



Genome Build GRCh37 (hg19)

Gene	GenBank Accession Number*	Exons
<i>ANKRD26</i>	NM_014915.2	5'UTR starting at c.-172, 1-4
<i>ASXL1</i>	NM_015338.5	10-13
<i>BCOR</i>	NM_001123385.1	4-15
<i>BCORL1</i>	NM_001184772.2	1-13
<i>BRAF</i>	NM_004333.4	11, 15
<i>CALR</i>	NM_004343.3	9
<i>CBL</i>	NM_005188.3	Intron 7 last 100 bp before start of exon 8, exon 8, all of intron 8 and exon 9
<i>CEBPA</i>	NM_004364.4	1
<i>CSF3R</i>	NM_000760.3	4, 13-14, 17
<i>DDX41</i>	NM_016222.2	1-17
<i>DNMT3A</i>	NM_022552.4	8-23
<i>ELANE</i>	NM_001972.2	1-5
<i>ETNK1</i>	NM_018638.4	2-5
<i>ETV6</i>	NM_001987.4	3-8
<i>EZH2</i>	NM_004456.4	2-20
<i>FLT3</i>	NM_004119.2	14-20, intron 14, spanning c.1837+1-c.1838-1 (90 bp)
<i>GATA1</i>	NM_002049.3	Starts at c.-19-30 before exon 2, 2 and 4
<i>GATA2</i>	NM_032638.4	1-6, Intron 4 c.1017+1-c.1017+870
<i>IDH1</i>	NM_005896.3	4, 6-8
<i>IDH2</i>	NM_002168.3	3-4, 6-8
<i>JAK2</i>	NM_004972.3	12-20
<i>KDM6A (UTX)</i>	NM_021140.3	1-29
<i>KIT</i>	NM_000222.2	8-11 and 17
<i>KRAS</i>	NM_033360.3	2-4
<i>MPL</i>	NM_005373.2	1-12
<i>NF1</i>	NM_001042492.2	1-58
<i>NPM1</i>	NM_002520.6	9-11, -3 bp before exon 11
<i>NRAS</i>	NM_002524.4	2-4
<i>PHF6</i>	NM_001015877.1	2-10
<i>PPM1D</i>	NM_003620.3	1-6
<i>PTPN1</i>	NM_002834.3	3-4 and 12-13
<i>RAD21</i>	NM_006265.2	1, 2, 4-7, 9-11, 13-14

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

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