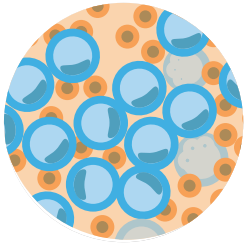
CLL MASTR Plus

The CLL MASTR Plus is a somatic molecular research assay for the identification of both SNVs and CNVs in 9 selected genes associated with Chronic Lymphocytic Leukemia (CLL). This ready-to-use assay offers robust performance with minimum hands-on time and is compatible with all current Next-Generation Sequencing (NGS) systems.



Research application

- For the detection of variants (SNVs and CNVs) in 9 selected genes associated with CLL using Illumina NGS Systems.

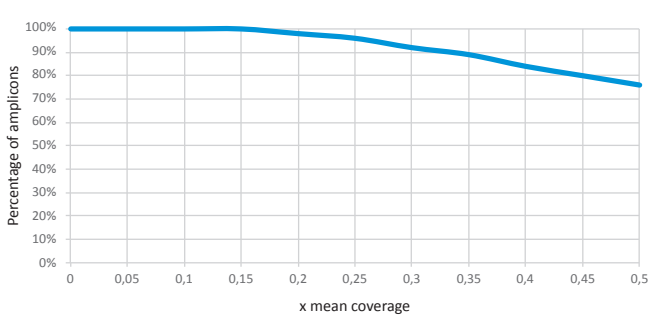
Assay characteristics

Genes	*TP53, BIRC3, NOTCH1, SF3B1, MYD88, FBXW7, ATM, POT1* and *XPO1*
Genomic region analyzed	60.9 kb
Number of amplicons	251
Amplicon length	261-437 bp
Number of plexes	6
Verified with NGS System	Illumina MiSeq System, MiSeq v3

Performance Characteristics

Uniformity of amplification (0.2X mean coverage)	98 %
On target read count	> 98 %
DNA input	as low as 20 ng per plex
Number of samples/run (20x per allele)	Miseq v3: 314* @ 50 % VAF sample MiSeq v3: 31 *@ 5 % VAF sample*

**only 192 MID combinations available.*



Graph representing the high coverage uniformity for all CLL MASTR Plus amplicons. To allow comparison between samples, the read pair counts were normalized. The data are based on 18 samples.

Background

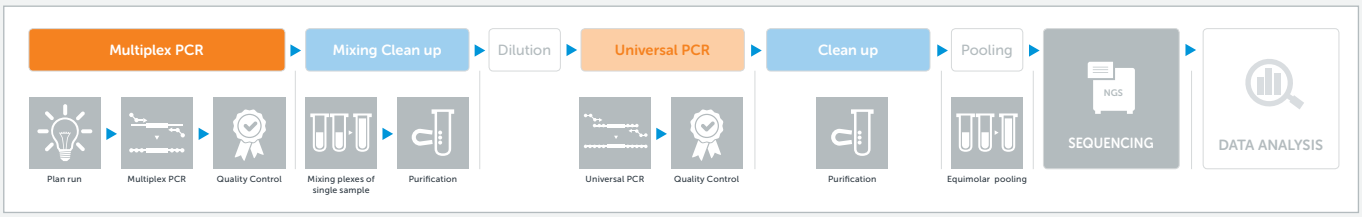
Gene panel CLL MASTR Plus	Gene name	Genomic location
9 genes SNV and CNA	*TP53*	17p13.1
	BIRC3	11q22.2
	ATM	11q22.3
	NOTCH1	9q34.3
	SF3B1	2q33.1
	XPO1	2p15
	MYD88	3p22.2
	FBXW7	4q31.3
	POT1	7q31.33

Data external verification study:

	No. samples	Concordance CLL MASTR Plus with reference method
SNVs	18 blood-derived DNA samples + 1 proficiency sample	31/31 variants
CNAs	Del11q22-q23, -> reported FISH-based frequency: ≥ 91 %	7/7 samples
	Del17p13 -> reported FISH-based frequency: ≥ 60 %	1/1 sample
	Duplication XPO1 (2p15)	3/3 samples

Reference methods: *FISH, Sanger, FASAY, microarray resequencing, NGS on MiSeq, RT-PCR, CGH microarray*

Workflow



Order info

Cat. No.	Product Name	Product type	Samples
MR-0300.024	*CLL MASTR Plus*	*Research*	*24*

MID (Molecular Identifiers) kits are necessary to complete the workflow.

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