

Supplementary Table

Name	Sequence of forward primer	Sequence of reverse primer	Amplified region
GAPDH +119	AGGTGAAGACGGGCGGAGAGA	GCGAACACATCCGGCCT	+78/+160 (TSS)
GAPDH +925	CTCGATGGGTGGAGTCGC	CTAGGAAAAGCATCACCCGGA	+881/+968 (TSS)
GAPDH +1675	GGTGGTGAAGCAGGCGTCGGAGGGC	GAGCCAGTCTCTGGCCCCAGCCACA	+3348/+3534 (TSS)
7SK	CTGATCTGGCTGGCTAGGCGGG	GAAGACCGGTCTCTCTATCGG	+11/+181 (TSS)
5'ETS rRNA	TGAGTGAGACGAGACGAGAC	GAAGTCAACCCACACACGA	+961/+1168 (TSS)
Leu74 tRNA	AGC TTG GCT TCC TCG TGT T	TGTCAGAAGTGGGATTCGAAC	+37/+105 (TSS)
TRPM7 -927	GATGGAGAGGGACGAGATGAAGG	GACATACCTGTGCACCCATG	-979/-876 (TSS)
TRPM7 +172	CTAGCGCCGGAGCTGAGTTAG	TTCCCGATAGATGGCTACAGG	+120/+225 (TSS)
TRPM7 +394	CGGTAAAGGAGAGACTTGCCA	GGGACGGGTGTGCAGTTCTTCT	+334/+455 (TSS)
TRPM7 +653	GGGACGGGTGTGCAGTTCTTCT	CAGTTGCTGGCAGATAAGGGAA	+614/+692 (TSS)
TRPM7 +898	GGAACCAAAGGGAGGGATT	CTGTCAGTCAGGATTTAAGTCGAAC	+830/+966 (TSS)
DHX9 +660	GATAACCTCGCCAACGCGAAG	CATGTGACTGGAGTGTGGCGA	+600/+720 (TSS)
DHX9 +949	GGTGAAGGTAGTAGATCTGGA	GGCTCACAGCAACGTCCGGTC	+878/+1020 (TSS)
DHX9 +1499	GAAATGTAGGGGTAGGGTGTGG	GGGTGAGTTAGTGCCACAGTTGGATG	+1388/+1611 (TSS)
DHX9 +2125	CATTCACCATGAGGGCTTGTGTTTAAT	TTCCCTTCGCCAAATGGATGACCA	+2066/+2184 (TSS)
PLK2 -1386	AAGTGCTCCTCTGTACCAGGA	GGAATCATGACCAGGAAATGTACGG	-1440/-1332 (TSS)
PLK2 +253	ACCGGGGTGTTGGGTGCTAGT	ATAGTCCGCAAAGCTCCATG	+185/+321 (TSS)
PLK2 +624	AGTGCTGGAAAGGTGACAAGCGG	ATCGGACCCCCGAAAACCCGGAA	+559/+689 (TSS)
PLK2 +988	GTTCCAACCTCCCTCATAAAGCTC	TTGAGGAATGGAGGAGGTGGACA	+916/+1061 (TSS)
EIF2S3 +420	AACCAGCGAACTTCAGACGCT	GTCCCCAGCTTGTCCAGAGA	-480/-360 (TSS)
EIF2S3 +335	GAGAAGCTGGAGTGACTCTAGG	CACTGACTAGTCCCAATACC	+264/+406 (TSS)
EIF2S3 +662	GGTGTCTGTCTGCATTACTT	CACAACAGACTACACCTCCAC	+610/+714 (TSS)
EIF2S3 +862	GATGGTGGCAAGATGTAGATAGCA	CGTCAACTTGGTAACATCCTGCAATG	+808/+917 (TSS)
EIF2S3 +1635	TACAGGCCTTGAACACTGCT	CTTAGCATAGTTGTTCCGGAGG	+1591/+1679 (TSS)
KPNB1 TSS+0.9	AGGGAAGGGAAGTTAGTTGCG	GAGCTTCCACATGGCCCTA	+900/+986 (TSS)
KPNB1 TSS+5.3	GCAAAGCAGGATACTAAGTGATCCGA	GAAGCCACAATTGACCTAGAGC	+5234/+5405 (TSS)
KPNB1 TSS+20.2	TGCAAGAGCCAGTGGGAACACTT	CCTCTACTCAGCAATGATACTTC	+20187/+20370 (TSS)
KPNB1 pA-4.8	CTGAGGAAACTGAAGAACCAAG	GAAGGCAGTGCTTGCCAGAAT	-4862/-4746 (end)
KPNB1 pA-2.9	GAGGAGTGTGCACGGATGCTGAA	CCAAGATGGCCGATGTTATGG	-3030/-2855 (end)
KPNB1 pA-0.4	TAGTTACCGTCTGCTTGGGAAGATG	CCTCTGACAGCAAGTCCAACATT	-510/-330 (end)
KPNB1 pA+1.4	GACTCATCACACCAAGGTCAC	GATAGTGCTGGGAAGGAAATGG	+1320/+1490 (end)
KPNB1 pA+2.6	GTACATCTCAGCTTTGGCATATG	GCCCAGAACATAGCAGGCATTGC	+2587/+2728 (end)
KPNB1 pA+4.1	GTTTCACCGTGTAGCCAGGATGG	CCACAGCCATGTTTATTCTGC	+4053/+4217 (end)
KPNB1 pA	CAGTCTGTGATGGCATTTAAG	TCTGACTTTCAAACATTTACCTCC	-114/+77 (end)
DHX9 +1118	CCTGCCTCAAGATGATCTCC	GCTAGCTACAGCTGTACAGC	+1028/+1208 (end)
DHX9 +1654	GAAAGTGCTTCCACATAGCCATGG	CTGGATTCCCCTTACAGCTATGAC	+1568/+1740 (end)
DHX9 -122	GGC ATG CTA TGT GTT ACG TG	CGAGGTCAACAAACAACTACAGGC	-272/+29 (end)

Supplementary Table . Sequences of primers used and their position relative to the TSS or the end of gene (end).