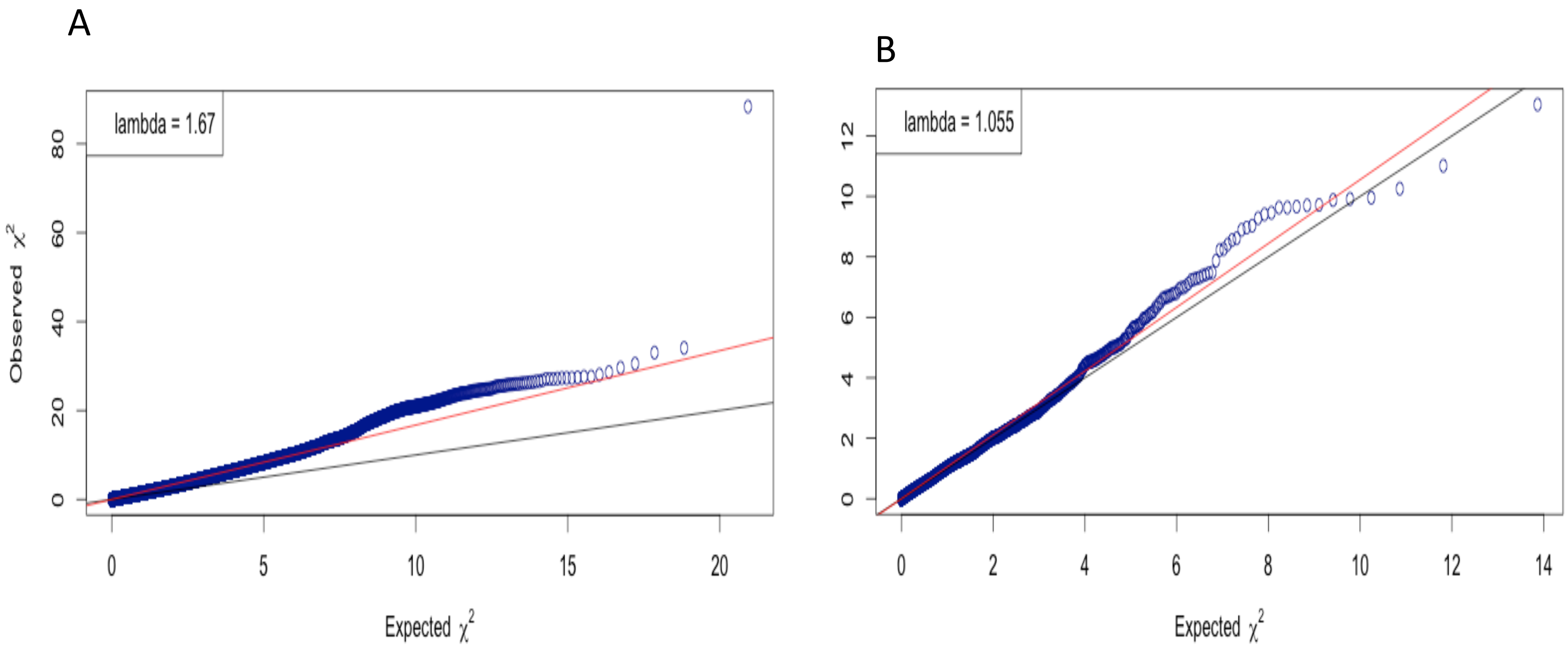
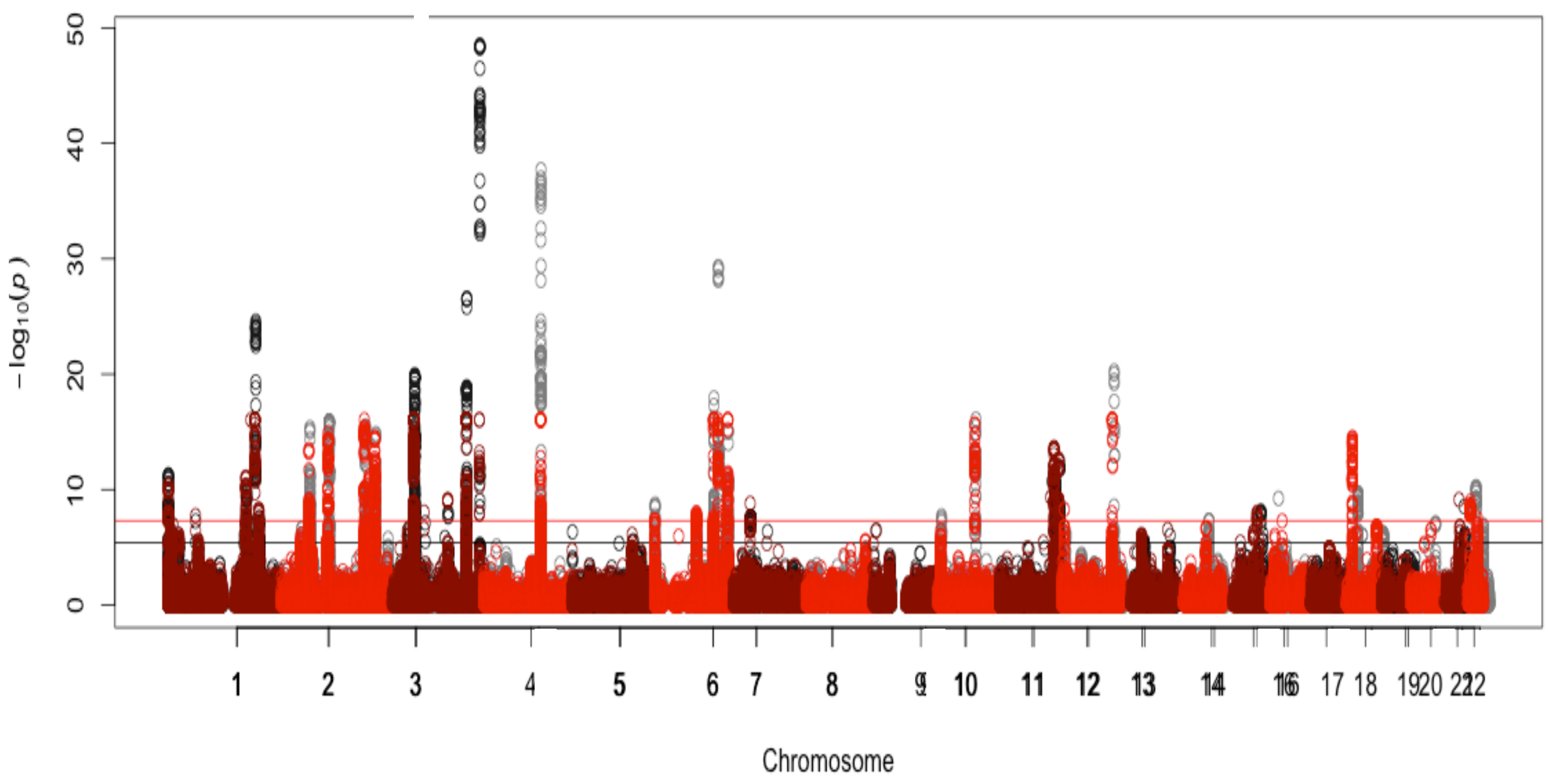
Supplementary Figure 1. QQ plots from the association results



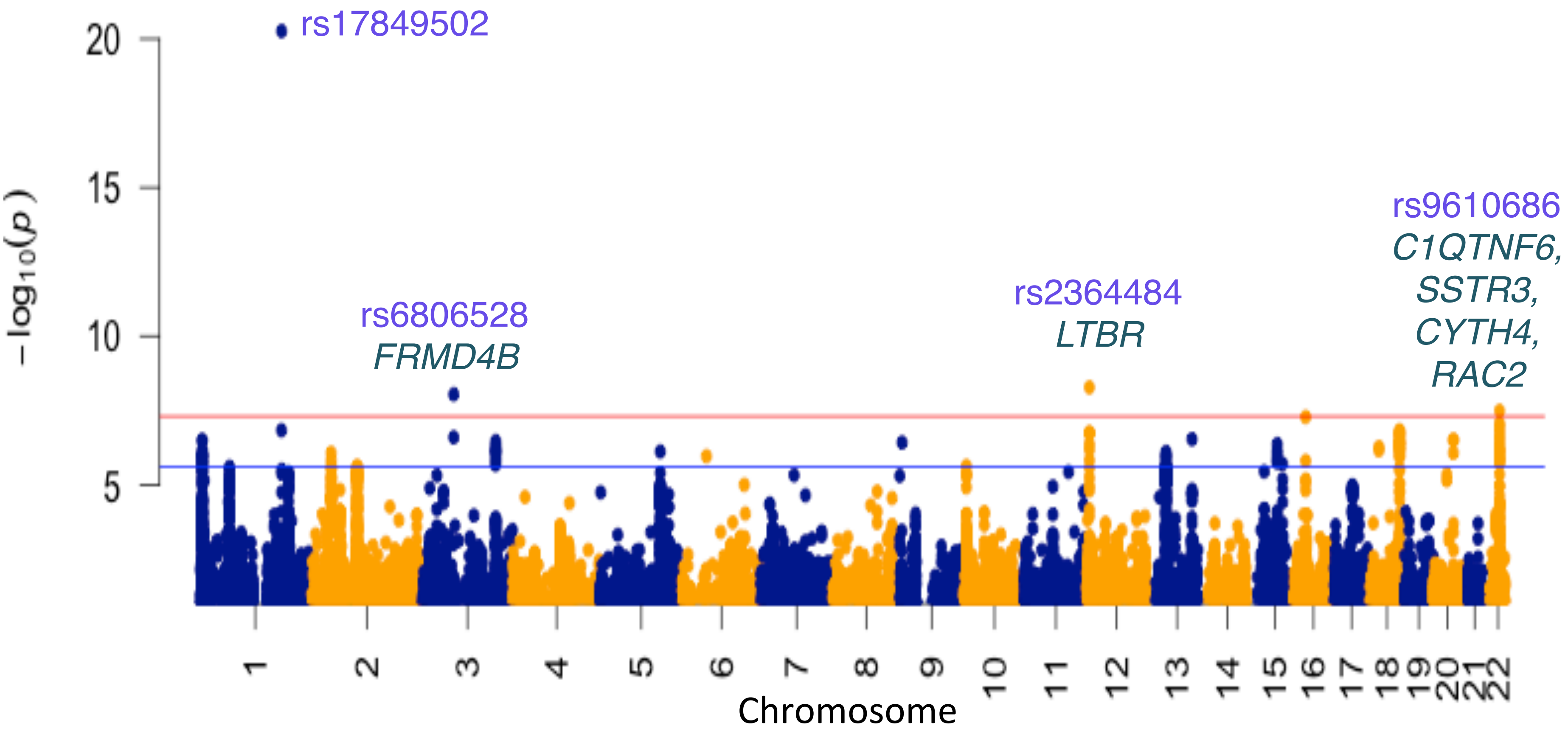
A. QQ plot of the associations results excluding the 41 loci reported previously B. QQ plot of the association in three loci associated to bipolar disorder.

Supplementary Figure 2. Overlapping manhattan plot of new and previous association results without the HLA region



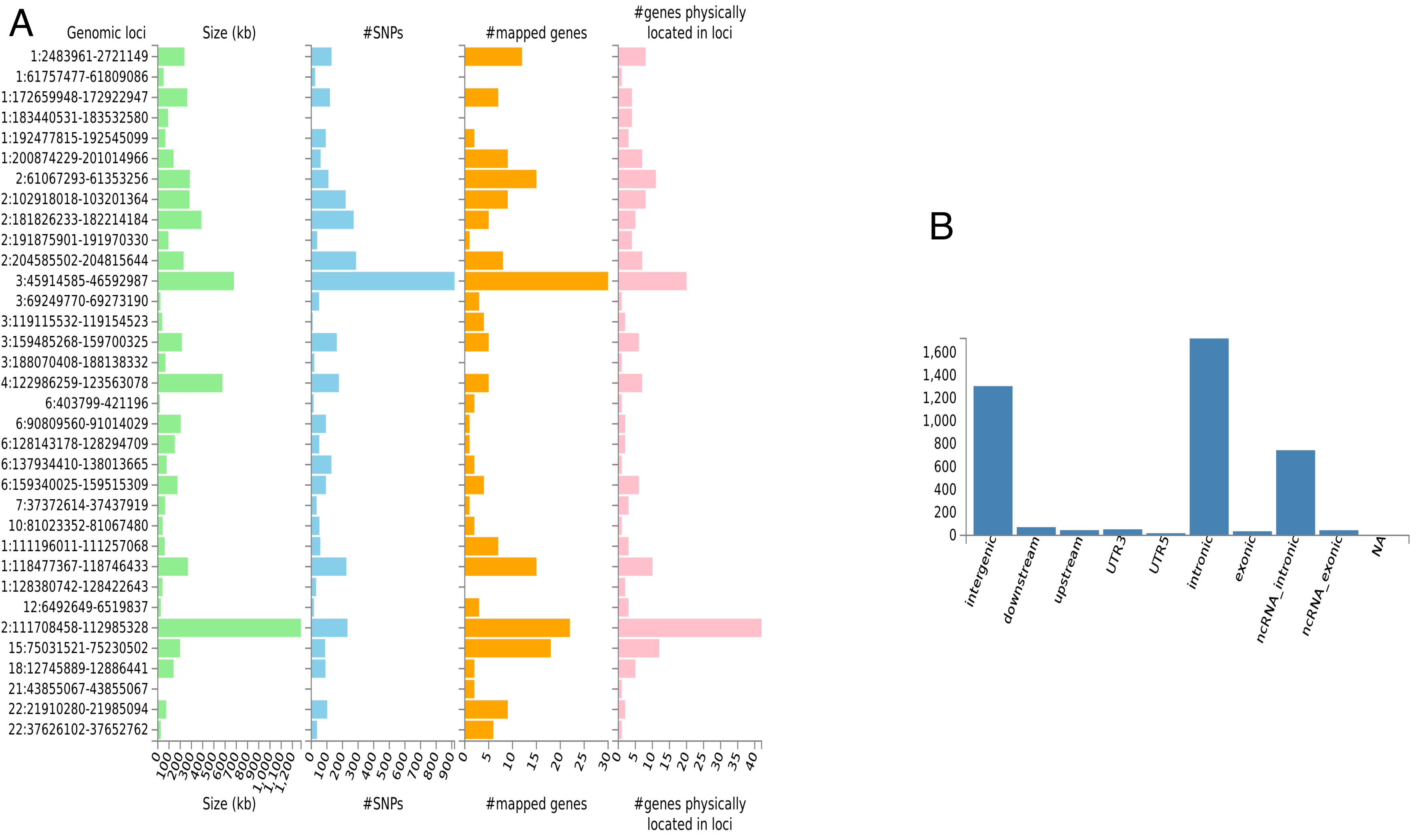
The results from the previous Immunochip analysis are showed in black, the results from this meta-analysis are showed in red. PLINK reports p-value below 2.22 $x10^{-16}$ as 0 for the meta-analysis, thus we gave an arbitrary value of $9.99x10^{-17}$ for this picture.

Supplementary Figure 3. Manhattan plot of genome-wide significant loci not reported in our previous Immunochip analysis



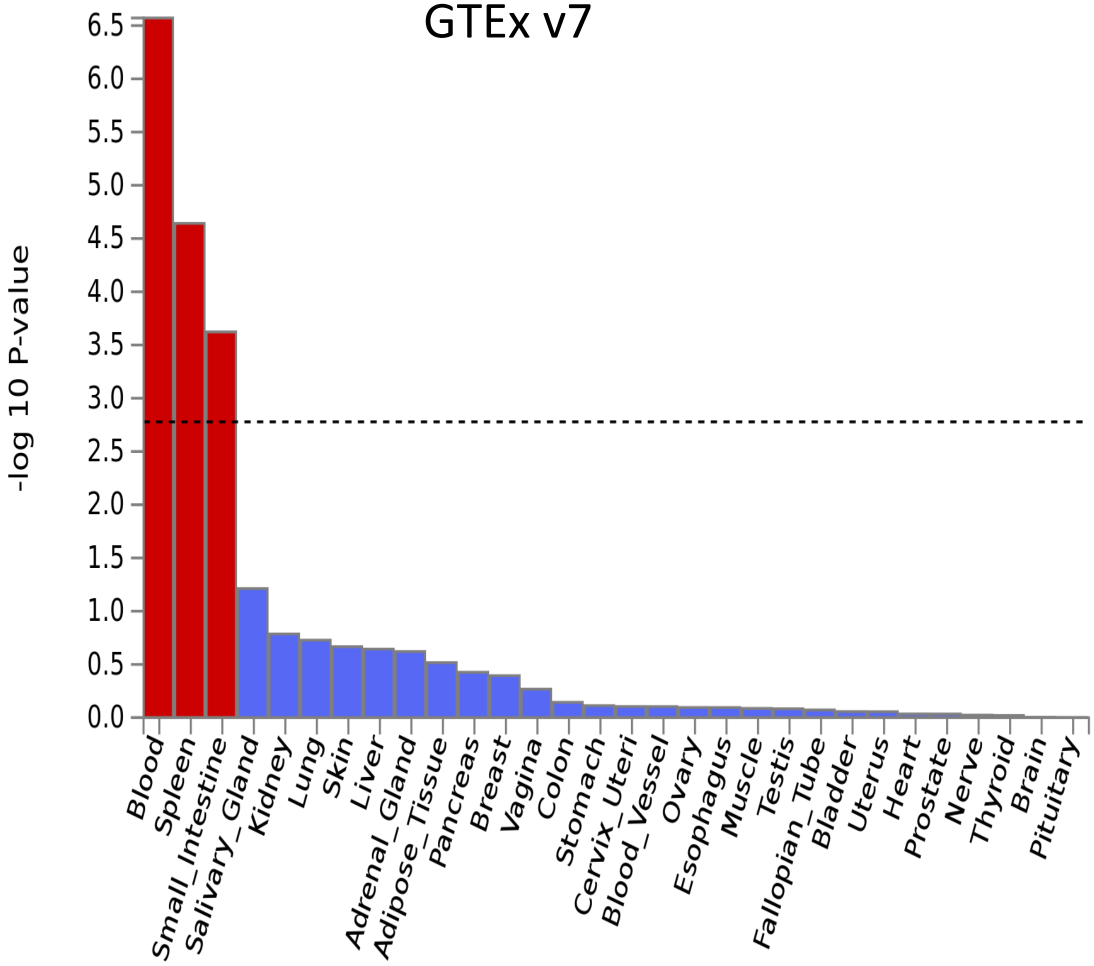
Manhattan plot of genome-wide significant loci not reported in our previous Immunochip study. The red line indicated the threshold for genome-wide associations and the blue line for suggestive associations. The SNP with the strongest association within the locus is showed in blue and the nearby genes whose expression is affected by the SNP are showed in grey.

Supplementary figure 4: Functional annotation of all genome-wide significant associated loci



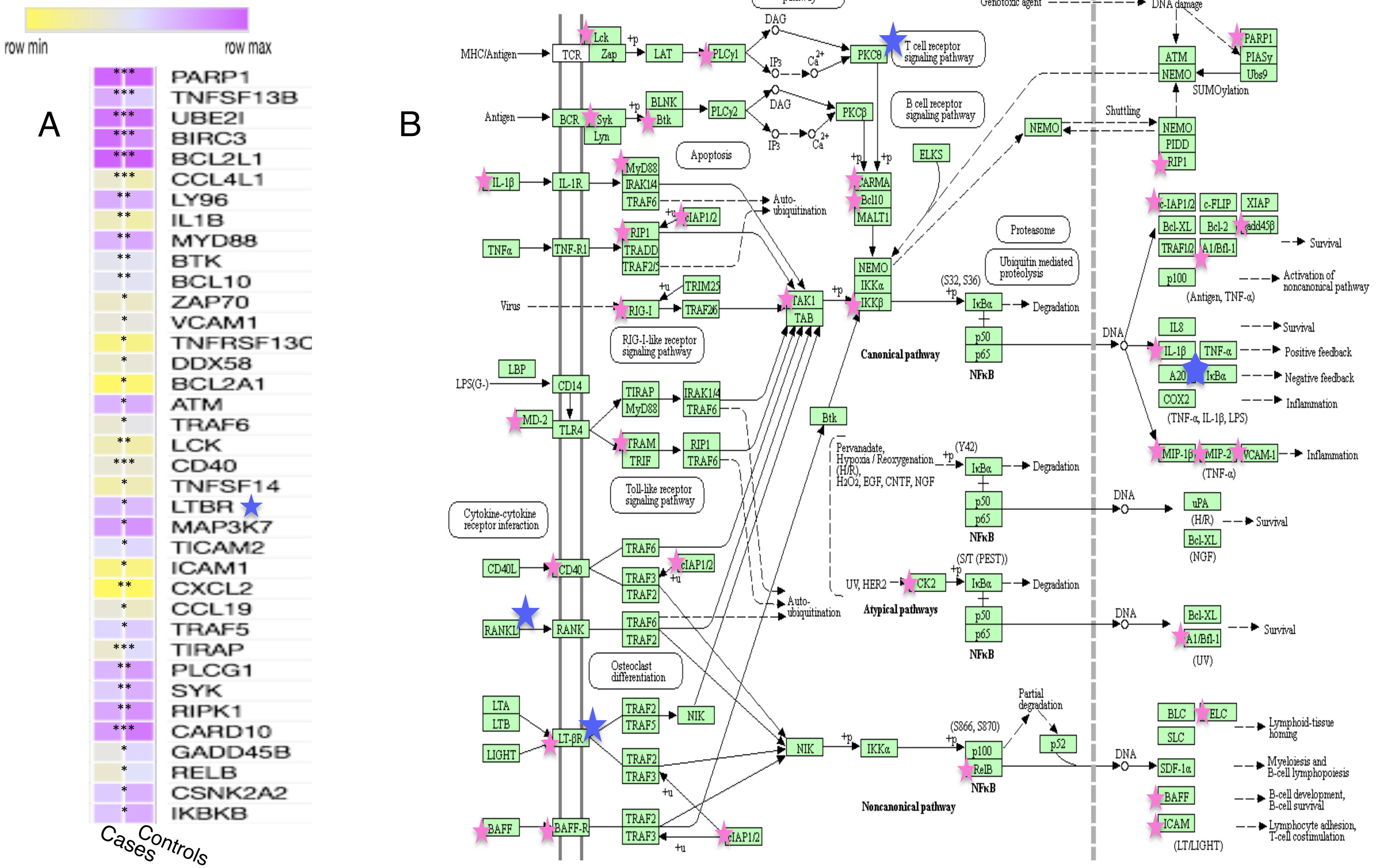
Functional annotation of genomic loci. A. Summary per genomic risk locus. The Y axis shows the genomic coordinates of each of the locus. In green is shown the size of the locus in kilobases, in blue the number of SNPs within the loci, in orange the number of mapped candidate genes and in pink the number of genes physically located within the locus. B. Functional consequences of SNPs on genes. The histogram displays the number all Top-SNPs and SNPs in LD with them which have corresponding functional annotation assigned by ANNOVAR. SNPs that have more than one annotation are counted for each annotation.

Supplementary figure 5: Tissue expression analysis in 30 tissue types from GTEx v7



The histogram shows the results of the gene-property tissue expression analysis by MAGMA. The dash line indicated the threshold for significance. In read are shown the significantly positive relationship between tissue specificity and genetic association of genes.

Figure 6. NFKB signaling genes related to CeD



NFKB signaling genes related to CeD. A. Heatmap showing 37 genes part of the NFKB signaling pathway that showed significant differences in their levels of expression (Pval <0.05) in CeD cases versus controls. The asterisk indicate the level of significance, one * indicated pval<0.5, two ** indicates pval=0.05-0.01, three *** Pval=0.01-0.001. Purple stars indicate the genes associated to CeD and the pink stars indicate the differentially expressed in intestinal biopsies of celiac cases vs. controls