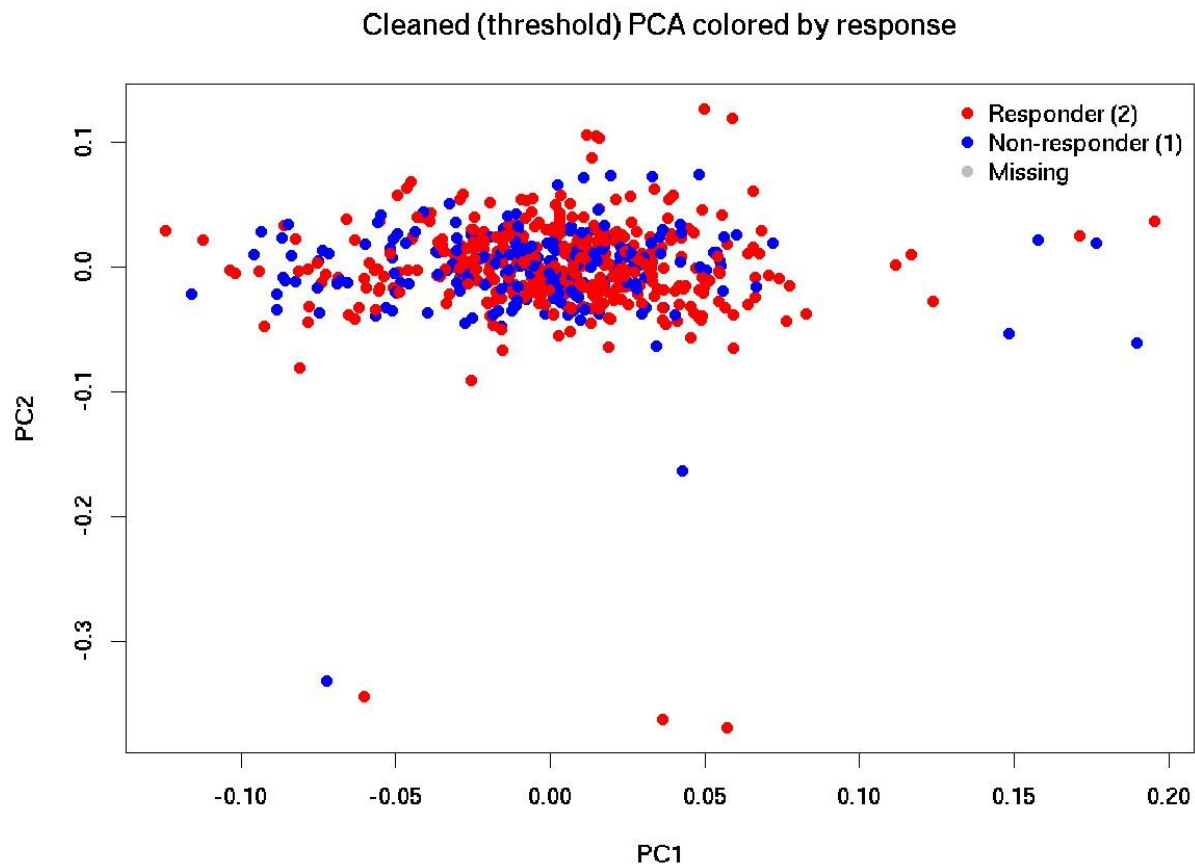




Supplementary Figure 1. Principal component analysis (PCA) of the study cohort colored by methadone treatment response. PCA was performed on linkage-disequilibrium-pruned autosomal SNPs to assess population structure. Shown are the first two principal components (PC1 and PC2), with individuals colored by treatment response status (responders, non-responders, and missing phenotype). Population outliers were identified as individuals exceeding ± 6 standard deviations on any principal component and were excluded prior to downstream analyses ($n = 8$). No additional outliers were detected following imputation. Principal components were retained as covariates in PRS and GWAS analyses to account for residual population stratification.