**Figure S1. LD Score regression and gene-set enrichment reveal genetic overlap between adult height and testicular cancer.** (A) LD Score regression summary for each phenotype. Mean chisq denotes the average chi-square statistic across all SNPs. The genomic control inflation factor (Lambda GC) quantifies potential population stratification. The LDSC intercept and its standard error (SE) capture residual confounding. The ratio and its SE indicate the fraction of inflation attributable to the polygenic signal. Observed SNP-based heritability (H2\_obs) and its SE reflect the proportion of phenotypic variance explained by SNPs; H2\_Z and H2\_p report the Z-score and p-value for the genetic correlation estimate. (B, C) Gene-set enrichment analysis of genes mapped from SNPs reaching genome-wide significance. The combined score integrates adjusted p-values and Z-scores. Panel B highlights top enrichment of the DisGeNET “Body height” category; Panel C highlights top enrichment of the Jensen\_DISEASES “TC” category (see Table S2).