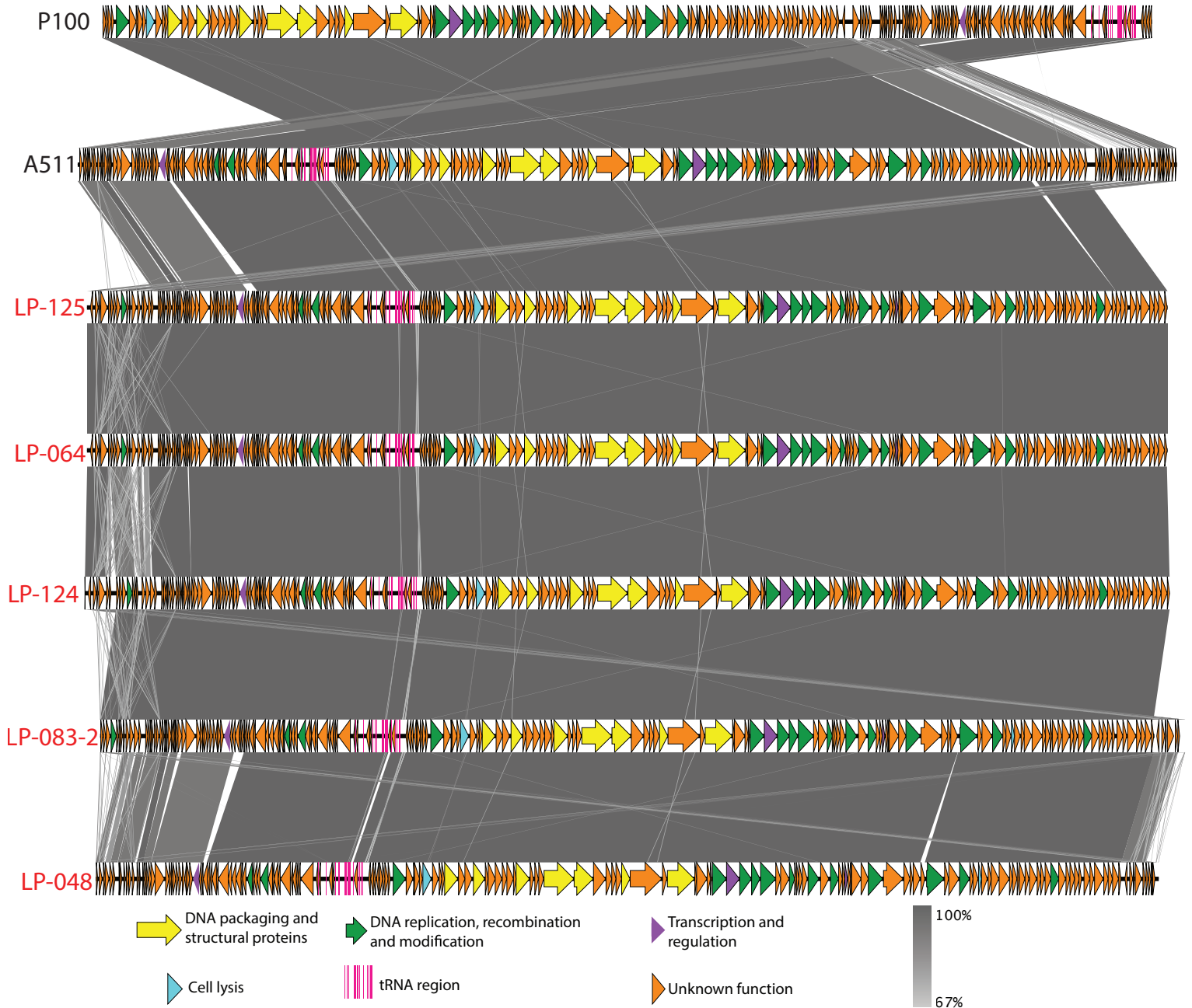


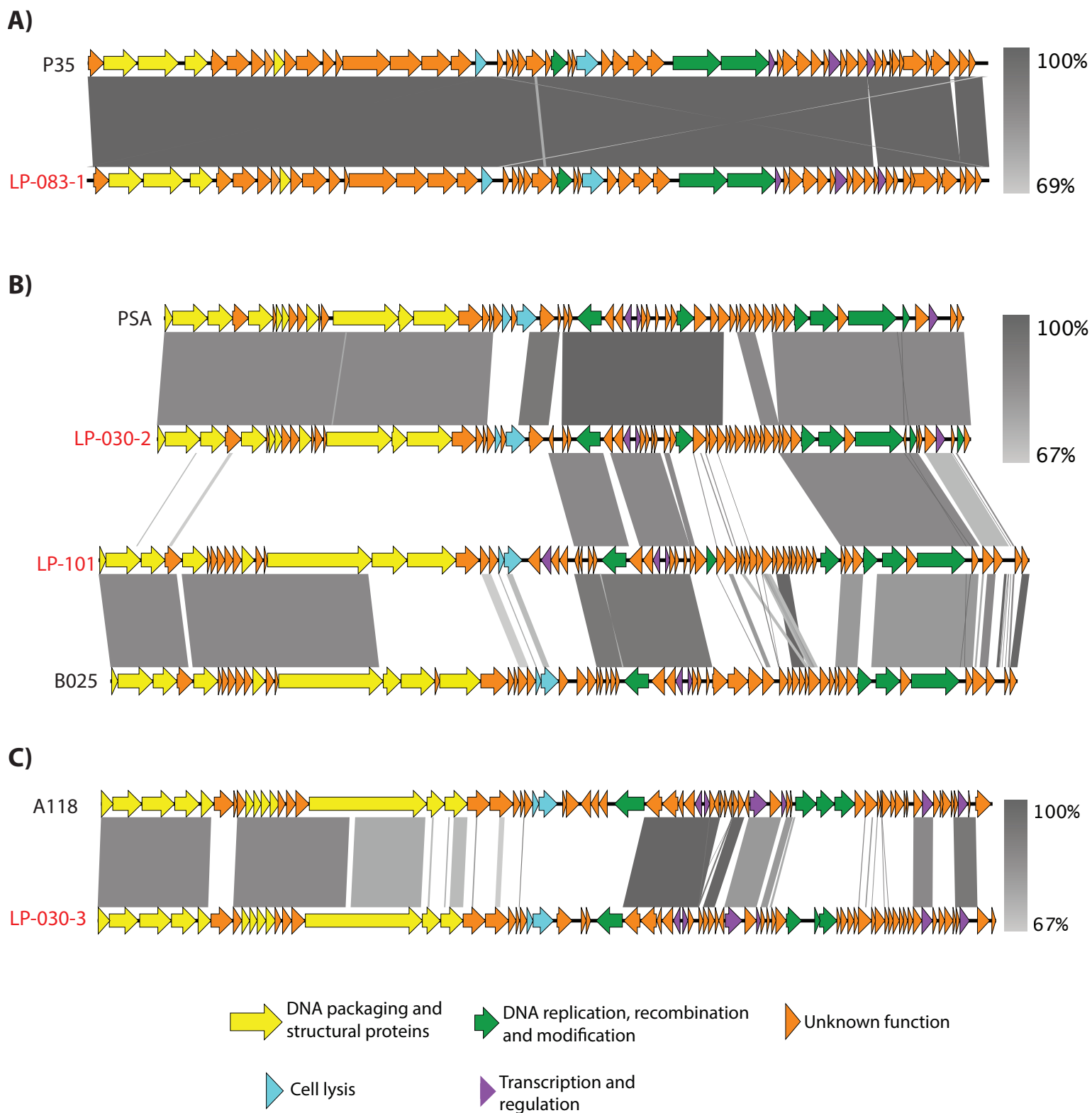
**Supplemental Table 1:** General characteristics of bacteriophages included in orthocluster analysis

Phage	Host	Accession no.	Genome Size (bp)	Family (morphotype)	References
42e	<i>Staphylococcus</i>	AY954955.1	45861	Siphoviridae (B1)	1
187	<i>Staphylococcus</i>	AY954950.1	39620	Siphoviridae (B2)	1
A006	<i>Listeria</i>	NC_009815.1	38124	Siphoviridae (B1)	2, 3
A9	<i>Brochothrix</i>	NC_015253.1	127065	Myoviridae	4, 5
A118	<i>Listeria</i>	NC_003216.1	40834	Siphoviridae (B1)	2, 3, 6
A500	<i>Listeria</i>	NC_009810.1	38867	Siphoviridae (B1)	2, 3
A511	<i>Listeria</i>	NC_009811.2	137619	Myoviridae	4, 7, 8
B025	<i>Listeria</i>	NC_009812.1	42653	Siphoviridae	2, 3
B054	<i>Listeria</i>	NC_009813.1	48172	Myoviridae	2, 3
BC-611	<i>Enterococcus</i>	NC_018086.1	53996	Siphoviridae	9
CaseusJM1	<i>Lactococcus</i>	KC522412.1	30692	Siphoviridae (B1)	10
Dp-1	<i>Streptococcus</i>	NC_015274.1	56506	Siphoviridae	11
EW	<i>Staphylococcus</i>	AY954959.1	45286	Siphoviridae <sup>ab</sup>	1
G	<i>Bacillus</i>	JN638751.1	497513	Myoviridae	37
G1	<i>Staphylococcus</i>	NC_007066.1	138715	Myoviridae	1
K	<i>Staphylococcus</i>	NC_005880.1	127395	Myoviridae	12
Lb338-1	<i>Lactobacillus</i>	NC_012530.1	142111	Myoviridae	5, 13
LP65	<i>Lactobacillus</i>	AY682195.1	131522	Myoviridae	5, 14
M102	<i>Streptococcus</i>	NC_012884.1	31147	Siphoviridae (B1)	15
P35	<i>Listeria</i>	NC_009814.1	35822	Siphoviridae (B1)	3
P40	<i>Listeria</i>	NC_011308.1	35638	Siphoviridae (B1)	3
P70	<i>Listeria</i>	NC_018831.1	67170	Siphoviridae (B3)	16
P100	<i>Listeria</i>	DQ004855.1	131384	Myoviridae	5, 17
Φ29	<i>Bacillus</i>	NC_011048.1	19282	Podoviridae (C2)	18, 19
Φ3626	<i>Clostridium</i>	NC_003524.1	33507	Siphoviridae (B1)	20
ΦAQ113	<i>Lactobacillus</i>	NC_019782.1	36566	Myoviridae (A1)	21
ΦCP24R	<i>Clostridium</i>	NC_019523.1	18919	Podoviridae (C1)	22
ΦCpV1	<i>Clostridium</i>	HM640230.1	16748	Podoviridae (C1)	23
phiD12	<i>Streptococcus</i>	KC581799.1	50470	Unclassified	24
ΦEf11	<i>Enterococcus</i>	NC_013696.1	42822	Siphoviridae (B1)	25, 26
ΦEF24C	<i>Enterococcus</i>	AP009390.1	142072	Myoviridae	4, 5, 27
ΦNJ2	<i>Streptococcus</i>	NC_019418.1	37282	Siphoviridae <sup>a</sup>	24, 28
P68	<i>Staphylococcus</i>	NC_004679.1	18227	Podoviridae (C1)	29
ΦPYB5	<i>Lactobacillus</i>	GU323708.1	32847	Siphoviridae (B1)	30, 31
PSA	<i>Listeria</i>	NC_003291.2	37618	Siphoviridae (B1)	3, 32
vB_SauM_Romulus	<i>Staphylococcus</i>	NC_020877.1	131332	Myoviridae	33
SAP6	<i>Enterococcus</i>	JF731128.1	58619	Siphoviridae	34
SPO1	<i>Bacillus</i>	FJ230960.1	132562	Myoviridae	5, 35
SPP1	<i>Bacillus</i>	X97918.2	44010	Siphoviridae	36
Twort	<i>Staphylococcus</i>	NC_007021.1	130706	Myoviridae	1, 5

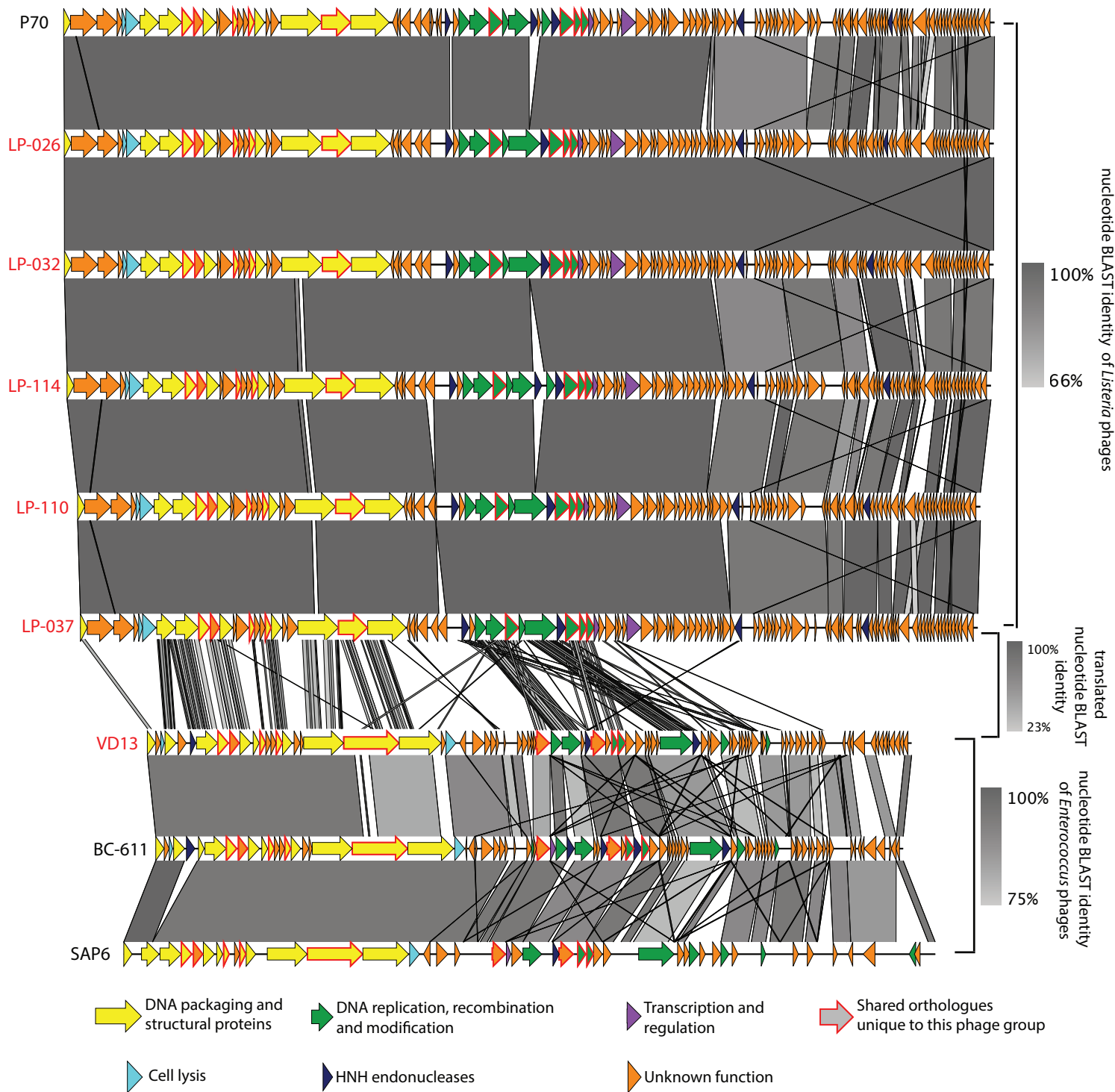
<sup>a</sup>Morphology as reported on NCBI. <sup>b</sup>Reference described phage as morphotype “A”; however, no micrograph or record of how this was determined could be found.



**Supplemental Figure 1.** Linear BLAST comparisons of orthocluster I *Listeria* phages. Predicted genes are indicated by arrows and are color coded by putative function. For LP-124, the original contig was reordered to move the terminal repeat sequences to the 5' end and to assure a 5' start for the genome comparison that is consistent with LP-064 (this required one single break of the original LP-124 contig; the GenBank accession for LP-124 represents the original, not re-ordered contig). The shade of gray drawn between genomes represents the level of nucleotide similarity (indicated on bottom right, darker is more similar). Phages in red text were sequenced in this study.



**Supplemental Figure 2.** Linear BLAST comparisons of orthocluster (A) II, (B) III, and (C) IV *Listeria* phages. Predicted genes are indicated by arrows and are color coded according to putative function. The shade of gray drawn between genomes represents the level of nucleotide similarity (indicated on right-hand side, darker is more similar). Phages in red text were sequenced in this study.



**Supplemental Figure 3.** Linear BLAST comparison of orthocluster V (LP-026, LP-032, LP-037, LP-110, and LP-114) and VI (VD13, SAP6, and BC-611) phages. Phages within orthoclusters are compared by average nucleotide identity. LP-037 and VD13 are compared by translated nucleotide identity. Predicted genes are indicated by arrows and are color coded by putative function. Bacteriophage genomes were reordered to start with the small terminase subunit. The shade of gray drawn between genomes represents the level of nucleotide or amino acid similarity (indicated on right-hand side, darker is more similar). Phages in red text were sequenced in this study.

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