

Supplementary Table 4 : Transcripts and DAVID pathways correlating with the expression of CD8a in lupus kidney biopsies

| Positive correlation |             |                                   |                            | Negative correlation |             |                                   |                         |
|----------------------|-------------|-----------------------------------|----------------------------|----------------------|-------------|-----------------------------------|-------------------------|
| Transcripts          | Gene Symbol | Correlation coefficient with CD8a | Pathways                   | Transcripts          | Gene Symbol | Correlation coefficient with CD8a | Pathways                |
| ILMN_2353732         | CD8A        | 1                                 | Annotation Cluster 1       | ILMN_1700771         | PRUNE2      | -0.40058295                       | Annotation Cluster 1    |
| ILMN_1768482         | CD8A        | 0.97986707                        | Enrichment Score: 13.42    | ILMN_1721549         | PLA2G1B     | -0.400328462                      | Enrichment Score: 18.91 |
| ILMN_1779324         | GZMA        | 0.87333729                        | SP_PIR_KEYWORDS            | ILMN_1780872         | KCN10       | -0.400468542                      | Enrichment Score: 10.74 |
| ILMN_2389765         | HGLL1       | 0.85188292                        | UP_SEQ_FEATURE             | ILMN_1796136         | RAB37       | -0.40052267                       | Enrichment Score: 10.74 |
| ILMN_2123274         | RAM9B       | 0.84721542                        | SP_PIR_KEYWORDS            | ILMN_1800919         | TM9P        | -0.400576232                      | Enrichment Score: 10.74 |
| ILMN_1763452         | EVH2B       | 0.84462941                        | UP_SEQ_FEATURE             | ILMN_1805534         | PP4R1L      | -0.400582979                      | Enrichment Score: 10.74 |
| ILMN_2083066         | IGLL3P      | 0.838996022                       | UP_SEQ_FEATURE             | ILMN_1665437         | CYP2E1      | -0.400598437                      | Enrichment Score: 10.74 |
| ILMN_1716651         | RUN2        | 0.831882364                       | GOTERM_BP_FAT              | ILMN_1731948         | PCK1        | -0.400774781                      | Enrichment Score: 10.74 |
| ILMN_1769129         | CCL19       | 0.818324657                       | GOTERM_BP_FAT              | ILMN_1803824         | ZDHHC8      | -0.400972943                      | Enrichment Score: 10.74 |
| ILMN_1754507         | HE4         | 0.810884807                       | GOTERM_BP_FAT              | ILMN_1658110         | C18orf19    | -0.400994389                      | Enrichment Score: 10.74 |
| ILMN_2105441         | IGJ         | 0.80713872                        | Enrichment Score: 10.81    | ILMN_1778611         | GBAS        | -0.401005236                      | Enrichment Score: 10.74 |
| ILMN_1659075         | HLA-DMA     | 0.803521768                       | SP_PIR_KEYWORDS            | ILMN_1721308         | FSTL4       | -0.401051404                      | Enrichment Score: 10.74 |
| ILMN_2208413         | ARHGAP15    | 0.802049622                       | UP_SEQ_FEATURE             | ILMN_2156971         | PRY         | -0.401104574                      | Enrichment Score: 10.74 |
| ILMN_2325837         | CD3E        | 0.788912749                       | SP_PIR_KEYWORDS            | ILMN_1776566         | GRB3        | -0.401116813                      | Enrichment Score: 10.74 |
| ILMN_1811049         | POU2AF1     | 0.781591378                       | GOTERM_CC_FAT              | ILMN_1870255         | MAGEA8B     | -0.401142424                      | Enrichment Score: 10.74 |
| ILMN_3240375         | abPpTs      | 0.779415662                       | GOTERM_CC_FAT              | ILMN_1674349         | HRA15L5     | -0.401239572                      | Enrichment Score: 10.74 |
| ILMN_1691341         | IL7R        | 0.774655206                       | GOTERM_CC_FAT              | ILMN_1743594         | UBO7        | -0.401307884                      | Enrichment Score: 10.74 |
| ILMN_2061043         | CD48        | 0.77459778                        | Enrichment Score: 9.01     | ILMN_1736077         | L1AS        | -0.401321098                      | Enrichment Score: 10.74 |
| ILMN_1607081         | CNMD        | 0.752331418                       | GOTERM_BP_FAT              | ILMN_2150284         | RNRC3       | -0.401378913                      | Enrichment Score: 10.74 |
| ILMN_2254635         | ITGAX       | 0.750603553                       | GOTERM_BP_FAT              | ILMN_1650985         | TEXT4D2     | -0.401388806                      | Enrichment Score: 10.74 |
| ILMN_1886655         | TRCVB       | 0.754105378                       | GOTERM_BP_FAT              | ILMN_1877996         | AI9159018   | -0.401439898                      | Enrichment Score: 10.74 |
| ILMN_1710734         | GZMK        | 0.752051991                       | ILMN_1710734               | GZMK                 | 0.752051991 | Enrichment Score: 9.01            | Enrichment Score: 10.74 |
| ILMN_1797875         | ALEXASP     | 0.749564057                       | GOTERM_BP_FAT              | ILMN_1737025         | PCL12       | -0.401835395                      | Enrichment Score: 10.74 |
| ILMN_2208093         | CD33        | 0.746012968                       | GOTERM_BP_FAT              | ILMN_1668270         | ZDHHC8      | -0.401927268                      | Enrichment Score: 10.74 |
| ILMN_1680274         | abPpTs      | 0.742033438                       | GOTERM_BP_FAT              | ILMN_2044895         | RQCD1       | -0.401956623                      | Enrichment Score: 10.74 |
| ILMN_2261416         | CD3D        | 0.739289893                       | GOTERM_BP_FAT              | ILMN_1756558         | FBXO36      | -0.401923292                      | Enrichment Score: 10.74 |
| ILMN_1739508         | abPpTs      | 0.73870528                        | GOTERM_BP_FAT              | ILMN_2211780         | S1C2S4A     | -0.40219111                       | Enrichment Score: 10.74 |
| ILMN_2098126         | CCL5        | 0.73807032                        | GOTERM_BP_FAT              | ILMN_2350607         | C2orf7      | -0.402299971                      | Enrichment Score: 10.74 |
| ILMN_1737994         | CD3E        | 0.732320986                       | Enrichment Score: 7.57     | ILMN_1743594         | UBO7        | -0.402340474                      | Enrichment Score: 10.74 |
| ILMN_1672357         | SLA2        | 0.73093111                        | GOTERM_BP_FAT              | ILMN_1744748         | HM13116     | -0.402390957                      | Enrichment Score: 10.74 |
| ILMN_1848887         | SAMS2N1     | 0.729702225                       | GOTERM_BP_FAT              | ILMN_1672515         | PO1A1       | -0.402468501                      | Enrichment Score: 10.74 |
| ILMN_2347693         | NC0A3       | 0.729002273                       | GOTERM_BP_FAT              | ILMN_2318745         | C14orf37    | -0.402678025                      | Enrichment Score: 10.74 |
| ILMN_1790529         | LUM         | 0.727307355                       | GOTERM_BP_FAT              | ILMN_1646340         | MAOA        | -0.402779011                      | Enrichment Score: 10.74 |
| ILMN_2246328         | PTPN22      | 0.725320263                       | GOTERM_BP_FAT              | ILMN_1784283         | USH1C       | -0.402780174                      | Enrichment Score: 10.74 |
| ILMN_3232921         | CCR2        | 0.721359808                       | GOTERM_BP_FAT              | ILMN_1762972         | CHD9        | -0.402794069                      | Enrichment Score: 10.74 |
| ILMN_2157441         | HLA-DRA     | 0.712117789                       | GOTERM_BP_FAT              | ILMN_1378950         | SPCC1       | -0.40282738                       | Enrichment Score: 10.74 |
| ILMN_1682993         | NGF7        | 0.712931182                       | GOTERM_BP_FAT              | ILMN_1868659         | PRODH2      | -0.402830211                      | Enrichment Score: 10.74 |
| ILMN_1715647         | VANGL2      | 0.710673789                       | GOTERM_BP_FAT              | ILMN_1812600         | NA          | -0.402957355                      | Enrichment Score: 10.74 |
| ILMN_1697554         | SASH3       | 0.714618446                       | GOTERM_BP_FAT              | ILMN_1973931         | S1C2ZAT7    | -0.40302308                       | Enrichment Score: 10.74 |
| ILMN_1674228         | abPpTs      | 0.712883949                       | GOTERM_BP_FAT              | ILMN_1710064         | SDR16C5     | -0.403059961                      | Enrichment Score: 10.74 |
| ILMN_1670824         | CD3E7       | 0.713598975                       | GOTERM_BP_FAT              | ILMN_2309999         | RECL6       | -0.403101358                      | Enrichment Score: 10.74 |
| ILMN_1686116         | THBS1       | 0.711465157                       | Enrichment Score: 7.14     | ILMN_1685636         | CKN2        | -0.403178511                      | Enrichment Score: 10.74 |
| ILMN_1662843         | CD53        | 0.711508893                       | INTERPRO                   | ILMN_1674021         | LOC401321   | -0.403218171                      | Enrichment Score: 10.74 |
| ILMN_1713751         | ADAM19      | 0.71086577                        | SP_PIR_KEYWORDS            | ILMN_3248363         | DBA62629    | -0.40324045                       | Enrichment Score: 10.74 |
| ILMN_1796962         | PPP1R1      | 0.710367708                       | INTERPRO                   | ILMN_1780625         | HR          | -0.403287979                      | Enrichment Score: 10.74 |
| ILMN_1706539         | CD43B       | 0.710798869                       | INTERPRO                   | ILMN_1756623         | NTS1C8      | -0.403424922                      | Enrichment Score: 10.74 |
| ILMN_2093343         | PLAC8       | 0.705048083                       | SMART                      | ILMN_1674021         | CKN2        | -0.403445983                      | Enrichment Score: 10.74 |
| ILMN_1690907         | CCR6        | 0.703261207                       | INTERPRO                   | ILMN_1752386         | MYO19       | -0.403459388                      | Enrichment Score: 10.74 |
| ILMN_1747775         | STX2        | 0.702612571                       | Enrichment Score: 5.52     | ILMN_1685796         | CSD1        | -0.403379863                      | Enrichment Score: 10.74 |
| ILMN_1800908         | PRKCB       | 0.701297604                       | UP_SEQ_FEATURE             | ILMN_1813341         | PTGER       | -0.40364001                       | Enrichment Score: 10.74 |
| ILMN_2795273         | CCL1A2      | 0.699409923                       | KEGG_PATHWAY               | ILMN_1827779         | A0023464    | -0.403680903                      | Enrichment Score: 10.74 |
| ILMN_1773352         | CCL5        | 0.700226821                       | KEGG_PATHWAY               | ILMN_2097522         | CEP350      | -0.403691928                      | Enrichment Score: 10.74 |
| ILMN_1797362         | ILMK1       | 0.699831127                       | GOTERM_BP_FAT              | ILMN_3274344         | NA          | -0.403833144                      | Enrichment Score: 10.74 |
| ILMN_1750805         | ARHGAP30    | 0.699046258                       | GOTERM_BP_FAT              | ILMN_1669572         | RNF126      | -0.403855056                      | Enrichment Score: 10.74 |
| ILMN_1807042         | MARCKS      | 0.697983994                       | KEGG_PATHWAY               | ILMN_1796969         | POU4F3      | -0.403864332                      | Enrichment Score: 10.74 |
| ILMN_1801504         | RUN1        | 0.69741376                        | INTERPRO                   | ILMN_324710          | LOC157627   | -0.403901277                      | Enrichment Score: 10.74 |
| ILMN_1743646         | VASP        | 0.697313722                       | GOTERM_BP_FAT              | ILMN_2187830         | CCN1        | -0.404138273                      | Enrichment Score: 10.74 |
| ILMN_1677950         | CCL21       | 0.695091586                       | SP_PIR_KEYWORDS            | ILMN_1786498         | STAR13      | -0.40418989                       | Enrichment Score: 10.74 |
| ILMN_2114568         | GAP5        | 0.693020938                       | INTERPRO                   | ILMN_3212469         | LOC401561   | -0.404269201                      | Enrichment Score: 10.74 |
| ILMN_1740283         | PRM2        | 0.692842392                       | UP_SEQ_FEATURE             | ILMN_324570          | CEP350      | -0.404302993                      | Enrichment Score: 10.74 |
| ILMN_1652613         | GUPR2       | 0.692781989                       | KEGG_PATHWAY               | ILMN_2097522         | CEP350      | -0.404319509                      | Enrichment Score: 10.74 |
| ILMN_1672611         | CDH11       | 0.691349791                       | UP_SEQ_FEATURE             | ILMN_2150019         | SUCLA2      | -0.404391617                      | Enrichment Score: 10.74 |
| ILMN_1682312         | CYPB        | 0.690837533                       | UP_SEQ_FEATURE             | ILMN_1742495         | CDKN2A      | -0.404421822                      | Enrichment Score: 10.74 |
| ILMN_1685943         | MABP4K1     | 0.690771136                       | SMART                      | ILMN_3244220         | DEFB107B    | -0.404479775                      | Enrichment Score: 10.74 |
| ILMN_1689913         | CD37        | 0.690407108                       | Region of interest:Alpha-1 | ILMN_1759448         | C92         | -0.404526886                      | Enrichment Score: 10.74 |
| ILMN_1794386         | IL2RG       | 0.689321564                       | GOTERM_CC_FAT              | ILMN_1674021         | CKN2        | -0.404561348                      | Enrichment Score: 10.74 |
| ILMN_1815734         | FCHSD2      | 0.689049551                       | GOTERM_BP_FAT              | ILMN_1781381         | AK123658    | -0.4047257                        | Enrichment Score: 10.74 |
| ILMN_2307861         | COL6A3      | 0.68508441                        | KEGG_PATHWAY               | ILMN_3238358         | SCARNA22    | -0.404878746                      | Enrichment Score: 10.74 |
| ILMN_1695774         | NP1         | 0.684677404                       | GOTERM_BP_FAT              | ILMN_1755554         | HR23        | -0.404926479                      | Enrichment Score: 10.74 |
| ILMN_3240231         | AEN         | 0.68424625                        | KEGG_PATHWAY               | ILMN_1676955         | A0052372    | -0.404971677                      | Enrichment Score: 10.74 |
| ILMN_1678143         | ARHGDB8     | 0.683898814                       | GOTERM_MF_FAT              | ILMN_2145781         | RCMY2FP     | -0.405033419                      | Enrichment Score: 10.74 |
| ILMN_2309848         | FXYD5       | 0.683177069                       | SP_PIR_KEYWORDS            | ILMN_1778104         | ABMD7       | -0.40540081                       | Enrichment Score: 10.74 |
| ILMN_2352303         | RASSF7      | 0.682971396                       | GOTERM_MF_FAT              | ILMN_3232128         | FLJ37786    | -0.405402756                      | Enrichment Score: 10.74 |
| ILMN_1689913         | HCT         | 0.679420315                       | GOTERM_BP_FAT              | ILMN_2277798         | NTNG1       | -0.405431845                      | Enrichment Score: 10.74 |
| ILMN_1752520         | SLFN11      | 0.679115884                       | KEGG_PATHWAY               | ILMN_1718135         | PRAMEF11    | -0.405290656                      | Enrichment Score: 10.74 |
| ILMN_1746090         | STT3A       | 0.678374943                       | KEGG_PATHWAY               | ILMN_2046429         | FTFD1       | -0.405525054                      | Enrichment Score: 10.74 |
| ILMN_1761788         | MXO1        | 0.678117121                       | INTERPRO                   | ILMN_3237473         | CBWD1       | -0.405741086                      | Enrichment Score: 10.74 |
| ILMN_1810559         | RHOQ        | 0.677993303                       | PIR_SUPERFAMILY            | ILMN_1655537         | ING1        | -0.405766784                      | Enrichment Score: 10.74 |
| ILMN_1800638         | NAPOR-1     | 0.676109361                       | GOTERM_BP_FAT              | ILMN_3251375         | WBPI1P1     | -0.40590988                       | Enrichment Score: 10.74 |
| ILMN_1695311         | HLA-DMA     | 0.675203098                       | UP_SEQ_FEATURE             | ILMN_1661363         | AF064105    | -0.405970404                      | Enrichment Score: 10.74 |
| ILMN_2340217         | PTPRC       | 0.674382701                       | UP_SEQ_FEATURE             | ILMN_1724156         | OR5G61      | -0.406209309                      | Enrichment Score: 10.74 |
| ILMN_1708791         | CDYR1       | 0.673957359                       | GOTERM_MF_FAT              | ILMN_246534          | TSG1        | -0.406224724                      | Enrichment Score: 10.74 |
| ILMN_1704286         | FYB8        | 0.67357359                        | PIR_SUPERFAMILY            | ILMN_2798231         | USP9        | -0.406231093                      | Enrichment Score: 10.74 |
| ILMN_1761733         | HLA-DMB     | 0.668044677                       | GOTERM_MF_FAT              | ILMN_1673752         | C1orf91     | -0.406371095                      | Enrichment Score: 10.74 |
| ILMN_3299520         | PRKCB       | 0.667521032                       | GOTERM_CC_FAT              | ILMN_3284840         | SNORA81     | -0.406389633                      | Enrichment Score: 10.74 |
| ILMN_1812392         | TMSB10      | 0.666931026                       | GOTERM_CC_FAT              | ILMN_3090959         | MIR93       | -0.406433778                      | Enrichment Score: 10.74 |
| ILMN_1760490         | CD78        | 0.666590291                       | UP_SEQ_FEATURE             | ILMN_1802192         | CDorf99     | -0.406439389                      | Enrichment Score: 10.74 |
| ILMN_1752526         | RNF144B     | 0.666509048                       | UP_SEQ_FEATURE             | ILMN_1652379         | US22        | -0.406474482                      | Enrichment Score: 10.74 |
|                      |             |                                   | INTERPRO                   | ILMN_2184556         | S1C4A4      | -0.406451017                      | Enrichment Score: 10.74 |

| Gene                  | Enrichment Score: 5.46 | Count | P_Value | Benjamini |
|-----------------------|------------------------|-------|---------|-----------|
| ILMN_1770673 AKNA     | 0.66359803             |       | 7       | 6.90E-03  |
| ILMN_1684040 THEMIS   | 0.66284937             |       | 7       | 8.30E-03  |
| ILMN_1695040 PFM22    | 0.66065533             |       | 3       | 2.10E-02  |
| ILMN_1665494 PHS      | 0.66241387             |       | 5       | 2.20E-02  |
| ILMN_2400947 CLF2     | 0.66183182             |       | 3       | 2.30E-02  |
| ILMN_2372024 LTB      | 0.660402766            |       | 3       | 9.10E-02  |
| ILMN_2314839 HLA-DQB1 | 0.657928071            |       | 14      | 1.10E-08  |
| ILMN_1709795 RAC2     | 0.65774761             |       | 13      | 1.00E-06  |
| ILMN_2369018 EVI2A    | 0.654152271            |       | 8       | 1.90E-05  |
| ILMN_1737015 RPL39    | 0.653659552            |       | 8       | 1.90E-05  |
| ILMN_1686623 CSF1R    | 0.65328217             |       | 8       | 1.60E-05  |
| ILMN_2159912 ITGB2    | 0.652838865            |       | 6       | 7.30E-05  |
| ILMN_1796409 C10B     | 0.65231085             |       | 6       | 7.30E-05  |
| ILMN_2087620 CYBB1    | 0.64947965             |       | 6       | 7.30E-05  |
| ILMN_1786216 C037     | 0.64910553             |       | 357     | 2.60E-10  |
| ILMN_1725992 RAP8F6   | 0.648411039            |       | 332     | 6.40E-08  |
| ILMN_2413808 CD53     | 0.647552799            |       | 280     | 7.10E-08  |
| ILMN_2376205 LTB      | 0.646931041            |       | 231     | 2.50E-07  |
| ILMN_1794447 CXCL12   | 0.646513676            |       | 462     | 1.20E-06  |
| ILMN_1794677 TM6C     | 0.646193931            |       | 318     | 1.90E-05  |
| ILMN_1659800 BCL11A   | 0.645472255            |       | 360     | 1.30E-04  |
| ILMN_1734740 GRP65    | 0.64483016             |       | 361     | 1.80E-04  |
| ILMN_2392624          | 0.644738871            |       | 399     | 1.00E-01  |
| ILMN_1807825 LY86     | 0.644540555            |       | 382     | 1.70E-01  |
| ILMN_1804601          | 0.644354221            |       | 124     | 7.30E-06  |
| ILMN_1790533 PHACTR2  | 0.643785252            |       | 121     | 1.10E-05  |
| ILMN_1653652 PTPRC    | 0.643224551            |       | 201     | 1.40E-05  |
| ILMN_1731233 GZMH     | 0.642744314            |       | 124     | 7.30E-06  |
| ILMN_1675979 RBMS5    | 0.642627652            |       | 57      | 1.30E-16  |
| ILMN_1763487 CTL4A    | 0.640579082            |       | 34      | 1.30E-09  |
| ILMN_1747622 CD33     | 0.640432382            |       | 36      | 8.70E-09  |
| ILMN_1708107 CD9F1    | 0.640213111            |       | 26      | 4.00E-08  |
| ILMN_1733579 EVI2A    | 0.639921311            |       | 27      | 7.90E-08  |
| ILMN_1687301 VCAN     | 0.639772457            |       | 26      | 1.10E-07  |
| ILMN_1663080 UFG      | 0.639770995            |       | 26      | 1.10E-07  |
| ILMN_1715566 TIMP1    | 0.639527029            |       | 22      | 1.30E-07  |
| ILMN_1794743 PHS17    | 0.639257881            |       | 23      | 1.50E-07  |
| ILMN_1652944          | 0.63924195             |       | 21      | 1.60E-07  |
| ILMN_1683271 TMS84X   | 0.63919967             |       | 21      | 1.60E-07  |
| ILMN_2327346 SSBP4    | 0.639157175            |       | 21      | 1.70E-07  |
| ILMN_1689655 HLA-DRA  | 0.639045709            |       | 21      | 1.70E-07  |
| ILMN_1706116 TNFRSF17 | 0.639034651            |       | 12      | 1.20E-04  |
| ILMN_2258816 SAMD3    | 0.639008811            |       | 15      | 5.90E-06  |
| ILMN_1786789 FAMI02B  | 0.639003574            |       | 18      | 1.30E-05  |
| ILMN_1762528 HLA-E    | 0.639027626            |       | 16      | 1.80E-05  |
| ILMN_1760347 SRGN     | 0.632136812            |       | 11      | 5.00E-05  |
| ILMN_1782057 ATR9B2   | 0.632136812            |       | 14      | 7.10E-05  |
| ILMN_1652799 CPS4B    | 0.631806459            |       | 14      | 8.70E-05  |
| ILMN_1685387 PIGR     | 0.63065527             |       | 14      | 8.70E-05  |
| ILMN_1774077 GBP2     | 0.630284046            |       | 11      | 1.80E-05  |
| ILMN_1665964 GAB2     | 0.629921037            |       | 13      | 1.40E-04  |
| ILMN_1754994 C1orf162 | 0.629798346            |       | 8       | 2.90E-02  |
| ILMN_3210187 ST       | 0.629579599            |       | 13      | 9.50E-04  |
| ILMN_1802106 APOBEC3G | 0.629574544            |       | 12      | 9.80E-04  |
| ILMN_2167755 MAA0895L | 0.629544511            |       | 9       | 2.00E-03  |
| ILMN_2104356 COL14A2  | 0.629491707            |       | 9       | 1.20E-03  |
| ILMN_1655935 ADCY7    | 0.629382878            |       | 9       | 1.20E-03  |
| ILMN_3249400 abp1arts | 0.629340664            |       | 9       | 1.20E-03  |
| ILMN_1739998 DHSR5    | 0.627644804            |       | 12      | 1.60E-03  |
| ILMN_2129563 LDLRAD3  | 0.627294665            |       | 12      | 2.80E-03  |
| ILMN_1797822 SEL1L3   | 0.627098346            |       | 9       | 7.20E-03  |
| ILMN_1672636 TPSA81   | 0.626740633            |       | 7       | 9.00E-03  |
| ILMN_1772218 HLA-DPA1 | 0.626402984            |       | 4       | 1.40E-02  |
| ILMN_2042651 EVI2B    | 0.625792931            |       | 5       | 2.10E-02  |
| ILMN_2101885 TUBB     | 0.625562301            |       | 5       | 2.10E-02  |
| ILMN_1655425 UCP2     | 0.625369053            |       | 40      | 2.90E-02  |
| ILMN_1740633 PRF1     | 0.625114691            |       | 5       | 2.30E-02  |
| ILMN_1757827 VOPP1    | 0.624264732            |       | 7       | 3.00E-02  |
| ILMN_2280548 FVB      | 0.623640974            |       | 79      | 1.50E-05  |
| ILMN_2079565 RLRI1    | 0.622892049            |       | 79      | 1.60E-05  |
| ILMN_2069134 CS2      | 0.622892049            |       | 39      | 6.80E-04  |
| ILMN_1788108 TNYDC5   | 0.620581685            |       | 41      | 6.80E-04  |
| ILMN_1738675 PTPN6    | 0.620434311            |       | 31      | 6.60E-09  |
| ILMN_2155228 CRLF3    | 0.620191302            |       | 23      | 5.50E-08  |
| ILMN_1653206 PLAC8    | 0.619913757            |       | 19      | 8.10E-07  |
| ILMN_2154598 CTRIC1   | 0.619879331            |       | 16      | 8.90E-06  |
| ILMN_1723684 DARC     | 0.618907069            |       | 15      | 1.20E-05  |
| ILMN_3208888 HLA-DRA1 | 0.615130022            |       | 18      | 1.50E-05  |
| ILMN_2127473 PCEBIP3  | 0.614721347            |       | 18      | 1.50E-05  |
| ILMN_1760590 EOMES    | 0.614145066            |       | 6       | 3.00E-02  |
| ILMN_2396991 HCST     | 0.613943988            |       | 6       | 4.60E-02  |
| ILMN_2340316 TMS84X   | 0.613180692            |       | 6       | 5.90E-02  |
| ILMN_1695951 RBM1     | 0.612812626            |       | 7       | 7.10E-02  |
| ILMN_1696494 OMT6A    | 0.611892445            |       | 46      | 2.20E-05  |
| ILMN_2359800 MS46A    | 0.611627525            |       | 70      | 3.00E-05  |
| ILMN_1727871 EGR3     | 0.611157445            |       | 68      | 3.60E-05  |
| ILMN_2105944 CD74     | 0.610747287            |       | 78      | 6.70E-05  |
| ILMN_2348788 CD44     | 0.610337518            |       | 78      | 8.50E-05  |
| ILMN_1719759 TNC      | 0.608756563            |       | 40      | 6.50E-05  |
| ILMN_1784661 TMEM2    | 0.608713078            |       | 40      | 6.50E-05  |
| ILMN_2421292 CH7      | 0.60818183             |       | 19      | 1.00E-04  |
| ILMN_1771333 CD47     | 0.606789531            |       | 19      | 1.00E-04  |
| ILMN_2384591 HNF1     | 0.606597268            |       | 42      | 1.60E-04  |

| Gene                   | Enrichment Score: 5.46 | Count | P_Value | Benjamini |
|------------------------|------------------------|-------|---------|-----------|
| ILMN_1723846 METTL21B  | -0.406466647           |       | 7       | 6.90E-03  |
| ILMN_1753026 LPR11     | -0.406482258           |       | 7       | 8.30E-03  |
| ILMN_1679555 TIMM23    | -0.406443891           |       | 3       | 2.10E-02  |
| ILMN_1656638 BHM17     | -0.405668635           |       | 5       | 2.20E-02  |
| ILMN_3307659 SFTD2     | -0.406739129           |       | 3       | 2.30E-02  |
| ILMN_1655892 BEZ6655   | -0.406773994           |       | 3       | 9.10E-02  |
| ILMN_1728799 FBP1      | -0.406801455           |       | 14      | 1.10E-08  |
| ILMN_2323801 MOC51     | -0.406814456           |       | 13      | 1.00E-06  |
| ILMN_205886 TCC38      | -0.406832136           |       | 8       | 1.90E-05  |
| ILMN_1708798 EAF2      | -0.406847717           |       | 8       | 1.90E-05  |
| ILMN_1685781 C14orf142 | -0.406876586           |       | 8       | 1.60E-05  |
| ILMN_1777559 FIGNL2    | -0.406882004           |       | 6       | 7.30E-05  |
| ILMN_1710312 TMEM33    | -0.406962311           |       | 6       | 7.30E-05  |
| ILMN_2085659 OTGGL     | -0.406965149           |       | 6       | 7.30E-05  |
| ILMN_2397876 VSTM2B    | -0.406973066           |       | 357     | 2.60E-10  |
| ILMN_1730572 HNRPLD    | -0.406992159           |       | 332     | 6.40E-08  |
| ILMN_1656227 GLT1D1    | -0.407003264           |       | 280     | 7.10E-08  |
| ILMN_2138754 C1orf68   | -0.407033822           |       | 231     | 2.50E-07  |
| ILMN_1680980 LOC148709 | -0.407063338           |       | 462     | 1.20E-06  |
| ILMN_2246510 TSC1      | -0.407092919           |       | 318     | 1.90E-05  |
| ILMN_339958 PCDH11Y    | -0.407191873           |       | 360     | 1.30E-04  |
| ILMN_1692056 H3S37A1   | -0.40722485            |       | 361     | 1.80E-04  |
| ILMN_1852793 RCM7908   | -0.407245476           |       | 399     | 1.00E-01  |
| ILMN_1757747 ASPOH     | -0.407277074           |       | 382     | 1.70E-01  |
| ILMN_1656672 MYX       | -0.407628229           |       | 124     | 7.30E-06  |
| ILMN_2306795 KIF27     | -0.407660624           |       | 121     | 1.10E-05  |
| ILMN_1784569 A4SB4     | -0.407977044           |       | 201     | 1.40E-05  |
| ILMN_1681221 Chr110    | -0.407982142           |       | 124     | 7.30E-06  |
| ILMN_1788894 TTL6      | -0.407751892           |       | 57      | 1.30E-16  |
| ILMN_2160706 FBX02205  | -0.40774573            |       | 34      | 1.30E-09  |
| ILMN_1751636 ANK3      | -0.40782564            |       | 36      | 8.70E-09  |
| ILMN_219189 NANOGB8    | -0.40785024            |       | 36      | 8.70E-09  |
| ILMN_2393341 LIAS      | -0.407850136           |       | 26      | 4.00E-08  |
| ILMN_1693664 POMGNT1   | -0.40785411            |       | 26      | 4.00E-08  |
| ILMN_1681651 FOLH1     | -0.407942371           |       | 27      | 7.90E-08  |
| ILMN_1697301 ST8B3A3   | -0.408004155           |       | 26      | 1.10E-07  |
| ILMN_1779634 MRG1      | -0.408098861           |       | 22      | 1.30E-07  |
| ILMN_1696474 ZNF703    | -0.408210795           |       | 23      | 1.50E-07  |
| ILMN_2343135 SNORA37   | -0.408411016           |       | 21      | 1.60E-07  |
| ILMN_1692535 DPP4      | -0.408540441           |       | 21      | 1.70E-07  |
| ILMN_1811933 SHMT1     | -0.408653126           |       | 21      | 1.70E-07  |
| ILMN_1855860 HGS3432   | -0.408794337           |       | 12      | 1.20E-04  |
| ILMN_1712288 ANKRD46   | -0.408816791           |       | 15      | 5.90E-06  |
| ILMN_1769547 DIO1      | -0.408840991           |       | 18      | 1.30E-05  |
| ILMN_1730411 OR5K2     | -0.408990927           |       | 16      | 1.80E-05  |
| ILMN_1708660 RW0D4     | -0.40905975            |       | 11      | 5.00E-05  |
| ILMN_1754234 ZMYND31   | -0.409207019           |       | 14      | 7.10E-05  |
| ILMN_1680025 SLC9A81   | -0.409207019           |       | 14      | 7.10E-05  |
| ILMN_1779751 C7orf55   | -0.409208618           |       | 14      | 8.70E-05  |
| ILMN_1795920 OR2M4     | -0.409249036           |       | 11      | 8.40E-05  |
| ILMN_1755843 SLC26A8   | -0.40928643            |       | 13      | 1.40E-04  |
| ILMN_1659616 FAM186A   | -0.409315146           |       | 8       | 2.90E-02  |
| ILMN_1751941 TMEM106A  | -0.409348261           |       | 13      | 9.50E-04  |
| ILMN_1755108 ANKSF6    | -0.409451602           |       | 12      | 9.80E-04  |
| ILMN_2396697 GRK2      | -0.409452906           |       | 9       | 2.00E-03  |
| ILMN_352006 SMC1A      | -0.409468178           |       | 9       | 1.20E-03  |
| ILMN_2133038 UGT3A3    | -0.409489243           |       | 9       | 1.20E-03  |
| ILMN_1811719 MYO7A     | -0.409495838           |       | 9       | 1.20E-03  |
| ILMN_1677384 PTGER3    | -0.409702223           |       | 12      | 1.60E-03  |
| ILMN_1765287 DPN193    | -0.409740692           |       | 12      | 2.80E-03  |
| ILMN_1658596 C1orf55   | -0.409902091           |       | 9       | 7.20E-03  |
| ILMN_237403 ALDH5A1    | -0.410057044           |       | 7       | 9.00E-03  |
| ILMN_1688146 FTH1      | -0.410131967           |       | 4       | 1.40E-02  |
| ILMN_2340173 MTS5L1    | -0.410150972           |       | 5       | 2.10E-02  |
| ILMN_1800874 MRO       | -0.410152152           |       | 5       | 2.10E-02  |
| ILMN_2323026 HGS34     | -0.410190531           |       | 40      | 2.90E-02  |
| ILMN_2134855 PIN4      | -0.410209718           |       | 5       | 2.30E-02  |
| ILMN_1888492 AOB3069   | -0.41052115            |       | 7       | 3.00E-02  |
| ILMN_1794643 ZPAT      | -0.410663413           |       | 79      | 1.50E-05  |
| ILMN_1728074 PHAX      | -0.410674711           |       | 79      | 1.60E-05  |
| ILMN_1800147N26        | -0.410874206           |       | 49      | 6.80E-04  |
| ILMN_1684106 NR113     | -0.410911299           |       | 41      | 6.80E-04  |
| ILMN_2326225 UTS2      | -0.410914628           |       | 31      | 6.60E-09  |
| ILMN_3191948 AKO91312  | -0.410984154           |       | 23      | 5.50E-08  |
| ILMN_2347625 SNORD98   | -0.411038046           |       | 19      | 8.10E-07  |
| ILMN_2146823 ZNF12     | -0.411282878           |       | 16      | 8.90E-06  |
| ILMN_1700042 TLN2      | -0.411298878           |       | 15      | 1.20E-05  |

| Gene              | Enrichment Score: 5.46 | Count | P_Value | Benjamini |
|-------------------|------------------------|-------|---------|-----------|
| ILMN_1740052 PRG6 | -0.411341197           |       | 18      | 1.50E-05  |
| ILMN_2048688 FSCD | -0.411446              |       |         |           |

|              |           |             |                        |  |       |          |           |
|--------------|-----------|-------------|------------------------|--|-------|----------|-----------|
| ILMN_2181968 | CBL       | 0.606045894 | GOTERM_BP_FAT          | <a href="#">regulation of protein kinase cascade</a>   | 34    | 2.30E-04 | 9.60E-03  |
| ILMN_2196550 | CL3orf18  | 0.605897828 | GOTERM_BP_FAT          | <a href="#">positive regulation of protein kinase cascade</a>  | 25    | 4.90E-04 | 1.90E-02  |
| ILMN_2120965 | SRGN      | 0.605538276 | Enrichment Score: 3.67 |  | Count | P_Value  | Benjamini |
| ILMN_1712722 | SRPNG1    | 0.605088424 | GOTERM_BP_FAT          | <a href="#">phosphoinositide binding</a>   | 26    | 4.70E-06 | 1.10E-03  |
| ILMN_1712722 | SRPNG1    | 0.605088424 | GOTERM_MF_FAT          | <a href="#">pattern binding</a>  | 26    | 2.60E-05 | 3.10E-03  |
| ILMN_1712722 | SRPNG1    | 0.605088424 | GOTERM_MF_FAT          | <a href="#">polya-achadine binding</a>   | 26    | 2.60E-05 | 3.10E-03  |
| ILMN_1662932 | LCPI      | 0.604545163 | GOTERM_MF_FAT          | <a href="#">carbohydrate binding</a>   | 11    | 6.40E-04 | 3.90E-02  |
| ILMN_1716080 | CBL       | 0.604504512 | SP_PIR_KEYWORDS        | <a href="#">hemagglutinin binding</a>  | 11    | 6.20E-03 | 5.50E-02  |
| ILMN_1706032 | WAS       | 0.604401483 | GOTERM_MF_FAT          | <a href="#">hemagglutinin binding</a>  | 15    | 1.70E-03 | 2.60E-01  |
| ILMN_1723486 | HK2       | 0.604279551 | Enrichment Score: 3.51 |  | Count | P_Value  | Benjamini |
| ILMN_1727284 | CD4       | 0.604201009 | SP_PIR_KEYWORDS        | <a href="#">extracellular matrix</a>   | 34    | 1.40E-05 | 3.80E-04  |
| ILMN_1700428 | HLA-DQB   | 0.604033998 | GOTERM_CC_FAT          | <a href="#">extracellular matrix</a>   | 43    | 3.40E-04 | 9.20E-03  |
| ILMN_1777998 | ARHGAP25  | 0.603919721 | GOTERM_CC_FAT          | <a href="#">proteasome-associated extracellular matrix</a>   | 40    | 3.90E-04 | 1.40E-02  |
| ILMN_1664691 | DAPP1     | 0.602275452 | GOTERM_CC_FAT          | <a href="#">extracellular matrix part</a>  | 17    | 6.70E-03 | 1.30E-01  |
| ILMN_1724293 | NDELR2    | 0.602021259 | Enrichment Score: 3.41 |  | Count | P_Value  | Benjamini |
| ILMN_1803560 | LAT2      | 0.601951917 | SP_PIR_KEYWORDS        | <a href="#">proteoglycan</a>   | 14    | 1.80E-05 | 4.50E-04  |
| ILMN_2113333 | LGALS9B   | 0.601702957 | UP_SEQ_FEATURE         | <a href="#">glycosylation site:O-linked (N-glycosaminoglycan)</a>                                      | 6     | 1.10E-03 | 1.70E-01  |
| ILMN_1809433 | YBP1      | 0.599335804 | SP_PIR_KEYWORDS        | <a href="#">rhodopsin sulfate proteoglycan</a>   | 6     | 2.90E-03 | 3.18E-02  |
| ILMN_1713058 | PSTPIP2   | 0.599335807 | Enrichment Score: 3.31 |  | Count | P_Value  | Benjamini |
| ILMN_1687888 | NTX1A1    | 0.598555999 | GOTERM_BP_FAT          | <a href="#">actin cytoskeleton organization</a>  | 37    | 2.00E-06 | 1.70E-04  |
| ILMN_1786720 | PROM1     | 0.597892998 | GOTERM_BP_FAT          | <a href="#">actin filament-based process</a>   | 37    | 9.00E-06 | 6.40E-04  |
| ILMN_1798379 | NFM       | 0.596966135 | SP_PIR_KEYWORDS        | <a href="#">actin binding</a>  | 32    | 1.30E-04 | 2.30E-03  |
| ILMN_1685403 | MMP7      | 0.596824843 | GOTERM_MF_FAT          | <a href="#">actin binding</a>  | 39    | 4.80E-04 | 3.70E-02  |
| ILMN_1701426 | ARL       | 0.596824843 | GOTERM_MF_FAT          | <a href="#">cytoskeleton organization</a>  | 44    | 1.10E-04 | 2.10E-01  |
| ILMN_1742427 | POLR1D    | 0.596482413 | GOTERM_MF_FAT          | <a href="#">cytoskeletal protein binding</a>   | 47    | 1.70E-02 | 3.80E-01  |
| ILMN_1756937 | STX4A     | 0.596483333 | GOTERM_CC_FAT          | <a href="#">actin cytoskeleton</a>   | 28    | 3.30E-02 | 3.90E-01  |
| ILMN_1712761 | SYNC      | 0.596409017 | Enrichment Score: 3.23 |  | Count | P_Value  | Benjamini |
| ILMN_2115005 | FGD2      | 0.595992623 | KEGG_PATHWAY           | <a href="#">Chemokine signaling pathway</a>  | 39    | 7.90E-08 | 1.50E-06  |
| ILMN_1673942 | GATAD2A   | 0.595497326 | GOTERM_BP_FAT          | <a href="#">chemokine activity</a>   | 14    | 5.70E-06 | 1.10E-03  |
| ILMN_1765446 | EMP3      | 0.595412119 | GOTERM_MF_FAT          | <a href="#">chemokine receptor binding</a>   | 14    | 1.20E-05 | 1.90E-03  |
| ILMN_1734653 | FND1C1    | 0.594373707 | SP_PIR_KEYWORDS        | <a href="#">chemotaxis</a>   | 16    | 2.70E-05 | 6.20E-04  |
| ILMN_2315979 | LBH       | 0.594161531 | GOTERM_BP_FAT          | <a href="#">chemotaxis</a>   | 27    | 3.60E-05 | 2.10E-03  |
| ILMN_1712025 | CHRD1D    | 0.593714732 | GOTERM_BP_FAT          | <a href="#">chemotaxis</a>   | 27    | 3.60E-05 | 2.10E-03  |
| ILMN_2193233 | AZD1      | 0.593714732 | INTERPRO               | <a href="#">Small chemokine, Interleukin-8-like</a>  | 12    | 1.10E-04 | 1.50E-02  |
| ILMN_1809400 | FAM98B    | 0.589782946 | SMART                  | <a href="#">SCY</a>  | 12    | 2.10E-04 | 1.50E-02  |
| ILMN_1787345 | FKBP11    | 0.591450109 | KEGG_PATHWAY           | <a href="#">Cytokine-cytokine receptor interaction</a>   | 39    | 2.90E-04 | 2.20E-03  |
| ILMN_2379644 | CD74      | 0.590905784 | INTERPRO               | <a href="#">Small chemokine, C-X-C, conserved site</a>   | 7     | 5.00E-04 | 6.40E-02  |
| ILMN_2115434 | RAB32     | 0.589980504 | PIR_SUPERFAMILY        | <a href="#">PIRSF002522:CXC chemokine</a>  | 6     | 2.60E-03 | 3.70E-01  |
| ILMN_1711416 | TRAM1     | 0.589781649 | SP_PIR_KEYWORDS        | <a href="#">cytokine</a>   | 8     | 8.00E-03 | 3.90E-02  |
| ILMN_1668417 | WIPF1     | 0.58952472  | Small chemokine, C-X-C |  | 6     | 2.00E-03 | 3.90E-01  |
| ILMN_2117987 | TRDP1     | 0.589297139 | BBID                   | <a href="#">109_Cytokine_families</a>  | 11    | 8.50E-03 | 5.10E-01  |
| ILMN_1651433 | DCK       | 0.588675286 | GOTERM_MF_FAT          | <a href="#">cytokine activity</a>  | 23    | 1.00E-02 | 2.90E-01  |
| ILMN_2109614 | NFISB     | 0.587491356 | INTERPRO               | <a href="#">Small chemokine, C-X-C/interleukin-8</a>   | 5     | 1.10E-02 | 4.60E-01  |
| ILMN_2115434 | RAB32     | 0.589980504 | GOTERM_BP_FAT          | <a href="#">chemokine behavior</a>   | 6     | 2.60E-03 | 3.70E-01  |
| ILMN_1711416 | TRAM1     | 0.589781649 | INTERPRO               | <a href="#">Small chemokine, C-X-C, conserved site</a>   | 6     | 2.00E-03 | 3.90E-01  |
| ILMN_1710937 | HF16      | 0.586048375 | PIR_SUPERFAMILY        | <a href="#">PIRSF001958:small inducible chemokine, C/CX types</a>                                      | 6     | 2.50E-02 | 8.70E-01  |
| ILMN_1780368 | GP118     | 0.586023222 | GOTERM_BP_FAT          | <a href="#">behavior</a>   | 38    | 2.20E-01 | 8.70E-01  |
| ILMN_1767448 | UHPF      | 0.585177803 | Enrichment Score: 3.14 |  | Count | P_Value  | Benjamini |
| ILMN_1814518 | TCF4      | 0.584885888 | SP_PIR_KEYWORDS        | <a href="#">sh3 binding</a>  | 18    | 1.70E-05 | 1.40E-02  |
| ILMN_1781515 | ITM       | 0.584813545 | GOTERM_MF_FAT          | <a href="#">SH3 domain binding</a>   | 18    | 1.70E-04 | 1.60E-02  |
| ILMN_1727402 | NCL1S     | 0.584687661 | GOTERM_MF_FAT          | <a href="#">protein domain specific binding</a>  | 38    | 1.20E-03 | 6.50E-02  |
| ILMN_2313926 | CDCA25E2  | 0.584512047 | UP_SEQ_FEATURE         | <a href="#">short sequence motif:SH3-binding</a>   | 9     | 1.90E-02 | 7.50E-01  |
| ILMN_2388701 | ST3GALS5  | 0.5844603   | Enrichment Score: 3.13 |  | Count | P_Value  | Benjamini |
| ILMN_2176063 | FCGR1C    | 0.58418888  | GOTERM_BP_FAT          | <a href="#">T cell selection</a>   | 8     | 1.80E-04 | 7.60E-03  |
| ILMN_2309520 | ITM       | 0.584183797 | BIOCARTA               | <a href="#">T Helper Cell Surface Molecules</a>  | 8     | 1.80E-04 | 1.00E-02  |
| ILMN_1724422 | SELL      | 0.583985345 | BIOCARTA               | <a href="#">Severe combined immunodeficiency, T cell-negative, B cell/natural killer cell positive</a> | 3     | 1.30E-02 | 6.90E-01  |
| ILMN_2058251 | WIM       | 0.583855607 | OMIM_DISEASE           |  | 3     | 1.30E-02 | 6.90E-01  |
| ILMN_2381237 | UMS1      | 0.583584967 | Enrichment Score: 3.12 |  | Count | P_Value  | Benjamini |
| ILMN_2179827 | RNF1      | 0.583085857 | GOTERM_BP_FAT          | <a href="#">cell motion</a>  | 6     | 5.20E-06 | 5.30E-04  |
| ILMN_1797988 | ILKAP1    | 0.583424679 | GOTERM_BP_FAT          | <a href="#">cell migration</a>   | 33    | 2.70E-03 | 7.70E-02  |
| ILMN_2400759 | CPVL      | 0.583355378 | GOTERM_BP_FAT          | <a href="#">cell motility</a>  | 35    | 4.20E-03 | 1.00E-01  |
| ILMN_2342328 | TPSAB1    | 0.582984476 | GOTERM_BP_FAT          | <a href="#">localization of cell</a>   | 35    | 4.20E-03 | 1.00E-01  |
| ILMN_1710482 | APF2      | 0.582731186 | SP_PIR_KEYWORDS        | <a href="#">localization of cell</a>   | 35    | 4.20E-03 | 1.00E-01  |
| ILMN_1778977 | TYROBP    | 0.582242767 | Enrichment Score: 2.97 |  | Count | P_Value  | Benjamini |
| ILMN_1785902 | CLCOP     | 0.581806467 | BIOCARTA               | <a href="#">Lck and Fyn tyrosine kinases in initiation of TCR Activation</a>                           | 9     | 5.40E-06 | 1.30E-03  |
| ILMN_1785902 | CLCOP     | 0.581806467 | BIOCARTA               | <a href="#">CTL mediated immune response against target cells</a>                                      | 10    | 1.40E-05 | 1.60E-03  |
| ILMN_1785902 | CLCOP     | 0.581806467 | BIOCARTA               | <a href="#">Activation of Cdk by cAMP-dependent Protein Kinase Inhibitors</a>                          | 10    | 1.40E-05 | 1.60E-03  |
| ILMN_1800091 | RARRES1   | 0.581578735 | BIOCARTA               | <a href="#">Signaling through the T Cell Receptor</a>  | 10    | 5.40E-05 | 4.20E-03  |
| ILMN_1705663 | NHL3D     | 0.581311766 | INTERPRO               | <a href="#">Phosphotyrosine immunoreceptor signaling (ITAM)</a>  | 6     | 5.50E-05 | 9.90E-03  |
| ILMN_1664699 | GLIS3     | 0.580988482 | GOTERM_CC_FAT          | <a href="#">T cell receptor complex</a>  | 7     | 7.00E-05 | 3.70E-03  |
| ILMN_2415162 | sept-01   | 0.580545891 | UP_SEQ_FEATURE         | <a href="#">domain:ITAM</a>  | 6     | 9.30E-05 | 2.50E-02  |
| ILMN_1781626 | C1S       | 0.580525801 | SMART                  | <a href="#">ITAM</a>   | 6     | 1.30E-04 | 1.90E-02  |
| ILMN_2143314 | SP1B      | 0.579798736 | BIOCARTA               | <a href="#">T Cytotoxic Cell Surface Molecules</a>   | 8     | 1.80E-04 | 1.00E-02  |
| ILMN_1652198 | CCM2      | 0.579493755 | BIOCARTA               | <a href="#">T Helper Cell Surface Molecules</a>  | 8     | 1.80E-04 | 1.00E-02  |
| ILMN_1717197 | CD3G      | 0.579237813 | BIOCARTA               | <a href="#">HIV Induced T Cell Apoptosis</a>   | 7     | 2.00E-04 | 9.10E-03  |
| ILMN_1872759 | BX099468  | 0.579211026 | GOTERM_CC_FAT          | <a href="#">alpha-beta-T cell receptor complex</a>   | 4     | 1.30E-03 | 3.30E-02  |
| ILMN_1711833 | STK4      | 0.579190057 | BIOCARTA               | <a href="#">IL-12 Signaling Pathway</a>  | 7     | 6.20E-03 | 2.10E-01  |
| ILMN_1793672 | SXS       | 0.578784885 | BIOCARTA               | <a href="#">T Cell Receptor and CD3 Complex</a>  | 4     | 6.70E-03 | 2.00E-01  |
| ILMN_1808634 | DRAM2     | 0.577489944 | PIR_SUPERFAMILY        | <a href="#">PIRSF001993:T cell surface glycoprotein CD3 delta chain</a>                                | 3     | 1.60E-02 | 7.60E-01  |
| ILMN_2060606 | HLA-DRB6  | 0.576693669 | BIOCARTA               | <a href="#">The Co-Stimulatory Signal During T-cell Activation</a>                                     | 7     | 2.20E-02 | 4.00E-01  |
| ILMN_1745356 | OC19L     | 0.5766773   | BIOCARTA               | <a href="#">Role of Top-1 in T-cell Activation</a>   | 5     | 3.00E-02 | 6.90E-01  |
| ILMN_1699205 | CD2       | 0.575943185 | BIOCARTA               | <a href="#">IL-12 and Stat4 Dependent Signaling Pathway in Th1 Development</a>                         | 6     | 8.90E-02 | 6.80E-01  |
| ILMN_2192072 | MMP7      | 0.575640117 | BIOCARTA               | <a href="#">T Cell Receptor Signaling Pathway</a>  | 8     | 1.10E-01 | 7.40E-01  |
| ILMN_1716563 | PRKCB     | 0.575596169 | BIOCARTA               | <a href="#">NO2-dependent IL-12 Pathway in NK cells</a>  | 4     | 2.10E-01 | 8.80E-01  |
| ILMN_1744505 | CD2A42    | 0.575231962 | Enrichment Score: 2.81 |  | Count | P_Value  | Benjamini |
| ILMN_1800058 | NKX2-5    | 0.575439851 | INTERPRO               | <a href="#">Plectin trimer homology</a>  | 34    | 5.60E-04 | 6.70E-02  |
| ILMN_1656129 | SLC3A10   | 0.575194973 | UP_SEQ_FEATURE         | <a href="#">domain:PH</a>  | 29    | 7.90E-04 | 1.40E-01  |
| ILMN_2200636 | NAA127    | 0.575073029 | INTERPRO               | <a href="#">Plectin trimer homology-type</a>   | 35    | 1.40E-03 | 1.30E-01  |
| ILMN_1805466 | SOX9      | 0.57439515  | SMART                  | <a href="#">Ph</a>   | 34    | 8.90E-03 | 3.50E-01  |
| ILMN_1790818 | 2NF238    | 0.57439515  | Enrichment Score: 3.78 |  | Count | P_Value  | Benjamini |
| ILMN_2312626 | HPGF      | 0.573737582 | GOTERM_MF_FAT          | <a href="#">immunoglobulin binding</a>   | 7     | 2.50E-04 | 2.10E-02  |
| ILMN_1729629 | LOC285074 | 0.572955663 | SP_PIR_KEYWORDS        | <a href="#">immunoglobulin receptor</a>  | 6     | 1.00E-04 | 4.50E-03  |
| ILMN_1800317 | WNT5A     | 0.572942095 | GOTERM_MF_FAT          | <a href="#">IgG binding</a>  | 5     | 1.10E-03 | 6.20E-02  |
| ILMN_2360710 | TPM1      | 0.572145797 | SP_PIR_KEYWORDS        | <a href="#">IgG binding protein</a>  | 4     | 6.80E-03 | 5.80E-02  |
| ILMN_1735538 | RPS10     | 0.572130739 | GOTERM_MF_FAT          | <a href="#">immunoglobulin receptor activity</a>   | 3     | 2.40E-02 | 4.10E-01  |
| ILMN_1672503 | DPVSL2    | 0.572204374 | Enrichment Score: 2.76 |  | Count | P_Value  | Benjamini |

|              |           |              |                        |  |       |          |           |
|--------------|-----------|--------------|------------------------|--|-------|----------|-----------|
| ILMN_1805271 | ABCA1P    | -0.412035845 | GOTERM_CC_FAT          | <a href="#">membrane-enclosed lumen</a>                        | 118   | 3.70E-01 | 9.70E-01  |
| ILMN_1764500 | C3orf10   | -0.412035845 | GOTERM_CC_FAT          | <a href="#">organelle lumen</a>                                | 111   | 5.80E-01 | 9.90E-01  |
| ILMN_1764861 | SOK1      | -0.412289975 | GOTERM_CC_FAT          | <a href="#">intracellular organelle lumen</a>                  | 107   | 6.50E-01 | 9.90E-01  |
| ILMN_1766551 | LOC253724 | -0.412488243 | GOTERM_CC_FAT          | <a href="#">nucleoplasm</a>                                    | 39    | 9.90E-01 | 1.00E+00  |
| ILMN_1742233 | LETM2     | -0.412532637 | GOTERM_CC_FAT          | <a href="#">nucleoplasm part</a>                               | 21    | 1.00E+00 | 1.00E+00  |
| ILMN_1785107 | KXT2      | -0.412556558 | GOTERM_CC_FAT          | <a href="#">nuclear lumen</a>                                  | 61    | 1.00E+00 | 1.00E+00  |
| ILMN_1715113 | HARS2     | -0.412694722 | Enrichment Score: 2.21 |  | Count | P_Value  | Benjamini |
| ILMN_1696935 | RBM39     | -0.412710201 | GOTERM_MF_FAT          | <a href="#">iron ion binding</a>                               | 39    | 1.30E-05 | 2.40E-03  |
| ILMN_1712985 | C16orf80  | -0.412892945 | SP_PIR_KEYWORDS        | <a href="#">iron ion binding</a>                               | 39    | 9.90E-01 | 3.20E-03  |
| ILMN_1690327 | CLCN5     | -0.412971979 | KEGG_PATHWAY           | <a href="#">linoleic acid metabolism</a>                       | 9     | 5.00E-04 | 5.30E-03  |
| ILMN_1724040 | ANKRD57   | -0.412970746 | SP_PIR_KEYWORDS        | <a href="#">metalloprotein</a>                                 | 17    | 1.40E-03 | 4.10E-02  |
| ILMN_3258084 | SILCA19   | -0.413041194 | COG_ONTOLOGY           | <a href="#">carbohydrate</a>                                   | 12    | 2.50E-03 | 2.80E-02  |
| ILMN_1681601 | SULCLN1   | -0.413116118 | UP_SEQ_FEATURE         | <a href="#">metal ion-binding site(iron heme axial ligand)</a> | 14    | 3.10E-01 | 5.60E-01  |
| ILMN_1757882 | PPP1R16A  | -0.413160256 | GOTERM_MF_FAT          | <a href="#">tetrapyrrole binding</a>                           | 17    | 3.90E-03 | 2.00E-01  |
| ILMN_2136971 | FABP3     | -0.413178929 | INTERPRO               | <a href="#">Cytochrome P450, C-terminal region</a>             | 10    | 4.30E-03 | 6.20E-01  |
| ILMN_2228180 | MSRA      | -0.413187877 | GOTERM_MF_FAT          | <a href="#">heme binding</a>                                   |       |          |           |



|              |               |             |                        |  |       |          |           |
|--------------|---------------|-------------|------------------------|--|-------|----------|-----------|
| ILMN_2364521 | AXL           | 0.542158719 | GOTERM_BP_FAT          | collagen biosynthetic process  | 3     | 4.10E-02 | 4.70E-01  |
| ILMN_1463230 | PITPNM1       | 0.542031299 | GOTERM_BP_FAT          | skin development   | 6     | 4.60E-02 | 4.90E-01  |
| ILMN_1714984 | MYH           | 0.541943618 | PIR_SUPERFAMILY        | PIR5F02255collagen alpha 1(I) chain  | 3     | 4.80E-02 | 9.50E-01  |
| ILMN_2395711 | AHRB2         | 0.541906357 | GO                     | COL1   | 4     | 4.80E-02 | 6.20E-01  |
| ILMN_1737683 | FGG           | 0.541293955 | UP_SEQ_FEATURE         | propeptide-N-terminal propeptide   | 3     | 4.90E-02 | 9.20E-01  |
| ILMN_1733937 | MMD           | 0.541175792 | GOTERM_BP_FAT          | multicellular organismal macromolecule metabolic process                                     | 6     | 5.90E-02 | 5.60E-01  |
| ILMN_2060413 | CD24          | 0.540993355 | UP_SEQ_FEATURE         | region of interest:Nonhealical region  | 3     | 8.40E-02 | 9.80E-01  |
| ILMN_2088124 | TMEM154       | 0.54081551  | UP_SEQ_FEATURE         | domain:VWF A 2   | 4     | 8.40E-02 | 9.80E-01  |
| ILMN_3309199 | RTN19         | 0.540551229 | GOTERM_BP_FAT          | multicellular organismal metabolic process   | 7     | 2.00E-01 | 1.15E+00  |
| ILMN_3192001 | CCLL15        | 0.540354123 | UP_SEQ_FEATURE         | domain:VWF A 1   | 3     | 2.60E-01 | 1.00E+00  |
| ILMN_1766275 | PKCDD         | 0.540185995 | Enrichment Score: 2.24 |  | Count | P_Value  | Benjamini |
| ILMN_2413622 | RFK4          | 0.539981118 | KEGG_PATHWAY           | fx receptor signaling pathway  | 17    | 4.50E-04 | 3.20E-03  |
| ILMN_1468898 | ZEB2          | 0.539496188 | KEGG_PATHWAY           | h cell receptor signaling pathway  | 15    | 2.60E-03 | 1.50E-02  |
| ILMN_1710434 | TBC1D10C      | 0.539283381 | KEGG_PATHWAY           | VEGF signaling pathway   | 10    | 1.60E-01 | 4.70E-01  |
| ILMN_1798006 | ANKRD35       | 0.539241711 | Enrichment Score: 2.19 |  | Count | P_Value  | Benjamini |
| ILMN_1717101 | MINK1         | 0.53925605  | UP_SEQ_FEATURE         | domain:Fibrinogen C-terminal   | 8     | 3.00E-03 | 3.10E-01  |
| ILMN_1661839 | ORS2A5        | 0.539195389 | INTERPRO               | Fibrinogen_alpha/beta/gamma chain_C-terminal globular  | 8     | 3.90E-03 | 2.80E-01  |
| ILMN_2125747 | CORO1A        | 0.538811741 | SMART                  | FBI  | 8     | 1.00E-02 | 3.40E-01  |
| ILMN_1693338 | CYP1B1        | 0.538794159 | INTERPRO               | Fibrinogen_alpha/beta/gamma chain_C-terminal globular_subdomain 1                            | 6     | 1.50E-02 | 4.90E-01  |
| ILMN_1769911 | SLC38A1       | 0.538354576 | Enrichment Score: 2.03 |  | Count | P_Value  | Benjamini |
| ILMN_1775542 | FAIM3         | 0.538105777 | GOTERM_BP_FAT          | regulation of inflammatory response  | 14    | 1.90E-03 | 6.10E-02  |
| ILMN_1742230 | SLZ1A         | 0.537949122 | GOTERM_BP_FAT          | positive regulation of defense response  | 13    | 4.40E-03 | 1.00E-01  |
| ILMN_2365465 | XBP1          | 0.537815715 | GOTERM_BP_FAT          | regulation of response to external stimulus  | 21    | 6.60E-03 | 1.50E-01  |
| ILMN_1763901 | C14orf43      | 0.537813281 | GOTERM_BP_FAT          | positive regulation of acute inflammatory response   | 5     | 7.10E-03 | 1.60E-01  |
| ILMN_1880403 | SSR4          | 0.537692812 | GOTERM_BP_FAT          | positive regulation of response to external stimulus   | 11    | 1.20E-02 | 2.20E-01  |
| ILMN_1803392 | P2RX5-TAX1BP3 | 0.53767956  | GOTERM_BP_FAT          | regulation of acute inflammatory response  | 6     | 1.20E-02 | 2.30E-01  |
| ILMN_2311078 | NRP1          | 0.537575315 | GOTERM_BP_FAT          | GOTERM_BP_FAT  | 7     | 1.50E-02 | 2.60E-01  |
| ILMN_2282641 | TBXAS1        | 0.53749085  | SP_PIR_KEYWORDS        | inflammation   | 5     | 6.50E-02 | 3.10E-01  |
| ILMN_1713749 | CORO1A        | 0.537065883 | Enrichment Score: 1.96 |  | Count | P_Value  | Benjamini |
| ILMN_1737964 | HAT11         | 0.53702627  | SP_PIR_KEYWORDS        | tyrosine-specific protein kinase   | 10    | 2.40E-03 | 2.70E-02  |
| ILMN_1681798 | sept-06       | 0.536288615 | SP_PIR_KEYWORDS        | transforming protein   | 8     | 4.10E-03 | 3.90E-02  |
| ILMN_1657353 | ACTG3         | 0.53581758  | SP_PIR_KEYWORDS        | transglutinin  | 8     | 9.00E-03 | 7.50E-02  |
| ILMN_1669447 | PHN1          | 0.535131608 | GOTERM_MF_FAT          | non-membrane spanning protein tyrosine kinase activity                                       | 8     | 1.70E-02 | 3.80E-01  |
| ILMN_1770247 | H0XA10-H0XA9  | 0.534469473 | SP_PIR_KEYWORDS        | cholesterol bond   | 7     | 2.20E-02 | 1.40E-01  |
| ILMN_1765557 | OLFML2B       | 0.534281024 | PIR_SUPERFAMILY        | PIR5F00601tyrosine-protein kinase, proto-oncogene SRC type                                   | 4     | 5.50E-02 | 9.40E-01  |
| ILMN_1898605 | BC1L1-9059    | 0.533821264 | Enrichment Score: 1.94 |  | Count | P_Value  | Benjamini |
| ILMN_2325379 | HAI5L8        | 0.533708741 | GOTERM_CC_FAT          | cell cortex  | 21    | 2.60E-03 | 6.00E-02  |
| ILMN_1718936 | LS1           | 0.53368528  | GOTERM_CC_FAT          | cell cortex part   | 13    | 1.20E-02 | 1.90E-01  |
| ILMN_1701441 | LPAR1         | 0.533584285 | GOTERM_CC_FAT          | cellular cytoskeleton  | 8     | 5.00E-02 | 5.00E-01  |
| ILMN_1696704 | TLE4          | 0.533575509 | Enrichment Score: 1.93 |  | Count | P_Value  | Benjamini |
| ILMN_1658327 | RAZ1A         | 0.533441732 | GOTERM_BP_FAT          | negative regulation of macromolecule metabolic process                                       | 73    | 1.40E-03 | 4.70E-02  |
| ILMN_1761463 | FHDH2         | 0.533391753 | SP_PIR_KEYWORDS        | resistor   | 43    | 2.70E-03 | 3.00E-02  |
| ILMN_1673708 | HDCA9         | 0.533243883 | GOTERM_BP_FAT          | negative regulation of RNA metabolic process   | 40    | 3.70E-03 | 9.70E-02  |
| ILMN_2059505 | ARPP19        | 0.533095609 | GOTERM_BP_FAT          | negative regulation of nitrogen compound metabolic process                                   | 52    | 6.50E-03 | 1.50E-01  |
| ILMN_1803825 | CCX12         | 0.532957472 | GOTERM_BP_FAT          | negative regulation of transcription, RNA-dependent  | 38    | 8.10E-03 | 1.70E-01  |
| ILMN_2326825 | RAPGEF5       | 0.532957273 | GOTERM_BP_FAT          | negative regulation of transcription   | 46    | 1.00E-02 | 2.10E-01  |
| ILMN_1691476 | MYXK          | 0.532906275 | GOTERM_BP_FAT          | negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 50    | 1.20E-02 | 2.30E-01  |
| ILMN_1732705 | HCF1          | 0.532655329 | GOTERM_BP_FAT          | negative regulation of transcription from RNA polymerase II                                  | 29    | 1.70E-02 | 2.80E-01  |
| ILMN_1740609 | CCLL15        | 0.532083263 | GOTERM_MF_FAT          | resistor   | 32    | 1.80E-02 | 3.90E-01  |
| ILMN_2388605 | ACTR2         | 0.531871163 | GOTERM_BP_FAT          | transcription repressor activity   | 48    | 2.10E-02 | 3.20E-01  |
| ILMN_2112580 | FCGR3A        | 0.531607296 | GOTERM_BP_FAT          | negative regulation of gene expression   | 51    | 2.40E-02 | 3.50E-01  |
| ILMN_2301624 | MACF1         | 0.531190638 | GOTERM_BP_FAT          | negative regulation of macromolecule biosynthetic process                                    | 53    | 2.50E-02 | 3.60E-01  |
| ILMN_2361427 | PM2P3         | 0.530483908 | GOTERM_BP_FAT          | negative regulation of biosynthetic process  | 53    | 2.50E-02 | 3.60E-01  |
| ILMN_1812973 | RBP1B         | 0.529983863 | GOTERM_BP_FAT          | negative regulation of cellular biosynthetic process   | 52    | 2.50E-02 | 3.60E-01  |
| ILMN_2375825 | CD37          | 0.529971865 | GOTERM_BP_FAT          | regulation of transcription from RNA polymerase II promoter                                  | 60    | 1.00E-01 | 7.10E-01  |
| ILMN_2201678 | FSTL1         | 0.529042966 | Enrichment Score: 1.88 |  | Count | P_Value  | Benjamini |
| ILMN_2094360 | NRP2          | 0.529095672 | GOTERM_CC_FAT          | histone methyltransferase complex  | 6     | 1.30E-02 | 2.00E-01  |
| ILMN_2355953 | USP8A         | 0.528695646 | GOTERM_CC_FAT          | methylytransferase complex   | 6     | 1.30E-02 | 2.00E-01  |
| ILMN_1745788 | GNFSF1B       | 0.528595986 | GOTERM_CC_FAT          | MuL1C complex  | 4     | 1.40E-02 | 2.10E-01  |
| ILMN_2104898 | G2M8          | 0.528278857 | Enrichment Score: 1.85 |  | Count | P_Value  | Benjamini |
| ILMN_1797813 | SUZ12         | 0.528141197 | INTERPRO               | Guanylate-binding protein_C-terminal   | 4     | 7.90E-03 | 4.10E-01  |
| ILMN_1739103 | MPZ1          | 0.5281348   | PIR_SUPERFAMILY        | PIR5F00552guanine nucleotide-binding protein 1   | 4     | 1.10E-02 | 7.10E-01  |
| ILMN_1728934 | PRC1          | 0.527854316 | INTERPRO               | Guanylate-binding protein_N-terminal   | 4     | 3.10E-02 | 6.20E-01  |
| ILMN_2282034 | HKS1T1        | 0.527795219 | Enrichment Score: 1.81 |  | Count | P_Value  | Benjamini |
| ILMN_1784774 | P2RY10        | 0.527700179 | GOTERM_BP_FAT          | response to molecule of bacterial origin   | 15    | 2.20E-03 | 4.60E-02  |
| ILMN_1717334 | VAV1          | 0.527665251 | GOTERM_BP_FAT          | response to lipopolysaccharide   | 11    | 3.80E-02 | 4.50E-01  |
| ILMN_3248562 | SNORD49A      | 0.52766457  | GOTERM_BP_FAT          | response to bacterium  | 21    | 4.50E-02 | 4.80E-01  |
| ILMN_1779257 | CD40          | 0.527673796 | Enrichment Score: 1.81 |  | Count | P_Value  | Benjamini |
| ILMN_2401938 | STAT3         | 0.527678962 | GOTERM_MF_FAT          | protein binding, binding   | 16    | 1.20E-03 | 6.30E-02  |
| ILMN_1747386 | GLIS3         | 0.526051034 | GOTERM_MF_FAT          | SH2/SH3 adaptor activity   | 8     | 4.10E-02 | 5.20E-01  |
| ILMN_1676528 | BTN3A2        | 0.525696218 | Enrichment Score: 1.75 |  | Count | P_Value  | Benjamini |
| ILMN_1813314 | HST1H2BK      | 0.525667946 | GOTERM_BP_FAT          | positive regulation of T cell differentiation  | 9     | 1.20E-03 | 4.10E-02  |
| ILMN_1633282 | CHRF          | 0.525573339 | SP_PIR_KEYWORDS        | acid   | 5     | 1.80E-02 | 1.30E-01  |
| ILMN_1861376 | FAHD8095      | 0.525551332 | GOTERM_BP_FAT          | positive regulation of T cell differentiation in the thymus                                  | 3     | 2.60E-02 | 3.70E-01  |
| ILMN_1746604 | IGST          | 0.525318987 | GOTERM_BP_FAT          | regulation of T cell differentiation in the thymus   | 3     | 1.70E-01 | 8.30E-01  |
| ILMN_1709486 | SRPX          | 0.524927756 | Enrichment Score: 1.75 |  | Count | P_Value  | Benjamini |
| ILMN_1683026 | PSMB10        | 0.524529619 | UP_SEQ_FEATURE         | short sequence motif:SH3-binding 3   | 4     | 9.10E-04 | 1.40E-01  |
| ILMN_1652306 | NRP7          | 0.523767182 | UP_SEQ_FEATURE         | short sequence motif:SH3-binding 2   | 4     | 2.20E-03 | 2.60E-01  |
| ILMN_1800021 | RTN1          | 0.523735881 | UP_SEQ_FEATURE         | short sequence motif:SH3-binding 1   | 4     | 2.20E-03 | 2.60E-01  |
| ILMN_1780533 | RNAS5E        | 0.523036373 | GOTERM_BP_FAT          | phospholipid scrambling  | 3     | 2.60E-02 | 3.70E-01  |
| ILMN_1738424 | CDCA2         | 0.522741055 | INTERPRO               | Scramblase   | 3     | 3.70E-02 | 6.60E-01  |
| ILMN_1734205 | RASSF1        | 0.522728233 | GOTERM_MF_FAT          | phospholipid transporter activity  | 6     | 4.00E-02 | 5.30E-01  |
| ILMN_1736178 | ABP1          | 0.522717341 | PIR_SUPERFAMILY        | PIR5F07928phospholipid scrambling  | 3     | 4.80E-02 | 9.50E-01  |
| ILMN_1719835 | OSCP1         | 0.522704627 | GOTERM_BP_FAT          | plasma membrane expansion  | 6     | 8.00E-02 | 6.90E-01  |
| ILMN_3183573 | NA            | 0.52263131  | GOTERM_MF_FAT          | lipid transporter activity   | 7     | 2.40E-01 | 9.20E-01  |
| ILMN_1677997 | MAZ           | 0.522238876 | Enrichment Score: 1.73 |  | Count | P_Value  | Benjamini |
| ILMN_1730842 | P7PRC         | 0.521762528 | GOTERM_BP_FAT          | extracellular matrix organization  | 16    | 5.10E-03 | 1.20E-01  |
| ILMN_1742332 | KCTD12        | 0.521545658 | GOTERM_BP_FAT          | collagen fibril organization   | 7     | 3.30E-02 | 2.40E-01  |
| ILMN_1749345 | STX5          | 0.521135791 | GOTERM_BP_FAT          | extracellular structure organization   | 17    | 9.80E-02 | 6.90E-01  |
| ILMN_3229033 | TDG           | 0.520773908 | Enrichment Score: 1.73 |  | Count | P_Value  | Benjamini |
| ILMN_1809488 | SPCS2         | 0.520711651 | UP_SEQ_FEATURE         | DNA-binding region:Tryptophan pentad repeat  | 4     | 1.50E-02 | 7.00E-01  |
| ILMN_2116714 | SLC39A1       | 0.520560078 | INTERPRO               | Interferon regulator factor_converted site   | 4     | 1.70E-02 | 5.20E-01  |
| ILMN_2391912 | SEC14L1       | 0.520405383 | INTERPRO               | Interferon regulator factor  | 4     | 1.70E-02 | 5.20E-01  |
| ILMN_2080242 | IGALS9C       | 0.520398144 | SMART                  | ITP  | 4     | 2.80E-02 | 5.40E-01  |
| ILMN_1669881 | TSKAN13       | 0.520298317 | Enrichment Score: 1.71 |  | Count | P_Value  | Benjamini |
| ILMN_1760858 | RAB8A         | 0.52012829  | GOTERM_BP_FAT          | regulation of inflammatory response  | 14    | 1.90E-03 | 6.10E-02  |
| ILMN_1782538 | VIM           | 0.51992954  | GOTERM_BP_FAT          | negative regulation of response to stimulus  | 15    | 8.60E-03 | 1.80E-01  |
| ILMN_2082244 | FOXK1         | 0.519593139 | GOTERM_BP_FAT          | regulation of defense response   | 8     | 1.00E-02 | 2.10E-01  |

|              |              |              |  |  |  |  |  |
|--------------|--------------|--------------|--|--|--|--|--|
| ILMN_3250798 | C11orf58     | -0.425834421 |  |  |  |  |  |
| ILMN_3236192 | NA           | -0.425843395 |  |  |  |  |  |
| ILMN_1892506 | CACNA1C      | -0.425805828 |  |  |  |  |  |
| ILMN_1898987 | BFS14393     | -0.426075959 |  |  |  |  |  |
| ILMN_3251373 | EEF1A1       | -0.426166297 |  |  |  |  |  |
| ILMN_3239073 | AY343892     | -0.426402786 |  |  |  |  |  |
| ILMN_2404085 | CLIP1        | -0.426519039 |  |  |  |  |  |
| ILMN_3234892 | MARCH11      | -0.426626181 |  |  |  |  |  |
| ILMN_1156699 | ACOT16       | -0.426634642 |  |  |  |  |  |
| ILMN_1897796 | IQ773461     | -0.426662393 |  |  |  |  |  |
| ILMN_1678919 | YOD1         | -0.426716693 |  |  |  |  |  |
| ILMN_1762714 | VGLL2        | -0.42674999  |  |  |  |  |  |
| ILMN_1679979 | PLK4         | -0.426809392 |  |  |  |  |  |
| ILMN_1659285 | PSMG1        | -0.426812772 |  |  |  |  |  |
| ILMN_1696708 | C14orf166    | -0.426884542 |  |  |  |  |  |
| ILMN_1744611 | DCAF13       | -0.426927838 |  |  |  |  |  |
| ILMN_1796165 | GLRX5        | -0.426984348 |  |  |  |  |  |
| ILMN_3308330 | MIR545       | -0.427153939 |  |  |  |  |  |
| ILMN_1788778 | sept-11      | -0.427244676 |  |  |  |  |  |
| ILMN_3286312 | NEK2         | -0.427250374 |  |  |  |  |  |
| ILMN_2057826 | PHF3         | -0.427296659 |  |  |  |  |  |
| ILMN_1861380 | B08B000      | -0.427315605 |  |  |  |  |  |
| ILMN_3204665 | LOC100132724 | -0.427342326 |  |  |  |  |  |
| ILMN_1738033 | ORTZ33       | -0.427420816 |  |  |  |  |  |
| ILMN_3296906 | SLC9A7P1     | -0.427436752 |  |  |  |  |  |
| ILMN_1760110 | A0023936     | -0.427439814 |  |  |  |  |  |
| ILMN_1697263 | BMS1P5       | -0.427451096 |  |  |  |  |  |
| ILMN_1685000 | DHDH         | -0.427850568 |  |  |  |  |  |
| ILMN_1787595 | B3GALNT1     | -0.428685747 |  |  |  |  |  |
| ILMN_1915734 | D4Z21262     | -0.428805689 |  |  |  |  |  |
| ILMN_1775814 | GHR          | -0.428936957 |  |  |  |  |  |
| ILMN_1628357 | NDUFAF2      | -0.428952134 |  |  |  |  |  |
| ILMN_1707649 | MPO2         | -0.428947541 |  |  |  |  |  |
| ILMN_1707665 | SALL3        | -0.42901524  |  |  |  |  |  |
| ILMN_3292122 | NA           | -0.4290776   |  |  |  |  |  |
| ILMN_1660186 | LOC282558    | -0.429136419 |  |  |  |  |  |
| ILMN_1660186 | SVY2         | -0.429338098 |  |  |  |  |  |
| ILMN_1886405 | KDR          | -0.429366603 |  |  |  |  |  |
| ILMN_2290118 | MEGF9        | -0.429391008 |  |  |  |  |  |
| ILMN_3264466 | FAM54B       | -0.429677162 |  |  |  |  |  |
| ILMN_1788678 | MC2OR14      | -0.429679257 |  |  |  |  |  |
| ILMN_1803850 | TSKAN15      | -0.429705446 |  |  |  |  |  |
| ILMN_1679919 | ASC2         | -0.430017785 |  |  |  |  |  |
| ILMN_1695717 | RBM41        | -0.430091428 |  |  |  |  |  |
| ILMN_1658413 | HYDIN        | -0.430108716 |  |  |  |  |  |
|              |              |              |  |  |  |  |  |

|              |              |             |                 |  |              |                |                  |  |
|--------------|--------------|-------------|-----------------|--|--------------|----------------|------------------|--|
| ILMN_1687533 | SEMA4D       | 0.519439179 | GOTERM_BP_FAT   | <a href="#">negative regulation of inflammatory response</a>   | 6            | 5.90E-02       | 5.60E-01         |  |
| ILMN_2367010 | GPR126       | 0.519409791 | GOTERM_BP_FAT   | <a href="#">negative regulation of response to external stimulus</a>   | 6            | 2.60E-01       | 9.10E-01         |  |
| ILMN_1693233 | KIAA4513     | 0.518984111 | INTERPRO        | <b>Enrichment Score: 1.71</b>  | <b>Count</b> | <b>P_Value</b> | <b>Benjamini</b> |  |
| ILMN_1738832 | SACS         | 0.51879672  | INTERPRO        | <a href="#">immunoglobulin subtype</a>   | 46           | 2.00E-06       | 5.70E-04         |  |
| ILMN_1651958 | MGP          | 0.518749732 | SMART           | <a href="#">Ig</a>   | 46           | 1.40E-04       | 1.30E-02         |  |
| ILMN_1713561 | C20orf103    | 0.518618413 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 1</a>  | 23           | 3.50E-03       | 3.40E-01         |  |
| ILMN_1748677 | H3F3A        | 0.518611689 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 3</a>  | 23           | 3.80E-03       | 3.50E-01         |  |
| ILMN_1706605 | COL5A1       | 0.518590399 | INTERPRO        | <a href="#">immunoglobulin</a>   | 22           | 2.30E-02       | 5.80E-01         |  |
| ILMN_1659905 | HSPD10       | 0.517798232 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 3</a>  | 13           | 7.60E-02       | 9.70E-01         |  |
| ILMN_1749789 | HIST1H1D     | 0.517385181 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 6</a>  | 6            | 7.60E-02       | 9.70E-01         |  |
| ILMN_1755353 | LOC646484    | 0.517359773 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 4</a>  | 9            | 9.80E-02       | 9.90E-01         |  |
| ILMN_1731418 | SP110        | 0.516672367 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 5</a>  | 7            | 1.20E-01       | 9.90E-01         |  |
| ILMN_1663739 | C6orf62      | 0.516400079 | UP_SEQ_FEATURE  | <a href="#">domain:like C2-type 7</a>  | 4            | 4.50E-01       | 1.00E+00         |  |
| ILMN_1730906 | FUPL1        | 0.516343457 | INTERPRO        | <a href="#">immunoglobulin subtype 2</a>   | 18           | 1.80E-01       | 9.50E-01         |  |
| ILMN_1752755 | VWF          | 0.51584319  | SMART           | <a href="#">Ig2</a>  | 18           | 4.30E-01       | 9.70E-01         |  |
| ILMN_2246882 | SP140        | 0.515398091 | INTERPRO        | <a href="#">immunoglobulin I-act</a>   | 8            | 8.00E-01       | 1.00E+00         |  |
| ILMN_1703692 | TUBB         | 0.515373368 |                 |  |              |                |                  |  |
| ILMN_1774733 | SOC1         | 0.515160688 | GOTERM_BP_FAT   | <a href="#">positive regulation of adaptive immune response</a>  | 10           | 1.70E-04       | 7.50E-03         |  |
| ILMN_1686401 | RFCO2        | 0.515156537 | GOTERM_BP_FAT   | <a href="#">regulation of immune effector process</a>  | 18           | 5.10E-04       | 2.00E-02         |  |
| ILMN_1765547 | IRF2         | 0.515132444 | GOTERM_BP_FAT   | <a href="#">positive regulation of immune effector process</a>   | 11           | 6.70E-04       | 2.60E-02         |  |
|              |              |             |                 | <a href="#">positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a> |              |                |                  |  |
| ILMN_1664644 | PTGDS        | 0.514995203 | GOTERM_BP_FAT   | <a href="#">regulation of adaptive immune response</a>   | 9            | 7.50E-04       | 2.80E-02         |  |
| ILMN_2414165 | PRDM1        | 0.514868207 | GOTERM_BP_FAT   | <a href="#">regulation of adaptive immune response</a>   | 12           | 1.30E-03       | 4.50E-02         |  |
| ILMN_2170813 | LAMP3        | 0.514854618 | GOTERM_BP_FAT   | <a href="#">regulation of leukocyte mediated immunity</a>  | 12           | 2.80E-03       | 7.90E-02         |  |
| ILMN_1768940 | COL15A1      | 0.514819308 | GOTERM_BP_FAT   | <a href="#">regulation of lymphocyte mediated immunity</a>   | 11           | 3.50E-03       | 9.30E-02         |  |
|              |              |             |                 | <a href="#">regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a>          |              |                |                  |  |
| ILMN_1653498 | IGSF6        | 0.51464226  | GOTERM_BP_FAT   | <a href="#">immunoglobulin superfamily domain</a>  | 11           | 4.00E-03       | 1.00E-01         |  |
| ILMN_3219558 | TUBA1C       | 0.51463854  | GOTERM_BP_FAT   | <a href="#">positive regulation of leukocyte mediated immunity</a>   | 8            | 7.60E-03       | 1.60E-01         |  |
| ILMN_1772359 | LAPTM5       | 0.514583115 | GOTERM_BP_FAT   | <a href="#">positive regulation of lymphocyte mediated immunity</a>  | 8            | 7.60E-03       | 1.60E-01         |  |
| ILMN_2379599 | CD163        | 0.51407854  | GOTERM_BP_FAT   | <a href="#">regulation of inflammatory response to antigenic stimulus</a>  | 4            | 1.40E-02       | 2.50E-01         |  |
|              |              |             |                 | <a href="#">positive regulation of inflammatory response to antigenic stimulus</a>   |              |                |                  |  |
| ILMN_1737586 | EIF4H        | 0.514073307 | GOTERM_BP_FAT   | <a href="#">positive regulation of B cell mediated immunity</a>  | 3            | 2.60E-02       | 3.70E-01         |  |
| ILMN_2388155 | CASP3        | 0.514056975 | GOTERM_BP_FAT   | <a href="#">positive regulation of B cell mediated immunity</a>  | 4            | 3.60E-02       | 4.30E-01         |  |
|              |              |             |                 | <a href="#">positive regulation of immunoglobulin mediated immune response</a>   |              |                |                  |  |
| ILMN_3248122 | MED1         | 0.514045603 | GOTERM_BP_FAT   | <a href="#">regulation of T cell mediated immunity</a>   | 4            | 3.60E-02       | 4.30E-01         |  |
| ILMN_1731800 | FRAT1        | 0.513913587 | GOTERM_BP_FAT   | <a href="#">regulation of T cell mediated immunity</a>   | 5            | 5.30E-02       | 5.30E-01         |  |
|              |              |             |                 | <a href="#">regulation of production of molecular mediator of immune response</a>  |              |                |                  |  |
| ILMN_1758315 | SLC9A9       | 0.513768304 | GOTERM_BP_FAT   | <a href="#">regulation of B cell mediated immunity</a>   | 7            | 6.10E-02       | 5.60E-01         |  |
| ILMN_1787844 | C13orf10     | 0.513285785 | GOTERM_BP_FAT   | <a href="#">regulation of B cell mediated immunity</a>   | 5            | 8.00E-02       | 6.40E-01         |  |
| ILMN_2113049 | OCY1         | 0.513038583 | GOTERM_BP_FAT   | <a href="#">regulation of immunoglobulin mediated immune response</a>  | 6            | 1.79E-02       | 6.9H11           |  |
| ILMN_1705442 | CDMT3        | 0.512363037 | GOTERM_BP_FAT   | <a href="#">positive regulation of T cell mediated immunity</a>  | 4            | 8.00E-02       | 6.40E-01         |  |
| ILMN_1805673 | AKXB4        | 0.512010829 | GOTERM_BP_FAT   | <a href="#">regulation of leukocyte mediated cytotoxicity</a>  | 5            | 9.00E-02       | 6.70E-01         |  |
| ILMN_2399304 | NAV2         | 0.511715806 | GOTERM_BP_FAT   | <a href="#">regulation of cell killing</a>   | 5            | 1.20E-01       | 7.50E-01         |  |
| ILMN_3243061 | SGLEC14      | 0.511462976 | GOTERM_BP_FAT   | <a href="#">regulation of T cell mediated cytotoxicity</a>   | 3            | 1.20E-01       | 7.50E-01         |  |
| ILMN_1775761 | GNAL2        | 0.511146532 | GOTERM_BP_FAT   | <a href="#">immunoglobulin production</a>  | 14           | 3.40E-01       | 6.50E-01         |  |
| ILMN_1672417 | PTPRCAP      | 0.510922759 | GOTERM_BP_FAT   | <a href="#">production of molecular mediator of immune response</a>  | 4            | 3.60E-01       | 9.50E-01         |  |
| ILMN_1772036 | STEAP4       | 0.510841905 | GOTERM_BP_FAT   | <a href="#">positive regulation of leukocyte mediated cytotoxicity</a>   | 3            | 4.30E-01       | 9.70E-01         |  |
| ILMN_1679880 | THOC6        | 0.510808899 | GOTERM_BP_FAT   | <a href="#">positive regulation of cell killing</a>  | 3            | 5.00E-01       | 9.80E-01         |  |
| ILMN_1769615 | FLRT2        | 0.510746445 |                 |  |              |                |                  |  |
| ILMN_1751572 | TLE1         | 0.510349743 | GOTERM_BP_FAT   | <a href="#">regulation of calcium-mediated signaling</a>   | 6            | 1.00E-02       | 2.00E-01         |  |
| ILMN_1654939 | TMED2        | 0.510307414 | GOTERM_BP_FAT   | <a href="#">positive regulation of calcium-mediated signaling</a>  | 5            | 2.60E-02       | 3.70E-01         |  |
| ILMN_3248324 | MGC16384     | 0.510283635 | GOTERM_BP_FAT   | <a href="#">positive regulation of alpha-beta T cell activation</a>  | 6            | 3.00E-02       | 4.00E-01         |  |
| ILMN_1773079 | COL3A1       | 0.510071055 |                 |  |              |                |                  |  |
| ILMN_1812795 | RUNX1T1      | 0.509851865 | UP_SEQ_FEATURE  | <a href="#">domain:DAPIN</a>   | 6            | 9.90E-03       | 6.30E-01         |  |
| ILMN_1659842 | CHAF1A       | 0.509555509 | INTERPRO        | <a href="#">Pain</a>   | 6            | 1.20E-02       | 4.70E-01         |  |
| ILMN_1707491 | FAM30A       | 0.509426057 | INTERPRO        | <a href="#">JH1_200/IF120</a>  | 3            | 3.30E-02       | 5.70E-01         |  |
| ILMN_1779234 | CXCL6        | 0.50910037  | INTERPRO        | <a href="#">DEATH-like</a>   | 9            | 6.90E-02       | 8.00E-01         |  |
| ILMN_1690004 | LRKK1        | 0.509125796 |                 |  |              |                |                  |  |
| ILMN_2366330 | FERM3T       | 0.50909588  | GOTERM_BP_FAT   | <a href="#">positive regulation of cytokine biosynthetic process</a>   | 10           | 5.00E-03       | 1.20E-01         |  |
| ILMN_1691693 | FCMB3        | 0.508919776 | GOTERM_BP_FAT   | <a href="#">regulation of interleukin-2 production</a>   | 7            | 1.50E-02       | 2.60E-01         |  |
| ILMN_2351466 | NTM          | 0.508739255 | GOTERM_BP_FAT   | <a href="#">regulation of cytokine biosynthetic process</a>  | 11           | 3.00E-02       | 4.00E-01         |  |
| ILMN_2320888 | CXCR4        | 0.508739089 | GOTERM_BP_FAT   | <a href="#">regulation of interleukin-2 biosynthetic process</a>   | 5            | 3.80E-02       | 4.50E-01         |  |
| ILMN_1700147 | VPRB3        | 0.508164615 | GOTERM_BP_FAT   | <a href="#">positive regulation of interleukin-2 biosynthetic process</a>  | 4            | 5.60E-02       | 5.40E-01         |  |
| ILMN_1724598 | RAB12A       | 0.507915242 | GOTERM_MF_FAT   | <a href="#">kinase binding</a>   | 21           | 1.50E-02       | 3.70E-01         |  |
| ILMN_1691662 | LOC100101266 | 0.507460597 | GOTERM_MF_FAT   | <a href="#">enzyme binding</a>   | 47           | 3.00E-02       | 4.70E-01         |  |
| ILMN_2077550 | RACGAP1      | 0.507273648 | GOTERM_MF_FAT   | <a href="#">protein-kinase binding</a>   | 17           | 3.40E-02       | 4.90E-01         |  |
| ILMN_1726392 | NIN          | 0.507098161 |                 |  |              |                |                  |  |
| ILMN_1783909 | COL6A2       | 0.506963109 | SP_PIR_KEYWORDS | <a href="#">GTPase activation</a>  | 19           | 9.30E-03       | 7.60E-02         |  |
| ILMN_1778401 | HLA-B        | 0.506796739 | UP_SEQ_FEATURE  | <a href="#">domain:Rho-GAP</a>   | 13           | 9.00E-02       | 7.30E-01         |  |
| ILMN_1681101 | MARCKH1      | 0.506702524 | INTERPRO        | <a href="#">RhoGAP</a>   | 10           | 2.90E-02       | 6.10E-01         |  |
| ILMN_1658586 | GPR161       | 0.506516035 | GOTERM_MF_FAT   | <a href="#">GTPase activator activity</a>  | 23           | 3.50E-02       | 4.90E-01         |  |
| ILMN_2169439 | ITGAV        | 0.506240584 | SMART           | <a href="#">RhoGAP</a>   | 10           | 7.40E-02       | 6.50E-01         |  |
| ILMN_2255133 | EC113A       | 0.505996909 |                 |  |              |                |                  |  |
| ILMN_2396441 | PTC9         | 0.505971823 | SP_PIR_KEYWORDS | <a href="#">tyrosine-specific protein kinase</a>   | 7            | 2.40E-03       | 2.70E-02         |  |
| ILMN_1724807 | NUDT3        | 0.505861202 | SP_PIR_KEYWORDS | <a href="#">autophosphorylation</a>  | 10           | 2.70E-03       | 3.00E-02         |  |
| ILMN_3234841 | RPL23AP7     | 0.505769005 | SP_PIR_KEYWORDS | <a href="#">phosphotransferase</a>   | 24           | 3.10E-03       | 3.20E-02         |  |
| ILMN_1724139 | TMEM123      | 0.505763396 | GOTERM_BP_FAT   | <a href="#">peptide:tyrosine modification</a>  | 9            | 1.60E-02       | 2.70E-01         |  |
| ILMN_2324447 | ABHD175      | 0.505759041 | GOTERM_MF_FAT   | <a href="#">non-membrane-spanning protein tyrosine kinase activity</a>   | 8            | 1.70E-02       | 3.80E-01         |  |
| ILMN_1673788 | CVS1         | 0.505494471 | SP_PIR_KEYWORDS | <a href="#">tyrosine protein kinase</a>  | 14           | 1.90E-02       | 3.20E-01         |  |
| ILMN_1722622 | CD163        | 0.505402829 | INTERPRO        | <a href="#">Tyrosine protein kinase</a>  | 15           | 2.10E-02       | 5.70E-01         |  |
| ILMN_1758418 | TNFSF13B     | 0.505239005 | INTERPRO        | <a href="#">Tyrosine protein kinase, active site</a>   | 13           | 2.40E-02       | 5.60E-01         |  |
| ILMN_1773389 | PLTP         | 0.505212684 | SP_PIR_KEYWORDS | <a href="#">ATP</a>  | 23           | 3.50E-02       | 2.00E-01         |  |
| ILMN_1304808 | TUBB         | 0.504963219 | GOTERM_BP_FAT   | <a href="#">peptide:tyrosine phosphorylation</a>   | 8            | 3.70E-02       | 4.40E-01         |  |
| ILMN_1692009 | FGF1         | 0.504780808 | GOTERM_MF_FAT   | <a href="#">non-tyrosine kinase activity</a>   | 18           | 4.30E-02       | 5.70E-01         |  |
| ILMN_1697377 | ANKRD36B     | 0.504188354 | SMART           | <a href="#">Tyrc</a>   | 15           | 7.30E-02       | 6.70E-01         |  |
| ILMN_2394750 | EXOC4        | 0.504148688 | GOTERM_MF_FAT   | <a href="#">transmembrane receptor protein tyrosine kinase activity</a>  | 9            | 7.40E-02       | 7.00E-01         |  |
| ILMN_1759312 | LAMP1        | 0.503895565 | INTERPRO        | <a href="#">Protein kinase, ATP binding site</a>   | 38           | 9.50E-02       | 8.60E-01         |  |
| ILMN_1701424 | LAMC2        | 0.503859319 | UP_SEQ_FEATURE  | <a href="#">binding site:ATP</a>   | 42           | 1.10E-01       | 9.90E-01         |  |
| ILMN_2329324 | CNE1         | 0.503494471 | INTERPRO        | <a href="#">Protein kinase, core</a>   | 39           | 1.10E-01       | 8.90E-01         |  |
| ILMN_2317923 | TMEM132A     | 0.503283566 | UP_SEQ_FEATURE  | <a href="#">domain:Protein kinase</a>  | 36           | 1.50E-01       | 1.00E+00         |  |
| ILMN_2352190 | CLIP2        | 0.503184367 |                 |  |              |                |                  |  |
| ILMN_1664010 | ELF1         | 0.50292913  |                 |  |              |                |                  |  |
| ILMN_1654586 | PAS3         | 0.502902143 | INTERPRO        | <a href="#">von Willebrand factor, type C</a>  | 8            | 1.40E-02       | 4.80E-01         |  |
| ILMN_1702708 | RP23A2A      | 0.502783714 | SMART           | <a href="#">YAGC</a>   | 8            | 3.30E-02       | 5.90E-01         |  |
| ILMN_1796762 | CCDC102A     | 0.502779007 | UP_SEQ_FEATURE  | <a href="#">region of interest:Heparin-binding</a>   | 4            | 1.20E-01       | 9.90E-01         |  |
| ILMN_1753608 | TMEM131      | 0.502769888 | GOTERM_BP_FAT   | <a href="#">regulation of cell-substrate adhesion</a>  | 4            | 6.20E-01       | 9.90E-01         |  |
| ILMN_1656920 | CRP1         | 0.502717157 |                 |  |              |                |                  |  |
| ILMN_1708416 | ARL6IP1      | 0.502712897 | GOTERM_BP_FAT   | <a href="#">positive regulation of immune effector process</a>   | 11           | 6.70E-04       | 2.60E-02         |  |
| ILMN_1813941 | SPTCL1       | 0.502717061 | GOTERM_BP_FAT   | <a href="#">positive regulation of immunoglobulin production</a>   | 3            | 5.90E-02       | 5.60E-01         |  |

|              |           |                |  |  |  |  |  |  |
|--------------|-----------|----------------|--|--|--|--|--|--|
| ILMN_3187680 | ACCS      | -0.434273601   |  |  |  |  |  |  |
| ILMN_1658548 | LOC101180 | -0.434301354   |  |  |  |  |  |  |
| ILMN_1775569 | CRSP2     | -0.434324694   |  |  |  |  |  |  |
| ILMN_232952  | CSO1      | -0.434332614   |  |  |  |  |  |  |
| ILMN_1813374 | C19orf28  | -0.434339413   |  |  |  |  |  |  |
| ILMN_1761049 | E1F2C3    | -0.434447469   |  |  |  |  |  |  |
| ILMN_1665621 | HSF1      | -0.434502935   |  |  |  |  |  |  |
| ILMN_2388425 | DKTL2     | -0.434522597   |  |  |  |  |  |  |
| ILMN_1646807 | CD44H1    | -0.434530741   |  |  |  |  |  |  |
| ILMN_2030908 | FAM71E2   | -0.434668528   |  |  |  |  |  |  |
| ILMN_1800049 | MAP2      | -0.434680407   |  |  |  |  |  |  |
| ILMN_3309234 | MIR181D   | -0.434711774   |  |  |  |  |  |  |
| ILMN_1683755 | SKD13     | -0.434840792   |  |  |  |  |  |  |
| ILMN_2310814 | MARF      | -0.435280042   |  |  |  |  |  |  |
| ILMN_1680420 | NUDT13    | -0.435267065   |  |  |  |  |  |  |
| ILMN_2388875 | CEK1      | -0.435436604</ |  |  |  |  |  |  |

|              |          |             |               |  |   |          |          |
|--------------|----------|-------------|---------------|--|---|----------|----------|
| ILMN_1668526 | GVN1     | 0.502134327 | GOTERM_BP_FAT | regulation of production of molecular mediator of immune response          | 7 | 6.10E-02 | 5.60E-01 |
| ILMN_1266471 | NHRPC    | 0.50206028  | GOTERM_BP_FAT | positive regulation of production of molecular mediator of immune response | 4 | 8.00E-02 | 6.40E-01 |
| ILMN_1792323 | HDC      | 0.501908382 | GOTERM_BP_FAT | regulation of immunoglobulin production                                    | 5 | 1.00E-01 | 7.00E-01 |
| ILMN_1250321 | PTPA43   | 0.501884874 |               |  |   |          |          |
| ILMN_1683658 | RKBP1A   | 0.500912724 |               |  |   |          |          |
| ILMN_1783182 | FN1      | 0.500903631 |               |  |   |          |          |
| ILMN_1708006 | MICA     | 0.50072348  |               |  |   |          |          |
| ILMN_1814822 | AEN      | 0.500720751 |               |  |   |          |          |
| ILMN_1768391 | ARL4C    | 0.500429722 |               |  |   |          |          |
| ILMN_1205783 | CXCL2    | 0.500390809 |               |  |   |          |          |
| ILMN_1727194 | CALL1    | 0.500369001 |               |  |   |          |          |
| ILMN_2161577 | CXCL6    | 0.500249011 |               |  |   |          |          |
| ILMN_2350634 | EFEF1    | 0.500206558 |               |  |   |          |          |
| ILMN_1806415 | TLL1     | 0.500133453 |               |  |   |          |          |
| ILMN_2145570 | TNC      | 0.499903436 |               |  |   |          |          |
| ILMN_1659158 | SAM03    | 0.499796669 |               |  |   |          |          |
| ILMN_2103107 | ADAMDEC1 | 0.499783162 |               |  |   |          |          |
| ILMN_1667966 | FAM132A  | 0.499777816 |               |  |   |          |          |
| ILMN_2289849 | FCG2A    | 0.499770278 |               |  |   |          |          |
| ILMN_2046730 | S100A11  | 0.499655898 |               |  |   |          |          |
| ILMN_1728478 | CXCL16   | 0.499648824 |               |  |   |          |          |
| ILMN_1720124 | RCC2     | 0.49959593  |               |  |   |          |          |
| ILMN_1773059 | GRP24    | 0.499553381 |               |  |   |          |          |
| ILMN_1770921 | TY1      | 0.499318867 |               |  |   |          |          |
| ILMN_2145501 | ANGPTL1  | 0.499287642 |               |  |   |          |          |
| ILMN_1739885 | SLC41A3  | 0.498939006 |               |  |   |          |          |
| ILMN_1732870 | FRM3B    | 0.498890752 |               |  |   |          |          |
| ILMN_1702787 | SEMA4A   | 0.498825311 |               |  |   |          |          |
| ILMN_3240005 | KDM5B    | 0.498036371 |               |  |   |          |          |
| ILMN_2328972 | DNMT3B   | 0.497852497 |               |  |   |          |          |
| ILMN_1776678 | GIMAP7   | 0.497755073 |               |  |   |          |          |
| ILMN_1777342 | PREX1    | 0.497650991 |               |  |   |          |          |
| ILMN_2384544 | ADAM15   | 0.49700085  |               |  |   |          |          |
| ILMN_1652237 | CR3      | 0.496843407 |               |  |   |          |          |
| ILMN_231523  | SACS     | 0.496414693 |               |  |   |          |          |
| ILMN_1713496 | ST3GAL5  | 0.496247538 |               |  |   |          |          |
| ILMN_1713676 | FLAOL30  | 0.496128814 |               |  |   |          |          |
| ILMN_2148459 | B2M      | 0.496016298 |               |  |   |          |          |
| ILMN_1738578 | FILP1L   | 0.495603084 |               |  |   |          |          |
| ILMN_1769705 | HIF3C    | 0.495596519 |               |  |   |          |          |
| ILMN_2384496 | STGAL1   | 0.495498269 |               |  |   |          |          |
| ILMN_1801767 | ABHD3    | 0.494887245 |               |  |   |          |          |
| ILMN_1673352 | HIF2A    | 0.494874549 |               |  |   |          |          |
| ILMN_1759915 | ARPC1A   | 0.494657516 |               |  |   |          |          |
| ILMN_1666050 | TM6B1    | 0.494520754 |               |  |   |          |          |
| ILMN_1773388 | CL3A1F8  | 0.494505622 |               |  |   |          |          |
| ILMN_2150258 | ZFP36L2  | 0.494331692 |               |  |   |          |          |
| ILMN_1790778 | PNMA2    | 0.493965071 |               |  |   |          |          |
| ILMN_1701613 | RARBES3  | 0.493865386 |               |  |   |          |          |
| ILMN_1675289 | SEMA4B   | 0.493656469 |               |  |   |          |          |
| ILMN_1768468 | TERF2    | 0.493630959 |               |  |   |          |          |
| ILMN_1750811 | TESC     | 0.493587988 |               |  |   |          |          |
| ILMN_1677765 | LRP8     | 0.49346876  |               |  |   |          |          |
| ILMN_1751368 | HNRNP0   | 0.493236882 |               |  |   |          |          |
| ILMN_1804117 | FAM98B   | 0.492879984 |               |  |   |          |          |
| ILMN_1734878 | C27B9    | 0.492621639 |               |  |   |          |          |
| ILMN_1751444 | NCAG     | 0.492263342 |               |  |   |          |          |
| ILMN_3194911 | ATF6B    | 0.492071889 |               |  |   |          |          |
| ILMN_1742450 | TAP8     | 0.491946553 |               |  |   |          |          |
| ILMN_1750271 | MOBP     | 0.491887629 |               |  |   |          |          |
| ILMN_2355981 | ATG16L1  | 0.491855287 |               |  |   |          |          |
| ILMN_1840742 | AA131235 | 0.491683004 |               |  |   |          |          |
| ILMN_2356991 | CD47     | 0.491672352 |               |  |   |          |          |
| ILMN_1674036 | BIRC7    | 0.49156155  |               |  |   |          |          |
| ILMN_1779828 | EDEM1    | 0.491418122 |               |  |   |          |          |
| ILMN_1768697 | TRIM9    | 0.491286869 |               |  |   |          |          |
| ILMN_2347145 | DCN      | 0.49086298  |               |  |   |          |          |
| ILMN_1793371 | KAA0430  | 0.490393749 |               |  |   |          |          |
| ILMN_1689968 | PLEKH02  | 0.490307169 |               |  |   |          |          |
| ILMN_1789502 | GPC4     | 0.490240829 |               |  |   |          |          |
| ILMN_1814998 | OTX1P    | 0.490214791 |               |  |   |          |          |
| ILMN_1716382 | CL21+75  | 0.49000653  |               |  |   |          |          |
| ILMN_2074258 | BARD1    | 0.489771583 |               |  |   |          |          |
| ILMN_1687538 | ETS1     | 0.48955585  |               |  |   |          |          |
| ILMN_1691165 | CLSPN    | 0.489179941 |               |  |   |          |          |
| ILMN_1676162 | ARHGAP22 | 0.489155297 |               |  |   |          |          |
| ILMN_1810910 | CH1      | 0.489085283 |               |  |   |          |          |
| ILMN_1716687 | TPM1     | 0.489048001 |               |  |   |          |          |
| ILMN_232724  | CALCA    | 0.488929487 |               |  |   |          |          |
| ILMN_1742544 | MEF2C    | 0.488487575 |               |  |   |          |          |
| ILMN_1676128 | ENAH7A   | 0.488320023 |               |  |   |          |          |
| ILMN_1678842 | THBS2    | 0.487925561 |               |  |   |          |          |
| ILMN_1674386 | PITX1    | 0.48785589  |               |  |   |          |          |
| ILMN_1781824 | FASLG    | 0.487431803 |               |  |   |          |          |
| ILMN_1666932 | FCG2A2   | 0.487320898 |               |  |   |          |          |
| ILMN_1795025 | MX1      | 0.487232145 |               |  |   |          |          |
| ILMN_1716988 | OPN3     | 0.487129838 |               |  |   |          |          |
| ILMN_1674533 | TRPV6    | 0.486954576 |               |  |   |          |          |
| ILMN_1782741 | CD300LB  | 0.486873453 |               |  |   |          |          |
| ILMN_3311700 | MIR338   | 0.486868487 |               |  |   |          |          |
| ILMN_1765144 | FNAB2    | 0.48685326  |               |  |   |          |          |
| ILMN_2145033 | CCDC5    | 0.486442397 |               |  |   |          |          |

|              |             |             |  |  |  |  |  |
|--------------|-------------|-------------|--|--|--|--|--|
| ILMN_1753498 | COASY       | 0.44184581  |  |  |  |  |  |
| ILMN_1687392 | NRK         | 0.441893837 |  |  |  |  |  |
| ILMN_2151281 | GABARAPL1   | 0.442144704 |  |  |  |  |  |
| ILMN_2145396 | AKR7A3      | 0.442315078 |  |  |  |  |  |
| ILMN_1737357 | AIFM1       | 0.442410762 |  |  |  |  |  |
| ILMN_1681674 | MAD1L1      | 0.442559235 |  |  |  |  |  |
| ILMN_1767649 | PCDHGC3     | 0.442560517 |  |  |  |  |  |
| ILMN_1720482 | CEND1       | 0.442682561 |  |  |  |  |  |
| ILMN_1766513 | KCNK18      | 0.442852728 |  |  |  |  |  |
| ILMN_1652037 | UPP2        | 0.442859322 |  |  |  |  |  |
| ILMN_1724021 | SLC6A19     | 0.442955601 |  |  |  |  |  |
| ILMN_1654526 | LOC10093698 | 0.443004156 |  |  |  |  |  |
| ILMN_1907451 | BCO38752    | 0.443040868 |  |  |  |  |  |
| ILMN_1792449 | ALS2CR11    | 0.443116937 |  |  |  |  |  |
| ILMN_1792564 | PSMG1       | 0.443242652 |  |  |  |  |  |
| ILMN_1798557 | FAM153A     | 0.443440132 |  |  |  |  |  |
| ILMN_1740949 | LRRC19      | 0.44360544  |  |  |  |  |  |
| ILMN_1801698 | ACSM5       | 0.443932605 |  |  |  |  |  |
| ILMN_1781104 | MAP2K7      | 0.444048565 |  |  |  |  |  |
| ILMN_2082130 | Clorf123    | 0.444076459 |  |  |  |  |  |
| ILMN_1742040 | GDPD4       | 0.444142814 |  |  |  |  |  |
| ILMN_324645  | UCRP        | 0.444175648 |  |  |  |  |  |
| ILMN_1494514 | ZDHHC11     | 0.444185751 |  |  |  |  |  |
| ILMN_1478202 | TRIM402     | 0.444219236 |  |  |  |  |  |
| ILMN_1681641 | XTPE        | 0.444253171 |  |  |  |  |  |
| ILMN_1840311 | DA984348    | 0.444326762 |  |  |  |  |  |
| ILMN_1792139 | UCRHR       | 0.444337518 |  |  |  |  |  |
| ILMN_1776077 | DSCC1       | 0.444443752 |  |  |  |  |  |
| ILMN_1705144 | ULK1        | 0.444481213 |  |  |  |  |  |
| ILMN_1703826 | UNC5D       | 0.444529337 |  |  |  |  |  |
| ILMN_2259949 | BCKPHB      | 0.444587731 |  |  |  |  |  |
| ILMN_1814316 | RFXO1       | 0.44459197  |  |  |  |  |  |
| ILMN_1762993 | PIGV        | 0.444738905 |  |  |  |  |  |
| ILMN_3239946 | LOC729375   | 0.445003494 |  |  |  |  |  |
| ILMN_1807397 | NDUF85      | 0.445175155 |  |  |  |  |  |
| ILMN_2330697 | NR13        | 0.445294152 |  |  |  |  |  |
| ILMN_1811478 | MF12        | 0.445303766 |  |  |  |  |  |
| ILMN_1713219 | RGS12       | 0.445360649 |  |  |  |  |  |
| ILMN_1782881 | DEU17       | 0.445374219 |  |  |  |  |  |
| ILMN_1783497 | PANCK1      | 0.445450884 |  |  |  |  |  |
| ILMN_1657641 | KACCA       | 0.445455635 |  |  |  |  |  |
| ILMN_3234735 | ER12        | 0.445520568 |  |  |  |  |  |
| ILMN_2188959 | ACOT2       | 0.446033483 |  |  |  |  |  |
| ILMN_1787591 | XPA         | 0.446132235 |  |  |  |  |  |
| ILMN_2183885 | C7orf11     | 0.446269591 |  |  |  |  |  |
| ILMN_1796556 | PFPRB2      | 0.446312466 |  |  |  |  |  |
| ILMN_3184595 | NA          | 0.446605606 |  |  |  |  |  |
| ILMN_1686291 | DIO1        | 0.446691529 |  |  |  |  |  |
| ILMN_3310281 | MIRLET7E    | 0.446768059 |  |  |  |  |  |
| ILMN_1698673 | EFCAB7      | 0.446801684 |  |  |  |  |  |
| ILMN_1684730 | POM1212     | 0.446853322 |  |  |  |  |  |
| ILMN_2352633 | ARHGAP24    | 0.446893923 |  |  |  |  |  |
| ILMN_1656940 | ABLIM3      | 0.44695517  |  |  |  |  |  |
| ILMN_1711217 | TRIM24      | 0.446969095 |  |  |  |  |  |
| ILMN_1798249 | A44         | 0.44712351  |  |  |  |  |  |
| ILMN_1769556 | HPH3        | 0.447158085 |  |  |  |  |  |
| ILMN_1704211 | IL2         | 0.447336104 |  |  |  |  |  |
| ILMN_1668012 | SLC25A13    | 0.447385447 |  |  |  |  |  |
| ILMN_3187862 | DNAH14      | 0.447428737 |  |  |  |  |  |
| ILMN_1739813 | HYAL1       | 0.447554496 |  |  |  |  |  |
| ILMN_1797332 | NARS2       | 0.447579401 |  |  |  |  |  |
| ILMN_2140799 | FAM24B      | 0.447620495 |  |  |  |  |  |
| ILMN_1660729 | ATP6V1C2    | 0.447713247 |  |  |  |  |  |
| ILMN_1786278 | FAM149A     | 0.448006985 |  |  |  |  |  |
| ILMN_1675365 | LRRP4       | 0.448013103 |  |  |  |  |  |
| ILMN_1752846 | NA          | 0.448098623 |  |  |  |  |  |
| ILMN_1685043 | CV3A7       | 0.448097164 |  |  |  |  |  |
| ILMN_1771061 | BRD4        | 0.448110561 |  |  |  |  |  |
| ILMN_1786433 | BCCP1       | 0.448134229 |  |  |  |  |  |
| ILMN_1721880 | LOC644075   | 0.448474355 |  |  |  |  |  |
| ILMN_2207986 | SFRPN1      | 0.448493869 |  |  |  |  |  |
| ILMN_3238353 | INASEH2C    | 0.448512818 |  |  |  |  |  |

|              |              |             |                        |  |         |           |          |          |
|--------------|--------------|-------------|------------------------|--|---------|-----------|----------|----------|
| ILMN_1789007 | APOC1        | 0.486258812 | GOTERM_MF_FAT          | <a href="#">identical protein binding</a>                                      | Count   | 57        | 1.90E-02 | 4.00E-01 |
| ILMN_1674855 | TRAM11       | 0.48617213  | GOTERM_MF_FAT          | <a href="#">protein dimerization activity</a>                                  | Count   | 49        | 2.40E-02 | 4.10E-01 |
| ILMN_1669727 | WNK          | 0.48616723  | GOTERM_MF_FAT          | <a href="#">protein homodimerization activity</a>                              | Count   | 29        | 1.20E-01 | 8.00E-01 |
| ILMN_2383435 | FSM410       | 0.486057524 | Enrichment Score: 1.4  |  | P_Value | Benjamini | Count    |          |
| ILMN_3203765 | FLJ0317      | 0.485864015 | GOTERM_BP_FAT          | <a href="#">cell separation during cytokinesis</a>                             | Count   | 3         | 2.60E-02 | 3.70E-01 |
| ILMN_1711361 | ZNF319       | 0.485740187 | GOTERM_BP_FAT          | <a href="#">cytokinetic process</a>  | Count   | 3         | 4.10E-02 | 4.70E-01 |
| ILMN_1790909 | NFE2L2       | 0.485575825 | GOTERM_BP_FAT          | <a href="#">cytokinesis</a>  | Count   | 7         | 6.10E-02 | 5.60E-01 |
| ILMN_1703803 | ADAMTS1      | 0.485564248 | Enrichment Score: 1.38 |  | P_Value | Benjamini | Count    |          |
| ILMN_2374962 | FAM158B1     | 0.485564134 | UP_SEQ_FEATURE         | <a href="#">glycosylation site-O-linked (Gal...)</a>                           | Count   | 7         | 4.00E-06 | 1.20E-03 |
| ILMN_1758100 | GALR3        | 0.485491993 | SP_PIR_KEYWORDS        | <a href="#">complement pathway</a>   | Count   | 6         | 3.00E-02 | 1.80E-01 |
| ILMN_1680102 | C11orf45     | 0.485368157 | GOTERM_BP_FAT          | <a href="#">complement activation, classical pathway</a>                       | Count   | 6         | 4.60E-02 | 4.90E-01 |
| ILMN_1791057 | IFNA2        | 0.485339991 | GOTERM_BP_FAT          | <a href="#">humoral immune response mediated by circulating immunoglobulin</a> | Count   | 6         | 5.90E-02 | 5.60E-01 |
| ILMN_1240011 | NECAP2       | 0.485335054 | PIR_SUPERFAMILY        | <a href="#">PIR5FD02477:complement subcomponent C1q chain A</a>                | Count   | 3         | 1.40E-01 | 1.00E+00 |
| ILMN_2414325 | TNFAIP8      | 0.485306836 | UP_SEQ_FEATURE         | <a href="#">domain:Collagen-like</a>   | Count   | 5         | 1.80E-01 | 1.00E+00 |
| ILMN_1754660 | ZCCHC24      | 0.485046115 | UP_SEQ_FEATURE         | <a href="#">domain:C1q</a>   | Count   | 4         | 3.00E-01 | 1.00E+00 |
| ILMN_2231051 | TCF11L2      | 0.484915625 | INTERPRO               | <a href="#">Complement C1q protein</a>   | Count   | 4         | 3.50E-01 | 9.90E-01 |
| ILMN_1699711 | DECE2        | 0.484669898 | SMART                  | <a href="#">C1q</a>  | Count   | 4         | 4.60E-01 | 9.70E-01 |
| ILMN_1757877 | HCFZ1R1      | 0.48437354  | Enrichment Score: 1.37 |  | P_Value | Benjamini | Count    |          |
| ILMN_1681679 | TSPO         | 0.484360858 | GOTERM_BP_FAT          | <a href="#">myeloid cell differentiation</a>                                   | Count   | 15        | 4.50E-03 | 1.10E-01 |
| ILMN_1743130 | PTGFRN       | 0.483998806 | GOTERM_BP_FAT          | <a href="#">erythrocyte differentiation</a>                                    | Count   | 7         | 7.30E-02 | 6.20E-01 |
| ILMN_2205050 | PRRX         | 0.483930978 | GOTERM_BP_FAT          | <a href="#">homeostasis of number of cells</a>                                 | Count   | 12        | 8.40E-02 | 6.50E-01 |
| ILMN_3200140 | LOC455638    | 0.483853466 | GOTERM_BP_FAT          | <a href="#">erythrocyte homeostasis</a>  | Count   | 7         | 1.20E-01 | 7.40E-01 |
| ILMN_1712950 | PNF1         | 0.483803209 | Enrichment Score: 1.35 |  | P_Value | Benjamini | Count    |          |
| ILMN_1716547 | NAGK         | 0.483708967 | INTERPRO               | <a href="#">von Willebrand factor, type A</a>                                  | Count   | 12        | 1.30E-02 | 4.70E-01 |
| ILMN_2162860 | SLFN11       | 0.483690165 | SMART                  | <a href="#">SMART</a>  | Count   | 12        | 4.10E-02 | 6.10E-01 |
| ILMN_1764036 | PRYR14       | 0.483557643 | UP_SEQ_FEATURE         | <a href="#">domain:VWFA 2</a>  | Count   | 4         | 8.40E-02 | 9.80E-01 |
| ILMN_1702129 | CECR6        | 0.483515626 | UP_SEQ_FEATURE         | <a href="#">domain:VWFA 2</a>  | Count   | 8         | 8.80E-02 | 9.80E-01 |
| ILMN_1808501 | SH3BP1       | 0.483483571 | Enrichment Score: 1.34 |  | P_Value | Benjamini | Count    |          |
| ILMN_1676241 | BCOR         | 0.483289888 | GOTERM_MF_FAT          | <a href="#">tumor necrosis factor receptor superfamily binding</a>             | Count   | 8         | 3.50E-03 | 1.60E-01 |
| ILMN_1808114 | LVEF1        | 0.483131065 | INTERPRO               | <a href="#">Tumour necrosis factor-like</a>                                    | Count   | 8         | 2.50E-02 | 5.80E-01 |
| ILMN_1726809 | BHLHE41      | 0.483043254 | INTERPRO               | <a href="#">Tumour Necrosis Factor</a>   | Count   | 4         | 9.50E-02 | 8.60E-01 |
| ILMN_1852236 | Gor12D4      | 0.483003621 | SMART                  | <a href="#">TNF</a>  | Count   | 4         | 1.40E-01 | 8.00E-01 |
| ILMN_2382500 | MSAL4        | 0.482912847 | GOTERM_MF_FAT          | <a href="#">tumor necrosis factor receptor binding</a>                         | Count   | 4         | 1.60E-01 | 8.60E-01 |
| ILMN_1683980 | PLEKHM2      | 0.482798316 | Enrichment Score: 1.34 |  | P_Value | Benjamini | Count    |          |
| ILMN_2062714 | PTGDR        | 0.482783702 | INTERPRO               | <a href="#">Hyalin</a>   | Count   | 3         | 1.20E-02 | 4.60E-01 |
| ILMN_1657793 | TERF2IP      | 0.482639283 | UP_SEQ_FEATURE         | <a href="#">domain:Sunh1</a>   | Count   | 8         | 1.80E-02 | 7.40E-01 |
| ILMN_1700795 | HNS2         | 0.482635422 | UP_SEQ_FEATURE         | <a href="#">domain:Sunh2</a>   | Count   | 8         | 7.60E-02 | 7.40E-01 |
| ILMN_2088990 | Chor21       | 0.482466462 | SP_PIR_KEYWORDS        | <a href="#">sushi</a>  | Count   | 9         | 2.10E-02 | 1.40E-01 |
| ILMN_1682799 | STAMBP1      | 0.482163417 | INTERPRO               | <a href="#">Sushi/SCR/CCP</a>  | Count   | 9         | 2.80E-02 | 6.00E-01 |
| ILMN_1869109 | NUCKS1       | 0.48210558  | INTERPRO               | <a href="#">Complement control module</a>                                      | Count   | 9         | 3.10E-02 | 6.20E-01 |
| ILMN_1790689 | CRISP1D2     | 0.481915025 | UP_SEQ_FEATURE         | <a href="#">domain:Sunh3</a>   | Count   | 6         | 4.50E-02 | 9.10E-01 |
| ILMN_1663313 | MYL1A        | 0.481831923 | SMART                  | <a href="#">CCP</a>  | Count   | 9         | 6.50E-02 | 6.50E-01 |
| ILMN_1709549 | PLEKHM1      | 0.481831437 | UP_SEQ_FEATURE         | <a href="#">domain:Sunh3</a>   | Count   | 3         | 4.00E-01 | 1.00E+00 |
| ILMN_1763907 | CENPW        | 0.481479699 | UP_SEQ_FEATURE         | <a href="#">domain:Sunh4</a>   | Count   | 3         | 5.10E-01 | 1.00E+00 |
| ILMN_2206722 | FER1L4       | 0.481574905 | Enrichment Score: 1.33 |  | P_Value | Benjamini | Count    |          |
| ILMN_1693994 | BCCKC        | 0.481319103 | GOTERM_BP_FAT          | <a href="#">regulation of protein modification process</a>                     | Count   | 32        | 1.20E-02 | 2.30E-01 |
| ILMN_2367001 | SECE1G       | 0.481263066 | GOTERM_BP_FAT          | <a href="#">regulation of protein amino acid phosphorylation</a>               | Count   | 21        | 1.60E-02 | 2.70E-01 |
| ILMN_1661266 | HLA-DQB1     | 0.481129497 | GOTERM_BP_FAT          | <a href="#">regulation of peptidyl-tyrosine phosphorylation</a>                | Count   | 11        | 1.80E-02 | 2.90E-01 |
| ILMN_3220265 | CP           | 0.481117153 | GOTERM_BP_FAT          | <a href="#">positive regulation of phosphorylation</a>                         | Count   | 13        | 3.50E-02 | 4.30E-01 |
| ILMN_1740842 | SALL2        | 0.481065402 | GOTERM_BP_FAT          | <a href="#">negative regulation of protein modification process</a>            | Count   | 15        | 3.50E-02 | 4.30E-01 |
| ILMN_2056032 | CD99         | 0.480999492 | GOTERM_BP_FAT          | <a href="#">negative regulation of cellular protein metabolic process</a>      | Count   | 20        | 4.20E-02 | 4.70E-01 |
| ILMN_1701643 | CD9P5        | 0.480975037 | GOTERM_BP_FAT          | <a href="#">negative regulation of phospholipid metabolic process</a>          | Count   | 13        | 4.20E-02 | 4.70E-01 |
| ILMN_1807088 | TC13         | 0.480561584 | GOTERM_BP_FAT          | <a href="#">positive regulation of phosphate metabolic process</a>             | Count   | 13        | 4.20E-02 | 4.70E-01 |
| ILMN_1776105 | PSPH         | 0.480298877 | GOTERM_BP_FAT          | <a href="#">negative regulation of protein metabolic process</a>               | Count   | 20        | 5.80E-02 | 5.50E-01 |
| ILMN_2308849 | MYADM        | 0.480151488 | GOTERM_BP_FAT          | <a href="#">positive regulation of protein modification process</a>            | Count   | 20        | 5.80E-02 | 5.50E-01 |
| ILMN_1660817 | DOB2         | 0.48010761  | GOTERM_BP_FAT          | <a href="#">regulation of cellular protein metabolic process</a>               | Count   | 42        | 7.80E-02 | 6.30E-01 |
| ILMN_1704980 | INCA1        | 0.479989585 | GOTERM_BP_FAT          | <a href="#">positive regulation of protein amino acid phosphorylation</a>      | Count   | 11        | 6.80E-02 | 7.00E-01 |
| ILMN_1809583 | REBP8        | 0.479496766 | GOTERM_BP_FAT          | <a href="#">positive regulation of peptidyl-tyrosine phosphorylation</a>       | Count   | 7         | 1.00E-01 | 7.00E-01 |
| ILMN_1681301 | AM2          | 0.479176522 | GOTERM_BP_FAT          | <a href="#">positive regulation of protein metabolic process</a>               | Count   | 23        | 1.20E-01 | 7.40E-01 |
| ILMN_1810584 | IL1R1        | 0.478315438 | GOTERM_BP_FAT          | <a href="#">positive regulation of cellular protein metabolic process</a>      | Count   | 22        | 1.30E-01 | 7.60E-01 |
| ILMN_2124437 | NCL          | 0.478175501 | Enrichment Score: 1.32 |  | P_Value | Benjamini | Count    |          |
| ILMN_3240793 | CD2A4        | 0.477860348 | UP_SEQ_FEATURE         | <a href="#">domain:FCM</a>   | Count   | 5         | 3.20E-02 | 8.40E-01 |
| ILMN_1815745 | SOX4         | 0.477196761 | INTERPRO               | <a href="#">Fcg/FcR/FCP4 homology</a>  | Count   | 5         | 4.40E-02 | 7.10E-01 |
| ILMN_1695356 | RNF166       | 0.477104279 | SMART                  | <a href="#">FCI</a>  | Count   | 5         | 7.50E-02 | 6.50E-01 |
| ILMN_1670926 | CHST15       | 0.476885777 | Enrichment Score: 1.32 |  | P_Value | Benjamini | Count    |          |
| ILMN_1751432 | OR9K2        | 0.476769892 | UP_SEQ_FEATURE         | <a href="#">nucleotide phosphate-binding region:GTP</a>                        | Count   | 32        | 2.90E-03 | 3.20E-01 |
| ILMN_1679548 | MYL2A        | 0.476731933 | SP_PIR_KEYWORDS        | <a href="#">gtp-binding</a>  | Count   | 34        | 4.10E-03 | 4.00E-02 |
| ILMN_1738116 | TMEM110      | 0.476661404 | GOTERM_MF_FAT          | <a href="#">GTPase activity</a>  | Count   | 25        | 6.60E-03 | 2.40E-01 |
| ILMN_2353202 | PTK7         | 0.476593963 | GOTERM_MF_FAT          | <a href="#">GTP binding</a>  | Count   | 37        | 1.40E-02 | 3.60E-01 |
| ILMN_3246957 | DKFZ6666P158 | 0.476218154 | SP_PIR_KEYWORDS        | <a href="#">prenylation</a>  | Count   | 18        | 1.60E-02 | 1.20E-01 |
| ILMN_1691290 | CELSR3       | 0.476204023 | GOTERM_MF_FAT          | <a href="#">guanylylribonucleotide binding</a>                                 | Count   | 37        | 2.00E-02 | 4.10E-01 |
| ILMN_1721344 | MOBR2A2      | 0.475910241 | GOTERM_MF_FAT          | <a href="#">guanyl nucleotide binding</a>                                      | Count   | 37        | 2.00E-02 | 4.10E-01 |
| ILMN_1237918 | CLQA         | 0.475527118 | UP_SEQ_FEATURE         | <a href="#">short sequence motif:Effector region</a>                           | Count   | 11        | 7.00E-02 | 9.60E-01 |
| ILMN_1698307 | DBNL         | 0.475506082 | GOTERM_BP_FAT          | <a href="#">small GTPase mediated signal transduction</a>                      | Count   | 29        | 7.40E-02 | 6.20E-01 |
| ILMN_1691892 | TAGLN2       | 0.475317368 | UP_SEQ_FEATURE         | <a href="#">lipid moiety-binding region:5-geranylgeranyl cysteine</a>          | Count   | 11        | 1.00E-01 | 9.90E-01 |
| ILMN_1651346 | TICAM2       | 0.475316666 | INTERPRO               | <a href="#">Ras</a>  | Count   | 12        | 1.90E-01 | 9.60E-01 |
| ILMN_1741727 | GCTF         | 0.475237221 | INTERPRO               | <a href="#">Ras-GTPase</a>   | Count   | 12        | 2.70E-01 | 9.80E-01 |
| ILMN_1673804 | ZNF426       | 0.475200205 | INTERPRO               | <a href="#">Ras-small GTPase: Rab-type</a>                                     | Count   | 6         | 3.70E-01 | 9.90E-01 |
| ILMN_1811313 | SLT3         | 0.474998531 | INTERPRO               | <a href="#">Small GTP-binding protein</a>                                      | Count   | 13        | 4.10E-01 | 1.00E+00 |
| ILMN_1772276 | WHAMML2      | 0.47453312  | SMART                  | <a href="#">RAB</a>  | Count   | 6         | 5.20E-01 | 9.80E-01 |
| ILMN_1746695 | FLJ40330     | 0.474396092 | Enrichment Score: 1.28 |  | P_Value | Benjamini | Count    |          |
| ILMN_2329165 | MYO1C        | 0.474311428 | INTERPRO               | <a href="#">Calponin-like actin-binding</a>                                    | Count   | 12        | 4.50E-03 | 3.50E-01 |
| ILMN_1757074 | GNG10        | 0.474209124 | UP_SEQ_FEATURE         | <a href="#">domain:CH</a>  | Count   | 8         | 1.40E-02 | 6.80E-01 |
| ILMN_1778561 | WEE1         | 0.474073424 | SMART                  | <a href="#">Ct</a>   | Count   | 12        | 1.80E-02 | 4.50E-01 |
| ILMN_2232121 | GNP65        | 0.474050626 | INTERPRO               | <a href="#">SM22/calponin</a>  | Count   | 4         | 3.10E-02 | 6.20E-01 |
| ILMN_1786168 | LOC400464    | 0.474003733 | INTERPRO               | <a href="#">Calponin repeat</a>  | Count   | 3         | 5.30E-02 | 7.50E-01 |
| ILMN_1898771 | TCRA         | 0.473921428 | CD5_ONTOLGY            | <a href="#">Calmodulin</a>   | Count   | 5         | 5.10E-02 | 7.80E-01 |
| ILMN_1657129 | SKAP2        | 0.473882901 | UP_SEQ_FEATURE         | <a href="#">domain:CH 1</a>  | Count   | 4         | 2.30E-01 | 1.00E+00 |
| ILMN_1701558 | MAP1A        | 0.473642983 | UP_SEQ_FEATURE         | <a href="#">domain:CH 2</a>  | Count   | 4         | 2.30E-01 | 1.00E+00 |
| ILMN_1755758 | RIF1         | 0.473496302 | INTERPRO               | <a href="#">Actinin-type_actin-binding_conserved_site</a>                      | Count   | 3         | 4.50E-01 | 1.00E+00 |
| ILMN_2160476 | CLC12        | 0.473235333 | Enrichment Score: 1.21 |  | P_Value | Benjamini | Count    |          |
| ILMN_1763286 | HD           | 0.473216071 | UP_SEQ_FEATURE         | <a href="#">propeptide/removed in mature form</a>                              | Count   | 7         | 2.10E-03 | 2.70E-01 |
| ILMN_1730777 | HRT19        | 0.473257177 | UP_SEQ_FEATURE         | <a href="#">lipid moiety-binding region:GPI-anchor amidated serine</a>         | Count   | 7         | 1.20E-01 | 9.90E-01 |
| ILMN_1808405 | HLA-DQA1     | 0.473094491 | SP_PIR_KEYWORDS        | <a href="#">phosphatidylinositol linkage</a>                                   | Count   | 5         | 1.20E-01 | 4.80E-01 |
| ILMN_1708537 | RBP1         | 0.473003542 | SP_PIR_KEYWORDS        | <a href="#">ILMN1808487 PLA2G12B</a>   | Count   | 12        | 1.50E-01 | 5.50E-01 |
| ILMN_2267783 | CIUB87675    | 0.472629627 | GOTERM_CC_FAT          | <a href="#">anchored to membrane</a>   | Count   | 20        | 1.90E-01 | 7.90E-01 |
| ILMN_1654560 | TR11         | 0.472627774 | Enrichment Score: 1.2  |  | P_Value | Benjamini | Count    |          |
| ILMN_1661737 | FDP1         | 0.472626305 | GOTERM_BP_FAT          | <a href="#">positive regulation of myeloid cell differentiation</a>            | Count   | 9         | 1.50E-03 | 4.80E-02 |
| ILMN_2404063 | APP          | 0.471859854 | GOTERM_BP_FAT          | <a href="#">regulation of myeloid cell differentiation</a>                     | Count   | 11        | 2.10E-02 | 3.20E-01 |
| ILMN_1792587 | VP54B        | 0.471590366 | GOTERM_BP_FAT          | <a href="#">positive regulation of erythrocyte differentiation</a>             | Count   | 4         | 3.60E-02 | 4.30E-01 |
| ILMN_1673757 | CASP8        | 0.471529578 | GOTERM_BP_FAT          | <a href="#">negative regulation of granulocyte differentiation</a>             | Count   | 3         | 4.10E-02 | 4.70E-01 |

|              |          |              |  |  |  |  |  |  |
|--------------|----------|--------------|--|--|--|--|--|--|
| ILMN_1861414 | BF593077 | -0.450741044 |  |  |  |  |  |  |
| ILMN_1827736 | PKD3     | -0.450796268 |  |  |  |  |  |  |
| ILMN_2247458 | HPP47    | -0.450913097 |  |  |  |  |  |  |
| ILMN_1901774 | BF531380 | -0.450910279 |  |  |  |  |  |  |
| ILMN_1657010 | FAM90A12 | -0.451001404 |  |  |  |  |  |  |
| ILMN_1797794 | AK126307 | -0.45100599  |  |  |  |  |  |  |
| ILMN_1860789 | BM974067 | -0.451014585 |  |  |  |  |  |  |



|              |          |             |                        |  |          |          |           |
|--------------|----------|-------------|------------------------|--|----------|----------|-----------|
| ILMN_3309021 | MIR142   | 0.471396045 | GOTERM_BP_FAT          | <a href="#">regulation of granulocyte differentiation</a>                      | 3        | 7.90E-02 | 6.40E-01  |
| ILMN_1791483 | PDE4D    | 0.471165152 | GOTERM_BP_FAT          | <a href="#">negative regulation of myeloid leukocyte differentiation</a>       | 4        | 1.10E-01 | 7.20E-01  |
| ILMN_2318455 | C2orf64  | 0.470851841 | GOTERM_BP_FAT          | <a href="#">positive regulation of myeloid leukocyte differentiation</a>       | 4        | 1.20E-01 | 7.50E-01  |
| ILMN_1769702 | GPRA1    | 0.470819971 | GOTERM_BP_FAT          | <a href="#">regulation of erythrocyte differentiation</a>                      | 4        | 1.20E-01 | 7.50E-01  |
| ILMN_2136133 | PABPC1   | 0.470772137 | GOTERM_BP_FAT          | <a href="#">negative regulation of myeloid cell differentiation</a>            | 5        | 1.50E-01 | 7.90E-01  |
| ILMN_2321578 | P2RY10   | 0.470628219 | GOTERM_BP_FAT          | <a href="#">regulation of myeloid leukocyte differentiation</a>                | 6        | 1.50E-01 | 7.90E-01  |
| ILMN_1860540 | AA709087 | 0.470532362 | GOTERM_BP_FAT          | <a href="#">regulation of osteoclast differentiation</a>                       | 3        | 4.50E-01 | 8.90E-01  |
| ILMN_3220952 | ANKRD36  | 0.470495107 | Enrichment Score: 1.14 |  | Count    | P_Value  | Benjamini |
| ILMN_1661454 | ILMN1    | 0.470365666 | UP_SEQ_FEATURE         | repeat:LRR 11  | 14       | 1.0E-02  | 6.40E-01  |
| ILMN_2331087 | MSA47    | 0.470165988 | INTERPRO               | <a href="#">Cysteine-rich flanking region, C-terminal</a>                      | 13       | 1.20E-02 | 4.60E-01  |
| ILMN_3176090 | RCC2     | 0.470072646 | UP_SEQ_FEATURE         | repeat:LRR 10  | 15       | 1.40E-02 | 6.80E-01  |
| ILMN_1796712 | S100A10  | 0.470064857 | UP_SEQ_FEATURE         | repeat:LRR 5   | 24       | 1.70E-02 | 7.30E-01  |
| ILMN_1657836 | PLEKHG2  | 0.469996733 | UP_SEQ_FEATURE         | repeat:LRR 9   | 14       | 2.00E-02 | 7.50E-01  |
| ILMN_2353901 | HAVCR1   | 0.469865103 | UP_SEQ_FEATURE         | repeat:LRR 6   | 22       | 2.10E-02 | 7.40E-01  |
| ILMN_3247494 | SNORA36B | 0.469639955 | UP_SEQ_FEATURE         | repeat:LRR 8   | 17       | 2.30E-02 | 7.60E-01  |
| ILMN_1684836 | AKAP12   | 0.469105751 | UP_SEQ_FEATURE         | repeat:LRR 7   | 19       | 2.70E-02 | 8.00E-01  |
| ILMN_2348905 | CTLA4    | 0.469093267 | INTERPRO               | <a href="#">Leucine-rich repeat</a>  | 22       | 3.80E-02 | 6.60E-01  |
| ILMN_1785846 | PMP22    | 0.469023995 | SMART                  | SMART  | 13       | 3.90E-02 | 6.20E-01  |
| ILMN_2351795 | CLCA4F1  | 0.468997397 | UP_SEQ_FEATURE         | repeat:LRR 4   | 24       | 4.10E-02 | 8.90E-01  |
| ILMN_1707700 | PCOLCE   | 0.468964933 | INTERPRO               | <a href="#">Leucine-rich repeat, tyrosyl subtype</a>                           | 15       | 4.60E-02 | 7.20E-01  |
| ILMN_2360448 | TAF1A    | 0.468931035 | UP_SEQ_FEATURE         | repeat:LRR 12  | 11       | 5.50E-02 | 9.40E-01  |
| ILMN_1709747 | EXOC     | 0.468906314 | INTERPRO               | <a href="#">Leucine-rich repeat, cysteine-rich flanking region, N-terminal</a> | 12       | 5.70E-02 | 7.70E-01  |
| ILMN_1652787 | PRKAP1   | 0.468888644 | SMART                  | SMART  | 15       | 5.40E-01 | 8.10E-01  |
| ILMN_1780898 | PRKCH    | 0.468726858 | SMART                  | SMART  | 12       | 1.50E-01 | 8.10E-01  |
| ILMN_1898518 | GRFAL    | 0.468572614 | UP_SEQ_FEATURE         | repeat:LRR 14  | 7        | 1.70E-01 | 1.00E+00  |
| ILMN_1809889 | CDC117   | 0.468515555 | UP_SEQ_FEATURE         | repeat:LRR 3   | 24       | 1.70E-01 | 1.00E+00  |
| ILMN_1754279 | FBXW7    | 0.468486392 | UP_SEQ_FEATURE         | repeat:LRR 1   | 25       | 1.80E-01 | 1.00E+00  |
| ILMN_1712112 | PCAN1    | 0.468451597 | UP_SEQ_FEATURE         | repeat:LRR 2   | 25       | 1.90E-01 | 1.00E+00  |
| ILMN_1680453 | TMC2C    | 0.468073991 | UP_SEQ_FEATURE         | repeat:LRR 13  | 8        | 1.00E-01 | 1.00E+00  |
| ILMN_1803686 | ADA      | 0.467907507 | SP_PIR_KEYWORDS        | <a href="#">Leucine-rich repeat</a>  | 25       | 1.90E-01 | 6.20E-01  |
| ILMN_3247893 | FBA1     | 0.467696547 | UP_SEQ_FEATURE         | repeat:LRR 15  | 5        | 3.90E-01 | 1.00E+00  |
| ILMN_1796738 | SPAST    | 0.467505404 | UP_SEQ_FEATURE         | repeat:LRR 18  | 4        | 5.10E-01 | 1.00E+00  |
| ILMN_1815656 | SERP1C   | 0.467409139 | UP_SEQ_FEATURE         | repeat:LRR 16  | 4        | 5.30E-01 | 1.00E+00  |
| ILMN_1706935 | CDC316   | 0.467373843 | UP_SEQ_FEATURE         | repeat:LRR 17  | 3        | 6.80E-01 | 1.00E+00  |
| ILMN_3242485 | TUJ2     | 0.467235007 | Enrichment Score: 1.13 |  | Count    | P_Value  | Benjamini |
| ILMN_3242067 | SNORA58  | 0.466849041 | GOTERM_BP_FAT          | <a href="#">regulation of organelle organization</a>                           | 25       | 1.50E-02 | 2.60E-01  |
| ILMN_1696243 | FLJ23152 | 0.466774251 | GOTERM_BP_FAT          | <a href="#">negative regulation of cellular component organization</a>         | 18       | 1.80E-02 | 2.90E-01  |
| ILMN_1805993 | GMP      | 0.466745036 | GOTERM_BP_FAT          | <a href="#">regulation of cellular component biosynthesis</a>                  | 17       | 3.60E-02 | 4.30E-01  |
| ILMN_1802456 | ACT1     | 0.466443135 | INTERPRO               | <a href="#">Thymosin beta-4, cytosolic</a>                                     | 3        | 3.70E-02 | 6.10E-01  |
| ILMN_1751034 | ITPRP12  | 0.466403331 | INTERPRO               | <a href="#">Thymosin beta-4</a>  | 3        | 3.70E-02 | 6.60E-01  |
| ILMN_1663618 | STAT3    | 0.466012799 | GOTERM_BP_FAT          | <a href="#">regulation of actin cytoskeleton organization</a>                  | 12       | 4.20E-02 | 4.70E-01  |
| ILMN_1864900 | MIAT     | 0.465927198 | GOTERM_BP_FAT          | <a href="#">regulation of protein complex assembly</a>                         | 12       | 4.50E-02 | 4.80E-01  |
| ILMN_1692398 | CNTNAP1  | 0.465412821 | PIRSF01828             | <a href="#">Thymosin_beta_4</a>  | 3        | 4.80E-02 | 9.50E-01  |
| ILMN_1748488 | TNXL4B   | 0.464957922 | SMART                  | THY  | 8        | 5.20E-02 | 6.20E-01  |
| ILMN_1714600 | NAV3     | 0.464963619 | GOTERM_BP_FAT          | <a href="#">regulation of actin filament-based process</a>                     | 12       | 5.20E-02 | 5.20E-01  |
| ILMN_3245764 | SNORA39  | 0.464882387 | GOTERM_BP_FAT          | <a href="#">negative regulation of organelle organization</a>                  | 11       | 5.50E-02 | 5.40E-01  |
| ILMN_1746565 | ITGB6    | 0.464796084 | GOTERM_BP_FAT          | <a href="#">sequestration of actin monomers</a>                                | 3        | 5.90E-02 | 5.60E-01  |
| ILMN_1789846 | FGBB     | 0.464763999 | GOTERM_BP_FAT          | 15   | 6.80E-02 | 6.60E-01 |           |
| ILMN_1916931 | PAD92585 | 0.464689473 | GOTERM_BP_FAT          | <a href="#">regulation of actin polymerization or depolymerization</a>         | 15       | 8.30E-01 | 7.50E-01  |
| ILMN_2390299 | PSM88    | 0.464119051 | GOTERM_BP_FAT          | <a href="#">regulation of actin filament length</a>                            | 8        | 1.40E-01 | 7.80E-01  |
| ILMN_1806782 | ZNF235   | 0.464072555 | GOTERM_BP_FAT          | <a href="#">regulation of actin filament polymerization</a>                    | 7        | 1.70E-01 | 8.20E-01  |
| ILMN_1679809 | GSTP1    | 0.463943885 | GOTERM_BP_FAT          | <a href="#">negative regulation of cytoskeleton organization</a>               | 7        | 1.80E-01 | 8.30E-01  |
| ILMN_1754249 | TARP     | 0.463843415 | GOTERM_BP_FAT          | <a href="#">regulation of protein polymerization</a>                           | 7        | 1.90E-01 | 8.40E-01  |
| ILMN_1713384 | SH2C1    | 0.463581258 | GOTERM_BP_FAT          | <a href="#">negative regulation of protein complex assembly</a>                | 6        | 2.10E-01 | 8.60E-01  |
| ILMN_1763842 | PRR11    | 0.463432626 | GOTERM_BP_FAT          | <a href="#">negative regulation of actin filament polymerization</a>           | 4        | 3.00E-01 | 9.30E-01  |
| ILMN_1657421 | YWHAE    | 0.463282516 | GOTERM_BP_FAT          | <a href="#">negative regulation of protein polymerization</a>                  | 4        | 3.20E-01 | 9.40E-01  |
| ILMN_1786357 | ARA1     | 0.463051253 | Enrichment Score: 1.11 |  | Count    | P_Value  | Benjamini |
| ILMN_1725206 | SMN1     | 0.462959453 | GOTERM_BP_FAT          | <a href="#">myeloid cell activation during immune response</a>                 | 6        | 6.20E-03 | 1.40E-01  |
| ILMN_1673727 | TRT1     | 0.462891734 | GOTERM_BP_FAT          | <a href="#">myeloid leukocyte mediated immunity</a>                            | 4        | 8.30E-01 | 7.74E-01  |
| ILMN_1786015 | CTCF     | 0.462699708 | GOTERM_BP_FAT          | <a href="#">leukocyte degranulation</a>  | 3        | 2.00E-01 | 8.60E-01  |
| ILMN_2313901 | PAM      | 0.462476555 | GOTERM_BP_FAT          | <a href="#">regulated secretory pathway</a>                                    | 3        | 3.60E-01 | 9.50E-01  |
| ILMN_1784320 | ELMO1    | 0.462362328 | Enrichment Score: 1.11 |  | Count    | P_Value  | Benjamini |
| ILMN_1732885 | SX4      | 0.462273136 | GOTERM_BP_FAT          | <a href="#">cytosolic motor activity</a>                                       | 10       | 9.50E-03 | 2.30E-01  |
| ILMN_1673727 | TRT1     | 0.462230401 | UP_SEQ_FEATURE         | short sequence motif: fib 1 motif  | 4        | 1.80E-01 | 1.00E+00  |
| ILMN_1779147 | ENCL1    | 0.46219442  | UP_SEQ_FEATURE         | short sequence motif: WSWWS motif  | 4        | 2.70E-01 | 1.00E+00  |
| ILMN_2140059 | LAMA4    | 0.461901018 | Enrichment Score: 1.09 |  | Count    | P_Value  | Benjamini |
| ILMN_1705750 | TGM2     | 0.461865708 | GOTERM_BP_FAT          | <a href="#">JAK-STAT cascade</a>   | 8        | 1.60E-02 | 2.70E-01  |
| ILMN_2399558 | SFRS18   | 0.461553932 | INTERPRO               | <a href="#">STAT transcription factor, all alpha</a>                           | 3        | 7.20E-02 | 8.00E-01  |
| ILMN_1767349 | ABCA4    | 0.461513825 | INTERPRO               | <a href="#">STAT transcription factor, DNA-binding</a>                         | 3        | 7.20E-02 | 8.00E-01  |
| ILMN_1775073 | ZNF273   | 0.461271332 | INTERPRO               | <a href="#">STAT transcription factor, protein interaction</a>                 | 3        | 7.20E-02 | 8.00E-01  |
| ILMN_1777190 | CFD      | 0.461258106 | INTERPRO               | <a href="#">STAT transcription factor, core</a>                                | 3        | 7.20E-02 | 8.00E-01  |
| ILMN_1809484 | TMO03    | 0.461247894 | INTERPRO               | <a href="#">STAT transcription factor, DNA-binding, subdomain</a>              | 3        | 7.20E-02 | 8.00E-01  |
| ILMN_2188264 | CYR61    | 0.461218262 | PIRSF01568             | <a href="#">signal transducer and transcription activator</a>                  | 3        | 9.10E-02 | 9.70E-01  |
| ILMN_1740466 | FAM46A   | 0.461145433 | Enrichment Score: 1.09 |  | Count    | P_Value  | Benjamini |
| ILMN_1653514 | RBBP4    | 0.461074783 | Enrichment Score: 1.09 |  | Count    | P_Value  | Benjamini |
| ILMN_1832656 | AWS78902 | 0.460798661 | GOTERM_BP_FAT          | <a href="#">leukocyte migration</a>  | 9        | 4.10E-02 | 4.60E-01  |
| ILMN_2196337 | CL21A011 | 0.460639796 | GOTERM_BP_FAT          | <a href="#">leukocyte chemotaxis</a>   | 3        | 7.90E-02 | 6.40E-01  |
| ILMN_2386849 | DSE      | 0.460637309 | GOTERM_BP_FAT          | <a href="#">leukocyte chemotaxis</a>   | 6        | 1.10E-01 | 7.20E-01  |
| ILMN_1814789 | UBAP2L   | 0.460294121 | GOTERM_BP_FAT          | <a href="#">cell chemotaxis</a>  | 6        | 1.30E-01 | 7.60E-01  |
| ILMN_2194577 | PLVAP    | 0.460281384 | Enrichment Score: 1.06 |  | Count    | P_Value  | Benjamini |
| ILMN_1741003 | ANKX5    | 0.460209295 | BIOCARTA               | <a href="#">IL_12 Signaling Pathway</a>  | 7        | 6.20E-03 | 2.10E-01  |
| ILMN_1808707 | F508L1   | 0.46013337  | Enrichment Score: 1.06 |  | Count    | P_Value  | Benjamini |
| ILMN_1730940 | HLIDC3   | 0.460024764 | Enrichment Score: 1.06 |  | Count    | P_Value  | Benjamini |
| ILMN_1656951 | APC0D1   | 0.459955462 | Enrichment Score: 1.06 |  | Count    | P_Value  | Benjamini |
| ILMN_2170814 | LAMP3    | 0.459909732 | INTERPRO               | <a href="#">Link</a>   | 4        | 5.90E-02 | 7.70E-01  |
| ILMN_3294414 | HA       | 0.459892135 | SMART                  | <a href="#">Link</a>   | 4        | 9.00E-02 | 7.00E-01  |
| ILMN_2286568 | ANKRD36  | 0.459861123 | INTERPRO               | <a href="#">C-type lectin-like</a>   | 11       | 8.00E-02 | 8.50E-01  |
| ILMN_1685202 | NBB2     | 0.459523259 | GOTERM_MF_FAT          | <a href="#">thymosin acid binding</a>  | 4        | 1.30E-01 | 8.20E-01  |
| ILMN_1814895 | POLM7    | 0.459433306 | Enrichment Score: 1.05 |  | Count    | P_Value  | Benjamini |
| ILMN_1757646 | UFM1     | 0.459334629 | GOTERM_BP_FAT          | <a href="#">integrin-mediated signaling pathway</a>                            | 13       | 2.80E-03 | 7.90E-02  |
| ILMN_1910180 | AKO24680 | 0.459313464 | GOTERM_CC_FAT          | <a href="#">integrin complex</a>   | 7        | 3.30E-02 | 1.90E-01  |
| ILMN_1803937 | CR3D671  | 0.458971842 | INTERPRO               | <a href="#">Zinc finger, homeobox/interdigitin</a>                             | 8        | 2.50E-02 | 8.60E-01  |
| ILMN_1684836 | S100A4   | 0.458842014 | Enrichment Score: 1.05 |  | Count    | P_Value  | Benjamini |
| ILMN_1740015 | CD14     | 0.458804422 | SMART                  | <a href="#">Integrin</a>   | 7        | 3.80E-02 | 2.20E-01  |
| ILMN_1655625 | GPATCH1  | 0.458604763 | INTERPRO               | <a href="#">Psi</a>  | 8        | 5.70E-02 | 6.40E-01  |
| ILMN_1749387 | TRPM2    | 0.458595151 | UP_SEQ_FEATURE         | <a href="#">integrin beta subunit, subregion</a>                               | 3        | 7.20E-02 | 8.00E-01  |
| ILMN_1800276 | RGN1     | 0.458526824 | PIRSF00525             | <a href="#">domain: WWFA</a>   | 8        | 8.80E-02 | 8.80E-01  |
| ILMN_2163871 | FNDC1    | 0.458298103 | PIRSF00525             | <a href="#">PIRSF00525: Integrin_B</a>   | 3        | 9.10E-02 | 9.70E-01  |
| ILMN_2370336 | MS4AAA   | 0.458186683 | INTERPRO               | <a href="#">PIRSF00525: Integrin_beta_subunit</a>                              | 3        | 9.10E-02 | 8.50E-01  |
| ILMN_1805750 | IFITM3   | 0.457809342 | UP_SEQ_FEATURE         | <a href="#">region of interest: Cysteine-rich tandem repeats</a>               | 3        | 1.00E-01 | 9.90E-01  |
| ILMN_2154950 | ZNF423   | 0.457682544 | INTERPRO               | <a href="#">integrin beta subunit, C-terminal</a>                              | 3        | 1.10E-01 | 8.90E-01  |

|              |               |              |                        |  |       |         |           |
|--------------|---------------|--------------|------------------------|--|-------|---------|-----------|
| ILMN_3237241 | FAM32A        | -0.458991045 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1664993 | SLX1B-SULT1A4 | -0.459082102 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1706441 | UPR1B         | -0.459136745 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1764175 | GP31          | -0.459352393 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1803218 | GRP139        | -0.459376636 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_3238143 | D2HGDH        | -0.459406668 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_3235584 | TRIM66        | -0.459694136 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1729650 | PKTX          | -0.459720821 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_4739303 | CACNA8        | -0.459789694 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1783835 | ZNF845        | -0.459836979 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2134039 | ACN9          | -0.46002319  | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1712999 | MGAM          | -0.460039898 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1804090 | SIL2SA10      | -0.460119625 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1702218 | POU1          | -0.460170057 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1905072 | CX78427       | -0.460261093 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_3226405 | PRAMEF11      | -0.46040765  | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1701507 | EHHADH        | -0.460466999 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2381959 | PAHA2         | -0.460477882 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2025550 | NDFAF4        | -0.460488426 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1733390 | LARP18        | -0.460626277 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2393968 | SYN1          | -0.460704607 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2320579 | RABGEF1       | -0.460812725 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1885917 | EMCN          | -0.460818784 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1796749 | KIEFC         | -0.460834566 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2195721 | KRTAP21-1     | -0.461018972 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2224333 | C3orf65       | -0.461713105 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1737240 | AKTIP         | -0.461812646 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_1730119 | HMK2          | -0.461886876 | Enrichment Score: 1.05 |  | Count | P_Value | Benjamini |
| ILMN_2027004 | EPF           | -0.461957892 | En                     |  |       |         |           |

|              |                |             |                        |  |    |          |          |
|--------------|----------------|-------------|------------------------|--|----|----------|----------|
| ILMN_178886  | TOX            | 0.457599277 | INTERPRO               | <a href="#">Integrin beta subunit</a>  | 3  | 1.10E-01 | 8.90E-01 |
| ILMN_171707  | MMP25          | 0.457535427 | INTERPRO               | <a href="#">fGc_receptorIIa</a>  | 8  | 1.10E-01 | 8.90E-01 |
| ILMN_2137084 | LHP            | 0.457451571 | SMART                  | <a href="#">TIR</a>  | 3  | 1.20E-01 | 7.90E-01 |
| ILMN_169921  | STAT2          | 0.457411543 | UP_SEQ_FEATURE         | <a href="#">repeatIII</a>  | 3  | 4.90E-01 | 1.00E+00 |
| ILMN_1745963 | FOLR2          | 0.457300409 | UP_SEQ_FEATURE         | <a href="#">repeatIV</a>   | 3  | 4.90E-01 | 1.00E+00 |
| ILMN_1723042 | CLDN3          | 0.457295007 | UP_SEQ_FEATURE         | <a href="#">repeatI</a>  | 3  | 4.90E-01 | 1.00E+00 |
| ILMN_2326021 | ANKRD36        | 0.457293548 | UP_SEQ_FEATURE         | <a href="#">repeatII</a>   | 3  | 4.90E-01 | 1.00E+00 |
| ILMN_1682928 | CPVL           | 0.457155899 | Enrichment Score: 1.04 | Count  | 58 | 6.00E-02 | 5.30E-01 |
| ILMN_1770585 | ITG2           | 0.457115098 | GOTERM_CC_FAT          | <a href="#">veicle</a>   | 55 | 7.60E-02 | 5.90E-01 |
| ILMN_1780268 | Clorf56        | 0.456978832 | GOTERM_CC_FAT          | <a href="#">cytoplasmic veicle</a>   | 48 | 1.10E-01 | 6.40E-01 |
| ILMN_2366041 | ITM2C          | 0.456972153 | GOTERM_CC_FAT          | <a href="#">membrane-bounded veicle</a>                                      | 46 | 1.40E-01 | 6.80E-01 |
| ILMN_1775004 | KCNQ3          | 0.456849586 | GOTERM_CC_FAT          | <a href="#">cytoplasmic membrane-bounded veicle</a>                          | 4  | 1.20E-01 | 7.50E-01 |
| ILMN_1688004 | THRF5F12A      | 0.456810235 | Enrichment Score: 1.03 | Count  | 8  | 1.00E-02 | 2.10E-01 |
| ILMN_1750153 | OR52A1         | 0.456795181 | GOTERM_BP_FAT          | <a href="#">regulation of alpha-beta T cell activation</a>                   | 6  | 3.00E-02 | 4.00E-01 |
| ILMN_2062524 | RBBP4          | 0.456639033 | GOTERM_BP_FAT          | <a href="#">positive regulation of alpha-beta T cell activation</a>          | 4  | 5.60E-02 | 5.40E-01 |
| ILMN_1778723 | AMICA1         | 0.456525593 | GOTERM_BP_FAT          | <a href="#">regulation of alpha-beta T cell proliferation</a>                | 3  | 1.20E-01 | 7.50E-01 |
| ILMN_2226304 | ANKRD50        | 0.45628001  | GOTERM_BP_FAT          | <a href="#">regulation of alpha-beta T cell differentiation</a>              | 3  | 2.80E-01 | 9.20E-01 |
| ILMN_1651826 | SASP1          | 0.456137482 | GOTERM_BP_FAT          | <a href="#">regulation of CD8-positive alpha-beta T cell differentiation</a> | 3  | 4.10E-01 | 9.70E-01 |
| ILMN_1682761 | CLTFR4         | 0.456001899 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1745583 | EYX1           | 0.455768392 | Enrichment Score: 1.03 | Count  | 8  | 3.00E-02 | 4.00E-01 |
| ILMN_1803988 | MCL1           | 0.455720645 | GOTERM_BP_FAT          | <a href="#">lymphocyte proliferation</a>                                     | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_2143485 | CLDN7          | 0.455662819 | GOTERM_BP_FAT          | <a href="#">hematopoietic cell proliferation</a>                             | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1748812 | TMEM130        | 0.455265602 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 6  | 9.00E-01 | 1.00E+00 |
| ILMN_1672834 | SH2            | 0.455165574 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 4.00E-01 | 1.00E+00 |
| ILMN_1715625 | C20orf94       | 0.45494532  | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1673543 | PGM2           | 0.454649266 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1725090 | CTHRC1         | 0.454547879 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2101278 | PGS1B          | 0.454540448 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_2141482 | SERPINC1       | 0.454440109 | Enrichment Score: 1.03 | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1781816 | AV723037       | 0.454308945 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1719905 | TLR10          | 0.454067984 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2137312 | KCNV5          | 0.454004146 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1706455 | TICS           | 0.453854886 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1670130 | AHD3A          | 0.453646396 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1755942 | O3FAR1         | 0.453635652 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1673023 | EP400          | 0.453546111 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1740903 | C7orf49        | 0.453471469 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1800956 | ATAD5          | 0.453339428 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1815552 | OLIG1 and IIG2 | 0.453098728 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1727917 | FAM26E         | 0.452860364 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1757019 | NTN4           | 0.452738855 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1755589 | DIP2B          | 0.452680461 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1905565 | CNKL1          | 0.452676977 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1699348 | MS4AE          | 0.452426636 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_2261600 | FCGR1B         | 0.452373964 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2257015 | AGER           | 0.452369798 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1715947 | HNRNP4A        | 0.452302743 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2059744 | IL2            | 0.452259998 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1911042 | PRKAZ2         | 0.452033462 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1735467 | NPIP2          | 0.452095592 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1793517 | RASAL1         | 0.452059448 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1769282 | FRMD6          | 0.451980801 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1806230 | PRFPR1         | 0.451812455 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1771057 | LAB2           | 0.451733153 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1790162 | ZC3H11A        | 0.451485196 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1671114 | ZNF865         | 0.451440317 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1708375 | IRF1           | 0.451382231 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_2328803 | RASAL3         | 0.451260258 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1901381 | MAG1           | 0.451234636 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1698444 | CFH            | 0.451194786 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1742001 | CD160          | 0.451060476 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1654571 | FCOH1          | 0.450815006 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1786197 | NDR1           | 0.450661682 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1744822 | BECN1          | 0.450345375 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1715639 | FLJ00310       | 0.45030731  | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_2094396 | LRR8C          | 0.450234879 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1801130 | STOML1         | 0.4500943   | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1715700 | HJAT           | 0.450065684 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2167416 | MRI1           | 0.450000896 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1799208 | CSGALNACT2     | 0.44978829  | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_3287952 | CDC27          | 0.449704602 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1678841 | UBD            | 0.44958398  | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1807277 | IR19           | 0.449577291 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2373821 | BTNGA3         | 0.449404235 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1665219 | LTBP4          | 0.449341699 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_3231881 | PTMA           | 0.449308018 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1666444 | RBM51          | 0.449302623 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_2346292 | RPL23A         | 0.449297272 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1791478 | MIFN           | 0.449296022 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1686388 | TPM3           | 0.448991138 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2244009 | LBH            | 0.448751199 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2337923 | TPD52L1        | 0.448593361 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1769229 | SCL2A1         | 0.447954958 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2092850 | HSE            | 0.447871525 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1677581 | RPGRIP1L       | 0.447862061 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1702301 | DOCK10         | 0.447692744 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1725427 | B2M            | 0.447573103 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1748290 | FAM175A        | 0.447540675 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2391150 | FLJ9141        | 0.447500883 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1803036 | TARBP1         | 0.447318586 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1815261 | PDIA4          | 0.447277622 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1772189 | ABCD1          | 0.447061328 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1800261 | TUBA1B         | 0.446650708 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_2348176 | C2CD4D         | 0.446650625 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1736700 | ALDOA          | 0.44662908  | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1783606 | MLL5           | 0.446478136 | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1652825 | IL10RA         | 0.446368695 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                              | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2089140 | FAM137B        | 0.446333669 | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                          | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1657683 | CLTFR2         | 0.446192535 | GOTERM_BP_FAT          | Count  | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_2347234 | PRMT1          | 0.446104955 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                               | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_1657627 | CBFA2T3        | 0.445938061 | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                                      | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2371685 | UBE2E1         | 0.445932641 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>   | 3  | 5.40E-01 | 9.90E-01 |

|              |           |              |                        |   |    |          |          |
|--------------|-----------|--------------|------------------------|---|----|----------|----------|
| ILMN_1685886 | MAPK4     | 0.47186298   | Enrichment Score: 1.04 | Count   | 58 | 6.00E-02 | 5.30E-01 |
| ILMN_3278903 | LOC644189 | -0.471904248 | GOTERM_BP_FAT          | <a href="#">cytoplasmic veicle</a>                                  | 48 | 1.10E-01 | 6.40E-01 |
| ILMN_1801400 | OR5D314   | -0.471916863 | GOTERM_BP_FAT          | <a href="#">membrane-bounded veicle</a>                             | 46 | 1.40E-01 | 6.80E-01 |
| ILMN_1667018 | ACE2      | -0.472008069 | GOTERM_BP_FAT          | <a href="#">cytoplasmic membrane-bounded veicle</a>                 | 4  | 1.20E-01 | 7.50E-01 |
| ILMN_1814333 | SERPIN1   | -0.472026311 | Enrichment Score: 1.03 | Count   | 8  | 1.00E-02 | 2.10E-01 |
| ILMN_1795304 | CLRF2     | -0.472077862 | GOTERM_BP_FAT          | <a href="#">regulation of alpha-beta T cell activation</a>          | 6  | 3.00E-02 | 4.00E-01 |
| ILMN_1753745 | HDDC2     | -0.472131    | GOTERM_BP_FAT          | <a href="#">positive regulation of alpha-beta T cell activation</a> | 4  | 5.60E-02 | 5.40E-01 |
| ILMN_1775742 | RNF128    | -0.472167675 | GOTERM_BP_FAT          | <a href="#">regulation of alpha-beta T cell proliferation</a>       | 3  | 1.20E-01 | 7.50E-01 |
| ILMN_1788332 | MTR       | -0.472272619 | GOTERM_BP_FAT          | <a href="#">regulation of alpha-beta T cell differentiation</a>     | 3  | 2.80E-01 | 9.20E-01 |
| ILMN_1694975 | GADD45A   | -0.472306322 | Enrichment Score: 1.03 | Count   | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_2181064 | GBA3      | -0.472319443 | GOTERM_BP_FAT          | <a href="#">lymphocyte proliferation</a>                            | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1735942 | LOC729970 | -0.472380253 | GOTERM_BP_FAT          | <a href="#">hematopoietic cell proliferation</a>                    | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_2142117 | LYPLAL1   | -0.472387677 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                      | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_3005942 | LOC729970 | -0.47245771  | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                             | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1717935 | SFTA1     | -0.472532677 | GOTERM_BP_FAT          | <a href="#">B cell proliferation</a>                                | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1772369 | PDHA1     | -0.47281696  | GOTERM_BP_FAT          | <a href="#">T cell proliferation</a>                                | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_2141118 | C15orf59  | -0.472931317 | GOTERM_BP_FAT          | <a href="#">regulation of DNA recombination</a>                     | 3  | 5.40E-01 | 9.90E-01 |
| ILMN_1735192 | COLEC11   | -0.47296937  | GOTERM_BP_FAT          | <a href="#">regulation of DNA metabolic process</a>                 | 3  | 6.00E-01 | 1.00E+00 |
| ILMN_1724658 | BNIP3     | -0.473087529 | GOTERM_BP_FAT          | Count   | 8  | 2.40E-02 | 3.50E-01 |
| ILMN_1674104 | S100A7L2  | -0.473170983 | GOTERM_BP_FAT          | <a href="#">mononuclear cell proliferation</a>                      | 5  | 1.10E-01 | 7.30E-01 |
| ILMN_2178116 | MMP20     | -0.47324418  | GOTERM_BP_FAT          | <a href="#">leukocyte proliferation</a>                             | 3  | 5.40E-01 | 9.90E    |

|              |           |             |
|--------------|-----------|-------------|
| ILMN_1706268 | PTGDR     | 0.445743173 |
| ILMN_1232673 | MSL2      | 0.445628891 |
| ILMN_1237883 | LUX4      | 0.445628691 |
| ILMN_1778630 | PYGB      | 0.445612914 |
| ILMN_1756204 | RPS6KA4   | 0.445574738 |
| ILMN_1704294 | CDH3      | 0.445524382 |
| ILMN_1656291 | TSKS      | 0.445412864 |
| ILMN_1706870 | CAPZA2    | 0.445310708 |
| ILMN_1755415 | SAMD3     | 0.445110312 |
| ILMN_1746408 | MIDN      | 0.445104553 |
| ILMN_2173004 | RAB8B     | 0.444895187 |
| ILMN_2278636 | CLUX1     | 0.444756064 |
| ILMN_2453553 | LST1      | 0.444655906 |
| ILMN_1763260 | HFE1A     | 0.444655587 |
| ILMN_1782977 | UBAS2     | 0.44439838  |
| ILMN_2313158 | MBNL1     | 0.444269661 |
| ILMN_1760360 | LTN1      | 0.444234099 |
| ILMN_2098616 | CCorf99   | 0.444213151 |
| ILMN_1767320 | MMPK1     | 0.444177474 |
| ILMN_1863308 | CV575492  | 0.443827134 |
| ILMN_1652412 | PHKB      | 0.443748828 |
| ILMN_3289508 | CR6D4709  | 0.443649544 |
| ILMN_1886097 | TOP2A     | 0.443524833 |
| ILMN_1733511 | COL3A3    | 0.443320372 |
| ILMN_2386008 | MPZL1     | 0.443253764 |
| ILMN_1694913 | LMO3      | 0.442734263 |
| ILMN_1778064 | FICD      | 0.442714305 |
| ILMN_2322177 | ACTN1     | 0.442626922 |
| ILMN_1811851 | PRKX1     | 0.442561044 |
| ILMN_1740298 | SGLEC5    | 0.442313042 |
| ILMN_1778144 | SILC4B1   | 0.442252615 |
| ILMN_2383964 | CDC4A     | 0.4420507   |
| ILMN_2402341 | MMPK3     | 0.442012153 |
| ILMN_1755173 | ELEK4A4   | 0.441991209 |
| ILMN_2342579 | IL7R      | 0.441898579 |
| ILMN_1724059 | GAS2L1    | 0.441891191 |
| ILMN_2077758 | CTDSP2    | 0.441825246 |
| ILMN_1711792 | GRBP1     | 0.441538966 |
| ILMN_1829845 | HA        | 0.441363733 |
| ILMN_1715508 | NNMT      | 0.441034435 |
| ILMN_1759154 | PABPN1    | 0.44088579  |
| ILMN_2114720 | SLP1      | 0.44088117  |
| ILMN_1700081 | FST       | 0.440882429 |
| ILMN_1728677 | CREB5     | 0.440552315 |
| ILMN_1847308 | FAM168A   | 0.440511603 |
| ILMN_2066849 | FAM26F    | 0.440508234 |
| ILMN_1697024 | STYX      | 0.440412277 |
| ILMN_2325514 | GPR183    | 0.440395974 |
| ILMN_1676123 | SRP2      | 0.440355745 |
| ILMN_1697370 | CTSL1     | 0.440232176 |
| ILMN_1652313 | RNF215    | 0.440217218 |
| ILMN_2106331 | H3F3A     | 0.440056216 |
| ILMN_1856670 | HLA-G     | 0.440031333 |
| ILMN_2058782 | IT2T      | 0.43993911  |
| ILMN_3241213 | FLJ00326  | 0.439881822 |
| ILMN_1681160 | CCT6P1    | 0.439874046 |
| ILMN_2151277 | LPGAT1    | 0.439852291 |
| ILMN_1789205 | NC2F      | 0.439789606 |
| ILMN_1863891 | TSP2C     | 0.439646024 |
| ILMN_2301193 | ATP8B2    | 0.439422945 |
| ILMN_1783771 | UBE2Z     | 0.439303883 |
| ILMN_1766916 | RAP3      | 0.439307011 |
| ILMN_1767556 | C10orf10  | 0.438985167 |
| ILMN_1655137 | ZCOC11    | 0.438903911 |
| ILMN_1670134 | FADS1     | 0.438907852 |
| ILMN_1730670 | FSTL3     | 0.438850911 |
| ILMN_1705892 | SH2D1A    | 0.438774921 |
| ILMN_2203271 | FRP3      | 0.438566056 |
| ILMN_2413799 | SEZL2     | 0.438322508 |
| ILMN_1723978 | LGALS1    | 0.438298858 |
| ILMN_3252556 | CARD16    | 0.438207912 |
| ILMN_2364174 | CSNK1A1   | 0.438207647 |
| ILMN_2389171 | RPS27     | 0.437948748 |
| ILMN_1739700 | MED7      | 0.437932752 |
| ILMN_1713182 | C3        | 0.43781048  |
| ILMN_1731714 | CREB5     | 0.437618078 |
| ILMN_1776464 | PARP4     | 0.437488843 |
| ILMN_1772074 | C10orf151 | 0.43741167  |
| ILMN_1811702 | GRN       | 0.437406544 |
| ILMN_1661337 | SRM       | 0.437380935 |
| ILMN_1704196 | DSG2      | 0.437234182 |
| ILMN_1758895 | CTSK      | 0.437080467 |
| ILMN_1680397 | PPL2A     | 0.437047873 |
| ILMN_1745523 | FR41      | 0.436897394 |
| ILMN_2219246 | ITPR1P2   | 0.436817642 |
| ILMN_1708858 | CSNK1E    | 0.436752795 |
| ILMN_1711899 | ANXA2     | 0.436657658 |
| ILMN_2376108 | PSMB9     | 0.436568056 |
| ILMN_1771385 | G8P4      | 0.436191759 |
| ILMN_1665601 | DUSP5     | 0.435948531 |
| ILMN_1724407 | TACC3     | 0.435703097 |
| ILMN_2230892 | HLI08B    | 0.435688228 |
| ILMN_1668039 | GPYC      | 0.435618056 |
| ILMN_1790951 | C19orf50  | 0.435581155 |
| ILMN_1730529 | CAB39L    | 0.435556408 |
| ILMN_2325763 | VCAM1     | 0.435519505 |
| ILMN_2383611 | PTRPE     | 0.435446843 |
| ILMN_2331525 | PRKQ2     | 0.435298616 |
| ILMN_1761519 | ESYT1     | 0.435216588 |
| ILMN_2410986 | STAT3     | 0.434897608 |
| ILMN_1690105 | STAT1     | 0.434806097 |
| ILMN_1715500 | SS18L1    | 0.434759963 |

|                |            |              |
|----------------|------------|--------------|
| ILMN_2413816   | GRB14      | -0.485224817 |
| ILMN_1728746   | GAB2       | -0.48523319  |
| ILMN_2318952   | VDR        | -0.48516093  |
| ILMN_2248640   | SNORD79    | -0.485110661 |
| ILMN_1735996   | NOK4       | -0.485684372 |
| ILMN_1676383   | ENPP6      | -0.485736049 |
| ILMN_1698487   | SDHD       | -0.48582935  |
| ILMN_1750880   | LOC196394  | -0.485908044 |
| ILMN_1600590   | LOC446462  | -0.486197245 |
| ILMN_1805024   | ERBB2IP    | -0.486467637 |
| ILMN_1662438   | SOD1       | -0.486520722 |
| ILMN_1786382   | LOC389834  | -0.486581677 |
| ILMN_1653793   | PDPK1      | -0.486733178 |
| ILMN_1745991   | GHRH1      | -0.4868385   |
| ILMN_1763975   | NCRNA00083 | -0.487142637 |
| ILMN_1671051   | CD276      | -0.487210861 |
| ILMN_2069196   | CAPZA3     | -0.487285448 |
| ILMN_1679797   | ADARB1     | -0.487561666 |
| ILMN_1608564   | CCorfE3    | -0.487599639 |
| ILMN_1726198   | CTS3       | -0.4876215   |
| ILMN_1774742   | MTTP       | -0.487946196 |
| ILMN_1694653   | CNDP1      | -0.488016894 |
| ILMN_2064898   | CCDC56     | -0.488160238 |
| ILMN_1668698   | CWIF19L2   | -0.488169807 |
| ILMN_1754241   | C16orf73   | -0.4882889   |
| ILMN_1761946   | PROM2      | -0.488445286 |
| ILMN_2103774   | PIPSKL1    | -0.488456324 |
| ILMN_2128931   | FAT2       | -0.488482639 |
| ILMN_1735044   | PPP1R3E    | -0.488500438 |
| ILMN_1667791   | PPFIA4     | -0.488939578 |
| ILMN_1757693   | C17orf51   | -0.48899806  |
| ILMN_1655377   | MRRP22     | -0.489004562 |
| ILMN_1690779   | SIC17A3    | -0.489168167 |
| ILMN_2381957   | HSPD1      | -0.489194309 |
| ILMN_1789096   | OStalpha   | -0.489209688 |
| ILMN_2079285   | ATP5L      | -0.489303322 |
| ILMN_2383229   | A1CF       | -0.489400688 |
| ILMN_1814526   | AOD3       | -0.489445534 |
| ILMN_1705212   | PRL5       | -0.489500023 |
| ILMN_1793578   | ZFP37      | -0.48993458  |
| ILMN_1670547   | GRM1       | -0.490038194 |
| ILMN_3294965   | RRA52      | -0.490159822 |
| ILMN_2355033   | KIAA1147   | -0.490174939 |
| ILMN_1685840   | GAPR2      | -0.490202698 |
| ILMN_1751943   | NME        | -0.490354886 |
| ILMN_1723414   | HACL1      | -0.490527151 |
| ILMN_1793832   | GRB14      | -0.490726285 |
| ILMN_1685840   | DDX25      | -0.49076395  |
| ILMN_2172174   | PWP        | -0.490777104 |
| ILMN_1745345   | MT4        | -0.490799854 |
| ILMN_1707464   | MST1       | -0.491048327 |
| ILMN_1720838   | DEC1       | -0.491263442 |
| ILMN_1712161   | BCL9       | -0.491554807 |
| ILMN_1738849   | SIC1A2     | -0.491600438 |
| ILMN_2131811   | CLPS       | -0.491694578 |
| ILMN_1829989   | LOC220930  | -0.491832265 |
| ILMN_1706690   | KHK        | -0.492025908 |
| ILMN_2236423   | RAB3GAP2   | -0.492151537 |
| ILMN_1650551   | PWB        | -0.492265911 |
| ILMN_1707548   | RAD18      | -0.492708727 |
| ILMN_1705049   | TMEM67     | -0.492782656 |
| ILMN_1782070   | NPL        | -0.492968704 |
| ILMN_1658318   | C11orf93   | -0.493056742 |
| ILMN_2117736   | MGA14C     | -0.493155881 |
| ILMN_1742444   | XG3359     | -0.493321817 |
| ILMN_1806330   | C17orf78   | -0.493325239 |
| ILMN_1790336   | C20orf202  | -0.493329884 |
| ILMN_2174650   | CAB        | -0.493330774 |
| ILMN_1654402   | IL18BP     | -0.493343558 |
| ILMN_1660635   | LACTB2     | -0.493890512 |
| ILMN_1812312   | NDUF54     | -0.493934591 |
| ILMN_1728798   | TEXT4P2    | -0.494220077 |
| ILMN_1803676   | ENOSF1     | -0.49442633  |
| ILMN_1788567   | PPP1R14D   | -0.494414997 |
| ILMN_1785284   | ALDH6A1    | -0.494556966 |
| ILMN_1674152   | NFKBIB     | -0.494661163 |
| ILMN_3234809   | H4BP2L2    | -0.494674317 |
| ILMN_1677043   | ARRB2A     | -0.494804549 |
| ILMN_2344079   | ZGPAT      | -0.494853029 |
| ILMN_2268068   | MAPKAP1    | -0.49530015  |
| ILMN_2052331   | MYOC       | -0.496146517 |
| ILMN_2058347   | NTSDC1     | -0.496224396 |
| ILMN_1726743   | MRRP50     | -0.496401513 |
| ILMN_1767674   | HACD2      | -0.496616467 |
| ILMN_1717757   | CALML4     | -0.496678661 |
| ILMN_1882485   | CFS52129   | -0.496938344 |
| ILMN_1699911   | GNCA4      | -0.496973117 |
| ILMN_163599753 | SUN3       | -0.497070211 |
| ILMN_1666273   | DEFB1      | -0.497495864 |
| ILMN_2292646   | GAD1       | -0.497584363 |
| ILMN_1810200   | ARPC2      | -0.497791751 |
| ILMN_3236472   | WEE2       | -0.4979425   |
| ILMN_2194667   | SGCG       | -0.498057682 |
| ILMN_1717853   | DMGDH      | -0.498148378 |
| ILMN_1686906   | TP53INP2   | -0.498317383 |
| ILMN_1783443   | ALOX15     | -0.498497757 |
| ILMN_1688543   | APA02      | -0.498559545 |
| ILMN_1809931   | NORG1      | -0.498566011 |
| ILMN_2393461   | DOD        | -0.498751158 |
| ILMN_3308168   | FAM41A1    | -0.49879344  |
| ILMN_1813270   | ELF5       | -0.499135583 |
| ILMN_2120210   | RCAN2      | -0.499184588 |

|              |           |             |
|--------------|-----------|-------------|
| ILMN_1772387 | TLR2      | 0.434622301 |
| ILMN_2099528 | BT1A      | 0.434543999 |
| ILMN_1721580 | TBX15     | 0.434356048 |
| ILMN_1815608 | ARRB1     | 0.434206762 |
| ILMN_2130525 | TSPAN13   | 0.434170357 |
| ILMN_2377669 | CD247     | 0.434110187 |
| ILMN_1737041 | HABP2     | 0.433447469 |
| ILMN_1776005 | OSTC      | 0.433355297 |
| ILMN_1719339 | UREG1G    | 0.433217588 |
| ILMN_1712419 | DCDC2     | 0.433121328 |
| ILMN_1759954 | PTMA      | 0.43311473  |
| ILMN_1672004 | TDB1      | 0.433087403 |
| ILMN_1712349 | PHF19     | 0.433038592 |
| ILMN_1785988 | CSML1A1   | 0.432985393 |
| ILMN_1772612 | ANGPT2    | 0.432925711 |
| ILMN_1652525 | FAM125B   | 0.432860995 |
| ILMN_1666208 | MIS18BP1  | 0.432634486 |
| ILMN_1809377 | GALNT1    | 0.432550814 |
| ILMN_1662768 | NHEK2     | 0.432545771 |
| ILMN_1737599 | TRIM5     | 0.432435355 |
| ILMN_1777344 | RP513     | 0.432353639 |
| ILMN_3246560 | EMB       | 0.432337279 |
| ILMN_1666715 | WHSC1L1   | 0.432327769 |
| ILMN_3236381 | NKX6A8    | 0.432292453 |
| ILMN_1656386 | SEC24D    | 0.431914267 |
| ILMN_2241953 | PILRA     | 0.43189174  |
| ILMN_1712887 | SLC10A3   | 0.431889181 |
| ILMN_1779677 | ZCCHC6    | 0.431738839 |
| ILMN_1658955 | IT4E      | 0.431614251 |
| ILMN_1690806 | CR613620  | 0.431600478 |
| ILMN_1789599 | Clorf151  | 0.431558138 |
| ILMN_3272603 | FAM60A    | 0.431376363 |
| ILMN_1768505 | IL13RA1   | 0.431185885 |
| ILMN_1767662 | LASS6     | 0.431176425 |
| ILMN_2333367 | FKBP1A    | 0.431137489 |
| ILMN_2272074 | TROVE2    | 0.431035481 |
| ILMN_1669692 | IKZF3     | 0.43083824  |
| ILMN_2064606 | TBC1D28   | 0.430761934 |
| ILMN_1786024 | KLHL34    | 0.430744076 |
| ILMN_1652161 | PNKD      | 0.430647752 |
| ILMN_1744113 | SCNM1     | 0.430643576 |
| ILMN_3270833 | NA        | 0.43058365  |
| ILMN_1725807 | TMS6M2    | 0.430379823 |
| ILMN_1733287 | RFGAP3    | 0.430371581 |
| ILMN_1657991 | LOC391722 | 0.430143759 |
| ILMN_1897254 | BX383912  | 0.430106436 |
| ILMN_1680772 | TCKGV     | 0.430076028 |
| ILMN_2386179 | ZMYND8    | 0.429998814 |
| ILMN_1655283 | INPP4A    | 0.429921382 |
| ILMN_1655572 | C6orf59   | 0.429948667 |
| ILMN_1718629 | NRIP1     | 0.429800467 |
| ILMN_3237946 | PXDN      | 0.429797978 |
| ILMN_1749658 | PRRC1     | 0.429755487 |
| ILMN_1782167 | RPL32     | 0.429593191 |
| ILMN_1910908 | BG205162  | 0.429518547 |
| ILMN_1714499 | TLK2      | 0.429477679 |
| ILMN_1722872 | MYH9      | 0.429400549 |
| ILMN_2053145 | KCNT2     | 0.429331195 |
| ILMN_1701114 | GPR1      | 0.429207189 |
| ILMN_1761442 | WDR24     | 0.429168867 |
| ILMN_1810037 | RUSC2     | 0.429130555 |
| ILMN_1651950 | TPST1     | 0.429020445 |
| ILMN_2096105 | TAGLN2    | 0.429008572 |
| ILMN_2407619 | CDC25C    | 0.428999816 |
| ILMN_2350574 | MYADM     | 0.428918454 |
| ILMN_2109994 | MIA-RAB4B | 0.428629613 |
| ILMN_3306628 | CLorf25   | 0.428601322 |
| ILMN_1785831 | ZDHHC13   | 0.428577225 |
| ILMN_1727135 | FREX1     | 0.428506665 |
| ILMN_3247223 | TPBG      | 0.428466645 |
| ILMN_1745130 | RBFCK2    | 0.428420918 |
| ILMN_1804444 | POA2      | 0.428411127 |
| ILMN_2213136 | LEP1      | 0.428344554 |
| ILMN_3302905 | RPL23A    | 0.428334223 |
| ILMN_3307693 | WFDC2     | 0.428222924 |
| ILMN_1669210 | RPL4      | 0.428202285 |
| ILMN_2063618 | RBBP8     | 0.427981058 |
| ILMN_1719695 | NFB2B2    | 0.427934866 |
| ILMN_2053178 | ACTG1     | 0.427897591 |
| ILMN_2063114 | TAF1D     | 0.427814401 |
| ILMN_1808059 | BCAS4     | 0.427514046 |
| ILMN_1780108 | PTPN22    | 0.427466872 |
| ILMN_1678669 | PRM2      | 0.427464083 |
| ILMN_2092693 | SMI2      | 0.427399574 |
| ILMN_1652512 | CXCO2     | 0.427377123 |
| ILMN_2402392 | COL8A1    | 0.42730106  |
| ILMN_3251100 | MEF2A     | 0.427118071 |
| ILMN_1685122 | COL9A2    | 0.426987984 |
| ILMN_1868260 | ZNF124    | 0.426935689 |
| ILMN_1793474 | INSIG1    | 0.426864599 |
| ILMN_1705763 | SCT       | 0.426754931 |
| ILMN_1740197 | ZNF234    | 0.426634136 |
| ILMN_1675479 | ZNF646    | 0.426526277 |
| ILMN_1744929 | PTGER1    | 0.426505259 |
| ILMN_2324421 | TXNRD1    | 0.426542949 |
| ILMN_3230521 | FLJ40330  | 0.426500061 |
| ILMN_3264073 | RP927     | 0.426413875 |
| ILMN_1703263 | SP140     | 0.426326277 |
| ILMN_1702691 | TNFAIP3   | 0.426321744 |
| ILMN_1652123 | HMGGN1    | 0.426303968 |
| ILMN_1748438 | POLR2G    | 0.426270248 |
| ILMN_2318568 | HCFPC1R1  | 0.426262679 |

|              |          |              |
|--------------|----------|--------------|
| ILMN_1662738 | ACSM3    | -0.499208254 |
| ILMN_3185020 | AR92A20  | -0.499249207 |
| ILMN_2379510 | RAD51L3  | -0.499280092 |
| ILMN_2393546 | DDO      | -0.499334417 |
| ILMN_1745887 | FBOXO1   | -0.499625604 |
| ILMN_1744534 | LVRM5    | -0.499749965 |
| ILMN_1738058 | CPN6E    | -0.499771275 |
| ILMN_1806473 | BEK5     | -0.49993877  |
| ILMN_1685074 | SLC5A33  | -0.500226991 |
| ILMN_1754423 | C3orf23  | -0.500300243 |
| ILMN_2357730 | CDK20    | -0.50036511  |
| ILMN_1818856 | BE49596  | -0.500533366 |
| ILMN_1653458 | FUT9     | -0.500859647 |
| ILMN_2358093 | ADP7P3   | -0.50089916  |
| ILMN_1758750 | EAR52    | -0.500906035 |
| ILMN_1748323 | CXCL14   | -0.500974665 |
| ILMN_1794875 | AGPAT9   | -0.500989569 |
| ILMN_3230880 | BEND7    | -0.501160509 |
| ILMN_1741695 | COL24A1  | -0.5014294   |
| ILMN_2331232 | TNFRSF68 | -0.501469367 |
| ILMN_3306482 | GCSH     | -0.501487404 |
| ILMN_1671791 | PCK2     | -0.502102533 |
| ILMN_2296510 | SLC5A12  | -0.50225117  |
| ILMN_1655513 | GSTA2    | -0.50235825  |
| ILMN_2142353 | GRTP1    | -0.502423665 |
| ILMN_1672479 | TRIM55   | -0.502816781 |
| ILMN_3187758 | SELE     | -0.503248184 |
| ILMN_1795300 | ARMHGF37 | -0.503315741 |
| ILMN_1739274 | PHM      | -0.50343916  |
| ILMN_1724504 | SETD3    | -0.503992383 |
| ILMN_1769433 | IQGAP2   | -0.504012224 |
| ILMN_1860963 | BM715829 | -0.504042576 |
| ILMN_1819515 | AR099300 | -0.50414379  |
| ILMN_2226228 | ZNF184   | -0.504221439 |
| ILMN_1733366 | MAST1    | -0.504424597 |
| ILMN_1875967 | BG222050 | -0.504471984 |
| ILMN_1701454 | OR2L13   | -0.504559082 |
| ILMN_1698880 | ARL7B    | -0.504668948 |
| ILMN_2427438 | C19orf69 | -0.504733896 |
| ILMN_1745817 | NELL1    | -0.505003682 |
| ILMN_1707585 | SLC46A2  | -0.505712375 |
| ILMN_1803743 | AX747098 | -0.506197539 |
| ILMN_2406334 | DNMT3L   | -0.506243129 |
| ILMN_2423788 | TMEM146  | -0.506261449 |
| ILMN_3180456 | NA       | -0.506333915 |
| ILMN_3225886 | NOKA     | -0.50637689  |
| ILMN_1658800 | BRPF3    | -0.506403267 |
| ILMN_1611880 | SLC24A3  | -0.506623239 |
| ILMN_1672605 | C7orf41  | -0.506646681 |
| ILMN_1651259 | UQP2     | -0.506794525 |
| ILMN_1789653 | PBLD     | -0.507117024 |
| ILMN_1676625 | SS18L1   | -0.507425975 |
| ILMN_1712943 | CKK      | -0.507951701 |
| ILMN_1778301 | C6orf132 | -0.507832521 |
| ILMN_2148497 | C2orf107 | -0.507935691 |
| ILMN_1758272 | MYPN     | -0.507953216 |
| ILMN_3298870 | FAM182B  | -0.508221693 |
| ILMN_1710903 | MAPP1    | -0.508311776 |
| ILMN_1807448 | FAM84A   | -0.509027419 |
| ILMN_1762531 | FGF9     | -0.50868513  |
| ILMN_1693270 | SUSD2    | -0.509007976 |
| ILMN_2244699 | MAPP7    | -0.509085121 |
| ILMN_1678170 | NMFI     | -0.509121703 |
| ILMN_1669123 | AK125437 | -0.509206616 |
| ILMN_1708672 | ACAT2    | -0.509242898 |
| ILMN_1803745 | SUOX     | -0.509517874 |
| ILMN_1761804 | ALDH9A1  | -0.509758034 |
| ILMN_2372698 | RGN      | -0.509770611 |
| ILMN_3048032 | NCCRP1   | -0.510109252 |
| ILMN_1739582 | HOKA10   | -0.510313253 |
| ILMN_2375879 | VEGFA    | -0.510415338 |
| ILMN_1661994 | ESRRG    | -0.510487705 |
| ILMN_1776601 | OR4F5    | -0.510501919 |
| ILMN_1660693 | CCN      | -0.510856919 |
| ILMN_1669617 | GRB10    | -0.511137899 |
| ILMN_2166865 | ENY2     | -0.511151344 |
| ILMN_1792671 | C12orf29 | -0.511357071 |
| ILMN_2373383 | AH461701 | -0.511387038 |
| ILMN_1742431 | AOC2     | -0.511745421 |
| ILMN_1662158 | RPL26L1  | -0.511950448 |
| ILMN_1680390 | GCNT2    | -0.512892865 |
| ILMN_1748650 | MRRPL45  | -0.513306647 |
| ILMN_1882763 | ALB      | -0.513404008 |
| ILMN_1694432 | PHO84    | -0.514517928 |
| ILMN_1780864 | PBLD     | -0.514555501 |
| ILMN_1809259 | HRASL52  | -0.513478157 |
| ILMN_1758034 | ETFDH    | -0.513764006 |
| ILMN_1887508 | AL20543  | -0.513965491 |
| ILMN_1813838 | CHEK4    | -0.514030853 |
| ILMN_1738346 | EHA1     | -0.514176572 |
| ILMN_1815203 | HMGCS2   | -0.514209731 |
| ILMN_2113470 | GSTA1    | -0.514312674 |
| ILMN_1715437 | CASC5    | -0.514444059 |
| ILMN_1691432 | PHO84    | -0.514517928 |
| ILMN_1780864 | MTRNR1   | -0.514688195 |
| ILMN_1778951 | C6orf203 | -0.515038647 |
| ILMN_1707592 | RGN      | -0.515175991 |
| ILMN_3251567 | FBW2     | -0.515813789 |
| ILMN_1779445 | NOTCH2   | -0.516231183 |
| ILMN_1658917 | SLC1A1   | -0.516353033 |
| ILMN_1815949 | SLC24A4  | -0.516558381 |
| ILMN_1733135 | TFAP2A   | -0.516837352 |
| ILMN_3272441 | PTPRQ    | -0.516966688 |

|              |              |             |
|--------------|--------------|-------------|
| ILMN_2188451 | HST11QAH     | 0.426236258 |
| ILMN_1705594 | NAT10        | 0.426166324 |
| ILMN_1679482 | TUBA3C       | 0.426144768 |
| ILMN_1808874 | AK127262     | 0.426144462 |
| ILMN_1728435 | C12orf45     | 0.425811025 |
| ILMN_2110271 | OLFM2        | 0.425709697 |
| ILMN_1702636 | TUBB6        | 0.425373273 |
| ILMN_2949439 | LOC100131289 | 0.425260739 |
| ILMN_1812559 | SLC7A6       | 0.425201753 |
| ILMN_2934947 | ATXN3        | 0.425072642 |
| ILMN_1766914 | MFAP4        | 0.425072282 |
| ILMN_2225135 | GCNT1        | 0.425036132 |
| ILMN_1651209 | SLC35E2      | 0.424909593 |
| ILMN_1655876 | TNEM159      | 0.424879729 |
| ILMN_1708841 | GOLPH3       | 0.424851811 |
| ILMN_1735594 | CDC42SE2     | 0.424633756 |
| ILMN_2227195 | CCDC65       | 0.424598883 |
| ILMN_1693986 | WHAMML2      | 0.424442196 |
| ILMN_1760374 | CSBA         | 0.424407406 |
| ILMN_1690139 | NAA0748      | 0.424156178 |
| ILMN_1715203 | DNAH7        | 0.424022883 |
| ILMN_1720819 | SPCS2        | 0.423789899 |
| ILMN_2233783 | CD38         | 0.423714979 |
| ILMN_1748529 | RLN2         | 0.423626949 |
| ILMN_1688279 | PVRG         | 0.423584213 |
| ILMN_2049536 | TRPV2        | 0.423572112 |
| ILMN_2278850 | RAB24        | 0.423526811 |
| ILMN_1738523 | MYO88        | 0.423488776 |
| ILMN_1774287 | CFB          | 0.423446323 |
| ILMN_1698766 | PFCARD       | 0.423321122 |
| ILMN_2090607 | IRF2         | 0.423291527 |
| ILMN_3199780 | GAP1         | 0.423239935 |
| ILMN_2206141 | BDGF         | 0.423183964 |
| ILMN_2351298 | WIPF1        | 0.423121778 |
| ILMN_1805519 | DQ893812     | 0.423097713 |
| ILMN_1804652 | PLEKH3       | 0.423061393 |
| ILMN_1773066 | CDKN2AIP     | 0.423047728 |
| ILMN_1789839 | GTF3C1       | 0.423022548 |
| ILMN_2070712 | RPS7         | 0.422918915 |
| ILMN_2163187 | FLJ35776     | 0.42280689  |
| ILMN_1660900 | SNORA7B      | 0.422800664 |
| ILMN_1824052 | AA909514     | 0.422769328 |
| ILMN_1783249 | ZC2N         | 0.422718765 |
| ILMN_1770281 | RFC1         | 0.422331227 |
| ILMN_1654031 | TPTE2        | 0.422210266 |
| ILMN_2414027 | CMTM1        | 0.422055341 |
| ILMN_1716983 | ULRA2        | 0.422022128 |
| ILMN_1672124 | FAM138B      | 0.421870139 |
| ILMN_1398918 | LOC45323     | 0.421855087 |
| ILMN_1681591 | PTPN1        | 0.421554524 |
| ILMN_1752923 | IFNAR1       | 0.421493221 |
| ILMN_1661359 | CXorf65      | 0.421419793 |
| ILMN_1654735 | SLCO3A1      | 0.421412848 |
| ILMN_1263586 | SOCBP        | 0.421295159 |
| ILMN_1772486 | ELF2         | 0.421264542 |
| ILMN_1766955 | VCAM1        | 0.421260966 |
| ILMN_1651767 | MKL1         | 0.421258711 |
| ILMN_1773964 | H1FX         | 0.421193858 |
| ILMN_1670178 | FAM115A      | 0.421144903 |
| ILMN_1718552 | CXCL13       | 0.421030719 |
| ILMN_1740426 | RASD1        | 0.420924785 |
| ILMN_2397934 | CTBP1        | 0.420879215 |
| ILMN_2396287 | RPX2         | 0.420771436 |
| ILMN_1656073 | NPFL2A       | 0.420645232 |
| ILMN_1736015 | PHF17        | 0.420607716 |
| ILMN_2410864 | RAB28        | 0.420492511 |
| ILMN_1683082 | RPUSD1       | 0.420466857 |
| ILMN_1660832 | RPL18A       | 0.420411273 |
| ILMN_2333366 | ASAP1        | 0.420392278 |
| ILMN_1743347 | AKT2         | 0.42028485  |
| ILMN_1722923 | SRGAP3       | 0.420100958 |
| ILMN_1692539 | SH3BP1       | 0.420043968 |
| ILMN_2355719 | NBRP1        | 0.419816012 |
| ILMN_1872122 | LCOR         | 0.419631791 |
| ILMN_1666078 | HLA-H        | 0.419592123 |
| ILMN_1683036 | BRWD1-IT2    | 0.419449867 |
| ILMN_1664063 | FAM129C      | 0.419349888 |
| ILMN_2348518 | SAMD3        | 0.419337104 |
| ILMN_1755024 | IRXK         | 0.419244023 |
| ILMN_1699440 | ZBTB47       | 0.419170676 |
| ILMN_1698067 | NBRP1        | 0.419120689 |
| ILMN_1763000 | ADAP2        | 0.419113398 |
| ILMN_1771593 | RRM1         | 0.419007709 |
| ILMN_2353787 | ARRDC5       | 0.418987921 |
| ILMN_1726114 | SLC45A3      | 0.418960459 |
| ILMN_1718558 | PARP12       | 0.418882561 |
| ILMN_2128293 | ARIP         | 0.41864951  |
| ILMN_2351733 | C19orf43     | 0.418617711 |
| ILMN_2085862 | SLC14A3      | 0.418636297 |
| ILMN_1760563 | PRRC2A       | 0.418610647 |
| ILMN_1770290 | CNN2         | 0.418497857 |
| ILMN_1744887 | RLN2         | 0.418274316 |
| ILMN_2309995 | MIR383       | 0.418262767 |
| ILMN_1720244 | NPRA2        | 0.418179382 |
| ILMN_3221499 | ZNF735       | 0.418155045 |
| ILMN_1762260 | C3           | 0.418085603 |
| ILMN_3275345 | RPS27        | 0.418077229 |
| ILMN_3270613 | NA           | 0.418005    |
| ILMN_2071809 | MGP          | 0.418040872 |
| ILMN_1692731 | TYRH3        | 0.417974627 |
| ILMN_1690561 | GZMM         | 0.417806132 |
| ILMN_1659029 | FAM116B      | 0.41773041  |

|              |           |              |
|--------------|-----------|--------------|
| ILMN_1736441 | PDXP      | -0.517129473 |
| ILMN_1662795 | CA2       | -0.517877699 |
| ILMN_1827211 | UHR50A    | -0.517809776 |
| ILMN_1738854 | CACHD1    | -0.51802405  |
| ILMN_1897333 | IXO85821  | -0.518589793 |
| ILMN_1826853 | NA        | -0.519285599 |
| ILMN_1662417 | LRPPRC    | -0.519916292 |
| ILMN_1770725 | AF1L1     | -0.520044771 |
| ILMN_1831214 | AW52010   | -0.520427228 |
| ILMN_3237589 | PHAX      | -0.520627824 |
| ILMN_1730229 | CGNL1     | -0.520771213 |
| ILMN_1686804 | CDKO2     | -0.521168852 |
| ILMN_1740233 | UGT1A1    | -0.521174601 |
| ILMN_1750800 | AC01      | -0.521249998 |
| ILMN_1731941 | APOM      | -0.521444993 |
| ILMN_1763558 | RGN       | -0.521548568 |
| ILMN_2163796 | RABGGTB   | -0.521763335 |
| ILMN_2369104 | TRAPPC8   | -0.521775481 |
| ILMN_1797210 | ATP9D     | -0.521837595 |
| ILMN_1804662 | NRG4      | -0.52201763  |
| ILMN_3307836 | SLCSA12   | -0.522149637 |
| ILMN_1741204 | KLHDC2    | -0.522396099 |
| ILMN_1661491 | SH3GL2    | -0.522598779 |
| ILMN_2297887 | SEZL2     | -0.522825419 |
| ILMN_1711245 | SCG3      | -0.523235608 |
| ILMN_1813350 | HSD11B2   | -0.5232935   |
| ILMN_1784834 | ORS2E6    | -0.523324668 |
| ILMN_1704566 | LWPI      | -0.523430022 |
| ILMN_1795778 | PH4A2     | -0.523449319 |
| ILMN_3261111 | IPK3      | -0.523734841 |
| ILMN_2371825 | AGL       | -0.523913857 |
| ILMN_1803882 | VEGFA     | -0.523969402 |
| ILMN_1770257 | COL3A1    | -0.52402098  |
| ILMN_2192730 | ZNF573    | -0.524066579 |
| ILMN_1790603 | ATPAF1    | -0.524461662 |
| ILMN_1652722 | C16orf2   | -0.524581174 |
| ILMN_1805147 | ACSM5     | -0.524782966 |
| ILMN_2128967 | C11orf1   | -0.524827605 |
| ILMN_1696450 | IKL5      | -0.52493008  |
| ILMN_1853824 | MGAT3     | -0.52519718  |
| ILMN_1669114 | WNK4      | -0.525564689 |
| ILMN_1814296 | TRPM6     | -0.525686444 |
| ILMN_1712786 | AHCY2     | -0.525943185 |
| ILMN_1778273 | PWVH      | -0.526349219 |
| ILMN_2224230 | TTY21     | -0.52598447  |
| ILMN_3237085 | NTF4      | -0.526155155 |
| ILMN_1683905 | C19orf21  | -0.526486266 |
| ILMN_1699520 | LOC39924  | -0.526605798 |
| ILMN_1802787 | CSX2      | -0.526670115 |
| ILMN_2183687 | LIME1     | -0.526839511 |
| ILMN_1691572 | TST       | -0.526977744 |
| ILMN_2143220 | ANGPTL3   | -0.527059729 |
| ILMN_1745688 | HPO       | -0.527222213 |
| ILMN_1722532 | KDM3A     | 0.527295305  |
| ILMN_1882652 | BGG97942  | -0.527716317 |
| ILMN_1699937 | HPS4      | -0.52790616  |
| ILMN_1749405 | KIAA1191  | -0.528195899 |
| ILMN_1646071 | TNNT2     | -0.528204728 |
| ILMN_1703174 | TREN2     | -0.528298078 |
| ILMN_3305339 | UBA5      | -0.529389579 |
| ILMN_1782937 | GSTA1     | -0.529390084 |
| ILMN_1797154 | AZGP1     | -0.52939045  |
| ILMN_1787734 | FANK1     | -0.529622636 |
| ILMN_1788322 | GSTAS     | -0.529974168 |
| ILMN_1765103 | C57R      | -0.530674355 |
| ILMN_1764494 | ATPSA1    | -0.530768756 |
| ILMN_2043306 | EPHA15    | -0.530984116 |
| ILMN_1759841 | KEFP5     | -0.53103745  |
| ILMN_2311020 | DNAC12    | -0.531187763 |
| ILMN_2052208 | GADD45A   | -0.531297129 |
| ILMN_1800659 | PGM1      | -0.531468513 |
| ILMN_1807101 | F11       | -0.531748271 |
| ILMN_2096985 | ALDH6A1   | -0.532271901 |
| ILMN_1786188 | RNF113A   | -0.532520805 |
| ILMN_1737152 | DAO       | -0.532909751 |
| ILMN_2290776 | AGBL5     | -0.533283314 |
| ILMN_1781242 | SOST      | -0.533354231 |
| ILMN_1756162 | EXOSC8    | -0.533846485 |
| ILMN_1728213 | BRP4      | -0.534297944 |
| ILMN_2373515 | HSP90AA1  | -0.535175503 |
| ILMN_1759973 | NDUFAS    | -0.535502407 |
| ILMN_1778844 | FAM58     | -0.535940023 |
| ILMN_1808238 | RBM52     | -0.536204866 |
| ILMN_1743484 | PCCA      | -0.536466934 |
| ILMN_2168228 | ATOH7     | -0.536831235 |
| ILMN_1764266 | CKMT2     | -0.537083454 |
| ILMN_1718853 | UQCRC2    | -0.537136305 |
| ILMN_1740365 | ACD77     | -0.537144734 |
| ILMN_2175020 | RPL32P3   | -0.537381679 |
| ILMN_1694359 | UPF0639   | -0.53741043  |
| ILMN_2057220 | HRSP12    | -0.537452901 |
| ILMN_1736954 | ZBTB78    | -0.537575523 |
| ILMN_1695193 | ANGPTL3   | -0.537664271 |
| ILMN_1690783 | TREN41    | -0.537930568 |
| ILMN_2216815 | MAP7      | -0.537730832 |
| ILMN_3236866 | ULK4      | -0.537747664 |
| ILMN_1811278 | RNF186    | -0.538336189 |
| ILMN_2209576 | VWAL1     | -0.538381839 |
| ILMN_1763661 | ALDH7A1   | -0.538402776 |
| ILMN_2380561 | PKLR      | -0.539004819 |
| ILMN_1726667 | LOC728758 | -0.539050257 |
| ILMN_2199676 | CEP152    | -0.539166845 |

|              |            |             |
|--------------|------------|-------------|
| ILMN_2186061 | PFKFB3     | 0.417660192 |
| ILMN_1761833 | SLC40A1    | 0.417650029 |
| ILMN_1095650 | FES        | 0.417542393 |
| ILMN_309920  | NA         | 0.417500011 |
| ILMN_1862018 | ATXN7L3    | 0.417422219 |
| ILMN_2325194 | PHFG       | 0.417394928 |
| ILMN_1717809 | RNF24      | 0.417357668 |
| ILMN_1656732 | LOC40300   | 0.4173066   |
| ILMN_1670101 | LELED      | 0.417290281 |
| ILMN_1749448 | GLMN       | 0.417254655 |
| ILMN_1741404 | MSC        | 0.417164353 |
| ILMN_1674640 | CXCR6      | 0.417146933 |
| ILMN_1703908 | NA         | 0.417115947 |
| ILMN_1808395 | ACAP1      | 0.417114521 |
| ILMN_1749662 | GPX1       | 0.417111988 |
| ILMN_2368318 | FRG        | 0.417014523 |
| ILMN_1807535 | YWHAE      | 0.416927101 |
| ILMN_2367384 | EPH2       | 0.416884046 |
| ILMN_2149526 | CAVI1      | 0.416843675 |
| ILMN_1713901 | NDEL3      | 0.416388066 |
| ILMN_1676091 | HNRNP1A1   | 0.41622215  |
| ILMN_2096784 | TAF2C      | 0.416209958 |
| ILMN_1726578 | ZNF93      | 0.41604881  |
| ILMN_1809477 | CARHSP1    | 0.41593852  |
| ILMN_1710221 | GPR35      | 0.415832341 |
| ILMN_2089073 | ATPSA      | 0.415818712 |
| ILMN_1691717 | RHBDP2     | 0.415769801 |
| ILMN_1686803 | LYPD1      | 0.415616137 |
| ILMN_1681238 | NYO1F      | 0.41557114  |
| ILMN_1726289 | CL2orf35   | 0.415514639 |
| ILMN_1710216 | AVEN       | 0.415414154 |
| ILMN_2402272 | TCEAL8     | 0.415399772 |
| ILMN_1720181 | CLSTN1     | 0.415206827 |
| ILMN_1752902 | CLPTM1L    | 0.415168609 |
| ILMN_1806721 | MS4A2      | 0.415164431 |
| ILMN_1661309 | XKR4       | 0.415157201 |
| ILMN_3238481 | SNORD60    | 0.415114925 |
| ILMN_1720476 | PHF2       | 0.415015791 |
| ILMN_2150161 | ZRANB3     | 0.414939412 |
| ILMN_1800220 | KCTD3      | 0.414858947 |
| ILMN_3248928 | UBN2       | 0.414582768 |
| ILMN_1680145 | SART1      | 0.414490626 |
| ILMN_1731528 | LIF        | 0.414434426 |
| ILMN_1803561 | FLJ245A    | 0.414133019 |
| ILMN_1767665 | GPX8       | 0.414133019 |
| ILMN_1801307 | TNFSF10    | 0.414066282 |
| ILMN_1664466 | KLHL9      | 0.413908363 |
| ILMN_1736806 | PAG1       | 0.413867396 |
| ILMN_1881714 | KIAA1016   | 0.413809879 |
| ILMN_1694223 | DGCR8      | 0.413708447 |
| ILMN_1675156 | CDC42      | 0.413692461 |
| ILMN_3241446 | QDF3B      | 0.413633306 |
| ILMN_2158902 | PDOL       | 0.413515069 |
| ILMN_1763640 | KCQAP5L    | 0.413450886 |
| ILMN_1703433 | PLSCR3     | 0.413294512 |
| ILMN_1749006 | RCS1       | 0.413284499 |
| ILMN_1751904 | EDNRB      | 0.413251946 |
| ILMN_3242753 | NBP1       | 0.413087545 |
| ILMN_1769671 | RYK        | 0.413087165 |
| ILMN_2112638 | SVEP1      | 0.41298778  |
| ILMN_1765829 | NUFIP2     | 0.412742373 |
| ILMN_2116127 | MEPP5      | 0.412697844 |
| ILMN_1731180 | EDCC2      | 0.412679758 |
| ILMN_1784141 | KAMMP1     | 0.412598732 |
| ILMN_2252309 | DPP7       | 0.412521148 |
| ILMN_1708959 | MFN1       | 0.412455127 |
| ILMN_2049021 | PTTG3      | 0.412410943 |
| ILMN_1733581 | CLIC4F35   | 0.41237078  |
| ILMN_1759883 | OTOP1      | 0.412196852 |
| ILMN_1666819 | PHLDB1     | 0.412185351 |
| ILMN_1695423 | CD9        | 0.412144435 |
| ILMN_1663925 | OR2L5      | 0.411991812 |
| ILMN_1858061 | HOXB00     | 0.411831354 |
| ILMN_3238560 | IT2I2      | 0.411724428 |
| ILMN_1671295 | MST1S1     | 0.411640204 |
| ILMN_3236169 | MACC1      | 0.411585575 |
| ILMN_1756360 | RPL35A     | 0.411556316 |
| ILMN_1802523 | H3S3T5     | 0.411548817 |
| ILMN_2385178 | NMR2       | 0.411417507 |
| ILMN_1701393 | TBX3       | 0.411322903 |
| ILMN_1694475 | GTPBP2     | 0.411230194 |
| ILMN_1759883 | SRP9       | 0.411170562 |
| ILMN_1757338 | PLSC4      | 0.411055498 |
| ILMN_1703228 | ASFG2      | 0.410957506 |
| ILMN_3246625 | KIAA1045   | 0.410797888 |
| ILMN_3244607 | FAM117B    | 0.410675233 |
| ILMN_1719986 | PKCIP1     | 0.410664945 |
| ILMN_1763382 | NPFR1      | 0.41017508  |
| ILMN_1726589 | CD248      | 0.410117271 |
| ILMN_2168520 | CL1orf70   | 0.410103311 |
| ILMN_1796244 | CD2BP2     | 0.409984858 |
| ILMN_2143795 | NCRNA00152 | 0.409976983 |
| ILMN_1712636 | NVL        | 0.40990025  |
| ILMN_3249866 | NA         | 0.409840864 |
| ILMN_2177413 | TBL3       | 0.409719664 |
| ILMN_2242463 | CTSC       | 0.409622204 |
| ILMN_2303166 | MBNL3      | 0.409593283 |
| ILMN_1702604 | KCNK3      | 0.40957905  |
| ILMN_1742947 | SECL4L4    | 0.409360464 |
| ILMN_1711994 | TCIRG1     | 0.409327091 |
| ILMN_2184184 | ANKA1      | 0.409291635 |
| ILMN_1692896 | JMID4      | 0.409240971 |

|              |              |              |
|--------------|--------------|--------------|
| ILMN_1731181 | TEX2         | -0.539457065 |
| ILMN_1712530 | AKAP1        | -0.539365608 |
| ILMN_1087515 | RORA         | -0.540826216 |
| ILMN_1727598 | MAP1LC1A     | -0.541130757 |
| ILMN_3269995 | LOC100129042 | -0.541942019 |
| ILMN_1809304 | PRAMEF12     | -0.541939361 |
| ILMN_1876924 | WNK1         | -0.542461742 |
| ILMN_1761260 | COR1L1       | -0.542512683 |
| ILMN_2238552 | POLB3        | -0.542891913 |
| ILMN_3246214 | B3GNT1       | -0.543174959 |
| ILMN_1703678 | DNM1P33      | -0.54344193  |
| ILMN_2285375 | SORD         | -0.543592997 |
| ILMN_1794968 | LRR28        | -0.543767953 |
| ILMN_2198239 | HGI          | -0.543885443 |
| ILMN_1688864 | CABP4        | -0.543889776 |
| ILMN_2317739 | ITSN2        | -0.544145111 |
| ILMN_3203059 | LOC100131176 | -0.544307725 |
| ILMN_2328269 | NDUFAB       | -0.54476094  |
| ILMN_1662605 | RNF123       | -0.545641659 |
| ILMN_3297082 | LOC729080    | -0.545746866 |
| ILMN_1739429 | HSS6T2       | -0.54579897  |
| ILMN_1794980 | SLC38A4      | -0.545811231 |
| ILMN_1688855 | KIAA0564     | -0.546087297 |
| ILMN_1647903 | UBAS         | -0.546474451 |
| ILMN_2244631 | STEAP1       | -0.546551755 |
| ILMN_1739659 | ZDHHC6       | -0.54779174  |
| ILMN_1752952 | MMP28        | -0.548653537 |
| ILMN_1966318 | LOC100130691 | -0.548705992 |
| ILMN_1739025 | SLC25A1      | -0.549264444 |
| ILMN_1676042 | NA           | -0.549144451 |
| ILMN_1881598 | AWA51118     | -0.549282264 |
| ILMN_2215155 | AK126539     | -0.549533144 |
| ILMN_1692517 | SORD         | -0.550630857 |
| ILMN_1781959 | LJPT2B28     | -0.550645189 |
| ILMN_2168747 | GSTA2        | -0.550689713 |
| ILMN_3305768 | GSTA7P       | -0.550784054 |
| ILMN_1807339 | HRG          | -0.551635717 |
| ILMN_1760174 | MCC1         | -0.55194636  |
| ILMN_2115421 | SLC5A16      | -0.55240474  |
| ILMN_2183772 | CCDC121      | -0.552384116 |
| ILMN_1777031 | PKLR         | -0.552412016 |
| ILMN_2166457 | HPGD         | -0.552644609 |
| ILMN_1796845 | ATP9E1E1     | -0.552733705 |
| ILMN_2136345 | CTAC2        | -0.553324211 |
| ILMN_2339779 | ATP9E1E1     | -0.553386787 |
| ILMN_2184049 | COX7B        | -0.554055405 |
| ILMN_1776724 | LYPD6        | -0.554080454 |
| ILMN_1891725 | BX11675      | -0.55418394  |
| ILMN_1782015 | FRLB         | -0.554272167 |
| ILMN_1806310 | AICF         | -0.55450949  |
| ILMN_2162819 | UGT2B11      | -0.554905065 |
| ILMN_1754491 | YD           | -0.555083178 |
| ILMN_1766896 | ZDHHC19      | -0.555800091 |
| ILMN_1751411 | PTRPQ        | -0.556309619 |
| ILMN_1736972 | GKAP1        | -0.55634514  |
| ILMN_1670385 | TUBAL3       | -0.556864698 |
| ILMN_3251540 | GSTA2        | -0.556889644 |
| ILMN_2113125 | LRR4C3       | -0.556913817 |
| ILMN_1718001 | PHK9         | -0.557140217 |
| ILMN_2363634 | ADHFE1       | -0.557389477 |
| ILMN_1699011 | GTD1         | -0.557551345 |
| ILMN_1800898 | ARG2         | -0.557982779 |
| ILMN_1720335 | ADSS1        | -0.55793379  |
| ILMN_1690733 | EGF          | -0.558118122 |
| ILMN_1728803 | HMP19        | -0.558583456 |
| ILMN_2296843 | GCDH         | -0.558638287 |
| ILMN_3245311 | DHRS4L1      | -0.558930928 |
| ILMN_1733333 | CALML3       | -0.559153649 |
| ILMN_1850274 | BGN43031     | -0.562963253 |
| ILMN_2374191 | FNTA         | -0.563012507 |
| ILMN_1702858 | ADHFE1       | -0.563346607 |
| ILMN_1806040 | TYMS         | -0.563573249 |
| ILMN_3305614 | ZNF812       | -0.564346479 |
| ILMN_1688886 | GPCS         | -0.565094193 |
| ILMN_2069224 | PVALB        | -0.565136982 |
| ILMN_2228780 | SLCSA11      | -0.56539883  |
| ILMN_2211546 | HAO1         | -0.566257024 |
| ILMN_2252609 | DGGL1        | -0.566755205 |
| ILMN_1758489 | ORAF17       | -0.567216459 |
| ILMN_1776493 | MTUS1        | -0.567659808 |
| ILMN_1861652 | BQ575680     | -0.567675662 |
| ILMN_1712231 | SH3YL1       | -0.567940667 |
| ILMN_1883133 | KLF15        | -0.567974457 |
| ILMN_1764607 | UGT1A1       | -0.568577404 |
| ILMN_3307954 | LMBTL4       | -0.568724889 |
| ILMN_1725352 | RUVBL1       | -0.569359348 |
| ILMN_1808677 | BC141517     | -0.569931014 |
| ILMN_262601  | RUF19        | -0.569857187 |
| ILMN_1687608 | ALDH7A1      | -0.57015289  |
| ILMN_1810324 | SGCB         | -0.570744689 |
| ILMN_1761511 | APOH         | -0.571018985 |
| ILMN_1702489 | TRIM63       | -0.571234802 |
| ILMN_1809352 | PRL          | -0.571379016 |
| ILMN_237001  | ATP9V1G3     | -0.571524254 |
| ILMN_2218104 | PAH          | -0.572114062 |
| ILMN_2380181 | MAG          | -0.573094942 |
| ILMN_1720998 | CA12         | -0.574295403 |
| ILMN_1754315 | MM4A4        | -0.574790064 |
| ILMN_1746788 | TRIM10       | -0.576504793 |
| ILMN_1749081 | AUTS2        | -0.577415214 |
| ILMN_3226181 | NUDT7        | -0.578374817 |
| ILMN_1772206 | CYP3A4       | -0.57903069  |

|              |            |             |
|--------------|------------|-------------|
| ILMN_1804339 | CAMK1G     | 0.409232738 |
| ILMN_1769293 | C17orf101  | 0.409167815 |
| ILMN_2225144 | EIF4E3     | 0.409058855 |
| ILMN_1683441 | NCAPD3     | 0.409039097 |
| ILMN_1739496 | P8RX1      | 0.409006761 |
| ILMN_1692261 | EPH81      | 0.408946755 |
| ILMN_2134224 | ATP13A1    | 0.408868275 |
| ILMN_1727991 | MIR671     | 0.408851244 |
| ILMN_1808590 | CUC1C43    | 0.408811581 |
| ILMN_1760683 | SRSF9      | 0.408767555 |
| ILMN_2151817 | PFN1       | 0.408751462 |
| ILMN_2206746 | BGN        | 0.408680759 |
| ILMN_2429388 | PELL1      | 0.408515236 |
| ILMN_1765409 | STAM1      | 0.408447493 |
| ILMN_1754746 | CN8B3      | 0.40837607  |
| ILMN_2354191 | CD88       | 0.408373244 |
| ILMN_3248247 | LOC349114  | 0.408338865 |
| ILMN_2082035 | GALNT1     | 0.408324549 |
| ILMN_1721333 | AURKC      | 0.408291834 |
| ILMN_1680367 | C10orf90   | 0.408250468 |
| ILMN_2402930 | H3FAA      | 0.408070068 |
| ILMN_1801118 | SNRNP25    | 0.408023057 |
| ILMN_2346801 | DNAJC30    | 0.407912599 |
| ILMN_1731048 | TLE1       | 0.407939551 |
| ILMN_1711617 | GMFG       | 0.407807931 |
| ILMN_1803429 | CD44       | 0.407755639 |
| ILMN_1777296 | ACTB       | 0.407726547 |
| ILMN_2295954 | SLA        | 0.407701178 |
| ILMN_2412922 | C14orf43   | 0.407638555 |
| ILMN_1741869 | WDR47      | 0.407482394 |
| ILMN_3247797 | abParts    | 0.407442946 |
| ILMN_1720511 | LRN1       | 0.407430882 |
| ILMN_1752953 | BCL2L1     | 0.407422789 |
| ILMN_1784294 | CPA4       | 0.407355544 |
| ILMN_2365307 | CD276      | 0.407303643 |
| ILMN_1744239 | FEM1B      | 0.407229805 |
| ILMN_2094952 | NUAK2      | 0.407222553 |
| ILMN_2367753 | ATP2B4     | 0.407218499 |
| ILMN_1741422 | TUBB       | 0.407201682 |
| ILMN_1771308 | BAAT       | 0.407199747 |
| ILMN_1708041 | PLEKHF1    | 0.407175881 |
| ILMN_1751161 | COL7A1     | 0.407096496 |
| ILMN_2400935 | TAGLN      | 0.407066588 |
| ILMN_1796082 | HKSF7      | 0.406959719 |
| ILMN_1673363 | CD97       | 0.406934185 |
| ILMN_1759983 | DRL1       | 0.406876211 |
| ILMN_1720996 | SLC12A2    | 0.406797011 |
| ILMN_1675162 | AKO97193   | 0.406746567 |
| ILMN_1754130 | TNFRSF2    | 0.406745522 |
| ILMN_2325506 | BCAS4      | 0.406577416 |
| ILMN_2219351 | CENPO      | 0.406461651 |
| ILMN_1789913 | SMPD13B    | 0.406272747 |
| ILMN_1700378 | ZWILCH     | 0.406259845 |
| ILMN_1761540 | EMAF3F     | 0.406238147 |
| ILMN_2409167 | ANXA2      | 0.406224506 |
| ILMN_3236752 | COA53      | 0.406143591 |
| ILMN_2368530 | IL32       | 0.406121209 |
| ILMN_2148785 | GBP1       | 0.406038882 |
| ILMN_1750761 | NCR1       | 0.405996254 |
| ILMN_2297864 | MTMR14     | 0.405988887 |
| ILMN_1730622 | EVL        | 0.405957415 |
| ILMN_1725644 | UBE2D2     | 0.405716669 |
| ILMN_1764754 | RAMP1      | 0.405714535 |
| ILMN_2199768 | SLITR84    | 0.405650391 |
| ILMN_2129015 | AF1        | 0.405500332 |
| ILMN_2390427 | FLT4       | 0.405493508 |
| ILMN_2360291 | UGCG1      | 0.405471767 |
| ILMN_2066588 | TNFSF13B   | 0.405415117 |
| ILMN_3211199 | TNFS16     | 0.405297968 |
| ILMN_1777564 | MAD2L1     | 0.405280667 |
| ILMN_1700067 | BTNSA2     | 0.405223794 |
| ILMN_1768197 | ROD1       | 0.405205631 |
| ILMN_2382857 | AHMGAP9    | 0.405204775 |
| ILMN_2148919 | TUBA1A     | 0.405149089 |
| ILMN_1687592 | WWC3       | 0.405141879 |
| ILMN_3220934 | NCRNA00152 | 0.405108576 |
| ILMN_1767377 | SMA4       | 0.405050431 |
| ILMN_2400352 | URD9       | 0.405005518 |
| ILMN_1669584 | IL3        | 0.405000466 |
| ILMN_1798679 | ANO9       | 0.40484745  |
| ILMN_2396982 | BCL2L12    | 0.404433884 |
| ILMN_1681542 | HIST1H4E   | 0.404382048 |
| ILMN_1762899 | EGR1       | 0.404364304 |
| ILMN_2194118 | CtcfP16    | 0.404300658 |
| ILMN_1766551 | CPA3       | 0.404148165 |
| ILMN_1747499 | EMID1      | 0.404049613 |
| ILMN_2343775 | RPL38      | 0.404012236 |
| ILMN_1733157 | HSD11      | 0.403989191 |
| ILMN_1742432 | CO9BA1     | 0.403981554 |
| ILMN_1738694 | WNT7B      | 0.403914993 |
| ILMN_1781752 | CLEC16A    | 0.403776549 |
| ILMN_1775327 | PKM2       | 0.403756842 |
| ILMN_1791097 | R8N1       | 0.403753679 |
| ILMN_3211187 | TUBB2A     | 0.403753581 |
| ILMN_1685830 | SLC7A2     | 0.403556149 |
| ILMN_1747451 | PLCOD1     | 0.403531645 |
| ILMN_3182487 | IG272090   | 0.403487818 |
| ILMN_1808777 | EH2D       | 0.403307383 |
| ILMN_3245293 | AKO31885   | 0.403293098 |
| ILMN_1655046 | NUTF2      | 0.402886751 |
| ILMN_1654392 | KHNYN      | 0.402880539 |
| ILMN_1786612 | PSME2      | 0.402718929 |

|              |             |              |
|--------------|-------------|--------------|
| ILMN_1651604 | MARK4       | -0.579185945 |
| ILMN_3246802 | ABCPC1      | -0.579440398 |
| ILMN_2149809 | PF8M1       | -0.578964821 |
| ILMN_1759910 | SERPINA5    | -0.580196376 |
| ILMN_1663538 | CLYBL       | -0.580771636 |
| ILMN_3182171 | FGGY        | -0.581109618 |
| ILMN_1701497 | CD5L        | -0.581893967 |
| ILMN_2128278 | ESM1        | -0.582004199 |
| ILMN_2134314 | TCF1        | -0.582316287 |
| ILMN_1808379 | PLCD4       | -0.583094515 |
| ILMN_2147503 | ALG13       | -0.583274376 |
| ILMN_1771084 | ACSM3       | -0.584096354 |
| ILMN_1752214 | BC141517    | -0.584419315 |
| ILMN_1738576 | SNA         | -0.585369606 |
| ILMN_1719468 | EPM2A       | -0.586245529 |
| ILMN_1712430 | ATP5G1      | -0.586448069 |
| ILMN_1748819 | MRRP22      | -0.586779542 |
| ILMN_1681437 | DCX4        | -0.587712567 |
| ILMN_1708635 | SIC8A11     | -0.587937657 |
| ILMN_1802027 | MGST2       | -0.588165283 |
| ILMN_1826447 | BXID7250    | -0.589681093 |
| ILMN_1712088 | LYBL        | -0.589726246 |
| ILMN_1732808 | TDK3        | -0.590095958 |
| ILMN_2067882 | LOC401431   | -0.591891252 |
| ILMN_1782579 | HMMT        | -0.59292823  |
| ILMN_1705066 | BTBD11      | -0.592983431 |
| ILMN_3288525 | NA          | -0.593028202 |
| ILMN_1725262 | ESM1        | -0.593092449 |
| ILMN_1784278 | LRRC37A3    | -0.593167415 |
| ILMN_1685978 | ATP1F1      | -0.594923735 |
| ILMN_1696675 | CE2         | -0.594988276 |
| ILMN_1678720 | SULT1C2P1   | -0.595613107 |
| ILMN_1858665 | AW429225    | -0.595837395 |
| ILMN_1722981 | SPH4        | -0.596505312 |
| ILMN_2078074 | MUT         | -0.596139871 |
| ILMN_1836218 | LOC25845    | -0.596157116 |
| ILMN_1792744 | SLC13A2     | -0.597663072 |
| ILMN_1763196 | WDR72       | -0.597813654 |
| ILMN_227817  | GSTA3       | -0.597837469 |
| ILMN_1896474 | AW269407    | -0.597824984 |
| ILMN_2226224 | BRP44L      | -0.598397894 |
| ILMN_1751258 | NDUFA4      | -0.598635717 |
| ILMN_1908274 | AW266020    | -0.599600223 |
| ILMN_2275239 | RNG1        | -0.600271458 |
| ILMN_1746819 | C5          | -0.600883539 |
| ILMN_1685496 | RG57        | -0.602245302 |
| ILMN_1727178 | C11orf92    | -0.602617445 |
| ILMN_1685703 | ACOX2       | -0.602707363 |
| ILMN_1466519 | MEI1        | -0.603278974 |
| ILMN_1809695 | CAMK2G      | -0.603207024 |
| ILMN_1726273 | ATP6V1G3    | -0.604313858 |
| ILMN_2376133 | KIAA1191    | -0.605124466 |
| ILMN_1740920 | ACAD5B      | -0.605260298 |
| ILMN_1729482 | PLT5        | -0.60583946  |
| ILMN_2196588 | C16orf32    | -0.608610031 |
| ILMN_1761058 | NHP3-ACAD11 | -0.60936502  |
| ILMN_3306997 | METTL1      | -0.60940641  |
| ILMN_3239925 | LOC25845    | -0.610644013 |
| ILMN_1824490 | RG618056    | -0.610809066 |
| ILMN_2054607 | CYP4V2      | -0.611190169 |
| ILMN_1728467 | GHTM        | -0.613134427 |
| ILMN_2161832 | VPS37A      | -0.613523403 |
| ILMN_1801443 | TKM1        | -0.615246496 |
| ILMN_1704247 | LAMA3       | -0.616805915 |
| ILMN_2143097 | NCALD       | -0.617285357 |
| ILMN_1685441 | ASAP3       | -0.617627034 |
| ILMN_1745988 | NUDT12      | -0.621088638 |
| ILMN_1788895 | SRO5A2      | -0.621494099 |
| ILMN_1736699 | SLITR83     | -0.623097006 |
| ILMN_1777797 | AFM         | -0.623559015 |
| ILMN_1670542 | AK2         | -0.62558549  |
| ILMN_2232036 | EFCAB7      | -0.625854312 |
| ILMN_1763992 | NCCO1       | -0.626401725 |
| ILMN_1798853 | CTSLP2      | -0.626849597 |
| ILMN_2341548 | MYO5B       | -0.62916488  |
| ILMN_1826572 | AKO94562    | -0.630831038 |
| ILMN_1878728 | DB22718     | -0.6308546   |
| ILMN_1684585 | ACSL1       | -0.631805074 |
| ILMN_1650059 | SLC25A6     | -0.631966776 |
| ILMN_1768719 | RDM11       | -0.632212543 |
| ILMN_2124361 | LEAP2       | -0.634775452 |
| ILMN_1791588 | S71824      | -0.642483736 |
| ILMN_1727309 | FAM82A2     | -0.642564793 |
| ILMN_2199439 | CA2         | -0.643390117 |
| ILMN_1700810 | HS900A1     | -0.645977781 |
| ILMN_1694106 | GPD1L       | -0.656480919 |
| ILMN_1779241 | CRYM        | -0.658657608 |
| ILMN_1748352 | CTSL2       | -0.659837865 |
| ILMN_1770245 | EP8A1L5     | -0.660070465 |
| ILMN_1753877 | MYADM2      | -0.660219722 |
| ILMN_1778357 | DNMT3L      | -0.660374324 |
| ILMN_3246634 | SDHA        | -0.662612025 |
| ILMN_2145250 | CTSLP8      | -0.665062308 |
| ILMN_2193936 | HMG         | -0.668100275 |
| ILMN_1654151 | COX6C       | -0.675159256 |
| ILMN_1706579 | SHBG        | -0.676413554 |
| ILMN_1803673 | LOC113230   | -0.677095151 |
| ILMN_2050911 | SLC22A4     | -0.686403787 |
| ILMN_3270242 | LICREF5     | -0.689758015 |
| ILMN_1678965 | FABP1       | -0.69801149  |
| ILMN_1740418 | CYP27B1     | -0.716855413 |
| ILMN_1794844 | THRSP       | -0.723994052 |

|              |              |             |
|--------------|--------------|-------------|
| ILMN_2230998 | TMEM186      | 0.402696872 |
| ILMN_1652611 | CID          | 0.402689208 |
| ILMN_2350206 | FBXO46       | 0.402655401 |
| ILMN_1685371 | SJMF2        | 0.402593428 |
| ILMN_1654065 | ATOX8        | 0.402590865 |
| ILMN_3246391 | SNORD52      | 0.402522447 |
| ILMN_2070375 | GPR82        | 0.402338398 |
| ILMN_1796085 | PPM1B        | 0.402315368 |
| ILMN_1706434 | CSDAP1       | 0.402292386 |
| ILMN_1704753 | EPAS1        | 0.402216039 |
| ILMN_3262298 | LOC100180357 | 0.402075502 |
| ILMN_1663866 | TGFB1        | 0.402040888 |
| ILMN_1674519 | ZP2          | 0.401815798 |
| ILMN_1814799 | S100A13      | 0.401656514 |
| ILMN_2364828 | OGT          | 0.401545481 |
| ILMN_1762787 | RNF26        | 0.401529643 |
| ILMN_1698100 | ANKZF2       | 0.40146465  |
| ILMN_2289346 | AK747493     | 0.401407661 |
| ILMN_2222234 | PRDM4        | 0.401386729 |
| ILMN_2243912 | RAB37        | 0.401302072 |
| ILMN_1784717 | RPS19        | 0.401267792 |
| ILMN_1779185 | SPECC1L      | 0.401240483 |
| ILMN_1697220 | NTSE         | 0.401130225 |
| ILMN_1719105 | KRTAP20-1    | 0.401072137 |
| ILMN_1733947 | FKBP8        | 0.401029305 |
| ILMN_3283015 | NSA2         | 0.400993922 |
| ILMN_1697417 | CEP170       | 0.400772249 |
| ILMN_1802251 | PTTG1IP      | 0.400745049 |
| ILMN_1717327 | KCNJ14       | 0.400746433 |
| ILMN_1680435 | NPEPPS       | 0.40068875  |
| ILMN_1784364 | STARO5       | 0.400666852 |
| ILMN_1842797 | AW293882     | 0.400634792 |
| ILMN_1830984 | BT509118     | 0.400628025 |
| ILMN_3178471 | ESPL1        | 0.400613827 |
| ILMN_2412214 | HUAT         | 0.400468568 |
| ILMN_1743137 | PRRC2C       | 0.400366982 |
| ILMN_1873838 | IGKC         | 0.400154093 |
| ILMN_1787951 | RABL5        | 0.400100335 |
| ILMN_1831763 | BCD99D11     | 0.400010768 |