

# Proteomic profiling of ovarian clear cell carcinomas identifies prognostic biomarkers for chemotherapy

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## Abstract

CCOC is a relatively rare subtype of ovarian cancer with high degree of resistance to standard chemotherapy. Little is known about the underlying molecular mechanisms, and it remains a challenge to predict its prognosis after chemotherapy. We analyzed the proteome of CCOC tissue samples from two independent cohorts using DIA-MS. A total of 8697 proteins were characterized in the first cohort (H1 cohort, 32 patients, 35 FFPE samples) and 9409 proteins in the second cohort (H2 cohort, 24 patients, 28 FF samples). After bioinformatics analysis, we narrowed our focus to 15 proteins significantly correlated with RFS in both cohorts. These proteins are mainly involved in DNA damage response, extracellular matrix, and mitochondrial metabolism. We further developed a 13-protein model to predict the prognosis of patients with CCOC in H2 cohort, and validated the model in the H1 cohort in both DIA and PRM data. Finally, we verified the modulated pathways from our CCOC proteomic dataset in several published CCOC transcriptome and proteome datasets. Taken together, this study presents a CCOC proteomic data resource and a promising 13-protein panel which could potentially predict the recurrence and survival of CCOC.

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