**Supplementary File**

**A Systems Biology Approach to Elucidating Functional and Genomic Signatures in Host-Pathogen Interactions of Triple Infections: Tuberculosis, HIV, and SARS-CoV-2**

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**Table s1:**

**Table s2:**

**Table s3:**

**Table s4:**

**Table s5:**

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| --- | --- | --- | --- | --- | --- |
| GeneID | Symbol | Description | log2(fold change) | #NAME? | Set |
| 9249 | DHRS3 | dehydrogenase/reductase 3 | -0.858 | 1.937 | Down |
| 2268 | FGR | FGR proto-oncogene, Src family tyrosine kinase | -2.122 | 1.554 | Down |
| 85028 | SNHG12 | small nucleolar RNA host gene 12 | -1.249 | 1.559 | Down |
| 51440 | HPCAL4 | hippocalcin like 4 | -0.946 | 2.263 | Down |
| 64744 | SMAP2 | small ArfGAP2 | -0.456 | 2.108 | Down |
| 8613 | PLPP3 | phospholipid phosphatase 3 | -5.38 | 2.063 | Down |
| 3725 | JUN | Jun proto-oncogene, AP-1 transcription factor subunit | -1.095 | 1.755 | Down |
| 8412 | BCAR3 | BCAR3 adaptor protein, NSP family member | -1.495 | 2.152 | Down |
| 8556 | CDC14A | cell division cycle 14A | -0.641 | 1.607 | Down |
| 128346 | C1orf162 | chromosome 1 open reading frame 162 | -0.968 | 1.398 | Down |
| 10628 | TXNIP | thioredoxin interacting protein | -1.016 | 4.495 | Down |
| 57326 | PBXIP1 | PBX homeobox interacting protein 1 | -0.704 | 4.862 | Down |
| 9103 | FCGR2C | Fc gamma receptor IIc (gene/pseudogene) | -2.554 | 2.263 | Down |
| 2213 | FCGR2B | Fc gamma receptor IIb | -3.035 | 4.599 | Down |
| 10223 | GPA33 | glycoprotein A33 | -1.286 | 1.365 | Down |
| 7292 | TNFSF4 | TNF superfamily member 4 | -0.721 | 1.437 | Down |
| 1.07E+08 | SNORA103 | small nucleolar RNA, H/ACA box 103 | -1.216 | 1.394 | Down |
| 1.05E+08 | LOC105371622 | uncharacterized LOC105371622 | -1.815 | 3.984 | Down |
| 81788 | NUAK2 | NUAK family kinase 2 | -0.983 | 2.096 | Down |
| 9214 | FCMR | Fc mu receptor | -0.957 | 1.338 | Down |
| 10472 | ZBTB18 | zinc finger and BTB domain containing 18 | -0.891 | 1.641 | Down |
| 8462 | KLF11 | KLF transcription factor 11 | -0.825 | 3.179 | Down |
| 678 | ZFP36L2 | ZFP36 ring finger protein like 2 | -1.155 | 2.216 | Down |
| 23177 | CEP68 | centrosomal protein 68 | -0.987 | 2.786 | Down |
| 11320 | MGAT4A | alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A | -0.576 | 1.381 | Down |
| 284996 | RNF149 | ring finger protein 149 | -0.65 | 2.299 | Down |
| 1.12E+08 | LOC112268426 |  | -1.84 | 7.182 | Down |
| 7852 | CXCR4 | C-X-C motif chemokine receptor 4 | -1.821 | 7.963 | Down |
| 5334 | PLCL1 | phospholipase C like 1 (inactive) | -0.689 | 3.123 | Down |
| 2043 | EPHA4 | EPH receptor A4 | -1.86 | 4.496 | Down |
| 57007 | ACKR3 | atypical chemokine receptor 3 | -2.249 | 4.291 | Down |
| 92106 | OXNAD1 | oxidoreductase NAD binding domain containing 1 | -0.66 | 1.588 | Down |
| 9975 | NR1D2 | nuclear receptor subfamily 1 group D member 2 | -1.029 | 4.595 | Down |
| 10491 | CRTAP | cartilage associated protein | -0.776 | 1.584 | Down |
| 10803 | CCR9 | C-C motif chemokine receptor 9 | -2.425 | 2.135 | Down |
| 131909 | FAM172BP | family with sequence similarity 172 member B, pseudogene | -0.845 | 1.496 | Down |
| 80325 | ABTB1 | ankyrin repeat and BTB domain containing 1 | -0.801 | 4.599 | Down |
| 54800 | KLHL24 | kelch like family member 24 | -1.254 | 6.363 | Down |
| 116211 | TM4SF19 | transmembrane 4 L six family member 19 | -3.866 | 1.384 | Down |
| 201895 | SMIM14 | small integral membrane protein 14 | -0.971 | 1.701 | Down |
| 10396 | ATP8A1 | ATPase phospholipid transporting 8A1 | -0.938 | 1.432 | Down |
| 27284 | SULT1B1 | sulfotransferase family 1B member 1 | -2.312 | 3.792 | Down |
| 6374 | CXCL5 | C-X-C motif chemokine ligand 5 | -6.125 | 8.004 | Down |
| 246175 | CNOT6L | CCR4-NOT transcription complex subunit 6 like | -0.969 | 3.63 | Down |
| 5530 | PPP3CA | protein phosphatase 3 catalytic subunit alpha | -0.691 | 1.645 | Down |
| 4126 | MANBA | mannosidase beta | -0.813 | 3.482 | Down |
| 1.08E+08 | LOC107986196 | uncharacterized LOC107986196 | -1.442 | 1.351 | Down |
| 23022 | PALLD | palladin, cytoskeletal associated protein | -2.172 | 1.698 | Down |
| 3575 | IL7R | interleukin 7 receptor | -1.817 | 5.458 | Down |
| 1601 | DAB2 | DAB adaptor protein 2 | -1.937 | 1.539 | Down |
| 79722 | ANKRD55 | ankyrin repeat domain 55 | -2.076 | 2.494 | Down |
| 4214 | MAP3K1 | mitogen-activated protein kinase kinase kinase 1 | -0.413 | 1.373 | Down |
| 5295 | PIK3R1 | phosphoinositide-3-kinase regulatory subunit 1 | -0.739 | 4.874 | Down |
| 51301 | GCNT4 | glucosaminyl (N-acetyl) transferase 4 | -1.201 | 3.609 | Down |
| 57561 | ARRDC3 | arrestin domain containing 3 | -1.184 | 1.516 | Down |
| 96459 | FNIP1 | folliculin interacting protein 1 | -0.482 | 1.404 | Down |
| 51523 | CXXC5 | CXXC finger protein 5 | -1.617 | 3.652 | Down |
| 1809 | DPYSL3 | dihydropyrimidinase like 3 | -4.654 | 6.274 | Down |
| 729678 | LINC00847 | long intergenic non-protein coding RNA 847 | -0.818 | 3.276 | Down |
| 51439 | FAM8A1 | family with sequence similarity 8 member A1 | -0.808 | 1.854 | Down |
| 2289 | FKBP5 | FKBP prolyl isomerase 5 | -0.734 | 4.448 | Down |
| 79627 | OGFRL1 | opioid growth factor receptor like 1 | -0.846 | 1.572 | Down |
| 58528 | RRAGD | Ras related GTP binding D | -0.783 | 1.844 | Down |
| 115330 | GPR146 | G protein-coupled receptor 146 | -1.056 | 1.984 | Down |
| 401303 | ZNF815P | zinc finger protein 815, pseudogene | -1.155 | 1.908 | Down |
| 10457 | GPNMB | glycoprotein nmb | -2.498 | 4.65 | Down |
| 5166 | PDK4 | pyruvate dehydrogenase kinase 4 | -5.584 | 2.132 | Down |
| 222255 | ATXN7L1 | ataxin 7 like 1 | -0.795 | 1.536 | Down |
| 728743 | LOC728743 | zinc finger domain-containing protein LOC728743 | -0.798 | 1.755 | Down |
| 170575 | GIMAP1 | GTPase, IMAP family member 1 | -0.646 | 1.527 | Down |
| 4023 | LPL | lipoprotein lipase | -5.699 | 5.542 | Down |
| 1.05E+08 | LOC105379326 |  | -1.741 | 2.391 | Down |
| 85479 | DNAJC5B | DnaJ heat shock protein family (Hsp40) member C5 beta | -1.978 | 1.526 | Down |
| 2167 | FABP4 | fatty acid binding protein 4 | -7.138 | 4.28 | Down |
| 94241 | TP53INP1 | tumor protein p53 inducible nuclear protein 1 | -0.773 | 1.419 | Down |
| 6383 | SDC2 | syndecan 2 | -3.531 | 7.188 | Down |
| 359809 | PEG13 | paternally expressed 13 | -1.473 | 2.391 | Down |
| 123 | PLIN2 | perilipin 2 | -1.077 | 4.595 | Down |
| 360 | AQP3 | aquaporin 3 (Gill blood group) | -1.002 | 1.447 | Down |
| 7088 | TLE1 | TLE family member 1, transcriptional corepressor | -1.571 | 1.419 | Down |
| 1514 | CTSL | cathepsin L | -1.361 | 1.487 | Down |
| 401548 | SNX30 | sorting nexin family member 30 | -0.579 | 1.4 | Down |
| 9966 | TNFSF15 | TNF superfamily member 15 | -4.682 | 1.868 | Down |
| 5742 | PTGS1 | prostaglandin-endoperoxide synthase 1 | -1.257 | 1.408 | Down |
| 1621 | DBH | dopamine beta-hydroxylase | -2.368 | 2.557 | Down |
| 138948 | DBH-AS1 | DBH antisense RNA 1 | -2.695 | 3.123 | Down |
| 84973 | SNHG7 | small nucleolar RNA host gene 7 | -1.054 | 2.434 | Down |
| 9022 | CLIC3 | chloride intracellular channel 3 | -2.899 | 2.581 | Down |
| 4360 | MRC1 | mannose receptor C-type 1 | -3.302 | 1.775 | Down |
| 220213 | OTUD1 | OTU deubiquitinase 1 | -0.509 | 1.95 | Down |
| 143098 | MPP7 | MAGUK p55 scaffold protein 7 | -1.305 | 1.942 | Down |
| 8829 | NRP1 | neuropilin 1 | -1.868 | 2.108 | Down |
| 219749 | ZNF25 | zinc finger protein 25 | -0.486 | 1.438 | Down |
| 80201 | HKDC1 | hexokinase domain containing 1 | -2.239 | 1.357 | Down |
| 10023 | FRAT1 | FRAT regulator of WNT signaling pathway 1 | -0.888 | 1.755 | Down |
| 4601 | MXI1 | MAX interactor 1, dimerization protein | -0.686 | 3.596 | Down |
| 282997 | PDCD4-AS1 | PDCD4 antisense RNA 1 | -1.142 | 1.844 | Down |
| 1.05E+08 | LOC105376548 | uncharacterized LOC105376548 | -2.12 | 2.038 | Down |
| 10418 | SPON1 | spondin 1 | -0.755 | 1.835 | Down |
| 5140 | PDE3B | phosphodiesterase 3B | -0.823 | 2.96 | Down |
| 219539 | YPEL4 | yippee like 4 | -2.201 | 1.998 | Down |
| 23642 | SNHG1 | small nucleolar RNA host gene 1 | -1.057 | 1.631 | Down |
| 10235 | RASGRP2 | RAS guanyl releasing protein 2 | -1.216 | 7.391 | Down |
| 4312 | MMP1 | matrix metallopeptidase 1 | -3.935 | 1.854 | Down |
| 6653 | SORL1 | sortilin related receptor 1 | -0.879 | 1.4 | Down |
| 928 | CD9 | CD9 molecule | -0.868 | 1.608 | Down |
| 1.08E+08 | LOC107987174 |  | -1.174 | 1.474 | Down |
| 25875 | LETMD1 | LETM1 domain containing 1 | -0.882 | 3.02 | Down |
| 319101 | KRT73 | keratin 73 | -2.824 | 2.299 | Down |
| 11213 | IRAK3 | interleukin 1 receptor associated kinase 3 | -1.634 | 2.299 | Down |
| 338773 | TMEM119 | transmembrane protein 119 | -3.291 | 1.474 | Down |
| 1.01E+08 | LINC02361 | long intergenic non-protein coding RNA 2361 | -0.976 | 1.438 | Down |
| 8848 | TSC22D1 | TSC22 domain family member 1 | -0.942 | 5.375 | Down |
| 283514 | SIAH3 | siah E3 ubiquitin protein ligase family member 3 | -3.581 | 1.849 | Down |
| 22821 | RASA3 | RAS p21 protein activator 3 | -0.776 | 1.569 | Down |
| 57161 | PELI2 | pellino E3 ubiquitin protein ligase family member 2 | -0.867 | 1.516 | Down |
| 1.05E+08 | LINC02320 | long intergenic non-protein coding RNA 2320 | -3.379 | 3.05 | Down |
| 145200 | LINC00239 | long intergenic non-protein coding RNA 239 | -1.594 | 3.179 | Down |
| 440253 | WHAMMP2 | WHAMM pseudogene 2 | -2.028 | 2.82 | Down |
| 1E+08 | WHAMMP4 | WHAMM pseudogene 4 | -1.136 | 1.357 | Down |
| 26585 | GREM1 | gremlin 1, DAN family BMP antagonist | -4.285 | 4.103 | Down |
| 7057 | THBS1 | thrombospondin 1 | -1.974 | 2.038 | Down |
| 283876 | LINC00921 | long intergenic non-protein coding RNA 921 | -1.475 | 2.442 | Down |
| 9665 | MARF1 | meiosis regulator and mRNA stability factor 1 | -0.591 | 1.4 | Down |
| 10261 | IGSF6 | immunoglobulin superfamily member 6 | -2.188 | 1.535 | Down |
| 283897 | C16orf54 | chromosome 16 open reading frame 54 | -1.152 | 7.793 | Down |
| 83719 | YPEL3 | yippee like 3 | -0.756 | 2.356 | Down |
| 85407 | NKD1 | NKD inhibitor of WNT signaling pathway 1 | -1.62 | 2.845 | Down |
| 64174 | DPEP2 | dipeptidase 2 | -1.734 | 9.369 | Down |
| 333929 | SNAI3 | snail family transcriptional repressor 3 | -1.18 | 3.125 | Down |
| 115992 | RNF166 | ring finger protein 166 | -0.773 | 1.338 | Down |
| 37 | ACADVL | acyl-CoA dehydrogenase very long chain | -0.805 | 3.042 | Down |
| 56985 | ADPRM | ADP-ribose/CDP-alcohol diphosphatase, manganese dependent | -0.902 | 1.766 | Down |
| 400581 | GRAPL | GRB2 related adaptor protein like | -1.247 | 1.416 | Down |
| 3690 | ITGB3 | integrin subunit beta 3 | -3.76 | 6.025 | Down |
| 81558 | FAM117A | family with sequence similarity 117 member A | -0.456 | 2.256 | Down |
| 388403 | YPEL2 | yippee like 2 | -1.44 | 1.451 | Down |
| 8313 | AXIN2 | axin 2 | -0.412 | 1.404 | Down |
| 124599 | CD300LB | CD300 molecule like family member b | -4.69 | 3.123 | Down |
| 10871 | CD300C | CD300c molecule | -2.574 | 1.326 | Down |
| 649446 | DLGAP1-AS1 | DLGAP1 antisense RNA 1 | -0.865 | 1.416 | Down |
| 753 | LDLRAD4 | low density lipoprotein receptor class A domain containing 4 | -1.028 | 4.554 | Down |
| 10449 | ACAA2 | acetyl-CoA acyltransferase 2 | -0.447 | 2.364 | Down |
| 5055 | SERPINB2 | serpin family B member 2 | -5.479 | 5.322 | Down |
| 199675 | MCEMP1 | mast cell expressed membrane protein 1 | -5.428 | 4.554 | Down |
| 374879 | ZNF699 | zinc finger protein 699 | -0.567 | 1.491 | Down |
| 10365 | KLF2 | KLF transcription factor 2 | -1.433 | 7.893 | Down |
| 27106 | ARRDC2 | arrestin domain containing 2 | -1.207 | 3.959 | Down |
| 126364 | LRRC25 | leucine rich repeat containing 25 | -5.779 | 2.953 | Down |
| 148113 | CILP2 | cartilage intermediate layer protein 2 | -1.703 | 3.596 | Down |
| 9170 | LPAR2 | lysophosphatidic acid receptor 2 | -0.927 | 7.893 | Down |
| 126375 | ZNF792 | zinc finger protein 792 | -0.863 | 1.443 | Down |
| 53822 | FXYD7 | FXYD domain containing ion transport regulator 7 | -0.943 | 1.437 | Down |
| 57677 | ZFP14 | ZFP14 zinc finger protein | -0.581 | 2.235 | Down |
| 57711 | ZNF529 | zinc finger protein 529 | -0.514 | 2.569 | Down |
| 25850 | ZNF345 | zinc finger protein 345 | -0.632 | 1.422 | Down |
| 163087 | ZNF383 | zinc finger protein 383 | -0.634 | 2.096 | Down |
| 728 | C5AR1 | complement C5a receptor 1 | -4.193 | 7.544 | Down |
| 1E+08 | SIGLEC14 | sialic acid binding Ig like lectin 14 | -2.786 | 1.691 | Down |
| 55769 | ZNF83 | zinc finger protein 83 | -0.585 | 1.56 | Down |
| 11027 | LILRA2 | leukocyte immunoglobulin like receptor A2 | -2.904 | 1.379 | Down |
| 54498 | SMOX | spermine oxidase | -1.915 | 3.961 | Down |
| 7056 | THBD | thrombomodulin | -4.121 | 9.875 | Down |
| 22918 | CD93 | CD93 molecule | -1.31 | 1.419 | Down |
| 9935 | MAFB | MAF bZIP transcription factor B | -3.411 | 4.289 | Down |
| 4318 | MMP9 | matrix metallopeptidase 9 | -3.317 | 1.822 | Down |
| 1.1E+08 | SLC12A5-AS1 | SLC12A5 and MMP9 antisense RNA 1 | -3.582 | 3.226 | Down |
| 56937 | PMEPA1 | prostate transmembrane protein, androgen induced 1 | -2.013 | 1.438 | Down |
| 1.01E+08 | MHENCR | melanoma highly expressed competing endogenous lncRNA for miR-425 and miR-489 | -1.295 | 4.617 | Down |
| 4987 | OPRL1 | opioid related nociceptin receptor 1 | -2.087 | 1.874 | Down |
| 645426 | TMEM191C | transmembrane protein 191C | -1.58 | 1.475 | Down |
| 3985 | LIMK2 | LIM domain kinase 2 | -0.745 | 3.287 | Down |
| 113791 | PIK3IP1 | phosphoinositide-3-kinase interacting protein 1 | -2.269 | 24.659 | Down |
| 8911 | CACNA1I | calcium voltage-gated channel subunit alpha1 I | -1.059 | 3.794 | Down |
| 340527 | NHSL2 | NHS like 2 | -1.703 | 2.803 | Down |
| 1831 | TSC22D3 | TSC22 domain family member 3 | -3.548 | 34.987 | Down |
| 340547 | VSIG1 | V-set and immunoglobulin domain containing 1 | -1.957 | 6.363 | Down |
| 2239 | GPC4 | glypican 4 | -3.998 | 3.652 | Down |
| 203523 | ZNF449 | zinc finger protein 449 | -0.709 | 1.631 | Down |
| 10726 | NUDC | nuclear distribution C, dynein complex regulator | 0.445 | 1.438 | Up |
| 3595 | IL12RB2 | interleukin 12 receptor subunit beta 2 | 1.699 | 1.399 | Up |
| 9898 | UBAP2L | ubiquitin associated protein 2 like | 0.435 | 1.392 | Up |
| 913 | CD1E | CD1e molecule | 4.948 | 1.4 | Up |
| 6846 | XCL2 | X-C motif chemokine ligand 2 | 1.653 | 2.285 | Up |
| 6375 | XCL1 | X-C motif chemokine ligand 1 | 2.013 | 1.633 | Up |
| 356 | FASLG | Fas ligand | 2.055 | 7.893 | Up |
| 3586 | IL10 | interleukin 10 | 2.515 | 4.865 | Up |
| 29949 | IL19 | interleukin 19 | 2.345 | 3.123 | Up |
| 386597 | GRASLND | glycosaminoglycan regulatory associated long non-coding RNA | 0.753 | 1.416 | Up |
| 10971 | YWHAQ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta | 0.512 | 1.701 | Up |
| 348654 | GEN1 | GEN1 Holliday junction 5' flap endonuclease | 0.515 | 1.438 | Up |
| 25940 | FAM98A | family with sequence similarity 98 member A | 0.591 | 1.325 | Up |
| 87178 | PNPT1 | polyribonucleotide nucleotidyltransferase 1 | 0.509 | 1.331 | Up |
| 5899 | RALB | RAS like proto-oncogene B | 0.735 | 2.96 | Up |
| 843 | CASP10 | caspase 10 | 0.545 | 2.138 | Up |
| 940 | CD28 | CD28 molecule | 0.605 | 1.786 | Up |
| 3431 | SP110 | SP110 nuclear body protein | 0.65 | 1.516 | Up |
| 5707 | PSMD1 | proteasome 26S subunit, non-ATPase 1 | 0.563 | 4.799 | Up |
| 55081 | IFT57 | intraflagellar transport 57 | 0.857 | 2.289 | Up |
| 79413 | ZBED2 | zinc finger BED-type containing 2 | 1.976 | 4.795 | Up |
| 4171 | MCM2 | minichromosome maintenance complex component 2 | 0.702 | 3.042 | Up |
| 28976 | ACAD9 | acyl-CoA dehydrogenase family member 9 | 0.495 | 2.182 | Up |
| 5359 | PLSCR1 | phospholipid scramblase 1 | 0.879 | 1.755 | Up |
| 8743 | TNFSF10 | TNF superfamily member 10 | 1.585 | 3.369 | Up |
| 5708 | PSMD2 | proteasome 26S subunit ubiquitin receptor, non-ATPase 2 | 0.412 | 2.072 | Up |
| 152579 | SCFD2 | sec1 family domain containing 2 | 0.678 | 1.69 | Up |
| 3627 | CXCL10 | C-X-C motif chemokine ligand 10 | 3.232 | 1.443 | Up |
| 10855 | HPSE | heparanase | 0.699 | 6.096 | Up |
| 59067 | IL21 | interleukin 21 | 2.297 | 1.844 | Up |
| 1.05E+08 | LINC02365 | long intergenic non-protein coding RNA 2365 | 2.066 | 1.442 | Up |
| 57491 | AHRR | aryl hydrocarbon receptor repressor | 0.955 | 1.943 | Up |
| 5810 | RAD1 | RAD1 checkpoint DNA exonuclease | 0.439 | 1.681 | Up |
| 5734 | PTGER4 | prostaglandin E receptor 4 | 1.123 | 7.893 | Up |
| 5019 | OXCT1 | 3-oxoacid CoA-transferase 1 | 0.502 | 1.854 | Up |
| 8507 | ENC1 | ectodermal-neural cortex 1 | 2.051 | 4.874 | Up |
| 80315 | CPEB4 | cytoplasmic polyadenylation element binding protein 4 | 0.634 | 4.25 | Up |
| 94081 | SFXN1 | sideroflexin 1 | 0.737 | 1.584 | Up |
| 1212 | CLTB | clathrin light chain B | 0.52 | 1.338 | Up |
| 26262 | TSPAN17 | tetraspanin 17 | 0.651 | 3.71 | Up |
| 3182 | HNRNPAB | heterogeneous nuclear ribonucleoprotein A/B | 0.599 | 1.998 | Up |
| 203068 | TUBB | tubulin beta class I | 0.591 | 3.088 | Up |
| 6891 | TAP2 | transporter 2, ATP binding cassette subfamily B member | 0.613 | 1.525 | Up |
| 6890 | TAP1 | transporter 1, ATP binding cassette subfamily B member | 0.865 | 1.631 | Up |
| 1.05E+08 | TAGAP-AS1 | TAGAP antisense RNA 1 | 1.123 | 3.062 | Up |
| 117289 | TAGAP | T cell activation RhoGTPase activating protein | 1.215 | 3.104 | Up |
| 3181 | HNRNPA2B1 | heterogeneous nuclear ribonucleoprotein A2/B1 | 0.557 | 1.582 | Up |
| 2783 | GNB2 | G protein subunit beta 2 | 0.39 | 1.302 | Up |
| 168537 | GIMAP7 | GTPase, IMAP family member 7 | 0.743 | 1.496 | Up |
| 4609 | MYC | MYC proto-oncogene, bHLH transcription factor | 0.882 | 1.889 | Up |
| 29126 | CD274 | CD274 molecule | 1.448 | 1.408 | Up |
| 401563 | LINC02908 | long intergenic non-protein coding RNA 2908 | 1.232 | 1.867 | Up |
| 2529 | FUT7 | fucosyltransferase 7 | 1.402 | 2.569 | Up |
| 10383 | TUBB4B | tubulin beta 4B class IVb | 0.755 | 1.343 | Up |
| 1763 | DNA2 | DNA replication helicase/nuclease 2 | 0.871 | 1.302 | Up |
| 3098 | HK1 | hexokinase 1 | 0.405 | 3.041 | Up |
| 79751 | SLC25A22 | solute carrier family 25 member 22 | 0.675 | 1.562 | Up |
| 2237 | FEN1 | flap structure-specific endonuclease 1 | 0.633 | 1.908 | Up |
| 113130 | CDCA5 | cell division cycle associated 5 | 0.962 | 2.655 | Up |
| 8726 | EED | embryonic ectoderm development | 0.544 | 1.945 | Up |
| 1111 | CHEK1 | checkpoint kinase 1 | 0.817 | 1.908 | Up |
| 57102 | C12orf4 | chromosome 12 open reading frame 4 | 0.602 | 1.998 | Up |
| 5777 | PTPN6 | protein tyrosine phosphatase non-receptor type 6 | 0.776 | 4.64 | Up |
| 5213 | PFKM | phosphofructokinase, muscle | 0.444 | 1.869 | Up |
| 10376 | TUBA1B | tubulin alpha 1b | 0.714 | 1.404 | Up |
| 3458 | IFNG | interferon gamma | 4.101 | 5.295 | Up |
| 4939 | OAS2 | 2'-5'-oligoadenylate synthetase 2 | 0.947 | 1.998 | Up |
| 27198 | HCAR1 | hydroxycarboxylic acid receptor 1 | 2.513 | 1.701 | Up |
| 4008 | LMO7 | LIM domain 7 | 0.881 | 1.487 | Up |
| 7027 | TFDP1 | transcription factor Dp-1 | 0.523 | 2.135 | Up |
| 10598 | AHSA1 | activator of HSP90 ATPase activity 1 | 0.434 | 1.443 | Up |
| 30844 | EHD4 | EH domain containing 4 | 0.839 | 1.922 | Up |
| 5371 | PML | PML nuclear body scaffold | 0.536 | 1.416 | Up |
| 6627 | SNRPA1 | small nuclear ribonucleoprotein polypeptide A' | 0.506 | 1.687 | Up |
| 79801 | SHCBP1 | SHC binding and spindle associated 1 | 1.25 | 1.537 | Up |
| 60528 | ELAC2 | elaC ribonuclease Z 2 | 0.322 | 1.323 | Up |
| 5717 | PSMD11 | proteasome 26S subunit, non-ATPase 11 | 0.392 | 1.69 | Up |
| 6351 | CCL4 | C-C motif chemokine ligand 4 | 2.389 | 2.48 | Up |
| 5709 | PSMD3 | proteasome 26S subunit, non-ATPase 3 | 0.544 | 1.572 | Up |
| 30009 | TBX21 | T-box transcription factor 21 | 2.182 | 7.893 | Up |
| 117246 | FTSJ3 | FtsJ RNA 2'-O-methyltransferase 3 | 0.569 | 1.863 | Up |
| 3959 | LGALS3BP | galectin 3 binding protein | 0.736 | 3.103 | Up |
| 8740 | TNFSF14 | TNF superfamily member 14 | 0.83 | 1.331 | Up |
| 4670 | HNRNPM | heterogeneous nuclear ribonucleoprotein M | 0.496 | 1.535 | Up |
| 684 | BST2 | bone marrow stromal cell antigen 2 | 0.909 | 1.699 | Up |
| 10452 | TOMM40 | translocase of outer mitochondrial membrane 40 | 0.642 | 1.351 | Up |
| 5536 | PPP5C | protein phosphatase 5 catalytic subunit | 0.49 | 1.615 | Up |
| 8775 | NAPA | NSF attachment protein alpha | 0.516 | 4.512 | Up |
| 160 | AP2A1 | adaptor related protein complex 2 subunit alpha 1 | 0.345 | 1.516 | Up |
| 26121 | PRPF31 | pre-mRNA processing factor 31 | 0.417 | 1.689 | Up |
| 27338 | UBE2S | ubiquitin conjugating enzyme E2 S | 0.763 | 1.353 | Up |
| 11237 | RNF24 | ring finger protein 24 | 0.716 | 2.847 | Up |
| 25939 | SAMHD1 | SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1 | 0.524 | 1.675 | Up |
| 85379 | KIAA1671 | KIAA1671 | 1.222 | 1.638 | Up |
| 57168 | ASPHD2 | aspartate beta-hydroxylase domain containing 2 | 0.516 | 1.516 | Up |
| 2130 | EWSR1 | EWS RNA binding protein 1 | 0.494 | 3.245 | Up |
| 162 | AP1B1 | adaptor related protein complex 1 subunit beta 1 | 0.5 | 1.631 | Up |
| 91370 | LIF-AS2 | LIF antisense RNA 2 | 1.685 | 4.426 | Up |
| 4174 | MCM5 | minichromosome maintenance complex component 5 | 0.679 | 2.676 | Up |
| 50 | ACO2 | aconitase 2 | 0.387 | 1.516 | Up |
| 27351 | DESI1 | desumoylating isopeptidase 1 | 0.459 | 1.671 | Up |
| 92745 | SLC38A5 | solute carrier family 38 member 5 | 0.669 | 2.442 | Up |
| 27316 | RBMX | RNA binding motif protein X-linked | 0.399 | 1.789 | Up |

**Table s6:**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GeneID | Symbol | Description | padj | pvalue | log2(fold change)(Control vs TB-PE) | Set | -log10(Pvalue)(Control vs TB-PE) | log2(fold change)(Control vs Activated) | Set | -log10(Pvalue)(Control vs Activated) | log2(fold change)(TB-PE vs Activated) | Set | -log10(Pvalue)(TB-PE vs Activated) | log2(fold change)(TB-PE vs Activated\_TB-PE) | Set | -log10(Pvalue)(TB-PE vs Activated\_TB-PE) | log2(fold change)(Activated vs Activated\_TB-PE) | Set | -log10(Pvalue)(Activated vs Activated\_TB-PE) |
| 2268 | FGR | FGR proto-oncogene, Src family tyrosine kinase | 7.09E-07 | 1.38E-07 | -1.95 | Down | 1.408 | 1.632 | Up | 1.818 | 3.582 | Up | 7.87 | 1.461 | Up | 1.405 | -2.122 | Down | 1.554 |
| 85028 | SNHG12 | small nucleolar RNA host gene 12 | 1.20E-11 | 1.24E-12 | -1.241 | Down | 1.744 | 1.437 | Up | 3.79 | 2.678 | Up | 12.628 | 1.429 | Up | 3.58 | -1.249 | Down | 1.559 |
| 356 | FASLG | Fas ligand | 1.04E-31 | 1.78E-33 | 1.209 | Up | 2.08 | -2.374 | Down | 13.398 | -3.583 | Down | 28.752 | -1.528 | Down | 4.911 | 2.055 | Up | 7.893 |
| 5899 | RALB | RAS like proto-oncogene B | 2.32E-54 | 8.06E-57 | 0.795 | Up | 3.58 | -1.739 | Down | 24.008 | -2.534 | Down | 50.175 | -1.799 | Down | 24.383 | 0.735 | Up | 2.96 |
| 7852 | CXCR4 | C-X-C motif chemokine receptor 4 | 1.85E-18 | 9.28E-20 | -1.382 | Down | 4.419 | 1.163 | Up | 4.322 | 2.545 | Up | 19.759 | 0.724 | Up | 1.68 | -1.821 | Down | 7.963 |
| 5707 | PSMD1 | proteasome 26S subunit, non-ATPase 1 | ######## | ######## | 0.336 | Up | 1.325 | -1.818 | Down | 66.739 | -2.154 | Down | 93.326 | -1.591 | Down | 49.17 | 0.563 | Up | 4.799 |
| 246175 | CNOT6L | CCR4-NOT transcription complex subunit 6 like | 1.75E-31 | 3.04E-33 | -0.837 | Down | 2.633 | 1.597 | Up | 13.877 | 2.434 | Up | 32.139 | 1.465 | Up | 11.264 | -0.969 | Down | 3.63 |
| 10855 | HPSE | heparanase | 1.39E-18 | 6.89E-20 | 0.593 | Up | 4.266 | -0.456 | Down | 3.778 | -1.049 | Down | 18.068 | -0.35 | Down | 1.919 | 0.699 | Up | 6.096 |
| 1601 | DAB2 | DAB adaptor protein 2 | 1.22E-08 | 1.83E-09 | -1.722 | Down | 1.448 | 1.86 | Up | 2.714 | 3.581 | Up | 9.577 | 1.644 | Up | 2.194 | -1.937 | Down | 1.539 |
| 6891 | TAP2 | transporter 2, ATP binding cassette subfamily B member | 2.09E-39 | 2.16E-41 | 0.582 | Up | 1.419 | -1.646 | Down | 18.973 | -2.227 | Down | 34.614 | -1.614 | Down | 17.623 | 0.613 | Up | 1.525 |
| 6890 | TAP1 | transporter 1, ATP binding cassette subfamily B member | 6.87E-30 | 1.32E-31 | 0.907 | Up | 1.968 | -1.892 | Down | 13.321 | -2.798 | Down | 28.991 | -1.933 | Down | 13.4 | 0.865 | Up | 1.631 |
| 10457 | GPNMB | glycoprotein nmb | 4.15E-70 | 5.85E-73 | -5.261 | Down | 34.562 | 1.635 | Up | 2.88 | 6.896 | Up | 51.256 | 4.398 | Up | 25.16 | -2.498 | Down | 4.65 |
| 5166 | PDK4 | pyruvate dehydrogenase kinase 4 | 7.10E-22 | 2.54E-23 | -5.369 | Down | 7.863 | 4.17 | Up | 2.041 | 9.539 | Up | 10.659 | 3.955 | Up | 5.862 | -5.584 | Down | 2.132 |
| 4023 | LPL | lipoprotein lipase | 3.16E-28 | 6.77E-30 | -4.232 | Down | 11.174 | 3.473 | Up | 2.814 | 7.705 | Up | 13.641 | 2.006 | Up | 3.364 | -5.699 | Down | 5.542 |
| 6383 | SDC2 | syndecan 2 | 5.75E-17 | 3.38E-18 | -1.951 | Down | 2.098 | 3.481 | Up | 8.932 | 5.432 | Up | 21.645 | 1.902 | Up | 3.009 | -3.531 | Down | 7.188 |
| 10418 | SPON1 | spondin 1 | ######## | ######## | 0.942 | Up | 5.921 | 5.407 | Up | 192.285 | 4.465 | Up | 129.43 | 3.71 | Up | 91.073 | -0.755 | Down | 1.835 |
| 23642 | SNHG1 | small nucleolar RNA host gene 1 | 9.62E-16 | 6.28E-17 | -0.939 | Down | 1.33 | 1.636 | Up | 6.833 | 2.575 | Up | 16.603 | 1.518 | Up | 5.637 | -1.057 | Down | 1.631 |
| 928 | CD9 | CD9 molecule | 4.29E-80 | 3.53E-83 | -1.729 | Down | 17.398 | 1.824 | Up | 14.432 | 3.554 | Up | 58.774 | 2.685 | Up | 35.486 | -0.868 | Down | 1.608 |
| 57161 | PELI2 | pellino E3 ubiquitin protein ligase family member 2 | 7.60E-15 | 5.55E-16 | -0.781 | Down | 1.336 | 1.296 | Up | 6.121 | 2.076 | Up | 15.437 | 1.209 | Up | 5.124 | -0.867 | Down | 1.516 |
| 1.05E+08 | LINC02320 | long intergenic non-protein coding RNA 2320 | 1.93E-14 | 1.46E-15 | -2.895 | Down | 4.393 | 2.312 | Up | 2.245 | 5.207 | Up | 11.242 | 1.827 | Up | 2.461 | -3.379 | Down | 3.05 |
| 145200 | LINC00239 | long intergenic non-protein coding RNA 239 | 1.05E-21 | 3.82E-23 | -1.962 | Down | 7.043 | 1.223 | Up | 2.97 | 3.186 | Up | 19.959 | 1.592 | Up | 5.444 | -1.594 | Down | 3.179 |
| 8313 | AXIN2 | axin 2 | 2.03E-81 | 1.55E-84 | 0.571 | Up | 4.393 | 2.011 | Up | 65.781 | 1.439 | Up | 33.005 | 1.027 | Up | 15.971 | -0.412 | Down | 1.404 |
| 4670 | HNRNPM | heterogeneous nuclear ribonucleoprotein M | 2.83E-28 | 6.04E-30 | 0.495 | Up | 1.645 | -1.068 | Down | 12.362 | -1.563 | Down | 26.288 | -1.067 | Down | 11.828 | 0.496 | Up | 1.535 |
| 126364 | LRRC25 | leucine rich repeat containing 25 | 5.24E-29 | 1.07E-30 | -3.845 | Down | 8.711 | 4.761 | Up | 3.06 | 8.606 | Up | 10.199 | 2.827 | Up | 6.332 | -5.779 | Down | 2.953 |
| 53822 | FXYD7 | FXYD domain containing ion transport regulator 7 | 3.89E-35 | 5.17E-37 | -0.801 | Down | 1.488 | 2.301 | Up | 16.65 | 3.102 | Up | 30.733 | 2.158 | Up | 15.046 | -0.943 | Down | 1.437 |
| 728 | C5AR1 | complement C5a receptor 1 | 2.64E-19 | 1.20E-20 | -2.817 | Down | 4.904 | 3.111 | Up | 5.299 | 5.928 | Up | 19.25 | 1.735 | Up | 2.499 | -4.193 | Down | 7.544 |
| 9935 | MAFB | MAF bZIP transcription factor B | 1.94E-60 | 4.57E-63 | -3.189 | Down | 17.411 | 3.654 | Up | 7.073 | 6.843 | Up | 25.618 | 3.432 | Up | 18.834 | -3.411 | Down | 4.289 |
| 2130 | EWSR1 | EWS RNA binding protein 1 | 7.61E-60 | 1.83E-62 | 0.419 | Up | 2.212 | -1.224 | Down | 28.695 | -1.643 | Down | 51.52 | -1.15 | Down | 24.428 | 0.494 | Up | 3.245 |
| 113791 | PIK3IP1 | phosphoinositide-3-kinase interacting protein 1 | 1.02E-66 | 1.67E-69 | -0.733 | Down | 1.771 | 3.188 | Up | 52.496 | 3.92 | Up | 79.999 | 1.651 | Up | 13.723 | -2.269 | Down | 24.659 |
| 1831 | TSC22D3 | TSC22 domain family member 3 | 8.08E-64 | 1.57E-66 | -1.838 | Down | 8.334 | 3.616 | Up | 38.153 | 5.454 | Up | 87.743 | 1.906 | Up | 10.446 | -3.548 | Down | 34.987 |

**Table s7:** **27 common elements in "SARS Cov-2" and "HIV-1/TB ":**

|  |
| --- |
| **FASLG** |
| **SPON1** |
| **PDK4** |
| **CD9** |
| **GPNMB** |
| **EWSR1** |
| **PIK3IP1** |
| **LPL** |
| **HNRNPM** |
| **C5AR1** |
| **SDC2** |
| **CXCR4** |
| **MAFB** |
| **TAP1** |
| **PELI2** |
| **PSMD1** |
| **AXIN2** |
| **DAB2** |
| **TSC22D3** |
| **FXYD7** |
| **TAP2** |
| **FGR** |
| **HPSE** |
| **RALB** |
| **LRRC25** |
| **SNHG12** |
| **SNHG1** |

**Table s8:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Category | Term | Pathway | Count | Genes | Fold Enrichment | Bonferroni | Benjamini | FDR |
| Biological Process | GO:0001934 | positive regulation of protein phosphorylation | 5 | DAB2, RALB, GPNMB, PELI2, AXIN2 | 18.42233 | 0.037721 | 0.038448 | 0.038448 |
| Biological Process | GO:0030335 | positive regulation of cell migration | 4 | FGR, DAB2, GPNMB, CXCR4 | 10.5784 | 0.823425 | 0.576404 | 0.576404 |
| Biological Process | GO:0019885 | antigen processing and presentation of endogenous peptide antigen via MHC class I | 2 | TAP2, TAP1 | 151.8 | 0.981101 | 0.985901 | 0.985901 |
| Biological Process | GO:0006915 | apoptotic process | 4 | DAB2, RALB, CXCR4, FASLG | 5.11973 | 0.999995 | 1 | 1 |
| Biological Process | GO:0031623 | receptor internalization | 2 | RALB, CD9 | 29.19231 | 1 | 1 | 1 |
| Biological Process | GO:0007165 | signal transduction | 5 | FGR, RALB, GPNMB, C5AR1, FASLG | 3.060484 | 1 | 1 | 1 |
| Biological Process | GO:0010718 | positive regulation of epithelial to mesenchymal transition | 2 | DAB2, AXIN2 | 27.10714 | 1 | 1 | 1 |
| Biological Process | GO:0015031 | protein transport | 3 | DAB2, TAP2, TAP1 | 5.486747 | 1 | 1 | 1 |
| Cellular Component | GO:0005886 | plasma membrane | 15 | RALB, SDC2, C5AR1, TAP1, CXCR4, LPL, FASLG, AXIN2, FGR, DAB2, GPNMB, PIK3IP1, EWSR1, CD9, FXYD7 | 2.075087 | 0.232602 | 0.188654 | 0.188654 |
| Cellular Component | GO:0042825 | TAP complex | 2 | TAP2, TAP1 | 386.7963 | 0.348519 | 0.188654 | 0.188654 |
| Cellular Component | GO:0043202 | lysosomal lumen | 3 | SDC2, FASLG, HPSE | 23.68141 | 0.433248 | 0.188654 | 0.188654 |
| Cellular Component | GO:0016020 | membrane | 13 | LRRC25, SDC2, PELI2, TAP2, TAP1, CXCR4, FASLG, HNRNPM, GPNMB, CD9, PSMD1, FXYD7, HPSE | 1.992215 | 0.637717 | 0.212955 | 0.212955 |
| Cellular Component | GO:0042824 | MHC class I peptide loading complex | 2 | TAP2, TAP1 | 154.7185 | 0.657478 | 0.212955 | 0.212955 |
| Cellular Component | GO:0009897 | external side of plasma membrane | 3 | CD9, CXCR4, FASLG | 5.409738 | 0.999873 | 0.879986 | 0.879986 |
| Molecular Function | GO:0005515 | protein binding | 24 | LRRC25, SPON1, RALB, TSC22D3, SDC2, PELI2, TAP2, TAP1, CXCR4, LPL, FASLG, AXIN2, FGR, HNRNPM, DAB2, MAFB, GPNMB, PIK3IP1, EWSR1, PDK4, CD9, PSMD1, FXYD7, HPSE | 1.453022 | 0.06087 | 0.062781 | 0.062781 |
| Molecular Function | GO:0015433 | ABC-type peptide antigen transporter activity | 2 | TAP2, TAP1 | 514.7733 | 0.308919 | 0.107635 | 0.107635 |
| Molecular Function | GO:1904680 | peptide transmembrane transporter activity | 2 | TAP2, TAP1 | 514.7733 | 0.308919 | 0.107635 | 0.107635 |
| Molecular Function | GO:0046978 | TAP1 binding | 2 | TAP2, TAP1 | 308.864 | 0.459826 | 0.107635 | 0.107635 |
| Molecular Function | GO:0031625 | ubiquitin protein ligase binding | 4 | RALB, PSMD1, CXCR4, AXIN2 | 9.931318 | 0.476869 | 0.107635 | 0.107635 |
| Molecular Function | GO:0023029 | MHC class Ib protein binding | 2 | TAP2, TAP1 | 220.6171 | 0.57779 | 0.122644 | 0.122644 |
| Molecular Function | GO:0005102 | signaling receptor binding | 4 | FGR, PIK3IP1, LPL, FASLG | 8.370298 | 0.645147 | 0.128831 | 0.128831 |
| Molecular Function | GO:0042605 | peptide antigen binding | 2 | TAP2, TAP1 | 24.13 | 0.999627 | 0.843169 | 0.843169 |
| KEGG Pathway | hsa05170 | Human immunodeficiency virus 1 infection | 4 | TAP2, TAP1, CXCR4, FASLG | 9.222744 | 0.463895 | 0.365579 | 0.365579 |
| KEGG Pathway | hsa05340 | Primary immunodeficiency | 2 | TAP2, TAP1 | 25.84795 | 0.998032 | 1 | 1 |
| KEGG Pathway | hsa02010 | ABC transporters | 2 | TAP2, TAP1 | 21.82716 | 0.999377 | 1 | 1 |
| Reactome Pathway | R-HSA-1236974 | ER-Phagosome pathway | 3 | TAP2, TAP1, PSMD1 | 16.80455 | 0.978912 | 1 | 1 |
| Reactome Pathway | R-HSA-1236975 | Antigen processing-Cross presentation | 3 | TAP2, TAP1, PSMD1 | 14.4039 | 0.99439 | 1 | 1 |
| Reactome Pathway | R-HSA-5663205 | Infectious disease | 6 | FGR, SDC2, CD9, PSMD1, CXCR4, FXYD7 | 2.959705 | 0.999995 | 1 | 1 |
| Reactome Pathway | R-HSA-983170 | Antigen Presentation: Folding, assembly and peptide loading of class I MHC | 2 | TAP2, TAP1 | 34.76803 | 1 | 1 | 1 |
| Reactome Pathway | R-HSA-6798695 | Neutrophil degranulation | 4 | FGR, C5AR1, PSMD1, HPSE | 4.201136 | 1 | 1 | 1 |
| Reactome Pathway | R-HSA-168256 | Immune System | 8 | FGR, C5AR1, PELI2, TAP2, TAP1, PSMD1, FASLG, HPSE | 1.96353 | 1 | 1 | 1 |
| Reactome Pathway | R-HSA-162582 | Signal Transduction | 9 | HNRNPM, RALB, GPNMB, C5AR1, PDK4, PSMD1, CXCR4, FASLG, AXIN2 | 1.745759 | 1 | 1 | 1 |

**Table s9:**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Annotation Cluster 1 | Enrichment Score: 1.7209275840680245 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| UP\_KW\_CELLULAR\_COMPONENT | KW-0472~Membrane | 19 | 70.37037 | 0.004343 | LRRC25, RALB, SDC2, PELI2, C5AR1, TAP2, TAP1, CXCR4, LPL, FASLG, FGR, DAB2, GPNMB, PIK3IP1, EWSR1, CD9, PSMD1, FXYD7, HPSE | 25 | 8340 | 17942 | 1.635002 | 0.083369 | 0.086862 | 0.086862 |
| UP\_SEQ\_FEATURE | TOPO\_DOM:Cytoplasmic | 11 | 40.74074 | 0.008624 | LRRC25, GPNMB, PIK3IP1, SDC2, C5AR1, TAP2, CD9, TAP1, CXCR4, FXYD7, FASLG | 25 | 3901 | 20569 | 2.32001 | 0.93524 | 0.681312 | 0.681312 |
| GOTERM\_CC\_DIRECT | GO:0016020~membrane | 13 | 48.14815 | 0.011737 | LRRC25, SDC2, PELI2, TAP2, TAP1, CXCR4, FASLG, HNRNPM, GPNMB, CD9, PSMD1, FXYD7, HPSE | 27 | 5048 | 20887 | 1.992215 | 0.637717 | 0.212955 | 0.212955 |
| UP\_SEQ\_FEATURE | TOPO\_DOM:Extracellular | 9 | 33.33333 | 0.016632 | LRRC25, GPNMB, PIK3IP1, SDC2, C5AR1, CD9, CXCR4, FXYD7, FASLG | 25 | 2992 | 20569 | 2.47488 | 0.995008 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical | 12 | 44.44444 | 0.032092 | LRRC25, GPNMB, PIK3IP1, SDC2, PELI2, TAP2, CD9, TAP1, PSMD1, CXCR4, FXYD7, FASLG | 25 | 5446 | 20569 | 1.812912 | 0.999967 | 1 | 1 |
| UP\_KW\_DOMAIN | KW-1133~Transmembrane helix | 13 | 48.14815 | 0.059617 | LRRC25, SDC2, PELI2, C5AR1, TAP2, TAP1, CXCR4, FASLG, GPNMB, PIK3IP1, CD9, PSMD1, FXYD7 | 21 | 5882 | 14597 | 1.536253 | 0.52175 | 0.385364 | 0.385364 |
| UP\_KW\_DOMAIN | KW-0812~Transmembrane | 13 | 48.14815 | 0.064227 | LRRC25, SDC2, PELI2, C5AR1, TAP2, TAP1, CXCR4, FASLG, GPNMB, PIK3IP1, CD9, PSMD1, FXYD7 | 21 | 5941 | 14597 | 1.520996 | 0.549138 | 0.385364 | 0.385364 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 2 | Enrichment Score: 1.3054230950558041 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_MF\_DIRECT | GO:0005102~signaling receptor binding | 4 | 14.81481 | 0.010411 | FGR, PIK3IP1, LPL, FASLG | 25 | 369 | 19304 | 8.370298 | 0.645147 | 0.128831 | 0.128831 |
| GOTERM\_CC\_DIRECT | GO:0005615~extracellular space | 6 | 22.22222 | 0.102324 | SPON1, PIK3IP1, CD9, LPL, FASLG, HPSE | 27 | 2033 | 20887 | 2.283107 | 0.999907 | 0.879986 | 0.879986 |
| GOTERM\_CC\_DIRECT | GO:0005576~extracellular region | 6 | 22.22222 | 0.113835 | FGR, CD9, LPL, PSMD1, FASLG, HPSE | 27 | 2101 | 20887 | 2.209213 | 0.999969 | 0.889986 | 0.889986 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 3 | Enrichment Score: 1.1227376478882118 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_BP\_DIRECT | GO:0006915~apoptotic process | 4 | 14.81481 | 0.038014 | DAB2, RALB, CXCR4, FASLG | 26 | 593 | 19734 | 5.11973 | 0.999995 | 1 | 1 |
| KEGG\_PATHWAY | hsa05200:Pathways in cancer | 4 | 14.81481 | 0.078908 | RALB, CXCR4, FASLG, AXIN2 | 18 | 533 | 8840 | 3.685637 | 0.999076 | 1 | 1 |
| GOTERM\_CC\_DIRECT | GO:0070062~extracellular exosome | 6 | 22.22222 | 0.142796 | FGR, HNRNPM, RALB, CD9, CXCR4, FASLG | 27 | 2258 | 20887 | 2.055605 | 0.999998 | 1 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 4 | Enrichment Score: 1.0724748086070106 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| KEGG\_PATHWAY | hsa05170:Human immunodeficiency virus 1 infection | 4 | 14.81481 | 0.007308 | TAP2, TAP1, CXCR4, FASLG | 18 | 213 | 8840 | 9.222744 | 0.463895 | 0.365579 | 0.365579 |
| KEGG\_PATHWAY | hsa05163:Human cytomegalovirus infection | 4 | 14.81481 | 0.008602 | TAP2, TAP1, CXCR4, FASLG | 18 | 226 | 8840 | 8.692232 | 0.520169 | 0.365579 | 0.365579 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=7 | 4 | 14.81481 | 0.09775 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 954 | 20569 | 3.449727 | 1 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=6 | 4 | 14.81481 | 0.115222 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 1026 | 20569 | 3.207641 | 1 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=5 | 4 | 14.81481 | 0.116731 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 1032 | 20569 | 3.188992 | 1 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=3 | 4 | 14.81481 | 0.122074 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 1053 | 20569 | 3.125394 | 1 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=4 | 4 | 14.81481 | 0.122845 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 1056 | 20569 | 3.116515 | 1 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=1 | 4 | 14.81481 | 0.127772 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 1075 | 20569 | 3.061433 | 1 | 1 | 1 |
| UP\_SEQ\_FEATURE | TRANSMEM:Helical; Name=2 | 4 | 14.81481 | 0.128033 | C5AR1, TAP2, TAP1, CXCR4 | 25 | 1076 | 20569 | 3.058587 | 1 | 1 | 1 |
| KEGG\_PATHWAY | hsa05168:Herpes simplex virus 1 infection | 3 | 11.11111 | 0.265566 | TAP2, TAP1, FASLG | 18 | 522 | 8840 | 2.822478 | 1 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0945~Host-virus interaction | 3 | 11.11111 | 0.296249 | TAP2, TAP1, CXCR4 | 19 | 690 | 11450 | 2.620137 | 0.999947 | 1 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 5 | Enrichment Score: 0.7420146049745282 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| UP\_KW\_PTM | KW-0325~Glycoprotein | 12 | 44.44444 | 0.060733 | LRRC25, SPON1, GPNMB, PIK3IP1, SDC2, C5AR1, CD9, LPL, CXCR4, FXYD7, FASLG, HPSE | 22 | 4813 | 14252 | 1.615171 | 0.609309 | 0.670528 | 0.670528 |
| GOTERM\_CC\_DIRECT | GO:0005615~extracellular space | 6 | 22.22222 | 0.102324 | SPON1, PIK3IP1, CD9, LPL, FASLG, HPSE | 27 | 2033 | 20887 | 2.283107 | 0.999907 | 0.879986 | 0.879986 |
| UP\_SEQ\_FEATURE | CARBOHYD:N-linked (GlcNAc...) asparagine | 9 | 33.33333 | 0.124386 | LRRC25, SPON1, GPNMB, C5AR1, CD9, LPL, CXCR4, FASLG, HPSE | 25 | 4422 | 20569 | 1.674545 | 1 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0130~Cell adhesion | 3 | 11.11111 | 0.17975 | SPON1, CD9, HPSE | 19 | 492 | 11450 | 3.674583 | 0.996105 | 1 | 1 |
| UP\_KW\_CELLULAR\_COMPONENT | KW-0964~Secreted | 5 | 18.51852 | 0.332358 | SPON1, CD9, LPL, FASLG, HPSE | 25 | 2180 | 17942 | 1.646055 | 0.99969 | 1 | 1 |
| UP\_KW\_PTM | KW-1015~Disulfide bond | 8 | 29.62963 | 0.346177 | SPON1, PIK3IP1, C5AR1, CD9, LPL, CXCR4, FASLG, HPSE | 22 | 3906 | 14252 | 1.326817 | 0.998294 | 0.867911 | 0.867911 |
| UP\_KW\_DOMAIN | KW-0732~Signal | 8 | 29.62963 | 0.400081 | LRRC25, SPON1, GPNMB, PIK3IP1, SDC2, CD9, LPL, HPSE | 21 | 4410 | 14597 | 1.260944 | 0.997827 | 1 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 6 | Enrichment Score: 0.5842574176163582 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_BP\_DIRECT | GO:0015031~protein transport | 3 | 11.11111 | 0.096415 | DAB2, TAP2, TAP1 | 26 | 415 | 19734 | 5.486747 | 1 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0653~Protein transport | 3 | 11.11111 | 0.271206 | DAB2, TAP2, TAP1 | 19 | 648 | 11450 | 2.789961 | 0.999858 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0813~Transport | 4 | 14.81481 | 0.675743 | DAB2, TAP2, TAP1, FXYD7 | 19 | 2124 | 11450 | 1.134899 | 1 | 1 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 7 | Enrichment Score: 0.5254842100972762 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| UP\_KW\_LIGAND | KW-0547~Nucleotide-binding | 5 | 18.51852 | 0.205876 | FGR, RALB, TAP2, PDK4, TAP1 | 10 | 1879 | 6947 | 1.84859 | 0.900256 | 0.941035 | 0.941035 |
| UP\_KW\_LIGAND | KW-0067~ATP-binding | 4 | 14.81481 | 0.282311 | FGR, TAP2, PDK4, TAP1 | 10 | 1443 | 6947 | 1.92571 | 0.963745 | 0.941035 | 0.941035 |
| GOTERM\_MF\_DIRECT | GO:0005524~ATP binding | 4 | 14.81481 | 0.299409 | FGR, TAP2, PDK4, TAP1 | 25 | 1541 | 19304 | 2.004309 | 1 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0391~Immunity | 3 | 11.11111 | 0.454429 | FGR, TAP2, TAP1 | 19 | 963 | 11450 | 1.877357 | 1 | 1 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 8 | Enrichment Score: 0.20549782908453454 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| UP\_KW\_MOLECULAR\_FUNCTION | KW-0678~Repressor | 3 | 11.11111 | 0.189926 | MAFB, EWSR1, FASLG | 16 | 636 | 11889 | 3.505012 | 0.98172 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0805~Transcription regulation | 3 | 11.11111 | 0.918289 | MAFB, EWSR1, FASLG | 19 | 2414 | 11450 | 0.748921 | 1 | 1 | 1 |
| UP\_KW\_BIOLOGICAL\_PROCESS | KW-0804~Transcription | 3 | 11.11111 | 0.926677 | MAFB, EWSR1, FASLG | 19 | 2483 | 11450 | 0.728109 | 1 | 1 | 1 |
| UP\_KW\_CELLULAR\_COMPONENT | KW-0539~Nucleus | 6 | 22.22222 | 0.932218 | HNRNPM, MAFB, EWSR1, TSC22D3, FASLG, HPSE | 25 | 5858 | 17942 | 0.735077 | 1 | 1 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Annotation Cluster 9 | Enrichment Score: 0.05731737974098145 |  |  |  |  |  |  |  |  |  |  |  |
| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
| GOTERM\_CC\_DIRECT | GO:0005654~nucleoplasm | 5 | 18.51852 | 0.76731 | FGR, HNRNPM, EWSR1, PSMD1, HPSE | 27 | 4030 | 20887 | 0.959792 | 1 | 1 | 1 |
| UP\_KW\_PTM | KW-0007~Acetylation | 4 | 14.81481 | 0.920348 | HNRNPM, DAB2, EWSR1, PSMD1 | 22 | 3511 | 14252 | 0.738044 | 1 | 1 | 1 |
| UP\_KW\_DOMAIN | KW-0677~Repeat | 5 | 18.51852 | 0.95307 | LRRC25, HNRNPM, SPON1, EWSR1, PSMD1 | 21 | 5064 | 14597 | 0.68631 | 1 | 1 | 1 |

**Table s10:**

|  |  |
| --- | --- |
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**Table s11:**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SUID | AverageShortestPathLength | BetweennessCentrality | ClosenessCentrality | ClusteringCoefficient | degree.layout | Eccentricity | EdgeCount | Indegree | Matching.Attribute | Matching.Attribute.1 | MCODE\_Cluster | MCODE\_Score | name | NeighborhoodConnectivity | Outdegree |
| 1342 | 1 | 0 | 1 | 0 | 5 | 1 | 7 | 0 | DAB2 | DAB2 |  | 0.25 | DAB2 | 8.142857 | 7 |
| 1343 | 0 | 0 | 0 | 0 | 5 | 0 | 5 | 5 | positive regulation of protein phosphorylation | positive regulation of protein phosphorylation |  | 0.285714 | positive regulation of protein phosphorylation | 6.4 | 0 |
| 1344 | 1 | 0 | 1 | 0 | 7 | 1 | 8 | 0 | RALB | RALB |  | 0.222222 | RALB | 8.5 | 8 |
| 1345 | 1 | 0 | 1 | 0 | 7 | 1 | 7 | 0 | GPNMB | GPNMB |  | 0.25 | GPNMB | 10.71429 | 7 |
| 1346 | 1 | 0 | 1 | 0 | 4 | 1 | 4 | 0 | PELI2 | PELI2 |  | 0.4 | PELI2 | 12.5 | 4 |
| 1347 | 1 | 0 | 1 | 0 | 5 | 1 | 6 | 0 | AXIN2 | AXIN2 |  | 0.285714 | AXIN2 | 9.833333 | 6 |
| 1348 | 0 | 0 | 0 | 0 | 5 | 0 | 4 | 4 | positive regulation of cell migration | positive regulation of cell migration |  | 0.333333 | positive regulation of cell migration | 8.25 | 0 |
| 1349 | 1 | 0 | 1 | 0 | 8 | 1 | 10 | 0 | CXCR4 | CXCR4 |  | 0.181818 | CXCR4 | 8.6 | 10 |
| 1350 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | antigen processing and presentation of endogenous peptide antigen via MHC class I | antigen processing and presentation of endogenous peptide antigen via MHC class I |  | 2 | antigen processing and presentation of endogenous peptide antigen via MHC class I | 19.5 | 0 |
| 1351 | 0 | 0 | 0 | 0 | 5 | 0 | 4 | 4 | apoptotic process | apoptotic process |  | 0.333333 | apoptotic process | 9.25 | 0 |
| 1352 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 2 | receptor internalization | receptor internalization |  | 0.5 | receptor internalization | 7 | 0 |
| 1353 | 1 | 0 | 1 | 0 | 4 | 1 | 6 | 0 | CD9 | CD9 |  | 0.285714 | CD9 | 10.5 | 6 |
| 1354 | 0 | 0 | 0 | 0.05 | 6 | 0 | 5 | 5 | signal transduction | signal transduction |  | 2 | signal transduction | 8.2 | 0 |
| 1355 | 1 | 0 | 1 | 0 | 4 | 1 | 5 | 0 | C5AR1 | C5AR1 |  | 0.333333 | C5AR1 | 8.2 | 5 |
| 1356 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 2 | positive regulation of epithelial to mesenchymal transition | positive regulation of epithelial to mesenchymal transition |  | 0.5 | positive regulation of epithelial to mesenchymal transition | 6.5 | 0 |
| 1357 | 0 | 0 | 0 | 0.166667 | 4 | 0 | 3 | 3 | protein transport | protein transport |  | 2 | protein transport | 15.33333 | 0 |
| 1358 | 0 | 0 | 0 | 0.004762 | 12 | 0 | 15 | 15 | plasma membrane | plasma membrane |  | 2 | plasma membrane | 7.2 | 0 |
| 1359 | 1 | 0 | 1 | 0 | 4 | 1 | 5 | 0 | SDC2 | SDC2 |  | 0.333333 | SDC2 | 12.2 | 5 |
| 1360 | 1 | 0 | 1 | 0 | 3 | 1 | 3 | 0 | LPL | LPL |  | 0.5 | LPL | 14.33333 | 3 |
| 1361 | 1 | 0 | 1 | 0 | 3 | 1 | 3 | 0 | PIK3IP1 | PIK3IP1 |  | 0.5 | PIK3IP1 | 14.33333 | 3 |
| 1362 | 1 | 0 | 1 | 0 | 4 | 1 | 4 | 0 | FXYD7 | FXYD7 |  | 0.4 | FXYD7 | 14.5 | 4 |
| 1363 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | TAP complex | TAP complex |  | 2 | TAP complex | 19.5 | 0 |
| 1364 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 3 | lysosomal lumen | lysosomal lumen |  | 0.4 | lysosomal lumen | 7.333333 | 0 |
| 1365 | 1 | 0 | 1 | 0 | 3 | 1 | 5 | 0 | HPSE | HPSE |  | 0.333333 | HPSE | 10.4 | 5 |
| 1366 | 1 | 0 | 1 | 0 | 2 | 1 | 2 | 0 | LRRC25 | LRRC25 |  | 0.666667 | LRRC25 | 18.5 | 2 |
| 1367 | 0 | 0 | 0 | 0.00641 | 10 | 0 | 13 | 13 | membrane | membrane |  | 2 | membrane | 8.230769 | 0 |
| 1368 | 1 | 0 | 1 | 0 | 6 | 1 | 9 | 0 | PSMD1 | PSMD1 |  | 0.2 | PSMD1 | 8.222222 | 9 |
| 1369 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | MHC class I peptide loading complex | MHC class I peptide loading complex |  | 2 | MHC class I peptide loading complex | 19.5 | 0 |
| 1370 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 3 | external side of plasma membrane | external side of plasma membrane |  | 0.4 | external side of plasma membrane | 9.333333 | 0 |
| 1371 | 0 | 0 | 0 | 0.005435 | 14 | 0 | 24 | 24 | protein binding | protein binding |  | 0.857143 | protein binding | 6.291667 | 0 |
| 1372 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | SPON1 | SPON1 |  | 0 | SPON1 | 24 | 1 |
| 1373 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | TSC22D3 | TSC22D3 |  | 0 | TSC22D3 | 24 | 1 |
| 1374 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | MAFB | MAFB |  | 0 | MAFB | 24 | 1 |
| 1375 | 1 | 0 | 1 | 0 | 2 | 1 | 2 | 0 | PDK4 | PDK4 |  | 0.666667 | PDK4 | 16.5 | 2 |
| 1376 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | ABC-type peptide antigen transporter activity | ABC-type peptide antigen transporter activity |  | 2 | ABC-type peptide antigen transporter activity | 19.5 | 0 |
| 1377 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | peptide transmembrane transporter activity | peptide transmembrane transporter activity |  | 2 | peptide transmembrane transporter activity | 19.5 | 0 |
| 1378 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | TAP1 binding | TAP1 binding |  | 2 | TAP1 binding | 19.5 | 0 |
| 1379 | 0 | 0 | 0 | 0 | 5 | 0 | 4 | 4 | ubiquitin protein ligase binding | ubiquitin protein ligase binding |  | 0.333333 | ubiquitin protein ligase binding | 8.25 | 0 |
| 1380 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | MHC class Ib protein binding | MHC class Ib protein binding |  | 2 | MHC class Ib protein binding | 19.5 | 0 |
| 1381 | 0 | 0 | 0 | 0.083333 | 3 | 0 | 4 | 4 | signaling receptor binding | signaling receptor binding |  | 2 | signaling receptor binding | 6.75 | 0 |
| 1382 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | peptide antigen binding | peptide antigen binding |  | 2 | peptide antigen binding | 19.5 | 0 |
| 1383 | 0 | 0 | 0 | 0.083333 | 5 | 0 | 4 | 4 | Human immunodeficiency virus 1 infection | Human immunodeficiency virus 1 infection |  | 2 | Human immunodeficiency virus 1 infection | 15.25 | 0 |
| 1384 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | Primary immunodeficiency | Primary immunodeficiency |  | 2 | Primary immunodeficiency | 19.5 | 0 |
| 1385 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | ABC transporters | ABC transporters |  | 2 | ABC transporters | 19.5 | 0 |
| 1386 | 0 | 0 | 0 | 0.166667 | 4 | 0 | 3 | 3 | ER-Phagosome pathway | ER-Phagosome pathway |  | 2 | ER-Phagosome pathway | 16 | 0 |
| 1387 | 0 | 0 | 0 | 0.166667 | 4 | 0 | 3 | 3 | Antigen processing-Cross presentation | Antigen processing-Cross presentation |  | 2 | Antigen processing-Cross presentation | 16 | 0 |
| 1388 | 0 | 0 | 0 | 0 | 6 | 0 | 6 | 6 | Infectious disease | Infectious disease |  | 0.25 | Infectious disease | 7.166667 | 0 |
| 1389 | 0 | 0 | 0 | 0.5 | 3 | 0 | 2 | 2 | "Antigen Presentation: Folding | "Antigen Presentation: Folding |  | 2 | "Antigen Presentation: Folding | 19.5 | 0 |
| 1390 | 0 | 0 | 0 | 0 | 5 | 0 | 4 | 4 | Neutrophil degranulation | Neutrophil degranulation |  | 0.333333 | Neutrophil degranulation | 7 | 0 |
| 1391 | 0 | 0 | 0 | 0.035714 | 8 | 0 | 8 | 8 | Immune System | Immune System | Cluster 1 | 1.2 | Immune System | 10.375 | 0 |
| 1392 | 0 | 0 | 0 | 0 | 8 | 0 | 9 | 9 | Signal Transduction | Signal Transduction |  | 0.181818 | Signal Transduction | 7 | 0 |
| 1393 | 1.4 | 0 | 0.714286 | 0.166667 | 3 | 2 | 3 | 0 | EWSR1 | EWSR1 |  | 2 | EWSR1 | 14.33333 | 3 |
| 1394 | 1 | 6.49E-04 | 1 | 0.083333 | 4 | 1 | 4 | 1 | HNRNPM | HNRNPM |  | 2 | HNRNPM | 12.25 | 3 |
| 1395 | 1.2 | 0 | 0.833333 | 0.037879 | 9 | 2 | 12 | 0 | FASLG | FASLG | Cluster 1 | 1.047619 | FASLG | 8.416667 | 12 |
| 1396 | 1 | 9.74E-04 | 1 | 0.069444 | 8 | 1 | 9 | 1 | FGR | FGR | Cluster 1 | 1.047619 | FGR | 9.111111 | 8 |
| 1397 | 1 | 0 | 1 | 0.047368 | 5 | 1 | 20 | 0 | TAP1 | TAP1 |  | 0.389474 | TAP1 | 5.7 | 20 |
| 1398 | 1 | 0 | 1 | 0.052632 | 4 | 1 | 19 | 1 | TAP2 | TAP2 |  | 0.389474 | TAP2 | 5.263158 | 18 |
| 1399 |  |  |  |  | 1 |  |  |  |  | assembly and peptide loading of class I MHC" |  | 0 | assembly and peptide loading of class I MHC" |  |  |
| 1400 |  |  |  |  | 3 |  |  |  |  | Reactome Pathway |  | 0.285714 | Reactome Pathway |  |  |
| 1401 |  |  |  |  | 3 |  |  |  |  | KEGG Pathway |  | 0.5 | KEGG Pathway |  |  |
| 1402 |  |  |  |  | 3 |  |  |  |  | Molecular Function |  | 0.222222 | Molecular Function |  |  |
| 1403 |  |  |  |  | 2 |  |  |  |  | Cellular Component |  | 0.285714 | Cellular Component |  |  |
| 1404 |  |  |  |  | 4 |  |  |  |  | Biological Process |  | 0.222222 | Biological Process |  |  |

**Table s12:** Top 30 in network Merged Network\_1 ranked by Degree method.

|  |  |  |
| --- | --- | --- |
| Rank | Name | Score |
| 1 | protein binding | 25 |
| 2 | TAP1 | 20 |
| 3 | TAP2 | 19 |
| 4 | plasma membrane | 16 |
| 5 | membrane | 14 |
| 6 | FASLG | 12 |
| 7 | CXCR4 | 10 |
| 7 | Signal Transduction | 10 |
| 9 | PSMD1 | 9 |
| 9 | Immune System | 9 |
| 9 | FGR | 9 |
| 12 | RALB | 8 |
| 12 | Molecular Function | 8 |
| 12 | Biological Process | 8 |
| 15 | DAB2 | 7 |
| 15 | GPNMB | 7 |
| 15 | Infectious disease | 7 |
| 18 | positive regulation of protein phosphorylation | 6 |
| 18 | AXIN2 | 6 |
| 18 | CD9 | 6 |
| 18 | signal transduction | 6 |
| 18 | Reactome Pathway | 6 |
| 18 | Cellular Component | 6 |
| 24 | positive regulation of cell migration | 5 |
| 24 | apoptotic process | 5 |
| 24 | C5AR1 | 5 |
| 24 | SDC2 | 5 |
| 24 | HPSE | 5 |
| 24 | ubiquitin protein ligase binding | 5 |
| 24 | signaling receptor binding | 5 |