SUPPLEMENTAL MATERIAL

Genome-wide association study identifies seven novel loci associating with circulating cytokines and cell adhesion molecules in Finns

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Table S1. Distributions of the unadjusted and untransformed inflammatory phenotypes in the NFBC1966.

Phenotype	N	Mean	SD	Median	IQR	Inter-assay CV %	Intra-assay CV %
sE-selectin (ng/ml)	5100	33.39	15.56	31.56	18.61	28.0	7.5
sICAM-1 (ng/ml)	5100	145.35	60.49	134.81	53.70	15.9	8.3
sVCAM-1 (ng/ml)	5100	1644.40	396.67	1609.73	481.99	13.9	7.9
VEGF (pg/ml)	4941	222.96	2840.43	62.77	164.39	20.6	7.5
IL17 (pg/ml)	4974	77.68	1331.38	21.86	40.76	8.4	2.5
IL1α (pg/ml)	4917	77.81	690.51	7.17	41.88	11.0	4.0
IL1β (pg/ml)	4971	7.48	87.60	0.72	5.34	9.5	3.0
IL1ra (pg/ml)	4864	85.02	1088.30	10.78	34.15	13.0	4.6
IL4 (pg/ml)	4962	49.16	912.08	2.36	19.45	10.4	3.0
IL6 (pg/ml)	4966	17.85	124.09	2.45	8.85	7.7	2.6
IL8 (pg/ml)	4974	46.20	454.39	16.33	24.99	7.6	2.2
IP10 (pg/ml)	4975	442.61	433.54	364.51	231.40	8.3	4.5
MCP1 (pg/ml)	4975	309.68	128.31	294.46	143.97	6.7	3.1
sCD40L (pg/ml)	4970	567.59	975.28	395.33	339.14	14.9	3.7
TNFα (pg/ml)	4971	10.99	97.63	5.94	4.06	7.2	2.6
PAI-1 (ng/ml)	5100	20.99	28.43	11.58	17.73	18.6	6.8

SD, standard deviation; IQR, interquartile range; CV, coefficient of variation.

Table S2. Genomic inflation factors for the 16 studied inflammatory markers.
The genomic inflation factors were calculated in R as median(Z^2)/qchisq(0.5,1), where Z is the effect estimate per standard error ratio.

Marker	Genomic lambda
sE-selectin	1.024
sICAM-1	1.022
sVCAM-1	1.011
VEGF	0.995
IL17	1.006
IL1α	1.023
IL1β	1.007
IL1ra	0.989
IL4	0.998
IL6	0.992
IL8	1.000
IP10	0.989
MCP1	0.991
sCD40L	1.006
TNFα	0.990
PAI-1	1.005

Table S3. Traits associated previously with the novel loci identified in the present study.

If multiple studies reported associations with the same trait or if multiple SNPs were associated with the same trait, the strongest SNP with the smallest P-value is given.

	Trait	P-value	SNP	PMID
sE-selectin in NFBC1966; ST3GAL4; 11q24.2; 11:126266665; rs11220471				
Biobank Engine (inquiry the lead SNP)	na			
Phenoscanner (inquiry the lead SNP)	Mean platelet volume	8.81e-06	rs11220471	27863252
GWAS Catalog (inquiry +-500 kb around the lead SNP)	Blood protein levels (Cell adhesion molecule-related/down-regulated by oncogenes, CDON.4541.49.2)	4.00e-86	rs562022020	29875488, 28240269
	C-reactive protein levels or LDL-cholesterol levels (pleiotropy)	6.00e-17	rs11220463	27286809
	Cholesterol, total	2.00e-15	rs11220462	28334899, 24097068, 20686565, 25961943
	Eosinophil percentage of granulocytes	1.00e-10	rs8177376	27863252
	LDL cholesterol	2.00e-22	rs17135399	28334899, 24097068, 20686565, 25961943
	Liver enzyme levels (alkaline phosphatase)	2.00e-09	rs2236653	22001757
	Lung function (FEV1)	5.00e-10	rs567508	28166213
	Mean platelet volume	3.00e-30	rs7949566	27863252
	Mumps	1.00e-08	rs3862630	28928442
	Neutrophil percentage of granulocytes	3.00e-12	rs8177376	27863252
	Neutrophil percentage of white cells	5.00e-10	rs73017399	27863252
	Platelet count	2.00e-18	rs4937127	27863252
	Platelet distribution width	4.00e-13	rs7949566	27863252
	Primary tooth development (time to first tooth eruption)	4.00e-08	rs4937076	23704328
	Serum alkaline phosphatase levels	6.00-41	rs10893506	29403010
sVAM-1 in NFBC1966; ABO; 9q34.2; 9:136131322; rs8176746				
Biobank Engine (inquiry the lead SNP)	Red blood cell (erythrocyte) count	5.13e-24	rs8176746	(https://biobankengine.stanford.edu)
	Platelet crit.	3.15e-18	rs8176746	(https://biobankengine.stanford.edu)
	Impedance of whole body	5.60e-13	rs8176746	(https://biobankengine.stanford.edu)
	Immature reticulocyte fraction	2.73e-10	rs8176746	(https://biobankengine.stanford.edu)
	Deep venous thrombosis	7.89e-15	rs8176746	(https://biobankengine.stanford.edu)
Phenoscanner (inquiry the lead SNP)	Reed blood cell count + multiple other red bood cell-related traits	1.95e-53	rs8176746	27863252
	Plasma carcinoembryonic antigen CEA levels	4.70e-36	rs8176746	23300138
	Activated partial thromboplastin time	1.77e-22	rs8176746	22703881
	Von Willebrand factor vWF	1.59e-17	rs8176746	23381943
	Factor XIII antigen	1.19e-14	rs8176746	23381943
	Blood clot in the leg	1.21e-14	rs8176746	UKBB
	TNFa	1.96e-14	rs8176746	18464913
	Impedance of whole body	6.25e-13	rs8176746	UKBB
	Angiotensin convertin enzyme ACE activity	2.92e-10	rs8176746	20066004
	Low-density lipoprotein	2.29e-08	rs8176746	24097068

Table S3. Continues.

	Trait	P-value	SNP	PMID
sVAM-1 in NFBC1966; *ABO*; 9q34.2; 9:136131322; rs8176746 (continues)				
GWAS Catalog (inquiry +-500 kb around the lead SNP)	ADAMTS13 levels	1.00e-57	rs28673647	29296746, 25934476
	Angiotensin-converting enzyme activity	3.00e-08	rs495828	20066004
	Basophil percentage of white cells + multiple other white blood cell-related traits	5.00e-25	rs550065584	27863252
	Blood protein levels (E-selectin)	1.00e-96	rs651007	28240269, 19729612
	Cholesterol, total	4.00e-49	rs579459	28334899, 24097068, 20686565, 25961943
	Coagulation factor levels	2.00e-138	rs687289	23267103
	Coronary artery disease or stroke	4.00e-14	rs579459	21378990, 29212778, 24262325, 27997041, 29531354
	Diastolic blood pressure	2.00e-18	rs6271	27618452
	Elevated serum carcinoembryonic antigen levels	2.00e-24	rs8176741	24941225
	End-stage coagulation	2.00e-25	rs651007	23381943
	Endothelial growth factor levels	2.00e-33	rs8176693	25552591
	GIP levels in response to oral glucose tolerance test (120 min)	7.00e-14	rs635634	29093273
	Hemoglobin + other corpuscular-related traits	2.00e-25	rs10901252	27863252, 29403010, 20139978, 28017375
	High serum lipase activity	1.00e-22	rs8176693	25028398
	Intraocular pressure	3.00e-11	rs8176743	25173106, 28073927, 29617998
	Iron status biomarkers (ferritin levels)	1.00e-08	rs651007	25352340
	Lactate dehydrogenase levels	7.00e-09	rs116552240	29403010
	LDL cholesterol	2.00e-51	rs579459	28334899, 24097068, 20686565, 25961943
	Liver enzyme levels	3.00e-123	rs579459	22001757
	Malaria	4.00e-21	rs8176719	22895189
	Serum alkaline phosphatase levels	1.00e-56	rs651007	24094242
	Smoking behavior	4.00e-08	rs3025343	20418890
	Soluble levels of adhesion molecules (P-selectin, ICAM)	2.00e-41	rs579459	20167578
	Tonsillectomy	9.00e-09	rs635634	27182965, 28928442
	Tumor biomarkers (CEA)	7.00e-105	rs8176749	23300138
	Type 2 diabetes	2.00e-08	rs635634	28566273
	Urinary metabolites (H-NMR features)	1.00e-28	rs579459	24586186
	Venous thromboembolism	4.00e-21	rs8176645	28373160, 22672568
sVAM-1 in NFBC1966; *HPS90B1*; 12q23.3; 12:104448391; rs117238625				
Biobank Engine (inquiry the lead SNP)	na			
Phenoscanner (inquiry the lead SNP)	na			
GWAS Catalog (inquiry +-500 kb around the lead SNP)	Adolescent idiopathic scoliosis	4.00e-08	rs7138824	30019117
	Blood protein levels (Endoplasmin. HSP90B1.6393.63.3)	8.00e-133	rs63658260	29875488
	Central corneal thickness/structure	2.00e-17	rs11553764	29760442, 23291589
	Intraocular pressure	4.00e-13	rs11553764	29617998
	vWF level	7.00e-10	rs4981022	20231535, 26486471
	Stem cell growth factor beta levels	1.00e-23	rs187503377	27989323

Table S3. Continues.

	Trait	P-value	SNP	PMID
sVAM-1 in NFBC1966; *ABCA8*; 17q24.2; 17:66823805; rs112001035				
Biobank Engine (inquiry the lead SNP)	na			
Phenoscanner (inquiry the lead SNP)	na			
GWAS Catalog (inquiry +-500 kb around the lead SNP)	Adolescent idiopathic scoliosis	7.00e-10	rs9893173	30019117
	Blood protein levels (C-C motif chemokine 22. CCL22.3508.78.3 + others)	7.00e-22	rs77542162	29875488
	HDL cholesterol	2.00e-15	rs1373067	28334899, 24097068, 20686565
	Hemoglobin concentration + other corpuscular-related traits	2.00e-16	rs77542162	27863252
	Intraocular pressure	8.00e-21	rs77542162	29617998
	LDL cholesterol	2.00e-18	rs77542162	25961943
	Musician’s dystonia	4.00e-09	rs11655081	24375517
	Phosphorus levels	1.00e-08	rs35186465	29403010
	Total cholesterol	2.00e-13	rs77542162	25961943
IL1b in meta-analysis; HLA locus; 6p22.1; 6:30017071; rs6917603				
Biobank Engine (inquiry the lead SNP)	na			
Phenoscanner (inquiry the lead SNP)	Lipid metabolism phenotypes	3.00e-29	rs6917603	22286219
	Gender	6.80e-20	rs6917603	22362730
	Rheumatoid arthrtitis	2.80e-13	rs6917603	24390342
GWAS Catalog (inquiry +-500 kb around the lead SNP)	Albumin-globulin ratio	3.00e-11	rs114180431	29403010
	Allergic disease (asthma. hay fever or eczema)	2.00e-09	rs9259819	29083406
	Autism spectrum disorder or schizophrenia	1.00e-22	rs151267808	28540026
	Beta-2 microglobulin plasma levels	2.00e-22	rs9260489	23417110
	Bipolar disorder lithium response or schizophrenia	1.00e-17	rs144373461	29121268
	Blood protein levels	4.00e-22	rs3132645	28240269, 29875488
	Chickenpox	1.00e-10	rs10947050	28928442
	Colonoscopy-negative controls vs population controls	2.00e-08	rs29234	29228715
	Crohn’s disease	2.00e-10	rs9258260	22412388
	Cutaneous lupus erythematosus	2.00e-11	rs3094067	25827949
	Depression, depressive symptoms	5.00e-13	rs2517601	29662059
	Drug-induced liver injury	2.00e-10	rs2523822	21570397, 28043905
	General cognitive ability	1.00e-11	rs885916	29844566
	Graves’ disease	2.00e-20	rs3893464	21900946
	Hand grip strength	2.00e-08	rs453325	29691431
	Heel bone mineral density	3.00e-11	rs9260426	28869591
	Height	2.00e-24	rs11970475	25429064
	Hepatocellular carcinoma in hepatitis B infection	9.00e-13	rs1110446	29784950
	HIV-1 control	2.00e-08	rs7758512	20041166
	IgA nephropathy	2.00e-11	rs2523946	22197929, 26028593
	IgE levels	1.00e-15	rs2571391	22075330

Table S3. Continues.

	Trait	P-value	SNP	PMID
IL1b in meta-analysis; HLA locus; 6p22.1; 6:30017071; rs6917603 (continues)				
GWAS Catalog (continues)	Itch intensity from mosquito bite	1.00e-10	rs2516703	28199695
	Late-onset myasthenia gravis	1.00e-11	rs150881176	26562150
	Lipid metabolism phenotypes	3.00e-29	rs6917603	22286219
	Lung cancer	4.00e-18	rs114601353	28604730
	Menarche (age at onset)	3.00e-10	rs16896742	25231870
	Mixed cellularity Hodgkin lymphoma	3.00e-23	rs1633096	29196614
	Moderate to vigorous physical activity levels	1.00e-09	rs3094622	29899525
	Multiple sclerosis	1.00e-17	rs2523393	19525953
	Multiple white or red blood cell-related traits	2.00e-74	rs9260620	27863252
	Mumps	2.00e-17	rs114193679	28928442
	Nasopharyngeal carcinoma	9.00e-17	rs29232	19664746
	Neuroticism	1.00e-09	rs2267633	29255261
	Non-albumin protein levels	3.00e-09	rs142014154	29403010
	Prostate cancer	2.00e-08	rs115457135	25217961, 29892016
	Sarcoidosis (Lofgren's syndrome vs non-Lofgren's syndrome)	4.00e-23	rs3130141	26651848
	Schizophrenia	2.00e-19	rs114200269	26198764, 27922604, 22883433, 21926974
	Shingles	2.00e-22	rs2523815	28928442
	Tonsillectomy	8.00e-10	rs10484552	28928442
	Tuberculosis	2.00e-12	rs181383036	28928442
	Type 1 diabetes and autoimmune thyroid diseases	2.00e-08	rs2523989	25936594
	Vitiligo	2.00e-66	rs60131261	27723757
TNFa in meta-analyses; *DLEU1*; 13q14.3; 13:51141997; rs17074575				
Biobank Engine (inquiry the lead SNP)	na			
Phenoscanner (inquiry the lead SNP)	na			
GWAS Catalog (inquiry +-500 kb around the lead SNP)	Adolescent idiopathic scoliosis	1.00e-08	rs797487	30019117
	Aortic root size	2.00e-15	rs2762049	28394258
	Circulating odd-numbered chain saturated fatty acid levels (C19:0)	7.00e-09	rs17363566	29738550
	Eosinophil percentage of white cells	5.00e-10	rs201798	27863252
	Heel bone mineral density	4.00e-10	rs1149821	28869591
	Height	1.00e-69	rs3118905	25282103
	Hemoglobin	2.00e-10	rs806293	29403010
	High light scatter reticulocyte percentage of red cells	1.00e-13	rs9535495	27863252
	Hip circumference adjusted for BMI	4.00e-15	rs558003	25673412
	Multiple sclerosis	3.00e-10	rs2812197	27386562
	Primary biliary cholangitis	1.00e-10	rs9591325	26394269
	Primary tooth development (number of teeth)	3.00e-08	rs9316505	23704328
	Prostate-specific antigen levels	3.00e-22	rs202346	28139693
	Reticulocyte fraction of red cells	3.00e-11	rs9535495	27863252

Table S4. The results of the supplemental GWAS.

Individuals who had reported having fever at the time of the blood sampling (N=32) or C-reactive protein (CRP) > 10 mg/l (N=212) were excluded from the supplementary GWAS completed in NFBC1966. The data adjustments (age, sex, BMI, and the first ten genetic principal components) and transformations were performed as in the primary analyses. The results are given for the locus lead SNPs as in the Table 2.

Marker	Locus	Chr:Position	Candidate gene	Nearest gene(s)	Annotation	dbSNP refrerence	EA	EAF	Beta	Se	P-value	Beta origNFBC1966	Se origNFBC1966	P-value origNFBC1966
sE-Selectin	9q34.2	9:136141870	*ABO*	*ABO*	Intronic	rs2519093	T	0.212	-0.908	0.025	8.01E-295	-0.903	0.024	4.48E-305
	11q24.2	11:126266665	*ST3GAL4*	*ST3GAL4*	Intronic	rs11220471	G	0.241	-0.157	0.024	8.76E-11	-0.162	0.024	7.72E-12
sICAM-1	9q34.2	9:136141870	*ABO*	*ABO*	Intronic	rs2519093	T	0.212	-0.350	0.025	2.26E-45	-0.352	0.024	7.43E-48
	19p13.2	19:10383403	*ICAM1*	*ICAM1*	Intronic	rs117960796	A	0.012	-1.769	0.132	8.75E-41	-1.669	0.126	8.03E-40
sVCAM-1	9q34.2	9:136131322	*ABO*	*ABO*	Missense	rs8176746	T	0.138	0.257	0.029	2.38E-18	0.256	0.029	5.06E-19
	12q23.3	12:104448391	*HSP90B1*	*GLT8D2*	Intronic	rs117238625	A	0.023	0.527	0.069	2.28E-14	0.510	0.067	2.90E-14
	17q24.2	17:66823805	*ABCA8*	*ABCA8*	Intergenic	rs112001035	A	0.062	-0.315	0.045	1.88E-12	-0.324	0.044	1.04E-13
IL1β	6p22.1	6:30017071		*HLA* locus	Intronic	rs6917603	C	0.291	-0.164	0.023	2.28E-12	-0.163	0.023	8.82E-13
IP10	4q21.1	4:76899176	*CXCL10*	*SAD1*	Intronic	rs192716315	C	0.003	1.472	0.205	6.35E-13	1.513	0.205	1.79E-13
MCP1	1q23.2	1:159175354	*ACKR1*	*ACKR1*	Missense	rs12075	G	0.507	0.028	0.020	0.174	0.031	0.020	0.123
TNFα	13q14.3	13:51141997	*DLEU1*	*DLEU1*	Intronic	rs17074575	G	0.001	2.560	0.414	6.40E-10	2.131	0.357	2.48E-09
VEGF	4p16.2	4:5636073	*STK32B*	*EVC2*	Intronic	rs186725382	A	0.001	-2.629	0.406	9.13E-11	-2.380	0.381	4.22E-10
	6p21.1	6:43927050	*VEGFA*	*C6orf223*	Intergenic	rs7767396	G	0.511	-0.015	0.021	0.452	-0.015	0.020	0.465
	9p24.2	9:2686273	*VLDLR*	*VLDLR, KCNV2*	Intergenic	rs7030781	T	0.392	0.036	0.021	0.097	0.042	0.021	0.044

All positions correspond to human genome build 37. $\text{Beta}_{\text{origNFBC1966}}$, $\text{Se}_{\text{origNFBC1966}}$ and $\text{P-value}_{\text{origNFBC1966}}$ indicate the test statistics as in the original discovery GWAS in the NFBC1966 population. EA, effect allele; EAF, effect allele frequency.

Figure S1. Correlation heatmap of the inflammatory phenotypes in NFBC1966.
Pearson's ρ calculated for the adjusted (age, sex, BMI, ten first genetic principal components) and transformed inflammatory phenotypes. Coloring represents the sign of the correlation (red-yellow positive, purple-blue negative) and the circle area is proportional to the absolute value of the correlation. Cells with statistically insignificant values (P≥0.05) are left blank.

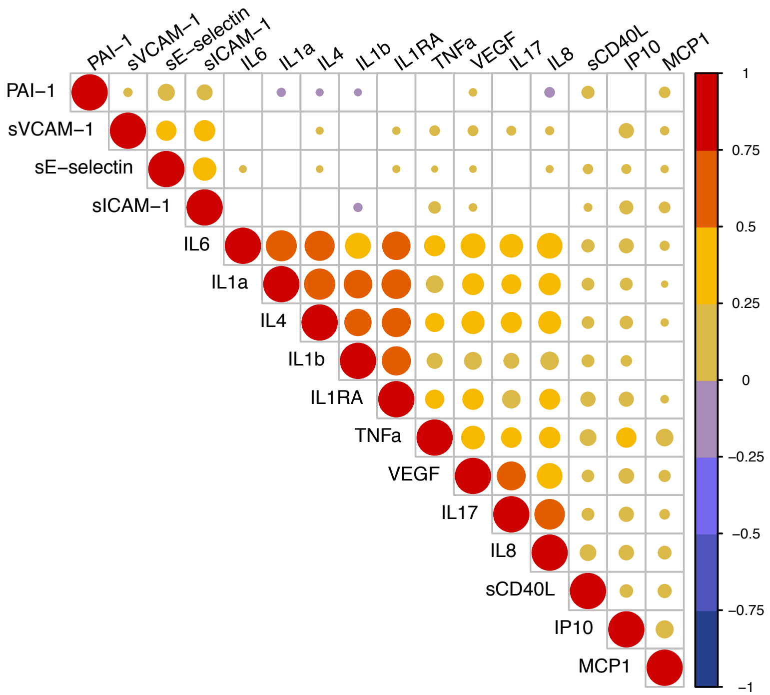


Figure S2 A) Manhattan, Q-Q, and LocusZoom plots for sE-selectin results in NFBC1966.

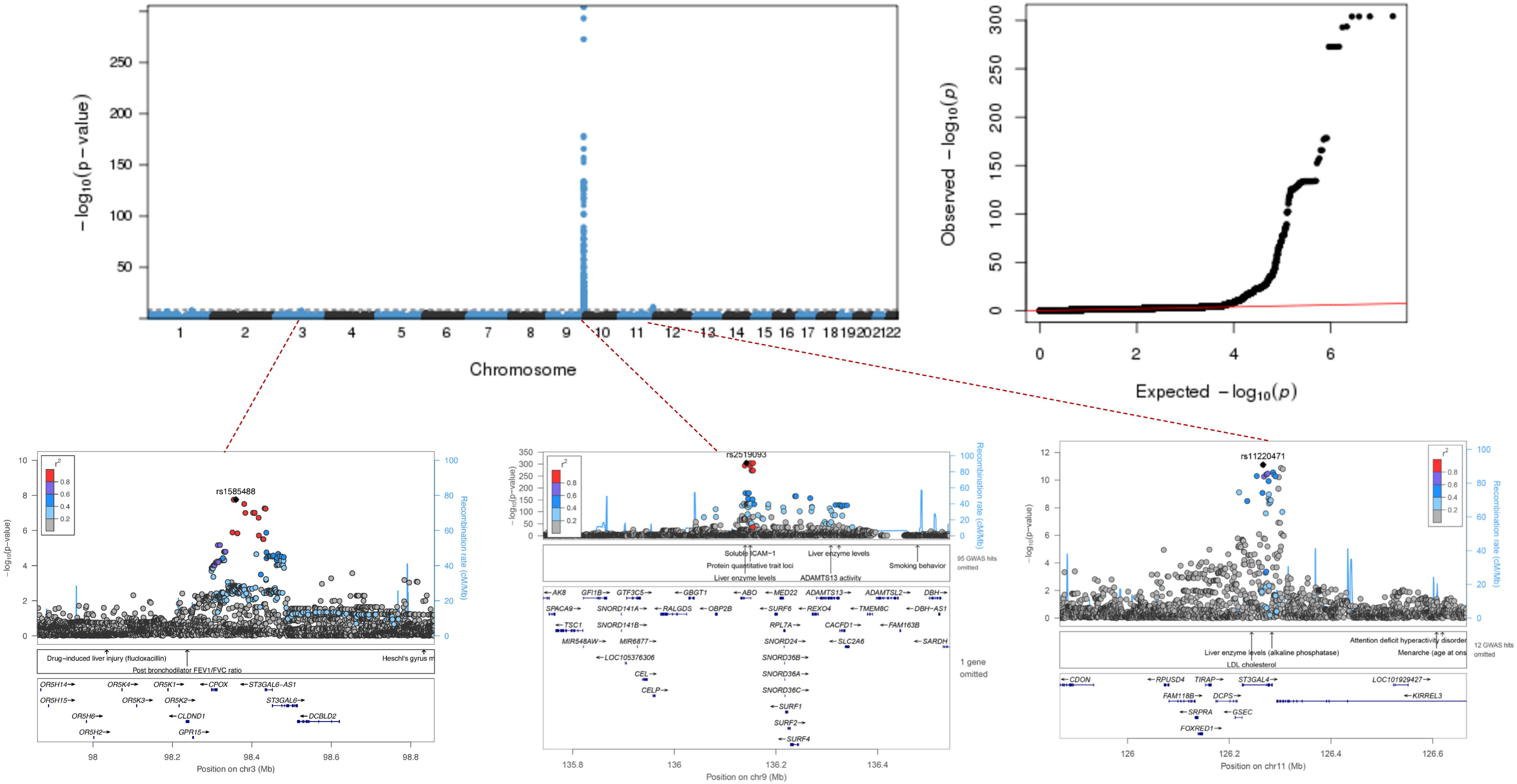


Figure S2 B) Manhattan, Q-Q, and LocusZoom plots for sICAM-1 results in NFBC1966.

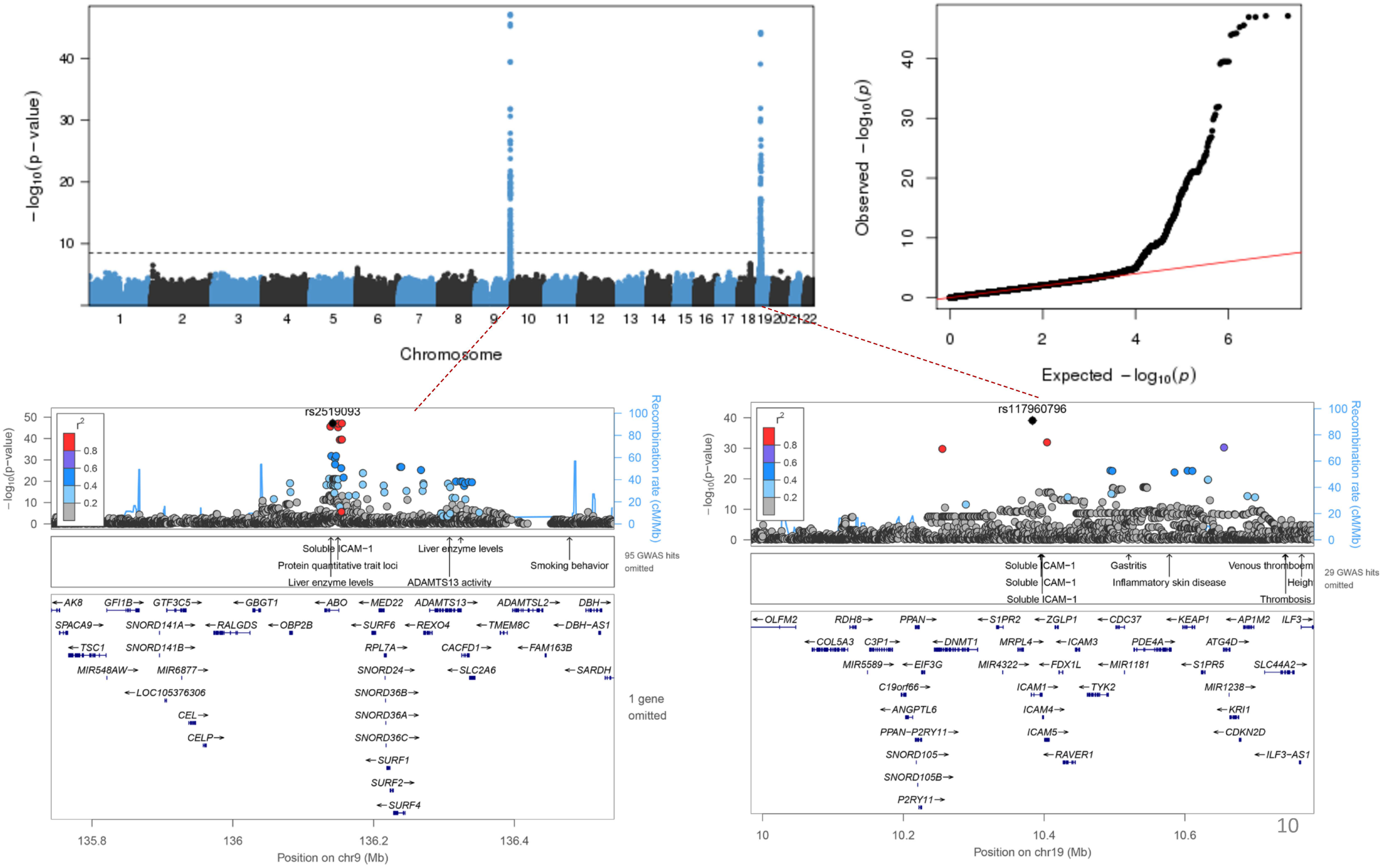


Figure S2 C) Manhattan, Q-Q, and LocusZoom plots for sVCAM-1 results in NFBC1966.

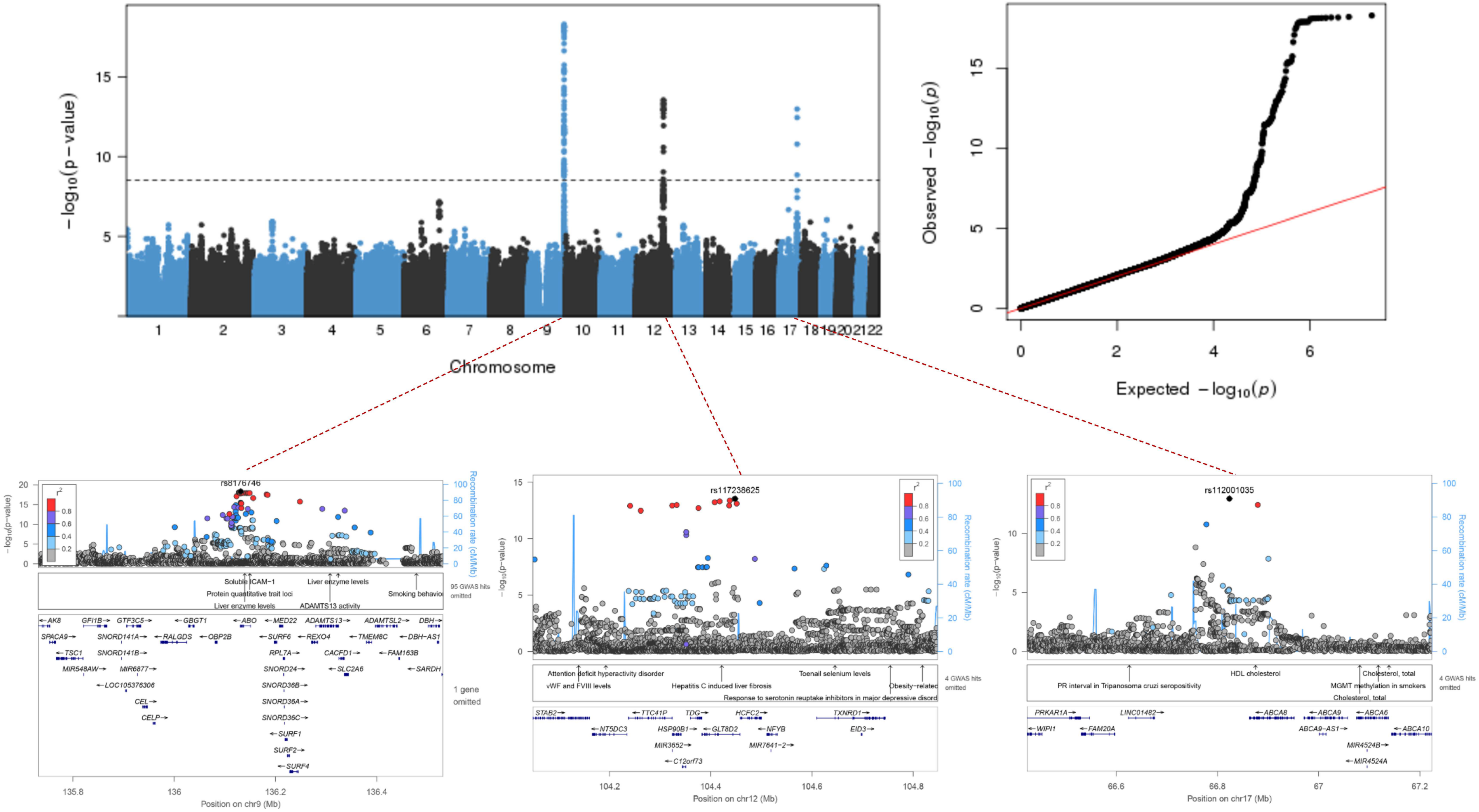


Figure S2 D) Manhattan, Q-Q, and LocusZoom plots for VEGF results in NFBC1966.

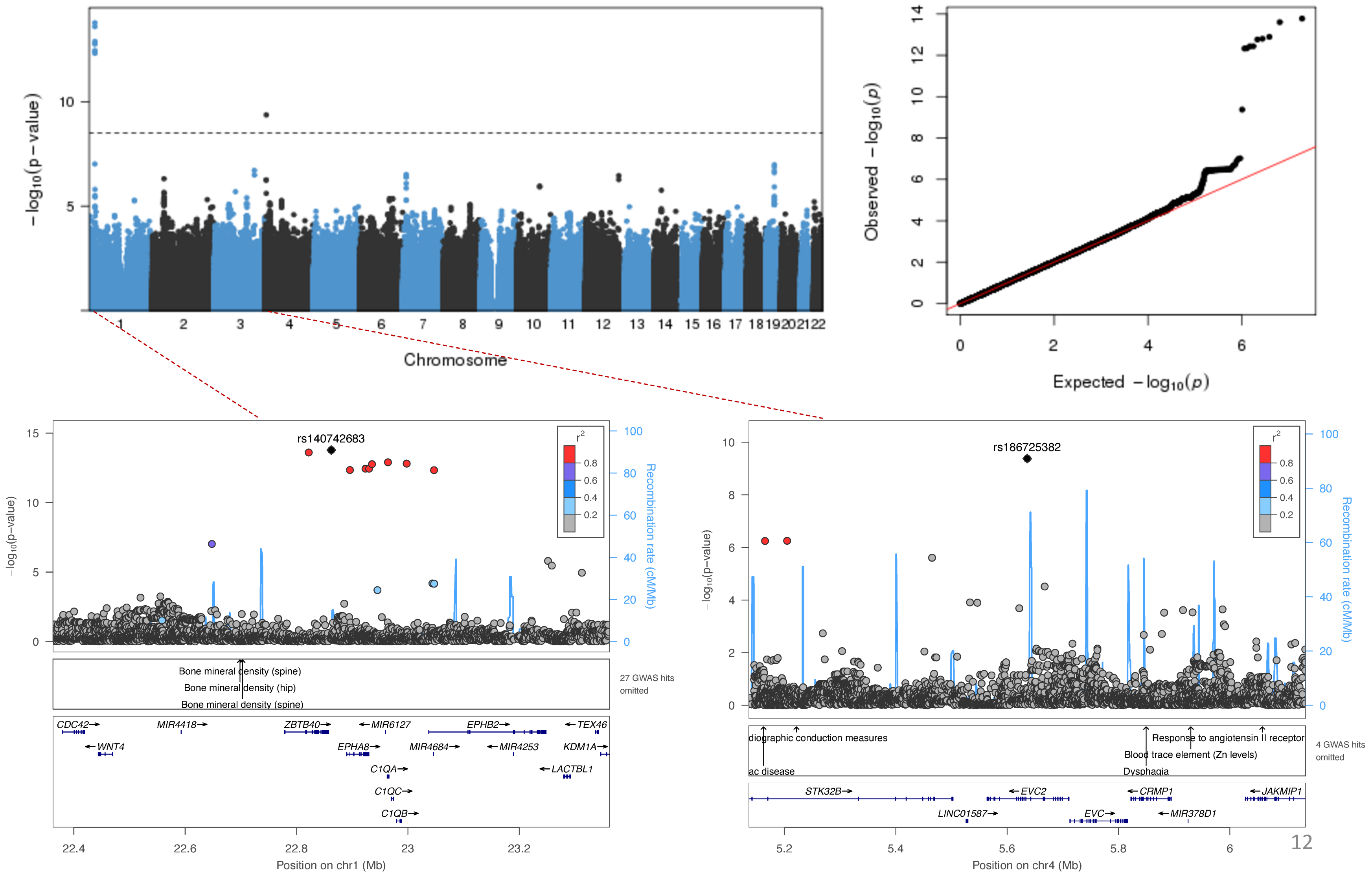


Figure S2 E) Manhattan, Q-Q, and LocusZoom plots for VEGF results in meta-analyses.

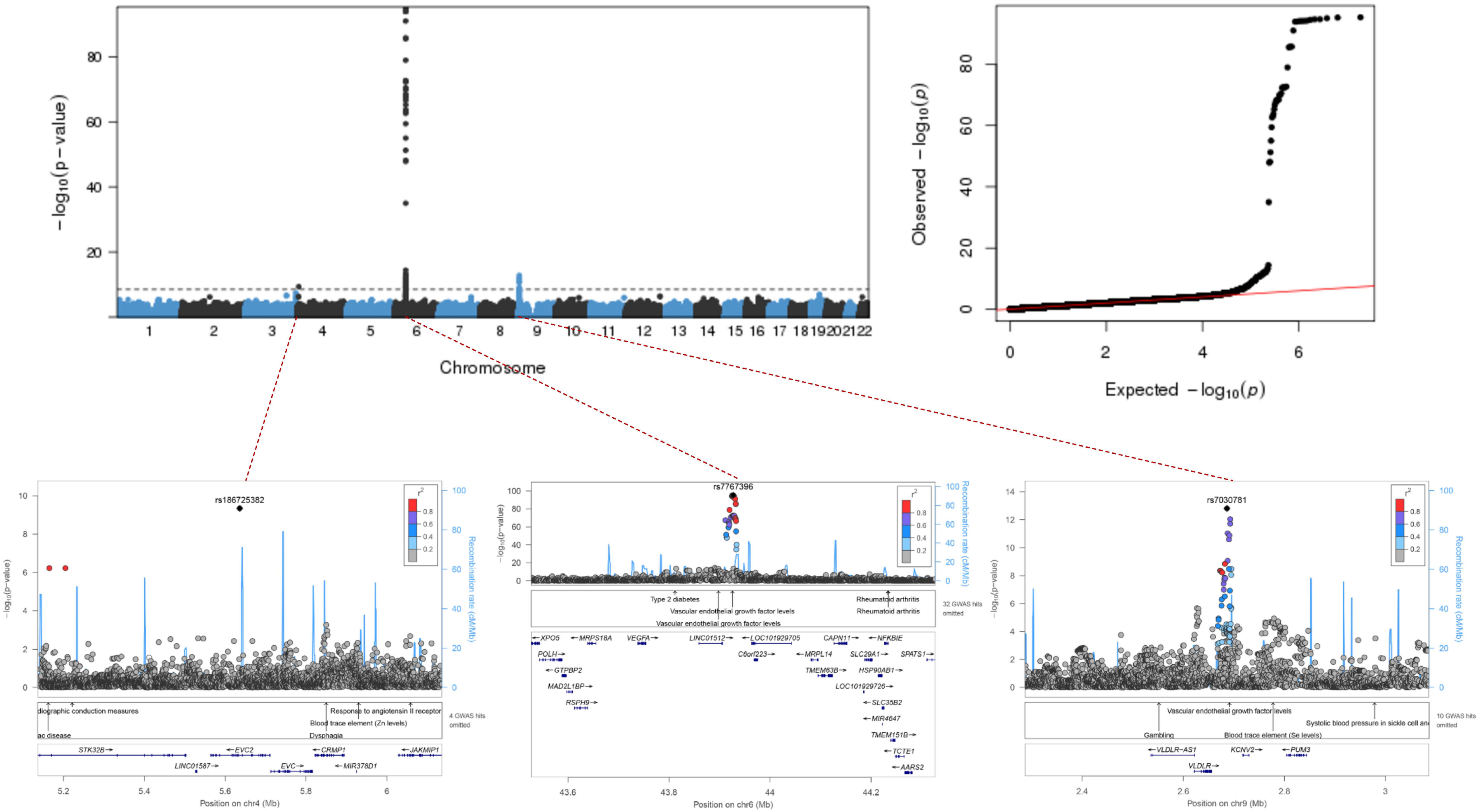


Figure S2 F) Manhattan, Q-Q, and LocusZoom plots for TNFa results in NFBC1966.

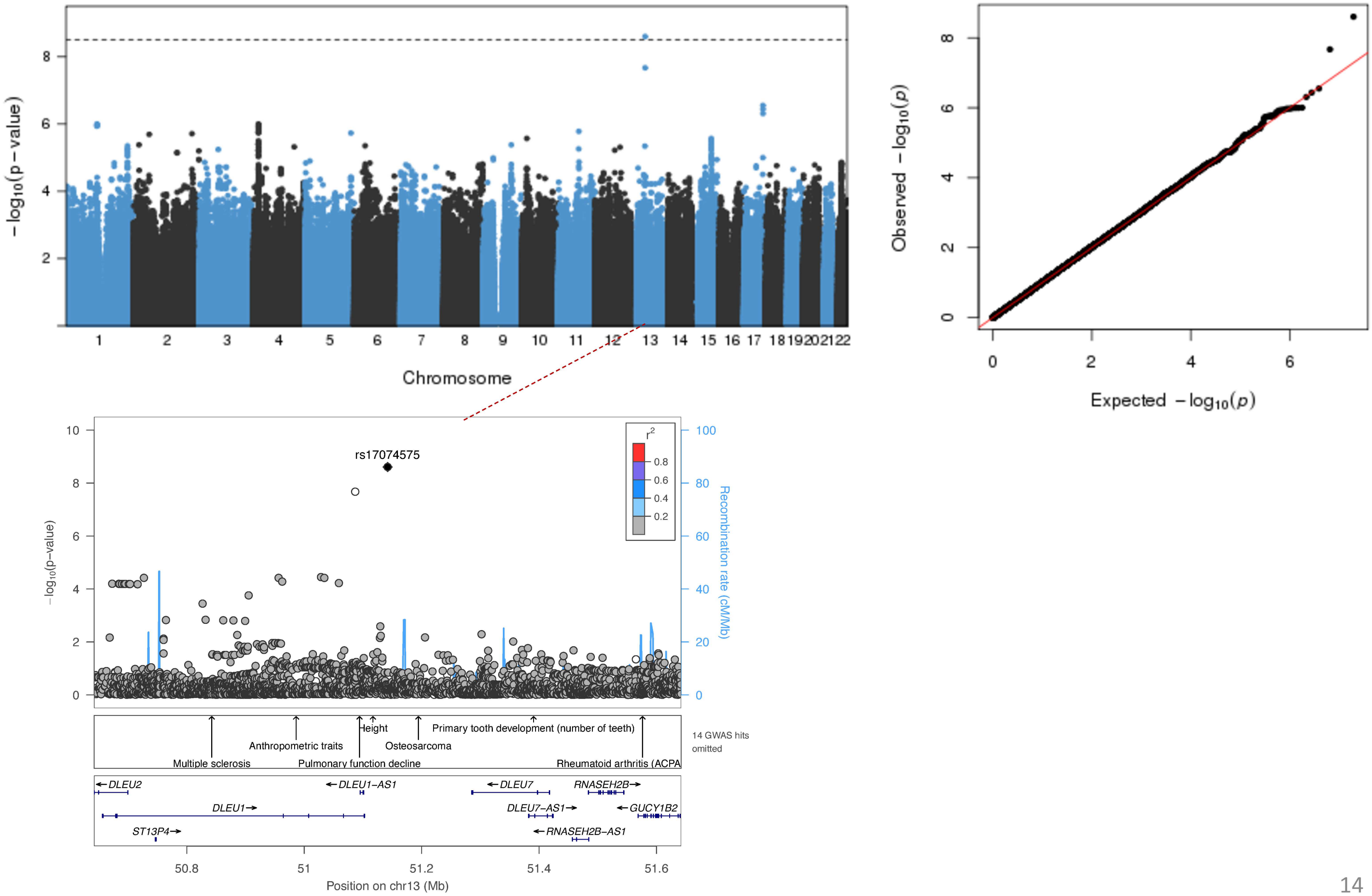


Figure S2 G) Manhattan, Q-Q, and LocusZoom plots for TNFa results in meta-analyses.

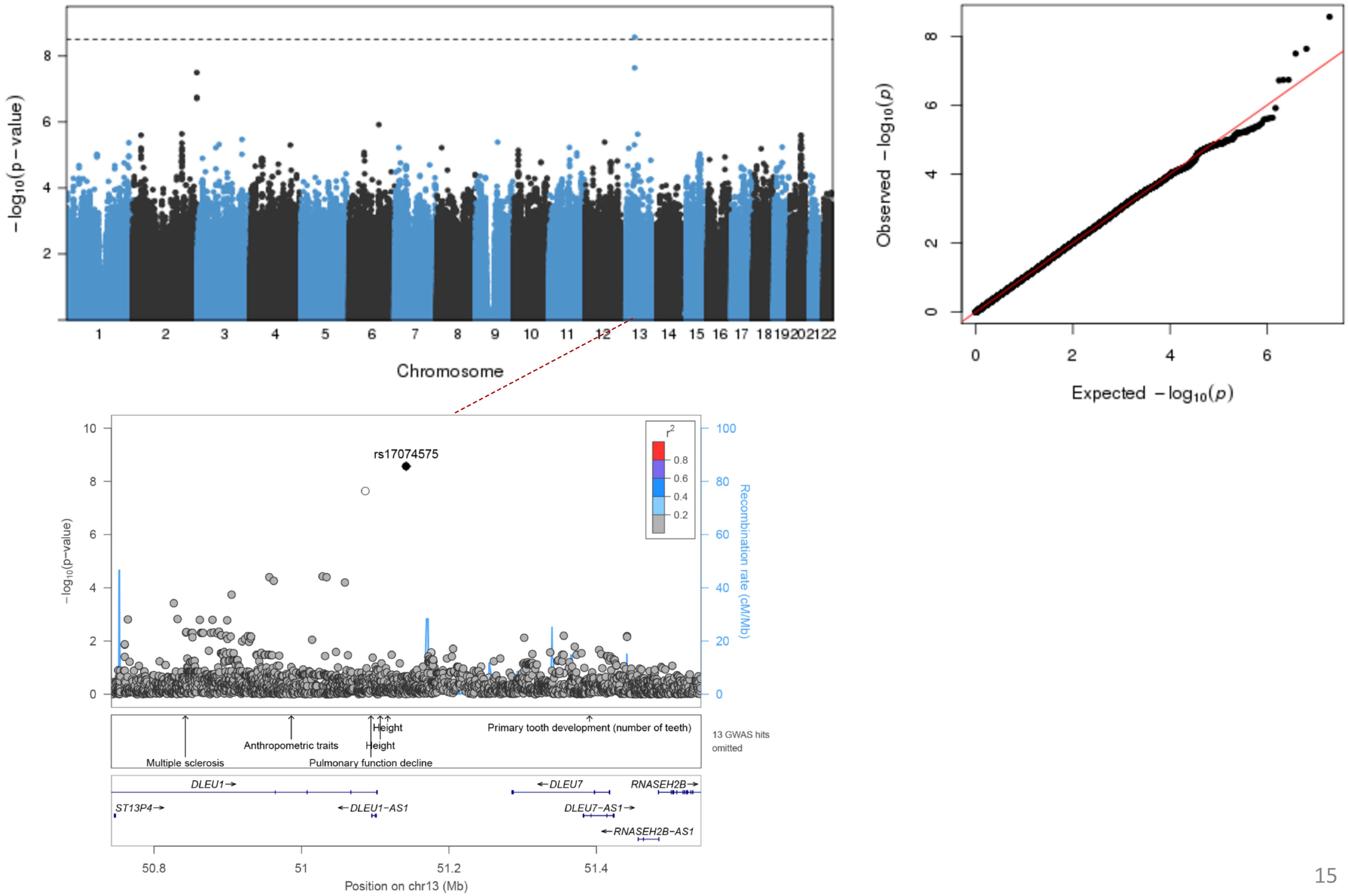
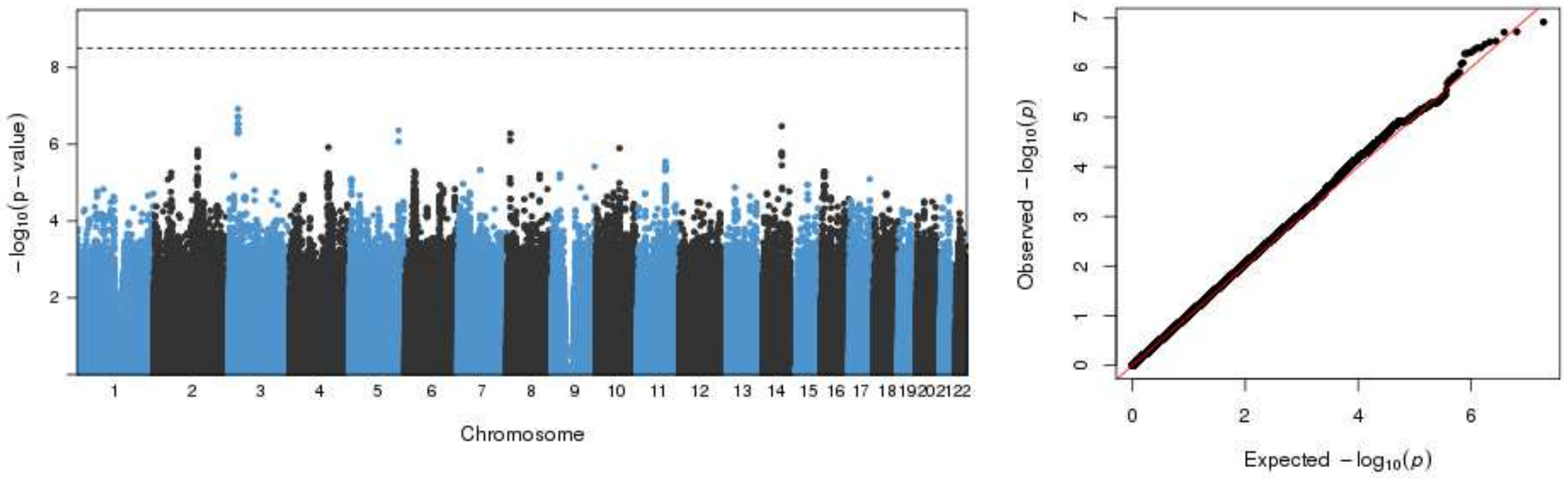


Figure S2 H) Manhattan, Q-Q, and LocusZoom plots for IL-1a results in NFBC1966.



No significant assocítions (p-value limit 3.1x10^{-9}).

Figure S2 I) Manhattan, Q-Q, and LocusZoom plots for IL-1b results in NFBC1966.

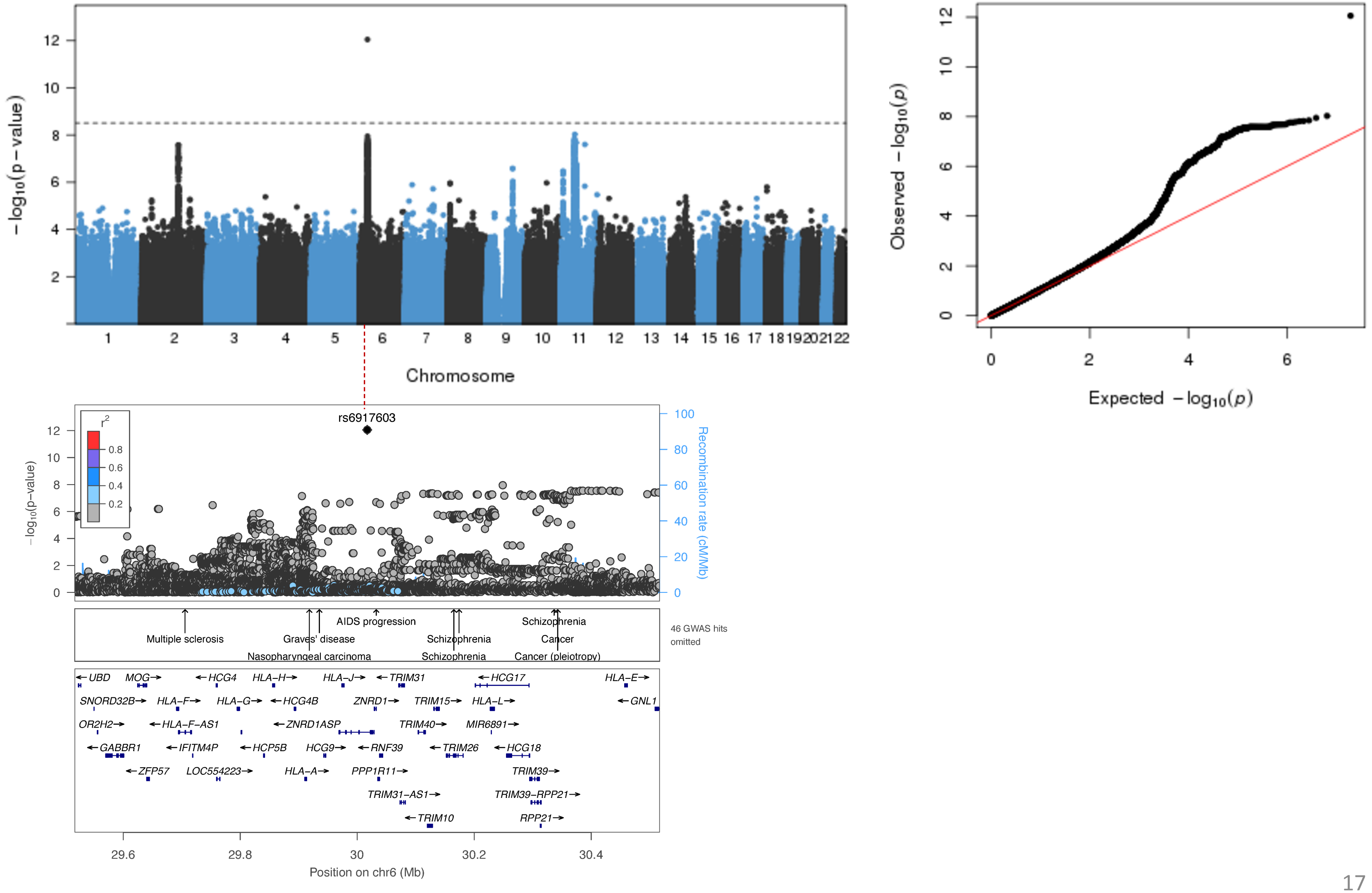


Figure S2 J) Manhattan, Q-Q, and LocusZoom plots for IL-1b results in meta-analyses.

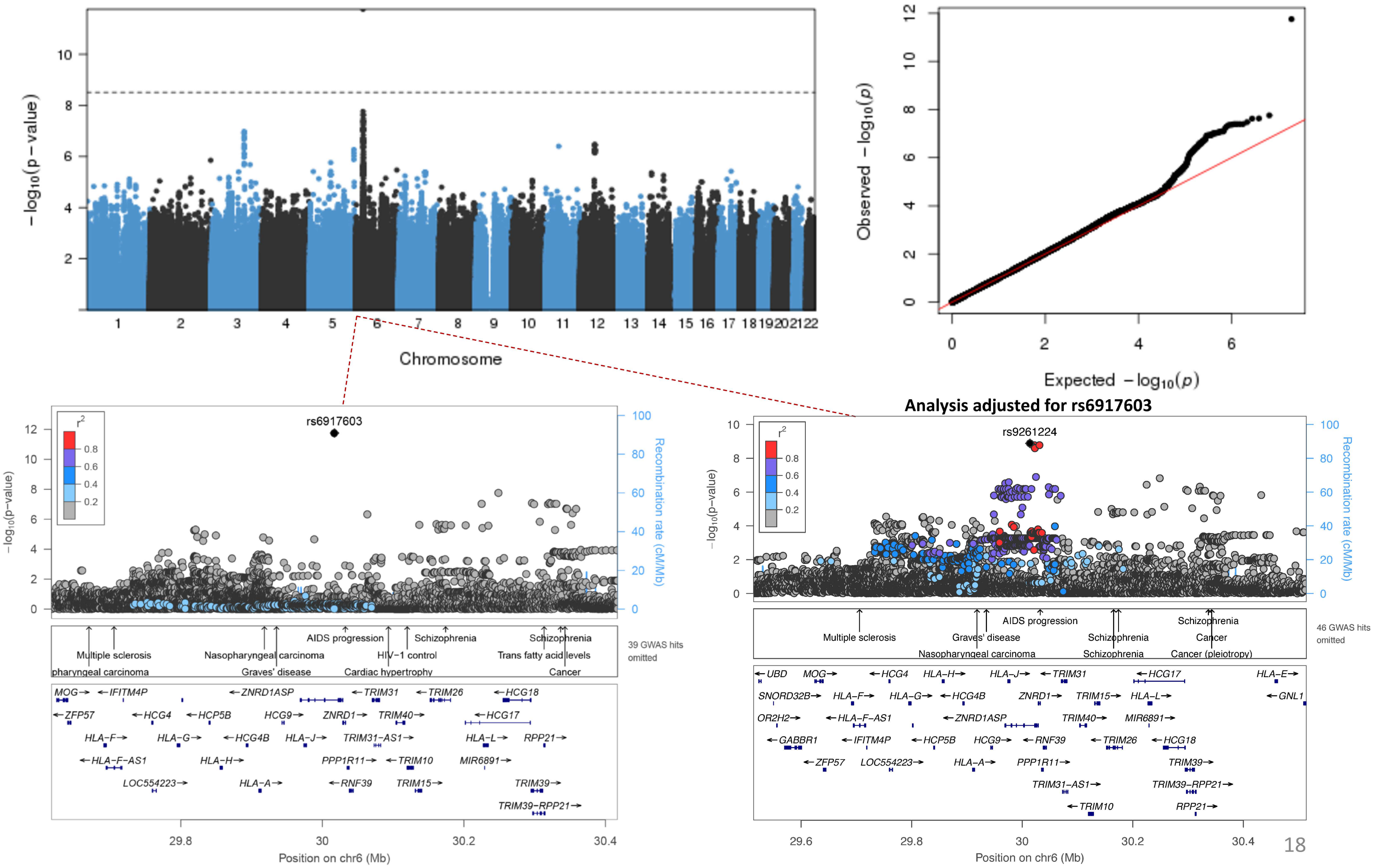
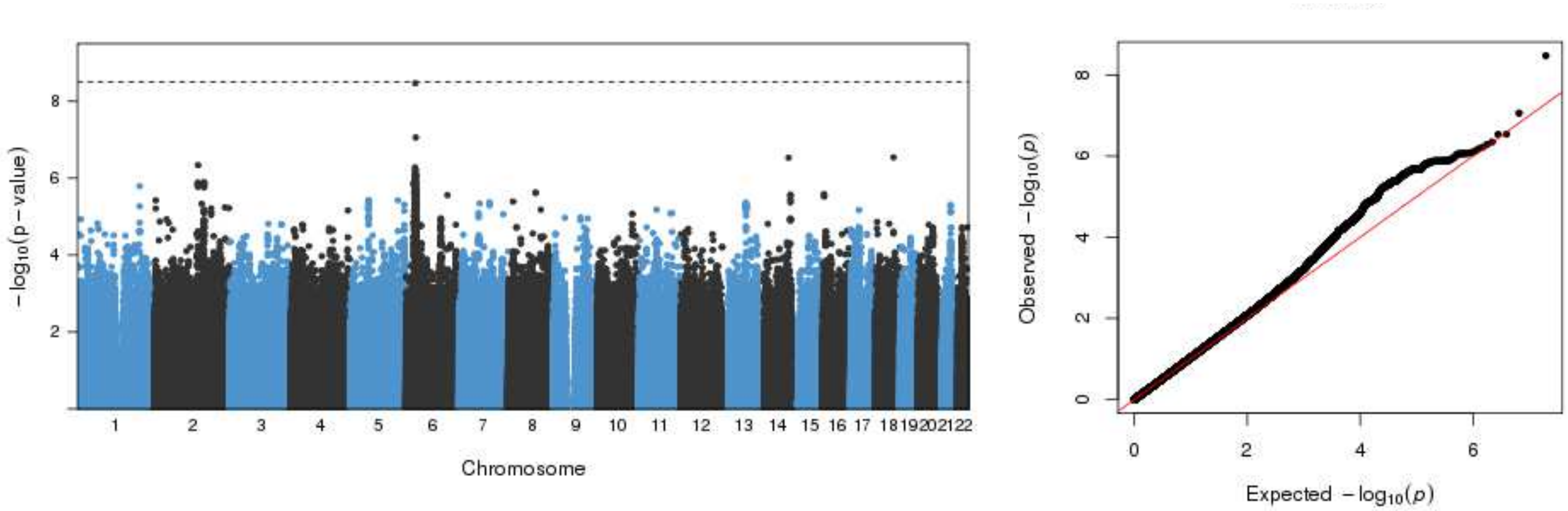
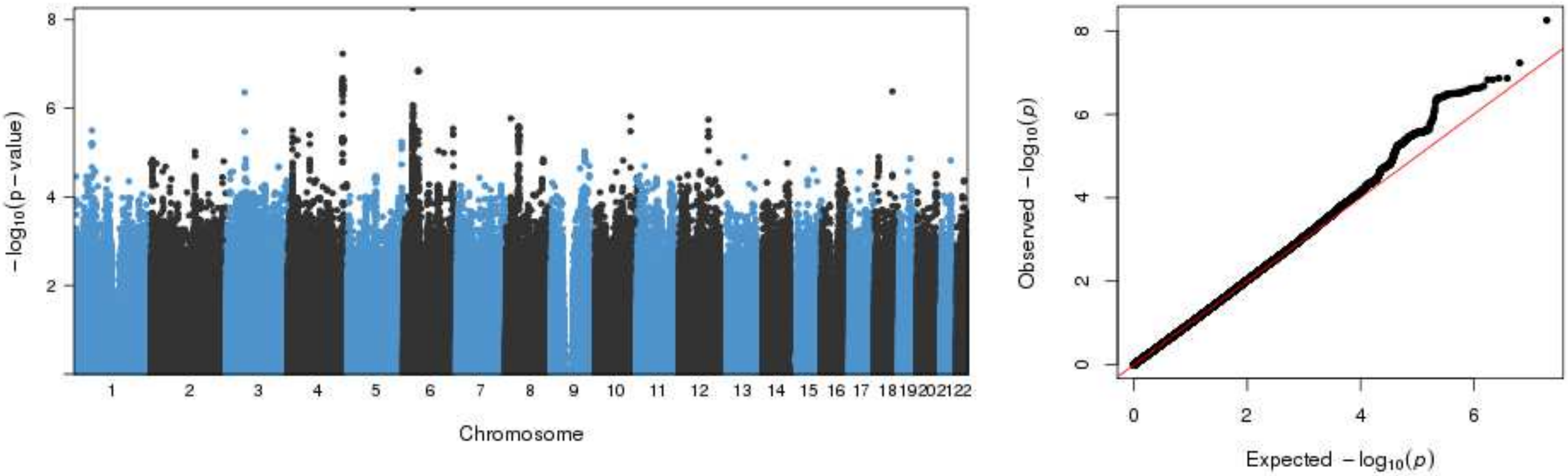


Figure S2 K) Manhattan, Q-Q, and LocusZoom plots for IL4 results in NFBC1966.



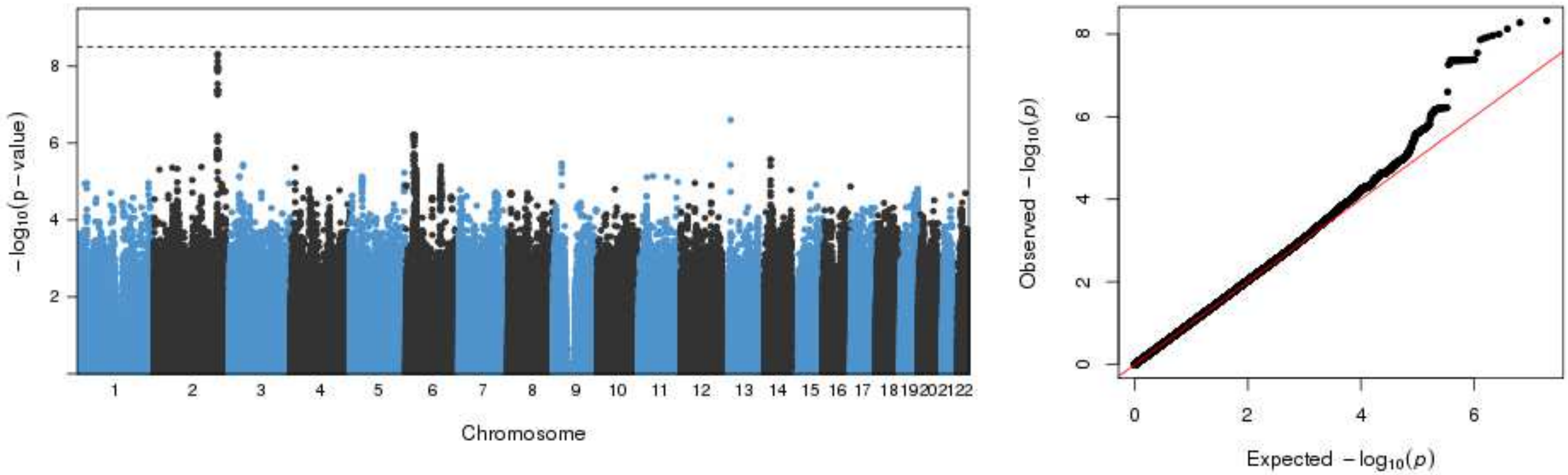
No significant assocition̲s (p-value limit 3.1×10^{-9}).

Figure S2 L) Manhattan, Q-Q, and LocusZoom plots for IL4 results in meta-analyses.



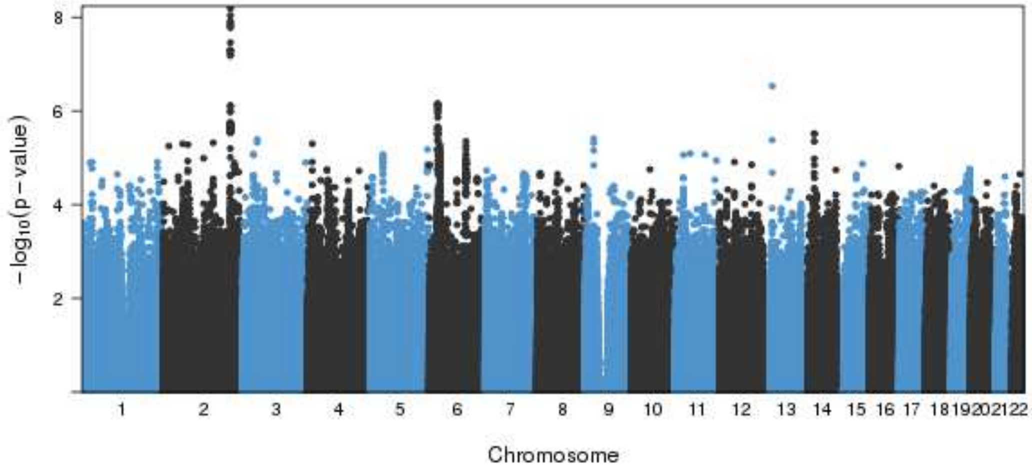
No significant associtions (p-value limit $3.1\text{x}10^{-9}$).

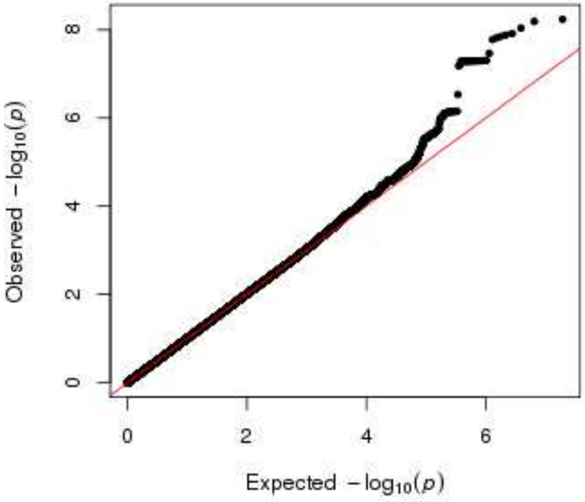
Figure S2 M) Manhattan, Q-Q, and LocusZoom plots for IL6 results in NFBC1966.



No significant associtions (p-value limit 3.1×10^{-9}).

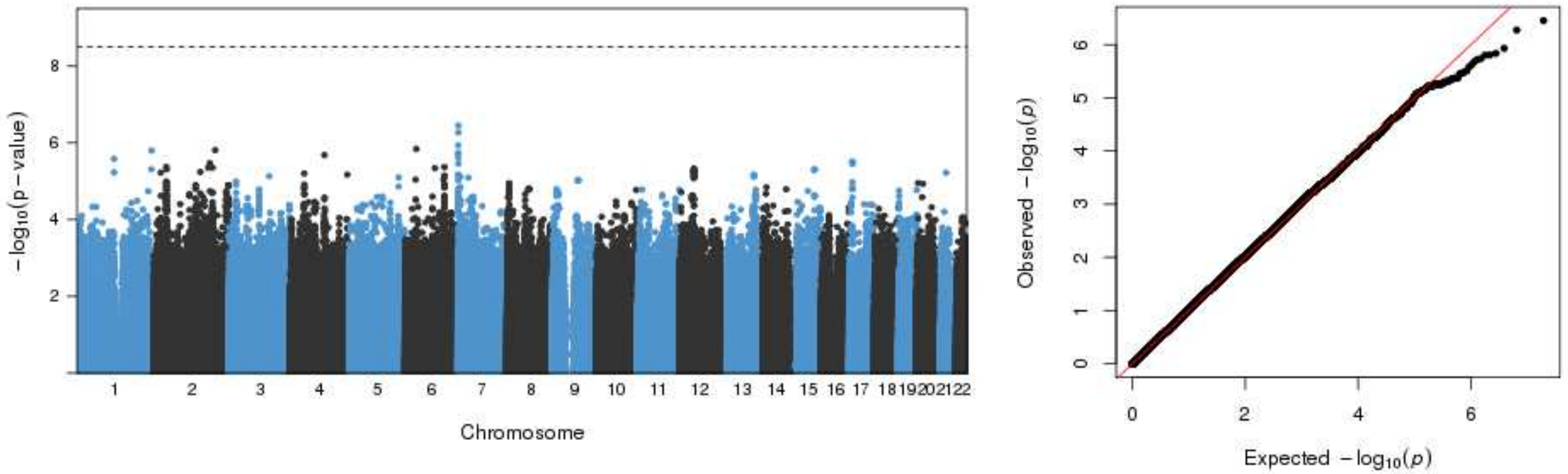
Figure S2 N) Manhattan, Q-Q, and LocusZoom plots for IL6 in meta-analyses.





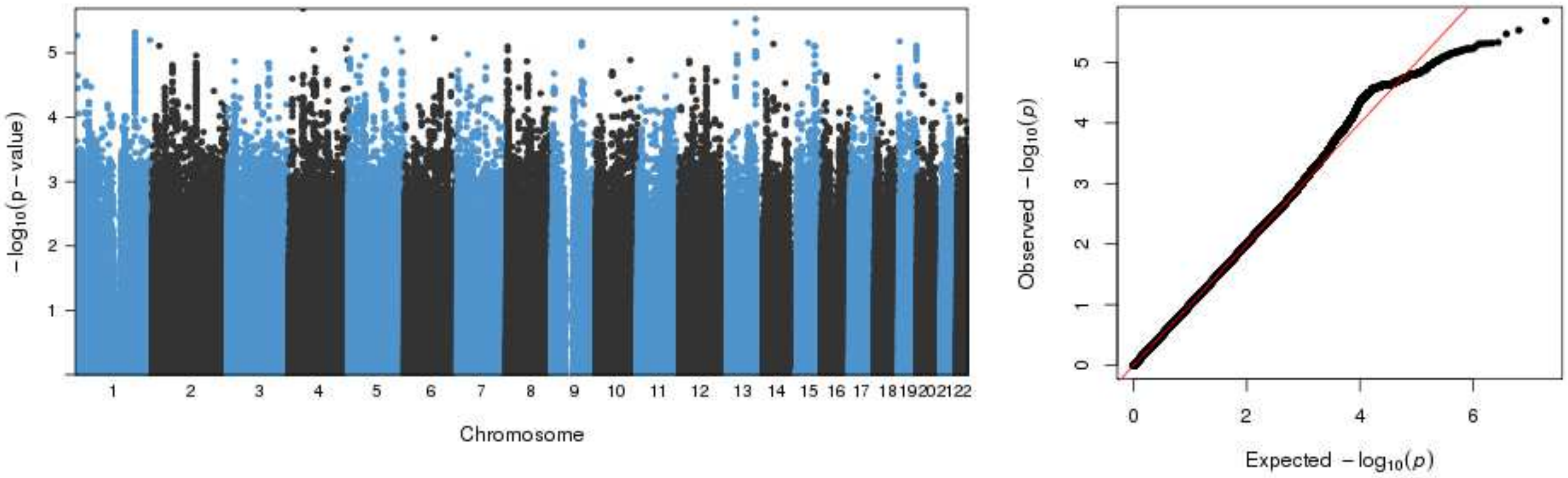
No significant assocititions (p-value limit $3.1x10^{-9}$).

Figure S2 O) Manhattan, Q-Q, and LocusZoom plots for IL8 results in NFBC1966.



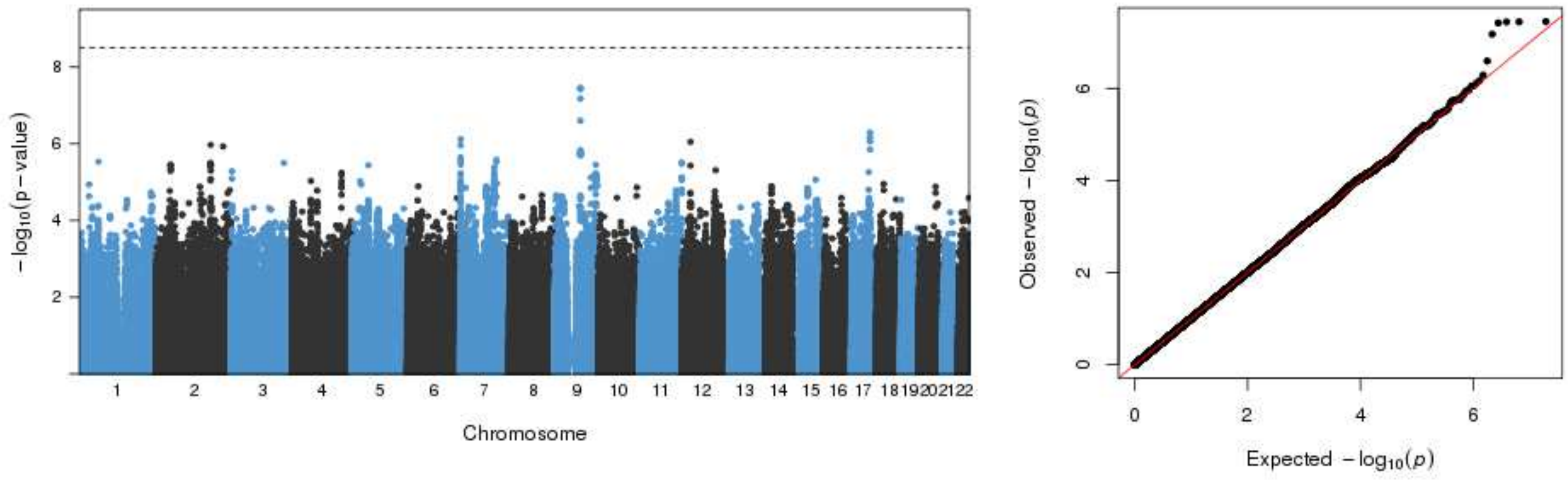
No significant associtions (p-value limit 3.1×10^{-9}).

Figure S2 P) Manhattan, Q-Q, and LocusZoom plots for IL8 results in meta-analyses.



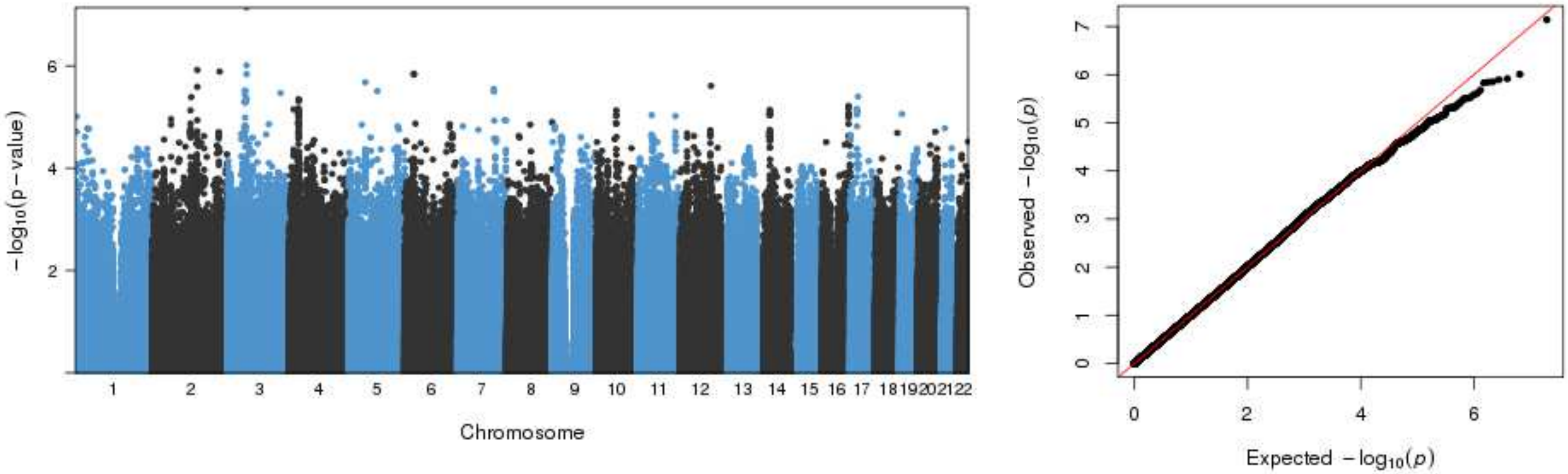
No significant associtions (p-value limit 3.1x10^{-9}).

Figure S2 Q) Manhattan, Q-Q, and LocusZoom plots for IL17 results in NFBC1966.



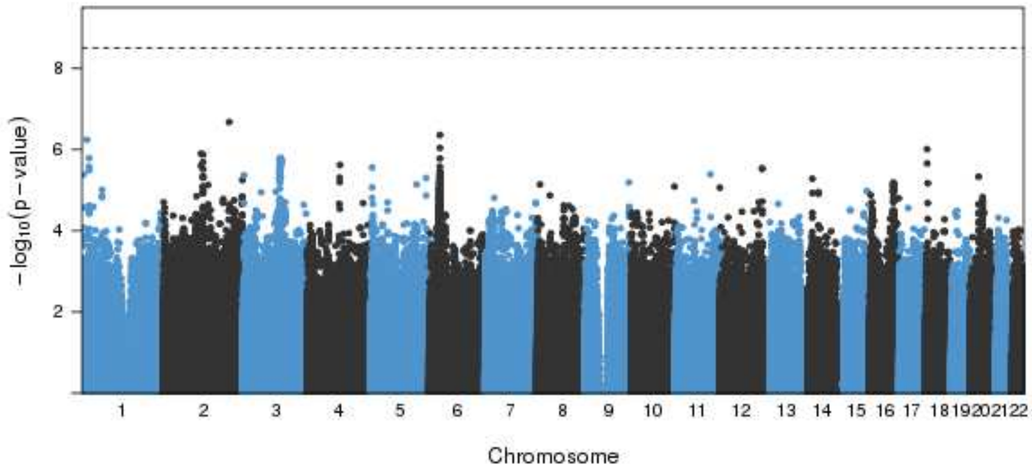
No significant associtions (p-value limit $3.1x10^{-9}$).

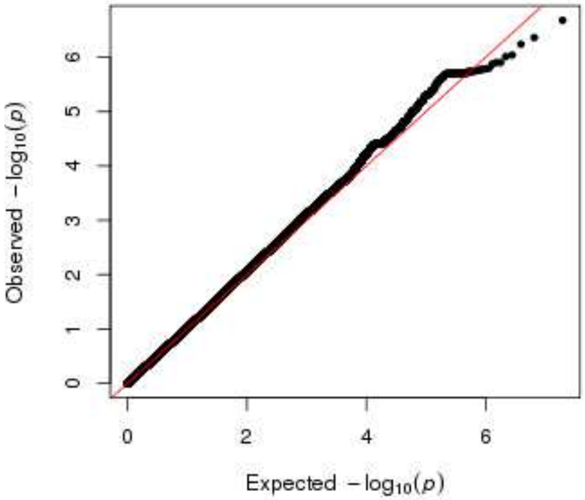
Figure S2 R) Manhattan, Q-Q, and LocusZoom plots for IL17 results in meta-analyses.



No significant associtions (p-value limit $3.1x10^{-9}$).

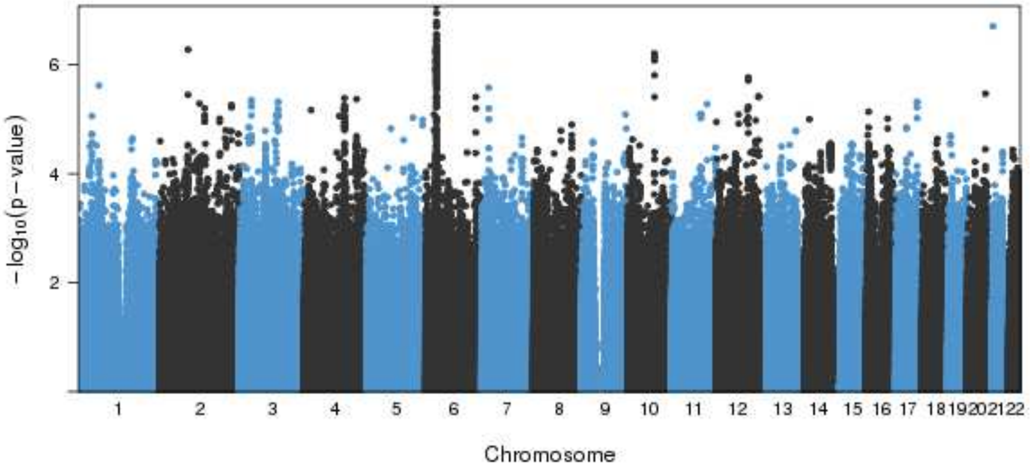
Figure S2 S) Manhattan, Q-Q, and LocusZoom plots for IL1ra results in NFBC1966.

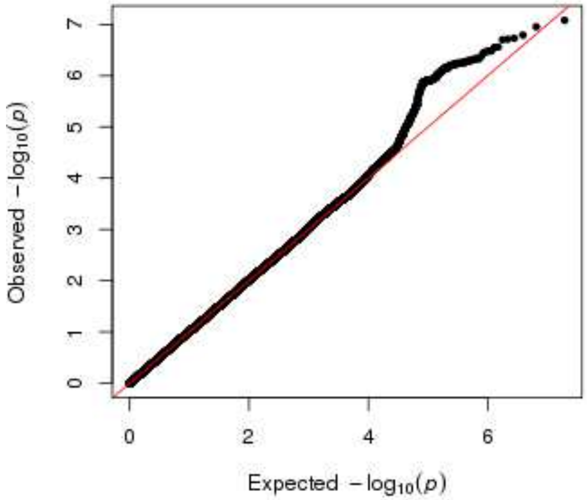




No significant associtions (p-value limit 3.1x10^{-9}).

Figure S2 T) Manhattan, Q-Q, and LocusZoom plots for IL1ra results in meta-analyses.





No significant associtions (p-value limit 3.1x10^{-9}).

Figure S2 U) Manhattan, Q-Q, and LocusZoom plots for IP10 results in NFBC1966.

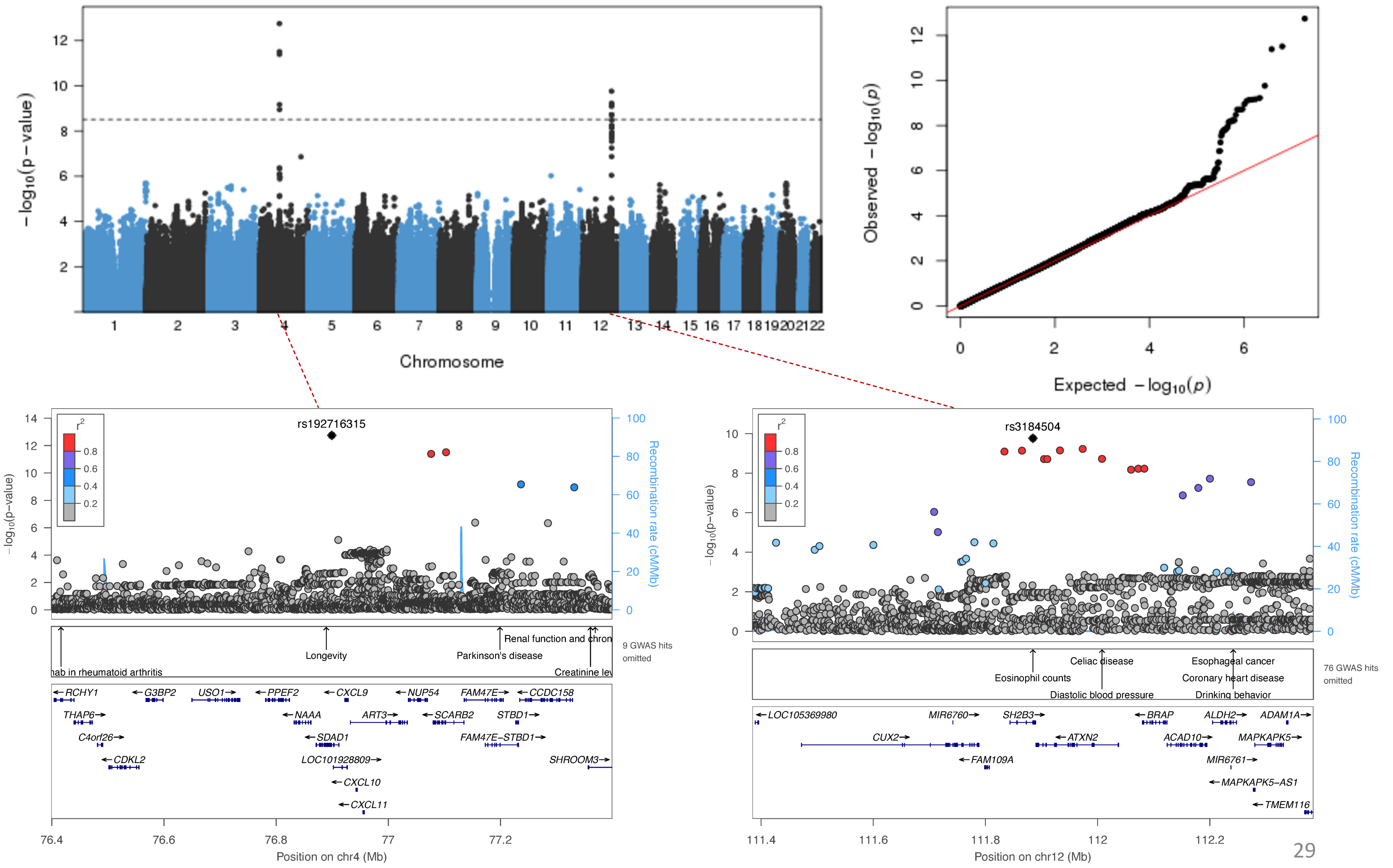


Figure S2 V) Manhattan, Q-Q, and LocusZoom plots for IP10 results in meta-analyses.

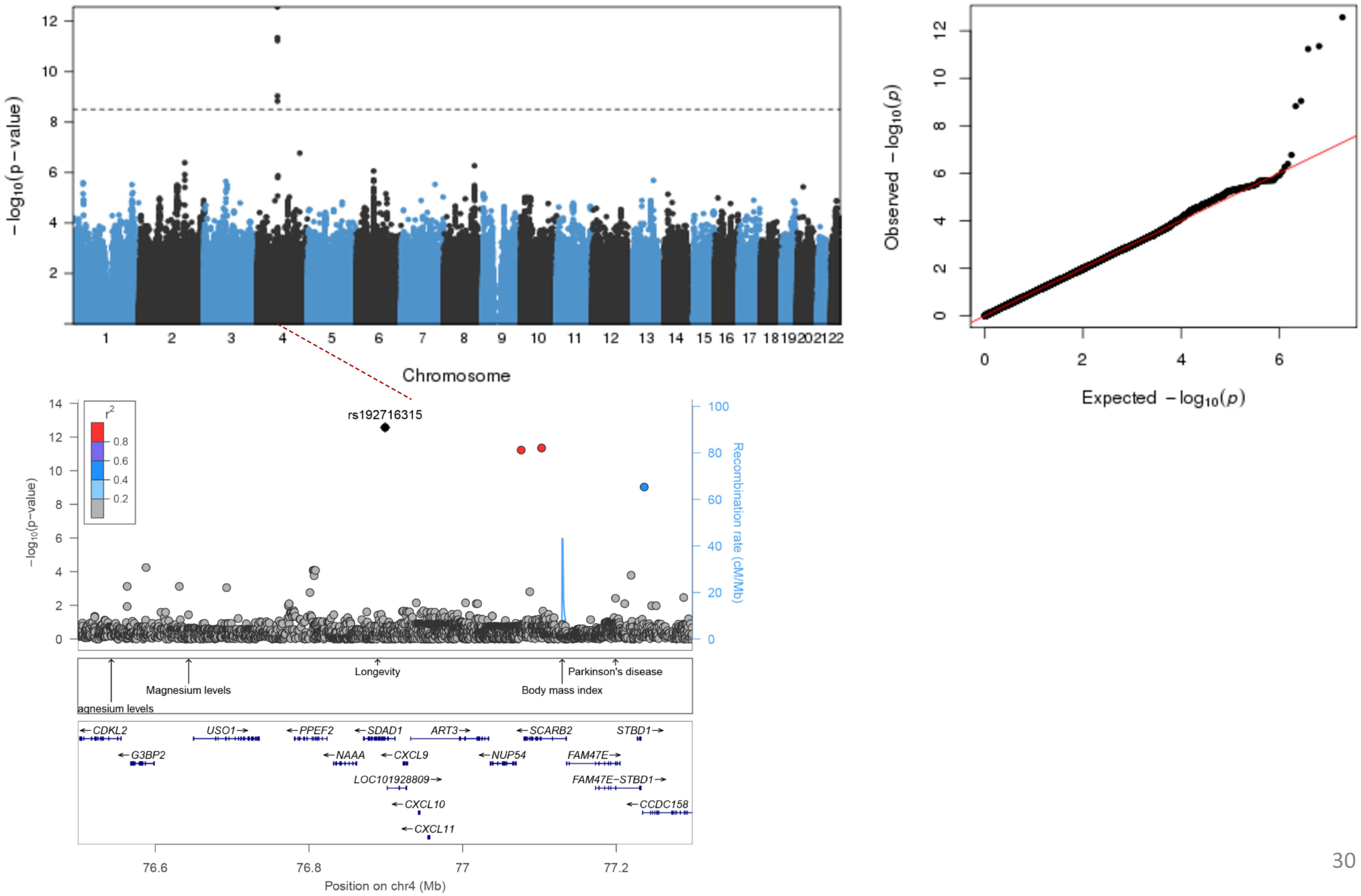


Figure S2 W) Manhattan, Q-Q, and LocusZoom plots for MCP1 results in NFBC1966.

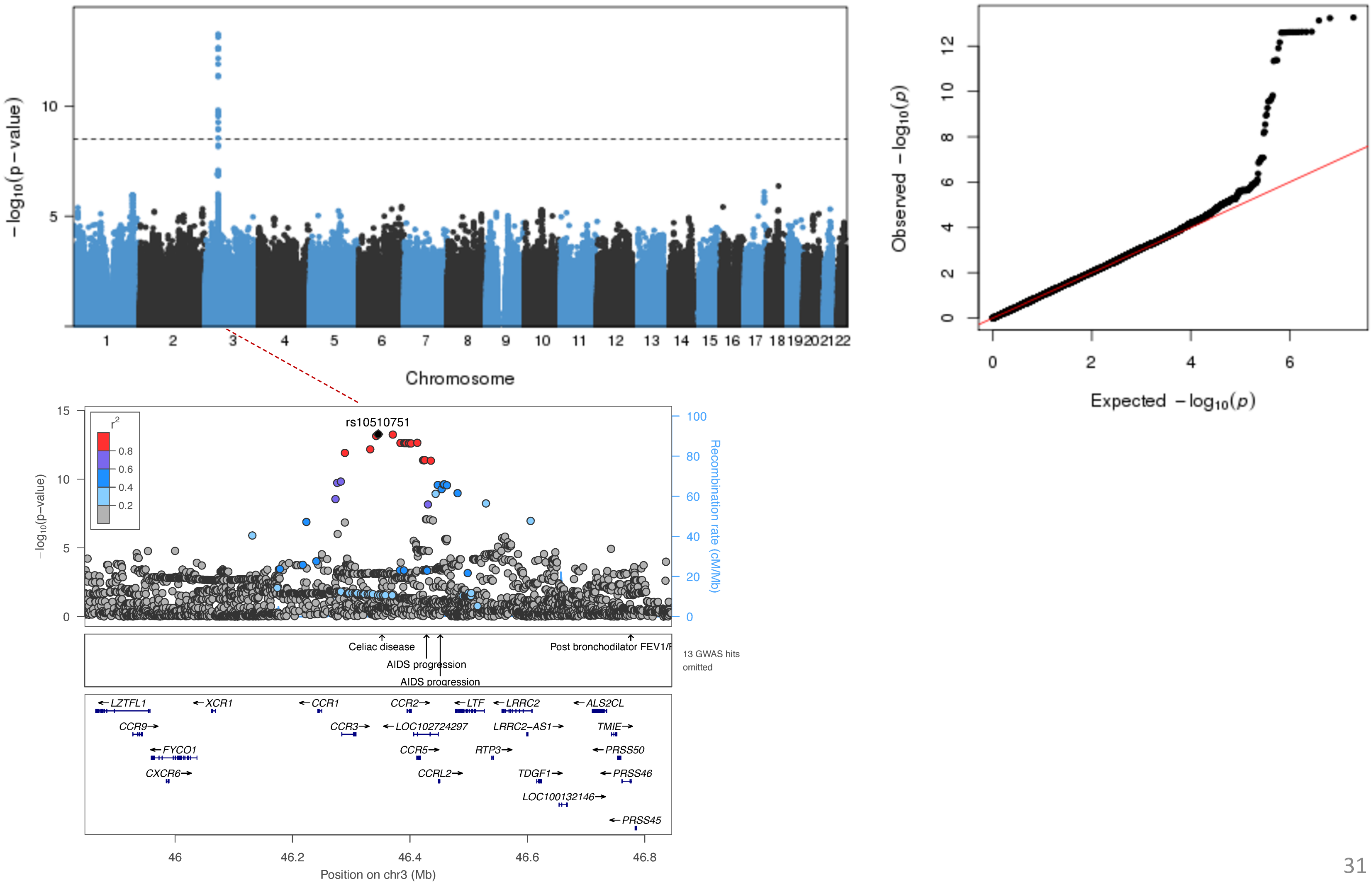


Figure S2 X) Manhattan, Q-Q, and LocusZoom plots for MCP1 results in meta-analyses.

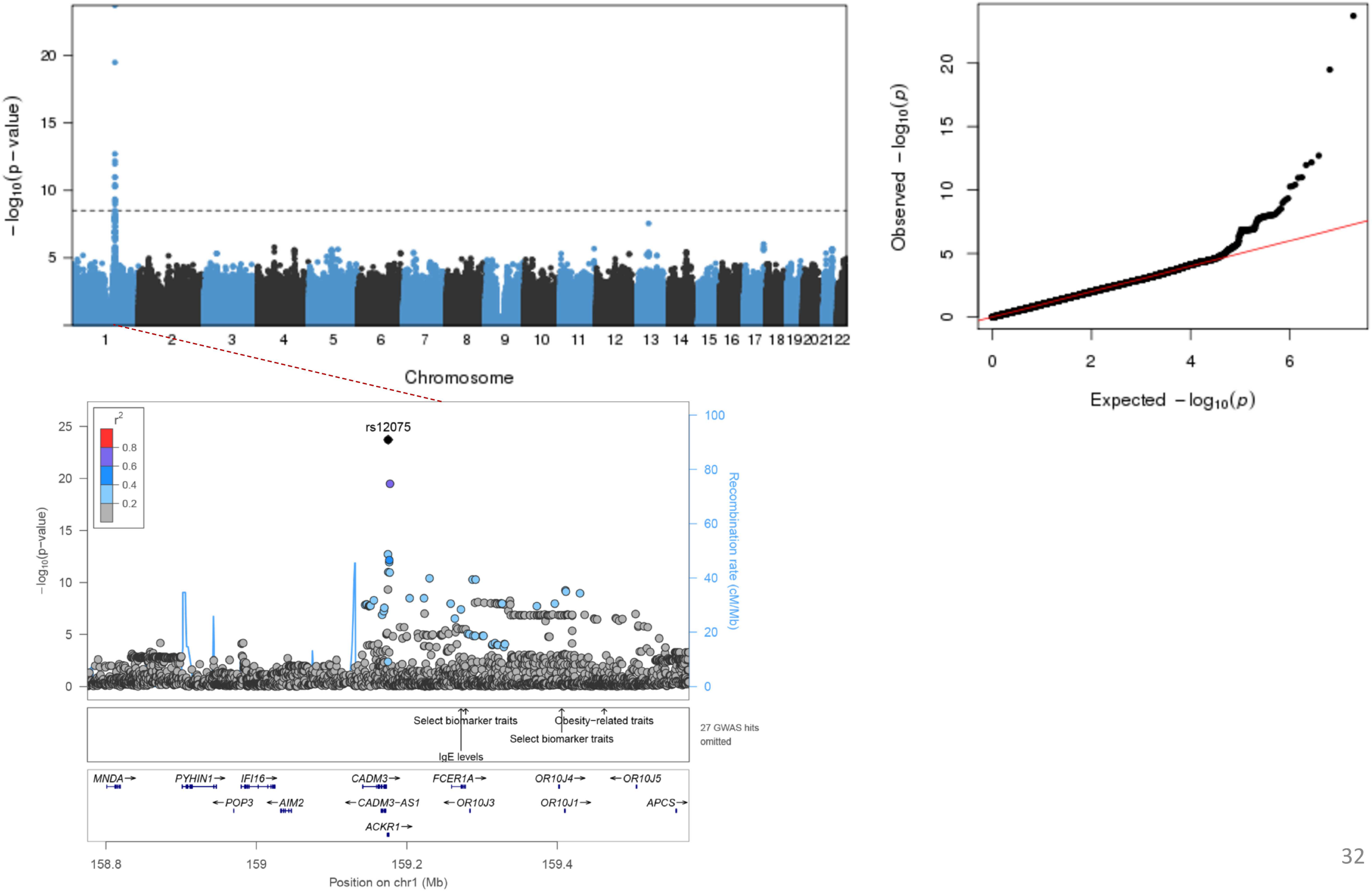
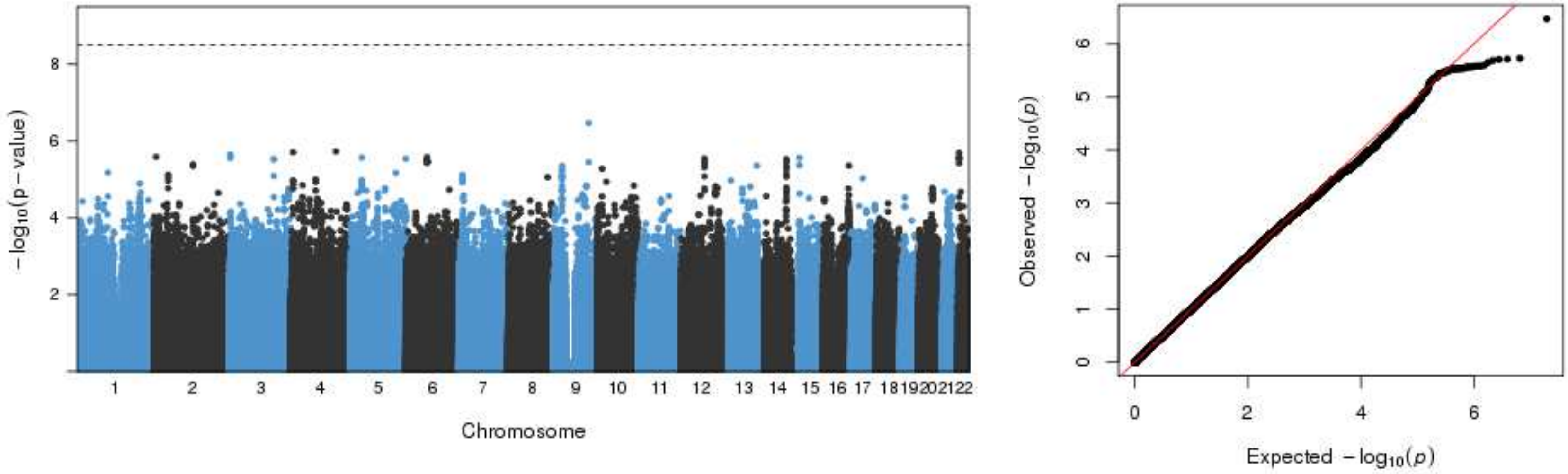
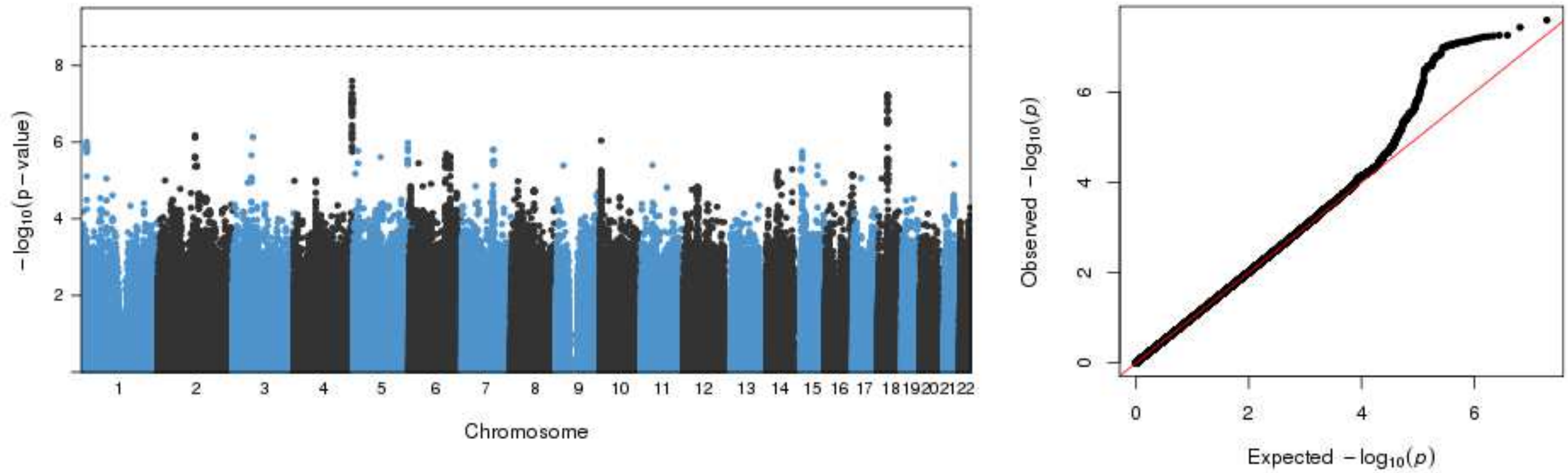


Figure S2 Y) Manhattan, Q-Q, and LocusZoom plots for sCD40L results in NFBC1966.



No significant associtions (p-value limit 3.1x10^{-9}).

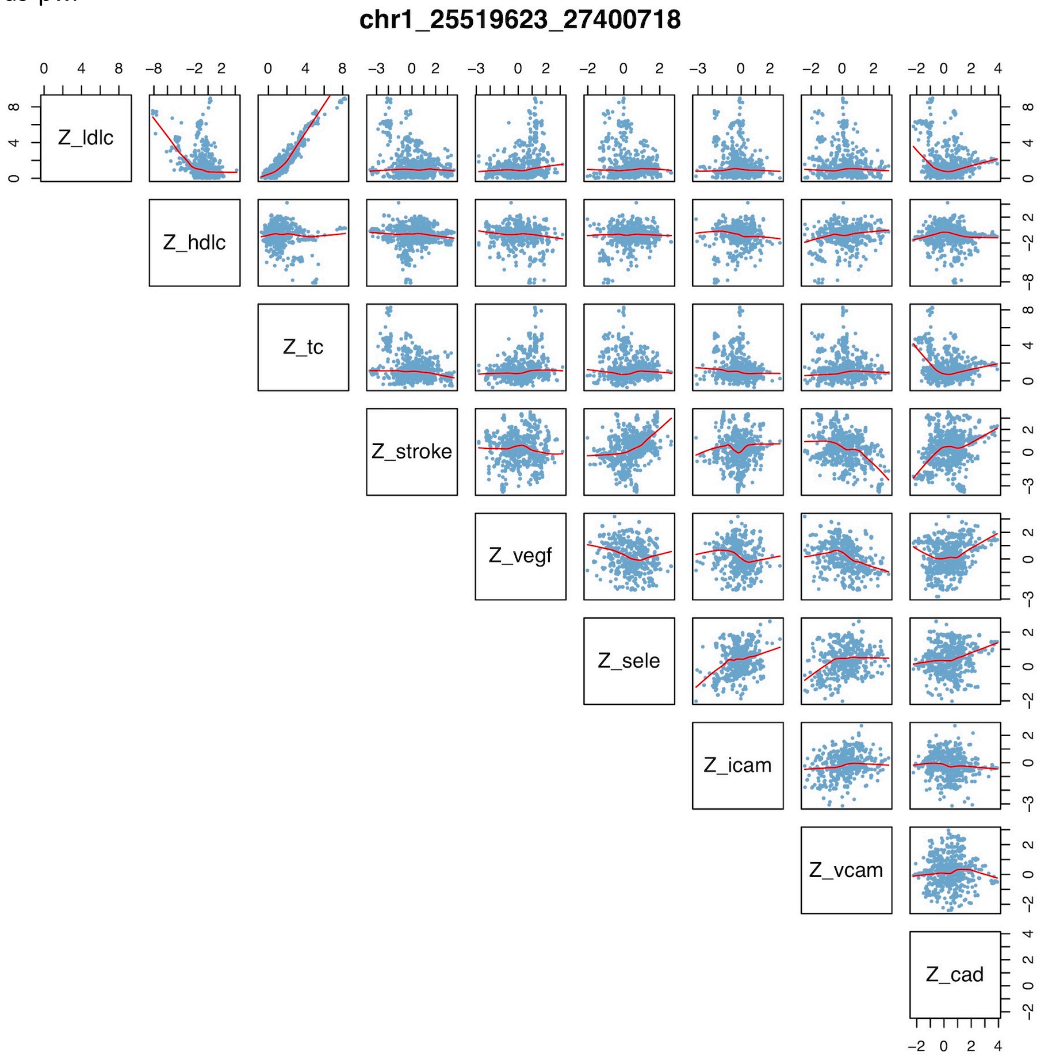
Figure S2 Z) Manhattan, Q-Q, and LocusZoom plots for PAI-1 results in NFBC1966.



No significant associtions (p-value limit 3.1x10^{-9}).

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (1/56)

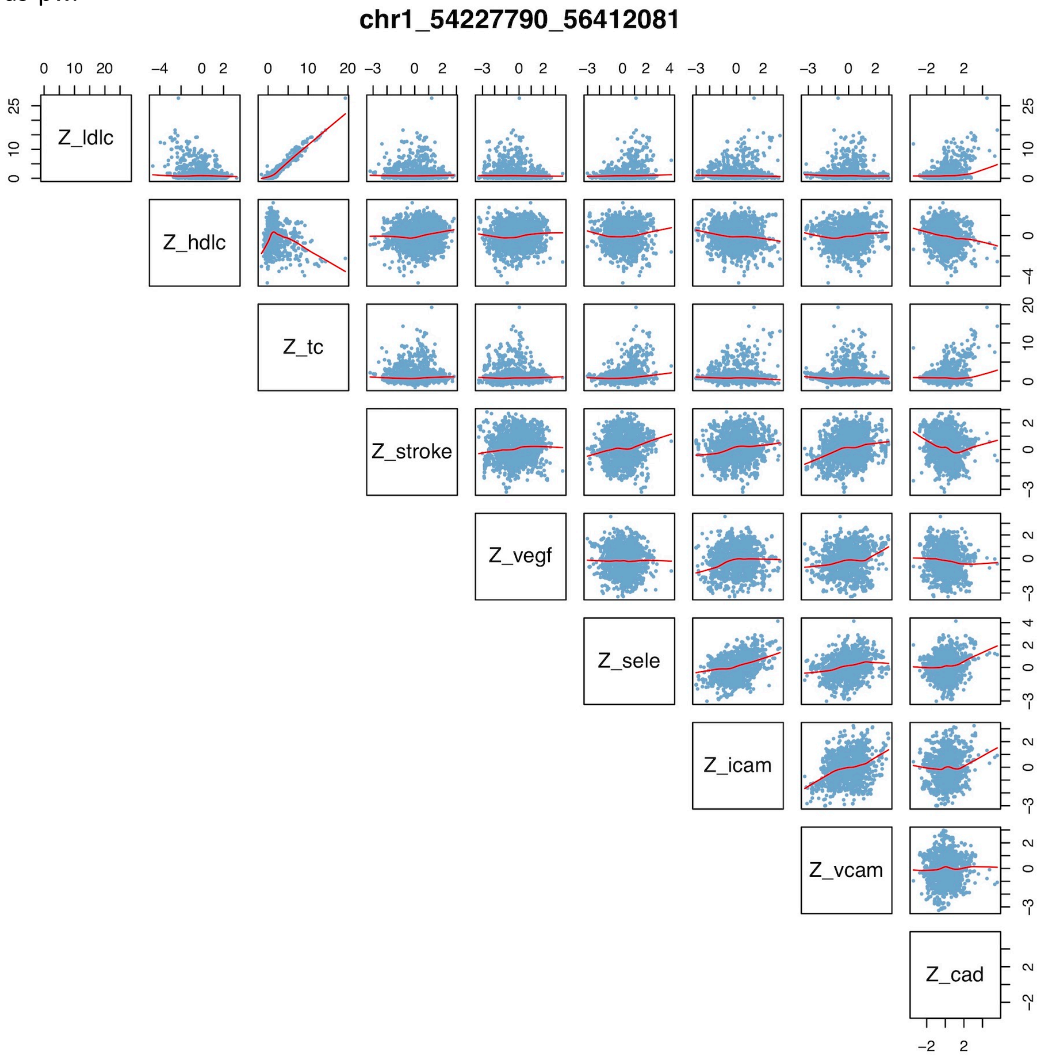
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr1_25519623_27400718	0.992	ldlc	cad
chr1_25519623_27400718	0.996	ldlc	hdlc
chr1_25519623_27400718	0.991	ldlc	icam
chr1_25519623_27400718	0.991	ldlc	stroke
chr1_25519623_27400718	1.000	ldlc	tc
chr1_25519623_27400718	0.991	ldlc	vcam
chr1_25519623_27400718	0.992	ldlc	vegf
chr1_25519623_27400718	0.991	sele	ldlc

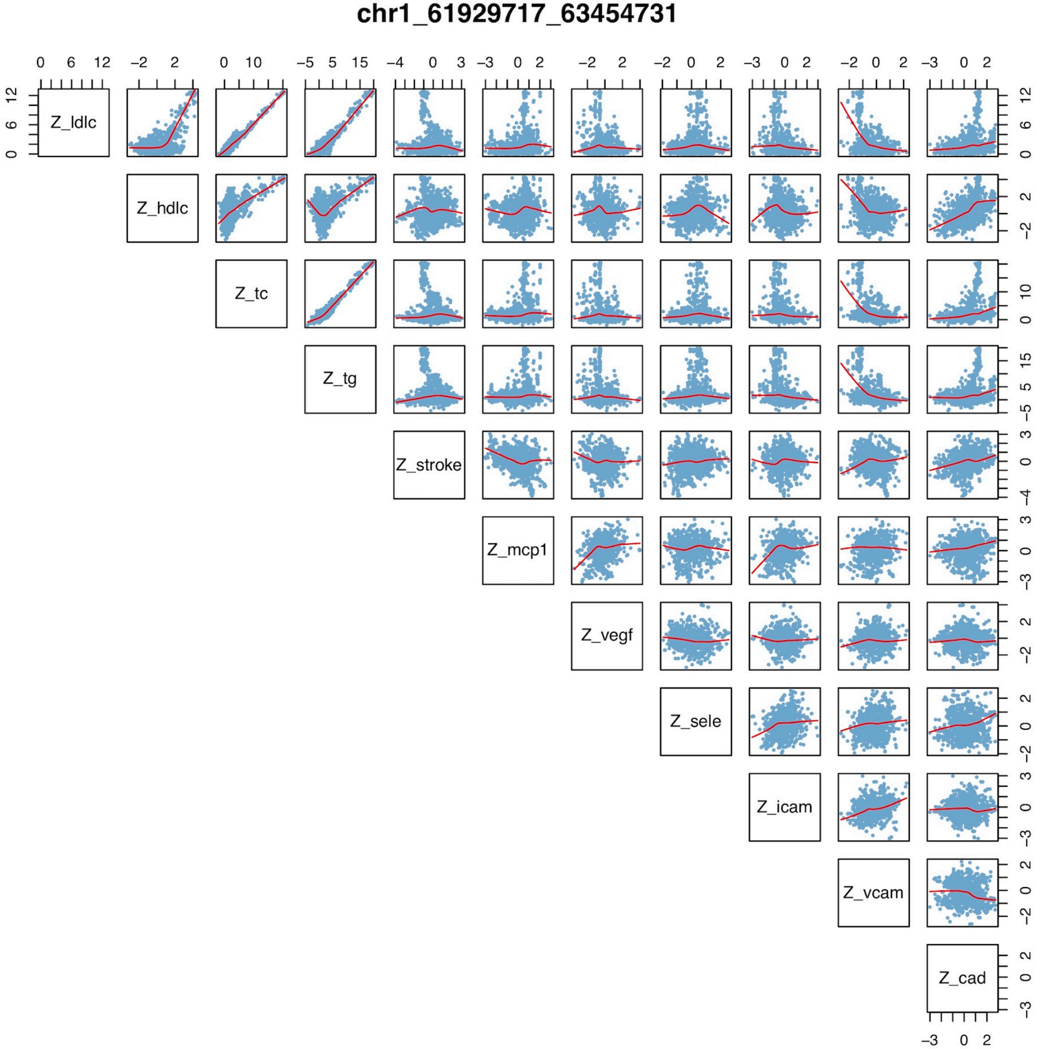
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (2/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



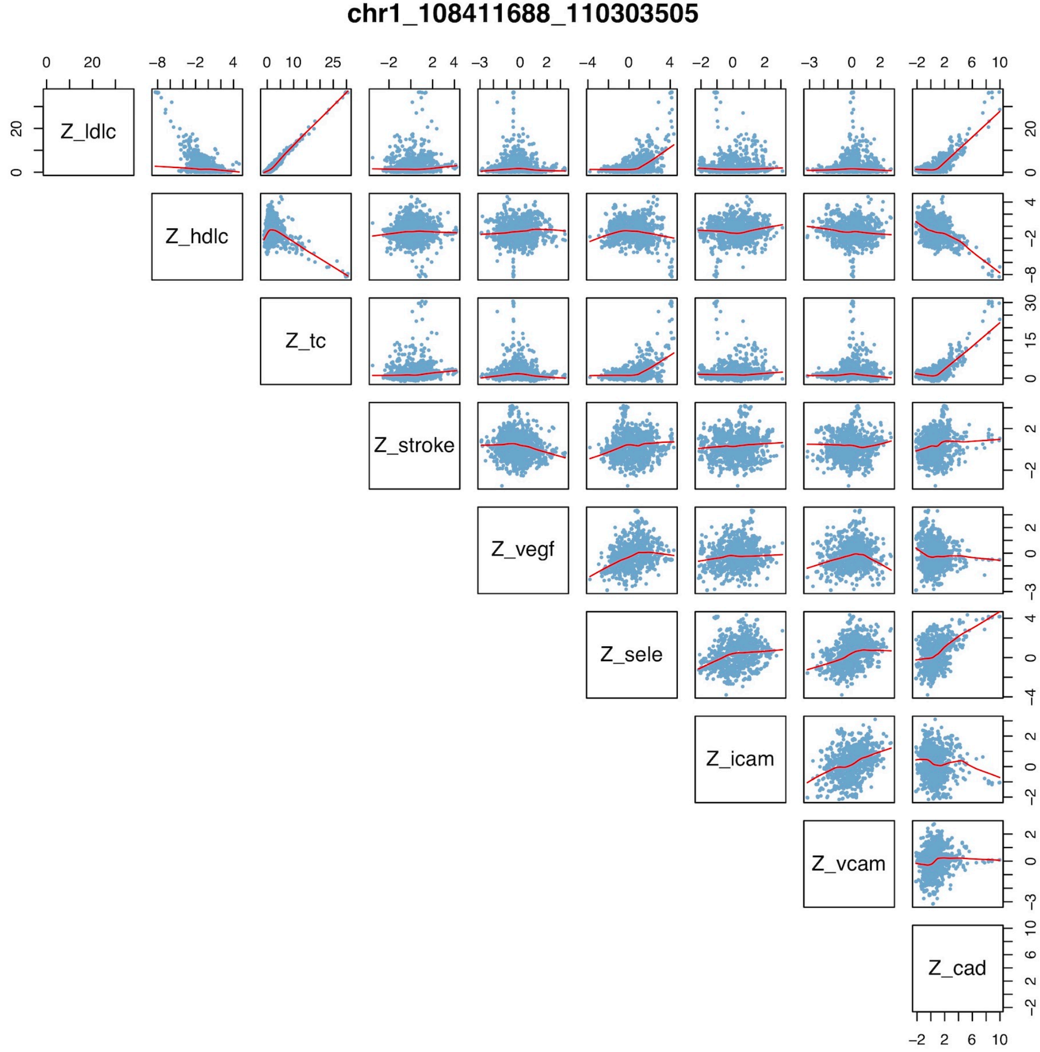
locus	PPA_3	pheno1	pheno2
chr1_54227790_56412081	0.999	ldlc	cad
chr1_54227790_56412081	1.000	ldlc	hdlc
chr1_54227790_56412081	0.999	ldlc	icam
chr1_54227790_56412081	0.999	ldlc	stroke
chr1_54227790_56412081	1.000	ldlc	tc
chr1_54227790_56412081	0.999	ldlc	vcam
chr1_54227790_56412081	0.999	ldlc	vegf
chr1_54227790_56412081	0.999	sele	ldlc
chr1_54227790_56412081	0.999	sele	tc
chr1_54227790_56412081	0.999	tc	cad
chr1_54227790_56412081	0.999	tc	icam
chr1_54227790_56412081	0.999	tc	stroke
chr1_54227790_56412081	0.999	tc	vcam
chr1_54227790_56412081	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (3/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



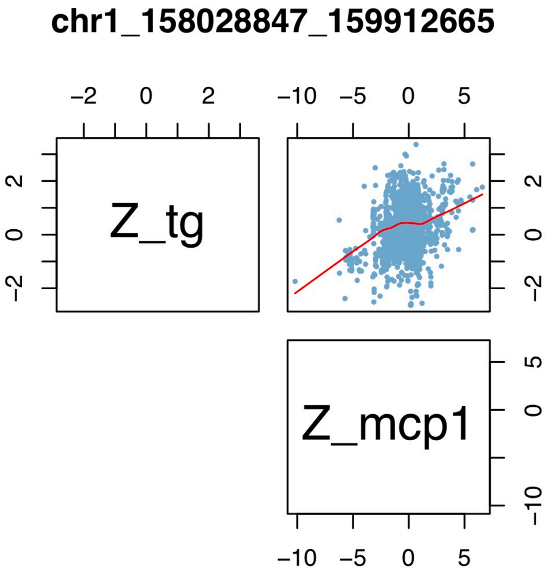
locus	PPA_3	pheno1	pheno2
chr1_61929717_63454731	0.996	hdlc	tc
chr1_61929717_63454731	1.000	hdlc	tg
chr1_61929717_63454731	0.999	ldlc	cad
chr1_61929717_63454731	1.000	ldlc	hdlc
chr1_61929717_63454731	0.999	ldlc	icam
chr1_61929717_63454731	0.999	ldlc	stroke
chr1_61929717_63454731	1.000	ldlc	tc
chr1_61929717_63454731	0.999	ldlc	tg
chr1_61929717_63454731	0.999	ldlc	vcam
chr1_61929717_63454731	0.999	ldlc	vegf
chr1_61929717_63454731	0.999	sele	ldlc
chr1_61929717_63454731	0.999	sele	tc
chr1_61929717_63454731	0.999	sele	tg
chr1_61929717_63454731	0.999	tc	cad
chr1_61929717_63454731	0.999	tc	icam
chr1_61929717_63454731	0.999	tc	stroke
chr1_61929717_63454731	1.000	tc	tg
chr1_61929717_63454731	0.999	tc	vcam
chr1_61929717_63454731	0.999	tc	vegf
chr1_61929717_63454731	0.999	tg	cad
chr1_61929717_63454731	0.999	tg	icam
chr1_61929717_63454731	0.999	tg	mcp1
chr1_61929717_63454731	0.999	tg	stroke
chr1_61929717_63454731	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (4/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



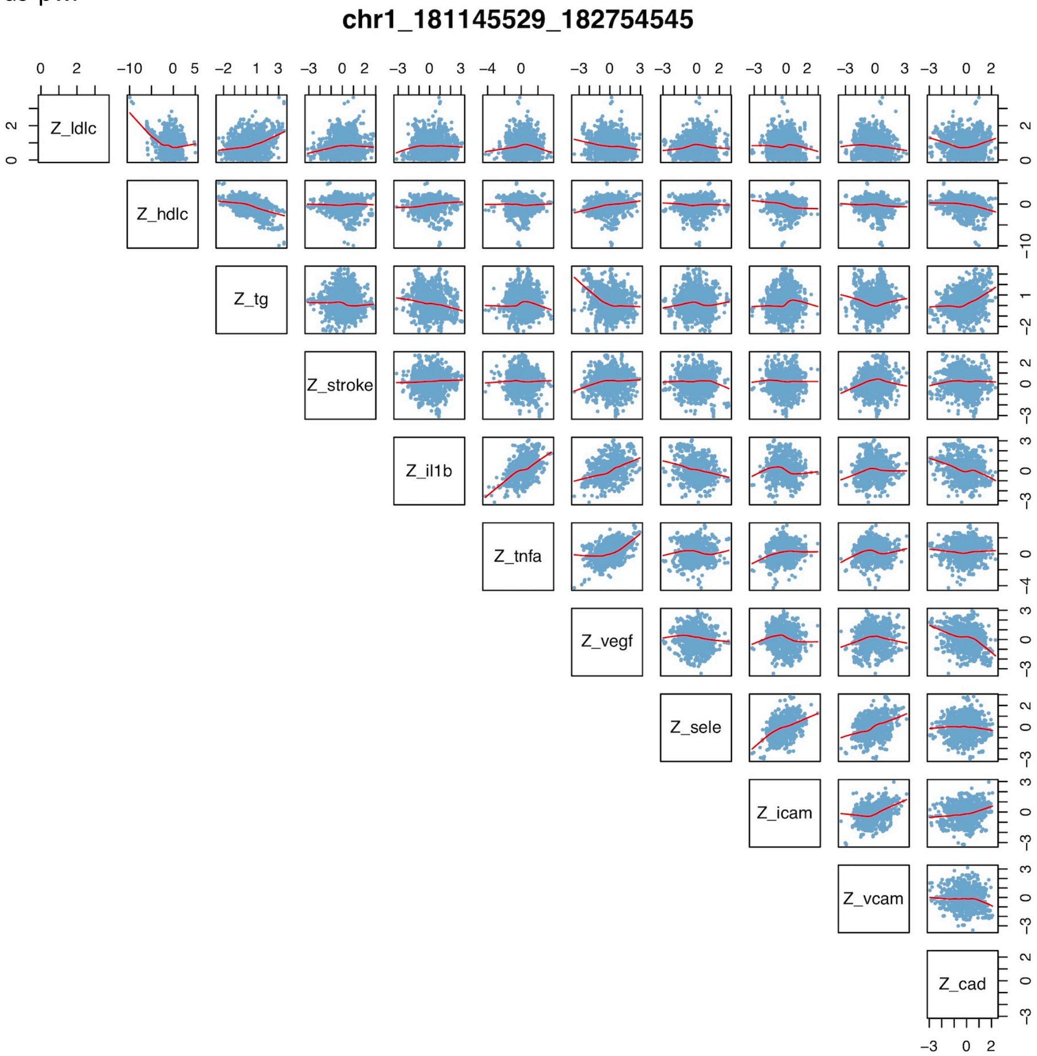
locus	PPA_3	pheno1	pheno2
chr1_108411688_110303505	1.000	hdlc	tc
chr1_108411688_110303505	1.000	ldlc	cad
chr1_108411688_110303505	1.000	ldlc	hdlc
chr1_108411688_110303505	0.999	ldlc	icam
chr1_108411688_110303505	0.999	ldlc	stroke
chr1_108411688_110303505	1.000	ldlc	tc
chr1_108411688_110303505	0.999	ldlc	vcam
chr1_108411688_110303505	0.999	ldlc	vegf
chr1_108411688_110303505	1.000	sele	ldlc
chr1_108411688_110303505	1.000	sele	tc
chr1_108411688_110303505	1.000	tc	cad
chr1_108411688_110303505	0.999	tc	icam
chr1_108411688_110303505	0.999	tc	stroke
chr1_108411688_110303505	0.999	tc	vcam
chr1_108411688_110303505	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (5/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



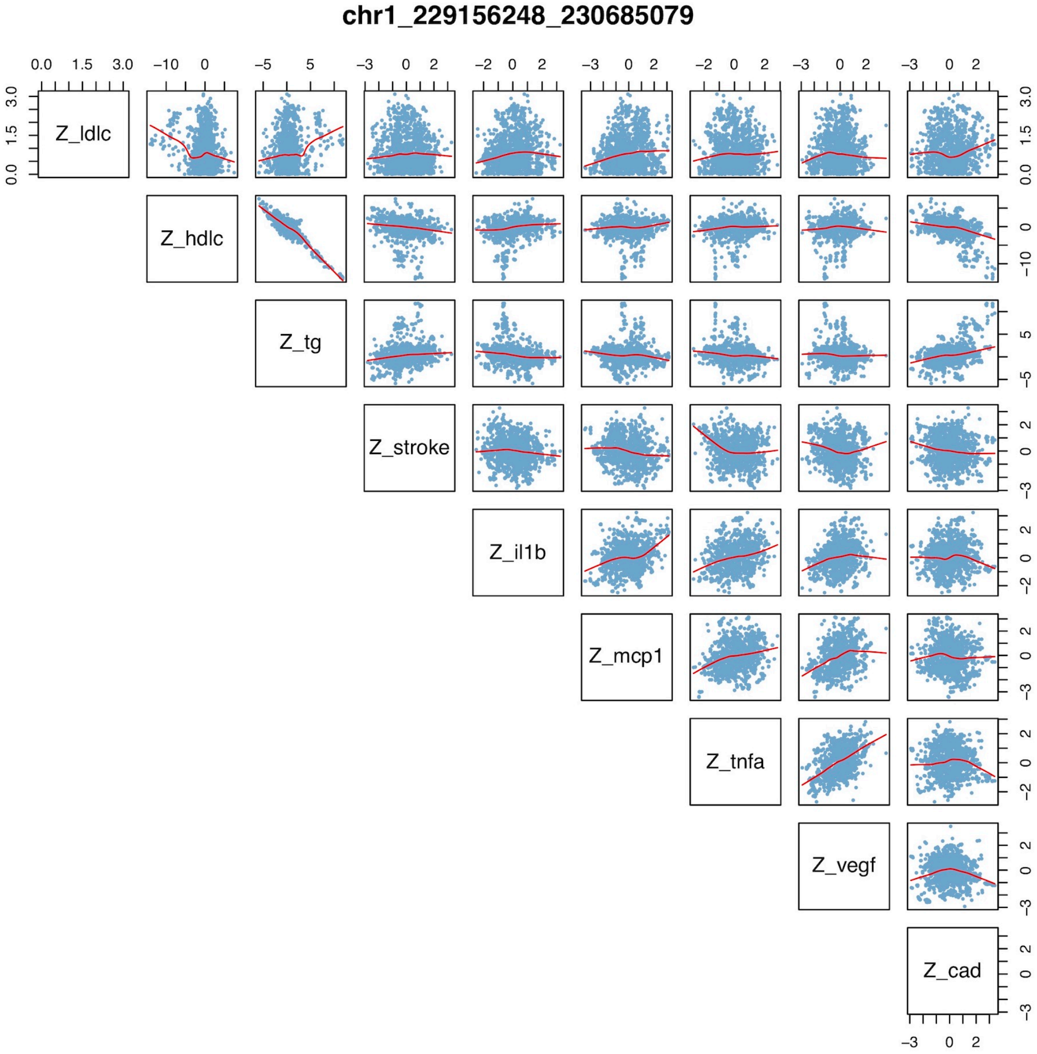
locus	PPA_3	pheno1	pheno2
chr1_158028847_159912665	0.996	tg	mcp1

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (6/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



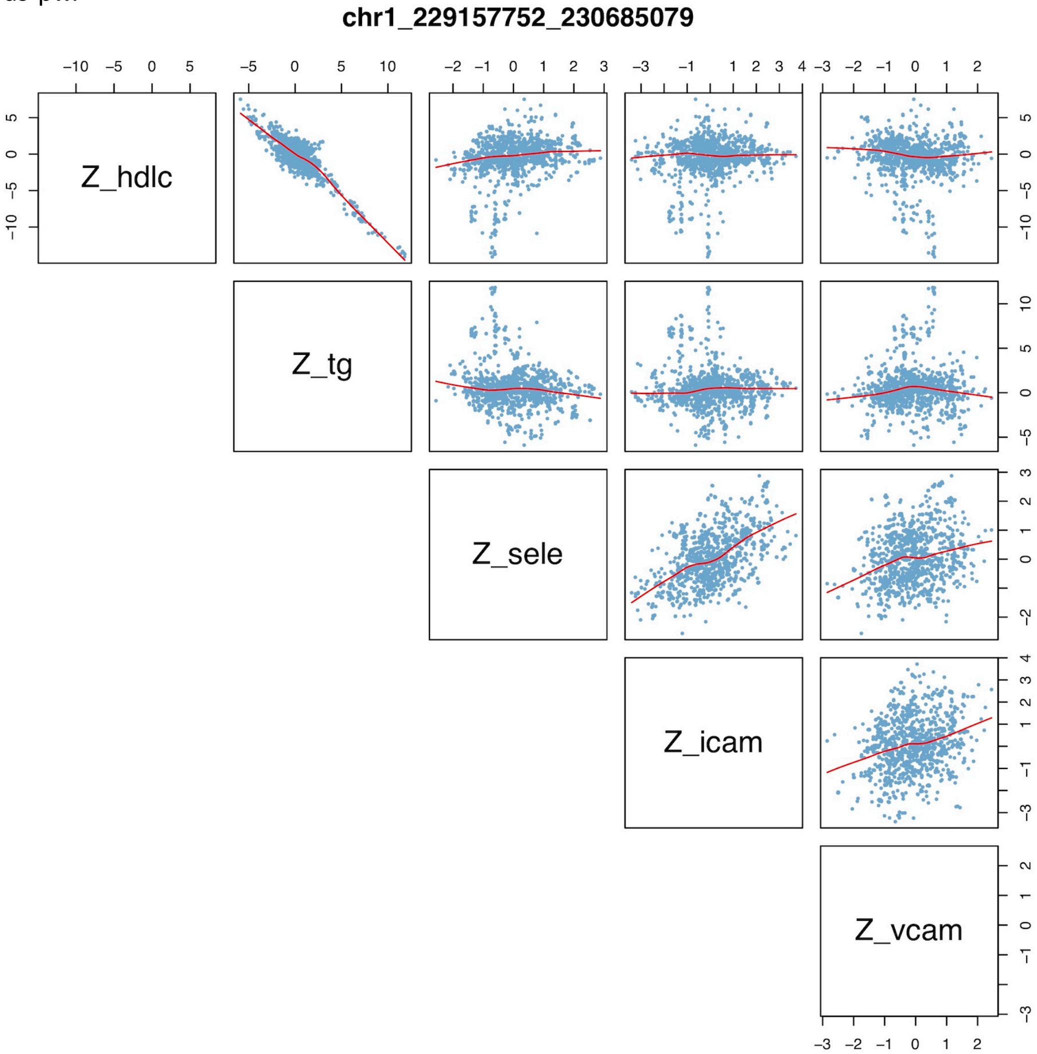
locus	PPA_3	pheno1	pheno2
chr1_181145529_182754545	0.992	hdlc	cad
chr1_181145529_182754545	0.992	hdlc	icam
chr1_181145529_182754545	0.992	hdlc	il1b
chr1_181145529_182754545	0.992	hdlc	stroke
chr1_181145529_182754545	0.998	hdlc	tg
chr1_181145529_182754545	0.991	hdlc	tnfa
chr1_181145529_182754545	0.992	hdlc	vcam
chr1_181145529_182754545	0.991	hdlc	vegf
chr1_181145529_182754545	0.997	ldlc	hdlc
chr1_181145529_182754545	0.992	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (7/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



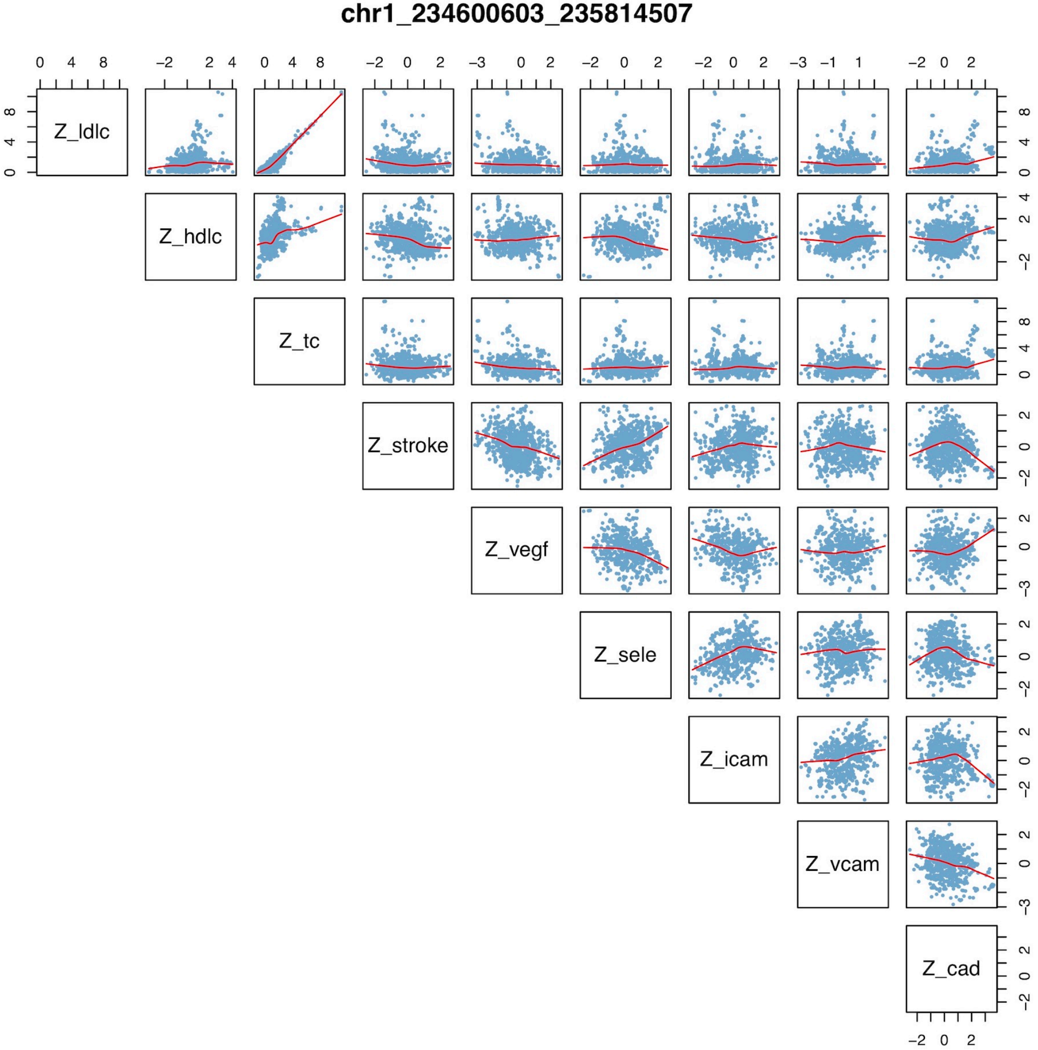
locus	PPA_3	pheno1	pheno2
chr1_229156248_230685079	0.999	hdlc	cad
chr1_229156248_230685079	0.999	hdlc	il1b
chr1_229156248_230685079	0.999	hdlc	stroke
chr1_229156248_230685079	1.000	hdlc	tg
chr1_229156248_230685079	0.999	hdlc	tnfa
chr1_229156248_230685079	0.999	hdlc	vegf
chr1_229156248_230685079	0.999	ldlc	hdlc
chr1_229156248_230685079	0.999	tg	cad
chr1_229156248_230685079	0.999	tg	mcp1
chr1_229156248_230685079	0.999	tg	stroke
chr1_229156248_230685079	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (8/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr1_229157752_230685079	0.999	hdlc	icam
chr1_229157752_230685079	0.999	hdlc	vcam
chr1_229157752_230685079	0.999	sele	hdlc
chr1_229157752_230685079	0.999	sele	tg
chr1_229157752_230685079	0.999	tg	icam

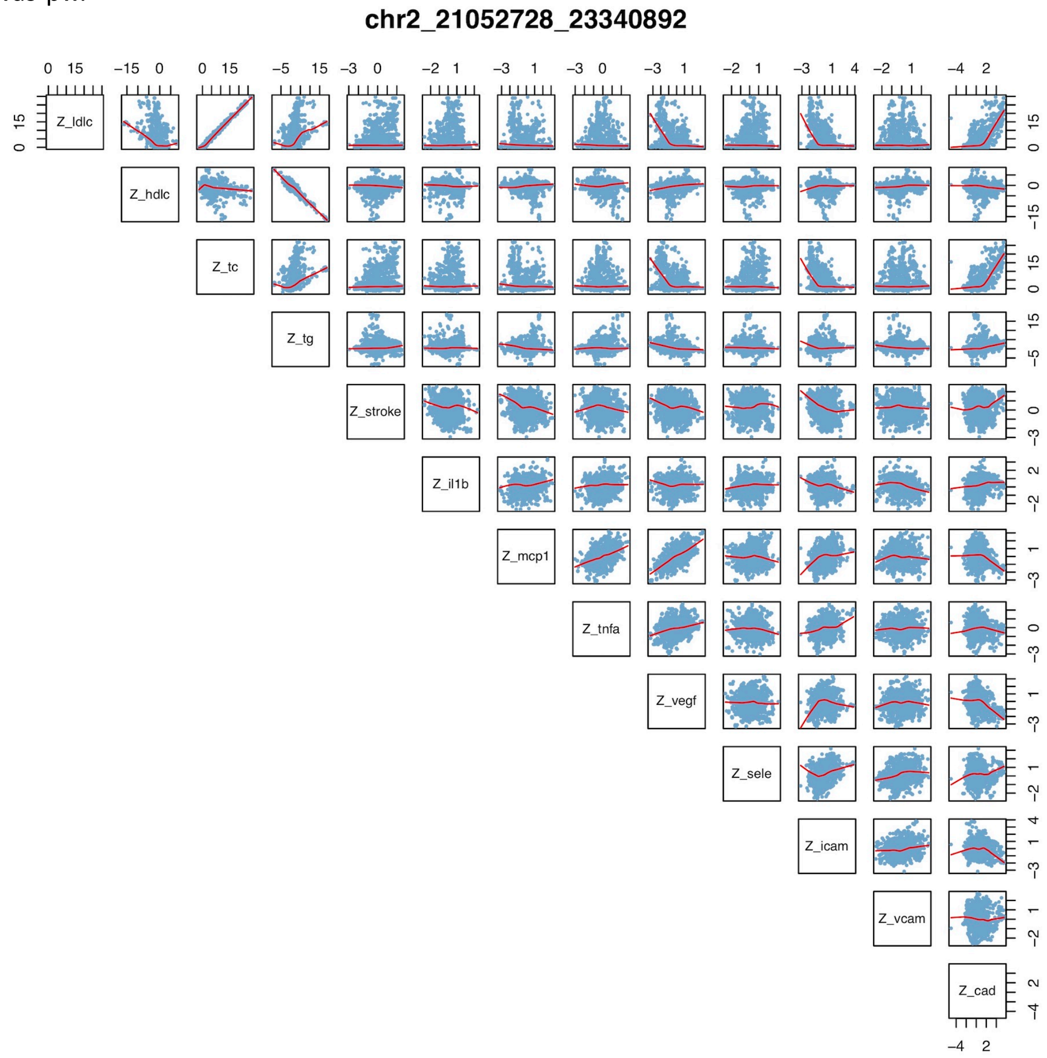
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (9/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr1_234600603_235814507	0.992	hdlc	tc
chr1_234600603_235814507	0.997	ldlc	cad
chr1_234600603_235814507	0.999	ldlc	hdlc
chr1_234600603_235814507	0.997	ldlc	icam
chr1_234600603_235814507	0.996	ldlc	stroke
chr1_234600603_235814507	1.000	ldlc	tc
chr1_234600603_235814507	0.996	ldlc	vcam
chr1_234600603_235814507	0.996	ldlc	vegf
chr1_234600603_235814507	0.996	sele	ldlc
chr1_234600603_235814507	0.998	sele	tc
chr1_234600603_235814507	0.998	tc	cad
chr1_234600603_235814507	0.998	tc	icam
chr1_234600603_235814507	0.998	tc	stroke
chr1_234600603_235814507	0.998	tc	vcam
chr1_234600603_235814507	0.998	tc	vegf

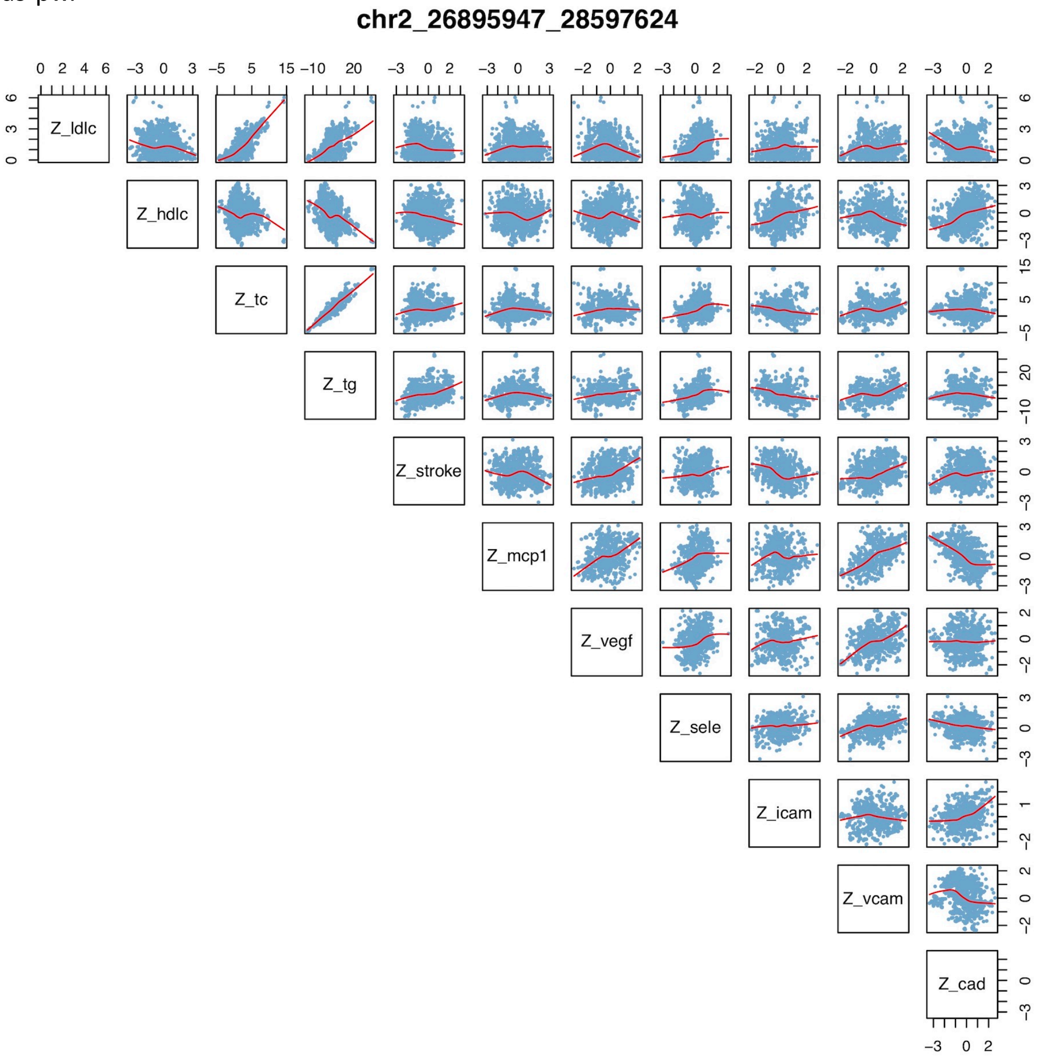
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (10/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr2_21052728_23340892	0.999	hdlc	cad
chr2_21052728_23340892	0.999	hdlc	icam
chr2_21052728_23340892	0.999	hdlc	il1b
chr2_21052728_23340892	0.999	hdlc	stroke
chr2_21052728_23340892	1.000	hdlc	tg
chr2_21052728_23340892	0.999	hdlc	tnfa
chr2_21052728_23340892	0.999	hdlc	vcam
chr2_21052728_23340892	0.999	hdlc	vegf
chr2_21052728_23340892	0.999	ldlc	cad
chr2_21052728_23340892	0.999	ldlc	icam
chr2_21052728_23340892	0.999	ldlc	stroke
chr2_21052728_23340892	1.000	ldlc	tc
chr2_21052728_23340892	0.999	ldlc	vcam
chr2_21052728_23340892	0.999	ldlc	vegf
chr2_21052728_23340892	0.999	sele	hdlc
chr2_21052728_23340892	0.999	sele	ldlc
chr2_21052728_23340892	0.999	sele	tc
chr2_21052728_23340892	0.999	sele	tg
chr2_21052728_23340892	0.999	tc	cad
chr2_21052728_23340892	0.999	tc	icam
chr2_21052728_23340892	0.999	tc	stroke
chr2_21052728_23340892	0.999	tc	vcam
chr2_21052728_23340892	0.999	tc	vegf
chr2_21052728_23340892	0.999	tg	cad
chr2_21052728_23340892	0.999	tg	icam
chr2_21052728_23340892	0.999	tg	mcp1
chr2_21052728_23340892	0.999	tg	stroke
chr2_21052728_23340892	0.999	tg	vegf

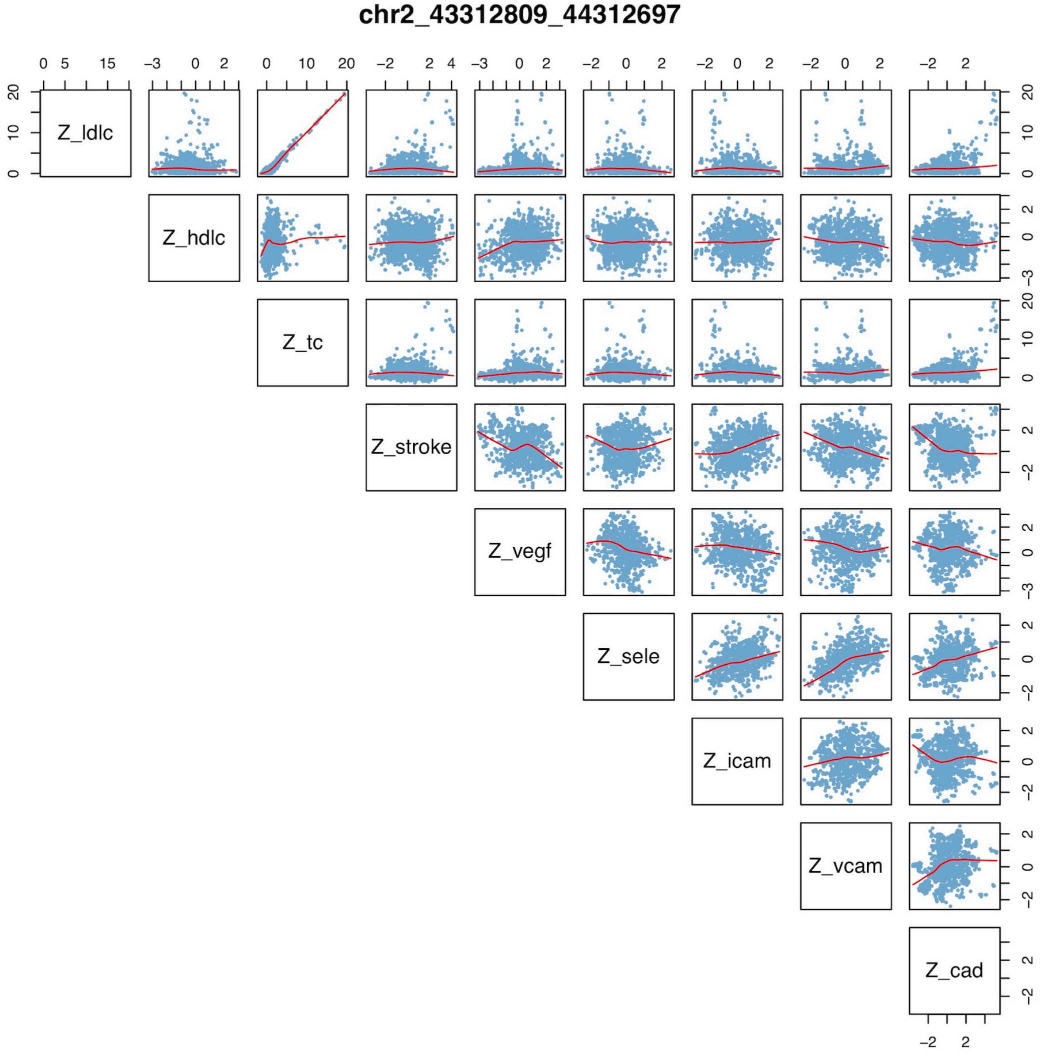
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (11/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr2_26895947_28597624	0.993	hdlc	tc
chr2_26895947_28597624	1.000	hdlc	tg
chr2_26895947_28597624	1.000	ldlc	tc
chr2_26895947_28597624	0.995	ldlc	tg
chr2_26895947_28597624	0.999	sele	tc
chr2_26895947_28597624	0.999	sele	tg
chr2_26895947_28597624	0.999	tc	cad
chr2_26895947_28597624	0.999	tc	icam
chr2_26895947_28597624	0.999	tc	stroke
chr2_26895947_28597624	1.000	tc	tg
chr2_26895947_28597624	0.999	tc	vcam
chr2_26895947_28597624	0.999	tc	vegf
chr2_26895947_28597624	0.999	tg	cad
chr2_26895947_28597624	0.999	tg	icam
chr2_26895947_28597624	0.999	tg	mcp1
chr2_26895947_28597624	0.999	tg	stroke
chr2_26895947_28597624	0.999	tg	vegf

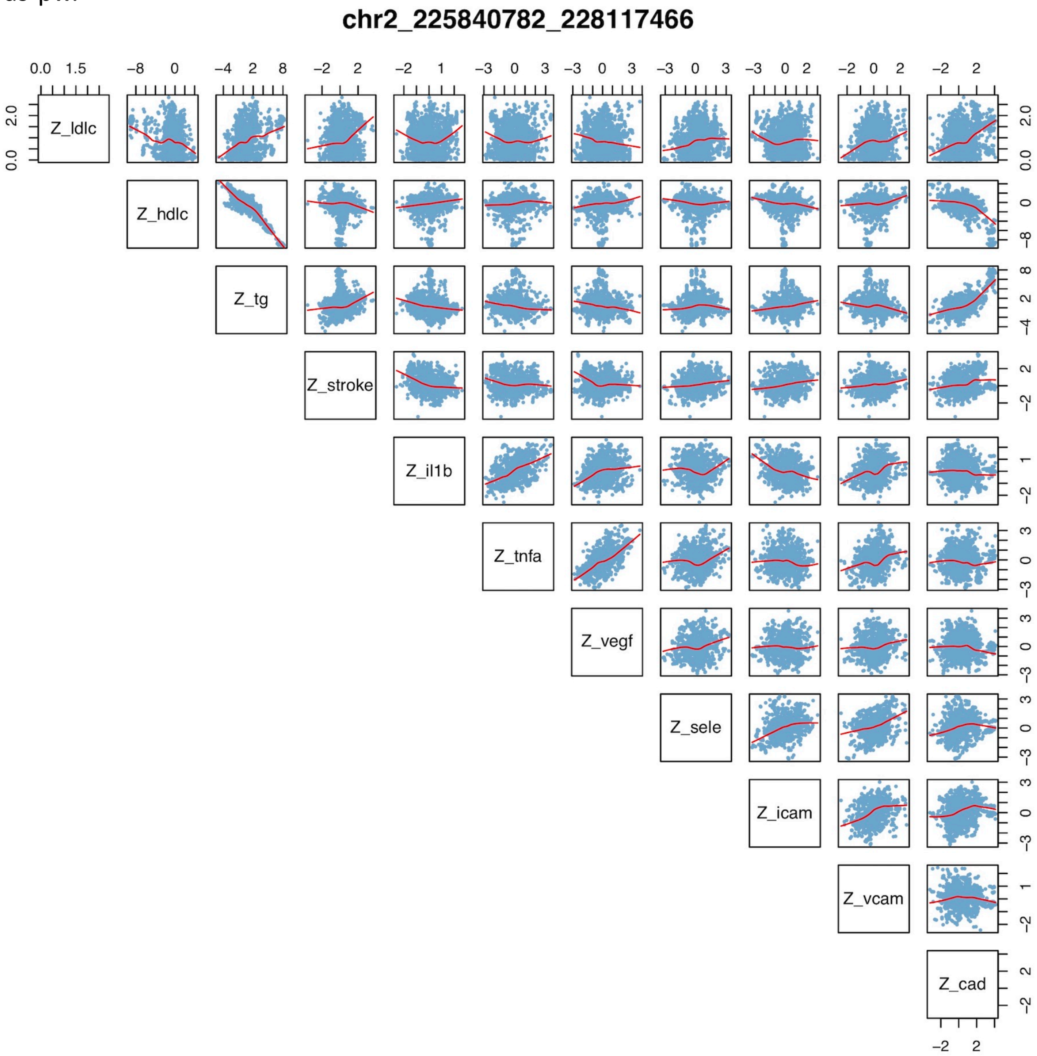
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (12/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



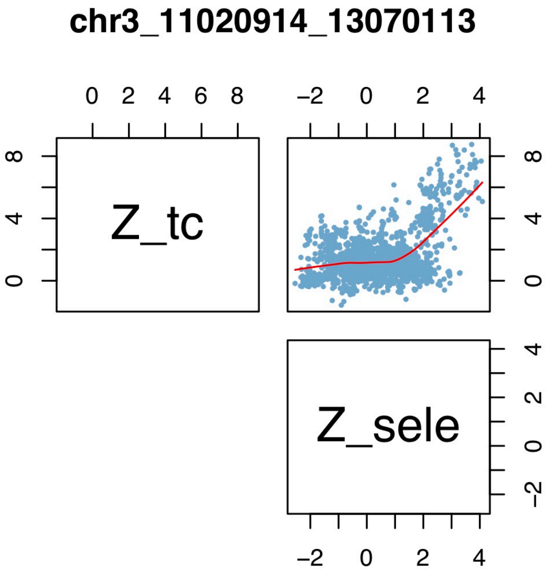
locus	PPA_3	pheno1	pheno2
chr2_43312809_44312697	0.999	ldlc	cad
chr2_43312809_44312697	0.999	ldlc	hdlc
chr2_43312809_44312697	0.999	ldlc	icam
chr2_43312809_44312697	0.999	ldlc	stroke
chr2_43312809_44312697	1.000	ldlc	tc
chr2_43312809_44312697	0.999	ldlc	vcam
chr2_43312809_44312697	0.999	ldlc	vegf
chr2_43312809_44312697	0.999	sele	ldlc
chr2_43312809_44312697	0.999	sele	tc
chr2_43312809_44312697	0.999	tc	cad
chr2_43312809_44312697	0.999	tc	icam
chr2_43312809_44312697	0.999	tc	stroke
chr2_43312809_44312697	0.999	tc	vcam
chr2_43312809_44312697	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (13/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr2_225840782_228117466

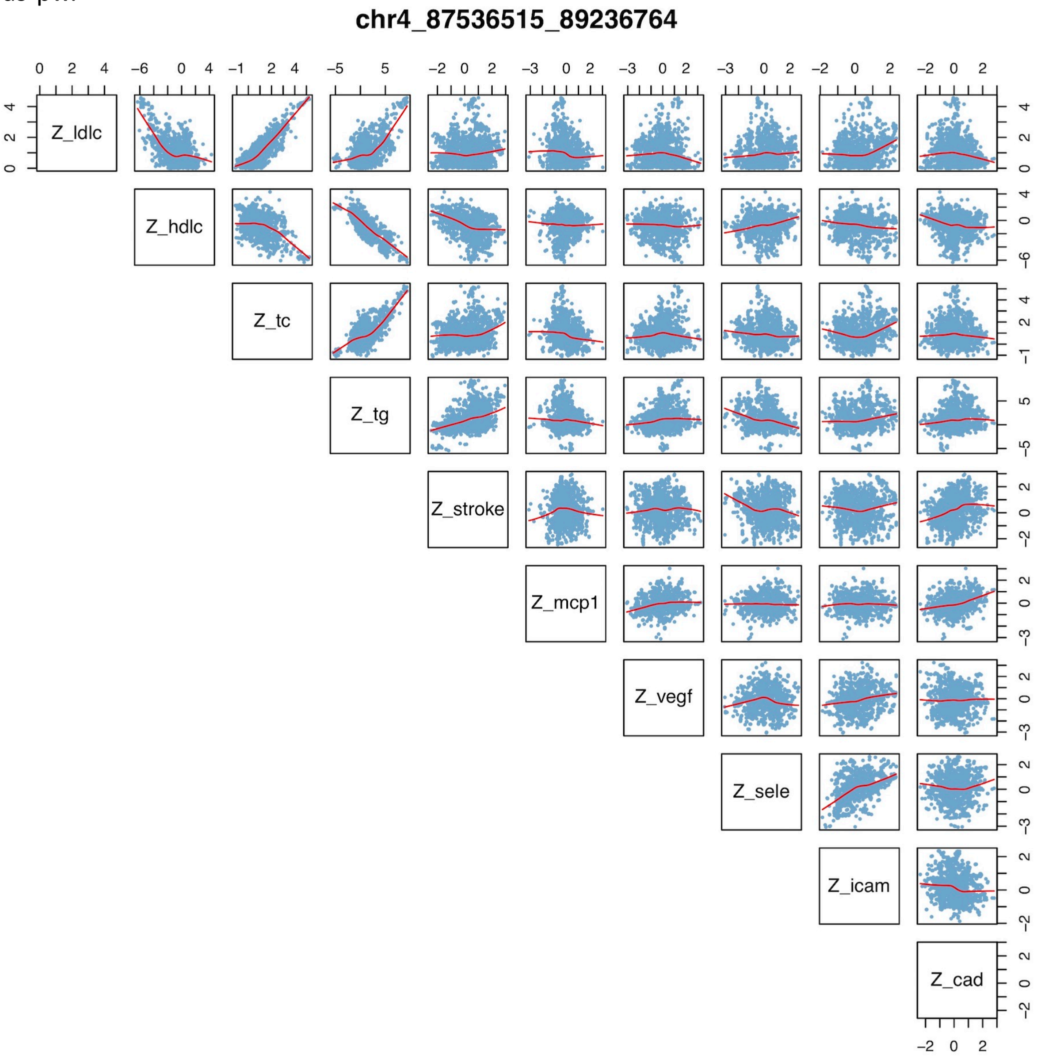
locus	PPA_3	pheno1	pheno2
chr2_225840782_228117466	0.997	hdlc	cad
chr2_225840782_228117466	0.997	hdlc	icam
chr2_225840782_228117466	0.996	hdlc	il1b
chr2_225840782_228117466	0.997	hdlc	stroke
chr2_225840782_228117466	1.000	hdlc	tg
chr2_225840782_228117466	0.996	hdlc	tnfa
chr2_225840782_228117466	0.997	hdlc	vcam
chr2_225840782_228117466	0.996	hdlc	vegf
chr2_225840782_228117466	0.998	ldlc	hdlc
chr2_225840782_228117466	0.997	sele	hdlc
chr2_225840782_228117466	0.990	sele	tg
chr2_225840782_228117466	0.992	tg	cad
chr2_225840782_228117466	0.991	tg	icam
chr2_225840782_228117466	0.990	tg	stroke
chr2_225840782_228117466	0.990	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (14/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr3_11020914_13070113	0.993	sele	tc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (15/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.

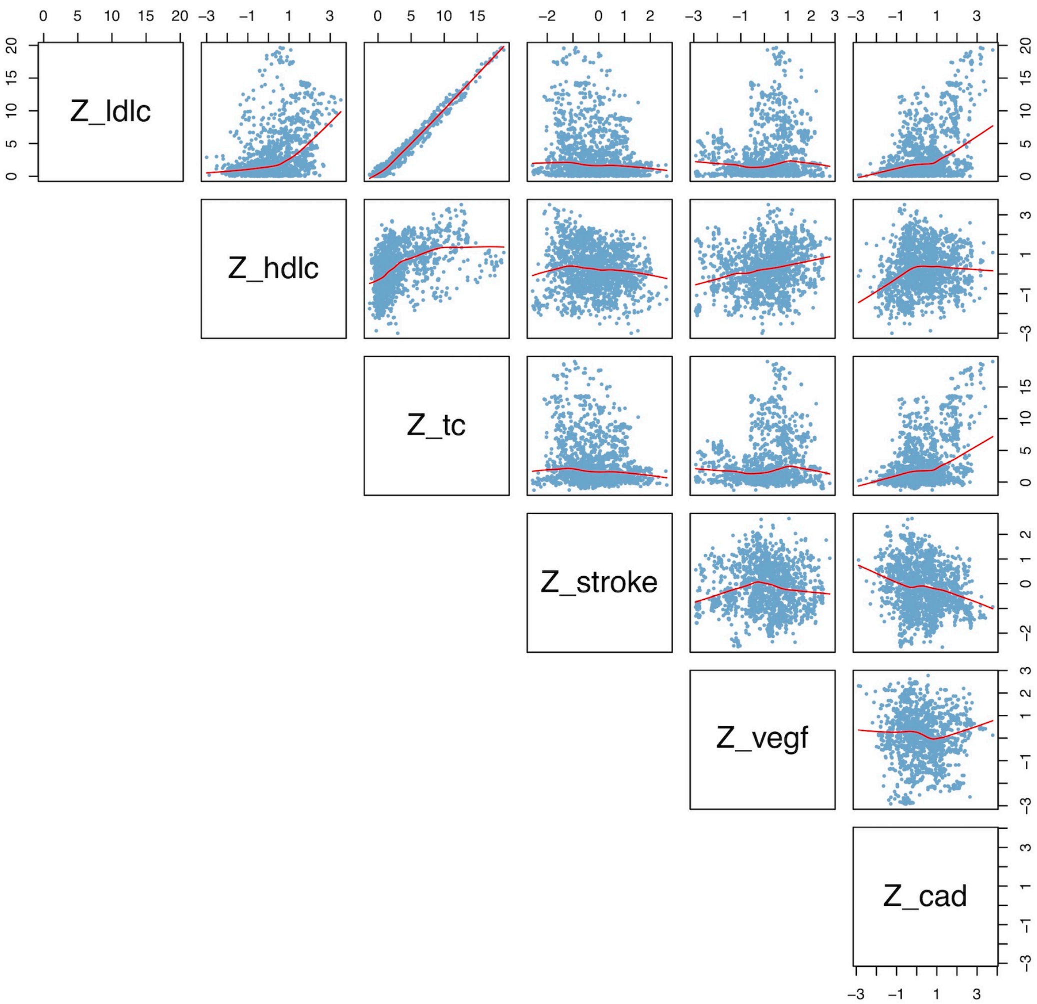


locus	PPA_3	pheno1	pheno2
chr4_87536515_89236764	1.000	hdlc	tg
chr4_87536515_89236764	0.991	ldlc	hdlc
chr4_87536515_89236764	0.997	sele	tg
chr4_87536515_89236764	0.991	tc	tg
chr4_87536515_89236764	0.998	tg	cad
chr4_87536515_89236764	0.997	tg	icam
chr4_87536515_89236764	0.997	tg	mcp1
chr4_87536515_89236764	0.997	tg	stroke
chr4_87536515_89236764	0.998	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (16/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.

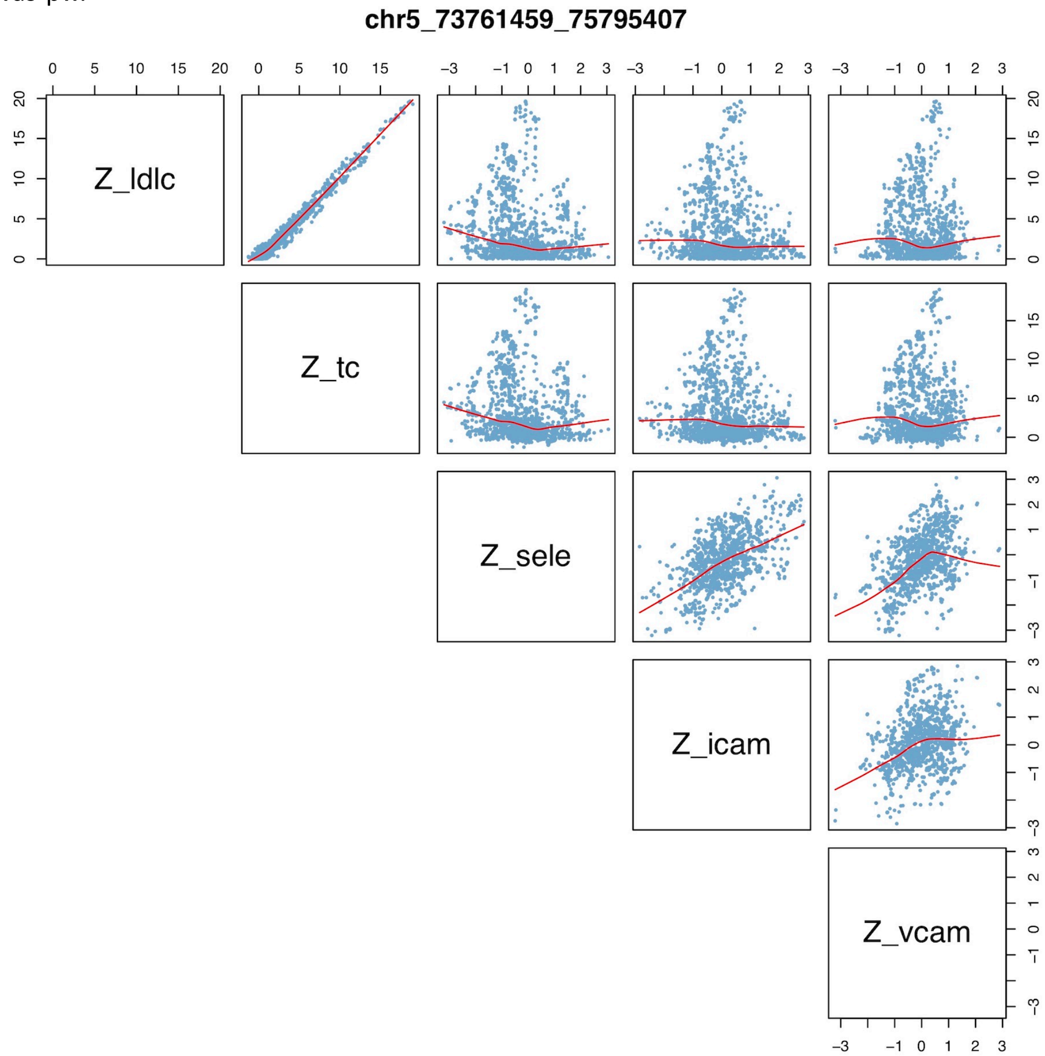
chr5_73760788_75795407



locus	PPA_3	pheno1	pheno2
chr5_73760788_75795407	0.999	ldlc	cad
chr5_73760788_75795407	0.999	ldlc	hdlc
chr5_73760788_75795407	0.999	ldlc	stroke
chr5_73760788_75795407	1.000	ldlc	tc
chr5_73760788_75795407	0.999	ldlc	vegf
chr5_73760788_75795407	0.999	tc	cad
chr5_73760788_75795407	0.999	tc	stroke
chr5_73760788_75795407	0.999	tc	vegf

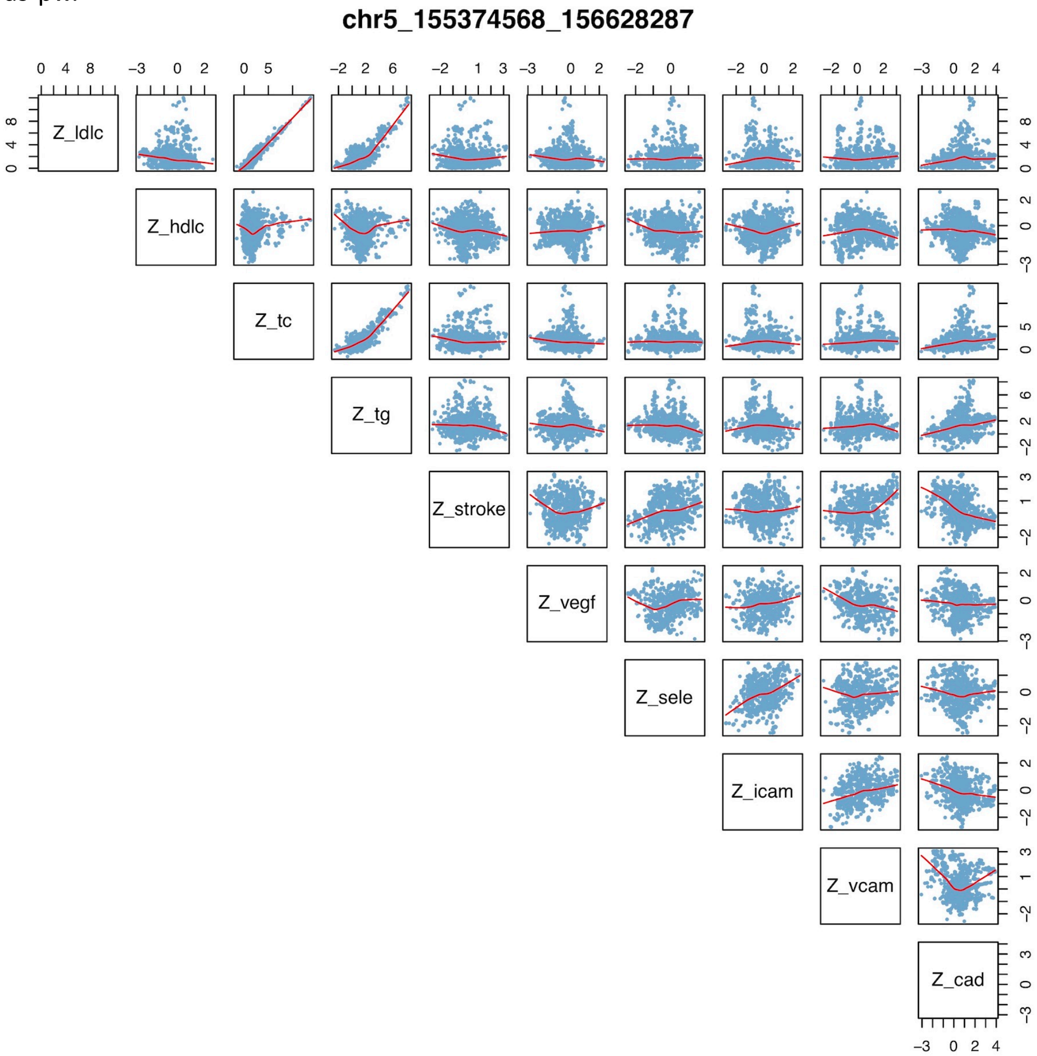
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (17/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr5_73761459_75795407	0.999	ldlc	icam
chr5_73761459_75795407	0.999	ldlc	vcam
chr5_73761459_75795407	0.999	sele	ldlc
chr5_73761459_75795407	0.999	sele	tc
chr5_73761459_75795407	0.999	tc	icam
chr5_73761459_75795407	0.999	tc	vcam

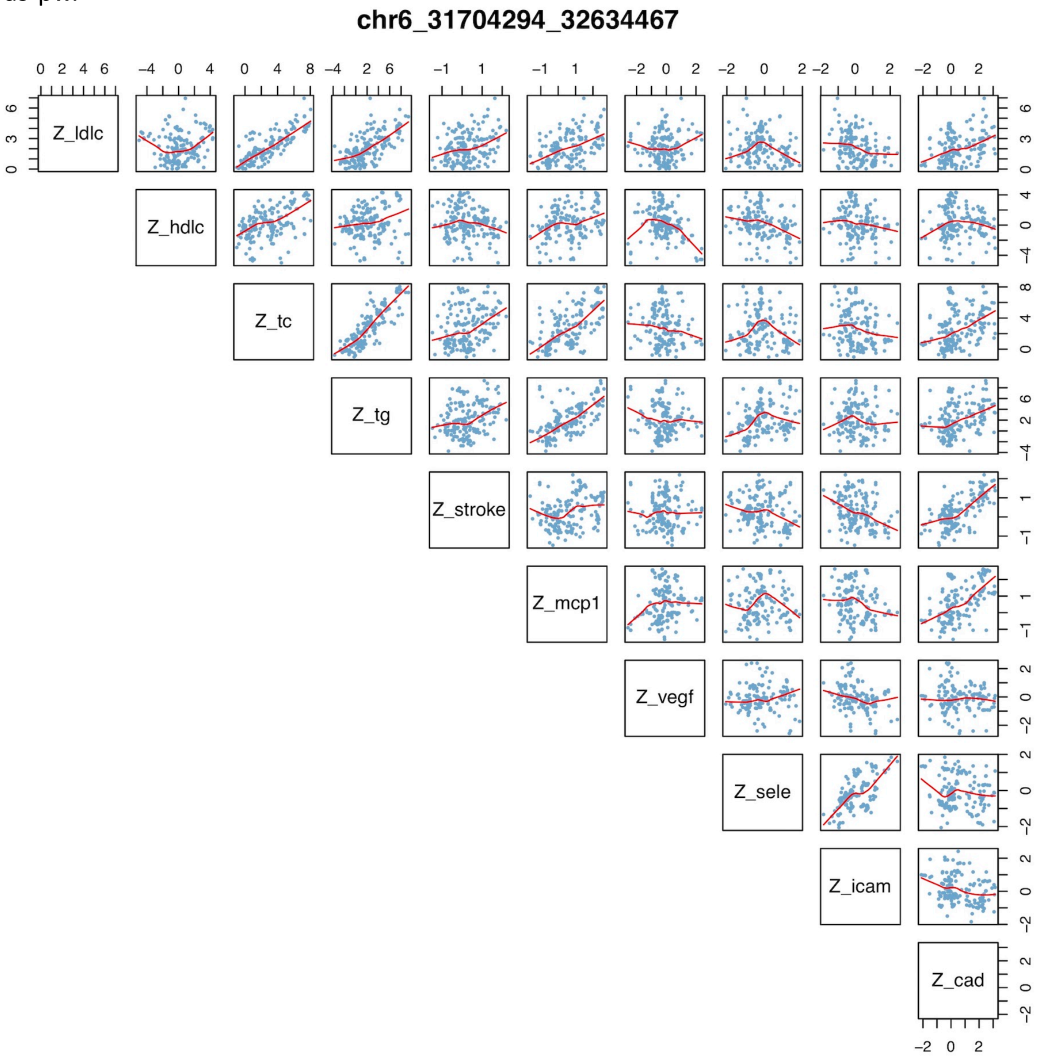
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (18/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr5_155374568_156628287	0.993	hdlc	tg
chr5_155374568_156628287	0.999	ldlc	cad
chr5_155374568_156628287	0.999	ldlc	hdlc
chr5_155374568_156628287	0.999	ldlc	icam
chr5_155374568_156628287	0.999	ldlc	stroke
chr5_155374568_156628287	1.000	ldlc	tc
chr5_155374568_156628287	1.000	ldlc	tg
chr5_155374568_156628287	0.999	ldlc	vcam
chr5_155374568_156628287	0.999	ldlc	vegf
chr5_155374568_156628287	0.999	sele	ldlc
chr5_155374568_156628287	0.999	sele	tc
chr5_155374568_156628287	0.999	tc	cad
chr5_155374568_156628287	0.999	tc	icam
chr5_155374568_156628287	0.999	tc	stroke
chr5_155374568_156628287	1.000	tc	tg
chr5_155374568_156628287	0.999	tc	vcam
chr5_155374568_156628287	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (19/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.

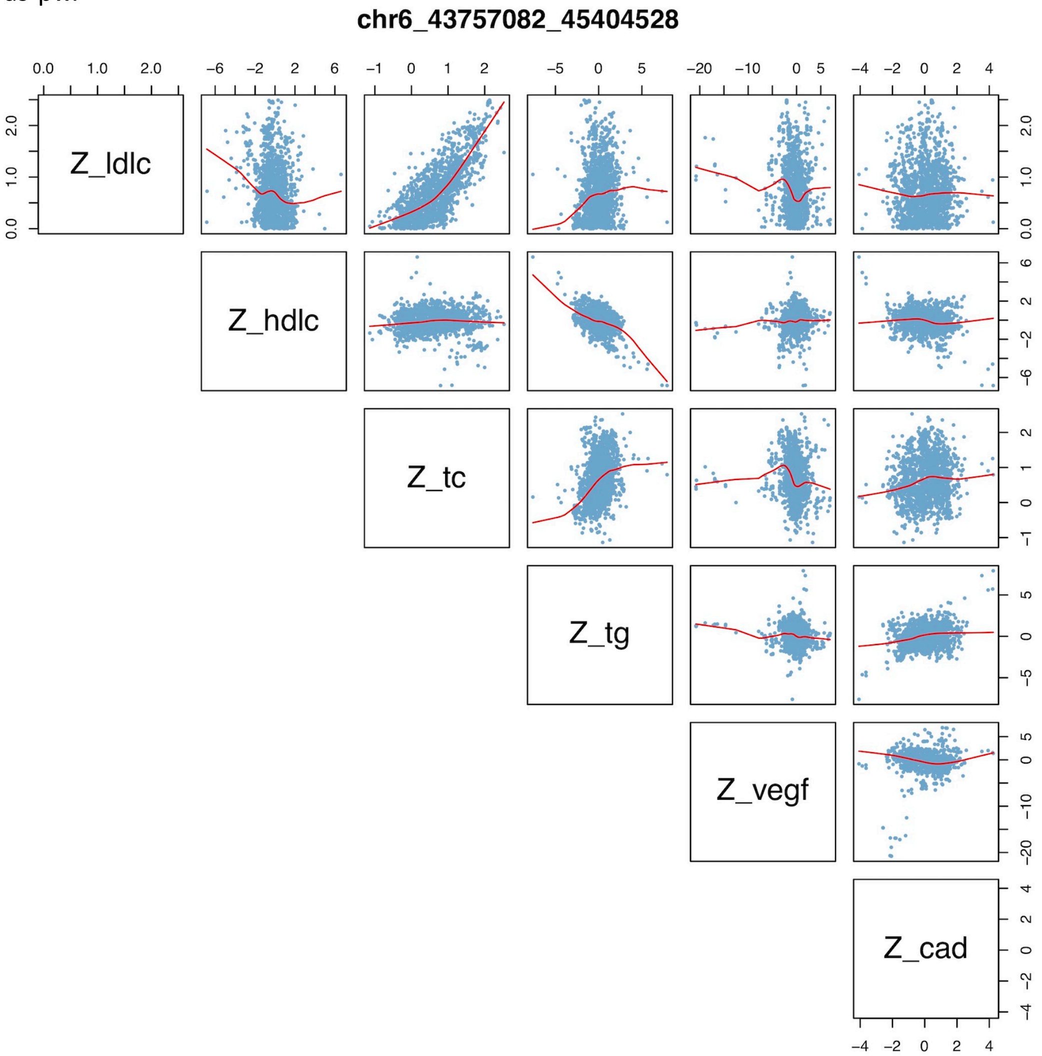


chr6_31704294_32634467

locus	PPA_3	pheno1	pheno2
chr6_31704294_32634467	0.998	hdlc	tg
chr6_31704294_32634467	0.998	ldlc	tc
chr6_31704294_32634467	0.996	sele	tg
chr6_31704294_32634467	0.998	tc	tg
chr6_31704294_32634467	0.997	tg	cad
chr6_31704294_32634467	0.996	tg	icam
chr6_31704294_32634467	0.998	tg	mcp1
chr6_31704294_32634467	0.996	tg	stroke
chr6_31704294_32634467	0.996	tg	vegf

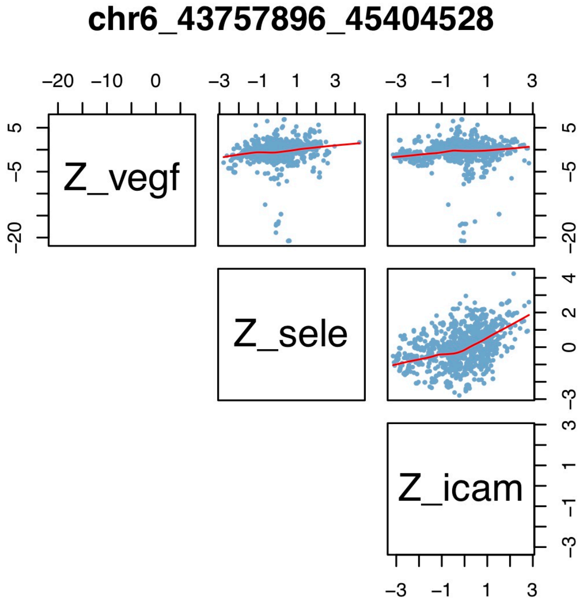
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (20/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr6_43757082_45404528	0.997	hdlc	tg
chr6_43757082_45404528	0.999	hdlc	vegf
chr6_43757082_45404528	0.999	ldlc	vegf
chr6_43757082_45404528	0.999	tc	vegf
chr6_43757082_45404528	0.999	tg	vegf
chr6_43757082_45404528	0.992	vegf	cad

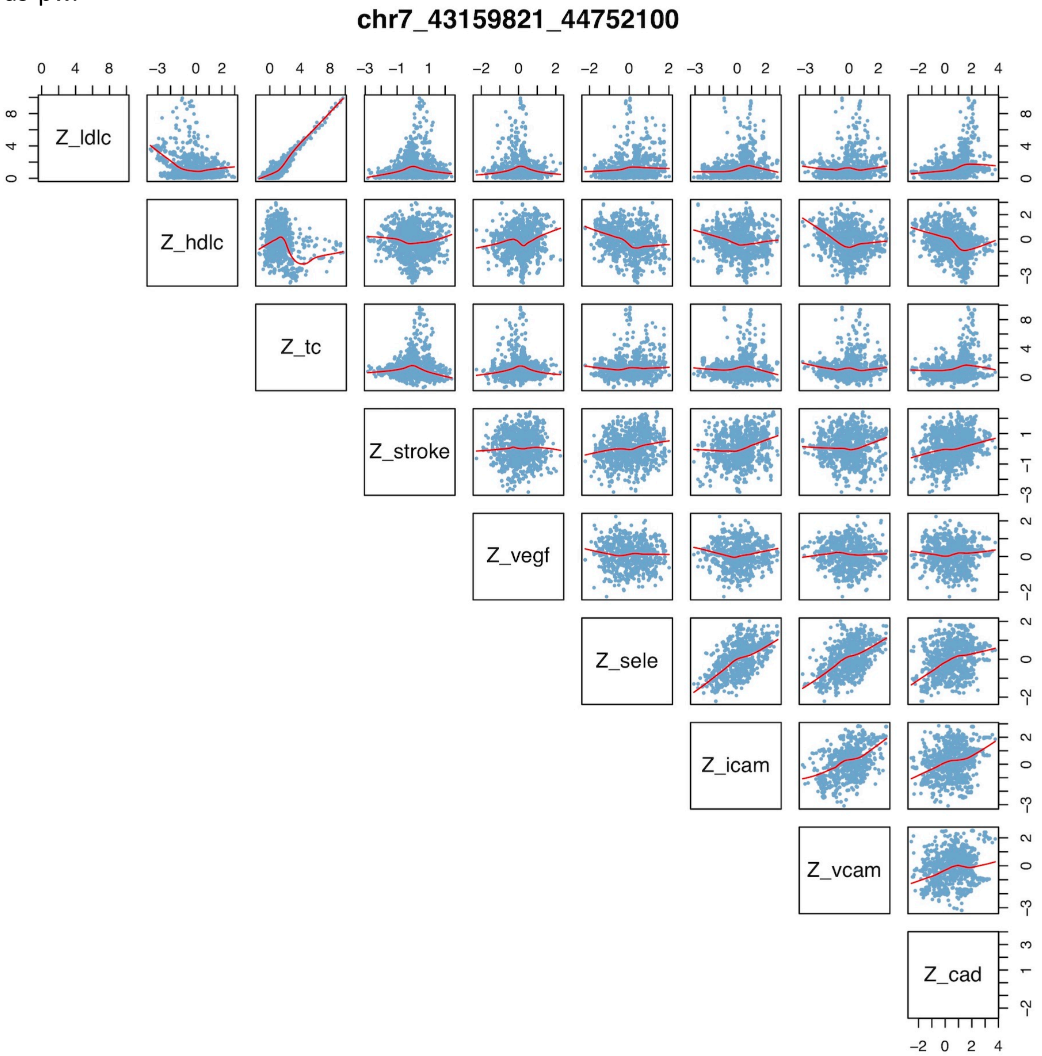
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (21/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr6_43757896_45404528	0.991	sele	vegf
chr6_43757896_45404528	0.992	vegf	icam

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (22/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



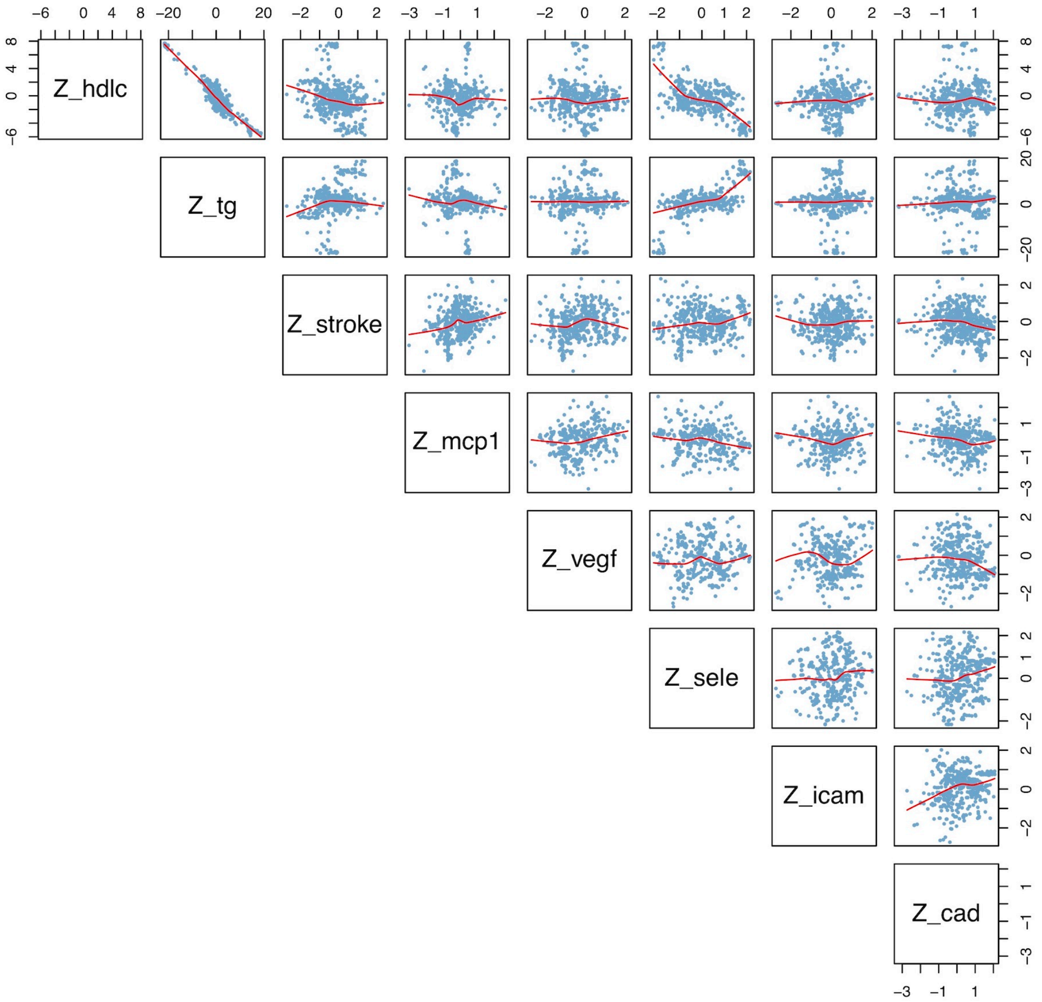
chr7_43159821_44752100

locus	PPA_3	pheno1	pheno2
chr7_43159821_44752100	0.993	ldlc	cad
chr7_43159821_44752100	0.996	ldlc	hdlc
chr7_43159821_44752100	0.992	ldlc	icam
chr7_43159821_44752100	0.992	ldlc	stroke
chr7_43159821_44752100	1.000	ldlc	tc
chr7_43159821_44752100	0.992	ldlc	vcam
chr7_43159821_44752100	0.992	ldlc	vegf
chr7_43159821_44752100	0.992	sele	ldlc
chr7_43159821_44752100	0.992	sele	tc
chr7_43159821_44752100	0.993	tc	cad
chr7_43159821_44752100	0.993	tc	icam
chr7_43159821_44752100	0.993	tc	stroke
chr7_43159821_44752100	0.993	tc	vcam
chr7_43159821_44752100	0.992	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (23/56)

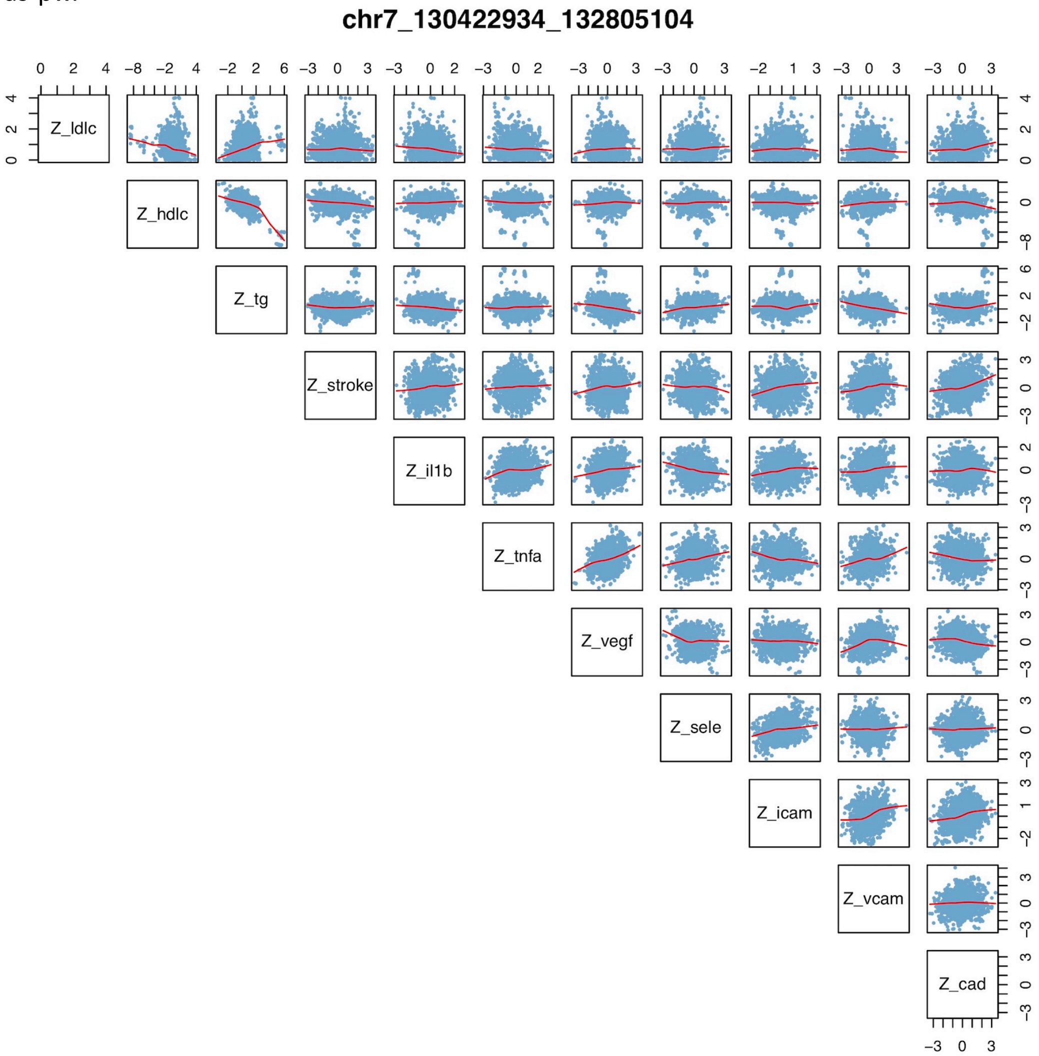
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.

chr7_71874997_73332055



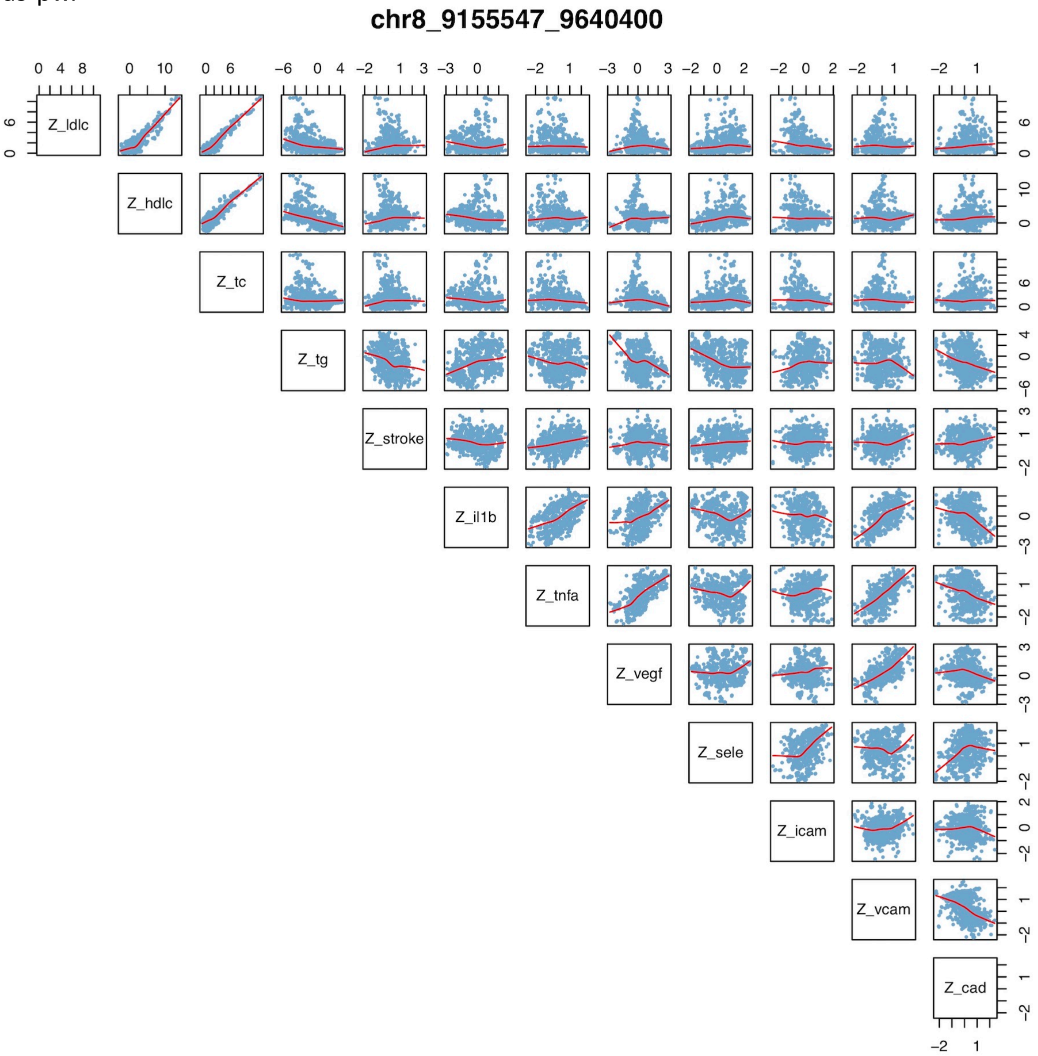
locus	PPA_3	pheno1	pheno2
chr7_71874997_73332055	1.000	hdlc	tg
chr7_71874997_73332055	0.999	sele	tg
chr7_71874997_73332055	0.999	tg	cad
chr7_71874997_73332055	0.999	tg	icam
chr7_71874997_73332055	0.999	tg	mcp1
chr7_71874997_73332055	0.999	tg	stroke
chr7_71874997_73332055	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (24/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr7_130422934_132805104

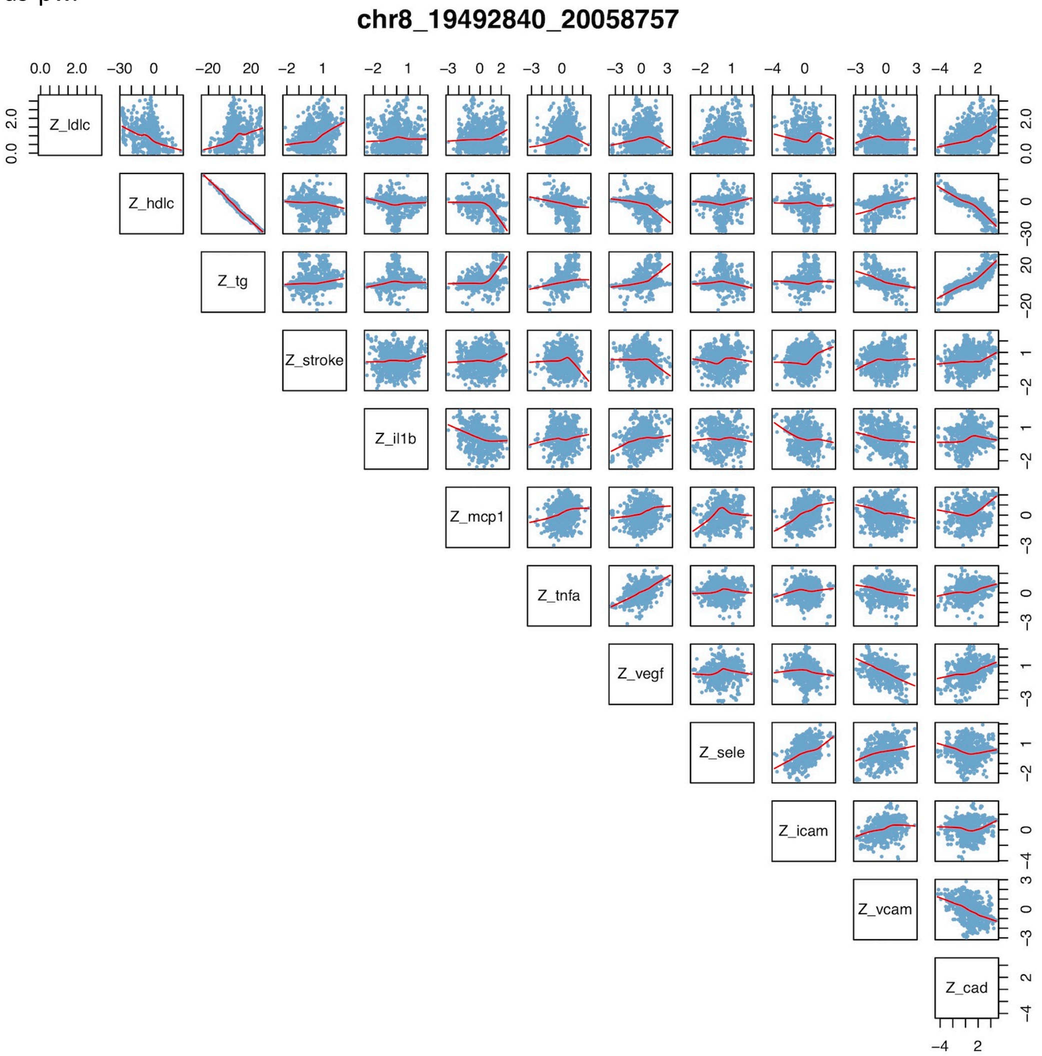
locus	PPA_3	pheno1	pheno2
chr7_130422934_132805104	0.991	hdlc	cad
chr7_130422934_132805104	0.991	hdlc	icam
chr7_130422934_132805104	0.991	hdlc	il1b
chr7_130422934_132805104	0.991	hdlc	stroke
chr7_130422934_132805104	0.999	hdlc	tg
chr7_130422934_132805104	0.990	hdlc	tnfa
chr7_130422934_132805104	0.990	hdlc	vcam
chr7_130422934_132805104	0.990	hdlc	vegf
chr7_130422934_132805104	0.995	ldlc	hdlc
chr7_130422934_132805104	0.991	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (25/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



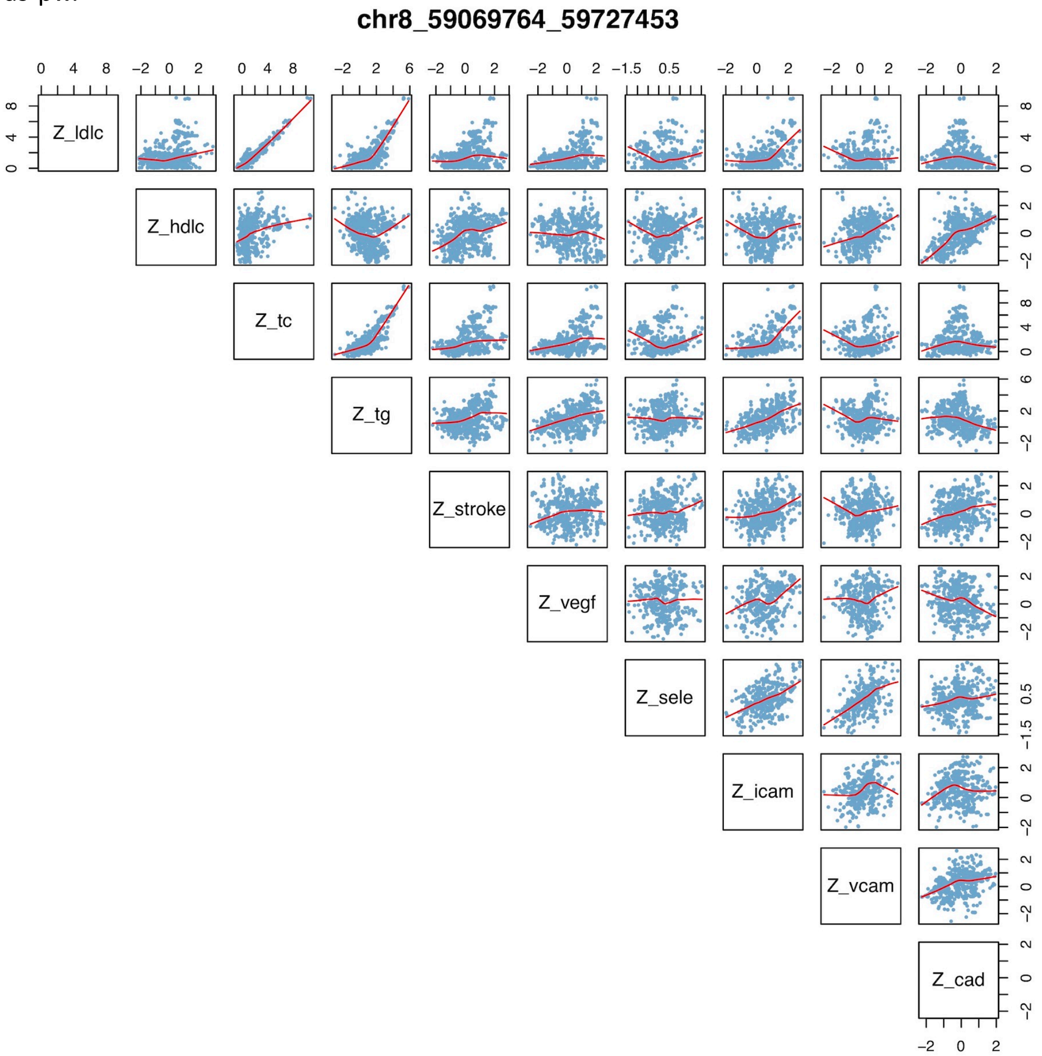
locus	PPA_3	pheno1	pheno2
chr8_9155547_9640400	0.996	hdlc	cad
chr8_9155547_9640400	0.996	hdlc	icam
chr8_9155547_9640400	0.996	hdlc	il1b
chr8_9155547_9640400	0.995	hdlc	stroke
chr8_9155547_9640400	1.000	hdlc	tc
chr8_9155547_9640400	0.999	hdlc	tg
chr8_9155547_9640400	0.995	hdlc	tnfa
chr8_9155547_9640400	0.995	hdlc	vcam
chr8_9155547_9640400	0.995	hdlc	vegf
chr8_9155547_9640400	1.000	ldlc	hdlc
chr8_9155547_9640400	1.000	ldlc	tc
chr8_9155547_9640400	0.996	sele	hdlc
chr8_9155547_9640400	0.992	sele	tc
chr8_9155547_9640400	0.992	tc	cad
chr8_9155547_9640400	0.993	tc	icam
chr8_9155547_9640400	0.992	tc	stroke
chr8_9155547_9640400	0.992	tc	vcam
chr8_9155547_9640400	0.992	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (26/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr8_19492840_20058757	0.999	hdlc	cad
chr8_19492840_20058757	0.999	hdlc	icam
chr8_19492840_20058757	0.999	hdlc	il1b
chr8_19492840_20058757	0.999	hdlc	stroke
chr8_19492840_20058757	1.000	hdlc	tg
chr8_19492840_20058757	0.999	hdlc	tnfa
chr8_19492840_20058757	0.999	hdlc	vcam
chr8_19492840_20058757	0.999	hdlc	vegf
chr8_19492840_20058757	1.000	ldlc	hdlc
chr8_19492840_20058757	0.999	sele	hdlc
chr8_19492840_20058757	0.999	sele	tg
chr8_19492840_20058757	0.999	tg	cad
chr8_19492840_20058757	0.999	tg	icam
chr8_19492840_20058757	0.999	tg	mcp1
chr8_19492840_20058757	0.999	tg	stroke
chr8_19492840_20058757	0.999	tg	vegf

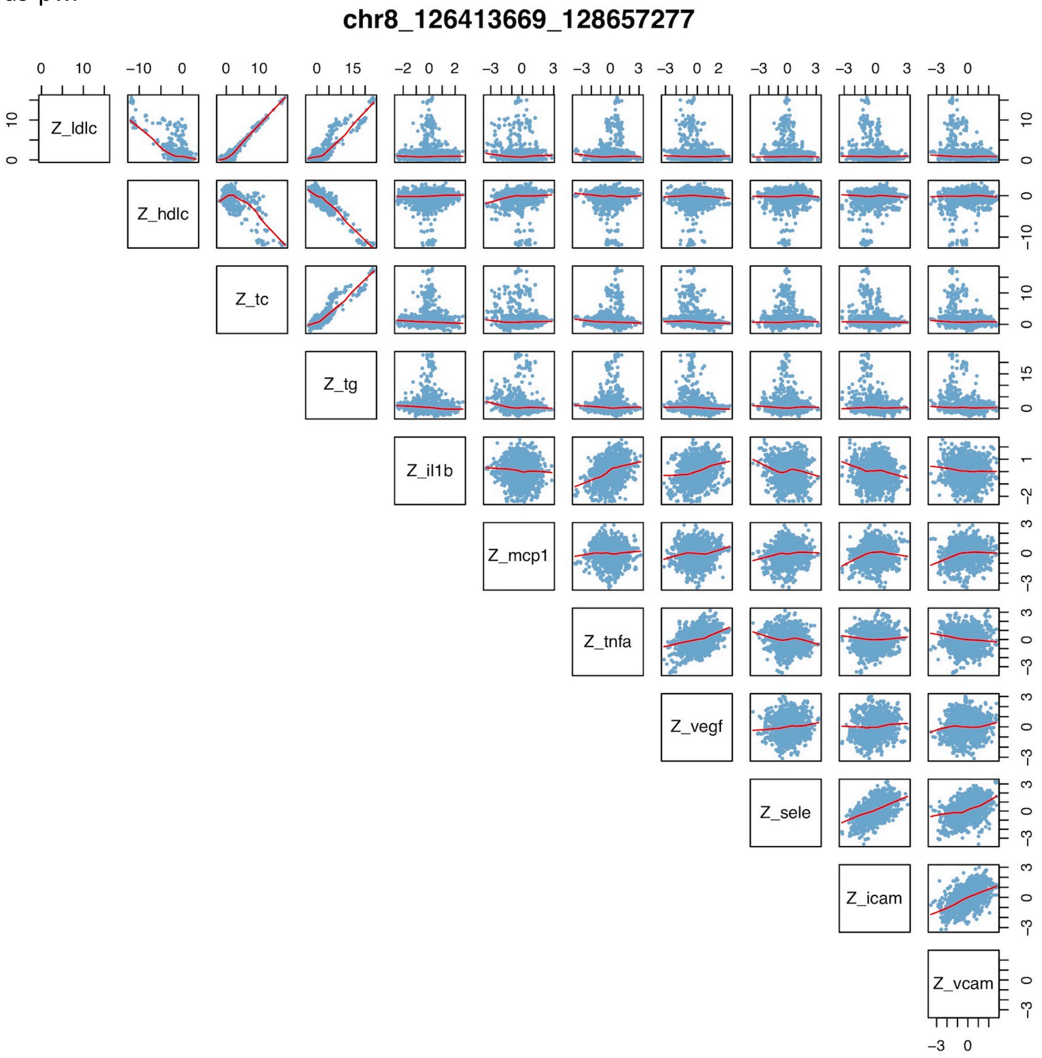
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (27/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr8_59069764_59727453

locus	PPA_3	pheno1	pheno2
chr8_59069764_59727453	0.994	ldlc	hdlc
chr8_59069764_59727453	0.990	ldlc	icam
chr8_59069764_59727453	1.000	ldlc	tc
chr8_59069764_59727453	0.990	ldlc	tg
chr8_59069764_59727453	0.998	sele	tc
chr8_59069764_59727453	0.998	tc	cad
chr8_59069764_59727453	0.999	tc	icam
chr8_59069764_59727453	0.998	tc	stroke
chr8_59069764_59727453	0.996	tc	tg
chr8_59069764_59727453	0.998	tc	vcam
chr8_59069764_59727453	0.999	tc	vegf

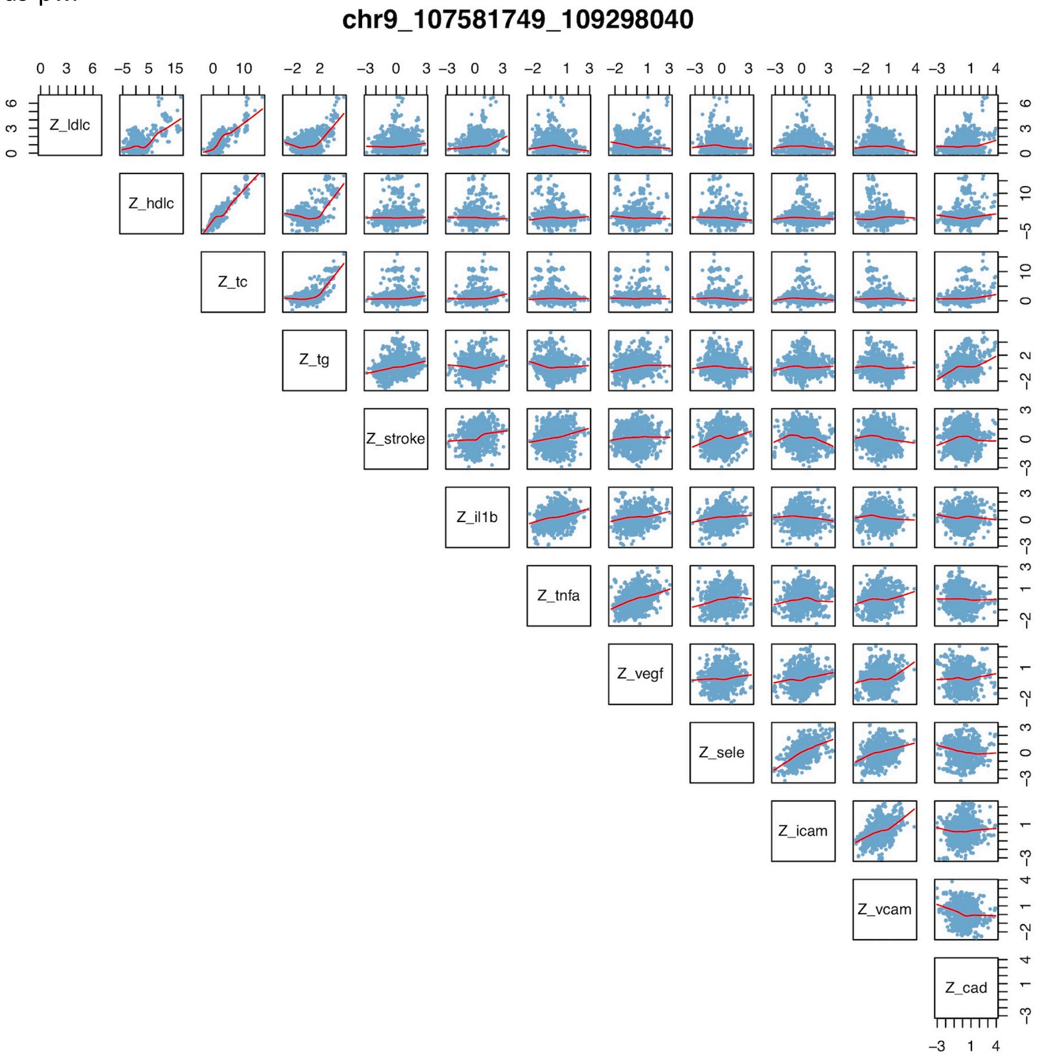
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (28/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



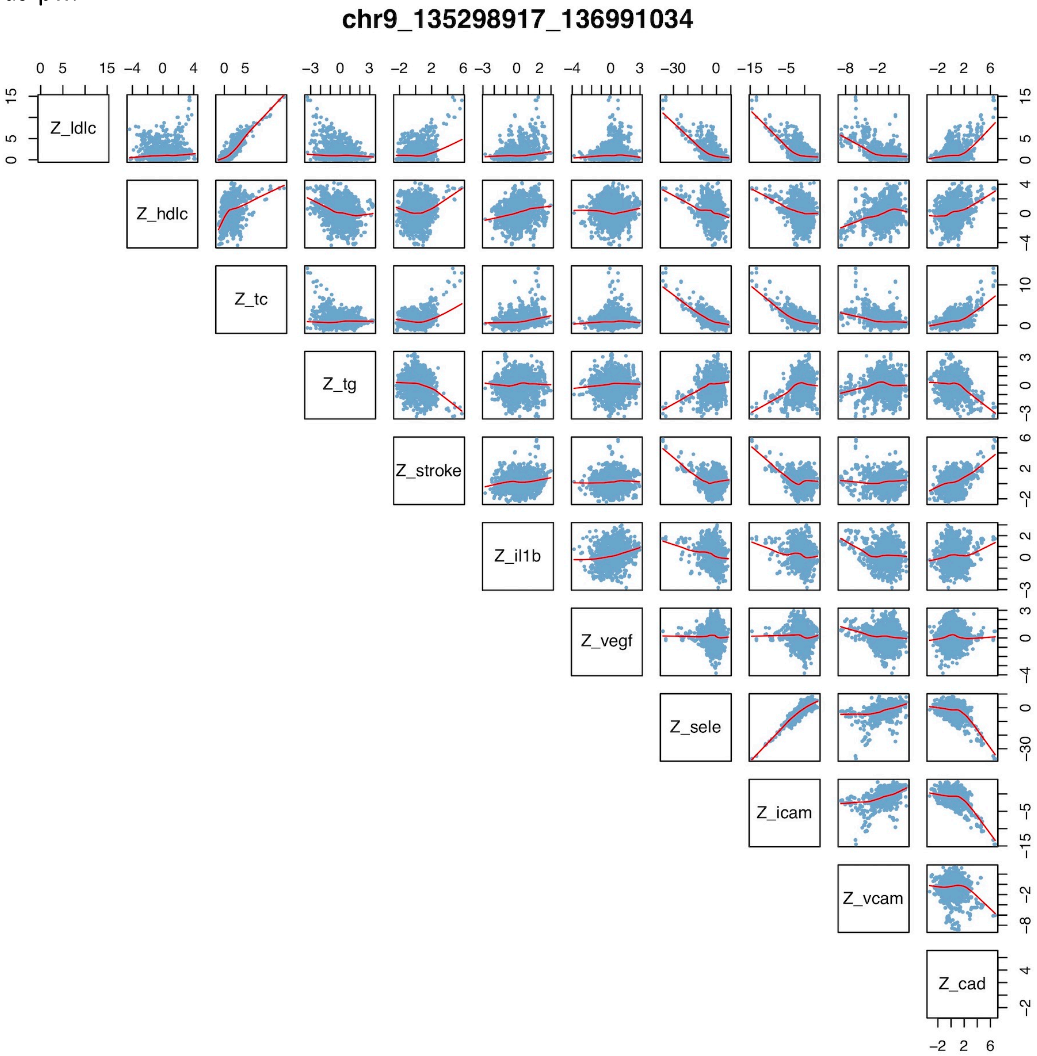
locus	PPA_3	pheno1	pheno2
chr8_126413669_128657277	0.999	hdlc	icam
chr8_126413669_128657277	0.999	hdlc	il1b
chr8_126413669_128657277	0.999	hdlc	tnfa
chr8_126413669_128657277	0.999	hdlc	vcam
chr8_126413669_128657277	0.999	hdlc	vegf
chr8_126413669_128657277	0.999	ldlc	icam
chr8_126413669_128657277	0.999	ldlc	vcam
chr8_126413669_128657277	0.999	ldlc	vegf
chr8_126413669_128657277	0.999	sele	hdlc
chr8_126413669_128657277	0.999	sele	ldlc
chr8_126413669_128657277	0.999	sele	tc
chr8_126413669_128657277	0.999	sele	tg
chr8_126413669_128657277	0.999	tc	icam
chr8_126413669_128657277	0.999	tc	vcam
chr8_126413669_128657277	0.999	tc	vegf
chr8_126413669_128657277	0.999	tg	icam
chr8_126413669_128657277	0.999	tg	mcp1
chr8_126413669_128657277	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (29/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr9_107581749_109298040

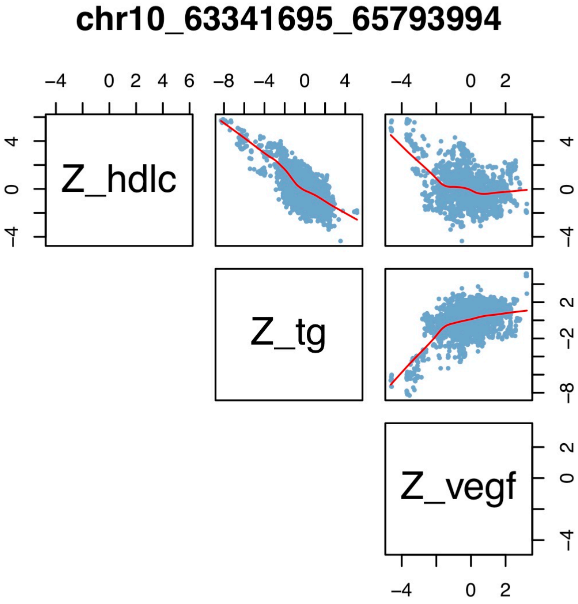
locus	PPA_3	pheno1	pheno2
chr9_107581749_109298040	0.999	hdlc	cad
chr9_107581749_109298040	0.999	hdlc	icam
chr9_107581749_109298040	0.999	hdlc	il1b
chr9_107581749_109298040	0.999	hdlc	stroke
chr9_107581749_109298040	1.000	hdlc	tc
chr9_107581749_109298040	1.000	hdlc	tg
chr9_107581749_109298040	0.999	hdlc	tnfa
chr9_107581749_109298040	0.999	hdlc	vcam
chr9_107581749_109298040	0.999	hdlc	vegf
chr9_107581749_109298040	1.000	ldlc	hdlc
chr9_107581749_109298040	1.000	ldlc	tc
chr9_107581749_109298040	0.999	sele	hdlc
chr9_107581749_109298040	0.999	sele	tc
chr9_107581749_109298040	0.999	tc	cad
chr9_107581749_109298040	0.999	tc	icam
chr9_107581749_109298040	0.999	tc	stroke
chr9_107581749_109298040	0.994	tc	tg
chr9_107581749_109298040	0.999	tc	vcam
chr9_107581749_109298040	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (30/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr9_135298917_136991034	1.000	hdlc	icam
chr9_135298917_136991034	0.993	hdlc	tc
chr9_135298917_136991034	0.995	icam	cad
chr9_135298917_136991034	0.999	icam	vcam
chr9_135298917_136991034	0.992	il1b	icam
chr9_135298917_136991034	0.999	ldlc	cad
chr9_135298917_136991034	1.000	ldlc	hdlc
chr9_135298917_136991034	1.000	ldlc	icam
chr9_135298917_136991034	0.999	ldlc	stroke
chr9_135298917_136991034	1.000	ldlc	tc
chr9_135298917_136991034	1.000	ldlc	vcam
chr9_135298917_136991034	0.999	ldlc	vegf
chr9_135298917_136991034	0.995	sele	cad
chr9_135298917_136991034	1.000	sele	hdlc
chr9_135298917_136991034	1.000	sele	icam
chr9_135298917_136991034	0.991	sele	il1b
chr9_135298917_136991034	1.000	sele	ldlc
chr9_135298917_136991034	1.000	sele	tc
chr9_135298917_136991034	0.999	sele	tg
chr9_135298917_136991034	0.999	sele	vcam
chr9_135298917_136991034	0.991	sele	vegf
chr9_135298917_136991034	0.990	stroke	icam
chr9_135298917_136991034	0.999	tc	cad
chr9_135298917_136991034	1.000	tc	icam
chr9_135298917_136991034	0.999	tc	stroke
chr9_135298917_136991034	1.000	tc	vcam
chr9_135298917_136991034	0.999	tc	vegf
chr9_135298917_136991034	0.999	tg	icam
chr9_135298917_136991034	0.992	vegf	icam

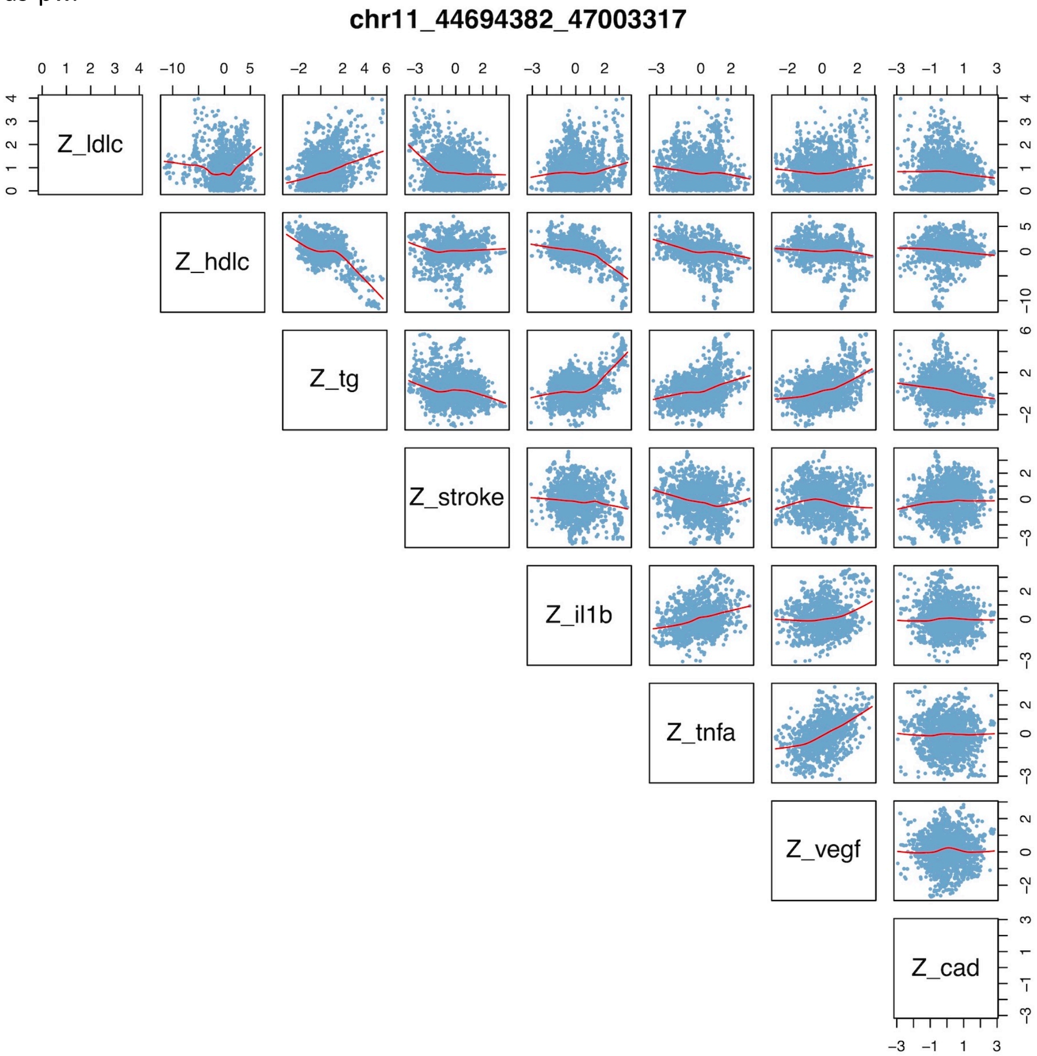
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (31/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr10_63341695_65793994	0.999	hdlc	tg
chr10_63341695_65793994	0.995	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (32/56)

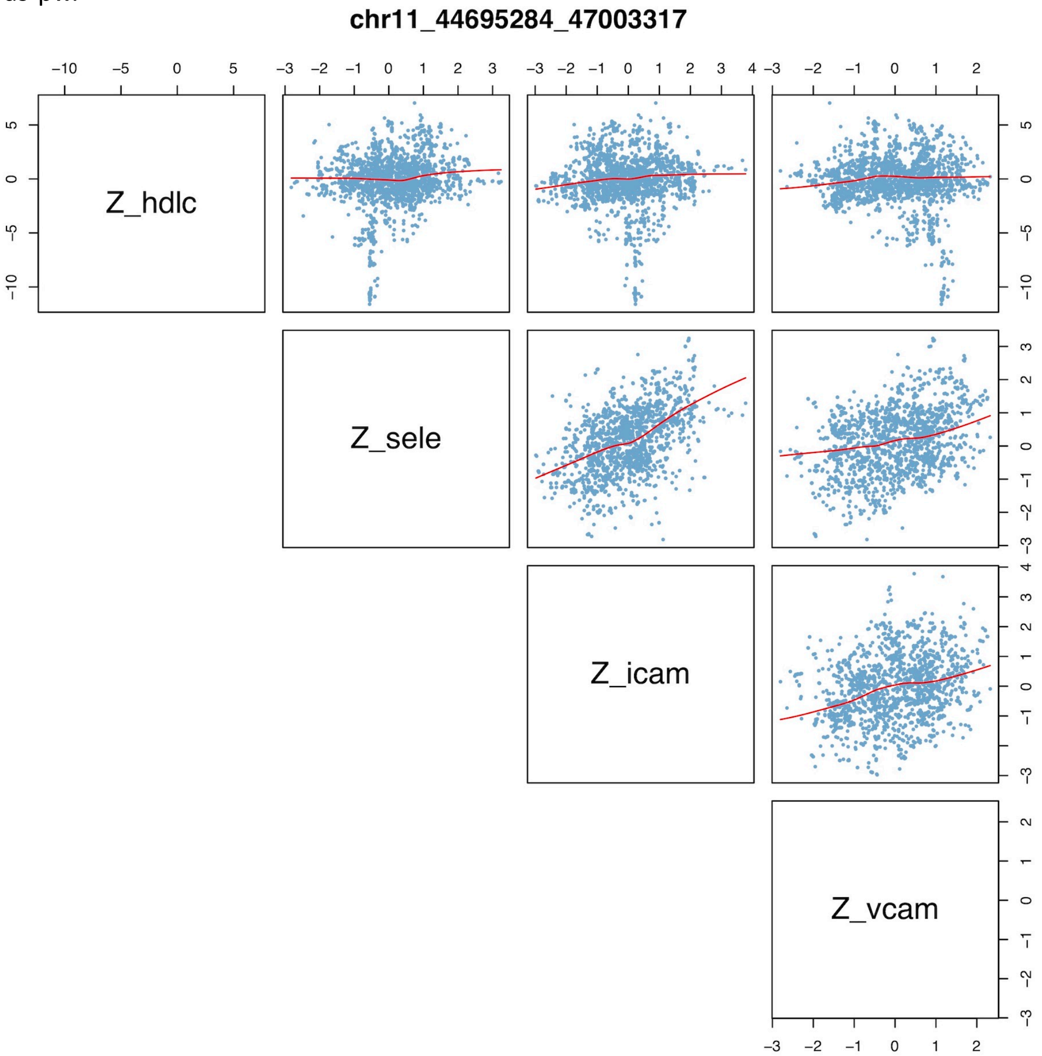
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



chr11_44694382_47003317

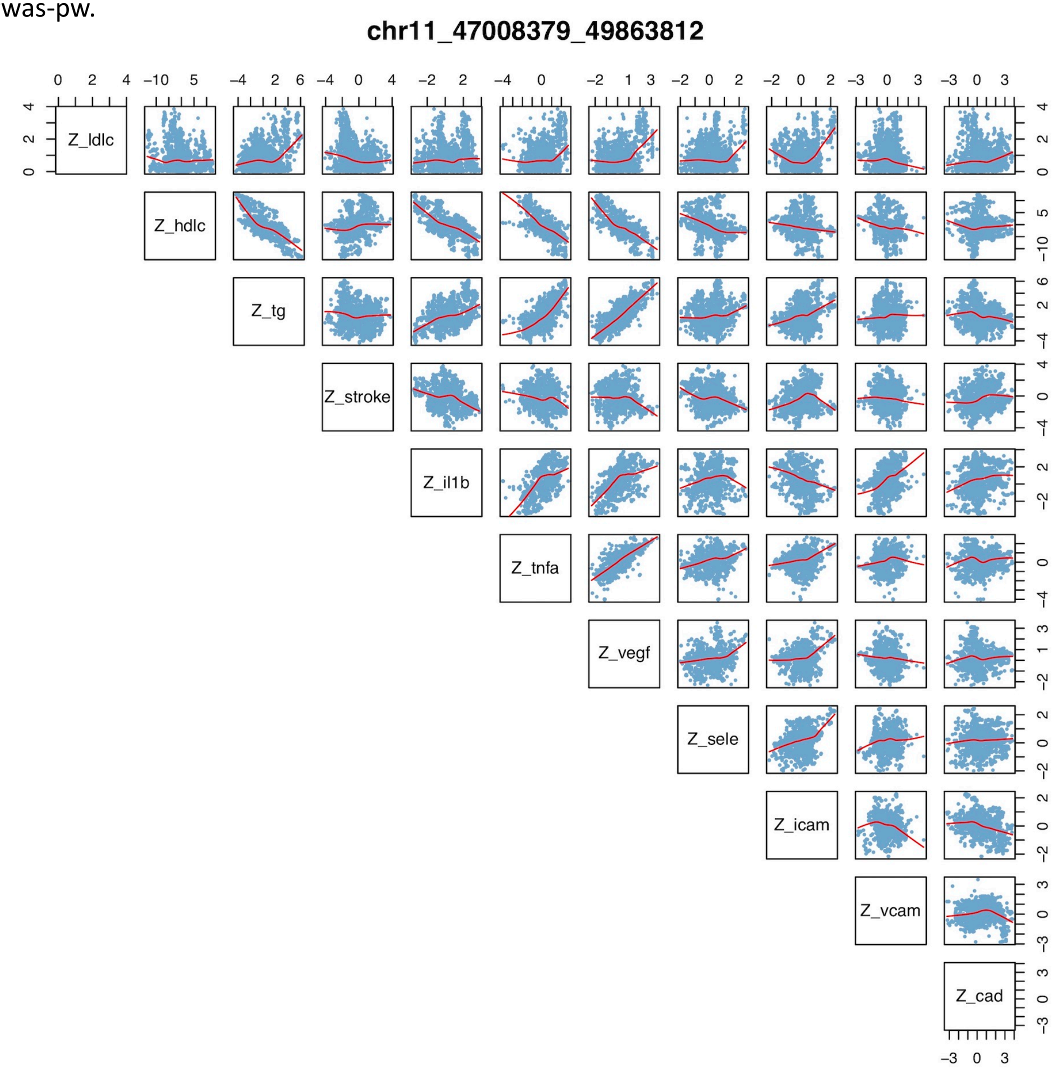
locus	PPA_3	pheno1	pheno2
chr11_44694382_47003317	0.992	hdlc	cad
chr11_44694382_47003317	0.995	hdlc	il1b
chr11_44694382_47003317	0.991	hdlc	stroke
chr11_44694382_47003317	0.998	hdlc	tg
chr11_44694382_47003317	0.991	hdlc	tnfa
chr11_44694382_47003317	0.992	hdlc	vegf
chr11_44694382_47003317	0.995	ldlc	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (33/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



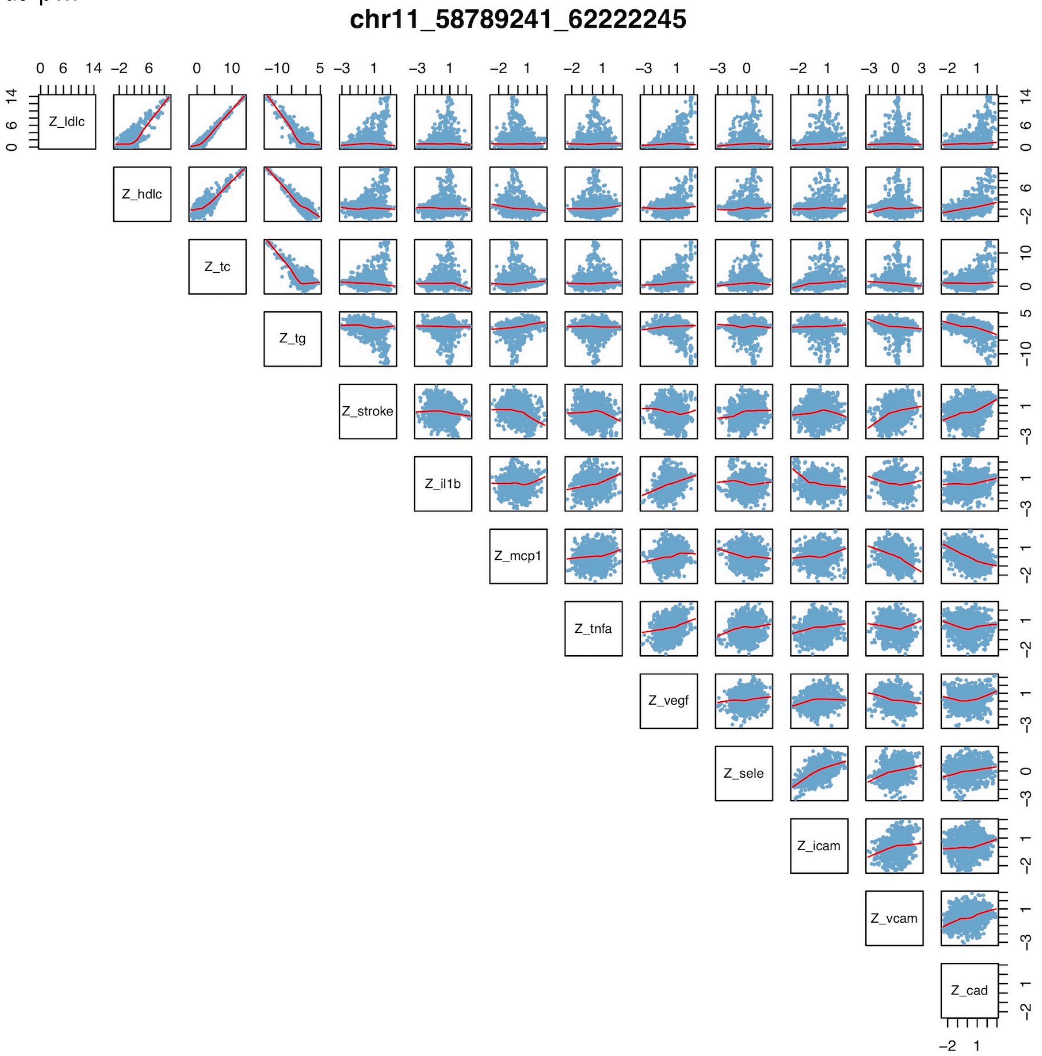
locus	PPA_3	pheno1	pheno2
chr11_44695284_47003317	0.991	hdlc	icam
chr11_44695284_47003317	0.992	hdlc	vcam
chr11_44695284_47003317	0.991	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (34/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



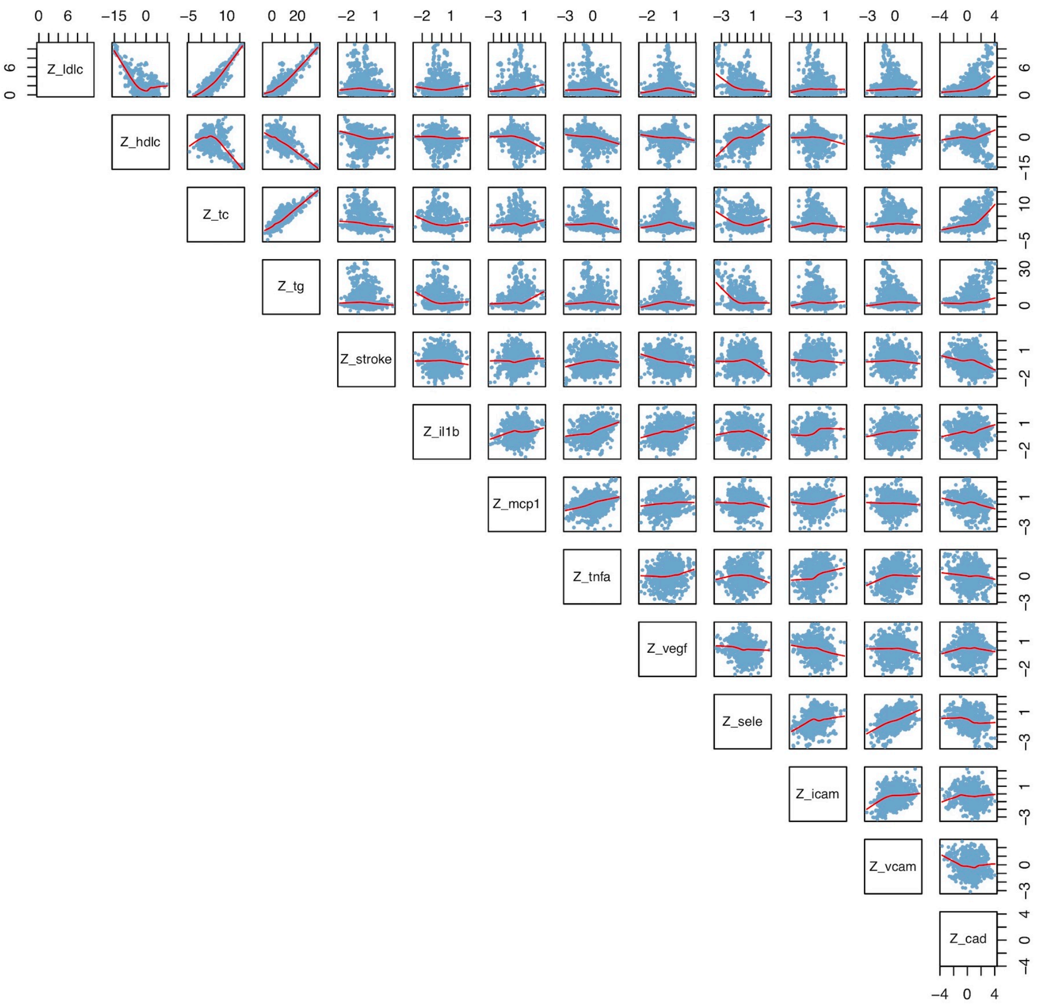
locus	PPA_3	pheno1	pheno2
chr11_47008379_49863812	0.999	hdlc	cad
chr11_47008379_49863812	0.999	hdlc	icam
chr11_47008379_49863812	1.000	hdlc	il1b
chr11_47008379_49863812	0.999	hdlc	stroke
chr11_47008379_49863812	1.000	hdlc	tg
chr11_47008379_49863812	0.999	hdlc	tnfa
chr11_47008379_49863812	0.999	hdlc	vcam
chr11_47008379_49863812	1.000	hdlc	vegf
chr11_47008379_49863812	1.000	ldlc	hdlc
chr11_47008379_49863812	0.999	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (35/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr11_58789241_62222245

locus	PPA_3	pheno1	pheno2
chr11_58789241_62222245	0.999	hdlc	cad
chr11_58789241_62222245	0.999	hdlc	icam
chr11_58789241_62222245	0.999	hdlc	il1b
chr11_58789241_62222245	0.999	hdlc	stroke
chr11_58789241_62222245	1.000	hdlc	tc
chr11_58789241_62222245	1.000	hdlc	tg
chr11_58789241_62222245	0.999	hdlc	tnfa
chr11_58789241_62222245	0.999	hdlc	vcam
chr11_58789241_62222245	0.999	hdlc	vegf
chr11_58789241_62222245	0.999	ldlc	cad
chr11_58789241_62222245	1.000	ldlc	hdlc
chr11_58789241_62222245	0.999	ldlc	icam
chr11_58789241_62222245	0.999	ldlc	stroke
chr11_58789241_62222245	1.000	ldlc	tc
chr11_58789241_62222245	1.000	ldlc	tg
chr11_58789241_62222245	0.999	ldlc	vcam
chr11_58789241_62222245	0.999	ldlc	vegf
chr11_58789241_62222245	0.999	sele	hdlc
chr11_58789241_62222245	0.999	sele	ldlc
chr11_58789241_62222245	0.999	sele	tc
chr11_58789241_62222245	0.999	sele	tg
chr11_58789241_62222245	0.999	tc	cad
chr11_58789241_62222245	0.999	tc	icam
chr11_58789241_62222245	0.999	tc	stroke
chr11_58789241_62222245	1.000	tc	tg
chr11_58789241_62222245	0.999	tc	vcam
chr11_58789241_62222245	1.000	tc	vegf
chr11_58789241_62222245	0.999	tg	cad
chr11_58789241_62222245	0.999	tg	icam
chr11_58789241_62222245	0.999	tg	mcp1
chr11_58789241_62222245	0.999	tg	stroke
chr11_58789241_62222245	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (36/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.

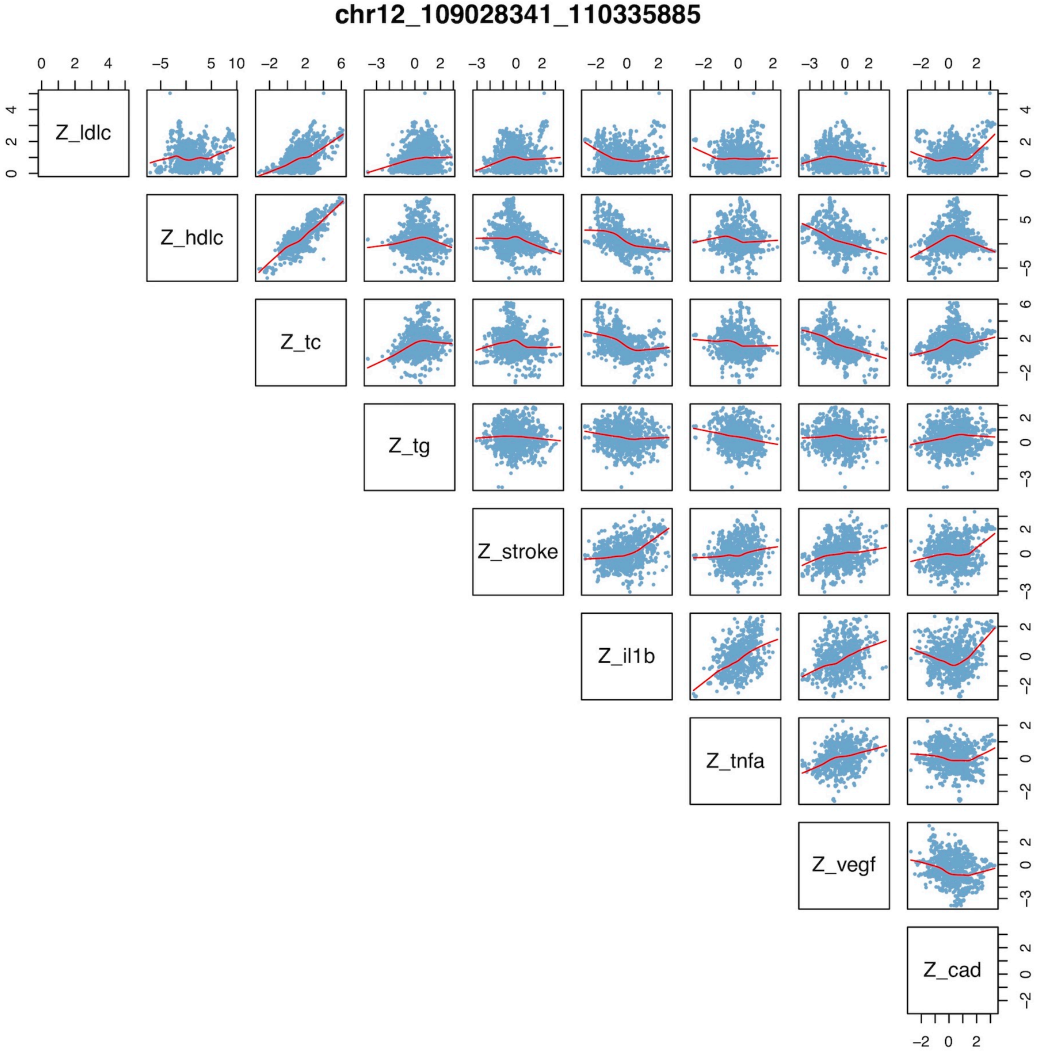


chr11_116384126_117745049

locus	PPA_3	pheno1	pheno2
chr11_116384126_117745049	0.999	hdlc	cad
chr11_116384126_117745049	0.999	hdlc	icam
chr11_116384126_117745049	0.999	hdlc	il1b
chr11_116384126_117745049	0.999	hdlc	stroke
chr11_116384126_117745049	1.000	hdlc	tc
chr11_116384126_117745049	1.000	hdlc	tg
chr11_116384126_117745049	0.999	hdlc	tnfa
chr11_116384126_117745049	0.999	hdlc	vcam
chr11_116384126_117745049	0.999	hdlc	vegf
chr11_116384126_117745049	1.000	ldlc	hdlc
chr11_116384126_117745049	1.000	ldlc	tc
chr11_116384126_117745049	0.995	ldlc	tg
chr11_116384126_117745049	0.999	sele	hdlc
chr11_116384126_117745049	0.999	sele	tc
chr11_116384126_117745049	0.999	sele	tg
chr11_116384126_117745049	0.999	tc	cad
chr11_116384126_117745049	0.999	tc	icam
chr11_116384126_117745049	0.999	tc	stroke
chr11_116384126_117745049	0.999	tc	tg
chr11_116384126_117745049	0.999	tc	vcam
chr11_116384126_117745049	0.999	tc	vegf
chr11_116384126_117745049	0.999	tg	cad
chr11_116384126_117745049	0.999	tg	icam
chr11_116384126_117745049	0.999	tg	mcp1
chr11_116384126_117745049	0.999	tg	stroke
chr11_116384126_117745049	0.999	tg	vegf

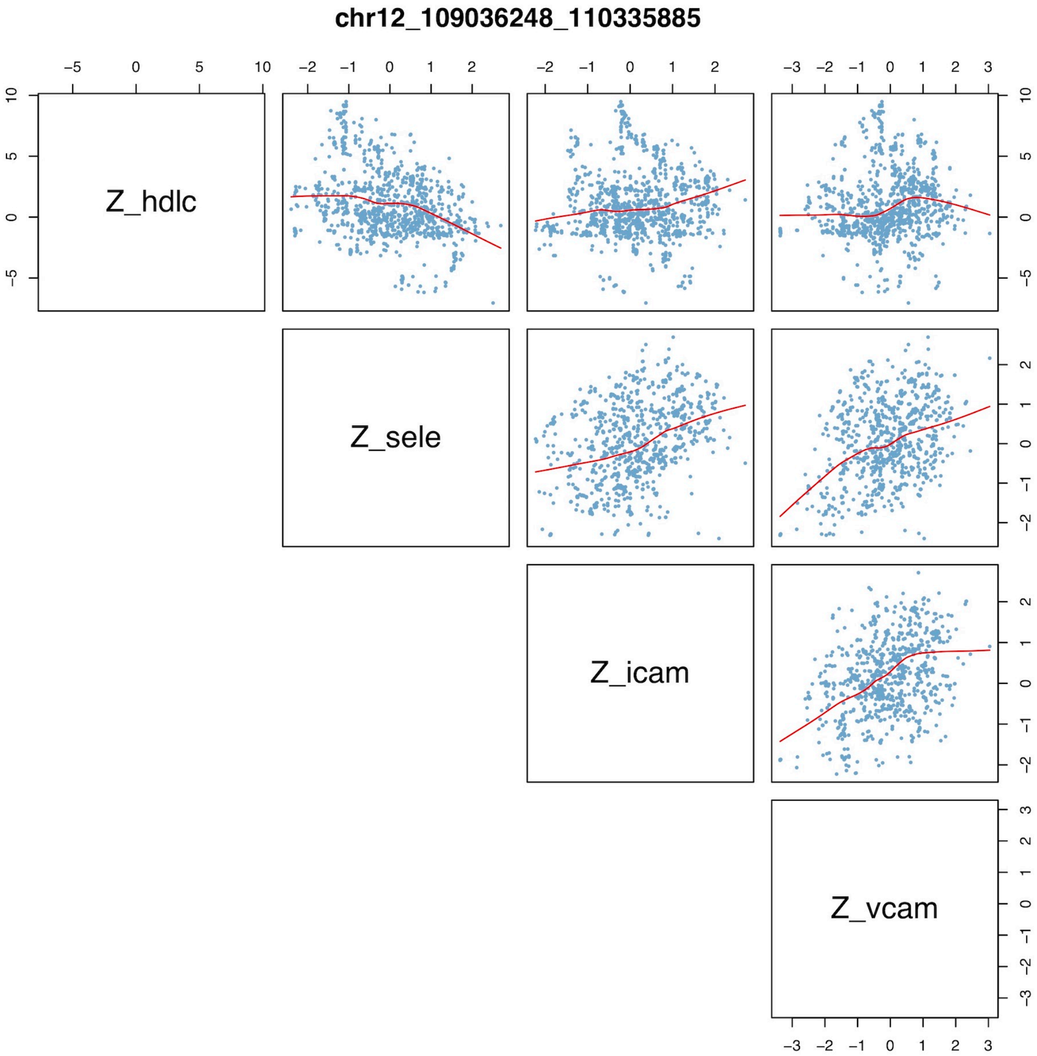
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (37/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



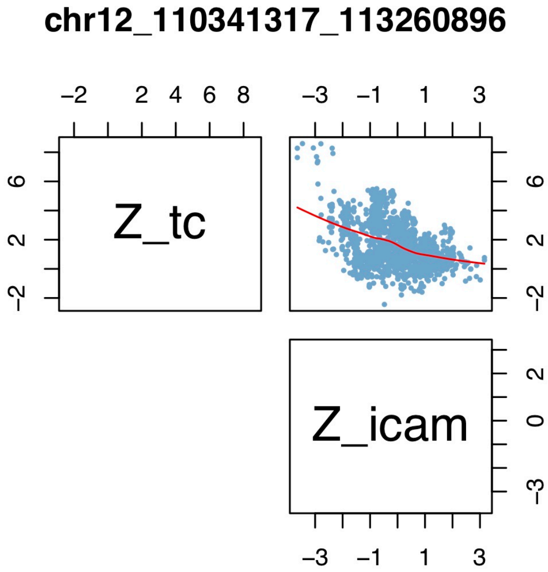
locus	PPA_3	pheno1	pheno2
chr12_109028341_110335885	0.998	hdlc	cad
chr12_109028341_110335885	0.998	hdlc	il1b
chr12_109028341_110335885	0.998	hdlc	stroke
chr12_109028341_110335885	0.999	hdlc	tc
chr12_109028341_110335885	0.999	hdlc	tg
chr12_109028341_110335885	0.997	hdlc	tnfa
chr12_109028341_110335885	0.998	hdlc	vegf
chr12_109028341_110335885	0.999	ldlc	hdlc
chr12_109028341_110335885	0.990	ldlc	tc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (38/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr12_109036248_110335885	0.997	hdlc	icam
chr12_109036248_110335885	0.997	hdlc	vcam
chr12_109036248_110335885	0.998	sele	hdlc

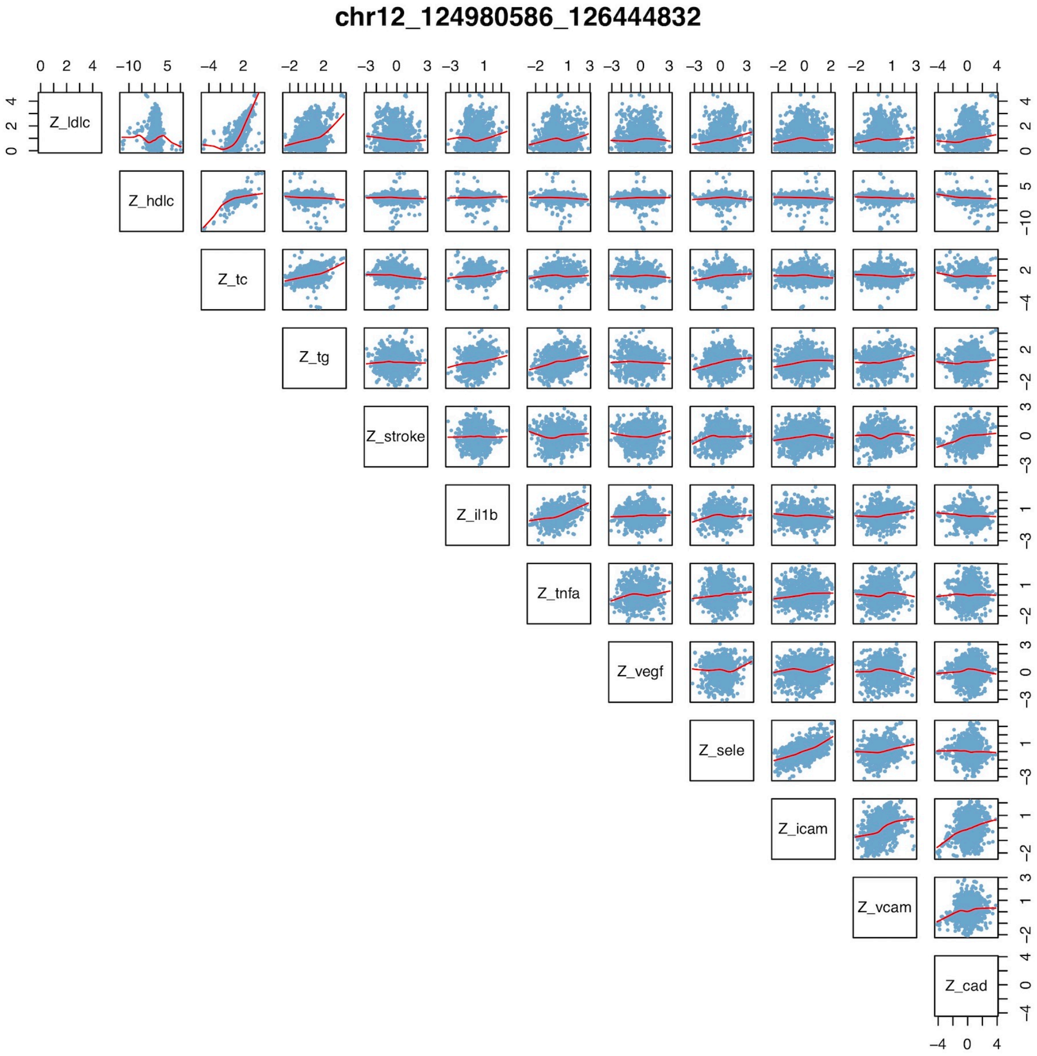
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (39/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr12_110341317_113260896	0.990	tc	icam

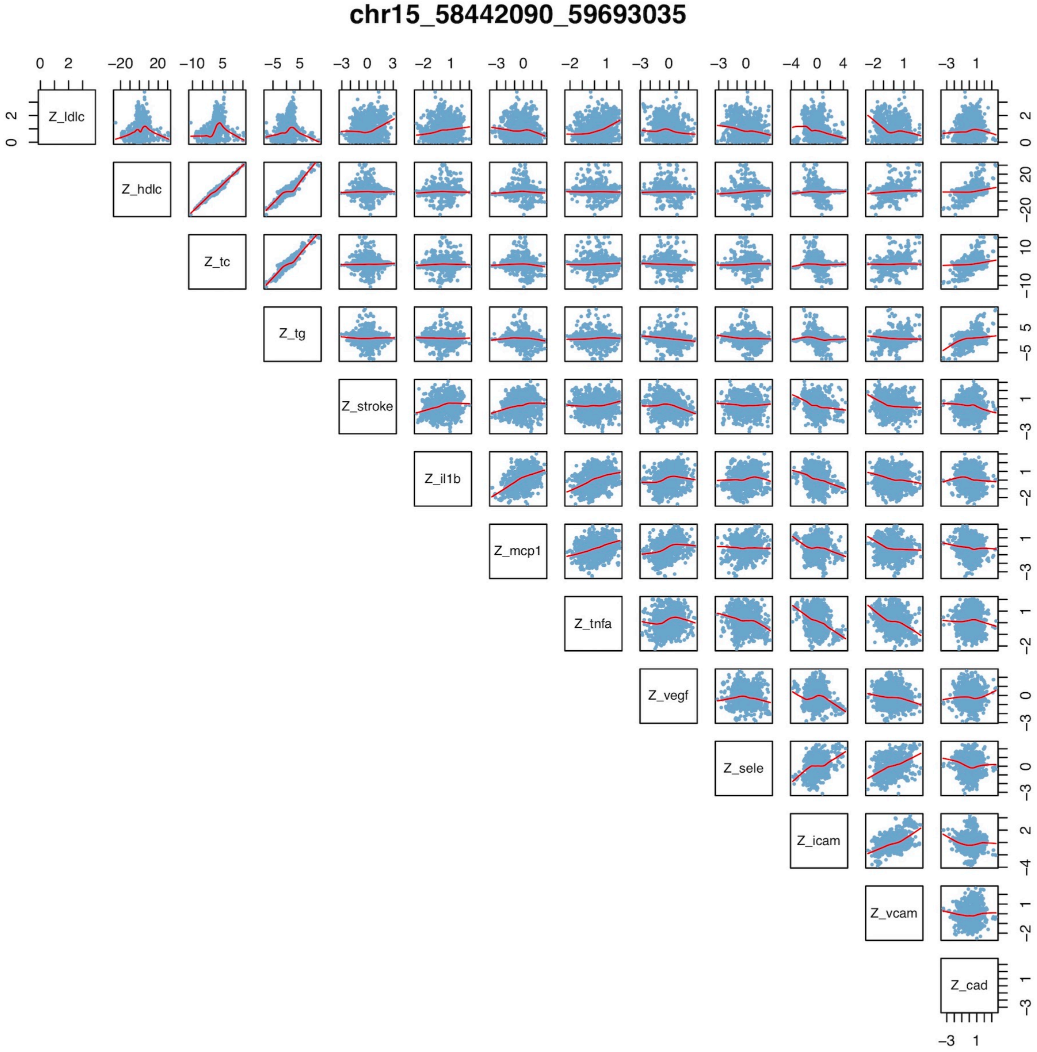
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (40/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



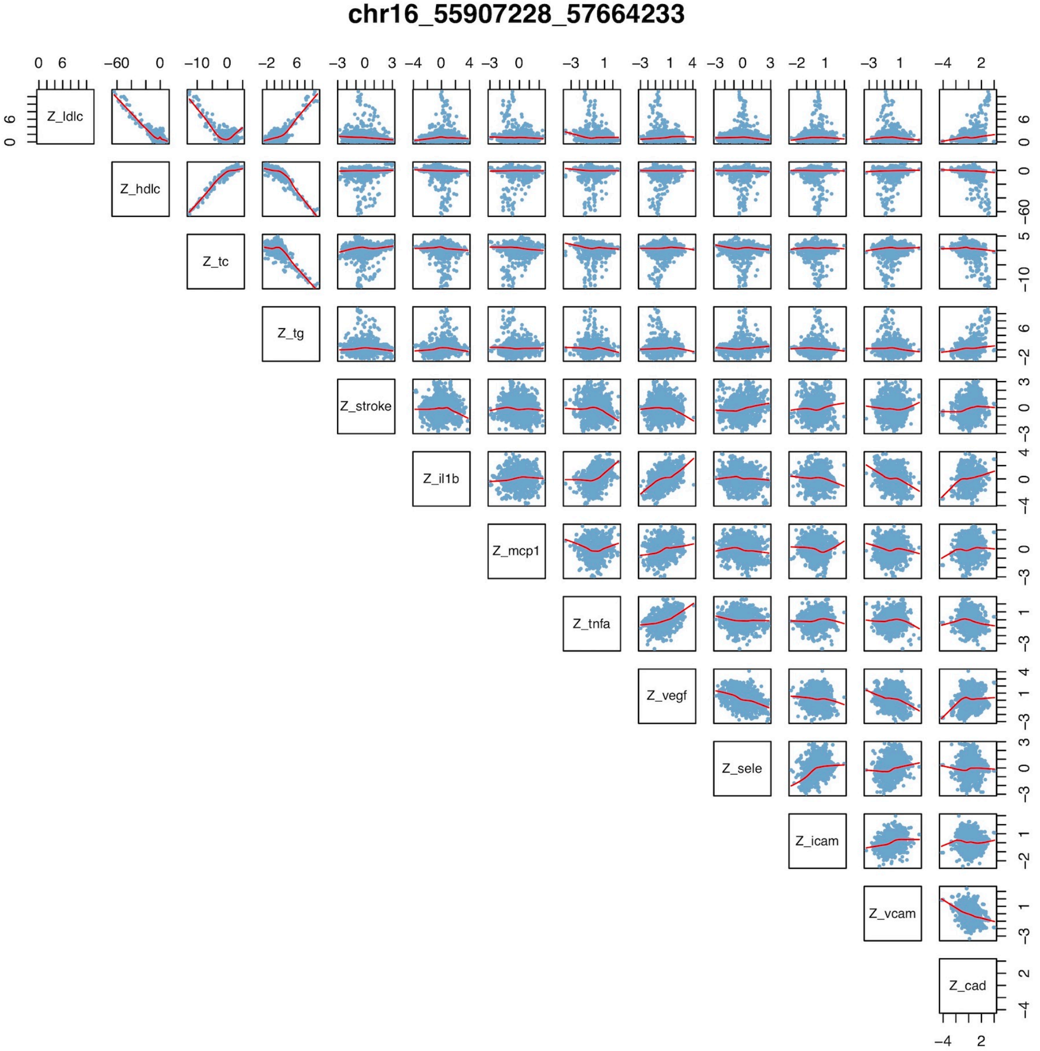
locus	PPA_3	pheno1	pheno2
chr12_124980586_126444832	0.999	hdlc	cad
chr12_124980586_126444832	0.999	hdlc	icam
chr12_124980586_126444832	0.999	hdlc	il1b
chr12_124980586_126444832	0.999	hdlc	stroke
chr12_124980586_126444832	0.997	hdlc	tc
chr12_124980586_126444832	1.000	hdlc	tg
chr12_124980586_126444832	0.999	hdlc	tnfa
chr12_124980586_126444832	0.999	hdlc	vcam
chr12_124980586_126444832	0.999	hdlc	vegf
chr12_124980586_126444832	0.999	ldlc	hdlc
chr12_124980586_126444832	0.999	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (41/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



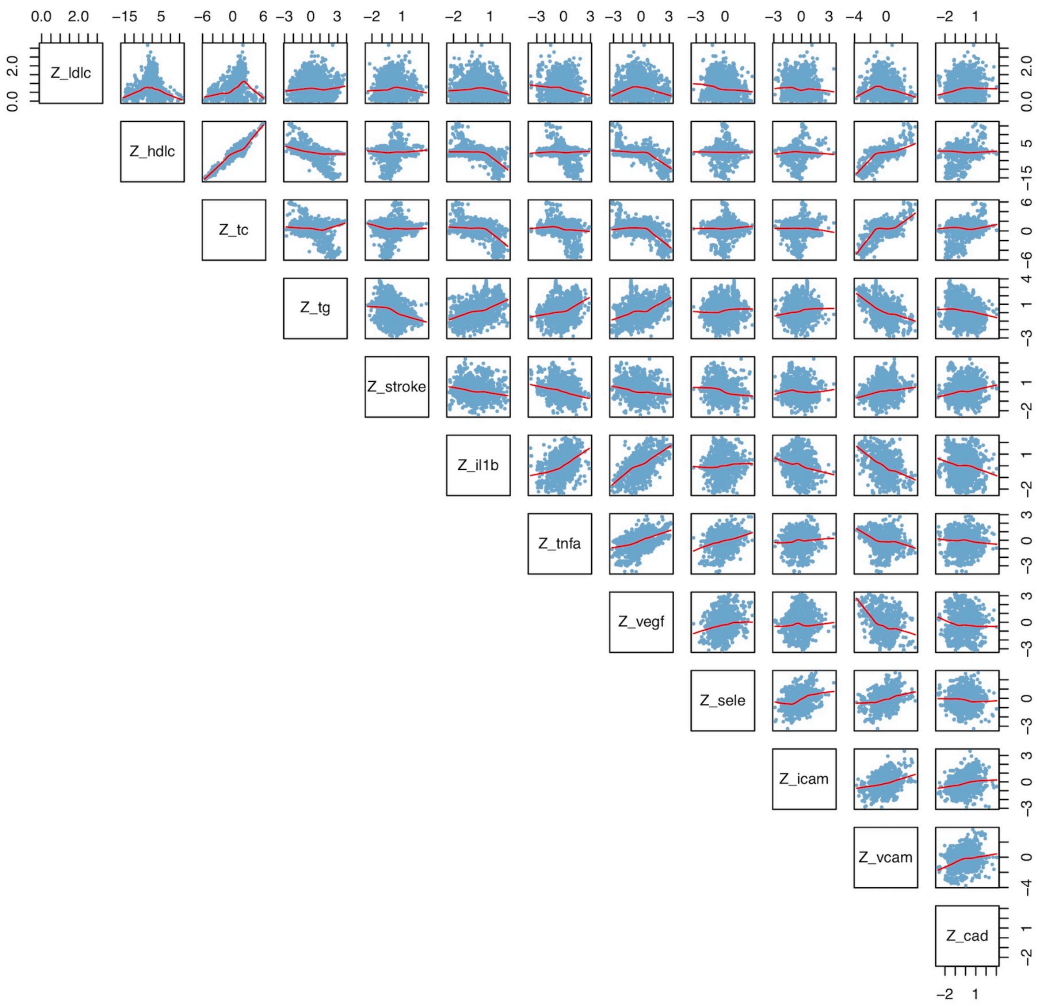
locus	PPA_3	pheno1	pheno2
chr15_58442090_59693035	0.999	hdlc	cad
chr15_58442090_59693035	0.999	hdlc	icam
chr15_58442090_59693035	0.999	hdlc	il1b
chr15_58442090_59693035	0.999	hdlc	stroke
chr15_58442090_59693035	1.000	hdlc	tc
chr15_58442090_59693035	1.000	hdlc	tg
chr15_58442090_59693035	0.999	hdlc	tnfa
chr15_58442090_59693035	1.000	hdlc	vcam
chr15_58442090_59693035	0.999	hdlc	vegf
chr15_58442090_59693035	0.999	ldlc	hdlc
chr15_58442090_59693035	1.000	ldlc	tc
chr15_58442090_59693035	0.999	sele	hdlc
chr15_58442090_59693035	0.999	sele	tc
chr15_58442090_59693035	0.998	sele	tg
chr15_58442090_59693035	0.999	tc	cad
chr15_58442090_59693035	0.999	tc	icam
chr15_58442090_59693035	0.999	tc	stroke
chr15_58442090_59693035	1.000	tc	tg
chr15_58442090_59693035	1.000	tc	vcam
chr15_58442090_59693035	0.999	tc	vegf
chr15_58442090_59693035	0.998	tg	cad
chr15_58442090_59693035	0.998	tg	icam
chr15_58442090_59693035	0.997	tg	mcp1
chr15_58442090_59693035	0.998	tg	stroke
chr15_58442090_59693035	0.998	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (42/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



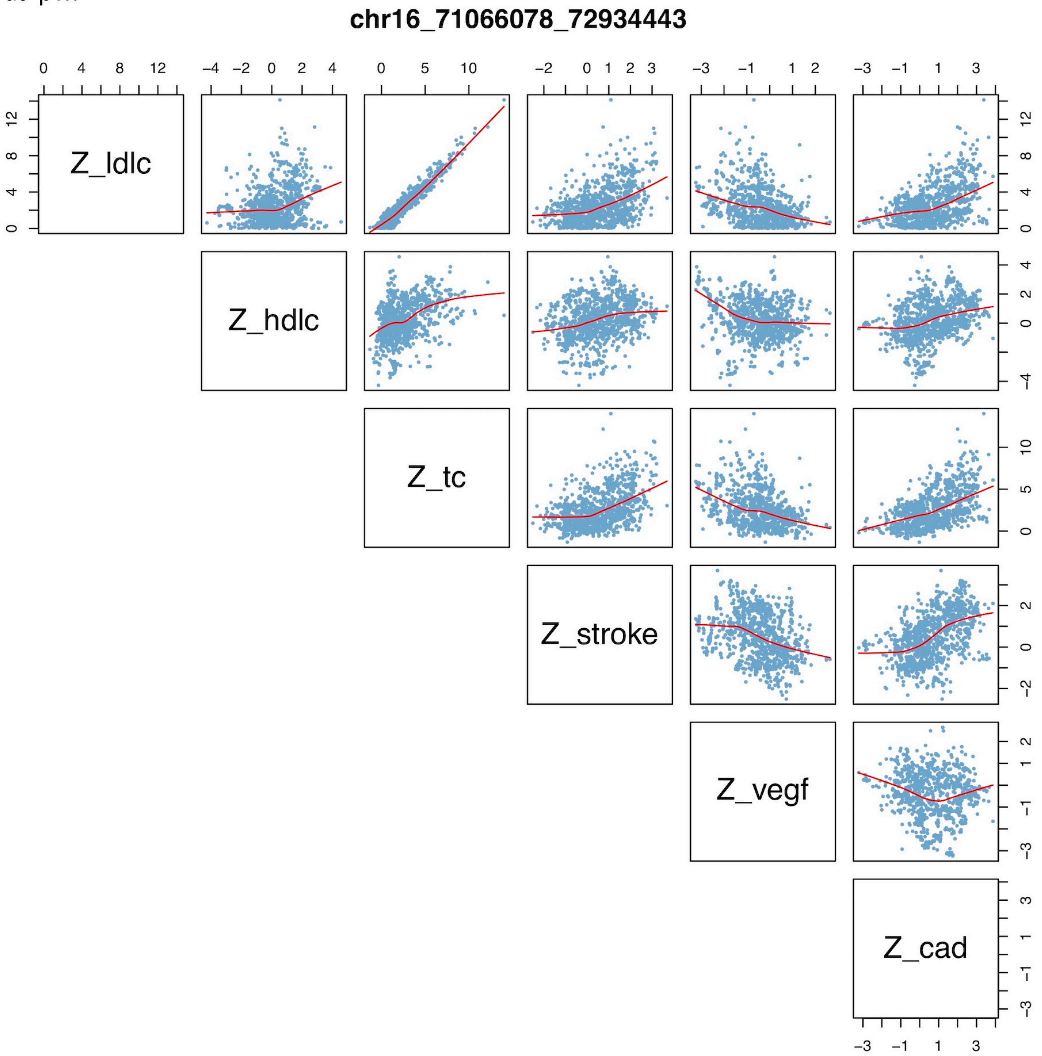
locus	PPA_3	pheno1	pheno2
chr16_55907228_57664233	0.999	hdlc	cad
chr16_55907228_57664233	0.999	hdlc	icam
chr16_55907228_57664233	0.999	hdlc	il1b
chr16_55907228_57664233	0.999	hdlc	stroke
chr16_55907228_57664233	1.000	hdlc	tc
chr16_55907228_57664233	1.000	hdlc	tg
chr16_55907228_57664233	0.999	hdlc	tnfa
chr16_55907228_57664233	0.999	hdlc	vcam
chr16_55907228_57664233	0.999	hdlc	vegf
chr16_55907228_57664233	0.999	ldlc	cad
chr16_55907228_57664233	1.000	ldlc	hdlc
chr16_55907228_57664233	0.999	ldlc	icam
chr16_55907228_57664233	0.999	ldlc	stroke
chr16_55907228_57664233	1.000	ldlc	tc
chr16_55907228_57664233	1.000	ldlc	tg
chr16_55907228_57664233	0.999	ldlc	vcam
chr16_55907228_57664233	0.999	ldlc	vegf
chr16_55907228_57664233	0.999	sele	hdlc
chr16_55907228_57664233	0.999	sele	ldlc
chr16_55907228_57664233	0.999	sele	tc
chr16_55907228_57664233	0.999	sele	tg
chr16_55907228_57664233	0.999	tc	cad
chr16_55907228_57664233	0.999	tc	icam
chr16_55907228_57664233	0.999	tc	stroke
chr16_55907228_57664233	1.000	tc	tg
chr16_55907228_57664233	0.999	tc	vcam
chr16_55907228_57664233	0.999	tc	vegf
chr16_55907228_57664233	0.999	tg	cad
chr16_55907228_57664233	0.999	tg	icam
chr16_55907228_57664233	0.999	tg	mcp1
chr16_55907228_57664233	0.999	tg	stroke
chr16_55907228_57664233	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (43/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr16_65938609_68840588

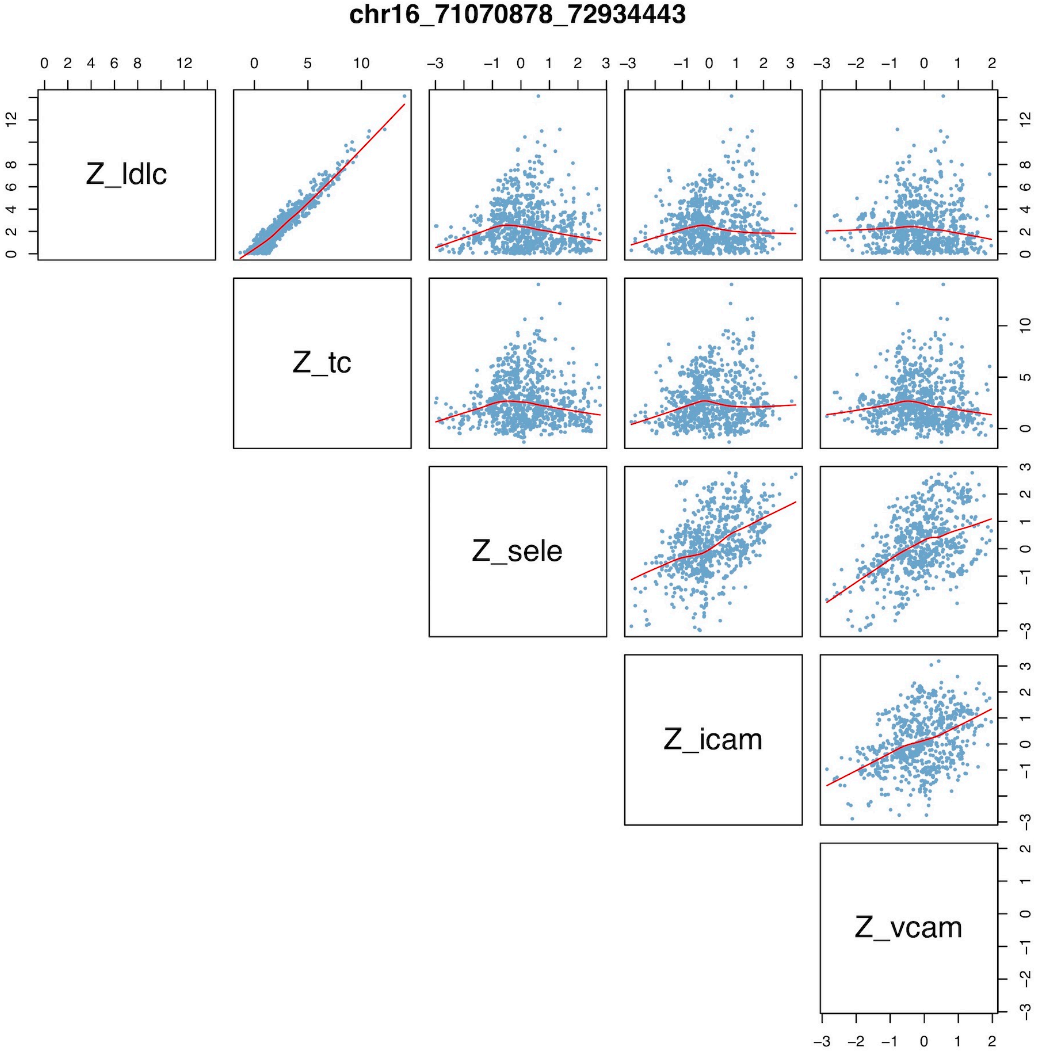
locus	PPA_3	pheno1	pheno2
chr16_65938609_68840588	0.999	hdlc	cad
chr16_65938609_68840588	0.999	hdlc	icam
chr16_65938609_68840588	0.999	hdlc	il1b
chr16_65938609_68840588	0.999	hdlc	stroke
chr16_65938609_68840588	0.996	hdlc	tc
chr16_65938609_68840588	1.000	hdlc	tg
chr16_65938609_68840588	0.999	hdlc	tnfa
chr16_65938609_68840588	0.999	hdlc	vcam
chr16_65938609_68840588	0.999	hdlc	vegf
chr16_65938609_68840588	0.999	ldlc	hdlc
chr16_65938609_68840588	0.999	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (44/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.


chr16_71066078_72934443

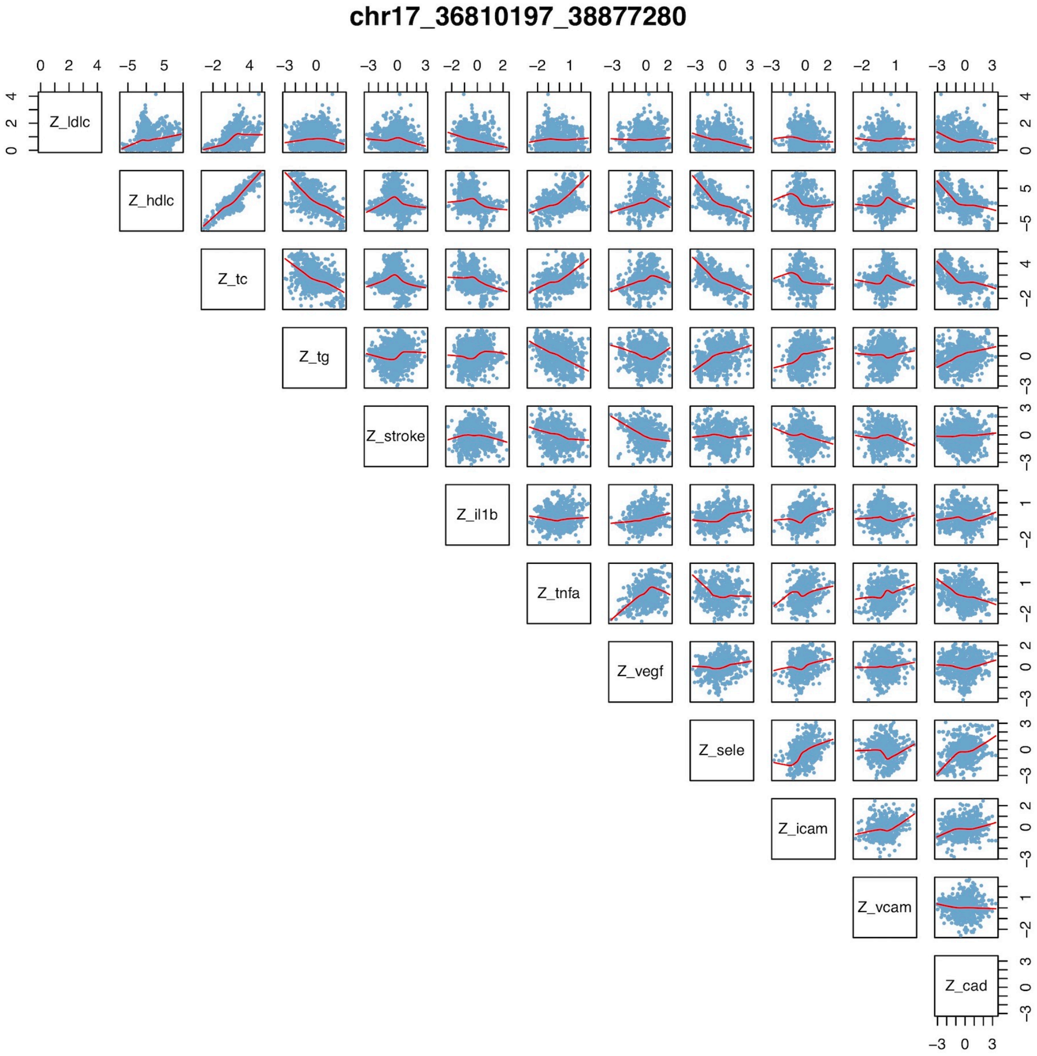
locus	PPA_3	pheno1	pheno2
chr16_71066078_72934443	0.999	ldlc	cad
chr16_71066078_72934443	0.999	ldlc	hdlc
chr16_71066078_72934443	0.998	ldlc	stroke
chr16_71066078_72934443	1.000	ldlc	tc
chr16_71066078_72934443	0.998	ldlc	vegf
chr16_71066078_72934443	0.999	tc	cad
chr16_71066078_72934443	0.999	tc	stroke
chr16_71066078_72934443	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (45/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr16_71070878_72934443	0.999	ldlc	icam
chr16_71070878_72934443	0.998	ldlc	vcam
chr16_71070878_72934443	0.998	sele	ldlc
chr16_71070878_72934443	0.999	sele	tc
chr16_71070878_72934443	0.999	tc	icam
chr16_71070878_72934443	0.999	tc	vcam

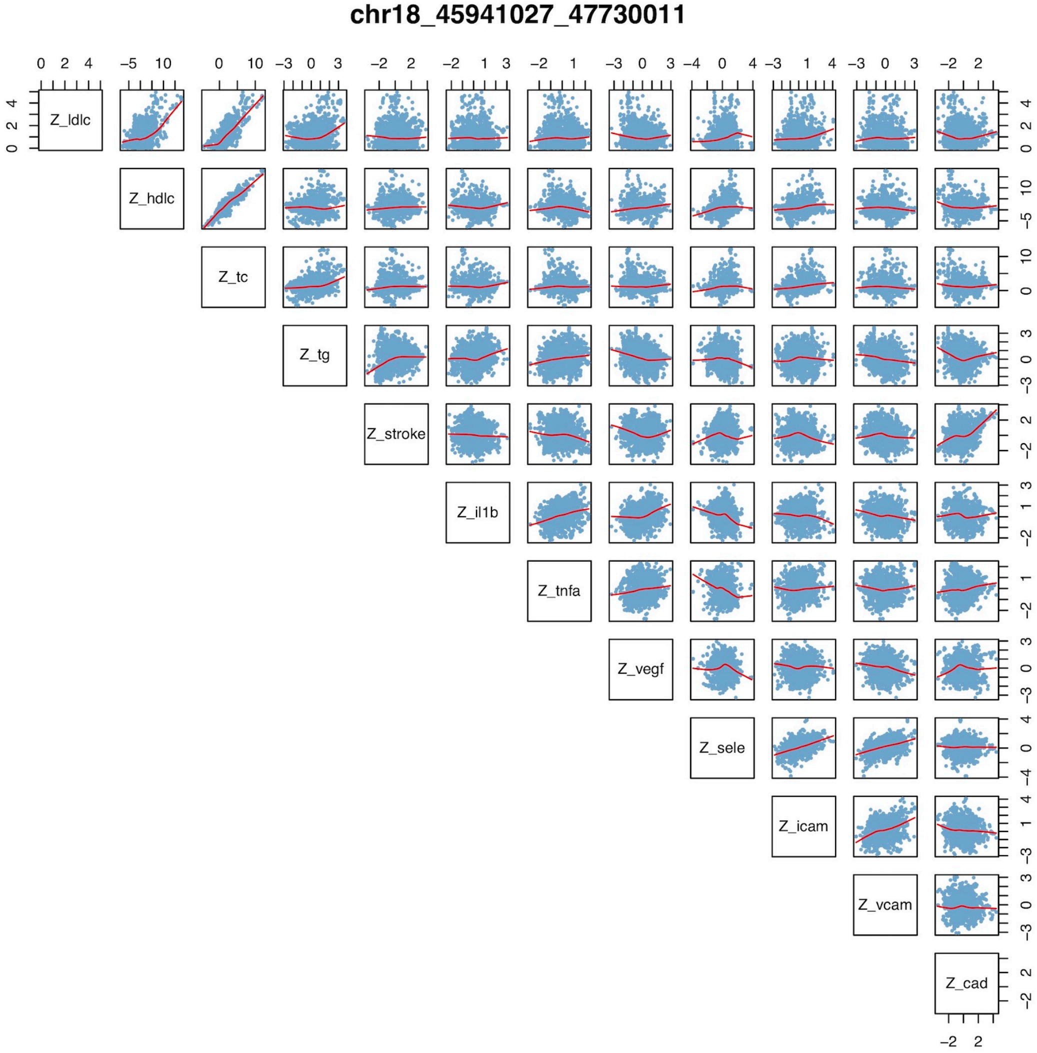
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (46/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr17_36810197_38877280	0.997	hdlc	cad
chr17_36810197_38877280	0.997	hdlc	icam
chr17_36810197_38877280	0.997	hdlc	il1b
chr17_36810197_38877280	0.997	hdlc	stroke
chr17_36810197_38877280	0.997	hdlc	tc
chr17_36810197_38877280	0.999	hdlc	tg
chr17_36810197_38877280	0.997	hdlc	tnfa
chr17_36810197_38877280	0.997	hdlc	vcam
chr17_36810197_38877280	0.997	hdlc	vegf
chr17_36810197_38877280	0.998	ldlc	hdlc
chr17_36810197_38877280	0.998	sele	hdlc

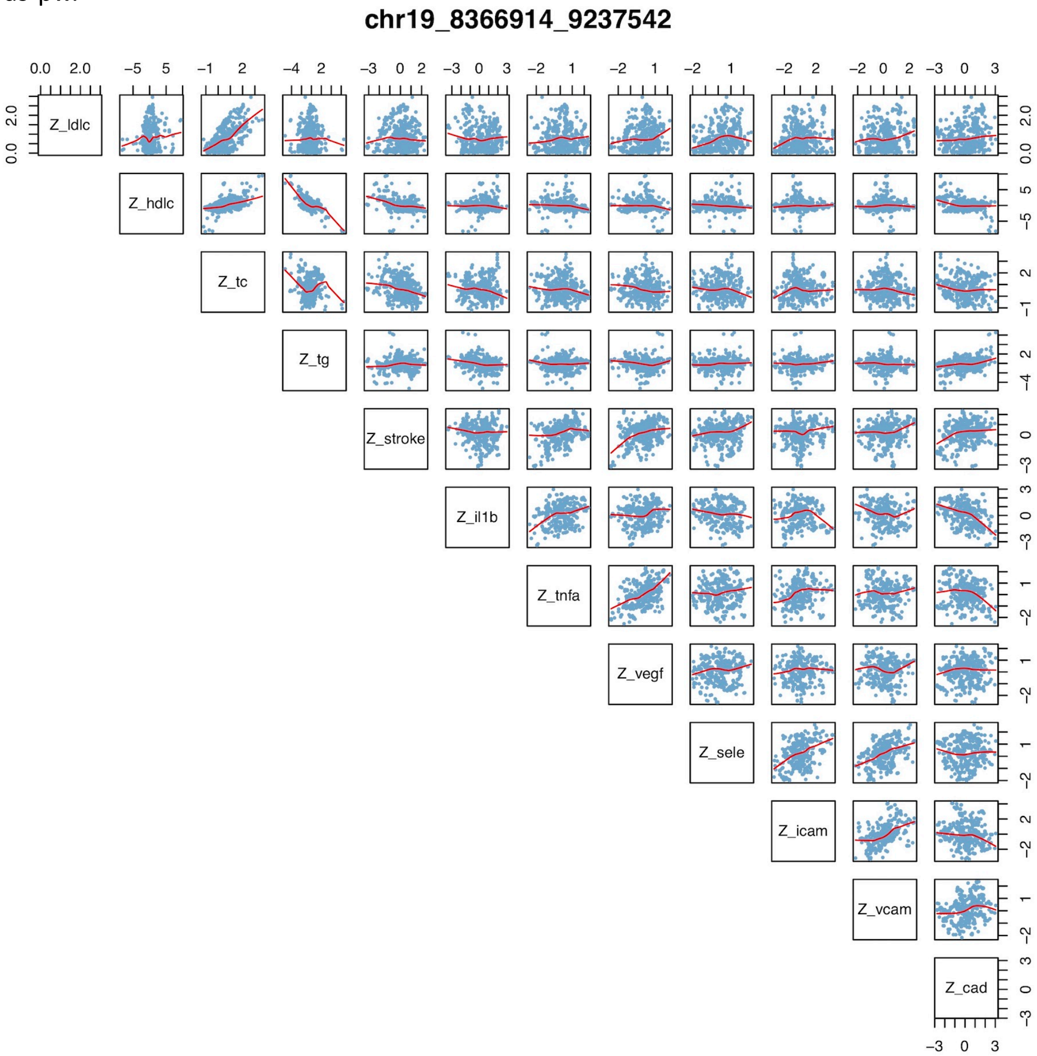
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (47/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr18_45941027_47730011	0.999	hdlc	cad
chr18_45941027_47730011	0.999	hdlc	icam
chr18_45941027_47730011	0.999	hdlc	il1b
chr18_45941027_47730011	0.999	hdlc	stroke
chr18_45941027_47730011	1.000	hdlc	tc
chr18_45941027_47730011	1.000	hdlc	tg
chr18_45941027_47730011	0.999	hdlc	tnfa
chr18_45941027_47730011	0.999	hdlc	vcam
chr18_45941027_47730011	0.999	hdlc	vegf
chr18_45941027_47730011	1.000	ldlc	hdlc
chr18_45941027_47730011	0.999	ldlc	tc
chr18_45941027_47730011	0.999	sele	hdlc
chr18_45941027_47730011	0.995	sele	tc
chr18_45941027_47730011	0.995	tc	cad
chr18_45941027_47730011	0.995	tc	icam
chr18_45941027_47730011	0.995	tc	stroke
chr18_45941027_47730011	0.995	tc	vcam
chr18_45941027_47730011	0.995	tc	vegf

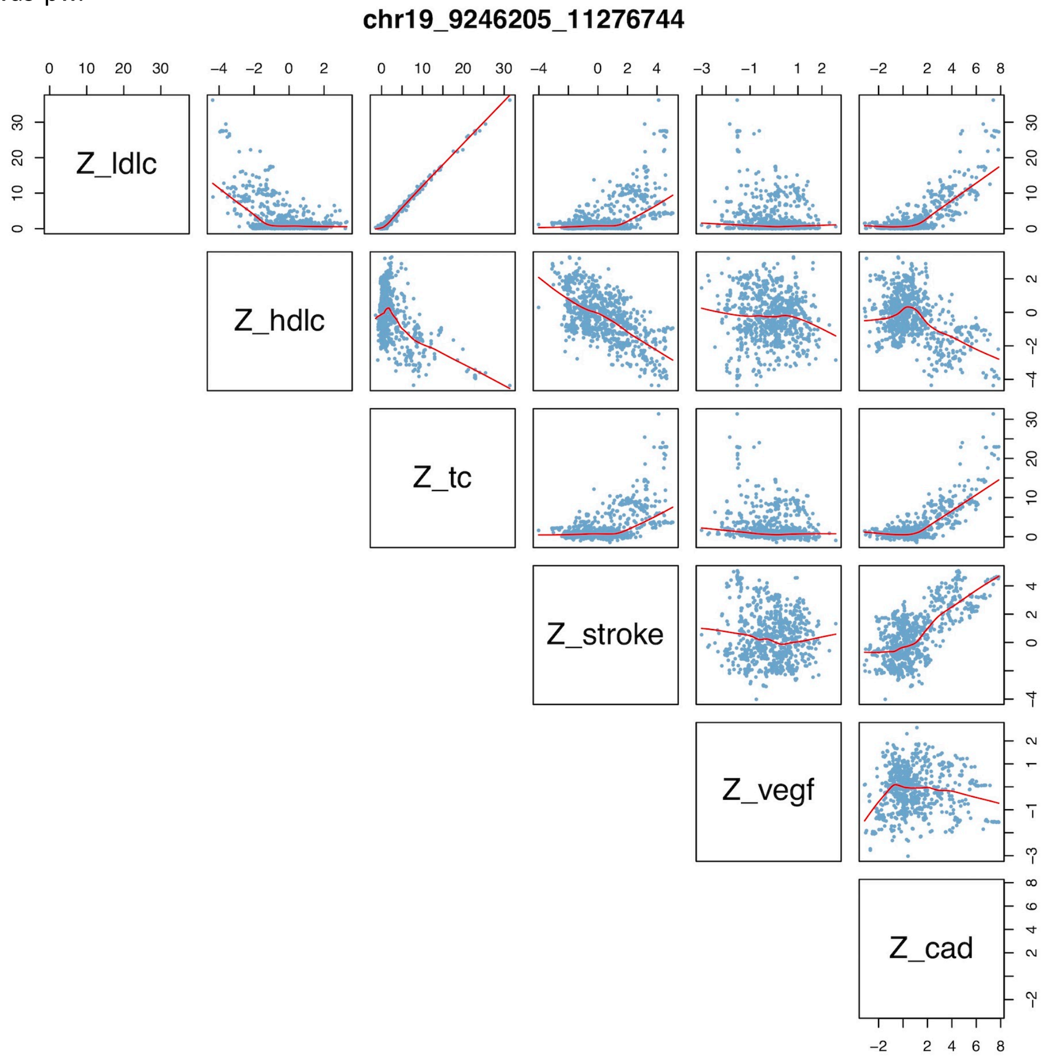
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (48/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr19_8366914_9237542	0.994	hdlc	cad
chr19_8366914_9237542	0.994	hdlc	icam
chr19_8366914_9237542	0.995	hdlc	il1b
chr19_8366914_9237542	0.994	hdlc	stroke
chr19_8366914_9237542	0.991	hdlc	tc
chr19_8366914_9237542	0.999	hdlc	tg
chr19_8366914_9237542	0.993	hdlc	tnfa
chr19_8366914_9237542	0.994	hdlc	vcam
chr19_8366914_9237542	0.993	hdlc	vegf
chr19_8366914_9237542	0.997	ldlc	hdlc
chr19_8366914_9237542	0.994	sele	hdlc

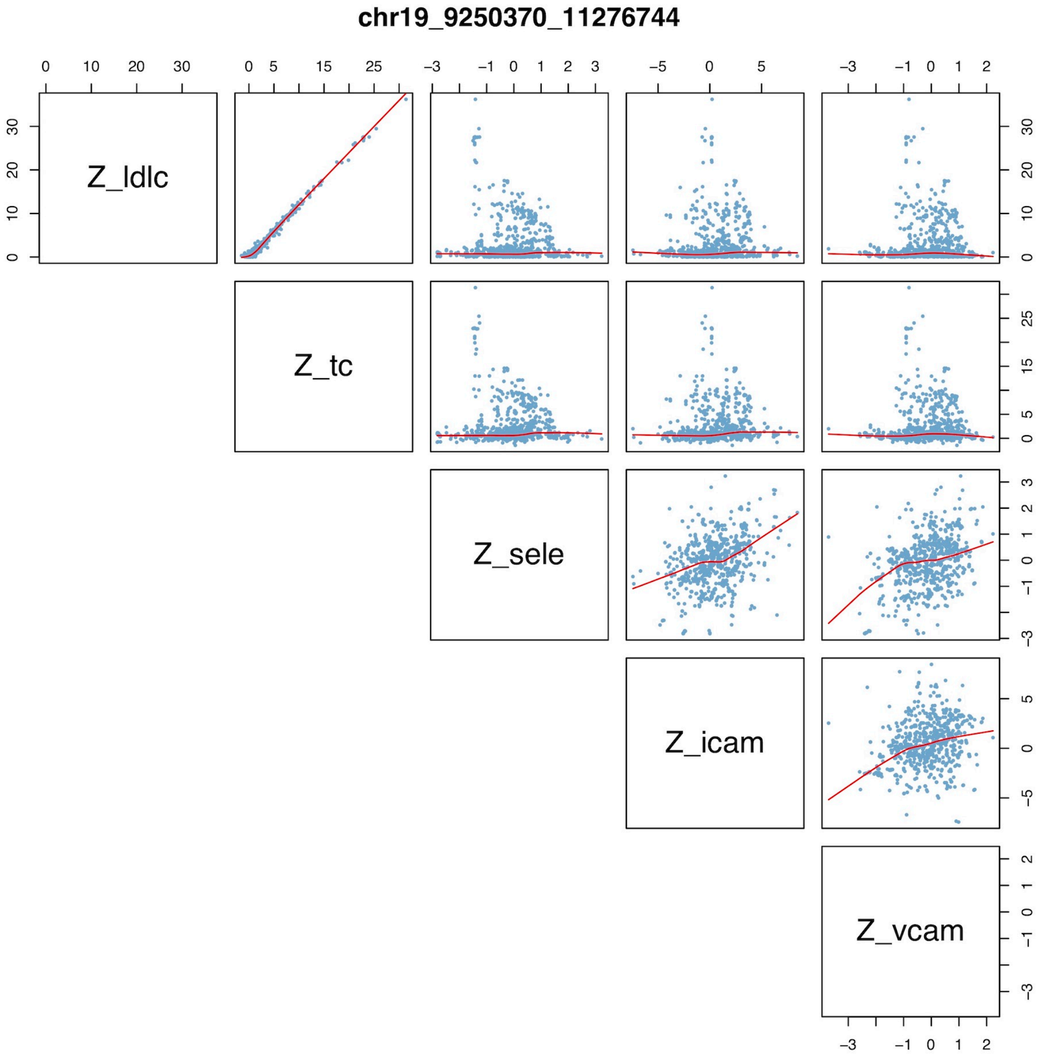
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (49/56)

The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



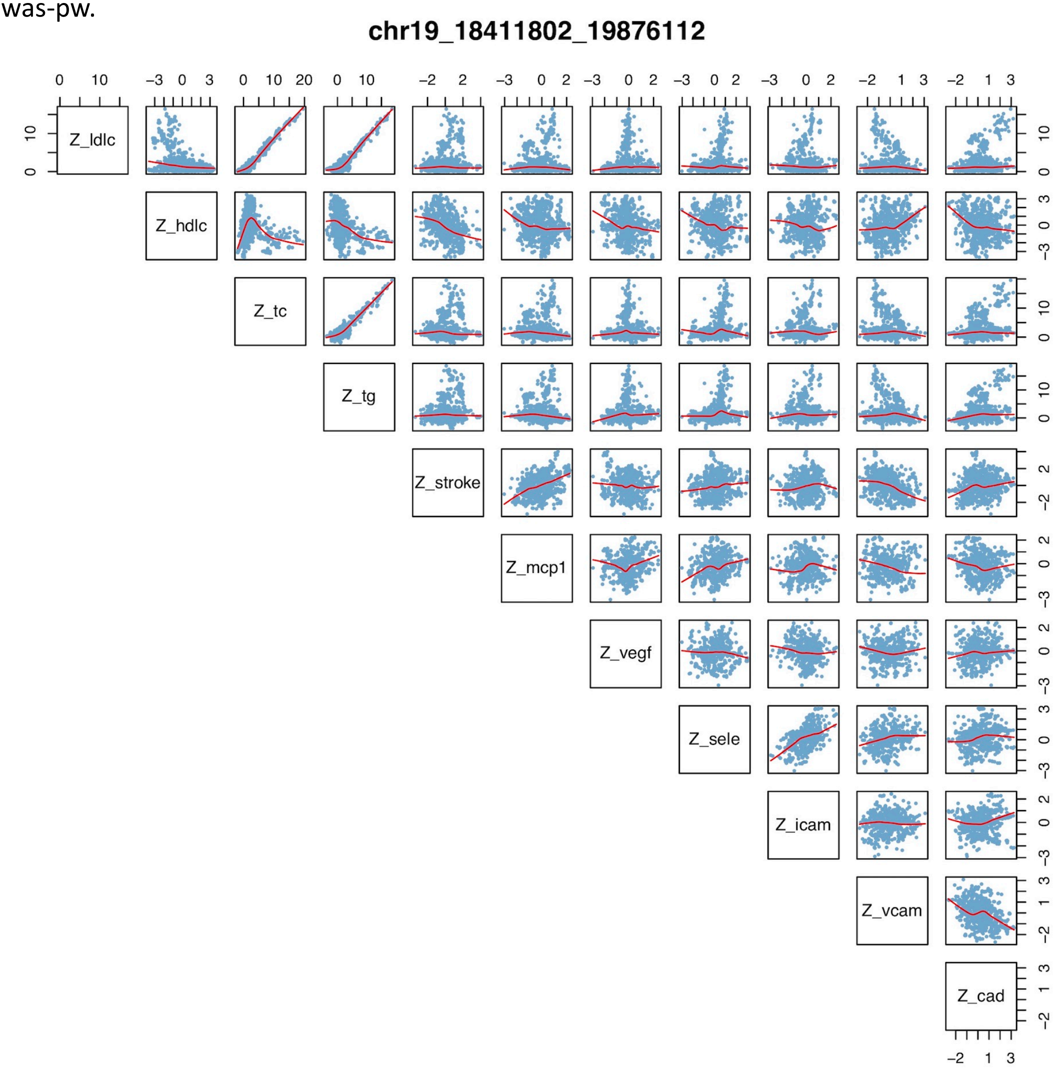
locus	PPA_3	pheno1	pheno2
chr19_9246205_11276744	0.992	hdlc	tc
chr19_9246205_11276744	0.999	ldlc	cad
chr19_9246205_11276744	1.000	ldlc	hdlc
chr19_9246205_11276744	0.999	ldlc	stroke
chr19_9246205_11276744	1.000	ldlc	tc
chr19_9246205_11276744	0.999	ldlc	vegf
chr19_9246205_11276744	0.999	tc	cad
chr19_9246205_11276744	0.999	tc	stroke
chr19_9246205_11276744	0.999	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (50/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr19_9250370_11276744	0.999	ldlc	icam
chr19_9250370_11276744	0.999	ldlc	vcam
chr19_9250370_11276744	0.999	sele	ldlc
chr19_9250370_11276744	0.999	sele	tc
chr19_9250370_11276744	0.999	tc	icam
chr19_9250370_11276744	0.999	tc	vcam

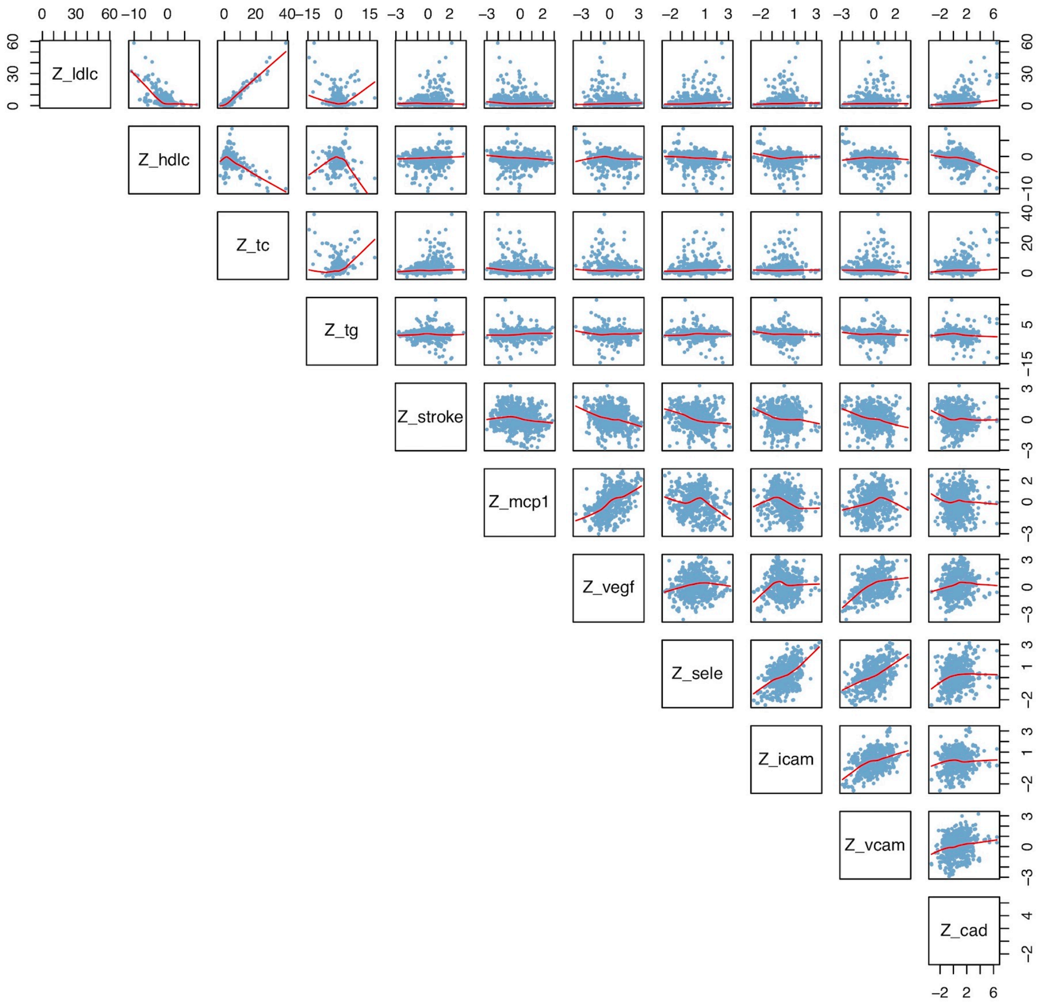
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (51/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr19_18411802_19876112	1.000	hdlc	tg
chr19_18411802_19876112	0.996	ldlc	cad
chr19_18411802_19876112	0.998	ldlc	hdlc
chr19_18411802_19876112	0.996	ldlc	icam
chr19_18411802_19876112	0.996	ldlc	stroke
chr19_18411802_19876112	1.000	ldlc	tc
chr19_18411802_19876112	0.999	ldlc	tg
chr19_18411802_19876112	0.996	ldlc	vcam
chr19_18411802_19876112	0.996	ldlc	vegf
chr19_18411802_19876112	0.996	sele	ldlc
chr19_18411802_19876112	0.999	sele	tc
chr19_18411802_19876112	0.999	sele	tg
chr19_18411802_19876112	0.999	tc	cad
chr19_18411802_19876112	0.999	tc	icam
chr19_18411802_19876112	0.999	tc	stroke
chr19_18411802_19876112	1.000	tc	tg
chr19_18411802_19876112	0.999	tc	vcam
chr19_18411802_19876112	0.999	tc	vegf
chr19_18411802_19876112	0.999	tg	cad
chr19_18411802_19876112	0.999	tg	icam
chr19_18411802_19876112	0.999	tg	mcp1
chr19_18411802_19876112	0.999	tg	stroke
chr19_18411802_19876112	0.999	tg	vegf

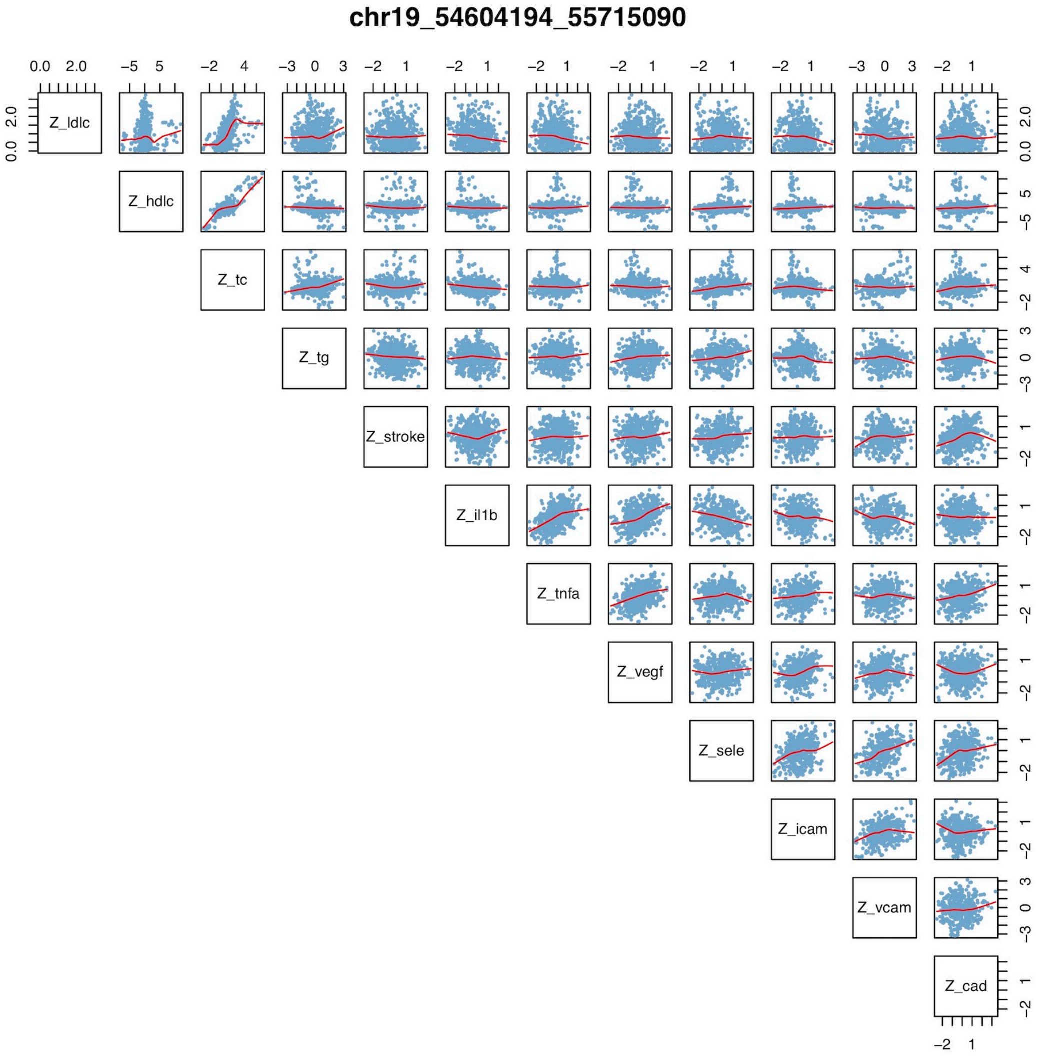
Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (52/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.

chr19_44744147_46098885



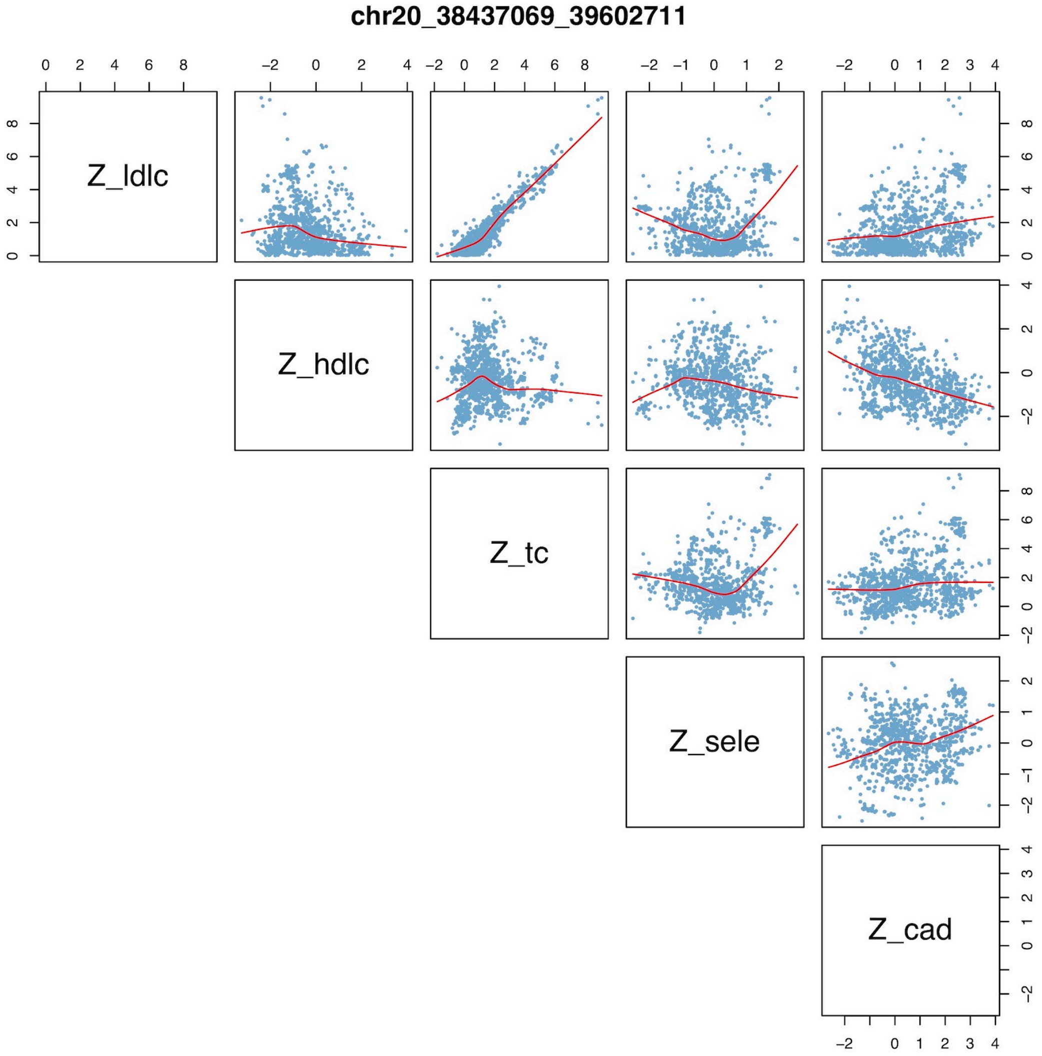
locus	PPA_3	pheno1	pheno2
chr19_44744147_46098885	0.998	hdlc	tc
chr19_44744147_46098885	1.000	hdlc	tg
chr19_44744147_46098885	0.991	hdlc	vegf
chr19_44744147_46098885	0.999	ldlc	cad
chr19_44744147_46098885	1.000	ldlc	hdlc
chr19_44744147_46098885	0.999	ldlc	icam
chr19_44744147_46098885	0.999	ldlc	stroke
chr19_44744147_46098885	1.000	ldlc	tc
chr19_44744147_46098885	0.999	ldlc	vcam
chr19_44744147_46098885	0.999	ldlc	vegf
chr19_44744147_46098885	0.999	sele	ldlc
chr19_44744147_46098885	0.999	sele	tc
chr19_44744147_46098885	0.999	sele	tg
chr19_44744147_46098885	0.999	tc	cad
chr19_44744147_46098885	0.999	tc	icam
chr19_44744147_46098885	0.999	tc	stroke
chr19_44744147_46098885	0.999	tc	vcam
chr19_44744147_46098885	0.999	tc	vegf
chr19_44744147_46098885	0.999	tg	cad
chr19_44744147_46098885	0.999	tg	icam
chr19_44744147_46098885	0.999	tg	mcp1
chr19_44744147_46098885	0.999	tg	stroke
chr19_44744147_46098885	0.999	tg	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (53/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



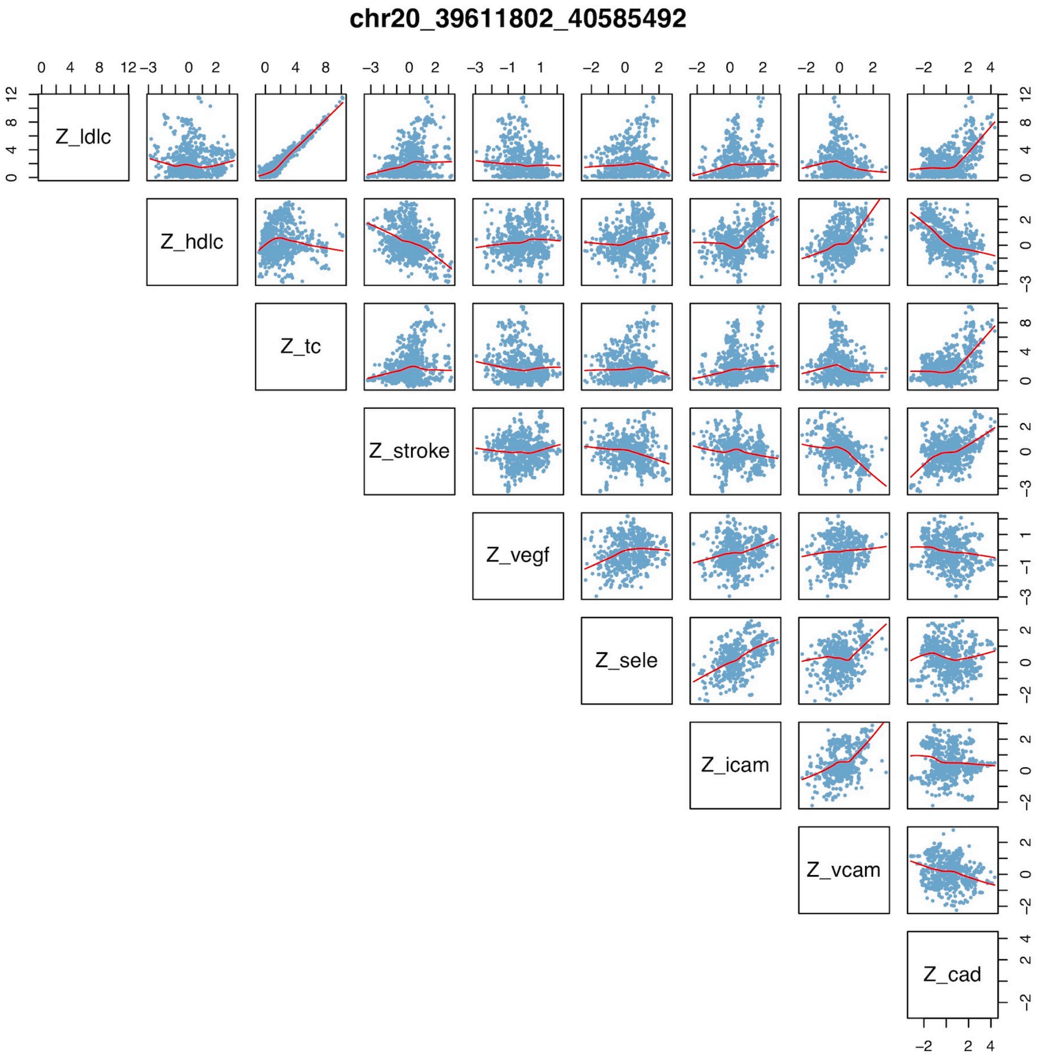
locus	PPA_3	pheno1	pheno2
chr19_54604194_55715090	0.997	hdlc	cad
chr19_54604194_55715090	0.997	hdlc	icam
chr19_54604194_55715090	0.997	hdlc	il1b
chr19_54604194_55715090	0.997	hdlc	stroke
chr19_54604194_55715090	0.998	hdlc	tc
chr19_54604194_55715090	0.999	hdlc	tg
chr19_54604194_55715090	0.997	hdlc	tnfa
chr19_54604194_55715090	0.998	hdlc	vcam
chr19_54604194_55715090	0.997	hdlc	vegf
chr19_54604194_55715090	0.998	ldlc	hdlc
chr19_54604194_55715090	0.997	sele	hdlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (54/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



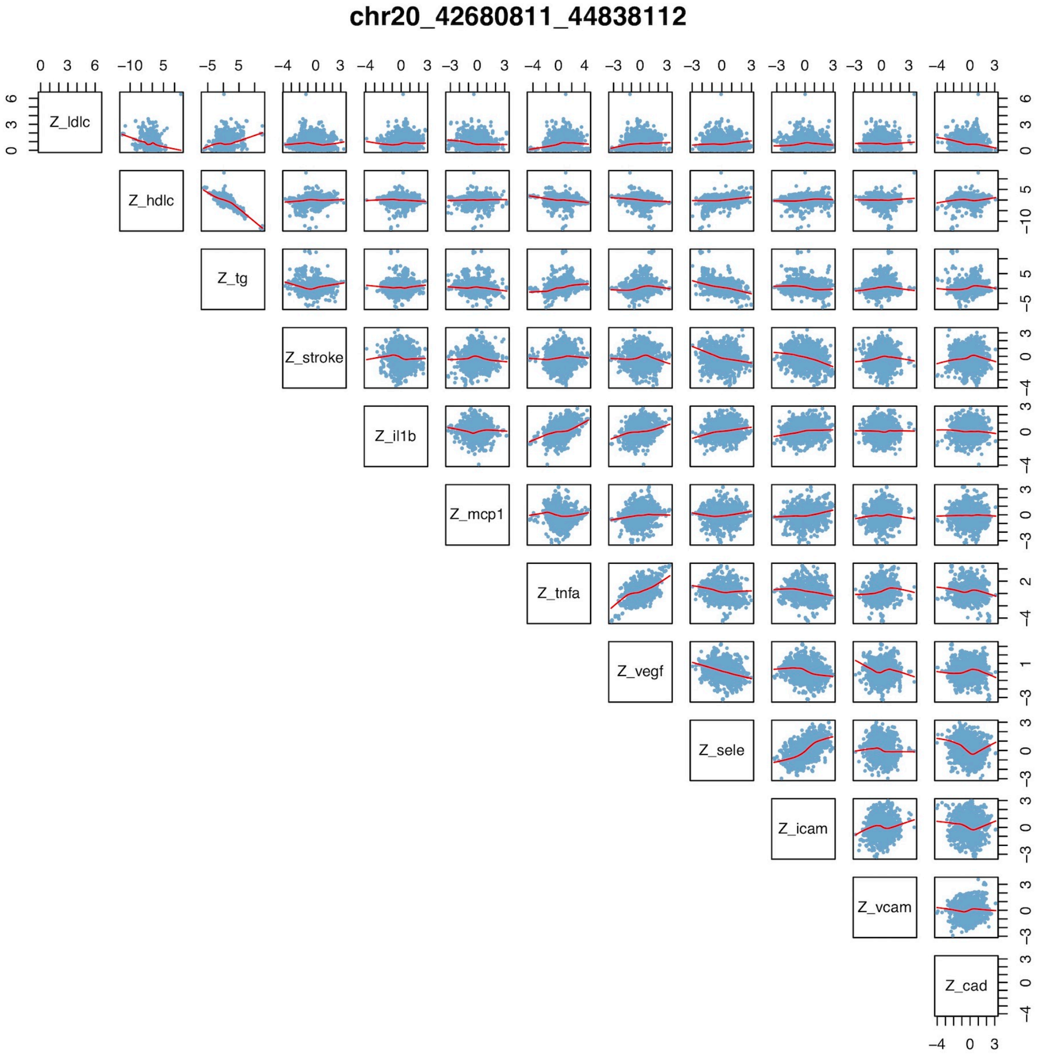
locus	PPA_3	pheno1	pheno2
chr20_38437069_39602711	0.990	ldlc	cad
chr20_38437069_39602711	0.996	ldlc	hdlc
chr20_38437069_39602711	1.000	ldlc	tc
chr20_38437069_39602711	0.990	sele	ldlc

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (55/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr20_39611802_40585492	0.999	ldlc	cad
chr20_39611802_40585492	0.999	ldlc	hdlc
chr20_39611802_40585492	0.999	ldlc	icam
chr20_39611802_40585492	0.999	ldlc	stroke
chr20_39611802_40585492	1.000	ldlc	tc
chr20_39611802_40585492	0.999	ldlc	vcam
chr20_39611802_40585492	0.999	ldlc	vegf
chr20_39611802_40585492	0.999	sele	ldlc
chr20_39611802_40585492	0.998	sele	tc
chr20_39611802_40585492	0.998	tc	cad
chr20_39611802_40585492	0.998	tc	icam
chr20_39611802_40585492	0.998	tc	stroke
chr20_39611802_40585492	0.998	tc	vcam
chr20_39611802_40585492	0.998	tc	vegf

Figure S3. Correlations of the genetic effects in the 56 genomic regions showing strong evidence for containing a genetic variant influencing on at least one of the inflammatory phenotypes and at the same time at least one of the other cardiovascular traits studied. (56/56)
The table lists the pairwise comparisons of traits with model 3 posterior propability (PPA_3) > 0.99 within the genomic region estimated using gwas-pw.



locus	PPA_3	pheno1	pheno2
chr20_42680811_44838112	0.999	hdlc	cad
chr20_42680811_44838112	0.999	hdlc	icam
chr20_42680811_44838112	0.999	hdlc	il1b
chr20_42680811_44838112	0.999	hdlc	stroke
chr20_42680811_44838112	1.000	hdlc	tg
chr20_42680811_44838112	0.999	hdlc	tnfa
chr20_42680811_44838112	0.999	hdlc	vcam
chr20_42680811_44838112	0.999	hdlc	vegf
chr20_42680811_44838112	0.999	ldlc	hdlc
chr20_42680811_44838112	0.999	sele	hdlc
chr20_42680811_44838112	0.999	sele	tg
chr20_42680811_44838112	0.999	tg	cad
chr20_42680811_44838112	0.999	tg	icam
chr20_42680811_44838112	0.999	tg	mcp1
chr20_42680811_44838112	0.999	tg	stroke
chr20_42680811_44838112	0.999	tg	vegf