Additional file 1.

Table 3: Changes observed in the T3 Δ 1.3A_E adaptation and recombination test of compensatory evolution.

change	Element	Function	T3A _E	R	1 st detected (hrs)
G->A G204S	0.7	protein kinase	+(2/2)	(0/5)	
deleted and insertion ¹	φ1.05p, 1.05, φ1.1	promoter, ?, promoter	+(1/2)	-	0
engineered deletion	1.3	ligase	+(2/2)	-	
deleted	1.5	?	+(2/2)	-	10
C->T R2C	1.6	?	+(2/2)	-	
G->A G3S	2.5	ssDNA binding	+(1/2)	-	20
T->G F63C	3	endonuclease	+(1/1)	-	0
A->G N143S	3.5	lysozyme	+(1p/2)	*	
G->A D22N	4A	primase	+(2/2)	-	20
T->C L514S	<i>4</i> A	primase	+(1/1)	-**	
T->C L452S	<i>4</i> B	helicase	+(1/1)	-**	
T->C W41R	4.2	?	+(1/1)	-**	
G->A A382T	5	DNA polymerase	(2/2)	+	
G->A	RNAse III 6.5		+(2/2)	-	40
A->C K4Q	6.7	adsorption	(1/1)	(1/2)	
C->T A36V	11	tail A	+(2/2)	-**	0
A->G Q545R	12	tail B	+(2/2)	-	20
G->A A2T	17	tail fiber	+(1/1)	-	0
T->C Y70H	17	"	+(1/1)	-	0
G->A L4L	19.5	?	+(1/1)	+/-	
deleted	1.05, <i>φ</i> 1.1	?, promoter	-(1/2)	-	0
C->T	RNAse III 1.3		+/-(1/2)	-	
G->A V260M	4A	primase	+/-(1p/1)	-	
G->A V198M	4B	helicase	+/-(1p/1)	-	
T->C W52R	5.3	?	+/-(1/2)	-**	
A->G H88R	5.3	?	+/-(1p/2)	-**	
	G->A G204S deleted and insertion ¹ engineered deletion deleted C->T R2C G->A G3S T->G F63C A->G N143S G->A D22N T->C L514S T->C L514S T->C L452S T->C W41R G->A A382T G->A A->C K4Q C->T A36V A->C K4Q C->T A36V A->G Q545R G->A A2T T->C Y70H G->A L4L deleted C->T G->A V260M G->A V198M T->C W52R	G->A G204S0.7deleted and insertion1 ϕ 1.05p, 1.05, ϕ 1.1engineered deletion1.3deleted1.5C->T R2C1.6G->A G3S2.5T->G F63C3A->G N143S3.5G->A D22N4AT->C L514S4AT->C L452S4BT->C W41R4.2G->A A382T5G->ARNAse III 6.5A->C K4Q6.7C->T A36V11A->G Q545R12G->A A2T17T->C Y70H17G->A L4L19.5deleted1.05, ϕ 1.1C->TRNAse III 1.3G->A V198M4BT->C W52R5.3	G->A G204S0.7protein kinasedeleted and insertion1 $\phi 1.05p, 1.05$, $\phi 1.1$ promoter, ?, promoterengineered deletion1.3ligasedeleted1.5?C->T R2C1.6?G->A G3S2.5ssDNA bindingT->G F63C3endonucleaseA->G N143S3.5lysozymeG->A D22N4AprimaseT->C L514S4AprimaseT->C L452S4BhelicaseT->C W41R4.2?G->A A382T5DNA polymeraseG->ARNAse III 6.5A->C K4Q6.7adsorptionC->T A36V11tail AA->G Q545R12tail BG->A L4L19.5?deleted1.05, $\phi 1.1$?, promoterC->TRNAse III 1.3G->A V260MG->A V198M4BhelicaseT->C W52R5.3?	G->A G204S0.7protein kinase $+(2/2)$ deleted and insertion1 ϕ 1.05p, 1.05, ϕ 1.1promoter, ?, promoter $+(1/2)$ engineered deletion1.3ligase $+(2/2)$ deleted1.5? $+(2/2)$ C->T R2C1.6? $+(2/2)$ G->A G3S2.5ssDNA binding $+(1/2)$ T->G F63C3endonuclease $+(1/1)$ A->G N143S3.5lysozyme $+(1/2)$ G->A D22N4Aprimase $+(2/2)$ G->A D22N4Aprimase $+(1/1)$ T->C L514S4Aprimase $+(1/1)$ T->C L452S4Bhelicase $+(1/1)$ G->A A382T5DNA polymerase $(2/2)$ G->ARNAse III 6.5 $+(2/2)$ A->C K4Q6.7adsorption $(1/1)$ C->T A36V11tail A $+(2/2)$ A->C Y70H17" $+(1/1)$ T->C Y70H17" $+(1/1)$ G->A L4L19.5? $+(1/1)$ G->A V260M4Aprimase $+/-(1/2)$ C->TRNAse III 1.3 $+/-(1/2)$ G->A V198M4Bhelicase $+/-(1p/1)$ T->C W52R5.3? $+/-(1/2)$	G->A G204S0.7protein kinase $+(2/2)$ $(0/5)$ deleted and insertion1 $\phi 1.05p, 1.05, \\ \phi 1.1$ promoter $+(1/2)$ $-$ engineered deleted1.3ligase $+(2/2)$ $-$ C->T R2C1.6? $+(2/2)$ $-$ G->A G3S2.5ssDNA binding $+(1/2)$ $-$ T->G F63C3endonuclease $+(1/1)$ $-$ A->G N143S3.5lysozyme $+(1p/2)$ $*$ G->A D22N4Aprimase $+(2/2)$ $-$ T->C L514S4Aprimase $+(1/1)$ $-**$ T->C W41R4.2? $+(1/1)$ $-**$ G->A A382T5DNA polymerase $(2/2)$ $+$ G->A A382T5DNA polymerase $(2/2)$ $-$ A->C K4Q6.7adsorption $(1/1)$ $(1/2)$ C->T A36V11tail A $+(2/2)$ $-$ A->G Q545R12tail B $+(2/2)$ $-$ G->A A2T17tail fiber $+(1/1)$ $-$ T->C Y70H17" $+(1/1)$ $-$ G->A V260M4Aprimase $+/-(1/2)$ $-$ G->A V198M4Bhelicase $+/-(1/2)$ $-$ T->C W52R5.3? $+/-(1/2)$ $-$

In the "T3A_E" and "R" columns, a ratio in parentheses indicates the number of isolates in which the mutation was observed over the number of isolates sequenced, whereas a + or - sign indicates the presence or absence of the change in a consensus sequence of the population; +/- indicates multiple peaks in the sequence file. Mutations that were polymorphic in or absent from the consensus of T3 Δ 1.3A_E are listed under the bold line. Column 'R' is for the recombinant test of compensatory evolution; a "-" entry indicates that the change did not ascend in the test and thus was strictly compensatory except for the engineered ligase deletion. Insertion¹ is a duplication of T3 nucleotides 6515-6551 inserted just after base 5659; this

insertion contains part of the promoter and RNaseIII site upstream of 1.3 and should restore functionality of the ϕ 1.05 promoter.

 ϕ – promoter; ? – function unknown; * = the mutation listed was absent in the recombinant, but a new mutation in the same codon had replaced it, so its status is ambiguous and is not considered strictly compensatory; -** = sequence was obtained from a mix of 10 isolates from the population; p = multiple sequence peaks;