ACCEL-AMPLICON™ PLUS 57G PAN-CANCER PROFILING PANEL

The 57G Pan-Cancer Profiling Panel offers comprehensive and hotspot coverage of 57 clinically-relevant oncology-related genes. The panel contains pre-validated content which covers over 16,000 COSMIC and 6,000 ClinVar mutations as well as 104 exonic and gender markers for sample identification. In addition, the panel includes full exon coverage of *TP53* and enables validated CNV detection in the *ERBB2* gene.

- Full exon coverage of *TP53*
- CNV detection in *ERBB2*
- Tracking of tumor/normal pairs
- Compatibility with wide range of samples
- Data analysis options including Primerclip and Genialis
- Addition of your own custom content

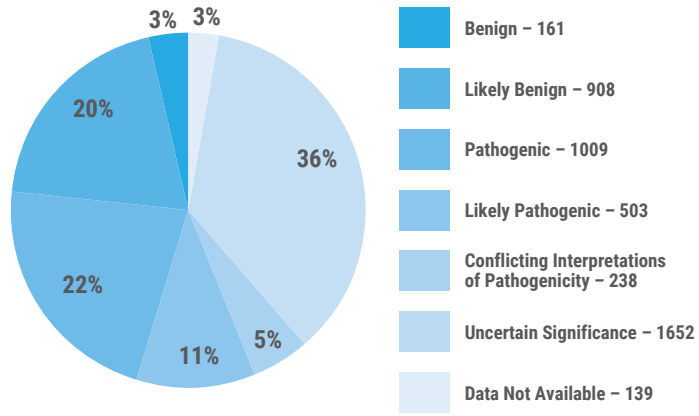

Figure 1. *ACMG and AMP-classified variants of clinical significance covered by the 57G Pan-Cancer Profiling Panel.*

Panel Specifications

Disease Relevance	Pan-Cancer
Amplicons	286
Average Amplicon Size	139 bp
Number of Genes	57
Gene List	*ABL1, AKT1, ALK, APC, ATM, BRAF, CDH1, CDKN2A, CSF1R, CTNNB1, DDR2, DNMT3A, EGFR, ERBB2, ERBB4, EZH2, FBXW7, FGFR1, FGFR2, FGFR3, FLT3, FOXL2, GNA11, GNAQ, GNAS, HNF1A, HRAS, IDH1, IDH2, JAK2, JAK3, KDR, KIT, KRAS, MAP2K1, MET, MLH1, MPL, MSH6, NOTCH1, NPM1, NRAS, PDGFRA, PIK3CA, PTEN, PTPN11, RB1, RET, SMAD4, SMARCB1, SMO, SRC, STK11,* ***TP53****, TSC1, TSC2, VHL* (**Bold** indicates whole CDS coverage)
CNV Detection	*ERBB2*
Total Target	25.9 kb
Input Recommended	10 ng amplifiable DNA
Assay Format	Single-tube Multiplex PCR reaction + Dual Indexed Adapters
Time Required	2 hours from DNA to library
Multiplexing on MiSeq v3 at 5000X depth (50M PE reads)	34 samples
Limit of Detection	1% SNV
Sample Compatibility	Cell line, whole blood, cell-free DNA, FFPE

Performance

Achieve Robust Sequencing Performance Over a Wide Range of Samples

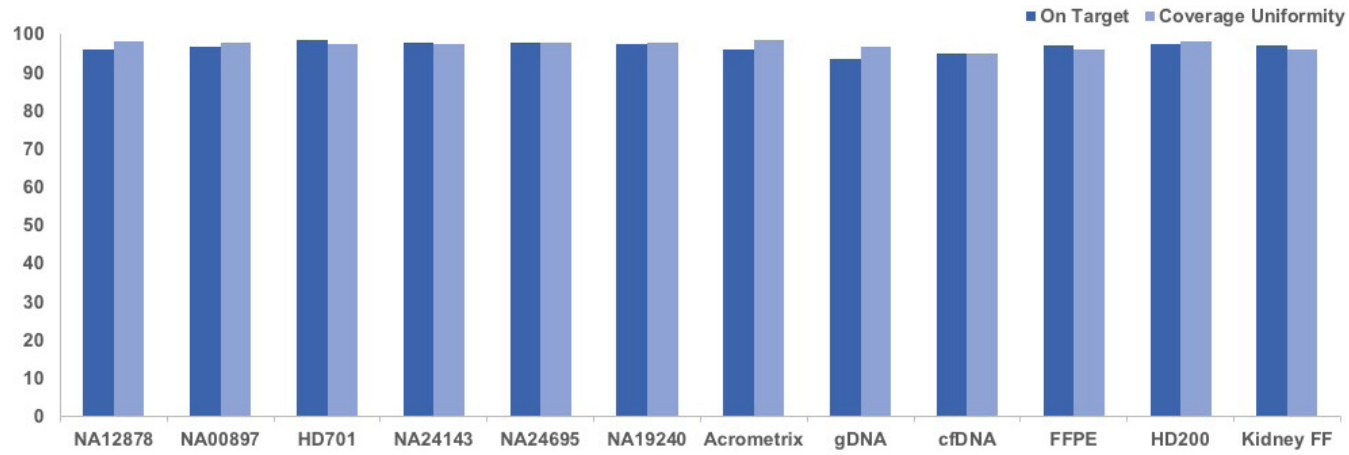

Figure 2. *An array of control DNA samples (10 ng input for each) was used to generate libraries with the Accel-Amplicon Plus 57G Pan-Cancer Profiling Panel. The samples include male and female Coriell repository DNAs of different ethnicities, Horizon HD701 Quantitative Multiplex Reference Standard, the Acrometrix™ Oncology Hotspot Control, gDNA and cfDNA extracted from human blood, circulating cell-free DNA, and three formalin-compromised samples, including Horizon HD200 FFPE. Libraries were sequenced on an Illumina MiniSeq instrument and the on target aligned reads and coverage uniformity percentages were plotted.*

Detect Low Frequency Variants Accurately from Formalin-Compromised DNA

CHR	POS	Gene	Mutation AA	Mutation Type	Expected Frequency (%)	Average Detected Frequency (%)
7	55241707	EGFR	G719S	SNV	24.5	23.3
3	178952085	PIK3CA	H1047R	SNV	17.5	17.5
12	25398281	KRAS	G13D	SNV	15.0	12.8
1	115256530	NRAS	Q61K	SNV	12.5	13.7
7	140453136	BRAF	V600E	SNV	10.5	10.9
4	55599321	KIT	D816V	SNV	10.0	10.4
3	178936091	PIK3CA	E545K	SNV	9.0	7.3
12	25398284	KRAS	G12D	SNV	6.0	5.2
7	55259515	EGFR	L858R	SNV	3.0	3.1
7	55242464	EGFR	ΔE746 - A750	DEL	2.0	1.0
7	55249071	EGFR	T790M	SNV	1.0	1.2

Figure 3. *The Accel-Amplicon Plus 57G Pan-Cancer Profiling Panel consistently detected validated variants at the expected frequency in replicates from 10 ng of the Horizon Diagnostics Quantitative Multiplex DNA Reference Standard HD200. Variants were called by LoFreq (Genome Institute of Singapore).*

Fully customizable. Rapidly create your own panel by building from our pre-designed Accel-Amplicon Plus panels. You can add any target gene including our pre-validated primers or novel targets. We will design, pool and validate your assay for you.

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