PRECISIONDIAGNOSTIC
LABORATORY

THE UNIVERSITY OF CHICAGO

OncoPlus 1200 Genes NGS PANEL

The OncoPlus panel is a targeted next generation sequencing (NGS) assay that has the capability to cover 1,213 cancer-related genes for personalized assessments of both solid tumors and hematological malignancies. Variant calling in 147 genes shown below are reportable for clinical patient care:

- 147 genes shown below are clinically reportable for mutations, insertions and deletions:

  ABL1, AKT1, ALK, APC, ARID1A, ARID2, ASXL1, ATM, ATR, ATRX, AXL, B2M, BAP1, BCOR, BCORL1, BIRC3, BLM, BRAF, BRCA1, BRCA2, BTK, CALR, CBL, CBLB, CCND1, CCND2, CCND3, CDH1, CDKN2A, CEBPA, CHEK1, CHEK2, CSF1R, CSF3R, CTCF, CTNNA1, CTNNB1, CUX1, CXCR4, DAXX, DDR2, DDX3X, DDX41, DICER1, DNMT3A, EGFR, EP300, EPHA3, EPHA5, ERBB2, ERBB3, ERBB4, ERCC3, ESR1, ETV6, EZH2, FANCA, FAT3, FBXW7, FGFR1, FGFR2, FGFR3, FH, FLT3, FOXL2, GATA1, GATA2, GNA11, GNAQ, GNAS, GRIN2A, H3F3A, HIST1H3B, HIST1H3C, HNF1A, HRAS, IDH1, IDH2, IKZF1, ITPKB, JAK2, KDM6A, KDR, KIT, KMT2A, KRAS, MAP2K1, MAPK1, MET, MLH1, MLH3, MPL, MRE11A, MSH2, MSH6, MTOR, MYD88, NBN, NF1, NF2, NFE2L2, NOTCH1, NOTCH2, NPM1, NRAS, PALB2, PBRM1, PDGFRA, PDGFRB, PHF6, PIK3CA, PIK3CB, PIK3R1, PLCG2, POLE, POT1, PPP2R1A, PTCH1, PTEN, PTPN11, RAD21, RAD51, RB1, RET, RUNX1, SDHB, SDHC, SDHD, SETBP1, SF3B1, SMAD4, SMARCB1, SMC1A, SMC3, SMO, SRSF2, STAG2, STK11, TERT, TET2, TP53, TSC1, TSC2, U2AF1, VHL, WT1, and ZRSR2.

- Genes reported for copy number gains and losses (136):

  ABL1, AKT1, ALK, APC, ARID1A, ARID2, ASXL1, ATM, ATR, AXL, B2M, BAP1, BIRC3, BLM, BRAF, BRCA1, BRCA2, CALR, CBL, CBLB, CCND1, CCND2, CCND3, CDH1, CDKN2A, CEBPA, CHEK1, CHEK2, CSF1R, CSF3R, CTCF, CTNNA1, CTNNB1, CUX1, CXCR4, DAXX, DDR2, DDX41, DICER1, DNMT3A, EGFR, EP300, EPHA3, EPHA5, ERBB2, ERBB3, ERBB4, ERCC3, ESR1, ETV6, EZH2, FANCA, FAT3, FBXW7, FGFR1, FGFR2, FGFR3, FH, FLT3, FOXL2, GATA2, GNA11, GNAQ, GNAS, GRIN2A, H3F3A, HIST1H3B, HIST1H3C, HNF1A, HRAS, IDH1, IDH2, IKZF1, ITPKB, JAK2, KDR, KIT, KMT2A, KRAS, MAP2K1, MAPK1, MET, MLH1, MLH3, MPL, MRE11A, MSH2, MSH6, MTOR, MYD88, NBN, NF1, NF2, NFE2L2, NOTCH1, NOTCH2, NPM1, NRAS, PALB2, PBRM1, PDGFRA,

PDGFRB, PIK3CA, PIK3CB, PIK3R1, PLCG2, POLE, POT1, PPP2R1A, PTCH1, PTEN, PTPN11, RAD21, RAD51, RB1, RET, RUNX1, SDHB, SDHC, SDHD, SETBP1, SF3B1, SMAD4, SMARCB1, SMC3, SMO, SRSF2, STK11, TERT, TET2, TP53, TSC1, TSC2, U2AF1, VHL, and WT1.

- Genes reported for fusions/translocations:

  ALK, RET, and ROS1.

Test includes

- Detection of mutations, insertions and deletions for 147 clinically reported genes.
- Detection and reporting of copy number variations (CNVs) for 136 genes.
- Detection and reporting of lung cancer-related gene fusions in ALK, RET, and ROS1.

Collection Instructions

Formalin-fixed, paraffin embedded tissue:

- 0.5x0.5 cm total area (5 micron tissue) with >20% tumor cells (typically >50,000 total cells) is required to yield sufficient total DNA.
- Slides/blocks received from outside laboratories must be received labeled with two patient identifiers and a surgical pathology ID.
- Specimens with less than 20% tumor cells may be tested at the discretion of the attending molecular pathologist.

FFPE tissues: a pathologist will review the respective case upon receiving a requisition to select the appropriate block for testing. Slides will be recut and evaluated, tumor-rich areas are selected for testing.

Test Methodology

The test procedure involves DNA extraction and quantity/quality assessment, fragmentation and library preparation, followed by pooled capture targeting the desired genomic loci. Next generation sequencing (NGS) is performed on the HiSeq 2500 system (Illumina) and downstream analysis for quality control and detection of mutations is performed via custom-design bioinformatics pipelines on a HIPAA-compliant high performance computing system within the Center for Research Informatics (CRI).