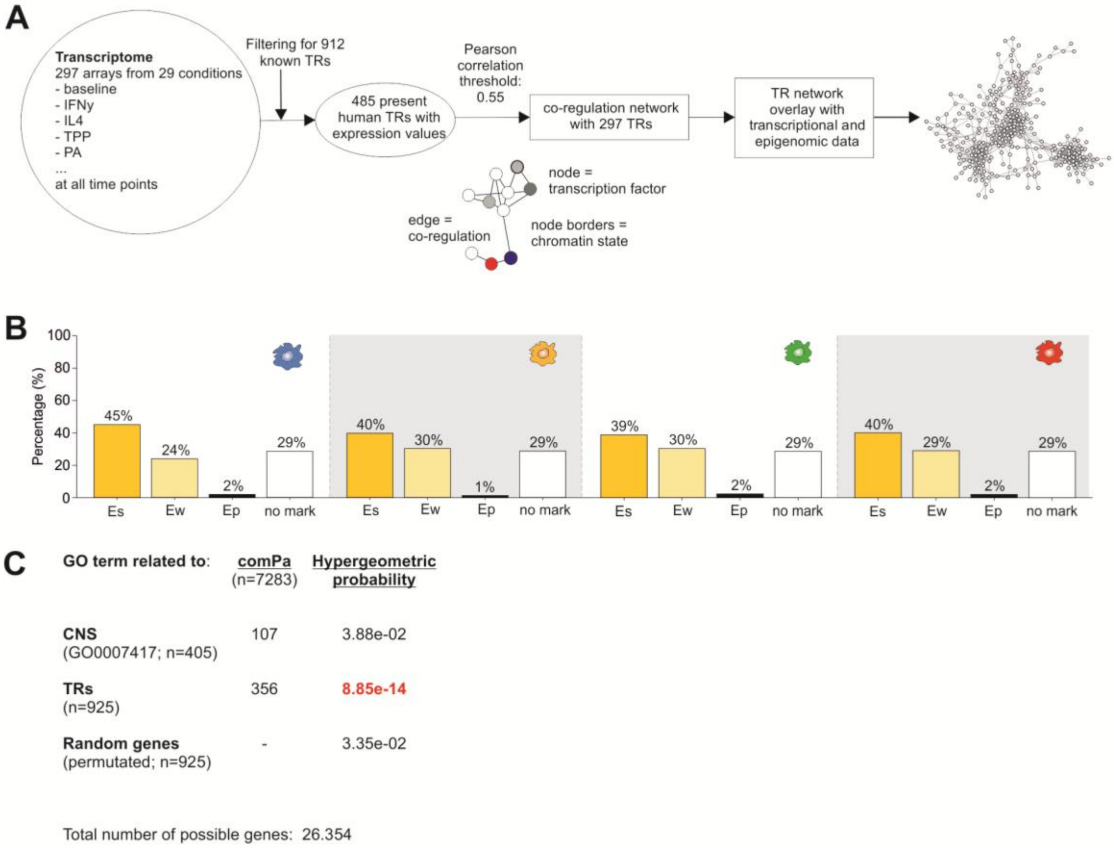
Supplementary information, Figure S4



GO term related to:	comPa (n=7283)	Hypergeometric probability
CNS (GO0007417; n=405)	107	3.88e-02
TRs (n=925)	356	**8.85e-14**
Random genes (permutated; n=925)	-	3.35e-02

Total number of possible genes: 26.354

Figure S4: Epigenetic landscape of transcriptional regulators in human inflammatory macrophages

(A) Workflow for the generation of the co-regulation network for 297 TRs expressed by human activated macrophages. **(B)** Distribution of TRs belonging to the TR network with strong (Es), weak (Ew) or poised (Ep) enhancers in all four investigated inflammatory macrophages. **(C)** Hypergeometric probability for the enrichment of accessible promoters (Pa) in the TR networks in gene sets grouped according biological functions.