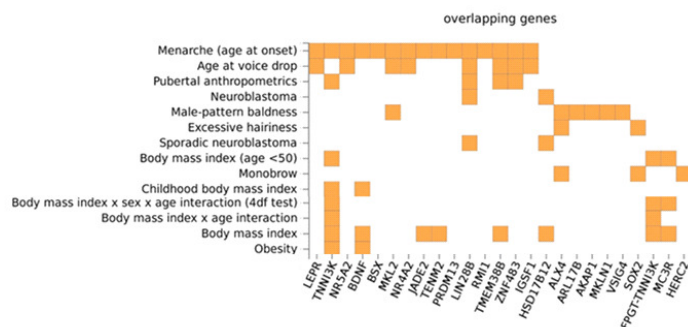
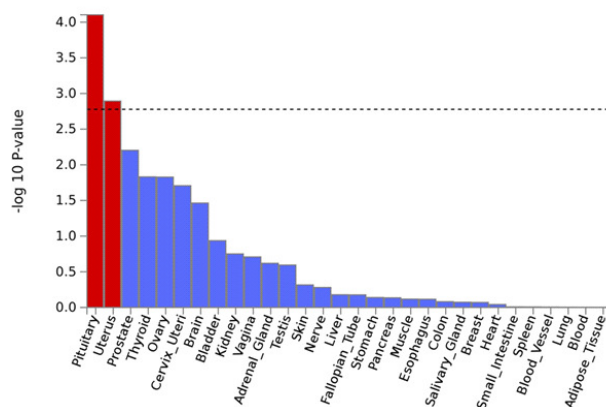


Supplementary Figure 1. GWAS catalog reported genes and tissue expression analysis extracted from GENE2FUNC function of FUMA platform (<https://fuma.ctglab.nl/>). A) Representation of genes of interest in a catalog of GWAS. B) Tissue expression analysis testing the positive relationship between all annotated genes using the full distribution of SNPs p-values and the average expression of genes per tissue type based on GTEx RNA-seq data. Significant enrichment at Bonferroni corrected P-value ≤ 0.05 are colored in red. C) Differential expression analysis of prioritized genes in a panel of 30 genes. Genes with P-value ≤ 0.05 after Bonferroni correction and absolute log fold change ≥ 0.58 were defined as differentially expressed genes in a given tissue compared to others.

A



B



C

