

Integrated Transcriptomic and Regulatory Network Analysis Identifies Candidate Molecular Signatures in Endometrioid Endometrial Cancer

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Background: Endometrial cancer is one of the most common gynecological malignancies, with endometrioid endometrial carcinoma representing its predominant histological subtype. Alterations in gene expression and transcriptional regulation contribute to tumor development and progression. This study aimed to identify differentially expressed genes and characterize their functional, interaction-network, and regulatory features in endometrioid endometrial cancer.

Methods: The publicly available microarray dataset GSE17025 was obtained from the Gene Expression Omnibus (GEO) database. Expression profiles from 79 endometrioid endometrial cancer samples and 11 non-malignant endometrial controls were analyzed. Differential expression analysis was performed using GEO2R based on the limma framework, with Benjamini–Hochberg correction for multiple testing. An adjusted $P < 0.05$ was considered statistically significant, while an absolute $\log_2$ fold-change threshold ≥ 1 was used to prioritize biologically relevant alterations. Significant genes were subjected to Gene Ontology (GO)-based functional characterization and protein–protein interaction analysis. Network organization and potential molecular modules were further explored using CytoCluster. Promoter sequences of selected genes were additionally investigated for regulatory motifs, with motif comparison and functional characterization performed using Tomtom and GOMO.

Results: Transcriptomic analysis identified 6,173 significantly altered probes/features between endometrioid endometrial cancer and normal endometrial tissues. Both increased and decreased expression patterns were observed. Functional and network analyses indicated broad molecular dysregulation involving multiple biological processes and interconnected gene modules. Promoter-level analysis further suggested potentially shared regulatory elements among selected differentially expressed genes.

Conclusion: Integrated analysis of GSE17025 revealed extensive transcriptional alterations associated with endometrioid endometrial cancer. Combining differential expression, functional annotation, network clustering, and promoter analysis may facilitate identification of candidate molecular signatures for further experimental and clinical investigation.

Keywords: Endometrial cancer; Transcriptomics; Bioinformatics