MAYO CLINIC LABORATORIES

Targeted Genes Interrogated by Myeloid Neoplasms, Comprehensive OncoHeme Next-Generation Sequencing

Genome Build GRCh37 (hg19)

Gene	GenBank Accession Number*	Exons
ANKRD26	NM_014915.2	5'UTR starting at c.-172, 1–4
ASXL1	NM_015338.5	10–13
BCOR	NM_001123385.1	4–15
BCORL1	NM_001184772.2	1–13
BRAF	NM_004333.4	11, 15
CALR	NM_004343.3	9
CBL	NM_005188.3	Intron 7 last 100 bp before start of exon 8, exon 8, all of intron 8 and exon 9
CEBPA	NM_004364.4	1
CSF3R	NM_000760.3	4, 13–14, 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, intron 14, spanning c.1837+1-c.1838-1 (90 bp)
GATA1	NM_002049.3	Starts at c.-19-30 before exon 2, 2 and 4
GATA2	NM_032638.4	1–6, Intron 4 c.1017+1-c.1017+870
IDH1	NM_005896.3	4, 6–8
IDH2	NM_002168.3	3–4, 6–8
JAK2	NM_004972.3	12–20
KDM6A (UTX)	NM_021140.3	1–29
KIT	NM_000222.2	8–11 and 17
KRAS	NM_033360.3	2–4
MPL	NM_005373.2	1–12
NF1	NM_001042492.2	1–58
NPM1	NM_002520.6	9–11, -3 bp before exon 11
NRAS	NM_002524.4	2–4
PHF6	NM_001015877.1	2–10
PPM1D	NM_003620.3	1–6
PTPN11	NM_002834.3	3–4 and 12–13
RAD21	NM_006265.2	1, 2, 4–7, 9–11, 13–14

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Targeted Genes Interrogated by Myeloid Neoplasms, Comprehensive OncoHeme Next-Generation Sequencing (continued)

Gene	GenBank Accession Number*	Exons
RUNX1	NM_001754.4	1–9, -13 bp before exon 8
SETBP1	NM_015559.2	Partial exon 4; amino acids 400–950
SF3B1	NM_012433.2	13–16
SH2B3 (LNK)	NM_005475.2	2–8
SMC3	NM_005445.3	7–8, 13, 17, 21, 29
SRSF2	NM_003016.4	1–2
STAG2	NM_001042750.1	4–34, exons 12 and 17, to -3 on the 5' end due to intronic poly T tracts
STAT3	NM_139276.2	2–24
TERT	NM_198253.2	2–16
TET2	NM_001127208.2	3–11
TP53	NM_000546.4	4–11
U2AF1	NM_001025203.1	2, 6, 8
UBA1	NM_003334.3	2–26
WT1	NM_024426.2	1–10
ZRSR2	NM_005089.3	1–11

Default is +/- 10 bp around each exon with some exception. For CBL, FLT3, GATA2, and RUNX1, there are some intronic regions of interest. SETBP1 only has partial coverage of exon 4. *ANKRD26* and *GATA1* have untranslated regions of interest. *NPM1* exon 11, *RAD21* exon 10, and *STAG2* exons 12 and 17 have coverage set to -3 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.