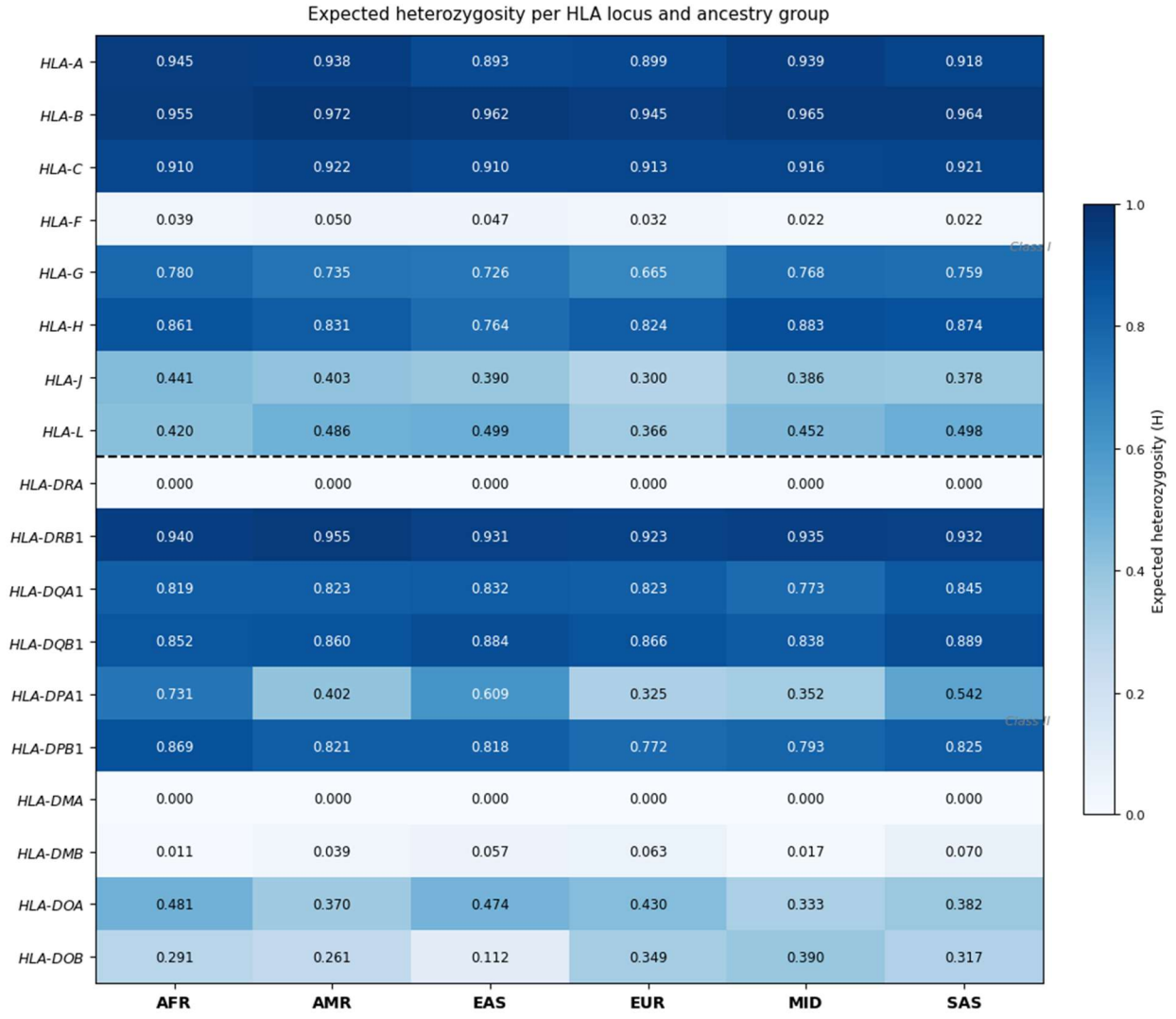
Supplementary Table 1. Cohort sizes for WGS analyses after removal of related individuals

AFR	AMR	EAS	EUR	MID	SAS	Total
77657	72151	9675	224559	1458	5323	390823

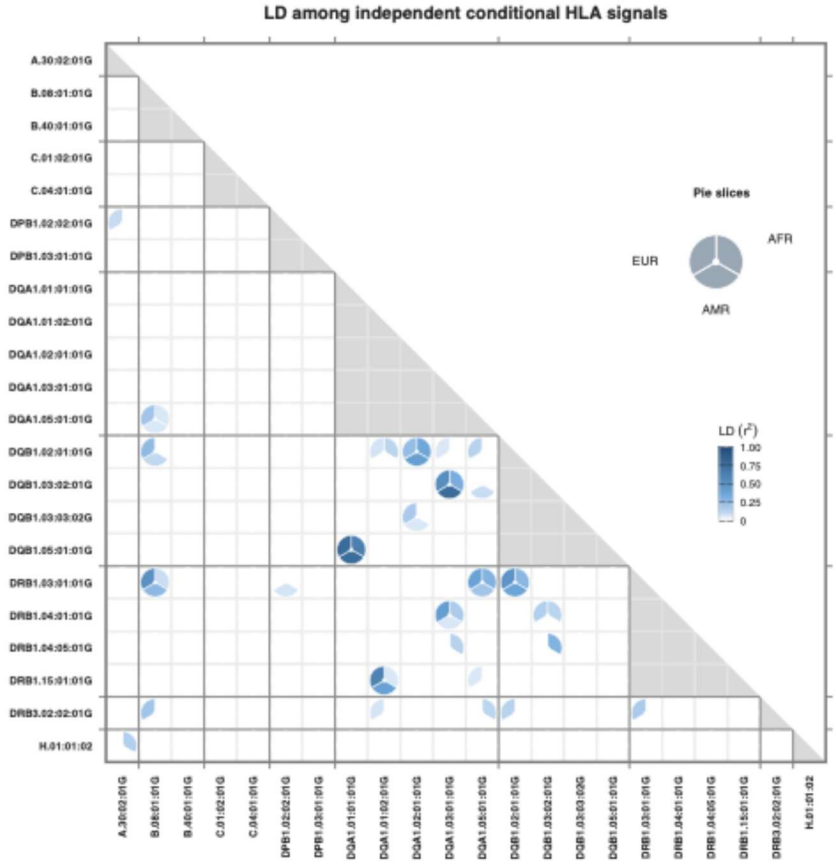
Number of unrelated participants included in HLA diversity and linkage disequilibrium analyses after exclusion of related individuals (identity-by-descent > 0.2). AFR, African; AMR, Admixed American; EAS, East Asian; EUR, European; MID, Middle Eastern; SAS, South Asian.

Supplementary Figure 1. Expected heterozygosity across HLA loci and ancestry groups.



Heatmap showing expected heterozygosity ($H = 1 - \Sigma p_i^2$) calculated from allele frequencies across HLA loci and ancestry groups. Higher values indicate greater allelic diversity. HLA-DRB3 and HLA-DRB5 were excluded because of haplotype-dependent gene presence.

Supplementary Figure 2. LD among independent conditional HLA alleles across ancestries



Heatmap of inter-locus allele-level linkage disequilibrium (LD; r^2) among 22 HLA alleles identified by stepwise conditional meta-analysis across five phenotypes. Alleles are ordered by gene, with black divider lines indicating gene boundaries. Within-gene comparisons (including the diagonal) are shown in light gray. Increasingly darker shades of blue indicate stronger LD.

Supplementary Data

Supplementary Data 1. HLA calling rates by locus and ancestry

Calling rates across HLA loci and ancestry groups following quality control.

Supplementary Data 2. Allele-level LD matrices across ancestry groups

Full allele-level linkage disequilibrium (r^2) matrices for all six ancestry groups.

Supplementary Data 3. Meta-analysis HLA–phenotype associations

All HLA–phenotype associations reaching FDR $q < 0.05$ in the cross-ancestry meta-analysis, including effect sizes and confidence intervals.

Supplementary Data 4. Ancestry-restricted HLA–phenotype association results

Associations restricted to allele–phecode pairs evaluable across EUR, AFR, and AMR populations, including signals significant in AFR only, AMR only, or jointly in AFR and AMR but not EUR.

Supplementary Data 5. Novel HLA–phenotype associations

Classification of candidate novel associations after accounting for prior evidence, linkage disequilibrium structure, and gene-level context.