SUPPLEMENTARY MATERIALS

Table S-1:   Oligonucleotide sequences used as primers.

G-1: $^{5'}$-GCGCATATGGCCAGCTCTGAGGGGACCCGC-$^{3'}$
G-2: $^{5'}$-GCGACTAGTTCACAAAGTACTCAAAAACTCTTTG-$^{3'}$
G-3: $^{5'}$-GGTCTTTTACCTTCCAAACGTATGCCTGTCTCAGTCG-$^{3'}$
G-4: $^{5'}$-CGACTGAGACAGGCATACGTTTGGAAGGTAAAAGACC-$^{3'}$

P-1: $^{5'}$-CGCGCAATTAACCCTCACTAAAG-$^{3'}$
P-2: $^{5'}$-GAATAAGGGCGACACGGAAATG-$^{3'}$
P-3: $^{5'}$-GCGAAATTAATACGACTCACTATAGGG-$^{3'}$
P-4: $^{5'}$-GCTAGTTATTGCTCAGCGG-$^{3'}$

R104NNS_f $^{5'}$-ATAAGAGCTCAGCTTGCCTCTCTGAATGG-$^{3'}$
R104NNS_r $^{5'}$-AAGCTGCGCTCTTATSNNACTGAGACAGGCATACG-$^{3'}$
D133NNS_f $^{5'}$-GGTATATTTTTGCATCTAATTTGTATGAATCTG-$^{3'}$
D133NNS_r $^{5'}$-TAGATGCAAAAATATACCTSNNACTATACACAGATCG-$^{3'}$

D133A_f: $^{5'}$-GTGTATAGTGCCAGGTATATTTTTGCATCTAA-$^{3'}$
D133A_r: $^{5'}$-ATATACCTGGCACTATACACAGATCGTTCAA-$^{3'}$
R104M_f: $^{5'}$-CTGTCTCAGTATGATAAGAGCTCAGCTTGCCTC-$^{3'}$
R104M_r: $^{5'}$-GAGGCAAGCTGAGCTCTTATCATACTGAGACAGGC-$^{3'}$
A100V_f: $^{5'}$-CAAACGTATGTCTGTCTCAGTATGATAAG-$^{3'}$
A100V_r: $^{5'}$-ACTGAGACAGACATACGTTTGGAAGGTAA-$^{3'}$
H202L_f: $^{5'}$-GCAAGGCATTCCTCTTGAATATTTAGAGAAGCT-$^{3'}$
H202L_r: $^{5'}$-CTAAATATTCAAGAGGAATGCCTTGCTCTTC-$^{3'}$
N133G_f: $^{5'}$-TGTGTATAGTGGCAGGTATATTTTTGC-$^{3'}$
N133G_r: $^{5'}$-AATATACCTGCCACTATACACAGATCG-$^{3'}$

Table S-2: Site-saturation mutagenesis; codon distributions in position 104 & 133.

		dA	dG	dC	T
N (ideal)		0.25	0.25	0.25	0.25
S (ideal)		0	0.5	0.5	0
position 104	N	0.27	0.21	0.33	0.19
	N	0.21	0.26	0.32	0.21
	S	0.08	0.45	0.47	0
position 133	N	0.17	0.17	0.5	0.16
	N	0.19	0.08	0.35	0.38
	S	0	0.7	0.3	0