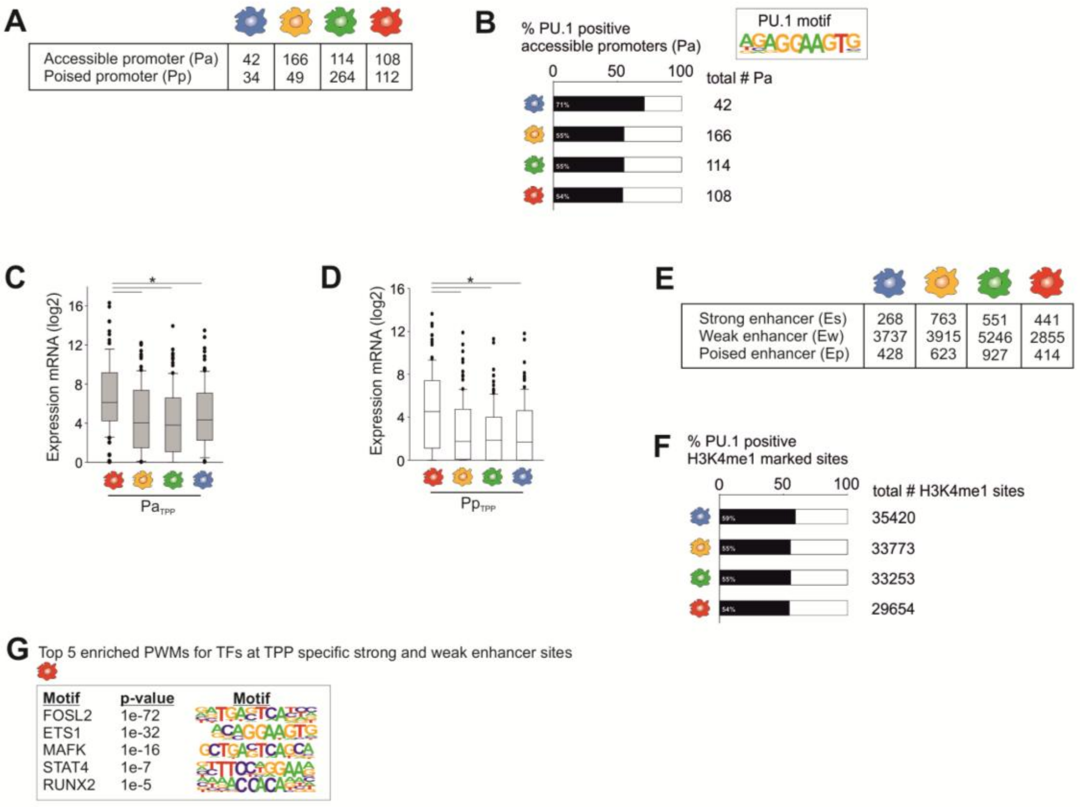
Supplementary information, Figure S2



A

	🟦	🟨	🟩	🟥
Accessible promoter (Pa)	42	166	114	108
Poised promoter (Pp)	34	49	264	112

E

	🟦	🟨	🟩	🟥
Strong enhancer (Es)	268	763	551	441
Weak enhancer (Ew)	3737	3915	5246	2855
Poised enhancer (Ep)	428	623	927	414

G Top 5 enriched PWMs for TFs at TPP specific strong and weak enhancer sites

🟥

Motif	p-value	Motif
FOSL2	1e-72	
ETS1	1e-32	
MAFK	1e-16	
STAT4	1e-7	
RUNX2	1e-5	

Figure S2: Activation-specific specific promoter and enhancer marks

(A) Numbers of genes with accessible (Pa) or poised (Pp) promoters in inflammatory GM-CSF derived macrophages and each macrophage activation condition. **(B)** Percentage of activation-specific gene loci with PU.1 binding (black bars) at accessible promoters determined by ChIP-seq analysis. **(C-D)** Box-and-Whiskers plots showing expression levels of genes with M^{TPP}-specific (C) accessible promoters (Pa_{TPP}) and (D) poised promoters (Pp_{TPP}) investigated in the three macrophage activation conditions (Kruskal-Wallis One Way ANOVA on ranks with pairwise multiple comparison according to Tukey test, ***$p<0.05$). **(E)** Numbers of genes with macrophage activation-specific strong (Es), weak (Ew) and poised (Ep) enhancer marks. **(F)** Percentage of PU-1 positive enhancer sites in ChIP-seq data from M^{b} and three other macrophage activation conditions. **(G)** Motif enrichment analysis for transcription factor (TF) binding sites in genes with strong and weak enhancers in TPP activated macrophages. Displayed are the top 5 positional weight matrices (PWM) ranked according the binomial p-values for the enrichment. 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.