

Supplementary Table 1. Genes with statistically significant splicing identified by all three bioinformatics methods (FIRMA, MIDAS, ANOSVA) with corresponding splicing scores and p values.

Gene symbol	Number of adjacent exons spliced	FIRMA scores	FIRMA p-values	MIDAS scores	MIDAS p-values	ASNOVA p-values
GALNT1	0	2.43	0	2.44	0.017303	2.79372E-05
RPN2	2	3.03	0	2.63	0.040224	0.00313795
SLC38A1	2	2.68	0.00001	5.37	0.02265	0.00159715
HMGXB4	1	-2.96	0.00001	-1.71	0.037055	0.00839021
RPL11	0	-2.11	0.00004	-3.15	0.017841	0.00996667
SPIN1	0	-1.98	0.00004	4.33	0.029267	4.14807E-07
SMC2	1	-2.29	0.00006	2.01	0.049588	2.27244E-07
ILF2	1	2.11	0.00007	-2.54	0.034805	6.02988E-05
SLC39A6	1	1.95	0.00007	4.46	0.037141	1.47252E-11
PRDX1	0	3.10	0.00008	3.84	0.02488	0.00158676
RABGAP1L	5	2.67	0.00009	2.08	0.029123	0.00557443
TTC17	0	-1.88	0.00009	2.50	0.042319	0.00115331
RAP2A	3	-2.61	0.00009	3.86	0.023404	2.08717E-06
COL5A2	11	-2.69	0.0001	3.78	0.018022	5.59315E-12
SOX4	2	-1.89	0.0001	-4.73	0.033221	0.00152663
CEP350	0	2.65	0.00011	2.07	0.04104	0.00654876
THBS2	8	-2.13	0.00012	-2.82	0.026826	1.82292E-10
GNA13	0	-1.92	0.00012	2.71	0.024925	4.43889E-05
TAOK1	1	-1.62	0.00013	1.91	0.039657	4.12566E-05
STXBP5	2	1.59	0.00016	-2.09	0.0353	0.0051397
CAPRIN1	4	-2.71	0.00016	1.77	0.016125	0.00401313
CCT2	5	-2.91	0.00017	-5.31	0.034639	1.66782E-08
SEC61A1	0	-2.89	0.00019	3.35	0.041778	1.60599E-05
PCGF2	0	1.90	0.00023	-3.09	0.022781	0.00870917
PTK2	4	-2.47	0.00024	1.05	0.029415	0.000841486
SPARC	2	1.93	0.00026	1.23	0.041602	1.34396E-05
MARS	2	2.46	0.0003	-3.46	0.022779	0.000409151
YTHDF1	1	-2.23	0.00033	3.19	0.025487	0.00245809
DARS	2	-1.63	0.00034	4.02	0.033051	0.00201025
TFRC	2	1.92	0.00034	2.19	0.026858	0.00014995
USP34	1	1.56	0.00035	2.54	0.033149	0.00176853
CAND1	7	2.94	0.00036	1.72	0.036665	1.18221E-05
ALCAM	6	1.95	0.00036	1.49	0.042686	3.01511E-06
ATP2A2	2	-1.81	0.00037	2.52	0.037323	0.00337872
KIF23	3	-2.61	0.00037	3.08	0.01916	3.14786E-11
PSMA7	2	-2.00	0.00037	2.69	0.040371	0.000465175
NEXN	0	1.90	0.00042	-2.67	0.042861	0.00545863
IARS2	6	-2.16	0.00043	4.17	0.02786	0.00132895
GNAS	4	2.09	0.00043	1.26	0.048403	3.58804E-06
RCC2	2	-1.60	0.00044	-2.10	0.049557	1.56397E-05
CLSPN	12	-1.71	0.00045	-2.78	0.018561	7.88203E-10
SIRT1	2	2.00	0.00045	6.12	0.026176	1.11635E-08
VCAN	1	-2.40	0.00049	2.01	0.01888	0.000133398
COL12A1	5	-2.16	0.00049	3.61	0.017637	1.24805E-11
YY1	3	2.56	0.0005	6.02	0.027863	2.08364E-10
MANF	8	-1.69	0.00051	4.77	0.028571	1.57539E-08
GNB1	3	-1.44	0.00052	2.12	0.034731	0.00462593
MED13	1	2.22	0.00052	-1.91	0.035959	0.00149218
ESYT1	4	1.78	0.00052	-3.86	0.024699	6.8431E-07
SLC17A5	4	-1.78	0.00054	3.04	0.030499	0.000364402
SSR1	1	1.75	0.00055	2.07	0.043299	0.000606738
MATR3	3	-2.40	0.00058	1.19	0.034371	3.28259E-06
ZBTB44	3	-2.08	0.00059	2.58	0.040439	0.00216664
CCNJ	3	1.70	0.00063	-3.53	0.032536	0.000314969
GATA6	1	-1.88	0.00063	3.67	0.048284	7.21843E-06
IDH1	1	-1.95	0.00064	-3.54	0.01861	9.24217E-05
APP	6	-1.94	0.00064	2.25	0.044619	0.000200504
EZH2	4	4.95	0.00067	3.06	0.046242	2.39594E-10
TPX2	10	-1.54	0.0007	2.58	0.048631	5.44606E-10
ZBTB41	1	-2.61	0.0007	2.16	0.023079	0.00520708
DSG2	1	1.72	0.0007	3.20	0.039713	1.23594E-09
CCNA2	4	-1.77	0.00072	2.83	0.032232	1.44783E-10
TRIM33	8	-2.05	0.00073	1.60	0.021483	0.00122048
PRKDC	2	-1.41	0.00073	-3.85	0.031811	4.25999E-06
GDE1	4	-1.61	0.00076	2.90	0.045743	7.47662E-08
PDIA6	0	1.97	0.00078	2.84	0.033651	0.0000354
RDH10	4	1.95	0.00078	1.91	0.02083	0.000160419
TCF3	1	-1.79	0.00081	-4.04	0.040331	0.00294546
ADAMTS9	10	-1.96	0.00086	-2.23	0.020655	0.000177544
BRAF	2	1.75	0.00086	-3.33	0.013879	0.00937293
LEMD3	7	2.09	0.0009	2.86	0.048904	0.000502659
BUB1	6	-3.24	0.0009	-2.30	0.020682	0.00287803
DLGAP5	2	1.63	0.00092	1.82	0.036205	3.41289E-09
LAT2	0	2.07	0.00094	3.42	0.047207	0.00462413
TNFRSF21	7	2.05	0.00098	3.26	0.030943	1.01738E-08
MTCH2	5	-1.68	0.00099	-3.38	0.013583	0.00801725