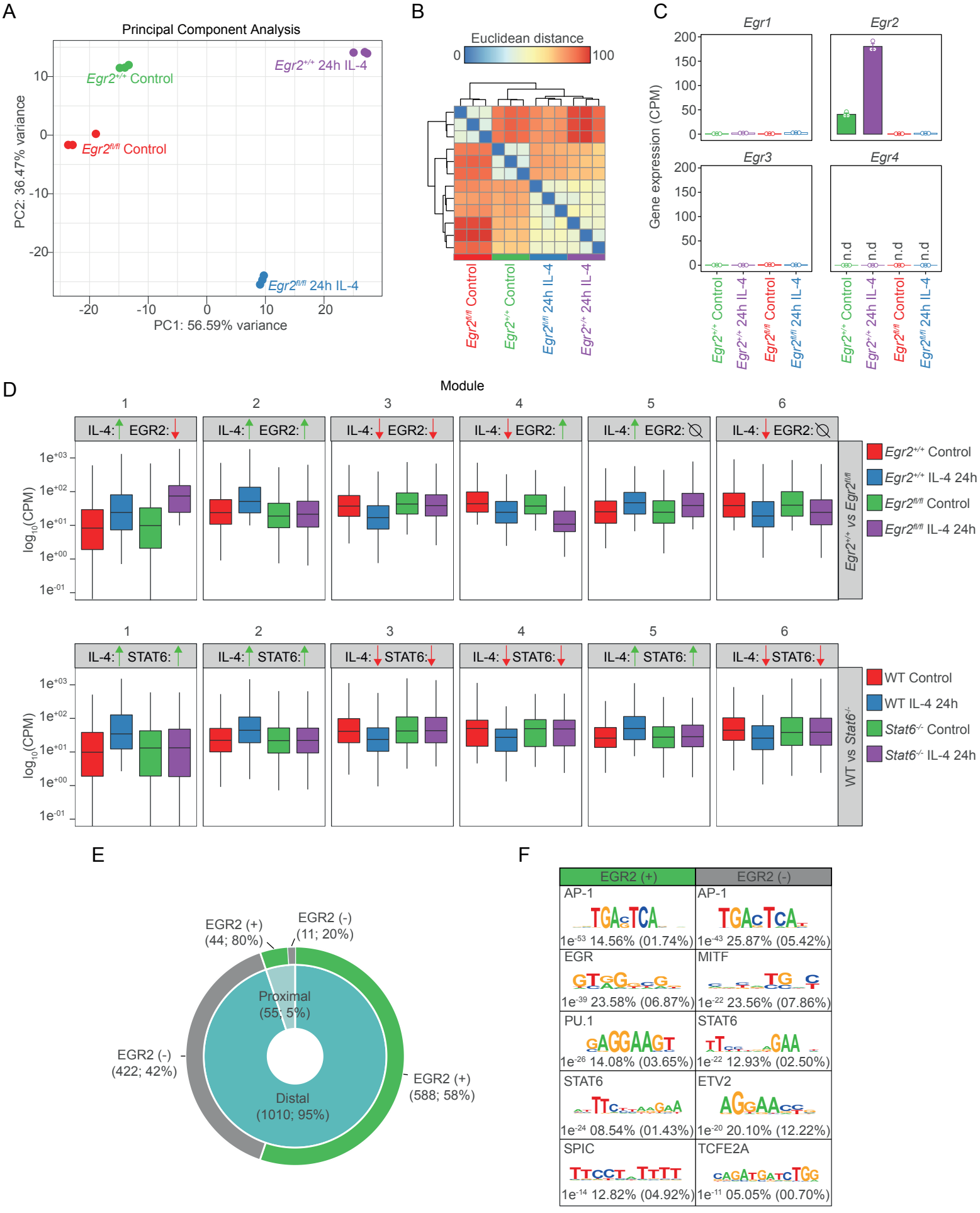
Supplemental Fig. S4



Supplementary Fig. S4. IL-4 and EGR2 controls the alternatively polarized macrophage phenotype. Related to Fig. 4.

A, Principal component analysis of RNA-seq experiments. Macrophage genotypes and treatment conditions are indicated.

B, Correlation heatmap visualizing Euclidean distance between the different conditions and genotypes based on the principal component analysis.

C, Boxplot representation of the *Egr2* gene family expression in BMDMs. Count per million values are plotted.

D, Boxplot representation of the expression of gene modules, exhibiting IL-4, STAT6 and EGR2 dependent expression. RNA-seq experiments were performed in *Egr2*$^{+/+}$, *Egr2*$^{-/-}$, *Stat6*$^{-/-}$ and wild type macrophages in the presence or absence of IL-4 (24h). Gene modules were defined based on IL-4 mediated gene expression changes and its dependence on STAT6 or EGR2. Green arrows indicate positive regulation of gene expression wither by the cytokine (IL-4) or the studied transcription factors (STAT6 or EGR2), whereas red arrows indicate negative regulation of gene expression by the same factors. Ø indicate no effect on gene expression. Log_{10} CPM (Count per million) values a plotted.

E, Genomic distribution of regulatory regions bound (EGR2 positive (+)) or not bound (EGR2 negative (-)) by EGR2 around IL-4/EGR2-induced genes in a genomic window of +/- 100kb around the transcription start sites.

F, Motif enrichment analysis on the regulatory regions bound (EGR2 positive (+)) or not bound (EGR2 negative (-)) by EGR2 around IL-4/EGR2-induced genes in a genomic window of +/- 100kb around the transcription start sites. For each motif logo, p-value and percentage of genomic regions that contain the given motif in the target (P300-bound) and background genomic regions (in parenthesis) are shown.