

Myeloid Mutation gDNA Reference Standard



Suitable for the performance verification and routine quality control of myeloid leukemia gene detection process



Myeloid mutation gDNA reference standard is a highly complex product covering various clinical-related mutations, especially the FLT3 internal tandem repeats (FLT3-ITDs) to better simulate real clinical samples. The allelic frequencies (AFs) of mutations are designated from 5% to 60% for validation of distinct variants detection processes and LoD determination.

Product Code	Product Name	Format	Specification	Shelf Life
IB-GW-OYC001	Myeloid Mutation gDNA Reference Standard	gDNA	30ng/ μ L, 0.5 μ g/tube	36 months (2-8°C)

Application



Highly multiplex reference standard, covering 22 mutation sites of 19 genes



Covers high and low AFs variants to supports the performance verification of somatic and germline mutations



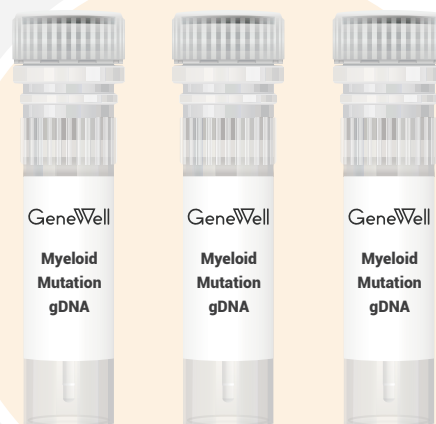
Suitable for the routine quality control of NGS and PCR platforms test processes



Covers drug targets and prognostic assessment sites to provide comprehensive quality control for clinical testing

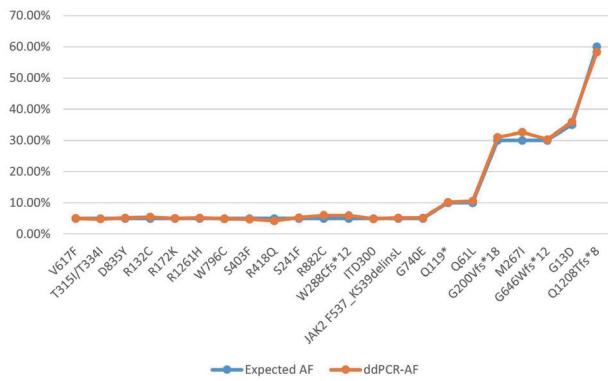


Contains common SNV and Indel mutation types, including FLT3 gene 300bp long insertion repeat sequence



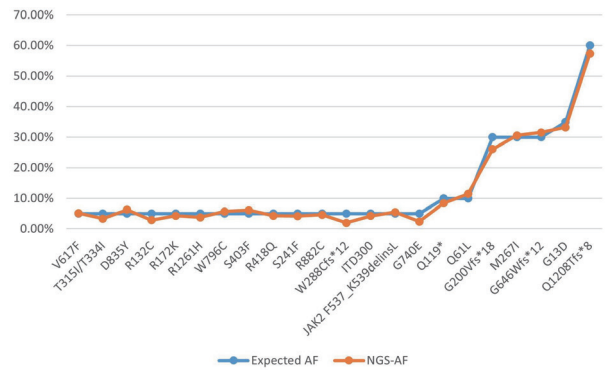
Application Demonstration

The expected AFs are consist with ddPCR verification



In the figure above, blue is the expected allelic frequencies (AFs) and orange is the AFs measured by ddPCR. This result demonstrates a high consistency between the expect and actual AFs.

The expected AFs are consist with WES verification



In the figure above, blue is the expected AFs, and orange is the value of the target variants detected by xGen Exome Research Panel V1. This result claims that the AFs of target variants of NGS whole exon verification was in good agreement with the expected AFs.

Note: NGS bioinformatics analysis methods vary from company to company, and the measured mutation frequency is for reference only

Hot spot mutation information

Gene	AA change	NA mutation	AF
ABL1	T315I/T334I	c.1001C>T	5%
ASXL1	G646Wfs*12	c.1934dup	30%
ASXL1	W796C	c.2388G>T	5%
BCOR	Q1208Tfs*8	c.3621dup	60%
CBL	S403F	c.1208C>T	5%
DNMT3A	R882C	c.2644C>T	5%
EZH2	R418Q	c.1253G>A	5%
FLT3	D835Y	c.2503G>T	5%
FLT3	ITD300	N/A	5%
GATA1	Q119*	c.355C>T	10%
GATA2	G200Vfs*18	c.599del	30%
IDH1	R132C	c.394C>T	5%
IDH2	R172K	c.515G>A	5%
JAK2	F537_K539delinsL	c.1611_1616del	5%
JAK2	V617F	c.1849G>T	5%
KRAS	G13D	c.38G>A	35%
NPM1	W288Cfs*12	c.860_863dup	5%
NRAS	Q61L	c.182A>T	10%
RUNX1	M267I	c.801G>A	30%
SF3B1	G740E	c.2219G>A	5%
TET2	R1261H	c.3782G>A	5%
TP53	S241F	c.722C>T	5%



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