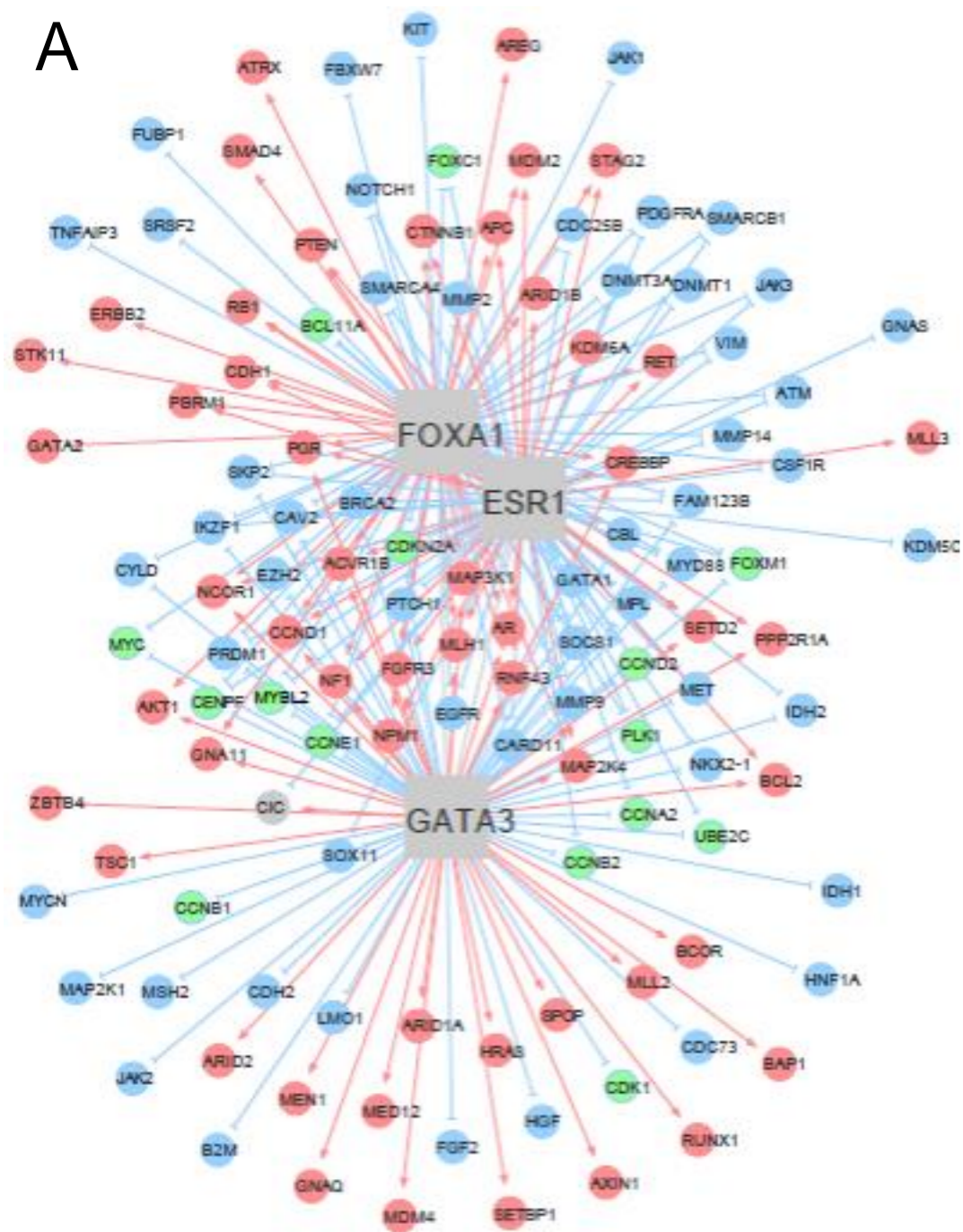


Figure S10. Validation of regulator-regulon interaction patterns in the Guedj cohort. Due to the smaller population size in the Guedj cohort, compared to the other two cohorts, we focus on the cross-subtype gene regulatory networks. See Figure S8 for nodes and edges. **A:** a gene regulatory network illustrating the interactions between three representative Group 1 MRs and cancer driver/related genes. Green nodes are highlighted for either cell cycle genes or Group 2 MRs. Other Group 1 MRs, such as *AR*, are up-regulated by the central regulators. However, Group 2 MRs, such as *FOXM1*, and the cell cycle genes, such as *CCNA2* and *CCNB2* are down-regulated by the central MRs. **B:** A gene regulatory network illustrating the interactions between the four Group 2-MRs and the regulons. Green nodes are highlighted for either the cell cycle genes or the Group 1 MRs. The cell cycle genes, such as *CDk1* and *CCNA2*, are up-regulated by the central MRs. However, the Group 1 MRs, such as *GATA3* and *FOXA1*, are down-regulated by the central MRs.

Figure S10

A



B

