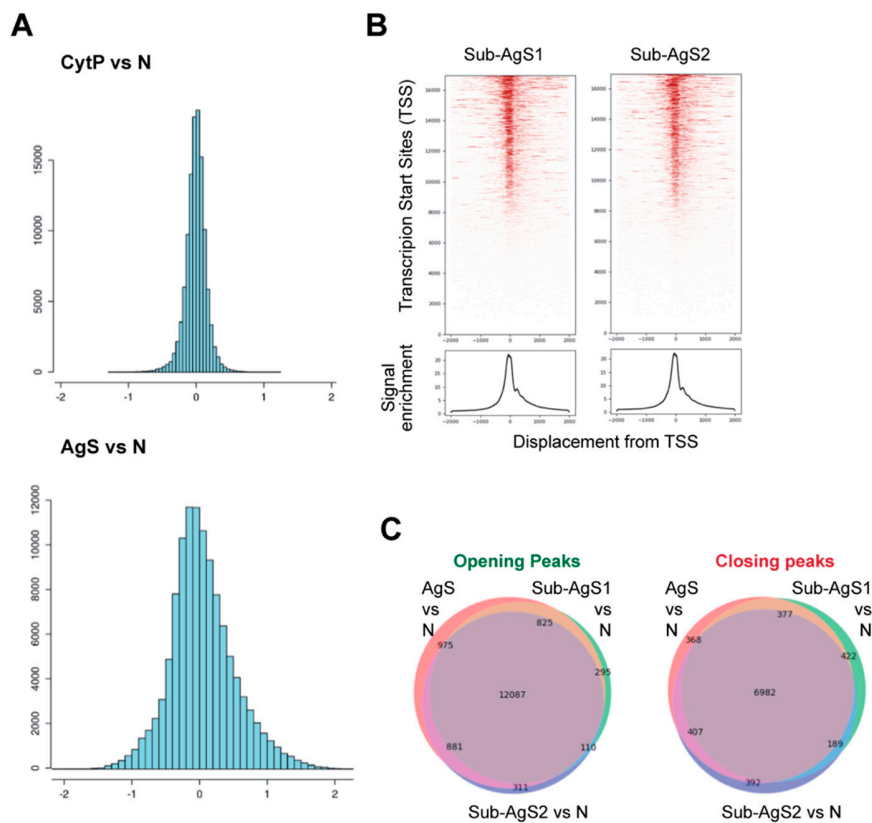
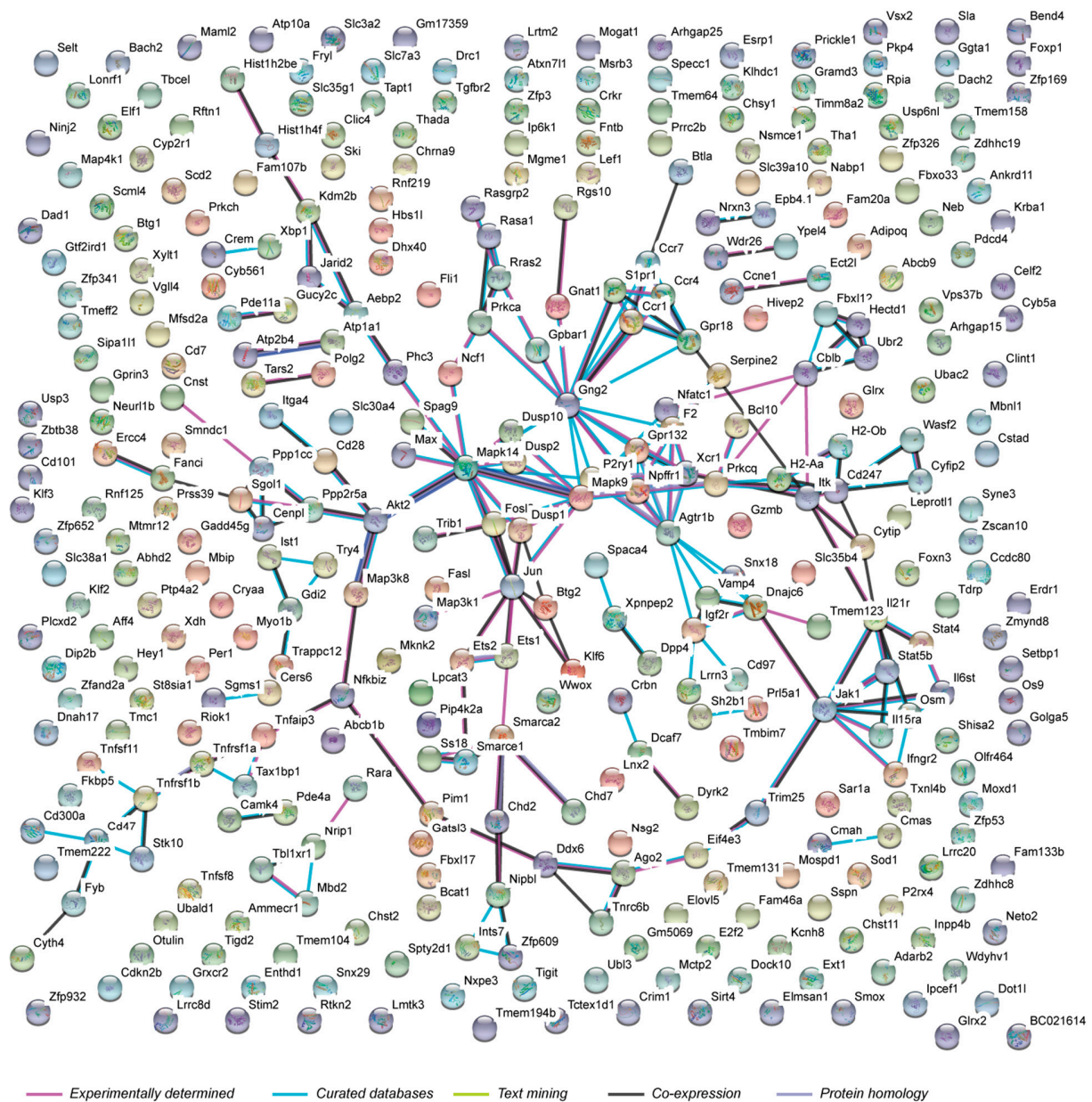


Inflammatory cytokines that enhance antigen responsiveness of naïve CD8⁺ T lymphocytes modulate chromatin accessibility of genes impacted by antigen stimulation

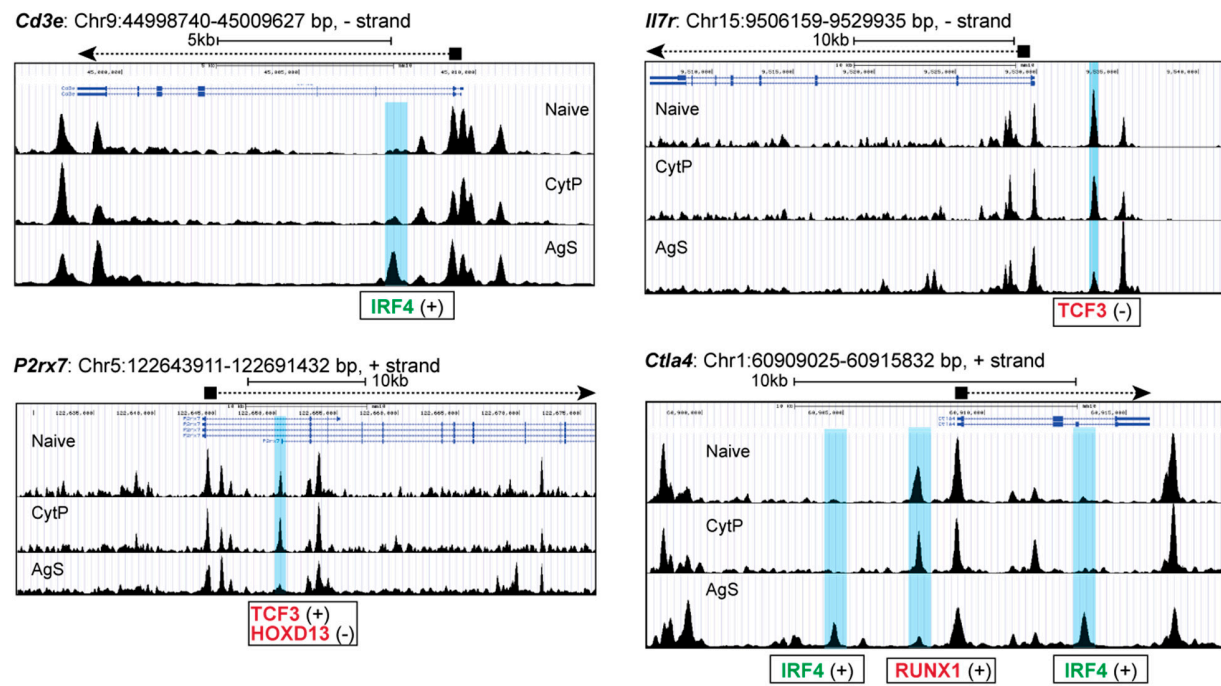
Quenum et al.,



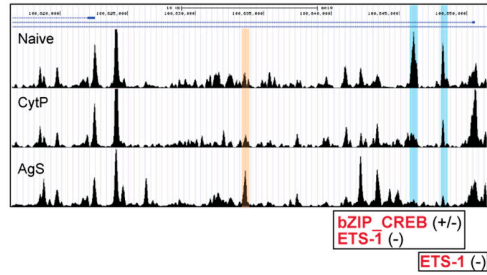
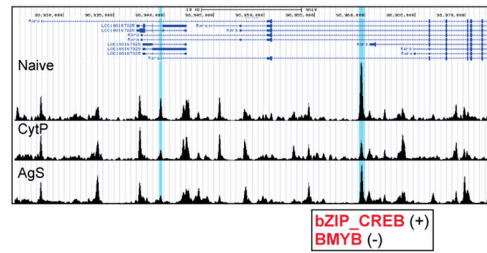
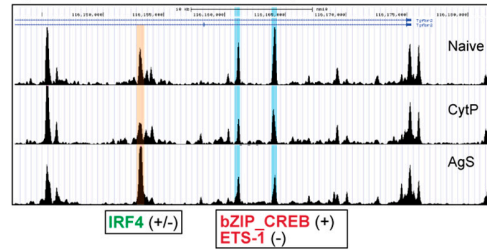
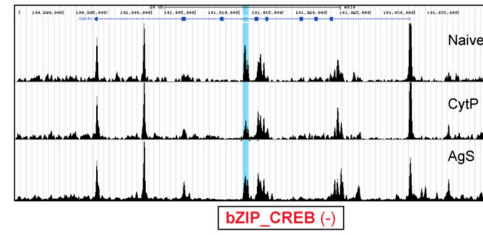
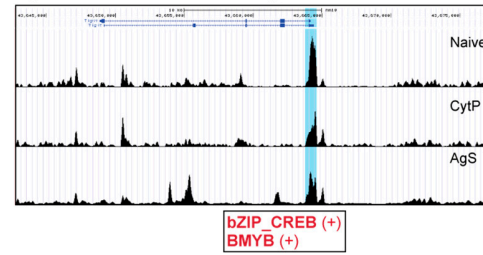
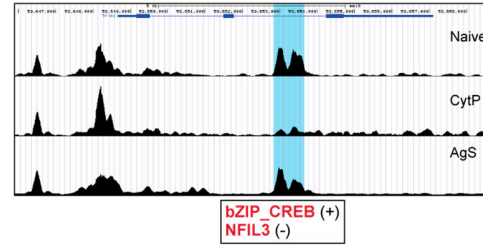
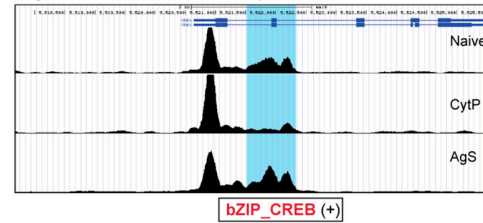
Supplementary Figure S1. Quality control of chromatin accessibility peaks in AgS cells. (A) Distribution of rlogFC values for comparison between CytP versus N and AgS versus N cells. (B) Fragment length distribution analysis of ATACseq reads from AgS cells randomly subgrouped to sub-AgS1 and sub-AgS2 reads. (C) Comparison of the opening and closing peaks in sub-AgS1 and sub-AgS2 ATACseq reads compared to naive cells.



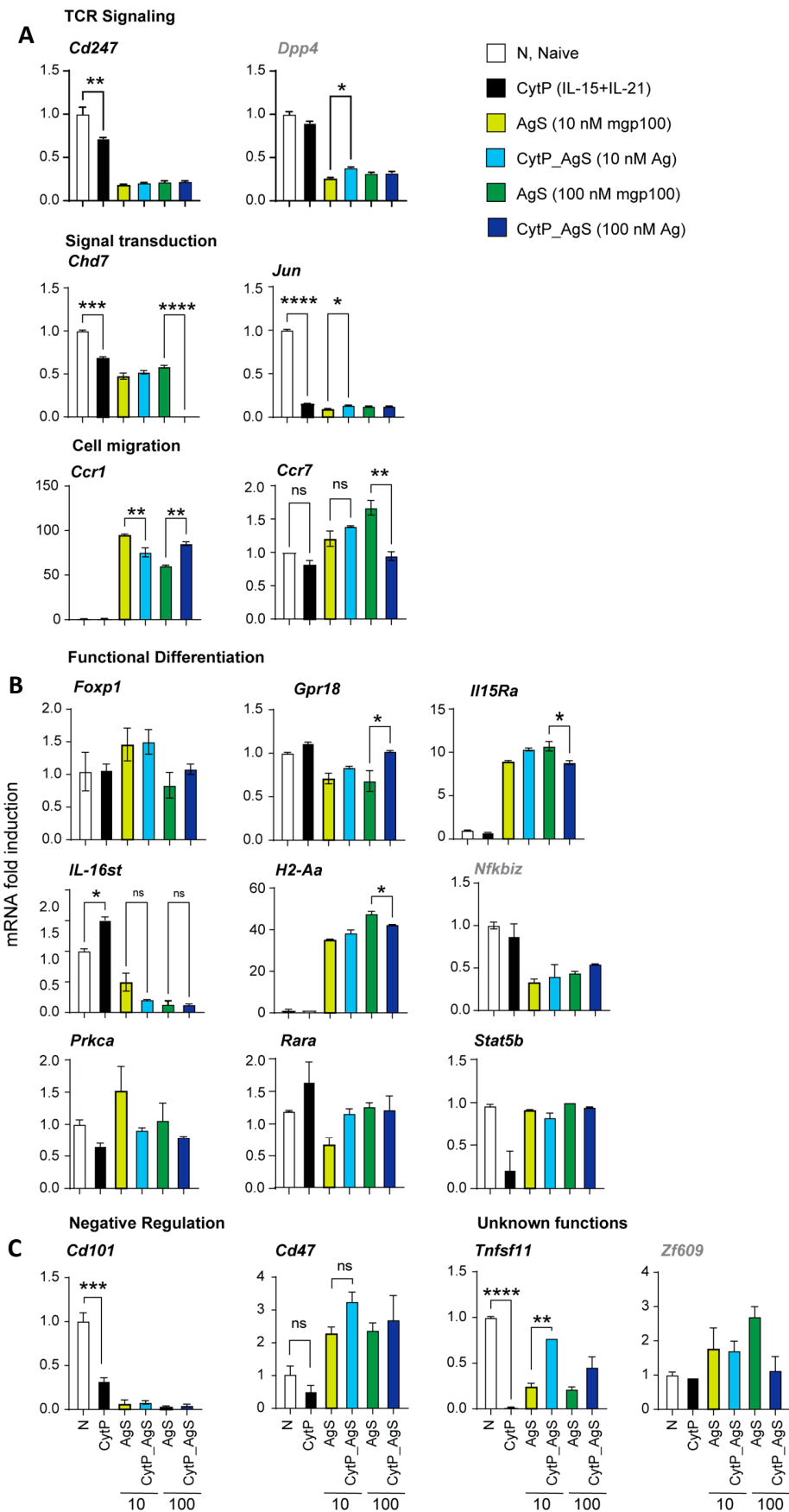
Supplementary Figure S2. Protein interaction network analysis of genes in the vicinity of the ATACseq peaks modulated in cytokine-primed PMEL-1 cells compared to naive cells.



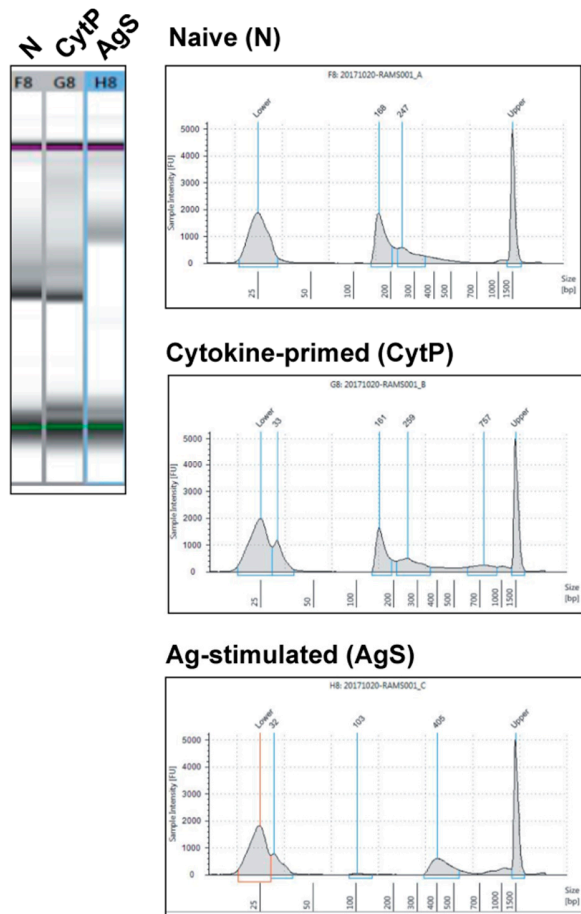
Supplementary Figure S3. Other examples of chromosome accessibility peaks opening (*Cd3e*), closing (*Il7ra*, *P2rx7*) or both opening and closing (*Ctla4*) in Ag-stimulated but not in cytokine-primed cells.

A Closing Peaks in CytP & AgS cells**Stat5b**: Chr11:100780731-100850724 bp, - strand**Rara**: Chr11:98927818-98974942 bp, + strand**Tgfb2**: Chr9:116087695-116175363 bp, - strand**B Peaks closing only in CytP cells****Cd101**: Chr3:100993529-101029495 bp, - strand**Tigit**: Chr16:43648867-43664146 bp, - strand**Trib1**: Chr15:59648654-59657099 bp, + strand**Xbp1**: Chr11:5520659-5525893 bp, + strand

Supplementary Figure S4. Chromosome accessibility peaks that are closing in both CytP and in AgS cells (A) or only in AgS cells (B).



Supplementary Figure S5. (A–C) RT-qPCR analysis of additional genes implicated in T cell activation, signaling, effector differentiation, negative regulation and exhaustion in naïve (N), cytokine-primed (CytP) and Ag-stimulated (10 or 100 nM of PMEL-1 peptide) cells without (AgS) or with cytokine priming (CytP_AgS). Fold induction was calculated based on the expression level in naïve PML-1 cells. Mean + SEM for 3 independent experiments are shown. Comparison by one-way ANOVA with Tukey's multiple comparison test. *, $p < 0.05$, ** < 0.01 , *** < 0.001 , **** < 0.0001 .



Supplementary Figure S6. Bioanalyzer quality assessment of ATACseq libraries of naive, cytokine-primed and Ag-stimulated PMEL-1 TCR transgenic CD8⁺ T lymphocytes.