



Genome Build GRCh37 (hg19)

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