Table 2. Characteristics of PSE-4 mutant libraries

	Library A	Library B	Library C	Library D
Nucleotides sequenced [*]	7,879	6,824	6,344	7,656
Synonymous substitutions	18	38	52	84
Nonsynonymous substitutions	41	57	114	191
Nucleotide deletions	3	4	6	5
Nonsynonymous substitutions producing stop codons	2	4	4	8
Library average nucleotide substitutions/gene ($\langle m_{\text{nt}} \rangle$) [†]	7.20 ± 1.23	13.27 ± 1.76	24.81 ± 2.62	33.46 ± 2.78
Fraction of clones surviving selection ($P_{\text{f}}(\langle m_{\text{nt}} \rangle)$)	0.13 ±0.015	0.0142 ±0.0032	0.00158 ±0.0004	0.00007 ±0.00007
Eq. **1** with $\nu = 0.54$ and auxiliary assumption	0.112	0.0170	0.00063	0.000049
Eq. **1** with $\nu = 0.54$, no auxiliary assumption	0.118	0.0196	0.00064	0.000049

[*] Nine to 10 clones were partially sequenced from each library.

[†] Library average nucleotide mutations per gene $\langle m_{\text{nt}} \rangle$ equals the sum of synonymous mutations, nonsynonymous mutations, and deletions divided by the number of gene equivalents sequenced (base pairs sequenced / 915). Errors are the expected standard errors calculated following the methods of ref. 1.

1. Drummond, D. A., Iverson, B. L., Georgiou, G., and Arnold, F. H. (2005) arXiv: q-bio.QM/0411041.