Comparative miRNA Profiling in Breast Cancer Tissue and Plasma

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Background

Micro-RNAs (miRNAs) have been shown to regulate oncogene and tumor suppressor pathways and are often dysregulated in breast cancer, impacting progression of malignancies. Their presence in circulation has led to interest in their potential use as non-invasive tumor biomarkers.

This study aims to characterize miRNA expression patterns in breast cancer tissues and compare them across clinical and demographic subgroups, with the future aim of comparing tumor expression and plasma levels.

Methods

Archived formalin-fixed paraffin-embedded (FFPE) breast cancer samples (n=106) are currently being processed using the Qiagen AllPrep DNA/RNA FFPE Kit.

Total RNA is quantified and quality assessed by Nanodrop, converted to cDNA via reverse transcription, and analyzed via quantitative PCR (qPCR).

Expression patterns of 9 candidate miRNAs are measured using miR-16 as loading control.
ΔCt values are compared between tumor and normal tissues, as well as across clinicopathologic subgroups using independent t-tests with Welch's correction. Fold changes are calculated from ΔΔCt values.

Results: Tumor vs Healthy

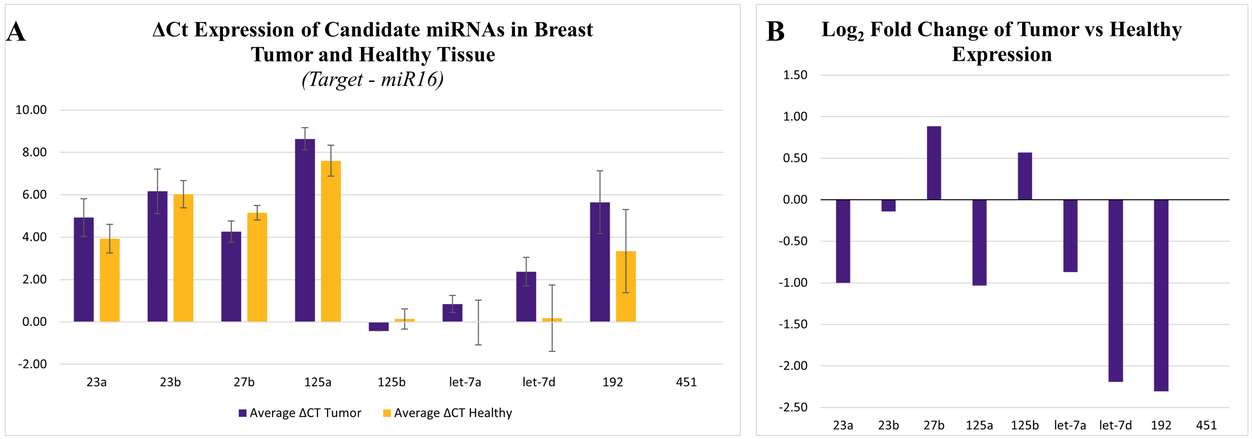

Figure 1. ΔCt expression (mean ± SD) and $\log_2$ fold change of candidate miRNAs in breast tumor and matched normal tissues, normalized to miR-16. Lower ΔCt values correspond to higher expression. Positive $\log_2$ fold change values indicate upregulation in tumor tissue, while negative values indicate downregulation.

Summary:

- Analysis was completed for a **subset of samples (n ≈ 30)**.
- Several candidate miRNAs showed differential expression between **tumor and matched normal breast tissue**.
- **let-7d** demonstrated a strong trend toward **downregulation in tumor tissue** compared to normal (*p=0.051*, n=12 vs 11).

Overall patterns suggest distinct miRNA expression differences between tumor and normal tissue, laying the groundwork for subsequent plasma–tissue correlation analyses.

Results: Exploratory Comparisons

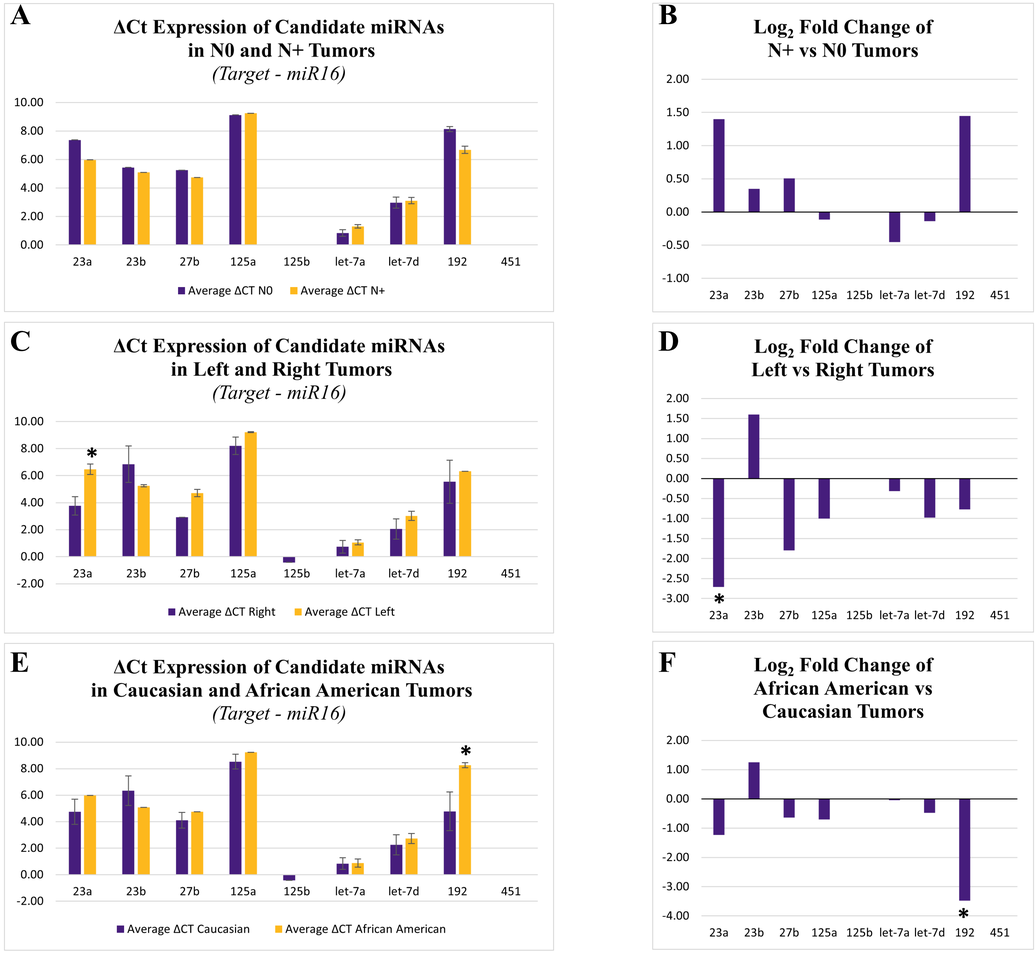

Figure 2. Exploratory comparisons of ΔCt expression (left panels) and $\log_2$ fold changes (right panels) across nodal status (A–B), race (C–D), and tumor laterality (E–F).

Summary:

- Subgroup analyses were performed for **nodal status (N0 vs N+)**, **race (Caucasian vs African American)**, and **tumor laterality (left vs right)**.
- **miR-192** showed increased expression in **N+ tumors** compared to N0 tumors (*p=0.097*).
- **miR-192** was upregulated in **African American tumors** compared to Caucasian tumors (*p=0.033*).
- **miR-23a** was upregulated in **left-sided tumors** compared to right-sided tumors (*p=0.022*).

These exploratory patterns highlight biologically meaningful subgroup differences that warrant further investigation with larger sample sizes.

Conclusions

Our preliminary analyses suggest that **let-7d**, **miR-192**, and **miR-23a** may play roles in breast cancer biology, with expression differences observed by tumor presence, nodal status, laterality, and race.

While plasma analyses and expanded clinical correlations are ongoing, these early findings highlight biological signals of interest, with continued processing and analysis underway.