

Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

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Study Populations

The SHIP dataset

SHIP (Study of Health in Pomerania) is a population-based project consisting of two independent cohorts, SHIP and SHIP-TREND. Baseline examinations for SHIP-TREND started in 2008. The study region of SHIP is West Pomerania, a region in the north-east of Germany. From the total population of West Pomerania comprising 212,157 inhabitants, a two-stage cluster sample of adults aged 20 to 79 years was drawn. Since the Federal State of Mecklenburg/West Pomerania has recently established a central population registry, we used this option for SHIP-TREND to draw a stratified random sample of 8,016 adults.

Stratification variables were age, sex, and city/country of residence. Subjects were sampled from the regional strata with a probability proportional to size design. Age/sex strata within countries were of equal size. Study design and sampling methods have been previously described¹.

The Rotterdam Study

The Rotterdam Study (RS) (www.epib.nl/rotterdamstudy) is a prospective, population-based cohort study in the district of Rotterdam, the Netherlands. The initial design of the study is straight-forward: a prospective cohort study among 7,983 persons living in the well-defined Ommoord district in the city of Rotterdam (78% of 10,215 invitees), called Rotterdam Study I (or RS-I). They were 55 years of age or older and the oldest participant at the start was 106 years. The study started in the second half of 1989. In 1999, 3,011 participants (out of 4,472 invitees) who had become 55 years of age or moved into the study district since the start of the study were added to the cohort, called Rotterdam Study II (or RS-II). In 2006, a further extension of the cohort was initiated in which 3,932 subjects were included, aged 45–54 years (out of 6,057 invited), called Rotterdam Study III (RS-III). The participants were all examined in some detail at baseline. They were interviewed at home and then had an extensive set of examinations in a specially built research facility in the centre of their district. These examinations were repeated every 3–4 years in characteristics that could change over time. The participants in the Rotterdam Study are followed for a variety of diseases that are frequent in the elderly. Informed consent was obtained from each participant, and the medical ethics committee of the Erasmus Medical Center Rotterdam approved the study. Study design and sampling methods have been described in detail^{2,3}.

Genotyping

SHIP-TREND

For the SHIP-TREND study DNA was isolated using the Genra Puregene Blood Kit (Qiagen) according to the manufacturer's protocol. Purity and concentration of DNA and RNA

was determined using a NanoDrop ND-1000 UV-Vis Spectrophotometer (Thermo Scientific). The integrity of all DNA preparations was validated by electrophoresis using 0.8% agarose-1x TBE gels stained with ethidium bromide. The Illumina HumanOmni2.5-Quad arrays were used for genotyping.

Genotypes were calculated from the raw intensity data using the Genotyping Module from Illumina's GenomeStudio V 2010.1, imputation to the HapMap v22 CEU reference panel was done using IMPUTE.

Rotterdam Study (RS)

For RS, DNA was isolated using standard salting-out methods. Illumina HumanHap 550K arrays were used for genotyping. Sample call rate was >97.5%, gender mismatches were excluded based on typing with X-linked markers, and samples with evidence for DNA contamination were excluded too (mean of autosomal heterozygosity >0.33). First-degree relatives and duplicated were excluded (estimated by pairwise IBD), and ethnic outliers were excluded (>4 SD from population mean using MDS). Genotypes were imputed for all polymorphic SNPs (MAF>0.01) using MACH, based upon phased autosomal chromosomes of the HapMap CEU Phase II panel (release 22, build 36), orientated on the positive strand.

Gene Expression Profiling

SHIP-TREND

RNA was prepared from whole blood under fasting conditions in PAXgene tubes (BD) using the PAXgene Blood miRNA Kit (Qiagen, Hilden, Germany). For SHIP-TREND this was done on a QIAcube according to protocols provided by the manufacturer (Qiagen). To ensure a constant high quality of the RNA preparations, all RNA samples were analyzed using RNA 6000 Nano LabChips (Agilent Technologies) on a 2100 Bioanalyzer (Agilent Technologies) according to the manufacturer's instructions. Using the Illumina TotalPrep-96 RNA Amp Kit (Ambion), 500ng of RNA was reverse transcribed into cRNA, and biotin-UTP-labeled. 3000ng

of cRNA were hybridized to the Illumina HumanHT-12 v3 Expression BeadChips, followed by washing steps as described in the Illumina protocol.

Processing of the SHIP-TREND DNA and RNA samples was performed at the Helmholtz Zentrum München.

Rotterdam Study (RS)

For RS-III, whole-blood was collected in PAXgene-tubes (BD). Total RNA was isolated using PAXgene Blood RNA kits (Qiagen).

To ensure a constant high quality of the RNA preparations, all RNA samples were analyzed using the Labchip GX (Calliper) according to the manufacturer's instructions. Samples with an RNA Quality Score > 7 were amplified and labelled (Ambion TotalPrep RNA), and hybridized to the Illumina HumanHT-12 v4 Expression Beadchips as described by the manufacturer's protocol.

Processing of the Rotterdam Study DNA and RNA samples was performed at the Genetic Laboratory of Internal Medicine, Erasmus University Medical Center Rotterdam.

Gene expression analysis

SHIP-TREND and RS-III

For gene expression analysis in SHIP-TREND, raw intensity data generated with the expression arrays were exported from Illumina's GenomeStudio V 2010.1 Gene Expression Module to the R environment and processed (quantile normalization and \log_2 -transformation) with the lumi 1.12.4 package from the Bioconductor open source software (<http://www.bioconductor.org/>).

For eQTL analysis in SHIP-TREND and RS-III, raw intensity data generated with the expression arrays were exported from Illumina's GenomeStudio V 2010.1 Gene Expression Module to the R environment and quantile normalized and \log_2 -transformed (with the lumi 1.12.4 package from the Bioconductor open source software (<http://www.bioconductor.org/>)) as well as probe-centered, and sample-standardized⁴.

Gene expression levels and bacterial load

SHIP-TREND

To investigate the association of gene expression levels and the fecal *H. pylori* antigen titer, we checked whether individuals with high bacterial load (based on fecal *H. pylori* antigen titers, OD>1) also exhibit the highest 25% of gene expression levels of the respective *4p14* region's genes.

cis-eQTL analysis

SHIP-TREND and RS-III

For *cis*-eQTL analysis we chose all genes in a ± 250 kb region of the two GWAS top SNPs rs10004195 and rs368433 representing the two loci *4p14* and *1q23.3*, respectively. Probes that mapped to those genes had to fulfil the following two criteria: 1) The probe must be available on both, the HumanHT-12 v3 as well as HumanHT-12 v4 Expression BeadChip. 2) The probe must be expressed in at least 10% of the samples. This was estimated based on the detection p-value (<0.05) provided by Illumina. Subsequently, we performed a regression analysis of transcript abundance represented by 26 probes present on the HumanHT-12 Expression BeadChips and the two GWAS top SNPs. The probes represent five genes at the *4p14* locus (*KLF3*, *TLR1*, *TLR10*, *TLR6*, *TMEM156*) as well as 11 genes at the *1q23.3* locus (*SDHC*, *FCGR2A*, *HSPA6*, *FCGR3A*, *HSPA7*, *FCGR3B*, *FCGR2B*, *FCRLA*, *FCRLB*, *DUSP12*). Linear regression analysis was carried out with adjustment for the first 50 eigenvectors of a principal component analysis. Associations with $P < 1.92 \times 10^{-3}$ were considered statistically significant (Bonferroni correction for 26 analyzed SNP-probe pairs).

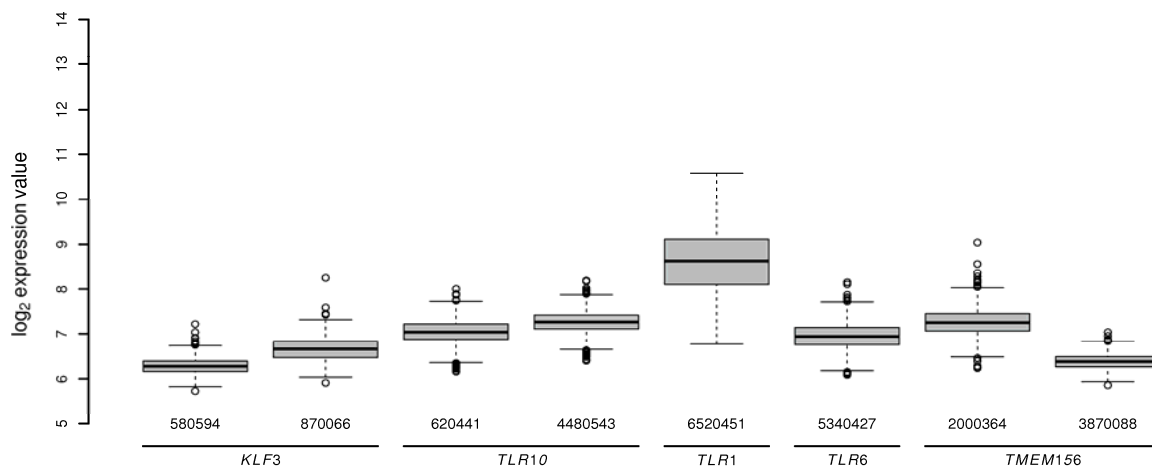
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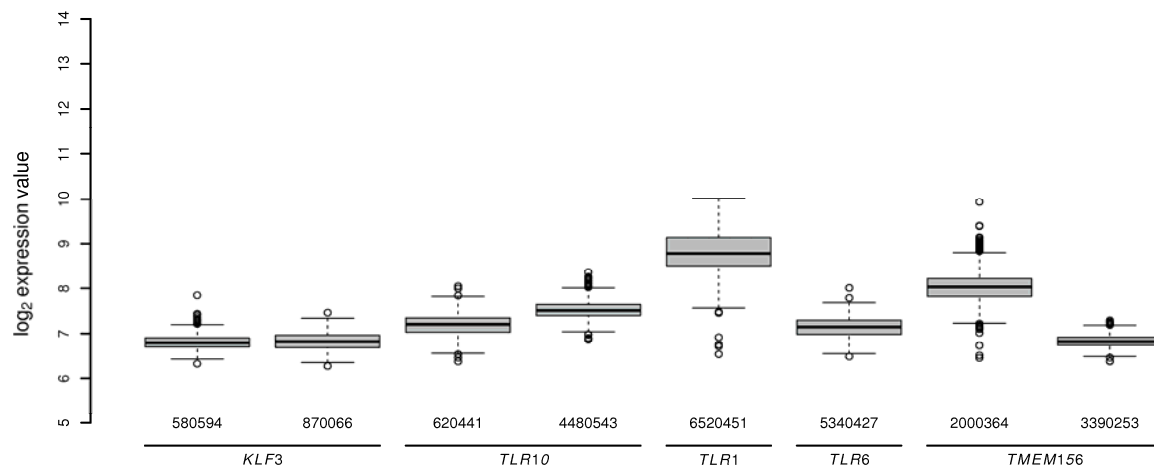
eFigure 1. Boxplot of the \log_2 -Transformed Expression Values of the Genes at *4p14* and *1q23.3*

Shown are the quantile normalized and \log_2 -transformed expression values for the analyzed *cis*-eQTL probes at *4p14* (Panel A and B for SHIP-TREND and RS-III, respectively) and *1q23.3* (Panel C-D and E-F for SHIP-TREND and RS-III, respectively). The bottom and top of the boxes are the lower and upper quartiles, respectively. The horizontal bar within the box is the median. The lower and upper ends of the whiskers represent the smallest and highest value within the 1.5 interquartile range of the lower and upper quartile, respectively. With respect to this convention, circles display outliers,

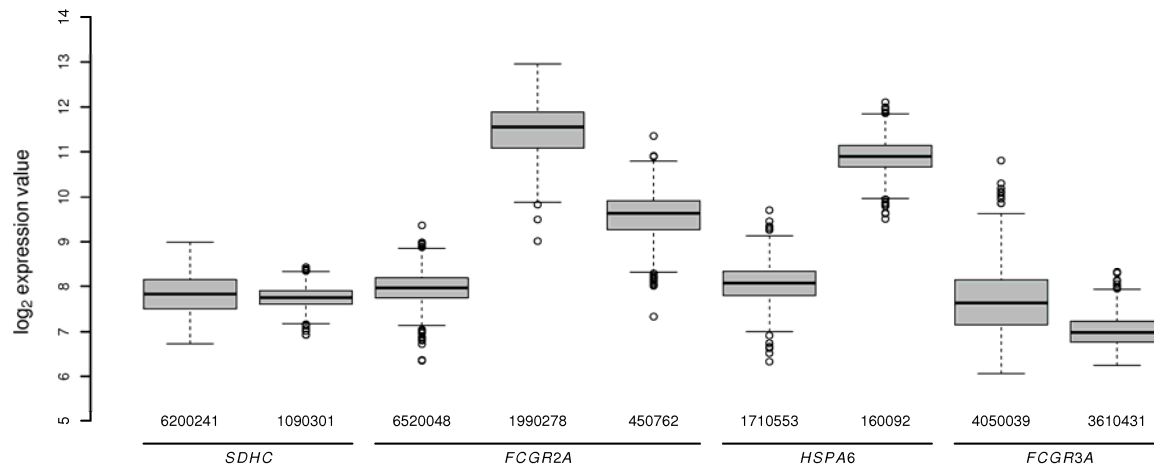
1A



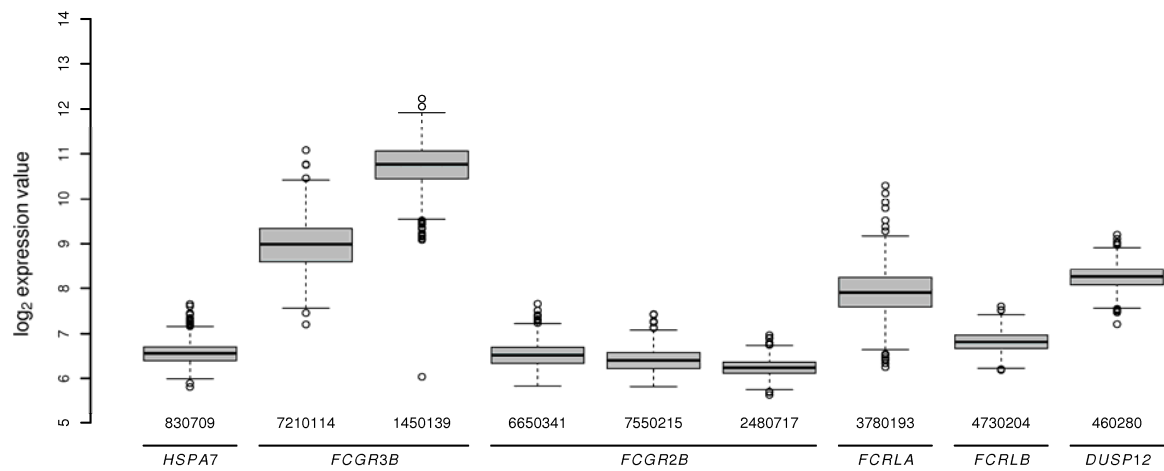
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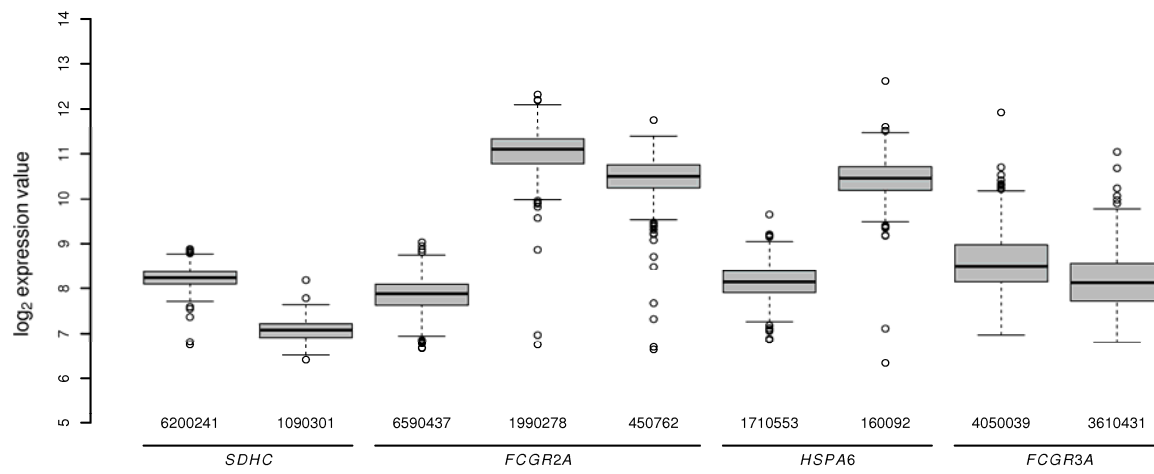
1C



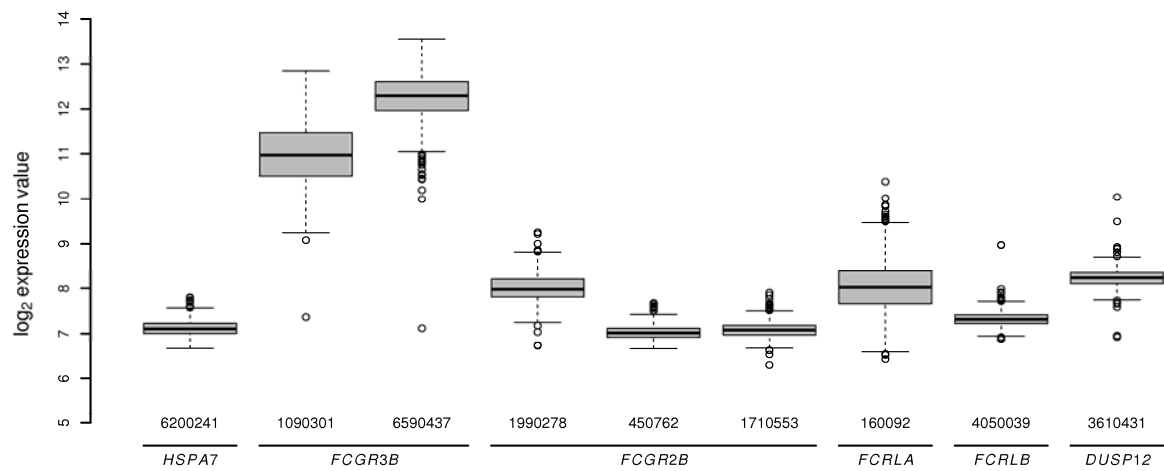
1D



1E

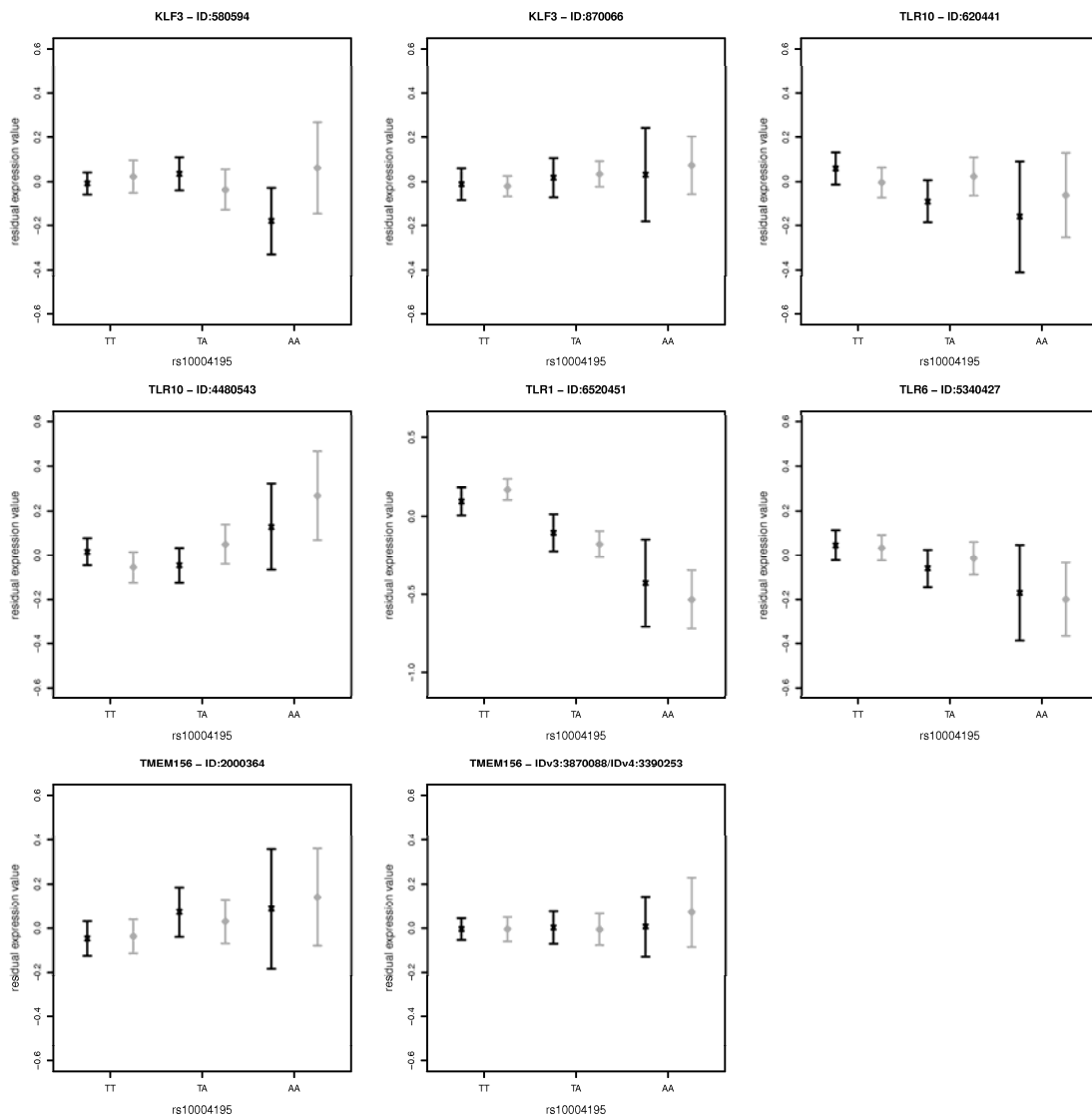


1F



eFigure 2. Visualization of the *cis*-eQTLs at *4p14*

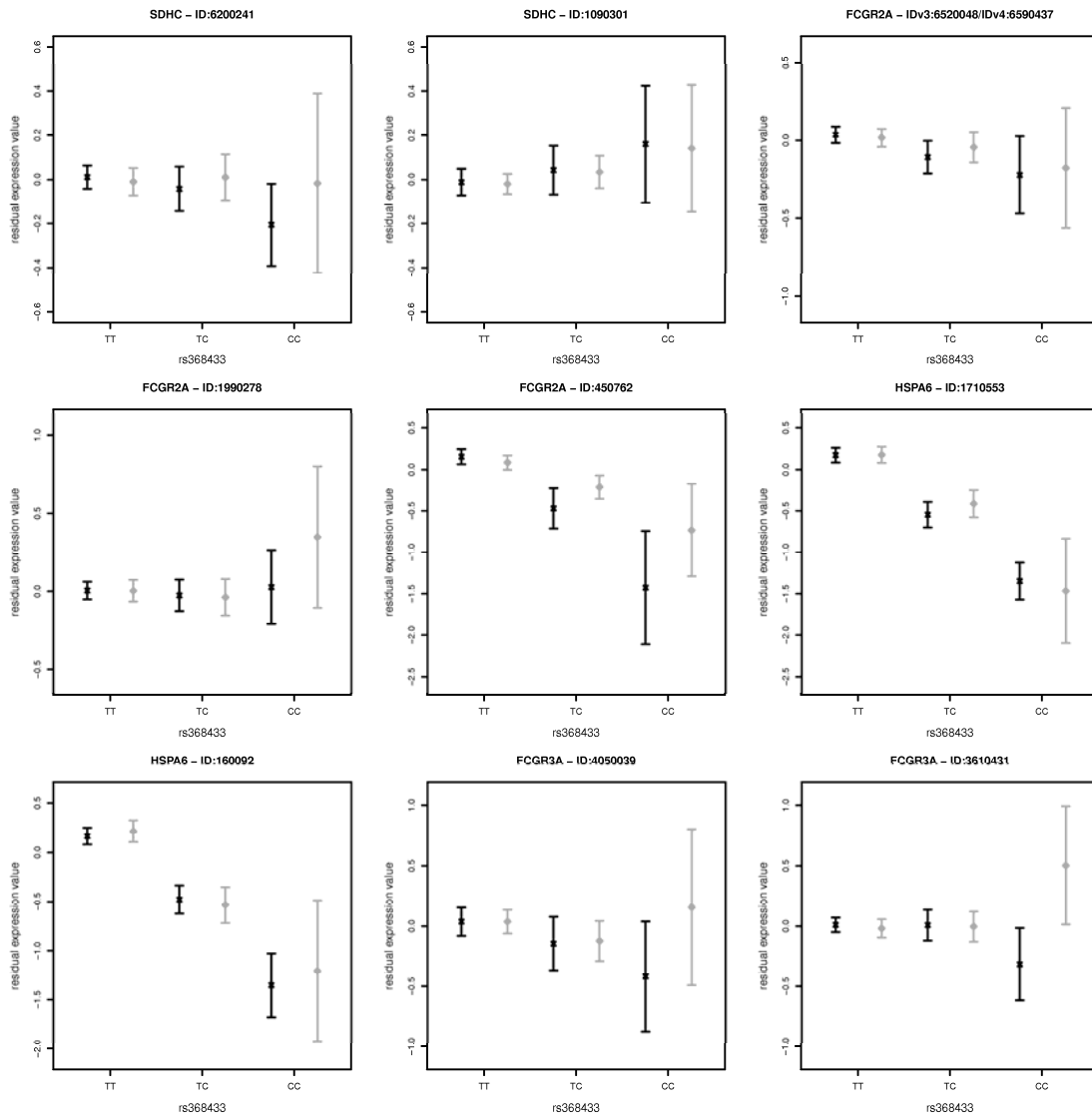
Shown are the residual mean \log_2 -transformed gene expression levels and 95% confidence intervals (CIs) (y-axis) per genotype group (x-axis) of *KLF3*, *TLR10*, *TLR1*, *TLR6*, and *TMEM156* adjusted for the first 50 eigenvectors with respect to rs10004195 for SHIP-TREND (black, genotype distribution: TT=614, TA=315, AA=47) and RS-III (grey, genotype distribution: TT=439, TA=269, AA=54).



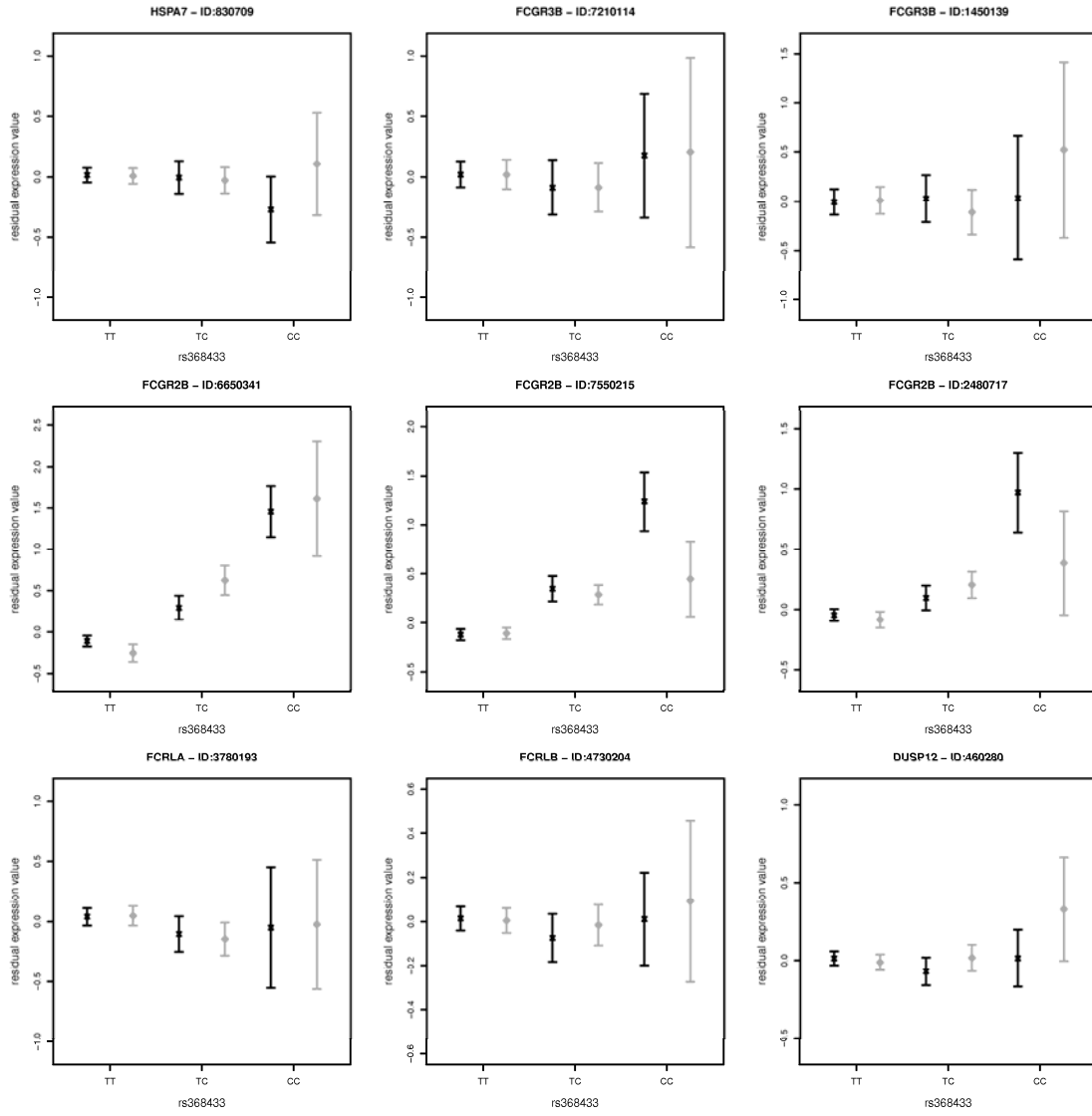
eFigure 3. Visualization of the *cis*-eQTLs at 1q23.3

Shown are the **residual mean log₂-transformed** gene expression levels and 95% CIs (y-axis) per genotype group (x-axis) of *SDHC*, *FCGR2A*, *HSPA6*, *FCGR3A* (**3A**), *HSPA7*, *FCGR3B*, *FCGR2B*, *FCRLA*, *FCRLB*, and *DUSP12* (**3B**) adjusted for the first 50 eigenvectors with respect to rs368433 for both SHIP-TREND (**black**, genotype distribution: TT=765, TC=191, CC=20) and RS-III (**grey**, genotype distribution: TT=551, TC=198, CC=13).

3A



3B



eTable 1A. Characteristics of the Probe at *4p14* Used for *cis*-eQTL Analysis in SHIP-TREND and RS-III

Gene	Array Address ID		SHIP-TREND			RS-III		
	HT-12 v3	HT-12 v4	Mean expression	SD expression	Significant expressed Probes [%]	Mean expression	SD expression	Significant expressed Probes [%]
<i>KLF3</i>	580594	580594	6.2848	0.1772	16.65	6.8126	0.1567	10.10
<i>KLF3</i>	870066	870066	6.6619	0.2573	76.99	6.8326	0.1878	23.38
<i>TLR10</i>	620441	620441	7.0345	0.2849	95.46	7.1901	0.2475	74.01
<i>TLR10</i>	4480543	4480543	7.2663	0.2598	99.29	7.5259	0.2111	97.50
<i>TLR1</i>	6520451	6520451	8.6078	0.6854	100.00	8.8020	0.4736	99.77
<i>TLR6</i>	5340427	5340427	6.9367	0.3128	92.03	7.1400	0.2286	68.10
<i>TMEM156</i>	2000364	2000364	7.2607	0.3112	99.39	8.0348	0.3653	99.09
<i>TMEM156</i>	3870088	3390253	6.3821	0.1608	34.91	6.8371	0.1379	16.00

Displayed is the mean and standard deviation (SD) of the quantile normalized and log₂-transformed gene expression data as well as the amount of significant expressed probes (detection p-value < 0.05)

eTable 1B. Characteristics of the Probe at *1q23.3* Used for *cis*-eQTL Analysis in SHIP-TREND and RS-III

Gene	Array Address ID		SHIP-TREND			RS-III		
	HT-12 v3	HT-12 v4	Mean expression	SD expression	Significant expressed Probes [%]	Mean expression	SD expression	Significant expressed Probes [%]
<i>SDHC</i>	6200241	6200241	7.8232	0.3870	100.00	8.2353	0.2180	100.00
<i>SDHC</i>	1090301	1090301	7.7570	0.2336	100.00	7.0715	0.2140	57.89
<i>FCGR2A</i>	6520048	6590437	7.9612	0.3636	99.80	7.8653	0.3587	97.73
<i>FCGR2A</i>	1990278	1990278	11.4887	0.5431	100.00	11.0409	0.4593	99.89
<i>FCGR2A</i>	450762	450762	9.5815	0.4889	100.00	10.4638	0.4721	99.89
<i>HSPA6</i>	1710553	1710553	8.0661	0.4194	99.90	8.1485	0.3760	99.43
<i>HSPA6</i>	160092	160092	10.8988	0.3767	100.00	10.4557	0.4387	100.00
<i>FCGR3A</i>	4050039	4050039	7.6802	0.7492	95.36	8.5940	0.6258	99.77
<i>FCGR3A</i>	3610431	3610431	7.0193	0.3492	97.07	8.1785	0.6132	98.98
<i>HSPA7</i>	830709	830709	6.5592	0.2455	68.11	7.1243	0.1783	72.08
<i>FCGR3B</i>	7210114	7210114	8.9866	0.5628	100.00	10.9708	0.6792	100.00
<i>FCGR3B</i>	1450139	1450139	10.7310	0.5098	99.90	12.2535	0.5521	99.89
<i>FCGR2B</i>	6650341	6650341	6.5289	0.2631	59.84	8.0154	0.3064	99.77
<i>FCGR2B</i>	7550215	7550215	6.4125	0.2511	43.79	7.0259	0.1582	50.96
<i>FCGR2B</i>	2480717	2480717	6.2408	0.1882	13.93	7.0936	0.1744	66.74
<i>FCRLA</i>	3780193	3780193	7.9134	0.4962	99.39	8.0386	0.6058	94.55
<i>FCRLB</i>	4730204	4730204	6.8194	0.2244	92.94	7.3280	0.1767	94.78
<i>DUSP12</i>	460280	460280	8.2476	0.2629	100.00	8.2228	0.2237	99.77

Displayed is the mean and standard deviation (SD) of the quantile normalized and log₂-transformed gene expression data as well as the amount of significant expressed probes (detection p-value < 0.05)

eTable 2. GWA Meta-analysis Results Using Random-Effects Model

	Fixed Effects Model		Random-Effects Model		Total variability due to heterogeneity	Total variability / sampling variability
	OR (95% CI)	p-value	OR (95% CI)	p-value		
rs10004195						
Meta-Analysis	0.70 (0.65-0.76)	1.4x10 ⁻¹⁸	0.69 (0.61-0.79)	6.5x10 ⁻⁹	56.52%	2.3
rs368433						
Meta-Analysis	0.73 (0.65-0.81)	2.1x10 ⁻⁸	0.73 (0.65-0.82)	9.2x10 ⁻⁸	7.83%	1.08

Abbreviations: OR = Odds Ratio, CI = Confidence Interval.

eTable 3. Results of the GWA Meta-analysis for all SNPs Within the Genomic Region or in a ± 100 Kilobase Window Around the Genes *TLR9*, *TLR2*, and *TLR4*

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs920160	3	52132766	<i>WDR51A</i>	0	C	0.084	0.88 (0.78-0.99)	0.029
rs9809977	3	52141187	<i>WDR51A</i>	0	C	0.063	1.08 (0.95-1.22)	0.264
rs9841469	3	52141636	<i>WDR51A</i>	0	A	0.063	1.08 (0.95-1.22)	0.258
rs4687809	3	52143015	<i>WDR51A</i>	0	A	0.084	0.88 (0.78-0.99)	0.029
rs4687810	3	52144135	<i>WDR51A</i>	0	C	0.146	0.96 (0.88-1.05)	0.348
rs2334961	3	52148665	<i>WDR51A</i>	0	C	0.146	0.96 (0.88-1.05)	0.348
rs735768	3	52150010	<i>WDR51A</i>	0	G	0.146	0.96 (0.88-1.05)	0.369
rs893055	3	52152388	<i>WDR51A</i>	0	C	0.146	0.96 (0.87-1.05)	0.352
rs17051977	3	52157984	<i>WDR51A</i>	0	C	0.063	1.08 (0.95-1.23)	0.249
rs2304505	3	52159800	<i>WDR51A</i>	0	C	0.063	1.08 (0.95-1.23)	0.245
rs6786592	3	52171281	<i>WDR51A</i>	7821	C	0.147	0.96 (0.87-1.05)	0.357
rs171294	3	52178639	<i>WDR51A</i>	15179	G	0.063	1.08 (0.95-1.23)	0.24
rs352148	3	52183938	<i>WDR51A</i>	20478	C	0.063	1.08 (0.95-1.23)	0.236
rs352149	3	52184570	<i>WDR51A</i>	21110	A	0.063	1.08 (0.95-1.23)	0.244
rs352151	3	52185312	<i>ALAS1</i>	21843	G	0.063	1.08 (0.95-1.23)	0.241
rs352152	3	52185740	<i>ALAS1</i>	21415	T	0.149	0.98 (0.89-1.08)	0.639
rs353556	3	52186862	<i>ALAS1</i>	20293	G	0.203	0.95 (0.87-1.04)	0.286
rs3852070	3	52187701	<i>ALAS1</i>	19454	C	0.443	0.94 (0.84-1.06)	0.296
rs352158	3	52192744	<i>ALAS1</i>	14411	C	0.451	0.99 (0.93-1.06)	0.866
rs614288	3	52195243	<i>ALAS1</i>	11912	T	0.441	1 (0.93-1.07)	0.962
rs352173	3	52204135	<i>ALAS1</i>	3020	G	0.03	1.09 (0.89-1.34)	0.418
rs181274	3	52208901	<i>ALAS1</i>	0	T	0.448	0.99 (0.93-1.06)	0.785
rs352171	3	52209243	<i>ALAS1</i>	0	A	0.452	0.99 (0.93-1.06)	0.796
rs352170	3	52211117	<i>ALAS1</i>	0	A	0.452	0.99 (0.93-1.06)	0.838
rs352169	3	52211802	<i>ALAS1</i>	0	G	0.452	0.99 (0.93-1.06)	0.825
rs352168	3	52213010	<i>ALAS1</i>	0	C	0.452	0.99 (0.93-1.06)	0.827
rs352167	3	52213696	<i>ALAS1</i>	0	T	0.447	0.99 (0.93-1.06)	0.796

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs352166	3	52213717	ALAS1	0	C	0.447	0.99 (0.93-1.06)	0.815
rs352165	3	52217942	ALAS1	0	A	0.447	0.99 (0.93-1.06)	0.797
rs11712164	3	52219091	ALAS1	0	T	0.442	1.01 (0.95-1.08)	0.768
rs352163	3	52222150	ALAS1	0	G	0.447	1 (0.93-1.06)	0.892
rs164640	3	52222354	ALAS1	0	C	0.447	1 (0.93-1.06)	0.896
rs352162	3	52228009	TLR9	2128	T	0.442	0.99 (0.93-1.06)	0.865
rs352140	3	52231737	TLR9	0	C	0.45	1 (0.93-1.07)	0.965
rs352139	3	52233412	TLR9	0	T	0.445	1 (0.93-1.06)	0.921
rs187084	3	52236071	TLR9	852	G	0.427	1 (0.94-1.07)	0.978
rs352143	3	52239947	TWF2	0	C	0.199	0.99 (0.91-1.07)	0.749
rs164637	3	52240255	TWF2	0	A	0.051	0.96 (0.83-1.12)	0.632
rs352142	3	52241422	TWF2	0	C	0.053	1 (0.86-1.17)	0.984
rs11717574	3	52243286	TWF2	0	C	0.145	1.01 (0.93-1.11)	0.76
rs353547	3	52243906	TWF2	0	T	0.423	1 (0.94-1.06)	0.932
rs4082828	3	52249782	TWF2	1559	C	0.11	1 (0.91-1.11)	0.97
rs7618915	3	52254634	PPM1M	630	A	0.354	1 (0.93-1.06)	0.92
rs11715391	3	52255418	PPM1M	0	T	0.11	1 (0.91-1.11)	0.967
rs1060330	3	52263985	WDR82	0	T	0.482	1.01 (0.94-1.07)	0.848
rs1767	3	52265514	WDR82	0	G	0.115	1 (0.91-1.11)	0.924
rs1769	3	52265590	WDR82	0	G	0.11	1 (0.9-1.11)	0.989
rs11717018	3	52268899	WDR82	0	G	0.11	1 (0.91-1.11)	0.968
rs7614727	3	52270935	WDR82	0	C	0.482	1.01 (0.94-1.07)	0.839
rs6793317	3	52274026	WDR82	0	C	0.115	1 (0.91-1.11)	0.928
rs7643913	3	52278253	WDR82	0	A	0.098	1 (0.9-1.12)	0.932
rs6445358	3	52283885	WDR82	0	C	0.482	1.01 (0.94-1.07)	0.847
rs6809248	3	52284378	WDR82	0	G	0.115	1 (0.91-1.11)	0.928
rs9844183	3	52290232	WDR82	2533	G	0.166	1 (0.91-1.09)	0.936

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs11707938	3	52294255	GLYCTK	2656	C	0.015	0.96 (0.63-1.47)	0.853
rs13071708	3	52297720	GLYCTK	0	A	0.023	0.86 (0.63-1.18)	0.357
rs3796343	3	52299209	GLYCTK	0	G	0.158	1.01 (0.93-1.1)	0.816
rs3733063	3	52303573	GLYCTK	1041	A	0.115	1 (0.91-1.11)	0.932
rs11708811	3	52303647	GLYCTK	1115	T	0.11	1 (0.91-1.11)	0.964
rs17052051	3	52306306	GLYCTK	3774	G	0.11	1 (0.91-1.11)	0.968
rs17052052	3	52306833	GLYCTK	4301	G	0.11	1 (0.91-1.11)	0.969
rs7622851	3	52308711	GLYCTK	6179	C	0.482	1.01 (0.94-1.07)	0.867
rs17052053	3	52309633	GLYCTK	7101	C	0.115	1.01 (0.91-1.11)	0.901
rs17052054	3	52312794	GLYCTK	10262	T	0.109	1 (0.9-1.1)	0.946
rs9311474	3	52313892	GLYCTK	11360	T	0.482	1 (0.94-1.07)	0.882
rs10461027	3	52316166	DNAH1	9393	A	0.11	1 (0.91-1.11)	0.966
rs3844291	3	52316255	DNAH1	9304	C	0.354	1 (0.93-1.06)	0.909
rs17052057	3	52316666	DNAH1	8893	T	0.016	1.12 (0.82-1.53)	0.486
rs699469	3	52317569	DNAH1	7990	G	0.136	1.04 (0.95-1.14)	0.414
rs10460962	3	52318719	DNAH1	6840	T	0.111	1 (0.91-1.11)	0.962
rs17052058	3	52319720	DNAH1	5839	G	0.166	1 (0.92-1.09)	0.973
rs6445385	3	52320499	DNAH1	5060	G	0.111	1 (0.91-1.11)	0.956
rs17052061	3	52321280	DNAH1	4279	G	0.166	1 (0.92-1.09)	0.979
rs730050	3	52323404	DNAH1	2155	A	0.357	1.01 (0.94-1.09)	0.764
rs3852064	3	52324452	DNAH1	1107	T	0.354	1 (0.93-1.06)	0.895
rs6445386	3	52325252	DNAH1	307	G	0.166	1 (0.92-1.09)	0.987
rs17052068	3	52327904	DNAH1	0	T	0.162	1 (0.91-1.09)	0.944
rs13064343	3	52332126	DNAH1	0	A	0.023	0.87 (0.64-1.19)	0.386
rs11711934	3	52333157	DNAH1	0	C	0.168	1 (0.92-1.09)	0.957
rs11707931	3	52333457	DNAH1	0	G	0.163	1 (0.92-1.09)	0.976
rs6796333	3	52334718	DNAH1	0	C	0.173	1.01 (0.92-1.1)	0.862
rs11710014	3	52335012	DNAH1	0	T	0.113	1.01 (0.91-1.12)	0.849

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs6857611	4	154725642	KIAA0922	0	G	0.011	1.31 (0.93-1.82)	0.118
rs10517574	4	154730293	KIAA0922	0	A	0.322	1 (0.94-1.07)	0.949
rs10222829	4	154730353	KIAA0922	0	C	0.027	0.89 (0.67-1.19)	0.434
rs1036615	4	154730588	KIAA0922	0	G	0.032	0.88 (0.66-1.16)	0.356
rs7664062	4	154732597	KIAA0922	0	T	0.334	1 (0.93-1.07)	0.973
rs1371158	4	154732981	KIAA0922	0	G	0.334	1 (0.93-1.07)	0.973
rs7669418	4	154733077	KIAA0922	0	G	0.336	1 (0.93-1.07)	0.983
rs7669741	4	154733172	KIAA0922	0	T	0.334	1 (0.93-1.07)	0.977
rs893628	4	154733306	KIAA0922	0	C	0.363	0.99 (0.93-1.06)	0.824
rs7670485	4	154733377	KIAA0922	0	C	0.334	1 (0.93-1.07)	0.972
rs13133464	4	154733995	KIAA0922	0	C	0.335	1 (0.93-1.07)	0.962
rs17370297	4	154734415	KIAA0922	0	C	0.336	1 (0.93-1.07)	0.963
rs12511694	4	154735206	KIAA0922	0	G	0.027	0.89 (0.67-1.18)	0.425
rs13147188	4	154735510	KIAA0922	0	A	0.337	1 (0.93-1.07)	0.965
rs13147416	4	154735631	KIAA0922	0	A	0.364	0.99 (0.93-1.06)	0.811
rs13147431	4	154735650	KIAA0922	0	A	0.337	1 (0.93-1.07)	0.981
rs1371156	4	154736189	KIAA0922	0	A	0.337	1 (0.93-1.07)	0.977
rs7690932	4	154736744	KIAA0922	0	T	0.338	1 (0.93-1.07)	0.978
rs7696772	4	154737479	KIAA0922	0	A	0.338	1 (0.93-1.07)	0.968
rs7697047	4	154737777	KIAA0922	0	A	0.338	1 (0.93-1.07)	0.967
rs12507192	4	154737794	KIAA0922	0	A	0.021	0.79 (0.55-1.12)	0.18
rs7655793	4	154738030	KIAA0922	0	T	0.338	1 (0.93-1.07)	0.962
rs7656141	4	154738075	KIAA0922	0	T	0.338	1 (0.93-1.07)	0.963
rs11943070	4	154739868	KIAA0922	0	A	0.338	1 (0.93-1.07)	0.965
rs9990596	4	154740230	KIAA0922	0	C	0.338	1 (0.93-1.07)	0.963
rs11734684	4	154741024	KIAA0922	0	A	0.347	0.99 (0.92-1.06)	0.778
rs11099889	4	154741113	KIAA0922	0	A	0.326	1 (0.93-1.07)	0.995
rs3891364	4	154741448	KIAA0922	0	C	0.347	0.99 (0.92-1.06)	0.777

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs3810766	4	154742647	KIAA0922	0	C	0.326	1 (0.93-1.07)	0.98
rs1063151	4	154744908	KIAA0922	0	T	0.117	1.05 (0.94-1.17)	0.431
rs12510162	4	154745944	KIAA0922	0	T	0.031	0.7 (0.49-0.99)	0.046
rs17030220	4	154746889	KIAA0922	0	G	0.072	1.13 (0.92-1.4)	0.237
rs10517575	4	154747065	KIAA0922	0	G	0.074	0.95 (0.82-1.1)	0.469
rs7686634	4	154747933	KIAA0922	0	C	0.397	1.01 (0.94-1.07)	0.839
rs6821970	4	154750089	KIAA0922	0	A	0.407	1.01 (0.95-1.08)	0.687
rs17030238	4	154751114	KIAA0922	0	G	0.029	1.02 (0.75-1.39)	0.897
rs13135353	4	154751497	KIAA0922	0	G	0.405	1.01 (0.94-1.08)	0.768
rs6535929	4	154753478	KIAA0922	0	C	0.028	1.35 (0.96-1.91)	0.087
rs1550344	4	154756174	KIAA0922	0	G	0.442	1.02 (0.95-1.09)	0.551
rs6535930	4	154759506	KIAA0922	0	T	0.362	0.98 (0.92-1.05)	0.559
rs17370492	4	154759980	KIAA0922	0	T	0.022	0.73 (0.4-1.32)	0.293
rs7674639	4	154760193	KIAA0922	0	T	0.365	0.98 (0.92-1.05)	0.591
rs11099891	4	154760746	KIAA0922	0	T	0.452	1.01 (0.94-1.08)	0.843
rs2241839	4	154763007	KIAA0922	0	A	0.431	1 (0.94-1.08)	0.922
rs2289319	4	154763717	KIAA0922	0	A	0.499	0.99 (0.89-1.1)	0.819
rs17030263	4	154768359	KIAA0922	0	T	0.016	0.74 (0.46-1.2)	0.229
rs6535932	4	154769113	KIAA0922	0	C	0.467	0.97 (0.9-1.04)	0.357
rs2083288	4	154770053	KIAA0922	0	T	0.254	1 (0.91-1.1)	0.987
rs2083290	4	154770175	KIAA0922	0	A	0.016	0.83 (0.51-1.36)	0.462
rs893631	4	154770562	KIAA0922	0	G	0.021	0.82 (0.58-1.16)	0.261
rs11099892	4	154773143	KIAA0922	0	G	0.41	0.95 (0.86-1.04)	0.236
rs2278576	4	154776248	KIAA0922	0	C	0.183	0.95 (0.85-1.06)	0.356
rs7687239	4	154778414	KIAA0922	1102	A	0.351	0.97 (0.87-1.07)	0.51
rs2033831	4	154778601	KIAA0922	1289	A	0.223	0.97 (0.89-1.05)	0.466
rs6851477	4	154778939	KIAA0922	1627	A	0.086	0.87 (0.74-1.03)	0.099
rs10517576	4	154781073	KIAA0922	3761	C	0.039	0.97 (0.78-1.21)	0.808

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs6835748	4	154782219	<i>KIAA0922</i>	4907	G	0.075	0.93 (0.8-1.07)	0.31
rs1025748	4	154783347	<i>KIAA0922</i>	6035	G	0.261	0.97 (0.9-1.05)	0.49
rs12650674	4	154788298	<i>KIAA0922</i>	10986	T	0.237	0.97 (0.88-1.06)	0.45
rs7656224	4	154791020	<i>KIAA0922</i>	13708	A	0.448	0.97 (0.9-1.05)	0.455
rs10007443	4	154792701	<i>KIAA0922</i>	15389	T	0.26	0.96 (0.89-1.05)	0.391
rs6819564	4	154799243	<i>KIAA0922</i>	21931	G	0.3	0.98 (0.91-1.06)	0.639
rs6819788	4	154799374	<i>KIAA0922</i>	22062	G	0.019	0.69 (0.49-0.96)	0.029
rs17279573	4	154799738	<i>KIAA0922</i>	22426	G	0.168	1.01 (0.93-1.1)	0.813
rs1595625	4	154804041	<i>TLR2</i>	20849	A	0.458	0.98 (0.92-1.05)	0.593
rs1595626	4	154804158	<i>TLR2</i>	20732	A	0.212	1 (0.92-1.08)	0.954
rs1595627	4	154804312	<i>TLR2</i>	20578	T	0.212	1 (0.92-1.08)	0.95
rs4696477	4	154804865	<i>TLR2</i>	20025	A	0.212	1 (0.92-1.08)	0.952
rs11727442	4	154805372	<i>TLR2</i>	19518	A	0.167	1.01 (0.93-1.1)	0.816
rs11736691	4	154806043	<i>TLR2</i>	18847	C	0.036	0.79 (0.65-0.96)	0.016
rs17030307	4	154808052	<i>TLR2</i>	16838	G	0.08	0.93 (0.83-1.05)	0.253
rs4629430	4	154808480	<i>TLR2</i>	16410	G	0.42	1.02 (0.96-1.09)	0.506
rs17370673	4	154809174	<i>TLR2</i>	15716	C	0.167	1.01 (0.92-1.1)	0.879
rs6835636	4	154809799	<i>TLR2</i>	15091	A	0.414	1.02 (0.96-1.09)	0.468
rs6814974	4	154810701	<i>TLR2</i>	14189	T	0.281	1.06 (0.98-1.14)	0.174
rs4696187	4	154814328	<i>TLR2</i>	10562	C	0.167	1.01 (0.92-1.1)	0.889
rs13150331	4	154819072	<i>TLR2</i>	5818	G	0.419	0.97 (0.91-1.04)	0.377
rs1898830	4	154827903	<i>TLR2</i>	0	G	0.347	1.01 (0.94-1.08)	0.85
rs1816702	4	154828973	<i>TLR2</i>	0	T	0.12	0.91 (0.82-1.01)	0.074
rs11099894	4	154834044	<i>TLR2</i>	0	T	0.016	1.12 (0.64-1.96)	0.694
rs4696483	4	154838705	<i>TLR2</i>	0	T	0.134	0.94 (0.85-1.03)	0.189
rs11938228	4	154841396	<i>TLR2</i>	0	A	0.355	0.97 (0.91-1.04)	0.384
rs3804099	4	154844106	<i>TLR2</i>	0	C	0.446	1.01 (0.95-1.08)	0.699
rs3804100	4	154844859	<i>TLR2</i>	0	C	0.065	0.95 (0.83-1.08)	0.442

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs5743704	4	154845401	<i>TLR2</i>	0	A	0.041	0.97 (0.81-1.15)	0.695
rs5743708	4	154845767	<i>TLR2</i>	0	A	0.057	1.16 (0.93-1.43)	0.18
rs7656411	4	154847105	<i>TLR2</i>	413	G	0.238	1.04 (0.97-1.12)	0.254
rs1339	4	154851013	<i>RNF175</i>	0	C	0.196	0.98 (0.91-1.07)	0.687
rs1337	4	154851037	<i>RNF175</i>	0	G	0.229	0.99 (0.92-1.07)	0.807
rs11935252	4	154851512	<i>RNF175</i>	0	G	0.33	1 (0.93-1.07)	0.922
rs17030340	4	154852288	<i>RNF175</i>	0	A	0.16	1.06 (0.97-1.16)	0.19
rs2289318	4	154853184	<i>RNF175</i>	0	C	0.216	0.98 (0.9-1.06)	0.567
rs7695605	4	154854886	<i>RNF175</i>	0	G	0.248	0.97 (0.9-1.04)	0.402
rs1036614	4	154858555	<i>RNF175</i>	0	T	0.018	0.97 (0.54-1.74)	0.921
rs7654018	4	154859117	<i>RNF175</i>	0	G	0.343	1.01 (0.94-1.08)	0.861
rs11936681	4	154859981	<i>RNF175</i>	0	A	0.33	1 (0.93-1.06)	0.886
rs11945694	4	154860007	<i>RNF175</i>	0	C	0.33	1 (0.93-1.07)	0.899
rs2606319	4	154860302	<i>RNF175</i>	0	A	0.367	0.99 (0.93-1.06)	0.844
rs1439166	4	154860939	<i>RNF175</i>	0	T	0.367	0.99 (0.93-1.06)	0.866
rs11733149	4	154861088	<i>RNF175</i>	0	C	0.04	1.02 (0.86-1.2)	0.839
rs12509119	4	154861140	<i>RNF175</i>	0	A	0.33	1 (0.93-1.07)	0.942
rs1439165	4	154861722	<i>RNF175</i>	0	G	0.33	1 (0.93-1.07)	0.963
rs2606322	4	154862672	<i>RNF175</i>	0	G	0.037	1.01 (0.86-1.2)	0.893
rs17279789	4	154862695	<i>RNF175</i>	0	C	0.26	0.98 (0.91-1.06)	0.626
rs1869947	4	154862953	<i>RNF175</i>	0	G	0.037	0.99 (0.84-1.17)	0.899
rs1439167	4	154863700	<i>RNF175</i>	0	T	0.376	1.02 (0.95-1.08)	0.645
rs10517577	4	154863987	<i>RNF175</i>	0	C	0.26	0.98 (0.91-1.06)	0.632
rs2118861	4	154864257	<i>RNF175</i>	0	C	0.33	1 (0.93-1.07)	0.95
rs11727144	4	154864631	<i>RNF175</i>	0	C	0.2	0.97 (0.9-1.05)	0.528
rs10006303	4	154864673	<i>RNF175</i>	0	A	0.258	0.98 (0.91-1.06)	0.67
rs10440446	4	154864921	<i>RNF175</i>	0	A	0.335	1 (0.94-1.07)	0.941
rs2124641	4	154865260	<i>RNF175</i>	0	T	0.201	0.97 (0.9-1.05)	0.497

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs2579907	4	154865820	RNF175	0	A	0.036	1 (0.84-1.19)	0.996
rs16998891	4	154865869	RNF175	0	G	0.201	0.97 (0.9-1.05)	0.506
rs10021447	4	154865909	RNF175	0	G	0.201	0.98 (0.9-1.06)	0.531
rs10021631	4	154866125	RNF175	0	C	0.201	0.97 (0.9-1.05)	0.507
rs2606343	4	154866202	RNF175	0	G	0.036	1 (0.84-1.18)	0.978
rs1530105	4	154866444	RNF175	0	G	0.201	0.97 (0.9-1.05)	0.523
rs10517578	4	154867602	RNF175	0	T	0.037	1.02 (0.87-1.21)	0.775
rs4426759	4	154869556	RNF175	0	C	0.499	1.04 (0.98-1.11)	0.224
rs6835960	4	154869910	RNF175	0	A	0.231	0.97 (0.9-1.05)	0.457
rs6835640	4	154869944	RNF175	0	T	0.231	0.97 (0.9-1.05)	0.447
rs17030382	4	154870337	RNF175	0	G	0.195	0.97 (0.89-1.05)	0.43
rs17370965	4	154870398	RNF175	0	T	0.231	0.97 (0.9-1.05)	0.447
rs981843	4	154871435	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.524
rs981844	4	154871478	RNF175	0	G	0.271	0.98 (0.91-1.05)	0.511
rs2579918	4	154871684	RNF175	0	C	0.271	0.98 (0.91-1.05)	0.527
rs2606324	4	154871897	RNF175	0	G	0.271	0.98 (0.91-1.05)	0.526
rs2579917	4	154872098	RNF175	0	G	0.271	0.98 (0.91-1.05)	0.525
rs2606325	4	154872131	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.525
rs2606327	4	154873079	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.52
rs2606328	4	154873314	RNF175	0	T	0.266	0.98 (0.91-1.06)	0.643
rs2251997	4	154873517	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.536
rs2251994	4	154873547	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.519
rs2251900	4	154873595	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.53
rs4145338	4	154873773	RNF175	0	C	0.037	0.99 (0.84-1.18)	0.942
rs2606329	4	154874093	RNF175	0	C	0.271	0.98 (0.91-1.05)	0.519
rs1371161	4	154874621	RNF175	0	C	0.307	0.99 (0.92-1.07)	0.754
rs12504286	4	154875651	RNF175	0	T	0.499	1.04 (0.98-1.11)	0.226
rs6848765	4	154875710	RNF175	0	T	0.499	1.04 (0.98-1.11)	0.226

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs2405431	4	154875846	RNF175	0	G	0.271	0.98 (0.91-1.05)	0.518
rs12504447	4	154875949	RNF175	0	T	0.332	1 (0.94-1.08)	0.922
rs2606335	4	154875986	RNF175	0	C	0.271	0.98 (0.91-1.05)	0.514
rs2606337	4	154876295	RNF175	0	T	0.272	0.97 (0.9-1.05)	0.454
rs8180349	4	154876488	RNF175	0	C	0.231	0.97 (0.9-1.05)	0.456
rs2263434	4	154877762	RNF175	0	G	0.271	0.98 (0.91-1.05)	0.514
rs2606341	4	154878152	RNF175	0	C	0.271	0.98 (0.91-1.05)	0.513
rs2445617	4	154878478	RNF175	0	C	0.499	1.04 (0.98-1.11)	0.23
rs1585110	4	154880394	RNF175	0	T	0.124	1.07 (0.95-1.21)	0.282
rs6827685	4	154881677	RNF175	0	T	0.284	0.99 (0.92-1.06)	0.697
rs12648400	4	154881881	RNF175	0	T	0.499	1.04 (0.98-1.11)	0.234
rs17298985	4	154883711	RNF175	0	T	0.271	0.98 (0.91-1.05)	0.528
rs17371021	4	154883745	RNF175	0	A	0.271	0.98 (0.91-1.05)	0.534
rs11931479	4	154883973	RNF175	0	G	0.037	0.99 (0.84-1.17)	0.91
rs11099896	4	154884147	RNF175	0	G	0.232	0.97 (0.9-1.05)	0.473
rs11099898	4	154884471	RNF175	0	T	0.499	1.04 (0.98-1.11)	0.231
rs12647687	4	154884663	RNF175	0	C	0.499	1.04 (0.98-1.11)	0.231
rs12641631	4	154884729	RNF175	0	G	0.195	0.97 (0.9-1.05)	0.499
rs10517579	4	154885771	RNF175	0	C	0.271	0.97 (0.91-1.05)	0.476
rs1598632	4	154886832	RNF175	0	G	0.499	1.04 (0.98-1.11)	0.212
rs11099899	4	154887037	RNF175	0	G	0.499	1.04 (0.98-1.11)	0.21
rs6851366	4	154887879	RNF175	0	C	0.499	1.04 (0.98-1.11)	0.21
rs11099900	4	154888921	RNF175	0	T	0.232	0.97 (0.9-1.05)	0.467
rs4637381	4	154889706	RNF175	0	G	0.499	1.04 (0.98-1.11)	0.213
rs5020754	4	154889894	RNF175	0	C	0.198	0.97 (0.9-1.06)	0.537
rs12643219	4	154890248	RNF175	0	C	0.194	0.97 (0.9-1.05)	0.517
rs17030417	4	154890263	RNF175	0	G	0.037	0.99 (0.83-1.16)	0.859
rs17299034	4	154890846	RNF175	0	G	0.271	0.97 (0.91-1.05)	0.453

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs17299041	4	154892577	<i>RNF175</i>	0	C	0.271	0.97 (0.91-1.05)	0.453
rs11946638	4	154893545	<i>RNF175</i>	0	T	0.037	0.99 (0.83-1.16)	0.861
rs13121180	4	154893642	<i>RNF175</i>	0	A	0.342	1.01 (0.94-1.08)	0.801
rs11099902	4	154893728	<i>RNF175</i>	0	C	0.499	1.04 (0.98-1.11)	0.209
rs12512426	4	154894051	<i>RNF175</i>	0	T	0.499	1.04 (0.98-1.11)	0.209
rs6857680	4	154897813	<i>RNF175</i>	0	A	0.463	0.96 (0.9-1.03)	0.241
rs4696491	4	154899315	<i>RNF175</i>	0	T	0.194	0.98 (0.91-1.06)	0.662
rs10009844	4	154901026	<i>RNF175</i>	189	C	0.308	0.97 (0.9-1.04)	0.338
rs6841173	4	154902013	<i>RNF175</i>	1176	T	0.285	0.94 (0.88-1.01)	0.117
rs1020702	4	154905162	<i>RNF175</i>	4325	A	0.311	0.97 (0.91-1.04)	0.382
rs11099905	4	154905633	<i>RNF175</i>	4796	T	0.188	0.98 (0.91-1.07)	0.662
rs17030422	4	154907490	<i>RNF175</i>	6653	G	0.037	0.98 (0.83-1.16)	0.818
rs4696495	4	154910629	<i>RNF175</i>	9792	G	0.037	0.98 (0.83-1.16)	0.816
rs11099906	4	154911140	<i>SFRP2</i>	10051	T	0.188	0.98 (0.9-1.06)	0.567
rs7653960	4	154916880	<i>SFRP2</i>	4311	T	0.311	0.97 (0.91-1.04)	0.386
rs11099909	4	154918283	<i>SFRP2</i>	2908	A	0.028	1.09 (0.84-1.4)	0.529
rs12639885	4	154919824	<i>SFRP2</i>	1367	A	0.187	0.98 (0.9-1.06)	0.57
rs10014299	4	154920308	<i>SFRP2</i>	883	G	0.187	0.98 (0.9-1.06)	0.57
rs17030428	4	154921733	<i>SFRP2</i>	0	C	0.037	0.98 (0.83-1.16)	0.851
rs17030432	4	154922910	<i>SFRP2</i>	0	A	0.037	0.98 (0.83-1.16)	0.857
rs17030434	4	154923046	<i>SFRP2</i>	0	C	0.188	0.97 (0.9-1.06)	0.517
rs17030437	4	154923675	<i>SFRP2</i>	0	A	0.278	0.98 (0.91-1.05)	0.537
rs6853435	4	154925466	<i>SFRP2</i>	0	A	0.499	1.04 (0.98-1.11)	0.233
rs6853522	4	154925670	<i>SFRP2</i>	0	A	0.188	0.97 (0.9-1.06)	0.516
rs3810765	4	154928930	<i>SFRP2</i>	0	A	0.499	1.04 (0.98-1.11)	0.235
rs4643790	4	154929304	<i>SFRP2</i>	0	A	0.169	1.06 (0.97-1.17)	0.175
rs11937424	4	154930636	<i>SFRP2</i>	958	A	0.334	1.02 (0.95-1.1)	0.531
rs12645134	4	154932880	<i>SFRP2</i>	3202	C	0.188	0.97 (0.9-1.05)	0.506

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs1456389	4	154933566	<i>SFRP2</i>	3888	T	0.5	1.04 (0.98-1.11)	0.22
rs952211	4	154937266	<i>SFRP2</i>	7588	C	0.188	0.97 (0.9-1.05)	0.49
rs11732581	4	154939688	<i>SFRP2</i>	10010	T	0.037	0.98 (0.83-1.16)	0.841
rs1456391	4	154939935	<i>SFRP2</i>	10257	G	0.188	0.97 (0.9-1.05)	0.481
rs732681	4	154944569	<i>SFRP2</i>	14891	A	0.465	0.96 (0.9-1.03)	0.235
rs1106708	4	154946307	<i>SFRP2</i>	16629	A	0.464	0.96 (0.9-1.03)	0.257
rs10026531	4	154946520	<i>SFRP2</i>	16842	A	0.188	0.97 (0.9-1.05)	0.489
rs1410850	9	119406886	<i>TLR4</i>	99544	T	0.175	0.99 (0.91-1.07)	0.731
rs1410849	9	119406996	<i>TLR4</i>	99434	C	0.192	1.02 (0.94-1.11)	0.596
rs7846865	9	119407193	<i>TLR4</i>	99237	C	0.021	0.88 (0.68-1.13)	0.323
rs17186662	9	119408297	<i>TLR4</i>	98133	A	0.045	0.98 (0.83-1.14)	0.771
rs10983712	9	119408557	<i>TLR4</i>	97873	C	0.365	1 (0.94-1.07)	0.947
rs4837402	9	119408696	<i>TLR4</i>	97734	A	0.175	0.99 (0.91-1.07)	0.744
rs7875849	9	119408849	<i>TLR4</i>	97581	G	0.191	1.02 (0.94-1.11)	0.605
rs10983715	9	119410227	<i>TLR4</i>	96203	T	0.015	1.07 (0.81-1.4)	0.632
rs13299223	9	119411227	<i>TLR4</i>	95203	T	0.05	0.89 (0.74-1.06)	0.2
rs7047007	9	119411355	<i>TLR4</i>	95075	C	0.453	0.99 (0.93-1.06)	0.855
rs11788798	9	119412661	<i>TLR4</i>	93769	C	0.03	1.04 (0.85-1.29)	0.688
rs1329055	9	119412703	<i>TLR4</i>	93727	T	0.145	0.98 (0.9-1.08)	0.707
rs2039126	9	119413742	<i>TLR4</i>	92688	A	0.191	1.02 (0.94-1.11)	0.603
rs2039125	9	119413754	<i>TLR4</i>	92676	A	0.199	1.03 (0.95-1.11)	0.515
rs4837409	9	119414115	<i>TLR4</i>	92315	A	0.32	0.98 (0.92-1.05)	0.565
rs9299254	9	119414216	<i>TLR4</i>	92214	G	0.453	0.99 (0.93-1.06)	0.863
rs10491854	9	119414301	<i>TLR4</i>	92129	T	0.247	1.01 (0.94-1.09)	0.813
rs1013985	9	119414729	<i>TLR4</i>	91701	C	0.453	0.99 (0.93-1.06)	0.863
rs1329053	9	119415942	<i>TLR4</i>	90488	G	0.19	1.02 (0.94-1.11)	0.608
rs10983716	9	119415955	<i>TLR4</i>	90475	C	0.075	0.96 (0.85-1.09)	0.552
rs7038943	9	119416999	<i>TLR4</i>	89431	C	0.365	1 (0.94-1.07)	0.938

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs10983717	9	119417293	<i>TLR4</i>	89137	T	0.089	0.98 (0.88-1.1)	0.714
rs4837414	9	119417575	<i>TLR4</i>	88855	T	0.145	0.98 (0.9-1.08)	0.7
rs1928295	9	119418304	<i>TLR4</i>	88126	C	0.453	0.99 (0.93-1.06)	0.859
rs12555132	9	119418503	<i>TLR4</i>	87927	C	0.038	1.08 (0.92-1.28)	0.353
rs9408902	9	119418785	<i>TLR4</i>	87645	G	0.453	0.99 (0.93-1.06)	0.866
rs1077206	9	119419698	<i>TLR4</i>	86732	T	0.038	1.08 (0.92-1.28)	0.35
rs9299255	9	119420307	<i>TLR4</i>	86123	C	0.453	0.99 (0.93-1.06)	0.865
rs1329056	9	119421355	<i>TLR4</i>	85075	T	0.19	1.02 (0.94-1.11)	0.632
rs9409189	9	119422748	<i>TLR4</i>	83682	C	0.453	0.99 (0.93-1.06)	0.87
rs7038925	9	119423543	<i>TLR4</i>	82887	A	0.19	1.02 (0.94-1.11)	0.631
rs12685267	9	119424637	<i>TLR4</i>	81793	A	0.145	0.98 (0.9-1.08)	0.707
rs10818053	9	119424888	<i>TLR4</i>	81542	C	0.089	0.98 (0.88-1.09)	0.702
rs716570	9	119427049	<i>TLR4</i>	79381	A	0.168	1 (0.91-1.09)	0.946
rs10983720	9	119427308	<i>TLR4</i>	79122	T	0.365	1 (0.94-1.07)	0.924
rs4443732	9	119428597	<i>TLR4</i>	77833	G	0.247	1.01 (0.94-1.09)	0.79
rs4443733	9	119428873	<i>TLR4</i>	77557	C	0.453	1 (0.93-1.06)	0.88
rs10283900	9	119428990	<i>TLR4</i>	77440	A	0.075	0.96 (0.85-1.09)	0.542
rs1155928	9	119429286	<i>TLR4</i>	77144	T	0.247	1.01 (0.94-1.09)	0.788
rs1887904	9	119430103	<i>TLR4</i>	76327	A	0.32	0.98 (0.92-1.05)	0.563
rs17187347	9	119431809	<i>TLR4</i>	74621	C	0.247	1.01 (0.94-1.09)	0.772
rs10983723	9	119434372	<i>TLR4</i>	72058	C	0.189	1.02 (0.94-1.1)	0.652
rs10491853	9	119437440	<i>TLR4</i>	68990	G	0.039	1.08 (0.92-1.27)	0.338
rs16905915	9	119437986	<i>TLR4</i>	68444	C	0.039	1.08 (0.92-1.27)	0.334
rs7026557	9	119438206	<i>TLR4</i>	68224	C	0.189	1.02 (0.94-1.1)	0.655
rs7026576	9	119438241	<i>TLR4</i>	68189	A	0.175	0.99 (0.91-1.07)	0.729
rs7032255	9	119439908	<i>TLR4</i>	66522	A	0.365	1 (0.94-1.07)	0.902
rs10491852	9	119441690	<i>TLR4</i>	64740	G	0.189	1.02 (0.94-1.1)	0.651
rs957512	9	119445526	<i>TLR4</i>	60904	C	0.35	1 (0.93-1.07)	0.965

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs12001662	9	119445830	<i>TLR4</i>	60600	T	0.438	0.99 (0.93-1.06)	0.78
rs1329065	9	119448271	<i>TLR4</i>	58159	T	0.033	1.08 (0.9-1.29)	0.4
rs4837462	9	119450040	<i>TLR4</i>	56390	G	0.476	0.99 (0.93-1.06)	0.797
rs765419	9	119452135	<i>TLR4</i>	54295	C	0.476	0.99 (0.93-1.06)	0.799
rs7020245	9	119452898	<i>TLR4</i>	53532	T	0.489	0.99 (0.93-1.06)	0.825
rs7034845	9	119453013	<i>TLR4</i>	53417	G	0.412	1.01 (0.95-1.08)	0.764
rs10818061	9	119453560	<i>TLR4</i>	52870	C	0.321	1 (0.93-1.07)	0.908
rs4836693	9	119453769	<i>TLR4</i>	52661	C	0.154	0.99 (0.9-1.08)	0.815
rs7024352	9	119453776	<i>TLR4</i>	52654	C	0.026	0.94 (0.76-1.15)	0.548
rs928052	9	119454033	<i>TLR4</i>	52397	G	0.474	0.99 (0.93-1.05)	0.686
rs13293271	9	119454590	<i>TLR4</i>	51840	A	0.474	0.99 (0.93-1.05)	0.686
rs16905925	9	119455831	<i>TLR4</i>	50599	G	0.13	1 (0.91-1.1)	0.977
rs10983735	9	119455887	<i>TLR4</i>	50543	A	0.154	0.99 (0.9-1.08)	0.793
rs10983736	9	119456069	<i>TLR4</i>	50361	A	0.154	0.99 (0.9-1.08)	0.792
rs10983737	9	119456223	<i>TLR4</i>	50207	G	0.08	0.97 (0.87-1.1)	0.662
rs1887905	9	119456941	<i>TLR4</i>	49489	C	0.473	0.99 (0.93-1.05)	0.695
rs12375686	9	119456993	<i>TLR4</i>	49437	G	0.081	0.97 (0.87-1.1)	0.666
rs12375692	9	119457078	<i>TLR4</i>	49352	G	0.081	0.97 (0.87-1.1)	0.666
rs10983738	9	119457144	<i>TLR4</i>	49286	T	0.039	1.12 (0.95-1.32)	0.184
rs12686163	9	119457710	<i>TLR4</i>	48720	A	0.154	0.99 (0.9-1.08)	0.797
rs16905939	9	119457793	<i>TLR4</i>	48637	G	0.028	1.05 (0.87-1.27)	0.621
rs913615	9	119457939	<i>TLR4</i>	48491	C	0.473	0.99 (0.93-1.05)	0.695
rs1329066	9	119458129	<i>TLR4</i>	48301	G	0.128	1 (0.91-1.1)	0.993
rs745507	9	119458580	<i>TLR4</i>	47850	C	0.067	1.07 (0.94-1.22)	0.323
rs1329067	9	119462020	<i>TLR4</i>	44410	A	0.128	1 (0.91-1.1)	0.991
rs16905962	9	119462953	<i>TLR4</i>	43477	C	0.028	1.05 (0.87-1.28)	0.602
rs1928296	9	119463408	<i>TLR4</i>	43022	T	0.473	0.99 (0.93-1.05)	0.683
rs1329068	9	119463524	<i>TLR4</i>	42906	G	0.473	0.99 (0.93-1.05)	0.683

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs1410851	9	119464417	<i>TLR4</i>	42013	G	0.168	1 (0.92-1.09)	0.932
rs1410852	9	119464729	<i>TLR4</i>	41701	G	0.473	0.99 (0.93-1.05)	0.683
rs7037542	9	119466039	<i>TLR4</i>	40391	A	0.168	1.01 (0.93-1.1)	0.871
rs7026433	9	119466290	<i>TLR4</i>	40140	T	0.193	0.99 (0.92-1.08)	0.86
rs11788318	9	119466329	<i>TLR4</i>	40101	G	0.472	0.99 (0.93-1.05)	0.687
rs10983741	9	119467140	<i>TLR4</i>	39290	C	0.472	0.99 (0.93-1.05)	0.687
rs1854447	9	119467220	<i>TLR4</i>	39210	A	0.317	0.98 (0.91-1.05)	0.553
rs1854448	9	119467305	<i>TLR4</i>	39125	G	0.317	0.98 (0.91-1.05)	0.555
rs10739495	9	119467736	<i>TLR4</i>	38694	A	0.192	0.99 (0.92-1.08)	0.856
rs10448253	9	119469292	<i>TLR4</i>	37138	A	0.081	0.98 (0.87-1.1)	0.691
rs13294726	9	119470318	<i>TLR4</i>	36112	T	0.472	0.99 (0.93-1.05)	0.687
rs16905976	9	119471100	<i>TLR4</i>	35330	T	0.028	1.05 (0.86-1.27)	0.63
rs7039637	9	119471324	<i>TLR4</i>	35106	C	0.202	1 (0.92-1.08)	0.961
rs7039756	9	119471366	<i>TLR4</i>	35064	A	0.202	1 (0.92-1.08)	0.96
rs10818066	9	119473222	<i>TLR4</i>	33208	C	0.229	0.99 (0.92-1.07)	0.79
rs2039124	9	119473338	<i>TLR4</i>	33092	T	0.162	1 (0.92-1.09)	0.984
rs10983744	9	119474903	<i>TLR4</i>	31527	T	0.212	0.98 (0.91-1.07)	0.714
rs4837494	9	119475962	<i>TLR4</i>	30468	T	0.144	1.02 (0.94-1.12)	0.595
rs10818067	9	119476882	<i>TLR4</i>	29548	T	0.184	0.96 (0.88-1.04)	0.304
rs1329061	9	119476938	<i>TLR4</i>	29492	G	0.329	0.98 (0.92-1.05)	0.638
rs1329060	9	119478298	<i>TLR4</i>	28132	T	0.143	1.03 (0.94-1.12)	0.591
rs1329057	9	119481767	<i>TLR4</i>	24663	C	0.192	1 (0.92-1.08)	0.983
rs1928297	9	119483076	<i>TLR4</i>	23354	T	0.249	1 (0.93-1.07)	0.961
rs12339064	9	119483117	<i>TLR4</i>	23313	A	0.081	0.96 (0.85-1.08)	0.467
rs960312	9	119483600	<i>TLR4</i>	22830	G	0.143	1.03 (0.94-1.12)	0.587
rs10491851	9	119484346	<i>TLR4</i>	22084	A	0.282	1.03 (0.96-1.11)	0.417
rs1252041	9	119484618	<i>TLR4</i>	21812	A	0.114	0.99 (0.9-1.09)	0.853
rs1360092	9	119484664	<i>TLR4</i>	21766	C	0.329	0.98 (0.92-1.05)	0.627

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs1252040	9	119484829	<i>TLR4</i>	21601	C	0.08	0.96 (0.85-1.08)	0.466
rs3904153	9	119485038	<i>TLR4</i>	21392	G	0.329	0.98 (0.92-1.05)	0.627
rs1252039	9	119485355	<i>TLR4</i>	21075	T	0.08	0.96 (0.85-1.08)	0.461
rs13296664	9	119486517	<i>TLR4</i>	19913	T	0.282	1.03 (0.96-1.11)	0.412
rs1928298	9	119486647	<i>TLR4</i>	19783	C	0.329	0.98 (0.92-1.05)	0.622
rs16906007	9	119487219	<i>TLR4</i>	19211	A	0.047	0.95 (0.82-1.11)	0.519
rs10818068	9	119487268	<i>TLR4</i>	19162	A	0.329	0.98 (0.92-1.05)	0.631
rs16906010	9	119487508	<i>TLR4</i>	18922	G	0.061	0.98 (0.85-1.12)	0.741
rs1252038	9	119488319	<i>TLR4</i>	18111	G	0.081	0.95 (0.84-1.07)	0.411
rs1360093	9	119488961	<i>TLR4</i>	17469	C	0.329	0.98 (0.92-1.05)	0.64
rs1360094	9	119489287	<i>TLR4</i>	17143	A	0.329	0.98 (0.92-1.05)	0.645
rs12346837	9	119489321	<i>TLR4</i>	17109	A	0.08	0.96 (0.85-1.08)	0.467
rs12337637	9	119489428	<i>TLR4</i>	17002	G	0.08	0.96 (0.85-1.08)	0.467
rs4837495	9	119490586	<i>TLR4</i>	15844	T	0.317	0.97 (0.91-1.04)	0.397
rs4837496	9	119490619	<i>TLR4</i>	15811	A	0.25	1 (0.93-1.07)	0.945
rs7873159	9	119490834	<i>TLR4</i>	15596	A	0.25	1 (0.93-1.07)	0.9
rs1252037	9	119491226	<i>TLR4</i>	15204	T	0.057	0.94 (0.82-1.08)	0.395
rs10818069	9	119493792	<i>TLR4</i>	12638	A	0.079	0.96 (0.85-1.08)	0.526
rs10818070	9	119496316	<i>TLR4</i>	10114	A	0.079	0.96 (0.85-1.09)	0.537
rs10983754	9	119498428	<i>TLR4</i>	8002	T	0.079	0.96 (0.85-1.08)	0.512
rs11789302	9	119499347	<i>TLR4</i>	7083	G	0.281	1.03 (0.96-1.1)	0.448
rs10759930	9	119501442	<i>TLR4</i>	4988	T	0.392	0.99 (0.93-1.06)	0.879
rs10513308	9	119502074	<i>TLR4</i>	4356	T	0.035	0.9 (0.75-1.08)	0.267
rs2737191	9	119502536	<i>TLR4</i>	3894	G	0.281	1.03 (0.96-1.1)	0.487
rs2770150	9	119502960	<i>TLR4</i>	3470	G	0.282	1.03 (0.96-1.1)	0.47
rs11536855	9	119503534	<i>TLR4</i>	2896	A	0.01	1.05 (0.64-1.75)	0.837
rs10116253	9	119504141	<i>TLR4</i>	2289	C	0.251	0.99 (0.92-1.07)	0.809
rs10983755	9	119504491	<i>TLR4</i>	1939	A	0.03	1.14 (0.95-1.38)	0.152

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs1927914	9	119504546	<i>TLR4</i>	1884	G	0.329	0.98 (0.91-1.05)	0.534
rs7866214	9	119504939	<i>TLR4</i>	1491	C	0.029	0.94 (0.77-1.15)	0.553
rs10759932	9	119504965	<i>TLR4</i>	1465	C	0.145	1.03 (0.94-1.12)	0.586
rs10818073	9	119507397	<i>TLR4</i>	0	T	0.062	0.91 (0.79-1.04)	0.158
rs12344353	9	119508470	<i>TLR4</i>	0	C	0.062	0.91 (0.79-1.04)	0.155
rs7864330	9	119509371	<i>TLR4</i>	0	G	0.062	0.91 (0.79-1.04)	0.167
rs11536869	9	119509653	<i>TLR4</i>	0	G	0.041	1.08 (0.92-1.28)	0.361
rs1927911	9	119509875	<i>TLR4</i>	0	A	0.251	0.99 (0.92-1.07)	0.812
rs11536879	9	119512032	<i>TLR4</i>	0	G	0.033	1 (0.83-1.2)	0.966
rs12377632	9	119512551	<i>TLR4</i>	0	C	0.39	1 (0.93-1.06)	0.936
rs1927907	9	119512585	<i>TLR4</i>	0	T	0.145	1.02 (0.93-1.13)	0.631
rs10983756	9	119513001	<i>TLR4</i>	0	T	0.062	0.9 (0.79-1.04)	0.145
rs2770146	9	119513159	<i>TLR4</i>	0	C	0.299	1.04 (0.97-1.11)	0.291
rs5030717	9	119513655	<i>TLR4</i>	0	G	0.12	0.98 (0.88-1.08)	0.62
rs2149356	9	119514020	<i>TLR4</i>	0	T	0.312	0.97 (0.9-1.04)	0.337
rs5030728	9	119514103	<i>TLR4</i>	0	A	0.297	1.04 (0.97-1.11)	0.319
rs4986790	9	119515123	<i>TLR4</i>	0	G	0.062	0.9 (0.79-1.03)	0.129
rs4986791	9	119515423	<i>TLR4</i>	0	T	0.062	0.9 (0.79-1.03)	0.131
rs5030721	9	119516186	<i>TLR4</i>	0	A	0.024	0.94 (0.67-1.31)	0.709
rs7869402	9	119517853	<i>TLR4</i>	0	T	0.03	1.16 (0.96-1.39)	0.127
rs11536889	9	119517952	<i>TLR4</i>	0	C	0.137	1.01 (0.92-1.11)	0.827
rs7873784	9	119518757	<i>TLR4</i>	0	C	0.148	0.95 (0.86-1.04)	0.239
rs11536897	9	119519831	<i>TLR4</i>	244	A	0.048	0.94 (0.81-1.1)	0.467
rs1927906	9	119519936	<i>TLR4</i>	349	C	0.093	0.99 (0.88-1.1)	0.801
rs11536898	9	119520031	<i>TLR4</i>	444	A	0.118	0.95 (0.86-1.05)	0.349
rs1554973	9	119520633	<i>TLR4</i>	1046	C	0.242	0.96 (0.89-1.03)	0.252
rs7044464	9	119521218	<i>TLR4</i>	1631	A	0.149	0.95 (0.86-1.04)	0.242
rs7856729	9	119521677	<i>TLR4</i>	2090	T	0.15	0.95 (0.86-1.04)	0.241

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs7846989	9	119522761	<i>TLR4</i>	3174	C	0.093	0.99 (0.88-1.1)	0.81
rs7860896	9	119522924	<i>TLR4</i>	3337	G	0.093	0.99 (0.88-1.1)	0.81
rs7037225	9	119523460	<i>TLR4</i>	3873	T	0.153	0.96 (0.88-1.05)	0.408
rs7037117	9	119523484	<i>TLR4</i>	3897	G	0.255	0.95 (0.88-1.02)	0.191
rs752998	9	119523597	<i>TLR4</i>	4010	T	0.243	0.96 (0.89-1.03)	0.241
rs913930	9	119523830	<i>TLR4</i>	4243	G	0.357	1.04 (0.97-1.11)	0.267
rs2183016	9	119525036	<i>TLR4</i>	5449	C	0.145	0.95 (0.86-1.05)	0.307
rs1927905	9	119525129	<i>TLR4</i>	5542	C	0.053	0.92 (0.8-1.07)	0.288
rs7045953	9	119525616	<i>TLR4</i>	6029	G	0.148	0.96 (0.88-1.06)	0.426
rs10759934	9	119528817	<i>TLR4</i>	9230	A	0.492	0.97 (0.91-1.04)	0.367
rs7025144	9	119536208	<i>TLR4</i>	16621	T	0.272	1 (0.93-1.08)	0.991
rs10465133	9	119537779	<i>TLR4</i>	18192	G	0.431	0.98 (0.92-1.05)	0.55
rs7034482	9	119540354	<i>TLR4</i>	20767	G	0.271	1 (0.93-1.07)	0.944
rs7866830	9	119542086	<i>TLR4</i>	22499	A	0.219	0.97 (0.9-1.05)	0.41
rs7870814	9	119543095	<i>TLR4</i>	23508	A	0.496	0.98 (0.92-1.04)	0.519
rs7860332	9	119543329	<i>TLR4</i>	23742	T	0.495	0.98 (0.92-1.04)	0.532
rs10759938	9	119544034	<i>TLR4</i>	24447	C	0.457	1.03 (0.97-1.1)	0.37
rs10818076	9	119544847	<i>TLR4</i>	25260	G	0.457	1.03 (0.97-1.1)	0.372
rs10983764	9	119546128	<i>TLR4</i>	26541	C	0.457	1.03 (0.97-1.1)	0.377
rs10818079	9	119549214	<i>TLR4</i>	29627	G	0.458	1.03 (0.97-1.1)	0.366
rs10983766	9	119549669	<i>TLR4</i>	30082	G	0.458	1.03 (0.97-1.1)	0.365
rs17323923	9	119549702	<i>TLR4</i>	30115	T	0.092	0.97 (0.87-1.09)	0.616
rs7350246	9	119549972	<i>TLR4</i>	30385	C	0.47	1.04 (0.97-1.1)	0.29
rs10818080	9	119550001	<i>TLR4</i>	30414	T	0.458	1.03 (0.97-1.1)	0.356
rs10818081	9	119550185	<i>TLR4</i>	30598	C	0.471	1.04 (0.98-1.11)	0.227
rs17330490	9	119550720	<i>TLR4</i>	31133	G	0.093	0.97 (0.87-1.08)	0.588
rs10818083	9	119551132	<i>TLR4</i>	31545	G	0.458	1.03 (0.97-1.1)	0.369
rs756136	9	119552087	<i>TLR4</i>	32500	C	0.458	1.03 (0.97-1.1)	0.367

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs756135	9	119552260	<i>TLR4</i>	32673	T	0.458	1.03 (0.96-1.1)	0.391
rs943840	9	119552361	<i>TLR4</i>	32774	C	0.452	1.03 (0.97-1.1)	0.347
rs17421726	9	119552652	<i>TLR4</i>	33065	T	0.092	0.97 (0.87-1.09)	0.616
rs7846760	9	119552688	<i>TLR4</i>	33101	C	0.458	1.03 (0.97-1.1)	0.365
rs7860993	9	119553006	<i>TLR4</i>	33419	T	0.458	1.03 (0.97-1.1)	0.375
rs10759939	9	119553261	<i>TLR4</i>	33674	A	0.458	1.03 (0.97-1.1)	0.376
rs10739498	9	119553617	<i>TLR4</i>	34030	A	0.458	1.03 (0.97-1.1)	0.379
rs10818084	9	119553922	<i>TLR4</i>	34335	A	0.457	1.03 (0.96-1.1)	0.415
rs10739499	9	119554082	<i>TLR4</i>	34495	C	0.324	1 (0.93-1.07)	0.973
rs10818085	9	119554092	<i>TLR4</i>	34505	T	0.181	0.97 (0.89-1.06)	0.526
rs1999066	9	119554285	<i>TLR4</i>	34698	G	0.325	1 (0.93-1.07)	0.999
rs1999065	9	119554395	<i>TLR4</i>	34808	T	0.325	1 (0.93-1.07)	0.996
rs10739501	9	119554504	<i>TLR4</i>	34917	C	0.325	1 (0.93-1.07)	0.986
rs2225207	9	119554591	<i>TLR4</i>	35004	C	0.325	1 (0.93-1.07)	0.985
rs10759941	9	119555490	<i>TLR4</i>	35903	G	0.355	0.99 (0.92-1.06)	0.733
rs2149355	9	119556094	<i>TLR4</i>	36507	A	0.231	1 (0.93-1.08)	0.981
rs2149354	9	119556621	<i>TLR4</i>	37034	A	0.231	1 (0.93-1.08)	0.981
rs2149353	9	119556664	<i>TLR4</i>	37077	A	0.231	1 (0.93-1.08)	0.981
rs3945581	9	119556792	<i>TLR4</i>	37205	T	0.231	1 (0.93-1.08)	0.981
rs7848124	9	119556947	<i>TLR4</i>	37360	A	0.216	0.99 (0.91-1.07)	0.744
rs1887780	9	119557377	<i>TLR4</i>	37790	G	0.231	1 (0.93-1.08)	0.98
rs4837502	9	119557665	<i>TLR4</i>	38078	G	0.233	1 (0.93-1.08)	0.99
rs4837503	9	119557703	<i>TLR4</i>	38116	G	0.231	1 (0.93-1.08)	0.979
rs10983772	9	119557801	<i>TLR4</i>	38214	T	0.231	1 (0.93-1.08)	0.996
rs10114960	9	119557880	<i>TLR4</i>	38293	T	0.221	0.99 (0.92-1.08)	0.9
rs10123941	9	119557983	<i>TLR4</i>	38396	C	0.253	0.99 (0.92-1.06)	0.738
rs10123955	9	119557995	<i>TLR4</i>	38408	C	0.231	1 (0.93-1.08)	0.988
rs10124679	9	119558206	<i>TLR4</i>	38619	G	0.236	1.01 (0.93-1.08)	0.886

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs10118506	9	119558218	<i>TLR4</i>	38631	A	0.231	1 (0.93-1.08)	0.987
rs10124632	9	119558239	<i>TLR4</i>	38652	C	0.231	1 (0.93-1.08)	0.997
rs7021145	9	119558337	<i>TLR4</i>	38750	T	0.438	0.97 (0.91-1.04)	0.394
rs7036316	9	119558612	<i>TLR4</i>	39025	G	0.231	1 (0.93-1.08)	0.997
rs10818087	9	119558680	<i>TLR4</i>	39093	G	0.206	0.96 (0.89-1.04)	0.309
rs1927902	9	119558812	<i>TLR4</i>	39225	T	0.231	1 (0.93-1.08)	0.991
rs1927900	9	119558976	<i>TLR4</i>	39389	G	0.231	1 (0.93-1.08)	0.991
rs1927899	9	119559025	<i>TLR4</i>	39438	T	0.231	1 (0.93-1.08)	0.999
rs7039838	9	119559295	<i>TLR4</i>	39708	A	0.212	1 (0.92-1.08)	0.92
rs1927898	9	119559515	<i>TLR4</i>	39928	C	0.231	1 (0.93-1.08)	0.999
rs1927897	9	119559586	<i>TLR4</i>	39999	G	0.414	0.98 (0.92-1.05)	0.586
rs1927896	9	119559699	<i>TLR4</i>	40112	A	0.231	1 (0.93-1.08)	0.989
rs4259480	9	119559912	<i>TLR4</i>	40325	A	0.429	0.97 (0.91-1.04)	0.381
rs4595203	9	119559957	<i>TLR4</i>	40370	G	0.231	1 (0.93-1.08)	0.988
rs7026297	9	119559971	<i>TLR4</i>	40384	T	0.231	1 (0.93-1.08)	0.988
rs7026522	9	119560098	<i>TLR4</i>	40511	T	0.184	1.01 (0.93-1.1)	0.733
rs7041060	9	119560158	<i>TLR4</i>	40571	C	0.436	0.97 (0.91-1.04)	0.416
rs12335791	9	119560233	<i>TLR4</i>	40646	G	0.206	0.96 (0.89-1.04)	0.341
rs1927894	9	119560529	<i>TLR4</i>	40942	A	0.436	0.97 (0.91-1.04)	0.417
rs1927893	9	119560567	<i>TLR4</i>	40980	A	0.436	0.97 (0.91-1.04)	0.417
rs1927892	9	119560615	<i>TLR4</i>	41028	T	0.436	0.97 (0.91-1.04)	0.417
rs10983776	9	119560953	<i>TLR4</i>	41366	T	0.442	0.97 (0.91-1.03)	0.34
rs17421927	9	119561760	<i>TLR4</i>	42173	G	0.047	0.95 (0.82-1.11)	0.55
rs12337267	9	119561825	<i>TLR4</i>	42238	C	0.231	1 (0.93-1.08)	0.984
rs7038716	9	119562433	<i>TLR4</i>	42846	T	0.231	1 (0.93-1.08)	0.983
rs10759943	9	119562694	<i>TLR4</i>	43107	A	0.184	1.01 (0.93-1.1)	0.753
rs7027711	9	119563999	<i>TLR4</i>	44412	G	0.184	1.01 (0.93-1.1)	0.752
rs10983777	9	119565801	<i>TLR4</i>	46214	G	0.206	0.96 (0.89-1.04)	0.313

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs17422114	9	119565832	<i>TLR4</i>	46245	G	0.047	0.95 (0.82-1.11)	0.554
rs10983778	9	119565933	<i>TLR4</i>	46346	A	0.191	1.02 (0.94-1.11)	0.608
rs4837505	9	119566153	<i>TLR4</i>	46566	A	0.184	1.02 (0.94-1.11)	0.657
rs10983781	9	119568239	<i>TLR4</i>	48652	T	0.184	0.97 (0.89-1.06)	0.521
rs1927890	9	119568427	<i>TLR4</i>	48840	T	0.184	1.02 (0.94-1.11)	0.651
rs10818088	9	119569415	<i>TLR4</i>	49828	G	0.238	0.97 (0.9-1.05)	0.42
rs17331131	9	119570843	<i>TLR4</i>	51256	C	0.048	0.96 (0.82-1.12)	0.58
rs4474091	9	119571518	<i>TLR4</i>	51931	T	0.184	1.02 (0.94-1.11)	0.631
rs1475546	9	119573243	<i>TLR4</i>	53656	T	0.441	0.98 (0.92-1.05)	0.553
rs10983782	9	119573326	<i>TLR4</i>	53739	A	0.16	0.96 (0.88-1.05)	0.43
rs4837506	9	119573818	<i>TLR4</i>	54231	C	0.059	1.01 (0.87-1.16)	0.926
rs928177	9	119573894	<i>TLR4</i>	54307	T	0.166	1.01 (0.92-1.1)	0.867
rs10983783	9	119574487	<i>TLR4</i>	54900	G	0.423	0.98 (0.92-1.05)	0.582
rs7357627	9	119575166	<i>TLR4</i>	55579	A	0.398	0.99 (0.92-1.06)	0.706
rs10739502	9	119576335	<i>TLR4</i>	56748	T	0.307	1 (0.93-1.07)	0.948
rs7046020	9	119576672	<i>TLR4</i>	57085	T	0.307	1 (0.93-1.07)	0.956
rs17331249	9	119576729	<i>TLR4</i>	57142	C	0.194	1 (0.92-1.09)	0.925
rs7030459	9	119577167	<i>TLR4</i>	57580	C	0.307	0.99 (0.93-1.07)	0.885
rs7855252	9	119577609	<i>TLR4</i>	58022	T	0.307	1 (0.93-1.07)	0.904
rs13302141	9	119577665	<i>TLR4</i>	58078	T	0.122	0.99 (0.9-1.09)	0.852
rs2149366	9	119577700	<i>TLR4</i>	58113	A	0.167	1 (0.92-1.09)	0.968
rs7032054	9	119578801	<i>TLR4</i>	59214	C	0.141	1 (0.91-1.09)	0.959
rs7046641	9	119578844	<i>TLR4</i>	59257	A	0.141	1 (0.91-1.09)	0.958
rs1927937	9	119579291	<i>TLR4</i>	59704	G	0.307	1 (0.93-1.07)	0.902
rs1927936	9	119579791	<i>TLR4</i>	60204	A	0.307	1 (0.93-1.07)	0.902
rs1927935	9	119579852	<i>TLR4</i>	60265	A	0.167	1 (0.92-1.09)	0.954
rs1927934	9	119580111	<i>TLR4</i>	60524	C	0.362	1.02 (0.95-1.09)	0.586
rs1927933	9	119580125	<i>TLR4</i>	60538	A	0.195	1.01 (0.93-1.1)	0.773

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs10759945	9	119580451	<i>TLR4</i>	60864	A	0.498	1 (0.94-1.06)	0.931
rs17331469	9	119580725	<i>TLR4</i>	61138	T	0.141	1 (0.91-1.1)	1
rs17422633	9	119581388	<i>TLR4</i>	61801	G	0.096	0.95 (0.85-1.07)	0.42
rs7028772	9	119581905	<i>TLR4</i>	62318	G	0.307	1 (0.93-1.07)	0.904
rs7045117	9	119581932	<i>TLR4</i>	62345	C	0.141	1 (0.91-1.09)	0.979
rs1927932	9	119582235	<i>TLR4</i>	62648	C	0.307	1 (0.93-1.07)	0.912
rs10983786	9	119582351	<i>TLR4</i>	62764	A	0.307	1 (0.93-1.07)	0.912
rs12342312	9	119582675	<i>TLR4</i>	63088	A	0.307	1 (0.93-1.07)	0.91
rs2149364	9	119582809	<i>TLR4</i>	63222	T	0.307	1 (0.93-1.07)	0.905
rs12342472	9	119582997	<i>TLR4</i>	63410	C	0.307	1 (0.93-1.07)	0.908
rs12337657	9	119583050	<i>TLR4</i>	63463	C	0.307	1 (0.93-1.07)	0.905
rs7018934	9	119583091	<i>TLR4</i>	63504	T	0.335	1.01 (0.94-1.08)	0.823
rs10983787	9	119583265	<i>TLR4</i>	63678	C	0.307	1 (0.93-1.07)	0.906
rs10983788	9	119583528	<i>TLR4</i>	63941	G	0.307	1 (0.93-1.07)	0.906
rs13299731	9	119583983	<i>TLR4</i>	64396	C	0.141	1 (0.91-1.1)	0.989
rs12338997	9	119584075	<i>TLR4</i>	64488	A	0.141	1 (0.91-1.1)	0.997
rs12339950	9	119584157	<i>TLR4</i>	64570	A	0.141	1 (0.91-1.1)	0.997
rs12340150	9	119584677	<i>TLR4</i>	65090	A	0.141	1 (0.91-1.1)	0.997
rs12349310	9	119585039	<i>TLR4</i>	65452	G	0.141	1 (0.91-1.1)	0.997
rs10983791	9	119585271	<i>TLR4</i>	65684	A	0.096	0.95 (0.85-1.07)	0.421
rs4416895	9	119585308	<i>TLR4</i>	65721	C	0.499	0.99 (0.93-1.06)	0.873
rs7045671	9	119585629	<i>TLR4</i>	66042	A	0.307	1 (0.93-1.07)	0.921
rs7046116	9	119585954	<i>TLR4</i>	66367	C	0.195	1.01 (0.94-1.1)	0.732
rs16906215	9	119586079	<i>TLR4</i>	66492	G	0.167	1 (0.91-1.09)	0.929
rs12342445	9	119586164	<i>TLR4</i>	66577	T	0.141	1 (0.91-1.1)	0.993
rs12342558	9	119586202	<i>TLR4</i>	66615	A	0.141	1 (0.91-1.1)	0.993
rs1411434	9	119586819	<i>TLR4</i>	67232	G	0.335	1.01 (0.94-1.08)	0.803
rs1411433	9	119586851	<i>TLR4</i>	67264	A	0.499	0.99 (0.93-1.06)	0.866

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs12352822	9	119587103	<i>TLR4</i>	67516	G	0.14	1 (0.91-1.1)	0.994
rs12348755	9	119587593	<i>TLR4</i>	68006	C	0.141	1 (0.91-1.1)	0.994
rs12555783	9	119587714	<i>TLR4</i>	68127	G	0.195	1.01 (0.94-1.1)	0.728
rs12344131	9	119587830	<i>TLR4</i>	68243	A	0.141	1 (0.91-1.1)	0.999
rs2149363	9	119587923	<i>TLR4</i>	68336	C	0.335	1.01 (0.94-1.08)	0.794
rs4837507	9	119588619	<i>TLR4</i>	69032	T	0.167	1 (0.92-1.09)	0.954
rs4836703	9	119588755	<i>TLR4</i>	69168	G	0.167	1 (0.92-1.09)	0.959
rs7021846	9	119592261	<i>TLR4</i>	72674	G	0.17	1.01 (0.93-1.1)	0.734
rs12352294	9	119595606	<i>TLR4</i>	76019	C	0.183	0.99 (0.91-1.07)	0.743
rs4604518	9	119595666	<i>TLR4</i>	76079	A	0.449	0.99 (0.93-1.05)	0.726
rs17423464	9	119596250	<i>TLR4</i>	76663	C	0.183	0.99 (0.91-1.07)	0.743
rs1927926	9	119596376	<i>TLR4</i>	76789	A	0.171	1.01 (0.93-1.1)	0.744
rs2225208	9	119596427	<i>TLR4</i>	76840	T	0.171	1.01 (0.93-1.1)	0.744
rs10123709	9	119597947	<i>TLR4</i>	78360	T	0.183	0.99 (0.91-1.07)	0.743
rs17423610	9	119598207	<i>TLR4</i>	78620	C	0.183	0.99 (0.91-1.07)	0.743
rs10115586	9	119598832	<i>TLR4</i>	79245	T	0.353	1 (0.93-1.07)	0.958
rs10116360	9	119599543	<i>TLR4</i>	79956	A	0.183	0.99 (0.91-1.07)	0.743
rs10125349	9	119599567	<i>TLR4</i>	79980	T	0.183	0.99 (0.91-1.07)	0.743
rs10119246	9	119599627	<i>TLR4</i>	80040	G	0.183	0.99 (0.91-1.07)	0.736
rs10125456	9	119599701	<i>TLR4</i>	80114	A	0.183	0.99 (0.91-1.07)	0.736
rs1927924	9	119599797	<i>TLR4</i>	80210	A	0.171	1.01 (0.93-1.1)	0.736
rs16906261	9	119599819	<i>TLR4</i>	80232	C	0.025	1.03 (0.83-1.28)	0.797
rs10125440	9	119599830	<i>TLR4</i>	80243	A	0.183	0.99 (0.91-1.07)	0.736
rs10116431	9	119599865	<i>TLR4</i>	80278	C	0.183	0.99 (0.91-1.07)	0.736
rs2149361	9	119600380	<i>TLR4</i>	80793	C	0.183	0.98 (0.91-1.07)	0.68
rs1927923	9	119602212	<i>TLR4</i>	82625	G	0.171	1.01 (0.93-1.1)	0.736
rs4481682	9	119603089	<i>TLR4</i>	83502	T	0.182	0.98 (0.91-1.07)	0.694
rs13297107	9	119604730	<i>TLR4</i>	85143	T	0.183	0.99 (0.91-1.07)	0.721

SNP	Chr	Pos	Gene	Gene Distance	Minor Allele	MAF	OR (95% CI)	p-value
rs1927922	9	119605057	<i>TLR4</i>	85470	T	0.183	0.99 (0.91-1.07)	0.72
rs1927921	9	119605136	<i>TLR4</i>	85549	C	0.183	0.99 (0.91-1.07)	0.719
rs7849955	9	119605150	<i>TLR4</i>	85563	A	0.171	1.01 (0.93-1.1)	0.736
rs7852849	9	119605315	<i>TLR4</i>	85728	T	0.171	1.01 (0.93-1.1)	0.752
rs17332972	9	119606160	<i>TLR4</i>	86573	G	0.182	0.98 (0.91-1.07)	0.716
rs17333006	9	119606224	<i>TLR4</i>	86637	A	0.182	0.98 (0.91-1.07)	0.716
rs16906265	9	119606610	<i>TLR4</i>	87023	T	0.171	1.01 (0.93-1.1)	0.771
rs9792558	9	119610016	<i>TLR4</i>	90429	C	0.333	0.97 (0.9-1.04)	0.353
rs2149360	9	119610340	<i>TLR4</i>	90753	T	0.198	1.02 (0.95-1.11)	0.55
rs13290714	9	119610613	<i>TLR4</i>	91026	T	0.022	0.75 (0.51-1.08)	0.123
rs7852394	9	119611072	<i>TLR4</i>	91485	C	0.45	0.99 (0.93-1.05)	0.727
rs2149359	9	119611087	<i>TLR4</i>	91500	G	0.182	0.98 (0.91-1.07)	0.691
rs2149358	9	119611129	<i>TLR4</i>	91542	G	0.199	1.02 (0.95-1.11)	0.547
rs10983799	9	119611867	<i>TLR4</i>	92280	A	0.38	1.01 (0.94-1.07)	0.872
rs7859808	9	119612283	<i>TLR4</i>	92696	C	0.199	1.02 (0.95-1.11)	0.553
rs10983800	9	119612373	<i>TLR4</i>	92786	G	0.182	0.98 (0.91-1.07)	0.685
rs10121310	9	119612415	<i>TLR4</i>	92828	A	0.199	1.02 (0.95-1.11)	0.541
rs10739504	9	119613013	<i>TLR4</i>	93426	C	0.38	1.01 (0.94-1.07)	0.867
rs10983803	9	119614184	<i>TLR4</i>	94597	G	0.182	0.98 (0.91-1.07)	0.684
rs4524861	9	119615806	<i>TLR4</i>	96219	T	0.38	1.01 (0.94-1.07)	0.868
rs12341434	9	119616054	<i>TLR4</i>	96467	T	0.182	0.98 (0.91-1.07)	0.684
rs12342517	9	119616208	<i>TLR4</i>	96621	T	0.182	0.98 (0.91-1.07)	0.684
rs10759948	9	119616455	<i>TLR4</i>	96868	C	0.333	0.97 (0.9-1.04)	0.35
rs10818091	9	119616945	<i>TLR4</i>	97358	T	0.333	0.97 (0.91-1.04)	0.356
rs12336133	9	119618941	<i>TLR4</i>	99354	G	0.182	0.98 (0.91-1.07)	0.675

eTable 4. Genome-Wide Significant SNPs From the GWAS Meta-analysis on the Defined Anti-*H pylori* IgG-Titer Phenotype in RS-I, RS-II and SHIP

SNP information					Meta-Analysis		SHIP		RS-I and RS-II	
SNP	nearest Gene	locus	Minor Allele	MAF	OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
rs10004195	TLR10	4p14	A	0.25	0.70 (0.65-0.76)	1.42E-18	0.62 (0.54-0.72)	4.95E-11	0.74 (0.67-0.81)	7.42E-10
rs4833095	TLR1	4p14	C	0.25	0.70 (0.65-0.76)	1.43E-18	0.62 (0.54-0.72)	5.33E-11	0.74 (0.67-0.81)	7.12E-10
rs4543123	TLR1	4p14	G	0.25	0.70 (0.65-0.76)	1.75E-18	0.62 (0.54-0.72)	5.12E-11	0.74 (0.67-0.82)	8.65E-10
rs5743604	TLR1	4p14	G	0.25	0.70 (0.65-0.76)	2.22E-18	0.63 (0.54-0.72)	5.86E-11	0.74 (0.67-0.82)	9.72E-10
rs12233670	TLR10	4p14	T	0.25	0.70 (0.65-0.76)	2.89E-18	0.63 (0.55-0.72)	1.31E-10	0.74 (0.67-0.81)	7.13E-10
rs17616434	TLR1	4p14	C	0.26	0.71 (0.65-0.76)	6.51E-18	0.62 (0.54-0.72)	6.55E-11	0.75 (0.68-0.82)	2.19E-09
rs6815814	TLR1	4p14	C	0.26	0.71 (0.66-0.77)	6.95E-18	0.63 (0.55-0.73)	1.51E-10	0.75 (0.68-0.82)	1.29E-09
rs2101521	TLR1	4p14	A	0.22	0.71 (0.65-0.77)	1.08E-15	0.63 (0.54-0.74)	4.56E-09	0.75 (0.67-0.82)	9.90E-09
rs6835514	FAM114A1	4p14	G	0.26	0.73 (0.67-0.79)	1.08E-15	0.67 (0.58-0.77)	9.75E-09	0.76 (0.69-0.83)	7.61E-09
rs7653908	TLR10	4p14	C	0.22	0.72 (0.66-0.78)	3.60E-15	0.64 (0.55-0.74)	2.74E-09	0.76 (0.68-0.84)	4.63E-08
rs6851685	FAM114A1	4p14	T	0.26	0.73 (0.68-0.79)	3.80E-15	0.68 (0.60-0.78)	5.09E-08	0.76 (0.69-0.83)	7.61E-09
rs7658893	TLR10	4p14	A	0.25	0.74 (0.69-0.80)	9.86E-14	0.68 (0.59-0.78)	5.47E-08	0.77 (0.70-0.85)	1.25E-07
rs5743592	TLR1	4p14	G	0.19	0.72 (0.66-0.78)	1.59E-13	0.61 (0.52-0.71)	7.45E-10	0.77 (0.70-0.86)	1.99E-06
rs11725309	TLR10	4p14	C	0.19	0.72 (0.66-0.79)	2.35E-13	0.62 (0.53-0.73)	3.94E-09	0.77 (0.69-0.85)	1.16E-06
rs5743557	TLR1	4p14	A	0.19	0.72 (0.66-0.79)	4.30E-13	0.62 (0.53-0.73)	2.85E-09	0.78 (0.70-0.86)	2.29E-06
rs7687447	TLR6	4p14	G	0.23	0.74 (0.68-0.81)	5.08E-13	0.67 (0.58-0.77)	3.87E-08	0.78 (0.71-0.86)	5.64E-07
rs5743563	TLR1	4p14	G	0.19	0.73 (0.67-0.79)	5.13E-13	0.63 (0.53-0.73)	3.93E-09	0.78 (0.70-0.86)	2.07E-06
rs5743565	TLR1	4p14	C	0.19	0.73 (0.66-0.79)	5.51E-13	0.63 (0.53-0.73)	3.99E-09	0.78 (0.70-0.86)	2.33E-06
rs5743571	TLR1	4p14	T	0.19	0.73 (0.67-0.79)	6.07E-13	0.63 (0.54-0.73)	4.87E-09	0.78 (0.70-0.86)	2.27E-06
rs7673348	TLR6	4p14	A	0.23	0.74 (0.69-0.81)	6.49E-13	0.67 (0.58-0.77)	3.86E-08	0.78 (0.71-0.86)	6.94E-07
rs5743595	TLR1	4p14	G	0.19	0.73 (0.67-0.79)	7.69E-13	0.64 (0.54-0.74)	1.23E-08	0.77 (0.70-0.86)	1.67E-06
rs3860069	FAM114A1	4p14	C	0.22	0.74 (0.68-0.80)	1.02E-12	0.66 (0.57-0.77)	5.57E-08	0.77 (0.70-0.86)	8.86E-07
rs11466640	TLR10	4p14	A	0.19	0.73 (0.67-0.80)	2.54E-12	0.64 (0.54-0.75)	2.07E-08	0.78 (0.70-0.86)	3.00E-06
rs11466645	TLR10	4p14	T	0.19	0.73 (0.67-0.80)	3.05E-12	0.64 (0.55-0.75)	2.90E-08	0.78 (0.70-0.86)	3.00E-06
rs4274855	TLR10	4p14	T	0.19	0.73 (0.67-0.80)	3.05E-12	0.64 (0.55-0.75)	2.91E-08	0.78 (0.70-0.86)	3.00E-06
rs11466617	TLR10	4p14	C	0.19	0.73 (0.67-0.80)	3.05E-12	0.64 (0.55-0.75)	2.76E-08	0.78 (0.70-0.86)	3.13E-06
rs4129009	TLR10	4p14	C	0.19	0.73 (0.67-0.80)	3.17E-12	0.64 (0.55-0.75)	2.72E-08	0.78 (0.70-0.87)	3.17E-06
rs5743794	TLR6	4p14	T	0.2	0.74 (0.68-0.81)	3.63E-12	0.64 (0.55-0.75)	1.32E-08	0.79 (0.71-0.87)	4.98E-06
rs9761637	TLR10	4p14	G	0.33	0.78 (0.73-0.84)	5.46E-12	0.74 (0.66-0.84)	2.26E-06	0.80 (0.73-0.87)	3.69E-07

SNP information					Meta-Analysis		SHIP		RS-I and RS-II	
SNP	nearest Gene	locus	Minor Allele	MAF	OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
rs5743562	TLR1	4p14	C	0.18	0.73 (0.67-0.80)	7.27E-12	0.62 (0.53-0.74)	1.84E-08	0.78 (0.70-0.87)	7.25E-06
rs10026553	KLF3	4p14	G	0.35	0.78 (0.73-0.84)	8.19E-12	0.75 (0.66-0.84)	1.63E-06	0.80 (0.73-0.87)	7.77E-07
rs2174284	FAM114A1	4p14	T	0.2	0.74 (0.68-0.81)	9.44E-12	0.66 (0.57-0.77)	1.01E-07	0.78 (0.71-0.87)	4.08E-06
rs4540058	TLR10	4p14	A	0.3	0.78 (0.72-0.84)	1.35E-11	0.72 (0.63-0.82)	6.05E-07	0.80 (0.74-0.88)	1.98E-06
rs1873195	FAM114A1	4p14	T	0.2	0.75 (0.69-0.82)	2.35E-11	0.67 (0.58-0.78)	1.86E-07	0.79 (0.71-0.87)	6.20E-06
rs17582921	FAM114A1	4p14	C	0.2	0.75 (0.69-0.82)	2.39E-11	0.67 (0.58-0.78)	1.81E-07	0.79 (0.71-0.87)	6.41E-06
rs5743596	TLR1	4p14	A	0.18	0.73 (0.67-0.80)	2.43E-11	0.64 (0.54-0.75)	6.60E-08	0.78 (0.70-0.87)	1.02E-05
rs1005938	KLF3	4p14	G	0.28	0.77 (0.72-0.84)	2.69E-11	0.73 (0.64-0.83)	2.66E-06	0.80 (0.73-0.87)	1.29E-06
rs17582830	FAM114A1	4p14	G	0.2	0.75 (0.69-0.82)	3.37E-11	0.69 (0.59-0.80)	6.26E-07	0.78 (0.71-0.87)	4.22E-06
rs2890620	KLF3	4p14	C	0.31	0.79 (0.73-0.84)	4.65E-11	0.72 (0.64-0.82)	6.61E-07	0.82 (0.75-0.89)	4.83E-06
rs17582893	FAM114A1	4p14	A	0.2	0.75 (0.69-0.82)	5.01E-11	0.68 (0.59-0.79)	5.68E-07	0.79 (0.71-0.87)	6.23E-06
rs4072590	TLR10	4p14	T	0.3	0.79 (0.73-0.85)	5.12E-11	0.73 (0.65-0.83)	1.17E-06	0.81 (0.75-0.89)	4.08E-06
rs7660102	KLF3	4p14	A	0.24	0.77 (0.71-0.83)	8.07E-11	0.70 (0.61-0.81)	1.04E-06	0.80 (0.73-0.88)	5.73E-06
rs13135770	KLF3	4p14	A	0.24	0.77 (0.71-0.83)	9.58E-11	0.70 (0.61-0.81)	1.04E-06	0.80 (0.73-0.88)	6.95E-06
rs12510962	KLF3	4p14	A	0.24	0.77 (0.71-0.83)	1.00E-10	0.70 (0.61-0.81)	1.11E-06	0.80 (0.73-0.88)	6.95E-06
rs4833103	TLR1	4p14	C	0.47	0.81 (0.76-0.86)	1.09E-10	0.73 (0.65-0.81)	1.33E-08	0.85 (0.79-0.93)	1.25E-04
rs10776483	TLR10	4p14	G	0.22	0.77 (0.71-0.83)	1.46E-10	0.70 (0.61-0.81)	1.34E-06	0.80 (0.72-0.88)	8.67E-06
rs11096956	TLR10	4p14	A	0.22	0.77 (0.71-0.83)	1.56E-10	0.70 (0.61-0.81)	1.30E-06	0.80 (0.72-0.88)	9.41E-06
rs10776482	TLR10	4p14	G	0.22	0.77 (0.71-0.83)	1.57E-10	0.70 (0.61-0.81)	1.35E-06	0.80 (0.72-0.88)	9.17E-06
rs13132956	KLF3	4p14	T	0.2	0.77 (0.71-0.84)	2.69E-09	0.69 (0.59-0.81)	3.99E-06	0.81 (0.73-0.89)	4.40E-05
rs7658334	KLF3	4p14	G	0.43	0.82 (0.76-0.87)	2.70E-09	0.80 (0.71-0.90)	1.61E-04	0.83 (0.76-0.90)	4.07E-06
rs7663292	KLF3	4p14	C	0.43	0.82 (0.76-0.87)	2.88E-09	0.80 (0.71-0.90)	1.60E-04	0.83 (0.76-0.90)	4.38E-06
rs4832786	KLF3	4p14	G	0.43	0.82 (0.77-0.88)	3.93E-09	0.81 (0.72-0.91)	2.47E-04	0.83 (0.76-0.90)	4.07E-06
rs13137984	KLF3	4p14	A	0.43	0.82 (0.77-0.88)	6.98E-09	0.82 (0.73-0.92)	4.68E-04	0.83 (0.76-0.90)	4.07E-06
rs11728133	KLF3	4p14	C	0.28	0.81 (0.75-0.87)	1.10E-08	0.78 (0.69-0.88)	8.89E-05	0.82 (0.75-0.90)	2.60E-05
rs11722813	TLR1	4p14	T	0.17	0.64 (0.55-0.75)	1.44E-08	0.64 (0.55-0.75)	1.44E-08	NA	NA
rs10008492	TLR10	4p14	T	0.39	0.83 (0.77-0.88)	2.06E-08	0.81 (0.72-0.90)	2.06E-04	0.84 (0.77-0.91)	2.41E-05
rs368433	FCGR2A	1q23.3	C	0.16	0.73 (0.65-0.81)	2.13E-08	0.67 (0.55-0.81)	2.40E-05	0.76 (0.66-0.87)	1.33E-04
rs10024216	TLR10	4p14	A	0.38	0.83 (0.78-0.89)	4.01E-08	0.80 (0.71-0.90)	1.28E-04	0.85 (0.78-0.92)	6.29E-05
rs9427401	HSPA6	1q23.3	G	0.14	0.73 (0.65-0.81)	4.57E-08	0.66 (0.54-0.81)	5.13E-05	0.76 (0.66-0.87)	1.35E-04
rs17400517	FCGR2A	1q23.3	T	0.15	0.73 (0.65-0.81)	4.95E-08	0.67 (0.55-0.81)	5.40E-05	0.76 (0.66-0.87)	1.46E-04

eTable 5. eQTL Results of rs10004195 and all TLR Genes Present on the HumanHT12 BeadChips

Gene	Chr	Array Address ID		SHIP-TREND						RS-III					
		HT-12 v3	HT-12 v4	beta	SE	p-value	Mean Expr	SD Expr.	Significant expressed Probes [%]	beta	SE	p-value	Mean Expr.	SD Expr.	Significant expressed Probes [%]
<i>TLR1</i>	4	6520451	6520451	-0.228	0.061	2.1x10 ⁻⁴	8.6078	0.6854	100.00%	-0.299	0.040	3.2x10 ⁻¹	8.8020	0.4736	99.74%
<i>TLR10</i>	4	620441	620441	-0.131	0.050	9.0x10 ⁻³	7.0345	0.2849	95.46%	-0.003	0.041	0.933	7.1901	0.2475	73.75%
<i>TLR6</i>	4	5340427	5340427	-0.107	0.047	0.021	6.9367	0.3128	92.03%	-0.086	0.036	0.018	7.1400	0.2286	68.50%
<i>TLR3</i>	4	2060377	2060377	-0.075	0.035	0.034	6.3398	0.1655	18.37%	-0.030	0.035	0.406	6.8419	0.1204	5.51%
<i>TLR10</i>	4	380639	380639	-0.061	0.033	0.063	6.3128	0.1412	15.34%	NA	NA	NA	NA	NA	0%
<i>TLR4</i>	9	1500180	1500180	-0.094	0.060	0.120	7.9968	0.3652	100.00%	-0.004	0.057	0.922	7.8373	0.3714	96.85%
<i>TLR3</i>	4	730762	730762	0.044	0.029	0.135	6.1831	0.1275	2.72%	NA	NA	NA	NA	NA	0%
<i>TLR8</i>	X	6480360	6480360	-0.054	0.042	0.202	9.7327	0.4622	100.00%	-0.043	0.048	0.239	9.5449	0.4075	99.87%
<i>TLR8</i>	X	6370487	6370487	-0.031	0.034	0.365	6.2242	0.1425	6.46%	-0.043	0.034	0.233	6.8569	0.1213	9.45%
<i>TLR7</i>	X	7200753	7200753	0.037	0.046	0.427	7.4971	0.2798	99.90%	0.016	0.041	0.657	7.2456	0.2757	76.77%
<i>TLR8</i>	X	3390612	3390612	0.023	0.04	0.567	8.9932	0.3489	100.00%	-0.042	0.043	0.244	8.4310	0.3872	99.21%
<i>TLR5</i>	1	830440	830440	-0.014	0.052	0.794	7.7393	0.4312	99.60%	-0.054	0.051	0.140	8.2489	0.3389	99.74%
<i>TLR10</i>	4	4480543	4480543	-0.009	0.042	0.83	7.2663	0.2598	99.29%	0.113	0.043	0.002	7.5259	0.2111	97.11%
<i>TLR9</i>	3	1820440	1820440	0.001	0.035	0.970	6.2503	0.144	8.58%	-0.033	0.029	0.361	6.6492	0.1171	0.52%
<i>TLR2</i>	4	6420750	6420750	-0.001	0.054	0.988	6.9843	0.3164	93.95%	0.031	0.042	0.390	7.1922	0.2928	69.95%

Abbreviations: Chr = Chromosome, SE = Standard Error, Expr = Expression value, SD = Standard Deviation, NA = Not Available

eTable 6. Results of the *cis*-eQTL Analysis of rs10004195 (*4p14*) and rs368433 (*1q23.3*)

Gene	Chr	Array Address ID		SHIP-TREND			RS-III		
		HT-12 v3	HT-12 v4	beta	CI	p-value	beta	CI	p-value
rs10004195, Effect allele = A									
<i>KLF3</i>	4	580594	580594	-0.015	(-0.086-0.056)	0.670	-0.016	(-0.104-0.072)	0.72
<i>KLF3</i>	4	870066	870066	0.026	(-0.068-0.12)	0.589	0.050	(-0.005-0.105)	0.073
<i>TLR10</i>	4	620441	620441	-0.131	(-0.229--0.033)	9.0x10 ⁻³	-0.003	(-0.083-0.077)	0.933
<i>TLR10</i>	4	4480543	4480543	-0.009	(-0.091-0.073)	0.830	0.136	(0.052-0.22)	2.0x10 ⁻³
<i>TLR1</i>	4	6520451	6520451	-0.228	(-0.348--0.108)	2.1x10⁻⁴	-0.35	(-0.428--0.272)	3.2x10⁻¹⁷
<i>TLR6</i>	4	5340427	5340427	-0.107	(-0.199--0.015)	0.021	-0.085	(-0.156--0.014)	0.018
<i>TMEM156</i>	4	2000364	2000364	0.096	(-0.014-0.206)	0.087	0.079	(-0.015-0.173)	0.097
<i>TMEM156</i>	4	3870088	3390253	0.006	(-0.063-0.075)	0.858	0.021	(-0.046-0.088)	0.542
rs368433, Effect allele = C									
<i>SDHC</i>	1	6200241	6200241	-0.093	(-0.197-0.011)	0.079	0.015	(-0.093-0.123)	0.788
<i>SDHC</i>	1	1090301	1090301	0.087	(-0.033-0.207)	0.150	0.060	(-0.016-0.136)	0.121
<i>FCGR2A</i>	1	6520048	6590437	-0.172	(-0.278--0.066)	1.6x10 ⁻³	-0.070	(-0.172-0.032)	0.181
<i>FCGR2A</i>	1	1990278	1990278	-0.034	(-0.146-0.078)	0.545	0.010	(-0.11-0.13)	0.87
<i>FCGR2A</i>	1	450762	450762	-0.819	(-1.017--0.621)	1.4x10⁻¹⁵	-0.325	(-0.472--0.178)	1.7x10⁻⁵
<i>HSPA6</i>	1	1710553	1710553	-0.766	(-0.938--0.594)	1.8x10⁻¹⁷	-0.648	(-0.817--0.479)	1.1x10⁻¹³
<i>HSPA6</i>	1	160092	160092	-0.717	(-0.882--0.552)	4.3x10⁻¹⁷	-0.741	(-0.931--0.551)	6.5x10⁻¹⁴
<i>FCGR3A</i>	1	4050039	4050039	-0.209	(-0.442-0.024)	0.079	-0.107	(-0.279-0.065)	0.223
<i>FCGR3A</i>	1	3610431	3610431	-0.047	(-0.169-0.075)	0.452	0.074	(-0.055-0.203)	0.262
<i>HSPA7</i>	1	830709	830709	-0.065	(-0.188-0.058)	0.301	-0.016	(-0.128-0.096)	0.78
<i>FCGR3B</i>	1	7210114	7210114	-0.025	(-0.241-0.191)	0.821	-0.057	(-0.265-0.151)	0.589
<i>FCGR3B</i>	1	1450139	1450139	0.030	(-0.227-0.287)	0.817	-0.029	(-0.264-0.206)	0.807
<i>FCGR2B</i>	1	6650341	6650341	0.614	(0.481-0.747)	9.5x10⁻¹⁹	0.892	(0.708-1.076)	2.5x10⁻²⁰
<i>FCGR2B</i>	1	7550215	7550215	0.595	(0.475-0.715)	1.4x10⁻²¹	0.368	(0.266-0.47)	3.0x10⁻¹²
<i>FCGR2B</i>	1	2480717	2480717	0.274	(0.172-0.376)	2.0x10⁻⁷	0.276	(0.162-0.39)	2.5x10⁻⁶

<i>FCRLA</i>	1	3780193	3780193	-0.124	(-0.273-0.025)	0.100	-0.155	(-0.298--0.012)	0.033
<i>FCRLB</i>	1	4730204	4730204	-0.038	(-0.148-0.072)	0.493	-0.005	(-0.103-0.093)	0.918
<i>DUSP12</i>	1	460280	460280	-0.057	(-0.147-0.033)	0.216	0.063	(-0.025-0.151)	0.165

Abbreviations: Chr = Chromosome, CI = 95% Confidence Interval. P-values in bold indicate significance after Bonferroni correction. Italic Array Address IDs indicate differences between the HumanHT-12 v3 and HumanHT-12 v4 BeadChips. The units of the betas are the log2-transformed gene expression values as measured with the Illumina HumanHT-12 BeadChips.