MAYO CLINIC LABORATORIES

Targeted Genes Interrogated by MayoComplete T-cell Lymphoma Next-Generation Sequencing

Genome Build GRCh37 (hg19)

Gene	GenBank Accession Number*	Coverage Region**
ARID1B	NM_001374820.1	Exons 2–20
CCR4	NM_005508.4	Exon 2
CXCR4	NM_003467.2	Exons 1–2
DNMT3A	NM_022552.4	Exons 2–23
DDX3X	NM_001356.4	Exons 1–17
EZH2	NM_004456.4	Exons 2–20
FYN	NM_002037.5	Exons 4–14
IDH1	NM_005896.3	Exon 4
IDH2	NM_002168.3	Exon 4
JAK1	NM_002227.3	Exons 2–25
JAK3	NM_000215.3	Exons 2–24
KMT2D	NM_003482.3	Exons 1–54
KRAS	NM_033360.3	Exons 2–4
MSC	NM_005098.3	Exons 1–2
NOTCH1	NM_017617.3	Exons 26, 27, 34
NRAS	NM_002524.4	Exons 2–4
PLCG1	NM_002660.2	Exons 1–32
RHOA	NM_001664.3	Exons 2–3
STAT3	NM_139276.2	Exons 2–24
STAT5B	NM_012448.3	Exons 14–19
TET2	NM_001127208.2	Exons 3–11
TP53	NM_000546.4	Exons 4–11

*Reference transcript numbers may have been updated due to database re-versioning. Refer to the patient report for the most updated gene transcript information.

**Default is +/- 5 bps of flanking intron surrounding each exon with some exceptions. *EZH2* exon 3 has -2 bp of flanking intron. *NOTCH1* contains additional coverage in the 3'UTR (chr9:g.139390143-139390152). *KMT2D* exon 10 has partial coverage, excluding regions from chr12:g.49444801-49445200 and chr12:g.49445333-49445686.

©2025 Mayo Foundation for Medical Education and Research