Time (hr)	Selection Strain	BC	DE	FG	HI	NM
0	BL21	AASGSYMGG	TRNNY	SAEGG	DRDAPP	WT
24	372	AASGSYMGG	TRNNY	SAGGG	DRGAPP	NM02
24	372	AASGSYMGG	TRNNY	SAGGG	DRGAPP	NM02
24	372	AASGSYMGG	TRNNY	SAGGG	DRGAPP	NM02
24	372	AASGSYMGG	TRNNY	SAGGG	DRGAPP	NM02
24	372	AASGSYMGG	TRNNY	SAGGG	DRGAPP	NM02
24	372	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
24	372	AASGSYMGG	TRNNY	SAGGG	DRDAPP	NM37
24	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
24	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
24	369	AASGSYMGG	TRNNY	SAEGG	NRGAPP	NM14
24	369	AASGSYMGG	TRNNY	SAEGG	NRGAPP	NM14
24	369	AASGSYMGG	TRNNY	SAEGG	NRGAPP	NM14
24	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
24	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
24	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
48	372	AASGSYMRG	TRNNY	SAEGG	DRDARP	NM21
48	372	AASGSYMRG	TRNNY	SAEGG	DRDARP	NM21
48	372	AASGSYMRG	TRNNY	SAEGG	DRDAHP	NM56
48	372	AASGSYMRG	TRNNY	SAEGG	DRDAHP	NM56
48	372	AASGSYMRG	TRNNY	SAEGG	DRDAHP	NM56
48	372	AASGSYMRG	TRNNY	SAEGG	DRDAHP	NM56
48	372	AASGSYMGG	TRNNY	SAEGG	DRGAHP	NM50
48	372	AASGSYMGG	TRNNY	SAEGG	DRGAHP	NM50
48	372	AASGSYMGG	TRNNY	SAEGG	DRGAHP	NM50
48	369	AASGSYMGG	TRNNY	SAGGG	DRDAPP	NM37
48	369	AASGSYMGG	TRNNY	SAEGG	DRDARP	NM33
48	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
48	369	AASGSYMGG	TRNNY	SAEGG	DRGAPP	NM55
48	369	AASGSYMRG	TRNNY	SAEGG	DRDAPP	NM34
48	369	AASGSYMRG	TRNNY	SAEGG	DRDAPP	NM34
48	369	AASGSYMRG	TRNNY	SAEGG	DRDAPP	NM34
48	369	AASGSYMRG	TRNNY	SAEGG	DRDAPP	NM34
48	369	AASGSYMRG	TRNNY	SAEGG	DRDARP	NM21
48	369	AASGSYMRG	TRNNY	SAEGG	DRDAHP	NM56

Table S1: Summary of Sanger sequencing results for the gp17 tip region of natural T3 phage mutants isolated from 24 and 48 hr co-cultures of T3 and BL21. Related to Figure 2.

A BL21 culture (5 mL; OD = 0.7) was infected with T3 (10^7 PFU) and was co-cultured for 24 and 48 hrs. After which, phage lysates were chloroform treated and filtered. Natural phage mutants were selected for and plaque purified on either isolation hosts: *ΔwaaC* or *ΔwaaG*.

Targeted loop	Theoretical diversity (number of different combinations from NNK codon randomization)	Number of libraries constructed	Cumulative coverage (% of theoretical diversity)	Number of phagebody libraries producing "hits" on *ΔwaaC*	Number of phagebody libraries producing "hits" on *ΔwaaG*
WT gp17	NA	21	NA	0	0
BC	3.5E+13	10	~0.0000005	4	7
BC[1-4]	1.0E+06	10	~60	4	6
BC[3-7]	3.4E+07	10	~90	2	5
BC[6-9]	1.0E+06	8	>100	2	4
DE	3.4E+07	10	~50	2	4
FG	3.4E+07	10	~0.3	0	0
HI	1.0E+06	15	>100	15	15
HI[+1]	3.4E+10	4	~0.00002	3	4
HI[+3]	3.4E+07	14	~20	10	10

Table S2: Cumulative summary of phagebody libraries constructed. Related to Figure 3.

The theoretical diversity expresses the total number of possible DNA combinations based on the number of NNK codons randomized ($4\times4\times2^{\#\text{ of codons mutagenized}}$). The cumulative coverage is the sum of the library transformation yields for all the libraries ever constructed for that loop. Calculated cumulative coverage is the percentage of theoretical diversity as determined by the total number of plasmid clones obtained for all repeats for each type of library. "Hits" are defined as obtaining at least one PFU on a lawn of the corresponding selective BL21 mutants, *ΔwaaC* or *ΔwaaG*.

Mutated sequence	Targeted loop	Loop DNA sequence	Loop protein sequence	Isolation method	Part of cocktail
T3	BC	**GCTGCTAGTGGTAGTTAC ATGGGAGGAGGT**	AASGSYMGGG		
T3(BC:AASGSHMHT)	BC	GCTGCTAGTGGTAGTCAT ATGCATACTGGC	AASGSHMHTG	panning on PRM01	Yes
T3(BC:AAGKNALGG)	BC+H	GCTGCTGGTAAGAATGCG CTTGGAGGAGGT//C163 1T	AAGKNALGGG// A544V	direct plaque picking	
T3(BC:AARKRGLGG)	BC	GCTGCTAGGAAGCGGGGT CTGGGAGGAGGT	AARKRGLGGG	panning on PRM01	Yes
T3(BC:MHGKSYMGG)	BC+FG	ATGCATGGTAAGAGTTAC ATGGGAGGAGGT//G157 0A	MHGKSYMGGG// A524T	direct plaque picking	
T3(BC:AIGRSHLKS)	BC	GCGATTGGTAGGTCTCAT TTGAAGAGTGGT	AIGRSHLKSG	direct plaque picking	
T3(HI:AASGSKLRH)	BC	GCTGCTAGTGGTAGTAAG CTGAGGCATGGC	AASGSKLRHG	panning on *ΔwaaC*	Yes
T3(BC:AASGSHMHK)	BC	GCTGCTAGTGGTAGTCAT ATGCATACTGGC	AASGSHMHKG	panning on *ΔwaaG*	Yes
T3	FG	**TCAGCCGAGGGCGGT**	SAEGG		
T3(FG:PLDGH)	FG	CCGTTGGATGGTCAT	PLDGH	panning on *ΔwaaG* and PRM01	Yes
T3	HI	**AGAGATGCGCCTCCA**	RDAPP		
T3(HI:GHLSL)	HI	AGACATGGGTTGTCTTTG	RGHLSL	panning on *ΔwaaG*	Yes
T3(HI:LGLAV)	HI	AGACTGGGTCTTGCTGTT	RLGLAV	panning on PRM01	Yes
T3(HI:HSVV)	FG+HI	G1570A//AGACATTCGG TGGTT	A524T//RHSVV	direct plaque picking	
T3(HI:NCHV)	HI	AGAAATTGTCATGTG	RNCHV	panning on PRM01	Yes
T3(HI:HTGI)	HI	AGACATACGGGTATT	RHTGI	panning on *ΔwaaG*	Yes
T3(HI:AYASP)	HI	AGAGCTTATGCGTCTCCA	RAYASP	direct plaque picking	
T3(HI:KSGV)	HI	AGAAAGAGTGGGGTG	RKSGV	direct plaque picking	
T3(HI:R546G KAGI)	H+HI	GGAAAGGCGGGGATT	GKAGI	direct plaque picking	
T3(HI:HTHP)	HI	AGACATACTCATCCT	RHTHP	panning on *ΔwaaG*	Yes
T3(HI:HSQP)	HI	AGACATTCTCAGCCG	RHSQP	panning on PRM01	Yes
T3(HI:KLNI)	HI	AGAAAGCTGAATATT	RKLNI	direct plaque picking	
T3(HI:GARV)	HI	AGAGGGGCGAGGGTG	RGARV	direct plaque picking	
T3(HI:ASRV)	HI	AGAGCGAGTAGGGTG	RASRV	direct plaque picking	
T3(HI:KAGI)	HI	AGAAAGGCGGGGATT	RKAGI	direct plaque picking	
T3(HI:RTFI)	HI	AGACGTACTTTTATT	RRTFI	direct plaque picking	
T3(HI:RDIRLSI)	HI	AGACGGGATATTAGGCTT AGTATT	RRDIRLSI	direct plaque picking	
T3(HI:RFFV)	HI	AGACGTTTTTTGTT	RRFFV	panning on *ΔwaaC*	Yes

Table S3: Summary of the phagebodies characterized. Related to Figure 3.

Summary of all the phagebodies isolated and characterized during this work showing mutated sequences (indicated by green), isolation method, and if used in the minimal cocktail (**Figure 4C**).

pSLM49 Construction	
gtacGAATTCagctGGATCCAGACCTAGGGGATATATTCCGCTTCCTCGCTCA	
gcatCCCGGGtgcaAAGCTTGACGTCGGAATTGCCAGCTGGGGCGCCCTC	
TAGCGGATCCTGAAGGAACGTGACCCAAACAAACCGTACA	
TCGACCCGGGATCTTATCGACTACCTTGGCACCAATCTGA	
subcloning phagebody tips into pSLM49	
GTACTAAGTGGGGAGGTAAGTGGCTT	
GTGTGATAGTCCATCCGTGGACTTAAAGTA	
AAGCCACTTACCTCCCCACTTAGTAC	
TACTTTAAGTCCACGGATGGACTATCACAC	
pSLM111alpha construction	
CCTGTGGGGCCCATGCCCTAGGTCATGAGATTATCAAAAAGGATCTTCACC	
GGTGCAGGGCCCTCGACAATTGTCAGCCAATCGACTGGCGAGCGGCATCGC	
TGCGAAgggcccGGATTCGAATTCGTGATCTTCCGTCACAGGTAGGCGC	
GTGGCAGGGCCCGCGTAAGCTAGCGGCGCGCCATTTAAATGAAGTTCCTATTCC	
***waaC* deletion**	
CGGATGCGGGTTTTGATCGTTAAAACATCGTCGATGGGCGGTGTAGGCTGGAGCTGCTTC	
ACCATCTGATTCTTCCCATACCCACCAATTAATCCCGGATATGGGAATTAGCCATGGTCC	
***waaG* deletion**	
CGGTTTGCAGCGCGATTTTATGCGTATTGCTCAGACAGTCGTGTAGGCTGGAGCTGCTTC	
CCAGACCACCCGTTATGATATCCGCCGCTTTCTCTGGCAGATGGGAATTAGCCATGGTCC	
direct transformation loop library construction	
CCTGTGGGAGAGTATCAGTCTGAGAACCMNNMNNMNNMNNMNNMNNMNNMNN MNNAGCCCATACTTGAGTCCAGGCC	BC FW
GGTTCTCAGACTGATACTCTCCCACAGG	BC RV
GGCAGGGTATTTAAGAACATAGCGGATAGANNKNNKNNKNNKACAGCAATAGCC GTAGAGGACGTG	HI FW
TCTATCCGCTATGTTCTTAAATACCCTGCC	HI RV
AACTGGTCCTGACGGTATCTACTTCCTTNNKNNKNNKNNKNNKTGGCTAAAATTC CAGATACACTCTAATGGC	FG FW
AAGGAAGTAGATACCGTCAGGACCAGTT	FG RV
CTTAATCCATATGTTGCGGAATCGC	DE FW
GCGATTCCGCAACATATGGATTAAGNNKNNKNNKNNKNNKTGGAACTTCTTCCGA ACTGGTCCTGACG	DE RV
GACAATGGCCTGGACTCAAGTATGGGCTNNKNNKNNKNNKNNKNNKNNKNNKNN KNNKGGTTCTCAGACTGATACTCTCCCAC	BC[10] FW
AGCCCATACTTGAGTCCAGGCCATTGTC	BC[10] RV
GGGTATTTAAGAACATAGCGGATAGANNKNNKNNKNNKNNKNNKNNKACAGCAA TAGCCGTAGAGGACGTG	HI[+3] FW
TCTATCCGCTATGTTCTTAAATACCC	HI[+3] RV

GGTTCTCAGACTGATACTCTCCCACAGG	BC FW
CCTGTGGGAGAGTATCAGTCTGAGAACCMNNMNNMNNMNNACTACCACTAGCAGCAGCCCATACTTGAGTCCAGGCC	BC[6-9] RV
CCTGTGGGAGAGTATCAGTCTGAGAACCTCCTCCCATGTAACTMNNMNNMNNMNNAGCCCATACTTGAGTCCAGGCC	BC[3-7] RV
PST1254 CCTGTGGGAGAGTATCAGTCTGAGAACCTCCTCCMNNMNNMNNMNNMNNAGCAGCAGCCCATACTTGAGTCCAGGCC	BC[1-4] RV
BsaI/religation loop library construction	
ctgactGGTCTCtAgCCMNNMNNMNNMNNACTACCACTAGCAGCAGCCCATACTTGAGTCCAGGCCATTGTC	BC[6-9] RV
ctgactGGTCTCtAgCCTCCTCCCATGTAACTMNNMNNMNNMNNAGCCCATACTTGAGTCCAGGCCATTGTC	BC[3-7] RV
ctgactGGTCTCtAgCCTCCTCCMNNMNNMNNMNNMNNAGCAGCAGCCCATACTTGAGTCCAGGCCATTGTC	BC[1-4] RV
agtcagGGTCTCtGGTTCTCAGACTGATACTCTCCCACAGG	BC FW
ctgactGGTCTCtaTTCCAMNNMNNMNNMNNMNNCTTAATCCATATGTTGCGGAATCGC	DE RV
agtcagGGTCTCtGAAtTTCTTCCGAACTGGTCCTGACGGTATC	DE FW
ctgactGGTCTCtcAaCCAMNNMNNMNNMNNMNNAAGGAAGTAGATACCGTCAGGACCAG	FG RV
agtcagGGTCTCtTGGCTAAAATTCCAGATACACTCTAATGG	FG FW
ctgactGGTCTCtCgGTMNNMNNMNNMNNTCTATCCGCTATGTTCTTAAATACCCTGC	HI RV
ctgactGGTCTCtCgGTMNNMNNMNNMNNMNNTCTATCCGCTATGTTCTTAAATACCCTGC	HI[+1] RV
agtcagGGTCTCtACcGCAATAGCCGTAGAGGACGTG	HI FW

Table S5: List of all oligonucleotides used in this study. Related to Figure 3.

FW: forward primer; RV: reverse primer