

Supplemental Table 1. List of 432 genes of interest prior to refinement. The table includes the Entrez gene identifier, the Dharmacon library from which the initial hit was identified, the gene symbol, the mean fold change in secreted ApoA-I that resulted from siRNA knockdown, the Z-score associated with the siRNA knockdown, a brief description of the known function of the gene. Genes are listed in alphabetical order by gene symbol. ROHG = rest of human genome, GPCR = G-protein coupled receptor

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
13	Human Druggable	AADAC	2.33	3.09	Arylacetamide deacetylase, may play a role in protein amino acid deacetylation and lipid metabolic process
16	ROHG	AARS	1.90	2.21	Alanyl-tRNA synthetase, a tRNA binding protein that is involved in humoral immune response and tRNA processing
27252	ROHG	AB026190	2.03	2.17	Kelch-like 20, binds actin filaments, forms a complex with CUL3 and ROC1 to form an E3 ubiquitin ligase, mediating ubiquitination of DAPK1 and subsequently controlling cellular responses to interferon
4363	Human Druggable	ABCC1	2.16	2.70	ATP-binding cassette subfamily C member 1, a multidrug transporter that acts in chemotaxis, apoptosis, and food intake
215	Human Druggable	ABCD1	1.91	2.11	ATP-binding cassette subfamily D (ALD) member 1, involved in the transport of acyl CoA esters across the peroxisomal membrane
225	ROHG	ABCD2	2.03	2.52	ATP-binding cassette sub-family D member 2, an ABC transporter that plays a role in very long chain fatty acid metabolism, regulates NF-kappaB, AP-1, and C/EBP transcription factors activities, nitric oxide synthesis, and cytokine production
171586	Human Druggable	ABHD3	1.90	2.07	Abhydrolase domain containing 3 (lung alpha/beta hydrolase 3), a member of the alpha/beta hydrolase family of enzymes
31	Human Druggable	ACACA	1.92	2.10	Acetyl-Coenzyme A carboxylase alpha, plays a role in fatty acid biosynthetic process, regulates apoptosis, cell proliferation, cell growth, insulin secretion, and glycogen biosynthetic process;

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
37	Human Druggable	ACADVL	1.87	2.08	Acyl-Coenzyme A dehydrogenase very long chain, acts in fatty acid beta-oxidation
84320	ROHG	ACBD6	2.42	2.98	Acyl-Coenzyme A binding domain containing 6, binds long chain acyl-CoAs with a preference for unsaturated, C18:1 CoA and C20:4 CoA, a cellular marker for primitive progenitor cells that function in hematopoiesis and vascular endothelium development
52	Human Druggable	ACP1	1.98	2.68	Acid phosphatase 1 soluble, a tyrosine phosphatase that acts in receptor-mediated signaling
51205	Human Druggable	ACP6	1.85	2.02	Acid phosphatase 6 lysophosphatidic, hydrolyzes lysophosphatidic acid to monoacylglycerol, may play a role in the mitochondrial lipid biosynthesis, gastrointestinal motor function, and in the pacemaker activity of interstitial cells
148	GPCR	ADRA1A	1.86	1.96	Adrenergic alpha-1A- receptor, a G protein-coupled receptor that functions in cytosolic calcium elevation, phospholipase C activation, apoptosis, cell-cell signaling, smooth muscle and heart contraction
9447	Human Druggable	AIM2	2.39	3.17	Absent in melanoma 2, regulates cytoplasmic DNA-induced caspase-1 activation and IL1 beta processing and inhibits cell proliferation
9863	Human Druggable	AIP1	1.88	2.04	Activin receptor interacting protein 1, binds to PTEN, plays a role in signal transduction
10840	ROHG	ALDH1L1	1.91	1.91	Aldehyde dehydrogenase 1 family member L1, an oxidoreductase that acts in 10-formyltetrahydrofolate catabolism and negative regulation of cell growth and proliferation
310	Human Druggable	ANXA7	2.27	2.96	Annexin A7, an voltage-dependent calcium channel, involved in vesicle fusion and cellular response to glucose starvation, regulates calcium-mediated signaling and cell proliferation

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
160	ROHG	AP2A1	1.98	2.41	Adaptor-related protein complex 2 alpha 1 subunit, a transporter that acts in receptor-mediated endocytosis, may play a role in membrane budding
115201	ROHG	APG4A	2.26	2.49	ATG4 autophagy related 4 homolog A, a cysteine endopeptidase that has specificity for ubiquitin-like proteins, may act in intra-Golgi transport by cleaving the intra-Golgi transport modulator GATE-16
335	Human Druggable	APOA1	0.14	-2.01	Apolipoprotein A-I, a cholesterol transporter that acts in cAMP biosynthesis
390	Human Druggable	ARHE	1.83	1.94	Rho family GTPase 3, a translation repressor that inhibits mitotic cell cycle, stress fiber assembly, cap-dependent translation, and cell proliferation, mediates cell migration and transcription
57584	ROHG	ARHGAP21	1.90	2.10	Rho GTPase activating protein 21, binds to protein kinase, acts in the regulation of cell migration, GTPase activity, and protein amino acid phosphorylation
64333	ROHG	ARHGAP9	0.13	-2.04	Rho GTPase activating protein 9, selective for RAC1 and CDC42, binds phosphoinositide ligands through a spectrin-like binding pocket, negatively regulates cell adhesion to fibronectin
84100	ROHG	ARL6	2.01	1.99	ADP-ribosylation factor-like 6, a GTP binding protein that may function in membrane-associated intracellular trafficking, ciliary disassembly and Wnt signaling
79754	ROHG	ASB13	2.17	2.74	Protein has moderate similarity to human ASB9, which inhibits mitochondrial function and cell growth, promotes protein ubiquitination, contains six ankyrin repeats
429	Human Druggable	ASCL1	2.03	2.34	Achaete-scute complex homolog 1, a transcriptional activator
79058	Human Druggable	ASPSCR1	1.89	2.08	Alveolar soft part sarcoma chromosome region candidate 1

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
471	Human Druggable	ATIC	1.97	2.31	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase, an IMP cyclohydrolase that acts in de novo IMP biosynthesis
487	Human Druggable	ATP2A1	0.23	-2.09	ATPase Ca ⁺⁺ transporting cardiac muscle fast twitch 1, plays a role in calcium ion transport, regulates action potential, heart contraction, and striated muscle contraction
10538	Human Druggable	BATF	2.04	2.36	Basic leucine zipper transcription factor ATF-like, an RNA polymerase II transcription factor, heterodimerizes with Jun proteins and IFI35, inhibits AP-1 mediated transcription and Ras-mediated transformation
8424	ROHG	BBOX1	2.14	2.40	Gamma-butyrobetaine dioxygenase, a putative enzyme that binds ferrous ion, may play a role in carnitine biosynthesis
607	Human Druggable	BCL9	2.28	2.97	B-cell CLL-lymphoma 9, a transcriptional activator that regulates Wnt receptor signaling, cell proliferation, epithelial to mesenchymal transition, and angiogenesis
113452	ROHG	BCLP	1.98	1.94	Beta-casein-like protein, a tumor associated antigen that may regulate tumor cell morphology and growth pattern
53630	ROHG	BCMO1	2.02	2.34	Beta-carotene 15-15'-monooxygenase 1, mediates retinal metabolism
10565	Human Druggable	BIG1	0.21	-2.16	ADP-ribosylation factor guanine nucleotide-exchange factor 1, binds to myosin and microtubule, maintains normal Golgi morphology and inhibits Rho GTPase activity, mediates endomembrane organization and N-glycosylation
274	Human Druggable	BIN1	1.96	2.24	Bridging integrator 1, involved in microtubule bundle formation, sarcomere organization, and myofiber development
666	Human Druggable	BOK	1.84	1.95	BCL2-related ovarian killer, interacts with BNIP3, induces apoptosis in response to DNA damage via TP53 signal transduction pathway,

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
686	Human Druggable	BTD	1.98	2.29	Biotinidase, catalyzes the hydrolysis of biocytin to release free biotin, may play a role in central nervous system and epidermis development
219771	Human Druggable	C10ORF9	2.32	3.07	Cyclin Y, regulates cell proliferation, colony formation, and cell cycle progression in glioma cells
79622	ROHG	C16ORF33	0.16	-2.00	Chromosome 16 open reading frame 33 (U11/U12 snRNP 25K protein), a component of the 18S U11/U12 snRNP that binds C6orf151 and U11 snRNA and plays a role in RNA splicing
8131	ROHG	C16ORF35	2.10	2.30	Protein with very strong similarity to uncharacterized mouse Mare
58509	ROHG	C19ORF29	0.16	-1.97	NY-REN-24 antigen, a renal cell carcinoma tumor antigen that is recognized by an autoantibody
10616	Human Druggable	C20ORF18	0.30	-1.90	RanBP-type and C3HC4-type zinc finger containing 1, a transcription regulator that plays a role in cytoplasmic sequestering of protein, protein ubiquitination, and proteasomal ubiquitin-dependent protein catabolic process
164312	ROHG	C20ORF75	2.02	2.43	Protein with high similarity to neuronal leucine rich repeat-4, which plays a key role in hippocampal-dependent long lasting memory, contains 6 leucine rich repeats and a fibronectin type III domain
200558	ROHG	C2ORF13	1.94	2.23	Aprataxin and PNKP like factor, an endo- and exonuclease that interacts with the DNA repair proteins, involved in the cellular response to chromosomal DNA strand breaks, activates ADP-ribosyltransferase
83648	ROHG	C8ORF13	0.20	-1.91	Family with sequence similarity 167 member A
786	ROHG	CACNG1	2.08	2.66	Calcium channel (voltage-dependent, gamma subunit 1), probably involved in calcium ion transport and coupling of excitation and contraction in muscle

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
790	ROHG	CAD	2.33	3.27	CAD trifunctional protein, a carbamoyl-phosphate synthase that plays a role in de novo pyrimidine base biosynthesis, MAPKKK cascade, and cell proliferation
152137	ROHG	CCDC50	1.98	1.94	Coiled-coil domain containing 50, suppresses ligand-mediated down regulation of the EGF receptor, binds several proteins to negatively regulate NF-kappaB signaling
6361	GPCR	CCL17	0.14	-1.95	Chemokine ligand 17, interacts with CCR4, acts in chemotaxis, cell-cell signaling, and platelet activation
896	Human Druggable	CCND3	1.88	2.00	Cyclin D3, a cyclin-dependent protein kinase regulator that modulates cell cycle, cell proliferation, and apoptosis, acts in Notch signaling, hemopoiesis, and skeletal muscle development
10983	Human Druggable	CCNI	1.95	2.16	Cyclin I, a putative cyclin dependent protein kinase regulator that may play a role in spermatogenesis
9973	Human Druggable	CCS	0.28	-1.98	Copper chaperone for superoxide dismutase, a copper ion transmembrane transporter that plays a role in superoxide metabolism and regulation of gene expression
50489	ROHG	CD207	1.98	2.23	CD207 molecule langerin, a receptor that plays a role in endocytosis, antigen processing and presentation, regulates natural killer T cell activation and IL-12 production
961	Human Druggable	CD47	1.96	2.18	CD47 molecule, an Rac GTPase activator and a receptor signaling protein that acts in cell adhesion, induction of apoptosis, and cell migration
963	Human Druggable	CD53	1.85	1.95	CD53 molecule, binds CD81 and CD82, involved in JNK activation, homophilic cell adhesion, and calcium ion transport, induces DNA synthesis, B-cell proliferation, and IgG and IgM production

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
972	Human Druggable	CD74	1.72	1.95	CD74 antigen, regulates antigen processing and presentation, T-cell immunity, B cell proliferation and differentiation, and MAPK and I-kappaB kinase/NF-kappaB cascades
976	GPCR	CD97	1.97	2.21	CD97 molecule, a chemoattractant receptor that promotes chemotaxis, angiogenesis, T-cell proliferation, and cytokine production, acts in integrin-mediated signaling
113130	ROHG	CDCA5	2.17	2.32	Cell division cycle associated 5, required for proper cohesion binding to chromatin during G2 phase, and efficient repair of DNA double strand breaks in G2
10423	ROHG	CDIPT	2.17	2.46	CDP diacylglycerol inositol 3 phosphatidyltransferase, a phosphatidylinositol transporter that plays a role in phosphatidylinositol biosynthesis and cell proliferation
634	ROHG	CEACAM1	1.78	1.92	Carcinoembryonic antigen-related cell adhesion molecule 1, binds to receptors, acts in activation of protein kinase B activity, cell proliferation, and lymphangiogenesis
1053	Human Druggable	CEBPE	2.15	2.62	CCAAT enhancer binding protein epsilon, a transcription regulator, regulates cell proliferation
1054	Human Druggable	CEBPG	2.30	2.96	CCAAT enhancer binding protein gamma, a transcription repressor that plays a role in DNA dependent regulation of transcription
1062	Human Druggable	CENPE	0.30	-1.92	Centromere protein E 312kDa, a kinesin-like motor protein that acts in mitotic cell cycle checkpoint, metaphase plate congression, and kinetochore-microtubule attachment, acts as an autoantigen in systemic sclerosis
1063	Human Druggable	CENPF	1.98	2.24	Centromere protein F 350-400ka, a transcription corepressor that acts in mitosis, cytokinesis, and apoptosis
9023	ROHG	CH25H	2.20	2.52	Cholesterol 25-hydroxylase, plays a role in lipid and cholesterol metabolism, inhibits cell proliferation

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
1122	Human Druggable	CHML	0.11	-2.44	Choroideremia-like Rab escort protein 2, a Rab GTPase binding protein that plays a role in protein geranylgeranylation
1133	Human Druggable	CHRM5	0.29	-1.94	Cholinergic receptor muscarinic 5, a G protein-coupled receptor that acts through stimulation of phospholipase C and elevation of intracellular calcium
1280	Human Druggable	COL2A1	1.84	1.93	Collagen type II alpha 1, binds to integrin, acts in skeletal system development, transforming growth factor beta receptor signaling pathway, and collagen fibril organization
1288	Human Druggable	COL4A6	2.10	2.56	Collagen type IV alpha 6, inhibits angiogenesis and endothelial cell proliferation
9276	Human Protein Kinase	COPB2	0.12	-1.97	Coatmer protein complex subunit beta 2, may play a role in exocytosis
10229	ROHG	COQ7	2.03	2.17	Coenzyme Q7 homolog ubiquinone, a putative oxidoreductase that plays a role in ubiquinone and quinone cofactor biosynthesis, mitochondrial organization and function, neuron generation, and embryonic development, regulates gluconeogenesis
51692	ROHG	CPSF3	1.94	2.15	Cleavage and polyadenylation specificity factor 3, a transcription repressor that acts in mRNA polyadenylation
1392	Human Druggable	CRH	2.47	3.43	Corticotropin releasing hormone, a nitric-oxide synthase regulator that is involved in steroidogenesis, synaptic transmission, and immune response
49860	ROHG	CRNN	1.93	2.12	Cornulin, a calcium binding protein that acts in cell cycle arrest and inhibits cell proliferation
1473	ROHG	CST5	2.42	3.49	Cystatin D, a cysteine protease inhibitor
1485	ROHG	CTAG1B	1.88	2.17	Cancer testis antigen 1, acts in humoral immune response and cellular defense response

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
10217	ROHG	CTDSPL	2.04	2.18	Carboxy terminal domain RNA polymerase II polypeptide A small phosphatase like, a putative phosphoprotein phosphatase that inhibits cell proliferation
1499	Human Druggable	CTNNB1	1.82	1.92	Catenin beta 1, a transcriptional activator that plays a role in antiapoptosis and cell differentiation, regulates G2-M transition of mitotic cell cycle and positive selection of thymocytes
1497	Human Druggable	CTNS	1.86	2.01	Cystinosis nephropathic, a lysosomal L-cystine transmembrane transporter that acts in lysosomal cystine transport
1509	Human Druggable	CTSD	1.88	2.02	Cathepsin D, a peptidase that acts in angiogenesis and apoptosis
1512	Human Druggable	CTSH	2.89	4.32	Cathepsin H, involved in response to low density lipoprotein stimulus
1513	Human Druggable	CTSK	2.75	4.00	Cathepsin K, a collagenolytic cysteine protease that acts in ossification, increased expression causes arteriosclerosis
1520	Human Druggable	CTSS	2.55	3.55	Cathepsin S, a cysteine-type peptidase that regulates angiogenesis and microglial cell migration, acts in antigen processing and presentation
58191	ROHG	CXCL16	1.92	2.15	Chemokine (C-X-C motif) ligand 16, a scavenger receptor that regulates oxidized LDL uptake, acts in angiogenesis and cell migration, upregulated in myocardial infarction and pancreatitis
220002	ROHG	CYBASC3	1.93	2.22	Protein with high similarity to mouse Cybrd1, which is a b-type cytochrome with ferric reductase activity that acts in the iron absorption pathway
79901	ROHG	CYBRD1	2.04	2.44	Cytochrome b reductase 1, involved in iron homeostasis, reduces monodehydroascorbate to ascorbate
1583	Human Druggable	CYP11A1	1.93	2.11	Cytochrome P450 family 11 subfamily A polypeptide 1, cholesterol monooxygenase that acts in steroid biosynthesis and osteoblast proliferation

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
1562	Human Druggable	CYP2C18	1.84	1.91	Cytochrome P450 family 2 subfamily C polypeptide 18, a monooxygenase and retinoic acid 4-hydroxylase that plays a role in retinoid and xenobiotic metabolic process
10858	ROHG	CYP46A1	1.96	2.01	Cytochrome P450 family 46 subfamily A polypeptide 1, catalyzes the conversion of cholesterol to 24S-hydroxycholesterol, may play a role in beta-amyloid metabolism and nervous system development
23002	Human Druggable	DAAM1	1.90	2.06	Dishevelled associated activator of morphogenesis 1, binds to Rho GTPase RHOA, RHOB, and RHOC, plays a role in actin assembly and Wnt receptor signaling
1621	Human Druggable	DBH	2.22	2.78	Dopamine beta-hydroxylase, catalyzes dopamine to norepinephrine conversion, acts in locomotory behavior and sensory perception
28983	Human Druggable	DESC1	1.93	2.11	Transmembrane protease serine 11E, hydrolyzes extracellular matrix components, including fibronectin, gelatin and fibrinogen, confers tumorigenic properties to Madin Darby canine kidney cells
1687	Human Druggable	DFNA5	2.12	2.55	Deafness autosomal dominant 5, may play a role in caspase activation, cell proliferation, and cell cycle arrest
54487	ROHG	DGCR8	2.23	2.82	DiGeorge syndrome critical region gene 8, binds to RNA and mediates stem cell division, pre-microRNA and primary microRNA processing
9249	ROHG	DHRS3	1.98	2.05	Dehydrogenase reductase SDR family member 3, catalyzes the NADPH-dependent reduction of all-trans-retinal, plays a role in fatty acid metabolism
22907	ROHG	DHX30	2.05	2.39	DEAH box polypeptide 30, a corepressor of photoreceptor cell-specific nuclear receptor (NR2E3)
26130	ROHG	DKFZP434C212	1.94	2.14	GTPase activating protein and VPS9 domains 1, a Rab guanyl-nucleotide exchange factor and Ras GTPase activator, plays a role in endocytosis

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
64753	ROHG	DKFZP434G156	2.29	3.03	Protein of unknown function
81556	ROHG	DKFZP564O1664	0.27	-1.92	Chromosome 15 open reading frame 44
84067	ROHG	DKFZP566M1046	2.22	2.41	Protein of unknown function, has strong similarity to uncharacterized rat MGC94288
10294	Human Druggable	DNAJA2	1.98	2.24	DnaJ (Hsp40) homolog subfamily A member 2, a HSC70 protein regulator that plays a role in protein folding and refolding, functions in mitochondrial translocation
1778	Human Druggable	DNCH1	0.26	-2.02	Dynein cytoplasmic 1 heavy chain 1, catalyzes the movement along a microtubule, plays a role in the mitotic spindle organization and biogenesis and retrograde axon cargo transport;
1786	Human Druggable	DNMT1	2.12	2.55	DNA (cytosine-5-)-methyltransferase, binds to DNMT3A and DNMT3B, acts in DNA methylation and gene silencing, interacts with HDAC2 and DMAP1 to mediate transcriptional repression
116092	Human Druggable	DNTTIP1	1.93	2.12	Deoxynucleotidyltransferase terminal interacting protein 1, a single-stranded DNA binding protein that interacts with and regulates the activity of DNNT
220164	ROHG	DOK5L	1.87	2.06	Docking protein 6, a RET substrate, promotes neurite outgrowth mediated by RET, member of the p62Dok family, contains a PH domain and a PTB domain
57171	Human Druggable	DOLPP1	0.29	-1.94	Protein with strong similarity to mouse Dolpp1, which plays a role in lipid metabolic process and protein amino acid N-linked glycosylation, member of the phosphatidic acid phosphatase-related phosphoesterase family
57628	ROHG	DPP10	2.01	2.37	Dipeptidylpeptidase 10, a potassium channel regulator that plays a role in intracellular protein transport

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
56896	ROHG	DPYSL5	1.97	2.29	Dihydropyrimidinase like 5, binds to kinases, may play a role in axon guidance, nervous system development, and signal transduction
4733	Human Druggable	DRG1	1.84	1.92	Developmentally regulated GTP binding protein 1, binds to TAL1 and inhibits prostate cancer metastasis
8624	ROHG	DSCR2	1.95	1.99	Proteasome assembly chaperone 1, exhibits protein heterodimerization activity, plays a role in proteasome assembly
51207	Human Druggable	DUSP13	1.96	2.62	Dual specificity phosphatase 13, a protein tyrosine-serine-threonine phosphatase that may inhibit MAPKKK cascade
1846	Human Protein Kinase	DUSP4	1.95	2.12	Dual specificity phosphatase 4, plays a role in cell aging, induction of apoptosis by oxidative stress, and inactivation of MAPK, regulates apoptosis
84651	ROHG	ECG2	2.06	2.09	Serine peptidase inhibitor Kazal type 7, binds to p53, mediates mitotic spindle checkpoint, apoptosis induction, and protein localization, inhibits ubiquitination
1842	Human Druggable	ECM2	1.88	2.02	Extracellular matrix protein 2 female organ and adipocyte specific, may play a role in cell-matrix adhesion
8661	Human Druggable	EIF3S10	0.09	-2.07	Eukaryotic translation initiation factor 3 subunit A, a putative translation initiation factor that inhibits epithelial cell differentiation
8668	Human Druggable	EIF3S2	0.16	-1.93	Eukaryotic translation initiation factor-3 subunit-I, a transcription corepressor that acts in regulation of TGF-beta receptor signaling pathway, cell cycle, and cell proliferation
8663	Human Druggable	EIF3S8	0.17	-1.90	Eukaryotic translation initiation factor 3 subunit C, a cytosolic small ribosomal subunit that binds and recruits EIF1 to 40S ribosomes, negatively regulates cell proliferation

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
2013	ROHG	EMP2	1.99	2.45	Epithelial membrane protein 2, acts in regulation of gene expression, induction of apoptosis, embryo implantation, cell-matrix adhesion, endosome to lysosome transport, and macroautophagy
94240	ROHG	EPSTI1	2.03	2.04	Epithelial stromal interaction 1, plays a role in regulation of breast tumor cell properties and epithelial-mesenchymal transition
345062	ROHG	ESSPL	1.97	2.56	Protein of unknown function, has moderate similarity to protease serine 21
2107	Human Druggable	ETF1	0.18	-1.90	Eukaryotic translation termination factor 1, binds to translation release factors, plays a role in selenocysteine incorporation
23474	ROHG	ETHE1	2.48	3.36	Ethylmalonic encephalopathy 1, a transcriptional suppressor that interacts with histone deacetylase acts in antiapoptosis, TP53 ubiquitylation and degradation
2113	Human Druggable	ETS1	1.99	2.27	Homolog 1 of v-ets erythroblastosis virus E26 oncogene, a transcription activator that acts in apoptosis, blood vessel remodeling, decidualization, and regulation of cytokine secretion
2117	Human Druggable	ETV3	1.90	2.07	Ets variant gene 3, a putative transcriptional repressor that may play a role in cell proliferation, macrophage differentiation, and multicellular organismal development
2149	GPCR	F2R	1.87	1.94	Coagulation factor II thrombin receptor, a RAP GTPase activator that acts in inflammatory response, blood coagulation, platelet activation, and degranulation, regulates vasodilation and cell cycle
84548	ROHG	FAM11A	2.30	2.56	Protein of unknown function, has strong similarity to uncharacterized mouse Tmem185b
10144	ROHG	FAM13A1	1.96	2.01	Family with sequence similarity 13 member A, a predicted Rho GTPase activator acting in Rho signal transduction
51063	ROHG	FAM26B	1.99	2.26	Protein of unknown function, has strong similarity to uncharacterized mouse Calhm2

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
23014	Human Druggable	FBXO21	2.12	2.55	Protein containing an F-box domain, which serves as a link between a target protein and a ubiquitin-conjugating enzyme
56929	ROHG	FEM1C	1.99	2.33	Fem-1 homolog c, a putative transcription regulator that may play a role in skeletal system development, signal transduction, and sex determination
152273	ROHG	FGD5	2.65	3.26	Protein containing two pleckstrin homology (PH) domains, which mediate protein-protein interactions, a RhoGEF (GTPase exchange factor) domain, and a FYVE zinc finger domain, has a region of low similarity to rat Fgd4, which crosslinks actin
2260	Human Protein Kinase	FGFR1	1.96	2.16	Fibroblast growth factor receptor 1, a putative protein tyrosine kinase that acts in cell proliferation and skeletal development
2288	Human Druggable	FKBP4	1.89	2.03	FK506 binding protein 4 59kDa, a cochaperone immunophilin that exhibits peptidyl-prolyl cis-trans isomerase activity, functions in copper ion transport and protein refolding
55113	ROHG	FLJ10307	2.05	2.41	Protein with weak similarity to <i>C. elegans</i> CED-8, which is a plasma membrane protein that appears to have a role in the modulation of the kinetics of cell corpse engulfment during development
55226	ROHG	FLJ10774	2.08	2.48	N-acetyltransferase 10, a DNA binding transcription activator that mediates histone acetylation and mitotic chromosome decondensation
79643	ROHG	FLJ11749	0.18	-1.96	Chromatin modifying protein 6, plays a role in endosome transport, may mediate cholesterol transport
64943	ROHG	FLJ12442	2.13	2.65	Protein with moderate similarity to Rice Os09g0424600, which is involved in response to anoxia
65251	ROHG	FLJ12644	1.82	1.92	Zinc finger protein 649, a nuclear transcriptional repressor that inhibits transcriptional activities of SRE and AP1

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
79815	ROHG	FLJ13955	2.07	2.51	Member of the DUF803 domain of unknown function family, has strong similarity to uncharacterized mouse Npal2
79903	ROHG	FLJ14154	0.18	-1.92	Member of the acetyltransferase (GNAT) family
54463	ROHG	FLJ20152	2.12	2.57	Family with sequence similarity 134 member B, localized to the cis-Golgi
54471	ROHG	FLJ20232	1.85	1.94	Protein of unknown function, has very strong similarity to uncharacterized mouse AI452372
60526	ROHG	FLJ21820	2.00	2.35	Protein of unknown function, has high similarity to uncharacterized mouse 1110057K04Rik
64772	Human Druggable	FLJ21865	2.00	2.28	Endo beta N acetylglucosaminidase, catabolizes free oligosaccharides in the cytosol
80233	ROHG	FLJ22175	0.17	-1.95	Protein of unknown function, has high similarity to uncharacterized mouse 2310003H01Rik
79733	ROHG	FLJ23311	2.09	2.57	E2F transcription factor 8, a transcriptional repressor that inhibits cell proliferation, may repress expression of E2F-target genes in the S-phase of the cell cycle
132332	ROHG	FLJ30834	2.33	2.62	Protein of unknown function
144577	ROHG	FLJ32549	2.25	2.47	Protein of unknown function, has strong similarity to uncharacterized mouse BC048403
255252	ROHG	FLJ36812	1.89	2.11	Protein containing four leucine rich repeats, which mediate protein-protein interactions, has low similarity to a region of suppressor of clear (soc-2) homolog, which forms a complex with Ras and Raf and has a role in ERK (MAPK1) signaling
283284	ROHG	FLJ37794	0.14	-2.05	Protein containing two fibronectin type III, three immunoglobulin (Ig), four immunoglobulin V-set, and six immunoglobulin I-set domain

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
284309	ROHG	FLJ38288	2.04	2.48	Protein with high similarity to human ZNF418, which is a transcriptional repressor that inhibits MAPKKK cascade, member of the KRAB box family, contains nine zinc finger C2H2 type repeats
126272	ROHG	FLJ38944	2.09	2.15	EID-2-like inhibitor of differentiation-3, a member of the EID family which negatively regulates transcription by preventing the recruitment of the co-activator complex, CBP-p300, to nuclear receptor regulated promoters
124989	ROHG	FLJ40342	2.45	2.86	Protein of unknown function
222194	ROHG	FLJ42526	1.93	2.22	Protein with high similarity to mouse Rsb1, which binds to protein kinase A
2316	Human Druggable	FLNA	1.86	2.00	Filamin A alpha, acts in actin cytoskeleton organization and apoptosis, regulates cell migration
2321	Human Protein Kinase	FLT1	1.98	2.19	Fms-related tyrosine kinase 1, a vascular endothelial growth factor receptor, acts in angiogenesis, ossification, response to hypoxia, cell phosphorylation, and proliferation
2339	Human Druggable	FNTA	2.02	2.33	Farnesyltransferase CAAX box alpha, a geranylgeranyltransferase that mediates insulin receptor and transforming growth factor beta receptor signaling, regulates Ras protein signal transduction
3170	Human Druggable	FOXA2	2.45	3.31	Forkhead box A2, a transcriptional regulator that mediates glucose metabolism, cell cycle, apoptosis, cell proliferation and differentiation, and tissue and organ development
84824	Human Druggable	FREB	1.85	1.97	Fc receptor-like A, a putative immunoglobulin receptor that may play a role in B cell differentiation
2529	ROHG	FUT7	2.26	3.10	Fucosyltransferase 7 (alpha (1,3) fucosyltransferase), forms the sialyl Lewis x moiety and functions in the glycosylation of selectin ligands

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
2531	Human Druggable	FVT1	1.89	2.04	3-ketodihydrosphingosine reductase, a 3-ketodihydrosphingosine reductase that catalyzes reduction of 3-ketodihydrosphingosine to dihydrosphingosine
53827	ROHG	FXYD5	1.97	2.22	FXD domain-containing ion transport regulator 5, a member of the FXD-domain family of small ion transport regulators or channels, inactivates cadherin-mediated cell-cell adhesion and promotes metastasis
50486	ROHG	G0S2	1.91	2.07	G0-G1switch 2, involved in response to retinoic acid
55879	Human Druggable	GABRQ	2.33	3.09	Gamma-aminobutyric acid (GABA) receptor subunit theta, a GABA-A receptor that plays a role in synaptic transmission
2581	Human Druggable	GALC	2.41	3.22	Galactosylceramidase, may play a role in galactosylceramide catabolism
130589	ROHG	GALM	1.97	1.92	Galactose mutarotase (aldose 1-epimerase), an enzyme that catalyzes the conversion of glucose and galactose between alpha and beta anomers,
8693	ROHG	GALNT4	1.94	1.96	UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylgalactosaminyltransferase 4, plays a role in protein amino acid O-linked glycosylation via serine and threonine
2520	Human Druggable	GAS	1.98	2.28	Gastrin, a putative hormone that is involved in gastric acid secretion, cell proliferation, and signal transduction
57798	ROHG	GATAD1	0.18	-1.93	GATA zinc finger domain containing 1 (ocular development-associated gene)
23464	ROHG	GCAT	1.85	1.95	Glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase), a putative transaminase that inhibits cell proliferation
81025	ROHG	GJA10	0.19	-2.12	Member of the connexin family of gap junction channel proteins, has moderate similarity to gap junction protein alpha 1 (connexin 43, human GJA1), which is a transporter that acts in cell-cell signaling

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
2735	Human Druggable	GLI	1.84	1.92	GLI family zinc finger 1, a transcriptional regulator that acts in central nervous system development, promotes cell proliferation, upregulated in prostate, breast, and several neoplasms
148423	ROHG	GM117	3.15	4.24	Protein of unknown function, has strong similarity to uncharacterized mouse 2410004B18Rik
26205	ROHG	GMEB2	2.52	3.45	Glucocorticoid modulatory element binding protein 2, an RNA polymerase II transcription factor that binds sequence specific promoter elements in a complex with GMEB1 to mediate transcription of target genes
2770	GPCR	GNAI1	1.87	1.95	Gi1 protein alpha subunit, a delta type-opioid receptor binding protein
23015	ROHG	GOLGIN-67	1.97	2.20	Golgin 67, a Golgi apparatus-specific protein, may play a role in Golgi structure maintenance, may play a role in vesicle tethering or docking
55105	ROHG	GPATC2	2.02	2.34	Member of the G-patch domain family, has strong similarity to uncharacterized mouse Gpatc2
2820	Human Druggable	GPD2	1.87	1.99	Glycerol-3-phosphate dehydrogenase 2 mitochondrial, acts in glycolysis, and oxygen and ROS metabolism, regulates fatty acid oxidation, decreased activity correlates with type 2 diabetes
11245	GPCR	GPR	2.51	3.38	Putative G protein-coupled receptor
10149	GPCR	GPR64	1.91	2.04	G protein-coupled receptor 64, an epididymal-specific member of the class B secretin-like G protein-coupled receptor family
8477	GPCR	GPR65	1.93	2.09	G protein-coupled receptor 65, a putative caspase activator that acts in apoptosis, cell proliferation, and neurogenesis

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
8111	GPCR	GPR68	1.88	1.98	G protein-coupled receptor 68, an Edg1 sphingosine 1 phosphate receptor binding protein that elevates intracellular calcium and activates MAP kinases, inhibits cell proliferation, regulates proton induced prostaglandin I2 production
2831	GPCR	GPR7	1.99	2.23	Neuropeptides B-W receptor 1, acts in activation of MAPK activity, elevation of cytosolic calcium ion concentration, generation of precursor metabolites and energy, neuropeptide signaling pathway, and regulation of adenylyl cyclase activity
10887	GPCR	GPR73	2.08	2.42	Prokineticin receptor 1, a GPCR that elevates cytosolic Ca ²⁺ , activates MAPK, may play a role in angiogenesis, nociception, placenta development, and smooth muscle contraction
128674	GPCR	GPR73L1	1.96	2.15	Prokineticin receptor 2, a GPCR that acts in the androgen metabolism, and neurogenesis, regulates hormone secretion, ion transport, and locomotion
10886	GPCR	GPR74	2.05	2.34	Neuropeptide FF receptor 2, a GPCR that binds neuropeptides AF and FF (NPFF), RFamide-related peptides (C7orf9), and prolactin releasing peptide (PRH), inhibits adenylyl cyclase and stimulates intracellular Ca ²⁺ flux
10888	GPCR	GPR83	2.16	2.59	G protein-coupled receptor 83, acts in the insulin receptor signaling pathway
2939	ROHG	GSTA2	2.01	2.48	Glutathione S-transferase A2, catalyzes conjugation of glutathione to toxic compounds, mediates detoxification of electrophilic xenobiotics
373156	ROHG	GSTK1	2.05	2.39	Glutathione S-transferase kappa 1, exhibits glutathione transferase and glutathione peroxidase activities, predicted to function in cellular and lipid metabolisms
2975	Human Druggable	GTF3C1	1.91	2.06	General transcription factor IIIC polypeptide 1 alpha subunit 220kD, a transcription factor TFIIC subunit, required for transcription from the RNA polymerase III promoter

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
23498	ROHG	HAAO	2.04	2.37	3 hydroxyanthranilate 3 4 dioxygenase, an electron carrier that may play a role in quinolinate synthetase A activity
3033	Human Druggable	HADHSC	1.95	2.16	Hydroxyacyl-Coenzyme A dehydrogenase, acts in fatty acid beta-oxidation, insulin secretion, and steroid hormone metabolism
57817	Human Druggable	HAMP	1.82	1.91	Hepcidin antimicrobial peptide, acts in cellular iron ion homeostasis
23438	ROHG	HARSL	2.12	2.56	Histidyl-tRNA synthetase 2 mitochondrial, a putative ATP binding protein that may play a role in the regulation of translation and histidyl-tRNA aminoacylation
3047	Human Druggable	HBG1	1.97	2.26	Hemoglobin gamma A, plays a role in erythropoiesis, may be associated with hemoglobin complex
10542	ROHG	HBXIP	2.05	2.20	Hepatitis B virus x-interacting protein, a transcription coactivator that regulates centrosome dynamics and spindle assembly, induces NF-kappaB transcription factor activity and inactivates caspase 9 activity
25875	Human Druggable	HCCR1	1.80	1.97	LETM1 domain containing 1, involved in protein stabilization, may mediate ubiquitin-dependent protein catabolism, regulation of growth, and transcription
79654	ROHG	HECTD3	1.93	2.18	HECT domain containing 3, likely facilitates cell cycle progression via regulating ubiquitination and degradation of Tara (TRIOBP)
57493	ROHG	HEG	0.14	-2.02	HEG homolog 1; mRNA expression is reduced in malignant serous epithelial ovarian tumors
3097	Human Druggable	HIVEP2	1.92	2.10	Human immunodeficiency virus type I enhancer binding protein 2, an RNA polymerase II transcription factor that promotes cell proliferation, involved in response to extracellular stimulus and retinoic acid

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
3188	ROHG	HNRPH2	1.80	1.96	Heterogeneous nuclear ribonucleoprotein H2 (H'), a component of mRNA cleavage and polyadenylation specificity factor complex and an RNA binding protein that recognizes the mRNA motifs GGGA and GGGGGC
3203	ROHG	HOXA6	2.02	2.51	Homeobox A6, a putative transcription factor that plays a role in embryonic pattern specification and skeletal system development
3211	Human Druggable	HOXB1	2.09	2.50	Homeobox B1, a transcription factor that plays a role in pattern specification, facial nerve structural organization, and brain development
3227	Human Druggable	HOXC11	2.18	2.71	Homeobox C11, a transcription factor that plays a role in ureteric bud development
3224	ROHG	HOXC8	2.25	3.08	Homeobox C8, a transcriptional repressor that plays a role in skeletal system development, pattern specification, and cartilage differentiation
3268	ROHG	HRBL	0.18	-2.02	HIV-1 Rev binding protein-like, a cellular cofactor of the human immunodeficiency virus Rev protein, contains a zinc finger domain and four EH domain-binding NPF motifs
27102	Human Protein Kinase	HRI	1.98	2.20	Eukaryotic translation initiation factor 2 alpha kinase 1, plays a role in protein amino acid phosphorylation, involved in response to nitric oxide
9953	ROHG	HS3ST3B1	2.01	2.13	Heparan sulfate 3 O sulfotransferase 3B1, a putative integral plasma membrane protein that plays a role in heparan sulfate proteoglycan biosynthetic process
11077	Human Druggable	HSF2BP	2.61	3.70	Heat shock transcription factor 2 binding protein
3363	GPCR	HTR7	1.96	2.15	5-hydroxytryptamine receptor 7, activates MAPK activity and adenylyl cyclase activity by serotonin receptor signaling pathway, plays a role in neuron projection development, micturition, and behavioral functions

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
127544	ROHG	IBRDC3	3.28	4.51	Protein with high similarity to human RNF19A, which is an ubiquitin ligase that regulates caspase activity, release of cytochrome C, and programmed cell death, contains a C3HC4 type (RING) zinc finger
3421	ROHG	IDH3G	1.83	2.05	Isocitrate dehydrogenase 3 (NAD ⁺) gamma, catalyzes the oxidative decarboxylation of isocitrate into alpha-ketoglutarate in the TCA cycle
3430	Human Druggable	IFI35	1.92	2.10	Interferon-induced protein 35, binds to transcription factor, exhibits homodimer and heterodimerization activity
23765	Human Druggable	IL17R	2.07	2.49	Interleukin 17 receptor A, acts in the regulation of interleukin-6 biosynthetic process and protein binding
29949	Human Druggable	IL19	2.28	2.97	Interleukin 19, a cytokine that induces apoptosis, IL-6, and TNF production,
3576	GPCR	IL8	2.15	2.57	Interleukin 8, acts in immune response, aberrantly expressed in digestive, lung, and immune system diseases, Behcet syndrome, multiple sclerosis, diabetes, pancreatitis, ischemia, psoriasis, arteriosclerosis, myelofibrosis, and several cancers
51147	Human Druggable	ING4	2.16	2.64	Inhibitor of growth family member 4, mediates G2-M transition of mitotic cell cycle, chromatin remodeling, and induction of apoptosis, regulates histone acetylation
3675	Human Druggable	ITGA3	2.11	2.58	Integrin alpha 3, a laminin receptor that plays a role in small GTPase mediated signaling, cell proliferation, migration, and adhesion, protein complex assembly, and phagocytosis
3699	ROHG	ITIH3	1.86	2.12	Inter-alpha inhibitor H3, a putative endopeptidase inhibitor
84962	ROHG	JUB	3.11	4.18	Jub ajuba homolog, an enzyme regulator and a signal transducer that plays a role in activation of Rac GTPase, homophilic cell adhesion, lamellipodium assembly, and G2-M transition of mitotic cell cycle, inhibits transcription

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
7881	Human Druggable	KCNAB1	1.83	2.04	Potassium voltage-gated channel shaker-related subfamily beta member 1, a potassium channel inhibitor that may act in cardiomyocyte excitement
23415	Human Druggable	KCNH4	1.82	1.91	Potassium voltage-gated channel subfamily H (eag-related) member 4, a ion channel that may play a role in synaptic transmission
27133	Human Druggable	KCNH5	1.84	2.29	Potassium voltage-gated channel subfamily H member 5, plays a role in potassium ion transport
23023	Human Druggable	KIAA0779	1.87	2.15	Transmembrane and coiled-coil domain family 1, a predicted DNA or RNA binding protein
57592	ROHG	KIAA1441	2.02	2.38	Zinc finger protein 687; gene translocation with the RUNX1 partner gene is associated with acute myeloid leukemia
57683	ROHG	KIAA1571	2.13	2.66	Protein of unknown function
57701	ROHG	KIAA1602	0.14	-2.02	Member of the amino acid permease family of membrane transporters, has moderate similarity to human SLC7A1
11278	Human Druggable	KLF12	2.45	3.31	Kruppel-like factor 12, a transcriptional corepressor, modulates activity of AP-2alpha promoter
3816	ROHG	KLK1	1.80	1.97	Kallikrein 1, a peptidase that cleaves kininogen, functions in glucose homeostasis, heart contraction, and vasoconstriction
25984	ROHG	KRT23	2.44	3.28	Protein with moderate similarity to keratin 19
9355	ROHG	LHX2	1.93	1.96	LIM homeobox 2, a transcription factor that acts in hair follicle development, thalamocortical tract pathfinding, and erythropoiesis
3978	Human Druggable	LIG1	1.85	1.95	Ligase I DNA ATP-dependent, acts in DNA replication and base excision repair
4009	Human Druggable	LMX1A	2.18	2.71	LIM homeobox transcription factor 1 alpha, a transcription activator that plays a role in neural plate development, neuron differentiation, and regulation of cell cycle
120224	ROHG	LOC120224	2.34	2.64	Member of the DUF716 domain of unknown function family

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
126731	ROHG	LOC126731	1.98	1.94	Protein of unknown function, has high similarity to uncharacterized mouse 1700054N08Rik
150084	ROHG	LOC150084	1.97	1.92	Protein of unknown function, has high similarity to uncharacterized rat LOC304000
150946	ROHG	LOC150946	2.26	2.48	family with sequence similarity 59, member B (NCBI)
163233	ROHG	LOC163233	1.88	2.08	Protein with high similarity to human ZNF85, which is involved in the negative regulation of transcription from RNA polymerase II promoter
163782	ROHG	LOC163782	1.94	2.22	Protein containing three ankyrin repeats, which may mediate protein binding, has low similarity to ankyrin repeat domain 15, which acts in cell cycle arrest, regulation of cell shape, and actin filament organization
203427	ROHG	LOC203427	2.23	2.93	Member of the mitochondrial carrier protein family of membrane transporters
221955	ROHG	LOC221955	1.81	1.92	Diacylglycerol lipase beta, a predicted diacylglycerol-lipase that may act in biosynthesis of the endocannabinoid 2-arachidnoyl glycerol
253012	ROHG	LOC253012	2.74	4.14	HEPACAM family member 2, plays a likely role in mitosis and nuclear morphology, localizes to mitotic spindles and centrosomes
339448	ROHG	LOC339448	0.17	-1.96	Protein of unknown function, has high similarity to uncharacterized mouse A430005L14Rik
339453	ROHG	LOC339453	2.44	3.44	Chromosome 1 open reading frame 70
346673	ROHG	LOC346673	0.26	-1.95	Protein with high similarity to stimulated by retinoic acid gene 8
349136	ROHG	LOC349136	1.76	1.99	Protein containing eight WD domain G-beta repeats, has weak similarity to C. elegans C14B1.4, which positively regulates histone H3-K4 methylation
375035	ROHG	LOC375035	1.89	2.11	Member of the SFT2-like protein family, which may be transmembrane proteins
51760	ROHG	LOC51760	1.87	1.98	Protein containing two C2 domains, which may be involved in calcium-dependent phospholipid binding

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
63928	ROHG	LOC63928	1.82	1.92	Calcineurin B homologous protein 2, binds to and stimulates phosphatase activity of calcineurin A, regulates sodium ion transport, and inhibits serum deprivation-induced cell death by increasing intracellular pH
83468	ROHG	LOC83468	1.97	2.32	Member of the glycosyl transferase family 8, which transfer sugar residues to donor molecules during lipopolysaccharide and glycogen biosynthesis
90167	ROHG	LOC90167	2.17	2.30	FERM domain containing 7, plays a likely role in control of eye movement and gaze stability
91966	ROHG	LOC91966	2.81	3.58	Chromosome X open reading frame 40A, interacts with MT2A
93343	ROHG	LOC93343	2.07	2.12	Protein of unknown function, has strong similarity to uncharacterized mouse 1110012M11Rik
121227	ROHG	LRIG3	2.28	2.53	Leucine-rich repeats and immunoglobulin-like domains 3, may regulate cell proliferation
92335	Human Protein Kinase	LYK5	0.12	-1.97	Protein kinase LYK5, a likely pseudokinase that regulates the kinase activity of LKB1 (STK11) and is required for LKB1-induced cell cycle arrest
4126	Human Druggable	MANBA	1.84	1.93	Mannosidase beta A lysosomal, may play a role in oligosaccharide metabolic process
4188	ROHG	MDFI	1.98	2.41	MyoD family inhibitor, a putative transcriptional repressor that mediates cytoplasmic sequestering of transcription factor, regulates striated muscle development, inhibits release of sequestered calcium ion into cytosol
78986	Human Druggable	MGC1136	1.90	2.46	Dual specificity phosphatase 26, a protein phosphatase that binds the HSF4 transcription factor, promotes anaplastic thyroid cancer cell growth by inhibiting p38 MAPK (MAPK14) activity
84283	ROHG	MGC13102	1.92	2.43	Protein of unknown function, has strong similarity to uncharacterized mouse 2310042N02Rik

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
84315	ROHG	MGC13272	1.86	2.26	Protein with strong similarity to MON1 homolog A, which is required for trafficking of ferroportin and regulation of cellular iron content and has a fundamental role in the secretory apparatus
84841	ROHG	MGC15634	2.19	2.36	Protein with high similarity to human ZNF85, which is a transcription repressor, member of the KRAB box family, contains many zinc finger C2H2 type repeats
84970	ROHG	MGC15882	2.75	3.45	Protein of unknown function
133383	ROHG	MGC33648	2.13	2.23	Protein of unknown function
256586	ROHG	MGC35274	2.08	2.56	Protein of unknown function, has strong similarity to uncharacterized mouse Lysmd2
79415	ROHG	MGC4368	0.12	-2.11	Protein of unknown function, has strong similarity to uncharacterized mouse Bc017643
253769	ROHG	MGC43690	1.93	2.22	Protein containing two WD domain G-beta repeats
79025	ROHG	MGC5356	1.91	2.14	Protein of unknown function, has strong similarity to uncharacterized mouse BC051628
4257	Human Druggable	MGST1	1.89	2.03	Microsomal glutathione S-transferase 1, involved in aging and response to oxidative stress
4284	Human Druggable	MIP	2.24	2.88	Major intrinsic protein of lens fiber, a calmodulin binding water channel that plays a role in visual perception and water transport
4297	Human Druggable	MLL	1.99	2.26	Mixed-lineage leukemia, a histone methyltransferase that acts in maintenance of Hox gene expression during embryonic development, regulates anteroposterior axis formation
58508	Human Druggable	MLL3	0.30	-1.92	Myeloid-lymphoid or mixed-lineage leukemia 3, a transcription coactivator that mediates histone H3-K4 methylation
4299	ROHG	MLLT2	1.83	2.03	AF4-FMR2 family member 1, a transcription activator that acts in histone methylation, eye, and hindbrain development, regulates insulin-like growth factor receptor signaling pathway

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
143098	ROHG	MPP7	1.97	1.92	Membrane protein palmitoylated 7 (MAGUK p55 subfamily member 7), forms a complex with LIN7A or LIN7C and DLG1 that regulates stability and localization of DLG1 to cell junctions, binds DLG1 to facilitate epithelial tight junction formation
3140	ROHG	MR1	0.21	-1.95	MHC class I-like antigen MR-1, a beta-2-microglobulin binding protein that plays a role in the regulation of MHC class I expression
65080	ROHG	MRPL44	2.04	2.45	Member of the RNase3 domain containing family, contains a double-stranded RNA binding domain
92259	ROHG	MRPS36	2.79	3.54	Mitochondrial ribosomal protein S36, a putative component of the small subunit of the mitochondrial ribosome
10797	ROHG	MTHFD2	2.09	2.28	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 methenyltetrahydrofolate cyclohydrolase, an electron carrier that may act in utero embryonic development, mitochondrion organization, and translation
219402	ROHG	MTIF3	2.10	2.60	Mitochondrial translational initiation factor 3, binds to mitochondrial ribosomal subunits, mediates dissociation of 55S ribosomal subunits and fMet-tRNA bound to mitochondrial 28S subunits
23026	ROHG	MYR8	2.15	2.61	Protein with high similarity to myosin heavy chain Myr 8, an unconventional myosin that binds actin, contains five ankyrin repeats, a myosin head domain (motor domain), and an IQ calmodulin-binding motif
55577	Human Protein Kinase	NAGK	0.12	-1.97	N-acetylglucosamine kinase, an enzyme that phosphorylates N-acetylglucosamine and N-acetylmannosamine, binds to ADP and glucose, plays a role in carbohydrate phosphorylation
22861	Human Druggable	NALP1	1.98	2.40	NLR family pyrin domain containing 1, binds to ATP and caspase, plays a role in caspase activation and induction of apoptosis by granzyme

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
222236	ROHG	NAPE-PLD	2.36	3.24	N-acyl phosphatidylethanolamine phospholipase D, hydrolyzes N-acyl phosphatidylethanolamines to the corresponding N-acylethanolamines, acts in neurotransmitter biosynthesis and embryo implantation and development
26151	ROHG	NAT9	2.12	2.55	N-acetyltransferase 9, a predicted N-acetyltransferase whose defective regulation by the RUNX1 transcription factor may be a determinant for susceptibility to psoriasis
81565	Human Druggable	NDEL1	2.30	3.19	NUDE-like protein, an endopeptidase that acts in microtubule anchoring at centrosome and chromosome segregation, regulates mitotic cell cycle, neurogenesis, and exocytosis
3340	ROHG	NDST1	2.19	2.91	N-deacetylase-N-sulfotransferase 1, a bifunctional enzyme that catalyzes both N-deacetylation and N-sulfation of glucosamine of glycosaminoglycan in heparan sulfate
4747	Human Druggable	NEFL	1.83	2.03	Neurofilament light polypeptide, a structural constituent of the cytoskeleton
29922	Human Protein Kinase	NME7	1.88	1.96	Protein containing two nucleoside diphosphate kinase domains, has low similarity to a region of thioredoxin domain containing 3, a microtubule binding protein with ciliary function
9111	Human Druggable	NMI	1.98	2.24	N-myc interactor, a transcription corepressor that is involved in JAK-STAT cascade, protein stabilization, and inflammatory response
10316	GPCR	NMUR1	2.10	2.46	Neuromedin U receptor 1, a peptide receptor that plays a role in elevation of cytosolic calcium ion concentration, inflammatory response, and regulation of cytokine production, involved in response to bacterium and hormone stimulus
57414	ROHG	NPD007	1.85	1.99	Rhomboid domain containing 2, positively regulates cell proliferation

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
64324	Human Druggable	NSD1	1.84	2.29	Nuclear receptor binding SET domain protein 1, a transcription coactivator that plays a role in skeletal development and cell growth
9423	Human Druggable	NTN1	0.12	-2.05	Netrin-1, regulates angiogenesis and plays a role in axon guidance, inhibits RhoA GTPase activity, highly expressed in non small cell lung cancer
83894	ROHG	NYD-SP14	3.25	4.45	Protein containing four type 2 and four type 1 tetratricopeptide repeats, which may mediate protein-protein interactions
84654	ROHG	NYD-TSP1	2.42	2.79	Spermatogenic leucine zipper 1, a putative transcription factor
22953	Human Druggable	P2RX2	1.89	2.08	Purinergic receptor P2X ligand-gated ion channel 2, an ATP-gated cation channel that plays a role in calcium ion transport
201161	ROHG	P30	2.10	2.62	Centromere protein V, acts in directional cell motility and progression of mitosis as a scaffolding molecule linking microtubules and Src family kinases, required for centromere organization, chromosome alignment and cytokinesis
26986	ROHG	PABPC1	0.20	-2.09	Poly(A)-binding protein cytoplasmic 1, binds to RNA, regulates cell migration, focal adhesion formation, and translation, may act in nucleocytoplasmic transport
55003	ROHG	PAK1IP1	1.96	2.20	PAK1 interacting protein 1, a serine-threonine protein kinase inhibitor that interacts with PAK1 to inhibit downstream JNK and NF-kappaB signaling pathways
5090	Human Druggable	PBX3	1.70	1.91	Pre-B-cell leukemia homeobox 3, a enhancer binding transcription factor that acts in spinal cord and limb development, proprioception, locomotion, and perception of sound
5097	Human Druggable	PCDH1	2.56	3.56	Protocadherin 1, plays a role in cell adhesion and embryonic development

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
26577	ROHG	PCOLCE2	1.79	2.08	Procollagen C-endopeptidase enhancer 2, enhances cleavage of type II procollagen by the procollagen C-proteinases, BMP1 and TLL1, accelerates proteolytic processing of pro-apolipoprotein AI (APOA1) to play a likely role in HDL biogenesis
79955	ROHG	PDZK7	1.82	1.94	PDZ domain containing 7, a component of the protein network related to Usher syndrome
5204	Human Druggable	PFDN5	1.84	1.92	Prefoldin subunit 5, a transcription corepressor that interacts and inhibits transcriptional activity of MYC, regulates cell proliferation
114770	ROHG	PGLYRP2	2.00	1.98	Peptidoglycan recognition protein 2, a N-acetylmuramoyl-L-alanine amidase that mediates cell response to bacteria
8225	ROHG	PGPL	2.06	2.22	Pseudoautosomal GTP-binding protein-like, a putative GTP-binding protein
54681	Human Druggable	PH-4	2.08	2.66	Hypoxia inducible factor prolyl 4 hydroxylase, a putative oxygen sensor that responds to hypoxia
51230	ROHG	PHF20	2.06	2.41	PHD finger protein 20, altered mRNA expression is observed in U937 macrophages following events that induce atherosclerosis
5283	ROHG	PIGH	2.23	2.59	Phosphatidylinositol glycan anchor biosynthesis class H, plays a role in GPI anchor biosynthesis and protein modification
30849	Human Protein Kinase	PIK3R4	2.13	2.53	Phosphoinositide-3-kinase regulatory subunit 4, forms a complex with and activates PtdIns 3-kinase, involved in macroautophagy induction, may be involved in protein trafficking and vesicle-mediated transport
114780	ROHG	PKD1L2	1.98	1.93	Polycystic kidney disease 1-like 2, binds specific G protein subunits
8605	Human Druggable	PLA2G4C	1.79	1.95	Phospholipase A2 group IVC, plays a role in metabolism of arachidonic acid, phosphatidylethanolamine, and prostaglandin, acts in phospholipid homeostasis

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
22925	Human Druggable	PLA2R1	1.87	2.13	Phospholipase A2 receptor 1, a phospholipase A2 activator that may play a role in phospholipase-mediated melanocyte dendricity and pigmentation
5325	Human Druggable	PLAGL1	2.00	2.29	Pleomorphic adenoma gene-like 1, a transcription activator that acts in cell cycle arrest, cell surface receptor linked signal transduction, and induction of apoptosis
59338	Human Druggable	PLEKHA1	2.01	2.29	Pleckstrin homology domain containing family A member 1, binds to phosphatidylinositol-3-4-bisphosphate, acts in B-cell receptor signaling pathway
5347	Human Protein Kinase	PLK1	0.11	-1.99	Polo-like kinase 1, an serine-threonine kinase that acts in Golgi organization, mitotic cell cycle G2-M transition DNA damage checkpoint, and protein amino acid phosphorylation,
10154	Human Druggable	PLXNC1	1.88	2.05	Plexin C1, a receptor for SEMA7A and virally-encoded semaphorins A39R and AHV, inhibits melanocyte spreading, involved in soluble CD100 (SEMA4D) mediated inhibition of monocyte migration
5368	ROHG	PNOC	2.26	2.64	Prepronociceptin, a neuropeptide hormone that activates MAPK activity, regulates chemotaxis, neutrophil degranulation, blood pressure, and heart contraction
84172	ROHG	POLR1B	2.19	2.35	Protein with strong similarity to mouse Rpo1-2, which inhibits apoptosis and plays a role in rRNA synthesis and nucleolus organization and biogenesis
64840	Human Druggable	PORCN	1.90	2.05	Porcupine homolog, a putative chaperone-like molecule that is involved in Wnt protein processing,
5511	Human Druggable	PPP1R8	2.57	4.29	Protein phosphatase 1 regulatory (inhibitor) subunit 8, a magnesium-dependent endoribonuclease that interacts with EZH2 and EED to inhibit transcription, binds and targets PPP1CA and PPP1CC to nuclear speckles, acts in cleavage of RNase E substrates

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
54886	ROHG	PRG-3	1.95	2.16	Protein with very strong similarity to plasticity-related protein 3 (rat Prg-3), member of the phosphatidic acid phosphatase-related (PAP2) phosphoesterase family
10216	Human Druggable	PRG4	2.18	2.90	Proteoglycan 4, plays a role in cell proliferation, may act in cell-matrix adhesion
5725	Human Druggable	PTBP1	0.23	-1.90	Polypyrimidine tract binding protein 1, plays a role in regulation of alternative splicing, translation, cell proliferation, and apoptosis, acts in G1-S phase cell cycle, focal adhesion formation and RNA stabilization
169714	ROHG	QSCN6L1	2.03	2.45	Quiescin Q6 sulfhydryl oxidase 2, regulates the sensitivity of neuroblastoma cells to interferon-gamma (IFNG)-induced apoptosis, member of the sulfhydryl oxidase-Quiescin6 family
5865	Human Druggable	RAB3B	0.26	-2.01	RAB3B member RAS oncogene family, a GTPase that binds to calmodulin, functions in exocytosis, may play a role in vesicle-mediated transport
23637	ROHG	RABGAP1	1.95	2.16	RAB GTPase activating protein 1, a tubulin binding protein that plays a role in Rab protein signal transduction and microtubule nucleation, regulates mitotic cell cycle
57610	ROHG	RANBP10	2.30	3.05	RAN binding protein 10, a transcription coactivator that plays a role in hemostasis, Ran protein signal transduction, and regulation of microtubule cytoskeleton organization
29098	ROHG	RANGNRF	2.37	3.13	RAN guanine nucleotide release factor, a Ran GTPase binding protein that mediates nuclear import, may play a role in intracellular protein transport
5914	Human Druggable	RARA	1.88	2.04	Retinoic acid receptor alpha, a DNA binding protein that regulates transcription, chondrocyte differentiation, and cell cycle

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
5932	Human Druggable	RBBP8	1.81	1.98	Retinoblastoma binding protein 8, a transcriptional corepressor that acts in DNA double-strand break repair, G2-M transition checkpoint, and in utero embryonic development
5948	ROHG	RBP2	2.70	3.56	Cellular retinol-binding protein 2, a fatty acid binding protein that may play a role in the transport of 9-cis retinoic acid to its nuclear receptor, increased serum level correlates with chronic renal failure
5954	ROHG	RCN1	2.40	2.93	Reticulocalbin 1, binds to calcium ions
6001	ROHG	RGS10	2.22	2.55	Regulator of G protein signaling 10, binds and stimulates the GTPase activity of GNAI, involved in HTR1A-mediated signaling, regulates the activity of potassium channels and adenylyl cyclase
22838	ROHG	RNF44	2.25	2.85	Protein with high similarity to RING finger protein OIP1, which binds to the sperm tail protein rat Odf1, contains a C3HC4 type (RING) zinc finger
10073	Human Druggable	RNUT1	1.90	2.06	Snurportin-1, plays a role in cajal body organization and nucleocytoplasmic transport, involved in small nucleolar ribonucleoprotein complex assembly and snRNP protein import into nucleus
4736	ROHG	RPL10A	0.20	-1.96	Ribosomal protein L10a, a putative structural constituent of ribosome that shows cellular response to X-rays and fission neutron-ionizing radiation
23521	Human Druggable	RPL13A	0.19	-1.98	Ribosomal protein L13a, binds to 3'-UTR mRNA and translation initiation factors and inhibits translation
6146	ROHG	RPL22	1.91	1.91	Ribosomal protein L22, a structural constituent of ribosome that plays a role in thymocyte development, regulates T cell apoptosis and CD4 and CD8-positive alpha-beta T cell differentiation
6167	Human Druggable	RPL37	0.12	-2.16	Ribosomal protein L37, a putative ribosomal protein that may bind to zinc ion and may play a role in translation

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
6125	Human Druggable	RPL5	0.12	-2.16	Ribosomal protein L5, a structural constituent of ribosome that plays a role in translation and protein complex assembly
6235	Human Druggable	RPS29	0.21	-1.95	Ribosomal protein S29, a zinc ion binding protein that plays a role in the regulation of cell shape
6242	ROHG	RTKN	2.57	3.30	Rhotekin, interacts with RHOA, plays a role in Rho protein signal transduction, I-kappaB kinase-NF-kappaB cascade, and regulation of survival gene product expression
57142	ROHG	RTN4	1.91	2.13	Reticulon 4, a growth inhibitor that modulates growth cone motility, acts in neuron development and maturation
9905	ROHG	RUTBC1	2.01	2.13	Small G protein signaling modulator 2, interacts with several members of the RAP and RAB small G protein superfamily to likely modulate their activity, contains a RUN domain and a TBC domain
8607	Human Druggable	RUVBL1	0.25	-2.06	RuvB-like 1, a ATPase that forms complex with ACTL6A and RUVBL2, binds to ssRNA, ssDNA, and dsDNA, regulates histone acetyltransferase activity of TIP60, involved in H2AX dephosphorylation
6385	Human Druggable	SDC4	2.29	2.94	Syndecan 4, involved in actin cytoskeleton organization, regulates inositol phospholipid binding and signaling, platelet aggregation, and dendritic cell motility
6386	ROHG	SDCBP	2.15	2.42	Syndecan binding protein, an antigen binding protein that plays a role in cell migration, protein complex assembly, and intracellular protein transport
10640	Human Druggable	SEC10L1	1.79	1.93	SEC10-like 1, a component of the exocyst complex, involved in the synthesis and delivery of secretory proteins in epithelial cells
6404	Human Druggable	SELPLG	1.91	2.12	Selectin P ligand, a kinase binding protein, mediates leukocyte adhesion and rolling, MAPK activation, inhibits hemopoiesis, may mediate hemostasis

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
10371	Human Druggable	SEMA3A	1.84	1.95	Semaphorin 3A, a putative chemorepellent that acts in apoptosis, angiogenesis, and spine and organ development
462	Human Druggable	SERPINC1	2.54	3.50	Antithrombin III, inhibits blood coagulation and angiogenesis
114132	Human Druggable	SIGLEC11	1.91	2.09	Sialic acid binding Ig-like lectin 11, a member of the CD33/Siglec-3-related Siglec family, binds alpha2-8-linked sialic acids and protein phosphatases SHP-1 and SHP-2
6490	Human Druggable	SILV	2.18	2.91	Silver homolog, a putative structural molecule that acts in T cell activation, melanocyte differentiation, and epidermis development
201780	ROHG	SLC10A4	1.98	2.34	Solute carrier family 10 member 4, exhibits regulated expression in dopaminergic neurons of the developing ventral mesencephalon
121260	ROHG	SLC15A4	2.27	2.51	Solute carrier family 15 member 4, a histidine transporter that plays a role in di- and tripeptide transport, regulates nucleotide-binding oligomerization domain containing-1 dependent NF kappaB signaling
114789	ROHG	SLC25A25	4.09	6.11	Solute carrier family 25 mitochondrial carrier phosphate carrier member 25, a putative calcium ion binding protein that may play a role in mitochondrial transport, expressed in the liver and skeletal muscle
10559	ROHG	SLC35A1	2.51	3.17	Solute carrier family 35 member A1, a CMP-sialic acid transmembrane transporter that mediates CMP-sialic acid transport and protein amino acid glycosylation
7355	ROHG	SLC35A2	2.95	4.08	Solute carrier family 35 member A2, catalyzes the transport of UDP-N-acetylgalactosamine across the membrane, involved in galactose metabolism and E-selectin mediated cell-cell adhesion
57181	ROHG	SLC39A10	2.14	2.68	Protein with moderate similarity to human SLC39A6, which plays a role in zinc ion transport, involved in cellular response to estrogen and progesterone

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
55630	Human Druggable	SLC39A4	1.91	2.13	Solute carrier family 39 member 4, a zinc ion transporter
84102	ROHG	SLC41A2	2.44	2.85	Solute carrier family 41 member 2, functions as a plasma membrane magnesium ion transporter
9497	ROHG	SLC4A7	2.00	2.11	Solute carrier family 4 sodium bicarbonate cotransporter member 7, plays a role in bicarbonate transport and regulation of pH
9498	ROHG	SLC4A8	1.93	1.95	Solute carrier family 4 sodium bicarbonate cotransporter member 8, regulates pH, acts in eye and ear development and sensory perception
340024	ROHG	SLC6A19	1.84	2.00	Solute carrier family 6 member 19, an neutral L-amino acid secondary active transmembrane transporter that plays a role in leucine and sodium ion transport
6534	ROHG	SLC6A7	2.04	2.19	Solute carrier family 6, an amino acid transmembrane transporter that plays a role in L-proline transport
23315	ROHG	SLC9A8	2.02	2.32	Protein with very strong similarity to mouse Slc9a8, which is a sodium-hydrogen antiporter that regulates pH
6578	ROHG	SLCO2A1	2.13	2.37	Solute carrier organic anion transporter family member 2A1, a prostaglandin transmembrane transporter that regulates prostaglandin uptake
10944	ROHG	SMAP	1.90	2.04	Protein of unknown function, has strong similarity to uncharacterized mouse 1110004F10Rik
64094	ROHG	SMOC2	0.19	-1.91	SPARC related modular calcium binding 2, plays a role in cell cycle progression by regulating integrin linked kinase (ILK) activity during G1 cell cycle progression, regulates growth factor induced cyclin D1 expression and DNA synthesis
6643	ROHG	SNX2	2.15	2.41	Sorting nexin 2, a putative protein transporter that plays a role in retrograde transport from endosome to Golgi and embryonic development, regulates epidermal growth factor receptor signaling

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
65244	ROHG	SPATS2	1.90	2.10	Protein with strong similarity to spermatogenesis associated serine-rich 2, which is developmentally regulated during spermatogenesis and downregulated in response to heat stress
90864	ROHG	SPSB3	0.24	-2.01	Member of the SPRY (SPLa and the RYanodine Receptor) domain containing family
6731	Human Druggable	SRP72	0.20	-1.97	Signal recognition particle 72kDa, a putative ribonucleoprotein that undergoes cleavage by caspase during apoptosis
256435	ROHG	ST6GALNAC3	1.92	2.20	ST6 N-acetylgalactosaminide alpha-2-6-sialyltransferase 3, catalyzes the formation of sialylglycoconjugates via transfer of the sialic acid group from CMP to one of several glycoconjugate acceptors, acts in O-glycan processing and protein modification
6775	Human Druggable	STAT4	1.87	2.02	Signal transducer and activator of transcription 4, acts in Th-1 cell differentiation
412	Human Druggable	STS	1.85	2.33	Steroid sulfatase arylsulfatase C isozyme S, catalyzes the conversion of sulfated steroid precursors to estrogens
6822	Human Druggable	SULT2A1	1.97	2.39	Sulfotransferase family cytosolic 2A dehydroepiandrosterone preferring member 1, a sulfotransferase that plays a role in drug, steroid, and xenobiotic metabolic processes
25870	ROHG	SUMF2	1.98	2.23	Sulfatase modifying factor 2, member of the formylglycine-generating family subgroup B, activates sulfatase activity of arylsulfatase A
6613	RefSeq 27 Supplement	SUMO2	2.55	3.38	SMT3 suppressor of mif two 3 homolog 2, a small conjugating protein ligase that plays a role in proteolysis and protein modification process, regulates protein localization
255928	ROHG	SYT14	1.89	2.11	Protein with high similarity to mouse Syt16, which is a phospholipid binding protein, contains two C2 domains, which may be involved in calcium-dependent phospholipid binding

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
6875	Human Druggable	TAF4B	1.95	2.17	TAF4b RNA polymerase II TATA box binding protein associated factor 105kDa, a transcription coactivator that plays a role in I-kappaB kinase-NF-kappaB cascade and antiapoptosis
221400	ROHG	TDRD6	2.09	2.59	Member of the tudor domain containing family, has a region of weak similarity to tudor domain containing 1 (mouse Tdrd1), which plays a role in male germ cell differentiation and nuage-germinal granule formation
64518	ROHG	TEKT3	1.98	2.29	Tektin 3, may play a role in sperm motility and in ciliary or flagellar motility
29841	ROHG	TFCP2L2	1.84	1.92	Grainyhead-like 1, a transcriptional activator that binds to the HIV-1 long terminal repeat
7032	ROHG	TFF2	2.04	2.17	Trefoil factor 2, a signal transducer that acts in JNK cascade and wound healing, regulates calcium flux, chemotaxis, angiogenesis, and inflammation
116179	ROHG	TGM7	2.71	3.38	Transglutaminase 7, a putative transglutaminase that may bind calcium
7057	Human Druggable	THBS1	1.99	2.30	Thrombospondin 1, a metalloendopeptidase inhibitor that acts in angiogenesis, downregulated in coronary artery disease
57187	ROHG	THOC2	1.89	2.08	THO complex 2, a protein that is a component of the TREX complex, which may couple transcription to mRNA export
757	ROHG	TMEM50B	2.47	3.61	Member of the UPF0220 uncharacterized protein family, has very strong similarity to uncharacterized mouse Tmem50b
7124	Human Druggable	TNF	1.87	2.03	Tumor necrosis factor, a proinflammatory cytokine that mediates responses to bacteria and injury
55504	Human Druggable	TNFRSF19	1.84	1.96	Tumor necrosis factor receptor superfamily member 19, mediates caspase-independent cell death, regulates mitochondrial membrane potential and cell shape, plays a role in vacuole organization and JNK (MAPK8) cascade

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
959	Human Druggable	TNFSF5	1.92	2.15	CD40 ligand, a caspase activator, mediates T-helper 1 type immunity, isotype switching, and sphingomyelin catabolism
79155	ROHG	TNIP2	1.83	1.95	TNFAIP3 interacting protein 2, a transcription coactivator that binds to SMARCD1 and TEK, inhibits NFkappaB import into the nucleus, plays a role in G1-S transition of mitotic cell cycle and endothelial cell apoptosis
10040	Human Druggable	TOM1L1	2.06	2.47	Target of myb1(chicken)-like 1, a TOLLIP binding protein that promotes keratinocyte differentiation, regulates cell proliferation and transcription, involved in the recruitment of clathrin to endosomes
7158	Human Druggable	TP53BP1	2.30	2.97	Tumor protein p53 binding protein 1, a transcriptional corepressor that is involved in DNA damage checkpoint, DNA repair and recombination, induction of apoptosis, and immune response
24150	Human Druggable	TP53TG3	1.90	2.05	TP53 target gene 3, a TP53 inducible gene that may play a role in TP53 signaling
9697	ROHG	TRAM2	0.18	-2.15	Translocation associated membrane protein 2, interacts with the SERCa2b calcium ATPase and with pro-alpha1 (I) collagen, involved in type I collagen synthesis and collagen assembly in hepatic stellate cells
10131	Human Druggable	TRAP1	1.86	2.00	TNF receptor-associated protein 1, an ATPase that regulates protein folding and mitochondrial membrane potential, involved in regulation of TNF-mediated signaling, Stat3 tyrosine phosphorylation, cell adhesion, and gene expression, inhibits apoptosis
287015	ROHG	TRIM42	2.27	3.03	Protein containing a C3HC4 type (RING) zinc finger, two B-box zinc finger domains, and a fibronectin type III domain, has a region of weak similarity to a region of human MID1
59341	Human Druggable	TRPV4	1.87	2.03	Transient receptor potential cation channel subfamily V member 4, an osmosensor that promotes cytoskeletal remodeling, mediates blood pressure, Ca ²⁺ influx, and ATP release

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
8100	ROHG	TTC10	2.38	2.90	Intraflagellar transport 88 homolog, may play a role in cell proliferation and excretion
81027	Human Druggable	TUBB1	0.25	-2.03	Tubulin beta 1, a putative structural molecule that may play a role in hemostasis
10381	Human Druggable	TUBB4	0.19	-2.20	Tubulin beta 3, may play a role in microtubule cytoskeleton organization and biogenesis
51061	ROHG	TXNDC11	1.94	2.14	Thioredoxin domain containing 11, interacts with DUOX1, DUOX2 and TPO
51060	ROHG	TXNDC12	1.87	1.98	Thioredoxin domain containing 12 (endoplasmic reticulum), a protein-disulfide oxidoreductase
23071	Human Druggable	TXNDC4	0.25	-2.05	Endoplasmic reticulum protein 44, exhibits protein disulfide isomerase activity, plays a role in cell redox homeostasis, platelet activation, neuron differentiation, protein retention in ER lumen, 'de novo' protein folding, and calcium-mediated signaling
7311	Human Druggable	UBA52	0.13	-2.04	Ubiquitin A-52 residue ribosomal protein fusion product 1, a putative structural constituent of ribosome that may play a role in protein ubiquitination
29914	ROHG	UBIAD1	2.04	2.36	UbiA prenyltransferase domain containing 1, inhibits cell proliferation
7342	ROHG	UBP1	2.69	3.55	Upstream binding protein 1, a transcriptional regulator that regulates angiogenesis, may be involved in steroid biosynthetic process
151887	ROHG	URB	2.55	3.06	Coiled coil domain containing 80, mediates growth inhibition in colon and pancreatic cancer cells
7391	Human Druggable	USF1	2.04	2.37	Upstream stimulatory factor 1, a transcription activator, regulates cell proliferation, loss of activity is associated with breast neoplasms
7392	Human Druggable	USF2	2.02	2.33	Upstream transcription factor 2 c-fos interacting, a transcription activator that plays a role in central nervous system and utero embryonic development and lactose biosynthetic process

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
10791	ROHG	VAMP5	1.94	1.96	Vesicle-associated membrane protein 5 (myobrevin), may function in vesicle-mediated transport, member of the Vamp subfamily of SNAREs
50853	ROHG	VILL	1.97	2.22	Villin-like, a putative structural constituent of cytoskeleton
55823	ROHG	VPS11	0.16	-1.98	Vacuolar protein sorting 11, binds to syntaxin 7 (STX7), vacuolar protein sorting 18 (VPS18) and vacuolar protein sorting 16 (VPS16), may be involved in endosome to lysosome vesicle docking and fusion
54832	ROHG	VPS13C	2.02	2.32	Vacuolar protein sorting 13 homolog C, may act in determining blood glucose levels after an oral glucose challenge, member of the VPS13 family
26276	ROHG	VPS33B	2.29	2.95	Vacuolar protein sorting 33b, a late endosomal and lysosomal protein that is involved in in megakaryocyte and platelet alpha granule biogenesis
7458	Human Druggable	WBSCR1	2.22	2.79	Eukaryotic translation initiation factor 4H, plays a role in mRNA catabolism and regulation of translational initiation
57539	ROHG	WDR35	1.95	2.22	Protein containing three WD domain G-beta repeats, has low similarity to C. elegans IFTA-1, which is involved in normal cilium axoneme biogenesis and retrograde intraflagellar transport
402415	ROHG	XKRX	2.16	3.06	Protein with moderate similarity to kell blood group precursor McLeod phenotype homolog
11260	Human Druggable	XPOT	1.93	2.28	Exportin tRNA, a Ran GTPase binding protein that binds and exports mature tRNAs from nucleus to the cytoplasm
10897	ROHG	YIF1	2.27	2.67	Yip1 interacting factor, contains five predicted transmembrane domains, localizes to cis-Golgi and endoplasmic reticulum membranes
54877	ROHG	ZCCHC2	1.90	2.05	Protein of unknown function, has strong similarity to uncharacterized mouse Zcchc2

Entrez Gene	Library	Gene Symbol	Fold Δ ApoA-I	Z-Score	Gene Summary
64145	ROHG	ZFYVE20	2.37	3.21	Zinc finger FYVE domain containing 20, a phosphatidylinositol binding protein that interacts with RAB4A, plays a role in endosome transport, recruits VPS45A to Rab5-containing complexes, stimulates transferrin (TF) recycling
7767	ROHG	ZNF224	2.00	2.10	Zinc finger protein 224, a transcription regulator
84364	ROHG	ZNF289	2.02	2.02	Protein with strong similarity to mouse Arfgap2, which is a small GTPase activator that plays a role in coatomer-mediated vesicular trafficking
7586	ROHG	ZNF36	2.40	2.94	Protein with high similarity to zinc finger protein 192 (human ZNF192), which is involved in protein binding
84307	ROHG	ZNF397	1.87	2.30	Zinc finger protein 397, contains a SCAN domain and nine C2H2 zinc finger repeats, forms homodimers and heterodimers with human ZNF396
57711	ROHG	ZNF529	0.16	-1.98	Protein with high similarity to human ZNF540, which is a transcription repressor that is involved in inactivation of MAPK activity, member of the KRAB box family, contains nine zinc finger C2H2 type repeats
137209	ROHG	ZNF572	2.44	2.84	Protein with high similarity to human ZNF436, which inhibits transcriptional activities of SRE and AP1, contains 12 zinc finger C2H2 type repeats
55752	Human Druggable	SEPT11	1.92	2.10	Septin 11, a GTPase that is involved in cytoskeleton organization, regulates cell size and Fc-gamma receptor mediated phagocytosis