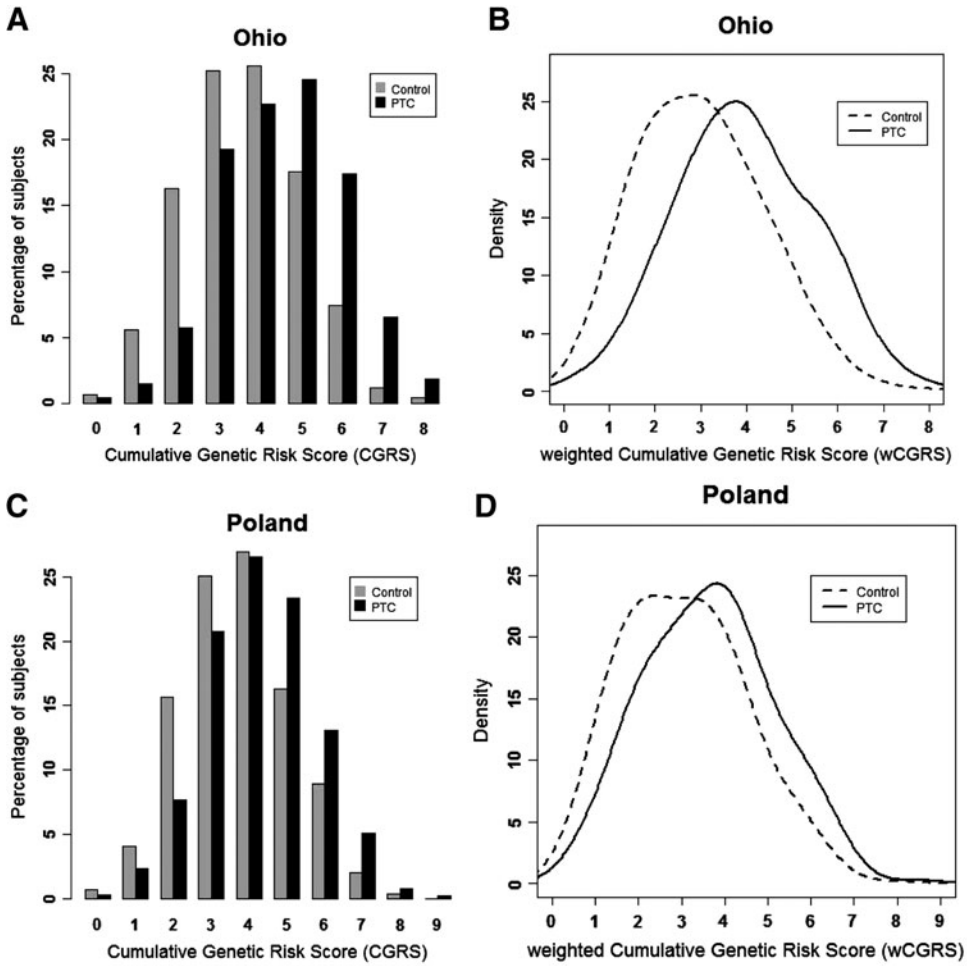
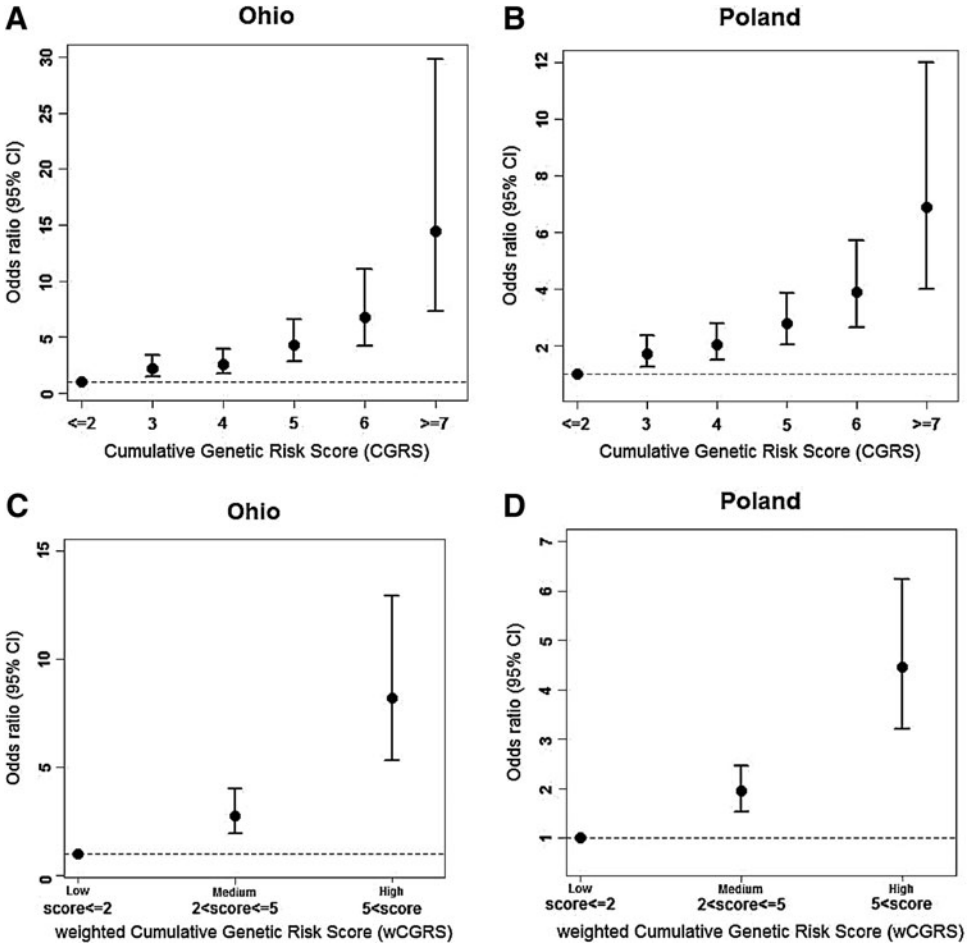
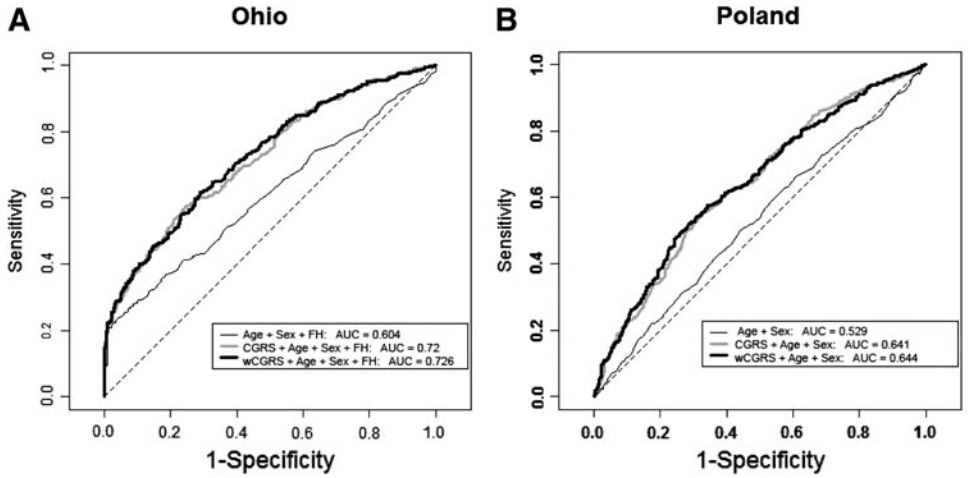
Supplementary Data



SUPPLEMENTARY FIG. S1. Cumulative risk scores in Ohio and Polish cohorts, after removing folicular variant papillary thyroid carcinoma (FVPTC) samples. **(A, C)** Distribution of number of risk alleles or cumulative genetic risk scores (CGRS) between cases and controls. **(B, D)** Distribution of weighted cumulative genetic risk scores (wCGRS) between cases and controls. **(A, B)** Ohio cohort; set of 916 controls and 488 cases without any missing genotypes were used for the analysis. **(C, D)** Polish cohort; set of 1663 controls and 1470 cases without any missing genotypes are used for the analysis.



SUPPLEMENTARY FIG. S2. Age- and sex-adjusted odds ratios (OR) and their 95% CI for the CGRSs **(A, B)** and wCGRSs **(C, D)**, after removing FVPTC samples. The groups with CGRS ≤ 2 and wCGRS ≤ 2 were set as reference groups. **(A, C)** Ohio cohort. **(B, D)** Polish cohort.



SUPPLEMENTARY FIG. S3. ROC curves. **(A)** ROC curves assessing the discriminative power of the unweighted and weighted cumulative genetic risk score models, after removing FVPTC samples. A random sample of age- and sex-matched cases ($n = 480$) and controls ($n = 480$) from the Ohio cohort was used for the analysis. Model was adjusted for the age, sex and family history (FH). **(B)** ROC curves assessing the discriminative power for the unweighted and weighted cumulative genetic risk score models. A random sample of age- and sex-matched cases ($n = 643$) and controls ($n = 643$) from the Polish cohort was used for the analysis. Model was adjusted for age and sex.