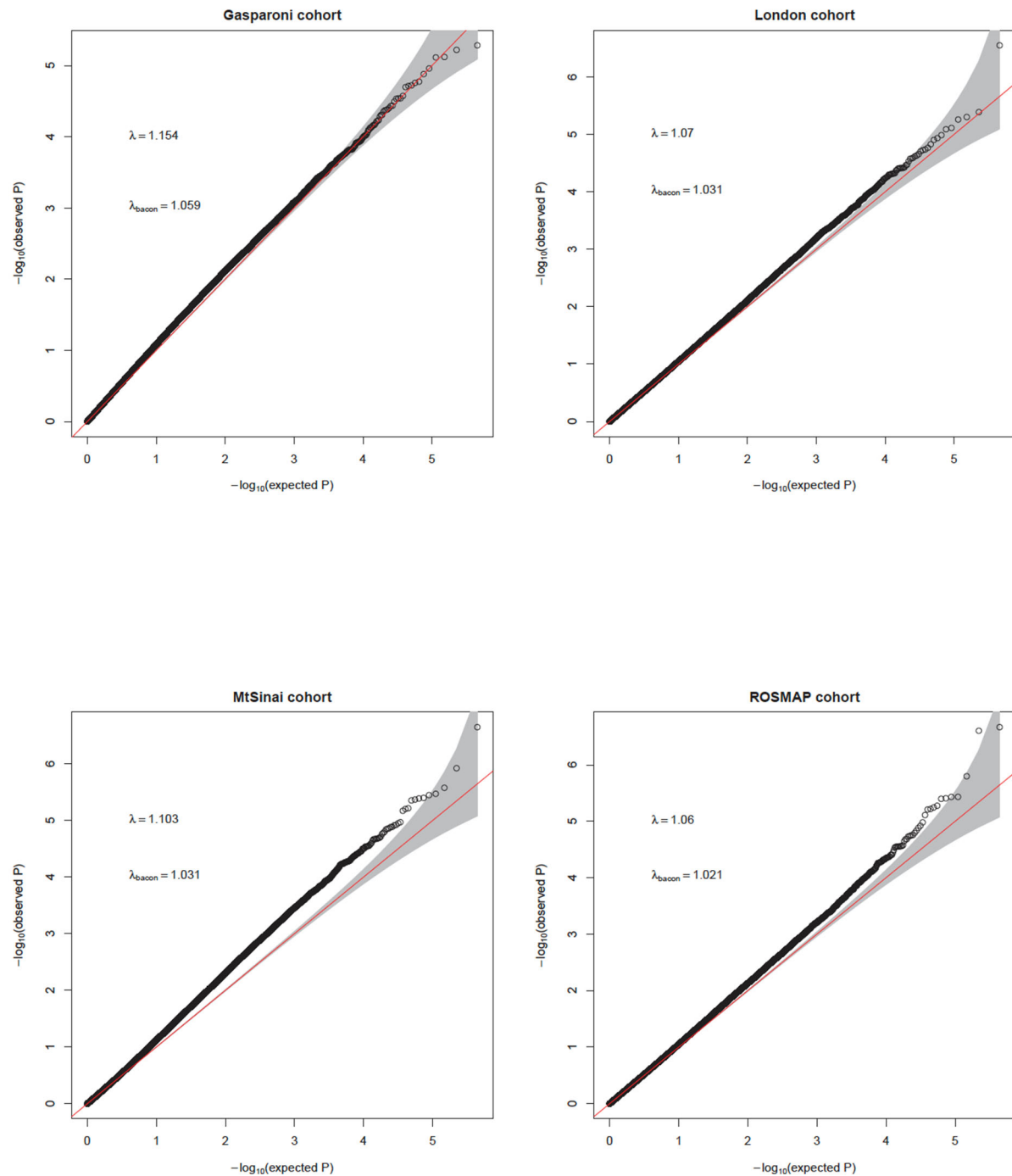
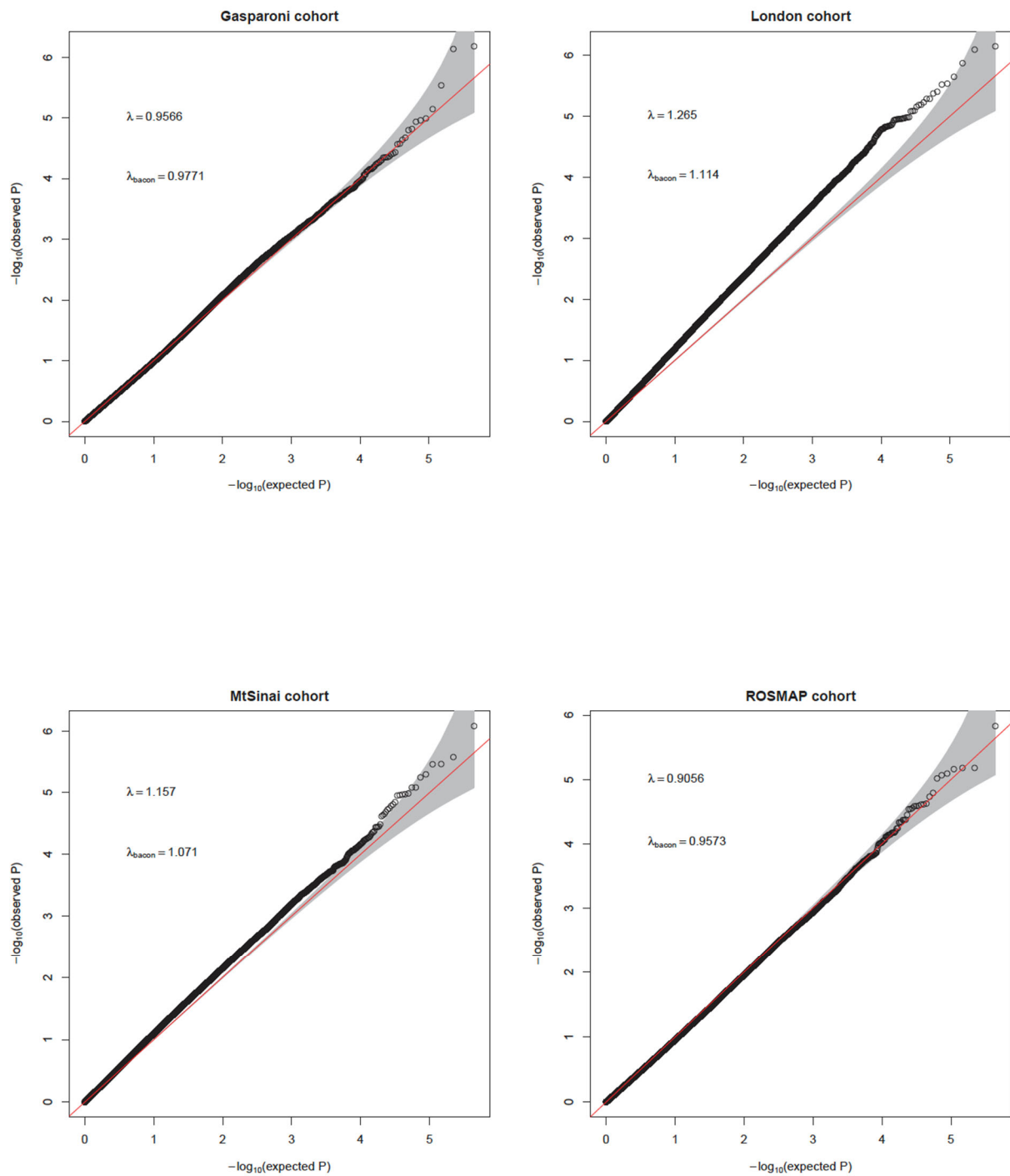


Supplementary Figure 1 Quantile-quantile (QQ) plots of observed and expected distributions of p-values in Gasparoni, London, Mount Sinai, and ROSMAP cohorts. λ is the genomic inflation factor, and λ_{bacon} is the genomic inflation factor estimated using the method of Iterson et al. (2017) (PMID: 28129774), as implemented in the bacon R package. Shading indicates 95% confidence intervals. Reference line in red indicates expected distribution of $-\log_{10}(\text{P-values})$ under the null hypothesis of no association.

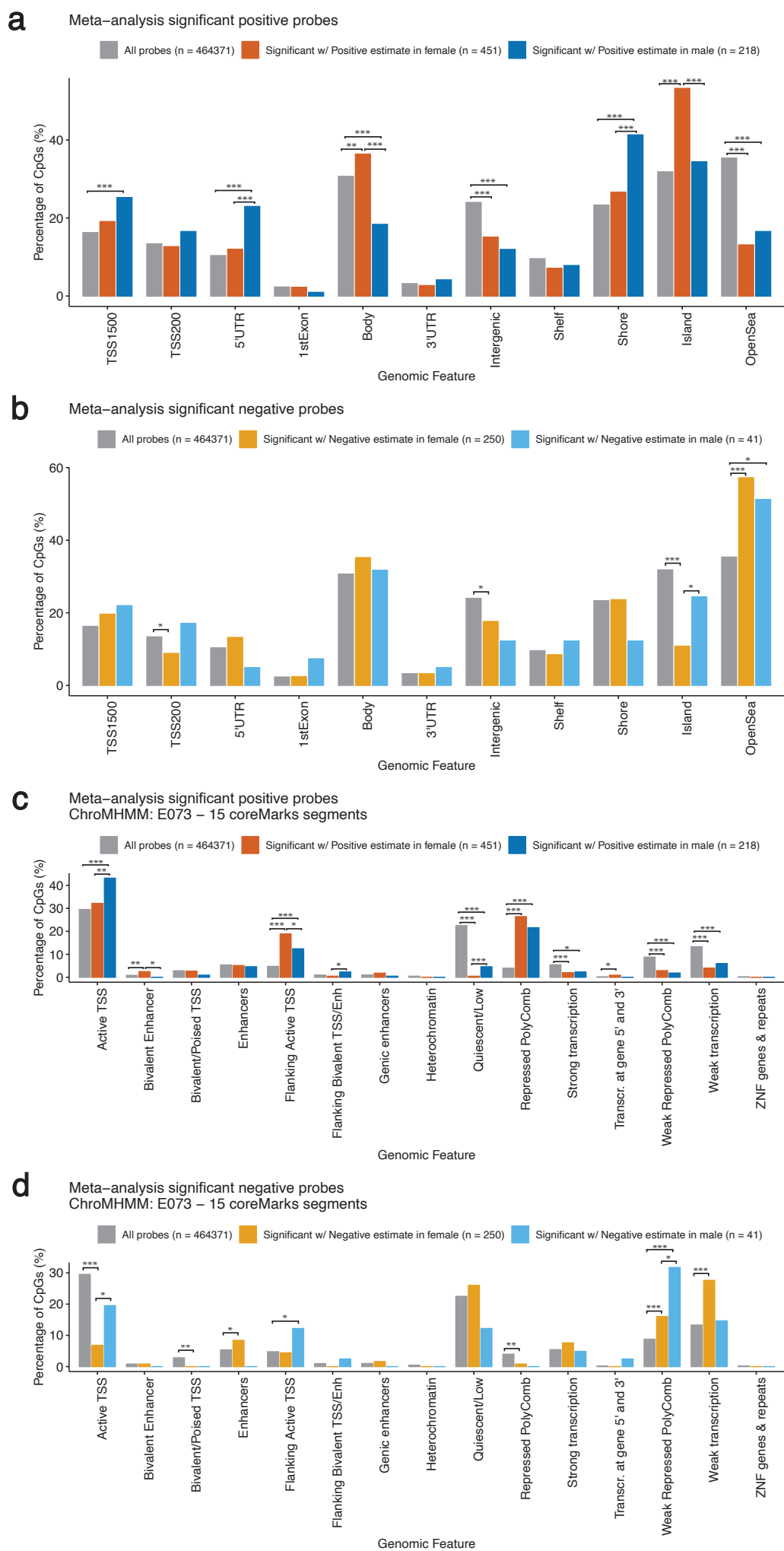
(A) for analysis results of female samples



(B) for analysis results of male samples

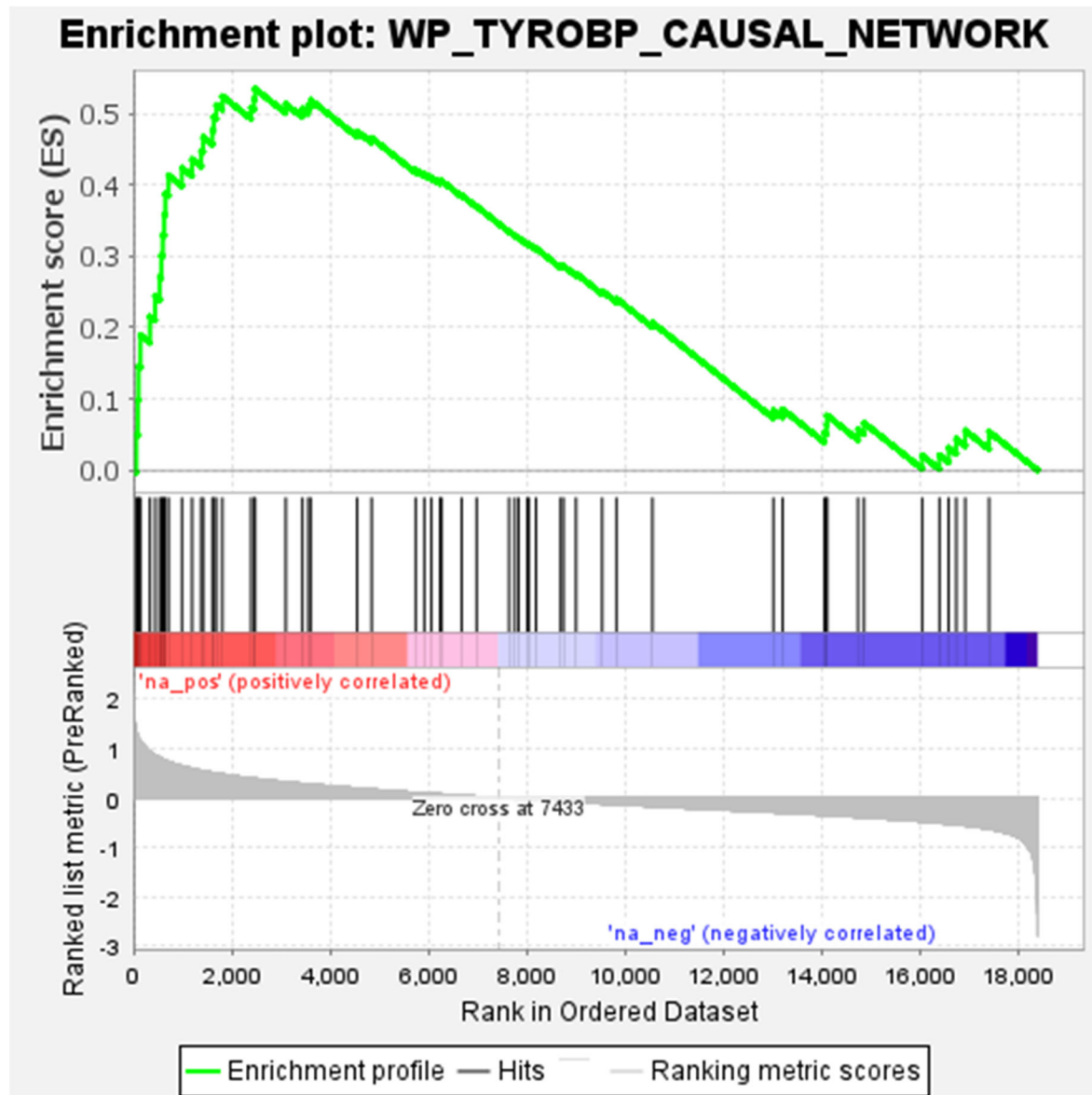


Supplementary Table 2 Enrichment of FDR significant CpGs and CpGs located within FDR significant DMRs with positive and negative effect estimates in various (A) (B) genomic features and (C) (D) chromatin states. *** indicates P-value < 0.001, ** indicates P-value < 0.01, * indicates P-value < 0.05



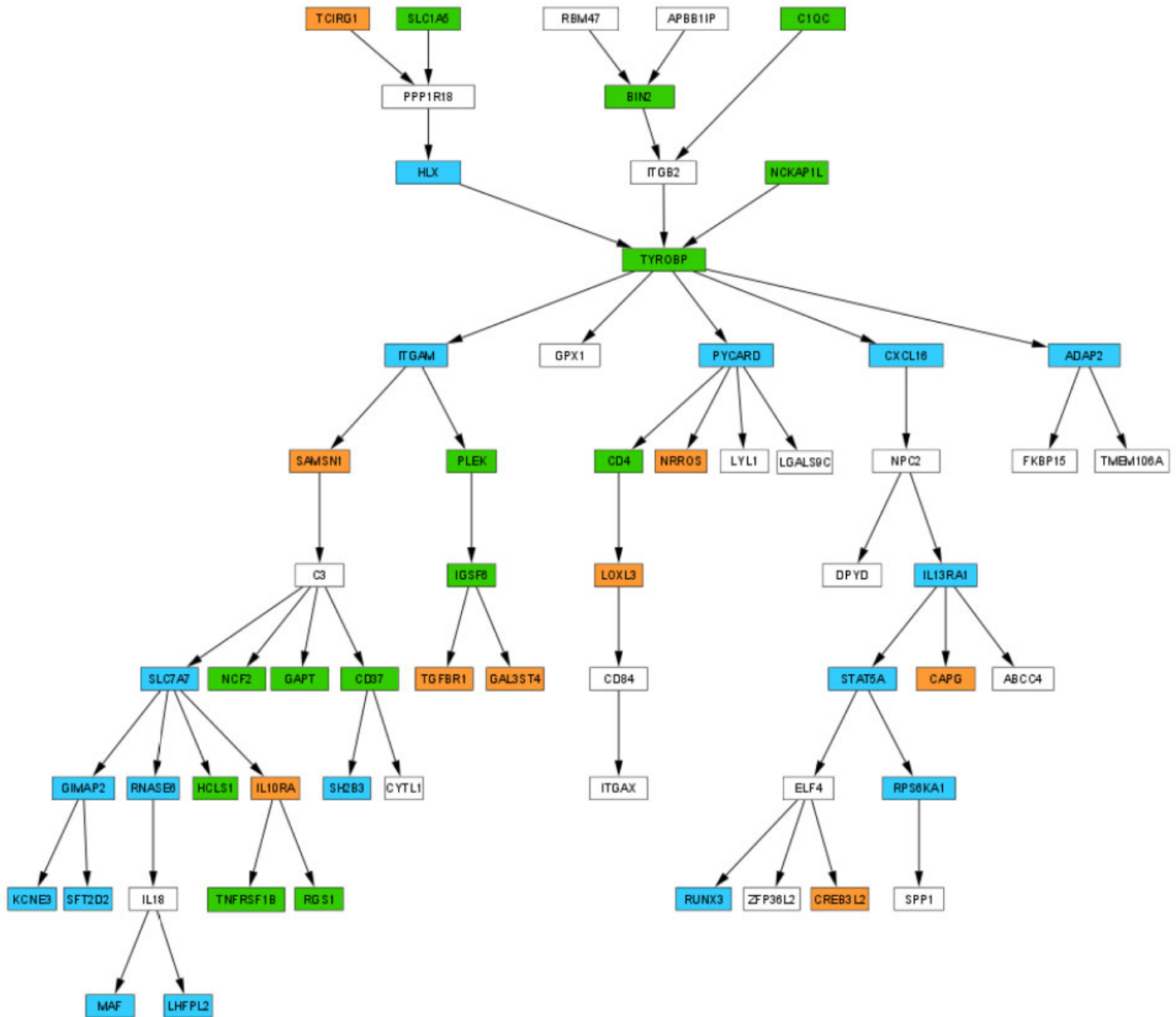
Supplementary Figure 3 The TYROBP causal network.

(A) Genes with significant DNA methylation changes in female samples are enriched in the TYROBP causal network (FDR = 0.014).

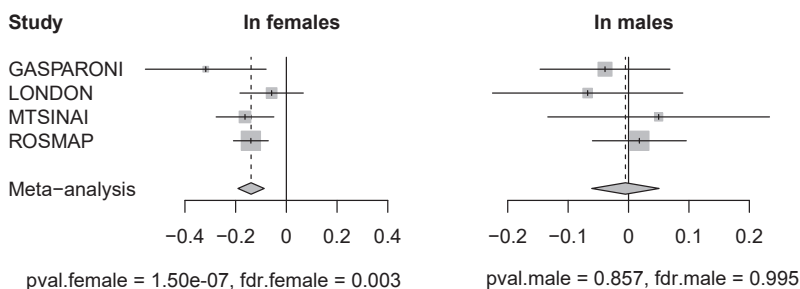


(B) Core enrichment genes identified by GSEA.

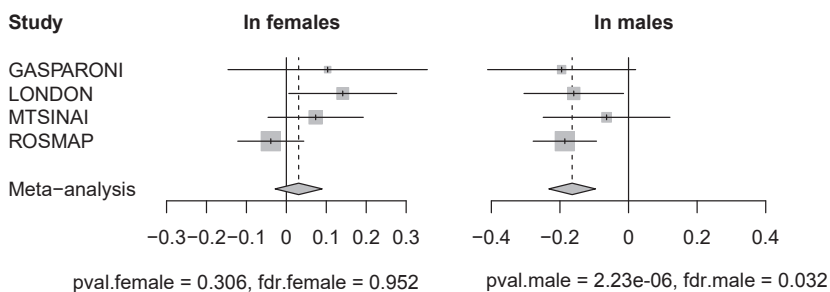
Orange = core enrichment genes identified by GSEA in the analysis of female samples, blue = core enrichment genes identified by GSEA in the analysis of male samples, and green = core enrichment genes identified by GSEA in both male and female samples analysis.



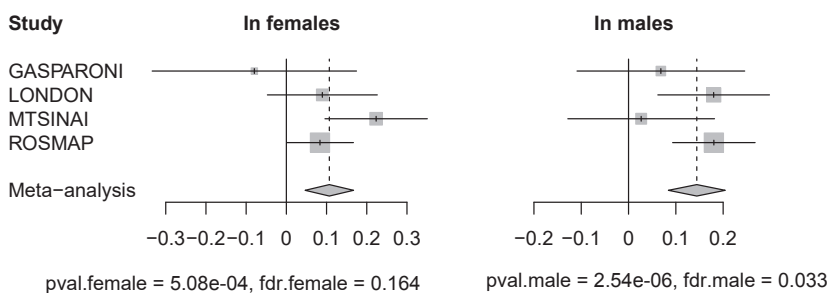
cg22632947(PRKCA)



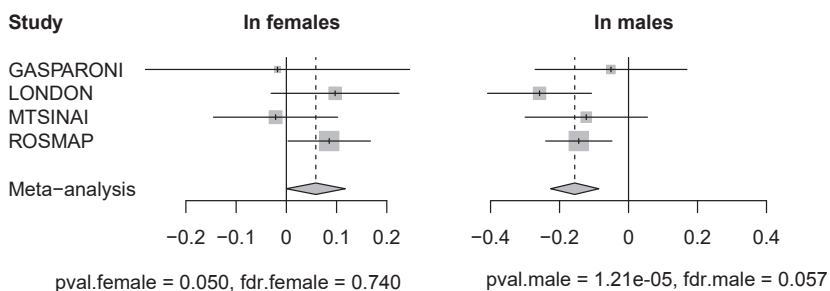
cg18942110(CRTC3)



cg15626350(ESR1)



cg25734825(TMEM39A)



cg21722170(TNXB;TNXA)

