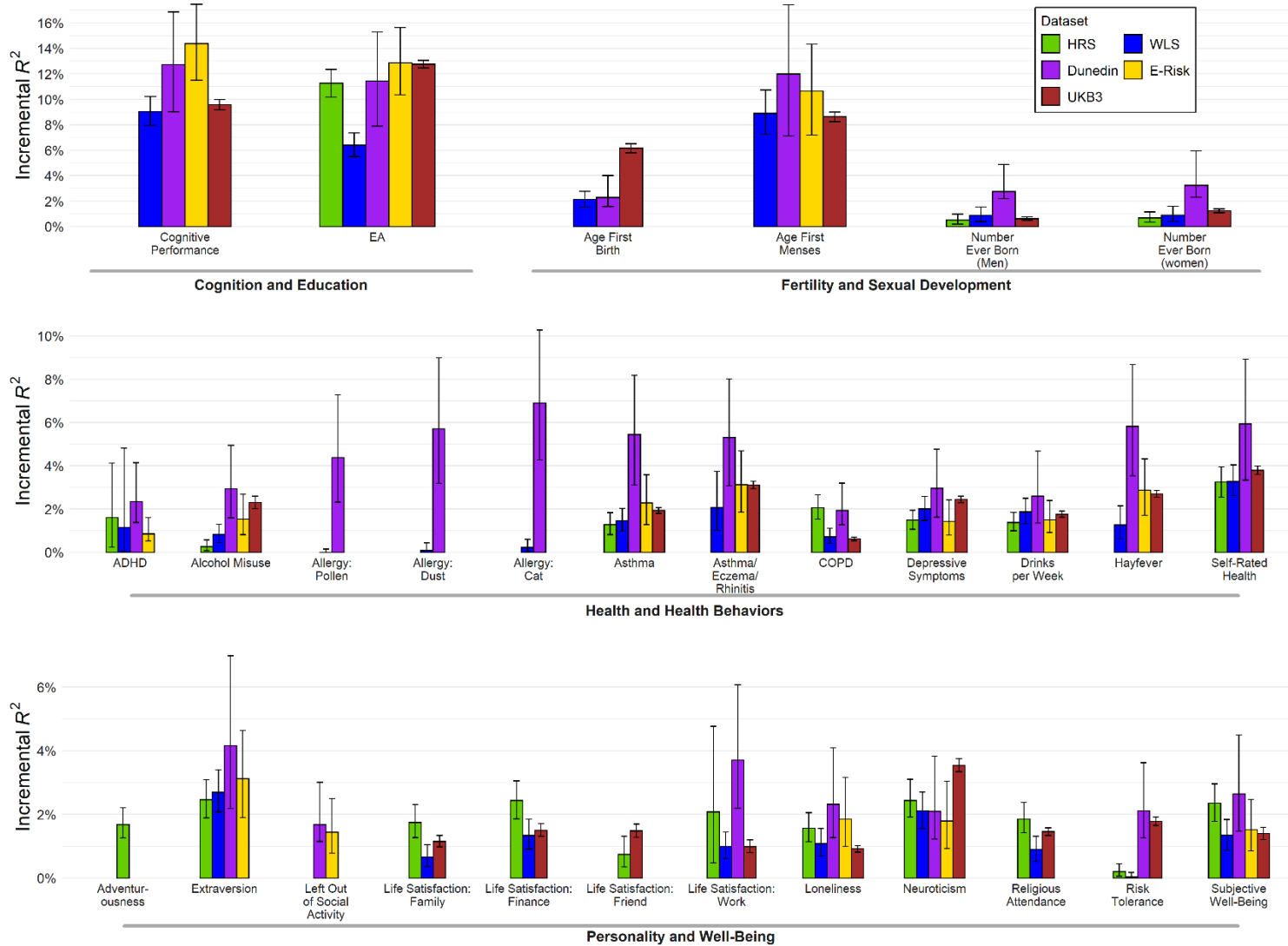
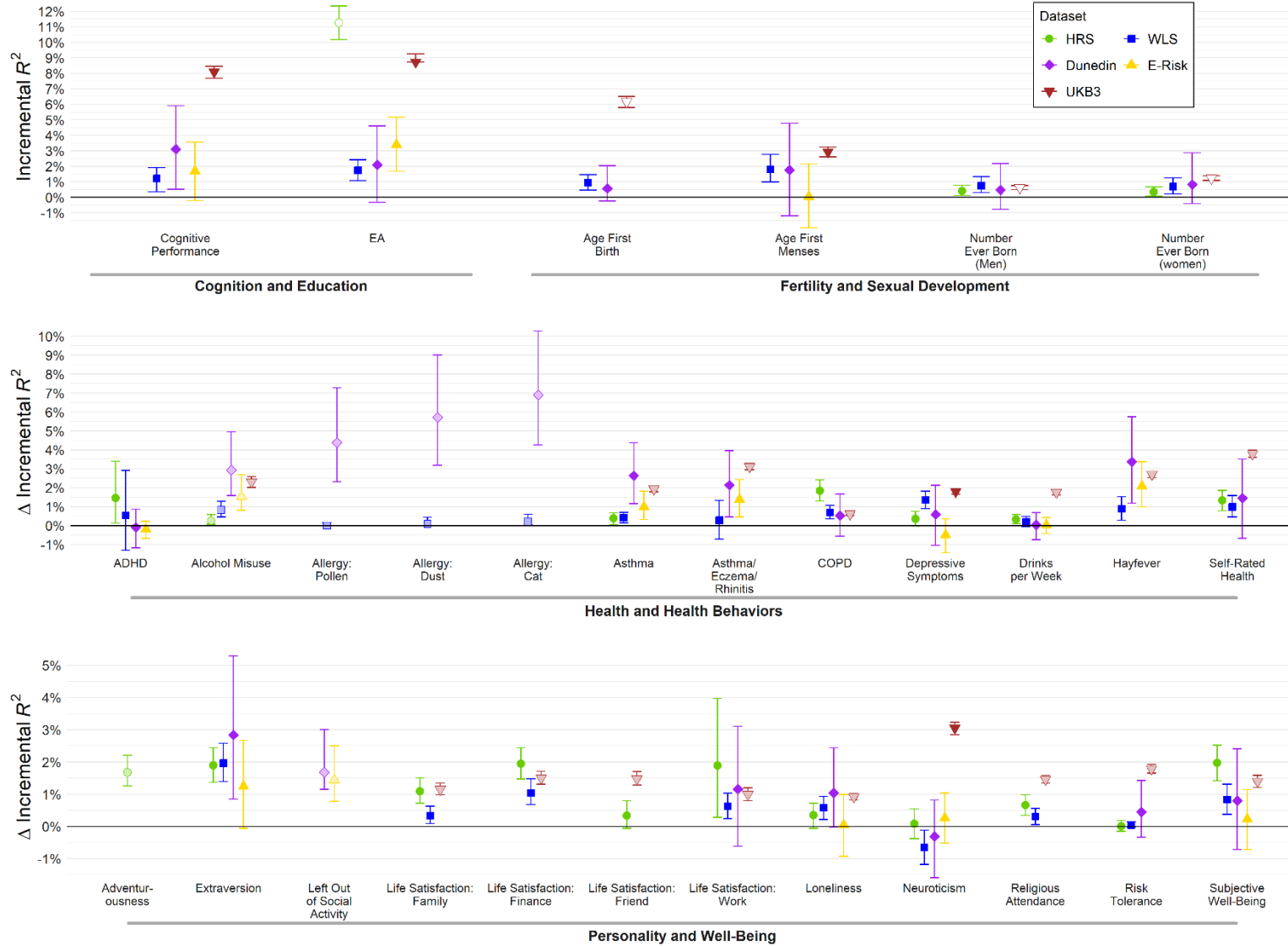


# Supplementary Figure 1. Predictive power of Repository multi-trait PGIs

(A)



(B)



**Notes:** Error bars show 95% confidence intervals from bootstrapping with 1,000 repetitions. Panel (A): Incremental  $R^2$  from adding Repository's multi-trait PGI to a regression of the phenotype on 10 principal components of the genetic relatedness matrix for HRS, WLS, Dunedin, and E-Risk, and on 20 principal components and 106 genotyping batch dummies for UKB. Prior to the regression, phenotypes are residualized on a second-degree polynomial for age or birth year, sex, and their interactions (see Supplementary Tables 5 and 12). For the GWAS-equivalent sample sizes of the summary statistics that the PGIs are based on, see Supplementary Table 10. Panel (B): Difference in incremental  $R^2$  between Repository multi-trait PGI and PGI constructed from publicly available summary statistics using our Repository pipeline. (Note that the latter do not include PGI directly available from datasets, such as the ones accessible from the HRS website.) If no publicly available summary statistics are available for a phenotype, then the difference in incremental  $R^2$  is equal to the incremental  $R^2$  of the single-trait PGI and is represented by an open circle. For the GWAS sample sizes of the PGIs based on publicly available summary statistics, see Supplementary Table 13.