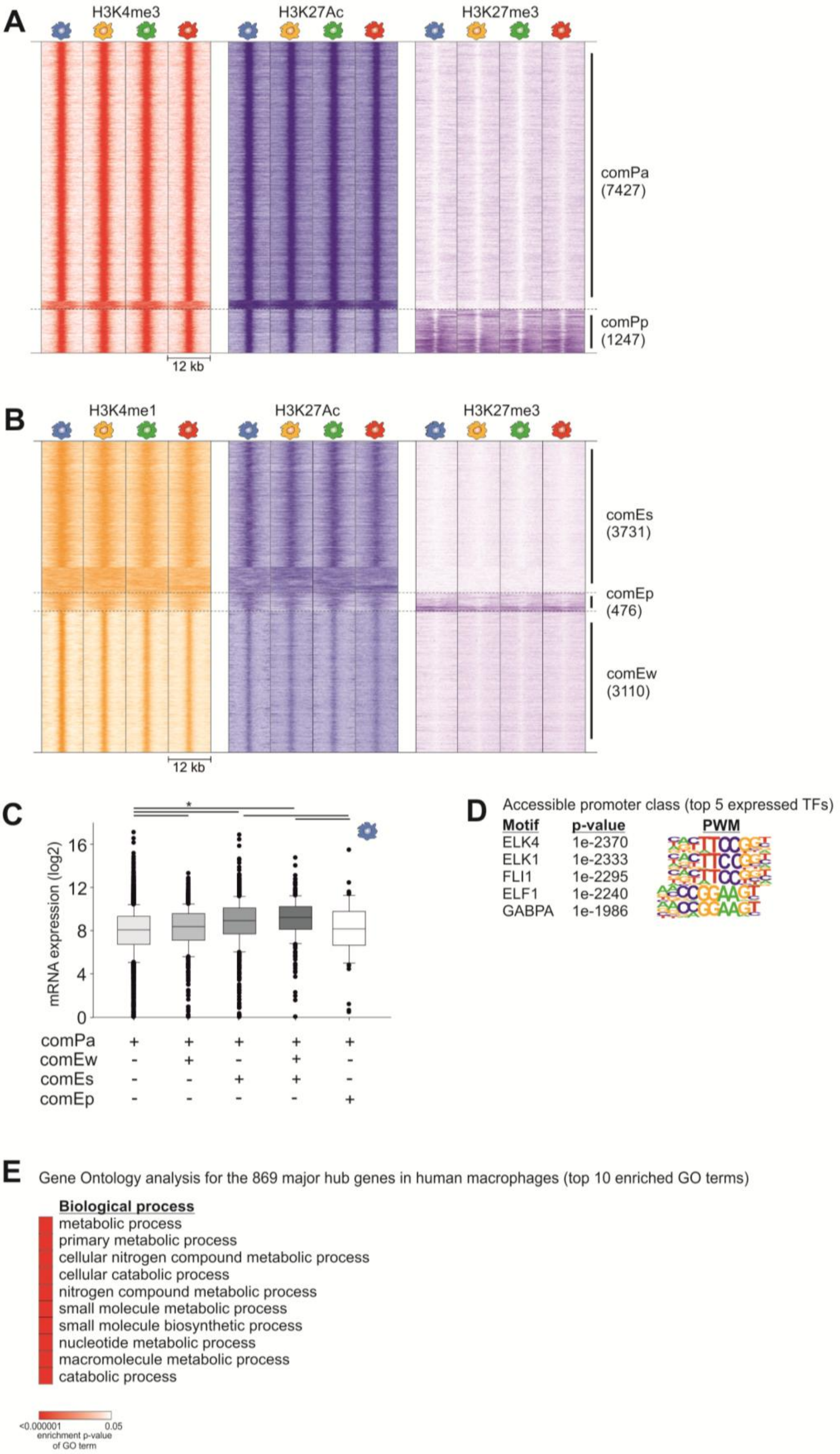
Supplementary information, Figure S1



Accessible promoter class (top 5 expressed TFs)

Motif	p-value	PWM
ELK4	1e-2370	
ELK1	1e-2333	
FLI1	1e-2295	
ELF1	1e-2240	
GABPA	1e-1986	

Gene Ontology analysis for the 869 major hub genes in human macrophages (top 10 enriched GO terms)

Biological process

metabolic process
primary metabolic process
cellular nitrogen compound metabolic process
cellular catabolic process
nitrogen compound metabolic process
small molecule metabolic process
small molecule biosynthetic process
nucleotide metabolic process
macromolecule metabolic process
catabolic process

Figure S1: Histone marks in common macrophage core signature genes

(A-B) Pile-up heatmaps of genomic positions with (A) common accessible (comPa) and poised (comPp) promoter marks and (B) common strong (comEs), weak (comEw) or poised (comEp) enhancers present in all four macrophage conditions. Heatmaps were centered to (A) H3K4me3 or (B) H3K4me1 peak midpoints. Signals were determined with 500bp windows 6kb up- and downstream of peak midpoints. Numbers of common promoters and enhancers are indicated in brackets. **(C)** Box-and-Whisker plots of RNA-seq data for common accessible promoters (comPa) in comparison to genes with simultaneous common marks for common Es (comEs), common Ew or a combination of Es and Ew, and common poised enhancers (comEp) (Kruskal-Wallis One Way ANOVA on ranks with pairwise multiple comparison according to Dunn's Method, $^*p<0.05$). **(D)** Motif enrichment analysis for transcription factor (TF) binding sites in equally expressed genes with accessible promoter marks found in all four macrophage conditions. Displayed are the positional weight matrices (PWM) and the binomial p-values for the enrichment of the top 5 expressed TFs. **(E)** Gene Ontology (GO) analysis for 869 genes which 10% of the most connected genes in macrophages defined previously [2]. M^{b} (blue), $M^{IFN\gamma}$ (yellow), M^{IL4} (green) and M^{TPP} (red); RNA-seq and ChIP-seq were derived from three independent experiments.