

Supplementary Material

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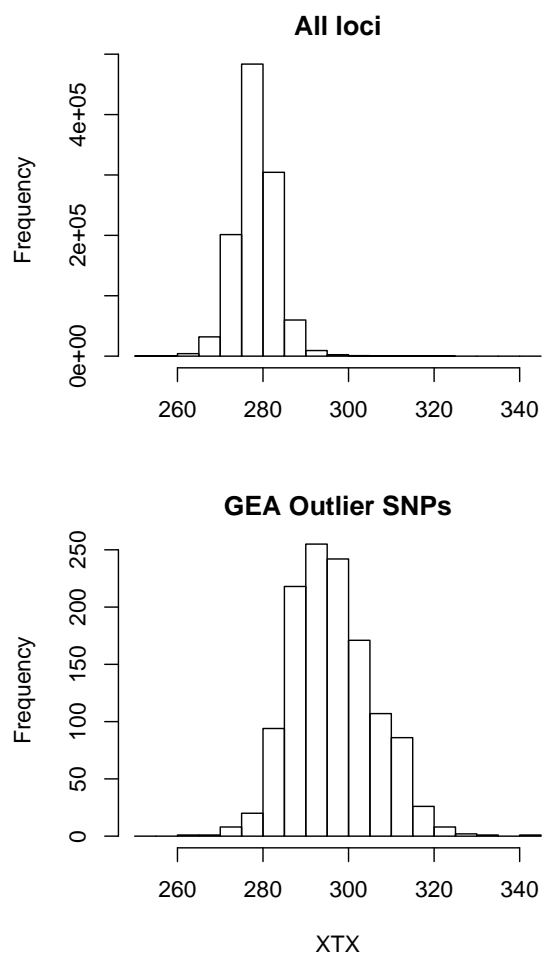
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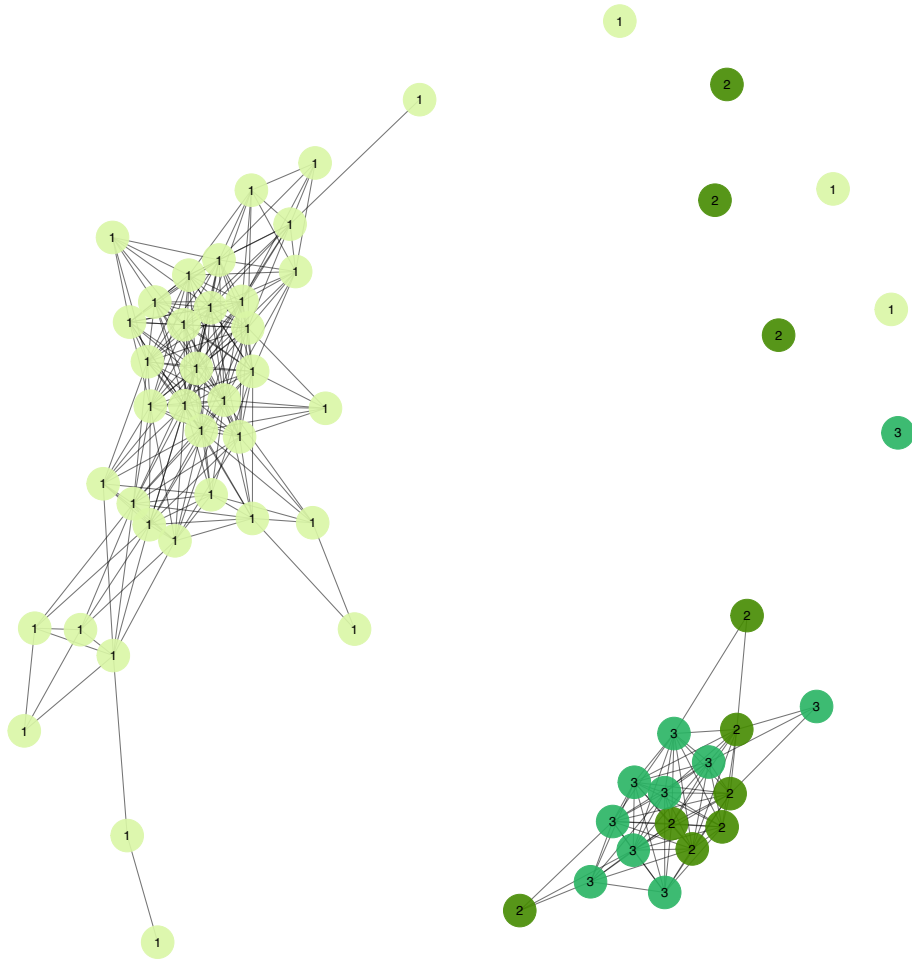
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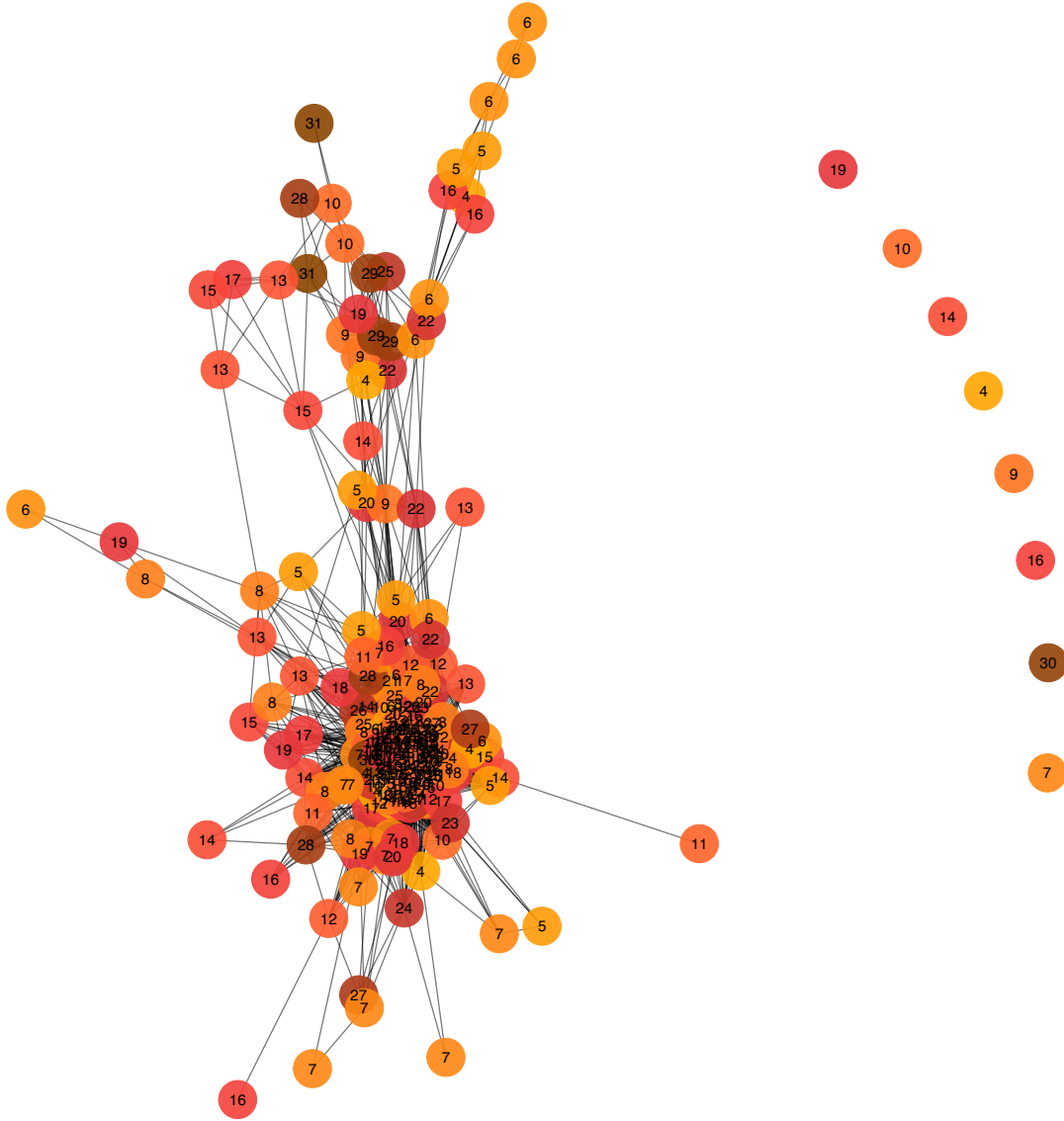
1. SUPPLEMENTARY FIGURES



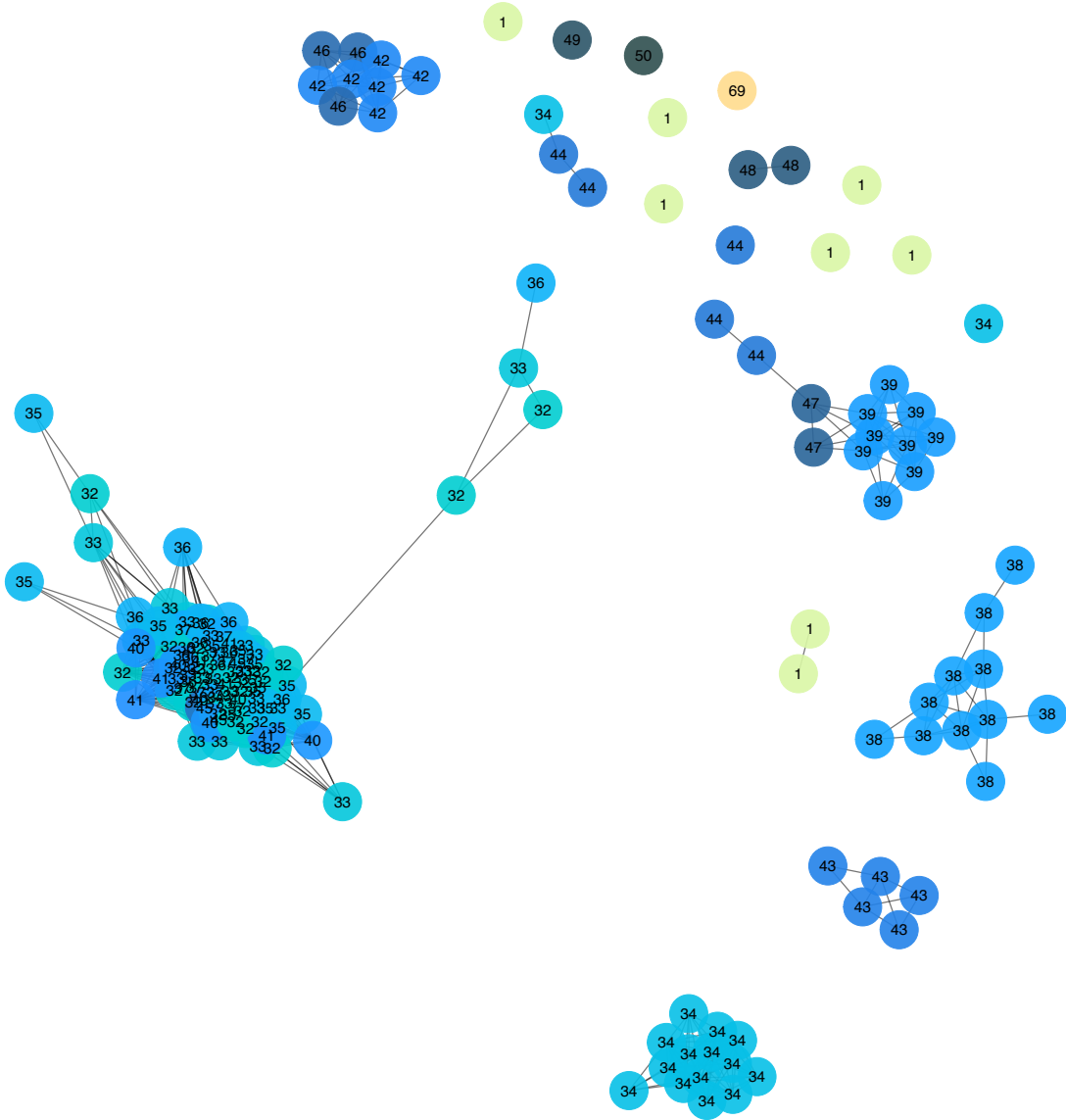
SUPPLEMENTARY FIGURE 1. Histogram of $X^T X$ estimated from Bayenv2 for all SNPs (top) and for top candidate SNPs (bottom).



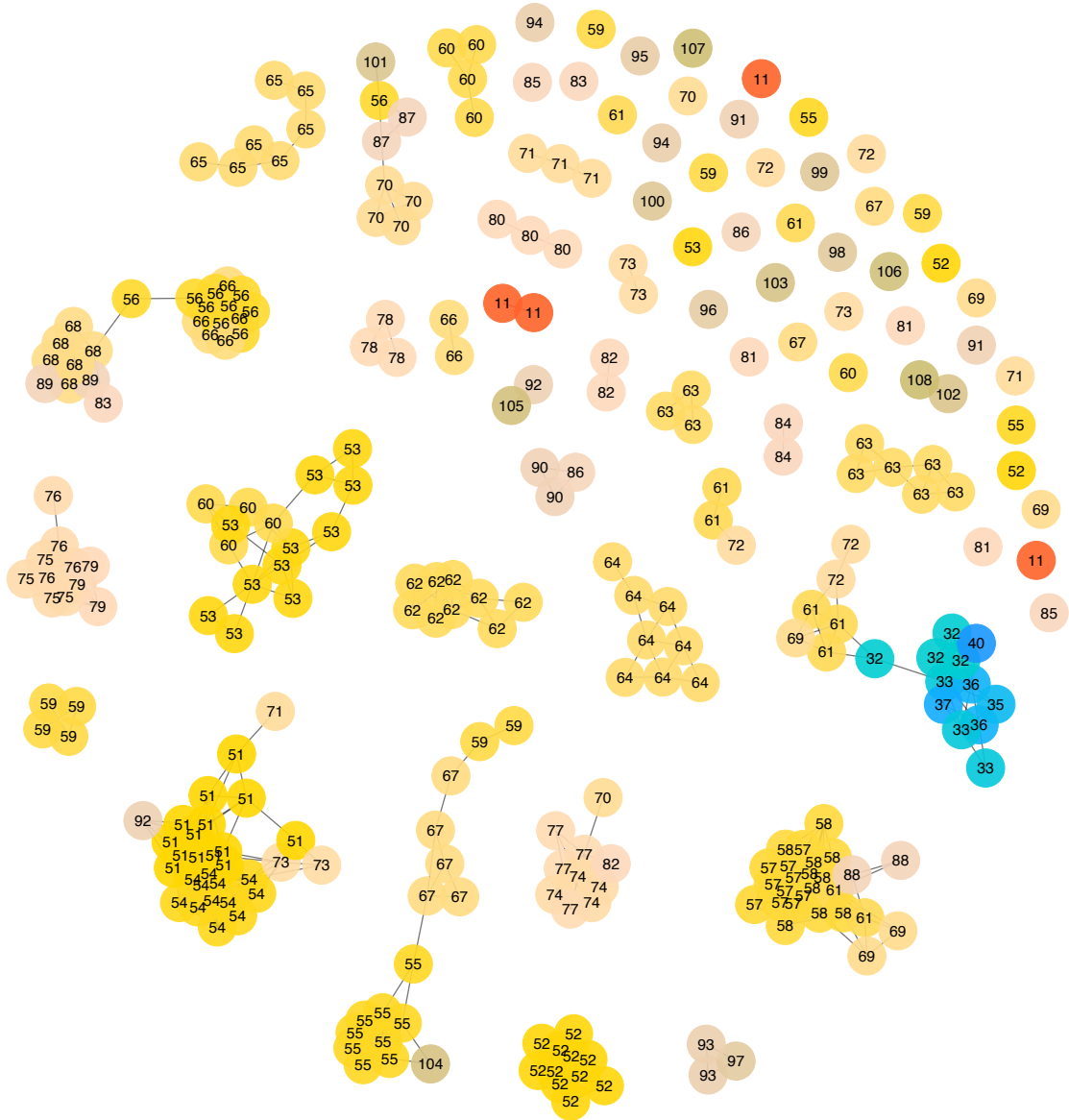
SUPPLEMENTARY FIGURE 2. Undirected graph network for the Multi group (enlarged version of Figure 1C).



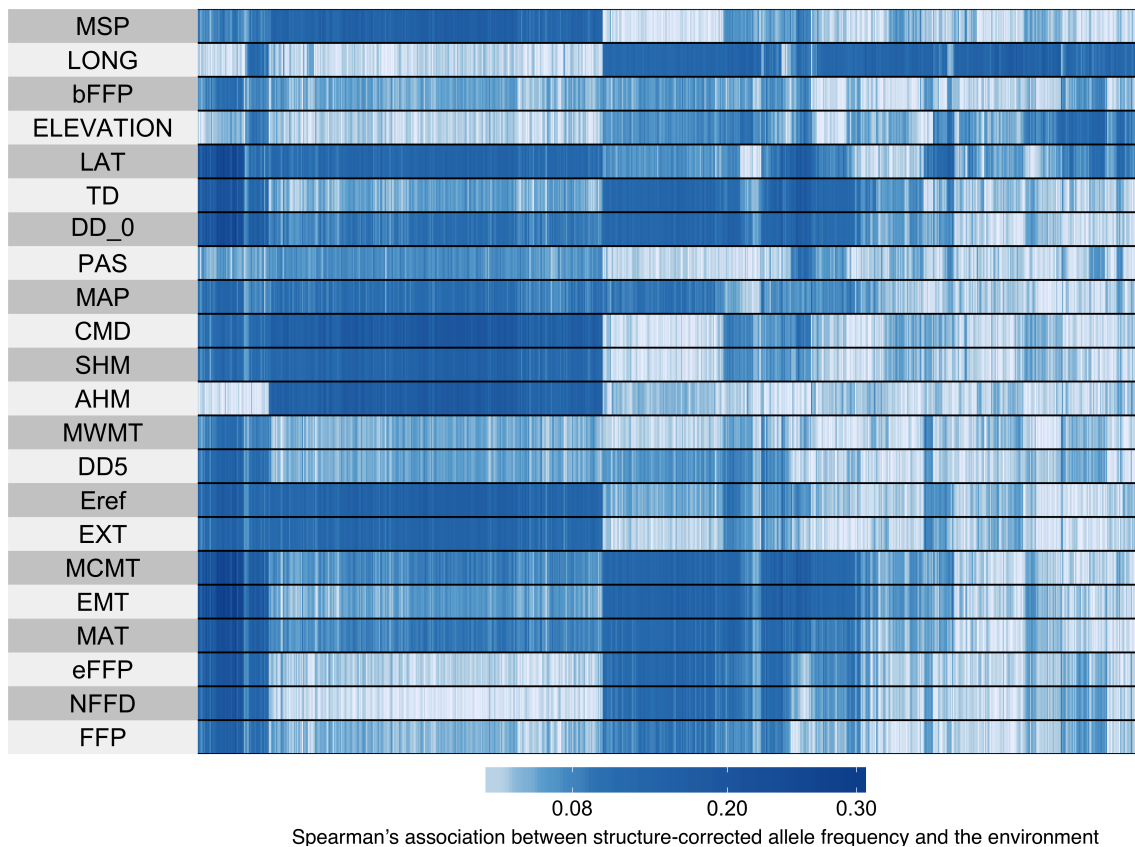
SUPPLEMENTARY FIGURE 3. Undirected graph network for the Aridity group (enlarged version of Figure 1D).



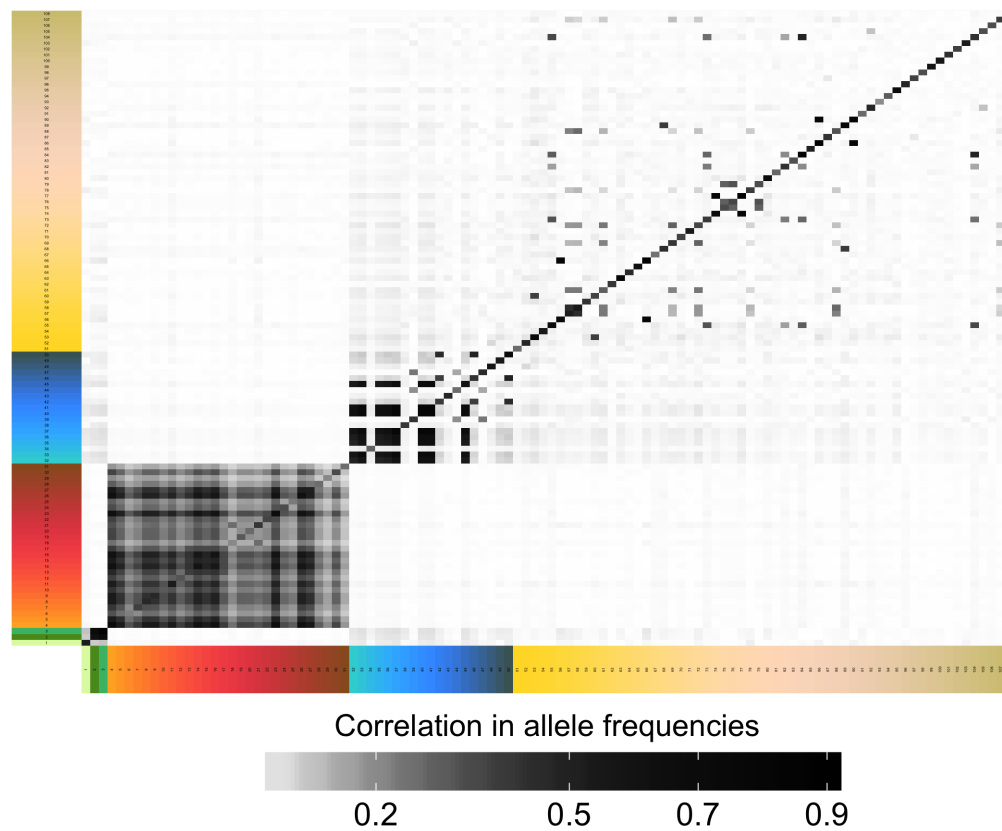
SUPPLEMENTARY FIGURE 4. Undirected graph network for the Freezing group (enlarged version of Figure 1E).



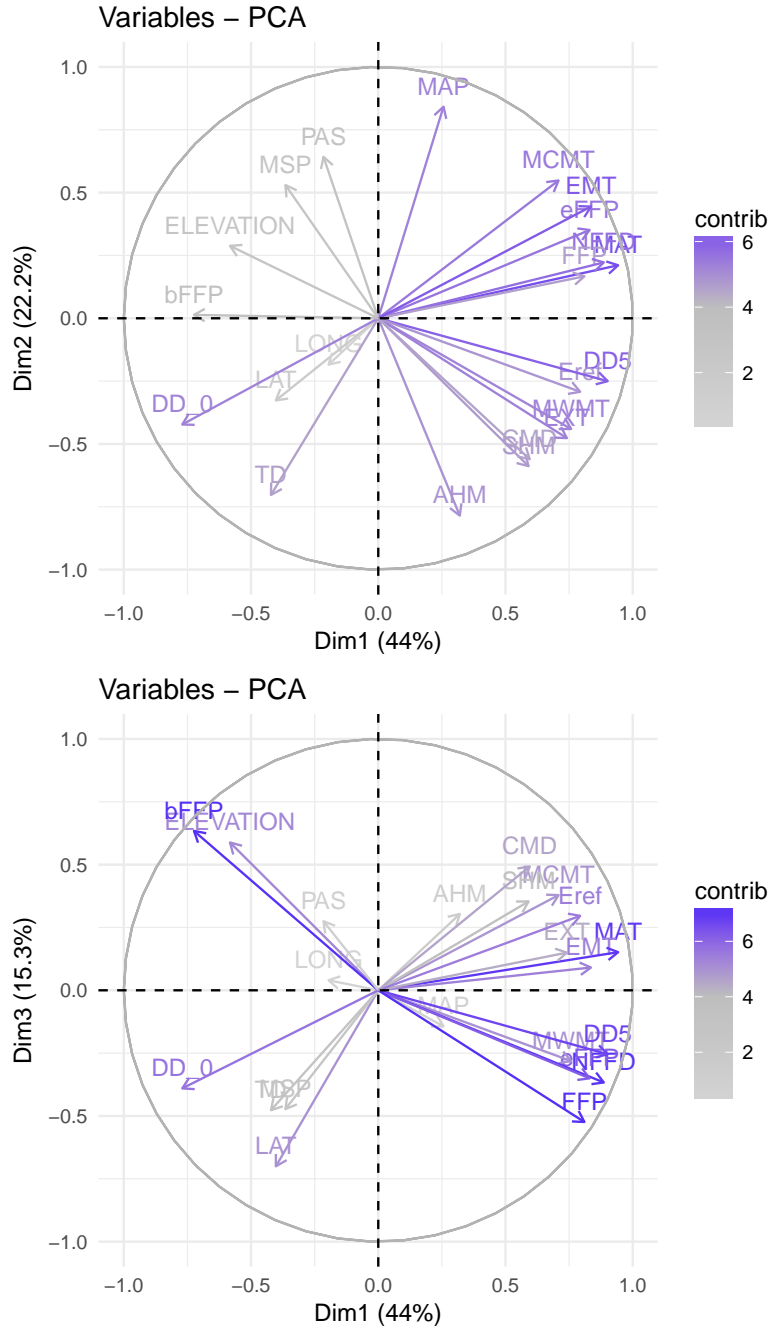
SUPPLEMENTARY FIGURE 5. Undirected graph network for the Geography group (enlarged version of Figure 1F).



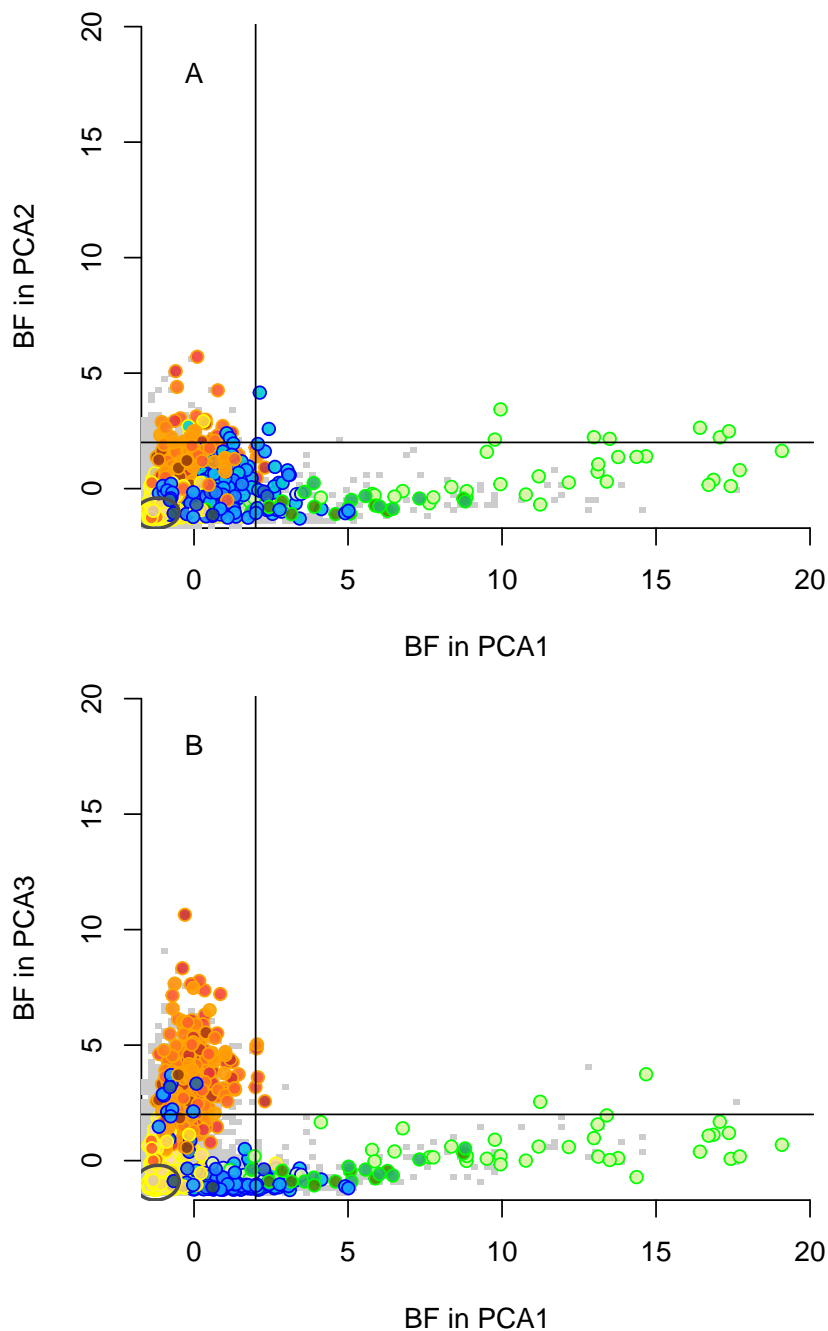
SUPPLEMENTARY FIGURE 6. Heatmap of structure-corrected allele associations with the environment, analogous to Figure 1B in the main paper. Note that although the pattern is very similar, the magnitude of allele correlations is smaller in the structure-corrected data.



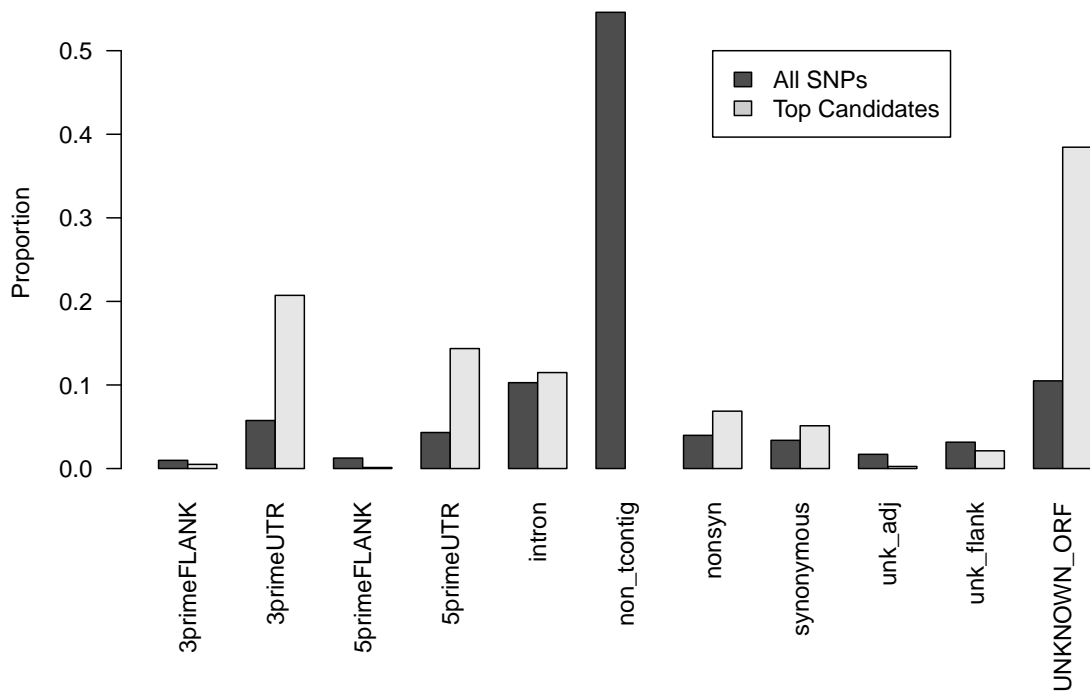
SUPPLEMENTARY FIGURE 7. Mean correlation among allele frequencies between top candidate contigs. Contigs are ordered the same as Figure 1G in the main paper.



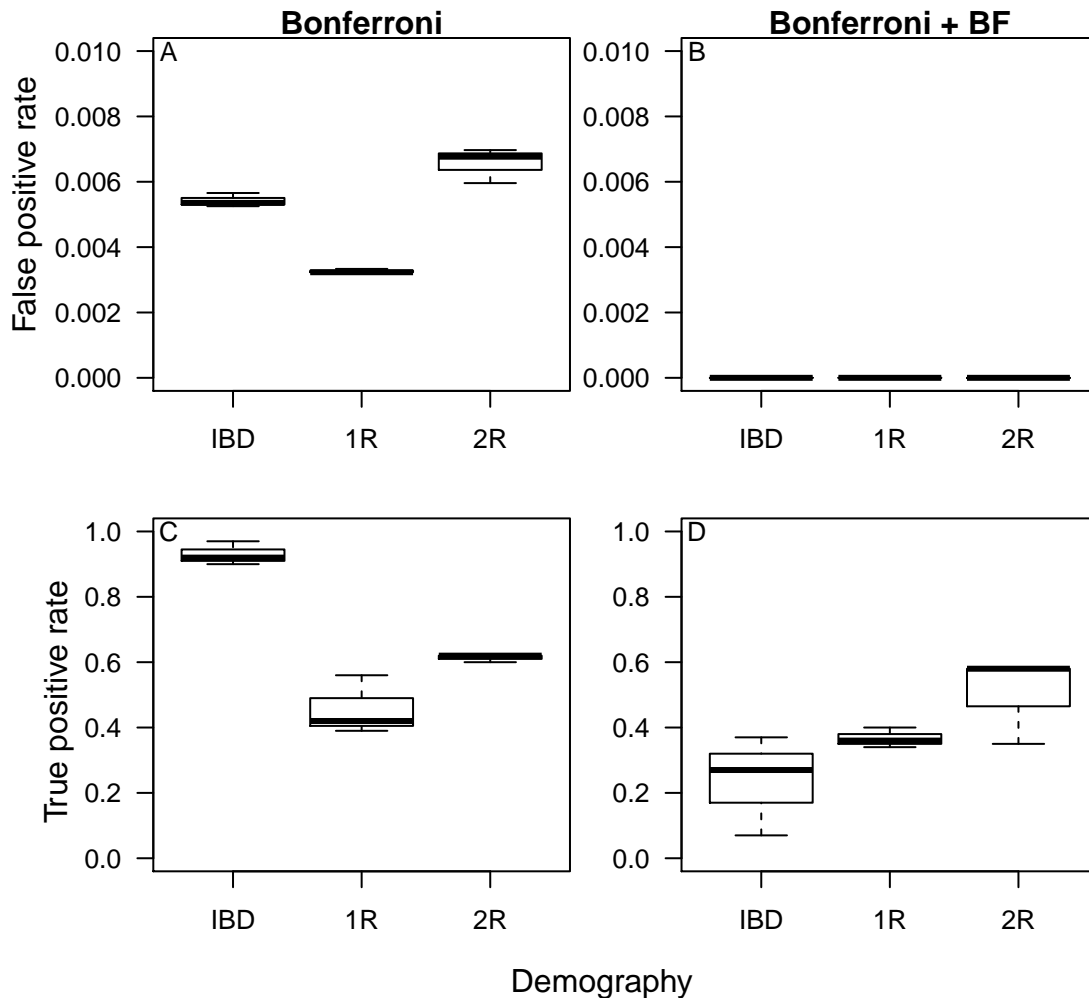
SUPPLEMENTARY FIGURE 8. The length and direction of each vector represents the scaled loading of that environmental variable onto the PC axis. The color of each vector represents the mean proportion of variance explained by that environment in the two axes plotted.



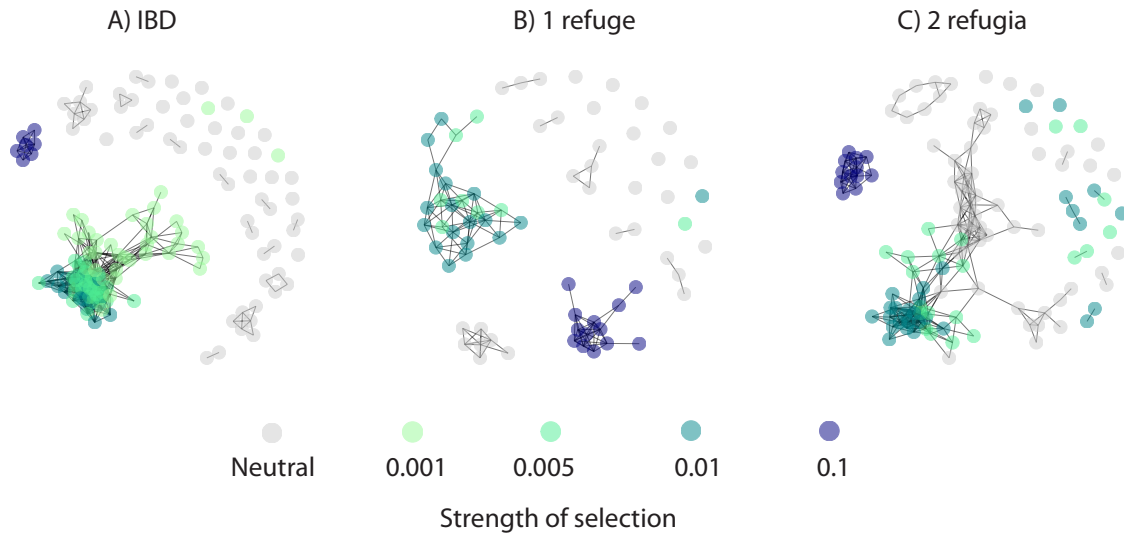
SUPPLEMENTARY FIGURE 9. The distribution of Bayes Factors for the association between SNPs and environments along the first three PC axes. Colored points correspond to the candidate described in the main paper: Aridity (orange), Multi (green), Freezing (blue), and Geography (yellow). Vertical and horizontal lines represent criteria for significance. Note that candidate SNPs all had $BF > 2$ with at least one univariate environmental variable.



SUPPLEMENTARY FIGURE 10. Proportion of SNPs falling into various categories for genomic features in the entire dataset compared to in the top candidate list. 3primeFLANK: 3' flanking region; 3primeUTR: 3' untranslated region; 5primeFLANK: 5' flanking region; 5primeUTR: 5' untranslated region; non-tcontig: not located in a transcriptomic contig (intergenic); nonsyn: non-synonymous substitution; unk-adj: unknown adjacent region; unk-flank: unknown flanking region; UNKNOWN-ORF: unknown open reading frame.



SUPPLEMENTARY FIGURE 11. Error rates from the simulations given a less stringent criteria (Bonferroni, left) and a more stringent criteria (Bonferroni and Bayes Factors from bayenv2, right). The less stringent criteria was used for the simulations because it had some false positives (A), while the more stringent criteria was used for the empirical data because it didn't have any false positives (B). While using the more stringent criteria resulted in no false positives, it also reduced the number of true positives (compare C and D), with the most severe reduction under isolation by distance.



SUPPLEMENTARY FIGURE 12. The simulated datasets were nested within randomly generated selective environments, such that different demographic histories were simulated on the same environmental landscape. For this randomly generated environment, loci simulated under stronger selection had a propensity to cluster differently than loci simulated under weaker selection.