TEMPUS | ONCOLOGY

NEW YORK STATE

# xF Gene Panel

A non-invasive, liquid biopsy panel of 105 genes focused on oncogenic and resistance mutations in cell-free DNA (cfDNA). This panel is designed to provide support for clinical decision making for solid tumors.

- SNVs (single nucleotide variants) and insertions and deletions (indels) are detected in all 105 genes
- Copy Number Amplifications (CNAs) and gene rearrangements (translocations) are detected in a subset of genes
- DNA Sequencing Depth: average 20,000x (raw reads) / 5,000x (unique reads)
- Specimen Requirements: Two Streck tubes of peripheral blood (8.5mL each)

The report includes genomic alterations in select genes, microsatellite instability-high status when present,[1] median variant allele fraction (mVAF), therapy options and clinical trials matched to the patient's genomic profile, as well as available clinical history.

## xF GENE PANEL

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| *AKT1* | *BAP1* | *CDH1* | *ESR1* | *GNA11* | *KDR* | *MPL* | *NOTCH1* | *PIK3R1* | *RHOA* | *TP53* |
| *AKT2* | *BRAF* | *CDK4* | *EZH2* | *GNAQ* | *KEAP1* | *MSH2* | *NPM1* | *PMS2* | *RIT1* | *TSC1* |
| *ALK* | *BRCA1* | *CDK6* | *FBXW7* | *GNAS* | *KIT* | *MSH3* | *NRAS* | *PTCH1* | *RNF43* | *TSC2* |
| *APC* | *BRCA2* | *CDKN2A* | *FGFR1* | *HNF1A* | *KMT2A* | *MSH6* | *NTRK1* | *PTEN* | *ROS1* | *UGT1A1* |
| *AR* | *BTK* | *CTNNB1* | *FGFR2* | *HRAS* | *KRAS* | *MTOR* | *PALB2* | *PTPN11* | *SDHA* | *VHL* |
| *ARAF* | *CCND1* | *DDR2* | *FGFR3* | *IDH1* | *MAP2K1* | *MYC* | *PBRM1* | *RAD51C* | *SMAD4* | |
| *ARID1A* | *CCND2* | *DPYD* | *FGFR4* | *IDH2* | *MAP2K2* | *MYCN* | *PDCD1LG2* | *RAF1* | *SMO* | |
| *ATM* | *CCND3* | *EGFR* | *FLT3* | *JAK1* | *MAPK1* | *NF1* | *PDGFRA* | *RB1* | *SPOP* | |
| *ATR* | *CCNE1* | *ERBB2 (HER2)* | *FOXL2* | *JAK2* | *MET* | *NF2* | *PDGFRB* | *RET* | *STK11* | |
| *B2M* | *CD274 (PD-L1)* | *ERRFI1* | *GATA3* | *JAK3* | *MLH1* | *NFE2L2* | *PIK3CA* | *RHEB* | *TERT* | |

## GENE REARRANGEMENTS

| | | | | | | |
|---|---|---|---|---|---|---|
| *ALK* | *BRAF* | *FGFR2* | *FGFR3* | *NTRK1* | *RET* | *ROS1* |

## COPY NUMBER GAINS

| | | | | | |
|---|---|---|---|---|---|
| *CCNE1* | *CD274 (PD-L1)* | *EGFR* | *ERBB2 (HER2)* | *MET* | *MYC* |

## PERFORMANCE SPECIFICATIONS

| | Variant Allele Fraction (VAF) | Sensitivity[2] |
|---|---|---|
| Single Nucleotide Variants (SNVs) | >0.50% | >99.9% |
| | 0.50% | >99.9% |
| | 0.25% | 97.0% |
| Insertions and Deletions | >0.50% | 98.8% |
| | 0.50% | 96.0% |
| Copy Number Amplifications (CNAs)[3] | >0.50% | >99.9% |
| | 0.50% | >99.9% |
| Rearrangements/Fusions[3] | >0.50% | 97.4% |
| | 0.50% | 70.8% |

## ANALYTICAL SPECIFICITY

| Variant Type | Specificity[2] |
|---|---|
| SNV | >99.9% |
| INDEL | >99.9% |
| CNA | 96.2% |
| Fusion | >99.9% |

1 MSI status will be reported when the specimen is determined to be MSI-High

2 Established using reference materials

3 Variant Allele Fraction (VAF) is based on limit of detection dilution studies