**Table A. Genes upregulated in response to both S6K1 and S6K2 siRNA.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Transcripts Cluster ID | Gene symbol | Gene description | S6K1 siRNA  Fold change | S6K1 siRNA  p-value | S6K2 siRNA  Fold change | S6K2 siRNA  p-value |
| 17109714 | SCARNA9L | small Cajal body-specific RNA 9-like | 0,80 | 0,0024 | 0,41 | 0,0212 |
| 16830577 | CD68 |  | 0,66 | 0,0032 | 0,34 | 0,0089 |
| 16868443 | ZNF562 | zinc finger protein 562 | 0,57 | 0,0464 | 0,5 | 0,0158 |
| 16967875 | PARM1 | prostate androgen-regulated mucin-like protein 1 | 0,51 | 0,0286 | 0,25 | 0,0252 |
| 17096728 | ABCA1 | ATP-binding cassette, sub-family A (ABC1), member 1 | 0,51 | 0,0039 | 0,34 | 0,0044 |
| 16777309 | ZDHHC20 | zinc finger, DHHC-type containing 20 | 0,48 | 0,0366 | 0,6 | 0,0181 |
| 17066065 | SLC7A2 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 | 0,48 | 0,0125 | 0,33 | 0,0337 |
| 16937855 | FBLN2 | fibulin 2 | 0,47 | 0,0293 | 0,36 | 0,0409 |
| 16723175 | ARL14EP | ADP-ribosylation factor-like 14 effector protein | 0,47 | 0,0062 | 0,37 | 0,0042 |
| 16974968 | SEL1L3 | sel-1 suppressor of lin-12-like 3 (C. elegans) | 0,46 | 0,0086 | 0,45 | 0,0130 |
| 16873049 | CADM4 | cell adhesion molecule 4 | 0,44 | 0,0468 | 0,49 | 0,0492 |
| 16735557 | SCUBE2 | signal peptide, CUB domain, EGF-like 2 | 0,44 | 0,0092 | 0,39 | 0,0164 |
| 16725619 | SDHAF2 | succinate dehydrogenase complex assembly factor 2 | 0,43 | 0,0228 | 0,45 | 0,0204 |
| 16875274 | TFPT | TCF3 (E2A) fusion partner (in childhood Leukemia) | 0,43 | 0,0482 | 0,34 | 0,0303 |
| 16954576 | VPRBP | Vpr (HIV-1) binding protein | 0,41 | 0,0490 | 0,46 | 0,0211 |
| 17001100 | NR3C1 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) | 0,41 | 0,0428 | 0,29 | 0,0472 |
| 16662123 | ZBTB8A | zinc finger and BTB domain containing 8A | 0,40 | 0,0455 | 0,4 | 0,0328 |
| 17110237 | CASK | calcium/calmodulin-dependent serine protein kinase (MAGUK family) | 0,40 | 0,0296 | 0,5 | 0,0247 |
| 16887993 | MTX2 | metaxin 2 | 0,39 | 0,0069 | 0,33 | 0,0079 |
| 16926029 | TFF3 | trefoil factor 3 (intestinal) | 0,39 | 0,0126 | 0,3 | 0,0099 |
| 16999259 | CEP120 | centrosomal protein 120kDa | 0,38 | 0,0243 | 0,28 | 0,0358 |
| 16841542 | COX10-AS1 | COX10 antisense RNA 1 (non-protein coding) | 0,38 | 0,0383 | 0,34 | 0,0271 |
| 16836457 | RAD51C | RAD51 homolog C (S. cerevisiae) | 0,37 | 0,0046 | 0,15 | 0,0249 |
| 17061048 | UPK3BL|POLR2J3 | uroplakin 3B-like | polymerase (RNA) II (DNA directed) polypeptide J3 | 0,37 | 0,0418 | 0,62 | 0,0441 |
| 16723614 | CD44 |  | 0,37 | 0,0249 | 0,26 | 0,0250 |
| 17014562 | QKI |  | 0,36 | 0,0229 | 0,42 | 0,0004 |
| 16698556 | SLC41A1 | solute carrier family 41, member 1 | 0,36 | 0,0247 | 0,23 | 0,0230 |
| 16860678 | LSM14A |  | 0,36 | 0,0374 | 0,39 | 0,0006 |
| 16687418 | TMEM48 | transmembrane protein 48 | 0,36 | 0,0010 | 0,42 | 0,0125 |
| 16989054 | RAD50 |  | 0,35 | 0,0361 | 0,28 | 0,0191 |
| 16771962 | SBNO1 | strawberry notch homolog 1 (Drosophila) | 0,35 | 0,0108 | 0,37 | 0,0217 |
| 16943548 | ALCAM | activated leukocyte cell adhesion molecule | 0,35 | 0,0076 | 0,38 | 0,0145 |
| 16692724 | ANP32E | acidic (leucine-rich) nuclear phosphoprotein 32 family, member E | 0,35 | 0,0346 | 0,38 | 0,0099 |
| 16700370 | PGBD5 | piggyBac transposable element derived 5 | 0,34 | 0,0093 | 0,4 | 0,0111 |
| 16671457 | IL6R | interleukin 6 receptor | 0,34 | 0,0353 | 0,21 | 0,0220 |
| 16940110 | SACM1L | SAC1 suppressor of actin mutations 1-like (yeast) | 0,34 | 0,0329 | 0,28 | 0,0201 |
| 16844356 | TNS4 | tensin 4 | 0,34 | 0,0129 | 0,49 | 0,0131 |
| 16918996 | SOGA1 | suppressor of glucose, autophagy associated 1 | 0,33 | 0,0361 | 0,28 | 0,0253 |
| 16929509 | HMGXB4 | HMG box domain containing 4 | 0,33 | 0,0243 | 0,31 | 0,0065 |
| 16730340 | CEP57 | centrosomal protein 57kDa | 0,33 | 0,0167 | 0,19 | 0,0148 |
| 16922292 | SON |  | 0,33 | 0,0116 | 0,39 | 0,0483 |
| 17093762 | TLN1 | talin 1 | 0,32 | 0,0107 | 0,41 | 0,0231 |
| 17000079 | SAR1B | SAR1 homolog B (S. cerevisiae) | 0,32 | 0,0426 | 0,34 | 0,0096 |
| 16822868 | MSRB1 | methionine sulfoxide reductase B1 | 0,32 | 0,0061 | 0,3 | 0,0489 |
| 16951601 | TOP2B | topoisomerase (DNA) II beta 180kDa | 0,32 | 0,0165 | 0,33 | 0,0017 |
| 16757831 | CCDC64 | coiled-coil domain containing 64 | 0,32 | 0,0184 | 0,35 | 0,0268 |
| 16906534 | STAT1 | signal transducer and activator of transcription 1, 91kDa | 0,31 | 0,0456 | 0,3 | 0,0346 |
| 16853234 | ATP9B | ATPase, class II, type 9B | 0,31 | 0,0037 | 0,33 | 0,0200 |
| 16766318 | PRIM1 | primase, DNA, polypeptide 1 (49kDa) | 0,31 | 0,0106 | 0,36 | 0,0008 |
| 16917173 | MKKS | McKusick-Kaufman syndrome | 0,31 | 0,0189 | 0,29 | 0,0325 |
| 16822356 | LUC7L | LUC7-like (S. cerevisiae) | 0,31 | 0,0388 | 0,32 | 0,0125 |
| 16964731 | LOC93622 | Morf4 family associated protein 1-like 1 pseudogene | 0,31 | 0,0292 | 0,54 | 0,0161 |
| 16670391 | BOLA1 | bolA homolog 1 (E. coli) | 0,31 | 0,0264 | 0,26 | 0,0196 |
| 17084936 | ZCCHC7 | zinc finger, CCHC domain containing 7 | 0,31 | 0,0393 | 0,22 | 0,0296 |
| 16754177 | TMEM19 | transmembrane protein 19 | 0,30 | 0,0008 | 0,27 | 0,0082 |
| 16906440 | OSGEPL1 | O-sialoglycoprotein endopeptidase-like 1 | 0,30 | 0,0067 | 0,27 | 0,0411 |
| 17112269 | ATRX | alpha thalassemia/mental retardation syndrome X-linked | 0,30 | 0,0355 | 0,36 | 0,0389 |
| 16926011 | ZNF295 | zinc finger protein 295 | 0,30 | 0,0196 | 0,34 | 0,0446 |
| 16698425 | RBBP5 | retinoblastoma binding protein 5 | 0,30 | 0,0337 | 0,28 | 0,0059 |
| 16972396 | GALNT7 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) | 0,30 | 0,0129 | 0,17 | 0,0350 |
| 16675354 | CDC73 | cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) | 0,30 | 0,0417 | 0,26 | 0,0054 |
| 17088576 | LOC100288842 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 pseudogene | 0,30 | 0,0077 | 0,48 | 0,0004 |
| 16667608 | HIAT1 | hippocampus abundant transcript 1 | 0,30 | 0,0331 | 0,33 | 0,0478 |
| 17010991 | CASP8AP2 | caspase 8 associated protein 2 | 0,29 | 0,0147 | 0,32 | 0,0296 |
| 16786243 | C14orf169 | chromosome 14 open reading frame 169 | 0,29 | 0,0303 | 0,24 | 0,0460 |
| 16708468 | BTRC | beta-transducin repeat containing E3 ubiquitin protein ligase | 0,29 | 0,0345 | 0,32 | 0,0118 |
| 16714798 | JMJD1C | jumonji domain containing 1C | 0,29 | 0,0048 | 0,31 | 0,0070 |
| 17055937 | OSBPL3 | oxysterol binding protein-like 3 | 0,29 | 0,0043 | 0,21 | 0,0161 |
| 16789258 | KLC1 | kinesin light chain 1 | 0,29 | 0,0219 | 0,18 | 0,0390 |
| 17024578 | PPIL4 | peptidylprolyl isomerase (cyclophilin)-like 4 | 0,28 | 0,0220 | 0,25 | 0,0170 |
| 16667037 | CDC7 | cell division cycle 7 homolog (S. cerevisiae) | 0,28 | 0,0145 | 0,32 | 0,0199 |
| 16857315 | SAFB | scaffold attachment factor B | 0,28 | 0,0372 | 0,36 | 0,0000 |
| 16821614 | COX4I1 | cytochrome c oxidase subunit IV isoform 1 | 0,28 | 0,0135 | 0,2 | 0,0063 |
| 16887702 | ITGA6 | integrin, alpha 6 | 0,28 | 0,0225 | 0,2 | 0,0005 |
| 16772004 | RILPL1 | Rab interacting lysosomal protein-like 1 | 0,28 | 0,0047 | 0,4 | 0,0119 |
| 16732856 | TBRG1 | transforming growth factor beta regulator 1 | 0,28 | 0,0018 | 0,21 | 0,0074 |
| 16914469 | SLC2A10 | solute carrier family 2 (facilitated glucose transporter), member 10 | 0,27 | 0,0108 | 0,25 | 0,0041 |
| 16740797 | MRPL11 | mitochondrial ribosomal protein L11 | 0,27 | 0,0020 | 0,43 | 0,0173 |
| 16781248 | DCUN1D2 | DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae) | 0,27 | 0,0271 | 0,33 | 0,0287 |
| 16890424 | SPAG16 | sperm associated antigen 16 | 0,27 | 0,0335 | 0,29 | 0,0178 |
| 16683061 | USP48 | ubiquitin specific peptidase 48 | 0,27 | 0,0188 | 0,38 | 0,0290 |
| 16909638 | USP40 | ubiquitin specific peptidase 40 | 0,26 | 0,0287 | 0,38 | 0,0348 |
| 16979389 | MAD2L1 | MAD2 mitotic arrest deficient-like 1 (yeast) | 0,26 | 0,0027 | 0,21 | 0,0196 |
| 16902570 | WDR33|SFT2D3 | WD repeat domain 33 | SFT2 domain containing 3 | 0,26 | 0,0154 | 0,3 | 0,0108 |
| 16824690 | ERI2 | ERI1 exoribonuclease family member 2 | 0,26 | 0,0268 | 0,28 | 0,0130 |
| 16969009 | PDLIM5 | PDZ and LIM domain 5 | 0,25 | 0,0263 | 0,26 | 0,0098 |
| 16668891 | LRIG2 | leucine-rich repeats and immunoglobulin-like domains 2 | 0,25 | 0,0023 | 0,42 | 0,0104 |
| 16685482 | YRDC | yrdC domain containing (E. coli) | 0,25 | 0,0202 | 0,36 | 0,0386 |
| 16816479 | CCP110 | centriolar coiled coil protein 110kDa | 0,25 | 0,0289 | 0,25 | 0,0157 |
| 16842766 | SDF2 | stromal cell-derived factor 2 | 0,25 | 0,0162 | 0,22 | 0,0498 |
| 17098642 | ST6GALNAC6 | ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 | 0,25 | 0,0312 | 0,19 | 0,0021 |
| 16838698 | RPTOR | regulatory associated protein of MTOR, complex 1 | 0,25 | 0,0051 | 0,28 | 0,0348 |
| 16964764 | TBC1D14 | TBC1 domain family, member 14 | 0,25 | 0,0278 | 0,23 | 0,0063 |
| 16970673 | PHF17 | PHD finger protein 17 | 0,25 | 0,0127 | 0,4 | 0,0188 |
| 16854904 | PSTPIP2 | proline-serine-threonine phosphatase interacting protein 2 | 0,24 | 0,0117 | 0,29 | 0,0073 |
| 16917655 | CRNKL1 | crooked neck pre-mRNA splicing factor-like 1 (Drosophila) | 0,24 | 0,0426 | 0,25 | 0,0060 |
| 17086784 | CENPP | centromere protein P | 0,24 | 0,0310 | 0,34 | 0,0209 |
| 16824143 | RRN3 |  | 0,24 | 0,0152 | 0,28 | 0,0016 |
| 16697438 | UCHL5 | ubiquitin carboxyl-terminal hydrolase L5 | 0,23 | 0,0397 | 0,21 | 0,0346 |
| 16861647 | KCNK6 | potassium channel, subfamily K, member 6 | 0,23 | 0,0186 | 0,23 | 0,0176 |
| 16974779 | GPR125 | G protein-coupled receptor 125 | 0,23 | 0,0206 | 0,19 | 0,0134 |
| 16923491 | PWP2 |  | 0,23 | 0,0036 | 0,19 | 0,0183 |
| 16918832 | NFS1 |  | 0,23 | 0,0311 | 0,38 | 0,0154 |
| 16937563 | BRK1|LOC100653323 | BRICK1, SCAR/WAVE actin-nucleating complex subunit | uncharacterized LOC100653323 | 0,23 | 0,0405 | 0,15 | 0,0168 |
| 16778433 | ELF1 | E74-like factor 1 (ets domain transcription factor) | 0,23 | 0,0141 | 0,15 | 0,0333 |
| 16852206 | HAUS1 | HAUS augmin-like complex, subunit 1 | 0,23 | 0,0350 | 0,35 | 0,0422 |
| 16686140 | MED8 | mediator complex subunit 8 | 0,23 | 0,0284 | 0,29 | 0,0140 |
| 17021385 | SYNCRIP | synaptotagmin binding, cytoplasmic RNA interacting protein | 0,23 | 0,0117 | 0,25 | 0,0084 |
| 17023592 | MED23 | mediator complex subunit 23 | 0,23 | 0,0443 | 0,21 | 0,0115 |
| 16820289 | NUTF2|LOC128322 | nuclear transport factor 2 | nuclear transport factor 2-like | 0,22 | 0,0077 | 0,38 | 0,0008 |
| 16706586 | C10orf57 | chromosome 10 open reading frame 57 | 0,22 | 0,0262 | 0,32 | 0,0132 |
| 16770733 | MED13L | mediator complex subunit 13-like | 0,22 | 0,0263 | 0,2 | 0,0341 |
| 17015434 | MUTED|EEF1E1-MUTED|MUTED-TXNDC5 | muted homolog (mouse) | EEF1E1-MUTED readthrough | MUTED-TXNDC5 readthrough (non-protein coding) | thioredoxin domain containing 5 (endoplasmic reticulum) | eukaryotic translation elongation factor 1 epsilon 1 | 0,22 | 0,0185 | 0,33 | 0,0002 |
| 16667011 | ZNF326 | zinc finger protein 326 | 0,22 | 0,0373 | 0,38 | 0,0191 |
| 17062915 | TSGA13|COPG2 | testis specific, 13 | coatomer protein complex, subunit gamma 2 | 0,22 | 0,0401 | 0,23 | 0,0284 |
| 17053019 | CUL1 | cullin 1 | 0,22 | 0,0026 | 0,21 | 0,0070 |
| 17061374 | ORC5 | origin recognition complex, subunit 5 | 0,21 | 0,0360 | 0,24 | 0,0451 |
| 16818672 | LONP2 | lon peptidase 2, peroxisomal | 0,21 | 0,0452 | 0,23 | 0,0310 |
| 16886105 | HNMT | histamine N-methyltransferase | 0,21 | 0,0481 | 0,2 | 0,0167 |
| 16886818 | TANC1 | tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 | 0,21 | 0,0427 | 0,29 | 0,0065 |
| 16789509 | SIVA1 |  | 0,21 | 0,0077 | 0,25 | 0,0084 |
| 16715031 | SLC25A16 | solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16 | 0,21 | 0,0024 | 0,46 | 0,0310 |
| 16915804 | C20orf11 | chromosome 20 open reading frame 11 | 0,21 | 0,0011 | 0,24 | 0,0137 |
| 16847996 | HELZ | helicase with zinc finger | 0,20 | 0,0311 | 0,19 | 0,0373 |
| 16681323 | RERE | arginine-glutamic acid dipeptide (RE) repeats | 0,20 | 0,0023 | 0,28 | 0,0409 |
| 16817090 | RBBP6 | retinoblastoma binding protein 6 | 0,20 | 0,0413 | 0,26 | 0,0256 |
| 16802795 | NEO1 | neogenin 1 | 0,20 | 0,0460 | 0,32 | 0,0189 |
| 17023308 | HDDC2 | HD domain containing 2 | 0,20 | 0,0110 | 0,28 | 0,0182 |
| 16753498 | TBK1 | TANK-binding kinase 1 | 0,20 | 0,0375 | 0,35 | 0,0179 |
| 16732067 | CCDC84 | coiled-coil domain containing 84 | 0,20 | 0,0226 | 0,25 | 0,0231 |
| 16780509 | DOCK9 | dedicator of cytokinesis 9 | 0,19 | 0,0080 | 0,27 | 0,0273 |
| 16669963 | GPR89C|GPR89A|GPR89B | G protein-coupled receptor 89C | G protein-coupled receptor 89A | G protein-coupled receptor 89B | 0,19 | 0,0013 | 0,25 | 0,0019 |
| 16868564 | EIF3G | eukaryotic translation initiation factor 3, subunit G | 0,19 | 0,0354 | 0,22 | 0,0178 |
| 17102668 | ATP6AP2 | ATPase, H+ transporting, lysosomal accessory protein 2 | 0,19 | 0,0434 | 0,21 | 0,0092 |
| 17003180 | RAB24|MXD3 | RAB24, member RAS oncogene family | MAX dimerization protein 3 | 0,19 | 0,0052 | 0,28 | 0,0380 |
| 16906509 | TMEM194B | transmembrane protein 194B | 0,19 | 0,0464 | 0,24 | 0,0106 |
| 17012404 | RNF146 | ring finger protein 146 | 0,19 | 0,0404 | 0,2 | 0,0407 |
| 16949611 | IL1RAP | interleukin 1 receptor accessory protein | 0,19 | 0,0499 | 0,2 | 0,0292 |
| 16773046 | SAP18 | Sin3A-associated protein, 18kDa | 0,18 | 0,0346 | 0,14 | 0,0373 |
| 16753712 | CAND1 | cullin-associated and neddylation-dissociated 1 | 0,18 | 0,0174 | 0,26 | 0,0068 |
| 17005922 | ZNF193 | zinc finger protein 193 | 0,18 | 0,0276 | 0,09 | 0,0200 |
| 17066036 | VPS37A | vacuolar protein sorting 37 homolog A (S. cerevisiae) | 0,18 | 0,0413 | 0,21 | 0,0076 |
| 17063448 | LUC7L2|LOC100129148 | LUC7-like 2 (S. cerevisiae) | uncharacterized LOC100129148 | 0,18 | 0,0193 | 0,17 | 0,0295 |
| 16989867 | PAIP2 | poly(A) binding protein interacting protein 2 | 0,18 | 0,0000 | 0,24 | 0,0236 |
| 16889054 | CCDC150 | coiled-coil domain containing 150 | 0,18 | 0,0119 | 0,12 | 0,0015 |
| 17066381 | XPO7 | exportin 7 | 0,18 | 0,0073 | 0,22 | 0,0007 |
| 16973375 | GAK | cyclin G associated kinase | 0,18 | 0,0142 | 0,21 | 0,0193 |
| 16771507 | KDM2B | lysine (K)-specific demethylase 2B | 0,17 | 0,0400 | 0,2 | 0,0139 |
| 17076372 | WHSC1L1 | Wolf-Hirschhorn syndrome candidate 1-like 1 | 0,17 | 0,0376 | 0,26 | 0,0039 |
| 17078342 | TCEB1 | transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C) | 0,17 | 0,0178 | 0,18 | 0,0385 |
| 16808322 | PPIP5K1 | diphosphoinositol pentakisphosphate kinase 1 | 0,17 | 0,0112 | 0,27 | 0,0316 |
| 16804294 | PDE8A | phosphodiesterase 8A | 0,17 | 0,0037 | 0,19 | 0,0183 |
| 16920454 | ZNF217 | zinc finger protein 217 | 0,17 | 0,0479 | 0,31 | 0,0075 |
| 16729611 | ANKRD42 | ankyrin repeat domain 42 | 0,17 | 0,0096 | 0,16 | 0,0111 |
| 16919138 | TTI1 | TELO2 interacting protein 1 | 0,17 | 0,0230 | 0,2 | 0,0195 |
| 16943284 | TBC1D23 | TBC1 domain family, member 23 | 0,17 | 0,0409 | 0,16 | 0,0414 |
| 16837451 | C17orf80 | chromosome 17 open reading frame 80 | 0,16 | 0,0205 | 0,2 | 0,0065 |
| 16878800 | BIRC6 | baculoviral IAP repeat containing 6 | 0,16 | 0,0094 | 0,2 | 0,0200 |
| 16966008 | KLF3 | Kruppel-like factor 3 (basic) | 0,16 | 0,0144 | 0,19 | 0,0034 |
| 17064724 | PAXIP1 | PAX interacting (with transcription-activation domain) protein 1 | 0,16 | 0,0252 | 0,24 | 0,0447 |
| 16916261 | PCMTD2 | protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 | 0,15 | 0,0376 | 0,21 | 0,0247 |
| 16861012 | FFAR3 | free fatty acid receptor 3 | 0,15 | 0,0087 | 0,39 | 0,0281 |
| 16975928 | USP46 | ubiquitin specific peptidase 46 | 0,15 | 0,0494 | 0,2 | 0,0156 |
| 16841982 | TOM1L2 | target of myb1-like 2 (chicken) | 0,15 | 0,0228 | 0,14 | 0,0437 |
| 16799084 | PGBD4 | piggyBac transposable element derived 4 | 0,15 | 0,0144 | 0,07 | 0,0370 |
| 16977970 | GPRIN3 | GPRIN family member 3 | 0,15 | 0,0325 | 0,3 | 0,0244 |
| 16873632 | SLC1A5 | solute carrier family 1 (neutral amino acid transporter), member 5 | 0,15 | 0,0075 | 0,21 | 0,0092 |
| 16808094 | LCMT2 | leucine carboxyl methyltransferase 2 | 0,15 | 0,0289 | 0,19 | 0,0035 |
| 16880277 | CCDC85A | coiled-coil domain containing 85A | 0,15 | 0,0459 | 0,09 | 0,0484 |
| 16994002 | LPCAT1 | lysophosphatidylcholine acyltransferase 1 | 0,14 | 0,0489 | 0,18 | 0,0154 |
| 16759977 | DCP1B | DCP1 decapping enzyme homolog B (S. cerevisiae) | 0,14 | 0,0043 | 0,12 | 0,0499 |
| 16697686 | ZNF281 | zinc finger protein 281 | 0,14 | 0,0294 | 0,26 | 0,0375 |
| 16855684 | KDSR | 3-ketodihydrosphingosine reductase | 0,14 | 0,0108 | 0,28 | 0,0261 |
| 16669121 | ATP1A1 | ATPase, Na+/K+ transporting, alpha 1 polypeptide | 0,14 | 0,0292 | 0,19 | 0,0261 |
| 16828357 | FA2H | fatty acid 2-hydroxylase | 0,14 | 0,0214 | 0,18 | 0,0389 |
| 16827353 | ZDHHC1 | zinc finger, DHHC-type containing 1 | 0,13 | 0,0246 | 0,15 | 0,0171 |
| 16731084 | SIK2 | salt-inducible kinase 2 | 0,13 | 0,0300 | 0,21 | 0,0302 |
| 16676150 | BTG2 | BTG family, member 2 | 0,13 | 0,0308 | 0,09 | 0,0187 |
| 16915220 | RAB22A |  | 0,13 | 0,0119 | 0,3 | 0,0336 |
| 16670141 | GPR89B|GPR89A|GPR89C | G protein-coupled receptor 89B | G protein-coupled receptor 89A | G protein-coupled receptor 89C | 0,13 | 0,0260 | 0,24 | 0,0009 |
| 16906921 | SF3B1 | splicing factor 3b, subunit 1, 155kDa | 0,13 | 0,0004 | 0,18 | 0,0374 |
| 16825923 | ZNF668 | zinc finger protein 668 | 0,12 | 0,0255 | 0,11 | 0,0207 |
| 16855318 | MEX3C | mex-3 homolog C (C. elegans) | 0,12 | 0,0106 | 0,2 | 0,0291 |
| 16696548 | RC3H1 | ring finger and CCCH-type domains 1 | 0,12 | 0,0065 | 0,18 | 0,0352 |
| 17074490 | PPP1R3B | protein phosphatase 1, regulatory subunit 3B | 0,12 | 0,0180 | 0,19 | 0,0183 |
| 16824400 | PKD1P1|NPIP|LOC399491|LOC100288332|LOC642799|LOC642778|LOC100506193|NPIPP1 | polycystic kidney disease 1 (autosomal dominant) pseudogene 1 | nuclear pore complex interacting protein | GPS, PLAT and transmembrane domain-containing protein | nuclear pore complex-interacting protein-like 1-like | nuclear pore complex interacting protein pseudogene 1 | 0,11 | 0,0147 | 0,17 | 0,0340 |
| 16726336 | PLCB3 | phospholipase C, beta 3 (phosphatidylinositol-specific) | 0,11 | 0,0182 | 0,07 | 0,0005 |
| 16971048 | SMARCA5 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 | 0,11 | 0,0206 | 0,18 | 0,0316 |
| 16958812 | RUVBL1 | RuvB-like 1 (E. coli) | 0,11 | 0,0247 | 0,2 | 0,0134 |
| 16776658 | ATP11A | ATPase, class VI, type 11A | 0,10 | 0,0001 | 0,24 | 0,0218 |
| 16899079 | DGUOK-AS1 | DGUOK antisense RNA 1 (non-protein coding) | 0,10 | 0,0342 | 0,09 | 0,0109 |
| 16760603 | MLF2 | myeloid leukemia factor 2 | 0,10 | 0,0087 | 0,14 | 0,0006 |
| 16801035 | AP4E1 | adaptor-related protein complex 4, epsilon 1 subunit | 0,09 | 0,0483 | 0,28 | 0,0298 |
| 16847117 | MTMR4 | myotubularin related protein 4 | 0,09 | 0,0103 | 0,09 | 0,0198 |
| 16924007 | DIP2A | DIP2 disco-interacting protein 2 homolog A (Drosophila) | 0,09 | 0,0388 | 0,18 | 0,0064 |
| 16890490 | ATIC | 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase | 0,08 | 0,0145 | 0,12 | 0,0042 |
| 16676130 | ADORA1 | adenosine A1 receptor | 0,08 | 0,0073 | 0,14 | 0,0143 |
| 16692787 | ENSA | endosulfine alpha | 0,07 | 0,0491 | 0,15 | 0,0255 |
| 16964050 | WHSC1 | Wolf-Hirschhorn syndrome candidate 1 | 0,07 | 0,0285 | 0,2 | 0,0247 |
| 16824429 | NOMO2|NOMO1|NOMO3 | NODAL modulator 2 | NODAL modulator 1 | NODAL modulator 3 | 0,07 | 0,0358 | 0,09 | 0,0401 |
| 16907488 | RAPH1 | Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 | 0,06 | 0,0497 | 0,31 | 0,0019 |
| 16849194 | PRPSAP1 | phosphoribosyl pyrophosphate synthetase-associated protein 1 | 0,06 | 0,0323 | 0,12 | 0,0205 |
| 16756310 | TCP11L2 | t-complex 11 (mouse)-like 2 | 0,06 | 0,0261 | 0,19 | 0,0036 |
| 17065109 | ERICH1-AS1 | ERICH1 antisense RNA 1 (non-protein coding) | 0,06 | 0,0314 | 0,06 | 0,0146 |
| 16713187 | NRP1 | neuropilin 1 | 0,06 | 0,0057 | 0,27 | 0,0249 |
| 16802605 | LRRC49 | leucine rich repeat containing 49 | 0,05 | 0,0374 | 0,21 | 0,0120 |
| 16677789 | BROX | BRO1 domain and CAAX motif containing | 0,04 | 0,0383 | 0,08 | 0,0321 |
| 16820486 | CDH1 | cadherin 1, type 1, E-cadherin (epithelial) | 0,03 | 0,0380 | 0,09 | 0,0078 |

**Table B. Pathways upregulated in response to both S6K1 and S6K2 siRNA.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| p-value | Term | Term ID | Term description | Genes |
| 2.69e-03 | GO:0044260 | BP | cellular macromolecule metabolic process | CDH1, NRP1, WHSC1, ADORA1, MTMR4, RUVBL1, SMARCA5, PPP1R3B, RC3H1, SF3B1, BTG2, SIK2, ZDHHC1, ZNF281, DCP1B, LCMT2, USP46, PAXIP1, KLF3, BIRC6, ANKRD42, ZNF217, PDE8A, TCEB1, WHSC1L1, KDM2B, PAIP2, VPS37A, CAND1, SAP18, RNF146, ATP6AP2, EIF3G, TBK1, NEO1, RBBP6, RERE, SIVA1, LONP2, ORC5, CUL1, ZNF326, MED23, SYNCRIP, MED8, ELF1, NFS1, UCHL5, RRN3, CENPP, CRNKL1, PHF17, RPTOR, ST6GALNAC6, SDF2, MAD2L1, USP40, USP48, MRPL11, TBRG1, ITGA6, SAFB, CDC7, PPIL4, JMJD1C, BTRC, CASP8AP2, CDC73, GALNT7, RBBP5, ZNF295, OSGEPL1, MKKS, PRIM1, STAT1, TOP2B, MSRB1, SAR1B, TLN1, SON, IL6R, SBNO1, RAD50, QKI, CD44, RAD51C, MTX2, CASK, ZBTB8A, NR3C1, SDHAF2, ABCA1, ZNF562 |
| 1.10e-02 | GO:0031981 | CC | nuclear lumen | WHSC1, ENSA, RUVBL1, SMARCA5, SF3B1, PAXIP1, ZNF217, TCEB1, KDM2B, SAP18, RBBP6, RERE, SIVA1, ORC5, CUL1, ZNF326, MED13L, MED23, SYNCRIP, MED8, PWP2, UCHL5, RRN3, CENPP, CRNKL1, PHF17, CDC7, JMJD1C, CASP8AP2, CDC73, RBBP5, ZCCHC7, PRIM1, STAT1, TOP2B, SON, RAD50, RAD51C, CASK, NR3C1, SDHAF2 |
| 6.39e-03 | BIOGRID:00000 | bi | BioGRID interaction data | CDH1, BROX, LRRC49, NRP1, TCP11L2, PRPSAP1, RAPH1, WHSC1, ENSA, ADORA1, ATIC, DIP2A, MTMR4, AP4E1, MLF2, ATP11A, RUVBL1, SMARCA5, PLCB3, PPP1R3B, RC3H1, MEX3C, SF3B1, RAB22A, BTG2, SIK2, ZDHHC1, FA2H, KDSR, ZNF281, DCP1B, LPCAT1, CCDC85A, LCMT2, SLC1A5, TOM1L2, USP46, PCMTD2, PAXIP1, KLF3, BIRC6, TBC1D23, TTI1, ANKRD42, ZNF217, PDE8A, PPIP5K1, TCEB1, WHSC1L1, KDM2B |

**Table C. Genes downregulated in response to both S6K1 and S6K2 siRNA.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Transcripts cluster ID | Gene symbol | Gene description | S6K1 siRNA  Fold change | S6K1 siRNA  p-value1 | S6K2 siRNA  Fold change | S6K2 siRNA  p-value1 |  |  |
| 17048563 | PEG10 | paternally expressed 10 | -0,63 | 0,0133 | -0,33 | 0,0318 |  |  |
| 17101292 | STS | steroid sulfatase (microsomal), isozyme S | -0,53 | 0,0471 | -0,34 | 0,0100 |  |  |
| 16859205 | UCA1 | urothelial cancer associated 1 (non-protein coding) | -0,50 | 0,0256 | -0,44 | 0,0119 |  |  |
| 16860123 | ZNF486 | zinc finger protein 486 | -0,48 | 0,0138 | -0,32 | 0,0417 |  |  |
| 16920475 | BCAS1 | breast carcinoma amplified sequence 1 | -0,44 | 0,0204 | -0,16 | 0,0497 |  |  |
| 16954761 | GLYCTK-AS1 | GLYCTK antisense RNA 1 (non-protein coding) | -0,42 | 0,0112 | -0,45 | 0,0113 |  |  |
| 16701023 | CHRM3-AS1 | CHRM3 antisense RNA 1 (non-protein coding) | -0,39 | 0,0359 | -0,37 | 0,0117 |  |  |
| 16762655 | KLHDC5 | kelch domain containing 5 | -0,37 | 0,0218 | -0,37 | 0,0190 |  |  |
| 16738333 | TRIM51HP | tripartite motif-containing 51H, pseudogene | -0,36 | 0,0068 | -0,35 | 0,0394 |  |  |
| 16761820 | MGP | matrix Gla protein | -0,36 | 0,0076 | -0,28 | 0,0330 |  |  |
| 16918294 | TSPY26P | testis specific protein, Y-linked 26, pseudogene | -0,33 | 0,0381 | -0,12 | 0,0453 |  |  |
| 16829718 | OR1A2 | olfactory receptor, family 1, subfamily A, member 2 | -0,32 | 0,0082 | -0,28 | 0,0028 |  |  |
| 17029847 | HLA-DPA1 | major histocompatibility complex, class II, DP alpha 1 | -0,28 | 0,0471 | -0,42 | 0,0344 |  |  |
| 17116583 | TTTY4| TTTY4B| TTTY4C | testis-specific transcript, Y-linked 4 (non-protein coding) | testis-specific transcript, Y-linked 4B (non-protein coding) | testis-specific transcript, Y-linked 4C (non-protein coding) | -0,27 | 0,0436 | -0,19 | 0,0386 |  |  |
| 16681468 | C1orf200 | chromosome 1 open reading frame 200 | -0,27 | 0,0447 | -0,25 | 0,0392 |  |  |
| 16754717 | MYF5 | myogenic factor 5 | -0,27 | 0,0039 | -0,31 | 0,0360 |  |  |
| 17104688 | ITGB1BP2 | integrin beta 1 binding protein (melusin) 2 | -0,26 | 0,0038 | -0,19 | 0,0438 |  |  |
| 16916396 | TMEM74B | transmembrane protein 74B | -0,25 | 0,0213 | -0,26 | 0,0491 |  |  |
| 16960771 | KCNAB1-AS1 | KCNAB1 antisense RNA 1 (non-protein coding) | -0,25 | 0,0198 | -0,09 | 0,0406 |  |  |
| 17006649 | LTA | lymphotoxin alpha (TNF superfamily, member 1) | -0,23 | 0,0295 | -0,26 | 0,0162 |  |  |
| 16703563 | BAMBI | BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) | -0,23 | 0,0154 | -0,17 | 0,0008 |  |  |
| 17033327 | LTA | lymphotoxin alpha (TNF superfamily, member 1) | -0,23 | 0,0352 | -0,27 | 0,0172 |  |  |
| 16815918 | TNFRSF17 | tumor necrosis factor receptor superfamily, member 17 | -0,22 | 0,0245 | -0,15 | 0,0220 |  |  |
| 17043355 | AIMP2 | aminoacyl tRNA synthetase complex-interacting multifunctional protein 2 | -0,22 | 0,0267 | -0,12 | 0,0158 |  |  |
| 16960844 | VEPH1 | ventricular zone expressed PH domain homolog 1 (zebrafish) | -0,22 | 0,0457 | -0,15 | 0,0346 |  |  |
| 16841295 | MYH1 | myosin, heavy chain 1, skeletal muscle, adult | -0,21 | 0,0257 | -0,22 | 0,0460 |  |  |
| 17075712 | CHRNA2 | cholinergic receptor, nicotinic, alpha 2 (neuronal) | -0,21 | 0,0438 | -0,26 | 0,0358 |  |  |
| 16800642 | HMGN2P46 | high mobility group nucleosomal binding domain 2 pseudogene 46 | -0,20 | 0,0291 | -0,21 | 0,0406 |  |  |
| 16829880 | GLTPD2 | glycolipid transfer protein domain containing 2 | -0,20 | 0,0206 | -0,21 | 0,0301 |  |  |
| 16881021 | GKN1 | gastrokine 1 | -0,19 | 0,0035 | -0,26 | 0,0194 |  |  |
| 17035408 | LTA | lymphotoxin alpha (TNF superfamily, member 1) | -0,19 | 0,0353 | -0,21 | 0,0121 |  |  |
| 16775626 | POU4F1-AS1 | POU4F1 antisense RNA 1 (non-protein coding) | -0,19 | 0,0117 | -0,17 | 0,0366 |  |  |
| 16946835 | WWTR1-AS1 | WWTR1 antisense RNA 1 (non-protein coding) | -0,19 | 0,0255 | -0,32 | 0,0101 |  |  |
| 16790138 | METTL17 | methyltransferase like 17 | -0,19 | 0,0161 | -0,25 | 0,0180 |  |  |
| 16923675 | KRTAP10-12 | keratin associated protein 10-12 | -0,19 | 0,0364 | -0,21 | 0,0175 |  |  |
| 16874878 | SIGLEC12 | sialic acid binding Ig-like lectin 12 (gene/pseudogene) | -0,18 | 0,0225 | -0,22 | 0,0186 |  |  |
| 17070713 | NECAB1 | N-terminal EF-hand calcium binding protein 1 | -0,18 | 0,0066 | -0,35 | 0,0408 |  |  |
| 17118019 | ATP1B3| LOC100507375 | ATPase, Na+/K+ transporting, beta 3 polypeptide | uncharacterized LOC100507375 | -0,18 | 0,0208 | -0,36 | 0,0004 |  |  |
| 17035225 | MDC1| MDC1-AS1 | mediator of DNA-damage checkpoint 1 | MDC1 antisense RNA 1 (non-protein coding) | -0,17 | 0,0426 | -0,24 | 0,0455 |  |  |
| 17113677 | RHOXF2B | Rhox homeobox family, member 2B | -0,17 | 0,0092 | -0,18 | 0,0314 |  |  |
| 16887463 | SP5 | Sp5 transcription factor | -0,17 | 0,0352 | -0,17 | 0,0138 |  |  |
| 16751420 | GRASP | GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein | -0,17 | 0,0283 | -0,14 | 0,0162 |  |  |
| 17026419 | PSMB9 | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2) | -0,17 | 0,0049 | -0,18 | 0,0257 |  |  |
| 16957807 | POPDC2|COX17 | popeye domain containing 2 | COX17 cytochrome c oxidase assembly homolog (S. cerevisiae) | -0,17 | 0,0365 | -0,16 | 0,0250 |  |  |
| 16835013 | SPPL2C | signal peptide peptidase like 2C | -0,15 | 0,0043 | -0,16 | 0,0307 |  |  |
| 16935994 | SMC1B | structural maintenance of chromosomes 1B | -0,15 | 0,0440 | -0,17 | 0,0378 |  |  |
| 16766283 | PTGES3| LOC100506732| PTGES3P3 | prostaglandin E synthase 3 (cytosolic) | uncharacterized LOC100506732 | prostaglandin E synthase 3 (cytosolic) pseudogene 3 | -0,14 | 0,0432 | -0,07 | 0,0329 |  |  |
| 17000180 | IL9 | interleukin 9 | -0,13 | 0,0312 | -0,09 | 0,0257 |  |  |
| 16724190 | CRY2 | cryptochrome 2 (photolyase-like) | -0,13 | 0,0034 | -0,12 | 0,0031 |  |  |
| 16904514 | SCN3A | sodium channel, voltage-gated, type III, alpha subunit | -0,12 | 0,0272 | -0,11 | 0,0428 |  |  |
| 16916462 | SIRPB2 | signal-regulatory protein beta 2 | -0,12 | 0,0155 | -0,14 | 0,0275 |  |  |
| 16857766 | CLEC4GP1 | C-type lectin domain family 4, member G pseudogene 1 | -0,10 | 0,0169 | -0,1 | 0,0339 |  |  |
| 16800117 | STARD9 | StAR-related lipid transfer (START) domain containing 9 | -0,10 | 0,0208 | -0,11 | 0,0442 |  |  |
| 16954068 | AMT | aminomethyltransferase | -0,09 | 0,0252 | -0,04 | 0,0051 |  |  |
| 17054312 | C7orf50 | chromosome 7 open reading frame 50 | -0,09 | 0,0295 | -0,09 | 0,0268 |  |  |
| 16939755 | ZNF662| KRBOX1 | zinc finger protein 662 | KRAB box domain containing 1 | -0,09 | 0,0309 | -0,14 | 0,0311 |  |  |
| 16981219 | DDX60 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 | -0,08 | 0,0384 | -0,17 | 0,0208 |  |  |
| 16752168 | OR6C65 | olfactory receptor, family 6, subfamily C, member 65 | -0,08 | 0,0075 | -0,17 | 0,0256 |  |  |
| 17020799 | MTO1 | mitochondrial translation optimization 1 homolog (S. cerevisiae) | -0,06 | 0,0005 | -0,05 | 0,0227 |  |  |
| 16881353 | DYSF | dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) | -0,05 | 0,0237 | -0,04 | 0,0421 |  |  |

1From Student’s t-test.