**IL-1R8 DEFICIENCY DRIVES AUTOIMMUNITY-ASSOCIATED LYMPHOMA DEVELOPMENT**

Running title: IL-1R8 in autoimmunity-associated B cell lymphoma

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| **Supplementary Table 1**: List of genes analyzed by Real Time PCR Array |
| **GENE** | **Full official name** | **Gene ID** | **Genebank link** |
| Actb\* | actin, beta - HOUSEKEEPING | 11461 | https://www.ncbi.nlm.nih.gov/gene/11461 |
| Adm | adrenomedullin | 11535 | https://www.ncbi.nlm.nih.gov/gene/11535 |
| Agt | angiotensinogen (serpin peptidase inhibitor, clade A, member 8) | 11606 | https://www.ncbi.nlm.nih.gov/gene/11606 |
| Akt1 | thymoma viral proto-oncogene 1 | 11651 | https://www.ncbi.nlm.nih.gov/gene/11651 |
| Aldh3a2 | aldehyde dehydrogenase family 3, subfamily A2 | 11671 | https://www.ncbi.nlm.nih.gov/gene/11671 |
| B2m\* | beta-2 microglobulin - HOUSEKEEPING | 12010 | https://www.ncbi.nlm.nih.gov/gene/12010 |
| Bcl2a1a | B cell leukemia/lymphoma 2 related protein A1a | 12044 | https://www.ncbi.nlm.nih.gov/gene/12044 |
| Bcl2l1 | BCL2-like 1 | 12048 | https://www.ncbi.nlm.nih.gov/gene/12048 |
| Birc2 | baculoviral IAP repeat-containing 2 | 11797 | https://www.ncbi.nlm.nih.gov/gene/11797 |
| Birc3 | baculoviral IAP repeat-containing 3 | 11796 | https://www.ncbi.nlm.nih.gov/gene/11796 |
| C3 | complement component 3 | 12266 | https://www.ncbi.nlm.nih.gov/gene/12266 |
| Ccl12 | chemokine (C-C motif) ligand 12 | 20293 | https://www.ncbi.nlm.nih.gov/gene/20293 |
| Ccl22 | chemokine (C-C motif) ligand 22 | 20299 | https://www.ncbi.nlm.nih.gov/gene/20299 |
| Ccl5 | chemokine (C-C motif) ligand 5 | 20304 | https://www.ncbi.nlm.nih.gov/gene/20304 |
| Ccnd1 | cyclin D1 | 12443 | https://www.ncbi.nlm.nih.gov/gene/12443 |
| Ccr5 | chemokine (C-C motif) receptor 5 | 12774 | https://www.ncbi.nlm.nih.gov/gene/12774 |
| Cd40 | CD40 antigen | 21939 | https://www.ncbi.nlm.nih.gov/gene/21939 |
| Cd74 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) | 16149 | https://www.ncbi.nlm.nih.gov/gene/16149 |
| Cd80 | CD80 antigen | 12519 | https://www.ncbi.nlm.nih.gov/gene/12519 |
| Cd83 | CD83 antigen | 12522 | https://www.ncbi.nlm.nih.gov/gene/12522 |
| Cdkn1a | cyclin-dependent kinase inhibitor 1A (P21) | 12575 | https://www.ncbi.nlm.nih.gov/gene/12575 |
| Cfb | complement factor B | 14962 | https://www.ncbi.nlm.nih.gov/gene/14962 |
| Csf1 | colony stimulating factor 1 (macrophage) | 12977 | https://www.ncbi.nlm.nih.gov/gene/12977 |
| Csf2 | colony stimulating factor 2 (granulocyte-macrophage) | 12981 | https://www.ncbi.nlm.nih.gov/gene/12981 |
| Csf2rb | colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) | 12983 | https://www.ncbi.nlm.nih.gov/gene/12983 |
| Csf3 | colony stimulating factor 3 (granulocyte) | 12985 | https://www.ncbi.nlm.nih.gov/gene/12985 |
| Cxcl1 | chemokine (C-X-C motif) ligand 1 | 14825 | https://www.ncbi.nlm.nih.gov/gene/14825 |
| Cxcl10 | chemokine (C-X-C motif) ligand 10 | 15945 | https://www.ncbi.nlm.nih.gov/gene/15945 |
| Cxcl3 | chemokine (C-X-C motif) ligand 3 | 330122 | https://www.ncbi.nlm.nih.gov/gene/330122 |
| Cxcl9 | chemokine (C-X-C motif) ligand 9 | 17329 | https://www.ncbi.nlm.nih.gov/gene/17329 |
| Egfr | epidermal growth factor receptor | 13649 | https://www.ncbi.nlm.nih.gov/gene/13649 |
| Egr2 | early growth response 2 | 13654 | https://www.ncbi.nlm.nih.gov/gene/13654 |
| F3 | coagulation factor III | 14066 | https://www.ncbi.nlm.nih.gov/gene/14066 |
| F8 | coagulation factor VIII | 14069 | https://www.ncbi.nlm.nih.gov/gene/14069 |
| Fas | Fas (TNF receptor superfamily member 6) | 14102 | https://www.ncbi.nlm.nih.gov/gene/14102 |
| Fasl | Fas ligand (TNF superfamily, member 6) | 14103 | https://www.ncbi.nlm.nih.gov/gene/14103 |
| Gadd45b | growth arrest and DNA-damage-inducible 45 beta | 17873 | https://www.ncbi.nlm.nih.gov/gene/17873 |
| Gapdh\* | glyceraldehyde-3-phosphate dehydrogenase - HOUSEKEEPING | 14433 | https://www.ncbi.nlm.nih.gov/gene/14433 |
| Gusb\* | glucuronidase, beta - HOUSEKEEPING | 110006 | https://www.ncbi.nlm.nih.gov/gene/110006 |
| Hprt\* | hypoxanthine guanine phosphoribosyl transferase - HOUSEKEEPING | 15452 | https://www.ncbi.nlm.nih.gov/gene/15452 |
| Hsp90ab1 | heat shock protein 90 alpha (cytosolic), class B member 1 | 15516 | https://www.ncbi.nlm.nih.gov/gene/15516 |
| Icam1 | intercellular adhesion molecule 1 | 15894 | https://www.ncbi.nlm.nih.gov/gene/15894 |
| Ifnb1 | interferon beta 1, fibroblast | 15977 | https://www.ncbi.nlm.nih.gov/gene/15977 |
| Ifng | interferon gamma | 15978 | https://www.ncbi.nlm.nih.gov/gene/15978 |
| Il12b | interleukin 12b | 16160 | https://www.ncbi.nlm.nih.gov/gene/16160 |
| Il15 | interleukin 15 | 16168 | https://www.ncbi.nlm.nih.gov/gene/16168 |
| Il1a | interleukin 1 alpha | 16175 | https://www.ncbi.nlm.nih.gov/gene/16175 |
| Il1b | interleukin 1 beta | 16176 | https://www.ncbi.nlm.nih.gov/gene/16176 |
| Il1r2 | interleukin 1 receptor, type II | 16178 | https://www.ncbi.nlm.nih.gov/gene/16178 |
| Il1rn | interleukin 1 receptor antagonist | 16181 | https://www.ncbi.nlm.nih.gov/gene/16181 |
| Il2 | interleukin 2 | 16183 | https://www.ncbi.nlm.nih.gov/gene/16183 |
| Il2ra | interleukin 2 receptor, alpha chain | 16184 | https://www.ncbi.nlm.nih.gov/gene/16184 |
| Il4 | interleukin 4 | 16189 | https://www.ncbi.nlm.nih.gov/gene/16189 |
| Il6 | interleukin 6 | 16193 | https://www.ncbi.nlm.nih.gov/gene/16193 |
| Ins2 | insulin II | 16334 | https://www.ncbi.nlm.nih.gov/gene/16334 |
| Irf1 | interferon regulatory factor 1 | 16362 | https://www.ncbi.nlm.nih.gov/gene/16362 |
| Lta | lymphotoxin A | 16992 | https://www.ncbi.nlm.nih.gov/gene/16992 |
| Ltb | lymphotoxin B | 16994 | https://www.ncbi.nlm.nih.gov/gene/16994 |
| Map2k6 | mitogen-activated protein kinase kinase 6 | 26399 | https://www.ncbi.nlm.nih.gov/gene/26399 |
| Mitf | microphthalmia-associated transcription factor | 17342 | https://www.ncbi.nlm.nih.gov/gene/17342 |
| Mmp9 | matrix metallopeptidase 9 | 17395 | https://www.ncbi.nlm.nih.gov/gene/17395 |
| Myc | myelocytomatosis oncogene | 17869 | https://www.ncbi.nlm.nih.gov/gene/17869 |
| Myd88 | myeloid differentiation primary response gene 88 | 17874 | https://www.ncbi.nlm.nih.gov/gene/17874 |
| Ncoa3 | nuclear receptor coactivator 3 | 17979 | https://www.ncbi.nlm.nih.gov/gene/17979 |
| Nfkb1 | nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 | 18033 | https://www.ncbi.nlm.nih.gov/gene/18033 |
| Nfkb2 | nuclear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 | 18034 | https://www.ncbi.nlm.nih.gov/gene/18034 |
| Nfkbia | nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha | 18035 | https://www.ncbi.nlm.nih.gov/gene/18035 |
| Nqo1 | NAD(P)H dehydrogenase, quinone 1 | 18104 | https://www.ncbi.nlm.nih.gov/gene/18104 |
| Nr4a2 | nuclear receptor subfamily 4, group A, member 2 | 18227 | https://www.ncbi.nlm.nih.gov/gene/18227 |
| Pdgfb | platelet derived growth factor, B polypeptide | 18591 | https://www.ncbi.nlm.nih.gov/gene/18591 |
| Plau | plasminogen activator, urokinase | 18792 | https://www.ncbi.nlm.nih.gov/gene/18792 |
| Ptgs2 | prostaglandin-endoperoxide synthase 2 | 19225 | https://www.ncbi.nlm.nih.gov/gene/19225 |
| Rel | reticuloendotheliosis oncogene | 19696 | https://www.ncbi.nlm.nih.gov/gene/19696 |
| Rela | v-rel reticuloendotheliosis viral oncogene homolog A (avian) | 19697 | https://www.ncbi.nlm.nih.gov/gene/19697 |
| Relb | avian reticuloendotheliosis viral (v-rel) oncogene related B | 19698 | https://www.ncbi.nlm.nih.gov/gene/19698 |
| Sele | selectin, endothelial cell | 20339 | https://www.ncbi.nlm.nih.gov/gene/20339 |
| Selp | selectin, platelet | 20344 | https://www.ncbi.nlm.nih.gov/gene/20344 |
| Snap25 | synaptosomal-associated protein 25 | 20614 | https://www.ncbi.nlm.nih.gov/gene/20614 |
| Sod2 | superoxide dismutase 2, mitochondrial | 20656 | https://www.ncbi.nlm.nih.gov/gene/20656 |
| Stat1 | signal transducer and activator of transcription 1 | 20846 | https://www.ncbi.nlm.nih.gov/gene/20846 |
| Stat3 | signal transducer and activator of transcription 3 | 20848 | https://www.ncbi.nlm.nih.gov/gene/20848 |
| Stat5b | signal transducer and activator of transcription 5B | 20851 | https://www.ncbi.nlm.nih.gov/gene/20851 |
| Tbp\* | TATA box binding protein - HOUSEKEEPING | 21374 | https://www.ncbi.nlm.nih.gov/gene/21374 |
| Tnf | tumor necrosis factor | 21926 | https://www.ncbi.nlm.nih.gov/gene/21926 |
| Tnfrsf1b | tumor necrosis factor receptor superfamily, member 1b | 21938 | https://www.ncbi.nlm.nih.gov/gene/21938 |
| Tnfsf10 | tumor necrosis factor (ligand) superfamily, member 10 | 22035 | https://www.ncbi.nlm.nih.gov/gene/22035 |
| Traf2 | TNF receptor-associated factor 2 | 22030 | https://www.ncbi.nlm.nih.gov/gene/22030 |
| Trp53 | transformation related protein 53 | 22059 | https://www.ncbi.nlm.nih.gov/gene/22059 |
| Vcam1 | vascular cell adhesion molecule 1 | 22329 | https://www.ncbi.nlm.nih.gov/gene/22329 |
| Xiap | X-linked inhibitor of apoptosis | 11798 | https://www.ncbi.nlm.nih.gov/gene/11798 |

\*Housekeeping genes.

**Supplementary Table 2** - Fold difference of mRNA expression mean ratio between the indicated groups of mice; statistically significant differences are indicated in red (p-value<0.05).

|  |  |  |  |
| --- | --- | --- | --- |
|  | versus *Il1r8+/+* | versus *Il1r8-/-* | versus *lpr* |
| **GENE** | ***Il1r8-/-*** | ***lpr***  | ***Il1r8-/--lpr***  | ***Il1r8-/--lpr***  | ***lpr***  | ***Il1r8-/--lpr***  |
| Cxcl9 | 1.84 | 20.91 | 8.51 | 4.63 | 11.36 | 0.41 |
| Ccnd1 | 1.25 | 3.97 | 8.39 | 6.7 | 3.17 | 2.11 |
| Il1b | 1.97 | 12.84 | 7.94 | 4.03 | 6.52 | 0.62 |
| Fas | 1.14 | 3.9 | 6.71 | 5.9 | 3.42 | 1.72 |
| Nr4a2 | 0.93 | 2.56 | 3.33 | 3.57 | 2.74 | 1.3 |
| Ifng | 0.72 | 3.06 | 3.29 | 4.56 | 4.25 | 1.07 |
| Adm | 0.85 | 2.71 | 3.19 | 3.74 | 3.18 | 1.18 |
| Csf1 | 0.78 | 3.24 | 2.96 | 3.8 | 4.17 | 0.91 |
| F8 | 1.17 | 2 | 2.47 | 2.11 | 1.71 | 1.23 |
| Stat1 | 1.02 | 2.63 | 2.43 | 2.39 | 2.59 | 0.92 |
| Il12b | 1.13 | 2.54 | 2.41 | 2.14 | 2.25 | 0.95 |
| Il15 | 1.14 | 2.96 | 1.52 | 1.33 | 2.59 | 0.51 |
| Akt1 | 0.77 | 1.62 | 1.49 | 1.95 | 2.11 | 0.92 |
| Bcl2a1a | 0.93 | 0.47 | 1.08 | 1.17 | 0.5 | 2.32 |

**Supplementary Table 3 -** GSEA analysis: pathways significantly enriched by genes positively correlated with IL-1R8 gene expression profile.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| NAME | SIZE | ES | NES | NOM p-val | FDR q-val |
| REACTOME\_IMMUNOREGULATORY\_INTERACTIONS\_BETWEEN\_A\_LYMPHOID\_AND\_A\_NON\_LYMPHOID\_CELL | 57 | 0.5560651 | 2.1149802 | 0 | 0.006631271 |
| REACTOME\_SEMAPHORIN\_INTERACTIONS | 63 | 0.5272512 | 2.0625565 | 0 | 0.004427689 |
| REACTOME\_APOPTOSIS | 135 | 0.46543798 | 2.0192509 | 0 | 0.005509295 |
| REACTOME\_SEMA4D\_IN\_SEMAPHORIN\_SIGNALING | 29 | 0.6114722 | 2.0106351 | 0 | 0.004679007 |
| REACTOME\_GENERATION\_OF\_SECOND\_MESSENGER\_MOLECULES | 24 | 0.6335456 | 1.9857982 | 0 | 0.006849419 |
| REACTOME\_IL\_2\_SIGNALING | 41 | 0.56653845 | 1.9849968 | 0 | 0.005707849 |
| REACTOME\_SEMA4D\_INDUCED\_CELL\_MIGRATION\_AND\_GROWTH\_CONE\_COLLAPSE | 24 | 0.63027036 | 1.968461 | 0 | 0.006471509 |
| REACTOME\_IL\_RECEPTOR\_SHC\_SIGNALING | 27 | 0.60233754 | 1.947832 | 0 | 0.007729077 |
| REACTOME\_THE\_ROLE\_OF\_NEF\_IN\_HIV1\_REPLICATION\_AND\_DISEASE\_PATHOGENESIS | 25 | 0.61866456 | 1.9468073 | 0 | 0.006870291 |
| REACTOME\_IL\_3\_5\_AND\_GM\_CSF\_SIGNALING | 43 | 0.54155475 | 1.9265699 | 0 | 0.008161997 |
| REACTOME\_ER\_PHAGOSOME\_PATHWAY | 55 | 0.5154725 | 1.925284 | 0 | 0.007524913 |
| REACTOME\_REGULATION\_OF\_ORNITHINE\_DECARBOXYLASE\_ODC | 45 | 0.5329246 | 1.9158075 | 0 | 0.008183328 |
| REACTOME\_PLATELET\_ACTIVATION\_SIGNALING\_AND\_AGGREGATION | 184 | 0.42759752 | 1.9112071 | 0 | 0.007889953 |
| REACTOME\_DESTABILIZATION\_OF\_MRNA\_BY\_AUF1\_HNRNP\_D0 | 46 | 0.52571225 | 1.8967216 | 0.002631579 | 0.009368315 |
| REACTOME\_VIF\_MEDIATED\_DEGRADATION\_OF\_APOBEC3G | 47 | 0.5094536 | 1.8831106 | 0.00128866 | 0.010375362 |
| REACTOME\_COSTIMULATION\_BY\_THE\_CD28\_FAMILY | 55 | 0.49536243 | 1.8799953 | 0 | 0.010000062 |
| REACTOME\_NEF\_MEDIATES\_DOWN\_MODULATION\_OF\_CELL\_SURFACE\_RECEPTORS\_BY\_RECRUITING\_THEM\_TO\_CLATHRIN\_ADAPTERS | 18 | 0.63335466 | 1.8777714 | 0 | 0.009606511 |
| REACTOME\_INTERFERON\_ALPHA\_BETA\_SIGNALING | 61 | 0.4942432 | 1.8699483 | 0 | 0.010796562 |
| REACTOME\_TCR\_SIGNALING | 46 | 0.5140592 | 1.869061 | 0.00127551 | 0.010403285 |
| REACTOME\_P53\_DEPENDENT\_G1\_DNA\_DAMAGE\_RESPONSE | 49 | 0.50641054 | 1.8481817 | 0 | 0.01404614 |
| REACTOME\_APOPTOTIC\_CLEAVAGE\_OF\_CELLULAR\_PROTEINS | 36 | 0.5295947 | 1.845216 | 0.001381216 | 0.013805647 |
| REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_ | 72 | 0.46877983 | 1.8421261 | 0 | 0.013381686 |
| REACTOME\_CDK\_MEDIATED\_PHOSPHORYLATION\_AND\_REMOVAL\_OF\_CDC6 | 43 | 0.50937605 | 1.8257669 | 0 | 0.015894147 |
| REACTOME\_POST\_CHAPERONIN\_TUBULIN\_FOLDING\_PATHWAY | 17 | 0.6184924 | 1.8248627 | 0 | 0.015278487 |
| REACTOME\_SMOOTH\_MUSCLE\_CONTRACTION | 21 | 0.59832734 | 1.8230551 | 0.002773925 | 0.015109732 |
| REACTOME\_SIGNAL\_AMPLIFICATION | 26 | 0.5731574 | 1.8095484 | 0.00141844 | 0.01779493 |
| REACTOME\_SIGNALING\_BY\_ILS | 102 | 0.43309763 | 1.7989638 | 0 | 0.019566141 |
| REACTOME\_SCFSKP2\_MEDIATED\_DEGRADATION\_OF\_P27\_P21 | 51 | 0.4794771 | 1.7814187 | 0 | 0.023977658 |
| REACTOME\_MUSCLE\_CONTRACTION | 44 | 0.4909483 | 1.777127 | 0.002574003 | 0.024215458 |
| REACTOME\_REGULATION\_OF\_MRNA\_STABILITY\_BY\_PROTEINS\_THAT\_BIND\_AU\_RICH\_ELEMENTS | 74 | 0.4400756 | 1.771664 | 0 | 0.024884202 |
| REACTOME\_APC\_C\_CDH1\_MEDIATED\_DEGRADATION\_OF\_CDC20\_AND\_OTHER\_APC\_C\_CDH1\_TARGETED\_PROTEINS\_IN\_LATE\_MITOSIS\_EARLY\_G1 | 57 | 0.4641212 | 1.7661825 | 0 | 0.025548024 |
| REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT | 57 | 0.46556526 | 1.764726 | 0.001261034 | 0.025270775 |
| REACTOME\_AUTODEGRADATION\_OF\_CDH1\_BY\_CDH1\_APC\_C | 50 | 0.48146138 | 1.7576708 | 0 | 0.02608101 |
| REACTOME\_HOST\_INTERACTIONS\_OF\_HIV\_FACTORS | 115 | 0.42015973 | 1.7574587 | 0 | 0.025379796 |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_DEGRADATION\_OF\_MITOTIC\_PROTEINS | 58 | 0.46135092 | 1.7555938 | 0.001265823 | 0.0251361 |
| REACTOME\_METABOLISM\_OF\_MRNA | 193 | 0.39280644 | 1.7548724 | 0 | 0.024592694 |
| REACTOME\_AUTODEGRADATION\_OF\_THE\_E3\_UBIQUITIN\_LIGASE\_COP1 | 43 | 0.49731064 | 1.7541634 | 0 | 0.024076857 |
| REACTOME\_SCF\_BETA\_TRCP\_MEDIATED\_DEGRADATION\_OF\_EMI1 | 46 | 0.47870278 | 1.7464118 | 0.001310616 | 0.02552312 |
| REACTOME\_APOPTOTIC\_EXECUTION\_PHASE | 50 | 0.47540772 | 1.7395765 | 0.002604167 | 0.02694393 |
| REACTOME\_ACTIVATION\_OF\_NF\_KAPPAB\_IN\_B\_CELLS | 57 | 0.45388073 | 1.7378933 | 0.00130719 | 0.026800659 |
| REACTOME\_PEPTIDE\_CHAIN\_ELONGATION | 81 | 0.43504187 | 1.7273188 | 0.001234568 | 0.029317182 |
| REACTOME\_ASSEMBLY\_OF\_THE\_PRE\_REPLICATIVE\_COMPLEX | 59 | 0.4554593 | 1.7214398 | 0.002587322 | 0.031143634 |
| REACTOME\_INFLUENZA\_VIRAL\_RNA\_TRANSCRIPTION\_AND\_REPLICATION | 97 | 0.41603833 | 1.720955 | 0 | 0.030650971 |
| REACTOME\_SRP\_DEPENDENT\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE | 102 | 0.4165638 | 1.7156625 | 0.001168224 | 0.031823423 |
| REACTOME\_HIV\_INFECTION | 181 | 0.38957876 | 1.713343 | 0 | 0.031957068 |
| REACTOME\_SIGNALING\_BY\_WNT | 59 | 0.449378 | 1.7073417 | 0.001283697 | 0.033359867 |
| REACTOME\_INTERFERON\_GAMMA\_SIGNALING | 52 | 0.46091112 | 1.7033194 | 0.002614379 | 0.03404304 |
| REACTOME\_FORMATION\_OF\_TUBULIN\_FOLDING\_INTERMEDIATES\_BY\_CCT\_TRIC | 19 | 0.57164603 | 1.702992 | 0.008759124 | 0.03340133 |
| REACTOME\_ACTIVATION\_OF\_CHAPERONE\_GENES\_BY\_XBP1S | 40 | 0.4788658 | 1.6994843 | 0.001342282 | 0.033926148 |
| REACTOME\_CDT1\_ASSOCIATION\_WITH\_THE\_CDC6\_ORC\_ORIGIN\_COMPLEX | 50 | 0.45630804 | 1.6907895 | 0.001270648 | 0.036716018 |
| REACTOME\_ORC1\_REMOVAL\_FROM\_CHROMATIN | 61 | 0.44581953 | 1.6894866 | 0.002487562 | 0.03677745 |
| REACTOME\_DOWNSTREAM\_SIGNALING\_EVENTS\_OF\_B\_CELL\_RECEPTOR\_BCR | 85 | 0.41550535 | 1.6843051 | 0 | 0.038091242 |
| REACTOME\_RAP1\_SIGNALLING | 16 | 0.5897599 | 1.6842521 | 0.013452915 | 0.03737254 |
| REACTOME\_ADAPTIVE\_IMMUNE\_SYSTEM | 446 | 0.35587052 | 1.6797129 | 0 | 0.038463127 |
| REACTOME\_SIGNALING\_BY\_RHO\_GTPASES | 91 | 0.40948877 | 1.6578765 | 0 | 0.04708154 |
| REACTOME\_HEMOSTASIS | 408 | 0.34873915 | 1.655229 | 0 | 0.047703303 |
| REACTOME\_PREFOLDIN\_MEDIATED\_TRANSFER\_OF\_SUBSTRATE\_TO\_CCT\_TRIC | 24 | 0.52445096 | 1.6495107 | 0.014285714 | 0.04984741 |
| REACTOME\_CELL\_CELL\_COMMUNICATION | 104 | 0.3989851 | 1.6480373 | 0.001175088 | 0.049832825 |
| REACTOME\_ADP\_SIGNALLING\_THROUGH\_P2RY12 | 16 | 0.58344877 | 1.6470783 | 0.012084592 | 0.049475666 |
| REACTOME\_P53\_INDEPENDENT\_G1\_S\_DNA\_DAMAGE\_CHECKPOINT | 45 | 0.45737544 | 1.6463854 | 0.005235602 | 0.048965402 |

**Supplementary Table 4** - Enriched genes of the apoptotic process.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| GENE SYMBOL | GENE\_TITLE | RANK IN GENE LIST | RANK METRIC SCORE | RUNNING ES | CORE ENRICHMENT |
| PSMB6 | proteasome (prosome, macropain) subunit, beta type, 6 | 52 | 0.41652301 | 0.019545525 | Yes |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | 111 | 0.379027456 | 0.036516022 | Yes |
| VIM | vimentin | 198 | 0.34844178 | 0.049621828 | Yes |
| PLEC | null | 209 | 0.34479329 | 0.06832451 | Yes |
| PSMB10 | proteasome (prosome, macropain) subunit, beta type, 10 | 247 | 0.334308475 | 0.0843737 | Yes |
| LMNA | lamin A/C | 274 | 0.328417122 | 0.10093016 | Yes |
| FADD | Fas (TNFRSF6)-associated via death domain | 279 | 0.325757533 | 0.119016245 | Yes |
| PRKCQ | protein kinase C, theta | 543 | 0.28244096 | 0.114881255 | Yes |
| PSMB9 | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2) | 598 | 0.27664268 | 0.12637676 | Yes |
| BAK1 | BCL2-antagonist/killer 1 | 629 | 0.273930728 | 0.13955164 | Yes |
| TRADD | TNFRSF1A-associated via death domain | 671 | 0.269125074 | 0.15161532 | Yes |
| PSME1 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) | 760 | 0.26119566 | 0.15964271 | Yes |
| PSMB8 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) | 943 | 0.245740891 | 0.15962034 | Yes |
| FAS | Fas (TNF receptor superfamily, member 6) | 978 | 0.243191808 | 0.17075437 | Yes |
| CASP6 | caspase 6, apoptosis-related cysteine peptidase | 992 | 0.24199158 | 0.18342404 | Yes |
| STK24 | serine/threonine kinase 24 (STE20 homolog, yeast) | 1011 | 0.240606546 | 0.19563375 | Yes |
| SATB1 | special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) | 1029 | 0.239358261 | 0.20784935 | Yes |
| BBC3 | BCL2 binding component 3 | 1062 | 0.237126738 | 0.21879366 | Yes |
| CDH1 | cadherin 1, type 1, E-cadherin (epithelial) | 1143 | 0.231702372 | 0.22576675 | Yes |
| PSMD13 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 | 1164 | 0.230314344 | 0.23724268 | Yes |
| BAX | BCL2-associated X protein | 1277 | 0.222801566 | 0.24126996 | Yes |
| PSMC5 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 | 1297 | 0.221761256 | 0.25233936 | Yes |
| BCAP31 | B-cell receptor-associated protein 31 | 1426 | 0.213666007 | 0.2546292 | Yes |
| GSN | gelsolin (amyloidosis, Finnish type) | 1513 | 0.20895645 | 0.25986 | Yes |
| SPTAN1 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) | 1581 | 0.205189586 | 0.26632884 | Yes |
| PSMC3 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 | 1637 | 0.201421753 | 0.2735012 | Yes |
| PSMB4 | proteasome (prosome, macropain) subunit, beta type, 4 | 1742 | 0.197212592 | 0.2766946 | Yes |
| CASP10 | caspase 10, apoptosis-related cysteine peptidase | 1811 | 0.194014773 | 0.2824562 | Yes |
| TP53 | tumor protein p53 (Li-Fraumeni syndrome) | 1883 | 0.190981865 | 0.28781748 | Yes |
| DFFB | DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase) | 2049 | 0.183593184 | 0.28558442 | Yes |
| PSMB1 | proteasome (prosome, macropain) subunit, beta type, 1 | 2095 | 0.181542188 | 0.29239795 | Yes |
| PSMF1 | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) | 2132 | 0.179984078 | 0.2998107 | Yes |
| FNTA | farnesyltransferase, CAAX box, alpha | 2149 | 0.178958476 | 0.30869263 | Yes |
| PSMB3 | proteasome (prosome, macropain) subunit, beta type, 3 | 2217 | 0.175969407 | 0.31351176 | Yes |
| CTNNB1 | catenin (cadherin-associated protein), beta 1, 88kDa | 2291 | 0.172614813 | 0.3176834 | Yes |
| UBA52 | ubiquitin A-52 residue ribosomal protein fusion product 1 | 2300 | 0.172053069 | 0.32678628 | Yes |
| PSMA4 | proteasome (prosome, macropain) subunit, alpha type, 4 | 2343 | 0.169935465 | 0.3331736 | Yes |
| TJP2 | tight junction protein 2 (zona occludens 2) | 2422 | 0.166432753 | 0.33661443 | Yes |
| HIST1H1B | histone cluster 1, H1b | 2453 | 0.165594146 | 0.34367287 | Yes |
| PSMA5 | proteasome (prosome, macropain) subunit, alpha type, 5 | 2479 | 0.164413571 | 0.35104644 | Yes |
| BCL2L1 | BCL2-like 1 | 2532 | 0.162730902 | 0.35626346 | Yes |
| HMGB1 | high-mobility group box 1 | 2543 | 0.162348092 | 0.36466572 | Yes |
| DAPK3 | death-associated protein kinase 3 | 2555 | 0.16198799 | 0.3729713 | Yes |
| PSMD6 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 | 2581 | 0.160928071 | 0.38014808 | Yes |
| PPP3R1 | protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I) | 2646 | 0.158675864 | 0.3842199 | Yes |
| TNFSF10 | tumor necrosis factor (ligand) superfamily, member 10 | 2782 | 0.153721586 | 0.38259098 | Yes |
| PSMC4 | proteasome (prosome, macropain) 26S subunit, ATPase, 4 | 2794 | 0.153471187 | 0.3904157 | Yes |
| CASP9 | caspase 9, apoptosis-related cysteine peptidase | 2849 | 0.151306331 | 0.39483503 | Yes |
| RIPK1 | receptor (TNFRSF)-interacting serine-threonine kinase 1 | 2867 | 0.150717303 | 0.40204617 | Yes |
| PSMD8 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 | 2909 | 0.14917843 | 0.40733793 | Yes |
| ADD1 | adducin 1 (alpha) | 2933 | 0.148253188 | 0.4139518 | Yes |
| TJP1 | tight junction protein 1 (zona occludens 1) | 3014 | 0.144911438 | 0.41602492 | Yes |
| PSMA1 | proteasome (prosome, macropain) subunit, alpha type, 1 | 3246 | 0.137312159 | 0.4061396 | Yes |
| TRAF2 | TNF receptor-associated factor 2 | 3267 | 0.136561528 | 0.4123225 | Yes |
| FASLG | Fas ligand (TNF superfamily, member 6) | 3304 | 0.13552995 | 0.41722545 | Yes |
| CASP7 | caspase 7, apoptosis-related cysteine peptidase | 3325 | 0.134987339 | 0.42331946 | Yes |
| BAD | BCL2-antagonist of cell death | 3366 | 0.13365902 | 0.42781138 | Yes |
| GAS2 | growth arrest-specific 2 | 3462 | 0.130408719 | 0.4279204 | Yes |
| PSMA7 | proteasome (prosome, macropain) subunit, alpha type, 7 | 3493 | 0.12949127 | 0.43294057 | Yes |
| DAPK2 | death-associated protein kinase 2 | 3562 | 0.127150416 | 0.43492714 | Yes |
| PSMD9 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 | 3649 | 0.123832248 | 0.43535203 | Yes |
| UNC5B | unc-5 homolog B (C. elegans) | 3662 | 0.123366199 | 0.44140074 | Yes |
| PSMD4 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 | 3683 | 0.122686043 | 0.44680023 | Yes |
| PSMB2 | proteasome (prosome, macropain) subunit, beta type, 2 | 3731 | 0.121151149 | 0.45005155 | Yes |
| PSMD14 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 | 3816 | 0.118051887 | 0.45030278 | Yes |
| GZMB | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) | 3850 | 0.117033623 | 0.4543906 | Yes |
| PSMD7 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) | 3897 | 0.116026208 | 0.45742887 | Yes |
| HIST1H1A | histone cluster 1, H1a | 3975 | 0.11394807 | 0.4579829 | Yes |
| H1F0 | H1 histone family, member 0 | 3982 | 0.11356803 | 0.46393657 | Yes |
| PAK2 | p21 (CDKN1A)-activated kinase 2 | 4046 | 0.111794814 | 0.46543798 | Yes |
| LMNB1 | lamin B1 | 4222 | 0.106737122 | 0.45810226 | No |
| PSMB7 | proteasome (prosome, macropain) subunit, beta type, 7 | 4628 | 0.094924688 | 0.4325384 | No |
| AKT1 | v-akt murine thymoma viral oncogene homolog 1 | 4654 | 0.09422037 | 0.435949 | No |
| PSMC1 | proteasome (prosome, macropain) 26S subunit, ATPase, 1 | 4729 | 0.09196727 | 0.4354911 | No |
| MAPT | microtubule-associated protein tau | 5074 | 0.082384244 | 0.41387677 | No |
| PSMD2 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 | 5099 | 0.081270099 | 0.4166326 | No |
| HIST1H1E | histone cluster 1, H1e | 5199 | 0.077871844 | 0.4134701 | No |
| PSMC6 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 | 5257 | 0.076524444 | 0.41343832 | No |
| BID | BH3 interacting domain death agonist | 5306 | 0.075060926 | 0.41401112 | No |
| NMT1 | N-myristoyltransferase 1 | 5319 | 0.074643262 | 0.41730908 | No |
| CASP8 | caspase 8, apoptosis-related cysteine peptidase | 5367 | 0.073361464 | 0.41786227 | No |
| PSMD5 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 | 5427 | 0.071343392 | 0.4173853 | No |
| PSMB5 | proteasome (prosome, macropain) subunit, beta type, 5 | 5588 | 0.066878699 | 0.40894458 | No |
| KPNA1 | karyopherin alpha 1 (importin alpha 5) | 5671 | 0.065234862 | 0.40636662 | No |
| DIABLO | diablo homolog (Drosophila) | 5861 | 0.05927572 | 0.3952824 | No |
| DAPK1 | death-associated protein kinase 1 | 5863 | 0.059258614 | 0.39855164 | No |
| TNF | tumor necrosis factor (TNF superfamily, member 2) | 5983 | 0.055305526 | 0.39258802 | No |
| PSMA2 | proteasome (prosome, macropain) subunit, alpha type, 2 | 6097 | 0.051621255 | 0.3868745 | No |
| PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 | 6153 | 0.050288383 | 0.38551423 | No |
| CASP3 | caspase 3, apoptosis-related cysteine peptidase | 6192 | 0.049306627 | 0.38539654 | No |
| DYNLL1 | dynein, light chain, LC8-type 1 | 6399 | 0.042980991 | 0.37209433 | No |
| PSMA3 | proteasome (prosome, macropain) subunit, alpha type, 3 | 6462 | 0.041139551 | 0.3696831 | No |
| YWHAB | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide | 6524 | 0.039215144 | 0.3672395 | No |
| HMGB2 | high-mobility group box 2 | 6534 | 0.038935993 | 0.36875057 | No |
| PSMD12 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 | 6599 | 0.037256908 | 0.3659674 | No |
| CFLAR | CASP8 and FADD-like apoptosis regulator | 6663 | 0.03534105 | 0.3631524 | No |
| BIRC2 | baculoviral IAP repeat-containing 2 | 6694 | 0.034608167 | 0.3628157 | No |
| ACIN1 | apoptotic chromatin condensation inducer 1 | 6722 | 0.033761207 | 0.36266023 | No |
| PTK2 | PTK2 protein tyrosine kinase 2 | 6768 | 0.032362424 | 0.36105144 | No |
| MST4 | null | 6920 | 0.027659044 | 0.35108364 | No |
| TFDP1 | transcription factor Dp-1 | 6951 | 0.026788058 | 0.35030544 | No |
| KPNB1 | karyopherin (importin) beta 1 | 7127 | 0.02140981 | 0.33815235 | No |
| DSP | desmoplakin | 7497 | 0.010311938 | 0.31056014 | No |
| PSMD1 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 | 7503 | 0.010136612 | 0.31075066 | No |
| E2F1 | E2F transcription factor 1 | 7650 | 0.006075256 | 0.29994607 | No |
| ROCK1 | Rho-associated, coiled-coil containing protein kinase 1 | 7674 | 0.005447912 | 0.29849753 | No |
| DNM1L | dynamin 1-like | 7804 | 0.001282528 | 0.28872034 | No |
| ARHGAP10 | Rho GTPase activating protein 10 | 7853 | -6.68E-04 | 0.2850931 | No |
| HIST1H1C | histone cluster 1, H1c | 7857 | -7.17E-04 | 0.28490454 | No |
| OCLN | occludin | 8238 | -0.012228195 | 0.25658062 | No |
| DFFA | DNA fragmentation factor, 45kDa, alpha polypeptide | 8241 | -0.012269149 | 0.2571206 | No |
| BCL2L11 | BCL2-like 11 (apoptosis facilitator) | 8433 | -0.017898289 | 0.2435476 | No |
| PSMD10 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 | 8618 | -0.024384446 | 0.23087527 | No |
| DSG1 | desmoglein 1 | 8711 | -0.027806591 | 0.22542065 | No |
| PMAIP1 | phorbol-12-myristate-13-acetate-induced protein 1 | 8754 | -0.029104063 | 0.22385697 | No |
| DSG2 | desmoglein 2 | 8862 | -0.03216894 | 0.21750334 | No |
| APAF1 | apoptotic peptidase activating factor | 8867 | -0.032486897 | 0.21903206 | No |
| BCL2 | B-cell CLL/lymphoma 2 | 8872 | -0.032803878 | 0.22057867 | No |
| TNFRSF10B | tumor necrosis factor receptor superfamily, member 10b | 9323 | -0.047694054 | 0.18891236 | No |
| PSMD11 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | 9681 | -0.059567343 | 0.16501723 | No |
| RPS27A | ribosomal protein S27a | 9684 | -0.059663501 | 0.16823299 | No |
| XIAP | null | 9766 | -0.062621981 | 0.16558385 | No |
| DSG3 | desmoglein 3 (pemphigus vulgaris antigen) | 9784 | -0.063103743 | 0.16784854 | No |
| BMX | BMX non-receptor tyrosine kinase | 10037 | -0.072316527 | 0.1526903 | No |
| MAGED1 | melanoma antigen family D, 1 | 10399 | -0.087206572 | 0.13005023 | No |
| APPL1 | null | 10698 | -0.099578418 | 0.11291888 | No |
| CYCS | cytochrome c, somatic | 10773 | -0.102455653 | 0.113053136 | No |
| MAPK8 | mitogen-activated protein kinase 8 | 10981 | -0.111080423 | 0.10351933 | No |
| PSME4 | proteasome (prosome, macropain) activator subunit 4 | 11063 | -0.114919037 | 0.10382276 | No |
| HIST1H1D | histone cluster 1, H1d | 11118 | -0.117366418 | 0.10632591 | No |
| PRKCD | protein kinase C, delta | 11244 | -0.122483566 | 0.10369687 | No |
| APC | adenomatosis polyposis coli | 11309 | -0.125610173 | 0.105901904 | No |
| PKP1 | plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) | 11526 | -0.137387902 | 0.09716618 | No |
| PSMC2 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 | 12516 | -0.208658576 | 0.033433072 | No |
| DCC | deleted in colorectal carcinoma | 13211 | -0.373435706 | 0.001527133 | No |

**Supplementary Table 5** - Enriched genes of the TP53-dependent G1 DNA damage response.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| GENE SYMBOL | GENE\_TITLE | RANK IN GENE LIST | RANK METRIC SCORE | RUNNING ES | CORE ENRICHMENT |
| PSMB6 | proteasome (prosome, macropain) subunit, beta type, 6 | 52 | 0.41652301 | 0.05551553 | Yes |
| PSMB10 | proteasome (prosome, macropain) subunit, beta type, 10 | 247 | 0.334308475 | 0.08852323 | Yes |
| PSMB9 | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2) | 598 | 0.27664268 | 0.10146552 | Yes |
| CDKN1B | cyclin-dependent kinase inhibitor 1B (p27, Kip1) | 651 | 0.271203846 | 0.13623628 | Yes |
| CDKN1A | cyclin-dependent kinase inhibitor 1A (p21, Cip1) | 744 | 0.262213349 | 0.1666894 | Yes |
| PSME1 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) | 760 | 0.26119566 | 0.2028381 | Yes |
| PSMB8 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) | 943 | 0.245740891 | 0.22411275 | Yes |
| PSMD13 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 | 1164 | 0.230314344 | 0.24030271 | Yes |
| PSMC5 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 | 1297 | 0.221761256 | 0.26194695 | Yes |
| PSMC3 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 | 1637 | 0.201421753 | 0.26498562 | Yes |
| PSMB4 | proteasome (prosome, macropain) subunit, beta type, 4 | 1742 | 0.197212592 | 0.2852494 | Yes |
| TP53 | tumor protein p53 (Li-Fraumeni syndrome) | 1883 | 0.190981865 | 0.30189294 | Yes |
| PSMB1 | proteasome (prosome, macropain) subunit, beta type, 1 | 2095 | 0.181542188 | 0.31180322 | Yes |
| PSMF1 | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) | 2132 | 0.179984078 | 0.33476573 | Yes |
| PSMB3 | proteasome (prosome, macropain) subunit, beta type, 3 | 2217 | 0.175969407 | 0.3535141 | Yes |
| UBA52 | ubiquitin A-52 residue ribosomal protein fusion product 1 | 2300 | 0.172053069 | 0.3718551 | Yes |
| PSMA4 | proteasome (prosome, macropain) subunit, alpha type, 4 | 2343 | 0.169935465 | 0.392928 | Yes |
| PSMA5 | proteasome (prosome, macropain) subunit, alpha type, 5 | 2479 | 0.164413571 | 0.40615812 | Yes |
| PSMD6 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 | 2581 | 0.160928071 | 0.42146975 | Yes |
| PSMC4 | proteasome (prosome, macropain) 26S subunit, ATPase, 4 | 2794 | 0.153471187 | 0.42729694 | Yes |
| PSMD8 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 | 2909 | 0.14917843 | 0.43994513 | Yes |
| PSMA1 | proteasome (prosome, macropain) subunit, alpha type, 1 | 3246 | 0.137312159 | 0.43405953 | Yes |
| PSMA7 | proteasome (prosome, macropain) subunit, alpha type, 7 | 3493 | 0.12949127 | 0.43388444 | Yes |
| PSMD9 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 | 3649 | 0.123832248 | 0.43980432 | Yes |
| PSMD4 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 | 3683 | 0.122686043 | 0.4548149 | Yes |
| PSMB2 | proteasome (prosome, macropain) subunit, beta type, 2 | 3731 | 0.121151149 | 0.46854445 | Yes |
| PSMD14 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 | 3816 | 0.118051887 | 0.4790249 | Yes |
| MDM2 | Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) | 3829 | 0.117791235 | 0.4949297 | Yes |
| PSMD7 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) | 3897 | 0.116026208 | 0.50641054 | Yes |
| PSMB7 | proteasome (prosome, macropain) subunit, beta type, 7 | 4628 | 0.094924688 | 0.46458697 | No |
| PSMC1 | proteasome (prosome, macropain) 26S subunit, ATPase, 1 | 4729 | 0.09196727 | 0.4701301 | No |
| PSMD2 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 | 5099 | 0.081270099 | 0.45374104 | No |
| PSMC6 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 | 5257 | 0.076524444 | 0.4527559 | No |
| PSMD5 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 | 5427 | 0.071343392 | 0.45012084 | No |
| PSMB5 | proteasome (prosome, macropain) subunit, beta type, 5 | 5588 | 0.066878699 | 0.44753116 | No |
| PSMA2 | proteasome (prosome, macropain) subunit, alpha type, 2 | 6097 | 0.051621255 | 0.41636577 | No |
| PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 | 6153 | 0.050288383 | 0.41937256 | No |
| PSMA3 | proteasome (prosome, macropain) subunit, alpha type, 3 | 6462 | 0.041139551 | 0.40188196 | No |
| PSMD12 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 | 6599 | 0.037256908 | 0.39688417 | No |
| PSMD1 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 | 7503 | 0.010136612 | 0.3298339 | No |
| CDK2 | cyclin-dependent kinase 2 | 7528 | 0.009388188 | 0.32935357 | No |
| CCNE2 | cyclin E2 | 8597 | -0.023701966 | 0.25172368 | No |
| PSMD10 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 | 8618 | -0.024384446 | 0.25368753 | No |
| CCNE1 | cyclin E1 | 9675 | -0.059321754 | 0.18205273 | No |
| PSMD11 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | 9681 | -0.059567343 | 0.19017689 | No |
| RPS27A | ribosomal protein S27a | 9684 | -0.059663501 | 0.19854234 | No |
| PSME4 | proteasome (prosome, macropain) activator subunit 4 | 11063 | -0.114919037 | 0.11041884 | No |
| ATM | ataxia telangiectasia mutated (includes complementation groups A, C and D) | 12016 | -0.168801442 | 0.06230158 | No |
| PSMC2 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 | 12516 | -0.208658576 | 0.05423648 | No |