

TABLE S1.

Single-nucleotide mutants of bacteriophage F1 obtained by site-directed mutagenesis

Nucleotide substitution	Gene	Amino acid substitution	Relative fitness effect, s ± SEM
T117A	II	None	0.006 ± 0.009
T178A	II	L194I	-1
G181A	II	V195I	-0.064 ± 0.017
A209C	II	Q204P	-1
C231A	II	S211R	-0.009 ± 0.038
T275A	II	L226STOP	-1
A333T	II	E245D	-1
T336A	II	None	-0.002 ± 0.039
C337A	II	None	0.024 ± 0.027
C370A	II	L258I	0.029 ± 0.051
A431G	II	D278G	-1
T470A	II	L290Q	-1
A499T	II	N301Y	-0.406 ± 0.021
G601A	II	G335S	-0.162 ± 0.021
T657A	II	None	0.008 ± 0.021
G671A	II	W358STOP	-1
A878G	V	None	-0.039 ± 0.021
C1088A	V	None	0.033 ± 0.021
C1161A	VII	None	-0.102 ± 0.016
G1205A	VII	R33K	-0.216 ± 0.008
A1433T	VIII	I45F	-1
T1441A	VIII	Y47STOP	-1
C1449A	VIII	A50E	-0.01 ± 0.035
T1544A	Intergenic	None	-0.514 ± 0.029
T1605A	III	None	-0.005 ± 0.009
T1655A	III	L26STOP	-1
G1739A	III	C54Y	-1
T2004A	III	None	-0.044 ± 0.026
A2045T	III	N156I	-0.25 ± 0.046
C2136A	III	Y186STOP	-1
A2408T	III	D277V	-0.046 ± 0.034
C2423A	III	A282E	-0.059 ± 0.057
T2592A	III	None	0.018 ± 0.016
T2727A	III	Y383STOP	-1
G2791A	III	V405I	0.002 ± 0.022
C2795A	III	A406D	-0.084 ± 0.053
C2799A	III	None	-0.026 ± 0.017

T2937A	VI	F28I	-0.052 ± 0.007
T3016A	VI	L54H	-0.521 ± 0.136
G3077A	VI	None	-0.114 ± 0.02
C3120A	VI	L89I	-0.129 ± 0.017
T3142A	VI	F96Y	-0.603 ± 0.029
G3264A	I	None	-0.007 ± 0.041
C3324A	I	None	-0.008 ± 0.041
C3389A	I	S66Y	-0.085 ± 0.035
T3395A	I	L67STOP	-1
T3564A	I	F123L	-0.663 ± 0.041
T3566A	I	L124H	-1
G3643A	I	D150N	-1
A3649G	I	I152V	-0.130 ± 0.004
G3664A	I	V157I	0.022 ± 0.025
C3748A	I	Q185K	0.074 ± 0.016
T3771A	I	None	-0.012 ± 0.05
G3795A	I	None	0.055 ± 0.024
T3855A	I	None	0.003 ± 0.024
T3927A	I	None	0.039 ± 0.022
T3966A	I	None	-0.007 ± 0.028
T4025A	I	V277D	-0.113 ± 0.011
A4218G	I	None	0.019 ± 0.035
C4266A	IV	S16STOP	-1
T4304A	IV	S29T	0.031 ± 0.017
A4417G	IV	None	0.034 ± 0.035
A4537C	IV	None	-0.032 ± 0.027
T4541A	IV	S108T	0.067 ± 0.016
A4547C	IV	N110H	0.044 ± 0.018
G4552A	IV	None	0.023 ± 0.018
T4603A	IV	N128K	-0.070 ± 0.02
T4615A	IV	None	0.001 ± 0.02
C4620A	IV	T134N	-0.788 ± 0.032
A4634G	IV	N139D	-0.694 ± 0.014
T4747A	IV	None	0.045 ± 0.017
C4938A	IV	S240Y	-0.280 ± 0.048
G5120A	IV	E301K	-0.096 ± 0.079
G5158A	IV	None	-0.001 ± 0.025
G5168A	IV	V317I	-0.006 ± 0.03
G5253A	IV	S345N	-0.037 ± 0.052
A5265C	IV	Q349P	-0.210 ± 0.071
G5271A	IV	S351N	-0.119 ± 0.027
A5286T	IV	N356I	-0.371 ± 0.058

A5322G	IV	D368G	-0.526 ± 0.053
G5389A	IV	None	0.015 ± 0.02
T5472A	IV	V418D	-1
C5575A	Intergenic	None	-0.03 ± 0.035
C5649A	Intergenic	None	-0.458 ± 0.091
C5727A	Intergenic	None	-0.019 ± 0.013
A5740C	Intergenic	None	-0.146 ± 0.053
C5753A	Intergenic	None	-0.008 ± 0.032
C5771A	Intergenic	None	-0.053 ± 0.024
G5876A	Intergenic	None	-0.105 ± 0.075
A5903G	Intergenic	None	0.030 ± 0.028
C5966A	Intergenic	None	-0.082 ± 0.042
G6028A	II	R8Q	-0.251 ± 0.026
G6090A	II	V29I	-0.006 ± 0.044
T6091A	II	V29E	-1
T6266A	II	None	-0.051 ± 0.018
A6276G	II	I91V	-0.152 ± 0.042
C6286A	II	S94Y	-1
T6308A	II	None	0.044 ± 0.031
C6344A	II	C112STOP	-1
T6362A	II	None	-0.012 ± 0.012