MAYO CLINIC LABORATORIES

Targeted Genes and Methodology Details for β-Catenin Mutation Analysis

Next-generation sequencing is performed to test for the presence of single nucleotide variations, deletions, and insertions in the 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 guanine-cytosine [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
CTNNB1	Ex2	chr3	41265558	41265574	NM_001904
CTNNB1	Ex3	chr3	41266015	41266246	NM_001904
CTNNB1	Ex4	chr3	41266443	41266700	NM_001904
CTNNB1	Ex5	chr3	41266823	41267065	NM_001904
CTNNB1	Ex6	chr3	41267149	41267354	NM_001904
CTNNB1	Ex7	chr3	41268697	41268845	NM_001904
CTNNB1	Ex8	chr3	41274830	41274937	NM_001904
CTNNB1	Ex9	chr3	41275018	41275360	NM_001904
CTNNB1	Ex10	chr3	41275628	41275790	NM_001904
CTNNB1	Ex11	chr3	41277213	41277336	NM_001904
CTNNB1	Ex12	chr3	41277838	41277992	NM_001904
CTNNB1	Ex13	chr3	41278077	41278202	NM_001904
CTNNB1	Ex14	chr3	41279505	41279569	NM_001904
CTNNB1	Ex15	chr3	41280623	41280835	NM_001904