Rational design of NGS gene panels to evaluate potential cancer treatment options as part of clinical decision support systems

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Nowadays, the effectiveness of cancer treatments is being questioned. Despite the increasing availability of treatment options, millions of patients die from cancer every year. Due to metastasis, relapse, heterogeneity, resistance to chemotherapy and radiotherapy, and also patient-specific molecular characteristics, existing cancer therapies respond differently in different patients. In this context, there is a great need for a personalized medicine approach. It is important to develop clinical decision support systems (CDSS) that interrogate treatment efficacy using biomarkers at the individual molecular level for precision oncology. The key components of these CDSSs are gene panels consisting of disease-specific molecular biomarkers that are targeted by currently approved drugs and guide treatment. In this study, we developed a novel strategy to develop next generation sequencing (NGS)-based gene panels that enable effective treatment decision-making by integrating data from multiple biological levels (genomics, pharmacogenomics, drug-protein interactions, drug-drug interactions, etc.). The goal was to develop gene panels primarily for colorectal, glioblastoma, breast, and lung cancers to address the most pressing needs of the clinic. These gene panels will enable more accurate decisions about effective cancer treatments and pave the way for new clinical trials, clinical applications, and scientific research projects. As a complement to CDSSs, they will help reduce the impact of disease and the economic burden on public health and the national health care system.