**Appendix table section**

## Appendix table S1. Differentially expressed genes upon SARS-CoV-2 early infection in HEK-293T-ACE2 cells that take part in “Calcium Signaling”.

The “$Ca^{2+}$signaling by reactome pathway” through RNAseq analyses from the differentially expressed genes in HEK293T-ACE2 cells infected with SARS-CoV-2 (VOC Delta, 24 h) *versus* Mock infected cells. Here, 157 genes involved in Calcium Signaling were significantly deregulated by SARS-CoV-2 after 24 h. Data given include gene name, BaseMean (average of the normalized count values), log2FoldChange, lfcSE (standard error), pValue and adjusted p value (padj) are listed. Red, membrane and endoplasmic reticulum $Ca^{2+}$ pumps (i.e., ATP2Bs and ATP2As, respectively).

| **Gene name** | **BaseMean** | **Log2FoldChange** | **lfcSE** | **pValue** | **pAdj** |
|---|---|---|---|---|---|
| EGF | 470.066.492.265.217 | -40.619.336.960.114 | 0.664028018529976 | 7,08E+03 | 1,05E+05 |
| CAMK1G | 364.858.544.902.485 | -340.754.771.922.581 | 0.913198249232395 | 8,34E+08 | 5,08E+09 |
| TNNC2 | 201.384.809.825.337 | -316.776.580.773.799 | 125.621.979.502.456 | 0.000426075476689886 | 0.00177089604329882 |
| KDR | 447.921.773.022.525 | -291.789.785.352.181 | 0.690679824706131 | 1,20E+08 | 8,54E+08 |
| PTGER3 | 2.631.393.772.017 | -259.177.710.593.284 | 0.807666047432124 | 6,24E+09 | 0.000316375821514552 |
| CACNA1I | 869.350.624.213.802 | -245.646.245.246.643 | 0.413068357989845 | 1,64E+04 | 2,27E+05 |
| FGF19 | 595.183.107.293.085 | -24.348.301.365.875 | 0.498409657835589 | 6,06E+06 | 5,46E+07 |
| ATP2B2 | 270.270.787.313.473 | -22.332.018.924.914 | 0.766386590862842 | 0.000168310855505058 | 0.000771084907017115 |
| MYLK4 | 359.196.817.041.812 | -218.249.512.123.712 | 0.653358723896032 | 4,44E+09 | 0.000231472468385037 |
| CACNA1G | 945.542.009.013.953 | -193.464.303.503.756 | 0.183028207937104 | 2,77E-13 | 3,38E-12 |
| NTRK3 | 280.665.734.128.966 | -191.862.731.213.666 | 0.798849668970072 | 0.000742655141446291 | 0.00289573206235725 |
| AVPR1A | 486.965.123.732.544 | -18.995.518.921.901 | 0.577352080972861 | 5,66E+09 | 0.00028951664775388 |
| RYR2 | 163.422.835.354.659 | -189.620.200.301.431 | 0.315137422842955 | 1,23E+04 | 1,74E+05 |
| PRKCG | 549.075.446.715.279 | -177.755.730.324.405 | 0.188372347832613 | 3,09E-09 | 2,15E-06 |
| RYR1 | 809.194.404.057.114 | -169.311.919.230.691 | 0.486468803564657 | 3,24E+08 | 0.000174489336118528 |
| PDGFRB | 324.832.730.647.174 | -166.275.196.192.471 | 0.771626078491638 | 0.00147511758120898 | 0.00532287697789966 |
| NGF | 301.570.589.660.459 | -15.325.074.691.358 | 0.745790834556926 | 0.0020175651560619 | 0.00702354442142255 |
| FGF18 | 298.564.044.685.259 | -148.439.847.088.366 | 0.828292832261265 | 0.00337210418608626 | 0.0110347633464023 |
| CALML6 | 490.099.528.433.961 | -131.370.510.943.569 | 0.825860210839343 | 0.00533449786994513 | 0.0164946648727855 |
| GRIN1 | 157.108.717.534.577 | -128.763.563.304.787 | 0.323378819942514 | 6,46E+08 | 4,02E+09 |
| NTRK2 | 262.623.726.884.291 | -128.054.971.330.727 | 0.243831076403219 | 1,58E+06 | 1,58E+07 |
| NTRK1 | 578.235.945.050.576 | -12.596.871.921.419 | 0.551982314520049 | 0.00162927852165569 | 0.00581799505388285 |
| GDNF | 558.396.367.605.257 | -125.541.837.244.765 | 0.531587287153423 | 0.00137309343890679 | 0.00500164697395093 |
| PHKG1 | 399.138.091.587.535 | -122.304.443.526.309 | 0.632694503323343 | 0.00358227204856374 | 0.0116168708830677 |
| PTGFR | 276.774.110.594.092 | -116.245.612.041.348 | 0.826887731548613 | 0.00858417601832968 | 0.0248084910809525 |
| ADRB2 | 103.466.364.639.335 | -115.829.451.291.408 | 0.424783537150509 | 0.00059891519425065 | 0.0023882746914971 |
| ATP2A1 | 203.108.013.385.034 | -107.280.686.165.945 | 0.262329863906071 | 5,49E+08 | 3,46E+09 |
| ERBB4 | 170.776.039.723.201 | -104.381.160.003.265 | 0.300596363974115 | 6,48E+09 | 0.00032742177194106 |
| CACNA1C | 393.319.540.235.024 | -102.106.063.979.435 | 0.192751646909679 | 1,72E+06 | 1,71E+07 |
| ADRA1B | 591.447.672.206.431 | -101.281.999.512.882 | 0.511038582291448 | 0.00457889299727663 | 0.0144293335681128 |
| SLC8A3 | 95.692.745.140.642 | -0.998473384007727 | 0.410221783240345 | 0.00169667248287767 | 0.00602970050421849 |
| PLCB4 | 853.137.293.137.909 | -0.980318301180731 | 0.140257942056366 | 4,46E+01 | 9,22E+02 |
| HRH1 | 274.954.013.122.704 | -0.960466468918194 | 0.835252217871031 | 0.0151214999321587 | 0.0400493571921168 |
| P2RX2 | 210.012.518.949.649 | -0.906096933837229 | 0.255316025097521 | 6,31E+09 | 0.000319747150885531 |
| CACNA1B | 420.417.802.824.201 | -0.887883543343921 | 0.188611910026867 | 4,54E+07 | 3,47E+07 |
| GRIN2C | 134.980.629.604.766 | -0.861218744558696 | 0.31162870962008 | 0.000932072365025747 | 0.00354992600479506 |
| SLC8A2 | 273.654.190.588.128 | -0.858567119679333 | 0.237358375185696 | 5,37E+08 | 0.000275901884465897 |
| MST1 | 588.954.201.846.589 | -0.829615004504173 | 0.243875246591338 | 0.000125608272597485 | 0.000592232918411347 |
| MCOLN3 | 165.355.435.122.002 | -0.827337601316473 | 0.128096033644867 | 2,26E+03 | 3,64E+04 |
| PDGFB | 116.038.571.818.564 | -0.802905099711672 | 0.413428970321733 | 0.00785763338500944 | 0.0230062180714721 |
| PLCD1 | 606.706.213.146.116 | -0.73419217381745 | 0.211338432292575 | 0.000128480351249161 | 0.000604624576401611 |
| PTAFR | 148.429.292.120.027 | -0.718467868052912 | 0.305326705403937 | 0.00398084691805461 | 0.0127481951469379 |

| | | | | | |
|---|---|---|---|---|---|
| SPHK1 | 425.399.369.213.307 | -0.707202397121825 | 0.201780650419755 | 0.000116061152317301 | 0.000552590774509452 |
| ADRB1 | 655.653.614.469.463 | -0.679205605810754 | 0.472803117372689 | 0.025791562973466 | 0.0629923986317459 |
| FLT1 | 700.355.766.267.359 | -0.669898202668207 | 0.185104262705454 | 8,28E+09 | 0.000409305590749802 |
| AGTR1 | 114.530.552.323.422 | -0.656048536313823 | 0.390155781513432 | 0.0194109134979577 | 0.049664781084052 |
| TPCN1 | 252.604.797.979.172 | -0.600289817556319 | 0.132545750778705 | 2,04E+07 | 1,39E+09 |
| PHKA2 | 175.224.737.675.515 | -0.561183955695007 | 0.120614441069424 | 1,27E+08 | 8,99E+08 |
| FGF2 | 107.171.213.660.927 | -0.52864644155335 | 0.131546499596881 | 2,52E+09 | 0.000138420306528569 |
| ERBB3 | 120.866.178.420.076 | -0.526562320203576 | 0.13331201305227 | 3,35E+09 | 0.000179921804431245 |
| CACNA1D | 336.171.601.170.013 | -0.513843498616443 | 0.231116856688361 | 0.0101629928909175 | 0.0285960922734542 |
| FGF9 | 481.838.217.511.183 | -0.440316618339933 | 0.201003686986393 | 0.0138044691557052 | 0.0370226603357302 |
| ITPR3 | 544.035.684.154.367 | -0.436844916967323 | 0.0858936274580685 | 2,85E+07 | 2,25E+07 |
| BDKRB2 | 432.395.097.685.611 | -0.433653663001909 | 0.497631594097063 | 0.0986511036863904 | 0.187638940694549 |
| SLC8A1 | 522.452.995.997.531 | -0.425640845179831 | 0.209128356637808 | 0.0207771460712456 | 0.0526173559586334 |
| PDE1B | 289.070.207.499.701 | -0.410559888941243 | 0.206926593742145 | 0.0245441014890181 | 0.0604941914017028 |
| VEGFA | 297.506.769.867.281 | -0.405780412554488 | 0.142594980006681 | 0.00247420124223248 | 0.00837757964418323 |
| FGF5 | 79.709.394.383.223 | -0.399984899482115 | 0.356896301574514 | 0.108219512397703 | 0.201880061965315 |
| ATP2B4 | 283.800.562.649.639 | -0.394169016228452 | 0.126855884293042 | 0.00112236419580121 | 0.00418746949373256 |
| RET | 577.232.271.862.126 | -0.353170332880125 | 0.170689077431222 | 0.0239340673097788 | 0.0592338298112563 |
| PDGFA | 579.364.106.716.877 | -0.322941855478592 | 0.173196187829469 | 0.0411391142990746 | 0.0926751594433211 |
| CCKBR | 126.784.008.566.849 | -0.320952603632085 | 0.304055604871576 | 0.161838087141715 | 0.276984470866739 |
| LTB4R2 | 189.584.854.807.253 | -0.313758791468503 | 0.26937952269752 | 0.146164169708267 | 0.255529602755143 |
| MCOLN2 | 113.978.857.145.436 | -0.301788122475556 | 0.137806208277608 | 0.0203855557780396 | 0.0517490197933601 |
| PRKCB | 25.235.847.386.427 | -0.29501851474154 | 0.109946339948008 | 0.00539312477447984 | 0.0166518138449238 |
| CAMK2B | 772.906.926.209.551 | -0.283029002203993 | 0.145730810888778 | 0.0383029245794291 | 0.0874986769446822 |
| PDGFRA | 109.866.805.847.052 | -0.282309320967817 | 0.2972729826783 | 0.211044616859362 | 0.340490350351324 |
| CHRM3 | 560.839.356.409.002 | -0.251888870437173 | 0.160119800958921 | 0.088376618755959 | 0.1719817480213 |
| FGF17 | 16.496.815.745.705 | -0.248096374729555 | 0.249482103006665 | 0.227384140460309 | 0.359420066595756 |
| ADCY7 | 599.531.283.129.749 | -0.242677303099414 | 0.155103300744442 | 0.0923579071335468 | 0.178067513485704 |
| HTR6 | 354.992.109.224.363 | -0.236382187781594 | 0.198583734709514 | 0.179234191122456 | 0.300143455269253 |
| NOS2 | 382.743.199.985.029 | -0.216942472653685 | 0.216414799478264 | 0.246028914267307 | 0.382173021389535 |
| CAMK1D | 115.738.679.551.248 | -0.20243741585522 | 0.144915532772324 | 0.1364996988295 | 0.242143975557365 |
| PTK2B | 3.347.654.773.982 | -0.198541912471893 | 0.198825455813247 | 0.259322322212717 | 0.397481473680127 |
| PLCG2 | 128.718.181.153.958 | -0.146004446908614 | 0.133411235660135 | 0.248733561997342 | 0.385274541913544 |
| CALML4 | 720.412.591.192.242 | -0.142650941830901 | 0.163982197735486 | 0.344385374689041 | 0.489805705022451 |
| OXTR | 148.277.035.788.061 | -0.141149910723466 | 0.274436307642278 | 0.508031589930453 | 0.648622564287605 |
| CHRNA7 | 489.354.993.796.243 | -0.137351331277486 | 0.16799105529875 | 0.373336159701828 | 0.519360460101477 |
| ITPR1 | 194.448.959.208.382 | -0.130765692109194 | 0.135837801130851 | 0.309257090522638 | 0.45335357342098 |
| PHKA1 | 179.591.123.826.724 | -0.125547564416148 | 0.103400902226699 | 0.210340488576319 | 0.339696463309899 |
| ADORA2A | 223.762.626.919.609 | -0.106559430507992 | 0.419538375673638 | 0.476481309897874 | 0.620376663464722 |
| PLCG1 | 699.101.491.751.449 | -0.104642450208333 | 0.0865004261930556 | 0.215520564598944 | 0.345427330349358 |
| FGFR4 | 208.232.993.177.581 | -0.101715568146048 | 0.102865746174184 | 0.308028355572787 | 0.452073453570876 |
| FGFR1 | 499.106.216.692.943 | -0.0923093100011115 | 0.0949481980581863 | 0.304396825481386 | 0.448217896866103 |
| PHKG2 | 314.206.921.479.836 | -0.0911508288462413 | 0.124077121364634 | 0.44208383855371 | 0.587814337568264 |
| ADCY9 | 235.254.942.195.309 | -0.0837295765189726 | 0.0974106513943221 | 0.376355915316127 | 0.522388753677872 |
| FGF8 | 464.562.300.432.542 | -0.0761848939011496 | 0.353716413037013 | 0.713462371093803 | 0.813931531496335 |
| ATP2B3 | 587.586.125.763.348 | -0.0626210328757565 | 0.439048123471953 | 0.0738189363850452 | 0.14885884758557 |
| CXCR4 | 122.446.292.826.757 | -0.0603388356624955 | 0.143329518789903 | 0.655120311029227 | 0.76759630744944 |
| PLCB1 | 994.674.848.651.785 | -0.0589275381309039 | 0.14056687275296 | 0.656669719144886 | 0.768689888118064 |
| MST1R | 165.032.670.287.062 | -0.0494471966447024 | 0.245291459692777 | 0.802995262899111 | 0.878339556478466 |
| CAMK4 | 891.013.810.454.115 | -0.0452814478563072 | 0.177434779926719 | 0.778334345320621 | 0.861379840200812 |
| STIM2 | 95.701.248.136.539 | -0.0390808211180951 | 0.140900346772734 | 0.76820715039287 | 0.854282496755984 |
| PLCE1 | 107.195.402.497.356 | -0.0341801457720718 | 0.145079723037892 | 0.801377847150615 | 0.87713678071911 |
| ITPKC | 70.396.087.492.243 | -0.0284050996316445 | 0.143515642077651 | 0.835382348472484 | 0.901049822420575 |
| ADCY1 | 190.640.441.243.435 | -0.0234347315901111 | 0.129135611085778 | 0.848319232392113 | 0.909983793161546 |
| PPP3CC | 594.164.875.490.275 | -0.0217191364607527 | 0.151752406462586 | 0.877965754946522 | 0.929456415592496 |
| ATP2A3 | 57.861.264.377.674 | -0.0129319930116038 | 0.154240920271403 | 0.926149963731589 | 0.958988807760499 |
| CACNA1H | 345.963.329.850.669 | -0.0119216426741543 | 0.105863576682641 | 0.924981441177746 | 0.958205598411089 |
| GRIN2D | 787.806.074.900.388 | -0.00313600612645953 | 0.165848797099175 | 0.982047635092185 | 0.988873258407805 |
| ORAI3 | 669.964.822.841.849 | -0.0029585841913774 | 0.154784193674808 | 0.980434132269063 | 0.987886621158221 |
| PRKACA | 511.052.546.711.711 | 8,08E+09 | 0.0944525021842156 | 0.992207464272 | 0.995423498362367 |
| MYLK | 499.839.296.301.556 | 0.00232286697512634 | 0.18351714058263 | 0.990738415795618 | 0.99448260200729 |
| FLT4 | 409.216.446.721.523 | 0.0279541004301016 | 0.0953640134258976 | 0.785110815522244 | 0.865849292306412 |
| ITPR2 | 185.378.863.744.044 | 0.02851082365659 | 0.141313453931377 | 0.830830585455922 | 0.898094050005188 |

| | | | | | |
|---|---|---|---|---|---|
| MYLK3 | 403.912.378.245.326 | 0.037299870072606 | 0.345347448460966 | 0.861313219529031 | 0.918180856193811 |
| PRKCA | 370.983.476.105.691 | 0.0516584120737146 | 0.124335893152742 | 0.665347986001177 | 0.776105971436831 |
| ASPH | 570.280.921.671.974 | 0.0628042195081283 | 0.0836495719479821 | 0.418065723667828 | 0.564821627755414 |
| MCOLN1 | 854.203.446.687.649 | 0.0870758272799398 | 0.128577790062911 | 0.478726811743744 | 0.622464822939255 |
| STIM1 | 279.598.609.555.574 | 0.0889388752105342 | 0.0880916879107226 | 0.302797288672749 | 0.446274957562273 |
| F2R | 166.748.356.309.198 | 0.110639447436645 | 0.110393117808017 | 0.300908480333341 | 0.444224780302863 |
| EDNRA | 206.182.690.976.498 | 0.11977237588773 | 0.239855306412242 | 0.583076385014544 | 0.710293050835899 |
| ATP2B1 | 461.626.628.987.639 | 0.138005263348501 | 0.104312447327456 | 0.173826346731307 | 0.29304324553352 |
| PLCB2 | 489.493.216.881.739 | 0.148460461120645 | 0.357200444519728 | 0.498085877010279 | 0.64013790333965 |
| EGFR | 183.157.545.910.826 | 0.15414471676835 | 0.147426537239317 | 0.262530900964082 | 0.401076892043935 |
| CAMK2G | 308.856.140.894.947 | 0.161321439499772 | 0.0861961767053738 | 0.0560495627231519 | 0.119042800166328 |
| TPCN2 | 962.925.542.934.949 | 0.163688229634313 | 0.127735585791043 | 0.180017322232568 | 0.301137783686921 |
| MCU | 232.326.143.842.897 | 0.221045523640019 | 0.0948496793645021 | 0.0166832275403525 | 0.0435548197581096 |
| TBXA2R | 2.791.255.953.813 | 0.221920495895446 | 0.210650643728027 | 0.22896567920061 | 0.361286110716458 |
| GNAQ | 335.459.683.975.552 | 0.224240766827919 | 0.119403166128341 | 0.0505041469254608 | 0.109429738958333 |
| VEGFC | 262.865.606.384.951 | 0.252700671951347 | 0.227767993537088 | 0.195701724209886 | 0.321311440786427 |
| MET | 320.453.265.120.091 | 0.266669221254998 | 0.140882757374689 | 0.0439163404621055 | 0.0976594709508658 |
| GNAL | 167.298.061.304.345 | 0.276532654299546 | 0.114951656898321 | 0.012100979045169 | 0.0331554640153218 |
| PDGFC | 851.803.632.271.765 | 0.277270899831492 | 0.134986267423683 | 0.0305866358113616 | 0.0727059910065298 |
| PLCD3 | 169.699.382.882.478 | 0.281311858492587 | 0.120781708407388 | 0.0150483628998168 | 0.0398840609001914 |
| ITPKA | 31.922.290.961.536 | 0.299758123828119 | 0.236373895471205 | 0.133703915861153 | 0.23828325479496 |
| ORAI2 | 198.370.882.017.582 | 0.307664239516031 | 0.120832479310531 | 0.00778793820930639 | 0.0228296793309466 |
| ATP2A2 | 153.064.511.889.483 | 0.315242341768931 | 0.0910620865403779 | 0.000357803271130382 | 0.00151709402930254 |
| P2RX4 | 670.723.664.696.776 | 0.319126310522452 | 0.166028279387448 | 0.03684946883754 | 0.0846902290966677 |
| CAMK2D | 277.091.778.625.274 | 0.349630625956543 | 0.110798494640924 | 0.00106991166438658 | 0.00401189901582001 |
| PLCB3 | 30.578.336.330.819 | 0.369227730401235 | 0.0885761252993303 | 1,91E+09 | 0.000108029201407511 |
| PPP3CA | 256.585.595.024.188 | 0.373235392209162 | 0.12771848546183 | 0.00217807704361912 | 0.00749461396054691 |
| PRKACB | 155.479.632.445.332 | 0.382557095457931 | 0.152796328493714 | 0.0077530204829596 | 0.0227452518074045 |
| ADCY3 | 35.157.160.555.465 | 0.384570165506337 | 0.10318861828844 | 0.00011816572969351 | 0.000561384634799467 |
| SLC25A4 | 222.886.070.310.512 | 0.426581089118532 | 0.129454666583038 | 0.000538905641752702 | 0.00217817459658416 |
| ORAI1 | 109.532.355.302.949 | 0.430951303438528 | 0.149874442423144 | 0.00215782305621755 | 0.00743753904020853 |
| ERBB2 | 466.302.801.935.591 | 0.453000747759762 | 0.0859070335582125 | 7,17E+06 | 6,35E+07 |
| PHKB | 335.349.384.106.186 | 0.459366904885841 | 0.110460336516651 | 1,67E+07 | 9,52E+09 |
| CALM1 | 120.000.433.254.103 | 0.473988326599753 | 0.0822585983329827 | 4,03E+05 | 4,40E+06 |
| FGFR3 | 412.173.682.384.824 | 0.478844958517372 | 0.0926416266480472 | 1,18E+07 | 1,01E+08 |
| GNAS | 432.993.639.253.567 | 0.505876338060198 | 0.0933872474831993 | 2,81E+06 | 2,69E+07 |
| ADORA2B | 662.365.757.868.432 | 0.555313439236578 | 0.153468486520173 | 0.000115645342097655 | 0.000550846120311868 |
| PPP3R1 | 311.618.175.694.851 | 0.55631882811167 | 0.11382605476247 | 4,12E+07 | 3,18E+08 |
| GNA11 | 419.075.116.639.903 | 0.557660312687605 | 0.114087597573777 | 4,22E+07 | 3,24E+08 |
| SLC25A5 | 31.554.050.213.949 | 0.591996841533849 | 0.0944225412316923 | 1,38E+03 | 1,94E+05 |
| VDAC2 | 128.821.388.697.325 | 0.59427964544448 | 0.105051143244051 | 5,78E+04 | 6,16E+06 |
| FGFR2 | 282.071.577.743.889 | 0.614594852851092 | 0.10179451505322 | 5,45E+04 | 6,90E+05 |
| SPHK2 | 990.013.366.279.113 | 0.617877886815798 | 0.16358013542891 | 5,28E+08 | 0.00027165538890307 |
| CALM2 | 139.947.481.397.403 | 0.658786203542567 | 0.0878843057258299 | 1,66E+00 | 4,31E+01 |
| VDAC3 | 615.721.313.965.366 | 0.659604486969271 | 0.0792079673505408 | 2,75E-03 | 1,01E-01 |
| VEGFB | 182.794.381.075.822 | 0.66583541826766 | 0.128523584142247 | 6,82E+06 | 6,07E+07 |
| SLC25A6 | 110.045.490.085.772 | 0.697750300545649 | 0.132019257663235 | 2,62E+06 | 2,52E+07 |
| PPP3CB | 282.723.784.431.472 | 0.737736854234094 | 0.1037294597725 | 3,04E+01 | 6,49E+02 |
| CALM3 | 237.389.641.209.479 | 0.740184385222163 | 0.070241951160023 | 3,98E-12 | 4,23E-10 |
| VDAC1 | 127.948.228.767.543 | 0.798029346731346 | 0.0882435705879339 | 2,97E-06 | 1,58E-04 |
| CAMK1 | 302.929.731.805.388 | 0.832051455658237 | 0.114559291649818 | 8,35E+00 | 1,95E+02 |

## Appendix table S2. Rare coding pathogenic variants in the *ATP2B1* locus.

Among the 351 coding variants of *ATP2B1* from "The Genome Aggregation Database" (GnomAD v2.1), 13 are reported as "pathogenic" according to "Functional Analysis through Hidden Markov Models" (FATHMM) prediction scores. These variants are rare and were thus excluded from further investigations. Data given include chromosomal locus, position, rsID, dbSNP ID, protein consequence, fathmm prediction, reference and alternative alleles, transcript consequence, variant annotation, and allele frequency.

| **Chr** | **Position** | **rsID** | **dbSNP** | **ID** | **Protein** | **FATHMM prediction** | **Ref** | **Alt** | **Transcript consequence** | **Annotation** | **Allele frequency** |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 12 | 89984832 | rs115449702 | rs115449702 | NP_001673.2 | I1198V | DAMAGING | T | C | c.3592A>G | missense_variant | 7,96096E-06 |
| 12 | 89984882 | rs142404163 | rs142404163 | NP_001673.2 | P1181H | DAMAGING | G | T | c.3542C>A | missense_variant | 0,000453695 |
| 12 | 89995138 | rs79015625 | rs79015625 | NP_001001323.1 | I1045V | DAMAGING | T | C | c.3133A>G | missense_variant | 0,000900653 |
| 12 | 89997018 | rs189003061 | rs189003061 | NP_001673.2 | F954L | DAMAGING | A | T | c.2862T>A | missense_variant | 4,24257E-06 |
| 12 | 90005121 | rs182212584 | rs182212584 | NP_001001323.1 | R699T | DAMAGING | C | G | c.2096G>C | missense_variant | 3,00153E-05 |
| 12 | 90010584 | rs145288143 | rs145288143 | NP_001001323.1 | P688T | DAMAGING | G | T | c.2062C>A | missense_variant | 1,99351E-05 |
| 12 | 90013932 | rs199582675 | rs199582675 | NP_001673.2 | R558Q | DAMAGING | C | T | c.1673G>A | missense_variant | 3,98137E-06 |
| 12 | 90018046 | rs184588664 | rs184588664 | NP_001673.2 | F420L | DAMAGING | A | G | c.1258T>C | missense_variant | 3,98096E-06 |
| 12 | 90018088 | rs116585190 | rs116585190 | NP_001001323.1 | A406S | DAMAGING | C | A | c.1216G>T | missense_variant | 0,000159293 |
| 12 | 90028654 | rs149203241 | rs149203241 | NP_001001323.1 | L230F | DAMAGING | G | C | c.688C>G | missense_variant | 4,00208E-06 |
| 12 | 90036125 | rs200832650 | rs200832650 | NP_001001323.1 | S72R | DAMAGING | A | T | c.216T>A | missense_variant | 8,22788E-06 |
| 12 | 90049575 | rs116694524 | rs116694524 | NP_001001323.1 | T30M | DAMAGING | G | A | c.89C>T | missense_variant | 0,000767591 |
| 12 | 90049584 | rs201371800 | rs201371800 | NP_001001323.1 | F27Y | DAMAGING | A | T | c.80T>A | missense_variant | 3,97712E-06 |

## Appendix table S3. Noncoding variants in the genomic region of the *ATP2B1* locus that act as "expression quantitative traits loci" (eQTLs).

In-silico analysis pipeline identifying the presence of noncoding variants in the ATP2B1 locus acting as expression quantitative traits. Data given include genecode ID, gene symbol, variant ID (chromosomal position, alternative and reference alleles), SNP ID, P-value, normalized enrichment score (NES) and tissue (using the "Genotype-Tissue Expression" GTex database).

| Gencode Id | Gene symbol | Variant Id | SNP Id | P-value | NES | Tissue |
|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_89615182_A_G_b38 | rs2681472 | 1,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89619312_T_C_b38 | rs2681492 | 3,40E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89632685_G_A_b38 | rs11105352 | 3,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89632686_C_A_b38 | rs11105353 | 3,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89632746_A_G_b38 | rs11105354 | 3,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89656726_A_G_b38 | rs12579302 | 3,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89665065_G_A_b38 | rs111478946 | 3,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89675499_T_G_b38 | rs11105364 | 3,60E-18 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89680664_G_C_b38 | rs11105368 | 7,40E-18 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89681466_C_T_b38 | rs4842675 | 7,40E-18 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89591515_AAAGT_A_b38 | rs10580742 | 1,20E-17 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89696964_C_T_b38 | rs11105378 | 1,30E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89666809_G_A_b38 | rs17249754 | 1,50E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89668599_G_A_b38 | rs6538195 | 1,50E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89678299_G_A_b38 | rs73437358 | 1,50E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89625401_C_G_b38 | rs57481061 | 1,50E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89548613_A_G_b38 | rs11105328 | 1,70E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89547772_T_C_b38 | rs4842666 | 2,10E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89694803_T_A_b38 | rs11105375 | 5,70E-17 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89697090_A_G_b38 | rs12230074 | 8,10E-17 | 0,33 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89660842_T_C_b38 | rs73437338 | 1,50E-16 | 0,33 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89597536_C_T_b38 | rs117742247 | 4,20E-16 | 0,34 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89599730_A_T_b38 | rs11105337 | 4,60E-16 | 0,33 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89694991_G_A_b38 | rs11105376 | 7,80E-16 | 0,33 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89709925_C_G_b38 | rs2280715 | 4,30E-14 | 0,31 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89713495_T_C_b38 | rs11105382 | 4,30E-14 | 0,31 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89713529_T_C_b38 | rs11105383 | 4,30E-14 | 0,31 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89719293_T_G_b38 | rs7299436 | 4,30E-14 | 0,31 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89709168_C_G_b38 | rs73437382 | 8,00E-14 | 0,3 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89698005_G_C_b38 | rs4842676 | 6,10E-13 | -0,27 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89701396_T_C_b38 | rs11105379 | 1,40E-12 | 0,3 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89695013_G_A_b38 | rs10858917 | 2,50E-12 | -0,26 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89556543_A_C_b38 | rs7302816 | 4,50E-12 | 0,25 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89713058_A_G_b38 | rs11105381 | 2,90E-11 | -0,25 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89715560_T_C_b38 | rs2408046 | 5,50E-11 | -0,24 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89703890_G_C_b38 | rs10745511 | 5,70E-11 | -0,25 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89705620_T_A_b38 | rs2113894 | 5,70E-11 | -0,25 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89696509_CAA_C_b38 | rs10550903 | 7,60E-11 | -0,23 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89738370_G_A_b38 | rs12579052 | 5,40E-10 | 0,28 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90001084_A_T_b38 | rs4408360 | 3,40E-08 | -0,18 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90024395_T_G_b38 | rs149193253 | 4,40E-08 | 1 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_90049701_T_C_b38 | rs150184539 | 4,40E-08 | 1 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_90137707_G_A_b38 | rs77187603 | 4,40E-08 | 1 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_90143905_A_G_b38 | rs150119566 | 4,40E-08 | 1 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_89677042_CAAAG_C_b38 | rs143087380 | 5,00E-08 | -0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90006794_TA_T_b38 | rs67882152 | 8,80E-08 | -0,18 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90006796_A_T_b38 | rs114744356 | 8,80E-08 | -0,18 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90010274_T_C_b38 | rs7488223 | 1,10E-07 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89973923_G_C_b38 | rs4842701 | 1,30E-07 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89997003_T_C_b38 | rs7968803 | 1,30E-07 | -0,18 | Esophagus - Mucosa |

| | | | | | | |
|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_89991517_A_G_b38 | rs10777217 | 1,60E-07 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89595822_G_A_b38 | rs1401982 | 2,30E-07 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89576142_A_AACTC_b38 | rs10689649 | 2,50E-07 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89968275_A_G_b38 | rs4466894 | 2,70E-07 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89584456_C_T_b38 | rs1689040 | 2,80E-07 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89951830_C_T_b38 | rs4842699 | 3,00E-07 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89631845_G_A_b38 | rs2681485 | 3,30E-07 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90140138_C_T_b38 | rs55849728 | 3,80E-07 | -0,18 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89571272_C_T_b38 | rs7313874 | 3,90E-07 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89434814_A_G_b38 | rs8181784 | 4,20E-07 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89435693_C_T_b38 | rs11105287 | 4,20E-07 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89569762_G_GAGA_b38 | rs35533953 | 4,20E-07 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89687411_T_C_b38 | rs7136259 | 5,00E-07 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89702568_T_C_b38 | rs10858918 | 5,00E-07 | -0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89943269_A_C_b38 | rs4842697 | 5,20E-07 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89436943_T_C_b38 | rs10777163 | 6,60E-07 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89643729_T_C_b38 | rs111337717 | 7,20E-07 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89713948_C_T_b38 | rs1590008 | 7,20E-07 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89717005_G_A_b38 | rs1980235 | 7,20E-07 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90156621_AG_A_b38 | rs369917221 | 7,60E-07 | 0,75 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90025415_G_A_b38 | rs10858944 | 8,30E-07 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90034251_A_G_b38 | rs73208536 | 8,40E-07 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90385245_G_A_b38 | rs1594565 | 8,60E-07 | 0,38 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90047438_T_C_b38 | rs10777221 | 8,70E-07 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90048224_G_A_b38 | rs7488974 | 8,70E-07 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89987295_A_ATGTT_b38 | rs10625779 | 9,80E-07 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89708115_T_A_b38 | rs1358350 | 9,90E-07 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89640625_G_GC_b38 | rs66786558 | 0,0000011 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89640630_T_C_b38 | rs78409878 | 0,0000011 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89648365_C_G_b38 | rs11105358 | 0,0000011 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90398938_C_T_b38 | rs7955801 | 0,0000012 | 0,38 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90392860_A_C_b38 | rs2116497 | 0,0000012 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_89437093_C_T_b38 | rs10858851 | 0,0000012 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90072266_A_G_b38 | rs6538223 | 0,0000012 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90168240_C_T_b38 | rs4842509 | 0,0000012 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90170518_A_G_b38 | rs17836934 | 0,0000014 | -0,17 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89482366_T_C_b38 | rs11105298 | 0,0000015 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90391772_A_C_b38 | rs7976895 | 0,0000016 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90393455_G_A_b38 | rs12580873 | 0,0000016 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90084874_G_A_b38 | rs10858948 | 0,0000016 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90079719_A_G_b38 | rs6538224 | 0,0000017 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90376827_T_C_b38 | rs11105589 | 0,0000018 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90386667_C_T_b38 | rs6538234 | 0,0000018 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90388244_T_A_b38 | rs7979392 | 0,0000018 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90390285_G_C_b38 | rs2043213 | 0,0000018 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_89526956_C_T_b38 | rs11105312 | 0,0000018 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89527498_C_T_b38 | rs10777185 | 0,0000018 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89625452_C_T_b38 | rs7297206 | 0,0000018 | -0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90059201_T_C_b38 | rs7959983 | 0,0000021 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90080698_G_A_b38 | rs7485419 | 0,0000021 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90376071_T_C_b38 | rs12582977 | 0,0000023 | 0,37 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_89533400_G_A_b38 | rs11105319 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89534012_A_G_b38 | rs10858902 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89534195_G_A_b38 | rs10858903 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89539669_T_C_b38 | rs4842662 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89539986_G_C_b38 | rs3741898 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89540697_C_T_b38 | rs10858906 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89541074_CAGAG_C_b38 | rs71897440 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89541195_G_C_b38 | rs12369195 | 0,0000024 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89528255_C_A_b38 | rs10858897 | 0,0000025 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89535128_A_G_b38 | rs12369685 | 0,0000026 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90068229_T_C_b38 | rs7310135 | 0,0000026 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90079906_G_A_b38 | rs6419356 | 0,0000026 | -0,15 | Esophagus - Mucosa |

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|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_90081169_G_A_b38 | rs7962435 | 0,0000026 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90084513_C_T_b38 | rs7132441 | 0,0000026 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89530034_G_C_b38 | rs10858899 | 0,0000027 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89530596_A_ATCT_b38 | rs112698976 | 0,0000027 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89530782_C_T_b38 | rs11105314 | 0,0000027 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89531423_T_G_b38 | rs11105316 | 0,0000027 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89933142_G_A_b38 | rs11105466 | 0,0000028 | -0,16 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89432148_T_C_b38 | rs10858848 | 0,0000029 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89497589_G_A_b38 | rs11105302 | 0,000003 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89497697_T_G_b38 | rs10858881 | 0,000003 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89441951_C_A_b38 | rs10858854 | 0,0000032 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89445295_C_T_b38 | rs11105291 | 0,0000032 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89445926_A_G_b38 | rs10858860 | 0,0000032 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90049705_A_G_b38 | rs10858945 | 0,0000032 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90050234_G_T_b38 | rs7958749 | 0,0000032 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89481583_G_A_b38 | rs75615848 | 0,0000035 | 0,32 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89439561_T_C_b38 | rs10858852 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89440336_C_T_b38 | rs4842653 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89440651_T_A_b38 | rs4842654 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89442082_C_G_b38 | rs10858855 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89442149_G_A_b38 | rs9795772 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89442895_G_C_b38 | rs11513812 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89443404_T_C_b38 | rs11105289 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89445026_A_T_b38 | rs11105290 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89445465_C_T_b38 | rs10858859 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89445949_A_G_b38 | rs10858861 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89448276_T_C_b38 | rs10858862 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89451080_T_TG_b38 | rs11461256 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89452453_C_T_b38 | rs10858864 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89452699_G_A_b38 | rs10858865 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89457389_C_T_b38 | rs10858867 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89463834_C_T_b38 | rs10858869 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89466542_C_A_b38 | rs3803128 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89467752_T_C_b38 | rs10506972 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89468253_G_T_b38 | rs12228177 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89477836_G_A_b38 | rs10858871 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89479155_C_T_b38 | rs10858872 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89483146_C_T_b38 | rs112511312 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89484166_A_G_b38 | rs11105299 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89487787_C_G_b38 | rs4842488 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89490501_C_T_b38 | rs10858877 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89490517_G_A_b38 | rs10858878 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89492146_C_A_b38 | rs6538189 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89492165_T_C_b38 | rs6538190 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89492801_T_A_b38 | rs10858879 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89493872_T_C_b38 | rs1008764 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89503120_C_T_b38 | rs10858885 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89503384_C_G_b38 | rs10858886 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89503557_C_T_b38 | rs11105305 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89503611_C_T_b38 | rs11105306 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89508827_G_A_b38 | rs10858889 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89513389_T_C_b38 | rs10858890 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89516073_T_C_b38 | rs11105309 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89519642_C_T_b38 | rs1054807 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89520484_T_C_b38 | rs10858894 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89529599_A_T_b38 | rs11105313 | 0,0000036 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90056289_A_G_b38 | rs12227543 | 0,0000036 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89524900_C_A_b38 | rs11105310 | 0,0000037 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89525791_C_T_b38 | rs10777184 | 0,0000037 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89526407_C_T_b38 | rs10858896 | 0,0000037 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89527500_G_A_b38 | rs10777186 | 0,0000037 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90052157_T_C_b38 | rs4842710 | 0,0000037 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90057274_A_G_b38 | rs10858947 | 0,0000037 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90068211_G_A_b38 | rs7139279 | 0,0000037 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90077187_C_T_b38 | rs7488228 | 0,0000037 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90083730_C_T_b38 | rs4842505 | 0,0000037 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90083900_C_T_b38 | rs7306280 | 0,0000037 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89996947_A_G_b38 | rs7953742 | 0,0000038 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89996827_CA_C_b38 | rs112780917 | 0,0000039 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90007154_C_CA_b38 | rs11396475 | 0,0000039 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90018978_A_C_b38 | rs4842705 | 0,0000039 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89531304_C_A_b38 | rs10858900 | 0,0000041 | 0,16 | Artery - Tibial |

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|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_89536622_A_G_b38 | rs4842661 | 0,0000047 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89539933_C_T_b38 | rs3825330 | 0,000005 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89541610_C_T_b38 | rs10858909 | 0,000005 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89544813_G_A_b38 | rs11105325 | 0,000005 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90050964_A_G_b38 | rs10777222 | 0,000005 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89540154_G_A_b38 | rs3741899 | 0,0000051 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90389431_C_T_b38 | rs1228496 | 0,0000052 | 0,49 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_89528334_A_G_b38 | rs10858898 | 0,0000052 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89544253_G_A_b38 | rs4842664 | 0,0000052 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90510721_G_T_b38 | rs12578110 | 0,0000055 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_89532881_G_A_b38 | rs11105318 | 0,0000056 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89931928_T_C_b38 | rs7970120 | 0,0000063 | -0,21 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89432335_C_G_b38 | rs11105286 | 0,0000064 | 0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90386667_C_T_b38 | rs6538234 | 0,0000083 | 0,51 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90388244_T_A_b38 | rs7979392 | 0,0000083 | 0,51 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90390285_G_C_b38 | rs2043213 | 0,0000083 | 0,51 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90398938_C_T_b38 | rs7955801 | 0,0000083 | 0,51 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90063091_G_A_b38 | rs6538220 | 0,0000084 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90516738_A_G_b38 | rs1347015 | 0,0000088 | 0,47 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90523189_C_T_b38 | rs1579534 | 0,0000088 | 0,47 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90510105_C_T_b38 | rs10858992 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90519613_A_T_b38 | rs61655253 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90528232_A_G_b38 | rs4274255 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90528837_C_T_b38 | rs11105663 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90532822_TTCTTAAGGACAA_T_b38 | rs6144807 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90533124_TA_T_b38 | rs36032096 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90535560_T_C_b38 | rs12580833 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90543285_C_T_b38 | rs11105668 | 0,0000088 | 0,46 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_89780365_G_T_b38 | rs116990534 | 0,0000092 | 0,35 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89719404_G_A_b38 | rs4842679 | 0,0000094 | -0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89504370_G_A_b38 | rs138808993 | 0,0000095 | 0,65 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_89538657_G_A_b38 | rs143285018 | 0,0000095 | 0,65 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_90129715_G_A_b38 | rs59313167 | 0,0000097 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90134908_C_T_b38 | rs7970711 | 0,0000097 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90136962_G_A_b38 | rs7979050 | 0,0000097 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89959608_C_T_b38 | rs11105474 | 0,00001 | -0,14 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89622750_A_G_b38 | rs147471906 | 0,000011 | 0,59 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_89643621_G_A_b38 | rs149731397 | 0,000011 | 0,59 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_90394122_TTTC_T_b38 | rs10543504 | 0,000011 | 0,52 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90385245_G_A_b38 | rs1594565 | 0,000011 | 0,5 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90088859_T_C_b38 | rs11105501 | 0,000011 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90089663_G_A_b38 | rs11105503 | 0,000011 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90089938_C_T_b38 | rs11105504 | 0,000011 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89926004_G_A_b38 | rs111342256 | 0,000012 | 0,65 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90195090_A_G_b38 | rs10858967 | 0,000012 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90407150_G_A_b38 | rs7969733 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90411424_C_G_b38 | rs10777244 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90411690_G_A_b38 | rs7958205 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90411780_G_A_b38 | rs7958308 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90414020_G_T_b38 | rs7966452 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90414588_CT_C_b38 | rs35829324 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90416671_A_G_b38 | rs2897862 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90416672_A_T_b38 | rs2408160 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90422109_C_T_b38 | rs7315821 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90425535_T_A_b38 | rs6538235 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90427858_G_A_b38 | rs10777245 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |

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|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_90430064_C_G_b38 | rs6538236 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90436231_T_C_b38 | rs1835768 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90436298_G_A_b38 | rs1835767 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90439201_G_A_b38 | rs34234695 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90439855_C_T_b38 | rs11105617 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90443686_G_A_b38 | rs66955893 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90451488_G_A_b38 | rs11105622 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90452503_C_T_b38 | rs7960740 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90457546_A_T_b38 | rs11105623 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90468635_G_A_b38 | rs7954409 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90474639_G_A_b38 | rs1864782 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90476135_C_T_b38 | rs7298940 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90478226_G_A_b38 | rs12818545 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90482472_AAC_A_b38 | rs67668093 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90484858_C_T_b38 | rs7311599 | 0,000013 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90559065_T_A_b38 | rs2520561 | 0,000013 | 0,31 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90391772_A_C_b38 | rs7976895 | 0,000014 | 0,48 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90392860_A_C_b38 | rs2116497 | 0,000014 | 0,48 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90393455_G_A_b38 | rs12580873 | 0,000014 | 0,48 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90552916_G_A_b38 | rs2520567 | 0,000014 | 0,44 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90001825_T_C_b38 | rs17192565 | 0,000014 | 0,43 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90459042_T_A_b38 | rs7132660 | 0,000014 | 0,34 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_90106317_C_CAT_b38 | rs148143712 | 0,000015 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90112140_G_A_b38 | rs7966278 | 0,000015 | -0,15 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89556543_A_C_b38 | rs7302816 | 0,000016 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89422110_G_A_b38 | rs80277599 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89428758_A_G_b38 | rs112370308 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89441431_T_C_b38 | rs113025676 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89457067_C_T_b38 | rs61435009 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89471149_A_G_b38 | rs74754458 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89478671_T_C_b38 | rs60772618 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89484136_C_G_b38 | rs74543833 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89487042_C_G_b38 | rs58117070 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89488169_C_T_b38 | rs185300284 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89488792_C_T_b38 | rs76672752 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_89490053_G_T_b38 | rs78332000 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90581088_T_TA_b38 | rs143922775 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90583461_C_T_b38 | rs17018043 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90586839_A_G_b38 | rs73358180 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90589431_T_C_b38 | rs73358183 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90593192_C_T_b38 | rs73358194 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90594592_G_A_b38 | rs2106528 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90599502_C_T_b38 | rs76134788 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90602009_G_C_b38 | rs73360109 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90602975_T_C_b38 | rs73360112 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90603192_A_G_b38 | rs17018088 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90606864_CAG_C_b38 | rs34639687 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90608792_A_G_b38 | rs7306918 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90609936_C_T_b38 | rs73360125 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90614576_G_T_b38 | rs73360133 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90626419_G_T_b38 | rs11829105 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90626488_A_T_b38 | rs11833692 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90628581_A_G_b38 | rs73360170 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90646115_A_G_b38 | rs11830515 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90650906_T_C_b38 | rs11105723 | 0,000017 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90661217_T_C_b38 | rs11105730 | 0,000017 | 1,4 | Brain - Hypothalamus |

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|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_89525853_ACC_A_b38 | rs67346689 | 0,000017 | 0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90637101_TTG_T_b38 | rs1491580271 | 0,000018 | 1,4 | Brain - Hypothalamus |
| ENSG00000070961.15 | ATP2B1 | chr12_90136354_G_A_b38 | rs143689254 | 0,000018 | 0,68 | Brain - Anterior cingulate cortex (BA24) |
| ENSG00000070961.15 | ATP2B1 | chr12_90241276_A_G_b38 | rs73196463 | 0,000018 | 0,62 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90554733_G_A_b38 | rs2520565 | 0,000018 | 0,44 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90556726_A_G_b38 | rs2520563 | 0,000018 | 0,44 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90557663_C_T_b38 | rs2520562 | 0,000018 | 0,44 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_90558072_T_C_b38 | rs2723917 | 0,000018 | 0,44 | Brain - Substantia nigra |
| ENSG00000070961.15 | ATP2B1 | chr12_89569279_G_A_b38 | rs372643302 | 0,000018 | 0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89950918_A_G_b38 | rs7294671 | 0,000018 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89956338_C_G_b38 | rs11105473 | 0,000018 | -0,14 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89957460_T_G_b38 | rs7132526 | 0,000018 | -0,14 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89704243_G_A_b38 | rs61926784 | 0,000019 | 0,19 | Brain - Frontal Cortex (BA9) |
| ENSG00000070961.15 | ATP2B1 | chr12_90326873_G_T_b38 | rs825954 | 0,000023 | -0,15 | Esophagus - Muscularis |
| ENSG00000070961.15 | ATP2B1 | chr12_90329398_C_T_b38 | rs10858974 | 0,000024 | -0,13 | Thyroid |
| ENSG00000070961.15 | ATP2B1 | chr12_90299326_G_A_b38 | rs11105563 | 0,000024 | -0,35 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_89876539_G_A_b38 | rs74851539 | 0,000025 | 0,41 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89940862_G_A_b38 | rs12368259 | 0,000027 | 0,22 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90299488_G_C_b38 | rs10506984 | 0,000027 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90303890_G_C_b38 | rs2056699 | 0,000027 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90306554_G_A_b38 | rs1587440 | 0,000027 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90311197_C_T_b38 | rs10858971 | 0,000027 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90631370_A_T_b38 | rs11105706 | 0,000028 | -0,28 | Colon - Transverse |
| ENSG00000070961.15 | ATP2B1 | chr12_90631458_A_G_b38 | rs11105707 | 0,000028 | -0,28 | Colon - Transverse |
| ENSG00000070961.15 | ATP2B1 | chr12_90632378_G_A_b38 | rs11105709 | 0,000028 | -0,28 | Colon - Transverse |
| ENSG00000070961.15 | ATP2B1 | chr12_90636015_C_A_b38 | rs11105712 | 0,000028 | -0,28 | Colon - Transverse |
| ENSG00000070961.15 | ATP2B1 | chr12_90638508_T_A_b38 | rs112784216 | 0,000028 | -0,28 | Colon - Transverse |
| ENSG00000070961.15 | ATP2B1 | chr12_90451210_G_A_b38 | rs1148676 | 0,000029 | 0,3 | Brain - Spinal cord (cervical c-1) |
| ENSG00000070961.15 | ATP2B1 | chr12_89973104_A_G_b38 | rs10777215 | 0,000029 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89999628_A_ATTC_b38 | rs10671258 | 0,000029 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90000940_A_G_b38 | rs4406875 | 0,000029 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90005097_T_A_b38 | rs4240746 | 0,000029 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89559134_C_T_b38 | rs112417857 | 0,000031 | 0,54 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89394010_T_C_b38 | rs11105273 | 0,000031 | 0,18 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89975574_A_G_b38 | rs7303123 | 0,000031 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89976239_C_T_b38 | rs10777216 | 0,000031 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89957885_A_G_b38 | rs4842700 | 0,000032 | -0,18 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90287401_C_T_b38 | rs11105559 | 0,000032 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90295570_G_A_b38 | rs2165035 | 0,000032 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90273379_C_A_b38 | rs12320693 | 0,000033 | -0,37 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_89995520_A_C_b38 | rs6538214 | 0,000034 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90007782_T_TATAAA_b38 | rs57291885 | 0,000034 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90008924_A_C_b38 | rs4842504 | 0,000034 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90018772_T_C_b38 | rs10858942 | 0,000034 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90061403_T_C_b38 | rs7303035 | 0,000037 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89042639_G_A_b38 | rs76671707 | 0,000037 | -0,57 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90266564_G_A_b38 | rs1347846 | 0,000039 | -0,33 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90259816_T_C_b38 | rs4381424 | 0,000039 | -0,34 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90303378_AT_A_b38 | rs141511768 | 0,000039 | -0,36 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90275487_CAA_C_b38 | rs3042884 | 0,000041 | -0,35 | Cells - EBV-transformed lymphocytes |
| ENSG00000070961.15 | ATP2B1 | chr12_90328476_T_C_b38 | rs1405527 | 0,000042 | -0,13 | Thyroid |
| ENSG00000070961.15 | ATP2B1 | chr12_90330109_G_A_b38 | rs12818395 | 0,000042 | -0,13 | Thyroid |
| ENSG00000070961.15 | ATP2B1 | chr12_90150155_C_T_b38 | rs7135166 | 0,000042 | -0,14 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89709017_C_A_b38 | rs12369944 | 0,000044 | 0,18 | Brain - Frontal Cortex (BA9) |
| ENSG00000070961.15 | ATP2B1 | chr12_89966286_A_G_b38 | rs10745520 | 0,000044 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89702020_T_A_b38 | rs11105380 | 0,000045 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90153750_C_G_b38 | rs2118803 | 0,000047 | -0,14 | Esophagus - Mucosa |

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|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_90568565_A_G_b38 | rs35520023 | 0,000048 | 0,13 | Adipose - Subcutaneous |
| ENSG00000070961.15 | ATP2B1 | chr12_90629207_G_A_b38 | rs11105704 | 0,000048 | -0,27 | Colon - Transverse |
| ENSG00000070961.15 | ATP2B1 | chr12_89666809_G_A_b38 | rs17249754 | 0,000051 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89668599_G_A_b38 | rs6538195 | 0,000051 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89678299_G_A_b38 | rs73437358 | 0,000051 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89913265_C_T_b38 | rs7972820 | 0,000053 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89784106_A_T_b38 | rs113133867 | 0,000054 | 0,55 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89632685_G_A_b38 | rs11105352 | 0,000054 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89632686_C_A_b38 | rs11105353 | 0,000054 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89632746_A_G_b38 | rs11105354 | 0,000054 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89656726_A_G_b38 | rs12579302 | 0,000054 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89665065_G_A_b38 | rs111478946 | 0,000054 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89675499_T_G_b38 | rs11105364 | 0,000054 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_90158457_G_GT_b38 | rs79468373 | 0,000054 | -0,14 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89909790_G_C_b38 | rs7957657 | 0,000057 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90328476_T_C_b38 | rs1405527 | 0,000057 | -0,15 | Esophagus - Muscularis |
| ENSG00000070961.15 | ATP2B1 | chr12_90329398_C_T_b38 | rs10858974 | 0,000057 | -0,15 | Esophagus - Muscularis |
| ENSG00000070961.15 | ATP2B1 | chr12_90330109_G_A_b38 | rs12818395 | 0,000057 | -0,15 | Esophagus - Muscularis |
| ENSG00000070961.15 | ATP2B1 | chr12_90026116_GT_G_b38 | rs11324040 | 0,000058 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89629273_T_C_b38 | rs116858620 | 0,00006 | 0,43 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90035251_A_G_b38 | rs7311631 | 0,00006 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89879521_G_A_b38 | rs2553100 | 0,00006 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89944741_G_A_b38 | rs4842698 | 0,000062 | -0,18 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89680664_G_C_b38 | rs11105368 | 0,000063 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_90577787_T_C_b38 | rs11105685 | 0,000063 | 0,13 | Adipose - Subcutaneous |
| ENSG00000070961.15 | ATP2B1 | chr12_89681466_C_T_b38 | rs4842675 | 0,000065 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89619312_T_C_b38 | rs2681492 | 0,000066 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89615182_A_G_b38 | rs2681472 | 0,000066 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89956222_G_A_b38 | rs10777213 | 0,000066 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89958659_C_T_b38 | rs7306228 | 0,000066 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90039790_A_G_b38 | rs6538218 | 0,000066 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89912752_T_C_b38 | rs7135197 | 0,000067 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89915156_G_A_b38 | rs7959788 | 0,000067 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90152680_A_G_b38 | rs10745525 | 0,000068 | -0,18 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89837533_A_G_b38 | rs2722224 | 0,000079 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89696964_C_T_b38 | rs11105378 | 0,00008 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89695013_G_A_b38 | rs10858917 | 0,00008 | -0,17 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_90050278_C_T_b38 | rs55846104 | 0,000081 | -0,19 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90147932_C_T_b38 | rs4608145 | 0,000083 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90087601_T_C_b38 | rs7316395 | 0,000087 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90087981_A_G_b38 | rs7300611 | 0,000087 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90089145_A_G_b38 | rs10735278 | 0,000087 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90089249_A_T_b38 | rs10735279 | 0,000087 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90089939_T_G_b38 | rs10858950 | 0,000087 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90090107_T_C_b38 | rs11105505 | 0,000087 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_89966684_C_T_b38 | rs4584633 | 0,00009 | -0,17 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89921101_C_G_b38 | rs4842693 | 0,000093 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90133970_C_T_b38 | rs11105516 | 0,000094 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90022580_A_C_b38 | rs10777219 | 0,000094 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90024345_G_A_b38 | rs10858943 | 0,000094 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90157130_AT_A_b38 | rs34734819 | 0,000099 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89694803_T_A_b38 | rs11105375 | 0,0001 | 0,18 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89697090_A_G_b38 | rs12230074 | 0,0001 | 0,18 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_90148406_A_C_b38 | rs1438984 | 0,0001 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90148426_G_A_b38 | rs1438983 | 0,0001 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90042305_C_T_b38 | rs7975953 | 0,0001 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90042794_T_C_b38 | rs7963304 | 0,0001 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90110385_A_C_b38 | rs10858955 | 0,00011 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90111572_G_A_b38 | rs10745523 | 0,00011 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90114532_G_T_b38 | rs10777224 | 0,00011 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90120301_C_G_b38 | rs10858956 | 0,00011 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_89336143_A_C_b38 | rs10161308 | 0,00012 | 0,22 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89660842_T_C_b38 | rs73437338 | 0,00012 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89591515_AAAGT_A_b38 | rs10580742 | 0,00012 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_89677042_CAAAG_C_b38 | rs143087380 | 0,00012 | -0,11 | Thyroid |
| ENSG00000070961.15 | ATP2B1 | chr12_90099780_G_A_b38 | rs7486390 | 0,00012 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90100728_G_C_b38 | rs7303398 | 0,00012 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_89694991_G_A_b38 | rs11105376 | 0,00013 | 0,19 | Artery - Aorta |
| ENSG00000070961.15 | ATP2B1 | chr12_90117803_G_C_b38 | rs7486630 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90119438_T_A_b38 | rs7139353 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90121102_T_C_b38 | rs10777226 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90122191_G_C_b38 | rs6538227 | 0,00013 | -0,13 | Lung |

| | | | | | | |
|---|---|---|---|---|---|---|
| ENSG00000070961.15 | ATP2B1 | chr12_90123327_G_T_b38 | rs10858957 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90123338_T_C_b38 | rs10858958 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90124075_G_A_b38 | rs7315166 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90124724_G_A_b38 | rs4842713 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90126369_C_T_b38 | rs7138547 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90127423_A_G_b38 | rs10777227 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90127443_A_G_b38 | rs10777228 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90128789_G_A_b38 | rs12303180 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90129235_T_C_b38 | rs4842714 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90130357_GCTC_G_b38 | rs35647353 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90132074_G_T_b38 | rs10858961 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90133198_A_AG_b38 | rs79553876 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90134620_G_C_b38 | rs6538228 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90137321_T_C_b38 | rs1595599 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90137388_G_A_b38 | rs1595598 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90137720_T_G_b38 | rs7304226 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90139086_C_T_b38 | rs7295818 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90141861_G_T_b38 | rs1438986 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90142076_T_G_b38 | rs1438985 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90142537_C_A_b38 | rs1470031 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90142786_G_A_b38 | rs1470030 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90144066_A_C_b38 | rs10745524 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90144234_A_G_b38 | rs1470029 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90144899_A_T_b38 | rs4842715 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90145400_C_A_b38 | rs4842716 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90145401_C_T_b38 | rs4842717 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90145987_C_A_b38 | rs1344962 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90146644_T_C_b38 | rs11105517 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90147279_C_G_b38 | rs1344961 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90147385_C_G_b38 | rs2218085 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90147644_A_C_b38 | rs2196783 | 0,00013 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_90002703_T_C_b38 | rs7964216 | 0,00013 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90004485_T_C_b38 | rs10777218 | 0,00013 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90005574_C_T_b38 | rs11105483 | 0,00013 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90015717_C_T_b38 | rs61926987 | 0,00013 | -0,14 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90159905_G_A_b38 | rs6538230 | 0,00014 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89547597_G_A_b38 | rs4842665 | 0,00015 | 0,12 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89865713_T_C_b38 | rs2722213 | 0,00015 | -0,12 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89866278_G_A_b38 | rs2553097 | 0,00015 | -0,12 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89875126_G_A_b38 | rs2553104 | 0,00015 | -0,12 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90071866_G_A_b38 | rs6538222 | 0,00015 | -0,13 | Lung |
| ENSG00000070961.15 | ATP2B1 | chr12_89851601_T_C_b38 | rs2553101 | 0,00015 | -0,13 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89637618_C_T_b38 | rs10858914 | 0,00017 | -0,12 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90010069_T_C_b38 | rs4393376 | 0,00017 | -0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90016872_A_C_b38 | rs6538217 | 0,00017 | -0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89904501_A_C_b38 | rs7965284 | 0,00017 | -0,18 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90128372_C_T_b38 | rs10858959 | 0,00019 | -0,13 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90129926_G_A_b38 | rs10858960 | 0,00019 | -0,13 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89943230_A_C_b38 | rs4842696 | 0,0002 | -0,14 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_89345678_C_G_b38 | rs11105262 | 0,00022 | 0,21 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89861997_C_A_b38 | rs1946327 | 0,00023 | -0,12 | Esophagus - Mucosa |
| ENSG00000070961.15 | ATP2B1 | chr12_90003409_T_C_b38 | rs4453292 | 0,00023 | -0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90162353_T_C_b38 | rs2731241 | 0,00023 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90164205_A_G_b38 | rs1438980 | 0,00023 | -0,16 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89434120_G_A_b38 | rs118130015 | 0,00027 | 0,33 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90173201_C_T_b38 | rs1347851 | 0,00027 | -0,15 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89623959_G_T_b38 | rs2070759 | 0,00028 | -0,11 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89646107_G_A_b38 | rs939329 | 0,00028 | -0,11 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_90149730_G_A_b38 | rs10777230 | 0,00028 | -0,12 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89857319_C_T_b38 | rs12371308 | 0,00028 | -0,13 | Artery - Tibial |
| ENSG00000070961.15 | ATP2B1 | chr12_89857983_T_C_b38 | rs11105439 | 0,00028 | -0,13 | Artery - Tibial |

**Appendix table S4. eQTLs SNPs for the *ATP2B1* gene from the "Genotype-Tissue Expression" (GTex) database (P <1 ×$10^{-6}$).**

In-silico analysis pipeline identifying the presence of noncoding variants in the ATP2B1 locus located in putative elements responsible for transcriptional regulation (EQTLs). The 77 SNPs that act as eQTLs for the *ATP2B1* gene annotated with prediction functional scores calculated from the "Genome-Wide Annotation of Variants" GWAVA tool. Eight SNPs are not reported in GWAVA, and are thus excluded. Data given include ID, chromosome, position, and region score. Bold: the top six SNPs selected.

| ID | Chr. | Position | Region score |
|---|---|---|---|
| **rs11105352** | **12** | **90.026.462** | **0,63** |
| **rs11105353** | **12** | **90.026.463** | **0,61** |
| **rs10777221** | **12** | **90.441.215** | **0,52** |
| **rs73437358** | **12** | **90.072.076** | **0,48** |
| **rs111337717** | **12** | **90.037.506** | **0,47** |
| **rs2681492** | **12** | **90.013.089** | **0,47** |
| rs7136259 | 12 | 90.081.188 | 0,46 |
| rs17249754 | 12 | 90.060.586 | 0,43 |
| rs11105382 | 12 | 90.107.272 | 0,43 |
| rs73437338 | 12 | 90.054.619 | 0,42 |
| rs2280715 | 12 | 90.103.702 | 0,42 |
| rs149193253 | 12 | 90.418.172 | 0,42 |
| rs4842699 | 12 | 90.345.607 | 0,41 |
| rs114744356 | 12 | 90.400.573 | 0,41 |
| rs7488223 | 12 | 90.404.051 | 0,41 |
| rs11105354 | 12 | 90.026.523 | 0,4 |
| rs11105337 | 12 | 89.993.507 | 0,39 |
| rs2681472 | 12 | 90.008.959 | 0,39 |
| rs11105364 | 12 | 90.069.276 | 0,39 |
| rs10777217 | 12 | 90.385.294 | 0,39 |
| rs10745511 | 12 | 90.097.667 | 0,38 |
| rs2408046 | 12 | 90.109.337 | 0,38 |
| rs1401982 | 12 | 89.989.599 | 0,37 |
| rs12579302 | 12 | 90.050.503 | 0,37 |
| rs4842675 | 12 | 90.075.243 | 0,37 |
| rs11105379 | 12 | 90.095.173 | 0,37 |
| rs7299436 | 12 | 90.113.070 | 0,37 |
| rs73208536 | 12 | 90.428.028 | 0,37 |
| rs8181784 | 12 | 89.828.591 | 0,36 |
| rs10777163 | 12 | 89.830.720 | 0,36 |
| rs6538195 | 12 | 90.062.376 | 0,35 |
| rs4842676 | 12 | 90.091.782 | 0,35 |
| rs2113894 | 12 | 90.099.397 | 0,35 |
| rs1980235 | 12 | 90.110.782 | 0,35 |
| rs7488974 | 12 | 90.442.001 | 0,35 |
| rs150184539 | 12 | 90.443.478 | 0,35 |
| rs150119566 | 12 | 90.537.682 | 0,35 |
| rs12230074 | 12 | 90.090.867 | 0,34 |
| rs1358350 | 12 | 90.101.892 | 0,34 |
| rs73437382 | 12 | 90.102.945 | 0,34 |
| rs11105381 | 12 | 90.106.835 | 0,34 |
| rs2681485 | 12 | 90.025.622 | 0,33 |

| | | | |
|---|---|---|---|
| rs11105368 | 12 | 90.074.441 | 0,33 |
| rs11105378 | 12 | 90.090.741 | 0,33 |
| rs7313874 | 12 | 89.965.049 | 0,32 |
| rs1689040 | 12 | 89.978.233 | 0,32 |
| rs111478946 | 12 | 90.058.842 | 0,32 |
| rs11105383 | 12 | 90.107.306 | 0,32 |
| rs12579052 | 12 | 90.132.147 | 0,32 |
| rs1594565 | 12 | 90.779.022 | 0,32 |
| rs10858918 | 12 | 90.096.345 | 0,31 |
| rs4408360 | 12 | 90.394.861 | 0,31 |
| rs11105287 | 12 | 89.829.470 | 0,3 |
| rs7968803 | 12 | 90.390.780 | 0,3 |
| rs4842666 | 12 | 89.941.549 | 0,29 |
| rs11105328 | 12 | 89.942.390 | 0,29 |
| rs10858917 | 12 | 90.088.790 | 0,29 |
| rs7302816 | 12 | 89.950.320 | 0,28 |
| rs1590008 | 12 | 90.107.725 | 0,28 |
| rs4466894 | 12 | 90.362.052 | 0,27 |
| rs55849728 | 12 | 90.533.915 | 0,27 |
| rs11105375 | 12 | 90.088.580 | 0,26 |
| rs4842697 | 12 | 90.337.046 | 0,26 |
| rs77187603 | 12 | 90.531.484 | 0,25 |
| rs10858944 | 12 | 90.419.192 | 0,24 |
| rs11105376 | 12 | 90.088.768 | 0,23 |
| rs4842701 | 12 | 90.367.700 | 0,19 |
| rs117742247 | 12 | 89.991.313 | 0,16 |
| rs57481061 | 12 | 90.019.178 | 0,14 |

### Appendix table S5. Differentially expressed genes in HEK-293T edited cells

Differentially expressed (DE) genes comparing differentially expressed genes from RNAseq analyses comparing HEK293T (WT T/T) and isogenic generated clones (C/C). Data given include gene name, BaseMean (average of the normalized count values), FoldChange, log2Fold Change, pValue and BH adjusted p value are listed.

| Gene Symbol | C.C. / T.T. base Mean | C.C. / T.T. Fold change | C.C. / T.T. Log2 Fold change | C.C. / T.T. .raw. pval | C.C. / T.T. .bh. pval |
|---|---|---|---|---|---|
| TMEM189-UBE2V1 | 83,432186 | -8,030776 | 0,449601396 | 2,31086E-11 | 4,1064E-07 |
| CCND1 | 1001,397770 | -5,516491 | 0,398915171 | 6,5693E-10 | 5,83682E-06 |
| BRINP3 | 286,533286 | 2,984710 | 0,262334776 | 1,81388E-09 | 1,07442E-05 |
| SGPP2 | 407,418822 | -2,731977 | 0,265271423 | 4,60582E-08 | 0,000204614 |
| ACTRT3 | 160,576777 | 2,871753 | 0,284993336 | 9,28257E-08 | 0,000329903 |
| KCNB1 | 82,902050 | -8,504763 | 0,594124921 | 2,01426E-07 | 0,000596558 |
| UBAC2-AS1 | 137,141414 | 3,239612 | 0,33518791 | 4,20766E-07 | 0,00097994 |
| LOC105274304 | 42,515853 | 5,209731 | 0,471500485 | 4,41166E-07 | 0,00097994 |
| DECR1 | 969,930136 | 2,615839 | 0,279833059 | 7,14043E-07 | 0,001409838 |
| TUNAR | 59,840352 | -7,617012 | 0,598726825 | 9,96018E-07 | 0,001769925 |
| AIFM2 | 413,442074 | 3,150496 | 0,344923044 | 1,58785E-06 | 0,002565095 |
| IFI30 | 824,717238 | 2,366240 | 0,263042902 | 2,31328E-06 | 0,003425588 |
| LINC00839 | 176,086803 | -3,580646 | 0,400302795 | 4,28474E-06 | 0,00585691 |
| IFIT1 | 334,126293 | 2,561404 | 0,306536035 | 9,56975E-06 | 0,012146741 |
| ZNF442 | 58,360208 | -5,030546 | 0,538613852 | 1,50985E-05 | 0,017471828 |
| LOC105374338 | 57,358380 | -10,111528 | 0,772992986 | 1,57315E-05 | 0,017471828 |
| STC1 | 61,570815 | -13,594827 | 0,874836971 | 1,68012E-05 | 0,017562241 |
| TP53I3 | 647,230208 | 3,278584 | 0,404223866 | 2,25589E-05 | 0,020025016 |
| SORCS1 | 580,443344 | -5,656138 | 0,587216634 | 2,07132E-05 | 0,020025016 |
| C11orf96 | 232,808814 | -3,155106 | 0,391077311 | 2,24744E-05 | 0,020025016 |
| ETNPPL | 89,902382 | 2,369733 | 0,29823272 | 2,99735E-05 | 0,02417569 |
| MAP6 | 113,007758 | -2,857277 | 0,364924211 | 3,31659E-05 | 0,024556566 |
| NAALAD2 | 172,160859 | 2,522826 | 0,324404345 | 3,86575E-05 | 0,027025416 |
| CRTAC1 | 151,000507 | -3,739295 | 0,464430892 | 4,18567E-05 | 0,027025416 |
| ZNF83 | 296,337238 | -4,632727 | 0,540401733 | 4,25837E-05 | 0,027025416 |
| SLC9A9 | 260,880735 | 2,474374 | 0,318723781 | 4,11494E-05 | 0,027025416 |
| DUSP4 | 199,388914 | -3,327344 | 0,425797324 | 4,63653E-05 | 0,027463719 |
| CACNA1C | 285,991249 | -2,298536 | 0,300564281 | 6,47297E-05 | 0,032293583 |
| KCND3 | 60,278431 | -3,500644 | 0,453509921 | 6,72404E-05 | 0,032293583 |
| TAC1 | 32,763155 | -6,635666 | 0,679767066 | 5,90848E-05 | 0,032293583 |
| HCAR1 | 30,689060 | 3,294148 | 0,427826276 | 5,81729E-05 | 0,032293583 |
| SH3BGRL3 | 1332,907483 | 2,280879 | 0,297318012 | 6,30567E-05 | 0,032293583 |
| ZFAS1 | 3127,906649 | -2,477187 | 0,326245427 | 6,03582E-05 | 0,032293583 |
| INSC | 111,875918 | -5,631494 | 0,631212073 | 7,80323E-05 | 0,034665871 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| CA5BP1-CA5B | 466,096834 | -2,141693 | 0,27781154 | 7,65262E-05 | 0,034665871 |
| CALCB | 550,253073 | -3,207646 | 0,427394581 | 8,34263E-05 | 0,034945057 |
| FAM189A1 | 428,197582 | -2,040489 | 0,261739715 | 8,45715E-05 | 0,034945057 |
| SLC10A4 | 97,279503 | 2,640249 | 0,356808371 | 8,65269E-05 | 0,034945057 |
| LOC105376600 | 64,661519 | 2,868588 | 0,3861753 | 8,25346E-05 | 0,034945057 |
| APOBEC3B | 398,824054 | 4,451726 | 0,552665277 | 9,69358E-05 | 0,038278864 |
| MYO7A | 138,110413 | 3,845872 | 0,500531182 | 0,000103389 | 0,039405917 |
| MIR503HG | 382,949889 | 2,740963 | 0,377910205 | 0,000118465 | 0,042102402 |
| DTX4 | 43,232806 | -2,915700 | 0,404222777 | 0,000133839 | 0,044873876 |
| RASGRP1 | 252,508176 | -2,536054 | 0,353223386 | 0,000144141 | 0,047433015 |
| GPR85 | 89,893659 | 3,055436 | 0,424745359 | 0,000148388 | 0,047942902 |
| INSM1 | 333,792159 | -2,640916 | 0,370350247 | 0,000154944 | 0,049167057 |
| FOXL2NB | 69,535137 | 2,242507 | 0,310092596 | 0,000171754 | 0,051335806 |
| ZNF887P | 141,080914 | -2,027753 | 0,271087935 | 0,000168438 | 0,051335806 |
| BCL11B | 128,012163 | -2,141969 | 0,293595502 | 0,000181812 | 0,052964053 |
| TNFSF12 | 92,089181 | 5,655907 | 0,674469239 | 0,000210342 | 0,057504346 |
| GFRA3 | 101,151302 | 6,134739 | 0,711668641 | 0,000235738 | 0,061603889 |
| FAM131B | 181,464732 | -5,544801 | 0,674009661 | 0,000246065 | 0,063370689 |
| ZNF44 | 448,348209 | -2,660575 | 0,386100663 | 0,000255784 | 0,064017982 |
| UNC5A | 171,595731 | -2,055024 | 0,284091889 | 0,000254375 | 0,064017982 |
| HLA-DPB1 | 257,589645 | 4,096743 | 0,557369411 | 0,000262095 | 0,0646866 |
| H4C11 | 59,272138 | 3,145864 | 0,456588286 | 0,000293094 | 0,070382225 |
| SERPINB9 | 222,213079 | 2,565982 | 0,376759785 | 0,000308057 | 0,072028525 |
| DCDC2 | 111,351198 | 3,554733 | 0,508187792 | 0,00031758 | 0,073290751 |
| B3GAT1 | 55,924350 | -6,020004 | 0,721809715 | 0,000333382 | 0,075951172 |
| H4C12 | 52,248215 | 2,875846 | 0,428253452 | 0,000372825 | 0,083861984 |
| ITGA8 | 1480,265031 | 2,565157 | 0,383623932 | 0,000396122 | 0,087988497 |
| EGR2 | 57,211147 | -3,256387 | 0,48351939 | 0,000427247 | 0,090382994 |
| CREG2 | 138,836938 | -3,811626 | 0,547340446 | 0,000420481 | 0,090382994 |
| GLT8D2 | 491,209835 | 2,068799 | 0,298657443 | 0,000445259 | 0,093085281 |
| MAGEH1 | 23,032460 | 3,765570 | 0,545761431 | 0,000456687 | 0,094364358 |
| KCNA3 | 174,522777 | -5,306064 | 0,694577979 | 0,0005276 | 0,099863623 |
| KCNH2 | 367,978109 | -2,119386 | 0,312378761 | 0,000522372 | 0,099863623 |
| PPP2R2C | 623,556841 | -3,178508 | 0,480416645 | 0,000515224 | 0,099863623 |
| H2BC11 | 104,296047 | 3,505272 | 0,521191634 | 0,000516785 | 0,099863623 |
| H2BC12 | 5516,018025 | 2,972387 | 0,452599321 | 0,000515759 | 0,099863623 |
| TMEM271 | 66,685863 | -5,078329 | 0,683493121 | 0,000603671 | 0,107272367 |
| TNC | 225,868755 | -3,865169 | 0,569370153 | 0,000613059 | 0,107861917 |
| MPPED1 | 79,902676 | -2,725473 | 0,422693183 | 0,000621349 | 0,10824876 |
| GRIP2 | 536,880773 | -2,409086 | 0,374771203 | 0,000712575 | 0,121754415 |
| H2BC4 | 158,261088 | 3,957894 | 0,587408093 | 0,000728037 | 0,123145543 |
| PLEKHB1 | 991,447366 | 2,364495 | 0,3682189 | 0,000746997 | 0,124057381 |
| CXCL12 | 497,709536 | 2,440144 | 0,383127391 | 0,000781944 | 0,127469281 |
| IGSF21 | 19,475213 | -3,463513 | 0,533943272 | 0,000789061 | 0,127469281 |
| CCDC144CP | 89,717015 | -2,343600 | 0,367716468 | 0,000833258 | 0,132440319 |

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|---|---|---|---|---|---|
| LOC105374985 | 122,075149 | 3,935212 | 0,591569805 | 0,000834739 | 0,132440319 |
| UTS2R | 669,584487 | 2,216588 | 0,345007443 | 0,000873299 | 0,135418787 |
| WFIKKN2 | 26,461499 | 3,677875 | 0,564654428 | 0,000876374 | 0,135418787 |
| H3C10 | 84,134491 | 4,237925 | 0,627580818 | 0,000901255 | 0,138062951 |
| EPSTI1 | 127,915454 | 2,507306 | 0,400637841 | 0,000932738 | 0,140464055 |
| H2AC19 | 254,781970 | 3,581659 | 0,55686518 | 0,000948618 | 0,141654904 |
| NHS | 387,764739 | -2,075790 | 0,320358692 | 0,001005432 | 0,146278352 |
| H2AC18 | 241,818396 | 3,582827 | 0,560110286 | 0,001012506 | 0,146278352 |
| CNFN | 134,566492 | 2,034835 | 0,311705432 | 0,00100874 | 0,146278352 |
| LOC102724334 | 45,875395 | 4,157796 | 0,626222775 | 0,001027497 | 0,147246965 |
| H2BS1 | 47,617542 | 4,141893 | 0,627330158 | 0,001082034 | 0,15260112 |
| RBP1 | 498,109755 | 2,335820 | 0,375359291 | 0,001111426 | 0,155512164 |
| MYT1 | 336,558529 | -2,496780 | 0,405195824 | 0,001122582 | 0,155845922 |
| IGSF10 | 166,452007 | 2,822054 | 0,460107759 | 0,001141803 | 0,157285548 |
| CLCNKB | 71,124774 | 2,626501 | 0,429119494 | 0,001168278 | 0,15854326 |
| CD2BP2-DT | 102,902309 | 2,125394 | 0,33505821 | 0,001168777 | 0,15854326 |
| SCN2A | 118,744369 | 4,382325 | 0,660897543 | 0,001257718 | 0,166966859 |
| LOC105377101 | 43,642001 | 2,453621 | 0,401504402 | 0,001259064 | 0,166966859 |
| GABBR2 | 275,256463 | -2,302025 | 0,37357461 | 0,001281988 | 0,167174498 |
| ADPRHL1 | 206,292022 | 2,044902 | 0,320362946 | 0,001275461 | 0,167174498 |
| GET1-SH3BGR | 244,495810 | -4,533027 | 0,678679707 | 0,001314393 | 0,169251913 |
| MYD88 | 450,900886 | 2,744254 | 0,45372257 | 0,001327711 | 0,1697369 |
| CHRNA4 | 93,363994 | -5,174757 | 0,743578819 | 0,001426209 | 0,175792593 |
| NOTUM | 121,190271 | -2,438830 | 0,402652245 | 0,00140174 | 0,175792593 |
| ABHD14A-ACY1 | 86,989168 | 4,121113 | 0,640588902 | 0,001426147 | 0,175792593 |
| RN7SL832P | 86,608086 | 2,603285 | 0,432534517 | 0,001416503 | 0,175792593 |
| PCDH1 | 249,128800 | -3,070607 | 0,514882728 | 0,001669514 | 0,193903631 |
| FSTL4 | 105,636621 | -3,452507 | 0,568575036 | 0,001666109 | 0,193903631 |
| LOC105379452 | 18,840817 | -7,236213 | 0,91124622 | 0,001728351 | 0,196876904 |
| LOC107987172 | 224,587454 | -2,233874 | 0,369907133 | 0,001720297 | 0,196876904 |
| CHGA | 52,623770 | 2,281134 | 0,380346509 | 0,001759575 | 0,197896488 |
| NEFL | 3076,889048 | -2,324726 | 0,39182036 | 0,001895273 | 0,211817637 |
| IRS2 | 774,762114 | -2,430070 | 0,412667393 | 0,001908012 | 0,211908554 |
| DGUOK-AS1 | 61,009747 | 3,091032 | 0,525311791 | 0,001939911 | 0,214113167 |
| RIC3 | 16,087736 | -6,163998 | 0,849278443 | 0,002004773 | 0,219906273 |
| LOC105372431 | 20,335433 | -3,024195 | 0,517910682 | 0,002051481 | 0,223616918 |
| OSTN | 265,011136 | -4,127151 | 0,669869737 | 0,002265276 | 0,235513736 |
| KCP | 63,009142 | 3,034456 | 0,524561128 | 0,002266339 | 0,235513736 |
| B4GALNT4 | 1789,211576 | -2,360494 | 0,406635152 | 0,002310023 | 0,23865763 |
| H2AC20 | 38,358109 | 3,148083 | 0,544654169 | 0,002384238 | 0,243495518 |
| GAPDHP21 | 66,226989 | 2,039074 | 0,338965735 | 0,002425363 | 0,243495518 |
| H2BC21 | 467,016242 | 2,680520 | 0,470178014 | 0,002482406 | 0,247822236 |
| CD70 | 238,434988 | -2,135637 | 0,362964621 | 0,00256215 | 0,252686977 |
| ZNF804A | 161,621028 | 2,502031 | 0,442391564 | 0,002782586 | 0,26727862 |

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| PDGFA | 321,135004 | -2,431151 | 0,432302092 | 0,003029935 | 0,284755132 |
| H2AC6 | 159,268699 | 3,655072 | 0,632378301 | 0,003107166 | 0,288759469 |
| LOC105376043 | 16,002502 | -7,968389 | 1,013067823 | 0,003119967 | 0,288759469 |
| LAMA2 | 84,810986 | 2,212674 | 0,390290428 | 0,003327536 | 0,30168526 |
| HLA-DRB1 | 261,379742 | 2,361657 | 0,423085885 | 0,003385552 | 0,305387139 |
| C1R | 326,419676 | 2,102984 | 0,366464971 | 0,003428663 | 0,306167512 |
| CDO1 | 280,605339 | 2,471103 | 0,446550508 | 0,003469559 | 0,308270276 |
| PTX3 | 196,772221 | -3,196000 | 0,575713778 | 0,003595448 | 0,310480211 |
| H4C8 | 36,880186 | 4,138057 | 0,703235663 | 0,003572774 | 0,310480211 |
| LINC00673 | 63,137675 | -2,367503 | 0,426173496 | 0,003528355 | 0,310480211 |
| RNF103-CHMP3 | 23,006288 | 4,909577 | 0,790049364 | 0,003665034 | 0,313975487 |
| DUSP5 | 188,637928 | -2,127848 | 0,376078681 | 0,003770855 | 0,315387624 |
| LGALS1 | 484,005465 | 3,165096 | 0,574286868 | 0,00379814 | 0,315387624 |
| RSU1 | 4483,402702 | 2,096227 | 0,368836706 | 0,003791163 | 0,315387624 |
| LOC100506691 | 154,987603 | -2,603430 | 0,477442577 | 0,003836928 | 0,317126558 |
| MAFF | 183,948512 | -2,747302 | 0,506155611 | 0,003969603 | 0,321912334 |
| C2orf50 | 30,828723 | 2,691050 | 0,496331917 | 0,004009059 | 0,321912334 |
| PAXIP1-AS2 | 96,613543 | 2,093501 | 0,370134505 | 0,003979131 | 0,321912334 |
| PPM1F-AS1 | 126,491921 | 2,321619 | 0,422439835 | 0,00402164 | 0,321912334 |
| RPL41P3 | 994,823529 | -6,363841 | 0,930643075 | 0,004119357 | 0,326790034 |
| ZNF441 | 217,268996 | -2,460594 | 0,453645679 | 0,004190123 | 0,327153842 |
| MIR3659HG | 35,909683 | -2,917769 | 0,539273373 | 0,004173825 | 0,327153842 |
| IFI6 | 516,531609 | 2,037603 | 0,359182836 | 0,00425093 | 0,328430553 |
| FAM20A | 18,469118 | -4,573073 | 0,769258599 | 0,004358061 | 0,330435232 |
| PHF21B | 829,424746 | -2,110548 | 0,377709072 | 0,004330359 | 0,330435232 |
| UBE2E1-AS1 | 30,518553 | 3,030628 | 0,561304591 | 0,004374402 | 0,330435232 |
| FOXI3 | 405,501943 | -2,235103 | 0,408071728 | 0,004462465 | 0,334590736 |
| FAM21EP | 28,952462 | 2,440531 | 0,454598738 | 0,004633063 | 0,344475022 |
| GNG11 | 177,289717 | 2,388944 | 0,444408438 | 0,004697628 | 0,347820231 |
| LOC151760 | 37,555359 | 4,055385 | 0,717594844 | 0,004881754 | 0,359953422 |
| EBF4 | 926,500813 | -2,105279 | 0,382956348 | 0,005039054 | 0,366983561 |
| CLTRN | 91,214118 | -2,208317 | 0,408660804 | 0,005160954 | 0,374310337 |
| HLA-DMA | 129,970696 | 2,791911 | 0,530479769 | 0,005233657 | 0,376526647 |
| DUSP8 | 1009,106859 | -2,124815 | 0,391010065 | 0,005421802 | 0,382323077 |
| AMER2 | 85,303773 | -4,903363 | 0,827422472 | 0,00556807 | 0,386300756 |
| NEXMIF | 152,020623 | -2,379328 | 0,451180425 | 0,005575786 | 0,386300756 |
| LOC105372793 | 60,164013 | -2,645564 | 0,505870059 | 0,005527368 | 0,386300756 |
| ARMC3 | 44,004830 | 3,301865 | 0,623115799 | 0,005682036 | 0,391355711 |
| H1-2 | 1253,717094 | 4,372085 | 0,778833812 | 0,006281695 | 0,402363213 |
| NGF | 28,998625 | -5,312023 | 0,878278419 | 0,006085037 | 0,402363213 |
| H2AC13 | 57,802894 | 2,912808 | 0,564885206 | 0,006324124 | 0,402363213 |
| SUSD2 | 48,559757 | 2,332326 | 0,44645699 | 0,006207968 | 0,402363213 |
| ZNF860 | 30,609216 | 3,327763 | 0,636034472 | 0,006388669 | 0,402363213 |
| SOX21-AS1 | 454,193051 | -2,288834 | 0,43839043 | 0,006430195 | 0,402363213 |
| STAB1 | 28,840577 | 4,147057 | 0,755452179 | 0,006600202 | 0,405872299 |

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|---|---|---|---|---|---|
| MARVELD3 | 125,416640 | -2,042442 | 0,378984335 | 0,006556484 | 0,405872299 |
| FOXCUT | 173,477735 | 2,678922 | 0,524240057 | 0,006691182 | 0,410007933 |
| ZNF460 | 293,617721 | -2,224608 | 0,427585615 | 0,006979412 | 0,411478038 |
| A2M-AS1 | 60,090907 | 2,706839 | 0,531927131 | 0,00691806 | 0,411478038 |
| LOC105375740 | 86,770649 | -2,370976 | 0,46056627 | 0,006846118 | 0,411478038 |
| NQO1 | 351,818692 | 2,235962 | 0,430797178 | 0,007043902 | 0,412818205 |
| TCN2 | 85,481631 | 3,841755 | 0,720806098 | 0,007062551 | 0,412818205 |
| H2AJ | 362,220293 | 2,430186 | 0,476221574 | 0,007143814 | 0,412818205 |
| LOC107985805 | 69,525191 | 2,079098 | 0,393589469 | 0,007298886 | 0,413061172 |
| PAX2 | 233,687579 | -2,136228 | 0,40852503 | 0,00735046 | 0,41334709 |
| ASNSP1 | 344,657840 | -3,151973 | 0,617752823 | 0,007338129 | 0,41334709 |
| TAPT1-AS1 | 123,498240 | -2,096041 | 0,39921997 | 0,00748669 | 0,418864575 |
| CXCR4 | 665,122921 | -2,221408 | 0,431640906 | 0,007637986 | 0,421512451 |
| HMOX1 | 1093,831527 | 2,024364 | 0,382354463 | 0,007789452 | 0,426123586 |
| SULF1 | 1407,221782 | -2,493240 | 0,495333451 | 0,007793714 | 0,426123586 |
| FAM78B | 54,049146 | -2,562930 | 0,511916417 | 0,007992772 | 0,430292346 |
| LINC01597 | 37,243723 | -2,502565 | 0,499487631 | 0,008060368 | 0,430292346 |
| EXOSC10-AS1 | 39,898137 | 2,091504 | 0,401575181 | 0,008027439 | 0,430292346 |
| SNHG32 | 4816,524514 | -2,008954 | 0,38031661 | 0,008136959 | 0,432915455 |
| H2AC11 | 72,462803 | 2,602216 | 0,522608452 | 0,008288056 | 0,435951051 |
| UBL4B | 8,989938 | -6,065390 | 0,984368804 | 0,008244327 | 0,435951051 |
| MASP1 | 21,080358 | -4,784451 | 0,85785675 | 0,008474581 | 0,441072181 |
| SETBP1 | 104,230686 | -4,504099 | 0,827547562 | 0,008697979 | 0,442373736 |
| DENND1C | 166,681322 | 2,236305 | 0,442279609 | 0,00865723 | 0,442373736 |
| ABCC6P2 | 58,605638 | 2,124452 | 0,414419093 | 0,00871163 | 0,442373736 |
| LOC105375519 | 123,303250 | 2,201741 | 0,43332124 | 0,008596054 | 0,442373736 |
| SPINK5 | 56,960169 | 3,380029 | 0,671658903 | 0,00889759 | 0,446638892 |
| DNAH17 | 660,196411 | -12,991896 | 1,415355257 | 0,008952578 | 0,44813329 |
| GNG4 | 2828,753979 | -2,154744 | 0,424255402 | 0,009041138 | 0,450555045 |
| CCDC116 | 50,743509 | 2,828669 | 0,574753817 | 0,009053493 | 0,450555045 |
| ABCF2-H2BE1 | 79,017769 | -3,696435 | 0,723836331 | 0,009167405 | 0,452063237 |
| SH2D3C | 173,250310 | -3,670695 | 0,722574101 | 0,009422087 | 0,452514835 |
| SOX21 | 192,512570 | -2,283514 | 0,457850407 | 0,009272394 | 0,452514835 |
| TMED10P2 | 13,875128 | -4,819407 | 0,871634639 | 0,009241487 | 0,452514835 |
| SHC2 | 684,471429 | -2,390509 | 0,485047011 | 0,009537637 | 0,453549176 |
| RFTN2 | 82,707924 | 2,864247 | 0,588418628 | 0,009878295 | 0,461769397 |
| LOC105379504 | 41,293086 | -2,451935 | 0,501916547 | 0,009938537 | 0,461769397 |
| IFIT3 | 43,831074 | 2,507580 | 0,51614904 | 0,010181648 | 0,462265878 |
| KCNA2 | 82,223961 | -2,978108 | 0,611573092 | 0,010043193 | 0,462265878 |
| PTPN6 | 78,379271 | 2,699979 | 0,557503478 | 0,010161193 | 0,462265878 |
| LDHD | 129,209991 | 2,010303 | 0,391882921 | 0,010149346 | 0,462265878 |
| LOC101927372 | 254,006279 | -2,567526 | 0,528534871 | 0,010056872 | 0,462265878 |
| LOC114841040 | 32,439531 | 2,586396 | 0,533564783 | 0,010187365 | 0,462265878 |
| DAB1 | 90,481342 | -3,717556 | 0,738909645 | 0,010355817 | 0,46706311 |
| LOC644285 | 414,486063 | -2,280702 | 0,463925576 | 0,010349105 | 0,46706311 |

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|---|---|---|---|---|---|
| LOC105374334 | 32,195839 | 4,638824 | 0,863822353 | 0,010384734 | 0,467181598 |
| ALOX5 | 68,900380 | -2,642849 | 0,54872954 | 0,010613777 | 0,473270214 |
| LOC105376483 | 15,592257 | 3,677065 | 0,735519121 | 0,010647714 | 0,473270214 |
| SLCO3A1 | 50,987492 | -2,509594 | 0,520864958 | 0,010816953 | 0,474027365 |
| KRT222 | 194,081512 | 2,808758 | 0,585660287 | 0,010958442 | 0,47441647 |
| PDE1A | 76,600583 | 2,668715 | 0,559252946 | 0,011334662 | 0,475644889 |
| WNT4 | 40,266779 | -3,593715 | 0,731933331 | 0,011689823 | 0,475644889 |
| ERAP2 | 220,731598 | 2,214322 | 0,454493509 | 0,011622886 | 0,475644889 |
| H3C14 | 19,132920 | 3,126135 | 0,649555568 | 0,011356085 | 0,475644889 |
| SCARA5 | 71,406056 | -4,983017 | 0,918286074 | 0,011629218 | 0,475644889 |
| LOC100420528 | 20,732670 | 2,665940 | 0,557335307 | 0,011141539 | 0,475644889 |
| MYOF | 98,844708 | 2,405213 | 0,503064848 | 0,011839179 | 0,477389443 |
| PTHLH | 67,818047 | -2,799376 | 0,591552441 | 0,012055277 | 0,482482583 |
| SAMD9 | 284,810135 | 2,572262 | 0,544851383 | 0,012360968 | 0,486358865 |
| LOC107986617 | 17,359839 | 3,855924 | 0,77857966 | 0,012391103 | 0,486358865 |
| LOC107987250 | 48,694225 | 2,309197 | 0,482601656 | 0,012355056 | 0,486358865 |
| CALCRL | 179,524358 | 2,819903 | 0,599296854 | 0,012572062 | 0,487190171 |
| H3C15 | 18,019846 | 3,213396 | 0,674335694 | 0,012510092 | 0,487190171 |
| LPP-AS2 | 27,195223 | 2,953635 | 0,626554803 | 0,01263898 | 0,487190171 |
| FOSL2 | 498,345889 | -2,160202 | 0,449119202 | 0,013357203 | 0,491346421 |
| GPER1 | 43,831085 | 2,068560 | 0,424244067 | 0,013445204 | 0,491346421 |
| ONECUT1 | 80,375529 | -2,513206 | 0,53652296 | 0,013210403 | 0,491346421 |
| LOC105378808 | 60,735803 | -2,405349 | 0,511242528 | 0,013256575 | 0,491346421 |
| LOC105370363 | 22,128300 | 2,915329 | 0,625509733 | 0,013593049 | 0,49295607 |
| GALR2 | 18,776678 | 2,690987 | 0,582278692 | 0,014180182 | 0,505122879 |
| MGC16275 | 19,913205 | 2,699908 | 0,584681385 | 0,014255746 | 0,505122879 |
| PURPL | 905,326998 | -2,178588 | 0,458829099 | 0,014349526 | 0,505122879 |
| PCAT7 | 44,179737 | 2,529582 | 0,547027132 | 0,014381473 | 0,505122879 |
| LOC107986673 | 32,149159 | -2,555470 | 0,55349272 | 0,014463524 | 0,505122879 |
| BHLHE40 | 3211,357365 | -2,035148 | 0,420187279 | 0,01469918 | 0,507367599 |
| ZNNT1 | 193,418348 | -2,055119 | 0,426198756 | 0,014754478 | 0,507367599 |
| ABCC2 | 147,085656 | -2,064318 | 0,429579076 | 0,014926274 | 0,5081224 |
| MID1 | 8398,040743 | 2,442604 | 0,530037031 | 0,015065038 | 0,509915674 |
| SCN3B | 251,318239 | -3,127228 | 0,678378073 | 0,015319743 | 0,513718244 |
| LOC105376504 | 61,762559 | -3,448586 | 0,737366292 | 0,015429375 | 0,515375921 |
| MAGEB2 | 150,733781 | 5,985202 | 1,066853118 | 0,015535903 | 0,517960597 |
| SAMD11 | 3551,242289 | 2,512037 | 0,550171652 | 0,015720042 | 0,520195799 |
| LMCD1 | 280,590523 | -2,331061 | 0,50615077 | 0,015852283 | 0,522625367 |
| LOC101928092 | 140,132142 | -2,301133 | 0,501431022 | 0,016492685 | 0,528692213 |
| LOC101927441 | 20,980243 | 2,953978 | 0,652620361 | 0,016645856 | 0,530308548 |
| LOC105371870 | 96,721458 | -2,043582 | 0,430801613 | 0,016690937 | 0,530308548 |
| H3C6 | 480,760988 | 2,091117 | 0,445043835 | 0,016784642 | 0,530717248 |
| PHYH | 1351,003601 | 2,079548 | 0,442799167 | 0,017058774 | 0,531333198 |
| VAMP8 | 885,013422 | 2,171423 | 0,468580666 | 0,016972804 | 0,531333198 |
| ZNF528 | 51,419408 | -2,789087 | 0,620849434 | 0,017149 | 0,531333198 |

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| LOC105379392 | 30,522192 | 2,168717 | 0,468142051 | 0,017047111 | 0,531333198 |
| H4C15 | 848,081978 | 2,326789 | 0,513961658 | 0,017764578 | 0,543333142 |
| ZSCAN18 | 496,028424 | -2,477565 | 0,553161678 | 0,01796893 | 0,544894016 |
| BST1 | 42,447076 | -2,733265 | 0,613235969 | 0,018004493 | 0,545042312 |
| H2BC5 | 325,329786 | 2,052075 | 0,43867119 | 0,018071646 | 0,546144805 |
| EXTL1 | 39,272401 | 2,955607 | 0,662931628 | 0,01835417 | 0,550006069 |
| FANCF | 24,796607 | 3,274535 | 0,726371963 | 0,01847581 | 0,55028118 |
| LOC105375010 | 29,577349 | -2,326060 | 0,51692616 | 0,018471957 | 0,55028118 |
| HCN4 | 200,515863 | -2,341954 | 0,52183483 | 0,018638418 | 0,551089327 |
| MIR1915HG | 622,393508 | 2,143832 | 0,467832047 | 0,018688765 | 0,551660042 |
| SHBG | 16,336178 | 2,600599 | 0,586773003 | 0,018779639 | 0,552506929 |
| LOC105374493 | 34,884114 | -2,082786 | 0,450736212 | 0,018853601 | 0,552852287 |
| SMIM2-AS1 | 39,907480 | 2,069649 | 0,447096195 | 0,018919456 | 0,553627805 |
| LOC112268241 | 16,162227 | 2,576821 | 0,58192947 | 0,018942358 | 0,553627805 |
| PTPRO | 109,503379 | -3,192074 | 0,717533457 | 0,019612448 | 0,564851214 |
| GABRQ | 117,505298 | -3,325180 | 0,743274717 | 0,019692484 | 0,565850958 |
| ST6GALNAC5 | 58,661560 | -2,277628 | 0,509295209 | 0,019715577 | 0,565850958 |
| AGGF1P1 | 75,236533 | -2,001329 | 0,429735175 | 0,019846073 | 0,566829963 |
| BTBD19 | 19,815384 | -2,256164 | 0,505427563 | 0,020204302 | 0,569046054 |
| TOP1P1 | 20,975574 | 2,395720 | 0,545105753 | 0,020760003 | 0,576763449 |
| LBH | 348,392939 | -2,007632 | 0,436482617 | 0,021243329 | 0,580922357 |
| JMJD1C-AS1 | 20,547817 | 2,177953 | 0,486735487 | 0,021046359 | 0,580922357 |
| CRHR1 | 74,163037 | -3,119579 | 0,714829279 | 0,021667636 | 0,587838014 |
| ALDH3A1 | 51,564457 | 2,030258 | 0,445706127 | 0,021892099 | 0,589428174 |
| TOGARAM2 | 64,410262 | 2,032265 | 0,446168429 | 0,021844844 | 0,589428174 |
| LY6G6F-LY6G6D | 30,422044 | 2,837476 | 0,656716005 | 0,021957089 | 0,589475932 |
| ISM1 | 168,213279 | 2,253060 | 0,514240247 | 0,022674901 | 0,596937774 |
| HLA-DRB5 | 66,684569 | 2,095448 | 0,474913907 | 0,024622952 | 0,6124707 |
| PLXNC1 | 125,599244 | -2,032641 | 0,455195742 | 0,024565674 | 0,6124707 |
| OLFM1 | 87,194852 | -2,502325 | 0,588324214 | 0,024498682 | 0,6124707 |
| ZMAT1 | 154,767848 | -2,057124 | 0,460991629 | 0,023984921 | 0,6124707 |
| COL23A1 | 161,782803 | -2,293905 | 0,533073397 | 0,024641254 | 0,6124707 |
| GRIN3B | 75,913529 | -2,122059 | 0,480329354 | 0,023831561 | 0,6124707 |
| TCAM1P | 292,359082 | -2,164467 | 0,494167664 | 0,024176086 | 0,6124707 |
| SNORA11F | 26,338611 | 2,425985 | 0,565904865 | 0,023862346 | 0,6124707 |
| LINC02154 | 46,614149 | -4,990886 | 1,026013531 | 0,023790692 | 0,6124707 |
| PVALB | 47,946661 | 2,151926 | 0,493283792 | 0,025002553 | 0,613180123 |
| LAMB2P1 | 81,418210 | -2,224735 | 0,515092519 | 0,025112833 | 0,613180123 |
| PLPP4 | 83,437231 | -2,586149 | 0,6118097 | 0,02505361 | 0,613180123 |
| HAPLN2 | 66,310597 | -2,150832 | 0,493860281 | 0,025269234 | 0,613519736 |
| ZNF136 | 547,872865 | -2,288885 | 0,537473715 | 0,026235772 | 0,618327315 |
| DLEC1 | 69,802038 | -2,346366 | 0,557397501 | 0,027282522 | 0,618327315 |
| ZNF681 | 67,945174 | -3,170104 | 0,753168711 | 0,027102651 | 0,618327315 |
| SOX1-OT | 27,428964 | -2,472606 | 0,588381895 | 0,026438999 | 0,618327315 |
| LOC107987248 | 27,404747 | -2,656373 | 0,638453499 | 0,027271334 | 0,618327315 |

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|---|---|---|---|---|---|
| LOC107987251 | 24,939658 | -2,492595 | 0,591782975 | 0,025975741 | 0,618327315 |
| LEF1-AS1 | 10,382565 | 2,965153 | 0,712581027 | 0,027764282 | 0,62136913 |
| DST-AS1 | 18,634134 | 2,385808 | 0,570050732 | 0,027761299 | 0,62136913 |
| LOC105369250 | 54,782954 | -2,358759 | 0,563292125 | 0,027960272 | 0,624188491 |
| INSM2 | 11,886420 | -4,562444 | 0,998014051 | 0,028223603 | 0,626134106 |
| CHST8 | 147,860459 | -2,191799 | 0,516440039 | 0,028368458 | 0,62747547 |
| LOC102724378 | 107,836594 | 2,044709 | 0,471499984 | 0,028630399 | 0,631967839 |
| CILP2 | 1056,471899 | 2,191085 | 0,51891651 | 0,029199336 | 0,638129205 |
| LOC105376328 | 35,957406 | 3,257089 | 0,781766807 | 0,029320919 | 0,638129205 |
| BST2 | 129,190668 | -2,603304 | 0,637831445 | 0,030455147 | 0,638242279 |
| HRH1 | 31,364331 | -3,547574 | 0,839254605 | 0,029500518 | 0,638242279 |
| IGF2 | 298,928826 | -2,190637 | 0,523733752 | 0,030760052 | 0,638242279 |
| SPOCK1 | 74,099071 | -2,533698 | 0,620688448 | 0,030703218 | 0,638242279 |
| HRK | 1442,061989 | -2,067082 | 0,482684959 | 0,029980322 | 0,638242279 |
| CEACAM19 | 421,866469 | -2,111206 | 0,496631935 | 0,029949543 | 0,638242279 |
| AGAP11 | 226,224745 | -4,149321 | 0,945037251 | 0,029835361 | 0,638242279 |
| LOC100132813 | 26,858145 | 3,591384 | 0,848840792 | 0,029779515 | 0,638242279 |
| TGM2 | 102,982558 | 2,036974 | 0,476814833 | 0,031344216 | 0,641216622 |
| GRM4 | 33,914389 | -2,166065 | 0,518157665 | 0,031397154 | 0,641295886 |
| IL6R | 455,226024 | -2,414722 | 0,597222214 | 0,033202873 | 0,657379503 |
| STUM | 712,383401 | -2,019302 | 0,475845422 | 0,033118578 | 0,657379503 |
| KRT8 | 1692,119095 | -3,237575 | 0,803462327 | 0,034900367 | 0,659904218 |
| PDE1B | 121,592956 | -2,420183 | 0,614313225 | 0,037923755 | 0,659904218 |
| TF | 53,626629 | -2,140486 | 0,526316224 | 0,036971291 | 0,659904218 |
| TNXB | 126,148950 | -2,777447 | 0,700142904 | 0,03529643 | 0,659904218 |
| H2AC17 | 44,397996 | 2,123504 | 0,514353935 | 0,034664515 | 0,659904218 |
| H3C2 | 37,279100 | 2,441449 | 0,611098822 | 0,035095964 | 0,659904218 |
| H4C14 | 171,407851 | 2,145295 | 0,529799692 | 0,037665465 | 0,659904218 |
| RBMXL2 | 7,056080 | -4,092136 | 0,970121257 | 0,036129778 | 0,659904218 |
| TBX21 | 23,823518 | -3,535255 | 0,87011824 | 0,036281811 | 0,659904218 |
| MXRA8 | 742,309992 | 4,938746 | 1,100322983 | 0,036254433 | 0,659904218 |
| FBXO43 | 27,910448 | 2,324499 | 0,586318879 | 0,037937867 | 0,659904218 |
| NKX1-2 | 328,033589 | -2,063241 | 0,498482414 | 0,03606565 | 0,659904218 |
| LOC101929174 | 40,160169 | -2,477070 | 0,620696243 | 0,03500213 | 0,659904218 |
| LOC105370910 | 97,580591 | -2,037697 | 0,492260299 | 0,03696304 | 0,659904218 |
| CCDC153 | 45,688284 | 2,117462 | 0,521734304 | 0,038033238 | 0,660655556 |
| GFAP | 56,207540 | 2,525608 | 0,645819608 | 0,038483651 | 0,665228083 |
| TXLNB | 67,542515 | 2,138848 | 0,532055281 | 0,039255018 | 0,672672778 |
| SUGT1P4-STRA6LP | 90,262837 | 2,070079 | 0,509493046 | 0,039374107 | 0,672767195 |
| ADCYAP1R1 | 465,193709 | -2,198484 | 0,551971334 | 0,039494182 | 0,674170625 |
| LOC105371532 | 14,132693 | 2,467460 | 0,634079108 | 0,039879884 | 0,676255363 |
| LOC729557 | 9,871495 | -3,513475 | 0,883260477 | 0,040120401 | 0,676413214 |
| SCARNA17 | 28,820570 | -2,044434 | 0,503553726 | 0,040477633 | 0,676756734 |
| MYRIP | 88,728956 | -3,270970 | 0,835919301 | 0,040823763 | 0,677578065 |
| LOC100128164 | 19,536298 | 2,490301 | 0,644092608 | 0,040985032 | 0,677578065 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| LOC107985770 | 68,489353 | 2,396833 | 0,617532415 | 0,041130972 | 0,677578065 |
| PTGER2 | 85,787112 | 2,029074 | 0,504340009 | 0,042962561 | 0,679242342 |
| SORCS2 | 32,286955 | -2,270660 | 0,580786738 | 0,04164157 | 0,679242342 |
| DLGAP3 | 87,714925 | -2,189738 | 0,557256084 | 0,042442684 | 0,679242342 |
| NOD2 | 29,843526 | -2,656171 | 0,696051762 | 0,042890477 | 0,679242342 |
| LRRTM4 | 150,016199 | 2,702259 | 0,707208258 | 0,042567824 | 0,679242342 |
| SYT9 | 129,882797 | -2,769766 | 0,722887965 | 0,042033928 | 0,679242342 |
| TCTE1 | 51,052442 | -2,897185 | 0,755715189 | 0,042282642 | 0,679242342 |
| LINC01402 | 10,805989 | -3,217822 | 0,829104117 | 0,041989727 | 0,679242342 |
| LOC105371017 | 36,450784 | -2,459946 | 0,637256278 | 0,041565889 | 0,679242342 |
| LOC105378833 | 20,204920 | -2,245461 | 0,576124057 | 0,042803151 | 0,679242342 |
| KCNMA1 | 74,965729 | -2,250091 | 0,579673145 | 0,043554829 | 0,679530352 |
| NTRK2 | 141,708054 | -2,044637 | 0,510582031 | 0,04328823 | 0,679530352 |
| PAX5 | 19,568319 | -2,734964 | 0,717831779 | 0,043166855 | 0,679530352 |
| LOC112268295 | 24,415084 | -2,997949 | 0,783904476 | 0,043318754 | 0,679530352 |
| IL11 | 44,702869 | -2,752191 | 0,725039729 | 0,043958762 | 0,67984961 |
| MRO | 15,883299 | 2,329972 | 0,605762425 | 0,043956368 | 0,67984961 |
| STAC2 | 260,470414 | 2,553762 | 0,6713543 | 0,043928815 | 0,67984961 |
| MSANTD1 | 33,984032 | -2,022199 | 0,50443212 | 0,044009807 | 0,680047188 |
| THBS4 | 76,990769 | -2,139081 | 0,545757687 | 0,044427726 | 0,681228534 |
| SUGT1P3 | 19,701491 | -2,308214 | 0,601111382 | 0,044688301 | 0,681311766 |
| TMEM178A | 54,875002 | -2,018488 | 0,505256216 | 0,04491301 | 0,681468869 |
| PHOSPHO1 | 96,998389 | 2,060482 | 0,520749767 | 0,045193765 | 0,682184047 |
| LOC107986246 | 15,956279 | -2,135533 | 0,546524024 | 0,045195192 | 0,682184047 |
| SMIM38 | 89,398948 | -4,752361 | 1,12486107 | 0,045603814 | 0,682746789 |
| PEG10 | 51,475601 | 2,171752 | 0,560292324 | 0,045833778 | 0,683667226 |
| C8orf34-AS1 | 36,077362 | -2,149353 | 0,55358984 | 0,046143368 | 0,683667226 |
| LOC105376010 | 162,695106 | -4,282941 | 1,050605227 | 0,045769033 | 0,683667226 |
| H2BC17 | 62,093953 | 2,172750 | 0,562547537 | 0,046580628 | 0,687489829 |
| TNFRSF12A | 702,530996 | -2,201738 | 0,572560751 | 0,046736058 | 0,688639922 |
| SNORD15A | 12,494615 | -3,166962 | 0,837004461 | 0,046926124 | 0,689367271 |
| GNAO1 | 354,579308 | -2,304205 | 0,606754546 | 0,047169963 | 0,69095057 |
| SATB2-AS1 | 24,904431 | 2,408586 | 0,640765043 | 0,047796243 | 0,69481449 |
| RPL5P30 | 13,576400 | -3,342785 | 0,880028155 | 0,04788322 | 0,69481449 |
| C15orf48 | 44,677075 | -2,657012 | 0,717744712 | 0,049505175 | 0,706024844 |
| LOC441087 | 36,410145 | -2,278663 | 0,606125248 | 0,049960668 | 0,707138674 |

| KEGG | N. of SigGenes | Pvalue | Bonferroni | FDR | Number of SigGenes UP | Number of SigGenes DOWN |
|---|---|---|---|---|---|---|
| Systemic lupus erythematosus | 31 | 1,23E-38 | 2,83E-36 | 2,83E-36 | 31 | 0 |
| Alcoholism | 32 | 8,62E-36 | 1,98E-33 | 9,88E-34 | 27 | 5 |
| Neutrophil extracellular trap formation | 26 | 2,57E-26 | 5,89E-24 | 1,96E-24 | 26 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Viral carcinogenesis | 15 | 2,83E-11 | 6,49E-09 | 1,62E-09 | 13 | 2 |
| **PI3K-Akt signaling pathway** | 14 | 2,63E-07 | 6,02E-05 | 1,20E-05 | 3 | 11 |
| Neuroactive ligand-receptor interaction | 14 | 3,96E-07 | 9,06E-05 | 1,51E-05 | 4 | 10 |
| Herpes simplex virus 1 infection | 15 | 3,00E-06 | 6,87E-04 | 9,81E-05 | 6 | 9 |
| Toxoplasmosis | 8 | 5,21E-06 | 1,19E-03 | 1,49E-04 | 6 | 2 |
| Necroptosis | 9 | 5,88E-06 | 1,35E-03 | 1,50E-04 | 9 | 0 |
| Intestinal immune network for IgA production | 6 | 1,17E-05 | 2,68E-03 | 2,68E-04 | 5 | 1 |
| Taste transduction | 7 | 1,41E-05 | 3,23E-03 | 2,93E-04 | 2 | 5 |
| Morphine addiction | 7 | 1,95E-05 | 4,46E-03 | 3,72E-04 | 2 | 5 |
| Pathways in cancer | 14 | 2,21E-05 | 5,06E-03 | 3,89E-04 | 6 | 8 |
| Viral myocarditis | 6 | 3,18E-05 | 7,29E-03 | 5,21E-04 | 5 | 1 |
| Inflammatory bowel disease | 6 | 4,70E-05 | 1,08E-02 | 7,17E-04 | 4 | 2 |
| Renin secretion | 6 | 6,27E-05 | 1,44E-02 | 8,97E-04 | 2 | 4 |
| **MAPK signaling pathway** | 10 | 9,54E-05 | 2,18E-02 | 1,28E-03 | 1 | 9 |
| Leishmaniasis | 6 | 1,06E-04 | 2,43E-02 | 1,35E-03 | 6 | 0 |
| **Calcium signaling pathway** | 9 | 1,60E-04 | 3,67E-02 | 1,93E-03 | 1 | 8 |
| Transcriptional misregulation in cancer | 8 | 1,80E-04 | 4,12E-02 | 2,06E-03 | 5 | 3 |
| GABAergic synapse | 6 | 2,10E-04 | 4,81E-02 | 2,29E-03 | 1 | 5 |

**Appendix table S6. Differentially expressed proteins in HEK293T-ACE2 cells upon treatment with 1 µM compound #7 for 24 h.**

Proteomic assay based on LC-MS/MS approach performed on HEK-293T-ACE2 cells treated with PI-7 molecule (1 µM) for 24 h. In the treated cells, there were found 17 downregulated and 66 upregulated proteins. Data given include protein entry, protein names, gene names, log2 fold changes (log2FC), fold change (FC), Student's *t*-test false discovery rate (FDR), number of peptides (Razor + unique peptides), and proportion of sequence coverage (Unique + razon sequence coverage).

| **Entry** | **Protein name** | **Gene name** | **log2FC** | **FC** | **Student's *t*-test FDR** | **Razor + unique peptides** | **Unique + razor sequence coverage (%)** |
|---|---|---|---|---|---|---|---|
| Q6FI81 | Anamorsin | CIAPIN1 | -0,92 | 0,53 | 3,71E-02 | 4 | 24,4 |
| P55145 | Mesencephalic astrocyte-derived neurotrophic factor | MANF | -0,87 | 0,55 | 4,88E-02 | 6 | 33 |
| P10412 | Histone H1.4 | HIST1H1E | -0,73 | 0,60 | 5,44E-04 | 12 | 32,4 |
| P51572 | B-cell receptor-associated protein 31 | BCAP31 | -0,72 | 0,61 | 6,31E-03 | 7 | 26 |
| P62280 | 40S ribosomal protein S11 | RPS11 | -0,70 | 0,61 | 5,76E-03 | 8 | 41,1 |
| P47813 | Eukaryotic translation initiation factor 1A, X-chromosomal | EIF1AX | -0,70 | 0,62 | 3,17E-03 | 6 | 34 |
| P62750 | 60S ribosomal protein L23a | RPL23A | -0,62 | 0,65 | 3,54E-03 | 9 | 37,2 |
| P62979 | Ubiquitin-40S ribosomal protein S27a | RPS27A | -0,62 | 0,65 | 5,82E-05 | 12 | 55,8 |
| P84090 | Enhancer of rudimentary homolog | ERH | -0,58 | 0,67 | 1,32E-02 | 4 | 37,5 |
| P60866 | 40S ribosomal protein S20 | RPS20 | -0,58 | 0,67 | 2,10E-03 | 4 | 28,6 |
| P35613 | Basigin | BSG | -0,57 | 0,67 | 2,79E-03 | 6 | 22,9 |
| Q9H444 | Charged multivesicular body protein 4b | CHMP4B | -0,57 | 0,67 | 5,54E-04 | 6 | 27,7 |
| Q07020 | 60S ribosomal protein L18 | RPL18 | -0,56 | 0,68 | 9,09E-03 | 7 | 35,6 |
| P42677 | 40S ribosomal protein S27 | RPS27 | -0,55 | 0,68 | 2,24E-04 | 5 | 40,5 |
| P25788 | Proteasome subunit alpha type-3 | PSMA3 | -0,52 | 0,70 | 5,44E-04 | 6 | 22,4 |
| P13073 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial | COX4I1 | -0,50 | 0,71 | 7,07E-03 | 6 | 31,4 |
| Q9BRA2 | Thioredoxin domain-containing protein 17 | TXNDC17 | -0,50 | 0,71 | 3,68E-03 | 4 | 46,3 |
| P38159 | RNA-binding motif protein, X chromosome | RBMX | -0,50 | 0,71 | 2,35E-04 | 10 | 26,1 |
| P48643 | T-complex protein 1 subunit epsilon | CCT5 | 0,50 | 1,41 | 6,28E-04 | 28 | 68,6 |
| P12532 | Creatine kinase U-type, mitochondrial | CKMT1A | 0,50 | 1,41 | 6,28E-04 | 7 | 35,5 |
| P04844 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 | RPN2 | 0,50 | 1,41 | 1,71E-04 | 16 | 39,9 |
| Q9Y5L0 | Transportin-3 | TNPO3 | 0,50 | 1,41 | 4,25E-02 | 6 | 11,1 |
| P63208 | S-phase kinase-associated protein 1 | SKP1 | 0,50 | 1,41 | 7,76E-03 | 5 | 33,7 |
| P06748 | Nucleophosmin | NPM1 | 0,51 | 1,42 | 3,58E-03 | 11 | 36,4 |
| O15160 | DNA-directed RNA polymerases I and III subunit RPAC1 | POLR1C | 0,52 | 1,43 | 3,37E-03 | 5 | 21,7 |
| Q9Y285 | Phenylalanine--tRNA ligase alpha subunit | FARSA | 0,52 | 1,44 | 1,69E-02 | 6 | 19,5 |
| P23921 | Ribonucleoside-diphosphate reductase large subunit | RRM1 | 0,53 | 1,44 | 8,05E-03 | 8 | 19,4 |
| Q13126 | S-methyl-5-thioadenosine phosphorylase | MTAP | 0,55 | 1,46 | 3,11E-03 | 8 | 48,1 |
| Q9BSJ8 | Extended synaptotagmin-1 | ESYT1 | 0,55 | 1,47 | 1,37E-02 | 5 | 6,4 |
| Q15435 | Protein phosphatase 1 regulatory subunit 7 | PPP1R7 | 0,55 | 1,47 | 4,65E-03 | 6 | 23,9 |
| Q92616 | eIF-2-alpha kinase activator GCN1 | GCN1 | 0,55 | 1,47 | 1,74E-04 | 35 | 21 |

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|---|---|---|---|---|---|---|---|
| P24534 | Elongation factor 1-beta | EEF1B2 | 0,56 | 1,47 | 2,75E-03 | 5 | 37,3 |
| P09104 | Gamma-enolase | ENO2 | 0,56 | 1,47 | 2,35E-04 | 13 | 48,6 |
| Q14257 | Reticulocalbin-2 | RCN2 | 0,57 | 1,49 | 6,68E-03 | 4 | 20,8 |
| P62917 | 60S ribosomal protein L8 | RPL8 | 0,58 | 1,50 | 9,79E-03 | 7 | 33,9 |
| Q8IY67 | Ribonucleoprotein PTB-binding 1 | RAVER1 | 0,58 | 1,50 | 2,35E-04 | 5 | 17,3 |
| Q8IZL8 | Proline-, glutamic acid- and leucine-rich protein 1 | PELP1 | 0,59 | 1,51 | 3,75E-03 | 6 | 9,4 |
| P61011 | Signal recognition particle 54 kDa protein | SRP54 | 0,60 | 1,51 | 2,37E-02 | 7 | 21 |
| Q9UBE0 | SUMO-activating enzyme subunit 1 | SAE1 | 0,60 | 1,52 | 4,37E-04 | 11 | 47,1 |
| Q6P1J9 | Parafibromin | CDC73 | 0,60 | 1,52 | 2,70E-02 | 4 | 9,6 |
| Q9ULC4 | Malignant T-cell-amplified sequence 1 | MCTS1 | 0,62 | 1,54 | 3,58E-03 | 7 | 57,5 |
| P47985 | Cytochrome b-c1 complex subunit Rieske, mitochondrial | UQCRFS1 | 0,62 | 1,54 | 3,37E-03 | 4 | 22,6 |
| Q8N3U4 | Cohesin subunit SA-2 | STAG2 | 0,63 | 1,55 | 1,48E-02 | 7 | 8,1 |
| P26038 | Moesin | MSN | 0,63 | 1,55 | 5,64E-03 | 7 | 15,8 |
| P60953 | Cell division control protein 42 homolog | CDC42 | 0,63 | 1,55 | 7,15E-03 | 8 | 48,2 |
| Q15021 | Condensin complex subunit 1 | NCAPD2 | 0,64 | 1,55 | 3,53E-03 | 14 | 16,2 |
| Q96P70 | Importin-9 | IPO9 | 0,66 | 1,58 | 1,03E-02 | 5 | 9,1 |
| P26599 | Polypyrimidine tract-binding protein 1 | PTBP1 | 0,66 | 1,59 | 2,24E-04 | 16 | 52 |
| Q9C0B1 | Alpha-ketoglutarate-dependent dioxygenase FTO | FTO | 0,67 | 1,59 | 6,56E-03 | 7 | 20,4 |
| Q92896 | Golgi apparatus protein 1 | GLG1 | 0,69 | 1,61 | 2,52E-02 | 4 | 4,8 |
| Q96CS3 | FAS-associated factor 2 | FAF2 | 0,69 | 1,62 | 2,35E-04 | 4 | 16,2 |
| P61970 | Nuclear transport factor 2 | NUTF2 | 0,70 | 1,62 | 3,58E-03 | 5 | 69,3 |
| P63010 | AP-2 complex subunit beta | AP2B1 | 0,70 | 1,63 | 2,39E-04 | 10 | 20,4 |
| P04632 | Calpain small subunit 1 | CAPNS1 | 0,71 | 1,63 | 3,81E-02 | 5 | 31 |
| Q9Y6G9 | Cytoplasmic dynein 1 light intermediate chain 1 | DYNC1LI1 | 0,73 | 1,65 | 2,07E-03 | 5 | 18,4 |
| Q9HAV4 | Exportin-5 | XPO5 | 0,73 | 1,65 | 2,21E-03 | 13 | 15,9 |
| O75947 | ATP synthase subunit d, mitochondrial | ATP5PD | 0,73 | 1,66 | 1,71E-03 | 8 | 64 |
| P08708 | 40S ribosomal protein S17 | RPS17 | 0,74 | 1,67 | 9,90E-04 | 8 | 60 |
| P20290 | Transcription factor BTF3 | BTF3 | 0,75 | 1,68 | 1,20E-03 | 6 | 48,1 |
| Q96AC1 | Fermitin family homolog 2 | FERMT2 | 0,75 | 1,68 | 1,48E-02 | 8 | 18,4 |
| Q5JTH9 | RRP12-like protein | RRP12 | 0,79 | 1,72 | 4,43E-02 | 11 | 12,8 |
| Q9H0A0 | RNA cytidine acetyltransferase | NAT10 | 0,79 | 1,73 | 5,44E-04 | 12 | 17,2 |
| Q96T76 | MMS19 nucleotide excision repair protein homolog | MMS19 | 0,80 | 1,75 | 5,44E-04 | 6 | 10,2 |
| P62081 | 40S ribosomal protein S7 | RPS7 | 0,82 | 1,76 | 2,31E-03 | 12 | 55,7 |
| O00429 | Dynamin-1-like protein | DNM1L | 0,82 | 1,77 | 1,42E-03 | 12 | 27,3 |
| P35270 | Sepiapterin reductase | SPR | 0,87 | 1,83 | 1,81E-02 | 4 | 24,5 |
| O00764 | Pyridoxal kinase | PDXK | 0,87 | 1,83 | 1,97E-02 | 4 | 21,2 |
| O15260 | Surfeit locus protein 4 | SURF4 | 0,88 | 1,83 | 1,82E-03 | 4 | 18,2 |
| Q9BXW7 | Haloacid dehalogenase-like hydrolase domain-containing 5 | HDHD5 | 0,92 | 1,89 | 2,99E-03 | 6 | 25,1 |
| P61086 | Ubiquitin-conjugating enzyme E2 K | UBE2K | 0,92 | 1,90 | 3,36E-02 | 4 | 33 |
| P99999 | Cytochrome c | CYCS | 0,97 | 1,95 | 6,59E-04 | 4 | 41 |
| Q14978 | Nucleolar and coiled-body phosphoprotein 1 | NOLC1 | 1,01 | 2,01 | 2,14E-02 | 8 | 15,2 |
| Q99436 | Proteasome subunit beta type-7 | PSMB7 | 1,01 | 2,02 | 7,16E-03 | 6 | 34,3 |
| Q9GZS3 | WD repeat-containing protein 61 | WDR61 | 1,02 | 2,02 | 2,21E-03 | 4 | 26,9 |
| Q9BWD1 | Acetyl-CoA acetyltransferase, cytosolic | ACAT2 | 1,03 | 2,04 | 2,07E-04 | 5 | 35 |
| Q05639 | Elongation factor 1-alpha 2 | EEF1A2 | 1,04 | 2,05 | 8,77E-04 | 8 | 38,2 |
| Q14011 | Cold-inducible RNA-binding protein | CIRBP | 1,06 | 2,09 | 4,55E-04 | 4 | 32 |
| Q16836 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial | HADH | 1,07 | 2,09 | 4,26E-04 | 8 | 42,4 |
| Q8N684 | Cleavage and polyadenylation specificity factor subunit 7 | CPSF7 | 1,08 | 2,11 | 2,71E-02 | 4 | 13,4 |
| Q99598 | Translin-associated protein X | TSNAX | 1,11 | 2,16 | 7,56E-03 | 4 | 22,8 |
| Q15428 | Splicing factor 3A subunit 2 | SF3A2 | 1,11 | 2,17 | 4,19E-02 | 7 | 24,4 |
| P25787 | Proteasome subunit alpha type-2 | PSMA2 | 1,12 | 2,17 | 1,71E-04 | 7 | 45,7 |
| P07602 | Prosaposin | PSAP | 1,31 | 2,47 | 2,35E-02 | 4 | 9,2 |
| Q7L1Q6 | Basic leucine zipper and W2 domain-containing protein 1 | BZW1 | 2,10 | 4,28 | 1,76E-03 | 8 | 23,4 |

**Appendix table S7. Proteins that take part in the interaction-network, according to those downregulated by compound #7 in HEK293T-ACE2 cells.**

A protein interaction network was generated using the Search Tool for the Retrieval of Interacting Genes/ Proteins (STRING) database (https://string-db.org), using only those proteins that were downregulated in PI-7- treated cells. Data given include term ID, term description, observed gene count in the network, background gene count, strength, false discovery rate (FDR), and matching network proteins.

| Term ID | Term description | Observed gene count | Background gene count | Strength | FDR | Matching proteins in the network |
|---|---|---|---|---|---|---|
| GO:0070972 | Protein localization to endoplasmic reticulum | 8 | 140 | 1.79 | 4.64e-09 | CHMP4B,RPS11,RPS27A,RPS27,RPL23A,BCAP31,RPS20,RPL18 |
| GO:0045047 | Protein targeting to endoplasmic reticulum | 7 | 110 | 1.84 | 4.39e-08 | CHMP4B,RPS11,RPS27A,RPS27,RPL23A,RPS20,RPL18 |
| GO:0006413 | Translational initiation | 7 | 141 | 1.73 | 1.16e-07 | RPS11,RPS27A,RPS27,EIF1AX,RPL23A,RPS20,RPL18 |
| GO:0006612 | Protein targeting to membrane | 7 | 165 | 1.66 | 2.69e-07 | CHMP4B,RPS11,RPS27A,RPS27,RPL23A,RPS20,RPL18 |
| GO:0006614 | SRP-dependent cotranslational protein targeting to membrane | 6 | 96 | 1.83 | 6.50e-07 | RPS11,RPS27A,RPS27,RPL23A,RPS20,RPL18 |
| GO:0019083 | Viral transcription | 6 | 115 | 1.75 | 1.38e-06 | RPS11,RPS27A,RPS27,RPL23A,RPS20,RPL18 |
| GO:0000184 | Nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 6 | 119 | 1.74 | 1.49e-06 | RPS11,RPS27A,RPS27,RPL23A,RPS20,RPL18 |
| GO:0072657 | Protein localization to membrane | 8 | 495 | 1.24 | 6.70e-06 | CHMP4B,RPS11,RPS27A,BSG,RPS27,RPL23A,RPS20,RPL18 |
| GO:0016032 | Viral process | 9 | 776 | 1.1 | 8.86e-06 | PSMA3,CHMP4B,RPS11,RPS27A,RPS27,RPL23A,BCAP31,RPS20,RPL18 |
| GO:0044265 | Cellular macromolecule catabolic process | 8 | 917 | 0.98 | 0.00035 | PSMA3,CHMP4B,RPS11,RPS27A,RPS27,RPL23A,RPS20,RPL18 |
| GO:0006886 | Intracellular protein transport | 8 | 999 | 0.94 | 0.00062 | CHMP4B,RPS11,RPS27A,RPS27,RPL23A,BCAP31,RPS20,RPL18 |
| GO:0016071 | mRNA metabolic process | 7 | 678 | 1.05 | 0.00065 | RPS11,RPS27A,RPS27,RBMX,RPL23A,RPS20,RPL18 |
| GO:0034613 | Cellular protein localization | 9 | 1610 | 0.78 | 0.0016 | CHMP4B,RPS11,RPS27A,BSG,RPS27,RPL23A,BCAP31,RPS20,RPL18 |
| GO:0044271 | Cellular nitrogen compound biosynthetic process | 8 | 1522 | 0.76 | 0.0095 | RPS11,RPS27A,RPS27,RBMX,EIF1AX,RPL23A,RPS20,RPL18 |
| GO:0034645 | Cellular macromolecule biosynthetic process | 8 | 1592 | 0.74 | 0.0118 | RPS11,RPS27A,RPS27,RBMX,EIF1AX,RPL23A,RPS20,RPL18 |
| GO:0008152 | Metabolic process | 16 | 8298 | 0.32 | 0.0167 | PSMA3,CHMP4B,TXNDC17,RPS11,RPS27A,HIST1H1E,BSG,RPS27,RBMX,EIF1AX,CIAPIN1,RPL23A,RPS20,RPL18,ERH,COX4I1 |
| GO:0034622 | Cellular protein-containing complex assembly | 6 | 816 | 0.9 | 0.0173 | CHMP4B,RPS27A,HIST1H1E,RPS27,RBMX,RPL23A |
| GO:0051641 | Cellular localization | 10 | 2967 | 0.56 | 0.0220 | CHMP4B,RPS11,RPS27A,BSG,RPS27,RPL23A,BCAP31,RPS20,MANF,RPL18 |
| GO:0051649 | Establishment of localization in cell | 9 | 2375 | 0.61 | 0.0247 | CHMP4B,RPS11,RPS27A,RPS27,RPL23A,BCAP31,RPS20,MANF,RPL18 |
| GO:0044237 | Cellular metabolic process | 15 | 7513 | 0.34 | 0.0294 | PSMA3,CHMP4B,RPS11,RPS27A,HIST1H1E,BSG,RPS27,RBMX,EIF1AX,CIAPIN1,RPL23A,RPS20,RPL18,ERH,COX4I1 |
| GO:0010629 | Negative regulation of gene expression | 8 | 2014 | 0.64 | 0.0485 | RPS11,RPS27A,HIST1H1E,RPS27,RBMX,RPL23A,RPS20,RPL18 |

**Appendix table S8. Proteins that take part in the interaction network, according to those upregulated by compound #7 in HEK293T-ACE2 cells.**

A protein interaction network was generated using STRING database (https://string-db.org) by using only those proteins found upregulated in PI-7-treated cells. Data given include term ID, term description, observed gene count in the network, background gene count, strength, false discovery rate (FDR), and matching network proteins.

| Term ID | Term description | Observed gene count | Background gene count | Strength | FDR | Matching proteins in the network |
|---|---|---|---|---|---|---|
| GO:0034641 | Cellular nitrogen compound metabolic process | 32 | 3282 | 0.46 | 3.69e-05 | EEF1A2,SF3A2,SPR,NAT10,RPL8,XPO5,WDR61,PDXK,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,PSAP,NOLC1,MMS19,FTO,ENO2,RRP12 |
| GO:0010608 | Posttranscriptional regulation of gene expression | 14 | 574 | 0.86 | 4.75e-05 | EEF1A2,PSMA2,NAT10,PSMB7,XPO5,NPM1,GCN1L1,PTBP1,TSNAX,MCTS1,EEF1B2,NOLC1,FTO,CIRBP |
| GO:0044237 | Cellular metabolic process | 48 | 7513 | 0.28 | 7.28e-05 | EEF1A2,SF3A2,PSMA2,SKP1,SPR,RPN2,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,ESYT1,WDR61,SAE1,PDXK,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,UQCRFS1,CYCS,FARSA,CECR5,RPS7,CPSF7,RPS17,PTBP1,TSNAX,ACAT2,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,PSAP,CDC42,NOLC1,CKMT1A,MMS19,FTO,ENO2,RRP12,HADH,AP2B1 |
| GO:0006807 | Nitrogen compound metabolic process | 45 | 6852 | 0.29 | 0.00015 | EEF1A2,SF3A2,PSMA2,SKP1,SPR,RPN2,CAPNS1,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,ESYT1,WDR61,SAE1,PDXK,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,CYCS,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,PSAP,CDC42,NOLC1,CKMT1A,MMS19,FTO,ENO2,RRP12,AP2B1 |
| GO:0071704 | Organic substance metabolic process | 48 | 7755 | 0.26 | 0.00015 | EEF1A2,SF3A2,PSMA2,SKP1,SPR,RPN2,CAPNS1,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,ESYT1,WDR61,SAE1,PDXK,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,CYCS,FARSA,CECR5,RPS7,CPSF7,RPS17,PTBP1,TSNAX,ACAT2,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,PSAP,CDC42,NOLC1,CKMT1A,MMS19,FTO,ENO2,RRP12,HADH,AP2B1 |
| GO:0010467 | Gene expression | 23 | 2056 | 0.52 | 0.00027 | EEF1A2,SF3A2,NAT10,RPL8,WDR61,RAVER1,GCN1L1,PELP1,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,MCTS1,POLR1C,BTF3,EEF1B2,PSAP,NOLC1,MMS19,RRP12 |
| GO:0006725 | Cellular aromatic compound metabolic process | 27 | 2882 | 0.44 | 0.00030 | SF3A2,SPR,NAT10,RPL8,XPO5,WDR61,PDXK,RAVER1,NPM1,RRM1,PELP1,ATP5H,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,POLR1C,MTAP,BTF3,NOLC1,MMS19,FTO,ENO2,RRP12 |
| GO:0008152 | Metabolic process | 49 | 8298 | 0.24 | 0.00030 | EEF1A2,SF3A2,PSMA2,SKP1,SPR,RPN2,CAPNS1,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,ESYT1,WDR61,SAE1,PDXK,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,UQCRFS1,CYCS,FARSA,CECR5,RPS7,CPSF7,RPS17,PTBP1,TSNAX,ACAT2,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,PSAP,CDC42,NOLC1,CKMT1A,MMS19,FTO,ENO2,RRP12,HADH,AP2B1 |
| GO:0016070 | RNA metabolic process | 20 | 1584 | 0.57 | 0.00030 | SF3A2,NAT10,RPL8,XPO5,WDR61,RAVER1,PELP1,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,POLR1C,BTF3,NOLC1,MMS19,FTO,RRP12 |
| GO:0022613 | Ribonucleoprotein complex biogenesis | 11 | 423 | 0.89 | 0.00030 | SF3A2,NAT10,NPM1,PELP1,RPS7,CPSF7,RPS17,CDC73,MCTS1,NOLC1,RRP12 |
| GO:0046483 | Heterocycle metabolic process | 27 | 2840 | 0.45 | 0.00030 | SF3A2,SPR,NAT10,RPL8,XPO5,WDR61,PDXK,RAVER1,NPM1,RRM1,PELP1,ATP5H,FARSA,R |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | PS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,POLR1C,MTAP,BTF3,NOLC1,MMS19,FTO,ENO2,RRP12 |
| GO:1901360 | Organic cyclic compound metabolic process | 28 | 3118 | 0.43 | 0.00033 | SF3A2,SPR,NAT10,RPL8,XPO5,WDR61,PDXK,RAVER1,NPM1,RRM1,PELP1,ATP5H,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,ACAT2,CDC73,POLR1C,MTAP,BTF3,NOLC1,MMS19,FTO,ENO2,RRP12 |
| GO:0044238 | Primary metabolic process | 45 | 7332 | 0.26 | 0.00043 | EEF1A2,SF3A2,PSMA2,SKP1,RPN2,CAPNS1,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,ESYT1,WDR61,SAE1,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,CYCS,FARSA,CECR5,RPS7,CPSF7,RPS17,PTBP1,TSNAX,ACAT2,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,PSAP,CDC42,NOLC1,MMS19,FTO,ENO2,RRP12,HADH,AP2B1 |
| GO:0044271 | Cellular nitrogen compound biosynthetic process | 19 | 1522 | 0.57 | 0.00043 | EEF1A2,SPR,RPL8,WDR61,PDXK,GCN1L1,RRM1,ATP5H,FARSA,RPS7,CPSF7,RPS17,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,MMS19 |
| GO:0006139 | Nucleobase-containing compound metabolic process | 25 | 2659 | 0.45 | 0.00068 | SF3A2,NAT10,RPL8,XPO5,WDR61,RAVER1,NPM1,RRM1,PELP1,ATP5H,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,POLR1C,MTAP,BTF3,NOLC1,MMS19,FTO,ENO2,RRP12 |
| GO:0006417 | Regulation of translation | 10 | 398 | 0.87 | 0.00081 | EEF1A2,NAT10,NPM1,GCN1L1,PTBP1,MCTS1,EEF1B2,NOLC1,FTO,CIRBP |
| GO:0016032 | Viral process | 13 | 776 | 0.7 | 0.0014 | SKP1,PSMB7,RPL8,XPO5,DYNC1LI1,NPM1,RPS7,RPS17,PTBP1,MSN,MCTS1,CDC42,AP2B1 |
| GO:0044085 | Cellular component biogenesis | 24 | 2583 | 0.44 | 0.0014 | STAG2,SF3A2,SKP1,NAT10,UBE2K,NPM1,RRM1,PELP1,FARSA,RPS7,FERMT2,CPSF7,RPS17,CDC73,MCTS1,PSAP,CDC42,NOLC1,MMS19,RRP12,DNM1L,SRP54,CIRBP,AP2B1 |
| GO:1901576 | Organic substance biosynthetic process | 24 | 2734 | 0.42 | 0.0032 | EEF1A2,SPR,RPN2,RPL8,WDR61,PDXK,GCN1L1,RRM1,ATP5H,FARSA,CECR5,RPS7,CPSF7,RPS17,ACAT2,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,CKMT1A,MMS19,ENO2 |
| GO:0090304 | Nucleic acid metabolic process | 21 | 2178 | 0.46 | 0.0036 | SF3A2,NAT10,RPL8,XPO5,WDR61,RAVER1,NPM1,PELP1,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,POLR1C,BTF3,NOLC1,MMS19,FTO,RRP12 |
| GO:0043170 | Macromolecule metabolic process | 38 | 6137 | 0.26 | 0.0054 | EEF1A2,SF3A2,PSMA2,SKP1,RPN2,CAPNS1,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,WDR61,SAE1,RAVER1,NPM1,GCN1L1,RRM1,PELP1,CYCS,FARSA,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,MCTS1,POLR1C,BTF3,EEF1B2,PSAP,CDC42,NOLC1,MMS19,FTO,RRP12,AP2B1 |
| GO:1903311 | Regulation of mrna metabolic process | 8 | 338 | 0.85 | 0.0104 | PSMA2,PSMB7,NPM1,CPSF7,PTBP1,CDC73,FTO,CIRBP |
| GO:0006396 | RNA processing | 12 | 854 | 0.62 | 0.0130 | SF3A2,NAT10,RAVER1,PELP1,RPS7,CPSF7,RPS17,PTBP1,TSNAX,CDC73,NOLC1,RRP12 |
| GO:0016055 | Wnt signaling pathway | 8 | 351 | 0.83 | 0.0130 | PSMA2,SKP1,PSMB7,WDR61,FERMT2,CDC73,CDC42,AP2B1 |
| GO:0051290 | Protein heterotetramerization | 3 | 15 | 1.77 | 0.0130 | RRM1,FARSA,CPSF7 |
| GO:0006412 | Translation | 8 | 366 | 0.81 | 0.0149 | EEF1A2,RPL8,GCN1L1,FARSA,RPS7,RPS17,MCTS1,EEF1B2 |
| GO:0031329 | Regulation of cellular catabolic process | 12 | 875 | 0.61 | 0.0149 | EEF1A2,PSMA2,CAPNS1,PSMB7,UBE2K,NPM1,RPS7,MSN,PSAP,FTO,DNM1L,CIRBP |
| GO:0046907 | Intracellular transport | 16 | 1520 | 0.49 | 0.0149 | NUTF2,FAF2,RPL8,XPO5,TNPO3,DYNC1LI1,NPM1,ATP5H,RPS7,RPS17,IPO9,PSAP,CDC42,DNM1L,SRP54,AP2B1 |
| GO:0009987 | Cellular process | 63 | 15024 | 0.09 | 0.0158 | GLG1,EEF1A2,STAG2,NUTF2,SF3A2,PSMA2,SKP1,SPR,RPN2,CAPNS1,NAT10,PSMB7,UBE2K,FAF2,RPL8,XPO5,TNPO3,ESYT1,WDR61,SAE1,DYNC1LI1,CCT5,PDXK,RAVER1,NPM1,GCN1L1,RRM1,PELP1,ATP5H,UQCRFS1,CYCS,FARSA,NCAPD2,CECR5,RPS7,FERMT2,CPSF7,RPS17,PTBP1,MSN,IPO9,TSNAX,ACAT2,CDC73,MCTS1,SURF4,POLR1C,MTAP,BTF3,EEF1B2,PSAP,CDC42,NOLC1,CKMT1A,MMS19,FTO,ENO2,RRP12,DNM1L,SRP54,CIRBP,HADH,AP2B1 |

| | | | | | | |
|---|---|---|---|---|---|---|
| GO:0032268 | Regulation of cellular protein metabolic process | 22 | 2693 | 0.38 | 0.0170 | GLG1,EEF1A2,SKP1,PPP1R7,NAT10,UBE2K,WDR61,SAE1,NPM1,GCN1L1,CYCS,RPS7,PTBP1,MSN,MCTS1,EEF1B2,PSAP,CDC42,NOLC1,FTO,DNM1L,CIRBP |
| GO:0034645 | Cellular macromolecule biosynthetic process | 16 | 1592 | 0.47 | 0.0226 | EEF1A2,RPN2,RPL8,WDR61,GCN1L1,RRM1,FARSA,RPS7,CPSF7,RPS17,CDC73,MCTS1,POLR1C,BTF3,EEF1B2,MMS19 |
| GO:0042254 | Ribosome biogenesis | 7 | 292 | 0.85 | 0.0226 | NAT10,NPM1,PELP1,RPS7,RPS17,NOLC1,RRP12 |
| GO:0051641 | Cellular localization | 23 | 2967 | 0.36 | 0.0226 | NUTF2,PSMA2,SKP1,PSMB7,FAF2,RPL8,XPO5,TNPO3,ESYT1,DYNC1LI1,PDXK,NPM1,ATP5H,RPS7,FERMT2,RPS17,IPO9,SURF4,PSAP,CDC42,DNM1L,SRP54,AP2B1 |
| GO:0034613 | Cellular protein localization | 16 | 1610 | 0.47 | 0.0239 | NUTF2,SKP1,FAF2,RPL8,XPO5,TNPO3,NPM1,RPS7,FERMT2,RPS17,IPO9,PSAP,CDC42,DNM1L,SRP54,AP2B1 |
| GO:0051649 | Establishment of localization in cell | 20 | 2375 | 0.4 | 0.0241 | NUTF2,PSMA2,PSMB7,FAF2,RPL8,XPO5,TNPO3,DYNC1LI1,PDXK,NPM1,ATP5H,RPS7,RPS17,IPO9,SURF4,PSAP,CDC42,DNM1L,SRP54,AP2B1 |
| GO:0006364 | rRNA processing | 6 | 212 | 0.92 | 0.0264 | NAT10,PELP1,RPS7,RPS17,NOLC1,RRP12 |
| GO:0019080 | Viral gene expression | 5 | 132 | 1.05 | 0.0264 | RPL8,RPS7,RPS17,PTBP1,MCTS1 |
| GO:0044249 | Cellular biosynthetic process | 21 | 2611 | 0.38 | 0.0264 | EEF1A2,SPR,RPN2,RPL8,WDR61,PDXK,GCN1L1,RRM1,ATP5H,FARSA,CECR5,RPS7,CPSF7,RPS17,CDC73,MCTS1,POLR1C,MTAP,BTF3,EEF1B2,MMS19 |
| GO:0071840 | Cellular component organization or biogenesis | 34 | 5633 | 0.25 | 0.0264 | STAG2,SF3A2,SKP1,CAPNS1,NAT10,UBE2K,FAF2,ESYT1,WDR61,DYNC1LI1,NPM1,RRM1,PELP1,ATP5H,CYCS,FARSA,NCAPD2,RPS7,FERMT2,CPSF7,RPS17,MSN,CDC73,MCTS1,SURF4,PSAP,CDC42,NOLC1,MMS19,RRP12,DNM1L,SRP54,CIRBP,AP2B1 |
| GO:0042274 | Ribosomal small subunit biogenesis | 4 | 70 | 1.23 | 0.0293 | NAT10,NPM1,RPS7,RPS17 |
| GO:0072594 | Establishment of protein localization to organelle | 8 | 433 | 0.74 | 0.0293 | NUTF2,RPL8,TNPO3,RPS7,RPS17,IPO9,SRP54,AP2B1 |
| GO:0006886 | Intracellular protein transport | 12 | 999 | 0.55 | 0.0301 | NUTF2,FAF2,RPL8,XPO5,TNPO3,NPM1,RPS7,RPS17,IPO9,PSAP,SRP54,AP2B1 |
| GO:1904666 | Regulation of ubiquitin protein ligase activity | 3 | 26 | 1.53 | 0.0302 | SKP1,RPS7,DNM1L |
| GO:1901566 | Organonitrogen compound biosynthetic process | 14 | 1346 | 0.49 | 0.0334 | EEF1A2,SPR,RPN2,RPL8,PDXK,GCN1L1,ATP5H,FARSA,RPS7,RPS17,MCTS1,MTAP,EEF1B2,CKMT1A |
| GO:0034660 | ncRNA metabolic process | 8 | 467 | 0.71 | 0.0419 | NAT10,XPO5,PELP1,FARSA,RPS7,RPS17,NOLC1,RRP12 |
| GO:0048522 | Positive regulation of cellular process | 33 | 5579 | 0.24 | 0.0423 | EEF1A2,NUTF2,SF3A2,PSMA2,SKP1,PPP1R7,CAPNS1,NAT10,PSMB7,UBE2K,XPO5,WDR61,SAE1,DYNC1LI1,CCT5,NPM1,GCN1L1,PELP1,CYCS,RPS7,PTBP1,MSN,CDC73,MCTS1,SURF4,PSAP,CDC42,NOLC1,MMS19,FTO,DNM1L,CIRBP,AP2B1 |
| GO:0033365 | Protein localization to organelle | 10 | 743 | 0.6 | 0.0427 | NUTF2,SKP1,RPL8,TNPO3,RPS7,RPS17,IPO9,DNM1L,SRP54,AP2B1 |
| GO:0048518 | Positive regulation of biological process | 35 | 6112 | 0.23 | 0.0427 | EEF1A2,NUTF2,SF3A2,PSMA2,SKP1,PPP1R7,CAPNS1,NAT10,PSMB7,UBE2K,XPO5,WDR61,SAE1,DYNC1LI1,CCT5,NPM1,GCN1L1,PELP1,CYCS,RPS7,PTBP1,MSN,CDC73,MCTS1,SURF4,POLR1C,PSAP,CDC42,NOLC1,MMS19,FTO,DNM1L,CIRBP,HADH,AP2B1 |
| GO:0019222 | Regulation of metabolic process | 38 | 6948 | 0.21 | 0.0453 | GLG1,EEF1A2,NUTF2,PSMA2,SKP1,PPP1R7,SPR,CAPNS1,NAT10,PSMB7,UBE2K,RPL8,XPO5,WDR61,SAE1,CCT5,NPM1,GCN1L1,PELP1,CYCS,RPS7,CPSF7,RPS17,PTBP1,MSN,TSNAX,CDC73,MCTS1,POLR1C,EEF1B2,PSAP,CDC42,NOLC1,MMS19,FTO,DNM1L,CIRBP,HADH |

## Appendix table S9

**Sequences of the primers used in this study for qPCR analyses.**

| | |
|---|---|
| **CoV-2 N Forward:** | GACCCCAAAATCAGCGAAAT |
| **CoV-2 N Reverse:** | TCTGGTTACTGCCAGTTGAATCTG |
| **ACTB Forward:** | GACCCAGATCATGTTTGAGACCTT |
| **ACTB Reverse:** | CCAGAGGCGTACAGGGATAGC |
| **IL-1β Forward:** | ATGATGGCTTATTACAGTGGCAA |
| **IL-1β Reverse:** | GTCGGAGATTCGTAGCTGGA |
| **TNFA Forward:** | CTCTTCTGCCTGCTGCACTTTG |
| **TNFA Reverse:** | ATGGGCTACAGGCTTGTCACTC |
| **ATP2B1 Forward:** | CGATCTCACTGGCTTATTCAGTCA |
| **ATP2B1 Reverse:** | TAGCTGTAGCATTTCCCATGGTT |
| **ATP2A1 Forward:** | AACGAGGCCAAAGGTGTCTA |
| **ATP2A1 Reverse:** | TCGAGAGGCTTCTCACATC |
| **IL-12 Forward:** | TGATGGCCCTGTGCCTTAGT |
| **IL-12 Reverse:** | GGATCCATCAGAAGCTTTGCAT |
| **ACE2 Forward:** | GAAATTCCCAAAGACCAGTGGA |
| **ACE2 Reverse:** | CCCCAACTATCTCTCGCTTCAT |
| **Spike Forward:** | ATTGCCACTAGTCTCTAGT |
| **Spike Reverse:** | AGGATCTGAAAACTTTGTCA |
| **TMEM16 Forward:** | GAAGCGGAAACAGATGCGACTC |
| **TMEM16 Reverse:** | CTGGCTTCGTATTCAGCTCTAGG |