Table S1. Errors in synthesis & construction of section *alpha*

Location on T7.1 (Genome Position)	**Nature of Difference**	**Probable Reason for Difference**	**Expected Outcome**
D1L (164-170), D1R & D2L (338-350)	Restriction sites were not added in construction	Difficulties in manipulating left end of genome resulted in using wild-type	Loss of manipulability in part 1 (containing A0)
gene *0.4* (1418)	Single base deletion	Unknown	Frameshift after 27th amino acid followed by early termination of gene *0.4*
D6L (1304-1310) D6R (1494-1500)	Restriction sites appear twice.	Inefficiency of digestion of scaffold	No expected change
gene *0.6B*	Single base addition	Error is known to be in stock of wild-type genome	Dependent upon nature of putative translational slippage in formation of gene *0.6B*
D11L (3302-3307)	Restriction site appears twice	Inefficiency of digestion of scaffold	No expected change
gene *1* (4877)	Single base mutation	Error in PCR or within wild-type genome	Silent mutation, no expected change
gene *1* (5159)	Single base mutation	Error in PCR or within wild-type genome	Silent mutation, no expected change
gene *1* (5399)	Single base mutation	Error in PCR or within wild-type genome	Silent mutation, no expected change
D14R (6591-6597)	Restriction site appears twice	Inefficiency of digestion of scaffold	No expected change
TE (7827)	Single base deletion	Primer synthesis error	Possible loss of function of transcriptional terminator.
D20L (8082-8086)	Restriction site appears twice	Inefficiency of digestion of scaffold	No expected change
U4 (8153-8159)	Restriction site was not added in construction	Failure in site-directed mutagenesis	Loss of manipulability of overlap in parts 18 and 19
D22L (8247-8253)	Restriction site appears twice	Inefficiency of digestion of scaffold	No expected change

Table S2. Errors in synthesis & construction of section *beta*

Location on T7.1	Nature of Difference	Probable Reason for Difference	Expected Outcome
gene *1.7* (8794)	Single base silent mutation	Error during PCR or within wild-type genome	No expected change
gene *1.8* (9245)	Single base mutation	Error during PCR or within wild-type genome	Amino acid change in gene *1.8* from Asp to Gly
gene *2.0* (9447)	Single base mutation	Error during PCR or within wild-type genome	Amino acid change in gene *2.0* from Glu to Val
gene *2.5* (10351)	Singe base deletion	Error during primer design	deletion in stop codon; read-through adding on 8AA
gene *2.8* (10627)	Single base mutation	Error during PCR	Amino acid change in gene *2.8* from Asp to Gly
gene *2.8* (10717-10803)	82 base deletion	Error in cloning of part	Loss of function in gene *2.8* in addition to unknown effect on translation of *3.0* due to read-through
gene *3.0* (10926)	Single base silent mutation	Error during PCR or within wild-type genome	No expected change