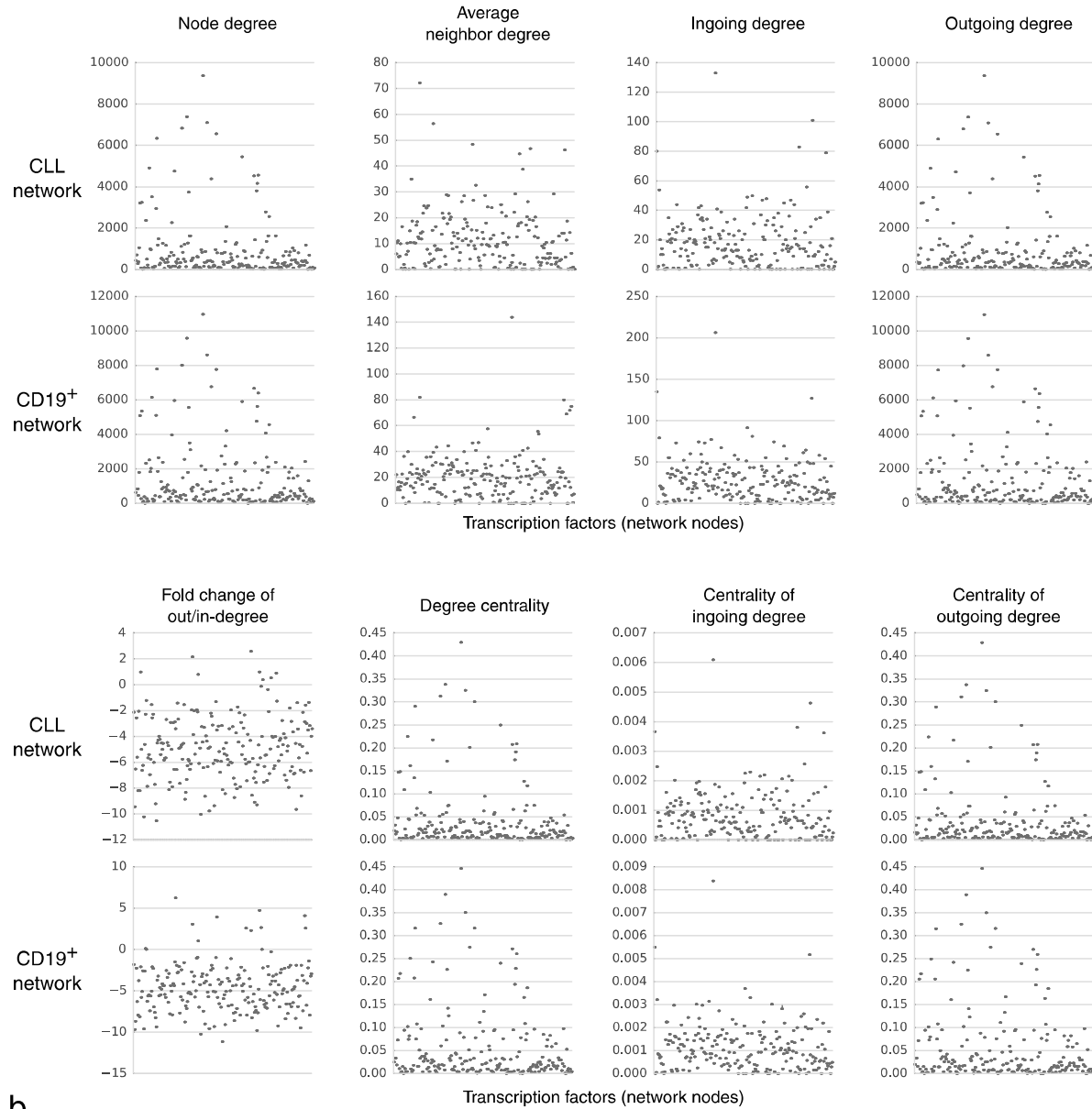
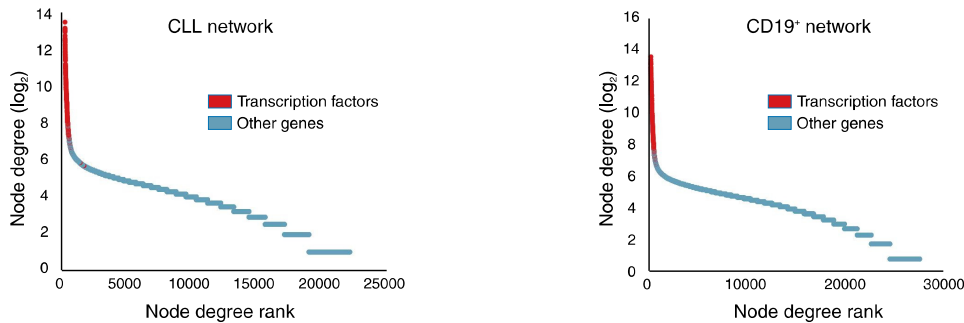


a



b



Supplementary Figure 18

Footprinting-based gene regulatory networks for ATAC-seq in CLL and DNase-seq in B cells show similar properties.

a) Structural properties of gene regulatory networks inferred from ATAC-seq data for the CLL cohort and from DNase-seq data for CD19⁺ B cells. b) Number of connections for all genes in the two gene regulatory networks (transcription factors are shown in red).