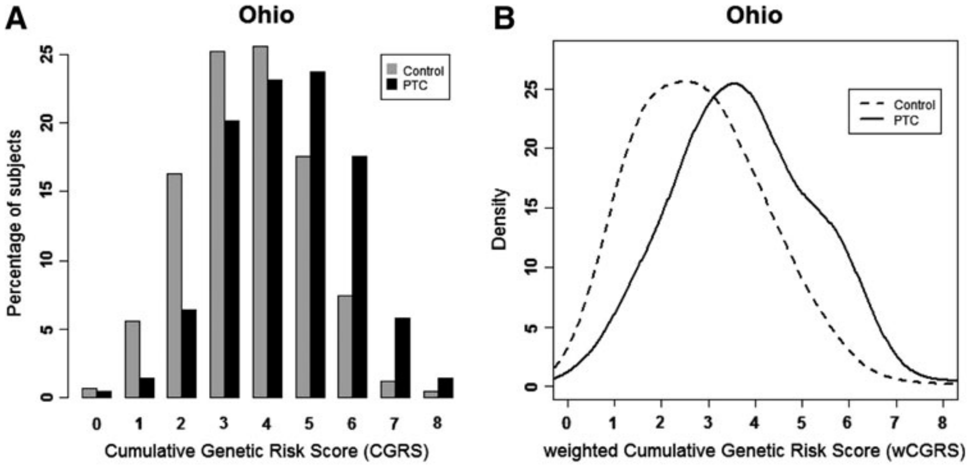
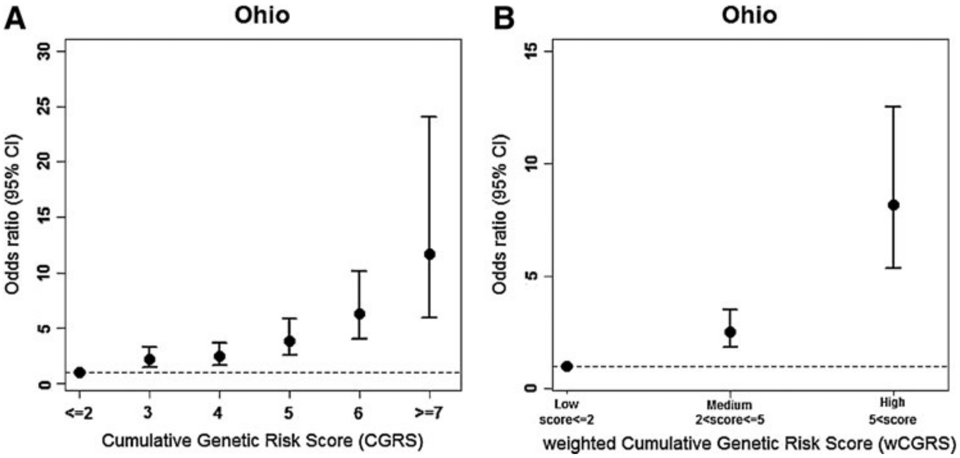
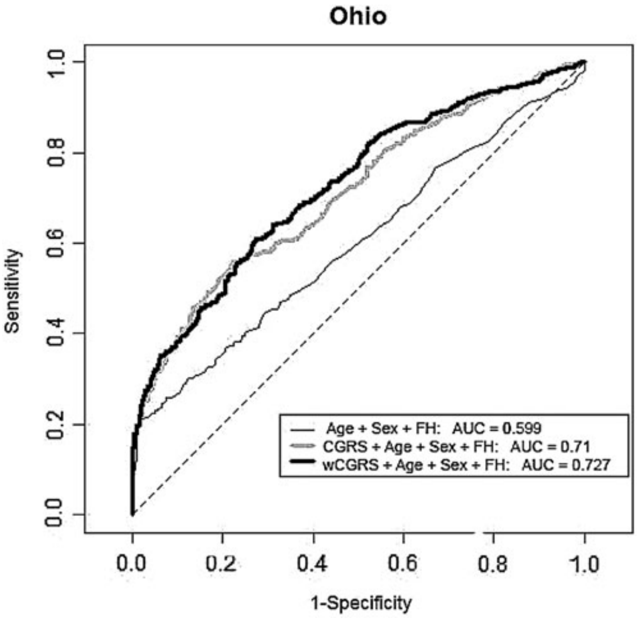


SUPPLEMENTARY FIG. S4. Cumulative risk scores in the Ohio cohort, after removing microPTC samples. **(A)** Distribution of number of risk alleles or CGRSs between cases and controls. **(B)** Distribution of wCGRS between cases and controls. **(A, B)** Sets of 916 controls and 501 cases without any missing genotypes were used for the analysis.



SUPPLEMENTARY FIG. S5. Age- and sex-adjusted odds ratios (OR) and their 95% CI for the CGRSs **(A)** and wCGRSs **(B)**, in the Ohio cohort after removing microPTC samples. The groups with CGRS ≤ 2 and wCGRS ≤ 2 were set as reference groups.



SUPPLEMENTARY FIG. S6. ROC curves, after removing microPTC samples. ROC curves assessing the discriminative power of the unweighted and weighted cumulative genetic risk score models. A random sample of age- and sex-matched cases ($n = 489$) and controls ($n = 489$) from the Ohio cohort was used for the analysis. Model was adjusted for age, sex, and family history (FH).