MAYO CLINIC LABORATORIES

Targeted Genes and Methodology Details for TP53 Mutation Analysis

Next-generation sequencing (NGS) is performed to test for the presence of single nucleotide variations, deletions, and insertions in coding regions and intron/exon boundaries of the genes listed. When appropriate, alterations detected are confirmed by an independent reference method, such as Sanger sequencing. Default reportable range offset is +/-2 base pairs around each targeted exon region.

As a result of technical limitations of the assay (including regions of homology, high GC content, and repetitive sequences), there are regions of some genes that cannot be effectively evaluated. Refer to gene regions table below for complete gene coverage information. To verify if a specific region/exon/variant is covered by this assay, contact the laboratory at 800-533-1710.

Genomic Build: GRCh37 (hg19) unless otherwise specified

Gene	Exon	Chromosome	Genomic Start	Genomic Stop	Reference Transcript
TP53	Ex2	chr17	7579837	7579914	NM_000546
TP53	Ex3	chr17	7579698	7579723	NM_000546
TP53	Ex4	chr17	7579310	7579592	NM_000546
TP53	Ex5	chr17	7578369	7578556	NM_000546
TP53	Ex6	chr17	7578175	7578291	NM_000546
TP53	Ex7	chr17	7577497	7577610	NM_000546
TP53	Ex8	chr17	7577017	7577157	NM_000546
TP53	Ex9	chr17	7576851	7576928	NM_000546
TP53	Ex10	chr17	7573925	7574035	NM_000546
TP53	Ex11	chr17	7572925	7573010	NM_000546