



HIGH-RESOLUTION CHARACTERIZATION OF HLA CLASS I AND CLASS II DIVERSITY IN SARASWAT BRAHMIN AND SINDHI POPULATIONS OF JAIPUR, RAJASTHAN

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Abstract

Background: The human leukocyte antigen (HLA) system is one of the most genetically varied segments of the human genome and plays a pivotal role in the regulation of the immune system, susceptibility to diseases, and success of hematopoietic stem cell or solid organ transplantation. Given the pronounced genetic diversity within the Indian population, acquiring high-resolution, population-specific HLA data is crucial.

Methods: High-resolution next-generation sequencing based HLA typing was performed for six classical loci (HLA-A, -B, -C, -DRB1, -DQB1, and -DPB1) in 296 healthy, unrelated individuals from two North Indian populations: Saraswat Brahmins (n = 148) and Sindhis (n = 148). Allele and haplotype frequencies, Hardy-Weinberg equilibrium (HWE), linkage disequilibrium (LD), and haplotypic associations were analyzed using established statistical methods.

Results: Extensive allelic diversity was observed across all loci in both populations, with HLA-B being the most polymorphic. High heterozygosity was maintained across class I and class II loci, whereas HLA-DPB1 showed comparatively higher homozygosity. A strong and consistent LD was observed between HLA-DRB1 and HLA-DQB1 in both populations of this study. Population-specific enrichment of alleles and haplotypes was evident, particularly for HLA-B and HLA-DPB1 genes. The Sindhi population demonstrated greater HLA-DPB1 allelic diversity, whereas the Saraswat Brahmin population showed stronger overall haplotypic conservation than the Sindhi population.

Conclusion: This study provides comprehensive four-field resolution HLA data for two distinct North Indian populations, highlighting both had population-specific genetic structures. These findings are relevant to transplantation immunogenetics, donor registry optimization, and population genetics research in India.

Keywords: HLA polymorphism; Next-generation sequencing; Saraswat Brahmin; Sindhi; North Indian populations; Transplantation immunogenetics; High-resolution HLA typing; Human Leukocyte Antigen; Allele frequency; India

1. Introduction

The human leukocyte antigen (HLA) region, a major histocompatibility complex present on chromosome 6 at 6p21.3 locus. HLA region is the most polymorphic region of the human genome and is critical for antigen presentation and immune regulation ^[1]. Variation within HLA genes influences susceptibility to infectious diseases, autoimmune disorders, malignancies, drug hypersensitivity reactions, and the outcomes of solid-organ and hematopoietic stem cell transplantation ^[2]. HLA allele and haplotype distributions vary substantially across populations as evolutionary selection, founder effects, migration, and long-standing endogamy. Consequently, population-specific HLA frequency data are essential for improving transplant matching strategies and advancing disease association and anthropological genetic studies ^[3]. India, the second largest populated country in the world, also called sub-continent, harbors exceptional genetic diversity, shaped by ancient migrations and rigid sociocultural practices. However, many previous Indian HLA studies have relied on serological or low-resolution typing, which limits their clinical applicability ^[4,5]. Advances in next-generation sequencing (NGS) now allow unambiguous three/ four-field HLA typing, enabling the precise characterization of both common and rare alleles. The present study applied high-resolution NGS-based HLA typing to characterize class I and class II diversity in the Saraswat Brahmin and Sindhi populations from Jaipur, Rajasthan.

2. Materials and Methods

2.1 Study Population

A total of 296 healthy, unrelated adult individuals were enrolled, including 148 Saraswat Brahmins and 148 Sindhis. Participants were recruited between 2022 and 2025 at Mahatma Gandhi Medical College and Hospital (MGMCH), Jaipur Rajasthan. Written informed consent was obtained from all participants prior to enrollment. The study was approved by the Institutional Ethics Committee of MGMCH. Individuals with known diseases, recent blood transfusion or transplantation, pregnancy, or incomplete consent were excluded.

2.2 DNA Extraction and HLA Typing

Peripheral blood (2-3 mL) samples were collected in EDTA vacutainer tubes (purple top). Genomic DNA was extracted using the QIAamp DNA Blood Mini Kit (Qiagen, Hilden, Germany), following the manufacturer's instructions. DNA concentration was assessed using a Qubit™ 4.0 Fluorometer with the Qubit™ dsDNA High Sensitivity Assay Kit (Thermo Fisher Scientific, Waltham, MA, USA). Samples meeting predefined laboratory quality criteria were processed for downstream analysis. High-resolution HLA typing was performed using the NGSgo® MX 6-1 HLA Typing Kit (GenDx, Utrecht, Netherlands). Libraries were prepared through locus-specific amplification, enzymatic fragmentation, adapter ligation and indexing. Sequencing was performed using the Illumina iSeq 100 platform (Illumina Inc., San Diego, CA, USA). Allele assignment and ambiguity resolution were performed using NGSengine® software (GenDx, Utrecht, Netherlands) with reference to the IPD-IMGT/HLA database (release 3.62 /2025-10).

2.3 Statistical Analysis

Allele and haplotype frequencies were calculated for each locus. Hardy-Weinberg equilibrium, linkage disequilibrium, and haplotypic associations were evaluated using the HLA.Net web application (<https://hla-net.eu/tools/basic-statistics/>) ^[6]. Statistical significance was assessed using permutation-based and asymptotic tests where appropriate, with a two-tailed significance threshold of $p < 0.05$.

3. Results

3.1 Demographic Characteristics

The demographic distribution of the study population is summarized in Table 1. The Saraswat Brahmin cohort comprised 85 men (57.4%) and 63 women (42.6%), whereas the Sindhi cohort included 90 men (60.8%) and 58 women (39.2%).

3.2 Homozygosity and Heterozygosity

HLA class I and class II loci homozygosity and heterozygosity estimates are presented in Table 2. High heterozygosity was observed at all loci in both populations. Among class I loci, HLA-C showed the highest heterozygosity, whereas HLA-DPB1 exhibited comparatively higher homozygosity than other loci. Despite this, heterozygosity predominated at all loci, reflecting a substantial genetic diversity.

3.3 Allelic Diversity

The total number of distinct alleles identified at each locus is listed in Table 3. A total of 44-62 alleles were observed across class I loci and 31-51 across class II loci, with HLA-B being the most polymorphic locus in both populations. Notably, HLA-DPB1 showed greater allelic diversity in the Sindhi population, whereas other class II loci displayed comparable diversity between groups. Detailed allele frequencies list provided in Tables 8-13 (Supplementary data)

3.4 Linkage Disequilibrium

The pairwise linkage disequilibrium analysis between the HLA loci is detailed in Chart 1. Strong and consistent LD was observed between HLA-DRB1 and HLA-DQB1 in both populations. Several extended haplotypes involving class I and class II loci also demonstrated significant LD. Overall, the Saraswat Brahmin population showed a higher proportion of significant LD pairs, suggesting greater haplotypic conservation, whereas the Sindhi population exhibited relatively weaker LD, consistent with a higher degree of admixture.

3.5 Haplotype Analysis

The most frequent six-locus HLA haplotypes identified in the Saraswat Brahmin and Sindhi populations are shown in Tables 4 and 5, respectively. The observed and expected frequencies of common two-locus haplotypes, along with standardized residuals (StdRes), are provided in Tables 6 (Saraswat Brahmins) and 7 (Sindhis). The observed and expected frequencies of common two-locus haplotypes, along with standardized residuals, are provided in Tables 6 (Saraswat Brahmins) and 7 (Sindhis).

Extensive six-locus haplotypic diversity was observed in both populations. A small number of haplotypes occurred at relatively high frequencies, whereas the majority were rare. Population-specific differences in the distribution and frequency of common haplotypes were evident, particularly for HLA-B and HLA-DPB1.

4. DISCUSSION

4.1 Overview and significance of the study

The present investigation provides a comprehensive high-resolution characterization of HLA class I (HLA-A, -B, -C) and class II (HLA-DRB1, -DQB1, -DPB1) diversity in the Saraswat Brahmin and Sindhi populations of Jaipur, Rajasthan. By employing next-generation sequencing based typing at three-field resolution, this study addresses a major gap in Indian immunogenetic literature, where many earlier studies relied on serology or low-resolution molecular methods. Given India's exceptional genetic heterogeneity and long-standing endogamous population structure, population-specific HLA datasets are essential for accurate disease association studies, transplantation matching, and evolutionary inference.

The findings demonstrate extensive allelic and haplotypic diversity, strong linkage disequilibrium within the HLA region, and clear genetic differentiation between the two populations despite

geographic proximity. These observations reinforce the concept that Indian populations cannot be treated as genetically homogeneous entities and highlight the clinical and anthropological importance of fine-scale immunogenetic mapping.

4.2 HLA heterozygosity and balancing selection

4.2.1 High heterozygosity across loci

Both Saraswat Brahmin and Sindhi populations exhibited very high heterozygosity across all classical HLA loci, particularly HLA-B, HLA-C, and HLA-DRB1. This pattern is consistent with the global hallmark of HLA diversity and reflects strong balancing selection acting on antigen-presenting genes. Numerous studies have demonstrated that heterozygosity at HLA loci confers a selective advantage by broadening the repertoire of peptides presented to T cells, thereby enhancing resistance to diverse pathogens.

Theoretical and empirical work has repeatedly shown that pathogen-mediated selection, including heterozygote advantage and frequency-dependent selection, is the primary evolutionary force maintaining HLA polymorphism worldwide^[7,8].

Indian population studies using NGS approaches report similarly high heterozygosity values, with HLA-B consistently emerging as the most polymorphic locus^[9]. The present study corroborates these findings while demonstrating that endogamy has not resulted in substantial loss of immunogenetic diversity at the population level.

4.2.2 HLA-DPB1: reduced heterozygosity but preserved diversity

HLA-DPB1 showed relatively higher homozygosity compared with other loci in both populations. This observation aligns with multiple global studies indicating weaker balancing selection at DPB1, higher recombination rates, and distinct evolutionary dynamics compared with DRB1–DQB1^[10].

Despite this, DPB1 retained substantial allelic diversity, particularly in the Sindhi population. This finding is clinically relevant, as DPB1 mismatches are now recognized to significantly influence haematopoietic stem cell transplantation outcomes, challenging earlier assumptions that DPB1 was of secondary importance^[11].

4.3 Allelic distributions in Indian and global context

4.3.1 HLA-A locus

The predominance of A01:01 and A11:01 in both populations mirrors findings from North Indian, Gujarati, Maharashtrian, and South Indian populations, as well as DKMS registry data from Indian donors^[12].

Globally, A11:01 is frequent across South and East Asia, whereas A01:01 is common in West Eurasian populations, suggesting historical admixture and shared ancestry across Eurasia. However, the enrichment of A26:01 and A32:01 in Saraswat Brahmins and A*68 lineage alleles in Sindhis indicates population-specific drift or founder effects, likely reinforced by strict endogamous marriage practices. Comparable patterns of allele enrichment have been reported in tribal and caste-based Indian populations, where unique allelic signatures persist despite broader regional similarities^[13].

4.3.2 HLA-B locus: extreme polymorphism

HLA-B emerged as the most polymorphic locus in both populations, consistent with virtually all Indian and global HLA studies. This extreme polymorphism is thought to reflect intense historical pathogen pressure, particularly from viral infections, where HLA-B molecules play a dominant role in CD8⁺ T-cell responses^[12].

The high frequency of B*51:01 in the Sindhi population is noteworthy. This allele has been reported at elevated frequencies in several Indian, Middle Eastern, and Mediterranean populations and is strongly associated with Behçet's disease^[14].

4.3.3 HLA-C locus and NK cell regulation

Distinct allele dominance at HLA-C (C06:02 in Saraswat Brahmins and C07:02 in Sindhis) parallels findings from Indian donor registries and regional studies. HLA-C molecules serve not only as classical antigen-presenting molecules but also as key ligands for killer immunoglobulin-like receptors (KIRs) on NK cells, influencing innate immune responses and pregnancy outcomes. Population-specific variation in HLA-C frequencies has been shown to co-evolve with KIR gene distributions, shaping NK cell education and function ^[15].

4.4 Class II loci and disease-associated haplotypes

4.4.1 DRB1 and DQB1 allele distributions

The dominance of DRB107:01, DRB113:01, DRB115 lineage alleles and corresponding DQB1 partners reflects conserved Indian class II haplotypes reported across multiple populations. Large-scale Indian datasets consistently report DRB107:01 and DRB1*15:01 among the most frequent alleles nationwide ^[9].

However, the enrichment of DRB113:01 and DRB103:01 in Sindhis and DRB1*15:02 in Saraswat Brahmins indicates population-specific differentiation with potential clinical implications. DRB1-DQB1 haplotypes are strongly associated with autoimmune diseases such as type 1 diabetes, rheumatoid arthritis, and systemic lupus erythematosus, as well as infectious disease susceptibility. South Indian tribal studies have demonstrated similar enrichment of DRB115 and DRB110 lineages, suggesting that certain class II alleles may confer selective advantages in tropical pathogen environments ^[13].

4.5 Linkage disequilibrium and conserved haplotypes

4.5.1 Strong DRB1-DQB1 linkage disequilibrium

The strongest LD was consistently observed between DRB1 and DQB1 in both populations, reflecting tight physical linkage and low recombination rates. This pattern is universally observed across human populations and has been extensively documented in Indian, European, and East Asian datasets.

High standardized residuals for specific DRB1-DQB1 haplotypes indicate long-standing conservation, likely maintained by selection for optimal antigen-presenting combinations. Similar conserved haplotypes have been reported in DKMS Indian registry data and global populations ^[13].

4.5.2 Extended haplotypes and evolutionary stability

Evidence of extended haplotypes spanning class I and class II loci suggests the presence of ancestral chromosomal segments preserved over long evolutionary timescales. Such extended haplotypes have been described in multiple populations and are thought to arise from selective sweeps or historical bottlenecks ^[14].

The weaker LD involving HLA-C is consistent with higher recombination rates at this locus and supports previous observations from global HLA studies.

4.6 Implications for transplantation and precision medicine

The high allelic and haplotypic diversity observed in both populations poses challenges for identifying fully matched unrelated donors but also provides opportunities for improving registry design. Population-specific HLA frequency data can substantially enhance donor recruitment strategies and improve match probabilities for Indian patients.

The distinct haplotypic profiles of Saraswat Brahmin and Sindhi populations highlight the inadequacy of treating Indian donors as a single genetic pool. This has direct consequences for hematopoietic stem cell transplantation (HSCT) outcomes, particularly when considering extended matching including DPB1.

5. Conclusion

The present study provides high-resolution four-field HLA allele and haplotype frequency data for the Saraswat Brahmin and Sindhi populations from Jaipur. The findings revealed extensive polymorphism, strong class II linkage disequilibrium, and clear population-specific genetic signatures. These data represent a valuable resource for transplantation immunogenetics, donor registry development, and population genetics research in India.

Ethics Statement

The study was conducted in accordance with the institutional ethical guidelines, and written informed consent was obtained from all participants. Ethics committee number: MGMCH/ IEC/ JPR/ 2021/ 484.

Data Availability

Allele and haplotype frequency data are available from the corresponding author upon reasonable requests.

Conflict of Interest

The authors declare no conflicts of interest.

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Abbreviations

- **DNA** – Deoxyribonucleic Acid
- **dsDNA** – Double-stranded Deoxyribonucleic Acid
- **EDTA** – Ethylenediaminetetraacetic Acid
- **HLA** – Human Leukocyte Antigen
- **HLA-A** – Human Leukocyte Antigen-A
- **HLA-B** – Human Leukocyte Antigen-B
- **HLA-C** – Human Leukocyte Antigen-C
- **HLA-DPB1** – Human Leukocyte Antigen-DP Beta 1
- **HLA-DQB1** – Human Leukocyte Antigen-DQ Beta 1
- **HLA-DRB1** – Human Leukocyte Antigen-DR Beta 1
- **HWE** – Hardy–Weinberg Equilibrium
- **IMGT** – ImMunoGeneTics Project
- **IPD** – Immuno Polymorphism Database
- **LD** – Linkage Disequilibrium
- **NGS** – Next-Generation Sequencing
- **StdRes** – Standardized Residuals

Tables

Table-1 Gender distribution		
Gender	Saraswat Brahmin population (n=148)	Sindhi population (n=148)
Male	85 (57.4%)	90 (60.8%)
Female	63 (42.6%)	58 (39.2%)

Table 1. Demographic characteristics of the Saraswat Brahmin and Sindhi study populations.

Table-2 Homozygosity vs Heterozygosity				
Loci	Saraswat Brahmin population		Sindhi population	
	Homozygosity	Heterozygosity	Homozygous	Heterozygous
HLA-A	0.06630266	0.93369734	0.08360491	0.91639509
HLA-B	0.06714605	0.93285395	0.05863818	0.94136182
HLA-C	0.03767166	0.96232834	0.05769707	0.94230293
HLA-DRB1	0.06478611	0.93521389	0.07643982	0.92356018
HLA-DQB1	0.08681614	0.91318386	0.07943126	0.92056874
HLA-DPB1	0.14651792	0.85348208	0.12708414	0.87291586

Table 2. Homozygosity and heterozygosity estimate for HLA-A, -B, -C, -DRB1, -DQB1, and -DPB1 loci in the Saraswat Brahmin and Sindhi populations. The values represent the proportional frequencies calculated from high-resolution four-field HLA genotyping.

Table3: Total number of Haplotypes observed in the two population (n=296) (148 individuals each group)		
Loci	Saraswat Brahmin	Sindhi
HLA-A	44	40
HLA-B	62	57
HLA-C	36	39
HLA-DRB1	35	34
HLA-DQB1	31	33
HLA-DPB1	43	51

Table 3. Number of distinct alleles identified at each HLA locus in the Saraswat Brahmin and Sindhi populations. Allelic diversity was reported at a four-field resolution according to the IPD-IMGT/HLA database.

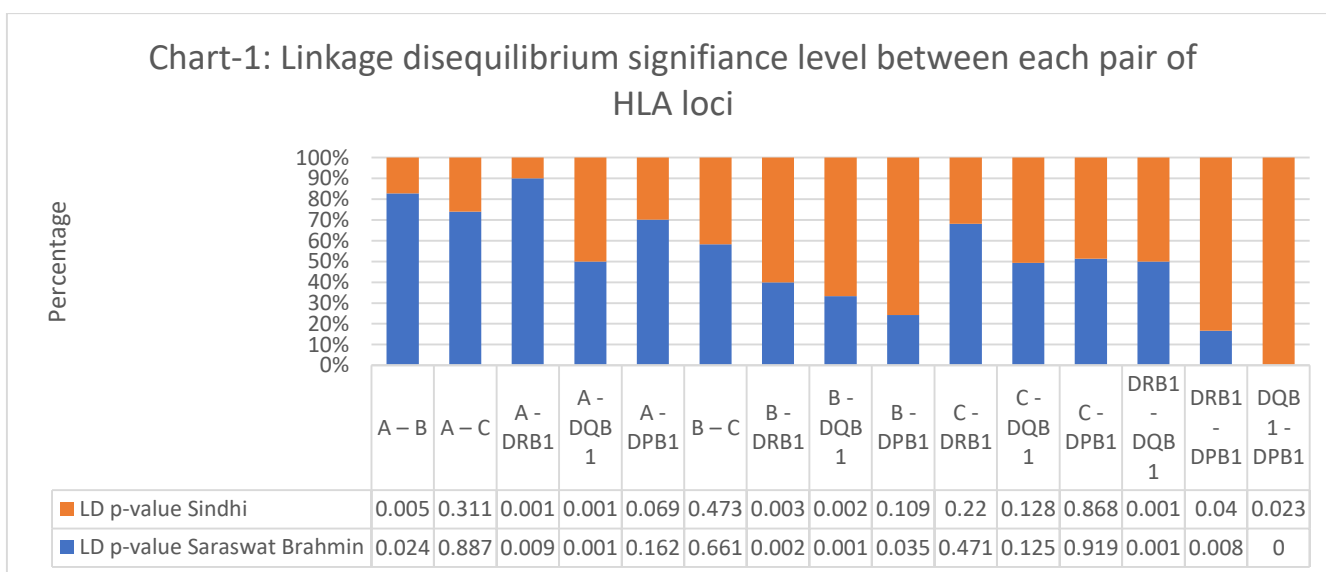


Chart 1: Pairwise linkage disequilibrium (LD) analysis among classical HLA class I and class II loci in the Saraswat Brahmin and Sindhi populations. Statistical significance was assessed using permutation-based P-values.

Table: 4 Saraswat Brahmin population Top-15 Haplotype with frequencies	frequency
A*24:02:01:04~B*18:01:01:02~C*12:03:01:01~DRB1*11:04:01:01~DQB1*03:01:01:02~DPB1*19:01:01:01	0.0169

A*33:01:01:01~B*14:02:01:01~C*08:02:01:01~DRB1*01:02:01:01~DQB1*05:01:01:01~DPB1*02:01:02:03	0.0169
A*02:11:01:01~B*40:06:01:02~C*15:02:01:01~DRB1*15:01:01:01~DQB1*06:01:01:01~DPB1*04:01:01:01	0.0135
A*32:01:01:01~B*18:01:01:02~C*02:02:02:01~DRB1*09:01:02:01~DQB1*03:02:01:01~DPB1*04:02:01:02	0.0135
A*26:01:01:01~B*44:03:02:01~C*07:06:01:01~DRB1*14:04:01:01~DQB1*05:03:01:01~DPB1*14:01:01:01	0.0135
A*30:01:01:01~B*13:02:01:01~C*06:02:01:01~DRB1*07:01:01:01~DQB1*02:02:01:01~DPB1*04:01:01:01	0.0135
A*11:01:01:01~B*52:01:01:01~C*12:02:02:01~DRB1*13:01:01:01~DQB1*06:03:01:01~DPB1*13:01:01:01	0.0101
A*33:03:01:01~B*58:01:01:01~C*03:02:02:01~DRB1*03:01:01:01~DQB1*02:01:01:01~DPB1*04:01:01:01	0.0101
A*26:01:01:01~B*08:01:01:02~C*07:02:01:01~DRB1*03:01:01:01~DQB1*02:01:01:01~DPB1*04:01:01:01	0.0101
A*01:01:01:01~B*57:01:01:01~C*06:02:01:01~DRB1*07:01:01:01~DQB1*03:03:02:01~DPB1*02:01:02:01	0.0101
A*68:01:02:01~B*55:01:01:01~C*01:02:01:01~DRB1*11:01:01:01~DQB1*03:01:01:02~DPB1*26:01:02:01	0.0101
A*26:01:01:01~B*27:05:02:01~C*02:02:02:01~DRB1*04:04:01:02~DQB1*03:02:01:01~DPB1*04:02:01:02	0.0101
A*23:01:01:01~B*49:01:01:01~C*07:01:01:01~DRB1*15:02:02:01~DQB1*06:01:01:01~DPB1*04:01:01:01	0.0101
A*11:01:01:01~B*40:06:01:02~C*15:02:01:01~DRB1*15:01:01:01~DQB1*06:01:01:01~DPB1*04:01:01:01	0.0101
A*01:01:01:01~B*37:01:01:01~C*06:02:01:01~DRB1*10:01:01:01~DQB1*05:01:01:05~DPB1*04:01:01:01	0.0068

Table 4. Top 15 most frequent six-locus HLA haplotypes (HLA-A, -B, -C, -DRB1, -DQB1, and -DPB1) observed in the Saraswat Brahmin population (n = 148).

Table: 5 Sindhi population Top-15 Haplotype with frequencies	frequency
A*02:11:01:01~B*40:06:01:02~C*15:02:01:01~DRB1*15:01:01:01~DQB1*06:01:01:01~DPB1*04:01:01:01	0.0135
A*26:01:01:01~B*08:01:01:02~C*07:02:01:01~DRB1*03:01:01:01~DQB1*02:01:01:01~DPB1*04:02:01:02	0.0135
A*01:01:01:01~B*57:01:01:01~C*06:02:01:01~DRB1*07:01:01:01~DQB1*03:03:02:01~DPB1*04:01:01:01	0.0101
A*24:02:01:01~B*07:02:01:01~C*07:02:01:03~DRB1*03:01:01:01~DQB1*02:01:01:01~DPB1*04:01:01:01	0.0101
A*01:01:01:01~B*15:17:01:01~C*07:01:02:01~DRB1*13:01:01:01~DQB1*06:03:01:01~DPB1*04:01:01:01	0.0101
A*33:03:01:01~B*58:01:01:01~C*03:02:02:01~DRB1*13:01:01:01~DQB1*06:03:01:01~DPB1*02:01:02:01	0.0101
A*01:01:01:01~B*51:01:01:01~C*12:02:02:01~DRB1*08:01:01:01~DQB1*04:02:01:01~DPB1*04:02:01:02	0.0068
A*68:01:02:02~B*35:01:01:02~C*04:01:01:01~DRB1*13:01:01:01~DQB1*06:03:01:01~DPB1*04:01:01:01	0.0068
A*11:01:01:01~B*37:01:01:01~C*06:02:01:01~DRB1*04:03:01:01~DQB1*03:02:01:01~DPB1*02:01:02:01	0.0068
A*03:02:01:01~B*41:02:01:01~C*17:03:01:01~DRB1*15:01:01:01~DQB1*06:01:01:01~DPB1*04:01:01:01	0.0068
A*11:01:01:01~B*44:02:01:01~C*05:01:01:02~DRB1*11:04:01:01~DQB1*03:01:01:02~DPB1*04:01:01:01	0.0068
A*68:01:02:02~B*35:03:01:01~C*12:03:01:01~DRB1*13:01:01:01~DQB1*06:03:01:01~DPB1*04:01:01:01	0.0068
A*11:01:01:01~B*35:01:01:02~C*04:01:01:05~DRB1*01:01:01:01~DQB1*05:01:01:02~DPB1*04:01:01:01	0.0068
A*24:02:01:01~B*51:01:01:01~C*15:02:01:01~DRB1*13:01:01:01~DQB1*06:03:01:01~DPB1*09:01:01:01	0.0068
A*01:01:01:01~B*15:17:01:01~C*07:01:02:01~DRB1*13:02:01:02~DQB1*06:04:01:01~DPB1*02:01:02:26	0.0068

Table 5. Top 15 most frequent six-locus HLA haplotypes (HLA-A, -B, -C, -DRB1, -DQB1, and -DPB1) observed in the Sindhi population (n = 148).

Table: 6 Saraswat Brahmin population top 15 haplotype with observed frequency				
Haplotype	observed	expected	difference	stdres
DRB1*13:01:01:01~DQB1*06:03:01:01	0.0946	0.009937	0.084663	14.53911
DQB1*06:01:01:01~DPB1*04:01:01:01	0.0907	0.060546	0.030154	2.043534
C*06:02:01:01~DPB1*04:01:01:01	0.0858	0.051058	0.034742	2.576805
DRB1*15:02:01:02~DQB1*06:01:01:01	0.0845	0.016885	0.067615	8.876316
DRB1*03:01:01:01~DQB1*02:01:01:01	0.0777	0.00714	0.07056	14.31496
A*01:01:01:01~C*06:02:01:01	0.0725	0.021112	0.051388	6.020155
DRB1*14:04:01:01~DQB1*05:03:01:01	0.0709	0.006301	0.064599	13.95645
B*40:06:01:02~C*15:02:01:01	0.0676	0.008135	0.059465	11.29661
A*11:01:01:01~DPB1*04:01:01:01	0.0661	0.037986	0.028114	2.43411
DRB1*07:01:01:01~DPB1*04:01:01:01	0.0642	0.034437	0.029763	2.711415
DRB1*15:01:01:01~DQB1*06:01:01:01	0.0642	0.014559	0.049641	7.026314
DRB1*15:01:01:01~DPB1*04:01:01:01	0.0565	0.029693	0.026807	2.636419
DRB1*07:01:01:01~DQB1*02:02:01:01	0.0541	0.005302	0.048798	11.49962

B*37:01:01:01~C*06:02:01:01	0.0538	0.00834	0.04546	8.528365
C*15:02:01:01~DQB1*06:01:01:01	0.053	0.01804	0.03496	4.437625

Table 6. Observed and expected frequencies of the top 15 two-locus HLA haplotypes in the Saraswat Brahmin population, including standardized residuals (StdRes), indicating linkage disequilibrium strength.

Table: 7 Sindhi population top 15 haplotype with observed frequency				
Haplotype	observed	expected	difference	stdres
DRB1*03:01:01:01~DQB1*02:01:01:01	0.1318	0.018254	0.113546	14.32628
DRB1*13:01:01:01~DQB1*06:03:01:01	0.1284	0.021112	0.107288	12.56891
A*01:01:01:01~DPB1*04:01:01:01	0.099	0.059573	0.039427	2.695098
C*07:02:01:01~DRB1*03:01:01:01	0.0755	0.015443	0.060057	8.250295
C*07:02:01:01~DQB1*02:01:01:01	0.074	0.014696	0.059304	8.354531
B*51:01:01:01~DPB1*04:01:01:01	0.0667	0.051362	0.015338	1.134039
DRB1*03:01:01:01~DPB1*04:01:01:01	0.0648	0.042118	0.022682	1.861028
DRB1*11:01:01:01~DQB1*03:01:01:02	0.0642	0.008317	0.055883	10.49817
DRB1*10:01:01:01~DQB1*05:01:01:05	0.0642	0.004122	0.060078	16.0669
DRB1*14:04:01:01~DQB1*05:03:01:01	0.0608	0.006625	0.054175	11.41344
DQB1*02:01:01:01~DPB1*04:01:01:01	0.0579	0.04008	0.01782	1.500361
B*08:01:01:02~C*07:02:01:01	0.0574	0.006779	0.050621	10.54165
B*40:06:01:02~C*15:02:01:01	0.0574	0.007672	0.049728	9.730114
B*08:01:01:02~DQB1*02:01:01:01	0.0538	0.008013	0.045787	8.764503
B*08:01:01:02~DRB1*03:01:01:01	0.0537	0.008421	0.045279	8.453404

Table 7. Observed and expected frequencies of the top 15 two-locus HLA haplotypes in the Sindhi population, including standardized residuals (StdRes).

Table 8: HLA-A Allele frequencies (n=296) (148 individuals each group)			
Saraswat Brahmin population (haplotype=44)		Sindhi population (haplotype=40)	
HLA-A	Frequency	HLA-A	Frequency
A*01:01:01:01	0.1453	A*01:01:01:01	0.1959
A*11:01:01:01	0.1081	A*11:01:01:01	0.1115
A*26:01:01:01	0.0845	A*68:01:02:02	0.0946
A*32:01:01:01	0.0811	A*24:02:01:01	0.0912
A*24:02:01:01	0.0777	A*26:01:01:01	0.0574
A*24:02:01:04	0.0473	A*02:06:01:01	0.0405
A*33:03:01:01	0.0473	A*33:03:01:01	0.0405
A*03:01:01:01	0.0473	A*02:11:01:01	0.0405
A*02:01:01:01	0.0439	A*03:01:01:01	0.0405
A*02:11:01:01	0.0338	A*32:01:01:01	0.0338
A*02:06:01:01	0.027	A*02:01:01:01	0.0304
A*33:01:01:01	0.0236	A*68:01:01:02	0.027
A*68:01:02:02	0.0236	A*68:01:02:01	0.027
A*68:01:02:01	0.0169	A*02:03:01:01	0.027
A*02:20:02:01	0.0169	A*31:01:02:01	0.0236
A*31:01:02:01	0.0169	A*03:02:01:01	0.0203
A*03:02:01:01	0.0169	A*24:02:01:04	0.0068
A*30:01:01:01	0.0135	A*02:20:02:01	0.0068
A*68:01:01:02	0.0101	A*02:09:01:01	0.0068

A*01:01:01:03	0.0101	A*01:01:01:03	0.0068
A*23:01:01:01	0.0101	A*24:33:01:01	0.0068
A*02:05:01:01	0.0101	A*32:01:01:09	0.0034
A*74:03:01:01	0.0068	A*23:01:01:01	0.0034
A*29:01:01:01	0.0068	A*24:17:01:01	0.0034
A*24:02:01:02L	0.0068	A*01:01:100:01	0.0034
A*11:01:26:01	0.0068	A*24:11N:01:01	0.0034
A*31:08:01:01	0.0034	A*24:02:01:02L	0.0034
A*33:129N:01:01	0.0034	A*03:03:01:01	0.0034
A*02:01:01:63	0.0034	A*23:02:01:02L	0.0034
A*24:02:13:01	0.0034	A*02:05:01:0	0.0034
A*23:01:01:07	0.0034	A*02:05:01:01	0.0034
A*24:33:01:01	0.0034	A*11:03:01:01	0.0034
A*24:03:01:01	0.0034	A*02:06:01:04	0.0034
A*31:01:02:44	0.0034	A*26:01:01:02	0.0034
A*31:16:01:01	0.0034	A*23:01:01:07	0.0034
A*11:01:01:25	0.0034	A*03:06:01:01	0.0034
A*33:191:01:01	0.0034	A*33:01:01:01	0.0034
A*33:243:01:01	0.0034	A*31:16:01:01	0.0034
A*02:20:02:02	0.0034	A*31:06:01:01	0.0034
A*24:02:01:02	0.0034	A*29:01:01:01	0.0034
A*26:01:01:02	0.0034	-	-
A*02:03:01:01	0.0034	-	-
A*02:131:01:01	0.0034	-	-
A*24:07:01:01	0.0034	-	-

Table 8. Allele frequency distribution of HLA-A in the Saraswat Brahmin and Sindhi populations.

Table 9: HLA-B Allele frequencies (n=296) (148 individuals each group)			
Saraswat Brahmin population (haplotype=62)		Sindhi population (haplotype=57)	
HLA-B	Frequency	HLA-B	Frequency
B*40:06:01:02	0.0777	B*51:01:01:01	0.1689
B*35:03:01:01	0.0709	B*40:06:01:02	0.0811
B*51:01:01:01	0.0608	B*35:03:01:01	0.0709
B*37:01:01:01	0.0574	B*08:01:01:02	0.0608
B*18:01:01:02	0.0574	B*07:02:01:01	0.0439
B*08:01:01:02	0.0507	B*58:01:01:01	0.0405
B*55:01:01:01	0.0439	B*35:01:01:02	0.0338
B*52:01:01:01	0.0439	B*44:03:02:01	0.0338
B*52:01:01:02	0.0405	B*40:01:02:01	0.0338
B*57:01:01:01	0.0372	B*55:01:01:01	0.0304
B*58:01:01:01	0.0338	B*52:01:01:01	0.0304
B*14:02:01:01	0.027	B*15:17:01:01	0.0304
B*07:02:01:01	0.0236	B*37:01:01:01	0.0236
B*44:03:02:01	0.0236	B*57:01:01:01	0.0236
B*27:05:02:01	0.0236	B*38:02:01:01	0.0203
B*13:02:01:01	0.0203	B*52:01:01:02	0.0203
B*15:17:01:01	0.0169	B*50:01:01:01	0.0169
B*35:01:01:02	0.0169	B*49:01:01:01	0.0135

B*49:01:01:01	0.0169	B*15:08:01:01	0.0135
B*50:01:01:01	0.0169	B*39:01:01:03	0.0135
B*13:01:01:01	0.0135	B*44:02:01:01	0.0135
B*37:04:02:01	0.0135	B*27:05:02:01	0.0135
B*36:01:01:01	0.0135	B*18:01:01:02	0.0101
B*15:02:01:01	0.0101	B*15:18:01:02	0.0101
B*56:01:01:01	0.0101	B*36:01:01:02	0.0068
B*39:01:01:03	0.0101	B*36:03:01:01	0.0068
B*40:01:02:01	0.0101	B*09:01:01:02	0.0068
B*41:06:01:02	0.0068	B*41:02:01:01	0.0068
B*59:01:01:01	0.0068	B*51:08:01:01	0.0068
B*44:02:01:01	0.0068	B*15:01:01:01	0.0068
B*51:01:05:01	0.0068	B*13:01:01:01	0.0068
B*27:07:01:01	0.0068	B*56:01:01:01	0.0068
B*27:02:01:04	0.0068	B*15:02:01:01	0.0068
B*51:06:01:01	0.0068	B*43:03:01:01	0.0068
B*35:08:01:01	0.0068	B*51:06:01:01	0.0068
B*56:01:01:03	0.0068	B*37:01:01:02	0.0034
B*07:05:01:01	0.0068	B*34:01:01:02	0.0034
B*55:02:01:03	0.0068	B*37:03:01:01	0.0034
B*54:01:01:01	0.0068	B*33:01:01:02	0.0034
B*15:75:01:01	0.0034	B*34:03:01:01	0.0034
B*36:01:01:03	0.0034	B*06:01:01:02	0.0034
B*37:03:01:01	0.0034	B*48:01:01:01	0.0034
B*15:18:01:02	0.0034	B*54:01:01:01	0.0034
B*15:01:01:01	0.0034	B*35:02:01:01	0.0034
B*15:08:01:01	0.0034	B*39:02:01:01	0.0034
B*44:03:01:01	0.0034	B*27:07:01:01	0.0034
B*47:01:01:01	0.0034	B*44:02:01:03	0.0034
B*46:01:01:01	0.0034	B*40:06:04:01	0.0034
B*53:01:01:02	0.0034	B*13:01:01:03	0.0034
B*56:02:01:03	0.0034	B*44:03:01:01	0.0034
B*09:02:01:02	0.0034	B*59:01:01:01	0.0034
B*51:01:01:02	0.0034	B*35:08:01:01	0.0034
B*07:02:01:03	0.0034	B*51:01:05:01	0.0034
B*50:01:01:03	0.0034	B*14:02:01:01	0.0034
B*36:04:02:01	0.0034	B*41:06:01:02	0.0034
B*53:01:01:01	0.0034	B*17:17:01:01	0.0034
B*41:01:02:01	0.0034	B*53:01:01:01	0.0034
B*39:01:02:01	0.0034	-	-
B*27:07:03:01	0.0034	-	-
B*34:03:01:01	0.0034	-	-
B*48:01:01:01	0.0034	-	-
B*38:02:01:01	0.0034	-	-

Table 9. Allele frequency distribution of HLA-B in the Saraswat Brahmin and Sindhi populations.

Table 10: HLA-C Allele frequencies (n=296) (148 individuals each group)	
Saraswat Brahmin population (haplotype=36)	Sindhi population (haplotype=39)

HLA-C	Frequency	HLA-C	Frequency
C*06:02:01:01	0.1453	C*07:02:01:01	0.1115
C*15:02:01:01	0.1047	C*15:02:01:01	0.0946
C*12:03:01:01	0.0912	C*04:01:01:01	0.0777
C*12:02:02:01	0.0743	C*12:03:01:01	0.0743
C*07:02:01:01	0.0709	C*12:02:02:01	0.0709
C*04:01:01:01	0.0574	C*06:02:01:01	0.0608
C*01:02:01:01	0.0541	C*16:02:01:01	0.0574
C*02:02:02:01	0.0507	C*01:02:01:01	0.0541
C*03:02:02:01	0.0405	C*07:02:01:03	0.0507
C*08:02:01:01	0.0338	C*14:02:01:01	0.0405
C*14:02:01:01	0.0304	C*07:01:02:01	0.0405
C*07:06:01:01	0.027	C*07:06:01:01	0.0338
C*07:01:02:01	0.0236	C*03:02:02:01	0.0338
C*07:02:01:03	0.0203	C*07:01:01:01	0.0304
C*16:02:01:01	0.0203	C*02:02:02:01	0.0203
C*04:03:01:01	0.0169	C*05:01:01:02	0.0169
C*07:01:01:01	0.0169	C*07:04:01:01	0.0135
C*04:01:01:06	0.0135	C*04:01:01:05	0.0135
C*06:02:01:02	0.0135	C*08:02:01:01	0.0101
C*08:01:01:01	0.0101	C*03:04:01:02	0.0101
C*07:04:01:01	0.0101	C*17:03:01:01	0.0068
C*15:05:02:01	0.0101	C*04:01:01:06	0.0068
C*03:03:01:01	0.0101	C*06:02:01:02	0.0068
C*05:01:01:02	0.0068	C*08:01:01:01	0.0068
C*03:04:01:02	0.0068	C*04:03:01:01	0.0068
C*15:04:01:01	0.0068	C*12:04:02:01	0.0068
C*06:27:00:01	0.0034	C*07:26:01:01	0.0034
C*11:03:01:01	0.0034	C*06:27:01:01	0.0034
C*03:04:01:01	0.0034	C*02:02:01:01	0.0034
C*12:09:01:01	0.0034	C*06:02:01:19	0.0034
C*12:04:02:01	0.0034	C*15:07:01:02	0.0034
C*15:07:01:02	0.0034	C*15:13:01:01	0.0034
C*06:02:01:03	0.0034	C*03:03:01:01	0.0034
C*06:02:01:04	0.0034	C*03:01:01:02	0.0034
C*16:04:01:01	0.0034	C*03:04:01:01	0.0034
C*51:01:01:01	0.0034	C*14:02:02:01	0.0034
-	-	C*12:09:01:01	0.0034
-	-	C*15:04:01:01	0.0034
-	-	C*15:05:02:01	0.0034

Table 10. Allele frequency distribution of HLA-C in the Saraswat Brahmin and Sindhi populations.

Table 11: HLA-DRB1 Allele frequencies (n=296) (148 individuals each group)			
Saraswat Brahmin population (haplotype=35)		Sindhi population (haplotype=34)	
HLA-DRB1	Frequency	HLA-DRB1	Frequency
DRB1*15:02:01:02	0.098	DRB1*13:01:01:01	0.1453
DRB1*07:01:01:01	0.098	DRB1*03:01:01:01	0.1385
DRB1*13:01:01:01	0.098	DRB1*11:01:01:01	0.0912

DRB1*03:01:01:01	0.0845	DRB1*07:01:01:01	0.0811
DRB1*15:01:01:01	0.0845	DRB1*15:01:01:01	0.0676
DRB1*14:04:01:01	0.0777	DRB1*14:04:01:01	0.0676
DRB1*10:01:01:01	0.0608	DRB1*10:01:01:01	0.0642
DRB1*11:01:01:01	0.0608	DRB1*15:02:01:02	0.0473
DRB1*04:03:01:01	0.0439	DRB1*04:03:01:01	0.0405
DRB1*11:04:01:01	0.0405	DRB1*13:02:01:02	0.0304
DRB1*01:02:01:01	0.0338	DRB1*01:01:01:01	0.0304
DRB1*09:01:02:01	0.0304	DRB1*14:54:01:01	0.0203
DRB1*04:04:01:02	0.0304	DRB1*04:04:01:02	0.0203
DRB1*15:02:02:01	0.0203	DRB1*04:01:01:01	0.0135
DRB1*13:02:01:02	0.0169	DRB1*11:04:01:01	0.0135
DRB1*13:02:01:01	0.0135	DRB1*12:02:01:01	0.0135
DRB1*01:01:01:01	0.0135	DRB1*13:02:01:01	0.0135
DRB1*11:11:01:01	0.0135	DRB1*08:01:01:01	0.0101
DRB1*12:02:01:01	0.0101	DRB1*08:02:01:01	0.0101
DRB1*04:05:01:01	0.0068	DRB1*15:04:01:01	0.0101
DRB1*08:02:01:01	0.0068	DRB1*09:01:02:01	0.0068
DRB1*13:03:01:01	0.0068	DRB1*15:06:01:01	0.0068
DRB1*14:54:01:01	0.0068	DRB1*12:01:01:01	0.0068
DRB1*15:04:01:01	0.0068	DRB1*15:02:02:01	0.0068
DRB1*12:01:01:01	0.0034	DRB1*04:02:01:01	0.0068
DRB1*04:01:01:01	0.0034	DRB1*11:11:01:01	0.0068
DRB1*14:05:01:01	0.0034	DRB1*08:03:02:01	0.0068
DRB1*08:01:01:01	0.0034	DRB1*12:02:01:02	0.0034
DRB1*04:07:01:01	0.0034	DRB1*14:02:01:01	0.0034
DRB1*16:02:01:01	0.0034	DRB1*14:202:01:01	0.0034
DRB1*14:02:01:01	0.0034	DRB1*11:06:01:01	0.0034
DRB1*03:71:01:01	0.0034	DRB1*09:05:01:01	0.0034
DRB1*04:03:01:0	0.0034	DRB1*04:05:01:01	0.0034
DRB1*10:01:01:0	0.0034	DRB1*16:02:01:01	0.0034
DRB1*04:02:01:01	0.0034	-	-

Table 11. Allele frequency distribution of HLA-DRB1 in the Saraswat Brahmin and Sindhi populations.

Table 12: HLA-DQB1 Allele frequencies (n=296) (148 individuals each group)			
Saraswat Brahmin population (haplotype=31)		Sindhi population (haplotype=33)	
HLA-DQB1	Frequency	HLA-DQB1	Frequency
DQB1*06:01:01:01	0.1723	DQB1*06:03:01:01	0.1453
DQB1*03:02:01:01	0.1115	DQB1*02:01:01:01	0.1318
DQB1*03:01:01:02	0.1014	DQB1*05:03:01:01	0.098
DQB1*06:03:01:01	0.1014	DQB1*03:01:01:02	0.0912
DQB1*02:01:01:01	0.0845	DQB1*06:01:01:01	0.0845
DQB1*05:03:01:01	0.0811	DQB1*03:02:01:01	0.0709
DQB1*05:01:01:05	0.0541	DQB1*05:01:01:05	0.0642
DQB1*02:02:01:01	0.0541	DQB1*02:02:01:01	0.0439
DQB1*05:01:01:01	0.0372	DQB1*05:01:01:02	0.0304
DQB1*03:03:02:01	0.0372	DQB1*06:04:01:01	0.027
DQB1*05:01:01:02	0.0203	DQB1*03:03:02:01	0.0236

DQB1*05:02:01:01	0.0169	DQB1*03:01:01:01	0.0236
DQB1*06:09:01:01	0.0135	DQB1*06:02:01:01	0.0236
DQB1*06:04:01:01	0.0135	DQB1*05:02:01:01	0.0203
DQB1*06:02:01:01	0.0101	DQB1*04:02:01:01	0.0169
DQB1*04:02:01:09	0.0101	DQB1*03:01:01:07	0.0135
DQB1*05:01:24:01	0.0101	DQB1*03:05:01:01	0.0101
DQB1*03:01:01:15	0.0101	DQB1*06:09:01:01	0.0101
DQB1*04:03:01:01	0.0068	DQB1*06:110:01:01	0.0101
DQB1*03:01:01:01	0.0068	DQB1*03:01:01:05	0.0068
DQB1*03:03:02:02	0.0068	DQB1*06:41:01:02	0.0068
DQB1*02:01:01:08	0.0068	DQB1*03:01:01:04	0.0068
DQB1*03:01:01:07	0.0068	DQB1*03:01:01:17	0.0068
DQB1*06:41:01:02	0.0034	DQB1*03:02:01:11	0.0034
DQB1*04:12:00:01	0.0034	DQB1*05:01:24:01	0.0034
DQB1*03:01:01:05	0.0034	DQB1*04:01:01:05	0.0034
DQB1*03:78:01:01	0.0034	DQB1*05:01:01:01	0.0034
DQB1*04:02:01:01	0.0034	DQB1*03:01:01:15	0.0034
DQB1*06:02:01:18Q	0.0034	DQB1*03:01:02:01	0.0034
DQB1*04:02:08:01	0.0034	DQB1*03:03:02:02	0.0034
DQB1*06:03:01:01	0.0034	DQB1*04:01:01:01	0.0034
-	-	DQB1*06:09:04:01	0.0034
-	-	DQB1*04:12:01:01	0.0034

Table 12. Allele frequency distribution of HLA-DQB1 in the Saraswat Brahmin and Sindhi populations.

Table 13: HLA-DPB1 Allele frequencies (n=296) (148 individuals each group)			
Saraswat Brahmin population (haplotype=43)		Sindhi population (haplotype=51)	
HLA-DPB1	Frequency	HLA-DPB1	Frequency
DPB1*04:01:01:01	0.3514	DPB1*04:01:01:01	0.3041
DPB1*02:01:02:01	0.0777	DPB1*02:01:02:01	0.125
DPB1*04:02:01:02	0.0676	DPB1*09:01:01:01	0.0946
DPB1*26:01:02:01	0.0608	DPB1*26:01:02:01	0.0473
DPB1*13:01:01:02	0.0405	DPB1*04:02:01:02	0.0372
DPB1*14:01:01:01	0.0372	DPB1*13:01:01:02	0.0372
DPB1*09:01:01:01	0.0338	DPB1*05:01:01:01	0.0304
DPB1*02:01:02:10	0.0338	DPB1*13:21:01:01	0.027
DPB1*02:01:02:03	0.0236	DPB1*03:01:02:01	0.0236
DPB1*19:01:01:01	0.0203	DPB1*03:01:01:01	0.0236
DPB1*04:01:01:41	0.0169	DPB1*13:15:01:01	0.0236
DPB1*13:01:01:01	0.0135	DPB1*02:01:02:26	0.0135
DPB1*05:01:01:01	0.0135	DPB1*14:01:01:01	0.0135
DPB1*03:01:01:01	0.0135	DPB1*104:01:01:01	0.0135
DPB1*04:01:01:75	0.0135	DPB1*17:01:01:01	0.0101
DPB1*10:01:01:01	0.0135	DPB1*10:01:01:01	0.0101
DPB1*105:01:01:05	0.0101	DPB1*04:01:01:41	0.0101
DPB1*06:01:01:01	0.0101	DPB1*02:01:02:52	0.0101
DPB1*13:21:01:01	0.0101	DPB1*04:02:01:04	0.0101
DPB1*104:01:01:03	0.0101	DPB1*414:01:01:02	0.0068
DPB1*02:01:02:26	0.0101	DPB1*04:01:01:28	0.0068

DPB1*02:01:01:01	0.0101	DPB1*04:01:01:03	0.0068
DPB1*232:01:01:01	0.0101	DPB1*15:01:01:01	0.0068
DPB1*15:01:01:01	0.0068	DPB1*05:01:01:02	0.0068
DPB1*13:15:01:01	0.0068	DPB1*08:01:01:01	0.0068
DPB1*01:01:01:04	0.0068	DPB1*02:01:02:03	0.0068
DPB1*04:02:01:04	0.0068	DPB1*27:01:02:01	0.0068
DPB1*104:01:01:01	0.0068	DPB1*01:01:02:01	0.0034
DPB1*08:01:01:01	0.0068	DPB1*06:01:01:28	0.0034
DPB1*14:01:01:02	0.0068	DPB1*05:01:01:28	0.0034
DPB1*12:12:01:01	0.0068	DPB1*16:01:01:01	0.0034
DPB1*04:02:01:01	0.0068	DPB1*03:01:01:02	0.0034
DPB1*04:02:01G:01	0.0034	DPB1*04:01:01:02	0.0034
DPB1*12:01:01:01	0.0034	DPB1*105:01:01:02	0.0034
DPB1*18:01:01:01	0.0034	DPB1*13:22:01:01	0.0034
DPB1*03:01:02:03	0.0034	DPB1*104:01:01:03	0.0034
DPB1*04:01:01:03	0.0034	DPB1*25:01:02:01	0.0034
DPB1*02:01:02:12	0.0034	DPB1*199:01:01:01	0.0034
DPB1*13:46:01:01	0.0034	DPB1*323:01:01:01	0.0034
DPB1*02:01:02:52	0.0034	DPB1*05:02:01:02	0.0034
DPB1*212:01:01:01	0.0034	DPB1*04:01:01:136	0.0034
DPB1*126:01:01:01	0.0034	DPB1*12:20:01:01	0.0034
DPB1*414:01:01:02	0.0034	DPB1*04:02:01:22	0.0034
-	-	DPB1*13:01:01:01	0.0034
-	-	DPB1*04:01:02:01	0.0034
-	-	DPB1*28:01:02:01	0.0034
-	-	DPB1*04:01:01:75	0.0034
-	-	DPB1*06:02:01:04	0.0034
-	-	DPB1*01:01:01:04	0.0034
-	-	DPB1*296:01:01:01	0.0034
-	-	DPB1*02:01:01:01	0.0034

Table 13. Allele frequency distribution of HLA-DPB1 in the Saraswat Brahmin and Sindhi populations.

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