Table S1 Table summarizing the currently known association with HDLc, LDLc, TC and TG. Only the single top signal per locus is shown plus statistically significant independently associated SNPs as identified by conditional analysis.

Locus	Chr	Lead SNP	Lead trait	Other traits	MAF	P
ANGPTL3	1	rs2131925	TG	TC, LDL	0.32	9 × 10−43
EVI5	1	rs7515577	TC		0.21	3 × 10−8
FCGR2A	1	rs1801274	TC		0.50	4 × 10−8
GALNT2	1	rs4846914	HDL	TG	0.40	4 × 10−21
IRF2BP2	1	rs514230	TC	LDL	0.48	5 × 10−14
LDLRAP1	1	rs12027135	TC	LDL	0.45	4 × 10−11
MOSC1	1	rs2642442	TC	LDL	0.32	6 × 10−13
PABPC4	1	rs4660293	HDL		0.23	4 × 10−10
PCSK9	1	rs2479409	LDL	TC	0.30	2 × 10−28
SORT1	1	rs629301	LDL	TC	0.22	1 × 10−170
ZNF648	1	rs1689800	HDL		0.35	3 × 10−10
ABCG5/8	2	rs4299376	LDL	TC	0.30	2 × 10−47
APOB	2	rs1367117	LDL	TC	0.30	4 × 10−114
APOB	2	rs1042034	TG	HDL	0.22	1 × 10−45
COBLL1	2	rs10195252	TG		0.40	2 × 10−10
COBLL1	2	rs12328675	HDL		0.13	3 × 10−10
GCKR	2	rs1260326	TG	TC	0.41	6 × 10−133
INSIG2	2	rs12464355	TC		0.93	1 × 10−8
IRS1	2	rs2972146	HDL	TG	0.37	3 × 10−9
RAB3GAP1	2	rs7570971	TC		0.34	2 × 10−8
UGT1A1	2	rs11563251	TC		0.09	3 × 10−9
MSL2L1	3	rs645040	TG		0.22	3 × 10−8
PPARG	3	rs12631819	HDL		0.03	8 × 10−6
RAF1	3	rs2290159	TC		0.22	4 × 10−9
KLHL8	4	rs442177	TG		0.41	9 × 10−12
SLC39A8	4	rs13107325	HDL		0.07	7 × 10−11
ARL15	5	rs6450176	HDL		0.26	5 × 10−8
HMGCR	5	rs12916	TC	LDL	0.39	9 × 10−47
MAP3K1	5	rs9686661	TG		0.20	1 × 10−10
TIMD4	5	rs6882076	TC	LDL, TG	0.35	7 × 10−28
C4B	6	rs389883	TG		0.63	1 × 10−18
C6orf106	6	rs2814944	HDL		0.16	4 × 10−9
C6orf106	6	rs2814982	TC		0.11	5 × 10−11
CITED2	6	rs605066	HDL		0.42	3 × 10−8
FRK	6	rs9488822	TC	LDL	0.35	2 × 10−10
HFE	6	rs1800562	LDL	TC	0.06	6 × 10−10
HLA	6	rs3177928	TC	LDL	0.16	4 × 10−19
HLA	6	rs2247056	TG		0.25	2 × 10−15
LPA	6	rs1564348	LDL	TC	0.17	2 × 10−17
LPA	6	rs1084651	HDL		0.16	3 × 10−8
LPAL2	6	rs3123629	TG		0.34	4 × 10−8
MYLIP	6	rs3757354	LDL	TC	0.22	1 × 10−11
DNAH11	7	rs12670798	TC	LDL	0.23	9 × 10−10
GCK	7	rs2070971	TG		0.13	2 × 10−7
KLF14	7	rs4731702	HDL		0.48	1 × 10−15
MLXIPL	7	rs17145738	TG	HDL	0.12	6 × 10−58
NPC1L1	7	rs2072183	TC	LDL	0.25	3 × 10−11
TYW1B	7	rs13238203	TG		0.04	1 × 10−9
CYP7A1	8	rs2081687	TC	LDL	0.35	2 × 10−12
GATA4	8	rs6983129	TG		0.49	3 × 10−8
GPIHBP1	8	rs7388248	HDL		0.29	3 × 10−9
LPL	8	rs12678919	TG	HDL	0.12	2 × 10−115
NAT2	8	rs1495741	TG	TC	0.22	5 × 10−14
PINX1	8	rs11776767	TG		0.37	1 × 10−8
PLEC1	8	rs11136341	LDL	TC	0.40	4 × 10−13
PPP1R3B	8	rs9987289	HDL	TC, LDL	0.09	6 × 10−25
TRIB1	8	rs2954029	TG	TC, LDL, HDL	0.47	3 × 10−55
TRPS1	8	rs2293889	HDL		0.41	6 × 10−11
TRPS1	8	rs2737229	TC		0.30	2 × 10−8
ABCA1	9	rs1883025	HDL	TC	0.25	2 × 10−33
ABO	9	rs9411489	LDL	TC	0.20	6 × 10−13
TTC39B	9	rs581080	HDL	TC	0.18	3 × 10−12
VLDLR	9	rs7024888	LDL		0.95	8 × 10−8
CHUK	10	rs11597086	TC		0.59	3 × 10−9

CYP26A1	10	rs2068888	TG		0.46	2 × 10−8
GPAM	10	rs2255141	TC	LDL	0.30	2 × 10−10
JMJD1C	10	rs10761731	TG		0.43	3 × 10−12
AMPD3	11	rs2923084	HDL		0.17	5 × 10−8
APOA1	11	rs964184	TG	TC, HDL, LDL	0.13	7 × 10−240
DGAT2	11	rs11236530	HDL		0.42	1 × 10−9
FADS1-2-3	11	rs174546	TG	HDL, TC, LDL	0.34	5 × 10−24
LRP4	11	rs3136441	HDL		0.15	3 × 10−18
SPTY2D1	11	rs10128711	TC		0.28	3 × 10−8
SPTY2D1	11	rs11024739	LDL		0.55	6 × 10−10
ST3GAL4	11	rs11220462	LDL	TC	0.14	1 × 10−15
UBASH3B	11	rs7941030	TC	HDL	0.38	2 × 10−10
BRAP	12	rs11065987	TC	LDL	0.42	7 × 10−12
HCAR2	12	rs4759361	HDL		0.16	2 × 10−12
HNF1A	12	rs1169288	TC	LDL	0.33	1 × 10−14
LRP1	12	rs11613352	TG	HDL	0.23	4 × 10−10
MVK	12	rs7134594	HDL		0.47	7 × 10−15
PDE3A	12	rs7134375	HDL		0.42	4 × 10−8
SBNO1	12	rs4759375	HDL		0.06	7 × 10−9
SCARB1	12	rs838880	HDL		0.31	3 × 10−14
UBE3B	12	rs7298565	TC		0.53	2 × 10−6
ZNF664	12	rs4765127	HDL	TG	0.34	3 × 10−10
BRCA2	13	rs9534275	LDL	TC	0.51	6 × 10−9
NYNRIN	14	rs8017377	LDL		0.47	5 × 10−11
CAPN3	15	rs2412710	TG		0.02	2 × 10−8
FRMD5	15	rs2929282	TG		0.05	2 × 10−11
LACTB	15	rs2652834	HDL		0.20	9 × 10−9
LIPC	15	rs1532085	HDL	TC, TG	0.39	3 × 10−96
CETP	16	rs3764261	HDL	TC, LDL, TG	0.32	7 × 10−380
CMIP	16	rs2925979	HDL		0.30	2 × 10−11
CTF1	16	rs11649653	TG		0.40	3 × 10−8
FTO	16	rs1421085	HDL		0.61	2 × 10−8
HPR	16	rs2000999	TC	LDL	0.20	3 × 10−24
LCAT	16	rs16942887	HDL		0.12	8 × 10−33
ABCA8	17	rs4148008	HDL		0.32	2 × 10−10
APOH	17	rs1801689	LDL		0.96	9 × 10−14
OSBPL7	17	rs7206971	LDL	TC	0.49	2 × 10−8
PGS1	17	rs4129767	HDL		0.49	8 × 10−9
SERPINF2	17	rs2070863	TG		0.21	2 × 10−5
SOCS3	17	rs4082919	TC	LDL	0.52	9 × 10−7
STARD3	17	rs11869286	HDL		0.34	1 × 10−13
LIPG	18	rs7241918	HDL	TC	0.17	3 × 10−49
MC4R	18	rs12967135	HDL		0.23	7 × 10−9
ANGPTL4	19	rs7255436	HDL		0.47	3 × 10−8
APOE	19	rs4420638	LDL	TC, HDL	0.17	9 × 10−147
APOE	19	rs439401	TG		0.36	1 × 10−30
CILP2	19	rs10401969	TC	TG, LDL	0.07	3 × 10−38
FLJ36070	19	rs492602	TC		0.49	2 × 10−10
INSR	19	rs8112883	TG		0.33	5 × 10−6
LDLR	19	rs6511720	LDL	TC	0.11	4 × 10−117
LILRA3	19	rs386000	HDL		0.20	4 × 10−16
LOC55908	19	rs737337	HDL		0.08	3 × 10−9
ERGIC3	20	rs2277862	TC		0.15	4 × 10−10
HNF4A	20	rs1800961	HDL	TC	0.03	1 × 10−15
MAFB	20	rs2902940	TC	LDL	0.29	6 × 10−11
PLTP	20	rs6065906	HDL	TG	0.18	2 × 10−22
TOP1	20	rs6029526	LDL	TC	0.47	4 × 10−19
PLA2G6	22	rs5756931	TG		0.40	4 × 10−8
UBE2L3	22	rs181362	HDL		0.20	1 × 10−8

Table S2 Biological process VLAD results, triglyceride trait associated genes

GO Term	P-value	k	M	Genes
GO:0008150: biological_process	1.00E+00	29	29612	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, CTF1, CYP26A1, FADS1, FADS2, FADS3, *FRMD5, GALNT2, GCKR, IRS1, JMJD1C, LIPC, LPL, LRP1, MAP3K1, MLXIPL, MSL2, NAT2, PINX1, PLA2G6, PLTP, TRIB1, TYW1B, *ZNF664
GO:0044710: single-organism metabolic process	4.68E-06	26	14505	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, CYP26A1, FADS1, FADS2, FADS3, GALNT2, GCKR, IRS1, JMJD1C, LIPC, LPL, LRP1, MAP3K1, MLXIPL, MSL2, NAT2, PINX1, PLA2G6, PLTP, TYW1B, ZNF664
GO:0008152: metabolic process	7.68E-06	26	14817	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, *CYP26A1, FADS1, FADS2, FADS3, GALNT2, GCKR, IRS1, JMJD1C, LIPC, LPL, LRP1, MAP3K1, MLXIPL, MSL2, NAT2, PINX1, PLA2G6, PLTP, TYW1B, ZNF664
GO:0044238: primary metabolic process	9.13E-06	25	13667	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, CYP26A1, FADS1, FADS2, FADS3, GALNT2, GCKR, IRS1, JMJD1C, LIPC, LPL, LRP1, MAP3K1, MLXIPL, MSL2, PINX1, PLA2G6, PLTP, TYW1B, ZNF664
GO:0071704: organic substance metabolic process	2.09E-05	25	14197	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, CYP26A1, FADS1, FADS2, FADS3, GALNT2, GCKR, IRS1, JMJD1C, LIPC, LPL, LRP1, MAP3K1, MLXIPL, MSL2, PINX1, PLA2G6, PLTP, TYW1B, ZNF664
GO:0044237: cellular metabolic process	9.92E-06	24	12556	ANGPTL3, APOA1, APOB, APOE, CETP, CYP26A1, FADS1, FADS2, FADS3, GALNT2, GCKR, JMJD1C, LIPC, LPL, LRP1, MAP3K1, MLXIPL, MSL2, NAT2, PINX1, PLA2G6, PLTP, TYW1B, ZNF664
GO:0044281: small molecule metabolic process	1.72E-09	17	3455	ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *CYP26A1, *FADS1, *FADS2, FADS3, *GCKR, LIPC, *LPL, LRP1, *MLXIPL, *NAT2, *PLA2G6, PLTP
GO:0065008: regulation of biological quality	1.50E-07	15	3451	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, CYP26A1, GCKR, IRS1, JMJD1C, LIPC, LPL, MAP3K1, MLXIPL, PINX1
GO:0009058: biosynthetic process	2.16E-04	15	6142	APOA1, APOB, APOE, FADS1, FADS2, FADS3, GALNT2, JMJD1C, LIPC, LPL, MLXIPL, PINX1, PLA2G6, PLTP, ZNF664
GO:0006629: lipid metabolic process	1.37E-11	15	1762	ANGPTL3, *APOA1, *APOB, *APOE, *CETP, CYP26A1, FADS1, FADS2, FADS3, IRS1, LIPC, *LPL, LRP1, PLA2G6, *PLTP
GO:0044249: cellular biosynthetic process	1.12E-04	15	5811	APOA1, APOB, APOE, FADS1, FADS2, FADS3, GALNT2, JMJD1C, LIPC, LPL, MLXIPL, PINX1, PLA2G6, PLTP, ZNF664
GO:1901576: organic substance biosynthetic process	1.54E-04	15	5967	APOA1, APOB, APOE, FADS1, FADS2, FADS3, GALNT2, JMJD1C, LIPC, LPL, MLXIPL, PINX1, PLA2G6, PLTP, ZNF664
GO:0042221: response to chemical stimulus	6.65E-06	14	3988	ANGPTL3, APOB, APOE, CAPN3, CYP26A1, FADS1, GCKR, IRS1, LPL, MAP3K1, MLXIPL, NAT2, PLA2G6, TRIB1
GO:0048518: positive regulation of biological process	5.35E-04	13	5136	ANGPTL3, APOA1, APOB, APOE, CAPN3, CTF1, GCKR, IRS1, LPL, LRP1, MAP3K1, MLXIPL, TRIB1
GO:0032879: regulation of localization	5.79E-08	12	1830	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, GCKR, IRS1, LPL, LRP1, MAP3K1, TRIB1
GO:0042592: homeostatic process	2.56E-08	12	1700	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, GCKR, IRS1, LIPC, LPL, MLXIPL, PINX1
GO:0044255: cellular lipid metabolic process	1.00E-09	12	1274	ANGPTL3, *APOA1, APOB, APOE, CETP, CYP26A1, *FADS1, FADS2, FADS3, LIPC, LPL, PLA2G6
GO:0033036: macromolecule localization	1.54E-05	11	2555	ANGPTL3, APOA1, APOB, APOE, CAPN3, CETP, GCKR, IRS1, LIPC, LRP1, PLTP
GO:0048878: chemical homeostasis	8.04E-08	10	1156	ANGPTL3, APOA1, APOB, APOE, CETP, GCKR, IRS1, LIPC, LPL, MLXIPL

GO:0010033: response to organic substance	1.80E-04	10	2751	ANGPTL3, APOB, APOE, CYP26A1, FADS1, GCKR, IRS1, MAP3K1, MLXIPL, TRIB1
GO:0065009: regulation of molecular function	2.66E-04	9	2329	ANGPTL3, APOA1, APOE, CAPN3, GCKR, IRS1, LRP1, PINX1, TRIB1
GO:0009893: positive regulation of metabolic process	9.89E-04	9	2783	ANGPTL3, APOA1, APOE, CAPN3, GCKR, IRS1, MAP3K1, MLXIPL, TRIB1
GO:0055088: lipid homeostasis	1.37E-15	9	115	*ANGPTL3, APOA1, APOB, APOE, *CETP, GCKR, LIPC, LPL, MLXIPL
GO:0050790: regulation of catalytic activity	4.35E-05	9	1840	ANGPTL3, APOA1, APOE, *CAPN3, GCKR, IRS1, LRP1, PINX1, TRIB1
GO:0009056: catabolic process	3.97E-04	9	2457	ANGPTL3, APOB, APOE, CYP26A1, IRS1, LIPC, LPL, MAP3K1, PLA2G6
GO:0043933: macromolecular complex subunit organization	5.29E-06	9	1414	APOA1, APOB, APOE, CAPN3, CETP, IRS1, LIPC, LPL, MAP3K1
GO:1901575: organic substance catabolic process	2.08E-04	9	2254	ANGPTL3, APOB, APOE, CYP26A1, IRS1, LIPC, LPL, MAP3K1, PLA2G6
GO:1901615: organic hydroxy compound metabolic process	1.24E-08	8	471	ANGPTL3, APOA1, APOB, APOE, CETP, LIPC, LRP1, PLA2G6
GO:0016042: lipid catabolic process	4.33E-10	8	307	ANGPTL3, APOB, APOE, CYP26A1, *IRS1, LIPC, LPL, *PLA2G6
GO:0070887: cellular response to chemical stimulus	7.99E-04	8	2141	APOB, APOE, CAPN3, CYP26A1, IRS1, MAP3K1, MLXIPL, NAT2
GO:0006066: alcohol metabolic process	2.05E-09	8	374	ANGPTL3, APOA1, APOB, APOE, CETP, LIPC, LRP1, PLA2G6
GO:0006082: organic acid metabolic process	1.28E-04	8	1635	ANGPTL3, CYP26A1, FADS1, FADS2, FADS3, GCKR, LIPC, LPL
GO:0044711: single-organism biosynthetic process	4.05E-06	7	702	APOA1, FADS1, FADS2, FADS3, LIPC, LPL, PLTP
GO:0051049: regulation of transport	2.27E-04	7	1321	APOA1, APOE, CAPN3, CETP, GCKR, IRS1, LRP1
GO:0019637: organophosphate metabolic process	4.86E-04	7	1497	ANGPTL3, APOA1, CETP, FADS1, LIPC, LPL, PLA2G6
GO:0032787: monocarboxylic acid metabolic process	1.80E-06	7	621	ANGPTL3, CYP26A1, FADS1, FADS2, FADS3, LIPC, LPL
GO:0070328: triglyceride homeostasis	1.02E-15	7	31	*ANGPTL3, *APOA1, *CETP, *GCKR, *LIPC, *LPL, *MLXIPL
GO:0055090: acylglycerol homeostasis	1.31E-15	7	32	*ANGPTL3, APOA1, CETP, GCKR, LIPC, LPL, MLXIPL
GO:0008203: cholesterol metabolic process	3.08E-11	7	126	*ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *LIPC, *LRP1
GO:0016125: sterol metabolic process	6.83E-11	7	141	ANGPTL3, APOA1, APOB, APOE, CETP, LIPC, LRP1
GO:0008202: steroid metabolic process	2.14E-08	7	322	ANGPTL3, APOA1, APOB, APOE, CETP, LIPC, LRP1
GO:0046486: glycerolipid metabolic process	2.22E-07	7	454	APOA1, APOB, APOE, CETP, LIPC, LPL, PLA2G6
GO:0006644: phospholipid metabolic process	5.96E-07	7	526	*ANGPTL3, APOA1, CETP, FADS1, LIPC, *LPL, *PLA2G6
GO:0008610: lipid biosynthetic process	8.76E-06	7	790	APOA1, FADS1, FADS2, FADS3, LIPC, LPL, PLA2G6
GO:0010876: lipid localization	6.71E-09	7	272	ANGPTL3, APOA1, APOB, APOE, CETP, LIPC, PLTP
GO:0044283: small molecule biosynthetic process	3.28E-06	7	680	APOA1, FADS1, FADS2, FADS3, LIPC, LPL, PLTP
GO:0019752: carboxylic acid metabolic process	4.63E-04	7	1485	ANGPTL3, CYP26A1, FADS1, FADS2, FADS3, LIPC, LPL
GO:0043436: oxoacid metabolic process	7.71E-04	7	1617	ANGPTL3, CYP26A1, FADS1, FADS2, FADS3, LIPC, LPL
GO:0030334: regulation of cell migration	1.51E-05	6	563	ANGPTL3, APOE, IRS1, LRP1, *MAP3K1, TRIB1
GO:2000145: regulation of cell motility	1.92E-05	6	588	ANGPTL3, APOE, IRS1, LRP1, MAP3K1, TRIB1
GO:0044092: negative regulation of molecular function	1.05E-04	6	798	ANGPTL3, APOA1, APOE, GCKR, PINX1, TRIB1
GO:0055092: sterol homeostasis	1.69E-10	6	82	ANGPTL3, APOA1, APOB, APOE, CETP, LIPC
GO:0042632: cholesterol homeostasis	1.69E-10	6	82	*ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *LIPC
GO:0006631: fatty acid metabolic process	3.42E-06	6	434	*ANGPTL3, FADS1, FADS2, FADS3, LIPC, LPL
GO:0006869: lipid transport	1.28E-07	6	247	APOA1, APOB, APOE, *CETP, LIPC, *PLTP
GO:0042157: lipoprotein metabolic process	1.50E-08	6	172	*APOA1, *APOB, *APOE, *CETP, *LPL, *LRP1
GO:0034369: plasma lipoprotein particle remodeling	1.48E-13	6	27	APOA1, APOB, APOE, CETP, LIPC, LPL
GO:0034368: protein-lipid complex remodeling	1.48E-13	6	27	APOA1, APOB, APOE, CETP, LIPC, LPL

GO:0034367: macromolecular complex remodeling	1.48E-13	6	27	APOA1, APOB, APOE, CETP, LIPC, LPL
GO:0071825: protein-lipid complex subunit organization	5.52E-13	6	33	APOA1, APOB, APOE, CETP, LIPC, LPL
GO:0071827: plasma lipoprotein particle organization	5.52E-13	6	33	APOA1, APOB, APOE, CETP, LIPC, LPL
GO:0019216: regulation of lipid metabolic process	2.79E-07	6	282	ANGPTL3, APOA1, APOB, APOE, IRS1, MLXIPL
GO:0043086: negative regulation of catalytic activity	2.30E-05	6	607	ANGPTL3, APOA1, APOE, GCKR, PINX1, TRIB1
GO:0051338: regulation of transferase activity	1.43E-04	6	844	APOA1, APOE, GCKR, IRS1, PINX1, TRIB1
GO:0097006: regulation of plasma lipoprotein particle levels	2.45E-11	6	60	APOA1, APOB, APOE, CETP, LIPC, LPL
GO:0048585: negative regulation of response to stimulus	7.40E-04	6	1148	APOA1, APOE, CYP26A1, IRS1, LRP1, TRIB1
GO:0040012: regulation of locomotion	2.88E-05	6	632	ANGPTL3, APOE, IRS1, LRP1, MAP3K1, TRIB1
GO:0051270: regulation of cellular component movement	2.96E-05	6	635	ANGPTL3, APOE, IRS1, LRP1, MAP3K1, TRIB1
GO:0042325: regulation of phosphorylation	7.19E-04	6	1142	APOA1, APOE, GCKR, IRS1, MLXIPL, TRIB1
GO:0015850: organic hydroxy compound transport	1.83E-08	5	84	APOA1, APOB, APOE, CETP, LIPC
GO:0009896: positive regulation of catabolic process	9.48E-07	5	185	ANGPTL3, APOE, IRS1, MLXIPL, TRIB1
GO:0055114: oxidation-reduction process	4.92E-04	5	686	APOA1, FADS1, FADS2, FADS3, MLXIPL
GO:0009894: regulation of catabolic process	6.33E-04	5	725	ANGPTL3, APOE, IRS1, MLXIPL, TRIB1
GO:0006641: triglyceride metabolic process	6.21E-08	5	107	APOB, *APOE, *CETP, LIPC, *LPL
GO:0006639: acylglycerol metabolic process	8.54E-08	5	114	APOB, APOE, CETP, LIPC, LPL
GO:0006638: neutral lipid metabolic process	9.32E-08	5	116	APOB, APOE, CETP, LIPC, LPL
GO:0044242: cellular lipid catabolic process	9.23E-07	5	184	ANGPTL3, APOB, CYP26A1, LIPC, LPL
GO:0006633: fatty acid biosynthetic process	1.29E-06	5	197	FADS1, FADS2, FADS3, *LIPC, *LPL
GO:0030301: cholesterol transport	2.77E-09	5	58	*APOA1, *APOB, APOE, *CETP, LIPC
GO:0015918: sterol transport	2.77E-09	5	58	APOA1, APOB, APOE, CETP, LIPC
GO:0045834: positive regulation of lipid metabolic process	1.25E-07	5	123	ANGPTL3, APOA1, APOE, IRS1, MLXIPL
GO:0072330: monocarboxylic acid biosynthetic process	5.82E-06	5	268	FADS1, FADS2, FADS3, LIPC, LPL
GO:0016053: organic acid biosynthetic process	9.81E-05	5	484	FADS1, FADS2, FADS3, LIPC, LPL
GO:0046394: carboxylic acid biosynthetic process	9.81E-05	5	484	FADS1, FADS2, FADS3, LIPC, LPL
GO:0048844: artery morphogenesis	3.25E-07	4	59	*ANGPTL3, *APOB, *APOE, LRP1
GO:0060840: artery development	6.89E-07	4	71	ANGPTL3, APOB, APOE, LRP1
GO:0006898: receptor-mediated endocytosis	6.62E-06	4	125	*APOB, *APOE, *CETP, *LRP1
GO:0006897: endocytosis	6.25E-04	4	405	APOB, APOE, CETP, LRP1
GO:0046470: phosphatidylcholine metabolic process	4.82E-07	4	65	APOA1, *CETP, LIPC, PLA2G6
GO:0006650: glycerophospholipid metabolic process	4.23E-04	4	365	APOA1, CETP, LIPC, PLA2G6
GO:0043691: reverse cholesterol transport	2.85E-09	4	19	*APOA1, *APOE, *CETP, *LIPC
GO:0034381: plasma lipoprotein particle clearance	5.35E-08	4	38	APOA1, APOB, APOE, LIPC
GO:0034372: very-low-density lipoprotein particle remodeling	2.59E-11	4	7	*APOE, *CETP, *LIPC, *LPL
GO:0034370: triglyceride-rich lipoprotein particle remodeling	1.55E-10	4	10	APOE, CETP, LIPC, LPL
GO:0034374: low-density lipoprotein particle remodeling	5.27E-10	4	13	*APOB, *APOE, *CETP, *LIPC

GO:0034375: high-density lipoprotein particle remodeling	1.00E-09	4	15	*APOA1, *APOE, *CETP, *LIPC
GO:0032374: regulation of cholesterol transport	2.62E-08	4	32	APOA1, APOE, CETP, *LRP1
GO:0032371: regulation of sterol transport	2.62E-08	4	32	APOA1, APOE, CETP, LRP1
GO:0032368: regulation of lipid transport	8.14E-07	4	74	APOA1, APOE, CETP, LRP1
GO:0051348: negative regulation of transferase activity	6.99E-05	4	228	APOE, GCKR, PINX1, TRIB1
GO:0009743: response to carbohydrate stimulus	9.38E-05	4	246	*APOB, FADS1, GCKR, MLXIPL
GO:0042439: ethanolamine-containing compound metabolic process	2.13E-06	4	94	APOA1, CETP, LIPC, PLA2G6
GO:0031331: positive regulation of cellular catabolic process	8.22E-06	4	132	APOE, IRS1, MLXIPL, TRIB1
GO:0044106: cellular amine metabolic process	1.63E-05	4	157	APOA1, CETP, LIPC, PLA2G6
GO:0006576: cellular biogenic amine metabolic process	1.63E-05	4	157	APOA1, CETP, LIPC, PLA2G6
GO:0009308: amine metabolic process	4.12E-05	4	199	APOA1, CETP, LIPC, PLA2G6
GO:0031400: negative regulation of protein modification process	6.19E-04	4	404	APOE, CAPN3, MLXIPL, TRIB1
GO:0033500: carbohydrate homeostasis	4.23E-04	3	150	GCKR, IRS1, MLXIPL
GO:0042593: glucose homeostasis	4.23E-04	3	150	GCKR, *IRS1, *MLXIPL
GO:0030336: negative regulation of cell migration	5.58E-04	3	165	APOE, LRP1, TRIB1
GO:2000146: negative regulation of cell motility	5.78E-04	3	167	APOE, LRP1, TRIB1
GO:0010743: regulation of macrophage derived foam cell differentiation	9.45E-06	3	42	APOB, CETP, LPL
GO:0015748: organophosphate ester transport	3.71E-05	3	66	APOA1, APOE, CETP
GO:0055091: phospholipid homeostasis	7.07E-08	3	9	*ANGPTL3, *APOA1, *CETP
GO:0019433: triglyceride catabolic process	1.48E-06	3	23	*APOB, *LIPC, *LPL
GO:0046464: acylglycerol catabolic process	2.16E-06	3	26	APOB, LIPC, LPL
GO:0046461: neutral lipid catabolic process	2.16E-06	3	26	APOB, LIPC, LPL
GO:0046503: glycerolipid catabolic process	4.11E-06	3	32	APOB, LIPC, LPL
GO:0006636: unsaturated fatty acid biosynthetic process	4.05E-05	3	68	*FADS1, *FADS2, *FADS3
GO:0042158: lipoprotein biosynthetic process	1.61E-04	3	108	*APOA1, *APOB, *APOE
GO:0033559: unsaturated fatty acid metabolic process	1.70E-04	3	110	*FADS1, *FADS2, FADS3
GO:0015914: phospholipid transport	8.78E-06	3	41	APOA1, APOE, *CETP
GO:0065005: protein-lipid complex assembly	3.81E-07	3	15	APOA1, APOB, APOE
GO:0034377: plasma lipoprotein particle assembly	3.81E-07	3	15	APOA1, APOB, APOE
GO:0010906: regulation of glucose metabolic process	1.44E-04	3	104	GCKR, IRS1, MLXIPL
GO:0010675: regulation of cellular carbohydrate metabolic process	2.59E-04	3	127	GCKR, IRS1, MLXIPL
GO:0006109: regulation of carbohydrate metabolic process	2.91E-04	3	132	GCKR, IRS1, MLXIPL
GO:0019218: regulation of steroid metabolic process	1.24E-04	3	99	APOA1, APOB, APOE
GO:0046890: regulation of lipid biosynthetic process	2.97E-04	3	133	APOB, APOE, MLXIPL
GO:0010874: regulation of cholesterol efflux	5.69E-07	3	17	APOE, *CETP, LRP1
GO:0051271: negative regulation of cellular component movement	6.40E-04	3	173	APOE, LRP1, TRIB1

GO:0040013: negative regulation of locomotion	8.66E-04	3	192	APOE, LRP1, TRIB1
GO:0022900: electron transport chain	8.66E-04	3	192	*FADS1, *FADS2, *FADS3
GO:0045862: positive regulation of proteolysis	7.90E-05	3	85	APOE, *CAPN3, TRIB1
GO:0030317: sperm motility	6.37E-04	2	38	*APOB, *PLTP
GO:0014912: negative regulation of smooth muscle cell migration	4.15E-05	2	10	*LRP1, *TRIB1
GO:0043651: linoleic acid metabolic process	2.58E-05	2	8	*FADS1, *FADS2
GO:0042159: lipoprotein catabolic process	5.07E-05	2	11	*APOB, *APOE
GO:0009395: phospholipid catabolic process	5.71E-04	2	36	*ANGPTL3, LIPC
GO:0033700: phospholipid efflux	6.07E-05	2	12	*APOA1, *APOE
GO:0033344: cholesterol efflux	2.97E-04	2	26	*APOA1, *APOE
GO:0034384: high-density lipoprotein particle clearance	1.94E-05	2	7	*APOA1, *APOE
GO:0034382: chylomicron remnant clearance	3.32E-05	2	9	*APOE, *LIPC
GO:0071830: triglyceride-rich lipoprotein particle clearance	3.32E-05	2	9	APOE, LIPC
GO:0042953: lipoprotein transport	7.18E-05	2	13	*APOB, *LRP1
GO:0034380: high-density lipoprotein particle assembly	1.39E-05	2	6	*APOA1, *APOE
GO:0010907: positive regulation of glucose metabolic process	4.51E-04	2	32	*IRS1, MLXIPL
GO:0010676: positive regulation of cellular carbohydrate metabolic process	7.78E-04	2	42	IRS1, MLXIPL
GO:0010873: positive regulation of cholesterol esterification	1.94E-05	2	7	*APOA1, *APOE
GO:0010872: regulation of cholesterol esterification	3.32E-05	2	9	APOA1, APOE
GO:0045540: regulation of cholesterol biosynthetic process	2.11E-04	2	22	*APOB, APOE
GO:0045940: positive regulation of steroid metabolic process	3.45E-04	2	28	APOA1, APOE
GO:0090181: regulation of cholesterol metabolic process	4.80E-04	2	33	APOB, APOE
GO:0045923: positive regulation of fatty acid metabolic process	5.71E-04	2	36	IRS1, MLXIPL
GO:0050996: positive regulation of lipid catabolic process	2.97E-04	2	26	*ANGPTL3, IRS1
GO:0010875: positive regulation of cholesterol efflux	5.07E-05	2	11	*APOE, *LRP1
GO:0032373: positive regulation of sterol transport	7.18E-05	2	13	APOE, LRP1
GO:0032376: positive regulation of cholesterol transport	7.18E-05	2	13	APOE, LRP1
GO:0032370: positive regulation of lipid transport	6.04E-04	2	37	APOE, *LRP1
GO:0010886: positive regulation of cholesterol storage	1.57E-04	2	19	*APOB, *LPL
GO:0010885: regulation of cholesterol storage	2.74E-04	2	25	APOB, LPL
GO:0010884: positive regulation of lipid storage	3.20E-04	2	27	*APOB, LPL
GO:0032489: regulation of Cdc42 protein signal transduction	1.92E-04	2	21	*APOA1, *APOE
GO:0036109: alpha-linolenic acid metabolic process	5.07E-05	2	11	*FADS1, *FADS2
GO:0010744: positive regulation of macrophage derived foam cell differentiation	3.70E-04	2	29	*APOB, *LPL
GO:0019915: lipid storage	4.51E-04	2	32	*ANGPTL3, *APOA1
GO:0014910: regulation of smooth muscle cell migration	5.40E-04	2	35	LRP1, TRIB1
GO:0006775: fat-soluble vitamin metabolic process	3.45E-04	2	28	CYP26A1, PLTP

k is the number of genes in the query set annotated to that node, and M is the number of genes in the database annotated to that node.
*next to the gene symbol indicates that the gene is annotated to the node, and not any of the child terms.
Based on annotation dataset 12th November 2012 and GO ontology from 27th November 2012.

Table S3 Biological process VLAD results, total cholesterol trait associated genes

GO Term	P-value	k	M	Genes
GO:0008150: biological_process	1.00E+00	49	29612	ABCA1, ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, BRAP, *C6orf106, CETP, CYP7A1, DNAH11, ERGIC3, EVI5, FADS1, FADS2, FADS3, FRK, GCKR, GPAM, HFE, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MAMSTR, MARC1, MYLIP, NAT2, NPC1L1, OSBPL7, PCSK9, PLEC, PPP1R3B, RAB3GAP1, RAF1, SORT1, *SPTY2D1, ST3GAL4, TOP1, TRIB1, TRPS1
GO:0008152: metabolic process	2.37E-04	37	14817	ABCA1, ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GCKR, GPAM, HFE, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MARC1, MYLIP, NAT2, NPC1L1, PCSK9, PPP1R3B, RAF1, ST3GAL4, TOP1, TRPS1
GO:0044237: cellular metabolic process	1.02E-05	36	12556	ABCA1, ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GCKR, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MARC1, MYLIP, NAT2, NPC1L1, PCSK9, PPP1R3B, RAF1, ST3GAL4, TOP1, TRPS1
GO:0044710: single-organism metabolic process	4.23E-04	36	14505	ABCA1, ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GCKR, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MARC1, MYLIP, NAT2, NPC1L1, PCSK9, PPP1R3B, RAF1, ST3GAL4, TOP1, TRPS1
GO:0044238: primary metabolic process	8.54E-04	34	13667	ABCA1, ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GCKR, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MYLIP, NPC1L1, PCSK9, PPP1R3B, RAF1, ST3GAL4, TOP1, TRPS1
GO:0044707: single-multicellular organism process	9.16E-06	28	8030	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, EVI5, GPAM, HFE, HMGCR, HNF1A, HNF4A, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MYLIP, NPC1L1, PCSK9, RAB3GAP1, RAF1, SORT1, TOP1, TRPS1
GO:0032501: multicellular organismal process	1.01E-05	28	8067	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, EVI5, GPAM, HFE, HMGCR, HNF1A, HNF4A, LDLR, LDLRAP1, LIPC, LIPG, LPA, MAFB, MYLIP, NPC1L1, PCSK9, RAB3GAP1, RAF1, SORT1, TOP1, TRPS1
GO:0019222: regulation of metabolic process	1.31E-05	26	7178	ABCA1, ANGPTL3, APOA1, APOB, APOE, CYP7A1, FADS1, GCKR, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPG, LPA, MAFB, MAMSTR, MYLIP, PCSK9, RAB3GAP1, RAF1, SORT1, TRIB1, TRPS1
GO:0044281: small molecule metabolic process	1.96E-12	26	3455	*ABCA1, *ABCG5, *ABCG8, ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *CYP7A1, *FADS1, *FADS2, FADS3, *GCKR, *GPAM, *HMGCR, HNF1A, HNF4A, *LDLR, LDLRAP1, LIPC, *LPA, MARC1, *NAT2, *NPC1L1, PCSK9, *ST3GAL4

GO:0080090: regulation of primary metabolic process	2.44E-05	24	6458	ABCA1, ANGPTL3, APOA1, APOB, APOE, CYP7A1, FADS1, GCKR, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPG, MAFB, MAMSTR, MYLIP, PCSK9, RAB3GAP1, RAF1, TRIB1, TRPS1
GO:0006629: lipid metabolic process	7.37E-16	23	1762	*ABCA1, *ABCG5, *ABCG8, ANGPTL3, *APOA1, *APOB, *APOE, *CETP, CYP7A1, FADS1, FADS2, FADS3, GPAM, HMGCR, HNF1A, *HNF4A, *LDLR, LDLRAP1, LIPC, *LIPG, *LPA, *NPC1L1, PCSK9
GO:0051179: localization	2.41E-05	23	5992	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, ERGIC3, GCKR, GPAM, HFE, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, LPA, NPC1L1, OSBPL7, PCSK9, SORT1, TRPS1
GO:0065008: regulation of biological quality	5.75E-09	22	3451	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GCKR, GPAM, HFE, HNF1A, HNF4A, LDLR, LDLRAP1, LIPC, LIPG, MYLIP, NPC1L1, PCSK9, RAF1
GO:0006810: transport	1.96E-06	22	4771	ABCA1, ABCG5, ABCG8, APOA1, APOB, APOE, CETP, ERGIC3, GCKR, GPAM, HFE, HNF1A, LDLR, *LDLRAP1, LIPC, LIPG, LPA, NPC1L1, OSBPL7, PCSK9, SORT1, TRPS1
GO:0051234: establishment of localization	2.83E-06	22	4875	ABCA1, ABCG5, ABCG8, APOA1, APOB, APOE, CETP, ERGIC3, GCKR, GPAM, HFE, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, LPA, NPC1L1, OSBPL7, PCSK9, SORT1, TRPS1
GO:1901360: organic cyclic compound metabolic process	4.34E-04	22	6677	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GCKR, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LDLRAP1, LIPC, MAFB, NPC1L1, PCSK9, TOP1, TRPS1
GO:0048878: chemical homeostasis	3.04E-17	21	1156	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GCKR, GPAM, HFE, HNF1A, HNF4A, LDLR, LDLRAP1, LIPC, LIPG, MYLIP, NPC1L1, PCSK9
GO:0009058: biosynthetic process	3.82E-04	21	6142	ABCA1, ABO, APOA1, APOB, APOE, CYP7A1, FADS1, FADS2, FADS3, GPAM, HFE, HMGCR, HNF1A, HNF4A, IRF2BP2, LIPC, MAFB, NPC1L1, ST3GAL4, TOP1, TRPS1
GO:0042592: homeostatic process	6.36E-14	21	1700	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GCKR, GPAM, HFE, HNF1A, HNF4A, LDLR, LDLRAP1, LIPC, LIPG, MYLIP, NPC1L1, PCSK9
GO:0042221: response to chemical stimulus	4.26E-07	21	3988	ABCA1, ABCG5, ANGPTL3, APOB, APOE, CYP7A1, FADS1, GCKR, GPAM, HMGCR, HNF1A, HNF4A, LDLR, LIPG, MARC1, NAT2, PCSK9, RAF1, SORT1, TOP1, TRIB1
GO:0031323: regulation of cellular metabolic process	8.66E-04	21	6511	ABCA1, APOA1, APOE, CYP7A1, FADS1, GCKR, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LDLR, LIPG, MAFB, MAMSTR, MYLIP, PCSK9, RAB3GAP1, RAF1, TRIB1, TRPS1
GO:1901576: organic substance biosynthetic process	7.52E-04	20	5967	ABCA1, ABO, APOA1, APOB, APOE, CYP7A1, FADS1, FADS2, FADS3, GPAM, HMGCR, HNF1A, HNF4A, IRF2BP2, LIPC, MAFB, NPC1L1, ST3GAL4, TOP1, TRPS1
GO:0071702: organic substance transport	3.71E-09	19	2430	ABCA1, ABCG5, ABCG8, APOA1, APOB, APOE, CETP, GCKR, GPAM, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, LPA, NPC1L1, OSBPL7, SORT1, TRPS1
GO:0033036: macromolecule localization	8.48E-09	19	2555	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GCKR, GPAM, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, LPA, NPC1L1, OSBPL7, TRPS1
GO:0048519: negative regulation of biological process	5.19E-05	19	4507	ABCA1, ABCG5, ABCG8, APOA1, APOE, BRAP, CETP, FRK, GPAM, HMGCR, HNF1A, HNF4A, MAFB, MYLIP, PCSK9, RAF1, SORT1, TRIB1, TRPS1
GO:0048518: positive regulation of biological process	3.09E-04	19	5136	ABCA1, ANGPTL3, APOA1, APOB, APOE, GCKR, GPAM, HMGCR, HNF1A, HNF4A, LDLR, LDLRAP1, LIPG, MAFB, MAMSTR, MYLIP, PCSK9, RAF1, TRIB1
GO:0055088: lipid homeostasis	5.62E-34	19	115	ABCA1, ABCG5, ABCG8, *ANGPTL3, APOA1, APOB, APOE, *CETP, CYP7A1, GCKR, GPAM, *HNF4A, LDLR, LDLRAP1, LIPC, LIPG, MYLIP, NPC1L1, PCSK9

GO:0032879: regulation of localization	2.53E-09	17	1830	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GCKR, GPAM, HNF1A, HNF4A, LDLRAP1, LIPG, PCSK9, RAF1, TRIB1
GO:0048523: negative regulation of cellular process	6.20E-04	16	4093	ABCA1, APOA1, APOE, BRAP, CETP, FRK, GPAM, HMGCR, HNF1A, HNF4A, MAFB, PCSK9, RAF1, SORT1, TRIB1, TRPS1
GO:0009893: positive regulation of metabolic process	5.81E-06	16	2783	ABCA1, ANGPTL3, APOA1, APOE, GCKR, GPAM, HNF1A, HNF4A, LDLR, LDLRAP1, MAFB, MAMSTR, MYLIP, PCSK9, RAF1, TRIB1
GO:0055092: sterol homeostasis	7.84E-30	16	82	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, LDLR, LDLRAP1, LIPC, LIPG, MYLIP, NPC1L1, PCSK9
GO:0042632: cholesterol homeostasis	7.84E-30	16	82	*ABCA1, *ABCG5, *ABCG8, *ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *CYP7A1, *LDLR, *LDLRAP1, *LIPC, *LIPG, *MYLIP, *NPC1L1, *PCSK9
GO:0044255: cellular lipid metabolic process	1.10E-10	16	1274	*ABCA1, ANGPTL3, *APOA1, APOB, APOE, CETP, *CYP7A1, *FADS1, FADS2, FADS3, *GPAM, *HMGCR, HNF1A, LIPC, LIPG, PCSK9
GO:0010876: lipid localization	4.20E-21	16	272	ABCA1, ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, LPA, NPC1L1, OSBPL7
GO:0006793: phosphorus metabolic process	2.06E-05	15	2720	ABCG5, ABCG8, ANGPTL3, APOA1, CETP, FADS1, FRK, GPAM, HMGCR, HNF4A, LIPC, LIPG, PCSK9, RAF1, TOP1
GO:0006869: lipid transport	5.25E-20	15	247	ABCA1, ABCG5, ABCG8, APOA1, APOB, APOE, *CETP, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, *LPA, NPC1L1, *OSBPL7
GO:0010033: response to organic substance	2.36E-05	15	2751	ABCA1, ANGPTL3, APOB, APOE, CYP7A1, FADS1, GCKR, GPAM, HNF1A, HNF4A, LDLR, PCSK9, RAF1, SORT1, TRIB1
GO:1901615: organic hydroxy compound metabolic process	2.22E-14	14	471	ABCA1, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, LIPC, NPC1L1, PCSK9
GO:0051239: regulation of multicellular organismal process	1.18E-04	14	2790	ABCG5, ABCG8, ANGPTL3, APOA1, APOE, GPAM, HMGCR, HNF4A, LIPG, MAFB, MAMSTR, MYLIP, PCSK9, TRPS1
GO:0008203: cholesterol metabolic process	1.80E-22	14	126	*ABCA1, *ANGPTL3, *APOA1, *APOB, *APOE, *CETP, CYP7A1, HMGCR, *HNF1A, *LDLR, *LDLRAP1, *LIPC, NPC1L1, *PCSK9
GO:0016125: sterol metabolic process	9.30E-22	14	141	ABCA1, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, LIPC, NPC1L1, PCSK9
GO:0008202: steroid metabolic process	1.17E-16	14	322	ABCA1, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, LIPC, NPC1L1, PCSK9
GO:0006066: alcohol metabolic process	9.33E-16	14	374	ABCA1, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, LIPC, NPC1L1, PCSK9
GO:0006796: phosphate-containing compound metabolic process	5.75E-05	14	2610	ABCG5, ABCG8, ANGPTL3, APOA1, CETP, FADS1, FRK, GPAM, HMGCR, LIPC, LIPG, PCSK9, RAF1, TOP1
GO:0015850: organic hydroxy compound transport	7.03E-23	13	84	ABCA1, ABCG5, ABCG8, APOA1, APOB, APOE, CETP, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, NPC1L1
GO:0051049: regulation of transport	1.53E-07	13	1321	ABCA1, ABCG5, ABCG8, APOA1, APOE, CETP, GCKR, GPAM, HNF1A, HNF4A, LDLRAP1, LIPG, PCSK9
GO:0065009: regulation of molecular function	7.58E-05	13	2329	ANGPTL3, APOA1, APOE, GCKR, HMGCR, HNF4A, LDLRAP1, LPA, PCSK9, RAB3GAP1, RAF1, SORT1, TRIB1
GO:0030301: cholesterol transport	3.65E-25	13	58	ABCA1, ABCG5, ABCG8, *APOA1, *APOB, APOE, *CETP, HNF1A, *LDLR, LDLRAP1, LIPC, LIPG, *NPC1L1
GO:0015918: sterol transport	3.65E-25	13	58	ABCA1, *ABCG5, *ABCG8, APOA1, APOB, APOE, CETP, HNF1A, LDLR, LDLRAP1, LIPC, LIPG, *NPC1L1
GO:0050793: regulation of developmental process	4.96E-05	13	2235	ABCA1, ANGPTL3, APOA1, APOB, APOE, CETP, FADS1, HMGCR, HNF4A, MAFB, MAMSTR, RAF1, TRPS1
GO:0031325: positive regulation of cellular metabolic process	9.49E-04	12	2626	ABCA1, APOA1, APOE, GPAM, HNF1A, HNF4A, LDLR, MAFB, MAMSTR, PCSK9, RAF1, TRIB1

GO:0006082: organic acid metabolic process	1.05E-05	12	1635	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GCKR, GPAM, HNF1A, HNF4A, LIPC, MARC1, ST3GAL4
GO:0016192: vesicle-mediated transport	7.00E-06	11	1300	ABCA1, APOA1, APOB, APOE, CETP, *ERGIC3, HFE, LDLR, LDLRAP1, LPA, SORT1
GO:0044092: negative regulation of molecular function	5.82E-08	11	798	ANGPTL3, APOA1, APOE, GCKR, HMGCR, HNF4A, LPA, PCSK9, RAF1, SORT1, TRIB1
GO:0019637: organophosphate metabolic process	2.62E-05	11	1497	ABCG5, ABCG8, ANGPTL3, APOA1, CETP, FADS1, GPAM, HMGCR, LIPC, LIPG, PCSK9
GO:0050790: regulation of catalytic activity	1.68E-04	11	1840	ANGPTL3, APOA1, APOE, GCKR, HMGCR, LPA, PCSK9, RAB3GAP1, RAF1, SORT1, TRIB1
GO:0043436: oxoacid metabolic process	5.30E-05	11	1617	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GPAM, HNF1A, HNF4A, LIPC, MARC1, ST3GAL4
GO:1901575: organic substance catabolic process	9.45E-04	11	2254	ABCG5, ABCG8, ANGPTL3, APOB, APOE, CYP7A1, LDLR, LIPC, LIPG, MYLIP, PCSK9
GO:0008610: lipid biosynthetic process	5.53E-07	10	790	APOA1, CYP7A1, FADS1, FADS2, FADS3, GPAM, HMGCR, HNF1A, LIPC, NPC1L1
GO:0043086: negative regulation of catalytic activity	4.87E-08	10	607	ANGPTL3, APOA1, APOE, GCKR, HMGCR, LPA, *PCSK9, RAF1, SORT1, TRIB1
GO:0009719: response to endogenous stimulus	3.13E-04	10	1650	ABCA1, ANGPTL3, APOB, FADS1, GPAM, HNF4A, LDLR, PCSK9, RAF1, SORT1
GO:0019220: regulation of phosphate metabolic process	2.63E-04	10	1614	ABCA1, APOA1, APOE, GCKR, HMGCR, HNF4A, LDLR, RAB3GAP1, RAF1, TRIB1
GO:0051174: regulation of phosphorus metabolic process	2.79E-04	10	1626	ABCA1, APOA1, APOE, GCKR, HMGCR, HNF4A, LDLR, RAB3GAP1, RAF1, TRIB1
GO:0006897: endocytosis	1.94E-08	9	405	ABCA1, APOB, APOE, CETP, HFE, *LDLR, LDLRAP1, LPA, *SORT1
GO:0044711: single-organism biosynthetic process	1.98E-06	9	702	APOA1, CYP7A1, FADS1, FADS2, FADS3, HMGCR, HNF1A, LIPC, NPC1L1
GO:0042157: lipoprotein metabolic process	1.03E-11	9	172	*ABCA1, *APOA1, *APOB, *APOE, *CETP, *LDLR, *LPA, *NPC1L1, *PCSK9
GO:0019216: regulation of lipid metabolic process	8.35E-10	9	282	ANGPTL3, APOA1, APOB, APOE, CYP7A1, GPAM, *HNF4A, LDLR, LDLRAP1
GO:0097006: regulation of plasma lipoprotein particle levels	5.92E-16	9	60	ABCA1, APOA1, APOB, APOE, CETP, LDLR, LDLRAP1, LIPC, LIPG
GO:0045595: regulation of cell differentiation	9.98E-04	9	1576	ABCA1, APOB, APOE, CETP, *FADS1, MAFB, MAMSTR, *RAF1, TRPS1
GO:0044283: small molecule biosynthetic process	1.52E-06	9	680	APOA1, CYP7A1, FADS1, FADS2, FADS3, HMGCR, HNF1A, LIPC, NPC1L1
GO:0019752: carboxylic acid metabolic process	6.53E-04	9	1485	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GPAM, HNF1A, HNF4A, LIPC
GO:0043933: macromolecular complex subunit organization	4.59E-04	9	1414	ABCA1, APOA1, APOB, APOE, CETP, HFE, HMGCR, LIPC, LIPG
GO:0032787: monocarboxylic acid metabolic process	7.56E-06	8	621	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GPAM, HNF1A, LIPC
GO:0006644: phospholipid metabolic process	2.24E-06	8	526	*ANGPTL3, APOA1, CETP, FADS1, *GPAM, LIPC, LIPG, *PCSK9
GO:0009725: response to hormone stimulus	5.75E-04	8	1157	*ANGPTL3, APOB, FADS1, GPAM, LDLR, PCSK9, RAF1, SORT1
GO:0006898: receptor-mediated endocytosis	1.49E-09	7	125	*APOB, *APOE, *CETP, *HFE, *LDLR, *LDLRAP1, *LPA
GO:0009894: regulation of catabolic process	1.80E-04	7	725	ANGPTL3, APOE, LDLR, MYLIP, PCSK9, RAB3GAP1, TRIB1
GO:0055091: phospholipid homeostasis	7.79E-19	7	9	*ABCA1, *ANGPTL3, *APOA1, *CETP, *GPAM, *HNF4A, *LIPG
GO:0006631: fatty acid metabolic process	6.99E-06	7	434	*ANGPTL3, FADS1, FADS2, FADS3, *GPAM, HNF1A, LIPC
GO:0046486: glycerolipid metabolic process	9.37E-06	7	454	APOA1, APOB, APOE, CETP, GPAM, LIPC, PCSK9
GO:0043691: reverse cholesterol transport	1.08E-15	7	19	*ABCA1, *APOA1, *APOE, *CETP, *HNF1A, *LIPC, *LIPG
GO:0071827: plasma lipoprotein particle organization	8.98E-14	7	33	ABCA1, APOA1, APOB, APOE, CETP, LIPC, LIPG
GO:0071825: protein-lipid complex subunit organization	8.98E-14	7	33	ABCA1, APOA1, APOB, APOE, CETP, LIPC, LIPG
GO:0045834: positive regulation of lipid metabolic process	1.33E-09	7	123	ANGPTL3, APOA1, APOE, GPAM, HNF4A, LDLR, LDLRAP1

GO:0032374: regulation of cholesterol transport	7.08E-14	7	32	ABCA1, ABCG5, ABCG8, APOA1, APOE, CETP, LIPG
GO:0032371: regulation of sterol transport	7.08E-14	7	32	ABCA1, ABCG5, ABCG8, APOA1, APOE, CETP, LIPG
GO:0032368: regulation of lipid transport	3.59E-11	7	74	ABCA1, ABCG5, ABCG8, APOA1, APOE, CETP, LIPG
GO:0009743: response to carbohydrate stimulus	1.60E-07	7	246	*APOB, CYP7A1, FADS1, GCKR, GPAM, HNF1A, HNF4A
GO:0031667: response to nutrient levels	1.22E-05	7	473	ABCG5, FADS1, *GPAM, HFE, HMGCR, LIPG, PCSK9
GO:0010243: response to organic nitrogen	9.30E-04	7	954	FADS1, GPAM, HNF4A, LDLR, PCSK9, RAF1, SORT1
GO:0009991: response to extracellular stimulus	2.22E-05	7	519	ABCG5, FADS1, GPAM, HFE, HMGCR, LIPG, PCSK9
GO:0015748: organophosphate ester transport	1.26E-09	6	66	ABCA1, ABCG8, APOA1, APOE, CETP, LDLR
GO:0055114: oxidation-reduction process	9.07E-04	6	686	APOA1, FADS1, FADS2, FADS3, *MARC1, PPP1R3B
GO:0051241: negative regulation of multicellular organismal process	1.68E-04	6	499	ABCG5, ABCG8, APOA1, APOE, MYLIP, PCSK9
GO:0070328: triglyceride homeostasis	1.07E-11	6	31	*ANGPTL3, *APOA1, *CETP, *GCKR, *HNF4A, *LIPC
GO:0055090: acylglycerol homeostasis	1.31E-11	6	32	*ANGPTL3, APOA1, CETP, GCKR, HNF4A, LIPC
GO:0006641: triglyceride metabolic process	2.38E-08	6	107	APOB, *APOE, *CETP, GPAM, LIPC, *PCSK9
GO:0006639: acylglycerol metabolic process	3.48E-08	6	114	APOB, APOE, CETP, GPAM, LIPC, PCSK9
GO:0006638: neutral lipid metabolic process	3.87E-08	6	116	APOB, APOE, CETP, GPAM, LIPC, PCSK9
GO:0016042: lipid catabolic process	1.14E-05	6	307	ANGPTL3, APOB, APOE, CYP7A1, LIPC, LIPG
GO:0015914: phospholipid transport	6.43E-11	6	41	ABCA1, *ABCG8, APOA1, APOE, *CETP, *LDLR
GO:0034381: plasma lipoprotein particle clearance	3.96E-11	6	38	APOA1, APOB, APOE, LDLR, LDLRAP1, LIPC
GO:0034369: plasma lipoprotein particle remodeling	4.31E-12	6	27	APOA1, APOB, APOE, CETP, LIPC, LIPG
GO:0034368: protein-lipid complex remodeling	4.31E-12	6	27	APOA1, APOB, APOE, CETP, LIPC, LIPG
GO:0034367: macromolecular complex remodeling	4.31E-12	6	27	APOA1, APOB, APOE, CETP, LIPC, LIPG
GO:0046890: regulation of lipid biosynthetic process	8.74E-08	6	133	APOB, APOE, CYP7A1, GPAM, HNF4A, LDLR
GO:0043434: response to peptide hormone stimulus	4.79E-04	6	607	FADS1, GPAM, LDLR, PCSK9, RAF1, SORT1
GO:1901652: response to peptide	5.40E-04	6	621	FADS1, GPAM, LDLR, PCSK9, RAF1, SORT1
GO:0072330: monocarboxylic acid biosynthetic process	5.24E-06	6	268	CYP7A1, FADS1, FADS2, FADS3, HNF1A, LIPC
GO:0016053: organic acid biosynthetic process	1.43E-04	6	484	CYP7A1, FADS1, FADS2, FADS3, HNF1A, LIPC
GO:0046394: carboxylic acid biosynthetic process	1.43E-04	6	484	CYP7A1, FADS1, FADS2, FADS3, HNF1A, LIPC
GO:0031329: regulation of cellular catabolic process	4.50E-04	6	600	APOE, LDLR, MYLIP, PCSK9, RAB3GAP1, TRIB1
GO:0006694: steroid biosynthetic process	4.81E-06	5	149	APOA1, CYP7A1, HMGCR, HNF1A, NPC1L1
GO:0006633: fatty acid biosynthetic process	1.86E-05	5	197	FADS1, FADS2, FADS3, *HNF1A, *LIPC
GO:0033344: cholesterol efflux	6.44E-10	5	26	*ABCA1, *ABCG5, *ABCG8, *APOA1, *APOE
GO:0034375: high-density lipoprotein particle remodeling	2.98E-11	5	15	*APOA1, *APOE, *CETP, *LIPC, *LIPG
GO:0019218: regulation of steroid metabolic process	6.40E-07	5	99	APOA1, APOB, APOE, CYP7A1, LDLRAP1
GO:0051346: negative regulation of hydrolase activity	8.79E-05	5	273	ANGPTL3, *APOA1, LPA, RAF1, SORT1
GO:0009746: response to hexose stimulus	9.95E-06	5	173	CYP7A1, GCKR, GPAM, HNF1A, HNF4A
GO:0034284: response to monosaccharide stimulus	1.82E-05	5	196	CYP7A1, GCKR, GPAM, HNF1A, HNF4A

GO:0032868: response to insulin stimulus	4.42E-04	5	387	*FADS1, GPAM, PCSK9, RAF1, *SORT1
GO:0046434: organophosphate catabolic process	2.72E-04	5	348	ABCG5, ABCG8, ANGPTL3, LIPC, LIPG
GO:0033500: carbohydrate homeostasis	1.12E-04	4	150	CYP7A1, GCKR, HNF1A, HNF4A
GO:0042593: glucose homeostasis	1.12E-04	4	150	CYP7A1, GCKR, *HNF1A, *HNF4A
GO:0044241: lipid digestion	6.54E-09	4	14	ABCG5, ABCG8, LDLR, NPC1L1
GO:0050892: intestinal absorption	1.32E-07	4	28	ABCG5, ABCG8, LDLR, NPC1L1
GO:0022600: digestive system process	1.44E-06	4	50	ABCG5, ABCG8, LDLR, NPC1L1
GO:0007586: digestion	4.57E-05	4	119	ABCG5, ABCG8, LDLR, NPC1L1
GO:0009896: positive regulation of catabolic process	2.51E-04	4	185	ANGPTL3, APOE, MYLIP, TRIB1
GO:0042176: regulation of protein catabolic process	7.46E-04	4	247	APOE, MYLIP, PCSK9, TRIB1
GO:0042158: lipoprotein biosynthetic process	3.12E-05	4	108	ABCA1, *APOA1, *APOB, *APOE
GO:0044242: cellular lipid catabolic process	2.46E-04	4	184	ANGPTL3, APOB, LIPC, LIPG
GO:0030299: intestinal cholesterol absorption	4.61E-10	4	8	*ABCG5, *ABCG8, *LDLR, *NPC1L1
GO:0034374: low-density lipoprotein particle remodeling	4.68E-09	4	13	*APOB, *APOE, *CETP, *LIPC
GO:0034377: plasma lipoprotein particle assembly	8.91E-09	4	15	ABCA1, APOA1, APOB, APOE
GO:0065005: protein-lipid complex assembly	8.91E-09	4	15	ABCA1, APOA1, APOB, APOE
GO:0033673: negative regulation of kinase activity	4.13E-04	4	211	APOE, GCKR, HMGCR, TRIB1
GO:0051348: negative regulation of transferase activity	5.53E-04	4	228	APOE, GCKR, HMGCR, TRIB1
GO:0009749: response to glucose stimulus	1.51E-04	4	162	CYP7A1, *GPAM, *HNF1A, *HNF4A
GO:0048844: artery morphogenesis	1.30E-04	3	59	*ANGPTL3, *APOB, *APOE
GO:0060840: artery development	2.25E-04	3	71	ANGPTL3, APOB, APOE
GO:0015758: glucose transport	1.89E-04	3	67	*GCKR, HNF1A, SORT1
GO:0008645: hexose transport	1.98E-04	3	68	*GCKR, HNF1A, SORT1
GO:0015749: monosaccharide transport	2.16E-04	3	70	GCKR, HNF1A, SORT1
GO:0030300: regulation of intestinal cholesterol absorption	8.49E-08	3	6	ABCG5, ABCG8, *APOA1
GO:0044058: regulation of digestive system process	1.68E-05	3	30	ABCG5, ABCG8, APOA1
GO:0032803: regulation of low-density lipoprotein particle receptor catabolic process	4.25E-08	3	5	APOE, *MYLIP, *PCSK9
GO:2000644: regulation of receptor catabolic process	8.49E-08	3	6	APOE, MYLIP, PCSK9
GO:0010743: regulation of macrophage derived foam cell differentiation	4.67E-05	3	42	ABCA1, APOB, CETP
GO:0045732: positive regulation of protein catabolic process	9.23E-04	3	115	APOE, *MYLIP, TRIB1
GO:0042159: lipoprotein catabolic process	6.96E-07	3	11	*APOB, *APOE, *LDLR
GO:0009395: phospholipid catabolic process	2.93E-05	3	36	*ANGPTL3, LIPC, *LIPG
GO:0006695: cholesterol biosynthetic process	4.34E-05	3	41	*APOA1, *HMGCR, *NPC1L1
GO:0016126: sterol biosynthetic process	8.89E-05	3	52	APOA1, HMGCR, NPC1L1
GO:0046470: phosphatidylcholine metabolic process	1.73E-04	3	65	APOA1, *CETP, LIPC
GO:0006636: unsaturated fatty acid biosynthetic process	1.98E-04	3	68	*FADS1, *FADS2, *FADS3
GO:0033559: unsaturated fatty acid metabolic process	8.11E-04	3	110	*FADS1, *FADS2, FADS3
GO:0033700: phospholipid efflux	9.27E-07	3	12	*ABCA1, *APOA1, *APOE
GO:0010984: regulation of lipoprotein particle clearance	1.20E-06	3	13	LIPG, MYLIP, PCSK9

GO:0034383: low-density lipoprotein particle clearance	1.91E-06	3	15	*APOB, *LDLR, LDLRAP1
GO:0034380: high-density lipoprotein particle assembly	8.49E-08	3	6	*ABCA1, *APOA1, *APOE
GO:0034372: very-low-density lipoprotein particle remodeling	1.48E-07	3	7	*APOE, *CETP, *LIPC
GO:0034370: triglyceride-rich lipoprotein particle remodeling	5.07E-07	3	10	APOE, CETP, LIPC
GO:0045940: positive regulation of steroid metabolic process	1.35E-05	3	28	APOA1, APOE, LDLRAP1
GO:0090181: regulation of cholesterol metabolic process	2.24E-05	3	33	APOB, APOE, LDLRAP1
GO:0050810: regulation of steroid biosynthetic process	2.44E-04	3	73	APOB, APOE, CYP7A1
GO:0046889: positive regulation of lipid biosynthetic process	1.05E-04	3	55	GPAM, HNF4A, LDLR
GO:0032376: positive regulation of cholesterol transport	1.20E-06	3	13	ABCA1, APOE, *LIPG
GO:0032373: positive regulation of sterol transport	1.20E-06	3	13	ABCA1, APOE, LIPG
GO:0010874: regulation of cholesterol efflux	2.85E-06	3	17	ABCA1, APOE, *CETP
GO:0032370: positive regulation of lipid transport	3.18E-05	3	37	ABCA1, APOE, LIPG
GO:0009267: cellular response to starvation	6.70E-04	3	103	*FADS1, HFE, *PCSK9
GO:0032489: regulation of Cdc42 protein signal transduction	5.55E-06	3	21	*ABCA1, *APOA1, *APOE
GO:0046164: alcohol catabolic process	1.89E-04	3	67	APOE, CYP7A1, LIPC
GO:0042439: ethanolamine-containing compound metabolic process	5.13E-04	3	94	APOA1, CETP, LIPC
GO:0008643: carbohydrate transport	6.33E-04	3	101	GCKR, HNF1A, SORT1
GO:0030802: regulation of cyclic nucleotide biosynthetic process	7.49E-04	3	107	ABCA1, APOE, RAF1
GO:0030808: regulation of nucleotide biosynthetic process	7.69E-04	3	108	ABCA1, APOE, RAF1
GO:1900371: regulation of purine nucleotide biosynthetic process	7.69E-04	3	108	ABCA1, APOE, RAF1
GO:0030799: regulation of cyclic nucleotide metabolic process	9.70E-04	3	117	ABCA1, APOE, RAF1
GO:0030804: positive regulation of cyclic nucleotide biosynthetic process	2.44E-04	3	73	ABCA1, APOE, RAF1
GO:1900373: positive regulation of purine nucleotide biosynthetic process	2.54E-04	3	74	ABCA1, APOE, RAF1
GO:0030810: positive regulation of nucleotide biosynthetic process	2.54E-04	3	74	ABCA1, APOE, RAF1
GO:0030801: positive regulation of cyclic nucleotide metabolic process	2.64E-04	3	75	ABCA1, APOE, RAF1
GO:1901616: organic hydroxy compound catabolic process	2.75E-04	3	76	APOE, CYP7A1, LIPC
GO:1900544: positive regulation of purine nucleotide metabolic process	2.86E-04	3	77	ABCA1, APOE, RAF1
GO:0045981: positive regulation of nucleotide metabolic process	2.86E-04	3	77	ABCA1, APOE, RAF1
GO:0046323: glucose import	1.61E-05	2	4	*HNF1A, *SORT1
GO:0010949: negative regulation of intestinal phytosterol absorption	2.68E-06	2	2	*ABCG5, *ABCG8
GO:0045796: negative regulation of intestinal cholesterol absorption	2.68E-06	2	2	*ABCG5, *ABCG8
GO:0060457: negative regulation of digestive system process	4.04E-04	2	18	ABCG5, ABCG8
GO:0010745: negative regulation of macrophage derived foam cell differentiation	2.07E-04	2	13	*ABCA1, *CETP
GO:0043651: linoleic acid metabolic process	7.46E-05	2	8	*FADS1, *FADS2

GO:0006707: cholesterol catabolic process	2.07E-04	2	13	*APOE, *CYP7A1
GO:0016127: sterol catabolic process	2.07E-04	2	13	APOE, CYP7A1
GO:0006699: bile acid biosynthetic process	6.64E-04	2	23	*CYP7A1, *HNF1A
GO:0019433: triglyceride catabolic process	6.64E-04	2	23	*APOB, *LIPC
GO:0046464: acylglycerol catabolic process	8.50E-04	2	26	APOB, LIPC
GO:0046461: neutral lipid catabolic process	8.50E-04	2	26	APOB, LIPC
GO:0035376: sterol import	8.04E-06	2	3	APOA1, LDLR
GO:0070508: cholesterol import	8.04E-06	2	3	*APOA1, *LDLR
GO:0035382: sterol transmembrane transport	8.04E-06	2	3	APOA1, LDLR
GO:0032367: intracellular cholesterol transport	7.46E-05	2	8	*ABCA1, LDLRAP1
GO:0032366: intracellular sterol transport	7.46E-05	2	8	ABCA1, LDLRAP1
GO:0032365: intracellular lipid transport	4.04E-04	2	18	ABCA1, LDLRAP1
GO:0034384: high-density lipoprotein particle clearance	5.60E-05	2	7	*APOA1, *APOE
GO:0034382: chylomicron remnant clearance	9.59E-05	2	9	*APOE, *LIPC
GO:0071830: triglyceride-rich lipoprotein particle clearance	9.59E-05	2	9	APOE, LIPC
GO:0010873: positive regulation of cholesterol esterification	5.60E-05	2	7	*APOA1, *APOE
GO:0010872: regulation of cholesterol esterification	9.59E-05	2	9	APOA1, APOE
GO:0045540: regulation of cholesterol biosynthetic process	6.07E-04	2	22	*APOB, APOE
GO:0010867: positive regulation of triglyceride biosynthetic process	1.46E-04	2	11	*GPAM, *LDLR
GO:0010866: regulation of triglyceride biosynthetic process	3.17E-04	2	16	GPAM, LDLR
GO:0090208: positive regulation of triglyceride metabolic process	3.59E-04	2	17	GPAM, LDLR
GO:0032375: negative regulation of cholesterol transport	1.46E-04	2	11	ABCG5, ABCG8
GO:0010875: positive regulation of cholesterol efflux	1.46E-04	2	11	*ABCA1, *APOE
GO:0032372: negative regulation of sterol transport	1.46E-04	2	11	ABCG5, ABCG8
GO:0010989: negative regulation of low-density lipoprotein particle clearance	1.61E-05	2	4	*MYLIP, *PCSK9
GO:0010988: regulation of low-density lipoprotein particle clearance	5.60E-05	2	7	MYLIP, PCSK9
GO:0010985: negative regulation of lipoprotein particle clearance	5.60E-05	2	7	MYLIP, PCSK9
GO:0051005: negative regulation of lipoprotein lipase activity	4.01E-05	2	6	*ANGPTL3, *SORT1
GO:0060192: negative regulation of lipase activity	2.07E-04	2	13	ANGPTL3, SORT1
GO:0010885: regulation of cholesterol storage	7.85E-04	2	25	ABCA1, APOB
GO:0009750: response to fructose stimulus	2.07E-04	2	13	*GCKR, *GPAM
GO:0036109: alpha-linolenic acid metabolic process	1.46E-04	2	11	*FADS1, *FADS2
GO:0060395: SMAD protein signal transduction	6.64E-04	2	23	*HNF1A, *HNF4A
GO:0006706: steroid catabolic process	8.50E-04	2	26	APOE, CYP7A1
GO:0090207: regulation of triglyceride metabolic process	9.17E-04	2	27	GPAM, LDLR
GO:0050663: cytokine secretion	9.17E-04	2	27	ABCA1, GPAM

GO:0032369: negative regulation of lipid transport	9.17E-04	2	27	ABCG5, ABCG8

k is the number of genes in the query set annotated to that node, and M is the number of genes in the database annotated to that node.
*next to the gene symbol indicates that the gene is annotated to the node, and not any of the child terms.
Based on annotation dataset 12th November 2012 and GO ontology from 27th November 2012.

Table S4 Biological process VLAD results, LDL cholesterol trait associated genes

GO Term	P-value	k	M	Genes
GO:0008150: biological_process	1.00E+00	38	29612	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, BRAP, CETP, CYP7A1, DNAH11, FADS1, FADS2, FADS3, FRK, GPAM, HFE, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MARC1, MYLIP, NPC1L1, *NYNRIN, OSBPL7, PCSK9, PLEC, PPP1R3B, PRKCA, SFN, SORT1, ST3GAL4, TOP1, TRIB1
GO:0009987: cellular process	8.23E-04	37	23018	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, BRAP, CETP, CYP7A1, DNAH11, FADS1, FADS2, FADS3, FRK, GPAM, HFE, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MARC1, MYLIP, NPC1L1, NYNRIN, PCSK9, PLEC, PPP1R3B, PRKCA, SFN, SORT1, ST3GAL4, TOP1, TRIB1
GO:0008152: metabolic process	5.86E-05	31	14817	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GPAM, HFE, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MARC1, MYLIP, NPC1L1, NYNRIN, PCSK9, PPP1R3B, PRKCA, ST3GAL4, TOP1
GO:0044237: cellular metabolic process	4.75E-06	30	12556	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GPAM, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MARC1, MYLIP, NPC1L1, NYNRIN, PCSK9, PPP1R3B, PRKCA, ST3GAL4, TOP1
GO:0044710: single-organism metabolic process	1.47E-04	30	14505	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GPAM, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MARC1, MYLIP, NPC1L1, NYNRIN, PCSK9, PPP1R3B, PRKCA, ST3GAL4, TOP1
GO:0044238: primary metabolic process	1.49E-04	29	13667	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GPAM, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MYLIP, NPC1L1, NYNRIN, PCSK9, PPP1R3B, PRKCA, ST3GAL4, TOP1
GO:0071704: organic substance metabolic process	3.40E-04	29	14197	ABCG5, ABCG8, ABO, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, FADS1, FADS2, FADS3, FRK, GPAM, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MYLIP, NPC1L1, NYNRIN, PCSK9, PPP1R3B, PRKCA, ST3GAL4, TOP1
GO:0044707: single-multicellular organism process	6.32E-05	22	8030	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GPAM, HFE, HMGCR, HNF1A, LDLR, LDLRAP1, LPA, MAFB, MYLIP, NPC1L1, PCSK9, PRKCA, SFN, SORT1, TOP1
GO:0032501: multicellular organismal process	6.82E-05	22	8067	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GPAM, HFE, HMGCR, HNF1A, LDLR, LDLRAP1, LPA, MAFB, MYLIP, NPC1L1, PCSK9, PRKCA, SFN, SORT1, TOP1

GO:0044281: small molecule metabolic process	9.53E-12	22	3455	*ABCG5, *ABCG8, ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *CYP7A1, *FADS1, *FADS2, FADS3, *GPAM, *HMGCR, HNF1A, *LDLR, LDLRAP1, *LPA, MARC1, *NPC1L1, PCSK9, *PRKCA, *ST3GAL4
GO:0019222: regulation of metabolic process	1.50E-04	20	7178	ANGPTL3, APOA1, APOB, APOE, CYP7A1, FADS1, GPAM, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, LPA, MAFB, MYLIP, PCSK9, PRKCA, SFN, SORT1, TRIB1
GO:0006629: lipid metabolic process	5.63E-14	19	1762	*ABCG5, *ABCG8, ANGPTL3, *APOA1, *APOB, *APOE, *CETP, CYP7A1, FADS1, FADS2, FADS3, GPAM, HMGCR, HNF1A, *LDLR, LDLRAP1, *LPA, *NPC1L1, PCSK9
GO:1901360: organic cyclic compound metabolic process	1.90E-04	19	6677	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, MAFB, NPC1L1, NYNRIN, PCSK9, PRKCA, TOP1
GO:0080090: regulation of primary metabolic process	4.22E-04	18	6458	ANGPTL3, APOA1, APOB, APOE, CYP7A1, FADS1, GPAM, HMGCR, HNF1A, IRF2BP2, LDLR, LDLRAP1, MAFB, MYLIP, PCSK9, PRKCA, SFN, TRIB1
GO:0051179: localization	1.58E-04	18	5992	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GPAM, HFE, HNF1A, LDLR, LDLRAP1, LPA, NPC1L1, OSBPL7, PCSK9, PRKCA, SORT1
GO:0048878: chemical homeostasis	1.34E-14	17	1156	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GPAM, HFE, HNF1A, LDLR, LDLRAP1, MYLIP, NPC1L1, PCSK9, PRKCA
GO:0065008: regulation of biological quality	3.31E-07	17	3451	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GPAM, HFE, HNF1A, LDLR, LDLRAP1, MYLIP, NPC1L1, PCSK9, PRKCA
GO:0048519: negative regulation of biological process	1.40E-05	17	4507	ABCG5, ABCG8, APOA1, APOE, BRAP, CETP, FRK, GPAM, HMGCR, HNF1A, MAFB, MYLIP, PCSK9, PRKCA, SFN, SORT1, TRIB1
GO:0009058: biosynthetic process	7.46E-04	17	6142	ABO, APOA1, APOB, APOE, CYP7A1, FADS1, FADS2, FADS3, GPAM, HFE, HMGCR, HNF1A, IRF2BP2, MAFB, NPC1L1, ST3GAL4, TOP1
GO:0042592: homeostatic process	6.70E-12	17	1700	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, GPAM, HFE, HNF1A, LDLR, LDLRAP1, MYLIP, NPC1L1, PCSK9, PRKCA
GO:0006810: transport	1.25E-04	16	4771	ABCG5, ABCG8, APOA1, APOB, APOE, CETP, GPAM, HFE, HNF1A, LDLR, *LDLRAP1, LPA, NPC1L1, OSBPL7, PCSK9, SORT1
GO:0051234: establishment of localization	1.63E-04	16	4875	ABCG5, ABCG8, APOA1, APOB, APOE, CETP, GPAM, HFE, HNF1A, LDLR, LDLRAP1, LPA, NPC1L1, OSBPL7, PCSK9, SORT1
GO:0042221: response to chemical stimulus	1.32E-05	16	3988	ABCG5, ANGPTL3, APOB, APOE, CYP7A1, FADS1, GPAM, HMGCR, HNF1A, LDLR, MARC1, PCSK9, PRKCA, SORT1, TOP1, TRIB1
GO:0032879: regulation of localization	2.67E-08	14	1830	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GPAM, HNF1A, LDLRAP1, PCSK9, PRKCA, SFN, TRIB1
GO:0071702: organic substance transport	8.83E-07	14	2430	ABCG5, ABCG8, APOA1, APOB, APOE, CETP, GPAM, HNF1A, LDLR, LDLRAP1, LPA, NPC1L1, OSBPL7, SORT1
GO:0033036: macromolecule localization	1.61E-06	14	2555	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, GPAM, HNF1A, LDLR, LDLRAP1, LPA, NPC1L1, OSBPL7
GO:0048523: negative regulation of cellular process	3.33E-04	14	4093	APOA1, APOE, BRAP, CETP, FRK, GPAM, HMGCR, HNF1A, MAFB, PCSK9, PRKCA, SFN, SORT1, TRIB1

GO:0055088: lipid homeostasis	6.99E-25	14	115	ABCG5, ABCG8, *ANGPTL3, APOA1, APOB, APOE, *CETP, CYP7A1, GPAM, LDLR, LDLRAP1, MYLIP, NPC1L1, PCSK9
GO:0055092: sterol homeostasis	1.06E-24	13	82	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, LDLR, LDLRAP1, MYLIP, NPC1L1, PCSK9
GO:0042632: cholesterol homeostasis	1.06E-24	13	82	*ABCG5, *ABCG8, *ANGPTL3, *APOA1, *APOB, *APOE, *CETP, *CYP7A1, *LDLR, *LDLRAP1, *MYLIP, *NPC1L1, *PCSK9
GO:0044255: cellular lipid metabolic process	3.23E-09	13	1274	ANGPTL3, *APOA1, APOB, APOE, CETP, *CYP7A1, *FADS1, FADS2, FADS3, *GPAM, *HMGCR, HNF1A, PCSK9
GO:0010876: lipid localization	1.10E-17	13	272	ABCG5, ABCG8, ANGPTL3, APOA1, APOB, APOE, CETP, HNF1A, LDLR, LDLRAP1, LPA, NPC1L1, OSBPL7
GO:1901615: organic hydroxy compound metabolic process	4.25E-13	12	471	ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, NPC1L1, PCSK9
GO:0006793: phosphorus metabolic process	9.80E-05	12	2720	ABCG5, ABCG8, ANGPTL3, APOA1, CETP, FADS1, FRK, GPAM, HMGCR, PCSK9, PRKCA, TOP1
GO:0009893: positive regulation of metabolic process	1.22E-04	12	2783	ANGPTL3, APOA1, APOE, GPAM, HNF1A, LDLR, LDLRAP1, MAFB, MYLIP, PCSK9, PRKCA, TRIB1
GO:0008203: cholesterol metabolic process	5.07E-20	12	126	*ANGPTL3, *APOA1, *APOB, *APOE, *CETP, CYP7A1, HMGCR, *HNF1A, *LDLR, *LDLRAP1, NPC1L1, *PCSK9
GO:0016125: sterol metabolic process	2.05E-19	12	141	ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, NPC1L1, PCSK9
GO:0008202: steroid metabolic process	4.68E-15	12	322	ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, NPC1L1, PCSK9
GO:0006869: lipid transport	1.94E-16	12	247	ABCG5, ABCG8, APOA1, APOB, APOE, *CETP, HNF1A, LDLR, LDLRAP1, *LPA, NPC1L1, *OSBPL7
GO:0010033: response to organic substance	1.09E-04	12	2751	ANGPTL3, APOB, APOE, CYP7A1, FADS1, GPAM, HNF1A, LDLR, PCSK9, PRKCA, SORT1, TRIB1
GO:0006066: alcohol metabolic process	2.78E-14	12	374	ANGPTL3, APOA1, APOB, APOE, CETP, CYP7A1, HMGCR, HNF1A, LDLR, LDLRAP1, NPC1L1, PCSK9
GO:0006796: phosphate-containing compound metabolic process	6.57E-05	12	2610	ABCG5, ABCG8, ANGPTL3, APOA1, CETP, FADS1, FRK, GPAM, HMGCR, PCSK9, PRKCA, TOP1
GO:0051049: regulation of transport	5.28E-07	11	1321	ABCG5, ABCG8, APOA1, APOE, CETP, GPAM, HNF1A, LDLRAP1, PCSK9, PRKCA, SFN
GO:0065009: regulation of molecular function	1.14E-04	11	2329	ANGPTL3, APOA1, APOE, HMGCR, LDLRAP1, LPA, PCSK9, PRKCA, SFN, SORT1, TRIB1
GO:0051239: regulation of multicellular organismal process	5.53E-04	11	2790	ABCG5, ABCG8, ANGPTL3, APOA1, APOE, GPAM, HMGCR, MAFB, MYLIP, PCSK9, PRKCA
GO:0015850: organic hydroxy compound transport	8.59E-18	10	84	ABCG5, ABCG8, APOA1, APOB, APOE, CETP, HNF1A, LDLR, LDLRAP1, NPC1L1
GO:0044092: negative regulation of molecular function	4.56E-08	10	798	ANGPTL3, APOA1, APOE, HMGCR, LPA, PCSK9, PRKCA, SFN, SORT1, TRIB1
GO:0030301: cholesterol transport	1.66E-19	10	58	ABCG5, ABCG8, *APOA1, *APOB, APOE, *CETP, HNF1A, *LDLR, LDLRAP1, *NPC1L1
GO:0015918: sterol transport	1.66E-19	10	58	*ABCG5, *ABCG8, APOA1, APOB, APOE, CETP, HNF1A, LDLR, LDLRAP1, *NPC1L1
GO:0043086: negative regulation of catalytic activity	3.43E-09	10	607	ANGPTL3, APOA1, APOE, HMGCR, LPA, *PCSK9, PRKCA, SFN, SORT1, TRIB1
GO:0050790: regulation of catalytic activity	7.94E-05	10	1840	ANGPTL3, APOA1, APOE, HMGCR, LPA, PCSK9, PRKCA, SFN, SORT1, TRIB1
GO:0016192: vesicle-mediated transport	3.03E-05	9	1300	APOA1, APOB, APOE, CETP, HFE, LDLR, LDLRAP1, LPA, SORT1

GO:0019637: organophosphate metabolic process	9.06E-05	9	1497	ABCG5, ABCG8, ANGPTL3, APOA1, CETP, FADS1, GPAM, HMGCR, PCSK9
GO:0008610: lipid biosynthetic process	5.33E-07	9	790	APOA1, CYP7A1, FADS1, FADS2, FADS3, GPAM, HMGCR, HNF1A, NPC1L1
GO:0043436: oxoacid metabolic process	1.63E-04	9	1617	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GPAM, HNF1A, MARC1, ST3GAL4
GO:0006082: organic acid metabolic process	1.77E-04	9	1635	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GPAM, HNF1A, MARC1, ST3GAL4
GO:0006897: endocytosis	3.90E-08	8	405	APOB, APOE, CETP, HFE, *LDLR, LDLRAP1, LPA, *SORT1
GO:0044711: single-organism biosynthetic process	2.50E-06	8	702	APOA1, CYP7A1, FADS1, FADS2, FADS3, HMGCR, HNF1A, NPC1L1
GO:0042157: lipoprotein metabolic process	4.64E-11	8	172	*APOA1, *APOB, *APOE, *CETP, *LDLR, *LPA, *NPC1L1, *PCSK9
GO:0019216: regulation of lipid metabolic process	2.34E-09	8	282	ANGPTL3, APOA1, APOB, APOE, CYP7A1, GPAM, LDLR, LDLRAP1
GO:0009725: response to hormone stimulus	9.11E-05	8	1157	*ANGPTL3, APOB, FADS1, GPAM, LDLR, PCSK9, PRKCA, SORT1
GO:0009719: response to endogenous stimulus	9.96E-04	8	1650	ANGPTL3, APOB, FADS1, GPAM, LDLR, PCSK9, PRKCA, SORT1
GO:0044283: small molecule biosynthetic process	1.97E-06	8	680	APOA1, CYP7A1, FADS1, FADS2, FADS3, HMGCR, HNF1A, NPC1L1
GO:0006898: receptor-mediated endocytosis	2.28E-10	7	125	*APOB, *APOE, *CETP, *HFE, *LDLR, *LDLRAP1, *LPA
GO:0055114: oxidation-reduction process	2.35E-05	7	686	APOA1, FADS1, FADS2, FADS3, *MARC1, PPP1R3B, PRKCA
GO:0051241: negative regulation of multicellular organismal process	2.97E-06	7	499	ABCG5, ABCG8, APOA1, APOE, MYLIP, PCSK9, PRKCA
GO:0032787: monocarboxylic acid metabolic process	1.24E-05	7	621	ANGPTL3, CYP7A1, FADS1, FADS2, FADS3, GPAM, HNF1A
GO:0009894: regulation of catabolic process	2.99E-04	6	725	ANGPTL3, APOE, LDLR, MYLIP, PCSK9, TRIB1
GO:0006631: fatty acid metabolic process	1.78E-05	6	434	*ANGPTL3, FADS1, FADS2, FADS3, *GPAM, HNF1A
GO:0046486: glycerolipid metabolic process	2.29E-05	6	454	APOA1, APOB, APOE, CETP, GPAM, PCSK9
GO:0006644: phospholipid metabolic process	5.20E-05	6	526	*ANGPTL3, APOA1, CETP, FADS1, *GPAM, *PCSK9
GO:0045834: positive regulation of lipid metabolic process	1.12E-08	6	123	ANGPTL3, APOA1, APOE, GPAM, LDLR, LDLRAP1
GO:0051338: regulation of transferase activity	6.67E-04	6	844	APOA1, APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0097006: regulation of plasma lipoprotein particle levels	1.40E-10	6	60	APOA1, APOB, APOE, CETP, LDLR, LDLRAP1
GO:0009743: response to carbohydrate stimulus	6.83E-07	6	246	*APOB, CYP7A1, FADS1, GPAM, HNF1A, PRKCA
GO:0031667: response to nutrient levels	2.88E-05	6	473	ABCG5, FADS1, *GPAM, HFE, HMGCR, PCSK9
GO:0043434: response to peptide hormone stimulus	1.14E-04	6	607	FADS1, GPAM, LDLR, PCSK9, *PRKCA, SORT1
GO:1901652: response to peptide	1.29E-04	6	621	FADS1, GPAM, LDLR, PCSK9, PRKCA, SORT1
GO:0009991: response to extracellular stimulus	4.83E-05	6	519	ABCG5, FADS1, GPAM, HFE, HMGCR, PCSK9
GO:0060341: regulation of cellular localization	6.35E-04	6	836	APOA1, GPAM, HNF1A, LDLRAP1, PRKCA, SFN
GO:0007568: aging	1.20E-04	5	380	*APOE, *FADS1, *HMGCR, *LDLR, *PRKCA
GO:0015748: organophosphate ester transport	2.23E-08	5	66	ABCG8, APOA1, APOE, CETP, LDLR
GO:0001933: negative regulation of protein phosphorylation	2.47E-05	5	272	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0006641: triglyceride metabolic process	2.56E-07	5	107	APOB, *APOE, *CETP, GPAM, *PCSK9
GO:0006639: acylglycerol metabolic process	3.51E-07	5	114	APOB, APOE, CETP, GPAM, PCSK9
GO:0006638: neutral lipid metabolic process	3.83E-07	5	116	APOB, APOE, CETP, GPAM, PCSK9
GO:0006694: steroid biosynthetic process	1.32E-06	5	149	APOA1, CYP7A1, HMGCR, HNF1A, NPC1L1

GO:0015914: phospholipid transport	1.92E-09	5	41	*ABCG8, APOA1, APOE, *CETP, *LDLR
GO:0034381: plasma lipoprotein particle clearance	1.29E-09	5	38	APOA1, APOB, APOE, LDLR, LDLRAP1
GO:0019218: regulation of steroid metabolic process	1.73E-07	5	99	APOA1, APOB, APOE, CYP7A1, LDLRAP1
GO:0046890: regulation of lipid biosynthetic process	7.55E-07	5	133	APOB, APOE, CYP7A1, GPAM, LDLR
GO:0032374: regulation of cholesterol transport	5.20E-10	5	32	ABCG5, ABCG8, APOA1, APOE, CETP
GO:0032371: regulation of sterol transport	5.20E-10	5	32	ABCG5, ABCG8, APOA1, APOE, CETP
GO:0032368: regulation of lipid transport	4.00E-08	5	74	ABCG5, ABCG8, APOA1, APOE, CETP
GO:0006469: negative regulation of protein kinase activity	5.60E-06	5	200	APOE, HMGCR, PRKCA, *SFN, *TRIB1
GO:0033673: negative regulation of kinase activity	7.26E-06	5	211	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0051348: negative regulation of transferase activity	1.06E-05	5	228	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0051346: negative regulation of hydrolase activity	2.51E-05	5	273	ANGPTL3, *APOA1, LPA, SFN, SORT1
GO:0042326: negative regulation of phosphorylation	3.19E-05	5	287	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0071900: regulation of protein serine/threonine kinase activity	4.34E-04	5	502	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0072330: monocarboxylic acid biosynthetic process	2.30E-05	5	268	CYP7A1, FADS1, FADS2, FADS3, HNF1A
GO:0016053: organic acid biosynthetic process	3.68E-04	5	484	CYP7A1, FADS1, FADS2, FADS3, HNF1A
GO:0046394: carboxylic acid biosynthetic process	3.68E-04	5	484	CYP7A1, FADS1, FADS2, FADS3, HNF1A
GO:0031329: regulation of cellular catabolic process	9.70E-04	5	600	APOE, LDLR, MYLIP, PCSK9, TRIB1
GO:0010563: negative regulation of phosphorus metabolic process	7.43E-05	5	343	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0045936: negative regulation of phosphate metabolic process	7.43E-05	5	343	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0031400: negative regulation of protein modification process	1.60E-04	5	404	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0032269: negative regulation of cellular protein metabolic process	5.99E-04	5	539	APOE, HMGCR, PRKCA, SFN, TRIB1
GO:0044241: lipid digestion	2.29E-09	4	14	ABCG5, ABCG8, LDLR, NPC1L1
GO:0050892: intestinal absorption	4.62E-08	4	28	ABCG5, ABCG8, LDLR, NPC1L1
GO:0022600: digestive system process	5.09E-07	4	50	ABCG5, ABCG8, LDLR, NPC1L1
GO:0007586: digestion	1.65E-05	4	119	ABCG5, ABCG8, LDLR, NPC1L1
GO:0009896: positive regulation of catabolic process	9.22E-05	4	185	ANGPTL3, APOE, MYLIP, TRIB1
GO:0042176: regulation of protein catabolic process	2.79E-04	4	247	APOE, MYLIP, PCSK9, TRIB1
GO:0055091: phospholipid homeostasis	2.89E-10	4	9	*ANGPTL3, *APOA1, *CETP, *GPAM
GO:0006633: fatty acid biosynthetic process	1.17E-04	4	197	FADS1, FADS2, FADS3, *HNF1A
GO:0016042: lipid catabolic process	6.33E-04	4	307	ANGPTL3, APOB, APOE, CYP7A1
GO:0030299: intestinal cholesterol absorption	1.61E-10	4	8	*ABCG5, *ABCG8, *LDLR, *NPC1L1
GO:0043691: reverse cholesterol transport	8.81E-09	4	19	*APOA1, *APOE, *CETP, *HNF1A
GO:0033344: cholesterol efflux	3.38E-08	4	26	*ABCG5, *ABCG8, *APOA1, *APOE
GO:0034369: plasma lipoprotein particle remodeling	3.96E-08	4	27	APOA1, APOB, APOE, CETP
GO:0034368: protein-lipid complex remodeling	3.96E-08	4	27	APOA1, APOB, APOE, CETP
GO:0034367: macromolecular complex remodeling	3.96E-08	4	27	APOA1, APOB, APOE, CETP
GO:0071827: plasma lipoprotein particle organization	9.18E-08	4	33	APOA1, APOB, APOE, CETP

GO:0071825: protein-lipid complex subunit organization	9.18E-08	4	33	APOA1, APOB, APOE, CETP
GO:0043405: regulation of MAP kinase activity	8.67E-04	4	334	APOE, HMGCR, PRKCA, *TRIB1
GO:0048844: artery morphogenesis	6.03E-05	3	59	*ANGPTL3, *APOB, *APOE
GO:0060840: artery development	1.05E-04	3	71	ANGPTL3, APOB, APOE
GO:0030300: regulation of intestinal cholesterol absorption	3.89E-08	3	6	ABCG5, ABCG8, *APOA1
GO:0044058: regulation of digestive system process	7.73E-06	3	30	ABCG5, ABCG8, APOA1
GO:0048259: regulation of receptor-mediated endocytosis	3.89E-05	3	51	LDLRAP1, PCSK9, *PRKCA
GO:0032803: regulation of low-density lipoprotein particle receptor catabolic process	1.95E-08	3	5	APOE, *MYLIP, *PCSK9
GO:2000644: regulation of receptor catabolic process	3.89E-08	3	6	APOE, MYLIP, PCSK9
GO:0045732: positive regulation of protein catabolic process	4.36E-04	3	115	APOE, *MYLIP, TRIB1
GO:0046165: alcohol biosynthetic process	5.82E-04	3	127	APOA1, HMGCR, NPC1L1
GO:0070328: triglyceride homeostasis	8.55E-06	3	31	*ANGPTL3, *APOA1, *CETP
GO:0055090: acylglycerol homeostasis	9.42E-06	3	32	*ANGPTL3, APOA1, CETP
GO:0042159: lipoprotein catabolic process	3.19E-07	3	11	*APOB, *APOE, *LDLR
GO:0006695: cholesterol biosynthetic process	2.01E-05	3	41	*APOA1, *HMGCR, *NPC1L1
GO:0016126: sterol biosynthetic process	4.13E-05	3	52	APOA1, HMGCR, NPC1L1
GO:0006636: unsaturated fatty acid biosynthetic process	9.22E-05	3	68	*FADS1, *FADS2, *FADS3
GO:0042158: lipoprotein biosynthetic process	3.63E-04	3	108	*APOA1, *APOB, *APOE
GO:0033559: unsaturated fatty acid metabolic process	3.83E-04	3	110	*FADS1, *FADS2, FADS3
GO:0034383: low-density lipoprotein particle clearance	8.78E-07	3	15	*APOB, *LDLR, LDLRAP1
GO:0034374: low-density lipoprotein particle remodeling	5.53E-07	3	13	*APOB, *APOE, *CETP
GO:0034377: plasma lipoprotein particle assembly	8.78E-07	3	15	APOA1, APOB, APOE
GO:0065005: protein-lipid complex assembly	8.78E-07	3	15	APOA1, APOB, APOE
GO:0034375: high-density lipoprotein particle remodeling	8.78E-07	3	15	*APOA1, *APOE, *CETP
GO:0045940: positive regulation of steroid metabolic process	6.25E-06	3	28	APOA1, APOE, LDLRAP1
GO:0090181: regulation of cholesterol metabolic process	1.04E-05	3	33	APOB, APOE, LDLRAP1
GO:0050810: regulation of steroid biosynthetic process	1.14E-04	3	73	APOB, APOE, CYP7A1
GO:0060191: regulation of lipase activity	6.09E-04	3	129	ANGPTL3, PRKCA, SORT1
GO:0009267: cellular response to starvation	3.16E-04	3	103	*FADS1, HFE, *PCSK9
GO:0031669: cellular response to nutrient levels	8.05E-04	3	142	FADS1, HFE, PCSK9
GO:0042594: response to starvation	9.26E-04	3	149	FADS1, HFE, PCSK9
GO:0043407: negative regulation of MAP kinase activity	1.85E-04	3	86	*APOE, *HMGCR, PRKCA
GO:0071901: negative regulation of protein serine/threonine kinase activity	4.82E-04	3	119	APOE, HMGCR, PRKCA
GO:0046323: glucose import	9.61E-06	2	4	*HNF1A, *SORT1
GO:0010949: negative regulation of intestinal phytosterol absorption	1.60E-06	2	2	*ABCG5, *ABCG8

GO:0045796: negative regulation of intestinal cholesterol absorption	1.60E-06	2	2	*ABCG5, *ABCG8
GO:0060457: negative regulation of digestive system process	2.42E-04	2	18	ABCG5, ABCG8
GO:0043651: linoleic acid metabolic process	4.47E-05	2	8	*FADS1, *FADS2
GO:0006707: cholesterol catabolic process	1.24E-04	2	13	*APOE, *CYP7A1
GO:0016127: sterol catabolic process	1.24E-04	2	13	APOE, CYP7A1
GO:0006699: bile acid biosynthetic process	3.99E-04	2	23	*CYP7A1, *HNF1A
GO:0035376: sterol import	4.81E-06	2	3	APOA1, LDLR
GO:0070508: cholesterol import	4.81E-06	2	3	*APOA1, *LDLR
GO:0035382: sterol transmembrane transport	4.81E-06	2	3	APOA1, LDLR
GO:0033700: phospholipid efflux	1.05E-04	2	12	*APOA1, *APOE
GO:0034384: high-density lipoprotein particle clearance	3.35E-05	2	7	*APOA1, *APOE
GO:0010984: regulation of lipoprotein particle clearance	1.24E-04	2	13	MYLIP, PCSK9
GO:0034380: high-density lipoprotein particle assembly	2.40E-05	2	6	*APOA1, *APOE
GO:0034372: very-low-density lipoprotein particle remodeling	3.35E-05	2	7	*APOE, *CETP
GO:0034370: triglyceride-rich lipoprotein particle remodeling	7.17E-05	2	10	APOE, CETP
GO:0010873: positive regulation of cholesterol esterification	3.35E-05	2	7	*APOA1, *APOE
GO:0010872: regulation of cholesterol esterification	5.74E-05	2	9	APOA1, APOE
GO:0045540: regulation of cholesterol biosynthetic process	3.64E-04	2	22	*APOB, APOE
GO:0010867: positive regulation of triglyceride biosynthetic process	8.76E-05	2	11	*GPAM, *LDLR
GO:0010866: regulation of triglyceride biosynthetic process	1.90E-04	2	16	GPAM, LDLR
GO:0090208: positive regulation of triglyceride metabolic process	2.15E-04	2	17	GPAM, LDLR
GO:0032375: negative regulation of cholesterol transport	8.76E-05	2	11	ABCG5, ABCG8
GO:0032372: negative regulation of sterol transport	8.76E-05	2	11	ABCG5, ABCG8
GO:0010874: regulation of cholesterol efflux	2.15E-04	2	17	APOE, *CETP
GO:0010989: negative regulation of low-density lipoprotein particle clearance	9.61E-06	2	4	*MYLIP, *PCSK9
GO:0010988: regulation of low-density lipoprotein particle clearance	3.35E-05	2	7	MYLIP, PCSK9
GO:0010985: negative regulation of lipoprotein particle clearance	3.35E-05	2	7	MYLIP, PCSK9
GO:0051005: negative regulation of lipoprotein lipase activity	2.40E-05	2	6	*ANGPTL3, *SORT1
GO:0060192: negative regulation of lipase activity	1.24E-04	2	13	ANGPTL3, SORT1
GO:0031664: regulation of lipopolysaccharide-mediated signaling pathway	1.24E-04	2	13	PRKCA, TRIB1
GO:0032489: regulation of Cdc42 protein signal transduction	3.32E-04	2	21	*APOA1, *APOE
GO:0036109: alpha-linolenic acid metabolic process	8.76E-05	2	11	*FADS1, *FADS2
GO:0006706: steroid catabolic process	5.11E-04	2	26	APOE, CYP7A1
GO:0090207: regulation of triglyceride metabolic process	5.52E-04	2	27	GPAM, LDLR
GO:0032369: negative regulation of lipid transport	5.52E-04	2	27	ABCG5, ABCG8
GO:0010543: regulation of platelet activation	7.28E-04	2	31	APOE, PRKCA

GO:0048260: positive regulation of receptor-mediated endocytosis	7.76E-04	2	32	*LDLRAP1, PCSK9
GO:0019915: lipid storage	7.76E-04	2	32	*ANGPTL3, *APOA1

k is the number of genes in the query set annotated to that node, and M is the number of genes in the database annotated to that node.
*next to the gene symbol indicates that the gene is annotated to the node, and not any of the child terms.
Based on annotation dataset 12th November 2012 and GO ontology from 27th November 2012.

Table S5 Biological process VLAD results, HDL cholesterol trait associated genes

Term	P-value	k	M	Genes
GO:0008150: biological process	1.00E+00	34	29612	ABCA1, ABCA8, ANGPTL4, APOA1, APOB, APOE, ARL15, *C6orf106, CETP, CITED2, FADS1, GALNT2, HNF4A, IRS1, KLF14, LCAT, LILRA3, LIPC, LPA, LRP4, MC4R, MLXIPL, PDE3A, PGS1, PLTP, PPP1R3B, *SBNO1, SLC39A8, STARD3, TRIB1, TRPS1, UBE2L3, ZNF648, *ZNF664
GO:0065007: biological regulation	3.92E-04	27	14777	ABCA1, ANGPTL4, APOA1, APOB, APOE, ARL15, CETP, CITED2, FADS1, HNF4A, IRS1, KLF14, LCAT, LILRA3, LIPC, LPA, LRP4, MC4R, MLXIPL, PDE3A, SBNO1, STARD3, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0050789: regulation of biological process	4.85E-04	26	13977	ABCA1, ANGPTL4, APOA1, APOB, APOE, ARL15, CETP, CITED2, FADS1, HNF4A, IRS1, KLF14, LCAT, LILRA3, LIPC, LPA, LRP4, MC4R, MLXIPL, PDE3A, SBNO1, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0044237: cellular metabolic process	8.30E-04	24	12556	ABCA1, ANGPTL4, APOA1, APOB, APOE, CETP, FADS1, GALNT2, HNF4A, KLF14, LCAT, LIPC, LPA, MC4R, MLXIPL, PDE3A, PGS1, PLTP, PPP1R3B, STARD3, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0019222: regulation of metabolic process	1.75E-05	20	7178	ABCA1, ANGPTL4, APOA1, APOB, APOE, CITED2, FADS1, HNF4A, IRS1, KLF14, LPA, LRP4, MC4R, MLXIPL, SBNO1, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0009058: biosynthetic process	3.39E-05	18	6142	ABCA1, APOA1, APOB, APOE, FADS1, GALNT2, HNF4A, KLF14, LCAT, LIPC, MLXIPL, PGS1, PLTP, STARD3, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0080090: regulation of primary metabolic process	6.87E-05	18	6458	ABCA1, APOA1, APOB, APOE, CITED2, FADS1, HNF4A, IRS1, KLF14, LRP4, MC4R, MLXIPL, SBNO1, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0044249: cellular biosynthetic process	1.54E-05	18	5811	ABCA1, APOA1, APOB, APOE, FADS1, GALNT2, HNF4A, KLF14, LCAT, LIPC, MLXIPL, PGS1, PLTP, STARD3, TRPS1, UBE2L3, ZNF648, ZNF664
GO:1901576: organic substance biosynthetic process	2.25E-05	18	5967	ABCA1, APOA1, APOB, APOE, FADS1, GALNT2, HNF4A, KLF14, LCAT, LIPC, MLXIPL, PGS1, PLTP, STARD3, TRPS1, UBE2L3, ZNF648, ZNF664
GO:1901360: organic cyclic compound metabolic process	4.12E-04	17	6677	ABCA1, APOA1, APOB, APOE, CETP, HNF4A, KLF14, LCAT, LIPC, MLXIPL, PDE3A, PLTP, STARD3, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0031323: regulation of cellular metabolic process	3.00E-04	17	6511	ABCA1, APOA1, APOE, CITED2, FADS1, HNF4A, IRS1, KLF14, LRP4, MC4R, MLXIPL, SBNO1, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0006629: lipid metabolic process	1.83E-11	16	1762	*ABCA1, ANGPTL4, *APOA1, *APOB, *APOE, *CETP, FADS1, *HNF4A, IRS1, *LCAT, LIPC, *LPA, *PDE3A, PGS1, *PLTP, *STARD3
GO:0051179: localization	3.98E-04	16	5992	ABCA1, ABCA8, APOA1, APOB, APOE, CETP, IRS1, LCAT, LIPC, LPA, LRP4, MC4R, PLTP, SLC39A8, STARD3, TRPS1

GO:0044281: small molecule metabolic process	3.16E-07	16	3455	*ABCA1, *ANGPTL4, *APOA1, *APOB, *APOE, *CETP, *FADS1, HNF4A, *LCAT, LIPC, *LPA, *MLXIPL, PDE3A, *PGS1, PLTP, STARD3
GO:0009889: regulation of biosynthetic process	5.78E-05	16	5118	ABCA1, APOB, APOE, CITED2, FADS1, HNF4A, IRS1, KLF14, MC4R, MLXIPL, SBNO1, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0065008: regulation of biological quality	2.03E-06	15	3451	ABCA1, ANGPTL4, APOA1, APOB, APOE, CETP, CITED2, HNF4A, IRS1, LCAT, LIPC, MC4R, MLXIPL, PDE3A, STARD3
GO:0006810: transport	1.07E-04	15	4771	ABCA1, *ABCA8, APOA1, APOB, APOE, CETP, LCAT, LIPC, LPA, LRP4, MC4R, PLTP, SLC39A8, STARD3, TRPS1
GO:0051234: establishment of localization	1.38E-04	15	4875	ABCA1, ABCA8, APOA1, APOB, APOE, CETP, LCAT, LIPC, LPA, LRP4, MC4R, PLTP, SLC39A8, STARD3, TRPS1
GO:0031326: regulation of cellular biosynthetic process	2.20E-04	15	5077	ABCA1, APOE, CITED2, FADS1, HNF4A, IRS1, KLF14, MC4R, MLXIPL, SBNO1, TRIB1, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0048523: negative regulation of cellular process	3.54E-04	13	4093	ABCA1, ANGPTL4, APOA1, APOE, CETP, CITED2, HNF4A, IRS1, LRP4, MLXIPL, PDE3A, TRIB1, TRPS1
GO:0048519: negative regulation of biological process	9.13E-04	13	4507	ABCA1, ANGPTL4, APOA1, APOE, CETP, CITED2, HNF4A, IRS1, LRP4, MLXIPL, PDE3A, TRIB1, TRPS1
GO:0010033: response to organic substance	5.32E-06	13	2751	ABCA1, APOB, APOE, CITED2, FADS1, HNF4A, IRS1, LCAT, MC4R, MLXIPL, PDE3A, TRIB1, UBE2L3
GO:0042221: response to chemical stimulus	2.73E-04	13	3988	ABCA1, APOB, APOE, CITED2, FADS1, HNF4A, IRS1, LCAT, MC4R, MLXIPL, PDE3A, TRIB1, UBE2L3
GO:0034645: cellular macromolecule biosynthetic process	6.13E-04	13	4326	ABCA1, APOA1, APOB, APOE, GALNT2, HNF4A, KLF14, LCAT, MLXIPL, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0009059: macromolecule biosynthetic process	7.19E-04	13	4397	ABCA1, APOA1, APOB, APOE, GALNT2, HNF4A, KLF14, LCAT, MLXIPL, TRPS1, UBE2L3, ZNF648, ZNF664
GO:0033036: macromolecule localization	1.50E-05	12	2555	ABCA1, APOA1, APOB, APOE, CETP, IRS1, LCAT, LIPC, LPA, LRP4, PLTP, TRPS1
GO:0042592: homeostatic process	2.07E-07	12	1700	ABCA1, ANGPTL4, APOA1, APOB, APOE, CETP, CITED2, HNF4A, IRS1, LCAT, LIPC, MLXIPL
GO:0048878: chemical homeostasis	3.83E-08	11	1156	ABCA1, ANGPTL4, APOA1, APOB, APOE, CETP, HNF4A, IRS1, LCAT, LIPC, MLXIPL
GO:0071702: organic substance transport	5.38E-05	11	2430	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC, LPA, MC4R, PLTP, TRPS1
GO:0051239: regulation of multicellular organismal process	1.87E-04	11	2790	ANGPTL4, APOA1, APOE, CITED2, HNF4A, LCAT, LRP4, MC4R, MLXIPL, PDE3A, TRPS1
GO:0050793: regulation of developmental process	2.48E-05	11	2235	ABCA1, ANGPTL4, APOA1, APOB, APOE, CETP, CITED2, FADS1, HNF4A, PDE3A, TRPS1
GO:0055088: lipid homeostasis	6.34E-17	10	115	ABCA1, ANGPTL4, APOA1, APOB, APOE, *CETP, *HNF4A, LCAT, LIPC, MLXIPL
GO:0044255: cellular lipid metabolic process	1.07E-06	10	1274	*ABCA1, *ANGPTL4, *APOA1, APOB, APOE, CETP, *FADS1, LCAT, LIPC, PGS1
GO:0009719: response to endogenous stimulus	1.07E-05	10	1650	ABCA1, APOB, CITED2, FADS1, HNF4A, IRS1, LCAT, MC4R, PDE3A, UBE2L3
GO:0032879: regulation of localization	1.65E-04	9	1830	ABCA1, APOA1, APOB, APOE, CETP, CITED2, HNF4A, IRS1, TRIB1
GO:0006869: lipid transport	7.39E-12	9	247	ABCA1, APOA1, APOB, APOE, *CETP, LCAT, LIPC, *LPA, *PLTP
GO:0010876: lipid localization	1.75E-11	9	272	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC, LPA, PLTP
GO:0070887: cellular response to chemical stimulus	5.30E-04	9	2141	ABCA1, APOB, APOE, CITED2, HNF4A, IRS1, MLXIPL, PDE3A, UBE2L3

GO:0019220: regulation of phosphate metabolic process	6.29E-05	9	1614	ABCA1, APOA1, APOE, HNF4A, IRS1, LRP4, MC4R, MLXIPL, TRIB1
GO:0051174: regulation of phosphorus metabolic process	6.66E-05	9	1626	ABCA1, APOA1, APOE, HNF4A, IRS1, LRP4, MC4R, MLXIPL, TRIB1
GO:0043933: macromolecular complex subunit organization	2.23E-05	9	1414	ABCA1, ANGPTL4, APOA1, APOB, APOE, CETP, IRS1, LCAT, LIPC
GO:1901615: organic hydroxy compound metabolic process	4.88E-08	8	471	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC, STARD3
GO:0008203: cholesterol metabolic process	1.42E-12	8	126	*ABCA1, *APOA1, *APOB, *APOE, *CETP, *LCAT, *LIPC, *STARD3
GO:0016125: sterol metabolic process	3.54E-12	8	141	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC, STARD3
GO:0008202: steroid metabolic process	2.54E-09	8	322	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC, *STARD3
GO:0071310: cellular response to organic substance	5.33E-04	8	1692	ABCA1, APOB, APOE, CITED2, IRS1, MLXIPL, PDE3A, UBE2L3
GO:0006066: alcohol metabolic process	8.19E-09	8	374	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC, STARD3
GO:0016192: vesicle-mediated transport	5.87E-04	7	1300	ABCA1, APOA1, APOB, APOE, CETP, LPA, LRP4
GO:0015850: organic hydroxy compound transport	5.79E-12	7	84	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0055092: sterol homeostasis	4.87E-12	7	82	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0042632: cholesterol homeostasis	4.87E-12	7	82	*ABCA1, *APOA1, *APOB, *APOE, *CETP, *LCAT, *LIPC
GO:0046486: glycerolipid metabolic process	7.15E-07	7	454	APOA1, APOB, APOE, CETP, LCAT, LIPC, PGS1
GO:0030301: cholesterol transport	3.92E-13	7	58	ABCA1, *APOA1, *APOB, APOE, *CETP, *LCAT, LIPC
GO:0015918: sterol transport	3.92E-13	7	58	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0042157: lipoprotein metabolic process	9.30E-10	7	172	*ABCA1, *APOA1, *APOB, *APOE, *CETP, *LCAT, *LPA
GO:0071825: protein-lipid complex subunit organization	5.69E-15	7	33	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0071827: plasma lipoprotein particle organization	5.69E-15	7	33	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0097006: regulation of plasma lipoprotein particle levels	5.03E-13	7	60	ABCA1, APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0033993: response to lipid	8.57E-05	7	949	ABCA1, APOB, CITED2, FADS1, LCAT, TRIB1, UBE2L3
GO:0009725: response to hormone stimulus	2.91E-04	7	1157	APOB, CITED2, FADS1, IRS1, LCAT, MC4R, UBE2L3
GO:0042325: regulation of phosphorylation	2.69E-04	7	1142	APOA1, APOE, HNF4A, IRS1, LRP4, MLXIPL, TRIB1
GO:0006897: endocytosis	6.13E-06	6	405	ABCA1, APOB, APOE, CETP, LPA, *LRP4
GO:0044711: single-organism biosynthetic process	1.33E-04	6	702	APOA1, FADS1, LCAT, LIPC, PLTP, STARD3
GO:0044092: negative regulation of molecular function	2.65E-04	6	798	ANGPTL4, APOA1, APOE, HNF4A, LPA, TRIB1
GO:0070328: triglyceride homeostasis	1.04E-12	6	31	*ANGPTL4, *APOA1, *CETP, *HNF4A, *LIPC, *MLXIPL
GO:0055090: acylglycerol homeostasis	1.27E-12	6	32	ANGPTL4, APOA1, CETP, HNF4A, LIPC, MLXIPL
GO:0006644: phospholipid metabolic process	2.69E-05	6	526	APOA1, CETP, FADS1, *LCAT, LIPC, *PGS1
GO:0008610: lipid biosynthetic process	2.51E-04	6	790	APOA1, FADS1, LCAT, LIPC, PGS1, STARD3
GO:0043691: reverse cholesterol transport	3.86E-14	6	19	*ABCA1, *APOA1, *APOE, *CETP, *LCAT, *LIPC
GO:0034369: plasma lipoprotein particle remodeling	4.18E-13	6	27	APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0034368: protein-lipid complex remodeling	4.18E-13	6	27	APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0034367: macromolecular complex remodeling	4.18E-13	6	27	APOA1, APOB, APOE, CETP, LCAT, LIPC
GO:0019216: regulation of lipid metabolic process	7.60E-07	6	282	APOA1, APOB, APOE, *HNF4A, IRS1, MLXIPL
GO:0044283: small molecule biosynthetic process	1.11E-04	6	680	APOA1, FADS1, LCAT, LIPC, PLTP, STARD3

GO:0014070: response to organic cyclic compound	9.25E-04	6	1011	CITED2, *FADS1, HNF4A, LCAT, PDE3A, UBE2L3
GO:0042158: lipoprotein biosynthetic process	1.50E-07	5	108	ABCA1, *APOA1, *APOB, *APOE, *LCAT
GO:0006639: acylglycerol metabolic process	1.97E-07	5	114	APOB, APOE, CETP, LIPC, PGS1
GO:0006638: neutral lipid metabolic process	2.15E-07	5	116	APOB, APOE, CETP, LIPC, PGS1
GO:0006650: glycerophospholipid metabolic process	5.74E-05	5	365	APOA1, CETP, LCAT, LIPC, PGS1
GO:0034375: high-density lipoprotein particle remodeling	4.37E-12	5	15	*APOA1, *APOE, *CETP, *LCAT, *LIPC
GO:0045834: positive regulation of lipid metabolic process	2.88E-07	5	123	APOA1, APOE, HNF4A, IRS1, MLXIPL
GO:0043086: negative regulation of catalytic activity	6.06E-04	5	607	ANGPTL4, APOA1, APOE, LPA, TRIB1
GO:0006898: receptor-mediated endocytosis	1.27E-05	4	125	*APOB, *APOE, *CETP, *LPA
GO:0015748: organophosphate ester transport	9.92E-07	4	66	ABCA1, APOA1, APOE, CETP
GO:0009896: positive regulation of catabolic process	5.91E-05	4	185	APOE, IRS1, MLXIPL, TRIB1
GO:0001933: negative regulation of protein phosphorylation	2.60E-04	4	272	APOE, HNF4A, MLXIPL, TRIB1
GO:0055091: phospholipid homeostasis	1.82E-10	4	9	*ABCA1, *APOA1, *CETP, *HNF4A
GO:0046470: phosphatidylcholine metabolic process	9.33E-07	4	65	APOA1, *CETP, LCAT, LIPC
GO:0006641: triglyceride metabolic process	6.87E-06	4	107	APOB, *APOE, *CETP, LIPC
GO:0008654: phospholipid biosynthetic process	3.86E-04	4	302	APOA1, *FADS1, LCAT, PGS1
GO:0016042: lipid catabolic process	4.11E-04	4	307	APOB, APOE, *IRS1, LIPC
GO:0015914: phospholipid transport	1.42E-07	4	41	ABCA1, APOA1, APOE, *CETP
GO:0034381: plasma lipoprotein particle clearance	1.04E-07	4	38	APOA1, APOB, APOE, LIPC
GO:0034372: very-low-density lipoprotein particle remodeling	5.06E-11	4	7	*APOE, *CETP, *LCAT, *LIPC
GO:0034370: triglyceride-rich lipoprotein particle remodeling	3.03E-10	4	10	APOE, CETP, LCAT, LIPC
GO:0034374: low-density lipoprotein particle remodeling	1.03E-09	4	13	*APOB, *APOE, *CETP, *LIPC
GO:0065005: protein-lipid complex assembly	1.96E-09	4	15	ABCA1, APOA1, APOB, APOE
GO:0034377: plasma lipoprotein particle assembly	1.96E-09	4	15	ABCA1, APOA1, APOB, APOE
GO:0046890: regulation of lipid biosynthetic process	1.62E-05	4	133	APOB, APOE, HNF4A, MLXIPL
GO:0032374: regulation of cholesterol transport	5.09E-08	4	32	ABCA1, APOA1, APOE, CETP
GO:0032371: regulation of sterol transport	5.09E-08	4	32	ABCA1, APOA1, APOE, CETP
GO:0032368: regulation of lipid transport	1.57E-06	4	74	ABCA1, APOA1, APOE, CETP
GO:0009743: response to carbohydrate stimulus	1.77E-04	4	246	*APOB, FADS1, HNF4A, MLXIPL
GO:0042326: negative regulation of phosphorylation	3.19E-04	4	287	APOE, HNF4A, MLXIPL, TRIB1
GO:0042439: ethanolamine-containing compound metabolic process	4.10E-06	4	94	APOA1, CETP, LCAT, LIPC
GO:0031331: positive regulation of cellular catabolic process	1.58E-05	4	132	APOE, IRS1, MLXIPL, TRIB1
GO:0044106: cellular amine metabolic process	3.12E-05	4	157	APOA1, CETP, LCAT, LIPC
GO:0006576: cellular biogenic amine metabolic process	3.12E-05	4	157	APOA1, CETP, LCAT, LIPC

GO:0009308: amine metabolic process	7.84E-05	4	199	APOA1, CETP, LCAT, LIPC
GO:0045936: negative regulation of phosphate metabolic process	6.23E-04	4	343	APOE, HNF4A, MLXIPL, TRIB1
GO:0010563: negative regulation of phosphorus metabolic process	6.23E-04	4	343	APOE, HNF4A, MLXIPL, TRIB1
GO:0048844: artery morphogenesis	4.30E-05	3	59	*APOB, *APOE, CITED2
GO:0060840: artery development	7.49E-05	3	71	APOB, APOE, CITED2
GO:0033500: carbohydrate homeostasis	6.79E-04	3	150	HNF4A, IRS1, MLXIPL
GO:0042593: glucose homeostasis	6.79E-04	3	150	*HNF4A, *IRS1, *MLXIPL
GO:0030336: negative regulation of cell migration	8.95E-04	3	165	APOE, *CITED2, TRIB1
GO:2000146: negative regulation of cell motility	9.27E-04	3	167	APOE, CITED2, TRIB1
GO:0010743: regulation of macrophage derived foam cell differentiation	1.54E-05	3	42	ABCA1, APOB, CETP
GO:0033700: phospholipid efflux	3.02E-07	3	12	*ABCA1, *APOA1, *APOE
GO:0033344: cholesterol efflux	3.53E-06	3	26	*ABCA1, *APOA1, *APOE
GO:0034380: high-density lipoprotein particle assembly	2.76E-08	3	6	*ABCA1, *APOA1, *APOE
GO:0010907: positive regulation of glucose metabolic process	6.70E-06	3	32	HNF4A, *IRS1, MLXIPL
GO:0010676: positive regulation of cellular carbohydrate metabolic process	1.54E-05	3	42	HNF4A, IRS1, MLXIPL
GO:0045913: positive regulation of carbohydrate metabolic process	2.46E-05	3	49	HNF4A, IRS1, MLXIPL
GO:0010906: regulation of glucose metabolic process	2.33E-04	3	104	HNF4A, IRS1, MLXIPL
GO:0010675: regulation of cellular carbohydrate metabolic process	4.18E-04	3	127	HNF4A, IRS1, MLXIPL
GO:0006109: regulation of carbohydrate metabolic process	4.68E-04	3	132	HNF4A, IRS1, MLXIPL
GO:0019218: regulation of steroid metabolic process	2.01E-04	3	99	APOA1, APOB, APOE
GO:0045923: positive regulation of fatty acid metabolic process	9.62E-06	3	36	HNF4A, IRS1, MLXIPL
GO:0019217: regulation of fatty acid metabolic process	2.26E-04	3	103	HNF4A, IRS1, MLXIPL
GO:0010874: regulation of cholesterol efflux	9.30E-07	3	17	ABCA1, APOE, *CETP
GO:0032489: regulation of Cdc42 protein signal transduction	1.81E-06	3	21	*ABCA1, *APOA1, *APOE
GO:0030802: regulation of cyclic nucleotide biosynthetic process	2.53E-04	3	107	ABCA1, APOE, MC4R
GO:0030808: regulation of nucleotide biosynthetic process	2.60E-04	3	108	ABCA1, APOE, MC4R
GO:1900371: regulation of purine nucleotide biosynthetic process	2.60E-04	3	108	ABCA1, APOE, MC4R
GO:0030799: regulation of cyclic nucleotide metabolic process	3.29E-04	3	117	ABCA1, APOE, MC4R
GO:0030804: positive regulation of cyclic nucleotide biosynthetic process	8.14E-05	3	73	ABCA1, APOE, MC4R
GO:1900373: positive regulation of purine nucleotide biosynthetic process	8.48E-05	3	74	ABCA1, APOE, MC4R
GO:0030810: positive regulation of nucleotide biosynthetic process	8.48E-05	3	74	ABCA1, APOE, MC4R
GO:0030801: positive regulation of cyclic nucleotide metabolic process	8.82E-05	3	75	ABCA1, APOE, MC4R

GO:1900544: positive regulation of purine nucleotide metabolic process	9.55E-05	3	77	ABCA1, APOE, MC4R
GO:0045981: positive regulation of nucleotide metabolic process	9.55E-05	3	77	ABCA1, APOE, MC4R
GO:0030317: sperm motility	8.77E-04	2	38	*APOB, *PLTP
GO:0010470: regulation of gastrulation	6.21E-04	2	32	APOA1, *HNF4A
GO:0010745: negative regulation of macrophage derived foam cell differentiation	9.90E-05	2	13	*ABCA1, *CETP
GO:0042159: lipoprotein catabolic process	6.99E-05	2	11	*APOB, *APOE
GO:0019433: triglyceride catabolic process	3.19E-04	2	23	*APOB, *LIPC
GO:0046464: acylglycerol catabolic process	4.09E-04	2	26	APOB, LIPC
GO:0046461: neutral lipid catabolic process	4.09E-04	2	26	APOB, LIPC
GO:0046503: glycerolipid catabolic process	6.21E-04	2	32	APOB, LIPC
GO:0034384: high-density lipoprotein particle clearance	2.68E-05	2	7	*APOA1, *APOE
GO:0034382: chylomicron remnant clearance	4.58E-05	2	9	*APOE, *LIPC
GO:0071830: triglyceride-rich lipoprotein particle clearance	4.58E-05	2	9	APOE, LIPC
GO:0010873: positive regulation of cholesterol esterification	2.68E-05	2	7	*APOA1, *APOE
GO:0010872: regulation of cholesterol esterification	4.58E-05	2	9	APOA1, APOE
GO:0045540: regulation of cholesterol biosynthetic process	2.91E-04	2	22	*APOB, APOE
GO:0045940: positive regulation of steroid metabolic process	4.75E-04	2	28	APOA1, APOE
GO:0090181: regulation of cholesterol metabolic process	6.61E-04	2	33	APOB, APOE
GO:0045723: positive regulation of fatty acid biosynthetic process	1.33E-04	2	15	*HNF4A, *MLXIPL
GO:0010875: positive regulation of cholesterol efflux	6.99E-05	2	11	*ABCA1, *APOE
GO:0032373: positive regulation of sterol transport	9.90E-05	2	13	ABCA1, APOE
GO:0032376: positive regulation of cholesterol transport	9.90E-05	2	13	ABCA1, APOE
GO:0032370: positive regulation of lipid transport	8.31E-04	2	37	ABCA1, APOE
GO:0010885: regulation of cholesterol storage	3.78E-04	2	25	ABCA1, APOB
GO:0034405: response to fluid shear stress	6.21E-04	2	32	ABCA1, *CITED2
GO:0019934: cGMP-mediated signaling	1.28E-05	2	5	*APOE, *PDE3A
GO:0002021: response to dietary excess	1.72E-04	2	17	*APOE, MC4R
GO:0006656: phosphatidylcholine biosynthetic process	4.41E-04	2	27	*APOA1, *LCAT
GO:0019935: cyclic-nucleotide-mediated signaling	5.10E-04	2	29	APOE, PDE3A
GO:0042304: regulation of fatty acid biosynthetic process	7.87E-04	2	36	HNF4A, *MLXIPL

k is the number of genes in the query set annotated to that node, and M is the number of genes in the database annotated to that node.
*next to the gene symbol indicates that the gene is annotated to the node, and not any of the child terms.
Based on annotation dataset 12th November 2012 and GO ontology from 27th November 2012.

Table S7 Combined biological process VLAD summary results, triglyceride, total cholesterol, LDL cholesterol and HDL cholesterol trait associated genes

GO term grouping	**Gene Ontology term**	**M**	**TG k**	**TC k**	**LDLc k**	**HDLc k**
coagulation	blood coagulation	533	-	-	-	-
development	aging	380	-	-	5	-
development	circulatory system development	1053	-	-	-	-
development	regulation of cell differentiation	1576	-	9	-	-
development	homeostatic process	1700	12	21	17	12
metabolism	cellular carbohydrate metabolic process	246	-	-	-	-
metabolism	digestion	119	-	4	4	-
metabolism	lipid metabolic process	1762	15	23	19	16
metabolism	lipoprotein metabolic process	172	6	9	8	7
metabolism	plasma lipoprotein particle clearance	38	4	6	5	4
metabolism	regulation of glucose metabolic process	104	3	-	-	3
metabolism	regulation of lipid metabolic process	282	6	9	8	6
metabolism	small molecule metabolic process	3455	17	26	22	16
metabolism	regulation of enzyme activity					
signalling	cell communication	6835	-	-	-	-
signalling	response to chemical stimulus	3988	14	21	16	13
signalling	response to nutrient levels	473	-	7	6	-
signalling	response to stress					
transport	vesicle-mediated transport	1300	-	11	9	7
transport	plasma lipoprotein particle organization	33	6	7	4	7
transport	regulation of lipid transport	74	4	7	5	4
transport	regulation of plasma lipoprotein particle levels	60	6	9	6	7
transport	establishment and maintenance of position					

k is the number of genes in the query set annotated to that node, and M is the number of genes in the database annotated to that node. Based on annotation dataset 12th November 2012 and GO ontology from 27th November 2012.

Individual lipid trait SNP datasets associated with each of the listed GO terms. HDL-C: HDL cholesterol trait, LDL-C: LDL cholesterol trait, TC: total cholesterol, TG: triglyceride.