

# GPU-accelerated linkage disequilibrium scans reveal non-independent assortment of human non-homologous chromosomes

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## Supplementary Figures

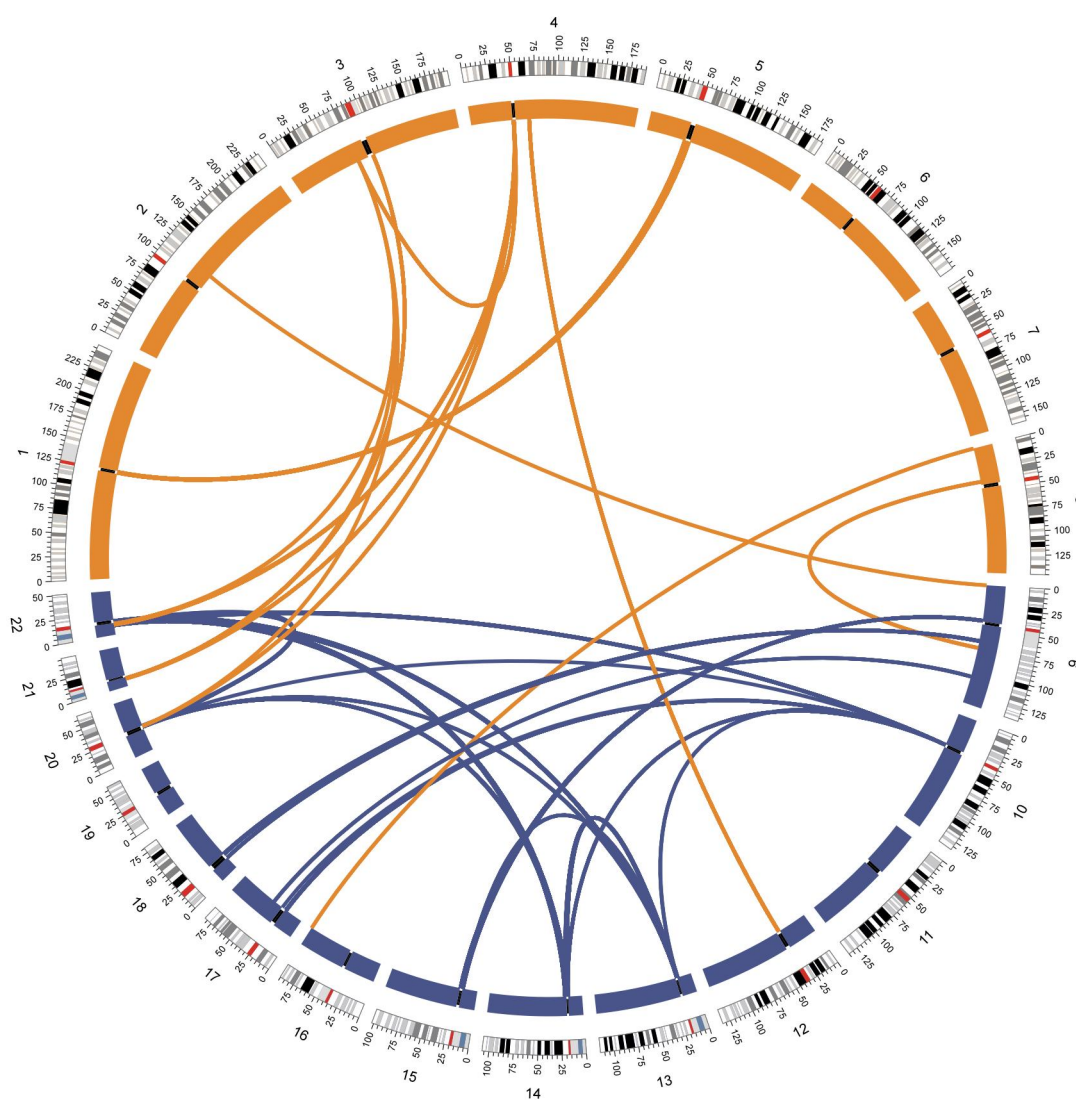
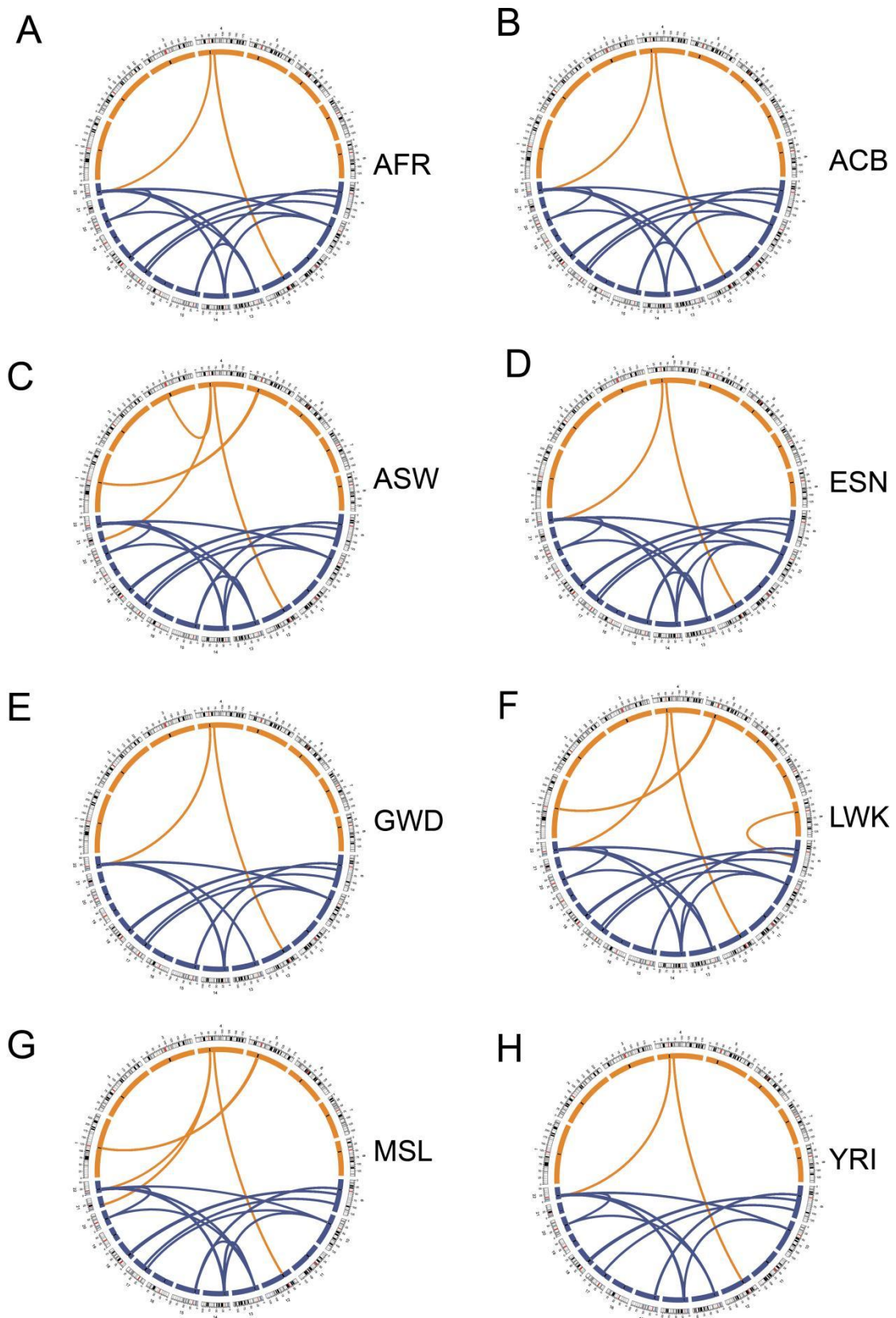
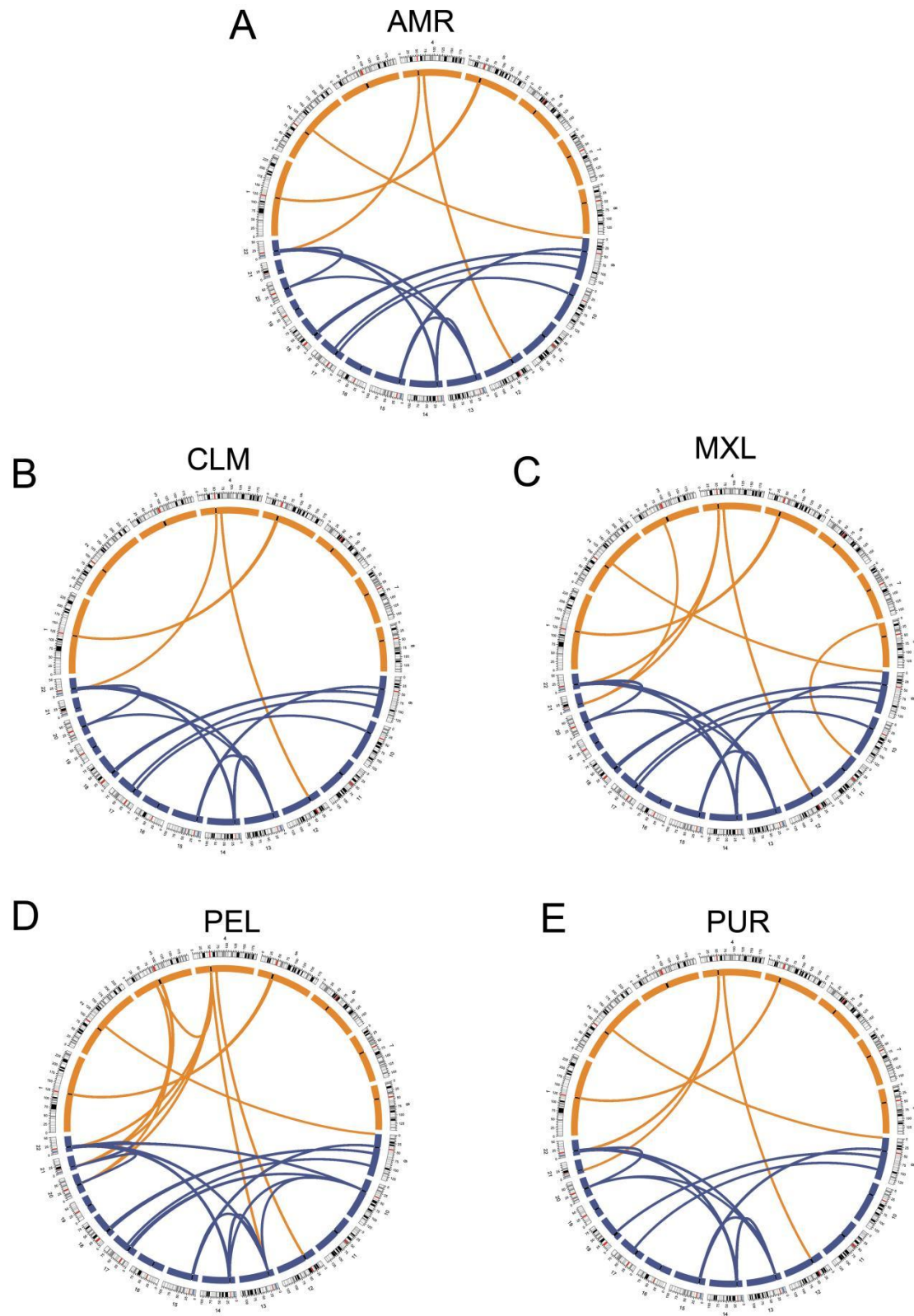


Figure S1. Circos plot of high LD pairs when  $r^2 \geq 0.5$  for overall populations.

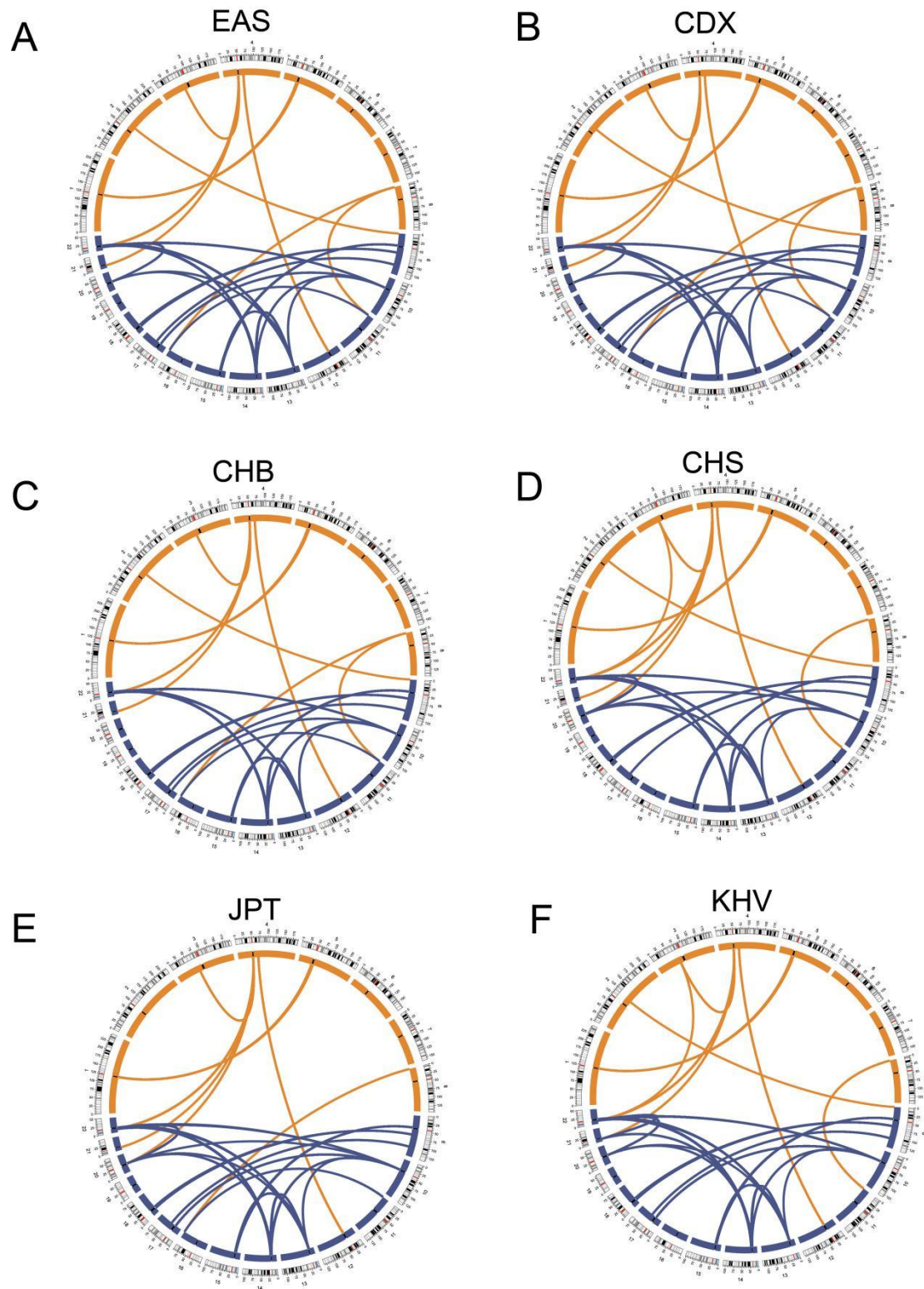


**Figure S2. Circos plot of high LD pairs when  $r^2 \geq 0.8$  for AFR super population (A) and the corresponding independent populations (B-H).**

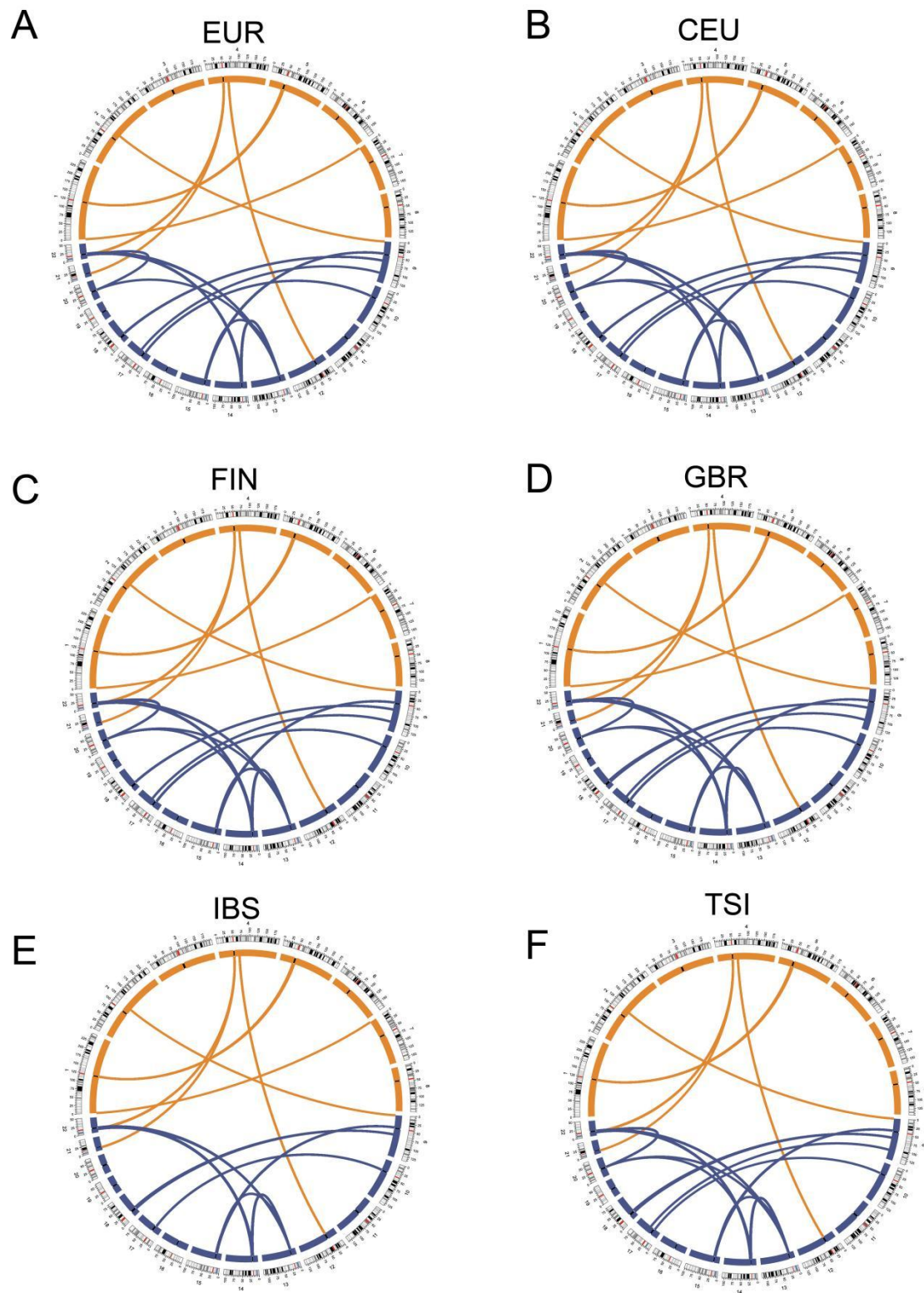


**Figure S3. Circos plot of high LD pairs when  $r^2 \geq 0.8$  for AMR super population (A) and the corresponding independent populations (B-E).**



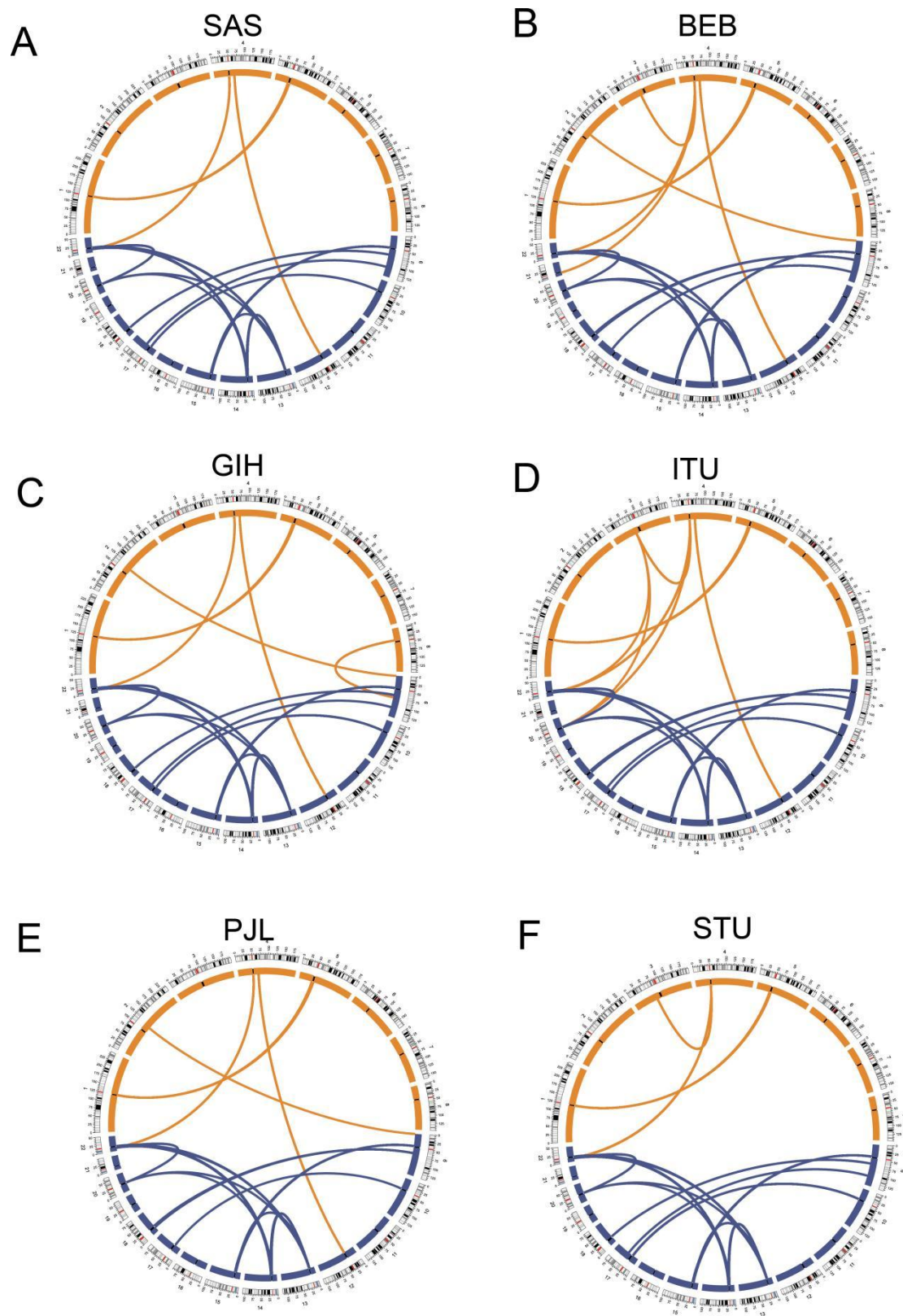


**Figure S4. Circos plot of high LD pairs when  $r^2 \geq 0.8$  for EAS super population (A) and the corresponding independent populations (B-F).**

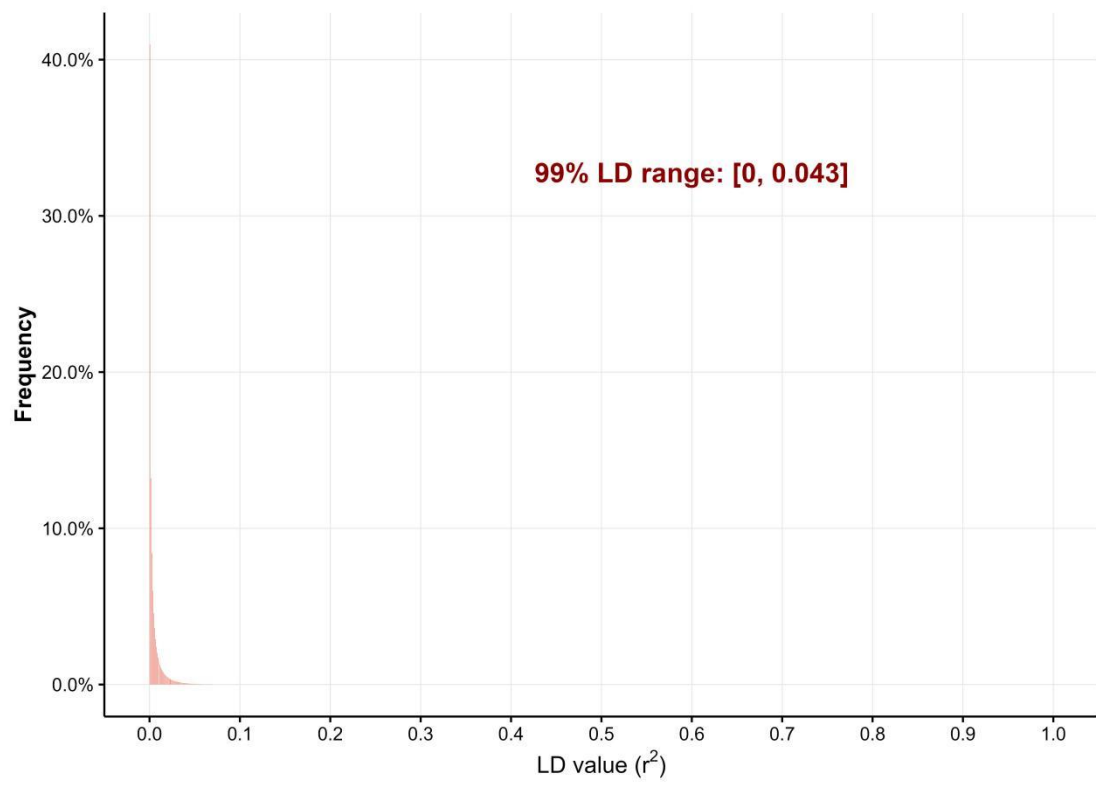


**Figure S5. Circos plot of high LD pairs when  $r^2 \geq 0.8$  for EUR super population (A) and the corresponding independent populations (B-F).**



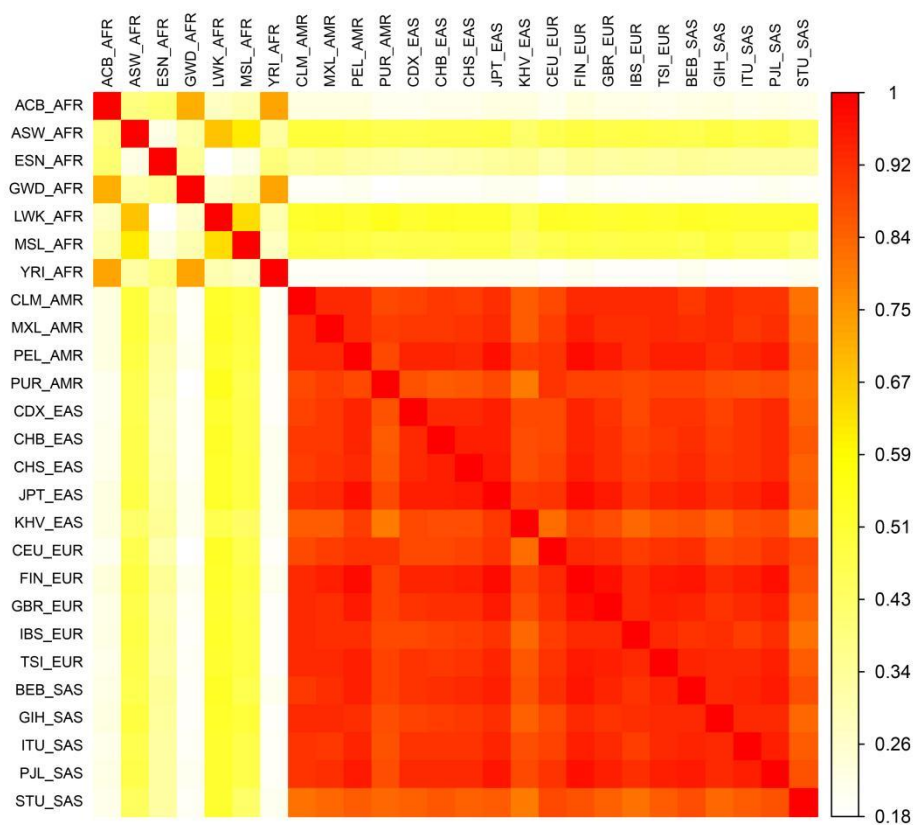


**Figure S6. Circos plot of high LD pairs when  $r^2 \geq 0.8$  for SAS super population (A) and the corresponding independent populations (B - F).**



**Figure S7. The frequency distribution of inter-chromosomal LD.**





**Figure S8. Jaccard similarity between each of 26 independent populations for 1,195 high LD SNP pairs identified in the whole population based analysis.**