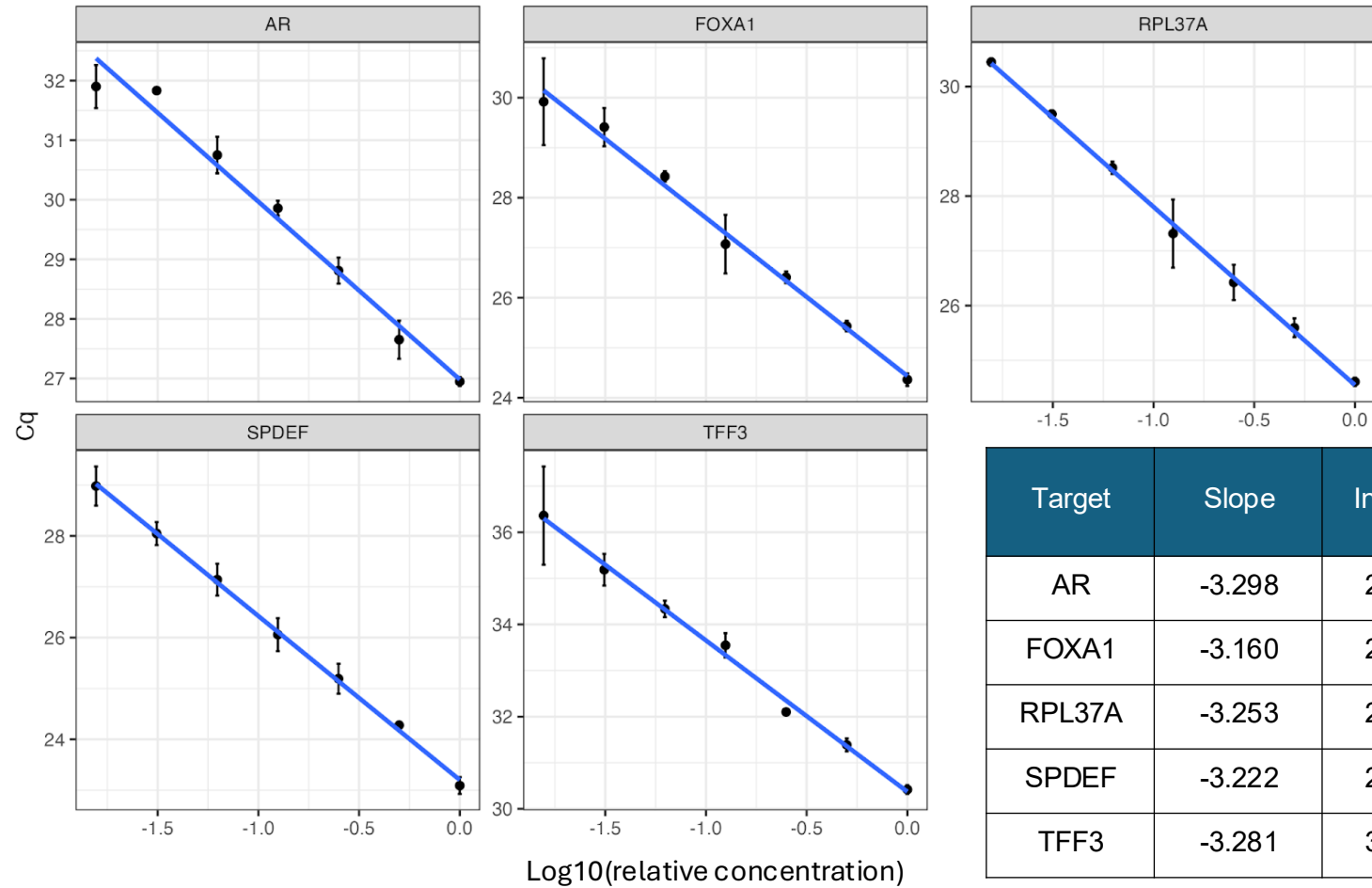
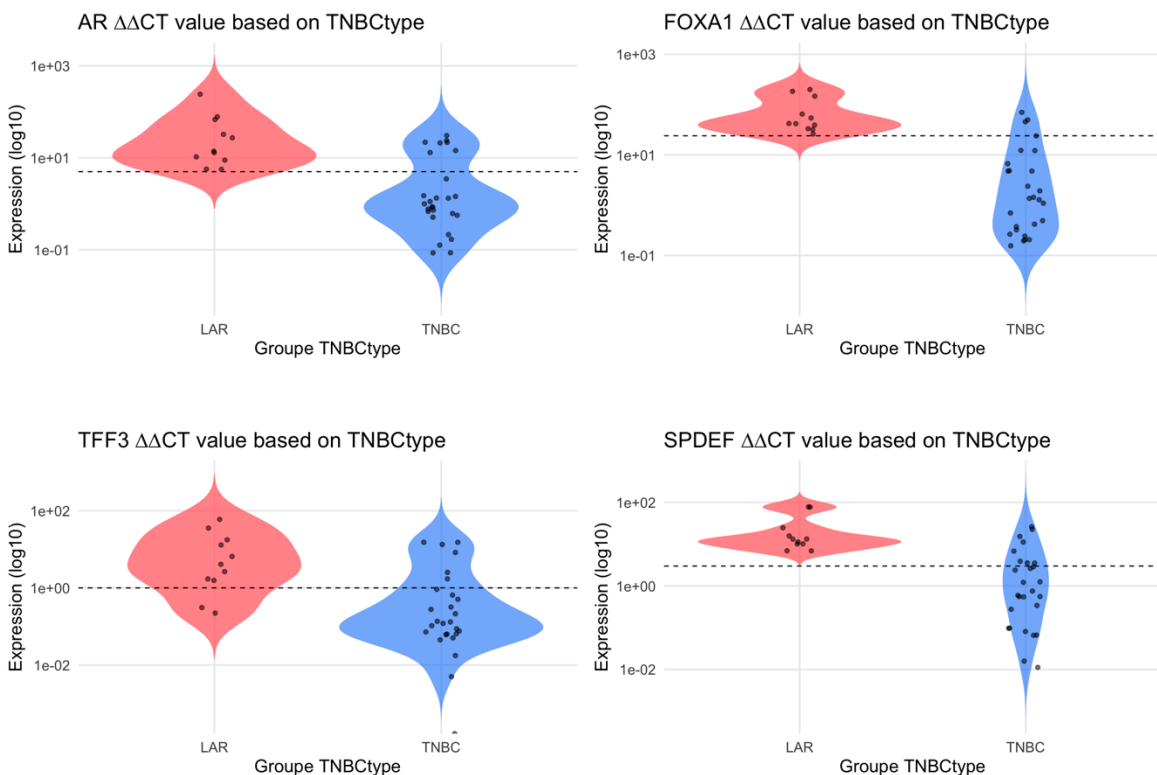
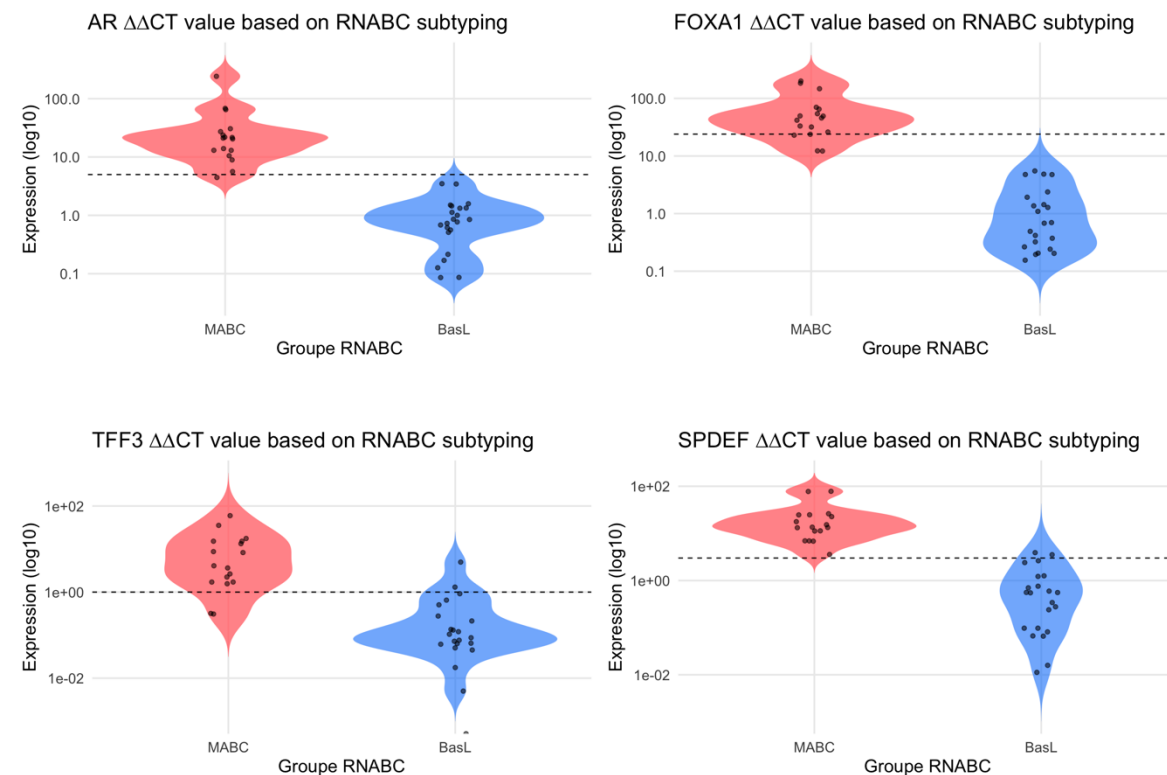




Supplementary Figure 1. RT-qPCR standard curves for the 4-gene signature and reference gene.

Standard curves were generated for *AR*, *FOXA1*, *SPDEF*, *TFF3*, and the housekeeping gene *RPL37A* using serial dilutions of cDNA. Each point represents the mean quantification cycle (Cq) ± standard deviation from technical replicates. The linear regression line (in blue) shows the expected inverse relationship between Cq values and the logarithm of relative cDNA concentration (log₁₀ scale), confirming high amplification efficiency and assay reproducibility for all targets.

A**SLSvalidation – TNBCtype subtyping****B****SLSvalidation – RNABC subtyping**

Supplementary Figure 2. Validation of the 4-gene expression signature in the SLSvalidation cohort using two independent molecular classifiers.

(A) Violin plots showing the $\Delta\Delta$ CT values (log10 scale) of *AR*, *FOXA1*, *SPDEF*, and *TFF3* in tumors classified as LAR or TNBC according to the TNBCtype-4 classifier. **(B)** Corresponding expression patterns in tumors classified as MABC or BasL according to the RNABC classifier.

For each gene, red indicates LAR/MABC tumors and blue indicates TNBC/BasL tumors. The dashed lines represent the median threshold used to distinguish high and low expression.