

Table S1: Mutation Rates and Spectra at the *lys2-TAG* allele in the *apn1*Δ strain.

	T	A	G	Mutation Rate $\times 10^{-8}$ (95% confidence interval)	N
	a	A	G	2.92	2
	c	A	G	2.92	2
Mutated sequence	g	A	G	8.75	6
	T	c	G	53.9	37
	T	A	c	1.46	1
Total				70 (58.5 – 93.8)	48

Mutated bases are indicated in lower case letters. Uracil-associated and cytosine-associated mutations are highlighted in yellow and blue, respectively.