Table S1

Non-P22-like phages and prophages in figure 1

Prophage[1] or Phage	Host strain	Locus_tag of *terS* gene	Phylum; Class of host
B171-1	*Escherichia coli* B171	EcB171_0867	Proteobacteria; Gammaproteobacteria
Bact1	*Bacteroides sp.* D2	BSGG_4618	Bacteroidetes; Bacteroidia
Bpert1	*Bordetella pertussis* Tohamal	BP3385	Proteobacteria; Betaproteobacteria
Bruc1	*Brucella sp.* NF2653	BROD_2255	Proteobacteria; Alphaproteobacteria
Crono1	*Cronobacter sakazakii* ATCCBAA-894	ESA_02744	Proteobacteria; Gammaproteobacteria
Delf1	*Delftia acidovoran*s SPH-1	Daci_1941	Proteobacteria; Betaproteobacteria
Dick1	*Dickeya zeae* Ech1591	Dd1591_4010	Proteobacteria; Gammaproteobacteria
Ent13047-1	*Enterobacter cloacae* ATCC13047	ECL_03566	Proteobacteria; Gammaproteobacteria
Ent9394-1	*Enterobacter cloacae* NCTC9394	ENC_27700	Proteobacteria; Gammaproteobacteria
ES-2*	*Cronobacter sakazakii*	teminase small subunit	Proteobacteria; Gammaproteobacteria
Kleb1	*Klebsiella pneumoniae* ATCC13884	HMPREF0484_3793	Proteobacteria; Gammaproteobacteria
Niss1	*Neisseria gonorrhoeae* FA1090	NGO0494	Proteobacteria; Betaproteobacteria
Rhodo1	*Rhodopseudomonas palustris* TIE-1	Rpa1_3055	Proteobacteria; Alphaproteobacteria
Robig1	*Robiginitalea biformata* HTCC2501	RB2501_01380	Bacteroidetes; Flavobacteria
T1*	*Escherichia coli*	T1p54	Proteobacteria; Gammaproteobacteria
Tcarb1	*Thermosinus carboxydivorans* Nor1	TcarDRAFT_1282	Firmicutes; Negativicutes
Yers1	*Yersinia pseudotuberculosis* YPIII	YPK_1220	Proteobacteria; Gammaproteobacteria
Zymob1	*Zymomonas mobilis* ZM4	ZMO0378	Proteobacteria; Alphaproteobacteria

* Fully functional phages (those without asterisks are putative prophages in bacterial genome sequences)

1. These are prophages that we have identified in bacterial genome sequenced in the extant GenBank database. Prophages are not generally named by the researchers who sequenced these bacterial genomes. These are provisional names we gave to these prophages during our studies (some prophage names are from our previous publication Casjens& Thuman-Commike (2011) Virology 411, 393-415).

Table S2

P22-like TerS proteins used in figures 1 and 2

Prophage[1] or Phage	Host species and strain	Genbank Locus_tag or *terS* gene name	Class; Family of host
Ars1	*Arsophonas nasoniae*	ARN_26050	*Gammaproteobacteria; Enterobacteriaceae*
APSE-1	*Hamiltonella defensa*	gene *17*	*Gammaproteobacteria; Enterobacteriaceae*
Cart1	*Pectobacterium carotovorum* PBR1692	PcarbP_010200010662	Gammaproteobacteria; Enterobacteriaceae
CUS-3*	*Escherichia coli* serotype K1	gene *22*	*Gammaproteobacteria; Enterobacteriaceae*
H591-1	*Escherichia coli* H591	ECPG_00988	*Gammaproteobacteria; Enterobacteriaceae*
HK620	*Escherichia coli* serotype H	gene *hkbO*	*Gammaproteobacteria; Enterobacteriaceae*
IME10*	*Enterobacteria* (host species not published)	gene *3*	*Gammaproteobacteria; Enterobacteriaceae*
Miss1	*Salmonella enterica* serotype Mississippi A4-633	LTSEMIS_1103	*Gammaproteobacteria; Enterobacteriaceae*
ϕSG1	*Sodalis glossinidius*	gene *01*	*Gammaproteobacteria; Enterobacteriaceae*
P22*	*Salmonella enterica* serotype Typhimurium	gene *3*	*Gammaproteobacteria; Enterobacteriaceae*
Rett1	*Providencia rettgeri* DSM 1131	PROVRETT_06006	Gammaproteobacteria; Enterobacteriaceae
Serr1	*Serratia plymuthica* AS9	SerAS9_2692	*Gammaproteobacteria; Enterobacteriaceae*
Sf6*	*Shigella flexneri* serotype Y	gene *1*	*Gammaproteobacteria; Enterobacteriaceae*
SPC-P1*	*Salmonella enterica* serotype Paratyphi B	gene *1*	*Gammaproteobacteria; Enterobacteriaceae*
TA124-1	*Escherichia coli* TA124	ESRG_00795	*Gammaproteobacteria; Enterobacteriaceae*
Ugan1	*Salmonella enterica* serotype Uganda R8-3404	LTSEUGA_0536	*Gammaproteobacteria; Enterobacteriaceae*
Wand1	*Salmonella enterica* serotype Wandsworth A4-580	LTSEWAN_0986	*Gammaproteobacteria; Enterobacteriaceae*

* Fully functional phages (those without asterisks are putative prophages in bacterial genome sequences)

1. These are prophages that we have identified in bacterial genome sequenced in the extant GenBank database. Prophages are not generally named by the researchers who sequenced these bacterial genomes. These are provisional names we gave to these prophages during our studies (some prophage names are from our previous publication Casjens& Thuman-Commike (2011) Virology 411, 393-415).

Table S3

Oligonucleotides used in this study

A
5'-GAGGGCGCGAAAGAGTCCTCAGCCTGAAATAACAACTAAGTGAGATGAATCCTGTTGACAATTAATCATCCGCA

B
5'-GATACGAGAGCGTCGCTTATCGCGATCTCCCTTATCAGGTGTCACGTCTTTCAGCACTGTCCTGCTCCTT

C
5'-GAGGGCGCGAAAGAGTCCTCAGCCTGAAATAACAACTAAGTGAGATGAATATGGCGACTGAACCAAAAGC

D
5'-GATACGAGAGCGTCGCTTATCGCGATCTCCCTTATCAGGTGTCACGTCCTTGTCGCCATACTTACGGG

E
5'-ACGATTCTAGAGACTTACCAAGCTGGTTACC

F
5'-CAATCAAGCTTCTGTTCACTACCGGAGCATG

G
5'-TCATTGAGGATTATATTAAAGAACATTTTACAATTAAATAACACCAAACACCCCCCAAAACC

H
5'-CGAAGAGCTATGGGAAATTTTTGTTGAAGAACAAATATAACACACAACCACACCACACCAC

I
5'-ATTAAGAGTAATAACTCCGTCTGTCGGCATGGTACACCGGTTAAGACCCACTTTCACATT

J
5'-AATGCTGAATTCAGACGCAGAATTTTGTCTGCTTACCGTCCTAAGCACTTGTCTCCTG

K
5'-CGGTCAGCGACATCCATTTTCGCGAATCCGGCCGCACTGGCCCCCGATGGTCAACCGTACCG

L
5'-CGGTCAGCGACATCCATTTTCGCGAATCCGGAGTATAAATATCGCCTGAGAGAAGATTTATCTGAAGTCGTTACGC
GAG

M
5'-ACCGGTACGGTTGACCATCGGGGGCCAGTGCGGGCGTTTCATCTCGCGTAACGACTTCAGATAAATCTTCTCTCAGGC
GATA