



Figure S1. Phage secretion from host *Pseudomonas carnis* M132: TEM images of the uninfected host and three timepoints post infection. Bacterial flagella are indicated with white arrows. Black arrows indicate the filamentous phage.

Table S1. *Pseudomonas* strains used in this study.

Strain description	Origin	Source/ Reference ^{1,2}
<i>P. fluorescens</i> L1-82	raw milk	TUM isolate
<i>P. fluorescens</i> L1-83	raw milk	TUM isolate
<i>P. fragi</i> L1-85	raw milk	TUM isolate
<i>P. gessardii</i> L1-88 (DSM 17152)	mineral water	Verhille et al. (1999) [47] emend. van den Beld et al.(2016) [48]
<i>P. gessardii</i> L1-89	raw milk	TUM isolate
<i>P. gessardii</i> L1-90	milk semifinished product	TUM isolate
<i>P. lactis</i> L1-91	raw milk	TUM isolate
<i>P. lactis</i> L1-92	raw milk	TUM isolate
<i>P. lactis</i> L1-93 (DSM 29167)	raw milk	Neubeck et al. (2017) [15]
<i>P. lundensis</i> L1-95	raw milk	TUM isolate
<i>P. lundensis</i> L1-96	milk semifinished product	TUM isolate
<i>P. meridiana</i> L1-98	raw milk	TUM isolate
<i>P. meridiana</i> L1-99	raw milk	TUM isolate
<i>P. protegens</i> L1-101	raw milk	TUM isolate
<i>P. protegens</i> L1-102	raw milk	TUM isolate
<i>P. proteolytica</i> L1-103 (DSM 15321)	cyanobacterial mat samples	Reddy et al. (2004) [49] emend. van den Beld et al. (2016) [48]
<i>P. proteolytica</i> L1-104	raw milk	TUM isolate
<i>P. proteolytica</i> L1-105	raw milk	TUM isolate
<i>P. proteolytica</i> L1-106	raw milk	TUM isolate
<i>P. proteolytica</i> L1-107	cream	TUM isolate
<i>P. haemolytica</i> L1-177 (DSM 108987)	raw milk	Hofmann et al. (2020) [50]
<i>P. iridis</i> L1-222 (M19)	raw milk	MRI isolate
<i>P. lundensis</i> M47	raw milk	MRI isolate
<i>P. rustica</i> L1-223 (M59) (DSM 112348)	raw milk	Fiedler et al., 2022 [51]
<i>P. sp.</i> M70	raw milk	MRI isolate
<i>P. bubulae</i> M72	raw milk	MRI isolate
<i>P. carnis</i> M132	raw milk	MRI isolate

¹TUM: Technical University of Munich. Strains have been isolated within the Industrial Collective Research (IGF) funded project AiF-FV 16588 N.

²MRI: Max Rubner-Institut. Strains have been isolated within the Industrial Collective Research (IGF) funded project AiF-FV 20027 N.

Table S2. Top 3 Blast hits of assembled contigs. Node 3 was identified as a filamentous phage.

Description	Scientific Name	Common Name	Taxid	Max Score	Total Score	Query cover	E Value	Per. Ident	Acc. Len	Accession
NODE_1										
<i>Pseudomonas monteilii</i> STW0522-72 plasmid pSTW0522-72-3 DNA,...	<i>Pseudomonas</i>	NA	76759	45142	69238	75%	0	99	44219	AP022476.1
<i>Pseudomonas putida</i> strain IEC33019 plasmid pIEC33019, complete...	<i>Pseudomonas</i>	NA	303	42125	76004	82%	0	99,3	52710	CP016446.1
<i>Pseudomonas mendocina</i> strain AOUC-01/15 plasmid pMEN15, comple.	<i>Pseudomonas</i>	NA	300	36221	71110	75%	0	100	55387	MK671727.1
NODE_2										
<i>Pseudomonas fragi</i> strain NMC25 plasmid unnamed2, complete...	<i>Pseudomonas</i>	NA	296	13682	36520	68%	0	87,9	54359	CP021134.1
<i>Pseudomonas migulae</i> strain R1-9 plasmid unnamed, complete...	<i>Pseudomonas</i>	NA	78543	9768	35396	68%	0	87,3	68338	CP043572.1
<i>Pseudomonas mandelii</i> JR-1 plasmid, complete sequence	<i>Pseudomonas</i>	NA	1147786	6482	7250	9%	0	100	410512	CP005961.1
NODE_3 (=PMBT54)										
<i>Inoviridae</i> sp. isolate ctbd3, complete genome	<i>Inoviridae</i> sp.	NA	2219103	11537	12845	100%	0	97,9	7321	MH616883.1
<i>Pseudomonas tolaasii</i> strain 2192T chromosome	<i>Pseudomonas</i>	NA	29442	65,8	65,8	4%	0,0001	70,7	6856683	CP020369.1
<i>Pseudomonas aeruginosa</i> strain PAAK095 chromosome, complete genome	<i>Pseudomonas</i>	NA	287	60,2	120	1%	0,006	79,6	6780782	CP054473.1
NODE_7										
Uncultured prokaryote from Rat gut metagenome metamobilome,...	uncultured p..	NA	198431	1657	2711	55%	0	93,8	4028	LN853216.1
<i>Pseudomonas aeruginosa</i> strain YTSY4 plasmid pYTSY4-VIM, comple...	<i>Pseudomonas</i>	NA	287	1530	2738	59%	0	91,2	14870	MT313930.1
Uncultured prokaryote from Rat gut metagenome metamobilome,...	uncultured p..	NA	198431	1391	1391	35%	0	88	2394	LN854271.1

Table S3. HMM alignments of the predicted ORFs against the databases UniProt, Pfam and PDB using HHsuite. Best hit and corresponding database is indicated next to the ORF number. Below are alignment statistics for each hit.

[illegible]

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ORF2, DB = PDB
>3VEA A Macrodomein Ter protein/DNA complex; macrodomains, chromosome, DNA condensation, DNA; 2.55A {Yersinia pestis}
Probab=92.51 E-value=0.045 Score=37.40 Aligned_cols=37 Identities=24% Similarity=0.424 Sum_probs=33.7
Template_Neff=6.100
```

ORF3, DB = PDB, Pfam, UniProt
no significant results

ORF5, DB = PDB
>1PFS_B PF3 SINGLE-STRANDED DNA BINDING PROTEIN; DNA-BINDING PROTEIN, VIRAL, BACTERIOPHAGE PF3; NMR {Pseudomonas phage PF3} SCOP: b.40.4.7
Probab=98.29 E-value=1.8e-09 Score=69.05 Aligned_cols=75 Identities=27% Similarity=0.515 Sum_probs=71.2
Template_Neff=6.500

Q ORF5	87	A	87	(94)
Q Consensus	87	a	87	(94)
		.		
T Consensus	77	~	77	(78)
T 1PFS_B	77	R	77	(78)
T ss_dssp		E		
T ss_pred		c		
Confidence		4		

[illegible]

Q ORF7	29	AAKWDTYTQITTTGVDFSGIATGVLVSAAVLAGIYAGIKGARIVLGLF	74	(76)
Q Consensus	29	aakwdytqtittgvdfsgiatgvlsvaavlagiyagikgarivlglf	74	(76)
		+.-+ +-.+...+..+ +.-+..+..+...+...+...+...+.. +.-+...+..		
T Consensus	13	a-a-d-t-v-t-I-----iG-av1-v-v-i-----k-vrr~	56	(56)
T 13CK69_9GAMM/1	13	vanITVTDIVDQLK--AGAPAIIVSITAATISLLAVIAVFKYVRGAL	56	(56)
T ss_pred		hhccCHHHHHHHHHH--hhHHHHHHHHHHHHHHHHHHHHHHHHHHhhc		
Confidence		344566777877665 67777888888888888888999999988876653		

[illegible]

Q ORF8	317	GSTGGTGdgetPgtGTGGGqgggGTGTGGSGnGSsgSSPGTgSGSgSSgSSGSSGEGDgSGSGdGLGSfESFPgdLTLS	396	(483)
Q Consensus	317	--gg-g--g--g--g--g--g--g--g--g--g--g--g--g--f----- ++.[.]++...[++++].[+..+++++++][+.].[+]++[++++].[[+]].[-.+].[+].[.]	396	(483)
T Consensus	162	gstgtgdgetpgtGttgggggggTgtggsgmgngssgspptGsgsgssgggsagsggedgsgsdglgfesapgdltls	241	(328)
T UniRef100 A0A3	162	GSTGGTGdgetPgtGTGGGqgggGTGTGGSGnGSsgSSPGTgSGSgSSgSSGSSGEGDgSGSGdGLGSfESFPgdLTLS	241	(328)

[illegible]

[illegible]

Table S4. Python script used to extract coding sequences from GenBank files and saving them as Fasta (.faa) files.

[illegible]