

Table S4 GO annotation of 22 genes

| Gene_name | GO_name |
|---------------|---|
| <i>ACSM2A</i> | Medium-chain fatty-acyl-CoA metabolic process |
| <i>ACSM2A</i> | Triglyceride homeostasis |
| <i>ACSM2A</i> | Fatty acid metabolic process |
| <i>ACSM2A</i> | Glucose homeostasis |
| <i>APOB</i> | Blood coagulation |
| <i>APOB</i> | Small molecule metabolic process |
| <i>APOB</i> | Cellular response to prostaglandin stimulus |
| <i>APOB</i> | Lipoprotein catabolic process |
| <i>APOB</i> | Triglyceride mobilization |
| <i>APOB</i> | Lipoprotein biosynthetic process |
| <i>APOB</i> | Regulation of cholesterol biosynthetic process |
| <i>APOB</i> | Positive regulation of lipid storage |
| <i>APOB</i> | Positive regulation of cholesterol storage |
| <i>APOB</i> | Response to carbohydrate stimulus |
| <i>APOB</i> | Response to selenium ion |
| <i>APOB</i> | Very-low-density lipoprotein particle assembly |
| <i>APOB</i> | Low-density lipoprotein particle clearance |
| <i>APOB</i> | Low-density lipoprotein particle remodeling |
| <i>APOB</i> | Positive regulation of macrophage derived foam cell differentiation |
| <i>APOB</i> | Cholesterol transport |
| <i>APOB</i> | Lipoprotein transport |
| <i>APOB</i> | Triglyceride catabolic process |
| <i>APOB</i> | Cholesterol efflux |
| <i>APOB</i> | Artery morphogenesis |
| <i>APOB</i> | Fertilization |
| <i>APOB</i> | Sperm motility |
| <i>APOB</i> | Lipoprotein metabolic process |
| <i>APOB</i> | Cellular response to tumor necrosis factor |
| <i>APOB</i> | Receptor-mediated endocytosis |
| <i>APOB</i> | Retinoid metabolic process |
| <i>APOB</i> | Phototransduction, visible light |
| <i>APOB</i> | Cholesterol homeostasis |
| <i>APOB</i> | Cholesterol metabolic process |
| <i>APOB</i> | Post-embryonic development |
| <i>APOB</i> | Leukocyte migration |
| <i>APOB</i> | Response to lipopolysaccharide |
| <i>APOB</i> | Response to virus |
| <i>APOB</i> | Lipid metabolic process |
| <i>APOB</i> | In utero embryonic development |

Table S4 (continued)**Table S4** (continued)

| Gene_name | GO_name |
|-----------------|---|
| <i>APOB</i> | Nervous system development |
| <i>APOB</i> | Spermatogenesis |
| <i>APOH</i> | Positive regulation of blood coagulation |
| <i>APOH</i> | Negative regulation of fibrinolysis |
| <i>APOH</i> | Triglyceride transport |
| <i>APOH</i> | Regulation of fibrinolysis |
| <i>APOH</i> | Negative regulation of myeloid cell apoptotic process |
| <i>APOH</i> | Negative regulation of smooth muscle cell apoptotic process |
| <i>APOH</i> | Plasminogen activation |
| <i>APOH</i> | Regulation of blood coagulation |
| <i>APOH</i> | Positive regulation of lipoprotein lipase activity |
| <i>APOH</i> | Negative regulation of blood coagulation |
| <i>APOH</i> | Negative regulation of endothelial cell migration |
| <i>APOH</i> | Blood coagulation, intrinsic pathway |
| <i>APOH</i> | Negative regulation of endothelial cell proliferation |
| <i>APOH</i> | Triglyceride metabolic process |
| <i>APOH</i> | Negative regulation of angiogenesis |
| <i>CDC42EP3</i> | Regulation of cell shape |
| <i>CDC42EP3</i> | Signal transduction |
| <i>CXCL14</i> | Signal transduction |
| <i>CXCL14</i> | Immune response |
| <i>CXCL14</i> | Inner ear development |
| <i>CXCL14</i> | Chemotaxis |
| <i>CXCL14</i> | Cell-cell signaling |
| <i>DDR2</i> | Positive regulation of extracellular matrix disassembly |
| <i>DDR2</i> | Collagen-activated tyrosine kinase receptor signaling pathway |
| <i>DDR2</i> | Regulation of extracellular matrix disassembly |
| <i>DDR2</i> | Endochondral bone growth |
| <i>DDR2</i> | Chondrocyte proliferation |
| <i>DDR2</i> | Positive regulation of fibroblast migration |
| <i>DDR2</i> | Regulation of bone mineralization |
| <i>DDR2</i> | Signal transduction |
| <i>DDR2</i> | Biomineral tissue development |
| <i>DDR2</i> | Cell adhesion |
| <i>DDR2</i> | Collagen fibril organization |
| <i>DDR2</i> | Positive regulation of protein kinase activity |
| <i>DDR2</i> | Positive regulation of fibroblast proliferation |

Table S4 (continued)

Table S4 (continued)

| Gene_name | GO_name |
|--------------|--|
| <i>DDR2</i> | Peptidyl-tyrosine phosphorylation |
| <i>DDR2</i> | Positive regulation of osteoblast differentiation |
| <i>DDR2</i> | Ossification |
| <i>DDR2</i> | Positive regulation of sequence-specific DNA binding transcription factor activity |
| <i>DDR2</i> | Protein autophosphorylation |
| <i>DOCK5</i> | Small gtpase mediated signal transduction |
| <i>F5</i> | Blood coagulation |
| <i>F5</i> | Platelet activation |
| <i>F5</i> | Platelet degranulation |
| <i>F5</i> | Cell adhesion |
| <i>F5</i> | Blood circulation |
| <i>FTCD</i> | Small molecule metabolic process |
| <i>FTCD</i> | Cytoskeleton organization |
| <i>FTCD</i> | Folic acid-containing compound metabolic process |
| <i>FTCD</i> | Histidine catabolic process to glutamate and formamide |
| <i>FTCD</i> | Histidine catabolic process to glutamate and formate |
| <i>FTCD</i> | Histidine catabolic process |
| <i>FTCD</i> | Tetrahydrofolate interconversion |
| <i>FTCD</i> | Cellular metabolic process |
| <i>FTCD</i> | Cellular nitrogen compound metabolic process |
| <i>GNAI1</i> | Blood coagulation |
| <i>GNAI1</i> | Platelet activation |
| <i>GNAI1</i> | Vesicle fusion |
| <i>GNAI1</i> | Adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway |
| <i>GNAI1</i> | Adenylate cyclase-modulating G-protein coupled receptor signaling pathway |
| <i>GNAI1</i> | Response to peptide hormone stimulus |
| <i>GNAI1</i> | Cell cycle |
| <i>GNAI1</i> | Cell division |
| <i>GNAI1</i> | G-protein coupled receptor signaling pathway |
| <i>GNAI1</i> | Synaptic transmission |
| <i>HPSE</i> | Positive regulation of blood coagulation |
| <i>HPSE</i> | Small molecule metabolic process |
| <i>HPSE</i> | Heparan sulfate proteoglycan catabolic process |
| <i>HPSE</i> | Regulation of hair follicle development |
| <i>HPSE</i> | Vascular wound healing |

Table S4 (continued)

Table S4 (continued)

| Gene_name | GO_name |
|--------------|---|
| <i>HPSE</i> | Positive regulation of hair follicle development |
| <i>HPSE</i> | Positive regulation of osteoblast proliferation |
| <i>HPSE</i> | Proteoglycan metabolic process |
| <i>HPSE</i> | Positive regulation vascular endothelial growth factor production |
| <i>HPSE</i> | Glycosaminoglycan catabolic process |
| <i>HPSE</i> | Positive regulation of protein kinase B signaling cascade |
| <i>HPSE</i> | Cell-matrix adhesion |
| <i>HPSE</i> | Glycosaminoglycan metabolic process |
| <i>HPSE</i> | Carbohydrate metabolic process |
| <i>IGKC</i> | Immune response |
| <i>IGKC</i> | Complement activation |
| <i>IGKC</i> | Complement activation, classical pathway |
| <i>IGKC</i> | Fc-gamma receptor signaling pathway involved in phagocytosis |
| <i>IGKC</i> | Regulation of immune response |
| <i>IGKC</i> | Innate immune response |
| <i>LYRM4</i> | Small molecule metabolic process |
| <i>MZB1</i> | Positive regulation of immunoglobulin biosynthetic process |
| <i>MZB1</i> | Regulation of B cell proliferation |
| <i>MZB1</i> | Negative regulation of glucose import in response to insulin stimulus |
| <i>MZB1</i> | Integrin activation |
| <i>MZB1</i> | Regulation of cell proliferation |
| <i>MZB1</i> | Positive regulation of cell proliferation |
| <i>MZB1</i> | Apoptotic process |
| <i>PARVA</i> | Actin-mediated cell contraction |
| <i>PARVA</i> | Regulation of cell shape |
| <i>PARVA</i> | Smooth muscle cell chemotaxis |
| <i>PARVA</i> | Heterotypic cell-cell adhesion |
| <i>PARVA</i> | Outflow tract septum morphogenesis |
| <i>PARVA</i> | Sprouting angiogenesis |
| <i>PARVA</i> | Establishment or maintenance of cell polarity |
| <i>PARVA</i> | Substrate adhesion-dependent cell spreading |
| <i>PARVA</i> | Cilium morphogenesis |
| <i>PARVA</i> | Cell junction assembly |
| <i>PLG</i> | Blood coagulation |
| <i>PLG</i> | Platelet activation |
| <i>PLG</i> | Platelet degranulation |
| <i>PLG</i> | Negative regulation of fibrinolysis |

Table S4 (continued)

Table S4 (*continued*)

| Gene_name | GO_name |
|-----------------|--|
| <i>PLG</i> | Negative regulation of cell-cell adhesion mediated by cadherin |
| <i>PLG</i> | Positive regulation of fibrinolysis |
| <i>PLG</i> | Tissue remodeling |
| <i>PLG</i> | Negative regulation of cell-substrate adhesion |
| <i>PLG</i> | Fibrinolysis |
| <i>PLG</i> | Extracellular matrix disassembly |
| <i>PLG</i> | Extracellular matrix organization |
| <i>PLG</i> | Negative regulation of cell proliferation |
| <i>PLG</i> | Proteolysis |
| <i>PLG</i> | Cellular protein metabolic process |
| <i>RNF138</i> | Wnt receptor signaling pathway |
| <i>RNF138</i> | Protein ubiquitination |
| <i>SERPINA1</i> | Blood coagulation |
| <i>SERPINA1</i> | Platelet activation |
| <i>SERPINA1</i> | Platelet degranulation |
| <i>SERPINA1</i> | Acute-phase response |
| <i>SERPINA1</i> | Regulation of proteolysis |
| <i>SERPINA1</i> | Negative regulation of endopeptidase activity |
| <i>SGCD</i> | Cytoskeleton organization |
| <i>SGCD</i> | Muscle organ development |
| <i>UPB1</i> | Small molecule metabolic process |
| <i>UPB1</i> | Beta-alanine biosynthetic process |
| <i>UPB1</i> | Nitrogen compound metabolic process |
| <i>UPB1</i> | Pyrimidine nucleoside catabolic process |
| <i>UPB1</i> | Pyrimidine nucleobase metabolic process |
| <i>UPB1</i> | Nucleobase-containing small molecule metabolic process |

GO, gene ontology.