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Identification of expression signatures for metastatic prostate cancer

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Metastatic prostate cancer usually has a poor prognosis. Identification of new molecular signatures associated with an aggressive form of prostate cancer and the creation of a prognostic multigenic panel will make it possible to assess the dynamics of the disease and choose the treatment tactics. The aim of our study was a bioinformatic search for a multigene panel whose transcriptomic profile would be associated with metastasis and survival of patients with prostate cancer. Prediction of the value of differentially expressed genes indicated that overexpression of a panel of seven genes FUS, PRC1, ASF1B, WDR5, RBM28, RUVBL1, SF3B6 correlated with recurrence-free survival in patients with prostate cancer. A review of the available literature sources in PUBMED over the past 15 years has shown that aberrant tissue-specific expression of some genes was observed in metastatic prostate cancer and served as an indicator of cell proliferation, and was well differentiated from control (healthy tissue). At the same time, there were no data on the potential of the multigene panel identified by us as a marker of poor prognosis of the disease. This fact testifies to the novelty of the results achieved. The modern gene diagnostics paradigm is focused primarily on the analysis of the several molecular determinants expression. Therefore, further verification of a multigene panel consisting of FUS, PRC1, ASF1B, WDR5, RBM28, RUVBL1, and SF3B6 will improve the transcriptional platform for predicting metastatic prostate cancer.