Alzheimer's
Research & Therapy

RESEARCH

Open Access

Convergent transcriptomic and genomic evidence supporting a dysregulation of *CXCL16* and *CCL5* in Alzheimer's disease

Xiao Li[1,2†], Deng-Feng Zhang[1,2†], Rui Bi[1,2,3], Li-Wen Tan[4], Xiaogang Chen[4], Min Xu[1,2*] and Yong-Gang Yao[1,2,3*]

Abstract

Background Neuroinflammatory factors, especially chemokines, have been widely reported to be involved in the pathogenesis of Alzheimer's disease (AD). It is unclear how chemokines are altered in AD, and whether dysregulation of chemokines is the cause, or the consequence, of the disease.

Methods We initially screened the transcriptomic profiles of chemokines from publicly available datasets of brain tissues of AD patients and mouse models. Expression alteration of chemokines in the blood from AD patients was also measured to explore whether any chemokine might be used as a potential biomarker for AD. We further analyzed the association between the coding variants of chemokine genes and genetic susceptibility of AD by targeted sequencing of a Han Chinese case–control cohort. Mendelian randomization (MR) was performed to infer the causal association of chemokine dysregulation with AD development.

Results Three chemokine genes (*CCL5*, *CXCL1*, and *CXCL16*) were consistently upregulated in brain tissues from AD patients and the mouse models and were positively correlated with Aβ and tau pathology in AD mice. Peripheral blood mRNA expression of *CXCL16* was upregulated in mild cognitive impairment (MCI) and AD patients, indicating the potential of *CXCL16* as a biomarker for AD development. None of the coding variants within any chemokine gene conferred a genetic risk to AD. MR analysis confirmed a causal role of CCL5 dysregulation in AD mediated by trans-regulatory variants.

Conclusions In summary, we have provided transcriptomic and genomic evidence supporting an active role of dysregulated *CXCL16* and *CCL5* during AD development.

Keywords Alzheimer's disease, Chemokine, mRNA expression, Pathology, Targeted sequencing, Mendelian randomization

†Xiao Li and Deng-Feng Zhang contributed equally to this work.

*Correspondence:
Min Xu
xumin@mail.kiz.ac.cn
Yong-Gang Yao
yaoyg@mail.kiz.ac.cn
[1] Key Laboratory of Animal Models and Human Disease Mechanisms of the Chinese Academy of Sciences & Yunnan Province, and KIZ/CUHK Joint Laboratory of Bioresources and Molecular Research in Common Diseases, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650204, Yunnan, China
[2] Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming 650204, China
[3] CAS Center for Excellence in Brain Science and Intelligence Technology, Chinese Academy of Sciences, Shanghai 200031, China
[4] Mental Health Institute of the Second Xiangya Hospital, Central South University, Changsha 410011, China

© The Author(s) 2023. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by/4.0/. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

Background

Alzheimer's disease (AD) is a progressive and incurable age-related neurodegenerative disease with cognitive decline caused by neuronal loss and brain atrophy [1, 2]. The neuropathological features of AD include the presence of abundant extracellular amyloid plaques laden with β-amyloid peptide (Aβ), intraneuronal neurofibrillary tangles formed by the hyperphosphorylated tau, neuritic dystrophy, loss of synapses and neuronal somata [1, 2]. Microglia activation and neuroinflammation are also hallmarks of AD [1, 2]. Genetic studies including genome-wide association studies (GWAS) [3–7], whole-exome sequencing (WES) [8, 9], and whole-genome sequencing (WGS) [10] studies have identified numerous genomic loci associated with AD, with immune genes being highlighted frequently.

The immune factors that are linked to neuroinflammation may accompany and contribute to neurodegenerative pathology [11]. Chemokines are small proteins with the ability to induce targeted chemotaxis of nearby reactive immune cells and have a well-established role in the immune system [12, 13]. Chemokines are a group of chemotactic cytokines and can be classified into two groups: the homeostatic chemokines and the inflammatory chemokines. The homeostatic chemokines are important for lymphoid organ development and immune cell trafficking. The inflammatory chemokines are actively involved in the mobilization of effector cells to the inflammatory sites [14]. Apart from their roles in the immune system, chemokines also take part in the physiological and pathological processes in the central nervous system (CNS). In the human brain, neurons and glial cells are able to express chemokines and also have chemokine receptors [15, 16]. Chemokines participate in the proliferation, differentiation, and migration of neural cells and are important for brain homeostasis [15]. The expression of chemokines and the functioning of their receptors may change in CNS diseases [14–16]. Chemokines have been reported to be actively involved in CNS development and neurological diseases [14]. Chemokine signaling affects a variety of cellular activities and functions, including the migration and survival of neuronal precursors [17], the migration and proliferation of oligodendrocyte progenitors [18], the maintenance of oligodendrocyte lineage, myelination, and white matter [19], the central synaptic transmission [20], glymphatic function and neuroinflammation [21], and aging-dependent neuronal regenerative decline [22].

There are several lines of evidence to show expression change, chemokine/chemokine receptor axis signaling, pathological correlation, and genetic regulation of chemokines, each take a part in the disease progression of AD. First, expression changes of chemokines have been implicated in the pathogenesis of AD. Some chemokines were reported to be significantly altered in brain tissues [23], cerebral microcirculation [24], cerebrospinal fluid (CSF) [25, 26], plasma [27] or peripheral blood cells [28, 29] of AD patients, and in a mouse model of AD [30]. Second, chemokine/chemokine receptor axes may affect AD pathologies in multiple ways. The impaired CCL2/CCR2 axis in blood-derived monocytes caused a deficit in cell migration in mild cognitive impairment (MCI) and AD patients [31]. Dysregulation of the CX3CL1/CX3CR1 axis has shown both neuroprotective and neurotoxic effects in different AD mouse models [32, 33]. Third, a growing body of evidence indicates the chemokine/chemokine receptor axes affect Aβ and tau pathologies [32, 34–36], glymphatic function, cognition, or neuroinflammation [21, 36] in AD mouse models. Despite the functional involvement, several genetic association studies focusing on a few chemokine genes showed no direct association between common genetic polymorphisms of chemokine genes and the genetic susceptibility to AD [13, 37–39]. However, one study has suggested that a haplotype of single nucleotide polymorphism (SNP) within a chemokine gene cluster may modify the age of onset of familial AD [40]. Since genetic variants play a role in the regulation and activation of chemokine/chemokine receptor signaling in AD [27], a systematic evaluation of the genetic variants and regulation of chemokines in AD is warranted.

In this study, we evaluated the transcriptomic dysregulation of chemokines in publicly available datasets of AD patients and mouse models. A three-stage genetic study of 31 chemokine genes was conducted in a Han Chinese cohort of 1280 AD cases and 5044 cognitively normal control subjects, to evaluate the potential association of genetic variation of chemokines with AD. Mendelian randomization (MR) was further used to evaluate the causally associated chemokine gene(s) in AD (Fig. 1). We found an active involvement of *CXCL16* and *CCL5* dysregulation in the development of AD.

Materials and methods

Gene assignment

We assigned 31 typical chemokine genes, including nine C–C motif chemokine ligands (CCLs) and seven receptors (CCRs), nine C-X-C motif chemokine ligands (CXCLs) and four receptors (CXCRs), C-X3-C motif chemokine receptor (CX3CR1) and X-C motif chemokine receptor (XCR1), as defined by the KEGG "Chemokine signaling pathway" (https://www.gsea-msigdb.org/gsea/msigdb/cards/KEGG_CHEMOKINE_SIGNALING_PATHWAY.html) and the Immport database (https://www.immport.org/shared/genelists) [45].

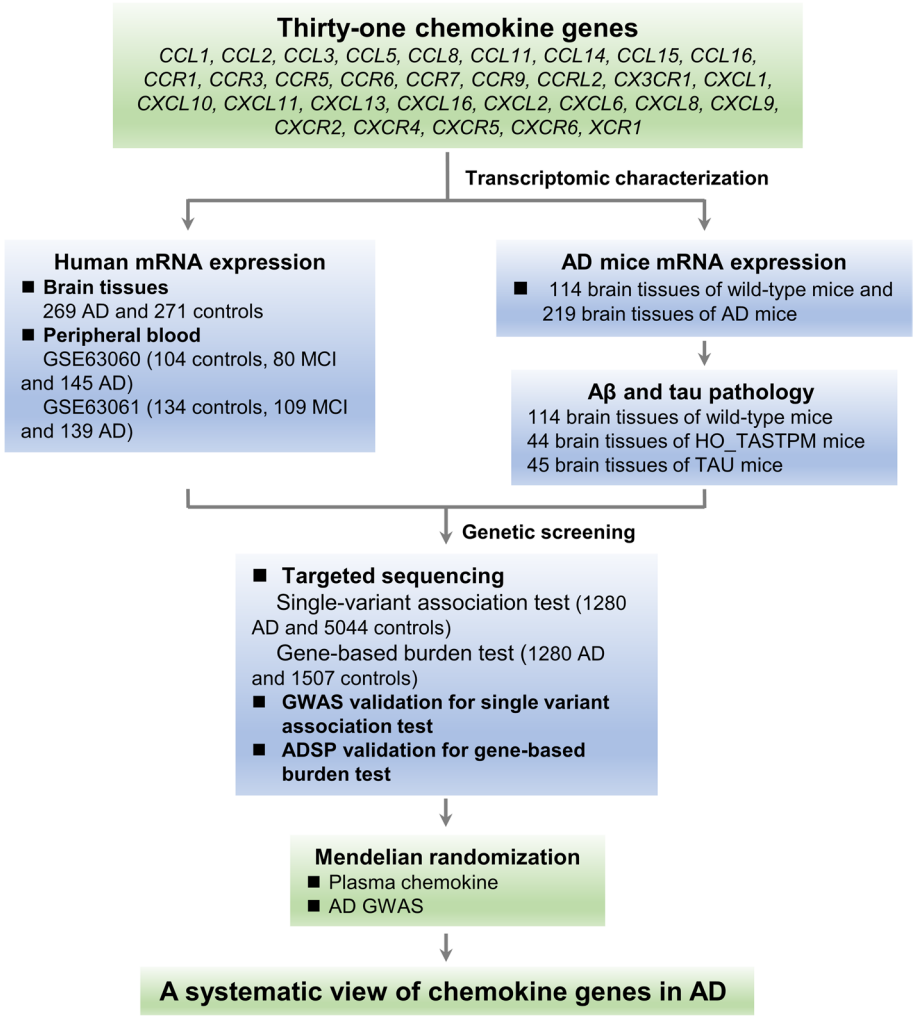

Fig. 1 Study design for integrative analysis and for identifying AD-associated chemokines. The mRNA expression profiling of 31 chemokine genes was analyzed by using the compiled microarray data of four brain regions (entorhinal cortex, hippocampus, frontal cortex, and temporal cortex) of AD patients and controls [41], two microarray data (GSE63060 and GSE63061) from peripheral blood of patients with mild cognitive impairment (MCI) or AD and controls [42], and expression data of AD mouse models [43]. The gene-based burden test and single-variant association analysis were performed using Han Chinese cohorts in this study and reported datasets [6, 44]. Mendelian randomization (MR) was used to assess the causal effect of the most significantly AD-associated chemokine genes on AD

mRNA expression profiling of chemokine genes in AD patients

The mRNA expression levels of the chemokine genes were analyzed in four AD-relevant brain regions (the entorhinal cortex, hippocampus, temporal cortex and frontal cortex) [41]. The microarray expression data of the four brain regions from 269 AD patients and 271 controls were retrieved from Gene Expression Omnibus (GEO: http://www.ncbi.nlm.nih.gov/geo) and were integrated to generate a normalized expression profile, as described in our previous study (http://www.alzdata.org/) [41]. In brief, for each original microarray data retrieved from the GEO database, we conducted data normalization, log2 transformation, probe filtration, and probe mapping to entrez gene IDs. Expression datasets for the same brain region were then combined and re-normalized to remove batch effects. The normalized expression data was used to detect if there were any differentially expressed chemokine genes between AD patients and controls. More details regarding to data processing of these reported datasets can be retrieved from our previous study ([41] and references therein).

The expression alterations of chemokines in peripheral blood from individuals with and without AD were explored in two large independent age-matched dementia case–control data sets [42]. The first dataset (GSE63060) includes 329 individuals containing 104 healthy controls, 80 MCI, and 145 AD patients from AddneuroMed

Cohort (batch 1, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63060). The second dataset (GSE63061) includes 388 individuals, among which 382 were explicitly defined (including 134 healthy controls, 109 MCI, and 139 AD patients) (batch 2, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63061) [42]. Patients with MCI and AD had different levels of cognitive impairments. Specifically, the MCI patients had problems with memory, but had normal daily activities. The healthy control subjects had no cognitive impairment. More description of these patients with AD, MCI, and healthy controls can be found in the original study [42]. The expression profiling of the original microarray expression matrix series was loaded using the R package *GEOquery*. The *limma* R package was used to process the data and differential expression analysis was conducted under the linear model. More information regarding the related datasets can be found in the original publication [42].

mRNA expression profiling and pathological correlation in AD mouse models

So as to investigate the dynamic alteration of chemokines before and during the development of AD pathology, we retrieved the spatial–temporal expression data of chemokine genes in AD mouse models from Mouseac (www.mouseac.org) [43]. We retrieved pathological scores of Aβ and tau of the AD mouse models and performed the correlation analysis between the mRNA expression level of chemokine genes and scored AD pathology by using the nonparametric Pearson correlation test with the GraphPad Prism software (GraphPad Software, La Jolla, CA, USA), as described in our previous study [46]. The original study [43] measured the gene expression changes in the brain tissues (including 113 hippocampus samples, 113 cortex samples, and 111 cerebellum samples) from different AD murine models at the age of 2, 4, 8, and 18 months. Also, the levels of amyloid burden and phosphorylated tau pathology were investigated through immunostaining with antibodies for Aβ40 or phosphorylated tau, and the semi-quantitative scores were based on the pathology severity [43]. In total, the expression data and pathological features of 114 brain tissues from wild-type mice (WILD) and 219 brain tissues from five AD transgenic mice with human APP, PSEN1 or MAPT mutant (TAS10 [with APP $^{K670N/M671L}$ mutant], TPM [with PSEN1 ^{M146V} mutant], HO_TASTPM [with homozygous mutant of APP and PSEN1 mentioned above], HET_TASTPM [with heterozygous mutant of APP and PSEN1 mentioned above], and TAU [with MAPT ^{P301L} mutant]) were analyzed. More information about these mouse models can be found in the original research [43].

Targeted sequencing of chemokine genes in Han Chinese

To investigate whether there is a potential genetic association between the chemokine gene variants and AD, we conducted targeted sequencing of 31 chemokine genes in Han Chinese with and without AD. The majority of Han Chinese samples have been described in our previous studies [46–49]. Briefly, two cohorts containing AD cases ($n=1280$) and controls ($n=5044$) were enrolled from Southern and Eastern China. All AD patients were confirmed to have no known pathogenic variants in *APP*, *PSEN1*, or *PSEN2*. The Southern cohort contains 635 sporadic AD patients (mean age 79.7 ± 8.2 years, 40.0% male) and 1507 controls (mean age 35.2 ± 15.5 years, 56.2% male) recruited from Sichuan, Hunan, and Yunnan Province of China. The Eastern cohort contains 645 AD patients (mean age 79.2 ± 9.1 years, 41.2% male) recruited from Shanghai and Zhejiang and 3537 controls from the general population with WGS data from the China Metabolic Analytics Project (ChinaMAP) [50]. The patients were diagnosed by at least two clinical psychiatrists following the Diagnostic and Statistical Manual of Mental Disorders (DSM-IV), as have been previously described [46–48]. Some of the control samples from the Yunnan Province of China have been reported in our previous study [51, 52]. The Southern and Eastern cohorts were used in stage 1 and stage 2 analyses, respectively. Written informed consents conforming to the tenets of the Declaration of Helsinki were obtained from all participants before the enrollment of this study. The experimental protocols were approved by the institutional review board of Kunming Institute of Zoology, Chinese Academy of Sciences.

Genomic DNA was extracted from peripheral blood by using the AxyPrep Blood Genomic DNA Miniprep Kit (Axygen Scientific). DNA probes were designed using the online NimbleDesign tool (now updated ashttps://www.hyperdesign.com/#/). Coding regions, exon–intron boundaries, the 5'- and 3'-untranslated regions (UTRs) of the 31 genes were captured with the NimbleGen SeqCap EZ Choice Enrichment Kit (Roche NimbleGen) according to the manufacturer's protocols, as described in our recent studies [51, 52]. Briefly, all captured DNA libraries were sequenced with the NovaSeq 6000 (150 bp paired-end). Raw reads were trimmed to remove sequencing adapters and low-quality reads by using the Trimmomatic (v0.33) [53]. Clean reads were aligned according to the human reference genome GRCh37/hg19 with the Burrows-Wheeler Aligner [54]. Post alignment quality control and variant calling were performed using the Genome Analysis Toolkit (GATK v4.1) following the best practices pipeline (https://www.broadinstitute.org/gatk/guide/best-practices) [55]. Quality control was performed based

on all of the sequencing data. Variants were excluded if the genotype rate were less than 90%, or deviated from Hardy–Weinberg equilibrium (HWE $p < 1 \times 10^{-6}$). Samples with an average genotype rate < 80% were also excluded.

Variants were annotated into different functional categories by using ANNOVAR [56]. A variant was defined as rare if it had a minor allele frequency (MAF) < 0.01, otherwise, it was defined as common. Rare variants were further classified into three categories: loss-of-function (LoF) variants, missense variants, and possibly pathogenic variants. Variants belonging to stop gain/loss, frameshift indels, initiation codon, and splice sites were defined as LoF variants. Rare missense variants with sensitivity score ≤ 0.95 were defined as possibly pathogenic by using the Mendelian Clinically Applicable Pathogenicity (M-CAP) [57].

Cross-genetic validation in European-ancestry populations

Data from two previous studies [6, 44] were used for cross-validation of the association of the single variants and genes with AD identified in this study. The summary data of the newly published GWAS meta-analysis [6] contains a total of 111,326 clinically diagnosed/ "proxy" AD cases and 677,663 controls. We used this dataset to validate the potential association of common variants with AD in Han Chinese. The WES data from the discovery case–control association results of the Alzheimer's Disease Sequencing Project (ADSP) [44] was used to validate the gene-based burden test discerned in this study. The cumulative minor allele counts from the 5740 AD cases and 5096 cognitively normal controls and the *p*-values adjusted for different covariates were extracted from the original study. More information regarding patient description and data quality control can be found in the original reports [6, 44].

MR analyses

In order to explore whether there was a causal effect of the observed association between chemokine and AD, we conducted MR analyses by using the R package "TwoSampleMR" [58]. The causal effect of chemokine on AD was measured using chemokine as the exposure and AD as the outcome. Genetic variants (SNPs) associated with chemokine expression (p-value $< 1 \times 10^{-5}$) were set as the instrumental variables and were investigated in GWAS of outcomes. The causal effect of chemokine-related instruments (significant SNPs) on AD outcomes was assessed in large-scale GWAS for AD. In brief, we extracted plasma protein data for chemokines from 3301 healthy blood donors [59] and 3394 individuals with multiple cardiovascular diseases [60]. GWAS data for AD were extracted from the stage 1 summary results of 21,982 diagnosed AD cases and 41,944 controls in a large GWAS meta-analysis study [3]. Data were retrieved from IEU GWAS database (https://gwas.mrcieu.ac.uk/) [58] using the gwasglue R package (https://mrcieu.github.io/gwasglue/).

In consideration of the fact that reverse causation is a common confounding factor in observational studies, we also checked the reverse causal effect setting AD as the exposure and chemokine as the outcome in the MR analyses. SNPs associated with AD (p-value $< 1 \times 10^{-5}$) were used as the instrumental variables. The effect of the instruments was estimated in the corresponding GWAS for each outcome with inverse-variance weighted (IVW) linear regression [58]. For the significance of the MR effect, a MR p-value < 0.05 was defined as significant. All MR analyses were conducted in R version 3.6.3 with packages.

Statistical analyses

We used Quanto software to evaluate the statistical power of our samples under the gene-only hypothesis and log additive model [61]. Fisher's exact test was applied to test if the allele frequency of a variant was significantly different between AD patients and controls. Meta-analyses combined the Southern and Eastern cohorts were performed using the metafor R package under the fixed effects model [62]. Nominal significance was defined as $p < 0.05$. The Bonferroni correction for multiple testing was performed based on the corresponding numbers of tested variants or genes. Rare variants within each gene were arranged into a gene-based burden test. Single rare and common variants were subjected to association analysis. The Bonferroni corrected significance requires a $p < 0.0016$ (0.05/31 genes) for gene-based analysis, $p < 5.96 \times 10^{-5}$ (0.05/839 rare variants identified in this study) for rare variant association analysis, and $p < 7.04 \times 10^{-4}$ (0.05/71 common variants identified in this study) for common variant association analysis. The burden of rare variants in each targeted gene was tested by using the optimized sequence kernel association test (SKAT-O) in the R package SKAT [63]. Rare variants classified into LoF, possibly pathogenic, or missense in each gene, were assessed. As we had no detailed genotype data of each individual from the ChinaMAP [50], we followed the same strategy as in our recent study [52] and performed the burden tests using only the 1507 healthy individuals from the Southern cohort as the control sample in the burden test.

Two-tailed Student's *t*-test was used to investigate the mRNA expression difference between AD patients and controls with the GraphPad Prism software. Correlations between mRNA levels of the chemokine genes and AD pathology scores from Mouseac [43] were measured by

using the nonparametric Pearson correlation test with the GraphPad Prism software.

Results

Upregulation of mRNA levels of chemokine genes in AD brain tissues

Since expression changes of chemokines are implicated in the pathogenesis of AD [32], we compared the mRNA expression levels of chemokine genes in four brain tissues (entorhinal cortex, hippocampus, temporal cortex, and frontal cortex) between AD patients and controls, using the normalized microarray data compiled in our previous study [41]. Among these 31 chemokine genes, no expression data of *CCL3*, *CCL14*, and *CCL15* were available for the analysis. The mRNA expression levels of 15 chemokine genes were nominally upregulated in one or more of the four AD-relevant tissues. Four genes, *CCL5*, *CXCL1*, *CXCL16*, and *CXCR4*, survived multiple-testing

Table 1 mRNA expression levels of chemokine genes in brain tissues from 269 AD patients and 271 controls

Gene	Entorhinal cortex		Hippocampus		Temporal cortex		Frontal cortex	
	logFC	*P*	logFC	*P*	logFC	*P*	logFC	*P*
C–C motif chemokine ligand								
CCL1	−0.13	0.413	0.09	0.498	−0.28	0.229	0.02	0.82
CCL2	0.68	0.021*	0.63	0.007*	0.52	0.094	0.19	0.351
CCL5	0.17	0.17	0.46	**0.001***	0.64	**0.001***	0.02	0.841
CCL8	0.43	0.017*	0.32	0.081	0.12	0.619	−0.19	0.066
CCL11	0.23	0.128	−0.16	0.213	0.19	0.409	0.01	0.901
CCL16	0.18	0.194	0.29	0.056	−0.07	0.785	−0.13	0.211
C–C motif chemokine receptor								
CCR1	0.28	0.127	0.32	0.006*	0.4	0.008*	0.26	0.008*
CCR3	0.11	0.398	0.22	0.143	0.01	0.973	−0.06	0.61
CCR5	NA	NA	0.38	0.006*	NA	NA	−0.02	0.864
CCR6	0.12	0.411	−0.02	0.892	−0.18	0.464	−0.08	0.46
CCR7	0.32	0.034*	0.15	0.279	−0.09	0.748	0.07	0.398
CCR9	0.27	0.036*	−0.08	0.61	−0.04	0.838	−0.04	0.692
CCRL2	0.18	0.206	NA	NA	0.28	0.207	−0.01	0.923
C-X-C motif chemokine ligand								
CXCL1	0.21	0.263	0.26	0.18	0.79	**8.89×10^{-5}***	0.39	0.012*
CXCL2	0.23	0.192	0.2	0.257	0.17	0.405	0.09	0.483
CXCL6	0.41	0.005*	0.04	0.805	−0.07	0.807	−0.06	0.635
CXCL8	0.28	0.274	0.53	0.004*	−0.06	0.729	0.03	0.816
CXCL9	0.31	0.016*	−0.16	0.281	0.43	0.07	0.2	0.133
CXCL10	0.45	0.097	0.35	0.168	0.71	0.007*	0.41	0.026*
CXCL11	0.24	0.165	0.12	0.406	−0.1	0.691	0.17	0.275
CXCL13	0.16	0.289	−0.06	0.655	−0.09	0.754	−0.03	0.752
CXCL16	0.38	0.011*	0.29	0.012*	0.64	**2.16×10^{-4}***	NA	NA
C-X-C motif chemokine receptor								
CXCR2	NA	NA	0.26	0.088	−0.05	0.849	−0.03	0.847
CXCR4	0.8	**3.3×10^{-4}***	0.56	**0.001***	0.55	0.003*	0.5	**3.79×10^{-5}***
CXCR5	0.03	0.776	0.11	0.32	0.08	0.712	−0.12	0.22
CXCR6	0.14	0.245	0.16	0.091	0.16	0.278	0.2	0.011*
C-X3-C motif chemokine receptor								
CX3CR1	0.06	0.759	−0.09	0.589	−0.12	0.535	0.08	0.569
X-C motif chemokine receptor								
XCR1	0.1	0.392	0	0.977	0.09	0.637	0.01	0.884

The mRNA expression data were retrieved from the AlzData database (www.alzdata.org) [41], with no data available for *CCL3*, *CCL14*, and *CCL15*

A *p* value < 0.05 was marked with "*," and a *p* value < 0.0018 after Bonferroni correction for the number of tested genes (0.05/28) was marked in bold

LogFC, log2 fold change of mRNA expressional mean value in AD patients relative to that in controls

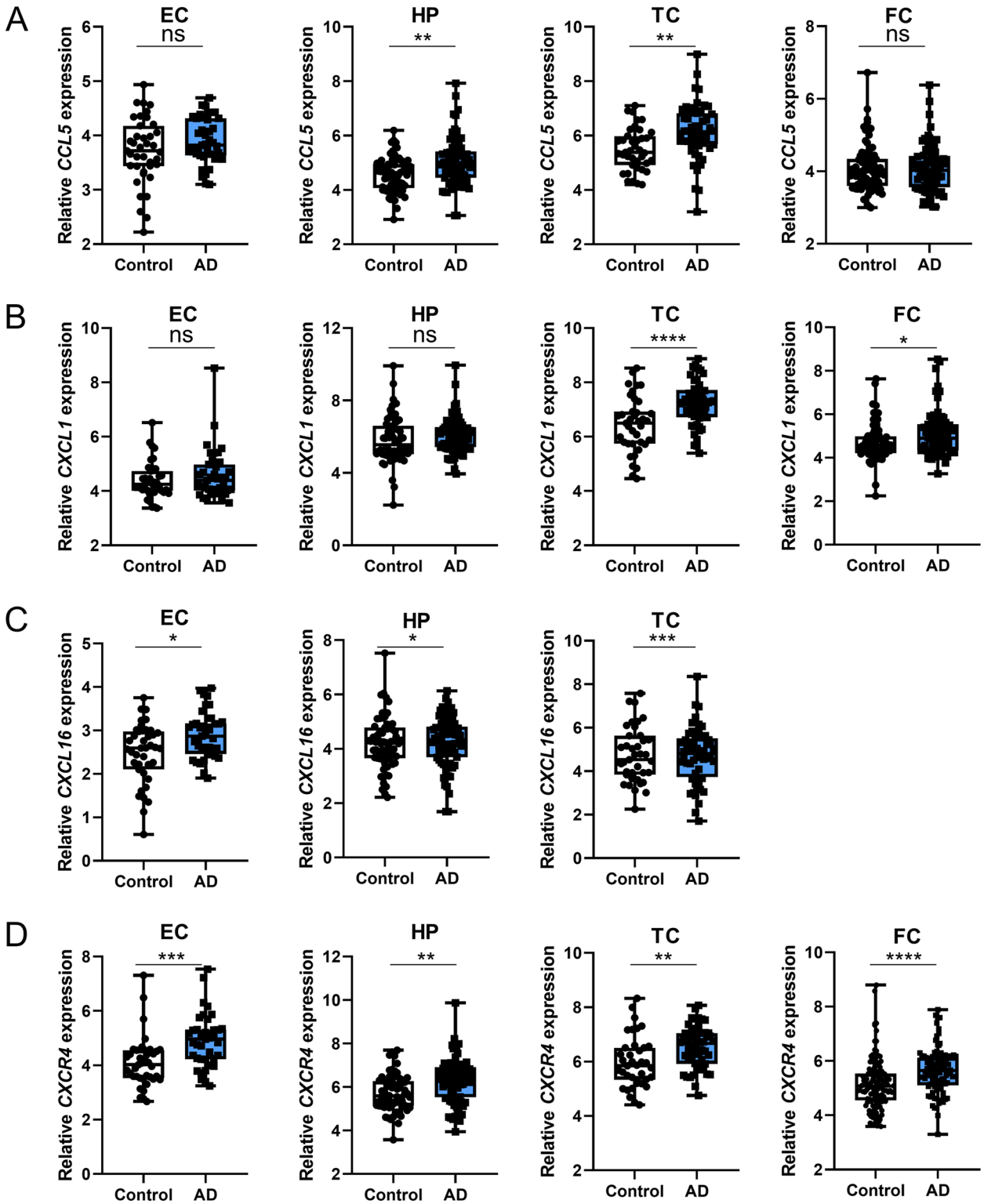

Fig. 2 Upregulated mRNA expression levels of chemokine genes in brain tissues of AD patients. **A**–**D** The mRNA expression data were retrieved from the AlzData (www.alzdata.org) [41]. Data of *CXCL16* was not available in the frontal cortex tissues. Data from min to max were presented by dots. The lower and upper hinges of the boxes represent the first and third quantiles, the whiskers extend from min to max, and the line represents the median. EC, entorhinal cortex; HP, hippocampus; TC, temporal cortex; FC, frontal cortex; Ns, not significant. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; two-tailed Student's *t*-test

and showed significant differential expression (Table 1 and Fig. 2), suggesting a robust dysregulation of these genes in AD. No significant alteration of mRNA expression was observed for the remaining 13 genes.

Correlation of chemokine mRNA expression levels with Aβ and tau pathology in AD mouse models

We reanalyzed the expression data of the AD mouse models and compared the gene expression levels of chemokines in brain tissues including 114 from WILD mice, 44 from HO_TASTPM mice, and 45 from TAU mice at different ages [43]. The mRNA expression levels of 10 chemokine genes (*Ccl3*, *Ccl5*, *Ccl8*, *Ccrl2*, *Cx3cr1*, *Cxcl1*, *Cxcl9*, *Cxcl10*, *Cxcl13*, and *Cxcl16*) were upregulated along with age and reached a significant level of differential expression at the late stage of AD. Among these 10 chemokines, six genes (*Ccl3*, *Ccl5*, *Cxcl1*, *Cxcl10*, *Cxcl13*, and *Cxcl16*) were upregulated in both HO_TASTPM and TAU mice (Additional file 1: Fig. S1). We observed a strong positive correlation between the mRNA expression of the above 10 genes and AD pathology. Except for the *Ccrl2* gene, whose mRNA expression was positively correlated only with Aβ pathology, the other nine genes showed a positive correlation of mRNA expression with both Aβ and tau pathology (Additional file 1: Fig. S2). These observations support an active involvement of chemokines in AD pathology in mouse models.

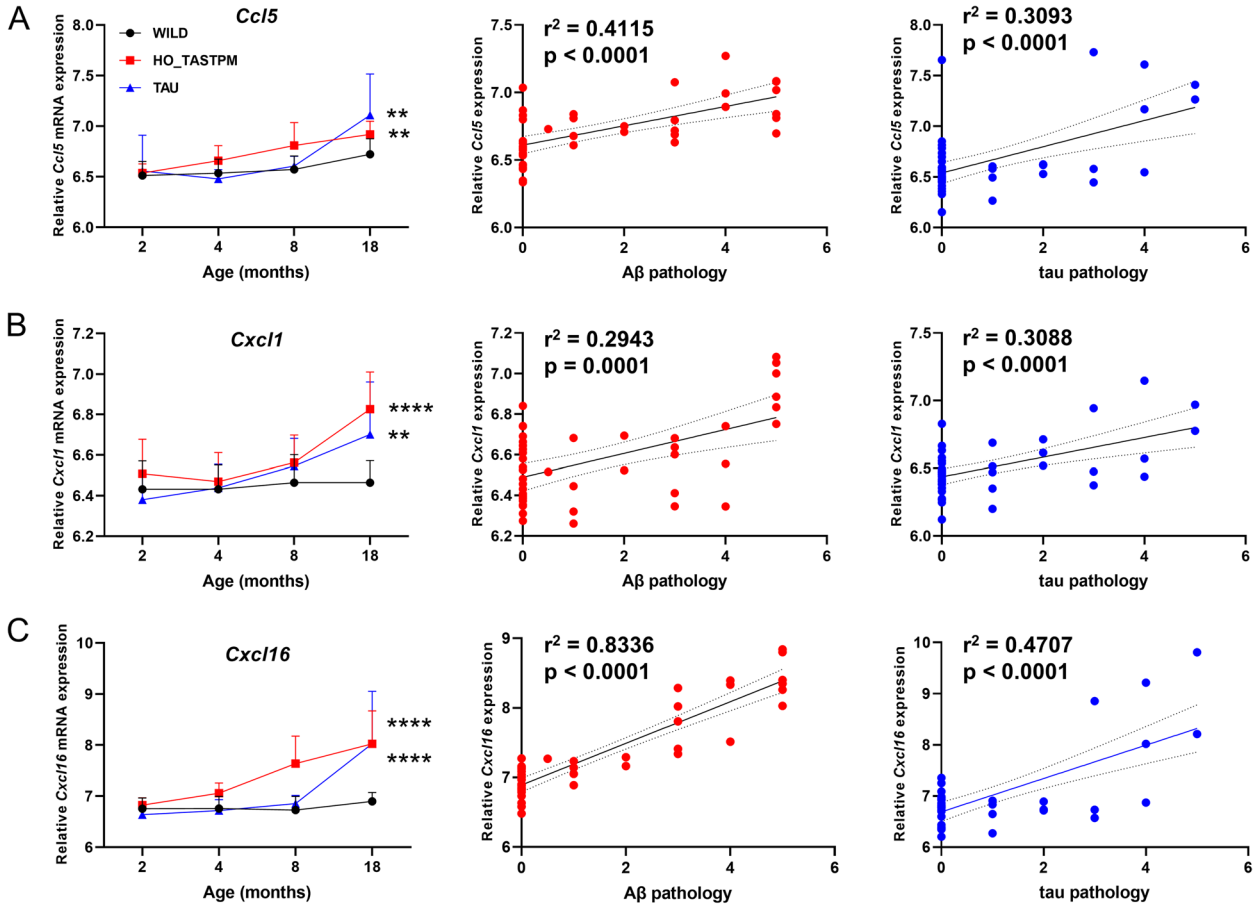

Fig. 3 Correlation of upregulated mRNA levels of *Ccl5* (**A**), *Cxcl1* (**B**), and *Cxcl16* (**C**) with Aβ and tau pathology in AD mouse models. Original data were retrieved from Mouseac (www.mouseac.org) [43]. The age-related mRNA expression level was measured in 114 brain tissues from wild-type mice (WILD), 44 brain tissues from homozygous APP/PSEN1 double mutant mice (HO_TASTPM), and 45 brain tissues from mutant human MAPT mice (TAU) at different ages. The scores of Aβ pathology and tau pathology were based on 44 brain tissues of HO_TASTPM mice and 45 brain tissues of TAU mice, respectively. Error bars represent the population standard deviation. **, $P < 0.01$; ****, $P < 0.0001$; two-tailed Student's *t*-test for comparison of mRNA expression between AD transgenic mice and WILD mice at month 18. The correlation between mRNA expression levels and pathology was measured using the Pearson correlation analysis. The solid and dashed lines represent the slope and the 95% confidence intervals in linear regression

We overlapped the genes with significant expression alteration in brain tissues from AD patients and the mouse models, as we speculated that these genes validated in two systems may be more reliable for being causal for AD development. Three genes, including *CCL5*, *CXCL1*, and *CXCL16* showed a consistent alteration pattern in AD patients and in the mouse models (Figs. 2 and 3).

Upregulation of *CXCL16* expression in peripheral blood of patients with MCI and AD

To investigate if any of these dysregulated chemokine genes could be used as a potential biomarker for AD development, we analyzed the mRNA expression alterations of these genes in the peripheral blood from MCI patients, AD patients, and healthy controls. Among

Table 2 mRNA expression levels of chemokine genes in peripheral blood of patients with MCI and AD and healthy controls

Gene	ID (GSE63060)	80 MCI/104 controls		145 AD/104 controls		ID (GSE63061)	109 MCI/134 controls		139 AD/134 controls	
		logFC	*P*	logFC	*P*		logFC	*P*	logFC	*P*
C–C motif chemokine ligand										
CCL2	ILMN_1720048	−0.013	0.210	0.003	0.793	ILMN_1720048	0.005	0.416	−0.002	0.670
CCL3	ILMN_1671509	0.043	0.012*	0.050	6.65×10^{-4}*	ILMN_1671509	0.006	0.647	0.015	0.216
CCL5	ILMN_1773352	0.086	0.241	6.75×10^{-4}	0.991	ILMN_1773352	0.011	0.853	0.032	0.575
CCL8	ILMN_1772964	0.038	0.036*	0.016	0.291	ILMN_1772964	0.029	0.482	−0.017	0.650
CCL11	ILMN_1725519	0.002	0.877	0.002	0.806	-	-	-	-	-
CCL14	-	-	-	-	-	ILMN_3192001	-6.72×10^{-4}	0.895	0.003	0.6
CCL15	ILMN_1670658	−0.002	0.809	−0.009	0.250	-	-	-	-	-
CCL16	ILMN_2045324	0.004	0.677	-7.10×10^{-4}	0.935	-	-	-	-	-
C–C motif chemokine receptor										
CCR1	ILMN_1678833	−0.166	0.001*	−0.037	0.420	ILMN_1678833	−0.039	0.319	−0.033	0.370
CCR3	ILMN_1763322	0.027	0.741	−0.085	0.219	ILMN_1763322	0.104	0.130	−0.032	0.601
CCR5	ILMN_2145033	−0.012	0.379	−0.006	0.609	ILMN_2145033	−0.001	0.795	0.004	0.464
CCR6	ILMN_2387696	0.054	0.084	0.034	0.189	ILMN_2387696	0.017	0.496	0.027	0.246
CCR7	ILMN_1715131	0.030	0.715	0.026	0.733	ILMN_1715131	−0.11	0.094	−0.092	0.166
CCR9	ILMN_2337386	−0.008	0.561	0.005	0.737	ILMN_2337386	−0.006	0.176	−0.005	0.222
CCRL2	ILMN_1675346	−0.015	0.387	−0.012	0.435	ILMN_1675346	0.001	0.804	−0.007	0.107
C-X-C motif chemokine ligand										
CXCL1	ILMN_1787897	−0.007	0.599	0.002	0.841	ILMN_1787897	−0.021	0.241	0.013	0.448
CXCL6	ILMN_2161577	−0.006	0.447	0.011	0.116	ILMN_2161577	−0.003	0.411	-7.16×10^{-5}	0.986
CXCL8	ILMN_1666733	−0.047	0.339	0.075	0.092	ILMN_1666733	−0.025	0.310	−0.004	0.875
CXCL9	ILMN_1745356	0.006	0.611	0.011	0.291	-	-	-	-	-
CXCL10	ILMN_1791759	−0.119	8.36×10^{-5}*	−0.046	0.138	ILMN_1791759	−0.034	0.043*	−0.036	0.025*
CXCL11	ILMN_2067890	0.010	0.270	0.002	0.809	ILMN_2067890	5.29×10^{-3}	0.229	0.006	0.168
CXCL13	ILMN_1718552	−0.014	0.136	−0.004	0.638	ILMN_1718552	0.002	0.637	−0.002	0.597
CXCL16	ILMN_1728478	0.124	0.017*	0.111	0.029*	ILMN_1728478	0.097	0.012*	0.118	0.003*
C-X-C motif chemokine receptor										
CXCR2	ILMN_1680397	0.264	2.30×10^{-5}*	0.155	0.037*	ILMN_1680397	0.158	0.010*	0.122	0.057
CXCR4	ILMN_2320888	0.083	0.066	0.165	3.79×10^{-5}*	ILMN_2320888	0.007	0.818	0.057	0.045
CXCR5	ILMN_2337928	0.069	0.321	−0.033	0.556	ILMN_2337928	−0.046	0.334	−0.11	0.01
CXCR6	ILMN_1674640	−0.003	0.902	0.004	0.864	ILMN_1674640	0.017	0.394	0.032	0.076
C-X3-C motif chemokine receptor										
CX3CR1	ILMN_1745788	0.067	0.098	0.013	0.716	ILMN_1745788	0.046	0.126	0.044	0.116
X-C motif chemokine receptor										
XCR1	ILMN_1764034	−0.006	0.637	−0.017	0.155	ILMN_1764034	0.008	0.416	0.008	0.323

The original data GSE63060 and GSE63061 [42] were extracted from GEO (https://www.ncbi.nlm.nih.gov/geo), with no data available for *CCL1* and *CXCL2*

Six individuals without explicit disease definition in GSE63061 were excluded from the analysis

A p value < 0.05 was marked with a "*"

-, missing data

ID Unique identifier for the probe

LogFC Log2 fold change of mRNA expressional mean value in MCI or AD patients relative to that in controls

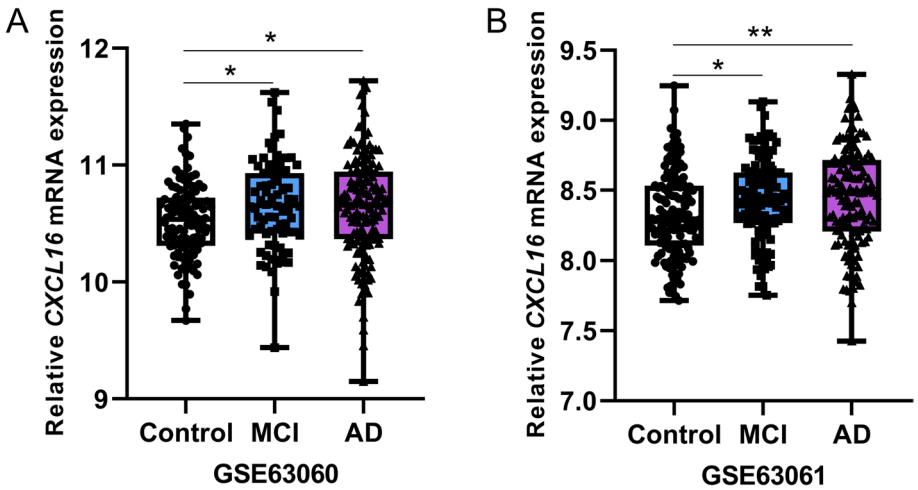

Fig. 4 Upregulated mRNA expression of *CXCL16* in peripheral blood of patients with MCI and AD. Datasets of (**A**) GSE63060 (104 controls, 80 MCI, and 145 AD patients) and (**B**) GSE63061 (134 controls, 109 MCI, and 139 AD patients) [42] were used for determining *CXCL16* mRNA expression levels. Data from min to max were presented by dots. *, $P<0.05$; **, $P<0.01$; two-tailed Student's *t*-test

the three genes (*CCL5*, *CXCL1*, and *CXCL16*) consistently upregulated in brain tissues of AD patients and the mouse models, only *CXCL16* showed an upregulated expression in peripheral blood of MCI and AD patients as compared to controls (Table 2 and Fig. 4). This result suggests the potential of *CXCL16* to be a biomarker for AD development.

No association of chemokine genetic variants with AD in Han Chinese

Among these Han Chinese subjected to targeted sequencing, the mean sequencing depth of each gene was higher than 90 × in targeted sequencing (Additional file 1: Table S1), and the sequencing depth for each variant was higher than 25 × (Additional files 2 and 3). A total of 910 genetic variants (including 839 rare and 71 common variants) in 31 chemokine genes passed the quality control and were analyzed subsequently. The SKAT-O analysis [63] was conducted using rare variants in each gene for each cohort. In the Southern cohort, possibly pathogenic variants in *CCR7* ($p=0.004$) and missense variants in *CCR9* ($p=0.009$) were enriched in AD patients. In the Eastern cohort, *CCL3*, *CCR5*, and *CCR9* showed an association with AD at the gene-burden level. When combined both cohorts together to achieve a better statistic power, we found that five genes (including *CCL3*, *CCR7*, *CCR9*, *CCRL2*, and *XCR1*) were associated with AD at the gene-burden level and had an enrichment of rare variants (Additional file 1: Table S2). However, none of these significances survived the multiple testing correction, partially due to the limited sample size.

To confirm the gene-based association between chemokine genes and AD identified in Han Chinese, we used the WES data in the discovery stage of ADSP (5740 AD cases and 5096 cognitively normal controls) [44] as a validation cohort. None of these chemokine genes associated with AD in our Han Chinese population could be validated in the ADSP dataset [44], although we found that four genes (*CCL2*, *CCR6*, *CXCL6*, *CX3CR1*) were associated with AD at the gene-burden level under correction for different covariates, including the principal components, sequencing center, sex, age, and *APOE* ε4 and ε2 dosages, with the SKAT-O analysis [63] by using the ADSP dataset [44] (Additional file 1: Table S3).

Next, we tested the single-variant association of 839 rare and 71 common variants with AD risk in each Han Chinese cohort and the combined sample. We observed nominally significant association with AD of eight rare variants in six of the 31 chemokine genes in meta-analysis, but none of these variants survived the multiple testing correction (Additional file 2). The MAF of 71 common variants ranged from 0.01 to 0.5 in the combined control samples. Under the gene-only hypothesis and log additive model with an average population MAF of 0.1, the statistical power to detect an odds ratio (OR) value of 1.25 for a risk allele using the current sample size (1280 cases and 5044 controls) was above 88.8%. We observed a significant association of rs181868085 ($p=0.006$, OR = 1.59) in *CXCL1* and rs2304973 ($p=0.045$, OR = 0.84) in *CXCL16* with AD in the meta-analysis (Additional file 3). The OR values of these two SNPs indicated a consistent direction of genetic effect on disease risk between the Southern and the Eastern cohorts, although the association did not survive the multiple testing correction. Note that we observed a significant association between *CCL3* and AD in the Eastern cohort of Han Chinese, even after the

Bonferroni correction ($p = 4.35 \times 10^{-4}$), but this association was weakened in the combined Han Chinese sample ($p = 0.008$; Additional file 1: Table S2), suggesting that population heterogeneity may exist even between our two cohorts under study. A reanalysis of the allele frequency data of 71 common variants in the newly published GWAS study [6] showed no association with AD in the European population (Additional file 1: Table S4).

Taken together, there seems to be no robust association of rare and common variants of chemokine genes with AD in both Han Chinese and European populations. The weak association between the chemokine gene and AD observed in the gene-based burden test might be caused by population substructure and stratification.

MR analyses prioritized *CCL5* as a causal gene for AD

The MR analysis based on large-scale proteomic data of plasma chemokine levels [59, 60] and a genetic study of AD [3] showed that *CCL5* ($p = 0.0055$, $\beta = -0.0667$, Table 3) was causally linked to AD without the reverse causal effect ($p = 0.7864$, $\beta = 0.0078$). This result, together with the observation of altered expression of *CCL5* in AD patients and the mouse models, indicated that CCL5 dysregulations might be actively involved in the development of AD.

Discussion

Alteration of chemokines has been frequently reported to be involved in AD [28, 31, 32]. However, the exact mechanisms of the upregulation or downregulation of chemokine genes during the development of AD have not been sufficiently clarified, and this has led to a dispute regarding whether the chemokine expression alterations are the drivers, or by-products, of AD pathobiology. In this study, we aimed to determine the role of mRNA expression and genetic variations of 31 chemokine genes in AD, with an intention of defining the involvement of chemokines in AD. By integrating the genetic analyses, mRNA expression alterations, and pathological correlation in both AD patients and mouse models, we found an involvement of CXCL16 and CCL5 in the development of AD. This comprehensive analysis enabled us to provide a systematic view for understanding the roles of chemokines in the development of AD. First, the mRNA expression levels of a small proportion of chemokines under study were upregulated in brain regions both in AD patients (Table 1 and Fig. 2) and AD mice (Fig. 3). This result is consistent with previous reports for a higher level of proinflammatory chemokines in peripheral blood and brain tissues in AD patients [28, 64], and supports the significant role of chemokines in the neuroinflammatory process of AD. Second, we found that the upregulated chemokines were positively correlated with Aβ and tau pathology in AD mice (Fig. 3). This observation suggested an active role of chemokines in AD progression although their function in regulating Aβ or tau pathology remains to be determined [32]. Third, the MR analysis showed that *CCL5* was prioritized to be causally linked to AD, indicating that chemokine gene may be involved in AD in different ways.

We did not obtain a firm conclusion regarding the association of genetic variants of 31 chemokine genes with AD. Although we found five genes (*CCL3*, *CCR7*, *CCR9*, *CCRL2*, and *XCR1*) were nominally associated with AD in the combined Han Chinese sample in the gene-based burden test (Additional file 1: Table S2), none of the associations can be verified in the populations of European ancestry based on a data-mining of the ADSP dataset [44] (Additional file 1: Table S3). Instead, four other genes, *CCL2*, *CCR6*, *CX3CR1*, and *CXCL6*, were suggested to be associated with AD in the populations of European ancestry [44]. Our analysis of the potential association between rare or common variants and AD risk showed the same pattern of mixed signal for positive

Table 3 Summary results of bi-direction MR estimates for causal effect between chemokines and Alzheimer's disease

Exposure	Exposure ID	Outcome	Outcome ID	Nsnp	β	SE	*P*	OR	95% CI
CCL5	prot-a-409	Alzheimer's disease	ieu-b-2	29	−0.0667	0.0240	**0.0055**	0.94	0.89–0.98
CXCL1	prot-b-16	Alzheimer's disease	ieu-b-2	8	−0.0251	0.0353	0.4773	0.98	0.91–1.05
CXCL16	prot-a-745	Alzheimer's disease	ieu-b-2	27	−0.0050	0.0246	0.8404	1.00	0.95–1.04
Alzheimer's disease	ieu-b-2	CCL5	prot-a-409	50	0.0078	0.0290	0.7864	1.01	0.95–1.07
Alzheimer's disease	ieu-b-2	CXCL1	Prot-b-16	32	0.0016	0.0380	0.9657	1.00	0.93–1.08
Alzheimer's disease	ieu-b-2	CXCL16	prot-a-745	50	−0.0404	0.0290	0.1636	0.96	0.91–1.02

Nsnp Number of SNPs used as instrumental variables with GWAS $p < 1.0 \times 10^{-5}$

β The effect size of exposure on outcome

SE Standard error of β

P P value of the causal effect inference by inverse-variance weighted (IVW) model

OR Odds ratio of the causal effect, *95% CI* 95% confidence interval of OR

association. Therefore, we were unable to make a firm conclusion that genetic variants of the chemokine genes had a role in conferring genetic risk to AD, and the current weak association could be real or could be explained by different genetic structures between Asian and European populations. Independent validation analysis with a large sample size in populations of different ancestral origins is needed to clarify this issue.

The dysregulation of CCL5 and CXCL16 in AD patients at the transcriptional level deserved further attention. The CCL5 was reported to be upregulated in peripheral blood mononuclear cells of AD patients [29, 65], and Aβ42 treatment could increase the expression of CCL5 and its receptor CCR5 in peripheral mononuclear cells [66]. The upregulation of CCL5 in the AD brain may play a possible neuroprotective role [24], as soluble CCL5 activated by Aβ had an ameliorating effect on AD in mice by recruiting bone marrow-induced microglia immune response [67]. In this study, we found that CCL5 increases with AD development in both mouse models and patients, and an increased CCL5 level was causally associated with decreased AD risk in the MR analysis, collectively supporting the active role of CCL5 in AD and the potential utility of CCL5 as a therapeutic target.

Concerning the involvement of CXCL16 in AD, there were only a few reports available until very recently, Piehl et al. highlighted the CXCL16-CXCR6 axis in CSF of aged and AD brain [68]. These researchers found that CXCL16, derived from inflamed microglia and increased in CSF, activated the $CD8^+$ T cell trafficking to the CSF through the CXCL16-CXCR6 pathway [68]. Note that dysregulation of CXCL16 was previously suggested as a possible mechanism of neurodegeneration in AD [69]. The consistent alteration pattern of CXCL16 in serum, CSF, and brain tissues of AD patients suggested that this chemokine might be used as a potential biomarker for monitoring AD development. A clinical observation study is needed to test this possibility.

This study has some limitations. First, the sample size used in genetic analyses was relatively small, and potential population stratification and different population structure might blur the potential association between chemokine genes and AD. Second, although we observed expression alterations of some chemokine genes in brain tissues of AD patients and the mouse models, we have not linked the expression changes to cell types and had no experimental data to discern its potential effect on cellular function of these affected cells. We also did not validate the causal role of the highlighted genes, such as *CCL5* and *CXCL16*, in animal models of AD [70]. Third, we only analyzed a proportion of chemokines in this study, and we could not exclude the possibility that other chemokine genes might have a prominent role in AD pathobiology. Nonetheless, the accumulating knowledge of chemokines' roles in AD, as exemplified in this study with an intention of comprehensive integrative analysis, is undoubtedly essential for guiding the development of potential novel immunotherapies for AD.

Conclusions

In short, through an extensive analysis of chemokine genes based on expressional, pathological, and genetic analysis data, we provide multiple lines of evidence to support the important role of chemokines CCL5 and CXCL16 in the development of AD. Further genetic studies with larger sample sizes and functional assays are needed to validate our conclusion and to depict the mechanisms of these two chemokines in AD pathogenesis.

Abbreviations

AD	Alzheimer's disease
MCI	Mild cognitive impairment
MR	Mendelian randomization
GWAS	Genome-wide association study
WES	Whole-exome sequencing study
WGS	Whole-genome sequencing study
CNS	Central nervous system
CSF	Cerebrospinal fluid
SNP	Single nucleotide polymorphism
WILD	Wild-type mice
HO_TASTPM	Homozygous mutant human APP $^{K670N/M671L}$ and PSEN1 ^{M146V} mice
TAU	Mutant human MAPT ^{P301L} mice
ChinaMAP	China Metabolic Analytics Project
DSM-IV	Diagnostic and Statistical Manual of Mental Disorders IV
HWE	Hardy-Weinberg equilibrium
MAF	Minor allele frequency
LoF	Loss-of-function
M-CAP	Mendelian Clinically Applicable Pathogenicity
IVW	Inverse-variance weighted linear regression
ADSP	The Alzheimer's Disease Sequencing Project
SKAT-O	The optimized sequence kernel association test

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13195-022-01159-5.

Additional file 1: Fig. S1. Up-regulation of mRNA expression of chemokine genes during aging in AD mouse models. **Fig. S2.** Correlation between the mRNA expression levels of chemokine genes with AD pathology in AD mouse models. **Table S1.** Sequence coverage of each gene in the targeted sequencing. **Table S2.** Results of SKAT-O analysis in Han Chinese with and without AD. **Table S3.** Results of gene-based burden test of chemokine genes from ADSP. **Table S4.** Association results of common variants in European population.

Additional file 2. Rare variants of 31 chemokine genes in Han Chinese.

Additional file 3. Association results of common variants in 31 chemokine genes in Han Chinese of AD.

Acknowledgements

We thank Dr. Ian Logan for language editing and Prof. Yanan Cao for sharing allele frequency data in the ChinaMAP project.

Authors' contributions
YGY and DFZ designed the study; XL, DFZ, MX, and RB performed the study; XL, MX, and DFZ analyzed the data. LWT and XC collected the sample for targeted sequencing; XL, YGY, and DFZ wrote the manuscript. All authors read and approved the final manuscript.

Funding
This study was supported by the Ministry of Science and Technology of China (grant number STI2030-Major Projects 2022ZD0213500), the National Natural Science Foundation of China (grant numbers 31730037, 82022017, 31970965); and the Strategic Priority Research Program (B) of the Chinese Academy of Sciences (CAS) (grant number XDB02020003), and the Youth Innovation Promotion Association of CAS.

Availability of data and materials
All data generated or analyzed during this study are included in this published article and its Additional files.

Declarations

Ethics approval and consent to participate
This study was approved by the institutional review board of Kunming Institute of Zoology, Chinese Academy of Sciences. Written informed consents were obtained from all participants in targeted sequencing. The study was adhered to the tenets of the Declaration of Helsinki.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

Received: 20 October 2022 Accepted: 29 December 2022
Published online: 21 January 2023

References

1. Querfurth HW, LaFerla FM. Alzheimer's disease. N Engl J Med. 2010;362:329–44.
2. Scheltens P, De Strooper B, Kivipelto M, Holstege H, Chetelat G, Teunissen CE, et al. Alzheimer's disease. Lancet. 2021;397:1577–90.
3. Kunkle BW, Grenier-Boley B, Sims R, Bis JC, Damotte V, Naj AC, et al. Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Abeta, tau, immunity and lipid processing. Nat Genet. 2019;51:414–30.
4. Jansen IE, Savage JE, Watanabe K, Bryois J, Williams DM, Steinberg S, et al. Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. Nat Genet. 2019;51:404–13.
5. Wightman DP, Jansen IE, Savage JE, Shadrin AA, Bahrami S, Holland D, et al. A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. Nat Genet. 2021;53:1276–82.
6. Bellenguez C, Küçükali F, Jansen IE, Kleineidam L, Moreno-Grau S, Amin N, et al. New insights into the genetic etiology of Alzheimer's disease and related dementias. Nat Genet. 2022;54:412–36.
7. Jia L, Li F, Wei C, Zhu M, Qu Q, Qin W, et al. Prediction of Alzheimer's disease using multi-variants from a Chinese genome-wide association study. Brain. 2021;144:924–37.
8. Guerreiro R, Wojtas A, Bras J, Carrasquillo M, Rogaeva E, Majounie E, et al. TREM2 variants in Alzheimer's disease. N Engl J Med. 2013;368:117–27.
9. Zhang DF, Fan Y, Xu M, Wang G, Wang D, Li J, et al. Complement C7 is a novel risk gene for Alzheimer's disease in Han Chinese. Natl Sci Rev. 2019;6:257–74.
10. Zhou X, Chen Y, Mok KY, Zhao Q, Chen K, Chen Y, et al. Identification of genetic risk factors in the Chinese population implicates a role of immune system in Alzheimer's disease pathogenesis. Proc Natl Acad Sci U S A. 2018;115:1697–706.
11. Heneka MT, Carson MJ, El Khoury J, Landreth GE, Brosseron F, Feinstein DL, et al. Neuroinflammation in Alzheimer's disease. Lancet Neurol. 2015;14:388–405.
12. Koelink PJ, Overbeek SA, Braber S, de Kruijf P, Folkerts G, Smit MJ, et al. Targeting chemokine receptors in chronic inflammatory diseases: an extensive review. Pharmacol Ther. 2012;133:1–18.
13. Su F, Bai F, Zhang Z. Inflammatory cytokines and Alzheimer's disease: a review from the perspective of genetic polymorphisms. Neurosci Bull. 2016;32:469–80.
14. Savarin-Vuaillat C, Ransohoff RM. Chemokines and chemokine receptors in neurological disease: raise, retain, or reduce? Neurotherapeutics. 2007;4:590–601.
15. Bajetto A, Bonavia R, Barbero S, Florio T, Schettini G. Chemokines and their receptors in the central nervous system. Front Neuroendocrinol. 2001;22:147–84.
16. Réaux-Le Goazigo A, Van Steenwinckel J, Rostène W, Mélik PS. Current status of chemokines in the adult CNS. Prog Neurobiol. 2013;104:67–92.
17. Dziembowska M, Tham TN, Lau P, Vitry S, Lazarini F, Dubois-Dalcq M. A role for CXCR4 signaling in survival and migration of neural and oligodendrocyte precursors. Glia. 2005;50:258–69.
18. Tsai HH, Frost E, To V, Robinson S, Ffrench-Constant C, Geertman R, et al. The chemokine receptor CXCR2 controls positioning of oligodendrocyte precursors in developing spinal cord by arresting their migration. Cell. 2002;110:373–83.
19. Padovani-Claudio DA, Liu L, Ransohoff RM, Miller RH. Alterations in the oligodendrocyte lineage, myelin, and white matter in adult mice lacking the chemokine receptor CXCR2. Glia. 2006;54:471–83.
20. Bertollini C, Ragozzino D, Gross C, Limatola C, Eusebi F. Fractalkine/CX3CL1 depresses central synaptic transmission in mouse hippocampal slices. Neuropharmacology. 2006;51:816–21.
21. Da Mesquita S, Herz J, Wall M, Dykstra T, de Lima KA, Norris GT, et al. Aging-associated deficit in CCR7 is linked to worsened glymphatic function, cognition, neuroinflammation, and beta-amyloid pathology. Sci Adv. 2021;7:eabe4601.
22. Zhou L, Kong G, Palmisano I, Cencioni MT, Danzi M, De Virgiliis F, et al. Reversible CD8 T cell-neuron cross-talk causes aging-dependent neuronal regenerative decline. Science. 2022;376:eabd5926.
23. Sokolova A, Hill MD, Rahimi F, Warden LA, Halliday GM, Shepherd CE. Monocyte chemoattractant protein-1 plays a dominant role in the chronic inflammation observed in Alzheimer's disease. Brain Pathol. 2009;19:392–8.
24. Tripathy D, Thirumangalakudi L, Grammas P. RANTES upregulation in the Alzheimer's disease brain: a possible neuroprotective role. Neurobiol Aging. 2010;31:8–16.
25. Kauwe JS, Bailey MH, Ridge PG, Perry R, Wadsworth ME, Hoyt KL, et al. Genome-wide association study of CSF levels of 59 alzheimer's disease candidate proteins: significant associations with proteins involved in amyloid processing and inflammation. PLoS Genet. 2014;10:e1004758.
26. Perea JR, Lleo A, Alcolea D, Fortea J, Avila J, Bolos M. Decreased CX3CL1 levels in the cerebrospinal fluid of patients with Alzheimer's disease. Front Neurosci. 2018;12:609.
27. Lee WJ, Liao YC, Wang YF, Lin IF, Wang SJ, Fuh JL. Plasma MCP-1 and cognitive decline in patients with Alzheimer's disease and mild cognitive impairment: a two-year follow-up study. Sci Rep. 2018;8:1280.
28. Goldeck D, Larbi A, Pellicano M, Alam I, Zerr I, Schmidt C, et al. Enhanced chemokine receptor expression on leukocytes of patients with Alzheimer's disease. PLoS ONE. 2013;8:e66664.
29. Iarlori C, Gambi D, Gambi F, Lucci I, Feliciani C, Salvatore M, et al. Expression and production of two selected beta-chemokines in peripheral blood mononuclear cells from patients with Alzheimer's disease. Exp Gerontol. 2005;40:605–11.
30. Jorda A, Cauli O, Santonja JM, Aldasoro M, Aldasoro C, Obrador E, et al. Changes in chemokines and chemokine receptors expression in a mouse model of Alzheimer's disease. Int J Biol Sci. 2019;15:453–63.
31. Guedes JR, Santana I, Cunha C, Duro D, Almeida MR, Cardoso AM, et al. MicroRNA deregulation and chemotaxis and phagocytosis impairment in Alzheimer's disease. Alzheimers Dement (Amst). 2016;3:7–17.
32. Guedes JR, Lao T, Cardoso AL, El Khoury J. Roles of microglial and monocyte chemokines and their receptors in regulating Alzheimer's disease-associated amyloid-beta and tau pathologies. Front Neurol. 2018;9:549.

33. Subbarayan MS, Joly-Amado A, Bickford PC, Nash KR. CX3CL1/CX3CR1 signaling targets for the treatment of neurodegenerative diseases. Pharmacol Ther. 2022;231:107989.
34. Bhaskar K, Konerth M, Kokiko-Cochran ON, Cardona A, Ransohoff RM, Lamb BT. Regulation of tau pathology by the microglial fractalkine receptor. Neuron. 2010;68:19–31.
35. Liu Z, Condello C, Schain A, Harb R, Grutzendler J. CX3CR1 in microglia regulates brain amyloid deposition through selective protofibrillar amyloid-beta phagocytosis. J Neurosci. 2010;30:17091–101.
36. Kiyota T, Gendelman HE, Weir RA, Higgins EE, Zhang G, Jain M. CCL2 affects beta-amyloidosis and progressive neurocognitive dysfunction in a mouse model of Alzheimer's disease. Neurobiol Aging. 2013;34:1060–8.
37. Vendramini AA, de Labio RW, Rasmussen LT, Minett T, Bertolucci PH, de Arruda Cardoso Smith M, et al. Interleukin-8 gene polymorphism -251T>A and Alzheimer's disease. J Alzheimers Dis. 2007;12:221–2.
38. Villa C, Venturelli E, Fenoglio C, Clerici F, Marcone A, Benussi L, et al. CCL8/MCP-2 association analysis in patients with Alzheimer's disease and frontotemporal lobar degeneration. J Neurol. 2009;256:1379–81.
39. Balistreri CR, Grimaldi MP, Vasto S, Listi F, Chiappelli M, Licastro F, et al. Association between the polymorphism of CCR5 and Alzheimer's disease: results of a study performed on male and female patients from Northern Italy. Ann N Y Acad Sci. 2006;1089:454–61.
40. Lalli MA, Bettcher BM, Arcila ML, Garcia G, Guzman C, Madrigal L, et al. Whole-genome sequencing suggests a chemokine gene cluster that modifies age at onset in familial Alzheimer's disease. Mol Psychiatry. 2015;20:1294–300.
41. Xu M, Zhang DF, Luo R, Wu Y, Zhou H, Kong LL, et al. A systematic integrated analysis of brain expression profiles reveals YAP1 and other prioritized hub genes as important upstream regulators in Alzheimer's disease. Alzheimers Dement. 2018;14:215–29.
42. Sood S, Gallagher IJ, Lunnon K, Rullman E, Keohane A, Crossland H, et al. A novel multi-tissue RNA diagnostic of healthy ageing relates to cognitive health status. Genome Biol. 2015;16:185.
43. Matarin M, Salih DA, Yasvoina M, Cummings DM, Guelfi S, Liu W, et al. A genome-wide gene-expression analysis and database in transgenic mice during development of amyloid or tau pathology. Cell Rep. 2015;10:633–44.
44. Bis JC, Jian X, Kunkle BW, Chen Y, Hamilton-Nelson KL, Bush WS, et al. Whole exome sequencing study identifies novel rare and common Alzheimer's-associated variants involved in immune response and transcriptional regulation. Mol Psychiatry. 2020;25:1859–75.
45. Bhattacharya S, Dunn P, Thomas CG, Smith B, Schaefer H, Chen J, et al. ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. Sci Data. 2018;5:180015.
46. Bi R, Zhang W, Zhang DF, Xu M, Fan Y, Hu QX, et al. Genetic association of the cytochrome c oxidase-related genes with Alzheimer's disease in Han Chinese. Neuropsychopharmacology. 2018;43:2264–76.
47. Zhang DF, Li J, Wu H, Cui Y, Bi R, Zhou HJ, et al. CFH variants affect structural and functional brain changes and genetic risk of Alzheimer's disease. Neuropsychopharmacology. 2016;41:1034–45.
48. Li GD, Bi R, Zhang DF, Xu M, Luo R, Wang D, et al. Female-specific effect of the BDNF gene on Alzheimer's disease. Neurobiol Aging. 2017;53(192):e11–9.
49. Wang HZ, Bi R, Hu QX, Xiang Q, Zhang C, Zhang DF, et al. Validating GWAS-identified risk loci for Alzheimer's disease in Han Chinese populations. Mol Neurobiol. 2016;53:379–90.
50. Cao Y, Li L, Xu M, Feng Z, Sun X, Lu J, et al. The ChinaMAP analytics of deep whole genome sequences in 10,588 individuals. Cell Res. 2020;30:717–31.
51. Wang D, Fan Y, Malhi M, Bi R, Wu Y, Xu M, et al. Missense variants in HIF1A and LACC1 contribute to leprosy risk in Han Chinese. Am J Hum Genet. 2018;102:794–805.
52. Li X, Xu M, Bi R, Tan LW, Yao YG, Zhang DF. Common and rare variants of EGF increase the genetic risk of Alzheimer's disease as revealed by targeted sequencing of growth factors in Han Chinese. Neurobiol Aging. 2022;S0197-4580(22)00223-8.
53. Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics. 2014;30:2114–20.
54. Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics. 2009;25:1754–60.
55. McKenna A, Hanna M, Banks E, Sivachenko A, Cibulskis K, Kernytsky A, et al. The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. Genome Res. 2010;20:1297–303.
56. Wang K, Li M, Hakonarson H. ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. Nucleic Acids Res. 2010;38:e164.
57. Jagadeesh KA, Wenger AM, Berger MJ, Guturu H, Stenson PD, Cooper DN, et al. M-CAP eliminates a majority of variants of uncertain significance in clinical exomes at high sensitivity. Nat Genet. 2016;48:1581–6.
58. Hemani G, Zheng J, Elsworth B, Wade KH, Haberland V, Baird D, et al. The MR-Base platform supports systematic causal inference across the human phenome. Elife. 2018;7:e34408.
59. Sun BB, Maranville JC, Peters JE, Stacey D, Staley JR, Blackshaw J, et al. Genomic atlas of the human plasma proteome. Nature. 2018;558:73–9.
60. Folkersen L, Fauman E, Sabater-Lleal M, Strawbridge RJ, Franberg M, Sennblad B, et al. Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genet. 2017;13:e1006706.
61. Gauderman WJ. Sample size requirements for matched case-control studies of gene-environment interaction. Stat Med. 2002;21:35–50.
62. Viechtbauer W. Conducting meta-analyses in R with the metafor package. J Stat Softw. 2010;36:1–48.
63. Lee S, Emond MJ, Bamshad MJ, Barnes KC, Rieder MJ, Nickerson DA, et al. Optimal unified approach for rare-variant association testing with application to small-sample case-control whole-exome sequencing studies. Am J Hum Genet. 2012;91:224–37.
64. Zuena AR, Casolini P, Lattanzi R, Maftei D. Chemokines in Alzheimer's disease: new insights into prokineticins, chemokine-like proteins. Front Pharmacol. 2019;10:622.
65. Pellicano M, Bulati M, Buffa S, Barbagallo M, Di Prima A, Misiano G, et al. Systemic immune responses in Alzheimer's disease: in vitro mononuclear cell activation and cytokine production. J Alzheimers Dis. 2010;21:181–92.
66. Reale M, Iarlori C, Feliciani C, Gambi D. Peripheral chemokine receptors, their ligands, cytokines and Alzheimer's disease. J Alzheimers Dis. 2008;14:147–59.
67. Lee JK, Schuchman EH, Jin HK, Bae JS. Soluble CCL5 derived from bone marrow-derived mesenchymal stem cells and activated by amyloid beta ameliorates Alzheimer's disease in mice by recruiting bone marrow-induced microglia immune responses. Stem Cells. 2012;30:1544–55.
68. Piehl N, van Olst L, Ramakrishnan A, Teregulova V, Simonton B, Zhang Z, et al. Cerebrospinal fluid immune dysregulation during healthy brain aging and cognitive impairment. Cell. 2022. https://doi.org/10.1016/j.cell.2022.11.019.
69. Yeung SS, Ho YS, Chang RC. The role of meningeal populations of type II innate lymphoid cells in modulating neuroinflammation in neurodegenerative diseases. Exp Mol Med. 2021;53:1251–67.
70. Chen ZY, Zhang Y. Animal models of Alzheimer's disease: Applications, evaluation, and perspectives. Zool Res. 2022;43:1026–40.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Supplementary files

This file contains two supplementary figures and four supplementary tables.

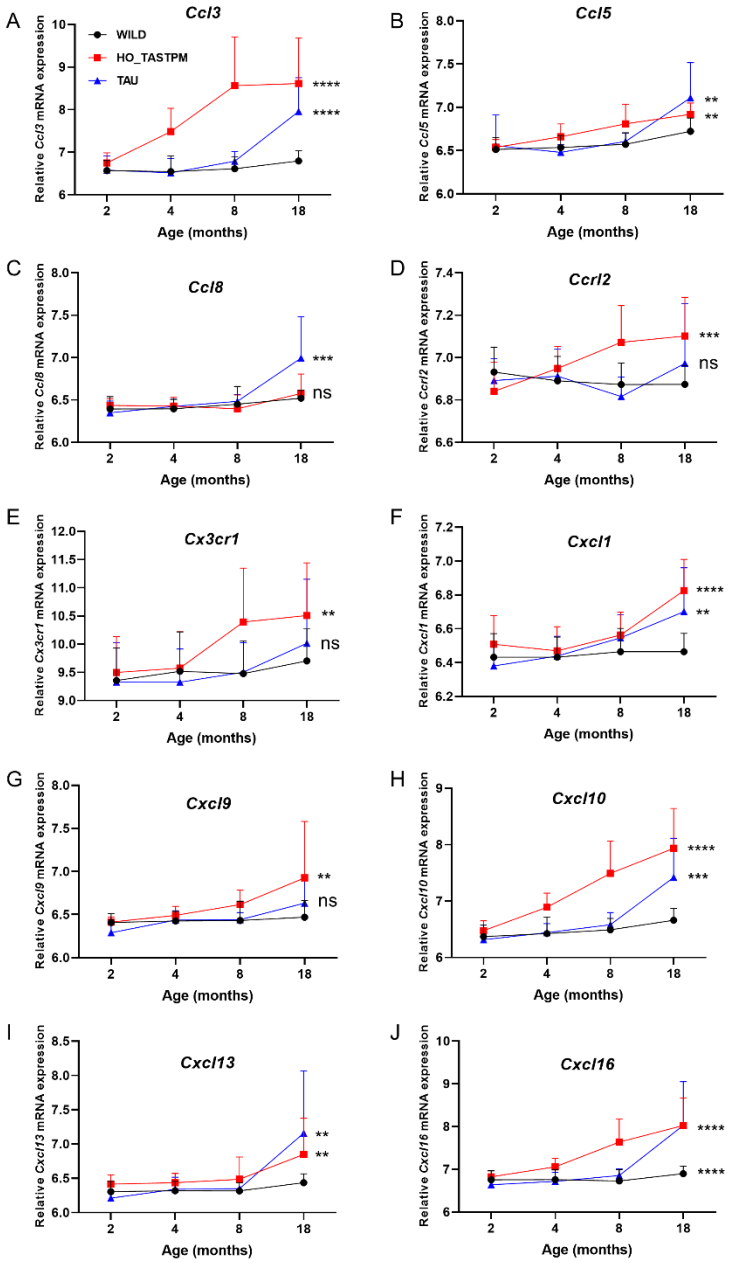

Fig. S1 Up-regulation of mRNA expression of chemokine genes during aging in AD mouse models. **A-J** The age-related mRNA expression alteration of each of the 10 chemokine genes. Data were retrieved from Mouseac (www.mouseac.org) [1]. The age-related mRNA expression level was measured in 114 brain tissues from WILD mice, 44 brain tissues from HO_TASTPM mice, and 45 brain tissues from TAU mice at different life stages. Statistical differences were calculated by two-tailed student's t-test. Error bars represent the population standard deviation. Ns, not significant; $^{**}P < 0.01$; $^{***}P < 0.001$; $^{****}P < 0.0001$.

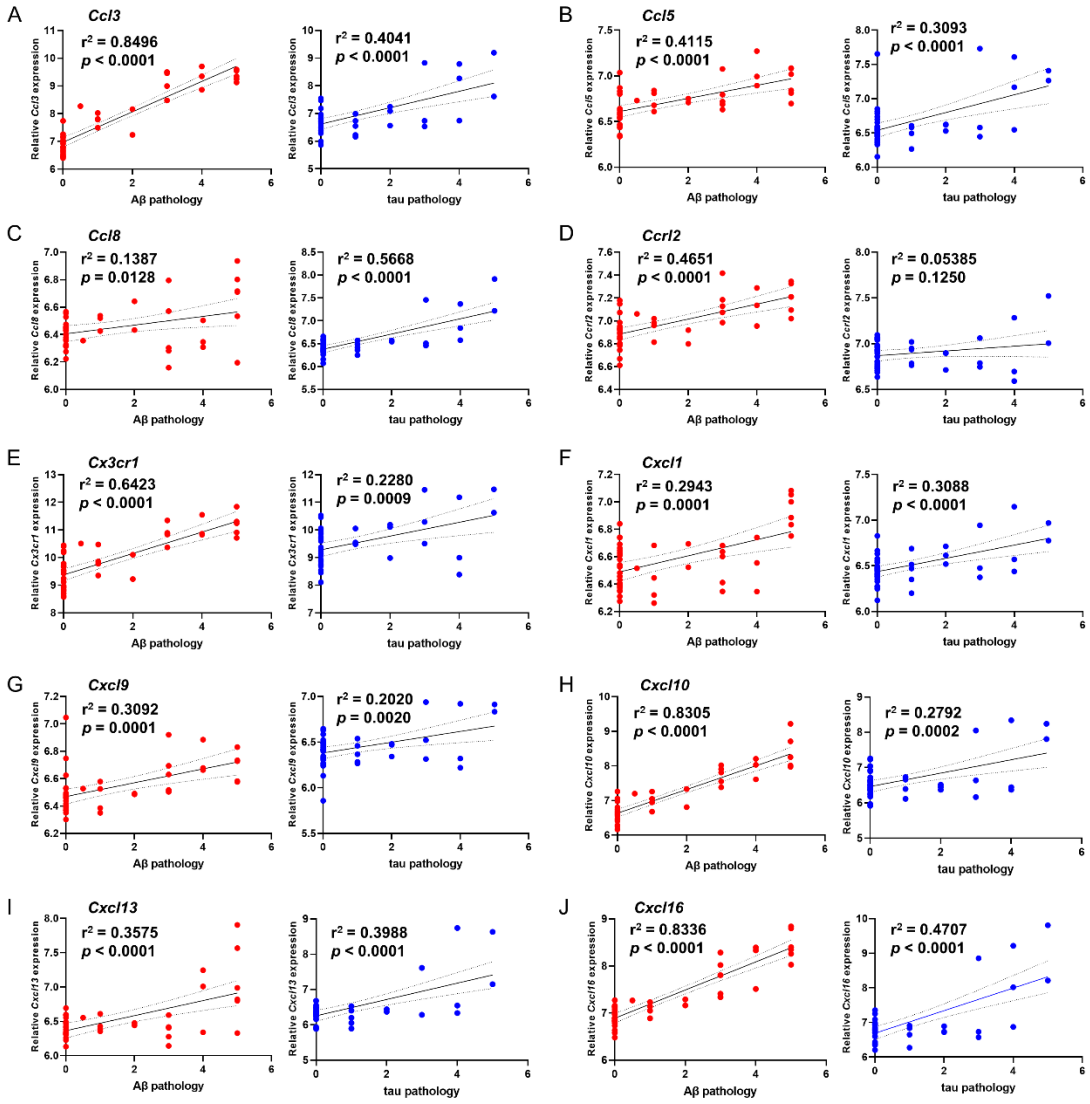

Fig. S2 Correlation between the mRNA expression levels of chemokine genes with AD pathology in AD mouse models. Data were retrieved from Mouseac (www.mouseac.org) [1]. **A-J** shows the correlation between each of the chemokine gene and the Aβ and tau pathology. The scores of Aβ pathology were retrieved from 44 brain tissues of HO_TASTPM mice, and the scores of tau pathology were retrieved from 45 brain tissues of TAU mice. The correlations between mRNA expression levels and Aβ or tau pathology were measured using the Pearson correlation analysis. The solid and dashed lines represent the slope and the 95% confidence intervals in linear regression.

Table S1 Sequence coverage of each gene in the targeted sequencing

Gene	Mean depth	10× Coverage (%)	20× Coverage (%)	30× Coverage (%)	50× Coverage (%)
C-C motif chemokine ligand					
CCL1	92.3	100	100	100	100
CCL2	94.1	100	100	100	97.0
CCL3	106.3	100	100	100	75.1
CCL5	118.7	100	100	100	100
CCL8	139.4	100	100	100	100
CCL11	134.2	100	100	100	100
CCL14	160.6	100	100	100	100
CCL15	146.2	100	100	100	98.4
CCL16	182.0	100	100	100	100
C-C motif chemokine receptor					
CCR1	229.2	100	100	100	100
CCR3	239.4	100	100	100	100
CCR5	250.2	100	100	100	100
CCR6	248.6	100	100	100	100
CCR7	139.7	100	100	100	100
CCR9	229.5	100	100	100	100
CCRL2	222.8	100	100	100	100
C-X-C motif chemokine ligand					
CXCL1	102.6	100	100	100	87.7
CXCL2	109.1	100	100	100	91.6
CXCL6	150.5	100	100	100	100
CXCL8	134.9	100	100	100	92.6
CXCL9	187.9	100	100	100	100
CXCL10	140.4	100	100	100	100
CXCL11	206.4	100	100	100	100
CXCL13	115.3	100	100	100	100
CXCL16	94.8	100	100	97.3	84.8
C-X-C motif chemokine receptor					
CXCR2	203.8	100	100	100	100
CXCR4	198.4	100	100	100	100
CXCR5	131.9	100	100	100	99.9
CXCR6	213.4	100	100	100	100
C-X3-C motif chemokine receptor					
CX3CR1	225.7	100	100	100	100
X-C motif chemokine receptor					
XCR1	171.3	100	100	100	100

The mean depth of a gene was calculated by an equation = total sequence data / gene length.
N× coverage was calculated by an equation = (the total number of nucleobases in a gene that was sequenced over N times / total gene length) × 100%.

Table S2 Results of SKAT-O analysis in Han Chinese with and without AD

Gene	Southern cohort (635 cases vs. 1507 controls)			Eastern cohort (645 cases vs. 1507 controls)			Combined (1280 cases vs. 1507 controls)		
	LoF	**Possibly pathogenic**	**Missense**	**LoF**	**Possibly pathogenic**	**Missense**	**LoF**	**Possibly pathogenic**	**Missense**
C-C motif chemokine ligand									
CCL1	NA	0.648 (1)	0.532 (2)	NA	0.650 (1)	0.515 (3)	NA	0.730 (1)	0.431 (3)
CCL2	NA	NA	0.780 (3)	NA	NA	0.755 (2)	NA	NA	0.798 (3)
CCL3	NA	1.000 (0)	0.763 (4)	NA	1.000 (0)	4.351×10^{-4} (5)*	NA	1.000 (0)	0.008 (6)*
CCL5	NA	0.648 (1)	0.456 (5)	NA	0.300 (2)	0.591 (4)	NA	0.752 (2)	0.824 (6)
CCL8	NA	NA	0.148 (1)	NA	NA	0.150 (1)	NA	NA	0.105 (2)
CCL11	NA	NA	0.753 (2)	NA	NA	0.755 (2)	NA	NA	0.357 (2)
CCL14	1.000 (0)	NA	0.532 (2)	1.000 (0)	NA	0.794 (2)	1.000 (0)	NA	0.608 (2)
CCL15	NA	NA	0.423 (3)	NA	NA	0.222 (4)	NA	NA	0.201 (5)
CCL16	NA	NA	0.125 (4)	NA	NA	0.435 (5)	NA	NA	0.110 (5)
C-C motif chemokine receptor									
CCR1	NA	0.532 (6)	0.973 (9)	NA	0.061 (9)	0.362 (12)	NA	0.187 (11)	0.740 (14)
CCR3	NA	0.897 (6)	0.930 (10)	NA	0.463 (9)	0.464 (14)	NA	0.671 (11)	0.853 (16)
CCR5	NA	0.798 (9)	0.650 (17)	NA	0.026 (12)*	0.025 (19)*	NA	0.121 (12)	0.072 (20)
CCR6	NA	1.000 (0)	0.772 (6)	NA	0.150 (1)	0.773 (6)	NA	0.230 (1)	0.847 (8)
CCR7	0.332 (1)	0.004 (4)*	0.142 (11)	0.851 (1)	1.000 (0)	0.927 (6)	0.418 (1)	0.022 (4)*	0.378 (12)
CCR9	NA	0.296 (2)	0.009 (11)*	NA	0.016 (5)*	0.117 (13)	NA	0.067 (6)	0.015 (15)*
CCRL2	NA	0.592 (7)	0.183 (15)	NA	0.672 (7)	0.089 (18)	NA	0.876 (9)	0.042 (20)*
C-X-C motif chemokine ligand									
CXCL1	NA	1.000 (0)	0.456 (4)	NA	1.000 (0)	0.755 (2)	NA	1.000 (0)	0.524 (4)
CXCL2	0.385 (1)	NA	0.290 (3)	0.387 (1)	NA	0.288 (6)	0.176 (1)	NA	0.457 (6)
CXCL6	NA	NA	0.057 (2)	NA	NA	0.109 (3)	NA	NA	0.118 (3)

CXCL8	NA	NA	0.456 (5)	NA	NA	0.562 (4)	NA	NA	0.457 (6)
CXCL9	NA	NA	0.516 (3)	NA	NA	0.526 (3)	NA	NA	0.413 (3)
CXCL10	NA	0.648 (1)	0.853 (2)	NA	0.650 (1)	0.853 (2)	NA	0.730 (1)	0.722 (2)
CXCL11	1.000 (0)	0.532 (2)	0.301 (7)	1.000 (0)	0.526 (3)	0.761 (8)	1.000 (0)	0.686 (3)	0.320 (8)
CXCL13	NA	NA	0.772 (2)	NA	NA	0.308 (3)	NA	NA	0.736 (3)
CXCL16	NA	0.408 (1)	0.232 (9)	NA	0.904 (1)	0.277 (9)	NA	0.502 (1)	0.178 (11)
C-X-C motif chemokine receptor									
CXCR2	NA	0.780 (3)	0.378 (12)	NA	0.755 (2)	0.710 (10)	NA	0.798 (3)	0.837 (13)
CXCR4	NA	1.000 (0)	0.739 (5)	NA	0.150 (1)	0.120 (5)	NA	0.230 (1)	0.329 (7)
CXCR5	NA	0.296 (2)	0.872 (6)	NA	0.121 (3)	0.559 (8)	NA	0.234 (4)	0.934 (9)
CXCR6	NA	0.780 (3)	0.666 (4)	NA	0.755 (2)	0.245 (5)	NA	0.798 (3)	0.603 (6)
C-X3-C motif chemokine receptor									
CX3CR1	NA	0.662 (3)	0.758 (13)	NA	0.469 (2)	0.362 (10)	NA	0.496 (3)	0.629 (14)
X-C motif chemokine receptor									
XCR1	NA	0.275 (8)	0.277 (18)	NA	0.054 (8)	0.106 (17)	NA	0.031 (9)*	0.069 (20)

Numbers of tested variants are shown in parentheses and association with nominal significance ($p < 0.05$) was marked with a "*".

LoF, loss-of-function variants.

Table S3 Results of gene-based burden test of chemokine genes from ADSP [2]

Gene	nSNPs	cMAC_all	p_m0	p_m1	p_m2
C-C motif chemokine ligand					
CCL1	10	15	0.508	0.580	0.516
CCL11	14	42	0.265	0.292	0.354
CCL14	21	1766	0.073	0.114	0.160
CCL15	11	1058	0.489	0.462	0.731
CCL16	17	382	0.651	0.401	0.313
CCL2	5	24	0.064	**0.033**	**0.030**
CCL3	14	81	0.144	0.374	0.294
CCL5	10	21	0.792	0.469	0.541
CCL8	14	559	0.175	0.348	0.413
C-C motif chemokine receptor					
CCR1	26	111	0.473	0.451	0.602
CCR3	36	535	0.662	0.787	0.811
CCR5	57	744	0.452	0.117	0.160
CCR6	24	31	**0.015**	0.058	0.147
CCR7	25	721	0.985	0.704	0.755
CCR9	32	360	0.239	0.601	0.333
CCRL2	46	798	0.472	0.941	0.912
C-X-C motif chemokine ligand					
CXCL1	12	60	0.331	0.064	0.053
CXCL10	10	136	0.699	0.095	0.107
CXCL11	16	179	0.104	0.645	0.445
CXCL13	11	16	0.300	0.407	0.614
CXCL16	21	273	0.322	0.491	0.487
CXCL2	14	490	0.681	0.350	0.286
CXCL6	13	107	**0.020**	0.101	0.115
CXCL9	11	33	0.442	0.804	0.864
C-X-C motif chemokine receptor					
CXCR2	29	154	0.282	0.254	0.349
CXCR4	23	40	0.665	0.948	0.830
CXCR5	26	44	0.752	0.432	0.348
CXCR6	15	163	0.990	0.599	0.601
C-X3-C motif chemokine receptor					
CX3CR1	27	436	**0.011**	**0.013**	**0.015**
X-C motif chemokine receptor					
XCR1	28	188	0.542	0.811	0.771

Data for *CXCL8* was not available in this study. nSNPs, number of SNPs tested; cMAC_all, cumulative minor allele count in all samples including 5740 AD cases and 5096 cognitively normal controls in discovery stage; p_mo, *p* values were adjusted for PCs and sequencing center; p_m1, *p* values were adjusted for sex and age at diagnosis or last follow-up in addition to those included in mo; p_m2, *p* values were adjusted for *APOE* ε4 & ε2 dosages in addition to those included in m1.

Table S4 Association results of common variants in European population

Gene	Variant_id	*P*	Chr	Location	Allele	Effect_allele_freq	OR	ci_lower	ci_upper	beta	se
CCL2	rs28730833	0.2523	17	34255475	A/T	0.0129	1.045	0.969	1.126	0.0436	0.0381
CCL2	rs4586	0.1808	17	34256250	T/C	0.6398	1.011	0.995	1.028	0.0113	0.0084
CCL2	rs13900	0.5038	17	34256892	T/C	0.2693	0.994	0.976	1.012	-0.0061	0.0091
CCL3	rs1130371	0.7399	17	36089191	A/G	0.2311	0.997	0.978	1.016	-0.0032	0.0098
CCL8	rs41410552	0.7661	17	34319112	A/G	0.107	1.004	0.978	1.03	0.0039	0.0132
CCL8	rs1133763	0.6492	17	34320812	A/C	0.8455	0.995	0.973	1.017	-0.0051	0.0113
CCL11	rs1129844	0.2609	17	34285875	A/G	0.1834	1.012	0.991	1.033	0.0118	0.0105
CCL14	rs75238886	0.9026	17	35986576	A/G	0.0317	1.003	0.958	1.049	0.0028	0.0231
CCL14	rs113937434	0.9316	17	35986638	A/G	0.0313	1.002	0.957	1.049	0.002	0.0232
CCL15	rs854625	0.7695	17	36001422	A/G	0.0451	0.994	0.955	1.034	-0.006	0.0203
CCL16	rs79254649	0.3018	17	35977569	A/C	0.0242	0.971	0.918	1.027	-0.0295	0.0286
CCL16	rs11080369	0.7433	17	35978128	A/C	0.9292	0.995	0.964	1.026	-0.0052	0.0159
CCL16	rs114853983	0.2714	17	35978326	T/C	0.0241	0.969	0.916	1.025	-0.0315	0.0287
CCR1	rs34423195	0.676	3	46208231	A/G	0.9218	1.006	0.977	1.037	0.0064	0.0153
CCR1	rs3181080	0.6745	3	46208438	A/T	0.9218	1.006	0.977	1.037	0.0064	0.0153
CCR3	rs9853223	0.5162	3	46242602	A/G	0.4376	0.995	0.979	1.011	-0.0053	0.0082
CCR3	rs4987053	0.3866	3	46265209	T/C	0.929	1.014	0.983	1.046	0.0137	0.0159
CCR5	rs1800452	0.9312	3	46373570	A/G	0.001	0.985	0.706	1.376	-0.0147	0.1704
CCR6	rs1012656	0.865	6	167111815	C/G	0.4645	1.001	0.986	1.017	0.0014	0.0081
CCR6	rs3093009	0.3378	6	167135989	A/G	0.7813	1.01	0.99	1.03	0.0096	0.01
CCR6	rs3093007	0.4998	6	167136287	T/C	0.8149	1.007	0.987	1.028	0.0072	0.0106
CCR6	rs2071171	0.489	6	167136554	T/C	0.6183	0.994	0.978	1.011	-0.0058	0.0084
CCR7	rs588019	0.7504	17	40558855	A/G	0.0732	0.995	0.963	1.028	-0.0053	0.0167
CCRL2	rs11266744	0.19	3	46408487	A/C	0.6008	0.989	0.973	1.005	-0.0109	0.0083

CCRL2	rs3204849	0.1942	3	46408579	A/T	0.3961	1.011	0.995	1.027	0.0108	0.0083
CCRL2	rs3204850	0.8376	3	46408806	A/G	0.9152	1.003	0.975	1.032	0.003	0.0147
CXCL1	rs11547681	0.1551	4	73869433	T/G	0.1814	0.985	0.965	1.006	-0.0151	0.0106
CXCL1	rs2071425	0.1036	4	73869527	A/G	0.7924	1.017	0.997	1.037	0.0165	0.0101
CXCL1	rs7656335	0.5066	4	73869807	C/G	0.0517	0.988	0.952	1.025	-0.0124	0.0187
CXCL1	rs4074	0.05719	4	73870427	A/G	0.3681	0.984	0.967	1.001	-0.0163	0.0086
CXCL9	rs2276886	0.7759	4	76007275	T/C	0.2484	0.997	0.979	1.016	-0.0027	0.0094
CXCL9	rs2276885	0.667	4	76007576	A/G	0.8049	0.996	0.976	1.016	-0.0044	0.0102
CXCL10	rs3921	0.7409	4	76021790	C/G	0.464	0.997	0.982	1.013	-0.0027	0.0081
CXCL11	rs6532111	0.764	4	76034761	T/C	0.4637	0.998	0.982	1.014	-0.0024	0.0081
CXCL11	rs6819597	0.7659	4	76036018	T/C	0.5362	1.002	0.987	1.018	0.0024	0.0081
CXCL13	rs17002743	0.3168	4	77610778	T/C	0.004	0.906	0.747	1.099	-0.0986	0.0985
CXCL16	rs1051009	0.9637	17	4734591	A/G	0.3402	1	0.983	1.017	-4.00×10^{-4}	0.0087
CXCL16	rs3744700	0.2228	17	4734715	T/G	0.3496	1.011	0.994	1.028	0.0106	0.0087
CXCL16	rs1876444	0.7667	17	4735189	T/C	0.4479	0.998	0.982	1.014	-0.0024	0.0082
CXCL16	rs2277680	0.5392	17	4735268	A/G	0.4295	0.995	0.979	1.011	-0.005	0.0082
CXCL16	rs1050998	0.5711	17	4735442	A/G	0.5679	1.005	0.989	1.021	0.0046	0.0082
CXCL16	rs1050997	0.3679	17	4738460	T/C	0.7611	1.009	0.99	1.029	0.0089	0.0099
CXCL16	rs2250333	0.1863	17	4738774	A/G	0.1824	0.986	0.964	1.007	-0.0146	0.011
CXCL16	rs2304973	0.7027	17	4738927	A/G	0.0822	0.994	0.965	1.025	-0.0059	0.0154
CXCR2	rs4674259	0.05653	2	218126282	A/G	0.5302	0.985	0.969	1	-0.0155	0.0081
CXCR2	rs11574750	0.115	2	218135569	T/C	0.046	0.97	0.933	1.008	-0.0307	0.0195
CXCR2	rs2230054	0.2085	2	218135587	T/C	0.4828	0.99	0.974	1.006	-0.0102	0.0081
CXCR4	rs2228014	0.8075	2	136115514	A/G	0.0397	1.005	0.964	1.048	0.0052	0.0212
CXCR5	rs2276344	0.5039	11	118883809	A/T	0.006	1.039	0.929	1.162	0.0381	0.057
CXCR5	rs10892307	0.266	11	118883940	C/G	0.8405	0.988	0.966	1.01	-0.0124	0.0112

CXCR5	rs598207	0.1642	11	118894558	C/G	0.2674	1.013	0.995	1.031	0.0129	0.0092
CXCR6	rs2234358	0.9427	3	45947552	T/G	0.4966	0.999	0.984	1.015	-6.00×10^{-4}	0.0081
CX3CR1	rs3732378	0.7644	3	39265671	A/G	0.1629	0.997	0.976	1.018	-0.0033	0.0109
CX3CR1	rs3732379	0.5591	3	39265765	T/C	0.2792	1.005	0.988	1.023	0.0052	0.009
CX3CR1	rs11715522	0.9979	3	39281672	A/C	0.6025	1	0.984	1.017	0	0.0084
XCR1	rs2230322	0.2389	3	46021837	T/C	0.893	1.016	0.99	1.043	0.0157	0.0133
XCR1	rs71327010	0.255	3	46027343	T/G	0.1035	0.985	0.959	1.011	-0.0153	0.0135
XCR1	rs7623476	0.1307	3	46027351	A/G	0.7796	0.985	0.967	1.004	-0.0148	0.0098

Summary statistics are available through the National Human Genome Research Institute-European Bioinformatics Institute GWAS catalog under accession number GCST90027158 (https://www.ebi.ac.uk/gwas/) [3].

Thirteen common variants (rs193057414, rs74842203, rs117290001, rs181868085, rs3732380, rs137916685, rs70937035, rs151132172, rs17038679, rs61758325, rs41339751, rs75158174, rs55901334) have no data in this GWAS study.

Chr, chromosome; Location, base pair location in GRCh38; Allele, effect allele/other allele; OR, odds ratio of the effect allele; ci, confidence interval of OR; se, standard error.

References

1. Matarin M, Salih DA, Yasvoina M, Cummings DM, Guelfi S, Liu W, et al. A genome-wide gene-expression analysis and database in transgenic mice during development of amyloid or tau pathology. Cell Rep. 2015;10:633-44.
2. Bis JC, Jian X, Kunkle BW, Chen Y, Hamilton-Nelson KL, Bush WS, et al. Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. Mol Psychiatry. 2020;25:1859-75.
3. Bellenguez C, Küçükali F, Jansen IE, Kleineidam L, Moreno-Grau S, Amin N, et al. New insights into the genetic etiology of Alzheimer's disease and related dementias. Nat Genet. 2022;54:412-36.

Gene	Chr[a]	Position[b]	Variant ID[c]	Alt[d]	Ref[c]	Location	Function	Amino acid change	MeanDP[f]	M-CAP[g]	M-CAP sensitivity score[h]	Stage 1 (Southern cohort)						Stage 2 (Eastern cohort)						Stage 3 (meta-analysis)					
												MAF of cases[i]	Allele no. of cases	MAF of controls[i]	Allele no. of controls	*P* value	OR[j]	95% CI[k]	MAF of cases[i]	Allele no. of cases	MAF of controls[i]	Allele no. of controls	*P* value	OR[j]	95% CI[k]	*P* value	OR[j]	95% CI[k]	Het I^2(%)[l]	Het *P*[m]
CCL1	17	32688760	rs73288091	A	G	intronic	regulatory	-	40.8	NA	NA	8.00E-04	1250	0.000333	3004	0.501	2.40	0.03-188.51	0.000781	1280	0.00099	7074	1.000	0.79	0.02-6.15	0.843	1.18	0.22-6.30	0.00	0.530
CCL1	17	32690253	chr17 32690253 G A	A	G	upstream	downstream	-	36.2	NA	NA	0	1242	0.000337	2968	1.000	0.00	0.00-93.06	0	1256	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL1	17	32690089	chr17 32690089 T C	C	T	intronic	intron	-	34.9	NA	NA	0	1246	0	2970	1.000	0.00	0.00-Inf	0.00079	1266	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL1	17	32687689	rs3136684	G	A	intronic	downstream	-	30.4	NA	NA	0	1156	0.000357	2800	1.000	0.00	0.00-94.33	0	1152	0	7074	1.000	0.00	0.00-Inf	0.637	1.82	0.15-21.69	0.00	0.432
CCL1	17	32687638	rs572840565	C	T	exonic	synonymous	CCL1:p.T77T	37.8	NA	NA	0	1252	0	2980	1.000	0.00	0.00-Inf	0	1270	0	7074	1.000	0.00	0.00-Inf	0.361	3.64	0.23-58.22	0.00	0.764
CCL1	17	32688811	rs772552276	G	C	exonic	regulatory	CCL1:p.G61R	44.7	0.007191	0.99231	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1288	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.11	0.00	0.333
CCL1	17	32687571	rs749704943	C	A	UTR3	3 prime UTR	-	39.1	NA	NA	0	1260	0	3002	1.000	0.00	0.00-Inf	0.000779	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL1	17	32690119	rs542632553	C	A	exonic	downstream	CCL1:p.V21G	38.5	0.00821	0.99	0	1262	0	3002	1.000	0.00	0.00-Inf	0.000783	1278	0.000848	7074	1.000	0.92	0.02-7.61	0.889	1.14	0.18-7.36	0.00	0.677
CCL1	17	32687650	chr17 32687650 G C	C	G	exonic	downstream	CCL1:p.C73W	36.9	0.201628	0.64692	0	1248	0.000337	2966	1.000	0.00	0.00-92.55	0	1262	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL1	17	32687522	rs1463966077	G	T	UTR3	downstream	-	34.5	NA	NA	0.000808	1238	0	2956	0.295	2.39	0.06-Inf	0	1256	0	7074	1.000	0.00	0.00-Inf	0.139	6.51	0.55-77.68	0.00	0.926
CCL1	17	32688738	chr17 32688738 A T	T	A	intronic	regulatory	-	37.1	NA	NA	0	1214	0.000334	2992	1.000	0.00	0.00-95.98	0.000801	1248	0	7074	0.150	5.67	0.15-Inf	0.254	3.74	0.39-35.95	41.93	0.189
CCL1	17	32690057	rs375569467	A	G	intronic	intron	-	29.3	NA	NA	0	1162	0.000352	2838	1.000	0.00	0.00-95.11	0	1168	0	7074	1.000	0.00	0.00-Inf	0.637	1.82	0.15-21.68	0.00	0.437
CCL1	17	32687511	rs3136683	C	G	UTR3	downstream	-	32.9	NA	NA	0	1220	0.000341	2930	1.000	0.00	0.00-93.53	0	1246	0	7074	1.000	0.00	0.00-Inf	0.658	1.75	0.15-20.91	0.00	0.448
CCL1	17	32688775	rs187174245	G	A	intronic	regulatory	-	42.5	NA	NA	0.003968	1260	0.003989	3008	1.000	0.99	0.27-3.04	0.000778	1286	0.000424	7074	0.487	1.83	0.03-22.86	0.833	1.11	0.43-2.86	0.00	0.631
CCL1	17	32690056	rs185823036	T	C	intronic	downstream	-	29	NA	NA	0.001712	1168	0.001413	2830	1.000	1.21	0.11-8.47	0.000853	1172	0.000848	7074	1.000	1.01	0.02-8.30	0.860	1.13	0.30-4.24	0.00	0.893
CCL1	17	32690231	chr17 32690231 G A	A	G	UTR5	5 prime UTR	-	38.5	NA	NA	0	1260	0.000333	3002	1.000	0.00	0.00-92.79	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL1	17	32688878	rs533149708	G	C	exonic	regulatory	CCL1:p.A38A	45.3	NA	NA	0.00237	1266	0.000995	3014	0.370	2.38	0.32-17.81	0	1290	0.00212	7074	0.149	0.00	0.00-1.53	0.743	1.26	0.31-5.08	59.67	0.115
CCL11	17	32614087	rs377267955	T	C	intronic	intron	-	49.1	NA	NA	0	1266	0	3014	1.000	0.00	0.00-Inf	0.000779	1284	0	7074	0.154	5.51	0.14-Inf	0.109	7.62	0.64-90.90	0.00	0.453
CCL11	17	32612684	rs897141820	T	C	upstream	upstream	-	41.8	NA	NA	0	1260	0	3000	1.000	0.00	0.00-Inf	0	1278	0.000424	7074	1.000	0.00	0.00-13.40	0.891	1.18	0.11-12.55	0.00	0.660
CCL11	17	32614128	chr17 32614128 C T	T	C	exonic	synonymous	CCL11:p.T30T	50.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612864	rs1345202009	C	A	exonic	regulatory	CCL11:p.I13L	44	0.002338	0.99846	0	1266	0.000332	3012	1.000	0.00	0.00-92.65	0	1288	0.000141	7074	1.000	0.00	0.00-213.49	0.872	1.20	0.13-11.58	0.00	0.717
CCL11	17	32614157	rs764694346	T	A	exonic	missense	CCL11:p.K40M	50.4	0.012144	0.98231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCL11	17	32614552	rs183026342	A	G	intronic	intron	-	39.1	NA	NA	0	1234	0	2996	1.000	0.00	0.00-Inf	0	1248	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612754	rs547574343	A	G	upstream	5 prime UTR	-	44.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCL11	17	32612665	rs762590301	G	A	upstream	upstream	-	38.5	NA	NA	8.00E-04	1250	0	2992	0.295	2.40	0.06-Inf	0.000796	1256	0.000141	7074	0.279	5.64	0.07-440.81	0.086	6.25	0.77-50.86	0.00	0.911
CCL11	17	32612703	rs1479581443	T	C	upstream	5 prime UTR	-	43.6	NA	NA	0.002366	1268	0.000995	3014	0.370	2.38	0.32-17.78	0.000779	1284	0.001272	7074	1.000	0.61	0.01-4.42	0.580	1.43	0.40-5.07	3.56	0.309
CCL11	17	32612937	rs370775153	A	G	intronic	regulatory	-	36.5	NA	NA	0.000843	1186	0	2968	0.286	2.50	0.06-Inf	0	1210	0.000424	7074	1.000	0.00	0.00-14.15	0.453	2.30	0.26-20.25	0.00	0.324
CCL11	17	32612691	rs1182975436	T	G	upstream	5 prime UTR	-	42.7	NA	NA	0	1266	0.000333	3004	1.000	0.00	0.00-92.41	0	1280	0.000565	7074	1.000	0.00	0.00-8.38	0.735	0.69	0.08-5.96	0.00	0.909
CCL11	17	32612839	rs185980467	T	C	exonic	regulatory	CCL11:p.S4S	45	NA	NA	0.01343	1266	0.008988	3004	0.188	1.50	0.76-2.87	0.01009	1288	0.006785	7074	0.211	1.49	0.74-2.81	0.068	1.50	0.97-2.31	0.00	0.990
CCL11	17	32612712	rs200213188	T	C	upstream	5 prime UTR	-	43.8	NA	NA	0	1268	0	3012	1.000	0.00	0.00-Inf	0.000776	1288	0.000424	7074	0.488	1.83	0.03-22.83	0.503	1.95	0.28-13.88	0.00	0.910
CCL11	17	32612731	rs199775798	G	A	upstream	5 prime UTR	-	44.5	NA	NA	0.000787	1270	0.000664	3014	1.000	1.19	0.02-22.82	0	1290	0.00099	7074	0.605	0.00	0.00-3.81	0.737	0.73	0.12-4.59	0.00	0.536
CCL11	17	32614658	chr17 32614658 G A	A	G	exonic	synonymous	CCL11:p.V81V	44.6	NA	NA	0	1266	0.000332	3012	1.000	0.00	0.00-92.65	0	1288	0	7074	1.000	0.00	0.00-Inf	0.668	1.72	0.14-20.52	0.00	0.454
CCL11	17	32614743	rs200369153	C	G	UTR3	3 prime UTR	-	38	NA	NA	0	1200	0.000336	2978	1.000	0.00	0.00-96.64	0.001631	1226	0.000424	7074	0.161	3.85	0.32-33.64	0.218	2.67	0.56-12.74	0.00	0.411
CCL11	17	32614577	chr17 32614577 T G	G	T	intronic	intron	-	42.4	NA	NA	0	1260	0	3012	1.000	0.00	0.00-Inf	0.000781	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32614551	rs1190477269	C	T	intronic	intron	-	39	NA	NA	0	1232	0	2998	1.000	0.00	0.00-Inf	0	1248	0.000141	7074	1.000	0.00	0.00-220.30	0.560	2.09	0.18-24.95	0.00	0.922
CCL11	17	32614556	chr17 32614556 A G	G	A	intronic	intron	-	40.1	NA	NA	0	1238	0.000332	3008	1.000	0.00	0.00-94.62	0	1254	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612814	rs137995665	G	C	UTR5	regulatory	-	45	NA	NA	0	1270	0	3012	1.000	0.00	0.00-Inf	0.002326	1290	0.000707	7074	0.112	3.30	0.51-16.95	0.093	3.17	0.83-12.17	0.00	0.877
CCL11	17	32612721	chr17 32612721 T C	C	T	upstream	5 prime UTR	-	44.1	NA	NA	0.000787	1270	0	3012	0.297	2.37	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.54	0.00	0.919
CCL11	17	32614165	chr17 32614165 C T	T	C	exonic	missense	CCL11:p.L43F	50.5	0.004421	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612842	rs757174131	T	A	exonic	regulatory	CCL11:p.A5A	44.4	NA	NA	0.00079	1266	0	3010	0.296	2.38	0.06-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612840	rs56120942	A	G	exonic	regulatory	CCL11:p.A5T	44.5	0.00424	0.99846	0	1264	0	3008	1.000	0.00	0.00-Inf	0	1288	0.000565	7074	1.000	0.00	0.00-8.32	0.994	0.99	0.10-10.32	0.00	0.585
CCL11	17	32614704	chr17 32614704 C A	A	C	exonic	missense	CCL11:p.P97T	43.1	0.015043	0.97615	0	1262	0	3010	1.000	0.00	0.00-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612756	rs1470484567	A	G	upstream	5 prime UTR	-	44.7	NA	NA	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32614703	chr17 32614703 G A	A	G	exonic	synonymous	CCL11:p.K96K	43.2	NA	NA	0	1264	0	3012	1.000	0.00	0.00-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL11	17	32612701	chr17 32612701 C T	T	C	upstream	5 prime UTR	-	43.4	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34313606	rs755332753	T	C	splicing	regulatory	-	45.9	0.00964	0.98538	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34312811	chr17 34312811 C A	A	C	exonic	regulatory	CCL14:p.V34F	50.7	0.002496	0.99846	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34313637	rs771441014	T	C	exonic	regulatory	CCL14:p.A17T	49.4	0.002919	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34311411	chr17 34311411 A G	G	A	exonic	NMD,3 prime UTR	CCL14:p.Y69H	44.4	0.010564	0.98462	0	1270	0	3012	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34311478	chr17 34311478 G C	C	G	exonic	NMD,3 prime UTR	CCL14:p.Y46X	43.4	NA	NA	0	1270	0	3004	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34311483	chr17 34311483 G C	C	G	exonic	NMD,3 prime UTR	CCL14:p.P45A	43.1	0.009029	0.98769	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34313607	rs186783049	C	G	exonic	regulatory	CCL14:p.R27G	46	0.004454	0.99846	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	17	34311433	rs148605501	T	C	exonic	synonymous	CCL14:p.P61P	44.3	NA	NA	0	1270	0.000332	3010	1.000	0.00	0.00-92.30	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL15	17	34324849	rs150213949	A	G	exonic	missense	CCL15:p.P99L	43.2	0.000585	1	0.002362	1270	0.001327	3014	0.430	1.78	0.26-10.55	0.001558	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL15	17	34325361	rs567687330	C	T	exonic	5 prime UTR	CCL15:p.K68R	44	0.00144	1	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0.000778	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL15	17	34325426	chr17 34325426 G C	C	G	exonic	regulatory	CCL15:p.S46R	42.6	0.001548	1	0.000789	1268	0	3010	0.296	2.38	0.06-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL15	17	34328523	chr17 34328523 G C	C	G	exonic	regulatory	CCL15:p.V3V	67.4	NA	NA	0.00079	1266	0	3012	0.296	2.38	0.06-Inf	0	1278	0	7074	1.000	0.00	0.00-Inf	0.141	6.45	0.54-76.97	0.00	0.921
CCL15	17	34328513	chr17 34328513 C A	A	C	exonic	regulatory	CCL15:p.A7S	67	0.001503	1	0	1264	0	3010	1.000	0.00	0.00-Inf	0.000784	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL15	17	34324876	rs745762672	T	C	exonic	missense	CCL15:p.R90Q	42.5	0.001033	1	0	1268	0	3004	1.000	0.00	0.00-Inf	0.00078	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304735	chr17 34304735 G A	A	G	exonic	regulatory	CCL16:p.T77I	62.3	0.004385	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304657	rs536870292	A	G	exonic	regulatory	CCL16:p.T103M	75.1	0.001475	1	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308597	rs565897451	A	T	upstream	regulatory	-	33.1	NA	NA	0	1158	0.000674	2968	1.000	0.00	0.00-13.65	0	1172	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304726	rs768847780	C	T	exonic	regulatory	CCL16:p.N80S	62.5	0.001551	1	0	1270	0.000995	3014	0.560	0.00	0.00-5.74	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34305241	chr17 34305241 C T	T	C	exonic	synonymous	CCL16:p.V45V	49.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308523	rs549950289	A	G	UTR5	regulatory	-	40.7	NA	NA	0	1264	0	2994	1.000	0.00	0.00-Inf	1.56E-03	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308565	chr17 34308565 G A	A	G	upstream	regulatory	-	37.3	NA	NA	0	1240	0.000334	2996	1.000	0.00	0.00-94.09	0	1254	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304806	rs772673314	T	C	intronic	regulatory	-	61.7	NA	NA	0.000789	1268	0	3008	0.297	2.37	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308476	rs369188602	G	A	UTR5	regulatory	-	41.7	NA	NA	0	1266	0.000332	3012	1.000	0.00	0.00-92.65	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304748	rs192887586	T	G	exonic	regulatory	CCL16:p.R73R	62.3	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308436	chr17 34308436 G C	C	G	exonic	regulatory	CCL16:p.A7A	41.3	NA	NA	0	1268	0	3012	1.000	0.00	0.00-Inf	0.000781	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308408	chr17 34308408 T A	A	T	exonic	regulatory	CCL16:p.I17F	39.8	0.002232	0.99923	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304538	chr17 34304538 T C	C	T	UTR3	regulatory	-	62.2	NA	NA	0	1268	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34305154	chr17 34305154 G A	A	G	intronic	intron	-	48.9	NA	NA	0	1268	0.000332	3012	1.000	0.00	0.00-92.51	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308475	rs1219037835	A	C	UTR5	regulatory	-	41.8	NA	NA	0.000789	1268	0	3010	0.296	2.38	0.06-Inf	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308350	rs200938478	A	G	intronic	regulatory	-	31.5	NA	NA	0	1202	0.002381	2940	0.204	0.00	0.00-1.70	0.004181	1196	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308364	chr17 34308364 G A	A	G	intronic	regulatory	-	33.9	NA	NA	0	1218	0.001008	2976	0.561	0.00	0.00-5.91	0	1246	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308561	chr17 34308561 C G	G	C	upstream	regulatory	-	38.1	NA	NA	0	1246	0.000666	3002	1.000	0.00	0.00-12.83	0	1258	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34305138	chr17 34305138 C T	T	C	intronic	intron	-	48.3	NA	NA	0	1268	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308491	rs371857407	T	C	UTR5	regulatory	-	41.6	NA	NA	0	1270	0.000665	3008	1.000	0.00	0.00-12.62	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308392	rs543053536	T	C	exonic	regulatory	CCL16:p.R22H	37.8	0.001615	0.99923	0	1266	0	2988	1.000	0.00	0.00-Inf	0.000786	1272	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34308401	rs199602184	A	G	exonic	regulatory	CCL16:p.S19L	39	0.004801	0.99846	0	1270	0.000665	3008	1.000	0.00	0.00-12.62	0	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34305092	chr17 34305092 A C	C	A	intronic	intron	-	43.7	NA	NA	0.000814	1228	0	2986	0.291	2.43	0.06-Inf	0	1252	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304774	chr17 34304774 A G	G	A	intronic	regulatory	-	62.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304786	chr17 34304786 A G	G	A	intronic	regulatory	-	62.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304508	chr17 34304508 G A	A	G	UTR3	regulatory	-	59.9	NA	NA	0.000808	1238	0	2998	0.292	2.42	0.06-Inf	0	1270	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34305100	rs189408858	T	C	intronic	intron	-	44.8	NA	NA	0.000803	1246	0	3000	0.293	2.41	0.06-Inf	0	1258	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

CCL16	17	34304703	chr17 34304703 T C	C	T	exonic	regulatory	CCL16:p.I88V	62.4	0.001549	1	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304845	chr17 34304845 A G	G	A	intronic	regulatory	-	58.7	NA	NA	0	1230	0	2984	1.000	0.00	0.00-Inf	0.000795	1258	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304819	rs763998359	A	G	intronic	regulatory	-	61.1	NA	NA	0.00079	1266	0	3006	0.296	2.38	0.06-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	17	34304796	rs774525937	C	G	intronic	regulatory	-	61.9	NA	NA	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32583350	chr17 32583350 A T	T	A	exonic	regulatory	CCL2:p.E62D	47.2	0.016174	0.97385	0.000789	1268	0	3010	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32582354	rs762750838	G	A	UTR5	regulatory	-	39.2	NA	NA	0.000791	1264	0	2996	0.297	2.37	0.06-Inf	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32583892	rs766347726	T	C	UTR3	regulatory	-	38.5	NA	NA	0	1214	0	2996	1.000	0.00	0.00-Inf	0	1230	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32582521	chr17 32582521 T C	C	T	intronic	regulatory	-	28.4	NA	NA	0	1114	0	2858	1.000	0.00	0.00-Inf	0	1114	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32583310	rs148937652	T	C	exonic	regulatory	CCL2:p.A49V	47.7	0.005519	0.99769	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32582498	rs1895570180	G	A	intronic	regulatory	-	32.7	NA	NA	0.003268	1224	0.004076	2944	1.000	0.80	0.19-2.65	0.003247	1232	0.001696	7074	0.281	1.92	0.45-6.34	0.600	1.24	0.56-2.76	12.15	0.286
CCL2	17	32582455	rs771009864	T	C	intronic	regulatory	-	39.2	NA	NA	0.00159	1258	0.000334	2992	0.211	4.76	0.25-280.58	0	1282	0.000283	7074	1.000	0.00	0.00-29.39	0.299	2.71	0.41-17.84	0.00	0.459
CCL2	17	32583309	rs760761240	A	G	exonic	regulatory	CCL2:p.A49T	47.7	0.01941	0.96846	0	1270	0.000333	3006	1.000	0.00	0.00-92.18	0	1288	0	7074	1.000	0.00	0.00-Inf	0.670	1.71	0.14-20.46	0.00	0.452
CCL2	17	32583861	rs773995779	G	A	UTR3	regulatory	-	41.9	NA	NA	0	1258	0.000333	3006	1.000	0.00	0.00-93.06	0	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	17	32582334	rs779422035	G	A	UTR5	regulatory	-	37.8	NA	NA	0	1262	0.000334	2996	1.000	0.00	0.00-92.45	0	1274	0.000141	7074	1.000	0.00	0.00-215.82	0.869	1.21	0.13-11.63	0.00	0.713
CCL2	17	32583311	chr17 32583311 G A	A	G	exonic	regulatory	CCL2:p.A49A	47.7	NA	NA	0	1270	0.000332	3010	1.000	0.00	0.00-92.30	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416500	rs201356193	C	T	intronic	regulatory	-	53	NA	NA	0	1266	0.000332	3010	1.000	0.00	0.00-92.59	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416045	rs1049114	G	A	exonic	synonymous	CCL3:p.Y84Y	28.6	NA	NA	0	1210	0	2736	1.000	0.00	0.00-Inf	0	1226	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417530	rs929424387	T	C	upstream	regulatory	-	42.9	NA	NA	0	1270	0.000999	3004	0.559	0.00	0.00-5.73	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416533	rs943179896	T	C	exonic	regulatory	CCL3:p.V62I	54.5	0.005527	0.99769	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416536	rs1130374	T	C	exonic	regulatory	CCL3:p.G61S	54.6	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.004658	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417531	rs983463958	A	G	upstream	regulatory	-	42.8	NA	NA	0	1270	0	3010	1.000	0.00	0.00-Inf	0.00078	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417493	chr17 34417493 G A	A	G	upstream	regulatory	-	44.3	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417571	chr17 34417571 T C	C	T	upstream	regulatory	-	36.7	NA	NA	0	1218	0.000338	2958	1.000	0.00	0.00-94.58	0	1232	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416665	rs1719133	A	G	intronic	regulatory	-	67.7	NA	NA	0	1266	0.000333	3004	1.000	0.00	0.00-92.41	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416063	chr17 34416063 C T	T	C	exonic	intron,non coding	CCL3:p.E78E	28.8	NA	NA	0	1204	0	2750	1.000	0.00	0.00-Inf	0	1236	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417541	rs909385570	G	A	upstream	regulatory	-	41.8	NA	NA	0	1262	0	3008	1.000	0.00	0.00-Inf	0.000781	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416499	rs118134981	C	A	intronic	regulatory	-	53	NA	NA	0.0142	1268	0.007979	3008	0.064	1.79	0.91-3.45	0.009346	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416559	rs771827521	A	G	exonic	regulatory	CCL3:p.T53M	65	0.021301	0.96231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416647	rs1851501	C	T	intronic	regulatory	-	63.3	NA	NA	0.001577	1268	0.000665	3006	0.587	2.37	0.17-32.76	0.00311	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417313	chr17 34417313 C A	A	C	intronic	regulatory	-	41.2	NA	NA	0	1256	0	3008	1.000	0.00	0.00-Inf	0.000784	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416486	rs184293561	A	C	intronic	regulatory	-	52.1	NA	NA	0.01422	1266	0.007973	3010	0.063	1.79	0.91-3.46	0.00939	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416507	rs1468375708	T	G	intronic	regulatory	-	53.4	NA	NA	0	1268	0.000665	3010	1.000	0.00	0.00-12.64	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416577	rs146554516	G	A	exonic	regulatory	CCL3:p.I47T	64.9	0.033626	0.92231	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416702	chr17 34416702 C T	T	C	intronic	regulatory	-	41.7	NA	NA	0	1236	0.000336	2978	1.000	0.00	0.00-93.83	0	1252	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416560	chr17 34416560 T A	A	T	exonic	regulatory	CCL3:p.T53S	65	0.011372	0.98308	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416578	chr17 34416578 T C	C	T	exonic	regulatory	CCL3:p.I47V	64.9	0.003122	0.99846	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416038	rs141182065	T	C	exonic	intron,non coding	CCL3:p.D87N	28.4	NA	NA	0.000824	1214	0.000366	2732	0.521	2.25	0.03-176.55	0	1224	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416039	rs1049121	A	G	exonic	intron,non coding	CCL3:p.S86S	28.4	NA	NA	0	1210	0	2718	1.000	0.00	0.00-Inf	0	1222	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416453	rs1719131	G	A	intronic	regulatory	-	47.8	NA	NA	0.000808	1238	0	2986	0.293	2.41	0.06-Inf	0	1246	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417475	chr17 34417475 T C	C	T	UTR5	regulatory	-	44.6	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416706	chr17 34416706 T C	C	T	intronic	regulatory	-	39.7	NA	NA	0	1194	0	2960	1.000	0.00	0.00-Inf	0	1204	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34417558	chr17 34417558 G A	A	G	upstream	regulatory	-	39	NA	NA	0.000809	1236	0	2988	0.293	2.42	0.06-Inf	0.000792	1262	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL3	17	34416655	rs749528977	T	G	intronic	regulatory	-	62.8	NA	NA	0	1266	0.000333	3004	1.000	0.00	0.00-92.41	0.000779	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199334	rs370171166	T	C	exonic	intron,non coding	CCL5:p.L135L	48.1	NA	NA	0	1258	0.000333	3006	1.000	0.00	0.00-93.06	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205623	rs776911285	G	A	exonic	regulatory	CCL5:p.C33R	44.9	0.057951	0.86	0	1262	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205670	chr17 34205670 C T	T	C	intronic	regulatory	-	42.9	NA	NA	0	1262	0.000333	3002	1.000	0.00	0.00-92.64	0	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205632	rs759918234	C	T	exonic	regulatory	CCL5:p.T30A	44.8	0.036341	0.91462	0	1262	0.000332	3012	1.000	0.00	0.00-92.95	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205717	chr17 34205717 T C	C	T	intronic	regulatory	-	35.3	NA	NA	0	1188	0.000339	2948	1.000	0.00	0.00-96.63	0	1196	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205533	rs766662990	T	C	exonic	regulatory	CCL5:p.V63I	41.7	0.01843	0.96923	0.000796	1256	0	3010	0.294	2.40	0.06-Inf	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34207221	chr17 34207221 G A	A	G	intronic	regulatory	-	34.9	NA	NA	0	1238	0.000336	2978	1.000	0.00	0.00-93.68	0	1244	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205680	rs191296440	T	C	intronic	regulatory	-	42	NA	NA	0.000794	1260	0	3008	0.295	2.39	0.06-Inf	0	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34205662	chr17 34205662 G A	A	G	intronic	regulatory	-	43.7	NA	NA	0	1262	0	3012	1.000	0.00	0.00-Inf	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199565	chr17 34199565 T G	G	T	intronic	upstream	-	39.3	NA	NA	0	1082	0	2920	1.000	0.00	0.00-Inf	0.000912	1096	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199474	chr17 34199474 G T	T	G	intronic	intron,non coding	-	49.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199514	rs572481560	T	C	intronic	upstream	-	48.8	NA	NA	0.00079	1266	0.000665	3008	1.000	1.19	0.02-22.84	0.00155	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34207303	chr17 34207303 C T	T	C	exonic	regulatory	CCL5:p.V3I	40.6	0.005751	0.99692	0	1270	0.000666	3004	1.000	0.00	0.00-12.60	0.00156	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34207416	chr17 34207416 C T	T	C	upstream	regulatory	-	34.3	NA	NA	0	1226	0.000342	2928	1.000	0.00	0.00-93.01	0	1244	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34207335	rs1168580925	A	G	UTR5	regulatory	-	41	NA	NA	0	1270	0.000333	3006	1.000	0.00	0.00-92.18	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199501	chr17 34199501 A T	T	A	intronic	intron	-	49.3	NA	NA	0.000789	1268	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34207436	chr17 34207436 T C	C	T	upstream	regulatory	-	30.5	NA	NA	0	1170	0.000703	2846	1.000	0.00	0.00-12.96	0	1176	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199282	rs752111320	T	C	exonic	upstream	CCL5:p.A153T	40.9	NA	NA	0	1182	0.000339	2946	1.000	0.00	0.00-97.06	0	1212	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL5	17	34199448	rs140271646	T	C	exonic	intron,non coding	CCL5:p.R70H	50	0.015458	0.97538	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646408	chr17 32646408 C A	A	C	upstream	5 prime UTR	-	48.2	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32647360	rs745389863	A	G	exonic	missense	CCL8:p.S50N	42.9	0.014066	0.97769	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1288	0.000141	7074	1.000	0.00	0.00-213.45	0.576	2.03	0.17-24.23	0.00	0.920
CCL8	17	32646157	rs200838025	A	G	upstream	regulatory	-	49.2	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0	7074	1.000	0.00	0.00-Inf	0.322	3.14	0.33-30.19	0.00	0.733
CCL8	17	32647463	chr17 32647463 G A	A	G	intronic	intron	-	33.1	NA	NA	0	1150	0.000678	2950	1.000	0.00	0.00-13.66	0	1170	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646426	rs1178525576	C	T	upstream	5 prime UTR	-	48	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32647927	rs1247688071	A	G	UTR3	3 prime UTR	-	36.2	NA	NA	0	1242	0.000338	2958	1.000	0.00	0.00-92.75	0	1258	0	7074	1.000	0.00	0.00-Inf	0.663	1.74	0.15-20.73	0.00	0.448
CCL8	17	32646186	rs144003271	T	C	upstream	regulatory	-	49.4	NA	NA	0.000787	1270	0.002322	3014	0.450	0.34	0.01-2.64	0.00155	1290	0.001555	7074	1.000	1.00	0.11-4.58	0.552	0.69	0.20-2.35	0.00	0.412
CCL8	17	32647299	rs769159848	T	A	exonic	missense	CCL8:p.I30F	41.1	0.01286	0.97923	0.000789	1268	0	3008	0.297	2.37	0.06-Inf	0	1278	0.000707	7074	1.000	0.00	0.00-6.04	0.645	1.66	0.19-14.19	30.97	0.229
CCL8	17	32646111	rs1263614226	T	C	upstream	regulatory	-	47.1	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CCL8	17	32646006	rs200083542	T	C	upstream	regulatory	-	38.1	NA	NA	0	1212	0	2954	1.000	0.00	0.00-Inf	0.000824	1214	0.000565	7074	0.547	1.46	0.03-14.75	0.609	1.65	0.24-11.16	0.00	0.822
CCL8	17	32646140	rs199521640	T	C	upstream	regulatory	-	49.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCL8	17	32646380	chr17 32646380 T C	C	T	upstream	regulatory	-	48.5	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646328	rs1367907135	A	G	upstream	regulatory	-	48.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646192	chr17 32646192 T C	C	T	upstream	regulatory	-	48.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.829	0.79	0.09-6.92	0.00	0.996
CCL8	17	32646575	chr17 32646575 C T	T	C	exonic	missense	CCL8:p.P19S	44.3	0.004058	0.99846	0	1266	0	3002	1.000	0.00	0.00-Inf	0.000783	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32647816	rs199534921	T	C	intronic	splice,intron	-	36.8	NA	NA	0.000801	1248	0	2994	0.294	2.40	0.06-Inf	0	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646501	rs768645764	C	T	UTR5	5 prime UTR	-	46.6	NA	NA	0	1270	0	3008	1.000	0.00	0.00-Inf	0.000783	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646272	rs183097812	T	C	upstream	regulatory	-	49.8	NA	NA	0.007874	1270	0.003981	3014	0.107	1.99	0.77-5.03	0.003101	1290	0.003958	7074	0.809	0.78	0.20-2.24	0.337	1.38	0.72-2.66	45.63	0.175
CCL8	17	32647410	chr17 32647410 G A	A	G	intronic	splice,intron	-	41	NA	NA	0	1266	0.000332	3012	1.000	0.00	0.00-92.65	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646583	chr17 32646583 A G	G	A	exonic	synonymous	CCL8:p.G21G	43.8	NA	NA	0	1266	0.000333	3004	1.000	0.00	0.00-92.41	0	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646134	chr17 32646134 C T	T	C	upstream	regulatory	-	49.1	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646324	rs1418329867	C	T	upstream	regulatory	-	48.8	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.623	1.67	0.22-12.95	0.00	0.713
CCL8	17	32646181	rs1168291809	G	A	upstream	regulatory	-	49.2	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646479	chr17 32646479 C T	T	C	UTR5	5 prime UTR	-	46.9	NA	NA	0	1266	0	3010	1.000	0.00	0.00-Inf	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	17	32646544	rs569040565	A	G	exonic	synonymous	CCL8:p.L8L	45.4	NA	NA	0.00158	1266	0.000333	3006	0.211	4.75	0.25-280.11	0	1286	0	7074	1.000	0.00	0.00-Inf	0.126	4.95	0.64-38.34	0.00	0.951
CCR1	3	46245772	rs762719844	A	G	exonic	intron	CCR1:p.D11D	51.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR1	3	46245465	chr3 46245465 A T	T	A	exonic	missense	CCR1:p.Y114N	50.6	0.224426	0.61692	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46249906	chr3 46249906 G C	C	G	upstream	regulatory	-	65.2	NA	NA	0	1270	0.000664	3012	1.000	0.00	0.00-12.63	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46249797	rs549636818	C	T	UTR5	regulatory	-	65.4	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245077	chr3 46245077 A G	G	A	exonic	intron	CCR1:p.V243A	50.2	0.02432	0.95077	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA	NA

CCR1	3	46245692	rs1192919970	A	G	exonic	missense	CCR1:p.P38L	51.1	0.186276	0.66538	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CCR1	3	46245447	chr3_46245447_C_T	T	C	exonic	intron	CCR1:p.E120K	50.5	0.03329	0.92538	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245532	rs570245777	A	G	exonic	synonymous	CCR1:p.I91I	50.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR1	3	46245721	rs146106258	A	G	exonic	intron	CCR1:p.N28N	51.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245177	chr3_46245177_A_G	G	A	exonic	synonymous	CCR1:p.L210L	50.3	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245280	rs201064013	C	T	exonic	synonymous	CCR1:p.Q175Q	50.4	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.267	3.61	0.38-34.70	0.00	0.556
CCR1	3	46245547	rs202204196	T	C	exonic	synonymous	CCR1:p.T86T	50.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.267	3.61	0.38-34.70	42.11	0.189
CCR1	3	46244879	rs201235369	T	C	exonic	intron	CCR1:p.R309Q	47.7	0.097548	0.78462	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR1	3	46245624	rs142817888	T	G	exonic	intron	CCR1:p.Q61K	51.2	0.006046	0.99615	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0.000775	1290	0.001555	7074	0.706	0.50	0.01-3.43	0.862	0.86	0.17-4.49	0.00	0.375
CCR1	3	46245169	chr3_46245169_C_A	A	C	exonic	missense	CCR1:p.L212F	50.3	0.061766	0.85385	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245807	rs41477748	T	C	UTR5	5_prime_UTR	-	51.4	NA	NA	0.001575	1270	0.001327	3014	1.000	1.19	0.11-8.30	0.004651	1290	0.001131	7074	0.013	4.13	1.18-13.59	0.020	2.91	1.18-7.15	32.80	0.223
CCR1	3	46245528	rs1303561388	G	A	exonic	intron	CCR1:p.Y93H	50.7	0.173318	0.67846	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46244850	rs181920971	A	G	exonic	missense	CCR1:p.R319C	47.5	0.05542	0.86692	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245394	rs768750994	A	G	exonic	intron	CCR1:p.H137H	50.5	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR1	3	46249796	rs188083799	A	G	UTR5	regulatory	-	65.5	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.567	1.75	0.26-11.97	0.00	0.542
CCR1	3	46245483	chr3_46245483_T_A	A	T	exonic	missense	CCR1:p.I108F	50.7	0.006556	0.99385	0.000787	1270	0.000995	3014	1.000	0.79	0.02-9.86	0	1290	0	7074	1.000	0.00	0.00-Inf	0.803	1.28	0.18-9.12	0.00	0.402
CCR1	3	46244948	rs201264930	A	G	exonic	intron	CCR1:p.T286M	50.1	0.158704	0.7	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46244902	rs141128686	A	G	exonic	synonymous	CCR1:p.Y301Y	47.8	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.13-11.57	0.00	0.717
CCR1	3	46245645	chr3_46245645_G_A	A	G	exonic	intron	CCR1:p.L54L	51.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245897	chr3_46245897_A_G	G	A	intronic	intron	-	39.7	NA	NA	0	1110	0	2944	1.000	0.00	0.00-Inf	0	1136	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245372	chr3_46245372_G_T	T	G	exonic	synonymous	CCR1:p.R145R	50.5	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0	7074	1.000	0.00	0.00-Inf	0.322	3.14	0.33-30.19	0.00	0.733
CCR1	3	46249787	chr3_46249787_A_G	G	A	UTR5	regulatory	-	65.4	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245473	chr3_46245473_C_T	T	C	exonic	intron	CCR1:p.G111E	50.6	0.108107	0.76538	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245546	chr3_46245546_G_A	A	G	exonic	missense	CCR1:p.L87F	50.8	0.112913	0.75846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245371	rs1213578557	T	C	exonic	intron	CCR1:p.R145Q	50.5	0.125817	0.74462	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46245378	rs368420597	A	G	exonic	missense	CCR1:p.R143W	50.5	0.193804	0.65385	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR1	3	46249864	rs1314075555	A	G	upstream	regulatory	-	65.4	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.924	0.90	0.10-8.13	0.00	0.549
CCR1	3	46245548	rs200700185	A	G	exonic	intron	CCR1:p.T86M	51	0.336949	0.51077	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307386	rs756281359	T	C	exonic	missense	CCR3:p.A267V	46.9	0.005948	0.99692	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR3	3	46283862	chr3_46283862_T_C	C	T	upstream	regulatory	-	49.9	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CCR3	3	46307432	rs939772784	T	C	exonic	synonymous	CCR3:p.L282L	46.9	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306940	chr3_46306940_T_A	A	T	exonic	missense	CCR3:p.H118Q	46.9	0.003683	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46283878	rs1336673814	T	G	UTR5	regulatory	-	50.1	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.623	1.67	0.22-12.95	0.00	0.713
CCR3	3	46306696	chr3_46306696_A_G	G	A	exonic	missense	CCR3:p.Y37C	46.1	0.164837	0.68692	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307756	rs774783220	A	G	UTR3	3_prime_UTR	-	38.1	NA	NA	0	1164	0	2970	1.000	0.00	0.00-Inf	0	1210	0	7074	1.000	0.00	0.00-Inf	0.340	3.86	0.24-61.75	0.00	0.769
CCR3	3	46283903	rs200506062	A	G	UTR5	regulatory	-	50.2	NA	NA	0.001575	1270	0	3014	0.088	4.75	0.45-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.158	4.89	0.54-44.32	0.00	0.406
CCR3	3	46307586	rs777668503	T	C	exonic	missense	CCR3:p.R334C	46.6	0.010008	0.98538	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46284039	rs201804545	C	G	intronic	regulatory	-	49.6	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307031	chr3_46307031_A_T	T	A	exonic	missense	CCR3:p.T149S	46.9	0.04721	0.88769	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000424	7074	0.488	1.83	0.03-22.79	0.504	1.95	0.27-13.86	0.00	0.910
CCR3	3	46307700	chr3_46307700_C_T	T	C	exonic	missense	CCR3:p.L372F	44.8	0.007629	0.99077	0	1258	0.000332	3010	1.000	0.00	0.00-93.18	0	1282	0	7074	1.000	0.00	0.00-Inf	0.665	1.73	0.14-20.63	0.00	0.454
CCR3	3	46307525	chr3_46307525_C_T	T	C	exonic	synonymous	CCR3:p.S313S	46.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306653	chr3_46306653_A_C	C	A	exonic	missense	CCR3:p.T23P	45.6	0.07865	0.81615	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000778	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307487	rs1265344373	A	G	exonic	missense	CCR3:p.D301N	46.8	0.050145	0.88231	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306902	rs201980677	A	G	exonic	missense	CCR3:p.V106I	47	0.004442	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307752	rs773365222	G	C	UTR3	3_prime_UTR	-	38.9	NA	NA	0	1184	0	2978	1.000	0.00	0.00-Inf	0	1220	0.000141	7074	1.000	0.00	0.00-225.34	0.546	2.15	0.18-25.62	0.00	0.919
CCR3	3	46307472	rs41276535	T	C	exonic	missense	CCR3:p.R296W	46.8	0.066221	0.84	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CCR3	3	46305808	chr3_46305808_G_T	T	G	intronic	regulatory	-	43.3	NA	NA	0	1264	0.000332	3010	1.000	0.00	0.00-92.74	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306822	rs760043296	A	T	exonic	missense	CCR3:p.I79N	47	0.047972	0.88538	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR3	3	46307367	rs761492821	T	C	exonic	missense	CCR3:p.L261F	46.9	0.029569	0.93846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CCR3	3	46307442	rs1289458889	A	C	exonic	missense	CCR3:p.Q286K	46.8	0.031989	0.93077	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CCR3	3	46307471	rs753893797	A	G	exonic	synonymous	CCR3:p.E295E	46.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR3	3	46307261	chr3_46307261_C_T	T	C	exonic	synonymous	CCR3:p.T225T	46.9	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307677	rs777044791	T	C	exonic	missense	CCR3:p.S364F	45.7	0.075711	0.82385	0.00158	1266	0.00166	3012	1.000	0.95	0.09-5.82	0	1288	0.002827	7074	0.060	0.00	0.00-1.11	0.447	0.58	0.14-2.38	28.67	0.236
CCR3	3	46284038	rs778498603	T	C	intronic	regulatory	-	49.6	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307211	chr3_46307211_C_T	T	C	exonic	missense	CCR3:p.P209S	46.8	0.02849	0.94	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR3	3	46307519	rs775542097	T	C	exonic	synonymous	CCR3:p.A311A	46.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CCR3	3	46305958	rs541912550	G	A	intronic	regulatory	-	44	NA	NA	0.000796	1256	0.000664	3014	1.000	1.20	0.02-23.07	0	1280	0.001696	7074	0.234	0.00	0.00-1.99	0.572	0.59	0.09-3.68	0.00	0.371
CCR3	3	46283870	rs984801958	G	A	upstream	regulatory	-	50	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46305950	rs903813800	T	C	intronic	regulatory	-	44.6	NA	NA	0	1264	0	3012	1.000	0.00	0.00-Inf	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307449	rs41515745	A	T	exonic	missense	CCR3:p.I288N	46.8	0.016805	0.97154	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306870	rs1371298356	G	T	exonic	missense	CCR3:p.L95R	46.9	0.080069	0.81231	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CCR3	3	46307033	rs570345529	G	A	exonic	synonymous	CCR3:p.T149T	46.9	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307089	rs61738836	C	T	exonic	missense	CCR3:p.V168A	46.9	0.03295	0.92538	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46307083	rs199999286	A	G	exonic	missense	CCR3:p.R166Q	46.9	0.043137	0.89462	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR3	3	46305952	chr3_46305952_T_C	C	T	intronic	regulatory	-	44.4	NA	NA	0	1262	0	3014	1.000	0.00	0.00-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306928	chr3_46306928_T_C	C	T	exonic	synonymous	CCR3:p.Y114Y	46.9	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR3	3	46306765	rs5742906	T	C	exonic	missense	CCR3:p.P60L	46.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CCR3	3	46283975	rs200200535	T	C	UTR5	regulatory	-	50.3	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0	7074	1.000	0.00	0.00-Inf	0.322	3.14	0.33-30.19	0.00	0.733
CCR3	3	46283902	rs184254690	T	C	UTR5	regulatory	-	50.2	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR3	3	46307620	rs768953812	C	T	exonic	missense	CCR3:p.L345P	46.4	0.036195	0.91462	0.001575	1270	0.001327	3014	1.000	1.19	0.11-8.30	0.00155	1290	0.002262	7074	1.000	0.68	0.08-2.92	0.801	0.87	0.29-2.64	0.00	0.632
CCR3	3	46307364	rs367876385	T	C	exonic	missense	CCR3:p.R260W	46.9	0.151397	0.70692	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.10	0.00	0.333
CCR3	3	46307379	chr3_46307379_A_G	G	A	exonic	missense	CCR3:p.I265V	46.9	0.009537	0.98538	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415209	chr3_46415209_T_A	A	T	exonic	regulatory	CCR5:p.S272S	49.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
CCR5	3	46415348	rs374959868	T	C	exonic	regulatory	CCR5:p.R319C	48.9	0.013967	0.97769	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CCR5	3	46414560	rs1459619557	A	T	exonic	regulatory	CCR5:p.I56K	47.6	0.030385	0.93462	0.000787	1270	0.000995	3014	1.000	0.79	0.02-9.86	0	1290	0	7074	1.000	0.00	0.00-Inf	0.803	1.28	0.18-9.12	0.00	0.402
CCR5	3	46414498	rs113471490	A	G	exonic	regulatory	CCR5:p.P35P	47.6	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.566	0.54	0.07-4.43	0.00	0.908
CCR5	3	46415447	rs1312722843	C	T	exonic	regulatory	CCR5:p.L352L	48.2	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415207	rs761483454	C	T	exonic	regulatory	CCR5:p.S272P	49.3	0.078931	0.81615	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.737	1.41	0.19-10.71	0.00	0.592
CCR5	3	46414470	rs189601230	G	A	exonic	regulatory	CCR5:p.K26R	47.9	0.005183	0.99846	0.001575	1270	0.002654	3014	0.733	0.59	0.06-2.98	0.003101	1290	0.001696	7074	0.293	1.83	0.43-6.05	0.650	1.24	0.50-3.09	24.48	0.250
CCR5	3	46415199	rs184279915	T	G	exonic	intron,non_coding	CCR5:p.C269F	49.3	0.033771	0.92231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR5	3	46414940	rs1281371966	T	C	exonic	regulatory	CCR5:p.P183S	48.3	0.014551	0.97615	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR5	3	46414925	rs199824195	C	T	exonic	regulatory	CCR5:p.C178R	49.1	0.098506	0.78308	0.00315	1270	0.002986	3014	1.000	1.05	0.24-3.79	0	1290	0	7074	1.000	0.00	0.00-Inf	0.741	1.21	0.39-3.74	0.00	0.430
CCR5	3	46415273	chr3_46415273_C_T	T	C	exonic	regulatory	CCR5:p.P294S	49.2	0.261782	0.58769	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46414436	rs200209014	C	T	exonic	regulatory	CCR5:p.Y15H	47.4	0.00634	0.99462	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.955	0.94	0.10-8.50	0.00	0.885
CCR5	3	46415394	rs764318467	A	G	exonic	regulatory	CCR5:p.R334Q	48.7	0.037835	0.91	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.924	0.90	0.10-8.13	0.00	0.549
CCR5	3	46415151	rs748818705	C	T	exonic	missense	CCR5:p.I253T	49.3	0.077761	0.81846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.655	0.61	0.07-5.25	0.00	0.834
CCR5	3	46415269	rs1392690733	T	C	exonic	regulatory	CCR5:p.I292I	49.2	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415067	chr3_46415067_G_T	T	G	exonic	missense	CCR5:p.R225L	49.1	0.034413	0.92154	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415060	rs200419576	T	C	exonic	intron,non_coding	CCR5:p.R223W	48.3	0.034994	0.91846	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.566	0.54	0.07-4.43	0.00	0.908
CCR5	3	46415014	chr3_46415014_G_T	T	G	exonic	synonymous	CCR5:p.L207L	48.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415415	rs751446924	A	G	exonic	regulatory	CCR5:p.R341Q	48.6	0.010331	0.98538	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46414922	rs777849486	T	A	exonic	regulatory	CCR5:p.T177S	48	0.009354	0.98615	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

CCR5	3	46414564	chr3 46414564 C T	T	C	exonic	regulatory	CCR5:p.N57N	47.6	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415255	rs150592242	G	A	exonic	regulatory	CCR5:p.T288A	49.3	0.011559	0.98308	0.000787	1270	0.000664	3014	1.000	1.19	0.02-22.82	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.739	1.39	0.20-9.46	0.00	0.833
CCR5	3	46415131	rs771408105	T	C	exonic	synonymous	CCR5:p.L246L	49.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415349	rs369373756	A	G	exonic	regulatory	CCR5:p.R319H	48.9	0.005125	0.99846	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.500	0.49	0.06-3.96	0.00	0.982
CCR5	3	46414852	rs574865763	T	G	exonic	regulatory	CCR5:p.W153C	49.1	0.279848	0.56692	0.001575	1270	0.002322	3014	1.000	0.68	0.07-3.57	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.785	0.82	0.20-3.37	0.00	0.586
CCR5	3	46414784	rs34418657	A	G	exonic	regulatory	CCR5:p.V131I	48.1	0.021061	0.96385	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.830	1.25	0.17-9.31	0.00	0.508
CCR5	3	46414926	chr3 46414926 G A	A	G	exonic	regulatory	CCR5:p.C178Y	48.2	0.045271	0.89	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46414538	rs1450402163	G	A	exonic	regulatory	CCR5:p.M49V	47.6	0.003158	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46414543	chr3 46414543 G A	A	G	exonic	regulatory	CCR5:p.L50L	47.6	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR5	3	46415400	rs765009973	T	G	exonic	regulatory	CCR5:p.S336I	48.9	0.027172	0.94385	0.002362	1270	0.001659	3014	0.701	1.42	0.22-7.34	0.000775	1290	0.001131	7074	1.000	0.69	0.02-5.12	0.844	1.13	0.35-3.66	0.00	0.570
CCR6	6	167550195	rs41510645	C	A	exonic	regulatory	CCR6:p.R159S	52.1	0.012295	0.98	0.000787	1270	0.000664	3014	1.000	1.19	0.02-22.82	0.000775	1290	0.001131	7074	1.000	0.69	0.02-5.12	0.859	0.87	0.18-4.18	0.00	0.735
CCR6	6	167549617	rs201769708	A	C	UTR5	5 prime UTR	-	63	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.267	3.61	0.38-34.70	0.00	0.556
CCR6	6	167550202	rs555430497	T	C	exonic	missense	CCR6:p.P162S	51.9	0.004721	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR6	6	167525398	chr6 167525398 C T	T	C	UTR5	regulatory	-	64.8	NA	NA	0.001575	1270	0	3014	0.088	4.75	0.45-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.019	13.87	1.53-125.54	0.00	0.885
CCR6	6	167549536	rs3093008	G	A	UTR5	5 prime UTR	-	62.6	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.039	10.83	1.13-104.14	0.00	0.717
CCR6	6	167549925	rs185551935	A	C	exonic	regulatory	CCR6:p.I69I	72.3	NA	NA	0	1270	0.000995	3014	0.560	0.00	0.00-5.74	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.784	0.74	0.08-6.49	0.00	0.449
CCR6	6	167550168	rs767267986	A	G	exonic	regulatory	CCR6:p.A150A	51.9	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CCR6	6	167549528	chr6 167549528 T C	C	T	UTR5	splice,5 prime UTI	-	62.5	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167550807	rs749935898	T	C	exonic	synonymous	CCR6:p.T363T	50.5	NA	NA	0	1268	0	3012	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.71	0.00	0.767
CCR6	6	167550790	rs188414355	T	C	exonic	regulatory	CCR6:p.R358W	51	0.047706	0.88769	0	1268	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.353	2.64	0.34-20.44	0.00	0.951
CCR6	6	167550808	rs145112098	A	G	exonic	non coding exon	CCR6:p.A364T	50.5	0.009638	0.98538	0	1268	0	3010	1.000	0.00	0.00-Inf	0.000776	1288	0	7074	0.154	5.50	0.14-Inf	0.109	7.59	0.64-90.62	0.00	0.453
CCR6	6	167549811	rs746424070	G	T	exonic	regulatory	CCR6:p.S31S	72.1	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CCR6	6	167525451	rs181845376	C	G	UTR5	regulatory	-	65.2	NA	NA	0.000787	1270	0.000995	3014	1.000	0.79	0.02-9.86	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.652	0.66	0.11-3.95	0.00	0.805
CCR6	6	167549695	chr6 167549695 C T	T	C	intronic	intron,non coding	-	64.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167550589	rs545727839	A	G	exonic	missense	CCR6:p.E291K	51.8	0.003151	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR6	6	167549537	chr6 167549537 C G	G	C	UTR5	non coding exon	-	62.6	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167549597	rs776702941	G	A	UTR5	5 prime UTR	-	62.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.567	1.75	0.26-11.97	0.00	0.542
CCR6	6	167550565	chr6 167550565 A G	G	A	exonic	missense	CCR6:p.K283E	51.8	0.018683	0.96846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167525342	chr6 167525342 G C	C	G	UTR5	regulatory	-	62.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167549432	chr6 167549432 G A	A	G	intronic	intron,non coding	-	50.5	NA	NA	0.000843	1186	0	2980	0.285	2.51	0.06-Inf	0	1214	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167550758	chr6 167550758 C G	G	C	exonic	regulatory	CCR6:p.S347C	51.5	0.010824	0.98385	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167550332	rs1359373359	T	C	exonic	missense	CCR6:p.S205L	51.9	0.005775	0.99692	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167525302	chr6 167525302 G A	A	G	UTR5	regulatory	-	45	NA	NA	0	1264	0	3008	1.000	0.00	0.00-Inf	0.00078	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR6	6	167549694	rs775830961	G	A	intronic	intron	-	64.9	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR7	17	38711815	rs187022118	C	G	exonic	missense	CCR7:p.L106V	47.9	0.00848	0.98846	0.004724	1270	0.002986	3014	0.400	1.58	0.46-5.00	0.003882	1288	0.004806	7074	0.825	0.81	0.25-2.08	0.798	1.10	0.55-2.20	0.00	0.344
CCR7	17	38715210	rs1183888660	T	C	intronic	intron	-	42	NA	NA	0	1266	0.000333	3002	1.000	0.00	0.00-92.35	0.000779	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38711222	rs2229095	C	T	exonic	regulatory	CCR7:p.Q303Q	48.5	NA	NA	0.01102	1270	0.009622	3014	0.737	1.15	0.56-2.25	0.01008	1290	0.014984	7074	0.201	0.67	0.34-1.20	0.467	0.85	0.55-1.31	33.14	0.221
CCR7	17	38715268	rs996657496	A	G	intronic	intron	-	33.3	NA	NA	0	1188	0.000343	2918	1.000	0.00	0.00-95.65	0.000833	1200	0.001414	7074	1.000	0.59	0.01-4.15	0.624	0.65	0.11-3.66	0.00	0.866
CCR7	17	38711270	chr17 38711270 C A	A	C	exonic	regulatory	CCR7:p.T287T	46.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38721710	rs756086011	A	G	UTR5	regulatory	-	50	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38711481	chr17 38711481 A G	G	A	exonic	regulatory	CCR7:p.V217A	43.8	0.004768	0.99846	0	1244	0.000665	3006	1.000	0.00	0.00-12.87	0	1272	0	7074	1.000	0.00	0.00-Inf	0.878	1.21	0.11-13.32	0.00	0.334
CCR7	17	38711893	rs778119660	T	C	exonic	missense	CCR7:p.V80M	47.9	0.038327	0.90769	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38721709	rs200743644	T	C	UTR5	regulatory	-	50	NA	NA	0.00315	1270	0.000332	3014	0.029	9.52	0.94-467.78	0	1290	0.001555	7074	0.234	0.00	0.00-2.18	0.325	2.39	0.42-13.53	75.46	0.044
CCR7	17	38711665	rs760286309	T	C	exonic	missense	CCR7:p.V156M	44.2	0.013669	0.97846	0.000795	1258	0.000332	3008	0.503	2.39	0.03-187.56	0.000789	1268	0	7074	0.152	5.58	0.14-Inf	0.111	5.51	0.68-44.79	0.00	0.368
CCR7	17	38711482	rs771518819	T	C	exonic	regulatory	CCR7:p.V217M	43.8	0.010028	0.98538	0.000801	1248	0	3006	0.293	2.41	0.06-Inf	0	1268	0	7074	1.000	0.00	0.00-Inf	0.138	6.52	0.55-77.79	0.00	0.920
CCR7	17	38715238	chr17 38715238 G A	A	G	intronic	intron	-	39.2	NA	NA	0.000796	1256	0	2994	0.296	2.39	0.06-Inf	0	1270	0	7074	1.000	0.00	0.00-Inf	0.140	6.47	0.54-77.26	0.00	0.923
CCR7	17	38715102	rs3136689	A	G	intronic	intron	-	41.3	NA	NA	0.009494	1264	0.008661	3002	0.858	1.10	0.50-2.26	0.007031	1280	0.00933	7074	0.520	0.75	0.33-1.52	0.710	0.91	0.56-1.49	0.00	0.450
CCR7	17	38721676	rs764612700	A	G	UTR5	regulatory	-	49.8	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38711182	rs200720683	T	C	exonic	missense	CCR7:p.V317I	46.5	0.006846	0.99385	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38715263	chr17 38715263 G A	A	G	intronic	intron	-	34.6	NA	NA	0	1208	0.00034	2938	1.000	0.00	0.00-94.71	0	1206	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38721802	rs1479661854	A	C	upstream	regulatory	-	54.2	NA	NA	0.001582	1264	0	2994	0.088	4.74	0.44-Inf	0.000781	1280	0.000707	7074	1.000	1.11	0.02-9.89	0.319	2.44	0.42-14.08	36.03	0.211
CCR7	17	38715067	rs557078450	T	C	intronic	intron	-	36.4	NA	NA	0.008885	1238	0.006069	2966	0.312	1.47	0.62-3.29	0.003968	1260	0.007068	7074	0.259	0.56	0.17-1.40	0.994	1.00	0.56-1.79	60.38	0.112
CCR7	17	38711894	rs114428166	C	G	exonic	synonymous	CCR7:p.V79V	48.1	NA	NA	0	1270	0.001327	3014	0.326	0.00	0.00-3.60	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.334	0.36	0.05-2.84	0.00	0.761
CCR7	17	38710991	rs372376814	T	C	UTR3	regulatory	-	37.3	NA	NA	0.000803	1246	0	2986	0.294	2.40	0.06-Inf	0	1268	0	7074	1.000	0.00	0.00-Inf	0.139	6.50	0.54-77.55	0.00	0.921
CCR7	17	38715084	chr17 38715084 C A	A	C	intronic	intron	-	38.9	NA	NA	0	1260	0	2994	1.000	0.00	0.00-Inf	0.00078	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38721760	rs11574661	A	G	upstream	regulatory	-	49.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CCR7	17	38712044	rs140039442	T	C	exonic	synonymous	CCR7:p.T29T	47.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.267	3.61	0.38-34.70	42.11	0.189
CCR7	17	38715185	rs111607645	G	A	exonic	missense	CCR7:p.M7T	42.9	0.011831	0.98231	0	1268	0	3014	1.000	0.00	0.00-Inf	0	1288	0.000141	7074	1.000	0.00	0.00-213.49	0.575	2.03	0.17-24.25	0.00	0.919
CCR7	17	38711291	rs754971665	G	A	exonic	regulatory	CCR7:p.N280N	46.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38715060	chr17 38715060 C A	A	C	intronic	intron	-	35	NA	NA	0.000821	1218	0.000676	2960	1.000	1.22	0.02-23.37	0	1238	0.000424	7074	1.000	0.00	0.00-13.83	0.969	1.04	0.16-6.70	0.00	0.838
CCR7	17	38711405	rs751684156	G	A	exonic	regulatory	CCR7:p.C242C	46.1	NA	NA	0.000789	1268	0.000332	3014	0.505	2.38	0.03-186.46	0.000776	1288	0.000707	7074	1.000	1.10	0.02-9.83	0.658	1.47	0.27-8.02	0.00	0.666
CCR7	17	38711920	rs375638802	T	C	exonic	missense	CCR7:p.V71M	48	0.012712	0.97923	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCR7	17	38712118	chr17 38712118 T C	C	T	intronic	intron	-	45	NA	NA	0	1256	0.000668	2996	1.000	0.00	0.00-12.71	0	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38721554	rs1343791765	G	A	intronic	regulatory	-	45	NA	NA	0	1254	0.000332	3008	1.000	0.00	0.00-93.42	0	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38715186	rs2228015	C	T	exonic	missense	CCR7:p.M7V	43	NA	NA	0.000787	1270	0.001995	3008	0.682	0.39	0.01-3.26	0.001553	1288	0.002262	7074	1.000	0.69	0.08-2.92	0.366	0.57	0.17-1.92	0.00	0.674
CCR7	17	38711107	chr17 38711107 T C	C	T	exonic	missense	CCR7:p.K342E	44.9	0.039243	0.90385	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38712111	chr17 38712111 G A	A	G	intronic	intron	-	45.7	NA	NA	0	1264	0	2998	1.000	0.00	0.00-Inf	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38715178	rs193282140	A	G	exonic	synonymous	CCR7:p.S9S	43.6	NA	NA	0.006299	1270	0.008976	3008	0.459	0.70	0.27-1.59	0.007776	1286	0.006927	7074	0.717	1.12	0.51-2.25	0.746	0.92	0.55-1.54	0.00	0.375
CCR7	17	38711031	chr17 38711031 C T	T	C	exonic	missense	CCR7:p.S367N	41.7	0.027378	0.94308	0.000789	1268	0	3010	0.296	2.38	0.06-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38712116	rs751950812	C	G	intronic	intron	-	45.3	NA	NA	0	1256	0	2996	1.000	0.00	0.00-Inf	0	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38711623	rs575312747	A	G	exonic	missense	CCR7:p.R170C	43.6	0.041629	0.89769	0.000794	1260	0	3008	0.295	2.39	0.06-Inf	0	1270	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR7	17	38711323	rs145153052	T	C	exonic	regulatory	CCR7:p.V270M	46.8	0.014446	0.97615	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR9	3	45942529	rs191809380	T	C	exonic	upstream	CCR9:p.T83T	48.2	NA	NA	0.001575	1270	0	3014	0.088	4.75	0.45-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.074	8.89	0.81-98.08	0.00	0.760
CCR9	3	45943371	chr3 45943371 C T	T	C	exonic	missense	CCR9:p.S364L	47.6	0.069684	0.83231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45943278	chr3 45943278 A G	G	A	exonic	missense	CCR9:p.K333R	48.2	0.005151	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45943351	chr3 45943351 T C	C	T	exonic	synonymous	CCR9:p.S357S	47.9	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR9	3	45943318	rs200106483	A	T	exonic	missense	CCR9:p.F346L	48.4	0.004304	0.99846	0	1270	0.001991	3014	0.189	0.00	0.00-2.01	0.00155	1290	0.000283	7074	0.115	5.49	0.40-75.66	0.451	1.86	0.37-9.42	72.80	0.055
CCR9	3	45942963	chr3 45942963 T C	C	T	exonic	missense	CCR9:p.V228A	48.2	0.007206	0.99231	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CCR9	3	45943394	rs753720491	A	G	UTR3	3 prime UTR	-	46.9	NA	NA	0	1266	0.000332	3012	1.000	0.00	0.00-92.65	0.000778	1286	0.000424	7074	0.487	1.83	0.03-22.86	0.729	1.39	0.22-8.80	0.00	0.675
CCR9	3	45943358	rs766123355	T	C	exonic	synonymous	CCR9:p.L360L	47.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.353	2.64	0.34-20.43	0.00	0.951
CCR9	3	45928136	rs1407616439	A	T	UTR5	regulatory	-	41.1	NA	NA	0.00079	1266	0.000333	3000	0.506	2.37	0.03-185.88	0	1282	0	7074	1.000	0.00	0.00-Inf	0.322	3.14	0.33-30.22	0.00	0.730
CCR9	3	45943249	rs199573914	G	A	exonic	synonymous	CCR9:p.R323R	48.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45943348	rs201669237	A	G	exonic	synonymous	CCR9:p.S356S	47.9	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CCR9	3	45943256	rs751139030	T	C	exonic	missense	CCR9:p.R326W	48.2	0.064403	0.84692	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45942460	rs769563630	T	C	exonic	synonymous	CCR9:p.I60I	48.1	0.012598	0.97923	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCR9	3	45943120	rs201673015	T	C	exonic	synonymous	CCR9:p.D280D	48.4	NA	NA	0	1270	0.000995	3014	0.560	0.00	0.00-5.74	0	1290	0	7074	1.000	0.00	0.00-Inf	0.954	0.93	0.09-9.91	18.89	0.267
CCR9	3	45943047	rs149823113	T	C	exonic	upstream	CCR9:p.T256I	48.6	0.002704	0.99846	0.000787	1270	0.000995	3014	1.000	0.79	0.02-9.86	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.676	1.42	0.27-7.37	0.00	0.460
CCR9	3	45936405	chr3 45936405 C T	T	C	UTR5	intron	-	47.3	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.482	2.12	0.26-17.26	0.00	0.903
CCR9	3	45942704	rs199541347	A	G	exonic	missense	CCR9:p.V142M	48.3	0.010384	0.98462	0.003937	1270	0.001327	3014	0.136	2.97	0.64-15.01	0	1290	0.001414	7074	0.378	0.00	0.00-2.45	0.280	1.93	0.59-6.38	57.02	0.127
CCR9	3	45942551	rs56325097	A	G	exonic	missense	CCR9:p.A91T	48.2	0.056301	0.86462	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.00099	7074	1.000	0.78	0.02-6.10	0.998	1.00	0.16-6.36	0.00	0.625
CCR9	3	45942608	rs56064700	A	G	exonic	missense	CCR9:p.D110N	50	NA	NA	0.0126	1270	0.005309	3014	0.018	2.39	1.12-5.12	0.007752	1290	0.010885	7074	0.371	0.71	0.33-1.38	0.340	1.26	0.78-2.04	83.72	0.013
CCR9	3	45942329	chr3 45942329 T C	C	T	exonic	regulatory	CCR9:p.Y17H	47.5	0.048802	0.88462	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

CCR9	3	45942956	chr3 45942956 C T	T	C	exonic	upstream	CCR9:p.P226S	48.3	0.050736	0.88077	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45942421	rs372974725	A	G	exonic	intron	CCR9:p.A47A	48	0.005286	0.99846	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45928052	rs191514046	T	C	UTR5	regulatory	-	40.8	NA	NA	0.004739	1266	0.003014	2986	0.402	1.58	0.46-4.97	0	1286	0.00099	7074	0.605	0.00	0.00-3.82	0.565	1.33	0.50-3.52	0.00	0.348
CCR9	3	45943073	rs200611238	G	T	exonic	intron	CCR9:p.L265V	48.5	0.008667	0.98846	0.000787	1270	0.000995	3014	1.000	0.79	0.02-9.86	0.00155	1290	0.000848	7074	0.356	1.83	0.18-10.24	0.627	1.38	0.37-5.11	0.00	0.553
CCR9	3	45943253	rs200417769	T	C	exonic	intron	CCR9:p.R325C	48.3	0.09706	0.78615	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45942566	rs200200496	A	C	exonic	missense	CCR9:p.L96I	48.3	0.019178	0.96846	0.000787	1270	0.000664	3014	1.000	1.19	0.02-22.82	0.00155	1290	0	7074	0.024	10.98	1.03-Inf	0.151	3.97	0.60-26.14	60.45	0.112
CCR9	3	45928138	rs41289608	A	G	UTR5	regulatory	-	41	NA	NA	0	1266	0.000334	2994	1.000	0.00	0.00-92.10	0	1280	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.451
CCR9	3	45942893	rs201973846	A	G	exonic	upstream	CCR9:p.D205N	48.3	0.009056	0.98692	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45943113	chr3 45943113 C A	A	C	exonic	intron	CCR9:p.T278N	48.3	0.021485	0.96077	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCR9	3	45943130	rs12721497	G	A	exonic	upstream	CCR9:p.M284V	49.4	NA	NA	0.003937	1270	0.001327	3014	0.136	2.97	0.64-15.01	0.004651	1290	0.004524	7074	1.000	1.03	0.35-2.50	0.342	1.42	0.69-2.95	42.38	0.188
CCR9	3	45942524	rs759011726	G	A	exonic	missense	CCR9:p.M82V	48.1	0.026958	0.94385	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CCRL2	3	46449684	chr3 46449684 C A	A	C	exonic	regulatory	CCRL2:p.A50A	49	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450333	rs757568035	G	A	exonic	regulatory	CCRL2:p.N267D	54	0.04337	0.89308	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.732	0.69	0.08-5.93	0.00	0.906
CCRL2	3	46448832	rs540361762	T	C	UTR5	regulatory	-	45.6	NA	NA	0	1268	0	3012	1.000	0.00	0.00-Inf	0.000776	1288	0	7074	0.154	5.50	0.14-Inf	0.109	7.59	0.64-90.65	0.00	0.453
CCRL2	3	46450596	rs146961841	T	C	exonic	regulatory	CCRL2:p.T354T	50.1	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449896	rs556407644	A	T	exonic	regulatory	CCRL2:p.L121Q	49.9	0.057329	0.86308	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0.00155	1290	0.000707	7074	0.295	2.20	0.21-13.42	0.550	1.55	0.37-6.58	0.00	0.384
CCRL2	3	46449923	rs749278347	T	C	exonic	regulatory	CCRL2:p.T130I	49.9	0.016926	0.97154	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.353	2.64	0.34-20.43	0.00	0.951
CCRL2	3	46449906	chr3 46449906 G C	C	G	exonic	regulatory	CCRL2:p.V124V	49.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449107	chr3 46449107 G A	A	G	UTR5	regulatory	-	47.8	NA	NA	0	1268	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.353	2.64	0.34-20.44	0.00	0.951
CCRL2	3	46449864	rs6808835	T	G	exonic	regulatory	CCRL2:p.G110G	49.8	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.765	0.72	0.08-6.17	0.00	0.702
CCRL2	3	46450034	rs1232278210	T	C	exonic	regulatory	CCRL2:p.A167V	162.5	0.02668	0.94385	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.573	1.80	0.23-13.97	26.57	0.243
CCRL2	3	46448821	rs569537650	A	G	UTR5	regulatory	-	45.4	NA	NA	0	1268	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.23	0.00	0.919
CCRL2	3	46449560	rs762524534	A	G	exonic	regulatory	CCRL2:p.G9D	43.3	0.024739	0.94923	0	1232	0.000335	2982	1.000	0.00	0.00-94.26	0	1256	0.000141	7074	1.000	0.00	0.00-218.91	0.858	1.23	0.13-11.83	0.00	0.715
CCRL2	3	46448970	rs1487259446	T	C	UTR5	regulatory	-	46.5	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1282	0	7074	1.000	0.00	0.00-Inf	0.668	1.72	0.14-20.55	0.00	0.452
CCRL2	3	46450394	rs560371668	A	G	exonic	regulatory	CCRL2:p.S287N	53.9	0.013917	0.97769	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450151	rs770117283	T	C	exonic	regulatory	CCRL2:p.T206I	58.4	0.036785	0.91308	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.648	1.65	0.19-14.12	31.48	0.227
CCRL2	3	46449103	chr3 46449103 C T	T	C	intronic	regulatory	-	47.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCRL2	3	46449857	chr3 46449857 A G	G	A	exonic	regulatory	CCRL2:p.H108R	49.4	0.014184	0.97769	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCRL2	3	46449811	rs377346921	A	G	exonic	regulatory	CCRL2:p.A93T	49.3	0.037245	0.91231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCRL2	3	46450453	chr3 46450453 A C	C	A	exonic	regulatory	CCRL2:p.I307L	52.4	0.007768	0.99	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449146	rs754865498	C	T	UTR5	regulatory	-	48.2	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449519	chr3 46449519 C T	T	C	intronic	regulatory	-	36.8	NA	NA	0	1112	0	2928	1.000	0.00	0.00-Inf	0.000868	1152	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450072	rs6441977	A	G	exonic	regulatory	CCRL2:p.V180M	58.7	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.765	0.72	0.08-6.17	0.00	0.702
CCRL2	3	46450607	chr3 46450607 C T	T	C	UTR3	regulatory	-	49.4	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449863	rs111863112	A	G	exonic	regulatory	CCRL2:p.G110E	49.6	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCRL2	3	46449513	chr3 46449513 A T	T	A	intronic	regulatory	-	35.6	NA	NA	0.000917	1090	0	2912	0.272	2.67	0.07-Inf	0	1110	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450591	chr3 46450591 T C	C	T	exonic	regulatory	CCRL2:p.S353P	50.2	0.015234	0.97538	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000424	7074	0.488	1.83	0.03-22.79	0.504	1.95	0.27-13.86	0.00	0.910
CCRL2	3	46450619	rs751640350	G	A	UTR3	regulatory	-	48.5	NA	NA	0	1258	0.001329	3010	0.327	0.00	0.00-3.62	0.000786	1272	0.000424	7074	0.484	1.85	0.04-23.11	0.903	0.89	0.15-5.36	5.86	0.303
CCRL2	3	46449289	rs770202632	T	C	intronic	regulatory	-	39.7	NA	NA	0	1152	0.000338	2962	1.000	0.00	0.00-100.12	0	1166	0.000141	7074	1.000	0.00	0.00-235.74	0.812	1.32	0.14-12.66	0.00	0.710
CCRL2	3	46450326	rs557325885	A	G	exonic	regulatory	CCRL2:p.A264A	54	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
CCRL2	3	46450336	rs746011785	G	A	exonic	regulatory	CCRL2:p.I268V	54	0.021203	0.96308	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450205	rs1175561646	T	C	exonic	regulatory	CCRL2:p.P224L	58.4	0.096294	0.78615	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CCRL2	3	46449932	rs770582861	G	A	exonic	regulatory	CCRL2:p.N133S	50.3	0.015631	0.97462	0	1270	0.002986	3014	0.066	0.00	0.00-1.20	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.408	0.41	0.05-3.41	33.83	0.219
CCRL2	3	46449072	chr3 46449072 C T	T	C	intronic	regulatory	-	47.2	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.454
CCRL2	3	46449672	chr3 46449672 G A	A	G	exonic	regulatory	CCRL2:p.Q46Q	48.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCRL2	3	46449269	chr3 46449269 G A	A	G	intronic	regulatory	-	44.4	NA	NA	0	1238	0.000334	2998	1.000	0.00	0.00-94.31	0	1264	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449996	chr3 46449996 G A	A	G	exonic	regulatory	CCRL2:p.R154R	162.4	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCRL2	3	46450586	rs184378837	G	A	exonic	regulatory	CCRL2:p.D351G	50.8	0.010161	0.98538	0.002362	1270	0.002324	3012	1.000	1.02	0.17-4.46	0.000776	1288	0.004382	7074	0.051	0.18	0.00-1.06	0.347	0.58	0.19-1.79	50.71	0.154
CCRL2	3	46450185	chr3 46450185 C G	G	C	exonic	regulatory	CCRL2:p.N217K	58.4	0.106462	0.76923	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449142	rs1296950838	A	C	UTR5	regulatory	-	48.2	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.728	1.40	0.21-9.19	0.00	0.374
CCRL2	3	46448963	rs541643583	T	C	UTR5	regulatory	-	46.6	NA	NA	0	1260	0	3014	1.000	0.00	0.00-Inf	0.000781	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450076	rs755804337	C	T	exonic	regulatory	CCRL2:p.V181A	58.5	0.050899	0.88077	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CCRL2	3	46449520	chr3 46449520 A G	G	A	intronic	regulatory	-	37.1	NA	NA	0	1126	0.000339	2946	1.000	0.00	0.00-101.88	0	1164	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46448920	rs1203835808	T	C	UTR5	regulatory	-	46.7	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.454
CCRL2	3	46448820	rs765805906	T	C	UTR5	regulatory	-	45.3	NA	NA	0	1268	0.000332	3012	1.000	0.00	0.00-92.51	0	1288	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.453
CCRL2	3	46448908	rs573204763	A	G	UTR5	regulatory	-	46.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CCRL2	3	46450071	rs369593534	T	C	exonic	regulatory	CCRL2:p.F179F	58.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CCRL2	3	46450046	chr3 46450046 C T	T	C	exonic	regulatory	CCRL2:p.A171V	162.4	0.028209	0.94077	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46450429	rs145501356	A	C	exonic	regulatory	CCRL2:p.L299I	53.9	0.015459	0.97538	0.009449	1270	0.005309	3014	0.146	1.79	0.77-4.04	0.01008	1290	0.008906	7074	0.634	1.13	0.57-2.09	0.206	1.35	0.85-2.16	0.00	0.353
CCRL2	3	46449723	rs778301112	T	C	exonic	regulatory	CCRL2:p.I63I	49.2	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449018	chr3 46449018 G C	C	G	intronic	regulatory	-	46	NA	NA	0	1264	0.000332	3010	1.000	0.00	0.00-92.74	0	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCRL2	3	46449834	chr3 46449834 G T	T	G	exonic	regulatory	CCRL2:p.L100F	49.4	0.039249	0.90385	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CX3CR1	3	39307494	rs149456270	A	C	exonic	missense	CX3CR1:p.K201N	47.4	0.022223	0.95769	0	1270	0.000995	3014	0.560	0.00	0.00-5.74	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.850	1.20	0.19-7.74	13.45	0.282
CX3CR1	3	39307587	rs758302878	A	C	exonic	missense	CX3CR1:p.M170I	47.7	0.016616	0.97308	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.651	0.61	0.07-5.11	0.00	0.817
CX3CR1	3	39323221	rs146251729	T	C	UTR5	regulatory	-	51.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CX3CR1	3	39307146	rs1173177338	G	A	exonic	synonymous	CX3CR1:p.H317H	46.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307785	chr3 39307785 G A	A	G	exonic	synonymous	CX3CR1:p.N104N	47.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307830	chr3 39307830 G A	A	G	exonic	synonymous	CX3CR1:p.T89T	47.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39308028	chr3 39308028 C T	T	C	intronic	intron	-	44.4	NA	NA	0	1252	0	2996	1.000	0.00	0.00-Inf	0	1258	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39323150	rs780911224	G	A	exonic	regulatory	CX3CR1:p.L13L	48.8	NA	NA	0.000787	1270	0.000664	3014	1.000	1.19	0.02-22.82	0	1290	0.000848	7074	0.599	0.00	0.00-4.66	0.787	0.78	0.12-4.90	0.00	0.588
CX3CR1	3	39307922	rs200139865	T	C	exonic	missense	CX3CR1:p.V59M	47.6	0.050424	0.88077	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307667	rs757198893	T	C	exonic	missense	CX3CR1:p.G144S	47.7	0.01881	0.96846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CX3CR1	3	39307933	rs750523600	G	A	exonic	missense	CX3CR1:p.I55T	47.6	0.027755	0.94154	0.000787	1270	0.000995	3014	1.000	0.79	0.02-9.86	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.962	1.05	0.16-6.64	0.00	0.676
CX3CR1	3	39307297	chr3 39307297 A G	G	A	exonic	missense	CX3CR1:p.L267P	47.5	0.048076	0.88538	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39323332	rs908648673	T	C	upstream	regulatory	-	37.7	NA	NA	0	1192	0.000346	2890	1.000	0.00	0.00-94.42	0	1200	0.000283	7074	1.000	0.00	0.00-31.42	0.989	0.99	0.11-8.92	0.00	0.867
CX3CR1	3	39307690	chr3 39307690 A C	C	A	exonic	missense	CX3CR1:p.F136C	47.7	0.016276	0.97385	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307962	rs41535248	A	C	exonic	missense	CX3CR1:p.E45D	47.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
CX3CR1	3	39323333	rs761713089	A	G	upstream	regulatory	-	37.7	NA	NA	0	1192	0.000347	2882	1.000	0.00	0.00-94.16	0	1202	0	7074	1.000	0.00	0.00-Inf	0.647	1.78	0.15-21.30	0.00	0.441
CX3CR1	3	39307832	rs199811198	C	T	exonic	missense	CX3CR1:p.T89A	47.8	0.007071	0.99308	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39323282	rs958914498	T	C	upstream	regulatory	-	47	NA	NA	0.00079	1266	0.000335	2984	0.507	2.36	0.03-184.89	0	1280	0	7074	1.000	0.00	0.00-Inf	0.323	3.13	0.33-30.13	0.00	0.728
CX3CR1	3	39323071	rs764402346	T	C	intronic	regulatory	-	39.5	NA	NA	0	1192	0.000337	2964	1.000	0.00	0.00-96.83	0	1232	0.000141	7074	1.000	0.00	0.00-223.16	0.842	1.26	0.13-12.11	0.00	0.717
CX3CR1	3	39307229	rs765564346	A	G	exonic	missense	CX3CR1:p.L290F	52.8	0.01154	0.98308	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0.001131	7074	0.618	0.00	0.00-3.21	0.370	0.39	0.05-3.09	0.00	0.856
CX3CR1	3	39307705	rs777824021	C	T	exonic	missense	CX3CR1:p.N131S	48.3	0.036127	0.91462	0	1270	0.001327	3014	0.326	0.00	0.00-3.60	0.000775	1290	0.000424	7074	0.488	1.83	0.03-22.79	0.893	0.88	0.15-5.29	5.28	0.304
CX3CR1	3	39307666	rs201442030	G	C	exonic	missense	CX3CR1:p.G144A	48.7	0.014771	0.97615	0.004724	1270	0.003981	3014	0.797	1.19	0.36-3.43	0.003876	1290	0.004806	7074	0.825	0.81	0.25-2.08	0.930	0.97	0.49-1.91	0.00	0.576
CX3CR1	3	39323115	chr3 39323115 C A	A	C	exonic	regulatory	CX3CR1:p.W24C	47.1	0.010452	0.98462	0.000789	1268	0	3004	0.297	2.37	0.06-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307472	rs868320190	T	C	exonic	missense	CX3CR1:p.G209S	47.3	0.003528	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307803	rs548178853	A	G	exonic	synonymous	CX3CR1:p.T98T	47.8	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.00155	1290	0	7074	0.024	10.98	1.03-Inf	0.147	5.11	0.56-46.31	59.72	0.115
CX3CR1	3	39323216	rs374777325	T	C	UTR5	regulatory	-	51.5	NA	NA	0.000787	1270	0.000332	3010	0.505	2.37	0.03-185.92	0.002326	1290	0.002403	7074	1.000	0.97	0.18-3.35	0.842	1.12	0.36-3.45	0.00	0.562
CX3CR1	3	39323167	rs187806548	A	G	exonic	regulatory	CX3CR1:p.A7V	51.5	0.003182	0.99846	0.000787	1270	0	3012	0.297	2.37	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.54	0.00	0.919
CX3CR1	3	39307784	rs776227760	A	G	exonic	synonymous	CX3CR1:p.L105L	47.8	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39323113	rs779788631	G	C	exonic	regulatory	CX3CR1:p.R25T	47	0.004764	0.99846	0	1268	0.000333	3000	1.000	0.00	0.00-92.14	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CX3CR1	3	39307682	rs535968351	T	C	exonic	missense	CX3CR1:p.A139T	47.7	0.015634	0.97462	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919

CXCL1	4	74735503	rs190901425	T	A	exonic	regulatory	CXCL1:p.E73V	47.3	0.044453	0.89154	0	1266	0	3012	1.000	0.00	0.00-Inf	0	1282	0.000141	7074	1.000	0.00	0.00-214.48	0.574	2.04	0.17-24.33	0.00	0.921
CXCL1	4	74735058	chr4_74735058_G_A	A	G	upstream	regulatory	-	37.5	NA	NA	0	1254	0	2932	1.000	0.00	0.00-Inf	0	1256	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735075	chr4_74735075_C_G	G	C	upstream	regulatory	-	38.7	NA	NA	0	1258	0	2954	1.000	0.00	0.00-Inf	0.000785	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735517	rs763506829	T	C	intronic	regulatory	-	47.4	NA	NA	0	1266	0.000997	3010	0.560	0.00	0.00-5.76	0	1274	0	7074	1.000	0.00	0.00-Inf	0.957	0.94	0.09-9.97	19.51	0.265
CXCL1	4	74735181	chr4_74735181_G_A	A	G	UTR5	regulatory	-	41.4	NA	NA	0	1244	0	2960	1.000	0.00	0.00-Inf	0.000796	1256	0.000141	7074	0.279	5.64	0.07-440.81	0.212	4.23	0.44-40.66	0.00	0.725
CXCL1	4	74735618	chr4_74735618_T_G	G	T	intronic	regulatory	-	48.4	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735566	rs375620205	T	C	intronic	regulatory	-	48	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0.000781	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735674	chr4_74735674_A_T	T	A	exonic	regulatory	CXCL1:p.I92I	48.4	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735294	rs199755915	C	A	intronic	regulatory	-	34.9	NA	NA	0	1150	0.00104	2884	0.563	0.00	0.00-6.07	0.000865	1156	0.000283	7074	0.365	3.06	0.05-58.87	0.778	1.31	0.20-8.45	17.80	0.270
CXCL1	4	74736268	chr4_74736268_G_A	A	G	UTR3	regulatory	-	52.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735137	rs1240344258	T	C	UTR5	regulatory	-	42.1	NA	NA	0	1254	0	2984	1.000	0.00	0.00-Inf	0	1274	0	7074	1.000	0.00	0.00-Inf	0.362	3.63	0.23-58.12	0.00	0.765
CXCL1	4	74735026	rs555081880	G	A	upstream	regulatory	-	34.7	NA	NA	0.002451	1224	0.002427	2884	1.000	1.01	0.17-4.43	0.002431	1234	0.002262	7074	0.755	1.08	0.20-3.76	0.925	1.04	0.42-2.60	0.00	0.947
CXCL1	4	74735319	rs746567439	C	G	intronic	regulatory	-	36.4	NA	NA	0	1214	0	2904	1.000	0.00	0.00-Inf	0	1196	0	7074	1.000	0.00	0.00-Inf	0.349	3.76	0.24-60.14	0.00	0.749
CXCL1	4	74735609	chr4_74735609_C_T	T	C	intronic	regulatory	-	48.4	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735519	rs559470228	T	G	intronic	regulatory	-	47.5	NA	NA	0.002377	1262	0.000665	3008	0.157	3.58	0.41-42.91	0.000783	1278	0.001272	7074	1.000	0.61	0.01-4.44	0.451	1.68	0.43-6.51	37.33	0.207
CXCL1	4	74736180	rs56078309	A	G	intronic	regulatory	-	51.8	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0.00155	1290	0.000141	7074	0.064	10.98	0.57-645.17	0.217	3.28	0.50-21.57	60.48	0.112
CXCL1	4	74735790	rs1294354786	G	A	intronic	regulatory	-	35.9	NA	NA	0	1074	0.000339	2950	1.000	0.00	0.00-106.95	0	1140	0	7074	1.000	0.00	0.00-Inf	0.593	1.97	0.16-23.49	0.00	0.459
CXCL1	4	74735444	rs769691514	T	C	exonic	regulatory	CXCL1:p.H53H	46.4	NA	NA	0	1262	0	3012	1.000	0.00	0.00-Inf	0.00078	1282	0.000283	7074	0.393	2.76	0.05-53.02	0.350	2.65	0.34-20.56	0.00	0.950
CXCL1	4	74735601	rs201005012	T	C	intronic	regulatory	-	48.4	NA	NA	0	1270	0.001327	3014	0.326	0.00	0.00-3.60	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.620	1.73	0.20-14.93	71.40	0.061
CXCL1	4	74735131	rs202228146	A	C	UTR5	regulatory	-	42.1	NA	NA	0.001595	1254	0.001004	2988	0.636	1.59	0.13-13.89	0	1272	0	7074	1.000	0.00	0.00-Inf	0.414	1.97	0.39-10.06	0.00	0.569
CXCL1	4	74736193	chr4_74736193_A_G	G	A	intronic	regulatory	-	52.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74736355	chr4_74736355_G_A	A	G	UTR3	regulatory	-	46.9	NA	NA	0	1228	0	2988	1.000	0.00	0.00-Inf	0.00079	1266	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735478	rs201878466	T	C	exonic	regulatory	CXCL1:p.P65S	47.1	0.008351	0.98923	0.000792	1262	0	3012	0.295	2.39	0.06-Inf	0	1280	0	7074	1.000	0.00	0.00-Inf	0.140	6.46	0.54-77.07	0.00	0.920
CXCL1	4	74735689	rs759232302	G	C	exonic	regulatory	CXCL1:p.I97M	48.1	0.014896	0.97615	0.000787	1270	0	3012	0.297	2.37	0.06-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.267	3.61	0.37-34.69	0.00	0.556
CXCL1	4	74735215	chr4_74735215_C_T	T	C	exonic	regulatory	CXCL1:p.P10S	39.2	0.00292	0.99846	0	1208	0.000338	2956	1.000	0.00	0.00-95.29	0	1212	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735332	rs374842435	A	G	intronic	regulatory	-	37.9	NA	NA	0	1234	0.00034	2942	1.000	0.00	0.00-92.85	0.001631	1226	0.000283	7074	0.107	5.78	0.42-79.61	0.155	3.36	0.63-17.90	6.83	0.300
CXCL1	4	74735579	chr4_74735579_C_T	T	C	intronic	regulatory	-	48.1	NA	NA	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735550	rs769188173	T	C	intronic	regulatory	-	47.8	NA	NA	0	1266	0.000664	3014	1.000	0.00	0.00-12.68	0	1280	0	7074	1.000	0.00	0.00-Inf	0.885	1.19	0.11-13.17	0.00	0.332
CXCL1	4	74736256	rs373235955	C	A	UTR3	regulatory	-	52.4	NA	NA	0.001575	1270	0	3014	0.088	4.75	0.45-Inf	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.317	2.95	0.35-24.61	36.63	0.209
CXCL1	4	74736267	rs568899629	A	G	UTR3	regulatory	-	52.4	NA	NA	0.000787	1270	0.001991	3014	0.682	0.40	0.01-3.26	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.331	0.43	0.08-2.37	0.00	0.899
CXCL1	4	74735238	rs201090116	G	A	exonic	regulatory	CXCL1:p.R17R	37	NA	NA	0.000845	1184	0.002409	2906	0.452	0.35	0.01-2.73	0	1176	0.001272	7074	0.625	0.00	0.00-3.05	0.207	0.34	0.06-1.83	0.00	0.955
CXCL1	4	74735068	rs116120548	G	C	upstream	regulatory	-	38.3	NA	NA	0.007154	1258	0.009196	2936	0.587	0.78	0.32-1.71	0.005529	1266	0.007492	7074	0.588	0.74	0.28-1.63	0.318	0.76	0.44-1.31	0.00	0.925
CXCL1	4	74735378	rs1336020337	C	T	intronic	regulatory	-	43	NA	NA	0.000795	1258	0	2990	0.296	2.38	0.06-Inf	0	1270	0	7074	1.000	0.00	0.00-Inf	0.140	6.46	0.54-77.12	0.00	0.924
CXCL1	4	74735493	chr4_74735493_G_T	T	G	exonic	regulatory	CXCL1:p.A70S	47.3	0.00884	0.98769	0	1266	0.000332	3014	1.000	0.00	0.00-92.72	0	1282	0.000283	7074	1.000	0.00	0.00-29.39	0.959	0.94	0.10-8.54	0.00	0.884
CXCL1	4	74735592	chr4_74735592_C_T	T	C	intronic	regulatory	-	48.3	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74736291	chr4_74736291_G_A	A	G	UTR3	regulatory	-	52	NA	NA	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735006	chr4_74735006_G_C	C	G	upstream	regulatory	-	32.7	NA	NA	0	1192	0.000347	2886	1.000	0.00	0.00-94.29	0	1202	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74735265	rs199791199	G	A	exonic	regulatory	CXCL1:p.V26V	34.7	NA	NA	0	1176	0.000343	2912	1.000	0.00	0.00-96.43	0	1162	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL1	4	74736305	chr4_74736305_C_T	T	C	UTR3	regulatory	-	51.6	NA	NA	0	1268	0	3012	1.000	0.00	0.00-Inf	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL10	4	76942953	chr4_76942953_C_A	A	C	UTR3	3_prime_UTR	-	39.5	NA	NA	0	1176	0.000337	2972	1.000	0.00	0.00-98.41	0	1230	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL10	4	76943942	chr4_76943942_A_G	G	A	exonic	intron	CXCL10:p.C30C	48	NA	NA	0	1264	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	0.000141	7074	0.284	5.50	0.07-429.89	0.217	4.16	0.43-40.01	0.00	0.733
CXCL10	4	76943857	rs756286152	T	G	exonic	missense	CXCL10:p.R59S	48.7	0.012536	0.98	0.000791	1264	0.000332	3014	0.504	2.39	0.03-187.05	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.112	5.46	0.67-44.39	0.00	0.371
CXCL10	4	76944641	chr4_76944641_G_A	A	G	UTR5	regulatory	-	50.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL10	4	76944631	rs765381166	G	A	UTR5	regulatory	-	50.4	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL10	4	76942966	rs1175655613	A	T	UTR3	3_prime_UTR	-	42.4	NA	NA	0.000817	1224	0.000334	2994	0.496	2.45	0.03-191.87	0.00159	1258	0.000283	7074	0.111	5.63	0.41-77.60	0.076	4.26	0.86-21.14	0.00	0.631
CXCL10	4	76942967	chr4_76942967_G_A	A	G	UTR3	intron	-	42.6	NA	NA	0	1222	0	2978	1.000	0.00	0.00-Inf	0	1262	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL10	4	76943561	rs755610178	A	G	exonic	intron	CXCL10:p.S79L	50.3	0.039041	0.90538	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.955	0.94	0.10-8.50	0.00	0.885
CXCL10	4	76943015	chr4_76943015_G_A	A	G	UTR3	intron	-	47.9	NA	NA	0	1268	0.000332	3010	1.000	0.00	0.00-92.45	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL10	4	76943046	rs542690649	G	C	UTR3	3_prime_UTR	-	49.5	NA	NA	0	1270	0.00166	3012	0.331	0.00	0.00-2.59	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL11	4	76957127	rs763762627	A	C	exonic	regulatory	CXCL11:p.G5V	67	0.015815	0.97385	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.454
CXCL11	4	76956449	rs766851546	T	C	exonic	regulatory	CXCL11:p.G36G	94.8	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL11	4	76955970	chr4_76955970_C_G	G	C	splicing	downstream	-	59.4	NA	NA	0	1244	0	3014	1.000	0.00	0.00-Inf	0	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL11	4	76956220	chr4_76956220_G_C	C	G	exonic	regulatory	CXCL11:p.Q81E	154.5	0.11097	0.76	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CXCL11	4	76956459	rs765371990	G	A	exonic	regulatory	CXCL11:p.I33T	94.8	0.005572	0.99769	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL11	4	76956378	rs780866387	G	A	exonic	regulatory	CXCL11:p.I60T	94.9	0.011911	0.98231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL11	4	76955947	rs61757197	A	T	exonic	downstream	CXCL11:p.K94X	59.7	NA	NA	0	1264	0	3014	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL11	4	76956468	rs1436351705	A	C	exonic	regulatory	CXCL11:p.C30F	94.7	0.191933	0.65615	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.267	3.61	0.37-34.68	42.13	0.189
CXCL11	4	76956271	rs763146774	C	T	exonic	regulatory	CXCL11:p.I64V	154.5	0.018075	0.97	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.732	0.69	0.08-5.93	0.00	0.906
CXCL11	4	76957080	rs749029946	A	C	exonic	regulatory	CXCL11:p.G21C	66.4	0.197274	0.65308	0	1268	0.000664	3014	1.000	0.00	0.00-12.66	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.12	0.00	0.334
CXCL11	4	76957097	chr4_76957097_C_T	T	C	exonic	regulatory	CXCL11:p.C15Y	66.7	0.003894	0.99846	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78531891	rs765631049	C	T	intronic	intron	-	43.2	NA	NA	0	1266	0.000332	3014	1.000	0.00	0.00-92.72	0	1282	0	7074	1.000	0.00	0.00-Inf	0.667	1.72	0.14-20.57	0.00	0.453
CXCL13	4	78532066	rs997310003	A	G	intronic	intron	-	36.1	NA	NA	0	1084	0.000341	2934	1.000	0.00	0.00-105.39	0	1140	0.000707	7074	1.000	0.00	0.00-6.78	0.741	0.70	0.08-5.96	0.00	0.831
CXCL13	4	78531703	rs531446649	G	T	intronic	intron	-	33.3	NA	NA	0	1160	0.000669	2990	1.000	0.00	0.00-13.73	0	1172	0	7074	1.000	0.00	0.00-Inf	0.832	1.30	0.12-14.30	0.00	0.331
CXCL13	4	78532296	rs1397356088	G	A	UTR3	3_prime_UTR	-	34.4	NA	NA	0.000906	1104	0.00034	2938	0.472	2.66	0.03-208.74	0	1136	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78532120	rs199748032	C	T	intronic	intron	-	44	NA	NA	0.002377	1262	0.004648	3012	0.425	0.51	0.09-1.83	0.00312	1282	0.001838	7074	0.316	1.70	0.40-5.51	0.987	0.99	0.43-2.29	49.34	0.160
CXCL13	4	78432857	chr4_78432857_A_G	G	A	upstream	upstream	-	39.2	NA	NA	0.000799	1252	0	3010	0.294	2.41	0.06-Inf	0	1274	0	7074	1.000	0.00	0.00-Inf	0.139	6.50	0.54-77.56	0.00	0.919
CXCL13	4	78432989	chr4_78432989_T_C	C	T	intronic	intron	-	36.9	NA	NA	0	1238	0.000335	2988	1.000	0.00	0.00-93.99	0	1238	0.000283	7074	1.000	0.00	0.00-30.45	0.976	0.97	0.11-8.76	0.00	0.876
CXCL13	4	78432901	rs183893867	T	C	upstream	upstream	-	41.5	NA	NA	0.000791	1264	0	3004	0.296	2.38	0.06-Inf	0	1278	0.000141	7074	1.000	0.00	0.00-215.15	0.265	3.63	0.38-34.88	0.00	0.558
CXCL13	4	78432953	rs1039780585	T	G	intronic	intron	-	40.4	NA	NA	0	1260	0	3012	1.000	0.00	0.00-Inf	0.000786	1272	0	7074	0.152	5.57	0.14-Inf	0.107	7.67	0.64-91.56	0.00	0.452
CXCL13	4	78432841	chr4_78432841_C_T	T	C	upstream	upstream	-	37.4	NA	NA	0	1246	0.000333	3000	1.000	0.00	0.00-93.76	0	1262	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78526933	chr4_78526933_T_G	G	T	intronic	intron	-	40.7	NA	NA	0	1256	0	3008	1.000	0.00	0.00-Inf	0	1270	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78532288	chr4_78532288_A_G	G	A	UTR3	3_prime_UTR	-	35.6	NA	NA	0	1156	0.000337	2968	1.000	0.00	0.00-99.98	0	1176	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78528775	rs764379787	A	G	intronic	intron	-	32.8	NA	NA	0	1050	0	2938	1.000	0.00	0.00-Inf	0	1082	0	7074	1.000	0.00	0.00-Inf	0.304	4.28	0.27-68.39	0.00	0.764
CXCL13	4	78527038	rs1446341803	A	T	exonic	missense	CXCL13:p.S7T	43.5	0.004731	0.99846	0	1268	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.59	0.64-90.59	0.00	0.454
CXCL13	4	78531897	rs368899779	T	G	intronic	intron	-	42.9	NA	NA	0.002381	1260	0.003324	3008	0.767	0.72	0.13-2.79	0.000781	1280	0.001272	7074	1.000	0.61	0.01-4.44	0.499	0.69	0.23-2.05	0.00	0.902
CXCL13	4	78528928	rs371680233	T	C	exonic	missense	CXCL13:p.R46C	45.7	0.00771	0.99	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.10	0.00	0.333
CXCL13	4	78527003	rs748252694	T	C	UTR5	5_prime_UTR	-	43.8	NA	NA	0	1264	0.000332	3014	1.000	0.00	0.00-92.86	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78532082	chr4_78532082_A_C	C	A	intronic	intron	-	39.2	NA	NA	0	1188	0.000335	2988	1.000	0.00	0.00-97.94	0	1232	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78528969	chr4_78528969_T_G	G	T	exonic	synonymous	CXCL13:p.G59G	45.1	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL13	4	78531812	rs115525661	T	C	exonic	missense	CXCL13:p.A81V	44.8	0.006413	0.99462	0.001575	1270	0.000995	3014	0.637	1.58	0.13-13.83	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.857	1.15	0.25-5.27	0.00	0.506
CXCL13	4	78529030	chr4_78529030_A_G	G	A	intronic	intron	-	39	NA	NA	0	1170	0	2964	1.000	0.00	0.00-Inf	0	1194	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638743	rs1403253124	A	G	exonic	downstream	CXCL16:p.P140L	42	0.006945	0.99308	0.000799	1252	0	2994	0.295	2.39	0.06-Inf	0	1268	0	7074	1.000	0.00	0.00-Inf	0.139	6.49	0.54-77.45	0.00	0.922
CXCL16	17	4638618	chr17_4638618_C_T	T	C	exonic	missense	CXCL16:p.E182K	59.8	0.00742	0.99154	0	1266	0	3006	1.000	0.00	0.00-Inf	0.000776	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4642136	rs200171443	T	C	exonic	regulatory	CXCL16:p.Q72Q	53	NA	NA	0	1270	0	3012	1.000	0.00	0.00-Inf	0.000775	1290	0.000707	7074	1.000	1.10	0.02-9.81	0.778	1.31	0.20-8.62	0.00	0.735
CXCL16	17	4638785	rs201243416	A	G	exonic	downstream	CXCL16:p.S126L	38.3	0.003956	0.99846	0.003284	1218	0.002363	2962	0.740	1.39	0.30-5.48	0.00081	1234	0.001555	7074	1.000	0.52	0.01-3.59	0.897	1.07	0.37-3.08	0.00	0.420
CXCL16	17	4641666	chr17_4641666_T_C	C	T	intronic	regulatory	-	42.2	NA	NA	0.000791	1264	0	3006	0.296	2.38	0.06-Inf	0	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4641999	chr17_4641999_T_C	C	T	intronic	regulatory	-	40.5	NA	NA	0.000838	1194	0.000674	2968	1.000	1.24	0.02-23.90	0	1226	0.00099	7074	0.604	0.00	0.00-4.00	0.776	0.77	0.12-4.82	0.00	0.538
CXCL16	17	4638427	rs758471159	T	C	exonic	downstream	CXCL16:p.L245L	44	NA	NA	0.000787	1270	0.000332	3008	0.506	2.37	0.03-185.79	0	1284	0.000424	7074	1.000	0.00	0.00-13.34	0.736	1.42	0.19-10.73	0.00	0.594
CXCL16	17	4641811	chr17_4641811_C_G	G	C	intronic	regulatory	-	43.7	NA	NA	0	1256	0.000334	2992	1.000	0.00	0.00-92.77	0	1266	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638713	rs1327594547	A	G	exonic	downstream	CXCL16:p.S150F	55.6	0.013706	0.97846	0.000799	1252	0	2998	0.295	2.40	0.06-Inf	0	1270	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4641994	chr17_4641994_C_T	T	C	intronic	regulatory	-	39.3	NA	NA	0	1156	0.00034	2944	1.000	0.00	0.00-99.17	0	1196	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638580	chr17_4638580_C_G	G	C	exonic	downstream	CXCL16:p.A194A	60.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

CXCL16	17	4638377	rs1245448303	C	T	intronic	downstream	-	38.4	NA	NA	0	1254	0.000335	2982	1.000	0.00	0.00-92.61	0	1260	0.000565	7074	1.000	0.00	0.00-8.51	0.741	0.70	0.08-6.02	0.00	0.914
CXCL16	17	4638744	rs1342445224	T	G	exonic	downstream	CXCL16:p.P140T	41.9	0.002007	0.99923	0.000799	1252	0.000334	2992	0.503	2.39	0.03-187.46	0	1270	0	7074	1.000	0.00	0.00-Inf	0.318	3.17	0.33-30.48	0.00	0.730
CXCL16	17	4637947	rs1402966715	C	T	exonic	upstream	CXCL16:p.D259G	40.1	0.003249	0.99846	0	1252	0	2988	1.000	0.00	0.00-Inf	0	1260	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4642195	rs545491433	G	C	exonic	regulatory	CXCL16:p.V53L	51.3	0.008525	0.98846	0	1268	0.000664	3012	1.000	0.00	0.00-12.65	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.11	0.00	0.334
CXCL16	17	4638360	rs548855958	C	G	intronic	downstream	-	35.3	NA	NA	0	1216	0	2962	1.000	0.00	0.00-Inf	0	1224	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4642237	rs752937120	A	G	intronic	regulatory	-	42.2	NA	NA	0	1254	0.002004	2994	0.189	0.00	0.00-2.03	0	1274	0	7074	1.000	0.00	0.00-Inf	0.671	0.60	0.06-6.15	47.09	0.169
CXCL16	17	4638401	rs754219984	A	G	exonic	downstream	CXCL16:p.P254L	42	0.003435	0.99846	0	1266	0.000334	2998	1.000	0.00	0.00-92.22	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638474	rs147630160	A	G	exonic	missense	CXCL16:p.L230F	46.5	0.040408	0.9	0.006309	1268	0.004316	3012	0.472	1.46	0.52-3.82	0.004658	1288	0.008623	7074	0.174	0.54	0.19-1.24	0.644	0.87	0.47-1.59	61.41	0.107
CXCL16	17	4642051	rs1269660062	C	G	intronic	regulatory	-	47.3	NA	NA	0	1264	0.000333	3006	1.000	0.00	0.00-92.62	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638652	rs747829747	A	G	exonic	downstream	CXCL16:p.P170P	58.4	NA	NA	0	1266	0.000999	3004	0.560	0.00	0.00-5.74	0.000783	1278	0.000424	7074	0.485	1.85	0.04-23.00	0.990	0.99	0.16-5.97	0.00	0.373
CXCL16	17	4637915	chr17 4637915 C T	T	C	exonic	missense	CXCL16:p.D270N	41.8	0.008524	0.98846	0	1264	0	3008	1.000	0.00	0.00-Inf	0	1270	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4641815	chr17 4641815 G A	A	G	intronic	regulatory	-	43	NA	NA	0	1252	0	2988	1.000	0.00	0.00-Inf	0	1262	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4641801	rs760611199	G	C	intronic	regulatory	-	45.4	NA	NA	0	1264	0.000332	3008	1.000	0.00	0.00-92.68	0	1274	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638608	rs756282432	T	C	exonic	downstream	CXCL16:p.R185H	60.1	0.002029	0.99923	0	1268	0	3010	1.000	0.00	0.00-Inf	0.000776	1288	0.000424	7074	0.488	1.83	0.03-22.83	0.503	1.95	0.28-13.88	0.00	0.911
CXCL16	17	4638530	rs61463072	C	G	exonic	downstream	CXCL16:p.P211R	88.9	0.00559	0.99769	0	1268	0.00365	3014	0.041	0.00	0.00-0.95	0.000775	1290	0.002403	7074	0.341	0.32	0.01-2.06	0.070	0.22	0.04-1.13	0.00	0.520
CXCL16	17	4641850	chr17 4641850 C G	G	C	intronic	regulatory	-	37	NA	NA	0.000895	1118	0	2932	0.276	2.62	0.07-Inf	0	1162	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4642148	chr17 4642148 C A	A	C	exonic	regulatory	CXCL16:p.P68P	52.9	NA	NA	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4642134	rs142895776	T	A	exonic	regulatory	CXCL16:p.F73Y	53.1	0.001993	0.99923	0	1270	0.001659	3014	0.330	0.00	0.00-2.59	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.880	1.17	0.16-8.64	60.09	0.113
CXCL16	17	4638625	rs151239052	T	C	exonic	synonymous	CXCL16:p.S179S	59.5	NA	NA	0	1266	0.000332	3008	1.000	0.00	0.00-92.53	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL16	17	4638485	rs771591021	A	G	exonic	missense	CXCL16:p.P226L	88.5	0.079667	0.81385	0	1268	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964830	rs186397980	T	C	exonic	regulatory	CXCL2:p.R3H	39.7	NA	NA	0	1260	0	2956	1.000	0.00	0.00-Inf	0.000783	1278	0.000141	7074	0.283	5.54	0.07-433.25	0.217	4.16	0.43-40.00	0.00	0.726
CXCL2	4	74964590	rs1181764749	T	C	exonic	regulatory	CXCL2:p.Q50Q	45.1	NA	NA	0.00079	1266	0	3004	0.296	2.37	0.06-Inf	0	1288	0	7074	1.000	0.00	0.00-Inf	0.142	6.42	0.54-76.61	0.00	0.920
CXCL2	4	74963554	chr4 74963554 C G	G	C	intronic	regulatory	-	47.3	NA	NA	0	1266	0	3014	1.000	0.00	0.00-Inf	0.000776	1288	0	7074	0.154	5.50	0.14-Inf	0.109	7.60	0.64-90.73	0.00	0.454
CXCL2	4	74965026	rs1480151838	T	C	upstream	regulatory	-	32.7	NA	NA	0	1226	0	2920	1.000	0.00	0.00-Inf	0.000814	1228	0	7074	0.148	5.77	0.15-Inf	0.104	7.82	0.66-93.38	0.00	0.443
CXCL2	4	74964861	chr4 74964861 G A	A	G	UTR5	regulatory	-	41.5	NA	NA	0	1266	0.000335	2988	1.000	0.00	0.00-91.92	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964664	rs918287928	A	T	intronic	regulatory	-	39.9	NA	NA	0	1246	0	2934	1.000	0.00	0.00-Inf	0	1254	0.000141	7074	1.000	0.00	0.00-219.25	0.569	2.06	0.17-24.55	0.00	0.931
CXCL2	4	74964237	rs1347966646	C	T	intronic	regulatory	-	35.1	NA	NA	0	1214	0.000338	2962	1.000	0.00	0.00-95.02	0	1226	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964247	rs1309518072	C	T	intronic	regulatory	-	37.1	NA	NA	0	1230	0.000671	2980	1.000	0.00	0.00-12.91	0	1246	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964526	rs773598787	C	T	exonic	regulatory	CXCL2:p.T72A	45.8	0.003761	0.99846	0	1264	0	3012	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.60	0.64-90.68	0.00	0.454
CXCL2	4	74964836	rs770759328	G	A	exonic	regulatory	CXCL2:p.M1?	40	0.217639	0.62769	0	1256	0.001011	2966	0.559	0.00	0.00-5.72	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74965015	chr4 74965015 C T	T	C	upstream	regulatory	-	34.9	NA	NA	0	1244	0.000339	2946	1.000	0.00	0.00-92.23	0	1250	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964525	chr4 74964525 G A	A	G	exonic	regulatory	CXCL2:p.T72I	45.8	0.004915	0.99846	0	1266	0	3012	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964356	rs200989587	T	C	exonic	regulatory	CXCL2:p.S90S	45.7	NA	NA	0.000787	1270	0.00365	3014	0.125	0.22	0.00-1.48	0.000775	1290	0.000424	7074	0.488	1.83	0.03-22.79	0.459	0.56	0.12-2.57	47.02	0.169
CXCL2	4	74963600	chr4 74963600 C T	T	C	intronic	regulatory	-	41.9	NA	NA	0.000838	1194	0	2982	0.286	2.50	0.06-Inf	0	1226	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964798	rs747593102	C	G	exonic	regulatory	CXCL2:p.R14G	37.1	0.007926	0.99	0	1222	0.000689	2902	1.000	0.00	0.00-12.65	0	1238	0.00099	7074	0.604	0.00	0.00-3.97	0.417	0.42	0.05-3.39	0.00	0.917
CXCL2	4	74964625	rs142264518	C	T	exonic	regulatory	CXCL2:p.T39A	43.9	NA	NA	0	1266	0.000334	2996	1.000	0.00	0.00-92.16	0	1286	0	7074	1.000	0.00	0.00-Inf	0.670	1.71	0.14-20.47	0.00	0.452
CXCL2	4	74964847	rs1403975975	G	C	UTR5	regulatory	-	40.6	NA	NA	0.000792	1262	0	2984	0.297	2.37	0.06-Inf	0.00078	1282	0.000283	7074	0.393	2.76	0.05-53.02	0.167	3.88	0.57-26.48	0.00	0.644
CXCL2	4	74964617	chr4 74964617 C A	A	C	exonic	regulatory	CXCL2:p.L41L	44.4	NA	NA	0	1264	0.000333	3006	1.000	0.00	0.00-92.62	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74963496	rs750117850	A	G	intronic	regulatory	-	48.1	NA	NA	0	1266	0.000332	3014	1.000	0.00	0.00-92.72	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.830	0.79	0.09-6.93	0.00	0.995
CXCL2	4	74964817	rs771730846	A	G	exonic	regulatory	CXCL2:p.S7S	39	NA	NA	0	1246	0.000677	2956	1.000	0.00	0.00-12.64	0.001577	1268	0.000848	7074	0.349	1.86	0.18-10.42	0.654	1.38	0.34-5.70	0.00	0.435
CXCL2	4	74964786	chr4 74964786 C A	A	C	exonic	regulatory	CXCL2:p.V18L	35.5	0.015128	0.97538	0	1194	0.000345	2898	1.000	0.00	0.00-94.52	0	1222	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964365	chr4 74964365 G C	C	G	exonic	regulatory	CXCL2:p.N87K	45.5	0.010474	0.98462	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74963493	rs201597863	G	A	intronic	regulatory	-	48.1	NA	NA	0	1266	0.000995	3014	0.560	0.00	0.00-5.76	0	1288	0.000141	7074	1.000	0.00	0.00-213.49	0.785	0.74	0.08-6.50	0.00	0.449
CXCL2	4	74964820	chr4 74964820 G A	A	G	exonic	regulatory	CXCL2:p.L6L	39.2	NA	NA	0	1254	0	2962	1.000	0.00	0.00-Inf	0.000786	1272	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL2	4	74964797	chr4 74964797 C G	G	C	exonic	regulatory	CXCL2:p.R14P	36.9	0.009358	0.98615	0	1224	0	2924	1.000	0.00	0.00-Inf	0	1244	0	7074	1.000	0.00	0.00-Inf	0.356	3.68	0.23-58.93	0.00	0.759
CXCL2	4	74963558	rs1233800719	G	C	intronic	regulatory	-	47.1	NA	NA	0	1266	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.77	0.00	0.768
CXCL2	4	74964428	rs201352382	G	A	intronic	regulatory	-	45.7	NA	NA	0	1270	0.000995	3014	0.560	0.00	0.00-5.74	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.850	1.20	0.19-7.74	13.45	0.282
CXCL2	4	74964216	chr4 74964216 G A	A	G	intronic	regulatory	-	30.9	NA	NA	0	1074	0	2910	1.000	0.00	0.00-Inf	0.000901	1110	0	7074	0.136	6.38	0.16-Inf	0.086	8.75	0.73-104.47	0.00	0.449
CXCL2	4	74965025	rs1350572240	A	G	upstream	regulatory	-	33.1	NA	NA	0	1232	0	2920	1.000	0.00	0.00-Inf	0	1232	0.001272	7074	0.373	0.00	0.00-2.91	0.678	0.61	0.06-6.14	0.00	0.404
CXCL6	4	74702292	chr4 74702292 C T	T	C	upstream	regulatory	-	39.8	NA	NA	0.000796	1256	0	2964	0.298	2.36	0.06-Inf	0	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702473	chr4 74702473 C T	T	C	exonic	regulatory	CXCL6:p.S2S	48.3	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702625	rs41401748	C	G	intronic	regulatory	-	46.9	NA	NA	0	1256	0	3000	1.000	0.00	0.00-Inf	0	1272	0.000141	7074	1.000	0.00	0.00-216.16	0.570	2.05	0.17-24.48	0.00	0.922
CXCL6	4	74702533	rs768136002	G	C	exonic	regulatory	CXCL6:p.L22L	47.7	NA	NA	0	1262	0.000333	3006	1.000	0.00	0.00-92.76	0	1284	0.000707	7074	1.000	0.00	0.00-6.01	0.658	0.62	0.07-5.27	0.00	0.834
CXCL6	4	74702570	rs770802849	A	G	exonic	regulatory	CXCL6:p.A35T	46.4	0.022263	0.95769	0	1248	0	2990	1.000	0.00	0.00-Inf	0.00079	1266	0.000283	7074	0.390	2.80	0.05-53.69	0.345	2.68	0.35-20.77	0.00	0.948
CXCL6	4	74703355	chr4 74703355 C T	T	C	exonic	synonymous	CXCL6:p.N114N	42.3	NA	NA	0	1262	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702447	chr4 74702447 G A	A	G	UTR5	regulatory	-	48.4	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702635	chr4 74702635 G A	A	G	intronic	regulatory	-	47.4	NA	NA	0	1260	0	3002	1.000	0.00	0.00-Inf	0	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703430	rs949337617	A	C	UTR3	3 prime UTR	-	36.6	NA	NA	0	1196	0.000336	2976	1.000	0.00	0.00-96.90	0	1238	0.000141	7074	1.000	0.00	0.00-222.08	0.843	1.26	0.13-12.08	0.00	0.719
CXCL6	4	74702557	rs754627748	A	G	exonic	regulatory	CXCL6:p.P30P	46.9	NA	NA	0	1260	0.000334	2994	1.000	0.00	0.00-92.54	0	1268	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702923	chr4 74702923 C G	G	C	exonic	regulatory	CXCL6:p.A82A	49.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703262	rs1324118047	T	C	intronic	intron	-	36.4	NA	NA	0	1174	0.000334	2990	1.000	0.00	0.00-99.17	0	1226	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703322	rs749690840	C	T	intronic	intron	-	41.9	NA	NA	0	1262	0.000332	3014	1.000	0.00	0.00-93.01	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.957	0.94	0.10-8.53	0.00	0.887
CXCL6	4	74702838	chr4 74702838 C G	G	C	intronic	regulatory	-	49.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703017	chr4 74703017 T C	C	T	intronic	regulatory	-	48.4	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703028	rs925068282	T	G	intronic	regulatory	-	48.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702588	chr4 74702588 T C	C	T	intronic	regulatory	-	46.1	NA	NA	0	1250	0	2986	1.000	0.00	0.00-Inf	0	1266	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703024	chr4 74703024 T C	C	T	intronic	regulatory	-	48.2	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000778	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74703416	chr4 74703416 G C	C	G	UTR3	3 prime UTR	-	38.1	NA	NA	0	1228	0	3000	1.000	0.00	0.00-Inf	0.000794	1260	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702370	chr4 74702370 G C	C	G	upstream	regulatory	-	47.9	NA	NA	0.000787	1270	0	3010	0.297	2.37	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.51	0.00	0.920
CXCL6	4	74702360	rs543723730	G	T	upstream	regulatory	-	47.6	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.00099	7074	1.000	0.78	0.02-6.10	0.998	1.00	0.16-6.36	0.00	0.625
CXCL6	4	74702951	rs140549348	G	C	exonic	regulatory	CXCL6:p.L92V	49.2	0.009104	0.98692	0.001575	1270	0	3014	0.088	4.75	0.45-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.019	13.87	1.53-125.54	0.00	0.885
CXCL6	4	74702752	rs1253736804	G	A	exonic	regulatory	CXCL6:p.K61E	49.2	0.008527	0.98846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.567	1.75	0.26-11.97	0.00	0.542
CXCL6	4	74702639	chr4 74702639 T A	A	T	intronic	regulatory	-	47.5	NA	NA	0	1262	0.000333	3002	1.000	0.00	0.00-92.64	0	1282	0	7074	1.000	0.00	0.00-Inf	0.667	1.72	0.14-20.56	0.00	0.452
CXCL6	4	74702907	rs1334652828	C	T	intronic	regulatory	-	49.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL6	4	74702572	rs146902260	T	C	exonic	regulatory	CXCL6:p.A35A	46.3	NA	NA	0	1252	0.000335	2986	1.000	0.00	0.00-92.88	0	1268	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607690	rs751369405	C	G	exonic	regulatory	CXCL8:p.E75D	48.2	0.002278	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74606472	rs909040696	T	C	intronic	regulatory	-	45.4	NA	NA	0	1262	0.000332	3014	1.000	0.00	0.00-93.01	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607378	rs140214046	A	G	exonic	regulatory	CXCL8:p.A62T	51.2	0.010269	0.98538	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74606303	chr4 74606303 G A	A	G	UTR5	regulatory	-	41.5	NA	NA	0	1248	0.001333	3000	0.328	0.00	0.00-3.64	0	1262	0	7074	1.000	0.00	0.00-Inf	0.845	0.79	0.08-8.24	32.88	0.222
CXCL8	4	74607303	rs1229729466	G	A	exonic	regulatory	CXCL8:p.I37V	51.4	0.008365	0.98923	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607164	chr4 74607164 G A	A	G	intronic	regulatory	-	42.8	NA	NA	0	1130	0.000336	2976	1.000	0.00	0.00-102.55	0	1182	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607340	rs1422350043	C	T	exonic	regulatory	CXCL8:p.I49T	51.4	0.01963	0.96769	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CXCL8	4	74607797	rs1216823634	C	T	UTR3	regulatory	-	43.2	NA	NA	0	1224	0.000333	3004	1.000	0.00	0.00-95.57	0	1268	0	7074	1.000	0.00	0.00-Inf	0.654	1.76	0.15-21.04	0.00	0.457
CXCL8	4	74607746	rs185040023	G	A	exonic	regulatory	CXCL8:p.K94R	48	0.010045	0.98538	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1288	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.11	0.00	0.333
CXCL8	4	74608282	chr4 74608282 G A	A	G	UTR3	regulatory	-	34.2	NA	NA	0	1200	0.00034	2942	1.000	0.00	0.00-95.47	0	1234	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607331	chr4 74607331 C A	A	C	exonic	regulatory	CXCL8:p.P46H	51.4	0.014832	0.97615	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CXCL8	4	74608299	rs537113120	G	A	UTR3	regulatory	-	31.9	NA	NA	0	1162	0	2922	1.000	0.00	0.00-Inf	0	1164	0	7074	1.000	0.00	0.00-Inf	0.335	3.91	0.24-62.50	0.00	0.755
CXCL8	4	74607757	rs747439661	G	A	UTR3	regulatory	-	47.5	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1288	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.73	0.00	0.767
CXCL8	4	74607197	chr4 74607197 A G	G	A	intronic	regulatory	-	47.6	NA	NA	0	1248	0	3014	1.000	0.00	0.00-Inf	0.000784	1276	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607827	chr4 74607827 T A	A	T	UTR3	regulatory	-	36	NA	NA	0	1086	0.00034	2938	1.000	0.00	0.00-105.34	0	1124	0	7074	1.000	0.00	0.00-Inf	0.595	1.96	0.16-23.41	0.00	0.452
CXCL8	4	74607824	rs1377623448	A	C	UTR3	regulatory	-	36.3	NA	NA	0	1092	0.000342	2928	1.000	0.00	0.00-104.40	0	1140	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74607419	chr4 74607419 T C	C	T	intronic	regulatory	-	48.4	NA	NA	0	1234	0.000333	3006	1.000	0.00	0.00-94.86	0	1234	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

CXCL8	4	74606355	rs56002960	T	A	UTR5	regulatory	-	45.6	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL8	4	74606318	chr4_74606318_T_C	C	T	UTR5	regulatory	-	43.3	NA	NA	0	1260	0.00133	3008	0.327	0.00	0.00-3.62	0	1278	0	7074	1.000	0.00	0.00-Inf	0.839	0.78	0.08-8.17	32.62	0.223
CXCL9	4	76928680	rs139049627	T	G	upstream	regulatory	-	49.9	NA	NA	0.004747	1264	0.006304	3014	0.663	0.75	0.25-1.96	0.007764	1288	0.004524	7074	0.134	1.72	0.75-3.60	0.418	1.26	0.72-2.22	48.66	0.163
CXCL9	4	76927268	chr4_76927268_T_A	A	T	intronic	intron	-	52.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76927220	rs1340874065	G	A	intronic	downstream	-	50.5	NA	NA	0	1262	0	3012	1.000	0.00	0.00-Inf	0.00155	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76928514	chr4_76928514_T_C	C	T	intronic	regulatory	-	49.7	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76927338	rs773967412	C	A	exonic	downstream	CXCL9:p.F52V	52.5	0.007597	0.99077	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0.000775	1290	0.00099	7074	1.000	0.78	0.02-6.10	0.640	1.52	0.26-8.77	21.80	0.258
CXCL9	4	76924776	rs764068063	T	C	exonic	intron,non_coding	CXCL9:p.R118H	52.9	0.003384	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CXCL9	4	76927420	rs140548865	G	T	exonic	downstream	CXCL9:p.P24P	52.1	NA	NA	0	1266	0.000332	3014	1.000	0.00	0.00-92.72	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.52	0.00	0.454
CXCL9	4	76927468	chr4_76927468_A_G	G	A	intronic	upstream	-	49.1	NA	NA	0.000804	1244	0	3004	0.293	2.42	0.06-Inf	0	1260	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76927497	chr4_76927497_G_T	T	G	intronic	upstream	-	41.8	NA	NA	0.000952	1050	0	2948	0.263	2.81	0.07-Inf	0	1120	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76927213	chr4_76927213_A_G	G	A	intronic	intron	-	50	NA	NA	0	1252	0	3008	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76927430	rs1035844912	T	G	intronic	downstream	-	51.9	NA	NA	0	1266	0	3012	1.000	0.00	0.00-Inf	0.000779	1284	0	7074	0.154	5.51	0.14-Inf	0.109	7.61	0.64-90.87	0.00	0.453
CXCL9	4	76927418	rs771431360	G	A	exonic	missense	CXCL9:p.V25A	52.2	0.012747	0.97923	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.414	2.39	0.29-19.46	0.00	0.370
CXCL9	4	76924770	rs752253991	T	C	exonic	missense	CXCL9:p.R120H	52.9	0.008143	0.99	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.10	0.00	0.333
CXCL9	4	76928473	chr4_76928473_G_A	A	G	intronic	regulatory	-	47	NA	NA	0	1260	0	3012	1.000	0.00	0.00-Inf	0	1268	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76928740	chr4_76928740_C_T	T	C	upstream	regulatory	-	43.5	NA	NA	0	1188	0	2984	1.000	0.00	0.00-Inf	0	1198	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76928490	chr4_76928490_T_C	C	T	intronic	regulatory	-	48.5	NA	NA	0.000792	1262	0	3012	0.295	2.39	0.06-Inf	0	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCL9	4	76928486	chr4_76928486_C_A	A	C	intronic	regulatory	-	48.2	NA	NA	0.000791	1264	0	3012	0.296	2.38	0.06-Inf	0	1276	0	7074	1.000	0.00	0.00-Inf	0.140	6.46	0.54-77.10	0.00	0.921
CXCL9	4	76928509	rs376172940	C	T	intronic	regulatory	-	49.6	NA	NA	0	1270	0.001659	3014	0.330	0.00	0.00-2.59	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.392	0.40	0.05-3.21	0.00	0.542
CXCR2	2	218994110	chr2_218994110_C_T	T	C	intronic	regulatory	-	45.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.218	4.15	0.43-39.91	0.00	0.732
CXCR2	2	218993970	rs532891105	T	G	intronic	regulatory	-	40.9	NA	NA	0	1266	0	2974	1.000	0.00	0.00-Inf	0.000786	1272	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	219000097	rs757932890	C	T	exonic	synonymous	CXCR2:p.N191N	55.2	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CXCR2	2	218999386	rs1462122778	G	A	intronic	intron	-	48.8	NA	NA	0.00082	1220	0.000333	3006	0.494	2.47	0.03-193.27	0	1234	0	7074	1.000	0.00	0.00-Inf	0.306	3.27	0.34-31.41	0.00	0.731
CXCR2	2	218999379	rs56288225	A	G	intronic	intron	-	47.5	NA	NA	0.00084	1190	0	2986	0.285	2.51	0.06-Inf	0	1198	0	7074	1.000	0.00	0.00-Inf	0.129	6.83	0.57-81.56	0.00	0.925
CXCR2	2	218994113	chr2_218994113_C_T	T	C	intronic	regulatory	-	45.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	219000634	rs749754060	A	G	UTR3	3_prime_UTR	-	49.1	NA	NA	0.000791	1264	0	3012	0.296	2.38	0.06-Inf	0	1282	0.000141	7074	1.000	0.00	0.00-214.48	0.265	3.63	0.38-34.88	0.00	0.556
CXCR2	2	219000055	rs201960181	T	C	exonic	synonymous	CXCR2:p.A177A	55.2	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0.000775	1290	0.00099	7074	1.000	0.78	0.02-6.10	0.644	0.67	0.12-3.74	0.00	0.790
CXCR2	2	218994170	rs1233606141	T	C	intronic	regulatory	-	41.4	NA	NA	0	1228	0.000335	2982	1.000	0.00	0.00-94.57	0	1252	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218994089	rs1268294652	T	G	splicing	regulatory	-	46	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.829	0.79	0.09-6.93	0.00	0.996
CXCR2	2	219000570	rs200917361	G	T	exonic	missense	CXCR2:p.V349G	51.6	0.016478	0.97385	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000776	1288	0	7074	0.154	5.50	0.14-Inf	0.266	3.61	0.38-34.72	42.17	0.189
CXCR2	2	218990949	rs1209622886	T	C	UTR5	regulatory	-	49.5	NA	NA	0.001577	1268	0.000332	3010	0.211	4.75	0.25-280.04	0	1286	0	7074	1.000	0.00	0.00-Inf	0.126	4.95	0.64-38.34	0.00	0.950
CXCR2	2	218990923	rs1438455528	T	C	UTR5	regulatory	-	45.9	NA	NA	0	1260	0	2994	1.000	0.00	0.00-Inf	0	1258	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	219000280	rs17844699	T	C	exonic	synonymous	CXCR2:p.V252V	55	NA	NA	0.000789	1268	0.000664	3014	1.000	1.19	0.02-22.85	0.00155	1290	0.000565	7074	0.233	2.74	0.25-19.17	0.302	2.08	0.52-8.31	0.00	0.577
CXCR2	2	218999400	rs916503546	G	A	intronic	intron	-	50.9	NA	NA	0.00321	1246	0	3010	0.007	9.69	1.60-Inf	0	1268	0.001131	7074	0.616	0.00	0.00-3.27	0.371	2.54	0.33-19.57	75.36	0.044
CXCR2	2	218999369	rs746065677	T	C	intronic	intron	-	45.4	NA	NA	0.000876	1142	0.000674	2966	1.000	1.30	0.02-24.97	0.000874	1144	0.001696	7074	1.000	0.51	0.01-3.49	0.728	0.76	0.16-3.59	0.00	0.565
CXCR2	2	218989983	rs751544158	T	C	upstream	upstream	-	49.2	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CXCR2	2	219000505	chr2_219000505_G_C	C	G	exonic	missense	CXCR2:p.K327N	52	0.021124	0.96385	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218990000	rs142516344	A	G	upstream	upstream	-	50.3	NA	NA	0.007087	1270	0.00564	3014	0.667	1.26	0.49-2.99	0.008527	1290	0.008058	7074	0.866	1.06	0.50-2.05	0.630	1.13	0.68-1.88	0.00	0.744
CXCR2	2	219000628	rs756813057	T	C	UTR3	3_prime_UTR	-	49.7	NA	NA	0	1264	0.000332	3014	1.000	0.00	0.00-92.86	0	1282	0.000565	7074	1.000	0.00	0.00-8.36	0.736	0.69	0.08-5.97	0.00	0.906
CXCR2	2	218993942	rs1234937921	A	G	intronic	regulatory	-	35.1	NA	NA	0	1218	0.000351	2846	1.000	0.00	0.00-91.00	0	1230	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	219000387	rs199642674	A	G	exonic	missense	CXCR2:p.R288H	52.1	0.06925	0.83308	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.955	0.94	0.10-8.50	0.00	0.885
CXCR2	2	218990948	chr2_218990948_C_G	G	C	UTR5	regulatory	-	49.3	NA	NA	0	1268	0.000332	3008	1.000	0.00	0.00-92.39	0	1284	0.000141	7074	1.000	0.00	0.00-214.15	0.872	1.20	0.13-11.58	0.00	0.715
CXCR2	2	218999545	chr2_218999545_G_A	A	G	exonic	synonymous	CXCR2:p.E7E	54.3	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.576	2.03	0.17-24.21	0.00	0.919
CXCR2	2	218994003	rs376479157	A	C	intronic	regulatory	-	44.8	NA	NA	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.365	3.60	0.23-57.64	0.00	0.767
CXCR2	2	218999480	rs189767843	A	C	intronic	intron	-	54	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218999551	rs776173448	T	C	exonic	synonymous	CXCR2:p.D9D	54.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CXCR2	2	219000114	rs1477862706	G	A	exonic	missense	CXCR2:p.Y197C	55.2	0.030097	0.93538	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218990043	rs558264941	T	C	UTR5	upstream	-	49.6	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.732	0.69	0.08-5.93	0.00	0.906
CXCR2	2	218999815	chr2_218999815_T_C	C	T	exonic	synonymous	CXCR2:p.F97F	55.1	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	219000417	chr2_219000417_C_T	T	C	exonic	missense	CXCR2:p.A298V	52	0.007339	0.99231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218999932	rs376503094	G	A	exonic	synonymous	CXCR2:p.L136L	55.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218999659	rs183812193	T	A	exonic	missense	CXCR2:p.E45D	54.5	0.0037	0.99846	0.001575	1270	0.000332	3014	0.211	4.75	0.25-279.97	0	1290	0.001131	7074	0.618	0.00	0.00-3.21	0.637	1.56	0.25-9.77	50.03	0.157
CXCR2	2	219000405	rs2228413	A	G	exonic	missense	CXCR2:p.R294Q	52	0.005961	0.99615	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CXCR2	2	218999762	rs138773569	T	C	exonic	missense	CXCR2:p.R80C	56.3	0.012619	0.97923	0.01024	1270	0.007631	3014	0.463	1.34	0.62-2.78	0.006977	1290	0.010178	7074	0.353	0.68	0.30-1.38	0.884	0.96	0.59-1.57	46.04	0.173
CXCR2	2	219000142	chr2_219000142_C_G	G	C	exonic	missense	CXCR2:p.N206K	55.2	0.004055	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218991066	chr2_218991066_A_G	G	A	UTR5	regulatory	-	52.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218999759	rs149364972	A	G	exonic	missense	CXCR2:p.G79S	54.3	0.00267	0.99846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218990927	chr2_218990927_A_G	G	A	UTR5	regulatory	-	46.7	NA	NA	0	1260	0.000334	2998	1.000	0.00	0.00-92.66	0	1264	0.000141	7074	1.000	0.00	0.00-217.53	0.866	1.22	0.13-11.69	0.00	0.711
CXCR2	2	218991009	rs1425656484	G	A	UTR5	regulatory	-	52.9	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CXCR2	2	219000272	rs755206310	C	A	exonic	missense	CXCR2:p.M250L	55	0.028216	0.94077	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
CXCR2	2	219000460	rs45606837	T	C	exonic	synonymous	CXCR2:p.L312L	52	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.113	5.44	0.67-44.27	0.00	0.370
CXCR2	2	219000404	rs141145934	T	C	exonic	missense	CXCR2:p.R294W	52	0.014588	0.97615	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CXCR2	2	218991167	rs1429141735	G	T	intronic	regulatory	-	44.4	NA	NA	0	1208	0.000336	2978	1.000	0.00	0.00-96.00	0	1230	0.000141	7074	1.000	0.00	0.00-223.52	0.844	1.25	0.13-12.07	0.00	0.714
CXCR2	2	218999933	rs369839517	T	C	exonic	synonymous	CXCR2:p.L137L	55.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218999595	rs764550414	A	G	exonic	missense	CXCR2:p.S24N	54.3	0.008359	0.98923	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR2	2	218990114	rs554061016	A	G	intronic	upstream	-	48.8	NA	NA	0.002366	1268	0.002988	3012	1.000	0.79	0.14-3.18	0.003106	1288	0.002686	7074	0.772	1.16	0.29-3.49	0.985	0.99	0.43-2.28	0.00	0.661
CXCR2	2	218999442	chr2_218999442_T_C	C	T	intronic	intron	-	53.4	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.454
CXCR2	2	218999767	rs372364370	T	C	exonic	synonymous	CXCR2:p.S81S	55.1	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CXCR4	2	136875738	rs1418351901	G	C	upstream	regulatory	-	35.7	NA	NA	0.000807	1240	0	2954	0.296	2.38	0.06-Inf	0	1262	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136872820	chr2_136872820_C_A	A	C	exonic	regulatory	CXCR4:p.L297L	47.6	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
CXCR4	2	136875554	rs908818052	A	G	intronic	regulatory	-	40.7	NA	NA	0	1262	0.000332	3008	1.000	0.00	0.00-92.82	0.000778	1286	0.000424	7074	0.487	1.83	0.03-22.86	0.728	1.39	0.22-8.81	0.00	0.676
CXCR4	2	136875720	chr2_136875720_G_A	A	G	upstream	regulatory	-	39.7	NA	NA	0.000794	1260	0	2988	0.297	2.37	0.06-Inf	0	1288	0	7074	1.000	0.00	0.00-Inf	0.142	6.42	0.54-76.59	0.00	0.920
CXCR4	2	136872946	rs770667555	G	A	exonic	regulatory	CXCR4:p.Y255Y	47.9	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0	7074	1.000	0.00	0.00-Inf	0.322	3.14	0.33-30.19	0.00	0.733
CXCR4	2	136875523	rs1420564690	C	T	intronic	regulatory	-	33.9	NA	NA	0.000812	1232	0	2968	0.293	2.41	0.06-Inf	0	1248	0.000283	7074	1.000	0.00	0.00-30.20	0.372	2.73	0.30-24.68	0.00	0.410
CXCR4	2	136873243	rs202097184	A	G	exonic	regulatory	CXCR4:p.L156L	50.2	NA	NA	0.002362	1270	0	3014	0.026	7.14	0.98-Inf	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.032	9.21	1.22-69.76	0.00	0.592
CXCR4	2	136872427	rs767404285	C	T	UTR3	regulatory	-	45.4	NA	NA	0	1258	0.000664	3014	1.000	0.00	0.00-12.76	0	1278	0.000424	7074	1.000	0.00	0.00-13.40	0.657	0.62	0.07-5.16	0.00	0.817
CXCR4	2	136872509	chr2_136872509_G_T	T	G	exonic	regulatory	CXCR4:p.S401Y	47.3	0.02269	0.95692	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136873511	chr2_136873511_C_T	T	C	UTR5	regulatory	-	49.8	NA	NA	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136873549	rs2680880	T	A	UTR5	regulatory	-	48.5	NA	NA	0	1264	0.00166	3012	0.330	0.00	0.00-2.60	0	1284	0.001131	7074	0.617	0.00	0.00-3.23	0.201	0.27	0.03-2.02	0.00	0.846
CXCR4	2	136873128	chr2_136873128_C_T	T	C	exonic	regulatory	CXCR4:p.V128I	50.3	0.014506	0.97615	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CXCR4	2	136872497	rs748189454	T	C	exonic	regulatory	CXCR4:p.R405Q	47.2	0.028584	0.94	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136872495	rs147214773	T	C	exonic	regulatory	CXCR4:p.G406S	47.2	0.015994	0.97385	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136872410	rs17848059	T	C	UTR3	regulatory	-	42.4	NA	NA	0	1244	0.000333	3000	1.000	0.00	0.00-93.91	0	1254	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136875617	chr2_136875617_C_T	T	C	exonic	regulatory	CXCR4:p.S5N	44.2	0.019541	0.96846	0	1268	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.73	0.00	0.768
CXCR4	2	136872988	chr2_136872988_G_A	A	G	exonic	regulatory	CXCR4:p.P241P	48	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136873409	rs923351521	T	C	exonic	regulatory	CXCR4:p.R101H	50.1	0.009549	0.98538	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.10	0.00	0.333
CXCR4	2	136873203	rs755899324	T	C	exonic	regulatory	CXCR4:p.V170M	50.1	0.008761	0.98846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CXCR4	2	136872637	rs535778934	A	G	exonic	regulatory	CXCR4:p.T358T	47.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136872976	chr2_136872976_A_G	G	A	exonic	regulatory	CXCR4:p.F245F	48	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136872823	chr2_136872823_C_T	T	C	exonic	regulatory	CXCR4:p.K296K	47.7	NA	NA	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	0	7074	1.000	0.00	0.00-Inf	0.888	1.19	0.11-13.10	0.00	0.333
CXCR4	2	136873327	rs533290861	C	T	exonic	regulatory	CXCR4:p.G128G	50	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

CXCR4	2	136872971	rs1274871337	C	T	exonic	regulatory	CXCR4:p.N247S	48	0.006636	0.99385	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136875748	chr2 136875748 T C	C	T	upstream	regulatory	-	33.4	NA	NA	0	1214	0.000348	2876	1.000	0.00	0.00-92.26	0	1226	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR4	2	136872813	rs772992625	T	A	exonic	regulatory	CXCR4:p.S300T	47.7	0.021408	0.96077	0.000787	1270	0.000664	3014	1.000	1.19	0.02-22.82	0.002326	1290	0.001414	7074	0.437	1.65	0.29-6.41	0.464	1.53	0.49-4.77	0.00	0.814
CXCR4	2	136875700	chr2 136875700 G C	C	G	UTR5	regulatory	-	42.4	NA	NA	0	1264	0	3004	1.000	0.00	0.00-Inf	0	1290	0.000424	7074	1.000	0.00	0.00-13.28	0.895	1.17	0.11-12.47	0.00	0.658
CXCR4	2	136873574	rs556724652	G	A	UTR5	regulatory	-	42.4	NA	NA	0.002547	1178	0.000669	2990	0.141	3.81	0.44-45.70	0.000816	1226	0.00099	7074	1.000	0.82	0.02-6.42	0.319	2.00	0.51-7.80	15.73	0.276
CXCR4	2	136873048	chr2 136873048 C T	T	C	exonic	regulatory	CXCR4:p.L221L	48.1	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CXCR4	2	136872969	rs767830104	T	C	exonic	regulatory	CXCR4:p.V248I	47.9	0.016854	0.97154	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118754525	rs1476432605	A	G	upstream	regulatory	-	31.9	NA	NA	0	1154	0.000347	2886	1.000	0.00	0.00-97.39	0	1176	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118754646	rs199805189	G	C	UTR5	regulatory	-	45	NA	NA	0	1270	0.001328	3012	0.326	0.00	0.00-3.59	0.001553	1288	0.001414	7074	1.000	1.10	0.12-5.16	0.760	0.81	0.21-3.12	0.00	0.395
CXCR5	11	118765339	rs749744362	A	G	exonic	3 prime UTR	CXCR5:p.E362E	48.9	NA	NA	0.000789	1268	0	3012	0.296	2.38	0.06-Inf	0.000775	1290	0.000707	7074	1.000	1.10	0.02-9.81	0.459	1.96	0.33-11.67	0.00	0.341
CXCR5	11	118754662	rs552138226	A	G	exonic	regulatory	CXCR5:p.P4P	45.6	NA	NA	0	1266	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764986	rs764486324	C	T	exonic	3 prime UTR	CXCR5:p.L245L	48.1	NA	NA	0.000787	1270	0.000332	3010	0.505	2.37	0.03-185.92	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.624	1.67	0.22-12.94	0.00	0.713
CXCR5	11	118764331	rs146150938	G	C	exonic	missense	CXCR5:p.N26K	43.5	0.01144	0.98308	0	1268	0	3006	1.000	0.00	0.00-Inf	0	1280	0	7074	1.000	0.00	0.00-Inf	0.363	3.62	0.23-57.87	0.00	0.765
CXCR5	11	118764922	rs771273984	C	T	exonic	synonymous	CXCR5:p.H223H	48.1	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0.000707	7074	1.000	0.00	0.00-5.99	0.648	1.65	0.19-14.12	31.48	0.227
CXCR5	11	118764574	rs369772789	T	C	exonic	synonymous	CXCR5:p.A107A	47.3	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118765087	rs2230321	T	C	exonic	3 prime UTR	CXCR5:p.V278V	48.2	NA	NA	0.000787	1270	0.000332	3012	0.505	2.37	0.03-186.04	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.482	2.12	0.26-17.25	0.00	0.904
CXCR5	11	118765165	rs187389271	A	C	exonic	3 prime UTR	CXCR5:p.I304I	48.2	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.002326	1290	0.000283	7074	0.029	8.24	0.94-98.75	0.023	6.65	1.30-33.88	0.00	0.571
CXCR5	11	118754530	rs1163258383	T	C	upstream	regulatory	-	32.7	NA	NA	0	1170	0	2886	1.000	0.00	0.00-Inf	0	1196	0.000424	7074	1.000	0.00	0.00-14.32	0.855	1.25	0.12-13.26	0.00	0.669
CXCR5	11	118765256	rs200126792	T	C	exonic	missense	CXCR5:p.R335W	47.6	0.072305	0.82923	0.00079	1266	0	3012	0.296	2.38	0.06-Inf	0	1288	0.000707	7074	1.000	0.00	0.00-6.00	0.647	1.65	0.19-14.15	31.52	0.227
CXCR5	11	118754686	rs755089290	A	G	exonic	regulatory	CXCR5:p.E12E	45.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000424	7074	0.488	1.83	0.03-22.79	0.504	1.95	0.27-13.86	0.00	0.910
CXCR5	11	118754533	chr11 118754533 T A	A	T	upstream	regulatory	-	33.7	NA	NA	0.000838	1194	0	2926	0.290	2.45	0.06-Inf	0	1210	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764412	rs373651751	T	C	exonic	downstream	CXCR5:p.F53F	46.3	NA	NA	0	1268	0.000332	3008	1.000	0.00	0.00-92.39	0	1286	0.000848	7074	0.599	0.00	0.00-4.67	0.594	0.56	0.07-4.75	0.00	0.776
CXCR5	11	118764972	chr11 118764972 G T	T	G	exonic	3 prime UTR	CXCR5:p.G240V	48.1	0.022799	0.95615	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764461	rs112901555	A	G	exonic	downstream	CXCR5:p.V70I	46.9	0.003644	0.99846	0	1270	0.000332	3008	1.000	0.00	0.00-92.24	0.000778	1286	0.000141	7074	0.284	5.50	0.07-430.56	0.414	2.39	0.29-19.47	0.00	0.369
CXCR5	11	118764664	chr11 118764664 C T	T	C	exonic	3 prime UTR	CXCR5:p.S137S	47.3	NA	NA	0	1270	0	3012	1.000	0.00	0.00-Inf	0.000779	1284	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118754731	rs370538221	T	C	intronic	regulatory	-	45.4	NA	NA	0	1266	0.000665	3010	1.000	0.00	0.00-12.66	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.572	1.80	0.23-13.98	26.46	0.244
CXCR5	11	118764418	chr11 118764418 C A	A	C	exonic	synonymous	CXCR5:p.P55P	46.5	NA	NA	0.000787	1270	0	3008	0.297	2.37	0.06-Inf	0	1288	0.000141	7074	1.000	0.00	0.00-213.49	0.267	3.61	0.38-34.69	0.00	0.557
CXCR5	11	118764989	rs753990934	T	C	exonic	missense	CXCR5:p.R246C	48.1	0.022514	0.95692	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764590	chr11 118764590 G C	C	G	exonic	missense	CXCR5:p.V113L	47.3	0.038269	0.90846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764990	chr11 118764990 G T	T	G	exonic	3 prime UTR	CXCR5:p.R246L	48.1	0.009834	0.98538	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118754668	rs373785028	A	G	exonic	regulatory	CXCR5:p.T6T	45.7	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118765115	chr11 118765115 A C	C	A	exonic	missense	CXCR5:p.K288Q	48.3	0.045774	0.89	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CXCR5	11	118764893	chr11 118764893 G T	T	G	exonic	3 prime UTR	CXCR5:p.A214S	48	0.025013	0.94923	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764326	chr11 118764326 G A	A	G	exonic	downstream	CXCR5:p.D25N	43.2	0.00259	0.99846	0	1266	0	3002	1.000	0.00	0.00-Inf	0.000781	1280	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118765231	rs12795395	T	C	exonic	3 prime UTR	CXCR5:p.G326G	47.6	NA	NA	0	1270	0.000332	3010	1.000	0.00	0.00-92.30	0.000776	1288	0.000141	7074	0.284	5.50	0.07-429.89	0.415	2.39	0.29-19.46	0.00	0.369
CXCR5	11	118764880	rs768071139	C	A	exonic	3 prime UTR	CXCR5:p.Q209H	48.1	0.031835	0.93077	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.109	7.58	0.64-90.53	0.00	0.453
CXCR5	11	118754521	rs1252498049	T	C	upstream	regulatory	-	31.3	NA	NA	0.000877	1140	0	2868	0.284	2.52	0.06-Inf	0	1148	0	7074	1.000	0.00	0.00-Inf	0.125	6.96	0.58-83.09	0.00	0.937
CXCR5	11	118764378	chr11 118764378 A T	T	A	exonic	missense	CXCR5:p.E42V	45.7	0.0187	0.96846	0	1270	0.000332	3010	1.000	0.00	0.00-92.30	0	1286	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR5	11	118764337	rs367828442	T	C	exonic	synonymous	CXCR5:p.N28N	43.9	NA	NA	0.001577	1268	0.000332	3008	0.212	4.75	0.25-279.85	0.000781	1280	0	7074	0.153	5.53	0.14-Inf	0.040	7.45	1.09-50.88	0.00	0.540
CXCR5	11	118764712	rs745706377	T	C	exonic	3 prime UTR	CXCR5:p.H153H	47.6	NA	NA	0	1270	0	3010	1.000	0.00	0.00-Inf	0	1286	0.000283	7074	1.000	0.00	0.00-29.30	0.755	1.47	0.13-16.18	0.00	0.762
CXCR6	3	45988100	rs753227593	T	G	exonic	regulatory	CXCR6:p.V43F	47.8	0.007363	0.99231	0	1270	0	3014	1.000	0.00	0.00-Inf	0.00155	1290	0.000424	7074	0.173	3.66	0.31-32.00	0.141	3.40	0.67-17.31	0.00	0.844
CXCR6	3	45984991	rs924193069	A	G	UTR5	intron	-	32.8	NA	NA	8.00E-04	1250	0	2940	0.298	2.35	0.06-Inf	0	1254	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45989018	rs371002459	T	C	UTR3	regulatory	-	46.4	NA	NA	0	1266	0	3010	1.000	0.00	0.00-Inf	0	1284	0	7074	1.000	0.00	0.00-Inf	0.363	3.62	0.23-57.87	0.00	0.766
CXCR6	3	45988498	rs61757198	T	C	exonic	regulatory	CXCR6:p.L175L	47.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.000775	1290	0.000141	7074	0.285	5.49	0.07-429.23	0.415	2.39	0.29-19.45	0.00	0.370
CXCR6	3	45988580	chr3 45988580 C G	G	C	exonic	regulatory	CXCR6:p.P203A	47.7	0.047799	0.88692	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45989074	rs116917020	T	C	UTR3	regulatory	-	44.1	NA	NA	0.002513	1194	0.000669	2988	0.144	3.76	0.43-45.06	0	1224	0.000283	7074	1.000	0.00	0.00-30.80	0.195	2.77	0.59-12.97	0.00	0.512
CXCR6	3	45989078	chr3 45989078 C A	A	C	UTR3	regulatory	-	43.4	NA	NA	0.000849	1178	0	2972	0.284	2.53	0.06-Inf	0	1212	0.000283	7074	1.000	0.00	0.00-31.11	0.355	2.83	0.31-25.62	0.00	0.406
CXCR6	3	45988612	rs1212760681	T	C	exonic	intron	CXCR6:p.V213V	47.7	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.267	3.61	0.38-34.70	0.00	0.556
CXCR6	3	45988789	rs150362180	A	G	exonic	synonymous	CXCR6:p.V272V	47.9	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0	1290	0.000565	7074	1.000	0.00	0.00-8.31	0.830	1.25	0.17-9.31	0.00	0.508
CXCR6	3	45987980	rs2234355	A	G	exonic	regulatory	CXCR6:p.E3K	47.5	NA	NA	0.001575	1270	0.000995	3014	0.637	1.58	0.13-13.83	0.000775	1290	0.000565	7074	0.567	1.37	0.03-13.88	0.570	1.49	0.37-5.98	0.00	0.921
CXCR6	3	45987962	chr3 45987962 A C	C	A	UTR5	regulatory	-	47	NA	NA	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988979	rs753824355	A	G	exonic	regulatory	CXCR6:p.A336T	47.5	0.007172	0.99231	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.353	2.64	0.34-20.43	0.00	0.951
CXCR6	3	45988282	rs746505246	C	G	exonic	missense	CXCR6:p.K103N	47.7	0.074866	0.82615	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
CXCR6	3	45988156	rs768543024	A	G	exonic	regulatory	CXCR6:p.K61K	47.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988924	rs775944730	G	A	exonic	regulatory	CXCR6:p.Q317Q	47.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	1.55E-03	1290	0.000141	7074	0.064	10.98	0.57-645.17	0.058	7.23	0.93-56.04	0.00	0.514
CXCR6	3	45988330	chr3 45988330 C A	A	C	exonic	synonymous	CXCR6:p.I119I	47.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988801	rs140098665	T	C	exonic	regulatory	CXCR6:p.I276I	47.8	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988525	rs61751654	T	C	exonic	regulatory	CXCR6:p.D184D	47.7	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
CXCR6	3	45988485	rs200297727	G	A	exonic	regulatory	CXCR6:p.N171S	47.6	0.034651	0.92077	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988828	rs200437385	C	T	exonic	regulatory	CXCR6:p.P285P	47.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.955	0.94	0.10-8.50	0.00	0.885
CXCR6	3	45988860	rs141955108	T	G	exonic	regulatory	CXCR6:p.R296L	47.9	0.076792	0.82231	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988190	chr3 45988190 C T	T	C	exonic	regulatory	CXCR6:p.L73L	47.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45988717	rs1221055000	T	C	exonic	synonymous	CXCR6:p.N248N	47.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
CXCR6	3	45988501	chr3 45988501 C T	T	C	exonic	regulatory	CXCR6:p.D176D	47.7	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CXCR6	3	45985030	rs983400643	T	C	UTR5	regulatory	-	32.4	NA	NA	0	1234	0	2956	1.000	0.00	0.00-Inf	0.000801	1248	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063484	rs767355373	T	G	intronic	intron	-	44.5	NA	NA	0	1262	0.000332	3010	1.000	0.00	0.00-92.89	0	1284	0	7074	1.000	0.00	0.00-Inf	0.667	1.72	0.14-20.58	0.00	0.453
XCR1	3	46062490	rs529280793	A	G	exonic	missense	XCR1:p.S317L	43.1	0.014446	0.97615	0	1266	0	3002	1.000	0.00	0.00-Inf	0.00078	1282	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063050	rs761886960	T	C	exonic	upstream	XCR1:p.S130S	46.6	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1286	0.000141	7074	1.000	0.00	0.00-213.82	0.872	1.20	0.13-11.58	0.00	0.716
XCR1	3	46068974	rs1193206012	G	T	UTR5	regulatory	-	47	NA	NA	0.001577	1268	0.000332	3014	0.211	4.76	0.25-280.41	0.000779	1284	0.000141	7074	0.284	5.51	0.07-431.23	0.080	5.07	0.83-31.13	0.00	0.937
XCR1	3	46068929	chr3 46068929 A T	T	A	UTR5	regulatory	-	47.9	NA	NA	0.000787	1270	0	3012	0.297	2.37	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063052	rs370879585	C	A	exonic	upstream	XCR1:p.S130A	46.9	0.004911	0.99846	0.004724	1270	0.001991	3014	0.201	2.38	0.63-8.92	0.000775	1290	0.000707	7074	1.000	1.10	0.02-9.81	0.172	2.01	0.74-5.48	0.00	0.532
XCR1	3	46062663	rs573724659	A	G	exonic	upstream	XCR1:p.C259C	46.5	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
XCR1	3	46063164	chr3 46063164 G A	A	G	exonic	synonymous	XCR1:p.H92H	46.9	NA	NA	0.000789	1268	0	3014	0.296	2.38	0.06-Inf	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.266	3.61	0.38-34.72	0.00	0.555
XCR1	3	46062816	rs922608630	A	G	exonic	upstream	XCR1:p.I208I	47	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0.000141	7074	1.000	0.00	0.00-213.16	0.873	1.20	0.12-11.56	0.00	0.717
XCR1	3	46062694	rs181118021	A	G	exonic	upstream	XCR1:p.T249M	47.2	0.016648	0.97231	0.002362	1270	0.004645	3014	0.425	0.51	0.09-1.82	0.00155	1290	0.001696	7074	1.000	0.91	0.10-4.11	0.372	0.65	0.25-1.69	0.00	0.554
XCR1	3	46068933	rs1159261362	A	G	UTR5	regulatory	-	47.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0.001553	1288	0.000565	7074	0.233	2.75	0.25-19.20	0.335	2.09	0.47-9.37	0.00	0.500
XCR1	3	46063503	chr3 46063503 T C	C	T	intronic	upstream	-	42.3	NA	NA	0	1246	0.000333	3002	1.000	0.00	0.00-93.83	0	1250	0	7074	1.000	0.00	0.00-Inf	0.657	1.75	0.15-20.93	0.00	0.450
XCR1	3	46062882	rs758777371	A	G	exonic	synonymous	XCR1:p.S186S	47	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.364	3.61	0.23-57.68	0.00	0.767
XCR1	3	46063383	rs758306508	T	G	exonic	upstream	XCR1:p.S19R	47.2	0.063759	0.84846	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1288	0.000141	7074	1.000	0.00	0.00-213.49	0.873	1.20	0.13-11.57	0.00	0.716
XCR1	3	46063023	rs752197806	A	G	exonic	synonymous	XCR1:p.R139R	46.7	NA	NA	0.000787	1270	0.001327	3014	1.000	0.59	0.01-6.00	0	1288	0.001131	7074	0.618	0.00	0.00-3.22	0.399	0.47	0.08-2.69	0.00	0.740
XCR1	3	46063003	chr3 46063003 C G	G	C	exonic	missense	XCR1:p.R146P	46.7	0.030521	0.93462	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063223	chr3 46063223 G A	A	G	exonic	synonymous	XCR1:p.L73L	47	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46062934	chr3 46062934 T G	G	T	exonic	upstream	XCR1:p.K169T	47	0.035934	0.91462	0	1270	0.001327	3014	0.326	0.00	0.00-3.60	0	1290	0	7074	1.000	0.00	0.00-Inf	0.834	0.78	0.07-8.11	32.47	0.224
XCR1	3	46063528	chr3 46063528 C A	A	C	intronic	intron	-	34.3	NA	NA	0	1126	0.000348	2870	1.000	0.00	0.00-99.25	0	1152	0.000141	7074	1.000	0.00	0.00-238.60	0.811	1.32	0.14-12.68	0.00	0.703
XCR1	3	46063087	rs1335381226	T	A	exonic	missense	XCR1:p.F118Y	46.6	0.012672	0.97923	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46062629	rs551972565	A	T	exonic	upstream	XCR1:p.I271F	46.6	0.027073	0.94385	0.002362	1270	0.000664	3014	0.158	3.57	0.41-42.72	0.003101	1290	0.00212	7074	0.520	1.46	0.35-4.60	0.191	1.87	0.73-4.79	0.00	0.407
XCR1	3	46063188	chr3 46063188 C A	A	C	exonic	upstream	XCR1:p.L84F	46.9	0.090865	0.79769	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.454
XCR1	3	46062656	chr3 46062656 T C	C	T	exonic	upstream	XCR1:p.K262E	46.5	0.018574	0.96846	0.000787	1270	0	3014	0.296	2.38	0.06-Inf	0	1290	0	7074	1.000	0.00	0.00-Inf	0.142	6.41	0.54-76.57	0.00	0.919
XCR1	3	46063363	chr3 46063363 G A	A	G	exonic	upstream	XCR1:p.A26V	47.2	0.016325	0.97385	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46062922	rs78405233	A	G	exonic	upstream	XCR1:p.S173L	47	0.005726	0.99769	0.000787	1270	0.001327	3014	1.000	0.59	0.01-6.00	0.000775	1290	0	7074	0.154	5.49	0.14-Inf	0.560	1.71	0.28-10.46	64.52	0.093
XCR1	3	46063378	rs750354912	A	G	exonic	upstream	XCR1:p.P21L	47.2	0.014362	0.97615	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063343	rs140218706	T	C	exonic	upstream	XCR1:p.A33T	47.2	0.004988	0.99846	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA

XCR1	3	46063030	chr3 46063030 G A	A	G	exonic	missense	XCR1:p.T137I	46.6	0.022592	0.95692	0.000787	1270	0	3012	0.297	2.37	0.06-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46069034	chr3 46069034 T G	G	T	upstream	regulatory	-	41.2	NA	NA	0	1224	0	2992	1.000	0.00	0.00-Inf	0.000799	1252	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46062567	chr3 46062567 C T	T	C	exonic	upstream	XCR1:p.G291G	45.9	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46062972	rs770851613	A	G	exonic	upstream	XCR1:p.A156A	46.8	NA	NA	0.000787	1270	0.000332	3014	0.505	2.37	0.03-186.16	0.000775	1290	0.000283	7074	0.395	2.74	0.05-52.69	0.306	2.58	0.42-15.84	0.00	0.938
XCR1	3	46063323	rs1399389370	C	G	exonic	upstream	XCR1:p.C39W	47	0.016556	0.97308	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	0.000283	7074	1.000	0.00	0.00-29.21	0.756	1.46	0.13-16.16	0.00	0.760
XCR1	3	46068799	chr3 46068799 T A	A	T	intronic	intron	-	32.4	NA	NA	0	1062	0.00034	2938	1.000	0.00	0.00-107.71	0	1134	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063281	rs779760487	T	C	exonic	upstream	XCR1:p.L53L	47	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063250	chr3 46063250 A G	G	A	exonic	upstream	XCR1:p.S64P	47.2	0.042005	0.89615	0	1270	0.000664	3014	1.000	0.00	0.00-12.64	0	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063009	rs181024730	T	C	exonic	upstream	XCR1:p.R144H	46.9	0.020311	0.96615	0.002362	1270	0.000995	3014	0.370	2.38	0.32-17.75	0.003106	1288	0.000848	7074	0.054	3.67	0.76-15.50	0.025	3.10	1.15-8.38	0.00	0.677
XCR1	3	46063033	rs1377358310	A	G	exonic	upstream	XCR1:p.S136F	46.6	0.024861	0.94923	0	1270	0.000332	3012	1.000	0.00	0.00-92.36	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.71	0.14-20.47	0.00	0.453
XCR1	3	46063199	rs377699037	T	C	exonic	upstream	XCR1:p.A81T	47	0.006561	0.99385	0	1268	0.000332	3014	1.000	0.00	0.00-92.57	0	1290	0	7074	1.000	0.00	0.00-Inf	0.669	1.72	0.14-20.50	0.00	0.454
XCR1	3	46062775	rs757552327	T	C	exonic	upstream	XCR1:p.R222H	46.9	0.042434	0.89538	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
XCR1	3	46069059	chr3 46069059 G C	C	G	upstream	regulatory	-	33.9	NA	NA	0	1074	0.000344	2904	1.000	0.00	0.00-105.28	0	1094	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46062771	rs148335914	T	C	exonic	synonymous	XCR1:p.T223T	46.9	NA	NA	0	1270	0	3014	1.000	0.00	0.00-Inf	0.000775	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
XCR1	3	46063406	rs778906589	C	A	exonic	upstream	XCR1:p.F12V	47.1	0.012927	0.97923	0	1270	0.000995	3014	0.560	0.00	0.00-5.74	0	1290	0.001696	7074	0.234	0.00	0.00-1.97	0.209	0.27	0.03-2.08	0.00	0.835
XCR1	3	46063377	rs368378214	T	C	exonic	synonymous	XCR1:p.P21P	47.3	NA	NA	0	1270	0.000332	3014	1.000	0.00	0.00-92.42	0	1290	0	7074	1.000	0.00	0.00-Inf	0.670	1.72	0.14-20.48	0.00	0.453
XCR1	3	46062782	rs745493157	A	G	exonic	missense	XCR1:p.R220C	46.9	0.133273	0.73077	0	1270	0	3014	1.000	0.00	0.00-Inf	0.00155	1290	0.000141	7074	0.064	10.98	0.57-645.17	0.058	7.23	0.93-56.04	0.00	0.514

[a]Chromosome. [b]hg19 position. [C]Variant ID with format "chromosome_position_reference allele_alternate allele (according to hg19)", or SNP (rs) number according to dbSNP build 151. [d]Alternative allele. [e]Reference allele. [f]Mean sequencing depth. [g]Mendelian Clinically Applicable Pathogenicity. [h]Variants with M-CAP sensitivity score $\leqslant$ 0.95 were judged as possibly pathogenic. [i]MAF, minor allele frequency. [j]odds ratio with respect to the alternative allele. [k]95% confidence interval of OR. [l]Heterogeneity statistic. [m]*P*-value for heterogeneity statistic.

Association results of common variants in 51 chemokine genes in Han Chinese with AD

Gene	Variant ID[a]	Chr[b]	Position[c]	Location	MeanDP[d]	Alt/Ref[e]	Stage 1 (Southern cohort)							Stage 2 (Eastern cohort)							Stage 3 (meta-analysis)				
							MAF of cases[f]	Allele no. of cases	MAF of controls[f]	Allele no. of controls	*P* value	OR[g]	95% CI[h]	MAF of cases[f]	Allele no. of cases	MAF of controls[f]	Allele no. of controls	*P* value	OR[g]	95% CI[h]	*P* value	OR[g]	95% CI[h]	Het I^2(%)[i]	Het P^j
CCL1	rs61758325	17	32688804	exonic	45.6	C/A	0.019	1268	0.023	3014	0.491	0.82	0.49-1.33	0.014	1288	0.016	7074	0.629	0.86	0.49-1.42	0.316	0.84	0.60-1.18	0.00	0.907
CCL11	rs1129844	17	32612894	exonic	49.3	A/G	0.179	1256	0.176	3004	0.826	1.02	0.85-1.21	0.144	1276	0.140	7074	0.694	1.04	0.87-1.23	0.664	1.03	0.91-1.16	0.00	0.895
CCL11	rs55901334	17	32614637	exonic	45.5	A/C	0.011	1268	0.011	3014	1.000	1.01	0.50-1.94	0.009	1288	0.008	7074	0.743	1.10	0.54-2.07	0.818	1.05	0.68-1.64	0.00	0.848
CCL14	rs113937434	17	34313674	exonic	51.3	A/G	0.029	1268	0.039	3014	0.127	0.74	0.49-1.08	0.024	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL14	rs75238886	17	34313612	exonic	49.1	A/G	0.030	1270	0.039	3014	0.153	0.76	0.51-1.11	0.025	1288	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL15	rs854625	17	34328461	exonic	66.4	A/G	0.314	1256	0.337	2998	0.153	0.90	0.78-1.04	0.288	1264	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	rs74842203	17	34304680	exonic	81.7	T/C	0.073	1270	0.056	3014	0.036	1.33	1.01-1.74	0.072	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	rs11080369	17	34305164	intronic	55.4	C/A	0.058	1268	0.070	3014	0.139	0.81	0.60-1.07	0.050	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	rs151132172	17	34308557	upstream	38.9	A/G	0.009	1252	0.010	3000	0.864	0.88	0.40-1.81	0.006	1256	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	rs114853983	17	34305362	intronic	38.3	T/C	0.079	1114	0.057	2958	0.014	1.42	1.07-1.86	0.079	1146	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL16	rs79254649	17	34304605	exonic	75.4	A/C	0.073	1270	0.056	3014	0.036	1.33	1.01-1.74	0.072	1290	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	rs13900	17	32583911	UTR3	42.2	C/T	0.449	1182	0.465	2954	0.388	0.94	0.82-1.08	0.416	1206	0.414	7074	0.899	1.01	0.89-1.14	0.622	0.98	0.89-1.07	0.00	0.452
CCL2	rs4586	17	32583269	exonic	71.8	T/C	0.451	1266	0.463	3006	0.460	0.95	0.83-1.09	0.429	1284	0.414	7074	0.310	1.06	0.94-1.20	0.801	1.01	0.93-1.11	34.27	0.217
CCL2	rs28730833	17	32582494	intronic	33.5	A/T	0.012	1228	0.012	2934	0.875	1.05	0.53-2.00	0.010	1242	0.009	7074	0.517	1.20	0.60-2.21	0.591	1.12	0.73-1.73	0.00	0.773
CCL3	rs1130371	17	34416537	exonic	79.6	A/G	0.395	1268	0.387	3006	0.631	1.03	0.90-1.18	0.392	1278	-	7074	NA	NA	NA	NA	NA	NA	NA	NA
CCL8	rs1133763	17	32647831	exonic	45.9	C/A	0.287	1254	0.300	2994	0.397	0.94	0.81-1.09	0.284	1266	0.287	7074	0.840	0.98	0.86-1.13	0.456	0.96	0.87-1.06	0.00	0.630
CCL8	rs70937035	17	32646017	upstream	40.8	A/T	0.014	1244	0.012	2976	0.646	1.16	0.61-2.14	0.011	1244	0.009	7074	0.525	1.23	0.63-2.22	0.395	1.20	0.79-1.80	0.00	0.900
CCL8	rs41410552	17	32646131	upstream	83.1	A/G	0.287	1270	0.302	3012	0.341	0.93	0.80-1.08	0.285	1290	0.285	7074	0.973	1.00	0.87-1.14	0.487	0.97	0.88-1.06	0.00	0.497
CCL8	rs41339751	17	32647298	exonic	41.8	T/C	0.022	1268	0.018	3008	0.398	1.21	0.74-1.96	0.017	1276	0.019	7074	0.737	0.91	0.55-1.44	0.777	1.05	0.76-1.45	0.00	0.382
CCR1	rs3181080	3	46249929	upstream	64	T/A	0.044	1260	0.036	3002	0.219	1.23	0.87-1.74	0.057	1286	0.055	7074	0.843	1.03	0.78-1.33	0.359	1.10	0.90-1.35	0.00	0.387
CCR1	rs137916685	3	46244920	exonic	51	G/A	0.013	1270	0.013	3014	1.000	1.01	0.53-1.83	0.024	1290	0.019	7074	0.233	1.27	0.82-1.89	0.328	1.18	0.85-1.63	0.00	0.522
CCR1	rs34423195	3	46249722	intronic	68.5	G/A	0.043	1266	0.036	3012	0.255	1.22	0.86-1.72	0.057	1290	0.055	7074	0.843	1.02	0.78-1.33	0.391	1.09	0.89-1.34	0.00	0.407
CCR3	rs4987053	3	46306700	exonic	53.6	C/T	0.039	1270	0.033	3014	0.315	1.21	0.84-1.72	0.047	1290	0.050	7074	0.626	0.92	0.68-1.22	0.828	1.02	0.82-1.27	29.46	0.234
CCR3	rs9853223	3	46284093	intronic	60.7	A/G	0.312	1228	0.320	2996	0.611	0.96	0.83-1.11	0.289	1258	0.290	7074	0.946	0.99	0.87-1.14	0.681	0.98	0.89-1.08	0.00	0.743
CCR5	rs1800452	3	46415061	exonic	69.1	A/G	0.061	1270	0.069	3014	0.347	0.87	0.66-1.15	0.068	1290	0.068	7074	0.952	1.01	0.79-1.28	0.542	0.95	0.79-1.13	0.00	0.423
CCR6	rs193057414	6	167549660	intronic	65.8	C/T	0.016	1270	0.013	3014	0.475	1.22	0.67-2.15	0.003	1290	0.008	7074	0.051	0.38	0.10-1.04	0.811	0.94	0.58-1.52	74.31	0.049
CCR6	rs3093007	6	167549775	exonic	74.1	C/T	0.043	1270	0.048	3014	0.474	0.89	0.63-1.23	0.057	1288	0.049	7074	0.238	1.17	0.89-1.52	0.660	1.05	0.86-1.28	42.67	0.187
CCR6	rs117290001	6	167525350	UTR5	64.9	G/C	0.028	1266	0.022	3014	0.270	1.27	0.81-1.95	0.030	1290	0.033	7074	0.732	0.92	0.63-1.30	0.724	1.05	0.80-1.37	27.39	0.241
CCR6	rs1012656	6	167525303	UTR5	64.8	C/G	0.406	1260	0.401	3008	0.732	1.02	0.89-1.17	0.410	1276	0.422	7074	0.423	0.95	0.84-1.07	0.701	0.98	0.90-1.07	0.00	0.413
CCR6	rs2071171	6	167550042	exonic	147.5	C/T	0.487	1270	0.497	3010	0.569	0.96	0.84-1.10	0.509	1288	0.517	7074	0.628	0.97	0.86-1.09	0.432	0.97	0.88-1.05	0.00	0.920
CCR6	rs3093009	6	167549477	intronic	63.5	G/A	0.131	1264	0.138	3010	0.591	0.95	0.77-1.15	0.131	1282	0.123	7074	0.408	1.08	0.90-1.29	0.826	1.01	0.89-1.16	0.00	0.330
CCR6	rs75158174	6	167525399	UTR5	65.9	A/G	0.017	1270	0.010	3014	0.094	1.62	0.88-2.92	0.012	1290	0.010	7074	0.540	1.21	0.64-2.15	0.094	1.40	0.94-2.08	0.00	0.475
CCR7	rs588019	17	38715107	intronic	44.2	A/G	0.068	1262	0.061	3002	0.409	1.12	0.85-1.47	0.056	1284	0.057	7074	0.948	0.99	0.75-1.28	0.611	1.05	0.87-1.26	0.00	0.499
CCRL2	rs3204849	3	46450070	exonic	179.6	T/A	0.457	1270	0.446	3014	0.523	1.05	0.91-1.20	0.470	1290	0.477	7074	0.649	0.97	0.86-1.10	0.920	1.00	0.92-1.10	0.00	0.419
CCRL2	rs11266744	3	46449978	exonic	169.4	A/C	0.457	1268	0.446	3014	0.523	1.05	0.91-1.20	0.471	1288	0.477	7074	0.693	0.98	0.86-1.10	0.888	1.01	0.92-1.10	0.00	0.444
CCRL2	rs3204850	3	46450297	exonic	65.8	G/A	0.043	1270	0.037	3014	0.437	1.14	0.80-1.60	0.043	1290	0.050	7074	0.324	0.85	0.63-1.14	0.769	0.97	0.78-1.20	39.95	0.197
CX3CR1	rs3732379	3	39307256	exonic	55.1	T/C	0.034	1270	0.028	3014	0.327	1.21	0.81-1.77	0.022	1290	0.024	7074	0.842	0.93	0.60-1.40	0.621	1.07	0.82-1.41	0.00	0.356
CX3CR1	rs11715522	3	39323163	exonic	91.4	A/C	0.350	1266	0.347	3010	0.860	1.01	0.88-1.17	0.333	1288	0.332	7074	0.949	1.01	0.88-1.14	0.849	1.01	0.92-1.11	0.00	0.930
CX3CR1	rs3732380	3	39307562	exonic	52.3	T/C	0.024	1270	0.023	3012	0.739	1.08	0.68-1.69	0.033	1290	0.034	7074	1.000	0.98	0.69-1.37	0.908	1.02	0.78-1.32	0.00	0.711
CX3CR1	rs3732378	3	39307162	exonic	52.8	A/G	0.034	1270	0.027	3014	0.235	1.25	0.84-1.85	0.022	1290	0.023	7074	1.000	0.98	0.63-1.46	0.438	1.11	0.85-1.46	0.00	0.370
CX3CR1	rs17038679	3	39307545	exonic	56.3	A/G	0.036	1270	0.040	3014	0.604	0.90	0.62-1.28	0.046	1290	0.045	7074	0.884	1.01	0.75-1.35	0.760	0.97	0.78-1.20	0.00	0.594
CXCL1	rs181868085	4	74735429	exonic	47.2	A/C	0.037	1262	0.031	3002	0.301	1.21	0.83-1.75	0.037	1278	0.023	7074	0.009	1.59	1.12-2.22	0.006	1.40	1.10-1.79	17.18	0.272
CXCL1	rs2071425	4	74735244	exonic	37.5	G/A	0.400	1210	0.382	2904	0.292	1.08	0.94-1.24	0.399	1206	0.407	7074	0.612	0.97	0.85-1.10	0.731	1.02	0.93-1.11	25.18	0.248
CXCL1	rs4074	4	74736144	intronic	65.8	A/G	0.470	1260	0.437	2996	0.050	1.14	1.00-1.31	0.457	1288	0.491	7074	0.027	0.87	0.77-0.99	0.747	0.99	0.90-1.08	88.69	0.003
CXCL1	rs7656335	4	74735524	intronic	54.2	C/G	0.132	1264	0.116	3010	0.136	1.16	0.95-1.42	0.118	1282	0.123	7074	0.643	0.95	0.79-1.15	0.517	1.05	0.91-1.20	53.25	0.144
CXCL1	rs11547681	4	74735150	UTR5	46.7	T/G	0.323	1244	0.305	2956	0.258	1.09	0.94-1.26	0.319	1256	0.335	7074	0.298	0.93	0.82-1.06	0.986	1.00	0.91-1.10	59.29	0.117
CXCL10	rs3921	4	76942943	UTR3	37.2	C/G	0.044	1118	0.054	2944	0.231	0.81	0.57-1.13	0.054	1176	0.047	7074	0.378	1.14	0.85-1.51	0.908	0.99	0.80-1.22	59.19	0.117
CXCL11	rs6532111	4	76955914	exonic	74.3	T/C	0.042	1266	0.054	3014	0.108	0.77	0.55-1.06	0.052	1286	0.047	7074	0.436	1.11	0.83-1.46	0.635	0.95	0.77-1.17	66.32	0.085
CXCL11	rs6815597	4	76957171	UTR5	172.5	C/T	0.042	1270	0.054	3014	0.108	0.77	0.55-1.06	0.052	1288	0.047	7074	0.478	1.11	0.83-1.45	0.620	0.95	0.77-1.17	66.63	0.083
CXCL13	rs17002743	4	78531932	intronic	39.7	T/C	0.051	1180	0.039	2976	0.088	1.32	0.94-1.83	0.043	1206	0.055	7074	0.096	0.78	0.57-1.05	0.947	0.99	0.80-1.23	82.51	0.017
CXCL16	rs1050997	17	4641755	exonic	78.5	C/T	0.287	1264	0.301	3010	0.360	0.93	0.81-1.08	0.295	1284	0.274	7074	0.119	1.11	0.97-1.27	0.585	1.03	0.93-1.13	66.95	0.082
CXCL16	rs2304973	17	4642222	intronic	48.8	A/G	0.087	1266	0.095	3004	0.452	0.91	0.71-1.15	0.065	1286	0.082	7074	0.043	0.78	0.61-0.99	0.045	0.84	0.72-1.00	0.00	0.378
CXCL16	rs1876444	17	4638484	exonic	91.9	T/C	0.375	1268	0.398	3010	0.160	0.91	0.79-1.04	0.395	1288	0.382	7074	0.383	1.06	0.93-1.19	0.760	0.99	0.90-1.08	63.36	0.099
CXCL16	rs1050998	17	4638737	exonic	56	A/G	0.378	1244	0.402	2990	0.138	0.90	0.79-1.04	0.394	1268	0.384	7074	0.552	1.04	0.92-1.18	0.592	0.98	0.89-1.07	56.61	0.129
CXCL16	rs2250333	17	4642069	intronic	80.5	A/G	0.281	1268	0.298	3006	0.270	0.92	0.79-1.07	0.291	1284	0.272	7074	0.174	1.10	0.96-1.25	0.789	1.01	0.92-1.12	68.21	0.076
CXCL16	rs1051009	17	4637886	UTR3	50.7	G/A	0.471	1244	0.501	2972	0.074	0.89	0.77-1.01	0.463	1258	0.467	7074	0.854	0.99	0.87-1.12	0.174	0.94	0.86-1.03	29.04	0.235
CXCL16	rs2277680	17	4638563	exonic	97.5	G/A	0.385	1266	0.405	3014	0.218	0.92	0.80-1.05	0.397	1288	0.385	7074	0.419	1.05	0.93-1.19	0.805	0.99	0.90-1.08	54.49	0.138
CXCL16	rs3744700	17	4638010	intronic	33.3	T/G	0.100	1160	0.106	2866	0.608	0.94	0.74-1.18	0.109	1176	0.111	7074	0.841	0.98	0.79-1.19	0.591	0.96	0.83-1.11	0.00	0.807
CXCL9	rs2276885	4	76928729	upstream	55.6	G/A	0.495	1220	0.500	2996	0.812	0.98	0.86-1.12	0.468	1244	0.470	7074	0.902	0.99	0.88-1.12	0.774	0.99	0.90-1.08	0.00	0.917
CXCL9	rs2276886	4	76928428	intronic	39.1	T/C	0.408	1126	0.390	2940	0.298	1.08	0.94-1.24	0.429	1140	0.429	7074	1.000	1.00	0.88-1.14	0.467	1.04	0.94-1.14	0.00	0.439
CXCR2	rs2230054	2	219000310	exonic	84	T/C	0.343	1270	0.329	3010	0.394	1.06	0.92-1.22	0.365	1286	0.345	7074	0.181	1.09	0.96-1.23	0.114	1.08	0.98-1.18	0.00	0.800
CXCR2	rs4674259	2	218991005	UTR5	97.8	A/G	0.376	1266	0.369	3012	0.677	1.03	0.90-1.18	0.394	1284	0.374	7074	0.169	1.09	0.96-1.23	0.186	1.06	0.97-1.16	0.00	0.552
CXCR2	rs11574750	2	219000292	exonic	59	T/C	0.032	1268	0.040	3014	0.254	0.81	0.55-1.17	0.030	1290	0.028	7074	0.716	1.07	0.74-1.53	0.593	0.93	0.73-1.20	19.34	0.266
CXCR4	rs2228014	2	136873084	exonic	77.3	A/G	0.133	1268	0.145	3012	0.314	0.90	0.74-1.10	0.121	1290	0.126	7074	0.647	0.96	0.79-1.15	0.285	0.93	0.82-1.06	0.00	0.676
CXCR5	rs10892307	11	118754649	UTR5	49.6	G/C	0.063	1268	0.067	3012	0.638	0.93	0.70-1.22	0.065	1288	0.060	7074	0.486	1.09	0.84-1.39	0.870	1.02	0.85-1.21	0.00	0.398
CXCR5	rs598207	11	118765267	exonic	63.8	C/G	0.184	1266	0.211	3006	0.050	0.85	0.71-1.00	0.210	1286	0.221	7074	0.400	0.94	0.81-1.09	0.053	0.90	0.80-1.00	0.00	0.356
CXCR5	rs2276344	11	118754518	upstream	30.9	A/T	0.158	1152	0.160	2876	0.886	0.98	0.81-1.19	0.145	1144	0.127	7074	0.087	1.17	0.97-1.40	0.262	1.08	0.95-1.23	42.76	0.186
CXCR6	rs2234358	3	45989044	UTR3	66.4	T/G	0.323	1252	0.330	3008	0.667	0.97	0.84-1.12	0.358	1268	0.360	7074	0.899	0.99	0.87-1.12	0.683	0.98	0.89-1.08	0.00	0.811
XCR1	rs71327010	3	46068835	intronic	42	T/G	0.046	1242	0.046	2998	1.000	1.00	0.72-1.39	0.071	1260	0.062	7074	0.258	1.15	0.90-1.46	0.348	1.09	0.91-1.32	0.00	0.505
XCR1	rs7623476	3	46068843	intronic	50.2	G/A	0.301	1256	0.298	2996	0.854	1.02	0.88-1.18	0.302	1280	0.316	7074	0.326	0.94	0.82-1.07	0.541	0.97	0.88-1.07	0.00	0.405
XCR1	rs2230322	3	46063329	exonic	56.9	C/T	0.046	1270	0.046	3014	1.000	1.00	0.72-1.38	0.070	1290	0.062	7074	0.291	1.13	0.89-1.44	0.408	1.08	0.90-1.31	0.00	0.522

[a]SNP (rs) number according to dbSNP build 151. [b]Chromosome. [c]hg19_Position. [d]Mean sequencing depth. [e]Alternative allele/reference allele. [f]MAF, Minor allele frequency. [g]Odds ratio calculated with respect to the alternative allele. [h]95% confidence interval of OR. [i]Heterogeneity statistic. [j]*P*-value for heterogeneity statistic.