

Figure S1. Comparison of MAF between genic and non-genic regions in array (left) and WGS (right) data.

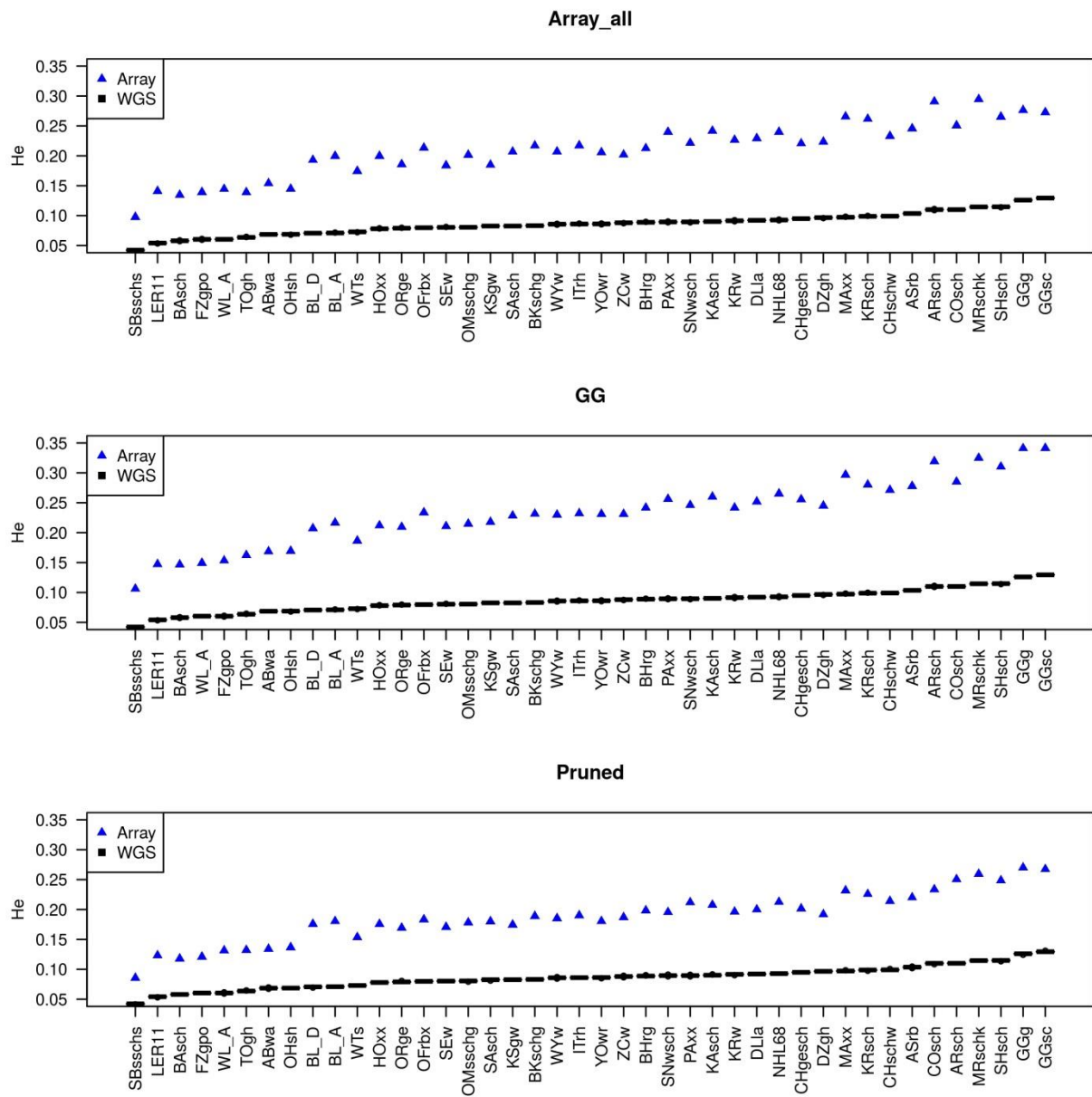


Figure S2. Comparisons of expected heterozygosity (H_e) estimates between WGS (boxplot of 100 replicates) and array (Array_all, GG and Pruned) data, for all 42 populations.

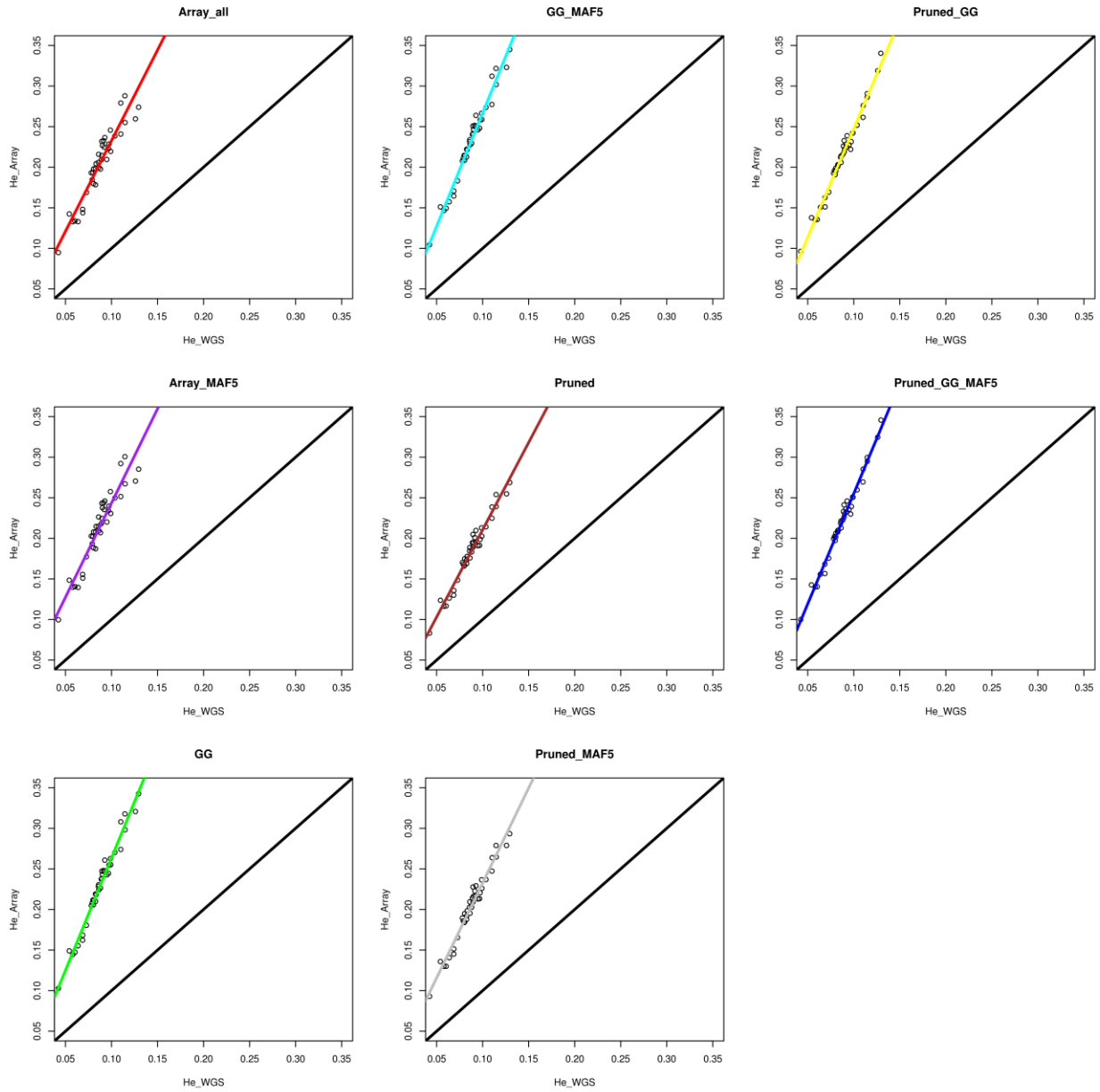


Figure S3. Expected heterozygosity (H_e) estimated with array vs. WGS data for the 39 populations.

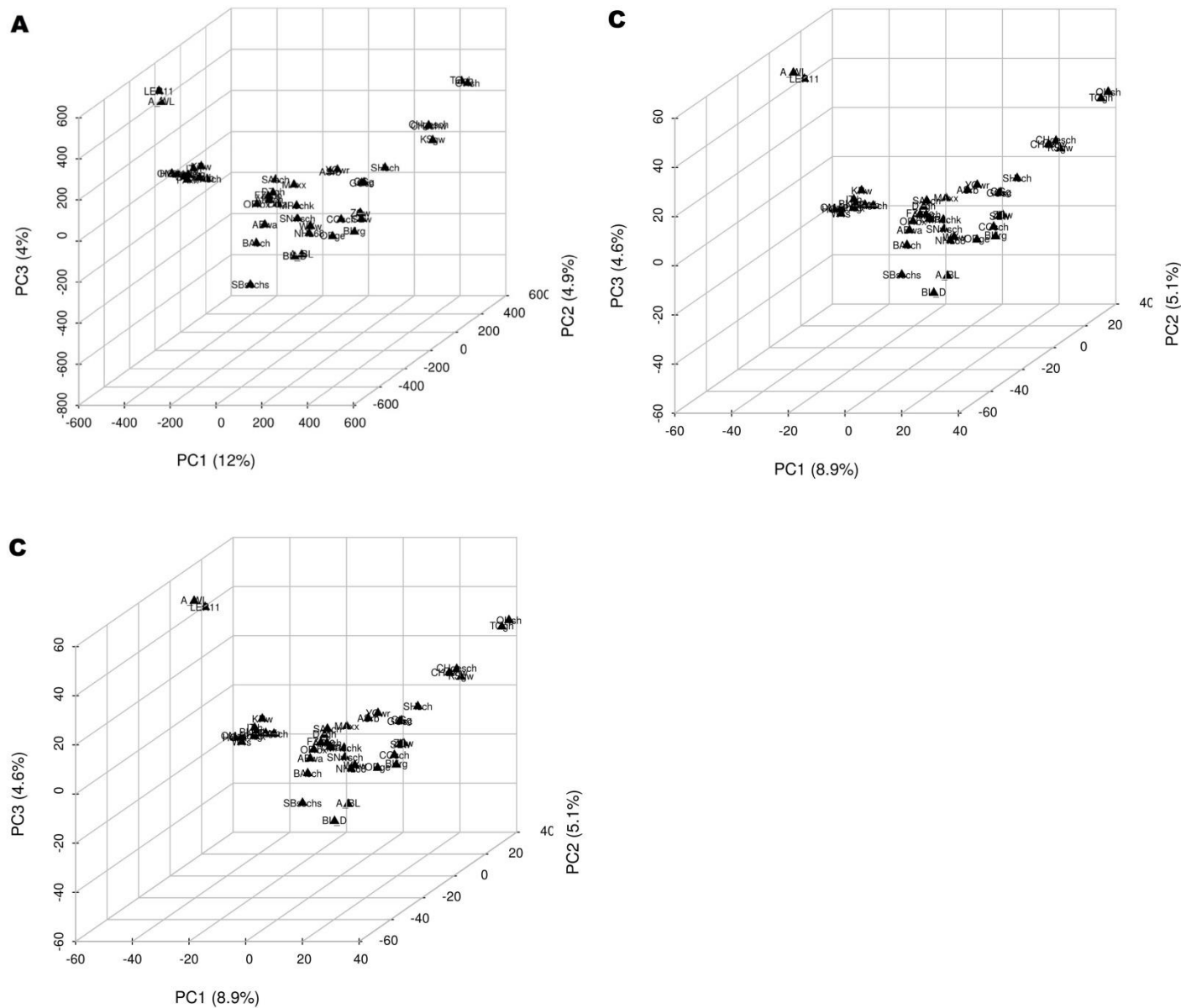


Figure S4. Three dimensional PCA plot of A) WGS, B) GG and C) Pruned array data.