EVOLUTIONARY GENETICS OF BEHCET’S DISEASE

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…to my father, Süleyman KAPLAN

ABSTRACT

EVOLUTIONARY GENETICS OF BEHÇET'S DISEASE

Behcet's Disease (BD) is an auto-immune/autoinflammatory complex disease that causes inflammation of the blood vessels. The underlying cause of BD is unknown. The highest prevalence is seen in populations along the ancient silk road, raising the possibility that it may have its origins along these historic trade routes. The genetic makeup that increases BD susceptibility in modern populations might have been advantageous for certain environmental stress factors such as resistance to infections and pathogens. Such an advantage is expected to leave signs of selection on the genes associated with BD. We have observed a possible recent selection on HLA-B as suggested in previous reports, but recent selection signature was not unique to HLA-B, 14 other BD-associated genes also showed recent selection including other MHC loci such as HLA-G, and other genes such as KCKN9 and NOD2 showed even a stronger selection than HLA-B. Results indicate that the BD alleles are not specific to East Asians. They are present in other world populations with appreciable frequencies. This shows that there is no selection favouring specifically these variants in populations with high BD prevalence. In conclusion, a variety of evolutionary processes have shaped the genetic diversity in BD risk genes, and it is difficult to understand the precise mechanisms of selection that underlie these processes. There are some common genes with BD and other inflammatory diseases. Consequently, our findings may not only apply to BD but also to other inflammatory illnesses in general.

ÖZET

BEHÇET HASTALIĞI'NIN EVRİMSEL GENETİĞİ

Behçet Hastalığı (BH), damarların iltihaplanmasına neden olan kompleks bir otoimmün/otoinflamatuar hastalıktır. BH'nin nedenleri bilinmemektedir. Hastalığın en sık görüldüğü popülasyonlar antik ipek yolu üzerindeki popülasyonlardır, bu da hastalığın kökeninin bu antik ticaret yoluna dayanma ihtimalini arttırır. Eğer, hastalığa neden olan genler seçilim geçirdiyse, bu seçilim bizi çeşitli patojenler ve bulaşıcı hastalıklar gibi stres faktörlerine karşı koruma amaçlı ortaya çıkmış olabilir. Böylesine bir seçilimin de izlerini BH ile ilişkilendirilmiş genlerde bulmayı bekleriz. Bu çalışmanın amacı BH'nin nötral veya seçilimsel süreçlerden nasıl etkilendiğini bulmaktır. Çalışmamızda HLA-B üzerinde önceki çalışmalarda da belirtildiği üzere bir seçilim tespit ettik, ancak seçilim izi sadece HLA-B'ye özgü değildi. HLA-B dışında BH ile ilişkilendirilmiş 14 genin daha seçilim geçirdiğini gördük. Bu seçilim izlerinden bazıları HLA-G gibi MHC lokusunda bulunan genlerdeyken, MHC lokusu dışında bulunan KCNK9 ve NOD2 gibi bazı genler HLA-B'den daha büyük bir seçilim izi göstermekte. Sonuçlar, BH alellerinin sadece BH'nin görüldüğü popülasyonlara özgü olmadığını, aksine diğer dünya popülasyonlarında da kayda değer bir miktarda bulunduğunu göstermekte. Bu da BH'nin sık görüldüğü popülasyonlarda BH alellerini özellikle destekleyen bir seçilim olma olasılığını düşürmekte. Çeşitli evrimsel süreçler, BH genlerindeki genetik çeşitliliği şekillendirmiştir ve bu süreçlerin altında yatan seçilim mekanizmalarını kesin olarak anlamak zordur. BH diğer inflamatuar hastalıklarla ortak bazı genlere sahip. Sonuç olarak, bulgularımız sadece BH için değil, genel olarak diğer inflamatuar hastalıklar için de geçerli olabilir.

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CHAPTER 1

INTRODUCTION

1.1. Behcet’s Disease

Behçet’s Disease (BD) is a multisystem disorder causing inflammation of the blood vessels and tissues showing symptoms mainly in the gastrointestinal systems, skin, nervous systems and eyes [1,2]. The underlying cause of BD is unknown but it is a complex disease, meaning several genes are involved along with the environmental factors in the disease pathogenesis [1].

The first official recognition of the disease was in 1937 by Hulusi Behçet, a Turkish dermatologist who described the three main symptoms as iritis, orogenital ulcerations, and hypopyon uveitis [3]. However, Hippocrates mentions a disease-specific to Asia Minor with similar symptoms to BD in his book *Epidemion* [4].

1.2. Epidemiology

BD mainly shows a distribution from East Asia to the Mediterranean and is rarely seen in the US, Northern European, Australian, African, and American Indian populations[5] [6]. Showing a high prevalence among East Asia, the Middle East, and the Mediterranean; BD is sometimes referred to as the “Silk Road Disease” [7].

1.3. Clinic Features

Even though BD can affect all systems by inflammation of blood vessels, its main clinical features include mucocutaneous lesions like oral and genital aphthae, articular and ocular inflammations/manifestations, neurological inflammations, and cutaneous lesions. [8]

1.3.1. Mucocutaneous lesions

Mucocutaneous lesions are the most important signs of BD since they are the most common symptoms seen in patients. Their identification carries a significant role in early diagnosis and treatment resulting in a better prognosis. [8]

1.3.1.1. Oral Aphthae

Oral aphthae are the most common symptoms seen in BD patients with an occurrence rate of 97%. [9] They usually take place on the lips' mucous sides, soft palate, tongue, and buccal mucosa. It takes 1-4 weeks for an oral aphtha to disappear and it returns within days or months. [8]

1.3.1.2. Genital Aphthae

Genital aphthae are seen in 60-70% of the patients. They can affect any part of the urogenital system and take weeks to heal. The most common part affected is the scrotum in males and the vulva in females. [9] The ulcers are deeper compared to the oral aphthae. [8]

1.3.2. Cutaneous/Skin Lesions

The main cutaneous lesions seen in BD patients are papulopustular lesions and erythema nodosum-like lesions. Papulopustular lesions are present in 50–96% of the patients while erythema nodosum-like lesions have an occurrence within half of the patients. [10]

1.3.3. Articular Manifestations

40–71 % of BD patients have articular manifestations according to different studies. Joint involvement is the first seen manifestation occurring in 11–34 % and can show itself years before other symptoms.

On the other hand, the most common articular symptom by being present in 80% of BD patients is Arthralgia. [11]

1.3.4. Ocular Manifestations

Ocular symptoms are present in nearly 50% of the patients and male patients are more prone (50–70%) to developing ocular involvement compared to females (20–30%). Males also are at a higher risk of visual morbidity. Ocular findings usually show themselves in the first 2-4 years of BD. [12]

1.3.5. Neurological Manifestations

Neurological symptoms are present in 3-9% of the patients.[13] The risk of involvement is higher in male patients. Symptoms are usually seen in the central nervous system and can be classified into two groups: parenchymal and non-parenchymal. In the parenchymal involvement, the major risk is meningoencephalitis while in the non-parenchymal involvement, it is thrombosis. [14]

1.4. Pathogenesis

The causes of BD are still unknown, however, it is a complex disease with environmental and genetic factors involved [1]. As symptoms, repeated inflammation of the mucocutaneous tissue, blood vessels, eyes, gastrointestinal tract and brain are present. These symptoms are thought to be triggered by a pathogen as Hulusi Behçet himself mentioned suspecting viruses and oral cavity infections [15].

Viral agents possibly associated with BD are herpes simplex virus-1, parvovirus B19, hepatitis C virus, Epstein-Barr virus, cytomegalovirus, and varicella zoster virus. Along with the viruses listed, several bacteria suspected to play a role in BD susceptibility are *Streptococcus sanguinis*, *Saccharomyces cerevisiae*, *Escherichia coli, mycobacterium, Helicobacter pylori*, *Borrelia burgdorferi*, *Mycoplasma fermentans,* and *Staphylococcus aureus.* [16]

As genetic factors, major histocompatibility complex (MHC) class I genes have been strongly associated with BD. Among the MHC class I genes, HLA-B51 is considered the main genetic factor while also being used as the genetic marker for the disease. Even though being used as a genetic marker, it is estimated that it contributes roughly 20% to overall genetic BD susceptibility. [17]

1.4.1. Nongenetic Factors

1.4.1.1. Viral Hypothesis

The first mention of a viral infection triggering BD was made by Hulusi Behçet himself. The most associated virus with the disease is herpes simplex virus-1 (HSV-1) because serum antibodies against HSV and HSV DNA were found higher in BD patients compared to the control groups. The HSV DNA was present in genital and intestinal ulcers. However, it was not found in oral ulcers. [16]

1.4.1.2. Bacterial Hypothesis

Given oral aphtha is the most common symptom and the decrease in some symptoms after usage of antibiotics such as minocycline and penicillin increased the suspicion of oral flora being involved in BD pathogenesis. The main focus has been on the Streptococci genus, especially *Streptococcus sanguis*. Research has shown *Streptococcus sanguis* of unique characteristics was present in BD patients’ oral flora and was found in higher proportions compared to the control group. [16,17]

1.4.2. Genetic Factors

1.4.2.1. HLA Region

Human leukocyte antigens (HLA), also known as major histocompatibility complex (MHC) molecules, are the cell surface proteins that present antigens, activate T cells, and aid in the immune system's recognition of foreign substances. [18]

1.4.2.1.1. HLA-B*51

HLA-B*51 was identified to be the major risk locus, however, it cannot be the sole and main factor of this disease because a third of patients from countries with high BD prevalence do not present HLA-B*51. [4]

Interestingly, this HLA-B subtype is thought to be passing to modern humans through Neanderthal admixture according to the latest admixture studies. [19]

1.5. Genome-Wide Association Study

To associate genetic variations with particular traits, Genome-Wide Association Study (GWAS) is conducted.

To perform a GWAS, the genomes of many people with and without disease are scanned. By using Single Nucleotide Polymorphisms (SNPs), the whole genome is searched to find a significant difference in a certain position. When the differences are found, they are suggested to be associated with the disease.

1.6. Evolution of Complex Diseases

Our genome carries traces of human history and evolution. Every stress factor in the environment such as infectious diseases, climate changes, and migration had impacts on our DNA. Humans have experienced changes in certain traits to adapt to their surroundings. With all these impacts, modern humans' genomes differ from their ancient relatives' genomes.

Some of these trait changes caused by infectious diseases have led to genetic disorders.

A few examples of infectious disease—genetic disorder pairings would be: Tuberculosis – Tay-Sachs Disease, Cholera – Cystic Fibrosis, *Yersinia pestis* (The Plague) - Familial Mediterranean Fever (FMF) [20]

1.7. Ancient DNA Studies

Ancient DNA (aDNA) studies started by collecting DNA samples from ancient specimens. The first extraction of aDNA was on a quagga and a child mummy from Egypt [21]. Due to the lack of better sequencing technologies and PCR, those samples were not as informative as samples collected later but they have surely opened a new perspective on evolution in general.

Even with high-throughput sequencing, there are many factors affecting the aDNA quality such as fragmentation, post-mortem mutations, contamination, etc. [21] All these factors make it hard to study the aDNA samples.

However, with all the drawbacks, aDNA is still an important source to compare modern individuals to ancient individuals. After the genome-wide association studies (GWAS), many loci have been associated with complex traits. Using these associations, we are able to compare past and present allele frequencies of certain traits and even see if there are any signs of selection. [22]

1.8. Hypothesis and Aims of the Study

1.8.1. Hypothesis

Behcet's Disease has a rather structured global distribution and is seen more commonly in populations along the ancient silk road. We hypothesize that there can be a selection or neutral processes behind BD, and if the disease is carrying marks of selection, it may be an environmental stress factor behind this particular geographic distribution.

The genetic makeup that increases BD susceptibility in modern populations might have been advantageous for certain environmental stress factors such as resistance to infections and pathogens. If so, there should be signs of selection on the genes associated with Behcet's Disease.

By looking at the ancient DNA data and variants in the global ancient DNA variant set, we want to find out the nature of this selection. We will also support our hypothesis by comparing the genomic variation in contemporary Asian populations with the European populations- which have a lower risk for Behcet's Disease.

1.8.2. Aims

To test whether BD susceptibility is a derived selected trait, we compared the distribution of disease risk status (susceptible vs. protective) of alleles with their respective ancestral and derived status among populations with high BD prevalence.

To conduct population differentiation analyses between East Asians, Europeans and Africans with BD-associated alleles and, compare the results with respect to genome-wide differentiation between these populations.

To conduct population genetic tests to identify possible selection on BD-associated genes

To compare the allele frequency difference between modern-day populations and ancient populations.

CHAPTER 2

MATERIALS AND METHODS

2.1. Variants and Genes Associated with Behçet's Disease

BD-associated variants and genes were found by reviewing articles till 31 May 2022 in PubMed (https://www.ncbi.nlm.nih.gov/pubmed/). The keywords used to search articles were "Behcet Disease", "Behcet Syndrome", "Behcet's Disease", and "genetics" for between 1980-2022. Only original studies written in English that reported on sample size, studied genes and their variations, and their statistical connection with Behcet's disease were further assessed. Seventy-seven articles in total met the search requirements. After filtering out unnecessary information, we used SNP and gene data from 18 papers in total (Appendix A).

BD-associated SNPs, their allelic states (derived vs ancestral), positions on the chromosomes, population frequencies, and their nature of change (coding, promoter, etc.) were collected from dbSNP (https://www.ncbi.nlm.nih.gov/snp/) and the 1000 Genomes database [23] (http://www.internationalgenome.org/) accessed till 31 May 2022.

2.2. Single Nucleotide Polymorphism (SNP) Based and Gene Sequence Based Population Genetics Analyses Samples

For the modern populations used for both gene sequence-based and SNP-based analyses, the 1000 Genomes database [23] (http://www.internationalgenome.org/) was used and they are listed in Appendix C. The analyses were conducted to focus on East Asians (high BD occurrence), Europeans (low/very low BD occurrence), and Africans (very low/no BD occurrence). VCF files and DNA sequences for BD-associated genes were downloaded using the ENSEMBL DataSlicer tool (http://grch37.ensembl.org/Homo_sapiens/Tools/DataSlicer) based on Phase 31,1000 Genomes data[23]. East Asian, European, and African populations included 504, 503, and 661 individuals, respectively.

The ancient populations used for both gene sequence and SNP-based analyses are taken from Allen Ancient DNA Resource (AADR) [24] (https://reich.hms.harvard.edu/allen-ancient-dna-resource-aadr-downloadable-genotypes-present-day-and-ancient-dna-data), version 44.3.

Turkish population allele frequencies of 3,362 individuals were taken from the Turkish Variome.[25] (https://figshare.com/articles/dataset/The_genetic_structure_of_the_Turkish_population_reveals_high_levels_of_variation_and_admixture/15147642).

2.3. Population Genetics and Selection Analyses

PLINK (a toolset for whole-genome association and population-based linkage analysis) versions 2.0 and 1.9 (www.cog-genomics.org/plink/2.0/) [26,27] was used to compare SNP-based fixation indices (Fst) between 1K Genome populations. For the gene-based analyses, we calculated the number of haplotypes, segregating sites (S), haplotype diversity, the total number of mutations (Eta), nucleotide diversity π (pi) [28], Watterson theta θW (ThetaW) [28,29], the average number of nucleotide differences θK (ThetaK) [30] for each population.

The θ (Theta), calculated by $4Ne\mu$ (effective population size and mutation rate multiplied), nucleotide diversity estimates are determined by the number of segregating sites. The average number of pairwise differences between gene sequences is used to estimate the π diversity. For allele frequency spectrum-based neutrality tests we estimated Fu and Li’s D [31], Fu’s Fs [32], Fu and Li’s F [31], Tajima’s D [33], Achaz’s Y [34], ZnS statistic [35], Ramos-Onsins and Rozas R2 [36]. Test results are given in Table 1.

Table 1. Comparison of ancestral and derived allele status versus population distribution of BD-associated SNPs with respect to their effect on BD. [a]Chi-square test result. [b]Pooling alleles and their effects from all reported studies. [c]Focusing only on reported alleles from studies with larger sample sizes and more significant BD associations (reported p values less than $p < 10^{-5}$). Populations represent study populations where BD genetic association study was conducted and variants were discovered.

	Susceptible		Protective		p[a]
	Ancestral N(%)	Derived N(%)	Ancestral N(%)	Derived N(%)	
Chinese	18 (31)	14 (24)	13 (22)	14 (22)	0.64
Japanese	35 (24)	47 (33)	20 (14)	41 (29)	0.23
Korean	5 (62)	3 (38)	-	-	-
Turkish	14 (35)	24 (60)	0 (0)	2 (100)	0.29
Total[b]	72 (29)	88 (35)	33 (13)	57 (23)	0.32
SNPs[c] with $p<10^{-4}$	32 (26)	53 (44)	15 (12)	21 (17)	0.68

Here, we provide a quick summary of various techniques. Tajima's D determines whether there is a statistically significant difference between the π and θ estimates of nucleotide diversity. The π and θ estimates of nucleotide diversity should be relatively comparable under neutral evolutionary processes, such as no selection and constant population size, leading to Tajima's D values around zero. While excessive intermediate frequency polymorphisms result in positive Tajima's D values, suggesting balancing selection, excessive rare polymorphisms result in negative Tajima's D values, implying negative selection, background selection, or abrupt population expansion. Using Fu and Li's D* and F* tests, the distribution of mutations on the internal branches and external branches of the gene are compared. On the external branches of the tree, rare frequency variants that have just evolved are found, whereas, on the internal branches, older, higher frequency variants occur. Negative Fu-Li test findings, therefore, imply a high prevalence of recent or novel mutations, whereas positive values indicate a high prevalence of old intermediate or high-frequency variants. The distribution of allele frequency spectrum under various demographic and evolutionary models can be modeled by Fu's Fs [32], Achaz's Y [34], and Ramos-Onsins and Rozas R2 [36]. They are statistically stronger than Tajima's D and Fu and Li tests and are significantly less dependent on sample size. The ZnS statistic [35] calculates the average linkage disequilibrium statistic between all pairs of segregating sites to estimate linkage disequilibrium.

We calculated the parameters for population differentiation Fst (fixation index), Hst (haplotype diversity-based differentiation) [37,38], and Dxy (average number of nucleotide changes per site between two populations). In our work, DnaSP 6 (DNA Sequence Polymorphism) software was used to estimate all population genetic parameters [39].

Inter-population haplotype differentiation-based cross-population extended haplotype homozygosity (XP-EHH) [40] and Intra-population linkage disequilibrium-based integrated haplotype score (iHS) [41] are used to detect recent selection on BD-related genomic regions using PopHuman. iHS scores are obtained for EAS, EUR, AFR, and SAS subpopulations whereas Pairwise XP-EHH is calculated by comparing CHB (Han-Chinese from Beijing, China), CEU (Utah Residents of Western and Northern European Ancestry) and YRI (Yoruba in Ibadan, Nigeria) populations. XP-EHH and iHS estimates are based on a sliding window of 10kb. The highest determined iHS and XP-EHH scores for each gene from the sliding window analyses are presented. To avoid compromising the selection signals from other SNPs in the gene, the windows are not always focused on the variants linked to BD.

McDonald and Kreitman test (MKT) [42], Alpha value (proportion of adaptive substitutions) [43], Neutrality index (NI) [44], and Direction of selection (DoS) [45] tests were performed using chimpanzee sequences in order to obtain adaptive protein evolution parameters.

Adaptive protein evolution and recent selection tests were performed using PopHuman (https://pophuman.uab.cat/) [46] tool. The selection tests mentioned above can be carried out using PopHuman, a web-based application with a focus on human genomics.

2.4. Statistical Analyses

Chi-square tests are used to compare the distribution of susceptible, protective, ancestral, and derived effect alleles among populations. Shapiro test is used to evaluate deviations from the Normal distribution for continuous variables. By using a non-parametric Kruskal-Wallis one-way ANOVA followed by non-parametric Wilcoxon pairwise testing, population genetic parameter estimates for each gene were compared among Asian, European, and African populations. R (https://www.r-project.org) was used to do the principal component analysis with allele frequencies, and factoextra version 1.0.7 (https://cran.r-project.org/web/packages/factoextra/index.html) was used to visualize the results. Rfit package version 0.23.0 [47] was used to perform rank-based regressions [48]. Every statistical analysis was done in R (https://www.r-project.org/).

2.5. Biological Pathway and Molecular Function Analyses

Protein class, molecular function identification, protein-protein interaction, and biological process enrichment analyses were performed using STRING-DB (Search Tool for the Retrieval of Interacting Genes/Proteins) [49] (https://stringdb.org), and PANTHER (Protein ANalysis THrough Evolutionary Relationships) [50] (http://www.pantherdb.org/) online tools. Using the online STRING tool, a protein-protein interaction network was built from primary interactions based only on functional and physical protein relationships from curated databases and empirically determined sources. Medium confidence was defined as the minimum required interaction score. Using the Cytoscape [51] tool, a protein-protein interaction network was created.

CHAPTER 3

RESULTS AND DISCUSSION

3.1. Annotation of Behçet's Disease Related Variants

241 variations from 114 genes were found to be linked with BD when candidate gene and genome-wide association studies were taken into account. In candidate gene research, the final list only contained genetic connections that had been verified in at least two separate studies and that were based on the largest sample size (Appendix A). Only 9% of the variants linked to BD were found in exons, and 64% of these were reported to raise the risk of BD. For all but two of the variants, dbSNP identification (rs number) was possible. Gene ontology and pathway analyses of genes with respect to molecular function, biological process, and protein class showed a common representation of immune response-related genes involved in antigen processing and presentation (such as HLA), cytokine and chemokine signalling pathways (such as IL10, CCR) in the list. However, only limited gene ontology data was discovered for the majority of the top-hit BD genes, including PSORS1C1 and CCHCR1.

3.2. Analyses Using Behçet's Disease-Related Variants

We focused on published findings from studies done with Chinese, Japanese, Korean, and Turkish populations for analyses with BD-related variants. To determine if susceptibility to BD is an ancestral or a derived trait; variant/SNP identification number, reported p-values, and effect on BD (susceptible vs protective) are used. First, we determined the derived and ancestral allele status of variants linked to BD and compared the distribution of allele status according to their impact on BD. Overall, both protective (23 vs 13%) and susceptible (35 vs 29%) variants had slightly more derived alleles than ancestral alleles, but the difference was not statistically significant (Table 1). When all the variations from all the studies were combined, there was no statistically significant difference in the distribution of ancestral and derived alleles with regard to their susceptibility or protection against BD (Table 1). The analysis was stratified by study populations once more, but there was no evidence of enrichment of ancestral or derived alleles within susceptible or protective traits in any populations (Table 1).

There were no appreciable differences in the ancestral/derived status or susceptible/protective effect partitioning in BD variants amongst the groups (Figure 1).

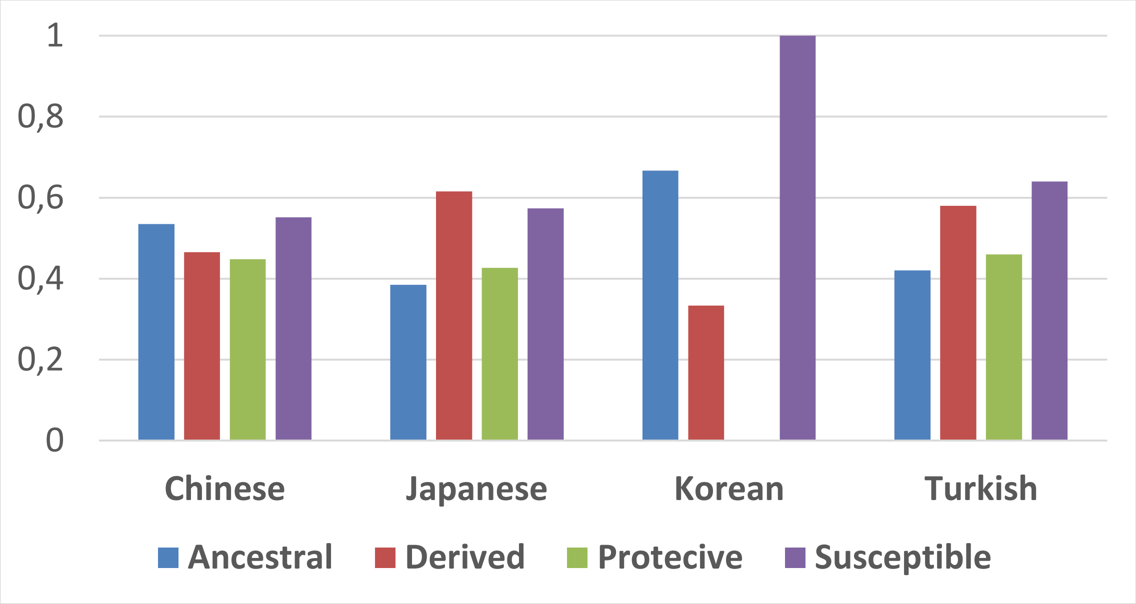

Figure 1. Ancestral and derived allele status distribution and their impact on BD in the populations with the highest frequency of BD. Table 1 provides information on allele counts.

For all twenty-six 1000 Genomes populations, allele frequencies of reported BD-related variants with rs numbers were collected (Appendix C). A principal component analysis was then performed on the resulting allele frequency matrix. The top two principal components (PCs) that provide the most significant information on population differentiation were displayed (Figure 2A).

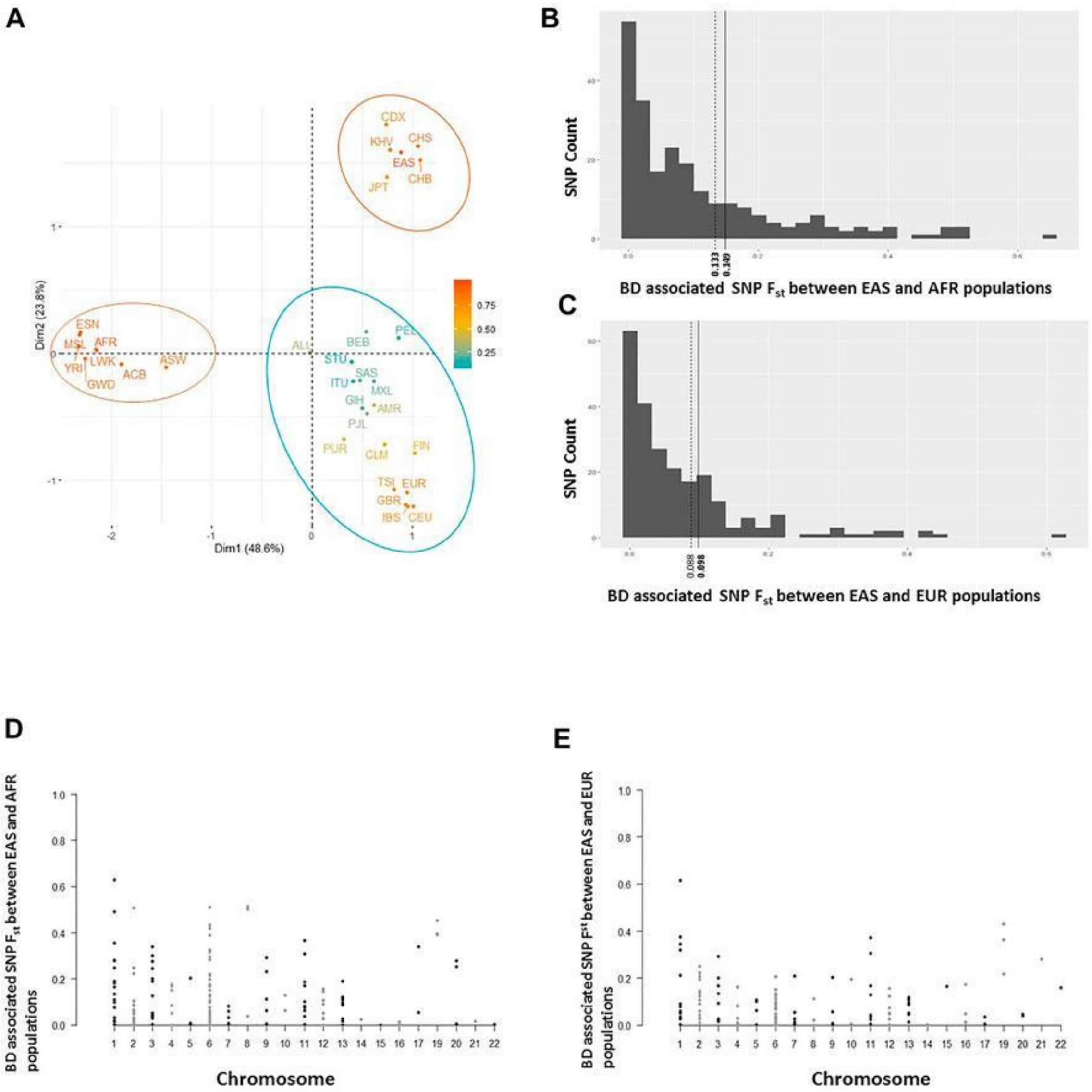

Figure 2. (A) Principal component analysis on a BD-related allele frequency matrix was used to separate the 26 1K Genome populations along the top 2 principal components (Dim1 and Dim2). Populations with ellipses around them denote clusters created using clustering analysis. (B) Estimates of population differentiation (Fst) for BD-associated SNPs between populations from East Asia (EAS) and Africa (AFR). Genome-wide SNP Fst and mean Fst of BD-related SNPs are depicted by solid and dashed vertical lines, respectively. (C) Fst estimations of BD-associated SNPs in populations from East Asia (EAS) and Europe (EUR). Genome-wide SNP Fst and mean Fst of BD-related SNPs are depicted by solid and dashed vertical lines, respectively. (D) Distribution of EAS-AFR Fst values for BD-related SNPs along human chromosomes. (E) Distribution of EAS-EUR Fst values for BD-related SNPs along human chromosomes.

The first PC made a distinct distinction between populations in Africa and the rest of the world. The first PC had the highest loading for BD-related variants in TNFAIP3, IL23R, EBF2, SMARCA2, ASB18, SAMD3, and COL12A1 indicating significant frequency differences between African and other populations. The second PC, interestingly, distinguished East Asian groups from the other populations, including Southeast Asians. On the second PC that separated East Asians from other populations, BD-associated variations in IL10, STAT4, TENM4, LYST, LILRB1, DTL, API5, LTN1, FUT2, TNFAIP3, and PMFBP1 made the biggest contributions. In comparison to the variants that contributed significantly to the first PC, these variants were also more significantly associated with BD in East Asian populations. Some of the most significant variants reported to be associated with BD making a contribution to the second PC include IL10 (rs1518111 and rs1800871), TNFAIP3 (rs9494885), and API5 (rs16937370) (Appendix A).

In addition to performing principal component analysis, we looked into population differentiation (Fst) amongst East Asian, European, and African populations. In comparison to genome-wide Fst estimates between East Asian and African (0.149) and East Asian and European (0.098) populations, the mean Fst estimates of BD-related SNPs between East Asian and African (0.133) and East Asian and European (0.088) populations were lower (Figures 2B, C). Between East Asians and Africans, seventy-four percent of the SNPs had lower Fst values than the mean Fst of all BD SNPs (less than 0.133; Figure 2B). Between East Asians and Europeans, sixty-eight percent of the SNPs had Fst values that were lower than the mean Fst of all BD SNPs (less than 0.088; Figure 2C). This suggests a small number of SNPs related to BD, significantly differentiate East Asians from other groups. There was no confounding from chromosomal stratification or genomic location, as shown by the even distribution of BD SNPs with high and low Fst values across the human chromosomes (Figures 2D, E). Additionally, in East Asians, population differentiation (Fst) in relation to African populations was greater for the ancestral BD-associated alleles than the derived BD-associated alleles (medians 0.09 vs 0.06, p = 0.008). (Appendix S).

Additional research on the allele frequency distributions of BD-associated SNPs in East Asian, African, and European populations revealed mainly overlapping histograms with various modalities (Appendix TA). No population showed any systematic enrichment or skew in favor of rare or more frequent alleles. We predicted that BD-associated variants with larger allele frequency differences and greater population differentiation (Fst) between East Asians (high BD prevalence) and other populations (low/no BD prevalence) would be more significantly associated with BD and would have a greater risk effect on BD. To test this theory, a rank regression analysis of the allele frequencies of BD-associated SNPs in East Asians was carried out, where the allele frequencies were regressed on the rank order by the reported p-values of these variants from BD GWAS studies in East Asian populations. There was no trend that was statistically significant (Appendix TB). But when the same rank regression analysis was carried out regressing allele frequency differences between East Asians and Europeans or East Asians and Africans on the rank order of the reported p-values of these variations, significant trends were seen (Figures 3A, B).

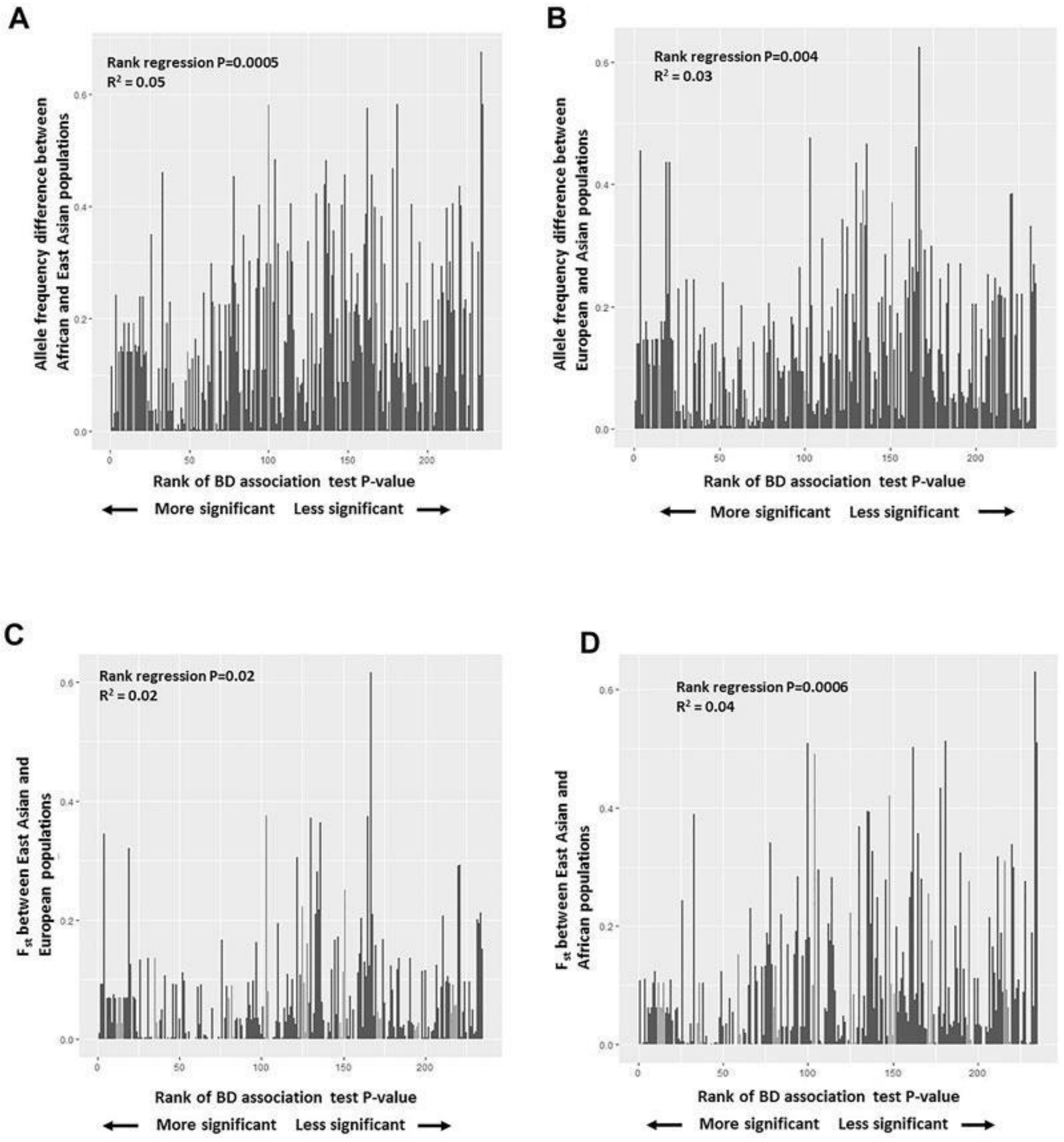

Figure 3. (A) Plot comparing the allele frequencies of BD-associated variants in populations from East Asia and Africa against the stated rank of BD association test p-values. (B) The plot of the rank of the reported BD association test p-values against the allele frequency difference between European and East Asian populations for BD-linked variants. (C) The plot of the rank of the reported BD association test p-values against the population differentiation (Fst) between East Asian and European populations. (D) The plot of the rank of the reported BD association test p-values against the population differentiation (Fst) between East Asian and African populations.

For variants associated with BD more significantly (having a greater effect on BD risk), the allele frequency differences between East Asians and Europeans or between East Asians and Africans were less. When the allele frequency differences between East Asians and Europeans or Africans were regressed on the actual reported p-values of these variations, the trend remained significant (Appendix U). Similar to this, a significant rank regression trend was seen between the rank order of the BD-related variant p-values and the East Asian-African and East Asian-European Fst estimations. Between East Asians and Europeans or Africans, more significant BD associations were seen to have lower Fst values (Figures 3C, D). Higher risk variants were shown to have less allele frequency differences and less population differentiation between East Asians and Europeans and East Asians and Africans when similar regression analyses were carried out using reported odds ratios (Appendix V).

3.3. Population Genetic Analyses with Behçet's Disease-Related Genes

3.3.1. Intra-population statistics

Following analyses that targeted particular BD-related variants, population genetic analyses focusing on the molecular evolution of BD-related genes were carried out (Appendices D-F). First, the cumulative distribution of summary statistics comparing 114 genes' population differentiation tests among African, East Asian, and European populations were compared. These statistics included estimates of nucleotide and haplotype diversity, allele frequency spectrum, and population differentiation tests (Table 2).

Table 2. Comparison of 114 BD-associated gene population genetic parameter estimations across the 1,000 Genomes populations of East Asian (EAS), African (AFR), and European (EUR). Medians and distributions of 114 BD-associated genes are compared by non-parametric Kruskal-Wallis one-way ANOVA, followed by non-parametric Wilcoxon pairwise tests. Small letters 'a' and 'b' represent significantly different pairwise comparisons between the three populations. S: segregating sites, Eta: total number of mutations, Hap: total number of haplotypes, Hd: Haplotype diversity, π (pi): nucleotide diversity, θK (ThetaK): average number of nucleotide differences, θW (ThetaW): Watterson theta.

Parameter	AFR Median (25%, 75%)	EAS Median (25%, 75%)	EUR Median (25%, 75%)	*p*
Nucleotide Diversity				
Total Sites	903 (246, 3695)	903 (246, 3695)	903 (246, 3695)	0.99
S	143 (15, 549)	113 (8, 400)	105 (11, 375)	0.05
Eta	553 (144, 1789)	400 (114, 1074)	375 (106, 1006)	0.05
Hap	482 (160, 1056)a	313 (96,877)b	278 (78, 819)b	0.004
Hd	0.99 (0.95, 0.99)	0.97 (0.86, 0.99)	0.97 (0.88, 0.92)	0.08
π	1.1 (0.8, 1.5)a	0.8 (0.6, 1.2)b	0.8 (0.6, 1.3)b	0.0002
θK	43.7 (14.7, 131.1)	35.3 (9.4, 107.2)	35.8 (11.1, 100.5)	0.37
θW	71.3 (18.5, 230.4)	53.4 (15.3, 143.4)	50.1 (14.1, 134.3)	0.08
Allele Frequency Spectrum				
Tajima's D	-1.2 (-1.5, -0.9)a	-0.8 (-1.3, -0.3)b	-0.7 (-1.2, -0.1)b	<0.001
Fu and Li's D*	-6.5 (-7.9, -4.3)a	-8.5 (-10.4, -4.0)b	-7.4 (-9.2, -4.0)a	0.0008
Fu and Li's F*	-3.7 (-4.5, -2.6)a	-4.5 (-5.6, -2.6)b	-3.9 (-4.8, -2.8)a	0.001
Fu's Fs	-31.4 (-34.4, -30.2)	-30.9 (-32.0, -9.6)	-31.0 (-32.2, -7.9)	0.06
Achaz's Y*	-0.7 (-1.2, -0.3)a	0.1 (-0.5, 0.7)b	0.2 (-0.4, 0.9)b	<0.001
R2	0.04 (0.03, 0.05)a	0.05 (0.04, 0.06)b	0.05 (0.04, 0.06)b	0.001
ZnS	0.02 (0.01, 0.05)a	0.04 (0.02, 0.07)b	0.04 (0.02, 0.07)b	0.0002
Population Differentiation				

Table 2 (cont.)

AFR - Fst	-	0.12 (0.07, 0.16)	0.09 (0.06, 0.14)	0.03
AFR - Dxy	-	0.001 (0.0008, 002)	0.001 (0.0008, 0.002)	0.9
AFR - Hst	-	0.009 (0.0003, 0.03)	0.008 (0.0004, 0.02)	0.31
Effect of Divergence on Nucleotide Diversity				
π/Fst	-	0.006 (0.004, 0,01)	0.007 (0.005, 0.02)	0.07
π/Dxy	-	0.76 (0.64, 0.88)	0.82 (0.71, 0.90)	0.02

African populations exhibited the highest nucleotide and haplotype diversity, followed by East Asian and European groups. East Asian people exhibited much more negative Fu and Li's D* and Fu and Li's F* test results than African populations, indicating a higher number of more recently derived singleton or rare variations, despite African populations having slightly more negative Tajima's D test results (Table 2, Appendix Y). East Asian and European populations had similar estimates for the Y*, R2, and ZnS parameters, indicating similar demographic and evolutionary histories (Table 2). Compared to African populations, East Asian and European populations' ZnS estimations were higher, indicating greater linkage disequilibrium and extended haplotypes (Table 2).

Gene parameter estimates were ordered from smallest to greatest for each population after comparisons between three populations using population genetics parameter estimates of all BD-associated genes (East Asian, European, and African). Within each population, each parameter—such as nucleotide diversity, haplotype diversity, Tajima's D, etc.—was rated separately. Genes within the lowest (values less than the 25th percentile) and highest (values more than the 75th percentile) quartiles for each parameter estimate were found. For the East Asian, African, and European populations separately, this ranking and the identification of genes with the lowest and highest quartile values were carried out by creating a list for each population. These lists were combined, and genes having values in the three populations' greatest and lowest quartiles for the population genetic parameter were compared. Most genes had overlapping rank orders when the highest and lowest quartile population genetic parameter values from the three populations were compared, however, several genes had values that were specific to East Asians (Appendices G, H, and R). In all three meta-populations, HLA genes, for instance, demonstrated balancing selection because of their great nucleotide diversity and quantity of intermediate frequency alleles (high positive Tajima's and Fu-Li test findings). But some genes reported to be among the most significantly associated with BD showed extreme reduction in nucleotide diversity, and excess of rare variants (such as DTL, NOD2, FUT2, IL23R, SMARCA2, STX8) only in East Asians, suggesting a unique evolutionary history of these genes in East Asians, where highest BD incidence and prevalence is reported.

3.3.2. Population differentiation and divergence

Inter-population statistics are used to assess population differentiation between East Asian, African, and European populations after intra-population analysis (Appendices I and J). Based on the Fst statistic of all 114 genes, population differentiation between Africans and East Asians was greater than population differentiation between Africans and Europeans (Table 2). Although average net nucleotide divergence (Dxy) and haplotype divergence (Hst) between Africans and East Asians, as well as between Africans and Europeans, were fairly similar, the effect of divergence on nucleotide diversity was greater, leading to a greater reduction in nucleotide diversity in East Asians (Table 2). The genes with the lowest Fst values were those with high nucleotide diversity, including HLA genes, and those with significant differences in rare allele profiles. While comparing the three populations for each gene, based on the highest and lowest quartile population differentiation and divergence parameters we have seen overlaps but also genes with divergence patterns found only in East Asians. IL6, OSR1, FUT2, HMP19, HNF4G, and IL1A have shown the highest Fst between East Asians and Africans (Appendices K, L, and R).

Furthermore, we compared the BD-related SNP Fst estimations with the corresponding genes of these variants (as described above in Section 3.2). We also want to determine whether SNPs associated with BD show greater population differentiation than other SNPs in the same gene between populations with high BD prevalence (East Asian) and those with extremely low/no BD prevalence (African). Since the frequency of the BD risk allele should be greater in the high BD prevalent population, we anticipate SNPs that have been reported to be significantly related to BD to show strong population differentiation across populations with high and very low/no BD prevalence. Only 39% (85/216) of the BD-associated SNPs showed population differentiation estimates (Fst) that were greater than those for the corresponding genes between East Asians and Africans (Appendix M). The remaining 61% (131/216) of BD SNPs had Fst values that were lower than the Fst estimations for respective genes (Appendix M). As predicted, some of the SNPs identified as having the strongest associations with BD, including those in PSORS1C1, POU5F1, MUC21, HLA-B, IL23R, and HLA-G, had Fst estimates higher than their corresponding genes, indicating a higher BD risk allele frequency difference and differentiation in these SNPs compared to other variants in those genes. Contrary to predictions, several SNPs that were shown to exhibit some of the strongest associations with BD, including those in the CCHCR1, IL-10, ERAP1, TLR4, and CCR1, had Fst estimates that were lower than the corresponding genes (Appendix M).

3.3.3. Recent selective sweeps

We used integrated haplotype score (iHS) and cross-population extended haplotype homozygosity (XP-EHH) testing to look for recent selections on BD-related genes. Since iHS values more than 2 make up the top 1% of the empirical distribution of genome-wide iHS values, absolute iHS values greater than 2 are regarded as suggesting recent selection. As values above 1.635 represent the top 90th percentile among HapMap Phase-2 SNPs [35,46], iHS values between 1.64 and 2.0 are viewed as suggesting moderate recent selection. About twenty genes associated with pattern recognition (i.e., NOD2), intracellular peptide processing (i.e., DTL, UBASH3B, GALNT10, LYST), adaptive immune regulation (HLA genes), immune cell differentiation (i.e., EBF2), and other molecular processes have undergone recent selection, which is unique to EAS populations (Appendix N).

3.3.4. Adaptive protein evolution

We investigated possible adaptive protein evolution in BD-associated genes in East Asians by utilizing variations of the McDonald and Kreitman (MK) test, comparing the proportion of adaptive substitutions in an MK test (alpha value), ratio of ratios in a MK 2x2 table (Neutrality index: NI), and the difference between the proportion of nonsynonymous divergence and nonsynonymous polymorphism (DoS: Direction of selection). Nearly all genes showed negative DoS results and NI values greater than one, which suggested that negative selection had occurred; however, only ABCB5, ATP8A1, CPVL, HIVEP3, PSORS1C1, and SLC22A23 showed statistical significance, indicating that there were many polymorphic changes but few divergent nonsynonymous (replacement) changes. None of the BD-related genes in East Asians is predicted to have undergone adaptive protein evolution or positive selection.

3.3.5. Gene expression profiles

For gene expression studies, we collected expression profiles of BD-related genes for 27 human tissues from the "NCBI normal tissue RNA-seq" collection (accessed in April 2022).[69] Considering all BD-related genes (Appendix Z.A) or just the genes that demonstrate recent selection in East Asians (Appendix P; Appendix Z.B), the highest gene expression was found in the gastrointestinal tissues. It's interesting to note that East Asians with BD tend to have gastrointestinal issues. Expression in immune function-related tissues such as thyroid, bone marrow, spleen, and lymph node was lower than in gastrointestinal tissues with a wider expression range (Appendix Z.B).

3.3.6. Genes with population genetic parameter and selection estimates unique to east Asians

Based on the difference between East Asian populations and African populations (Fst), detection of a selective sweep, and abundance of rare/singleton variants, we found 36 genes with various roles and different evolutionary histories that are unique to East Asians. Recent soft selective sweep was inferred for KCNK9, NOD2, RALGAPA2, CTNNA2, HLA-G, EBF2, DTL, NAV2, GALNT10, SEMA6D, LYST, and UBASH3B by concentrating on iHS values greater than 2. The genes KCNK9, NOD2, RALGAPA2, EBF2, and NAV2 all displayed significant frequency of recent rare/singleton mutations as well (Appendix R, Figure 4). For UBAC2, STX8, SMARCA2, and IL23R, high-frequency recent rare/singleton variants were seen, but there was no recent selective sweep signal. Low nucleotide diversity and high Fst with regard to African populations were found in FUT2, HMP19, HNF4G, and LYST. On the other side, IL6, IL1A, and OSR1 showed significant Fst and low haplotype diversity. HLA-F, RNF39, PSORS1C1, PPP1R11, ZNRD1, and SLC44A4 showed low Fst and high nucleotide diversity in contrast to the genes with reduced nucleotide and haplotype diversity (Appendix R, Figure 4).

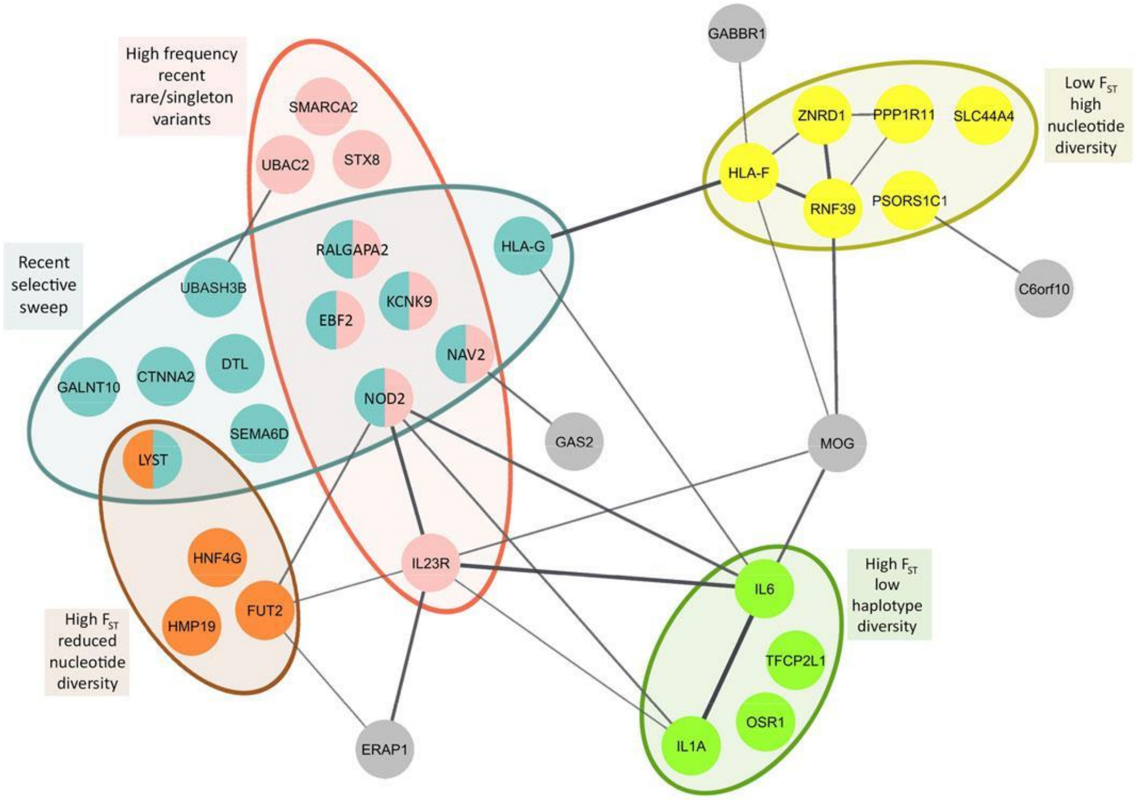

Figure 4. Population genetic parameter and selection estimates superposed on to protein-protein interaction network of BD-associated genes with population genetic parameter and selection estimates unique to East Asians. Primary interactions based on functional and physical protein associations only from curated databases and experimentally determined sources are presented. The line thickness of the edges indicates the strength of data support. High and low Fst represent the population differentiation of East Asians with respect to Africans.

With these 36 genes, we did a protein-protein interaction network analysis and discovered two main networks that were interconnected. One of the networks included the genes HLA-G, HLA-F, RNF39, PPP1R11, ZNRD1, GABBR1, and MOG. Surprisingly, nearly all of the genes in this network displayed the highest nucleotide diversity (Figure 4). All of these genes are located on Chromosome 6 in the extended HLA area, with immune-related tissues often exhibiting the highest levels of expression

(Appendices P and R). The second network includes ERAP1, IL1A, NOD2, FUT2, IL6, and IL23R, the center node of this network. The genes in this network display a variety of the aforementioned population genetic parameter estimations and selection signatures, in contrast to the first network (Figure 4). In the gastrointestinal tissues, this network's genes exhibit their highest levels of expression (Appendices P and R).

3.4. Ancient vs Modern Allele Frequency Differences

We observed a possible recent selection on HLA-B as suggested in previous reports, but the recent selection signature was not unique to HLA-B, 14 other BD-associated genes also showed recent selection including other MHC loci such as HLA-G, and other genes such as KCNK9 and NOD2 showed even a stronger selection than HLA-B.

Therefore, we hypothesized that we can independently test and compare the recent selection suggestion by comparing the allele frequencies of BD-associated alleles in ancient and modern populations.

The recent selection might have increased BD-associated allele frequencies in modern-day populations compared to ancient populations, through adaptation to or selection from environmental factors.

Unfortunately, we weren’t able to find SNPs from the genes showing high recent selection signs such as KCNK9.

Below in Table 3, the mean value of protective and susceptible alleles’ absolute frequency difference is shown. As seen in the table, there is not a significant allele frequency difference in either protective or susceptible SNPs.

Table 3. The mean value of protective and susceptible alleles' absolute frequency difference.

	Turkey	China	Israel	Central Europe
Mean of the Protective Alleles' Absolute Frequency Differences	0.069	0.079	0.125	0.076
Mean of the Susceptible Alleles' Absolute Frequency Differences	0.058	0.106	0.105	0.072

To detect the BD SNPs showing the most absolute frequency difference in Turkish, Chinese (CHB), Israeli and Central European (CEU) populations, SNPs within the highest 15th percentile in terms of the allele frequency difference between ancient and modern populations are listed and compared among four populations (Tables 4, 5, 6, 7).

Table 4. SNPs within the highest 15th percentile in terms of the allele frequency difference between ancient and modern populations in Turkey.

Gene	Behcet Allele			Turkey		
	SNP	Allele	Status	Ancient (n=152)	Modern (n= 3362)	Difference
IL23R, IL12RB2	rs1495965	G	Susceptible	0.373	0.547	-0.173
TCF19	rs2073723	T	Protective	0.343	0.192	0.151
POU5F1	rs3130501	A	Protective	0.337	0.192	0.145
MICA	rs2523467	A	Protective	0.144	0.418	-0.274
SAMD3	rs899276	A	Protective	0.500	0.274	0.226

Table 5. SNPs within the highest 15th percentile in terms of the allele frequency difference between ancient and modern populations in Israel.

Gene	Behcet Allele			Israel		
	SNP	Allele	Status	Ancient (n=94)	Modern (n=137)	Difference
HIVEP3	rs4660590	A	Protective	0.714	0.493	0.222
IL23R, IL12RB2	rs1495965	G	Susceptible	0.333	0.533	-0.200
STAT4	rs7574070	A	Susceptible	0.200	0.482	-0.282
SACM1L	rs1969624	C	Protective	0.636	0.489	0.147
CCR1	rs7631551	A	Protective	0.030	0.243	-0.212
CCR3	rs9990343	G	Protective	0.160	0.386	-0.226
ERAP1	rs17482078	T	Susceptible	0.265	0.084	0.181
LOC285830 (HLA-F antisense RNA1)	rs2523386	A	Susceptible	0.364	0.164	0.199
LOC285830 (HLA-F antisense RNA1)	rs1633041	T	Susceptible	0.120	0.405	-0.285
MUC21	rs2530710	A	Protective	0.368	0.120	0.248
MUC21	rs1634717	T	Susceptible	0.107	0.357	-0.250
MICA	rs2523467	A	Protective	0.278	0.477	-0.199
TSBP1	rs539703	C	Susceptible	1.000	0.569	0.431
HLA-DQA1	rs9272346	G	Protective	0.667	0.302	0.365
SAMD3	rs899276	A	Protective	1.000	0.407	0.593
TNFAIP3	rs10499194	C	Susceptible	0.000	0.677	-0.677
GIMAP2	rs10266069	A	Susceptible	1.000	0.485	0.515
SMARCA2	rs7033529	A	Protective	1.000	0.827	0.173
TLR4	rs4986790	G	Protective	0.333	0.022	0.311
TMEM132B	rs4435061	A	Protective	0.087	0.257	-0.170

Table 6. SNPs within the highest 15th percentile in terms of the allele frequency difference between ancient and modern populations in China.

Gene	Behcet Allele			China		
	SNP	Allele	Status	Ancient (n=64)	Modern (n=103)	Difference
IL-10	rs1554286	C	Protective	0.500	0.267	0.233
IL-10	rs1800871	T	Susceptible	0.444	0.743	-0.298
DNMT3A	rs1465825	C	Protective	0.241	0.422	-0.181
STAT4	rs7572482	A	Susceptible	0.348	0.617	-0.269
POU5F1	rs3130501	A	Protective	0.103	0.320	-0.217
HLA-C	rs3905495	C	Protective	0.375	0.612	-0.237
HLA-B	rs9266406	A	Susceptible	0.125	0.354	-0.229
BAG6 (BAT3)	rs2077102	T	Susceptible	0.460	0.165	0.294
SLC44A4	rs11965547	A	Susceptible	0.482	0.209	0.273
TSBP1	rs574710	G	Susceptible	0.700	0.408	0.292
TSBP1	rs539703	C	Susceptible	0.550	0.398	0.152
BTNL2	rs2076530	G	Protective	0.192	0.335	-0.143
SAMD3	rs899276	A	Protective	0.548	0.364	0.184
TNFAIP3	rs10499194	C	Susceptible	0.000	0.981	-0.981
KLRC4	rs2617170	C	Protective	0.735	0.549	0.187
SLC41A2	rs2731031	A	Susceptible	0.240	0.422	-0.182
UBAC2	rs2892976	G	Susceptible	0.438	0.291	0.146

Table 7. SNPs within the highest 15th percentile in terms of the allele frequency difference between ancient and modern populations in CEU.

Gene	Behcet Allele			CEU		
	SNP	Allele	Status	Ancient (n=432)	Modern (n=99)	Difference
IL23R	Rs11209032	A	Susceptible	0.188		0.188
IL23R, IL12RB2	rs1495965	G	Susceptible	0.267	0.424	-0.157
HLA-G	rs2523408	G	Susceptible	0.408	0.263	0.146
LOC285830 (HLA-F antisense RNA1)	rs2523386	A	Susceptible	0.321	0.096	0.225
MUC21	rs2517411	G	Susceptible	0.343	0.101	0.242
C6orf15	rs1265048	A	Protective	0.452	0.682	-0.230
HLA-B	rs9266409	C	Susceptible	0.402	0.182	0.220
BTNL2	rs2076530	G	Protective	0.263	0.475	-0.211
HLA-DQA1	rs9272346	G	Protective	0.721	0.434	0.286
SAMD3	rs899276	A	Protective	0.520	0.343	0.176
GIMAP2	rs10266069	A	Susceptible	0.732	0.485	0.247

3.5. Discussion

We have conducted population genetic analyses on BD associated genes and their variants to see if the increased BD risk in specific populations is due to past selection.

The SNP-based analyses have proved that both ancestral and derived alleles play a role in increasing or decreasing the BD risk. In addition to this, the allele frequency differences showed a similar distribution throughout the East Asians, Africans, and Europeans. These results indicate that BD-associated alleles are not specific to East Asians, they are present in other world populations with similar frequencies. A selection scenario favoring the BD-associated alleles in populations with high BD occurrence seems unlikely.

BD is considered an autoimmune disease [1,2]. Autoimmune diseases are believed to be triggered by a more active immune system [53]. Some derived traits causing autoimmune diseases are the result of selection against pathogens [19,53–56]. Based on this information, we expected derived traits to have a high population differentiation in BD-susceptible populations. However, the results do not support this hypothesis. Both ancestral and derived traits play a role in BD susceptibility. Therefore, further alternative selection (or neutral) explanations for BD variants are required in light of our data. For instance, changes in environmental factors may result in a relaxation of negative selection on derived alleles related to BD. Or eventually, allele dynamics related to BD may be the outcome of neutral demographic processes unaffected by any form of selection. Since it is not possible to differentiate these alternative selection scenarios by focusing only on allele type and frequency-based analyses, we have decided to proceed with population genetic analyses on the genes of the alleles associated with BD.

Several HLA region genes, including HLA-F, PPP1R11, RNF39, ZNRD1, and PSORS1C1, showed much higher nucleotide diversity in East Asians compared to other groups, indicating selection for high nucleotide and haplotype diversity in East Asians.

The pathogenesis of BD is thought to be triggered by the innate immune system's recognition of infectious organisms' proteins or human proteins due to molecular mimicry [57,58]. Interestingly, only in East Asians, we have identified recent selection sweep in genes involved in immune regulation (HLA-G), regulation of migration and cellular growth (CTNNA2, NAV2, SEMA6D, RALGAPA2), differentiation of B cells (EBF2), intracellular pattern recognition (NOD2), and intracellular processing of (foreign) peptides (UBASH3B, GALNT10, DTL, LYST). All the BD-associated derived and ancestral alleles in these genes affect BD susceptibility suggesting recent selection is influencing both ancestral and derived alleles. The results of the selective sweep rely on the strongest selective sweep signal seen on a gene, and the selective sweep windows are not always concentrated on variants that are linked to BD. This helps to not lose any selection signal on an undiscovered variant affecting BD susceptibility.

Highest population differentiation, high frequency of singleton/rare variants, low haplotype and nucleotide diversity were observed in genes responsible for microbial recognition (FUT2), stimulation of neutrophils and T helper 17 cells (IL23R), triggering of inflammation (IL1A, IL6), cell differentiation and maturation (SMARCA2), transcriptional regulation (HNF4G, TCFP2L1, OSR1). No selective sweep is seen for these genes, despite the fact that these genetic patterns are typically seen in sweeps. Despite the fact that some of the genes exhibit recent selective sweep signals, the sweep should be regarded as a soft sweep due to the low iHS values of the genes. This could be the primary cause of the genome-wide selection scans' failure to detect these BD risk genes. Soft sweep model suggests that beneficial mutations can appear at a locus on various genomic backgrounds, and these variants can simultaneously increase in frequency while none of them can reach fixation [59]. Pathogen identification, immune response modulation, self vs. non-self recognition, cellular differentiation, and other unidentified tasks reflecting many biological pathways are only a few of the diverse roles performed by genes related to BD. These genes also affect other inflammatory conditions [56]. For instance, certain IL23R variations that block IL23 signalling have protective effects not just in BD but also in psoriasis, inflammatory bowel disease (IBD), and ankylosing spondylitis (AS) [55,60–62]. Important elements of the immune response against pathogens, such as neutrophil-driven inflammation and Th17 T-cell-driven inflammation, are modulated by IL23R. Different variants and their derived and ancestral status may have a survival advantage against certain infections. Therefore, it's possible that no specific variant was the major object of selection resulting in a selective sweep. Similarly, among European and East Asian populations, distinct haplotypes and ancestral genetic polymorphisms influence a variety of inflammatory disorders in different degrees [63]. In BD, the ERAP1 effect is only seen in those who have the HLA-B51* type, suggesting that there may be an interaction between ERAP1 and HLA-B51* [64]. For both East Asians and Europeans, a soft selective sweep in HLA-B is seen in this study. These findings draw attention to the potential significance of interactions and epistasis in influencing the selection affecting BD genes. Soft selective signals were population specific. Most signals were only observed in Chinese samples (such as CHS, CHB, CDX). However Japanese samples did not show as soft selective sweep signals as many. This again shows the importance of analysing local populations to see soft selective sweep signals instead of focusing only on meta-populations. Finally, BD can affect the success of reproduction, but this effect is limited because the condition typically develops after sexual development [65,66]. Therefore, it is unlikely that a strong sexual selection against risk alleles would drive a hard selective sweep. It is significantly more difficult to identify and comprehend the underlying mechanisms of soft sweeps than hard sweeps, and often much higher sample sizes are needed. Future research can find novel sweeps and potential underlying mechanisms by collecting high-density SNP or sequencing data from various East Asian populations.

Compared to their BD-associated variations, certain gene-based analyses of genes including IL-10, MEFV, ERAP1, TLR4, and CCHCR1 exhibit larger population differentiation estimates. This implies the existence of additional variants with higher population differentiation than those that have been reported. These untested variants may have an impact on BD and may be to blame for BD's lack of heredity. In fact, individuals with BD who underwent targeted sequencing of the genes ERAP1, MEFV, TLR4, and IL10 revealed unique population-specific functional rare variants that were substantially related to BD [55,67]. We suggest that sequencing of genes with population differentiation estimates greater than their BD-linked variants can uncover novel BD risk variants and help us understand the molecular etiology of BD.

Finally, we summarized our thorough examination of the molecular evolutionary genetic etiology of BD. The genetic diversity in BD risk genes is shaped by a variety of evolutionary processes, and it is undoubtedly difficult to understand the precise mechanisms of selection that underlie these processes. We discovered a modest number of BD risk genes among East Asians with distinct evolutionary histories. The selection mechanisms and their historical causes in these genes can be uncovered in future studies using larger sequence data from BD patients and healthy controls recruited from local East Asian populations as well as from other groups with high BD prevalence. Several of the genes looked at in this study have been linked to other inflammatory illnesses as risk factors. Consequently, our findings and recommendations are not just applicable to BD but also to those inflammatory diseases.

The study has a number of drawbacks. To start with one, we did not use DNA sequence information from BD patients. Our findings should be validated by whole genome or candidate gene resequencing investigations in BD patients. Future studies using patient sequence data, we believe, will confirm our findings and uncover even better selection outcomes. For instance, BD patients had a frequency of a recently selected single extended HLA-B haplotype that was three times greater than that of controls [68]. Secondly, we restricted our analysis to East Asian groups. Future research should be done using high-quality genome sequence data from groups in Turkey, the Middle East, and Central Asia that have a high prevalence of BD. In addition to testing our findings, analyses of various populations can reveal intriguing evolutionary histories in BD genes that are unique to each population. Third, non-coding areas like the extended promoter and downstream sections of BD genes were not included in our analysis; instead, we focused solely on the coding regions, which were delineated by well-defined start and finish nucleotide locations. Future population genetic research should concentrate on these non-coding regions since several identified BD-related SNPs are in non-coding regions.

Comparing the BD-related variants showing an allele frequency difference higher than 15 percent among the ancient and modern populations, the Turkish population shows the highest allele frequency difference in the protective MICA variant rs2523467. This SNP shows an allele frequency difference among the highest 15th percentile in the Israeli population as well. However, in the Chinese population and the CEU population, we did not observe a major difference in terms of the MICA variant rs2523467. The second highest allele frequency difference observed in the Turkish population was protective SAMD3 variant rs899276, notably, this variant is present in the highest 15th percentile in all four populations. In Israeli and Chinese populations, the highest allele frequency is seen in the susceptible variant rs10499194, interestingly this variant has an allele frequency of 0 in the Israeli and Chinese ancient populations. These results support our previous findings about both protective and susceptible variants going under selection and no certain pattern is affecting the disease susceptibility. Therefore, further aDNA analyses including the genes of interest and related variants that are showing recent selection marks, are required to properly create a perspective on BD evolution.

CHAPTER 4

CONCLUSION

BD is not driven only by derived alleles. Both ancestral and derived alleles are involved in BD susceptibility. Among these variants, both susceptible and protective properties are present.

Alleles reported to be associated with BD are not only unique to East Asians but are also found in other world populations with appreciable frequencies. Some protective and susceptible variants present in populations included in this thesis even show similar frequencies.

Gene-based analyses show possible recent selection on a number of genes involved in pathogen recognition, pattern recognition (i.e. NOD2), intracellular processing of peptides (i.e. DTL, UBASH3B, GALNT10, LYST), adaptive immune regulation (HLA genes), differentiation of immune cells (i.e. EBF2), and other molecular processes. Since these genes are related to the immune system and show a selection sign, they can be responsible for disease susceptibility and progression.

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APPENDICES

APPENDIX A. GENES AND THEIR VARIANTS REPORTED TO BE ASSOCIATED WITH BEHCET DISEASE.

Gene	Variant/SNP	Type	Behcet Allele	Effect on Behcet Disease	OR	P value	Study Population	Reference
PSORS1C1	rs4959053	Intron	A	Susceptible	3.18	1.8x10^{-26}	Japanese	(Mizuki et al., 2010)
POU5F1	rs9501063	Exon	G	Susceptible	2.54	1.2x10^{-23}	Japanese	(Mizuki et al., 2010)
CCHCR1	rs2073716	Intron	C	Susceptible	2.57	1.7x10^{-23}	Japanese	(Mizuki et al., 2010)
IL-10	rs1518111	Intron	A	Susceptible	1.45	3.54x10^{-18}	Turkish	(Zhou et al., 2012; Remmers et al., 2010; Takeuchi et al., 2015)
MUC21	rs2517446	Upstream	C	Susceptible	2.28	1.5x10^{-17}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs1610637	Upstream	C	Susceptible	2.17	8.3x10^{-17}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs885940	Upstream	A	Susceptible	2.13	2.4x10^{-16}	Japanese	(Mizuki et al., 2010)
HLA-B	rs9266409	Upstream	C	Susceptible	1.92	2.4x10^{-16}	Japanese	(Mizuki et al., 2010)
POU5F1	rs3130501	Intron	A	Protective	0.50	2.5x10^{-16}	Japanese	(Mizuki et al., 2010)
HLA-G	rs2523408	Upstream	G	Susceptible	2.10	2.7x10^{-16}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs1633041	Upstream	T	Susceptible	2.15	6.2x10^{-16}	Japanese	(Mizuki et al., 2010)
POU5F1	rs9263804	Intron	C	Protective	0.52	1.2x10^{-15}	Japanese	(Mizuki et al., 2010)
HLA-G	rs9258466	Upstream	G	Susceptible	2.08	1.4x10^{-15}	Japanese	(Mizuki et al., 2010)
HLA-G	rs1736963	Upstream	T	Susceptible	2.08	1.5x10^{-15}	Japanese	(Mizuki et al., 2010)
POU5F1	rs3132524	Intron	A	Protective	0.52	2x10^{-15}	Japanese	(Mizuki et al., 2010)
HLA-B	rs9266406	Upstream	A	Susceptible	1.86	2.1x10^{-15}	Japanese	(Mizuki et al., 2010)
HLA-G	rs753544	Upstream	T	Susceptible	2.08	3.3x10^{-15}	Japanese	(Mizuki et al., 2010)
HLA-B	rs6910516	Upstream	C	Susceptible	1.86	6x10^{-15}	Japanese	(Mizuki et al., 2010)

(cont. on the next page)

Appendix A (cont.)

IL-10	rs1800871	Upstream	T	Susceptible	1.45	$1x10^{-14}$	Japanese	(Zhou et al., 2012; Mizuki et al., 2010; Takeuchi et al., 2015)
HLA-G	rs407238	Downstream	C	Susceptible	2.01	$1.6x10^{-14}$	Japanese	(Mizuki et al., 2010)
IL-10	rs1800872	Upstream	A	Susceptible	1.45	$2.1x10^{-14}$	Japanese, Turkish, Korean	(Zhou et al., 2012; Mizuki et al., 2010)
HLA-G	rs1633002	Upstream	A	Susceptible	2.01	$1.1x10^{-13}$	Japanese	(Mizuki et al., 2010)
HLA-G	rs1632973	Upstream	A	Susceptible	2.00	$1.6x10^{-13}$	Japanese	(Mizuki et al., 2010)
MUC21	rs2844673	Downstream	A	Susceptible	1.96	$1.7x10^{-13}$	Japanese	(Mizuki et al., 2010)
MUC21	rs2252926	Downstream	G	Susceptible	1.97	$1.8x10^{-13}$	Japanese	(Mizuki et al., 2010)
CCR1	rs7616215	Downstream	T	Protective	0.72	$4.3x10^{-13}$	Turkish-Japanese-Han Chinese	(Kirino et al., 2013a)
MUC21	rs2517411	Downstream	G	Susceptible	1.95	$4.9x10^{-13}$	Japanese	(Mizuki et al., 2010)
MEFV	rs61752717	Exon	G	Susceptible	2.65	$1.79x10^{-12}$	Turkish	(Deng et al., 2018; Kirino et al., 2013b)
CCHCR1	rs2240063	Intron	A	Protective	0.55	$2.1x10^{-12}$	Japanese	(Mizuki et al., 2010)
RNF39	rs9261317	Exon	A	Susceptible	2.25	$3.1x10^{-12}$	Japanese	(Mizuki et al., 2010)
MUC21	rs1632854	Downstream	T	Susceptible	1.82	$3.2x10^{-12}$	Japanese	(Mizuki et al., 2010)
MUC21	rs2523915	Downstream	T	Susceptible	1.90	$7.7x10^{-12}$	Japanese	(Mizuki et al., 2010)
TNFAIP3	rs9494885	Upstream	T	Protective	0.50	$8.26x10^{-12}$	Han Chinese	(Li et al., 2013)
HLA-F	rs3116788	Upstream	G	Protective	0.48	$8.4x10^{-12}$	Japanese	(Mizuki et al., 2010)
IFNγ	UTR-5644	Downstream	A	Susceptible	3.53	$1x10^{-11}$	Turkish	(Zhou et al., 2012)
MUC21	rs1634717	Downstream	T	Susceptible	1.80	$1.6x10^{-11}$	Japanese	(Mizuki et al., 2010)
TCF19	rs2073723	Intron	T	Protective	0.57	$1.9x10^{-11}$	Japanese	(Mizuki et al., 2010)
MUC21	rs2252925	Downstream	G	Susceptible	1.87	$2.1x10^{-11}$	Japanese	(Mizuki et al., 2010)
C6orf15 (STG)	rs1265048	Upstream	A	Protective	0.59	$2.6x10^{-11}$	Japanese	(Mizuki et al., 2010)
HLA-C	rs3905495	Upstream	C	Protective	0.59	$4.7x10^{-11}$	Japanese	(Mizuki et al., 2010)
BTNL2	rs2076530	Exon	G	Protective	0.59	$4.7x10^{-11}$	Japanese	(Mizuki et al., 2010)

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Appendix A (cont.)

ERAP1	rs17482078	Exon	T	Susceptible	4.56	4.73x10^{-11}	Turkish	(Kirino et al., 2013a; Takeuchi et al., 2015)
HLA-F	rs1610584	Upstream	T	Protective	0.51	6.5x10^{-11}	Japanese	(Mizuki et al., 2010)
ZNRD1	rs9261265	Upstream	C	Susceptible	2.04	7.3x10^{-11}	Japanese	(Mizuki et al., 2010)
HLA-F	rs1611388	Upstream	C	Protective	0.52	7.8x10^{-11}	Japanese	(Mizuki et al., 2010)
HLA-DQA1	rs9272346	Upstream	G	Protective	0.60	8.7x10^{-11}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs2844845	Intron	A	Susceptible	2.07	9.5x10^{-11}	Japanese	(Mizuki et al., 2010)
HCG9	rs9260954	Downstream	G	Susceptible	2.06	1.2x10^{-10}	Japanese	(Mizuki et al., 2010)
GABBR1	rs29273	Upstream	G	Susceptible	2.03	1.4x10^{-10}	Japanese	(Mizuki et al., 2010)
MUC21	rs2530710	Upstream	A	Protective	0.53	3x10^{-10}	Japanese	(Mizuki et al., 2010)
HLA-F	rs1610585	Upstream	C	Protective	0.52	3.3x10^{-10}	Japanese	(Mizuki et al., 2010)
HCG9	rs6926792	Downstream	A	Susceptible	1.75	3.3x10^{-10}	Japanese	(Mizuki et al., 2010)
DHFRP2	rs7761068	Exon	T	Protective	0.48	3.5x10^{-10}	Japanese	(Mizuki et al., 2010)
UBD	rs3025657	Downstream	G	Protective	0.48	3.8x10^{-10}	Japanese	(Mizuki et al., 2010)
HCG27	rs3130944	Downstream	C	Susceptible	1.70	4.3x10^{-10}	Japanese	(Mizuki et al., 2010)
HLA-F	rs1610593	Upstream	T	Protective	0.53	4.5x10^{-10}	Japanese	(Mizuki et al., 2010)
MICA	rs3094584	Downstream	T	Susceptible	1.69	4.7x10^{-10}	Japanese	(Mizuki et al., 2010)
HLA-F	rs1611381	Upstream	T	Protective	0.53	5.6x10^{-10}	Japanese	(Mizuki et al., 2010)
ABCB5	rs2190411	Intron	C	Susceptible	2.51	8.77x10^{-10}	Han Chinese	(Hou et al., 2012c)
C6orf10 (TSBP1)	rs574710	Intron	G	Susceptible	1.65	9.7x10^{-10}	Japanese	(Mizuki et al., 2010)
C6orf47 (G4)	rs2242655	Exon	C	Susceptible	1.70	1.1x10^{-09}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs2523386	Intron	A	Susceptible	2.02	1.2x10^{-09}	Japanese	(Mizuki et al., 2010)
KLRC4 Appendix A (cont.)	rs2617170	Exon	C	Protective	0.78	1.34x10^{-09}	Turkish-Japanese	(Kirino et al., 2013a; Takeuchi et al., 2015)
SGPP2	rs17562982	Intron	T	Susceptible	2.79	1.91x10^{-09}	Han Chinese	(Hou et al., 2012c)
TRIM31	rs9261376	Downstream	G	Susceptible	1.67	2.2x10^{-09}	Japanese	(Mizuki et al., 2010)
MICA	rs2523467	Upstream	A	Protective	0.59	2.3x10^{-09}	Japanese	(Mizuki et al., 2010)

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Appendix A (cont.)

SUSD1	rs2782932	Intron	T	Susceptible	2.41	2.47x10^{-09}	Han Chinese	(Hou et al., 2012c)
TRIM31	rs6923832	Downstream	A	Susceptible	2.00	2.5x10^{-09}	Japanese	(Mizuki et al., 2010)
HLA-F	rs1627465	Upstream	C	Protective	0.54	2.6x10^{-09}	Japanese	(Mizuki et al., 2010)
C6orf10 (TSBP1)	rs544358	Intron	C	Susceptible	1.63	2.8x10^{-09}	Japanese	(Mizuki et al., 2010)
RIMBP2	rs2895135	Intron	A	Susceptible	2.55	3.35x10^{-09}	Han Chinese	(Hou et al., 2012c)
HLA-F	rs1611356	Upstream	G	Protective	0.55	3.4x10^{-09}	Japanese	(Mizuki et al., 2010)
HLA-DQA1	rs9272723	Intron	T	Protective	0.61	4.8x10^{-09}	Japanese	(Mizuki et al., 2010)
C6orf10 (TSBP1)	rs926591	Intron	T	Susceptible	1.62	5.1x10^{-09}	Japanese	(Mizuki et al., 2010)
BAG6(BAT3)	rs2077102	Intron	T	Susceptible	1.64	5.2x10^{-09}	Japanese	(Mizuki et al., 2010)
C6orf10 (TSBP1)	rs539703	Intron	C	Susceptible	1.61	5.3x10^{-09}	Japanese	(Mizuki et al., 2010)
FUT2	rs681343	Exon	T	Susceptible	1.30	5.9x10^{-09}	Iranian-Turkish	(Takeuchi et al., 2015)
API5 (LINC01499)	rs16937370	Upstream	G	Susceptible	2.46	6.01x10^{-09}	Han Chinese	(Hou et al., 2012c)
TRIM31	rs9261389	Downstream	G	Susceptible	1.64	6.1x10^{-09}	Japanese	(Mizuki et al., 2010)
SMG6	rs749240	Exon	T	Susceptible	2.49	6.43x^{-09}	Han Chinese	(Hou et al., 2012c)
IL23R,IL12RB2	rs924080	Down/Up-stream	T	Susceptible	1.28	6.69x10^{-09}	Japanese-Turkish	(Zhou et al., 2012; Remmers et al., 2010)
HLA-G	rs1077433	Upstream	A	Susceptible	1.79	6.9x10^{-09}	Japanese	(Mizuki et al., 2010)
C6orf10 (TSBP1)	rs4959093	Intron	C	Susceptible	1.62	8.6x10^{-09}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs9258205	Intron	C	Protective	0.56	9.5x10^{-09}	Japanese	(Mizuki et al., 2010)
SLC44A4	rs11965547	Intron	A	Susceptible	1.65	1x10^{-08}	Japanese	(Mizuki et al., 2010)
MOG	rs3129045	Downstream	T	Susceptible	1.78	1.2x10^{-08}	Japanese	(Mizuki et al., 2010)
ZNRD1	rs9261189	Upstream	T	Susceptible	1.64	1.4x10^{-08}	Japanese	(Mizuki et al., 2010)
HLA-F	rs7741807	Upstream	G	Protective	0.54	1.5x10^{-08}	Japanese	(Mizuki et al., 2010)
HCG9	rs6931776	Downstream	G	Susceptible	1.63	1.7x10^{-08}	Japanese	(Mizuki et al., 2010)
SLC43A3	rs549630	Downstream	G	Susceptible	2.27	2.04x10^{-08}	Han Chinese	(Hou et al., 2012c)
HLA-DQB1	rs6457617	Upstream	C	Protective	0.63	2.1x10^{-08}	Japanese	(Mizuki et al., 2010)
GALNTL1	rs12589991	Intron	A	Susceptible	2.51	2.16x10^{-08}	Han Chinese	(Hou et al., 2012c)

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Appendix A (cont.)

PPP1R11	rs2074482	Exon	T	Susceptible	1.60	2.2x10^{-08}	Japanese	(Mizuki et al., 2010)
HLA-G	rs1736951	Upstream	A	Susceptible	1.75	2.3x10^{-08}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs1615251	Upstream	T	Susceptible	1.62	2.7x10^{-08}	Japanese	(Mizuki et al., 2010)
IL23R,IL12RB2	rs12119179	Down/Up-stream	A	Susceptible	1.55	2.7x10^{-08}	Japanese-Turkish	(Mizuki et al., 2010)
UBD	rs6933331	Downstream	A	Protective	0.55	2.8x10^{-08}	Japanese	(Mizuki et al., 2010)
ZNRD1	rs3869068	Upstream	A	Susceptible	1.61	3.3x10^{-08}	Japanese	(Mizuki et al., 2010)
SLIT2	rs13435197	Intron	A	Susceptible	2.46	3.59x10^{-08}	Han Chinese	(Hou et al., 2012c)
HCG9	rs6911737	Downstream	A	Susceptible	1.60	4.1x10^{-08}	Japanese	(Mizuki et al., 2010)
LOC285830 *(HLA-F antisense RNA1)*	rs1737031	Upstream	A	Susceptible	1.59	4.4x10^{-08}	Japanese	(Mizuki et al., 2010)
ASB18	rs7561555	Intron	C	Susceptible	2.28	4.7x10^{-08}	Han Chinese	(Hou et al., 2012c)
IL23R,IL12RB2	rs11209033	Down/Up-stream	C	Susceptible	1.54	5.5x10^{-08}	Japanese-Turkish	(Mizuki et al., 2010)
GIMAP4	rs1608157	Upstream	C	Susceptible	2.53	6.01x10^{-08}	Korean	(Lee et al., 2013; Deng et al., 2018)
IL-10	rs1554286	Intron	C	Protective	0.62	8x10^{-08}	Chinese	(Mizuki et al., 2010)
IL23R,IL12RB2	rs12141431	Down/Up-stream	C	Susceptible	1.52	1.1x10^{-07}	Han Chinese	(Mizuki et al., 2010)
CPLX1	rs11248047	Upstream	A	Susceptible	1.36	1.26x10^{-07}	Turkish	(Remmers et al., 2010)
COL12A1	rs4640857	Downstream	G	Protective	0.65	1.3x10^{-07}	Japanese	(Mizuki et al., 2010)
GIMAP4	rs1916012	Upstream	T	Susceptible	2.38	2.62x10^{-07}	Korean	(Lee et al., 2013)
GIMAP4	rs1522596	Upstream	T	Susceptible	2.38	3.47x10^{-07}	Korean	(Lee et al., 2013; Deng et al., 2018)
DNMT3A	rs1465825	Intron	C	Protective	0.49	3.83x10^{-07}	Han Chinese	(Hou et al., 2012c)
C10orf11 (LRMDA)	rs1323076	Intron	G	Protective	0.61	1.2x10^{-06}	Japanese	(Mizuki et al., 2010)
PAX8	rs11123169	Downstream	C	Susceptible	1.53	1.3x10^{-06}	Japanese	(Mizuki et al., 2010)
MSX2	rs10516130	Downstream	A	Protective	0.23	2.98x10^{-06}	Han Chinese	(Hou et al., 2012c)
SORBS2	rs4493590	Intron	G	Susceptible	1.86	4.88x10^{-06}	Han Chinese	(Hou et al., 2012c)

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Appendix A (cont.)

HIVEP3	rs4660590	Intron	A	Protective	0.69	5.7x10^{-06}	Japanese	(Mizuki et al., 2010)
CEP135	rs2593082	Intron	T	Susceptible	1.42	6.2x10^{-06}	Japanese	(Mizuki et al., 2010)
UBAC2	rs3825427	Upstream	T	Susceptible	1.50	6.9x10^{-06}	Chinese	(Hou et al., 2012a; Deng et al., 2018)
RALGAPA2	rs6082210	Upstream	A	Protective	0.17	7.01x10^{-06}	Han Chinese	(Hou et al., 2012c)
GIMAP1	rs2286900	Exon	T	Susceptible	1.81	9.22x10^{-06}	Korean	(Lee et al., 2013; Deng et al., 2018)
TTLL7	rs11163772	Downstream	A	Susceptible	1.52	9.5x10^{-06}	Japanese	(Mizuki et al., 2010)
HMP19	rs1909704	Downstream	A	Susceptible	1.43	9.5x10^{-06}	Japanese	(Mizuki et al., 2010)
TFCP2L1	rs17006292	Intron	A	Protective	0.13	1.03x10^{-05}	Han Chinese	(Hou et al., 2012c)
TENM4(ODZ4)	rs2156215	Intron	T	Protective	0.69	1.1x10^{-05}	Japanese	(Mizuki et al., 2010)
OSR1	rs4666492	Upstream	G	Protective	0.62	1.2x10^{-05}	Japanese	(Mizuki et al., 2010)
KLRK1	rs2617151	Intron	A	Protective	0.63	1.2x10^{-05}	Japanese	(Mizuki et al., 2010)
CTNNA2	rs4852547	Intron	G	Protective	0.62	1.3x10^{-05}	Japanese	(Mizuki et al., 2010)
IL12A	rs17810546	Upstream	A	Susceptible	1.66	1.49x10^{-05}	Turkish-mixed	(Remmers et al., 2010; Takeuchi et al., 2015)
MN1	rs134006	Downstream	C	Susceptible	1.46	1.6x10^{-05}	Japanese	(Mizuki et al., 2010)
CEP135	rs2611826	Intron	G	Susceptible	1.40	1.6x10^{-05}	Japanese	(Mizuki et al., 2010)
PSMD14	rs6744214	Intron	T	Susceptible	1.76	1.67x10^{-05}	Han Chinese	(Hou et al., 2012c)
API5 (LINC01499)	rs420798	Intron	C	Susceptible	1.72	1.79x10^{-05}	Han Chinese	(Hou et al., 2012c)
C6orf85(SLC22A23)	rs12194547	Intron	C	Protective	0.16	1.91x10^{-05}	Han Chinese	(Hou et al., 2012c)
PSMD14	rs6733456	Intron	C	Susceptible	1.75	1.98x10^{-05}	Han Chinese	(Hou et al., 2012c)
LTN1(RNF160)	rs2832137	Downstream	T	Protective	0.64	2.1x10^{-05}	Japanese	(Mizuki et al., 2010)
HERPUD2	rs11763983	Downstream	T	Protective	0.66	2.1x10^{-05}	Japanese	(Mizuki et al., 2010)
LILRA1	rs103294	Upstream	C	Susceptible	1.76	2.19x10^{-05}	Han Chinese	(Hou et al., 2012c)
LILRB1	rs798887	Upstream	A	Susceptible	1.83	2.23x10^{-05}	Han Chinese	(Hou et al., 2012c)
SAMD3(TMEM200A)	rs9483115	Intron	T	Protective	0.72	2.5x10^{-05}	Japanese	(Mizuki et al., 2010)
GALNT10	rs574750	Intron	A	Susceptible	1.66	2.5x10^{-05}	Japanese	(Mizuki et al., 2010)

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Appendix A (cont.)

GIMAP2	rs10266069	Upstream	A	Susceptible	1.83	2.57x10^{-05}	Korean	(Lee et al., 2013; Deng et al., 2018)
KLRK1	rs2733852	Intron	G	Protective	0.65	2.8x10^{-05}	Japanese	(Mizuki et al., 2010)
DEPDC1	rs6692084	Upstream	A	Susceptible	1.89	2.81x10^{-05}	Han Chinese	(Hou et al., 2012c)
GIMAP2	rs10256482	Upstream	T	Susceptible	1.83	2.82x10^{-5}	Korean	(Lee et al., 2013; Deng et al., 2018)
UBAC2	rs9517701	Intron	G	Susceptible	1.40	2.9x10^{-05}	Chinese	(Hou et al., 2012a)
DEPDC1	rs12134670	Upstream	C	Susceptible	2.15	3.13x10^{-05}	Han Chinese	(Hou et al., 2012c)
SEMA6D	rs470151	Downstream	T	Susceptible	1.54	3.2x10^{-05}	Japanese	(Mizuki et al., 2010)
CDH26	rs817277	Downstream	A	Susceptible	1.78	3.24x10^{-05}	Han Chinese	(Hou et al., 2012c)
PMFBP1	rs11862324	Upstream	T	Susceptible	1.39	3.3x10^{-05}	Japanese	(Mizuki et al., 2010)
SAMD3	rs4897380	Intron	C	Susceptible	1.38	3.4x10^{-05}	Japanese	(Mizuki et al., 2010)
NAV2	rs2707110	Intron	C	Susceptible	1.43	3.5x10^{-05}	Japanese	(Mizuki et al., 2010)
UBAC2	rs9517668	Intron	T	Susceptible	2.62	3.61x10^{-05}	Turkish-Italy	(Sawalha et al., 2011)
STK39	rs2390639	Intron	A	Susceptible	1.72	3.97x10^{-05}	Han Chinese	(Hou et al., 2012c)
TMEM132B	rs4435061	Intron	A	Protective	0.73	4x10^{-05}	Japanese	(Mizuki et al., 2010)
STX8	rs1549332	Intron	A	Susceptible	1.59	4x10^{-05}	Japanese	(Mizuki et al., 2010)
SAMD3(TMEM200A)	rs4141940	Intron	A	Protective	0.73	4x10^{-05}	Japanese	(Mizuki et al., 2010)
CCDC180	rs2061634	Exon	G	Susceptible	2.04	4.2x10^{-05}	Turkish	(Fei et al., 2009; Hou et al., 2012a)
OVCH1	rs1436321	Downstream	A	Susceptible	1.39	4.4x10^{-05}	Japanese	(Mizuki et al., 2010)
SLC41A2	rs2731031	Intron	A	Susceptible	1.40	4.7x10^{-05}	Japanese	(Mizuki et al., 2010)
NAV2	rs873764	Intron	G	Susceptible	1.42	4.7x10^{-05}	Japanese	(Mizuki et al., 2010)
HNF4G	rs2980221	Upstream	A	Protective	0.71	4.8x10^{-05}	Japanese	(Mizuki et al., 2010)
IL1 (IL1A)	rs1800587	Exon	C	Susceptible	2.90	5x10^{-05}	Turkish	(Zhou et al., 2012)
SMARCA2	rs7033529	Intron	A	Protective	0.73	5.1x10^{-05}	Japanese	(Mizuki et al., 2010)
EBF2	rs4570167	Intron	C	Susceptible	1.47	5.2x10^{-05}	Japanese	(Mizuki et al., 2010)
GAS2	rs10833804	Intron	G	Protective	0.73	5.4x10^{-05}	Japanese	(Mizuki et al., 2010)
PAX8	rs10864912	Intron	T	Susceptible	1.47	5.7x10^{-05}	Japanese	(Mizuki et al., 2010)

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Appendix A (cont.)

DTL	rs1472224	Downstream	G	Protective	0.16	5.73x10^{-05}	Han Chinese	(Hou et al., 2012c)
STAT4	rs897200	Intron	A	Susceptible	1.45	5.88x10^{-05}	Han Chinese	(Hou et al., 2012c; Takeuchi et al., 2015)
LYST/NID1	rs7354999	Down/Up-stream	G	Susceptible	1.38	6.1x10^{-05}	Japanese	(Mizuki et al., 2010)
STK39	rs3769393	Intron	G	Susceptible	1.70	6.17x10^{-05}	Han Chinese	(Hou et al., 2012c)
TMEM132B	rs10846917	Intron	T	Susceptible	1.39	6.3x10^{-05}	Japanese	(Mizuki et al., 2010)
LOC100132252	rs9469615	Intergenic	C	Protective	0.63	6.3x10^{-05}	Japanese	(Mizuki et al., 2010)
CDH26	rs817283	Downstream	A	Susceptible	1.74	6.42x10^{-05}	Han Chinese	(Hou et al., 2012c)
SAMD3(TMEM200A)	rs899276	Intron	A	Protective	0.73	6.5x10^{-05}	Japanese	(Mizuki et al., 2010)
LOC107984355	rs872837	Intron	A	Susceptible	1.46	6.5x10^{-05}	Japanese	(Mizuki et al., 2010)
SACM1L	rs1969624	Intron	C	Protective	0.67	6.8x10^{-05}	Japanese	(Mizuki et al., 2010)
IL23R	rs11209026	Intron	A	Protective	0.68	6.9x10^{-05}	Turkish-Japanese	(Deng et al., 2018)
IL23R	rs76418789	Intron	A	Protective	0.54	6.9x10^{-05}	Turkish-Japanese	(Deng et al., 2018)
PLEKHB1	rs591804	Intron	G	Protective	0.72	7.4x10^{-05}	Japanese	(Mizuki et al., 2010)
SAMD3(TMEM200A)	rs7758496	Intron	G	Protective	0.73	7.7x10^{-05}	Japanese	(Mizuki et al., 2010)
TMEM132B	rs10846924	Intron	T	Protective	0.74	8x10^{-05}	Japanese	(Mizuki et al., 2010)
ATP8A1	rs2100766	Upstream	T	Protective	0.62	8.2x10^{-05}	Japanese	(Mizuki et al., 2010)
IL23R, IL12RB2	rs1495965	Down/Up-stream	G	Susceptible	1.25	8.4x10^{-05}	Japanese-Turkish	(Zhou et al., 2012; Mizuki et al., 2010)
EBF2	rs4242425	Intron	T	Susceptible	1.44	8.4x10^{-05}	Japanese	(Mizuki et al., 2010)
UBAC2	rs9554581	Intron	T	Susceptible	2.48	8.53x10^{-05}	Turkish-Italy	(Sawalha et al., 2011)
STAT4	rs7574070	Intron	A	Susceptible	1.27	8.56x10^{-05}	Turkish-Japanese	(Kirino et al., 2013a; Hou et al., 2012c; Takeuchi et al., 2015)
CCR1	rs17282391	Downstream	G	Protective	0.15	8.66x10^{-05}	Han Chinese	(Hou et al., 2012b)
CCR1	rs13084057	Downstream	G	Protective	0.15	8.66x10^{-05}	Han Chinese	(Hou et al., 2012b)

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CCR1	rs7631551	Downstream	A	Protective	0.15	$8.66x10^{-05}$	Han Chinese	(Hou et al., 2012b)
C10orf11(LRMDA)	rs17434565	Intron	G	Protective	0.64	$9x10^{-05}$	Japanese	(Mizuki et al., 2010)
SAMD3(TMEM200A)	rs724324	Intron	G	Protective	0.74	$9.5x10^{-05}$	Japanese	(Mizuki et al., 2010)
KCNK9	rs1961261	Downstream	A	Protective	0.69	$9.5x10^{-05}$	Japanese	(Mizuki et al., 2010)
STAT4	rs7572482	Intron	A	Susceptible	1.68	$9.77x10^{-05}$	Turkish	(Hou et al., 2012c)
CCR3	rs13075270	Intron	C	Protective	0.13	$9.9x10^{-05}$	Han Chinese	(Hou et al., 2012b)
CCR3	rs13092160	Intron	C	Protective	0.13	$9.9x10^{-05}$	Han Chinese	(Hou et al., 2012b)
CCR3	rs2373156	Intron	T	Protective	0.13	$9.9x10^{-05}$	Han Chinese	(Hou et al., 2012b)
CCR3	rs1542755	Intron	A	Protective	0.13	$9.9x10^{-05}$	Han Chinese	(Hou et al., 2012b)
UBAC2	rs727263	Intron	A	Susceptible	2.45	$1x10^{-04}$	Turkish-Italy	(Sawalha et al., 2011)
CPVL	rs317711	Intron	C	Susceptible	2.26	$1x10^{-04}$	Turkish	(Fei et al., 2009; Hou et al., 2012a)
IL17F-A126G, (Glu126Gly)	rs2397084	Exon	T	Protective	0.06	$1x10^{-04}$	Korean	(Jang et al., 2008)
UBAC2	rs7332161	Intron	A	Susceptible	2.43	$1.1x10^{-04}$	Turkish-Italy	(Sawalha et al., 2011)
IL23R	rs17375018	Intron	G	Susceptible	1.57	$1.11x10^{-04}$	Han Chinese	(Zhou et al., 2012; Jiang et al., 2010)
CCR1	rs10510749	Downstream	T	Protective	0.16	$1.22x10^{-04}$	Han Chinese	(Hou et al., 2012b)
IL23R	rs11209032	Downstream	A	Susceptible	1.48	$1.58x10^{-04}$	Han Chinese	(Zhou et al., 2012; Jiang et al., 2010)
UBAC2	rs17575643	Intron	T	Susceptible	2.91	$1.8x10^{-04}$	Turkish-Italy	(Sawalha et al., 2011)
SUMO4	rs237024	Downstream	C	Susceptible	1.70	$2x10^{-04}$	Han Chinese	(Deng et al., 2018)
IL1	rs16944	Upstream	G	Susceptible	2.19	$2x10^{-04}$	Turkish	(Zhou et al., 2012)
CCR3	rs13067058	Intron	A	Protective	0.14	$2x10^{-04}$	Han Chinese	(Hou et al., 2012b)
UBAC2	rs2892976	Downstream	G	Susceptible	1.96	$2.3x10^{-04}$	Turkish-Italy	(Sawalha et al., 2011)
LOC100129342	rs11206377	Intergenic	G	Susceptible	1.84	$3x10^{-04}$	Turkish	(Fei et al., 2009; Hou et al., 2012a)
UBAC2	rs7999348	Intron	G	Susceptible	1.78	$5.8x10^{-04}$	Turkish-Italy	(Sawalha et al., 2011)
TNFAIP3	rs10499194	Upstream	C	Susceptible	1.92	$1x10^{-03}$	Han Chinese	(Li et al., 2013)

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Appendix A (cont.)

TNFAIP3	rs7753873	Upstream	C	Susceptible	1.49	1x10^{-03}	Han Chinese	(Li et al., 2013; Deng et al., 2018)
UBAC2	rs6491493	Intron	G	Susceptible	1.74	1.1x10^{-03}	Turkish-Italy	(Sawalha et al., 2011)
UBAC2	rs9554573	Intron	A	Susceptible	1.73	1.2x10^{-03}	Turkish-Italy	(Sawalha et al., 2011)
UBAC2	rs9517644	Upstream	T	Susceptible	1.72	1.3x10^{-03}	Turkish-Italy	(Sawalha et al., 2011)
CCR3	rs13092160	Intron	C	Protective	0.13	1.48x10^{-03}	Han Chinese	(Hou et al., 2012b)
UBASH3B	rs4936742	Intron	T	Susceptible	1.71	1.5x10^{-03}	Turkish	(Fei et al., 2009; Hou et al., 2012a)
UBAC2	rs11069357	Upstream	A	Susceptible	1.68	2x10^{-03}	Turkish-Italy	(Sawalha et al., 2011)
TLR4	rs4986790	Exon	G	Protective	0.64	3x10^{-03}	Turkish-Japanese	(Deng et al., 2018)
TLR4	rs4986791	Exon	T	Protective	0.82	3x10^{-03}	Turkish-Japanese	(Deng et al., 2018)
CCR3	rs9990343	Downstream	G	Protective	0.48	3.4x10^{-03}	Han Chinese	(Hou et al., 2012b)
CCR3	rs6803980	Downstream	A	Protective	0.48	3.4x10^{-03}	Han Chinese	(Hou et al., 2012b)
TNFα	rs1799724	Upstream	T	Protective	0.76	4x10^{-03}	Turkish	(Zhou et al., 2012)
IL12	rs3212227	Downstream	A	Susceptible	1.84	4x10^{-03}	Turkish	(Zhou et al., 2012)
UBAC2	rs984477	Intron	G	Susceptible	1.65	4.3x10^{-03}	Turkish-Italy	(Sawalha et al., 2011)
UBAC2	rs9513584	Intron	G	Susceptible	1.61	5.8x10^{-03}	Turkish-China	(Fei et al., 2009; Hou et al., 2012a)
TNFα	rs361525	Upstream	A	Susceptible	1.51	6x10^{-03}	Turkish	(Zhou et al., 2012)
TNFα	rs1799964	Upstream	C	Susceptible	1.35	7x10^{-03}	Turkish	(Zhou et al., 2012)
UBAC2	rs912130	Intron	C	Susceptible	1.58	7.1x10^{-03}	Turkish-Italy	(Sawalha et al., 2011)
CCR3	rs7651539	Intron	T	Protective	0.35	8x10^{-03}	Han Chinese	(Hou et al., 2012b)
IL18	rs1946518	promoter	C	Susceptible	1.67	1.01x10^{-02}	Korean	(Zhou et al., 2012)
IL1beta	+3962T/C	Exon	C	Susceptible	2.60	1.5x10^{-02}	Turkish	(Akman et al., 2008)
NOD2	rs2066844	Exon	T	Protective	0.40	2x10^{-02}	Turkish-Japanese	(Deng et al., 2018)
NOD2	rs2066845	Exon	C	Protective	0.66	2x10^{-02}	Turkish-Japanese	(Deng et al., 2018)

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Appendix A (cont.)

NOD2	rs2066847	Exon	ins-C	Protective	0.38	2x10^{-02}	Turkish-Japanese	(Deng et al., 2018)
CCR3	rs7649764	Downstream	C	Protective	0.69	2.2x10^{-02}	Han Chinese	(Hou et al., 2012b)
IL1	rs1143634	Exon	T	Susceptible	1.74	2.4x10^{-02}	Turkish	(Zhou et al., 2012)
IL23R	rs1343151	Intron	T	Protective	0.50	2.9x10^{-02}	Han Chinese	(Jiang et al., 2010)
TNFAIP3	rs610604	Intron	A	Protective	0.80	5.5x10^{-02}	Han Chinese	(Li et al., 2013)
IL6	VNTR	Downstream	C	Susceptible	3.45	4x10^{-02}	Korean	(Chang et al., 2005)

Notes: Although over seventy publications that reported genetic associations with BD were found in the literature, redundant findings are not included in this final list. For candidate gene studies, only genetic associations that were replicated in at least two independent studies, and the result based on the largest sample size were included the final list. P values are the statistical associations reported in the original publications.

VNTR: Variable number tandem repeat; ins-C: Insertion of C nucleotide

APPENDIX B. GENE ONTOLOGY ANALYSES OF BEHCET DISEASE ASSOCIATED GENES

Gene	Family Name	GO-Slim Molecular Function	GO-Slim Biological Process	GO-Slim Cellular Component	Panther Protein Class
ABCB5	ATP-BINDING CASSETTE SUB-FAMILY B MEMBER 5 (PTHR24221:SF217)	ATPase activity(GO:0016887);phospholipid transporter activity(GO:0005548);ATPase-coupled intramembrane lipid transporter activity(GO:0140326);active transmembrane transporter activity(GO:0022804)	transmembrane transport(GO:0055085);lipid translocation(GO:0034204);amide transport(GO:0042886)	integral component of membrane(GO:0016021)	ATP-binding cassette (ABC) transporter(PC00003)
API5	APOPTOSIS INHIBITOR 5 (PTHR12758:SF23)	RNA binding(GO:0003723)	negative regulation of apoptotic process(GO:0043066);apoptotic process(GO:0006915)	nucleus(GO:0005634)	
ASB18	ANKYRIN REPEAT AND SOCS BOX PROTEIN 18 (PTHR24118:SF76)				membrane traffic protein(PC00150)
ATP8A1	PHOSPHOLIPID-TRANSPORTING ATPASE IA (PTHR24092:SF150)	ATPase activity(GO:0016887);ATPase-coupled intramembrane lipid transporter activity(GO:0140326)	phospholipid translocation(GO:0045332)	plasma membrane(GO:0005886)	primary active transporter(PC00068)
BAG6	LARGE PROLINE-RICH PROTEIN BAG6 (PTHR15204:SF0)	polyubiquitin modification-dependent protein binding(GO:0031593)	ubiquitin-dependent ERAD pathway(GO:0030433)	cytosol(GO:0005829);protein-containing complex(GO:0032991)	chaperone(PC00072)
BTNL2	BTNL2-RELATED (PTHR24100:SF105)	signaling receptor binding(GO:0005102)	immune response(GO:0006955);cytokine production(GO:0001816);regulation of cytokine production(GO:0001817);T cell receptor signaling pathway(GO:0050852)	leaflet of membrane bilayer(GO:0097478);external side of plasma membrane(GO:0009897)	immunoglobulin receptor superfamily(PC00124)

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C10orf11 (LRMDA)	LEUCINE-RICH MELANOCYTE DIFFERENTIATION-ASSOCIATED PROTEIN (PTHR46282:SF2)				
C6orf10 (TSBP1)	TESTIS-EXPRESSED BASIC PROTEIN 1	nucleus (GO:0005634), integral component of membrane (GO:0016021)			
C6orf15	MUCIN 18B, ISOFORM A (PTHR15817:SF2)				
C6orf47	SI:CH73-25F10.6 (PTHR14307:SF0)				
CCDC180	COILED-COIL DOMAIN-CONTAINING PROTEIN 180 (PTHR21444:SF14)				
CCHCR1	COILED-COIL ALPHA-HELICAL ROD PROTEIN 1 (PTHR46822:SF1)		protein export from nucleus(GO:0006611)	centriole(GO:0005814)	
CCR1	C-C CHEMOKINE RECEPTOR TYPE 1 (PTHR10489:SF711)	C-C chemokine binding(GO:0019957)	inflammatory response(GO:0006954);immune response(GO:0006955)	cytoplasm(GO:0005737)	
CCR3	C-C CHEMOKINE RECEPTOR TYPE 3 (PTHR10489:SF649)		inflammatory response(GO:0006954);immune response(GO:0006955)	cytoplasm(GO:0005737)	
CDH26	CADHERIN-LIKE PROTEIN 26 (PTHR24027:SF78)	cadherin binding(GO:0045296);calcium ion binding(GO:0005509)	cell-cell junction assembly(GO:0007043);multicellular organism development(GO:0007275);cell morphogenesis(GO:0000902);cell-cell adhesion via plasma-membrane adhesion molecules(GO:0098742)	adherens junction(GO:0005912);plasma membrane protein complex(GO:0098797);extrinsic component of plasma membrane(GO:0019897)	cadherin(PC00057)
CEP135	CENTROSOMAL PROTEIN OF 135 KDA (PTHR23159:SF18)				chromatin/chromatin-binding, or -regulatory protein(PC00077)

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COL12A1	COLLAGEN ALPHA-1(XII) CHAIN (PTHR24020:SF17)		cell differentiation(GO:0030154);ectoderm formation(GO:0001705);endoderm formation(GO:0001706);mesoderm formation(GO:0001707)	collagen-containing extracellular matrix(GO:0062023)	extracellular matrix structural protein(PC00103)
CTLA4	CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 (PTHR11494:SF8)		T cell differentiation (GO:0030217), regulation of hemopoiesis (GO:1903706), immune response (GO:0006955), regulation of cell differentiation (GO:0045595), negative regulation of multicellular organismal process (GO:0051241), negative regulation of T cell activation (GO:0050868), T cell receptor signaling pathway (GO:0050852), leukocyte cell-cell adhesion (GO:0007159), B cell receptor signaling pathway (GO:0050853)	leaflet of membrane bilayer (GO:0097478), external side of plasma membrane (GO:0009897)	immunoglobulin receptor superfamily (PC00124)
CPLX1	COMPLEXIN-1 (PTHR16705:SF6)	syntaxin-1 binding(GO:0017075)	regulation of neurotransmitter secretion(GO:0046928);vesicle fusion to plasma membrane(GO:0099500);synaptic vesicle exocytosis(GO:0016079)	terminal bouton(GO:0043195);SNARE complex(GO:0031201);plasma membrane region(GO:0098590)	
CPVL	SERINE CARBOXYPEPTIDASE CPVL-RELATED (PTHR11802:SF98)	carboxypeptidase activity(GO:0004180);serine-type peptidase activity(GO:0008236)			serine protease(PC00203)
CTNNA2	CATENIN ALPHA-2 (PTHR18914:SF23)				non-motor actin binding protein(PC00165)
DEPDC1	DEP DOMAIN-CONTAINING PROTEIN 1A (PTHR16206:SF12)				scaffold/adaptor protein(PC00226)
DHFRP2	dihydrofolate reductase pseudogene 2				
DNMT3A	DNA (CYTOSINE-5)-METHYLTRANSFERASE 3A (PTHR23068:SF10)				DNA methyltransferase(PC00013)

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DTL	DENTICLELESS PROTEIN HOMOLOG (PTHR22852:SF0)				
EBF2	TRANSCRIPTION FACTOR COE2 (PTHR10747:SF33)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nuclear chromatin(GO:0000790)	DNA-binding transcription factor(PC00218)
ERAP1	ENDOPLASMIC RETICULUM AMINOPEPTIDASE 1 (PTHR11533:SF156)	zinc ion binding(GO:0008270);peptide binding(GO:0042277);metallopeptidase activity(GO:0008237)	peptide metabolic process(GO:0006518);proteolysis(GO:0006508);organonitrogen compound catabolic process(GO:1901565);cellular catabolic process(GO:0044248)	cytoplasm(GO:0005737)	metalloprotease(PC00153)
FUT2	GALACTOSIDE ALPHA-(1,2)-FUCOSYLTRANSFERASE 2 (PTHR11927:SF2)	fucosyltransferase activity(GO:0008417)	protein glycosylation(GO:0006486)		glycosyltransferase (PC00111)
GABBR1	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR SUBUNIT 1 (PTHR10519:SF73)	G protein-coupled receptor activity(GO:0004930)	G protein-coupled receptor signaling pathway(GO:0007186)	integral component of plasma membrane(GO:0005887);plasma membrane protein complex(GO:0098797);receptor complex(GO:0043235)	G-protein coupled receptor(PC00021)
GALNT1	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE 1 (PTHR11675:SF123)			Golgi apparatus(GO:0005794);vacuole(GO:0005773);plasma membrane(GO:0005886)	glycosyltransferase (PC00111)
GALNT10	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE 10 (PTHR11675:SF41)			Golgi apparatus(GO:0005794);vacuole(GO:0005773);plasma membrane(GO:0005886)	glycosyltransferase (PC00111)
GAS2	GROWTH ARREST-SPECIFIC PROTEIN 2 (PTHR46756:SF9)	actin filament binding(GO:0051015);protein-macromolecule adaptor activity(GO:0030674);microtubule binding(GO:0008017)	actin filament organization(GO:0007015);microtubule cytoskeleton organization(GO:0000226)	actin filament(GO:0005884);microtubule(GO:0005874)	

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GIMAP1	GTPASE IMAP FAMILY MEMBER 1 (PTHR10903:SF74)			endoplasmic reticulum(GO:0005783);vacuole(GO:0005773);plasma membrane(GO:0005886)	small GTPase(PC00208)
GIMAP2	GTPASE IMAP FAMILY MEMBER 2 (PTHR10903:SF7)			endoplasmic reticulum(GO:0005783);vacuole(GO:0005773);plasma membrane(GO:0005886)	small GTPase(PC00208)
GIMAP4	GTPASE IMAP FAMILY MEMBER 4 (PTHR10903:SF62)				small GTPase(PC00208)
HCG27					
HCG9					
HERPUD2	HOMOCYSTEINE-RESPONSIVE ENDOPLASMIC RETICULUM-RESIDENT UBIQUITIN-LIKE DOMAIN MEMBER 2 PROTEIN (PTHR12943:SF5)		endoplasmic reticulum unfolded protein response(GO:0030968)		
HIVEP3	TRANSCRIPTION FACTOR HIVEP3 (PTHR45944:SF5)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nucleus(GO:0005634)	

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HLA-B	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B ALPHA CHAIN (PTHR16675:SF251)		T cell mediated immunity(GO:0002456);positive regulation of adaptive immune response(GO:0002821);positive regulation of cellular process(GO:0048522);antigen processing and presentation(GO:0019882);positive regulation of lymphocyte mediated immunity(GO:0002708);cellular process(GO:0009987)	extracellular space(GO:0005615);leaflet of membrane bilayer(GO:0097478);external side of plasma membrane(GO:0009897)	major histocompatibility complex protein(PC00149)
HLA-C	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C ALPHA CHAIN (PTHR16675:SF252)	peptide binding(GO:0042277);signaling receptor binding(GO:0005102)	T cell mediated immunity(GO:0002456);positive regulation of adaptive immune response(GO:0002821);positive regulation of cellular process(GO:0048522);antigen processing and presentation(GO:0019882);positive regulation of lymphocyte mediated immunity(GO:0002708);cellular process(GO:0009987)	extracellular space(GO:0005615);leaflet of membrane bilayer(GO:0097478);external side of plasma membrane(GO:0009897)	major histocompatibility complex protein(PC00149)
HLA-DQ		antigen processing and presentation of peptide or polysaccharide antigen via MHC class II(GO:0002504);cellular defense response(GO:0006968)	major histocompatibility complex antigen(PC00149)	T cell activation->MHC-antigen;;	
HLA-DQA1	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ ALPHA 1 CHAIN (PTHR19944:SF59)				major histocompatibility complex protein(PC00149)
HLA-DQA2	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ ALPHA 2 CHAIN (PTHR19944:SF94)				major histocompatibility complex protein(PC00149)

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HLA-DQB1		antigen processing and presentation(GO:0019882)	immunoglobulin receptor superfamily(PC00124);major histocompatibility complex antigen(PC00149)		
HLA-F	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F (PTHR16675:SF187)	peptide binding(GO:0042277);signaling receptor binding(GO:0005102)	T cell mediated immunity(GO:0002456);positive regulation of adaptive immune response(GO:0002821);positive regulation of cellular process(GO:0048522);antigen processing and presentation(GO:0019882);positive regulation of lymphocyte mediated immunity(GO:0002708);cellular process(GO:0009987)	extracellular space(GO:0005615);leaflet of membrane bilayer(GO:0097478);external side of plasma membrane(GO:0009897)	major histocompatibility complex protein(PC00149)
HLA-G	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN G (PTHR16675:SF169)	peptide binding(GO:0042277);signaling receptor binding(GO:0005102)	T cell mediated immunity(GO:0002456);positive regulation of adaptive immune response(GO:0002821);positive regulation of cellular process(GO:0048522);antigen processing and presentation(GO:0019882);positive regulation of lymphocyte mediated immunity(GO:0002708);cellular process(GO:0009987)	extracellular space(GO:0005615);leaflet of membrane bilayer(GO:0097478);external side of plasma membrane(GO:0009897)	major histocompatibility complex protein(PC00149)
HMP19	NEURONAL VESICLE TRAFFICKING-ASSOCIATED PROTEIN 2 (PTHR28546:SF2)	clathrin binding(GO:0030276)	cellular protein-containing complex assembly(GO:0034622);endosomal transport(GO:0016197)	endosome(GO:0005768);integral component of membrane(GO:0016021);vacuole(GO:0005773);plasma membrane(GO:0005886)	
HNF4G	HEPATOCYTE NUCLEAR FACTOR 4-GAMMA (PTHR24083:SF42)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	anatomical structure development(GO:0048856);cell differentiation(GO:0030154);transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nuclear chromatin(GO:0000790)	C4 zinc finger nuclear receptor(PC00169)

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IFNG	INTERFERON GAMMA (PTHR11419:SF0)				interferon superfamily(PC00127)
IL10	Interkulin-10		interleukin superfamily(PC00128)	Interleukin signaling pathway->Interleukin;;	
IL12A	Interkulin-12		interleukin superfamily(PC00128)	Interleukin signaling pathway->Interleukin;;	
IL17A	Interkulin-17		interleukin superfamily(PC00128)	Interleukin signaling pathway->Interleukin;;	
IL1A	INTERLEUKIN-1 ALPHA (PTHR10078:SF33)		T cell differentiation(GO:0030217);inflammatory response(GO:0006954);cellular response to lipopolysaccharide(GO:0071222);cytokine-mediated signaling pathway(GO:0019221);positive regulation of T cell differentiation(GO:0045582);positive regulation of gene expression(GO:0010628);T cell proliferation(GO:0042098);regulation of catalytic activity(GO:0050790);gene expression(GO:0010467);oxidation-reduction process(GO:0055114);positive regulation of T cell proliferation(GO:0042102);leukocyte cell-cell adhesion(GO:0007159)	extracellular space(GO:0005615)	interleukin superfamily(PC00128)
IL23R	INTERLEUKIN-23 RECEPTOR (PTHR23036:SF112)	growth factor receptor binding(GO:0070851);cytokine binding(GO:0019955);cytokine receptor activity(GO:0004896);cytokine receptor binding(GO:0005126)	cytokine-mediated signaling pathway(GO:0019221)	integral component of plasma membrane(GO:0005887);leaflet of membrane bilayer(GO:0097478);plasma membrane protein complex(GO:0098797);external side of plasma membrane(GO:0009897);receptor complex(GO:0043235)	transmembrane signal receptor(PC00197)
IL6	INTERLEUKIN-6 (PTHR10511:SF3)				

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KCNK9	POTASSIUM CHANNEL SUBFAMILY K MEMBER 9 (PTHR11003:SF75)	potassium channel activity(GO:0005267)	potassium ion transmembrane transport(GO:0071805);regulation of membrane potential(GO:0042391)	integral component of plasma membrane(GO:0005887)	ion channel(PC00133)
KLRC4	NKG2-F TYPE II INTEGRAL MEMBRANE PROTEIN (PTHR22800:SF185)				
KLRK1	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN (PTHR47494:SF1)				
LILRA1	LEUKOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR SUBFAMILY A MEMBER 1-RELATED (PTHR11738:SF165)				immunoglobulin receptor superfamily(PC00124)
LILRB1	LEUKOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR SUBFAMILY A MEMBER 1-RELATED (PTHR11738:SF165)				immunoglobulin receptor superfamily(PC00124)
LOC100129342					
LOC100132252					
LOC107984355					
LOC285830					
LTN1	E3 UBIQUITIN-PROTEIN LIGASE LISTERIN (PTHR12389:SF0)	ubiquitin protein ligase activity(GO:0061630);ribonucleoprotein complex binding(GO:0043021)	regulation of translation(GO:0006417);proteasome-mediated ubiquitin-dependent protein catabolic process(GO:0043161);translational elongation(GO:0006414)	cytosol(GO:0005829);protein-containing complex(GO:0032991)	ubiquitin-protein ligase(PC00234)
LYST	LYSOSOMAL-TRAFFICKING REGULATOR (PTHR13743:SF86)	protein kinase binding(GO:0019901)	protein localization(GO:0008104)	membrane(GO:0016020);cytosol(GO:0005829)	

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MEFV	PYRIN (PTHR24103:SF606)	ubiquitin protein ligase activity(GO:0061630)	protein ubiquitination(GO:0016567)	cytoplasm(GO:0005737)	ubiquitin-protein ligase(PC00234)
MICA	MHC CLASS I POLYPEPTIDE-RELATED SEQUENCE A-RELATED				
MN1	TRANSCRIPTIONAL ACTIVATOR MN1 (PTHR15821:SF0)				
MOG	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (PTHR24100:SF71)	signaling receptor binding(GO:0005102)	immune response(GO:0006955);cytokine production(GO:0001816);regulation of cytokine production(GO:0001817);T cell receptor signaling pathway(GO:0050852)	leaflet of membrane bilayer(GO:0097478);external side of plasma membrane(GO:0009897)	immunoglobulin receptor superfamily(PC00124)
MSX2	HOMEOBOX PROTEIN MSX-2 (PTHR24338:SF10)	RNA polymerase II transcription regulatory region sequence-specific DNA binding(GO:0000977);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	embryonic morphogenesis(GO:0048598)	nucleus(GO:0005634)	homeodomain transcription factor(PC00119)
MUC21	MUCIN-21 (PTHR39408:SF3)				
NAV2	NEURON NAVIGATOR 2 (PTHR12784:SF6)		nervous system development(GO:0007399)		

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NOD2	NUCLEOTIDE-BINDING OLIGOMERIZATION DOMAIN-CONTAINING PROTEIN 2 (PTHR24106:SF64)		transcription, DNA-templated(GO:0006351);positive regulation of I-kappaB kinase/NF-kappaB signaling(GO:0043123);response to peptide(GO:1901652);I-kappaB kinase/NF-kappaB signaling(GO:0007249);defense response to bacterium(GO:0042742);positive regulation of NF-kappaB transcription factor activity(GO:0051092)	cytosol(GO:0005829)	scaffold/adaptor protein(PC00226)
OSR1	PROTEIN ODD-SKIPPED-RELATED 1 (PTHR14196:SF5)	RNA polymerase II transcription regulatory region sequence-specific DNA binding(GO:0000977);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	embryo development(GO:0009790);urogenital system development(GO:0001655);transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nucleus(GO:0005634)	zinc finger transcription factor(PC00244)
OVCH1	OVOCHYMASE-1 (PTHR24251:SF21)				serine protease(PC00203)
PAX8	PAIRED BOX PROTEIN PAX-8 (PTHR45636:SF6)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	anatomical structure development(GO:0048856);transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nuclear chromatin(GO:0000790)	
PLEKHB1	PLECKSTRIN HOMOLOGY DOMAIN-CONTAINING FAMILY B MEMBER 1 (PTHR14309:SF7)		regulation of cell differentiation(GO:0045595);cell differentiation(GO:0030154)	integral component of membrane(GO:0016021)	
PMFBP1	POLYAMINE-MODULATED FACTOR 1-BINDING PROTEIN 1 (PTHR18881:SF2)				

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POU5F1	POU DOMAIN, CLASS 5, TRANSCRIPTION FACTOR 1 (PTHR11636:SF86)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nuclear chromatin(GO:0000790)	
PPP1R11	E3 UBIQUITIN-PROTEIN LIGASE PPP1R11 (PTHR20835:SF4)	phosphoprotein phosphatase activity(GO:0004721);protein phosphatase inhibitor activity(GO:0004864);protein phosphatase 1 binding(GO:0008157)	negative regulation of phosphatase activity(GO:0010923);protein dephosphorylation(GO:0006470);negative regulation of protein dephosphorylation(GO:0035308);regulation of phosphoprotein phosphatase activity(GO:0043666)	nucleus(GO:0005634)	ubiquitin-protein ligase(PC00234)
PSMD14	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 14 (PTHR10410:SF5)	thiol-dependent ubiquitin-specific protease activity(GO:0004843);proteasome binding(GO:0070628);metallopeptidase activity(GO:0008237)	protein deubiquitination(GO:0016579);proteasome-mediated ubiquitin-dependent protein catabolic process(GO:0043161)	proteasome regulatory particle, lid subcomplex(GO:0008541)	translation initiation factor(PC00224)
PSORS1C1	Psoriasis susceptibility 1 candidate gene 1 protein;PSORS1C1;ortholog				
PTPN22	TYROSINE-PROTEIN PHOSPHATASE NON-RECEPTOR TYPE 22 (PTHR45983:SF1)	protein tyrosine phosphatase activity (GO:0004725)	peptidyl-tyrosine dephosphorylation (GO:0035335)	Nucleus cytoplasm (GO:0005737)	
RALGAPA2	RAL GTPASE-ACTIVATING PROTEIN SUBUNIT ALPHA-2 (PTHR10063:SF2)	GTPase activity(GO:0003924);GTPase activator activity(GO:0005096)		cytoplasm(GO:0005737)	GTPase-activating protein(PC00257)

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Appendix B(cont.)

RIMBP2	RIMS-BINDING PROTEIN 2 (PTHR14234:SF18)		neuromuscular synaptic transmission(GO:0007274)		
RNF39	RING FINGER PROTEIN 39 (PTHR24103:SF646)	ubiquitin protein ligase activity(GO:0061630)	innate immune response(GO:0045087);regulation of gene expression(GO:0010468);gene expression(GO:0010467);protein ubiquitination(GO:0016567)	cytoplasm(GO:0005737)	ubiquitin-protein ligase(PC00234)
SACM1L	PHOSPHATIDYLINOSITOL-3-PHOSPHATASE SAC1 PTHR45662:SF2)	phosphatase activity(GO:0016791)	phospholipid dephosphorylation(GO:0046839);phosphatidylinositol metabolic process(GO:0046488)	endoplasmic reticulum(GO:0005783);vacuole(GO:0005773);plasma membrane(GO:0005886)	phosphatase(PC00181)
SAMD3	STERILE ALPHA MOTIF DOMAIN-CONTAINING PROTEIN 3 (PTHR47302:SF1)				

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Appendix B(cont.)

SEMA6D	SEMAPHORIN-6D (PTHR11036:SF65)	receptor ligand activity(GO:0048018)	negative regulation of locomotion(GO:0040013);neural crest cell development(GO:0014032);negative regulation of cellular component movement(GO:0051271);negative regulation of neuron differentiation(GO:0045665);axon guidance(GO:0007411);cell surface receptor signaling pathway(GO:0007166);axon extension(GO:0048675);regulation of axonogenesis(GO:0050770);regulation of cell growth(GO:0001558);negative regulation of response to external stimulus(GO:0032102);negative regulation of cellular component organization(GO:0051129);regulation of cellular component size(GO:0032535);regulation of chemotaxis(GO:0050920);cell migration(GO:0016477);positive regulation of cell migration(GO:0030335)	integral component of plasma membrane(GO:0005887);extracellular space(GO:0005615)	membrane-bound signaling molecule(PC00152)
SGPP2	SPHINGOSINE-1-PHOSPHATE PHOSPHATASE 2 (PTHR14969:SF14)	phosphatase activity(GO:0016791)	phospholipid dephosphorylation(GO:0046839);alcohol metabolic process(GO:0006066);sphingolipid metabolic process(GO:0006665)	endoplasmic reticulum membrane(GO:0005789);endoplasmic reticulum(GO:0005783);vacuole(GO:0005773);plasma membrane(GO:0005886)	phosphatase(PC00181)
SLC22A23	SOLUTE CARRIER FAMILY 22 MEMBER 23 (PTHR24064:SF192)				secondary carrier transporter(PC00258)
SLC41A2	SOLUTE CARRIER FAMILY 41 MEMBER 2 (PTHR16228:SF25)			plasma membrane(GO:0005886)	secondary carrier transporter(PC00258)
SLC43A3	SOLUTE CARRIER FAMILY 43 MEMBER 3 (PTHR20765:SF1)				amino acid transporter(PC00046)

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Appendix B(cont.)

SLC44A4	CHOLINE TRANSPORTER-LIKE PROTEIN 4 (PTHR12385:SF37)	organic cation transmembrane transporter activity(GO:0015101);organophosphate ester transmembrane transporter activity(GO:0015605);organic anion transmembrane transporter activity(GO:0008514)	choline transport(GO:0015871);anion transmembrane transport(GO:0098656);cation transmembrane transport(GO:0098655);organophosphate ester transport(GO:0015748);organic anion transport(GO:0015711)	plasma membrane(GO:0005886)	secondary carrier transporter(PC00258)
SLIT2	SLIT HOMOLOG 2 PROTEIN	heparin binding(GO:0008201);signaling receptor binding(GO:0005102)			
SMARCA2	GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2-RELATED (PTHR10799:SF541)	DNA binding(GO:0003677);DNA-dependent ATPase activity(GO:0008094);transcription factor binding(GO:0008134)	ATP-dependent chromatin remodeling(GO:0043044);transcription by RNA polymerase II(GO:0006366);positive regulation of transcription by RNA polymerase II(GO:0045944)	nucleus(GO:0005634)	DNA helicase(PC00011)
SMG6	TELOMERASE-BINDING PROTEIN EST1A (PTHR15696:SF0)	telomerase RNA binding(GO:0070034);telomeric DNA binding(GO:0042162)	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay(GO:0000184);gene expression(GO:0010467)	telomerase holoenzyme complex(GO:0005697)	RNA metabolism protein(PC00031)
SORBS2	SORBIN AND SH3 DOMAIN-CONTAINING PROTEIN 2 (PTHR14167:SF56)				

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Appendix B(cont.)

STAT4	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 4 (PTHR11801:SF19)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription factor activity, RNA polymerase II-specific(GO:0000981)	cell population proliferation(GO:0008283);cytokine-mediated signaling pathway(GO:0019221);transcription by RNA polymerase II(GO:0006366);defense response(GO:0006952);response to peptide hormone(GO:0043434);regulation of cell population proliferation(GO:0042127);receptor signaling pathway via JAK-STAT(GO:0007259);regulation of transcription by RNA polymerase II(GO:0006357)	nuclear chromatin(GO:0000790)	DNA-binding transcription factor(PC00218)
STK39	STE20/SPS1-RELATED PROLINE-ALANINE-RICH PROTEIN KINASE (PTHR48012:SF14)				
STX8	SYNTAXIN-8 (PTHR19957:SF322)	SNARE binding(GO:0000149);protein-macromolecule adaptor activity(GO:0030674)	organelle localization(GO:0051640);vesicle fusion(GO:0006906);intracellular protein transport(GO:0006886)	integral component of membrane(GO:0016021);SNARE complex(GO:0031201);endomembrane system(GO:0012505);vacuole(GO:0005773);plasma membrane(GO:0005886)	SNARE protein(PC00034)
SUMO4	SMALL UBIQUITIN-RELATED MODIFIER 3-RELATED (PTHR10562:SF79)	ubiquitin-like protein ligase binding(GO:0044389)	protein sumoylation(GO:0016925)	nucleus(GO:0005634)	
SUSD1	SUSHI DOMAIN-CONTAINING PROTEIN 1 (PTHR24051:SF5)				extracellular matrix glycoprotein(PC00100)
TCF19	TRANSCRIPTION FACTOR 19 (PTHR15464:SF1)		regulation of gene expression(GO:0010468);gene expression(GO:0010467)	nucleus(GO:0005634)	DNA-binding transcription factor(PC00218)

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Appendix B(cont.)

TENM4	TENEURIN-4 (PTHR11219:SF9)	protein homodimerization activity(GO:0042803);cell adhesion molecule binding(GO:0050839)	cell-cell adhesion via plasma-membrane adhesion molecules(GO:0098742);neuron development(GO:0048666)	plasma membrane region(GO:0098590);neuron projection(GO:0043005)	
TFCP2L1	TRANSCRIPTION FACTOR CP2-LIKE PROTEIN 1 (PTHR11037:SF18)	RNA polymerase II cis-regulatory region sequence-specific DNA binding(GO:0000978);DNA-binding transcription activator activity, RNA polymerase II-specific(GO:0001228)	transcription by RNA polymerase II(GO:0006366);regulation of transcription by RNA polymerase II(GO:0006357)	nucleus(GO:0005634)	DNA-binding transcription factor(PC00218)
TLR4	TOLL-LIKE RECEPTOR 4 (PTHR24365:SF521)	signaling receptor activity(GO:0038023);lipopolysaccharide binding(GO:0001530)	toll-like receptor signaling pathway(GO:0002224);inflammatory response(GO:0006954);defense response to Gram-negative bacterium(GO:0050829)	integral component of plasma membrane(GO:0005887)	
TMEM132B	TRANSMEMBRANE PROTEIN 132B (PTHR13388:SF12)				
TNF	TUMOR NECROSIS FACTOR (PTHR11471:SF23)	tumor necrosis factor receptor binding(GO:0005164);cytokine activity(GO:0005125)	tumor necrosis factor-mediated signaling pathway(GO:0033209);transcription by RNA polymerase II(GO:0006366);extrinsic apoptotic signaling pathway via death domain receptors(GO:0008625);positive regulation of transcription by RNA polymerase II(GO:0045944);positive regulation of NF-kappaB transcription factor activity(GO:0051092)	extracellular space(GO:0005615);cell surface(GO:0009986)	

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Appendix B(cont.)

TNFAIP3	TUMOR NECROSIS FACTOR ALPHA-INDUCED PROTEIN 3 (PTHR13367:SF3)	thiol-dependent ubiquitin-specific protease activity(GO:0004843);K63-linked polyubiquitin modification-dependent protein binding(GO:0070530)	protein deubiquitination(GO:0016579);cytoskeleton organization(GO:0007010);Wnt signaling pathway(GO:0016055);positive regulation of Wnt signaling pathway(GO:0030177);cell migration(GO:0016477);ubiquitin-dependent protein catabolic process(GO:0006511)	nucleus(GO:0005634);cytoplasm(GO:0005737)	cysteine protease(PC00081)
TRIM31	E3 UBIQUITIN-PROTEIN LIGASE TRIM31 (PTHR24103:SF87)	ubiquitin protein ligase activity(GO:0061630)	innate immune response(GO:0045087);regulation of gene expression(GO:0010468);gene expression(GO:0010467);protein ubiquitination(GO:0016567)	cytoplasm(GO:0005737)	ubiquitin-protein ligase(PC00234)
TTLL7	TUBULIN POLYGLUTAMYLASE TTLL7 (PTHR12241:SF147)	tubulin binding(GO:0015631);catalytic activity, acting on a protein(GO:0140096);ligase activity(GO:0016874)	peptidyl-amino acid modification(GO:0018193);microtubule cytoskeleton organization(GO:0000226)	cilium(GO:0005929);intraciliary transport particle(GO:0030990);plasma membrane region(GO:0098590)	microtubule or microtubule-binding cytoskeletal protein(PC00157)
UBAC2	Ubiquitin-associated domain-containing protein 2;UBAC2;ortholog				

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Appendix B(cont.)

UBASH3B	UBIQUITIN-ASSOCIATED AND SH3 DOMAIN-CONTAINING PROTEIN B (PTHR16469:SF29)	protein tyrosine phosphatase activity(GO:0004725)	transmembrane receptor protein tyrosine kinase signaling pathway(GO:0007169);regulation of bone resorption(GO:0045124);protein phosphorylation(GO:0006468);negative regulation of protein kinase activity(GO:0006469);osteoclast differentiation(GO:0030316);regulation of release of sequestered calcium ion into cytosol(GO:0051279);regulation of hemopoiesis(GO:1903706);negative regulation of signal transduction(GO:0009968);regulation of cell differentiation(GO:0045595);bone resorption(GO:0045453);negative regulation of multicellular organismal process(GO:0051241);sequestering of calcium ion(GO:0051208);release of sequestered calcium ion into cytosol(GO:0051209);peptidyl-tyrosine dephosphorylation(GO:0035335);platelet aggregation(GO:0070527)	cytoplasm(GO:0005737)	

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Appendix B(cont.)

UBD	UBIQUITIN D (PTHR47731:SF1)	proteasome binding(GO:0070628)	transcription, DNA-templated(GO:0006351);innate immune response(GO:0045087);apoptotic process(GO:0006915);positive regulation of apoptotic process(GO:0043065);positive regulation of I-kappaB kinase/NF-kappaB signaling(GO:0043123);I-kappaB kinase/NF-kappaB signaling(GO:0007249);positive regulation of NF-kappaB transcription factor activity(GO:0051092);protein ubiquitination(GO:0016567);response to tumor necrosis factor(GO:0034612);ubiquitin-dependent protein catabolic process(GO:0006511)	nucleus(GO:0005634)	
ZNRD1	DNA-DIRECTED RNA POLYMERASE I SUBUNIT RPA12 (PTHR11239:SF14)	DNA-directed 5'-3' RNA polymerase activity(GO:0003899)	transcription by RNA polymerase I(GO:0006360)	RNA polymerase I complex(GO:0005736)	DNA-directed RNA polymerase(PC00019)

APPENDIX C. DISTRIBUTION OF BEHCET DISEASE ASSOCIATED VARIANTS AMONG 1000 GENOMES POPULATION SAMPLES

A. Abbreviations of the 1000 Genomes populations

AFR	**African**
ACB	African Caribbeans in Barbados
ASW	Americans of African Ancestry in SW USA
ESN	Esan in Nigeria
GWD	Gambian in Western Divisions in the Gambia
LWK	Luhya in Webuye, Kenya
MSL	Mende in Sierra Leone
YRI	Yoruba in Ibadan, Nigeria
AMR	**Ad Mixed American**
CLM	Colombians from Medellin, Colombia
MXL	Mexican Ancestry from Los Angeles USA
PEL	Peruvians from Lima, Peru
PUR	Puerto Ricans from Puerto Rico
EAS	**East Asian**
CDX	Chinese Dai in Xishuangbanna, China
CHB	Han Chinese in Bejing, China
CHS	Southern Han Chinese
JPT	Japanese in Tokyo, Japan
KHV	Kinh in Ho Chi Minh City, Vietnam
EUR	**European**
CEU	Utah Residents (CEPH) with Northern and Western European Ancestry
FIN	Finnish in Finland
GBR	British in England and Scotland
IBS	Iberian Population in Spain
TSI	Toscani in Italia
SAS	**South Asian**
BEB	Bengali from Bangladesh
GIH	Gujarati Indian from Houston, Texas
ITU	Indian Telugu from the UK
PJL	Punjabi from Lahore, Pakistan
STU	Sri Lankan Tamil from the UK

B. 1000 Genomes African population samples

Gene	**Variant/SNP**	**Behcet Allele**	**ALL**	**AFR**	ACB	ASW	ESN	GWD	LWK	MSL	YRI
IL-10	rs1518111	A	0.427	0.434	0.385	0.377	0.449	0.473	0.394	0.471	0.463
IL-10	rs1800871	T	0.435	0.436	0.391	0.377	0.449	0.473	0.389	0.476	0.468
IL-10	rs1800872	A	0.435	0.436	0.391	0.377	0.449	0.473	0.394	0.476	0.468
IL-10	rs1554286	C	0.592	0.569	0.625	0.623	0.556	0.527	0.606	0.529	0.542
IL23R,IL12RB2	rs1495965	G	0.466	0.422	0.422	0.484	0.409	0.363	0.419	0.471	0.426
IL23R,IL12RB2	rs924080	T	0.604	0.495	0.484	0.541	0.530	0.403	0.515	0.547	0.481
IL23R,IL12RB2	rs12119179	A	0.644	0.801	0.797	0.746	0.788	0.876	0.778	0.806	0.787
IL23R,IL12RB2	rs11209033	C	0.644	0.797	0.792	0.746	0.783	0.876	0.773	0.806	0.778
IL23R,IL12RB2	rs12141431	C	0.294	0.023	0.036	0.131	0.005	0.013	0.010	0	0.005
TNFAIP3	rs9494885	T	0.794	0.477	0.536	0.639	0.505	0.363	0.551	0.447	0.384
TNFAIP3	rs10499194	C	0.809	0.870	0.833	0.811	0.838	0.876	0.929	0.841	0.926
TNFAIP3	rs610604	A	0.613	0.318	0.354	0.369	0.384	0.292	0.278	0.247	0.315
TNFAIP3	rs7753873	C	0.191	0.463	0.458	0.295	0.449	0.522	0.409	0.441	0.579
STAT4	rs7574070	A	0.494	0.734	0.688	0.623	0.828	0.704	0.753	0.759	0.750
STAT4	rs897200	A	0.499	0.734	0.688	0.615	0.828	0.704	0.753	0.765	0.750
STAT4	rs7572482	A	0.484	0.697	0.635	0.607	0.763	0.699	0.702	0.735	0.704
CCR1	rs17282391	G	0.093	0.003	0.010	0.016	0	0	0	0	0
CCR1	rs10510749	T	0.122	0.111	0.052	0.082	0.056	0.173	0.141	0.141	0.116
CCR1	rs13084057	G	0.122	0.111	0.052	0.082	0.056	0.173	0.141	0.141	0.116
CCR1	rs7631551	A	0.180	0.307	0.198	0.262	0.232	0.336	0.449	0.365	0.292
CCR1	rs7616215	T	0.652	0.523	0.609	0.574	0.566	0.513	0.369	0.512	0.537
CCR3	rs7649764	C	0.634	0.722	0.609	0.656	0.722	0.792	0.662	0.776	0.801
CCR3	rs9990343	G	0.409	0.523	0.432	0.402	0.470	0.673	0.424	0.606	0.593
CCR3	rs6803980	A	0.418	0.559	0.458	0.467	0.500	0.704	0.465	0.624	0.639

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Appendix C (cont.)

CCR3	rs13075270	C	0.156	0.220	0.255	0.230	0.217	0.168	0.227	0.235	0.222
CCR3	rs13092160	C	0.125	0.124	0.130	0.164	0.076	0.097	0.146	0.141	0.134
CCR3	rs2373156	T	0.195	0.374	0.344	0.311	0.359	0.381	0.399	0.441	0.370
CCR3	rs7651539	T	0.195	0.374	0.344	0.311	0.359	0.381	0.399	0.441	0.370
CCR3	rs1542755	A	0.084	0.003	0.010	0.016	0	0	0	0	0
CCR3	rs13067058	A	0.079	0.003	0.010	0.016	0	0	0	0	0
CCR3	rs13092160	C	0.125	0.124	0.130	0.164	0.076	0.097	0.146	0.141	0.134
KLRC4	rs2617170	C	0.557	0.433	0.474	0.516	0.434	0.341	0.455	0.365	0.477
MEFV	rs61752717	G	0.0002	0	0	0	0	0	0	0	0
ERAP1	rs17482078	T	0.101	0.054	0.073	0.074	0.035	0.031	0.040	0.071	0.065
FUT2	rs681343	T	0.322	0.491	0.516	0.508	0.566	0.469	0.439	0.388	0.542
IL12A	rs17810546	A	0.960	0.998	0.995	0.992	1.000	1.000	1.000	1.000	1.000
IL23R	rs11209026	A	0.023	0.003	0	0.016	0	0	0.005	0	0.005
IL23R	rs76418789	A	0.0112	0.0008	0	0.0082	0	0	0	0	0
IL23R	rs17375018	G	0.694	0.794	0.812	0.795	0.854	0.752	0.692	0.818	0.843
IL23R	rs11209032	A	0.354	0.198	0.198	0.246	0.222	0.124	0.212	0.194	0.218
IL23R	rs1343151	T	0.338	0.728	0.703	0.598	0.788	0.730	0.712	0.771	0.750
TLR4	rs4986790	G	0.060	0.071	0.042	0.057	0.051	0.128	0.096	0.076	0.037
TLR4	rs4986791	T	0.041	0.005	0	0	0.010	0.018	0	0.006	0
NOD2	rs2066844	T	0.014	0.002	0.005	0.016	0	0	0	0	0
NOD2	rs2066845	C	0.005	0	0	0	0	0	0	0	0
NOD2	rs2066847	ins-C	0.006	0.004	0.005	0.033	0	0	0	0	0
IL1	rs1800587	C	0.721	0.596	0.568	0.664	0.641	0.531	0.606	0.641	0.565
IL1	rs1143634	T	0.133	0.123	0.130	0.123	0.126	0.168	0.111	0.088	0.102
IL1	rs16944	G	0.491	0.427	0.464	0.443	0.434	0.478	0.359	0.400	0.412
TNFα	rs1799964	C	0.219	0.149	0.130	0.156	0.076	0.164	0.207	0.188	0.130
TNFα	rs361525	A	0.061	0.038	0.016	0.041	0.010	0.084	0.061	0.047	0.005
TNFα	rs1799724	T	0.099	0.024	0.031	0.049	0.025	0.022	0.010	0.024	0.019

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Appendix C (cont.)

IL12	rs3212227	A	0.641	0.648	0.682	0.713	0.616	0.659	0.591	0.647	0.648
IL18	rs1946518	C	0.592	0.650	0.661	0.672	0.662	0.606	0.657	0.635	0.667
IL17F-A126G	rs2397084	T	0.967	0.997	0.995	0.992	1.000	1.000	0.990	1.000	1.000
LOC100129342	rs11206377	G	0.540	0.274	0.271	0.320	0.308	0.319	0.212	0.271	0.231
CCDC180	rs2061634	G	0.278	0.410	0.411	0.402	0.434	0.420	0.394	0.371	0.426
CPVL	rs317711	C	0.173	0.203	0.177	0.246	0.212	0.146	0.222	0.247	0.199
UBASH3B	rs4936742	T	0.389	0.163	0.203	0.230	0.136	0.124	0.182	0.159	0.144
UBAC2	rs9513584	G	0.532	0.728	0.667	0.656	0.763	0.770	0.697	0.771	0.741
UBAC2	rs9517644	T	0.526	0.705	0.641	0.631	0.758	0.743	0.677	0.753	0.704
UBAC2	rs11069357	A	0.526	0.707	0.641	0.639	0.758	0.748	0.677	0.753	0.704
UBAC2	rs984477	G	0.546	0.712	0.641	0.648	0.753	0.757	0.682	0.759	0.718
UBAC2	rs9554573	A	0.559	0.809	0.745	0.746	0.874	0.810	0.773	0.788	0.894
UBAC2	rs6491493	G	0.533	0.726	0.656	0.656	0.768	0.770	0.697	0.771	0.736
UBAC2	rs9517668	T	0.266	0.404	0.385	0.369	0.545	0.319	0.369	0.424	0.417
UBAC2	rs7999348	G	0.555	0.741	0.672	0.680	0.823	0.717	0.747	0.735	0.782
UBAC2	rs9554581	T	0.192	0.135	0.099	0.139	0.167	0.159	0.111	0.171	0.102
UBAC2	rs17575643	T	0.096	0.048	0.031	0.082	0.056	0.044	0.040	0.059	0.042
UBAC2	rs727263	A	0.188	0.121	0.099	0.115	0.136	0.146	0.131	0.147	0.074
UBAC2	rs7332161	A	0.189	0.121	0.104	0.115	0.131	0.146	0.131	0.147	0.074
UBAC2	rs912130	C	0.527	0.705	0.635	0.631	0.717	0.765	0.712	0.729	0.708
UBAC2	rs2892976	G	0.344	0.467	0.490	0.443	0.490	0.376	0.556	0.465	0.454
UBAC2	rs3825427	T	0.194	0.135	0.104	0.139	0.167	0.159	0.121	0.159	0.102
UBAC2	rs9517701	G	0.190	0.121	0.104	0.115	0.131	0.146	0.131	0.147	0.074
GIMAP4	rs1916012	T	0.506	0.452	0.521	0.410	0.480	0.434	0.530	0.388	0.389
GIMAP4	rs1522596	T	0.530	0.541	0.536	0.459	0.631	0.588	0.581	0.488	0.463
GIMAP4	rs1608157	C	0.505	0.452	0.516	0.410	0.480	0.434	0.530	0.388	0.389
GIMAP2	rs10266069	A	0.412	0.327	0.396	0.352	0.313	0.270	0.359	0.347	0.278
GIMAP2	rs10256482	T	0.501	0.455	0.484	0.418	0.480	0.447	0.470	0.471	0.407

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Appendix C (cont.)

GIMAP1	rs2286900	T	0.123	0.118	0.115	0.066	0.146	0.150	0.126	0.076	0.116
CPLX1	rs11248047	A	0.440	0.424	0.438	0.434	0.485	0.394	0.343	0.359	0.505
DEPDC1	rs6692084	A	0.293	0.495	0.432	0.500	0.515	0.544	0.480	0.535	0.463
DEPDC1	rs12134670	C	0.068	0.012	0.026	0.008	0.005	0.009	0.015	0.012	0.009
DTL	rs1472224	G	0.452	0.592	0.552	0.557	0.662	0.606	0.551	0.553	0.634
DNMT3A	rs1465825	C	0.364	0.405	0.411	0.385	0.308	0.478	0.318	0.500	0.426
TFCP2L1	rs17006292	A	0.048	0.118	0.156	0.090	0.101	0.093	0.172	0.106	0.102
PSMD14	rs6744214	T	0.374	0.368	0.302	0.393	0.414	0.332	0.379	0.412	0.366
PSMD14	rs6733456	C	0.428	0.582	0.542	0.557	0.576	0.593	0.510	0.676	0.616
STK39	rs2390639	A	0.639	0.632	0.661	0.598	0.657	0.522	0.712	0.671	0.616
STK39	rs3769393	G	0.697	0.720	0.734	0.689	0.758	0.664	0.803	0.682	0.704
SGPP2	rs17562982	T	0.368	0.288	0.260	0.320	0.298	0.270	0.359	0.282	0.245
ASB18	rs7561555	C	0.437	0.822	0.781	0.639	0.828	0.863	0.833	0.859	0.875
SLIT2	rs13435197	A	0.311	0.389	0.417	0.385	0.389	0.442	0.369	0.365	0.347
SORBS2	rs4493590	G	0.174	0.038	0.031	0.057	0.030	0.062	0.025	0.041	0.023
MSX2	rs10516130	A	0.268	0.486	0.438	0.467	0.495	0.496	0.510	0.535	0.463
C6orf85(LOC100507336)	rs12194547	C	0.087	0.115	0.115	0.082	0.146	0.106	0.066	0.141	0.139
ABCB5	rs2190411	C	0.235	0.260	0.250	0.303	0.278	0.248	0.116	0.329	0.319
SUSD1	rs2782932	T	0.140	0.009	0.036	0.033	0	0	0	0	0.005
LINC01499(API5)	rs420798	C	0.795	0.913	0.906	0.926	0.929	0.907	0.874	0.912	0.940
API5	rs16937370	G	0.039	0	0	0	0	0	0	0	0
SLC43A3	rs549630	G	0.364	0.579	0.573	0.516	0.611	0.500	0.667	0.624	0.560
RIMBP2	rs2895135	A	0.174	0.039	0.052	0.115	0.010	0.058	0.015	0.018	0.028
GALNTL1	rs12589991	A	0.109	0.089	0.109	0.115	0.056	0.049	0.121	0.065	0.120
SMG6	rs749240	T	0.426	0.691	0.641	0.607	0.697	0.699	0.667	0.729	0.764
LILRB1	rs798887	A	0.695	0.825	0.891	0.803	0.788	0.823	0.798	0.835	0.833
LILRA1	rs103294	C	0.782	0.926	0.938	0.885	0.975	0.867	0.934	0.918	0.954
RALGAPA2	rs6082210	A	0.100	0.165	0.125	0.156	0.182	0.181	0.177	0.106	0.208

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Appendix C (cont.)

CDH26	rs817277	A	0.447	0.692	0.661	0.623	0.722	0.743	0.707	0.753	0.616
CDH26	rs817283	A	0.441	0.669	0.620	0.590	0.687	0.726	0.707	0.729	0.597
UBD	rs6933331	A	0.079	0.123	0.099	0.082	0.121	0.150	0.141	0.129	0.120
UBD	rs3025657	G	0.079	0.123	0.099	0.074	0.116	0.146	0.152	0.147	0.111
GABBR1	rs29273	G	0.863	0.864	0.870	0.844	0.859	0.854	0.894	0.871	0.852
MOG	rs3129045	T	0.386	0.580	0.630	0.525	0.525	0.558	0.556	0.606	0.644
HLA-F	rs3116788	G	0.310	0.312	0.292	0.270	0.338	0.323	0.359	0.329	0.259
HLA-F	rs1610584	T	0.310	0.312	0.292	0.270	0.338	0.323	0.359	0.329	0.259
HLA-F	rs1610585	C	0.310	0.312	0.292	0.270	0.338	0.323	0.359	0.329	0.259
HLA-F	rs1610593	T	0.311	0.312	0.292	0.270	0.338	0.323	0.359	0.329	0.264
HLA-F	rs1611356	G	0.689	0.688	0.708	0.730	0.662	0.677	0.641	0.671	0.736
HLA-F	rs1611381	T	0.311	0.312	0.292	0.270	0.338	0.323	0.359	0.329	0.264
HLA-F	rs7741807	G	0.939	0.934	0.958	0.934	0.955	0.867	0.960	0.947	0.931
HLA-F	rs1611388	C	0.310	0.312	0.292	0.270	0.338	0.323	0.354	0.329	0.264
HLA-F	rs1627465	C	0.311	0.312	0.292	0.270	0.338	0.323	0.359	0.329	0.264
LOC285830 (HLA-F antisense RNA1)	rs9258205	C	0.217	0.223	0.229	0.164	0.268	0.204	0.247	0.212	0.218
LOC285830 (HLA-F antisense RNA1)	rs2523386	A	0.088	0.044	0.026	0.082	0.035	0.080	0.051	0.012	0.028
LOC285830 (HLA-F antisense RNA1)	rs2844845	A	0.094	0.063	0.052	0.082	0.056	0.097	0.106	0.012	0.032
LOC285830 (HLA-F antisense RNA1)	rs1633041	T	0.232	0.251	0.240	0.320	0.227	0.265	0.278	0.194	0.250
LOC285830 (HLA-F antisense RNA1)	rs1737031	A	0.329	0.486	0.505	0.500	0.480	0.518	0.404	0.412	0.565
LOC285830 (HLA-F antisense RNA1)	rs885940	A	0.232	0.250	0.240	0.320	0.222	0.265	0.278	0.194	0.250
LOC285830 (HLA-F antisense RNA1)	rs1610637	C	0.232	0.250	0.240	0.320	0.222	0.265	0.278	0.194	0.250
LOC285830 (HLA-F antisense RNA1)	rs1615251	T	0.616	0.402	0.370	0.393	0.439	0.327	0.510	0.429	0.356
HLA-G	rs1633002	A	0.771	0.757	0.781	0.689	0.778	0.735	0.742	0.806	0.755

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Appendix C (cont.)

HLA-G	rs1632973	A	0.232	0.250	0.240	0.320	0.222	0.261	0.278	0.194	0.250
HLA-G	rs1736963	T	0.232	0.250	0.240	0.320	0.222	0.265	0.278	0.194	0.250
HLA-G	rs2523408	G	0.001	0	0	0	0	0	0	0	0
HLA-G	rs1611172	G	0.232	0.250	0.240	0.320	0.222	0.265	0.278	0.194	0.250
HLA-G	rs753544	T	0.232	0.250	0.240	0.320	0.222	0.265	0.278	0.194	0.250
HLA-G	rs1077433	A	0.232	0.250	0.240	0.320	0.222	0.265	0.278	0.194	0.250
HLA-G	rs1736951	A	0.302	0.374	0.375	0.418	0.318	0.438	0.389	0.353	0.333
HLA-G	rs407238	C	0.260	0.241	0.260	0.213	0.222	0.212	0.278	0.206	0.278
HCG9	rs9260954	G	0.041	0.050	0.052	0.041	0.051	0.080	0.061	0.006	0.046
HCG9	rs6911737	A	0.192	0.300	0.286	0.270	0.253	0.345	0.288	0.324	0.315
HCG9	rs6926792	A	0.191	0.299	0.286	0.270	0.253	0.345	0.278	0.324	0.319
HCG9	rs6931776	G	0.191	0.299	0.286	0.270	0.253	0.345	0.278	0.324	0.319
ZNRD1	rs9261189	T	0.192	0.300	0.286	0.270	0.253	0.350	0.278	0.324	0.319
ZNRD1	rs3869068	A	0.191	0.299	0.286	0.270	0.253	0.345	0.278	0.324	0.319
ZNRD1	rs9261265	C	0.041	0.048	0.052	0.041	0.051	0.071	0.061	0.006	0.046
PPP1R11	rs2074482	T	0.191	0.299	0.286	0.270	0.253	0.345	0.278	0.324	0.319
RNF39	rs9261317	A	0.958	0.950	0.948	0.959	0.949	0.920	0.939	0.994	0.954
TRIM31	rs9261376	G	0.317	0.507	0.490	0.434	0.465	0.580	0.449	0.600	0.505
TRIM31	rs9261389	G	0.315	0.503	0.490	0.434	0.460	0.580	0.449	0.600	0.486
TRIM31	rs6923832	A	0.041	0.050	0.052	0.041	0.051	0.080	0.061	0.006	0.046
MUC21	rs2530710	A	0.139	0.021	0.026	0.057	0.010	0.009	0.030	0.035	0
MUC21	rs2517446	C	0.154	0.154	0.172	0.156	0.116	0.146	0.111	0.229	0.157
MUC21	rs2517411	G	0.155	0.154	0.172	0.156	0.116	0.146	0.111	0.229	0.157
MUC21	rs2844673	A	0.173	0.154	0.172	0.156	0.116	0.146	0.111	0.229	0.157
MUC21	rs2252925	G	0.155	0.154	0.172	0.156	0.116	0.146	0.111	0.229	0.157
MUC21	rs2252926	G	0.155	0.154	0.172	0.156	0.116	0.146	0.111	0.229	0.157
MUC21	rs1634717	T	0.305	0.273	0.286	0.246	0.253	0.279	0.268	0.324	0.255
MUC21	rs2523915	T	0.845	0.846	0.828	0.844	0.884	0.854	0.889	0.771	0.843

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Appendix C (cont.)

MUC21	rs1632854	T	0.695	0.727	0.714	0.754	0.747	0.721	0.732	0.676	0.745
C6orf15	rs1265048	A	0.606	0.705	0.661	0.689	0.732	0.642	0.793	0.735	0.690
PSORS1C1	rs4959053	A	0.093	0.012	0.031	0.041	0.005	0	0	0.012	0.009
CCHCR1	rs2240063	A	0.427	0.438	0.469	0.475	0.500	0.420	0.455	0.347	0.407
CCHCR1	rs2073716	C	0.895	0.849	0.854	0.852	0.884	0.854	0.879	0.794	0.819
TCF19	rs2073723	T	0.231	0.131	0.120	0.189	0.106	0.155	0.101	0.129	0.134
POU5F1	rs9501063	G	0.891	0.811	0.844	0.811	0.813	0.810	0.838	0.771	0.787
POU5F1	rs9263804	C	0.237	0.130	0.120	0.189	0.101	0.155	0.101	0.129	0.134
POU5F1	rs3130501	A	0.231	0.130	0.120	0.189	0.101	0.155	0.101	0.129	0.134
POU5F1	rs3132524	A	0.237	0.130	0.120	0.189	0.101	0.155	0.101	0.129	0.134
HCG27	rs3130944	C	0.779	0.862	0.901	0.811	0.879	0.836	0.778	0.912	0.907
HLA-C	rs3905495	C	0.555	0.508	0.432	0.615	0.500	0.544	0.586	0.441	0.468
DHFRP2	rs7761068	T	0.358	0.402	0.401	0.451	0.348	0.491	0.399	0.412	0.329
HLA-B	rs9266406	A	0.296	0.238	0.255	0.148	0.182	0.248	0.207	0.259	0.329
HLA-B	rs9266409	C	0.297	0.240	0.266	0.148	0.182	0.248	0.207	0.259	0.329
HLA-B	rs6910516	C	0.297	0.240	0.266	0.148	0.182	0.248	0.207	0.259	0.329
MICA	rs2523467	A	0.436	0.554	0.536	0.566	0.667	0.447	0.606	0.565	0.514
MICA	rs3094584	T	0.204	0.253	0.276	0.230	0.177	0.283	0.162	0.265	0.361
BAG6(BAT3)	rs2077102	T	0.127	0.076	0.057	0.131	0.040	0.159	0.045	0.076	0.032
C6orf47	rs2242655	C	0.873	0.924	0.943	0.869	0.960	0.841	0.955	0.924	0.968
SLC44A4	rs11965547	A	0.127	0.077	0.052	0.123	0.040	0.133	0.040	0.082	0.079
C6orf10	rs544358	C	0.327	0.135	0.146	0.164	0.081	0.235	0.111	0.135	0.079
C6orf10	rs574710	G	0.337	0.135	0.146	0.164	0.081	0.235	0.111	0.135	0.079
C6orf10	rs539703	C	0.327	0.135	0.146	0.164	0.081	0.235	0.111	0.135	0.079
C6orf10	rs926591	T	0.326	0.135	0.151	0.164	0.086	0.235	0.101	0.135	0.079
C6orf10	rs4959093	C	0.327	0.135	0.151	0.164	0.086	0.235	0.101	0.135	0.079
BTNL2	rs2076530	G	0.387	0.328	0.312	0.311	0.182	0.522	0.192	0.459	0.301
HLA-DQA1	rs9272346	G	0.475	0.533	0.630	0.598	0.530	0.394	0.682	0.329	0.579

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Appendix C (cont.)

HLA-DQB1	rs6457617	C	0.465	0.459	0.568	0.459	0.586	0.274	0.449	0.329	0.551
COL12A1	rs4640857	G	0.318	0.056	0.099	0.156	0.035	0.018	0.061	0.012	0.051
C10orf11	rs1323076	G	0.365	0.348	0.417	0.393	0.318	0.319	0.409	0.288	0.310
C10orf11	rs17434565	G	0.167	0.023	0.057	0.057	0.015	0.004	0.025	0.012	0.005
PAX8	rs11123169	C	0.322	0.378	0.422	0.328	0.303	0.367	0.414	0.459	0.352
PAX8	rs10864912	T	0.384	0.433	0.484	0.434	0.485	0.358	0.409	0.365	0.495
HIVEP3	rs4660590	A	0.536	0.716	0.677	0.672	0.717	0.765	0.692	0.729	0.731
CEP135	rs2593082	T	0.542	0.686	0.693	0.623	0.687	0.655	0.687	0.718	0.722
CEP135	rs2611826	G	0.460	0.357	0.354	0.410	0.348	0.394	0.374	0.329	0.306
HMP19	rs1909704	A	0.538	0.509	0.526	0.557	0.475	0.473	0.535	0.512	0.509
TTLL7	rs11163772	A	0.220	0.354	0.349	0.328	0.359	0.288	0.379	0.400	0.380
TENM4(ODZ4)	rs2156215	T	0.233	0.248	0.240	0.238	0.308	0.195	0.258	0.235	0.264
KLRK1	rs2617151	A	0.176	0.231	0.229	0.221	0.192	0.336	0.172	0.294	0.167
KLRK1	rs2733852	G	0.315	0.540	0.531	0.475	0.500	0.628	0.601	0.588	0.435
OSR1	rs4666492	G	0.312	0.248	0.281	0.303	0.182	0.279	0.268	0.212	0.227
CTNNA2	rs4852547	G	0.384	0.492	0.531	0.385	0.500	0.460	0.475	0.465	0.579
MN1	rs134006	C	0.213	0.315	0.255	0.254	0.409	0.292	0.313	0.365	0.301
LTN1(RNF160)	rs2832137	T	0.340	0.111	0.135	0.164	0.076	0.102	0.136	0.100	0.088
HERPUD2	rs11763983	T	0.294	0.086	0.146	0.131	0.045	0.084	0.096	0.065	0.056
GALNT10	rs574750	A	0.313	0.460	0.396	0.451	0.540	0.456	0.470	0.476	0.431
SAMD3(TMEM200A)	rs9483115	T	0.544	0.878	0.849	0.738	0.889	0.881	0.924	0.912	0.903
SAMD3(TMEM200A)	rs4141940	A	0.518	0.790	0.781	0.680	0.788	0.783	0.818	0.829	0.815
SAMD3(TMEM200A)	rs899276	A	0.514	0.772	0.776	0.672	0.753	0.779	0.808	0.829	0.759
SAMD3(TMEM200A)	rs7758496	G	0.557	0.937	0.880	0.795	0.955	0.978	0.960	0.976	0.958
SAMD3(TMEM200A)	rs724324	G	0.544	0.877	0.854	0.738	0.909	0.903	0.879	0.906	0.894
SAMD3	rs4897380	C	0.567	0.937	0.865	0.803	0.960	0.978	0.965	0.971	0.963
SEMA6D	rs470151	T	0.197	0.257	0.224	0.295	0.303	0.235	0.247	0.247	0.264
PMFBP1	rs11862324	T	0.381	0.542	0.458	0.492	0.561	0.504	0.662	0.500	0.588

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Appendix C (cont.)

NAV2	rs2707110	C	0.433	0.571	0.615	0.557	0.571	0.588	0.571	0.576	0.519
NAV2	rs873764	G	0.518	0.615	0.651	0.648	0.606	0.615	0.591	0.582	0.620
TMEM132B	rs4435061	A	0.444	0.689	0.688	0.541	0.727	0.735	0.672	0.682	0.713
TMEM132B	rs10846917	T	0.472	0.269	0.286	0.336	0.202	0.239	0.268	0.306	0.282
TMEM132B	rs10846924	T	0.330	0.355	0.396	0.328	0.364	0.358	0.338	0.335	0.352
STX8	rs1549332	A	0.135	0.216	0.229	0.172	0.207	0.204	0.308	0.206	0.171
OVCH1	rs1436321	A	0.489	0.747	0.677	0.648	0.813	0.810	0.763	0.782	0.699
SLC41A2	rs2731031	A	0.373	0.238	0.203	0.287	0.192	0.257	0.273	0.253	0.218
HNF4G	rs2980221	A	0.479	0.483	0.469	0.410	0.520	0.558	0.495	0.441	0.449
SMARCA2	rs7033529	A	0.570	0.152	0.193	0.262	0.126	0.133	0.141	0.141	0.116
EBF2	rs4570167	C	0.493	0.825	0.828	0.656	0.838	0.876	0.864	0.794	0.838
EBF2	rs4242425	T	0.495	0.832	0.839	0.656	0.864	0.885	0.864	0.794	0.843
GAS2	rs10833804	G	0.603	0.598	0.615	0.631	0.601	0.650	0.449	0.612	0.634
LYST/NID1	rs7354999	G	0.738	0.762	0.760	0.803	0.798	0.721	0.823	0.682	0.755
LOC100132252	rs9469615	C	0.097	0.129	0.083	0.115	0.136	0.195	0.146	0.129	0.083
LOC107984355	rs872837	A	0.293	0.275	0.297	0.246	0.308	0.221	0.263	0.288	0.301
SACM1L	rs1969624	C	0.403	0.421	0.411	0.426	0.414	0.540	0.303	0.447	0.394
PLEKHB1	rs591804	G	0.383	0.489	0.438	0.492	0.535	0.429	0.525	0.524	0.495
ATP8A1	rs2100766	T	0.145	0.294	0.302	0.230	0.354	0.243	0.278	0.294	0.338
KCNK9	rs1961261	A	0.209	0.129	0.078	0.164	0.126	0.119	0.121	0.200	0.116
SUMO4	rs237024	C	0.702	0.970	0.948	0.926	0.990	0.973	0.975	0.982	0.981

C. 1000 Genomes Ad-mixed American and East Asian populations population samples

Gene	**Variant/SNP**	**Behcet Allele**	**AMR**	CLM	MXL	PEL	PUR	**EAS**	CDX	CHB	CHS	JPT	KHV
IL-10	rs1518111	A	0.329	0.287	0.422	0.371	0.274	0.676	0.651	0.743	0.686	0.644	0.652
IL-10	rs1800871	T	0.333	0.298	0.422	0.371	0.279	0.676	0.651	0.743	0.686	0.639	0.657
IL-10	rs1800872	A	0.333	0.298	0.422	0.371	0.279	0.676	0.651	0.743	0.686	0.639	0.657
IL-10	rs1554286	C	0.693	0.729	0.594	0.647	0.760	0.339	0.360	0.267	0.338	0.365	0.369
IL23R,IL12RB2	rs1495965	G	0.354	0.378	0.289	0.371	0.361	0.517	0.565	0.510	0.529	0.433	0.556
IL23R,IL12RB2	rs924080	T	0.581	0.521	0.523	0.765	0.519	0.759	0.769	0.791	0.800	0.707	0.727
IL23R,IL12RB2	rs12119179	A	0.769	0.718	0.773	0.806	0.784	0.494	0.430	0.505	0.495	0.587	0.444
IL23R,IL12RB2	rs11209033	C	0.769	0.718	0.773	0.806	0.784	0.499	0.435	0.515	0.500	0.591	0.444
IL23R,IL12RB2	rs12141431	C	0.215	0.277	0.195	0.176	0.202	0.506	0.575	0.490	0.505	0.413	0.556
TNFAIP3	rs9494885	T	0.863	0.846	0.914	0.900	0.817	0.938	0.973	0.922	0.952	0.875	0.975
TNFAIP3	rs10499194	C	0.722	0.750	0.688	0.806	0.649	0.967	0.973	0.981	0.976	0.933	0.975
TNFAIP3	rs610604	A	0.605	0.580	0.617	0.629	0.601	0.900	0.935	0.883	0.890	0.947	0.843
TNFAIP3	rs7753873	C	0.131	0.144	0.086	0.100	0.173	0.066	0.032	0.078	0.057	0.135	0.025
STAT4	rs7574070	A	0.341	0.319	0.336	0.300	0.399	0.612	0.737	0.612	0.605	0.500	0.621
STAT4	rs897200	A	0.344	0.330	0.328	0.300	0.404	0.614	0.737	0.617	0.605	0.500	0.626
STAT4	rs7572482	A	0.334	0.319	0.320	0.282	0.399	0.614	0.737	0.617	0.605	0.500	0.626
CCR1	rs17282391	G	0.049	0.064	0.031	0.053	0.043	0.044	0.027	0.068	0.043	0.048	0.030
CCR1	rs10510749	T	0.059	0.069	0.039	0.065	0.058	0.043	0.027	0.068	0.043	0.043	0.030
CCR1	rs13084057	G	0.059	0.069	0.039	0.065	0.058	0.043	0.027	0.068	0.043	0.043	0.030
CCR1	rs7631551	A	0.095	0.085	0.055	0.076	0.144	0.043	0.027	0.068	0.043	0.043	0.030
CCR1	rs7616215	T	0.736	0.718	0.789	0.818	0.654	0.873	0.914	0.850	0.876	0.822	0.909
CCR3	rs7649764	C	0.666	0.676	0.711	0.571	0.707	0.403	0.317	0.369	0.424	0.486	0.409
CCR3	rs9990343	G	0.378	0.372	0.391	0.318	0.423	0.122	0.075	0.141	0.110	0.202	0.076
CCR3	rs6803980	A	0.382	0.378	0.398	0.318	0.428	0.122	0.075	0.141	0.110	0.202	0.076
CCR3	rs13075270	C	0.091	0.101	0.062	0.059	0.125	0.038	0.016	0.083	0.033	0.029	0.025

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CCR3	rs13092160	C	0.058	0.074	0.031	0.059	0.058	0.038	0.016	0.083	0.033	0.029	0.025
CCR3	rs2373156	T	0.121	0.133	0.086	0.059	0.183	0.038	0.016	0.083	0.033	0.029	0.025
CCR3	rs7651539	T	0.121	0.133	0.086	0.059	0.183	0.038	0.016	0.083	0.033	0.029	0.025
CCR3	rs1542755	A	0.048	0.064	0.039	0.041	0.043	0.038	0.016	0.083	0.033	0.029	0.025
CCR3	rs13067058	A	0.046	0.059	0.039	0.041	0.043	0.036	0.011	0.083	0.033	0.029	0.020
CCR3	rs13092160	C	0.058	0.074	0.031	0.059	0.058	0.038	0.016	0.083	0.033	0.029	0.025
KLRC4	rs2617170	C	0.667	0.707	0.727	0.682	0.582	0.550	0.500	0.549	0.610	0.601	0.480
MEFV	rs61752717	G	0.001	0	0	0.006	0	0	0	0	0	0	0
ERAP1	rs17482078	T	0.124	0.170	0.070	0.053	0.173	0.058	0.054	0.063	0.057	0.072	0.040
FUT2	rs681343	T	0.343	0.388	0.320	0.124	0.495	0.004	0	0.015	0	0	0.005
IL12A	rs17810546	A	0.899	0.899	0.875	0.929	0.889	1.000	1.000	1.000	1.000	1.000	1.000
IL23R	rs11209026	A	0.052	0.053	0.062	0.012	0.077	0	0	0	0	0	0
IL23R	rs76418789	A	0	0	0	0	0	0.0526	0.0376	0.0631	0.0429	0.10	0.0152
IL23R	rs17375018	G	0.504	0.569	0.516	0.265	0.635	0.680	0.715	0.689	0.695	0.644	0.657
IL23R	rs11209032	A	0.229	0.282	0.227	0.188	0.216	0.497	0.570	0.471	0.495	0.409	0.551
IL23R	rs1343151	T	0.277	0.324	0.234	0.082	0.418	0.053	0.038	0.024	0.038	0.101	0.061
TLR4	rs4986790	G	0.037	0.053	0.031	0.006	0.053	0	0	0	0	0	0
TLR4	rs4986791	T	0.036	0.064	0.031	0	0.043	0	0	0	0	0	0
NOD2	rs2066844	T	0.024	0.053	0	0.006	0.029	0	0	0	0	0	0
NOD2	rs2066845	C	0.013	0.021	0.023	0	0.010	0	0	0	0	0	0
NOD2	rs2066847	ins-C	0.016	0.016	0.008	0.006	0.029	0	0	0	0	0	0
IL1	rs1800587	C	0.725	0.691	0.766	0.724	0.731	0.928	0.930	0.937	0.948	0.865	0.960
IL1	rs1143634	T	0.125	0.170	0.086	0.053	0.168	0.023	0.011	0.019	0.010	0.062	0.010
IL1	rs16944	G	0.450	0.548	0.469	0.300	0.471	0.531	0.500	0.549	0.543	0.534	0.525
TNFα	rs1799964	C	0.219	0.181	0.258	0.182	0.260	0.195	0.210	0.218	0.190	0.135	0.227
TNFα	rs361525	A	0.082	0.059	0.102	0.118	0.062	0.031	0.011	0.034	0.038	0.014	0.056
TNFα	rs1799724	T	0.183	0.170	0.203	0.282	0.101	0.125	0.129	0.141	0.071	0.163	0.121
IL12	rs3212227	A	0.659	0.755	0.602	0.541	0.702	0.499	0.457	0.568	0.486	0.466	0.515

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IL18	rs1946518	C	0.509	0.511	0.508	0.471	0.538	0.473	0.489	0.408	0.514	0.394	0.566
IL17F-A126G	rs2397084	T	0.952	0.931	0.945	0.994	0.942	0.996	0.995	0.995	0.995	1.000	0.995
LOC100129342	rs11206377	G	0.633	0.670	0.633	0.753	0.500	0.568	0.575	0.500	0.519	0.688	0.561
CCDC180	rs2061634	G	0.304	0.314	0.266	0.394	0.245	0.184	0.194	0.131	0.248	0.154	0.192
CPVL	rs317711	C	0.147	0.176	0.156	0.059	0.188	0.152	0.134	0.170	0.138	0.082	0.237
UBASH3B	rs4936742	T	0.418	0.452	0.438	0.394	0.394	0.569	0.618	0.539	0.629	0.428	0.641
UBAC2	rs9513584	G	0.504	0.346	0.547	0.700	0.462	0.494	0.602	0.413	0.448	0.538	0.480
UBAC2	rs9517644	T	0.499	0.340	0.539	0.694	0.457	0.494	0.602	0.413	0.448	0.538	0.480
UBAC2	rs11069357	A	0.499	0.340	0.539	0.694	0.457	0.492	0.602	0.408	0.448	0.538	0.475
UBAC2	rs984477	G	0.526	0.372	0.570	0.700	0.495	0.494	0.602	0.413	0.448	0.538	0.480
UBAC2	rs9554573	A	0.509	0.351	0.547	0.706	0.466	0.507	0.618	0.417	0.462	0.548	0.500
UBAC2	rs6491493	G	0.504	0.346	0.547	0.700	0.462	0.493	0.597	0.413	0.448	0.538	0.480
UBAC2	rs9517668	T	0.287	0.170	0.398	0.441	0.197	0.317	0.398	0.267	0.267	0.356	0.308
UBAC2	rs7999348	G	0.507	0.351	0.539	0.712	0.462	0.495	0.597	0.413	0.448	0.538	0.490
UBAC2	rs9554581	T	0.267	0.149	0.383	0.418	0.178	0.320	0.403	0.272	0.267	0.356	0.313
UBAC2	rs17575643	T	0.219	0.144	0.234	0.376	0.149	0.057	0.038	0.102	0.071	0.034	0.035
UBAC2	rs727263	A	0.267	0.154	0.375	0.418	0.178	0.318	0.403	0.277	0.262	0.341	0.318
UBAC2	rs7332161	A	0.268	0.154	0.375	0.424	0.178	0.319	0.403	0.277	0.262	0.346	0.318
UBAC2	rs912130	C	0.504	0.346	0.555	0.694	0.462	0.495	0.602	0.422	0.443	0.534	0.485
UBAC2	rs2892976	G	0.346	0.229	0.414	0.488	0.293	0.349	0.344	0.291	0.319	0.452	0.338
UBAC2	rs3825427	T	0.264	0.149	0.367	0.418	0.178	0.315	0.398	0.267	0.262	0.351	0.308
UBAC2	rs9517701	G	0.271	0.154	0.383	0.429	0.178	0.322	0.409	0.282	0.262	0.351	0.318
GIMAP4	rs1916012	T	0.463	0.537	0.461	0.335	0.500	0.513	0.570	0.485	0.529	0.490	0.495
GIMAP4	rs1522596	T	0.473	0.548	0.461	0.335	0.524	0.509	0.554	0.485	0.524	0.490	0.495
GIMAP4	rs1608157	C	0.463	0.537	0.461	0.335	0.500	0.513	0.570	0.485	0.529	0.490	0.495
GIMAP2	rs10266069	A	0.408	0.447	0.438	0.271	0.466	0.501	0.548	0.500	0.476	0.457	0.530
GIMAP2	rs10256482	T	0.484	0.553	0.477	0.335	0.548	0.516	0.565	0.515	0.500	0.462	0.545
GIMAP1	rs2286900	T	0.091	0.106	0.109	0.071	0.082	0.213	0.247	0.189	0.205	0.212	0.217

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CPLX1	rs11248047	A	0.555	0.516	0.617	0.624	0.495	0.438	0.371	0.461	0.429	0.500	0.419
DEPDC1	rs6692084	A	0.336	0.282	0.305	0.371	0.375	0.138	0.134	0.146	0.190	0.115	0.101
DEPDC1	rs12134670	C	0.032	0.032	0.023	0.012	0.053	0.099	0.097	0.107	0.124	0.091	0.076
DTL	rs1472224	G	0.403	0.431	0.422	0.188	0.543	0.135	0.086	0.141	0.129	0.202	0.111
DNMT3A	rs1465825	C	0.285	0.282	0.297	0.271	0.293	0.381	0.360	0.422	0.376	0.409	0.333
TFCP2L1	rs17006292	A	0.010	0.005	0	0	0.029	0.032	0.022	0.044	0.014	0.058	0.020
PSMD14	rs6744214	T	0.251	0.202	0.273	0.265	0.269	0.488	0.452	0.476	0.514	0.438	0.561
PSMD14	rs6733456	C	0.275	0.245	0.273	0.259	0.317	0.462	0.441	0.461	0.500	0.361	0.551
STK39	rs2390639	A	0.693	0.691	0.695	0.694	0.692	0.420	0.446	0.388	0.386	0.500	0.379
STK39	rs3769393	G	0.723	0.755	0.711	0.694	0.726	0.492	0.543	0.447	0.495	0.534	0.444
SGPP2	rs17562982	T	0.530	0.473	0.617	0.706	0.385	0.200	0.226	0.214	0.186	0.125	0.258
ASB18	rs7561555	C	0.256	0.282	0.211	0.194	0.312	0.242	0.226	0.277	0.257	0.216	0.232
SLIT2	rs13435197	A	0.316	0.335	0.281	0.294	0.337	0.133	0.140	0.121	0.124	0.183	0.096
SORBS2	rs4493590	G	0.137	0.176	0.164	0.071	0.139	0.246	0.237	0.262	0.262	0.250	0.217
MSX2	rs10516130	A	0.274	0.229	0.281	0.312	0.279	0.165	0.215	0.189	0.167	0.101	0.157
C6orf85(LOC100507336)	rs12194547	C	0.035	0.021	0.078	0.012	0.038	0.104	0.048	0.136	0.095	0.188	0.045
ABCB5	rs2190411	C	0.252	0.298	0.211	0.212	0.269	0.192	0.172	0.199	0.152	0.255	0.182
SUSD1	rs2782932	T	0.174	0.207	0.133	0.147	0.192	0.231	0.220	0.252	0.252	0.240	0.187
LINC01499(API5)	rs420798	C	0.703	0.846	0.633	0.506	0.779	0.490	0.473	0.471	0.462	0.505	0.540
API5	rs16937370	G	0	0	0	0	0	0.168	0.124	0.136	0.200	0.202	0.172
SLC43A3	rs549630	G	0.255	0.309	0.289	0.059	0.346	0.276	0.306	0.248	0.233	0.332	0.263
RIMBP2	rs2895135	A	0.197	0.261	0.156	0.088	0.255	0.182	0.204	0.155	0.152	0.183	0.217
GALNTL1	rs12589991	A	0.052	0.064	0.039	0.006	0.087	0.162	0.183	0.131	0.186	0.178	0.131
SMG6	rs749240	T	0.357	0.441	0.281	0.229	0.433	0.237	0.242	0.223	0.243	0.216	0.263
LILRB1	rs798887	A	0.571	0.665	0.516	0.353	0.697	0.343	0.618	0.189	0.305	0.188	0.449
LILRA1	rs103294	C	0.756	0.846	0.641	0.712	0.784	0.487	0.855	0.243	0.452	0.260	0.672
RALGAPA2	rs6082210	A	0.049	0.048	0.047	0.059	0.043	0.128	0.086	0.155	0.148	0.139	0.106
CDH26	rs817277	A	0.298	0.277	0.234	0.212	0.428	0.289	0.409	0.204	0.229	0.260	0.359

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CDH26	rs817283	A	0.298	0.277	0.234	0.206	0.433	0.286	0.409	0.194	0.229	0.231	0.384
UBD	rs6933331	A	0.042	0.043	0.031	0.024	0.062	0.129	0.070	0.107	0.057	0.216	0.192
UBD	rs3025657	G	0.042	0.043	0.031	0.024	0.062	0.129	0.070	0.107	0.057	0.216	0.192
GABBR1	rs29273	G	0.800	0.782	0.734	0.871	0.798	0.954	0.984	0.956	0.976	0.894	0.965
MOG	rs3129045	T	0.375	0.351	0.500	0.194	0.466	0.231	0.247	0.282	0.252	0.159	0.217
HLA-F	rs3116788	G	0.265	0.287	0.250	0.176	0.327	0.308	0.306	0.330	0.290	0.250	0.364
HLA-F	rs1610584	T	0.265	0.287	0.250	0.176	0.327	0.309	0.306	0.330	0.290	0.255	0.364
HLA-F	rs1610585	C	0.265	0.287	0.250	0.176	0.327	0.309	0.306	0.330	0.290	0.255	0.364
HLA-F	rs1610593	T	0.265	0.287	0.250	0.176	0.327	0.309	0.306	0.330	0.290	0.255	0.364
HLA-F	rs1611356	G	0.735	0.713	0.750	0.824	0.673	0.691	0.694	0.670	0.710	0.745	0.636
HLA-F	rs1611381	T	0.265	0.287	0.250	0.176	0.327	0.309	0.306	0.330	0.290	0.255	0.364
HLA-F	rs7741807	G	0.981	0.979	0.992	0.988	0.971	0.895	0.930	0.903	0.948	0.784	0.914
HLA-F	rs1611388	C	0.265	0.287	0.250	0.176	0.327	0.309	0.306	0.330	0.290	0.255	0.364
HLA-F	rs1627465	C	0.265	0.287	0.250	0.176	0.327	0.309	0.306	0.330	0.290	0.255	0.364
LOC285830 (HLA-F antisense RNA1)	rs9258205	C	0.146	0.106	0.156	0.141	0.178	0.291	0.301	0.291	0.271	0.250	0.343
LOC285830 (HLA-F antisense RNA1)	rs2523386	A	0.125	0.154	0.156	0.059	0.135	0.041	0.011	0.039	0.014	0.106	0.030
LOC285830 (HLA-F antisense RNA1)	rs2844845	A	0.128	0.160	0.156	0.059	0.139	0.041	0.011	0.039	0.014	0.106	0.030
LOC285830 (HLA-F antisense RNA1)	rs1633041	T	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
LOC285830 (HLA-F antisense RNA1)	rs1737031	A	0.280	0.271	0.289	0.341	0.231	0.187	0.081	0.238	0.110	0.303	0.192
LOC285830 (HLA-F antisense RNA1)	rs885940	A	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
LOC285830 (HLA-F antisense RNA1)	rs1610637	C	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
LOC285830 (HLA-F antisense RNA1)	rs1615251	T	0.630	0.644	0.609	0.612	0.644	0.805	0.919	0.733	0.890	0.683	0.808
HLA-G	rs1633002	A	0.759	0.777	0.734	0.665	0.837	0.893	0.989	0.850	0.943	0.798	0.894
HLA-G	rs1632973	A	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106

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HLA-G	rs1736963	T	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
HLA-G	rs2523408	G	0	0	0	0	0	0.001	0	0	0.005	0	0
HLA-G	rs1611172	G	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
HLA-G	rs753544	T	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
HLA-G	rs1077433	A	0.245	0.223	0.281	0.341	0.163	0.109	0.011	0.160	0.057	0.202	0.106
HLA-G	rs1736951	A	0.346	0.319	0.383	0.406	0.298	0.120	0.011	0.199	0.057	0.216	0.106
HLA-G	rs407238	C	0.252	0.293	0.234	0.282	0.202	0.127	0.011	0.175	0.076	0.207	0.157
HCG9	rs9260954	G	0.035	0.037	0.062	0.012	0.034	0.036	0.011	0.029	0.010	0.101	0.025
HCG9	rs6911737	A	0.174	0.165	0.266	0.100	0.188	0.190	0.091	0.194	0.095	0.303	0.263
HCG9	rs6926792	A	0.174	0.165	0.266	0.100	0.188	0.188	0.086	0.194	0.095	0.303	0.258
HCG9	rs6931776	G	0.174	0.165	0.266	0.100	0.188	0.190	0.091	0.194	0.095	0.303	0.263
ZNRD1	rs9261189	T	0.174	0.165	0.266	0.100	0.188	0.190	0.091	0.194	0.095	0.303	0.263
ZNRD1	rs3869068	A	0.174	0.165	0.266	0.100	0.188	0.190	0.091	0.194	0.095	0.303	0.263
ZNRD1	rs9261265	C	0.040	0.048	0.062	0.018	0.038	0.036	0.011	0.029	0.010	0.101	0.025
PPP1R11	rs2074482	T	0.174	0.165	0.266	0.100	0.188	0.190	0.091	0.194	0.095	0.303	0.263
RNF39	rs9261317	A	0.960	0.952	0.938	0.982	0.962	0.964	0.989	0.971	0.990	0.899	0.975
TRIM31	rs9261376	G	0.256	0.266	0.336	0.141	0.293	0.208	0.091	0.223	0.110	0.303	0.308
TRIM31	rs9261389	G	0.256	0.266	0.336	0.141	0.293	0.208	0.091	0.223	0.110	0.303	0.308
TRIM31	rs6923832	A	0.040	0.048	0.062	0.018	0.038	0.036	0.011	0.029	0.010	0.101	0.025
MUC21	rs2530710	A	0.125	0.112	0.125	0.100	0.159	0.163	0.156	0.126	0.100	0.221	0.212
MUC21	rs2517446	C	0.261	0.250	0.258	0.371	0.183	0.119	0.075	0.155	0.110	0.159	0.091
MUC21	rs2517411	G	0.262	0.250	0.266	0.371	0.183	0.118	0.075	0.155	0.110	0.154	0.091
MUC21	rs2844673	A	0.262	0.250	0.266	0.371	0.183	0.208	0.317	0.189	0.214	0.154	0.177
MUC21	rs2252925	G	0.261	0.245	0.266	0.371	0.183	0.118	0.075	0.155	0.110	0.154	0.091
MUC21	rs2252926	G	0.261	0.245	0.266	0.371	0.183	0.118	0.075	0.155	0.110	0.154	0.091
MUC21	rs1634717	T	0.535	0.500	0.602	0.571	0.495	0.161	0.075	0.233	0.152	0.188	0.146
MUC21	rs2523915	T	0.739	0.755	0.734	0.629	0.817	0.882	0.925	0.845	0.890	0.846	0.909
MUC21	rs1632854	T	0.465	0.500	0.398	0.429	0.505	0.839	0.925	0.767	0.848	0.812	0.854

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Appendix C(cont.)

C6orf15	rs1265048	A	0.520	0.516	0.477	0.382	0.663	0.475	0.263	0.510	0.457	0.606	0.520
PSORS1C1	rs4959053	A	0.091	0.080	0.070	0.147	0.067	0.128	0.172	0.107	0.095	0.082	0.192
CCHCR1	rs2240063	A	0.367	0.367	0.352	0.318	0.418	0.399	0.274	0.437	0.410	0.481	0.379
CCHCR1	rs2073716	C	0.970	0.968	0.961	0.982	0.966	0.817	0.796	0.854	0.814	0.803	0.818
TCF19	rs2073723	T	0.186	0.181	0.195	0.212	0.163	0.323	0.199	0.320	0.338	0.457	0.288
POU5F1	rs9501063	G	0.968	0.952	0.969	0.982	0.971	0.817	0.796	0.854	0.814	0.803	0.818
POU5F1	rs9263804	C	0.192	0.181	0.203	0.218	0.173	0.323	0.199	0.320	0.338	0.457	0.288
POU5F1	rs3130501	A	0.186	0.181	0.195	0.218	0.159	0.323	0.199	0.320	0.338	0.457	0.288
POU5F1	rs3132524	A	0.192	0.181	0.203	0.218	0.173	0.323	0.199	0.320	0.338	0.457	0.288
HCG27	rs3130944	C	0.780	0.782	0.797	0.718	0.817	0.698	0.597	0.728	0.724	0.707	0.727
HLA-C	rs3905495	C	0.546	0.590	0.594	0.506	0.510	0.594	0.715	0.612	0.629	0.404	0.626
DHFRP2	rs7761068	T	0.304	0.319	0.242	0.171	0.438	0.273	0.242	0.277	0.357	0.216	0.268
HLA-B	rs9266406	A	0.223	0.186	0.273	0.229	0.221	0.391	0.457	0.354	0.357	0.361	0.434
HLA-B	rs9266409	C	0.225	0.191	0.273	0.229	0.221	0.391	0.457	0.354	0.357	0.361	0.434
HLA-B	rs6910516	C	0.225	0.191	0.273	0.229	0.221	0.391	0.457	0.354	0.357	0.361	0.434
MICA	rs2523467	A	0.520	0.590	0.453	0.494	0.519	0.324	0.360	0.301	0.295	0.337	0.333
MICA	rs3094584	T	0.187	0.191	0.164	0.100	0.269	0.119	0.032	0.131	0.048	0.303	0.071
BAG6(BAT3)	rs2077102	T	0.187	0.181	0.148	0.276	0.144	0.130	0.065	0.165	0.105	0.264	0.040
C6orf47	rs2242655	C	0.813	0.819	0.852	0.724	0.856	0.869	0.935	0.830	0.895	0.736	0.960
SLC44A4	rs11965547	A	0.183	0.197	0.180	0.265	0.106	0.148	0.070	0.209	0.100	0.284	0.066
C6orf10	rs544358	C	0.501	0.415	0.539	0.718	0.380	0.361	0.306	0.398	0.410	0.365	0.318
C6orf10	rs574710	G	0.517	0.431	0.570	0.735	0.385	0.382	0.344	0.408	0.433	0.370	0.348
C6orf10	rs539703	C	0.500	0.415	0.531	0.718	0.380	0.361	0.306	0.398	0.410	0.365	0.318
C6orf10	rs926591	T	0.496	0.399	0.531	0.718	0.380	0.360	0.301	0.398	0.410	0.365	0.318
C6orf10	rs4959093	C	0.496	0.399	0.531	0.718	0.380	0.361	0.301	0.398	0.410	0.370	0.318
BTNL2	rs2076530	G	0.484	0.532	0.531	0.435	0.452	0.292	0.231	0.335	0.181	0.519	0.182
HLA-DQA1	rs9272346	G	0.321	0.447	0.289	0.171	0.351	0.492	0.640	0.422	0.452	0.510	0.449
HLA-DQB1	rs6457617	C	0.318	0.372	0.266	0.194	0.404	0.443	0.312	0.476	0.462	0.404	0.556

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Appendix C(cont.)

COL12A1	rs4640857	G	0.313	0.346	0.328	0.259	0.317	0.390	0.376	0.393	0.390	0.365	0.424
C10orf11	rs1323076	G	0.460	0.532	0.367	0.441	0.466	0.188	0.156	0.204	0.176	0.216	0.182
C10orf11	rs17434565	G	0.229	0.250	0.211	0.335	0.135	0.171	0.156	0.175	0.176	0.183	0.162
PAX8	rs11123169	C	0.316	0.426	0.312	0.253	0.269	0.220	0.194	0.214	0.238	0.212	0.242
PAX8	rs10864912	T	0.353	0.452	0.367	0.276	0.317	0.231	0.247	0.228	0.238	0.159	0.288
HIVEP3	rs4660590	A	0.693	0.707	0.680	0.800	0.601	0.311	0.269	0.296	0.290	0.385	0.308
CEP135	rs2593082	T	0.640	0.601	0.648	0.718	0.606	0.385	0.360	0.374	0.405	0.447	0.333
CEP135	rs2611826	G	0.362	0.394	0.352	0.282	0.404	0.567	0.597	0.597	0.529	0.505	0.616
HMP19	rs1909704	A	0.595	0.644	0.570	0.600	0.562	0.440	0.457	0.447	0.429	0.409	0.465
TTLL7	rs11163772	A	0.146	0.160	0.117	0.076	0.207	0.272	0.263	0.248	0.267	0.255	0.328
TENM4(ODZ4)	rs2156215	T	0.278	0.223	0.289	0.453	0.178	0.376	0.414	0.364	0.390	0.274	0.444
KLRK1	rs2617151	A	0.125	0.138	0.109	0.041	0.192	0.214	0.269	0.155	0.190	0.207	0.258
KLRK1	rs2733852	G	0.228	0.245	0.133	0.071	0.399	0.262	0.344	0.209	0.219	0.226	0.323
OSR1	rs4666492	G	0.343	0.394	0.320	0.224	0.409	0.197	0.215	0.160	0.186	0.183	0.247
CTNNA2	rs4852547	G	0.441	0.457	0.500	0.329	0.481	0.154	0.145	0.194	0.143	0.135	0.152
MN1	rs134006	C	0.190	0.160	0.219	0.288	0.120	0.279	0.349	0.214	0.290	0.260	0.288
LTN1(RNF160)	rs2832137	T	0.418	0.367	0.453	0.476	0.394	0.172	0.151	0.189	0.138	0.202	0.177
HERPUD2	rs11763983	T	0.427	0.463	0.383	0.424	0.423	0.234	0.220	0.272	0.210	0.250	0.217
GALNT10	rs574750	A	0.215	0.261	0.195	0.088	0.288	0.144	0.156	0.131	0.129	0.159	0.146
SAMD3(TMEM200A)	rs9483115	T	0.445	0.415	0.492	0.476	0.418	0.473	0.538	0.364	0.443	0.534	0.495
SAMD3(TMEM200A)	rs4141940	A	0.435	0.399	0.500	0.465	0.404	0.473	0.538	0.364	0.443	0.534	0.495
SAMD3(TMEM200A)	rs899276	A	0.434	0.394	0.500	0.465	0.404	0.474	0.543	0.364	0.443	0.534	0.495
SAMD3(TMEM200A)	rs7758496	G	0.44	0.41	0.508	0.476	0.42	0.47	0.538	0.36	0.44	0.534	0.48
SAMD3(TMEM200A)	rs724324	G	0.445	0.410	0.500	0.476	0.418	0.473	0.538	0.364	0.443	0.534	0.495
SAMD3	rs4897380	C	0.45	0.43	0.523	0.471	0.41	0.48	0.522	0.40	0.45	0.577	0.46
SEMA6D	rs470151	T	0.159	0.133	0.172	0.259	0.091	0.259	0.269	0.248	0.281	0.144	0.359
PMFBP1	rs11862324	T	0.476	0.367	0.484	0.735	0.356	0.455	0.376	0.505	0.529	0.495	0.359
NAV2	rs2707110	C	0.354	0.335	0.336	0.382	0.361	0.338	0.301	0.335	0.329	0.332	0.394

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Appendix C(cont.)

NAV2	rs873764	G	0.500	0.457	0.469	0.624	0.457	0.408	0.376	0.432	0.405	0.394	0.429
TMEM132B	rs4435061	A	0.341	0.372	0.352	0.329	0.317	0.476	0.468	0.490	0.486	0.438	0.500
TMEM132B	rs10846917	T	0.588	0.574	0.570	0.571	0.625	0.376	0.430	0.364	0.357	0.346	0.389
TMEM132B	rs10846924	T	0.290	0.314	0.328	0.329	0.212	0.476	0.468	0.485	0.486	0.442	0.500
STX8	rs1549332	A	0.104	0.128	0.117	0.035	0.130	0.091	0.070	0.078	0.086	0.149	0.071
OVCH1	rs1436321	A	0.274	0.266	0.188	0.194	0.399	0.465	0.516	0.456	0.467	0.365	0.530
SLC41A2	rs2731031	A	0.284	0.261	0.312	0.259	0.308	0.390	0.414	0.422	0.381	0.322	0.414
HNF4G	rs2980221	A	0.431	0.521	0.391	0.259	0.514	0.343	0.323	0.350	0.338	0.346	0.359
SMARCA2	rs7033529	A	0.761	0.729	0.742	0.700	0.851	0.538	0.527	0.539	0.557	0.510	0.556
EBF2	rs4570167	C	0.363	0.335	0.359	0.253	0.481	0.250	0.290	0.228	0.238	0.202	0.298
EBF2	rs4242425	T	0.362	0.330	0.359	0.253	0.481	0.250	0.290	0.228	0.238	0.202	0.298
GAS2	rs10833804	G	0.715	0.777	0.727	0.618	0.731	0.400	0.387	0.325	0.371	0.486	0.429
LYST/NID1	rs7354999	G	0.885	0.910	0.891	0.824	0.909	0.364	0.371	0.320	0.357	0.404	0.369
LOC100132252	rs9469615	C	0.086	0.069	0.078	0.053	0.135	0.058	0.005	0.053	0.019	0.173	0.030
LOC107984355	rs872837	A	0.370	0.335	0.352	0.441	0.356	0.240	0.290	0.233	0.243	0.197	0.242
SACM1L	rs1969624	C	0.454	0.410	0.445	0.382	0.558	0.265	0.317	0.204	0.224	0.240	0.348
PLEKHB1	rs591804	G	0.329	0.319	0.328	0.306	0.356	0.310	0.306	0.350	0.290	0.317	0.283
ATP8A1	rs2100766	T	0.082	0.085	0.047	0.094	0.091	0.156	0.113	0.170	0.167	0.188	0.136
KCNK9	rs1961261	A	0.226	0.207	0.250	0.218	0.236	0.233	0.253	0.282	0.148	0.216	0.273
SUMO4	rs237024	C	0.615	0.532	0.594	0.700	0.635	0.736	0.753	0.728	0.714	0.726	0.763

D. 1000 Genomes European and South Asian populations

Gene	**Variant/SNP**	**Behcet Allele**	**EUR**	CEU	FIN	GBR	IBS	TSI	**SAS**	BEB	GIH	ITU	PJL	STU
IL-10	rs1518111	A	0.221	0.202	0.207	0.176	0.234	0.276	0.443	0.459	0.403	0.436	0.443	0.475
IL-10	rs1800871	T	0.24	0.207	0.237	0.187	0.262	0.294	0.458	0.494	0.408	0.456	0.448	0.49
IL-10	rs1800872	A	0.240	0.207	0.237	0.187	0.262	0.294	0.458	0.494	0.408	0.456	0.448	0.490
IL-10	rs1554286	C	0.815	0.833	0.813	0.841	0.818	0.776	0.582	0.547	0.621	0.574	0.620	0.544
IL23R,IL12RB2	rs1495965	G	0.480	0.424	0.646	0.445	0.439	0.449	0.537	0.599	0.529	0.505	0.484	0.574
IL23R,IL12RB2	rs924080	T	0.553	0.515	0.697	0.555	0.505	0.500	0.661	0.703	0.655	0.598	0.677	0.676
IL23R,IL12RB2	rs12119179	A	0.665	0.697	0.611	0.698	0.664	0.659	0.475	0.407	0.481	0.510	0.536	0.436
IL23R,IL12RB2	rs11209033	C	0.665	0.697	0.611	0.698	0.664	0.659	0.478	0.407	0.485	0.510	0.542	0.436
IL23R,IL12RB2	rs12141431	C	0.304	0.288	0.323	0.275	0.313	0.318	0.488	0.547	0.461	0.471	0.453	0.515
TNFAIP3	rs9494885	T	0.913	0.904	0.960	0.907	0.916	0.879	0.902	0.924	0.917	0.922	0.875	0.873
TNFAIP3	rs10499194	C	0.720	0.727	0.763	0.720	0.654	0.738	0.715	0.797	0.636	0.725	0.682	0.745
TNFAIP3	rs610604	A	0.662	0.601	0.707	0.654	0.650	0.696	0.674	0.715	0.689	0.637	0.661	0.672
TNFAIP3	rs7753873	C	0.087	0.096	0.040	0.093	0.084	0.121	0.101	0.081	0.083	0.078	0.125	0.137
STAT4	rs7574070	A	0.342	0.343	0.313	0.379	0.318	0.360	0.314	0.366	0.291	0.343	0.297	0.279
STAT4	rs897200	A	0.357	0.364	0.313	0.401	0.341	0.369	0.319	0.372	0.301	0.343	0.292	0.294
STAT4	rs7572482	A	0.343	0.343	0.313	0.385	0.318	0.360	0.315	0.360	0.296	0.343	0.292	0.289
CCR1	rs17282391	G	0.094	0.101	0.141	0.099	0.061	0.075	0.293	0.209	0.325	0.275	0.359	0.289
CCR1	rs10510749	T	0.094	0.101	0.141	0.099	0.061	0.075	0.292	0.209	0.325	0.275	0.359	0.284
CCR1	rs13084057	G	0.094	0.101	0.141	0.099	0.061	0.075	0.293	0.209	0.325	0.275	0.359	0.289
CCR1	rs7631551	A	0.100	0.101	0.141	0.099	0.079	0.084	0.293	0.209	0.325	0.275	0.365	0.284
CCR1	rs7616215	T	0.643	0.616	0.616	0.648	0.631	0.701	0.549	0.640	0.519	0.525	0.500	0.574
CCR3	rs7649764	C	0.735	0.753	0.697	0.769	0.785	0.673	0.628	0.570	0.675	0.603	0.656	0.627
CCR3	rs9990343	G	0.507	0.510	0.566	0.571	0.509	0.393	0.472	0.378	0.515	0.490	0.516	0.451
CCR3	rs6803980	A	0.506	0.510	0.566	0.571	0.509	0.388	0.466	0.384	0.515	0.480	0.495	0.446
CCR3	rs13075270	C	0.098	0.101	0.131	0.099	0.070	0.093	0.299	0.221	0.354	0.265	0.370	0.275

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Appendix C(cont.)

CCR3	rs13092160	C	0.092	0.101	0.131	0.099	0.061	0.075	0.299	0.221	0.354	0.265	0.370	0.275
CCR3	rs2373156	T	0.089	0.091	0.106	0.077	0.075	0.098	0.276	0.203	0.316	0.240	0.349	0.265
CCR3	rs7651539	T	0.089	0.091	0.106	0.077	0.075	0.098	0.276	0.203	0.316	0.240	0.349	0.265
CCR3	rs1542755	A	0.080	0.091	0.106	0.077	0.051	0.075	0.272	0.215	0.311	0.245	0.312	0.270
CCR3	rs13067058	A	0.078	0.096	0.111	0.071	0.047	0.065	0.253	0.198	0.301	0.211	0.297	0.250
CCR3	rs13092160	C	0.092	0.101	0.131	0.099	0.061	0.075	0.299	0.221	0.354	0.265	0.370	0.275
KLRC4	rs2617170	C	0.663	0.687	0.591	0.720	0.696	0.626	0.544	0.552	0.515	0.515	0.589	0.554
ERAP1	rs17482078	T	0.224	0.263	0.227	0.253	0.182	0.201	0.065	0.058	0.058	0.078	0.068	0.064
FUT2	rs681343	T	0.440	0.535	0.298	0.473	0.425	0.472	0.283	0.238	0.252	0.240	0.427	0.260
IL12A	rs17810546	A	0.906	0.909	0.894	0.885	0.916	0.921	0.967	0.983	0.942	0.966	0.958	0.990
IL23R	rs11209026	A	0.062	0.051	0.030	0.071	0.065	0.089	0.012	0.006	0.010	0.015	0.016	0.015
IL23R	rs76418789	A	0.002	0	0	0.0055	0.0047	0	0	0	0	0	0	0
IL23R	rs17375018	G	0.714	0.717	0.697	0.747	0.664	0.748	0.686	0.733	0.660	0.667	0.714	0.667
IL23R	rs11209032	A	0.334	0.303	0.389	0.297	0.336	0.341	0.525	0.593	0.515	0.495	0.458	0.569
IL23R	rs1343151	T	0.322	0.343	0.207	0.363	0.336	0.360	0.164	0.122	0.155	0.167	0.203	0.167
TLR4	rs4986790	G	0.057	0.040	0.116	0.044	0.037	0.047	0.126	0.134	0.102	0.142	0.109	0.142
TLR4	rs4986791	T	0.058	0.040	0.116	0.038	0.047	0.047	0.117	0.093	0.092	0.147	0.078	0.167
NOD2	rs2066844	T	0.051	0.071	0.030	0.049	0.056	0.047	0.001	0.006	0	0	0	0
NOD2	rs2066845	C	0.010	0.020	0	0.005	0.009	0.014	0.004	0	0	0.005	0.016	0
NOD2	rs2066847	ins-C	0.014	0.030	0	0.022	0.014	0.005	0	0	0	0	0	0
IL1	rs1800587	C	0.713	0.747	0.722	0.637	0.743	0.706	0.685	0.715	0.704	0.642	0.693	0.676
IL1	rs1143634	T	0.248	0.232	0.237	0.313	0.196	0.266	0.147	0.122	0.194	0.132	0.146	0.137
IL1	rs16944	G	0.650	0.652	0.626	0.681	0.673	0.621	0.400	0.401	0.403	0.382	0. 438	0.377
TNFα	rs1799964	C	0.210	0.212	0.202	0.220	0.178	0.238	0.348	0.436	0.383	0.373	0.286	0.270
TNFα	rs361525	A	0.064	0.066	0.040	0.077	0.051	0.084	0.105	0.105	0.170	0.132	0.047	0.069
TNFα	rs1799724	T	0.094	0.056	0.066	0.077	0.131	0.136	0.119	0.076	0.107	0.118	0.151	0.137
IL12	rs3212227	A	0.777	0.808	0.813	0.753	0.780	0.734	0.626	0.674	0.655	0.583	0.667	0.559
IL18	rs1946518	C	0.577	0.636	0.545	0.621	0.579	0.509	0.712	0.750	0.772	0.691	0.646	0.701

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Appendix C(cont.)

IL17F-A126G	rs2397084	T	0.921	0.924	0.934	0.907	0.935	0.907	0.953	0.953	0.961	0.956	0.938	0.956
LOC100129342	rs11206377	G	0.542	0.596	0.530	0.533	0.500	0.551	0.802	0.756	0.859	0.789	0.766	0.828
CCDC180	rs2061634	G	0.200	0.237	0.121	0.209	0.215	0.215	0.261	0.227	0.223	0.275	0.328	0.250
CPVL	rs317711	C	0.249	0.247	0.247	0.236	0.234	0.276	0.095	0.087	0.034	0.098	0.120	0.137
UBASH3B	rs4936742	T	0.419	0.369	0.328	0.451	0.439	0.505	0.458	0.465	0.485	0.475	0.396	0.466
UBAC2	rs9513584	G	0.273	0.202	0.359	0.258	0.234	0.313	0.593	0.558	0.597	0.627	0.536	0.637
UBAC2	rs9517644	T	0.276	0.202	0.359	0.264	0.238	0.318	0.594	0.552	0.602	0.623	0.552	0.632
UBAC2	rs11069357	A	0.277	0.202	0.359	0.264	0.238	0.322	0.594	0.552	0.602	0.623	0.552	0.632
UBAC2	rs984477	G	0.341	0.308	0.455	0.319	0.290	0.336	0.599	0.570	0.602	0.627	0.547	0.642
UBAC2	rs9554573	A	0.275	0.202	0.364	0.264	0.234	0.313	0.603	0.576	0.597	0.642	0.547	0.647
UBAC2	rs6491493	G	0.273	0.202	0.359	0.258	0.234	0.313	0.599	0.576	0.607	0.627	0.542	0.637
UBAC2	rs9517668	T	0.115	0.096	0.146	0.137	0.075	0.126	0.168	0.174	0.165	0.176	0.151	0.172
UBAC2	rs7999348	G	0.285	0.202	0.364	0.286	0.243	0.332	0.677	0.651	0.650	0.725	0.604	0.745
UBAC2	rs9554581	T	0.114	0.096	0.146	0.137	0.075	0.121	0.166	0.169	0.165	0.176	0.146	0.172
UBAC2	rs17575643	T	0.100	0.091	0.131	0.126	0.070	0.089	0.109	0.110	0.121	0.118	0.062	0.132
UBAC2	rs727263	A	0.114	0.096	0.146	0.137	0.075	0.121	0.163	0.169	0.155	0.172	0.146	0.172
UBAC2	rs7332161	A	0.114	0.096	0.146	0.137	0.075	0.121	0.167	0.174	0.165	0.176	0.146	0.172
UBAC2	rs912130	C	0.274	0.207	0.364	0.258	0.234	0.308	0.595	0.570	0.592	0.627	0.542	0.637
UBAC2	rs2892976	G	0.202	0.162	0.247	0.203	0.150	0.248	0.317	0.250	0.306	0.338	0.292	0.387
UBAC2	rs3825427	T	0.116	0.096	0.146	0.143	0.075	0.126	0.178	0.186	0.175	0.181	0.167	0.181
UBAC2	rs9517701	G	0.115	0.096	0.146	0.137	0.079	0.121	0.167	0.174	0.165	0.176	0.146	0.172
GIMAP4	rs1916012	T	0.554	0.525	0.475	0.637	0.584	0.551	0.551	0.465	0.587	0.529	0.573	0.588
GIMAP4	rs1522596	T	0.555	0.525	0.475	0.637	0.589	0.551	0.551	0.465	0.587	0.529	0.573	0.588
GIMAP4	rs1608157	C	0.554	0.525	0.475	0.637	0.584	0.551	0.551	0.465	0.587	0.529	0.573	0.588
GIMAP2	rs10266069	A	0.494	0.485	0.455	0.489	0.514	0.523	0.356	0.366	0.393	0.324	0.349	0.348
GIMAP2	rs10256482	T	0.597	0.556	0.571	0.654	0.603	0.607	0.463	0.430	0.505	0.412	0.500	0.466
GIMAP1	rs2286900	T	0.092	0.096	0.126	0.082	0.070	0.089	0.090	0.064	0.083	0.127	0.099	0.074
CPLX1	rs11248047	A	0.466	0.480	0.500	0.505	0.453	0.402	0.359	0.355	0.427	0.363	0.328	0.319

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DEPDC1	rs6692084	A	0.232	0.242	0.308	0.187	0.210	0.210	0.214	0.198	0.214	0.186	0.245	0.225
DEPDC1	rs12134670	C	0.082	0.076	0.126	0.066	0.065	0.075	0.122	0.087	0.112	0.137	0.141	0.127
DTL	rs1472224	G	0.597	0.616	0.465	0.670	0.621	0.617	0.474	0.384	0.481	0.495	0.495	0.505
DNMT3A	rs1465825	C	0.262	0.258	0.227	0.236	0.322	0.262	0.451	0.465	0.413	0.485	0.432	0.461
TFCP2L1	rs17006292	A	0.002	0	0	0	0.005	0.005	0.043	0.070	0.053	0.054	0.010	0.029
PSMD14	rs6744214	T	0.313	0.227	0.414	0.330	0.304	0.294	0.415	0.453	0.403	0.412	0.396	0.417
PSMD14	rs6733456	C	0.317	0.232	0.419	0.330	0.304	0.304	0.406	0.442	0.374	0.412	0.391	0.417
STK39	rs2390639	A	0.790	0.833	0.753	0.808	0.808	0.752	0.681	0.645	0.646	0.740	0.703	0.667
STK39	rs3769393	G	0.818	0.843	0.808	0.808	0.841	0.790	0.734	0.686	0.728	0.765	0.750	0.735
SGPP2	rs17562982	T	0.402	0.384	0.333	0.396	0.388	0.500	0.500	0.442	0.529	0.529	0.443	0.544
ASB18	rs7561555	C	0.304	0.343	0.354	0.247	0.285	0.290	0.383	0.419	0.393	0.348	0.380	0.382
SLIT2	rs13435197	A	0.397	0.419	0.379	0.396	0.355	0.435	0.297	0.262	0.257	0.333	0.354	0.275
SORBS2	rs4493590	G	0.280	0.343	0.323	0.269	0.271	0.201	0.199	0.256	0.218	0.137	0.182	0.211
MSX2	rs10516130	A	0.141	0.126	0.141	0.176	0.131	0.136	0.203	0.215	0.194	0.255	0.198	0.157
C6orf85(LOC100507336)	rs12194547	C	0.062	0.066	0.081	0.082	0.065	0.019	0.096	0.116	0.068	0.064	0.120	0.118
ABCB5	rs2190411	C	0.273	0.283	0.187	0.269	0.262	0.360	0.192	0.169	0.194	0.181	0.219	0.196
SUSD1	rs2782932	T	0.181	0.157	0.192	0.165	0.196	0.192	0.158	0.134	0.146	0.142	0.161	0.206
LINC01499(API5)	rs420798	C	0.925	0.934	0.924	0.923	0.911	0.935	0.882	0.831	0.898	0.892	0.896	0.887
API5	rs16937370	G	0	0	0	0	0	0	0.026	0.047	0.010	0.020	0.036	0.020
SLC43A3	rs549630	G	0.380	0.449	0.253	0.407	0.393	0.397	0.223	0.186	0.228	0.206	0.229	0.260
RIMBP2	rs2895135	A	0.324	0.303	0.384	0.302	0.374	0.257	0.178	0.215	0.136	0.162	0.219	0.167
GALNTL1	rs12589991	A	0.142	0.091	0.202	0.143	0.164	0.112	0.087	0.099	0.117	0.069	0.083	0.069
SMG6	rs749240	T	0.362	0.328	0.338	0.352	0.369	0.416	0.378	0.384	0.413	0.368	0.312	0.412
LILRB1	rs798887	A	0.810	0.823	0.682	0.802	0.836	0.897	0.852	0.767	0.898	0.902	0.818	0.858
LILRA1	rs103294	C	0.820	0.833	0.702	0.824	0.836	0.897	0.872	0.820	0.908	0.917	0.828	0.877
RALGAPA2	rs6082210	A	0.046	0.025	0.141	0.038	0.009	0.019	0.077	0.058	0.092	0.078	0.083	0.069
CDH26	rs817277	A	0.431	0.500	0.409	0.407	0.416	0.425	0.399	0.401	0.383	0.373	0.411	0.426
CDH26	rs817283	A	0.433	0.500	0.424	0.401	0.421	0.421	0.403	0.424	0.388	0.373	0.411	0.422

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UBD	rs6933331	A	0.012	0.010	0.005	0	0.023	0.019	0.063	0.093	0.058	0.044	0.057	0.069
UBD	rs3025657	G	0.012	0.010	0.005	0	0.023	0.019	0.063	0.093	0.058	0.044	0.057	0.069
GABBR1	rs29273	G	0.813	0.889	0.894	0.786	0.724	0.780	0.863	0.901	0.850	0.907	0.792	0.868
MOG	rs3129045	T	0.347	0.247	0.212	0.385	0.472	0.407	0.333	0.413	0.286	0.294	0.354	0.333
HLA-F	rs3116788	G	0.304	0.298	0.429	0.291	0.234	0.276	0.349	0.390	0.320	0.328	0.354	0.358
HLA-F	rs1610584	T	0.304	0.298	0.429	0.291	0.234	0.276	0.349	0.390	0.320	0.328	0.354	0.358
HLA-F	rs1610585	C	0.304	0.298	0.429	0.291	0.234	0.276	0.349	0.390	0.320	0.328	0.354	0.358
HLA-F	rs1610593	T	0.304	0.298	0.429	0.291	0.234	0.276	0.350	0.390	0.320	0.333	0.354	0.358
HLA-F	rs1611356	G	0.696	0.702	0.571	0.709	0.766	0.724	0.650	0.610	0.680	0.667	0.646	0.642
HLA-F	rs1611381	T	0.304	0.298	0.429	0.291	0.234	0.276	0.350	0.390	0.320	0.333	0.354	0.358
HLA-F	rs7741807	G	0.978	0.980	0.975	0.978	0.991	0.967	0.921	0.942	0.927	0.931	0.891	0.917
HLA-F	rs1611388	C	0.302	0.298	0.419	0.291	0.234	0.276	0.350	0.390	0.320	0.333	0.354	0.358
HLA-F	rs1627465	C	0.304	0.298	0.429	0.291	0.234	0.276	0.353	0.407	0.320	0.333	0.354	0.358
LOC285830 (HLA-F antisense RNA1)	rs9258205	C	0.115	0.121	0.111	0.159	0.079	0.112	0.287	0.343	0.262	0.279	0.302	0.260
LOC285830 (HLA-F antisense RNA1)	rs2523386	A	0.174	0.096	0.126	0.187	0.234	0.220	0.081	0.041	0.117	0.039	0.130	0.074
LOC285830 (HLA-F antisense RNA1)	rs2844845	A	0.179	0.096	0.126	0.187	0.248	0.229	0.082	0.041	0.117	0.044	0. 130	0.074
LOC285830 (HLA-F antisense RNA1)	rs1633041	T	0.255	0.232	0.202	0.275	0.280	0.285	0.299	0.209	0.417	0.304	0.328	0.221
LOC285830 (HLA-F antisense RNA1)	rs1737031	A	0.280	0.258	0.207	0.286	0.313	0.332	0.350	0.262	0.451	0.333	0.401	0.289
LOC285830 (HLA-F antisense RNA1)	rs885940	A	0.255	0.232	0.202	0.275	0.280	0.285	0.301	0.209	0.417	0.314	0.328	0.221
LOC285830 (HLA-F antisense RNA1)	rs1610637	C	0.255	0.232	0.202	0.275	0.280	0.285	0.303	0.215	0.417	0.314	0.333	0.221
LOC285830 (HLA-F antisense RNA1)	rs1615251	T	0.690	0.712	0.783	0.681	0.650	0.631	0.626	0.727	0.524	0.623	0.573	0.696
HLA-G	rs1633002	A	0.745	0.768	0.798	0.725	0.720	0.715	0.700	0.791	0.587	0.686	0.672	0.779
HLA-G	rs1632973	A	0.254	0.232	0.202	0.269	0.280	0.285	0.302	0.209	0.417	0.314	0.333	0.221
HLA-G	rs1736963	T	0.256	0.232	0.202	0.280	0.280	0.285	0.302	0.209	0.417	0.314	0.333	0.221

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HLA-G	rs2523408	G	0	0	0	0	0	0	0.005	0.017	0.005	0.005	0	0
HLA-G	rs1611172	G	0.256	0.237	0.202	0.275	0.280	0.285	0.301	0.209	0.417	0.314	0.328	0.221
HLA-G	rs753544	T	0.255	0.232	0.202	0.275	0.280	0.285	0.303	0.215	0.417	0.314	0.328	0.225
HLA-G	rs1077433	A	0.255	0.232	0.202	0.275	0.280	0.285	0.302	0.209	0.417	0.314	0.333	0.221
HLA-G	rs1736951	A	0.303	0.283	0.237	0.324	0.322	0.346	0.362	0.227	0.476	0.431	0.411	0.245
HLA-G	rs407238	C	0.348	0.333	0.424	0.335	0.276	0.374	0.340	0.297	0.417	0.299	0.328	0.353
HCG9	rs9260954	G	0.051	0.030	0.010	0.060	0.070	0.079	0.028	0.017	0.010	0.039	0.016	0.054
HCG9	rs6911737	A	0.095	0.061	0.030	0.082	0.126	0.168	0.158	0.238	0.121	0.123	0.104	0.216
HCG9	rs6926792	A	0.095	0.061	0.030	0.082	0.126	0.168	0.157	0.238	0.121	0.123	0.099	0.216
HCG9	rs6931776	G	0.096	0.061	0.030	0.088	0.126	0.168	0.157	0.238	0.121	0.123	0.099	0.216
ZNRD1	rs9261189	T	0.095	0.061	0.030	0.082	0.126	0.168	0.158	0.238	0.121	0.123	0.099	0.221
ZNRD1	rs3869068	A	0.095	0.061	0.030	0.082	0.126	0.168	0.156	0.238	0.121	0.123	0.099	0.211
ZNRD1	rs9261265	C	0.051	0.030	0.010	0.060	0.070	0.079	0.027	0.017	0.010	0.039	0.016	0.049
PPP1R11	rs2074482	T	0.095	0.061	0.030	0.082	0.126	0.168	0.157	0.238	0.121	0.123	0.099	0.216
RNF39	rs9261317	A	0.949	0.970	0.990	0.940	0.930	0.921	0.972	0.983	0.990	0.961	0.979	0.951
TRIM31	rs9261376	G	0.189	0.146	0.061	0.187	0.248	0.290	0.346	0.372	0.398	0.333	0.302	0.324
TRIM31	rs9261389	G	0.189	0.146	0.061	0.187	0.248	0.290	0.345	0.372	0.398	0.333	0.297	0.324
TRIM31	rs6923832	A	0.051	0.030	0.010	0.060	0.070	0.079	0.027	0.017	0.010	0.039	0.016	0.049
MUC21	rs2530710	A	0.182	0.212	0.232	0.176	0.150	0.145	0.237	0.209	0.199	0.240	0.255	0.279
MUC21	rs2517446	C	0.143	0.101	0.086	0.121	0.224	0.173	0.125	0.145	0.073	0.152	0.130	0.127
MUC21	rs2517411	G	0.146	0.101	0.096	0.121	0.224	0.178	0.127	0.151	0.078	0.152	0.130	0.127
MUC21	rs2844673	A	0.146	0.101	0.096	0.121	0.224	0.178	0.127	0.151	0.078	0.152	0.130	0.127
MUC21	rs2252925	G	0.146	0.101	0.096	0.121	0.224	0.178	0.127	0.151	0.078	0.152	0.130	0.127
MUC21	rs2252926	G	0.146	0.101	0.096	0.121	0.224	0.178	0.127	0.151	0.078	0.152	0.130	0.127
MUC21	rs1634717	T	0.405	0.354	0.293	0.423	0.477	0.467	0.232	0.227	0.180	0.289	0.266	0.201
MUC21	rs2523915	T	0.854	0.899	0.904	0.879	0.776	0.822	0.873	0.849	0.922	0.848	0.870	0.873
MUC21	rs1632854	T	0.595	0.646	0.707	0.577	0.523	0.533	0.768	0.773	0.820	0.711	0.734	0.799
C6orf15	rs1265048	A	0.603	0.682	0.510	0.621	0.579	0.626	0.673	0.744	0.684	0.632	0.609	0.701

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PSORS1C1	rs4959053	A	0.082	0.086	0.076	0.082	0.079	0.084	0.178	0.221	0.146	0.157	0.250	0.127
CCHCR1	rs2240063	A	0.437	0.439	0.359	0.423	0.495	0.463	0.474	0.535	0.466	0.451	0.458	0.471
CCHCR1	rs2073716	C	0.957	0.965	0.955	0.962	0.939	0.967	0.922	0.953	0.942	0.931	0.901	0.887
TCF19	rs2073723	T	0.216	0.247	0.232	0.253	0.173	0.182	0.317	0.407	0.243	0.284	0.339	0.328
POU5F1	rs9501063	G	0.957	0.965	0.955	0.956	0.949	0.963	0.950	0.977	0.971	0.961	0.943	0.902
POU5F1	rs9263804	C	0.219	0.247	0.232	0.258	0.182	0.182	0.344	0.424	0.272	0.314	0.380	0.343
POU5F1	rs3130501	A	0.217	0.253	0.232	0.253	0.173	0.182	0.318	0.407	0.243	0.289	0.339	0.328
POU5F1	rs3132524	A	0.220	0.247	0.232	0.258	0.182	0.187	0.344	0.424	0.272	0.314	0.380	0.343
HCG27	rs3130944	C	0.763	0.727	0.808	0.731	0.794	0.752	0.767	0.826	0.733	0.735	0.760	0.789
HLA-C	rs3905495	C	0.607	0.641	0.510	0.648	0.626	0.612	0.532	0.651	0.578	0.475	0.490	0.480
DHFRP2	rs7761068	T	0.512	0.641	0.434	0.555	0.542	0.397	0.268	0.250	0.282	0.221	0.271	0.314
HLA-B	rs9266406	A	0.215	0.182	0.202	0.148	0.224	0.304	0.412	0.483	0.393	0.436	0.375	0.382
HLA-B	rs9266409	C	0.215	0.182	0.202	0.148	0.224	0.304	0.412	0.483	0.393	0.436	0.375	0.382
HLA-B	rs6910516	C	0.215	0.182	0.202	0.148	0.224	0.304	0.412	0.483	0.393	0.436	0.375	0.382
MICA	rs2523467	A	0.388	0.293	0.369	0.418	0.444	0.411	0.381	0.419	0.456	0.382	0.271	0.377
MICA	rs3094584	T	0.179	0.121	0.051	0.132	0.318	0.252	0.261	0.302	0.223	0.275	0.255	0.255
BAG6(BAT3)	rs2077102	T	0.163	0.146	0.328	0.165	0.093	0.093	0.115	0.110	0.107	0.093	0.099	0.162
C6orf47	rs2242655	C	0.837	0.854	0.672	0.835	0.907	0.907	0.888	0.890	0.898	0.907	0.901	0.843
SLC44A4	rs11965547	A	0.116	0.101	0.212	0.104	0.056	0.112	0.144	0.128	0.126	0.142	0.130	0.191
C6orf10	rs544358	C	0.372	0.414	0.313	0.368	0.350	0.411	0.383	0.355	0.437	0.338	0.401	0.382
C6orf10	rs574710	G	0.379	0.414	0.333	0.368	0.360	0.416	0.395	0.349	0.442	0.343	0.417	0.417
C6orf10	rs539703	C	0.372	0.414	0.313	0.368	0.350	0.411	0.381	0.337	0.437	0.343	0.401	0.382
C6orf10	rs926591	T	0.374	0.414	0.313	0.368	0.350	0.421	0.381	0.343	0.437	0.338	0.401	0.382
C6orf10	rs4959093	C	0.374	0.414	0.313	0.368	0.350	0.421	0.381	0.343	0.437	0.338	0.401	0.382
BTNL2	rs2076530	G	0.447	0.475	0.444	0.478	0.477	0.369	0.435	0.494	0.388	0.471	0.385	0.441
HLA-DQA1	rs9272346	G	0.451	0.434	0.535	0.407	0.444	0.435	0.511	0.541	0.505	0.520	0.495	0.500
HLA-DQB1	rs6457617	C	0.455	0.480	0.369	0.467	0.491	0.467	0.608	0.610	0.549	0.569	0.729	0.593
COL12A1	rs4640857	G	0.414	0.404	0.465	0.379	0.421	0.397	0.505	0.547	0.500	0.554	0.505	0.426

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Appendix C(cont.)

C10orf11	rs1323076	G	0.500	0.510	0.444	0.484	0.500	0.556	0.367	0.401	0.311	0.382	0.385	0.363
C10orf11	rs17434565	G	0.214	0.192	0.298	0.181	0.206	0.192	0.265	0.331	0.199	0.270	0.271	0.265
PAX8	rs11123169	C	0.329	0.374	0.359	0.253	0.322	0.332	0.349	0.401	0.383	0.353	0.323	0.289
PAX8	rs10864912	T	0.456	0.470	0.510	0.456	0.416	0.435	0.420	0.436	0.456	0.387	0.422	0.402
HIVEP3	rs4660590	A	0.472	0.444	0.535	0.533	0.411	0.449	0.481	0.401	0.408	0.554	0.495	0.534
CEP135	rs2593082	T	0.508	0.455	0.515	0.484	0.547	0.533	0.476	0.477	0.471	0.436	0.464	0.534
CEP135	rs2611826	G	0.490	0.545	0.485	0.516	0.444	0.467	0.527	0.535	0.544	0.574	0.531	0.451
HMP19	rs1909704	A	0.670	0.702	0.636	0.665	0.645	0.701	0.501	0.471	0.500	0.510	0.495	0.525
TTLL7	rs11163772	A	0.159	0.187	0.116	0.143	0.168	0.178	0.102	0.122	0.073	0.103	0.083	0.132
TENM4(ODZ4)	rs2156215	T	0.033	0.005	0.086	0.027	0.033	0.014	0.237	0.262	0.214	0.304	0.203	0.206
KLRK1	rs2617151	A	0.183	0.172	0.222	0.137	0.164	0.215	0.090	0.110	0.083	0.078	0.089	0.093
KLRK1	rs2733852	G	0.294	0.293	0.308	0.264	0.280	0.322	0.150	0.157	0.150	0.127	0.161	0.157
OSR1	rs4666492	G	0.418	0.404	0.470	0.385	0.402	0.430	0.385	0.343	0.388	0.392	0.396	0.402
CTNNA2	rs4852547	G	0.484	0.455	0.525	0.495	0.467	0.481	0.333	0.390	0.272	0.333	0.359	0.324
MN1	rs134006	C	0.058	0.040	0.076	0.055	0.042	0.075	0.185	0.186	0.155	0.250	0.161	0.172
LTN1(RNF160)	rs2832137	T	0.562	0.571	0.611	0.632	0.486	0.523	0.538	0.523	0.539	0.549	0.557	0.520
HERPUD2	rs11763983	T	0.571	0.601	0.636	0.588	0.533	0.505	0.259	0.262	0.296	0.245	0.240	0.250
GALNT10	rs574750	A	0.293	0.308	0.258	0.302	0.304	0.294	0.379	0.419	0.403	0.314	0.401	0.368
SAMD3(TMEM200A)	rs9483115	T	0.348	0.354	0.348	0.363	0.318	0.360	0.438	0.471	0.413	0.436	0.370	0.500
SAMD3(TMEM200A)	rs4141940	A	0.343	0.343	0.348	0.357	0.313	0.355	0.435	0.471	0.413	0.431	0.370	0.490
SAMD3(TMEM200A)	rs899276	A	0.343	0.343	0.348	0.357	0.313	0.355	0.438	0.471	0.413	0.436	0.370	0.500
SAMD3(TMEM200A)	rs7758496	G	0.34	0.34	0.36	0.35	0.31	0.36	0.42	0.471	0.40	0.43	0.35	0.45
SAMD3(TMEM200A)	rs724324	G	0.349	0.354	0.348	0.363	0.322	0.360	0.439	0.477	0.413	0.436	0.370	0.500
SAMD3	rs4897380	C	0.36	0.37	0.38	0.36	0.33	0.37	0.44	0.471	0.42	0.49	0.37	0.45
SEMA6D	rs470151	T	0.043	0.066	0.035	0.055	0.019	0.042	0.237	0.314	0.165	0.240	0.135	0.338
PMFBP1	rs11862324	T	0.170	0.182	0.232	0.181	0.126	0.136	0.237	0.279	0.218	0.186	0.260	0.250
NAV2	rs2707110	C	0.300	0.348	0.217	0.308	0.304	0.322	0.534	0.541	0.592	0.529	0.448	0.554
NAV2	rs873764	G	0.430	0.470	0.460	0.462	0.360	0.411	0.601	0.599	0.655	0.613	0.526	0.608

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Appendix C(cont.)

TMEM132B	rs4435061	A	0.286	0.263	0.328	0.308	0.257	0.280	0.317	0.337	0.345	0.289	0.297	0.319
TMEM132B	rs10846917	T	0.669	0.662	0.631	0.621	0.720	0.701	0.562	0.541	0.544	0.588	0.620	0.520
TMEM132B	rs10846924	T	0.230	0.227	0.288	0.264	0.192	0.187	0.279	0.314	0.296	0.260	0.240	0.289
STX8	rs1549332	A	0.124	0.126	0.071	0.104	0.168	0.145	0.103	0.134	0.087	0.083	0.120	0.098
OVCH1	rs1436321	A	0.308	0.283	0.374	0.286	0.290	0.308	0.505	0.552	0.529	0.451	0.505	0.495
SLC41A2	rs2731031	A	0.372	0.374	0.455	0.352	0.350	0.332	0.603	0.541	0.607	0.603	0.589	0.667
HNF4G	rs2980221	A	0.586	0.611	0.545	0.566	0.570	0.636	0.537	0.442	0.573	0.510	0.547	0.598
SMARCA2	rs7033529	A	0.849	0.843	0.793	0.896	0.822	0.893	0.747	0.738	0.767	0.750	0.724	0.755
EBF2	rs4570167	C	0.344	0.313	0.343	0.297	0.350	0.407	0.542	0.453	0.495	0.627	0.589	0.534
EBF2	rs4242425	T	0.344	0.313	0.343	0.297	0.350	0.407	0.542	0.453	0.495	0.627	0.589	0.534
GAS2	rs10833804	G	0.664	0.657	0.646	0.687	0.696	0.636	0.677	0.756	0.665	0.647	0.661	0.667
LYST/NID1	rs7354999	G	0.989	1.000	0.960	0.995	0.995	0.995	0.731	0.680	0.791	0.667	0.776	0.735
LOC100132252	rs9469615	C	0.143	0.126	0.136	0.143	0.117	0.192	0.057	0.041	0.068	0.039	0.094	0.044
LOC107984355	rs872837	A	0.363	0.394	0.449	0.324	0.322	0.327	0.244	0.256	0.277	0.172	0.307	0.216
SACM1L	rs1969624	C	0.564	0.520	0.540	0.516	0.584	0.645	0.319	0.250	0.291	0.363	0.391	0.294
PLEKHB1	rs591804	G	0.354	0.354	0.318	0.352	0.355	0.388	0.383	0.331	0.403	0.392	0.396	0.387
ATP8A1	rs2100766	T	0.034	0.025	0.061	0.060	0.009	0.019	0.093	0.081	0.107	0.083	0.094	0.098
KCNK9	rs1961261	A	0.230	0.232	0.263	0.264	0.201	0.196	0.261	0.326	0.252	0.230	0.260	0.245
SUMO4	rs237024	C	0.483	0.490	0.480	0.522	0.481	0.449	0.593	0.628	0.553	0.613	0.562	0.613

APPENDIX D. POPULATION GENETIC PARAMETER ESTIMATES OF BEHCET DISEASE ASSOCIATED GENES IN THE 1000 GENOMES ASIAN POPULATIONS

Gene	Total Sites	Eta	Segregating Sites	Haplotypes	Haplotype Diversity	ThetaK	Pi	Theta (Watterson)	Tajima's D	FuLi's D	FuLi's F	Achaz Y	R2
ABCB5	4810	1406	1404	959	1.00	108.64	0.0008	187.66	-1.24	-9.90	-5.16	-0.46	0.04
API5	788	204	203	163	0.92	7.17	0.0002	27.23	-2.11	-10.59	-6.77	-1.59	0.02
ASB18	1984	616	616	452	0.98	62.04	0.0009	82.22	-0.72	-9.44	-4.78	0.36	0.05
ATP8A1	7037	1920	1915	902	1.00	176.94	0.0007	256.26	-0.91	-10.73	-5.26	0.14	0.05
BAG6	382	144	143	157	0.95	10.73	0.0008	19.22	-1.25	-5.57	-3.81	-0.82	0.04
BTNL2	642	454	450	240	0.97	94.45	0.0077	60.59	1.63	1.91	2.01	1.43	0.10
C10ORF11 (LRMDA)	30401	8102	8093	1008	1.00	651.76	0.0006	1081.36	-1.17	-12.52	-6.10	-0.05	0.04
C6ORF10 (TSBP1)	2086	1083	1081	445	0.99	215.55	0.0027	144.55	1.44	-0.19	0.93	1.57	0.10
C6ORF15	56	24	24	17	0.69	4.85	0.0038	3.20	1.23	-2.13	-0.84	2.08	0.10
C6ORF47	49	13	13	15	0.72	0.97	0.0004	1.74	-0.94	-2.57	-2.34	-0.45	0.04
C6ORF85 (SLC22A23)	5961	1763	1762	998	1.00	233.92	0.0012	235.30	-0.02	-9.54	-4.13	1.34	0.07
CCDC180	2020	578	578	373	0.98	62.87	0.0009	77.14	-0.54	-10.11	-4.98	0.78	0.05
CCHCR1	492	250	250	132	0.94	38.36	0.0024	33.37	0.43	-1.46	-0.44	0.67	0.08
CCR1	157	39	39	33	0.28	0.99	0.0002	5.21	-2.09	-5.83	-4.98	-1.74	0.01
CCR3	702	206	206	160	0.86	19.57	0.0008	27.49	-0.83	-7.92	-4.56	0.15	0.05
CDH26	1524	399	399	440	0.98	18.42	0.0003	53.25	-1.90	-10.83	-6.39	-1.32	0.02
CEP135	2132	531	530	362	0.98	35.47	0.0004	70.87	-1.46	-10.60	-5.86	-0.64	0.03
COL12A1	3133	811	810	878	1.00	57.55	0.0005	108.24	-1.37	-12.75	-6.63	-0.22	0.03
CPLX1	1427	438	437	527	0.99	48.92	0.0012	58.46	-0.48	-8.87	-4.46	0.71	0.06
CPVL	5291	1550	1545	988	1.00	154.73	0.0008	206.88	-0.74	-9.78	-4.75	0.29	0.05
CTLA4	145	48	48	48	0.67	1.47	0.0002	6.41	-2.03	-7.68	-6.03	-1.43	0.02
CTNNA2	34316	9730	9718	1008	1.00	955.57	0.0008	1298.64	-0.78	-9.70	-4.63	0.16	0.05
DEPDC1	532	145	145	103	0.74	11.13	0.0005	19.35	-1.20	-6.30	-4.14	-0.60	0.04
DHFRP2	150	110	109	35	0.81	22.25	0.0064	14.68	1.44	0.53	1.23	1.45	0.10
DNMT3A	2863	707	706	774	1.00	47.29	0.0004	94.36	-1.46	-13.07	-6.88	-0.31	0.03
DTL	1831	485	485	342	0.97	30.97	0.0004	64.73	-1.52	-9.65	-5.50	-0.85	0.03
EBF2	6081	1629	1625	953	1.00	135.43	0.0007	217.42	-1.11	-10.45	-5.30	-0.20	0.04
ERAP1	1453	435	435	317	0.97	57.39	0.0011	58.06	-0.03	-5.62	-2.64	0.73	0.07
FUT2	356	103	103	116	0.88	4.26	0.0004	13.75	-1.93	-6.39	-4.80	-1.59	0.02
GABBR1	704	273	273	147	0.94	25.63	0.0008	36.44	-0.86	-4.06	-2.56	-0.51	0.05
GALNT1	2769	781	781	780	1.00	81.82	0.0009	104.24	-0.63	-9.17	-4.53	0.42	0.05
GALT10	6235	1875	1873	971	1.00	162.96	0.0007	250.25	-1.03	-9.56	-4.83	-0.19	0.04

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GAS2	4319	1159	1159	882	1.00	129.32	0.0009	154.69	-0.48	-9.70	-4.59	0.70	0.06
GIMAP1	226	62	62	55	0.72	5.30	0.0007	8.28	-0.97	-7.21	-4.97	0.27	0.04
GIMAP2	238	63	63	77	0.86	5.93	0.0007	8.41	-0.80	-4.90	-3.45	-0.05	0.05
GIMAP4	197	60	60	51	0.84	6.17	0.0009	8.01	-0.62	-6.15	-4.14	0.56	0.05
HCG27	212	121	120	98	0.95	25.94	0.0043	16.15	1.71	-1.45	0.32	2.21	0.11
HCG9	158	117	116	79	0.82	20.11	0.0062	15.62	0.81	0.70	0.87	0.69	0.09
HERPUD2	212	121	120	98	0.95	25.94	0.0043	16.15	1.71	-1.45	0.32	2.21	0.11
HIVEP3	14415	3684	3679	1004	1.00	299.71	0.0006	491.70	-1.15	-11.35	-5.63	-0.17	0.04
HLA_B	297	270	248	690	0.99	54.89	0.0166	36.04	1.51	-0.94	0.52	1.76	0.11
HLA_DQ	836	798	783	578	0.98	241.87	0.0347	106.51	3.72	4.08	4.43	3.13	0.15
HLA_F	128	52	51	33	0.81	8.47	0.0022	6.94	0.59	-2.66	-1.41	1.12	0.08
HLA_G	185	99	98	41	0.80	22.60	0.0055	13.21	1.98	-1.66	0.34	2.63	0.12
HLA_C	319	233	222	532	0.98	55.02	0.0163	31.10	2.21	-0.35	1.26	2.39	0.12
HLADQB1	905	861	861	646	0.99	278.42	0.0386	114.92	4.17	4.36	4.82	3.45	0.16
HMP19	1774	452	452	319	0.98	9.99	0.0002	60.33	-2.43	-10.29	-6.44	-2.27	0.01
HNF4G	808	234	234	154	0.88	25.21	0.0009	31.23	-0.55	-9.89	-5.30	0.99	0.05
IFNG	118	28	28	28	0.62	1.45	0.0003	3.74	-1.51	-7.84	-6.16	0.05	0.03
IL10	142	38	38	33	0.73	2.87	0.0006	5.07	-1.12	-5.98	-4.54	-0.08	0.04
IL12A	178	43	43	37	0.59	3.75	0.0005	5.74	-0.90	-5.29	-3.92	0.02	0.04
IL17A	224	62	61	52	0.87	5.89	0.0008	8.28	-0.78	-6.48	-4.44	0.35	0.05
IL1A	269	72	72	47	0.57	8.09	0.0007	9.61	-0.43	-6.45	-4.10	0.84	0.06
IL23R	3296	853	852	680	1.00	74.90	0.0006	113.85	-1.00	-11.43	-5.77	0.20	0.04
IL6	145	52	52	42	0.50	1.53	0.0003	6.94	-2.07	-4.63	-4.10	-1.88	0.01
KCNK9	3439	929	928	885	1.00	82.86	0.0008	123.99	-0.97	-12.62	-6.26	0.46	0.04
KLRC4	473	144	144	119	0.93	17.22	0.0008	19.22	-0.30	-6.36	-3.58	0.74	0.06
KLRK1	429	116	116	103	0.79	15.81	0.0009	15.48	0.06	-6.76	-3.69	1.46	0.07
LILRA1	461	171	171	149	0.91	8.89	0.0010	22.82	-1.74	-6.12	-4.32	-1.42	0.03
LILRB1	901	307	306	248	0.94	24.16	0.0012	40.97	-1.19	-6.14	-3.76	-0.70	0.04
LOC100129342	207	53	53	44	0.65	4.90	0.0007	7.07	-0.82	-5.58	-3.96	0.14	0.05
LOC100132252	1039	385	384	428	0.99	38.60	0.0013	51.39	-0.72	-6.34	-3.49	-0.07	0.05
LOC107984355	617	179	179	309	0.98	11.38	0.0007	23.89	-1.50	-9.53	-5.90	-0.61	0.03
LOC285830	655	347	346	117	0.90	71.36	0.0032	46.31	1.57	-1.06	0.55	1.85	0.10
LTN1	1567	430	430	337	0.98	33.70	0.0005	57.39	-1.20	-11.92	-6.38	0.08	0.04
LYST	5588	1257	1257	828	1.00	38.18	0.0002	167.77	-2.27	-13.74	-7.58	-1.84	0.01
MEFV	584	169	169	259	0.96	18.87	0.0013	22.56	-0.47	-8.59	-4.78	0.95	0.06
MICA	686	418	413	149	0.95	64.73	0.0042	55.79	0.47	-3.67	-1.40	1.05	0.08
MN1	1555	459	458	873	1.00	35.53	0.0007	61.26	-1.22	-8.90	-4.97	-0.47	0.04
MOG	427	185	183	88	0.86	9.16	0.0006	24.69	-1.80	-8.51	-5.57	-1.28	0.03
MSX2	199	51	51	43	0.65	1.94	0.0003	6.81	-1.90	-4.02	-3.62	-1.70	0.02

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MUC21	209	114	112	164	0.86	8.35	0.0014	15.22	-1.27	-3.31	-2.62	-0.99	0.04
NAV2	24008	6560	6550	1008	1.00	664.45	0.0009	875.55	-0.71	-10.54	-4.95	0.39	0.05
NOD2	1185	321	320	282	0.88	12.18	0.0003	42.84	-2.07	-11.73	-7.04	-1.50	0.02
OSR1	178	33	33	32	0.44	0.48	0.0001	4.40	-2.25	-9.61	-7.66	-1.33	0.01
OVCH1	1882	556	556	515	0.99	52.31	0.0007	74.21	-0.86	-8.17	-4.32	-0.05	0.05
PAX8	1700	507	506	448	0.98	50.28	0.0008	67.67	-0.75	-7.92	-4.16	0.09	0.05
PLEKHB1	459	119	119	111	0.84	13.49	0.0008	15.88	-0.42	-5.74	-3.42	0.47	0.06
PMFBP1	1461	401	401	340	0.98	29.81	0.0006	53.52	-1.29	-11.16	-6.12	-0.20	0.04
POU5F1	190	103	103	64	0.87	17.20	0.0027	13.75	0.70	-2.77	-1.12	1.31	0.08
PPP1R11	73	33	32	21	0.62	2.16	0.0007	4.40	-1.29	-1.38	-1.65	-1.24	0.03
PSMD14	2268	531	530	424	0.99	35.12	0.0003	70.87	-1.47	-13.68	-7.28	-0.16	0.03
PSORS1C1	920	567	561	272	0.97	101.02	0.0040	75.68	0.98	-0.76	0.33	1.16	0.09
PTPN22	1249	313	313	243	0.91	24.69	0.0004	41.78	-1.18	-9.58	-5.42	-0.23	0,04
RALGAPA2	8018	1953	1950	958	1.00	113.86	0.0004	260.66	-1.66	-13.06	-6.78	-0.79	0.03
RIMBP2	11477	3395	3385	1008	1.00	412.77	0.0013	453.12	-0.26	-9.19	-4.09	0.87	0.06
RNF39	173	89	89	49	0.84	10.65	0.0019	11.88	-0.29	-1.53	-1.06	-0.08	0.06
SACM1L	1481	447	446	275	0.94	64.48	0.0011	59.66	0.24	-7.77	-3.46	1.53	0.07
SAMD3	6653	2044	2037	962	1.00	308.60	0.0014	272.81	0.39	-9.19	-3.68	1.87	0.08
SEMA6D	15970	4670	4662	1003	1.00	471.63	0.0008	623.29	-0.72	-10.41	-4.91	0.37	0.05
SGPP2	3802	1099	1096	974	1.00	80.10	0.0006	146.68	-1.33	-9.81	-5.23	-0.61	0.04
SLC41A2	3845	1111	1110	650	1.00	120.88	0.0008	148.28	-0.54	-10.17	-4.84	0.69	0.05
SLC43A3	603	162	162	164	0.89	6.28	0.0003	21.62	-2.02	-10.16	-6.64	-1.43	0.02
SLC44A4	406	156	156	141	0.94	16.72	0.0011	20.82	-0.56	-4.38	-2.67	-0.02	0.05
SLIT2	10545	2845	2840	1004	1.00	205.09	0.0006	379.72	-1.35	-11.29	-5.77	-0.52	0.04
SMARCA2	6721	1809	1808	1001	1.00	177.36	0.0010	241.44	-0.78	-11.90	-5.68	0.58	0.05
SMG6	6965	1975	1974	920	1.00	173.24	0.0007	263.60	-1.01	-12.11	-5.91	0.22	0.04
SORBS2	11721	3518	3501	1008	1.00	434.77	0.0012	469.54	-0.22	-9.06	-4.00	0.92	0.06
STAT4	3720	989	989	894	1.00	94.74	0.0007	132.00	-0.83	-11.46	-5.63	0.48	0.05
STK39	8547	2341	2339	966	1.00	321.08	0.0011	312.45	0.08	-9.04	-3.82	1.37	0.07
STX8	10346	2820	2815	1008	1.00	217.81	0.0007	376.38	-1.24	-11.57	-5.81	-0.29	0.04
SUMO4	36	8	8	8	0.40	0.79	0.0010	1.07	-0.48	-2.98	-2.49	0.46	0.05
SUSD1	3622	1048	1048	974	1.00	102.97	0.0008	139.87	-0.77	-10.86	-5.31	0.45	0.05
TCF19	190	92	91	52	0.88	12.50	0.0016	12.28	0.05	-3.47	-1.99	0.63	0.07
TENM4	23487	6209	6203	1008	0.30	558.50	0.0007	828.70	-0.96	-11.78	-5.65	0.20	0.04
TFCP2L1	2031	532	531	679	0.33	49.23	0.0007	71.00	-0.89	-10.39	-5.38	0.28	0.05
TLR4	338	80	80	95	0.85	3.69	0.0003	10.68	-1.80	-9.49	-6.65	-0.85	0.02
TMEM132B	9972	2766	2764	1007	1.00	256.79	0.0008	369.17	-0.90	-10.43	-5.08	0.11	0.05
TNF	61	13	13	13	0.33	0.47	0.0002	1.74	-1.55	-2.57	-2.64	-1.29	0.02
TNFAIP3	381	116	116	110	0.69	3.72	0.0002	15.48	-2.13	-8.63	-6.11	-1.73	0.02

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Appendix C(cont.)

TRIM31	338	146	146	166	0.95	14.92	0.0015	19.49	-0.67	-2.90 -1.97	-0.36	0.05
TTLL7	3060	874	873	605	0.99	56.74	0.0004	116.65	-1.51	-9.93 -5.45	-0.85	0.03
UBAC2	5101	1406	1405	808	1.00	110.54	0.0006	187.66	-1.21	-10.66 -5.47	-0.31	0.04
UBASH3B	4485	1324	1324	985	1.00	141.49	0.0009	176.71	-0.59	-8.72 -4.21	0.36	0.05
UBD	120	48	48	30	0.79	6.17	0.0015	6.41	-0.10	-2.08 -1.38	0.30	0.06
ZNRD1	85	53	53	38	0.81	4.43	0.0012	7.07	-1.00	-0.67 -1.00	-0.97	0.04

APPENDIX E. POPULATION GENETIC PARAMETER ESTIMATES OF BEHCET DISEASE ASSOCIATED GENES IN THE 1000 GENOMES AFRICAN POPULATIONS

Gene	Total Sites	Eta	Segregating Sites	Haplotypes	Haplotype Diversity	ThetaK	Pi	Theta (Watterson)	Tajima's D	FuLi's D	FuLi's F	Achaz Y	R2
ABCB5	4810	2530	2527	1249	1.00	204.23	0.0014	325.87	-1.09	-7.03	-3.64	-0.65	0.04
API5	788	328	327	247	0.97	11.20	0.0003	42.25	-2.10	-8.57	-5.45	-1.87	0.02
ASB18	1984	1028	1025	697	1.00	104.25	0.0015	132.41	-0.62	-5.14	-2.61	-0.20	0.05
ATP8A1	7037	3530	3511	1143	1.00	238.82	0.0010	454.68	-1.38	-7.55	-4.05	-1.02	0.03
BAG6	382	180	180	206	0.96	11.07	0.0008	23.18	-1.47	-6.64	-4.35	-1.03	0.03
BTNL2	642	526	520	160	0.96	43.65	0.0035	67.75	-1.03	-4.52	-2.73	-0.76	0.04
C10ORF11 (LRMDA)	30401	14818	14778	1322	1.00	872.90	0.0008	1908.62	-1.58	-9.29	-4.84	-1.18	0.03
C6ORF10 (TSBP1)	2086	1267	1264	591	0.99	203.66	0.0026	163.19	0.72	-2.76	-0.64	1.10	0.08
C6ORF15	56	38	38	37	0.74	3.58	0.0028	4.89	-0.68	-2.70	-2.15	-0.27	0.05
C6ORF47	49	24	24	24	0.75	1.11	0.0005	3.09	-1.52	-3.39	-3.16	-1.18	0.02
C6ORF85 (SLC22A23)	5961	3108	3098	1285	1.00	277.29	0.0015	400.32	-0.89	-6.62	-3.33	-0.44	0.04
CCDC180	2020	907	905	481	0.99	67.38	0.0010	116.83	-1.23	-8.53	-4.50	-0.67	0.04
CCHCR1	492	293	293	228	0.97	43.68	0.0028	37.74	0.45	-2.42	-0.84	0.80	0.07
CCR1	157	74	74	69	0.76	2.61	0.0004	9.53	-1.96	-5.43	-4.40	-1.71	0.02
CCR3	702	366	366	285	0.95	24.89	0.0010	47.14	-1.35	-7.69	-4.48	-0.85	0.03
CDH26	1524	720	720	606	0.99	43.21	0.0008	92.74	-1.54	-8.99	-4.97	-1.07	0.03
CEP135	2132	1052	1051	567	0.99	46.61	0.0006	135.50	-1.90	-7.39	-4.46	-1.70	0.02
COL12A1	3133	1501	1495	1052	1.00	82.26	0.0007	193.33	-1.67	-9.44	-5.11	-1.25	0.03
CTLA4	145	60	60	56	0.82	2.44	0.0004	7.73	-1.82	-6.47	-5.04	-1.35	0.02
CPLX1	1427	712	711	683	1.00	59.49	0.0015	91.71	-1.02	-7.79	-4.08	-0.43	0.04
CPVL	5291	2705	2695	1232	1.00	199.51	0.0011	348.41	-1.24	-6.51	-3.54	-0.91	0.04
CTNNA2	34316	17541	17485	1322	1.00	1314.89	0.0012	2259.35	-1.22	-8.04	-4.08	-0.76	0.04
DEPDC1	532	253	253	199	0.94	20.03	0.0009	32.59	-1.10	-6.28	-3.78	-0.60	0.04
DHFRP2	150	126	125	69	0.83	23.84	0.0069	16.23	1.30	-0.84	0.40	1.55	0.10
DNMT3A	2863	1278	1274	936	1.00	65.59	0.0006	164.61	-1.75	-9.60	-5.25	-1.34	0.03
DTL	1831	921	920	486	0.99	44.44	0.0006	118.63	-1.81	-7.66	-4.54	-1.56	0.02
EBF2	6081	3026	3007	1187	1.00	197.84	0.0010	389.76	-1.43	-8.20	-4.36	-1.04	0.03
ERAP1	1453	762	760	538	0.99	66.40	0.0012	98.15	-0.94	-6.15	-3.31	-0.49	0.04
FUT2	356	178	178	227	0.93	19.94	0.0020	22.93	-0.37	-6.09	-3.34	0.44	0.06
GABBR1	704	371	370	228	0.96	19.66	0.0006	47.79	-1.69	-4.81	-3.38	-1.52	0.03
GALNT1	2769	1380	1380	1027	1.00	101.99	0.0011	177.75	-1.24	-7.29	-3.92	-0.82	0.04
GALT10	6235	3215	3206	1189	1.00	292.02	0.0013	414.10	-0.86	-6.92	-3.42	-0.37	0.05

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Appendix E(cont.)

GAS2	4319	2263	2253	1052	1.00	192.97	0.0013	291.48	-0.98	-6.70	-3.44	-0.54	0.04
GIMAP1	226	114	113	113	0.95	6.67	0.0009	14.68	-1.51	-2.80	-2.49	-1.36	0.03
GIMAP2	238	132	132	187	0.95	6.45	0.0008	17.00	-1.73	-6.56	-4.63	-1.36	0.02
GIMAP4	197	86	86	82	0.89	7.37	0.0011	11.08	-0.91	-2.91	-2.24	-0.63	0.04
HCG27	212	143	143	130	0.95	22.84	0.0038	18.42	0.67	-0.48	0.18	0.78	0.08
HCG9	158	127	124	186	0.96	25.05	0.0077	16.36	1.48	0.55	1.26	1.46	0.10
HERPUD2	212	143	143	130	0.95	22.84	0.0038	18.42	0.67	-0.48	0.18	0.78	0.08
HIVEP3	14415	7323	7298	1312	1.00	519.53	0.0010	943.23	-1.31	-8.02	-4.16	-0.89	0.04
HLA_B	297	282	261	975	1.00	50.66	0.0153	36.32	1.13	2.56	1.93	0.72	0.10
HLA_DQ	836	799	784	761	0.97	236.97	0.0340	102.91	3.77	3.96	4.37	3.23	0.15
HLA_F	128	74	73	58	0.91	10.41	0.0027	9.53	0.25	-5.00	-2.88	1.18	0.07
HLA_G	185	125	124	69	0.90	25.63	0.0062	16.10	1.64	-1.91	0.04	2.17	0.10
HLAC	319	284	270	805	1.00	63.54	0.0188	36.58	2.10	1.95	2.36	1.86	0.12
HLADQB1	905	866	865	794	0.98	244.95	0.0340	111.54	3.46	-0.10	2.39	3.66	0.14
HMP19	1774	842	838	483	0.99	49.72	0.0008	108.45	-1.57	-8.50	-4.75	-1.16	0.03
HNF4G	808	421	419	301	0.97	23.39	0.0009	54.23	-1.63	-7.01	-4.33	-1.34	0.03
IFNG	118	59	59	51	0.85	2.26	0.0005	7.60	-1.86	-4.54	-3.89	-1.62	0.02
IL10	142	58	58	59	0.85	4.59	0.0010	7.47	-1.02	-5.32	-3.88	-0.32	0.04
IL12A	178	82	82	75	0.90	5.98	0.0009	10.56	-1.18	-4.79	-3.51	-0.71	0.04
IL17A	224	110	110	102	0.93	6.17	0.0008	14.17	-1.56	-6.51	-4.58	-1.09	0.03
IL1A	269	139	139	108	0.94	10.77	0.0009	17.90	-1.11	-4.62	-3.17	-0.73	0.04
IL23R	3296	1664	1659	806	1.00	118.55	0.0010	214.33	-1.30	-7.46	-4.01	-0.89	0.04
IL6	145	66	65	77	0.92	4.51	0.0010	8.50	-1.26	-3.47	-2.83	-0.91	0.03
KCNK9	3439	1758	1751	1214	1.00	124.64	0.0012	226.44	-1.31	-7.11	-3.87	-0.95	0.04
KLRC4	473	240	240	160	0.95	24.78	0.0012	30.91	-0.56	-5.74	-3.18	0.06	0.05
KLRK1	429	199	199	155	0.95	26.10	0.0015	25.63	0.05	-4.32	-2.13	0.66	0.07
LILRA1	461	239	239	240	0.97	18.64	0.0021	30.78	-1.12	-5.65	-3.51	-0.70	0.04
LILRB1	901	508	505	638	0.99	43.66	0.0021	65.43	-0.96	-5.15	-2.95	-0.58	0.04
LOC100129342	207	97	97	79	0.92	3.99	0.0006	12.49	-1.87	-5.04	-4.02	-1.65	0.02
LOC100132252	1039	574	570	560	0.99	53.55	0.0018	73.93	-0.80	-3.94	-2.29	-0.51	0.05
LOC107984355	617	276	274	642	0.99	17.80	0.0010	35.55	-1.42	-8.77	-5.20	-0.88	0.03
LOC285830	655	443	442	257	0.98	77.78	0.0035	57.06	1.04	-3.19	-0.72	1.58	0.09
LTN1	1567	743	742	471	0.99	40.87	0.0006	95.70	-1.66	-9.26	-5.17	-1.22	0.03
LYST	5588	2713	2702	1066	1.00	183.39	0.0008	349.45	-1.38	-8.61	-4.49	-0.93	0.03
MEFV	584	278	277	481	0.99	22.98	0.0016	35.81	-1.02	-5.18	-3.16	-0.61	0.04
MICA	686	533	526	260	0.98	67.66	0.0044	68.65	-0.04	0.26	0.09	-0.07	0.06
MN1	1555	743	739	1062	1.00	40.16	0.0008	95.70	-1.68	-7.98	-4.63	-1.36	0.03
MOG	427	259	257	169	0.96	23.05	0.0015	33.36	-0.88	-6.94	-3.95	-0.22	0.04
MSX2	199	94	94	104	0.94	8.05	0.0013	12.11	-0.92	-5.00	-3.40	-0.36	0.04

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Appendix E(cont.)

MUC21	209	146	141	233	0.96	9.74	0.0016	18.81	-1.35	-0.68	-1.26	-1.41	0.03
NAV2	24008	12463	12414	1322	1.00	988.67	0.0013	1605.28	-1.12	-7.20	-3.68	-0.70	0.04
NOD2	1185	530	529	420	0.99	26.67	0.0007	68.27	-1.76	-8.55	-5.03	-1.40	0.02
OSR1	178	88	88	103	0.79	2.87	0.0004	11.33	-2.04	-7.26	-5.43	-1.69	0.02
OVCH1	1882	953	950	692	0.99	80.03	0.0011	122.75	-1.01	-6.88	-3.64	-0.54	0.04
PAX8	1700	850	848	606	0.99	66.97	0.0011	109.48	-1.12	-7.23	-3.89	-0.66	0.04
PLEKHB1	459	256	254	251	0.96	24.15	0.0015	32.97	-0.76	-5.46	-3.14	-0.22	0.05
PMFBP1	1461	635	633	486	0.99	37.36	0.0007	81.79	-1.57	-10.36	-5.64	-1.01	0.03
POU5F1	190	107	107	67	0.92	14.46	0.0023	13.78	0.13	-2.35	-1.21	0.51	0.07
PPP1R11	73	35	33	30	0.85	3.02	0.0010	4.51	-0.83	-2.49	-2.18	-0.58	0.05
PSMD14	2268	998	996	608	0.99	30.15	0.0003	128.55	-2.22	-9.73	-5.69	-2.03	0.01
PSORS1C1	920	582	577	366	0.97	94.74	0.0038	74.96	0.76	-3.23	-0.90	1.24	0.08
PTPN22	1249	541	541	375	0.97	22.73	0.0004	69.68	-1.94	-8.07	-4.93	-1.69	0.02
RALGAPA2	8018	3639	3634	1224	1.00	137.17	0.0004	468.72	-2.06	-9.72	-5.41	-1.83	0.02
RIMBP2	11477	6072	6045	1322	1.00	506.77	0.0016	782.10	-1.03	-6.49	-3.34	-0.63	0.04
RNF39	173	94	94	70	0.92	12.41	0.0022	12.11	0.07	-2.48	-1.36	0.47	0.07
SACM1L	1481	749	749	441	0.99	77.14	0.0014	96.47	-0.58	-6.50	-3.21	0.01	0.05
SAMD3	6653	3684	3669	1205	1.00	319.27	0.0014	474.51	-0.95	-5.16	-2.78	-0.65	0.04
SEMA6D	15970	8188	8160	1317	1.00	556.11	0.0009	1054.65	-1.38	-9.12	-4.65	-0.90	0.03
SGPP2	3802	1907	1903	1165	1.00	133.19	0.0010	245.63	-1.33	-8.36	-4.40	-0.88	0.03
SLC41A2	3845	1894	1891	817	1.00	124.14	0.0008	243.95	-1.43	-6.37	-3.64	-1.15	0.03
SLC43A3	603	264	264	260	0.98	15.57	0.0008	34.00	-1.54	-6.38	-4.11	-1.21	0.03
SLC44A4	406	211	211	217	0.97	18.01	0.0011	27.18	-0.96	-5.18	-3.21	-0.52	0.04
SLIT2	10545	5088	5069	1298	1.00	278.11	0.0008	655.35	-1.68	-9.28	-4.94	-1.31	0.03
SMARCA2	6721	3437	3427	1299	1.00	243.11	0.0014	442.70	-1.31	-8.31	-4.31	-0.86	0.04
SMG6	6965	3153	3142	1159	1.00	225.72	0.0009	406.12	-1.29	-10.61	-5.23	-0.61	0.04
SORBS2	11721	6134	6122	1321	1.00	561.34	0.0015	790.08	-0.84	-6.80	-3.34	-0.36	0.05
STAT4	3720	1762	1757	1057	1.00	116.54	0.0008	226.95	-1.41	-8.69	-4.59	-0.96	0.03
STK39	8547	4545	4536	1218	1.00	405.22	0.0014	585.41	-0.90	-7.29	-3.59	-0.39	0.04
STX8	10346	5399	5381	1319	1.00	437.06	0.0013	695.41	-1.08	-7.72	-3.88	-0.60	0.04
SUMO4	36	15	15	14	0.54	0.69	0.0009	1.93	-1.39	-0.05	-0.71	-1.45	0.02
SUSD1	3622	1798	1794	1195	1.00	120.52	0.0009	231.59	-1.39	-8.23	-4.38	-0.96	0.03
TCF19	190	100	99	69	0.90	11.74	0.0015	12.88	-0.24	-4.24	-2.54	0.40	0.06
TENM4	23487	11678	11642	1320	1.00	838.79	0.0011	1504.17	-1.29	-8.38	-4.27	-0.83	0.04
TFCP2L1	2031	955	953	862	1.00	66.90	0.0010	123.01	-1.32	-8.25	-4.44	-0.83	0.03
TLR4	338	167	167	211	0.97	9.55	0.0007	21.51	-1.56	-5.62	-3.92	-1.25	0.03
TMEM132B	9972	5241	5227	1305	1.00	370.74	0.0011	675.06	-1.31	-7.77	-4.07	-0.91	0.04
TNF	61	27	27	28	0.42	0.75	0.0003	3.48	-1.89	-6.20	-5.27	-1.31	0.01
TNFAIP3	381	167	165	179	0.93	12.19	0.0008	21.51	-1.22	-7.52	-4.66	-0.48	0.04

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Appendix E(cont.)

TRIM31	338	191	191	275	0.98	20.99	0.0021	24.60	-0.41	-2.49	-1.53	-0.16	0.05
TTLL7	3060	1380	1379	748	1.00	77.70	0.0006	177.75	-1.63	-8.33	-4.63	-1.28	0.03
UBAC2	5101	2372	2367	960	1.00	110.87	0.0006	305.52	-1.85	-9.22	-5.10	-1.56	0.02
UBASH3B	4485	2372	2363	1215	1.00	182.56	0.0012	305.52	-1.17	-6.95	-3.67	-0.77	0.04
UBD	120	67	66	53	0.81	9.70	0.0023	8.63	0.33	-3.39	-1.79	1.16	0.07
ZNRD1	85	39	39	32	0.80	5.38	0.0015	5.02	0.18	-0.86	-0.46	0.36	0.07

APPENDIX F. POPULATION GENETIC PARAMETER ESTIMATES OF BEHCET DISEASE ASSOCIATED GENES IN THE 1000 GENOMES EUROPEAN POPULATIONS

“Gene	**Total Sites**	**Eta**	**Segregating Sites**	**Haplotypes**	**Haplotype Diversity**	**ThetaK**	**Pi**	**Theta (Watterson)**	**Tajima’s D**	**FuLi’s D**	**FuLi’s F**	**Achaz Y**	**R2**
ABCB5	4810	1331	1330	937	1.00	154.70	0.0011	177.69	-0.38	-9.64	-4.47	0.83	0.06
API5	788	197	196	159	0.93	11.00	0.0003	26.30	-1.67	-10.45	-6.44	-0.81	0.03
ASB18	1984	674	674	443	0.98	67.32	0.0010	89.98	-0.74	-8.56	-4.37	0.17	0.05
ATP8A1	7037	1794	1790	842	1.00	224.55	0.0009	239.50	-0.18	-8.66	-3.87	0.91	0.06
BAG6	382	132	131	123	0.96	10.40	0.0007	17.62	-1.16	-7.78	-4.94	-0.21	0.04
BTNL2	642	438	434	98	0.94	38.91	0.0032	58.47	-0.97	2.77	0.61	-1.24	0.04
C10ORF11 (LRMDA)	30401	7855	7846	1005	1.00	618.55	0.0005	1048.67	-1.21	-11.28	-5.61	-0.30	0.04
C6ORF10 (TSBP1)	2086	1171	1166	432	0.98	214.66	0.0027	156.33	1.10	-0.44	0.58	1.23	0.09
C6ORF15	56	27	27	25	0.73	4.58	0.0036	3.60	0.66	-1.25	-0.51	1.05	0.08
C6ORF47	49	15	15	15	0.68	0.87	0.0004	2.00	-1.24	-3.63	-3.26	-0.62	0.03
C6ORF85 (SLC22A23)	5961	1749	1747	965	1.00	210.03	0.0011	233.50	-0.30	-7.99	-3.66	0.65	0.06
CCDC180	2020	526	525	329	0.98	50.52	0.0007	70.22	-0.82	-9.19	-4.78	0.19	0.05
CCHCR1	492	255	254	146	0.96	45.27	0.0029	34.04	0.95	-1.40	-0.05	1.25	0.09
CCR1	157	48	48	43	0.47	2.10	0.0003	6.41	-1.77	-8.05	-6.12	-0.85	0.02
CCR3	702	178	178	116	0.93	23.77	0.0010	23.76	0.00	-5.94	-3.08	1.00	0.07
CDH26	1524	442	440	380	0.99	15.04	0.0003	59.01	-2.17	-10.92	-6.57	-1.79	0.02
CEP135	2132	536	536	348	0.98	42.06	0.0005	71.56	-1.20	-10.11	-5.46	-0.28	0.04
COL12A1	3133	786	785	818	1.00	28.39	0.0002	104.93	-2.14	-11.40	-6.57	-1.74	0.02
CTLA4	145	26	26	24	0.66	1.37	0.0002	3.47	-1.48	-6.18	-5.04	-0.47	0.03
CPLX1	1427	426	425	522	1.00	55.09	0.0013	56.87	-0.09	-7.04	-3.36	0.90	0.06
CPVL	5291	1639	1634	950	1.00	177.83	0.0009	218.81	-0.55	-7.94	-3.82	0.28	0.05
CTNNA2	34316	9396	9386	1006	1.00	861.27	0.0008	1254.40	-0.92	-10.11	-4.91	-0.01	0.05
DEPDC1	532	140	140	98	0.83	14.99	0.0007	18.69	-0.56	-7.31	-4.28	0.57	0.05

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Appendix F(cont.)

DHFRP2	150	92	92	35	0.90	24.58	0.0071	12.28	2.78	1.05	2.32	2.64	0.13
DNMT3A	2863	726	725	695	1.00	57.53	0.0005	96.92	-1.19	-10.87	-5.70	-0.18	0.04
DTL	1831	504	504	302	0.97	38.64	0.0006	67.29	-1.24	-7.87	-4.48	-0.64	0.04
EBF2	6081	1738	1727	878	1.00	170.09	0.0008	232.03	-0.79	-9.23	-4.54	0.12	0.05
ERAP1	1453	517	514	371	0.99	77.47	0.0015	69.02	0.36	-6.06	-2.53	1.33	0.07
FUT2	356	103	103	126	0.85	15.32	0.0015	13.75	0.32	-5.93	-3.13	1.65	0.07
GABBR1	704	305	304	151	0.91	18.32	0.0006	40.72	-1.59	-7.39	-4.64	-1.13	0.03
GALNT1	2769	754	754	714	1.00	89.96	0.0010	100.66	-0.31	-8.15	-3.86	0.72	0.06
GALT10	6235	1806	1803	929	1.00	247.65	0.0011	241.11	0.08	-8.27	-3.51	1.24	0.07
GAS2	4319	1189	1186	831	1.00	127.31	0.0009	158.74	-0.58	-10.62	-5.06	0.70	0.05
GIMAP1	226	48	48	45	0.72	4.58	0.0006	6.41	-0.75	-4.69	-3.41	0.05	0.05
GIMAP2	238	53	53	54	0.81	5.78	0.0007	7.08	-0.49	-4.53	-3.11	0.36	0.05
GIMAP4	197	52	52	41	0.81	5.15	0.0008	6.94	-0.69	-5.34	-3.74	0.29	0.05
HCG27	212	122	121	115	0.95	24.85	0.0041	16.29	1.48	-1.01	0.40	1.80	0.10
HCG9	158	115	113	72	0.87	21.00	0.0065	15.35	1.03	0.18	0.73	1.03	0.09
HERPUD2	212	122	121	115	0.95	24.85	0.0041	16.29	1.48	-1.01	0.40	1.80	0.10
HIVEP3	14415	3943	3934	1003	1.00	356.88	0.0007	526.40	-0.95	-9.31	-4.62	-0.14	0.04
HLA_B	297	246	226	710	0.99	54.42	0.0165	32.84	1.89	1.99	2.24	1.60	0.12
HLA_DQ	836	793	778	595	0.98	259.20	0.0372	105.87	4.24	4.03	4.76	3.61	0.17
HLA_F	128	51	50	32	0.84	8.12	0.0021	6.81	0.51	-2.37	-1.27	0.97	0.08
HLA_G	185	95	94	38	0.83	24.09	0.0058	12.68	2.50	0.35	1.77	2.59	0.13
HLAC	319	268	254	602	0.99	62.61	0.0185	35.78	2.17	2.30	2.59	1.86	0.12
HLADQB1	905	860	860	624	0.98	257.90	0.0358	114.81	3.65	4.36	4.46	2.97	0.15
HMP19	1774	478	477	293	0.97	23.06	0.0004	63.81	-1.86	-9.07	-5.47	-1.43	0.02
HNF4G	808	252	250	163	0.95	30.33	0.0011	33.64	-0.28	-5.41	-2.88	0.41	0.06
IFNG	118	25	25	22	0.74	1.96	0.0004	3.34	-1.00	-5.84	-4.57	0.32	0.04
IL10	142	53	53	51	0.84	5.15	0.0011	7.08	-0.72	-4.88	-3.47	0.10	0.05
IL12A	178	46	46	40	0.81	5.50	0.0008	6.14	-0.28	-3.00	-2.07	0.30	0.06

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Appendix F(cont.)

IL17A	224	60	59	53	0.77	5.79	0.0007	8.01	-0.75	-5.71	-3.94	0.30	0.05
IL1A	269	67	66	45	0.81	11.49	0.0010	8.94	0.77	-5.45	-2.82	2.38	0.09
IL23R	3296	884	883	603	1.00	97.96	0.0008	118.02	-0.50	-9.41	-4.53	0.64	0.06
IL6	145	44	44	40	0.75	4.20	0.0009	5.87	-0.75	-4.76	-3.48	0.11	0.05
KCNK9	3439	964	959	888	1.00	85.38	0.0008	128.70	-0.99	-10.46	-5.31	0.03	0.04
KLRC4	473	114	114	74	0.88	15.18	0.0007	15.22	-0.01	-5.63	-3.12	1.06	0.07
KLRK1	429	127	127	90	0.87	13.87	0.0008	16.95	-0.51	-6.82	-4.04	0.57	0.05
LILRA1	461	144	143	107	0.89	9.28	0.0011	19.22	-1.47	-5.57	-3.91	-1.04	0.03
LILRB1	901	283	282	256	0.95	33.40	0.0016	37.78	-0.33	-3.85	-2.09	0.13	0.06
LOC100129342	207	67	67	52	0.83	4.73	0.0007	8.94	-1.28	-7.26	-5.14	-0.29	0.03
LOC100132252	1039	444	442	413	0.99	41.13	0.0014	59.28	-0.89	-5.44	-3.13	-0.42	0.05
LOC107984355	617	173	172	252	0.97	10.83	0.0006	23.10	-1.52	-9.40	-5.90	-0.71	0.03
LOC285830	655	365	364	151	0.94	70.75	0.0032	48.73	1.31	-0.81	0.51	1.53	0.10
LTN1	1567	368	368	281	0.98	32.87	0.0005	49.13	-0.96	-9.34	-5.08	0.05	0.04
LYST	5588	1265	1261	789	1.00	100.14	0.0004	168.88	-1.20	-14.32	-7.08	0.34	0.04
MEFV	584	150	149	190	0.94	20.70	0.0014	20.03	0.10	-7.88	-4.10	1.78	0.07
MICA	686	343	340	165	0.96	62.33	0.0040	45.79	1.05	0.00	0.71	1.10	0.09
MN1	1555	388	386	819	1.00	30.54	0.0006	51.80	-1.19	-8.75	-4.93	-0.39	0.04
MOG	427	214	212	106	0.92	14.15	0.0009	28.57	-1.45	-3.59	-2.77	-1.27	0.03
MSX2	199	60	60	50	0.75	3.77	0.0006	8.01	-1.43	-5.83	-4.41	-0.79	0.03
MUC21	209	113	111	198	0.94	9.84	0.0016	15.09	-0.98	-0.09	-0.66	-1.02	0.04
NAV2	24008	6660	6649	1006	1.00	642.34	0.0008	889.13	-0.82	-9.11	-4.42	0.02	0.05
NOD2	1185	303	303	257	0.96	24.00	0.0006	40.45	-1.18	-9.67	-5.47	-0.20	0.04
OSR1	178	47	47	51	0.71	1.39	0.0002	6.27	-2.05	-4.05	-3.75	-1.89	0.01
OVCH1	1882	522	521	455	0.99	60.17	0.0009	69.69	-0.40	-8.77	-4.31	0.74	0.06
PAX8	1700	472	471	415	0.98	62.38	0.0010	63.01	-0.03	-7.72	-3.60	1.11	0.07
PLEKHB1	459	141	141	95	0.88	13.85	0.0008	18.82	-0.75	-4.90	-3.11	-0.17	0.05

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Appendix F(cont.)

PMFBP1	1461	383	381	306	0.98	38.15	0.0007	51.13	-0.74	-8.90	-4.70	0.33	0.05
POU5F1	190	88	88	47	0.92	16.43	0.0026	11.75	1.10	-1.32	-0.08	1.46	0.09
PPP1R11	73	41	40	35	0.72	2.16	0.0007	5.47	-1.57	-3.72	-3.31	-1.26	0.03
PSMD14	2268	550	549	423	0.99	33.03	0.0003	73.43	-1.61	-12.09	-6.63	-0.68	0.03
PSORS1C1	920	491	487	258	0.98	100.68	0.0040	65.55	1.56	-2.10	0.10	2.04	0.10
PTPN22	1249	323	323	257	0.97	31.68	0.0005	43.12	-0.77	-9.48	-5.08	0.42	0.05
RALGAPA2	8018	1879	1879	898	1.00	64.85	0.0002	250.85	-2.18	-13.97	-7.54	-1.67	0.02
RIMBP2	11477	3617	3603	1006	1.00	403.01	0.0013	482.88	-0.49	-8.65	-4.02	0.45	0.06
RNF39	173	77	77	48	0.89	7.65	0.0014	10.28	-0.70	-2.12	-1.68	-0.46	0.05
SACM1L	1481	459	459	275	0.97	73.72	0.0013	61.28	0.59	-8.06	-3.34	2.11	0.08
SAMD3	6653	2122	2116	878	1.00	290.04	0.0013	283.29	0.07	-5.75	-2.42	0.79	0.07
SEMA6D	15970	4321	4316	997	1.00	478.33	0.0008	576.87	-0.50	-9.10	-4.21	0.49	0.06
SGPP2	3802	1020	1015	882	1.00	94.38	0.0007	136.17	-0.90	-8.79	-4.51	-0.09	0.05
SLC41A2	3845	1127	1126	550	0.99	89.81	0.0006	150.46	-1.18	-10.05	-5.23	-0.34	0.04
SLC43A3	603	164	164	170	0.95	8.76	0.0004	21.89	-1.71	-10.50	-6.61	-0.80	0.03
SLC44A4	406	138	138	136	0.94	17.17	0.0011	18.42	-0.19	-4.87	-2.74	0.57	0.06
SLIT2	10545	2767	2761	991	1.00	246.09	0.0007	369.40	-0.98	-9.51	-4.76	-0.17	0.04
SMARCA2	6721	1835	1824	966	1.00	141.14	0.0008	244.98	-1.25	-9.18	-4.83	-0.57	0.04
SMG6	6965	1925	1923	859	1.00	206.73	0.0008	256.99	-0.58	-11.25	-5.24	0.80	0.05
SORBS2	11721	3862	3857	1003	1.00	483.58	0.0013	515.59	-0.18	-8.12	-3.58	0.81	0.06
STAT4	3720	946	943	833	1.00	87.81	0.0006	126.29	-0.89	-8.99	-4.60	-0.03	0.05
STK39	8547	2574	2572	915	1.00	286.69	0.0010	343.64	-0.49	-9.89	-4.57	0.67	0.06
STX8	10346	3118	3112	1004	1.00	288.84	0.0009	416.26	-0.90	-10.07	-4.93	0.04	0.05
SUMO4	36	11	11	11	0.51	1.02	0.0013	1.47	-0.62	-5.61	-4.49	1. 74	0.05
SUSD1	3622	960	959	891	1.00	102.66	0.0008	128.16	-0.58	-9.97	-4.81	0.61	0.05
TCF19	190	80	79	42	0.92	14.48	0.0019	10.68	0.98	-0.98	0.02	1.25	0.09
TENM4	23487	6583	6569	1004	1.00	607.65	0.0008	878.85	-0.91	-10.63	-5.12	0.10	0.05

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Appendix F(cont.)

TFCP2L1	2031	536	535	575	0.99	42.00	0.0006	71.56	-1.21	-8.82	-4.87	-0.46	0.04
TLR4	338	75	75	73	0.87	5.31	0.0004	10.01	-1.29	-4.76	-3.60	-0.81	0.04
TMEM132B	9972	2823	2820	995	1.00	282.41	0.0008	376.88	-0.74	-7.41	-3.68	-0.07	0.05
TNF	61	19	19	21	0.36	0.64	0.0002	2.54	-1.72	-6.05	-5.18	-0.84	0.02
TNFAIP3	381	96	96	89	0.78	6.07	0.0004	12.82	-1.46	-6.69	-4.71	-0.83	0.03
TRIM31	338	163	163	194	0.96	19.32	0.0019	21.76	-0.32	-3.76	-2.18	0.18	0.06
TTLL7	3060	835	835	537	0.99	76.29	0.0006	111.48	-0.92	-8.28	-4.33	-0.17	0.05
UBAC2	5101	1355	1353	722	1.00	111.15	0.0006	180.90	-1.13	-9.02	-4.72	-0.42	0.04
UBASH3B	4485	1274	1272	934	1.00	151.43	0.0010	170.08	-0.32	-8.16	-3.79	0.66	0.06
UBD	120	50	49	29	0.77	4.12	0.0010	6.68	-1.01	-3.95	-3.06	-0.43	0.04
ZNRD1	85	33	33	29	0.82	3.28	0.0009	4.41	-0.65	0.19	-0.22	-0.71	0.05

APPENDIX G. GENES WITH HIGHEST QUARTILE POPULATION GENETIC PARAMETER VALUES IN EAST ASIAN, AFRICAN, AND EUROPEAN 1K GENOMES POPULATIONS. ONLY THE HIGHEST QUARTILE VALUES ARE PRESENTED FOR CLARITY.

	East Asians							**Africans**							**Europeans**						
Gene	**HD**	**θ_k**	**Pi**	**θ_W**	**TD**	**FLD**	**FLF**	**HD**	**θ_k**	**Pi**	**θ_W**	**TD**	**FLD**	**FLF**	**HD**	**θ_k**	**Pi**	**θ_W**	**TD**	**FLD**	**FLF**
ABCB5	1.00							1.00							1.00						
ASB18								1.00													
ATP8A1	1.00							1.00			454.68				1.00						
BTNL2			0.0077		1.63	1.91	2.01			0.0035							0.0032			2.77	0.61
C10ORF11 (LRMDA)	1.00	651.76		1081.36				1.00	872.90		1908.62				1.00	618.55		1048.67			
C6ORF10 (TSBP1)			0.0027		1.44	-0.19	0.93					0.72		-0.64					1.1	-0.44	0.58
C6ORF15			0.0038		1.23		-0.84			0.0028							0.0036				
C6ORF85	1.00	233.92						1.00	277.29						1.00						
CCHCR1						-1.46	-0.44			0.0028		0.45	-2.42	-0.84			0.0029				
COL12A1	1.00							1.00							1.00						
CPLX1								1.00							1.00						
CPVL	1.00							1.00							1.00						
CTNNA2	1.00	955.57		1298.64				1.00	1314.89		2259.35				1.00	861.27		1254.40			
DHFRP2			0.0064		1.44	0.53	1.23			0.0069		1.30	-0.84	0.40			0.0071		2.78	1.05	2.32

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Appendix G(cont.)

DNMT3A	1.00							1.00							1.00						
EBF2	1.00							1.00							1.00						
GALNT1	1.00							1.00							1.00						
GALT10	1.00							1.00	292.02						1.00	247.65					
GAS2	1.00							1.00							1.00						
HCG27			0.0043		1.71	-1.45	0.32			0.0038		0.67	-0.48	0.18			0.0041		1.48	-1.01	0.40
HCG9			0.0062		0.81	0.70	0.87			0.0077		1.48	0.55	1.26			0.0065		1.03	0.18	0.73
HERPUD2			0.0043		1.71	-1.45	0.32			0.0038		0.67	-0.48	0.18			0.0041		1.48	-1.01	0.40
HIVEP3	1.00	299.71		491.7				1.00	519.53						1.00	356.88		526.40			
HLA_B			0.0166		1.51	-0.94	0.52	1.00		0.0153		1.13	2.56	1.93			0.0165		1.89	1.990	2.24
HLA_DQ		241.87	0.0347		3.72	4.08	4.43			0.0340		3.77	3.96	4.37		259.20	0.0372		4.24	4.030	4.76
HLA_F												0.25									
HLA_G			0.00550		1.98		0.34			0.0062		1.64	-1.91	0.04			0.0058		2.5	0.350	1.77
HLAC			0.01630		2.21	-0.35	1.26	1.00		0.0188		2.10	1.95	2.36			0.0185		2.17	2.300	2.59
HLADQB1		278.42	0.03860		4.17	4.36	4.82			0.0340		3.46	-0.10	2.39		257.90	0.0358		3.65	4.360	4.46
IL23R	1.00							1.00							1.00						
KCNK9	1.00							1.00							1.00						

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Appendix G(cont.)

LOC285830			0.00320		1.57	-1.06	0.55			0.0035		1.04		-0.72			0.0032		1.31	-0.810	0.51
LYST	1.00							1.00							1.00						
MICA			0.00420							0.0044			0.26	0.09			0.0040		1.05	0.000	0.71
MN1	1.00							1.00							1.00						
MUC21													-0.68							-0.090	
NAV2	1.00	664.45		875.55				1.00	988.67		1605.28				1.00	642.34		889.13			
POU5F1					0.70								-2.35						1.1		
PPP1R11						-1.38															
PSORS1C1			0.00400		0.98	-0.76	0.33			0.0038		0.76					0.0040		1.56		0.10
RALGAPA2	1.00			260.66				1.00			468.72				1.00			250.85			
RIMBP2	1.00	412.77		453.12				1.00	506.77		782.10				1.00	403.01		482.88			
SAMD3	1.00	308.60		272.81				1.00	319.27		474.51				1.00	290.04		283.29			
SEMA6D	1.00	471.63		623.29				1.00	556.11		1054.65				1.00	478.33		576.87			
SGPP2	1.00							1.00							1.00						
SLC41A2	1.00							1.00													
SLIT2	1.00			379.72				1.00	278.11		655.35				1.00			369.40			
SMARCA2	1.00							1.00							1.00						

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Appendix G(cont.)

SMG6	1.00			263.60				1.00							1.00			256.99			
SORBS2	1.00	434.77		469.54				1.00	561.34		790.08				1.00	483.58		515.59			
STAT4	1.00							1.00							1.00						
STK39	1.00	321.08		312.45				1.00	405.22		585.41				1.00	286.69		343.64			
STX8	1.00	217.81		376.38				1.00	437.06		695.41				1.00	288.84		416.26			
SUMO4													-0.05	-0.71							
SUSD1	1.00							1.00							1.00						
TCF19																			0.98	-0.98	0.02
TENM4		558.50		828.70				1.00	838.79		1504.17				1.00	607.65		878.85			
TFCP2L1								1.00													
TMEM132B	1.00	256.79		369.17				1.00	370.74		675.06				1.00	282.41		376.88			
TTLL7								1.00													
UBAC2	1.00							1.00							1.00						
UBASH3B	1.00							1.00							1.00						
UBD												0.33									
ZNRD1						-0.67							-0.86	-0.46							

(cont. on the next page)

Appendix G(cont.)

																				0.19	

HD: Haplotype diversity; θ_k:Theta-K; θ_W:Theta-Watterson; TD:Tajima's D; FLD: Fu-Li's D; FLF: Fu-Li's F

APPENDIX H. GENES WITH LOWEST QUARTILE POPULATION GENETIC PARAMETER VALUES IN EAST ASIAN, AFRICAN, AND EUROPEAN 1K GENOMES POPULATIONS. ONLY THE LOWEST QUARTILE VALUES ARE PRESENTED FOR CLARITY.

	East Asians							**Africans**							**Europeans**						
Gene	**HD**	**θ_k**	**Pi**	**θ_W**	**TD**	**FLD**	**FLF**	**HD**	**θ_k**	**Pi**	**θ_W**	**TD**	**FLD**	**FLF**	**HD**	**θ_k**	**Pi**	**θ_W**	**TD**	**FLD**	**FLF**
API5			0.0002		-2.11		-6.77			0.0003		-2.1		-5.45			0.0003		-1.67	-10.45	-6.44
C10ORF11 (LRMDA)						-12.52							-9.29							-11.28	-5.61
C6ORF15				3.2				0.74	3.58		4.89				0.73	4.58		3.6			
C6ORF47		0.97		1.74				0.75	1.11	0.0005	3.09				0.68	0.87		2			
CCR1	0.28	0.99	0.0002	5.21	-2.09			0.76	2.61	0.0004	9.53	-1.96			0.47	2.1	0.0003	6.41	-1.77		-6.12
CDH26					-1.9		-6.39						-8.99	-4.97			0.0003		-2.17	-10.92	-6.57
CEP135												-1.9								-10.11	-5.46
COL12A1						-12.75	-6.63						-9.44	-5.11			0.0002		-2.14	-11.4	-6.57
CTLA4	0.67	1.47	0.00024	6.41	-2.03			0.82	2.44	0.0004	7.73	-1.82		-5.04	0.66	1.37	0.00023	3.47	-1.48		
CTNNA2																				-10.11	

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Appendix H(cont.)

DHFRP2								0.83													
DNMT3A						-13.07	-6.88					-1.75	-9.6	-5.25						-10.87	-5.7
DTL												-1.81									
FUT2		4.26			-1.93																
GABBR1										0.0006									-1.59		
GAS2																				-10.62	
GIMAP1															0.72	4.58		6.41			
GIMAP4								0.89			11.08										
HLA_F				6.94							9.53							6.81			
HMP19			0.0002		-2.43		-6.44										0.0004		-1.86		-5.47
IFNG	0.62	1.45	0.0003	3.74			-6.16	0.85		0.0005	7.6	-1.86			0.74	1.96	0.0004	3.34			
IL10		2.87		5.07				0.85	4.59		7.47										
IL12A	0.59	3.75		5.74					5.98		10.56							6.14			
IL17A									6.17						0.77						
IL1A	0.57																				

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Appendix H(cont.)

IL23R						-11.43															
IL6	0.5	1.53	0.0003	6.94	-2.07				4.51		8.5				0.75	4.2		5.87			
KCNK9						-12.62	-6.26													-10.46	-5.31
LILRA1																			-1.47		
LOC100129342	0.65								3.99	0.0006		-1.87				4.73					
LOC107984355													-8.77	-5.2					-1.52		-5.9
LTN1						-11.92	-6.38			0.0006			-9.26	-5.17							
LYST			0.0002		-2.27	-13.74	-7.58						-8.61				0.0004			-14.32	-7.08
MOG					-1.8																
MSX2	0.65	1.94	0.0003	6.81	-1.9										0.75	3.77					
NOD2			0.0003		-2.07	-11.73	-7.04					-1.76		-5.03							-5.47
OSR1	0.44	0.48	0.0001	4.4	-2.25		-7.66	0.79	2.87	0.0004		-2.04		-5.43	0.71	1.39	0.0002	6.27	-2.05		
PMFBP1													-10.36	-5.64							

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Appendix H(cont.)

PPP1R11		2.16		4.4				0.85	3.02		4.51				0.72	2.16		5.47	-1.57		
PTPN22										0.00039		-1.94									
PSMD14			0.0003			-13.68	-7.28			0.0003		-2.22	-9.73	-5.69			0.0003		-1.61	-12.09	-6.63
RALGAPA2						-13.06	-6.78			0.0004		-2.06	-9.72	-5.41			0.0002		-2.18	-13.97	-7.54
SEMA6D													-9.12								
SLC43A3			0.0003		-2.02		-6.64										0.0004		-1.71	-10.5	-6.61
SLIT2													-9.28								
SMARCA2						-11.9															
SMG6						-12.11							-10.61	-5.23						-11.25	
STAT4						-11.46							-8.69								
STX8						-11.57															
SUMO4	0.4	0.79		1.07				0.54	0.69		1.93				0.51	1.02		1.47			
TCF19								0.9													
TENM4	0.3					-11.78														-10.63	

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Appendix H(cont.)

TFCP2L1	0.33																				
TLR4		3.69	0.0003		-1.8		-6.65										0.0004				
TNF	0.33	0.47	0.0002	1.74				0.42	0.75	0.0003	3.48	-1.89		-5.27	0.36	0.64	0.0002	2.54	-1.72		
TNFAIP3	0.69	3.72	0.0002		-2.13										0.78		0.0004				
TTLL7										0.0006											
UBAC2										0.0006		-1.85	-9.22	-5.1							
UBD				6.41				0.81			8.63				0.77	4.12		6.68			
ZNRD1								0.8	5.38		5.02					3.28		4.41			

HD: Haplotype diversity; θ_k:Theta-K; θ_W:Theta-Watterson; TD:Tajima's D; FLD: Fu-Li’s D; FLF: Fu-Li’s F

APPENDIX I. GENETIC DIFFERENTIATION PARAMETER ESTIMATES OF EAST ASIANS (EAS) WITH RESPECT TO AFRICANS (AFR), AND ITS EFFECT ON NUCLEOTIDE DIVERSITY IN EAST ASIANS

Gene	**AFR_EAS_Dxy**	**AFR_EAS_Hst**	**AFR_EAS_Fst**	**EAS_Pi/AFR_EAS_Fst**	**EAS_Pi/AFR_EAS_Dxy**
ABC5	0.0012805	5.7482E-05	0.13561221	0.005899174	0.624756645
API5	0.00038164	0.02132157	0.25981622	0.000769775	0.52405105
ASB18	0.00156873	0.00630468	0.23580367	0.003816734	0.57371188
ATP8A1	0.00097434	0.00018203	0.14205202	0.004927772	0.718438701
BAG6	0.00086794	0.01234207	0.10969875	0.007292699	0.921726246
BTNL2	0.00592129	0.01035004	0.05537937	0.139040939	1.300392174
C10ORF11	0.00079738	0	0.15079451	0.003978925	0.752466944
C6ORF10	0.00283765	0.00432596	0.06756536	0.039961305	0.951489924
C6ORF15	0.00386485	0.03733819	0.14358921	0.026464383	0.983220968
C6ORF47	0.00048594	0.04189384	0.12416654	0.00322148	0.823152535
C6ORF85	0.0015689	1.7216E-05	0.13048273	0.009196619	0.764866461
CCDC180	0.00102377	0.00623006	0.08668254	0.010382714	0.879107419
CCHCR1	0.0027174	0.01776057	0.04246738	0.056513964	0.88319623
CCR1	0.00033504	0.06951883	0.16353413	0.001222986	0.596951819
CCR3	0.00099889	0.04256231	0.08311031	0.009625761	0.800890712
CDH26	0.00072376	0.00565823	0.22993393	0.001304723	0.414504764
CEP135	0.00053182	0.00671425	0.08494813	0.004708756	0.75212784
COL12A1	0.00062252	0.00027683	0.07571757	0.006603487	0.803191889
CPLX1	0.00155238	0.00269676	0.14803493	0.008106195	0.773005484
CPVL	0.00113394	5.8396E-05	0.17756689	0.004505344	0.705503304
CTNNA2	0.00115792	0	0.13686432	0.005845205	0.690893376
DEPDC1	0.00079559	0.04686008	0.14581231	0.003429066	0.628467084
DHFRP2	0.00693959	0.05326073	0.04487538	0.142617171	0.922245075
DNMT3A	0.00052854	0.00061307	0.06197857	0.006453844	0.756797469

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Appendix I(cont.)

DTL	0.00059926	0.00990656	0.09099666	0.004395766	0.667486599
EBF2	0.00104801	0.00012816	0.21797327	0.003211403	0.667932773
ERAP1	0.00121127	0.00582362	0.03866646	0.028448425	0.908136337
FUT2	0.00190189	0.04106919	0.35903835	0.001114087	0.210317018
GABBR1	0.00075628	0.01310144	0.02821912	0.028349576	1.057803914
GALNT1	0.00114819	0.00054958	0.15271414	0.005893364	0.783845176
GALT10	0.00137402	9.6625E-05	0.28090408	0.002491954	0.509455183
GAS2	0.00136807	0.00036999	0.19504514	0.004614316	0.657859544
GIMAP1	0.00087205	0.07078605	0.1044166	0.006703915	0.802709041
GIMAP2	0.00087793	0.03306419	0.12058733	0.005804922	0.797329212
GIMAP4	0.00112319	0.01932429	0.07458924	0.012066083	0.801291022
HCG27	0.00430921	0.01785309	0.06183716	0.069537481	0.997862876
HCG9	0.0075162	0.03944051	0.07293072	0.085012184	0.824884685
HERPUD2	0.00430921	0.01785309	0.06183716	0.069537481	0.997862876
HIVEP3	0.00095579	5.2317E-06	0.19064344	0.003147237	0.627756078
HLA_B	0.01658694	0.00149874	0.03703837	0.448183816	1.000787179
HLA_DQ	0.0350457	0.00541328	0.02026803	1.712056034	0.990135681
HLA_F	0.00253558	0.03020028	0.04248372	0.051784543	0.867651627
HLA_G	0.00601565	0.04240733	0.0319909	0.171923902	0.914281449
HLAC	0.01841791	0.00267751	0.0474322	0.343648389	0.885008135
HLADQB1	0.03806229	0.00315063	0.04591025	0.840770787	1.014127159
HMP19	0.00066317	0.00705015	0.29147223	0.000686172	0.30158349
HNF4G	0.00135791	0.03520107	0.32921853	0.002733746	0.662784924
IFNG	0.00041096	0.03768679	0.06903799	0.004345433	0.730001401
IL10	0.00093886	0.06975995	0.16665197	0.003600317	0.639074899
IL12A	0.00085772	0.08349891	0.18491592	0.002703932	0.582943132
IL17AAFR	0.00086359	0.02754838	0.10323376	0.007749403	0.92636176
IL1A	0.00122824	0.11040593	0.33105719	0.002114438	0.569922383
IL23R	0.00094427	0.00106876	0.15359628	0.003906345	0.635414347

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Appendix I(cont.)

IL6	0.00093007	0.12486276	0.31535736	0.000951302	0.32255781
KCNK9	0.00116044	0.00019911	0.12503356	0.006398282	0.68939099
KLRC4	0.00109544	0.02193595	0.07486845	0.010685409	0.730302964
KLRK1	0.00139076	0.05874657	0.14554428	0.006183685	0.647130337
LILRA1	0.00194443	0.01924533	0.1929125	0.005183697	0.514290003
LILRB1	0.00184951	0.01527878	0.10957954	0.01095095	0.648819171
LOC100129342	0.00071645	0.06571282	0.14274365	0.004903896	0.977036941
LOC100132252	0.00171863	0.0038551	0.10534126	0.012340844	0.75641656
LOC107984355	0.00103659	0.00698551	0.18986785	0.003686775	0.675291826
LOC285830	0.00347845	0.02443881	0.04205956	0.076082587	0.91994973
LTN1	0.00062583	0.00685825	0.07963906	0.006278326	0.798941191
LYST	0.00083235	0.00057678	0.4019478	0.000497577	0.240282246
MEFV	0.00161378	0.01214822	0.10975776	0.011844265	0.805560302
MICA	0.00460319	0.01547815	0.07197141	0.058356508	0.912409979
MN1	0.00076324	0.00030085	0.0669336	0.010458126	0.917139604
MOGAFR	0.00118343	0.02867243	0.11134111	0.005388845	0.507002463
MSX2	0.00131581	0.08216862	0.39264893	0.000764041	0.227997021
MUC21	0.00154524	0.03987265	0.04844684	0.028897653	0.906006414
NAV2	0.00127905	0	0.16165851	0.005567291	0.703646463
NOD2	0.0005754	0.03120405	0.14295169	0.002098611	0.52137946
OSR1	0.0003497	0.17034855	0.31979811	0.000312697	0.285959471
OVCH1	0.00107319	0.00300444	0.12001921	0.005832399	0.65226093
PAX8	0.00107414	0.00706631	0.13199385	0.006060888	0.744784568
PLEKHB1	0.00143004	0.02504576	0.20566454	0.00388983	0.559425944
PMFBP1	0.00076224	0.00900844	0.17306362	0.003466933	0.787149131
POU5F1	0.0026603	0.02410504	0.05677237	0.047558346	1.014923474
PPP1R11	0.00091637	0.06804128	0.06856516	0.010209267	0.763886964
PSMD14	0.00033656	0.00428091	0.06169975	0.004862257	0.891384462
PSOR1C1	0.00403958	0.01319398	0.03884967	0.102960973	0.990202199

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Appendix I(cont.)

RALGAPA2	0.00041099	7.5897E-05	0.05459431	0.007326771	0.973250129
RIMBP2	0.00160778	0	0.10625923	0.012234231	0.808566731
RNF39	0.00217146	0.04268575	0.04424423	0.04294345	0.874986307
SACM1L	0.00138771	0.01265404	0.09031849	0.012179124	0.792672555
SAMD3	0.00178214	8.1994E-05	0.20306306	0.00689441	0.785573739
SEMA6D	0.00103527	3.8249E-06	0.1586915	0.005041228	0.772742683
SGPP2	0.00090821	0.00012231	0.1523515	0.003938261	0.660640923
SLC41A2	0.00083339	0.0013528	0.05825233	0.013733355	0.959933742
SLC43A3	0.00060286	0.02201781	0.11820887	0.002537881	0.497631377
SLC44A4	0.00114936	0.02203171	0.04140163	0.026569001	0.95705508
SLT2	0.00074611	9.5314E-06	0.11904523	0.005040101	0.804170423
SMARC2	0.0013588	9.8568E-06	0.13191343	0.007580729	0.735946152
SMG6	0.00101546	0.00013985	0.19441147	0.003600611	0.689345669
SORBS2	0.00154635	2.8136E-07	0.13213861	0.009081373	0.776020577
STAT4	0.0008424	0.00029377	0.12284807	0.005698095	0.830963347
STK39	0.00138592	7.2581E-05	0.10738987	0.010243051	0.793699383
STX8	0.00122767	8.4409E-07	0.1805072	0.003877962	0.570187426
SUMO4	0.00101322	0.05277707	0.07741019	0.012918196	0.986953026
SUSD1	0.00095676	6.6496E-05	0.12994052	0.006156663	0.836158943
TCF19	0.00163821	0.02722069	0.04890716	0.032715045	0.976673455
TENM4	0.00107669	5.6273E-07	0.17615867	0.00397369	0.650140548
TFCP2L1	0.00092116	0.0013199	0.08050129	0.008695513	0.759914024
TLR4	0.00058999	0.04346907	0.1557513	0.001926148	0.508484303
TMEM132B	0.0010682	6.3923E-06	0.12510237	0.006394763	0.748921159
TNF	0.00023183	0.01357753	0.03728786	0.005363676	0.862691442
TNFAIP3	0.0007473	0.08480455	0.33596092	0.000595307	0.267630519
TRIM31	0.00194462	0.0153796	0.09192719	0.016317262	0.771359266
TTLL7	0.0005391	0.00231745	0.03903041	0.01024842	0.74197783
UBAC2	0.00066078	0.00053521	0.09926092	0.006044675	0.908019365

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Appendix I(cont.)

UBASH3B	0.00116633	5.4219E-05	0.12463549	0.007221057	0.771652069
UBD	0.00224815	0.04191855	0.16089466	0.00932287	0.667214369
ZNRD1	0.00142082	0.03006726	0.04379919	0.02739777	0.844585397

APPENDIX J. GENETIC DIFFERENTIATION PARAMETER ESTIMATES OF EUROPEANS (EUR) WITH RESPECT TO AFRICANS (AFR), AND ITS EFFECT ON NUCLEOTIDE DIVERSITY IN EUROPEANS

Gene	**AFR_EUR_Dxy**	**AFR_EUR_Hst**	**AFR_EUR_Fst**	**EUR_Pi/AFR_EUR_Fst**	**EUR_Pi/AFR_EUR_Dxy**
ABC5	0.001412	0.000075	0.100525	0.010943	0.779197
API5	0.000413	0.018703	0.173589	0.001728	0.726256
ASB18	0.001509	0.004776	0.180450	0.005542	0.662568
ATP8A1	0.001033	0.000261	0.098049	0.009179	0.871318
BAG6	0.000838	0.011501	0.091561	0.007645	0.835478
BTNL2	0.003402	0.012698	0.016995	0.188291	0.940694
C10ORF11	0.000795	0.000000	0.167094	0.002992	0.628718
C6ORF10	0.002846	0.005320	0.072190	0.037401	0.948798
C6ORF15	0.003266	0.019265	0.019080	0.188681	1.102235
C6ORF47	0.000420	0.014030	0.033528	0.011930	0.952274
C6ORF85	0.001530	0.000045	0.150117	0.007328	0.718882
CCDC180	0.000971	0.004941	0.128244	0.005458	0.721022
CCHCR1	0.002864	0.010337	0.014996	0.193391	1.012509
CCR1	0.000422	0.039052	0.133073	0.002254	0.710094
CCR3	0.001098	0.027901	0.087291	0.011456	0.910614
CDH26	0.000714	0.005159	0.262583	0.001142	0.419941
CEP135	0.000558	0.005157	0.058716	0.008516	0.895281
COL12A1	0.000522	0.000404	0.127789	0.001565	0.383082
CPLX1	0.001543	0.001988	0.094168	0.013805	0.842408
CPVL	0.001156	0.000082	0.140615	0.006400	0.778582
CTNNA2	0.001125	0.000000	0.148768	0.005378	0.710891
DEPDC1	0.000804	0.020362	0.049995	0.014001	0.870791
DHFRP2	0.007067	0.024985	0.014712	0.482601	1.004626

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Appendix J(cont.)

DNMT3A	0.000573	0.000700	0.055874	0.008949	0.872941
DTL	0.000675	0.007949	0.110614	0.005424	0.889237
EBF2	0.001054	0.000187	0.141344	0.005660	0.759193
ERAP1	0.001441	0.003379	0.061116	0.024543	1.040678
FUT2	0.001895	0.045052	0.062705	0.023922	0.791561
GABBR1	0.000621	0.019467	0.008297	0.072315	0.965589
GALNT1	0.001085	0.000637	0.064009	0.015623	0.921322
GALT10	0.001328	0.000132	0.117350	0.009374	0.828447
GAS2	0.001315	0.000423	0.167481	0.005374	0.684662
GIMAP1	0.000846	0.072735	0.132964	0.004513	0.708830
GIMAP2	0.000864	0.046750	0.117293	0.005968	0.810147
GIMAP4	0.001077	0.037086	0.107608	0.007434	0.742523
HCG27	0.003998	0.015163	0.011426	0.358845	1.025491
HCG9	0.007599	0.021169	0.065147	0.099775	0.855368
HERPUD2	0.003998	0.015163	0.011426	0.358845	1.025491
HIVEP3	0.000981	0.000004	0.156547	0.004472	0.713444
HLA_B	0.016342	0.001889	0.026934	0.612616	1.009647
HLA_DQ	0.036176	0.003354	0.016535	2.249749	1.028309
HLA_F	0.002472	0.022757	0.035964	0.058391	0.849587
HLA_G	0.006193	0.023564	0.030697	0.188946	0.936536
HLAC	0.018984	0.003129	0.016678	1.109275	0.974479
HLADQB1	0.035234	0.001781	0.009714	3.685572	1.016071
HMP19	0.000685	0.009133	0.164031	0.002439	0.583915
HNF4G	0.001197	0.013143	0.158690	0.006932	0.919325
IFNG	0.000481	0.039100	0.097258	0.004113	0.831024
IL10	0.001114	0.042168	0.082892	0.013270	0.987203
IL12A	0.000877	0.034856	0.059971	0.013340	0.912036
IL17AAFR	0.000888	0.055895	0.135822	0.005154	0.788166

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Appendix J(cont.)

IL1A	0.001027	0.033194	0.055795	0.017923	0.973796
IL23R	0.000949	0.001274	0.057794	0.013842	0.842685
IL6	0.001082	0.065066	0.150816	0.005968	0.832133
KCNK9	0.001193	0.000152	0.138913	0.005759	0.670307
KLRC4	0.001072	0.033609	0.100728	0.006949	0.652741
KLRK1	0.001354	0.035483	0.162666	0.004918	0.590927
LILRA1	0.001995	0.014263	0.202056	0.005444	0.551510
LILRB1	0.002119	0.010055	0.116921	0.013684	0.755035
LOC100129342	0.000750	0.032040	0.196365	0.003565	0.933627
LOC100132252	0.001719	0.003235	0.081030	0.017278	0.814366
LOC107984355	0.000951	0.007402	0.133498	0.004494	0.630985
LOC285830	0.003417	0.015764	0.028848	0.110926	0.936442
LTN1	0.000626	0.005884	0.089969	0.005557	0.798859
LYST	0.000771	0.000471	0.173626	0.002304	0.518919
MEFV	0.001599	0.013875	0.062230	0.022497	0.875486
MICA	0.004379	0.009338	0.042159	0.094878	0.913433
MN1	0.000760	0.000376	0.125368	0.004786	0.788980
MOGAFR	0.001292	0.014070	0.059619	0.015096	0.696829
MSX2	0.001253	0.052144	0.245412	0.002445	0.478697
MUC21	0.001619	0.016486	0.017253	0.092738	0.988121
NAV2	0.001275	0.000000	0.170525	0.004691	0.627240
NOD2	0.000711	0.010178	0.096053	0.006247	0.843349
OSR1	0.000332	0.014196	0.088487	0.002260	0.603124
OVCH1	0.001096	0.003706	0.087037	0.010340	0.821281
PAX8	0.001087	0.005800	0.053431	0.018716	0.920293
PLEKHB1	0.001440	0.018330	0.203640	0.003928	0.555560
PMFBP1	0.000806	0.008134	0.120451	0.005811	0.868857
POU5F1	0.002522	0.014189	0.029626	0.087760	1.030750

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Appendix J(cont.)

PPP1R11	0.000945	0.039497	0.096530	0.007252	0.741020
PSMD14	0.000329	0.004181	0.071006	0.004225	0.911808
PSOR1C1	0.004252	0.009081	0.088544	0.045175	0.940657
RALGAPA2	0.000339	0.000128	0.078150	0.002559	0.589625
RIMBP2	0.001602	0.000000	0.112800	0.011525	0.811259
RNF39	0.001999	0.022618	0.096979	0.014436	0.700293
SACM1L	0.001452	0.006519	0.074012	0.017565	0.895220
SAMD3	0.001651	0.000169	0.165229	0.007868	0.787356
SEMA6D	0.001068	0.000006	0.178827	0.004474	0.749363
SGPP2	0.000916	0.000202	0.103034	0.006794	0.764427
SLC41A2	0.000742	0.001880	0.075972	0.007898	0.808997
SLC43A3	0.000644	0.010035	0.080716	0.004956	0.621221
SLC44A4	0.001163	0.017147	0.040281	0.027308	0.945978
SLT2	0.000757	0.000016	0.058277	0.012012	0.924471
SMARC2	0.001385	0.000032	0.221828	0.003606	0.577531
SMG6	0.001006	0.000206	0.118683	0.006741	0.795141
SORBS2	0.001542	0.000002	0.086857	0.014967	0.843234
STAT4	0.000855	0.000342	0.164389	0.003650	0.701533
STK39	0.001351	0.000110	0.127867	0.007821	0.740031
STX8	0.001263	0.000002	0.116917	0.007698	0.712691
SUMO4	0.001489	0.125437	0.275543	0.004718	0.873064
SUSD1	0.000935	0.000174	0.110669	0.007229	0.855871
TCF19	0.001732	0.014951	0.027187	0.069886	1.096701
TENM4	0.001059	0.000002	0.133050	0.006013	0.755329
TFCP2L1	0.000901	0.001700	0.118498	0.005063	0.665846
TLR4	0.000639	0.030590	0.125253	0.003194	0.625970
TMEM132B	0.001117	0.000012	0.128899	0.006206	0.716416
TNF	0.000259	0.006762	0.013679	0.014621	0.771760

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Appendix J(cont.)

TNFAIP3	0.000742	0.046074	0.232158	0.001723	0.539226
TRIM31	0.002100	0.013805	0.055961	0.033952	0.904858
TTLL7	0.000688	0.002327	0.137268	0.004371	0.872325
UBAC2	0.000719	0.000636	0.170168	0.003526	0.834237
UBASH3B	0.001189	0.000110	0.114932	0.008701	0.841099
UBD	0.002341	0.049420	0.298478	0.003350	0.427116
ZNRD1	0.001321	0.011900	0.092085	0.009774	0.681345

APPENDIX K. GENES WITH HIGHEST QUARTILE GENETIC DIFFERENTIATION PARAMETER VALUES WITH RESPECT TO AFRICAN POPULATION FOR EAST ASIAN, AND EUROPEAN 1K GENOMES POPULATIONS.

Only the highest quartile values are presented for clarity.

	African-East Asian differentiation				**African-European differentiation**			
Gene	**Dxy**	**Fst**	**Pi/Fst**	**Pi/Dxy**	**Dxy**	**Fst**	**Pi/Fst**	**Pi/Dxy**
API5		0.259816218				0.173588795		
ASB18		0.235803671				0.180449526		
BTNL2	0.005921291		0.139040939	1.300392174	0.003401745		0.188291449	
C6ORF10 (TSBP1)	0.002837655							
C6ORF15	0.003864848			0.983220968	0.003266093		0.188681168	1.102234516
CCHCR1			0.056513964		0.002864173		0.193390552	1.012508718
CDH26		0.229933931				0.262582705		
DHFRP2	0.006939587		0.142617171		0.007067305		0.482600785	1.00462617
EBF2		0.217973266						
ERAP1								1.040678078
FUT2		0.359038352						
GABBR1				1.057803914				
GALT10		0.280904079						
HCG27	0.004309209		0.069537481	0.997862876	0.003998085		0.358845411	1.025490924
HCG9	0.007516202		0.085012184		0.007599069		0.09977476	
HERPUD2	0.004309209		0.069537481	0.997862876	0.003998085		0.358845411	1.025490924
HLA_B	0.016586943		0.448183816	1.000787179	0.016342352		0.612616157	1.0096466

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Appendix K(cont.)

HLA_DQ	0.035045702		1.712056034	0.990135681	0.036175883		2.24974912	1.02830939
HLA_F			0.051784543					
HLA_G	0.006015653		0.171923902		0.006193034		0.188946431	
HLAC	0.01841791		0.343648389		0.018984499		1.10927539	0.974479235
HLADQB1	0.038062288		0.840770787	1.014127159	0.035233771		3.68557176	1.016070626
HMP19		0.291472228						
HNF4G		0.329218533						
IL10								0.987202548
IL1A		0.33105719						0.973796208
IL6		0.315357355						
LILRA1						0.202055579		
LOC100129342				0.977036941		0.196364814		
LOC285830	0.003478451		0.076082587		0.003417189		0.110926227	
LYST		0.401947798				0.173625837		
MICA	0.004603194		0.058356508		0.004379082		0.094878298	
MSX2		0.392648927				0.245412479		
MUC21							0.092737696	0.988121381
NAV2						0.170525014		
OSR1		0.319798114						
PLEKHB1						0.203640191		
POU5F1				1.014923474				1.030750321
PSOR1C1	0.004039579		0.102960973	0.990202199	0.004252348			
PTPN22		0.343023						1.003747
RALGAPA2				0.973250129				
SEMA6D						0.1788275		

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Appendix K(cont.)

SLC41A2				0.959933742				
SMARC2						0.221827969		
SUMO4				0.986953026		0.275542803		
TCF19				0.976673455				1.096701152
TNFAIP3		0.33596092				0.232158083		
UBAC2						0.17016835		
UBD						0.298477524		

Fst: fixation index, Dxy: average number of nucleotide substitutions per site between two populations, Hst: haplotype diversity based differentiation

APPENDIX L. GENES WITH LOWEST QUARTILE GENETIC DIFFERENTIATION PARAMETER VALUES WITH RESPECT TO AFRICAN POPULATION FOR EAST ASIAN, AND EUROPEAN 1K GENOMES POPULATIONS.

Only the lowest quartile values are presented for clarity.

	African- East Asian differentiation				**African-European differentiation**			
Gene	**Dxy**	**Fst**	**Pi/Fst**	**Pi/Dxy**	**Dxy**	**Fst**	**Pi/Fst**	**Pi/Dxy**
API5	0.00038164		0.000769775	0.52405105	0.000413077		0.001728222	
BTNL2						0.01699493		
C10ORF11 (LRMDA)							0.002992327	
C6ORF15						0.019079806		
C6ORF47	0.00048594				0.000420047			
CCHCR1		0.042467381				0.014995562		
CCR1	0.00033504		0.001222986		0.000422479		0.002254396	
CDH26			0.001304723	0.414504764			0.001142497	0.419940629
CEP135	0.00053182				0.000558484			
COL12A1					0.000522081		0.001565075	0.383082319
CTLA4	0.000346638				0.000321733	0.027420825		
DHFRP2		0.044875382				0.014711953		
DNMT3A	0.00052854				0.000572776			
DTL	0.00059926							
ERAP1		0.038666464						

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Appendix L(cont.)

FUT2			0.001114087	0.210317018				
GABBR1		0.028219117			0.000621382	0.008297016		
GALT10			0.002491954	0.509455183				
HCG27						0.011425533		
HERPUD2						0.011425533		
HLA_B		0.037038374				0.026933668		
HLA_DQ		0.020268028				0.016535177		
HLA_F		0.04248372						
HLA_G		0.031990898						
HLAC						0.016677554		
HLADQB1						0.009713554		
HMP19			0.000686172	0.30158349			0.002438571	0.583914759
IFNG	0.00041096				0.000481334			
IL1A			0.002114438					
IL6			0.000951302	0.32255781				
KLRK1								0.590926657
LILRA1				0.514290003				0.551510331
LOC100129342							0.003564793	
LOC285830		0.042059558						
LTN1					0.000625893			
LYST			0.000497577	0.240282246			0.002303805	0.518919173
MOG				0.507002463				
MSX2			0.000764041	0.227997021			0.002444863	0.478696557
MUC21						0.017252963		
NOD2	0.0005754		0.002098611	0.52137946				

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Appendix L(cont.)

OSR1	0.0003497		0.000312697	0.285959471	0.000331607		0.002260214	0.603123994
PLEKHB1								0.555559952
PSMD14	0.00033656				0.000329016			
PSOR1C1		0.038849672						
PTPN22			0.001242394		0.000544698			
RALGAPA2	0.00041099				0.000339199		0.002559187	0.589625155
RNF39		0.044244233						
SLC43A3				0.497631377				0.621221301
SLC44A4		0.041401632						
SMARC2								0.577530778
TCF19						0.027187253		
TLR4	0.00058999		0.001926148	0.508484303			0.003193536	0.625969814
TNF	0.00023183	0.037287858			0.000259148	0.013678583		
TNFAIP3			0.000595307	0.267630519			0.001722964	0.539226222
TTLL7	0.0005391	0.039030407						
UBAC2							0.00352592	
UBD							0.003350336	0.427115547
ZNRD1		0.043799185						

Fst: fixation index, Dxy: average number of nucleotide substitutions per site between two populations, Hst: haplotype diversity based differentiation

APPENDIX M. COMPARISON OF BD ASSOCIATED SNP FST VS. GENE FST VALUES. FST VALUES ESTIMATED COMPARING EAST ASIAN VS. AFRICAN POPULATIONS.

A. SNPs with Fst values greater than their respective Gene Fst estimates

SNP	Gene	SNP Fst	Gene Fst
rs1343151	IL23R	0.63	0.15
rs4242425	EBF2	0.51	0.22
rs610604	TNFAIP3	0.51	0.34
rs7561555	ASB18	0.51	0.24
rs4570167	EBF2	0.50	0.22
rs12141431	IL23R, IL12RB2	0.49	0.15
rs681343	FUT2	0.45	0.36
rs7758496	SAMD3(TMEM200A)	0.43	0.20
rs4897380	SAMD3	0.42	0.20
rs103294	LILRA1	0.40	0.19
rs798887	LILRB1	0.39	0.11
rs9494885	TNFAIP3	0.39	0.34
rs1472224	DTL	0.36	0.09
rs749240	SMG6	0.34	0.19
rs6803980	CCR3	0.34	0.08
rs9483115	SAMD3(TMEM200A)	0.33	0.20
rs724324	SAMD3(TMEM200A)	0.32	0.20
rs4936742	UBASH3B	0.31	0.12
rs9990343	CCR3	0.30	0.08
rs4640857	COL12A1	0.30	0.08
rs7033529	SMARCA2	0.29	0.13

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Appendix M(cont.)

rs1615251	LOC285830 (HLA-F antisense RNA1)	0.28	0.04
rs4660590	HIVEP3	0.28	0.19
rs817277	CDH26	0.28	0.23
rs2373156	CCR3	0.28	0.08
rs7651539	CCR3	0.28	0.08
rs817283	CDH26	0.26	0.23
rs6692084	DEPDC1	0.25	0.15
rs7616215	CCR1	0.24	0.16
rs2782932	SUSD1	0.23	0.13
rs4852547	CTNNA2	0.22	0.14
rs3129045	MOG	0.22	0.11
rs237024	SUMO4	0.21	0.08
rs7631551	CCR1	0.20	0.16
rs12119179	IL23R, IL12RB2	0.19	0.15
rs7649764	CCR3	0.19	0.08
rs9554573	UBAC2	0.19	0.10
rs11209033	IL23R, IL12RB2	0.18	0.15
rs1737031	LOC285830 (HLA-F antisense RNA1)	0.18	0.04
rs4493590	SORBS2	0.18	0.13
rs549630	SLC43A3	0.17	0.12
rs9261389	TRIM31	0.17	0.09
rs2593082	CEP135	0.17	0.08
rs11206377	LOC100129342	0.17	0.14
rs1436321	OVCH1	0.16	0.12
rs574710	C6orf10	0.15	0.07
rs1736951	HLA-G	0.15	0.03
rs13435197	SLIT2	0.15	0.12

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Appendix M(cont.)

rs544358	C6orf10	0.13	0.07
rs539703	C6orf10	0.13	0.07
rs4959093	C6orf10	0.13	0.07
rs926591	C6orf10	0.13	0.07
rs13075270	CCR3	0.13	0.08
rs2523408	HLA-G	0.12	0.03
rs2530710	MUC21	0.12	0.05
rs7999348	UBAC2	0.12	0.10
rs9517701	UBAC2	0.12	0.10
rs2061634	CCDC180	0.11	0.09
rs7332161	UBAC2	0.11	0.10
rs727263	UBAC2	0.11	0.10
rs9513584	UBAC2	0.11	0.10
rs6491493	UBAC2	0.11	0.10
rs4959053	PSORS1C1	0.11	0.04
rs9263804	POU5F1	0.10	0.06
rs3130501	POU5F1	0.10	0.06
rs3132524	POU5F1	0.10	0.06
rs2073723	TCF19	0.10	0.05
rs2523467	MICA	0.10	0.07
rs11763983	HERPUD2	0.08	0.06
rs3130944	HCG27	0.08	0.06
rs1799724	TNFα	0.08	0.04
rs1633041	LOC285830 (HLA-F antisense RNA1)	0.06	0.04
rs1632973	HLA-G	0.06	0.03
rs1736963	HLA-G	0.06	0.03
rs1611172	HLA-G	0.06	0.03

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Appendix M(cont.)

rs753544	HLA-G	0.06	0.03
rs1077433	HLA-G	0.06	0.03
rs885940	LOC285830 (HLA-F antisense RNA1)	0.06	0.04
rs1610637	LOC285830 (HLA-F antisense RNA1)	0.06	0.04
rs1633002	HLA-G	0.06	0.03
rs9266406	HLA-B	0.05	0.04
rs9266409	HLA-B	0.05	0.04
rs6910516	HLA-B	0.05	0.04
rs29273	GABBR1	0.05	0.03
rs407238	HLA-G	0.04	0.03

B. SNPs with Fst values less than their respective Gene Fst estimates

SNP	Gene	SNP Fst	Gene Fst
rs7753873	TNFAIP3	0.32	0.34
rs7354999	LYST/NID1	0.28	0.40
rs574750	GALNT10	0.20	0.28
rs10516130	MSX2	0.20	0.39
rs4141940	SAMD3(TMEM200A)	0.20	0.20
rs16937370	API5	0.19	0.26
rs899276	SAMD3(TMEM200A)	0.18	0.20
rs924080	IL23R, IL12RB2	0.14	0.15
rs17434565	C10orf11	0.13	0.15
rs1518111	IL-10	0.11	0.17
rs1800871	IL-10	0.11	0.17
rs1265048	C6orf15	0.10	0.14
rs3769393	STK39	0.10	0.11
rs2707110	NAV2	0.10	0.16
rs1554286	IL-10	0.10	0.17
rs9554581	UBAC2	0.10	0.10
rs984477	UBAC2	0.10	0.10
rs11069357	UBAC2	0.09	0.10
rs3825427	UBAC2	0.09	0.10
rs4435061	TMEM132B	0.09	0.13
rs9517644	UBAC2	0.09	0.10
rs912130	UBAC2	0.09	0.10
rs10864912	PAX8	0.09	0.13
rs2390639	STK39	0.09	0.11
rs873764	NAV2	0.08	0.16

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Appendix M(cont.)

rs12134670	DEPDC1	0.08	0.15
rs10833804	GAS2	0.08	0.20
rs591804	PLEKHB1	0.06	0.21
rs4986790	TLR4	0.06	0.16
rs1323076	C10orf11	0.06	0.15
rs10266069	GIMAP2	0.06	0.12
rs10499194	TNFAIP3	0.06	0.34
rs11123169	PAX8	0.06	0.13
rs3094584	MICA	0.06	0.07
rs1549332	STX8	0.06	0.18
rs2731031	SLC41A2	0.05	0.06
rs2100766	ATP8A1	0.05	0.14
rs1969624	SACM1L	0.05	0.09
rs17006292	TFCP2L1	0.05	0.08
rs13092160	CCR3	0.05	0.08
rs17282391	CCR1	0.04	0.16
rs2980221	HNF4G	0.04	0.33
rs2156215	TENM4(ODZ4)	0.04	0.18
rs7761068	DHFRP2	0.04	0.04
rs1961261	KCNK9	0.04	0.13
rs1634717	MUC21	0.04	0.05
rs1632854	MUC21	0.04	0.05
rs1542755	CCR3	0.03	0.08
rs17375018	IL23R	0.03	0.15
rs7574070	STAT4	0.03	0.12
rs2286900	GIMAP1	0.03	0.10
rs897200	STAT4	0.03	0.12
rs6926792	HCG9	0.03	0.07

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Appendix M(cont.)

rs10510749	CCR1	0.03	0.16
rs13084057	CCR1	0.03	0.16
rs13067058	CCR3	0.03	0.08
rs6911737	HCG9	0.03	0.07
rs6931776	HCG9	0.03	0.07
rs2074482	PPP1R11	0.03	0.07
rs9261189	ZNRD1	0.03	0.04
rs3869068	ZNRD1	0.03	0.04
rs10846924	TMEM132B	0.03	0.13
rs6744214	PSMD14	0.03	0.06
rs9469615	LOC100132252	0.03	0.11
rs6733456	PSMD14	0.03	0.06
rs2892976	UBAC2	0.03	0.10
rs2617170	KLRC4	0.03	0.07
rs11965547	SLC44A4	0.03	0.04
rs10846917	TMEM132B	0.03	0.13
rs12589991	GALNTL1	0.02	0.15
rs17562982	SGPP2	0.02	0.15
rs1495965	IL23R, IL12RB2	0.02	0.15
rs2242655	C6orf47	0.02	0.12
rs2077102	BAG6(BAT3)	0.02	0.11
rs11163772	TTLL7	0.02	0.04
rs9517668	UBAC2	0.02	0.10
rs3905495	HLA-C	0.01	0.05
rs2832137	LTN1(RNF160)	0.01	0.08
rs11862324	PMFBP1	0.01	0.17
rs7572482	STAT4	0.01	0.12

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Appendix M(cont.)

rs9258205	LOC285830 (HLA-F antisense RNA1)	0.01	0.04
rs2844673	MUC21	0.01	0.05
rs317711	CPVL	0.01	0.18
rs1909704	HMP19	0.01	0.29
rs10256482	GIMAP2	0.01	0.12
rs1608157	GIMAP4	0.01	0.07
rs1799964	TNFα	0.01	0.04
rs1916012	GIMAP4	0.01	0.07
rs4666492	OSR1	0.01	0.32
rs2844845	LOC285830 (HLA-F antisense RNA1)	0.00	0.04
rs2517446	MUC21	0.00	0.05
rs2517411	MUC21	0.00	0.05
rs2252925	MUC21	0.00	0.05
rs2252926	MUC21	0.00	0.05
rs2523915	MUC21	0.00	0.05
rs6082210	RALGAPA2	0.00	0.05
rs4986791	TLR4	0.00	0.16
rs2073716	CCHCR1	0.00	0.04
rs2076530	BTNL2	0.00	0.06
rs2240063	CCHCR1	0.00	0.04
rs9260954	HCG9	0.00	0.07
rs9272346	HLA-DQA1	0.00	0.02
rs11209026	IL23R	0.00	0.15
rs872837	LOC107984355	0.00	0.19
rs134006	MN1	0.00	0.07
rs2066847	NOD2	0.00	0.14
rs9261317	RNF39	0.00	0.04

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Appendix M(cont.)

rs6923832	TRIM31	0.00	0.09
rs1522596	GIMAP4	0.00	0.07
rs2066844	NOD2	0.00	0.14
rs9261265	ZNRD1	0.00	0.04
rs12194547	C6orf85(LOC100507336)	0.00	0.13
rs11248047	CPLX1	0.00	0.15
rs1465825	DNMT3A	0.00	0.06
rs17482078	ERAP1	0.00	0.04
rs6457617	HLA-DQB1	0.00	0.05
rs3116788	HLA-F	0.00	0.04
rs1610584	HLA-F	0.00	0.04
rs1610585	HLA-F	0.00	0.04
rs1610593	HLA-F	0.00	0.04
rs1611356	HLA-F	0.00	0.04
rs1627465	HLA-F	0.00	0.04
rs17810546	IL12A	0.00	0.18
rs2617151	KLRK1	0.00	0.15
rs2523386	LOC285830 (HLA-F antisense RNA1)	0.00	0.04
rs9501063	POU5F1	0.00	0.06
rs470151	SEMA6D	0.00	0.16
rs361525	TNFα	0.00	0.04
rs17575643	UBAC2	0.00	0.10
rs6933331	UBD	0.00	0.16
rs3025657	UBD	0.00	0.16

APPENDIX N. CROSS POPULATION EXTENDED HAPLOTYPE HOMOZYGOSITY (XP-EHH), AND INTEGRATED HAPLOTYPE SCORE (IHS) ANALYSES OF BD ASSOCIATED GENES. PAIRWISE XP-EHH ANALYSES COMPARES YRI, CEU, AND CHB POPULATIONS. IHS SCORES ARE CALCULATED WITHIN AFR, EAS, EUR, AND SAS SUBPOPULATIONS.

Highest values from 10kb sliding window analyses are presented.

	XP-EHH			**iHS**																							
Gene	**CEU-YRI**	**CHB-CEU**	**CHB-YRI**	**ACB-AFR**	**ASW-AFR**	**ESN-AFR**	**GWD-AFR**	**LWK-AFR**	**MSL-AFR**	**YRI-AFR**	**CDX-EAS**	**CHB-EAS**	**CHS-EAS**	**JPT-EAS**	**KHV-EAS**	**CEU-EUR**	**FIN-EUR**	**GBR-EUR**	**IBS-EUR**	**TSI-EUR**	**BEB-SAS**	**GIH-SAS**	**ITU-SAS**	**PJL-SAS**	**STU-SAS**
ABCB5	0.31	0.24	0.54	0.87	0.57	0.87	0.76	1.29	0.77	0.89	1.12	0.67	0.82	1.21	0.68	0.47	0.47	0.42	0.48	0.52	0.47	0.41	0.54	0.46	0.31
API5	0.14	0.48	0.30	0.61	0.95	0.54	0.66	0.52	0.42	0.66	1.78	1.59	1.46	0.85	1.07	1.53	1.14	1.74	**2.09**	1.00	0.92	0.88	1.08	1.50	0.99
ASB18	1.40	0.20	1.52	0.31	0.51	0.43	0.75	0.42	0.89	0.34	1.58	1.41	1.41	1.48	1.71	1.15	1.56	**2.00**	**2.31**	**2.03**	0.95	1.32	1.20	1.32	0.66
ATP8A1	0.29	0.19	0.39	0.45	0.34	0.32	0.49	0.38	0.35	0.31	0.72	0.76	0.82	0.74	0.89	0.67	0.72	0.69	0.54	0.85	0.64	0.53	0.63	0.47	0.66

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Appendix N(cont.)

BAG6	0.13	0.08	0.15	0.37	0.74	0.99	0.83	0.75	0.56	0.43	0.77	0.79	0.72	0.69	1.19	0.79	0.90	0.96	0.82	0.97	1.53	1.24	1.29	1.09	1.60
BTNL2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C10ORF11	0.93	0.41	0.59	0.78	0.58	0.98	0.93	1.50	0.80	0.82	1.31	0.78	1.23	1.35	1.54	0.82	0.70	0.66	0.48	0.64	0.76	1.05	0.84	0.50	0.81
C6ORF10*	0.66	0.48	0.19	0.32	0.40	0.30	0.52	0.51	0.31	0.30	1.85	1.24	1.28	0.83	1.56	0.79	0.70	0.74	1.16	1.28	1.37	0.79	0.97	1.58	1.44
C6ORF15	0.31	0.24	0.11	0.60	0.69	1.05	0.91	1.03	0.90	0.50	0.94	0.62	0.53	0.42	0.77	0.50	0.37	0.55	0.60	0.66	0.72	0.82	0.66	0.67	0.96
C6ORF47	0.27	0.08	0.32	1.02	0.99	1.59	1.27	0.84	0.85	1.01	0.69	0.72	1.14	0.78	1.47	1.37	1.63	1.67	0.98	1.88	1.61	1.57	1.34	0.96	1.64
C6ORF85	**2.23**	0.79	1.25	0.72	1.09	0.61	0.70	0.72	0.84	0.73	0.64	0.59	0.36	1.03	0.40	1.87	1.63	**2.03**	**2.13**	1.82	1.32	1.65	1.05	1.52	0.95
CCDC180	0.53	0.08	0.57	0.72	0.68	0.88	0.84	0.71	0.82	0.62	0.93	0.54	0.60	0.38	0.86	0.77	0.80	0.71	0.63	0.92	0.32	0.50	0.34	0.51	0.67
CCHCR1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CCR1	0.19	0.30	0.36	1.96	1.20	**2.04**	**2.86**	1.42	**2.26**	**2.63**	0.00	0.68	0.00	0.00	0.00	0.69	0.87	0.74	0.60	0.54	0.72	0.50	0.49	0.62	0.41
CCR3	0.04	0.55	0.41	**2.91**	1.82	**2.90**	**3.50**	**2.57**	**4.12**	**4.24**	0.00	0.41	0.00	0.00	0.00	0.56	0.31	0.50	0.73	0.60	0.27	0.75	0.67	1.04	0.23
CDH26	0.47	0.37	0.93	0.69	0.87	0.77	0.88	0.72	0.70	0.62	-	-	0.71	-	-	0.72	0.53	0.62	0.58	0.75	0.70	1.02	0.65	0.95	0.64

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Appendix N(cont.)

CEP135	0.25	0.30	0.58	0.52	0.60	0.59	0.65	0.79	0.42	0.50	1.35	1.05	1.13	0.91	1.22	0.72	1.09	0.72	0.95	0.66	0.92	0.93	0.86	0.95	0.88
COL12A1	0.92	0.22	0.72	0.61	0.81	0.52	0.42	0.55	0.59	0.55	0.52	0.60	0.47	0.90	0.67	0.44	0.00	0.58	0.43	0.28	0.52	0.38	0.59	0.87	0.85
CPLX1	0.16	0.09	0.08	0.88	0.55	0.86	1.01	1.01	1.19	0.79	0.49	0.66	0.74	0.60	0.76	0.55	0.51	0.46	0.46	0.63	0.48	0.50	0.44	0.50	0.43
CPVL	0.94	0.34	1.28	1.08	0.51	0.96	0.57	0.88	0.66	0.70	1.32	1.08	0.86	1.08	0.66	0.63	0.48	0.62	0.67	0.73	0.93	0.79	0.92	1.07	0.84
CTNNA2	0.81	0.79	**1.59**	0.67	0.67	0.47	0.58	0.41	0.47	0.66	**1.60**	**1.82**	**2.47**	**2.23**	**2.11**	0.53	1.52	0.82	0.82	0.70	0.74	0.94	0.81	0.37	0.41
DEPDC1	0.54	0.41	1.12	0.48	0.74	0.88	0.76	0.50	0.90	0.76	0.43	0.53	0.38	0.83	0.71	1.04	0.95	0.99	1.13	1.51	0.48	0.41	0.33	0.23	0.51
DHFRP2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DNMT3A	0.33	0.09	0.43	0.67	0.53	0.67	0.51	0.62	0.39	1.03	0.84	0.76	0.30	0.83	0.37	0.68	0.64	0.92	1.02	0.67	0.67	0.66	1.06	0.71	0.44
DTL*	0.08	0.35	0.43	0.94	1.05	0.51	0.83	1.42	0.77	0.94	**1.77**	1.01	**2.29**	**1.73**	**1.78**	0.40	0.30	0.67	0.49	0.37	0.39	0.77	0.52	0.68	0.73
EBF2*	0.58	0.94	**1.63**	0.46	0.42	0.41	0.58	0.35	0.38	0.42	**1.93**	**2.30**	**2.40**	**1.89**	**1.98**	0.71	0.54	0.68	0.70	0.57	0.62	0.54	0.64	0.65	0.58
ERAP1*	0.08	0.38	0.54	0.94	0.68	0.62	1.11	0.47	1.13	0.88	1.25	1.16	1.04	0.63	1.18	0.61	0.49	0.56	0.54	0.65	0.77	0.97	0.74	1.01	0.90
FUT2*	0.60	0.23	0.89	0.79	0.53	0.44	0.79	0.76	0.33	0.66	0.22	0.30	0.46	1.00	0.79	1.19	0.83	0.97	0.76	1.06	0.39	0.95	0.58	0.94	0.46

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Appendix N(cont.)

GABBR1*	0.17	0.12	0.16	0.30	0.37	0.43	0.24	0.44	0.49	0.36	0.67	0.76	0.87	0.95	0.81	0.77	0.65	0.76	1.00	0.75	1.03	0.63	0.49	0.86	0.90
GALNT1	1.07	0.23	0.98	0.45	0.67	1.22	0.84	0.79	0.55	0.63	0.82	1.11	1.66	1.42	0.83	0.67	0.44	0.57	0.10	0.73	0.19	1.41	0.82	1.02	0.57
GALNT10*	0.12	1.23	1.18	0.86	0.93	1.33	0.70	1.30	1.22	1.33	**2.09**	**1.99**	**2.09**	1.44	**2.00**	0.67	0.71	0.42	0.85	0.75	0.84	0.80	0.68	0.53	0.67
GAS2	1.44	0.41	**1.95**	0.45	0.83	0.41	0.60	0.39	0.43	0.66	1.76	1.47	0.90	1.55	1.29	1.62	1.33	1.52	1.68	1.40	1.36	1.62	1.55	1.39	1.59
GIMAP1	1.38	0.19	1.20	0.58	0.35	0.37	0.39	0.47	0.49	0.53	0.79	0.58	0.83	0.69	0.59	0.94	0.85	1.09	1.08	1.26	0.72	0.82	0.71	0.68	0.83
GIMAP2	0.27	0.04	0.26	0.43	0.39	0.43	0.43	0.50	0.53	0.42	0.61	0.57	0.55	0.61	0.74	0.56	0.74	0.74	0.76	0.70	0.74	0.87	0.78	0.71	0.90
GIMAP4	0.21	0.06	0.16	0.46	0.71	0.51	0.52	0.64	0.61	0.57	0.97	0.79	0.93	0.86	0.98	1.08	1.29	1.43	1.56	1.53	1.13	1.19	1.27	1.04	1.18
HCG27	0.23	0.28	0.06	0.45	0.74	0.57	0.54	0.55	0.66	0.46	0.97	1.05	0.70	1.09	1.38	0.99	1.00	0.98	1.47	1.41	0.99	0.86	1.07	1.11	1.67
HCG9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
HERPUD2	1.09	0.51	0.65	0.94	0.54	0.67	0.57	0.39	0.70	0.91	0.88	0.90	0.93	0.90	0.65	0.59	0.88	0.65	0.97	0.68	0.38	0.72	0.89	1.26	1.10
HIVEP3	1.03	0.15	1.12	0.82	0.82	1.03	0.92	0.78	0.70	0.87	0.80	0.66	1.26	0.91	0.69	0.41	0.62	0.52	0.39	0.57	0.44	0.66	0.55	0.46	0.55
HLA-B	0.08	0.05	0.07	0.97	1.24	1.14	1.68	1.00	0.79	0.98	**3.17**	**3.04**	**2.24**	**2.74**	**3.10**	**3.65**	**1.98**	**2.66**	**2.31**	**2.15**	**2.53**	**2.02**	1.48	**2.22**	1.72

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Appendix N(cont.)

HLA-DQA1	0.29	0.22	0.40	1.36	1.00	1.32	0.79	1.38	0.76	1.92	1.43	1.25	1.61	1.72	1.19	**2.27**	**1.64**	**2.10**	**1.83**	**2.05**	1.43	1.37	0.97	1.38	**2.00**
HLA-F*	0.43	0.10	0.40	0.37	0.52	0.43	0.34	0.41	0.54	0.60	0.26	0.53	0.39	0.86	0.64	0.53	1.03	0.53	0.55	0.72	0.77	0.90	0.80	0.52	0.85
HLA-G*	0.65	0.03	0.63	1.53	1.22	1.57	1.55	1.49	1.63	1.46	0.74	**2.43**	**1.74**	**2.11**	**2.60**	1.10	0.74	0.70	1.31	1.81	**2.36**	**1.80**	**2.31**	**1.61**	**1.78**
HLA-C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
HLA-DQB1	0.29	0.22	0.40	1.36	1.00	1.32	0.79	1.38	0.76	1.92	1.43	1.25	1.61	1.72	1.19	**2.27**	**1.64**	**2.10**	**1.83**	**2.05**	1.43	1.37	0.97	1.38	**2.00**
HMP19*	1.19	0.06	1.10	0.60	0.72	0.75	1.06	0.37	0.93	0.33	0.65	0.96	1.79	**1.97**	-	1.00	1.18	0.84	0.97	1.37	0.24	0.43	0.26	0.76	0.30
HNF4G*	0.10	0.55	0.59	0.56	1.14	0.70	0.61	0.62	0.58	0.98	1.18	1.00	0.89	1.16	1.34	0.75	0.67	1.21	1.14	1.05	1.33	0.74	1.20	1.31	0.71
IFNG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
IL10	0.13	0.70	0.67	0.55	0.51	0.49	0.72	0.68	0.85	0.58	0.96	1.06	0.80	0.93	0.96	0.49	0.50	0.82	0.69	0.59	0.27	0.61	0.63	0.57	0.48
IL12A	0.69	0.86	1.53	0.44	0.61	0.56	0.39	0.48	0.61	0.51	1.49	1.41	1.38	1.27	1.68	0.65	0.49	0.63	0.69	0.58	0.41	0.50	1.01	0.50	0.66
IL17A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
IL1A*	1.18	0.58	1.60	0.78	0.75	0.68	0.44	0.41	0.60	0.58	1.05	0.84	0.99	0.48	0.73	0.29	1.03	0.72	0.26	0.30	0.40	0.58	0.55	0.52	0.58

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Appendix N(cont.)

IL23R*	1.05	0.16	1.24	0.91	1.56	0.60	0.53	0.61	0.94	0.92	0.56	0.77	1.40	1.24	0.89	0.65	0.35	1.12	0.52	1.05	1.14	1.57	1.50	1.17	1.26
IL6*	0.59	0.33	1.04	0.53	0.49	0.58	0.41	0.58	0.38	0.35	1.08	1.39	1.67	1.70	0.91	0.62	0.63	0.41	0.43	0.46	0.64	0.51	0.60	0.72	0.62
KCNK9	0.91	0.49	1.40	0.74	0.98	1.08	0.72	1.40	0.55	1.03	**2.54**	**3.46**	**3.20**	**2.64**	**2.47**	0.72	0.40	0.64	0.55	0.74	0.89	0.99	0.77	0.59	0.89
KLRC4	0.70	0.18	0.51	0.66	0.57	1.16	0.70	0.91	0.80	1.09	0.60	0.74	0.37	0.91	0.69	0.72	1.12	0.61	0.75	0.98	1.39	0.92	1.28	0.99	1.02
KLRK1	0.60	0.18	0.76	0.79	0.46	0.68	0.66	0.85	0.70	0.69	0.74	0.81	0.54	0.66	0.70	0.84	0.93	0.50	0.63	0.62	0.74	0.62	0.71	0.80	0.50
LILRA1	0.67	0.25	0.50	1.16	1.06	1.03	1.38	1.02	0.93	1.01	0.66	0.46	0.13	0.57	0.36	0.29	0.05	0.80	0.44	0.49	1.03	1.04	0.78	0.74	1.04
LILRB1	0.50	0.47	0.95	0.71	0.73	0.76	0.79	0.88	0.64	0.49	1.76	1.16	0.63	0.64	0.54	0.58	0.43	0.45	0.62	0.38	0.51	0.66	0.44	0.46	0.40
LOC100129342	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LOC100132252	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LOC107984355	0.39	0.71	1.19	0.74	0.47	1.02	0.59	0.52	0.86	0.92	1.05	1.04	0.87	1.03	1.04	0.38	0.52	0.43	0.77	0.43	0.39	0.46	0.46	0.47	0.42
LOC285830	0.45	0.09	0.45	0.31	0.50	0.34	0.23	0.43	0.43	0.58	0.26	0.52	0.37	0.72	0.70	0.58	0.91	0.56	0.61	0.67	0.63	0.86	0.95	0.52	0.90

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Appendix N(cont.)

LTN1	0.71	0.06	0.65	1.26	1.07	1.12	1.41	1.10	1.20	1.71	1.75	1.07	1.46	1.38	1.39	1.25	0.94	0.74	0.92	0.90	0.93	1.13	0.81	0.55	0.70
LYST	0.55	1.18	**2.10**	0.70	0.76	0.45	0.70	0.86	1.07	0.64	0.97	1.33	1.13	0.75	**2.06**	0.61	0.79	0.76	0.53	0.50	0.55	0.90	0.54	0.62	1.02
MEFV	0.80	0.28	0.51	0.57	0.50	0.83	0.61	0.90	0.55	1.10	0.79	0.34	0.48	0.32	0.71	0.29	0.31	0.24	0.30	0.27	0.45	0.43	0.32	0.22	0.28
MICA	0.22	0.33	0.15	0.27	0.42	0.47	0.57	0.37	0.44	0.51	0.80	0.87	1.26	0.98	0.73	1.07	0.81	0.97	0.69	0.69	0.70	0.77	0.74	0.69	0.74
MN1	0.61	0.15	0.55	0.46	0.72	0.63	0.65	0.86	0.68	0.56	0.99	0.82	1.30	1.01	1.27	0.80	0.88	0.86	0.62	0.75	0.75	0.62	1.01	0.85	0.99
MOG*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
MSX2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
MUC21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
NAV2	1.70	0.27	**2.00**	0.62	0.50	0.77	0.57	0.65	0.65	0.67	**2.25**	1.47	1.47	0.77	**2.08**	1.21	1.28	1.09	0.84	0.90	1.03	1.12	1.23	1.09	1.22
NOD2*	0.93	0.75	**1.65**	1.16	1.62	1.38	1.26	0.89	1.42	1.42	**3.13**	**2.01**	**2.56**	**1.80**	**2.10**	0.90	0.33	0.49	0.31	0.37	1.44	1.35	1.24	1.15	0.86
OSR1*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
OVCH1	0.98	0.12	1.02	0.95	1.17	1.19	0.99	0.82	0.81	0.78	0.89	0.53	0.45	0.55	0.97	1.08	0.87	1.17	1.56	1.38	1.00	1.24	0.87	0.91	1.23
PAX8	0.56	0.25	0.87	0.84	0.70	0.59	0.65	0.60	0.81	0.70	1.11	0.93	1.38	0.87	0.81	0.36	0.41	0.55	0.87	0.59	0.45	0.52	0.62	0.73	0.48

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Appendix N(cont.)

PLEKHB1	0.84	0.11	0.95	0.47	0.53	0.77	0.97	0.58	1.17	0.73	0.66	0.86	0.82	0.84	0.85	0.73	0.58	0.87	0.79	0.73	0.75	0.56	0.60	0.68	0.42
PMFBP1	0.21	0.18	0.38	0.57	0.46	0.46	0.39	0.77	1.05	0.36	0.67	0.61	0.82	0.40	0.60	0.47	0.72	0.42	0.67	0.78	0.51	0.39	0.48	0.42	0.42
POU5F1	0.29	0.08	0.17	0.42	0.62	0.51	0.53	0.42	0.45	0.52	0.38	1.29	0.70	0.63	1.22	1.12	1.27	1.47	1.59	1.57	0.81	1.00	1.38	1.42	1.62
PPP1R11*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PSMD14	0.52	0.10	0.41	0.45	0.31	0.37	0.30	0.89	0.67	0.17	0.97	0.94	0.87	0.39	0.99	0.67	0.41	0.61	0.24	0.16	0.38	0.47	0.40	0.42	0.51
PSOR1C1*	0.07	0.07	0.09	0.74	0.50	0.87	0.56	0.56	0.72	0.68	0.95	0.65	0.73	0.54	0.52	0.50	0.40	0.44	0.52	0.57	0.55	0.71	0.71	0.70	0.71
RALGAPA2*	0.82	0.28	0.52	1.65	1.59	1.76	**1.97**	1.79	1.53	1.48	**2.61**	**2.05**	**2.70**	**2.84**	**2.04**	0.00	**3.01**	**2.23**	**2.99**	0.00	**2.08**	**2.39**	**1.60**	1.24	0.52
RIMBP2	0.37	0.14	0.47	0.82	1.03	1.14	0.97	1.01	0.98	0.97	1.27	1.06	1.12	1.01	1.10	1.34	0.91	1.64	1.19	1.19	0.78	0.75	0.72	0.69	0.76
RNF39*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SACM1L	0.20	0.86	1.06	0.76	1.00	0.73	0.84	0.74	0.75	0.76	0.72	0.67	0.61	1.08	0.61	0.89	0.71	1.11	0.71	0.71	1.26	0.90	1.77	1.50	1.61
SAMD3	0.66	0.29	0.91	0.99	0.87	0.78	1.35	1.08	1.22	1.07	1.48	1.37	1.40	1.24	1.58	1.36	1.31	1.16	1.52	1.72	1.05	1.38	1.31	1.18	0.82
SEMA6D	1.35	0.10	1.25	0.74	0.45	0.78	0.91	0.99	0.70	0.66	**2.08**	1.26	1.25	1.41	1.43	0.94	1.60	1.03	0.63	0.76	0.69	0.58	0.45	0.35	0.41

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Appendix N(cont.)

SGPP2	0.51	0.30	0.76	0.87	0.46	0.82	0.87	0.86	0.82	0.65	1.15	0.85	1.10	1.16	0.95	1.04	1.05	0.94	1.02	0.61	1.12	1.17	0.56	1.10	0.58
SLC41A2*	1.17	0.37	0.60	1.15	0.97	1.14	1.04	1.08	0.75	1.19	1.24	1.20	1.42	1.39	1.30	0.40	0.78	0.45	0.40	0.41	1.48	0.86	1.11	1.34	0.82
SLC43A3	0.54	0.47	1.01	0.65	0.89	0.54	0.59	0.49	0.64	0.63	0.87	1.07	0.92	0.70	1.20	0.50	0.76	0.51	0.46	0.60	1.36	1.24	1.24	1.26	1.14
SLC44A4*	0.19	0.06	0.16	0.30	0.50	0.48	0.55	0.27	0.84	0.45	0.74	0.69	0.44	0.37	0.69	0.58	0.39	0.56	0.79	0.79	0.77	0.64	0.79	0.77	0.83
SLIT2	0.23	0.48	0.68	1.40	1.03	1.13	1.00	1.20	1.29	1.44	0.83	1.22	1.12	1.03	0.85	**2.40**	**2.05**	**2.38**	**2.49**	**2.32**	1.11	1.57	1.14	1.59	1.11
SMARCA2*	0.45	0.11	0.58	1.14	1.01	1.40	1.68	1.12	1.92	1.03	0.72	1.22	0.87	1.43	0.77	0.66	1.42	0.73	1.22	1.68	1.04	0.75	1.32	1.36	1.32
SMG6	0.21	0.45	0.59	1.16	0.87	0.98	1.04	1.03	0.94	0.73	0.92	1.13	1.63	1.24	1.00	1.50	1.46	1.37	1.24	0.98	1.23	1.05	0.91	1.43	1.18
SORBS2	0.24	0.61	0.81	1.02	1.10	1.16	1.12	1.01	1.21	1.24	0.90	1.10	0.87	1.39	0.98	0.41	0.44	0.39	0.40	0.37	0.53	0.56	0.50	0.40	0.61
STAT4	0.95	0.40	0.55	1.00	0.49	1.69	0.79	1.20	0.91	0.94	0.42	0.42	0.48	0.59	0.48	1.40	1.61	1.25	1.48	1.56	1.57	1.91	1.56	1.91	1.83
STK39	0.98	0.40	0.57	0.57	0.51	0.41	0.68	0.59	0.65	0.55	0.87	0.94	1.29	1.32	1.23	0.40	0.62	0.84	1.08	0.96	0.74	0.83	0.98	1.14	0.95
STX8*	0.30	0.69	0.96	0.99	0.82	1.40	0.87	1.06	0.86	0.79	1.63	1.79	1.72	1.62	1.53	0.65	0.71	0.64	0.61	0.64	0.61	0.65	0.54	0.72	0.68

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Appendix N(cont.)

SUMO4	0.74	0.19	0.91	1.60	1.38	1.25	1.66	1.56	1.94	1.42	1.04	0.73	0.72	0.65	0.36	0.64	1.02	0.73	0.33	0.88	0.98	1.11	1.03	1.17	1.01
SUSD1	0.28	0.09	0.19	0.63	0.31	0.75	0.56	0.76	0.68	0.61	1.37	1.46	1.06	0.99	1.42	0.76	1.38	0.68	0.60	0.94	0.51	0.92	0.67	0.93	1.05
TCF19	0.29	0.08	0.17	0.42	0.62	0.51	0.53	0.42	0.45	0.52	0.38	1.29	0.70	0.63	1.22	1.12	1.27	1.47	1.59	1.57	0.81	1.00	1.38	1.42	1.62
TENM4	0.95	0.60	1.51	0.31	0.33	0.59	0.55	0.70	0.34	0.36	0.76	1.32	1.48	1.44	0.97	0.61	0.43	0.56	0.63	0.59	1.10	1.24	1.13	0.64	1.17
TFCP2L1*	1.21	0.58	0.58	0.56	0.34	0.48	0.26	0.52	0.27	0.44	0.64	0.85	0.48	0.83	0.89	0.82	0.60	0.77	0.89	1.15	0.31	0.57	0.80	0.75	0.78
TLR4	0.89	0.27	1.20	0.49	0.55	0.50	0.70	0.73	0.50	0.52	0.54	0.93	0.76	0.91	0.49	0.81	0.48	0.55	0.77	0.74	0.73	1.00	0.66	0.93	0.76
TMEM132B	0.58	0.68	1.28	0.78	0.77	0.92	0.62	0.83	0.84	0.94	1.89	1.51	1.56	1.43	1.49	0.40	0.51	0.33	0.51	0.35	0.34	0.49	0.52	0.31	0.63
TNF	0.11	0.07	0.18	1.12	1.01	0.98	1.00	0.70	1.01	1.13	0.49	0.65	0.30	0.73	0.51	0.46	0.19	0.37	0.60	0.61	0.99	1.10	1.25	0.95	1.09
TNFAIP3	0.89	0.02	1.10	0.34	0.44	0.45	0.53	0.54	0.73	0.69	0.64	1.03	1.36	0.49	0.84	0.87	1.16	0.66	0.79	1.37	0.85	0.77	0.83	0.86	0.78
TRIM31	0.08	0.07	0.11	0.53	0.43	0.21	0.76	0.57	0.85	0.71	0.41	0.65	0.68	0.36	0.55	0.95	0.37	0.80	0.91	1.03	0.56	0.64	0.34	0.90	0.73
TTLL7*	0.13	0.30	0.39	0.46	0.79	0.40	0.61	0.46	0.89	0.42	1.08	1.11	1.01	0.92	1.01	1.22	1.13	1.39	0.78	0.68	0.62	0.72	0.56	0.68	0.78

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Appendix N(cont.)

UBAC2	0.38	0.11	0.41	0.89	0.72	0.51	0.72	0.71	0.84	0.97	**1.83**	**1.67**	**1.81**	**1.94**	**1.69**	**2.00**	**2.20**	**2.08**	**2.03**	**1.98**	**2.02**	**2.11**	**2.63**	**2.49**	**2.18**
UBASH3B	0.60	0.60	1.24	1.30	1.32	0.88	1.32	1.47	0.73	0.87	**2.05**	**1.72**	**1.82**	**1.60**	**1.69**	1.41	1.14	1.32	1.32	1.42	1.15	0.64	1.16	0.41	1.36
UBD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ZNRD1*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

* Genes with highest or lowest quartile population genetic parameter and frequency spectrum test results unique to East Asians (EAS)

APPENDIX O. DIRECTION OF SELECTION (DOS), MCDONALD-KREITMAN TEST P VALUE, NEUTRALITY INDEX (NI), AND ALPHA (Α) PARAMETER ESTIMATES OF BEHCET DISEASE ASSOCIATED GENES IN THE 1000 GENOMES EAST ASIAN POPULATIONS.

	CDX				**CHB**				**CHS**				**JPT**				**KHV**			
Gene	**DoS[a]**	**P[b]**	**NI[c]**	**α[d]**	**DoS**	**P**	**NI**	**α**	**DoS**	**P**	**NI**	**α**	**DoS**	**P**	**NI**	**α**	**DoS**	**P**	**NI**	**α**
ABCB5	-0.5	0.04	1.45	-0.45	-0.5	0.23	1.55	-0.55	-0.5	0.04	1.31	-0.31	-0.5	0.01	7.1	-6.1	-0.5	0.05	5.3	-4.3
API5	-1	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
ASB18	-1	1	0	0	-1	1	0	0	-1	0.25	0	0	-1	0.33	0	0	-1	0.33	0	1
ATP8A1	-1	1	0	1	-1	1	0	1	-1	0.33	0	1	-1	0.024	0	1	-1	1	0	1
BAG6	-0.27	0.3	0	0	0.47	0.09	0.12	0.87	0.12	0.61	0.57	0.42	0.39	0.22	0.19	0.8	0.22	0.35	0.38	0.61
BTNL2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C10orf11	-1	1	0	0	-1	1	0	0	-1	1	0	0	-1	1	0	0	-1	1	1	0
C6orf10	0	1	0	0	0.05	1	0	1	0	1	0	0	0.05	1	0	1	0.06	1	0	1
C6orf47	-0.03	1	1.2	-0.2	-0.28	1	0	0	0.05	1	0.8	0.2	-0.03	1	1.2	-0.2	-0.11	1	2	-1
SLC22A23/C6orf85	-0.62	0.007	24	-23	-0.48	0.03	12.6	-12	-0.6	0.02	21	-20	-0.56	0.01	18	-17	-0.56	0.01	18	-17
CCDC180	0.04	1	0.75	0.25	0.04	1	0.75	0.25	0.09	0.61	0.56	0.43	0.17	0.38	0.37	0.62	0.04	1	0.75	0.25
CCHCR1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
CCR1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0

(cont. on the next page)

Appendix O(cont.)

CCR3	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
CDH26	-0.01	1	1.07	-0.07	0.23	0.37	0.35	0.64	0.13	0.6	0.53	0.46	0.23	0.55	0.35	0.64	-0.01	1	1.07	-0.07
CEP135	-0.03	1	1.2	-0.2	-0.28	1	0	0	0.21	1	0.4	0.6	-0.28	1	0	0	-0.28	1	0	0
COL12A1	-0.44	0.14	6.75	-5.75	-0.7	0.16	5.33	-4.3	-0.56	0.36	15.75	-15	-0.69	0.14	6.66	-5.6	-0.51	0.14	10.12	-9.12
CPLX1	-0.35	0.3	5	-4	-0.3	0.55	3.75	-2.75	-0.05	1	1.25	-0.25	-0.05	1	1.25	-0.25	-0.22	1	2.5	-1.5
CPVL	0.5	0.18	0	1	0.57	0.06	0	1	0.6	0.06	0	1	0.8	0.01	0	1	0.6	0.06	0	1
CTNNA2	0	—	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DEPDC1	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
DNMT3A	-0.16	1	2	-1	-0.33	1	4	-3	-0.16	1	2	-1	-0.5	0.4	2	-1	-0.33	1	2	-1
DTL	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
EBF2	-1	1	0	1	1	1	0	1	0	1	0	0	0	1	0	0	0	1	0	0
ERAP1	-0.36	0.26	5	-4	-0.18	0.58	2.2	-1.2	-0.36	0.27	4.9	-3.9	-0.35	0.28	4.5	-3.5	-0.41	0.11	6.5	-5.5
FUT2	-0.25	0.57	3	-2	-0.08	1	1.5	-0.5	-0.25	0.57	3	-2	-0.5	0.46	0	0	-0.08	1	1.5	-0.5
GABBR1	-0.1	0.73	1.52	-0.52	-0.2	0.17	2.32	-1.32	-0.2	0.21	2.43	-1.43	-0.03	1	1.14	-0.14	-0.17	0.35	2.08	-1.08
GALNT10	1	1	1.5	1	1	1	1	1	1	1	0.75	1	1	1	0.5	1	1	1	0.75	1
GALNTL1	-0.46	0.24	8	-7	-0.46	0.46	8	-7	-0.3	0.54	4	-3	-0.6	0.2	16	-15	-0.4	0.52	6	-5
GAS2	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	-1	1	0	0
GIMAP1	0.25	1	0.33	0.66	0.25	1	0.33	0.66	0.75	1	0	1	0.41	1	0.16	0.83	0.75	1	0	1

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Appendix O(cont.)

GIMAP2	0.16	1	0.5	0.5	0.16	1	0.5	0.5	0.16	1	0.5	0.5	0.16	1	0.5	0.5	0.16	1	0.5	0.5
GIMAP4	0	—	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HCG27	0.5	1	0	1	0.5	1	0	1	0.5	1	0	1	0.5	1	0	1	0.5	1	0	1
HCG9	0	—	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HERPUD2	-0.66	0.14	0	0	-0.66	0.1	0	0	-0.46	0.46	8	-7	-0.66	0.14	0	0	-0.66	0.4	0	0
HIVEP3	-0.17	0.43	2	-1	-0.5	0.009	13.5	-12.5	-0.34	0.08	4.2	-3.2	-0.41	0.03	6.75	-5.75	-0.25	0.37	2.8	-1.8
HLA-B	0.26	0.55	2.43	1	0.28	0.54	2.81	1	0.27	0.55	2.43	1	0.28	0.54	2.43	1	0.25	0.55	2.2	1
HLA-C	-0.16	0.31	2.43	-1.43	-0.18	0.26	2.81	-1.81	-0.16	0.31	2.43	-1.43	-0.16	0.31	2.43	-1.43	-0.14	0.6	2.2	-1.2
HLA-DQA1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
HLA-DQB1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
HLA-F	-0.14	1	0	0	0	1	1	0	0.02	1	0.83	0.16	0.02	1	0.83	0.16	0.02	1	0.83	0.16
HLA-G	0.37	0.11	0.19	0.8	0.17	0.6	0.44	0.55	0.06	1	0.74	0.25	0.16	0.37	0.44	0.55	0.2	0.35	0.39	0.6
HMP19	0.35	0.41	0.16	0.83	0.35	0.49	0.16	0.83	0.19	1	0.33	0.66	0.52	0.18	0.08	0.91	0.35	0.41	0.16	0.83
HNF4G	-1	0.2	0	0	-1	0.25	0	0	-0.66	1	0	0	-1	0.33	0	0	-1	0.33	0	0
IL-10	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
IL12A	-0.16	1	2	-1	0	1	0	0	-1	0.33	0	0	-0.5	1	0	0	-1	0.33	0	0
IL17F	-0.25	1	0	0	-0.25	1	0	0	-0.25	1	0	0	-0.25	1	0	0	-0.25	0.44	0	0

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Appendix O(cont.)

IL23R	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
IL6	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
KCNK9	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
KLRC4	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
KLRK1	-1	0.33	0	1	-1	0.33	0	1	-1	1	0	1	-1	0.33	0	1	-1	1	0	1
LILRA1	-0.19	0.09	0.38	0.61	0.04	0.76	0.77	0.22	0.11	0.46	0.54	0.45	0.08	0.39	0.62	0.37	0.22	0.06	0.33	0.66
LILRB1	0.01	1	0.95	0.05	-0.08	0.71	1.63	-0.63	-0.05	1	1.31	-0.31	-0.1	0.71	1.83	-0.83	-0.11	0.71	1.89	-0.89
LINC01499(API5)	-1	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
LOC285830 (HLA-F antisense RNA1)	-0.14	1	0	0	0	1	1	0	0.02	1	0.83	0.16	0.02	1	0.83	0.16	0.02	1	0.83	0.16
LTN1(RNF160)	0.08	0.71	0.7	0.3	0.06	0.74	0.75	0.25	0.09	0.72	0.65	0.34	0.05	1	0.78	0.21	0.09	0.72	0.65	0.34
LYST/NID1	0	—	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MEFV	0.08	1	0.6	0.4	0.03	1	0.8	0.2	0.03	1	0.8	0.2	-0.02	1	1.2	-0.2	-0.04	1	1.4	-0.4
MICA	-0.16	0.16	4.7	-3.7	-0.17	0.15	5.5	-4.5	-0.12	0.31	2.6	-1.63	-0.16	0.15	4.7	-3.7	-0.12	0.31	2.6	-1.63
MN1	0.52	1	0	1	-0.47	0.13	0	0	-0.47	1	0	0	-0.22	0.6	2.66	-1.66	0.2	1	0.44	0.55
MOG	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
MSX2	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0

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Appendix O(cont.)

MUC21	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
NAV2	-0.36	1	4.6	-3.6	-0.41	1	10	-9	-0.2	1	4	-3	-0.03	1	1.16	-0.16	-0.2	1	2.33	-1.33
NOD2	-0.03	1	1.14	-0.14	-0.2	1	2.85	-1.85	-0.03	1	1.14	-0.14	-0.2	1	2.85	-1.85	0.03	1	0.85	0.14
OSR1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
OVCH1	-0.24	0.2	3.75	-2.75	-0.25	0.19	4.06	-3.06	-0.21	0.22	3.12	-2.12	-0.22	0.23	3.09	-2.09	-0.26	0.18	4.68	-3.68
PAX8	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
PLEKHB1	0	1	0	0	-0.2	1	0	0	-0.2	1	0	0	0	1	0	0	-0.2	1	0	0
PMFBP1	-0.38	0.26	0.44	0.55	-0.38	0.11	1.4	-0.4	-0.24	0.35	3.75	-2.75	-0.38	0.12	0.76	0.23	-0.38	0.11	0.89	0.1
POU5F1	0.09	1	0.66	0.33	-0.28	0.59	3.33	-2.33	0.02	1	0.88	0.11	-0.23	0.59	2.66	-1.6	-0.28	0.59	3.33	-2.3
PPP1R11	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
PSMD14	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
PSORS1C1	-0.14	0.19	1.86	-0.8	-0.17	0.05	2.25	-1.2	-0.12	0.2	1.76	-0.7	-0.15	0.13	2.01	-1.01	-0.17	0.05	2.25	-1.2
RALGAPA2	-0.16	1	2	-1	-0.16	1	2	-1	0.33	1	0	1	-0.16	1	2	-1	-0.16	1	3	-1
RIMBP2	-0.38	1	5	-4	-0.54	1	12.5	-11.5	-0.25	1	3	-2	-0.38	1	5	-4	-0.26	1	3.33	-2.33
RNF39	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
SACM1L	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0

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Appendix O(cont.)

SAMD3 (TMEM200A)	-0.01	1	1.09	-0.09	-0.2	1	0	0	-0.01	1	1.09	-0.09	-0.26	0.53	0	0	-0.16	0.61	3.27	-2.27
SEMA6D	0.07	1	0.75	0.25	-0.3	0.32	3.5	-2.5	-0.17	1	2	-1	-0.17	1	2	-1	0	1	1	0
SGPP2	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
SLC41A2	0.5	1	0	1	0.5	1	0	1	0.5	1	0	1	-0.66	1	1	0	0.5	1	0	1
SLC43A3	0.66	0.4	0	1	0	1	0	0	0.06	1	0.75	0.25	-0.33	1	0	0	0.66	0.4	0	1
SLC44A4	-0.6	0.08	18	-17	-0.5	0.19	15	-14	-0.4	0.24	7.5	-6.5	-0.5	0.21	10.5	-9.5	-0.6	0.08	18	-17
SLIT2	0.04	1	0.83	0.16	0.175	1	0.41	0.58	-0.5	1	1.66	-0.66	-0.025	1	1.11	-0.11	0.04	1	0.83	0.16
SMARCA2	0	1	0	0	-0.5	1	0	0	-0.25	1	0	0	-1	0.2	0	0	-0.5	0.16	0	0
SMG6	0	1	0	0	-1	1	0	0	-1	1	0	0	-1	1	0	0	0	1	0	0
SORBS2	-0.09	1	1.55	-0.55	-0.02	1	1.12	-0.12	0.24	0.23	0.36	0.63	0.05	1	0.77	0.22	-0.34	0.3	0.5	0.5
STAT4	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
STK39	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
STX8	-0.5	1	0	0	-0.5	0.46	0	0	-0.5	1	0	0	0.16	1	0.5	0.5	-0.5	1	0	0
SUMO4	0	1	0	0	0.5	1	0	1	0	1	0	0	0.33	1	0	1	0	1	0	0
SUSD1	-0.16	1	2	-1	-0.16	1	2	-1	-0.26	1	3	-2	-0.16	1	2	-1	-0.26	1	3	-2
TCF19	0.09	1	0.66	0.33	-0.28	0.59	3.33	-2.33	0.02	1	0.88	0.11	-0.23	0.59	2.66	-1.66	-0.28	0.59	3.33	-2.33

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Appendix O(cont.)

TENM4(ODZ4)	-0.5	1	2.66	1	-1	1	1.62	1	0.5	1	3	1	-1	1	4.87	1	-1	1	2.4	1
TFCP2L1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
TLR4	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0
TMEM132B	-0.3	1	0.4	0.6	-0.3	1	0.66	0.33	0	1	1	0	-0.3	1	4	-3	-0.29	1	0.66	0.33
TNFAIP3	-0.66	0.4	0	0	-1	0.33	0	0	-1	0.1	0	0	-1	0.33	0	0	-1	0.33	0	0
TNFalfa	-0.33	1	0	0	-0.33	1	0	0	-0.33	0.37	0	0	-0.33	1	0	0	-0.33	0.37	0	0
TRIM31	-0.16	1	1	0	-0.5	1	0	0	-0.42	1	0	0	-0.4	1	0	0	-0.5	1	0	0
TTLL7	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
UBAC2	0.58	0.19	0.06	0.93	0.33	0.46	0.2	0.8	0.33	0.46	0.2	0.8	0.16	1	0.4	0.6	0.16	1	0.4	0.6
UBASH3B	-0.6	0.18	0	0	-0.33	0.5	0	0	-0.2	1	0	0.2	-0.22	1	0	0	-0.4	0.46	0	0
UBD	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0
ZNRD1	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0	0	—	0	0

a. DoS: Direction of Selection

b. P value of 2x2 McDonald-Kreitman test

c. NI: Neutrality Index

d. Alpha value (proportion of adaptive substitutions)

APPENDIX P. TISSUE SPECIFIC EXPRESSION PROFILES OF BD ASSOCIATED GENES WITH POPULATION GENETIC PARAMETER AND SELECTION ESTIMATES UNIQUE TO EAST ASIANS.

Gene	appendix	bone marrow	brain	colon	duodenum	endometrium	fat	gall bladder	heart	kidney	liver	lung	lymph node	ovary	pancreas	placenta	prostate	salivary gland	skin	small intestine	spleen	stomach	testis	urinary bladder
C6ORF10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.3	0.0
DTL	2.8	8.0	0.4	1.6	1.2	0.8	0.4	0.5	0.1	0.1	0.6	1.3	3.2	0.1	0.0	2.7	0.3	0.0	1.0	1.7	1.6	0.9	9.7	1.2
EBF2	0.5	0.0	0.0	0.1	0.0	0.2	8.5	1.9	4.4	0.3	0.0	0.3	0.4	0.2	0.1	0.2	0.5	0.3	0.1	0.1	0.0	0.0	0.5	1.0
ERAP1	12.1	6.1	4.5	10.4	16.1	6.6	20.3	8.9	5.2	5.5	4.5	8.4	10.1	7.4	1.1	13.3	6.5	2.5	10.6	14.8	9.6	9.5	4.5	10.2
FUT2	2.6	0.0	0.3	10.5	17.3	0.5	0.1	6.5	0.1	0.5	0.0	0.3	0.2	0.3	0.4	0.1	0.6	5.7	1.7	8.7	0.2	11.2	0.3	2.6
GABBR1	5.1	5.6	71.2	2.1	1.9	13.0	5.4	6.9	4.3	2.5	0.5	6.7	5.4	6.8	0.6	3.7	9.0	2.0	9.1	3.1	14.5	2.6	3.5	4.1
GALNT10	9.5	7.7	5.7	10.1	7.7	4.9	5.5	12.5	3.9	5.4	0.8	9.5	5.6	33.4	1.1	2.8	5.4	3.3	2.9	7.2	9.2	11.9	4.1	8.4
HLA_F	15.8	7.3	1.7	10.9	12.3	5.7	6.1	7.8	3.0	2.9	2.1	14.3	20.5	2.6	0.4	2.8	3.9	5.2	7.6	14.2	30.7	11.5	2.2	7.7
HLA_G	4.6	3.5	1.3	14.0	3.1	2.6	2.4	2.6	1.3	1.4	1.2	8.3	6.8	1.1	0.3	29.3	1.0	1.0	3.4	2.9	9.5	2.2	2.0	2.4
HMP19	1.5	0.0	115.0	1.7	1.1	0.0	0.4	0.1	0.1	0.2	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	1.9	0.0	1.8	2.7	0.0
HNF4G	1.4	0.0	0.2	10.4	45.9	0.2	0.1	6.8	0.0	7.8	2.8	0.1	0.0	0.0	0.6	0.0	0.3	0.1	0.0	54.2	0.0	3.2	1.4	0.5
IL1A	0.5	0.2	0.5	0.1	0.0	1.9	0.0	1.1	0.0	0.0	0.0	0.8	0.1	0.0	0.0	0.5	0.0	0.0	0.2	0.0	0.1	0.0	5.2	2.1
IL23R	0.2	0.0	0.0	0.3	0.2	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.6	0.2
IL6	6.8	4.9	0.5	0.3	0.3	0.9	1.9	7.8	0.9	0.3	1.4	4.3	1.4	0.0	0.6	1.5	2.4	0.0	0.0	0.2	0.8	0.2	0.2	10.7

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Appendix P(cont.)

MOG	0.0	0.0	52.1	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
NOD2	2.4	3.2	0.1	0.3	0.4	0.2	0.1	0.6	0.1	0.1	0.1	1.0	1.0	0.1	0.0	0.4	0.2	0.5	2.3	0.3	1.1	0.4	0.3	0.7
OSR1	1.3	0.0	0.2	2.2	0.5	5.3	2.8	3.1	2.6	0.3	0.0	2.8	0.2	1.1	0.2	1.8	3.1	5.4	1.1	0.9	0.1	0.9	3.1	4.4
PPP1R11	32.3	18.0	40.2	35.4	43.8	39.6	21.2	36.4	25.8	30.3	19.0	37.4	31.1	31.3	8.3	31.7	35.7	18.5	19.0	46.0	28.0	35.2	30.5	32.1
PSOR1C1 (C6orf16)	0.1	0.0	0.1	0.5	0.4	0.1	0.1	0.3	0.1	0.1	0.0	0.3	0.0	0.1	0.0	0.3	0.1	0.0	0.9	0.4	0.0	0.7	11.6	0.1
RALGAPA2	2.5	5.1	1.4	4.9	3.3	2.8	5.6	5.1	1.4	3.3	2.8	5.7	2.2	1.8	0.9	6.4	3.8	2.2	4.2	3.4	1.4	5.3	3.6	5.6
SLC41A2	1.8	0.0	1.8	4.1	5.7	0.8	1.6	3.4	0.3	1.5	11.2	1.1	0.8	1.0	0.7	0.8	0.7	1.1	0.2	5.0	0.6	5.6	1.9	0.9
SLC44A4	12.9	0.6	0.1	98.0	60.1	5.8	0.4	44.7	0.0	19.9	0.0	11.6	0.2	1.3	1.3	3.1	69.0	1.8	0.1	48.0	1.4	72.0	0.3	20.9
SMARCA2	13.0	8.9	24.7	12.5	6.4	16.1	22.7	17.3	9.9	17.8	12.9	17.3	16.2	42.3	2.7	18.6	16.6	7.4	17.3	9.2	16.2	10.0	29.1	13.6
STX8	5.3	6.2	7.2	6.1	4.8	6.4	9.6	6.8	6.9	7.0	5.2	5.4	6.4	7.1	2.1	6.0	7.0	4.3	5.1	5.2	6.1	5.4	14.5	8.2
TFCP2L1	1.0	0.1	0.5	11.8	0.3	0.3	0.1	2.0	0.0	25.0	0.0	2.0	0.1	0.0	0.8	5.0	3.2	24.0	2.5	0.2	0.6	5.2	0.9	1.5
TTLL7	0.9	0.0	17.7	1.1	1.1	2.3	2.7	3.0	1.2	0.4	0.4	2.3	0.3	0.5	0.6	0.1	3.5	0.8	0.3	1.2	0.4	1.2	2.9	2.1
ZNRD1	10.8	7.5	3.2	8.4	8.6	8.5	5.1	7.2	4.3	6.4	3.5	6.3	12.3	8.0	1.6	5.9	6.5	3.0	5.9	7.9	8.8	7.8	9.6	8.7

APPENDIX R. GENES WITH GENETIC DIVERSITY, ALLELE FREQUENCY SPECTRUM, DIVERGENCE, AND SELECTION PROFILES UNIQUE TO EAST ASIANS.

Gene	**AFR_EAS Dxy**	**AFR_EAS Hst**	**AFR_EAS Fst**	**Pi/Fst**	**Pi/Dxy**	**HD**	**θk**	**Pi**	**θW**	**TD**	**FLD**	**FLF**	**XP-EHH CHB-CEU**	**XP-EHH CHB-YRI**	**iHS[a]**	**DoS**	**Tissue of Major Expression**
DTL	0.000599	0.009907	0.090997	0.004396	0.667487	0.97	30.97	0.0004	64.73	-1.52	-9.65	-5.5	0.35	0.43	2.29	0	testis,bone marrow
EBF2	0.001048	0.000128	0.217973	0.003211	0.667933	1	135.43	0.0007	217.42	-1.11	-10.45	-5.3	0.94	1.63	2.40	1	fat, heart
ERAP1	0.001211	0.005824	0.038666	0.028448	0.908136	0.97	57.39	0.0011	58.06	-0.03	-5.62	-2.64	0.38	0.54	1.25	-0.35	fat, duodenum, small intestine
FUT2	0.001902	0.041069	0.359038	0.001114	0.210317	0.88	4.26	0.0004	13.75	-1.93	-6.39	-4.8	0.23	0.89	1.00	-0.5	duodenum, colon, stomach, small intestine
GABBR1	0.000756	0.013101	0.028219	0.02835	1.057804	0.94	25.63	0.0008	36.44	-0.86	-4.06	-2.56	0.12	0.16	0.95	-0.2	brain, spleen, endometrium

(cont. on the next page)

GALNT10	0.001374	9.66E-05	0.280904	0.002492	0.509455	1	162.96	0.0007	250.25	-1.03	-9.56	-4.83	1.23	1.18	2.09	1	ubiquitous
HLA-F	0.002536	0.0302	0.042484	0.051785	0.867652	0.81	8.47	0.0022	6.94	0.59	-2.66	-1.41	0.10	0.40	0.86	-0.14	spleen, lymph node,appendix, small intestine
HLA-G	0.006016	0.042407	0.031991	0.171924	0.914281	0.8	22.6	0.0055	13.21	1.98	-1.66	0.34	0.03	0.63	2.43	0.37	placenta, colon, spleen
HMP19	0.000663	0.00705	0.291472	0.000686	0.301583	0.98	9.99	0.0002	60.33	-2.43	-10.29	-6.44	0.06	1.10	1.97	0.52	brain, adrenal, small intestine
HNF4G	0.001358	0.035201	0.329219	0.002734	0.662785	0.88	25.21	0.0009	31.23	-0.55	-9.89	-5.3	0.55	0.59	1.18	1	small intestine, duodenum, colon
IL1A	0.001228	0.110406	0.331057	0.002114	0.569922	0.57	8.09	0.0007	9.61	-0.43	-6.45	-4.1	0.58	1.60	1.05		testis, esophagus, endometrium
IL23R	0.000944	0.001069	0.153596	0.003906	0.635414	1	74.9	0.0006	113.85	-1	-11.43	-5.77	0.16	1.24	1.40	0	adrenal, testis, colon
IL6	0.00093	0.124863	0.315357	0.000951	0.322558	0.5	1.53	0.0003	6.94	-2.07	-4.63	-4.1	0.33	1.04	1.70	0	urinary bladder, gall bladder

(cont. on the next page)

Appendix R(cont.)

MOG	0.001183	0.028672	0.111341	0.005389	0.507002	0.86	9.16	0.0006	24.69	-1.8	-8.51	-5.57				0	brain
NOD2	0.000575	0.031204	0.142952	0.002099	0.521379	0.88	12.18	0.0003	42.84	-2.07	-11.73	-7.04	0.75	1.65	3.13	-0.02	bone marrow, appendix,skin, esophagus
OSR1	0.00035	0.170349	0.319798	0.000313	0.285959	0.44	0.48	0.0001	4.4	-2.25	-9.61	-7.66	—	—	—	0	endometrium, salivary gland, urinary bladder
PPP1R11	0.000916	0.068041	0.068565	0.010209	0.763887	0.62	2.16	0.0007	4.4	-1.29	-1.38	-1.65	—	—	—	0	ubiquitous
PSORS1C1	0.00404	0.013194	0.03885	0.102961	0.990202	0.97	101.02	0.004	75.68	0.98	-0.76	0.33	0.07	0.09	0.73	-0.17	testis, skin, small intestine, stomach
RALGAPA2	0.000411	7.59E-05	0.054594	0.007327	0.97325	1	113.86	0.0004	260.66	-1.66	-13.06	-6.78	0.28	0.52	2.84	-0.16	thyroid
RNF39	0.002171	0.042686	0.044244	0.042943	0.874986	0.84	10.65	0.0019	11.88	-0.29	-1.53	-1.06	—	—		0	ubiquitous

(cont. on the next page)

Appendix R(cont.)

SLC41A2	0.000833	0.001353	0.058252	0.013733	0.959934	1	120.88	0.0008	148.28	-0.54	-10.17	-4.84	0.37	0.60	1.42	0.5	liver, duodenum, stomach, small intestine, colon
SLC44A4	0.001149	0.022032	0.041402	0.026569	0.957055	0.94	16.72	0.0011	20.82	-0.56	-4.38	-2.67	0.47	1.01	0.74	-0.6	colon, stomach, prostate, duodenum
SMARCA2	0.001359	9.86E-06	0.131913	0.007581	0.735946	1	177.36	0.001	241.44	-0.78	-11.9	-5.68	0.11	0.58	1.43	-0.5	ovary, testis, brain, fat
STX8	0.001228	8.44E-07	0.180507	0.003878	0.570187	1	217.81	0.0007	376.38	-1.24	-11.57	-5.81	0.69	0.96	1.79	-0.5	ubiquitous
TFCP2L1	0.000921	0.00132	0.080501	0.008696	0.759914	0.33	49.23	0.0007	71	-0.89	-10.39	-5.38	0.58	0.58	1.29	0	kidney, salivary gland, thyroid, colon
TSBP1	0.002838	0.004326	0.067565	0.039961	0.95149	0.99	215.55	0.0027	144.55	1.44	-0.19	0.93	—	—	—	0	testis
TTLL7	0.000539	0.002317	0.03903	0.010248	0.741978	0.99	56.74	0.0004	116.65	-1.51	-9.93	-5.45	0.30	0.39	1.11	0	ubiquitous

(cont. on the next page)

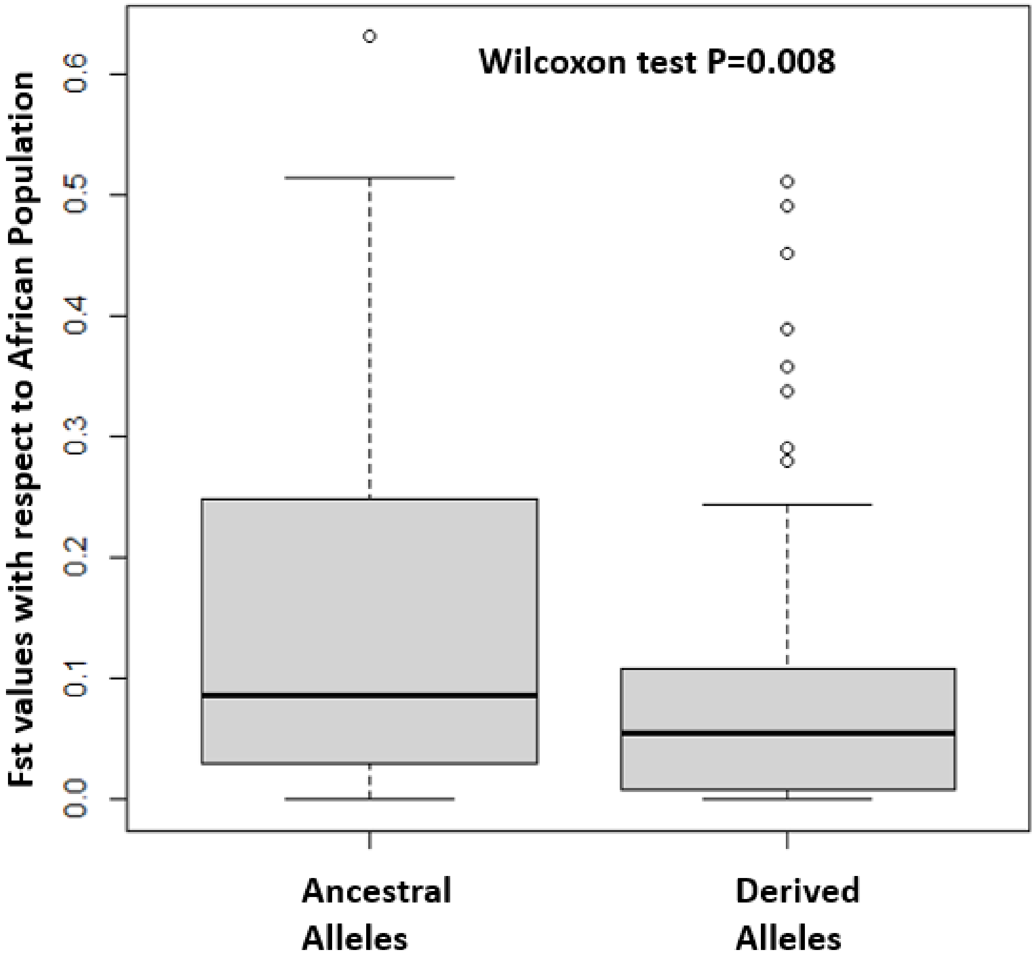
Appendix R(cont.)

ZNRD1	0.001421	0.030067	0.043799	0.027398	0.844585	0.81	4.43	0.0012	7.07	-1	-0.67	-1	—	—	—	—	ubiquitous
GAS2	0.001368	0.00037	0.195045	0.004614	0.65786	1	129.32	0.0009	154.69	-0.48	-9.7	-4.59	0.41	1.95	1.76	0	Liver, small intestine, stomach
LYST	0.000832	0.000577	0.401948	0.000498	0.240282	1	38.18	0.0002	167.77	-2.27	-13.74	-7.58	1.18	2.10	2.06	0	Bone marrow, spleen, lymph node
NAV2	0.001279	0	0.161659	0.005567	0.703646	1	664.45	0.0009	875.55	-0.71	-10.54	-4.95	0.27	2.00	2.25	-0.41	ubiquitous
CTNNA2	0.001158	0	0.136864	0.005845	0.690893	1	955.57	0.0008	1298.64	-0.78	-9.7	-4.63	0.79	1.59	2.47	0	Brain
KCNK9	0.00116	0.000199	0.125034	0.006398	0.689391	1	82.86	0.0008	123.99	-0.97	-12.62	-6.26	0.49	1.40	3.46	0	Brain, adrenal, Duodenum
SEMA6D	0.001035	3.82E-06	0.158692	0.005041	0.772743	1	471.63	0.0008	623.29	-0.72	-10.41	-4.91	0.10	1.25	2.08	-0.17	Small intestine, duodenum
UBAC2	0.000661	0.000535	0.099261	0.006045	0.908019	1	110.54	0.0006	187.66	-1.21	-10.66	-5.47	0.11	0.41	1.94	0.33	ubiquitous
UBASH3B	0.001166	5.42E-05	0.124635	0.007221	0.771652	1	141.49	0.0009	176.71	-0.59	-8.72	-4.21	0.60	1.24	2.05	-0.2	spleen, lymph node,bone marrow

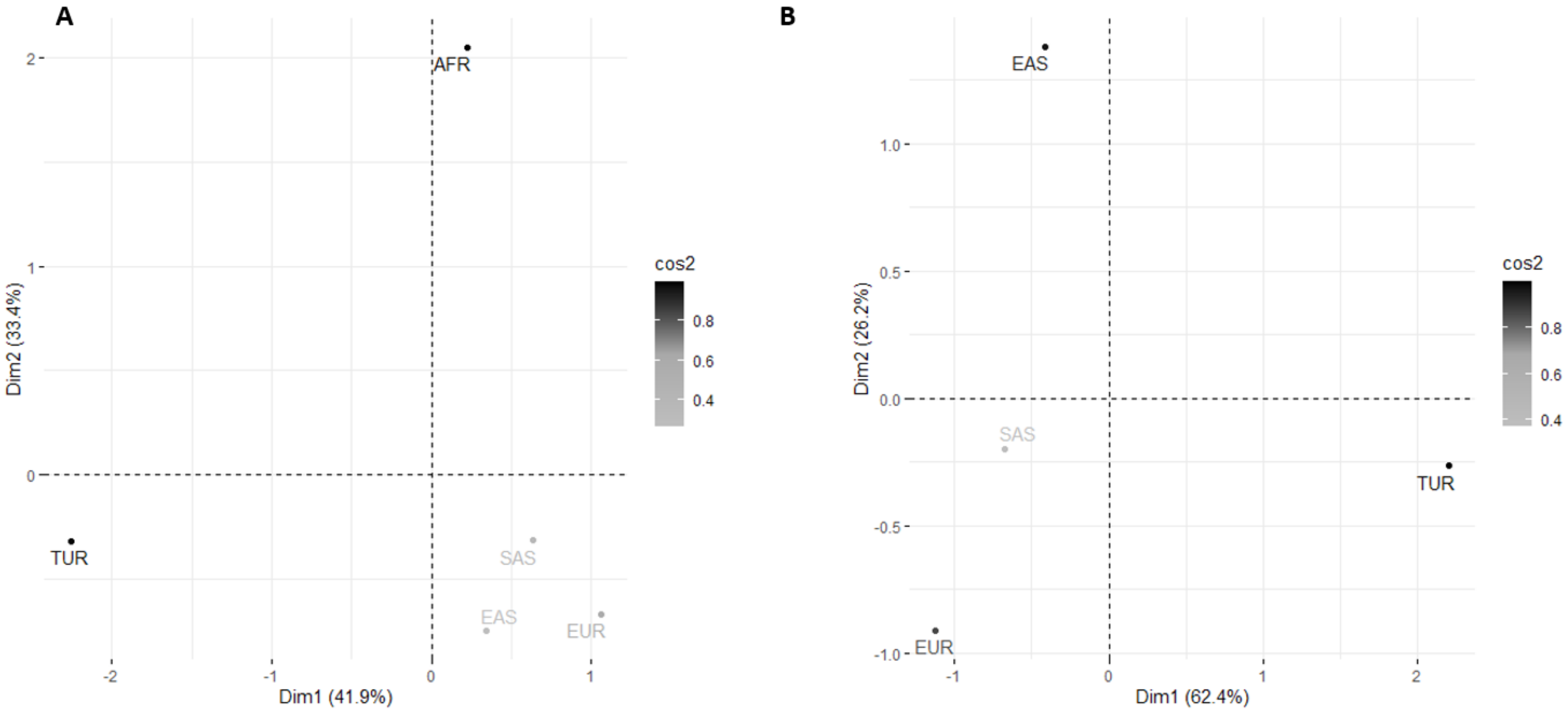
HD: Haplotype diversity; θ_k:Theta-K; θ_W:Theta-Watterson; TD:Tajima's D; FLD: Fu-Li’s D; FLF: Fu-Li’s F; Fst: fixation index, Dxy: average number of nucleotide substitutions per site between two populations; Hst: haplotype diversity based differentiation; XP-EHH: Cross population extended haplotype homozygosity; iHS: Integrated haplotype score; DoS: Direction of Selection

a. Highest iHS value is reported.

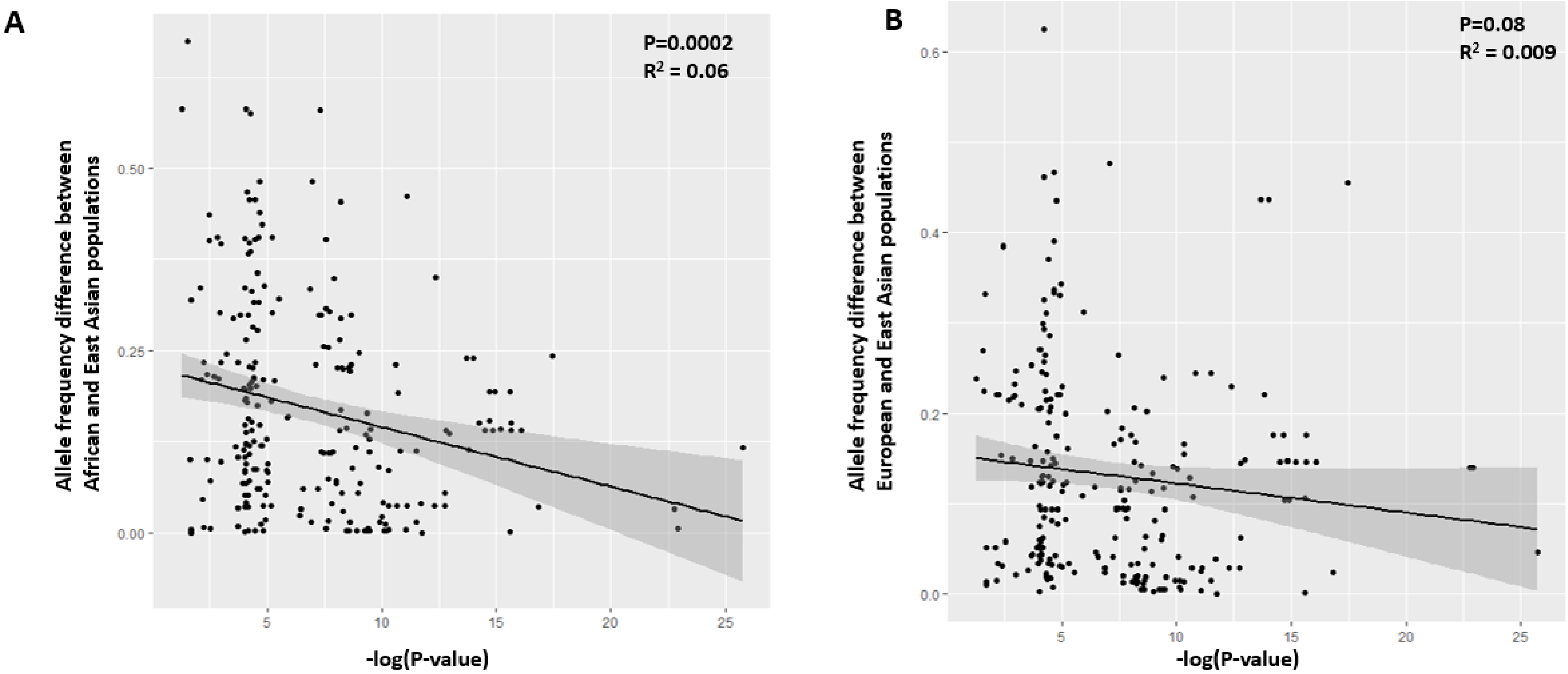
APPENDIX S


Wilcoxon test P=0.008
Fst values with respect to African Population
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Ancestral Alleles
Derived Alleles

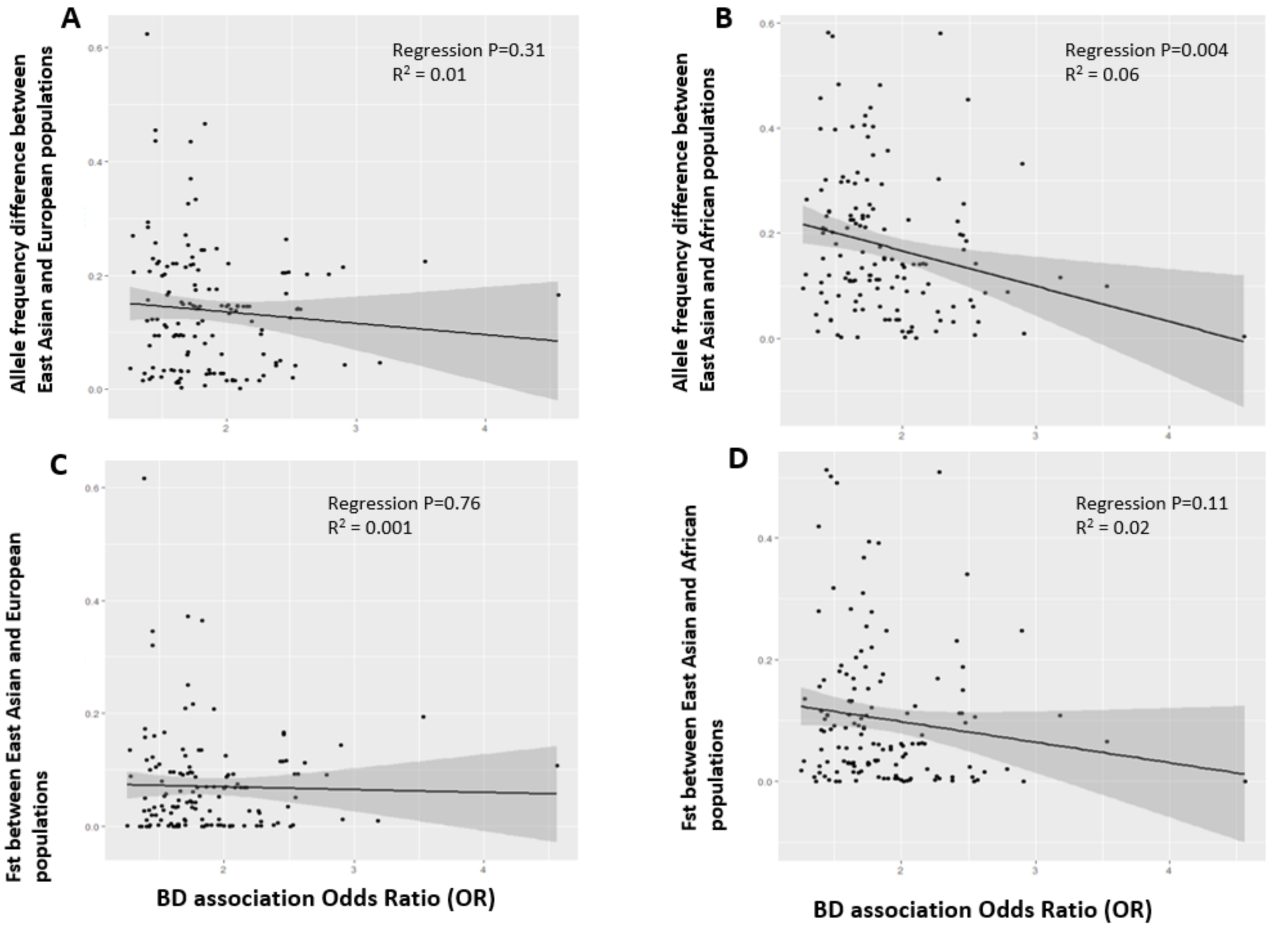
APPENDIX T


A
AFR
TUR
SAS
EAS
EUR
Dim1 (41.9%)
Dim2 (33.4%)
-2
-1
0
1
2
cos2
0.8
0.6
0.4
B
EAS
SAS
TUR
EUR
Dim1 (62.4%)
Dim2 (26.2%)
1.0
0.5
0.0
-0.5
-1.0
-1
0
1
2
cos2
0.8
0.6
0.4

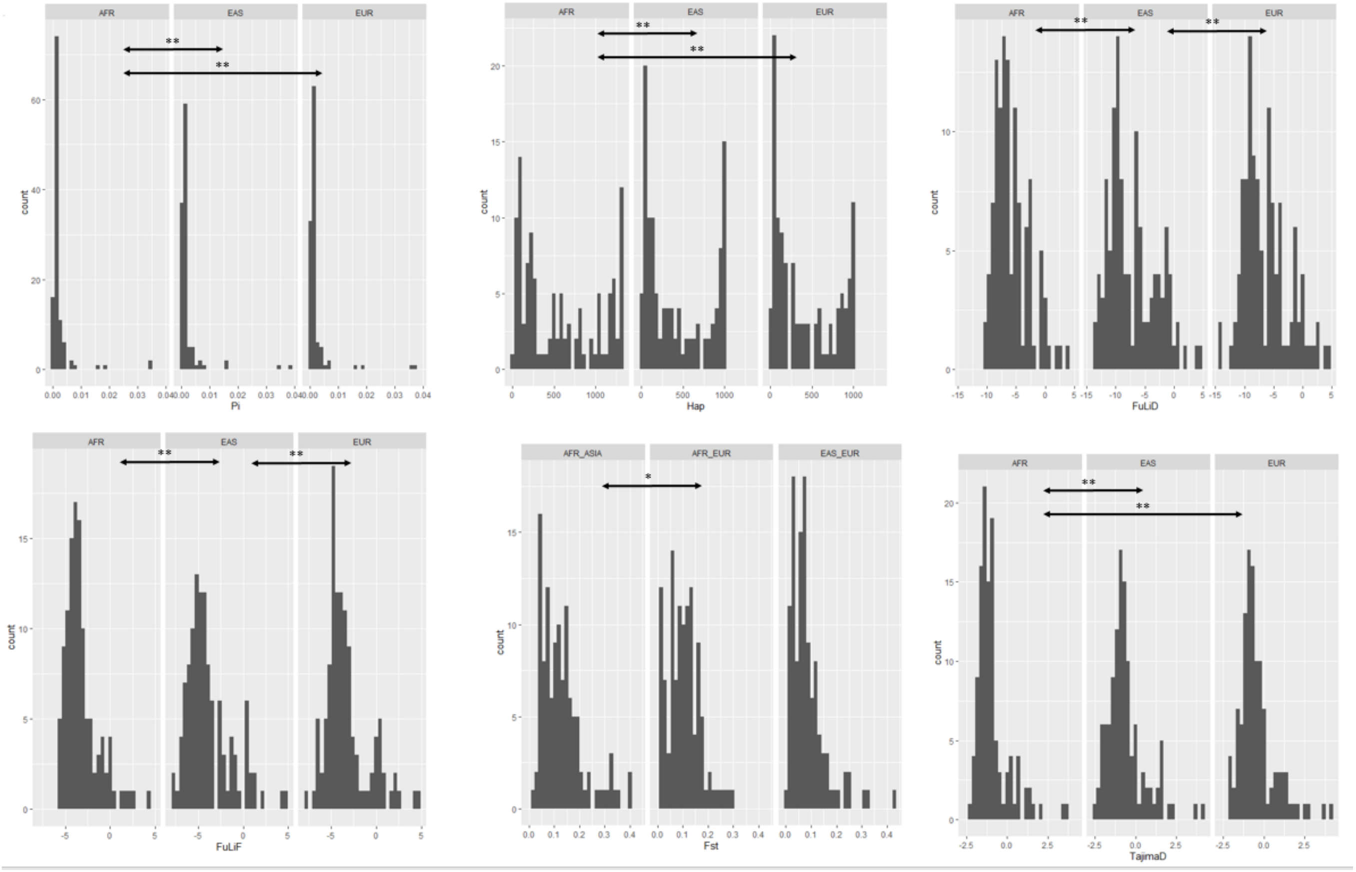
APPENDIX U


A
P=0.0002
$R^2 = 0.06$
Allele frequency difference between African and East Asian populations
0.00
0.25
0.50
5
10
15
20
25
-log(P-value)
B
P=0.08
$R^2 = 0.009$
Allele frequency difference between European and East Asian populations
0.0
0.2
0.4
0.6
5
10
15
20
25
-log(P-value)

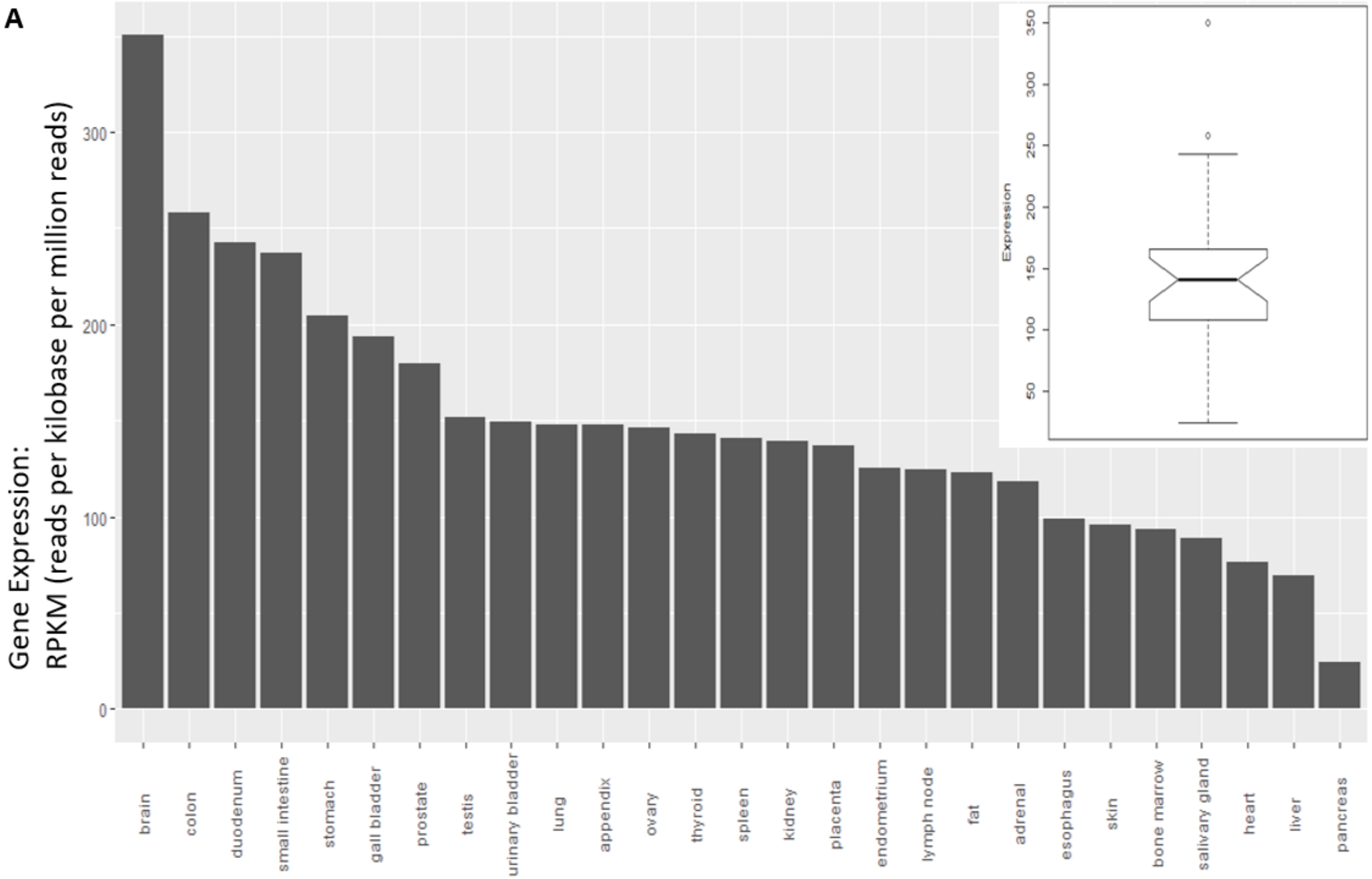
APPENDIX V


A
Regression P=0.31
R^2 = 0.01
Allele frequency difference between East Asian and European populations
0.0
0.2
0.4
0.6
2
3
4
B
Regression P=0.004
R^2 = 0.06
Allele frequency difference between East Asian and African populations
0.0
0.2
0.4
0.6
2
3
4
C
Regression P=0.76
R^2 = 0.001
Fst between East Asian and European populations
0.0
0.2
0.4
0.6
2
3
4
BD association Odds Ratio (OR)
D
Regression P=0.11
R^2 = 0.02
Fst between East Asian and African populations
0.0
0.2
0.4
2
3
4
BD association Odds Ratio (OR)

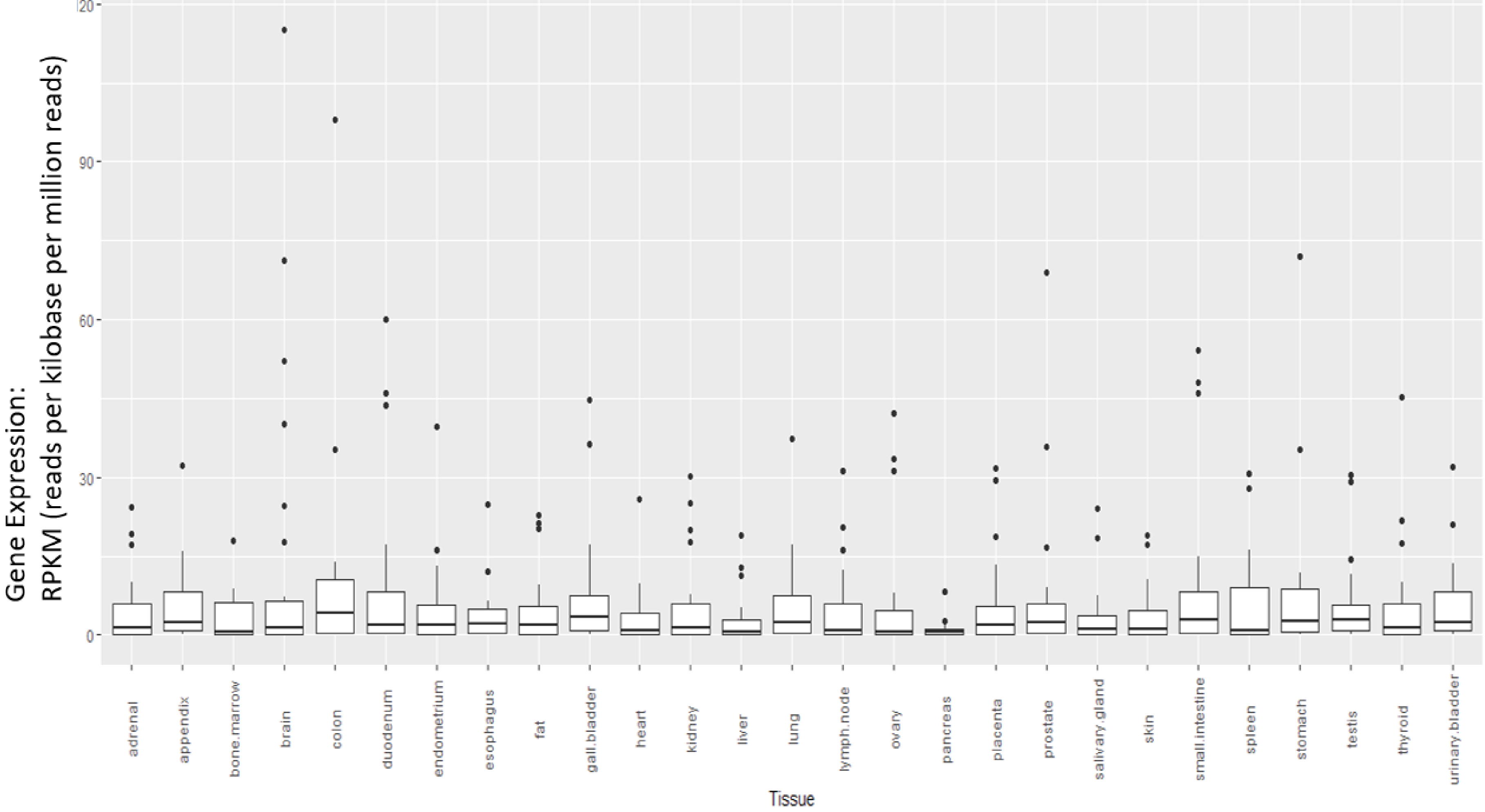
APPENDIX Y


AFR
EAS
EUR
**
**
count
Pi
0.00
0.01
0.02
0.03
0.04
AFR
EAS
EUR
**
**
count
Hap
0
500
1000
AFR
EAS
EUR
**
**
count
FuLiD
-15
-10
-5
0
5
AFR
EAS
EUR
**
**
count
FuLiF
-5
0
5
AFR_ASIA
AFR_EUR
EAS_EUR
*
count
Fst
0.0
0.1
0.2
0.3
0.4
AFR
EAS
EUR
**
**
count
TajimaD
-2.5
0.0
2.5

APPENDIX Z


A
Gene Expression:
RPKM (reads per kilobase per million reads)
0
100
200
300
brain
colon
duodenum
small intestine
stomach
gall bladder
prostate
testis
urinary bladder
lung
appendix
ovary
thyroid
spleen
kidney
placenta
endometrium
lymph node
fat
adrenal
esophagus
skin
bone marrow
salivary gland
heart
liver
pancreas
Expression
50
100
150
200
250
300
350

B


Gene Expression:
RPKM (reads per kilobase per million reads)
120
90
60
30
0
adrenal
appendix
bone.marrow
brain
colon
duodenum
endometrium
esophagus
fat
gall.bladder
heart
kidney
liver
lung
lymph.node
ovary
pancreas
placenta
prostate
salivary.gland
skin
small.intestine
spleen
stomach
testis
thyroid
urinary.bladder
Tissue