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ORIGINAL ARTICLE

Discovery of Lipid Metabolism Networks as Key Pathways in Breast Cancer via Genomic Data Integration and WGCNA

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SUMMARY

Background: **Breast cancer remains a major global health issue, requiring innovative approaches for early detection and treatment. This study employs weighted gene co-expression network analysis (WGCNA) to uncover the complex biological processes and pathways involved in tumorigenesis by focusing on gene modules rather than individual genes. The aim of this study was to integrate multiple datasets and utilize WGCNA to identify the key genes involved in breast cancer. By combining various gene expression datasets, we aimed to identify significant gene modules and regulatory networks that contribute to breast cancer progression**.

Methods: **Four gene expression datasets from the NCBI Gene Expression Omnibus (GEO) were integrated to explore the genetic profiles of breast cancer. Using high-throughput genomic data, WGCNA identified key regulatory networks and hub genes involved in disease progression, and RT-qPCR was performed for validation.**

Results: **The study identified 9,707 DEGs, showing significant alterations in gene expression between tumor and adjacent normal tissues. Four critical genes, ADIPOQ, CHRDL1, FABP4, and PLIN1, were highlighted, with their expression closely linked to lipid metabolism pathways, which are crucial in breast cancer biology. Notably, ADIPOQ expression was significantly reduced in tumor samples.**

Conclusions: **The integration of Omics data through WGCNA uncovered key interconnected gene modules, emphasizing the critical role of lipid metabolism in cancer progression. These results underscore the need for targeted therapeutic strategies to restore hub gene expression and to present potential biomarkers for early diagnosis**

and treatment. Moreover, lipid metabolism emerged as a pivotal pathway in breast cancer progression, suggesting that its regulation could be essential not only for targeted therapies but also for the prevention and control of the disease. This approach offers promising avenues for early intervention that could potentially reduce cancer risk.
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Supplementary Data

Table S1. Primer list for qPCR.

F ADIPOQ	**CTGTTGCTGGGAGCTGTTCTA**
R ADIPOQ	**TGGATCTCCTTTCTCACCCT**
F CHRDL1	**CCTGGAACC TTATGGGTTGGT**
R CHRDL1	**AACATTTGGACATCTG ACTCGG**
F FABP4	**TCG CTG ATG CAC TGC CTA TG**
R FABP4	**GAG AGG TCC ACA GAG CTG ATT**
F PLIN1	**GCCTGACTTTGCTGGATGG**
R PLIN1	**CTTGGTGCTGGTGTAGGTCTTCT**
F gapdh	**GAGTCA ACG GAT TTG GTC GT**
R agpdh	**GGTGCCATG GAATTTGCCAT**

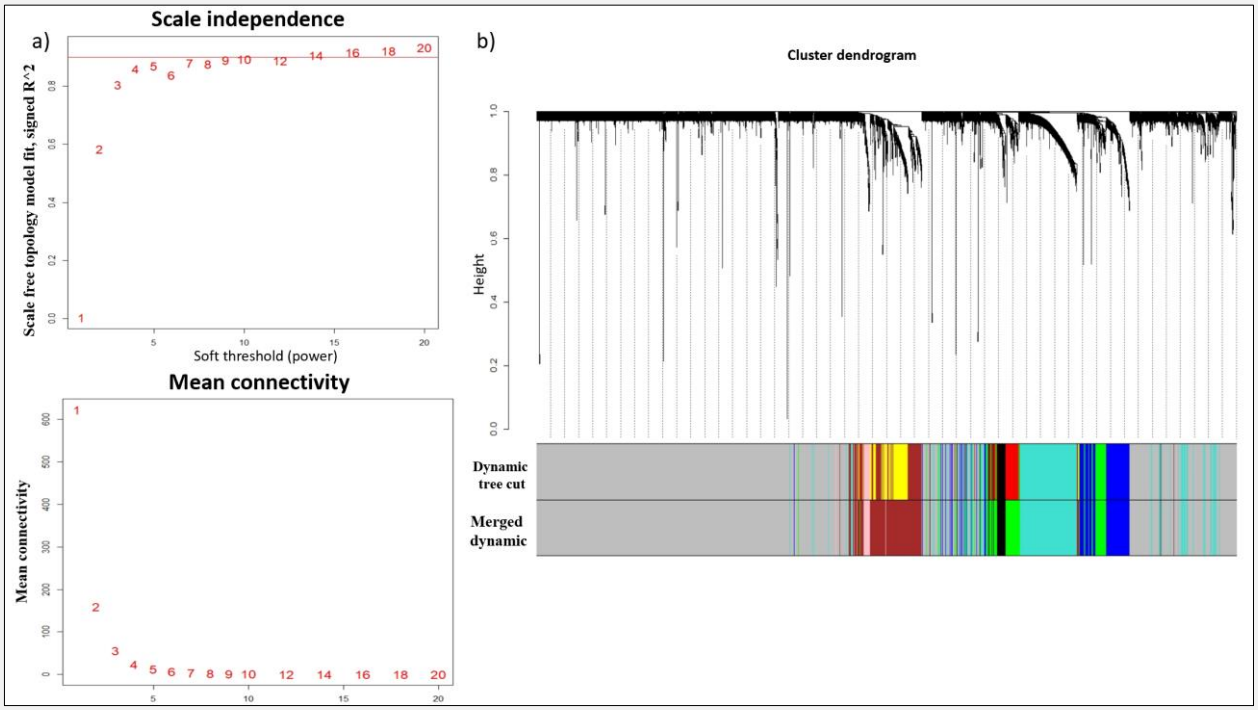

Figure S1. Determination of soft threshold and gene cluster dendrogram from WGCNA analysis.

a) By using a cutoff R^2 value of 0.9, a soft threshold β value was selected, b) cluster dendrogram and module assignment from WGCNA. The branches represent clusters of genes that are highly connected.