



Fig. 1| Schematic overview of EpiCon. **A.** Input of EpiCon. The input of EpiCon is the single cell multiome data, including TF expression and RE chromatin accessibility. The motif binding affinity is calculated by Homer software. **B.** Construct the TF-RE regulatory network. The foreground network is constructed by the correlation, while the background networks are generated by the permutation of expression data. The TF-RE regulatory network weight is the z-score across the background networks. **C.** Epi-controllability score. Epi-controllability score is defined as the weighted average chromatin accessibility of the downstream REs for the TF. **D.** Motif enrichment analysis for the cell type specific REs, which will be used to remove the non-enriched motifs from the EpiCon cell type specific score.