

Supplementary information

Supplementary Data 01. Gene annotation mapping file used for downstream analyses. The table reports the correspondence between Ensembl gene identifiers (ensg) and gene symbols, together with gene biotype classification and the mean expression value (mean_expr) calculated across samples.

Supplementary Data 02. Differential gene expression analysis results for mRNA across the analyzed disease stages. For each gene (ID), the table reports the log2 fold change (logFC), average expression level (AveExpr), nominal p value (P.Value), and multiple testing adjusted p value (adj.P.Val).

Supplementary Data 03. Differential gene expression analysis results for microRNA across the analyzed disease stages obtained from an additional comparison. Reported columns include gene identifier (ID), log2 fold change (logFC), average expression level (AveExpr), nominal p value (P.Value), and adjusted p value (adj.P.Val).

Supplementary Data 04. Results of the microRNA–mRNA correlation analysis. The table includes the microRNA name, predicted target gene (Target), direction of microRNA differential expression (microRNA.Direction), Spearman correlation coefficient (Corr.Coefficient), nominal correlation p value (Corr.P.Value), and multiple testing adjusted p value (Corr.Adjusted.P.Val).

Supplementary Figure 01. Multidimensional scaling (MDS) plots of normalized gene counts for mRNA and microRNA datasets. Samples are labeled according to sex, where M indicates male and F indicates female.

