**Supplemental Table S3.** Significantly overrepresented GO terms related to the genes in the top 200 dataset SNPs in ADRC dataset.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **GO term identifier** | **GO term description** | **Gene Symbol** |
| **BP** | GO:0033700 | phospholipid efflux | APOC1, APOE |
| *GO:0033344* | *cholesterol efflux* | *APOC1, APOE* |
| *GO:0032368* | *regulation of lipid transport* | *APOC1* |
| *GO:0032374* | *regulation of cholesterol transport* | *APOC1* |
| *GO:0032375* | *negative regulation of cholesterol transport* | *APOC1* |
| GO:0060282 | positive regulation of oocyte development | PDE5A, PDE3A |
| *GO:0002021* | *response to dietary excess* | *APOE* |
| GO:0031589 | cell-substrate adhesion | SMAD6, VWF |
| *GO:0007155* | *cell adhesion* | *ADAM12, VWF, CNTN4, NTM, PDZD2* |
| GO:0032060 | bleb assembly | MYLK |
| GO:0090162 | establishment of epithelial cell polarity | PARD3 |
| GO:0008356 | asymmetric cell division | PARD3 |
| GO:0046135 | pyrimidine nucleoside catabolic process | NT5E, DPYD |
| *GO:0009166* | *nucleotide catabolic process* | *NT5E* |
| *GO:0009187* | *cyclic nucleotide metabolic process* | *PDE5A* |
| *GO:0006214* | *thymidine catabolic process* | *DPYD* |
| *GO:0006222* | *UMP biosynthetic process* | *DPYD* |
| GO:0007154 | cell communication | SLC8A1, SNTG1 |
| GO:0042157 | lipoprotein metabolic process | APOC1, APOE |
| GO:0006629 | lipid metabolic process | APOC1, GDPD4, APOE, PDE3A |
| GO:0034587 | piRNA metabolic process | TDRD9 |
| GO:0090073 | positive regulation of protein homodimerization activity | CRBN |
| GO:0060401 | cytosolic calcium ion transport | SLC8A1 |
| GO:0019934 | cGMP-mediated signaling | APOE, PDE3A |
| *GO:0030828* | *positive regulation of cGMP biosynthetic process* | *APOE* |
| *GO:0007191* | *activation of adenylate cyclase activity by dopamine receptor signaling pathway* | *GNAL, OPRM1* |
| *GO:0007193* | *inhibition of adenylate cyclase activity by G-protein signaling pathway* | *GNAL, OPRM1* |
| GO:0071918 | urea transmembrane transport | SLC14A2 |
| *GO:0015840* | *urea transport* | *SLC14A2* |
| GO:0043457 | regulation of cellular respiration | PRDM16 |
| GO:0006641 | triglyceride metabolic process | APOC1, APOE |
| GO:0006003 | fructose 2,6-bisphosphate metabolic process | PFKFB3 |
| GO:0034616 | response to laminar fluid shear stress | SMAD6 |
| GO:0071321 | cellular response to cGMP | PDE3A |
| GO:0030512 | negative regulation of transforming growth factor beta receptor signaling pathway | SMAD6, PRDM16 |
| *GO:0010991* | *negative regulation of SMAD protein complex assembly* | *SMAD6* |
| *GO:0060394* | *negative regulation of pathway-restricted SMAD protein phosphorylation* | *SMAD6* |
| GO:0006554 | lysine catabolic process | SLC25A21 |
| GO:0055086 | nucleobase-containing small molecule metabolic process | NT5E, DPYD |
| GO:0042159 | lipoprotein catabolic process | APOE |
| *GO:0042158* | *lipoprotein biosynthetic process* | *APOE* |
| GO:0006196 | AMP catabolic process | NT5E |
| *GO:0046069* | *cGMP catabolic process* | *PDE5A* |
| GO:0010793 | regulation of mRNA export from nucleus | ZC3H3 |
| *GO:0016973* | *poly(A)+ mRNA export from nucleus* | *ZC3H3* |
| GO:0032488 | Cdc42 protein signal transduction | APOE |
| GO:0007352 | zygotic specification of dorsal/ventral axis | SMAD6 |
| *GO:0021513* | *spinal cord dorsal/ventral patterning* | *RAB23* |
| GO:0034447 | very-low-density lipoprotein particle clearance | APOC1, APOE |
| *GO:0034375* | *high-density lipoprotein particle remodeling* | *APOC1,APOE* |
| *GO:0034380* | *high-density lipoprotein particle assembly* | *APOE* |
| *GO:0034379* | *very-low-density lipoprotein particle assembly* | *APOC1* |
| *GO:0034384* | *high-density lipoprotein particle clearance* | *APOE* |
|  | *GO:0034382* | *chylomicron remnant clearance* | *APOC1, APOE* |
| *GO:0034372* | *very-low-density lipoprotein particle remodeling* | *APOE* |
| *GO:0034369* | *plasma lipoprotein particle remodeling* | *APOC1* |
| *GO:0010916* | *negative regulation of very-low-density lipoprotein particle clearance* | *APOC1* |
| GO:0006145 | purine base catabolic process | DPYD |
| *GO:0006212* | *uracil catabolic process* | *DPYD* |
| *GO:0006210* | *thymine catabolic process* | *DPYD* |
| *GO:0006208* | *pyrimidine base catabolic process* | *DPYD* |
| *GO:0006207* | *'de novo' pyrimidine base biosynthetic process* | *DPYD* |
| *GO:0006206* | *pyrimidine base metabolic process* | *NT5E, DPYD* |
| GO:0009414 | response to water deprivation | SLC14A2 |
| *GO:0071476* | *cellular hypotonic response* | *MYLK* |
| GO:0042311 | vasodilation | PDE5A,APOE |
| *GO:0007596* | *blood coagulation* | *PDE5A, SLC8A1, VWF, PDE3A* |
| *GO:0055118* | *negative regulation of cardiac muscle contraction* | *PDE5A* |
| *GO:0030168* | *platelet activation* | *PDE5A, SLC8A1, VWF, PDE3A* |
| *GO:0007599* | *hemostasis* | *VWF* |
| *GO:0010613* | *positive regulation of cardiac muscle hypertrophy* | *PDE5A* |
| *GO:0043117* | *positive regulation of vascular permeability* | *PDE3A* |
| *GO:0043116* | *negative regulation of vascular permeability* | *PDE3A* |
| *GO:0010544* | *negative regulation of platelet activation* | *APOE* |
| *GO:0003093* | *regulation of glomerular filtration* | *PTPRO* |
| GO:0042742 | defense response to bacterium | DEFB114, DEFB133 |
| GO:0051005 | negative regulation of lipoprotein lipase activity | APOC1 |
| GO:0048070 | regulation of developmental pigmentation | ADAMTS9 |
| *GO:0045636* | *positive regulation of melanocyte differentiation* | *ADAMTS9* |
| GO:0005513 | detection of calcium ion | SYT1 |
| *GO:0000302* | *response to reactive oxygen species* | *APOE* |
| GO:0006516 | glycoprotein catabolic process | ADAMTS9 |
| *GO:0034205* | *beta-amyloid formation* | *PION* |
| GO:0046086 | adenosine biosynthetic process | NT5E |
| GO:0051260 | protein homooligomerization | SYT1, VWF |
| *GO:0032463* | *negative regulation of protein homooligomerization* | *CRBN* |
| GO:0051651 | maintenance of location in cell | APOE |
| GO:0010873 | positive regulation of cholesterol esterification | APOC1, APOE |
| *GO:0045833* | *negative regulation of lipid metabolic process* | *APOC1* |
| *GO:0008203* | *cholesterol metabolic process* | *APOC1, APOE* |
| *GO:0010900* | *negative regulation of phosphatidylcholine catabolic process* | *APOC1* |
| *GO:0045541* | *negative regulation of cholesterol biosynthetic process* | *APOE* |
| *GO:0006704* | *glucocorticoid biosynthetic process* | *HSD11B1* |
| *GO:0045717* | *negative regulation of fatty acid biosynthetic process* | *APOC1* |
| *GO:0046839* | *phospholipid dephosphorylation* | *PPAPDC1A* |
| GO:0045750 | positive regulation of S phase of mitotic cell cycle | SMAD6 |
| *GO:0007128* | *meiotic prophase I* | *SYCP2* |
| *GO:0040020* | *regulation of meiosis* | *PDE3A* |
| GO:0032805 | positive regulation of low-density lipoprotein particle receptor catabolic process | APOE |
| GO:0006874 | cellular calcium ion homeostasis | SLC8A1, APOE |
| GO:0060267 | positive regulation of respiratory burst | CAMK1D |
| GO:0034766 | negative regulation of ion transmembrane transport | CRBN |
| *GO:0048261* | *negative regulation of receptor-mediated endocytosis* | *APOC1* |
| *GO:0017158* | *regulation of calcium ion-dependent exocytosis* | *SYT1* |
| *GO:0043271* | *negative regulation of ion transport* | *BEST3* |
| GO:0014820 | tonic smooth muscle contraction | MYLK |
| *GO:0055119* | *relaxation of cardiac muscle* | *PDE5A* |
| GO:0010430 | fatty acid omega-oxidation | CYP4V2 |
| GO:0071622 | regulation of granulocyte chemotaxis | CAMK1D |
| *GO:0007626* | *locomotory behavior* | *OPRM1, NPAS3* |
| *GO:0007614* | *short-term memory* | *PDE5A* |
| *GO:0002678* | *positive regulation of chronic inflammatory response* | *PDE5A* |
| *GO:0050728* | *negative regulation of inflammatory response* | *NT5E, APOE* |
| *GO:0042711* | *maternal behavior* | *NPAS3* |
| *GO:0030853* | *negative regulation of granulocyte differentiation* | *PRDM16* |
| GO:0072358 | cardiovascular system development | APOE |
| *GO:0090303* | *positive regulation of wound healing* | *MYLK* |
| *GO:0060414* | *aorta smooth muscle tissue morphogenesis* | *MYLK* |
| *GO:0007399* | *nervous system development* | *PDE5A, DAB1, CNTN4, CAMK1D, RAB23* |
| *GO:0007409* | *axonogenesis* | *PARD3, CNTN4* |
| *GO:0008038* | *neuron recognition* | *NTM* |
| *GO:0055001* | *muscle cell development* | *SGCZ* |
| *GO:0030516* | *regulation of axon extension* | *APOE* |
| *GO:0050773* | *regulation of dendrite development* | *CAMK1D* |
| *GO:0043586* | *tongue development* | *PRDM16* |
| *GO:0060596* | *mammary placode formation* | *NRG3* |
| *GO:0014012* | *peripheral nervous system axon regeneration* | *APOE* |
| **MF** | GO:0005516 | calmodulin binding | SLC8A1, SYT1, MYO1B, MYLK, CAMK1D |
| GO:0008081 | phosphoric diester hydrolase activity | PDE5A, PDE3A |
| *GO:0004331* | *fructose-2,6-bisphosphate 2-phosphatase activity* | *PFKFB3* |
| GO:0015204 | urea transmembrane transporter activity | SLC14A2 |
| GO:0030617 | transforming growth factor beta receptor, inhibitory cytoplasmic mediator activity | SMAD6 |
| GO:0060228 | phosphatidylcholine-sterol O-acyltransferase activator activity | APOC1, APOE |
| GO:0070524 | 11-beta-hydroxysteroid dehydrogenase (NADP+) activity | HSD11B1 |
| *GO:0003845* | *11-beta-hydroxysteroid dehydrogenase [NAD(P)] activity* | *HSD11B1* |
| GO:0004687 | myosin light chain kinase activity | MYLK |
| GO:0046911 | metal chelating activity | APOE |
| GO:0071208 | histone pre-mRNA DCP binding | SNRPD3 |
| GO:0071813 | lipoprotein particle binding | APOE |
| GO:0005543 | phospholipid binding | SYT1, SYT14, APOE |
| *GO:0005547* | *phosphatidylinositol-3,4,5-trisphosphate binding* | *PARD3,MYO1B* |
| *GO:0005546* | *phosphatidylinositol-4,5-bisphosphate binding* | *PARD3,MYO1B* |
| GO:0016787 | hydrolase activity | PDE5A, PTPRO, GDPD4,NT5E, ABHD12B, PPAPDC1A, PDE3A, PFKFB3, TDRD9 |
| GO:0000166 | nucleotide binding | GNAL, PDE5A, ABCA12, MYO1B, NT5E, MYLK, PFKFB3, HSD11B1, CAMK1D, RAB23, CHD9, TDRD9 |
| GO:0017113 | dihydropyrimidine dehydrogenase (NADP+) activity | DPYD |
| *GO:0004158* | *dihydroorotate oxidase activity* | *DPYD* |
| GO:0046872 | metal ion binding | GNAL, PDE5A, BNC2, ZNF787, GDPD4, ADAM12, NT5E, ZC3H3, MYLK, PDE3A, PRDM16, CYP4V2, ADAMTS9, DPYD |
| GO:0015085 | calcium ion transmembrane transporter activity | SLC8A1 |
| *GO:0005432* | *calcium:sodium antiporter activity* | *SLC8A1* |
| GO:0003873 | 6-phosphofructo-2-kinase activity | PFKFB3 |
| GO:0001540 | beta-amyloid binding | APOE, PION |
| GO:0050750 | low-density lipoprotein particle receptor binding | SYT1, APOE |
| *GO:0070326* | *very-low-density lipoprotein particle receptor binding* | *APOE* |
| GO:0070698 | type I activin receptor binding | SMAD6 |
| GO:0019865 | immunoglobulin binding | VWF |
| GO:0055102 | lipase inhibitor activity | APOC1 |
| GO:0004119 | cGMP-inhibited cyclic-nucleotide phosphodiesterase activity | PDE3A |
| GO:0003779 | actin binding | MYO1B,MYLK,PHACTR3,SNTG1 |
| GO:0030297 | transmembrane receptor protein tyrosine kinase activator activity | NRG3 |
| **CC** | GO:0005576 | extracellular region | APOC1, NRG3, DEFB114, ADAM12, VWF, APOE, NPFF, CNTN4, DEFB133, SNED1, EYS, PDZD2, ADAMTS9, ITFG1 |
| GO:0005783 | endoplasmic reticulum | APOC1, OPRM1, SEL1L, VWF, HSD11B1, CYP4V2, PDZD2, KIAA0368 |
| GO:0016020 | membrane | CSMD1, ABCA12, SLC8A1, TMEM217, SYT1, PTPRO, GDPD4, CRBN, TMEM206, SYT14, UNC5D, SEL1L, TSPAN13, AGPAT4, PPAPDC1A,TOMM40, PDE3A, FER1L5, HSD11B1, CYP4V2, TRAF3IP3, SLC25A21, ITFG1 |
| GO:0031225 | anchored to membrane | NT5E, CNTN4, NTM |
| GO:0042627 | chylomicron | APOC1, APOE |
| *GO:0034364* | *high-density lipoprotein particle* | *APOC1, APOE* |
| *GO:0034361* | *very-low-density lipoprotein particle* | *APOC1, APOE* |
| GO:0016013 | syntrophin complex | SNTG1 |
| GO:0033093 | Weibel-Palade body | VWF |
| *GO:0060203* | *clathrin sculpted glutamate transport vesicle membrane* | *SYT1* |
| *GO:0070083* | *clathrin sculpted monoamine transport vesicle membrane* | *SYT1* |
| GO:0016021 | integral to membrane | CSMD1, ABCA12, OPRM1, SLC8A1, TMEM217, SYT1, PTPRO, SGCZ, GDPD4, TMEM206, SYT14, ADAM12, UNC5D, SEL1L, SLC14A2, AGPAT4, PPAPDC1A, PDE3A, FER1L5, HSD11B1, CYP4V2, TRAF3IP3, BEST3, SLC25A21, ITFG1 |
| GO:0005770 | late endosome | APOE, KIAA0368 |
| GO:0031232 | extrinsic to external side of plasma membrane | APOE |

*MF:* GO molecular function; *CC:* GO cellular compartment; *BP:* biological process. Italicized entries represent redundant terms; they are placed under their most informative common ancestor (in normal font).