

Table S2. Statistical results of experiment set 2: 12 gBlocks samples with each mutant present at 5%.

nr.	NT notation	AA notation	pos-9	pos-10	pos-12	pos-13
7.	12C→A	G13C	0.2 (0.1)	0.3 (0.1)	45 (3.2)	0.3 (0.1)
8.	9C→G	G12R	49 (4.2)	0.0 (0.2)	0.0 (0.1)	0.1 (0.3)
9.	10C→T	G12D	0.8 (0.1)	69 (1.6)	0.5 (0.1)	0.2 (0.2)
10.	9C→A	G12C	49 (2.6)	0.9 (0.1)	0.0 (0.1)	0.3 (0.1)
11.	10C→G	G12A	1.5 (0.0)	42 (3.5)	1.7 (0.0)	0.1 (0.1)
12.	12C→T	G13S	0.5 (0.0)	0.5 (0.0)	54 (2.5)	0.2 (0.1)
13.	9C→T	G12S	74 (3.2)	2.0 (0.1)	0.8 (0.0)	1.0 (0.0)
14.	10C→A	G12V	0.4 (0.1)	72 (4.1)	0.2 (0.1)	0.9 (0.1)
15.	13C→G	G13A	0.0 (0.5)	0.8 (0.1)	0.8 (0.0)	63 (4.2)
16.	13C→A	G13V	0.6 (0.1)	0.2 (0.2)	0.2 (0.2)	65 (4.2)
17.	12C→G	G13R	0.2 (0.3)	0.3 (0.1)	65 (4.6)	0.2 (0.1)
18.	13C→T	G13D	0.6 (0.1)	0.5 (0.1)	0.8 (0.1)	36 (2.4)
19.	WT	WT	0.0 (0.2)	0.0 (0.3)	0.0 (0.3)	0.0 (0.2)

The tested gBlock samples are listed with mutations in nucleotide (NT) and amino acid (AA) notation, except for the WT control (experiment 19). Per sample (row) and per nucleotide position (column) the p' (ρ) values are shown for the most significant mutation hypothesis (out of three possible mutations). The highest p' -values that lead to the identification of the experimental nucleotide mutation in each gBlock sample are indicated in bold.