Recent natural selection conferred protection against schizophrenia by non-antagonistic pleiotropy

SUPPLEMENTARY FIGURES

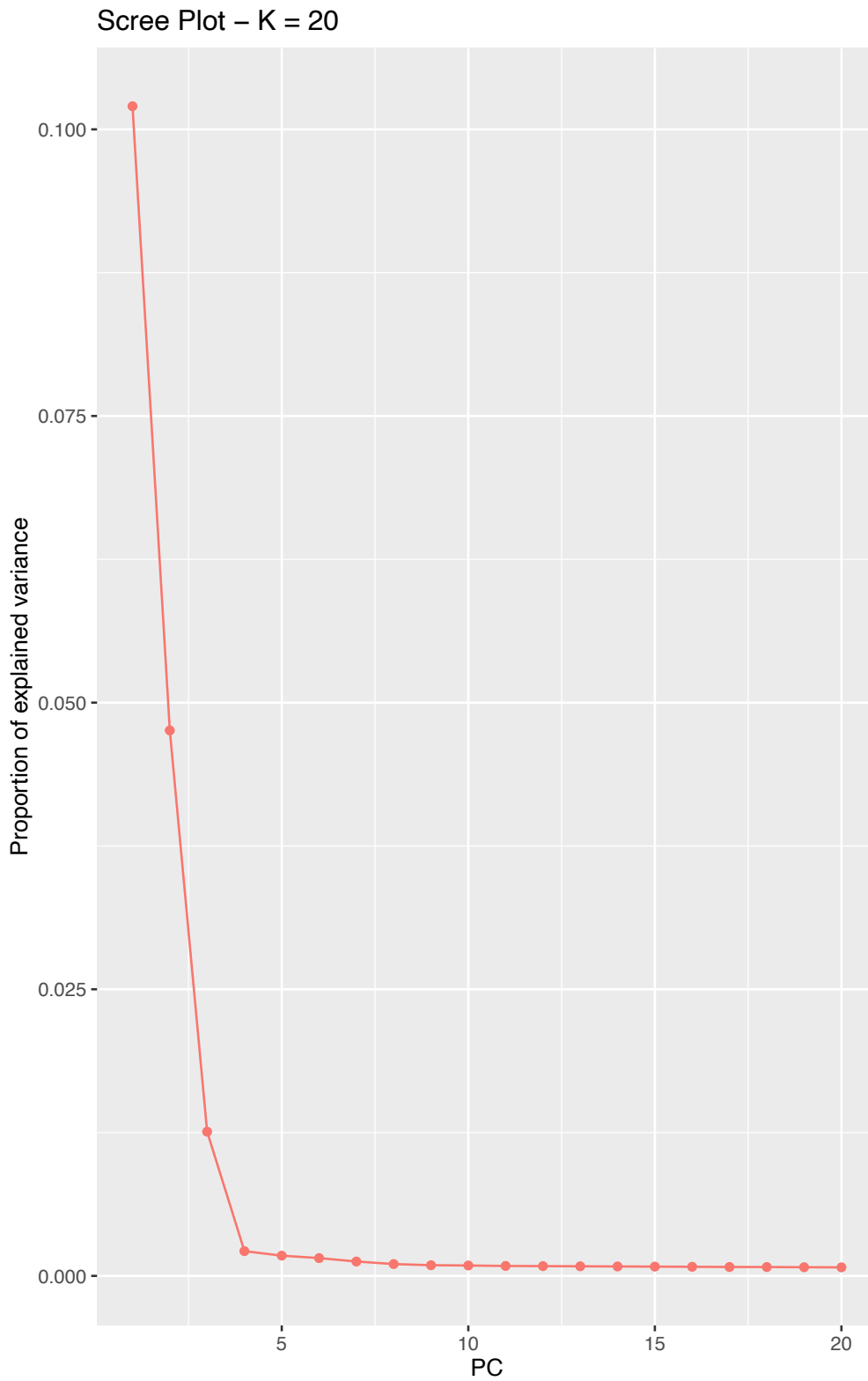**Supplementary Figure 1. Scree plot displaying the percentage of variance explained by each PC.** The number of PCs selected corresponds to the point where the scree plot is a steep curve followed by a bend and a straight line (Cattell's rule). Here, K = 3 is the optimal choice for K.

**Supplementary Figure 2. Principal components analysis (PCA) on 1000 genomes populations.** Score plot from PCA describing population structure of the subjects included in the study. 3 principal components were chosen based on Cattell's rule (**Supplementary Figure 1**). 1000 genomes phase 3 sequencing data 3 across African, European and Asiatic populations were used. We retained common biallelic genetic variation (MAF > 0.05), overlapped with summary data from the SCZ GWAS used in this study and with high imputation quality (score > 0.9). A total of 5,220,878 SNPs were used.
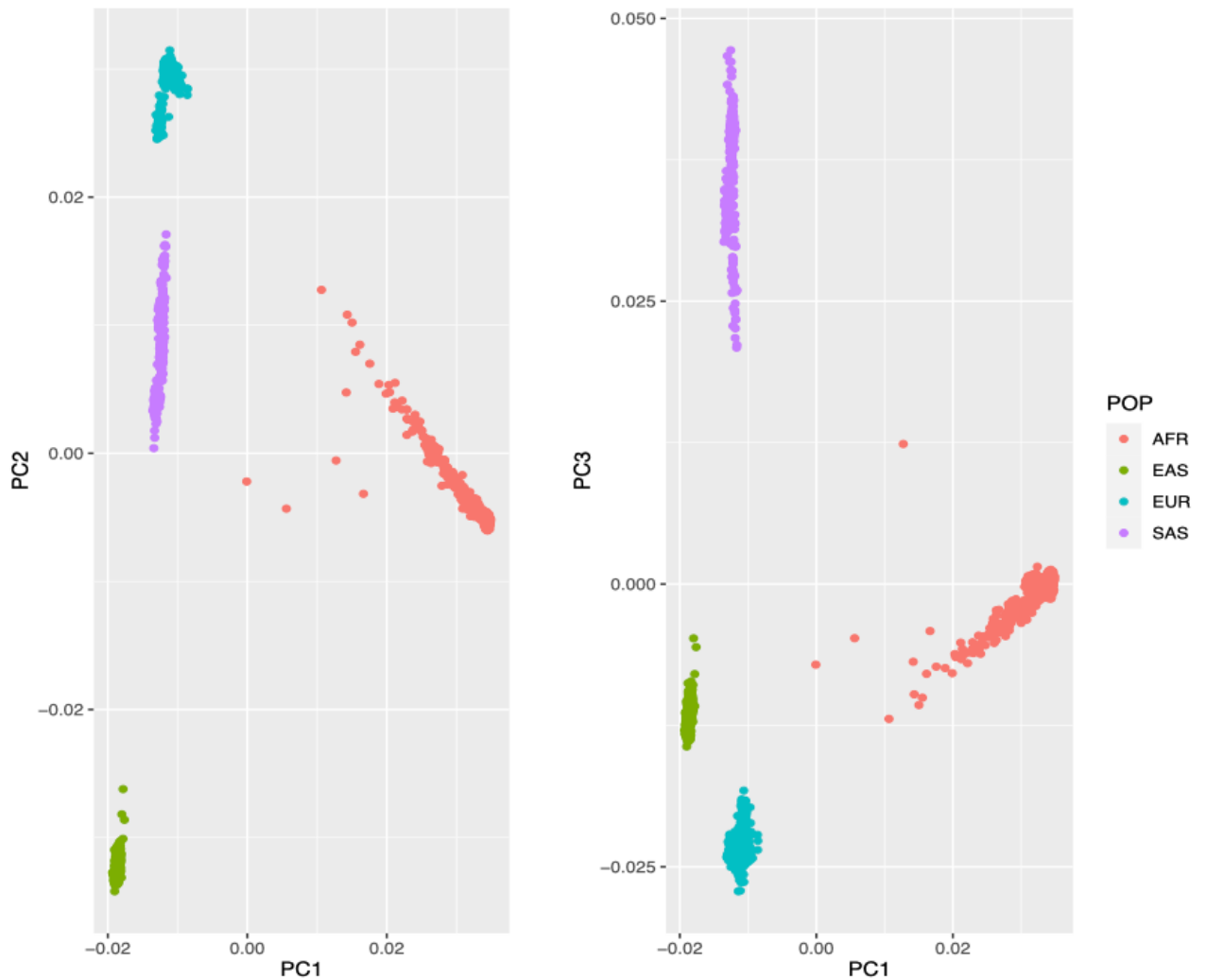
Supplementary Figure 3. Genome-wide display of RNS loci across the genome. Manhattan plot displaying probability to be a RNS signal ($-\log_{10}(p_{RNS})$) across autosomes is shown. 1000 genomes phase 3 sequencing data 3 across African, European and Asiatic populations were used. We retained common biallelic genetic variation (MAF > 0.05), overlapped with summary data from the SCZ GWAS used in this study and with high imputation quality (score > 0.9). A total of 5,554,437 SNPs were used. In the estimation of p_{RNS} for all SNP data, LD-genome structure (window size =200 SNP, $r^2 = 0.1$) was considered by pcadapt to avoid bias in PCA.
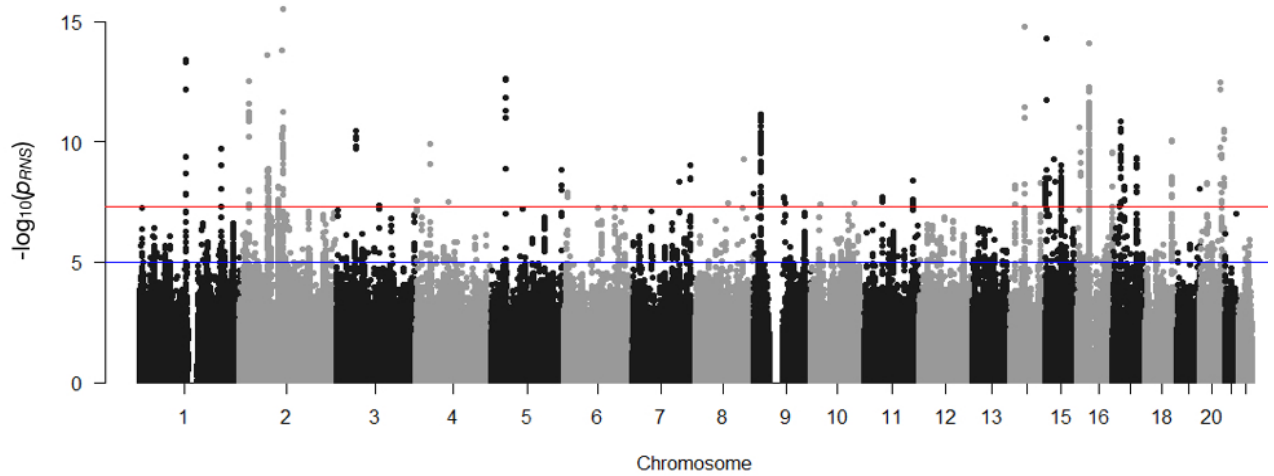
Supplementary Figure 4. Distribution of SNP studied accumulation p_{RNS} quantiles. Histogram of p_{RNS} indicating the higher accumulation of SNP with low p_{RNS} values than expected by chance.
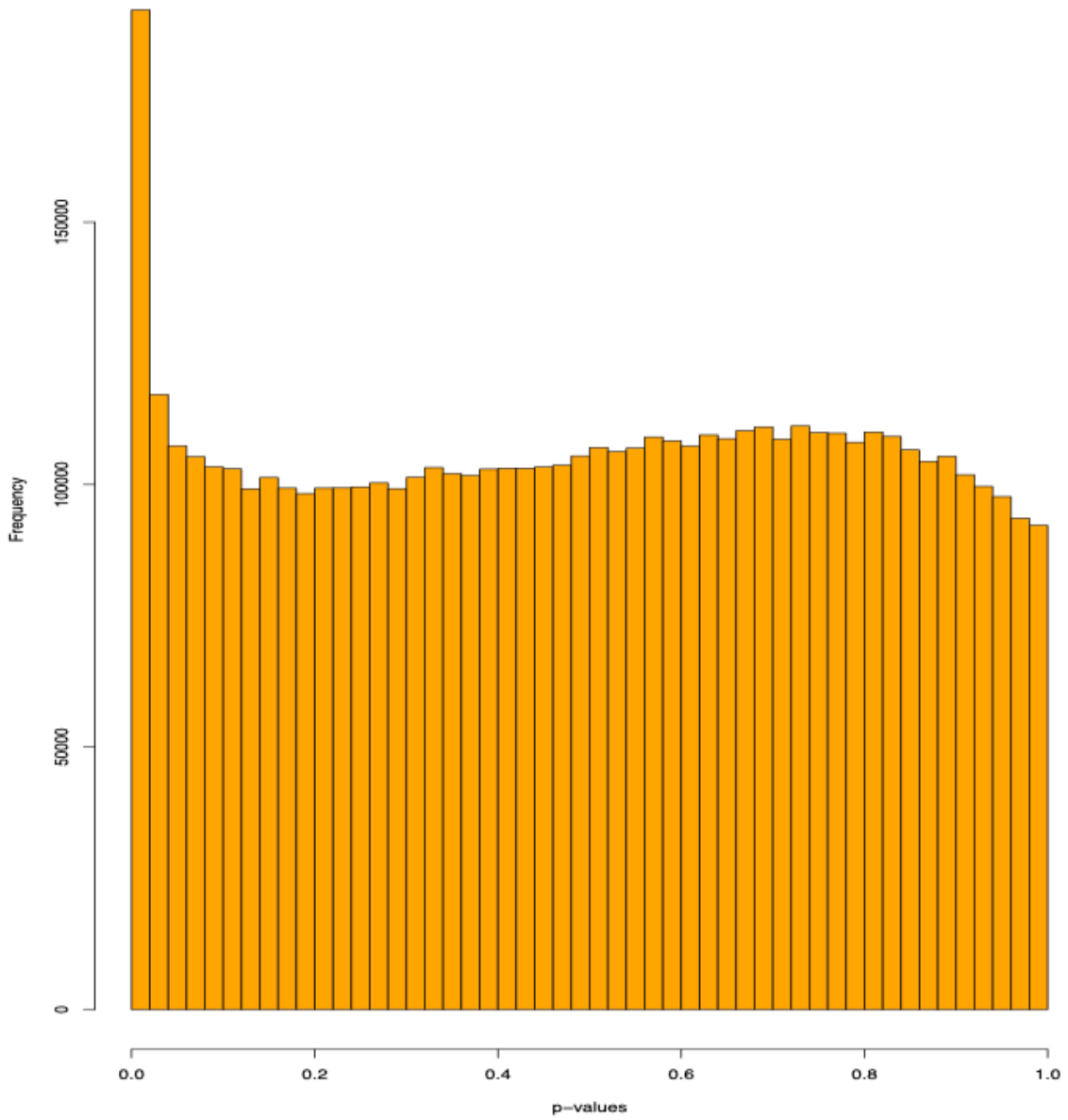
Supplementary Figure 5. Visual evaluation for the presence of recent natural selection outliers (Q-Q plot). A) Q-Q plot comparing the expected vs observed p-values for the SNP here studied. B) Statistical distribution of the Mahalanobis distance between each SNP and the PCs (K = 3).