

## Additional file 2

Table 4: Changes observed in the T3Δ1.3B<sub>E</sub> adaptation and recombination test of compensatory evolution.

Bases affected (GenBank AJ318471)	Change	Element	Function	T3B <sub>E</sub>	R
5781	T->C F22S	1.05	?	+	-
6595-7635	engineered deletion	1.3	ligase	+	-
7719	G->A W2X	1.5	?	+	-
8807	A->G T46A	2	inhibit host RNAP	+	-
9745	C->A P54T	3	endonuclease	+	-
10307	A->G K91E	3.5	lysozyme	+	-
11211	C->T A181V	4A	primase	+	-
“	C->T A119V	4B	helicase	+	-
13037	G->A	IG (5)	Ribosomal binding site	+	-
15145	A->G K701K	5	DNA polymerase	+	-
15265	G->A S33N	5.3	?	+	-
16737	A->C T201P	6	exonuclease	+	-
17495	A->C K4N	6.7	adsorption	+	*
21390	T->A V167D	10A	major capsid	+	-
“	T->A V167D	10B	minor capsid	+	-
32319	C->A R1173S	16	internal core	+ <sup>2</sup>	-
33186	G->A D119N	17	tail fiber	+	-
36424	C->T Y278Y	19	DNA packaging	+	-
“	C->T T63M	19.2	?	+	-

T3Δ1.3B<sub>E</sub> changes were determined in the sequence of an isolate. The recombination test was started with a mix of this isolate and with the initial, pre-adapted T3<sup>+</sup><sub>E</sub> population; all sequences from the recombination test are based on consensus of the adapted, recombinant population. +<sup>2</sup> = change was present in initial deletion isolate, T3Δ1.3B<sub>0</sub>; IG – intergenic change; ? = 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. Otherwise as in Additional file 1.