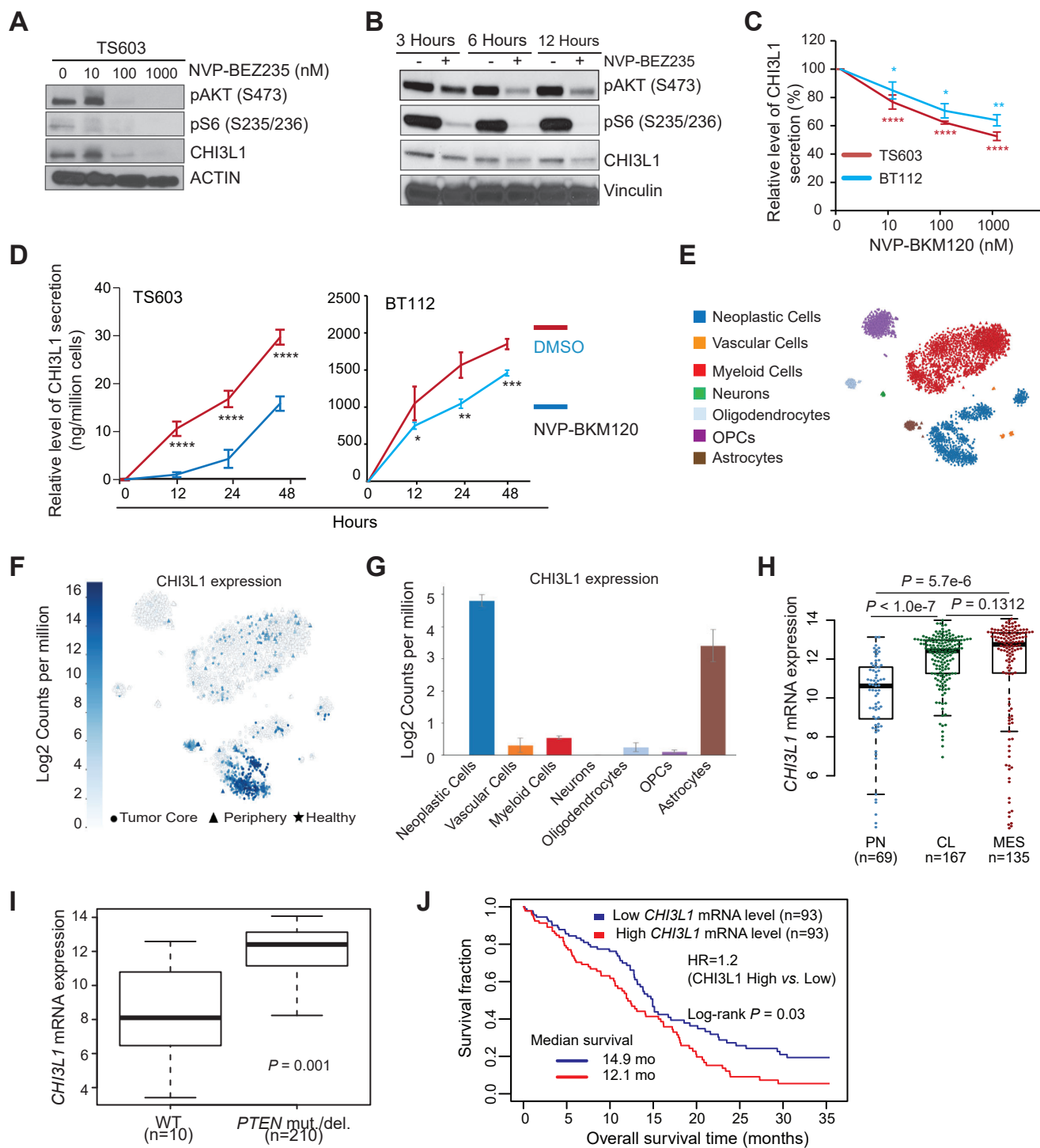


## **Supplemental Data**

Supplemental Figures 1-7

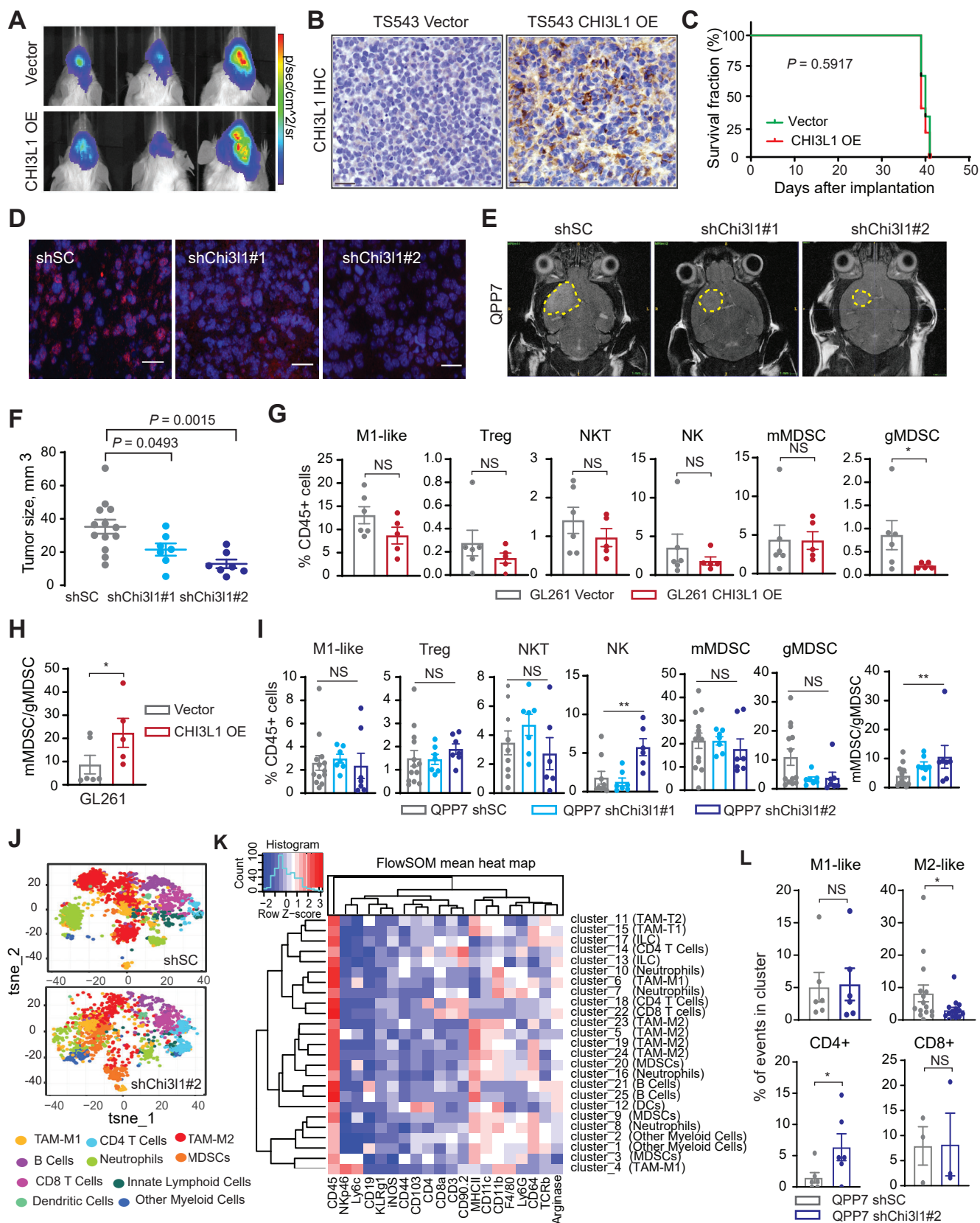
Supplemental Tables 1-3

Supplemental Methods



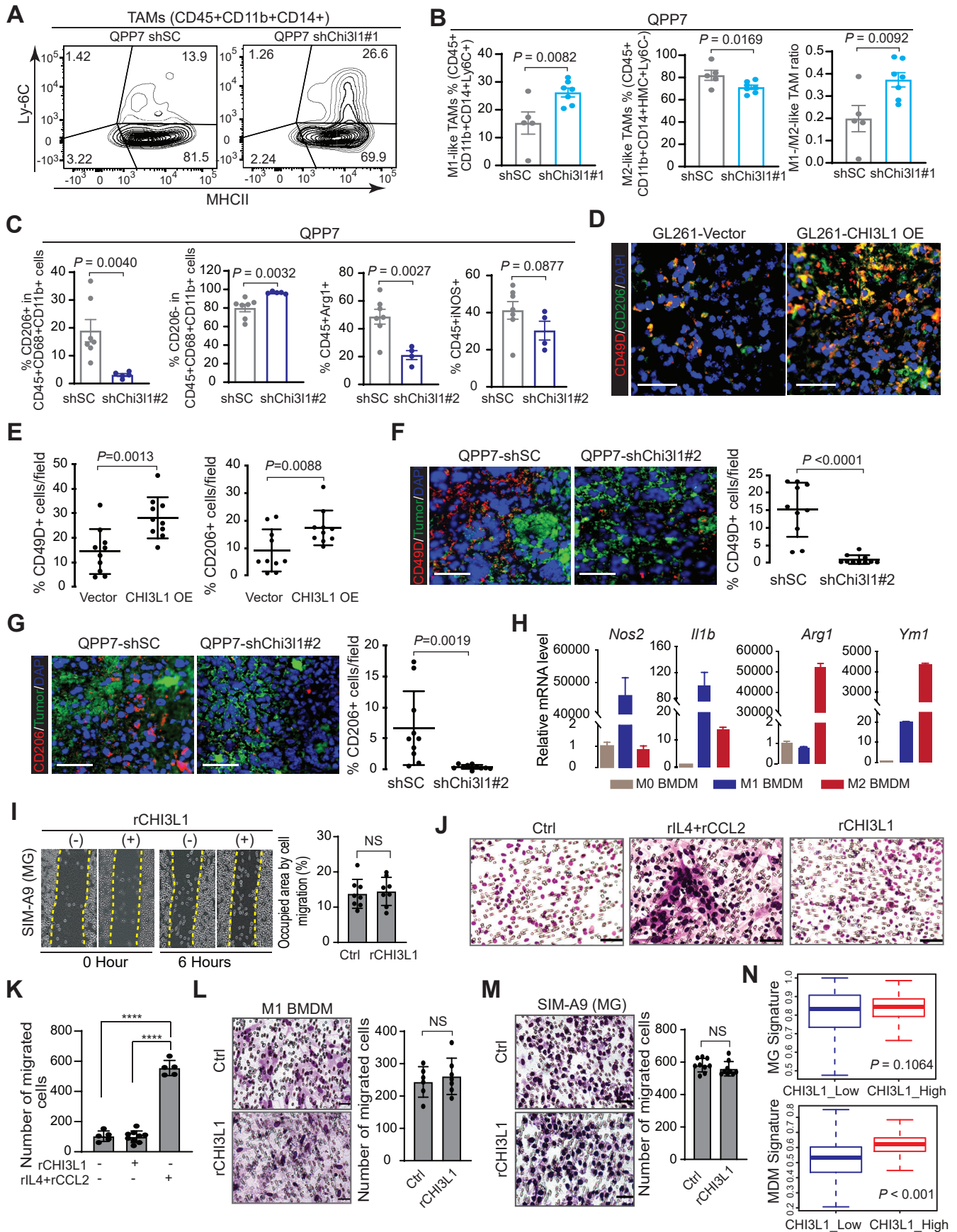
**Supplemental Figure 1. CHI3L1 is regulated by PI3K/AKT/mTOR signaling and is related to molecular and clinical features of GBM.**

Immunoblot analysis (IB) of indicated proteins in patient GBM neurosphere line TS603 treated with NVP-BEZ235 in a dose (A) and time (B) dependent manner. CHI3L1 secretion in the conditioned cell culture media was assessed by ELISA from patient GBM neurosphere lines treated with NVP-BKM120 at indicated concentrations after 24 hours of treatment (C) or at the concentration of 1  $\mu$ M in indicated times (D); error bars represent the mean  $\pm$  SD ( $n \geq 3$  replicates);  $P$ -value was calculated by a one-tailed unpaired  $t$  test; \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ , and \*\*\*\* $P < 0.0001$ . (E-G) CHI3L1 expression in various cell types within the TME from GBM patients' specimens based on analyzing a publicly available single-cell RNA seq dataset (19). The data were generated by a web tool (<http://www.gbmseq.org/>). (H) *CHI3L1* mRNA expression in proneural (PN), classical (CL), and mesenchymal (MS) subtypes.  $P$ -value was calculated by two-way ANOVA with Tukey's multiple comparison test. (I) Enrichment of *CHI3L1* mRNA expression in GBM with *PTEN* alterations (mutation and deletion) vs *PTEN* wildtype based on TCGA dataset analysis.  $P$ -value was calculated by Wilcoxon rank-sum test. (J) Overall survival analysis of TCGA GBM. Red and blue lines show survival curves of the top 25% tumors with the highest and lowest *CHI3L1* mRNA expression, respectively.



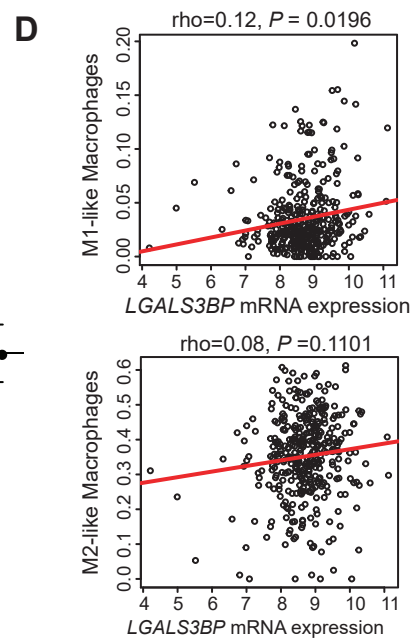
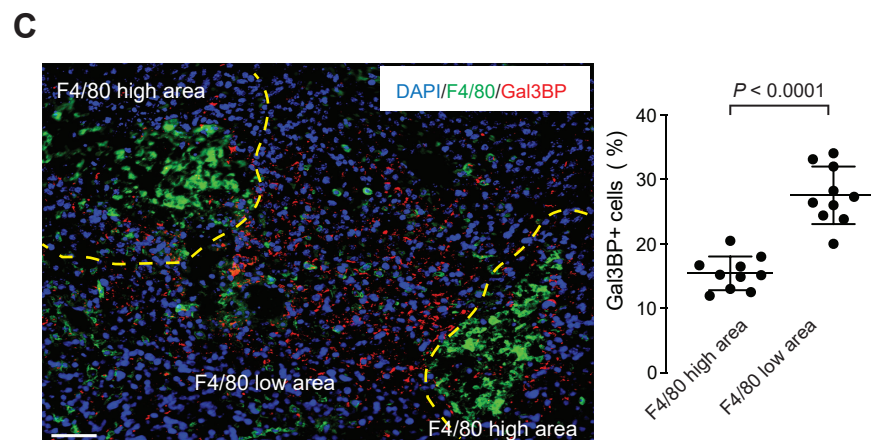
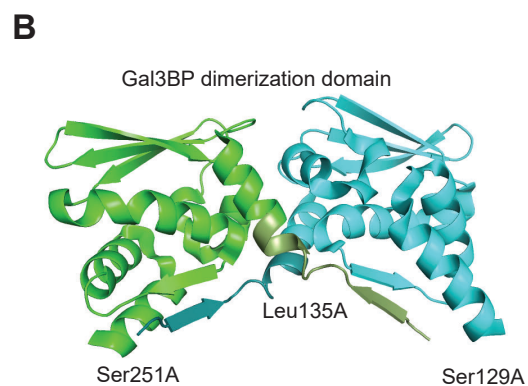
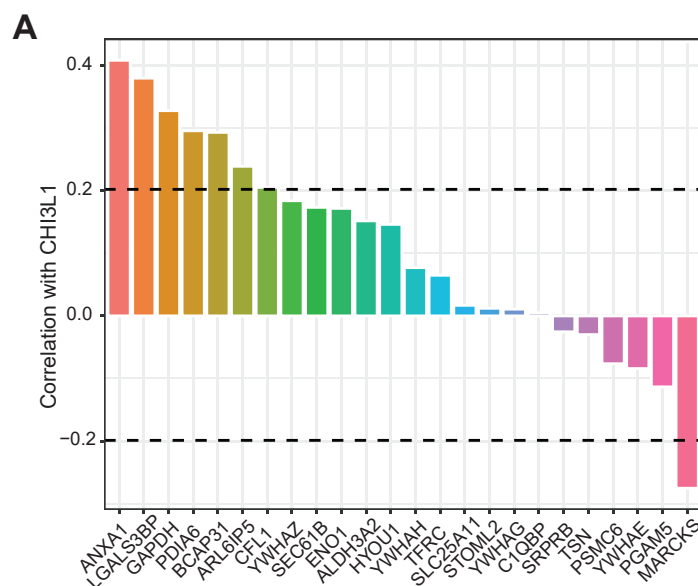
**Supplemental Figure 2. Overexpression and knockdown of CHI3L1 affect the frequency of immune cell types in glioma mouse models.**

(A) Representative *in vivo* images (IVIS) of luminescence shown in the brain of SCID mice carrying intracranial tumor derived from TS543 overexpressing vector control or CHI3L1 at 39 days after implantation. (B) Representative IHC images showing CHI3L1 expression in tumors derived from TS543 overexpressing CHI3L1 vs vector control. Scale bar, 50  $\mu$ m. (C) Kaplan–Meier tumor-free survival analysis. *P*-value was calculated by log-rank test. (D) Representative images showing CHI3L1 levels in tumors derived from QPP7 glioma-bearing mice by IF staining. Scale bar, 50  $\mu$ m. (E) Representative MRI from a syngeneic glioma mouse model bearing QPP7 with shChi3l1#1 and shChi3l1#2 vs shSC. (F) Tumor volume was measured by the T2 MRI scan in mice from (E). *P*-value was calculated by one-way ANOVA with Dunnett's multiple comparison test. Flow cytometry analyses of the indicated cell populations in GL261 (G, H) and QPP7 (I) derived syngeneic mouse models, including M1-like TAMs (CD45<sup>+</sup>CD11b<sup>+</sup>CD14<sup>+</sup>Ly6C<sup>+</sup>), Treg cells (CD45<sup>+</sup>CD3<sup>+</sup>CD4<sup>+</sup>CD25<sup>+</sup>CD127<sup>-</sup>), NKT cells (CD45<sup>+</sup>CD3<sup>+</sup>NK1.1<sup>+</sup>), NK cells (CD45<sup>+</sup>CD3<sup>+</sup>NK1.1<sup>+</sup>), monocytic MDSC (mMDSC, CD45<sup>+</sup>CD11b<sup>+</sup>Ly6G<sup>-</sup>Ly6C<sup>+</sup>), granulocytic MDSC (gMDSC, CD45<sup>+</sup>CD11b<sup>+</sup>Ly6G<sup>+</sup>Ly6C<sup>-</sup>), and the ratio of mMDSC/gMDSC. Each dot represents one mouse from the groups; error bars represent mean  $\pm$  SEM; *P*-value was calculated by a one-tailed unpaired *t* test in (G, H) and one-way ANOVA in (I); \**P* < 0.05, \*\**P* < 0.01; NS represents no significance. (J) t-distributed Stochastic Neighbor Embedding (t-SNE) plot of cell types in three pairs of tumors derived QPP7 glioma-bearing mice with shChi3l1#2 vs shSC. (K) Heatmap showing the degree of expression of genes on indicated clusters to define each immune cell type. (L) Quantitation of the percent of events identified as indicated cell populations from QPP7-derived tumors with shSC and shChi3l1#2 (n=3). *P*-value was calculated by a one-tailed unpaired *t* test; data are presented as the mean  $\pm$  SEM; \**P* < 0.05; NS represents no significance.



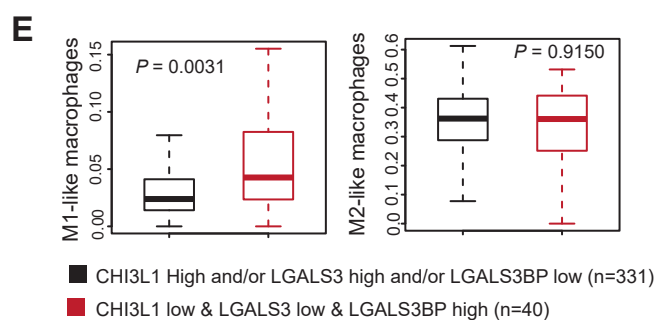
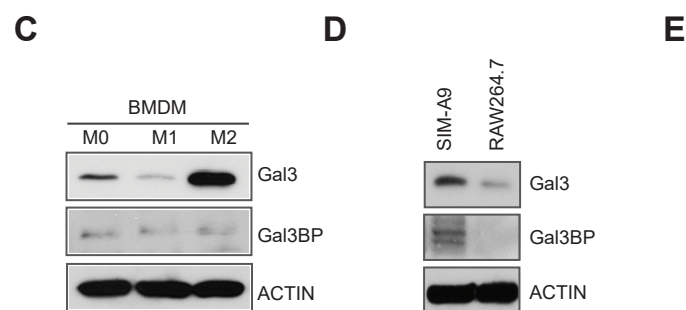
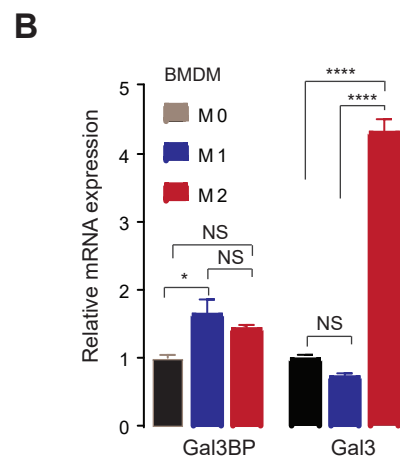
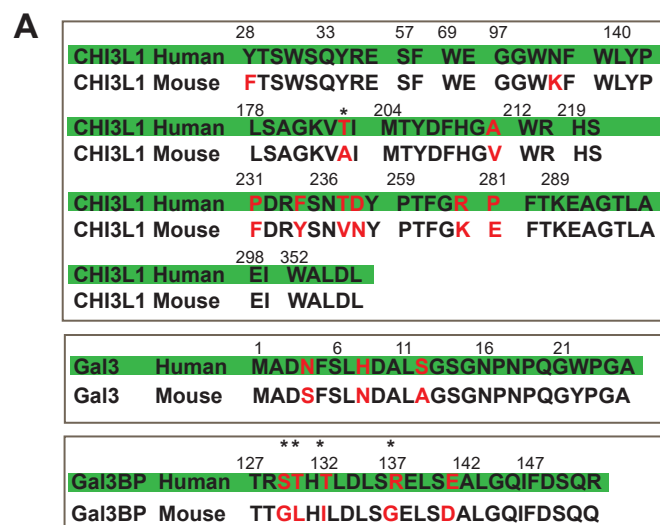
### Supplemental Figure 3. CHI3L1 regulates BMDM and microglial cell migration.

Representative flow cytometry analyses (**A**) and quantitation (**B**) showing the percentage of M1- and M2-like MDMs in tumors derived from QPP7 glioma-bearing mice with shChi3l1#1 vs shSC. (**C**) Quantitation of the percentage of indicated cell populations in tumors derived QPP7 glioma-bearing mice with shChi3l1#2 vs shSC. Each dot represents 1 mouse; data are presented as the mean  $\pm$  SEM; *P*-value was calculated by a one-tailed unpaired *t* test. Representative IF images and quantitation for CD49D and CD206 staining in tumor sections from GL261 (**D** and **E**) and QPP7 (**F** and **G**) derived glioma models, respectively. Each dot represents one field of indicated tumor regions ( $n \geq 3$ ); data are presented as the mean  $\pm$  SD; *P*-value was calculated by a one-tailed unpaired *t* test; scale bar, 50  $\mu$ m. (**H**) qRT-PCR for the hallmark gene expression of polarized BMDMs. (**I**) Representative brightfield images and quantitation showing microglial cell migration in 0 and 6 hours after treatment with CHI3L1 recombinant protein (rCHI3L1) at the concentration of 0.6  $\mu$ g/mL in the scratch-wound healing assay. Migration was assessed by quantifying occupied areas by migrated cells. Representative brightfield images and quantitation for cell migration of M0 BMDMs (**J** and **K**), M1 BMDMs (**L**), and microglial cell line (**M**) in the Transwell assay. Recombinant CCL2 protein (rCCL2, 20 ng/mL) and IL4 protein (rIL4, 20 ng/mL) were used as the positive control. Cell migration was assessed by determining the number of migrated cells. Data are presented as the mean  $\pm$  SD from at least three independent experiments; *P*-value was calculated by a one-tailed unpaired *t* test in (**I**, **L**, and **M**) or one-way ANOVA with Tukey's multiple comparison test in (**K**); \*\*\*\**P* < 0.0001; NS represents no significance; scale bar, 50  $\mu$ m. (**N**) Enrichment of MDM and MG signature in TCGA GBM with low and high levels of CHI3L1. *P*-value was calculated by Wilcoxon rank-sum test.



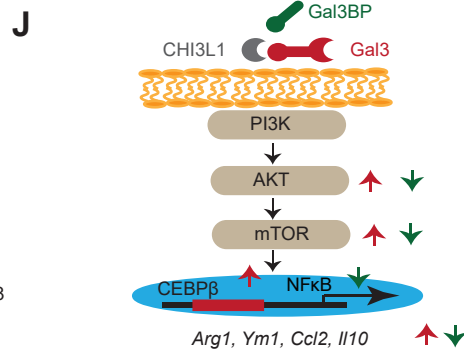
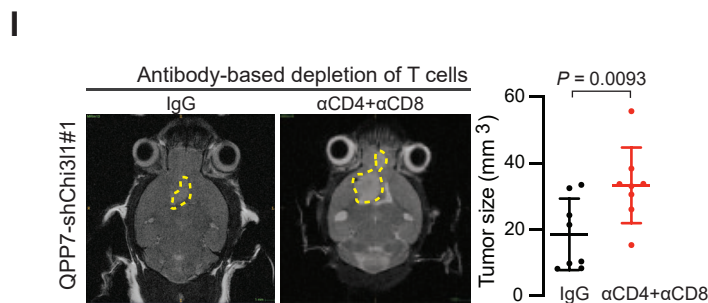
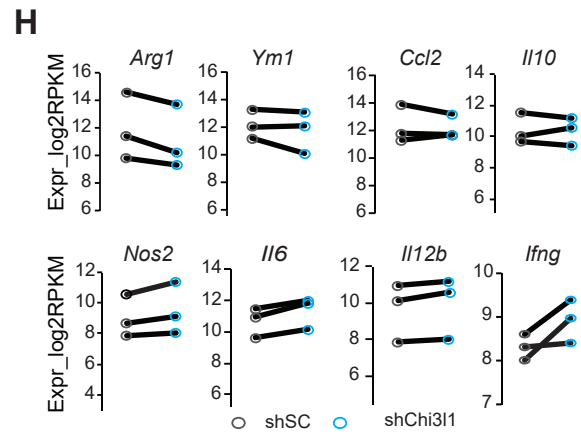
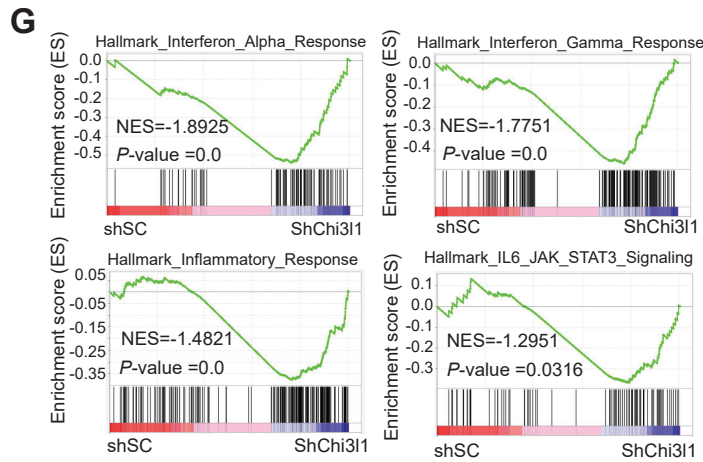
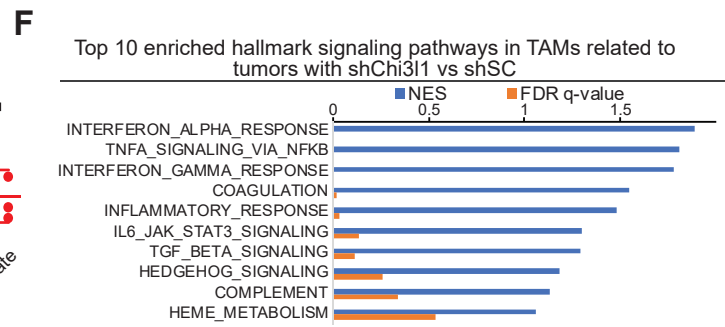
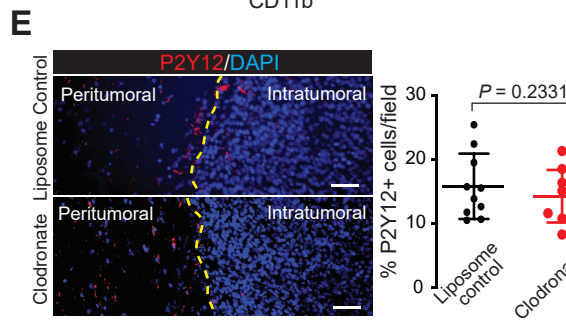
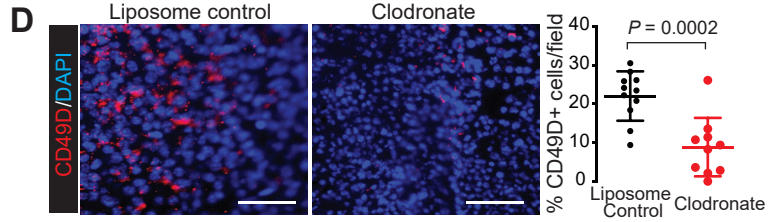
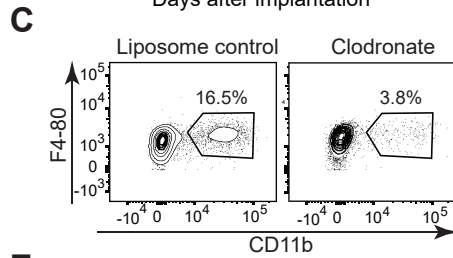
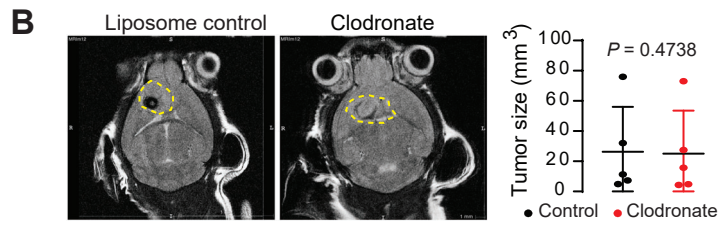
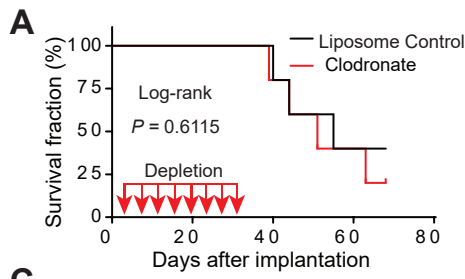
#### **Supplemental Figure 4. Identification of Gal3BP and association with macrophages.**

(A) The colorful histogram showing candidate genes of putative binding protein with CHI3L1 and their Pearson correlation coefficient in TCGA IDHwt GBM datasets. (B) Gal3BP dimerization domain (PDB 6GFB). Two monomers are shown in green/cyan. The dimer is mostly stabilized by antiparallel strand between Ser129-Leu135 of one monomer and Arg215 and Thr220 on the other. Confirmation is reminiscent of a domain swapping interaction. (C) Representative IF image showing expression of F4/80 and Gal3BP in tumors derived from syngeneic mice bearing GL261-CHI3L1. Quantitation was based on the percentage of Gal3BP<sup>+</sup> cells in the tumor regions with higher and lower levels of F4/80 expression separated by yellow dash lines. Each dot represents one field of indicated regions from indicated tumors (n≥3); data are presented as the mean ± SD; *P*-value was calculated by a one-tailed unpaired *t* test; scale bar, 50 μm. (D) Correlation between *LGALS3BP* mRNA expression and M1/M2-like macrophage signature in IDHwt GBM. *P*-value was calculated by Spearman rank correlation.



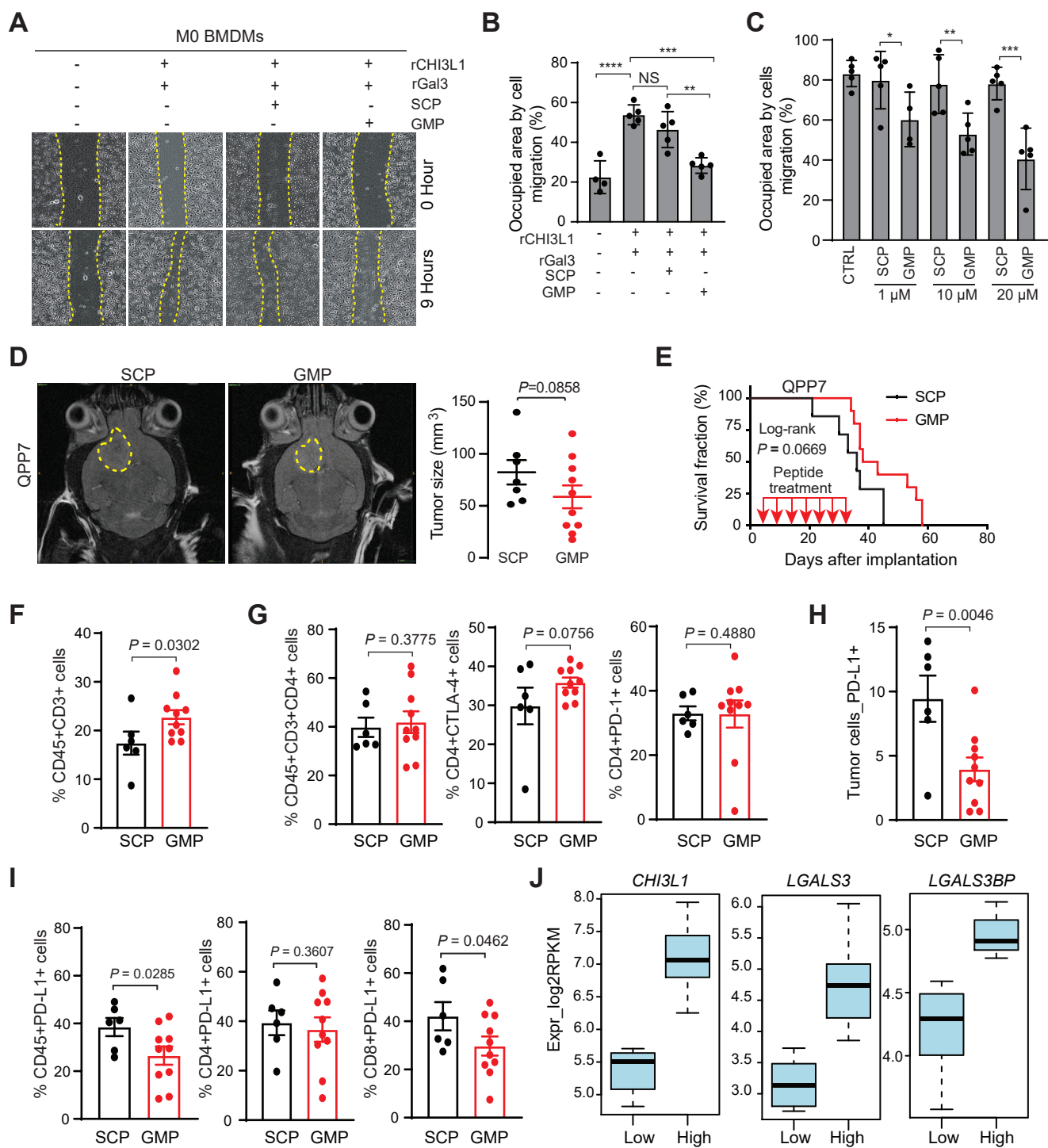
**Supplemental Figure 5. Sequence alignment and association among CHI3L1, Gal3, and Gal3BP.**

(A) Sequence alignments of binding domains of CHI3L1, Gal3, and Gal3BP in the human and mouse. The red letters (without star sign) represent different amino acids in the human and mouse but have similar properties. Different amino acids in the human and mouse are indicated with star signs. (B) qRT-PCR for mouse *Lgals3bp* gene expression in polarized BMDMs. Data are presented as the mean  $\pm$  SD from three replicates; *P*-value was calculated by one-way ANOVA with Tukey's multiple comparison test, \**P* < 0.05, \*\*\*\**P* < 0.0001; NS represents no significance. (C) Immunoblot analysis of Gal3 and Gal3BP levels in polarized BMDMs. (D) Immunoblot analysis of Gal3 and Gal3BP levels in a microglial cell line (SIM-A9) and mouse macrophage cell line (RAW264.7). (E) Boxplots showing enrichment of M1/M2-like macrophage signature in two indicated groups of TCGA GBMs. *P*-value was calculated by Wilcoxon rank-sum test.



**Supplemental Figure 6. *Chi3l1* gene knockdown reprograms MDMs toward a proinflammatory phenotype in tumor regression.**

Depletion of macrophages in C57BL/6 mice bearing glioma with GL261-CHI3L1 by an intravenous injection of clodronate liposomes vs control liposomes (100  $\mu$ L per mouse) every 2 days for a total of 8 times. **(A)** Kaplan–Meier tumor-free survival analysis of the mice with the treatment of clodronate vs control liposomes. **(B)** Tumor volume was measured by the T2 MRI scan. Each dot represents one mouse in the groups; data are presented as the mean  $\pm$  SD; *P*-value was calculated by a one-tailed unpaired *t* test. **(C)** Representative flow cytometry analysis showing the percentage of CD11b<sup>+</sup>F4/80<sup>+</sup> cells in blood from the mice with the treatment of clodronate vs control liposomes. Representative IF images for CD49D<sup>+</sup> **(D)** and P2Y12<sup>+</sup> **(E)** cells in tumor regions from mice with the treatment of clodronate vs control liposomes. Each dot represents one field of tumor regions from the groups; data are presented as the mean  $\pm$  SD; *P*-value was calculated by a one-tailed unpaired *t* test; scale bar 50  $\mu$ m **(D)** and 100  $\mu$ m **(E)**. **(F)** Top 10 enrich hallmark signaling pathways in TAMs derived from C57BL/6 mice bearing QPP7 with shChi3l1 compared to shSC. **(G)** GSEA plots depicting indicated signaling pathways in TAMs derived from C57BL/6 mice bearing QPP7 with shChi3l1 compared to shSC. NES stands for normalized enrichment score. **(H)** RNA-seq data showing indicated gene expression in TAMs isolated from three pairs of C57BL/6 mice bearing QPP7 with shChi3l1 compared to shSC. **(I)** Representative MRI from syngeneic glioma mouse models bearing QPP7 with shChi3l1 treating with antibodies against CD4 and CD8 (10 mg/kg) by intraperitoneal injection every 2 days for a total of 8 times after tumor implantation. Tumor volume was measured by the T2 MRI scan. Each dot represents 1 mouse; data are presented as the mean  $\pm$  SD; *P*-value was calculated by a one-tailed unpaired *t* test. **(J)** The schematic model depicts that the CHI3L1-Gal3 protein complex regulates the PI3K/AKT/mTOR signaling pathway in MDM, leading to inhibiting NF $\kappa$ B activation, but promoting CEBP $\beta$  activation, thereby upregulating protumor factors for immune suppression and tumor growth. Gal3BP can negatively regulate this signaling pathway by competing with Gal3 to bind CHI3L1.



**Supplemental Figure 7. Treatment with Gal3BP mimetic peptide leads to inhibiting BMDM migration *in vitro* and tumor immunity *in vivo*.**

(A) Representative brightfield images for cell migration of M0 BMDMs treated with rCHI3L1 (2.5  $\mu\text{g/mL}$ ), rGal3 (2.5  $\mu\text{g/mL}$ ), GMP (30  $\mu\text{M}$ ), SCP (30  $\mu\text{M}$ ), and indicated combinations in the scratch-wound healing assay. (B) Cell migration was assessed by quantifying the occupied area of migrated cells. (C) Histogram showing cell migration assessed by quantifying the occupied area of migrated cells in M2 BMDMs under the treatment with rCHI3L1 (0.6  $\mu\text{g/mL}$ ) with the different concentrations of GMP or SCP for 6 hours. Data are presented as the mean  $\pm$  SD from at least three independent experiments; *P*-value was calculated by one-way ANOVA with Tukey's multiple comparison test (B) and one-tailed unpaired *t* test (C); \**P* < 0.05, \*\**P* < 0.01; \*\*\**P* < 0.001; \*\*\*\**P* < 0.0001; NS represents no significance. (D) Representative MRI from mice bearing QPP7 tumors after the treatment with SCP and GMP, respectively. Tumor volume was measured by T2 sequences for infiltrative tumors in the mouse brain (yellow line). (E) Kaplan–Meier tumor-free survival analysis of mice bearing QPP7 tumors treating with indicated peptides. (F–I) Frequency of indicated immune cell types in tumors derived from mice bearing GL261-CHI3L1 cells under the treatment with GMP vs SCP. Each dot represents 1 mouse; data are presented as the mean  $\pm$  SEM; *P*-value was calculated by a one-tailed unpaired *t* test. (I) Boxplots showing low and high mRNA expression levels of indicated genes in GBM patients following anti-PD-1 immune checkpoint therapy based on a published RNA-seq dataset (41).

**Supplemental Table S1 Genes are significantly correlated to CHI3L1 in TCGA GBM dataset**

| Gene     | case.mean  | control.mean | s2n        | p        | FDR      |
|----------|------------|--------------|------------|----------|----------|
| CHI3L1   | 12.6953396 | 8.963619543  | 1.33038382 | 4.76E-73 | 5.74E-69 |
| PLA2G5   | 7.17859191 | 4.940500435  | 0.83306618 | 7.86E-42 | 9.46E-38 |
| PBEF1    | 10.9067009 | 9.282892573  | 0.80299784 | 9.24E-42 | 1.11E-37 |
| RNASE2   | 7.18101322 | 5.645627102  | 0.7563372  | 5.21E-37 | 6.27E-33 |
| HRH1     | 7.53076212 | 6.217493106  | 0.74758178 | 3.27E-37 | 3.93E-33 |
| PTX3     | 8.8135652  | 6.455513002  | 0.74552202 | 2.69E-37 | 3.23E-33 |
| CHI3L2   | 9.28194518 | 6.802699691  | 0.73843268 | 1.60E-36 | 1.93E-32 |
| MAN1C1   | 9.36784354 | 7.498898898  | 0.72934947 | 1.66E-36 | 1.99E-32 |
| TIMP1    | 11.8400831 | 10.51626828  | 0.71441624 | 3.22E-38 | 3.87E-34 |
| TNFRSF1A | 8.52074945 | 7.611531774  | 0.70252371 | 6.70E-35 | 8.06E-31 |
| PDPN     | 8.9515335  | 7.110154077  | 0.68780607 | 2.65E-33 | 3.19E-29 |
| FCGBP    | 10.3520235 | 8.104821549  | 0.68047071 | 2.56E-31 | 3.08E-27 |
| CEBPD    | 8.46340582 | 7.604622564  | 0.67134104 | 2.52E-32 | 3.03E-28 |
| SERPINA3 | 12.4101076 | 10.35777802  | 0.65916496 | 1.51E-31 | 1.81E-27 |
| STEAP3   | 7.69133605 | 6.414198684  | 0.65342489 | 1.64E-30 | 1.97E-26 |
| CA12     | 7.96352599 | 6.329209587  | 0.65278869 | 2.58E-31 | 3.10E-27 |
| CXCL14   | 9.24083534 | 6.698386634  | 0.6513333  | 1.88E-30 | 2.27E-26 |
| SOD2     | 8.13638176 | 6.769062406  | 0.64941343 | 4.94E-31 | 5.94E-27 |
| CLEC5A   | 6.50774426 | 5.105047372  | 0.64864938 | 1.96E-30 | 2.35E-26 |
| LTF      | 9.55214681 | 6.379816619  | 0.64169903 | 5.82E-30 | 7.00E-26 |
| DPYD     | 8.8856625  | 7.328917712  | 0.64104848 | 2.68E-32 | 3.23E-28 |
| CHST2    | 8.89886404 | 7.687568659  | 0.64086132 | 3.51E-32 | 4.22E-28 |
| EMP3     | 9.4544323  | 7.992512062  | 0.63808785 | 6.68E-30 | 8.02E-26 |
| EFEMP2   | 8.1677509  | 7.050469169  | 0.63042925 | 1.47E-29 | 1.76E-25 |
| C21orf62 | 7.58331744 | 5.814259535  | 0.62826617 | 1.80E-26 | 2.16E-22 |
| PLTP     | 9.65916208 | 8.278175279  | 0.62206116 | 3.67E-27 | 4.41E-23 |
| CCL2     | 9.48877403 | 7.465487826  | 0.62175537 | 1.60E-28 | 1.92E-24 |
| LGALS3   | 11.8177087 | 10.49960509  | 0.62070081 | 5.28E-30 | 6.34E-26 |
| PMP22    | 11.2380702 | 10.13386308  | 0.60459724 | 7.59E-30 | 9.13E-26 |
| CD44     | 8.92317691 | 7.688712909  | 0.60242432 | 2.21E-27 | 2.66E-23 |
| PLA2G2A  | 7.59760808 | 5.42437722   | 0.60146788 | 3.72E-29 | 4.47E-25 |
| EFEMP1   | 10.2560276 | 8.541825843  | 0.59390981 | 1.93E-26 | 2.32E-22 |
| RHOG     | 8.69520281 | 7.967732469  | 0.59318556 | 9.53E-28 | 1.14E-23 |
| FPR1     | 6.32091846 | 5.688231389  | 0.59133725 | 1.46E-26 | 1.76E-22 |
| CFI      | 8.08891828 | 6.641087851  | 0.59059157 | 3.51E-27 | 4.22E-23 |
| CHPT1    | 9.44734605 | 8.621008248  | 0.58925641 | 5.24E-29 | 6.30E-25 |
| ABCC3    | 6.77436499 | 5.422688862  | 0.58746074 | 3.06E-27 | 3.68E-23 |
| VAMP5    | 6.80622516 | 5.975032855  | 0.58632505 | 9.54E-27 | 1.15E-22 |
| C5AR1    | 6.84227451 | 5.724859176  | 0.58415392 | 2.79E-27 | 3.35E-23 |
| SERPING1 | 9.06862183 | 7.602303704  | 0.58217825 | 1.20E-25 | 1.44E-21 |
| C1RL     | 6.95094076 | 5.836031604  | 0.57971471 | 1.61E-25 | 1.93E-21 |
| HAMP     | 7.67090827 | 6.044289351  | 0.57809147 | 6.95E-26 | 8.34E-22 |
| C1S      | 9.82394733 | 8.320822144  | 0.57563779 | 3.76E-25 | 4.51E-21 |
| MRC2     | 7.98005186 | 7.092448145  | 0.57390182 | 5.67E-26 | 6.80E-22 |
| CCDC109B | 8.32849431 | 7.358296331  | 0.57357386 | 5.38E-27 | 6.45E-23 |
| CTSB     | 10.6616567 | 9.860565076  | 0.57185034 | 3.08E-28 | 3.70E-24 |
| CD63     | 12.6276631 | 12.16043846  | 0.56616911 | 1.50E-25 | 1.80E-21 |

|            |            |             |            |          |          |
|------------|------------|-------------|------------|----------|----------|
| TPP1       | 8.80677417 | 7.959364046 | 0.56415846 | 6.57E-26 | 7.88E-22 |
| DIRAS3     | 7.32309718 | 5.826391284 | 0.56237297 | 1.85E-25 | 2.22E-21 |
| STAB1      | 7.92761907 | 6.83647896  | 0.55951021 | 7.61E-25 | 9.11E-21 |
| NR2E1      | 7.82842743 | 6.075190181 | 0.5590407  | 9.88E-20 | 1.17E-15 |
| FCGR2A     | 7.77477694 | 6.650291106 | 0.55862813 | 8.58E-26 | 1.03E-21 |
| PTRF       | 7.41259487 | 6.46158509  | 0.55862561 | 8.55E-25 | 1.02E-20 |
| DPY19L1    | 9.20491951 | 8.265651876 | 0.55837638 | 3.05E-24 | 3.65E-20 |
| TNC        | 10.7283844 | 9.272990918 | 0.55741657 | 2.89E-24 | 3.46E-20 |
| PYGL       | 7.93206766 | 6.907096313 | 0.55651198 | 4.05E-24 | 4.85E-20 |
| C1orf54    | 9.17494623 | 8.222044342 | 0.55646838 | 2.05E-26 | 2.45E-22 |
| NRCAM      | 9.13011281 | 7.988490855 | 0.55623885 | 4.46E-22 | 5.32E-18 |
| SRPX2      | 7.00416422 | 5.655734381 | 0.55444154 | 7.20E-25 | 8.63E-21 |
| SCG2       | 9.67272414 | 7.916335277 | 0.55292685 | 1.64E-23 | 1.96E-19 |
| GLIPR1     | 7.88139956 | 6.746399958 | 0.5507341  | 5.53E-24 | 6.62E-20 |
| CPVL       | 8.31844681 | 7.125762793 | 0.55000935 | 4.12E-25 | 4.93E-21 |
| GBP2       | 7.96732764 | 6.915312559 | 0.55000308 | 3.30E-25 | 3.95E-21 |
| LHFPL2     | 8.23634045 | 7.452322742 | 0.54873016 | 3.69E-24 | 4.41E-20 |
| C3         | 11.5281995 | 10.09685559 | 0.54545827 | 6.17E-26 | 7.40E-22 |
| SERPINE1   | 7.86257991 | 6.436710435 | 0.54524872 | 2.39E-24 | 2.86E-20 |
| TIPARP     | 9.7102123  | 8.897557541 | 0.54499216 | 9.30E-24 | 1.11E-19 |
| BHLHB3     | 9.03638001 | 7.817110279 | 0.54415569 | 1.45E-21 | 1.72E-17 |
| DKFZP586H2 | 7.58323923 | 6.293481601 | 0.54227448 | 2.92E-23 | 3.48E-19 |
| ANGPTL4    | 6.8101082  | 5.606362971 | 0.54156645 | 8.93E-24 | 1.07E-19 |
| CD163      | 9.87899835 | 8.149671167 | 0.541449   | 1.34E-25 | 1.61E-21 |
| CDKN1A     | 8.51529808 | 7.563167362 | 0.54134268 | 3.90E-23 | 4.66E-19 |
| SLC11A1    | 5.60629168 | 5.064832597 | 0.54025908 | 1.19E-24 | 1.43E-20 |
| MAOB       | 10.1190345 | 8.423654883 | 0.54024142 | 2.36E-23 | 2.82E-19 |
| ARSJ       | 5.83690697 | 4.756101225 | 0.53962062 | 4.50E-25 | 5.40E-21 |
| CD14       | 10.0691678 | 8.70774506  | 0.53724438 | 1.81E-26 | 2.18E-22 |
| LOC26010   | 7.67202788 | 7.087453364 | 0.53669905 | 1.17E-24 | 1.40E-20 |
| SLA        | 7.80414969 | 6.72359688  | 0.53589449 | 8.18E-23 | 9.77E-19 |
| GADD45A    | 10.2166133 | 9.280926924 | 0.53589098 | 3.56E-23 | 4.25E-19 |
| FZD7       | 7.67751299 | 6.456056908 | 0.53466047 | 5.88E-24 | 7.03E-20 |
| F3         | 8.72377976 | 7.660787781 | 0.53396104 | 1.20E-23 | 1.43E-19 |
| CSF1R      | 8.52256851 | 7.409005637 | 0.53352755 | 2.44E-23 | 2.91E-19 |
| CCR1       | 6.93950938 | 6.014655122 | 0.53303906 | 1.08E-23 | 1.29E-19 |
| ITGA5      | 7.46444174 | 6.642937958 | 0.53301022 | 4.47E-25 | 5.36E-21 |
| VSIG4      | 10.1932438 | 8.638554407 | 0.53277426 | 4.87E-24 | 5.82E-20 |
| ALOX5AP    | 10.1009853 | 8.546222942 | 0.53250924 | 2.93E-25 | 3.51E-21 |
| M6PRBP1    | 8.86545787 | 8.158925021 | 0.53046233 | 1.13E-23 | 1.35E-19 |
| SLC39A14   | 9.45501488 | 8.522999725 | 0.52844964 | 1.34E-24 | 1.60E-20 |
| CLU        | 11.962617  | 10.70301618 | 0.52817908 | 2.44E-23 | 2.91E-19 |
| EMP1       | 9.74829451 | 8.59798662  | 0.52744423 | 1.00E-23 | 1.20E-19 |
| SLC2A5     | 6.88306435 | 5.86550867  | 0.52724433 | 8.23E-23 | 9.83E-19 |
| TRIP6      | 8.28099389 | 7.370639665 | 0.52719244 | 8.94E-21 | 1.06E-16 |
| CSRP2      | 10.84429   | 9.723842973 | 0.52590801 | 1.10E-22 | 1.31E-18 |
| ITGAM      | 5.61227751 | 5.152434015 | 0.52269749 | 1.27E-23 | 1.52E-19 |
| FLJ21963   | 6.87721514 | 5.713068377 | 0.52218229 | 4.10E-21 | 4.88E-17 |
| TNFSF12    | 5.96206672 | 5.47456119  | 0.52202693 | 2.66E-21 | 3.17E-17 |

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| SH3BGRL3 | 9.3749445  | 8.759764899 | 0.52177873 | 3.79E-24 | 4.53E-20 |
| LGALS1   | 11.727482  | 10.90338964 | 0.51989859 | 6.63E-25 | 7.94E-21 |
| ILK      | 8.75766162 | 8.229700147 | 0.51574413 | 5.26E-23 | 6.28E-19 |
| ADORA1   | 5.6184696  | 5.116587744 | 0.51480473 | 1.11E-21 | 1.33E-17 |
| PIPOX    | 8.22060358 | 6.739152482 | 0.5141336  | 5.81E-20 | 6.89E-16 |
| IQGAP1   | 8.79985539 | 8.034942682 | 0.51327291 | 6.20E-22 | 7.39E-18 |
| NNMT     | 9.50904244 | 7.647626721 | 0.51315793 | 3.87E-21 | 4.61E-17 |
| SEC14L2  | 6.13392204 | 5.318039618 | 0.51300018 | 3.99E-21 | 4.75E-17 |
| HMOX1    | 8.92249574 | 7.673176563 | 0.51298289 | 1.69E-23 | 2.02E-19 |
| GAL3ST4  | 7.37727288 | 6.735786116 | 0.51146658 | 2.76E-22 | 3.29E-18 |
| GLUL     | 10.5867344 | 9.678923293 | 0.51133116 | 8.13E-23 | 9.71E-19 |
| LRP10    | 8.95914807 | 8.322827314 | 0.5109314  | 9.85E-22 | 1.17E-17 |
| RAMP1    | 9.24018044 | 7.941057593 | 0.51085358 | 1.02E-18 | 1.21E-14 |
| SIPA1L1  | 7.4924026  | 6.757137465 | 0.51020174 | 2.03E-21 | 2.41E-17 |
| MYO1F    | 6.5818967  | 5.876559829 | 0.5099277  | 3.94E-22 | 4.70E-18 |
| GADD45B  | 7.15289831 | 6.368353511 | 0.50990851 | 4.97E-24 | 5.94E-20 |
| KCNMB1   | 5.97765079 | 5.047060942 | 0.50984484 | 1.48E-23 | 1.77E-19 |
| GAP43    | 9.64461393 | 8.055460062 | 0.5092569  | 8.25E-18 | 9.73E-14 |
| TAGLN    | 9.0582132  | 7.622517101 | 0.5080596  | 2.15E-21 | 2.56E-17 |
| FLOT1    | 7.79114542 | 7.459227625 | 0.50758919 | 3.33E-22 | 3.98E-18 |
| ZYX      | 8.54240789 | 7.58099265  | 0.50649451 | 1.53E-21 | 1.82E-17 |
| F13A1    | 8.33044636 | 6.55641997  | 0.50645464 | 1.96E-20 | 2.33E-16 |
| ITGA7    | 7.28376067 | 6.239474178 | 0.5059957  | 2.47E-20 | 2.93E-16 |
| ITGB2    | 8.98350736 | 7.908498056 | 0.50426814 | 2.03E-22 | 2.43E-18 |
| CD4      | 6.87032079 | 6.095237992 | 0.5041994  | 1.13E-21 | 1.34E-17 |
| ADORA3   | 7.28663573 | 6.194521611 | 0.50357895 | 5.24E-21 | 6.23E-17 |
| ACTN1    | 9.40875166 | 8.439833006 | 0.50283319 | 1.12E-20 | 1.33E-16 |
| TLR2     | 7.07824042 | 6.108257441 | 0.50270638 | 3.10E-21 | 3.69E-17 |
| SPOCK2   | 7.15754813 | 6.384570897 | 0.50195899 | 2.22E-21 | 2.64E-17 |
| ANXA1    | 10.6551161 | 9.440293034 | 0.50174955 | 4.57E-18 | 5.39E-14 |
| OSBPL3   | 6.76508577 | 5.959825337 | 0.50121634 | 2.53E-20 | 3.00E-16 |
| IFITM3   | 10.8850343 | 10.10807652 | 0.499051   | 2.60E-22 | 3.11E-18 |
| CA2      | 10.1161566 | 8.83910827  | 0.49884346 | 3.63E-22 | 4.32E-18 |
| NDP      | 8.55245786 | 7.112912887 | 0.49746347 | 1.20E-17 | 1.41E-13 |
| CD151    | 7.31025887 | 6.647151705 | 0.49720084 | 9.51E-21 | 1.13E-16 |
| MT1G     | 9.42636892 | 8.452809443 | 0.49717436 | 1.38E-20 | 1.63E-16 |
| TMBIM1   | 7.67034066 | 7.006971867 | 0.49710234 | 5.83E-21 | 6.94E-17 |
| BBOX1    | 8.78546809 | 7.184873352 | 0.49684908 | 9.98E-18 | 1.18E-13 |
| CEBPB    | 9.68065166 | 8.90411578  | 0.49555806 | 1.14E-22 | 1.36E-18 |
| CARD9    | 5.2610044  | 4.915996275 | 0.49552992 | 3.85E-20 | 4.57E-16 |
| RCAN1    | 8.81067453 | 7.585003067 | 0.49511711 | 3.92E-21 | 4.67E-17 |
| FCER1G   | 9.57679315 | 8.378691713 | 0.4945374  | 9.45E-23 | 1.13E-18 |
| FCGRT    | 8.14458029 | 7.405014105 | 0.49407987 | 2.60E-21 | 3.09E-17 |
| LAMP2    | 9.50669522 | 8.879204326 | 0.49364681 | 3.97E-22 | 4.73E-18 |
| PCSK5    | 6.26149323 | 5.375504939 | 0.49186258 | 5.83E-21 | 6.94E-17 |
| LAIR1    | 6.17796314 | 5.470953035 | 0.49153956 | 5.59E-22 | 6.67E-18 |
| LCP2     | 6.69837933 | 5.892682213 | 0.49134528 | 7.00E-21 | 8.32E-17 |
| SERPINB6 | 9.33527077 | 8.764287083 | 0.4909522  | 3.56E-23 | 4.25E-19 |
| CHRNA9   | 6.17127076 | 5.024969731 | 0.49010797 | 1.24E-24 | 1.48E-20 |

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| FEM1C    | 7.56147934 | 6.779328603 | 0.48919549 | 9.13E-20 | 1.08E-15 |
| STBD1    | 6.05750337 | 5.589655224 | 0.48821836 | 1.70E-21 | 2.02E-17 |
| ITPKB    | 8.82142723 | 7.681757176 | 0.48755213 | 8.44E-18 | 9.95E-14 |
| UPP1     | 7.18729197 | 6.252261619 | 0.48753084 | 1.28E-19 | 1.51E-15 |
| PKM2     | 10.4292957 | 9.726919413 | 0.48720131 | 8.19E-21 | 9.73E-17 |
| RAB13    | 10.6901312 | 10.15288374 | 0.48698053 | 1.37E-20 | 1.62E-16 |
| FAM129A  | 7.95575768 | 6.861202117 | 0.48668767 | 2.62E-20 | 3.12E-16 |
| TREM1    | 6.88236324 | 5.634679501 | 0.48625405 | 2.62E-22 | 3.13E-18 |
| ITPKC    | 5.89919109 | 5.409109032 | 0.48536578 | 4.71E-21 | 5.60E-17 |
| ANXA5    | 11.160568  | 10.58919413 | 0.48533764 | 2.05E-19 | 2.43E-15 |
| PRUNE2   | 8.02176189 | 7.026121834 | 0.48520878 | 1.23E-17 | 1.44E-13 |
| LOX      | 5.713575   | 4.734456346 | 0.48429658 | 1.99E-22 | 2.38E-18 |
| AKAP12   | 8.96338234 | 7.679154243 | 0.48253794 | 1.61E-19 | 1.90E-15 |
| HCLS1    | 8.64868111 | 7.561738951 | 0.48251411 | 2.95E-20 | 3.50E-16 |
| C3AR1    | 8.01411181 | 7.064260858 | 0.4822867  | 4.56E-21 | 5.43E-17 |
| TNFRSF1B | 6.68282854 | 5.874532921 | 0.48158744 | 7.02E-20 | 8.33E-16 |
| CST3     | 12.3105008 | 11.29025162 | 0.48125304 | 2.46E-16 | 2.88E-12 |
| CTSZ     | 6.3759595  | 5.856777785 | 0.47992833 | 1.25E-21 | 1.49E-17 |
| ACOX2    | 6.05280545 | 5.190435073 | 0.47959046 | 3.56E-22 | 4.24E-18 |
| COPZ2    | 7.53618425 | 6.572096868 | 0.4792159  | 7.37E-20 | 8.74E-16 |
| ENDOD1   | 7.6271072  | 6.836158557 | 0.47921303 | 2.97E-19 | 3.52E-15 |
| IBSP     | 5.71080885 | 4.816836306 | 0.47843861 | 1.12E-19 | 1.32E-15 |
| LMO2     | 9.0895242  | 7.946887738 | 0.47827828 | 8.89E-18 | 1.05E-13 |
| LIF      | 5.77189786 | 4.845103182 | 0.47751635 | 4.46E-23 | 5.32E-19 |
| HTRA1    | 11.5839268 | 10.54963532 | 0.47542771 | 1.17E-17 | 1.38E-13 |
| SRPX     | 10.3027825 | 8.804436371 | 0.47408717 | 6.13E-20 | 7.28E-16 |
| CENTA2   | 7.5843213  | 6.895333193 | 0.47393312 | 2.64E-19 | 3.12E-15 |
| SLC2A10  | 7.89739233 | 6.900155543 | 0.47386862 | 2.51E-16 | 2.94E-12 |
| CNIH3    | 6.69938137 | 5.680812251 | 0.47382387 | 9.13E-20 | 1.08E-15 |
| APH1B    | 6.36266377 | 5.931199598 | 0.47373688 | 3.16E-19 | 3.74E-15 |
| SIGLEC9  | 4.55822017 | 4.309747295 | 0.47259714 | 6.29E-21 | 7.48E-17 |
| GDPD2    | 6.47741252 | 5.725201795 | 0.47257051 | 5.78E-19 | 6.85E-15 |
| TBXAS1   | 6.06445369 | 5.353317437 | 0.47143946 | 8.80E-20 | 1.04E-15 |
| ABCA1    | 7.97958926 | 7.149234483 | 0.47066314 | 5.32E-19 | 6.30E-15 |
| PGCP     | 7.05801062 | 6.381512637 | 0.47049921 | 1.47E-18 | 1.73E-14 |
| RNASET2  | 9.72319594 | 8.971247296 | 0.4703803  | 1.21E-20 | 1.44E-16 |
| PLOD3    | 8.47355174 | 7.904769694 | 0.4698071  | 5.46E-20 | 6.48E-16 |
| TPST1    | 9.25362364 | 8.392314277 | 0.46967061 | 2.73E-17 | 3.21E-13 |
| LAPTM5   | 10.1078115 | 9.090302222 | 0.46956801 | 2.29E-21 | 2.72E-17 |
| KCTD12   | 10.213615  | 9.23529993  | 0.46850174 | 1.79E-18 | 2.12E-14 |
| KCNE4    | 6.4073697  | 5.551832101 | 0.46843066 | 3.52E-18 | 4.15E-14 |
| CLIC4    | 8.96954066 | 8.205708923 | 0.46825321 | 3.18E-18 | 3.76E-14 |
| SPI1     | 5.66666229 | 5.097795783 | 0.46727231 | 2.56E-21 | 3.05E-17 |
| CXorf9   | 6.23038996 | 5.371085824 | 0.46709877 | 4.19E-19 | 4.96E-15 |
| RAB31    | 11.2456012 | 10.44768551 | 0.46521225 | 5.44E-16 | 6.36E-12 |
| VIM      | 13.1220354 | 12.32535627 | 0.46489026 | 3.97E-22 | 4.73E-18 |
| C1QA     | 9.79170528 | 8.598100592 | 0.46439062 | 5.66E-20 | 6.72E-16 |
| SIGLEC7  | 5.21745781 | 4.898475475 | 0.46423612 | 1.14E-17 | 1.34E-13 |
| AIF1     | 7.82461362 | 7.017661488 | 0.46383467 | 5.99E-19 | 7.09E-15 |

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| EHD2      | 6.43204523 | 5.839078986 | 0.46376016 | 6.75E-19 | 7.99E-15 |
| ZFP36     | 9.12907814 | 8.232289416 | 0.46322338 | 1.18E-20 | 1.40E-16 |
| HSPA6     | 6.12840032 | 5.352359648 | 0.46314229 | 5.94E-21 | 7.07E-17 |
| RRAS      | 7.18636493 | 6.447428944 | 0.46254493 | 1.47E-22 | 1.75E-18 |
| CSRP1     | 10.2608961 | 9.4181888   | 0.46152869 | 9.53E-19 | 1.13E-14 |
| SPP1      | 12.9829211 | 11.92087856 | 0.46131281 | 3.94E-22 | 4.70E-18 |
| TMEM158   | 9.77086425 | 8.492465124 | 0.46065222 | 9.05E-18 | 1.07E-13 |
| ADAM9     | 9.75770581 | 9.074199611 | 0.4606217  | 1.89E-20 | 2.24E-16 |
| SLC4A3    | 6.23571532 | 5.480995686 | 0.46011052 | 3.39E-17 | 3.98E-13 |
| MAFB      | 9.83589498 | 8.704419269 | 0.45916505 | 2.06E-19 | 2.44E-15 |
| MT1X      | 11.1553045 | 10.21627097 | 0.45883382 | 4.57E-17 | 5.36E-13 |
| SAT1      | 10.5371839 | 9.979125162 | 0.45875434 | 7.12E-19 | 8.43E-15 |
| MLC1      | 8.66039921 | 7.393040421 | 0.45858706 | 1.06E-13 | 1.22E-09 |
| S100A8    | 7.38139742 | 6.069002213 | 0.45829431 | 1.55E-18 | 1.83E-14 |
| SYNPO     | 7.00859865 | 6.064164626 | 0.45801943 | 1.72E-19 | 2.04E-15 |
| DNAJB1    | 9.08865565 | 8.416213497 | 0.45790284 | 2.53E-20 | 3.00E-16 |
| TRIM22    | 9.18822894 | 8.143802038 | 0.45666053 | 4.66E-19 | 5.52E-15 |
| RNASE6    | 8.53278761 | 7.518828268 | 0.45658845 | 6.67E-19 | 7.90E-15 |
| ANXA2     | 11.9338461 | 11.09158075 | 0.45600692 | 5.04E-18 | 5.95E-14 |
| FGF1      | 6.34872272 | 5.54256371  | 0.45597901 | 7.79E-20 | 9.24E-16 |
| C10orf10  | 7.25837099 | 6.436457525 | 0.45571294 | 5.10E-20 | 6.06E-16 |
| GLRX      | 8.11264134 | 7.488125719 | 0.4549694  | 2.23E-21 | 2.66E-17 |
| ATP1B2    | 9.75915777 | 8.264661211 | 0.45475431 | 4.27E-17 | 5.01E-13 |
| S100A10   | 11.6502071 | 10.6302368  | 0.45465663 | 9.41E-20 | 1.12E-15 |
| PLK3      | 5.88519317 | 5.470015992 | 0.4538368  | 9.76E-19 | 1.15E-14 |
| SLC1A3    | 11.7637333 | 10.41099425 | 0.45373991 | 2.19E-11 | 2.46E-07 |
| NPC2      | 11.1075962 | 10.40115537 | 0.45368286 | 7.65E-19 | 9.05E-15 |
| FCGR1A    | 7.1165608  | 6.201127756 | 0.45359969 | 3.36E-18 | 3.96E-14 |
| CNTNAP1   | 7.2575697  | 6.546525223 | 0.45359422 | 7.48E-18 | 8.82E-14 |
| ADM       | 9.35875533 | 8.020859351 | 0.45357741 | 2.19E-17 | 2.57E-13 |
| TNFRSF12A | 7.77434544 | 6.999538148 | 0.45291778 | 6.32E-18 | 7.46E-14 |
| PLEKHQ1   | 7.03945683 | 6.495325168 | 0.45290562 | 5.75E-17 | 6.75E-13 |
| C1QB      | 10.7125617 | 9.486083795 | 0.45231586 | 3.57E-20 | 4.24E-16 |
| LAMA2     | 6.38424576 | 5.481124186 | 0.45151823 | 5.69E-21 | 6.77E-17 |
| CLCF1     | 5.33851944 | 4.944834283 | 0.44972257 | 2.16E-20 | 2.57E-16 |
| GPR65     | 6.23797691 | 5.405489763 | 0.44970707 | 1.28E-17 | 1.51E-13 |
| HRASLS3   | 8.74807837 | 8.043196722 | 0.4496784  | 5.71E-19 | 6.76E-15 |
| CD33      | 5.41460294 | 4.919673415 | 0.4479033  | 9.93E-19 | 1.17E-14 |
| CYBRD1    | 7.28282759 | 6.415108581 | 0.44788623 | 7.14E-18 | 8.42E-14 |
| ADAM12    | 5.41626461 | 4.959450794 | 0.44732217 | 9.88E-20 | 1.17E-15 |
| TGFB111   | 8.1437137  | 7.329951187 | 0.44653551 | 1.57E-18 | 1.86E-14 |
| IFITM2    | 9.67333645 | 8.882558491 | 0.44531614 | 3.54E-19 | 4.19E-15 |
| MICALL2   | 6.87317493 | 6.241996387 | 0.44519323 | 1.14E-18 | 1.35E-14 |
| CYFIP1    | 8.6702992  | 8.277910859 | 0.44277856 | 7.27E-18 | 8.57E-14 |
| A2M       | 11.3550309 | 10.34201711 | 0.44254907 | 2.27E-22 | 2.71E-18 |
| JUNB      | 8.08838516 | 7.391626599 | 0.44240811 | 8.66E-19 | 1.03E-14 |
| MT1E      | 9.80660032 | 8.926628859 | 0.44225802 | 5.47E-16 | 6.39E-12 |
| FLJ11286  | 8.25552095 | 7.535641487 | 0.4419871  | 1.10E-15 | 1.28E-11 |
| OXTR      | 6.85021781 | 5.616906859 | 0.44192059 | 9.98E-18 | 1.18E-13 |

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| FJX1     | 9.07300163 | 8.039149861 | 0.44138011 | 2.43E-16 | 2.85E-12 |
| CHL1     | 9.02901478 | 7.543611083 | 0.44045877 | 2.51E-14 | 2.90E-10 |
| TFE3     | 7.27013936 | 6.843910077 | 0.43931907 | 1.30E-16 | 1.53E-12 |
| CD93     | 7.70122726 | 6.766878962 | 0.43909387 | 7.88E-18 | 9.29E-14 |
| CAPG     | 8.05260297 | 7.221996298 | 0.43891845 | 1.99E-16 | 2.34E-12 |
| ZFP36L2  | 5.9841764  | 5.374410917 | 0.43820478 | 8.71E-17 | 1.02E-12 |
| GFPT2    | 7.95677431 | 6.846773007 | 0.4381413  | 3.50E-18 | 4.13E-14 |
| CH25H    | 6.7353148  | 5.516988948 | 0.43778408 | 2.45E-19 | 2.91E-15 |
| RARRES3  | 8.23384711 | 7.243795476 | 0.43734634 | 4.55E-16 | 5.31E-12 |
| FCGR2B   | 6.87601527 | 5.712759328 | 0.43685383 | 4.02E-18 | 4.75E-14 |
| GBP1     | 8.96000738 | 7.842322019 | 0.43637693 | 5.20E-17 | 6.11E-13 |
| FAS      | 6.54061804 | 5.708564938 | 0.43575865 | 6.40E-20 | 7.60E-16 |
| PAM      | 10.6623467 | 10.03294031 | 0.43537302 | 1.37E-18 | 1.63E-14 |
| CASP1    | 7.35953388 | 6.520352191 | 0.43528731 | 8.39E-18 | 9.90E-14 |
| BHLHB2   | 7.49883289 | 6.690208346 | 0.43499957 | 4.41E-18 | 5.21E-14 |
| HP       | 5.91311938 | 4.769516251 | 0.43391711 | 7.62E-17 | 8.94E-13 |
| RHBDF2   | 6.53999386 | 6.058798772 | 0.43352544 | 2.61E-17 | 3.07E-13 |
| JAM2     | 9.55621441 | 8.613131747 | 0.43296015 | 5.12E-13 | 5.86E-09 |
| IGFBP7   | 12.4338942 | 11.68389488 | 0.432533   | 2.00E-24 | 2.39E-20 |
| PTPN9    | 6.85578892 | 6.32915847  | 0.43201614 | 1.97E-16 | 2.31E-12 |
| S100A11  | 9.37071308 | 8.514201885 | 0.43176677 | 7.65E-18 | 9.03E-14 |
| LIMS1    | 8.49263724 | 7.992892828 | 0.43174056 | 1.36E-18 | 1.61E-14 |
| TREM2    | 8.31195351 | 7.300374736 | 0.43156576 | 4.21E-16 | 4.92E-12 |
| FAH      | 6.09942033 | 5.500728623 | 0.43155983 | 6.40E-20 | 7.60E-16 |
| RYR3     | 6.05342122 | 4.842417994 | 0.43153885 | 4.34E-17 | 5.10E-13 |
| LAP3     | 10.1001634 | 9.514618334 | 0.43146167 | 1.81E-18 | 2.14E-14 |
| CAMK2N1  | 10.713114  | 9.67670117  | 0.43104827 | 1.90E-16 | 2.22E-12 |
| UGCG     | 9.10000274 | 8.479880059 | 0.4308697  | 5.66E-17 | 6.64E-13 |
| RFTN1    | 9.18561064 | 8.298329662 | 0.43067597 | 6.51E-18 | 7.68E-14 |
| SWAP70   | 7.3301357  | 6.673265945 | 0.4306314  | 1.02E-16 | 1.20E-12 |
| HCK      | 6.75282362 | 5.854149293 | 0.43060074 | 1.17E-17 | 1.37E-13 |
| CROT     | 7.7007939  | 7.075384316 | 0.43015021 | 1.40E-16 | 1.64E-12 |
| GBE1     | 9.57730086 | 8.926174378 | 0.43012286 | 2.01E-16 | 2.35E-12 |
| MSN      | 9.99306136 | 9.278068023 | 0.42986451 | 1.02E-15 | 1.19E-11 |
| GALNT2   | 7.06109165 | 6.527653633 | 0.42984373 | 2.93E-18 | 3.47E-14 |
| LAMB2    | 7.57430241 | 6.876674917 | 0.42967404 | 6.73E-16 | 7.85E-12 |
| LILRB1   | 5.82045283 | 5.098340079 | 0.42916691 | 3.90E-17 | 4.58E-13 |
| RNASE3   | 4.947474   | 4.576081302 | 0.42881766 | 2.09E-17 | 2.46E-13 |
| BCL3     | 5.33650348 | 4.995522381 | 0.42849222 | 1.11E-18 | 1.31E-14 |
| FABP7    | 10.9807899 | 9.158891479 | 0.42840516 | 3.00E-11 | 3.37E-07 |
| PLEKHA4  | 5.52808151 | 5.077500617 | 0.42787236 | 3.09E-17 | 3.63E-13 |
| PDLIM4   | 5.94988137 | 5.267313978 | 0.42785297 | 3.22E-16 | 3.77E-12 |
| SPATA20  | 8.04568753 | 7.303191845 | 0.42772227 | 2.87E-15 | 3.34E-11 |
| FYB      | 6.23524943 | 5.585263385 | 0.42749934 | 1.75E-17 | 2.06E-13 |
| IL6ST    | 7.00507418 | 6.421878296 | 0.42686853 | 7.41E-15 | 8.60E-11 |
| SERPINA1 | 8.28431181 | 7.094868198 | 0.42644598 | 1.61E-18 | 1.91E-14 |
| FHL3     | 5.85971157 | 5.476520201 | 0.42524566 | 3.22E-16 | 3.77E-12 |
| SLC7A7   | 7.39384954 | 6.698352713 | 0.42499971 | 3.86E-17 | 4.53E-13 |
| RIN3     | 5.1495143  | 4.824574274 | 0.42429068 | 2.94E-17 | 3.45E-13 |

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|------------|------------|-------------|-------------|----------|----------|
| APOC2      | 8.95627944 | 7.821608547 | 0.4235504   | 6.47E-15 | 7.51E-11 |
| DYNLT3     | 9.84573968 | 9.130887539 | 0.42317811  | 1.77E-17 | 2.08E-13 |
| REEP5      | 9.9488547  | 9.538117743 | 0.42307608  | 9.91E-17 | 1.16E-12 |
| SAMSN1     | 8.02149442 | 7.069139034 | 0.42237486  | 2.85E-16 | 3.34E-12 |
| CLIC1      | 10.5983035 | 9.969088265 | 0.42218256  | 9.18E-15 | 1.06E-10 |
| SDCBP      | 11.6879523 | 11.26436226 | 0.42199111  | 3.61E-16 | 4.22E-12 |
| NFKBIA     | 10.313756  | 9.724551931 | 0.42165881  | 1.97E-17 | 2.32E-13 |
| GIMAP4     | 7.84923784 | 7.018313483 | 0.42144537  | 1.58E-16 | 1.85E-12 |
| CORO2B     | 8.61496086 | 7.488859542 | 0.4199121   | 1.34E-12 | 1.53E-08 |
| FAM26B     | 5.93135191 | 5.40541402  | 0.41982496  | 9.92E-18 | 1.17E-13 |
| CD86       | 6.15704561 | 5.493270937 | 0.41971807  | 6.02E-17 | 7.06E-13 |
| PLSCR1     | 8.59556867 | 7.868723942 | 0.41963787  | 6.99E-16 | 8.16E-12 |
| STAT3      | 9.57863235 | 9.037087367 | 0.41962689  | 3.94E-16 | 4.61E-12 |
| SH2B3      | 7.35238573 | 6.68938098  | 0.41916892  | 4.68E-18 | 5.52E-14 |
| GPR37      | 8.88551164 | 7.373769977 | 0.41898954  | 5.27E-12 | 5.97E-08 |
| GYS1       | 7.24734573 | 6.60852406  | 0.41802205  | 2.43E-15 | 2.83E-11 |
| ODZ4       | 8.04191467 | 7.123485815 | 0.4177829   | 1.86E-14 | 2.15E-10 |
| SLCO2B1    | 6.42233972 | 5.864381706 | 0.4177484   | 3.48E-16 | 4.07E-12 |
| CHPF       | 6.93254505 | 6.470408599 | 0.41702356  | 1.30E-15 | 1.52E-11 |
| MAP1B      | 10.6530945 | 9.626924048 | 0.41687103  | 3.03E-13 | 3.48E-09 |
| MS4A6A     | 8.88152308 | 7.897120654 | 0.41645437  | 5.84E-16 | 6.82E-12 |
| MAF        | 6.57997938 | 6.086748798 | 0.41586112  | 2.39E-14 | 2.77E-10 |
| FEZ2       | 7.96336696 | 7.649405493 | 0.41543772  | 9.58E-18 | 1.13E-13 |
| MVP        | 7.10042461 | 6.412563976 | 0.41503617  | 1.15E-17 | 1.36E-13 |
| LZTS1      | 4.74256215 | 4.56236509  | 0.41499889  | 1.34E-15 | 1.57E-11 |
| PLOD1      | 8.38278994 | 7.773452378 | 0.41482299  | 4.55E-16 | 5.31E-12 |
| SH3TC1     | 5.49158105 | 4.956641228 | 0.41469264  | 3.33E-16 | 3.89E-12 |
| TLR1       | 6.11051661 | 5.469936487 | 0.41446344  | 6.34E-16 | 7.40E-12 |
| PLP2       | 9.24567887 | 8.313110067 | 0.41420059  | 9.77E-16 | 1.14E-11 |
| TGFB1      | 6.14660065 | 5.585191675 | 0.41409075  | 2.93E-16 | 3.43E-12 |
| TMEPAI     | 6.96251116 | 6.29506164  | 0.41387915  | 6.13E-16 | 7.16E-12 |
| MS4A4A     | 8.55208353 | 7.364441852 | 0.41369217  | 9.74E-17 | 1.14E-12 |
| ELOVL2     | 6.92925622 | 5.780613841 | 0.4136572   | 4.67E-17 | 5.49E-13 |
| TYROBP     | 9.94422179 | 8.928320746 | 0.41337065  | 2.14E-16 | 2.51E-12 |
| CSG1cA-T   | 7.02872525 | 6.520653558 | 0.41302999  | 1.55E-16 | 1.82E-12 |
| MTMR11     | 6.53044627 | 5.914535296 | 0.41289699  | 1.50E-15 | 1.75E-11 |
| CD53       | 9.49086965 | 8.536832334 | 0.41277027  | 6.19E-17 | 7.27E-13 |
| SPRY2      | 9.37989042 | 8.409908433 | 0.41265204  | 1.88E-13 | 2.16E-09 |
| AEBP1      | 9.23912202 | 8.13014334  | 0.41258738  | 1.71E-14 | 1.98E-10 |
| DENND3     | 5.56201566 | 5.130810189 | 0.41224446  | 2.74E-17 | 3.23E-13 |
| IL13RA1    | 7.24172693 | 6.588712274 | 0.41128125  | 1.80E-16 | 2.10E-12 |
| GSTK1      | 9.0463021  | 8.560193875 | 0.411111307 | 5.27E-16 | 6.15E-12 |
| tcag7.1314 | 7.57671736 | 6.790827382 | 0.41051211  | 1.27E-15 | 1.48E-11 |
| MOXD1      | 8.13045264 | 6.724120096 | 0.41008019  | 6.34E-16 | 7.40E-12 |
| GNG5       | 10.6585647 | 10.267414   | 0.4100099   | 2.81E-16 | 3.28E-12 |
| PROS1      | 8.55022304 | 7.63621725  | 0.409839    | 1.70E-15 | 1.98E-11 |
| SYNC1      | 6.64969392 | 5.723758074 | 0.40953423  | 4.14E-16 | 4.84E-12 |
| ARHGDIB    | 9.76857732 | 9.066271209 | 0.40934529  | 6.55E-18 | 7.72E-14 |
| CHSY1      | 8.73497655 | 8.152010356 | 0.40906546  | 7.96E-16 | 9.29E-12 |

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| PLAUR    | 6.64827481 | 5.918471593 | 0.40882927 | 3.90E-18 | 4.61E-14 |
| FND C4   | 7.38622989 | 6.7875727   | 0.40866159 | 1.78E-15 | 2.07E-11 |
| TGFB3    | 6.48242981 | 5.931316083 | 0.40840095 | 8.87E-16 | 1.03E-11 |
| ANGPT2   | 7.07656112 | 6.097546868 | 0.408376   | 3.66E-14 | 4.22E-10 |
| ITGAV    | 10.5343057 | 9.971342202 | 0.40815004 | 8.53E-15 | 9.90E-11 |
| AK3L1    | 8.80651178 | 8.036579843 | 0.40772872 | 2.27E-14 | 2.63E-10 |
| AP1B1    | 6.90502241 | 6.556384722 | 0.40772313 | 9.72E-16 | 1.13E-11 |
| SMAD1    | 9.00758778 | 8.29807218  | 0.4077066  | 3.26E-15 | 3.79E-11 |
| DTNA     | 7.50644686 | 6.619051069 | 0.40744396 | 3.57E-12 | 4.05E-08 |
| DMN      | 6.47470757 | 6.05826239  | 0.40714119 | 9.38E-15 | 1.09E-10 |
| LY86     | 8.36889371 | 7.399360623 | 0.40691007 | 8.40E-15 | 9.75E-11 |
| PSRC1    | 9.4285263  | 8.50715888  | 0.40641961 | 1.52E-13 | 1.75E-09 |
| WAS      | 6.2313978  | 5.989000482 | 0.40605112 | 2.12E-17 | 2.50E-13 |
| ARHGAP29 | 8.09210894 | 7.326379479 | 0.40515561 | 5.47E-18 | 6.46E-14 |
| NRP1     | 5.77588765 | 5.299750821 | 0.40463667 | 6.65E-16 | 7.77E-12 |
| NFIC     | 7.36582409 | 6.701450809 | 0.40455038 | 3.78E-15 | 4.39E-11 |
| C1QTNF1  | 6.29338811 | 5.624481354 | 0.40446801 | 9.64E-18 | 1.14E-13 |
| LILRA2   | 5.3403609  | 5.043361732 | 0.40446581 | 6.40E-17 | 7.51E-13 |
| ANKRD25  | 7.30852375 | 6.737534198 | 0.40345182 | 8.58E-16 | 1.00E-11 |
| CSF1     | 5.03232708 | 4.862559089 | 0.403403   | 9.70E-19 | 1.15E-14 |
| PFKFB3   | 9.46508453 | 8.742576495 | 0.40299089 | 1.02E-14 | 1.18E-10 |
| C1orf38  | 6.23239976 | 5.525158357 | 0.40283708 | 5.71E-16 | 6.68E-12 |
| PHLDA3   | 6.27362075 | 5.831640834 | 0.4028366  | 3.44E-16 | 4.02E-12 |
| AGTRL1   | 8.16765926 | 6.933180636 | 0.40281777 | 4.72E-15 | 5.48E-11 |
| TNFAIP6  | 8.00538726 | 6.925403729 | 0.402647   | 7.15E-14 | 8.24E-10 |
| ANG      | 6.28309054 | 5.616424426 | 0.40260339 | 6.94E-18 | 8.18E-14 |
| MAN2B1   | 7.51193921 | 7.011256859 | 0.40255846 | 1.26E-15 | 1.47E-11 |
| SQSTM1   | 9.27934351 | 8.762424378 | 0.40244845 | 9.72E-16 | 1.13E-11 |
| SLC16A4  | 6.70928663 | 5.911689403 | 0.40237784 | 1.13E-15 | 1.32E-11 |
| CCR5     | 6.19429877 | 5.686651343 | 0.40224654 | 1.08E-17 | 1.27E-13 |
| DOCK2    | 6.03824985 | 5.349095042 | 0.40109283 | 9.53E-17 | 1.12E-12 |
| KCNJ8    | 6.50504158 | 5.77904125  | 0.40037519 | 8.71E-15 | 1.01E-10 |
| RENBP    | 5.30214144 | 4.867041909 | 0.40004075 | 1.21E-14 | 1.40E-10 |
| PCDH9    | 8.66205642 | 7.525495114 | 0.39938765 | 4.62E-12 | 5.24E-08 |
| CLEC7A   | 6.81174125 | 6.117232789 | 0.39932496 | 4.92E-15 | 5.72E-11 |
| EBI2     | 6.24813261 | 5.37081017  | 0.39929076 | 2.64E-16 | 3.09E-12 |
| JUN      | 8.4144482  | 7.831061915 | 0.39834636 | 7.11E-15 | 8.25E-11 |
| RAB20    | 7.57447235 | 6.931256871 | 0.3980976  | 5.05E-15 | 5.87E-11 |
| RNASE4   | 6.79089178 | 6.006636449 | 0.39790911 | 1.29E-16 | 1.52E-12 |
| CYBB     | 7.03581849 | 6.35556105  | 0.39785215 | 3.77E-16 | 4.41E-12 |
| PLOD2    | 9.03706627 | 8.308621132 | 0.39782432 | 4.55E-16 | 5.31E-12 |
| DFNA5    | 9.71701359 | 8.993094689 | 0.3969682  | 4.78E-11 | 5.35E-07 |
| MYBPC1   | 7.52841861 | 6.222388704 | 0.39674979 | 1.15E-13 | 1.33E-09 |
| NPL      | 7.07689178 | 6.281392524 | 0.39661914 | 1.26E-14 | 1.46E-10 |
| IL10RA   | 6.75245488 | 5.919202591 | 0.39648659 | 1.55E-14 | 1.80E-10 |
| NRN1     | 8.96177235 | 7.939407229 | 0.39616337 | 1.74E-11 | 1.96E-07 |
| CD300A   | 5.72890475 | 5.305494719 | 0.39614315 | 2.54E-16 | 2.98E-12 |
| P2RY5    | 7.65280577 | 7.029126051 | 0.39606059 | 9.23E-15 | 1.07E-10 |
| LY96     | 7.87259222 | 6.887829707 | 0.39601019 | 3.45E-15 | 4.02E-11 |

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|-----------|------------|-------------|------------|----------|------------|
| RGS19     | 7.3648146  | 6.997800039 | 0.39585307 | 2.17E-14 | 2.51E-10   |
| GIMAP6    | 7.01899275 | 6.327485052 | 0.39545332 | 6.23E-15 | 7.24E-11   |
| CAMK1     | 6.32434841 | 5.726877946 | 0.3953938  | 3.09E-13 | 3.55E-09   |
| ACP2      | 7.84348185 | 7.358283046 | 0.39499017 | 8.06E-17 | 9.45E-13   |
| ARHGEF6   | 9.98456798 | 9.127328263 | 0.39460067 | 4.80E-08 | 0.00050627 |
| TXNDC15   | 8.53760384 | 8.096748512 | 0.39417411 | 4.05E-16 | 4.74E-12   |
| GATM      | 10.0937373 | 8.927634111 | 0.39395685 | 7.71E-12 | 8.73E-08   |
| SSBP2     | 8.28120041 | 7.662958581 | 0.39347129 | 1.06E-13 | 1.22E-09   |
| ITPR2     | 6.25561574 | 5.720407346 | 0.39275571 | 2.24E-14 | 2.59E-10   |
| CAST      | 7.34338108 | 6.877406046 | 0.39275441 | 8.94E-18 | 1.05E-13   |
| TLR7      | 5.78887199 | 5.037838406 | 0.39183745 | 1.93E-15 | 2.25E-11   |
| HLA-E     | 11.0251542 | 10.49405401 | 0.39151818 | 2.00E-14 | 2.31E-10   |
| MKL2      | 9.09461185 | 8.545373819 | 0.3906745  | 2.65E-17 | 3.12E-13   |
| MAP3K6    | 5.28803735 | 4.865071413 | 0.39052815 | 3.90E-17 | 4.58E-13   |
| CD74      | 11.1658724 | 10.23900879 | 0.39021461 | 4.43E-15 | 5.15E-11   |
| KIAA0247  | 8.35373459 | 7.773845261 | 0.38996898 | 7.26E-15 | 8.42E-11   |
| METTL7A   | 9.37944791 | 8.590188604 | 0.38995055 | 2.10E-13 | 2.42E-09   |
| STOM      | 7.98493413 | 7.440086422 | 0.38929715 | 6.13E-16 | 7.16E-12   |
| GNAI2     | 9.51301795 | 8.944187637 | 0.38880606 | 3.86E-13 | 4.42E-09   |
| TNFRSF11B | 5.76373245 | 5.047773459 | 0.38872661 | 5.16E-18 | 6.09E-14   |
| FCGR3B    | 6.05911479 | 5.471927364 | 0.3885932  | 5.88E-15 | 6.83E-11   |
| CD302     | 8.51428991 | 7.751437553 | 0.38843666 | 2.73E-14 | 3.16E-10   |
| HLA-A     | 12.4356471 | 12.03257336 | 0.38838658 | 1.52E-13 | 1.75E-09   |
| TWSG1     | 6.32813408 | 5.693972705 | 0.38836611 | 3.87E-14 | 4.47E-10   |
| CD37      | 5.92753407 | 5.208000061 | 0.38828547 | 6.81E-17 | 7.99E-13   |
| SMPD1     | 5.54116753 | 5.264192232 | 0.38795787 | 3.16E-14 | 3.64E-10   |
| CHST7     | 7.08819215 | 6.304250318 | 0.38788013 | 7.75E-14 | 8.93E-10   |
| GALC      | 6.81342868 | 6.368858707 | 0.38756762 | 1.13E-13 | 1.30E-09   |
| ST5       | 7.87533565 | 7.268402443 | 0.38732195 | 1.51E-12 | 1.72E-08   |
| BCKDK     | 7.10289848 | 6.697685486 | 0.38561751 | 1.55E-13 | 1.79E-09   |
| SLC2A3    | 7.18465841 | 6.375745483 | 0.38557755 | 2.80E-14 | 3.24E-10   |
| SP100     | 5.98268861 | 5.590164971 | 0.3854431  | 7.00E-15 | 8.12E-11   |
| PTGS1     | 6.37343608 | 5.651610078 | 0.38519637 | 1.32E-20 | 1.56E-16   |
| ARNTL     | 7.42504945 | 6.765667847 | 0.38502863 | 8.48E-14 | 9.77E-10   |
| IRS2      | 10.1346787 | 9.411358586 | 0.38429508 | 1.03E-12 | 1.18E-08   |
| DDR2      | 6.77116108 | 5.986810351 | 0.38422814 | 1.75E-14 | 2.02E-10   |
| SNFT      | 6.75354278 | 6.044943246 | 0.38416923 | 1.77E-14 | 2.05E-10   |
| GALNT10   | 6.93166213 | 6.252511838 | 0.38407924 | 9.10E-14 | 1.05E-09   |
| MFSD1     | 9.99310566 | 9.558414166 | 0.38376294 | 3.78E-15 | 4.39E-11   |
| CENTD1    | 8.32660905 | 7.46424341  | 0.38347618 | 6.93E-12 | 7.85E-08   |
| SLC22A4   | 6.13468821 | 5.522577882 | 0.38329247 | 2.11E-15 | 2.45E-11   |
| TCIRG1    | 6.6023916  | 6.032038547 | 0.38299787 | 5.14E-17 | 6.04E-13   |
| GNA12     | 7.47022745 | 6.888500219 | 0.38270334 | 5.57E-12 | 6.31E-08   |
| AMPD3     | 5.79368642 | 5.496641141 | 0.38261415 | 4.22E-14 | 4.87E-10   |
| SRGN      | 10.4077127 | 9.554467306 | 0.38253625 | 8.49E-15 | 9.85E-11   |
| PODXL     | 8.44427415 | 7.714093273 | 0.38234648 | 1.13E-12 | 1.29E-08   |
| MREG      | 8.22276466 | 7.434655925 | 0.38222111 | 2.19E-14 | 2.54E-10   |
| SDC2      | 7.78705298 | 7.004292603 | 0.38201344 | 6.89E-15 | 8.00E-11   |
| NUCB1     | 7.56019365 | 7.010231986 | 0.38178081 | 2.19E-13 | 2.51E-09   |

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| CREBL2   | 7.8891287  | 7.362813577 | 0.38161276 | 2.76E-14 | 3.19E-10   |
| NDRG1    | 9.0518357  | 8.202615974 | 0.38128687 | 6.63E-14 | 7.64E-10   |
| ERBB2IP  | 10.0142983 | 9.488737368 | 0.38108766 | 1.12E-11 | 1.26E-07   |
| CALR     | 8.18462625 | 7.892739342 | 0.38064118 | 4.01E-14 | 4.63E-10   |
| IGFBP2   | 9.58857184 | 8.474780578 | 0.38052856 | 2.03E-11 | 2.28E-07   |
| C13orf18 | 6.85230036 | 6.03249409  | 0.38050928 | 4.64E-13 | 5.32E-09   |
| SCG5     | 10.3431604 | 9.244451447 | 0.38016323 | 3.26E-10 | 3.60E-06   |
| TMEM140  | 6.76948532 | 6.049469481 | 0.38013173 | 1.01E-14 | 1.18E-10   |
| PLS3     | 10.2426551 | 9.508679947 | 0.38011982 | 9.70E-13 | 1.11E-08   |
| ARL4C    | 7.79332583 | 7.143525225 | 0.38001993 | 1.29E-12 | 1.48E-08   |
| ACTB     | 12.6373061 | 12.27150785 | 0.37922155 | 1.35E-12 | 1.54E-08   |
| CTSL1    | 8.96236782 | 8.412949823 | 0.37890885 | 6.26E-17 | 7.35E-13   |
| LTBP3    | 7.99011376 | 7.3465577   | 0.37815105 | 5.92E-13 | 6.77E-09   |
| PDGFA    | 7.88663195 | 7.008546329 | 0.37779135 | 5.56E-13 | 6.36E-09   |
| PLXND1   | 6.90694828 | 6.387966414 | 0.37753465 | 4.03E-13 | 4.62E-09   |
| MNDA     | 6.84885764 | 5.974204547 | 0.37748923 | 6.36E-14 | 7.34E-10   |
| HSPB1    | 11.0476053 | 10.47562273 | 0.37741604 | 1.26E-13 | 1.45E-09   |
| GPC1     | 7.08741589 | 6.463745477 | 0.37721593 | 1.68E-12 | 1.91E-08   |
| DUSP3    | 6.40492433 | 6.058586432 | 0.3769742  | 9.24E-13 | 1.06E-08   |
| DOK5     | 9.90092345 | 8.877514557 | 0.37651007 | 5.21E-08 | 0.00054894 |
| PPAP2B   | 9.98412404 | 9.212397226 | 0.37599841 | 5.25E-11 | 5.87E-07   |
| GJA1     | 11.8947293 | 10.97517599 | 0.37571293 | 2.98E-11 | 3.34E-07   |
| TAPBP    | 7.04763397 | 6.718404562 | 0.37542813 | 5.79E-15 | 6.73E-11   |
| REXO2    | 9.97547759 | 9.551539168 | 0.37542258 | 5.32E-15 | 6.19E-11   |
| IDS      | 6.47720901 | 6.148944774 | 0.37403631 | 1.60E-14 | 1.85E-10   |
| SOCS3    | 4.54571521 | 4.401934391 | 0.37395564 | 1.70E-13 | 1.95E-09   |
| LYPLA3   | 6.04974309 | 5.74171011  | 0.37386514 | 1.10E-12 | 1.25E-08   |
| GRB10    | 7.47994132 | 6.776549716 | 0.37375914 | 1.26E-13 | 1.45E-09   |
| OLFML3   | 9.09713589 | 8.274995611 | 0.37373146 | 7.88E-13 | 9.01E-09   |
| PTN      | 11.6985235 | 10.53833785 | 0.37363714 | 1.91E-07 | 0.00196823 |
| BIN2     | 5.75684696 | 5.295321474 | 0.37361149 | 1.11E-16 | 1.31E-12   |
| FSTL1    | 10.0504331 | 9.320506501 | 0.37339686 | 1.49E-13 | 1.72E-09   |
| HEBP1    | 9.32905841 | 8.730032163 | 0.37319599 | 1.36E-12 | 1.55E-08   |
| PTPRC    | 7.16911415 | 6.404855105 | 0.37315455 | 9.47E-15 | 1.10E-10   |
| LGI1     | 6.68724678 | 5.516008954 | 0.37301561 | 3.33E-13 | 3.82E-09   |
| PCSK1    | 6.7316198  | 5.691666525 | 0.37296267 | 2.54E-14 | 2.94E-10   |
| EPAS1    | 7.72537926 | 7.277805834 | 0.37284853 | 1.36E-15 | 1.59E-11   |
| LILRB4   | 5.3246876  | 4.797028735 | 0.3727822  | 2.97E-14 | 3.43E-10   |
| SMOX     | 6.13235201 | 5.796518592 | 0.37268075 | 8.19E-13 | 9.36E-09   |
| VWA1     | 6.26164567 | 5.744716172 | 0.37263639 | 1.24E-12 | 1.41E-08   |
| PGDS     | 6.50322231 | 5.655605457 | 0.37241465 | 5.84E-13 | 6.68E-09   |
| PJA2     | 10.1962049 | 9.637841413 | 0.3720823  | 2.71E-12 | 3.07E-08   |
| GGTLA1   | 5.60464977 | 5.086373673 | 0.37195079 | 1.99E-14 | 2.30E-10   |
| PLEKHF1  | 5.78966281 | 5.345698053 | 0.37191441 | 1.23E-16 | 1.44E-12   |
| GPX1     | 10.8534699 | 10.45285098 | 0.37133631 | 1.74E-14 | 2.01E-10   |
| EMR2     | 5.18788912 | 4.646139354 | 0.37126011 | 1.85E-14 | 2.14E-10   |
| GPSM3    | 5.74357131 | 5.423058234 | 0.37106023 | 9.77E-15 | 1.13E-10   |
| NCF4     | 5.25933089 | 4.742554207 | 0.37075957 | 6.96E-15 | 8.08E-11   |
| SPARC    | 11.5485208 | 10.82560807 | 0.37070996 | 2.10E-11 | 2.36E-07   |

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| PHC2     | 8.84414977 | 8.439213593 | 0.37064556 | 3.69E-12 | 4.19E-08   |
| FLJ13236 | 4.89613008 | 4.437341599 | 0.37058599 | 2.46E-18 | 2.91E-14   |
| SSPN     | 8.01236201 | 7.245346794 | 0.37030562 | 1.78E-11 | 2.00E-07   |
| AHNAK2   | 6.2391607  | 5.247285645 | 0.37021608 | 1.19E-17 | 1.40E-13   |
| DLC1     | 5.74853747 | 5.448790324 | 0.37017339 | 1.68E-15 | 1.96E-11   |
| G6PC3    | 8.31781045 | 7.862892437 | 0.37017237 | 1.64E-11 | 1.85E-07   |
| EVI2B    | 7.52320192 | 6.702216133 | 0.36979883 | 6.11E-14 | 7.05E-10   |
| HLA-DMA  | 9.04334178 | 8.168199301 | 0.36958029 | 6.93E-14 | 7.99E-10   |
| TCTN1    | 7.85231789 | 7.392898482 | 0.36947671 | 1.38E-12 | 1.57E-08   |
| PPP1CB   | 9.20684266 | 8.811511839 | 0.36895454 | 2.48E-13 | 2.84E-09   |
| FBLN5    | 7.11147429 | 6.159255482 | 0.36878965 | 8.19E-13 | 9.36E-09   |
| OGFRL1   | 6.59220352 | 6.03264677  | 0.3684915  | 9.57E-15 | 1.11E-10   |
| EMID1    | 6.59493345 | 6.069775684 | 0.36810437 | 1.71E-13 | 1.96E-09   |
| LOXL1    | 6.67479769 | 5.787986392 | 0.36804992 | 3.04E-14 | 3.52E-10   |
| GMFG     | 7.89751841 | 7.194171121 | 0.36787048 | 9.15E-14 | 1.05E-09   |
| ANK2     | 8.15546663 | 7.25265     | 0.36744826 | 2.73E-08 | 0.00028948 |
| MR1      | 5.3410301  | 5.017342512 | 0.36703113 | 1.54E-15 | 1.80E-11   |
| TMEM22   | 7.9524863  | 7.179435755 | 0.36699665 | 1.78E-10 | 1.97E-06   |
| SH3BP2   | 5.63171475 | 5.341458116 | 0.36660399 | 1.89E-13 | 2.17E-09   |
| DHRS3    | 8.48525906 | 7.863284609 | 0.36649679 | 3.66E-11 | 4.10E-07   |
| CTBS     | 6.80969833 | 6.267475664 | 0.36648915 | 6.85E-13 | 7.83E-09   |
| FKBP15   | 6.30134433 | 6.083096161 | 0.36637834 | 2.46E-13 | 2.83E-09   |
| BCAP29   | 6.00489479 | 5.738379087 | 0.36618742 | 4.72E-14 | 5.44E-10   |
| LRP1     | 7.21253327 | 6.586037657 | 0.36618585 | 1.24E-14 | 1.44E-10   |
| CX3CR1   | 9.24982076 | 7.980338236 | 0.36580151 | 1.89E-10 | 2.10E-06   |
| CD180    | 4.81501117 | 4.468484828 | 0.36560246 | 9.96E-14 | 1.15E-09   |
| PTP4A2   | 10.3887801 | 10.04756855 | 0.36524269 | 8.85E-15 | 1.03E-10   |
| ERMAP    | 6.22869828 | 5.859096858 | 0.36486396 | 3.95E-13 | 4.53E-09   |
| LYN      | 7.76717108 | 7.130019074 | 0.36452903 | 9.56E-13 | 1.09E-08   |
| ICAM1    | 5.84044739 | 5.219819529 | 0.36450734 | 1.22E-18 | 1.44E-14   |
| AXL      | 6.61940323 | 6.138616188 | 0.36445262 | 1.17E-14 | 1.35E-10   |
| C21orf7  | 6.19839776 | 5.453256913 | 0.36400455 | 1.09E-16 | 1.28E-12   |
| PTTG1IP  | 11.8571237 | 11.46674286 | 0.36393106 | 8.00E-12 | 9.05E-08   |
| MXRA8    | 7.28890156 | 6.641692859 | 0.3638356  | 1.71E-15 | 1.99E-11   |
| RAB36    | 5.46909765 | 5.025047303 | 0.3632426  | 3.15E-13 | 3.62E-09   |
| HOPX     | 11.3739347 | 10.20412075 | 0.36314659 | 8.39E-13 | 9.59E-09   |
| CNN3     | 10.6343825 | 9.919167782 | 0.3629668  | 1.38E-11 | 1.56E-07   |
| MPP1     | 7.28219119 | 6.778285996 | 0.36236001 | 1.48E-12 | 1.69E-08   |
| TGFB2    | 5.05219739 | 4.590175435 | 0.3622814  | 5.24E-16 | 6.12E-12   |
| TGFBI    | 10.3417569 | 9.423923235 | 0.36186991 | 2.88E-14 | 3.32E-10   |
| SIPA1    | 5.75909124 | 5.423455589 | 0.36184926 | 8.26E-12 | 9.35E-08   |
| EML3     | 6.01758256 | 5.709418639 | 0.36170419 | 1.08E-11 | 1.22E-07   |
| FAM134B  | 5.96612317 | 5.661124129 | 0.36117897 | 1.97E-10 | 2.19E-06   |
| UBE2L6   | 9.75390171 | 9.280027964 | 0.36091113 | 1.10E-12 | 1.25E-08   |
| RGS2     | 10.0036081 | 9.234237133 | 0.36080118 | 1.29E-13 | 1.48E-09   |
| CCDC102B | 5.88772253 | 5.229976581 | 0.36050664 | 8.19E-13 | 9.36E-09   |
| CAP1     | 10.9043699 | 10.65346339 | 0.36035634 | 2.38E-13 | 2.73E-09   |
| MRAS     | 6.9959361  | 6.385463273 | 0.36024949 | 9.91E-09 | 0.00010644 |
| EMILIN1  | 5.12576044 | 4.641248533 | 0.3599215  | 1.36E-14 | 1.58E-10   |

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|-----------|------------|-------------|------------|----------|------------|
| CECR1     | 8.09583618 | 7.267719073 | 0.3599205  | 2.20E-12 | 2.50E-08   |
| SYDE1     | 5.48052704 | 5.274916143 | 0.35988134 | 2.00E-15 | 2.32E-11   |
| STK17A    | 7.54255475 | 6.944065508 | 0.3597163  | 3.20E-13 | 3.67E-09   |
| SH3GLB1   | 9.41571193 | 8.987567294 | 0.35964121 | 9.10E-14 | 1.05E-09   |
| SIRPA     | 6.45133461 | 6.027779496 | 0.35953604 | 7.40E-13 | 8.46E-09   |
| RRAGC     | 9.20991818 | 8.855592263 | 0.3586494  | 6.11E-14 | 7.05E-10   |
| DKK3      | 7.52615679 | 6.856149744 | 0.35845996 | 2.67E-10 | 2.96E-06   |
| TCN2      | 6.28253359 | 5.858128407 | 0.35841122 | 8.19E-12 | 9.27E-08   |
| SCARA3    | 6.86911424 | 6.279922206 | 0.35820162 | 2.28E-12 | 2.59E-08   |
| MYL9      | 7.05527076 | 6.231430548 | 0.35806404 | 2.49E-13 | 2.86E-09   |
| MGAT4A    | 6.16897013 | 5.64297371  | 0.35795161 | 9.52E-13 | 1.09E-08   |
| LOH11CR2A | 7.40364397 | 6.853316271 | 0.3579379  | 6.43E-12 | 7.29E-08   |
| RGS1      | 8.79218905 | 7.831513129 | 0.35745732 | 1.57E-11 | 1.77E-07   |
| C8orf4    | 7.37462598 | 6.514313019 | 0.35745468 | 3.70E-14 | 4.27E-10   |
| ST8SIA4   | 4.94960313 | 4.606116733 | 0.35736636 | 2.47E-11 | 2.78E-07   |
| FTL       | 10.7514683 | 10.50293696 | 0.35668387 | 8.08E-13 | 9.23E-09   |
| COL4A2    | 9.23056714 | 8.373063406 | 0.35654831 | 4.83E-11 | 5.40E-07   |
| ANXA2P2   | 7.38488356 | 6.852510105 | 0.35634837 | 7.91E-14 | 9.11E-10   |
| PRSS23    | 8.34888626 | 7.570356545 | 0.35634792 | 2.67E-13 | 3.06E-09   |
| ECM2      | 7.97517187 | 7.055578989 | 0.356335   | 4.99E-13 | 5.72E-09   |
| TMEM132A  | 7.01171092 | 6.464108897 | 0.35616975 | 5.78E-13 | 6.61E-09   |
| AQP9      | 6.02682178 | 5.322730602 | 0.35580208 | 4.47E-15 | 5.20E-11   |
| COL4A1    | 9.66360482 | 8.738400337 | 0.35553485 | 2.62E-11 | 2.95E-07   |
| HEXB      | 10.0744333 | 9.634986593 | 0.35544463 | 2.57E-16 | 3.01E-12   |
| ENG       | 5.88413825 | 5.538243608 | 0.35536576 | 3.71E-13 | 4.25E-09   |
| CP        | 7.36604557 | 6.307606082 | 0.35524204 | 6.10E-16 | 7.12E-12   |
| FLJ20273  | 7.20519255 | 6.450930641 | 0.35503327 | 9.31E-16 | 1.09E-11   |
| SECTM1    | 5.99746052 | 5.574908406 | 0.35430033 | 3.26E-15 | 3.79E-11   |
| CALD1     | 8.19507499 | 7.672406721 | 0.35418563 | 1.47E-11 | 1.66E-07   |
| PIK3CG    | 4.36630038 | 4.186201737 | 0.35405565 | 2.28E-15 | 2.66E-11   |
| HSPA5     | 11.2769603 | 10.88465802 | 0.35389332 | 5.87E-13 | 6.71E-09   |
| NDFIP1    | 10.2882542 | 9.819700918 | 0.35385491 | 1.24E-09 | 1.35E-05   |
| PLEKHC1   | 9.0708215  | 8.480907431 | 0.35382533 | 2.77E-12 | 3.15E-08   |
| SRI       | 11.0091253 | 10.43858908 | 0.35353401 | 1.01E-07 | 0.00105698 |
| CYB5R1    | 8.77016045 | 8.278895241 | 0.35345573 | 4.09E-14 | 4.72E-10   |
| FOSL1     | 5.37158739 | 4.800722983 | 0.35337158 | 8.26E-19 | 9.78E-15   |
| NOTCH3    | 5.93887022 | 5.730058137 | 0.35300753 | 6.62E-12 | 7.49E-08   |
| MAFF      | 8.10659055 | 7.378505283 | 0.35294362 | 5.17E-12 | 5.86E-08   |
| LAT2      | 5.58291457 | 5.306407856 | 0.35270789 | 1.48E-15 | 1.72E-11   |
| BACE1     | 8.51400311 | 7.97848593  | 0.35243144 | 1.91E-09 | 2.08E-05   |
| IFNGR2    | 8.75841095 | 8.382462661 | 0.35238857 | 4.39E-12 | 4.98E-08   |
| WTAP      | 7.61031049 | 7.167335191 | 0.35207497 | 3.00E-13 | 3.44E-09   |
| AGT       | 11.2023656 | 9.920918392 | 0.35202906 | 8.80E-07 | 0.00889515 |
| LDHA      | 12.5286448 | 12.07612715 | 0.35191809 | 4.45E-11 | 4.99E-07   |
| LGALS9    | 7.09000067 | 6.605973606 | 0.35189233 | 1.90E-12 | 2.16E-08   |
| CIDEB     | 5.4466936  | 5.152888635 | 0.35180691 | 7.52E-14 | 8.66E-10   |
| MSR1      | 4.87620885 | 4.561224998 | 0.35171869 | 1.26E-17 | 1.48E-13   |
| LRRC2     | 4.98563188 | 4.398733588 | 0.35164535 | 1.26E-13 | 1.45E-09   |
| AP1S2     | 9.47001981 | 8.810958961 | 0.35162915 | 2.24E-09 | 2.44E-05   |

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| ALDH9A1     | 10.2322827 | 9.907403272 | 0.35144272 | 2.81E-11 | 3.15E-07   |
| CSF3R       | 5.04500616 | 4.777779288 | 0.35140368 | 6.30E-16 | 7.36E-12   |
| COL8A2      | 5.3975467  | 4.887280686 | 0.35115867 | 1.22E-14 | 1.42E-10   |
| MAP4        | 8.40103951 | 7.90621794  | 0.35089281 | 9.38E-09 | 0.00010086 |
| SEP7        | 12.1245144 | 11.78111935 | 0.3508733  | 1.87E-08 | 0.00019944 |
| RNF130      | 9.58399796 | 9.104439115 | 0.35065652 | 3.64E-12 | 4.13E-08   |
| GUSB        | 9.69868514 | 9.249831063 | 0.35013928 | 2.58E-12 | 2.93E-08   |
| LILRB2      | 5.02064192 | 4.58693799  | 0.35001875 | 7.10E-16 | 8.29E-12   |
| HOM-TES-10: | 7.34205695 | 6.783212276 | 0.34974392 | 1.13E-09 | 1.24E-05   |
| HHLA3       | 6.81810576 | 6.246825572 | 0.34937436 | 3.53E-10 | 3.90E-06   |
| PEPD        | 8.14298056 | 7.730642303 | 0.34936913 | 4.62E-13 | 5.29E-09   |
| RUFY1       | 8.40330598 | 7.999330599 | 0.34935693 | 5.04E-14 | 5.82E-10   |
| SPEG        | 6.19497385 | 5.830213385 | 0.34893377 | 1.93E-11 | 2.17E-07   |
| SCIN        | 8.03782038 | 7.395508609 | 0.34888525 | 4.25E-13 | 4.87E-09   |
| ITGA3       | 5.83989921 | 5.240586589 | 0.34884589 | 8.15E-18 | 9.62E-14   |
| CD81        | 11.4886843 | 11.08514111 | 0.34872246 | 1.22E-10 | 1.36E-06   |
| IL4R        | 6.09287222 | 5.621877699 | 0.34871448 | 7.08E-14 | 8.16E-10   |
| PALLD       | 9.75529628 | 9.231247315 | 0.34848236 | 5.07E-11 | 5.67E-07   |
| ADFP        | 8.96141147 | 8.102377631 | 0.34821284 | 6.38E-11 | 7.13E-07   |
| FLNA        | 7.18317965 | 6.589646955 | 0.34814725 | 2.89E-12 | 3.28E-08   |
| SLC4A4      | 7.42522768 | 6.565037187 | 0.34811912 | 3.72E-11 | 4.17E-07   |
| HLA-B       | 11.3738437 | 10.83249773 | 0.3477611  | 3.33E-11 | 3.73E-07   |
| CD84        | 4.83650563 | 4.688604634 | 0.34773395 | 1.30E-12 | 1.48E-08   |
| NAGA        | 6.58429302 | 6.206482897 | 0.34729959 | 1.77E-11 | 1.99E-07   |
| PTPRE       | 7.65509779 | 7.036728719 | 0.34697378 | 1.51E-11 | 1.70E-07   |
| EGR1        | 9.04630694 | 8.28091156  | 0.3469021  | 3.72E-11 | 4.17E-07   |
| C1orf78     | 6.21643653 | 5.717483202 | 0.34677723 | 8.35E-13 | 9.54E-09   |
| PRDX6       | 10.5163711 | 10.17051179 | 0.34677091 | 2.96E-12 | 3.36E-08   |
| CTNNA1      | 9.9814542  | 9.643810734 | 0.3467297  | 2.11E-12 | 2.41E-08   |
| IL8         | 7.30052268 | 6.14107478  | 0.34659102 | 2.82E-13 | 3.23E-09   |
| TMEM176A    | 8.39741111 | 7.487779977 | 0.34651982 | 1.01E-11 | 1.14E-07   |
| CYR61       | 8.19529333 | 7.331156407 | 0.34636002 | 1.70E-12 | 1.93E-08   |
| MGAT1       | 7.25166626 | 6.852981936 | 0.34605401 | 7.52E-11 | 8.39E-07   |
| FOSL2       | 5.14999781 | 4.853519546 | 0.34603326 | 1.55E-13 | 1.78E-09   |
| PADI2       | 8.06323841 | 7.181837491 | 0.3457568  | 1.38E-08 | 0.00014822 |
| DENND2A     | 7.34062242 | 6.597495233 | 0.34522822 | 1.06E-09 | 1.16E-05   |
| C21orf25    | 7.3091983  | 6.802870732 | 0.34505236 | 1.03E-11 | 1.16E-07   |
| FER1L3      | 7.5426847  | 6.816572816 | 0.34505136 | 6.78E-15 | 7.87E-11   |
| LPXN        | 7.22595365 | 6.675457645 | 0.34423993 | 6.30E-14 | 7.26E-10   |
| RALBP1      | 8.67087511 | 8.217270234 | 0.34402848 | 3.44E-13 | 3.95E-09   |
| PLAU        | 6.28366545 | 5.476067105 | 0.34399241 | 7.14E-18 | 8.42E-14   |
| SGSH        | 6.68082349 | 6.345998565 | 0.3439815  | 2.60E-12 | 2.96E-08   |
| IFI30       | 9.6785526  | 8.9372204   | 0.34388613 | 2.67E-12 | 3.03E-08   |
| ROM1        | 5.62720451 | 5.299734941 | 0.34371342 | 3.77E-11 | 4.23E-07   |
| CDH2        | 8.23310566 | 7.540201793 | 0.34364326 | 1.04E-08 | 0.00011151 |
| JAM3        | 9.1520685  | 8.441176926 | 0.34350332 | 8.57E-09 | 9.23E-05   |
| UBC         | 12.7621681 | 12.48637994 | 0.34346441 | 8.11E-14 | 9.34E-10   |
| FAM46A      | 8.72073192 | 8.064184623 | 0.34332133 | 8.85E-12 | 1.00E-07   |
| ALDH1L1     | 7.46552957 | 6.479906985 | 0.34298934 | 1.77E-11 | 1.99E-07   |

|          |            |             |            |          |            |
|----------|------------|-------------|------------|----------|------------|
| RIN1     | 5.02548958 | 4.792635422 | 0.34266935 | 2.81E-11 | 3.15E-07   |
| CHMP2A   | 10.3059769 | 9.983706788 | 0.34195034 | 3.52E-12 | 4.00E-08   |
| IGFBP6   | 6.31800557 | 5.473993563 | 0.34125422 | 1.22E-14 | 1.42E-10   |
| TACC1    | 6.99102705 | 6.631640868 | 0.34119294 | 3.38E-13 | 3.87E-09   |
| MXRA7    | 11.0035552 | 10.48102331 | 0.34095037 | 2.63E-13 | 3.02E-09   |
| PARVA    | 7.48935439 | 6.983958837 | 0.34093961 | 3.61E-11 | 4.05E-07   |
| PHF11    | 8.7546513  | 8.187849636 | 0.34089006 | 8.03E-10 | 8.82E-06   |
| VCAM1    | 8.71245832 | 7.609100756 | 0.34074672 | 8.53E-12 | 9.66E-08   |
| RIC8A    | 8.96045372 | 8.628549191 | 0.3407172  | 2.39E-11 | 2.68E-07   |
| KLF9     | 6.69475552 | 6.151998717 | 0.34061874 | 3.41E-09 | 3.70E-05   |
| CARS     | 9.04877391 | 8.704355154 | 0.34059216 | 7.65E-11 | 8.53E-07   |
| SLC1A2   | 7.29713549 | 6.398178211 | 0.34010203 | 4.96E-11 | 5.54E-07   |
| CAPNS1   | 10.3044511 | 9.93998739  | 0.34007773 | 1.05E-12 | 1.20E-08   |
| EXT2     | 8.15631201 | 7.815310819 | 0.34006925 | 5.66E-11 | 6.33E-07   |
| MSX1     | 7.66332595 | 6.987034784 | 0.33972868 | 2.90E-08 | 0.00030741 |
| RGL1     | 9.26954488 | 8.747348233 | 0.33943476 | 1.34E-10 | 1.49E-06   |
| TAF10    | 10.1089202 | 9.801842163 | 0.33893334 | 5.44E-11 | 6.08E-07   |
| SCAMP4   | 6.64909992 | 6.085396948 | 0.33886895 | 3.12E-10 | 3.45E-06   |
| EFNB2    | 8.24913675 | 7.511465686 | 0.33862793 | 1.77E-11 | 1.99E-07   |
| LTBP1    | 7.69985186 | 6.988386867 | 0.33851722 | 6.22E-11 | 6.94E-07   |
| C2       | 6.43180916 | 5.784557579 | 0.3385047  | 4.51E-13 | 5.16E-09   |
| DSE      | 7.68347607 | 6.968158285 | 0.33838582 | 1.12E-11 | 1.26E-07   |
| IL6R     | 4.88011753 | 4.673106964 | 0.33805417 | 1.39E-15 | 1.63E-11   |
| CITED1   | 7.47006021 | 6.595485155 | 0.33730452 | 1.74E-10 | 1.93E-06   |
| GEM      | 8.75826603 | 8.008256736 | 0.33727344 | 4.98E-11 | 5.57E-07   |
| UGP2     | 10.3049456 | 9.878687915 | 0.33718445 | 5.27E-13 | 6.03E-09   |
| MAST4    | 6.75375235 | 6.241163978 | 0.33714229 | 1.53E-12 | 1.74E-08   |
| FES      | 4.52069014 | 4.257783555 | 0.33664011 | 1.45E-14 | 1.68E-10   |
| ARID5A   | 5.87152305 | 5.563568802 | 0.33628501 | 2.46E-12 | 2.80E-08   |
| TICAM1   | 5.47328853 | 5.173733094 | 0.33594361 | 1.50E-11 | 1.69E-07   |
| SDC4     | 8.31697976 | 7.492386514 | 0.33583093 | 2.13E-11 | 2.40E-07   |
| SHC1     | 7.34028166 | 6.820905225 | 0.33576536 | 4.67E-14 | 5.39E-10   |
| S100A13  | 9.94938886 | 9.2204559   | 0.33571478 | 1.29E-10 | 1.44E-06   |
| C20orf29 | 6.76752547 | 6.445491993 | 0.33564139 | 6.13E-11 | 6.85E-07   |
| GNA14    | 4.94919784 | 4.593361966 | 0.3355758  | 7.13E-12 | 8.07E-08   |
| LTC4S    | 5.50044183 | 5.109017063 | 0.33540358 | 2.01E-11 | 2.26E-07   |
| IL1RAP   | 6.28516929 | 5.685532251 | 0.33534656 | 2.62E-12 | 2.97E-08   |
| VEGFA    | 8.48914358 | 7.60588683  | 0.33524886 | 2.73E-11 | 3.07E-07   |
| BMP2K    | 5.94377841 | 5.501407518 | 0.33522082 | 1.59E-11 | 1.80E-07   |
| IGFBP5   | 7.68491337 | 7.026854194 | 0.3351146  | 4.44E-10 | 4.90E-06   |
| KLHL4    | 6.26472095 | 5.327168052 | 0.33501733 | 3.66E-12 | 4.15E-08   |
| NEDD9    | 7.37350252 | 6.83204471  | 0.33483499 | 3.10E-12 | 3.52E-08   |
| HEXA     | 8.7351401  | 8.301817889 | 0.33468483 | 2.17E-12 | 2.46E-08   |
| SLAMF8   | 5.64101463 | 5.104601325 | 0.33442969 | 3.80E-12 | 4.31E-08   |
| CADM1    | 9.31246203 | 8.707990231 | 0.33409026 | 5.84E-08 | 0.00061476 |
| AQP4     | 8.68609014 | 7.573831214 | 0.33356207 | 1.39E-07 | 0.00143734 |
| CAPN2    | 10.8744451 | 10.46794336 | 0.33350375 | 2.34E-14 | 2.71E-10   |
| HECTD3   | 7.29739128 | 6.886974871 | 0.33328687 | 1.85E-10 | 2.05E-06   |
| CXCL2    | 7.11351604 | 6.095261305 | 0.33317966 | 1.94E-15 | 2.26E-11   |

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|-----------|------------|-------------|------------|----------|------------|
| TM9SF1    | 7.90330222 | 7.49490089  | 0.33309703 | 1.77E-12 | 2.02E-08   |
| RAC1      | 12.2155052 | 11.95898867 | 0.33302686 | 3.65E-10 | 4.03E-06   |
| FN1       | 9.51551426 | 8.946964344 | 0.33280632 | 1.19E-11 | 1.34E-07   |
| FMNL1     | 4.93193175 | 4.65046613  | 0.3323824  | 1.24E-12 | 1.41E-08   |
| DYRK3     | 5.962499   | 5.639710279 | 0.33197615 | 1.07E-11 | 1.21E-07   |
| TRIM5     | 6.13502925 | 5.702257799 | 0.33182659 | 3.67E-11 | 4.12E-07   |
| DOCK4     | 9.24910981 | 8.640728069 | 0.33136761 | 1.02E-08 | 0.00010937 |
| SMPDL3A   | 7.15791718 | 6.63164695  | 0.33087491 | 2.47E-11 | 2.78E-07   |
| MMP19     | 5.5239183  | 5.231468202 | 0.33081037 | 5.27E-12 | 5.97E-08   |
| S100A6    | 11.1976077 | 10.68346254 | 0.33067907 | 4.62E-11 | 5.17E-07   |
| RHOC      | 9.29410298 | 8.928156745 | 0.33065501 | 4.31E-10 | 4.75E-06   |
| RPS27L    | 10.1303372 | 9.770173019 | 0.33045338 | 1.59E-11 | 1.79E-07   |
| TAPBPL    | 6.06208696 | 5.603811243 | 0.33042041 | 1.35E-12 | 1.54E-08   |
| POLR2L    | 9.36524531 | 9.001009793 | 0.33038092 | 3.67E-10 | 4.05E-06   |
| FOS       | 9.1760502  | 8.33030067  | 0.32973782 | 2.61E-11 | 2.93E-07   |
| GNA15     | 5.69517337 | 5.251614754 | 0.32969466 | 3.11E-17 | 3.65E-13   |
| APLP2     | 8.53888156 | 8.11892419  | 0.32968922 | 1.08E-10 | 1.20E-06   |
| S100A9    | 7.51901996 | 6.567306149 | 0.32951916 | 4.55E-15 | 5.28E-11   |
| EEA1      | 5.57576663 | 5.252046099 | 0.32938274 | 1.74E-11 | 1.96E-07   |
| HMGCL     | 8.02214275 | 7.684045157 | 0.32936444 | 4.20E-11 | 4.71E-07   |
| LYVE1     | 5.19171234 | 4.574867146 | 0.32926273 | 3.13E-12 | 3.56E-08   |
| RASSF2    | 10.0348743 | 9.129654704 | 0.32891931 | 5.91E-07 | 0.00600189 |
| TLR5      | 5.7003308  | 5.164106119 | 0.32883596 | 4.98E-12 | 5.65E-08   |
| FLVCR2    | 5.50805294 | 5.158465599 | 0.32883179 | 5.07E-11 | 5.67E-07   |
| TMEM176B  | 8.70910257 | 7.764698783 | 0.32881765 | 3.21E-10 | 3.55E-06   |
| LEPROT    | 9.58787996 | 9.30829381  | 0.32881663 | 1.94E-10 | 2.15E-06   |
| FADS3     | 6.45700916 | 6.068103391 | 0.32839942 | 1.28E-09 | 1.40E-05   |
| FGR       | 5.87833371 | 5.375037934 | 0.32823215 | 3.60E-13 | 4.13E-09   |
| ARRB2     | 6.72972458 | 6.343220718 | 0.32818453 | 5.72E-10 | 6.29E-06   |
| HLA-C     | 11.7433371 | 11.28703045 | 0.32802755 | 2.56E-10 | 2.84E-06   |
| TANK      | 7.42311337 | 7.051654069 | 0.32778741 | 2.79E-11 | 3.14E-07   |
| HIF1A     | 11.6929518 | 11.32872817 | 0.32772311 | 1.23E-10 | 1.37E-06   |
| PRNP      | 9.3724744  | 8.895790146 | 0.3276596  | 4.36E-09 | 4.72E-05   |
| TNFRSF10C | 4.19869466 | 4.032601439 | 0.32754157 | 3.96E-10 | 4.37E-06   |
| PILRA     | 5.3055751  | 4.926547705 | 0.32746187 | 4.03E-13 | 4.62E-09   |
| 2-Mar     | 7.53454975 | 7.021774049 | 0.32733217 | 4.20E-09 | 4.55E-05   |
| PFKL      | 6.80314363 | 6.462239633 | 0.32714682 | 3.11E-10 | 3.44E-06   |
| MAN2B2    | 7.51847139 | 7.046917104 | 0.32713236 | 2.66E-11 | 2.99E-07   |
| GFAP      | 8.70867994 | 8.341365021 | 0.32701313 | 9.74E-07 | 0.00981994 |
| APOBEC3G  | 7.14041047 | 6.474440549 | 0.32677471 | 5.09E-11 | 5.69E-07   |
| ABCA8     | 7.80118308 | 6.7606358   | 0.32674599 | 4.50E-10 | 4.96E-06   |
| GAPDH     | 13.0860555 | 12.77198963 | 0.32668978 | 2.01E-11 | 2.26E-07   |
| C17orf60  | 4.75270285 | 4.394758435 | 0.32652021 | 2.67E-12 | 3.03E-08   |
| FNDC3B    | 8.59328073 | 8.019762666 | 0.32624173 | 1.83E-11 | 2.07E-07   |
| HIG2      | 9.6711927  | 8.831480265 | 0.32604686 | 1.64E-11 | 1.85E-07   |
| GLT25D2   | 8.31585499 | 7.415617079 | 0.3259596  | 2.44E-08 | 0.00025978 |
| CALCOCO2  | 8.91605256 | 8.566742473 | 0.32562483 | 4.33E-12 | 4.91E-08   |
| WIPI1     | 7.19254066 | 6.554643956 | 0.3255511  | 7.26E-13 | 8.30E-09   |
| MCFD2     | 8.33540259 | 8.00806633  | 0.32514187 | 2.36E-13 | 2.71E-09   |

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| CTSA     | 9.27908781 | 8.801353904 | 0.32463743 | 2.61E-13 | 3.00E-09   |
| TBC1D1   | 5.9626484  | 5.732969824 | 0.32444284 | 1.73E-10 | 1.92E-06   |
| IL17RA   | 5.9660212  | 5.621202713 | 0.32377332 | 4.67E-10 | 5.15E-06   |
| WWTR1    | 5.8218902  | 5.302229958 | 0.32364594 | 7.40E-14 | 8.53E-10   |
| MYO1E    | 5.99193604 | 5.604270905 | 0.32314848 | 1.20E-14 | 1.39E-10   |
| TK2      | 6.23487855 | 5.947172036 | 0.32308745 | 5.83E-09 | 6.29E-05   |
| BLVRB    | 8.0177058  | 7.516017897 | 0.32284538 | 8.04E-12 | 9.10E-08   |
| GNB2     | 8.52914776 | 8.213704156 | 0.32277759 | 1.02E-09 | 1.12E-05   |
| SNX3     | 12.1999835 | 11.87328001 | 0.32266777 | 4.54E-10 | 5.00E-06   |
| LILRB3   | 5.8751749  | 5.623025764 | 0.32262972 | 3.52E-12 | 4.00E-08   |
| ETV5     | 7.28004144 | 6.717595952 | 0.32250179 | 1.09E-09 | 1.20E-05   |
| GMPPA    | 6.27015162 | 5.959160179 | 0.32249763 | 2.39E-11 | 2.68E-07   |
| MYD88    | 8.67775352 | 8.262710938 | 0.32234527 | 1.21E-10 | 1.35E-06   |
| SORT1    | 6.27516964 | 5.952631534 | 0.32187456 | 4.24E-11 | 4.75E-07   |
| SQRDL    | 8.40175122 | 7.748934367 | 0.32181925 | 1.92E-11 | 2.16E-07   |
| CTDSP1   | 7.32136753 | 6.978681599 | 0.32181764 | 1.86E-10 | 2.06E-06   |
| ASL      | 6.99762798 | 6.559774685 | 0.32181049 | 3.93E-11 | 4.40E-07   |
| ARID5B   | 9.21321982 | 8.671927274 | 0.32163555 | 1.51E-11 | 1.70E-07   |
| CORO1A   | 6.99091167 | 6.376963299 | 0.32153474 | 2.54E-11 | 2.86E-07   |
| GAA      | 6.89995717 | 6.479324117 | 0.3208595  | 2.94E-09 | 3.19E-05   |
| CD59     | 9.66037059 | 9.232095793 | 0.32072889 | 5.87E-11 | 6.55E-07   |
| GRN      | 8.76903707 | 8.331212913 | 0.32051463 | 5.22E-12 | 5.91E-08   |
| SREBF1   | 6.67085181 | 6.231425616 | 0.32038811 | 1.20E-10 | 1.34E-06   |
| LPP      | 6.82524962 | 6.452754717 | 0.32021611 | 1.26E-10 | 1.40E-06   |
| DUSP1    | 7.47870552 | 6.919339316 | 0.32016441 | 2.29E-11 | 2.58E-07   |
| FGL2     | 6.66320572 | 6.096351432 | 0.31984091 | 8.85E-11 | 9.86E-07   |
| TNFAIP3  | 7.00017997 | 6.419159175 | 0.31974856 | 6.59E-13 | 7.54E-09   |
| ACTN4    | 7.51386443 | 7.119388164 | 0.31968111 | 6.91E-11 | 7.72E-07   |
| PSCD4    | 4.96178928 | 4.784035877 | 0.31950282 | 1.53E-10 | 1.70E-06   |
| SERPINH1 | 8.08223484 | 7.469211746 | 0.31946123 | 4.87E-10 | 5.37E-06   |
| DERL2    | 8.33350867 | 8.023878394 | 0.319068   | 2.89E-10 | 3.20E-06   |
| CTSD     | 7.07106353 | 6.605071643 | 0.31895879 | 6.97E-10 | 7.66E-06   |
| PYCARD   | 7.20397719 | 6.571483426 | 0.31894768 | 5.20E-11 | 5.82E-07   |
| SAMD4A   | 5.64581236 | 5.416356858 | 0.31881754 | 1.44E-10 | 1.60E-06   |
| DCTD     | 7.90955912 | 7.494249239 | 0.31866268 | 6.33E-09 | 6.83E-05   |
| PI3      | 5.75178123 | 4.655180226 | 0.31829595 | 4.44E-17 | 5.22E-13   |
| HS2ST1   | 7.56090271 | 7.149363505 | 0.31827474 | 3.02E-10 | 3.34E-06   |
| APOE     | 8.15343936 | 7.663104975 | 0.31808554 | 4.82E-07 | 0.00491106 |
| STIM1    | 5.61493541 | 5.343335075 | 0.31789597 | 3.07E-09 | 3.34E-05   |
| NPC1     | 8.57220533 | 8.17495677  | 0.31787444 | 2.88E-12 | 3.27E-08   |
| COL5A3   | 6.34350217 | 5.796368242 | 0.31714321 | 3.42E-11 | 3.84E-07   |
| HK3      | 4.65248974 | 4.330065447 | 0.3166021  | 2.62E-14 | 3.03E-10   |
| LPL      | 9.75702795 | 8.716157683 | 0.31646592 | 5.40E-08 | 0.00056941 |
| RAB7L1   | 6.93868134 | 6.400330801 | 0.31627181 | 4.75E-10 | 5.24E-06   |
| TRIM21   | 6.1215792  | 5.736288996 | 0.31610686 | 9.53E-11 | 1.06E-06   |
| KIAA1199 | 6.10028641 | 5.374909391 | 0.31595118 | 6.95E-13 | 7.95E-09   |
| P2RY13   | 5.95987524 | 5.280278792 | 0.31591147 | 6.03E-11 | 6.73E-07   |
| TIMP2    | 7.95321351 | 7.543867166 | 0.31590902 | 9.49E-11 | 1.06E-06   |
| SLN      | 7.87209081 | 6.586953535 | 0.31583558 | 2.52E-11 | 2.83E-07   |

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| KLHL26   | 6.5551109  | 6.03762464  | 0.31578973 | 6.68E-10 | 7.34E-06   |
| ATP6V0E1 | 8.5261087  | 8.272192838 | 0.31561879 | 2.13E-10 | 2.36E-06   |
| PPP1R3C  | 8.28815388 | 7.627214039 | 0.31560166 | 1.21E-07 | 0.00125956 |
| STOML1   | 6.73983673 | 6.388937656 | 0.31556485 | 1.80E-09 | 1.97E-05   |
| TNFAIP2  | 5.57346254 | 5.150766497 | 0.31551811 | 2.56E-13 | 2.94E-09   |
| GNS      | 8.35461548 | 7.919626493 | 0.31539212 | 1.40E-12 | 1.59E-08   |
| KCNJ2    | 7.23555594 | 6.654209351 | 0.31538405 | 3.20E-10 | 3.54E-06   |
| PDZD2    | 7.81414149 | 6.878182432 | 0.3151728  | 2.99E-10 | 3.31E-06   |
| HLA-DRB1 | 10.8908544 | 10.08280322 | 0.31502802 | 1.54E-10 | 1.71E-06   |
| TDO2     | 6.04645287 | 5.098346406 | 0.31495497 | 4.66E-11 | 5.21E-07   |
| CYP27A1  | 7.0074745  | 6.641979363 | 0.31446547 | 3.47E-10 | 3.83E-06   |
| SUCLG2   | 7.08154516 | 6.752699473 | 0.31433105 | 1.20E-09 | 1.31E-05   |
| LST1     | 6.60840319 | 6.037406641 | 0.31419993 | 7.93E-10 | 8.71E-06   |
| ARHGAP26 | 5.36767021 | 5.090525117 | 0.31417072 | 1.99E-10 | 2.21E-06   |
| CPD      | 7.32680576 | 6.765535108 | 0.31411831 | 4.11E-12 | 4.66E-08   |
| ACP6     | 7.16098065 | 6.627347055 | 0.31404115 | 3.00E-11 | 3.37E-07   |
| MGC14376 | 6.93184078 | 6.417364386 | 0.31403676 | 2.06E-11 | 2.32E-07   |
| HEPH     | 6.79778391 | 5.944319845 | 0.31368169 | 2.48E-10 | 2.74E-06   |
| FTHP1    | 9.29140237 | 9.00927953  | 0.31340711 | 3.43E-10 | 3.79E-06   |
| LHFP     | 9.09221839 | 8.389385855 | 0.31333674 | 2.07E-07 | 0.00213329 |
| SCAMP2   | 8.02028737 | 7.673711988 | 0.31333671 | 4.20E-10 | 4.64E-06   |
| CTNS     | 6.57215221 | 6.213135582 | 0.31330089 | 1.01E-09 | 1.10E-05   |
| BCL2A1   | 6.04433131 | 5.305072214 | 0.31322261 | 9.49E-12 | 1.07E-07   |
| B4GALT5  | 8.88083587 | 8.435506475 | 0.31273607 | 2.93E-10 | 3.24E-06   |
| SNAPC2   | 5.2050388  | 5.024530822 | 0.31252001 | 2.95E-10 | 3.27E-06   |
| NCF1     | 5.16750951 | 4.789045261 | 0.31239876 | 9.74E-17 | 1.14E-12   |
| RBMS1    | 8.1440716  | 7.613914512 | 0.31235575 | 8.65E-11 | 9.65E-07   |
| ALOX5    | 5.14283575 | 4.844125479 | 0.31232671 | 6.21E-20 | 7.37E-16   |
| AGPAT5   | 9.98303536 | 9.511293365 | 0.31225248 | 3.73E-08 | 0.00039482 |
| TUBB6    | 9.57081175 | 8.829659915 | 0.31217314 | 8.51E-10 | 9.34E-06   |
| IGFBP3   | 9.46002217 | 8.479987765 | 0.31204123 | 1.19E-09 | 1.30E-05   |
| TMEM112B | 6.98545546 | 6.731159735 | 0.3119822  | 5.77E-10 | 6.35E-06   |
| FLJ20699 | 6.18628911 | 5.905367338 | 0.31196206 | 3.11E-10 | 3.44E-06   |
| IL10     | 4.30874196 | 4.143767981 | 0.31164297 | 4.33E-12 | 4.91E-08   |
| HSPB6    | 5.41565229 | 4.89881825  | 0.31133815 | 1.25E-14 | 1.45E-10   |
| PPARD    | 6.30662598 | 6.103799228 | 0.31105023 | 2.93E-10 | 3.24E-06   |
| SLC15A3  | 5.71178835 | 5.281854767 | 0.31090602 | 1.15E-11 | 1.30E-07   |
| ARPC1B   | 8.61638605 | 8.103632782 | 0.31069877 | 5.98E-13 | 6.84E-09   |
| TBC1D9B  | 7.00968439 | 6.744984332 | 0.31045068 | 1.64E-10 | 1.82E-06   |
| PTPN6    | 6.70324304 | 6.241683221 | 0.31019065 | 1.11E-12 | 1.27E-08   |
| ACTA2    | 9.65447604 | 8.917377614 | 0.31002424 | 7.58E-11 | 8.46E-07   |
| NCF2     | 6.00005475 | 5.405312925 | 0.31001746 | 1.50E-12 | 1.71E-08   |
| IFI35    | 7.29730932 | 6.725185009 | 0.30988953 | 1.08E-09 | 1.19E-05   |
| BICD1    | 6.73126838 | 6.380264722 | 0.30987031 | 2.72E-09 | 2.96E-05   |
| GPR3     | 4.66526196 | 4.433731374 | 0.30974792 | 1.00E-09 | 1.10E-05   |
| DRAM     | 7.10180861 | 6.53234208  | 0.30972476 | 2.29E-11 | 2.58E-07   |
| HLA-DPA1 | 10.8981773 | 10.11687131 | 0.30892818 | 6.85E-11 | 7.65E-07   |
| ATP1A1   | 9.63054854 | 9.233944474 | 0.30867117 | 5.94E-10 | 6.54E-06   |
| COTL1    | 8.38635581 | 7.896667999 | 0.30862196 | 1.83E-09 | 1.99E-05   |

|           |            |             |            |          |            |
|-----------|------------|-------------|------------|----------|------------|
| PTPN12    | 6.54901292 | 6.313858103 | 0.30849329 | 5.13E-09 | 5.55E-05   |
| WIPF1     | 6.56362924 | 6.192182182 | 0.30820641 | 7.62E-11 | 8.50E-07   |
| LILRA1    | 4.58119047 | 4.471827328 | 0.30774385 | 1.65E-09 | 1.80E-05   |
| TNFRSF11A | 4.6133152  | 4.404549602 | 0.30705992 | 2.25E-09 | 2.45E-05   |
| ATF3      | 8.34696578 | 7.637910062 | 0.30677613 | 4.77E-10 | 5.26E-06   |
| CXCL3     | 5.4325594  | 4.837702059 | 0.30669954 | 1.25E-15 | 1.45E-11   |
| ARHGEF3   | 8.33295038 | 7.890693338 | 0.30649068 | 1.69E-08 | 0.00018002 |
| POLD4     | 6.32994672 | 5.980080175 | 0.30644528 | 5.54E-11 | 6.19E-07   |
| OSMR      | 5.88607999 | 5.299868619 | 0.30633753 | 5.95E-12 | 6.74E-08   |
| ARL6IP5   | 10.3388581 | 10.06617619 | 0.3062139  | 6.21E-09 | 6.70E-05   |
| CD97      | 6.37925743 | 5.87777708  | 0.30607009 | 9.10E-12 | 1.03E-07   |
| SLC9A1    | 6.37039248 | 6.120852867 | 0.30586608 | 1.46E-10 | 1.63E-06   |
| THBD      | 5.82943484 | 5.271919942 | 0.30565403 | 3.37E-14 | 3.89E-10   |
| FKBP5     | 5.99382521 | 5.327253729 | 0.30551333 | 3.99E-10 | 4.41E-06   |
| COL6A1    | 5.32047894 | 5.115201165 | 0.30527883 | 6.40E-13 | 7.32E-09   |
| ETHE1     | 7.85223056 | 7.428107491 | 0.30504356 | 2.86E-10 | 3.17E-06   |
| SLC2A4RG  | 6.94418277 | 6.522487206 | 0.3045769  | 8.95E-10 | 9.82E-06   |
| PSCDBP    | 5.62822425 | 5.053120919 | 0.30446153 | 1.04E-14 | 1.21E-10   |
| CPE       | 10.5400855 | 9.767808228 | 0.30405787 | 3.70E-07 | 0.00378461 |
| KLHDC8A   | 6.92674808 | 6.204893066 | 0.30346369 | 3.42E-08 | 0.00036249 |
| GAS7      | 7.08022571 | 6.500953285 | 0.30341377 | 1.16E-09 | 1.27E-05   |
| SP110     | 6.86050751 | 6.454749153 | 0.30324144 | 6.24E-11 | 6.97E-07   |
| SORL1     | 9.20102794 | 8.602380125 | 0.30323577 | 7.90E-09 | 8.51E-05   |
| ENPEP     | 5.61307916 | 5.182175339 | 0.30310945 | 8.48E-10 | 9.30E-06   |
| MERTK     | 6.02089839 | 5.558513806 | 0.30293765 | 1.60E-09 | 1.74E-05   |
| CXCR4     | 8.1386871  | 7.477450703 | 0.30287782 | 4.22E-09 | 4.57E-05   |
| HMHA1     | 6.12428393 | 5.737355652 | 0.30276359 | 3.13E-11 | 3.51E-07   |
| ANGPT1    | 6.65194888 | 5.907049923 | 0.3026942  | 5.82E-11 | 6.50E-07   |
| XKR8      | 7.50692821 | 7.216928175 | 0.30263285 | 2.73E-09 | 2.97E-05   |
| SPSB1     | 5.91592267 | 5.527634348 | 0.30253482 | 4.17E-09 | 4.52E-05   |
| TPM4      | 8.17143891 | 7.70975633  | 0.30234078 | 2.15E-08 | 0.00022936 |
| KIF13B    | 7.19990566 | 6.69338754  | 0.30229258 | 5.64E-09 | 6.10E-05   |
| ELL2      | 4.93135104 | 4.735904136 | 0.30219488 | 1.28E-12 | 1.45E-08   |
| TOMM7     | 11.9781138 | 11.74806785 | 0.30199277 | 2.66E-09 | 2.89E-05   |
| LYL1      | 5.67630071 | 5.408509208 | 0.3016843  | 1.29E-09 | 1.41E-05   |
| MANBA     | 6.91883259 | 6.626532085 | 0.30167408 | 4.91E-10 | 5.42E-06   |
| NTAN1     | 7.35913987 | 6.95065857  | 0.30161642 | 2.48E-09 | 2.70E-05   |
| RHOB      | 10.4585355 | 9.821951336 | 0.3015113  | 4.04E-07 | 0.00412461 |
| MAN2A1    | 8.01046139 | 7.493760051 | 0.30115539 | 8.44E-10 | 9.27E-06   |
| TCTA      | 7.820773   | 7.37876513  | 0.30106818 | 2.05E-08 | 0.0002184  |
| ZFP106    | 8.54536741 | 8.08424735  | 0.30101228 | 8.41E-10 | 9.23E-06   |
| FBXO17    | 6.3679196  | 5.896468372 | 0.30073573 | 1.22E-07 | 0.00126401 |
| PLEK      | 6.53860096 | 6.069265716 | 0.30065706 | 2.46E-11 | 2.77E-07   |
| RAB4B     | 7.1684553  | 6.82621259  | 0.30043116 | 1.19E-08 | 0.00012719 |
| HYPE      | 6.505636   | 6.08171389  | 0.30034138 | 1.11E-08 | 0.00011959 |
| VAV1      | 5.20122665 | 4.899350461 | 0.29991618 | 3.87E-12 | 4.39E-08   |
| SERPINF1  | 8.3491913  | 7.566490386 | 0.29983886 | 1.78E-10 | 1.98E-06   |
| NCKAP1L   | 5.8010182  | 5.350092538 | 0.29972218 | 2.53E-12 | 2.88E-08   |
| TAGLN2    | 8.69680236 | 8.188757958 | 0.29965098 | 3.27E-08 | 0.00034668 |

|          |            |             |            |          |            |
|----------|------------|-------------|------------|----------|------------|
| SLC22A18 | 6.48699719 | 5.95856278  | 0.29956556 | 2.27E-11 | 2.55E-07   |
| CTSO     | 8.61943116 | 8.062189269 | 0.29937763 | 2.00E-07 | 0.002067   |
| GLB1L    | 5.49751867 | 5.222412925 | 0.2992959  | 1.67E-09 | 1.82E-05   |
| ORAI2    | 5.4643389  | 5.224872877 | 0.29926278 | 1.57E-08 | 0.00016744 |
| ARHGAP25 | 6.07681062 | 5.720320488 | 0.29924886 | 8.30E-10 | 9.12E-06   |
| HLA-DMB  | 8.6798074  | 8.039122716 | 0.29877846 | 1.60E-09 | 1.75E-05   |
| LSP1     | 5.80776772 | 5.406025116 | 0.298737   | 2.67E-11 | 3.00E-07   |
| LAPTM4A  | 11.6214745 | 11.40108434 | 0.29868688 | 3.49E-10 | 3.85E-06   |
| BNIP3L   | 10.5517271 | 10.21588616 | 0.29841442 | 5.53E-09 | 5.98E-05   |
| NPAS2    | 5.03231157 | 4.757366063 | 0.2982716  | 1.97E-11 | 2.22E-07   |
| KCNF1    | 6.06839609 | 5.425636086 | 0.2981688  | 8.95E-10 | 9.82E-06   |
| GAS2L1   | 6.91154669 | 6.530232145 | 0.29807995 | 7.43E-08 | 0.00077893 |
| IER5     | 9.14351099 | 8.672635827 | 0.29806674 | 1.70E-09 | 1.86E-05   |
| CHN1     | 9.84351095 | 9.183854266 | 0.2980031  | 6.75E-08 | 0.0007089  |
| CYP19A1  | 4.592221   | 4.315317052 | 0.29789533 | 3.14E-07 | 0.00321942 |
| SPRY1    | 8.03670896 | 7.327732347 | 0.29772781 | 1.54E-08 | 0.00016491 |
| TGFBR2   | 6.23569252 | 5.840475273 | 0.29742628 | 3.97E-13 | 4.55E-09   |
| BST2     | 7.84458647 | 7.113905009 | 0.29706996 | 3.67E-09 | 3.98E-05   |
| SLC2A1   | 8.75453288 | 8.194078447 | 0.29700647 | 5.44E-10 | 5.99E-06   |
| BGN      | 6.64140749 | 6.224094558 | 0.29677452 | 2.45E-08 | 0.00026075 |
| MOSPD2   | 6.9788354  | 6.654190128 | 0.29675836 | 2.15E-08 | 0.00022936 |
| SPRY4    | 7.89429669 | 7.07634606  | 0.29674636 | 4.73E-08 | 0.00049891 |
| MEF2A    | 6.89210976 | 6.575720815 | 0.2967272  | 1.74E-09 | 1.90E-05   |
| NOD1     | 5.65532971 | 5.355590413 | 0.29661702 | 2.14E-10 | 2.37E-06   |
| APBB1IP  | 5.09144735 | 4.823280203 | 0.29657943 | 1.74E-11 | 1.96E-07   |
| PIGT     | 8.44640007 | 8.140945861 | 0.29650412 | 2.37E-09 | 2.58E-05   |
| SCRN1    | 9.60734789 | 8.994078989 | 0.29646988 | 1.45E-07 | 0.00150542 |
| CFL1     | 12.6017777 | 12.38693948 | 0.29638823 | 1.56E-09 | 1.70E-05   |
| LGALS3BP | 8.82751275 | 8.350880326 | 0.29614152 | 6.41E-10 | 7.04E-06   |
| SEC14L1  | 8.46729876 | 7.946661267 | 0.29611528 | 1.13E-09 | 1.24E-05   |
| ZFP36L1  | 7.95487829 | 7.503500177 | 0.29598371 | 2.00E-08 | 0.00021273 |
| ZMAT3    | 8.52673718 | 7.868093365 | 0.29596948 | 1.52E-08 | 0.00016243 |
| ADAM28   | 5.43340157 | 5.100830047 | 0.29594511 | 5.07E-13 | 5.80E-09   |
| MAPKAPK2 | 5.98759485 | 5.758374015 | 0.29545136 | 5.34E-08 | 0.00056326 |
| VAMP3    | 9.08449317 | 8.631930053 | 0.29525425 | 1.63E-09 | 1.78E-05   |
| CD248    | 6.68548765 | 6.278952385 | 0.29502519 | 5.83E-09 | 6.29E-05   |
| YIPF1    | 7.46862022 | 7.183156391 | 0.29470162 | 5.76E-08 | 0.00060583 |
| HSD17B12 | 10.5567797 | 10.22983562 | 0.29467387 | 8.13E-10 | 8.93E-06   |
| COL5A2   | 8.57904781 | 7.775340137 | 0.29461106 | 2.71E-09 | 2.95E-05   |
| FGF2     | 6.18405232 | 5.775998677 | 0.29428636 | 1.53E-09 | 1.67E-05   |
| ITGB8    | 5.50527259 | 5.060933631 | 0.29401292 | 2.44E-11 | 2.74E-07   |
| RAP1A    | 9.33664791 | 9.081930528 | 0.29389598 | 1.01E-09 | 1.11E-05   |
| RGN      | 6.64282591 | 6.013251761 | 0.29383361 | 1.24E-08 | 0.00013315 |
| NUAK2    | 5.96550218 | 5.468444152 | 0.29383078 | 1.44E-12 | 1.65E-08   |
| ELTD1    | 7.25649685 | 6.637610239 | 0.29371686 | 3.61E-08 | 0.0003819  |
| CCPG1    | 6.75537799 | 6.349859402 | 0.29364435 | 3.46E-10 | 3.82E-06   |
| CNGA3    | 6.30001006 | 5.493697054 | 0.2935876  | 2.28E-10 | 2.53E-06   |
| DDEFL1   | 6.27296124 | 5.938273591 | 0.2932473  | 5.09E-09 | 5.50E-05   |
| COMMD9   | 8.22945885 | 7.939697641 | 0.29316444 | 5.57E-08 | 0.0005862  |

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|-------------|------------|-------------|------------|----------|------------|
| SIGLEC5     | 4.86227004 | 4.674281676 | 0.292956   | 2.55E-08 | 0.0002706  |
| ATP8B4      | 4.46108686 | 4.159235783 | 0.2928848  | 8.77E-12 | 9.92E-08   |
| GLB1        | 8.43778488 | 8.075768833 | 0.29288073 | 5.19E-10 | 5.72E-06   |
| SNX5        | 9.06024042 | 8.692627482 | 0.29262978 | 5.29E-08 | 0.00055712 |
| UBTD1       | 4.91109214 | 4.706435897 | 0.2925918  | 2.48E-10 | 2.74E-06   |
| CNDP2       | 9.8266651  | 9.518507279 | 0.29237613 | 1.51E-08 | 0.00016122 |
| PKD2        | 7.53897919 | 7.123849555 | 0.292302   | 6.04E-09 | 6.52E-05   |
| CLEC2B      | 7.39786709 | 6.686895522 | 0.2922744  | 2.25E-10 | 2.50E-06   |
| RASSF4      | 6.70408898 | 6.273972179 | 0.291941   | 5.29E-08 | 0.00055712 |
| CAV1        | 9.46937148 | 8.635727354 | 0.29129925 | 1.95E-09 | 2.13E-05   |
| TMEM51      | 6.73554864 | 6.403778723 | 0.29115614 | 4.13E-10 | 4.56E-06   |
| EGR2        | 6.66678981 | 6.099636072 | 0.29092137 | 8.12E-09 | 8.74E-05   |
| SERPINB8    | 5.19365145 | 4.837807698 | 0.29075637 | 4.16E-11 | 4.66E-07   |
| C20orf116   | 8.16194478 | 7.868968309 | 0.29068493 | 6.20E-10 | 6.81E-06   |
| CSDA        | 7.45912121 | 7.114482232 | 0.29059911 | 2.01E-10 | 2.23E-06   |
| OLR1        | 6.30698905 | 5.604511393 | 0.29019952 | 4.87E-10 | 5.37E-06   |
| HLA-DRA     | 10.8393139 | 9.971618893 | 0.29013071 | 1.42E-09 | 1.55E-05   |
| TMED10      | 10.3839491 | 10.08078037 | 0.28997867 | 2.18E-10 | 2.41E-06   |
| ADAMTS1     | 6.63030277 | 5.973966038 | 0.28996805 | 3.11E-10 | 3.44E-06   |
| TM6SF1      | 6.23121555 | 5.802063818 | 0.28981316 | 6.13E-09 | 6.62E-05   |
| DAB2        | 7.59855923 | 7.010518919 | 0.28946529 | 2.07E-09 | 2.26E-05   |
| ZDHHC24     | 5.82853667 | 5.549334698 | 0.28934388 | 7.11E-10 | 7.82E-06   |
| BCL6        | 7.81358932 | 7.345227782 | 0.28876917 | 1.08E-08 | 0.00011639 |
| SLC4A7      | 5.46689346 | 5.310646108 | 0.28876793 | 8.92E-09 | 9.59E-05   |
| GABARAP     | 11.1723464 | 10.92661913 | 0.2885372  | 2.52E-07 | 0.00259685 |
| GYPC        | 7.83732442 | 7.234972231 | 0.28851785 | 4.66E-09 | 5.04E-05   |
| MFAP3L      | 5.52066308 | 5.282958823 | 0.28782366 | 8.99E-09 | 9.67E-05   |
| BBS1        | 8.28857278 | 7.795396755 | 0.28770036 | 5.09E-07 | 0.00518703 |
| MEOX2       | 7.0391589  | 5.872283149 | 0.28761766 | 1.25E-08 | 0.00013417 |
| NME5        | 7.41430375 | 6.784940622 | 0.28760961 | 1.85E-07 | 0.00190763 |
| CPEB1       | 6.39458097 | 5.914339092 | 0.28757788 | 2.12E-08 | 0.00022599 |
| YAP1        | 6.0424881  | 5.453274878 | 0.2875662  | 5.17E-08 | 0.00054497 |
| TRIM6-TRIM3 | 5.94351534 | 5.52121761  | 0.28725757 | 2.07E-09 | 2.26E-05   |
| HLA-DPB1    | 9.94568858 | 9.19901709  | 0.28718563 | 1.78E-09 | 1.94E-05   |
| SIL1        | 6.72719756 | 6.415517714 | 0.287026   | 7.71E-09 | 8.31E-05   |
| TLN1        | 6.98019407 | 6.508633458 | 0.28701891 | 4.35E-08 | 0.00045997 |
| GPC4        | 6.2154262  | 5.744642784 | 0.28692689 | 5.82E-10 | 6.40E-06   |
| NUPR1       | 7.86850368 | 7.289861267 | 0.28689007 | 7.96E-09 | 8.57E-05   |
| CTSS        | 7.33003705 | 6.705973204 | 0.2868824  | 5.37E-10 | 5.91E-06   |
| PCGF1       | 7.24873123 | 6.899215835 | 0.28672876 | 8.02E-09 | 8.64E-05   |
| MTM1        | 6.00252931 | 5.63998072  | 0.28664185 | 1.76E-08 | 0.00018771 |
| PGLS        | 8.86749376 | 8.570155406 | 0.28651369 | 3.83E-08 | 0.00040523 |
| RPS6KA2     | 7.35845365 | 6.853418592 | 0.28649509 | 2.61E-07 | 0.00268869 |
| ARHGAP1     | 6.46648905 | 6.284148691 | 0.28645878 | 1.44E-08 | 0.00015457 |
| OBSL1       | 6.00767485 | 5.713908598 | 0.28632481 | 7.94E-08 | 0.00083118 |
| RGS6        | 5.05382288 | 4.77273261  | 0.28612616 | 4.30E-09 | 4.66E-05   |
| TFEC        | 5.47778175 | 4.996804697 | 0.28611745 | 1.54E-10 | 1.71E-06   |
| MAP3K14     | 5.58949169 | 5.297016282 | 0.28596977 | 2.86E-08 | 0.00030284 |
| TPI1        | 10.4365507 | 10.15513167 | 0.28583422 | 6.43E-08 | 0.00067611 |

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|----------|------------|-------------|------------|----------|------------|
| CDH11    | 8.95797282 | 8.350047659 | 0.28580937 | 8.79E-08 | 0.00091885 |
| BDH2     | 8.88324857 | 8.470033183 | 0.28542454 | 4.24E-09 | 4.59E-05   |
| MAP1LC3B | 9.69257429 | 9.309590424 | 0.2854202  | 8.73E-08 | 0.0009125  |
| PH-4     | 8.44860875 | 8.040043116 | 0.28529648 | 1.02E-07 | 0.00106063 |
| UROD     | 8.72715765 | 8.461461841 | 0.28526946 | 5.45E-09 | 5.88E-05   |
| PFN1     | 10.5034038 | 10.15094857 | 0.28499722 | 5.00E-08 | 0.00052711 |
| COLEC12  | 7.25168312 | 6.457771626 | 0.28497347 | 4.55E-09 | 4.93E-05   |
| WDR41    | 8.46686242 | 8.098015619 | 0.28493701 | 6.06E-09 | 6.54E-05   |
| NLRX1    | 6.1797909  | 5.895644103 | 0.28478977 | 1.74E-09 | 1.90E-05   |
| KIAA1033 | 8.12588141 | 7.801810791 | 0.28473598 | 8.18E-09 | 8.81E-05   |
| LEFTY2   | 6.44829266 | 5.833301256 | 0.28437762 | 1.48E-08 | 0.00015817 |
| IL1B     | 6.41030322 | 5.74940746  | 0.28419268 | 3.53E-11 | 3.96E-07   |
| CENTD3   | 7.46128562 | 6.80797739  | 0.28397802 | 7.32E-08 | 0.00076784 |
| CHCHD7   | 7.39460916 | 7.050720016 | 0.28386841 | 9.42E-09 | 0.00010124 |
| TEGT     | 10.8849705 | 10.62611125 | 0.28385734 | 2.23E-10 | 2.48E-06   |
| TRIM38   | 6.04068874 | 5.602589882 | 0.28371989 | 1.19E-10 | 1.32E-06   |
| CSTA     | 7.27523213 | 6.475889655 | 0.28357304 | 2.75E-15 | 3.20E-11   |
| RIPK1    | 5.55791406 | 5.248955974 | 0.28353328 | 7.91E-09 | 8.52E-05   |
| PLCG2    | 6.32157107 | 5.851287608 | 0.28348712 | 1.92E-10 | 2.13E-06   |
| SYK      | 6.54569855 | 6.060456692 | 0.28347686 | 5.35E-10 | 5.89E-06   |
| FOLR2    | 6.76824738 | 6.17789461  | 0.28306477 | 2.21E-07 | 0.00228128 |
| ADCK2    | 6.59700867 | 6.294537471 | 0.28300083 | 2.96E-09 | 3.22E-05   |
| IRF2     | 6.84552036 | 6.444100256 | 0.28283711 | 1.58E-08 | 0.00016937 |
| ENTPD1   | 6.39901524 | 6.049488287 | 0.28281131 | 5.30E-09 | 5.72E-05   |
| BIRC3    | 5.54666508 | 4.939811494 | 0.28249358 | 2.40E-14 | 2.78E-10   |
| CPSF4    | 8.05480054 | 7.790584294 | 0.28236024 | 9.57E-08 | 0.00099821 |
| PDE4B    | 8.75807954 | 8.107389254 | 0.28205393 | 5.42E-08 | 0.00057148 |
| EGF      | 4.66294507 | 4.355165595 | 0.28203977 | 1.08E-12 | 1.23E-08   |
| BDKRB2   | 5.3032422  | 4.946965239 | 0.28180406 | 1.90E-10 | 2.10E-06   |
| ORAI3    | 6.84225654 | 6.521780554 | 0.28175921 | 5.36E-08 | 0.0005653  |
| BRP44L   | 9.7206281  | 9.346821132 | 0.28169057 | 2.68E-07 | 0.00275515 |
| TLR3     | 5.48387896 | 5.076972993 | 0.28164228 | 3.15E-09 | 3.42E-05   |
| RCN1     | 8.62702406 | 8.275417975 | 0.28162687 | 1.37E-07 | 0.00142214 |
| FMOD     | 6.82382559 | 6.098446831 | 0.28151896 | 2.30E-10 | 2.55E-06   |
| HSPA2    | 8.3987665  | 7.639217008 | 0.28148925 | 5.51E-08 | 0.00057987 |
| RAB8B    | 6.09483503 | 5.735117897 | 0.28138746 | 8.68E-09 | 9.34E-05   |
| OGDH     | 7.22272204 | 6.834145844 | 0.28138591 | 2.90E-08 | 0.00030741 |
| DDB2     | 6.37245376 | 5.9238495   | 0.28112398 | 1.66E-09 | 1.81E-05   |
| POSTN    | 8.97918653 | 7.36991361  | 0.28043182 | 1.24E-08 | 0.00013266 |
| MKNK1    | 7.45074967 | 7.077184559 | 0.2804266  | 3.70E-08 | 0.0003919  |
| TMED5    | 8.48959003 | 8.182305727 | 0.28030457 | 2.66E-08 | 0.00028199 |
| BTK      | 5.70994475 | 5.374069406 | 0.28027424 | 8.94E-12 | 1.01E-07   |
| GPSN2    | 9.17389112 | 8.84207947  | 0.27956994 | 7.40E-08 | 0.00077621 |
| C12orf5  | 7.94001353 | 7.49148674  | 0.27950476 | 1.21E-09 | 1.32E-05   |
| SYPL1    | 9.15643208 | 8.664288395 | 0.27930254 | 1.81E-07 | 0.00186806 |
| APOC1    | 10.7310116 | 10.03808244 | 0.27916017 | 1.40E-07 | 0.0014476  |
| GRAMD3   | 8.9806462  | 8.307473488 | 0.27887323 | 8.00E-07 | 0.0080988  |
| RDH5     | 5.79870764 | 5.524188725 | 0.27871216 | 8.91E-10 | 9.78E-06   |
| PMFBP1   | 4.97129525 | 4.804056965 | 0.27870503 | 2.22E-08 | 0.00023634 |

|          |            |             |            |          |            |
|----------|------------|-------------|------------|----------|------------|
| FNBP1    | 7.89484069 | 7.534333641 | 0.27843034 | 5.42E-09 | 5.86E-05   |
| DUSP6    | 8.67345928 | 8.100313605 | 0.27827442 | 3.57E-07 | 0.00365725 |
| CSNK1A1  | 8.8757578  | 8.633289141 | 0.27822436 | 2.53E-08 | 0.00026858 |
| KIAA1539 | 5.90503406 | 5.687354705 | 0.27796218 | 3.62E-07 | 0.00370798 |
| ATP6V1B2 | 9.45112264 | 9.073532096 | 0.2779576  | 3.35E-08 | 0.00035458 |
| PRKCSH   | 8.60113386 | 8.211587693 | 0.27789021 | 2.56E-07 | 0.00263332 |
| VAT1     | 8.84625681 | 8.490293269 | 0.27775556 | 2.98E-07 | 0.00305746 |
| RNF24    | 7.40284835 | 7.038865107 | 0.2776655  | 6.63E-08 | 0.00069606 |
| OR3A1    | 4.11300797 | 4.015912085 | 0.27751133 | 1.13E-11 | 1.28E-07   |
| ITM2B    | 11.001338  | 10.73120974 | 0.27749688 | 9.71E-08 | 0.0010123  |
| LRPAP1   | 8.33535855 | 8.050675445 | 0.27740314 | 8.31E-09 | 8.94E-05   |
| C6orf62  | 9.04796755 | 8.713978531 | 0.27737271 | 1.84E-08 | 0.00019647 |
| TRIM14   | 6.12166536 | 5.882893386 | 0.27735568 | 2.02E-08 | 0.00021512 |
| TRAF6    | 5.93021618 | 5.666760728 | 0.27734093 | 6.77E-09 | 7.30E-05   |
| STAC     | 6.37808975 | 5.667141221 | 0.2772698  | 1.89E-10 | 2.10E-06   |
| ABCB9    | 4.93031094 | 4.735488383 | 0.27725704 | 6.25E-10 | 6.87E-06   |
| FTH1     | 12.0349648 | 11.71346226 | 0.27713405 | 1.28E-08 | 0.00013731 |
| RUNX1    | 4.57222349 | 4.478793971 | 0.2770261  | 7.82E-11 | 8.72E-07   |
| PVRL2    | 6.12865306 | 5.796019917 | 0.2766143  | 1.30E-08 | 0.0001389  |
| PRF1     | 5.39140011 | 4.964109386 | 0.27658634 | 1.41E-11 | 1.60E-07   |
| PDGFD    | 7.05465781 | 6.285876065 | 0.27652399 | 1.91E-08 | 0.00020402 |
| EMR1     | 4.5822057  | 4.217542273 | 0.27648399 | 1.76E-11 | 1.98E-07   |
| SLC27A3  | 6.95057532 | 6.450818014 | 0.27636674 | 8.48E-08 | 0.00088691 |
| ATP6V1D  | 9.52268565 | 9.23303962  | 0.27617603 | 6.11E-09 | 6.59E-05   |
| DOK1     | 5.19026608 | 5.02433499  | 0.27606623 | 1.73E-09 | 1.89E-05   |
| TMEM47   | 8.79807099 | 8.10978019  | 0.27605617 | 8.03E-07 | 0.00812554 |
| FVT1     | 7.62666747 | 7.346396107 | 0.27592251 | 2.12E-08 | 0.00022599 |
| APOBEC3C | 6.76953023 | 6.465191881 | 0.2758191  | 5.28E-09 | 5.70E-05   |
| GMPR     | 6.0559466  | 5.534505035 | 0.27579232 | 5.04E-10 | 5.55E-06   |
| SELPLG   | 6.04551588 | 5.736628897 | 0.27565278 | 9.25E-10 | 1.01E-05   |
| SCN1B    | 5.8824321  | 5.536697986 | 0.27564223 | 2.61E-08 | 0.00027679 |
| TMEM43   | 8.1208781  | 7.786866653 | 0.27562673 | 1.24E-08 | 0.00013266 |
| CAPZB    | 9.23223817 | 8.98586143  | 0.27526718 | 2.05E-07 | 0.00211104 |
| PRKACA   | 5.70663615 | 5.560839299 | 0.27517367 | 1.32E-08 | 0.00014157 |
| YKT6     | 7.15735403 | 6.803374883 | 0.27505439 | 2.86E-08 | 0.00030284 |
| MYH9     | 7.03153315 | 6.622355334 | 0.27493022 | 6.91E-11 | 7.72E-07   |
| MOCS1    | 5.4585523  | 5.234335798 | 0.27491194 | 2.45E-08 | 0.00026075 |
| ATP6AP1  | 9.59643392 | 9.286518339 | 0.27441592 | 3.32E-09 | 3.60E-05   |
| SNX10    | 9.21901585 | 8.454638512 | 0.27426758 | 9.46E-09 | 0.00010161 |
| NCSTN    | 7.8356783  | 7.491821807 | 0.27424733 | 1.98E-07 | 0.00203833 |
| FAM63B   | 5.19899677 | 4.954438366 | 0.27418924 | 5.17E-08 | 0.00054497 |
| CNR1     | 5.42826591 | 5.114033224 | 0.27413401 | 7.00E-10 | 7.69E-06   |
| F8       | 7.48001806 | 7.010615057 | 0.27373188 | 3.62E-07 | 0.00370798 |
| PPT1     | 11.5853808 | 11.36965435 | 0.27335852 | 4.39E-08 | 0.00046338 |
| FXYS5    | 7.47438362 | 6.927690048 | 0.27317402 | 5.99E-10 | 6.59E-06   |
| PIGB     | 6.07793239 | 5.65694712  | 0.27313708 | 4.25E-09 | 4.61E-05   |
| MGP      | 9.80628074 | 8.938379044 | 0.27310377 | 1.83E-07 | 0.00188766 |
| PARVB    | 5.25926333 | 4.914470983 | 0.27303768 | 9.10E-12 | 1.03E-07   |
| TEX2     | 7.58897325 | 7.293494593 | 0.27266301 | 5.93E-08 | 0.00062371 |

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|-----------|------------|-------------|------------|----------|------------|
| WDR1      | 8.17608913 | 7.84491416  | 0.27231274 | 2.21E-08 | 0.00023547 |
| COL6A2    | 6.16219821 | 5.545179163 | 0.27228044 | 4.07E-11 | 4.56E-07   |
| ELOVL1    | 7.50806781 | 7.193461057 | 0.27222304 | 4.71E-08 | 0.0004971  |
| MYO7A     | 4.78699975 | 4.633209387 | 0.27217469 | 4.79E-09 | 5.19E-05   |
| KCNQ1     | 4.76279793 | 4.659999628 | 0.27196908 | 2.94E-09 | 3.19E-05   |
| KDELR1    | 7.32142335 | 6.938425838 | 0.27195519 | 2.96E-09 | 3.22E-05   |
| TPCN1     | 7.33217626 | 6.967808287 | 0.27185501 | 2.28E-07 | 0.00234654 |
| C9orf167  | 4.99331452 | 4.756999713 | 0.27113733 | 1.59E-12 | 1.81E-08   |
| HOMER3    | 6.14640539 | 5.882745519 | 0.2709145  | 4.93E-09 | 5.33E-05   |
| KLF6      | 7.44984572 | 7.002071506 | 0.27088969 | 5.02E-10 | 5.53E-06   |
| CD58      | 7.12194058 | 6.69497581  | 0.27057333 | 3.31E-07 | 0.00339162 |
| ALDOA     | 12.0153185 | 11.74584158 | 0.27047757 | 3.39E-07 | 0.00347375 |
| PPP1R15A  | 5.92406817 | 5.590402371 | 0.27043141 | 1.96E-11 | 2.21E-07   |
| ALPK3     | 5.29228798 | 4.983422644 | 0.27035773 | 4.18E-11 | 4.68E-07   |
| RRBP1     | 5.96595711 | 5.735393661 | 0.27032901 | 1.11E-09 | 1.21E-05   |
| TPK1      | 5.89773496 | 5.521707752 | 0.26994895 | 2.95E-08 | 0.00031319 |
| GM2A      | 6.4706004  | 6.187006256 | 0.26987274 | 3.80E-09 | 4.12E-05   |
| NINJ1     | 7.82118179 | 7.4717602   | 0.26965136 | 3.92E-08 | 0.00041438 |
| TGOLN2    | 7.89809069 | 7.613921313 | 0.26947834 | 9.49E-09 | 0.00010199 |
| ACSL3     | 8.9722267  | 8.516063928 | 0.26944063 | 2.71E-08 | 0.00028734 |
| SNX24     | 6.62718002 | 6.268025396 | 0.26940107 | 2.80E-07 | 0.00287256 |
| APOBEC3F  | 4.26232515 | 4.111728049 | 0.26914192 | 1.97E-09 | 2.15E-05   |
| TMED7     | 8.20889638 | 7.932836074 | 0.2690227  | 8.35E-08 | 0.00087425 |
| CASP4     | 6.83665239 | 6.314635531 | 0.26878344 | 9.53E-10 | 1.04E-05   |
| TRADD     | 5.67574779 | 5.498538273 | 0.2687536  | 2.38E-10 | 2.64E-06   |
| TSPO      | 8.01297667 | 7.611769516 | 0.26846892 | 1.89E-08 | 0.00020171 |
| HK1       | 8.97803519 | 8.639749977 | 0.26845493 | 1.35E-08 | 0.00014486 |
| CLIP1     | 6.58332788 | 6.245353353 | 0.26842073 | 1.74E-07 | 0.00180345 |
| ACSBG1    | 7.641933   | 6.818109401 | 0.26841825 | 4.22E-07 | 0.00431232 |
| ZNF395    | 7.86877017 | 7.439603953 | 0.26830056 | 7.79E-08 | 0.0008166  |
| EHBP1     | 8.36070666 | 8.01442999  | 0.2681461  | 2.38E-07 | 0.0024546  |
| RAB11FIP5 | 6.31513987 | 6.017594706 | 0.26801077 | 1.30E-07 | 0.00134805 |
| PLCD1     | 7.31644933 | 6.912285488 | 0.26770479 | 1.14E-07 | 0.00118981 |
| GPX3      | 8.93252636 | 8.12364933  | 0.26750265 | 8.63E-08 | 0.00090287 |
| HBEGF     | 5.86905714 | 5.576630847 | 0.2674025  | 1.74E-10 | 1.93E-06   |
| ITGB4     | 5.04410134 | 4.804484852 | 0.26733194 | 9.42E-09 | 0.00010124 |
| C17orf62  | 8.04917073 | 7.792893774 | 0.26727792 | 1.27E-07 | 0.00131486 |
| TMSB10    | 12.8561889 | 12.63572376 | 0.26691723 | 6.85E-08 | 0.00071923 |
| PTK2B     | 4.82926908 | 4.643562268 | 0.26675758 | 3.63E-11 | 4.06E-07   |
| DHX58     | 5.35959971 | 5.089737505 | 0.2666875  | 1.65E-08 | 0.00017662 |
| MPV17     | 8.9808367  | 8.655227623 | 0.26668359 | 1.41E-08 | 0.00015109 |
| YTHDF1    | 9.58855796 | 9.266934342 | 0.26666046 | 4.39E-07 | 0.00447927 |
| BACH1     | 5.57653584 | 5.394733905 | 0.26663432 | 1.54E-08 | 0.00016491 |
| GNPDA1    | 8.56222441 | 8.273249744 | 0.26636372 | 2.15E-08 | 0.00022853 |
| ARSF      | 5.05952571 | 4.606023963 | 0.26633465 | 7.92E-13 | 9.05E-09   |
| P2RY1     | 5.24306979 | 4.838654575 | 0.2661691  | 1.19E-10 | 1.33E-06   |
| C7orf42   | 9.16899858 | 8.845738888 | 0.26560612 | 3.10E-07 | 0.00317577 |
| DAG1      | 7.31139444 | 7.016990269 | 0.26535493 | 2.88E-07 | 0.0029532  |
| BCL2L1    | 5.92823247 | 5.647049706 | 0.26514137 | 2.73E-09 | 2.97E-05   |

|          |            |             |            |          |            |
|----------|------------|-------------|------------|----------|------------|
| KIAA0409 | 6.33732866 | 6.077064692 | 0.26510957 | 4.82E-08 | 0.00050811 |
| CANX     | 10.1030424 | 9.750981029 | 0.26500397 | 1.33E-09 | 1.46E-05   |
| NMI      | 8.09196507 | 7.652869088 | 0.26469802 | 2.84E-07 | 0.00291275 |
| FABP5    | 10.0545391 | 9.168545459 | 0.26462832 | 1.13E-07 | 0.00117277 |
| WBP2     | 7.36206659 | 6.918689789 | 0.26425903 | 7.20E-07 | 0.00729921 |
| HLA-G    | 8.03748727 | 7.769789305 | 0.26424643 | 2.20E-08 | 0.00023461 |
| TMEM149  | 6.10262925 | 5.761595319 | 0.26408839 | 1.72E-07 | 0.00178487 |
| CHRNE    | 6.61525093 | 6.368477683 | 0.26379928 | 7.88E-08 | 0.00082542 |
| VWF      | 8.75035854 | 8.141341378 | 0.2637705  | 6.52E-07 | 0.00662231 |
| MGST2    | 8.0690967  | 7.65307757  | 0.26366138 | 2.30E-08 | 0.00024446 |
| FILIP1L  | 7.74562695 | 7.180476716 | 0.26344216 | 2.58E-08 | 0.00027368 |
| RDX      | 8.55865659 | 8.165004412 | 0.2634307  | 1.68E-07 | 0.0017351  |
| GLT25D1  | 6.55893948 | 6.284991437 | 0.26335331 | 1.32E-08 | 0.00014103 |
| XAF1     | 6.82162598 | 6.144076991 | 0.26316972 | 4.55E-09 | 4.93E-05   |
| SLC24A6  | 5.59430662 | 5.365552055 | 0.26316056 | 5.02E-07 | 0.00511642 |
| ECOP     | 10.2500136 | 9.6589335   | 0.2628628  | 8.41E-10 | 9.23E-06   |
| MAP3K8   | 5.28058109 | 4.802376153 | 0.26252641 | 2.71E-09 | 2.95E-05   |
| IRAK1    | 9.34243397 | 9.025018943 | 0.26235814 | 9.06E-09 | 9.74E-05   |
| PLXNB2   | 6.6396946  | 6.42613882  | 0.26223418 | 4.44E-08 | 0.00046847 |
| FZD1     | 5.9572925  | 5.607226788 | 0.26220937 | 1.05E-09 | 1.15E-05   |
| GALNT11  | 8.61720422 | 8.294374278 | 0.26213251 | 1.81E-08 | 0.00019352 |
| PARP3    | 5.41038397 | 5.163629247 | 0.26187198 | 3.01E-09 | 3.27E-05   |
| GPR4     | 4.66692213 | 4.499173809 | 0.26183903 | 3.12E-08 | 0.00033013 |
| TNIP1    | 7.63872605 | 7.298117352 | 0.26161473 | 8.57E-08 | 0.00089637 |
| SOCS6    | 5.70146128 | 5.403272718 | 0.26124811 | 2.83E-08 | 0.00030058 |
| C1orf166 | 6.32317334 | 6.072672149 | 0.26104116 | 1.02E-07 | 0.00106063 |
| ZNF217   | 7.01798485 | 6.475420164 | 0.26089833 | 3.85E-08 | 0.00040672 |
| GLT8D1   | 8.60941832 | 8.324867649 | 0.26087408 | 7.84E-07 | 0.00793939 |
| BACE2    | 7.1582386  | 6.590108105 | 0.26079212 | 5.65E-10 | 6.22E-06   |
| PTAFR    | 5.25711335 | 5.004881201 | 0.26061629 | 1.56E-09 | 1.70E-05   |
| SLC12A7  | 7.38602206 | 7.02371355  | 0.2601743  | 1.66E-08 | 0.00017729 |
| LOC93349 | 5.99532275 | 5.563432826 | 0.26008547 | 1.88E-08 | 0.00020096 |
| ZC3HAV1  | 7.13532452 | 6.896290235 | 0.25983754 | 1.51E-08 | 0.00016122 |
| ASAH1    | 5.31812159 | 5.105562954 | 0.25969665 | 1.96E-07 | 0.00202404 |
| PSAP     | 10.7882683 | 10.5090557  | 0.25960567 | 4.70E-07 | 0.00479641 |
| TAX1BP3  | 6.34262387 | 6.126332736 | 0.25948323 | 2.52E-08 | 0.00026758 |
| ARSA     | 4.99517152 | 4.764235175 | 0.25927761 | 2.96E-07 | 0.00303662 |
| APOL6    | 5.64785464 | 5.276832224 | 0.25886583 | 1.93E-09 | 2.11E-05   |
| PSMB9    | 8.66225847 | 8.151624446 | 0.25874373 | 8.35E-08 | 0.00087425 |
| KIAA0323 | 6.3479184  | 5.97380534  | 0.25868154 | 2.41E-08 | 0.00025588 |
| INSIG2   | 7.52022081 | 7.176137945 | 0.25854005 | 3.56E-07 | 0.00364485 |
| ITGB5    | 6.76443522 | 6.410670607 | 0.25849352 | 2.15E-08 | 0.00022936 |
| MTTP     | 5.1346873  | 4.643056666 | 0.25837654 | 9.86E-14 | 1.14E-09   |
| LMBRD1   | 10.1665618 | 9.84233637  | 0.25819198 | 3.34E-07 | 0.00342644 |
| FAM82C   | 8.34251549 | 8.043092309 | 0.257934   | 8.48E-07 | 0.00857428 |
| AP2A2    | 7.10866737 | 6.850439163 | 0.25751357 | 1.68E-07 | 0.0017351  |
| CRIM1    | 7.18518083 | 6.738536201 | 0.2573357  | 3.42E-07 | 0.00349678 |
| LAMC3    | 5.46764907 | 5.136218265 | 0.25726803 | 4.92E-08 | 0.00051946 |
| GIMAP5   | 6.46329409 | 6.164347065 | 0.25718746 | 9.60E-08 | 0.00100157 |

|            |            |             |            |          |            |
|------------|------------|-------------|------------|----------|------------|
| ECM1       | 6.31279067 | 5.863641682 | 0.25709731 | 2.21E-10 | 2.46E-06   |
| DPP8       | 9.04803996 | 8.742652546 | 0.2570684  | 2.56E-07 | 0.00263332 |
| ATP6AP2    | 8.24693874 | 8.09387425  | 0.25681165 | 3.75E-08 | 0.00039627 |
| ETF1       | 8.51036664 | 8.259758271 | 0.25642081 | 8.71E-09 | 9.37E-05   |
| SOAT1      | 6.21367365 | 5.801081982 | 0.25637261 | 9.38E-09 | 0.00010086 |
| TUBA1C     | 12.0568657 | 11.82951215 | 0.256358   | 4.74E-07 | 0.00482877 |
| NRP2       | 4.49022901 | 4.291091184 | 0.25618367 | 5.65E-10 | 6.22E-06   |
| LAMC1      | 8.24217367 | 7.827294031 | 0.25616833 | 1.53E-07 | 0.001588   |
| NLRP3      | 4.11199999 | 4.026681231 | 0.25611547 | 3.61E-08 | 0.0003819  |
| TMED9      | 8.80705994 | 8.550132942 | 0.25609833 | 4.18E-10 | 4.62E-06   |
| LEF1       | 5.55423593 | 5.295966727 | 0.25602707 | 7.65E-08 | 0.00080181 |
| B2M        | 12.9124339 | 12.70122705 | 0.25591105 | 2.52E-07 | 0.00258794 |
| LRRC16     | 6.13766744 | 5.69657184  | 0.25584265 | 9.06E-08 | 0.0009456  |
| ZMYM6      | 6.44443767 | 6.18520342  | 0.25579289 | 8.14E-08 | 0.00085233 |
| ZNF226     | 7.48751893 | 7.012439556 | 0.25492256 | 1.48E-07 | 0.001538   |
| TWF2       | 5.91609115 | 5.719442126 | 0.25482441 | 5.00E-08 | 0.00052711 |
| TADA3L     | 6.07868426 | 5.915186789 | 0.25477044 | 5.46E-07 | 0.00555279 |
| CSTB       | 10.9232018 | 10.64503129 | 0.25473309 | 1.15E-11 | 1.29E-07   |
| S100A4     | 8.24580858 | 7.547710543 | 0.25472559 | 3.72E-10 | 4.10E-06   |
| PCDH8      | 6.11660496 | 5.388609235 | 0.25451548 | 2.71E-08 | 0.00028734 |
| CFLAR      | 6.64126872 | 6.334515124 | 0.25431686 | 1.23E-08 | 0.00013217 |
| LYZ        | 8.42891796 | 7.592593483 | 0.25426173 | 1.22E-08 | 0.00013065 |
| HPS5       | 7.1233975  | 6.849315391 | 0.25415897 | 1.87E-07 | 0.00192744 |
| NOD2       | 5.04560812 | 4.756139231 | 0.25402135 | 1.34E-09 | 1.47E-05   |
| HLA-F      | 8.89788603 | 8.567519869 | 0.25395733 | 7.85E-08 | 0.00082247 |
| GRIK1      | 5.37658316 | 4.872269211 | 0.25374665 | 7.17E-10 | 7.88E-06   |
| BCL7B      | 7.13431233 | 6.853597861 | 0.2536546  | 2.04E-07 | 0.00210374 |
| FAM49A     | 6.37198923 | 6.007084309 | 0.25315998 | 8.73E-08 | 0.0009125  |
| PRRX1      | 6.00206334 | 5.472151738 | 0.25297214 | 3.64E-08 | 0.00038464 |
| PDLIM2     | 6.9532225  | 6.625865842 | 0.25284485 | 2.15E-08 | 0.00022853 |
| GALNAC4S-6 | 7.78479868 | 7.263450406 | 0.25266469 | 5.57E-07 | 0.00566527 |
| FLII       | 6.76288461 | 6.494345247 | 0.25263571 | 1.17E-08 | 0.00012574 |
| IDUA       | 4.48964129 | 4.397078707 | 0.25259566 | 2.66E-07 | 0.00273631 |
| PTPN18     | 6.65989702 | 6.366748002 | 0.25218345 | 6.94E-07 | 0.00703605 |
| CXCL6      | 4.49646818 | 4.08976771  | 0.25215279 | 4.54E-07 | 0.00463546 |
| FYCO1      | 6.75028952 | 6.407095832 | 0.25173807 | 1.30E-07 | 0.00134805 |
| CHST1      | 6.56993633 | 6.035618517 | 0.25132899 | 1.44E-08 | 0.00015399 |
| RGS10      | 7.09578218 | 6.706873082 | 0.25109898 | 1.65E-07 | 0.00170477 |
| CAPRIN2    | 7.84411382 | 7.433007954 | 0.25101917 | 5.55E-07 | 0.00564748 |
| ALDH3B1    | 5.38950926 | 5.127070986 | 0.2505393  | 1.69E-14 | 1.95E-10   |
| SLC39A1    | 7.48839101 | 7.236993755 | 0.25047119 | 2.14E-08 | 0.00022768 |
| WARS       | 8.18248477 | 7.755818563 | 0.25035527 | 3.25E-09 | 3.53E-05   |
| EYA2       | 6.15562601 | 5.652183801 | 0.25028471 | 9.29E-10 | 1.02E-05   |
| TLN2       | 6.09724086 | 5.786865532 | 0.25020029 | 1.20E-07 | 0.00125083 |
| LASS2      | 9.02431286 | 8.742668152 | 0.24968908 | 2.30E-09 | 2.51E-05   |
| PPBP       | 5.07208506 | 4.479493854 | 0.24930133 | 1.37E-08 | 0.00014652 |
| MAP3K5     | 6.87593884 | 6.446228356 | 0.24926097 | 6.84E-07 | 0.00694201 |
| CSNK1D     | 7.20877254 | 6.934600609 | 0.24925634 | 1.03E-07 | 0.00107578 |
| RETSAT     | 7.40438025 | 7.107148532 | 0.24916899 | 3.17E-07 | 0.00325317 |

|          |            |             |            |          |            |
|----------|------------|-------------|------------|----------|------------|
| PARP4    | 8.0414263  | 7.736784283 | 0.24912011 | 3.49E-08 | 0.00036928 |
| TMED1    | 7.33754152 | 7.054300669 | 0.24896252 | 4.21E-07 | 0.00429821 |
| MTHFS    | 6.7838363  | 6.536354685 | 0.248672   | 6.01E-09 | 6.49E-05   |
| NOL3     | 6.07372662 | 5.731776319 | 0.24849617 | 1.94E-07 | 0.00200289 |
| TNS1     | 6.24956853 | 5.994560883 | 0.24811004 | 1.85E-07 | 0.00190763 |
| CLPB     | 6.17740856 | 5.896700791 | 0.24771584 | 5.55E-07 | 0.00564748 |
| RTN4     | 11.8689277 | 11.65156494 | 0.24755078 | 7.38E-07 | 0.00747165 |
| C19orf28 | 7.60608203 | 7.243138532 | 0.2474223  | 3.96E-08 | 0.000419   |
| TMEM127  | 7.30242221 | 7.067547927 | 0.24727744 | 4.54E-07 | 0.00463546 |
| KIAA0152 | 8.85105533 | 8.520052488 | 0.24714365 | 8.48E-08 | 0.00088691 |
| TRPM3    | 4.62351943 | 4.398813409 | 0.24713301 | 7.59E-08 | 0.00079609 |
| TBXA2R   | 4.84581128 | 4.717627294 | 0.24707734 | 6.46E-08 | 0.00067855 |
| EFHC1    | 7.56203465 | 7.126251948 | 0.2468971  | 4.70E-07 | 0.00479641 |
| NOX4     | 5.97933343 | 5.533150533 | 0.24686699 | 2.81E-07 | 0.00288241 |
| GMIP     | 5.71886062 | 5.485173834 | 0.24661058 | 5.55E-07 | 0.00564748 |
| ABCD1    | 4.9757251  | 4.791698208 | 0.24654781 | 1.74E-07 | 0.00179718 |
| FGFR1    | 5.98778452 | 5.760517657 | 0.24652939 | 3.88E-09 | 4.20E-05   |
| CALU     | 8.35484736 | 7.938487866 | 0.24652154 | 3.32E-07 | 0.00340319 |
| STAT5A   | 5.23815255 | 5.021817149 | 0.24641816 | 1.20E-08 | 0.00012867 |
| HLA-DQB1 | 7.82439393 | 7.122238581 | 0.24628739 | 5.24E-07 | 0.00533057 |
| SSFA2    | 8.90489571 | 8.501204899 | 0.24621968 | 8.42E-07 | 0.00851722 |
| TNFSF4   | 5.39383357 | 5.039150929 | 0.2458152  | 2.76E-10 | 3.05E-06   |
| P4HA2    | 6.92846886 | 6.37755501  | 0.24569754 | 1.21E-08 | 0.00012965 |
| PLD3     | 7.10727701 | 6.845737825 | 0.24514804 | 1.20E-07 | 0.00125083 |
| AP2S1    | 10.0722305 | 9.844685129 | 0.24507897 | 7.18E-07 | 0.00727582 |
| ACTG1    | 13.0077038 | 12.84028523 | 0.2450041  | 7.28E-07 | 0.00737129 |
| NQO2     | 8.24687881 | 7.907705087 | 0.24485479 | 2.39E-07 | 0.00246307 |
| CDH5     | 6.97767855 | 6.489590512 | 0.24484681 | 9.74E-08 | 0.00101581 |
| VASP     | 6.61690122 | 6.397137577 | 0.24482181 | 3.62E-08 | 0.00038323 |
| IRAK3    | 4.76447655 | 4.541256074 | 0.24460161 | 2.24E-10 | 2.49E-06   |
| SEC61G   | 11.7612916 | 11.16235763 | 0.24432616 | 3.41E-08 | 0.00036116 |
| IRF1     | 6.55594519 | 6.14280272  | 0.24425421 | 2.41E-09 | 2.62E-05   |
| RNF14    | 7.72468183 | 7.372639189 | 0.2441513  | 5.01E-07 | 0.00509929 |
| OR2F2    | 4.06850787 | 3.991083201 | 0.24381571 | 3.70E-07 | 0.00378461 |
| AMD1     | 9.01536001 | 8.677581682 | 0.24364264 | 7.29E-08 | 0.00076509 |
| CHST12   | 7.43652484 | 7.154048588 | 0.24354952 | 9.81E-10 | 1.07E-05   |
| SERINC3  | 8.97686377 | 8.720532667 | 0.24315266 | 1.04E-07 | 0.00108739 |
| IL1R1    | 5.26355877 | 4.962474776 | 0.24304655 | 1.62E-10 | 1.80E-06   |
| ACSL1    | 7.63751783 | 7.158439628 | 0.24290357 | 3.85E-07 | 0.00393068 |
| COL3A1   | 9.27078333 | 8.326587174 | 0.24288062 | 1.81E-07 | 0.00186806 |
| IL1R2    | 5.40342449 | 4.863102148 | 0.24264345 | 3.29E-09 | 3.57E-05   |
| PTPN14   | 4.49234842 | 4.338481869 | 0.24259289 | 1.07E-09 | 1.17E-05   |
| PHF15    | 5.40689709 | 5.180914072 | 0.24237949 | 1.77E-07 | 0.0018353  |
| SNTA1    | 6.38783667 | 5.973881684 | 0.24231237 | 3.35E-08 | 0.00035458 |
| THBS4    | 7.61576932 | 6.897218326 | 0.24224785 | 7.91E-08 | 0.00082822 |
| PIM1     | 5.78504718 | 5.503677607 | 0.24195795 | 3.44E-08 | 0.00036383 |
| ARL8B    | 10.5053594 | 10.28529635 | 0.24185137 | 2.61E-07 | 0.00267947 |
| DNAL11   | 6.08928235 | 5.741484991 | 0.2418403  | 2.34E-07 | 0.00241266 |
| LOXL2    | 5.39713397 | 5.208874709 | 0.24176493 | 6.97E-11 | 7.78E-07   |

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|----------|------------|-------------|------------|----------|------------|
| FLT3LG   | 4.30811696 | 4.137858182 | 0.24158595 | 2.27E-08 | 0.00024177 |
| G0S2     | 6.41146209 | 5.898124377 | 0.24145338 | 6.01E-07 | 0.00610454 |
| KIAA0828 | 6.74520253 | 6.389448443 | 0.24143881 | 4.79E-07 | 0.00487865 |
| SERPINB1 | 6.99377922 | 6.448096041 | 0.24134914 | 1.80E-08 | 0.00019205 |
| UBE1L    | 6.02632107 | 5.739572055 | 0.24115392 | 4.18E-08 | 0.00044154 |
| IL18     | 5.5921916  | 5.154793837 | 0.24105619 | 6.80E-08 | 0.00071401 |
| PCDH12   | 6.2837303  | 5.948798304 | 0.24083221 | 4.80E-07 | 0.00489459 |
| SEC61A1  | 9.19481907 | 8.920577084 | 0.24081055 | 8.51E-08 | 0.00088999 |
| IFNAR1   | 4.88662145 | 4.703785627 | 0.24068516 | 9.35E-07 | 0.00944076 |
| PDIA3    | 10.2573595 | 9.948563597 | 0.24064205 | 1.20E-08 | 0.00012867 |
| CA3      | 6.08938065 | 5.262527394 | 0.24040879 | 8.05E-09 | 8.67E-05   |
| IFT122   | 6.96941079 | 6.663320927 | 0.24038464 | 2.06E-07 | 0.00212592 |
| TRIP10   | 6.11391595 | 5.834801374 | 0.240254   | 5.84E-08 | 0.00061476 |
| PXN      | 5.41523428 | 5.257699231 | 0.24013286 | 3.82E-09 | 4.14E-05   |
| CA9      | 6.07800723 | 5.553179458 | 0.23996642 | 3.99E-09 | 4.32E-05   |
| CAMK2B   | 5.99664684 | 5.395938623 | 0.23986089 | 9.64E-08 | 0.00100514 |
| WHDC1L1  | 4.83770884 | 4.592064057 | 0.23974274 | 4.78E-08 | 0.00050443 |
| ZCCHC6   | 7.35430715 | 7.052193223 | 0.23962985 | 9.64E-07 | 0.00972307 |
| ARHGAP15 | 6.17499922 | 5.773255586 | 0.23916711 | 9.12E-08 | 0.00095245 |
| HGSNAT   | 7.41807616 | 7.044163953 | 0.2389064  | 1.41E-07 | 0.00145766 |
| LITAF    | 9.21642738 | 8.892650195 | 0.23867288 | 8.86E-07 | 0.00895375 |
| DENND1C  | 4.84727233 | 4.66599622  | 0.23803999 | 2.50E-09 | 2.72E-05   |
| GSTM4    | 6.02133028 | 5.726720355 | 0.23775989 | 9.10E-07 | 0.00919279 |
| SERGEF   | 5.19740502 | 5.061122975 | 0.23723982 | 2.84E-07 | 0.00291275 |
| SGCB     | 7.94543741 | 7.545504984 | 0.23707772 | 3.04E-07 | 0.003122   |
| RBPMS    | 5.59847755 | 5.278763441 | 0.23693768 | 2.46E-08 | 0.00026169 |
| OLFML2B  | 6.56773955 | 6.060774282 | 0.23692995 | 9.80E-07 | 0.00988339 |
| COL4A3BP | 7.4497961  | 7.160880732 | 0.23674128 | 1.84E-07 | 0.00190101 |
| ISG20    | 6.31237427 | 5.873243371 | 0.23630744 | 2.71E-10 | 3.00E-06   |
| 9-Sep    | 8.20064007 | 7.942027606 | 0.23607217 | 1.22E-07 | 0.00127296 |
| FLNC     | 7.18972621 | 6.637294098 | 0.23602065 | 6.11E-08 | 0.00064223 |
| MAP2K3   | 5.98555587 | 5.769919187 | 0.23593701 | 6.98E-08 | 0.00073248 |
| TBC1D2B  | 6.51848801 | 6.186048921 | 0.23578281 | 7.58E-07 | 0.00767633 |
| GATAD1   | 7.89079103 | 7.571812484 | 0.23521862 | 6.80E-07 | 0.00689545 |
| FLJ20254 | 7.34151478 | 7.047680753 | 0.23505849 | 1.05E-07 | 0.00109125 |
| PDK3     | 5.16342285 | 4.935202198 | 0.23459182 | 1.22E-09 | 1.34E-05   |
| AOAH     | 5.47353787 | 5.160177552 | 0.23446643 | 3.32E-07 | 0.00340319 |
| VCL      | 6.76154237 | 6.563017266 | 0.234096   | 1.18E-08 | 0.00012671 |
| LEPREL1  | 6.21583724 | 5.770324114 | 0.23408115 | 8.80E-10 | 9.66E-06   |
| FZD5     | 5.50806056 | 5.226257876 | 0.23399712 | 1.35E-07 | 0.00140189 |
| SAP30L   | 6.54047832 | 6.31453555  | 0.23395176 | 1.71E-07 | 0.0017723  |
| LENG4    | 6.48060079 | 6.30842603  | 0.23349257 | 9.36E-08 | 0.00097685 |
| NR1D1    | 6.39859464 | 6.122587313 | 0.2333343  | 5.59E-08 | 0.00058833 |
| CDH4     | 5.75281962 | 5.235869301 | 0.23287208 | 3.85E-09 | 4.17E-05   |
| LAMB1    | 7.55068879 | 6.95586805  | 0.23271937 | 1.16E-07 | 0.00121137 |
| CYP1B1   | 6.136804   | 5.531286614 | 0.23259924 | 7.59E-08 | 0.00079609 |
| TNFRSF14 | 5.33767059 | 5.086480832 | 0.23232555 | 1.37E-09 | 1.49E-05   |
| MCC      | 5.49518458 | 5.135207122 | 0.23197084 | 7.00E-08 | 0.00073505 |
| GPI      | 9.73442817 | 9.374550235 | 0.23190687 | 3.12E-07 | 0.00319752 |

|             |            |             |            |          |            |
|-------------|------------|-------------|------------|----------|------------|
| RNH1        | 8.61028882 | 8.343909484 | 0.23179508 | 2.33E-07 | 0.00240436 |
| SELL        | 6.08473279 | 5.549666985 | 0.23172581 | 5.64E-09 | 6.10E-05   |
| FUCA1       | 8.58531502 | 8.177632193 | 0.23153445 | 3.24E-07 | 0.00332202 |
| PCOLCE      | 7.29595943 | 6.682380979 | 0.23128299 | 1.38E-07 | 0.00142714 |
| CRELD2      | 8.13739488 | 7.878101479 | 0.23107381 | 1.94E-07 | 0.00200289 |
| EDNRA       | 6.82891467 | 6.343596416 | 0.2307039  | 8.68E-07 | 0.00877644 |
| VNN2        | 5.23838235 | 4.830396147 | 0.2302543  | 6.96E-09 | 7.50E-05   |
| DNAJC3      | 6.2549009  | 6.041910259 | 0.23013284 | 4.89E-08 | 0.00051565 |
| NFE2L2      | 10.2967907 | 10.04897667 | 0.23012335 | 5.49E-08 | 0.00057783 |
| SLC16A6     | 5.32082894 | 5.017437211 | 0.22918528 | 1.80E-09 | 1.96E-05   |
| LRCH4       | 5.62909759 | 5.508144053 | 0.22890469 | 1.63E-07 | 0.00169291 |
| COL5A1      | 6.37861417 | 5.745074102 | 0.22866622 | 1.39E-09 | 1.52E-05   |
| DPP4        | 4.86721296 | 4.494208474 | 0.22803815 | 1.47E-10 | 1.64E-06   |
| MCL1        | 7.22008949 | 6.976230769 | 0.22788575 | 5.93E-08 | 0.00062371 |
| OAZ2        | 8.16107571 | 7.92242378  | 0.22770711 | 9.61E-07 | 0.00969227 |
| CLPTM1      | 6.96632744 | 6.678572329 | 0.2272014  | 9.38E-07 | 0.0094708  |
| IL32        | 6.08146531 | 5.635410607 | 0.22682952 | 4.57E-10 | 5.04E-06   |
| PALMD       | 6.14581705 | 5.749413686 | 0.22650545 | 9.96E-08 | 0.00103799 |
| BAX         | 6.09340955 | 5.802055392 | 0.22631352 | 3.90E-07 | 0.00398467 |
| DNASE2      | 6.9146205  | 6.674145696 | 0.22622914 | 5.18E-07 | 0.00527623 |
| DNAH9       | 4.8634463  | 4.57986864  | 0.22479546 | 8.44E-09 | 9.08E-05   |
| IRF7        | 6.4777779  | 6.170338278 | 0.22438723 | 3.54E-08 | 0.00037481 |
| ZNF576      | 6.46018078 | 6.220946783 | 0.22429833 | 9.32E-07 | 0.00940988 |
| GLG1        | 9.66839584 | 9.336173076 | 0.22407495 | 1.87E-07 | 0.00192744 |
| CIITA       | 4.37171942 | 4.289034308 | 0.2237424  | 2.03E-07 | 0.00208901 |
| CNOT2       | 8.54521398 | 8.25594173  | 0.22357389 | 4.48E-07 | 0.00457254 |
| VRK3        | 6.91839736 | 6.707448659 | 0.22353974 | 3.42E-07 | 0.00349678 |
| HERPUD1     | 9.75789678 | 9.492019531 | 0.22254623 | 4.47E-07 | 0.00455717 |
| CCL20       | 5.30413656 | 4.69535749  | 0.22201264 | 1.71E-12 | 1.94E-08   |
| P2RY6       | 4.95219415 | 4.728683648 | 0.22095688 | 4.80E-13 | 5.50E-09   |
| NEO1        | 6.57300595 | 6.253817228 | 0.22094878 | 9.74E-07 | 0.00981994 |
| RAB21       | 8.40054364 | 8.100212545 | 0.22039    | 1.59E-07 | 0.00165138 |
| FURIN       | 5.87940649 | 5.703244496 | 0.22006865 | 4.21E-07 | 0.00429821 |
| SLC16A3     | 5.6428811  | 5.34001456  | 0.21991975 | 3.23E-10 | 3.57E-06   |
| SAA4        | 4.53651357 | 4.370692991 | 0.21981924 | 5.73E-07 | 0.00582094 |
| SLC39A8     | 5.60657776 | 5.322158618 | 0.21940333 | 1.19E-11 | 1.35E-07   |
| IL21R       | 4.50672821 | 4.321140304 | 0.21892931 | 5.71E-09 | 6.17E-05   |
| SFRP4       | 6.22366956 | 5.68496153  | 0.21879843 | 5.36E-08 | 0.0005653  |
| DKFZp434K1! | 4.5202936  | 4.32881098  | 0.21808378 | 4.18E-07 | 0.00426928 |
| TNXB        | 5.15009514 | 5.056560246 | 0.21713313 | 8.08E-08 | 0.00084634 |
| CRYBB1      | 4.62294164 | 4.469718263 | 0.2165404  | 1.73E-07 | 0.00179093 |
| SLC6A9      | 4.93132926 | 4.672047235 | 0.21596296 | 9.71E-08 | 0.0010123  |
| PPP1R3D     | 5.3399953  | 5.125570282 | 0.21530666 | 6.22E-07 | 0.00631556 |
| SGEF        | 5.62767269 | 5.247816625 | 0.21463935 | 1.55E-07 | 0.00161068 |
| GNG11       | 8.82157586 | 8.412240196 | 0.21415837 | 9.48E-07 | 0.00956525 |
| CKMT2       | 5.28171379 | 5.030111499 | 0.21302488 | 2.00E-08 | 0.0002135  |
| FLJ22662    | 6.67841967 | 6.228802865 | 0.21279418 | 2.35E-09 | 2.56E-05   |
| EMX2        | 5.82671531 | 5.154465736 | 0.21261661 | 8.99E-08 | 0.0009388  |
| IER3        | 7.76079262 | 7.172496236 | 0.21217048 | 6.00E-08 | 0.0006305  |

|           |            |             |            |          |            |
|-----------|------------|-------------|------------|----------|------------|
| FLOT2     | 6.25743926 | 6.04600731  | 0.21035388 | 3.62E-07 | 0.00370798 |
| NAGPA     | 5.87984785 | 5.684490133 | 0.21001189 | 5.65E-07 | 0.00574316 |
| HPD       | 4.24771116 | 4.045613193 | 0.20972522 | 3.03E-08 | 0.00032154 |
| LY75      | 5.77410466 | 5.317958927 | 0.20941954 | 4.79E-07 | 0.00487865 |
| NPEPL1    | 5.7042506  | 5.55062027  | 0.2080573  | 1.03E-07 | 0.00107578 |
| ERBB2     | 5.30640469 | 5.116096032 | 0.20715344 | 6.96E-07 | 0.0070594  |
| TNFRSF10B | 5.76428156 | 5.514007823 | 0.20686884 | 7.88E-08 | 0.00082542 |
| GDF15     | 5.10804143 | 4.873577672 | 0.20630586 | 1.51E-08 | 0.00016122 |
| UBD       | 6.26374467 | 5.610704515 | 0.20557985 | 2.15E-09 | 2.34E-05   |
| FPRL1     | 4.17974928 | 4.08494769  | 0.20548385 | 1.14E-08 | 0.0001224  |
| ANXA4     | 8.15489665 | 7.729063559 | 0.20529205 | 1.52E-07 | 0.00157111 |
| CDH6      | 5.04390197 | 4.840001069 | 0.20469397 | 3.27E-11 | 3.67E-07   |
| ITGAX     | 5.39606553 | 5.155985847 | 0.20349445 | 2.78E-07 | 0.00285266 |
| GPR37L1   | 5.25080216 | 5.016515749 | 0.20191233 | 6.32E-07 | 0.00642338 |
| EBI3      | 4.96913266 | 4.729601861 | 0.20175465 | 1.72E-08 | 0.00018348 |
| PML       | 4.90144388 | 4.786998291 | 0.20135051 | 6.25E-08 | 0.00065652 |
| RAB27A    | 6.31686424 | 5.939320509 | 0.20076276 | 7.68E-11 | 8.57E-07   |
| C9orf116  | 5.79515057 | 5.535695535 | 0.19993087 | 8.73E-08 | 0.0009125  |
| TMEM109   | 7.15472745 | 6.903725067 | 0.19983546 | 7.25E-07 | 0.00734695 |
| CUL7      | 5.60127647 | 5.437394795 | 0.19920125 | 1.02E-07 | 0.0010643  |
| PTGS2     | 5.45455805 | 4.945962382 | 0.1987489  | 5.92E-09 | 6.39E-05   |
| CSF2RB    | 5.55348742 | 5.215008918 | 0.19871553 | 7.92E-07 | 0.00801911 |
| AFF1      | 5.49954899 | 5.405585031 | 0.1986133  | 9.41E-07 | 0.00950187 |
| SPAG4     | 5.58780787 | 5.19491659  | 0.19781546 | 4.57E-08 | 0.00048256 |
| LTBP2     | 6.81871531 | 6.380627943 | 0.19676842 | 9.20E-09 | 9.89E-05   |
| CLEC4A    | 5.36690653 | 5.099370861 | 0.19661562 | 6.96E-07 | 0.0070594  |
| GAS6      | 6.75609783 | 6.479313292 | 0.19631751 | 4.15E-07 | 0.00424013 |
| ANPEP     | 4.69158412 | 4.340862198 | 0.19429943 | 5.67E-08 | 0.00059701 |
| IKZF1     | 4.89190658 | 4.760171629 | 0.1941751  | 4.82E-08 | 0.00050811 |
| CXCL5     | 4.55256666 | 4.167150108 | 0.19378325 | 2.52E-09 | 2.74E-05   |
| LCP1      | 6.76556461 | 6.422477725 | 0.19376154 | 5.55E-08 | 0.00058414 |
| HFE       | 4.77001334 | 4.67045998  | 0.19358871 | 2.24E-08 | 0.00023813 |
| COL1A1    | 6.50828645 | 6.017162051 | 0.1935398  | 2.29E-08 | 0.00024356 |
| CD300C    | 4.71538249 | 4.592402768 | 0.19292898 | 3.45E-08 | 0.00036516 |
| AIM1      | 6.18134351 | 5.67309044  | 0.19218243 | 2.00E-07 | 0.00206004 |
| SLPI      | 7.36518168 | 6.588383304 | 0.19067981 | 3.68E-07 | 0.00375865 |
| SLFN12    | 4.96512436 | 4.701571409 | 0.18944529 | 9.57E-08 | 0.00099821 |
| PROCR     | 5.98300312 | 5.722281719 | 0.18893275 | 8.51E-08 | 0.00088999 |
| CCDC46    | 5.44978997 | 5.181949385 | 0.18838762 | 1.60E-08 | 0.00017131 |
| PIK3CD    | 5.14486508 | 5.023336179 | 0.18780695 | 1.35E-08 | 0.00014486 |
| TRPV2     | 5.02250077 | 4.828043415 | 0.18770239 | 1.19E-07 | 0.00123754 |
| EAF2      | 5.87089661 | 5.591052479 | 0.18702499 | 7.50E-07 | 0.00759914 |
| CASP8     | 5.56420001 | 5.341519294 | 0.18553284 | 1.23E-08 | 0.00013217 |
| TSPAN4    | 6.14182507 | 5.904312009 | 0.18453478 | 6.66E-09 | 7.19E-05   |
| FSTL3     | 5.14687989 | 4.953914168 | 0.18359318 | 1.39E-09 | 1.52E-05   |
| DDIT3     | 7.6092382  | 7.217317537 | 0.18346721 | 9.35E-07 | 0.00944076 |
| LMNA      | 6.79002296 | 6.581233451 | 0.18153316 | 2.75E-08 | 0.00029166 |
| BNC2      | 5.24404082 | 4.937991252 | 0.17984303 | 5.65E-07 | 0.00574316 |
| OXA1L     | 8.6622018  | 8.438485739 | 0.17797108 | 9.04E-07 | 0.00913269 |

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| IGFBP1   | 4.96835818 | 4.652890255 | 0.1776759   | 1.17E-09 | 1.28E-05   |
| SERPINA5 | 5.49529518 | 5.176871526 | 0.1755949   | 3.80E-10 | 4.19E-06   |
| PRKCD    | 5.35158936 | 5.122089694 | 0.1724013   | 3.81E-07 | 0.00389094 |
| CFB      | 4.82479943 | 4.624080941 | 0.17162153  | 9.87E-09 | 0.00010603 |
| PF4V1    | 3.67780109 | 3.610110768 | 0.16713296  | 3.39E-07 | 0.00347375 |
| STXBP2   | 5.23504429 | 5.057281088 | 0.16609296  | 9.61E-07 | 0.00969227 |
| C4orf18  | 4.80205393 | 4.556029169 | 0.16115845  | 9.36E-08 | 0.00097685 |
| GALNT4   | 4.10392448 | 3.969996874 | 0.15881577  | 4.09E-09 | 4.43E-05   |
| TEAD3    | 4.86364034 | 4.719912513 | 0.15630205  | 9.04E-07 | 0.00913269 |
| KCTD14   | 4.94332352 | 4.688348302 | 0.15412004  | 8.59E-07 | 0.00868949 |
| MARCO    | 4.82646429 | 4.547430221 | 0.15042033  | 1.15E-08 | 0.00012382 |
| PTPN7    | 4.86345137 | 4.752396645 | 0.14754025  | 3.87E-07 | 0.00395778 |
| MMP14    | 5.61610825 | 5.474220762 | 0.14696308  | 1.93E-07 | 0.00198884 |
| IL6      | 5.61938466 | 5.220046461 | 0.14110198  | 6.05E-07 | 0.00614535 |
| IL7R     | 5.55587046 | 5.293172947 | 0.13666448  | 3.25E-08 | 0.00034411 |
| PHKG1    | 5.40976392 | 5.180225209 | 0.12917074  | 5.27E-07 | 0.00536691 |
| RAC2     | 5.95878988 | 5.761999295 | 0.12859824  | 1.23E-10 | 1.37E-06   |
| FBP1     | 5.59065016 | 5.381704569 | 0.12576577  | 5.95E-08 | 0.00062591 |
| PTHR1    | 4.73785018 | 4.609425331 | 0.12196801  | 9.13E-07 | 0.00922298 |
| CDCP1    | 5.22629628 | 5.006850635 | 0.12114743  | 2.28E-08 | 0.00024267 |
| MAN1A1   | 4.64153407 | 4.497713952 | 0.11987707  | 2.00E-07 | 0.00206004 |
| IL1A     | 4.40515513 | 4.260150972 | 0.11545085  | 1.07E-07 | 0.00111513 |
| KDELR3   | 5.78970995 | 5.58726221  | 0.11156176  | 7.08E-07 | 0.00717799 |
| TRAF3IP3 | 4.35404888 | 4.26981806  | 0.08925621  | 5.42E-07 | 0.00551577 |
| IL15RA   | 4.99726025 | 4.907893182 | 0.07199878  | 3.94E-07 | 0.00402613 |
| VDR      | 4.5893918  | 4.553478514 | 0.05482279  | 2.94E-07 | 0.00301563 |
| GPRC5A   | 5.63125938 | 5.558846162 | 0.02693881  | 5.75E-07 | 0.0058404  |
| MUC1     | 5.24737679 | 5.260185835 | -0.00679344 | 6.38E-10 | 7.02E-06   |
| KYNU     | 4.87352108 | 4.918700982 | -0.0296076  | 8.17E-08 | 0.00085538 |
| MARCKSL1 | 10.2935904 | 10.57307833 | -0.1341241  | 7.97E-07 | 0.00807215 |
| GHRH     | 3.90443985 | 4.049732035 | -0.16363157 | 2.20E-07 | 0.00226557 |
| CBX1     | 8.57033841 | 8.799542274 | -0.16957633 | 8.39E-08 | 0.00087729 |
| MAGEH1   | 7.76134959 | 8.126288917 | -0.17236267 | 1.63E-07 | 0.00168701 |
| HMGB2    | 9.94166185 | 10.23539561 | -0.18031223 | 3.83E-07 | 0.00391777 |
| GP2      | 4.0926731  | 4.21189151  | -0.18186613 | 1.40E-08 | 0.00014936 |
| CLC      | 4.01719067 | 4.191514086 | -0.18403339 | 6.70E-07 | 0.00680456 |
| AHSG     | 4.16386073 | 4.352582329 | -0.19106341 | 1.96E-09 | 2.13E-05   |
| RHAG     | 3.91827151 | 4.017467497 | -0.19133774 | 6.70E-07 | 0.00680456 |
| KLRC4    | 3.61852358 | 3.860005098 | -0.19651446 | 1.95E-11 | 2.20E-07   |
| GSTA4    | 9.6701478  | 10.00015628 | -0.19689396 | 1.71E-12 | 1.94E-08   |
| PAIP2B   | 5.20386519 | 5.521036337 | -0.19906914 | 1.28E-07 | 0.00132908 |
| ATP1A3   | 4.65353462 | 4.963582931 | -0.20329235 | 2.20E-07 | 0.00226557 |
| SATB1    | 8.21161059 | 8.676668153 | -0.20535301 | 3.17E-09 | 3.44E-05   |
| PTPRS    | 4.53713402 | 4.689227005 | -0.20592823 | 6.68E-07 | 0.00678202 |
| MUC13    | 4.08058477 | 4.266670981 | -0.20600941 | 2.34E-07 | 0.00241266 |
| POU4F2   | 3.75308039 | 3.901408469 | -0.20709682 | 5.21E-09 | 5.64E-05   |
| GNAL     | 4.00037052 | 4.131072428 | -0.20907265 | 7.84E-07 | 0.00793939 |
| TOP2B    | 9.58984589 | 9.875121816 | -0.20925878 | 2.79E-08 | 0.00029609 |
| POU4F1   | 4.2624976  | 4.630284042 | -0.21185285 | 3.48E-09 | 3.78E-05   |

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| MLF1IP   | 8.36929946 | 8.903038348 | -0.21211682 | 2.49E-08 | 0.00026465 |
| SIX6     | 4.29781278 | 4.63255082  | -0.21214101 | 4.82E-07 | 0.00491106 |
| BCL2L14  | 3.93687287 | 4.069091113 | -0.21355125 | 4.82E-07 | 0.00491106 |
| FAAH     | 4.43038013 | 4.606622622 | -0.21464843 | 1.84E-08 | 0.00019647 |
| TPX2     | 7.34972406 | 7.851020622 | -0.21606382 | 1.20E-07 | 0.00125083 |
| LAPTM4B  | 9.98048233 | 10.32996041 | -0.21993278 | 1.17E-08 | 0.00012526 |
| CCNB2    | 7.43277712 | 7.965276937 | -0.22016695 | 4.24E-07 | 0.0043269  |
| COLQ     | 4.29488629 | 4.425654807 | -0.22139864 | 3.89E-09 | 4.22E-05   |
| PTCH1    | 4.9903461  | 5.220715782 | -0.22147917 | 1.55E-07 | 0.00160506 |
| MCM2     | 7.31198621 | 7.752686592 | -0.22158023 | 6.46E-07 | 0.00655535 |
| FGB      | 4.18660404 | 4.468201887 | -0.22161224 | 3.51E-07 | 0.0035946  |
| RIMS1    | 4.70022639 | 4.829127035 | -0.22174482 | 8.44E-10 | 9.27E-06   |
| ASPSCR1  | 5.50673472 | 5.733346498 | -0.22285865 | 1.66E-07 | 0.00171671 |
| SMARCE1  | 9.09452624 | 9.291339295 | -0.22331412 | 5.49E-08 | 0.00057783 |
| ACACA    | 7.74893333 | 8.033450141 | -0.22434515 | 5.67E-07 | 0.00576181 |
| CLIC5    | 4.16917597 | 4.430906775 | -0.22607967 | 1.26E-09 | 1.37E-05   |
| KCNK7    | 4.04711715 | 4.127027814 | -0.22708862 | 3.38E-07 | 0.00346194 |
| MAGEC1   | 3.87948231 | 4.036533377 | -0.22742821 | 1.86E-07 | 0.00192076 |
| HOXC8    | 4.53827181 | 4.672480717 | -0.22748902 | 4.56E-07 | 0.00465017 |
| CCT5     | 10.1313942 | 10.39832632 | -0.22762296 | 5.75E-07 | 0.0058404  |
| KIAA0907 | 8.75646697 | 9.04215897  | -0.22811261 | 1.29E-07 | 0.00134331 |
| XRCC5    | 9.54849077 | 9.798517095 | -0.22817701 | 4.69E-08 | 0.00049529 |
| TCP1     | 9.0739942  | 9.326570053 | -0.22877288 | 8.81E-09 | 9.48E-05   |
| HLTF     | 8.60537199 | 8.904223585 | -0.22954556 | 2.02E-08 | 0.00021512 |
| BRCA2    | 4.28574133 | 4.477807258 | -0.23021122 | 1.25E-07 | 0.00130079 |
| WASF1    | 7.68487418 | 8.214850584 | -0.23037849 | 1.97E-08 | 0.00021032 |
| TMPRSS2  | 4.11521174 | 4.272096695 | -0.23118356 | 8.80E-07 | 0.00889515 |
| MEOX1    | 3.9414416  | 4.148289796 | -0.23159315 | 1.34E-08 | 0.00014375 |
| UBE2S    | 7.68154046 | 8.129076866 | -0.23198683 | 1.91E-07 | 0.00196823 |
| CDC20    | 7.03452927 | 7.577673455 | -0.23229976 | 3.93E-08 | 0.0004159  |
| MAGEB4   | 4.07608466 | 4.132940872 | -0.2324068  | 3.40E-07 | 0.0034849  |
| PIK3R3   | 5.88384437 | 6.149732093 | -0.23248035 | 6.77E-07 | 0.00687262 |
| NOL11    | 8.28572502 | 8.533861333 | -0.23363812 | 1.48E-07 | 0.001538   |
| EZH2     | 6.98743005 | 7.513423128 | -0.23479816 | 1.64E-07 | 0.00169883 |
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| PAX1     | 3.85462642 | 4.010234528 | -0.23496561 | 8.05E-08 | 0.00084332 |
| HSD17B2  | 3.66376484 | 3.806743145 | -0.23507341 | 7.03E-07 | 0.00713061 |
| SLC22A3  | 3.64645671 | 3.858791879 | -0.23523615 | 1.09E-07 | 0.00113548 |
| TAF2     | 7.83486871 | 8.076094335 | -0.23589568 | 7.32E-08 | 0.00076784 |
| INTS8    | 8.17834127 | 8.416690555 | -0.23589959 | 9.54E-07 | 0.00962903 |
| TSHR     | 4.03682706 | 4.220655569 | -0.23630016 | 6.98E-08 | 0.00073248 |
| CTBP2    | 8.29585832 | 8.546240988 | -0.23761754 | 8.79E-08 | 0.00091885 |
| CDC123   | 7.97387656 | 8.286473842 | -0.23783289 | 4.48E-07 | 0.00457254 |
| SFRS3    | 9.66024988 | 9.880941958 | -0.23804713 | 9.39E-08 | 0.00098024 |
| SMC3     | 7.48121595 | 7.850272232 | -0.23848516 | 2.30E-07 | 0.00237096 |
| DTL      | 6.62164472 | 7.198558782 | -0.23853481 | 6.29E-08 | 0.00066134 |
| JARID1B  | 6.98216783 | 7.325403789 | -0.23959119 | 3.11E-07 | 0.00318663 |
| EYA1     | 4.9223036  | 5.518914411 | -0.23993233 | 1.22E-07 | 0.00126401 |
| SRC      | 4.72055416 | 4.810521253 | -0.23998314 | 4.58E-07 | 0.00466585 |

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| RFC4      | 8.26511479 | 8.702870245 | -0.24131709 | 1.74E-07 | 0.00180345 |
| SGCD      | 4.29242772 | 4.407443031 | -0.24149519 | 1.46E-08 | 0.00015576 |
| ARMC1     | 8.06517582 | 8.388878016 | -0.24151745 | 6.90E-08 | 0.00072449 |
| PQBP1     | 6.51440203 | 6.724224789 | -0.24200191 | 2.28E-07 | 0.00234654 |
| RACGAP1   | 8.07372846 | 8.508456047 | -0.24210847 | 1.79E-08 | 0.0001906  |
| SRPK3     | 4.71133773 | 4.881171523 | -0.24215342 | 3.37E-08 | 0.0003572  |
| UBE2C     | 8.35277633 | 8.930107205 | -0.24311685 | 1.59E-09 | 1.74E-05   |
| VDAC3     | 8.06203923 | 8.252087007 | -0.24315806 | 7.23E-07 | 0.0073234  |
| ELAVL2    | 4.24473295 | 4.526012902 | -0.24316342 | 2.35E-07 | 0.00242053 |
| TAS2R14   | 3.81488686 | 3.90713267  | -0.24341091 | 1.90E-07 | 0.00196179 |
| TOPBP1    | 8.27647388 | 8.620676484 | -0.24381103 | 3.58E-09 | 3.88E-05   |
| ZSCAN16   | 5.59556578 | 5.873597792 | -0.24394903 | 3.44E-07 | 0.00352065 |
| NVL       | 6.77253308 | 7.058994591 | -0.24404164 | 7.03E-07 | 0.00713061 |
| SS18L1    | 6.86725142 | 7.258392939 | -0.24412203 | 9.64E-07 | 0.00972307 |
| HNRNPL    | 8.52592588 | 8.808703584 | -0.24467711 | 7.27E-08 | 0.00076235 |
| C8orf51   | 4.42265505 | 4.532163748 | -0.24475449 | 8.95E-07 | 0.00904235 |
| B4GALT6   | 4.23249658 | 4.499357445 | -0.24549774 | 1.90E-07 | 0.00196179 |
| C11orf30  | 4.72161965 | 4.892602852 | -0.24561396 | 5.16E-07 | 0.00525859 |
| HIST1H4L  | 4.18491266 | 4.266161775 | -0.24562704 | 3.37E-08 | 0.0003572  |
| BZW2      | 9.47773937 | 9.849832306 | -0.2462106  | 1.90E-07 | 0.00196179 |
| CKS2      | 9.29694661 | 9.817628757 | -0.24624043 | 5.97E-09 | 6.44E-05   |
| UBAP2     | 7.59140183 | 7.931374417 | -0.24702521 | 1.49E-07 | 0.00154325 |
| GPSM2     | 7.29012448 | 7.702231098 | -0.24725555 | 5.61E-08 | 0.00059046 |
| MSH5      | 4.8937923  | 5.20604013  | -0.24745713 | 1.40E-07 | 0.0014476  |
| NARS2     | 7.03958132 | 7.392474197 | -0.24746486 | 3.39E-07 | 0.00347375 |
| PAX9      | 3.94109369 | 4.038487827 | -0.24783233 | 9.29E-07 | 0.0093791  |
| KCNIP2    | 3.83038981 | 3.925658329 | -0.24836303 | 1.62E-07 | 0.0016751  |
| NXN       | 7.23939444 | 7.711038623 | -0.24908037 | 3.40E-08 | 0.00035984 |
| CKAP2     | 7.53708472 | 7.94900826  | -0.24909783 | 9.42E-09 | 0.00010124 |
| CRHR1     | 3.98975701 | 4.051759985 | -0.24989563 | 3.09E-07 | 0.00316495 |
| RAD51AP1  | 6.2049129  | 6.673162942 | -0.24999791 | 7.58E-07 | 0.00767633 |
| DNASE1    | 3.96444589 | 4.091295168 | -0.25009245 | 8.99E-10 | 9.86E-06   |
| CCNB1IP1  | 8.23011931 | 8.5965359   | -0.25101407 | 1.56E-07 | 0.00161633 |
| ZNF32     | 7.47222624 | 7.786649935 | -0.25155892 | 4.00E-07 | 0.00408218 |
| MMP17     | 4.10122078 | 4.201299179 | -0.25192374 | 2.19E-07 | 0.00225776 |
| C16orf80  | 9.39777199 | 9.72394053  | -0.25265141 | 1.09E-09 | 1.19E-05   |
| MTX2      | 7.63772309 | 7.931541447 | -0.25301728 | 3.34E-07 | 0.00342644 |
| AKAP1     | 6.19430025 | 6.419179344 | -0.25324698 | 8.28E-07 | 0.00837577 |
| TMEM97    | 7.88477286 | 8.278972689 | -0.25325445 | 1.74E-08 | 0.00018559 |
| RCL1      | 6.40601425 | 6.671645188 | -0.25330416 | 7.23E-07 | 0.0073234  |
| IL26      | 4.0618069  | 4.148190416 | -0.25345548 | 1.42E-08 | 0.00015166 |
| GLRA3     | 3.79314759 | 3.869401154 | -0.25361778 | 1.79E-07 | 0.00185161 |
| PAQR5     | 3.93128935 | 4.032499493 | -0.25403521 | 7.18E-07 | 0.00727582 |
| KCNK1     | 5.5353769  | 6.188277721 | -0.25411112 | 6.87E-07 | 0.00696506 |
| LOC400506 | 6.30465502 | 6.567467526 | -0.25482604 | 6.43E-07 | 0.0065336  |
| BNC1      | 3.63988912 | 3.891199993 | -0.25499051 | 6.50E-08 | 0.00068352 |
| HOXD1     | 4.7355617  | 5.012704998 | -0.25543622 | 1.31E-08 | 0.00013996 |
| HSPA14    | 7.48981045 | 7.855727629 | -0.25548878 | 2.28E-07 | 0.00234654 |
| TTC13     | 6.79077394 | 7.12914525  | -0.25556908 | 1.10E-07 | 0.00114771 |

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| GTSE1     | 5.64256388 | 5.996606532 | -0.25594331 | 8.89E-07 | 0.00898319 |
| VASH2     | 4.57943196 | 4.957772922 | -0.25598427 | 1.16E-07 | 0.00120272 |
| MYH14     | 4.35053119 | 4.439842188 | -0.25608117 | 7.97E-08 | 0.00083416 |
| NCAPD2    | 6.54361622 | 6.968081075 | -0.25613754 | 2.66E-07 | 0.00273631 |
| CDSN      | 4.12218177 | 4.199852948 | -0.25669538 | 6.22E-07 | 0.00631556 |
| CSE1L     | 7.81858153 | 8.052477749 | -0.25683418 | 2.63E-08 | 0.00027885 |
| LEFTY1    | 4.62804674 | 4.829196807 | -0.25688238 | 1.00E-10 | 1.12E-06   |
| TIMELESS  | 6.3769994  | 6.782199451 | -0.2568955  | 1.31E-07 | 0.00135744 |
| SLC38A1   | 7.76229568 | 8.430022836 | -0.25755345 | 1.14E-08 | 0.00012193 |
| SIX1      | 4.9156578  | 5.223935109 | -0.25758568 | 6.63E-08 | 0.00069606 |
| PTTG3     | 5.17455503 | 5.419770293 | -0.25838384 | 8.95E-07 | 0.00904235 |
| PCGF2     | 6.1679761  | 6.443403187 | -0.25846913 | 2.73E-07 | 0.00280336 |
| LOC541469 | 4.18521374 | 4.281789646 | -0.25861014 | 9.81E-08 | 0.00102315 |
| HNRPH3    | 6.96903479 | 7.278440839 | -0.2586143  | 6.75E-08 | 0.0007089  |
| NR4A1     | 5.30979853 | 5.486240869 | -0.25865052 | 6.73E-07 | 0.0068265  |
| E2F1      | 5.06497193 | 5.225587535 | -0.25875519 | 8.89E-07 | 0.00898319 |
| MKRN3     | 4.63241827 | 4.936244056 | -0.25882835 | 5.40E-07 | 0.00549736 |
| CENPM     | 5.75767865 | 6.109481062 | -0.25908052 | 3.44E-07 | 0.00352065 |
| CCNJ      | 4.7058224  | 4.998614132 | -0.25950814 | 3.03E-07 | 0.00311136 |
| ANKZF1    | 5.92368693 | 6.135195621 | -0.25957717 | 6.03E-07 | 0.00612491 |
| RPL35A    | 11.3767515 | 11.61273746 | -0.26022753 | 1.19E-07 | 0.00124191 |
| PKP4      | 6.69778009 | 7.162850163 | -0.26028638 | 2.90E-08 | 0.00030741 |
| NASP      | 6.96699585 | 7.351467155 | -0.26036049 | 2.30E-07 | 0.00237096 |
| FANCI     | 6.49003885 | 7.05669194  | -0.26042397 | 1.11E-07 | 0.00115597 |
| LOC196993 | 4.03333613 | 4.128831198 | -0.26087623 | 3.65E-07 | 0.00373287 |
| EDC4      | 6.13395885 | 6.357908698 | -0.26117092 | 2.99E-08 | 0.00031674 |
| STYK1     | 4.05131997 | 4.252490527 | -0.26138511 | 4.84E-07 | 0.00492662 |
| DLL3      | 5.84364609 | 6.657463864 | -0.26169986 | 4.54E-07 | 0.00463546 |
| SFRS6     | 7.85866644 | 8.163113644 | -0.26184254 | 2.20E-08 | 0.00023461 |
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| COMMD3    | 8.81771845 | 9.150925415 | -0.26213001 | 1.69E-07 | 0.00174725 |
| OSR2      | 4.39243236 | 4.836258953 | -0.26244996 | 8.11E-08 | 0.00084929 |
| TOP2A     | 7.97444481 | 8.696041943 | -0.26275932 | 8.53E-12 | 9.66E-08   |
| MCF2      | 3.87087256 | 3.978654752 | -0.26295997 | 2.73E-07 | 0.00280336 |
| CKS1B     | 8.6125857  | 9.150660208 | -0.2629729  | 1.02E-07 | 0.0010643  |
| MAGI1     | 4.70839157 | 5.151692119 | -0.26338687 | 9.92E-08 | 0.00103431 |
| ACTR5     | 5.2220885  | 5.40079579  | -0.26497848 | 2.72E-07 | 0.00279376 |
| NOLC1     | 6.5498394  | 6.805874522 | -0.26566663 | 7.95E-07 | 0.00804559 |
| DCC       | 4.03090891 | 4.187831439 | -0.26588937 | 1.85E-07 | 0.00190763 |
| COQ3      | 6.16108884 | 6.512699081 | -0.26606976 | 3.83E-07 | 0.00391777 |
| PCDH21    | 4.89912259 | 5.127303905 | -0.26690269 | 7.24E-08 | 0.00075962 |
| RAB26     | 4.73987424 | 5.07863066  | -0.26691075 | 8.63E-08 | 0.00090287 |
| HSF2      | 5.4984985  | 5.790334863 | -0.26704716 | 1.18E-07 | 0.0012245  |
| HNRNPU    | 6.31531649 | 6.426251621 | -0.26741082 | 2.49E-08 | 0.00026465 |
| RAD52     | 4.46852706 | 4.588500354 | -0.26762262 | 1.06E-07 | 0.00110715 |
| HIST3H2A  | 6.41398352 | 7.093593625 | -0.26778899 | 1.81E-07 | 0.00187439 |
| HOXA11    | 4.25198127 | 4.478031503 | -0.26803058 | 3.93E-09 | 4.25E-05   |
| RBMX      | 8.97887462 | 9.280711187 | -0.26883649 | 1.62E-08 | 0.00017262 |
| LMNB1     | 6.1187111  | 6.637222017 | -0.26924446 | 7.88E-08 | 0.00082542 |

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| STXBP6      | 4.52473897 | 5.007139284 | -0.26931901 | 3.04E-07 | 0.003122   |
| NDST4       | 3.97424026 | 4.189731337 | -0.2693231  | 8.13E-10 | 8.93E-06   |
| UBE2I       | 6.77032087 | 6.913531375 | -0.2694712  | 2.25E-07 | 0.00231369 |
| GPR85       | 4.44894211 | 4.617195866 | -0.26949131 | 7.54E-08 | 0.00079033 |
| ZNF323      | 5.67961046 | 6.035826017 | -0.26967295 | 5.48E-07 | 0.00557138 |
| BIRC5       | 6.49667945 | 7.070036536 | -0.26978582 | 7.77E-09 | 8.37E-05   |
| KIT         | 5.98549202 | 6.640778977 | -0.26980373 | 8.59E-07 | 0.00868949 |
| BAAT        | 4.24790258 | 4.366650905 | -0.27021668 | 5.42E-07 | 0.00551577 |
| FXR1        | 8.20417391 | 8.506416193 | -0.27024069 | 8.86E-08 | 0.00092534 |
| PSMD4       | 7.17803584 | 7.328057547 | -0.27045748 | 1.34E-07 | 0.00139194 |
| EPHB3       | 5.12894775 | 5.554758177 | -0.2704661  | 4.18E-07 | 0.00426928 |
| MLLT10      | 4.7302404  | 4.915233273 | -0.27065494 | 6.18E-08 | 0.00064934 |
| RFC5        | 6.047329   | 6.461802971 | -0.27094037 | 4.04E-07 | 0.00412461 |
| CENPE       | 5.5377087  | 6.036649871 | -0.27148477 | 8.32E-08 | 0.00087113 |
| ZSCAN2      | 3.96334751 | 4.054593049 | -0.2716837  | 2.37E-07 | 0.00243751 |
| CHD7        | 6.62887841 | 7.166700726 | -0.27173619 | 2.48E-09 | 2.70E-05   |
| RAD21       | 9.38328214 | 9.66335648  | -0.2718759  | 2.36E-10 | 2.62E-06   |
| DLG3        | 4.86106622 | 5.039873273 | -0.27191451 | 4.76E-08 | 0.0005026  |
| ITFG2       | 4.52539058 | 4.684767242 | -0.27218228 | 9.19E-08 | 0.00095935 |
| EIF2B5      | 6.92734834 | 7.183802984 | -0.27237383 | 6.88E-09 | 7.42E-05   |
| KLK1        | 4.39714982 | 4.530572588 | -0.27242133 | 1.18E-07 | 0.0012245  |
| LHX1        | 4.00854808 | 4.183029244 | -0.27262274 | 9.22E-08 | 0.00096277 |
| ISL1        | 4.23067623 | 4.411096902 | -0.2732584  | 6.21E-09 | 6.70E-05   |
| SIM2        | 4.35126008 | 4.610396889 | -0.27419326 | 9.64E-08 | 0.00100514 |
| MKI67       | 5.2410282  | 5.697843469 | -0.27429045 | 1.76E-07 | 0.00182257 |
| MXD3        | 5.41913433 | 5.726576733 | -0.27463556 | 7.00E-08 | 0.00073505 |
| ZWINT       | 7.5686437  | 8.116005663 | -0.27478114 | 2.51E-09 | 2.73E-05   |
| TLX1        | 4.08739517 | 4.252216884 | -0.27483594 | 4.40E-08 | 0.00046503 |
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| ILF2        | 9.32660746 | 9.707958141 | -0.27624224 | 8.61E-12 | 9.74E-08   |
| FCHO1       | 4.26584374 | 4.414496235 | -0.27651879 | 7.48E-08 | 0.00078461 |
| TRIT1       | 5.46590003 | 5.650106401 | -0.27656951 | 5.95E-07 | 0.00604263 |
| CDCA3       | 5.34892616 | 5.837142314 | -0.27706581 | 5.51E-07 | 0.00560931 |
| MEGF6       | 4.53297629 | 4.726623684 | -0.27728266 | 3.70E-09 | 4.01E-05   |
| DCT         | 4.50059085 | 4.906044176 | -0.27756956 | 1.19E-10 | 1.32E-06   |
| AIM1L       | 4.56206694 | 4.679667943 | -0.2785754  | 2.58E-07 | 0.00265148 |
| GDF9        | 4.15669423 | 4.31155494  | -0.27885836 | 1.26E-08 | 0.00013521 |
| KCNB2       | 3.75918092 | 3.854857533 | -0.27890736 | 6.80E-09 | 7.33E-05   |
| DLX4        | 4.06992268 | 4.151938234 | -0.27902525 | 1.77E-07 | 0.00182565 |
| C1orf35     | 5.51989679 | 5.699910702 | -0.2793526  | 1.72E-07 | 0.00178487 |
| HSPB3       | 4.46163857 | 4.838654969 | -0.27960974 | 4.26E-08 | 0.0004498  |
| PLCB1       | 5.6371092  | 5.963040549 | -0.27961912 | 6.74E-09 | 7.27E-05   |
| AZI1        | 5.21714304 | 5.407366391 | -0.27990953 | 2.62E-08 | 0.00027782 |
| DCX         | 6.26846599 | 7.492678622 | -0.2801915  | 2.08E-07 | 0.00214069 |
| SFPQ        | 8.23745549 | 8.500960328 | -0.28019849 | 4.29E-09 | 4.64E-05   |
| ATAD2       | 5.95224735 | 6.461116785 | -0.28056941 | 8.63E-08 | 0.00090287 |
| PFDN2       | 8.70707483 | 9.035888779 | -0.28087539 | 1.64E-08 | 0.00017528 |
| KIF14       | 5.39583921 | 5.857697012 | -0.2812359  | 8.08E-08 | 0.00084634 |

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| TRIP13      | 6.38676028 | 6.969292325 | -0.28135781 | 3.27E-07 | 0.00335648 |
| ZNF750      | 3.6321787  | 3.93096377  | -0.28176237 | 1.43E-07 | 0.00148403 |
| GRID2       | 3.99069965 | 4.187308001 | -0.28177161 | 4.44E-08 | 0.00046847 |
| HMGCS1      | 6.04728527 | 6.475472755 | -0.28199434 | 4.93E-09 | 5.33E-05   |
| ZNF639      | 4.89737838 | 5.062256462 | -0.28200016 | 1.42E-08 | 0.00015166 |
| FANCG       | 6.58021912 | 7.038424516 | -0.28215015 | 5.78E-08 | 0.00060802 |
| TFAP2A      | 4.78079924 | 5.138877818 | -0.28255526 | 1.85E-08 | 0.00019719 |
| TDRKH       | 4.06055024 | 4.208193816 | -0.28269206 | 7.40E-08 | 0.00077621 |
| COIL        | 7.03441538 | 7.315896175 | -0.28272438 | 9.57E-09 | 0.00010279 |
| FGFR4       | 4.15008204 | 4.319518451 | -0.28327542 | 1.31E-09 | 1.43E-05   |
| GUCY1B2     | 4.07663575 | 4.211720733 | -0.28336094 | 3.89E-07 | 0.0039712  |
| CENPF       | 6.68017236 | 7.312772307 | -0.28337421 | 2.58E-09 | 2.81E-05   |
| PAFAH1B3    | 7.65838591 | 8.125376049 | -0.28370972 | 5.92E-09 | 6.39E-05   |
| KIF11       | 5.78323012 | 6.400747659 | -0.28432039 | 4.39E-08 | 0.00046338 |
| SCML2       | 5.3872609  | 5.586262755 | -0.28432424 | 1.58E-08 | 0.00016937 |
| ECT2        | 6.67776808 | 7.291173934 | -0.28473908 | 1.49E-08 | 0.00015938 |
| RELN        | 4.74504186 | 5.272870662 | -0.28482756 | 9.57E-08 | 0.00099821 |
| TEX10       | 7.00987895 | 7.382541392 | -0.28516856 | 3.75E-08 | 0.00039627 |
| ATP6V0A4    | 3.81763811 | 4.091180721 | -0.28534792 | 2.56E-09 | 2.78E-05   |
| C17orf75    | 5.71851947 | 6.125007943 | -0.28545767 | 1.40E-07 | 0.00145255 |
| KRTAP2-4    | 4.12786408 | 4.230834331 | -0.28570904 | 4.47E-08 | 0.0004719  |
| PTGER3      | 4.02321735 | 4.080738588 | -0.28579654 | 5.55E-08 | 0.00058414 |
| NCAPG       | 5.62237523 | 6.182000817 | -0.28585697 | 9.13E-09 | 9.82E-05   |
| HIC2        | 4.76173236 | 4.945617657 | -0.2860591  | 6.50E-08 | 0.00068352 |
| POLR2B      | 9.05126018 | 9.356510175 | -0.2860911  | 1.63E-10 | 1.81E-06   |
| ATP2C2      | 4.20351552 | 4.434157904 | -0.2863157  | 1.88E-09 | 2.05E-05   |
| GPR87       | 3.66778837 | 4.125683529 | -0.28648312 | 1.30E-07 | 0.00135267 |
| NEIL3       | 5.02587263 | 5.309478974 | -0.28652496 | 1.71E-08 | 0.00018209 |
| PLEKHG3     | 4.81562869 | 4.932976986 | -0.28768769 | 1.75E-09 | 1.91E-05   |
| CTPS        | 6.56843529 | 7.035700618 | -0.2883052  | 1.53E-08 | 0.00016366 |
| RBM4        | 7.14251627 | 7.383572538 | -0.2886416  | 2.02E-09 | 2.20E-05   |
| FANCE       | 5.06393972 | 5.31724529  | -0.28891379 | 5.67E-08 | 0.00059701 |
| DFFB        | 4.56258118 | 4.794287163 | -0.28892056 | 2.51E-08 | 0.00026659 |
| C13orf27    | 6.43124286 | 6.892480206 | -0.28926495 | 8.24E-09 | 8.87E-05   |
| C19orf40    | 4.59320985 | 4.758762902 | -0.28955799 | 2.05E-08 | 0.0002184  |
| ICA1        | 4.93370885 | 5.160433094 | -0.29027546 | 2.91E-07 | 0.00298426 |
| HOXD9       | 4.32673264 | 4.460147554 | -0.29053993 | 1.93E-08 | 0.00020556 |
| RP4-691N24. | 5.4161712  | 5.822927339 | -0.29079409 | 8.79E-08 | 0.00091885 |
| AMOTL2      | 7.49560408 | 8.095385993 | -0.29084059 | 2.19E-09 | 2.38E-05   |
| BUB3        | 7.87952195 | 8.254228395 | -0.29153649 | 3.58E-09 | 3.88E-05   |
| OTUB2       | 4.17202762 | 4.353564352 | -0.2915504  | 2.69E-09 | 2.92E-05   |
| FUBP1       | 5.68176733 | 5.96116595  | -0.29168677 | 7.38E-09 | 7.96E-05   |
| C10orf95    | 4.00551666 | 4.10599219  | -0.29223993 | 2.47E-08 | 0.00026267 |
| NMU         | 5.68793882 | 6.491283039 | -0.29231764 | 8.05E-09 | 8.67E-05   |
| ITGB6       | 3.71006185 | 3.966539859 | -0.29238801 | 3.41E-09 | 3.70E-05   |
| KIAA1324    | 4.19470895 | 4.458068444 | -0.29242522 | 6.04E-09 | 6.52E-05   |
| B3GNT3      | 4.30769226 | 4.487148814 | -0.29244001 | 9.80E-07 | 0.00988339 |
| NKX2-1      | 3.96701018 | 4.210123888 | -0.29244008 | 4.98E-11 | 5.57E-07   |
| ASPM        | 6.3346036  | 7.068204817 | -0.29247029 | 7.96E-10 | 8.75E-06   |

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| SLC6A14  | 3.59296788 | 3.928011437 | -0.29295446 | 8.33E-07 | 0.00843191 |
| ACVR2B   | 5.16587207 | 5.464798317 | -0.2930543  | 4.05E-09 | 4.39E-05   |
| TSC22D2  | 5.06183179 | 5.170884158 | -0.29321677 | 7.07E-09 | 7.62E-05   |
| EDAR     | 4.33002086 | 4.525766945 | -0.29349617 | 4.47E-11 | 5.01E-07   |
| PATZ1    | 4.9097621  | 5.092618705 | -0.29387036 | 1.09E-09 | 1.20E-05   |
| INTS7    | 6.21871496 | 6.623907646 | -0.29396799 | 1.86E-08 | 0.00019869 |
| TNR      | 4.16031557 | 4.271181642 | -0.29403878 | 2.74E-09 | 2.98E-05   |
| RALGPS1  | 4.96789536 | 5.286720464 | -0.29431488 | 4.79E-09 | 5.19E-05   |
| CDC2     | 6.54093013 | 7.224990561 | -0.29466294 | 1.53E-08 | 0.00016304 |
| CENPA    | 5.78836575 | 6.307776502 | -0.29502194 | 1.75E-08 | 0.00018629 |
| TIAL1    | 6.21002007 | 6.390414428 | -0.29519618 | 1.32E-07 | 0.0013721  |
| ZSCAN21  | 4.02901794 | 4.140784287 | -0.29551158 | 1.30E-08 | 0.00013943 |
| ACRV1    | 3.92805101 | 4.072021958 | -0.29605585 | 8.86E-08 | 0.00092534 |
| PAPD1    | 6.31813396 | 6.717903612 | -0.29702634 | 3.61E-08 | 0.0003819  |
| LDB1     | 5.52605662 | 5.785578474 | -0.29707811 | 2.19E-09 | 2.38E-05   |
| CDC6     | 4.54470413 | 5.015019549 | -0.29785895 | 1.18E-07 | 0.0012245  |
| DUSP26   | 5.43970995 | 5.919388883 | -0.29788332 | 2.49E-08 | 0.00026465 |
| TEX14    | 4.00572958 | 4.27169926  | -0.29846852 | 4.92E-08 | 0.00051946 |
| CEP152   | 4.43252695 | 4.739901496 | -0.29858522 | 7.11E-08 | 0.00074582 |
| TCF20    | 5.25192404 | 5.394157691 | -0.29873793 | 1.83E-08 | 0.00019574 |
| ARVCF    | 5.30114531 | 5.466220693 | -0.29898646 | 9.13E-09 | 9.82E-05   |
| GPRIN2   | 4.60315306 | 4.796624012 | -0.29917987 | 3.12E-07 | 0.00319752 |
| CARD10   | 4.38091913 | 4.496124041 | -0.29943202 | 3.57E-07 | 0.00365725 |
| TMEM28   | 4.29066249 | 4.581733437 | -0.2996032  | 8.57E-12 | 9.70E-08   |
| MCM7     | 7.49338386 | 8.028067249 | -0.29962445 | 7.74E-10 | 8.50E-06   |
| TTK      | 6.19991085 | 6.92693319  | -0.29977365 | 1.30E-09 | 1.43E-05   |
| RFC3     | 6.48155974 | 6.963762552 | -0.30018688 | 3.13E-09 | 3.40E-05   |
| HPGD     | 4.22065783 | 4.565434045 | -0.30034088 | 2.54E-07 | 0.00261503 |
| DLK2     | 4.73422617 | 4.921981287 | -0.30074564 | 5.91E-08 | 0.00062152 |
| CACYBP   | 7.89111906 | 8.1738833   | -0.30078528 | 3.28E-10 | 3.63E-06   |
| C1orf159 | 4.83282639 | 4.978536019 | -0.30108202 | 2.48E-09 | 2.70E-05   |
| SCD5     | 5.02515361 | 5.3853242   | -0.30171286 | 1.01E-07 | 0.00105698 |
| C17orf53 | 4.48574919 | 4.624464831 | -0.30174667 | 1.17E-09 | 1.28E-05   |
| CEP72    | 4.90312114 | 5.230737581 | -0.30230869 | 7.82E-08 | 0.00081953 |
| KIAA1166 | 5.66991513 | 6.125926938 | -0.30239925 | 1.75E-09 | 1.90E-05   |
| HYAL1    | 4.3349903  | 4.697976476 | -0.30256329 | 9.77E-07 | 0.00985113 |
| MAGEA9   | 4.05535563 | 4.354124206 | -0.30313073 | 1.19E-10 | 1.33E-06   |
| KRT5     | 4.18880404 | 4.700896291 | -0.30377958 | 2.61E-09 | 2.84E-05   |
| KCNK2    | 4.08298383 | 4.419361093 | -0.30388604 | 1.23E-11 | 1.39E-07   |
| ANKRD26  | 4.21447749 | 4.374334061 | -0.30402504 | 3.77E-09 | 4.09E-05   |
| DACH1    | 4.45806973 | 4.937991228 | -0.30421564 | 3.25E-07 | 0.00333336 |
| CELSR3   | 5.5677544  | 6.084609031 | -0.30438636 | 6.54E-10 | 7.19E-06   |
| SPATS2   | 6.219552   | 6.615715859 | -0.30443273 | 9.06E-10 | 9.94E-06   |
| WDR62    | 4.83993099 | 5.025755577 | -0.30462437 | 1.62E-09 | 1.76E-05   |
| ALCAM    | 8.68001745 | 9.283798814 | -0.30466578 | 1.19E-11 | 1.35E-07   |
| CDT1     | 3.85037902 | 4.140828433 | -0.30473216 | 2.07E-08 | 0.00022004 |
| NTF3     | 4.44841652 | 4.61577322  | -0.3048678  | 2.34E-07 | 0.00241266 |
| POLG2    | 5.95771956 | 6.298241781 | -0.30488035 | 1.01E-08 | 0.0001081  |
| TBPL1    | 7.68062456 | 8.163014418 | -0.30558304 | 1.44E-10 | 1.60E-06   |

|           |            |             |             |          |            |
|-----------|------------|-------------|-------------|----------|------------|
| SUPV3L1   | 6.26247434 | 6.637012209 | -0.30596309 | 2.35E-09 | 2.56E-05   |
| CYP2E1    | 3.96614254 | 4.077580607 | -0.30639749 | 2.00E-08 | 0.00021273 |
| KIF21B    | 5.79747683 | 6.528094755 | -0.30650279 | 4.87E-09 | 5.27E-05   |
| SQLE      | 6.51969482 | 6.939888981 | -0.30667435 | 4.96E-08 | 0.00052325 |
| LRRC1     | 6.04561722 | 6.567011047 | -0.30672743 | 9.72E-09 | 0.0001044  |
| MAD2L1    | 7.41781847 | 8.13098634  | -0.3071449  | 8.62E-11 | 9.61E-07   |
| CDC7      | 6.57345823 | 7.228584693 | -0.30734638 | 1.67E-09 | 1.82E-05   |
| RPS6KA5   | 5.4953849  | 5.934861771 | -0.30773964 | 1.86E-10 | 2.06E-06   |
| CSDC2     | 4.90521193 | 5.306529071 | -0.30780943 | 7.27E-09 | 7.84E-05   |
| SPAG5     | 6.12505853 | 6.648811202 | -0.30817519 | 4.55E-09 | 4.93E-05   |
| MMP15     | 4.81070638 | 5.141617295 | -0.30818831 | 5.35E-10 | 5.89E-06   |
| C2orf27   | 4.95155962 | 5.164400612 | -0.30843129 | 1.28E-07 | 0.00133376 |
| C10orf18  | 7.44129532 | 7.879104405 | -0.30864662 | 9.33E-10 | 1.02E-05   |
| TOX3      | 5.80903102 | 6.836237856 | -0.30892749 | 4.10E-10 | 4.52E-06   |
| COL11A2   | 4.3201312  | 4.494817009 | -0.30924662 | 3.45E-11 | 3.87E-07   |
| CDCA8     | 5.99753895 | 6.504795222 | -0.31035466 | 3.08E-09 | 3.35E-05   |
| SETDB1    | 5.69665527 | 5.93714768  | -0.31125407 | 7.75E-11 | 8.65E-07   |
| MYBL2     | 5.27445159 | 5.681791157 | -0.31200674 | 9.02E-09 | 9.70E-05   |
| POLE      | 5.27668834 | 5.584311825 | -0.31230198 | 5.51E-10 | 6.06E-06   |
| POF1B     | 3.97476641 | 4.153455042 | -0.31288398 | 5.19E-10 | 5.72E-06   |
| ELMO3     | 3.89447889 | 4.171390332 | -0.31295638 | 2.70E-07 | 0.00277439 |
| CCT3      | 9.66036873 | 9.968333337 | -0.31300117 | 4.91E-11 | 5.50E-07   |
| PRIM1     | 6.890224   | 7.456068802 | -0.31359409 | 2.83E-10 | 3.13E-06   |
| HCRP1     | 4.43612823 | 4.576911681 | -0.31420883 | 2.65E-08 | 0.00028095 |
| RECQL4    | 4.82488854 | 5.049388873 | -0.31549859 | 7.36E-09 | 7.93E-05   |
| ALDH3B2   | 3.75672024 | 3.873228371 | -0.31558758 | 1.09E-07 | 0.0011395  |
| TAS2R1    | 4.5724485  | 4.700868665 | -0.31560045 | 1.71E-09 | 1.87E-05   |
| PODXL2    | 4.94074314 | 5.334138225 | -0.31568617 | 7.75E-11 | 8.65E-07   |
| GADD45G   | 5.68441794 | 6.209917978 | -0.31571275 | 2.86E-07 | 0.00293277 |
| MUC4      | 3.89754374 | 4.185785561 | -0.31581143 | 2.74E-11 | 3.08E-07   |
| ODC1      | 10.1994069 | 10.68540768 | -0.31605664 | 6.25E-13 | 7.15E-09   |
| MAST1     | 4.24707252 | 4.433565149 | -0.31632633 | 1.33E-12 | 1.52E-08   |
| TRAF4     | 5.58250005 | 6.004394569 | -0.31687586 | 8.84E-10 | 9.70E-06   |
| DUSP9     | 3.8198459  | 4.00564462  | -0.31759375 | 1.60E-11 | 1.80E-07   |
| TMPRSS4   | 4.01068269 | 4.459783099 | -0.31765929 | 2.28E-08 | 0.00024267 |
| RPRM      | 5.49897246 | 6.145234525 | -0.31819663 | 8.55E-10 | 9.38E-06   |
| PCDHA9    | 4.29264098 | 4.653455695 | -0.31850918 | 8.34E-12 | 9.44E-08   |
| CTSE      | 4.24200698 | 4.599754671 | -0.31903212 | 8.77E-11 | 9.78E-07   |
| KLRK1     | 4.50181591 | 5.073109494 | -0.31908757 | 4.15E-10 | 4.58E-06   |
| CYP2C9    | 4.054285   | 4.133260251 | -0.31934666 | 1.82E-10 | 2.03E-06   |
| CCNA2     | 5.61424036 | 6.306153678 | -0.31957389 | 5.19E-10 | 5.72E-06   |
| TARBP1    | 6.09088726 | 6.536891136 | -0.32049987 | 3.38E-10 | 3.74E-06   |
| NBLA00301 | 3.80592623 | 3.974548995 | -0.32131864 | 9.58E-12 | 1.08E-07   |
| IDI1      | 7.75051656 | 8.212979916 | -0.32180124 | 3.65E-10 | 4.03E-06   |
| ZBTB5     | 7.29883865 | 7.670005938 | -0.32339365 | 1.33E-10 | 1.48E-06   |
| ATP7B     | 4.32458122 | 4.621268821 | -0.32379826 | 2.88E-10 | 3.18E-06   |
| PCDH7     | 4.04281751 | 4.212426799 | -0.32435856 | 5.65E-12 | 6.40E-08   |
| DLX5      | 4.48588568 | 5.386595711 | -0.32503689 | 1.91E-08 | 0.00020402 |
| RAB3B     | 4.11269793 | 4.366197114 | -0.32521168 | 4.13E-12 | 4.69E-08   |

|          |            |             |             |          |            |
|----------|------------|-------------|-------------|----------|------------|
| HN1      | 8.62572652 | 9.185577491 | -0.32538128 | 1.64E-11 | 1.85E-07   |
| DDX11    | 5.08889979 | 5.409979403 | -0.32617527 | 3.34E-09 | 3.63E-05   |
| BUB1     | 4.57796877 | 4.921844029 | -0.32682588 | 1.69E-09 | 1.84E-05   |
| CACNA2D2 | 4.68780952 | 5.203302954 | -0.32683123 | 1.72E-10 | 1.92E-06   |
| TNRC4    | 4.68684099 | 4.810202119 | -0.3283205  | 6.94E-10 | 7.62E-06   |
| KIF2C    | 5.72792991 | 6.311041099 | -0.32844035 | 2.90E-10 | 3.21E-06   |
| TAF4B    | 3.87380909 | 4.037946339 | -0.32844621 | 2.97E-07 | 0.00304702 |
| SKP2     | 5.62386123 | 5.948506366 | -0.32863058 | 5.40E-09 | 5.84E-05   |
| SMPD3    | 3.97746889 | 4.210418829 | -0.32871506 | 3.51E-12 | 3.98E-08   |
| SEPHS1   | 7.16086179 | 7.57749709  | -0.32878612 | 1.76E-11 | 1.98E-07   |
| SUSD5    | 4.40225269 | 5.043484054 | -0.32947783 | 1.65E-07 | 0.00170477 |
| VRK1     | 6.51852766 | 7.076057364 | -0.32972408 | 6.35E-10 | 6.99E-06   |
| RAD51    | 4.95486963 | 5.229666948 | -0.32987572 | 8.70E-08 | 0.00090925 |
| TFAM     | 5.96923592 | 6.31875664  | -0.32996468 | 7.86E-09 | 8.47E-05   |
| HR       | 4.41048703 | 4.532155474 | -0.33056662 | 1.25E-10 | 1.39E-06   |
| HMG4L    | 5.39149723 | 5.732413091 | -0.33120508 | 1.67E-10 | 1.86E-06   |
| TROAP    | 5.31508105 | 5.767170817 | -0.33145873 | 3.64E-10 | 4.02E-06   |
| KIF22    | 4.79379197 | 5.111852565 | -0.33221374 | 5.00E-11 | 5.59E-07   |
| PLK4     | 4.88372215 | 5.194094142 | -0.33285635 | 2.03E-10 | 2.25E-06   |
| CDH1     | 4.47965859 | 4.981896895 | -0.3334414  | 5.91E-08 | 0.00062152 |
| MTSS1    | 5.43435669 | 5.616844511 | -0.33510517 | 1.58E-11 | 1.78E-07   |
| C12orf48 | 5.14896453 | 5.5658318   | -0.33514256 | 8.03E-07 | 0.00812554 |
| RLN2     | 3.87506897 | 4.149512854 | -0.33524344 | 7.60E-07 | 0.00770096 |
| AOF2     | 7.42455294 | 7.895433076 | -0.33527306 | 1.44E-13 | 1.65E-09   |
| LIG3     | 4.83083355 | 5.103243712 | -0.33551038 | 2.73E-10 | 3.03E-06   |
| PKP2     | 3.88437433 | 4.071625088 | -0.33601162 | 7.68E-09 | 8.28E-05   |
| RFXAP    | 4.37989638 | 4.566832781 | -0.33616978 | 2.20E-10 | 2.44E-06   |
| FDFT1    | 9.20014675 | 9.635928638 | -0.33676952 | 2.62E-11 | 2.95E-07   |
| BCL11B   | 4.19426553 | 4.629210807 | -0.3374702  | 6.87E-12 | 7.78E-08   |
| GABRA3   | 3.94439323 | 4.334496142 | -0.33789314 | 7.61E-15 | 8.83E-11   |
| SUV39H2  | 3.74477916 | 3.919708021 | -0.33793625 | 5.54E-11 | 6.19E-07   |
| CABYR    | 4.18423827 | 4.568252698 | -0.33799126 | 1.46E-07 | 0.00151616 |
| BCCIP    | 6.24525383 | 6.645897406 | -0.33806987 | 7.20E-10 | 7.91E-06   |
| KLRG1    | 4.48613458 | 4.684736949 | -0.33833904 | 7.96E-13 | 9.10E-09   |
| HIST1H4C | 9.96443281 | 10.44189717 | -0.33872618 | 1.28E-10 | 1.42E-06   |
| NPR3     | 3.9916951  | 4.296259157 | -0.33885021 | 5.21E-09 | 5.64E-05   |
| MAPK8    | 4.22111219 | 4.371799973 | -0.33912412 | 2.84E-10 | 3.14E-06   |
| SRPK1    | 6.61453785 | 6.941942037 | -0.33943467 | 2.67E-10 | 2.96E-06   |
| ZNF643   | 4.10857461 | 4.390037717 | -0.34009698 | 3.73E-12 | 4.23E-08   |
| CENPJ    | 4.3391811  | 4.666024256 | -0.3404192  | 3.28E-11 | 3.68E-07   |
| GNG4     | 6.73075094 | 7.474926529 | -0.34066656 | 1.42E-10 | 1.58E-06   |
| BRIP1    | 4.08590962 | 4.377397484 | -0.34088218 | 1.01E-10 | 1.13E-06   |
| CLGN     | 4.49080774 | 5.260188445 | -0.34108471 | 1.11E-11 | 1.26E-07   |
| KLRC3    | 4.86449442 | 5.710584237 | -0.34135559 | 5.39E-10 | 5.94E-06   |
| CXXC4    | 5.41801099 | 6.050581791 | -0.3416618  | 3.17E-11 | 3.56E-07   |
| KCNS3    | 5.11032772 | 5.74667505  | -0.34212981 | 8.73E-08 | 0.0009125  |
| DLEU2    | 4.68587535 | 4.92355529  | -0.34303337 | 1.87E-10 | 2.08E-06   |
| REPS2    | 5.03714109 | 5.421542138 | -0.34548525 | 3.98E-10 | 4.39E-06   |
| POLB     | 8.07566815 | 8.550668007 | -0.34591863 | 1.16E-11 | 1.31E-07   |

|           |            |             |             |          |            |
|-----------|------------|-------------|-------------|----------|------------|
| PTH2R     | 3.89686142 | 4.37163476  | -0.34658208 | 3.53E-16 | 4.13E-12   |
| WDR67     | 5.45398288 | 5.839264101 | -0.3466597  | 1.02E-10 | 1.13E-06   |
| C14orf93  | 4.44778109 | 4.653843937 | -0.34732394 | 3.51E-11 | 3.94E-07   |
| NCAPH     | 5.44599443 | 5.940709382 | -0.34740324 | 9.41E-11 | 1.05E-06   |
| PYCR1     | 5.99386295 | 6.333746123 | -0.34830897 | 5.00E-11 | 5.59E-07   |
| C16orf59  | 4.91402778 | 5.160156015 | -0.34980746 | 2.44E-11 | 2.74E-07   |
| TAF5      | 5.58231589 | 6.03132178  | -0.35002421 | 9.19E-12 | 1.04E-07   |
| FUT1      | 4.39091263 | 4.637428143 | -0.35028881 | 1.16E-09 | 1.27E-05   |
| VIPR2     | 4.63945777 | 5.066920162 | -0.35042257 | 4.84E-14 | 5.58E-10   |
| MYT1      | 4.7187164  | 5.17801262  | -0.35062067 | 2.90E-11 | 3.25E-07   |
| MYCN      | 4.74318299 | 4.909473565 | -0.35121295 | 3.42E-11 | 3.84E-07   |
| C16orf67  | 4.75028176 | 5.016178753 | -0.35137141 | 2.18E-11 | 2.45E-07   |
| RMND5A    | 5.12760139 | 5.396718034 | -0.35175703 | 4.59E-10 | 5.06E-06   |
| FABP6     | 4.08675909 | 4.636545017 | -0.35259906 | 2.46E-12 | 2.80E-08   |
| C10orf137 | 5.50504964 | 5.848238967 | -0.35363651 | 4.20E-10 | 4.64E-06   |
| ESPL1     | 5.78315693 | 6.29218383  | -0.35404998 | 1.15E-10 | 1.28E-06   |
| HMGB3     | 6.94753053 | 7.491883302 | -0.35499976 | 5.72E-13 | 6.55E-09   |
| NSMCE4A   | 6.8345674  | 7.275584912 | -0.35507608 | 2.70E-10 | 2.99E-06   |
| LAD1      | 4.58459493 | 4.827009508 | -0.35533882 | 1.91E-07 | 0.00197489 |
| MNX1      | 5.09819779 | 5.554479092 | -0.35540799 | 9.29E-13 | 1.06E-08   |
| CORO2A    | 3.95346502 | 4.369588514 | -0.35553501 | 1.34E-08 | 0.00014321 |
| ZNF804A   | 4.57419836 | 5.252259451 | -0.35626429 | 2.40E-09 | 2.61E-05   |
| HDAC2     | 8.40634781 | 8.896032446 | -0.3566327  | 7.95E-14 | 9.15E-10   |
| CCNF      | 4.78395959 | 5.047940272 | -0.35666929 | 7.82E-12 | 8.85E-08   |
| BCOR      | 5.05152659 | 5.562571367 | -0.35701264 | 1.79E-12 | 2.04E-08   |
| KLF12     | 4.55833246 | 4.740557214 | -0.35705875 | 1.94E-13 | 2.23E-09   |
| FAM60A    | 7.89485757 | 8.650698601 | -0.35792346 | 6.97E-11 | 7.78E-07   |
| SHANK2    | 4.38842561 | 4.585315271 | -0.35812878 | 9.32E-12 | 1.05E-07   |
| ARHGEF16  | 4.4302362  | 4.646541781 | -0.35920089 | 6.60E-10 | 7.25E-06   |
| DAB1      | 4.1470362  | 4.321864684 | -0.35953535 | 7.74E-12 | 8.77E-08   |
| AURKB     | 5.44293208 | 5.99378848  | -0.36017099 | 6.19E-11 | 6.91E-07   |
| MAP2K6    | 4.90310089 | 5.123787208 | -0.36111412 | 1.11E-12 | 1.27E-08   |
| RALGPS2   | 4.05887596 | 4.220240013 | -0.36249622 | 2.07E-12 | 2.35E-08   |
| KLHL23    | 6.72671695 | 7.296452249 | -0.36269743 | 4.62E-13 | 5.29E-09   |
| NET1      | 5.65811873 | 6.403039275 | -0.36463639 | 3.77E-11 | 4.23E-07   |
| SOX4      | 7.29263107 | 8.086938243 | -0.36557304 | 1.57E-13 | 1.80E-09   |
| HOOK1     | 4.52739227 | 4.91084651  | -0.36598905 | 6.43E-10 | 7.07E-06   |
| CDC14A    | 4.04976316 | 4.134872695 | -0.36677008 | 1.51E-13 | 1.73E-09   |
| CDC45L    | 5.43693677 | 6.046907194 | -0.36697509 | 8.43E-11 | 9.40E-07   |
| DCUN1D2   | 5.34846682 | 5.748745176 | -0.36701779 | 1.57E-13 | 1.80E-09   |
| PRSS16    | 3.84151846 | 4.126460205 | -0.36718936 | 9.31E-09 | 0.00010008 |
| GSDML     | 4.59095671 | 4.912503508 | -0.36881964 | 8.65E-12 | 9.79E-08   |
| PRAME     | 4.17487926 | 4.914034866 | -0.36913308 | 6.46E-12 | 7.32E-08   |
| POLQ      | 4.60701622 | 4.949032769 | -0.36994106 | 4.54E-12 | 5.14E-08   |
| NEK2      | 4.89403224 | 5.438922687 | -0.3708646  | 3.55E-11 | 3.97E-07   |
| RASL11B   | 4.94286859 | 5.833316104 | -0.37135908 | 3.42E-17 | 4.02E-13   |
| FXD3      | 4.55849702 | 5.246114394 | -0.37240317 | 1.03E-09 | 1.12E-05   |
| C1orf135  | 5.18350814 | 5.585735476 | -0.37247029 | 1.44E-12 | 1.65E-08   |
| SPINK5    | 4.40267198 | 4.807387214 | -0.37302142 | 5.47E-11 | 6.11E-07   |

|          |            |             |             |          |            |
|----------|------------|-------------|-------------|----------|------------|
| DNMT3B   | 4.9134054  | 5.354978541 | -0.37391657 | 3.17E-14 | 3.66E-10   |
| ORC6L    | 6.82907995 | 7.383543379 | -0.37406497 | 3.26E-13 | 3.74E-09   |
| FAM77C   | 4.79175204 | 5.267065931 | -0.37614667 | 4.67E-14 | 5.39E-10   |
| EXO1     | 5.23417159 | 5.848234546 | -0.37702137 | 4.23E-12 | 4.80E-08   |
| NR0B1    | 4.18115804 | 5.157453104 | -0.37776064 | 2.70E-08 | 0.00028628 |
| ZNF10    | 4.54795915 | 4.822702894 | -0.37816794 | 3.01E-15 | 3.50E-11   |
| PKMYT1   | 4.31845644 | 4.598016653 | -0.37831436 | 1.24E-13 | 1.42E-09   |
| FUT3     | 3.96774266 | 4.196156629 | -0.3785747  | 1.35E-13 | 1.55E-09   |
| BCL7A    | 5.46469299 | 5.999539121 | -0.37900483 | 1.05E-13 | 1.21E-09   |
| H2AFY2   | 5.19387611 | 5.792509783 | -0.37923617 | 2.45E-11 | 2.76E-07   |
| ERBB3    | 5.54018308 | 6.860574452 | -0.37972152 | 6.37E-13 | 7.28E-09   |
| PRSS8    | 3.96817115 | 4.426299041 | -0.38064245 | 8.56E-07 | 0.00866098 |
| CDC25A   | 4.97451979 | 5.266584549 | -0.38178179 | 2.39E-13 | 2.75E-09   |
| GPR63    | 4.09328235 | 4.244433749 | -0.38267964 | 1.01E-14 | 1.18E-10   |
| LRRC20   | 5.31632388 | 5.618361559 | -0.38309155 | 2.91E-14 | 3.36E-10   |
| PEO1     | 5.37760605 | 5.785011897 | -0.38437843 | 8.60E-13 | 9.82E-09   |
| ATAD5    | 5.09559636 | 5.384195664 | -0.38471763 | 2.73E-13 | 3.14E-09   |
| C20orf42 | 5.43200084 | 6.491510726 | -0.38914142 | 1.49E-11 | 1.69E-07   |
| RANBP1   | 6.26290641 | 6.570794865 | -0.38918919 | 3.69E-12 | 4.19E-08   |
| RBM35B   | 4.17474358 | 4.721773953 | -0.39215723 | 3.05E-07 | 0.00313208 |
| EDG4     | 4.53844632 | 4.791819697 | -0.3923041  | 2.29E-12 | 2.61E-08   |
| LOC81691 | 4.75966624 | 5.325843771 | -0.39288903 | 2.43E-15 | 2.83E-11   |
| TRAIP    | 4.48856526 | 4.756591415 | -0.39521345 | 1.46E-13 | 1.68E-09   |
| DOK4     | 4.28095214 | 4.473791171 | -0.39716062 | 4.01E-13 | 4.59E-09   |
| RAC3     | 4.29322012 | 4.666326785 | -0.39921546 | 2.60E-12 | 2.96E-08   |
| FGF9     | 4.77434617 | 5.546758078 | -0.40049681 | 2.09E-15 | 2.44E-11   |
| ORC1L    | 4.37440922 | 4.753477851 | -0.40229452 | 1.77E-12 | 2.02E-08   |
| MCM10    | 4.23869877 | 4.932611279 | -0.40267655 | 8.06E-15 | 9.35E-11   |
| PASK     | 4.74904691 | 5.032778258 | -0.40308461 | 9.47E-18 | 1.12E-13   |
| BCL11A   | 5.20878969 | 5.900075041 | -0.40365369 | 2.32E-14 | 2.68E-10   |
| MCM3APAS | 4.78244999 | 5.365650857 | -0.40427389 | 9.42E-17 | 1.11E-12   |
| RBM35A   | 3.90030897 | 4.631312748 | -0.4050661  | 6.58E-08 | 0.00069101 |
| ZNF492   | 4.79229123 | 5.055012465 | -0.40650863 | 3.85E-14 | 4.44E-10   |
| CDC25C   | 4.36009993 | 4.598585769 | -0.4066299  | 9.27E-12 | 1.05E-07   |
| FANCA    | 4.09267496 | 4.295984787 | -0.41197208 | 3.56E-15 | 4.15E-11   |
| RAD54L   | 4.95503565 | 5.39871261  | -0.41384463 | 1.59E-13 | 1.83E-09   |
| HOXD3    | 4.16967484 | 4.485322323 | -0.41686547 | 1.94E-13 | 2.23E-09   |
| STMN1    | 7.78423224 | 8.396763879 | -0.41738362 | 1.86E-15 | 2.17E-11   |
| PAK7     | 4.14649546 | 4.842780226 | -0.41835731 | 1.52E-16 | 1.78E-12   |
| TACSTD1  | 3.92961977 | 5.24712316  | -0.4195415  | 5.30E-10 | 5.84E-06   |
| ZNF248   | 5.40816318 | 5.921705089 | -0.42193017 | 3.60E-15 | 4.19E-11   |
| RANBP17  | 4.64960385 | 4.886017322 | -0.42608915 | 2.10E-12 | 2.39E-08   |
| PHF16    | 5.51140384 | 6.135036868 | -0.42698196 | 9.58E-17 | 1.12E-12   |
| MYCL1    | 4.87400728 | 5.167656214 | -0.42808779 | 6.40E-15 | 7.43E-11   |
| C1orf106 | 5.55818591 | 6.362082251 | -0.42874669 | 3.76E-15 | 4.37E-11   |
| KIFC1    | 5.64245941 | 6.185653514 | -0.42959649 | 3.62E-15 | 4.21E-11   |
| ZNF74    | 4.4411421  | 4.800743113 | -0.43610659 | 9.98E-18 | 1.18E-13   |
| MYB      | 4.12255984 | 4.726463065 | -0.43981556 | 8.46E-19 | 1.00E-14   |
| PLS1     | 4.65049632 | 5.640713117 | -0.45508801 | 5.30E-15 | 6.15E-11   |

|        |            |             |             |          |          |
|--------|------------|-------------|-------------|----------|----------|
| PLCB4  | 4.47109356 | 5.187874186 | -0.46627699 | 2.79E-24 | 3.34E-20 |
| DNA2L  | 4.32554838 | 4.77481105  | -0.47224701 | 4.44E-18 | 5.24E-14 |
| CNKSR1 | 4.29908303 | 4.570677232 | -0.48758361 | 1.37E-17 | 1.61E-13 |

**Supplemental Table S2 Potential candidates interact with CHI3L1 by liquid chromatography–mass spectrometry (LC-MS) assay**

| Identified Proteins                                                                                         | Accession Num | Molecular Weight |
|-------------------------------------------------------------------------------------------------------------|---------------|------------------|
| E9PL22_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=2 SV=1                              | E9PL22 (+1)   | 105 kDa          |
| ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2                                                  | P06733        | 47 kDa           |
| 1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1                                    | P63104        | 28 kDa           |
| 1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2                                         | P61981        | 28 kDa           |
| 1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1                                       | P62258        | 29 kDa           |
| LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1                                | Q08380        | 65 kDa           |
| TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2                                 | P02786        | 85 kDa           |
| BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3                       | P51572 (+1)   | 28 kDa           |
| J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1                              | J3QRD1 (+2)   | 45 kDa           |
| ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2                                                   | P04083        | 39 kDa           |
| G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3                       | P04406 (+1)   | 36 kDa           |
| PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1                          | P62333        | 44 kDa           |
| C1QBP_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP   | Q07021        | 31 kDa           |
| PRAF3_HUMAN PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=1 SV=1                                      | O75915        | 22 kDa           |
| SEC61B_HUMAN Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2               | P60468        | 10 kDa           |
| STML2_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1                      | Q9UJZ1        | 39 kDa           |
| M2OM_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3        | Q02978        | 34 kDa           |
| PGAM5_HUMAN Isoform 2 of Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 | Q96HS1-2      | 28 kDa           |
| 1433F_HUMAN 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4                                           | Q04917        | 28 kDa           |
| SRPRB_HUMAN Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3            | Q9Y5M8        | 30 kDa           |
| TSN_HUMAN Translin OS=Homo sapiens GN=TSN PE=1 SV=1                                                         | Q15631        | 26 kDa           |
| MARCS_HUMAN Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4               | P29966        | 32 kDa           |

SupplementalTable S3 Primers for RT-PCR

| Gene            | Forward Seq           | Reverse Seq           | Source        |
|-----------------|-----------------------|-----------------------|---------------|
| <b>Human</b>    |                       |                       |               |
| <i>RPL39</i>    | CAGCTTCCCTCCTCTTCCTT  | GCCAGGAATCGCTTAATCC   | Sigma-Aldrich |
| <i>CHI3L1</i>   | GTGAAGGCGTCTCAAACAGG  | CTTCCCGGTACTGGGACCA   | Sigma-Aldrich |
| <b>Mouse</b>    |                       |                       |               |
| <i>Chi3l1</i>   | GTACAAGCTGGTCTGCTACTT | (ATGTGCTAAGCATGTTGTCG | Sigma-Aldrich |
| <i>Lgals3bp</i> | TGCTGGTTCCAGGGACTCAA  | CCACCGGCCTCTGTAGAAGA  | Sigma-Aldrich |
| <i>Lgals3</i>   | AGACAGCTTTTCGCTTAACGA | GGGTAGGCACTAGGAGGAG   | Sigma-Aldrich |

| Commerical Primers | Source | Cat#   | GeneGlobe ID |
|--------------------|--------|--------|--------------|
| <b>Mouse</b>       |        |        |              |
| <i>18S rRNA</i>    | QIAGEN | 249900 | QT02448075   |
| <i>Ccl2</i>        | QIAGEN | 249900 | QT00167832   |
| <i>Arg1</i>        | QIAGEN | 249900 | QT00134288   |
| <i>Chil3 (Ym1)</i> | QIAGEN | 249900 | QT00108829   |
| <i>Il-10</i>       | QIAGEN | 249900 | QT00106169   |
| <i>Nos2</i>        | QIAGEN | 249900 | QT00068740   |
| <i>IL-1β</i>       | QIAGEN | 249900 | QT01048355   |

## Supplemental Methods

*Lentivirus production.* The expression vectors pLenti6.3-GFP, -p53DN, -myr-AKT, -CHI3L1, and -CHI3L1\_V5 were generated by cloning the respective open reading frame (ORF) into the vector using the Gateway Cloning System. The pLKO.1 target gene set for the mouse *Chi3l1* gene was purchased from Sigma-Aldrich. Lentiviruses were generated in 293T cells with a packaging system including pCMVR8.74, pMD2.0G, and pRSV-Rev according to the manufacturer's protocol (Invitrogen). Lentiviruses from the medium of infected 293T cells were concentrated to a final concentration of 13% of polyethylene glycol (PEG)-8000 and 0.5 M NaCl (1). Target cells were infected with lentivirus with 1:1000 dilution of polybrene (Sigma-Aldrich, Cat# TR-1003). Gene expression was confirmed by qRT-PCR and immunoblotting.

*Macrophage and T cell depletion.* Three days after intracranial implantation of tumor cells, 100  $\mu$ L/20 g per mouse of Chodrosome or control liposome was injected into animals through the tail vein. Clodronate liposomes or control liposomes were injected every three days for a total of eight times. Blood was collected after four injections, and monocytes were treated with RBC Lysis Buffer (Invitrogen, Cat# 00-4300-54), stained with F4/80-APC (Invitrogen, Cat# 47-4801-80) and CD11b-PE (BD Biosciences, Cat# 553311), and analyzed by flow cytometry.

For T cell depletion, one day after intracranial implantation of tumor cells, 200  $\mu$ g/20 g per mouse of IgG or anti-mouse CD4 and anti-mouse CD8 antibodies were injected into animals through intraperitoneal injection. IgG or anti-mouse CD4 and anti-mouse CD8 antibodies were injected every three days for a total of eight times. Brain tumors and spleens were collected for cell isolation and subsequent staining with CD45-PerCP-Cy5.5 (Cat# 103132, 30-F11), CD4-APC-Cy7 (Cat# 100414, GK1.5), CD8a-BV711 (Cat# 100747, 53-6.7), and Live/Dead Fixable Blue Dead Cell Stain Kit for UV excitation (Invitrogen, Cat# L34961), followed by flow cytometry analysis.

*Peptide delivery to mouse brain in Situ.* For intracranial xenograft tumor models treated with peptides, mice were implanted with a guide screw prior to intracranial injection. To install the screw, mice were anesthetized by intraperitoneal (IP) injection with ketamine/xylazine solution (1.75 mL of 100 mg/mL ketamine and 0.25 mL of 100 mg/mL xylazine in 8 mL sterile water) at a dosage of 100  $\mu$ L/20 g body weight. The screw was covered by

sealing the skin, and mice were allowed to recover for one week before intracranial implantation. GL261 cells overexpressing CHI3L1 ( $1 \times 10^5$ ) were injected in 5  $\mu$ L of DPBS containing 20  $\mu$ M of either scrambled control peptide (SCP) or Gal3BP mimetic peptide (GMP). SCP (20  $\mu$ M) or GMP (20  $\mu$ M) was subsequently given once every 3 days with a total of seven times by intracranial injection via the guide screw.

*Co-Immunoprecipitation (Co-IP) and mass spectrometry (MS).* To confirm Co-IP experiments in TS603 cells by immunoblotting, the magnetic beads of protein G (Bio-Rad, Cat# 161-4023) were used following the manufacturer's protocol. The following antibodies were used for Co-IP confirmation experiments: Rabbit anti-V5 (Abcam, Cat# ab9116), Mouse anti-Galectin-3 (Santa Cruz Biotechnology, Cat# SC-32790), Rabbit anti-Galectin-3BP (Proteintech, Cat# 10281-1-AP), Mouse IgG (Santa Cruz Biotechnology, Cat# SC-2025), and Rabbit IgG (R&D Systems, Cat# AF008). For *in vivo* THP-1 cell or *in vitro* recombinant protein Co-IP experiments, additional following antibodies were used: Mouse anti-CHI3L1 (Santa Cruz Biotechnology, Cat# SC-393590), Rat anti-Galectin-3 (Santa Cruz Biotechnology, Cat# SC-23938), anti-Galectin-3BP (Santa Cruz Biotechnology, Cat# SC-374541), Rabbit anti-CHI3L1 (Cell Signaling Technology, Cat#47066), and Rat IgG (BioXCell, Cat# BE0090).

For protein identification by MS, the short gel fractionation method was used for sample preparation (2). The SDS-PAGE gel was run at 150 V for about 30 min until all samples fully migrated into the resolving gel. The gel was washed with ultrapure water twice, stained with Coomassie Blue for 4 hours at RT, and then de-stained until the bands appeared. The bands were excised and placed in 1.5 mL Eppendorf microcentrifuge tubes containing 200  $\mu$ L of ultrapure water. The samples were digested with Sequencing Grade TPCK-Treated Trypsin (Promega, Cat# V511A) followed by liquid chromatography (LC) (Dionex, nanoLC; NEW Objective, nano-ESI) separation and MS (ThermoFisher, LTQ XL linear ion trap) analysis. MS results were searched using MASCOT (Matrix Sciences) and returned using Scaffold (Proteome Software, Inc.). Only extracellular and cell membrane-associated proteins (Table S2) from the LC-MS list were used for correlation analysis with CHI3L1.

*Immunoblotting (IB), Immunohistochemistry (IHC), and Immunofluorescence (IF).* The antibodies used for IB were purchased from Cell Signaling Technology unless otherwise noted: Phospho-Akt (Thr308; Cat# 4056; RRID: AB\_331163), Phospho-Akt (Ser 473; Cat# 9271; RRID: AB\_329825), AKT (Cat# 9272; RRID: AB\_329827), Phospho-S6 Ribosomal Protein (Ser235/236; Cat# 4858S; RRID: AB\_916156), Phospho-NF- $\kappa$ B p65 (Ser536; Cat# 3033; RRID: AB\_331284), NF- $\kappa$ B p65 (Cat# 8242S; RRID: AB\_10859369), Phospho-C/EBP $\beta$  (Thr235;

Cat# 3084; RRID: AB\_2260359), Phospho-mTOR (Ser2448; Cat# 5536; RRID: AB\_10691552), C/EBP  $\beta$  (Santa Cruz, Cat# sc-150; RRID: AB\_2260363), p53 (Santa Cruz, Cat# sc-6243; RRID: AB\_653753),  $\beta$ -Actin (Sigma-Aldrich, Cat# A2228; RRID: AB\_476697), and Vinculin (Santa Cruz, Cat# sc-25336; RRID: AB\_628438). The following antibodies were used for IB, IHC, and/or IF: Galectin-3 (Santa Cruz, Cat# sc-32790; RRID: AB\_627657), Lgals3bp (Galectin-3BP; Proteintech; Cat# 10281-1-AP; RRID: AB\_2137066), CHI3L1 (Santa Cruz, Cat# sc-30465; RRID: AB\_2081268), and V5 (Abcam, Cat# ab9116; RRID: AB\_307024). The following antibodies were used for IF staining: TMEM119 (Proteintech; Cat# 27585-1-AP), P2Y12 (ANASPEC; Cat# AS-55043A), F4/80 (Invitrogen; Cat# MF48000), CD49D (Invitrogen; Cat# PA5-20599), CD206 (Invitrogen; Cat# MA5-16871), Alexa Fluor 594 donkey anti-rabbit IgG (Invitrogen; Cat# A21207; RRID: AB\_141637), Alexa Fluor 594 donkey anti-mouse IgG (Invitrogen; Cat# A21203; RRID: AB\_141633), Cy3 AffiniPure Donkey anti-Goat IgG (Jackson Immuno Research; Cat# 705-165-147; RRID: AB\_2307351), Alexa Fluor 488 AffiniPure Donkey anti-Mouse IgG (Jackson Immuno Research; Cat# 715-545-151; RRID: AB\_2341099), Alexa Fluor 488 AffiniPure Donkey anti-Goat IgG (Jackson Immuno Research; Cat# 705-545-147; RRID: AB\_2336933), and Alexa Fluor 488 donkey anti-rabbit IgG (Invitrogen; Cat# A21206; RRID: AB\_2535792).

*Magnetic resonance imaging (MRI).* **Anesthesia for in vivo MRI:** All mice received general inhalation anesthesia with Isoflurane for in vivo brain imaging. Mice were placed in a clear plexiglass anesthesia induction box that allowed unimpeded visual monitoring of the animals. Induction was achieved by administration of 3% Isoflurane mixed with oxygen for a few minutes. Depth of anesthesia was monitored by toe reflex (extension of limbs, spine positioning) and respiration rate. Once the plane of anesthesia was established, it was maintained with 1-2% Isoflurane in oxygen via a nose cone, and the mouse was transferred to the animal bed for imaging. Respiration was monitored using a pneumatic sensor placed between the animal bed and the mouse's abdomen, rectal temperature was measured with a fiberoptic sensor, and core temperature was maintained at  $36.8 \pm 0.2^\circ\text{C}$  with a feedback-controlled warm air source (SA Instruments). **In vivo MRI Acquisition:** In vivo MRI brain image was carried out using a Bruker BioSpec 70/30 USR spectrometer (Bruker BioSpin MRI) operating at 7-Tesla field strength, equipped with an actively shielded B-GA12S2 gradient system with 440 mT/m gradient strength and slew rate of 3440 T/m/s, as well as a quadrature radiofrequency volume coil with an inner diameter of 35 mm. Multi-planar  $T_2$ -weighted anatomical imaging of 11 to 21 slices (depending on tumor size and to cover the whole brain volume) was acquired with Rapid Imaging with Refocused Echoes (RARE) pulse sequence with the

following parameters: field of view (FOV) = 2.0 cm, matrix = 256 × 256, slice thickness = 0.6 mm, in-plane resolution = 78 μm × 78 μm, RARE factor = 8, echo time (TE) = 12 msec, effective echo time (TE) = 48 msec, repetition time (TR) = 1600 msec, and flip angle (FA) = 180°. **Volumetric Analysis of T<sub>2</sub>-weighted MRI:** The multi-planar T<sub>2</sub>-weighted RARE images were exported to DICOM format and analyzed by blinded independent observers using the open-source ITK-SNAP (<http://www.itksnap.org>) brain segmentation software (3). Tumor volume was defined as areas of hyperintensity; hemorrhage volume was defined as areas of hypointensity.

*Flow cytometry and CyTOF.* The antibodies used for flow cytometry were purchased from BioLegend unless otherwise noted: CD45-PerCP-Cy5.5 (Cat# 103132, 30-F11), CD3-APC (Cat# 100236, 17A2), CD4-APC-Cy7 (Cat# 100414, GK1.5), CD8a-BV711 (Cat# 100747, 53-6.7), CD25-BV650 (Cat# 102037, PC61), NK1.1-PE (Cat# 108708, PK136), CD127-PE-Dazzle 594 (Cat# 135032, A7R34), PD-1-PE (Cat# 135206, 29F.1A12), PD-L1-BV421 (Cat# 124315, 10F.9G2), CTLA-4-PE-Dazzle 594 (Cat# 106318, UC10-4B9), CD14-PE (Cat# 123310, Sa14-2), Ly-6G-BV421 (Cat# 127627, 1A8), Ly-6C-BV711 (Cat# 128037, HK1.4), MHC II-APC-Cy7 (Cat# 107628, M5/114.15.2), CD11b-PE-Cy7 (Cat# 101216, M1/70), F4/80-APC (Cat# 123116, BM8), CD68-BV421 (Cat# 137017, FA-11), CD206-PE (Cat# 141706, C068C2), iNOS-APC-eFluor 780 (Thermo Fisher Scientific, Cat# 47-5920-82, CXNFT), Arginase 1-APC (Thermo Fisher Scientific, Cat# 17-3697-82, A1exF5), and Live/Dead Fixable Blue Dead Cell Stain Kit for UV excitation (Invitrogen, Cat# L34961).

For CyTOF, 500 mM of Rh103 intercalator (Fluidigm, Cat# 201103A) was used to stain dead cells (10 min at RT), followed by incubation with 5 μL of FcX-Block (BioLegend, Cat# 422302) for an additional 10 min at RT. Then a cocktail of surface marker antibodies was added, and samples were incubated for 30 min at RT. All CyTOF antibodies were commercially available and purchased directly from the CyTOF Core-Lederer Lab (Brigham Women's Hospital, Harvard Medical School) with conjugated metals (<http://ledererlab.bwh.harvard.edu/cytof-core/>). Samples were washed twice with 500 μL of CyTOF staining buffer (CSB; 500 mL low-barium PBS containing 2.5 g BSA [Sigma-Aldrich, Cat# A3059] and 100 mg sodium azide [Sigma-Aldrich, Cat# 71289]). Cells were then resuspended in 500 μL of FoxP3 fix/perm (ThermoFisher, Cat# 00-5523) and incubated for 45 min at RT. After cells were washed twice with 1 mL of FoxP3 permeabilization buffer (ThermoFisher, Cat# 00-5523), a cocktail of intracellular marker antibodies was added to each sample and incubated for 45 min at RT. Cells were washed twice with 500 μL of CSB followed by incubation in 500 μL of 1.6% paraformaldehyde for 10 min at RT. Cells were pelleted and resuspended in 500

μL of CSB. Prior to the acquisition, samples were pelleted, resuspended in 500 μL of CSB containing 125 μM iridium intercalator (Fluidigm, Cat# 201192A), and incubated for 20 min at RT. Cells were washed twice with 500 μL of CSB, twice with 500 μL of water (Fluidigm, Cat# 201069), and resuspended in water at [a final concentration of]  $\sim 5 \times 10^5$  cells/mL. Then EQ beads (Fluidigm, Cat# 201078) were added to samples (1:1000 dilution) for normalization, followed by acquisition on a Helios2 CyTOF system (Fluidigm).

*Clinical GBM datasets analysis.* TCGA GBM datasets include gene mutations, copy number, gene expression, proteomics (RPPA), tumor subtypes, and patient survival information (<https://tcga-data.nci.nih.gov>). Data from 10 normal and 371 IDH wild-type GBM samples were analyzed. Wilcoxon rank-sum tests were used to examine the significance of the differences between groups (**Figure 1, M and O; Figure 5G; Figure 7E; Supplemental Figure 1, H and I; Supplemental Figure 3N; Supplemental Figure 5E**). Spearman's tests were used to assess the significance of the correlation between groups (**Figure 1N; Figure 4D; Supplemental Figure 4D**). A log-rank test was used to examine the significance of patient overall survival (**Supplemental Figure 1J**).

Regarding correlation analysis between gene expression (*CHI3L1*, *LGALS3*, and *LGALS3BP*) and GBM patient response to anti-PD-1 treatment, a published clinical dataset contains RNA-seq-based gene expression filing from 16 patients with one or more biospecimens before treatment with anti-PD-1 inhibitors (nivolumab or pembrolizumab) (4). The gene expression mean was used for patients with more than one biospecimen for RNA-seq. Gene expression was ranked and used to separate patients into two groups with equal size, designated as high and low expression groups, for each gene (**Supplemental Figure 7J**). The number of patients in the group with a combination of genes with high and low expression is counted by taking the intersection of patients in the corresponding high/low gene expression groups. The anti-PD-1 treatment response rate in each patient group is calculated as the number of positive responders over the total number of patients in the group (**Figure 10A**).

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