

Table S1.

	GOLD Meta-analysis (n= 7176)				NASH CRN /MIGen/iCONT analyses		
	AGES	AMISH	Family Heart Study	Framingham Heart Study	NASH CRN	MIGen	iCONT
Demographics							
N (% male)	2,868 (39.7)	541 (46.7)	886 (50.6)	2,932 (49.2)	592 (36.5)	1,405 (60.1)	3212(41.5)
Mean age (SD), years	76.4 (5.5)	56.9 (12.9)	61.8 (11.6)	51.0 (10.4)	49.4 (10.7)	47.4 (0.22)	N/A
Median drinks per week (P25, P75)	3(0, 16)	*	0 (0, 2.0)	3 (0, 8)	0 (0, 0.25)	N/A	N/A
Never drinkers (%)	639 (22.2)	*	497 (56.1)	759(25.9)	313(53)	N/A	N/A
European Ancestry (%)	2,868 (100)	541 (100)	886 (100)	2,932 (100)	592 (100)	1,405 (100)	3212(100)
Mean body mass index (SD), kg/m ²	27.0 (4.5)	27.7 (4.9)	29.2 (5.6)	27.5 (5.2)	34.8 (6.5)	27.1 (0.14)	N/A
CT liver phenotype characteristics							
Reference	Phantom LD	Spleen	Phantom LD	Phantom HD	N/A	N/A	N/A
Median raw liver measure (P25, P75)	60(57,64)	64(60,68)	61(55,66)	68(63,71)	N/A	N/A	N/A
Histologic Characteristics							
Steatosis >5% (%)	N/A	N/A	N/A	N/A	81.7	N/A	N/A
NASH (%)	N/A	N/A	N/A	N/A	79.2	N/A	N/A
Fibrosis (%)	N/A	N/A	N/A	N/A	78.6	N/A	N/A
Lobular inflammation (%)	N/A	N/A	N/A	N/A	99.5	N/A	N/A
Ballooning (%)	N/A	N/A	N/A	N/A	68.2	N/A	N/A

Table S2.

Samples	Genotyping						Imputation				Association analyses
	Platform	Calling algorithm	SNP MAF before imp'n	SNP call rate before imp'n	SNP HWE before imp'n	# SNPs for imp'n	Software	MAF	Imp'n quality*	SNPs in meta-analysis	Software
GOLD cohorts											
AGES	Illumina	GenCall	>0.01	>0.95	1 x 10 ⁻⁶	329,804	MACH (1.0.16)	>0.01	>0.30	2,408,992	ProbABEL/R
Amish	Affymetrix	Birdseed	>0.01	>0.95	1 x 10 ⁻⁶	338,598	MACH (1.0.15)	>0.01	>0.30	2,404,474	MMAP
Family Heart Study	Illumina	GenCall	>0.01	>0.98	1 x 10 ⁻⁶	456,293	MACH (1.0.15)	>0.01	>0.30	2,543,887	SAS
Framingham Heart Study	Affymetrix 500K & Affymetrix 50K	BRLMM	>0.01	>0.99	1 x 10 ⁻⁶	413,905	MACH (1.0.16)	>0.01	>0.30	2,420,081	R
Follow-up samples											
NASH-CRN	iPLEX™ Sequenom MassARRAY®	-	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	PLINK
MIGen	Affymetrix	Birdseed	>0.01	>0.95	1 x 10 ⁻⁶	618,475	MACH (1.0.15)	>0.01	>0.30	N/A	PLINK
iCONT	Illumina	GenCall	>0.01	>0.95	1 x 10 ⁻⁴	472,431	MACH (1.0.16)	>0.01	>0.30	N/A	PLINK

Table S3.

Cohort	Total sample	Call rate(*)	Other exclusions	Samples in analyses
GOLD Meta-analysis cohorts				
AGES	4,773	>99%	No genotype or imputed data for a number of samples (n=1,905)	2,868
Amish	880	>99%	No genotype or imputed data for a number of samples (n=339)	541
Family Heart Study	982	>98%	Gender incorrect (n=5) African American (n=3) Framingham Heart Study participants (n=86) Subjects on amiodarone (n= 2)	886
Framingham Heart Study	3,177	>99%	Principal component outliers (n=1) Lack full covariate data (n=66) Individual genotype missingness >3% (n=43) Contaminated/poor DNA (n=7) No genotypes (n=128)	2,932
Follow up samples				
NASH-CRN	879	>99%	Non European ancestry (n= 201) No histology (n=86)	592
MIGen	1,406	>99%	Not well matched to NASH CRN (n= 1)	1,405
iCONT	3,294	>99%	Individual genotype missingness >5% or IBD pi hat >0.15 (n=82)	3,212

Table S4.

Locus						GOLD						
Nearby Gene	SNP	Chr.	Pos.	EA	OA	EAf	Effect	SE	P	% Var	P het	N
<i>PNPLA3</i>	rs738409	22	42656060	G	C	0.231	0.261	0.021	4.30E-34	2.41	1.57E-01	7,176
<i>PPP1R3B</i>	rs4240624	8	9221641	A	G	0.923	0.288	0.033	3.68E-18	1.18	2.22E-01	7,176
<i>NCAN</i>	rs2228603	19	19190924	T	C	0.075	0.238	0.035	1.22E-11	0.79	4.63E-01	7,176
<i>TP73L</i>	rs9817981	3	191046224	A	G	0.574	0.089	0.018	6.21E-07	0.39	2.59E-01	7,176
<i>BMS1L</i>	rs1592158	10	42593362	A	G	0.181	0.109	0.023	1.70E-06	0.35	5.70E-01	7,176
<i>MSRA</i>	rs17151287	8	10089602	C	G	0.023	0.259	0.057	6.21E-06	0.3	1.49E-03	7,176
<i>ARL15</i>	rs11748223	5	53531996	C	T	0.907	0.127	0.030	1.79E-05	0.27	4.41E-01	7,176
<i>RBMS3</i>	rs9878305	3	29310430	A	G	0.889	0.119	0.028	1.84E-05	0.28	4.34E-01	7,176
<i>LOC442213</i>	rs12204829	6	48220567	G	A	0.087	0.137	0.033	2.69E-05	0.3	6.55E-01	7,176
<i>RPRM</i>	rs13402721	2	153770202	T	A	0.094	0.133	0.032	2.81E-05	0.3	1.47E-01	7,176
<i>MT1P2</i>	rs1252138	1	235207583	G	T	0.160	0.112	0.027	2.86E-05	0.34	4.66E-01	7,176
<i>SOCS6</i>	rs1282645	18	66589560	G	A	0.109	0.131	0.032	3.48E-05	0.33	7.12E-01	7,176
<i>KCNJ4</i>	rs9610956	22	37169820	A	G	0.069	0.163	0.039	3.54E-05	0.34	8.76E-01	6,635
<i>STC2</i>	rs13178402	5	172792898	A	G	0.881	0.113	0.028	3.97E-05	0.27	7.90E-01	7,176
<i>HEMK2</i>	rs7276221	21	28422813	G	A	0.562	0.071	0.017	4.52E-05	0.25	7.71E-01	7,176
<i>C18orf55</i>	rs1790856	18	69998062	A	G	0.401	0.077	0.019	4.64E-05	0.28	2.61E-01	7,176
<i>SHROOM3</i>	rs9996493	4	77660038	G	A	0.230	0.108	0.027	5.70E-05	0.41	7.23E-01	7,176
<i>LRPPRC</i>	rs6759184	2	44085473	A	G	0.296	0.075	0.019	6.44E-05	0.24	1.59E-01	7,176
<i>CYLC2</i>	rs1375213	9	104852166	C	A	0.564	0.069	0.017	7.13E-05	0.23	7.37E-01	7,176
<i>FGD2</i>	rs708010	6	37071350	A	C	0.252	0.082	0.021	7.35E-05	0.26	9.78E-01	7,176
<i>SAMD12</i>	rs1013456	8	119821110	G	A	0.655	0.073	0.018	7.65E-05	0.24	9.83E-02	7,176
<i>CCDC28A</i>	rs6927344	6	139144059	T	C	0.973	0.208	0.053	8.72E-05	0.22	2.51E-01	7,176
<i>ACTL7B</i>	rs593932	9	110223976	A	G	0.547	0.068	0.018	1.03E-04	0.23	3.43E-01	7,176
<i>IMPG1</i>	rs2125215	6	77526970	T	C	0.136	0.097	0.025	1.03E-04	0.22	4.60E-01	7,176
<i>LYPLAL1</i>	rs12137855	1	217515001	C	T	0.785	0.083	0.021	1.06E-04	0.23	9.74E-01	7,176
<i>TMEM16C</i>	rs10501021	11	25712104	A	G	0.851	0.103	0.027	1.16E-04	0.27	6.18E-01	7,176
<i>CDH4</i>	rs6513576	20	59352421	C	T	0.775	0.080	0.021	1.18E-04	0.23	9.69E-01	7,176
<i>SRD5A2L2</i>	rs1483293	4	64918291	A	G	0.047	0.159	0.042	1.48E-04	0.22	6.37E-01	7,176
<i>CCDC66</i>	rs3732513	3	56649343	C	T	0.167	0.090	0.024	1.70E-04	0.22	6.48E-02	7,176
<i>ASPH</i>	rs7836571	8	63006280	T	A	0.834	0.090	0.024	1.77E-04	0.22	4.53E-01	7,176
<i>ADH7</i>	rs971074	4	100560884	C	T	0.891	0.115	0.031	1.97E-04	0.26	9.95E-01	7,176
<i>PLD5</i>	rs6673239	1	240694244	T	A	0.373	0.066	0.018	2.00E-04	0.2	3.63E-02	7,176
<i>TLE3</i>	rs2668606	15	68386797	A	G	0.029	0.230	0.062	2.12E-04	0.29	7.04E-03	6,635
<i>PELI2</i>	rs9323291	14	55464800	G	A	0.907	0.119	0.032	2.43E-04	0.24	1.05E-01	7,176
<i>GCKR</i>	rs780094	2	27594741	T	C	0.393	0.065	0.018	2.56E-04	0.2	8.65E-01	7,176
<i>KIAA1345</i>	rs2160043	4	15108349	C	T	0.480	0.065	0.018	2.62E-04	0.21	8.95E-01	7,176
<i>ATXN7L4</i>	rs6953952	7	105246348	C	T	0.066	0.132	0.036	2.65E-04	0.21	1.86E-01	7,176
<i>ZHX2</i>	rs11783697	8	123886375	C	A	0.325	0.077	0.021	2.87E-04	0.26	8.61E-01	7,176
<i>PTPRG</i>	rs9860802	3	61986250	T	G	0.223	0.077	0.021	3.22E-04	0.2	6.35E-01	7,176
<i>RPS6KA1</i>	rs190737	1	26772031	C	A	0.475	0.062	0.018	4.40E-04	0.19	3.96E-02	7,176
<i>CACHD1</i>	rs11208510	1	64940125	A	T	0.196	0.099	0.028	4.85E-04	0.31	2.16E-01	6,635
<i>HS3ST3B1</i>	rs9896612	17	14259726	G	T	0.359	0.070	0.020	5.41E-04	0.22	8.72E-01	7,176
<i>RYR3</i>	rs7179722	15	31920794	T	A	0.517	0.065	0.019	7.25E-04	0.21	4.25E-01	7,176
<i>SLC6A15</i>	rs11116503	12	83541313	A	G	0.585	0.064	0.019	8.70E-04	0.2	9.14E-01	7,176
<i>SOCS7</i>	rs4794776	17	33734136	T	C	0.918	0.112	0.035	1.25E-03	0.19	9.65E-01	7,176

Table S4. (cont'd)

Locus						AGES					
Nearby Gene	SNP	Chr.	Pos.	EA	OA	EAF	Effect	SE	P	Imp	N
<i>PNPLA3</i>	rs738409	22	42656060	G	C	0.227	0.232	0.032	2.35E-13	0.984	2,868
<i>PPP1R3B</i>	rs4240624	8	9221641	A	G	0.926	0.265	0.049	6.31E-08	0.998	2,868
<i>NCAN</i>	rs2228603	19	19190924	T	C	0.068	0.184	0.053	4.99E-04	0.998	2,868
<i>TP73L</i>	rs9817981	3	191046224	A	G	0.576	0.064	0.026	1.47E-02	0.998	2,868
<i>BMS1L</i>	rs1592158	10	42593362	A	G	0.194	0.091	0.033	5.94E-03	0.999	2,868
<i>MSRA</i>	rs17151287	8	10089602	C	G	0.021	0.222	0.103	3.15E-02	0.793	2,868
<i>ARL15</i>	rs11748223	5	53531996	C	T	0.918	0.153	0.048	1.45E-03	0.998	2,868
<i>RBMS3</i>	rs9878305	3	29310430	A	G	0.898	0.115	0.043	7.78E-03	0.996	2,868
<i>LOC442213</i>	rs12204829	6	48220567	G	A	0.070	0.172	0.053	1.23E-03	0.938	2,868
<i>RPRM</i>	rs13402721	2	153770202	T	A	0.085	0.140	0.050	4.67E-03	0.940	2,868
<i>MT1P2</i>	rs1252138	1	235207583	G	T	0.146	0.133	0.044	2.48E-03	0.728	2,868
<i>SOCS6</i>	rs1282645	18	66589560	G	A	0.101	0.155	0.044	3.88E-04	0.998	2,868
<i>KCNJ4</i>	rs9610956	22	37169820	A	G	0.068	0.181	0.053	6.23E-04	0.997	2,868
<i>STC2</i>	rs13178402	5	172792898	A	G	0.875	0.082	0.041	4.59E-02	0.922	2,868
<i>HEMK2</i>	rs7276221	21	28422813	G	A	0.560	0.068	0.026	9.61E-03	0.984	2,868
<i>C18orf55</i>	rs1790856	18	69998062	A	G	0.371	0.077	0.028	4.94E-03	0.995	2,868
<i>SHROOM3</i>	rs9996493	4	77660038	G	A	0.222	0.119	0.041	3.94E-03	0.582	2,868
<i>LRPPRC</i>	rs6759184	2	44085473	A	G	0.290	0.100	0.029	5.66E-04	0.979	2,868
<i>CYLC2</i>	rs1375213	9	104852166	C	A	0.545	0.065	0.027	1.44E-02	0.973	2,868
<i>FGD2</i>	rs708010	6	37071350	A	C	0.250	0.083	0.032	9.37E-03	0.905	2,868
<i>SAMD12</i>	rs1013456	8	119821110	G	A	0.645	0.096	0.028	6.55E-04	0.988	2,868
<i>CCDC28A</i>	rs6927344	6	139144059	T	C	0.976	0.189	0.089	3.33E-02	0.906	2,868
<i>ACTL7B</i>	rs593932	9	110223976	A	G	0.579	0.054	0.027	4.54E-02	0.975	2,868
<i>IMPG1</i>	rs2125215	6	77526970	T	C	0.125	0.094	0.039	1.59E-02	1.000	2,868
<i>LYPLAL1</i>	rs12137855	1	217515001	C	T	0.777	0.083	0.032	1.01E-02	0.964	2,868
<i>TMEM16C</i>	rs10501021	11	25712104	A	G	0.845	0.137	0.037	2.26E-04	0.999	2,868
<i>CDH4</i>	rs6513576	20	59352421	C	T	0.753	0.078	0.030	1.09E-02	0.997	2,868
<i>SRD5A2L2</i>	rs1483293	4	64918291	A	G	0.046	0.159	0.064	1.26E-02	1.000	2,868
<i>CCDC66</i>	rs3732513	3	56649343	C	T	0.164	0.098	0.037	8.10E-03	0.918	2,868
<i>ASPH</i>	rs7836571	8	63006280	T	A	0.841	0.078	0.037	3.29E-02	0.980	2,868
<i>ADH7</i>	rs971074	4	100560884	C	T	0.913	0.112	0.048	1.94E-02	0.999	2,868
<i>PLD5</i>	rs6673239	1	240694244	T	A	0.389	0.097	0.027	3.06E-04	0.998	2,868
<i>TLE3</i>	rs2668606	15	68386797	A	G	0.025	0.455	0.102	8.44E-06	0.670	2,868
<i>PELI2</i>	rs9323291	14	55464800	G	A	0.910	0.187	0.048	8.83E-05	0.926	2,868
<i>GCKR</i>	rs780094	2	27594741	T	C	0.351	0.056	0.027	4.01E-02	0.999	2,868
<i>KIAA1345</i>	rs2160043	4	15108349	C	T	0.477	0.067	0.027	1.18E-02	1.000	2,868
<i>ATXN7L4</i>	rs6953952	7	105246348	C	T	0.070	0.168	0.052	1.33E-03	1.000	2,868
<i>ZHX2</i>	rs11783697	8	123886375	C	A	0.345	0.071	0.028	1.07E-02	0.996	2,868
<i>PTPRG</i>	rs9860802	3	61986250	T	G	0.205	0.073	0.033	2.79E-02	0.990	2,868
<i>RPS6KA1</i>	rs190737	1	26772031	C	A	0.508	0.028	0.026	2.78E-01	0.999	2,868
<i>CACHD1</i>	rs11208510	1	64940125	A	T	0.197	0.114	0.041	5.35E-03	0.640	2,868
<i>HS3ST3B1</i>	rs9896612	17	14259726	G	T	0.341	0.071	0.031	1.96E-02	0.834	2,868
<i>RYR3</i>	rs7179722	15	31920794	T	A	0.529	0.074	0.027	6.42E-03	0.954	2,868
<i>SLC6A15</i>	rs11116503	12	83541313	A	G	0.544	0.065	0.027	1.66E-02	0.945	2,868
<i>SOCS7</i>	rs4794776	17	33734136	T	C	0.916	0.122	0.051	1.64E-02	0.894	2,868

Table S4. (cont'd)

Locus						AMISH					
Nearby Gene	SNP	Chr.	Pos.	EA	OA	EAF	Effect	SE	P	Imp	N
<i>PNPLA3</i>	rs738409	22	42656060	G	C	0.245	0.129	0.092	1.59E-01	0.627	541
<i>PPP1R3B</i>	rs4240624	8	9221641	A	G	0.967	0.400	0.263	1.28E-01	0.396	541
<i>NCAN</i>	rs2228603	19	19190924	T	C	0.116	0.181	0.122	1.37E-01	0.706	541
<i>TP73L</i>	rs9817981	3	191046224	A	G	0.498	0.140	0.091	1.24E-01	0.510	541
<i>BMS1L</i>	rs1592158	10	42593362	A	G	0.170	0.227	0.097	1.96E-02	0.810	541
<i>MSRA</i>	rs17151287	8	10089602	C	G	0.016	0.284	0.298	3.40E-01	0.692	541
<i>ARL15</i>	rs11748223	5	53531996	C	T	0.946	0.331	0.155	3.27E-02	0.793	541
<i>RBMS3</i>	rs9878305	3	29310430	A	G	0.857	0.259	0.119	2.97E-02	0.565	541
<i>LOC442213</i>	rs12204829	6	48220567	G	A	0.048	-0.063	0.206	7.61E-01	0.483	541
<i>RPRM</i>	rs13402721	2	153770202	T	A	0.158	0.223	0.098	2.36E-02	0.848	541
<i>MT1P2</i>	rs1252138	1	235207583	G	T	0.213	0.147	0.095	1.20E-01	0.693	541
<i>SOCS6</i>	rs1282645	18	66589560	G	A	0.230	0.055	0.078	4.84E-01	0.910	541
<i>KCNJ4</i>	rs9610956	22	37169820	A	G	1.000					
<i>STC2</i>	rs13178402	5	172792898	A	G	0.852	0.137	0.094	1.45E-01	0.998	541
<i>HEMK2</i>	rs7276221	21	28422813	G	A	0.606	0.119	0.069	8.54E-02	0.900	541
<i>C18orf55</i>	rs1790856	18	69998062	A	G	0.536	-0.076	0.084	3.69E-01	0.605	541
<i>SHROOM3</i>	rs9996493	4	77660038	G	A	0.249	0.055	0.092	5.48E-01	0.599	541
<i>LRPPRC</i>	rs6759184	2	44085473	A	G	0.269	0.168	0.072	1.99E-02	1.000	541
<i>CYLC2</i>	rs1375213	9	104852166	C	A	0.516	0.006	0.065	9.31E-01	0.991	541
<i>FGD2</i>	rs708010	6	37071350	A	C	0.144	0.097	0.093	2.97E-01	0.982	541
<i>SAMD12</i>	rs1013456	8	119821110	G	A	0.626	-0.090	0.070	2.01E-01	0.895	541
<i>CCDC28A</i>	rs6927344	6	139144059	T	C	0.961	0.126	0.232	5.88E-01	0.867	541
<i>ACTL7B</i>	rs593932	9	110223976	A	G	0.405	0.031	0.065	6.35E-01	0.993	541
<i>IMPG1</i>	rs2125215	6	77526970	T	C	0.070	0.114	0.124	3.62E-01	1.000	541
<i>LYPLAL1</i>	rs12137855	1	217515001	C	T	0.860	0.126	0.097	1.95E-01	0.863	541
<i>TMEM16C</i>	rs10501021	11	25712104	A	G	0.912	0.057	0.129	6.60E-01	0.719	541
<i>CDH4</i>	rs6513576	20	59352421	C	T	0.713	0.064	0.075	3.92E-01	0.879	541
<i>SRD5A2L2</i>	rs1483293	4	64918291	A	G	0.020	0.468	0.248	5.85E-02	0.964	541
<i>CCDC66</i>	rs3732513	3	56649343	C	T	0.177	0.021	0.092	8.22E-01	0.825	541
<i>ASPH</i>	rs7836571	8	63006280	T	A	0.752	0.215	0.083	9.09E-03	0.862	541
<i>ADH7</i>	rs971074	4	100560884	C	T	0.816	0.122	0.077	1.15E-01	0.988	541
<i>PLD5</i>	rs6673239	1	240694244	T	A	0.271	-0.085	0.076	2.61E-01	0.998	541
<i>TLE3</i>	rs2668606	15	68386797	A	G	1.000					
<i>PELI2</i>	rs9323291	14	55464800	G	A	0.893	-0.118	0.125	3.43E-01	0.755	541
<i>GCKR</i>	rs780094	2	27594741	T	C	0.312	0.115	0.069	9.24E-02	0.999	541
<i>KIAA1345</i>	rs2160043	4	15108349	C	T	0.635	0.113	0.075	1.33E-01	0.784	541
<i>ATXN7L4</i>	rs6953952	7	105246348	C	T	0.052	0.035	0.169	8.35E-01	0.764	541
<i>ZHX2</i>	rs11783697	8	123886375	C	A	0.335	0.112	0.100	2.60E-01	0.475	541
<i>PTPRG</i>	rs9860802	3	61986250	T	G	0.340	0.131	0.072	6.75E-02	0.866	541
<i>RPS6KA1</i>	rs190737	1	26772031	C	A	0.431	-0.012	0.072	8.73E-01	0.767	541
<i>CACHD1</i>	rs11208510	1	64940125	A	T	1.000					
<i>HS3ST3B1</i>	rs9896612	17	14259726	G	T	0.414	0.112	0.082	1.70E-01	0.671	541
<i>RYR3</i>	rs7179722	15	31920794	T	A	0.544	0.164	0.088	6.13E-02	0.513	541
<i>SLC6A15</i>	rs11116503	12	83541313	A	G	0.489	0.102	0.076	1.77E-01	0.717	541
<i>SOCS7</i>	rs4794776	17	33734136	T	C	0.971	0.031	0.218	8.88E-01	0.735	541

Table S4. (cont'd)

Locus						Family Heart Study					
Nearby Gene	SNP	Chr.	Pos.	EA	OA	EAF	Effect	SE	P	Imp	N
<i>PNPLA3</i>	rs738409	22	42656060	G	C	0.232	0.349	0.069	4.45E-07	0.811	835
<i>PPP1R3B</i>	rs4240624	8	9221641	A	G	0.904	0.143	0.093	1.25E-01	0.987	835
<i>NCAN</i>	rs2228603	19	19190924	T	C	0.078	0.301	0.091	9.35E-04	1.000	835
<i>TP73L</i>	rs9817981	3	191046224	A	G	0.592	0.174	0.051	6.30E-04	0.997	835
<i>BMS1L</i>	rs1592158	10	42593362	A	G	0.170	0.141	0.067	3.50E-02	0.999	835
<i>MSRA</i>	rs17151287	8	10089602	C	G	0.018	0.660	0.123	8.08E-08	0.916	835
<i>ARL15</i>	rs11748223	5	53531996	C	T	0.904	0.078	0.077	3.11E-01	0.973	835
<i>RBMS3</i>	rs9878305	3	29310430	A	G	0.884	0.183	0.078	1.82E-02	0.997	835
<i>LOC442213</i>	rs12204829	6	48220567	G	A	0.090	0.153	0.085	7.26E-02	0.952	835
<i>RPRM</i>	rs13402721	2	153770202	T	A	0.078	0.270	0.091	3.10E-03	0.899	835
<i>MT1P2</i>	rs1252138	1	235207583	G	T	0.154	0.187	0.077	1.46E-02	0.853	835
<i>SOCS6</i>	rs1282645	18	66589560	G	A	0.067	0.166	0.113	1.41E-01	0.981	835
<i>KCNJ4</i>	rs9610956	22	37169820	A	G	0.076	0.138	0.088	1.20E-01	0.997	835
<i>STC2</i>	rs13178402	5	172792898	A	G	0.883	0.149	0.080	6.26E-02	0.936	835
<i>HEMK2</i>	rs7276221	21	28422813	G	A	0.568	0.102	0.051	4.48E-02	0.987	835
<i>C18orf55</i>	rs1790856	18	69998062	A	G	0.457	0.142	0.082	8.22E-02	0.554	835
<i>SHROOM3</i>	rs9996493	4	77660038	G	A	0.241	0.150	0.058	9.73E-03	0.996	835
<i>LRPPRC</i>	rs6759184	2	44085473	A	G	0.303	0.091	0.050	6.69E-02	0.991	835
<i>CYLC2</i>	rs1375213	9	104852166	C	A	0.576	0.091	0.049	6.41E-02	0.992	835
<i>FGD2</i>	rs708010	6	37071350	A	C	0.252	0.103	0.062	1.00E-01	0.935	835
<i>SAMD12</i>	rs1013456	8	119821110	G	A	0.665	0.098	0.053	6.42E-02	0.987	835
<i>CCDC28A</i>	rs6927344	6	139144059	T	C	0.978	0.432	0.126	5.86E-04	0.998	835
<i>ACTL7B</i>	rs593932	9	110223976	A	G	0.534	0.152	0.051	2.84E-03	0.997	835
<i>IMPG1</i>	rs2125215	6	77526970	T	C	0.117	-0.011	0.076	8.82E-01	0.987	835
<i>LYPLAL1</i>	rs12137855	1	217515001	C	T	0.786	0.076	0.059	2.03E-01	0.997	835
<i>TMEM16C</i>	rs10501021	11	25712104	A	G	0.829	0.053	0.070	4.51E-01	0.999	835
<i>CDH4</i>	rs6513576	20	59352421	C	T	0.804	0.108	0.063	8.51E-02	0.998	835
<i>SRD5A2L2</i>	rs1483293	4	64918291	A	G	0.048	0.115	0.138	4.05E-01	0.992	835
<i>CCDC66</i>	rs3732513	3	56649343	C	T	0.160	0.236	0.065	2.97E-04	0.950	835
<i>ASPH</i>	rs7836571	8	63006280	T	A	0.847	0.096	0.071	1.76E-01	0.955	835
<i>ADH7</i>	rs971074	4	100560884	C	T	0.979	0.048	0.274	8.61E-01	0.304	835
<i>PLD5</i>	rs6673239	1	240694244	T	A	0.373	-0.017	0.048	7.28E-01	0.999	835
<i>TLE3</i>	rs2668606	15	68386797	A	G	0.029	0.261	0.130	4.54E-02	0.815	835
<i>PELI2</i>	rs9323291	14	55464800	G	A	0.891	0.087	0.076	2.54E-01	0.998	835
<i>GCKR</i>	rs780094	2	27594741	T	C	0.411	0.051	0.054	3.38E-01	0.985	835
<i>KIAA1345</i>	rs2160043	4	15108349	C	T	0.469	0.044	0.051	3.89E-01	0.999	835
<i>ATXN7L4</i>	rs6953952	7	105246348	C	T	0.059	-0.097	0.117	4.06E-01	0.999	835
<i>ZHX2</i>	rs11783697	8	123886375	C	A	0.289	0.117	0.058	4.51E-02	0.997	835
<i>PTPRG</i>	rs9860802	3	61986250	T	G	0.215	0.124	0.060	3.81E-02	0.999	835
<i>RPS6KA1</i>	rs190737	1	26772031	C	A	0.451	0.171	0.047	2.66E-04	0.952	835
<i>CACHD1</i>	rs11208510	1	64940125	A	T	0.195	0.172	0.065	7.70E-03	0.902	835
<i>HS3ST3B1</i>	rs9896612	17	14259726	G	T	0.380	0.089	0.051	7.85E-02	0.898	835
<i>RYR3</i>	rs7179722	15	31920794	T	A	0.493	0.093	0.057	1.04E-01	0.978	835
<i>SLC6A15</i>	rs11116503	12	83541313	A	G	0.634	0.076	0.052	1.45E-01	0.943	835
<i>SOCS7</i>	rs4794776	17	33734136	T	C	0.915	0.083	0.094	3.81E-01	0.932	835

Table S4. (cont'd)

Locus						Framingham Heart Study					
Nearby Gene	SNP	Chr.	Pos.	EA	OA	EAF	Effect	SE	P	Imp	N
<i>PNPLA3</i>	rs738409	22	42656060	G	C	0.233	0.289	0.034	7.48E-18	0.931	2,932
<i>PPP1R3B</i>	rs4240624	8	9221641	A	G	0.924	0.352	0.051	6.27E-12	0.999	2,932
<i>NCAN</i>	rs2228603	19	19190924	T	C	0.073	0.293	0.060	1.03E-06	0.753	2,932
<i>TP73L</i>	rs9817981	3	191046224	A	G	0.572	0.085	0.028	2.49E-03	0.995	2,932
<i>BMS1L</i>	rs1592158	10	42593362	A	G	0.170	0.105	0.038	5.19E-03	0.949	2,932
<i>MSRA</i>	rs17151287	8	10089602	C	G	0.028	0.082	0.085	3.38E-01	0.903	2,932
<i>ARL15</i>	rs11748223	5	53531996	C	T	0.896	0.105	0.044	1.73E-02	1.000	2,932
<i>RBMS3</i>	rs9878305	3	29310430	A	G	0.886	0.085	0.042	4.63E-02	0.941	2,932
<i>LOC442213</i>	rs12204829	6	48220567	G	A	0.101	0.115	0.048	1.62E-02	0.905	2,932
<i>RPRM</i>	rs13402721	2	153770202	T	A	0.090	0.057	0.051	2.66E-01	0.915	2,932
<i>MT1P2</i>	rs1252138	1	235207583	G	T	0.163	0.067	0.040	9.49E-02	0.867	2,932
<i>SOCS6</i>	rs1282645	18	66589560	G	A	0.057	0.120	0.063	5.94E-02	0.854	2,932
<i>KCNJ4</i>	rs9610956	22	37169820	A	G	0.067	0.143	0.076	6.02E-02	0.473	2,932
<i>STC2</i>	rs13178402	5	172792898	A	G	0.896	0.134	0.046	3.29E-03	0.994	2,932
<i>HEMK2</i>	rs7276221	21	28422813	G	A	0.554	0.057	0.027	3.71E-02	0.996	2,932
<i>C18orf55</i>	rs1790856	18	69998062	A	G	0.411	0.085	0.028	2.49E-03	0.969	2,932
<i>SHROOM3</i>	rs9996493	4	77660038	G	A	0.227	0.076	0.049	1.21E-01	0.445	2,932
<i>LRPPRC</i>	rs6759184	2	44085473	A	G	0.305	0.026	0.030	3.94E-01	1.000	2,932
<i>CYLC2</i>	rs1375213	9	104852166	C	A	0.590	0.078	0.028	5.00E-03	0.992	2,932
<i>FGD2</i>	rs708010	6	37071350	A	C	0.266	0.074	0.031	1.75E-02	0.984	2,932
<i>SAMD12</i>	rs1013456	8	119821110	G	A	0.667	0.069	0.029	1.88E-02	0.994	2,932
<i>CCDC28A</i>	rs6927344	6	139144059	T	C	0.971	0.140	0.081	8.48E-02	0.992	2,932
<i>ACTL7B</i>	rs593932	9	110223976	A	G	0.544	0.065	0.028	1.94E-02	0.997	2,932
<i>IMPG1</i>	rs2125215	6	77526970	T	C	0.156	0.123	0.037	7.92E-04	0.999	2,932
<i>LYPLAL1</i>	rs12137855	1	217515001	C	T	0.785	0.079	0.034	1.81E-02	0.950	2,932
<i>TMEM16C</i>	rs10501021	11	25712104	A	G	0.863	0.076	0.048	1.11E-01	0.698	2,932
<i>CDH4</i>	rs6513576	20	59352421	C	T	0.808	0.079	0.035	2.35E-02	0.998	2,932
<i>SRD5A2L2</i>	rs1483293	4	64918291	A	G	0.049	0.148	0.061	1.57E-02	0.989	2,932
<i>CCDC66</i>	rs3732513	3	56649343	C	T	0.172	0.043	0.038	2.59E-01	0.926	2,932
<i>ASPH</i>	rs7836571	8	63006280	T	A	0.841	0.073	0.038	5.44E-02	0.948	2,932
<i>ADH7</i>	rs971074	4	100560884	C	T	0.896	0.118	0.047	1.28E-02	0.973	2,932
<i>PLD5</i>	rs6673239	1	240694244	T	A	0.370	0.081	0.028	4.23E-03	0.998	2,932
<i>TLE3</i>	rs2668606	15	68386797	A	G	0.032	0.015	0.096	8.78E-01	0.743	2,932
<i>PELI2</i>	rs9323291	14	55464800	G	A	0.916	0.087	0.058	1.33E-01	0.726	2,932
<i>GCKR</i>	rs780094	2	27594741	T	C	0.442	0.069	0.027	1.17E-02	0.999	2,932
<i>KIAA1345</i>	rs2160043	4	15108349	C	T	0.466	0.061	0.028	2.83E-02	0.957	2,932
<i>ATXN7L4</i>	rs6953952	7	105246348	C	T	0.063	0.156	0.058	6.85E-03	0.981	2,932
<i>ZHX2</i>	rs11783697	8	123886375	C	A	0.296	0.063	0.041	1.28E-01	0.526	2,932
<i>PTPRG</i>	rs9860802	3	61986250	T	G	0.217	0.053	0.034	1.24E-01	0.995	2,932
<i>RPS6KA1</i>	rs190737	1	26772031	C	A	0.450	0.075	0.030	1.26E-02	0.842	2,932
<i>CACHD1</i>	rs11208510	1	64940125	A	T	0.194	0.036	0.049	4.60E-01	0.499	2,932
<i>HS3ST3B1</i>	rs9896612	17	14259726	G	T	0.361	0.052	0.033	1.18E-01	0.749	2,932
<i>RYR3</i>	rs7179722	15	31920794	T	A	0.503	0.030	0.033	3.63E-01	0.688	2,932
<i>SLC6A15</i>	rs11116503	12	83541313	A	G	0.646	0.049	0.033	1.47E-01	0.741	2,932
<i>SOCS7</i>	rs4794776	17	33734136	T	C	0.919	0.115	0.055	3.75E-02	0.811	2,932

Table S5.

Nearby Gene	SNP	Chr.	Pos.	EA	OA	EAFA	EAFB	Imp ^b	OR NAFLD (95%CI)	P NAFLD
<i>PNPLA3</i>	rs738409	22	42656060	G	C	0.49	0.23	0.9455	3.26 (2.11 - 7.21)	3.6E-43
<i>PPP1R3B</i>	rs4240624	8	9221641	A	G	0.89	0.91	0.9601	0.93 (0.68 - 1.18)	0.285
<i>NCAN</i>	rs2228603	19	19190924	T	C	0.12	0.08	0.7491	1.65 (1.15 - 2.87)	5.29E-05
<i>TP73L</i>	rs9817981	3	191046224	A	G	0.6	0.59	0.9803	1.04 (0.89 - 1.20)	0.0195
<i>BMS1L</i>	rs1592158	10	42593362	A	G	0.16	0.17	0.864	0.91 (0.70 - 1.12)	0.0427
<i>MSRA</i>	rs17151287	8	10089602	C	G	0.02	0.03	0.9165	0.86 (0.35 - 1.37)	0.14
<i>ARL15</i>	rs11748223	5	53531996	C	T	0.9	0.9	0.9872	1.22 (0.96 - 1.47)	0.00579
<i>RBMS3</i>	rs9878305	3	29310430	A	G	0.89	0.89	0.9593	0.96 (0.72 - 1.20)	0.0913
<i>LOC442213</i>	rs12204829	6	48220567	G	A	0.1	0.11	0.9017	1.19 (0.91 - 1.71)	0.0181
<i>RPRM</i>	rs13402721	2	153770202	T	A	0.08	0.08	0.9249	0.92 (0.73 - 1.24)	0.0195
<i>MT1P2</i>	rs1252138	1	235207583	G	T	0.14	0.16	0.9097	0.96 (0.75 - 1.17)	0.0449
<i>SOCS6</i>	rs1282645	18	66589560	G	A	0.08	0.08	0.9991	1.02 (0.80 - 1.43)	0.174
<i>KCNJ4</i>	rs9610956	22	37169820	A	G	0.06	0.08	0.7558	0.92 (0.61 - 1.24)	0.0324
<i>STC2</i>	rs13178402	5	172792898	A	G	0.88	0.89	0.9997	1.00 (0.78 - 1.24)	0.056
<i>HEMK2</i>	rs7276221	21	28422813	G	A	0.6	0.55	0.9896	1.21 (1.03 - 1.48)	0.000406
<i>C18orf55</i>	rs1790856	18	69998062	A	G	0.41	0.41	0.9948	1.04 (0.89 - 1.19)	0.0143
<i>SHROOM3</i>	rs9996493	4	77660038	G	A	0.21	0.18	0.9761	1.16 (0.95 - 1.47)	0.00292
<i>LRPPRC</i>	rs6759184	2	44085473	A	G	0.32	0.3	1	1.09 (0.93 - 1.25)	0.0241
<i>CYLC2</i>	rs1375213	9	104852166	C	A	0.57	0.58	0.9956	1.02 (0.88 - 1.20)	0.0654
<i>FGD2</i>	rs708010	6	37071350	A	C	0.27	0.25	0.9997	1.12 (0.95 - 1.29)	0.00794
<i>SAMD12</i>	rs1013456	8	119821110	G	A	0.63	0.65	0.9921	0.95 (0.83 - 1.11)	0.0189
<i>CCDC28A</i>	rs6927344	6	139144059	T	C	0.97	0.97	0.9702	1.17 (0.78 - 2.35)	0.0115
<i>ACTL7B</i>	rs593932	9	110223976	A	G	0.55	0.57	0.9954	0.97 (0.82 - 1.13)	0.122
<i>IMPG1</i>	rs2125215	6	77526970	T	C	0.15	0.14	0.9998	1.24 (0.98 - 1.68)	0.00138
<i>LYPLAL1</i>	rs12137855	1	217515001	C	T	0.83	0.79	0.9586	1.37 (1.17 - 1.57)	4.12E-05
<i>TMEM16C</i>	rs10501021	11	25712104	A	G	0.83	0.81	0.9968	1.13 (0.93 - 1.33)	0.00716
<i>CDH4</i>	rs6513576	20	59352421	C	T	0.8	0.81	0.9984	0.99 (0.81 - 1.18)	0.0439
<i>SRD5A2L2</i>	rs1483293	4	64918291	A	G	0.05	0.06	0.9963	1.05 (0.71 - 1.38)	0.0399
<i>CCDC66</i>	rs3732513	3	56649343	C	T	0.14	0.17	0.9578	0.85 (0.64 - 1.06)	0.0177
<i>ASPH</i>	rs7836571	8	63006280	T	A	0.84	0.82	0.9676	1.07 (0.88 - 1.37)	0.0196
<i>ADH7</i>	rs971074	4	100560884	C	T	0.88	0.9	0.8858	0.77 (0.52 - 1.01)	0.0008
<i>PLD5</i>	rs6673239	1	240694244	T	A	0.36	0.37	1	0.98 (0.85 - 1.15)	0.0191
<i>TLE3</i>	rs2668606	15	68386797	A	G	0.03	0.04	0.9102	1.10 (0.67 - 1.54)	0.0212
<i>PELI2</i>	rs9323291	14	55464800	G	A	0.88	0.91	0.8401	0.77 (0.65 - 0.95)	0.00172
<i>GCKR</i>	rs780094	2	27594741	T	C	0.47	0.41	0.9999	1.45 (1.19 - 1.86)	2.59E-08
<i>KIAA1345</i>	rs2160043	4	15108349	C	T	0.48	0.46	0.9641	1.05 (0.91 - 1.20)	0.0277
<i>ATXN7L4</i>	rs6953952	7	105246348	C	T	0.06	0.05	0.9681	1.26 (0.93 - 1.60)	0.0111
<i>ZHX2</i>	rs11783697	8	123886375	C	A	0.29	0.34	0.8394	0.89 (0.78 - 1.04)	0.00421
<i>PTPRG</i>	rs9860802	3	61986250	T	G	0.23	0.22	0.9999	1.02 (0.86 - 1.25)	0.0266
<i>RPS6KA1</i>	rs190737	1	26772031	C	A	0.47	0.47	0.993	1.03 (0.90 - 1.22)	0.0177
<i>CACHD1</i>	rs11208510	1	64940125	A	T	0.19	0.21	0.9528	0.94 (0.74 - 1.13)	0.0368
<i>HS3ST3B1</i>	rs9896612	17	14259726	G	T	0.38	0.36	0.8794	1.09 (0.93 - 1.25)	0.00899
<i>RYR3</i>	rs7179722	15	31920794	T	A	0.49	0.49	0.7424	1.04 (0.89 - 1.25)	0.0224
<i>SLC6A15</i>	rs11116503	12	83541313	A	G	0.63	0.6	0.7462	1.20 (1.03 - 1.36)	0.00287
<i>SOCS7</i>	rs4794776	17	33734136	T	C	0.92	0.9	0.7673	1.31 (0.95 - 2.10)	0.00188

Table S6.

Nearby Gene	SNP	EA	OA	EA ^a	EA ^b	Imp ^b	OR NAFLD (95%CI)	P NAFLD
<i>PNPLA3</i>	rs738409	G	C	0.49	0.228385	0.9729	3.24(2.83-3.72)	2.16E-64
<i>NCAN</i>	rs2228603	T	C	0.12	0.066702	0.9975	1.90(1.55-2.34)	6.82E-10
<i>LYPLAL1</i>	rs12137855	C	T	0.83	0.800741	0.997	1.21(1.02-1.43)	0.02938
<i>GCKR</i>	rs780094	T	C	0.47	0.425565	0.999	1.18(1.05-1.34)	0.007514
<i>PPP1R3B</i>	rs4240624	A	G	0.89	0.906658	0.9916	0.86(0.70-1.06)	0.1524

Table S7.

Platform	R2 hat	N SNPs	concordance
Affymetrix 6.0	>0.3-0.4	7444	0.85
	>0.4-0.5	9906	0.87
	>0.5-0.6	13040	0.89
	>0.6-0.7	18724	0.91
	>0.7-0.8	29002	0.93
	>0.8-0.9	56310	0.96
	>0.9-1.0	432150	0.99
Illumina	>0.3-0.4	6055	0.89
	>0.4-0.5	8179	0.91
	>0.5-0.6	10998	0.92
	>0.6-0.7	15928	0.93
	>0.7-0.8	27504	0.95
	>0.8-0.9	63354	0.96
	>0.9-1.0	573286	0.99

Table S8.

Nearby Gene	SNP	Imp ^a	Concordance ^a	Imp ^b	Concordance ^b
<i>PNPLA3</i>	rs738409	0.9455	0.99	0.9729	0.99
<i>NCAN</i>	rs2228603	0.7491	0.93	0.9975	0.99
<i>LYPLAL1</i>	rs12137855	0.9586	0.99	0.997	0.99
<i>GCKR</i>	rs780094	0.9999	0.99	0.999	0.99
<i>PPP1R3B</i>	rs4240624	0.9601	0.99	0.9916	0.99

Table S9.

Nearby Gene	SNP	EA	OA	2 hour glucose				2 hour glucose controlled for BMI				Fasting Glucose			
				Effect	SE	P	N	Effect	SE	P	N	Effect	SE	P	N
<i>PNPLA3</i>	rs738409	G	C	-0.0156	0.0228	0.493	15,252	-0.0161	0.0224	0.4745	15,234	0.0057	0.0043	0.1867	45,727
<i>NCAN</i>	rs2228603	T	C	-0.0213	0.0369	0.5647	15,252	-0.0187	0.0365	0.6086	15,234	0.0064	0.0075	0.3934	44,603
<i>LYPLAL1</i>	rs12137855	C	T	-0.0163	0.0221	0.4599	15,252	-0.0153	0.0218	0.4839	15,234	-1.00E-04	0.0044	0.9815	45,042
<i>GCKR</i>	rs780094	T	C	0.0905	0.0191	2.27E-06	15,239	0.0911	0.0189	1.45E-06	15,221	-0.0261	0.0037	2.49E-12	45,044
<i>PPP1R3B</i>	rs4240624	A	G	0.0696	0.0309	0.02427	15,252	0.074	0.0305	0.01525	15,234	-0.0279	0.0062	7.83E-06	46,182

Table S9. (cont'd)

Nearby Gene	SNP	EA	OA	HOMA-B				HOMA-IR				Fasting Insulin			
				Effect	SE	P	N	Effect	SE	P	N	Effect	SE	P	N
<i>PNPLA3</i>	rs738409	G	C	7.00E-04	0.0039	0.8522	36,030	0.007	0.0047	0.1384	36,601	0.0049	0.0045	0.2802	37,802
<i>NCAN</i>	rs2228603	T	C	0.0053	0.0066	0.4259	35,012	0.0097	0.0081	0.2329	35,478	0.0082	0.0078	0.2917	36,776
<i>LYPLAL1</i>	rs12137855	C	T	0.0052	0.0039	0.1796	35,428	0.0035	0.0048	0.4694	35,894	0.0047	0.0046	0.312	37,192
<i>GCKR</i>	rs780094	T	C	-0.0039	0.0034	0.2515	35,433	-0.0201	0.0041	7.63E-07	35,899	-0.0152	0.0039	9.77E-05	37,197
<i>PPP1R3B</i>	rs4240624	A	G	-0.0011	0.0052	0.8325	36,463	-0.0208	0.0066	0.001657	37,034	-0.021	0.0064	0.001006	38,235

Table S9. (cont'd)

Nearby Gene	SNP	EA	OA	LDL			HDL			TG		
				Effect	P	N	Effect	P	N	Effect	P	N
<i>PNPLA3</i>	rs738409	G	C	-	0.01406	93,996	-	0.006189	98,406	+	0.2208	95,067
<i>NCAN</i>	rs2228603	T	C	-	1.42E-19	93,999	-	0.6776	98,409	-	1.49E-23	95,070
<i>LYPLAL1</i>	rs12137855	C	T	+	0.08711	95,454	-	0.1467	99,900	+	0.7338	96,598
<i>GCKR</i>	rs780094	T	C	+	0.000437	95,404	-	0.03961	99,849	+	7.08E-125	96,546
<i>PPP1R3B</i>	rs4240624	A	G	+	1.27E-12	95,454	+	1.44E-23	99,900	-	0.01944	96,598

Table S9. (cont'd)

Nearby Gene	SNP	EA	OA	BMI				Waist to hip ratio controlled for BMI				Diabetes mellitus					
				Effect	SE	P	N	Effect	SE	P	N	OR	L95%	U95%	P	CASES	CONTROLS
<i>PNPLA3</i>	rs738409	G	C	-0.0085	0.005644	0.137272	123,905	0.0044	0.0055	0.4207	77,218	1.04	1	1.1	0.0693	8,130	38,987
<i>NCAN</i>	rs2228603	T	C	-0.0057	0.009214	0.537516	123,842	0.0223	0.009	0.01311	77,163	1.09	1.01	1.18	0.0213	8,130	38,987
<i>LYPLAL1</i>	rs12137855	C	T	-0.0057	0.005759	0.325462	123,866	0.0112	0.0056	0.04484	77,169	1	0.96	1.05	0.885	8,130	38,987
<i>GCKR</i>	rs780094	T	C	-0.0081	0.004838	0.093909	123,805	0.0177	0.0047	0.000136	77,136	0.99	0.95	1.03	0.596	8,130	38,987
<i>PPP1R3B</i>	rs4240624	A	G	-0.0069	0.008408	0.412868	123,831	-0.0196	0.008	0.01446	77,170	0.96	0.9	1.03	0.234	8,130	38,987

Table S10.

	SNP	EA	tissue	N	Gene	Effect ^a	P	P _{adj} ^b	Peak SNP ^c	R _{sq} ^d	P peak	P _{adj} ^e
<i>PNPLA3</i>	rs738409	G	omental fat	741	<i>SAMM50</i>	-	6.86E-07	0.001235	rs6006595	0.053228	2.54E-16	1.30E-12
			subcutaneous fat	608	<i>SAMM50</i>	-	1.49E-07	0.000588	rs6006595	0.058679	2.36E-21	6.72E-17
<i>GCKR</i>	rs780094	T	liver	561	<i>C2orf16</i>	+	6.74E-06	NA	NA	NA	NA	NA
			liver	555	<i>IFT172</i>	+	1.53E-27	0.798425	rs4665978	0.386731	1.11E-86	1.93E-33
			omental fat	705	<i>IFT172</i>	+	1.70E-63	0.924709	rs1647276	0.449273	1.28E-222	1.39E-69
			subcutaneous fat	582	<i>IFT172</i>	+	8.85E-52	0.442351	rs10205219	0.415029	1.58E-176	9.26E-59
<i>PPP1R3B</i>	rs4240624	A	liver	566	<i>AW673036_RC</i>	+	4.05E-21	NA	NA	NA	NA	NA
			liver	566	<i>PPP1R3B</i>	+	1.22E-15	NA	NA	NA	NA	NA
			liver	565	<i>AK055863</i>	-	2.50E-15	0.997045	rs4841133	0.972937	2.36E-15	0.995253