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Original research

COVID-19 host-genetics: Known and novel variants in an admixed population

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ABSTRACT

Introduction: The investigation of host gene variants associated to COVID-19 has led to causal relationships and potential therapeutic targets, but most of these studies have taken place in individuals of European descent. **Objective:** Here, we aimed to confirm allele frequency differences in host genetic variants previously associated to COVID-19 in admixed individuals i.e., Mestizos from Mexico. Genes studied included those previously reported and replicated including, *ABO, CCR2, CCR9, CXCR6,*

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DPP9, FYCO1, IL10RB/IFNAR2, LZTFL1, OAS1, OAS2, OAS3, SLC6A20, TYK2, and *XCR1*. **Methods**: DNA from 106 COVID-19 patients and 2677 individuals were genotyped using the Illumina GSA array. Variants not probed in the array or that did not pass quality controls were imputed for these 14 genes using the 1000G phase 3 hg19 as reference following current standard protocols. Allele frequencies were computed and compared between COVID-19 patients and the general population. **Results:** We confirmed allele frequency differences for *ABO* rs657152, *DPP9* rs2109069, *LZTFL1* rs11385942, *OAS1* rs10774671, *OAS1* rs2660, *OAS2* rs1293767, and *OAS3* rs1859330 p<0.03. In addition, we identified over 100 SNVs with significant allele frequency differences (p-value <10 -2). Of these, there were four variants on *ABO, OAS1/2* and *FYCO1* with a high functional impact assessed in-silico. **Conclusions:** our observations confirm allele frequency differences in genes associated to COVID-19 in an admixed population and prompts for the development of metanalyses to validate local and geographical patterns of COVID-19 severity and infection associated to genetic variation.

Key words: COVID-19; host genetics; gene variation; admixed population.

RESUMEN

Introducción: Las variantes genéticas asociadas a la COVID-19 son indicadoras de genes causales y potenciales blancos terapéuticos. Desafortunadamente, la mayoría de estos estudios se han realizado en individuos de ancestría europea y desconocemos la presencia de éstas en otras poblaciones. **Objetivo:** Identificar y confirmar la frecuencia alélica de variantes relacionadas con la COVID-19 en población mexicana mestiza en los genes *ABO, CCR2, CCR9, CXCR6, DPP9, FYCO1, IL10RB/IFNAR2, LZTFL1, OAS1, OAS2, OAS3, SLC6A20, TYK2,* and *XCR1*. **Métodos**: El ADN de 106 pacientes y 2677 individuos sin infección previa y al momento de la entrevista fueron genotipados mediante microarreglo e imputación. Se determinó la frecuencia alélica y esta se comparó entre pacientes versus la población general. **Resultados:** Se confirmaron diferencias en la frecuencia alélica para las variantes ya reportadas, *ABO* rs657152, *DPP9* rs2109069, *LZTFL1* rs11385942, *OAS1* rs10774671, *OAS1* rs2660, *OAS2* rs1293767, y *OAS3* rs1859330 p<0.03. También reportamos más de 100 variantes con diferencias en la frecuencia alélica entre pacientes y la población general (p-value <10-2), se determinó el impacto funcional in-silico de éstas identificando 4 variantes con un impacto alto en *ABO, OAS1/2* and *FYCO1*. **Conclusiones:** Se confirman diferencias en la frecuencia alélica entre pacientes con COVID-19 y la población general en mestizos mexicanos, para genes previamente asociados con COVID-19, validando estudios previos, y fomentando el desarrollo de metaanálisis que validen y complementen la información genética relacionada con la infección y severidad a la COVID-19.

Palabras clave: COVID-19; genética humana; variantes genéticas; población mestiza.

INTRODUCTION

The World Health Organization (WHO) announced the COVID-19 pandemic as a world health emergency on January 30th, 2020, following the confirmation of 7,818 cases across 18 countries. The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection develops with a wide range of symptoms, from asymptomatic, to mild, to severe manifestations, and lethality related to respiratory failure, septic shock, and multiple organ dysfunction. Different factors including clinical biomarkers, anthropometric, and demographic parameters have been associated to COVID-19 outcomes highlighting the heterogeneity of these components linked to SARS-CoV-2 infection. Parallel to the method development for the identification of SARS-CoV2 strains we have been witnessing much progress in the characterization of the host genetics and its association with disease symptoms and clinical outcomes.[1]

The host genetics of COVID-19 has been intensively studied showing that several variants can impact immunity, inflammation through the cytokine cascade, severity, and susceptibility to SARS-CoV-2.[2,4] A consistent set of genetic variants have been associated to COVID-19 including some for the virus receptors *ACE2*, *TMPRSS2*, immune components *IFNAR1/2*, *TYK2*, interleukins IL6, antiviral genes OAS1-3, toll-like receptors of innate responses, *TLR3/4/7*, *HLA* genes, *APOE* and the locus 3p21.31 (several genes including, *SLC6A20*).[3,5] At the time of this study there are about 22 genome wide association studies (GWAs) for COVID-19 adding to the collection of variants that link, in part, disease risk, severity, and susceptibility mostly in populations of European descent.[6,7] Several of these have been

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confirmed in more than one study and these consistently include variants on genes, ACE2, ABO, OAS1-3, and the 3p21.31 locus that holds 6 genes, *SLC6A20*, *LZTFL1*, *CCR9*, *FYCO1*, *CXCR6*.[8,9] It is important to mention that there is still ongoing research in the field including the development of associations between the host genome and a myriad of clinical characteristics and outcomes that have been reported during SARS-CoV-2 infection, these might include key endpoints as mentioned above, and specific symptoms such as headache, pharyngalgia, dyspnea, diarrhea, myalgia, vomiting, sputum production, anxiety, chest pain, fatigue, nausea, anorexia, abdominal pain, rhinorrhea, runny nose, nasal congestion, dizziness, chills, systemic pain, mental confusion, hemoptysis, asthma, taste disorder, smell disorder, belching and tachycardia, with or without fever and normal, or dry cough, accentuating the complexity of these genetic associations.[10] The current literature indicates that up-to 15% of COVID-19 patients evolve to a severe disease[11] which can be in part due to gene variants that favor COVID-19 infection, susceptibility, respiratory failure, inflammation, immune exacerbated reactivity, and death.[12-16] Initial reports of the COVID-19 pandemic identified male and older age as risk determinants for increased severity, respiratory stress, and death.[17,18] This prompted to the creation of collaborative research groups such as The Sex, Gender and COVID-19 Project, that attempted to explain why more males were hospitalized compared to women.[19] T. Takahashi et al. reported that females show a more robust T cell activation while immune cytokines, associated with a worse progression, are higher in males.[20] Other hypotheses revolved around variation on the X chromosome such as a hypercoagulation karyotype, and genetic variation on *TLR7* and *ACE2* on the X chromosome.[21-23] Today it is still no clear whether sex differences have a genetic basis. Nevertheless, a faulty adaptive and innate immune system can partly explain the cytokine storm and the inability of the immune system to efficiently fight against SARS-CoV-2[24] and over 100 genetic variants on genes related to the immune function have been associated to exacerbated responses and immune-related death after SARS-CoV-2 infection including variants *on IFNAR1*, *IL6*, *OAS1-3*, and *TYK2*. Of all these studies only 2 were performed in non-Europeans, showing the lack of completion of the collection of genetic knowledge associated to COVID-19 for all world populations. The coverage of this paucity in genetic information could be of relevance to explain discrepancies of epidemiological studies which have shown that people from non-white ethnic backgrounds are at higher risk of infection and of severe COVID-19.[7] Research on COVID-19 host genetics provides an opportunity to fill the population knowledge gap, to determine whether genetic differences might be relevant risk factors for COVID-19, and if these associations are population independent. Up-to August 2023, twenty-two GWAS have identified relevant genetic variation associated to COVID-19 with 15 variants confirmed by more than one research group including, The COVID-19 Host Genetics Initiative,[9] The UK based Genetics of Mortality in Critical Care (GenOMICC),[6] and The Severe COVID-19 GWAS Group.[25,26] Results from these investigations motivated the development of models to predict the risk of severe COVID-19 and in March 2021, G. Dite et. al. published a validated model to assess the risk of COVID-19 for participants of the UK Biobank. The model included genetic variants from previous research, new variations from The COVID-19 Host Genetics Initiative, and variants from P. Castineira *et al.*[6,27,28] The final prediction model showed that 7 out of 116 variants, rs112641600, rs10755709, 118072448, rs7027911, rs71481792, rs112317747, rs2034831, can partially predict COVID-19 severity.[28] These predictions were based on 22 studies of which only two were performed in non-Europeans, one in China and another with East Asian participants.[7] This points towards the need to expand and replicate risk model assessments in different populations including those admixed and from Latin-America. Here, we sought to investigate allele frequencies of COVID-19 associated variants in Mexican individuals of mixed ancestry according to previously published GWAs that were available at the onset of this investigation.[1,6,29-31]

MATERIALS AND METHODS

Study population

One-hundred and six COVID-19 patients and 2677 non-infected individuals were recruited by three different institutions in Mexico City: Hospital General de Zona 48, Instituto Politécnico Nacional (IPN, ENCB), Código 46, and Instituto Mexicano del Seguro Social (IMSS). All participants signed informed consent, protocols followed the principles of the declaration of Helsinki, and were approved by the Committees of Research, Ethics and Biosafety at INMEGEN No. CEI2017/04 and IMSS No. 23/2016/I. SARS-CoV-2 infection was confirmed in 106 patients by a nasal PCR or an antigen test (Table 1). DNA was extracted from a blood sample using the Puregene blood kit (Qiagen). The comparison group was defined as the general population consisting of 2677 individuals (Table 1) with no COVID-19 infection confirmed by a PCR test (N=803, 30%), an antigen test (N=900, 34%) or a follow-up call (N=977, 36%).

Table 1. Population characteristics

	COVID-19	General Population
N	106	2677
males*	64	1148
age y	42 (17 – 73)	58 (17 -97)
BMI kg/m²*	28(20 – 31)	33 (17 - 55)
T2D*	85	1832
Hypertensive*	76	1272
Hospitalized	14	none
COVID antigen confirmed	44	803
COVID PCR confirmed	72	900
Severe COVID	16	none
Moderate COVID	43	none
Asymptomatic	47	none

Mean (range); *denotes differences between group comparisons; T2D: type-2 diabetes, HT: hypertension, Hosp.: hospitalized, PCR and antigen tests refer to COVID-19 diagnostic laboratory tests; * indicate significant differences, p-value<0.05.

Genetic analyses

Genotyping was performed with the Infinium GSA microarray v.1.0 (Illumina) focusing on genes previously associated to COVID-19, *ABO, CCR2, CCR9, CXCR6, DPP9, FYCO1, IL-10RB/IFNAR2, LZTFL1, OAS1, OAS2, OAS3, SLC6A20, TYK2,* and *XCR1* with special interest in variants with consistently reported allele frequency differences, *ABO* rs657152, rs8176747, rs41302905, *CCR9/LZTFL1, CXCR6, FYCO1, XCR1* Locus 3p21.31 (lead rs11385942), *DPP9* rs2109069, *IL10/IFNAR2* rs2236757, OAS1-3 rs10774671, rs2660, rs10735079, rs1293767, rs1859330, rs2285932, *SLC6A20* rs2742396, and *TYK2* rs1108572, rs74956615 (Table 2).[27,32]

Table 2. Single nucleotide variants previously associated with COVID-19 variants replicated in this admixed population

Gene, rs AF reported for Latin America	AF COVID-19	AF General Pop.	p-value	Ref.
ABO rs8176747, AF:0.064	0.0425	0.0579	NS	European (8,32)
ABO rs41302905, AF:0.009	0.0100	0.0139	NS	
ABO rs657152, AF:0.239	0.3600	0.244	7.50×10^{-5}	
DPP9, AF:0.238	0.3208	0.2462	1.35×10^{-2}	Multiple ancestries (4,11,16)
IFNAR2 rs2236757, AF:0.454	0.4380	0.4563	NS	
OAS1 rs10774671, AF:0.224	0.1840	0.2748	2.71×10^{-2}	British, Multiple (3,11,39)
OAS2 rs2660, AF:0.194	0.1085	0.1806	3.10×10^{-2}	
OAS3 rs10735079, AF:0.213	0.1274	0.1950	1.41×10^{-2}	
OAS3 rs1859330, AF:0.211	0.1462	0.2762	2.90×10^{-2}	
OAS3 rs2285932, AF:0.184	0.1040	0.137	NS	

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SLC6A20 rs2742396, AF:0.398	0.2123	0.4449	1.80×10^{-11}	European (3,39)
TYK2 rs1108572, AF:0.102	0.0047	0.0003	3.75×10^{-3}	
LZTFL1 rs11385942, AF:0.039	0.0094	0.0383	2.92×10^{-2}	Italy/Spain (3,39)

AF: Allele frequency, Gral Pop.: general population, Latin America AF from GnomAd and the ALFA project from https://www.ncbi.nlm.nih.gov/snp/. *TYK2* rs74956615 and *OAS2* rs1293767 were not detected.

Statistical and bioinformatic analyses

Variants that were not probed by the Infinium GSA array or did not pass microarray quality controls we imputed according to standard protocols with the software MACH v.1.0 and recommendations for human genetic imputation.[33,34] Public data from the 1000G phase 3, and the human genome assembly hg19 were included in the imputation protocol.[35] Allele frequency comparisons were performed using PLINK for variants that passed imputation bioinformatic quality controls.[33,36] Population admixture was calculated with 56,663 microarray variants using a model-based likelihood estimation with the program ADMIXTURE 3.0 (Supplemental Figure 1).[37] The selection of the informative ancestry variants was based on allele frequency of the minor allele (MAF > 0.05) between the four main parental groups; variants were excluded if they were in linkage disequilibrium ($r2 \geq 0.1$) or within a predefined physical distance of at least 500 kb.[21,22] COVID-19 samples and the general population showed very similar genetic ancestry proportions and did not impact allele frequency differences. All patients were admixed Mexicans from the metropolitan area showing on average, 45% Native, 34% Caucasian, 12% Asian, and 8% African ancestral proportions determined by comparing their genotypes with continental populations. Northern Europeans from Utah (CEU), Chinese Han from Beijing (CHB) and Yoruba Ibadan from Nigeria (YRI) from the 1000 genomes data base. No individual showed exclusively Native or European ancestries, no differences in admixture proportions between study groups were detected and admixture observations were in accordance with previous reports (Supplemental Figure 1).[38,39] In addition, kinship and inbreeding analyses using PLINK and an IBD proportion <0.5 showed that individuals were not related in first or second degrees, on average the population showed an inbreeding proportion similar to average populations between 10-15%. Allele frequency differences between groups were determined using a Chi-square test considering a p-value<0.05 as significant, calculations were computed using the Software R v4.0.5 and PLINK.[36,40]

Variant functional impact assessment

The functional impact of novel variants was determined in-silico using the Ensembl Variant Effect Predictor (VEP v.111). Variation was annotated according to the GRCh37.p13 genome assembly. VEP assessed functional consequences across coding and noncoding regions by comparing each variant to its corresponding transcript in the ENSEMBL/GENCODE 19 database matching the transcript location of the variant with molecular consequences computed and reported using the Sequence Ontology nomenclature. Here, we report the last iteration of this functional analysis, which represents the variant to the closest gene, and the one with the highest precision from all iterations performed.

It is important to mention that the differences in sample size between study groups did not allow for the development of association models, but future studies with additional COVID-19 samples may incorporate different covariates such as genetic ancestry to better account for population stratification.

RESULTS

Available clinical information for COVID-19 patients is presented in Table 1. On average individuals were 42 years old, 50% were diabetic and 70% hypertensive and showed an average BMI of 28 kg/m^2. The general population was on average 58 years of age, showed a BMI of 33 kg/m^2, 68% were diabetic and 48% hypertensive.

Genomic analyses and descriptive statistics

We genotyped and imputed single nucleotide variants (SNVs) on genes previously associated with COVID-19, only variants that passed bioinformatic quality controls for microarray and imputation processes were considered for further analysis. We detected most previously reported

variants including, *ABO* rs657152, rs8176747, rs41302905, *CCR9/LZTFL1, CXCR6, FYCO1, XCR1* Locus 3p21.31 (lead rs11385942), *DPP9* rs2109069, *IL10/IFNAR2* rs2236757, OAS1-3 rs10774671, rs2660, rs10735079, rs1293767, rs1859330, rs2285932, *SLC6A20* rs2742396, and *TYK2* rs1108572, rs74956615, but *TYK2* rs74956615 and *OAS2* rs1293767 known to impact COVID-19 outcomes, were not identified here; either because these did not pass bioinformatic quality control, they were not found in this population, or due to imputation limitations. Supplemental Table 1 lists all variants identified on these genes with an allele frequency ≥0.01%.

Allele frequency differences in COVID-19 associated variants

We confirmed allele frequency differences in 9 of the 13 detected SNVs (Table 2 and Figure 1), these were on *ABO* rs657152 p-value=7.2x10-5, *DPP9* rs2109069 p-value=0.014, *LZTFL1* rs11385942 p-value=0.029, *OAS1* rs10774671 p-value=0.0035, *OAS1* rs2660 p-value=0.007, *OAS2* rs1293767 p-value=0.00501, and *OAS3* rs1859330 p-value=2.9 x10-5. Allele frequencies in this admixed population were compared with that of ancestral populations, CEU, YRI, CHB based on data from the 1000 Genomes database, as mentioned above. Most allele frequency (AF) values were similar when compared to continental populations, but some apparent differences were detected for key variants including, *FYCO rs200040076, CXCR6 rs113318190, XCR1 rs181118021, ABO rs56390333,* and *OAS3 rs2072134*. Figure 1 shows AF key differences; for example, *FYCO* rs200040076 in COVID-19 patients showed an AF of 0.014, but it was almost absent in other populations. Similarly, *CXCR6* rs113318190 and *XCR1* rs181118021 showed an allele frequency around 0.10 in COVID-19 samples and were significantly less frequent in all other continental groups including admixed Mexicans (AF:0.0002). A more common variant was *OAS3* rs2072134 which showed an allele frequency of 0.10 in COVID-19 patients similar to that reported for CHB, but with an AF of 0.008 in this admixed population, and absent in other continental groups, potentially hinting towards the ancestral line that led this variant to Mexico (Figure 1). Intriguingly, *ABO* rs56390333 was present in COVID-19 patients and in individuals with YRI ancestry (AF: 0.080 and 0.050), but absent in other populations. We also found interesting differences in allele frequencies on *CXCR6 rs113318190, XCR1 rs181118021, and OAS3 rs2072134* between Mexicans from Los Angeles (MXL) from the 1000 Genome database and Mexicans from this study. The *OAS3 rs2072134* variant was present as a heterozygous only showing a low allele frequency <0.001, but these variants, *CXCR6 rs113318190, XCR1 rs181118021, and OAS3 rs2072134*, were absent in MXL likely due to the small group representing MXL. This highlights the importance of studying admixed populations in larger sample sizes.

Novel variation on COVID-related genes

We identified over 100 SNVs, not previously reported, with apparent and significant allele frequency differences between COVID-19 patients and the general population. The most relevant were listed in Table 3 and Figure 1, all showing the presence of the alternative allele more frequently in COVID-19 patients compared to the average population. Genes with the largest number of variants showing significant allele frequency differences between groups were *ABO (8 SNVs)*, *FYCO1 (5 SNVs),* and *XCR1 (5 SNVs)*, (p-value<10^{-50}).

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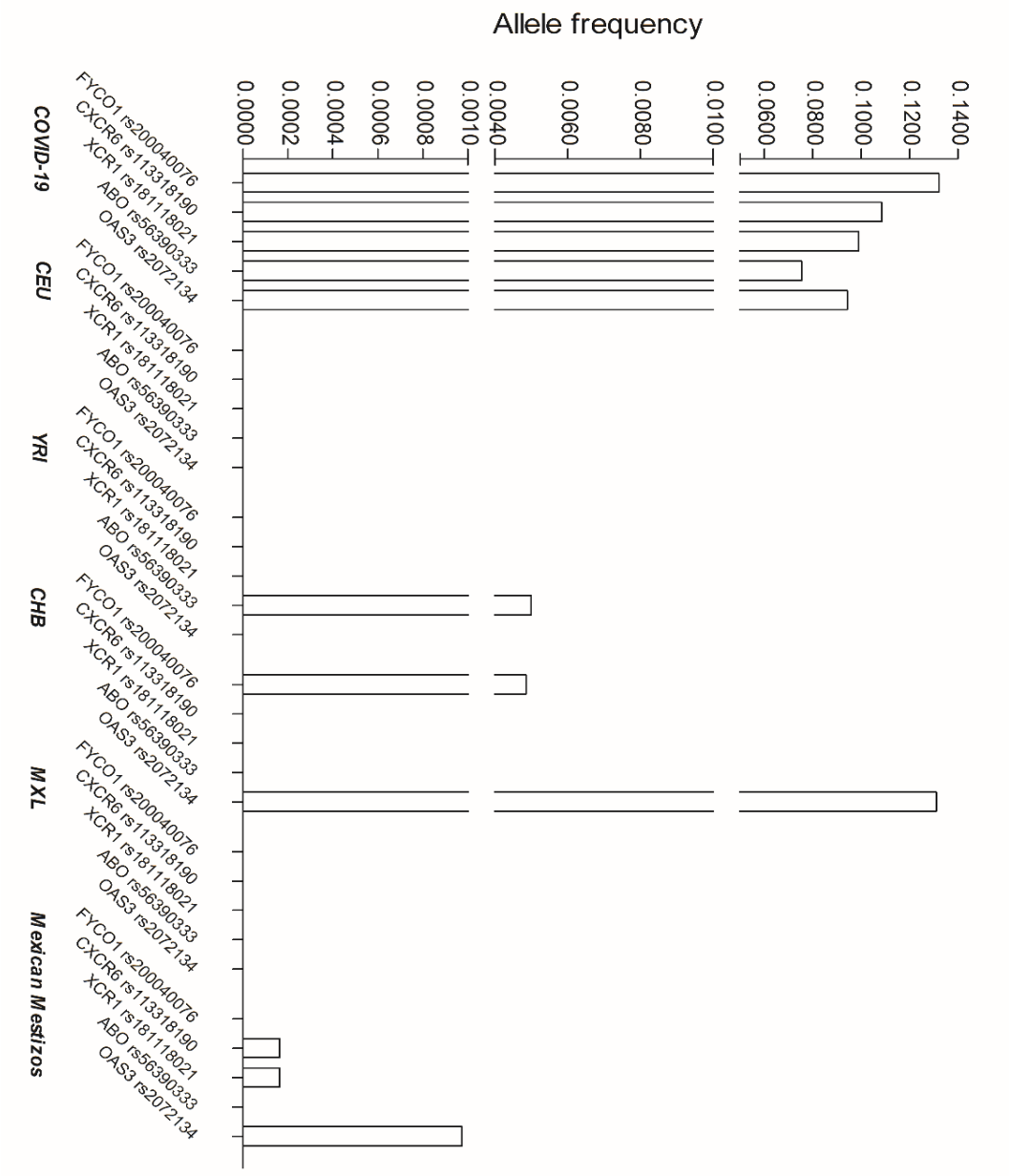
Table 3. Top novel variation of allele frequency differences in COVID-19 samples

Gene	rs identifier	allele	AF COVID-19	AF Gral Pop	p-value
FYCO1	rs200040076	C>T	0.1321	0	$1.14\ 10^{-179}$
CXCR6	rs113318190	G>A	0.1085	0.00016	$2.30\ 10^{141}$
XCR1	rs181118021	G>A	0.0991	0.00016	$1.15\ 10^{-128}$
ABO	rs56390333	G>A	0.0755	0	$2.47\ 10^{-103}$
OAS3	rs2072134	G>A	0.0943	0.00097	$1.40\ 10^{-97}$
ABO	rs35494115	G>A	0.0802	0.00049	$1.86\ 10^{-92}$
OAS3	rs16942374	G>A	0.066	0.00016	$2.54\ 10^{-84}$
DPP9	rs118149076	G>A	0.0708	0.00081	$1.23\ 10^{-71}$
ABO	rs371569951	G>A	0.0613	0.00049	$8.44\ 10^{-68}$
ABO	rs200932155	G>A	0.066	0.00097	$3.07\ 10^{-62}$
DPP9	rs75191837	T>C	0.0755	0.00227	$7.01\ 10^{-53}$
ABO	rs8176716	G>A	0.1179	0.00796	$7.28\ 10^{-49}$
SLC6A20	rs184655598	G>A	0.033	0	$3.50\ 10^{-46}$
CCR9	rs41289608	G>A	0.2264	0.03313	$9.74\ 10^{-46}$
IFNAR2	rs144511372	C>T	0.0283	0	$7.91\ 10^{-40}$
CCR9	rs79006711	G>A	0.1981	0.0302	$2.70\ 10^{-38}$
TYK2	rs35018800	G>A	0.0613	0.00276	$1.79\ 10^{-34}$
ABO	rs9411372	G>A	0.0377	0.00065	$1.81\ 10^{-34}$
ABO	rs61736301	G>A	0.0283	0.00016	$5.14\ 10^{-34}$
CCR9	rs6775854	G>A	0.2028	0.03556	$1.76\ 10^{-33}$
CCR9	rs7648467	C>A	0.2028	0.03556	$1.76\ 10^{-33}$
FYCO1	rs141064206	C>T	0.0236	0	$1.80\ 10^{-33}$
FYCO1	rs141476300	G>A	0.0236	0	$1.80\ 10^{-33}$
FYCO1	rs7619256	G>A	0.1934	0.03264	$2.24\ 10^{-33}$
CCR9	rs17078408	T>G	0.2028	0.03573	$2.65\ 10^{-33}$
ABO	rs1053878	G>A	0.2028	0.03654	$1.95\ 10^{-32}$
FYCO1	rs140002692	G>A	0.0377	0.00081	$1.09\ 10^{-31}$

AF: allele frequency, NS, not significant.



Bars indicate the allele frequency of each genetic variant, note the scale in the Y axis for low and higher allele frequencies. COVID-19: patients from this study, CEU: Europeans, YRI: Africans South of the Sahara, CHB: Chinese Han from Beijing, MXL: Mexicans from Los Angeles from The 1000G database, Mexican Mestizos: individuals from this study.

Figure 1. Allele frequency differences on genes associated to COVID-19 compared to continental populations. COVID-19 refers to patients from this study, CEU, YRI, CHB and MXL data were taken from the 1000G database, Mexican Mestizos refers to the general population data from this study.

We also identified genetic variation exclusive of COVID-19 samples including, 43 SNVs with a null allele frequency in the general population but present in COVID-19 samples. Of these, *ABO* rs56390333 (AF=0.076) and *FYCO1* rs200040076 (AF=0.132) were the most common (Table 3).

Other genes also showing variation exclusively in COVID-19 samples were, *CCR9* (9 SNVs), *OAS2* (3 SNVs), *LZTFL1* (12 SNVs), *SLC6A20* (8 SNVs), *IFNAR2*, *DPP9*, and *IL10RB*, statistical significance ranged from p-value < 10-8 (Supplemental Table 1).

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In-silico functional impact of genetic variants

The functional impact of these variants was assessed in-silico using the Ensembl Variant Effect Predictor (VEP) algorithm as mentioned earlier.[41,42] Table 4 and Figure 2 list and depict the functional impact of the top 100 novel variants most of these were either upstream (26%) or non-coding (22%). We also detected 9% of missense variants (N=17), 4 on *ABO*, 6 on *FYCO1*, 3 on *OAS3*, 2 on *TYK2*, and one on XCR1 and LZTFL1, all of them showing a moderate impact on protein function.

Table 4. Summary of the functional impact analysis of newly reported variants

Gene variant	AF difference, p-value	Functional impact
ABO rs56390333	$2.47\ 10^{-103}$	moderate/intron
FYCO1 rs200040076	$1.14\ 10^{-179}$	moderate/intron
OAS3 rs2072134	$1.40\ 10^{-97}$	moderate/intron
TYK2 rs35018800	$1.79\ 10^{-34}$	moderate/intron
XCR1 rs181118021	$1.15\ 10^{-128}$	moderate/intron
OAS1 rs2660	$7.00\ 10^{-03}$	high/stop codon
OAS1 rs10774671	$5.00\ 10^{-02}$	high/stop codon
OAS2 rs15895	$1.63\ 10^{-04}$	high/stop codon
FYCO1 rs13079869	$1.00\ 10^{-02}$	high/stop codon
ABO rs2014439325	$1.50\ 10^{-02}$	high/stop codon

The first five variants represent those with the largest differences in AF between COVID-19 samples and the general population. The latter five refer to those variants with the highest functional impact by VEP analysis, but they all have a lower statistical significance.

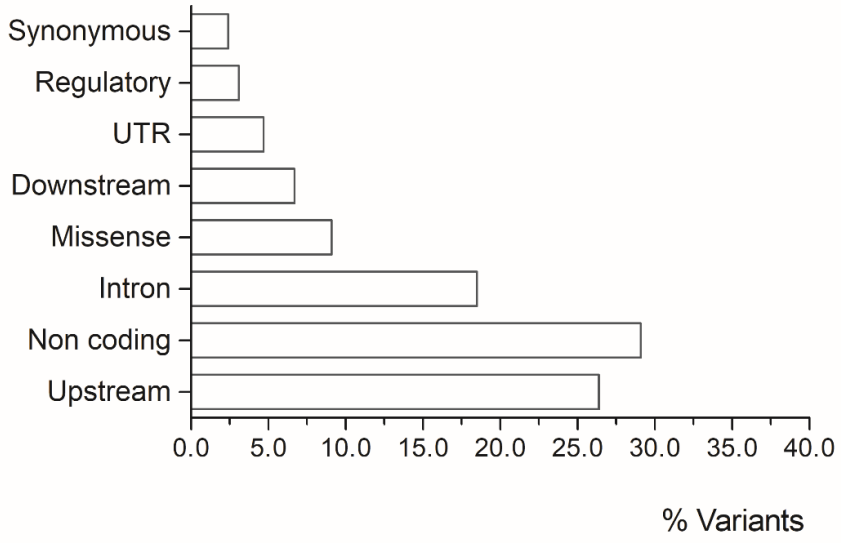

Figure 2. *In-silico* functional impact of top 100 variants with allele frequency differences.

DISCUSSION

Infection with SARS-CoV-2 presents an unpredictable course which can go from asymptomatic, to serious complications many of which have been associated to metabolic diseases.[10,43] According to the WHO and the Institutional Repository for Information Sharing (IRIS), Mexico showed a 18 – 25-fold higher COVID-19 risk compared to other countries.[44] It is known that within the country's demographic and geographical regions there are clusters of genetic variation with apparent differences meaningful for biomedical traits.[38] Moreover, Z. Yildirim et al. noted that for certain populations a higher COVID-19 incidence is seldom explained by behavior, environment, vitamin D levels, socioeconomic status, or cardiovascular risk, which prompts for the identification host genetic variants.[45] In this study we confirmed and expanded the list of COVID-19 associated gene variants in an admixed population from Mexico, below we discuss the relevance of these observations in the scope of what it is currently known about these loci.

Variation on the ABO gene

Initial reports on the host genetics of severe COVID-19 linked results almost immediately to blood type. Several research groups have reported ABO variants, rs8176747, rs657152, and rs41302905 which enhance the activation of the complement increasing COVID-19 severity.[46-48] Significant allele frequency differences in *ABO* rs657152 and rs8176747 (Table 2) were confirmed here (Table 2 and Supplemental Table S1). Here, we listed 157 additional COVID-19-associated variants on the *ABO* gene of which rs56390333 was the most significant and rs2014439325 showed a high detrimental impact in-silico, predicting a stop codon (Table 4). These observations expanded the relevance and variation of this gene in relation to COVID-19.

Variation on the OAS1-3 genes

Variation on *OAS1-3* may alter the proteins antiviral properties as their products trigger viral mRNA degradation.[29] *OAS3* rs1859330 reported here is a missense variant with a moderate impact on protein function, rs10735079 is located in a UTR region with an in-vivo functional impact not yet clear, rs10774671 and rs2660 showed an in-silico high detrimental impact as stop codons (Table 4). All *OAS1-3* variants here reported showed a lower allele frequency in COVID-19 samples compared to the general population (Table 3) supporting the notion that certain *OAS1-3* variation, putatively inherited from Neanderthals, may confer protection against severe COVID-19.[49]

Variation on the SLC6A20 gene

SLC6A20 is a glycine transporter needed for cytokine deployment during COVID-19 infection,[8] it is associated with T2D, and its product, SIT1, co-expresses and may interact with the SARS-CoV-2 receptor, ACE2. It is still not known if SIT1 affects the recognition of ACE2 by SARS-CoV-2,[50] but it may influence the proinflammatory cytokine secretion after SARS-CoV-2 infection.[8] Allele frequency differences on *SLCO6A20* rs2742396 were confirmed here (Table 3), and even though the *in-silico* functional analysis predicted it as a modifier variant, its actual impact on its product and its relation to COVID-19 has yet to be clarified.

Variation on the TYK2 gene

TYK2, tyrosine kinase 2 is part of the effector cascade of activated interferon receptors, its presence increases susceptibility to microbial infections and has been suggested as a drug target to treat COVID-19.[1] *TYK2* was first associated with severe COVID-19 by Pairo-Castineira et. al, and *TYK2* rs1108572 and rs35018800 were confirmed here, both predicted as modifier variants in-silico and more frequently present in COVID-19 patients (Table 3). Their clear role in COVID-19 severity is not evident, *TYK2* rs1108572 and rs35018800 are intron and missense variants so, it is possible that *TYK2* genetic variation alters the cytokine storm observed in severe cases.[6,51]

Variation on the DPP9 gene

DPP9 codes for the dipeptidyl peptidase, also known as CD26, is mainly responsible for T cell activation. Variants DPP9 rs13015258 and rs2109069 have been associated with severe COVID-1912,45 through its impact on the disease's immunogenetics52. We confirmed previous reports regarding *DPP9* rs2109069 by identifying significant a higher allele frequency o *DPP9* rs118149076, and rs75191837 in COVID-19 samples (Table 3, Supplemental Table S1). These variants were intronic or located on untranslated regions with a modifier impact in-silico, its causal association to COVID-19 remains to be investigated.

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Variation on the LZFTL1 gene

LZFTL1 rs11385942 is an intron variant with a modifier *in-silico* effect on the protein function, linked to the activation of the complement in individuals with severe COVID-19,[25] and more recently to a weakened airway viral clearance,[12] *LZFTL1* rs11385942 was confirmed here with a 4-fold lower allele frequency in COVID-19 patients (Table 3) supporting previous results.[53]

LZFTL1 codes for leucine zipper transcription factor like 1 and this variant did not show a relevant functional prediction *in-silico* analysis. Other variants here observed on *LZFTL1* seemed to have a modifier impact in protein function (Figure 2, Supplemental Figure SF2, and Supplemental Table ST2).

In-silico functional impact analysis of all 400 variants revealed five SNVs with a high functional impact, these were on *ABO, FYCO1, OAS1*, and *OAS2*, all affecting the stop codon and showing allele frequency differences between COVID-19 samples and the general population (Table 4 and Supplemental Table ST2). Future studies may seek to uncover its relevance in COVID-19 severity and clinical outcomes.

As COVID-19 research continues more variants will be identified as potential causal targets. For example, a recent multicenter metanalysis identified 113 variants associated to COVID-19 mortality most of them related to the modulation of the immune response directing more studies into regulating gene expression in immunity and lung function pathways.

Moreover, translational research has started to look into hindering the entrance of the virus by targeting the lipid platform needed for its entry i.e., inhibiting acid sphingomyelinase.[54] Minnai et al. have identified several drug candidates for inhibiting acid sphingomyelinase including the known drugs, amiodarone and astemizole.[55] Consequently, it is only logical to hypothesize that by increasing genetics and omics research the scientific community will complete the collection of genetic variation that may lead to identifying individuals at risk with a mechanistic explanation.

To summarize, our study confirmed allele frequency differences in genes previously associated with COVID-19 on *ABO, OAS1-3, SLC6A20, TYK2,* and *DPP9*. In addition, we provide a list of over 100 variants on these genes with significant allele frequency differences between COVID-19 patients and the general population that have not been previously reported. It is important to mention that the available clinical information and small sample size of the COVID-19 patients limited our statistical analyses for the development of association models.[25,29] Mexico is within the top fifteen countries with the highest number of COVID cases and 4th in COVID-related deaths. Infection and mortality rate are not consistent nor in proportion with population density highlighting the relevance of investigating all potential factors including genetic variation that may explain infection and mortality. Therefore, it is of relevance to continue genetics research related to COVID-19 to complement biomedical parameters that would possibly lead to the identification of populations at risk and therapeutic targets.

CONCLUSIONS

COVID-19 host genetic variation is slowly being completed and current endeavors are focused on quantitatively identifying individuals or populations at risk for all world populations. Our results confirm and complement previous reports on host gene variation in an admixed population. As more research becomes available it will be possible to validate the impact of host genetic variants on SARS-CoV-2 infection susceptibility, disease severity and treatment efficacy for all countries. Metanalyses considering admixture will enable the development of prediction models to discern if the impact of genetic variation for COVID-19 is population independent.

CONFLICT OF INTEREST

The authors declare no conflict of interests.

ACKNOWLEDGMENTS

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SUPPLEMENTAL MATERIAL

All supplemental information is consolidated in a pdf and includes Supplemental Table 1. Allele frequencies of all

genotyped variants; Supplemental Table 2. In-silico functional impact of all observed variants; and Supplemental Figure 1. Population admixture.

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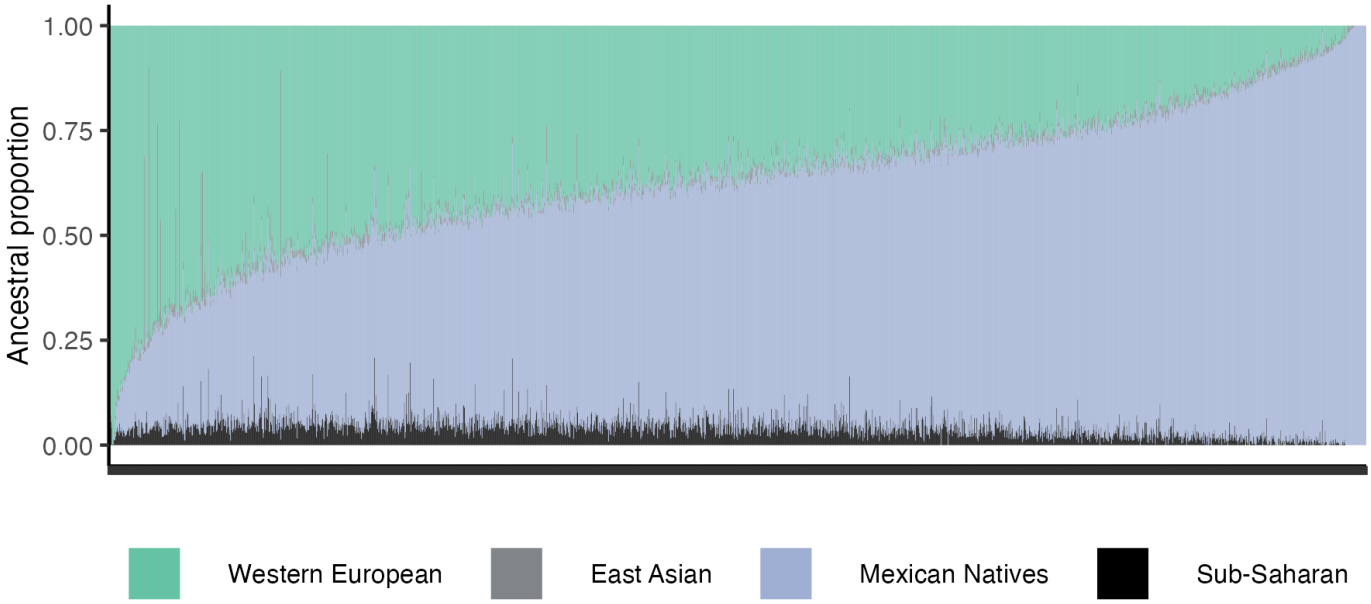
ALLSUPPLMATS COVID

Figure S1. Study population admixture proportions



Supplemental Table S1. Allele frequency on genes associated with COVID-19

SNP	CHR	GENE	Reference alelle	Alternative allele	Alternative allele frequency in General population	Alternative allele frequency in COVID-19 patients
rs56390333	9	ABO	A	G	0	0.07547
rs35494115	9	ABO	C	T	0.0004872	0.08019
rs371569951	9	ABO	A	G	0.0004872	0.06132
rs200932155	9	ABO	A	G	0.0009743	0.06604
rs113318190	3	CXCR6	A	G	0.0001624	0.1085
rs118149076	19	DPP9	A	G	0.000812	0.07075
rs200040076	3	FYCO1	C	T	0	0.1321
rs181118021	3	NRBF2P2	C	G	0.0001624	0.09906
rs16942374	12	OAS3	T	C	0.0001624	0.06604
rs2072134	12	OAS3	T	C	0.0009743	0.09434
rs7466899	9	ABO	T	C	0.0009743	0.03302
rs8176739	9	ABO	A	G	0.005196	0.07075
rs1053878	9	ABO	T	C	0.03654	0.2028
rs8176716	9	ABO	C	G	0.007957	0.1179
rs9411372	9	ABO	A	C	0.0006496	0.03774
rs8176705	9	ABO	G	A	0.004547	0.07075
rs61736301	9	ABO	C	A	0.0001624	0.0283
rs543040	9	ABO	G	A	0.2335	0.5708
rs613534	9	ABO	A	T	0.2442	0.5708
rs544873	9	ABO	C	G	0.2442	0.566
rs545971	9	ABO	A	G	0.2335	0.5519
rs612169	9	ABO	T	C	0.2335	0.5519
rs597988	9	ABO	C	T	0.2332	0.5519
rs597974	9	ABO	T	C	0.2332	0.5519
rs576123	9	ABO	G	C	0.2332	0.5519
rs8176663	9	ABO	C	A	0.2335	0.5519
rs491626	9	ABO	C	A	0.2332	0.5425
rs492488	9	ABO	A	T	0.2332	0.5425
rs493246	9	ABO	G	C	0.2332	0.5425
rs494242	9	ABO	G	A	0.2439	0.5519
rs495203	9	ABO	T	C	0.2332	0.5425
rs582118	9	ABO	A	G	0.2161	0.5142
rs582094	9	ABO	C	T	0.217	0.5425
rs79006711	3	CCR9	A	G	0.0302	0.1981
rs41289608	3	CCR9	T	C	0.03313	0.2264
rs6775854	3	CCR9	C	T	0.03556	0.2028
rs7648467	3	CCR9	G	A	0.03556	0.2028
rs17078408	3	CCR9	T	C	0.03573	0.2028

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rs75192040	3	CCR9	A	G	0.03621	0.1792
rs113305890	19	DPP9	G	A	0.02273	0.1321
rs73539528	19	DPP9	T	C	0.02192	0.1321
rs75894880	19	DPP9	G	A	0.01786	0.1321
rs57034092	19	DPP9	A	G	0.02209	0.1321
rs74840661	19	DPP9	T	C	0.01007	0.09434
rs78788550	19	DPP9	G	T	0.01056	0.09434
rs16992502	19	DPP9	G	A	0.01185	0.09434
rs79945697	19	DPP9	C	T	0.01056	0.09906
rs75191837	19	DPP9	C	G	0.002273	0.07547
rs114625537	19	DPP9	T	G	0.01056	0.09434
rs60431156	3	FYCO1	T	G	0.01559	0.1038
rs564601460	3	FYCO1	A	G	0.001949	0.04245
rs146554934	3	FYCO1	CT	C	0.002111	0.04245
rs114548859	3	FYCO1	A	G	0.002111	0.04245
rs141155944	3	FYCO1	A	G	0.001949	0.04245
rs150785981	3	FYCO1	A	G	0.001949	0.04245
rs140002692	3	FYCO1	T	C	0.000812	0.03774
rs77896301	3	FYCO1	A	G	0.002111	0.04245
rs75726990	3	FYCO1	A	G	0.002111	0.04245
rs145828326	3	FYCO1	T	A	0.000812	0.03774
rs181518477	3	FYCO1	C	G	0.001949	0.04245
rs140228956	3	FYCO1	T	C	0.001949	0.04245
rs189847748	3	FYCO1	T	G	0.001949	0.04245
rs141064206	3	FYCO1	G	C	0	0.02358
rs141476300	3	FYCO1	T	C	0	0.02358
rs7619256	3	FYCO1	C	T	0.03264	0.1934
rs3947589	3	FYCO1	G	T	0.06772	0.2406
rs144511372	21	IFNAR2	C	T	0	0.0283
rs61732395	12	OAS3	T	C	0.001462	0.03774
rs184655598	3	SLC6A20	A	G	0	0.03302
rs35018800	19	TYK2	A	G	0.002761	0.06132
rs55882956	19	TYK2	T	C	0.0203	0.1415
rs569981396	9	ABO	A	C	0	0.004717
rs10901251	9	ABO	A	G	0.1431	0.3208
rs34266669	9	ABO	T	C	0.05278	0.1274
rs199969472	9	ABO	C	G	0.05278	0.1274
rs35184739	9	ABO	C	G	0.05261	0.1274
rs7849280	9	ABO	T	C	0.05294	0.1274
rs9411475	9	ABO	C	T	0.04449	0.1179
rs13291798	9	ABO	G	A	0.0354	0.1085
rs34085694	9	ABO	T	C	0.06073	0.1792
rs4962113	9	ABO	AT	A	0.4209	0.3349

rs111590440	9	ABO	T	C	0.01104	0.0283
rs73660468	9	ABO	C	T	0.008282	0.04717
rs7870156	9	ABO	C	T	0.01023	0.04245
rs62574565	9	ABO	T	C	0.4638	0.5613
rs58081338	9	ABO	G	C	0.4729	0.6274
rs62574567	9	ABO	T	C	0.4729	0.6274
rs60484807	9	ABO	G	A	0.4688	0.3255
rs12554580	9	ABO	A	G	0.4688	0.3302
rs12554336	9	ABO	A	T	0.4726	0.6274
rs12554339	9	ABO	G	T	0.4657	0.5755
rs10901253	9	ABO	G	A	0.4726	0.6274
rs10751502	9	ABO	A	C	0.4657	0.3208
rs11244052	9	ABO	T	C	0.4657	0.5755
rs11244053	9	ABO	T	C	0.4726	0.6274
rs4962114	9	ABO	A	G	0.4726	0.6274
rs4962115	9	ABO	T	C	0.4726	0.6274
rs4962116	9	ABO	A	C	0.4726	0.6274
rs8176757	9	ABO	G	C	0.4696	0.3302
rs111207633	9	ABO	C	G	0.00682	0.0283
rs11244054	9	ABO	T	C	0.3157	0.2264
rs530909128	9	ABO	A	G	0.0003248	0.004717
rs7469795	9	ABO	C	A	0.4701	0.3255
rs7466519	9	ABO	T	C	0.00682	0.0283
rs8176748	9	ABO	C	T	0.4657	0.5802
rs8176745	9	ABO	A	G	0.4662	0.5802
rs201439325	9	ABO	A	C	0.0004872	0.004717
rs56116432	9	ABO	G	T	0.0006496	0.004717
rs557530257	9	ABO	A	G	0	0.004717
rs7855255	9	ABO	A	C	0.06642	0.1085
rs8176735	9	ABO	C	A	0.04027	0.009434
rs8176733	9	ABO	A	G	0.06642	0.1085
rs2073823	9	ABO	A	C	0.06642	0.1085
rs8176730	9	ABO	G	A	0.06642	0.1085
rs8176729	9	ABO	T	C	0.04027	0.009434
rs8176725	9	ABO	T	C	0.0669	0.1085
rs111310794	9	ABO	T	C	0.06155	0.01415
rs45610939	9	ABO	A	G	0.009256	0.02358
rs4962040	9	ABO	G	A	0.2092	0.1509
rs138164693	9	ABO	A	G	0.008769	0.02358
rs8176710	9	ABO	C	T	0.0669	0.01415
rs183228393	9	ABO	A	T	0.008769	0.02358
rs8176702	9	ABO	C	G	0.2082	0.1321
rs8176698	9	ABO	C	G	0.00406	0.01415

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rs8176696	9	ABO	C	G	0.00406	0.01415
rs687621	9	ABO	G	A	0.233	0.3019
rs687289	9	ABO	C	G	0.2319	0.3019
rs150372066	9	ABO	A	G	0.00341	0.0283
rs143174772	9	ABO	G	A	0.009419	0.06604
rs151155628	9	ABO	A	G	0.009419	0.06604
rs8176694	9	ABO	C	T	0.2186	0.1368
rs150326069	9	ABO	G	A	0.0001624	0.004717
rs8176692	9	ABO	C	G	0.01072	0.06604
rs145090216	9	ABO	C	G	0.009419	0.06604
rs8176691	9	ABO	A	G	0.2134	0.1415
rs8176687	9	ABO	T	G	0.06479	0.01415
rs8176684	9	ABO	A	C	0.007957	0.04717
rs147279040	9	ABO	T	C	0.0112	0.0566
rs657152	9	ABO	T	C	0.2436	0.3632
rs8176682	9	ABO	G	A	0.2135	0.1274
rs139568229	9	ABO	A	G	0.01072	0.0566
rs149756392	9	ABO	A	G	0.01072	0.0566
rs145595975	9	ABO	AG	A	0.01072	0.0566
rs148824570	9	ABO	A	G	0.01072	0.0566
rs146458069	9	ABO	C	T	0.01072	0.0566
rs181170522	9	ABO	A	G	0	0.004717
rs141515001	9	ABO	T	C	0.01072	0.0566
rs8176679	9	ABO	A	G	0.06479	0.01415
rs587736740	9	ABO	A	G	0.01072	0.05189
rs138313692	9	ABO	C	T	0.0003248	0.01415
rs149567216	9	ABO	G	T	0.01072	0.0566
rs8176676	9	ABO	C	T	0.0001624	0.009434
rs143159728	9	ABO	C	T	0.01072	0.0566
rs587682147	9	ABO	T	C	0.01072	0.05189
rs587774481	9	ABO	G	A	0.01072	0.05189
rs587635767	9	ABO	T	G	0.01056	0.03774
rs1752339	9	ABO	C	T	0.4602	0.5425
rs148667000	9	ABO	A	G	0.0003248	0.01415
rs142141716	9	ABO	G	T	0.01072	0.05189
rs587716454	9	ABO	G	C	0.01072	0.05189
rs587682443	9	ABO	T	C	0.001949	0.01887
rs587764387	9	ABO	T	C	0.001949	0.01887
rs587637585	9	ABO	T	C	0.001949	0.01887
rs144140881	9	ABO	AG	A	0.01072	0.05189
rs1927315	9	ABO	T	C	0.4602	0.5425
rs514659	9	ABO	T	C	0.2335	0.3679
rs644234	9	ABO	A	G	0.2442	0.4292

rs140796254	9	ABO	G	A	0.01072	0.05189
rs143309559	9	ABO	C	T	0.01072	0.05189
rs643434	9	ABO	C	T	0.2442	0.4292
rs145489959	9	ABO	G	A	0.0003248	0.01415
rs587698906	9	ABO	A	G	0.0004872	0.004717
rs139081859	9	ABO	CA	C	0.0003248	0.01415
rs142956930	9	ABO	T	C	0.006983	0.03302
rs8176668	9	ABO	T	C	0.2278	0.07547
rs574311	9	ABO	A	G	0.4615	0.6415
rs587663040	9	ABO	T	C	0	0.004717
rs488775	9	ABO	C	G	0.4588	0.6415
rs7036642	9	ABO	A	G	0.2116	0.07547
rs8176661	9	ABO	G	A	0.00747	0.05189
rs596141	9	ABO	C	T	0.4682	0.3538
rs587763606	9	ABO	G	A	0.0004872	0.004717
rs587707823	9	ABO	A	C	0.1853	0.3962
rs34357864	9	ABO	T	C	0.2334	0.4245
rs2769071	9	ABO	C	G	0.2321	0.4292
rs7041458	9	ABO	T	C	0.00747	0.05189
rs677355	9	ABO	T	C	0.2321	0.4198
rs676457	9	ABO	G	A	0.2317	0.4151
rs79343853	9	ABO	A	C	0.05083	0.01415
rs527210	9	ABO	T	C	0.2314	0.4009
rs675201	9	ABO	T	G	0.4547	0.5472
rs550057	9	ABO	A	T	0.1652	0.283
rs674302	9	ABO	T	C	0.2332	0.4057
rs551100	9	ABO	T	C	0.4562	0.5519
rs663054	9	ABO	A	G	0.4454	0.5425
rs7046674	9	ABO	C	T	0.2119	0.1226
rs554833	9	ABO	C	T	0.2324	0.4057
rs8176649	9	ABO	C	T	0.209	0.1226
rs660340	9	ABO	C	T	0.2777	0.4575
rs581107	9	ABO	T	C	0.2778	0.4575
rs8176647	9	ABO	A	G	0.06138	0.009434
rs659104	9	ABO	G	A	0.2775	0.4151
rs647800	9	ABO	C	A	0.2882	0.4151
rs473533	9	ABO	A	G	0.2775	0.4151
rs147960974	9	ABO	C	A	0.0001624	0.004717
rs475419	9	ABO	T	C	0.2766	0.4104
rs476410	9	ABO	T	C	0.2775	0.4151
rs645982	9	ABO	C	A	0.2775	0.4151
rs500498	9	ABO	T	C	0.2775	0.4151
rs145218729	9	ABO	C	A	0.0001624	0.004717

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rs8176644	9	ABO	T	C	0.04953	0.01415
rs505922	9	ABO	A	T	0.2283	0.3302
rs507666	9	ABO	C	T	0.1374	0.2453
rs529565	9	ABO	C	T	0.229	0.3349
rs8176641	9	ABO	G	A	0.05992	0.009434
rs532436	9	ABO	C	A	0.1811	0.2406
rs8176639	9	ABO	A	C	0.05992	0.009434
rs8176760	9	ABO	A	G	0.0003248	0.009434
rs3749461	3	CCR2	G	A	0.02842	0.1179
rs3918362	3	CCR2	A	G	0.02842	0.1179
rs3092963	3	CCR2	T	C	0.2892	0.4198
rs3918365	3	CCR2	A	G	0.02842	0.1179
rs1799865	3	CCR2	AAT	A	0.2892	0.4198
rs3138042	3	CCR2	C	T	0.2892	0.4198
rs140253702	3	CCR2	C	A	0.0003248	0.004717
rs1860264	3	CCR9	G	A	0.2621	0.4528
rs186153536	3	CCR9	T	C	0.0003248	0.004717
rs74808020	3	CCR9	C	T	0.0354	0.08491
rs530595037	3	CCR9	A	G	0.0003248	0.004717
rs552329766	3	CCR9	T	C	0.0003248	0.004717
rs12631321	3	CCR9	T	A	0.0354	0.08491
rs150667470	3	CCR9	C	G	0.0004872	0.004717
rs6441930	3	CCR9	G	A	0.2621	0.4528
rs138421181	3	CCR9	T	C	0	0.004717
rs115004584	3	CCR9	C	T	0.0003248	0.004717
rs78414305	3	CCR9	A	G	0.0003248	0.004717
rs115826613	3	CCR9	A	G	0	0.004717
rs74739895	3	CCR9	C	T	0.0003248	0.004717
rs75018424	3	CCR9	C	G	0.03524	0.08491
rs78044818	3	CCR9	T	G	0.0003248	0.004717
rs74337052	3	CCR9	A	G	0	0.004717
rs7636844	3	CCR9	A	G	0.1406	0.08491
rs2286486	3	CCR9	C	A	0.1406	0.08019
rs116350857	3	CCR9	C	T	0	0.004717
rs6441931	3	CCR9	G	A	0.1406	0.08491
rs34338823	3	CCR9	A	T	0.04141	0.01415
rs115227401	3	CCR9	C	T	0.0003248	0.004717
rs76478208	3	CCR9	G	A	0.0003248	0.004717
rs6783694	3	CCR9	A	ATTC	0.0003248	0.004717
rs6441932	3	CCR9	G	A	0.272	0.4481
rs116264461	3	CCR9	T	C	0.0003248	0.004717
rs77676459	3	CCR9	C	A	0.0003248	0.004717
rs114406614	3	CCR9	C	T	0	0.004717

rs144180015	3	CCR9	A	G	0.0003248	0.004717
rs9862611	3	CCR9	G	T	0.2714	0.4481
rs71325091	3	CCR9	CG	C	0.04141	0.01415
rs6441933	3	CCR9	A	G	0.272	0.4481
rs141167007	3	CCR9	A	G	0	0.004717
rs57527954	3	CCR9	A	G	0.272	0.4481
rs9834860	3	CCR9	A	G	0.272	0.4481
rs116207980	3	CCR9	AT	A	0	0.004717
rs12638201	3	CCR9	AT	A	0.03037	0.07547
rs56058226	3	CCR9	C	T	0.3823	0.3113
rs75078036	3	CCR9	G	A	0.02939	0.07075
rs9855205	3	CCR9	A	G	0.05213	0.009434
rs3764864	3	CCR9	A	T	0.07373	0.03774
rs6782814	3	CCR9	G	A	0.08672	0.2264
rs9823523	3	CCR9	A	C	0.05602	0.02358
rs3774642	3	CCR9	A	G	0.02923	0.07547
rs3774641	3	CCR9	C	T	0.1172	0.05189
rs1488371	3	CCR9	G	A	0.2761	0.4434
rs147753307	3	CCR9	C	T	0.001624	0.01415
rs2236938	3	CCR9	A	G	0.1159	0.25
rs17764980	3	CCR9	C	T	0.04157	0.01415
rs79663567	3	CCR9	T	G	0	0.004717
rs73830609	3	CCR9	A	C	0.002436	0.01415
rs17714101	3	CCR9	T	A	0.04157	0.01415
rs1985356	3	CCR9	C	T	0.1567	0.3538
rs1985463	3	CCR9	C	T	0.207	0.3821
rs59817490	3	CCR9	G	A	0.003897	0.01415
rs7614342	3	CCR9	C	G	0.1565	0.3538
rs79587259	3	CCR9	T	C	0.02907	0.07075
rs61751653	3	CCR9	G	A	0.001786	0.009434
rs74718475	3	CCR9	C	A	0	0.004717
rs73830610	3	CCR9	A	T	0.003897	0.01415
rs17714228	3	CCR9	T	C	0.04157	0.01415
rs875891	3	CCR9	G	T	0.1554	0.3538
rs875890	3	CCR9	T	C	0.2069	0.3821
rs62245098	3	CCR9	T	C	0.1565	0.3585
rs28595837	3	CCR9	A	G	0.02225	0.05189
rs9881306	3	CCR9	A	G	0.05213	0.009434
rs28501674	3	CCR9	G	A	0.1552	0.3538
rs61565453	3	CCR9	A	T	0.1565	0.3585
rs71325092	3	CCR9	G	A	0.04157	0.01415
rs79179998	3	CCR9	A	C	0.05213	0.009434
rs57295094	3	CCR9	G	C	0.1549	0.3538

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rs6791859	3	CCR9	G	A	0.1609	0.3443
rs4683147	3	CCR9	A	G	0.3966	0.566
rs74945326	3	CCR9	C	T	0.04108	0.009434
rs62245101	3	CCR9	G	A	0.1146	0.2311
rs62245102	3	CCR9	A	C	0.1593	0.3396
rs7638236	3	CXCR6	T	C	0.019	0.04245
rs4535265	3	CXCR6	T	C	0.4108	0.5094
rs9869848	3	CXCR6	A	G	0.1111	0.1887
rs9875616	3	CXCR6	A	G	0.109	0.1887
rs13091979	3	CXCR6	A	G	0.4105	0.5094
rs13091821	3	CXCR6	A	G	0.4105	0.5094
rs17078449	3	CXCR6	C	T	0.1471	0.08019
rs936938	3	CXCR6	A	G	0.4074	0.5
rs2171531	3	CXCR6	T	C	0.04579	0.009434
rs17078454	3	CXCR6	C	T	0.1466	0.08019
rs57204020	3	CXCR6	T	C	0.1465	0.08019
rs7634640	3	CXCR6	G	A	0.07616	0.1651
rs55920693	3	CXCR6	T	G	0.04579	0.009434
rs3774640	3	CXCR6	G	A	0.1465	0.08019
rs3774639	3	CXCR6	A	G	0.4105	0.5094
rs3774638	3	CXCR6	A	G	0.1465	0.08019
rs7627147	3	CXCR6	T	C	0.01851	0.04245
rs2234350	3	CXCR6	T	C	0.1259	0.1887
rs2234351	3	CXCR6	T	A	0.1462	0.08019
rs191811571	3	CXCR6	C	T	0.0001624	0.004717
rs3774635	3	CXCR6	A	C	0.4074	0.5
rs936939	3	CXCR6	C	T	0.1465	0.08019
rs143980719	3	CXCR6	T	C	0.001949	0.01415
rs2234355	3	CXCR6	A	G	0.02533	0.06132
rs17078464	3	CXCR6	A	G	0.01835	0.04245
rs2054866	3	CXCR6	G	A	0.4074	0.5
rs58442576	3	CXCR6	C	T	0.01851	0.04245
rs4683156	3	CXCR6	T	C	0.4105	0.5094
rs56239523	3	CXCR6	T	C	0.01851	0.04245
rs58050797	3	CXCR6	C	A	0.01835	0.04245
rs1994488	3	CXCR6	T	C	0.4074	0.5
rs35501575	3	CXCR6	A	G	0.04596	0.009434
rs1552489	3	CXCR6	C	A	0.4074	0.5
rs8107316	19	DPP9	A	G	0.2243	0.3066
rs72977966	19	DPP9	A	G	0	0.004717
rs8105807	19	DPP9	C	G	0.3037	0.3679
rs10421782	19	DPP9	A	C	0.3027	0.3679
rs2885734	19	DPP9	A	T	0.3037	0.3679

rs114346470	19	DPP9	T	C	0.0001624	0.004717
rs34136596	19	DPP9	A	G	0.0006496	0.004717
rs113439332	19	DPP9	A	T	0.0328	0.1321
rs113094386	19	DPP9	AC	A	0.005684	0.01887
rs2277735	19	DPP9	A	G	0.2947	0.3821
rs60199752	19	DPP9	C	T	0.2241	0.3066
rs35408525	19	DPP9	G	A	0.0006496	0.004717
rs11671605	19	DPP9	C	T	0.2241	0.3066
rs4401152	19	DPP9	T	A	0.2244	0.3019
rs72977989	19	DPP9	G	T	0.2241	0.3019
rs139518006	19	DPP9	G	A	0.0001624	0.004717
rs11670257	19	DPP9	C	T	0.3514	0.5
rs2277733	19	DPP9	C	A	0.3365	0.25
rs732631	19	DPP9	T	A	0.2756	0.3396
rs2006231	19	DPP9	A	T	0.4292	0.3443
rs2109069	19	DPP9	T	A	0.2462	0.3208
rs2109070	19	DPP9	T	A	0.2446	0.3208
rs3833278	19	DPP9	A	G	0.3909	0.3208
rs1467941	19	DPP9	G	A	0.3988	0.3255
rs1467942	19	DPP9	G	A	0.404	0.3349
rs56945978	19	DPP9	C	G	0.4256	0.3443
rs758510	19	DPP9	C	G	0.3474	0.2783
rs2277732	19	DPP9	C	T	0.1504	0.2925
rs10420007	19	DPP9	G	A	0.3953	0.3208
rs10420225	19	DPP9	T	C	0.4292	0.3443
rs530191556	19	DPP9	T	C	0.3964	0.3255
rs4683148	3	FYCO1	T	C	0.4112	0.5377
rs2171530	3	FYCO1	T	C	0.2196	0.316
rs9831315	3	FYCO1	G	A	0.4055	0.5283
rs560966886	3	FYCO1	T	C	0.0001624	0.004717
rs72622922	3	FYCO1	T	C	0.0003248	0.01415
rs185588322	3	FYCO1	T	C	0.001624	0.01415
rs7129	3	FYCO1	T	C	0.4058	0.5283
rs1994492	3	FYCO1	T	G	0.04222	0.009434
rs1994493	3	FYCO1	T	G	0.04222	0.009434
rs3796373	3	FYCO1	T	G	0.2212	0.3208
rs3733103	3	FYCO1	A	G	0.4112	0.533
rs75928798	3	FYCO1	A	G	0.04206	0.009434
rs2291470	3	FYCO1	A	G	0.4057	0.5283
rs11130078	3	FYCO1	A	G	0.2204	0.3349
rs148655132	3	FYCO1	C	G	0.001624	0.01415
rs11707672	3	FYCO1	C	G	0.0112	0.04245
rs6800954	3	FYCO1	T	C	0.1502	0.09906

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rs140100519	3	FYCO1	T	C	0.001624	0.01415
rs2248228	3	FYCO1	T	G	0.4094	0.5094
rs60237998	3	FYCO1	C	T	0.1512	0.08962
rs60110056	3	FYCO1	C	G	0.01543	0.04245
rs58491168	3	FYCO1	T	A	0.019	0.04245
rs4683149	3	FYCO1	C	T	0.4052	0.5047
rs2373087	3	FYCO1	A	G	0.04417	0.009434
rs7631809	3	FYCO1	A	G	0.1504	0.08962
rs2373088	3	FYCO1	A	G	0.06414	0.1557
rs62245106	3	FYCO1	A	G	0.113	0.0566
rs12638598	3	FYCO1	G	C	0.207	0.1132
rs35831747	3	FYCO1	T	C	0.04417	0.009434
rs77709797	3	FYCO1	T	C	0.1166	0.0566
rs1532070	3	FYCO1	A	G	0.06431	0.1557
rs6778225	3	FYCO1	A	G	0.1484	0.08491
rs13099120	3	FYCO1	A	T	0.04417	0.009434
rs6778324	3	FYCO1	T	C	0.1483	0.08491
rs60779624	3	FYCO1	G	A	0.1484	0.08491
rs190039371	3	FYCO1	T	C	0.1166	0.0566
rs41289614	3	FYCO1	A	T	0.03459	0.009434
rs35477280	3	FYCO1	C	G	0.04417	0.009434
rs4683152	3	FYCO1	A	C	0.4094	0.5094
rs13066516	3	FYCO1	A	G	0.04417	0.009434
rs200582580	3	FYCO1	C	T	0.04401	0.009434
rs1072755	3	FYCO1	T	C	0.4055	0.5
rs77902290	3	FYCO1	C	T	0.04417	0.009434
rs532777636	3	FYCO1	G	A	0.04579	0.009434
rs62242787	3	FYCO1	A	G	0.1543	0.07547
rs17078471	3	FYCO1	C	T	0.002111	0.009434
rs35257780	3	FYCO1	T	C	0.04628	0.009434
rs34000569	3	FYCO1	C	T	0.04628	0.009434
rs34324101	3	FYCO1	T	C	0.04628	0.009434
rs13069079	3	FYCO1	T	C	0.04628	0.009434
rs34849862	3	FYCO1	T	C	0.04628	0.009434
rs62242788	3	FYCO1	T	C	0.1263	0.0566
rs35209528	3	FYCO1	T	C	0.04628	0.009434
rs75918913	3	FYCO1	T	C	0.03995	0.009434
rs57036895	3	FYCO1	G	A	0.01543	0.03774
rs13079869	3	FYCO1	A	G	0.04677	0.009434
rs33910087	3	FYCO1	A	G	0.04693	0.009434
rs3796376	3	FYCO1	A	G	0.1354	0.0566
rs17215008	3	FYCO1	C	T	0.04644	0.009434
rs71325098	3	FYCO1	G	A	0.04644	0.009434

rs71325100	3	FYCO1	C	T	0.04644	0.009434
rs41289622	3	FYCO1	T	C	0.04644	0.009434
rs11130081	3	FYCO1	A	G	0.002111	0.009434
rs12639598	3	FYCO1	A	G	0.405	0.5047
rs144873702	3	FYCO1	G	A	0.000812	0.01415
rs751552	3	FYCO1	A	G	0.4053	0.5142
rs751553	3	FYCO1	T	C	0.4053	0.5142
rs904634	3	FYCO1	T	C	0.08379	0.1604
rs13066062	3	FYCO1	C	T	0.04644	0.009434
rs6781668	3	FYCO1	G	A	0.1351	0.0566
rs9844821	3	FYCO1	A	G	0.07161	0.1509
rs57228214	3	FYCO1	T	C	0.02192	0.05189
rs9849771	3	FYCO1	G	A	0.09337	0.1604
rs9849818	3	FYCO1	C	T	0.08396	0.1604
rs4682801	3	FYCO1	A	G	0.1291	0.2547
rs35537559	3	FYCO1	T	C	0.1971	0.09434
rs59767267	3	FYCO1	A	G	0.1314	0.0566
rs3821883	3	FYCO1	G	A	0.1346	0.0566
rs36122610	3	FYCO1	G	A	0.04628	0.009434
rs138017682	3	FYCO1	T	C	0.0006496	0.009434
rs34442130	3	FYCO1	T	C	0.04628	0.009434
rs931704	3	FYCO1	T	C	0.4039	0.4764
rs4683159	3	FYCO1	A	G	0.203	0.316
rs13075758	3	FYCO1	T	A	0.04628	0.009434
rs11130082	3	FYCO1	T	G	0.2035	0.3208
rs6802312	3	FYCO1	T	C	0.1159	0.2547
rs56972507	3	FYCO1	T	C	0.02144	0.04717
rs3733097	3	FYCO1	A	G	0.4058	0.5189
rs17078495	3	FYCO1	T	C	0.4058	0.5189
rs13086858	3	FYCO1	C	G	0.2035	0.3208
rs139886125	3	FYCO1	G	A	0.000812	0.01415
rs737452	3	FYCO1	G	C	0.4058	0.5189
rs730983	3	FYCO1	G	A	0.4039	0.4906
rs59226168	3	FYCO1	T	C	0.1898	0.1038
rs67044455	3	FYCO1	T	C	0.4058	0.533
rs62242796	3	FYCO1	C	T	0.1898	0.1038
rs7653682	3	FYCO1	A	T	0.1159	0.2877
rs72891712	3	FYCO1	A	T	0.02257	0.07547
rs1873000	3	FYCO1	A	G	0.203	0.3538
rs7628447	3	FYCO1	G	T	0.2035	0.3538
rs12635657	3	FYCO1	T	G	0.4057	0.5283
rs2133660	3	FYCO1	G	A	0.2371	0.3774
rs146216196	3	FYCO1	T	C	0.001786	0.01887

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rs139044419	3	FYCO1	A	G	0.001786	0.01887
rs1846615	3	FYCO1	C	T	0.2371	0.3774
rs1873001	3	FYCO1	C	T	0.2371	0.3774
rs142154067	3	FYCO1	AT	A	0.001786	0.01887
rs146285477	3	FYCO1	C	T	0.04628	0.009434
rs182171107	3	FYCO1	C	G	0.0006496	0.009434
rs1500003	3	FYCO1	A	G	0.2371	0.3774
rs79067698	3	FYCO1	A	G	0.001786	0.01887
rs1392288	3	FYCO1	C	G	0.1673	0.3349
rs17330872	3	FYCO1	C	T	0.04628	0.009434
rs188114046	3	FYCO1	A	G	0.001786	0.01887
rs142571332	3	FYCO1	G	C	0.04579	0.009434
rs71327003	3	FYCO1	G	T	0.04612	0.009434
rs188401375	21	IFNAR2	T	C	0.0006496	0.004717
rs17860118	21	IFNAR2	G	A	0.01754	0.08962
rs566208153	21	IFNAR2	C	T	0.02907	0.0566
rs13052526	21	IFNAR2	G	A	0.01608	0.04717
rs574424283	21	IFNAR2	A	C	0.4208	0.3491
rs2248420	21	IFNAR2	A	G	0.4227	0.3443
rs189110596	21	IFNAR2	T	C	0.002273	0.01415
rs7509997	21	IFNAR2	A	C	0.02452	0.0566
rs17860142	21	IFNAR2	C	A	0.4229	0.3443
rs8130779	21	IFNAR2	A	G	0.02631	0.0566
rs9974669	21	IFNAR2	G	A	0.02631	0.0566
rs570824030	21	IFNAR2	C	T	0.02663	0.0566
rs3153	21	IFNAR2	A	G	0.4227	0.3443
rs1187	21	IFNAR2	T	G	0.0004872	0.004717
rs12482014	21	IFNAR2	T	C	0.4229	0.3443
rs17860160	21	IFNAR2	A	G	0.01608	0.04717
rs12482193	21	IFNAR2	G	A	0.4285	0.3491
rs17860165	21	IFNAR2	T	C	0.4229	0.3443
rs117489085	21	IFNAR2	T	C	0.0003248	0.004717
rs545411453	21	IFNAR2	G	T	0.0003248	0.004717
rs8128785	21	IFNAR2	G	C	0.03215	0.0566
rs2229207	21	IFNAR2	T	C	0.01803	0.06132
rs1051393	21	IFNAR2	G	A	0.4329	0.316
rs62226154	21	IFNAR2	C	T	0.02436	0.04717
rs62226157	21	IFNAR2	G	C	0.4112	0.3396
rs144683777	21	IFNAR2	T	C	0.000812	0.01887
rs10211925	21	IFNAR2	C	A	0.0229	0.04717
rs17860183	21	IFNAR2	A	T	0.1669	0.04245
rs2834159	21	IFNAR2	C	G	0.02079	0.04245
rs12053666	21	IFNAR2	G	A	0.4104	0.2925

rs2834160	21	IFNAR2	G	C	0.01689	0.04245
rs2834162	21	IFNAR2	T	C	0.01786	0.04245
rs17860211	21	IFNAR2	A	G	0.01786	0.04245
rs2073362	21	IFNAR2	T	C	0.01689	0.06132
rs17860220	21	IFNAR2	T	C	0.01673	0.06132
rs147496374	21	IFNAR2	A	C	0.00341	0.02358
rs4817555	21	IFNAR2	T	C	0.04027	0.1226
rs59738559	21	IFNAR2	G	C	0.04108	0.1226
rs2834166	21	IFNAR2	C	A	0.3357	0.2547
rs11911133	21	IFNAR2	G	A	0.4732	0.3774
rs181597872	21	IFNAR2	C	T	0.0003248	0.004717
rs2300371	21	IFNAR2	A	G	0.4048	0.2925
rs1058961	3	LZTFL1	C	T	0.2408	0.4481
rs35624553	3	LZTFL1	G	C	0.03638	0.009434
rs139540257	3	LZTFL1	T	C	0.007145	0.02358
rs2064061	3	LZTFL1	T	G	0.3459	0.5189
rs67959919	3	LZTFL1	A	T	0.03638	0.009434
rs148112944	3	LZTFL1	G	T	0	0.004717
rs11385942	3	LZTFL1	T	C	0.03832	0.009434
rs11130077	3	LZTFL1	A	G	0.2311	0.3019
rs6796097	3	LZTFL1	A	G	0.001299	0.009434
rs190577088	3	LZTFL1	T	C	0.0004872	0.004717
rs35508621	3	LZTFL1	A	G	0.03459	0.004717
rs758389	3	LZTFL1	T	C	0.0009743	0.009434
rs34288077	3	LZTFL1	T	C	0.03443	0.004717
rs141146648	3	LZTFL1	A	G	0.0151	0.0566
rs150719194	3	LZTFL1	C	T	0.0001624	0.004717
rs35081325	3	LZTFL1	G	A	0.03443	0.009434
rs35731912	3	LZTFL1	C	T	0.03459	0.009434
rs17078371	3	LZTFL1	C	G	0.001462	0.009434
rs112101762	3	LZTFL1	A	G	0.001137	0.009434
rs113181700	3	LZTFL1	T	C	0.001137	0.009434
rs4683146	3	LZTFL1	T	G	0.3344	0.434
rs34326463	3	LZTFL1	A	G	0.03426	0.004717
rs73064425	3	LZTFL1	T	C	0.03475	0.009434
rs138727962	3	LZTFL1	T	C	0.0001624	0.004717
rs184214751	3	LZTFL1	T	G	0.0009743	0.009434
rs71325089	3	LZTFL1	A	G	0.02907	0.004717
rs61185149	3	LZTFL1	T	C	0.008931	0.02358
rs13081482	3	LZTFL1	G	A	0.03491	0.009434
rs75826707	3	LZTFL1	G	A	0.003248	0.01415
rs9871972	3	LZTFL1	T	C	0.3407	0.5
rs140227473	3	LZTFL1	A	G	0.001624	0.009434

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rs75507082	3	LZTFL1	A	G	0.02907	0
rs79657519	3	LZTFL1	C	A	0.001624	0.009434
rs148060386	3	LZTFL1	A	G	0.0001624	0.004717
rs2191031	3	LZTFL1	G	C	0.1161	0.0566
rs28607988	3	LZTFL1	T	C	0.04498	0.01415
rs77009309	3	LZTFL1	A	G	0.02972	0.1132
rs12639224	3	LZTFL1	A	G	0.138	0.2075
rs12639252	3	LZTFL1	T	A	0.0004872	0.004717
rs2373086	3	LZTFL1	T	G	0.02842	0.1226
rs112212287	3	LZTFL1	T	C	0.01624	0.06132
rs7614687	3	LZTFL1	A	G	0.01072	0.0566
rs57319220	3	LZTFL1	G	A	0.0544	0.02358
rs34518147	3	LZTFL1	G	C	0.04125	0.01415
rs9852270	3	LZTFL1	T	C	0.2621	0.4528
rs560506883	3	LZTFL1	T	C	0.0001624	0.004717
rs77000397	3	LZTFL1	G	A	0	0.004717
rs114742054	3	LZTFL1	A	G	0	0.004717
rs12633699	3	LZTFL1	A	G	0.05505	0.01415
rs34847985	3	LZTFL1	A	G	0.2131	0.3726
rs34549672	3	LZTFL1	C	G	0.2811	0.4434
rs75442536	3	LZTFL1	A	G	0.02273	0.0566
rs59451221	3	LZTFL1	T	C	0.06041	0.1745
rs9836836	3	LZTFL1	G	A	0.1341	0.0566
rs35280891	3	LZTFL1	T	C	0.04157	0.009434
rs181980885	3	LZTFL1	A	G	0.001624	0.01415
rs186530132	3	LZTFL1	T	C	0.001624	0.01415
rs112707117	3	LZTFL1	G	A	0.001624	0.01415
rs34068335	3	LZTFL1	C	A	0.04206	0.009434
rs558702333	3	NRBF2P2	A	T	0.0006496	0.004717
rs35334665	3	NRBF2P2	T	C	0.04726	0.009434
rs115932896	3	NRBF2P2	T	A	0.001299	0.01415
rs71327009	3	NRBF2P2	A	G	0.04726	0.009434
rs189659509	3	NRBF2P2	C	T	0.001299	0.009434
rs35161099	3	NRBF2P2	A	G	0.04726	0.009434
rs12054287	3	NRBF2P2	A	G	0.1323	0.05189
rs60080146	3	NRBF2P2	T	C	0.0177	0.03774
rs59676542	3	NRBF2P2	C	T	0.01819	0.03774
rs58035200	3	NRBF2P2	C	T	0.1958	0.1085
rs7623460	3	NRBF2P2	C	T	0.2658	0.1934
rs71327010	3	NRBF2P2	T	C	0.04726	0.009434
rs7623476	3	NRBF2P2	G	A	0.1957	0.1085
rs7956880	12	OAS1	A	G	0.1728	0.08962
rs10744785	12	OAS1	TC	T	0.2512	0.1557

rs4766662	12	OAS1	C	A	0.2407	0.1415
rs2240190	12	OAS1	T	G	0.03491	0.1274
rs34137742	12	OAS1	A	G	0.07616	0.1226
rs45542343	12	OAS1	G	A	0.03215	0.1038
rs75344264	12	OAS1	T	C	0.1082	0.184
rs2057778	12	OAS1	C	T	0.1772	0.1179
rs2285934	12	OAS1	A	C	0.2459	0.1509
rs4767023	12	OAS1	T	C	0.2621	0.1604
rs45495393	12	OAS1	C	T	0.07567	0.1274
rs56006713	12	OAS1	A	T	0.0009743	0.009434
rs12423440	12	OAS1	T	C	0.0492	0.08491
rs10774671	**12**	**OAS1**	C	A	**0.2748**	**0.184**
rs1131476	12	OAS1	T	C	0.1806	0.1132
rs2660	**12**	**OAS1**	T	C	**0.1806**	**0.1085**
rs7135577	12	OAS1	T	G	0.1806	0.1226
rs4767024	12	OAS1	T	C	0.1801	0.1226
rs4767025	12	OAS1	A	G	0.1801	0.1226
rs4767026	12	OAS1	A	G	0.1807	0.1226
rs4767027	12	OAS1	A	G	0.1801	0.1226
rs4767028	12	OAS1	A	G	0.1806	0.1226
rs4767029	12	OAS1	C	G	0.1801	0.1226
rs75628555	12	OAS1	C	T	0.04758	0.08491
rs4767030	12	OAS1	T	C	0.1806	0.1226
rs10850092	12	OAS1	G	A	0.1801	0.1226
rs6489864	12	OAS1	A	G	0.1801	0.1226
rs6489865	12	OAS1	G	T	0.1801	0.1226
rs10850093	12	OAS1	C	G	0.1801	0.1226
rs10850094	12	OAS1	C	T	0.1801	0.1226
rs10850095	12	OAS1	G	A	0.1801	0.1226
rs10774672	12	OAS1	C	T	0.1807	0.1226
rs10850096	12	OAS1	G	C	0.1801	0.1226
rs10850097	12	OAS1	C	T	0.1981	0.1415
rs10774673	12	OAS1	G	A	0.1801	0.1226
rs10774674	12	OAS1	C	G	0.1801	0.1226
rs3803057	12	OAS1	A	G	0.1312	0.06132
rs1298962	12	OAS2	T	G	0.1702	0.09906
rs1298301	12	OAS2	A	G	0.1632	0.2453
rs1293774	12	OAS2	A	T	0.1702	0.09906
rs117666908	12	OAS2	A	G	0.03361	0.06604
rs1293773	12	OAS2	A	AC	0.1629	0.2406
rs1293772	12	OAS2	T	G	0.1819	0.08019
rs531734809	12	OAS2	C	G	0	0.004717
rs1293771	12	OAS2	T	C	0.1819	0.08019

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rs1293770	12	OAS2	T	C	0.163	0.2358
rs12301619	12	OAS2	C	T	0.003735	0.01415
rs1293768	12	OAS2	A	G	0.1798	0.08019
rs150169230	12	OAS2	T	A	0.0001624	0.004717
rs1293767	12	OAS2	A	G	0.1259	0.06132
rs1293766	12	OAS2	A	G	0.1575	0.2311
rs1293765	12	OAS2	C	A	0.1645	0.07547
rs1293764	12	OAS2	A	G	0.1639	0.07547
rs1293763	12	OAS2	G	A	0.1523	0.2217
rs11066464	12	OAS2	A	G	0.2085	0.2736
rs757402	12	OAS2	G	A	0.1366	0.0566
rs200629605	12	OAS2	A	T	0.02744	0.06132
rs7975318	12	OAS2	G	C	0.1682	0.2311
rs757401	12	OAS2	AAT	A	0.1366	0.0566
rs557969944	12	OAS2	C	T	0	0.004717
rs5800979	12	OAS2	A	T	0.3746	0.5047
rs34886194	12	OAS2	G	A	0.2075	0.2689
rs1293762	12	OAS2	A	C	0.1845	0.08962
rs1293760	12	OAS2	C	T	0.1846	0.08962
rs1293759	12	OAS2	T	G	0.1177	0.04245
rs1293758	12	OAS2	A	G	0.2949	0.1038
rs1298961	12	OAS2	A	T	0.3303	0.1179
rs1635142	12	OAS2	A	G	0.1189	0.04245
rs1293757	12	OAS2	T	C	0.1189	0.04245
rs1293756	12	OAS2	A	G	0.1189	0.04245
rs1293754	12	OAS2	G	A	0.1192	0.04245
rs1293753	12	OAS2	T	G	0.1184	0.04245
rs1293752	12	OAS2	A	G	0.1315	0.04717
rs1293751	12	OAS2	T	C	0.1315	0.04717
rs2525848	12	OAS2	C	A	0.1315	0.04717
rs1296061	12	OAS2	A	G	0.1315	0.04717
rs2072137	12	OAS2	C	T	0.4147	0.6038
rs1293749	12	OAS2	T	C	0.134	0.05189
rs2003480	12	OAS2	C	T	0.4367	0.283
rs1293748	12	OAS2	T	A	0.134	0.05189
rs2240185	12	OAS2	T	A	0.4834	0.6698
rs929291	12	OAS2	A	G	0.1497	0.07547
rs1293747	12	OAS2	A	G	0.2986	0.2217
rs1293746	12	OAS2	A	G	0.285	0.2075
rs16942430	12	OAS2	T	C	0.05797	0.01887
rs1293745	12	OAS2	T	C	0.2858	0.2028
rs1293744	12	OAS2	C	G	0.2858	0.2028
rs1293743	12	OAS2	A	G	0.1613	0.06604

rs15895	12	OAS2	T	C	0.1624	0.06604
rs574059077	12	OAS2	A	G	0	0.004717
rs13311	12	OAS2	T	C	0.4721	0.684
rs1058480	12	OAS2	T	C	0.1626	0.06604
rs3815178	12	OAS3	T	C	0.1884	0.1226
rs1859331	12	OAS3	C	T	0.2756	0.1462
rs1859330	12	OAS3	T	C	0.2762	0.1462
rs1859329	12	OAS3	T	C	0.1884	0.1226
rs7299132	12	OAS3	T	C	0.1884	0.1226
rs6489879	12	OAS3	G	C	0.1884	0.1226
rs4238033	12	OAS3	C	T	0.1884	0.1226
rs4767041	12	OAS3	T	C	0.1954	0.1321
rs10850102	12	OAS3	T	C	0.1177	0.2642
rs7955267	12	OAS3	T	C	0.1954	0.1321
rs7311182	12	OAS3	T	C	0.188	0.1226
rs73433165	12	OAS3	A	G	0.0001624	0.004717
rs10735079	12	OAS3	G	T	0.195	0.1274
rs6489880	12	OAS3	T	G	0.1884	0.1226
rs7980275	12	OAS3	T	C	0.1949	0.1321
rs7977345	12	OAS3	A	G	0.1954	0.1321
rs6489881	12	OAS3	A	G	0.1954	0.1321
rs6489882	12	OAS3	T	C	0.1884	0.1226
rs7131998	12	OAS3	A	G	0.1853	0.1274
rs2269899	12	OAS3	A	G	0.1924	0.1368
rs11066456	12	OAS3	C	T	0.1452	0.2075
rs12427406	12	OAS3	C	T	0.126	0.1887
rs10850104	12	OAS3	A	C	0.3358	0.4292
rs11066457	12	OAS3	T	C	0.3688	0.4528
rs34647135	12	OAS3	A	G	0.3358	0.4292
rs7965570	12	OAS3	A	C	0.1332	0.2123
rs1974518	12	OAS3	G	A	0.4003	0.4764
rs71465868	12	OAS3	C	T	0.0328	0
rs12824584	12	OAS3	C	T	0.0006496	0.004717
rs146042277	12	OAS3	T	C	0.0004872	0.004717
rs10850105	12	OAS3	G	A	0.1475	0.08962
rs7310667	12	OAS3	G	A	0.1665	0.1132
rs4767042	12	OAS3	A	G	0.4003	0.4764
rs78069989	12	OAS3	C	G	0.00341	0.01887
rs78220999	12	OAS3	T	C	0.1468	0.08962
rs4435062	12	OAS3	A	C	0.3709	0.4481
rs150390228	12	OAS3	T	C	0.1468	0.08962
rs10744789	12	OAS3	G	A	0.1468	0.08962
rs140303054	12	OAS3	G	C	0.0004872	0.004717

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rs57771566	12	OAS3	C	G	0.002923	0.01415
rs138971703	12	OAS3	G	A	0.002436	0.01415
rs4238034	12	OAS3	A	C	0.147	0.08962
rs4766677	12	OAS3	A	G	0.4021	0.4764
rs4766678	12	OAS3	G	A	0.4029	0.4858
rs58603713	12	OAS3	T	C	0.002923	0.01415
rs2158393	12	OAS3	T	C	0.3707	0.4481
rs2072136	12	OAS3	T	G	0.3704	0.4481
rs2072135	12	OAS3	T	C	0.1466	0.2028
rs60439830	12	OAS3	A	G	0.00341	0.01887
rs55688670	12	OAS3	A	G	0.03556	0.07075
rs45607836	12	OAS3	C	T	0.03556	0.07075
rs4767044	12	OAS3	A	G	0.1174	0.06132
rs2240189	12	OAS3	T	C	0.1565	0.2123
rs1557866	12	OAS3	T	C	0.1172	0.06132
rs45489899	12	OAS3	G	A	0.00341	0.01887
rs3937434	12	OAS3	T	C	0.1174	0.06132
rs2016831	12	OAS3	T	C	0.1174	0.06132
rs11837165	12	OAS3	T	C	0.0003248	0.004717
rs757405	12	OAS3	T	G	0.1179	0.0566
rs73422036	12	OAS3	A	G	0.003248	0.01887
rs45620632	12	OAS3	T	C	0.001624	0.0283
rs11837367	12	OAS3	G	T	0.003248	0.01887
rs2010604	12	OAS3	C	T	0.1387	0.08491
rs739903	12	OAS3	A	G	0.1772	0.2358
rs2072133	12	OAS3	T	C	0.195	0.2594
rs4767045	12	OAS3	C	G	0.1181	0.05189
rs45583340	12	OAS3	A	C	0.0001624	0.004717
rs75755877	12	OAS3	C	T	0.002923	0.01415
rs10744791	12	OAS3	G	A	0.1181	0.05189
rs73422042	12	OAS3	A	G	0.002923	0.01415
rs7023	12	OAS3	C	T	0.1772	0.2358
rs2251109	3	SLC6A20	T	C	0.2369	0.3538
rs116082988	3	SLC6A20	A	G	0	0.004717
rs17078308	3	SLC6A20	A	G	0.004385	0.01887
rs144151884	3	SLC6A20	C	A	0	0.004717
rs116590098	3	SLC6A20	A	G	0	0.004717
rs2531750	3	SLC6A20	A	G	0.2363	0.1509
rs7621856	3	SLC6A20	A	G	0.4756	0.3821
rs2286489	3	SLC6A20	A	G	0.448	0.6085
rs113497906	3	SLC6A20	A	T	0.0001624	0.004717
rs6770261	3	SLC6A20	A	G	0.2834	0.3585
rs7634267	3	SLC6A20	A	G	0.02079	0.08019

rs9857669	3	SLC6A20	T	C	0.1639	0.2264
rs7641997	3	SLC6A20	G	C	0.1655	0.1132
rs575208313	3	SLC6A20	T	C	0.2441	0.316
rs143341618	3	SLC6A20	A	G	0.0001624	0.004717
rs567829326	3	SLC6A20	A	G	0	0.004717
rs62242259	3	SLC6A20	C	G	0.1807	0.09434
rs9867918	3	SLC6A20	C	T	0.1622	0.217
rs186253736	3	SLC6A20	G	A	0.0001624	0.004717
rs74850924	3	SLC6A20	C	T	0.001299	0.01415
rs369845989	3	SLC6A20	T	C	0.0006496	0.004717
rs4327428	3	SLC6A20	C	G	0.1468	0.2358
rs2108917	3	SLC6A20	A	G	0.2746	0.5142
rs720626	3	SLC6A20	A	G	0.01932	0.04717
rs6768156	3	SLC6A20	G	T	0.2813	0.5047
rs189427751	3	SLC6A20	A	G	0.0001624	0.004717
rs758388	3	SLC6A20	T	G	0.01965	0.0566
rs2077017	3	SLC6A20	G	A	0.01965	0.06132
rs9818982	3	SLC6A20	A	G	0.1504	0.2075
rs17279437	3	SLC6A20	T	A	0.05196	0.1226
rs1468541	3	SLC6A20	A	G	0.02371	0.09906
rs565220072	3	SLC6A20	A	G	0.0001624	0.004717
rs13314717	3	SLC6A20	G	C	0.003735	0.0283
rs17078335	3	SLC6A20	A	G	0.000812	0.009434
rs57133084	3	SLC6A20	T	C	0.004547	0.01415
rs2742396	3	SLC6A20	G	A	0.4449	0.2123
rs2531748	3	SLC6A20	T	C	0.4591	0.2264
rs6771661	3	SLC6A20	A	G	0.001462	0.009434
rs59375543	3	SLC6A20	A	C	0.0004872	0.004717
rs2252547	3	SLC6A20	T	C	0.3509	0.5283
rs543762608	3	SLC6A20	C	G	0.0006496	0.004717
rs12493913	3	SLC6A20	C	G	0.3553	0.25
rs576940167	3	SLC6A20	C	T	0.0006496	0.004717
rs17078339	3	SLC6A20	G	A	0.3115	0.1981
rs34987516	3	SLC6A20	A	G	0.3284	0.2075
rs142086756	3	SLC6A20	G	A	0.0003248	0.004717
rs184263104	3	SLC6A20	T	C	0.0003248	0.004717
rs2531747	3	SLC6A20	T	C	0.1843	0.3349
rs9848415	3	SLC6A20	G	A	0.302	0.1887
rs57126329	3	SLC6A20	A	C	0.2267	0.09906
rs2159272	3	SLC6A20	A	G	0.2808	0.467
rs7644870	3	SLC6A20	C	A	0.3404	0.2075
rs1860263	3	SLC6A20	T	C	0.3454	0.2123
rs545193808	3	SLC6A20	C	A	0	0.004717

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rs13064991	3	SLC6A20	G	A	0.2272	0.1415
rs28437706	3	SLC6A20	T	C	0.06382	0.1038
rs9852457	3	SLC6A20	T	C	0.06382	0.1038
rs182605899	3	SLC6A20	A	C	0.0003248	0.004717
rs59776512	3	SLC6A20	A	G	0.06285	0.1179
rs73062389	3	SLC6A20	T	C	0.004385	0.01415
rs7615978	3	SLC6A20	C	T	0.06479	0.1179
rs543563855	3	SLC6A20	T	C	0	0.004717
rs7618553	3	SLC6A20	T	C	0.06479	0.1038
rs147310206	3	SLC6A20	A	G	0.0003248	0.004717
rs188376831	3	SLC6A20	T	C	0	0.004717
rs2271616	3	SLC6A20	A	T	0.01153	0.0283
rs11085726	19	TYK2	T	C	0.0003248	0.004717
rs2304256	19	TYK2	A	G	0.2061	0.316
rs12720270	19	TYK2	T	G	0.1916	0.283
rs34725611	19	TYK2	T	C	0.2061	0.3019
rs569826524	19	TYK2	C	G	0.4432	0.6038
rs12610298	19	TYK2	T	C	0.1892	0.25
rs62130729	19	TYK2	T	C	0.189	0.2594
rs280499	19	TYK2	T	C	0.07584	0.1179
rs280500	19	TYK2	G	A	0.03832	0.1132
rs12720218	19	TYK2	T	G	0.02793	0.08962
rs280501	19	TYK2	T	G	0.04206	0.1132
rs71327006	3	XCR1	A	G	0.04726	0.009434
rs547178387	3	XCR1	T	C	0.0004872	0.004717
rs559851604	3	XCR1	T	C	0.0004872	0.004717
rs71327007	3	XCR1	T	G	0.04726	0.009434

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SNP	Location	Allele	Consequence	IMPACT	SYMBOL	Gene	Feature_type	REF_ALLELE
rs200040076	3:46008467-46008467	A	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	G
rs113318190	3:45978012-45978012	A	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	G
rs181118021	3:46062694-46062694	A	missense_variant	MODERATE	XCR1	ENSG00000173578	Transcript	G
rs56390333	9:136131064-136131064	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs2072134	12:113409176-113409176	A	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs35494115	9:136131389-136131389	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs16942374	12:113403751-113403751	A	missense_variant	MODERATE	OAS3	ENSG00000111331	Transcript	G
rs118149076	19:4724025-4724025	A	upstream_gene_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs371569951	9:136131590-136131590	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs72977997	19:4716147-4716147	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs200932155	9:136131635-136131635	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs75191837	19:4707472-4707472	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs8176716	9:136133065-136133065	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs184655598	3:45806282-45806282	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs41289608	3:45928138-45928138	A	5_prime_UTR_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs144511372	21:34635175-34635175	T	upstream_gene_variant	MODIFIER	IL10RB	ENSG00000243646	Transcript	C
rs79006711	3:45925881-45925881	A	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs35018800	19:10464843-10464843	A	missense_variant	MODERATE	TYK2	ENSG00000105397	Transcript	G
rs9411372	9:136134068-136134068	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs61736301	9:136137555-136137555	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs6775854	3:45934927-45934927	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs7648467	3:45936322-45936322	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs141064206	3:46021058-46021058	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs141476300	3:46021220-46021220	A	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	G
rs7619256	3:46029181-46029181	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs17078408	3:45939924-45939924	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs1053878	9:136131651-136131651	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs140002692	3:46010179-46010179	A	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	G
rs145828326	3:46011836-46011836	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs8176705	9:136135506-136135506	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs55882956	19:10469919-10469919	A	missense_variant	MODERATE	TYK2	ENSG00000105397	Transcript	G

rs75894880	19:4690630-4690630	T	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs543040	9:136143000-136143000	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs582094	9:136145484-136145484	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs79945697	19:4707056-4707056	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs8176739	9:136131523-136131523	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs613534	9:136143120-136143120	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs74840661	19:4700652-4700652	T	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs597988	9:136144284-136144284	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs597974	9:136144297-136144297	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs576123	9:136144308-136144308	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs545971	9:136143372-136143372	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs612169	9:136143442-136143442	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs8176663	9:136144427-136144427	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs544873	9:136143212-136143212	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs78788550	19:4701151-4701151	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs114625537	19:4709231-4709231	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs75192040	3:45949240-45949240	T	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs491626	9:136144873-136144873	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs492488	9:136144960-136144960	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs493246	9:136144994-136144994	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs495203	9:136145240-136145240	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs582118	9:136145471-136145471	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs7466899	9:136131069-136131069	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs494242	9:136145118-136145118	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs564601460	3:45997814-45997814	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs141155944	3:46008820-46008820	T	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	C
rs150785981	3:46008841-46008841	A	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	G
rs181518477	3:46012975-46012975	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs140228956	3:46016969-46016969	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs189847748	3:46018207-46018207	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs61732395	12:113405328-113405328	A	missense_variant	MODERATE	OAS3	ENSG00000111331	Transcript	G

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rs73539528	19:4685259-4685259	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs57034092	19:4695384-4695384	A	splice_donor_region_variant,intron_variant	LOW	DPP9	ENSG00000142002	Transcript	G
rs16992502	19:4705580-4705580	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs146554934	3:46006955-46006955	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs114548859	3:46008108-46008108	G	synonymous_variant	LOW	FYCO1	ENSG00000163820	Transcript	A
rs77896301	3:46011634-46011634	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs75726990	3:46011654-46011654	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs113305890	19:4680128-4680128	T	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs3947589	3:46034086-46034086	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs60431156	3:45961954-45961954	C	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs62245098	3:45945762-45945762	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs61565453	3:45946576-45946576	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs57295094	3:45947101-45947101	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs28501674	3:45946460-45946460	T	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs2373086	3:45918670-45918670	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs875891	3:45945157-45945157	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs143174772	9:136137600-136137600	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs151155628	9:136137641-136137641	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs145090216	9:136138074-136138074	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs587707823	9:136145409-136145409	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs7614342	3:45940817-45940817	T	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs1985356	3:45940441-45940441	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs45620632	12:113407773-113407773	A	missense_variant	MODERATE	OAS3	ENSG00000111331	Transcript	G
rs113439332	19:4696103-4696103	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs2108917	3:45809843-45809843	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs7653682	3:46029271-46029271	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs17860118	21:34602794-34602794	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs3749461	3:46395313-46395313	G	5_prime_UTR_variant	MODIFIER	CCR2	ENSG00000121807	Transcript	A
rs3918362	3:46395930-46395930	G	intron_variant	MODIFIER	CCR2	ENSG00000121807	Transcript	A
rs3918365	3:46398364-46398364	G	intron_variant	MODIFIER	CCR2	ENSG00000121807	Transcript	A
rs10901251	9:136126129-136126129	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A

rs8176692	9:136137937-136137937	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs138313692	9:136140283-136140283	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs148667000	9:136141177-136141177	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs145489959	9:136142447-136142447	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs139081859	9:136143192-136143192	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs72622922	3:45957055-45957055	A	downstream_gene_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs6768156	3:45810604-45810604	T	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs6791859	3:45948216-45948216	G	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs62245102	3:45948930-45948930	T	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs6782814	3:45936945-45936945	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs2240190	12:113346127-113346127	A	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs34085694	9:136127605-136127605	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs144683777	21:34615486-34615486	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs1058961	3:45865006-45865006	A	3_prime_UTR_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	T
rs8176661	9:136144640-136144640	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs7041458	9:136145988-136145988	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs1468541	3:45814303-45814303	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs77009309	3:45913521-45913521	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs2742396	3:45819701-45819701	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs2531748	3:45819837-45819837	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs59451221	3:45951550-45951550	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs2769071	9:136145974-136145974	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs1298961	12:113434156-113434156	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs10850102	12:113378835-113378835	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs1392288	3:46034791-46034791	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs677355	9:136146046-136146046	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs676457	9:136146227-136146227	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs1860264	3:45923085-45923085	C	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs6441930	3:45924953-45924953	C	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs9852270	3:45921043-45921043	C	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	T
rs875890	3:45945287-45945287	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T

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rs1985463	3:45940636-45940636	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs8176676	9:136140577-136140577	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs644234	9:136142217-136142217	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs643434	9:136142355-136142355	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs6802312	3:46025941-46025941	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs13311	12:113448652-113448652	A	3_prime_UTR_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1293758	12:113433587-113433587	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs139568229	9:136139383-136139383	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs149756392	9:136139395-136139395	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs145595975	9:136139460-136139460	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs148824570	9:136139589-136139589	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs146458069	9:136139672-136139672	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs141515001	9:136139833-136139833	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs149567216	9:136140469-136140469	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs143159728	9:136140613-136140613	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs7614687	3:45919904-45919904	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs2236938	3:45938939-45938939	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs2159272	3:45829995-45829995	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs8176684	9:136138874-136138874	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs554833	9:136147160-136147160	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs4817555	21:34626124-34626124	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs147279040	9:136138978-136138978	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs674302	9:136146664-136146664	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs73660468	9:136127907-136127907	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs660340	9:136147553-136147553	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs527210	9:136146431-136146431	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs581107	9:136147702-136147702	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs59738559	21:34626338-34626338	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	-
rs7634267	3:45806056-45806056	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs9862611	3:45931982-45931982	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs6441932	3:45930222-45930222	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A

rs6441933	3:45932847-45932847	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs57527954	3:45933344-45933344	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs9834860	3:45933647-45933647	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs2277732	19:4723670-4723670	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs45542343	12:113349099-113349099	A	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	G
rs34847985	3:45949753-45949753	G	downstream_gene_variant	MODIFIER	Y_RNA	ENSG00000201635	Transcript	A
rs2531747	3:45828586-45828586	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs13291798	9:136127481-136127481	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs2072137	12:113440921-113440921	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs280500	19:10490402-10490402	G	upstream_gene_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	A
rs587736740	9:136140169-136140169	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs587682147	9:136141110-136141110	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs587774481	9:136141113-136141113	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs142141716	9:136141226-136141226	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs587716454	9:136141304-136141304	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs144140881	9:136141877-136141877	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs140796254	9:136142304-136142304	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs143309559	9:136142339-136142339	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs144873702	3:46016687-46016687	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs139886125	3:46027293-46027293	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs569981396	9:136125870-136125870	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs557530257	9:136131779-136131779	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs181170522	9:136139715-136139715	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs587663040	9:136144145-136144145	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs138421181	3:45925170-45925170	T	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs115826613	3:45926390-45926390	A	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs74337052	3:45927163-45927163	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs116350857	3:45928008-45928008	A	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs114406614	3:45930947-45930947	T	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs141167007	3:45933141-45933141	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs116207980	3:45933969-45933969	T	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C

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rs79663567	3:45939088-45939088	A	5_prime_UTR_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs74718475	3:45943737-45943737	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs72977966	19:4681093-4681093	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs148112944	3:45872918-45872918	T	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs77000397	3:45921511-45921511	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	T
rs114742054	3:45921627-45921627	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs531734809	12:113421261-113421261	T	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs557969944	12:113429808-113429808	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs574059077	12:113448578-113448578	A	3_prime_UTR_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs116082988	3:45797352-45797352	C	3_prime_UTR_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs144151884	3:45799142-45799142	G	3_prime_UTR_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs116590098	3:45799278-45799278	G	3_prime_UTR_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs567829326	3:45807402-45807402	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs545193808	3:45834349-45834349	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs543563855	3:45835585-45835585	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs188376831	3:45837089-45837089	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs2240185	12:113444117-113444117	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1488371	3:45938089-45938089	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs1873000	3:46029458-46029458	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs2252547	3:45821624-45821624	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs7628447	3:46030003-46030003	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs4682801	3:46021218-46021218	T	synonymous_variant	LOW	FYCO1	ENSG00000163820	Transcript	G
rs488775	9:136144534-136144534	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs8176668	9:136144059-136144059	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs2373088	3:45968404-45968404	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs13314717	3:45817328-45817328	T	synonymous_variant	LOW	SLC6A20	ENSG00000163817	Transcript	C
rs1532070	3:45970842-45970842	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs8176760	9:136150379-136150379	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs2064061	3:45871203-45871203	C	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs12720218	19:10490888-10490888	A	upstream_gene_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	G
rs574311	9:136144110-136144110	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G

rs62245101	3:45948875-45948875	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs34549672	3:45949954-45949954	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs146216196	3:46032144-46032144	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs139044419	3:46032210-46032210	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs142154067	3:46033101-46033101	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs79067698	3:46034560-46034560	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs188114046	3:46035925-46035925	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs9411475	9:136127268-136127268	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs4683147	3:45948264-45948264	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs280501	19:10491322-10491322	T	upstream_gene_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	C
rs72891712	3:46029398-46029398	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs112212287	3:45919528-45919528	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs587682443	9:136141355-136141355	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs587764387	9:136141356-136141356	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs587637585	9:136141358-136141358	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs17860183	21:34616549-34616549	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs7036642	9:136144626-136144626	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs9871972	3:45909090-45909090	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs17860220	21:34623919-34623919	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs2073362	21:34620801-34620801	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs7634640	3:45982119-45982119	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs2133660	3:46031957-46031957	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs1846615	3:46032388-46032388	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs1873001	3:46032847-46032847	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs1500003	3:46033819-46033819	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs34266669	9:136126495-136126495	T	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs199969472	9:136126498-136126498	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs141146648	3:45889587-45889587	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs7849280	9:136126636-136126636	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs2286489	3:45804069-45804069	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs147496374	21:34625037-34625037	G	missense_variant	MODERATE	IFNAR2	ENSG00000159110	Transcript	C

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rs514659	9:136142203-136142203	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs550057	9:136146597-136146597	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs2229207	21:34614250-34614250	A	missense_variant	MODERATE	IFNAR2	ENSG00000159110	Transcript	T
rs17279437	3:45814094-45814094	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs11670257	19:4713430-4713430	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs2003480	12:113443225-113443225	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs507666	9:136149399-136149399	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs12554336	9:136128663-136128663	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs10901253	9:136128772-136128772	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs11244053	9:136129360-136129360	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs4962114	9:136129611-136129611	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs4962115	9:136129642-136129642	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs4962116	9:136129716-136129716	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs115932896	3:46062389-46062389	G	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	A
rs74850924	3:45808345-45808345	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs58081338	9:136128329-136128329	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs62574567	9:136128421-136128421	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs57126329	3:45829562-45829562	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs659104	9:136147823-136147823	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs473533	9:136148035-136148035	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs476410	9:136148368-136148368	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs645982	9:136148409-136148409	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs500498	9:136148647-136148647	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs7870156	9:136128080-136128080	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs9844821	3:46019722-46019722	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs475419	9:136148231-136148231	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs142956930	9:136143330-136143330	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs1859330	12:113376388-113376388	A	missense_variant	MODERATE	OAS3	ENSG00000111331	Transcript	G
rs1859331	12:113376331-113376331	A	5_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs10751502	9:136129079-136129079	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs2077017	3:45812473-45812473	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A

rs7469795	9:136130893-136130893	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs11130082	3:46025518-46025518	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs13086858	3:46026699-46026699	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs60484807	9:136128467-136128467	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs3092963	3:46396938-46396938	G	intron_variant	MODIFIER	CCR2	ENSG00000121807	Transcript	A
rs1799865	3:46399798-46399798	C	synonymous_variant	LOW	CCR2	ENSG00000121807	Transcript	T
rs3138042	3:46401032-46401032	G	intron_variant	MODIFIER	CCR2	ENSG00000121807	Transcript	A
rs138017682	3:46024528-46024528	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs182171107	3:46033769-46033769	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs11707672	3:45964389-45964389	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs7644870	3:45830886-45830886	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs1860263	3:45832052-45832052	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs8176757	9:136130012-136130012	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs4683159	3:46025013-46025013	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs647800	9:136148000-136148000	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs12554580	9:136128603-136128603	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs147753307	3:45938484-45938484	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs185588322	3:45959697-45959697	T	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs148655132	3:45964352-45964352	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs140100519	3:45965077-45965077	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs181980885	3:45953578-45953578	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs186530132	3:45953925-45953925	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs112707117	3:45954246-45954246	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs657152	9:136139265-136139265	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs11130078	3:45964168-45964168	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs2251109	3:45796951-45796951	T	3_prime_UTR_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs904634	3:46017304-46017304	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs9849818	3:46020594-46020594	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs2304256	19:10475652-10475652	A	missense_variant	MODERATE	TYK2	ENSG00000105397	Transcript	C
rs5800979	12:113429904-113429904	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	-
rs3774642	3:45937782-45937782	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C

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rs1293772	12:113420604-113420604	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs1293771	12:113421295-113421295	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs1058480	12:113449116-113449116	A	3_prime_UTR_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs75018424	3:45926947-45926947	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs15895	12:113448288-113448288	C	stop_lost	HIGH	OAS2	ENSG00000111335	Transcript	A
rs74808020	3:45924167-45924167	C	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs12631321	3:45924897-45924897	T	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs1293768	12:113424501-113424501	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs1293743	12:113447572-113447572	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs17078335	3:45818419-45818419	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs35537559	3:46021452-46021452	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs67044455	3:46028791-46028791	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs758388	3:45812104-45812104	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs150326069	9:136137847-136137847	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs147960974	9:136148224-136148224	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs145218729	9:136148697-136148697	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs191811571	3:45984372-45984372	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs114346470	19:4691102-4691102	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs139518006	19:4713387-4713387	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs560966886	3:45956874-45956874	T	downstream_gene_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs150719194	3:45889656-45889656	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs138727962	3:45901597-45901597	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs148060386	3:45910289-45910289	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs560506883	3:45921382-45921382	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs150169230	12:113424858-113424858	G	missense_variant	MODERATE	OAS2	ENSG00000111335	Transcript	C
rs73433165	12:113379823-113379823	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs45583340	12:113409691-113409691	T	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs113497906	3:45804597-45804597	T	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs143341618	3:45806320-45806320	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs186253736	3:45807903-45807903	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs189427751	3:45811313-45811313	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A

rs565220072	3:45816798-45816798	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs4683148	3:45956060-45956060	T	downstream_gene_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs12638201	3:45934279-45934279	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs587635767	9:136141122-136141122	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs73422036	12:113407260-113407260	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs11837367	12:113407993-113407993	G	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs9875616	3:45979877-45979877	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs1293752	12:113437814-113437814	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1293751	12:113438413-113438413	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs2525848	12:113439622-113439622	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs1296061	12:113439881-113439881	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs143980719	3:45986795-45986795	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs529565	9:136149500-136149500	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs9831315	3:45956362-45956362	C	downstream_gene_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs4327428	3:45809329-45809329	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs2291470	3:45962942-45962942	A	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs12635657	3:46031029-46031029	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs7129	3:45959759-45959759	A	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs111207633	9:136130214-136130214	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs7466519	9:136131002-136131002	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs9848415	3:45828841-45828841	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs3733103	3:45962595-45962595	G	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs78069989	12:113393875-113393875	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs60439830	12:113399653-113399653	G	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs45489899	12:113405472-113405472	G	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs1293760	12:113431578-113431578	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs1293762	12:113430836-113430836	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs17078339	3:45822437-45822437	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs9869848	3:45978806-45978806	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs1293749	12:113442257-113442257	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1293748	12:113444024-113444024	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T

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rs79587259	3:45941187-45941187	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs1293765	12:113425493-113425493	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs75344264	12:113350105-113350105	G	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs505922	9:136149229-136149229	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs1293764	12:113425679-113425679	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs12053666	21:34618439-34618439	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs13052526	21:34604737-34604737	C	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	T
rs17860160	21:34611320-34611320	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs75078036	3:45935443-45935443	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs12054287	3:46067586-46067586	A	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	G
rs1293754	12:113436597-113436597	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs758389	3:45886399-45886399	C	upstream_gene_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	T
rs184214751	3:45904011-45904011	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs56006713	12:113354384-113354384	A	missense_variant	MODERATE	OAS1	ENSG00000089127	Transcript	G
rs3796373	3:45960851-45960851	G	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs1635142	12:113434518-113434518	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs1293757	12:113435109-113435109	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs1293756	12:113435293-113435293	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1293753	12:113437706-113437706	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1051393	21:34614255-34614255	A	missense_variant	MODERATE	IFNAR2	ENSG00000159110	Transcript	T
rs1293759	12:113431643-113431643	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs34725611	19:10477067-10477067	G	intron_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	A
rs757402	12:113429102-113429102	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs757401	12:113429468-113429468	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs4766662	12:113345699-113345699	C	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs12638598	3:45969992-45969992	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs3796376	3:46009491-46009491	T	synonymous_variant	LOW	FYCO1	ENSG00000163820	Transcript	C
rs4767023	12:113352159-113352159	A	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs2171530	3:45956110-45956110	A	downstream_gene_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs6781668	3:46019283-46019283	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs7965570	12:113386624-113386624	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C

rs12720270	19:10475760-10475760	A	intron_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	G
rs3821883	3:46022704-46022704	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs189110596	21:34606840-34606840	C	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs3733097	3:46026259-46026259	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs17078495	3:46026641-46026641	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs737452	3:46027410-46027410	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs596141	9:136144689-136144689	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs9836836	3:45951602-45951602	C	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs8176748	9:136131289-136131289	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs2300371	21:34632241-34632241	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs8176745	9:136131347-136131347	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs9849771	3:46020509-46020509	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs62242259	3:45807626-45807626	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs2234355	3:45987980-45987980	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs59776512	3:45835415-45835415	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	-
rs59767267	3:46021559-46021559	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs75442536	3:45950911-45950911	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs751552	3:46016851-46016851	G	splice_polypyrimidine_tract_variant,intron_variant	LOW	FYCO1	ENSG00000163820	Transcript	A
rs751553	3:46016944-46016944	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs58035200	3:46068681-46068681	A	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	C
rs7956880	12:113345167-113345167	C	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs2285934	12:113351520-113351520	A	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs10744785	12:113345256-113345256	A	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs7623476	3:46068843-46068843	G	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	A
rs112101762	3:45892596-45892596	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs113181700	3:45893133-45893133	C	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs73830609	3:45939238-45939238	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs59226168	3:46028320-46028320	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs62242796	3:46029193-46029193	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs138971703	12:113397082-113397082	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs1298301	12:113418899-113418899	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G

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rs12493913	3:45822072-45822072	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs12554339	9:136128737-136128737	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs11244052	9:136129125-136129125	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs62242787	3:45995908-45995908	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs7046674	9:136147012-136147012	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176647	9:136147755-136147755	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs8176641	9:136149802-136149802	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176639	9:136150317-136150317	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176710	9:136134537-136134537	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs8176649	9:136147295-136147295	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs60110056	3:45966671-45966671	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs7615978	3:45835570-45835570	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs62242788	3:46001649-46001649	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs8176682	9:136139297-136139297	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs4683146	3:45898221-45898221	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs929291	12:113444418-113444418	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs1293773	12:113420551-113420551	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs3803057	12:113368734-113368734	A	intron_variant,NMD_transcript_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	G
rs8176687	9:136138658-136138658	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs8176679	9:136139955-136139955	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs17078308	3:45797991-45797991	C	3_prime_UTR_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs4767045	12:113409413-113409413	A	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs10744791	12:113410316-113410316	A	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs6796097	3:45878988-45878988	G	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs189659509	3:46065278-46065278	G	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	A
rs13064991	3:45834811-45834811	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs3774641	3:45937833-45937833	T	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs10774671	12:113357193-113357193	A	splice_acceptor_variant	HIGH	OAS1	ENSG00000089127	Transcript	G
rs200629605	12:113429326-113429326	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs2248228	3:45965386-45965386	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs4683152	3:45974886-45974886	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C

rs7509997	21:34607358-34607358	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs12639598	3:46016464-46016464	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs4683149	3:45967869-45967869	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs530909128	9:136130463-136130463	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs140253702	3:46401606-46401606	G	3_prime_UTR_variant	MODIFIER	CCR2	ENSG00000121807	Transcript	A
rs186153536	3:45923622-45923622	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs530595037	3:45924287-45924287	C	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs552329766	3:45924288-45924288	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs115004584	3:45925363-45925363	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs78414305	3:45925618-45925618	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs74739895	3:45926749-45926749	G	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs78044818	3:45926972-45926972	A	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs115227401	3:45929086-45929086	T	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs76478208	3:45929426-45929426	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs6783694	3:45929800-45929800	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs116264461	3:45930581-45930581	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs77676459	3:45930814-45930814	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs144180015	3:45931297-45931297	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs576036480	21:34607449-34607449	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs117489085	21:34611986-34611986	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs545411453	21:34612133-34612133	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs181597872	21:34629420-34629420	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs11837165	12:113406699-113406699	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs142086756	3:45823690-45823690	A	synonymous_variant	LOW	SLC6A20	ENSG00000163817	Transcript	G
rs184263104	3:45827195-45827195	T	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	A
rs182605899	3:45835228-45835228	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs147310206	3:45836492-45836492	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs11085726	19:10465609-10465609	A	intron_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	G
rs2531750	3:45799599-45799599	A	3_prime_UTR_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs13091979	3:45980110-45980110	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs13091821	3:45980115-45980115	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A

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rs3774639	3:45983654-45983654	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs4683156	3:45991087-45991087	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs1293766	12:113425282-113425282	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs57228214	3:46019939-46019939	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs4535265	3:45977866-45977866	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs12639224	3:45916222-45916222	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs111310794	9:136132986-136132986	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176694	9:136137646-136137646	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs720626	3:45810138-45810138	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs10850104	12:113385375-113385375	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs34647135	12:113386616-113386616	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs60199752	19:4705004-4705004	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs11671605	19:4705508-4705508	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs28595837	3:45946025-45946025	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs8107316	19:4680805-4680805	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs1293767	12:113425154-113425154	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs1293770	12:113421869-113421869	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs57771566	12:113396978-113396978	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs58603713	12:113398147-113398147	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs75755877	12:113409965-113409965	G	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs73422042	12:113410421-113410421	T	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs62574565	9:136128259-136128259	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs663054	9:136146920-136146920	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs9855205	3:45935698-45935698	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs9881306	3:45946147-45946147	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs79179998	3:45947066-45947066	A	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs2834160	21:34620113-34620113	C	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	T
rs45495393	12:113352708-113352708	A	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs11244054	9:136130225-136130225	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs1072755	3:45975983-45975983	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs551100	9:136146740-136146740	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T

rs11911133	21:34629175-34629175	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs17078371	3:45892477-45892477	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs6771661	3:45820507-45820507	G	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs1293763	12:113426632-113426632	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs757405	12:113406945-113406945	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs2277735	19:4700187-4700187	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs1298962	12:113418850-113418850	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs1293774	12:113419177-113419177	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	C
rs17078449	3:45980673-45980673	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs17078454	3:45981215-45981215	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs57204020	3:45981877-45981877	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs3774640	3:45983479-45983479	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs3774638	3:45983887-45983887	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs936939	3:45986623-45986623	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs2660	12:113357442-113357442	A	3_prime_UTR_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	G
rs77709797	3:45970409-45970409	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs190039371	3:45972170-45972170	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs8176702	9:136136146-136136146	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs936938	3:45980769-45980769	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs3774635	3:45986219-45986219	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs2054866	3:45990217-45990217	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs1994488	3:45992977-45992977	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs1552489	3:45993973-45993973	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs139540257	3:45869678-45869678	A	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs2234350	3:45984300-45984300	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs2234351	3:45984323-45984323	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs12427406	12:113383802-113383802	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs7621856	3:45802134-45802134	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs71465868	12:113390363-113390363	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs2191031	3:45910870-45910870	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs55688670	12:113400746-113400746	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C

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rs45607836	12:113401212-113401212	A	missense_variant	MODERATE	OAS3	ENSG00000111331	Transcript	G
rs8130779	21:34608625-34608625	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	T
rs9974669	21:34608954-34608954	C	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs72977989	19:4708568-4708568	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs675201	9:136146466-136146466	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs9869542	3:45934588-45934588	C	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs4401152	19:4708102-4708102	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs1293745	12:113446198-113446198	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs1293744	12:113446727-113446727	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs2277733	19:4714044-4714044	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs570824030	21:34609388-34609388	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs75826707	3:45908859-45908859	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs2834162	21:34620409-34620409	C	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs17860211	21:34620668-34620668	C	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	A
rs12633699	3:45922735-45922735	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs35334665	3:46061218-46061218	A	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	T
rs71327009	3:46064626-46064626	G	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	C
rs35161099	3:46067507-46067507	G	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	T
rs71327010	3:46068835-46068835	A	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	G
rs71327006	3:46058908-46058908	A	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	G
rs71327007	3:46059249-46059249	T	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	C
rs140227473	3:45909287-45909287	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs79657519	3:45910031-45910031	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs6778225	3:45970940-45970940	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs60779624	3:45971263-45971263	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs33910087	3:46009487-46009487	A	missense_variant	MODERATE	FYCO1	ENSG00000163820	Transcript	G
rs62245106	3:45968668-45968668	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs6778324	3:45971022-45971022	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs13079869	3:46008087-46008087	A	synonymous_variant	LOW	FYCO1	ENSG00000163820	Transcript	G
rs62130729	19:10486936-10486936	A	intron_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	G
rs17215008	3:46012279-46012279	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T

rs71325098	3:46012391-46012391	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs71325100	3:46013832-46013832	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs41289622	3:46014545-46014545	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs13066062	3:46018344-46018344	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs34000569	3:45999209-45999209	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs34324101	3:46000728-46000728	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs13069079	3:46000870-46000870	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs34849862	3:46001367-46001367	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs35209528	3:46003496-46003496	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs36122610	3:46022833-46022833	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs34442130	3:46024529-46024529	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs13075758	3:46025048-46025048	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs17330872	3:46035097-46035097	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs71327003	3:46036521-46036521	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs117666908	12:113420087-113420087	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs57036895	3:46007419-46007419	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs35501575	3:45993645-45993645	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs2109070	19:4719485-4719485	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs730983	3:46028056-46028056	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs8176691	9:136138229-136138229	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs2171531	3:45981171-45981171	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs55920693	3:45983476-45983476	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs11066456	12:113383431-113383431	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs17078464	3:45990117-45990117	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs58050797	3:45992445-45992445	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs75507082	3:45909496-45909496	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs1131476	12:113357209-113357209	A	missense_variant	MODERATE	OAS1	ENSG00000089127	Transcript	G
rs4767044	12:113402899-113402899	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs3937434	12:113406196-113406196	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs2016831	12:113406460-113406460	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs1557866	12:113405181-113405181	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A

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rs2286486	3:45927741-45927741	C	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	T
rs4962113	9:136127641-136127641	C	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs56972507	3:46025992-46025992	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs7627147	3:45984097-45984097	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs58442576	3:45990277-45990277	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs56239523	3:45991123-45991123	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs11066457	12:113386245-113386245	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs34137742	12:113348661-113348661	T	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs75628555	12:113359445-113359445	T	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs60237998	3:45965954-45965954	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs2109069	19:4719443-4719443	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs1293746	12:113445768-113445768	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs2834166	21:34626654-34626654	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs2006231	19:4719123-4719123	T	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs10420225	19:4724157-4724157	A	upstream_gene_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs10735079	12:113380008-113380008	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs2373087	3:45968043-45968043	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs35831747	3:45970391-45970391	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs13099120	3:45970944-45970944	G	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs35477280	3:45974092-45974092	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs13066516	3:45975443-45975443	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs77902290	3:45976662-45976662	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs7631809	3:45968325-45968325	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs61751653	3:45942971-45942971	A	missense_variant	MODERATE	CCR9	ENSG00000173585	Transcript	G
rs113094386	19:4699126-4699126	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs16942430	12:113446009-113446009	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	T
rs201439325	9:136131407-136131407	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs587698906	9:136142533-136142533	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs587763606	9:136145172-136145172	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs79343853	9:136146310-136146310	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs150667470	3:45924901-45924901	A	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G

rs1187	21:34610893-34610893	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	T
rs190577088	3:45880233-45880233	G	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs12639252	3:45916386-45916386	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs3815178	12:113376320-113376320	A	5_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs1859329	12:113376452-113376452	A	synonymous_variant	LOW	OAS3	ENSG00000111331	Transcript	C
rs7299132	12:113376913-113376913	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs6489879	12:113377822-113377822	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs4238033	12:113378081-113378081	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs6489880	12:113380271-113380271	G	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs6489882	12:113381376-113381376	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs146042277	12:113391245-113391245	G	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs140303054	12:113396695-113396695	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs4766678	12:113397691-113397691	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs59375543	3:45820990-45820990	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs547178387	3:46059120-46059120	A	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	-
rs559851604	3:46059121-46059121	A	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	C
rs1293747	12:113444845-113444845	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs7638236	3:45977641-45977641	C	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs58491168	3:45966939-45966939	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs7311182	12:113379123-113379123	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs9857669	3:45806066-45806066	T	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs7855255	9:136131895-136131895	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176733	9:136132168-136132168	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs2073823	9:136132516-136132516	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs8176730	9:136132525-136132525	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs11130077	3:45877712-45877712	A	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs7975318	12:113429329-113429329	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs575208313	3:45806200-45806200	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs6770261	3:45804734-45804734	T	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	C
rs35508621	3:45880481-45880481	C	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	T
rs687289	9:136137106-136137106	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G

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rs34288077	3:45888690-45888690	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs1994492	3:45960646-45960646	C	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs1994493	3:45960700-45960700	T	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs1752339	9:136141135-136141135	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs1927315	9:136142000-136142000	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs8176644	9:136149150-136149150	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176725	9:136132617-136132617	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs34326463	3:45899651-45899651	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs56945978	19:4721927-4721927	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs75928798	3:45962603-45962603	C	3_prime_UTR_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	A
rs34068335	3:45954339-45954339	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs7623460	3:46068764-46068764	C	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	A
rs10850105	12:113391363-113391363	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs12301619	12:113423203-113423203	C	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs12423440	12:113356309-113356309	T	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs35280891	3:45951647-45951647	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs4238034	12:113397143-113397143	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs78220999	12:113395457-113395457	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs150390228	12:113395704-113395704	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs10744789	12:113396010-113396010	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs687621	9:136137065-136137065	G	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs2072133	12:113409260-113409260	A	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs28437706	3:45834878-45834878	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs9852457	3:45835076-45835076	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs74945326	3:45948464-45948464	T	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs7636844	3:45927211-45927211	T	upstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs6441931	3:45928730-45928730	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs111590440	9:136127783-136127783	G	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs12482193	21:34611545-34611545	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	T
rs2072136	12:113398919-113398919	A	synonymous_variant	LOW	OAS3	ENSG00000111331	Transcript	G
rs4767041	12:113378677-113378677	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G

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rs7955267	12:113379039-113379039	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs7977345	12:113380708-113380708	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs6489881	12:113381217-113381217	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs2158393	12:113398422-113398422	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs11066464	12:113428717-113428717	A	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	G
rs4435062	12:113395660-113395660	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs10211925	21:34615732-34615732	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs7980275	12:113380529-113380529	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs9818982	3:45812514-45812514	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs17860142	21:34607870-34607870	G	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs12482014	21:34611318-34611318	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs17860165	21:34611730-34611730	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs8176735	9:136132008-136132008	T	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs8176729	9:136132528-136132528	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs2248420	21:34605778-34605778	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs3153	21:34609505-34609505	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs2072135	12:113399179-113399179	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs59817490	3:45940809-45940809	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs73830610	3:45943819-45943819	T	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs75918913	3:46006917-46006917	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs280499	19:10489606-10489606	G	upstream_gene_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	A
rs7618553	3:45835828-45835828	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs2010604	12:113408208-113408208	C	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs2057778	12:113350796-113350796	C	intron_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	G
rs1974518	12:113389603-113389603	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs4767042	12:113393284-113393284	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	T
rs138164693	9:136134118-136134118	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs183228393	9:136134835-136134835	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs12610298	19:10485242-10485242	A	intron_variant	MODIFIER	TYK2	ENSG00000105397	Transcript	C
rs532436	9:136149830-136149830	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	G
rs2271616	3:45838013-45838013	A	upstream_gene_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G

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rs739903	12:113408874-113408874	G	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs7023	12:113410975-113410975	A	3_prime_UTR_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs2240189	12:113403497-113403497	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs8176698	9:136136593-136136593	A	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	T
rs8176696	9:136136773-136136773	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs10420007	19:4724069-4724069	A	upstream_gene_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs11385942	3:45876461-45876461	A	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	-
rs61185149	3:45907384-45907384	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs4767026	12:113359132-113359132	C	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs10774672	12:113360737-113360737	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	G
rs4766677	12:113397630-113397630	G	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs7135577	12:113358106-113358106	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs4767028	12:113359188-113359188	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs4767030	12:113359577-113359577	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs17078471	3:45996583-45996583	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs11130081	3:46015182-46015182	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	G
rs34886194	12:113430203-113430203	G	intron_variant	MODIFIER	OAS2	ENSG00000111335	Transcript	A
rs28607988	3:45913338-45913338	C	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs4767024	12:113358791-113358791	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs4767025	12:113358794-113358794	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs4767027	12:113359157-113359157	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs4767029	12:113359318-113359318	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	G
rs10850092	12:113359703-113359703	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs6489864	12:113360025-113360025	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs6489865	12:113360302-113360302	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	A
rs10850093	12:113360468-113360468	T	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs10850094	12:113360563-113360563	C	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs10850095	12:113360575-113360575	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs10850096	12:113360786-113360786	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T
rs10774673	12:113361158-113361158	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs10774674	12:113361174-113361174	A	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	T

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rs1467941	19:4720523-4720523	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs7131998	12:113381695-113381695	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs2834159	21:34618089-34618089	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs60080146	3:46067618-46067618	G	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	A
rs9867918	3:45807699-45807699	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs931704	3:46024671-46024671	A	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	T
rs71325089	3:45904548-45904548	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs56058226	3:45935018-45935018	T	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	C
rs45610939	9:136133396-136133396	C	intron_variant,non_coding_transcript_variant	MODIFIER	ABO	ENSG00000175164	Transcript	A
rs62226154	21:34614901-34614901	T	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs35624553	3:45867440-45867440	G	3_prime_UTR_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs67959919	3:45871908-45871908	A	intron_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs62226157	21:34615088-34615088	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	G
rs56116432	9:136131429-136131429	A	non_coding_transcript_exon_variant	MODIFIER	ABO	ENSG00000175164	Transcript	C
rs34136596	19:4693903-4693903	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs35408525	19:4705215-4705215	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs758510	19:4721991-4721991	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs188401375	21:34602242-34602242	A	upstream_gene_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C
rs558702333	3:46060618-46060618	G	3_prime_UTR_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	C
rs12824584	12:113390957-113390957	A	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	G
rs369845989	3:45808361-45808361	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs543762608	3:45821742-45821742	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs576940167	3:45822241-45822241	C	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	T
rs6800954	3:45964959-45964959	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs59676542	3:46068160-46068160	T	intron_variant	MODIFIER	XCR1	ENSG00000173578	Transcript	C
rs4962040	9:136133531-136133531	G	splice_polypyrimidine_tract_variant,intron_variant	LOW	ABO	ENSG00000175164	Transcript	A
rs7310667	12:113392182-113392182	C	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	A
rs732631	19:4719025-4719025	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	C
rs73062389	3:45835417-45835417	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs10850097	12:113361117-113361117	G	downstream_gene_variant	MODIFIER	OAS1	ENSG00000089127	Transcript	C
rs9823523	3:45937117-45937117	G	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A

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rs10421782	19:4685276-4685276	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs2269899	12:113381956-113381956	T	intron_variant	MODIFIER	OAS3	ENSG00000111331	Transcript	C
rs7641997	3:45806173-45806173	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs1467942	19:4720532-4720532	A	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	G
rs13081482	3:45908116-45908116	C	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs73064425	3:45901089-45901089	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs8105807	19:4684642-4684642	G	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	A
rs2885734	19:4690259-4690259	C	intron_variant	MODIFIER	DPP9	ENSG00000142002	Transcript	T
rs41289614	3:45972492-45972492	T	intron_variant	MODIFIER	FYCO1	ENSG00000163820	Transcript	C
rs35731912	3:45889949-45889949	T	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	C
rs17764980	3:45939016-45939016	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs17714101	3:45939802-45939802	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs17714228	3:45945132-45945132	C	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs71325092	3:45947018-45947018	G	downstream_gene_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	A
rs3764864	3:45936237-45936237	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs35081325	3:45889921-45889921	G	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	A
rs34338823	3:45928769-45928769	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs71325091	3:45932407-45932407	A	intron_variant	MODIFIER	CCR9	ENSG00000173585	Transcript	G
rs57133084	3:45819197-45819197	A	intron_variant	MODIFIER	SLC6A20	ENSG00000163817	Transcript	G
rs34518147	3:45920298-45920298	C	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	T
rs57319220	3:45919992-45919992	A	intron_variant,NMD_transcript_variant	MODIFIER	LZTFL1	ENSG00000163818	Transcript	G
rs8128785	21:34613967-34613967	A	intron_variant	MODIFIER	IFNAR2	ENSG00000159110	Transcript	C

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