MAYO CLINIC LABORATORIES

Targeted Genes and Methodology Details for Hereditary Thyroid Cancer Panel

The following applies to THYRP / Hereditary Thyroid Cancer Panel. Testing is performed to evaluate for the presence of variants in coding regions and extending to +/- 10 base pairs of adjacent intronic sequence on either side of the coding exons of the genes analyzed. In addition, the analysis will cover select noncoding variants. Next-generation sequencing and/or a polymerase chain reaction-based quantitative method is performed to test for the presence of copy number variants (CNV) in the genes analyzed. Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

This list is current from November 2021 to the present. This document is intended to highlight additional evaluations for variants of high clinical interest as well as technical limitations. However, this document does not comprehensively reflect all genomic regions covered by this test. For questions regarding transcripts, genes or regions covered, contact the laboratory at 800-533-1710.

Genomic Build: GRCh37 (hg19) unless otherwise specified

Gene	Reference Transcript	Additional Evaluations	Technical Limitations
APC	NM_000038.6	Promoter 1A: c.-172 to c.-19 (variants between c.-565 to c.-173 may be detected) Promoter 1B: c.-30632 to c.-30046	-
DICER1	NM_177438.2	-	-
PRKAR1A	NM_002734.4	-	-
PTEN	NM_000314.8	Promoter: c.-1302 to c.-589	-
RET	NM_020975.6	-	-
TP53	NM_000546.5	-	-
WRN	NM_000553.6	-	-

Effective Date	Version	Synopsis of Test Change
June 2023	V2	Updated format (additional columns: Additional Evaluations and Technical Limitations)