

Genome wide Association with HLA-DPB2 and RNA expression in European and African : Suggesting expression quantitative trait loci of HLA-DPB2 that might function as inducing Anti-topoisomerase antibodies.

IlGwon Jo, School of Systems Biomedical Science, Soongsil University

Abstract

Racial disparities have been major concern that Blacks are more susceptible to SSc than White population. Disparities in economic status and access to medical management do not fully explain the differences in mortality. It is important to determine which genetic factors cause significant difference observed in SSc among 2 populations.

By identifying these racial disparities especially disparity in African, we approach at the point of lncRNA not protein coding gene. HLA-DPB2 was performed as a susceptible factor because significant difference of RNA expression in HLA-DPB2 was detected between European and African. Genome wide association analyses were performed to identify expression quantitative trait loci of HLA-DPB2 among European and African. It was difficult to further analyze signal in European, however, Single Linkage Disequilibrium block was detected in African. This block suggests important functional sites regulating expression of HLA-DPB2.

This study suggests significant eQTLs regulating RNA expression of HLA-DPB2 especially in African. Regulating mechanism how HLA-DPB2 leads to produce Anti-DNA topoisomerase I antibodies(ATA) was not studied. Further studies are needed that frequency of positive ATA really depends on expression of HLA-DPB2.

Introduction

Systemic sclerosis (SSc) is a complex connective tissue disease, innate and adaptive immune systems are one of associated pathologic targets [6]. Production of autoantibodies and cell-mediated autoimmunity, hyper-productivity between Anti-DNA topoisomerase I antibodies (ATA) interaction with type I topoisomerase leads to abnormality of innate and immune systems [3, 8]. Especially, many genome wide association analyses are proceeded identifying genetic associations in MHC – human leukocyte antigen (HLA, initiating immune responses) [7]. In other words, significantly high frequencies of ATA in patients compared to normal subjects were detected in HLA-regions as genetic loci for SSc.

In addition, it has been major concern that racial disparities between European and African are present in response to SSc and this phenomenon makes African responsible for a greater financial problems. Many studies show that Blacks are more likely to get SSc than Whites and to experience greater morbidity and less survival rate [1,2,12-15]. Abnormality of auto-antibody rate is also the one of major indicators determining racial differences in these association studies.

Actually, many genome wide association studies argue that HLA-regions are one of genetic indicators, however, it is still difficult to identify specific genetic loci for SSc[3], because HLA region is widely related. Furthermore, study of identifying association that non coding RNA leads to regulate Ssc is still lacking. It has been reported that HLA-DPB1 and HLA-DPB2 are genetic loci for Ssc in one study, however, it is localized in Korean population only[4].

In this project we present results of SNP variants associated with RNA expression of non-coding RNA (HLA-DPB2) after detecting significantly difference of RNA expression between European and African by t-test. This project suggest not only genetic basis of regulating mechanism of lncRNA but also uninvestigated insight for linking genetic loci of racial disparities especially in African in Ssc.

Material and Methods

Study Subjects

Statistical Analyses of t-test and expression quantitative trait loci (eQTLs) were performed using 1000 Geuvadis RNA-sequencing project as expression data from lymphoblastoid cell lines, where samples were associated with genome sequencing data of the same samples provided by the 1000 Genomes Project. Samples were consist of 5 populations, CEPH (CEU), Finns (FIN), British (GBR), Toscani (TSI) and Yoruba (YRI) which CEU, FIN, GBR and TSI were clustered to EUR(European) as a control, YRI was represented to AFR(African) as a case. After ‘quality controlling’ genotypes with minor allele frequency 5% , Hardy-Weinburg Equilibrium test under 1×10^{-6} , genotypes of 5,913,163SNPs in 373 Europeans and 9,360,676SNPs in 77 African were conducted for final analysis. Sex chromosomes were excluded in analysis. Insertion/Deletion data in 9,360,676SNPs were excluded after eQTL analysis. Gene expression of lymphoblastoid cell lines was determined by the sum of Reads Per Kilobase of transcript per Million mapped reads (RPKM) of individuals’ single gene

Measuring the mean difference between two samples.

By estimating whether significant difference of mean between gene expression from European(n=373) and African(n=77) exist, statistical significance was determined by two-tailed unpaired Welch’s t-test, and p<0.05 was considered as a significant value. Mean of gene expression of each sample is calculated by RPKM of HLA-DPB2.

Genome-wide association Analysis

The analyses through standard linear regression were implemented to identify eQTLs of HLA-DPB2. PLINK was conducted as a statistical analyzing tool, eQTLs of HLA-DPB2 from RNA expression depends on SNP allele change. Genome-wide significance level(α , 5×10^{-8}) threshold was evaluated as a significant indicator in multiple tests. Among detected SNPs of HLA-DPB2, Linkage Disequilibrium blocks were formulated using Haploview. Confidence intervals were determined as a block algorithm of association signals. After identifying eQTLs of HLA-DPB2, association between 10,229 genes and individual SNPs were conducted to investigate association with the expression of HLA-DPB2 using PLINK as well. The threshold for significance level(α) 4.89×10^{-6} after Bonferroni correction($=0.05$ divided by total gene numbers 10,229) for multiple tests.

Results

Significant mean differences of RNA expression in HLA-DPB2 between European and African were detected after performing unpaired t test (p-value 0.023, Figure1). RNA expression of HLA-DPB2 in African was higher than European (8.819>7.020,Figure 1)

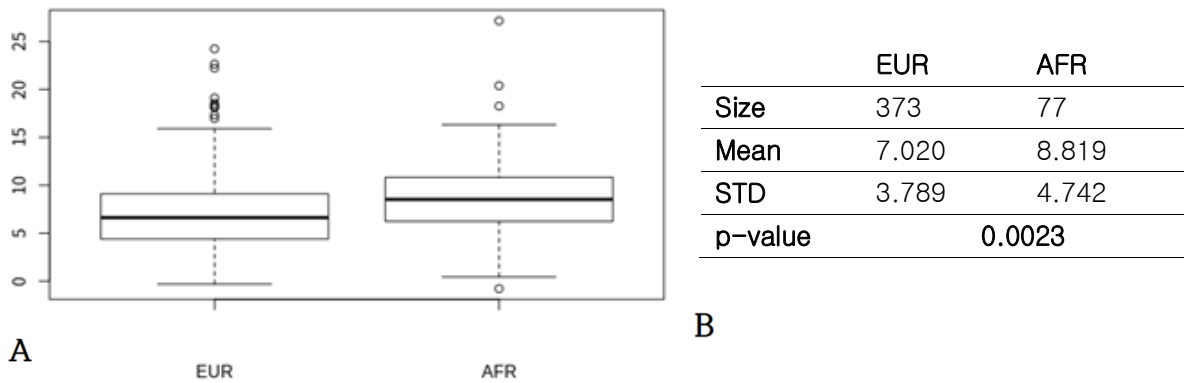


Figure1
Unpaired t test(Welch’s two sample t test) was performed to identify significant difference of RNA expression of HLA-DPB2 between European(n=373) and African(n=77). Table A shows RNA expression distribution of two samples. Table B indicates that RNA expression difference between two samples are significant.(P-value 0.0023 < significance level 0.05), HLA-DPB2= major histocompatibility complex, class II, DP beta 2(lncRNA), STD=Standard Deviation

Both European and African were detected in chr6 through genome wide association analysis of SNPs with RNA expression in HLA-DPB2(Figure2). However, region of significant SNPs association with HLA-DPB2 were different in two samples. For example, about 10kb of eQTLs containing HLA-DPB2 region were revealed in European with very strong scores($P < 5 \times 10^{-8}$). In control(EUR), 712eQTLs were detected in chr6 universally(Supplementary table2), but only single eQTL(rs115378869) was detected in case(AFR,p=3.076e-08, AFR, 11kb 3' of HLA-DPB1). Top 3 eQTLs(rs115378869,rs140554467,rs114535942) sorted by p-value score were used as analyzing loci. Rs114535942 were excluded because AA allele samples were too small to cause an error(Supplementary figure1) only 1 sample with AA allele exist among 77 samples(association between eQTLs and RNA expression of HLA-DPB2 in European are described in supplementary table2)

Table1
Genome wide associations of SNPs with RNA expression of HLA-DPB2 in African.

SNP	Gene	Position(hg38)	Allele	MAF	beta	p-value
rs115378869	11kb 3' of HLA-DPB1(LncRNA)	6:33082306	C/A	0.45	6.178	3.076e-08
rs140554467	HLA-DPB1(Intronic variant)	6:33098546	A/G	0.46	6.02	5.957e-08
rs114535942	2.6kb 3' of LGALS12(LncRNA)	11:33098546	T/A	0.11	5.944	8.192e-08

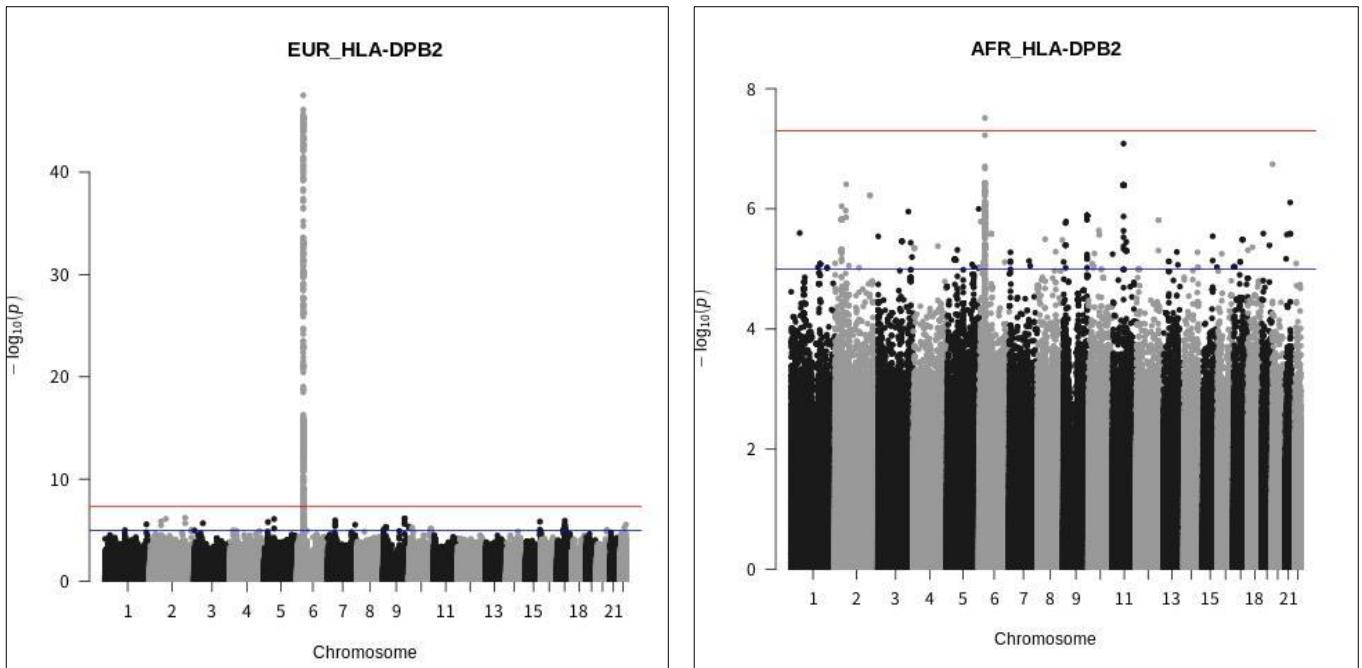


Figure 2. Manhattan plot shows genome-wide association between eQTLs and logistic value($-\log_{10}P$) of RNA expression of HLA-DPB2 between European($n=373$) and African($n=77$). The red line denotes a genome-wide significance level(WGS) threshold ($P=5 \times 10^{-8}$), and the blue line denotes p-value below 5×10^{-5} (“suggestive” threshold).

Linkage Disequilibrium blocks analysis showed that 712eQTLs in European were grouped as 9 blocks and 2eQTLs were revealed as single block in African. rs115378869, rs140554467 were clustered as a single signal with strong scores.(Figure3)

Analyzing association between individual SNP and whole 10,229 genes were performed. The threshold for declaring significance after Bonferroni correction for multiple tests was $p < 4.89 \times 10^{-6}$. 2 significant SNPs of HLA-DPB2 in African were analyzed and it was revealed that both 2SNPs were associated only in HLA-DPB2(all p-value against 10,229 genes were higher than 4.89×10^{-6} except HLA-DPB2.)

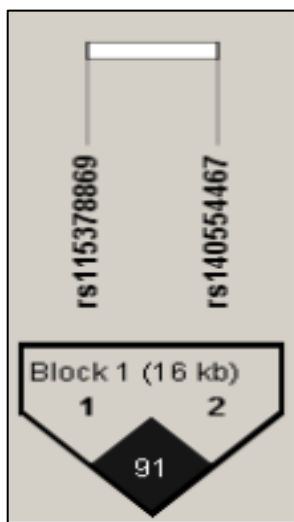


Figure3

Linkage disequilibrium block were identified to have association between base position and RNA expression of HLA-DPB2. R squared score(r^2) over 80 was performed as cut-off value identifying LD-block. Single block signal indicates that blocked region is more likely to inherit dependently in next generation. Base position from chr 6: 33082306 to chr6: 33098546 were clustered to indicate single signal(strong LD block) in African. Base position from chr6: 32978587 to 3139757 were clustered to indicate 9 signals in European(LD block was described in Supplementary table1)

Discussion

Systemic sclerosis is a rare chronic disease of unspecified cause which is characterized by diffuse fibrosis and vascular abnormalities in the skin and internal organs. Identifying treatments of this disease are still in progress as well. It has been reported that incidence of SSc among Blacks is approximately 2.5 fold higher than for whites[10]. Prior study of SSc mortality in the US reported that death rates are significantly higher for blacks than for whites (7.1 vs 4.4 deaths per million population per year)[11]. Also genome wide association study has identified that HLA-DPB1 and HLA-DPB2 are genetic loci for SSc with significantly high proportion of positive ATA in Korean SSc patients[4].

In the point of view that most of lncRNA regulates functional pathway, we hypothesized that HLA-DPB2 is one of genetic regulating factor that cause racial disparities of SSc, genome wide association study between eQTLs of 2 population and RNA expression of HLA-DPB2 was performed in this project.

It was revealed that RNA expression of HLA-DPB2 was significantly different among 2 populations. Especially, RNA expression of HLA-DPB2 was more higher in African than European. As significant difference between 2 populations support our hypothesis, we further statistically analyze association between eQTLs and HLA-DPB2 of 2 population respectively.

As a result, 9 blocks from chr6:32978587 to chr6:3319759 were detected universally in Europe. It was difficult to detect specific significant genetic Loci because these association signals spread widely(contain 3 HLA genes, and 4 other genes which are COLLA2,RXRB,SLC39A7,RING1). However single block from chr6:33082306 to 33098546 were detected as an association signal in African. It was revealed that both rs115378869 and rs140554467 expressed positively when reference allele changes to minor allele with 6.178 and 6.02 beta score each. Above all, 2SNPs have high proportion of MAF with 45% and 46% each. Each 2 eQTLs were excluded by quality controlling in European, however, according to 1000 genomes project samples, rs115378869 and rs140554467 have lower MAF with 4 % each in European. This quiet different proportion between 2 populations in minor SNP variants is an important genetic factor, and this different conservation rate might regulates functional pathways differently among 2 populations to cause different frequency of positive ATA differently indeed. Further studies are needed either rs115378869 and rs140554467 in European are really associated with HLA-DPB2 or dependent from HLA-DPB2.

Functional researches were conducted using variant annotation tool(HaploReg v4.1: decoding regulatory chromatin states, CHIPBase v2.0: decoding the transcriptional regulatory networks of lncRNA based on CHIP-Seq experiment, Roadmap Epigenomics Consortium, 2015). It was suggested that H3K4me1 and H3K27ac were detected in rs115378869 in GM12878,B-Lymphocyte which is an indicator raising the probability as an enhancer(Haploreg v4.0). In other words, rs115378869 is indicated as an important genetic marker which might function as an enhancer and also regulate the expression of HLA-DPB2. Functional research on rs115378869 is required to understand how this SNP regulates RNA expression of HLA-DPB2.

Among this significant single block of HLA-DPB2 in African(chr6:33082306 to 33098546), it was corresponded to a transcription factor binding sites. It was uncovered that from chr6:33092150 to 33092168,upstream were regulated as a CTCF binding locus in GM12878(CHIPbase v2.0). Binding interaction CTCF and its locus usually function negatively to RNA expression. Binding affinity of CTCF with allele change in African is not studied, however, this evidences suggest that this locus involving rs115378869 is functionally important regulating mechanism than other loci. Further studies are needed interacting binding affinity with allele change and association with RNA expression.

Pathway mechanisms of HLA genes are well studied. HLA-DPB plays a role in MHC(major histocompatibility complex) class2 beta chain. HLA-DPB function as an antigen presenting cell, set of genes that code for cell surface proteins essential for the acquired immune system to recognize foreign molecules. The reason why proportion of ATA increased in Human immune systems are not specifically identified, however, Expression disorders of genes(HLA-DP) responsible for MHC class2 might recognize type I topoisomerase as an antigen that leads to hyper-produce ATA.

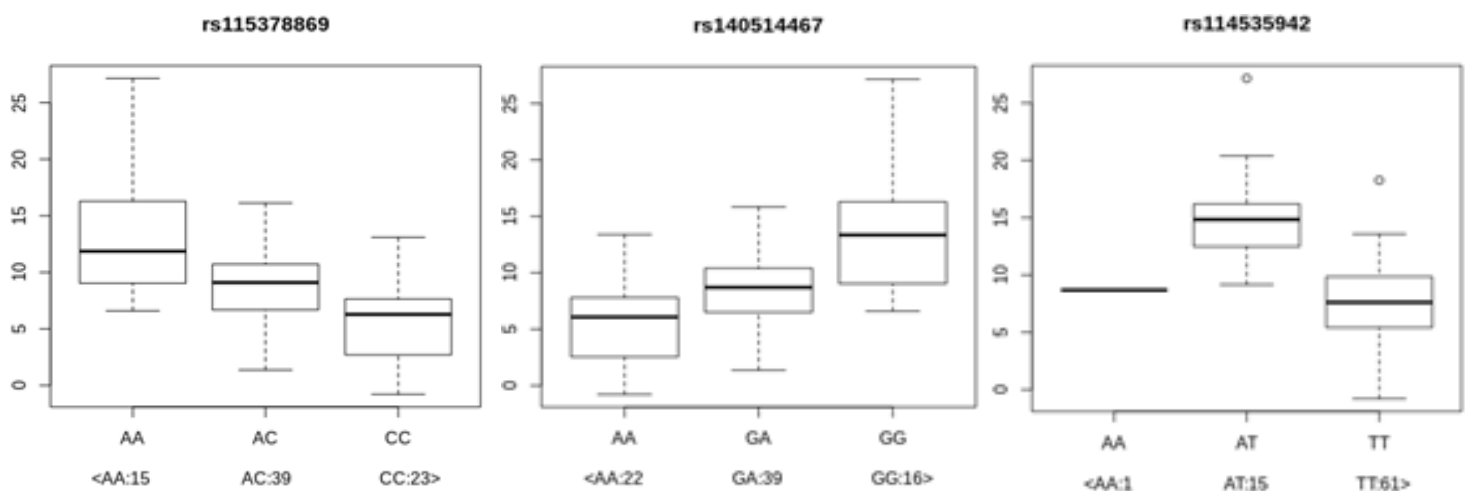
According to Pathcards(based on gene enrichment analysis comparison and Jaccard similarity coefficient computed for the gene contents of the entire source). HLA-DPB2 was detected that it is related to G-protein signaling N-RAS regulation pathway which contains Immune response Antigen presentation by MHC class II with 1.089 relevance score, however, its specific pathway is not studied and also the evidences how lncRNA, HLA-DPB2 regulates the functional pathway to produce ATA are still limited.

By supporting the hypothesis that expression of lncRNA leads to SSc, identification project(GapmeR, for example) that expression of positive ATA frequency really depends on the difference of lncRNA has to be preceded first. GapmeR is a chimeric antisense oligonucleotide that contains a central block of deoxynucleotide monomers sufficiently long to induce RNase H cleavage [16]. By constructing case-control experiment, comparing inactivated HLA-DPB2 and activated HLA-DPB2 cells independently; we might obtain the the expression data of ATA based on expression of HLA-DPB2.

Reference

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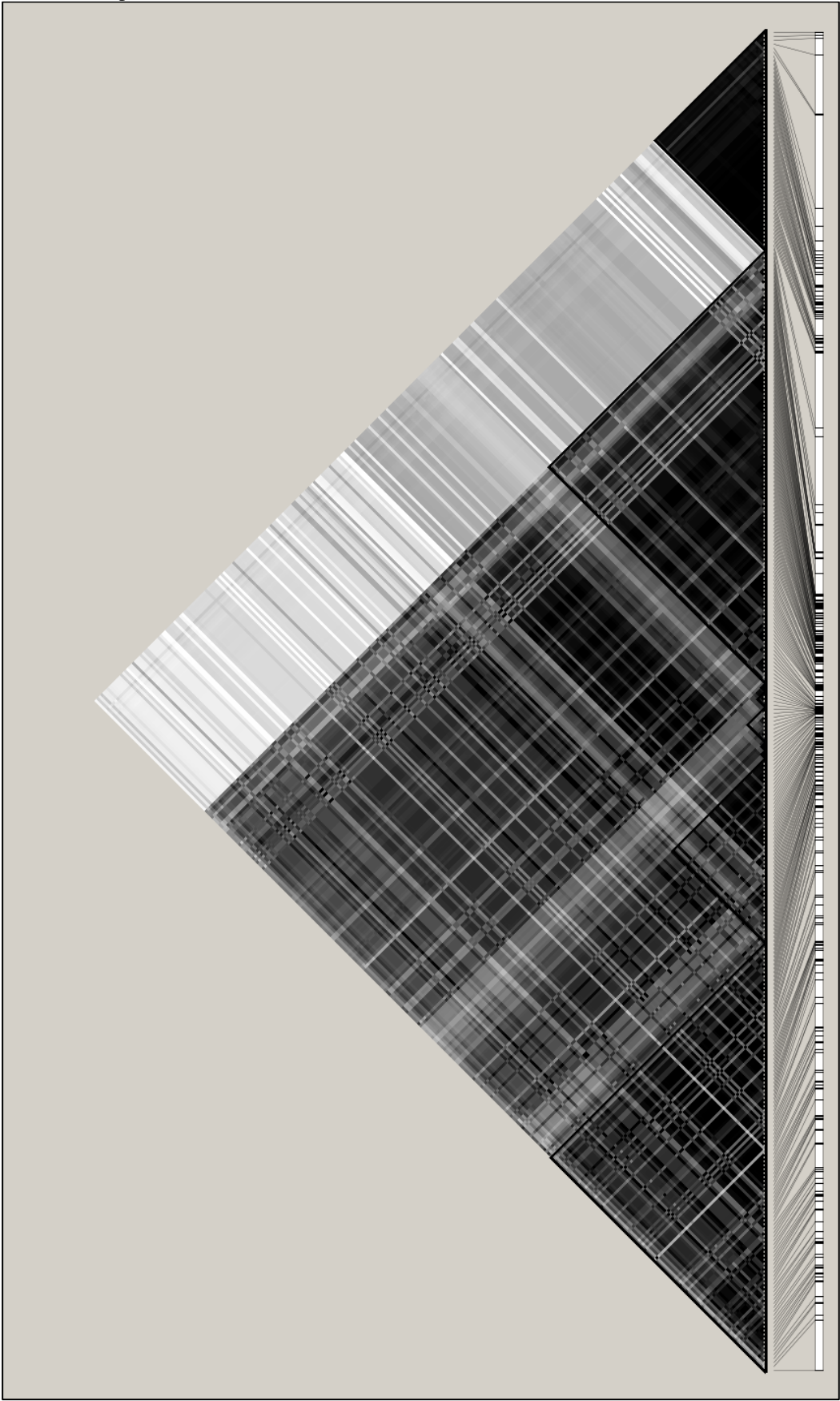
Supplementary Figure1



RNA expression of HLA-DPB2 with allele change. Both minor allele in rs115378869 and rs140514467 act positively against RNA expression(Minor allele, rs115378869: A, rs140514467 : G). rs114535942(chr11) has only 1 AA sample(which is too small to statistically analyze).

Supplementary table 1

Linkage disequilibrium block were identified to have association between base position and RNA expression of HLA-DPB2 in European.



Supplementary table2

Genome wide associations of SNPs with RNA expression of HLA-DPB2 in European. Hg19version was used as identifying position.

SNP	chr6:position	Ref	BETA	P	SNP	chr6:position	Ref	BETA	P	SNP	chr6:position	Ref	BETA	P
rs429916	32978587	A	2.819	4.33E-09	rs114852189	33036003	C	2.839	3.76E-16	rs114985917	33054142	C	3.333	1.74E-28
rs114040890	33000143	G	1.972	1.08E-09	rs115512814	33036085	G	2.765	1.56E-15	rs144086333	33054152	G	3.378	7.87E-30
rs114483226	33000150	T	2.425	1.37E-11	rs114382269	33036116	G	2.765	1.56E-15	rs147338815	33054155	T	3.338	2.16E-28
rs116603377	33001066	T	1.972	1.08E-09	rs116341739	33036177	G	2.765	1.56E-15	rs140877726	33054156	G	3.338	2.16E-28
rs114340858	33001488	G	1.972	1.08E-09	rs115697889	33036210	T	2.765	1.56E-15	rs114801185	33054167	A	3.18	1.88E-27
rs115045099	33001735	C	2.425	1.37E-11	rs116102701	33036233	G	2.765	1.56E-15	rs116535837	33054176	A	3.178	1.57E-23
rs116776695	33002105	A	1.972	1.08E-09	rs114609938	33036242	C	2.765	1.56E-15	rs116089975	33054177	C	3.178	1.57E-23
rs115604121	33003065	C	1.972	1.08E-09	rs114841510	33036312	G	2.765	1.56E-15	rs116308528	33054207	G	2.986	1.70E-19
rs115130984	33003120	G	1.876	7.17E-09	rs115315602	33036388	T	2.786	1.04E-15	rs115621867	33054208	T	2.986	1.70E-19
rs115712191	33003562	C	2.425	1.37E-11	rs115765369	33036394	A	2.786	1.04E-15	rs114109293	33054215	C	3.006	7.57E-24
rs116462477	33004230	C	1.972	1.08E-09	rs116257952	33036505	C	2.786	1.04E-15	rs114808487	33054227	A	3.069	1.93E-25
rs115527825	33004427	C	1.972	1.08E-09	rs115504766	33036617	T	2.786	1.04E-15	rs115745278	33054231	T	3.06	2.70E-25
rs115459187	33004935	T	1.972	1.08E-09	rs114881201	33036630	T	2.792	3.90E-15	rs116134208	33054235	G	3.034	6.52E-25
rs116636304	33005208	T	1.972	1.08E-09	rs115776286	33036631	C	2.844	8.43E-16	rs116707706	33054268	A	3.482	4.95E-34
rs116111601	33005273	A	1.972	1.08E-09	rs116044065	33036708	T	2.83	1.34E-15	rs115714329	33054280	C	3.385	6.85E-31
rs116408613	33005472	G	1.972	1.08E-09	rs114839492	33036709	G	2.83	1.34E-15	rs115781260	33054281	A	3.385	6.85E-31
rs147779666	33005564	G	1.972	1.08E-09	rs115563059	33036717	G	2.786	1.04E-15	rs114203387	33054302	C	3.73	6.32E-40
rs114154646	33005600	A	1.972	1.08E-09	rs115979901	33036853	C	2.786	1.04E-15	rs114988017	33054325	C	3.716	2.02E-40
rs114851789	33005644	C	2.425	1.37E-11	rs115704503	33036951	G	2.756	5.82E-15	rs114535545	33054331	C	3.732	7.56E-41
rs115579000	33005689	T	1.972	1.08E-09	rs116200742	33036959	A	2.765	1.56E-15	rs116393422	33054413	G	3.364	2.54E-29
rs114291191	33006869	C	1.972	1.08E-09	rs114397850	33036971	T	2.765	1.56E-15	rs115638518	33054414	A	3.364	2.54E-29
rs115414793	33007192	C	1.972	1.08E-09	rs114085168	33036999	C	2.765	1.56E-15	rs114717252	33054457	G	3.969	7.53E-47
rs114946771	33007321	T	1.972	1.08E-09	rs114702614	33037080	A	2.83	1.60E-15	rs115174485	33054550	A	3.863	7.79E-44
rs115424521	33017082	A	2.293	6.96E-10	rs114525450	33037082	G	2.751	2.48E-15	rs114009998	33054552	G	3.863	7.79E-44
rs114930983	33023792	C	1.815	1.77E-08	rs116424807	33037104	T	2.765	1.56E-15	rs114385226	33054619	A	3.908	6.65E-45
rs115257164	33024711	C	2.46	4.73E-08	rs115871636	33037142	G	2.765	1.56E-15	rs114899534	33054711	T	3.954	4.80E-46
rs114286263	33024738	T	2.46	4.73E-08	rs114516265	33037187	G	2.816	2.20E-16	rs116653986	33054721	T	3.954	4.80E-46
rs114941340	33024762	C	2.46	4.73E-08	rs115811196	33037265	A	2.765	1.56E-15	rs115967922	33054807	G	3.954	4.80E-46
rs116118029	33024795	T	2.46	4.73E-08	rs114870604	33037279	G	2.765	1.56E-15	rs114459399	33054861	G	3.523	1.26E-30
rs115673219	33024814	C	2.594	3.49E-12	rs115768631	33037294	C	2.765	1.56E-15	rs115107409	33054890	T	3.954	4.80E-46
rs115407957	33024823	C	2.691	6.08E-13	rs116826956	33037304	T	2.765	1.56E-15	rs114782971	33055009	A	3.954	4.80E-46
rs114935065	33024908	C	2.691	6.08E-13	rs116036234	33037419	A	2.765	1.56E-15	rs115639939	33055047	G	3.943	4.09E-45
rs116486262	33024972	G	2.691	6.08E-13	rs114535226	33037424	C	2.765	1.56E-15	rs116162451	33055079	G	3.51	1.65E-32
rs114930606	33025044	G	2.691	6.08E-13	rs114025661	33037522	C	2.878	2.09E-16	rs116735758	33055123	G	3.954	4.80E-46
rs114142782	33025050	G	2.691	6.08E-13	rs115720261	33037557	T	2.631	6.37E-12	rs114289471	33055158	G	3.954	4.80E-46
rs114211943	33025174	G	2.765	1.56E-15	rs114758358	33037560	A	2.577	4.30E-12	rs115854500	33055247	C	3.954	4.80E-46
rs116176189	33025386	A	2.691	6.08E-13	rs114101076	33037579	T	2.701	1.02E-13	rs115973003	33055308	T	3.827	6.31E-42
rs115320733	33025671	G	2.765	1.56E-15	rs115020570	33037580	G	2.701	1.02E-13	rs116250555	33055323	T	3.465	1.50E-31
rs116400397	33025712	T	2.691	6.08E-13	rs114123941	33037626	G	2.53	9.49E-10	rs115475465	33055346	G	3.845	4.24E-43
rs115820704	33025740	C	2.691	6.08E-13	rs114313264	33037675	A	2.871	6.48E-16	rs115561363	33055355	G	3.222	5.69E-11
rs116669206	33026084	A	2.765	1.56E-15	rs116512529	33037690	T	2.829	3.81E-16	rs115044571	33055367	A	3.954	4.80E-46
rs116519092	33026087	G	2.765	1.56E-15	rs115867762	33037768	A	2.911	2.07E-16	rs115497102	33055390	T	3.954	4.80E-46
rs114164262	33026169	A	2.716	6.72E-15	rs116603518	33037865	T	2.885	3.65E-15	rs114515918	33055419	G	3.954	4.80E-46
rs114861986	33026185	A	2.632	3.56E-12	rs115336552	33037866	G	2.885	3.65E-15	rs116649724	33055487	C	3.834	7.45E-43
rs114420525	33026246	G	2.765	1.56E-15	rs115779188	33037878	A	2.883	5.43E-16	rs116087639	33055494	T	3.834	7.45E-43
rs115028475	33026316	T	2.765	1.56E-15	rs116378027	33037891	T	2.883	5.43E-16	rs116385655	33055501	T	3.179	2.97E-22
rs114747995	33026388	A	2.691	6.08E-13	rs115478098	33037955	A	2.921	3.62E-14	rs114195294	33055516	C	3.954	4.80E-46
rs114531325	33026423	T	2.765	1.56E-15	rs114508533	33037957	A	2.921	3.62E-14	rs115222756	33055538	T	3.954	4.80E-46
rs115254361	33026433	C	2.691	6.08E-13	rs116597648	33037991	G	2.911	2.07E-16	rs115802743	33055551	A	3.342	3.81E-12
rs115997647	33026517	T	2.776	2.13E-15	rs116696897	33038052	T	2.777	1.78E-14	rs114105346	33055605	A	3.567	1.03E-33
rs116287528	33026524	C	2.753	4.20E-15	rs116082819	33038053	T	2.777	1.78E-14	rs115186402	33055780	T	3.954	4.80E-46
rs114055112	33026540	A	2.753	4.20E-15	rs116470580	33038117	T	2.934	3.85E-14	rs116737096	33055818	G	3.954	4.80E-46
rs116831804	33026553	A	2.745	4.60E-15	rs114757491	33038134	T	2.942	4.70E-14	rs114386240	33055899	A	2.889	1.47E-16
rs115889469	33026604	T	2.765	1.56E-15	rs115002929	33038144	T	2.88	3.38E-16	rs115298492	33055946	A	2.889	1.47E-16
rs115060883	33026606	G	2.765	1.56E-15	rs115714626	33038167	A	2.859	6.59E-16	rs114331767	33056069	A	3.523	1.26E-30
rs114429910	33026673	T	2.765	1.56E-15	rs114435069	33038178	T	2.859	6.59E-16	rs114984291	33056097	G	3.135	8.71E-22
rs114543070	33026697	G	2.765	1.56E-15	rs116604900	33038187	C	2.859	6.59E-16	rs116335534	33056207	T	3.515	5.33E-31
rs147684894	33028758	G	2.685	1.99E-14	rs115778668	33038223	G	2.747	1.50E-14	rs116790970	33056253	A	3.515	5.33E-31
rs116204831	33028830	T	2.754	2.34E-15	rs115508585	33038229	T	2.747	1.50E-14	rs114150262	33056405	T	3.515	5.33E-31
rs114926731	33028988	C	2.741	3.24E-15	rs115587006	33038237	G	2.747	1.50E-14	rs114108056	33056435	T	3.954	3.99E-46
rs115823344	33029009	G	2.741	3.24E-15	rs114811226	33038322	T	2.878	2.09E-16	rs114068262	33056566	C	3.523	1.26E-30
rs114135783	33029035	G	2.666	1.17E-12	rs116629007	33038369	A	2.878	2.09E-16	rs116423220	33056694	C	3.519	1.54E-30
rs115150035	33029125	A	2.768	7.13E-15	rs115631330	33038548	C	2.813	1.01E-15	rs115864736	33056711	T	3.512	2.11E-30
rs115832690	33029137	T	2.765	8.68E-15	rs114127259	33038579	G	2.813	1.01E-15	rs116261754	33056731	C	3.388	2.34E-27
rs114842290	33029148	C	2.751	6.39E-15	rs116457253	33038597	G	2.813	1.01E-15	rs115783656	33056738	G	2.996	3.23E-19
rs114348357	33029205	T	2.716	1.33E-14	rs115760825	33038766	T	2.886	2.19E-16	rs116788710	33056749	C	3.028	9.19E-20

rs114788682	33029216	T	2.669	5.41E-12	rs116140561	33038802	G	2.896	3.65E-14	rs116028586	33056840	C	3.342	3.81E-12
rs116391956	33029255	T	2.777	2.35E-15	rs115106824	33038830	T	2.865	4.30E-16	rs116365955	33056897	T	3.135	8.71E-22
rs115503245	33029276	C	2.759	2.91E-15	rs116786614	33038850	T	2.886	2.19E-16	rs115533527	33056916	T	3.954	4.80E-46
rs115460452	33029326	A	2.759	2.91E-15	rs115242781	33038862	G	2.886	2.19E-16	rs116819823	33057013	C	3.135	8.71E-22
rs114390018	33029384	T	2.21	8.27E-09	rs116542321	33038979	T	2.863	3.55E-16	rs116771249	33057055	C	3.569	9.46E-34
rs116916694	33029385	G	2.21	8.27E-09	rs116686655	33038982	A	2.864	6.13E-14	rs114716868	33057176	C	3.954	4.80E-46
rs116447375	33029392	C	2.623	2.63E-13	rs115336831	33039180	A	2.835	6.31E-16	rs115162296	33057198	C	2.992	1.24E-27
rs116602645	33029409	G	2.635	6.30E-14	rs116041988	33039196	T	2.828	1.13E-13	rs114001470	33057213	T	3.544	3.13E-33
rs114841687	33029456	A	2.625	1.27E-13	rs114832037	33039295	A	2.829	9.38E-16	rs114636429	33057232	T	-1.959	2.42E-13
rs115769355	33029460	G	2.625	1.27E-13	rs115557410	33039376	T	2.863	3.55E-16	rs115294331	33057244	G	3.55	8.03E-33
rs114505388	33029491	A	2.579	2.56E-13	rs115984483	33039405	G	2.863	3.55E-16	rs114480463	33057440	T	3.971	2.21E-45
rs115886783	33029506	G	2.709	3.70E-14	rs114807333	33039446	A	2.863	3.55E-16	rs114279440	33057651	T	3.55	8.03E-33
rs116203190	33029511	A	2.753	2.80E-14	rs116627480	33039484	G	2.863	3.55E-16	rs115320918	33057659	A	3.55	8.03E-33
rs115015915	33029514	G	2.809	3.87E-15	rs114310791	33039503	T	2.863	3.55E-16	rs116030909	33057711	A	3.954	4.80E-46
rs116686328	33029599	A	2.798	8.53E-16	rs115552421	33039606	T	2.863	3.55E-16	rs116367343	33057835	T	3.954	4.80E-46
rs114284752	33029639	A	2.786	1.03E-15	rs115380031	33039652	T	2.864	6.13E-14	rs115757902	33058114	T	3.567	1.03E-33
rs116207449	33029668	T	2.77	1.72E-15	rs116167529	33039697	G	2.918	6.48E-14	rs116757551	33058268	C	3.567	1.03E-33
rs114069180	33029687	C	2.741	1.73E-15	rs115565467	33039719	G	2.863	3.55E-16	rs114133784	33058436	A	3.567	1.03E-33
rs114430594	33029690	T	2.741	1.73E-15	rs115808002	33039729	G	2.863	3.55E-16	rs114776596	33058583	T	-1.959	2.42E-13
rs114377982	33029729	A	2.787	2.14E-16	rs116100104	33039767	G	2.863	3.55E-16	rs116222088	33058774	C	3.567	1.03E-33
rs115884113	33029775	G	2.545	2.16E-13	rs115382010	33039837	A	2.863	3.55E-16	rs115859925	33058874	T	3.368	5.76E-27
rs116689886	33029827	C	2.797	7.70E-16	rs114814166	33039848	A	2.863	3.55E-16	rs116764828	33059262	C	3.567	1.03E-33
rs116108798	33029925	G	2.776	1.09E-14	rs114267632	33039855	G	2.863	3.55E-16	rs114485939	33059336	C	3.567	1.03E-33
rs114620642	33029926	G	2.776	1.09E-14	rs116574766	33039899	T	2.808	7.78E-14	rs114581730	33059625	C	2.849	2.17E-15
rs116601221	33029930	G	2.77	1.72E-15	rs114320513	33039927	C	2.863	3.55E-16	rs115489506	33059796	G	2.889	1.47E-16
rs116690489	33029937	T	2.77	1.72E-15	rs115898443	33039980	G	2.863	3.55E-16	rs115749842	33059996	G	3.567	1.03E-33
rs114027443	33030099	A	2.765	1.56E-15	rs115416482	33040044	G	2.864	6.13E-14	rs116134790	33060064	A	3.567	1.03E-33
rs115713476	33030441	A	2.807	6.68E-16	rs114308029	33040478	A	2.892	1.70E-13	rs115913474	33060892	T	3.954	4.80E-46
rs114980670	33030449	C	2.835	1.18E-15	rs115009697	33040596	G	2.912	1.11E-16	rs116217859	33060949	T	3.567	1.03E-33
rs116051038	33030470	T	2.765	1.56E-15	rs116711188	33040654	G	2.927	1.87E-14	rs114323359	33061229	C	2.889	1.47E-16
rs116376149	33030484	A	2.765	1.56E-15	rs116569567	33040715	A	2.883	2.37E-16	rs114454844	33061626	A	3.567	1.03E-33
rs115773154	33030511	G	2.765	1.56E-15	rs115978008	33040736	C	2.863	3.55E-16	rs116533547	33061690	C	3.567	1.03E-33
rs116769906	33030585	T	2.765	1.56E-15	rs114267348	33040744	C	2.863	3.55E-16	rs116083894	33061871	C	3.567	1.03E-33
rs114819211	33030620	G	2.765	1.56E-15	rs115487731	33040781	G	2.8	1.37E-15	rs115639392	33061947	T	3.118	1.61E-21
rs114160973	33030730	A	2.751	2.48E-15	rs115570040	33040798	C	2.863	3.55E-16	rs114011636	33062554	G	3.594	2.58E-34
rs114602039	33030755	C	2.794	1.06E-15	rs114401366	33040835	G	2.863	3.55E-16	rs116083158	33062560	C	3.594	2.58E-34
rs116459727	33030787	C	2.765	1.56E-15	rs115651830	33040877	C	2.863	3.55E-16	rs116704764	33062581	C	3.567	1.03E-33
rs115939339	33030875	G	2.751	2.48E-15	rs116793085	33041034	G	2.863	3.55E-16	rs114266857	33062587	A	3.567	1.03E-33
rs116231912	33030883	T	2.751	2.48E-15	rs114902907	33041073	C	2.577	1.71E-10	rs116476256	33062673	T	3.567	1.03E-33
rs116545111	33031103	G	2.716	1.90E-14	rs116654855	33041176	T	2.863	3.55E-16	rs115227134	33062715	A	2.875	2.39E-16
rs114851008	33031186	T	2.685	5.27E-11	rs114027335	33041186	A	2.863	3.55E-16	rs115358060	33062822	G	3.567	1.03E-33
rs115511505	33031195	G	2.822	4.48E-12	rs115022481	33041226	T	2.863	3.55E-16	rs114192693	33062889	A	3.567	1.03E-33
rs114538694	33031198	C	2.768	6.99E-12	rs114917710	33042368	G	2.864	6.13E-14	rs116791961	33063196	G	3.567	1.03E-33
rs149796140	33031250	A	2.667	1.20E-11	rs116254741	33042406	G	2.864	6.13E-14	rs115709346	33063219	C	2.341	3.92E-08
rs148918284	33031261	A	2.745	1.93E-12	rs115189254	33042492	C	2.864	6.13E-14	rs116565081	33063237	C	3.609	4.50E-34
rs149303805	33031287	G	2.891	1.93E-15	rs115505532	33042880	G	2.864	6.13E-14	rs115977521	33063271	A	3.547	4.63E-31
rs114448960	33031315	C	2.818	1.79E-15	rs115979025	33043930	G	2.863	3.55E-16	rs114866036	33063272	T	3.547	4.63E-31
rs115098652	33031406	G	2.559	1.72E-11	rs115475655	33044188	A	2.864	6.13E-14	rs115679387	33063403	G	3.954	4.80E-46
rs114181649	33031414	A	2.468	5.40E-09	rs116102562	33044257	C	2.973	4.27E-16	rs116390444	33063699	G	3.567	1.03E-33
rs114626190	33031417	T	2.491	1.22E-10	rs116543263	33044258	A	2.95	3.95E-14	rs115632616	33063931	G	3.567	1.03E-33
rs116733694	33031467	G	2.408	1.38E-09	rs114118792	33044388	C	2.864	6.13E-14	rs116162918	33063982	A	3.136	7.16E-08
rs114279792	33031468	T	2.283	7.17E-09	rs116652483	33045500	C	3.066	8.65E-11	rs116477784	33064605	T	3.494	3.76E-32
rs190763247	33031503	G	2.273	2.51E-08	rs115499023	33045823	G	3.078	1.94E-15	rs115800130	33064786	G	3.567	1.03E-33
rs114129321	33031612	T	2.749	2.05E-13	rs116739537	33045835	G	2.601	5.68E-08	rs114764676	33064796	A	2.875	2.39E-16
rs114987986	33031677	A	2.686	1.53E-14	rs114390786	33045838	A	2.592	7.59E-08	rs116097191	33064916	A	1.874	7.53E-12
rs115795025	33031689	C	2.6	6.78E-12	rs116511231	33045839	T	2.592	7.59E-08	rs115305991	33065676	G	3.567	1.03E-33
rs116230747	33031691	C	2.673	2.64E-14	rs116425258	33046726	C	2.689	5.78E-14	rs116024094	33065711	A	2.889	1.47E-16
rs115404392	33031767	A	2.765	1.56E-15	rs114120159	33046742	C	3.195	1.20E-22	rs116649912	33065813	A	3.567	1.03E-33
rs114621696	33031809	C	2.765	1.56E-15	rs116285914	33046915	A	2.689	5.78E-14	rs147836064	33065993	G	3.135	8.71E-22
rs114785098	33031819	T	2.765	1.56E-15	rs115596400	33047031	C	3.858	5.21E-41	rs116745032	33066176	T	3.555	1.79E-33
rs116774728	33031934	T	2.773	1.45E-15	rs114396961	33047432	C	3.614	2.99E-37	rs116332566	33066236	A	3.567	1.03E-33
rs114933776	33031986	C	2.765	1.56E-15	rs115714173	33047466	C	3.052	5.65E-22	rs116495063	33066262	A	2.341	3.92E-08
rs116105320	33031994	C	2.765	1.56E-15	rs116100529	33047612	C	2.738	2.47E-14	rs114137435	33066465	A	3.567	1.03E-33
rs115655291	33032096	C	2.765	1.56E-15	rs116199894	33048348	A	2.682	8.10E-10	rs114777723	33066481	C	3.567	1.03E-33
rs114873240	33032159	C	2.763	2.91E-15	rs114172275	33048457	G	3.237	2.11E-28	rs115986757	33066594	G	2.69	3.66E-24
rs115768406	33032174	G	2.767	2.08E-15	rs115118356	33048459	G	3.226	9.28E-28	rs116737306	33067211	T	3.567	1.03E-33
rs115771088	33032188	A	2.767	2.08E-15	rs115929243	33048461	A	3.226	9.28E-28	rs149993072	33067281	C	3.567	1.03E-33
rs115039414	33032206	C	2.767	2.08E-15	rs142425820	33048466	T	2.724	2.75E-16	rs114977107	33067636	G	3.567	1.03E-33
rs116717442	33032272	T	2.765	1.56E-15	rs147762051	33048467	T	2.724	2.75E-16	rs115850157	33067663	T	3.567	1.03E-33
rs114307898	33032277	G	2.765	1.56E-15	rs114994560	33048539	A	3.137	2.96E-12	rs114477500	33067753	T	3.567	1.03E-33

rs114939328	33032347	G	2.765	1.56E-15	rs116768010	33048606	C	2.237	2.60E-09	rs115531966	33067769	G	3.567	1.03E-33
rs116112607	33032358	T	2.753	2.39E-15	rs115274041	33048628	C	2.646	7.22E-14	rs115793996	33067857	A	3.567	1.03E-33
rs114859249	33032430	C	2.765	1.56E-15	rs114462698	33048661	G	3.335	3.15E-24	rs116270006	33067897	A	3.58	1.94E-33
rs114617390	33032585	C	2.787	9.94E-16	rs116119081	33048663	A	3.439	1.27E-26	rs116246789	33068302	T	3.567	1.03E-33
rs116572398	33032600	G	2.766	1.92E-15	rs116369303	33048686	A	3.496	6.28E-36	rs139783835	33068848	T	-1.959	2.42E-13
rs115092330	33032623	A	2.582	1.44E-11	rs115008006	33048694	G	3.497	1.83E-35	rs115463704	33068864	C	3.501	9.14E-32
rs115893826	33032627	G	2.778	5.16E-17	rs116679521	33048921	G	2.749	2.07E-12	rs116819310	33068865	A	2.86	1.91E-15
rs114837706	33032636	G	2.619	9.30E-14	rs114495751	33048937	G	3.346	1.39E-14	rs114585416	33068917	A	3.567	1.03E-33
rs116108687	33032663	A	2.442	4.40E-12	rs114800151	33049074	T	3.342	3.81E-12	rs114827855	33068964	G	2.875	2.39E-16
rs114615156	33032668	G	2.465	2.49E-12	rs114115575	33049211	T	3.649	6.97E-39	rs149215820	33068994	A	3.118	1.61E-21
rs114913099	33032692	T	2.465	2.49E-12	rs116712283	33049565	G	2.587	6.78E-10	rs141258788	33068999	G	3.567	1.03E-33
rs116657559	33032698	T	2.465	2.49E-12	rs115380538	33049726	T	3.447	9.82E-13	rs116351963	33069367	A	3.543	3.20E-33
rs114766478	33032703	T	2.617	6.53E-14	rs116039258	33049727	T	3.447	9.82E-13	rs146250732	33069405	C	3.135	8.71E-22
rs116658390	33032788	A	2.765	1.56E-15	rs115978422	33049902	A	3.136	7.16E-08	rs116189829	33069873	C	3.567	1.03E-33
rs114025444	33032822	A	2.765	1.56E-15	rs116626328	33049979	G	3.915	4.67E-44	rs115209476	33069893	G	3.567	1.03E-33
rs114662916	33032831	A	2.765	1.56E-15	rs114304162	33049983	T	3.915	4.67E-44	rs116733240	33070749	A	3.512	5.16E-32
rs114181663	33032865	C	2.765	1.56E-15	rs116309049	33050024	A	3.887	2.35E-43	rs116504932	33070817	T	3.512	5.16E-32
rs116258000	33032905	C	2.789	1.08E-15	rs114240803	33050036	C	2.869	5.20E-16	rs114444712	33070822	A	2.889	1.47E-16
rs114311974	33032968	A	2.765	1.56E-15	rs116758096	33050045	C	3.887	2.35E-43	rs115856514	33070907	A	2.87	2.72E-16
rs115357514	33032975	C	2.64	4.02E-13	rs115402263	33050084	T	2.837	2.06E-15	rs137857089	33071022	G	2.145	5.23E-08
rs116047128	33033022	G	2.765	1.56E-15	rs115337572	33050144	T	2.863	2.01E-15	rs114325112	33071134	G	3.368	5.76E-27
rs114841893	33033055	T	2.765	1.56E-15	rs116759462	33050196	C	3.801	2.62E-41	rs115427324	33071322	G	3.567	1.03E-33
rs116660207	33033058	C	2.765	1.56E-15	rs116268983	33050203	G	3.839	3.25E-42	rs114459295	33071335	C	3.368	5.76E-27
rs115980081	33033146	C	2.732	4.01E-15	rs116655782	33050223	A	3.47	4.16E-31	rs116820500	33071600	A	3.368	5.76E-27
rs116344226	33033170	C	2.732	4.01E-15	rs115432596	33050232	G	3.49	1.52E-31	rs115000033	33071708	A	3.368	5.76E-27
rs115214595	33033235	C	2.732	4.01E-15	rs114456271	33050279	G	3.971	2.21E-45	rs116588010	33071754	A	3.368	5.76E-27
rs116744469	33033266	A	2.587	3.74E-13	rs115334414	33050325	C	2.889	1.47E-16	rs114144253	33071777	G	3.368	5.76E-27
rs114417021	33033267	A	2.577	5.18E-13	rs115107243	33050369	G	3.971	2.21E-45	rs114790869	33071983	C	3.567	1.03E-33
rs115877819	33033287	C	2.686	1.56E-14	rs114140675	33050394	A	2.889	1.47E-16	rs114003378	33072240	T	3.512	5.16E-32
rs114522401	33033313	T	2.56	3.22E-12	rs115504989	33050441	A	3.934	2.05E-43	rs114988419	33072266	T	3.368	5.76E-27
rs115240491	33033351	T	2.728	6.88E-15	rs114761768	33050442	A	3.934	2.05E-43	rs115858374	33072287	A	3.512	5.16E-32
rs116817204	33033357	G	2.728	6.88E-15	rs114145420	33050463	G	2.924	7.26E-17	rs115279634	33072729	T	3.368	5.76E-27
rs114409513	33033388	C	2.728	6.88E-15	rs115187464	33050473	G	3.971	2.21E-45	rs115556524	33073068	G	3.412	2.29E-28
rs115504820	33033390	T	2.728	6.88E-15	rs115610465	33050499	G	3.971	2.21E-45	rs115967254	33073076	A	3.412	2.29E-28
rs116512952	33033484	T	2.725	5.91E-15	rs114303287	33050521	T	3.971	2.21E-45	rs114692341	33073322	G	3.954	4.80E-46
rs114700485	33033494	G	2.725	5.91E-15	rs114607095	33050654	A	3.971	2.21E-45	rs116084582	33073440	A	3.368	5.76E-27
rs114214553	33033507	T	2.725	5.91E-15	rs116569811	33050671	C	3.971	2.21E-45	rs114983705	33073463	A	3.412	2.29E-28
rs115261015	33033520	A	2.725	5.91E-15	rs115978192	33050683	G	3.971	2.21E-45	rs116589260	33073515	A	2.889	1.47E-16
rs116756871	33033630	T	2.696	3.08E-14	rs116252464	33050742	A	3.971	2.21E-45	rs114151875	33073902	C	3.567	1.03E-33
rs114866421	33033639	A	2.696	3.08E-14	rs114918174	33050829	C	3.954	4.80E-46	rs116169905	33073984	G	3.386	6.79E-28
rs115123194	33033710	C	2.577	1.06E-11	rs115668285	33050877	G	3.954	4.80E-46	rs115745772	33074288	T	3.798	4.51E-39
rs114411298	33033738	T	2.717	6.46E-15	rs114393291	33050970	T	3.954	4.80E-46	rs114007167	33074348	C	3.368	5.76E-27
rs116516255	33033787	C	2.611	1.24E-13	rs116791231	33051051	G	3.954	4.80E-46	rs114641502	33074389	C	3.412	2.29E-28
rs115874768	33033791	T	2.611	1.24E-13	rs114894162	33051139	A	3.954	4.80E-46	rs115267328	33074569	G	3.412	2.29E-28
rs116664945	33033811	T	2.316	2.17E-09	rs116651593	33051277	G	3.799	2.12E-41	rs114469285	33074612	A	3.412	2.29E-28
rs115551265	33033824	T	2.31	2.66E-09	rs114049315	33051280	C	3.799	2.12E-41	rs116090438	33074707	A	3.368	5.76E-27
rs115386596	33033837	A	2.515	1.46E-11	rs114358313	33051307	G	3.757	5.50E-40	rs114227365	33074712	C	2.341	3.92E-08
rs115576446	33033849	C	2.693	1.32E-14	rs117320751	33051316	A	3.683	3.82E-38	rs115308137	33074853	T	3.479	1.07E-29
rs114716019	33033894	T	2.717	6.46E-15	rs116425814	33051394	T	3.954	4.80E-46	rs116027249	33074908	G	3.55	8.03E-33
rs116600732	33033919	C	2.72	6.77E-15	rs116837548	33051460	T	3.796	4.55E-42	rs116363691	33074963	A	-1.953	3.59E-13
rs116574777	33033939	A	2.717	6.46E-15	rs114742809	33051467	G	3.842	6.88E-43	rs114786264	33075443	T	3.221	1.10E-23
rs116371244	33033952	G	2.725	5.95E-15	rs116519180	33051493	C	3.848	3.99E-44	rs114139463	33075635	G	3.368	5.76E-27
rs115760308	33033961	T	2.725	5.95E-15	rs116015319	33051500	G	3.827	1.92E-43	rs114778875	33075666	T	3.573	9.99E-33
rs115035211	33034007	C	2.717	6.46E-15	rs115688984	33051554	C	3.897	1.66E-45	rs115023932	33076090	A	3.221	1.10E-23
rs115879511	33034076	T	2.717	6.46E-15	rs114210736	33051558	C	3.902	1.24E-45	rs114059064	33076268	C	2.685	1.57E-23
rs116201424	33034079	G	2.717	6.46E-15	rs115238630	33051562	A	3.88	6.24E-45	rs114481538	33077271	G	-1.885	1.34E-12
rs115014444	33034113	C	2.717	6.46E-15	rs115810879	33051624	G	3.954	4.80E-46	rs116395195	33077776	T	3.136	7.16E-08
rs114721650	33034120	T	2.717	6.46E-15	rs116255670	33051640	A	3.954	4.80E-46	rs148825442	33078020	C	2.341	3.92E-08
rs114213276	33034177	G	2.657	1.40E-14	rs115190895	33051683	T	3.954	4.80E-46	rs115492133	33078082	T	2.8	1.44E-16
rs114857469	33034223	A	2.663	2.43E-14	rs116739017	33051689	T	3.954	4.80E-46	rs115995433	33078163	A	2.341	3.92E-08
rs114505458	33034240	C	2.663	2.43E-14	rs115295510	33051790	A	3.794	9.52E-42	rs114830950	33110341	C	3.174	8.23E-08
rs115590896	33034296	C	2.635	5.84E-14	rs116021664	33051845	A	3.637	6.37E-38	rs115045413	33125973	A	1.781	1.38E-08
rs116768728	33034305	T	2.635	5.84E-14	rs115470008	33051865	C	3.637	6.37E-38	rs116699562	33126064	C	1.749	2.50E-08
rs116629512	33034353	A	2.604	7.83E-13	rs115385068	33051910	A	3.724	1.03E-40	rs2071025	33143756	G	1.83	1.71E-08
rs115683439	33034354	C	2.604	7.83E-13	rs114818321	33051969	T	3.904	1.90E-45	rs9277935	33160425	T	1.994	2.65E-09
rs114199772	33034399	A	2.665	2.59E-14	rs116653007	33051976	A	3.904	1.90E-45	rs2076310	33166034	G	1.819	2.09E-08
rs116458532	33034404	A	2.663	2.43E-14	rs116527890	33052007	A	3.726	4.40E-40	rs116493714	33173842	A	1.819	2.09E-08
rs115763111	33034421	G	2.756	2.21E-15	rs116074141	33052008	C	3.726	4.40E-40	rs114270432	33174783	G	1.799	3.71E-09
rs116141115	33034471	G	2.846	6.13E-15	rs115863713	33052028	T	3.884	3.91E-44	rs114399730	33175575	T	1.807	2.60E-08
rs114657860	33034473	G	2.844	1.25E-12	rs116193012	33052072	T	3.883	8.04E-45	rs116656565	33176958	T	1.794	3.98E-09

rs115317932	33034478	T	2.788	4.84E-14	rs114775991	33052128	T	3.944	8.22E-46	rs114746671	33178010	T	1.807	2.60E-08
rs115194707	33034484	T	2.794	4.89E-14	rs116735198	33052250	G	3.928	2.03E-45	rs148234917	33187355	T	1.979	1.64E-10
rs115662265	33034507	A	2.597	3.74E-13	rs114384365	33052303	T	3.908	6.58E-45	rs116873213	33191784	C	1.962	2.47E-10
rs116684342	33034518	A	2.742	3.88E-15	rs116460236	33052315	A	3.878	3.61E-44	rs116347854	33192662	A	1.838	9.07E-09
rs114505980	33034530	G	2.742	3.88E-15	rs115940431	33052327	T	3.833	4.60E-43	rs116089594	33192867	C	2	1.02E-10
rs116542824	33034577	T	2.742	3.88E-15	rs116508927	33052354	A	3.938	1.02E-45	rs148431844	33194477	A	1.962	2.47E-10
rs115893108	33034653	A	2.742	3.88E-15	rs116035345	33052382	C	3.894	6.72E-44	rs139853115	33197589	G	1.873	4.38E-09
rs115354528	33034699	T	2.803	1.57E-15	rs145619190	33052414	G	3.954	4.80E-46	rs114852189	33036003	C	2.839	3.76E-16
rs116047253	33034702	G	2.745	8.36E-15	rs115475053	33052439	G	3.954	4.80E-46	rs114332526	33054141	C	3.445	1.01E-30
rs115765574	33034745	C	2.713	9.17E-14	rs114300209	33052492	C	3.927	1.69E-43					
rs116019428	33034746	A	2.713	9.17E-14	rs115537548	33052498	C	3.901	3.19E-44					
rs114808855	33034785	A	2.767	2.33E-15	rs116751915	33052502	T	3.307	3.66E-37					
rs116628019	33034876	C	2.593	1.89E-13	rs116196108	33052711	C	3.26	4.09E-23					
rs114314360	33034900	G	2.593	1.89E-13	rs114009083	33052768	C	3.954	4.80E-46					
rs115056012	33034906	C	2.593	1.89E-13	rs114642386	33052803	A	3.954	4.80E-46					
rs115050691	33034930	G	2.454	1.75E-11	rs115866623	33052950	C	3.954	4.80E-46					
rs116487412	33034931	G	2.494	7.14E-12	rs116283696	33052958	T	3.954	4.80E-46					
rs116271556	33034956	A	2.711	7.51E-15	rs115288819	33052986	C	3.954	4.80E-46					
rs115586819	33034992	C	2.744	2.96E-15	rs116678934	33053026	A	3.064	9.13E-09					
rs116713787	33035020	A	2.744	2.96E-15	rs114398048	33053167	C	3.954	4.80E-46					
rs114526284	33035088	G	2.508	5.32E-10	rs115440545	33053248	G	3.954	4.80E-46					
rs146542010	33035095	G	2.461	1.78E-09	rs116471469	33053252	A	3.954	4.80E-46					
rs115242443	33035134	G	2.746	1.38E-14	rs114025565	33053270	A	3.972	7.37E-45					
rs114887705	33035143	C	2.689	4.04E-14	rs115347121	33053271	C	3.972	7.37E-45					
rs116101195	33035272	G	2.643	5.34E-14	rs116633022	33053307	T	3.954	4.80E-46					
rs115770992	33035288	G	2.748	2.43E-14	rs116366252	33053352	T	3.523	1.26E-30					
rs115714567	33035330	A	2.726	1.33E-14	rs115755801	33053396	G	3.523	1.26E-30					
rs115133743	33035395	G	2.767	2.36E-15	rs115424889	33053399	C	3.954	4.80E-46					
rs115933867	33035398	G	2.767	2.36E-15	rs115105101	33053444	C	3.821	3.03E-48					
rs114266380	33035424	T	2.649	1.68E-12	rs115603897	33053455	T	3.954	4.80E-46					
rs115399739	33035436	A	2.698	1.04E-14	rs115296214	33053468	T	3.954	4.80E-46					
rs114619293	33035513	G	2.636	1.23E-13	rs116592890	33053477	C	3.954	4.80E-46					
rs116573452	33035514	G	2.631	1.23E-13	rs115930026	33053682	A	3.954	4.80E-46					
rs115447191	33035518	C	2.755	1.06E-15	rs114391795	33053812	G	3.448	3.59E-29					
rs114912283	33035829	C	2.761	1.93E-15	rs115046195	33053820	G	3.421	3.41E-32					
rs115415207	33035845	A	2.761	1.93E-15	rs115224451	33053942	C	3.476	1.02E-29					
rs115255503	33035855	A	2.761	1.93E-15	rs114926188	33053968	A	3.904	1.19E-44					
rs115693065	33035877	G	2.784	1.07E-15	rs9277491	33053971	C	3.904	1.19E-44					
rs114420400	33035887	C	2.765	1.56E-15	rs116449581	33053982	C	3.954	4.80E-46					
rs116398066	33035925	T	2.765	1.56E-15	rs9277493	33054046	G	3.989	2.12E-46					
rs115815701	33035969	G	2.641	1.97E-13	rs116603005	33054057	A	3.879	2.03E-43					
rs116259312	33035974	G	2.653	1.35E-13	rs114938175	33054074	T	3.161	3.73E-21					