Table S1: Primers

Primers for EMT splicing signatures

Gene Symbol	Exon coordinate (hg19)	Left primer	Right primer	Skipping size (bp)	Inclusion size (bp)
ENAH	chr1:225,692,695-225,692,755	TGCTTCAGCCTGTCATAGTCA	TGGCAGCAAGTCACCTGTTA	105	168
FLNB	chr3:58,127,585-58,127,656	GGCGAAGAAGTAGGCTTTGTGG	GCCGTTCATGTCACTCACTGG	261	333 & 300
FNIP1	chr5:131,046,271-131,046,354	TCAGGACAACAATACATTAAAGGCTG	CAGACCGTGCTATGCCACTG	137	221
ARFGAP2	chr11:47,194,261-47,194,302	CCCCAACACAGACCTGCTT	CTTAGCTGCTGCTGGCTTCT	91	133
SLC37A2	chr11:124,956,100-124,956,156	GATCTTGGCCTGGAAGGTGT	TTCCCTGCTTGTGGAAGTTT	148	205
SLK	chr10:105,770,574-105,770,666	AGACTATCGAACGCCTGGAA	AACTCTGCCTTCTGCTGCTG	205	298
ARHGEF11	chr1:156,908,210-156,908,305	CAGAGCAGGAAGACATGGGT	TGAGCCTGTTGAGCTTGAGA	399	495
MAGI1	chr3:65,433,697-65,433,732	TAGACCCTCGGTGCCTAAAC	AATCTTTTCCCAACCAGCAG	119	83
SCRIB	chr8:144,889,722-144,889,784	AGCACTGAGGAGGAGGACAA	TATAGGGTGTGGAGCCCTTG	130	193

Primers for splicing factor realtime PCR

Gene Symbol	Left primer	Right primer	PCR amplicon size (bp)
GAPDH	TGGTATCGTGGAAGGACTCA	ACAGTCTTCTGGGTGGCAGT	60
ESRP1	ACAGAATGCGTTGAGGAAGC	AGAGGGGCCGAGGAGAAT	114
ESRP2	AGGAGATGAGCCGAGTGCT	GCTTGGAAGGTGGTGTAGGT	109
NOVA1	CCGGCAGCACCAAGAG	GTCTGTCCTCCCTTCCCAAT	106
RBFOX2	TAGAGGGCCGTAAAATCGAG	CTGGGCTTAATTTCCAACCA	99
MBNL3	CCTGGAAACCCACCTCTTG	CTCCCCACGGGTACAATTT	111
RBM39	GGGAACAACTGGTCGTCTTC	ATGCCAAAGAGCCACTCATC	107

Primers for differentially spliced exons

Gene Symbol	Exon coordinate (hg19)	Left primer	Right primer	Skipping size (bp)	Inclusion size (bp)
ACLY	chr17:40052872-40052902	CCAGCAGGACAGCATCTTTT	TCGGGAGCAGACATAGTCAA	185	215
AKAP9	chr7:91671359-91671500	CCAAGAACATCAACAGGCAA	CAGGAGGCACATCTTCAGGT	209	350
FLNA	chrX:153585618-153585642	CAAGCCGAAGAAGACACACA	ATTCTCCACCACGTCCACAT	319	343
MAP4K4	chr2:102487955-102488147	GCAATGGTGAAACGGAATCT	TCCGCTAGATGGAGAAATCTG	203	395
MYO6	chr6:76621388-76621415	GGCAGCTTGCAGAGAAGAAT	CACAAGTAGGATGGGTGGCT	334	361
PLD1	chr3:171404474-171404588	GCCTGTTCAAAACCTACCCA	GCAGTAGTCCTTTCCATGCC	247	361
SPAG9	chr17:49053223-49053262	GGGACAGGAAATGGTGTCAT	GGGACTGCCACAAAGAATTT	218	257
TRERF1	chr6:42231057-42231306	GTTTGGGGAGCAGTTTGATG	TGCCGGAACTTTTTCTTCTC	216	465
TRIM37	chr17:57078958-57079075	AGGTCATCTGGAAGGACTGC	GGGCCTATTTGTTCACCATC	144	261
MADD	chr11:47310518-47310578	ATCGGAACCACAGTACCAGC	TCTGATCCACTAACGCCCTC	120	180
GRHL1	chr2:10102583-10102660	TGGGCATTGATAAGAGAGGC	TGGGATAGAACTGGCCTTTG	379	456
IGF2BP3	chr7:23383336-23383472	CACAGAAGAGATCCCCTTGAA	TGAAGTGGGTGGGAACAGAC	186	322
RPAP3	chr12:48073275-48073377	GGAACCTGGAAATAAGCAAGC	TATTCTCTGGAGCAGCAGCA	143	245
STK36	chr2:219553113-219553216	ACCACTGAGCCTGTGCCTAT	TGTTGCTCTCCTGACTGTGC	274	377
ARHGEF12	chr11:120280102-120280159	CACATGATTTTGACCCCACA	GGATTGTCTCCACTGACCGT	94	151
CA12	chr15:63620296-63620329	CCTTCCCCCAGAGAAATGAT	AAAAGCCAAATGGACACCAC	155	188
ITGA6	chr2:173366499-173366629	GGGAGTACCTTGGTGGATCA	GTTGGAAAAAGCAGTTTGGG	296	426
MAP3K7	chr6:91254270-91254351	GGAGCAGTGTGGAGAGCTTG	GGATGGATCTACGTCTTGGC	123	204
MYOF	chr10:95152673-95152712	TAAAATTGCTGCCTCTGGTG	CGTGTACTCTCTGGGGCTTC	118	157
NFYA	chr6:41048549-41048636	CAGGAATCTCACTTGGAGGG	TGATGGTTTGACCTTGTCCA	207	294
OSBPL3	chr7:24902818-24902911	CCTGGTAGAAATGAGCCAGC	CTGATGAGGTTTCAGAGCCA	194	287
PDGFA	chr7:540067-540136	ACGTCAGGAAGAAGCCAAAA	TGGCAATAAAGCACCGTACA	207	276
USO1	chr4:76716488-76716509	GAAAATGCCACCCAGAAAGA	GGAACATTGGCTGAATTGTG	213	234
UTRN	chr6:145148483-145148522	TCTGGGGAAGATGTACGAGA	CAGTTGAGGAGATTGTGAGGG	154	193
SNX14	chr6:86248555-86248582	AATCACCAACACGCAATTCA	TAGGCAACATAGCTCCCTCC	132	159
NDEL1	chr17:8366637-8366672	ACCAAGCATCACGAAAATCC	GCAATCATGTGAAACCAACG	440	475
INSR	chr19:7150507-7150543	AATGCTGCTCCTGTCCAAAG	CGACTCCTTGTTCACCACCT	263	299
TBX3	chr12:115117717-115117777	CGAAATGCCAAAGAGGATGT	GGGGAACAAGTATGTCCGAA	229	289
NCOR2	chr12:124858958-124859009	GTGGAGGATGAGGAGATGGA	TCTCGGTGTCTGAGCTGTTG	100	151
TSC2	chr16:2127598-2127727	CGGTCCAATGTCCTCTTGTC	TCCAGGTGGAGGTTTTTCAG	182/185	314