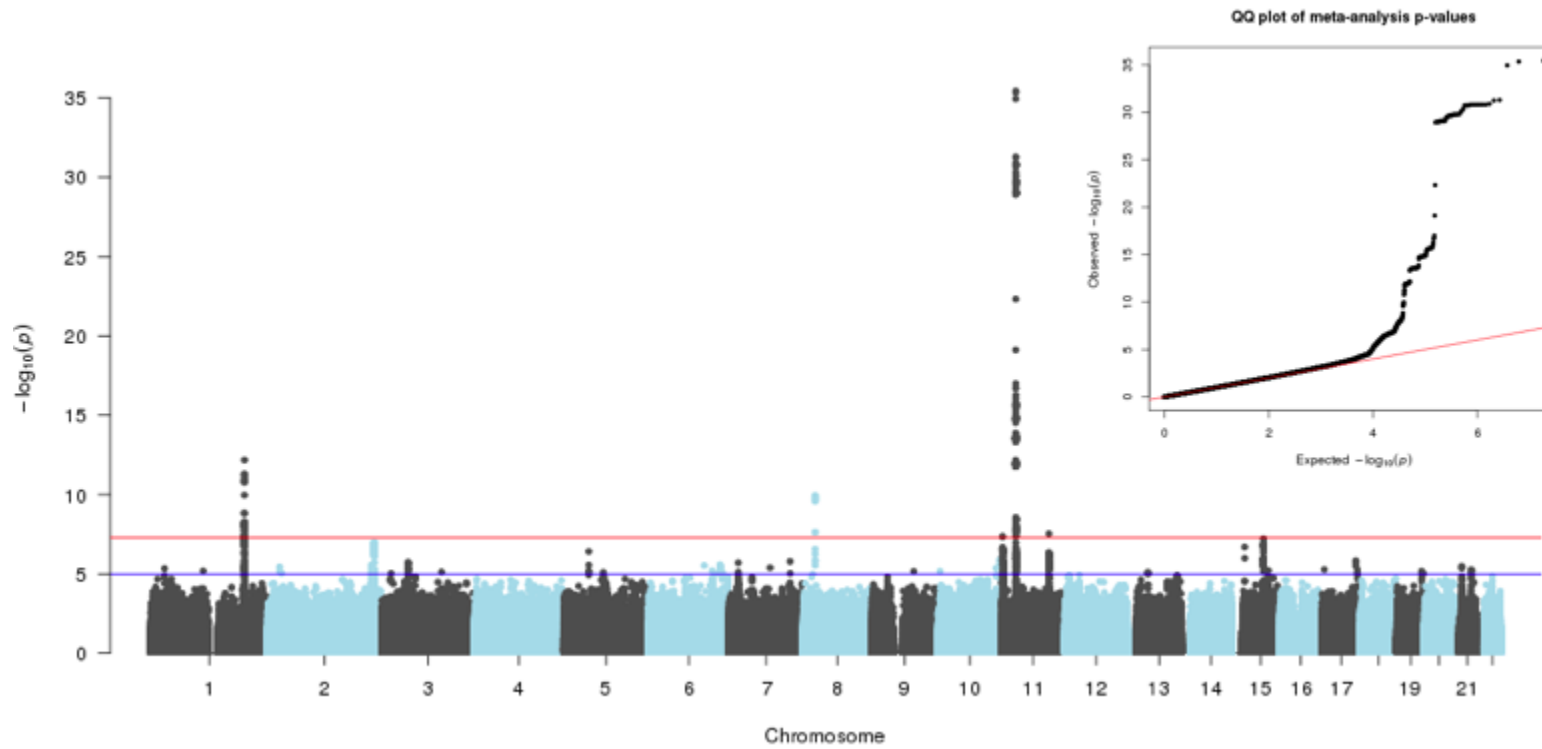
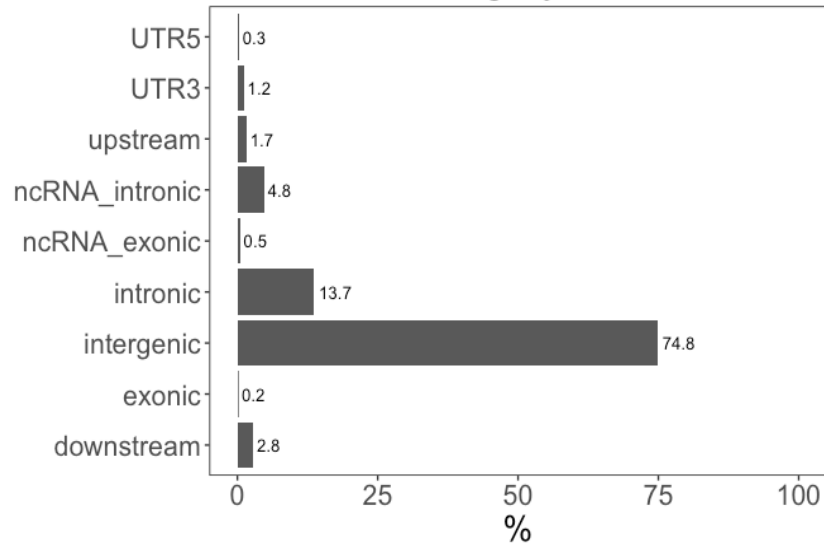


Supplementary Figures

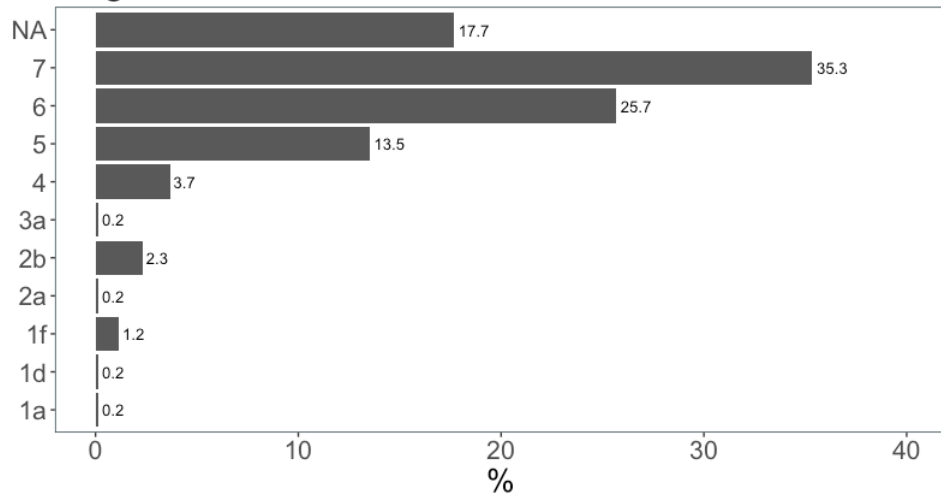


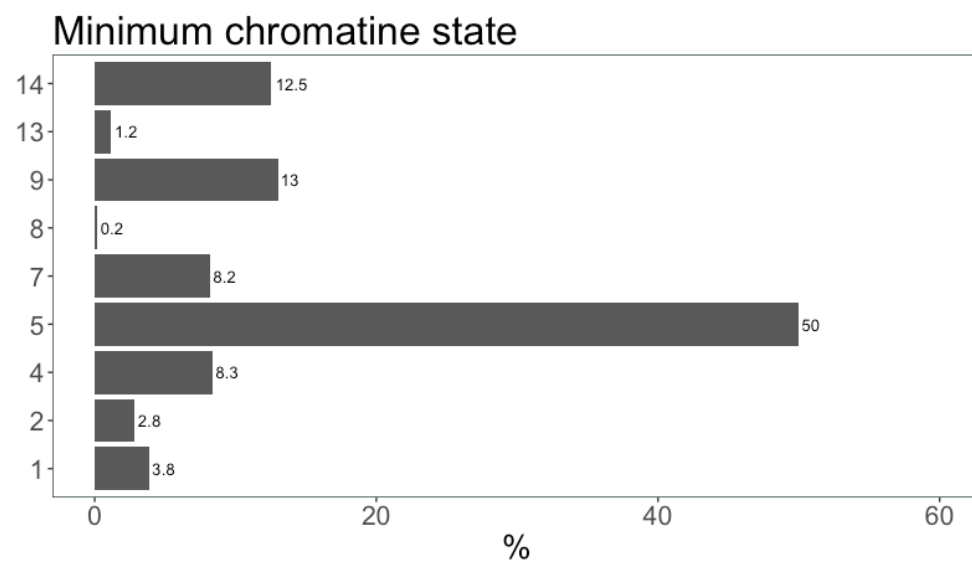
Supplementary Figure 1. Manhattan and QQ plot for menstrual cycle length GWAS meta-analysis.

Functional category

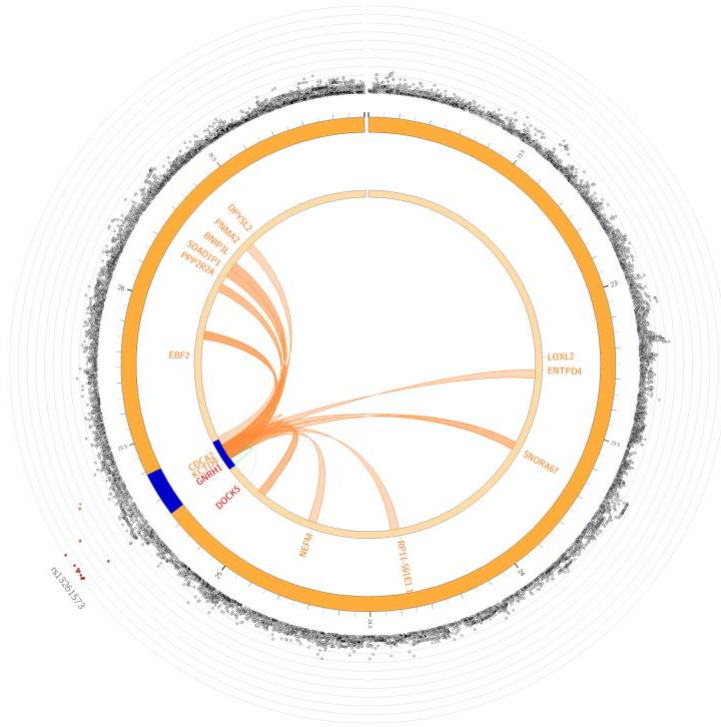


Regulome DB score



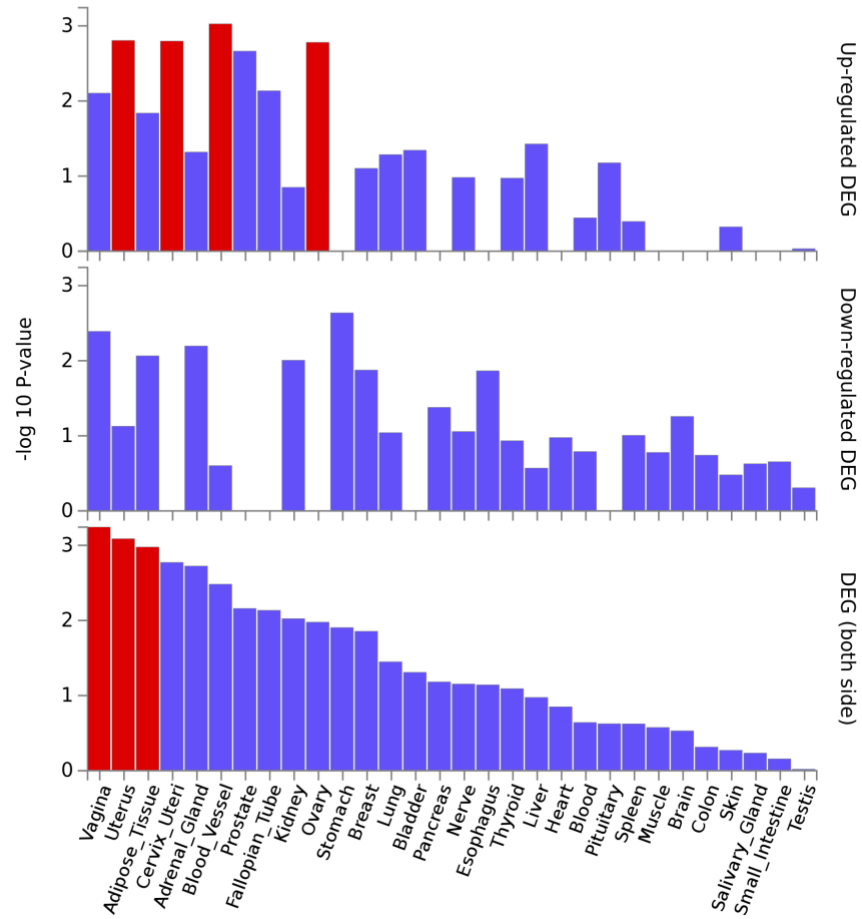


Supplementary Figure 2. Functional annotation for all SNPs with $r^2 \geq 0.6$ with the sentinel SNPs. a) Percentage of SNPs according to their functional category; b) Percentage of SNPs according to their RegulomeDB score. Lower score indicates a more likely regulatory role; c) Percentage of SNPs according to their minimum chromatin state across 127 tissues. Lower score indicates a more likely regulatory role.



Supplementary Figure 3. Circos plots demonstrating the results of eQTL and chromatin interaction mapping for loci on chromosome 11, 1, and 8, respectively. The outermost layer depicts SNPs with a $P < 0.05$ in a Manhattan-style plot. SNPs in detected genomic risk locus are coloured according to their r^2 value to the most significant variant at the locus. Y-axis values range from 0 to the maximum $-\log_{10}(P\text{-value})$ of the SNPs. The second and third layer represent the chromosome ring, where the risk locus is coloured in blue, and genes mapped by chromatin interactions with this region, depicted by orange ribbons, are displayed. eQTL associations are shown by green ribbons, and genes that were mapped by both eQTL associations and chromatin interaction data are highlighted in red.

B)



Supplementary Figure 4. a) Heatmap displaying average expression of prioritized genes and b) differential expression analysis of prioritized genes across GTEx v7 30 general tissue types.