[BIOINFO 2023]

IFN-γ–related transcriptome profile as favorable prognostic factors in high-grade serous ovarian cancer

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Although less than half of HGSC patients survive more than 5 years after diagnosis, those with exceptionally long survival may provide new insights into tumor prediction and treatment approaches. We obtained publicly available transcriptome data on HGSC patients and conducted RNA-seq analysis, comparing differentially expressed genes (DEGs), cell type composition and consensus molecular subtype (CMS) between both the long-term (LT) and short-term (ST) group of 126 patients (with 10 years cutoff). We found a number of differentially expressed genes between the two groups (FDR < 0.05), and several cell types significantly differed in CIBERSORT analysis between LT survivors and ST, including B-cell-naive, Macrophages M1, T-cell CD8 and Plasma cell. The immuno-reactive subtype among CMSs was highly enriched in LT samples, while the mesenchymal subtype was enriched in ST. Furthermore we investigated the expression pattern at the single-cell level (3 good and 3 poor response). We found markers showing consistent expression pattern with bulk transcriptome such as *CXCL9*, *GZMA* and *SECTM1*, which are functionally involved in interferon gamma signaling. These findings will enhance the understanding of the molecular mechanism in HGSC that exist among patients with different prognoses and better inform treatments by identifying new targets for drug development.