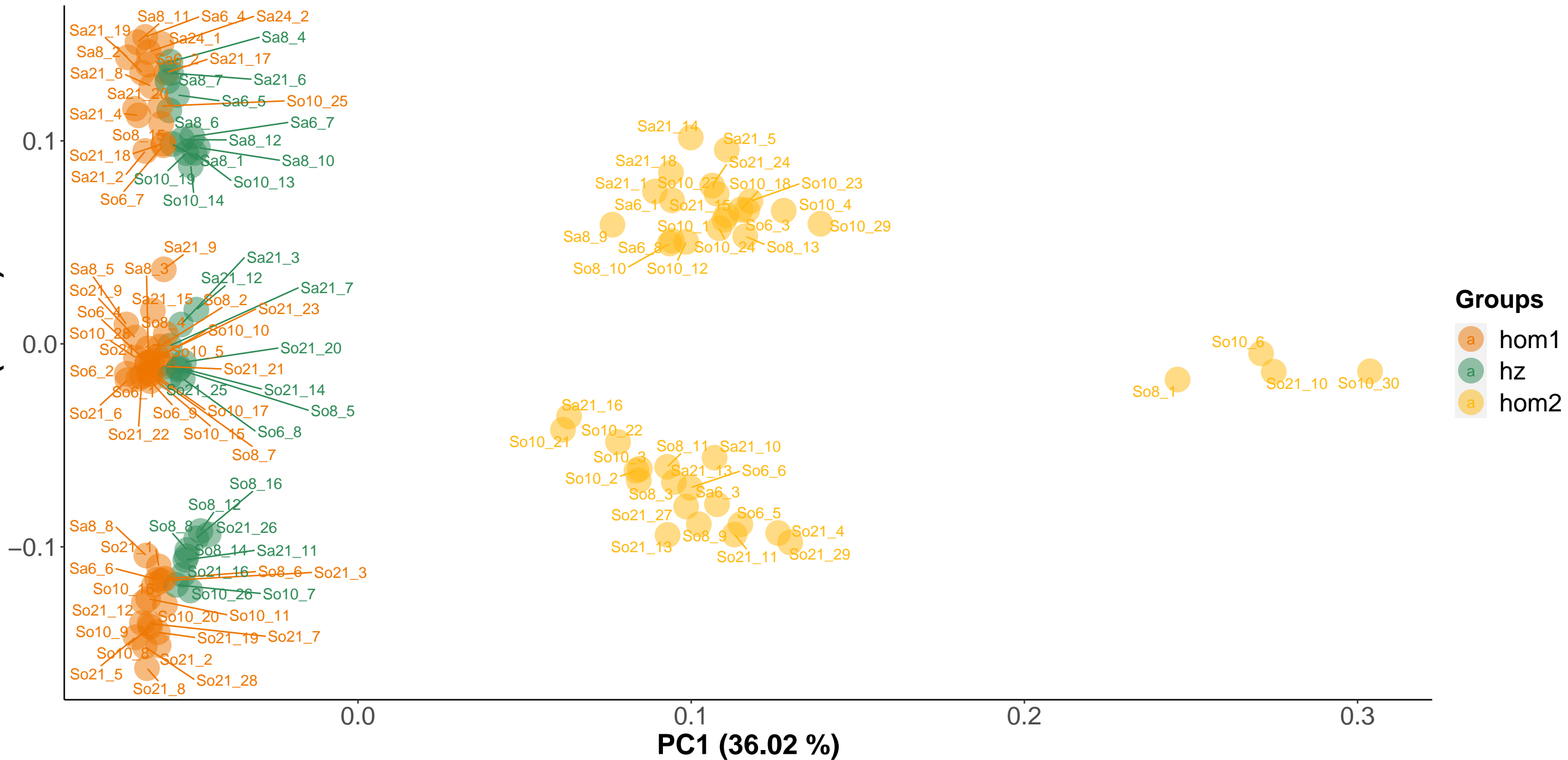


Best K-means clustering plot

PCA based on SNPs present in candidate structural variant

PC2 (9.79 %)



PC1 (36.02 %)

Heterozygosity between the Kmeans-based groups

