

Table S4: Estimation of P_{TDH3} -YFP fluorescence mutation rate from validated mutants

All validated mutants

Phenotype	cell fraction ¹	relative viability ²	c.f.u. fraction ³	mutants ⁴	screened ⁵	frequency ⁶	mutant frequency ⁷
High YFP	0.010	0.784	0.008	162	503	0.322	0.0026
Typical YFP	0.977	1.000	0.977				
Low YFP	0.012	0.843	0.010	69	561	0.119	0.0012
Total	1.000		0.996	231	1064		0.0039
						⁸ Inflation factor due to EMS	5797
						⁹ Spontaneous mutation rate (x10 ⁻⁷)	6.6476

Validated mutants, excluding known CNVs

Phenotype	cell fraction ¹	relative viability ²	c.f.u. fraction ³	mutants ⁴	screened ⁵	frequency ⁶	mutant frequency ⁷
High YFP	0.010	0.784	0.008	141	503	0.280	0.0023
Typical YFP	0.977	1.000	0.977				
Low YFP	0.012	0.843	0.010	68	561	0.119	0.0012
Total	1.000		0.996	209	1064		0.0035
						⁸ Inflation factor due to EMS	5797
						⁹ Spontaneous mutation rate (x10 ⁻⁷)	6.0605

¹ proportion of all FACS events ("cells") with this phenotype

² proportion of c.f.u. with this phenotype relative to the proportion of c.f.u. in the wild-type YFP expression class

³ proportion of all c.f.u. with this phenotype

⁴ number of c.f.u. with significant changes in YFP fluorescence

⁵ number of c.f.u. subjected to secondary screening

⁶ proportion of c.f.u. screened that are fluorescence mutants

⁷ frequency of fluorescence mutants among all c.f.u. in the population used for sorting

⁸ measured by comparing the observed frequency of canavanine resistance mutants to a published estimate of the spontaneous canavanine resistance mutation rate.

⁹ spontaneous mutation rate of fluorescence changes suggested by observed EMS-induced mutant frequency; measured per haploid genome, per generation.