

Table of Contents

Table 1. Genotyping, quality control, imputation, and analysis methods in the participating studies	2
Figure 1. QQ-Plot.....	3
Figure 2a. Regional Association Plot, rs17216707.....	4
Figure 2b. Regional Association Plot, rs2769071.....	5
Figure 2c. Regional Association Plot, rs11741640.....	6
Figure 2d. Regional Association Plot, rs17479566.....	7
Figure 2e. Regional Association Plot, rs9925837.....	8
Figure 3. Manhattan Plot, Model 2, European Ancestry	9
Figure 4a. Forest plot of beta-coefficients for rs17216707 from individual studies (Model 1)	10
Figure 4b. Forest plot of beta-coefficients for rs2769071 from individual studies (Model 1)	10
Figure 4c. Forest plot of beta-coefficients for rs11741640 from individual studies (Model 1)	11
Figure 4d. Forest plot of beta-coefficients for rs17479566 from individual studies (Model 1)	11
Figure 4e. Forest plot of beta-coefficients for rs9925837 from individual studies (Model 1)	12
Supplementary Table 2. Annotated SNPs demonstrating suggestive significance.....	13
Supplementary Table 3. Associations of top SNPs with ln-transformed intact FGF23 concentration..	25
Supplementary Table 4. Genetically predicted gene expression results	26

Table 1. Genotyping, quality control, imputation, and analysis methods in the participating studies

Study	Genotyping Platform/Chip	SNP Inclusion Criteria			Genomic control parameter
		SNP Call rate	MAF	HWE p-value	
ARIC	Affymetrix 6.0	≥ 0.95	≥ 0.01	$\geq 10^{-4}$	1.036
CHS	European ancestry: Illumina 370CNV BeadChip merged with IBC Illumina iSELECT African ancestry: Illumina Human Omni1-Quad_v1	≥ 0.97	≥ 0.01	$\geq 10^{-4}$	1.009
Indiana	Illumina Quad 660 BeadChip	≥ 0.95	≥ 0.03	$\geq 10^{-4}$	1.175
MESA	Affymetrix 6.0	≥ 0.95	≥ 0.01	$\geq 10^{-4}$	1.020
MrOS (GBG and Malmo)	Illumina Human Omni1-Quad_v1	≥ 0.98	≥ 0.01	$\geq 10^{-4}$	1.023
OPRA	Affymetrix 6.0	≥ 0.97	≥ 0.01	$\geq 10^{-4}$	1.014

*CHS additionally excluded for heterozygote frequency=0, ≥ 1 duplicate error, or Mendelian inconsistency in HapMap controls.

All cohorts used EIGENSTRAT for principal components of ancestry computation.

Figure 1. QQ-Plot (Genomic inflation factor $\lambda=1.007$)

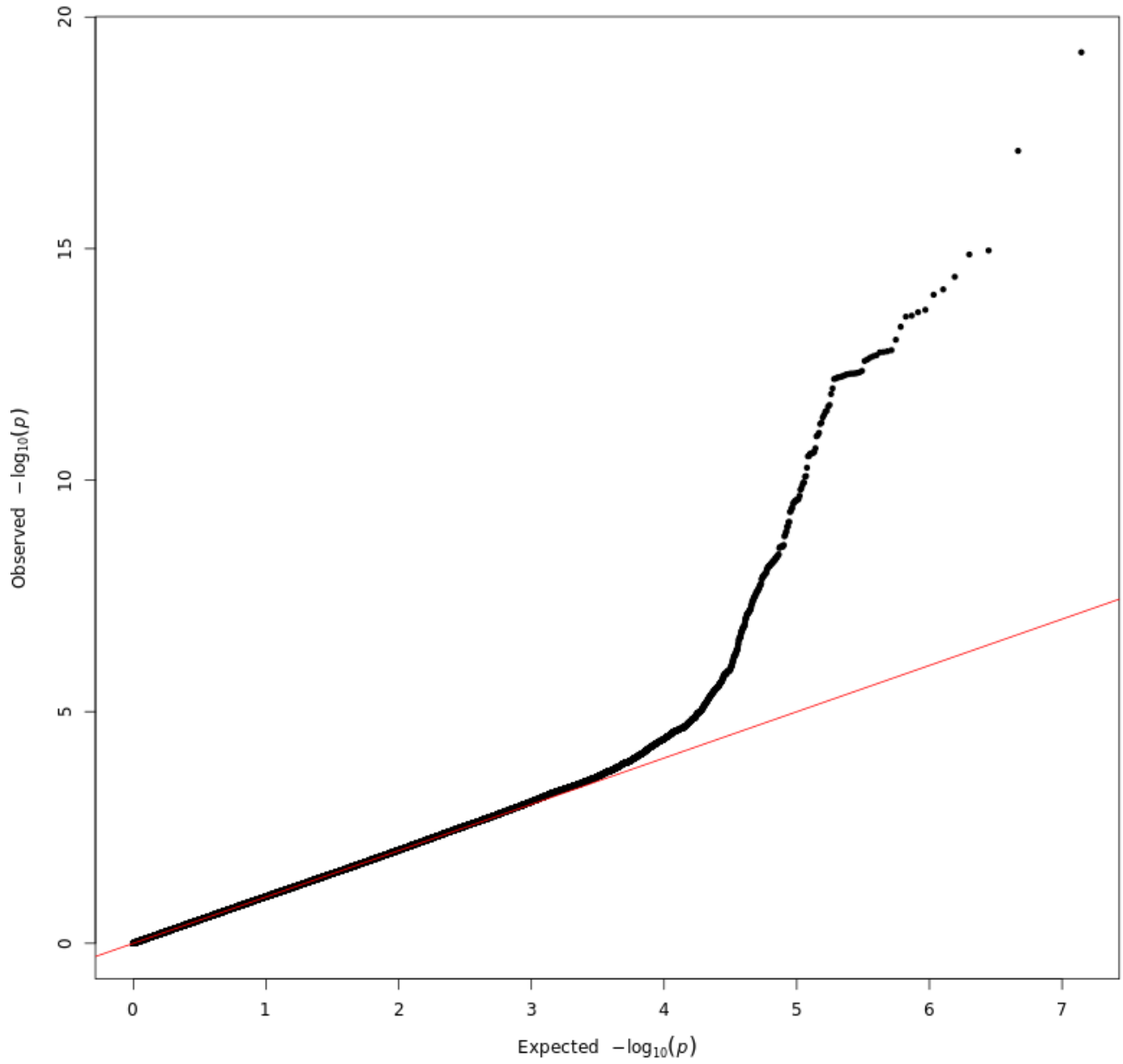


Figure 2a. Regional Association Plot, rs17216707

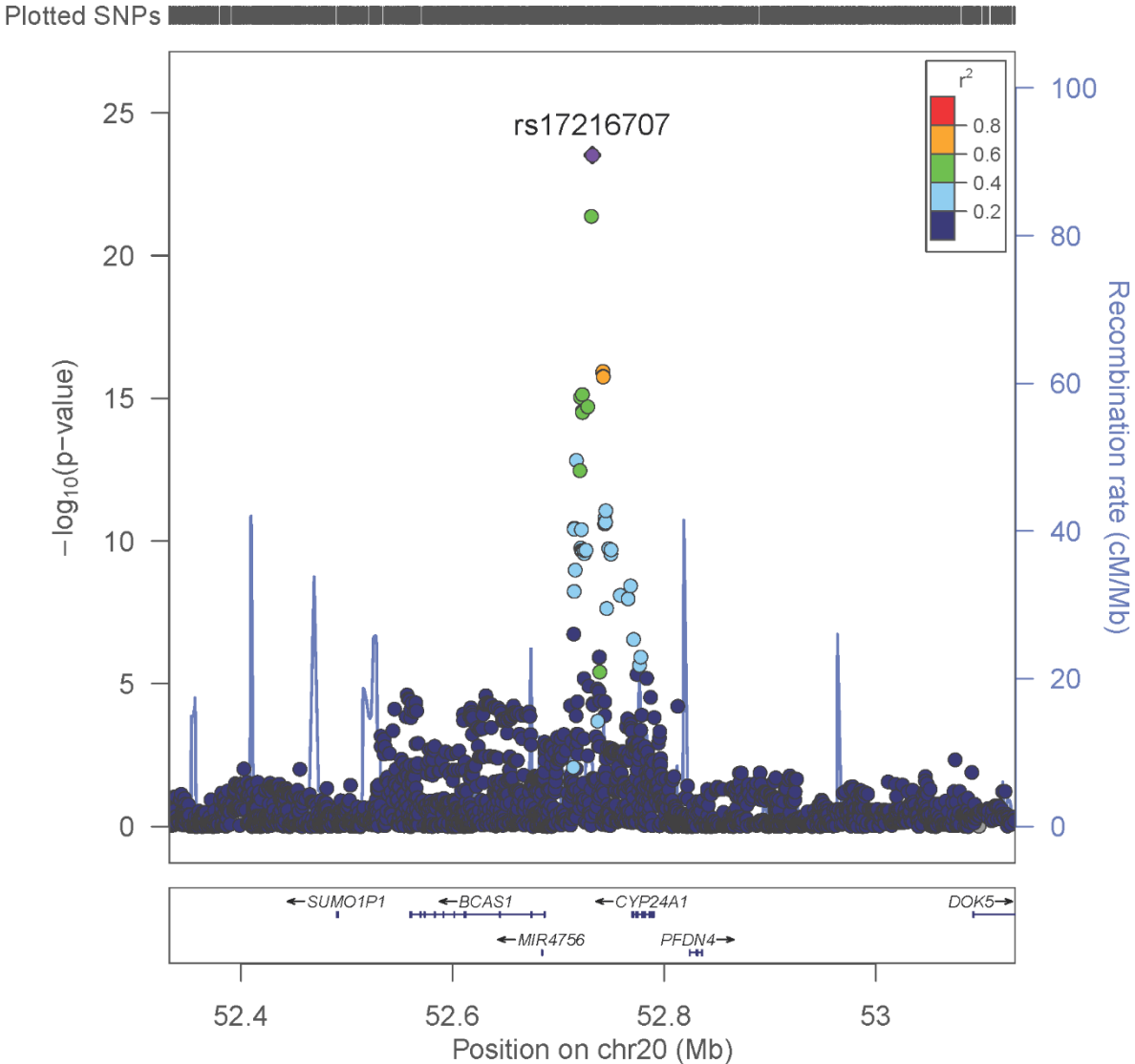


Figure 2b. Regional Association Plot, rs2769071

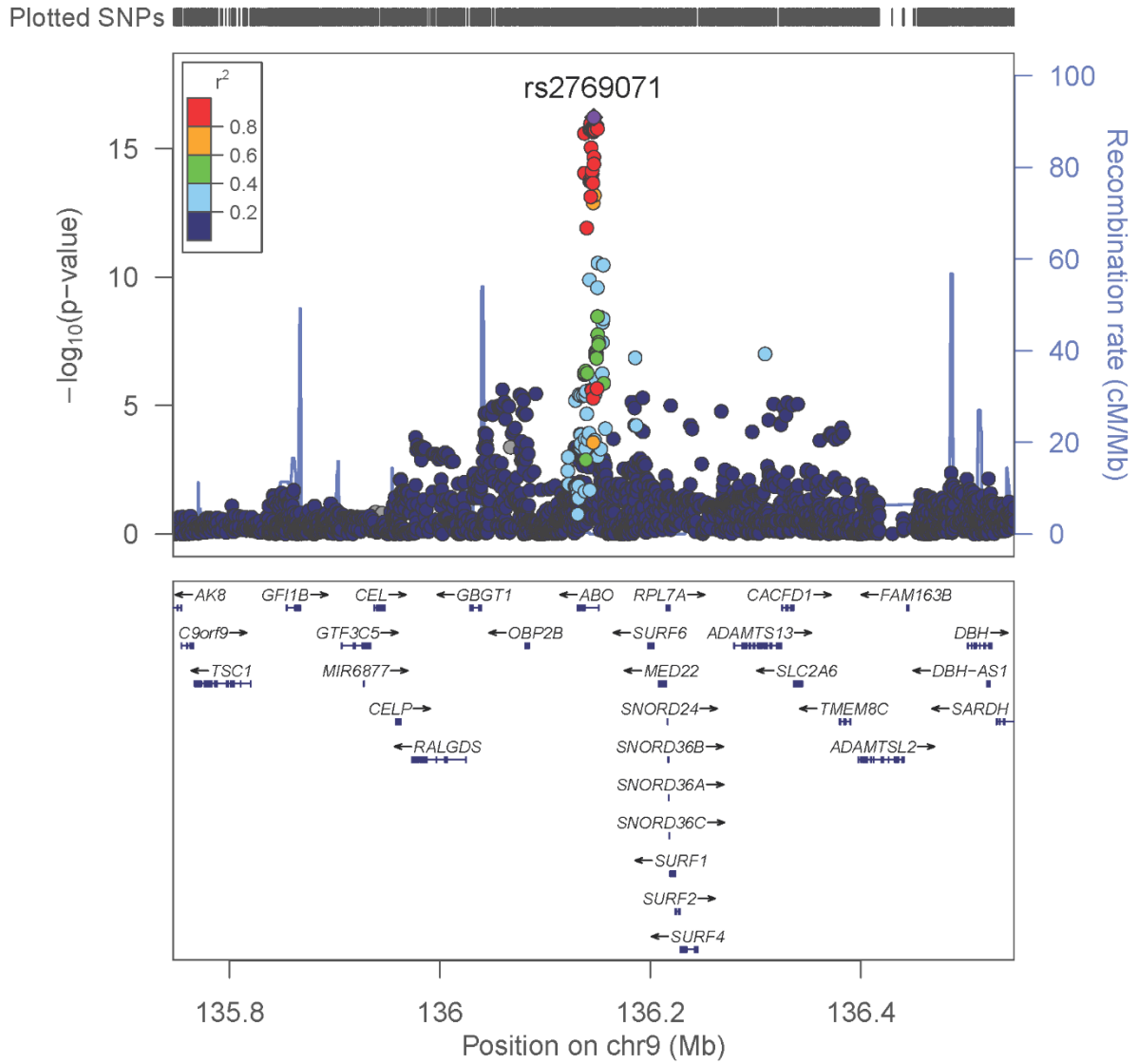


Figure 2c. Regional Association Plot, rs11741640

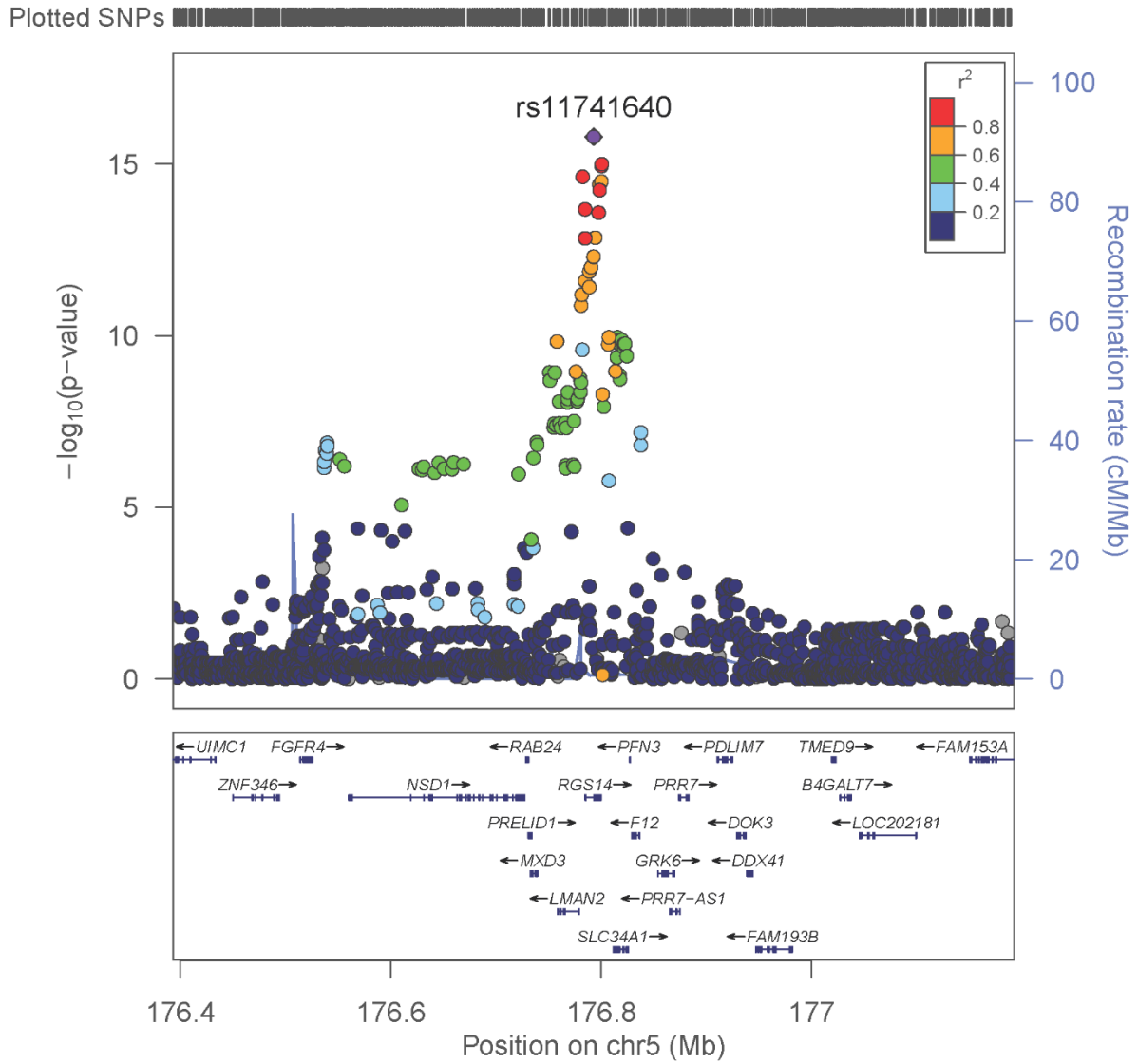


Figure 2d. Regional Association Plot, rs17479566

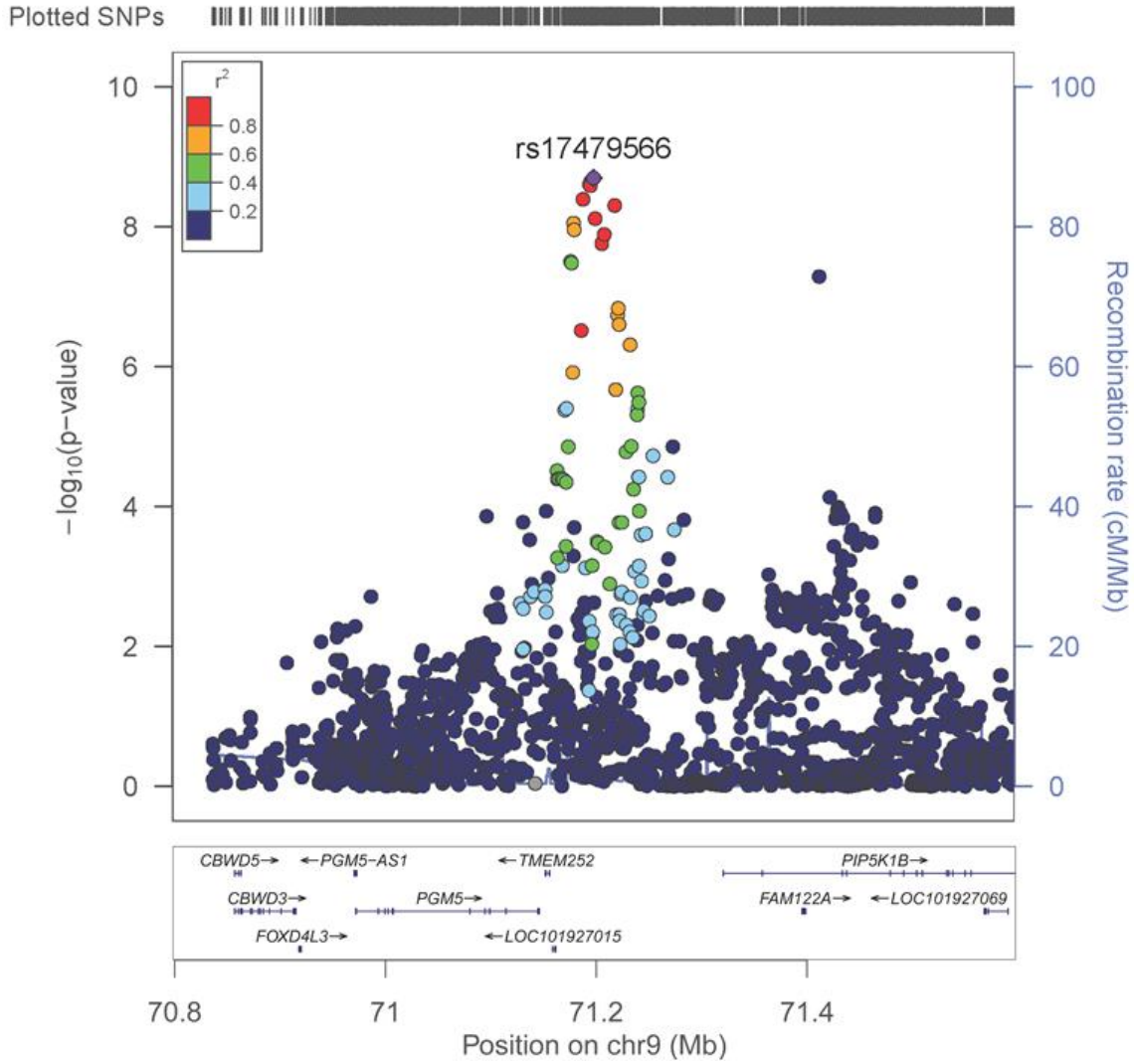


Figure 2e. Regional Association Plot, rs9925837

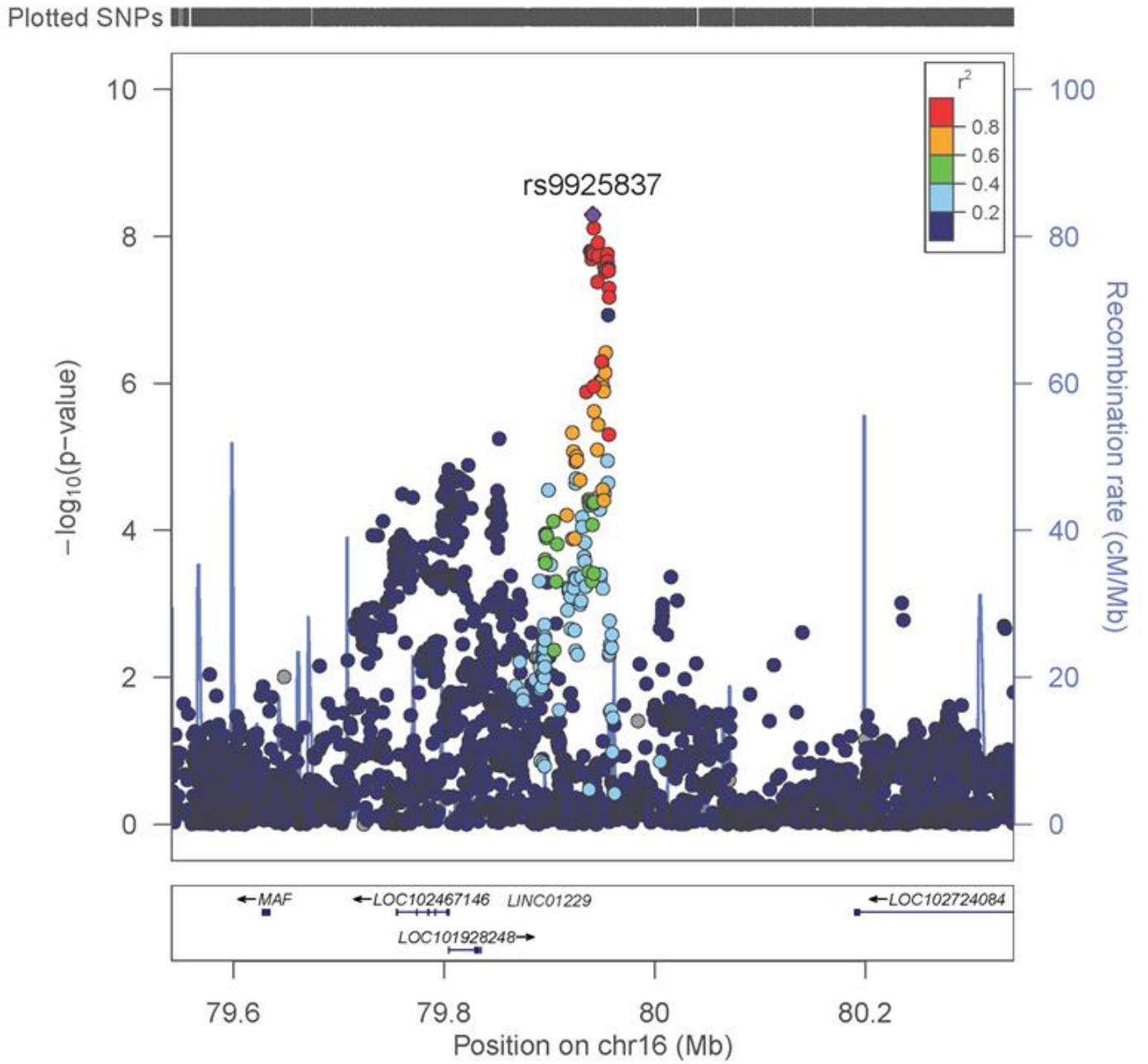


Figure 3. Manhattan Plot, Model 2, European Ancestry

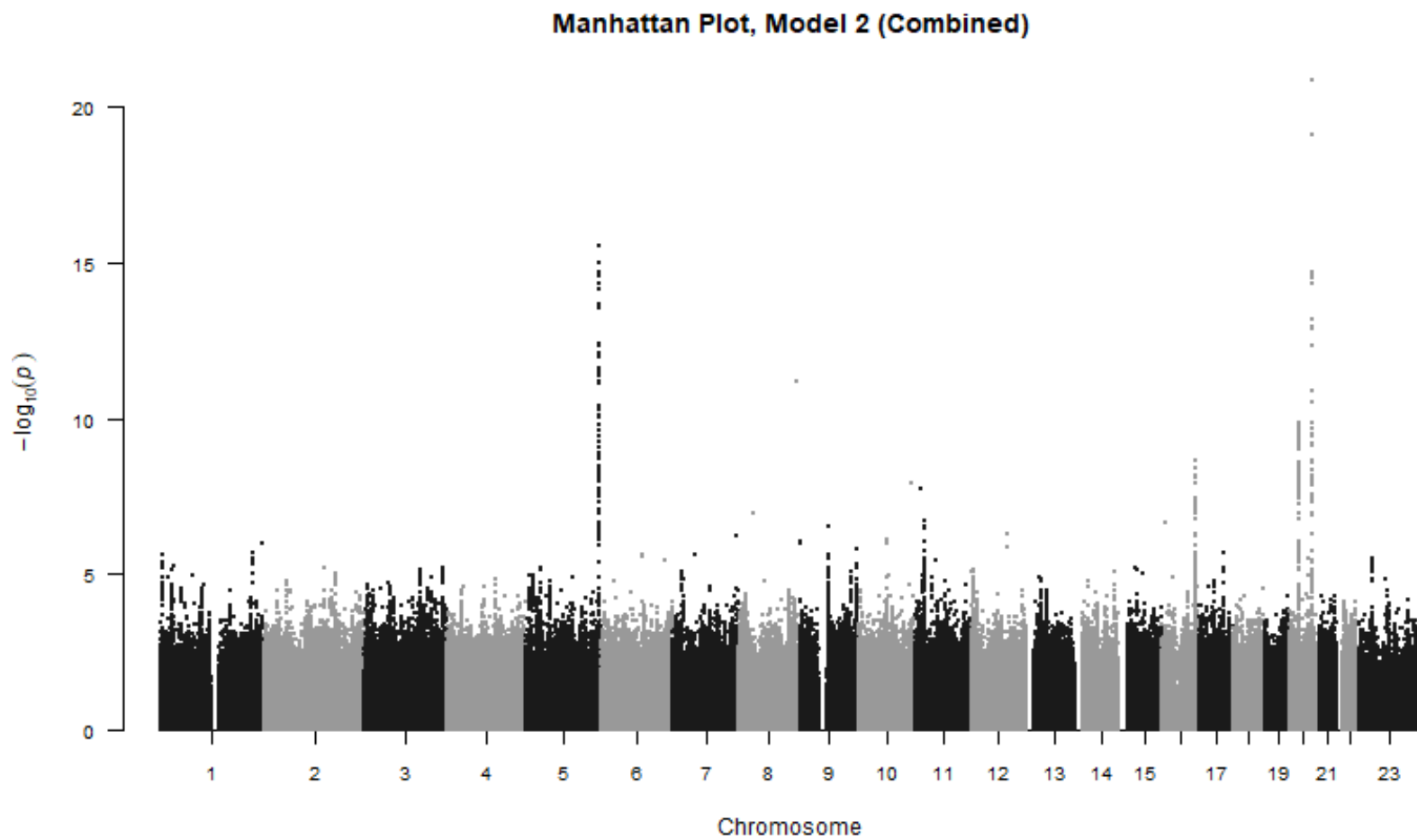


Figure 4a. Forest plot of beta-coefficients for rs17216707 from individual studies (Model 1)

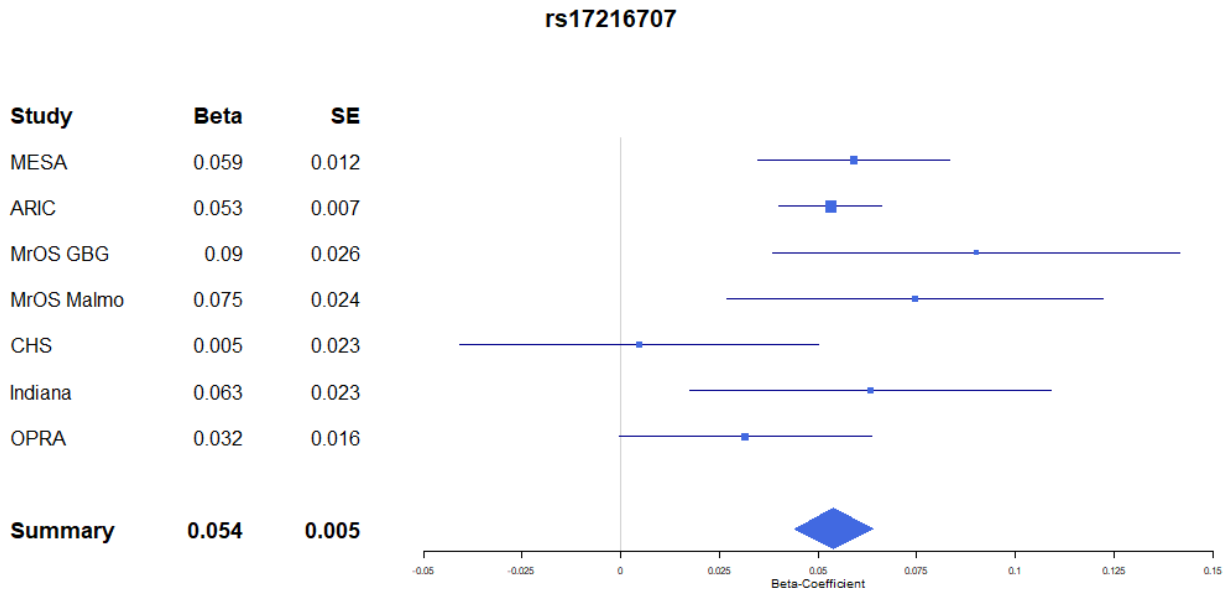


Figure 4b. Forest plot of beta-coefficients for rs2769071 from individual studies (Model 1)

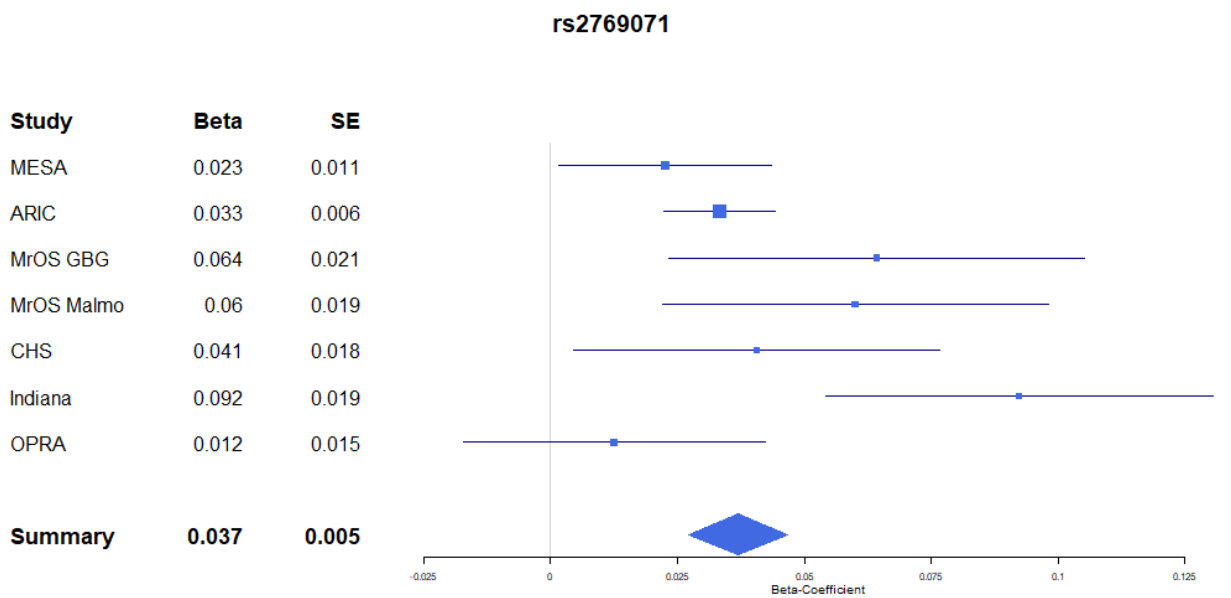


Figure 4c. Forest plot of beta-coefficients for rs11741640 from individual studies (Model 1)

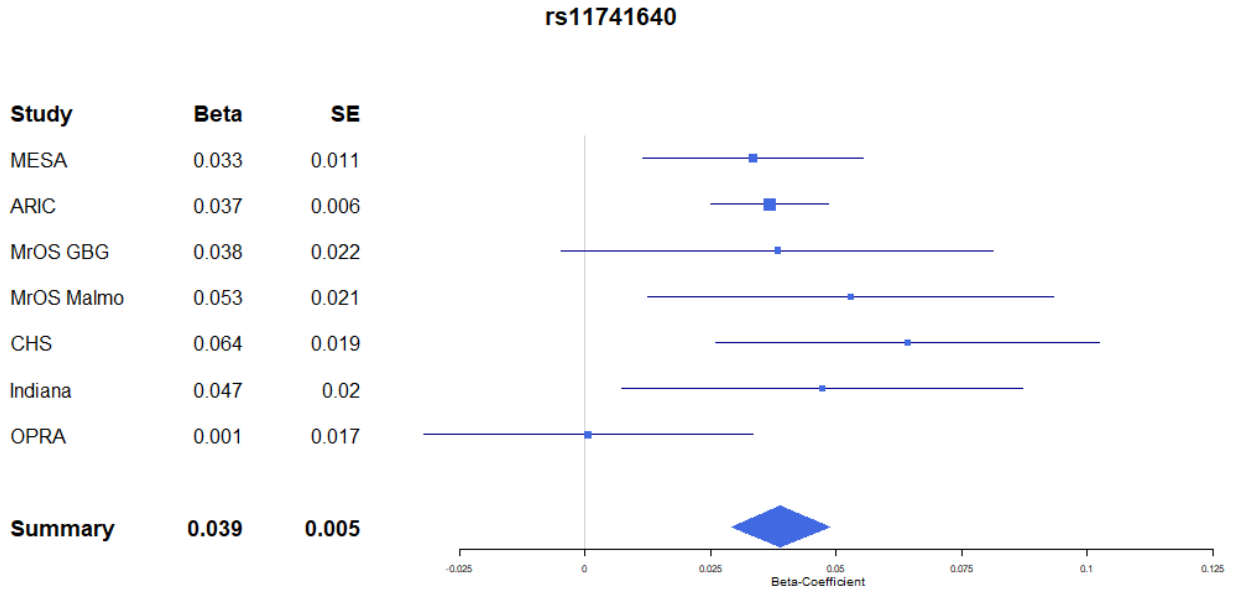


Figure 4d. Forest plot of beta-coefficients for rs17479566 from individual studies (Model 1)

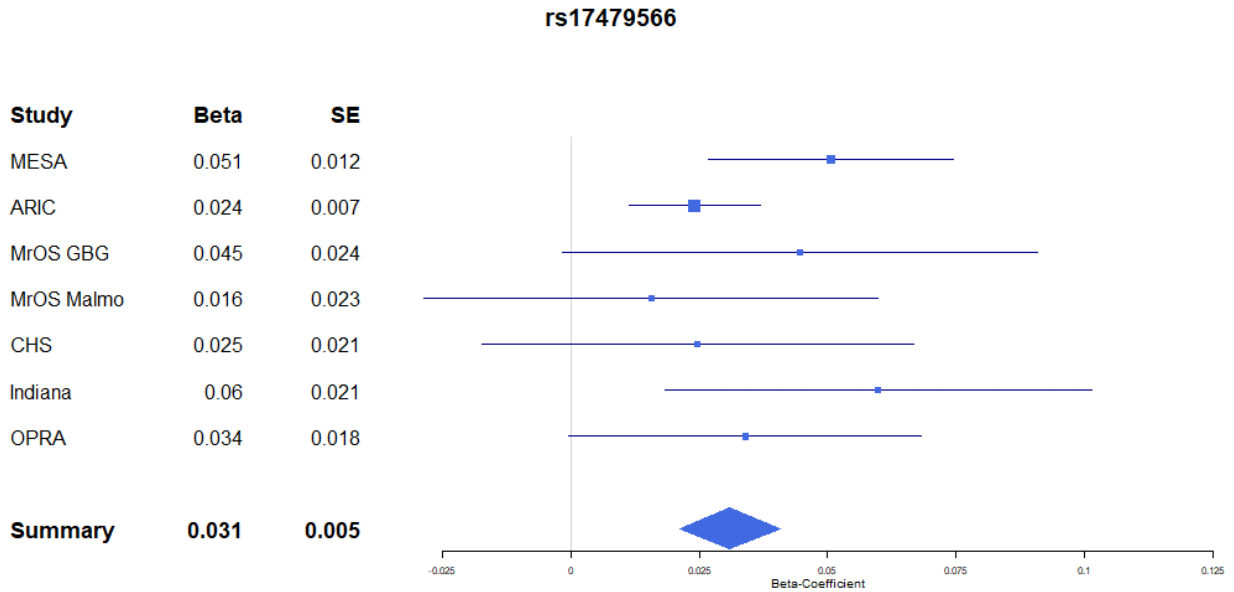
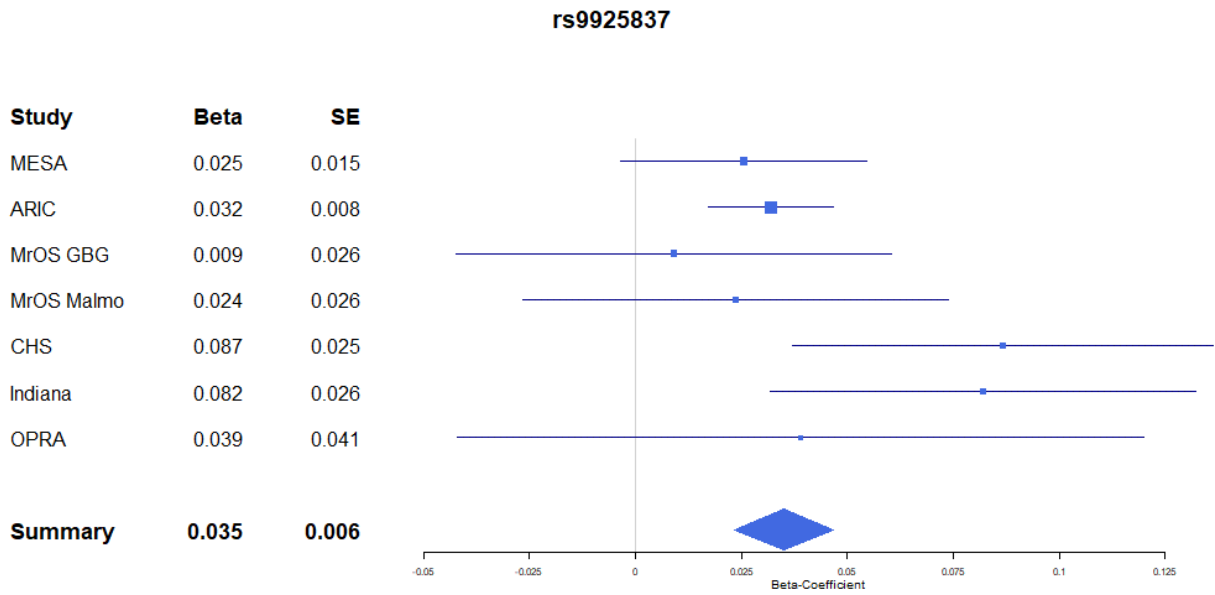


Figure 4e. Forest plot of beta-coefficients for rs9925837 from individual studies (Model 1)



Supplementary Table 2. Annotated SNPs demonstrating suggestive significance ($P < 5 \times 10^{-6}$) (Model 1)

MarkerName	Effect Allele	Other Allele	Effect Allele Frequency	Effect	SE	P.value.FE	P.value.RE	Chr	Position	Overlapped Gene	Nearest Upstream Gene	Nearest Downstream Gene
rs17216707	t	c	0.7997	0.0542	0.005	3.00E-24	1.10E-11	chr20	52732362		BCAS1	CYP24A1
rs6127099	a	t	0.7207	0.0477	0.005	4.16E-22	5.80E-16	chr20	52731402		BCAS1	CYP24A1
rs2769071	a	g	0.6491	-0.037	0.005	6.08E-17	4.79E-07	chr9	136145974	ABO		
rs527210	t	c	0.3428	0.038	0.005	6.38E-17	3.49E-07	chr9	136146431	ABO		
rs687289	a	g	0.3434	0.0379	0.005	7.34E-17	1.42E-06	chr9	136137106	ABO		
rs543040	a	t	0.6583	-0.038	0.005	1.06E-16	6.00E-07	chr9	136143000	ABO		
rs8121940	c	g	0.7902	0.0457	0.006	1.13E-16	4.80E-19	chr20	52742306		BCAS1	CYP24A1
rs35194449	t	c	0.2095	-0.046	0.006	1.18E-16	4.84E-19	chr20	52742047		BCAS1	CYP24A1
rs505922	t	c	0.6516	-0.037	0.005	1.43E-16	7.37E-07	chr9	136149229	ABO		
rs8176663	t	c	0.6501	-0.037	0.005	1.56E-16	6.74E-07	chr9	136144427	ABO		
rs11741640	a	g	0.2684	-0.039	0.005	1.59E-16	6.10E-17	chr5	176792743	RGS14		
rs17217119	a	g	0.79	0.0451	0.006	1.63E-16	3.72E-17	chr20	52742590		BCAS1	CYP24A1
rs6013897	a	t	0.2102	-0.045	0.006	1.66E-16	7.48E-19	chr20	52742479		BCAS1	CYP24A1
rs529565	t	c	0.6519	-0.037	0.005	1.69E-16	7.25E-07	chr9	136149500	ABO		
rs491626	t	c	0.3484	0.037	0.005	1.76E-16	7.29E-07	chr9	136144873	ABO		
rs514659	a	c	0.6503	-0.037	0.005	1.77E-16	7.00E-07	chr9	136142203	ABO		
rs492488	a	g	0.3504	0.0369	0.005	1.86E-16	7.36E-07	chr9	136144960	ABO		
rs545971	t	c	0.3497	0.0369	0.005	1.88E-16	6.94E-07	chr9	136143372	ABO		
rs554833	t	c	0.3499	0.0369	0.005	1.89E-16	7.52E-07	chr9	136147160	ABO		
rs674302	a	t	0.3498	0.0369	0.005	1.94E-16	7.76E-07	chr9	136146664	ABO		
rs676457	a	t	0.6504	-0.037	0.005	1.98E-16	7.79E-07	chr9	136146227	ABO		
rs493246	a	g	0.3507	0.0368	0.005	1.99E-16	6.82E-07	chr9	136144994	ABO		
rs495203	t	c	0.3505	0.0368	0.005	2.12E-16	7.58E-07	chr9	136145240	ABO		
rs582094	a	t	0.6502	-0.037	0.005	2.22E-16	7.01E-07	chr9	136145484	ABO		

rs582118	a	g	0.6502	-0.037	0.005	2.22E-16	7.01E-07	chr9	136145471	ABO		
rs687621	a	g	0.6492	-0.037	0.005	2.55E-16	1.09E-06	chr9	136137065	ABO		
rs11746443	a	g	0.2675	-0.039	0.005	6.67E-16	6.16E-11	chr5	176798306	RGS14		
rs612169	a	g	0.6509	-0.036	0.005	9.10E-16	1.16E-06	chr9	136143442	ABO		
rs11748297	a	g	0.2758	-0.038	0.005	9.96E-16	3.74E-16	chr5	176800361		RGS14	SLC34A1
rs4075958	a	g	0.2687	-0.038	0.005	1.04E-15	2.91E-15	chr5	176784512		LMAN2	RGS14
rs11748165	t	c	0.2788	-0.038	0.005	1.13E-15	4.09E-16	chr5	176800054		RGS14	SLC34A1
rs2870308	a	c	0.2918	-0.039	0.005	1.96E-15	1.37E-17	chr20	52727953		BCAS1	CYP24A1
rs677355	a	g	0.3407	0.0362	0.005	2.15E-15	8.82E-07	chr9	136146046	ABO		
rs4074995	a	g	0.2771	-0.037	0.005	2.31E-15	1.35E-09	chr5	176797343	RGS14		
rs13153019	t	c	0.7444	0.0392	0.005	2.33E-15	8.73E-16	chr5	176782218		LMAN2	RGS14
rs209956	a	g	0.7208	0.0373	0.005	2.78E-15	2.65E-16	chr20	52722856		BCAS1	CYP24A1
rs209954	a	t	0.7204	0.0373	0.005	3.10E-15	2.68E-16	chr20	52722943		BCAS1	CYP24A1
rs209955	t	c	0.2796	-0.037	0.005	3.14E-15	6.45E-17	chr20	52722871		BCAS1	CYP24A1
rs10051765	t	c	0.6765	0.0378	0.005	3.19E-15	8.61E-12	chr5	176799992		RGS14	SLC34A1
rs56235845	t	g	0.6884	0.0383	0.005	3.90E-15	1.25E-15	chr5	176798040	RGS14		
rs676996	t	g	0.6589	-0.036	0.005	3.96E-15	1.03E-06	chr9	136146077	ABO		
rs209957	a	g	0.72	0.0369	0.005	4.93E-15	1.09E-16	chr20	52721095		BCAS1	CYP24A1
rs576125	a	g	0.3187	0.0371	0.005	7.29E-15	2.32E-06	chr9	136144309	ABO		
rs597974	a	g	0.6802	-0.037	0.005	9.58E-15	2.93E-06	chr9	136144297	ABO		
rs643434	a	g	0.3711	0.0342	0.005	1.68E-14	5.84E-07	chr9	136142355	ABO		
rs657152	a	c	0.372	0.0341	0.005	1.76E-14	6.04E-07	chr9	136139265	ABO		
rs597988	a	t	0.3202	0.0364	0.005	1.79E-14	2.15E-06	chr9	136144284	ABO		
rs644234	t	g	0.629	-0.034	0.005	1.85E-14	5.44E-07	chr9	136142217	ABO		
rs544873	a	g	0.3707	0.0341	0.005	1.92E-14	5.65E-07	chr9	136143212	ABO		
rs494242	t	c	0.3718	0.034	0.005	2.19E-14	6.35E-07	chr9	136145118	ABO		
rs12654812	a	g	0.3272	-0.036	0.005	5.45E-14	4.52E-10	chr5	176794191	RGS14		
rs550057	t	c	0.2741	0.0361	0.005	6.51E-14	3.00E-07	chr9	136146597	ABO		
rs543968	t	c	0.6413	-0.034	0.005	7.51E-14	4.78E-07	chr9	136143121	ABO		
rs613534	a	g	0.6412	-0.034	0.005	7.54E-14	4.82E-07	chr9	136143120	ABO		

rs9411378	a	c	0.245	0.0385	0.005	1.29E-13	4.14E-07	chr9	136145425	ABO		
rs4075959	a	g	0.286	-0.035	0.005	1.44E-13	5.51E-14	chr5	176784612		LMAN2	RGS14
rs4976688	t	c	0.7138	0.0347	0.005	1.44E-13	5.52E-14	chr5	176784439		LMAN2	RGS14
rs209958	t	g	0.2785	-0.035	0.005	1.47E-13	2.44E-14	chr20	52717172		BCAS1	CYP24A1
rs158530	a	g	0.2911	-0.034	0.005	3.36E-13	8.08E-14	chr20	52720530		BCAS1	CYP24A1
rs11135015	t	c	0.6774	0.0344	0.005	4.92E-13	1.59E-13	chr5	176792557	RGS14		
rs6556313	a	g	0.676	0.0344	0.005	5.00E-13	1.67E-13	chr5	176792491	RGS14		
rs67111717	a	g	0.6724	0.034	0.005	1.00E-12	3.37E-13	chr5	176790162	RGS14		
rs4976647	a	c	0.6745	0.0338	0.005	1.33E-12	4.55E-13	chr5	176788622	RGS14		
rs4976646	t	c	0.6729	0.0337	0.005	1.54E-12	1.33E-12	chr5	176788570	RGS14		
rs4976689	c	g	0.6779	0.0331	0.005	2.51E-12	9.31E-13	chr5	176784448		LMAN2	RGS14
rs7713145	a	g	0.2807	-0.035	0.005	6.33E-12	3.13E-12	chr5	176781209		LMAN2	RGS14
rs4131290	a	c	0.7042	0.0323	0.005	1.31E-11	8.72E-12	chr5	176780682		LMAN2	RGS14
rs2762918	t	c	0.8388	0.0403	0.006	1.55E-11	5.20E-12	chr20	52744121		BCAS1	CYP24A1
rs2585448	c	g	0.8387	0.0399	0.006	2.13E-11	7.24E-12	chr20	52744537		BCAS1	CYP24A1
rs2762919	t	c	0.8387	0.0398	0.006	2.18E-11	7.48E-12	chr20	52744742		BCAS1	CYP24A1
rs2585449	a	g	0.1614	-0.04	0.006	2.27E-11	7.77E-12	chr20	52744679		BCAS1	CYP24A1
rs2585447	t	c	0.8388	0.0399	0.006	2.34E-11	7.95E-12	chr20	52744437		BCAS1	CYP24A1
rs2616278	t	c	0.8387	0.0398	0.006	2.41E-11	8.24E-12	chr20	52744525		BCAS1	CYP24A1
rs2616279	t	c	0.1623	-0.04	0.006	2.49E-11	8.52E-12	chr20	52743897		BCAS1	CYP24A1
rs532436	a	g	0.2052	0.0359	0.005	2.83E-11	2.02E-07	chr9	136149830	ABO		
rs507666	a	g	0.2052	0.0359	0.005	2.85E-11	4.20E-06	chr9	136149399	ABO		
rs33921462	a	g	0.2675	-0.034	0.005	2.88E-11	3.99E-10	chr5	176814656	SLC34A1		
rs635634	t	c	0.2046	0.0357	0.005	3.40E-11	2.07E-07	chr9	136155000		ABO	Y_RNA
rs458385	a	t	0.6881	0.0312	0.005	3.50E-11	2.50E-11	chr20	52715186		BCAS1	CYP24A1
rs458386	a	t	0.6825	0.0312	0.005	3.78E-11	2.74E-11	chr20	52715187		BCAS1	CYP24A1
rs2616277	t	c	0.1609	-0.039	0.006	4.07E-11	3.28E-12	chr20	52745040		BCAS1	CYP24A1
rs5030873	t	c	0.6864	0.0324	0.005	1.09E-10	6.88E-11	chr5	176815124	SLC34A1		
rs12659266	t	c	0.2449	-0.032	0.005	1.10E-10	6.47E-11	chr5	176807197	SLC34A1		
rs2519093	t	c	0.202	0.0349	0.005	1.27E-10	7.49E-07	chr9	136141870	ABO		

rs6556314	t	c	0.3157	-0.032	0.005	1.33E-10	8.62E-11	chr5	176819252	SLC34A1		
rs35610898	c	g	0.3142	-0.032	0.005	1.36E-10	8.71E-11	chr5	176815766	SLC34A1		
rs35630910	a	c	0.7064	0.0297	0.005	1.46E-10	1.04E-10	chr5	176757841		MXD3	LMAN2
rs6862195	t	g	0.3158	-0.032	0.005	1.70E-10	1.12E-10	chr5	176822512	SLC34A1		
rs158529	t	c	0.6591	0.0287	0.005	1.73E-10	9.01E-11	chr20	52721424		BCAS1	CYP24A1
rs6420095	a	c	0.6842	0.0322	0.005	1.73E-10	1.15E-10	chr5	176821449	SLC34A1		
rs6420094	a	g	0.6843	0.032	0.005	1.76E-10	1.19E-10	chr5	176817636	SLC34A1		
rs35716097	t	c	0.2894	-0.032	0.005	1.77E-10	1.99E-06	chr5	176806636	SLC34A1		
rs3812035	t	g	0.3155	-0.032	0.005	1.79E-10	1.87E-07	chr5	176817143	SLC34A1		
rs139415780	a	g	0.1559	-0.038	0.006	1.81E-10	7.74E-11	chr20	52747748		BCAS1	CYP24A1
rs2762921	a	g	0.156	-0.037	0.006	2.00E-10	8.82E-11	chr20	52749937		BCAS1	CYP24A1
rs158523	t	c	0.6602	0.0286	0.005	2.04E-10	1.07E-10	chr20	52724309		BCAS1	CYP24A1
rs210068	a	g	0.3392	-0.029	0.005	2.06E-10	1.12E-10	chr20	52726291		BCAS1	CYP24A1
rs158520	t	c	0.3398	-0.029	0.005	2.12E-10	1.11E-10	chr20	52724718		BCAS1	CYP24A1
rs158527	c	g	0.3399	-0.029	0.005	2.12E-10	1.11E-10	chr20	52722150		BCAS1	CYP24A1
rs10866705	a	c	0.7438	0.0312	0.005	2.16E-10	1.24E-10	chr5	176801131		RGS14	SLC34A1
rs6556316	t	c	0.3156	-0.032	0.005	2.19E-10	1.46E-10	chr5	176821375	SLC34A1		
rs158526	a	t	0.6601	0.0285	0.005	2.21E-10	1.16E-10	chr20	52722628		BCAS1	CYP24A1
rs158525	t	c	0.6599	0.0285	0.005	2.24E-10	1.17E-10	chr20	52722810		BCAS1	CYP24A1
rs158528	a	g	0.34	-0.029	0.005	2.25E-10	2.07E-11	chr20	52721956		BCAS1	CYP24A1
rs67190252	t	c	0.2089	-0.038	0.006	2.54E-10	9.67E-11	chr5	176781905		LMAN2	RGS14
rs158521	t	c	0.34	-0.028	0.005	2.74E-10	1.45E-10	chr20	52724665		BCAS1	CYP24A1
rs2762920	a	g	0.1561	-0.037	0.006	2.86E-10	1.32E-10	chr20	52749823		BCAS1	CYP24A1
rs7447593	c	g	0.6844	0.0321	0.005	3.87E-10	2.66E-10	chr5	176824137	SLC34A1		
rs3812036	t	c	0.2527	-0.03	0.005	1.08E-09	6.44E-10	chr5	176813404	SLC34A1		
rs34604271	t	c	0.2986	-0.028	0.005	1.11E-09	9.90E-10	chr5	176775851	LMAN2		
rs62397245	c	g	0.7688	0.0309	0.005	1.15E-09	8.47E-10	chr5	176750688		MXD3	LMAN2
rs6860069	t	c	0.3092	-0.028	0.005	1.17E-09	6.53E-10	chr5	176755841		MXD3	LMAN2
rs34316179	a	g	0.3184	-0.028	0.005	1.75E-09	8.39E-10	chr5	176779689		LMAN2	RGS14
rs55785724	a	t	0.6815	0.03	0.005	1.82E-09	1.49E-09	chr5	176817583	SLC34A1		

rs113955164	a	g	0.2233	-0.032	0.005	1.97E-09	1.31E-09	chr5	176750988		MXD3	LMAN2
rs151014368	a	g	0.2216	-0.031	0.005	2.01E-09	1.30E-09	chr5	176751059		MXD3	LMAN2
rs17479566	t	c	0.2207	0.0313	0.005	2.01E-09	7.17E-07	chr9	71198014	RP11-274B18.4		
rs4131289	a	g	0.3211	-0.028	0.005	2.27E-09	1.15E-09	chr5	176780545		LMAN2	RGS14
rs2026351	a	g	0.2221	0.0309	0.005	2.47E-09	1.00E-06	chr9	71194024	RP11-274B18.4		
rs72716037	t	c	0.2221	0.0308	0.005	2.58E-09	8.67E-07	chr9	71194967	RP11-274B18.4		
rs954453	t	c	0.2215	0.0306	0.005	3.37E-09	5.70E-09	chr9	71186301	RP11-274B18.4		
rs630510	a	g	0.4679	-0.025	0.004	3.40E-09	1.12E-05	chr9	136149581	ABO		
rs600038	t	c	0.7738	-0.031	0.005	3.61E-09	6.41E-08	chr9	136151806		ABO	Y_RNA
rs630014	a	g	0.468	-0.025	0.004	3.69E-09	8.83E-05	chr9	136149722	ABO		
rs12237628	t	c	0.7763	-0.031	0.005	4.04E-09	8.26E-07	chr9	71187957	RP11-274B18.4		
rs495828	t	g	0.226	0.0307	0.005	4.18E-09	1.17E-07	chr9	136154867		ABO	Y_RNA
rs13362309	a	g	0.6819	0.0277	0.005	4.31E-09	2.51E-09	chr5	176780137		LMAN2	RGS14
rs13190259	t	c	0.3003	-0.028	0.005	4.38E-09	2.05E-09	chr5	176768110	LMAN2		
rs651007	t	c	0.226	0.0305	0.005	4.84E-09	6.48E-08	chr9	136153875		ABO	Y_RNA
rs1888722	t	g	0.2128	0.0304	0.005	4.95E-09	1.02E-07	chr9	71218049	RP11-274B18.4		
rs9925837	a	g	0.8519	-0.035	0.006	5.11E-09	1.39E-04	chr16	79927303		RP11-345M22.3	RP11-148M9.1
rs579459	t	c	0.7742	-0.031	0.005	5.23E-09	1.15E-06	chr9	136154168		ABO	Y_RNA
rs209961	t	c	0.2847	-0.028	0.005	5.75E-09	2.72E-09	chr20	52715154		BCAS1	CYP24A1
rs649129	t	c	0.2252	0.0305	0.005	5.78E-09	6.88E-08	chr9	136154304		ABO	Y_RNA
rs209960	t	c	0.2852	-0.027	0.005	6.73E-09	4.80E-10	chr20	52716084		BCAS1	CYP24A1
rs13190105	a	g	0.7105	0.0281	0.005	6.79E-09	3.41E-09	chr5	176768090	LMAN2		
rs4976645	a	g	0.321	-0.027	0.005	6.86E-09	3.61E-09	chr5	176777493	LMAN2		
rs58256061	a	g	0.2142	0.03	0.005	7.62E-09	1.76E-07	chr9	71199513	RP11-274B18.4		
rs11644393	a	t	0.1572	0.0335	0.006	7.70E-09	2.63E-04	chr16	79928128		RP11-345M22.3	RP11-148M9.1
rs2585412	a	t	0.1494	-0.035	0.006	7.89E-09	4.04E-09	chr20	52758649		BCAS1	CYP24A1
rs4397143	a	c	0.6789	0.0266	0.005	8.08E-09	4.31E-09	chr5	176777022	LMAN2		
rs35582636	a	c	0.2521	-0.029	0.005	8.18E-09	5.41E-09	chr5	176759778	LMAN2		
rs111566909	a	g	0.6918	0.0265	0.005	8.68E-09	5.35E-09	chr5	176767817	LMAN2		
rs17479209	a	g	0.2036	0.0302	0.005	8.84E-09	3.14E-06	chr9	71178959	RP11-274B18.4		

rs10869048	a	c	0.7959	-0.03	0.005	9.35E-09	4.40E-08	chr9	71178178	RP11-274B18.4		
rs2762928	a	t	0.8504	0.0343	0.006	1.05E-08	5.64E-09	chr20	52766085		BCAS1	CYP24A1
rs869950	a	t	0.7968	-0.03	0.005	1.10E-08	3.95E-06	chr9	71179545	RP11-274B18.4		
rs13157098	a	g	0.144	-0.038	0.007	1.17E-08	3.98E-07	chr5	176802250		RGS14	SLC34A1
rs4627365	t	c	0.1449	0.0342	0.006	1.21E-08	4.00E-05	chr16	79932213		RP11-345M22.3	RP11-148M9.1
rs11143037	t	c	0.2158	0.0293	0.005	1.28E-08	3.26E-07	chr9	71208171	RP11-274B18.4		
rs11649114	a	g	0.8489	-0.033	0.006	1.58E-08	4.14E-04	chr16	79924857		RP11-345M22.3	RP11-148M9.1
rs28384289	t	c	0.1507	0.033	0.006	1.61E-08	2.88E-04	chr16	79925400		RP11-345M22.3	RP11-148M9.1
rs11646139	a	g	0.1506	0.033	0.006	1.62E-08	2.82E-04	chr16	79926321		RP11-345M22.3	RP11-148M9.1
rs9935686	a	c	0.1506	0.033	0.006	1.62E-08	2.91E-04	chr16	79927218		RP11-345M22.3	RP11-148M9.1
rs11644400	t	c	0.849	-0.033	0.006	1.65E-08	2.46E-05	chr16	79928186		RP11-345M22.3	RP11-148M9.1
rs9925120	c	g	0.849	-0.033	0.006	1.72E-08	1.31E-07	chr16	79941214		RP11-345M22.3	RP11-148M9.1
rs4745134	t	c	0.7836	-0.029	0.005	1.73E-08	6.08E-07	chr9	71205791	RP11-274B18.4		
rs4745135	t	c	0.7836	-0.029	0.005	1.74E-08	6.16E-07	chr9	71205800	RP11-274B18.4		
rs11647905	c	g	0.1508	0.033	0.006	1.75E-08	2.83E-04	chr16	79928065		RP11-345M22.3	RP11-148M9.1
rs9928026	a	g	0.8493	-0.033	0.006	1.78E-08	2.87E-04	chr16	79927537		RP11-345M22.3	RP11-148M9.1
rs4078173	a	g	0.8497	-0.033	0.006	1.83E-08	4.71E-06	chr16	79932332		RP11-345M22.3	RP11-148M9.1
rs2762932	t	c	0.8501	0.0336	0.006	1.96E-08	2.06E-09	chr20	52768391		BCAS1	CYP24A1
rs13330604	a	t	0.8497	-0.033	0.006	2.03E-08	2.93E-04	chr16	79926101		RP11-345M22.3	RP11-148M9.1
rs11641371	t	c	0.1488	0.0331	0.006	2.03E-08	9.83E-09	chr16	79940725		RP11-345M22.3	RP11-148M9.1
rs11641245	c	g	0.8482	-0.033	0.006	2.13E-08	4.71E-07	chr16	79940478		RP11-345M22.3	RP11-148M9.1
rs11641084	c	g	0.1507	0.0327	0.006	2.16E-08	1.50E-07	chr16	79940800		RP11-345M22.3	RP11-148M9.1
rs9925132	t	c	0.1508	0.0327	0.006	2.18E-08	1.58E-07	chr16	79941233		RP11-345M22.3	RP11-148M9.1
rs2616275	t	c	0.215	-0.03	0.005	2.28E-08	1.15E-08	chr20	52745825		BCAS1	CYP24A1
rs7188156	t	g	0.8491	-0.033	0.006	2.52E-08	2.49E-06	chr16	79938114		RP11-345M22.3	RP11-148M9.1
rs16951648	c	g	0.1527	0.0323	0.006	2.67E-08	4.17E-06	chr16	79942149		RP11-345M22.3	RP11-148M9.1
rs12103233	a	c	0.8487	-0.032	0.006	2.70E-08	4.67E-07	chr16	79941973		RP11-345M22.3	RP11-148M9.1
rs7189003	a	t	0.1508	0.0324	0.006	2.79E-08	1.50E-07	chr16	79939801		RP11-345M22.3	RP11-148M9.1
rs28623477	a	g	0.8482	-0.032	0.006	2.80E-08	2.17E-06	chr16	79942318		RP11-345M22.3	RP11-148M9.1
rs8053565	t	g	0.1517	0.0323	0.006	2.83E-08	1.40E-07	chr16	79941892		RP11-345M22.3	RP11-148M9.1

rs8060495	a	g	0.8493	-0.033	0.006	2.92E-08	4.13E-07	chr16	79942385		RP11-345M22.3	RP11-148M9.1
rs9313758	t	g	0.678	0.025	0.005	2.98E-08	9.22E-09	chr5	176773091	LMAN2		
rs35286975	c	g	0.1519	0.0323	0.006	3.03E-08	2.20E-06	chr16	79938996		RP11-345M22.3	RP11-148M9.1
rs36102285	t	c	0.3207	-0.025	0.005	3.03E-08	1.72E-08	chr5	176774018	LMAN2		
rs4532376	a	g	0.3208	-0.025	0.005	3.07E-08	8.42E-09	chr5	176774403	LMAN2		
rs11142926	t	g	0.2747	0.027	0.005	3.13E-08	2.24E-05	chr9	71176227	RP11-274B18.4		
rs4745107	a	g	0.7242	-0.027	0.005	3.29E-08	1.79E-08	chr9	71177110	RP11-274B18.4		
rs11748912	a	g	0.3224	-0.025	0.005	3.42E-08	1.89E-08	chr5	176765395	LMAN2		
rs616154	t	c	0.5209	0.0238	0.004	3.46E-08	3.28E-05	chr9	136150466	ABO		
rs4976643	a	c	0.6774	0.0249	0.005	3.50E-08	1.96E-08	chr5	176760227	LMAN2		
rs11949401	t	c	0.6778	0.0248	0.005	3.53E-08	1.13E-08	chr5	176765989	LMAN2		
rs6876677	t	c	0.6777	0.0249	0.005	3.56E-08	2.02E-08	chr5	176755342		MXD3	LMAN2
rs12055081	t	c	0.3222	-0.025	0.005	4.09E-08	2.32E-08	chr5	176757191		MXD3	LMAN2
rs4077451	a	t	0.8391	-0.032	0.006	4.15E-08	7.96E-06	chr16	79931720		RP11-345M22.3	RP11-148M9.1
rs559723	a	g	0.4871	-0.024	0.004	4.25E-08	2.55E-05	chr9	136150484	ABO		
rs6875461	t	c	0.6783	0.0246	0.005	4.67E-08	2.70E-08	chr5	176754665		MXD3	LMAN2
rs11738681	a	g	0.6774	0.0246	0.005	4.78E-08	2.72E-08	chr5	176761535	LMAN2		
rs11749830	a	g	0.323	-0.025	0.005	4.80E-08	2.63E-08	chr5	176766547	LMAN2		
rs28581385	a	t	0.852	-0.033	0.006	5.04E-08	2.81E-07	chr16	79942679		RP11-345M22.3	RP11-148M9.1
rs952436	t	c	0.2082	0.0287	0.005	5.13E-08	4.53E-09	chr9	71219086	RP11-274B18.4		
rs8058927	a	g	0.151	0.032	0.006	5.83E-08	8.24E-10	chr16	79942562		RP11-345M22.3	RP11-148M9.1
rs2252316	a	g	0.1396	-0.043	0.008	6.49E-08	5.41E-08	chr5	176837504	GRK6		
rs28555498	a	g	0.8453	-0.032	0.006	6.70E-08	8.13E-09	chr16	79942776		RP11-345M22.3	RP11-148M9.1
rs581107	t	c	0.5602	0.0233	0.004	7.98E-08	1.25E-03	chr9	136147702	ABO		
rs475419	t	c	0.5581	0.0232	0.004	8.68E-08	1.27E-03	chr9	136148231	ABO		
rs28446901	c	g	0.8145	-0.03	0.006	9.71E-08	6.81E-04	chr9	136308796	ADAMTS13		
rs645982	a	g	0.4415	-0.023	0.004	9.93E-08	1.21E-03	chr9	136148409	ABO		
rs473533	t	c	0.4415	-0.023	0.004	1.06E-07	1.28E-03	chr9	136148035	ABO		
rs476410	c	g	0.5586	0.023	0.004	1.06E-07	1.31E-03	chr9	136148368	ABO		
rs659104	t	g	0.4414	-0.023	0.004	1.10E-07	1.33E-03	chr9	136147823	ABO		

rs660340	a	g	0.4414	-0.023	0.004	1.11E-07	1.33E-03	chr9	136147553	ABO		
rs8054786	c	g	0.8417	-0.031	0.006	1.17E-07	1.31E-07	chr16	79941881		RP11-345M22.3	RP11-148M9.1
rs62397242	a	c	0.2379	-0.027	0.005	1.24E-07	8.71E-08	chr5	176738538	MXD3		
rs500498	t	c	0.4599	-0.023	0.004	1.25E-07	1.27E-03	chr9	136148647	ABO		
rs244730	a	g	0.2435	-0.026	0.005	1.30E-07	8.18E-08	chr5	176539212		FGFR4	NSD1
rs11789139	c	g	0.8258	-0.031	0.006	1.38E-07	2.44E-04	chr9	136185324		LCN1P2	SURF6
rs500499	c	g	0.5378	0.0232	0.004	1.44E-07	1.57E-03	chr9	136148648	ABO		
rs12238108	t	c	0.2083	0.0275	0.005	1.46E-07	6.86E-08	chr9	71221469	RP11-274B18.4		
rs72813185	a	c	0.2363	-0.027	0.005	1.48E-07	1.07E-07	chr5	176739110	MXD3		
rs2252317	t	g	0.8582	0.0414	0.008	1.54E-07	1.37E-07	chr5	176837490	GRK6		
rs633862	t	c	0.5512	0.0227	0.004	1.54E-07	1.49E-03	chr9	136155444		ABO	Y_RNA
rs244731	a	g	0.2435	-0.026	0.005	1.63E-07	1.00E-07	chr5	176539679		FGFR4	NSD1
rs6123359	a	g	0.9037	-0.041	0.008	1.79E-07	3.96E-08	chr20	52714706		BCAS1	CYP24A1
rs10869099	t	c	0.7915	-0.027	0.005	1.83E-07	8.67E-08	chr9	71220831	RP11-274B18.4		
rs244728	t	c	0.2347	-0.027	0.005	2.17E-07	1.36E-07	chr5	176537407		FGFR4	NSD1
rs4637914	a	t	0.2091	0.0269	0.005	2.49E-07	1.20E-07	chr9	71222223	RP11-274B18.4		
rs244729	c	g	0.755	0.0254	0.005	2.66E-07	1.72E-07	chr5	176539018		FGFR4	NSD1
rs67008484	t	c	0.7613	0.0255	0.005	3.61E-07	2.60E-07	chr5	176735383	MXD3		
rs7205649	t	c	0.1428	0.0303	0.006	3.80E-07	1.23E-04	chr16	79939504		RP11-345M22.3	RP11-148M9.1
rs3105419	c	g	0.2403	-0.025	0.005	3.98E-07	2.56E-07	chr5	176551396		FGFR4	NSD1
rs28579821	t	c	0.2808	0.0325	0.006	4.22E-07	3.66E-07	chr7	155287014	CNPY1		
rs8176690	a	g	0.5862	0.022	0.004	4.48E-07	9.59E-05	chr9	136138317	ABO		
rs75719543	t	c	0.9688	0.0809	0.016	4.64E-07	3.85E-07	chr12	85953371		RP11-408B11.2	RP11-629O19.1
rs244727	t	c	0.2378	-0.026	0.005	4.71E-07	2.98E-07	chr5	176536549		FGFR4	NSD1
rs12235842	t	c	0.2008	0.0271	0.005	4.86E-07	2.40E-07	chr9	71232678	RP11-274B18.4		
rs7724098	a	g	0.7594	0.0248	0.005	4.87E-07	3.77E-07	chr5	176659570	NSD1		
rs9313752	a	c	0.7595	0.0248	0.005	4.95E-07	3.77E-07	chr5	176645435	NSD1		
rs13331920	c	g	0.8582	-0.03	0.006	5.02E-07	4.21E-05	chr16	79935590		RP11-345M22.3	RP11-148M9.1
rs7193332	a	g	0.8595	-0.03	0.006	5.19E-07	3.75E-05	chr16	79936215		RP11-345M22.3	RP11-148M9.1
rs2073828	a	g	0.4132	-0.022	0.004	5.26E-07	6.44E-05	chr9	136137140	ABO		

rs8176681	t	c	0.5859	0.0218	0.004	5.44E-07	6.69E-05	chr9	136139754	ABO		
rs2073827	c	g	0.4132	-0.022	0.004	5.45E-07	5.86E-05	chr9	136137133	ABO		
rs918459	a	g	0.7594	0.0247	0.005	5.50E-07	4.34E-07	chr5	176669030	NSD1		
rs11244061	t	c	0.1172	0.0322	0.006	5.68E-07	3.52E-04	chr9	136153981		ABO	Y_RNA
rs35929305	t	c	0.2187	0.0293	0.006	6.03E-07	6.22E-07	chr1	35092426		RP4-657M3.2	MIR552
rs2073826	t	g	0.413	-0.022	0.004	6.17E-07	5.68E-05	chr9	136136963	ABO		
rs244707	a	t	0.7623	0.025	0.005	6.27E-07	4.41E-07	chr5	176555636		FGFR4	NSD1
rs887258	c	g	0.2195	0.0257	0.005	6.43E-07	2.46E-05	chr17	59479580	TBX2		
rs1476781	t	c	0.2203	0.0257	0.005	6.53E-07	7.81E-05	chr17	59476415	RP11-332H18.5		
rs7721671	t	c	0.24	-0.025	0.005	6.54E-07	4.96E-07	chr5	176630984	NSD1		
rs2109019	a	c	0.2201	0.0256	0.005	6.75E-07	1.61E-07	chr17	59475888	RP11-332H18.5		
rs6561600	a	g	0.7392	-0.024	0.005	6.90E-07	1.58E-06	chr13	33431045		PDS5B	LINC00423
rs244726	a	g	0.2507	-0.025	0.005	7.04E-07	4.56E-07	chr5	176536408		FGFR4	NSD1
rs11648875	t	c	0.1415	0.0296	0.006	7.13E-07	2.45E-05	chr16	79939049		RP11-345M22.3	RP11-148M9.1
rs4976685	a	g	0.6681	0.0221	0.005	7.21E-07	5.56E-07	chr5	176766177	LMAN2		
rs6872952	a	g	0.2561	-0.025	0.005	7.35E-07	5.34E-07	chr5	176650489	NSD1		
rs12652509	a	g	0.24	-0.025	0.005	7.50E-07	5.70E-07	chr5	176626441	NSD1		
rs10037110	a	t	0.2431	-0.024	0.005	7.67E-07	5.72E-07	chr5	176658066	NSD1		
rs78463612	c	g	0.9261	0.0422	0.009	8.09E-07	7.46E-07	chr6	100284585		Y_RNA	MCHR2
rs4976677	a	g	0.7599	0.0244	0.005	8.09E-07	6.14E-07	chr5	176629546	NSD1		
rs4325578	a	g	0.8561	-0.029	0.006	9.06E-07	3.11E-06	chr16	79936589		RP11-345M22.3	RP11-148M9.1
rs60715095	c	g	0.8574	-0.029	0.006	9.07E-07	5.73E-05	chr16	79935768		RP11-345M22.3	RP11-148M9.1
rs28580467	c	g	0.8577	-0.029	0.006	9.26E-07	4.11E-05	chr16	79934279		RP11-345M22.3	RP11-148M9.1
rs59520813	a	g	0.143	0.0292	0.006	9.45E-07	9.70E-05	chr16	79936068		RP11-345M22.3	RP11-148M9.1
rs60280876	c	g	0.1427	0.0292	0.006	9.61E-07	6.39E-05	chr16	79935778		RP11-345M22.3	RP11-148M9.1
rs647800	a	g	0.4203	-0.021	0.004	9.64E-07	2.72E-03	chr9	136148000	ABO		
rs6556307	a	g	0.2404	-0.024	0.005	9.68E-07	7.49E-07	chr5	176641434	NSD1		
rs6872021	a	g	0.7575	0.0242	0.005	1.05E-06	6.24E-07	chr5	176610012	NSD1		
rs11740250	c	g	0.2399	-0.024	0.005	1.07E-06	8.28E-07	chr5	176721272	NSD1		
rs78097283	a	t	0.9261	0.0414	0.009	1.11E-06	1.02E-06	chr6	100280629		Y_RNA	MCHR2

rs79480825	a	t	0.9261	0.0414	0.009	1.11E-06	1.02E-06	chr6	100280611		Y_RNA	MCHR2
rs9907379	t	c	0.2205	0.025	0.005	1.12E-06	8.99E-08	chr17	59489893	C17orf82		
rs12479682	t	c	0.1118	0.0329	0.007	1.13E-06	5.00E-07	chr20	52738937		BCAS1	CYP24A1
rs2762937	a	g	0.8091	0.028	0.006	1.15E-06	2.24E-07	chr20	52778025	CYP24A1		
rs1570669	a	g	0.6581	-0.022	0.004	1.15E-06	4.74E-05	chr20	52774427	CYP24A1		
rs7197544	t	g	0.1433	0.0289	0.006	1.16E-06	1.41E-04	chr16	79937201		RP11-345M22.3	RP11-148M9.1
rs12480880	t	c	0.8886	-0.033	0.007	1.19E-06	5.41E-07	chr20	52738743		BCAS1	CYP24A1
rs7203258	a	g	0.143	0.0289	0.006	1.25E-06	1.18E-06	chr16	79937727		RP11-345M22.3	RP11-148M9.1
rs7204126	t	c	0.143	0.0288	0.006	1.29E-06	5.55E-05	chr16	79937504		RP11-345M22.3	RP11-148M9.1
rs74038093	a	t	0.1435	0.0293	0.006	1.30E-06	1.79E-03	chr16	79921081		RP11-345M22.3	RP11-148M9.1
rs2762934	a	g	0.1831	-0.027	0.006	1.33E-06	5.55E-08	chr20	52771261	CYP24A1		
rs115325566	t	c	0.0788	-0.047	0.01	1.67E-06	2.85E-04	chr5	176807191	SLC34A1		
rs13295207	a	c	0.3538	0.0221	0.005	1.96E-06	4.78E-04	chr9	136075679		GBGT1	OBP2B
rs887461	a	t	0.7244	-0.023	0.005	2.19E-06	1.45E-06	chr7	90493764	CDK14		
rs41340944	a	g	0.0861	0.0369	0.008	2.22E-06	8.74E-07	chr10	70002020	RP11-153K11.3		
rs751088	a	t	0.1935	-0.027	0.006	2.25E-06	3.79E-07	chr20	52776892	CYP24A1		
rs10869158	a	g	0.7554	-0.024	0.005	2.37E-06	1.15E-04	chr9	71240051	RP11-274B18.4		
rs11795370	t	g	0.2777	0.0249	0.005	2.38E-06	5.83E-07	chr9	136059193		GBGT1	OBP2B
rs8176668	a	t	0.6072	0.0208	0.004	2.38E-06	1.85E-05	chr9	136144059	ABO		
rs58323452	a	g	0.8196	-0.026	0.006	2.40E-06	1.26E-03	chr16	79928440		RP11-345M22.3	RP11-148M9.1
rs10823164	t	c	0.9139	-0.037	0.008	2.44E-06	9.94E-07	chr10	70002705		RP11-153K11.3	KRT19P4
rs8068318	t	c	0.7221	-0.022	0.005	2.51E-06	2.08E-04	chr17	59483766	TBX2		
rs576123	t	c	0.6536	-0.054	0.012	2.52E-06	2.17E-06	chr9	136144308	ABO		
rs933992	t	c	0.1535	0.0268	0.006	2.58E-06	2.56E-06	chr3	69764203		RP11-444P10.1	MITF
rs62071306	a	c	0.344	0.0231	0.005	2.62E-06	5.98E-05	chr17	59476066	RP11-332H18.5		
rs10998033	a	g	0.914	-0.037	0.008	2.64E-06	1.04E-06	chr10	70002749		RP11-153K11.3	KRT19P4
rs7358139	t	c	0.0861	0.0367	0.008	2.65E-06	1.08E-06	chr10	70002260		RP11-153K11.3	KRT19P4
rs7036642	a	g	0.3931	-0.021	0.004	2.66E-06	1.01E-05	chr9	136144626	ABO		
rs9783267	c	g	0.0861	0.0367	0.008	2.69E-06	1.07E-06	chr10	70002494		RP11-153K11.3	KRT19P4
rs73271107	a	g	0.9138	-0.037	0.008	2.70E-06	1.08E-06	chr10	70002971		RP11-153K11.3	KRT19P4

rs12494375	c	g	0.8465	-0.027	0.006	2.71E-06	2.69E-06	chr3	69765396		RP11-444P10.1	MITF
rs7046674	t	c	0.3928	-0.021	0.004	2.74E-06	2.29E-05	chr9	136147012	ABO		
rs8176686	t	c	0.5869	0.0209	0.005	2.76E-06	NA	chr9	136138776	ABO		
rs12952625	a	g	0.7213	-0.022	0.005	2.91E-06	1.52E-05	chr17	59478644	TBX2		
rs3802030	t	g	0.2798	0.0223	0.005	2.93E-06	1.96E-06	chr7	90484578	CDK14		
rs4855446	a	g	0.1537	0.0266	0.006	3.13E-06	5.68E-06	chr3	69768996		RP11-444P10.1	MITF
rs8074151	a	g	0.7238	-0.022	0.005	3.15E-06	1.26E-03	chr17	59485017	TBX2		
rs8078036	a	g	0.7238	-0.022	0.005	3.18E-06	1.25E-03	chr17	59485120	TBX2		
rs10869160	a	g	0.2428	0.0232	0.005	3.18E-06	2.18E-05	chr9	71241343	RP11-274B18.4		
rs10781095	a	g	0.7571	-0.023	0.005	3.23E-06	1.85E-04	chr9	71240969	RP11-274B18.4		
rs1057987	t	c	0.7237	-0.022	0.005	3.28E-06	1.19E-03	chr17	59485555	TBX2		
rs6767501	t	c	0.1537	0.0266	0.006	3.33E-06	3.30E-06	chr3	69770411		RP11-444P10.1	MITF
rs34446110	c	g	0.7219	-0.022	0.005	3.35E-06	1.51E-03	chr17	59478354	TBX2		
rs1000423	t	c	0.7219	-0.022	0.005	3.36E-06	1.90E-03	chr17	59475642	RP11-332H18.5		
rs4855322	a	t	0.1536	0.0265	0.006	3.41E-06	3.38E-06	chr3	69769363		RP11-444P10.1	MITF
rs2240736	t	c	0.7254	-0.022	0.005	3.41E-06	1.56E-03	chr17	59485393	TBX2		
rs2270114	c	g	0.7095	-0.022	0.005	3.42E-06	1.12E-03	chr17	59478776	TBX2		
rs11794634	t	c	0.6613	-0.023	0.005	3.43E-06	1.22E-03	chr9	136090813		OBP2B	LCN1P1
rs8176649	a	g	0.3927	-0.02	0.004	3.45E-06	2.68E-05	chr9	136147295	ABO		
rs75973613	a	t	0.9863	0.1088	0.023	3.46E-06	5.25E-07	chr13	46364453	SIAH3		
rs7625281	t	c	0.1536	0.0265	0.006	3.47E-06	3.45E-06	chr3	69768940		RP11-444P10.1	MITF
rs4855443	a	g	0.8463	-0.026	0.006	3.54E-06	3.56E-06	chr3	69766382		RP11-444P10.1	MITF
rs4855445	t	c	0.154	0.0264	0.006	3.55E-06	3.57E-06	chr3	69766596		RP11-444P10.1	MITF
rs2289804	a	g	0.9286	-0.04	0.009	3.55E-06	2.18E-06	chr10	69993032	RP11-153K11.3		
rs8176682	t	c	0.3924	-0.02	0.004	3.56E-06	1.88E-06	chr9	136139297	ABO		
rs8073698	t	c	0.7238	-0.022	0.005	3.60E-06	1.29E-03	chr17	59484833	TBX2		
rs4078174	a	g	0.8245	-0.026	0.006	3.63E-06	5.66E-04	chr16	79932322		RP11-345M22.3	RP11-148M9.1
rs7873635	t	c	0.3915	-0.021	0.004	3.74E-06	9.77E-06	chr9	136132012	ABO		
rs11697119	a	g	0.3207	-0.022	0.005	3.83E-06	1.64E-06	chr20	52739292		BCAS1	CYP24A1
rs7215775	a	g	0.2745	0.022	0.005	3.93E-06	1.67E-03	chr17	59484316	TBX2		

rs12376362	a	c	0.8057	-0.025	0.005	3.95E-06	8.75E-07	chr9	71172306	RP11-274B18.4		
rs17597865	t	c	0.0517	-0.051	0.011	3.98E-06	3.18E-06	chr15	39030873		C15orf53	RP11-326N17.1
rs8176691	t	c	0.3919	-0.02	0.004	4.04E-06	1.28E-05	chr9	136138229	ABO		
rs8176702	a	g	0.3915	-0.02	0.004	4.06E-06	1.30E-05	chr9	136136146	ABO		
rs4962040	a	g	0.6081	0.0203	0.004	4.08E-06	1.76E-05	chr9	136133531	ABO		
rs10781092	a	g	0.2915	0.0221	0.005	4.10E-06	1.55E-05	chr9	71239648	RP11-274B18.4		
rs11791611	a	g	0.3509	0.0215	0.005	4.15E-06	9.84E-04	chr9	136077441		GBGT1	OBP2B
rs1411992	c	g	0.8074	-0.025	0.005	4.17E-06	7.50E-07	chr9	71170702	RP11-274B18.4		
rs4855444	t	c	0.8407	-0.026	0.006	4.43E-06	4.56E-06	chr3	69766592		RP11-444P10.1	MITF
rs1980513	t	g	0.0769	0.0366	0.008	4.55E-06	5.26E-05	chr14	35581151	FAM177A1		
rs9891115	a	g	0.6476	-0.023	0.005	4.60E-06	2.41E-04	chr17	59482173	TBX2		
rs13330024	a	t	0.856	-0.027	0.006	4.68E-06	1.42E-03	chr16	79907901		RP11-345M22.3	RP11-148M9.1
rs7616567	a	g	0.1539	0.0261	0.006	4.70E-06	4.72E-06	chr3	69766794		RP11-444P10.1	MITF
rs62252967	t	c	0.121	0.0285	0.006	4.83E-06	5.90E-06	chr3	69718556		RP11-444P10.1	MITF
rs10869153	a	c	0.7663	-0.023	0.005	4.87E-06	1.38E-04	chr9	71239400	RP11-274B18.4		
rs729781	a	g	0.276	0.0218	0.005	4.92E-06	1.52E-03	chr17	59486799	TBX2		
rs558599	a	c	0.4145	0.0238	0.005	4.94E-06	9.28E-04	chr9	136192551		LCN1P2	SURF6

P.value.FE: SNP P-value from fixed-effects model

P.value.RE: SNP P-value from random-effects mode

Supplementary Table 3. Associations of top single nucleotide polymorphisms with ln-transformed intact FGF23 concentration (exclusion of CHS and OPRA GWAS from meta-analysis)

SNP	Nearest gene [‡]	Chr	Position	FGF23 Increasing Allele	Other Allele	FGF23 Increasing Allele Frequency [‡]	Model 1		Model 2 [†]	
							(N=13,670)		(N=12,519)	
							β^{\ddagger} (SE)	p-value	β (SE)	p-value
rs17216707	<i>CYP24A1</i>	20	52732362	T	C	0.80	0.057 (0.006)	1.0 x 10 ⁻²⁵	0.054 (0.005)	1.5 x 10 ⁻²³
rs2769071	<i>ABO</i>	9	136145974	G	A	0.37	0.037 (0.005)	7.1 x 10 ⁻¹⁶	0.032 (0.008)	1.3 x 10 ⁻⁴
rs11741640	<i>RGS14</i>	5	176792743	G	A	0.73	0.038 (0.005)	1.6 x 10 ⁻¹⁴	0.037 (0.005)	3.6 x 10 ⁻¹⁴
rs17479566	<i>LINC01506</i>	9	71198013	T	C	0.22	0.032 (0.005)	3.8 x 10 ⁻⁹	0.044 (0.009)	3.8 x 10 ⁻⁶
rs9925837	<i>LINC01229</i>	16	79927303	G	A	0.13	0.032 (0.006)	2.2 x 10 ⁻⁷	0.032 (0.006)	1.0 x 10 ⁻⁷

Chr = chromosome

Only top SNP from each region shown.

Model 1 includes age, sex and first 10 principal components of ancestry

Model 2 additionally adjusts for BMI, eGFR and eGFR-squared.

[†]*Results for Model 2 were not available for the Indiana Sisters Study*

[‡]*Minor allele frequency data from 1000 Genome Phase 1 genotype data*

[‡]*Beta-estimates are interpreted as the relative difference in FGF23 concentration per minor allele, e.g. 0.055 is a 5.5% higher FGF23 concentration per additional allele*

Supplementary Table 4. Genetically predicted gene expression results from GWAS summary statistics

Tissue	Gene	Chr	Z -score	P value	Variance	R ²	N SNPs	Model N
Skeletal Muscle	RGS14*	5	7.956	1.78E-15	0.104	0.166	26	36
Subcutaneous Adipose	RGS14*	5	7.017	2.26E-12	0.079	0.178	4	4
Heart: Atrial Appendage	RGS14*	5	7.005	2.47E-12	0.18	0.305	14	14
Aortic Artery	RGS14*	5	6.887	5.70E-12	0.279	0.378	30	31
Transformed Fibroblast Cells	RGS14*	5	6.748	1.50E-11	0.418	0.568	22	23
Heart: Left Ventricle	RGS14*	5	6.219	5.00E-10	0.192	0.313	22	23
Coronary Artery	RGS14*	5	4.649	3.34E-06	0.149	0.21	27	29
Subcutaneous Adipose	TBX2*	17	4.581	4.62E-06	0.046	0.024	32	34
Subcutaneous Adipose	HDDC2	6	4.527	5.97E-06	0.135	0.125	46	50
Skeletal Muscle	NSD1*	5	-4.33	1.50E-05	0.012	0.035	6	6
Skeletal Muscle	TBX2*	17	4.043	5.27E-05	0.008	0.031	6	6
Skeletal Muscle	EIF3F	11	-4.04	5.28E-05	0.078	0.145	23	24
Subcutaneous Adipose	ARHGAP29	1	3.981	6.86E-05	0.048	0.05	40	42
Subcutaneous Adipose	EIF3F	11	-3.96	7.40E-05	0.084	0.164	17	18
Subcutaneous Adipose	JPH2	20	-3.93	8.36E-05	0.036	0.023	33	38
Aortic Artery	SNX7	1	-3.91	9.16E-05	0.082	0.168	14	14
Skeletal Muscle	MXD3*	5	3.908	9.30E-05	0.065	0.095	40	41
Transformed Fibroblast Cells	KCTD6	3	-3.85	1.19E-04	0.027	0.01	20	20
Heart: Atrial Appendage	MXD3*	5	3.821	1.33E-04	0.062	0.148	15	15
Skeletal Muscle	RPL29	3	3.809	1.39E-04	0.232	0.322	33	47
Skeletal Muscle	ZNF404	19	3.789	1.51E-04	0.062	0.163	34	38
Skeletal Muscle	WARS2	1	3.756	1.73E-04	0.266	0.41	21	21
Whole Blood Cells	EIF3F	11	-3.72	1.98E-04	0.093	0.149	25	25
Transformed Fibroblast Cells	LTBP4	19	3.714	2.04E-04	0.081	0.091	39	40
Transformed Fibroblast Cells	DOK5*	20	-3.7	2.17E-04	0.002	0.007	9	9
Spleen	REXO1	19	-3.66	2.55E-04	0.078	0.049	26	26
Subcutaneous Adipose	WARS2	1	3.631	2.82E-04	0.347	0.497	18	19
Skeletal Muscle	PDLIM7*	5	3.63	2.83E-04	0.202	0.268	28	35
Heart: Atrial Appendage	KDM4A	1	3.626	2.87E-04	0.002	0.052	4	4
Liver	SMYD2	1	3.616	2.99E-04	0.1	0.139	25	26
Heart: Atrial Appendage	PVRL2	19	3.6	3.18E-04	0.146	0.126	47	48
Transformed Fibroblast Cells	ENO1	1	-3.57	3.53E-04	0.008	0.02	14	15
Transformed Fibroblast Cells	PPP2CB	8	-3.56	3.65E-04	0.052	0.075	30	33
Transformed Fibroblast Cells	FAM124A	13	3.533	4.11E-04	0.01	0.016	5	6
Subcutaneous Adipose	PYGL	14	-3.53	4.12E-04	0.029	0.039	29	32
Skeletal Muscle	SVIP	11	-3.53	4.12E-04	0.162	0.191	33	41
Subcutaneous Adipose	BTBD19	1	3.532	4.13E-04	0.005	0.028	10	13
Skeletal Muscle	CCNDBP1	15	3.496	4.73E-04	0.007	0.007	7	7

*represents genes which localize to top GWAS signals (Table 2)

Performance prediction R²

Variance of the gene's predicted expression, calculated as $W'x G x W$ (where W is the vector of SNP weights in a gene's model, W' is its transpose, and G is the covariance matrix)

Number of SNPs included in the prediction model for that gene available in the FGF23GWAS summary statistics

Number of SNPs used to construct the prediction model for the gene in the tissue of interest using the GTExdata