Primers and fold changes of the 50 selected genes for qPCR validation

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene name | Forward primer (5' to 3') | Reverse primer (5' to 3') | qPCR.FC.D14 | RNA-seq.FC.D14 | qPCR.FC.D10 | RNA-seq.FC.D10 | qPCR.FC.D8 | RNA-seq.FC.D8 | qPCR.FC.D5 | RNA-seq.FC.D5 | qPCR.FC.D7 | RNA-seq.FC.D7 |
| *TNFRSF10D* | GTTGGCTTTTCATGTCGGAAGA | CCCAGGAACTCGTGAAGGAC | 0.772094921 | 0.552671625 | 0.534486856 | 0.437203331 | 0.644877012 | 0.717783757 | 0.183163997 | 0.202984105 | 0.54749965 | 0.427290639 |
| *RNASE1* | ACTGTAACCAAATGATGAGGCG | GTACCTGGAGCCGTTTGTCA | 0.224636611 | 0.124310096 | 0.497083233 | 0.206403406 | 0.382688527 | 0.256448189 | 0.287744424 | 0.335601912 | 0.282457831 | 0.171429697 |
| *SCG2* | ACCAGACCTCAGGTTGGAAAA | AAGTGGCTTTCATCGCCATTT | 0.267667271 | 0.233486448 | 0.218306572 | 0.145675174 | 0.406854065 | 0.363346778 | 0.083449075 | 0.087535695 | 0.382167256 | 0.236351419 |
| *TYROBP* | ACTGAGACCGAGTCGCCTTAT | ATACGGCCTCTGTGTGTTGAG | 0.187754055 | 0.081133258 | 0.682737306 | 0.288086757 | 0.496751687 | 0.954998635 | 0.310819975 | 0.280537969 | 0.427689953 | 0.213956034 |
| *FCER1G* | AGCAGTGGTCTTGCTCTTACT | TGCCTTTCGCACTTGGATCTT | 0.1144839 | 0.219056537 | 0.532472289 | 0.363228472 | 0.460116065 | 0.369523674 | 0.307352609 | 0.226114278 | 0.340364154 | 0.420828677 |
| *HOXB7* | TTCCCAGAACAAACTTCTTGTGC | GCATGTTGAAGGAACTCGGCT | 0.035417953 | 0.628877184 | 0.424685361 | 0.233135962 | 0.905227206 | 0.483695638 | 0.317741688 | 0.359173942 | 0.335576984 | 0.004444384 |
| *SPP1* | GAAGTTTCGCAGACCTGACAT | GTATGCACCATTCAACTCCTCG | 0.119877256 | 0.092165121 | 0.381671083 | 0.187674462 | 0.463819052 | 0.359135224 | 0.311497097 | 0.277075345 | 0.267266983 | 0.198303247 |
| *INHBA* | CAACAGGACCAGGACCAAAGT | GAGAGCAACAGTTCACTCCTC | 0.401721528 | 0.329829347 | 0.343017059 | 0.282096965 | 0.803777367 | 0.879542734 | 0.565309644 | 0.520837322 | 0.191327737 | 0.139092324 |
| *FUCA1* | GAAGCCAAGTTCGGGGTGTT | GGGTAGTTGTCGCGCATGA | 0.045719216 | 0.492397196 | 0.32527535 | 0.374000476 | 0.589518078 | 0.543087234 | 0.125324549 | 0.387342863 | 0.566190496 | 0.320510288 |
| *IL33* | GTGACGGTGTTGATGGTAAGAT | AGCTCCACAGAGTGTTCCTTG | 0.552800697 | 0.390958835 | 0.763811585 | 0.571076194 | 0.254248146 | 0.222642465 | 0.153028204 | 0.114294186 | 0.236136164 | 0.143466998 |
| *CCL2* | CAGCCAGATGCAATCAATGCC | TGGAATCCTGAACCCACTTCT | 0.608279277 | 0.377572346 | 0.374521804 | 0.214034295 | 0.388801054 | 0.487779243 | 0.274456595 | 0.292691452 | 0.559305412 | 0.680624081 |
| *IL6* | ACTCACCTCTTCAGAACGAATTG | CCATCTTTGGAAGGTTCAGGTTG | 0.481887341 | 0.274840067 | 0.323998786 | 0.33180777 | 0.472658769 | 0.49781895 | 0.404006799 | 0.42417837 | 0.421352643 | 0.266856552 |
| *ENC1* | GCTGCTGTCTGATGCACAC | AGAGTTGCACTACCATGTCCT | 0.417663516 | 0.146991015 | 0.37480596 | 0.285116922 | 0.469459587 | 0.508187668 | 0.528333641 | 0.390176247 | 0.254814266 | 0.145116475 |
| *CD74* | CCGGCTGGACAAACTGACA | GGTGCATCACATGGTCCTCTG | 0.347596352 | 0.182214156 | 0.497017081 | 0.181914774 | 0.584208017 | 0.448271551 | 0.472742928 | 0.324101405 | 0.468406269 | 0.24049948 |
| *MCAM* | AGCTCCGCGTCTACAAAGC | CTACACAGGTAGCGACCTCC | 0.301119719 | 0.217368875 | 0.490659539 | 0.128720503 | 0.466479365 | 0.277791238 | 0.286034721 | 0.388328883 | 0.414202595 | 0.207058172 |
| *CDC20* | ATCTGGAATGTGTGCTCTGG | CCTGAGATGAGCTCCTTGTAATG | 4.649827093 | 3.339881139 | 3.140922214 | 2.780965004 | 3.160741524 | 3.526285687 | 14.73622292 | 17.4259159 | 3.265618217 | 2.177696604 |
| *CDK1* | GGATGTGCTTATGCAGGATTCC | CATGTACTGACCAGGAGGGATAG | 2.527397953 | 2.072922071 | 2.966232102 | 2.702226926 | 3.024288485 | 3.643557062 | 9.719896888 | 11.39609736 | 3.361519966 | 2.031537271 |
| *BIRC5* | AGGACCACCGCATCTCTACAT | AAGTCTGGCTCGTTCTCAGTG | 2.992048424 | 3.482257961 | 2.146808041 | 2.37811387 | 2.539652655 | 3.747816542 | 11.25689328 | 11.01648718 | 2.693535753 | 1.797252625 |
| *CDKN2C* | GGGGACCTAGAGCAACTTACT | CAGCGCAGTCCTTCCAAAT | 2.135217333 | 1.360281559 | 2.772705525 | 2.799099923 | 2.38385403 | 2.06763129 | 5.981644814 | 5.456339835 | 3.057367686 | 2.003751425 |
| *CENPF* | GTGGAATATGGGAGAATGGTAGAG | GTGTCTTCTGCAGGGTGAATA | 3.864576666 | 3.113061356 | 2.284029192 | 2.07843765 | 2.581039726 | 2.911723609 | 10.83471281 | 14.64977199 | 3.166609728 | 2.571658699 |
| *AURKB* | CAGTGGGACACCCGACATC | GTACACGTTTCCAAACTTGCC | 1.985111856 | 1.435744388 | 3.576639243 | 2.967937192 | 3.024292485 | 3.363360014 | 7.052923581 | 14.57154509 | 3.391766002 | 2.271491309 |
| *KIFC1* | TCTGGGTGGTAGTGCTAAGA | AGGCAAAGCGTAGAGAGTTG | 2.979004652 | 2.043194939 | 3.193771681 | 2.452249249 | 3.606046726 | 2.121871816 | 11.39102783 | 12.36317294 | 3.206626542 | 2.187126296 |
| *FHL1* | TGCTGCCTGAAATGCTTTGAC | GCCAGAAGCGGTTCTTATAGTG | 2.421723302 | 1.493811176 | 3.46239037 | 2.439361839 | 2.501133813 | 2.085616269 | 9.516206353 | 7.469328996 | 7.001417653 | 4.13807738 |
| *DLGAP5* | AAGTGGGTCGTTATAGACCTGA | TGCTCGAACATCACTCTCGTTAT | 4.168099594 | 3.061867004 | 2.298734738 | 1.487081662 | 2.62358681 | 2.552068471 | 15.64704783 | 15.64515963 | 3.444360795 | 2.500638457 |
| *KIF2C* | TTAGGAAACGCCCACTGAATAA | GGTTCATGTACCAAGAGGAGAC | 3.934061582 | 3.423181556 | 4.140477219 | 2.066097194 | 3.599887668 | 2.835096169 | 13.35128653 | 12.36635111 | 3.644567074 | 2.422551863 |
| *MKI67* | ACGCCTGGTTACTATCAAAAGG | CAGACCCATTTACTTGTGTTGGA | 4.269675373 | 3.094355712 | 2.983390066 | 1.433712951 | 3.21897985 | 2.41855865 | 18.24120179 | 14.37448823 | 3.218942968 | 2.45718857 |
| *BUB1* | ACAATCAACGGAGAAAGCATGA | CTCCACCACCTGATGCAACT | 2.792350954 | 3.268601872 | 2.49026309 | 1.422025659 | 2.744452133 | 2.433857908 | 9.618754293 | 10.24853289 | 2.730464256 | 2.119958639 |
| *BUB1B* | TGGCACTTGAGAAAGAAGAAGA | CACCTCCTACACGGATGATTG | 5.556377482 | 5.686740566 | 2.810414754 | 1.092090182 | 2.542740178 | 2.903089777 | 15.32112245 | 10.76969099 | 3.275987739 | 3.028753541 |
| *NCAPG* | TGGTGTGCCCTTTGTGAATA | CTGGAATGCTCTGGATGTAACT | 3.37890148 | 2.904752285 | 3.226066333 | 2.239270323 | 3.20129076 | 2.313001853 | 13.37259105 | 8.250975465 | 3.332600909 | 2.426409043 |
| *KIF11* | TCCCTTGGCTGGTATAATTCCA | GTTACGGGGATCATCAAACATCT | 2.191329896 | 1.810965413 | 2.781789363 | 1.890412018 | 2.984615668 | 2.565581014 | 11.88571528 | 9.774117455 | 3.663136091 | 2.02013623 |
| *CDCA8* | CTTCGCCCTTGGAGGAAACAA | GGTGTCTGAATAGCTTCTGCTG | 1.39255985 | 2.538139411 | 2.315945426 | 2.367993193 | 2.983199433 | 2.481529828 | 4.594222848 | 11.63673039 | 3.224612262 | 2.281483843 |
| *GTSE1* | CGGCGAGATTCCTGTCTAAAT | GCGAAAGCTTTGGTGTTGAG | 2.58300825 | 3.397399714 | 2.792766923 | 1.830394635 | 3.013046132 | 2.598329074 | 7.62376939 | 10.46382146 | 3.179146502 | 2.077675013 |
| *CKS2* | TTCGACGAACACTACGAGTACC | GGACACCAAGTCTCCTCCAC | 2.004224513 | 1.767552437 | 2.228732232 | 4.617476112 | 2.415768013 | 5.270196825 | 5.644990411 | 4.808163435 | 3.008973802 | 1.645907277 |
| *TTK* | GCCACCAGAAGCAATCAAAG | ACATCCTAAGGACCAAACATCA | 2.293106139 | 2.673798791 | 2.754816119 | 2.049424661 | 2.637344434 | 1.902895793 | 8.251891093 | 13.67685596 | 3.801709929 | 2.424687499 |
| *FAM83D* | GGGAAGGTTCACGAAAAGTTCA | GACTGGGCATACAGGATTCGG | 2.884982457 | 3.404493169 | 2.995874719 | 2.303648106 | 2.918040842 | 2.968554265 | 13.95134741 | 15.93910271 | 3.541919825 | 2.635205974 |
| *NCAPH* | GTCCTCGAAGACTTTCCTCAGA | TGAAATGTCAATACTCCTGCTGG | 1.276923362 | 3.315138052 | 2.681169394 | 2.067399641 | 2.580333463 | 3.131952503 | 5.452639302 | 9.004444174 | 2.879090521 | 2.715145984 |
| *NEK2* | GGATTACCATCGACCTTCTGTT | CTAATTGTCGCCCTCTTCTCTC | 3.374038769 | 5.046107565 | 3.561883499 | 2.824260139 | 3.282667324 | 2.748662134 | 14.21160207 | 15.79354482 | 3.961350706 | 2.535874584 |
| *CENPA* | TTCCTCCCATCAACACAGTCG | CACACCACGAGTGAATTTAACAC | 3.391836246 | 1.402809747 | 3.131364514 | 2.920453646 | 3.07137579 | 7.791206677 | 12.87739481 | 14.77069363 | 4.95807946 | 2.318074304 |
| *ASPM* | GAGAGAGAGAAAGCTGCAAGAA | GAATGACGAGTGCTGCATTAAC | 2.669097401 | 2.158478695 | 2.356897284 | 1.801262133 | 3.226273907 | 2.528889133 | 11.83443685 | 15.61326503 | 3.499858884 | 2.626835954 |
| *KIF4A* | TACTGCGGTGGAGCAAGAAG | CATCTGCGCTTGACGGAGAG | 1.066308332 | 2.286126102 | 1.691316062 | 1.65028387 | 2.532976443 | 3.056499587 | 2.986115479 | 10.83360744 | 2.708681787 | 2.046520621 |
| *CENPE* | GATTCTGCCATACAAGGCTACAA | TGCCCTGGGTATAACTCCCAA | 2.095899783 | 1.678339811 | 1.650453646 | 1.64819896 | 2.936489353 | 1.529314295 | 10.05685988 | 9.038169608 | 3.226536948 | 2.406073908 |
| *CCNB1* | AATAAGGCGAAGATCAACATGGC | TTTGTTACCAATGTCCCCAAGAG | 2.112294526 | 2.303599113 | 1.94203147 | 2.290942467 | 2.614763753 | 2.943813532 | 6.045483053 | 7.918460777 | 2.850469007 | 2.05457515 |
| *KIF14* | CCTCACCCACAGTAGCCGA | AAGTGCCAATCTACCTACAGGA | 3.140712511 | 2.686490648 | 3.651496062 | 2.186289404 | 2.341867139 | 1.974931938 | 7.920146065 | 9.813718895 | 2.910246806 | 2.352349332 |
| *WDR62* | GCCTTCTCACCCAATATGAAGC | GCCACTACGATGTCTTTCTTCC | 1.99902807 | 1.834945968 | 1.945017202 | 1.758747291 | 2.859151076 | 2.359394153 | 5.428945188 | 5.802485688 | 2.902130821 | 2.320751501 |
| *UBE2C* | CCTGTCCTTGTGTCGTCTTT | GGCTCAACCGAGGCTTAAT | 3.077988115 | 3.81837502 | 2.808428862 | 1.77295714 | 2.635197464 | 3.233674599 | 12.47826408 | 13.61534218 | 3.440462002 | 2.25400537 |
| *TOP2A* | GCTACACATTTCCCAGATGAAAC | TAGTGGAGGTGGAAGACTGA | 3.593010694 | 2.92210656 | 3.217044077 | 1.712409198 | 2.798270087 | 2.034823031 | 11.13024719 | 11.06284457 | 3.832309248 | 2.541567557 |
| *NUSAP1* | AGCCCATCAATAAGGGAGGG | ACCTGACACCCGTTTTAGCTG | 2.422128884 | 2.685323163 | 2.103106408 | 1.647655475 | 2.716450711 | 2.400855441 | 9.125590287 | 10.56417369 | 3.588829759 | 1.796051779 |
| *TPX2* | ATGGAACTGGAGGGCTTTTTC | TGTTGTCAACTGGTTTCAAAGGT | 2.584762979 | 2.547301928 | 2.074770574 | 1.440849128 | 2.717086452 | 1.922548728 | 11.32543132 | 11.12840464 | 3.247708618 | 2.21660189 |
| *RACGAP1* | ATGATGCTGAATGTGCGGAAT | CGCCAACTGGATAAATTGGACTT | 1.618934745 | 2.207441715 | 2.360799654 | 1.719205529 | 2.577837541 | 2.357871901 | 5.423347272 | 7.219077239 | 1.962751466 | 1.863346559 |
| *KIF23* | AGAGCAGAAGGGAACAGATTAC | GGTTCTCTCTTAGGACATCCATAC | 3.606919274 | 1.457710977 | 3.462367483 | 1.763727661 | 2.953199352 | 2.638643471 | 11.96287842 | 7.51181639 | 3.377451453 | 2.160311462 |

Gene name: gene symbel; forward primer (5' to 3'): the forward primer sequence; reverse primer (5' to 3'): the reverse primer sequence; qPCR.FC: fold change of gene expression by qPCR; RNA-seq.FC: fold change of gene expression by RNA-seq. qPCR, quantitative PCR; FC, fold change.