

## Supplementary Data 1

Regional association plots of each significant locus from the EA GWAS meta-analysis of 137,136 PTSD cases and 1,085,746 controls. The x-axis represents the base pair (hg19) genetic position of SNPs. The y-axis represents  $-\log$  p-values of SNP association with PTSD. LD estimates of surrounding SNPs with the labeled index SNP (LD  $r^2$  values estimated based on 1KGP3 Europeans) is indicated by color (color bar on side of plot indicates color coding of  $r^2$  values). Local estimates of recombination rate are indicated in light blue (legend on vertical axis at right). Gene names, strands, and boundaries are shown in the box below the regional plot.





















































































































































































