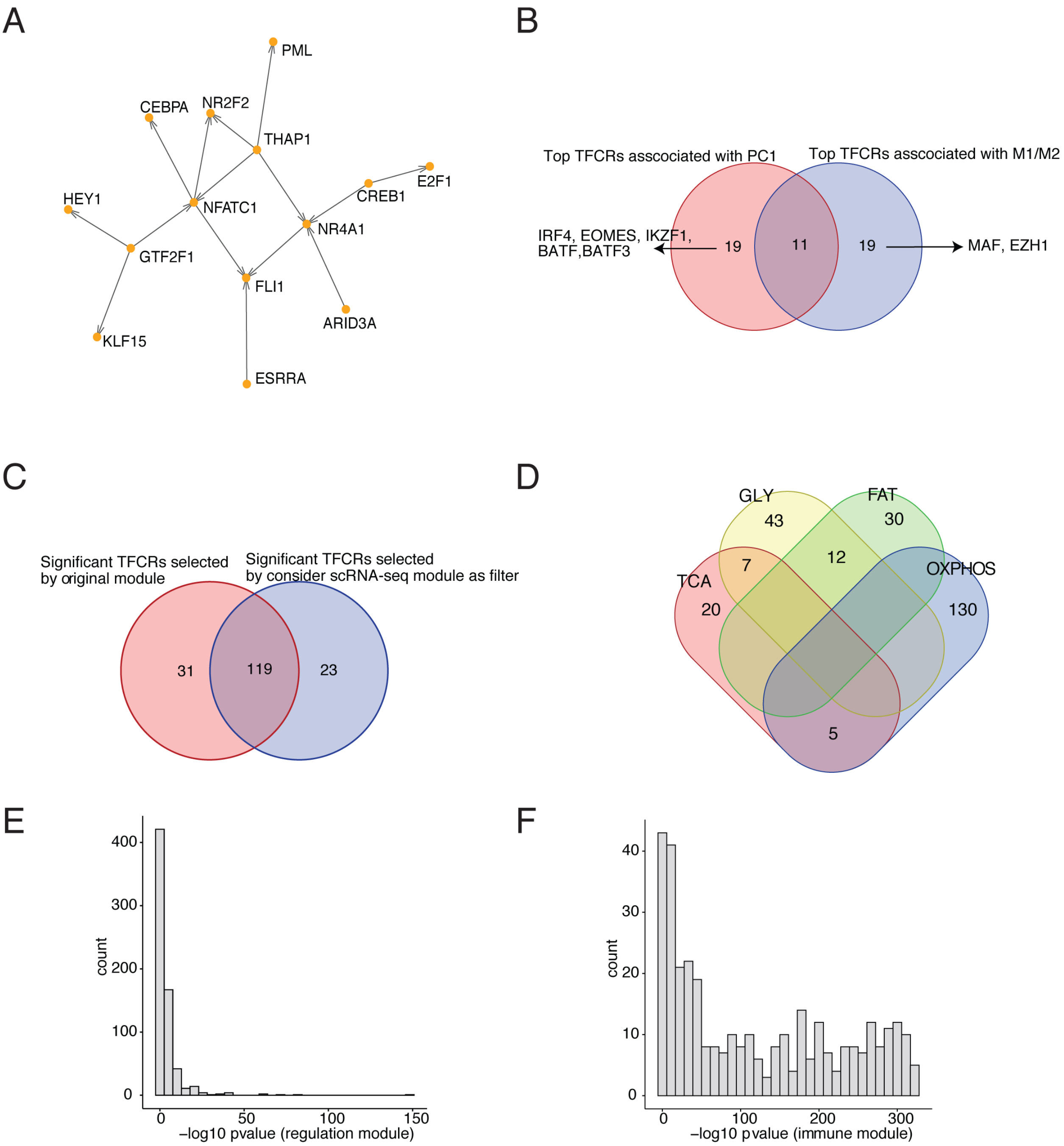

Fig. S18. Evaluation of BipotentR.

(**A**) Arrows directed from upstream TFCRs to their likely targets TFCRs, which were inferred using the knockTF database. (**B**) Overlap of top 30 significant TFCRs (adjusted p value<0.05) identified using M1/M2 or PC1. (**C**) Comparison of TFCRs identified by BipotentR immune-module and immune-module with scRNA sub-module as a filter. (**D**) Overlap among genes in the KEGG database metabolic pathways. GLY: glycolysis gluconeogenesis; FAT, fatty acid metabolism; TCA, citrate cycle TCA cycle; OXPHOS, oxidative phosphorylation. (**E, F**) Distribution of TFCR p-values of (**E**) regulation and (**F**) immune modules.