MAYO CLINIC LABORATORIES

Targeted Genes Interrogated by OncoHeme Next-Generation Sequencing

Genome Build GRCh37 (hg19)

Gene	GenBank Accession Number*	Exons
ANKRD26	NM_014915.2	1–4, 5'UTR c.-172
ASXL1	NM_015338.5	10–13
BCOR	NM_001123385.1	4–15
CALR	NM_004343.3	9
CBL	NM_005188.3	8–9, intron 7 100bp before exon 8 and intron 8
CEBPA	NM_004364.4	1
CSF3R	NM_000760.3	14 and 17
DDX41	NM_016222.2	1–17
DNMT3A	NM_022552.4	8–23
ELANE	NM_001972.2	1–5
ETNK1	NM_018638.4	2–5
ETV6	NM_001987.4	3–8
EZH2	NM_004456.4	2–20
FLT3	NM_004119.2	14–20
GATA1	NM_002049.3	2 and 4
GATA2	NM_001145661.1	3–7, intron 5 c.1017+1 to 1017+730
IDH1	NM_005896.3	4
IDH2	NM_002168.3	4
JAK2	NM_004972.3	12–16
KDM6A (UTX)	NM_021140.3	1–29
KIT	NM_000222.2	8–11 and 17
KRAS	NM_033360.3	2–3
MPL	NM_005373.2	10–12
NPM1	NM_002520.6	9–11, intron 10 30bp before exon 11
NRAS	NM_002524.4	2 and 3
PHF6	NM_001015877.1	2–10
PTPN11	NM_002834.3	3–4 and 12–13
RAD21	NM_006265.2	1, 2, 4–7, 9–11, 13, 14
RUNX1	NM_001001890.2	1–6, intron 4 c.725–13T>A and intron 5 c.886+1–4del
SETBP1	NM_015559.2	partial exon 4; amino acids 400–950
SH2B3 (LNK)	NM_005475.2	2–8
SF3B1	NM_012433.2	13–16

SRP72	NM_006947.3	6, 10
SMC3	NM_005445.3	7, 8, 13, 17, 19, 21, 29
SRSF2	NM_003016.4	1 and 2
STAG2	NM_001042750.1	4–34
TERT	NM_198253.2	2–16
TET2	NM_001127208.2	3–11
TP53	NM_000546.4	4–9
U2AF1	NM_001025203.1	2, 6, 8
WT1	NM_024426.2	1–10
ZRSR2	NM_005089.3	1–11

Default offset is +/- 10bps around each exon with exceptions for *CBL, GATA2* and *RUNX1*, which have certain intron regions of interest. For *SETBP1*, only part of exon 4 is evaluated. *NPM1* has coverage set to -30bps before exon 11 because of a downstream polymorphic region. *ANKRD26* has a region of interest in the 5' untranslated region (5'UTR). *RAD21* exon 10 and *STAG2* exons 12, 17, and 22 have coverage set to -15bps before the exons due to homopolymer regions.

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