**Integrative Omics Analysis Reveals DTX1 as a Key Marker and Drug Target in Breast Cancer**

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**Purpose**

The E3 ubiquitin ligase Deltex1 (DTX1) holds promise as a novel marker and therapeutic target for breast cancer. This study aims to elucidate the detailed molecular regulatory mechanisms of DTX1 in breast cancer cells and employ pharmacogenomic strategies to identify potential drugs.

**Method**

We conducted a comprehensive analysis of DTX1's clinical relevance using multi-omics data, including single-cell RNA sequencing and spatial transcriptomics. Raw data from the TCGA were validated against our dataset to ensure reliability. Additionally, pharmacogenomics was utilized to explore potential small molecule drugs targeting DTX1, and a 3D spheroid model was employed for drug screening.

**Results**

The mRNA and protein expression levels of DTX1 were significantly lower in breast cancer (BRCA) tissues compared to adjacent non-cancerous tissues. Importantly, low DTX1 expression was associated with poor prognosis in BRCA patients. Spatial transcription analysis and single-cell RNA-seq further confirmed that DTX1 is an independent prognostic factor for BRCA. Functional enrichment analysis using KEGG pathways and gene ontology (GO) revealed that low DTX1 expression in malignant breast cancer is primarily associated with macrophage infiltration. Furthermore, pharmacogenomic screening identified small molecule drugs that modulate DTX1 expression in breast cancer cells, effectively inhibiting their growth.

**Conclusion**

This study uncovers novel diagnostic and prognostic implications of DTX1 in breast cancer and introduces new small molecule drugs that can effectively slow cancer progression.