Additional Table 4 - Additional RT-PCR Primer Sequences

Gene	Exons	Probeset ID(s)	Primer F	Primer R	Splicing Index P-Value Rank	SI Magnitude Rank	VALIDATEDED?
GLCCI1	Ex1/3	97494957	GAGCAGCTCACCTGAGAGA	TCCTTACTGTGACGACTAC	2	596	🟥
TBC1D9B	Ex17/20	97891655	CAAGGTGCTCTACAAGCTAC	TTGCTCTTCCTGTGGTAGTG	6	303	🟩
ANK3	Ex36/37	96180441, 96180431	CAGATAGACGACAGAGCTTC	GGCCCAGGCACTGTAATCG	7	400	🟩
NPTN	Ex1/3	94749260	TTCTGCTAGGGAGGATGTC	TCTTTGTCCAGTAGCTGTATG	8	628	🟩
FEZ2	Ex5/8	99307244	TGGGAAGAATGAGAGAAGTCA	TTTCACTGTCCTCCTTCATG	10	48	🟩
TPD52L2	Ex5/8	93583452	GCAGGACAGAAGACTTCAG	TCGGTCCTCAAACGACTTG	16	49	🟩
ACTN4	Ex6/8b	93861390	ACAGACCAGAGCTGATTGAG	TTCTCATCTGGCCTCAGAG	21	233	🟩
ZYFVE21	Ex5/7	95078447	ACATTTCCACCGTGCAGATC	CCACCACTGTCAGCTTCAG	22	323	🟩
D87470	Ex2/5	95787339	CCTAAGAACATGGCCTACAC	GCCACAGGAAGACGAGTTC	24	312	🟩
MICAL2	Ex17/24	96051659, 96052696	GCTGCTGGCCAAGTTTGAG	TCAGCCGTTCCATCACGTAC	25	144	🟩
MYO6	Ex32/34	97796794	TGCTCCAAAGTCTGTTACTG	TACTCTGAGGGTCTTTGTAC	28	313	🟩
TJAP1	Ex7/8	97821142, 97821137	AGGAGTTGGAGGACAAGCT	GCTCTTCCAGCTTGTTGATG	29	292	🟩
KIF1B	Ex24/26	100266293	AAAGCGAAACCACTGTGACT	CACCTTTCTCACTGACGATG	31	187	🟩
LAS1L	Ex11b/12	105353418, 100363607	TGCTGGTCTCGGAGAAGTC		33	364	🟩
GDI1	Ex2/4	105358575	TCTGTGAACGGGAAGAAGGT	CACCTTGAAGTCCAGGTAG	34	1100	🟥
CLTB	Ex4/6	105557570	GCCAGAGTGAACAAGTAGAG	ACACATCTTTGCACTGCTTG	36	72	🟩
DUSP16	Ex6/7	95521258	TCGCTATCGCCTACATCATG	TTTGCTCTTTGGCCCTGATG	45	484	🟥
ARAF	Ex11/12	100506032	CGACACACGCTTCGACATG	ACTTGAGATCTCGGTGGATG	47	432	🟥
RECK1	Ex2/5	96694017, 96694012	TAACCAAATGTGCCGTGATG	CCAGTTCACAGCAGCCTAAG	58	791	🟩
THYN1	Ex1/2	95715606	GCAGTCGAGTCTGCAGAGT	AATGCCTCACCTGAGTTCTC	60	799	🟩
MAPK9	Ex6a/7	104808736	TGGTCCTCCATAAAGTCCTG	TTCCTCACAGTTGGCTGAAG	62	268	🟩
CADPS2	Ex22/24	97162001	TCCGCTATGTGGATCTCATG	GTTTAAGTCTTTGCTCTAAGTG	63	130	🟩
Y652	Ex11/14	96016281	GTCTGTAGAAGACTCTCAAG	GTCAGCCTGGGTACCATG	68	33	🟩
PRKCBP1	Ex15/16	103802407	GCTTTTACCGAAGGAGACTG	GGACACAAGGGTGCTCATG	69	661	🟩
CAMK2D	Ex12/15	98337652, 98337647	ACAACTATGCTGGCTACAAG	TTCACATCTTCATCCTCAATTG	70	203	🟩
SDCCAG8	Ex13/16	105282261	CGAATCTGAGCACCAACTG	TGCTTCATCGTCTCATGTAC	75	722	🟥
SORBS2	Ex15/16	98280250	TGGACCTCCCAGGATCAAGC	CAGTCGTCGTTTAGGAGATC	340	8	🟩
ACTN4	Ex18/20	93860469	CATCAGCCAGGAGCAGATG	CTCATGATGCGGTTGAACTC	151	13	🟩
UNC13B	Ex10b/11	104676985	ACCTCAACAAGTGCATCAAC	CCTTCCGGGAGCCACTGAG	679	14	🟩
EHBP1	Ex7/9	99566362	TATGAAGCAGGCTGACATTG	CAGCATCAGGATCATCAAATG	107	17	🟩
TPD52L2	Ex5/8	103811692	GCAGGACAGAAGACTTCAG	TCGGTCCTCAAACGACTTG	126	32	🟩
MLLT4	Ex8/10	97705870	AAACACTTGGAAGGCAAGAC	TGGCTTATCTCTAGAGTCAG	279	34	🟩
PTPRM	Ex12/15	94095691	TTTCCAAGCTGCTAGTAGAG	CTGTCGGGTGCTGCTCATG	78	35	🟩
NIBP	Ex17/19	96746277	CGACTACAGCCACGTGAAG	TCGGTGGAGTTGAAGACATC	283	43	🟥
FAT	Ex26/27	98278505	CCTGTCTGAAGTGCAGTCT	GGCATCCAATCTGATGTATC	517	44	🟩
SMTN	Ex11/12	93390005	GGGCAGTGTCACTCATGTC	TTCTGGTGCTTTGTTCACTC	480	50	🟥
ITSN2	Ex16/18	99323041	AACTGCATCTAAGCTGTCAG	CTTGCAGCCTCATCTTCTAG	378	54	🟩
BIN1	Ex6/8	105077962	AAGCTGGTGGACTACGACA	CTCCTGCAGATCCACATTC	430	58	🟩
APLP2	Ex13/15	104546949	GTGCAGATATGGACCAGTTC	TCTCTTCGGCACCGATCAG	150	871	🟩
RBM9	Ex9/13	93318444	CGGACAGTATATGGTGCAGT	CAGGCTGTGCATATCTGTAG	206	783	🟩
EPB41L3	Ex15/17	94016008	AGACACTGCCGTAACGAATG	ACCACCTTCTCAGTGCTAAG	226	157	🟩
PTPRK	Ex15/16	97560338	CACTCTGCATGCAGAAGATC	GGTAGCGAGGTACGTCTAG	227	538	🟩
GIT1	Ex6/9	94213279	GCCAATATGAGCTCACTGAC	TTGGCCAATTCGGATAAGTC	229	141	🟩
STAU	Ex3/5	93520304	CTTAACCTCTCAGAACTGAAC	GACTGCATCCGAGAGTAAG	242	762	🟩
KIAA0562	Ex18/19	99950716	TCTCATGCTGACAAGATGTG	CTCACTGCAACGGTAACAC	249	396	🟥
EPB41L1	Ex12/14	93626410	GTCAGCGAGAACCATGATG	CTTCAGCAAGACATCTTCTG	337	1066	🟩
SPIRE1	Ex8/9	94005738	CCAGAGGAGATTAGACGTAG	GCACCTGCTGTGAGGTACT	345	118	🟩
HM13	Ex11/13	93637662	GGCCAAGGGAGAAGTGACA	GATGCTGATGCCTCTGTTC	611	428	🟩
EPB41L3	Ex11/14	94015893	CCTTACTTTGAACGCTCATC	CCGTGCGCTCACTGTCAG	703	548	🟩
EPB41L3	Ex14/16	94015918	GACAGTGAGCGCACGGAC	TTACGGCAGTGTCTGTTGAG	753	250	🟩
MARK4	Ex15/18	93843376	AACCTCTTCACCAAGCTGAC	GTTTGATCCCAAGGTAGATG	860	343	🟩
APLP2	Ex6/8	104546909	TGAGGAGAATCCTACTGAAC	GAGCATGCTCATTATCATCTG	929	1046	🟩
DCNI2	Ex5/7	105158206	TGTGAGCACTCCAAGTGAAG	AGTTTCCTTTGTATACGTGAC			🟩