Our aim was to search for potential predictive biomarker(s) of cisplatin resistance in high-grade serous ovarian cancer (HGSOC). We have re-analyzed the data published by Koti et al.1. Data encompassed 28 HGSOC gene expression profiles obtained using Affymetrix U133-Plus-2.0-GeneChips. Based on progression free survival (PFS) after first-line chemotherapy, 16 samples were classified as platinum-sensitive (PFS>18 months), 12 as platinum-resistant (PFS<6). Data was filtered using Gaussian Mixture Modeling decomposition,2 in order to select transcripts that were characterized by large value of variance. Normality of data distribution was checked with Shapiro-Wilk test. Because of non-normal distribution U Mann-Whitney Test was performed and U Mann Whitney effect size was calculated for up- and down-regulated transcripts. Transcripts with p-values<0.001 and large or very large effect size were considered significant.

Our approach resulted in 356 probe-sets. Based on literature review we selected 40 potential candidate biomarkers for further validation. Selected probe-sets correspond to proteins related with mitochondrial function, nuclear- and cellular-membrane transport, that are processes related with drug resistance.

Our computational approach resulted in a larger list of probe-sets than that of Koti et al.1. In our opinion, their analysis suffered from the combination of parametric and non-parametric tests, inappropriately used for the data with non-normal distribution. Using non-parametric test suited for non-normal distributed dataset and analysis of effect size allowed to receive more reliable results, although selected candidate biomarkers must be further validated.

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