ACCEL-AMPLICON™ PLUS MYELOID PANEL

The Myeloid Panel offers comprehensive and exon-level hotspot coverage of 23 clinically-relevant myeloid genes, covering 12,000 COSMIC and 1,900 ClinVar mutations. This panel generates targeted libraries compatible with Illumina® sequencing platforms.

The panel enables:

- Full exon coverage of *TP53*
- Compatibility with wide range of samples
- Data analysis options including Primerclip and Genialis
- Addition of your own custom content

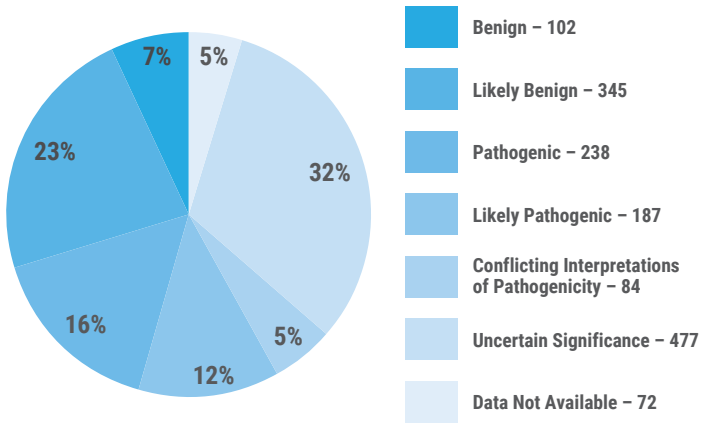

Figure 1. *ACMG and AMP-classified variants of clinical significance covered by the Myeloid Panel.*

Panel Specifications

Disease Relevance	Myeloid
Amplicons	478
Average Amplicon Size	142 bp
Number of Genes	23
Gene List	*ASXL1, CALR, CEBPA, CSF3R, DNMT3A, EZH2, FLT3, HRAS, IDH1, IDH2, JAK2, JAK3, KDM6A, KIT, MPL, NPM1, RUNX1, SETBP1, SF3B1, SRSF2, TET2,* ***TP53****, U2AF1* (**Bold** indicates whole CDS coverage)
Total Target	42 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)	20 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

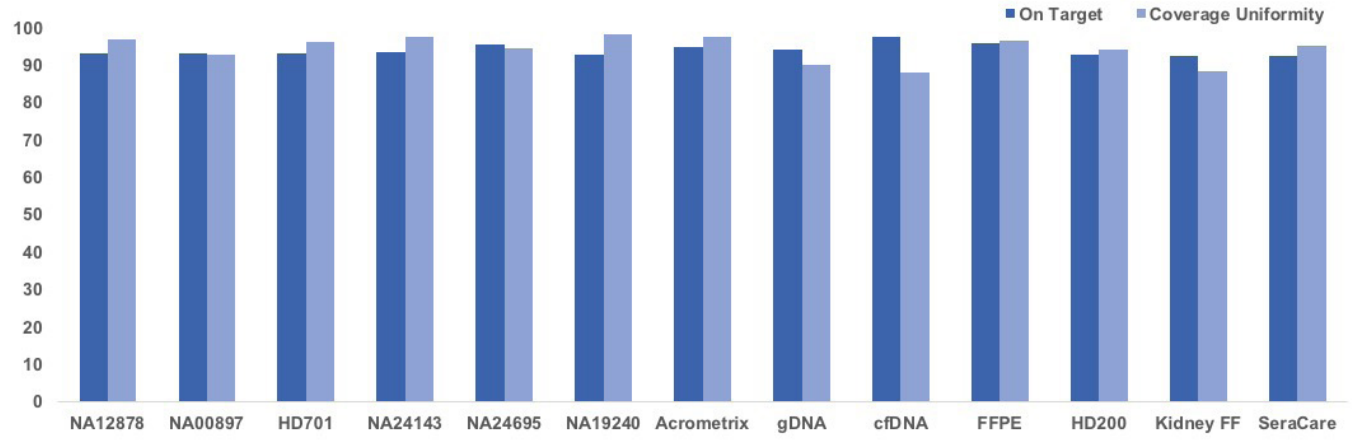

Figure 2. *An array of control DNA samples (10 ng input for each) was used to generate libraries with the Accel-Amplicon Plus Myeloid Panel. The samples include male and female Coriell repository DNAs of different ethnicities, Horizon HD701 quantitative multiplex reference standard, the Acrometrix™ Oncology Hotspot Control, gDNA and cfDNA extracted from human blood, circulating cell-free DNA, and three formalin-compromised samples, including Horizon HD200 FFPE. The SeraCare Myeloid standard DNA contains 23 clinically-relevant DNA mutations for myeloid cancers across 16 genes, with mutation targets quantitated with digital PCR at 5, 10, or 15% allele frequencies. 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

Myeloid malignancies are characterized by a wide variety of variant types, including SNVs, insertions/deletions, and internal tandem duplications at a range of allelic frequencies. The Accel-Amplicon Plus Myeloid Panel was run against a reference standard containing clinically-relevant DNA mutations across 16 genes. Mutation targets consist of different variant types and were quantitated by the manufacturer with digital PCR at 5, 10, or 15% allele frequencies. All variants covered by the core panel design were detected at the expected frequency with the Accel-Amplicon Plus Myeloid Panel. A subset of these variants are described below, and the full reference dataset is available for download from www.swiftbiosci.com.

CHR	POS	Gene	Mutation AA	Mutation Type	Expected Frequency (%)	Average Detected Frequency (%)
19	33792381	CEBPA	p.K313_V314insK	Ins	15	16.7
13	28608249	FLT3	N/A	ITD	10	11.7
20	31022402	ASXL1	p.E635fs*15	Del	10	9.6
2	209113113	IDH1	p.R132C	SNV	5	6.9
19	13054564	CALR	p.L367fs*46	Del	5	2.0
9	5073770	JAK2	p.V617F	SNV	5	6.0

Figure 3. *The Accel-Amplicon Plus Myeloid Panel consistently detected the validated variants at the expected frequency in replicates from 10 ng of the Seraseq™ Myeloid Reference Material. Variants were called by LoFreq (Genome Institute of Singapore) and GATK-HC (obtained by calculating the ratio of Alternate Alleles and total Allele Depth (AD).*

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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