

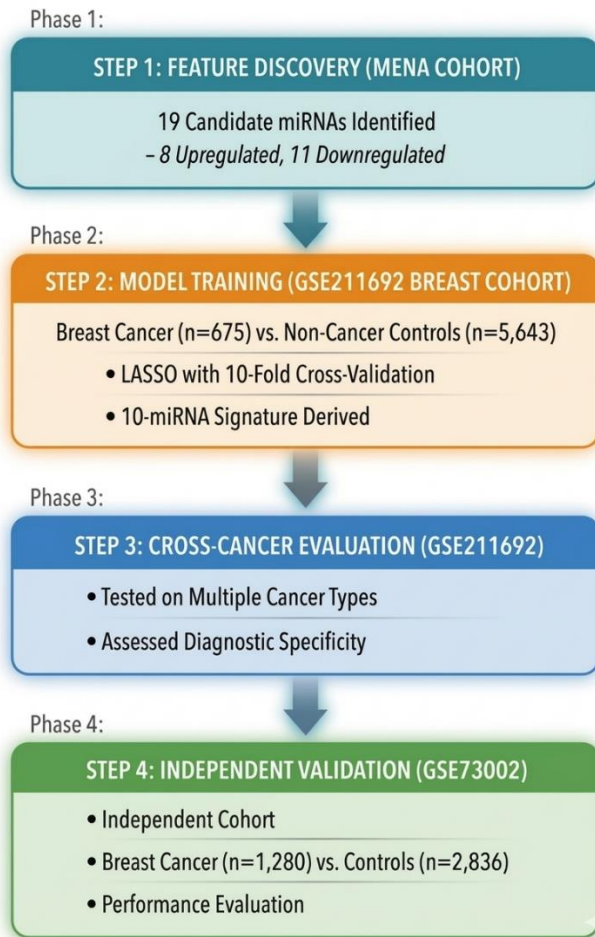


Figure S1. Workflow of miRNA diagnostic signature development and validation. Candidate miRNAs were first identified through differential expression analysis in the MENA cohort (feature discovery stage). These miRNAs were used as predefined input features for LASSO logistic regression modeling in the GSE211692 breast cancer cohort, where a 10-miRNA diagnostic signature was derived using 10-fold cross-validation. The resulting model was subsequently applied to other cancer types within GSE211692 to evaluate cross-cancer diagnostic specificity. Finally, the fixed LASSO coefficients were validated in an independent external dataset (GSE73002) comprising 1,280 breast cancer cases and 2,836 non-cancer controls.