Table 2. Summary of GWAS Meta-analysis Stage 1 Results (includes all signals with p < 5 x 10^{-7})

	Locus		Association Signal				Corroborating Signals (p < 10^{-6})		Nearby Genes
SNP	Chr	Position (Mb)	Allele (+/-)	Freq (+)	Effect (mg/dl)	P-value	SNPs	LD Groups (r^2 < 0.2)	(Relative Position) (-upstream, +downstream)
HDL Cholesterol (N = 8,656)									
rs3764261	16	55.6	A/C	.29	2.42	**2.8x10^{-19}**	14	2	*CETP* (-2.4kb)
rs12678919	8	19.9	G/A	.12	2.44	**1.3x10^{-11}**	84	2	*LPL* (+19.5kb)
rs10468017	15	56.5	T/C	.32	1.76	**8.6x10^{-11}**	18	2	*LIPC* (-45.7kb)
rs1323432	9	101.4	A/G	.87	1.93	**2.5x10^{-8}**	4	1	*GRIN3A* (Intron 6); *PPP3R2* (-5.7kb)
rs4149274	9	104.7	G/A	.69	1.51	7.4x10^{-8}	20	1	*ABCA1* (Intron 5)
rs4939883	18	45.4	C/T	.86	1.87	1.4x10^{-7}	2	1	*LIPG* (+47.9kb)
rs4846914	1	226.6	A/G	.62	1.15	2.9x10^{-7}	4	1	*GALNT2* (Intron 1)
LDL Cholesterol (N = 8,589)									
rs4420638	19	50.1	G/A	.16	8.02	**3.2x10^{-21}**	2	1	*APOE/APOC* cluster
rs515135	2	21.2	C/T	.83	6.08	**3.1x10^{-14}**	116	3	*APOB* (-19.1kb)
rs602633	1	109.5	G/T	.80	6.09	**4.8x10^{-14}**	8	1	*CELSR2* (+3.1kb); *PSRC1* (+668bp); *SORT1* (-30kb)
rs6511720	19	11.1	G/T	.91	8.03	**6.8x10^{-10}**	1	1	*LDLR* (Intron 1)
rs2228603	19	19.2	C/T	.93	6.46	1.8x10^{-7}	3	1	*NCAN* (Pro92Ser)
Triglycerides (N = 8,684)									
rs964184	11	116.2	G/C	.12	18.12	**1.5x10^{-16}**	29	2	*APOA5* (+11.2kb)
rs1260326	2	27.6	T/C	.40	10.25	**1.5x10^{-15}**	52	2	*GCKR* (Leu446Pro)
rs6993414	8	19.9	A/G	.88	14.20	**1.4x10^{-13}**	85	2	*LPL* (+78.1kb)
rs2954029	8	126.6	A/T	.56	6.42	**2.8x10^{-8}**	15	1	*TRIB1* (+40.3kb)
rs10401969	19	19.3	T/C	.92	12.28	2.3x10^{-7}	5	1	*NCAN* (+44.7 kb); *SF4* (Intron 8)

The table summarizes association signals observed in the analysis of lipid levels in three GWAS scans. Chromosome assignments, position, and gene annotations all refer to the March 2006 Genome Build (UCSC). Alleles are ordered such that the first allele (+) is associated with increased lipid levels. Effect sizes are measured as additive effects, which correspond to the average change in phenotype when one (-) allele is replaced with one (+) allele. Summaries of LD information around the strongest hit in each locus (number of LD groups, r^2 < 0.20, among nearby SNPs with p < 10^{-6}) are based on the HapMap CEU sample. Corroborating signals refers to the number of additional SNPs within 1 Mb with p < 10^{-6}. P-values in **bold** exceed a threshold of 5 x 10^{-8}, which corresponds to false positive rate of 0.05 after adjustment for 1 million independent tests, comparable to the number of independent common SNPs in the Phase II CEU HapMap. For each locus, the most strongly associated SNP is indicated together with its position relative to nearby genes, with a focus on genes previously implicated in lipid metabolism. In the nearby gene column, positions are relative to the transcription start for the nearest gene.

Table 3. Summary of Most Significant Stage 1+2 Results.

						Association p-values			Sample sizes		
SNP	Chr	Pos (Mb)	Alleles (+/-)	Freq (+)	Effect (mg/dl)	Stage 1 (two-sided)	Stage 2 (one-sided)	Combined (two-sided)	Stage 1	Stage 2	Nearby Genes
						SNPs Associated with HDL Cholesterol					
rs3764261	16	55.6	A/C	.31	3.47	2.8×10^{-19}	6.4×10^{-43}	2.3×10^{-57}	8,656	8,072	*CETP*
rs1864163	16	55.6	G/A	.80	4.12	3.0×10^{-17}	4.3×10^{-28}	6.9×10^{-39}	8,656	3,684	*CETP*
rs9989419	16	55.5	G/A	.65	1.72	8.0×10^{-16}	1.8×10^{-17}	3.2×10^{-31}	8,656	6,981	*CETP*
rs12596776	16	55.5	G/C	.13	1.26	3.7×10^{-5}	1.0×10^{-4}	2.8×10^{-8}	8,656	7,030	*CETP*
rs1566439	16	55.6	C/T	.45	0.96	2.0×10^{-5}	2.1×10^{-4}	3.3×10^{-8}	8,656	4,881	*CETP*
rs4775041	15	56.5	C/G	.33	1.38	2.8×10^{-9}	9.6×10^{-13}	3.2×10^{-20}	8,656	11,426	*LIPC*
rs261332	15	56.5	A/G	.19	1.41	1.7×10^{-9}	1.3×10^{-7}	2.3×10^{-15}	8,656	6,956	*LIPC*
rs10503669	8	19.9	A/C	.10	2.09	3.2×10^{-10}	9.4×10^{-11}	4.1×10^{-19}	8,656	11,431	*LPL*
rs2197089	8	19.9	A/G	.58	1.38	3.4×10^{-8}	3.2×10^{-5}	1.0×10^{-11}	8,656	3,644	*LPL*
rs6586891	8	20	A/C	.66	1.00	3.5×10^{-5}	9.7×10^{-6}	2.9×10^{-9}	8,656	7,017	*LPL*
rs2144300	1	226.6	T/C	.60	1.11	6.6×10^{-7}	4.0×10^{-9}	2.6×10^{-14}	8,656	11,406	*GALNT2*
rs2156552	18	45.4	T/A	.84	1.20	8.4×10^{-7}	7.1×10^{-7}	6.4×10^{-12}	8,656	11,437	*LIPG*
rs4149268	9	104.7	C/T	.64	0.82	3.3×10^{-7}	2.2×10^{-5}	1.2×10^{-10}	8,656	11,327	*ABCA1*
rs2338104	12	108.4	G/C	.45	0.48	1.9×10^{-6}	7.6×10^{-4}	3.4×10^{-8}	8,656	11,399	*MVK/MMAB*
rs255052	16	66.6	A/G	.17	0.74	1.5×10^{-6}	.0087	1.2×10^{-7}	8,656	4,534	*LCAT*
rs1323432	9	101.4	A/G	.88	-0.03	2.5×10^{-8}	.82	7.7×10^{-4}	8,656	8,176	*GRIN3A*
						SNPs Associated with LDL Cholesterol					
rs4420638	19	50.1	G/A	.18	6.61	3.2×10^{-21}	4.9×10^{-24}	3.0×10^{-43}	8,589	10,806	*APOE/C1/C4*
rs10402271	19	50	G/T	.33	2.62	9.8×10^{-6}	1.5×10^{-5}	1.2×10^{-9}	8,589	6,519	*APOE/C1/C4*
rs599839	1	109.5	A/G	.77	5.48	1.2×10^{-13}	2.7×10^{-21}	6.1×10^{-33}	8,589	10,783	*CELSR2/PSRC1/SORT1*
rs6511720	19	11.1	G/T	.90	9.17	6.8×10^{-10}	3.3×10^{-19}	4.2×10^{-26}	8,589	7,442	*LDLR*
rs562338	2	21.2	G/A	.82	4.89	1.2×10^{-11}	3.6×10^{-12}	5.6×10^{-22}	8,589	10,849	*APOB*
rs754523	2	21.2	G/A	.28	2.78	7.0×10^{-7}	1.3×10^{-6}	8.3×10^{-12}	8,589	6,542	*APOB*
rs693	2	21.1	A/G	.42	2.44	1.2×10^{-7}	.0034	3.1×10^{-9}	8,589	3,222	*APOB*
rs11206510	1	55.2	T/C	.81	3.04	7.5×10^{-6}	5.4×10^{-7}	3.5×10^{-11}	8,589	10,805	*PCSK9*
rs16996148	19	19.5	G/T	.89	3.32	2.4×10^{-6}	8.3×10^{-5}	2.7×10^{-9}	8,589	10,841	*NCAN/CILP2*
rs2254287	6	33.3	G/C	.38	1.91	2.9×10^{-6}	.0015	5.1×10^{-8}	8,589	7,440	*B3GALT4*
rs12695382	3	120.4	A/G	.90	2.23	4.9×10^{-6}	.0067	1.0×10^{-6}	8,589	10,802	*B4GALT4*

| | | Pos | Alleles | Freq | Effect | Association p-values Stage 1 | Stage 2 | Combined | Sample sizes Stage 1 | Stage 2 | |
SNP	Chr	(Mb)	(+/-)	(+)	(mg/dl)	(two-sided)	(one-sided)	(two-sided)	Stage 1	Stage 2	Nearby Genes
						SNPs Associated with Triglycerides					
rs780094	**2**	**27.7**	**T/C**	**.39**	**8.59**	1.7×10^{-14}	2.0×10^{-19}	6.1×10^{-32}	**8,684**	**9,723**	*GCKR*
rs11127129	2	28.0	C/G	.79	3.77	2.0×10^{-4}	3.2×10^{-4}	4.7×10^{-7}	8,684	9,700	*RBKS/GCKR*
rs12286037	**11**	**116.2**	**T/C**	**.06**	**25.82**	1.1×10^{-7}	1.6×10^{-22}	1.0×10^{-26}	**8,684**	**9,738**	*APOA5/A4/C3/A1*
rs662799	**11**	**116.2**	**G/A**	**.05**	**16.88**	4.3×10^{-8}	2.7×10^{-10}	2.4×10^{-15}	**8,684**	**3,248**	*APOA5/A4/C3/A1*
rs2000571	11	116.1	A/G	.17	6.93	4.7×10^{-5}	8.7×10^{-5}	5.7×10^{-8}	8,684	3,209	*APOA5/A4/C3/A1*
rs486394	11	116.0	C/A	.28	1.50	1.7×10^{-4}	.0073	7.4×10^{-6}	8,684	3,597	*APOA5/A4/C3/A1*
rs10503669	**8**	**19.9**	**C/A**	**.90**	**11.57**	1.4×10^{-9}	1.6×10^{-14}	3.9×10^{-22}	**8,684**	**9,711**	*LPL*
rs2197089	**8**	**19.9**	**G/A**	**.42**	**3.38**	3.1×10^{-11}	.0029	1.1×10^{-12}	**8,684**	**3,202**	*LPL*
rs6586891	8	20.0	C/A	.34	4.60	2.4×10^{-4}	5.0×10^{-4}	1.1×10^{-6}	8,684	3,622	*LPL*
rs17321515	**8**	**126.6**	**A/G**	**.56**	**6.42**	6.8×10^{-8}	1.0×10^{-6}	7.0×10^{-13}	**8,684**	**5,312**	*TRIB1*
rs17145738	**7**	**72.4**	**C/T**	**.84**	**8.21**	4.1×10^{-6}	5.0×10^{-8}	2.0×10^{-12}	**8,684**	**9,741**	*MLXIPL*
rs1748195	**1**	**62.8**	**C/G**	**.70**	**7.12**	2.3×10^{-4}	5.4×10^{-8}	1.7×10^{-10}	**8,684**	**9,559**	*ANGPTL3*
rs16996148	**19**	**19.5**	**G/T**	**.92**	**6.10**	6.3×10^{-7}	2.4×10^{-4}	2.5×10^{-9}	**8,684**	**9,707**	*NCAN/CILP2*
rs4775041	**15**	**56.5**	**C/G**	**.33**	**3.62**	7.3×10^{-5}	2.9×10^{-5}	1.6×10^{-8}	**8,684**	**8,462**	*LIPC*
rs2144300	1	226.6	C/T	.40	4.25	4.9×10^{-4}	2.4×10^{-4}	7.9×10^{-7}	8,684	8,473	*GALNT2*

The table summarizes association signals after follow-up of the promising SNPs in Stage 2 samples. Column headings are as described for Table 2, with the addition of one-sided p-values for the Stage 2 samples, in which we tested for the same direction of effect as Stage 1 – consistent with current best practice for replication of GWAS findings. The effect sizes shown were estimated from Stage 2 samples only. SNPs with a Combined (Stage 1 + 2) p-value < 10^{-5} were included, although we also show GRIN3A for completeness because it was significant in the initial scan. SNPs in this table may not match those in Table 2, which only displays the strongest signal in each locus. The discrepancy also reflects our bias towards genotyped Affymetrix 500K SNPs in the Stage 2 follow-up. Association p-values for each of the six Stage 2 samples are shown in Supplemental Table 4.