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Novel unsupervised classification of cancer patients and statistical prediction model of metastatic status based on NGS-generated molecular profiles

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Next generation Sequencing and other advanced genomic sequencing technologies have largely revolutionized basic and clinical cancer research. Emerging genomic analysis tools and growing databases facilitates clinical diagnosis and treatment plan decisions. In addition to traditional histopathological techniques and genomic assays, NGS have been used to identify biomarkers of tumor proliferation, cell cycle checkpoints, hypoxia, DNA repair, apoptosis, and androgen synthesis, which predict response to radiotherapy. In this study, we analyzed publically available whole exome/genome sequencing data, and summarized genes with frequently altered copy number variants in metastatic cancer patients. We identified a few novel gene clusters that are specific in predicting survival rate in cancer patients and could potentially serve as prognosis biomarkers. We generated an 80 gene biomarker panel based on unsupervised classification method in prostate cancer. By performing machine learning using statistical models, we analyzed cancer cohorts for different cancer types, and confirmed the sensitivity and overall accuracy of our biomarker panel in predicting metastatic status. These results could benefit the discovery of novel clinical biomarkers, drug targets, as well as early detection and diagnosis of metastatic cancer patients.

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