

Amino acid position	Forward primer	Reverse primer
170	TGACGGGACGACG N KGT CAACATGGTTG	CAACCATGTTGACMNNCGT CGTCCCGTCA
171	GGACGACGCTT N KAACA TGGTTGATTTC	GAAATCAACCATGTTMNA AGCGTCGTCC
244	ATACCGCCCGCTACGAT N NKTCCGTTCCC	GGGAACGGAMNNATCGTA GCGGGCGGTAT
319	GAACGACGGC N KGTCA ATACCATTTCGA	TCGAAATGGTATTGACMNN GCCGTCGTTC
358	GTCGAC N KTTGGAAATC ATCGGCGTTGACCC	GGGTCAACGCCGATGATTT CCAAMNNGTCGAC
359	AATGTGACCAT N KGAA ATCATCGGCGT	ACGCCGATGATTTMNNAT GGTCGACATT

Amino acid position	Forward primer	Reverse primer
170 and 171	GACGGGACGACGG G TTG GAACATGGTTG	CAACCATGTTCCAACCCGT CGTCCCGTC
359	GTCGACCATT G TGAAATC ATCGGCG	CGCCGATGATTTACAATG GTCGAC
171	GGACGACGCTTCTCAACA T	ATGTTGAGAAGCGTCGTCC
183	GCTTTTTTGACTT C ATGA AAGCG	CGCTTTCATGAAGTCAAAA AAGC

Table S1: Primers used in SSM (Top) and for SDM (Bottom).
Mutations are shown in bold.