Supplementary Table 1. Sample demographics for participants included in genome-wide association analyses. Mean ± s.d. are given.

Sample Characteristic	**FHS (up to n=2,753)**	**GS EA (up to n=1,238)**	**GS AA (up to n=840)**
% Male	46.55	44.89	38.17
% Diabetic †	8.68	5.82	11.65
% Hypertension ‡	21.82	26.35	40.16
% Smoking	18.28	22.87	30.09
Age (years)	54.8±9.8	44.5±13.2	43.3±12.3
Body mass index (kg/m^2)	27.4±5.0	28.6±6.2	31.8±8.0
LDL cholesterol (mg/dl)	126.9±33.1	125.3±37.1	120.9±38.6
Fibrinogen (mg/dl)	305.4±57.8	373.9±111.5	417.4±127.9
Maximal aggregation to lower ADP dose used in meta-analysis (%)	67.3 ± 24.8 (ADP 3uM)	44.2 ± 26.3 (ADP 2*u*M)	40.6 ± 28.3 (ADP 2*u*M)
Maximal aggregation to higher ADP dose used in meta-analysis (%)	77.6 ± 18.5 (ADP 5*u*M)	79.0 ± 14.1 (ADP 10*u*M)	76.2 ± 17.6 (ADP 10*u*M)
Threshold concentration (EC50) for 50% response to ADP (*u*M)	3.29 ± 1.5	n/a	n/a
Maximal aggregation to lower epinephrine dose used in meta-analysis (%)	57.1 ± 31.0 (Epi 1*u*M)	55.2 ± 33.5 (Epi 2*u*M)	50.2 ± 36.2 (Epi 2*u*M)
Maximal aggregation to higher epinephrine dose used in meta-analysis (%)	65.9 ± 28.4 (Epi 3*u*M)	70.8 ± 28.0 (Epi 10*u*M)	62.3 ± 34.5 (Epi 10*u*M)
Threshold concentration (EC50) for 50% response to epinephrine (*u*M)	1.93 ± 2.9	n/a	n/a
Lag time to collagen (seconds)	82.1±20.1 (190 µg/ml)	103.1 ± 60.8 (2 µg/ml)	114.5 ± 69.8 (2 µg/ml)

Values given are mean ± 1 s.d. Sample sizes for specific phenotypes are found in the Online Methods section.

†definition of Type II diabetes: fasting blood glucose > 126 mg/dL and/or anti-hypoglycemic medication use

‡definition of Hypertension: systolic blood pressure of >140 and diastolic blood pressure >90 and/or anti-hypertensive medication use

EA = European-ancestry, AA = African-ancestry.

Supplementary Table 2. Loci with 5.0x10^{-8} <p<1.0x10^{-4} in European-ancestry (EA) cohorts and p<0.05 in GS African-ancestry (AA) for platelet aggregation phenotypes.

SNP Information: SNPid, location, gene	Coded allele	Top EA SNP in region:[1] SNPid, p-value, r^2	FHS phenotype	FHS result: p-value, beta(sem), MAF	GS phenotype	GS (EA) result: p-value, beta(sem), MAF	EA meta-analysis p-value	GS (AA) result: p-value, beta(sem), MAF	EA + AA meta-analysis p-value
Loci associated with ADP aggregation									
rs525455 (A>G)* Chr 10: 13,143,291 Gene: ***MST151***	G	rs525455 5.5x10^{-5} Same SNP	ADP EC50 †	7.6x10^{-4} -0.02 (0.01) 45.9%	ADP 10*u*M	0.023 1.34 (0.59) 46.2%	5.5x10^{-5}	1.4x10^{-3} -3.52 (1.1) 26.6%	6.7x10^{-7}
rs179429 (G>A) Chr 11: 2,507,306 Gene: ***KCNQ1***	A	rs179428 5.9x10^{-6} r^2=0.87	ADP EC50 †	0.015 -0.02 (0.01) 16.7%	ADP 10*u*M	4.1x10^{-4} 2.47 (0.70) 17.6%	6.3x10^{-5}	0.033 2.54 (1.2) 17.3%	7.0x10^{-6}
rs1457806 (C>T) Chr 4: 160,934,451 Gene: ***RAPGEF2***	T	rs9996294 9.1x10^{-7} r^2=0.55	ADP 5*u*M	0.013 0.02 (0.01) 13.4%	ADP 10*u*M	7.2x10^{-5} 3.22 (0.81) 12.1%	1.2x10^{-5}	0.028 -2.29 (1.0) 41.4%	3.9x10^{-3}
Loci associated with epinephrine aggregation									
rs7071247 (G>T)* Chr 10: 105,247,776 Gene: ***NEURL***	T	rs3014183 3.5x10^{-5} r^2=0.92	Epi EC50 †	0.019 -0.07 (0.03) 11.9%	Epi 10*u*M	2.0x10^{-4} 5.54 (1.5) 15.6%	5.6x10^{-5}	1.8x10^{-4} 8.60 (2.3) 21.7%	2.0x10^{-7}
rs6052699 (G>A) Chr 20: 4,559,877 Gene: **nearest *PRNP***	A	rs6052699 9.5x10^{-5} Same SNP	Epi EC50 †	6.1x10^{-4} 0.07 (0.02) 49.3% ‡	Epi 2*u*M	0.047 -2.80 (1.4) 46.8%	9.5x10^{-5}	2.5x10^{-3} 6.56 (2.2) 23.6% ‡	1.7x10^{-6}
rs4947339 (C>T)* Chr 6: 29,024,231 Gene: **near *TRIM27***	T	rs6906909 2.0x10^{-5} r^2=1.00	Epi EC50 †	1.4x10^{-3} -0.06 (0.02) 43.8%	Epi 10*u*M	5.2x10^{-3} 3.14 (1.1) 44.3%	2.8x10^{-5}	0.025 -5.47 (2.4) 14.5% ‡	2.4x10^{-6}
rs1903595 (A>G) Chr 8: 14,433,852 Gene: ***SGCZ***	G	rs10111879 1.8x10^{-5} r^2=0.25	Epi 3*u*M	0.021 0.11 (0.05) 30.3%	Epi 10*u*M	2.1x10^{-4} 0.16 (0.04) 31.8%	3.4x10^{-5}	0.033 0.21 (0.10) 7.9%	4.5x10^{-6}
rs1874445 (C>T) Chr 11: 10,648,297 Gene: ***MRVI1***	T	rs4909945 7.6x10^{-7} r^2=0.61	Epi 3*u*M	0.010 0.11 (0.04) 37.6%	Epi 10*u*M	1.8x10^{-3} 0.13 (0.04) 40.2%	1.9x10^{-3}	0.05 0.10 (0.05) 39.3%	2.0x10^{-5}
rs7526348 (A>G) Chr 1: 190,390,334 Gene: **near *RGS18***	G	rs9996294 6.7x10^{-6} r^2=1.00	Epi EC50 †	1.6x10^{-4} -0.06 (0.02) 49.1%	Epi 2*u*M	0.014 3.67 (1.5) 49.9%	8.3x10^{-6}	0.030 4.33 (2.0) 32.6%	1.9x10^{-3}

rs6590203 (A>G)*		rs2236653		1.4x10^{-3}		4.5x10^{-3}		0.029	
Chr 11: 125,779,407	G	3.0x10^{-6}	Epi EC50 †	-0.06 (0.02)	Epi 10*u*M	3.50 (1.2)	2.6x10^{-5}	-3.95 (1.8)	4.0x10^{-3}
Gene: ***ST3GAL4***		r^2=0.87		41.0%		38.1%		44.9% ‡	
rs9888055 (C>T)*		rs11007689		9.1x10^{-4}		0.021		1.4x10^{-3}	
Chr 10: 29,995,655	T	4.4x10^{-5}	Epi EC50 †	0.08 (0.02)	Epi 2*u*M	-4.11 (1.8)	6.4x10^{-5}	7.27 (2.3)	0.02
Gene: ***SVIL***		r^2=1.00		17.7%		20.2%		40.6%	
Loci associated with collagen lag time									
rs7044355 (A>G)*		rs9299064		8.8x10^{-5}		0.037		8.2x10^{-4}	
Chr 9: 8,186,511	G	1.3x10^{-5}	Lag 190 *u*g/mL	0.01 (0.004)	Lag 2*u*g/mL	0.012 (0.006)	1.3x10^{-5}	-0.081 (0.024)	1.2x10^{-7}
Gene: **near *PTPRD***		r^2=0.60		49.9% ‡		49.9% ‡		27.0%	
rs6581827 (T>C)		rs6581827		7.3x10^{-4}		4.5x10^{-3}		0.036	
Chr 12: 67,170,158	C	1.5x10^{-5}	Lag 190 *u*g/mL	-0.01 (0.003)	Lag 2*u*g/mL	-0.017 (0.006)	1.5x10^{-5}	-0.057 (0.027)	3.2x10^{-3}
Gene: **near *RAP1B***		Same SNP		46.2%		48.9%		21.0% ‡	
rs12367822 (G>T)*		rs1870672		4.8x10^{-4}		6.6x10^{-3}		0.038	
Chr 12: 55,490,427	T	1.2x10^{-5}	Lag 190 *u*g/mL	0.01 (0.003)	Lag 2*u*g/mL	0.018 (0.007)	1.3x10^{-5}	0.063 (0.030)	1.1x10^{-6}
Gene:***HSD17B6***		r^2=0.90		27.7%		28.6%		15.3%	
rs2602376 (C>T)		rs6715829		0.018		7.4x10^{-5}		0.032	
Chr 2: 234,246,790	T	1.2x10^{-5}	Lag 190 *u*g/mL	-0.01 (0.003)	Lag 2 *u*g/mL	-0.026 (0.0066)	3.6x10^{-5}	0.099 (0.046)	0.01
Gene: ***UGT1A10***		r^2=0.56		28.6%		28.5%		6.7%	

Maximum sample sizes in GS AA were for ADP 10*u*M (n=836), epinephrine 10*u*M (n=840) and collagen 2*u*g/mL (n=763). For full details see Online Methods.

[1] The top meta-analysis SNP and p-value in EA for the same trait, and LD with the selected replication SNP based on HapMap CEU using SNAP[1] (Johnson et al., 2008).

*multiple SNPs in the gene region had p<0.05 in GS AA but only the most significant SNP in combined analysis is given

†The betas presented in the Table relate directly to the coded alleles and phenotypes presented. Because threshold concentrations (EC50 traits) are inversely related with maximal aggregation response, the signs of the betas for EC50 traits were flipped before meta-analysis.

‡For this population the coded allele was not the same as the minor allele

EA = European-ancestry, AA = African-ancestry.

Supplementary Table 3. Platelet aggregation GWAS results for SNPs associated with 2 different agonists with the same direction of effect in meta-analyses in European-ancestry (EA) cohorts (both SNPs $p<1.0\text{x}10^{-4}$), with the same SNP or a highly correlated SNP ($r^2>0.9$) being associated.

Gene(s) in region	Chr	Pos (Mb)	Agonist meta-analysis	SNP	Meta-analysis p-value in EA	Agonist meta-analysis	SNP	Meta-analysis p-value in EA	Relationship between agonist SNPs	Replication evidence in AA with genotyped SNP?
PEAR1	1	155.1	ADP3um2um	rs12566888	3.4e-12 (++)	EpiEC50 2um	rs12566888	7.3e-10 (++)	Same SNP	Yes
RGS18	1	190.4	ADP5um10um	rs4128880	4.0e-05(++)	EpiEC50 2um	rs4128880	6.8e-07 (++)	Same SNP	Yes
NUP210	3	13.3	ADPEC50 10um	rs9841645	8.8e-05 (++)	EpiEC50 10um	rs9841645	4.2e-05 (++)	Same SNP	No (1 SNP in region)
FBXL7	5	15.5	ADP5um10um	rs304586	2.3e-05 (++)	Epi1um2um	rs304586	2.9e-06 (++)	Same SNP	No (1 SNP in region)
ADAMTS2	5	178.7	ADP3um2um	rs467053	7.1e-05 (--)	Epi3um10um	rs467053	6.8e-05 (--)	Same SNP	No (1 SNP in region)
GMDS	6	2.3	ADP3um2um	rs2479008	6.1e-05 (++)	Epi1um2um	rs2505675	8.1e-05 (++)	r^2=1.00	No (1 SNP in region)
KLHL31	6	53.6	ADP5um10um	rs9474604	6.3e-05 (++)	Epi1um2um	rs6901352	6.0e-05 (++)	r^2=1.00	No (1 SNP in region)
WBSCR17	7	70.6	ADPEC50 2um	rs4236251	1.7e-05 (++)	Epi3um10um	rs4236251	6.3e-05 (++)	Same SNP	No (2 SNPs in region)
STMN4	8	27.1	ADPEC50 10um	rs17366330	5.6e-05 (++)	EpiEC50 10um	rs17366330	9.0e-05 (++)	Same SNP	n/a
PSKH2, ATP6V0D2	8	87.1	ADPEC50 10um	rs16876805	8.7e-06 (++)	EpiEC50 2um	rs16876805	7.9e-06 (++)	Same SNP	No (1 SNP in region)
PIP5K1B	9	70.7	ADPEC50 2um	rs11144351	2.2e-07 (++)	EpiEC50 10um	rs11144351	8.0e-06 (++)	Same SNP	No (8 SNPs in region)
CUBN	10	17.1	ADP3um2um	rs12359150	1.9e-05 (++)	EpiEC50 2um	rs12359150	8.1e-05 (++)	Same SNP	No (1 SNP in region)
SVIL	10	29.9	ADPEC50 10um	rs3847393	8.2e-05 (--)	EpiEC50 2um	rs3847393	5.9e-05 (--)	Same SNP	Yes
MRVI1	11	10.6	ADP5um10um	rs7940646	2.0e-08 (++)	EpiEC50 10um	rs4909945	7.6e-07 (++)	r^2=0.96	Yes
MIPOL1	14	36.8	ADPEC50 2um	rs7143938	4.9e-05 (++)	Epi3um10um	rs7143938	2.2e-05 (++)	Same SNP	No (16 SNPs in region)
THSD4	15	69.6	ADPEC50 10um	rs12443484	4.4e-05 (++)	EpiEC50 10um	rs12443484	8.2e-05 (++)	Same SNP	n/a
FLJ39743	15	96.7	ADP3um2um	rs8030441	1.5e-05 (--)	Epi1um2um	rs8030441	3.3e-05 (--)	Same SNP	No (1 SNP in region)
KIAA0802	18	8.8	ADP3um2um	rs689607	7.2e-05 (++)	Epi1um2um	rs689607	9.6e-06 (++)	Same SNP	No (1 SNP in region)
SETBP1	18	39.9	ADP5um10um	rs17686693	5.4e-06 (++)	Epi3um10um	rs17686693	1.3e-06 (++)	Same SNP	n/a
HMG1L1,PCK1,CTCFL	20	55.5	ADPEC50 2um	rs6123703	1.1e-06 (++)	EpiEC50 10um	rs6123703	5.2e-06 (++)	Same SNP	No (1 SNP in region)

p-values are given in columns with the direction of effect relative to the minor allele is indicated in parentheses for FHS and then GS EA cohorts, respectively. For those regions with no replication evidence in AA the number of SNPs with $p<1.0\text{x}10^{-4}$ in EA cohorts that were genotyped and tested in AA is listed. "n/a" indicates no genotyped SNPs were available for testing.

EA = European-ancestry, AA = African-ancestry.

Supplementary Table 4. Overview of loci associated with platelet aggregation in response to agonists in the current study including known functions particularly of relevance to platelet biology, known gene expression in platelets or megakaryocytes, and other genes in the region.

Locus	Representative gene and description of known functions	Effects of minor alleles on platelet aggregation to agonists	Expression in platelets	Expression in megakaryocytes[†]	Other genes ± 60kb of peak SNP
Loci with $p<5.0x10^{-8}$					
1q23.1	*PEAR1* – a transmembrane receptor phosphorylated upon platelet-platelet contact[2], expressed in platelets and endothelial cells, activation inhibited by inhibitors of platelet aggregation	↓ ADP, ↓ epinephrine	Yes[2,3]	not measured	*NTRK1, C1orf92, ARHGEF11, INSRR*
11p15.4	*MRVI1* – inositol-1,4,5-triphosphate receptor-kinase I, expressed in platelets, deletion of a phosphorylated domain in mice inhibits fibrinogen-receptor activation and platelet aggregation, deletion also causes failure of NO to prevent arterial thrombosis in a mouse model[4]	↑ ADP, ↑ epinephrine	Yes[4]	↑ 1.1 fold[5]	
7q36.3	*SHH* – key protein influencing developmental patterning and embryogenesis, SHH-positive microvesicles may induce differentiation along megakaryocyte lineages[6]	↑ ADP	Unknown	↓ 0.7 fold	
10q25.2	*ADRA2A*- epinephrine receptor on platelet cell surface, prior associations implicate the gene in inter-individual variability in epinephrine-induced aggregation[7-9] with suggested mediation via RNA and protein levels[10]	↓ epinephrine	Yes[9,10]	↑ 2.3 fold	
7q22.3	*PIK3CG* - phosphatidylinositol 3-kinase, animal models indicate a role in $\alpha_{IIb}\beta_3$ activated platelet aggregation and thrombosis[11], in macrophage activation[12] and wound healing[13]. Specific inhibitors show effects on arthritis[14] and SLE[15]. Prior human associations with platelet volume[16]	↓ epinephrine	Yes[16]	↑ 3.7 fold	*FLJ36031*

10q21.2	*JMJD1C* – member of the jumonji family of transcription factors, classified as a thyroid hormone receptor. Animal models support a role for jumonji in development of cardiac myocytes as well as proliferation of megakaryocytes[17]	↑ epinephrine	Unknown	↑ 4.0 fold	
19q13.42	*GP6* – direct receptor for activation of platelet aggregation on collagen contact, previous functional variation described[18,19], critical to wound closure while also a factor in thrombus formation[20]	↑ collagen lag	Yes[18,19,20]	↑ 7.0 fold	*NLRP2, RDH13*
Selected suggestive regions (consistent across ≥2 populations, $p>5.0x10^{-8}$)					
4q32.1	*RAPGEF2* - guanine nucleotide exchange factor involved in signaling, with a role in the activation of RAP1[21,22] (see below)	↑ ADP	Unknown	not measured	
11p15.5	*KCNQ1* – voltage-gated potassium channel, mutated in some long QT syndromes	↑ ADP	Unknown	↓ 0.7 fold	
17q11.2	*TAOK1* – serine-threonine protein kinase, may regulate mitotic progression, previously associated with mean platelet volume[23]	↑ ADP	Unknown	↑ 6.8 fold	
3q25.1	*P2RY12* - purinergic receptor involved in ADP activation of platelet aggregation, prior candidate gene associations implicate in ADP response and bleeding disorders	↓ ADP	Yes	↓ 0.6 fold	*MED12L, GPR87, P2RY13*
1q31.2	*RGS18* - regulator of G-protein signaling 18, highly expressed in platelets and megakaryocytes[24-27], its phosphorylation may be an important mediator of platelet signaling[27]	↑ ADP , ↑ epinephrine	Yes[24-27]	↑36.8 fold	
11q24.2	*ST3GAL4* - sialyltransferase that interacts with Ashwell receptors for clearance of desialylated platelets with effects on platelet homestasis[28]. Genetic lesion in mice and expression defects in humans indicate a role in bleeding disorder[29]	↑ epinephrine	Yes	↑ 1.5 fold	*KIRREL3*

20p13	*PRNP* – human prion protein (PrP^{C}), a sialyoglycoprotein expressed on platelets and upregulated upon platelet activation[30]. Notably human prion protein is normally isolated from platelets and this is a hypothesized tissue for transmission of Creutzfeldt-Jakob disease[31]. A variant (rs1799990) has been noted to be associated with the ability to amplify PrP^{C} from individual platelet samples[31]	↓ epinephrine	Yes[30,31]	↑ 5.2 fold	
12q15	*RAP1B* – RAS-like protein similar to small GTP-binding proteins, has a demonstrated role in platelet aggregation[32-34], specific role in collagen-mediated aggregation[34], with known signaling relation with PIK3CG and RAPGEF2 (see above). Rap1b -/- mice have a bleeding defect due to defective platelet function, with decreased response to agonists and protection from arterial thrombosis[35]	↓ collagen lag	Yes[32-34]	↑17.8 fold	
1q23.3	*FCER1G* – high affinity IgE receptor subunit, critical to allergic reactions, gene previously associated with response to a collagen-related peptide[3]	↓ collagen lag	Yes[3]	↑ 26.2 fold	*NDUFS2, APOA2, TOMM40L, NR1I3, PCP4L1, MPZ, SDHC*

[†] indicates the average fold intensity of a representative gene transcript relative to the mean background intensity across stem-cell derived megakaryocytes measured with the Illumina Human WG-6 v2 (n=4 individuals), further described in Watkins *et al.*[36]

Supplementary Table 5. Platelet aggregation meta-analysis GWAS results for prior candidate SNPs and gene regions.

5a. Platelet aggregation results for candidate SNPs.

Gene	SNP	Position	ADP2uM3uM	ADP5uM10uM	ADPEC50 2uM	ADPEC50 10uM	Epi1uM2uM	Epi3uM10uM	EpiEC50	EpiEC50 10uM	Collagen
ITGB3	rs5918	Leu33Pro	0.38 (++)	0.91 (-+)	0.92 (-+)	0.73 (-+)	0.58 (+-)	0.96 (-+)	0.99 (-+)	0.71 (-+)	0.26 (--)
ITGA2	**rs1126643**	**Phe224Phe**	0.93 (-+)	0.20 (++)	0.82 (-+)	0.98 (-+)	0.65 (-+)	0.97 (+-)	0.41 (-+)	0.24 (--)	**8.8e-03 (--)**
GPIbα	**rs6065**	**Thr161Met**	0.71 (-+)	0.54 (-+)	0.83 (-+)	0.74 (-+)	**0.03 (--)**	0.07 (--)	**0.032 (--)**	**0.027 (--)**	0.58 (++)
	rs2243093	-5 T/C	0.48 (+-)	0.42 (--)	0.71 (+-)	0.21 (+-)	0.67 (++)	0.19 (++)	0.60 (++)	0.24 (++)	0.77 (--)
*P2RY1**	rs701265	Val262Val	0.051 (--)	0.93 (-+)	0.06 (--)	0.34 (-+)	0.12 (--)	0.054 (--)	0.22 (--)	0.11 (--)	0.68 (+-)
P2RY12	**rs1472122**	**5'UTR adj.**	**2.0e-04 (--)**	**0.048 (--)**	**9.5e-04 (--)**	**8.0e-03 (--)**	0.19 (--)	0.08 (-+)	0.07 (-+)	0.10 (-+)	0.27 (++)
	rs10935839	**intronic**	0.10 (--)	0.21 (--)	**0.029 (--)**	**0.018 (--)**	0.51 (--)	0.35 (-+)	0.13 (-+)	0.14 (-+)	0.50 (++)
***PIK3CG*[1]**	**rs342293**	**intergenic**	0.28 (++)	0.44 (++)	**4.5e-03 (++)**	**2.0e-03 (++)**	**8.4e-04 (++)**	0.17 (++)	**6.2e-09 (++)**	**4.3e-07 (++)**	0.82 (-+)
***ARHGEF3*[2]**	**rs12485738**	**intronic**	**7.8e-03 (++)**	0.45 (++)	**0.049 (++)**	0.16 (++)	0.80 (-+)	0.67 (--)	**0.047 (++)**	0.15 (+-)	0.22 (--)
TAOK1[2]	rs2138852	intergenic	0.94 (-+)	0.55 (-+)	0.43 (-+)	0.19 (-+)	0.27 (-+)	0.18 (-+)	0.49 (-+)	0.35 (-+)	0.16 (--)
WDR66[2]	rs7961894	intronic	0.09 (--)	0.21 (--)	0.74 (+-)	0.62 (+-)	0.12 (++)	0.07 (++)	0.08 (++)	0.21 (++)	0.19 (--)

5b. Platelet aggregation results for candidate gene regions.

Gene	Reason	# SNPs tested	ADP trait meta-analysis	SNP with lowest p-val.	p-value	Epi trait meta-analysis	SNP with lowest p-val.	p-value	Collagen	SNP with lowest p-val.	p-value
ITGB3	Candidate	156	ADP5um10um	rs11871477	0.025(--)	Epi1um2um	rs2071438	0.018 (++)	Collagen	rs2071438	0.013(--)
ITGA2	Candidate	381	ADP5um10um	rs10059321	0.0017(--)	Epi1um2um	rs2056401	0.0012 (--)	Collagen	rs3212603	0.00030(++
GPIbα	Candidate	72	ADPEC50 10um	rs9901006	0.016(++)	EpiEC50 10um	rs2302318	0.0068 (++)	Collagen	rs2243107	0.15(++)
P2RY1	Candidate	81	ADP3um2um	rs6803505	0.020(--)	Epi1um2um	rs9289876	0.022 (+-)	Collagen	rs2165045	0.22(--)
P2RY12	**Candidate**	**218**	**ADP3um2um**	**rs16863323**	**8.2e-06 (--)**	EpiEC50 10um	rs16863336	0.0011 (--)	Collagen	rs6793061	0.035(--)
ARHGEF3	MPV[2]	144	ADP5um10um	rs4455300	0.00058(--)	Epi1um2um	rs9851853	0.0029 (++)	Collagen	rs11716680	0.016(--)
TAOK1	**MPV[2]**	**113**	**ADP5um10um**	**rs12936923**	**6.9e-05 (++)**	Epi3um10um	rs2586150	0.0029 (--)	Collagen	rs8070136	0.051(++)
WDR66	MPV[2]	116	ADPEC50 2um	rs1169076	0.0049(--)	EpiEC50 10um	rs830120	0.013 (++)	Collagen	rs7976716	0.055(++)
RAF1	ADP[3]	120	ADP3um2um	rs9809501	0.0051(++)	Epi3um10um	rs3773341	0.028 (++)	Collagen	rs4684111	0.0014(++)
JAK2	ADP[3]	207	ADPEC50 2um	rs12377744	0.015(++)	Epi3um10um	rs10974892	0.023 (++)	Collagen	rs2182726	0.0030(++)
GNAZ	ADP[3]	139	ADPEC50 2um	rs6003461	0.020(--)	Epi3um10um	rs737818	0.06 (++)	Collagen	rs6003461	0.07(++)
VAV3	ADP[3]	563	ADPEC50 10um	rs6583042	0.0021(--)	EpiEC50 10um	rs17019729	0.00038 (++)	Collagen	rs11185128	0.026(--)
MAP2K2	ADP[3]	50	ADPEC50 10um	rs350856	0.0049(--)	EpiEC50 2um	rs3760905	0.012 (++)	Collagen	rs164631	0.056(++)

MAPK14	ADP[3]	127	ADP3um2um	rs2145361	0.0080(--)	EpiEC50 10um	rs13196204	0.015 (--)	Collagen	rs17715303	0.0017(--)
FCER1G	**Collagen[3]**	**92**	ADP3um2um	rs10494345	0.0075(++)	Epi1um2um	rs4489574	0.028 (++)	**Collagen**	**rs2501865**	**1.6e-05(--)**
CD36	Collagen[3]	188	ADP3um2um	rs9649529	0.021(++)	EpiEC50 10um	rs3212009	0.012 (--)	Collagen	rs13239216	0.012(++)
AKT2	Collagen[3]	65	ADP5um10um	rs10402740	0.030(--)	EpiEC50 2um	rs8111561	0.0035 (++)	Collagen	rs10415181	0.034(--)
MAP2K4	Collagen[3]	123	ADP3um2um	rs1468501	0.0039(--)	Epi3um10um	rs7215869	0.053 (--)	Collagen	rs8067785	0.0021(++)
ITPR1	Collagen[3]	646	ADP5um10um	rs9858750	9.2e-05 (++)	Epi1um2um	rs6793265	0.0011 (--)	Collagen	rs304048	0.0015(--)

p-values are given in columns with the direction of effect for FHS and then GS European-ancestry cohorts, respectively, indicated in parentheses.

SNPs in bold have p-values <0.05 in Supplementary Table 5a, or survive a Bonferroni threshold of 0.05/n where n is the number of SNPs tested in the gene region in Supplementary Table 5b.

All SNPs in the meta-analysis within 60 kb of either end of the full length transcript were examined to determine the strongest SNP association in Supplementary Table 5b.

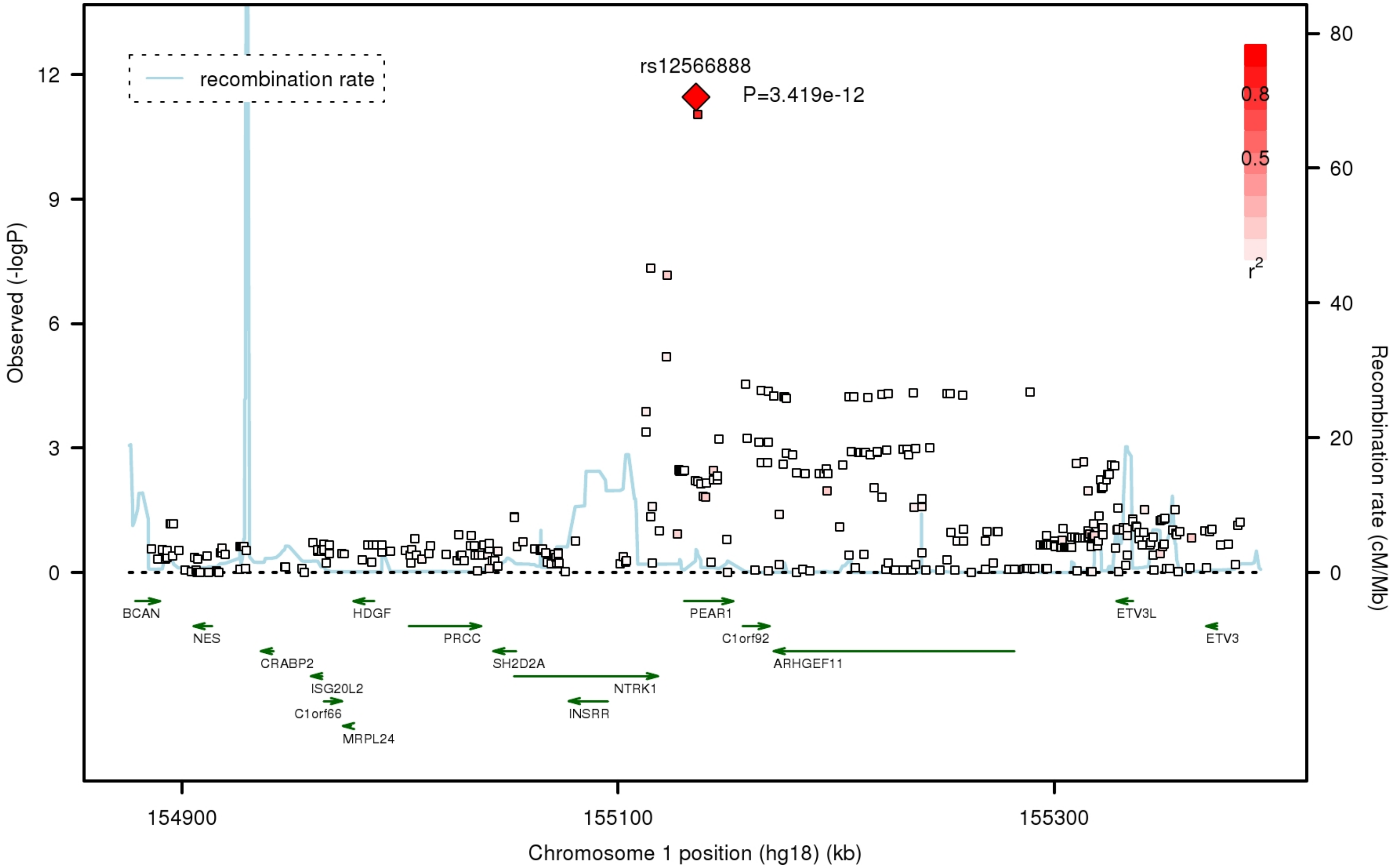
*note candidate SNP P2RY1 893 C>T (rs1065776) is not found in HapMap or in the meta-analysis dataset

[1] Region and trait identified from Soranzo et al., 2009[16].

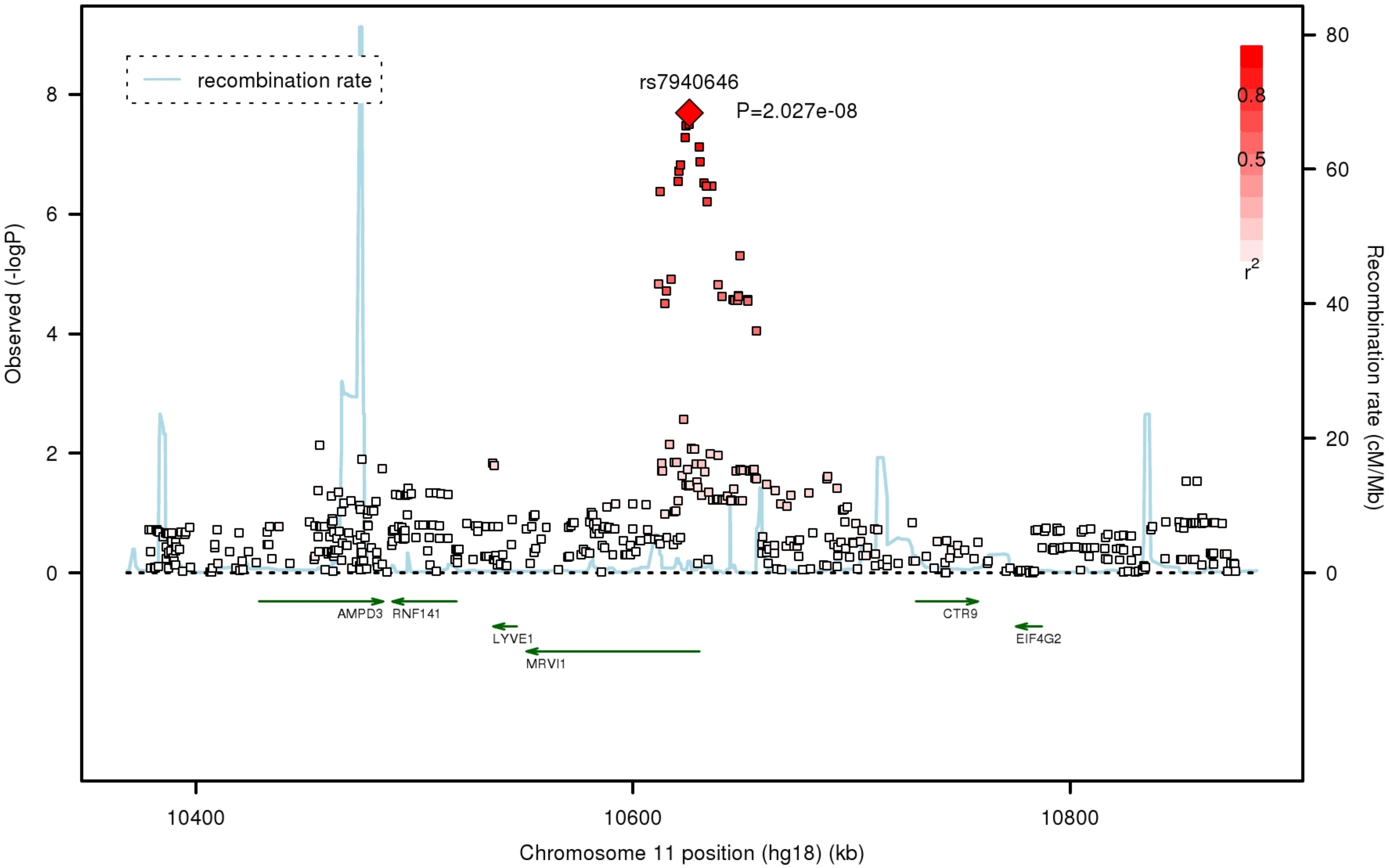
[2] Regions and traits identified from Meisinger et al., 2009[23].

[3] Regions and traits identified from Jones et al., 2009[3].

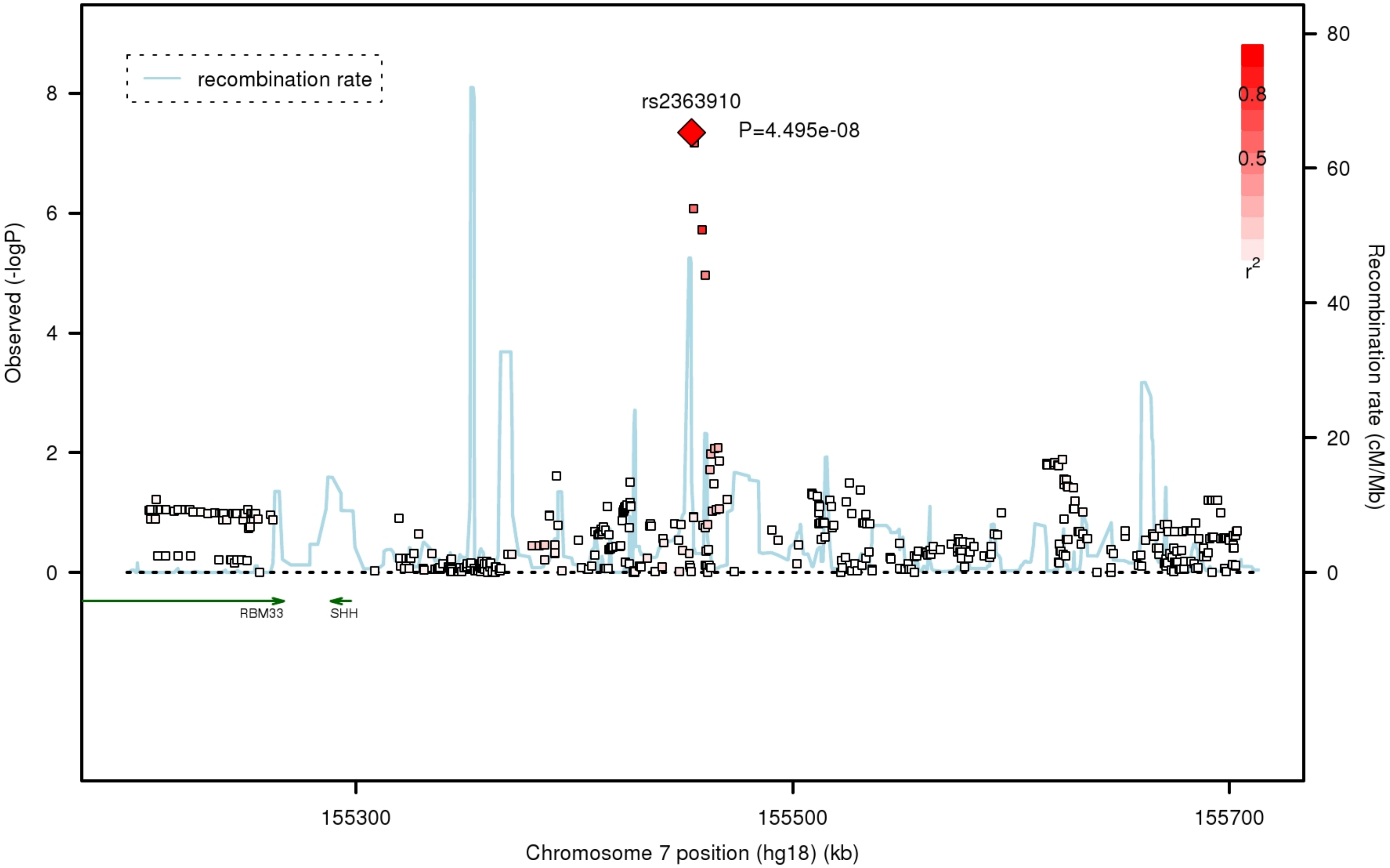
Supplementary Figure 1. SNAP[1] regional plots of meta-analysis associations. ADP-induced aggregation **1a:** (3 *u*M FHS, 2 *u*M GS) at 1q23.1, **1b:** (5 *u*M FHS, 10 *u*M GS) at 11p15.4, **1c:** (EC50 FHS, 10 *u*M GS) at 7q36.3, epinephrine-induced aggregation **1d:** (EC50 FHS, 2 *u*M GS) at 10q25.2, **1e:** (EC50 FHS, 2 *u*M GS) at 1q23.3, **1f:** (EC50 FHS, 2 *u*M GS) at 7q22.3, **1g:** (EC50 FHS, 2 *u*M GS) at 10q21.2, and lag time to collagen, **1h:** (2 *u*g/mL FHS, 190 *u*g/mL GS) at 19q13.42.



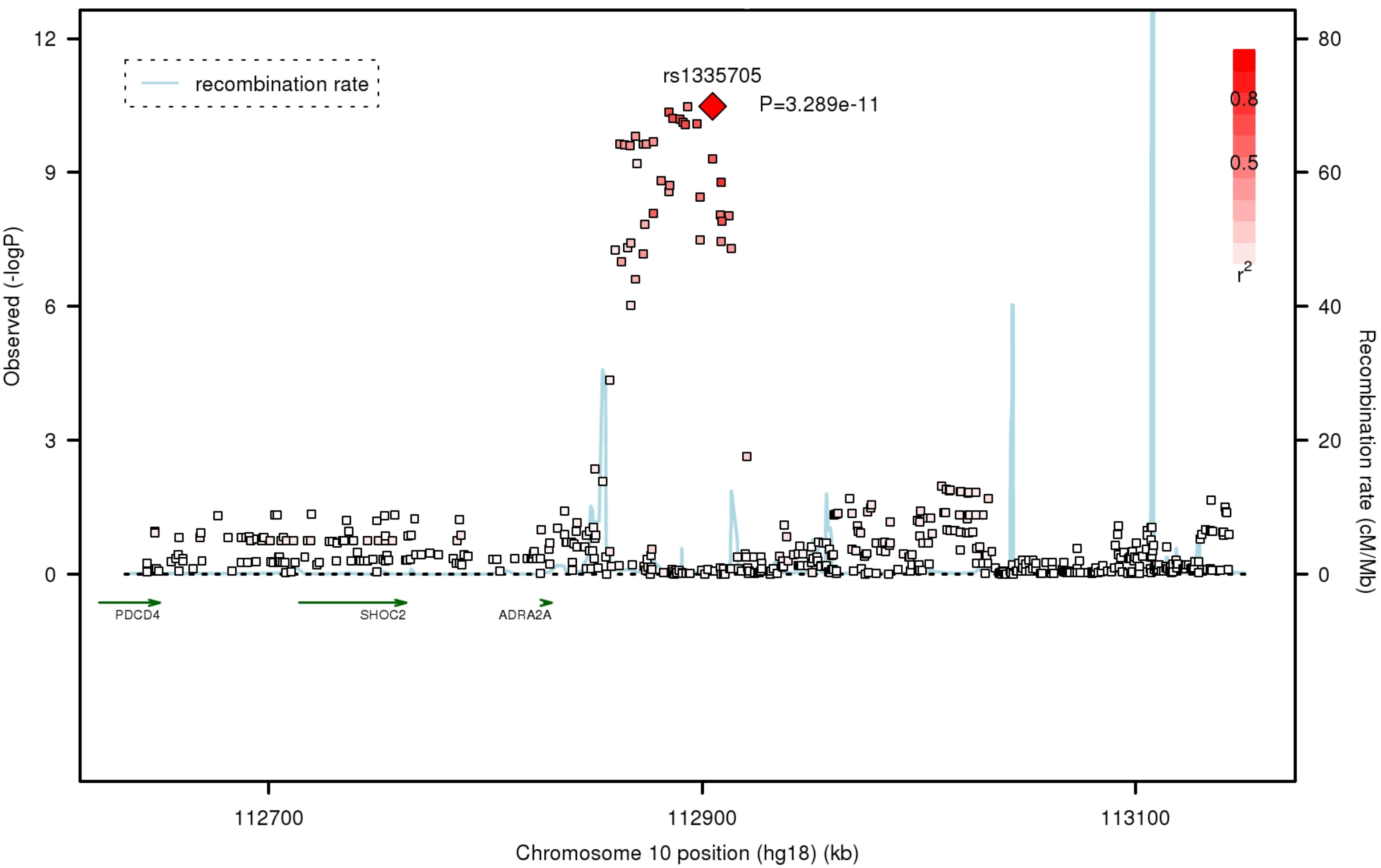
Supplementary Figure 1b



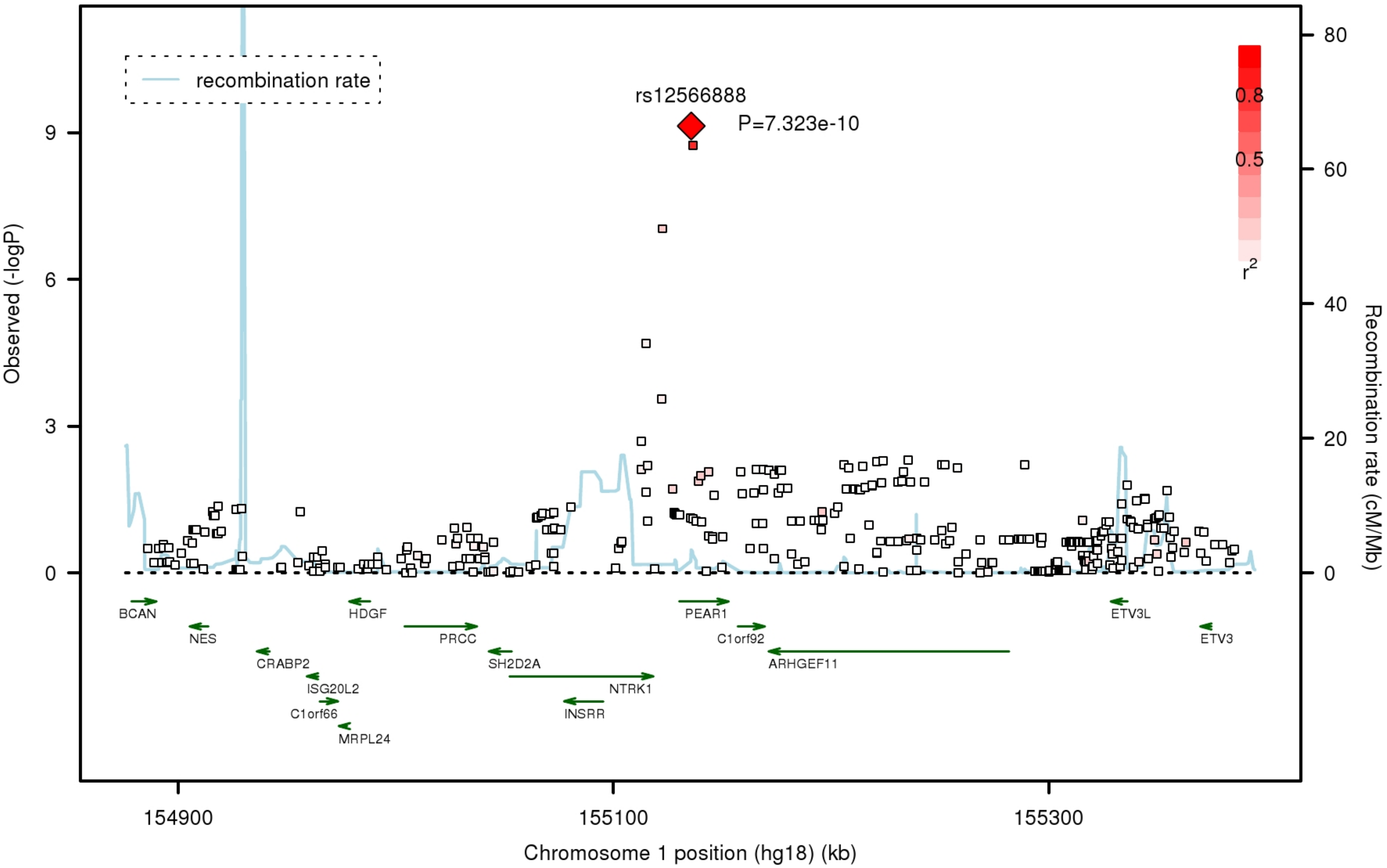
Supplementary Figure 1c



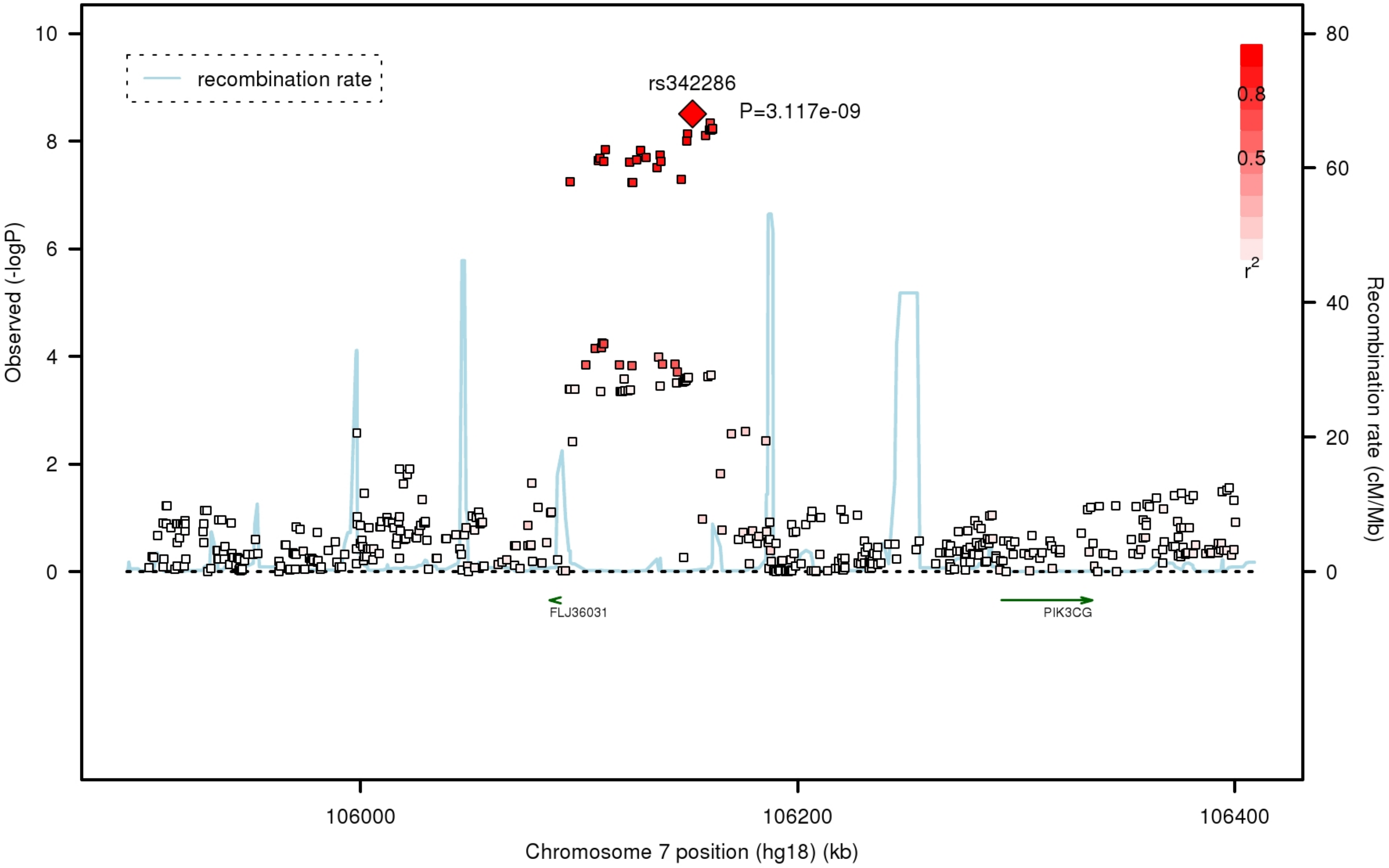
Supplementary Figure 1d



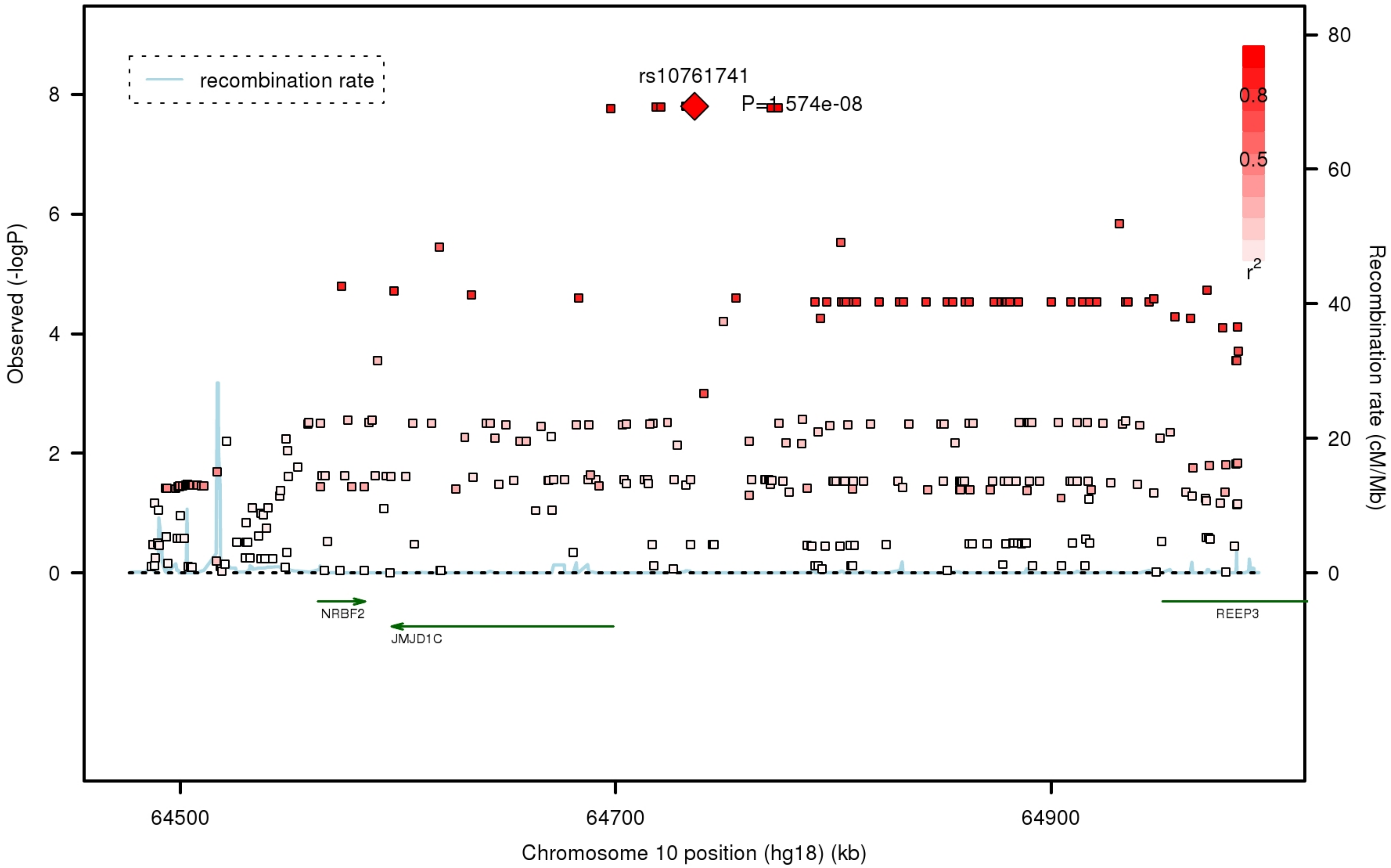
Supplementary Figure 1e



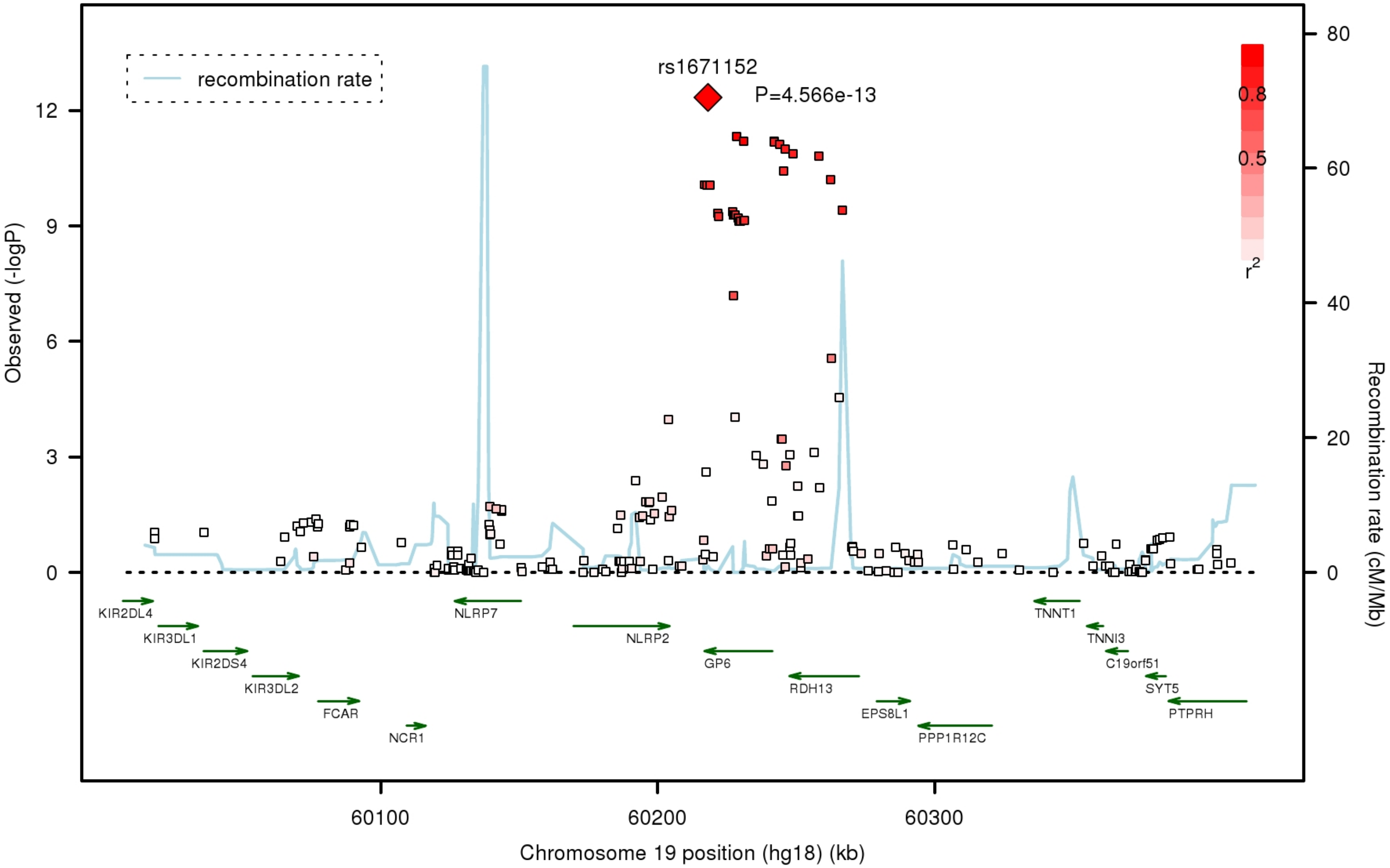
Supplementary Figure 1f



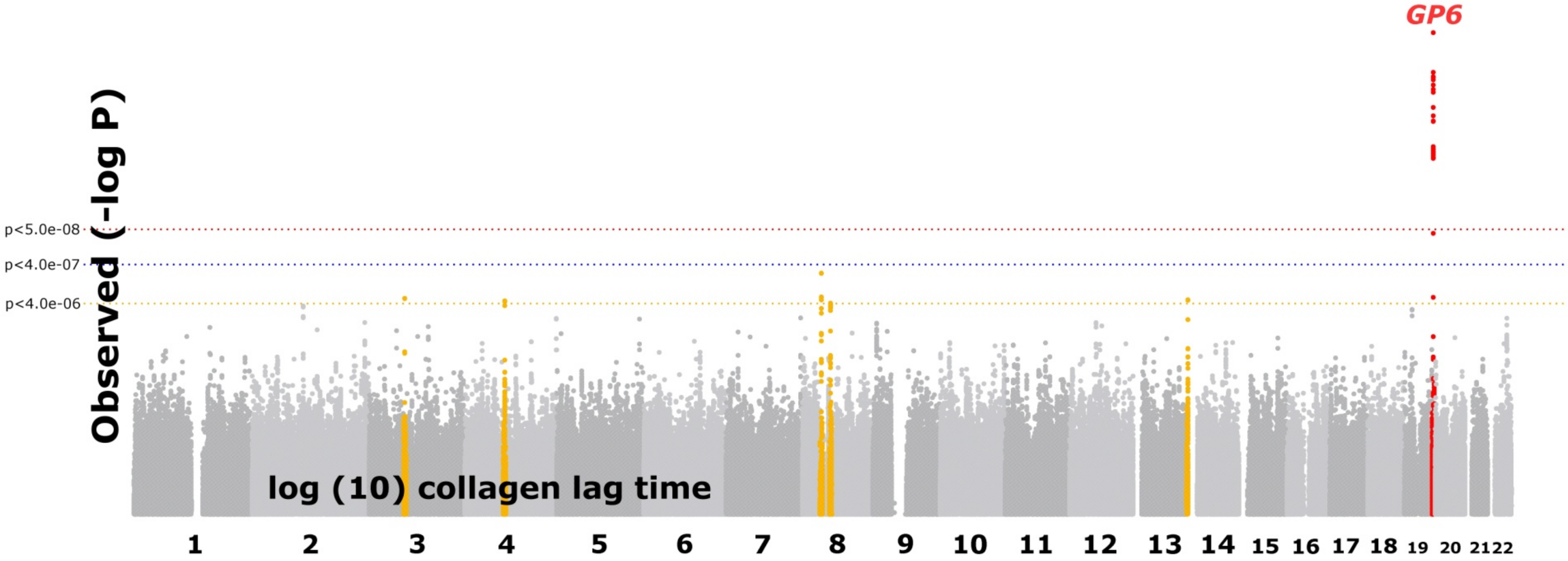
Supplementary Figure 1g



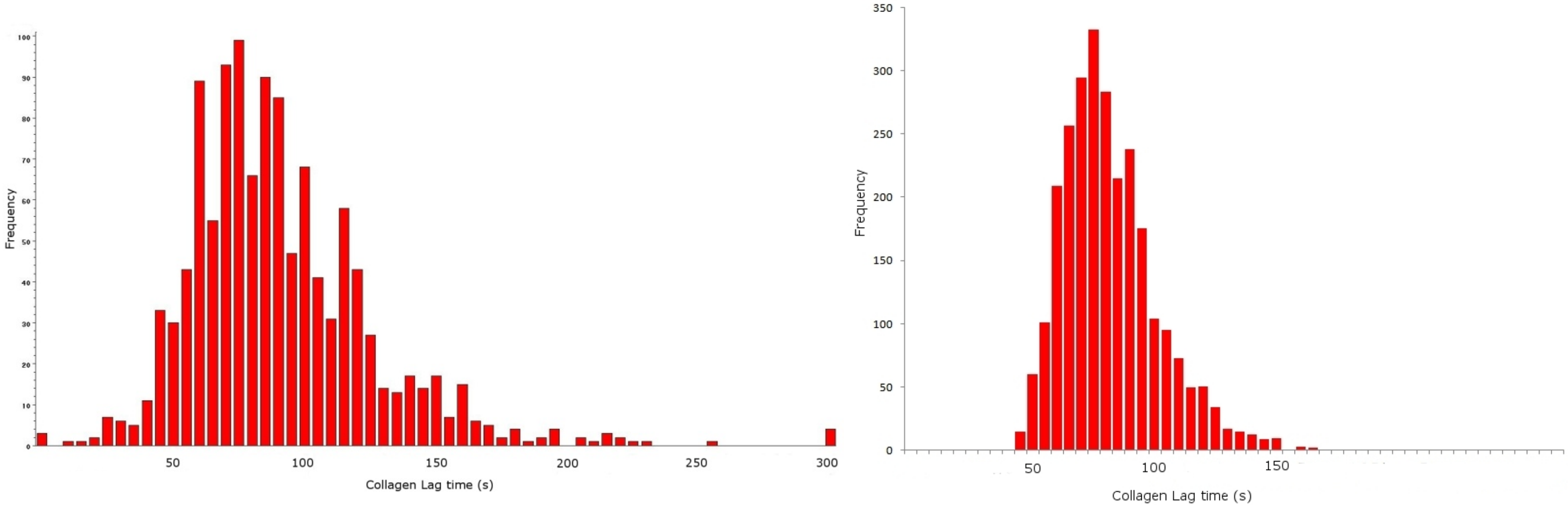
Supplementary Figure 1h



Supplementary Figure 2. Genome-wide association meta-analysis plot of associations with $\log_{10}$ lag time in response to collagen after filtering of SNPs for QC. Colored points are SNPs ± 250 kb from a SNP with association stronger than a p-value threshold as follows: red ($p<5.0\times10^{-8}$) and orange ($p<4.0\times10^{-6}$).



Supplementary Figure 3. Collagen lag time distributions. Distributions for GS at left (to 2 *u*g/ml equine-tendon derived collagen) and FHS at right (to 190 *u*g/ml calf-skin derived collagen).



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