**Table 1: Sequence of primers for RT-qPCR**

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| --- | --- | --- |
| Targets | Sequence of primer | |
| Forward | Reverse |
| DGKQ | GTCTCCCGAGGAGTACAGCA | CAAAGCAGGCAACGTCCAAC |
| DALRD3 | AGGAGTTCCAGCAACAGAAG | CTTTCACAGGGCCACAGAT |
| CAB39L | GATGAACCTCCTTCGGGATAAA | AACAGGATCTCCACAATAGGC |
| SV2C | TCCAAGGTTATGGCTTCTTTCT | GTACGAGAACACAGTGGGTATG |
| DLG2 | GTGCGTAGAAGACGACCTATTT | GCTGTTGTCTCCAGGAATGT |
| RIMS1 | TTCTTGATGGATTGGGACCAG | GTGCTCTAATGACTTCCACTTCTA |
| ITPKB | GTTCAGGATCGAGGGAATCAAG | CGATAGGCGATCAGGATGTTATG |
| LGALS3 | CCTCGCATGCTGATAACAATTC | CTCATTGAAGCGTGGGTTAAAG |
| BAG3 | AGAAACCACTCAGCCAGATAAA | GATGAGGATGAGCAGTCAGAG |
| BIN3 | GACTGTGATCGAGCCCTTAAA | TTTCCTCATACTTCTCCACCTTG |
| BRIP1 | TGTGCATGCCATTCAAAGGA | CTTTGCAGCCAGAGTGGTTT |
| CLCN3 | TGCAGTTTCCCTGGTAAAGG | CCACAGCCAGGACTAATGTG |
| CPLX1 | GTGATGAAGCAGGCTCTAGG | CCGCTCCTCCTCCTTCTT |
| CNOT1 | CCCAATCAGACCACTGCAT | CCAAGAGCACCAGTTCCTATAC |
| CTSB | TTCGATGCACGGGAACAA | GTCAGAGATGGCTTCCACAG |
| FYN | GGTGTGAACTCTTCGTCTCATAC | CTTCTGTCCGTGCTTCATAGTC |
| GIN1 | GGTATATCCAGGACCCTCACT | CTTGGCAATGCTGACAAGC |
| KRTCAP2 | CTCGCTCACTGCCTTCAATAA | GATGAGGCCAGATGCAAAGA |
| INPP5F | CTTGCCTGGAATCCCATTTG | GCCCACCAATGCTTTCTG |
| DYRK1A | CCAAACGCAGTGCAATCAAG | GCACCTCTGGAGACCGATAA |
| IP6K2 | GTCCTTCTGGAGCCCTTTG | GGAGGGTCTCGTAGAACTGA |
| NEK1 | GGAGAGAAGTTGCAGTATTGGC | CCCTCCCTCACAGTAATCCA |
| PAM | ACCAGACCCGTAGTTCCTATT | GCTTCCTCATCCACTGGTATTC |
| CRLS1 | CCCAGTTCTGGGCTATTTGA | GGCCCAGTTTCGAGCAATA |
| CAMK2D | AATTTAGTGGAAGGGATGGATTTT | TATGCAGGCGGCATCATC |
| FAM49B | ATGCACAGACCTTGAGCAGG | GCAAGTCCTCCAAGATGCCT |
| GAK | GAAGATCTTCTACCAGACGTG | ATGGTCCCTTGGTTACTAAGC |
| GBF1 | CATCGGCTCAGGTGTGAAG | GATCCAGGCTCACGTCATTC |
| HCN3 | GCCACAAAGCAGTGGAAATC | GCATGATCAGGTCCCAGTAAA |
| HIST1H3J | CATCCGCAAACTGCCATTTC | CTTCAAAGAGACCCACCAGATAG |
| MED12L | TGGAGATGAACATGGCTCAG | CCGTGTCCTGGAAAGTGTTA |
| NUPL2 | GCAGCAGCCTTCAGGTAATA | CATGGTGTGGATTTGGAGAAAC |
| RNF141 | AGTGGTTGTACGGGTGGTCT | ACTCCTGCTGCTTGACTTGT |
| RPS6KL1 | AGGCGGCCTTCAACCAC | CCCGCCGCAGGTATTTG |
| SEC23IP | GCTTCAATGTGCCCTTCATC | CTGTCCTCCTCACCAACATC |
| SETD1A | ATGGAACCCATTGCTGCTGA | TCGATGATGGTGTCGTGGTC |
| LCORL | TGACTGACTGGTCTATGGATGA | CTCCTCTGTTGGTGTTGACTG |
| MBNL2 | CCAGGAACACCACTTCATCC | GGTGCTAGGTAAGGAGCAAAG |
| MEX3C | TCCGAGCACGTCGCCGAG | CCTTCCAGTGACAACAAAAATGGG |
| HIP1R | CACGGGCAAGTATGAGGAG | GACTGTGCGAGAACATTCCT |
| HIST1H2AL | CAACAAGAAGACCCGCATTATC | CCCTGAGCGATGGTTACTTT |
| SNCA | AAGAGGGTGTTCTCTATGTAGGC | GCTCCTCCAACATTTGTCACTT |
| TIAL1 | CGGGTAGTTAAAGACATGGCA | CCCATATGCACAATCGCATTT |
| SPPL2B | CAGCTACAAAGACATGCTGGA | CCACAGCCATGATGAAGATGA |
| C5ORF24 | GCTGCGGGATACAAAGTC | CAAAATAAAACCAAGAAGCTTTGG |
| CNTN1 | ACGTCCTGAGGTCAGAGTAA | GAAGCCAGCGATAGCTAAGA |
| SCARB2 | CCCTACATCATCATGGCGCT | GTTCGAATGAGGGGTGCTCT |
| STK39 | CCCACCCAATGCTAATGAAGA | TCCTGGAGTAAACTCAAATCGTATG |
| TMEM175 | GTCTTCTCGTTTGACCTCCAC | GAACCTCTCCTTCACATCCTTG |
| ARIH2 | CTGGTTCACGATGTCAGGATT | GCTGGATGTGTCTAGGAGATTG |
| COASY | GGTGGGAGTAGCAGACAAAG | CTCAGATGTTCCACACGTTCT |
| IMPDH2 | CCAGGCCAAGAACCTCATT | GTGCATACTCTGACACCTTGTA |
| PRKAR2A | CTGCTACCATTGTTGCTACCT | TTCAAACATCTTCCTCTTCTTTGC |
| PYGO2 | AAAGAAGCGAAGGAAGTCAAATAC | GGCTCCGAAGTCATCTTCAA |
| USP19 | CCACTGCGAGCGAAGTATT | GGGTAGGAACACACGATGAAA |
| ZNF668 | GACCTCCGCAACCATGAG | CACGTGAGCGAGGATGAG |
| UBTF | GATGAGCAACCTGGACCTAAC | CGCTCGAACTCCTGTTTCTC |
| STX1B | GACCACCACCAACGAAGAA | TTGTGCCTCGTCTCAATCTC |
| QARS | CCCAATGGAATCCTGCATATTG | CTTCTCAGGGTTGGTGTCAT |
| VAMP4 | TTCTTACCTCGGCTTCCTACT | GCTTCTCAACAGGATAGTCACC |
| AMPD3 | CACCATCAGCGGAGATTACTG | CGGATCATTAGGGCCTTGG |
| ARID2 | CTAATGCCGGGGTGTTTGAC | TCTGTCAGAAATGAGGTCACGA |
| ASL | GATCAATGTCCTGCCCCTG | CACAAAGTCCCGCTCACTAG |
| ATP6V0A1 | AGGAAATGGCTTCTGGAGTG | CCTTCATCTTCCGCACTTTG |
| CAMLG | CGGAACAGCGCATCAACCG | TCACCCAGCACTACTCGCTTT |
| CCDC58 | GCTCATGCCAGTAGAGACAG | TCCAGCTCCTGTCATTTACCA |
| CCDC71 | GCCATGTTGGAGCAGCGGAG | TGGGTATCCGCAAACCAGCG |
| CLN3 | CCTGCTGTCCATGCTGGGTA | CCTGGGCCTCAGGAGATGTG |
| C5orf30 | CCTGGGCCATCGTACCTGGA | GAAGGGCAAGGTGGTCAGGG |
| CYLD | GGGCTCATTGGCTGAAGTTA | CGTACAGCCTGCACACTCAT |
| DCAF16 | CAAGCACCTCTGAAGTCTTCTC | GGAATGACGGGATGAGCTGT |
| DEPDC1B | CCCAGTGAGGCCAGTTGTGA | CTCTGTCAGCTGTCTGCGGT |
| DLST | TCTGAAGGAGGCCCAGAATA | ATGCCGACATGAAGCCTAGT |
| ERCC8 | GGAGACCAGGAAACTGCTAAT | GTTGGTACTAGAGGACCCAAAG |
| FAM162A | ACCTACGGATTGGCAGAAAA | ACCGTCAGGGCAATCATTAG |
| FLAD1 | CTAGGGCCTCTGAACTTTCTC | GTGTTGGTGTCCTGAGTGT |
| GOT2 | ATCCGTCCCATGTATTCCAA | TGAGGTTGGAGACCAGTTGA |
| HLA-A | TGGAGCTGTGATCACTGGAG | AGGCAGCTGTCTCACACTTT |
| DDX46 | GCTGAGCTGAAAAGAGGTGCT | GCGCATGACCTGGGGTTCAA |
| IGF2BP3 | GCACGGGAAACCCATAGAA | CAGCACCTCCCACTGTAAAT |
| ITGA2B | GCTCTATGGGCGATTCGG | CCAGGAACACCAGCACTTG |
| KCTD7 | AGGGCCGGTACTTCATCGAC | ACCTTCTCGCCCTTCAGTGG |
| KLHL7 | CTGGATGCAGCAAACCAATATC | CACTCCGCTAGCACACTTATAC |
| LAMB2 | ATTTGGTGCCCAAGGATGA | GATGCAGCTTGTAGGAGATACC |
| LRRN4 | GTCGCCACACACATCTTTCA | AGGAGCCAAGACAAGTCACA |
| MED13 | TGGAGTGTGGGAGAATGGACTT | GGTGAAGGAGCAGGACAAGTG |
| MLX | TCCAGTCCTTCAATGCCTCC | GCAGGACGCCAATCACAATC |
| MRPS5 | GCGGGACGGCAGGTCATTTA | TCAAGCTGGCGTAGGGATGG |
| MRVI1 | CGACGTCTCTTCACCTCACC | CCTGCCCTGAGACACTTTCC |
| NAGLU | GCACATCAAGCAGCTTTACCT | CAACTGCCCATCTTCGTGAC |
| INTS2 | TGCCTGGTTCTTGTGTCTCT | CTTGAGGGCCTGAGAAGGAT |
| KPNA1 | GCTTGGGCCATCACAAATG | ATCACAGAGCGGCTTGATAC |
| NCAPG | GTCCACATAGAGAAGAATGATGCTG | AGTCCACAGCATCCCAAGCATA |
| NFKB2 | TCCCACTGTCAAGATCTGTAACT | CCAGGTTGTTAAATTGGGCAG |
| NMD3 | AACCACCAGGAACTTGGATAC | CATCTACAAGCCGTACCTTACTC |
| NOD2 | AGGTGTATGTTCTCTCGCAGA | GGAGCCAGACTTCCAGGATG |
| NUP54 | GGACTGGGATTTGGAGGATTT | CTTGTGTAGGCTGACTGAAGAG |
| PARP9 | GCCAAAGACCATGTAAAACACC | GCATCTTGGACCTCTTTGCC |
| PBXIP1 | ACAGAGCCTGCCTTCAAC | GTCCACGTCGGTGTCATC |
| PCBD2 | AAGCAGCAGGATGGTCGGAA | GCTTGTAGGGCAACTCGGGA |
| PGF | GGCCTTGTCTGCTGGGAA | CAGGATGGGCTGAACATGTG |
| PGS1 | GACAACAGCGTCATCTTGAGCG | AAGAAGTCGGCAATCTCCGCAC |
| NFATC2IP | CCTTCGCCTTATCCCAGATG | GTCCTCAGCTTTGTCTTCCAG |
| P4HTM | GATGACTCCAGAGAGCATTCAG | CGAAGGTCCATGTTGGAGAA |
| POLR2A | ACTGGCTGCTTGGGGAGATT | GGCAGGTTCTCCAAGGGACT |
| PPIP5K2 | CGAAGACGCAGATCAGGGGA | CCGCACAGTGAGACCCTACA |
| RABGEF1 | GTTACGCCTCAGATGCTGTGTG | TCGAGGCACACGCTTGGAATCC |
| SAR1B | CCGAAGAACTGACCATTGCTGG | GACTCTAACAGCCTTTCGTGGTC |
| SH2B1 | GAGCTGTCCTGCCTGAATCA | ATCGAGTCAAAATGGGAGGC |
| SLC25A20 | CGTGTGCTTCTTTGGGTTTG | CTGTGGTGAATACGCCAGATAA |
| SPNS1 | ATAGTGGCGGTGCTGTGCTACA | GATGAACACGGTCTGGATGAGC |
| SOCS4 | GCTCTCCAGTGACTTCCGTT | GCAGGAAGTTTCTTCTGGGC |
| SLC38A7 | TAGCCCAAACTCTTCCCTCTGC | CACCTGTTTGGGGCTGTTAGC |
| SBDS | TGCTCACATGAGGCTTCGGT | CAGCCCGGGTCAATCAGACA |
| SULT1A1 | TTCCCAAGAGCTCAGGAACAT | ACCCCCTTCACGTACTCCAG |
| TPST1 | GTGTCTCTGTCAAAAGTGGAGA | TGGGTTGGCATATGGGTCAT |
| TUFM | GTGCCCTTGAGGGTCGG | CGCTCTAGTGTACCTGTCACC |
| C4orf27 | TCGCTTGAACAGAGAACCGTGA | TGGAACAACCAAGCCTGCAC |
| FAM134C | TTCTGCTGTCCTACTTGATGCT | GCGGCGTAATTGTCTCTCTCT |
| SFRS2IP | GACCTCGGTCTGAGGAAACCC | ATTGGGCATCTGTCAGCCTCA |
| CCDC101 | GTCTGCCGATTCCCGCATTG | TGCATCCGCTCATGGGTCTT |
| C6orf192 | GCGCACCAGGAGGTGATGAT | TGCTGGCTCCCTTCTTTTCAG |
| ZNF192 | TCTGAGGCAACCCAACATAAA | CTGGTCTCCAGAACTTCCTTTC |
| CRCP | CCTGTGACTGCTGTGGAGAT | GGTGACGGTGTGGAGAAGAG |
| RPP21 | GGGAGCCAAGCAGATTCCA | AGGAAGGCGGTCTGAAATGG |
| PPP1R11 | AGGGAAGGGTGTCTCATCC | AGTTTGATGGTAAGGCTCCG |
| B3GALNT1 | CCTGTTGGCTCTTCCCGCT | GCGAGCCGAAGGTTCTTTACAC |
| BCL7C | GGGCCAAGAGAGAGATCCCG | CAGGTGGCACTGGCTCAAAGA |
| DCUN1D1 | AGGCCCAGATACCCAAGATG | AGCACTAAGTTCCAGTAGGCA |
| DLGAP5 | GGGTTGTGAGGGTTCCTGCT | CCTTCCTGTGTCGACTGGCA |
| EFNA1 | GAAGTTCCAGCGCTTCACACC | TTCAACCTCAAGCAGCGGTC |
| KCNN3 | ACTCCATGTTTTCGTTGGCC | GTAGGTCATGGCTATCCGCC |
| NDUFAF3 | TAAACGGAAACCGCGTGCTC | ACCACCACGATCTCTATCCG |
| PPM1L | GTGTACTCCATCCAGGGCCG | TATTCAGCTGCAGTCTCTCCCC |
| PRSS3 | ACTGCTACAAGACCCGCATC | ATTGATGACGGCAGGTGAGG |
| QRICH1 | CGGGTCACTCCACTTGGCTAT | TGAGGGTGGTCAGCAAGGTG |
| HIST1H2BN | AGCGGTAGGTTGACAGAGC | CGGGCATGACTGGGAGTAAC |
| DPM3 | ACGTGGGGTAGAGTGACCAT | ACACGATAGCCCACAGTGCC |
| SLC41A1 | GTGTTGTACTCGGGCTGGGA | AGATTGCCCCCAACACCATT |
| TXNDC15 | AGGTGAACTGTGAGGAGAGA | ACGGGGTGTAAAACAGGACT |
| TYW1 | TCTTTGTGTCTGGAGTGAAGATT | AGTGTATGTCGCAACCAGGA |
| UBE2R2 | GTGGCACCCCAACATTTATGAG | CATCGACATTGGCTGGGGAG |
| WDR5B | AGTTTCGGTGGCTTCGTAGG | CCTCCCCAGGTCGAAATGTT |
| ZBTB4 | GAAGTACCCCTGCCGCTATT | GCTGGTGGGTCTTCAGGTTA |
| ZBTB7B | TTCTTCCCACACTGTGAGCC | GCTCCCCATCTTCTCCTCTCA |
| ZNF646 | GGCTGCAGTTAGGGCCTTGG | GTCCTCCATGGGGCAACGTA |
| ZNRD1 | GCCGATGAAGGGCAAACTGT | ACCAGACAGGATGGACAAGGC |
| ZSCAN16 | GTGCACACCATCCAGAGACT | CATATGGCCTTCCCAAGGGG |
| UBAP2 | AACAGATGCGTCTCGCTCAA | AGGGCCACTATGCATTCATCC |
| ZNF514 | CATTCTGGGCCTTCTAGTATCC | GACCTTCTCTTCCAGTCTGAGT |
| KIAA1967 | TGGGAGCTCAGCCTCAGTTG | GCCCGCTGTTTGCGTTTCTT |
| RAG1AP1 | CACGGAAGTCAACAACCTGGG | GAGCACAACACGCTTCCGAG |
| CLK2 | CAAGGAAGCAGCTCGACTTG | GGGTAGGGCAGGTAGTTGTT |
| KIAA1267 | CCCCAGAGCATACAACAGAC | GACAGGTCTGAGTGCTCCAC |
| EFNA3 | ACAGCCCCATCAAGTTCTCG | GAGTGGGCGTGGAGATGTAG |
| WNT3 | TCCACTGGTGCTGCTACGTC | CAGCCACACACTTCACCCCT |
| SCAMP3 | CAATTGGCCCCCTCTACCTT | GCGCCATTGTTGGTTTCCAC |
| GBA | ATTTGGAGGGGCCATGACAG | ATGGAGAAGTCACAGCTGGC |
| KIAA0317 | TTGCTGGCCCAATATCGGCT | TGCCATGAGCCACCAACAAC |
| C7orf30 | TCGGACGCGGCAGATCATA | ATGGCATGTAAGTGTCGGGT |
| VKORC1 | GGACAGGACAGCATCCTCAATCA | TGTCCGCAGGCAACCTAACAA |
| ATXN2L | AGTTCACCGATTCAGCCATTG | GTCTTCACACCGTAGTTCTCC |
| DTX3L | TGCTGTGGATTCCTGTCTCC | GGAAGTCACCACACACCTTC |
| FBXL19 | CCGCTGGATCGAGGATGTTA | CAGGGAGGCATCTGTCAGC |
| FBXO34 | TTGCATCCCACCAGTGTAGT | ACCTGCTGTTAACCTCCCTC |
| GRN | GTCCAATCCCAGAGGCTGTC | CTGGGGTGGGATAAGGAAGC |
| MAPK1IP1L | GTCCTTATCCAGCCCCAACT | ATACTGCCCTCCCATTCCTG |
| NDUFAF2 | GCAGTACAAGAACTGGAGAGGACA | CCAAGCTTCCCATTCTGTTGGA |
| NOL4 | GGCGAGAGAAAATGGAAGCA | CTCCGAATCGTCATGGTCCT |
| PDLIM2 | GGAAGTCTTCAAGATGCTGCA | GTGCCACCTCTCTCCTCAG |
| SLC45A3 | GGGGTAGAGGAGAAGTTCATGA | AGAAAGAGGCTCAGCAGGAT |
| C8orf58 | GTCCTGCTCAACCGGATCT | CGTTGCTTCTTAACCACTAATGA |
| TUBG1 | CCCCACCCAGGTCCACAA | CATACTGGCGACAGGTTCTCT |
| ZNF165 | CCCTGTCCGAGAGATGGCTAC | ACTGCCTAAAAAGCTGCCTGC |
| C7orf42 | TGGTATTCACAGCCTGCATG | GCGTATTTTGTGTTGGCATCTC |
| SYT17 | AGAACTGAGAGGAAGCTGACTA | CCCACTGAGCTTGTGATCTATG |
| ADAM15 | ATCGATGCCAGCGTGTGGAT | GCAGTGCCTGTTGCTGTCAC |
| BST1 | CCCTGAGCGATGTTCTGTATG | CTTCTGATGTAGGGCAGGATTG |
| CKS1B | GACGACGAGGAGTTTGAGTATC | CGCCAAGATTCCTCCATTCA |
| FDFT1 | CAACTCTATGGGCCTGTTTCT | CATACCTGCTCCAAACCTCTT |
| FDPS | AGGAATTGATGGCGAGAAGG | CCCAAAGAGGTCAAGGTAATCA |
| GALC | GCTCTGACTGATGGCTTAGG | AGGAAGAAATGGCCGTATGC |
| GCH1 | CCTGGAAGCTGTTGCCTTAT | TGTGTTTCTGTGGAGGAGTTG |
| ITGA8 | GTGAGCCTGCAAATCAACATC | CCTCTTCTGGTTCCCAGTTATG |
| MAP4K4 | ATAGCCAGGCAGGACAGAGA | CTGAGTTGCTGGACCCTGAG |
| MCCC1 | GCACATGATCAATTCTCTCCATTT | CCATCTTTAAGAGTCATGTTTCTGG |
| MTX1 | ACAAGATCATCACCCACCTTCG | GACATGAAGGCCAGGGTGTCT |
| NUCKS1 | CAGCTATGCTGACTGACACTAC | ATCTGAGGTGAGGAGGACTAAA |
| PMVK | CTTTGACTGGGTCATCGAGAA | GACTAAAGTCTGGAGCGGATAAA |
| RUSC1 | CAGTGAGTGTGTTGGCTCTT | CTATGGGTTTGCACCATCCT |
| SHC1 | CCAAGAAGGTGAGTGCTTGT | GAAGCCCAGAGGTGTGATTT |
| STX4 | GATGGTGTCTGATGAGGAGTTG | CTGCGTGTCCTTCAGGATATT |
| THBS3 | ACATTCGGGTGAAGCTCTATG | TCTTGGGAGAAGCAGAATAC |
| WDHD1 | GAGGAGGAAGATGGTCAAGAAG | CGGTGTAGAACCTGACTGAAA |
| WDR6 | GGGCATCTGCGGATGATAAA | CTCCAAGTCAAGGTCTCCATTAG |