

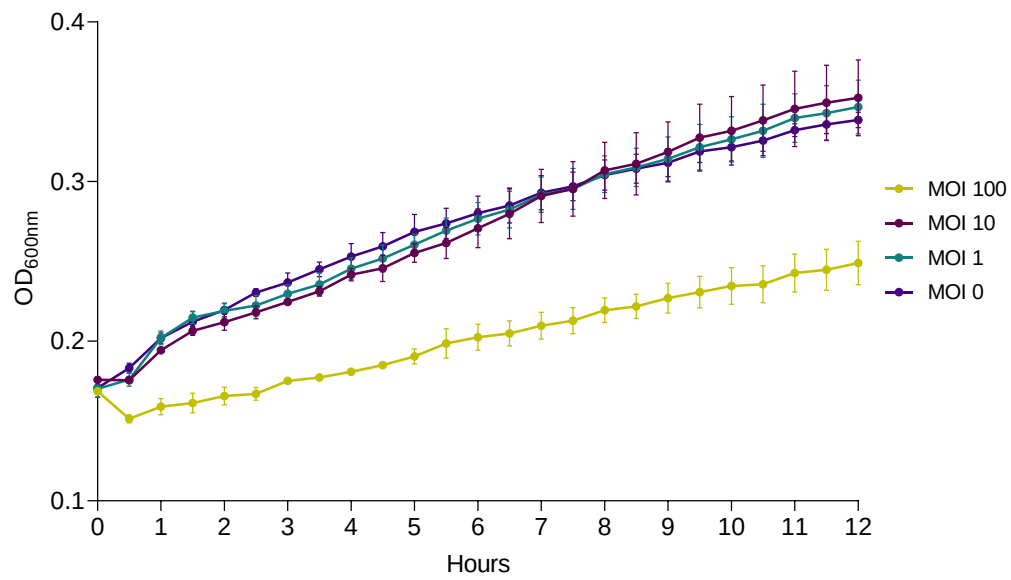


Figure S1. The bacteriolytic effect of phage Savoy against *Pseudomonas syringae* pv. *syringae*

Table S1. Functional annotation of predicted open reading frames (ORFs) in the phage Savoy genome.

gene	start	stop	annot	category
CDS_0001	40438	40950	head-tail adaptor Ad1	connector
CDS_0002	40943	41326	head closure Hc1	connector
CDS_0003	41323	41751	tail terminator	connector
CDS_0004	44116	44562	tail completion or Neck1 protein	connector
CDS_0005	1277	234	DNA polymerase processivity factor	DNA, RNA and nucleotide metabolism
CDS_0006	10211	8445	DNA helicase	DNA, RNA and nucleotide metabolism
CDS_0007	11137	10211	Cas4-domain exonuclease	DNA, RNA and nucleotide metabolism
CDS_0008	12914	12177	Sak4-like ssDNA annealing protein	DNA, RNA and nucleotide metabolism
CDS_0009	13901	12978	ATP-dependent DNA ligase	DNA, RNA and nucleotide metabolism
CDS_0010	18482	16041	DNA primase	DNA, RNA and nucleotide metabolism
CDS_0011	20049	19582	dCMP deaminase	DNA, RNA and nucleotide metabolism
CDS_0012	31634	32089	RusA-like Holliday junction resolvase	DNA, RNA and nucleotide metabolism
CDS_0013	61506	59239	DNA polymerase	DNA, RNA and nucleotide metabolism
CDS_0014	34147	35700	terminase large subunit	head and packaging
CDS_0015	35700	37220	portal protein	head and packaging
CDS_0016	37284	38090	head scaffolding protein	head and packaging
CDS_0017	38222	39247	major head protein	head and packaging
CDS_0018	48672	49418	virion structural protein	head and packaging
CDS_0019	32103	32444	endolysin	lysis
CDS_0020	32533	32868	holin	lysis
CDS_0021	3009	2068	queuine tRNA-ribosyltransferase	moron, auxiliary metabolic gene and host takeover
CDS_0022	5045	4566	QueD-like 6-pyruvoyl-tetrahydropterin synthase	moron, auxiliary metabolic gene and host takeover
CDS_0023	6057	5203	QueC-like queuosine biosynthesis	moron, auxiliary metabolic gene and host takeover
CDS_0024	7049	6273	QueE-like radical SAM domain	moron, auxiliary metabolic gene and host takeover
CDS_0025	4556	3738	GTP cyclohydrolase	other
CDS_0026	16273	15239	MazG-like pyrophosphatase	other
CDS_0027	41762	43264	minor tail protein	tail
CDS_0028	43274	43714	Tail assembly chaperone	tail
CDS_0029	43741	44103	tail chaperonin	tail
CDS_0030	44546	48586	tail length tape measure protein	tail
CDS_0031	49420	49950	minor tail protein	tail
CDS_0032	49999	53919	central tail fiber J	tail
CDS_0033	56611	56982	tail fiber assembly	tail
CDS_0034	139	2	hypothetical protein	unknown function
CDS_0035	237	136	hypothetical protein	unknown function
CDS_0036	1616	1380	hypothetical protein	unknown function
CDS_0037	2068	1616	hypothetical protein	unknown function
CDS_0038	3281	3009	hypothetical protein	unknown function
CDS_0039	3675	3283	hypothetical protein	unknown function
CDS_0040	5206	5042	hypothetical protein	unknown function

CDS_0041	6289	6065	hypothetical protein	unknown function
CDS_0042	7725	7105	hypothetical protein	unknown function
CDS_0043	7825	7718	hypothetical protein	unknown function
CDS_0044	8445	7813	hypothetical protein	unknown function
CDS_0045	12177	11203	hypothetical protein	unknown function
CDS_0046	14197	13904	hypothetical protein	unknown function
CDS_0047	14714	14178	hypothetical protein	unknown function
CDS_0048	15167	14739	hypothetical protein	unknown function
CDS_0049	18719	18483	hypothetical protein	unknown function
CDS_0050	19601	18786	hypothetical protein	unknown function
CDS_0051	20285	20106	hypothetical protein	unknown function
CDS_0052	20545	20288	hypothetical protein	unknown function
CDS_0053	21206	20523	hypothetical protein	unknown function
CDS_0054	21763	21203	hypothetical protein	unknown function
CDS_0055	22032	21829	hypothetical protein	unknown function
CDS_0056	22226	22029	hypothetical protein	unknown function
CDS_0057	23058	22291	hypothetical protein	unknown function
CDS_0058	23761	22994	unknown function	unknown function
CDS_0059	24024	23830	hypothetical protein	unknown function
CDS_0060	24352	24092	hypothetical protein	unknown function
CDS_0061	24627	24349	hypothetical protein	unknown function
CDS_0062	25009	24638	hypothetical protein	unknown function
CDS_0063	25216	25031	hypothetical protein	unknown function
CDS_0064	25393	25304	hypothetical protein	unknown function
CDS_0065	25789	25409	hypothetical protein	unknown function
CDS_0066	26580	25786	hypothetical protein	unknown function
CDS_0067	26947	26708	hypothetical protein	unknown function
CDS_0068	27087	26947	hypothetical protein	unknown function
CDS_0069	27107	27277	hypothetical protein	unknown function
CDS_0070	27393	27578	hypothetical protein	unknown function
CDS_0071	27650	27844	hypothetical protein	unknown function
CDS_0072	27841	28626	hypothetical protein	unknown function
CDS_0073	28685	28777	hypothetical protein	unknown function
CDS_0074	28788	28919	hypothetical protein	unknown function
CDS_0075	28919	29161	hypothetical protein	unknown function
CDS_0076	29338	30093	hypothetical protein	unknown function
CDS_0077	30184	30879	hypothetical protein	unknown function
CDS_0078	30883	31557	hypothetical protein	unknown function
CDS_0079	32977	33321	hypothetical protein	unknown function
CDS_0080	34123	33254	hypothetical protein	unknown function
CDS_0081	39299	39511	hypothetical protein	unknown function
CDS_0082	39586	40287	hypothetical protein	unknown function
CDS_0083	40298	40438	hypothetical protein	unknown function
CDS_0084	53919	54218	hypothetical protein	unknown function
CDS_0085	54219	54950	hypothetical protein	unknown function
CDS_0086	54962	56599	hypothetical protein	unknown function
CDS_0087	57037	57264	hypothetical protein	unknown function
CDS_0088	57456	57268	hypothetical protein	unknown function
CDS_0089	57634	57425	hypothetical protein	unknown function
CDS_0090	58146	57631	hypothetical protein	unknown function
CDS_0091	58328	58161	hypothetical protein	unknown function
CDS_0092	58726	58394	hypothetical protein	unknown function
CDS_0093	58842	58723	hypothetical protein	unknown function
CDS_0094	59228	58908	hypothetical protein	unknown function
CDS_0095	61707	61546	hypothetical protein	unknown function
CDS_0096	61923	61714	hypothetical protein	unknown function

Table S2. Closely related phages to Savoy identified by BLASTn analysis.

Scientific Name	Max Score	Total Score	Query Cover	E value	Per. ident	Acc. Len	Accession
<i>Pseudomonas</i> phage Knedl	516	516	1%	2.00E-139	77.97	59205	OR805297.1
<i>Pseudomonas</i> phage vB_PaeS_HTN2	510	510	1%	9.00E-138	77.85	60453	PP916319.1
<i>Pseudomonas</i> virus PBPA162	503	503	1%	2.00E-135	77.68	60626	NC_070971.1
<i>Pseudomonas</i> phage Iggy	492	492	1%	3.00E-132	77.45	60628	NC_070970.1
<i>Pseudomonas</i> phage PaMx25	383	572	2%	2.00E-99	74	57899	NC_041953.1
<i>Pseudomonas</i> phage Quinobequin-P09	383	383	2%	2.00E-99	74.13	58277	NC_072501.1
<i>Pseudomonas</i> phage BL5	383	628	2%	2.00E-99	74.08	58933	PP791527.1
<i>Pseudomonas</i> phage vB_PaeS_PAJD-1	377	377	2%	1.00E-97	73.9	57919	NC_072500.1
<i>Pseudomonas</i> phage TIVP-H6	372	372	2%	5.00E-96	73.83	57534	PP203295.1
<i>Pseudomonas</i> phage JG012	355	355	2%	5.00E-91	73.52	58359	KX898399.1
<i>Pseudomonas</i> phage JG054	311	545	2%	1.00E-77	74.07	57839	NC_072498.1
<i>Stenotrophomonas</i> phage BUCT627	246	246	1%	3.00E-58	73.27	61860	NC_071021.1
<i>Stenotrophomonas</i> phage BUCT626	243	243	1%	4.00E-57	72.71	61662	NC_071020.1
<i>Pseudomonas</i> phage pPA-3099-2aT.3	237	237	1%	2.00E-55	74.14	57911	OP784576.1
<i>Stenotrophomonas</i> phage vB_SmaS_BUCT548	222	222	1%	5.00E-51	72.84	62354	NC_071019.1
<i>Sphingomonas</i> phage vB_StuS_MMDA13	215	215	1%	8.00E-49	73.26	63743	NC_072503.1
<i>Pseudomonas</i> phage 20Sep420	213	213	1%	3.00E-48	72.44	62357	OQ319938.1
Prokaryotic dsDNA virus sp.	147	147	1%	3.00E-28	74.44	58944	MK892813.1
Alphaproteobacteria phage PhiJL001	124	124	0%	1.00E-21	76.13	63649	NC_006938.1
Prokaryotic dsDNA virus sp.	117	117	1%	2.00E-19	73.22	62844	MK892759.1
Roseobacter phage RDJL3	111	111	1%	1.00E-17	70.63	61503	OK283305.1
Prokaryotic dsDNA virus sp.	106	106	1%	5.00E-16	70.72	61408	MK892620.1