

BRAF Variant Allele Frequencies
8/27/2008

Notes: These summary statistics were compiled from clinical tests.

Only variants that are within the coding regions and about 50 base pairs of flanking sequence on each side are reported.

At this time, these summary statistics do NOT include insertion/deletion variants.

Exon	Left Flanking	Sequence Variation	Right Flanking	Coding Change	SNP Reference	Allele Frequencies
6	CGAAAAACGTTTTTC	c.730 A>C	CCTTAGCATTTTGTG	p.Thr244Pro		A-99.5% C-0.5%
6	GAAAGCTGCTTTTCC	c.770 A>G	GGGTTTCCGCTGTCA	p.Gln257Arg		A-97% G-3%
7	CTTCTGCTCTGGGC	c.980+27 G>A	ACATGCTACTTGAAC	Intronic		G-93.3% A-6.7%
11	AACACTTGGTAGACG	c.1332 G>A	GACTCGAGTGATGAT	p.Arg444Arg		G-99.5% A-0.5%
11	TGGGACAAAGAATTG	c.1391 G>T	ATCTGGATCATTTGG	p.Gly464Val		G-99% T-1%
11	CAAAGAATTGGATCT	c.1396 G>A	GATCATTTGGAACAG	p.Gly466Arg		G-99.5% A-0.5%
11	AGAATTGGATCTGGA	c.1399 T>G	CATTTGGAACAGTCT	p.Ser467Ala		T-99.5% G-0.5%
11	TTGGATCTGGATCAT	c.1403 T>C	TGGAACAGTCTACAA	p.Phe468Ser		T-99.5% C-0.5%
11	GATCTGGATCATTTG	c.1406 G>A	AACAGTCTACAAGGG	p.Gly469Glu		G-99% A-1%
12	TGGCAGTGAAAATGT	c.1454 T>C	GAATGTGACAGCACCC	p.Leu485Ser		T-99.5% C-0.5%
12	GGCAGTGAAAATGTT	c.1455 G>C	AATGTGACAGCACCT	p.Leu485Phe		G-99.5% C-0.5%
12	TGAAAATGTTGAATG	c.1460 T>G	GACAGCACCTACACC	p.Val487Gly		T-99.5% G-0.5%
12	CAGTTACAAGCCTTC	c.1495 A>G	AAAATGAAGTAGGAG	p.Lys499Glu		A-99.5% G-0.5%
13	-TTTTGTAAGAATTG	c.1518-48 C>T	TAAAGTTTGTGCGACA	Intronic		C-99% T-1%
13	ACCCAGTGGTGTGAG	c.1600 G>C	GCTCCAGCTTGTATC	p.Gly534Arg		G-99.5% C-0.5%
14	GACCTCAAGAGTAAT	c.1741 A>G	GTATCCTTCCTGAAA	p.Asn581Asp		A-99.5% G-0.5%
15	AAAATAGGTGATTT	c.1785 T>G	GGTCTAGCTACAGTG	p.Phe595Leu		T-99.5% G-0.5%
15	ATTTTGGTCTAGCTA	c.1796 C>G	AGTGAAATCTCGATG	p.Thr599Arg		C-99.5% G-0.5%
16	GTAATATTTACCAC	c.1992+16 G>C	TCTTGGTGTTTATTT	Intronic	rs3789806	G-95.4% C-4.6%
16	CAGCTTTCAGTCAGA	c.1914 T>A	GTATATGCATTTGGA	p.Asp638Glu		T-99.5% A-0.5%
16	TGTATATGCATTTGG	c.1929 A>G	ATTGTTCTGTATGAA	p.Gly643Gly	rs9648696	A-95.4% G-4.6%