

TWIST ONCOLOGY DNA CGP PANEL – 2.4 mb

Comprehensive analysis for tumor research

Comprehensive Genomic Profiling (CGP)

CGP is an assay that utilizes next-generation sequencing (NGS) to assess multiple established biomarkers present within a solid tumor. CGP detects at a genomic resolution that allows for the identification of variant classes such as Single Nucleotide Variants (SNV), indels, Copy Number Variants (CNV), fusions, splice variants, as well as cancer genomic signatures such as Tumor Mutational Burden (TMB) and Microsatellite Instability (MSI).

The breadth of this single assay allows for a robust understanding of a tumor profile, alleviating the need to use multiple tumor-specific panels or different modalities of testing. The panel is also compatible with Twist's enzymatic fragmentation library preparation and target enrichment reagents. Twist's CGP panel can also be supplemented with custom targets to include additional biomarkers.

PANEL CONTENT:

- 562 genes for Single Nucleotide Variants (SNV) and Hotspot coverage
- 57 genes for Copy Number Variant (CNV) Analysis
- 50 genomic loci for microsatellite instability scoring
- Inclusion of selected gene fusions
- Enables tumor mutational burden (TMB) analysis

PANEL TARGET SIZE	2.4 Mb
MEAN TARGET COVERAGE	515x
ON-TARGET RATE	77%
FOLD-80 BASE PENALTY	1.32
DUPLICATION RATE	20%
TARGET BASES COVERED >100X	99.5%

Table 1. Example Sequencing Metrics.
Relevant sequencing QC metrics averaged across data downsampled to 2000x raw coverage (32M 2x150 reads).

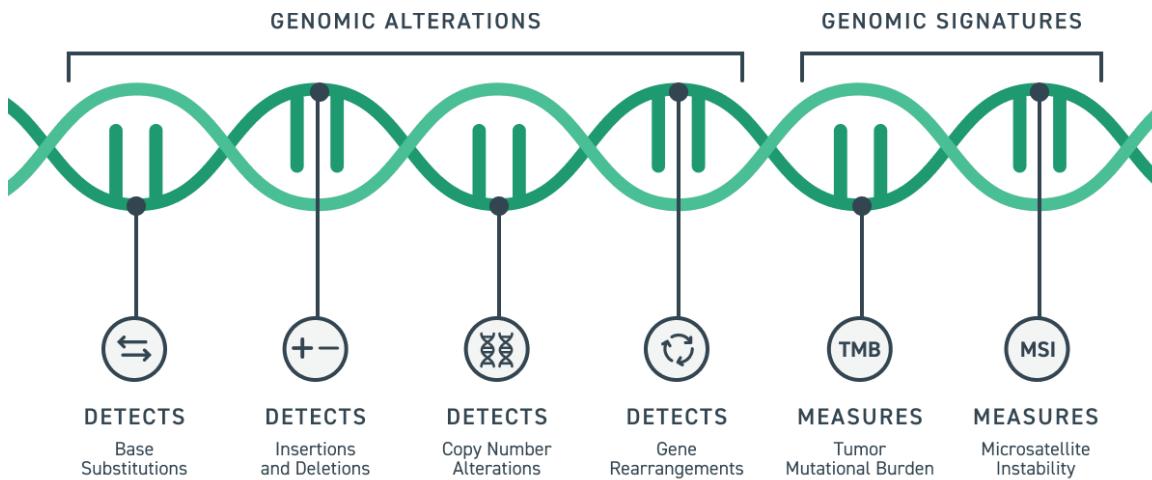


Figure 1. Comprehensive Genomic Profiling enables the detection of genomic alterations such as SNPs, Indels, and CNVs while also capturing genomic signatures which are important to understanding tumor biology such as TMB and MSI.

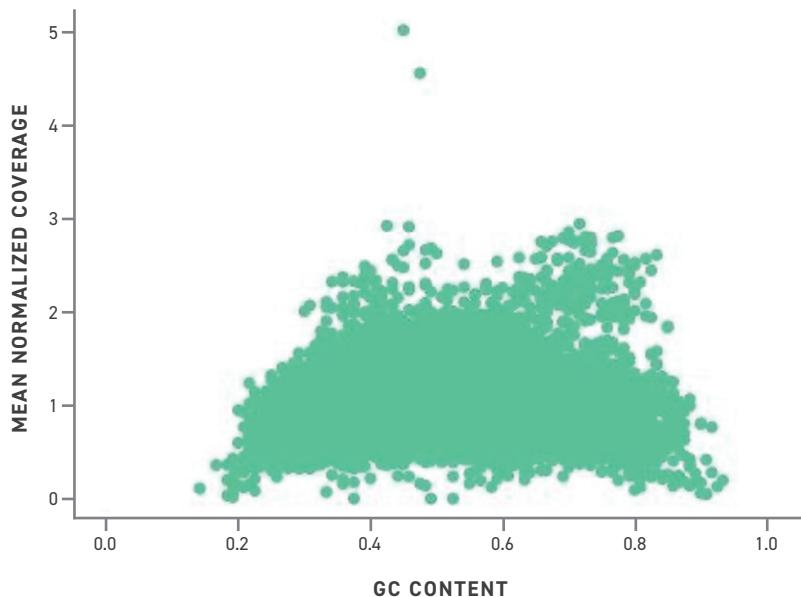


Figure 2. Uniform coverage of CGP targets with Twist Chemistry and Probe design. Panel sequencing with a complete Twist workflow exhibits uniform coverage and read distribution across %CG profiles

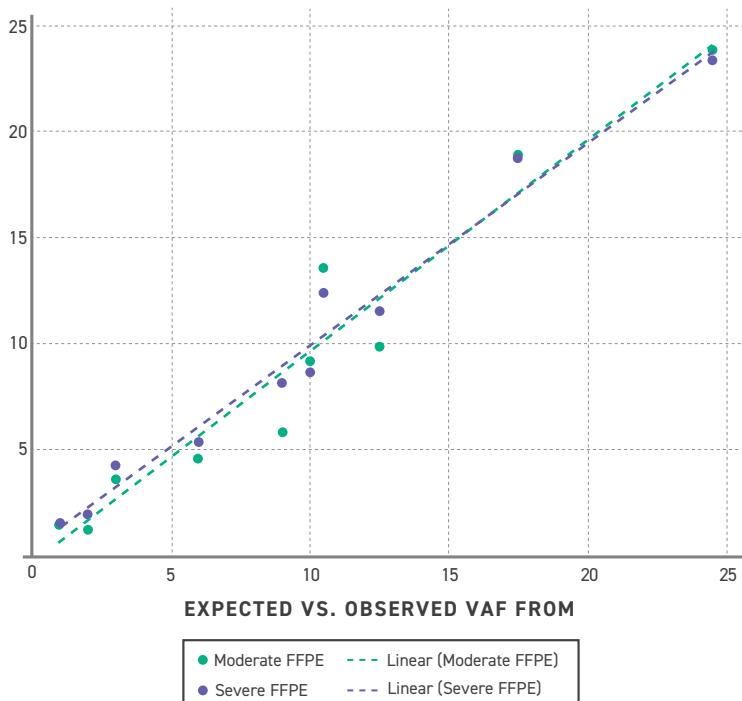


Figure 3. Variant calling concordance with a leading partner analysis solution using commercial FFPE control material. Correlation between observed and expected VAF of variants present in three common commercially available cancer reference controls. Enrichment of control samples containing 11 different SNV and Indels with the Twist Oncology DNA CGP panel. Samples were run in triplicate in material that represented degraded formalin-fixed DNA based on the fragmentation profiles. Data points shown represent the average of 3 replicates with a linear regression and Pearson's correlation of $R^2=0.945$ for "moderately" degraded and $R^2=0.975$ for severely degraded DNA. "Moderately" compromised FFPE is defined by the manufacturer as an average fragment length of between 2,000 to 4,000 bases and DNA integrity Number (DIN) in the range of 2.9 to 3.5. "Severely" compromised FFPE is defined by the manufacturer as an average fragment length >2,000 bases and a DIN in the range of 1.5 to 1.9.

LEARN MORE

twistbioscience.com/ngs
sales@twistbioscience.com

ORDERING INFORMATION

Twist Oncology – DNA CGP Panel – 2.4 Mb

116352: Oncology - DNA CGP Panel, 2.4 Mb, 2 Reactions
 116353: Oncology - DNA CGP Panel, 2.4 Mb, 12 Reactions
 116359: Oncology - DNA CGP Panel, 2.4 Mb, 96 Reactions

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