|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Enrichment FDR** | **Genes in list** | **Total genes** | **Functional Category** | **Genes** |
| 3.14E-10 | 16 | 1018 | Positive regulation of cell differentiation | SYK LPL IGF1 SYT1 APOB IL1B TGFBR2 NTN1 ZBTB16 CXCR4 AP3B1 SCARB2 ADAMTS9 ADIPOQ PRKD1 VEGFA |
| 1.95E-09 | 17 | 1433 | Positive regulation of developmental process | VEGFA IL1B SYK LPL IGF1 SYT1 APOB ZBTB16 TGFBR2 NTN1 CXCR4 AP3B1 SCARB2 ADAMTS9 CDK1 ADIPOQ PRKD1 |
| 4.64E-09 | 21 | 2763 | Regulation of developmental process | VEGFA RHOU IL1B SYK LPL IGF1 SYT1 APOB ZBTB16 TGFBR2 ADIPOQ NTN1 HNF4A LAMA1 CXCR4 AP3B1 SCARB2 SPTA1 ADAMTS9 CDK1 PRKD1 |
| 8.49E-09 | 19 | 2220 | Vesicle-mediated transport | SYT1 RHOU SYK CACNG2 ANK1 VEGFA ADIPOQ AP3B1 SCARB2 TGFBR2 CADPS ADAMTS9 PRKD1 IL1B IGF1 APOB KIF11 VAV2 SPTA1 |
| 1.05E-07 | 17 | 1954 | Regulation of cell differentiation | SYK LPL IGF1 SYT1 APOB IL1B TGFBR2 ADIPOQ NTN1 ZBTB16 CXCR4 AP3B1 SCARB2 ADAMTS9 PRKD1 VEGFA CDK1 |
| 1.14E-07 | 12 | 769 | Endocytosis | SYT1 RHOU CACNG2 VEGFA ADIPOQ SCARB2 TGFBR2 SYK IL1B APOB VAV2 PRKD1 |
| 1.14E-07 | 11 | 604 | Positive regulation of kinase activity | MAP3K1 PRKD1 VEGFA IL1B ADIPOQ VAV2 TGFBR2 SYK IGF1 CXCR4 CDK1 |
| 1.14E-07 | 11 | 603 | Blood vessel morphogenesis | VEGFA IL1B APOB LAMA1 CXCR4 VAV2 TGFBR2 ADAMTS9 SYK PRKD1 COL4A1 |
| 2.13E-07 | 17 | 2138 | Regulation of multicellular organismal development | VEGFA IL1B SYK IGF1 SYT1 ZBTB16 TGFBR2 ADIPOQ NTN1 HNF4A LAMA1 CXCR4 AP3B1 SCARB2 ADAMTS9 CDK1 PRKD1 |
| 2.13E-07 | 17 | 2139 | Movement of cell or subcellular component | VEGFA CXCR4 IL1B KIF11 IGF1 SYK ADIPOQ NTN1 APOB LAMA1 AP3B1 VAV2 TGFBR2 ADAMTS9 PRKD1 SPTA1 CDK1 |
| 2.25E-07 | 12 | 860 | Tube morphogenesis | VEGFA IL1B NTN1 APOB LAMA1 CXCR4 VAV2 TGFBR2 ADAMTS9 SYK PRKD1 COL4A1 |
| 2.25E-07 | 13 | 1077 | Circulatory system development | VEGFA IL1B TGFBR2 IGF1 APOB LAMA1 CXCR4 VAV2 ADAMTS9 SYK CDK1 PRKD1 COL4A1 |
| 2.50E-07 | 12 | 887 | Import into cell | SYT1 RHOU CACNG2 VEGFA ADIPOQ SCARB2 TGFBR2 SYK IL1B APOB VAV2 PRKD1 |
| 2.50E-07 | 11 | 687 | Blood vessel development | VEGFA IL1B APOB LAMA1 CXCR4 VAV2 TGFBR2 ADAMTS9 SYK PRKD1 COL4A1 |
| 2.50E-07 | 11 | 682 | Positive regulation of transferase activity | MAP3K1 PRKD1 VEGFA IL1B ADIPOQ VAV2 TGFBR2 SYK IGF1 CXCR4 CDK1 |
| 3.34E-07 | 11 | 715 | Vasculature development | VEGFA IL1B APOB LAMA1 CXCR4 VAV2 TGFBR2 ADAMTS9 SYK PRKD1 COL4A1 |
| 3.58E-07 | 11 | 724 | Cardiovascular system development | VEGFA IL1B APOB LAMA1 CXCR4 VAV2 TGFBR2 ADAMTS9 SYK PRKD1 COL4A1 |
| 5.04E-07 | 7 | 177 | Positive regulation of developmental growth | IGF1 SYT1 NTN1 CXCR4 TGFBR2 CDK1 VEGFA |
| 5.66E-07 | 11 | 765 | Regulation of cell adhesion | SYK IGF1 VEGFA CXCR4 IL1B TGFBR2 ADIPOQ LAMA1 ZBTB16 AP3B1 SPTA1 |
| 7.26E-07 | 18 | 2785 | Anatomical structure morphogenesis | VEGFA RHOU IL1B SYT1 ADIPOQ NTN1 APOB HNF4A LAMA1 ZBTB16 CXCR4 VAV2 TGFBR2 SPTA1 ADAMTS9 SYK PRKD1 COL4A1 |
| 7.26E-07 | 14 | 1506 | Cell migration | VEGFA CXCR4 IL1B IGF1 SYK ADIPOQ NTN1 LAMA1 VAV2 TGFBR2 ADAMTS9 PRKD1 APOB CDK1 |
| 7.26E-07 | 3 | 4 | Positive regulation of NK T cell differentiation | ZBTB16 AP3B1 TGFBR2 |
| 1.22E-06 | 12 | 1062 | Tube development | VEGFA IL1B NTN1 APOB LAMA1 CXCR4 VAV2 TGFBR2 ADAMTS9 SYK PRKD1 COL4A1 |
| 1.22E-06 | 18 | 2905 | Regulation of localization | RHOU SYT1 VEGFA SYK CACNG2 IGF1 APOB IL1B ADIPOQ NTN1 HNF4A LAMA1 CXCR4 TGFBR2 ADAMTS9 LPL PRKD1 CDK1 |
| 1.37E-06 | 19 | 3354 | Macromolecule localization | RHOU ANK1 CACNG2 APOB IL1B CDK1 ADIPOQ HNF4A ZBTB16 AP3B1 SCARB2 TGFBR2 CADPS ADAMTS9 SYK LPL PRKD1 IGF1 IDE |
| 1.37E-06 | 15 | 1921 | Locomotion | VEGFA CXCR4 IL1B IGF1 SYK ADIPOQ NTN1 APOB LAMA1 VAV2 TGFBR2 ADAMTS9 PRKD1 SPTA1 CDK1 |
| 1.37E-06 | 22 | 4671 | Cellular developmental process | RHOU CXCR4 SYK LPL IGF1 SYT1 APOB VEGFA IL1B TGFBR2 ADIPOQ NTN1 HNF4A LAMA1 ZBTB16 AP3B1 SCARB2 SPTA1 ADAMTS9 CDK1 PRKD1 COL4A1 |
| 1.37E-06 | 15 | 1911 | Positive regulation of multicellular organismal process | VEGFA IL1B SYK IGF1 SYT1 ZBTB16 TGFBR2 ADIPOQ NTN1 CXCR4 AP3B1 SCARB2 CDK1 LPL PRKD1 |
| 1.37E-06 | 17 | 2592 | Nitrogen compound transport | RHOU SYT1 CACNG2 IL1B ADIPOQ APOB HNF4A AP3B1 SCARB2 TGFBR2 CADPS ADAMTS9 SYK LPL PRKD1 IGF1 IDE |
| 1.48E-06 | 18 | 2988 | Protein localization | RHOU ANK1 CACNG2 IL1B CDK1 ADIPOQ APOB HNF4A ZBTB16 AP3B1 SCARB2 CADPS ADAMTS9 SYK LPL PRKD1 IGF1 IDE |

Table S1 Gene Ontology Enrichment analysis of 34 T2DM genes identified by diffusion algorithm on PPI network from query genes of PD

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **ID** | **adj.P.Val** | **P.Value** | **t** | **B** | **logFC** | **display name** | **Column1** |
| 227816\_at | 0.153646 | 0.000594 | -3.91808 | -0.25253 | -0.85467 | NTN1 | netrin 1 |
| 225927\_at | 0.1912905 | 0.001465 | 3.565465 | -1.02044 | 0.511316 | MAP3K1 | mitogen-activated protein kinase kinase kinase 1 |
| 234220\_at | 0.2945571 | 0.007704 | -2.89293 | -2.42452 | -1.36373 | CADPS | calcium dependent secretion activator |
| 217028\_at | 0.3157817 | 0.011404 | 2.726779 | -2.75269 | 1.113953 | CXCR4 | C-X-C motif chemokine receptor 4 |
| 207087\_x\_at | 0.3157817 | 0.011522 | -2.72237 | -2.76128 | -1.14525 | ANK1 | ankyrin 1 |
| 208353\_x\_at | 0.3277474 | 0.013377 | -2.6581 | -2.88555 | -0.94251 | ANK1 | ankyrin 1 |
| 205389\_s\_at | 0.3293293 | 0.013599 | -2.65097 | -2.89925 | -1.3106 | ANK1 | ankyrin 1 |
| 204814\_at | 0.3293881 | 0.013637 | -2.64976 | -2.90156 | -0.86775 | CADPS | calcium dependent secretion activator |
| 209201\_x\_at | 0.3352493 | 0.014577 | 2.620841 | -2.95689 | 0.897217 | CXCR4 | C-X-C motif chemokine receptor 4 |
| 211919\_s\_at | 0.3570433 | 0.018195 | 2.523633 | -3.14047 | 0.801451 | CXCR4 | C-X-C motif chemokine receptor 4 |
| 205391\_x\_at | 0.378696 | 0.022359 | -2.43189 | -3.31016 | -1.67367 | ANK1 | ankyrin 1 |
| 205390\_s\_at | 0.3831148 | 0.024397 | -2.3926 | -3.38172 | -1.69523 | ANK1 | ankyrin 1 |
| 205880\_at | 0.385206 | 0.025323 | 2.375737 | -3.41221 | 0.422647 | PRKD1 | protein kinase D1 |
| 226068\_at | 0.4068981 | 0.031453 | 2.276531 | -3.58897 | 0.968114 | SYK | spleen associated tyrosine kinase |
| 203327\_at | 0.4461579 | 0.045077 | 2.107336 | -3.8793 | 0.256321 | IDE | insulin degrading enzyme |
| 244023\_at | 0.4524469 | 0.046875 | 2.088571 | -3.91058 | 0.482342 | SYK | spleen associated tyrosine kinase |
| 203999\_at | 0.5058075 | 0.067349 | -1.91065 | -4.19748 | -1.18048 | SYT1 | synaptotagmin 1 |
| 208352\_x\_at | 0.5106699 | 0.069504 | -1.89481 | -4.22214 | -1.07838 | ANK1 | ankyrin 1 |
| 231534\_at | 0.5200402 | 0.074854 | 1.857259 | -4.28 | 0.958374 | CDK1 | cyclin dependent kinase 1 |
| 1555816\_at | 0.5375479 | 0.083064 | 1.803918 | -4.3607 | 1.221512 | THSD4 | thrombospondin type 1 domain containing 4 |
| 1568604\_a\_at | 0.5431287 | 0.085479 | -1.78909 | -4.38282 | -1.21021 | CADPS | calcium dependent secretion activator |
| 240363\_at | 0.5479406 | 0.087991 | -1.77405 | -4.40512 | -0.33543 | ANK1 | ankyrin 1 |
| 214495\_at | 0.5495015 | 0.089085 | -1.76761 | -4.41463 | -0.66776 | CACNG2 | calcium voltage-gated channel auxiliary subunit gamma 2 |
| 203998\_s\_at | 0.5659647 | 0.102548 | -1.69344 | -4.52218 | -1.12041 | SYT1 | synaptotagmin 1 |
| 210512\_s\_at | 0.5676699 | 0.103869 | 1.686611 | -4.53189 | 0.683731 | VEGFA | vascular endothelial growth factor A |
| 211527\_x\_at | 0.5758421 | 0.109475 | 1.658432 | -4.57169 | 0.80563 | VEGFA | vascular endothelial growth factor A |
| 1568603\_at | 0.57853 | 0.111896 | -1.64664 | -4.58819 | -1.27551 | CADPS | calcium dependent secretion activator |
| 210513\_s\_at | 0.5979332 | 0.124206 | 1.589753 | -4.66645 | 0.433301 | VEGFA | vascular endothelial growth factor A |
| 203549\_s\_at | 0.6210264 | 0.146226 | 1.498687 | -4.78711 | 0.49257 | LPL | lipoprotein lipase |
| 217496\_s\_at | 0.6259821 | 0.149598 | -1.48575 | -4.80378 | -0.27144 | IDE | insulin degrading enzyme |
| 207540\_s\_at | 0.6266597 | 0.150044 | 1.484054 | -4.80595 | 0.905116 | SYK | spleen associated tyrosine kinase |
| 214851\_at | 0.6320059 | 0.154089 | 1.468876 | -4.82534 | 0.738072 | HNF4A | hepatocyte nuclear factor 4 alpha |
| 205883\_at | 0.6384503 | 0.159693 | 1.448366 | -4.85127 | 0.426936 | ZBTB16 | zinc finger and BTB domain containing 16 |
| 233785\_at | 0.652038 | 0.171405 | -1.4073 | -4.90227 | -0.6538 | ADAMTS9 | ADAM metallopeptidase with thrombospondin type 1 motif 9 |
| 223169\_s\_at | 0.6626077 | 0.181 | -1.37528 | -4.94118 | -0.46783 | RHOU | ras homolog family member U |
| 201646\_at | 0.6691008 | 0.187257 | -1.35512 | -4.9653 | -0.25125 | SCARB2 | scavenger receptor class B member 2 |
| 210559\_s\_at | 0.6783793 | 0.197537 | 1.323103 | -5.00296 | 0.650968 | CDK1 | cyclin dependent kinase 1 |
| 229942\_at | 0.6873337 | 0.20776 | -1.29252 | -5.03821 | -0.86217 | BNC2 | basonuclin 2 |
| 226814\_at | 0.6954177 | 0.218217 | 1.262413 | -5.07222 | 0.996885 | ADAMTS9 | ADAM metallopeptidase with thrombospondin type 1 motif 9 |
| 222346\_at | 0.704342 | 0.227092 | 1.237713 | -5.09959 | 0.608467 | LAMA1 | laminin subunit alpha 1 |
| 203213\_at | 0.7196793 | 0.246557 | 1.185981 | -5.15539 | 0.590272 | CDK1 | cyclin dependent kinase 1 |
| 206937\_at | 0.7231758 | 0.250076 | -1.17696 | -5.1649 | -0.77288 | SPTA1 | spectrin alpha, erythrocytic 1 |
| 205536\_at | 0.7277824 | 0.256381 | -1.16102 | -5.18156 | -0.24397 | VAV2 | vav guanine nucleotide exchange factor 2 |
| 226063\_at | 0.7453628 | 0.279068 | -1.10595 | -5.23753 | -0.25213 | VAV2 | vav guanine nucleotide exchange factor 2 |
| 1552626\_a\_at | 0.7481545 | 0.282633 | 1.097593 | -5.24581 | 0.309088 | TMEM163 | transmembrane protein 163 |
| 212171\_x\_at | 0.7573854 | 0.297472 | 1.063603 | -5.2789 | 0.288853 | VEGFA | vascular endothelial growth factor A |
| 223168\_at | 0.7580185 | 0.298558 | -1.06116 | -5.28124 | -0.23352 | RHOU | ras homolog family member U |
| 217705\_at | 0.7623647 | 0.304063 | 1.048889 | -5.29293 | 0.569186 | PRKD1 | protein kinase D1 |
| 238478\_at | 0.765761 | 0.310269 | -1.03524 | -5.30579 | -0.23298 | BNC2 | basonuclin 2 |
| 211577\_s\_at | 0.7666318 | 0.31159 | -1.03236 | -5.30848 | -0.49514 | IGF1 | insulin like growth factor 1 |
| 220287\_at | 0.7676662 | 0.313434 | 1.028354 | -5.31222 | 0.417335 | ADAMTS9 | ADAM metallopeptidase with thrombospondin type 1 motif 9 |
| 203141\_s\_at | 0.7699816 | 0.317434 | -1.01972 | -5.32023 | -0.20282 | AP3B1 | adaptor related protein complex 3 beta 1 subunit |
| 244099\_at | 0.7736137 | 0.324147 | -1.00539 | -5.33337 | -0.43973 | CACNG2 | calcium voltage-gated channel auxiliary subunit gamma 2 |
| 230722\_at | 0.7765809 | 0.328806 | -0.99557 | -5.34229 | -0.24442 | BNC2 | basonuclin 2 |
| 207175\_at | 0.7799362 | 0.335589 | 0.981444 | -5.35497 | 0.342458 | ADIPOQ | adiponectin, C1Q and collagen domain containing |
| 233950\_at | 0.7945945 | 0.361941 | -0.92832 | -5.40116 | -0.51231 | CADPS | calcium dependent secretion activator |
| 234323\_at | 0.7951462 | 0.362938 | -0.92636 | -5.40282 | -0.44986 | THSD4 | thrombospondin type 1 domain containing 4 |
| 201647\_s\_at | 0.8068949 | 0.386913 | -0.8803 | -5.44085 | -0.17525 | SCARB2 | scavenger receptor class B member 2 |
| 203548\_s\_at | 0.8068949 | 0.387075 | 0.879995 | -5.4411 | 0.351363 | LPL | lipoprotein lipase |
| 208429\_x\_at | 0.8086774 | 0.390329 | 0.87389 | -5.446 | 0.419329 | HNF4A | hepatocyte nuclear factor 4 alpha |
| 205067\_at | 0.8134366 | 0.397492 | 0.860566 | -5.45659 | 0.561664 | IL1B | interleukin 1 beta |
| 223579\_s\_at | 0.8226341 | 0.41792 | -0.82338 | -5.48534 | -0.49464 | APOB | apolipoprotein B |
| 1555517\_at | 0.8333411 | 0.441588 | -0.78169 | -5.51615 | -0.40482 | GABRG3 | gamma-aminobutyric acid type A receptor gamma3 subunit |
| 39402\_at | 0.8413583 | 0.459259 | 0.751447 | -5.53754 | 0.341057 | IL1B | interleukin 1 beta |
| 209542\_x\_at | 0.843977 | 0.465592 | -0.74078 | -5.5449 | -0.3704 | IGF1 | insulin like growth factor 1 |
| 241072\_s\_at | 0.8525873 | 0.48481 | 0.708906 | -5.56628 | 0.438023 | IGF1 | insulin like growth factor 1 |
| 230772\_at | 0.8555178 | 0.491158 | -0.69854 | -5.57304 | -0.2751 | HNF4A | hepatocyte nuclear factor 4 alpha |
| 208944\_at | 0.856663 | 0.493519 | 0.694704 | -5.57551 | 0.14603 | TGFBR2 | transforming growth factor beta receptor 2 |
| 214832\_at | 0.8585881 | 0.496751 | -0.68947 | -5.57887 | -0.18725 | HNF4A | hepatocyte nuclear factor 4 alpha |
| 1555817\_s\_at | 0.862197 | 0.506272 | -0.67416 | -5.58855 | -0.48355 | THSD4 | thrombospondin type 1 domain containing 4 |
| 215754\_at | 0.8626493 | 0.508321 | 0.670887 | -5.5906 | 0.126581 | SCARB2 | scavenger receptor class B member 2 |
| 214786\_at | 0.8652828 | 0.514125 | 0.661653 | -5.59631 | 0.300783 | MAP3K1 | mitogen-activated protein kinase kinase kinase 1 |
| 209269\_s\_at | 0.8740973 | 0.536756 | 0.626185 | -5.61754 | 0.366127 | SYK | spleen associated tyrosine kinase |
| 220272\_at | 0.8761267 | 0.543404 | -0.61592 | -5.62348 | -0.16192 | BNC2 | basonuclin 2 |
| 226506\_at | 0.8773023 | 0.546614 | -0.61099 | -5.62629 | -0.13198 | THSD4 | thrombospondin type 1 domain containing 4 |
| 216889\_s\_at | 0.8877351 | 0.576246 | -0.56614 | -5.6509 | -0.25732 | HNF4A | hepatocyte nuclear factor 4 alpha |
| 230914\_at | 0.8879065 | 0.576752 | 0.565383 | -5.6513 | 0.316658 | HNF4A | hepatocyte nuclear factor 4 alpha |
| 209540\_at | 0.8927912 | 0.592165 | -0.54252 | -5.66313 | -0.2852 | IGF1 | insulin like growth factor 1 |
| 225961\_at | 0.9063886 | 0.628239 | 0.490118 | -5.68844 | 0.076288 | KLHL42 | kelch like family member 42 |
| 227048\_at | 0.9088447 | 0.635261 | 0.480079 | -5.693 | 0.108008 | LAMA1 | laminin subunit alpha 1 |
| 1554697\_at | 0.911043 | 0.644931 | -0.46634 | -5.69909 | -0.31881 | ADAMTS9 | ADAM metallopeptidase with thrombospondin type 1 motif 9 |
| 203142\_s\_at | 0.9225882 | 0.678604 | 0.419165 | -5.71869 | 0.050635 | AP3B1 | adaptor related protein complex 3 beta 1 subunit |
| 224983\_at | 0.9307963 | 0.702825 | -0.38582 | -5.7313 | -0.05842 | SCARB2 | scavenger receptor class B member 2 |
| 243445\_at | 0.9340713 | 0.716262 | -0.36752 | -5.73778 | -0.19881 | BNC2 | basonuclin 2 |
| 203328\_x\_at | 0.9389844 | 0.732687 | -0.34532 | -5.74523 | -0.04979 | IDE | insulin degrading enzyme |
| 223503\_at | 0.9408851 | 0.743958 | 0.330182 | -5.75004 | 0.112552 | TMEM163 | transmembrane protein 163 |
| 204444\_at | 0.9465219 | 0.767924 | -0.29826 | -5.75949 | -0.20471 | KIF11 | kinesin family member 11 |
| 208005\_at | 0.9572704 | 0.805508 | 0.248799 | -5.77225 | 0.130735 | NTN1 | netrin 1 |
| 225732\_at | 0.9657298 | 0.838911 | -0.20537 | -5.78156 | -0.02739 | KLHL42 | kelch like family member 42 |
| 216895\_at | 0.9675217 | 0.844452 | 0.19821 | -5.78292 | 0.095931 | GABRG3 | gamma-aminobutyric acid type A receptor gamma3 subunit |
| 219153\_s\_at | 0.9688622 | 0.854742 | -0.18494 | -5.78533 | -0.09649 | THSD4 | thrombospondin type 1 domain containing 4 |
| 239884\_at | 0.9726519 | 0.869983 | 0.165335 | -5.78857 | 0.033624 | CADPS | calcium dependent secretion activator |
| 207334\_s\_at | 0.9754645 | 0.881212 | -0.15094 | -5.79072 | -0.0491 | TGFBR2 | transforming growth factor beta receptor 2 |
| 225963\_at | 0.9819635 | 0.908838 | -0.11565 | -5.79517 | -0.02093 | KLHL42 | kelch like family member 42 |
| 209541\_at | 0.9838095 | 0.920448 | -0.10086 | -5.79668 | -0.04581 | IGF1 | insulin like growth factor 1 |
| 211980\_at | 0.9882033 | 0.940883 | -0.07489 | -5.79884 | -0.03766 | COL4A1 | collagen type IV alpha 1 chain |
| 203214\_x\_at | 0.9894221 | 0.946488 | 0.067782 | -5.79932 | 0.033984 | CDK1 | cyclin dependent kinase 1 |
| 237847\_at | 0.990439 | 0.950565 | 0.06261 | -5.79964 | 0.030813 | NTN1 | netrin 1 |
| 205108\_s\_at | 0.9933109 | 0.966484 | 0.042433 | -5.80064 | 0.01856 | APOB | apolipoprotein B |
| 211981\_at | 0.9970086 | 0.981225 | -0.02376 | -5.80123 | -0.01721 | COL4A1 | collagen type IV alpha 1 chain |
| 205537\_s\_at | 0.9983826 | 0.992775 | 0.009144 | -5.80145 | 0.002829 | VAV2 | vav guanine nucleotide exchange factor 2 |
| 222835\_at | 0.9992453 | 0.996618 | -0.00428 | -5.80148 | -0.0012 | THSD4 | thrombospondin type 1 domain containing 4 |
| 235723\_at | 0.9994232 | 0.997758 | -0.00284 | -5.80149 | -0.00145 | BNC2 | basonuclin 2 |

*Table S2 shows differential expression, PD vs control, in tissue from brain donors, in the 34 T2DM genes chosen as candidate PD genes.*