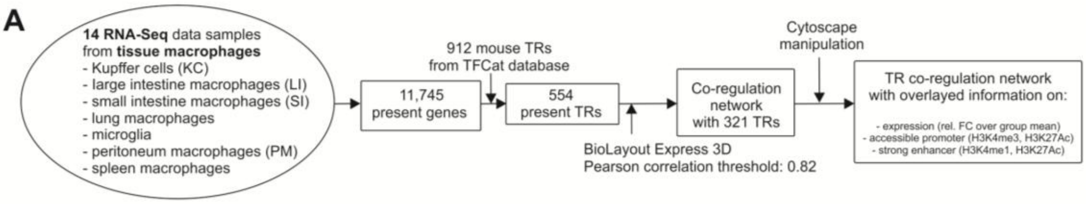
Supplementary information, Figure S6



B Histone modification state of 358 TRs being not present in murine macrophages:

Colonic	not expr.	**Ileal**	not expr.	**Microgl.**	not expr.	**Periton.**	not expr.	**Kupffer**	not expr.	**Spleen**	not expr.	**Lung**	not expr.
Pa	7 %	Pa	5 %	Pa	6 %	Pa	8 %	Pa	8 %	Pa	6 %	Pa	5 %
Pp	39 %	Pp	25 %	Pp	50 %	Pp	53 %	Pp	44 %	Pp	43 %	Pp	42 %
no mark	54 %	no mark	70 %	no mark	44 %	no mark	39 %	no mark	48 %	no mark	51 %	no mark	53 %
Es	9 %	Es	0 %	Es	4 %	Es	13 %	Es	9 %	Es	31 %	Es	0 %
Ep	24 %	Ep	0 %	Ep	12 %	Ep	28 %	Ep	31 %	Ep	3 %	Ep	0 %
no mark	67 %	no mark	100 %	no mark	84 %	no mark	59 %	no mark	60 %	no mark	66 %	no mark	100 %

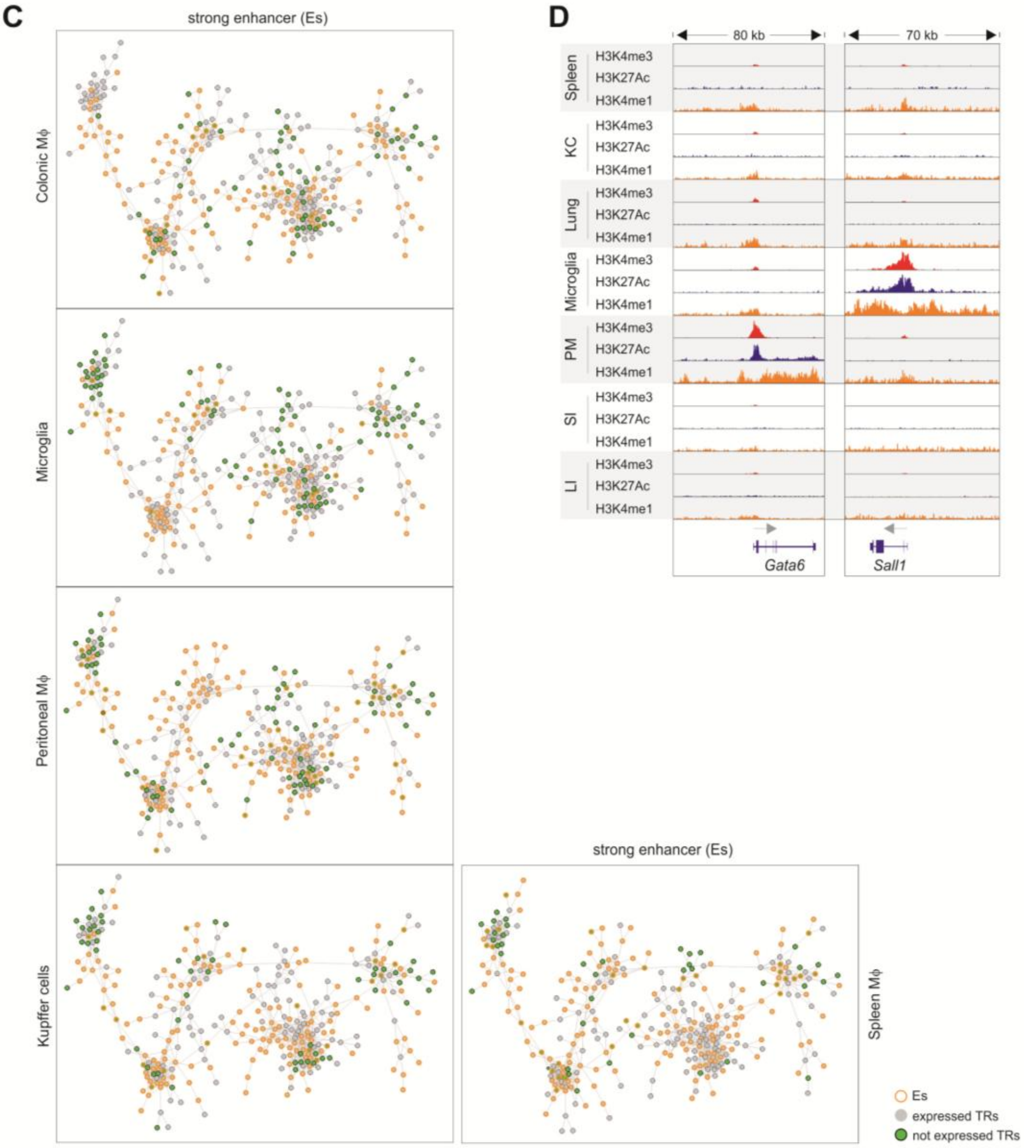


Figure S6: Epigenetic landscape of TR of murine tissue macrophages

(A) Bioinformatics approach for the generation of a murine tissue macrophage-related TR network build from 321 TRs. **(B)** Distribution of accessible (Pa) and poised promoters (Pp) and strong (Es) and poised (Ep) enhancers in the group of 358 TRs not being expressed in any of the analyzed tissue macrophages. **(C)** TR network overlaid with information on strong enhancer marks. Expressed TRs presented in grey, not expressed TRs in green/black. **(D)** Tissue macrophage-specific promoter marks for the TFs Gata6 and Sall1. RNA-seq and ChIP-seq were derived from two independent experiments [6].