



Next-generation sequencing (NGS) is performed to test for the presence of single nucleotide variations, deletions, and insertions in coding regions and intron/exon boundaries of the genes listed. When appropriate, alterations detected are confirmed by an independent reference method, such as Sanger sequencing. Default reportable range offset is +/-2 base pairs around each targeted exon region.

Genomic Build: GRCh37 (hg19) unless otherwise specified

As a result of technical limitations of the assay (including regions of homology, high GC content, and repetitive sequences), there are regions of some genes that cannot be effectively evaluated. Refer to gene regions table below for complete gene coverage information. To verify if a specific region/exon/variant is covered by this assay, contact the laboratory at 800-533-1710.

<b>Gene</b>	<b>Exon</b>	<b>Chromosome</b>	<b>Genomic Start</b>	<b>Genomic Stop</b>	<b>Reference Transcript</b>
<i>BRAF</i>	Ex1	chr7	140624364	140624505	NM_004333
<i>BRAF</i>	Ex2	chr7	140549909	140550014	NM_004333
<i>BRAF</i>	Ex3	chr7	140534407	140534674	NM_004333
<i>BRAF</i>	Ex4	chr7	140508690	140508797	NM_004333
<i>BRAF</i>	Ex5	chr7	140507758	140507864	NM_004333
<i>BRAF</i>	Ex6	chr7	140501210	140501362	NM_004333
<i>BRAF</i>	Ex7	chr7	140500160	140500283	NM_004333
<i>BRAF</i>	Ex8	chr7	140494106	140494269	NM_004333
<i>BRAF</i>	Ex9	chr7	140487346	140487386	NM_004333
<i>BRAF</i>	Ex10	chr7	140482819	140482959	NM_004333
<i>BRAF</i>	Ex11	chr7	140481374	140481495	NM_004333
<i>BRAF</i>	Ex12	chr7	140477789	140477877	NM_004333
<i>BRAF</i>	Ex13	chr7	140476710	140476890	NM_004333
<i>BRAF</i>	Ex14	chr7	140453985	140454035	NM_004333
<i>BRAF</i>	Ex15	chr7	140453073	140453195	NM_004333
<i>BRAF</i>	Ex16	chr7	140449085	140449220	NM_004333
<i>BRAF</i>	Ex17	chr7	140439610	140439748	NM_004333
<i>BRAF</i>	Ex18	chr7	140434395	140434572	NM_004333
<i>KIT</i>	Ex1	chr4	55524180	55524250	NM_000222
<i>KIT</i>	Ex2	chr4	55561676	55561949	NM_000222
<i>KIT</i>	Ex3	chr4	55564448	55564733	NM_000222
<i>KIT</i>	Ex4	chr4	55565794	55565934	NM_000222
<i>KIT</i>	Ex5	chr4	55569888	55570060	NM_000222
<i>KIT</i>	Ex6	chr4	55573262	55573455	NM_000222
<i>KIT</i>	Ex7	chr4	55575588	55575707	NM_000222
<i>KIT</i>	Ex8	chr4	55589748	55589866	NM_000222
<i>KIT</i>	Ex9	chr4	55592021	55592218	NM_000222
<i>KIT</i>	Ex10	chr4	55593382	55593492	NM_000222
<i>KIT</i>	Ex11	chr4	55593580	55593710	NM_000222
<i>KIT</i>	Ex12	chr4	55593987	55594095	NM_000222

***Targeted Genes and Methodology Details  
for BRAF/KIT Mutation Analysis*** (continued)

<b>Gene</b>	<b>Exon</b>	<b>Chromosome</b>	<b>Genomic Start</b>	<b>Genomic Stop</b>	<b>Reference Transcript</b>
<i>KIT</i>	Ex13	chr4	55594175	55594289	NM_000222
<i>KIT</i>	Ex14	chr4	55595499	55595653	NM_000222
<i>KIT</i>	Ex15	chr4	55597492	55597587	NM_000222
<i>KIT</i>	Ex16	chr4	55598035	55598166	NM_000222
<i>KIT</i>	Ex17	chr4	55599234	55599360	NM_000222
<i>KIT</i>	Ex18	chr4	55602662	55602777	NM_000222
<i>KIT</i>	Ex19	chr4	55602885	55602988	NM_000222
<i>KIT</i>	Ex20	chr4	55603339	55603448	NM_000222
<i>KIT</i>	Ex21	chr4	55604593	55604725	NM_000222