

Table S3. Assumptions and References for construction of phage stoichiometry reactions.

Viral mRNA production reactions	
Nucleotide stoichiometry for all 60 T7 bacteriophage mRNAs from genome sequence and to date publications.	GenBank (NC 001604)
Each added NTP was assumed to produce one pyrophosphate during polymerization.	[1]
Viral Gene Product production reactions	
Amino acid stoichiometry for all 60 T7 bacteriophage proteins.	GenBank
tRNA charging was assumed to hydrolyze 1 ATP to AMP and pyrophosphate	[1]
Aminoacyl-tRNA binding was assumed hydrolyze 1 GTP to GDP	[1]
tRNA translocation during translation was assumed to hydrolyze 1 GTP to GDP	[1]
Polymerization initiation was assumed to hydrolyze 1 GTP to GDP	[1]
Host genome degradation and recycling reaction	
Nucleotide stoichiometry for T7 bacteriophage and E. coli genomes	GenBank (U00096)
During host genome degradation dNMPs were assumed to be produced in proportion to their content in the E. coli genome.	-
During viral genome production dNTPs were assumed to be used in proportion to their content in the T7 genome and converted into 1 viral dNTP.	-
T7 Genome synthesis reaction	
Nucleotide stoichiometry for T7 bacteriophage genome	GenBank
Each added dNTP was assumed to produce one pyrophosphate during polymerization	[1]
DNA helicase was assumed to hydrolyze 2 ATP to ADP per base pair of DNA unwound	[2]
Lagging strand synthesis: RNAmers primers 4 nucleotides long were assumed to hydrolyze 2 high energy phosphate bonds per polymerized NTP (8 high energy phosphate bonds total)	[1, 3]
Lagging strand synthesis: Okazaki fragments were assumed to be 3,500 bases long on average	[3]
Lagging strand synthesis: 2 high energy phosphate bonds were hydrolyzed to regenerate the NAD used in ligation	[1]
Proofreading: Error rate in T7 DNA polymerase was assumed to be 10 percent for dATP, 5 percent for dTTP, 1 percent for dGTP and dCTP. These were counted as additional A,T,G,C incorporated into the genome and then hydrolyzed to dNMPs	[1, 4]
In all cases high energy phosphate bonds were accounted for as ATP being hydrolyzed to ADP.	-

Changes relative to rules in iMC1010v2 [5]. Rules relaxed indicates regulatory boolean expression altered to TRUE.

References

1. Neidhardt FC, Ingraham JL, Schaechter M (1990) Physiology of the bacterial cell. a molecular approach. Sinauer Associates Inc.
2. Lee SJ, Richardson CC (2010) Molecular Basis for Recognition of Nucleoside Triphosphate by Gene 4 Helicase of Bacteriophage T7. *Journal of Biological Chemistry* 285: 31462–31471.
3. Engler MJ, Richardson CC (1983) Bacteriophage T7 DNA replication. Synthesis of lagging strands in a reconstituted system using purified proteins. *The Journal of biological chemistry* 258: 11197–11205.
4. Rappaport H (2004) The fidelity of replication of the three-base-pair set adenine/thymine, hypoxanthine/cytosine and 6-thiopurine/5-methyl-2-pyrimidinone with T7 DNA polymerase. *Biochemical Journal* 381: 709.
5. Covert MW, Knight EM, Reed JL, Herrgard MJ, Palsson BO (2004) Integrating high-throughput and computational data elucidates bacterial networks. *Nature* 429: 92–96.