_001104262	MECP2	-0.63	-0.62	-0.65	22222350	14508813	14160000	FALSE		
XP_011515999	PSIP1	-0.63	-0.62	-0.65	28049917	18283160	17930000	FALSE		
NP_003860	CES2	-0.63	-0.57	-0.69	33261252	22393834	20640000	FALSE		
NP_078916	YRDC	-0.63	-0.55	-0.71	45874965	31381264	28140000	FALSE		
NP_001119603	POLG	-0.62	-0.75	-0.50	31526676	18768967	22310000	TRUE	insensitive	-0.325728917
XP_005273256	PSEN2	-0.62	-0.61	-0.64	53847928	35277062	34630000	FALSE		
NP_001379	DRG2	-0.62	-0.61	-0.63	155046732	101458924	99900000	FALSE		
NP_006160	NNMT	-0.62	-0.79	-0.45	1258328234	726281469	920300000	FALSE		
XP_011534145	MLLT4	-0.62	-0.46	-0.78	173609736	126029547	101000000	FALSE		
NP_001018114	FAHD1	-0.62	-0.50	-0.74	420178164	296529120	251900000	FALSE		
NP_001338	DGKQ	-0.62	-0.57	-0.67	17650070	11874244	11130000	TRUE	insensitive	0.107147088
NP_002473	NASP	-0.62	-0.66	-0.57	1447762170	915465927	972700000	TRUE	insensitive	-0.499036495
NP_001171846	PCYT2	-0.62	-0.60	-0.63	50272267	33146985	32460000	FALSE		

XP_011533470	COG6	-0.61	-0.54	-0.69	86120167	59427276	53330000	FALSE		
NP_037364	PDCD6	-0.61	-0.55	-0.67	391877191	268034671	246100000	FALSE		
NP_006597	RBBP9	-0.61	-0.68	-0.53	83077051	51813185	57370000	FALSE		
NP_005724	KIF20A	-0.61	-0.63	-0.58	157709458	101926046	105200000	FALSE		
NP_055764	KIAA0907	-0.61	-0.51	-0.70	85739777	60118617	52750000	FALSE		
NP_000273	PCCA	-0.60	-0.55	-0.66	97912239	66975969	61950000	FALSE		
NP_612467	WDR92	-0.60	-0.60	-0.60	25204604	16582835	16590000	FALSE		
NP_071732	RAB38	-0.60	-0.69	-0.52	85207232	52990333	59350000	FALSE		
XP_005251033	PLEC	-0.60	-0.63	-0.58	165012935	106970965	110300000	FALSE		
NP_002899	REL	-0.60	-0.70	-0.51	42238442	26028044	29730000	FALSE		
NP_115709	FAM213A	-0.60	-0.52	-0.68	584810709	407517336	364500000	FALSE		
NP_003376	VSNL1	-0.60	-0.52	-0.68	212333380	147610589	132800000	FALSE		
NP_056281	PTPN23	-0.60	-0.65	-0.55	125148122	79504184	85660000	FALSE		
XP_005248331	NNT	-0.60	-0.58	-0.62	596146314	399576260	388000000	FALSE		
NP_060037	NAGK	-0.60	-0.53	-0.66	113660362	78541913	72030000	FALSE		
NP_076945	CUEDC2	-0.59	-0.55	-0.64	35703352	24393117	22920000	FALSE		
NP_003861	IQGAP1	-0.59	-0.54	-0.65	5854954103	4024724167	3739000000	FALSE		
NP_064710	C16orf62	-0.59	-0.63	-0.55	31648401	20394552	21560000	FALSE		
XP_011512245	SUB1	-0.59	-0.63	-0.56	2471009736	1599426132	1681000000	FALSE		
XP_006719780	RNF10	-0.59	-0.73	-0.45	5536949	3339923	4049000	FALSE		
NP_001344	AKR1C1	-0.59	-0.66	-0.52	1285716273	812231939	898200000	FALSE		
XP_006720161	RALGAPA1	-0.59	-0.58	-0.59	28262935	18909103	18730000	FALSE		
NP_036369	SIRT2	-0.59	-0.63	-0.54	79729624	51364748	54960000	FALSE		
NP_060225	NSUN2	-0.59	-0.65	-0.52	1103890125	704793851	768200000	FALSE		
XP_005253361	FGD4	-0.58	-0.66	-0.51	63426134	40116447	44640000	TRUE	insensitive	-0.319493581
NP_065805	ARHGAP31	-0.58	-0.51	-0.65	5250135	3679988	3335000	FALSE		
XP_005266896	AIM1	-0.58	-0.60	-0.57	370499305	244771990	250100000	FALSE		
XP_005249025	SIRT5	-0.58	-0.61	-0.55	54350042	35576020	37060000	FALSE		
XP_005264506	BIRC6	-0.58	-0.62	-0.54	90304451	58642511	62120000	TRUE	insensitive	-0.248172174
XP_006718142	SH3PXD2A	-0.58	-0.48	-0.68	57263825	41003980	35730000	FALSE		
NP_001171725	ESYT1	-0.58	-0.58	-0.58	1066611961	714977114	711500000	FALSE		
NP_000013	ADA	-0.58	-0.68	-0.48	151242837	94265243	108600000	FALSE		
NP_003906	CPNE1	-0.58	-0.63	-0.53	501048957	323902477	347400000	FALSE		
XP_011530230	IRF2	-0.58	-0.56	-0.59	8688095	5895081	5767000	FALSE		
NP_066949	MPST	-0.57	-0.68	-0.47	357109597	222443553	258700000	FALSE		
XP_005266791	RAB27B	-0.57	-0.69	-0.46	39020348	24243638	28350000	FALSE		
NP_001284529	HSPBP1	-0.57	-0.51	-0.64	165621558	116406832	106500000	TRUE	insensitive	0.008131207
NP_004901	PITPNM1	-0.57	-0.58	-0.56	27798860	18582118	18840000	FALSE		
NP_951032	NDUFAF3	-0.57	-0.48	-0.66	62695786	45086627	39690000	FALSE		
NP_872319	SPC24	-0.57	-0.52	-0.62	117312100	82045329	76540000	FALSE		
NP_659500	OARD1	-0.57	-0.52	-0.61	30644172	21431563	20020000	FALSE		
XP_006723467	ITPKC	-0.56	-0.61	-0.52	87793880	57698924	61250000	FALSE		
NP_077719	NOTCH2	-0.56	-0.61	-0.51	38830153	25439471	27210000	FALSE		
NP_002532	OGDH	-0.56	-0.54	-0.58	725402643	497765329	485600000	FALSE		
NP_006701	COPS8	-0.56	-0.63	-0.49	97988317	63210965	69840000	FALSE		
NP_940684	HACD2	-0.55	-0.58	-0.53	204877747	137333903	141900000	FALSE		
NP_002205	ITGB8	-0.55	-0.59	-0.51	19179235	12705722	13460000	FALSE		
XP_005275157	HLA-B	-0.55	-0.48	-0.62	26581613	19039898	17270000	FALSE		
NP_757345	TAPBP	-0.55	-0.62	-0.48	199324061	129299402	143100000	FALSE		
XP_011537723	DOCK1	-0.55	-0.47	-0.62	48659416	35118241	31670000	TRUE	insensitive	0.085497703
NP_001101	ADAM10	-0.54	-0.58	-0.51	95934214	64388113	67180000	FALSE		
XP_011535053	KTN1	-0.54	-0.49	-0.60	857397775	611462852	566300000	FALSE		
NP_001129204	TOM1	-0.54	-0.50	-0.58	29639944	21001810	19840000	FALSE		
NP_689729	COMMD1	-0.54	-0.51	-0.56	73209750	51233954	49660000	FALSE		
NP_079431	PAAF1	-0.54	-0.54	-0.53	48446398	33277780	33510000	FALSE		
XP_005268745	DGKA	-0.54	-0.53	-0.54	216517663	149946200	148800000	FALSE		
XP_006719589	PTPN11	-0.54	-0.53	-0.54	164404312	113977797	112900000	FALSE		
XP_011515869	PRKDC	-0.53	-0.48	-0.58	3441002782	2465470538	2295000000	FALSE		
XP_006724163	HMGXB4	-0.53	-0.52	-0.55	13732058	9604031	9409000	FALSE		
XP_011540001	RNF220	-0.53	-0.50	-0.56	165621558	116873954	112700000	FALSE		
NP_003713	TP63	-0.53	-0.45	-0.61	146830320	107251238	96530000	FALSE		
XP_006720965	PPL	-0.53	-0.51	-0.55	137929207	97161401	94270000	FALSE		
XP_011534258	PDSS2	-0.52	-0.58	-0.46	22290821	14873168	16190000	FALSE		
NP_002809	PSME2	-0.52	-0.53	-0.52	906087622	629400342	633000000	FALSE		
XP_005268263	ELMSAN1	-0.52	-0.49	-0.56	23348303	16657575	15890000	FALSE		
NP_061914	MTRF1L	-0.52	-0.50	-0.54	15755730	11164219	10830000	FALSE		
XP_011514658	NCAPG2	-0.52	-0.54	-0.49	10407455	7135757	7415000	FALSE		
NP_001032671	SCD5	-0.51	-0.52	-0.51	213854937	149479078	149900000	FALSE		
NP_071903	LMBR1	-0.51	-0.52	-0.51	30164882	21057865	21180000	FALSE		
NP_001435	FABP5	-0.51	-0.54	-0.48	1664584145	1144449189	1190000000	FALSE		
NP_001293009	LMO7	-0.51	-0.47	-0.56	21263769	15358975	14470000	FALSE		
NP_001135452	TP53BP1	-0.51	-0.51	-0.51	159839638	112109308	112600000	TRUE	insensitive	0.041639261
NP_443182	WDFY2	-0.51	-0.50	-0.52	78284145	55456738	54610000	FALSE		
XP_011520393	EDC3	-0.51	-0.48	-0.53	60337371	43283535	41740000	FALSE		

Table S7. Proteins upregulated in SF3B1-mutant MCF-10A cells. Protein abundance derived from peptide counts is shown for the TWT1, K700E1, and K700E2 MCF-10A clones in this 3-way SILAC experiment. Proteins with SF3B1-mutant/SF3B1-wild type log2 ratios > 0.5 are included. If the corresponding mRNA was misspliced by mutant SF3B1 in our RNA-seq analysis, the predicted effect of the missplicing event on nonsense-mediated decay (NMD) is shown, along with the mutant/wild type whole gene mRNA ratio.

Accession	Gene name	Avg log2	Log2 K700E1/TWT1	Log2 K700E2/TWT1	Abun TWT1	Abun K700E1	Abun K700E2	Misspliced	NMD predict	log2FC mRNA
XP_011531456	DHX57	3.67	1.37	5.97	22617955	58418292	1419000000	FALSE		
NP_005644	TFCP2	3.50	3.59	3.42	11875758	143032792	126700000	FALSE		
NP_001020366	CES1	2.48	2.32	2.64	55696620	277470538	346600000	FALSE		
NP_001146	ANXA6	2.12	2.13	2.11	30164882	131728437	130300000	FALSE		
NP_005971	S100P	2.02	2.18	1.86	4650641	21076550	16840000	FALSE		
XP_011539949	CPSF3L	1.97	1.99	1.94	12918025	51448830	49580000	FALSE		
NP_073615	CEP85	1.94	2.18	1.71	7122412	32222084	23340000	FALSE		
NP_001091952	CRTC1	1.77	1.96	1.57	7207619	27989957	21450000	FALSE		
XP_011515035	DMTF1	1.70	1.70	1.70	2483943	8064396	8052000	FALSE		
NP_065699	TWSG1	1.69	1.41	1.97	11457330	30362938	44970000	FALSE		
XP_011513787	OCM	1.68	1.67	1.70	135875104	431714261	440300000	FALSE		
NP_001158297	SMIM12	1.61	1.48	1.75	25022017	69638565	84170000	FALSE		
NP_003812	RIPK2	1.60	1.95	1.25	12712615	49038480	30270000	FALSE		
XP_005254590	DNAJC17	1.59	1.83	1.35	12750654	45479009	32530000	FALSE		
NP_001893	CTH	1.56	1.13	1.98	10194437	22309752	40330000	FALSE		
NP_036294	FBXL6	1.55	1.53	1.58	27471725	79205226	82170000	FALSE		
NP_003607	GEMIN2	1.52	1.18	1.87	6907872	15629906	25230000	FALSE		
NP_004266	MED20	1.51	1.52	1.51	25569777	73272775	72710000	FALSE		
XP_011515603	GSDMD	1.50	1.15	1.85	61782851	137053629	222700000	FALSE		
NP_003829	FPGT	1.49	1.81	1.17	16067650	56204133	36100000	FALSE		
NP_055889	KIF1B	1.46	0.93	1.99	6958844	13284953	27730000	FALSE		
NP_598001	NEK7	1.43	2.28	0.58	25592601	123880786	38370000	FALSE		
XP_011517190	PTPN3	1.42	2.23	0.60	24892684	117154227	37810000	FALSE		
XP_005278096	OTUD5	1.40	1.72	1.08	3864757	12743091	8185000	FALSE		
NP_056299	SYF2	1.40	1.67	1.12	9281502	29578173	20160000	FALSE		
XP_005267216	FBXO30	1.39	1.61	1.16	29647552	90799197	66320000	FALSE		
NP_057183	GOLGA7	1.37	1.19	1.55	6655293	15144099	19460000	FALSE		
NP_060193	TOR4A	1.36	1.23	1.49	12857163	30101349	36080000	FALSE		
NP_001026788	COX19	1.36	1.28	1.44	21005104	50897626	56820000	FALSE		
NP_073557	DGCR8	1.34	1.08	1.60	12902809	27205192	39180000	FALSE		
XP_005271769	UBASH3B	1.31	1.36	1.27	14378720	36809223	34670000	FALSE		
XP_011506903	LOC105369243	1.30	0.59	2.01	52493741	79065090	211100000	FALSE		
NP_036323	NAT6	1.29	1.77	0.81	13161474	44825038	23020000	FALSE		
NP_002764	PRSS8	1.28	1.94	0.61	4150809	15919522	6350000	FALSE		
NP_803882	CYP20A1	1.27	2.06	0.48	14873227	61968420	20680000	FALSE		
NP_001244273	BCS1L	1.25	0.99	1.50	103313769	205440307	292700000	FALSE		
XP_006718056	CAMK2G	1.23	1.28	1.17	52463310	127430914	118400000	TRUE	insensitive	0.281013344
NP_001018121	PODXL	1.22	0.76	1.68	9144562	15443057	29300000	FALSE		
NP_932343	C1orf52	1.21	1.68	0.74	9935772	31811016	16640000	FALSE		
NP_006065	TRIM22	1.18	1.30	1.06	17604423	43320905	36800000	FALSE		
NP_001128245	STX16	1.17	1.16	1.17	81327260	181336806	183400000	FALSE		
NP_002679	SEPT5	1.16	1.16	1.16	32462434	72609462	72530000	FALSE		
NP_001026893	DNAJB14	1.15	1.43	0.88	11921405	32100632	21870000	FALSE		
NP_055049	HSD17B8	1.15	1.23	1.08	25318720	59259112	53430000	FALSE		
NP_733468	CASC5	1.15	1.44	0.86	8794604	23935337	15910000	FALSE		
NP_064528	PNO1	1.14	1.13	1.15	153601252	336514774	340600000	FALSE		
NP_057256	UBAC1	1.12	1.13	1.12	75400793	164894108	163900000	FALSE		
NP_000205	JAG1	1.12	1.01	1.23	8383783	16881793	19620000	FALSE		
NP_524558	SCAMP4	1.12	1.21	1.02	31770125	73637131	64400000	FALSE		
XP_006724250	RBFOX2	1.12	1.11	1.13	45060932	96974552	98310000	FALSE		
NP_036269	DDAH1	1.11	1.17	1.05	11541015	26037387	23820000	FALSE		
NP_005637	TARBP1	1.11	1.06	1.15	8330529	17414313	18550000	TRUE	insensitive	0.190606493
NP_001291373	ALAS1	1.09	0.95	1.22	16387177	31624167	38300000	FALSE		
NP_060921	CENPJ	1.07	1.21	0.93	5353601	12406763	10190000	FALSE		
NP_001648	AREG	1.07	1.26	0.87	86880946	208616738	159200000	FALSE		
NP_000393	G6PD	1.06	1.07	1.05	52957816	111361913	110000000	FALSE		
XP_011529712	KLHL13	1.05	1.38	0.72	15953533	41545841	26360000	FALSE		
NP_078939	NPEPL1	1.05	0.77	1.33	18753199	31876413	47280000	FALSE		
NP_057303	MAN1B1	1.04	1.09	0.99	20297580	43339590	40400000	FALSE		
XP_005250059	PRKAG2	1.04	1.28	0.80	7072200	17171409	12310000	FALSE		
NP_113680	RBM4B	1.04	0.92	1.16	26277302	49832588	58520000	FALSE		
NP_001288005	AP2S1	1.04	1.06	1.01	237134771	494495474	477600000	FALSE		
NP_003163	SURF1	1.04	1.43	0.64	11533408	31035594	18000000	FALSE		
XP_011520261	TCF12	1.02	0.96	1.08	3995611	7791597	8469000	TRUE	sensitive	-0.063666171
NP_055572	MAML1	1.02	0.58	1.46	23858025	35772212	65740000	FALSE		
NP_060354	PINX1	1.02	1.02	1.03	33375369	67723365	67950000	FALSE		
XP_011523836	MED24	1.02	0.84	1.19	12545243	22533971	28530000	FALSE		
NP_055299	MOCS3	1.01	0.92	1.11	8695702	16424014	18740000	FALSE		

NP_598395	MED22	1.01	0.89	1.13	50203797	93218890	109800000	FALSE		
XP_011533519	ZMYM2	1.01	0.99	1.03	34638261	68564184	70820000	FALSE		
NP_112494	KIF18A	1.01	1.40	0.62	12355049	32493015	18960000	FALSE		
XP_005263738	ARHGEF4	1.00	0.67	1.34	14272211	22674108	36160000	FALSE		
XP_011513874	STARD3NL	1.00	0.88	1.13	4585214	8444634	10020000	FALSE		
NP_064547	DHX33	1.00	1.29	0.71	27000042	66135149	44190000	FALSE		
XP_011542696	AGPAT6	0.99	1.27	0.72	10057497	24234295	16550000	FALSE		
NP_789788	GATC	0.99	1.14	0.84	24048220	53046388	42910000	FALSE		
XP_011522518	TLK2	0.98	1.15	0.82	4971690	11033424	8769000	FALSE		
NP_001002814	RAB11FIP1	0.98	0.65	1.32	32941725	51794500	81990000	FALSE		
XP_005277005	LSM14A	0.98	1.11	0.85	212713769	460302135	384500000	FALSE		
NP_065695	TMEM9B	0.97	1.18	0.77	24793783	56166763	42200000	FALSE		
XP_011516498	ZNF618	0.96	1.10	0.83	23120070	49542972	41030000	FALSE		
NP_079291	HSPA12A	0.95	1.41	0.48	5299586	14107088	7407000	FALSE		
XP_011536904	CALCOCO1	0.94	1.12	0.76	2366022	5127132	4017000	FALSE		
NP_001824	CLTA	0.94	1.19	0.69	334134075	760101110	540000000	FALSE		
XP_011516855	TOR2A	0.93	1.12	0.75	12263755	26635303	20600000	FALSE		
NP_997239	C1orf174	0.91	0.65	1.17	14150487	22272383	31920000	FALSE		
NP_036514	TTC33	0.90	0.84	0.96	37985688	67966268	74010000	FALSE		
NP_000480	ATRX	0.90	1.19	0.62	56251989	127898036	86180000	FALSE		
NP_001093095	MTFR1L	0.90	0.99	0.80	18601043	37042784	32390000	FALSE		
NP_006112	KRT1	0.89	0.77	1.01	393855216	670600512	794000000	FALSE		
NP_075387	UPF3A	0.88	0.91	0.85	6239147	11706080	11210000	TRUE	sensitive	-0.082808011
NP_003477	SLC7A5	0.87	0.82	0.93	2006173853	3537982921	3825000000	FALSE		
XP_011521752	MTSS1L	0.87	1.13	0.62	5503474	12061093	8433000	FALSE		
XP_011539841	MECR	0.87	0.73	1.02	42725341	70684919	86620000	FALSE		
XP_011530429	BDH2	0.87	0.98	0.77	9243463	18208420	15720000	FALSE		
NP_057150	GLRX2	0.87	0.77	0.98	65830195	111922459	129400000	FALSE		
XP_011517075	C9orf114	0.87	0.97	0.77	47556287	92891904	81010000	FALSE		
NP_705902	PANK2	0.86	1.01	0.72	9768401	19637814	16060000	FALSE		
XP_011534179	C6orf203	0.86	0.77	0.95	87413491	149011956	169000000	FALSE		
NP_001188409	OSBPL6	0.86	0.73	0.99	11472545	18983843	22820000	FALSE		
XP_005264437	AFTPH	0.86	0.64	1.07	4598908	7174061	9687000	FALSE		
NP_001278709	RBM38	0.86	1.12	0.60	4400345	9566661	6650000	FALSE		
NP_004086	EIF4EBP1	0.85	0.74	0.96	312680111	523737319	607600000	FALSE		
XP_005259320	GEMIN7	0.85	0.86	0.84	23447204	42480085	42100000	FALSE		
XP_011541730	PAIP2	0.85	0.81	0.89	16942545	29680939	31330000	FALSE		
XP_006712274	RABL2A	0.85	0.66	1.03	19749819	31278497	40290000	FALSE		
NP_001062	TYMS	0.85	0.85	0.84	101716134	183392143	182100000	FALSE		
NP_002426	MPI	0.84	1.15	0.53	5586399	12406763	8092000	FALSE		
NP_057158	BOLA1	0.84	0.84	0.83	30431154	54625260	54070000	FALSE		
NP_079090	CBLL1	0.84	0.67	1.00	21324631	33959778	42680000	FALSE		
XP_011523367	USP36	0.83	0.63	1.04	8969583	13845500	18390000	FALSE		
NP_001276048	ZCCHC7	0.83	0.97	0.69	6678878	13098104	10770000	FALSE		
NP_060831	AGPAT5	0.83	0.79	0.87	85511544	148171136	155800000	FALSE		
NP_919307	RPS19BP1	0.83	0.80	0.86	60116745	104822203	108800000	FALSE		
NP_001026897	MRI1	0.83	0.85	0.80	96390682	173676003	168400000	FALSE		
NP_001182132	EEF1D	0.82	1.12	0.52	74183547	160783433	106500000	FALSE		
NP_001032412	HELZ2	0.81	0.68	0.95	11814896	18890418	22750000	FALSE		
NP_060401	TTC38	0.81	0.87	0.75	49549527	90266678	83160000	FALSE		
XP_011532889	SPDL1	0.80	0.69	0.91	10772629	17386285	20290000	FALSE		
NP_695005	IP6K1	0.79	0.70	0.87	2774561	4519874	5065000	FALSE		
NP_757386	SUGP1	0.78	0.83	0.74	57712684	102673442	96210000	FALSE		
NP_060551	WRAP53	0.78	0.89	0.67	14454798	26794125	22970000	FALSE		
NP_036360	MSRB2	0.78	0.59	0.97	7843630	11790162	15320000	FALSE		
NP_055250	NAAA	0.77	0.90	0.64	30347469	56493749	47410000	FALSE		
XP_005244788	DVL1	0.77	1.04	0.50	20617107	42489428	29070000	FALSE		
XP_005257251	GAA	0.77	0.89	0.65	8201196	15153442	12870000	FALSE		
NP_001231630	ZFP36L1	0.76	0.83	0.69	43402434	77336738	70120000	FALSE		
XP_005248605	SGTB	0.76	0.79	0.73	31861419	55232519	52840000	FALSE		
NP_149080	ZCCHC3	0.76	0.90	0.63	11875758	22113561	18330000	FALSE		
NP_997717	BOLA3	0.76	0.77	0.75	50378776	86025209	84690000	FALSE		
NP_612482	SP1	0.76	0.80	0.71	9578206	16722972	15650000	FALSE		
XP_005248684	CCNH	0.76	0.82	0.70	38716036	68181144	62690000	FALSE		
NP_060818	CMTR2	0.76	0.60	0.91	29183477	44283177	54790000	FALSE		
NP_003646	CBX4	0.75	0.80	0.70	9829263	17096670	16020000	FALSE		
NP_463459	MGAT4B	0.75	0.94	0.57	28164033	53896550	41680000	FALSE		
NP_060919	UBAP2	0.75	0.92	0.58	126669680	239259949	189400000	FALSE		
NP_060934	CISD1	0.75	0.89	0.60	73118456	135839112	110600000	FALSE		
NP_859067	CENPV	0.74	0.77	0.71	54677177	93022699	89520000	FALSE		
NP_076968	SPATA5L1	0.74	0.77	0.70	34980612	59473988	57010000	FALSE		
NP_002219	JUN	0.73	0.78	0.68	70311182	121078053	112600000	FALSE		
NP_005504	GTF2E1	0.73	0.74	0.72	24329708	40742391	39990000	FALSE		
NP_689620	GRPEL2	0.73	0.63	0.83	56343282	87361178	99960000	FALSE		

XP_006714934	UIMC1	0.73	0.85	0.61	27601057	49748506	42050000	FALSE		
NP_001284694	CETN3	0.73	0.85	0.61	35132768	63267020	53560000	FALSE		
NP_689419	SNX6	0.73	0.69	0.76	115029764	185821178	195400000	FALSE		
XP_011541156	NPAT	0.72	0.99	0.45	3520124	6992818	4816000	FALSE		
NP_899648	RNF14	0.72	0.70	0.74	114268985	185634330	190900000	TRUE	sensitive	0.28006034
NP_060473	UACA	0.72	0.69	0.74	18722768	30288198	31360000	FALSE		
NP_001202	BUB1B	0.72	0.74	0.69	62345828	104074808	100800000	TRUE	insensitive	0.220559369
XP_011520549	ZNF592	0.71	0.68	0.75	15641613	25047088	26310000	FALSE		
NP_067007	C6orf47	0.71	0.90	0.52	4262644	7929865	6117000	FALSE		
NP_085054	TMEM177	0.70	0.64	0.77	40869040	63650060	69660000	FALSE		
NP_112236	SHARPIN	0.70	0.90	0.49	5489780	10267344	7724000	FALSE		
NP_714924	LIX1L	0.70	0.60	0.80	29738846	44974518	51670000	FALSE		
NP_056251	RCHY1	0.69	0.60	0.78	14340682	21795918	24560000	FALSE		
NP_671717	FBXO22	0.69	0.75	0.63	115486231	193949103	178800000	FALSE		
NP_001139669	CCDC168	0.68	0.71	0.66	310397775	507201196	489500000	FALSE		
NP_612457	ACYP2	0.68	0.81	0.55	41089666	72076943	60150000	FALSE		
XP_011509269	STK39	0.67	0.70	0.64	117236022	190398975	182900000	FALSE		
XP_011541049	CHORDC1	0.67	0.75	0.59	249383310	418074295	376000000	FALSE		
NP_065970	ALS2	0.66	0.85	0.48	38107413	68536157	53110000	FALSE		
NP_775752	MISP	0.66	0.84	0.48	46719430	83754996	65310000	FALSE		
NP_004789	KIF3B	0.66	0.76	0.57	15405772	26037387	22820000	FALSE		
NP_001664	ASNS	0.66	0.65	0.67	317092629	497111358	506100000	FALSE		
NP_620599	CD151	0.66	0.83	0.49	32713491	58109991	45940000	FALSE		
NP_008869	SNRPD1	0.66	0.66	0.65	1239308762	1960978651	1951000000	FALSE		
XP_006711623	ISG20L2	0.66	0.62	0.69	66073644	101552348	106900000	FALSE		
XP_005256854	MIS12	0.66	0.59	0.72	17901127	26962289	29540000	FALSE		
XP_005255105	RNPS1	0.66	0.74	0.57	421015021	704326729	624500000	FALSE		
NP_060224	UHRF1BP1	0.64	0.61	0.67	23173324	35463911	36910000	FALSE		
NP_077007	WDR77	0.64	0.66	0.62	403288873	639303330	619300000	FALSE		
NP_002309	LOXL2	0.64	0.73	0.55	34759986	57726951	50950000	FALSE		
XP_006717123	GLE1	0.64	0.80	0.48	43280709	75141264	60570000	FALSE		
XP_011519985	ZFAND6	0.64	0.57	0.70	41097274	60875354	66970000	FALSE		
XP_011537005	STAT6	0.63	0.65	0.61	37339026	58390265	56850000	FALSE		
XP_006719907	PSPC1	0.62	0.61	0.64	378943950	576428693	590400000	FALSE		
NP_000566	IL1A	0.62	0.69	0.55	73696648	119209564	107900000	FALSE		
NP_277050	ARHGAP18	0.62	0.73	0.51	21956078	36314073	31300000	FALSE		
NP_073210	DGCR14	0.62	0.68	0.56	38099805	60856670	56170000	FALSE		
NP_056943	GTF2A1	0.62	0.61	0.62	255773853	390327242	394200000	FALSE		
NP_006490	LGALS8	0.62	0.55	0.68	75598595	110801366	121300000	FALSE		
NP_945339	LENG9	0.62	0.57	0.66	19300960	28578531	30590000	FALSE		
XP_011540267	RBM15	0.60	0.59	0.62	105367872	158167549	161600000	FALSE		
NP_001014433	CUTA	0.60	0.69	0.51	748226008	1205175064	1064000000	FALSE		
NP_065070	ANKRD50	0.59	0.72	0.46	18669513	30820717	25640000	FALSE		
NP_006268	ITSN2	0.59	0.61	0.56	8992406	13742733	13240000	FALSE		
XP_005254003	KCTD10	0.58	0.62	0.55	16189374	24944321	23640000	FALSE		
NP_001142	SLC25A4	0.58	0.61	0.55	122941864	187969940	180500000	FALSE		
XP_011519114	BICD1	0.58	0.58	0.59	10795452	16087686	16210000	FALSE		
XP_005256832	VAMP2	0.58	0.58	0.58	795013908	1184621691	1187000000	FALSE		
NP_001910	ECI1	0.57	0.56	0.59	377650626	554847652	567500000	FALSE		
XP_005273855	AMOTL1	0.57	0.60	0.54	5282088	8016750	7672000	FALSE		
NP_001029345	ALDH1L2	0.57	0.62	0.51	502037969	772806832	716200000	FALSE		
NP_060631	NADSYN1	0.57	0.58	0.55	38997524	58446319	57120000	FALSE		
NP_077748	PSTPIP2	0.56	0.58	0.55	16699096	24963006	24430000	FALSE		
YP_003024028	COX1	0.55	0.61	0.50	93271488	141911699	132000000	FALSE		
NP_005429	FOSL1	0.55	0.56	0.54	62695786	92677028	91060000	FALSE		
NP_078954	NARS2	0.55	0.60	0.49	33732935	51121845	47510000	FALSE		
NP_060592	DARS2	0.55	0.56	0.53	228081502	336514774	329100000	FALSE		
NP_001295140	EARS2	0.54	0.64	0.45	55399917	86156003	75820000	FALSE		
XP_005256149	PAPD5	0.54	0.61	0.46	12963672	19768608	17850000	FALSE		
XP_011534268	NHSL1	0.53	0.57	0.48	35589235	52756772	49800000	FALSE		
NP_061848	TERF2IP	0.53	0.59	0.46	55430348	83418668	76400000	FALSE		
NP_079239	FBXL18	0.52	0.57	0.47	44589249	66256601	61790000	FALSE		

Table S8. Quantitative energy metabolite changes induced by mutant SF3B1. Fold change of metabolite abundance in SF3B1-mutant versus wild type MCF-10A isogenic cells. Data are from three biologic replicates in each group. P values from t tests are shown.

Metabolite	**Fold Change**	**p value**
Glucose	1.345	0.043498
Ribose	0.732	0.015966
2-HG	0.683	0.007568
α-KG	0.958	0.725804
Fumarate	0.585	0.029078
Malate	0.568	0.001218
Succinate	0.676	0.005205
3-HBA	1.222	0.001642
Lactate	1.172	0.398827
Pyruvate + OAA	1.285	0.115278
Citrate	1.172	0.097363
Alanine	0.527	0.000042
Arginine	0.980	0.493121
Asparagine	0.398	0.001059
Aspartate	0.316	0.000680
Glutamine	0.613	0.000825
Glutamate	0.557	0.000627
Glycine	0.344	0.001212
Serine	0.497	0.001136

Table S9. Quantification of serine isotopomers in WT and K700E hTERT-IMECs. Ion abundance values from three biologic replicates per condition were normalized by total protein, and mean values are shown. FC = fold change. P value for t-test comparing WT to K700E.

	WT +SG	**K700E +SG**	**FC K700E/WT**	**p value**
M+0 serine	3754813	2253679	0.600	0.0492
M+1 serine	159312	85093	0.534	0.0176
M+2 serine	31439	11560	0.368	8.28E-04
M+3 serine	110777	4476	0.040	7.56E-05
Total serine	4056340	2354807	0.581	0.0387

	WT -SG	**K700E -SG**	**FC K700E/WT**	**p value**
M+0 serine	22022	19842	0.901	0.471
M+1 serine	2936	1875	0.638	0.360
M+2 serine	211	0	0.000	0.125
M+3 serine	85004	572	0.007	3.67E-04
Total serine	110173	22290	0.202	9.89E-05

Table S10. Primer sequences. Primers used for amplification of homology arms in SF3B1 AAV gene targeting vector are shown with underlining of the restriction site sequence used for directional cloning into pSEPT cassette, with corresponding enzyme following the sequence. Primers used for validation of cryptic splicing by PCR of cDNA for MUT, DLST, and PHGDH are also shown.

5' arm homology arm forward primer	TCTAATGCGGCCGCTCCTTTGCACAAGTACAC	NotI
5' arm homology arm reverse primer	CACACGACTAGTGTGTGTGTACCTCTAGTCC	SpeI
3' arm homology arm forward primer	GTGCCAATCGATAGCCTGTCCATGTTTAATAG	BspDI
3' arm homology arm reverse primer	TAGTCACTCGAGGCGGCCGCAACTGTGTCCATGTTTCATC	NotI
MUT forward primer	ATTCCCAAAGTGGCTGATCC	
MUT reverse primer	CCAACAATTACTTCAGAACCAGAATC	
DLST forward primer	AGCTGTATGCAAGGATGACTTGG	
DLST reverse primer	CATCTTCTGCAACTGTGTCTCC	
PHGDH forward primer	CCTCCTTTGGTGTTCAGCAGC	
PHGDH reverser primer	GGCAAAGGTGTTGTCATTCAGC	