General Cancer Panels for Clinical Next Generation Sequencing (NGS) Testing

GENOME EXPLORATIONS
A DIVISION OF COMPASS LABORATORY SERVICES LLC

GenOnc Cancer Panel 1 - Actionable	**(8 Genes)**
GenOnc Cancer Panel 2 - Clinically Relevant	**(24 Genes)**
GenOnc Cancer Panel 3 - Hotspot	**(50 Genes)**
GenOnc Cancer Panel 4 - Comprehensive	**(160 Genes)**
GenOnc Cancer Panel 5 - Predisposition	**(143Genes)**

GenOnc Cancer Panel 1 - Actionable

Introduction

GenOnc Cancer Panel 1 – Actionable Mutations is a collection of multiplexed PCR primer assays for targeted enrichment of the key regions of 8 genes identified by the National Comprehensive Cancer Network (NCCN), College of American Pathologists (CAP), and American Society of Clinical Oncology (ASCO) to be clinically actionable somatic mutations in solid tumors. There are many genes that are somatically mutated during carcinogenesis. However, few of these mutations have confirmed prognostic or diagnostic importance. The guidelines and published opinions of the above medical bodies identify variants that are clinically relevant. Since the key mutations in each gene have also been identified through clinical trials, this targeted enrichment panel will focus on only those relevant genomic locations, saving sequencing space for higher throughput or greater sequencing depth to detect variants at lower minor allele frequencies

GenOnc Cancer Panel 1 Genes

BRAF, EGFR, IDH1, IDH2, KIT, KRAS, NRAS, PDGFRA

GenOnc Cancer Panel 2 - Clinically Relevant

Introduction

GenOnc Cancer Panel 2 - Clinically Relevant Tumor Targeted Panel is a collection of multiplexed PCR primer assays for targeted enrichment of the key regions of 24 genes identified by medical groups and peer-reviewed research to be functionally relevant in the treatment of solid tumors. Clinically relevant mutations in these genes have been identified by guidelines and published opinions from groups such as the National Comprehensive Cancer Network (NCCN), College of American Pathologists (CAP), and American Society of Clinical Oncology (ASCO). There are many genes that are somatically mutated during carcinogenesis. However, few of these genes have confirmed prognostic of diagnostic importance. Since the key mutations in some genes have been identified through clinical trials, this targeted enrichment panel will focus only on those relevant genomic locations, saving sequencing space for higher throughput or greater sequencing depth to detect variants at lower minor allele frequencies. In addition, this panel includes variants identified in retrospective studies as relevant to the prognosis or diagnosis of cancer. These variants re not yet included in published guidelines and opinions, but may be under review for future opinions. However, some genes require additional sequence information depending on their function. Tumor suppressor genes often do not have mutational “hotspots”; any mutation throughout their coding region may be functionally relevant. Therefore, the panel includes full coding region coverage of tumor suppressor genes. In addition, mutations for some oncogenes may lie elsewhere within entire exons or functional domains. Therefore, full coverage of relevant exons for certain genes is also included. This panel has been developed for molecular biology applications only. This panel is not intended for the diagnosis, prevention, or treatment of a disease.

GenOnc Cancer Panel 2 Genes

AKT1, ALK, AR, BRAF, CTNNB1, DDR2, EGFR, ERBB2, FGFR3, GNA11, GNAQ, IDH1, IDH2, KIT, KRAS, MAP2K1, MET, NRAS, PDGFRA, PIK3CA, PTEN, RET, STK11, TP53