5' RACE Target	Number of clones	start position (nt #)	Cloned Sequence (adaptors removed)
ITGB1-B-Site	4	+1547	CTTTAAAATTAGGCCTCTGGGCTTTACGGAGGAAGTAGAGGTTATTCTTCAGTACATCTGTGAATGTGAATGCCAAAGCGAAGGCATCCCTGAAAGTCCCAAGTGTCATGAAGGAAATGGGACATTTGAGTGTGGCGCGTGCAGGTGCAATGAAGGGCGTGTTGGTAGACATTGTGAATGCAGCACAGATGAAGTTAACAGTGAAGACATGGATGCTTACTGCAGGAAAGAAAACAGTTCAGAAATCTGCAGTAACAATGGAGAGTGCGTCTGCGGACAGTGTGTTTGTAGGAAGAGGGATAATACAAATGAAA
ITGB1-B-Site	1	+1553	AATTAGGCCTCTGGGCTTTACGGAGGAAGTAGAGGTTATTCTTCAGTACATCTGTGAATGTGAATGCCAAAGCGAAGGCATCCCTGAAAGTCCCAAGTGTCATGAAGGAAATGGGACATTTGAGTGTGGCGCGTGCAGGTGCAATGAAGGGCGTGTTGGTAGACATTGTGAATGCAGCACAGATGAAGTTAACAGTGAAGACATGGATGCTTACTGCAGGAAAGAAAACAGTTCAGAAATCTGCAGTAACAAT
ITGB1-B-Site	1	+1553	AATTAGGCCTCTGGGCTTTACGGAGGAAGTAGAGGTTATTCTTCAGTACATCTGTGAATGTGAATGCCAAAGCGAAGGCATCCCTGAAAGTCCCAAGTGTCATGAAGGAAATGGGACATTTGAGTGTGGCGCGTGCAGGTGCAATGAAGGGCGTGTTGGTAGACATTGTGAATGCAGCACAGATGAAGTTAACAGTGAAGACATGGATGCTTACTGCAGGAAAGAAAACAGTTCAGAAATCTGCAGTAACAAT
ITGB1-C-Site	4	+2229	ATTACCAAGGTAGAAAGTCGGGACAAATTACCCCAGCCGGTCCAACCTGATCCGGTGTCCCATTGTAAGGAGAAGGATGTTGACGACTGTTGGTTCTATTTTACGTATTCAGTGAATGGGAACAACGAGGTCATGGTTCATGTTGTGGAGAATCCAGAGTGTCCCANTGGTCCAGACATCATTCCAATTGTAGCTGGTGTGGTTGCTGGAATTGTTCTTATTGG
ITGB1-C-Site	1	+2229	ATTACCAAGGTAGAAAGTCGGGACAAATTACCCCAGCCGGTCCAACCTGATCCGGTGTCCCATTGTAAGGAGAAGGATGTTGACGACTGTTGGTTCTATTTTACGTATTCAGTGAATGGGAACAACGAGGTCATGGTTCATGTTGTGGAGAATCCAGAGTGTCCCANTGGTCCAGACATCATTCCAATTGTAGCTGGTGTGGTTGCTGGAATTGTTCTTATTGG
ITGB1-C-Site	4	+2281	CTGTGTCCCATTGTAAGGAGAAGGATGTTGACGACTGTTGGTTCTATTTTACGTATTCAGTGAATGGGAACAACGAGGTCATGGTTCATGTTGTGGAGAATCCAGAGTGTCCCACTGGTCCAGACATCATTCCAATTGTAGCTGGTGTGGTTGCTGGAATTGTTCTTATTGG
SARS-A-Site	4	+40	ACAGGCTGAGTGCTGCGGCGCGATTCTTGCTTCCCTGAGCGTTGGCCCGGGAGGAAAGAAGATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAGCGCTTCAAG
SARS-A-Site	2	+46	TGAGTGCTGCGGCGCGATCCTTGCTTCCCTGAGCGTTGGCCCGGGAGGAAAGAAGATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAGCGCTTCAAG
SARS-A-Site	2	+47	GAGTGCTGCGGCGCGATCCTTGCTTCCCTGAGCGTTGGCCCGGGAGGAAAGAAGATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAGCGCTTCAAG
SARS-B-Site	6	+188	CCGGGACTAGTGGACCAGCTGGTGAAGGCAGACAGCGAGTGGCGACGATGTAGATTTCGGGCAGACAACTTGAACAAGCTGAAGAACCTATGCAGCAAGACAATCGGAGAGAAAATGAAGAAAAAAGAGCCAGTGGGAGATGATGAGTCTGTCCCAGAGAATGTGCTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTCTCACAAATCAGAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGATGCGGACAACAAAGCAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGATGGTAGATGGCTTTGAAGGCGAAAAGGGA
SARS-B-Site	1	+188	CCGGGACTAGTGGACCAGCTGGTGAAGGCAGACAGCGAGTGGCGACGATGTAGATTTCGGGCAGACAACTTGAACAAGCTGAAGAACCTATGCAGCAAGACAATCGGAGAGAAAATGAAGAAAAAAGAGCCAGTGGGAGATGATGAGTCTGTCCCAGAGAATGTGCTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTCTCACAAATCAGAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGATGCGGACAACAAAGCAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGATGGTAGATGGCTTTGAAGGCGAAAAGGGA
SARS-B-Site	1	+267	acaagctgaagaacctatgcagcaagacaatcggagagaaaatgaagaaaaaagagccagtgggagatgatgagtctgtcccagagaatgtgctgagtttcgatgaccttactgcagacgctttagctaacctgaaagtctcacaaatcaaaaaagtccgactcctcattgatgaagccatcctgaagtgtgacgcggagcggataaagttggaagcagagcggtttgagaacctccgagagattgggaaccttctgcacccttctgtacccatcagtaacgatgaggatgtggacaacaaagtagagaggatttggggtgattgtacagtcaggaagaa

SARS-B-Site	1	+353	CTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTCTCACAAATTAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGA AGTGTGACGCGGAGCGGACAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGT AACGATGAGGATGTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGATGGTA GATGGCTTTGAAGGCGAAAAGGGA
SARS-B-Site	3	+360	TCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTCTCACAAATCAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGA CGCGGAGCGGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATG AGGATGTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGATGGTAGATGGC TTTGAAGGCGAAAAGGG
SARS-B-Site	1	+362	GATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTCTCACAAATCAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACG CGGAGCGGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAG GATGTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGATGGTAGATGGCTTT GAAGGCGAAAAGGG
SARS-B-Site	1	+368	CTTACTGCAGACGCTTTAGCTAACCTGAAAGTCTCACAAATCAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGC GGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGATGTGG ACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGATGGTAGATGGCTTTGAAGGCG AAAAGGG
SARS-B-Site	9	+440	ATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACC CATCAGTAACGATGAGGATGTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGT GATGGTAGATGGCTTTGAAGGCGAAAAGGG
SARS-B-Site	2	+440	ATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAAGCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACC CATCAGTAACGATGAGGATGTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGT GATGGTAGATGGCTTTGAAGGCGAAAAGGG
SARS-B-Site	2	+477	CAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGATGTGGACAACAAAGTAGAGA GGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTGAGGGTAGATGGCTTTGAAGGCGAAAAGGG
ZNF207-A site	1	+76	AAGTGAAGGATTTTTGGCCTNGTTTCTCCTGCTTCTTTTCTCCTCCCTTTTACTTTGCCGGTAGAACACAGTTATGGGTCGCAAGAAGAAGAACA GCTGAAGCCGTGGTGCTGGTATTGTAATAGAGATTTTGATGATGAGAAGATCCTTATTCAGCACCAAAAAGCAAAGCATTTTAAATGCCATATA NTCACAAGAA
ZNF207-A site	1	+124	TTTACTTTGCCGGTAGAACACAGTTATGGGTCGCAAGAAGAAGAAGCAGCTGAAGCCGTGGTGCTGGTATTGTAATAGAGATTTTGATGATGA GAAGATCCTT
ZNF207-A site	5	+124	TTTACTTTGCCGGTAGAACACAGTTATGGGTCGCAAGAGGAAGAAGCAGCTGAAGCCGTGGTGCTGGTATTGTAATAGAGATTTTGATGATGA GAAGATCCTTATTCAGCACCAAAAAGCAAAGCATTTTAAATGCCATATATGTCACAAGAAATTGTATACAGGACCTGGCTTAGCTATTCATTGCA TGCNGGT
ZNF207-A site	6	+147	TTATGGGTCGCAAGAAGAAGAAACAGCTGAAGCCGTGGTGCTGGTATTGTAATAGAGATTTTGATGATGAGAAGATCCTTATTCAGCACCAAAA AGCAAAGCATTTTAAATGCCATATATGTCACAAGAAATTGTATACAGGACCTGGCTTAGCTATTCATTGCATGCNGGT
ZNF207-A site	1	+147	TTATGGGTCGCAAGAAGAAGAAACAGCTGAAGCCGTGGTGCTGGTATTGTAATAGAGATTTTGATGATGAGAAGATCCTTATTCAGCACCAAAA AGCAAAGCATTTTAAATGCCATATATGTCACAAGAAATTGTATACAGGACCTGGCTTAGCTATTCATTGCATGCNGGT
ZNF207-B-site	1	+180	CGTGGTGNTGGTATNGTAATAGAGATTTTGATGATGAGAAGATCNTTATTCAGCACCAAAAAGCAAAGCATTTTAAATGCCATATATGTCACAAG AAATTGTATACAGGACCTGGCTTAGCTATTCATTGCATGCAGGTACATAAAGAAACAATAGATGCCGTACCAAATGCAATACCTGGAAGAACAG ACATAGAGTTGGAAATATATGGTATGGAAGGTATTCCAGAAAAAGACATGGATGAAAGACGACGACTTCTTGAACAGAAAACACAAGAAAGTCA AAAAAAGAAGCAACAAGATGATTCTGATGAATATGATGATGACGACTCTGCAGCCTCAACTTCATTTCAGCCACAGCCTGTTCAACCTCAGCAA GGTTATATTCCTCCAANGGCACAGCCAGGACTGCCACCAGTAC

ZNF207-B-site	7	+279	caagaaattgtatacaggacctggcttagctattcattgcatgcaggtacataaagaaacaatagatgccgtaccaaatgcaatacctggaagaacagacatagagttggaaatatatggtatggaaggtattcc agaaaaagacatggatgaaagacgacgacttcttgaacagaaaacacaagaaagtcaaaaaaagaagcaacaagatgattctgatgaatatgatgatgacgactctgcagcctcaacttcatttcagccac agcctgttcaacctcagcaaggttatattcctccaatggcacagccaggactgccaccagtacc
ZNF207-B-site	1	+400	TATTCCAGAAAAAGACATGGATGAAAGACGACGACTTCTTGAACAGAAAACACAAGAAAGTCAAAAAAAGAAGCAACAAGATGATTCTGATGAA TATGATGATGACGACTCTGCAGCCTCAACTTCATTTCAGCCACAGCCTGTTCAACCTCAGCAAGGTTATATTCCTCCAATGGCACAGCCAGGAC TGCCACCAGTACCAGGAGCACCAGGAATGCCTCCNGGCATACCTCCATTAATGCCA
ZNF207-B-site	2	+401	ATTCCAGAAAAAGACATGGATGAAAGACGACGACTTCTTGAACAGAAAACACAAGAAAGTCAAAAAAAGAAGCAACAAGATGATTCTGATGAAT ATGATGATGACGACTCTGCAGCCTCAACTTCATTTCAGCCACAGCCTGTTCAACCTCAGCAAGGTTATATTCCTCCAATGGCACAGCCAGGACT GCCACCAGTACCAGGAGCACCAGGAATGCCTCCNGGCATACCTCCATTAATGCCA
ZNF207-B-site	1	+401	ATTCNNGAANAAGACNTGGATGAAAGACGACGACTTCTTGAACAGAAAACNCAANANAGTCANAAAAAGAANCAACANNATGATTCTGATGANT ATGATGANGACGACTCTGCAGCCTCANCTTCATTTCANCCACNACCTGTTCAACCTCAGCAAGGTNATATTCCTCCAATGGCACAGCCAGGACT GCCNNCAGTACCAGGAGCACCAGGAATGCCTCCNGGCATACCTCCATTAATGCCA
ZNF207-B-site	1	+401	ATTCCAGAAAAAGACATGGATGAAAGACGACGACTTCTTGAACAGAAAACACAAGAAAGTCAAAAAAAGAAGCAACAAGATGATTCTGATGAAT ATGATGATGACGACTCTGCAGCCTCAACTTCATTTCAGCCACAGCCTGTTCAACCTCAGCAAGGTTATATTCCTCCAATGGCACAGCCAGGACT GCCACCAGTACCAGGAGCACCAGGAATGCCTCCNGGCATACCTCCATTAATGCCA
ZNF207-B-site	1	+411	aagacatggatgaaagacgacgacttcttgaacagaaaacacaagaaagtcaaaaaaagaagcaacaagatgattctgatgaatatgatgatgacgactctgcagcctcaacttcatttcagccacagcctg ttcaacctcagcaaggttatattcctccaatggcacagccaggactgccaccagtacc
ZNF207-C-site	1	+776	CCTGGACCAGGAATACCACCTCTGATGCCTGGAATGCCACCAGGTATGCCCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCA CAGGCTGTTTCAGCGCCAGGTATTCTTAATGGACCACCTGCACCAACAGCAACTGTACCTGCCCCACAGCCTCCAGTTACTAAGCCTCTTTTCC CCAGTGCTGGACAGGCTCAGGCAGCTGTCCAAGGACCTGTTGGTACAGANNNCNAACCCTTAAATAGTAC
ZNF207-C-site	1	+776	CCTGGACCAGGAATACCACCTCTGATGCCTGGAATGCCACCAGGTATGCCCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCA CAGGCTGTTTCAGCGCCAGGTATTCTTAATAGACCACCTGCACCAACAGCAACTGTACCTGCCCCACAGCCTCCAGTTACTAAGCCTCTTCCC CAGTGC
ZNF207-C-site	1	+783	CAGGAATANCANNTTTGGTGCCNGGAANNCCACCAGGTANGCCCCCACCTGTTNCACGTCCNGGAATTCCTCNAANGANTCAGGCACAGGCT GACGCAGCGCCT
ZNF207-C-site	1	+783	CAGGAATACCACNTNTGATGCCTGGAATGCCACCAGGTATGCCCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCACAGGCTG TTTCAGCGCCAGGTATTCTTAATAG
ZNF207-C-site	1	+783	CAGGAATACCANNNCTGATGCCTGGAATGCCACCAGGTATGCCCCCACCTGTTCCACGTCCTGGAANNCCTCCAATGACTCAAGCACAGGCT GCNNCAGCGCCAGGTANNNTTAATAGACCACCTGCACCAACAGCAACTGTACCTGCCCCACAGCCTCCAGTTANTAAGCCTCTTNCCCCNGTG CTGGACAGGCTCAGGCNGCTGTNCAANGACCTGTNNGTACAGATNTCAAACC
ZNF207-C-site	5	+783	CAGGAATACCACCTCTGATGCCTGGAATGCCACCAGGTATGCCCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCACAGGCTG TTTCAGCGCCAGGTATTCTTAATAGACCACCTGCACCAACAGCAACTGTACCTGCCCCACAGCCTCCAGTTACTAAGCCTCTTTTCCCCAGTGC TGGACAGGCTCAGGCAGCTGTCCAAGGACCTGTTGGTACAGATTTCAAACCCTTAAATAGTAC
ZNF207-C-site	4	+823	GCCCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCACAGGCTGTTTCAGCGCCAGGTATTCTTAATAGACCACCTGCACCAAC AGCAACTGTACCTGCCCCACAGCCTCCAGTTACTAAGCCTCTTTTCCCCAGTGCTGGACAGGCTCAGGCAGCTGTCCAAGGACCTGTTGGTAC AGATTTCAAACCCTTAAATAGTAC
ZNF207-C-site	5	+824	CCCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCACAGGCTGTTTCAGCGCCAGGTATTCTTAATAGACCACCTGCACCAACA GCAACTGTACCTGCCCCACAGCCTCCAGTTACTAAGCCTCTTTTCCCCAGTGCTGGACAGGCTCAGGCAGCTGTCCAAGGACCTGTTGGTACA GATTTCAAACCCTTAAATAGTAC
ZNF207-C-site	1	+825	CCCCACCTGTTCCACGTCCTGGAATTCCTCCAATGACTCAAGCACAGGCTGTTTCAGCGCCAGGTATTCTTAATAGACCACCTGCACCAACAG CAACTGTACCTGCCCCACAGCCTCCAGTTACTAAGCCTCTTTTCCCCAGTGCTGGACAGGCTCAGGCAGCTGTCCAAGGACCTGTTGGTACAG ATTTCAAACCCTTAAATAGTAC

mRNA	# of hits	start (nt#) of cloned sequence	Cloned Sequence directly after 5' RACE adaptor	Note(s)
ADK	1	+648	AGTGATGCATGCAGCACAAGTTCCTGTTGGCTGCTCATTCTGCTCGTAGT AATGAGCATCCACATGGGCTTCAGCAGCTTTTCTCTTCAGGATCTCCCCA AATTTATCTATCCCAATGCAT	
ARPC1B	1	+392	CGAGAACAAGTTTGCTGTGGGCAGCGGCTCTCGTGTGATCTCCATCTGT TATTTCGAGCAGGGGAATGACTGGTGGGTTTGCAAGCACATCAAGAAGC CCATCCGCTCCACCGTCCTCAGCCTGGACTGGCACCCCAACAATGTGCT GCTGGCTGCCGGCTCCTGTGACTTCAAGTGTCGGATCTTTTCAGCCTAC ATCAAGGAGGTGGAGGAACGGCCGGCACCCACCCCGTGGGGCTCCAA GATGCCCTTTGGGGAACTGATGTTCGAATCCAGCAGTAGCTGCGGCTGG GTACATGGCGTCTGTTTCTCAGCCAGCGGGAGCCGCGTGGCCTGGGTA AGCCACGACAGCACCGTCTGCCGGGCTGATGCCGACAAGAAGATGATC GTCG	
ATP6AP1	1	+1705	CAGGGTTCGTCGCTGTGAGGCGTAAGGGACGTGAATTCTAGGGTCTCCT TTCTCCTTATTTATTCTTGTGGCTACATCATCCCTGGCTGTGGATAGTGCT TTTGTGTAGCAAATGCTCCCTCCTTAAGGTTATAGGGCTCCCTGAGTTTG GGAGTGTGGAAGTACTACTTAACTGTCTGTCCTGCTTGGCTGTCGTTATC GTTTTCTGGTGATGTTGTGCTAACAATAAGCAGTACACGGGTTTATTTCT GTGGCCTGAGAAGGAAGGGACCTCCACGACAGGTGGGCTGGGTGC	3' UTR sequence only
CSDE1	1	+1737	TAGGATTAAAAAACTTCCCAAGGGCACGGTTTCATTCCATTCCCATTCMS ATCACCGTTTTCTGGGCACGGWARAAAAAGAAGCCGCTTTTTCCAATCC TAAAACCACTAGCCCAAATAAAGGCAAAGAGAAGGAGGCTGAGGATGGC ATTATTGCTTATGATGACTGTGGGGTGAAACTGACTATTGCTTTTCAAGC CAAGGATGTGGAAGGACCTACTTCTCCTCAAATAGGAGATAAGGTTGAAT TTAGTATTARTGACAAACAGAGGCCTGGACAGCAGGTTGCAACTTGTGT GCGACTTTTAGGTCGTAATTCTAACTCCAAGAGGCTCTTGGGTTATGTGG CAACTCTGAAGGATAATTTTGGATTTATTGAAACAGCCAATCATGATAAG GAAATCTTTTTCCATTACAGTGAGTTCTCTGGTGATGTT	
CTTN	1	+369	ATACACAAGCTGAGGGAGAATGTCTTTCAAGAGCATCAGACCCTTAAGG AGAAGGAACCTGAAACAGGACCAAAAGCTTCCCATGGCTATGGAGGGAA ATTTGGTGTGGAACAAGACCGAATGGATAAGTCAGCTGTCGGCCACGAA TATCAGTCGAAACTTTCCAAGCACTGCTCGCAGGTGGACTCGGTCCGTG GCTTCGGAGGCAAGTTTGGTGTCCAGATGGACAGAGTT	
DAPK3	1	+1784	GAGGCGGAGTGGGAGGAGCTGGAGCCAGGCCCGTAAGTACGCAGGCA GGGGTGGGTGTGGGACGGGGCTGCTTCTCTACACAGCCTCTACGCTGG CCTTCACCTTCACCCCTGCATCGTCGGTGACCCTGGGACCCTCCAGGCA GCGTGGCCTGTGGCACCGTGAGGGTTGGGACCCACCGAGGCGCGGAG GCGGCCCGAATGCAGCCCTGGTTCAGGCCCGGAGGAGGGTTTGCGGG TAGTTGCACGGACAATTCGGCGGGGTGCTGCCTGTTGCTGCCATTAGCC CAGGAGGA	3' UTR sequence only

DDX5	1	+1302	ATTTGCTGAAGCACTATATTCGTAGGACGTTGGTGCGAGTGATCTGARTG GWCACCACAATGCTCTTCCAATTGTGGATGTGCGTCATGACGTAGAAAA GGATGAAAAACTTATTCGTCTAATGGAAGAGATCATGAGTGAGAAGGAG AATAAAACCATTGTTTTTGTGGAAACCAAAAGAAGATGTGATGAGCTTAC CAGAAAAATGAGGAGAGATGGGTGGCCTGCCATGGGTATCCATGGTGA CAAGAGTCAACAAGAGCGTGACTGGGTTCTAAATGAATTCAAACATGGA AAAACTCCTATTCTGATTGCTACAGATGTGGCCTCCAGAGGGCTAGGTC CTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGGCCCTAC TGCGCAGAAGCATTCAGATGTCACTTGATGATCTATGTGGAAGATGTGAA ATTTGTCATCAATTATGACTACCCTAACTCCTCAGAGGATTATATTCATCG AATTGGAAGAACTGCTCACAGTACCAAAACAGGCACAGCATACACTTTCT TTACACCTAATAACATAAAGCAAGTGAGCGACCTTATCTCTGTGCTTCGT GAAGCTAATCAAGCAATTAATCCCAAGTTGCTTCAGTTGGTCGAAGACAG AGGTTCAGGTCGTTCCAGGGGTAGAGGAGGCATGAAGGAT	specific splice isoform only
DDX5	1	+1390	TGACGTAGAAAAGGATGAAAAACTTATTCGTCTAATGGAAGAGATCATGA GTGAGAAGGAGAATGAAACCATTGTTTTTGTGGAAACCAAAAGTAGATGT GATGAGCTTACCAGAAAAATGAGGAGAGATGGGTGGCCTGCCATGGGTA TCCATGGTGACAAGAGTCAACAAGAGCGTGACTGGGTTCTAAATGAATT CAAACATGGAAAAGCTCCTATTCTGATTGCTACAGATGTGGCCTCCAGAG GGCTAG	
DDX5	1	+1562	GAACGTGACTGGGTTCTAAATGAATTCAAACGTGGAAGAGCTCCTATTCT GATTGCTACAGATGTGGCCTCCAGAGGGCTAGATGTGGAAGATGTGAAA TTTGTCATCAATTATGACTACCCTAACTCCTCAGAGGATTATATTCATCGA ATTGGAAGAACTGCTCGCAGTACCAAAACAGGCACAGCATACACTTTCTT TACACCTAATAACATAAAGCAAGTGAGCGACCTTATCTCTGTGCTTCGTG AAGCTAATCAAGCAATTA	
DNAJB5	5	+1598	CTTAAGCAGCACCTACCCCGTTCCTAGGCTCTGCCCCAGCCAGTCCAGA GCCTACCACAGCAATACCCCCAACACTCACTCCACTCAATGTGCACCCA GCTTGATGTCCACTGGACACTGGCAACTTTTTCTAAAATGCAAAAAAAAG CCACTGGTTTTCAGGAAAA	Close to stop, no possible ORF
EDF1-alpha	1	+30	TCTAGCAGCTGCCGCTGAGCCGCCGGACGGACGCTCGTCTTCGCCCGC CATGGCCGAGAGCGACTGGGACACGGTGACGGTGCTGCGCAAGAAGG GCCCTACGGCCGCCCAGGCCAAATCCAAGCAGGCTATCTTAGCGGCAC AGAGACGAGGAGAAGATGTGGAGACCTCCAAGAAATGGGCTGCTGGCC AGAACAACAACATTCTATTACCAAGAACACGGCCAAGCTGGACCGGGAG ACAGAGGAGCTGCACCATGACAGGGTGACCCTGGAGGTGGGCAAGGTG ATCCAGCAAGGTCGGCAGAGCAAGGGGCTTACGCAGAAGGACCTGGCC ACGAAAATCAATGAGAAGCCACAGGT	specific splice isoform only
EEF1A1	2	+920	CAACGGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGGGTGAGGC TCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAG GATGTTCGTCGTGGCAAYGTTGCTGGTGACAGCAAAAATGACCCACCGA TGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGG CCAAATAAGCGCCGGCTATGCCCCTGTATTGGATTGCCACACGGCTCAC ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATT	
EEF1D	1	+2291	TTCAGTGTGTGGTGGAGGACGACAAGGTGGGGACAGACTTGCTGGAGG AGGAGATCACCAAGTTTGAGGAGCACGTGCAGAGTGTCGATATCGCAGC TTTCAACAAGATCTGAAGCCTGAGTGTGTGTACGTGCGCGCGTGCGTGA GGCCCTGCCACGATTAAAGACTGAGACCG	Close to stop, no possible ORF

EIF3D	1	+ 162	GAAGATGGCAAAGTTCATGACACCCGTGATCCAGGACAACCCCTCAGGC TGGGGTCCCTGTGCGGTTCCCTAGCAGTTTCGGGATATGCCCTACCAGC CGTTCAGCAAAGGAGATCGGCTAGGAAAGGTTGCAGACTGGACAGGAG CCACATACCAAGATAAGAGGTACACAAATAAGTACTCCTCTCAGTTTGGT GGTGGAAGTCAATATGCTTATTTCCATGAGGAGATGAAAGTAGCTTCCAG CTGGTGGATACAGCGCGCACACAGAAGACGGCCTACCAGCGGAATCGA ATGAGATTTGCCCAGAGGAACCTCCGCAGAGACAAA	
EIF4E2	1	+ 456	CCTGACAGGCCACAGTGACTTCCATCTCTTCAAAGAAGGAATTAAACCCA TGTGGGAGGATGATGCAAATAAAAATGGTGGCAAGTGGATTATTCGGCT GCGGAAGGGCTTGGCCTCCCGTTGCTGGGAGAATCTCATTTGGCCCTG CTGGGGGAACAGTTCATGGTTGGGGAGGA	
EMC6	2	+561	GAACAAATATTCCAAATCACGGAGACCTCTCTTTACAGGAGGCCTCATCG GGGGCCTCTTCACCTACGTCCTGTTCTGGACGTTCCTCTACGGCATGGT GCACGTCTACTGAAATGGGGGCCCGGGGGACTTTTTTAAAAAACCA	
EML4	1	+2334	GTACCTTCCTGGCTGTAGGATCTCATGACAACTTTATTTACCTCTATGTAG TCTCTGAAAATGGAAGAAAATATAGCAGATATGGAAGGTGCACTGGACAT TCCAGCTGCATCACACACCTTGACTGGTCCCCAGACAACAAGTATATAAT GTCTAACTCGGGAGACTATGAAATACTGTACTGGGACATTCCAAATGGCT GCAAACTAATCAGGG	specific splice isoform only
GPCPD1	1	+565	AGGCTGCAAGCCATAACCACACTCCGGCTGTGAATGCCTGCACTTAAAC TCATTGTCGCTTATTAAGGATATCTCCAAGCTATTGGACATTTTGTGGAGT ACAGTGGGAGATACCCTATCATCGTCATCTTCCTCCAGGCCTTCTAGTGT CAGCTTCACCCTAAATCTAGATTCTTTTAATTTTTTCTTGGTTATTGACACA GGAGGTTTTTCAGAATAATGCAAACGTAATCTTATTTCAGTCTGACATGTC AGCCATCCAGAATCCAGAGTTTCAACACCCCGTC	
GPX4	1	+148	GAAGCCAGCGCTGCTCTGTGGGGCTCTGGCCGCGCCTGGCCTGGCCG GGACCATGTGCGCGTCCCGGGACGACTGGCGCTGTGCGCGCTCCATGC ACGAGTTTTCCGCCAAGGACATCGACGGGCACATGGTTAACCTGGACAA GTACCGGGGCTTCGTGTGCATCGTCACCAACGTGGCCTCCCAGTGAGG CAAGACCGAAGTAAACTACACTCAGCTCGTCGACCTGCACGCCCGATAC GCTGAGTGTGGTTTGCGGATCCTGGCCTTCCCGTGTAACCAGTTCGGGA AGCAGGAGCCAGGGAGTAACGAAGAGATC	specific splice isoform only
HMCES	1	+239	GTTGCGAGGGGCGGTGTTGAAGAATGTGTGGGCGAACATCCTGTCACTT ACCTAGAGATGTTCTCACGAGAACTTGCGCCTACCAG	
HNRNPA1	0.5	+455	AAAGAAGACACTGAAGAACATCATCTAAGAGATTATTTTGAACAGTATGG AAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGCAAGAAA AGGGGCTTTGCCTTTGTAACCTTTGACGACCATGACTCCGTGGATAAGAT TGTCATTCAGAAATACCATACTGTAAATGGCCACAACTGTGAAGTTAGAA AAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGG TCGAAGTGGTTCTGGAAACTTTGGTGGT	ambiguous, can be either RNA
HNRNPA1L2	0.5	+1410	AAAGAAGACACTGAAGAACATCATCTAAGAGATTATTTTGAACAGTATGG AAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGCAAGAAA AGGGGCTTTGCCTTTGTAACCTTTGACGACCATGACTCCGTGGATAAGAT TGTCATTCAGAAATACCATACTGTAAATGGCCACAACTGTGAAGTTAGAA AAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGG TCGAAGTGGTTCTGGAAACTTTGGTGGT	ambiguous, can be either RNA

LRP5L-2	1	+335	TGAGCGCCCTCTACTCAGCATGGATATCAGGTGCTGAGCCAGGAGCAG CAGCCTTTCTGAGCCAAGGAGGTCCTGCTGCTGGCCCGGTAGACGGAC CAATGGAGGGTCTCGCTGGACACACCGGACTTCACCGACATCGTGCTG CAGCTGGACGACATCCAGCATGCCATCGCCATCAACTATGACACAATGG AGGGCCACGTCTACTGGACGGATGACGAGGTGTGGGCCATCCGCAGGG CATACCTGGATGGGTCTGGGGCGCAGACGCTGATCAACACCAAGATCAA CGACCCCGATGACATCGCAGTCAACTGGGTGGCCCGAAGCCTCTATTG GCCCCACACAGGCACTGAACACATCGAGGTGACGTGCCACAACAGCAC CTCCCACAAGATCCTGGTGTCAGAGGACATGGACGAGCCCCGTGCCATT GCACTGCATCCCGAGATGGGCCTCACGTACTGGATAGACTGGGGAGAG AACCCTGAAATCAAGCGTGCCAACCTGGACAGACAGGAGCTGCGCGTG CTGGTCAATGCTTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTG CAGGAAGGGAAGCTCTACTGGGGAGATGCCAAGACAGATAAGATCGAG GCGATCAGTGTCGATGAGACGAAGAGGCAGACCCTCCTGAAGGACAAG CTCCCACACATTTTCAGGTTCACCCTGCTGGGGGACTTCATCTACTGGA CCGCCTGGCAGCACCACAGCATCAAGCGGGTACACAAGGTC	specific splice isoform only
LYSMD1	1	+156	ACAAATTCTTGCAWTCCCCACGCTCTTCGTCTGCGGCGACAGTTCACCT GGGGTGGGCCTGATTTGTTCCTGACTCTAGCAAACAAACCCCGGGACCG GGGAGAGCTGGGATGTTGGAGCGCCCTGAGGCCAGGCTACTTGGGGG CAAACTGAGGAAAGAGTGTTGAGGATTATTTCTAGAGTTCAAAGGTCAGA GGTCAATGTAGCGAGGAGTTGTGGGG	
MED15	1	+1683	AGCTCTGTCATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAG TACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGC CGCATGATCAACAAGATCGACAAGAACGAAGACAGAAAAAAGGACCTGA GTAAGATGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTG TCCCCCGAAGACCTTGCAAAAGTGTGA	
METTL16	1	+21	AAGATGGCGGCGCGCTGGGAGCGTATCATCTGCGTTTCTAGGAGCTTC GCTATGCGGCTGCTTTAAGATTCTAGGGTTGTACAGGCCCACGCCAGAC ACGACGTCTGGCAGGAACCTCGGCCTCAGAGATGGCTCTGAGTAAGTCA ATGCATGCAAGAAGTAGATACAAGGACAAACCTCCTGACTTTGCATATCT GGCATCCAAATATCCAGATTTTAAGCAGCATGTTCAGATAAATCTGAATG GAAGAGTGAGCCTTAATTTTAAAGACCCCGAAGCAGTCAGAGCTCTGAC GTGTACTCTCCTAAGGGAAGATTTTGGACTTT	
MTX3	1	+7668	CAATGTTGGCCATAATTTCAATATTCTAGCCTTGCCGAGTGTGAATATATT TTACTCAGAGACTATGTACAAATACACTAAAGTGGTGATGGTGATCAATA TTGTAAAGAATT	3' UTR sequence only
MYO5B	1	+4531	AAGCTGGAGAAGAATGAGAGGAAGCTCAAAAAGCAACTGAAGATTTACA TGAAGAAAGCCCAGGACCTAGAAGCTGCCCAGGCATTGGCCCAGAGTG AGAGGAAGCGCCATGAGCTCAACAGGCAGGTCACGGTCCAGCGGAAAG AGAAGGATTTCCAGGGCATGCTGGAGTACCACAAAGAGGACGAGGCCC TCCTCATCCGGAACCTGGTGACAGACTTGAAGCCCCAGATGCTGTCGGG CACAGTGCCCTGTCTCCCCGCCTACATCCTCTACATGTGCGTCCGGCAC GCGGACTGTAGAACTCGATCGTCGGACTGTAGAACTC	
NDUFA6	3	+523	CATGAAGTCATTCAGTGGAAAGATGCACGTTGATACTATTTTAGAGCACA AATAAACTCACTATACAATGGTCAA	Close to stop, no possible ORF
PARD3	1	+ 3521	AAGCCAAAACTCGAGAATTTAGGGAACGACAAGCTCGAGAGCGTGACTA TGCTGAAATTCAAGATTTTCATCGGACATTTGGCTGTGATGATGAGTTAAT GTATGGGGGAGTTTCTTCTTATGAAGGTTCCGTGGCTCTCAACGCTAGA CCTCAGAGCCCACGAGGAGGGCATATGATGGATGCTTTGTATGCCCAAG TCAAGAAGCCGCGGAATTCCAAACCCTCACCTGTAGACAGTAACAGATC AACTCCTAGCAATCATGATCGGATACAGCGTCTGAGGCAAGAACTTCAG CAAGCAAAGCAAGATGAAGATGTAGAA	

PRDX5	1	+375	AAGGGCAAGAAGGGTGTGCTGTTTGGAGTTCCTGGGGCCTTCACCCCT GGATGTTCCAAGACACACCTGCCAGGGTTTGTGGAGCAGGCTGAGGCT CTGAAGGCCAAGGGAGTCCAGGTGGTGGCCTGTCTGAGTGTTAATGATG CCTTTGTGACTGGCGAGTGGGGCCGAGCCCACAAGGCGGAAGGCAAG GTTCGGCTCCTGGCTGATCCCACTGGGGCCTTTGGGAAGGAGACAGAC TTATTACTAGATGATTCGCTGGTGTCCATCTTTGGGAATCGACGTCTCAA GAGGTTCTCCATGGTGGTACAGGATGGCATAGTGAAGGCCCTGAATGTG GAACCAGATGGCACAGGCCTCACCTGCAGCCTGGCACCCAATATCATCT CACAGCTCTGAGGCCCTGGGCCAGATTACTTCCTCCACCCCTCCCTACC TCACCTGCCCAGCCCTGTGCTGGGGCCCTGCAATTGGAATGTTGGCCA GATTTCTGCAATAAACACTTGTGGTTTGCG	specific splice isoform only
PRKCE	1	+54	GGGTCAGCACTAGTGGTGAGAATTCTGGAGAACATTTTCTTTACCCAGAA ACTTAAAATCATGGACTCTTGGGGAGAAAGGAATGAGAAAAGGCAGCAT GCGGAATTACCAGTTTGTTATTTGGATCCCATCTGGATTTAAAACCGAAG ATCCCAAACTCGGATTGATCTGGAGCCAGAAGGAAGAGTGTATGTGATC ATCGATCTCTCAG	specific splice isoform only
PSMC6	1	+259	GCTACCRCTGGACCAWGATATGTTGTGGGTTGTCGTCCACAGCTTGTCA AAAGTATGCTGAAGCCTGGAACARGAGTTGCTTTGGATATGACTACMCT AACTATCAKGAGATATTTGCCGAGAGAGGTGGATCCWCTGGTTTATGAC ATGTCTCATGAGGACCCTGGGAATGTTTCTTATTCAGA	specific splice isoform only
RIT1	1	+216	CSATTCCCAGAAGATCATGATCCCGCCATTGAAGATGCTTATAAGATCAG GATCCGTATTGATGATGAGCCTGCCAATCTGGACATTTTGGATACAGCTG GACAGGCAGAGTTTACAGCCATGCGGGACCAGTATATGAGGGCAGGAG AAGGGTTTATCATCTGTTACTCTATCACG	
RPL18A	1	+530	AAGTTCCCGCTGCCCCACCGGGTCCTGCGCCGTCAGCACAAGCCACGC TTCACCACCAAGAGGCCCAACACCTTCTTCTAGGTGCAGGGCCCTCGTC CGGGTGTGCCCCAAATAAACTCAGGAACGCCCCGGTGAAAAAAAAAAAA AAA	Close to stop, no possible ORF
RPL31	4	+65	CTTTCCAACTTGGACGSTGCRGAATGGCTCCCGCAAAGAAGGGTGGCGA GAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAACCCGAGAATAC ACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTG CACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGG AACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCC AAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAAAA AACGTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACC TATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGA GAACTAATCGCT	specific splice isoform only
RPL31	1	+139	AACGAAGTGGTAGCCGAGAATACACCATCAACATTCACAAGCGCATCCA TGGAGTGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCG GAAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACC AGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACC GAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGGTTCACC AAATAAGCTATATACT	
RPL31	1	+194	TGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATT TGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTC AACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCC GTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCACCAAATAA GCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACA GACAGTCAATGTGGATGAGAACTAATCGCT	specific splice isoform only
RPL31	1	+194	TGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATT TGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTC AACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCC GTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCACCAAATAA GCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACA GACAGTCAATGTGGATGAGAACTAATCGCT	specific splice isoform only

RPL31	1	+202	AAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGA AGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGC TGTCTGGGCCAAAGGAATATGGAATGTGCCATACCGAATCCGTGTGCGG CTGTCCAGAAAACGCAATGAGGATGAAGATTCACCAAATAAGCTATATAC TTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAA TGTGGATGAGAACTAATCGCT	specific splice isoform only
RPL31	1	+204	GAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAG GAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTG TCTGGGCCAAAGGAATATGGAATGTGCCATACCGAATCCGTGTGCGGCT GTCCAGAAAACGCAATGAGGATGAAGATTCACCAAATAAGCTATATACTT TGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATG TGGATGAGAACTAATCGCT	specific splice isoform only
RPL31	1	+214	GTATATAGCTTATTTGGTGAATCTTCATCCTCATTACGTTTTCTGGACAGC CGCACACGGATTCGGTATGGCACATTCCTTATTCCTTTGGCCCAGACAG CTTTGTTGAGCCTGGTGTCAATGCGCACATCTGGAGTTCCCATCTCCTTC ATGGCAAATTTCCGAATCTCTTTGAGTGCCCGAGG	
RPL31	1	+226	TTTGGTGAATCTTCATCCTCATTACGTTTTCTGGACAGCCGCACACGGAT TCGGTATGGCACATTCCTTATTCCTTTGGCCCAGACAGCTTTGTTGAGCC TGGTGTCAATGCGCACATCTGGAGTTCCCATCTCCTTCATGGCAAATTTC CGAATCTCTTTGAGTGCCCGAGG	
RPL31	1	+228	TGGTGAATCTTCATCCTCATTACGTTTTCTGGACAGCCGCACACGGATTC GGTATGGCACATTCCTTATTCCTTTGGCCCAGACAGCTTTGTTGAGCCTG GTGTCAATGCGCACATCTGGAGTTCCCATCTCCTTCATGGCAAATTTCCG AATCTCTTTGAGTGCCCGAGG	specific splice isoform only
RPL31	1	+255	GATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTC TGGGCCAGAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGT CCAGAAAACGTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTG GTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGTG GATGAGAACTAATCGCT	specific splice isoform only
RPL31	1	+268	GATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAA TAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAGACGTAA TGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTAC CTGTTACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGAGAACTAA TCGCT	specific splice isoform only
RPL4	1	+1038	ATGTTGAAGCTAAACCCATATGCAAAGACCATGCGCCGGAACACCATTC TTCGCCAGGCCAGGAATCACAAGCTCCGGGTGGATAAGGCAGCTGCTG CAGCAGCGGCACTACAAGCCAAATCAGATGAGAAGGCGGCGGTTGCAG GCAAGAAGCCTGTGGTAGGTAAGAAAGGAAAGAAGGCTGCTGTTGGTGT TAAGAAGCAGAAGAAGCCTCTGGTGGGAAAAAAGGCAGCAGCTACCAA GAAACCAGCCCCTGAAAAGAAGCCTGCAGAGAAGAAACCTACTACAGAG GAGAAGAAGCCTGCTGCATAAACTCTTAAATTTGATTATTCCATAAAGGT CAAATCATTTTGGACAGCTTCTTTTGAATAAAGACCTGATTATACA	
RPL41	3	+44	CTCTCGGCCTTAGCGCCATTTTTTTGGAAACCTCTGCGCCATGAGAGCC AAGTGGAGGAAGAAGCGAATGCGCAGGCGAAGCGCAAAAGAAGAAAGA TGAGGCAGAGGTCCAAGTAAACCGCTAGCTTGTTGCACCGTGGAGGCC ACAGGAGCAGAAACATGGAGTGCCAGACGCTGGGGATGCTGGTACAAG TTGTGGGACTGCATGCTACTGTCTAGAGCTTGCCTCAATGGATCTAGAAC TTCATCGCCCTCTG	specific splice isoform only
RPS12	1	+294	AACGCCAAATCAACCTAATTAAGGTTGATGACAACAAGAAACTAGGAGAA TGGGTAGGCCTTTGTAAAATTGACAGAGAGGGGAAACCCCGTAAAGTGG TTGGTTGCAGTTGTGTAGTAGTTAAGGACTATGGCAAGGAGTCTCAGGC CAAGGATGTCATTGAAGAGTATTTCAAATGCAAGAAATGAAGAAATAAAT CTTTGGCTCCGGCAAAAAAAAAAAAA	

RPS19	1	+674	AAGAGTGTGGCCCGCCGGGTCCTCCAAGCCCTGGAGGGGCTGAAAATG GTGGAAAAGGACCAAGATGGCGGCCGCAAACTGACACCTCAGGGACAA AGAGATCTGGACAGAATCGCCGGACAGGTGGCAGCTGCCAACAAGAAG CATTAGAACAAACCATGCTGGGTTAATAAATTGCCTCATT	
RPS5	1	+250	CGSTTYCGCAAAGSTCAGTGTCCCMTTGTGGAGSGCCTCACTAAMTCCA WGATGATGCACGGCCGCAACAAMGGCAAGAAGSTCATGAMTGTGSGSA TWGTCAAGCAWGCCTTTGAGATCATACACCTGSTCMCAGGGGAGAACC CTTTGCAGGTCCTGGTGAAMGCCATYATCAACAGTGGTCCCCGGGAGG ACTCCACACSCMTTGGGSGSSCCGGGAMTGTGAGAMGACCGGSTGKGG ATGTGTCCCCCCTGSSCCGTGTGAACCCGGCCATTTGGSTGSTGKGCMC AGGSGCTYGKGAGGSTSCCTTCCGGAACATTAAAACCATTKSTGAGKGC CTGGCAGATGAGSTCATCAAWGSTGCCAAGGGCTCCTYGAAMTCCTATG CCCTTAAGAAGAAGGRCGAGSTGGAGSGTGTGGCCAAGTCCCACCSST GATTTTYCCMGSTGSTGCCCMAWAAACCYKTTTKCCCTTTGGGGCMGTY CC	
RRP36	1	+468	AAACAGTTGAAGAAGCACCTTTCAGGAGAGGAGCATGAGAAACTGCAGC AACTGCTTCAGCGAATGGAGCAGCAAGAAATGGCACAGCAGGAACGAAA GCAACAGCAGGAGCTGCACCTGGCCCTGAAGCAA	
SCAMP1	1	+209	CTCAACAATCCCTTCAAGGATCCATCAGTTACACAAGTGACAAGAAATGT TCCACCAGGACTTGATGAATATAATCCATTCTCGGATTCTAGAACACCCC CACCAGGCGGTGTGAAGATGCCTAATGTACCCAATACACAACCAGCAAT AATGAAACCAACAGAGGAACATCCAGCTTATACACAGATTGCAA	specific splice isoform only
SCAMP1	1	+281	AATCCATTCTCGGATTCTAGAACACCCCCACCAGGCGGTGTGAAGATGC CTAATGTACCCAATACACAACCAGCAATAATGAAACCAACAGAGGAACAT CCAGCTTATACACAGATTGCAAAGGAACATGCATTGGCCCAAGCTGAAC TTCTTAAGCGCCAGGAAGAACTAGAAAGAAAAGCCGCAGAATTA	specific splice isoform only
SPARC	1	+1385	CACATGGGTGGACATCCATCTGCTGGGGACGGCCTTATAGACACTTTGA TRCTGCCACTTTTCTGTTTAAGGTTCTGTTTGAAACTAATACTTACCGAGT CAGACTTTGTGTTCATTACATTTCAGGGTCTTGGCTGCCTGTGGGCTTCC CCAGGTGGCCTGGAGGTGGGCAAAGGGAAGTAACAGACACACGATGTT GTCAAGGATGGTCTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCT GCAGAACCCACCAACCAGAACGTGGTTTGCCTGAGGCTGTAACTGAGAG AAAGATTCTGGGGCTGTGTTATGAAAATATAGACATTCTCACATAAGCCC AGTTCATCACCATTTCCTCCTTTACCTTTCAGTGCAGTTTCTTTTCACATTA GGCTGTTGGTTCAAACTTTTGGGAGCACGGACTGTCAGTTCTCTGGGAA GTGGTCAGCGCATCCTGCAGGGCTTCTCCTCCTCTGTCTTTTGGAGAAC CAGGGCTCTTCTCAGGGGCTCTAGGGACTGCCAGGCTGTTTCAGCCAG GAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAAATAGAAAAAGT GGAGTTGGTGAATCGGTTGTTCTTTCCTCACATTTGGATGATTGTCATAA GGTTTTTAGCATGTTCCTCCTTTTCTTCACCCTCCCCTTTTTTCTTCTATTA ATCAAGAGAAACTTCAAAGTTAATGG	3' UTR sequence only
SPARC	1	+1733	TCATCACCATTTCCTCCTTTACCTTTCAGTGCAGTTTCTTTTCACATTAGG CTGTTGGTTCAAACTTTTGGGAGCACGGACTGTCAGTTCTCTGGGAAGT GGTCAGCGCATCCTGCAGGGCTTCTCCTCCTCCGTCTTTTGGAGAACCA GGGCTCTTCTCAGGGGCTCTAGGGACTGCCAGGCTGTTTCAGCCAGGA AGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAAATAGGAGAAGTG GAGTTGGTGAATCGGTTGTTCTTTCCTCACATTTGGATGATTGTCATAAG GTTTT	3' UTR sequence only
TAF10	2	+446	CCAGATGCAGAGACTGGTTACTACCTGAACCGTGCTGGCTTTGAGGCCT CAGACCCACGCATAATTCGGCTCATCTCCTTAGCTGCCCAGAAATTCATC TCAGATATTGCCAATGATGCCCTACAGCACTGCAAAATGAAGGGCACAG CCTCCGGCAGCTCCCGGAGCAAGAGCAAGGGCCGCAAGT	

TIAM2	1	+2888	ACGAAGACTGGGAGTGTGTGTGACTTTGGGTTTGCAGTTACAGCGCAGG TGGATGAGCGTCAGCATCTCAGCCGGATATTTATAAGCGACGTTCTTCC CGATGGCCTGGCGTATGGGGAAGGGCTGAGGAAGGGCAATGAGATCGT GACCTTAAATGGGGAAGCTGTGTCTGATCTTGACCTTAAGCAGATGGAG GCCCTGTTTTCTGAGAA	
UBE2J2	1	+195	CAGCACCAGCAGTAAGAGGGCTCCGACCACGGCAACCCAGAGGCTGAA GCAGGACTACCTTCGCATTAAGAAAGACCCGGTGCCTTACATCTGTGCC GAGCCCCTCCCTTYGAATATTCTCGAGTGGCACTATGTCGTCCGAGGCC CAGAGATGACCCCTTATGAAGGTGGCTATTATCATGGAAAACTAATTTTT CCCAGAGAATTTCCTTTCAAACTTYCCAGTATCTATATGATCACTCCCAAC GGGAGGTTTAAGTGCAACACCAGGYTGTGTCTTTCTATCACGGATTTCCA CCCGGACACGTGGAACCCGGCCYGG	specific splice isoform only
UBR1	2	+635	CCAGGAAAATATTTCCTTCAGTGATAAAGTATGTCGTAGAAATGACTATAT GGGAAGAGGAAGAAGAACTGCCTCCTGAACTCCAGATAAGGGAGAAAAA TGAAAGATACTATTGTGTCCTTTTCAATGATGAACACCATTCATATGACCA CGTCATATACAGCCTACAAAGAGCTCTTGACTGTGAGCTCGCAGAGGCC CAGTTGCATACCACTGCCATTGACAAAGAG	
YES1	1	+778	AGAGTGAAACAACTAAAGGTGCTAATTCCCTTTCTATTCGTGATTGGGAT GAGATAAGGGGTGACAATGTGAAACACTACAAAATTAGGAAACTTGACAA TGGTGGATACTATATCACAACCAGAGCACAATTTGATACTCTGCAGAAAT TGGTGAAACACTACACAGAACATGCTGATGGTTTATGCCACAAGTTGACA ACTGTGTGTCCAACTGTGAAACCTCAGACTCAAGGTCTAGCAAAAGATG CTTGGGAAATCCCTCGAGGATCTTTGCGACTAGAGGTTAAACTAGGACA AGGATGTTTCGGCGAAGTGTGGATGGGAACATGGAATGGAGCCACGAA AGTAGCAATCAAAACACTAAAACCAGGTACAATGATGCCAGAAGCTTTCC TTCAAGAAGCTCAGATAATGAAAAAATTAAGACATGATAAACTTGTTCCAC TATATGCTGTTGTTTCTGAAGAACCAATTTACATTGTCACTGAATTTATGT CAAAAGGAAGCTTATTAGATTTCCTTAAGGAAGGAGATGGAAAGTATTTG AAGCTTCCACAGCTGGTTGATATGGCTGCTCAGATTGCTGATGGTATGG CATATATTGAAAGAATGAACTATATTCACCGAGGTCGTCGGACTG	

