

Research application

• For detection of germline variants, SNVs, in exons 18-21 of EGFR in FFPE-derived DNA.

Assay characteristics

Genes	Full coding region of exons 18-21 of EGFR	
Genomic region analyzed	0.6 kb	
Number of amplicons	4	
Amplicon length	100-180 bp	
Number of plexes	1	
Designed to be compatible with	MiSeq, MiniSeq, NextSeq, Ion Torrent NGS Systems	

DNA input	as low as 4 ng per plex reaction
Number of samples/run** (20 reads/allele):	@ 5 % VAF sample Illumina MiSeq V2: 2,057* Illumina MiSeq V3: 3,771*

^{*} only 192 MID combinations available.

^{**} Number of samples per run for Illumina θ IonTorrent NGS Systems can be calculated via the Sequencing Calculator.





Order information

Cat. No.	Product Name	Reactions
MR-0130.024	EGFR 18-21 MASTR	1

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

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