Supplementary Material to

A Genome-wide Association Meta-analysis on Apolipoprotein A-IV Concentrations

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Supplementary Tables

Supplementary Table 1: Baseline characteristics of contributing studies

	Discovery stage					Replication stage	
	CoLaus (n=3996)	FamHS (n=1712)	KORA F3 (n=3075)	KORA F4 (n=2926)	YFS (n=2104)	Bruneck (n=802)	SAPHIR (n=1465)
Age (in years)	58.54 ± 10.52 [50, 58, 67]	51.5 ± 14.1 [39, 53, 63]	57.31 ± 12.89 [46, 57, 67]	56.15 ± 13.31 [44, 56, 67]	31.73 ± 4.99 [27, 33, 36]	62.7 ± 11.1 [53, 62, 71]	51 ± 6.02 [46, 52, 55]
Women, n (%)	1858 (46.50%)	1022 (54.0%)	1577 (51.28%)	1509 (51.57%)	1156 (54.94%)	402 (49.26%)	476 (32.49%)
ApoA-IV (mg/dl)	16.28 ± 4.73 [13.20, 15.77, 18.74]	14.3 ± 4.1 [11.6, 13.9, 16.6]	17.25 ± 4.67 [14.16, 16.72, 19.80]	15.31 ± 4.34 [12.40, 14.95, 17.62]	13.13 ± 3.84 [10.44, 12.84, 15.23]	14.27 ± 3.61 [11.90, 12.20, 16.50]	14.55 ± 3.3 [12.31, 14.50, 16.60]
Triglycerides (mg/dl)	120.02 ± 77.62 [71, 97, 142]	149.2 ± 104.4 [84, 125, 185]	164.66 ± 125.84 [88, 135, 200]	125.04 ± 89.18 [72, 105, 151]	118.35 ± 75.69 [71, 97, 142]	131.52 ± 79.87 [81, 111, 157]	126.38 ± 89.81 [72.0, 101.5, 151.0]
HDL cholesterol (mg/dl)	63.59 ± 18.02 [50, 62, 73]	49.8 ± 15.0 [39, 48, 58]	58.85 ± 17.14 [47, 56, 69]	55.91 ± 14.45 [45, 54, 65]	49.83 ± 12.23 [41, 49, 58]	58.75 ± 16.13 [47, 57, 67]	59.19 ± 15.6 [48, 57, 68]
eGFR (CKD-EPI) (mL/min/1.73 m2)	81.93 ± 14.87 [72.17, 82.53, 92.61]	81.7 ± 16.7 [71.0, 81.4, 93.2]	82.73 ± 17.61 [71.55, 84.43, 95.26]	83.76 ± 17.15 [72.72, 84.84, 96.05]	114.11 ± 6.45 [109.80, 113.80, 118.46]	79.24 ± 15.03 [69.35, 80.61, 89.66]	95.46 ± 11.83 [86.24, 98.54, 104.16]

Continuous variables are shown as mean +/- stdev and [25%, 50%, 75%]-Percentiles

Supplementary Table 2: Genotyping and imputation information of contributing studies at the discovery stage

	CoLaus	FamHS	KORA F3	KORA F4	YFS
SNP-chip	Affymetrix GeneChip® Human Mapping 500K	Illumina Human 1M-Duo v3 Illumina 610-Quadv1 Illumina Human Hap550K	Illumina Omni 2.5/ Illumina Omni Express	Affymetrix Axiom	Illumina 670k
QC before imputation	callrate >70%, p-value HWE > 10^{-7}	callrate >98%, p-value HWE > 10^{-6}, MAF>1%	callrate >98%, p-value HWE > 10^{-10}	callrate >98%, p-value HWE > 10^{-10}	callrate >95%, p-value HWE > 10^{-6}, MAF>1%
Program used for Imputation	minimac	MACH	IMPUTE	IMPUTE	IMPUTE
Reference panel for imputation	1000G phase 1 v3	1000G phase 1 v3	1000G phase 1 v3	1000G phase 1 v3	1000G phase 1 v3
Program used for GWA analysis	In-house Matlab code	PROBABEL	SNPTest	SNPTest	SNPTest 2.4.1
Genomic inflation factor λ	1.038	1.015	1.023	1.011	1.014

Supplementary Table 3: Characteristics of selected SNPs for replication (p-value < 1E-06 in the GWAs stage)

SNP	Chr	Position[#]	Nearest Gene	a*	A*	Reason for selection	MAF (range in studies)	MAF (1000G EUR)*
APOA4 gene region								
rs1729407	11	116677370	*APOA4*	C	G	Lead SNP	0.485-0.546	0.498
rs5104	11	116692334	*APOA4*	C	T	Missense variant & independently associated (cond. analysis)	0.128-0.204	0.174
rs5110	11	116691634	*APOA4*	A	C	Missense variant & Known from literature	0.035- 0.080	0.066
APOA4 gene region, selected from literature								
rs675	11	116691675	*APOA4*	A (C)	T	Missense variant & known from literature	0.158-0.209	0.180 (<0.001)
Other gene regions								
rs4241819	4	187157140	*KLKB1*	C	T	Lead SNP, but could not be genotyped → used in GWAs stage	0.452-0.565[$]	0.478
rs4253311	4	187174683	*KLKB1*	A	G	Proxy SNP with lead SNP and with missense variant → used in replication stage		0.477
rs59698941	5	132154912	*SOWAHA*	G	A	Lead SNP	0.140-0.167	0.127
rs2292030	5	132161294	*SHROOM1*	A	G	Missense variant	0.138-0.160	0.120

* MAF, minor (a) and major alleles (A) derived from 1000 Genomes, phase 3 v5, all European populations
[$] In GWAs discovery stage studies; [#]Based on build 37, HG19

Supplementary Table 4: Study-specific results of SNPs that were selected for replication

	MAF	HWE	Info*	Call-rate**	$\beta^{\#}$	se$^{\#}$	p$^{\#}$	$\beta^{\&}$	se$^{\&}$	p$^{\&}$
rs1729407										
CoLaus	0.510	0.884	0.892	--	-0.8440	0.1053	1.11E-15	-0.0509	0.0064	1.39E-15
FamHS	0.485	0.685	0.778	--	-0.5303	0.1473	3.16E-04	-0.0397	0.0104	1.29E-04
KORA F3	0.509	0.248	0.975	--	-0.7803	0.1187	5.68E-11	-0.0452	0.0068	3.55E-11
KORA F4	0.498	0.579	0.977	--	-0.7970	0.1102	5.95E-13	-0.0527	0.0071	1.14E-13
YFS	0.546	0.291	0.924	--	-0.0904	0.0326	0.0056	-0.0951	0.0326	0.0035
Bruneck	0.510	0.926	--	0.988	-0.3382	0.1808	0.0617	-0.0209	0.0135	0.1231
SAPHIR	0.510	0.949	--	0.992	-0.5568	0.1206	4.24E-06	-0.0394	0.0087	6.95e-06
rs5104										
CoLaus	0.151	0.477	0.965	--	-0.6960	0.1414	8.54E-07	-0.0425	0.0086	6.81E-07
FamHS	0.128	0.944	0.713	--	-0.5951	0.2148	0.0056	-0.0383	0.0151	0.0113
KORA F3	0.140	0.084	0.979	--	-0.9772	0.1719	1.43E-08	-0.0557	0.0099	1.75E-08
KORA F4	0.144	0.598	0.947	--	-0.8742	0.1601	5.14E-08	-0.0602	0.0103	5.08E-09
YFS	0.204	0.503	0.885	--	-0.1130	0.0402	0.0050	-0.1105	0.0402	0.0061
Bruneck	0.109	0.605	--	0.984	-0.4327	0.2889	0.1346	-0.0341	0.0216	0.1153
SAPHIR	0.143	0.157	--	0.986	-0.4603	0.1692	0.0066	-0.0344	0.01223	0.0049
rs5110										
CoLaus	0.072	0.849	0.517	--	0.8257	0.2663	0.0019	0.0432	0.0161	0.0074
FamHS	0.080	0.274	0.631	--	0.5338	0.2980	0.0732	0.0385	0.0209	0.0658
KORA F3	0.074	0.293	1.000	--	0.5140	0.2201	0.0196	0.0342	0.0126	0.0068
KORA F4	0.065	0.541	0.771	--	0.6306	0.2531	0.0128	0.0442	0.0162	0.0065
YFS	0.035	1.000	0.787	--	0.0182	0.0953	0.8484	0.0405	0.0953	0.6711
Bruneck	0.082	0.482	--	0.995	-0.1301	0.3214	0.6857	-0.0122	0.0240	0.6121
SAPHIR	0.067	0.193	--	0.994	0.1591	0.2465	0.5188	0.0092	0.0179	0.6066
rs675										
CoLaus	0.197	0.497	0.969	--	-0.2894	0.1282	0.0240	-0.0187	0.0078	0.0156
FamHS	0.207	0.026	0.842	--	-0.1456	0.1822	0.4244	-0.0141	0.0128	0.2725
KORA F3	0.208	0.353	0.997	--	-0.1200	0.1426	0.4001	-0.0069	0.0082	0.3977
KORA F4	0.209	0.313	0.923	--	-0.2091	0.1399	0.1351	-0.0143	0.0090	0.1119
YFS	0.158	0.935	0.932	--	-0.0693	0.0439	0.1147	-0.0625	0.0439	0.1546
Bruneck	0.249	0.700	--	0.999	-0.0838	0.2051	0.6830	-0.0025	0.0154	0.8692
SAPHIR	0.228	0.754	--	0.991	-0.1774	0.1449	0.2210	-0.0122	0.0105	0.2458
rs4241819 in GWAs stage / rs4253311 in replication stage										
CoLaus	0.540	0.975	0.787	--	0.4756	0.1138	2.92E-05	0.0307	0.0069	7.87e-06
FamHS	0.534	0.513	0.884	--	0.2440	0.1464	0.0955	0.0187	0.0103	0.0688
KORA F3	0.565	0.741	0.935	--	0.3102	0.1212	0.0105	0.0183	0.0070	0.0083
KORA F4	0.553	0.370	0.932	--	0.5290	0.1136	3.36E-06	0.0343	0.0073	2.63e-06
YFS	0.452	0.965	0.937	--	0.0728	0.0320	0.0229	0.0920	0.0320	0.0040
Bruneck	0.530	0.973	--	0.988	0.3800	0.1810	0.0362	0.0307	0.0135	0.0236
SAPHIR	0.510	0.710	--	0.993	0.1789	0.1211	0.1397	0.0143	0.0087	0.1032
rs59698941										
CoLaus	0.157	0.770	0.781	--	-0.4363	0.1555	0.0050	-0.0246	0.0094	0.0089
FamHS	0.148	0.001	0.913	--	-0.8484	0.2062	3.87E-05	-0.0649	0.0145	7.58E-06
KORA F3	0.155	0.581	0.994	--	-0.1263	0.1627	0.4375	-0.0057	0.0093	0.5423
KORA F4	0.167	0.894	0.894	--	-0.4603	0.1562	0.0032	-0.0284	0.0100	0.0047
YFS	0.140	0.928	0.959	--	-0.0557	0.0453	0.2183	-0.0766	0.0452	0.0907
Bruneck	0.156	0.014	--	0.990	0.1860	0.2372	0.4332	0.0107	0.0177	0.5485
SAPHIR	0.133	0.948	--	0.994	-0.1488	0.1815	0.4124	-0.0138	0.0132	0.2956
rs2292030										
CoLaus	0.138	0.470	0.877	--	-0.4162	0.1549	0.0072	-0.0226	0.0094	0.0160
FamHS	0.140	0.001	0.952	--	-0.8228	0.2081	7.71E-05	-0.0628	0.0146	1.79E-05
KORA F3	0.148	0.223	0.988	--	-0.1339	0.1672	0.4231	-0.0056	0.0096	0.5629
KORA F4	0.160	0.945	0.913	--	-0.4801	0.1573	0.0023	-0.0296	0.0101	0.0034
YFS	0.140	1.000	0.965	--	-0.0540	0.0452	0.2321	-0.0750	0.0451	0.0967
Bruneck	0.150	0.051	--	0.967	0.1072	0.2461	0.6632	0.0039	0.0184	0.8316
SAPHIR	0.126	0.965	--	0.976	-0.0973	0.1874	0.6036	-0.0104	0.0136	0.4430

*Info: imputation quality, for all discovery stage cohorts; **For replication cohorts; $^{\#}$B on original scale of ApoA-IV; $^{\&}$ Based on log-transformed ApoA-IV values; all β-estimates and MAF refer to the minor allele (1000G EUR, Table 3)

Supplementary Table 5: Results of pathway association analysis with all included genes in each pathway; Pathways are sorted by the Bonferroni-corrected p-value in ascending order.

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT	0.00000014	15					
			APOA5	2.14E-38	11	116660085	134
			APOC3	7.2E-38	11	116700623	173
			APOA1	1.23E-29	11	116706468	171
			P4HB	0.07675	17	79801033	141
			APOB	0.10523	2	21224300	174
			SDC1	0.23886	2	20400557	240
			APOA2	0.32657	1	161192082	112
			LPL	0.45164	8	19796581	293
			HSPG2	0.48969	1	22148724	548
			APOC2	0.52755	19	45449238	151
			LIPC	0.54093	15	58724174	659
			LDLRAP1	0.63487	1	25870075	157
			LDLR	0.73131	19	11200037	338
			SAR1B	0.80991	5	133936838	98
			APOE	0.91052	19	45409657	140
REACTOME_LIPOPROTEIN_METABOLISM	0.000000893	27					
			APOA5	2.14E-38	11	116660085	134
			APOC3	7.2E-38	11	116700623	173
			APOA1	1.23E-29	11	116706468	171
			LCAT	0.07266	16	67973786	46
			P4HB	0.07675	17	79801033	141
			APOB	0.10523	2	21224300	174
			CETP	0.13017	16	56995834	235
			SCARB1	0.14549	12	125262173	458
			AMN	0.21923	14	103388992	135
			SDC1	0.23886	2	20400557	240
			BMP1	0.2825	8	22022652	291
			APOA2	0.32657	1	161192082	112
			ABCG1	0.37514	21	43640007	537

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			LPL	0.45164	8	19796581	293
			CUBN	0.46678	10	16865964	1440
			HSPG2	0.48969	1	22148724	548
			APOC2	0.52755	19	45449238	151
			LIPC	0.54093	15	58724174	659
			LDLRAP1	0.63487	1	25870075	157
			ABCA1	0.72544	9	107543283	775
			LDLR	0.73131	19	11200037	338
			PLTP	0.7649	20	44527258	148
			SAR1B	0.80991	5	133936838	98
			ALB	0.8635	4	74269971	121
			LPA	0.89897	6	160952514	346
			APOE	0.91052	19	45409657	140
			A2M	0.96774	12	9220303	194
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	0.00000401	44					
			APOA5	2.14E-38	11	116660085	134
			APOC3	7.2E-38	11	116700623	173
			APOA1	1.23E-29	11	116706468	171
			PNLIPRP2	0.0078	10	118380464	247
			PRKACB	0.06885	1	84647314	367
			LCAT	0.07266	16	67973786	46
			P4HB	0.07675	17	79801033	141
			LIPE	0.09676	19	42905658	77
			APOB	0.10523	2	21224300	174
			CETP	0.13017	16	56995834	235
			SCARB1	0.14549	12	125262173	458
			PNLIP	0.17251	10	118305427	113
			MGLL	0.18105	3	127407904	475
			PPP1CC	0.19497	12	111157612	154
			AMN	0.21923	14	103388992	135
			SDC1	0.23886	2	20400557	240
			BMP1	0.2825	8	22022652	291

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			ABCG5	0.28784	2	44039610	296
			APOA2	0.32657	1	161192082	112
			ABCG1	0.37514	21	43640007	537
			LPL	0.45164	8	19796581	293
			CUBN	0.46678	10	16865964	1440
			HSPG2	0.48969	1	22148724	548
			APOC2	0.52755	19	45449238	151
			LIPC	0.54093	15	58724174	659
			ABCG8	0.56245	2	44066102	447
			PLIN1	0.58966	15	90207599	162
			CLPS	0.60749	6	35762758	165
			LDLRAP1	0.63487	1	25870075	157
			FABP4	0.64051	8	82390731	130
			PRKACA	0.647	19	14202506	96
			PRKACG	0.69531	9	71627448	125
			ABCA1	0.72544	9	107543283	775
			LDLR	0.73131	19	11200037	338
			PLTP	0.7649	20	44527258	148
			SAR1B	0.80991	5	133936838	98
			ALB	0.8635	4	74269971	121
			PPP1CA	0.8795	11	67165651	79
			CAV1	0.8919	7	116166411	216
			LPA	0.89897	6	160952514	346
			APOE	0.91052	19	45409657	140
			ABHD5	0.95474	3	43732374	195
			A2M	0.96774	12	9220303	194
			PPP1CB	0.97427	2	28974625	197
KEGG_PPAR_SIGNALING_PATHWAY	0.0000144	67					
			APOA5	2.14E-38	11	116660085	134
			APOC3	7.2E-38	11	116700623	173
			APOA1	1.23E-29	11	116706468	171
			FABP2	0.002	4	120238404	274

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			ACOX2	0.01785	3	58490862	174
			RXRG	0.02237	1	165406164	347
			CYP8B1	0.04114	3	42913683	123
			PPARD	0.04218	6	35310334	362
			ACOX1	0.06478	17	73937588	248
			SCD	0.06679	10	102106771	147
			DBI	0.08871	2	120125250	188
			FABP3	0.12868	1	31838099	136
			RXRB	0.14515	6	33161361	123
			UBC	0.15962	12	125396190	142
			PPARG	0.16454	3	12393000	482
			SLC27A4	0.16824	9	131102838	129
			ILK	0.19735	11	6625039	118
			SLC27A1	0.19767	19	17581252	259
			UCP1	0.25521	4	141481049	127
			ACSL3	0.26547	2	223725731	358
			RXRA	0.27856	9	137298427	491
			CYP27A1	0.27923	2	219646471	163
			MMP1	0.3174	11	102660640	189
			APOA2	0.32657	1	161192082	112
			ACSL6	0.3356	5	131285666	171
			CPT2	0.34885	1	53662100	125
			ACADM	0.39328	1	76190031	310
			LPL	0.45164	8	19796581	293
			AQP7	0.50619	9	33384947	169
			OLR1	0.51463	12	10310898	222
			SLC27A6	0.52504	5	128301212	618
			FABP7	0.53044	6	123100645	140
			HMGCS2	0.56216	1	120290618	148
			PLIN1	0.58966	15	90207599	162
			SCD5	0.63508	4	83581039	1017
			FABP4	0.64051	8	82390731	130

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			FADS2	0.69986	11	61595504	228
			FABP5	0.71816	8	82192717	69
			PCK1	0.72845	20	56136136	226
			ADIPOQ	0.7557	3	186560462	193
			PLTP	0.7649	20	44527258	148
			PPARA	0.76737	22	46546498	340
			SLC27A5	0.81851	19	59009699	114
			ACADL	0.83862	2	211052715	82
			GK2	0.8464	4	80327506	63
			CD36	0.86119	7	80275968	350
			CPT1C	0.86906	19	50194364	171
			ANGPTL4	0.87016	19	8429010	176
			ACSL1	0.87476	4	185676748	379
			NR1H3	0.8767	11	47279467	158
			FABP1	0.89514	2	88422507	153
			CPT1A	0.92095	11	68522350	303
			FABP6	0.92298	5	159656436	449
			SORBS1	0.92504	10	97071529	1051
			PDPK1	0.94277	16	2587964	62
			SLC27A2	0.94331	15	50474392	394
			PCK2	0.95745	14	24563489	79
			ACAA1	0.98709	3	38164200	80
			ME1	0.98836	6	83920109	615
			SCP2	0.98858	1	53480609	626
			CYP4A11	0.99122	1	47394845	152
			EHHADH	0.99302	3	184908411	229
			CYP7A1	0.99403	8	59402736	127
			ACOX3	0.9988	4	8368008	513
			ACSL5	0.99882	10	114135955	206
			CPT1B	0.9994	22	51007289	282
			CYP4A22	0.99993	1	47603096	175
YAMASHITA_LIVER_CANCER_STEM_CELL_DN	0.0000186	73					

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			APOA5	2.14E-38	11	116660085	134
			KLKB1	5.86E-11	4	187148671	258
			F11	9.03E-10	4	187187117	222
			FMO3	0.00234	1	171060017	277
			CYP8B1	0.04114	3	42913683	123
			C1R	0.04702	12	7187514	111
			SAA4	0.06727	11	18252901	184
			C8B	0.09652	1	57394882	375
			UGT2B7	0.09948	4	69962192	278
			SERPINC1	0.10496	1	173872941	135
			ADCY8	0.13823	8	131792546	1117
			CYP3A7	0.15094	7	99302659	130
			GSTP1	0.25614	11	67351065	139
			ACSL3	0.26547	2	223725731	358
			ABCG5	0.28784	2	44039610	296
			SLC10A1	0.30116	14	70242551	136
			MASP2	0.30869	1	11104854	142
			SOD1	0.31	21	33031934	124
			GSTA1	0.32154	6	52656177	150
			SNAI2	0.33088	8	49830238	67
			THBS1	0.3414	15	39873279	119
			MAPK13	0.36382	6	36098260	97
			NR1I3	0.36512	1	161199455	153
			CD14	0.36598	5	140011312	113
			ALDH6A1	0.38319	14	74524367	244
			ESR1	0.4032	6	152128813	1500
			CES2	0.41484	16	66968373	77
			PRKCD	0.41655	3	53195536	193
			CES1	0.42738	16	55836763	294
			SULT1C4	0.43638	2	108994420	150
			APCS	0.44131	1	159557615	179
			CRABP1	0.48296	15	78632665	120

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			DNAJA4	0.48797	15	78558559	204
			HNF4A	0.49621	20	43029895	394
			MAP2K2	0.54286	19	4090319	234
			FKBP5	0.55259	6	35548333	473
			ABCB4	0.55526	7	87031360	267
			CYP3A4	0.59613	7	99354582	68
			HMGCR	0.64022	5	74632992	162
			C8A	0.64583	1	57320442	377
			CYP7B1	0.66661	8	65508528	492
			FABP5	0.71816	8	82192717	69
			RARG	0.74134	12	53604349	125
			MAP3K5	0.74356	6	136878186	504
			APOC4	0.76133	19	45445494	147
			UGT2B15	0.77481	4	69512314	287
			MASP1	0.81646	3	186964141	380
			NR1I2	0.84307	3	119501556	214
			ALDH8A1	0.85237	6	135238527	148
			ALDH1L1	0.85926	3	125822403	517
			PIK3C3	0.8607	18	39535162	286
			ACSL1	0.87476	4	185676748	379
			PIK3C2G	0.88602	12	18414473	1398
			PPARGC1A	0.88709	4	23793643	418
			CDKN2A	0.91225	9	21967750	125
			ABCB11	0.92614	2	169779448	483
			ABCB1	0.92683	7	87133178	557
			KNG1	0.92929	3	186435097	363
			C6	0.93688	5	41142247	547
			SLC27A2	0.94331	15	50474392	394
			CYP2C8	0.95427	10	96796528	293
			GSTM4	0.95504	1	110198697	138
			GADD45A	0.95666	1	68150859	129
			HRG	0.96356	3	186383740	169

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			FMO4	0.96567	1	171283321	136
			CYP1A2	0.97051	15	75041183	144
			SULT2A1	0.9764	19	48373722	237
			AOX1	0.98877	2	201450730	375
			GSTM1	0.99151	1	110230417	196
			NQO2	0.99165	6	3000049	408
			GADD45B	0.99243	19	2476122	188
			CYP7A1	0.99403	8	59402736	127
			ACSL5	0.99882	10	114135955	206
HSIAO_LIVER_SPECIFIC_GENES	0.0000199	233					
			APOC3	7.2E-38	11	116700623	173
			APOA1	1.23E-29	11	116706468	171
			KLKB1	5.86E-11	4	187148671	258
			F11	9.03E-10	4	187187117	222
			FMO3	0.00234	1	171060017	277
			HRSP12	0.01276	8	99114566	194
			C1S	0.01508	12	7167979	79
			MBL2	0.01605	10	54525139	217
			ACOX2	0.01785	3	58490862	174
			CYP2A6	0.02038	19	41349442	213
			FGFR4	0.02077	5	176516550	190
			AKR1C1	0.03062	10	5005453	300
			PCBD1	0.04028	10	72643264	163
			SAA1	0.04225	11	18287807	184
			ACAT1	0.04427	11	107992257	133
			C1R	0.04702	12	7187514	111
			FGG	0.06555	4	155525727	77
			CYP2A7	0.06713	19	41381343	280
			SAA4	0.06727	11	18252901	184
			UGT2B4	0.07005	4	70345882	505
			LCAT	0.07266	16	67973786	46
			CRHBP	0.09248	5	76248679	201

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			C8B	0.09652	1	57394882	375
			HPN	0.09852	19	35531409	201
			UGT2B7	0.09948	4	69962192	278
			SERPINC1	0.10496	1	173872941	135
			APOB	0.10523	2	21224300	174
			BAAT	0.11249	9	104122698	221
			HPD	0.11632	12	122277432	205
			HPX	0.12314	11	6452267	115
			ARG1	0.13078	6	131894343	98
			PROS1	0.13263	3	93591880	148
			TST	0.13698	22	37406899	198
			SEPP1	0.14069	5	42799981	150
			GATM	0.14447	15	45653321	146
			GSTZ1	0.14522	14	77787229	155
			F13B	0.14765	1	197008320	157
			ACADSB	0.15142	10	124768428	317
			CPS1	0.15434	2	211458078	679
			VTN	0.15877	17	26694298	84
			CYP4F2	0.15966	19	15988833	347
			NAMPT	0.16302	7	105888731	199
			NR1H4	0.16331	12	100897137	259
			F10	0.16522	13	113777112	183
			MGST2	0.17173	4	140586921	394
			ALAS1	0.17301	3	52232098	72
			HSD17B4	0.19103	5	118788191	377
			AKR1D1	0.1957	7	137761177	262
			HABP2	0.19607	10	115312777	305
			ALDOB	0.19616	9	104182841	211
			ORM1	0.20744	9	117085302	127
			TAT	0.20781	16	71600753	108
			POR	0.21279	7	75544419	236
			LGALS4	0.21655	19	39292310	189

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			C4BPB	0.22218	1	207262627	108
			CDH2	0.23519	18	25530926	594
			CYP2E1	0.24962	10	135340866	264
			ALDH2	0.25057	12	112204690	94
			ITIH2	0.25357	10	7745235	394
			IL13	0.25912	5	131993864	81
			PCSK6	0.26021	15	101923952	1089
			GHR	0.26821	5	42565965	822
			PZP	0.27685	12	9301435	279
			CYP27A1	0.27923	2	219646471	163
			SERPINF2	0.28202	17	1646319	211
			IGFBP1	0.28328	7	45927958	134
			SERPINA5	0.2877	14	95047705	298
			PLOD2	0.29236	3	145787227	383
			RGL2	0.29618	6	33259430	115
			SLC10A1	0.30116	14	70242551	136
			SOD1	0.31	21	33031934	124
			PON3	0.3106	7	94989183	153
			SERPINF1	0.31498	17	1665258	247
			G6PC	0.32608	17	41052813	76
			GPT	0.32648	8	145729464	73
			APOA2	0.32657	1	161192082	112
			CBS	0.33032	21	44473300	350
			PTGR1	0.33412	9	114325246	339
			F7	0.33884	13	113760101	193
			TF	0.34212	3	133464976	250
			F12	0.34372	5	176829138	83
			CFB	0.35454	6	31913720	129
			GYS2	0.36235	12	21689122	394
			FMO5	0.36946	1	146657839	453
			PLGLB2	0.37232	2	88047605	14
			PYGL	0.37412	14	51371934	338

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			C4BPA	0.37606	1	207277606	184
			ALDH6A1	0.38319	14	74524367	244
			KYNU	0.3906	2	143635194	537
			MGST1	0.39757	12	16506350	235
			HSD11B1	0.39862	1	209878135	195
			AGXT	0.39981	2	241808161	280
			HMGCL	0.4065	1	24128366	85
			CES2	0.41484	16	66968373	77
			BDH1	0.42601	3	197236653	498
			CES1	0.42738	16	55836763	294
			TAF6	0.43814	7	99704692	105
			APCS	0.44131	1	159557615	179
			AGTR1	0.45479	3	148447966	256
			F2	0.45845	11	46740715	120
			SERPINE1	0.46027	7	100770369	188
			CYB5A	0.4699	18	71920526	330
			DHCR24	0.4701	1	55315299	333
			DPYS	0.47086	8	105391651	385
			GSTA2	0.47522	6	52614884	187
			ABCC6	0.47947	16	16315043	340
			SLC39A14	0.47986	8	22225049	346
			FGL1	0.48075	8	17721899	509
			PLIN2	0.48447	9	19115758	190
			SUPT4H1	0.48841	17	56422535	107
			SERPINA1	0.4915	14	94843083	260
			CYP2J2	0.50272	1	60358979	184
			SSRP1	0.50616	11	57093458	132
			ACAA2	0.52542	18	47309873	195
			APOC2	0.52755	19	45449238	151
			LIPC	0.54093	15	58724174	659
			SERPIND1	0.54159	22	21128382	167
			SERPINA3	0.54326	14	95078713	253

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			MUT	0.55365	6	49398072	156
			ABCB4	0.55526	7	87031360	267
			HMGCS2	0.56216	1	120290618	148
			LPIN2	0.56276	18	2916991	448
			ACSM3	0.5804	16	20775311	144
			ANG	0.5949	14	21156931	219
			CYP3A4	0.59613	7	99354582	68
			RBP4	0.60611	10	95351592	207
			APOF	0.61214	12	56754354	38
			HGFAC	0.62211	4	3443659	168
			C9	0.62631	5	39284377	360
			C8A	0.64583	1	57320442	377
			SPP2	0.64696	2	234959345	309
			CDO1	0.65842	5	115140429	120
			CFHR2	0.65887	1	196912897	129
			MSMO1	0.66863	4	166248817	207
			C2	0.68129	6	31895253	254
			AKR1C4	0.68534	10	5238797	405
			ADH1B	0.68613	4	100227543	179
			CP	0.69549	3	148890289	371
			TDO2	0.69743	4	156824844	249
			RNASE4	0.71543	14	21156935	247
			AHSG	0.7164	3	186330849	141
			CFHR4	0.72714	1	196857143	179
			PCK1	0.72845	20	56136136	226
			CASC3	0.73425	17	38296506	126
			TTR	0.73808	18	29171729	103
			GSTO1	0.74747	10	106014467	109
			CAT	0.75028	11	34460471	283
			AZGP1	0.75588	7	99564349	135
			SLC2A2	0.75641	3	170714136	172
			APOC4	0.76133	19	45445494	147

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			UGT2B15	0.77481	4	69512314	287
			CYP2D6	0.78617	22	42522500	191
			ITIH4	0.79136	3	52847005	129
			ASGR1	0.79352	17	7076750	91
			ASL	0.8029	7	65540833	156
			SORD	0.80714	15	45315301	257
			ASS1	0.80981	9	133320093	357
			GGCX	0.81198	2	85785847	193
			NR0B2	0.82128	1	27237974	71
			LSR	0.82367	19	35739558	212
			NAT2	0.82486	8	18248754	333
			RARRES2	0.82916	7	150035406	135
			ITIH3	0.82926	3	52828783	116
			GLUD1	0.83584	10	88809958	209
			FST	0.84512	5	52776263	172
			PLG	0.84724	6	161123224	281
			ADH4	0.84753	4	100044807	351
			EPHX1	0.8582	1	226013001	328
			AADAC	0.86311	3	151531860	257
			ALB	0.8635	4	74269971	121
			NNMT	0.86563	11	114166534	150
			ITIH1	0.86641	3	52813941	112
			TFPI	0.86828	2	188343304	330
			CYP2C9	0.87177	10	96698414	353
			ACSL1	0.87476	4	185676748	379
			PCCB	0.8751	3	135969166	208
			DDT	0.88228	22	24313553	213
			BZW1	0.88698	2	201677055	91
			NCOR2	0.88962	12	124808956	1036
			FABP1	0.89514	2	88422507	153
			CFI	0.89635	4	110661847	304
			LPA	0.89897	6	160952514	346

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			APOE	0.91052	19	45409657	140
			HGD	0.91112	3	120347014	342
			GCH1	0.91706	14	55308723	317
			SLC38A3	0.92335	3	50242678	96
			FCN2	0.92475	9	137772657	242
			AFM	0.92659	4	74347461	178
			KNG1	0.92929	3	186435097	363
			FBP1	0.93068	9	97365420	319
			HNMT	0.93144	2	138721807	197
			F5	0.93674	1	169481191	483
			SERPINA6	0.9395	14	94770584	207
			CRP	0.94134	1	159682078	99
			C5	0.94256	9	123714613	334
			SEPHS2	0.94713	16	30454945	71
			BHMT	0.95279	5	78407603	200
			DECR1	0.95387	8	91013579	220
			PCK2	0.95745	14	24563489	79
			C8G	0.95891	9	139839697	155
			ABCC2	0.95892	10	101542354	277
			HRG	0.96356	3	186383740	169
			SC5D	0.96537	11	121163576	144
			HP	0.96694	16	72088507	132
			FAH	0.96878	15	80445232	239
			AGT	0.96945	1	230838271	261
			TM4SF4	0.97119	3	149192367	437
			SERPING1	0.97294	11	57365704	134
			SULT2A1	0.9764	19	48373722	237
			CXCR2	0.97662	2	218990735	96
			APOH	0.97663	17	64208146	245
			CPB2	0.97664	13	46627321	280
			RBM4	0.97682	11	66406087	76
			C3	0.98118	19	6677845	342

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			CPN2	0.98685	3	194060493	287
			ACAA1	0.98709	3	38164200	80
			ASGR2	0.98771	17	7004640	235
			AOX1	0.98877	2	201450730	375
			PROC	0.98993	2	128175995	150
			HAL	0.9905	12	96366439	272
			CYP4A11	0.99122	1	47394845	152
			ALDH1A1	0.99132	9	75515577	198
			MTHFD1	0.99165	14	64854758	320
			ADH6	0.99242	4	100125878	155
			FGA	0.99269	4	155506428	78
			SHMT1	0.99521	17	18231173	213
			SDS	0.99592	12	113830250	112
			ATP13A3	0.99658	3	194123402	273
			FURIN	0.99704	15	91416107	138
			CYP2C18	0.99767	10	96443250	237
			APOC1	0.99865	19	45417920	129
			CRADD	0.999	12	94071150	553
			FGB	0.99946	4	155484131	122
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	0.0000506	15					
			APOC3	7.2E-38	11	116700623	173
			APOA1	1.23E-29	11	116706468	171
			LCAT	0.07266	16	67973786	46
			CETP	0.13017	16	56995834	235
			SCARB1	0.14549	12	125262173	458
			AMN	0.21923	14	103388992	135
			BMP1	0.2825	8	22022652	291
			ABCG1	0.37514	21	43640007	537
			CUBN	0.46678	10	16865964	1440
			APOC2	0.52755	19	45449238	151
			ABCA1	0.72544	9	107543283	775
			PLTP	0.7649	20	44527258	148

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			ALB	0.8635	4	74269971	121
			APOE	0.91052	19	45409657	140
			A2M	0.96774	12	9220303	194
REACTOME_INTRINSIC_PATHWAY	0.0000506	15					
			KLKB1	5.86E-11	4	187148671	258
			F11	9.03E-10	4	187187117	222
			C1QBP	0.01044	17	5336098	182
			GP1BA	0.13138	17	4835569	115
			GP1BB	0.14987	22	19711065	84
			F10	0.16522	13	113777112	183
			F12	0.34372	5	176829138	83
			VWF	0.44368	12	6058039	862
			F2	0.45845	11	46740715	120
			GP9	0.63864	3	128779609	49
			KNG1	0.92929	3	186435097	363
			A2M	0.96774	12	9220303	194
			SERPING1	0.97294	11	57365704	134
			GP5	0.98428	3	194115549	194
			PRCP	0.98928	11	82535408	360
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_23	0.0000823	19					
			PAFAH1B2	1.32E-18	11	117014999	259
			PCSK7	3.59E-16	11	117075786	225
			SDHD	0.02994	11	111957547	94
			ZBTB16	0.07566	11	113931287	755
			FLI1	0.11259	11	128563810	559
			PICALM	0.12433	11	85668213	466
			ARHGEF12	0.218	11	120256002	359
			CBL	0.22815	11	119076985	194
			NUMA1	0.3904	11	71713909	250
			BIRC3	0.56556	11	102188180	116
			MAML2	0.57217	11	95709756	1392
			KMT2A	0.60235	11	118307204	193

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			CCND1	0.66236	11	69455872	138
			ATM	0.84155	11	108093558	288
			POU2AF1	0.92852	11	111222980	233
			CLP1	0.93511	11	57425215	69
			MEN1	0.93969	11	64570985	90
			DDX6	0.94747	11	118618472	228
			DDX10	0.99978	11	108535751	612
BIOCARTA_INTRINSIC_PATHWAY	0.0000823	19					
			KLKB1	5.86E-11	4	187148671	258
			F11	9.03E-10	4	187187117	222
			F2R	0.03064	5	76011867	201
			FGG	0.06555	4	155525727	77
			COL4A1	0.08922	13	110843087	1008
			SERPINC1	0.10496	1	173872941	135
			COL4A2	0.12205	13	110959630	1264
			PROS1	0.13263	3	93591880	148
			F10	0.16522	13	113777112	183
			COL4A4	0.18121	2	227867426	645
			F12	0.34372	5	176829138	83
			COL4A3	0.35329	2	228029280	972
			F2	0.45845	11	46740715	120
			KNG1	0.92929	3	186435097	363
			F5	0.93674	1	169481191	483
			SERPING1	0.97294	11	57365704	134
			PROC	0.98993	2	128175995	150
			FGA	0.99269	4	155506428	78
			FGB	0.99946	4	155484131	122
HASLINGER_B_CLL_WITH_11Q23_DELETION	0.00011	22					
			SIK3	2.78E-29	11	116714117	1128
			PCSK7	3.59E-16	11	117075786	225
			HS3ST1	0.04979	4	11399987	268
			CSPG5	0.07208	3	47603727	101

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			LPCAT1	0.07676	5	1461541	383
			PICALM	0.12433	11	85668213	466
			DMXL2	0.16869	15	51739920	522
			PABPC4	0.20457	1	40026484	144
			GSN	0.23708	9	124062078	294
			SLC4A7	0.24798	3	27414211	515
			CTSK	0.30492	1	150768683	87
			FUT8	0.47825	14	65879447	938
			BIRC2	0.47977	11	102218104	162
			CNR1	0.66202	6	88849584	192
			AHR	0.7134	7	17338275	124
			HIST1H2BG	0.78042	6	26216427	176
			UBE4A	0.78133	11	118230295	137
			PPP2R1B	0.84056	11	111608604	176
			ATM	0.84155	11	108093558	288
			CASP1	0.90713	11	104896236	181
			ADRBK2	0.95992	22	25960860	543
			DDX10	0.99978	11	108535751	612
OHGUCHI_LIVER_HNF4A_TARGETS_DN	0.00014	144					
			APOA4	4.06E-38	11	116691417	179
			F11	9.03E-10	4	187187117	222
			CYP4V2	1.21E-09	4	187112673	269
			SLC22A7	0.00013	6	43265997	101
			FABP2	0.002	4	120238404	274
			CEACAM1	0.01551	19	43011457	57
			MBL2	0.01605	10	54525139	217
			NECAB1	0.01799	8	91803920	444
			TMEM30B	0.02245	14	61744088	112
			FAM107B	0.02539	10	14560555	1243
			SARDH	0.02612	9	136528683	494
			ELOVL3	0.03382	10	103986034	66
			CYP8B1	0.04114	3	42913683	123

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			ENPP3	0.04155	6	131958374	310
			GCGR	0.06722	17	79762007	72
			SAA4	0.06727	11	18252901	184
			IYD	0.06921	6	150690027	417
			UGT2B4	0.07005	4	70345882	505
			CCBL1	0.09147	9	131595391	217
			C8B	0.09652	1	57394882	375
			BAAT	0.11249	9	104122698	221
			KMO	0.11771	1	241695433	313
			SULT1B1	0.1393	4	70592685	276
			NUDT7	0.14281	16	77756388	423
			PDZK1	0.14564	1	145727665	46
			F13B	0.14765	1	197008320	157
			MPDZ	0.15472	9	13105702	373
			PROZ	0.16373	13	113812967	114
			APOM	0.17091	6	31623670	158
			NLRP12	0.17415	19	54296854	439
			MCM10	0.18651	10	13203553	357
			PLA2G12B	0.1895	10	74694937	61
			SRD5A1	0.19321	5	6633499	314
			GJB2	0.19452	13	20761603	181
			ERBB3	0.21321	12	56473891	117
			AGMAT	0.24284	1	15898193	233
			HSD3B7	0.24654	16	30996518	67
			LIFR	0.24869	5	38475064	275
			PCYT2	0.26035	17	79860776	29
			ARHGAP9	0.26285	12	57866037	113
			SLC30A10	0.26568	1	220087605	150
			HSD17B2	0.29807	16	82068857	292
			EGFR	0.3089	7	55086724	681
			TLCD2	0.31206	17	1606083	152
			SERPINF1	0.31498	17	1665258	247

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			GCHFR	0.32083	15	41056284	102
			INSC	0.32343	11	15170647	571
			F12	0.34372	5	176829138	83
			AQP8	0.35189	16	25228284	182
			NR1I3	0.36512	1	161199455	153
			CFHR1	0.36826	1	196788860	282
			C4BPA	0.37606	1	207277606	184
			RDH5	0.39133	12	56114150	59
			HYKK	0.39367	15	78799905	181
			BDH1	0.42601	3	197236653	498
			B3GALT1	0.43352	2	168675181	320
			SLC22A9	0.44783	11	63137260	275
			ABCC6	0.47947	16	16315043	340
			S100A10	0.48769	1	151955385	163
			SERPINA1	0.4915	14	94843083	260
			TKFC	0.51557	11	61100653	51
			SERPINA4	0.51603	14	95027756	251
			APOC2	0.52755	19	45449238	151
			HEBP1	0.53897	12	13127798	173
			LIPC	0.54093	15	58724174	659
			BBOX1	0.55166	11	27062508	415
			SOAT2	0.56002	12	53497273	175
			PGLYRP2	0.56415	19	15579456	131
			ENTPD8	0.56736	9	140328815	93
			ADRA1B	0.56932	5	159343739	286
			UGT2A3	0.56981	4	69794176	255
			ABAT	0.5923	16	8814572	920
			SHMT2	0.59889	12	57624148	60
			FAM35A	0.6225	10	88854952	322
			C9	0.62631	5	39284377	360
			C8A	0.64583	1	57320442	377
			SPP2	0.64696	2	234959345	309

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			ETHE1	0.6486	19	44010870	190
			RARRES1	0.66197	3	158422439	257
			CYP7B1	0.66661	8	65508528	492
			SDR9C7	0.66821	12	57316937	135
			AADAT	0.67617	4	170981372	200
			SLC23A2	0.68744	20	4833001	591
			SLC45A3	0.7123	1	205626980	230
			CA5A	0.71425	16	87921624	537
			NLRP6	0.72352	11	278569	211
			PNPLA7	0.72702	9	140354403	240
			TFPI2	0.74012	7	93514708	184
			MFSD2A	0.77294	1	40420783	97
			TFR2	0.77807	7	100218038	100
			SLC47A1	0.7803	17	19437166	194
			AQP11	0.79209	11	77300679	154
			ASGR1	0.79352	17	7076750	91
			ZFAND4	0.81089	10	46135153	274
			CLDN1	0.81614	3	190023489	321
			MASP1	0.81646	3	186964141	380
			CIDEB	0.81663	14	24774392	137
			SLC27A5	0.81851	19	59009699	114
			RARRES2	0.82916	7	150035406	135
			FAAH	0.83599	1	46859938	153
			SLCO2B1	0.84272	11	74870843	273
			SPATA2L	0.84704	16	89762764	185
			ADH4	0.84753	4	100044807	351
			ALDH8A1	0.85237	6	135238527	148
			CMAHP	0.85392	6	25108200	424
			UGT3A2	0.85883	5	36035118	226
			ACSM1	0.85888	16	20634558	315
			DIO1	0.86196	1	54359860	205
			AADAC	0.86311	3	151531860	257

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			CYP2F1	0.86359	19	41620352	308
			PRKD3	0.87092	2	37477645	416
			PRODH2	0.87561	19	36290891	152
			GLYAT	0.87916	11	58477560	254
			CFI	0.89635	4	110661847	304
			MBL1P	0.91641	10	81679933	232
			TNFAIP8L1	0.92181	19	4640028	241
			CTSH	0.92445	15	79214091	210
			CYP2C19	0.9256	10	96522437	379
			HAO1	0.92625	20	7863630	318
			PXDC1	0.93052	6	3722835	382
			TTC39C	0.93176	18	21693316	477
			PERP	0.93423	6	138409641	225
			C6	0.93688	5	41142247	547
			VWCE	0.9483	11	61025757	72
			TPMT	0.95143	6	18128544	261
			SUCNR1	0.95188	3	151591430	150
			C8G	0.95891	9	139839697	155
			FITM1	0.95902	14	24600674	71
			DDC	0.96031	7	50560344	674
			HAAO	0.9607	2	42994228	256
			ASPDH	0.96246	19	51014856	136
			KCNN2	0.96285	5	113769226	447
			HRG	0.96356	3	186383740	169
			SC5D	0.96537	11	121163576	144
			SERPINA12	0.96892	14	94953619	290
			ACP5	0.97058	19	11685474	145
			IL1RAP	0.9791	3	190231839	618
			SLC17A3	0.98342	6	25845327	212
			CPN2	0.98685	3	194060493	287
			XYLB	0.98978	3	38388250	354
			QPRT	0.99476	16	29690440	102

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			SLC3A1	0.99557	2	44502596	245
			NOX4	0.99687	11	89222020	646
			TMC7	0.99986	16	18995608	403
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	0.00021	30					
			KLKB1	5.86E-11	4	187148671	258
			F11	9.03E-10	4	187187117	222
			C1QBP	0.01044	17	5336098	182
			FGG	0.06555	4	155525727	77
			PF4	0.09802	4	74846541	88
			SERPINC1	0.10496	1	173872941	135
			GP1BA	0.13138	17	4835569	115
			PROS1	0.13263	3	93591880	148
			F13B	0.14765	1	197008320	157
			GP1BB	0.14987	22	19711065	84
			F10	0.16522	13	113777112	183
			F7	0.33884	13	113760101	193
			F12	0.34372	5	176829138	83
			VWF	0.44368	12	6058039	862
			F2	0.45845	11	46740715	120
			GP9	0.63864	3	128779609	49
			F3	0.84123	1	94994731	101
			TFPI	0.86828	2	188343304	330
			KNG1	0.92929	3	186435097	363
			F13A1	0.93279	6	6144310	879
			F5	0.93674	1	169481191	483
			THBD	0.95391	20	23026269	122
			PF4V1	0.9557	4	74719012	141
			A2M	0.96774	12	9220303	194
			SERPING1	0.97294	11	57365704	134
			GP5	0.98428	3	194115549	194
			PRCP	0.98928	11	82535408	360
			PROC	0.98993	2	128175995	150

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			FGA	0.99269	4	155506428	78
			FGB	0.99946	4	155484131	122
LEE_LIVER_CANCER_SURVIVAL_UP	0.00023	171					
			APOA5	2.14E-38	11	116660085	134
			APOC3	7.2E-38	11	116700623	173
			KLKB1	5.86E-11	4	187148671	258
			LEAP2	0.0000166	5	132209357	87
			FMO3	0.00234	1	171060017	277
			TTBK1	0.00288	6	43211221	230
			AMT	0.00807	3	49454210	98
			TMEM176B	0.01473	7	150488375	211
			ACOX2	0.01785	3	58490862	174
			MSRA	0.03708	8	9953061	1852
			DENND5B	0.04919	12	31535156	943
			CGREF1	0.05517	2	27323461	96
			KHK	0.0672	2	27309610	84
			UGT2B4	0.07005	4	70345882	505
			FAM134C	0.09457	17	40731525	127
			LDHAL6A	0.10043	11	18477373	203
			SERPINC1	0.10496	1	173872941	135
			FLJ30679	0.11105	16	86588925	165
			MRM1	0.11236	17	34958024	124
			BAAT	0.11249	9	104122698	221
			HPD	0.11632	12	122277432	205
			SGPL1	0.11801	10	72575703	377
			MORN1	0.12502	1	2306292	446
			TTPA	0.1386	8	63972047	233
			STK32B	0.13916	4	5053243	2322
			CABIN1	0.14165	22	24407819	366
			F13B	0.14765	1	197008320	157
			MPDZ	0.15472	9	13105702	373
			F10	0.16522	13	113777112	183

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			ALAS1	0.17301	3	52232098	72
			HAGH	0.1825	16	1859103	532
			SRD5A1	0.19321	5	6633499	314
			RUNDC3B	0.21064	7	87257728	407
			NECAB2	0.21185	16	84002236	607
			C4BPB	0.22218	1	207262627	108
			CUX2	0.22606	12	111471827	512
			CYP4F11	0.23122	19	16023179	321
			ACSM5	0.25264	16	20420855	346
			ZP3	0.25956	7	76054271	336
			PCSK6	0.26021	15	101923952	1089
			PCYT2	0.26035	17	79860776	29
			DEPDC7	0.26449	11	33037727	265
			CRYL1	0.27054	13	20977805	619
			ECHS1	0.28049	10	135175986	181
			FAM169A	0.28464	5	74073398	289
			SEPT4	0.28491	17	56597610	112
			ABCG5	0.28784	2	44039610	296
			VPREB1	0.30007	22	22599191	267
			MASP2	0.30869	1	11104854	142
			SALL1	0.30886	16	51169885	103
			INSR	0.31153	19	7112265	958
			SERPINF1	0.31498	17	1665258	247
			G6PC	0.32608	17	41052813	76
			C1QTNF4	0.33232	11	47611215	63
			ACSL6	0.3356	5	131285666	171
			SELENBP1	0.33918	1	151336777	94
			F12	0.34372	5	176829138	83
			CPT2	0.34885	1	53662100	125
			CES3	0.35101	16	67001377	97
			LPIN1	0.35166	2	11886721	672
			ANXA9	0.35487	1	150954498	139

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			NDUFS2	0.35577	1	161171936	123
			STARD10	0.36599	11	72465773	199
			PKLR	0.36753	1	155259083	80
			OGDHL	0.37142	10	50942686	198
			DCXR	0.37437	17	79993756	126
			AMFR	0.38882	16	56395363	304
			RDH5	0.39133	12	56114150	59
			ABHD6	0.39473	3	58223258	386
			UNKL	0.40469	16	1448305	251
			CES2	0.41484	16	66968373	77
			C6orf106	0.41775	6	34555056	354
			PLPP1	0.41981	5	54720669	389
			MAP4K1	0.42254	19	39078279	154
			BDH1	0.42601	3	197236653	498
			CES1	0.42738	16	55836763	294
			APCS	0.44131	1	159557615	179
			C1orf115	0.44166	1	220863627	229
			DPYS	0.47086	8	105391651	385
			MTSS1	0.47932	8	125563010	865
			SLC35D1	0.48225	1	67465014	318
			CRABP1	0.48296	15	78632665	120
			ITPR2	0.48378	12	26488269	1882
			AMACR	0.49227	5	33987090	159
			CYP2J2	0.50272	1	60358979	184
			RRN3P1	0.50605	16	21807950	62
			CAND2	0.51572	3	12838170	294
			PIPOX	0.53801	17	27369917	114
			HSD17B6	0.54112	12	57157001	141
			SERPIND1	0.54159	22	21128382	167
			ABCG8	0.56245	2	44066102	447
			PINK1	0.57519	1	20959947	243
			CYP3A4	0.59613	7	99354582	68

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			NDRG2	0.61144	14	21484921	292
			AQP9	0.62001	15	58430407	338
			ZBTB22	0.62054	6	33282181	98
			KIRREL2	0.63321	19	36347951	122
			SLC6A12	0.65821	12	299242	280
			CDO1	0.65842	5	115140429	120
			ZBTB20	0.66705	3	114033346	1795
			ENPP5	0.6716	6	46126918	149
			C2	0.68129	6	31895253	254
			ALDH4A1	0.68537	1	19197923	367
			PRDX6	0.69548	1	173446485	112
			IVD	0.72431	15	40697685	145
			INSIG1	0.72537	7	155089485	279
			ABCA6	0.72579	17	67074846	210
			CRAT	0.72813	9	131857072	118
			PCK1	0.72845	20	56136136	226
			EGLN2	0.72872	19	41305333	185
			NF1	0.73007	17	29421944	456
			SLC2A2	0.75641	3	170714136	172
			ATG16L1	0.76597	2	234160216	237
			CFHR5	0.76911	1	196946666	151
			COBLL1	0.77056	2	165536694	630
			UGT2B15	0.77481	4	69512314	287
			MYRIP	0.77544	3	40141501	1597
			CYP2D6	0.78617	22	42522500	191
			ASGR1	0.79352	17	7076750	91
			MRPL46	0.79377	15	89002708	51
			IL6R	0.7999	1	154377668	258
			SLC27A5	0.81851	19	59009699	114
			SLC22A18	0.83881	11	2923649	230
			ACADS	0.84747	12	121163540	199
			SEC14L2	0.84848	22	30792929	207

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			RHBG	0.85023	1	156338979	118
			AMDHD1	0.85382	12	96337070	271
			EPHX1	0.8582	1	226013001	328
			ALDH1L1	0.85926	3	125822403	517
			DIO1	0.86196	1	54359860	205
			ITIH1	0.86641	3	52813941	112
			CLRN1	0.86787	3	150644353	276
			PAH	0.86965	12	103232103	433
			WNT11	0.87245	11	75897369	191
			ACSL1	0.87476	4	185676748	379
			PCCB	0.8751	3	135969166	208
			UGT1A6	0.87702	2	234601511	518
			SPINK2	0.87807	4	57676025	274
			GLYAT	0.87916	11	58477560	254
			SLC25A10	0.88037	17	79679265	192
			HGD	0.91112	3	120347014	342
			TACO1	0.9194	17	61678230	41
			SLC38A3	0.92335	3	50242678	96
			HAO1	0.92625	20	7863630	318
			KNG1	0.92929	3	186435097	363
			CDHR5	0.93781	11	616564	204
			ADCK3	0.93844	1	227127937	249
			TSKU	0.94036	11	76494284	148
			MOGAT1	0.94667	2	223536456	248
			PC	0.94819	11	66615996	261
			HYAL1	0.95348	3	50337319	74
			UGT3A1	0.95428	5	35960857	234
			ABCC2	0.95892	10	101542354	277
			MST1	0.96138	3	49721379	94
			AGL	0.96331	1	100326765	405
			MIR1-1HG	0.9656	20	61147659	322
			PARD3B	0.96683	2	205410515	2893

Gene set	Gene set p-value (Hypergeometric test, Bonferroni-corrected)	Number of genes in gene set	Gene name	Gene-based p-value	chr	Start	Number of SNPs
			TRIM55	0.96904	8	67039277	239
			ECHDC2	0.97109	1	53361581	93
			SERPING1	0.97294	11	57365704	134
			PHLPP1	0.97414	18	60382671	598
			SULT2A1	0.9764	19	48373722	237
			CPB2	0.97664	13	46627321	280
			CPN2	0.98685	3	194060493	287
			FBXO31	0.98707	16	87360592	369
			DSG1	0.98836	18	28898051	339
			AOX1	0.98877	2	201450730	375
			MLXIPL	0.99269	7	73007523	221
			EHHADH	0.99302	3	184908411	229
			CCL16	0.99599	17	34303528	202
			MVK	0.99811	12	110011499	244

Supplementary Table 6: HDL-susceptibility SNPs derived from Willer et al. (1) including the original association result on HDL cholesterol and the p-value from the apoA-IV GWA meta-analysis.

			Reported results from original publication					
SNP	Chr	position	Reported Gene	n total	effect estimate	effect allele	reported p-value	p-value from apoA-IV GWA&
rs964184	11	116648917	APOA1	94000	0.106	C	6.00E-48	**0.0001**
rs16942887	16	67928042	LCAT	186000	0.083	A	8.00E-54	0.0022
rs4650994	1	178515312	ANGPTL1	187000	0.02	G	7.00E-09	0.0046
rs7241918	18	47160953	LIPG	93000	-0.09	G	1.00E-44	0.0114
rs2290547	3	47061183	SETD2	187000	-0.03	A	4.00E-09	0.0144
rs4142995	7	17919258	SNX13	165000	-0.03	T	9.00E-12	0.0216*
rs4765127	12	124460167	ZNF664	94000	0.032	T	8.00E-10	0.0424
rs11869286	17	37813856	STARD3	178000	-0.032	G	3.00E-17	0.0442*
rs4731702	7	130433384	KLF14	187000	0.029	T	5.00E-17	0.0521
rs4148008	17	66875294	ABCA8	166000	-0.028	G	1.00E-12	0.0594
rs4917014	7	50305863	IKZF1	187000	0.02	G	1.00E-08	0.0758
rs12678919	8	19844222	LPL	187000	0.155	G	1.00E-149	0.1142*
rs7255436	19	8433196	ANGPTL4	93000	-0.032	C	2.00E-08	0.1258
rs838880	12	125261593	SCARB1	173000	0.048	C	6.00E-32	0.1584
rs13326165	3	52532118	STAB1	187000	0.03	A	9.00E-11	0.1623
rs4420638	19	45422946	APOE	100000	-0.067	G	2.00E-21	0.1780
rs1532085	15	58683366	LIPC	185000	0.107	A	1.00E-188	0.1834
rs2923084	11	10388782	AMPD3	187000	-0.026	G	5.00E-08	0.1907
rs2293889	8	116599199	TRPS1	180000	-0.031	T	4.00E-17	0.1976
rs12967135	18	57849023	MC4R	154000	-0.026	A	4.00E-08	0.2071
rs17145738	7	72982874	MLXIPL	185000	0.041	T	5.00E-13	0.2152
rs2925979	16	81534790	CMIP	186000	-0.035	T	1.00E-19	0.2277
rs12748152	1	27138393	PIGV-NR0B2	187000	-0.05	T	1.00E-15	0.2281
rs17173637	7	150529449	TMEM176A	184000	-0.04	C	2.00E-08	0.2311
rs1121980	16	53809247	FTO	186000	-0.02	A	7.00E-09	0.3018*
rs605066	6	139829666	CITED2	94000	-0.028	C	3.00E-08	0.3127
rs3764261	16	56993324	CETP	178000	0.241	A	1.00E-769	0.3175
rs2954029	8	126490972	TRIB1	187000	0.04	T	3.00E-29	0.3220
rs12145743	1	156700651	HDGF-PMVK	181000	0.02	G	2.00E-08	0.3399
rs2013208	3	50129399	RBM5	170000	0.03	T	9.00E-12	0.3723
rs13076253	3	131751775	ACAD11	187000	0.0283	A	5.00E-09	0.3749
rs702485	7	6449272	DAGLB	187000	0.02	G	6.00E-12	0.3881*
rs1936800	6	127436064	RSPO3	187000	0.02	C	3.00E-10	0.3956
rs6065906	20	44554015	PLTP	186000	-0.059	C	5.00E-40	0.4024
rs12801636	11	65391317	KAT5	187000	0.02	A	3.00E-08	0.4104
rs4129767	17	76403984	PGS1	185000	-0.024	G	2.00E-11	0.4460*
rs174546	11	61569830	FADS1-2-3	187000	-0.039	T	8.00E-28	0.4712
rs2972146	2	227100698	IRS1	184000	0.032	G	2.00E-17	0.4814
rs7941030	11	122522375	UBASH3B	187000	0.027	C	1.00E-14	0.4970
rs10019888	4	26062990	C4orf52	187000	-0.03	G	5.00E-08	0.5123

… to be continued

Supplementary Table 6: continued

			Reported results from original publication					
SNP	Chr	position	Reported Gene	n total	effect estimate	effect allele	reported p-value	p-value from apoA-IV GWA[&]
rs181362	22	21932068	UBE2L3	178000	-0.038	T	4.00E-18	0.5324
rs6805251	3	119560606	GSK3B	186000	0.02	T	1.00E-08	0.5399
rs4846914	1	230295691	GALNT2	187000	-0.048	G	4.00E-41	0.5637
rs11246602	11	51512090	OR4C46	176000	0.03	C	2.00E-10	0.5641
rs3822072	4	89741269	FAM13A	187000	-0.03	A	4.00E-12	0.5749
rs2652834	15	63396867	LACTB	186000	-0.028	A	4.00E-11	0.5868
rs998584	6	43757896	VEGFA	184000	-0.026	A	2.00E-11	0.5968
rs1689800	1	182168885	ZNF648	187000	-0.034	G	5.00E-20	0.6055
rs3136441	11	46743247	LRP4	187000	0.054	C	7.00E-29	0.6095
rs7134594	12	110000193	MVK	94000	-0.035	C	2.00E-13	0.6132
rs731839	19	33899065	PEPD	185000	-0.022	G	3.00E-09	0.6304
rs6450176	5	53298025	ARL15	187000	-0.025	A	7.00E-10	0.6483
rs4759375	12	123796238	SBNO1	94000	0.056	T	3.00E-08	0.6621
rs1800961	20	43042364	HNF4A	158000	-0.127	T	2.00E-34	0.6627
rs4660293	1	40028180	PABPC4	187000	-0.035	G	3.00E-18	0.6827
rs386000	19	54792761	LILRA3	165000	0.048	C	3.00E-23	0.6950
rs2602836	4	100014805	ADH5	187000	0.02	A	5.00E-08	0.7217
rs12328675	2	165540800	COBLL1	187000	0.045	C	2.00E-15	0.7230
rs581080	9	15305378	TTC39B	187000	-0.042	G	1.00E-19	0.7231
rs1047891	2	211540507	CPS1	182000	-0.03	A	9.00E-10	0.7985
rs9987289	8	9183358	PPP1R3B	169000	-0.082	A	2.00E-41	0.8036
rs1883025	9	107664301	ABCA1	186000	-0.07	T	2.00E-65	0.8095
rs499974	11	75455021	MOGAT2-DGAT2	187000	-0.03	A	1.00E-08	0.8164
rs11613352	12	57792580	LRP1	187000	0.028	T	2.00E-13	0.8307
rs13107325	4	103188709	SLC39A8	179000	-0.071	T	1.00E-15	0.8452
rs2606736	3	11400249	ATG7	129000	0.03	C	5.00E-08	0.8523
rs4983559	14	105277209	ZBTB42-AKT1	184000	0.02	G	1.00E-08	0.8870
rs970548	10	46013277	MARCH8-ALOX5	187000	0.03	C	2.00E-10	0.9003
rs7134375	12	20473758	PDE3A	187000	0.021	A	1.00E-08	0.9112
rs17695224	19	52324216	HAS1	185000	-0.03	A	2.00E-13	0.9841

[&] P-value derived from meta-analysis results of the discovery studies on log-transformed ApoA-IV levels (age-and sex-adjusted); p-values based on a fixed effect(FE) model, besides the one marked with a star (*), where RE model was used. Significant p-values are written in bold font.

Supplementary Table 7: TG-susceptibility SNPs, derived from Willer et al. (1) with their original association result on TG and the p-value from the apoA-IV GWA meta-analysis.

			Reported results from original publication (Willer et al.)					
SNP	Chr	position	Reported Gene	n total	effect estimate	effect allele	reported p-value	p-value from apoA-IV GWA[&]
rs964184	11	116648917	APOA1	91000	-0.234	C	7.00E-224	**0.0001**
rs10761731	10	65027610	JMJD1C	91000	-0.031	T	8.00E-12	0.0039
rs4765127	12	124460167	ZNF664	91000	-0.029	T	2.00E-08	0.0424
rs2068888	10	94839642	CYP26A1	178000	-0.024	A	2.00E-11	0.0555
rs11776767	8	10683929	PINX1	177000	0.022	C	3.00E-11	0.0958
rs1260326	2	27730940	GCKR	178000	0.115	T	2.00E-239	0.1092
rs12678919	8	19844222	LPL	178000	-0.17	G	2.00E-199	0.1142*
rs442177	4	88030261	KLHL8	178000	-0.031	G	1.00E-18	0.1230
rs10401969	19	19407718	CILP2	176000	-0.121	C	1.00E-69	0.1351
rs6831256	4	3473139	LRPAP1	177000	0.026	G	2.00E-12	0.1401
rs1532085	15	58683366	LIPC	176000	0.031	A	2.00E-18	0.1834
rs17145738	7	72982874	MLXIPL	176000	-0.115	T	9.00E-99	0.2152
rs2412710	15	42683787	CAPN3	154000	0.099	A	2.00E-11	0.2219
rs12748152	1	27138393	PIGV, NR0B2	178000	0.037	T	1.00E-09	0.2281
rs8077889	17	41878166	MPP3	176000	0.025	C	1.00E-08	0.2333
rs4722551	7	25991826	MIR148A	178000	0.023	C	9.00E-11	0.2603
rs645040	3	135926622	MSL2L1	178000	-0.029	G	2.00E-12	0.2965
rs1121980	16	53809247	FTO	155000	0.021	A	3.00E-08	0.3018*
rs3764261	16	56993324	CETP	169000	-0.04	A	2.00E-25	0.3175
rs2954029	8	126490972	TRIB1	178000	-0.076	T	1.00E-107	0.3220
rs1936800	6	127436064	RSPO3	168000	-0.02	C	3.00E-08	0.3956
rs6065906	20	44554015	PLTP	176000	0.053	C	2.00E-34	0.4024
rs174546	11	61569830	FADS1, FADS2, FADS3	178000	0.045	T	7.00E-38	0.4712
rs2972146	2	227100698	IRS1	175000	-0.028	G	3.00E-15	0.4814
rs7248104	19	7224431	INSR	176000	-0.022	A	5.00E-10	0.4870
rs9686661	5	55861786	MAP3K1	177000	0.038	T	3.00E-16	0.4889
rs2131925	1	63025942	ANGPTL3	178000	-0.066	G	3.00E-74	0.4977
rs38855	7	116358044	MET	178000	-0.019	G	2.00E-08	0.5377
rs4846914	1	230295691	GALNT2	178000	0.04	G	7.00E-31	0.5637
rs998584	6	43757896	VEGFA	175000	0.029	A	3.00E-15	0.5968
rs731839	19	33899065	PEPD	176000	0.022	G	3.00E-09	0.6304
rs2929282	15	44245931	FRMD5	84000	0.072	T	2.00E-09	0.6703
rs3198697	16	15129940	PDXDC1	176000	-0.02	T	2.00E-08	0.6871
rs5756931	22	38546033	PLA2G6	174000	-0.02	C	3.00E-08	0.7652
rs6882076	5	156390297	TIMD4	178000	-0.029	T	2.00E-15	0.8102
rs11613352	12	57792580	LRP1	178000	-0.028	T	9.00E-14	0.8307
rs1832007	10	5254847	AKR1C4	178000	-0.033	G	2.00E-12	0.9346
rs1495741	8	18272881	NAT2	88000	0.04	G	3.00E-12	0.9535

[&] P-value derived from meta-analysis results of the discovery studies on log-transformed ApoA-IV levels (age-and sex-adjusted); p-values based on a fixed effect(FE) model, besides the one marked with a star (*), where RE model was used. Significant p-values are written in bold font.

Supplementary Table 8: Kidney function-susceptibility SNPs, derived from Pattaro et al. (2) with their original association result on eGFRcrea and the p-value from the apoA-IV GWA meta-analysis.

		Reported results from original publication (Willer et al.)						
SNP	Chr	position	Reported Gene	n total	effect estimate	effect allele	reported p-value	p-value from apoA-IV GWA
rs13329952	16	20366507	UMOD	133413	-0.0158	T	9.47E-43	0.0069
rs807601	2	15793014	DDX1	133413	0.0064	T	6.60E-12	0.0115
rs716877	13	72347448	DACH1	133413	0.0049	C	6.22E-08	0.0317
rs12460876	19	33356891	SLC7A9	133413	-0.0066	T	1.86E-13	0.0414
rs11657044	17	59450105	BCAS3	133413	-0.0115	T	7.89E-22	0.0486
rs17216707	20	52732362	BCAS1	175579	-0.0077	T	8.83E-15	0.0533
rs9916302	17	37499949	CDK12 / FBXL20	133413	-0.008	T	4.78E-15	0.0631
rs2467853	15	45698793	GATM	133413	0.0126	T	1.05E-42	0.0636
rs4014195	11	65506822	AP5B1	175579	0.0055	C	1.10E-11	0.0970
rs1260326	2	27730940	GCKR	133413	0.0068	T	3.38E-14	0.1092
rs3758086	8	23714992	STC1	133413	-0.0071	A	1.71E-15	0.1161
rs2861422	3	141724644	TFDP2	133413	0.0074	T	9.12E-14	0.1226
rs17319721	4	77368847	SHROOM3	133413	-0.0114	A	1.32E-37	0.1266
rs10277115	7	1285195	UNCX	175579	0.009	A	8.72E-14	0.1315
rs267734	1	150951477	LASS2	133413	-0.0079	T	4.01E-13	0.1740
rs6420094	5	176817636	SLC34A1	133413	0.0096	A	4.92E-22	0.1754
rs2802729	1	243501763	SDCCAG8	175579	-0.0046	A	2.20E-08	0.1819
rs4744712	9	71434707	PIP5K1B	133413	-0.0071	A	4.29E-15	0.1918
rs4667594	2	170008506	LRP2	175579	-0.0044	A	3.52E-08	0.2112
rs228611	4	103561709	NFKB1	175579	-0.0056	A	3.58E-12	0.2149
rs10491967	12	3368093	TSPAN9	175579	-0.0095	A	5.18E-14	0.2285
rs3750082	7	32919927	KBTBD2	175579	0.0045	A	3.22E-08	0.2509
rs163160	11	2789955	KCNQ1	154881	0.0065	A	2.26E-09	0.2710
rs164748	16	89708292	DPEP1	154881	0.0046	C	1.95E-08	0.2925
rs8091180	18	77164243	NFATC1	154881	-0.006	A	1.28E-09	0.2970
rs848490	7	77555005	TMEM60	133413	0.0073	C	7.80E-13	0.3122
rs3850625	1	201016296	CACNA1S	154881	0.0083	A	6.82E-11	0.3264
rs12136063	1	110014170	SYPL2	175579	0.0045	A	4.71E-08	0.3633
rs963837	11	30749090	MPPED2	133413	-0.0078	T	5.69E-18	0.3795
rs1800615	1	15832281	CASP9	133413	-0.0058	T	1.90E-09	0.4011
rs6088580	20	33285053	TP53INP2	175579	-0.0049	C	1.79E-09	0.4764
rs9682041	3	170091902	SKIL	154881	-0.0068	T	2.58E-08	0.4933
rs7805747	7	151407801	PRKAG2	133413	-0.013	A	7.96E-29	0.4942
rs7956634	12	15321194	PTPRO	175579	-0.0068	T	7.17E-12	0.5277
rs6795744	3	13906850	WNT7A	175579	0.006	A	3.33E-08	0.5444
rs6459680	7	156258568	RNF32	175579	-0.0055	T	1.07E-09	0.5552
rs9472135	6	43809802	VEGFA	133413	-0.008	T	3.34E-15	0.5823
rs7422339 / rs1047891	2	211540507	CPS1	133413	-0.0106	A	2.18E-23	0.7985
rs316009	6	160675764	SLC22A2	133413	0.0131	T	4.38E-19	0.8113
rs1106766	12	57809456	INHBC	175579	0.0061	T	2.41E-09	0.8303

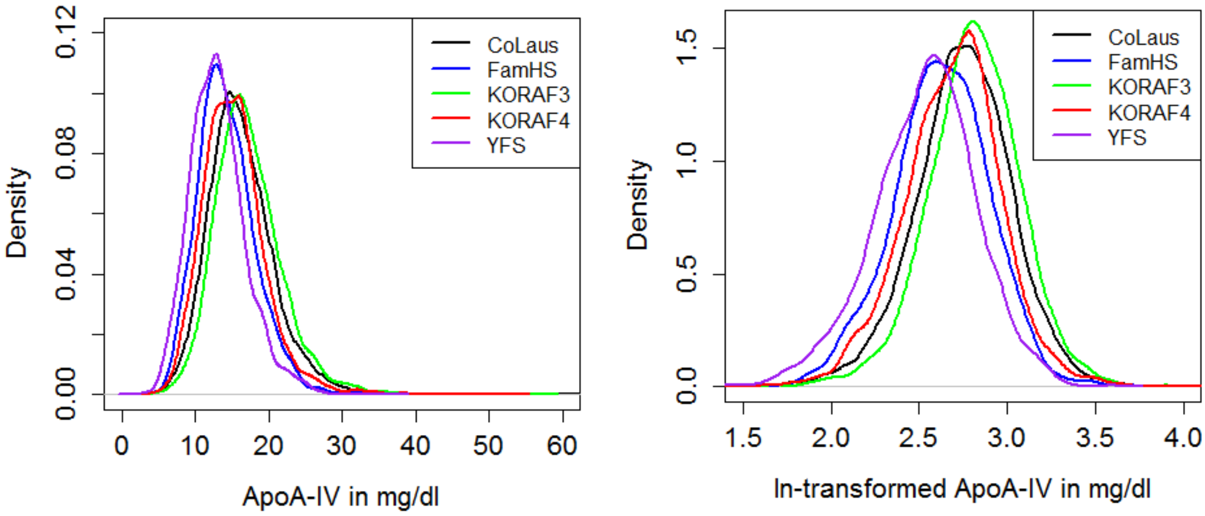
… to be continued

Supplementary Table 8: continued

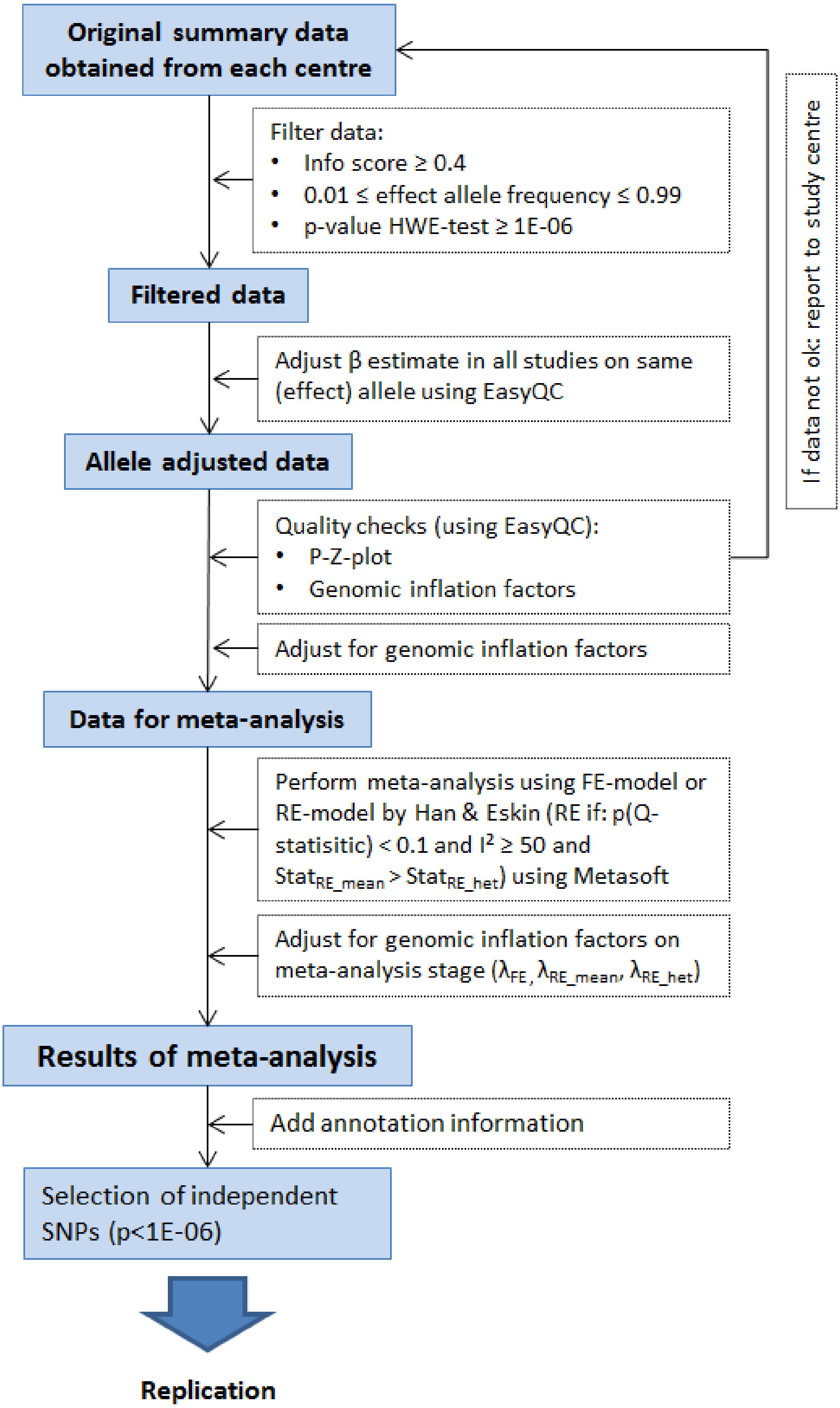
			Reported results from original publication (Willer et al.)					
SNP	Chr	position	Reported Gene	n total	effect estimate	effect allele	reported p-value	p-value from apoA-IV GWA
rs11959928	5	39397132	DAB2	133413	-0.0083	A	1.66E-20	0.8314
rs11666497	19	38464262	SIPA1L3	175579	-0.0058	T	4.25E-08	0.8406
rs491567	15	53946593	WDR72	133413	-0.0084	A	2.86E-15	0.8697
rs1394125	15	76158983	UBE2Q2	133413	-0.0073	A	5.47E-14	0.9061
rs476633	15	41392134	INO80	133413	0.0051	C	8.90E-09	0.9220
rs6546838	2	73679280	ALMS1	133413	-0.0093	A	7.72E-20	0.9222
rs1044261	10	1065710	WDR37	133413	-0.0113	T	1.21E-11	0.9339
rs2453580	17	19438321	SLC47A1	133413	0.0064	T	2.93E-11	0.9433
rs10774021	12	349298	SLC6A13	133413	-0.0063	T	4.77E-12	0.9478
rs2712184	2	217682779	IGFBP5	154881	-0.0053	A	1.33E-10	0.9498
rs10994860	10	52645424	A1CF	154881	0.0077	T	1.07E-12	0.9694
rs10513801	3	185822353	ETV5	154881	0.0072	T	1.03E-09	0.9805
rs7759001	6	27341409	ZNF204	175579	-0.0051	A	1.75E-08	0.9842

[&] P-value derived from meta-analysis results of the discovery studies on log-transformed ApoA-IV levels (age-and sex-adjusted); p-values based on a fixed effect(FE) model, besides the one marked with a star (*), where RE model was used. Significant p-values are written in bold font.

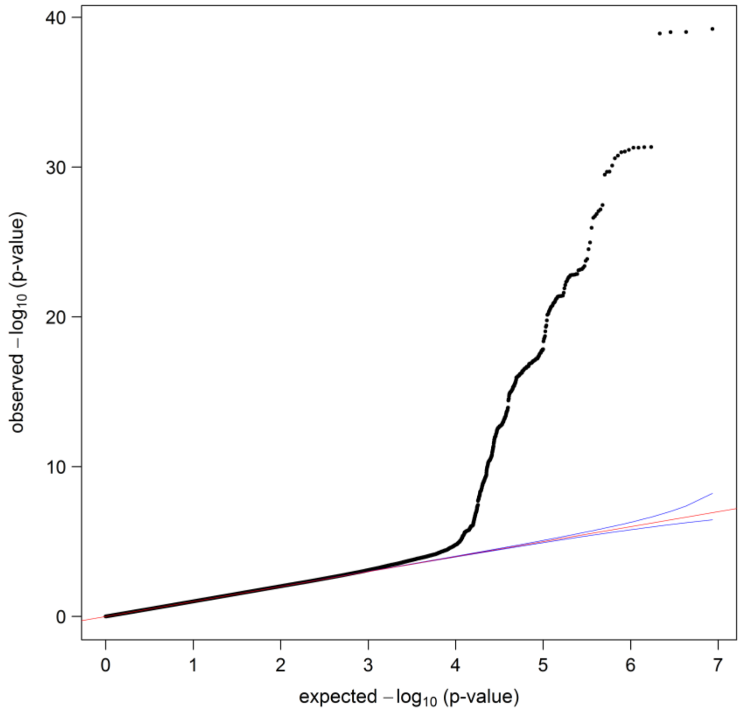
Supplementary Figures



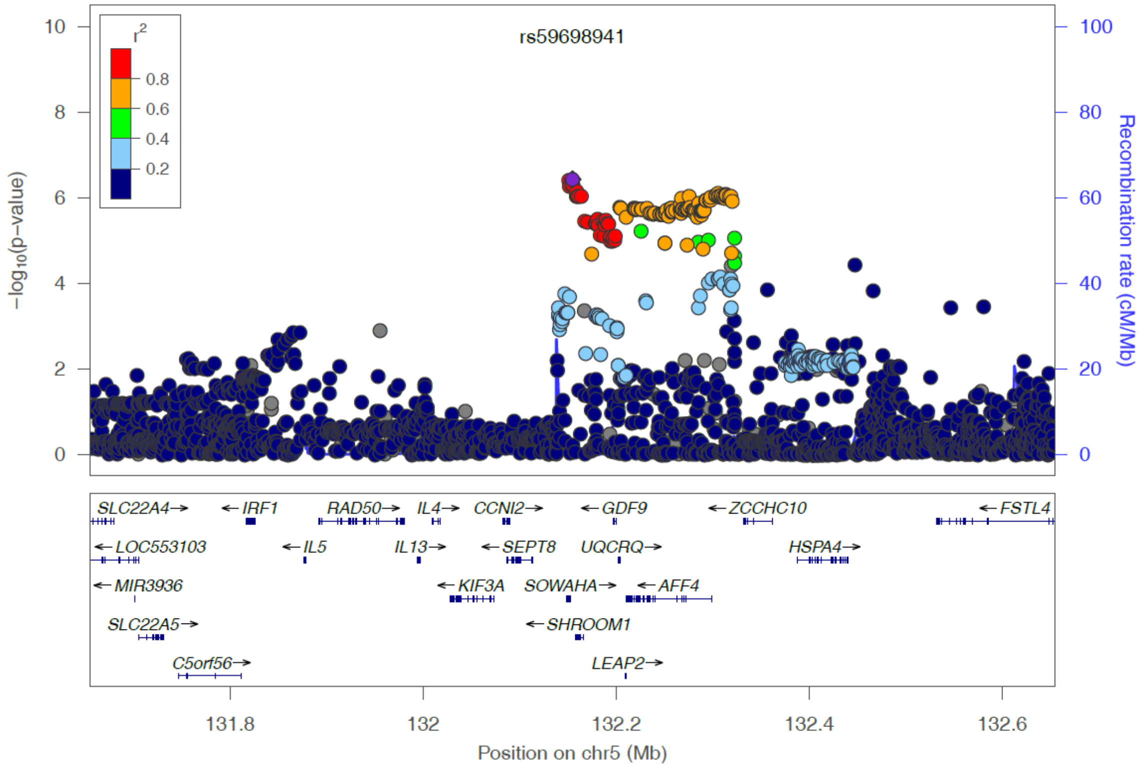
Supplementary Figure 1: Distribution of apoA-IV concentrations in all discovery cohorts



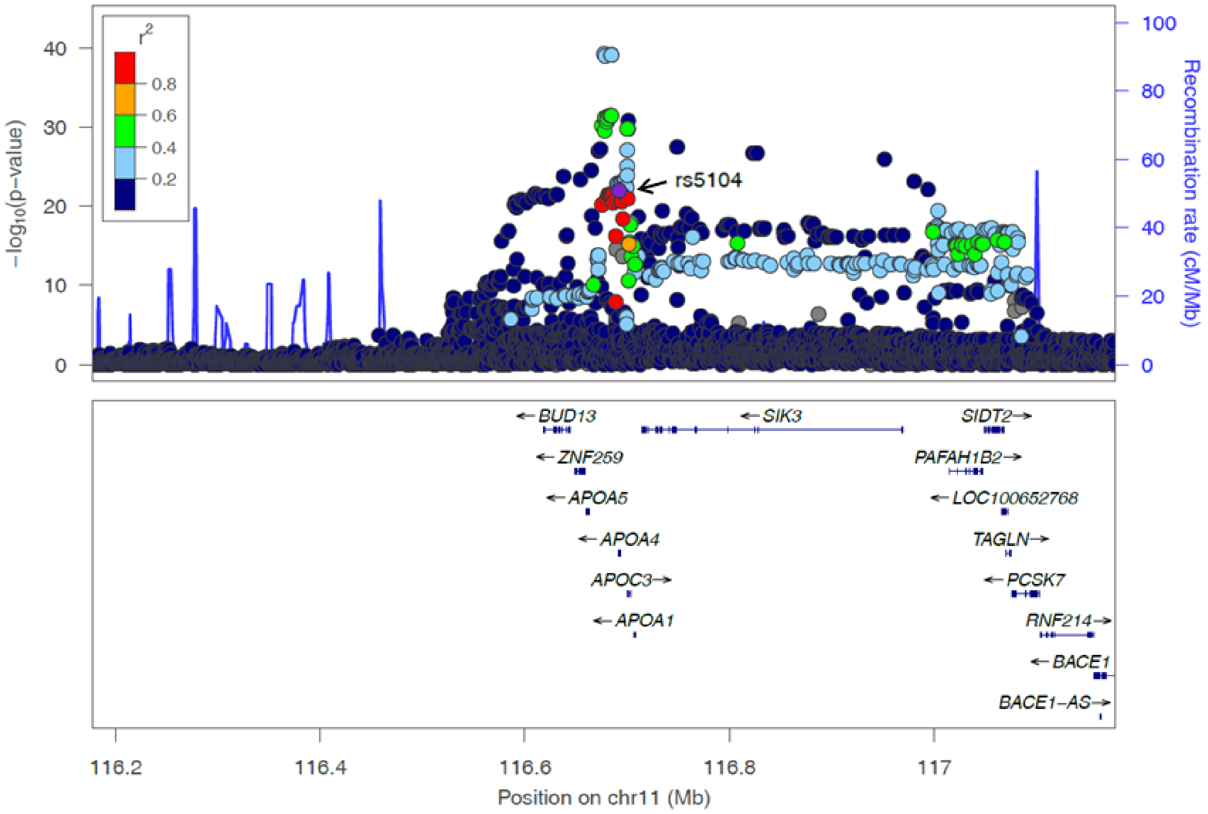
Supplementary Figure 2: Quality control and Meta-Analysis Workflow



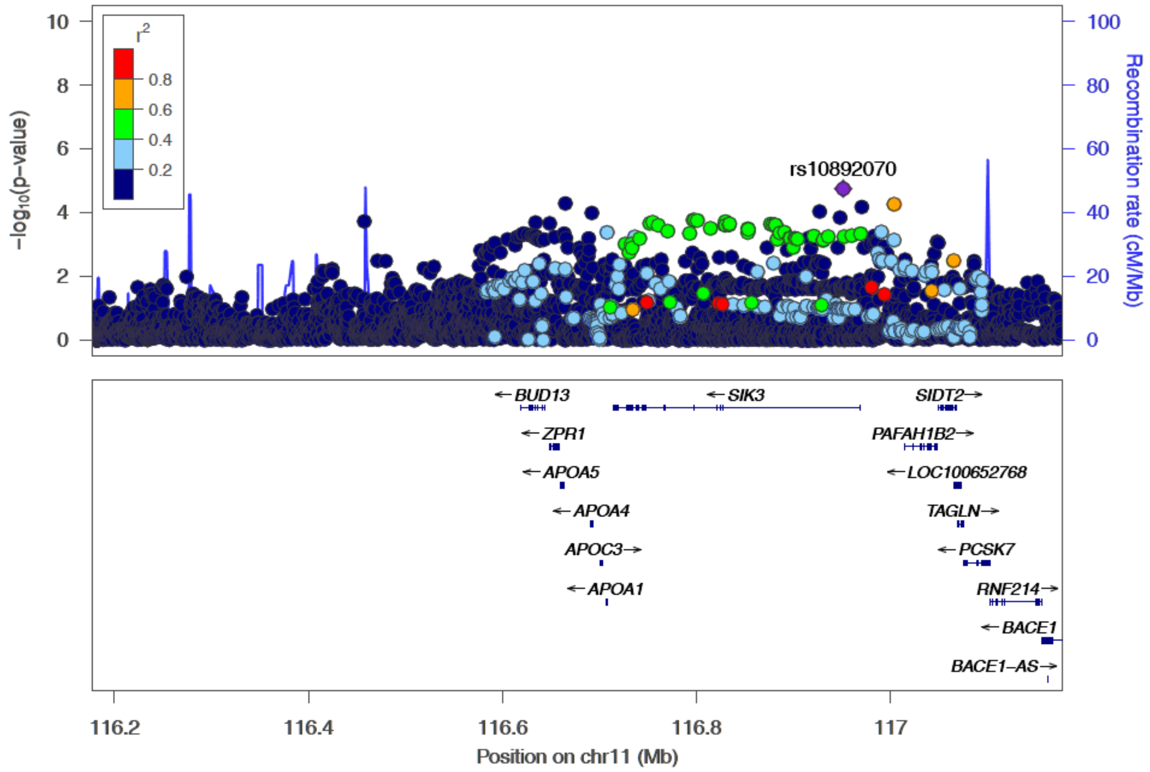
Supplementary Figure 3: QQ-plot for the meta-analysis on log-transformed apoA-IV values



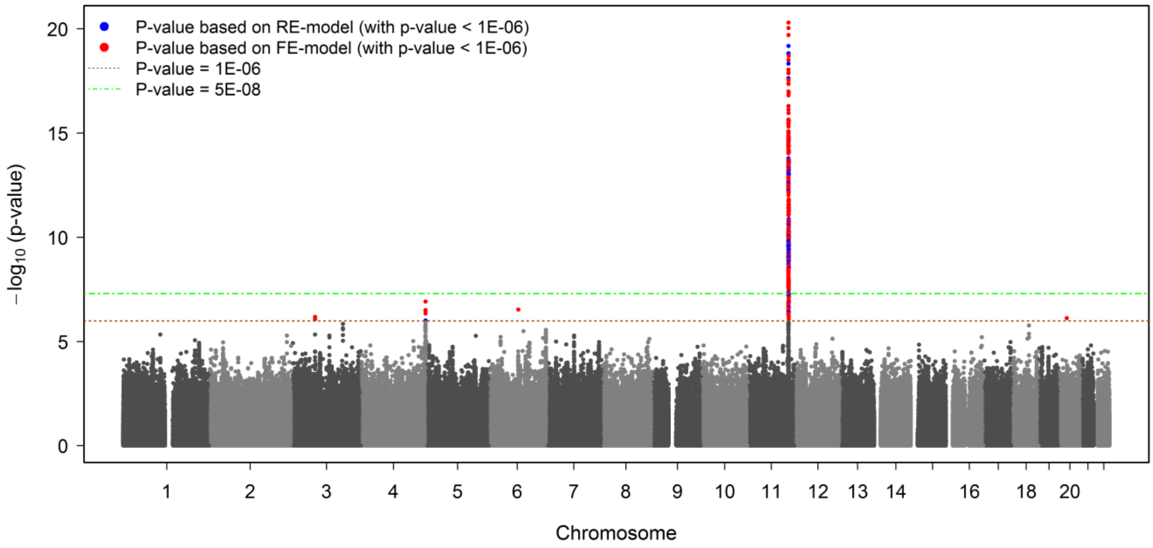
Supplementary Figure 4: Regional plot showing the genomic region defined by the *SOWAHA*-lead SNP rs59698941 +/- 500 kB (LD refers to rs59698941, based on 1000G EUR); p-values are derived from the meta-analysis on the five discovery cohorts on log-transformed apoA-IV concentrations.



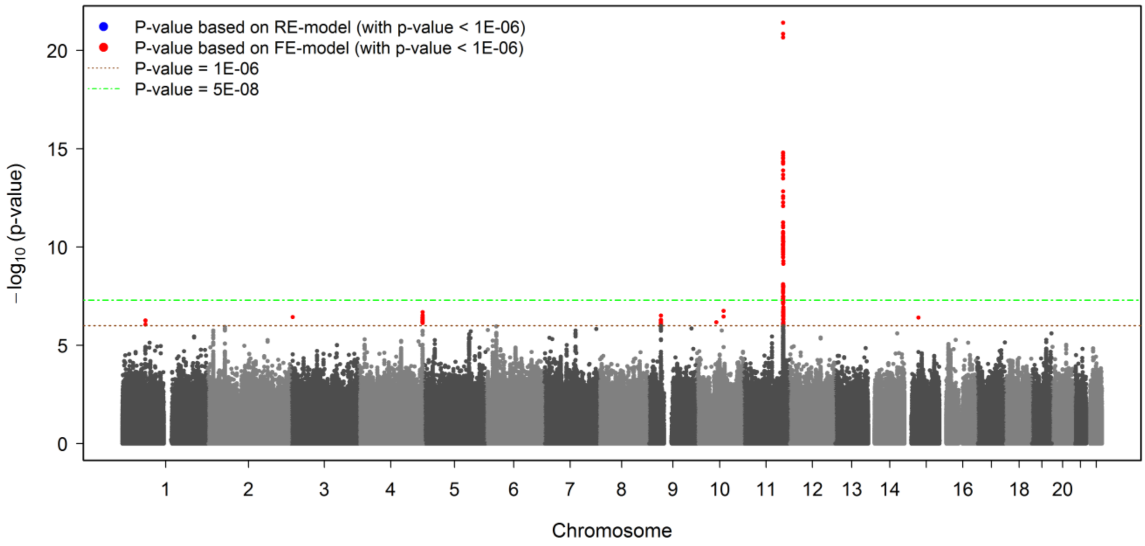
Supplementary Figure 5: Regional plot showing the genomic region defined by the *APOA4*-lead SNP rs1729407 +/- 500 kB (LD refers to rs5104, based on 1000G EUR); p-values are derived from the meta-analysis on the five discovery cohorts on log-transformed apoA-IV concentrations.



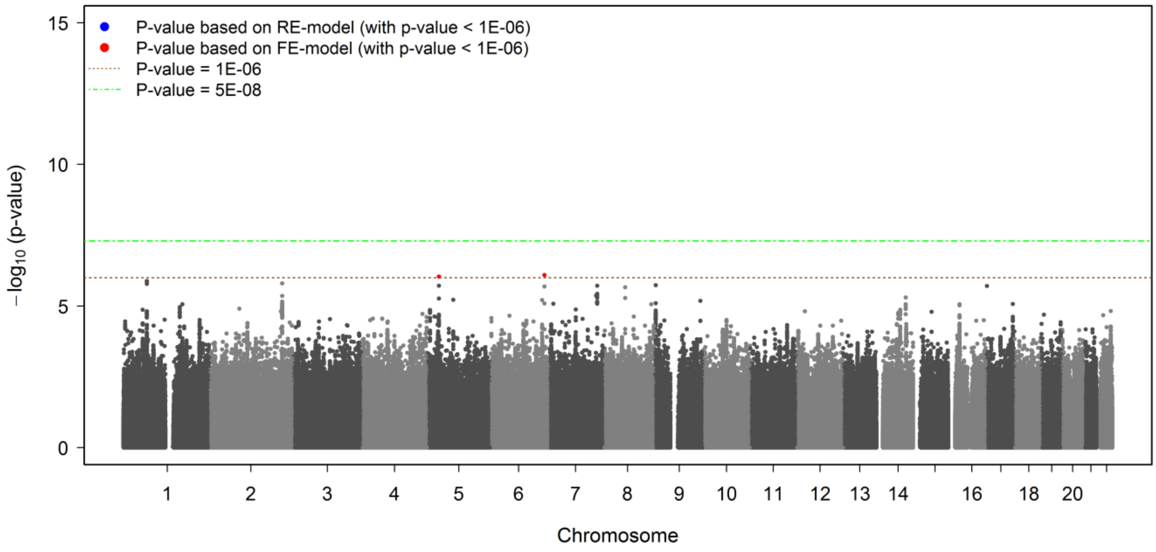
Supplementary Figure 6: Regional plot showing the genomic region defined by the *APOA4*-lead SNP rs1729407 +/- 500 kB (LD refers to rs10892070, based on 1000G EUR); p-values are derived from a conditional analysis, adjusting for rs1729407 and rs5104 (based on meta-analyzed results from the five discovery cohorts).



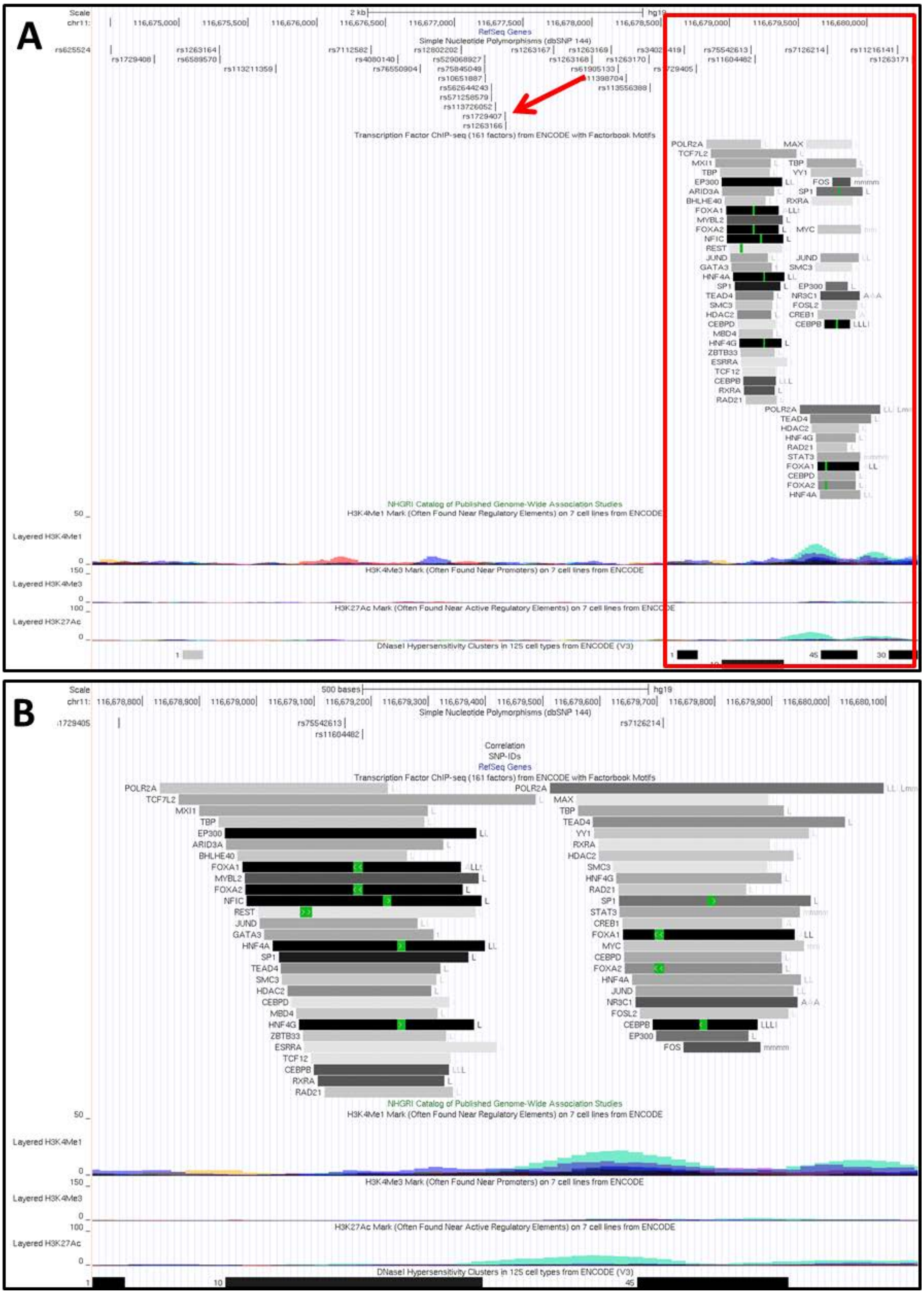
Supplementary Figure 7: Manhattan-plot for the meta-analysis on log-transformed apoA-IV values, only in men, based on five discovery cohorts.



Supplementary Figure 8: Manhattan-plot for the meta-analysis on log-transformed apoA-IV values, only in women, based on five discovery cohorts.



Supplementary Figure 9: Manhattan-plot for the meta-analysis on gender-interaction effects on log-transformed apoA-IV values, based on the five discovery cohorts.



Supplementary Figure 10: Regulatory chromatin elements from ENCODE near rs1729407. Panel A: Six kb large region centered on rs1729407 (indicated by a red arrow.)The top row shows the location of all SNPs from dbSNP144 with a MAF > 1%. The rows below indicate the binding sites of transcription factors (grey to black boxes), known GWAS hits (green, no hits present in the figure), regulatory element-specific histone marks, promoter-specific histone marks, active regulatory elements-specific histone marks and DNAse I hypersensitivity sites. Data was retrieved from the UCSC Genome browser (3) hg19 as described before (4). A large cluster of transcription factor binding sites is present about 1-1.5 kb downstream of rs1729407 (red box) Panel B. Enlarged transcription factor binding sites cluster. Four SNPs with a MAF > 1% are located in this region. The r^2 (D') with rs1729407 are: rs1729405: r^2=1(1); rs75542613: r^2<0.1 (n.a.) rs11604482: no data in SNiPA; rs7216214: r^2=0.1 (-1).

Supplementary References

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