

Regions Sequenced for Mutation Detection

Gene	Exon	GenBank Accession#	Chromosome	Hg19 Start	Hg19 Stop
AKT1	3	NM_001014431.1	chr14	105,246,446	105,246,556
ALK	21	NM_004304.4	chr2	29,445,380	29,445,476
ALK	22	NM_004304.4	chr2	29,445,209	29,445,277
ALK	23	NM_004304.4	chr2	29,443,573	29,443,702
ALK	24	NM_004304.4	chr2	29,436,847	29,436,950
ALK	25	NM_004304.4	chr2	29,432,655	29,432,735
AR	6	NM_000044.3	chrX	66,941,718	66,941,808
AR	8	NM_000044.3	chrX	66,943,525	66,943,592
BRAF	11	NM_004333.4	chr7	140,481,373	140,481,457
BRAF	15	NM_004333.4	chr7	140,453,103	140,453,196
CDK4	2	NM_000075.3	chr12	58,145,353	58,145,481
CTNNB1	3	NM_001904.3	chr3	41,266,031	41,266,147
DDR2	5	NM_006182.2	chr1	162,724,506	162,724,631
EGFR	3	NM_005228.3	chr7	55,211,045	55,211,126
EGFR	7	NM_005228.3	chr7	55,221,793	55,221,848
EGFR	12	NM_005228.3	chr7	55,227,951	55,228,034
EGFR	15	NM_005228.3	chr7	55,232,970	55,233,053
EGFR	18	NM_005228.3	chr7	55,241,636	55,241,729
EGFR	19	NM_005228.3	chr7	55,242,412	55,242,516
EGFR	20	NM_005228.3	chr7	55,248,983	55,249,100
EGFR	21	NM_005228.3	chr7	55,259,421	55,259,538
ERBB2	8	NM_004448.3	chr17	37,868,178	37,868,259
ERBB2	17	NM_004448.3	chr17	37,879,608	37,879,696
ERBB2	18	NM_004448.3	chr17	37,879,813	37,879,913
ERBB2	19	NM_004448.3	chr17	37,880,213	37,880,266
ERBB2	20	NM_004448.3	chr17	37,880,976	37,881,061
ERBB2	21	NM_004448.3	chr17	37,881,325	37,881,453
ERBB2	22	NM_004448.3	chr17	37,881,577	37,881,644
ERBB3	2	NM_001982.3	chr12	56,477,590	56,477,689
ERBB3	3	NM_001982.3	chr12	56,478,804	56,478,904
ERBB3	6	NM_001982.3	chr12	56,481,576	56,481,698
ERBB3	8	NM_001982.3	chr12	56,482,324	56,482,388
ERBB3	9	NM_001982.3	chr12	56,482,529	56,482,652
ERBB4	18	NM_005235.2	chr2	212,488,708	212,488,772
ESR1	9	NM_001122740.1	chr6	152,419,911	152,420,029
FGFR2	7	NM_000141.4	chr10	123,279,608	123,279,686
FGFR2	8	NM_000141.4	chr10	123,276,873	123,276,980
FGFR2	9	NM_000141.4	chr10	123,274,722	123,274,835
FGFR2	12	NM_000141.4	chr10	123,258,006	123,258,045
FGFR2	14	NM_000141.4	chr10	123,247,506	123,247,600
FGFR3	7	NM_000142.4	chr4	1,803,559	1,803,653
FGFR3	9	NM_000142.4	chr4	1,806,082	1,806,187
FGFR3	14	NM_000142.4	chr4	1,807,834	1,807,903
FGFR3	16	NM_000142.4	chr4	1,808,312	1,808,399
GNA11	4	NM_002067.4	chr19	3,114,967	3,115,073
GNA11	5	NM_002067.4	chr19	3,118,919	3,118,973

GNAQ	4	NM_002072.4	chr9	80,412,454	80,412,545
GNAQ	5	NM_002072.4	chr9	80,409,376	80,409,498
HRAS	2	NM_001130442.1	chr11	534,247	534,351
HRAS	3	NM_001130442.1	chr11	533,813	533,930
IDH1	4	NM_005896.3	chr2	209,113,104	209,113,206
IDH2	4	NM_002168.2	chr15	90,631,825	90,631,954
JAK1	14	NM_002227.2	chr1	65,312,329	65,312,407
JAK1	15	NM_002227.2	chr1	65,311,193	65,311,257
JAK1	16	NM_002227.2	chr1	65,310,460	65,310,574
JAK2	14	NM_004972.3	chr9	5,073,730	5,073,788
JAK3	11	NM_000215.3	chr19	17,949,118	17,949,191
JAK3	12	NM_000215.3	chr19	17,948,740	17,948,872
JAK3	15	NM_000215.3	chr19	17,945,894	17,946,019
KIT	8	NM_000222.2	chr4	55,589,747	55,589,817
KIT	9	NM_000222.2	chr4	55,592,158	55,592,219
KIT	11	NM_000222.2	chr4	55,593,579	55,593,695
KIT	13	NM_000222.2	chr4	55,594,174	55,594,279
KIT	17	NM_000222.2	chr4	55,599,246	55,599,361
KRAS	2	NM_033360.3	chr12	25,398,205	25,398,304
KRAS	3	NM_033360.3	chr12	25,380,261	25,380,349
KRAS	4	NM_033360.3	chr12	25,378,550	25,378,658
MAP2K1	2	NM_002755.3	chr15	66,727,414	66,727,529
MAP2K1	3	NM_002755.3	chr15	66,729,108	66,729,226
MAP2K1	6	NM_002755.3	chr15	66,774,090	66,774,199
MAP2K2	2	NM_030662.3	chr19	4,117,518	4,117,630
MET	14	NM_001127500.1	chr7	116,411,957	116,412,046
MET	16	NM_001127500.1	chr7	116,417,440	116,417,526
MET	19	NM_001127500.1	chr7	116,423,408	116,423,492
MTOR	30	NM_004958.3	chr1	11,217,206	11,217,311
MTOR	39	NM_004958.3	chr1	11,190,767	11,190,837
MTOR	40	NM_004958.3	chr1	11,189,792	11,189,898
MTOR	43	NM_004958.3	chr1	11,188,058	11,188,099
MTOR	43	NM_004958.3	chr1	11,188,157	11,188,186
MTOR	47	NM_004958.3	chr1	11,184,552	11,184,658
MTOR	53	NM_004958.3	chr1	11,174,373	11,174,495
NRAS	2	NM_002524.4	chr1	115,258,690	115,258,774
NRAS	3	NM_002524.4	chr1	115,256,505	115,256,584
NRAS	4	NM_002524.4	chr1	115,252,191	115,252,305
PDGFRA	12	NM_006206.4	chr4	55,141,005	55,141,103
PDGFRA	14	NM_006206.4	chr4	55,144,102	55,144,176
PDGFRA	18	NM_006206.4	chr4	55,152,025	55,152,133
PIK3CA	2	NM_006218.2	chr3	178,916,683	178,916,793
PIK3CA	2	NM_006218.2	chr3	178,916,848	178,916,953
PIK3CA	5	NM_006218.2	chr3	178,921,465	178,921,570
PIK3CA	6	NM_006218.2	chr3	178,922,288	178,922,365
PIK3CA	8	NM_006218.2	chr3	178,927,971	178,928,022
PIK3CA	8	NM_006218.2	chr3	178,928,070	178,928,129
PIK3CA	10	NM_006218.2	chr3	178,936,053	178,936,125
PIK3CA	14	NM_006218.2	chr3	178,938,832	178,938,948

PIK3CA	19	NM_006218.2	chr3	178,947,819	178,947,896
PIK3CA	21	NM_006218.2	chr3	178,951,997	178,952,097
RAF1	7	NM_002880.3	chr3	12,645,648	12,645,734
RAF1	12	NM_002880.3	chr3	12,632,342	12,632,448
RET	10	NM_020975.4	chr10	43,609,067	43,609,126
RET	11	NM_020975.4	chr10	43,609,925	43,610,010
RET	13	NM_020975.4	chr10	43,613,818	43,613,893
RET	15	NM_020975.4	chr10	43,615,547	43,615,654
RET	16	NM_020975.4	chr10	43,617,391	43,617,433
ROS1	36	NM_002944.2	chr6	117,638,333	117,638,438
ROS1	38	NM_002944.2	chr6	117,641,028	117,641,147
SMO	4	NM_005631.4	chr7	128,845,493	128,845,622
SMO	6	NM_005631.4	chr7	128,846,338	128,846,419
SMO	8	NM_005631.4	chr7	128,849,127	128,849,239
SMO	9	NM_005631.4	chr7	128,850,270	128,850,363