Table 2 A: Peptide mass fingerprinting (MALDI-MS) of tryptic fragments Cps-L of A118

Fragment [aa]	MW (exp) [Da] [a]	MW (calc) [Da] [b]	Δ MW [%] [c]	Corresponding aa-sequence [d]
15-31	1769.91	1770.00	0.00	TGSIPINISEQIITGVK
69-78	1150.59	1150.65	0.00	IQTSKPTFTK
86-94	959.47	959.56	0.01	MGVIIPTTK
119-138	2356.08	2356.20	0.00	KFDQAVFTGVESPYNWNILK
120-138	2228.00	2228.10	0.00	FDQAVFTGVESPYNWNILK
139-153	1549.65	1549.73	0.01	SATDASNLVEETANK
154-178	2744.17	2744.36	0.01	YDDLNEAIGLIEAEDLEPNGIATIR
218-241	2823.16	2823.36	0.01	YTFGDKDISELVGDWNQAYYGILR
224-241	2111.94	2112.04	0.00	DISELVGDWNQAYYGILR
242-269	3033.30	3033.56	0.01	GVEYEILTEATLTTVADETGKPLNLAER
276-286	1227.59	1227.64	0.00	ATFEVGFMVVK
287-299	**1347.56**	**1347.69**	**0.01**	DEAFSAVQPKAG**K**
305-314	**1003.48**	**1003.54**	**0.01**	**SGKTDSAPIK**
308-325	**1951.90**	**1952.00**	**0.01**	**TDSAPIKDFSVMTVAELK**
332-340	**993.46**	**993.50**	**0.00**	**NIEFASNAK**
341-352	**1258.62**	**1258.69**	**0.01**	**KAELVALLEGSE**

Table 2 B: Peptide mass fingerprinting (MALDI-MS) of tryptic fragments of Tsh-L of A118

Fragment [aa]	MW (exp) [Da] [a]	MW (calc) [Da] [b]	Δ MW [%] [c]	Corresponding aa-sequence [d]
10-25	1692.05	1691.83	0.01	YSVAEIVAGAGEPDWK
30-55	2860.46	2860.13	0.01	WITNVSDDGSDNTEEQGDYDGDGNEK
56-73	2045.25	2044.96	0.01	TVVLGYSEAYTFEGTHDR
97-108	1286.87	1286.68	0.01	IEIPDTETAIGK
116-132	1599.91	1599.69	0.01	GSAGGGDATEFPAFGCR
133-161	**3128.91**	**3128.56**	**0.01**	IAYDETPTVTKP**EESPSSVEVGHNTITVK**
162-190	**2993.87**	**2993.51**	**0.01**	**VGETFTINASVLPVGASQEVTYTSSNPPK**
193-214	**2075.34**	**2075.06**	**0.01**	**INSVGTGEGVAEGTANITVASK**

a. Expected molecular weight determined from the observed molecular mass of the protonated ions.

b. Molecular weight of the corresponding fragment claculated from the deduced aa sequence.

c. Difference between the expected and the calculated molecular weights.

d. Amino acid residues resulting from the frameshift are indicated in bold letters

Table S3 A: Peptide mass fingerprinting (MALDI-MS) of tryptic fragments of Csp-L of A500

Fragment [aa]	MW (exp) [Da] [a]	MW (calc) [Da] [b]	Δ MW [%] [c]	Corresponding aa-sequence [d]
8-24	1799.05	1798.94	0.01	LANLIDPEVMGPMISAK
34-53	2065.28	2065.08	0.01	IAPIDNSLEGQPGSEITVPK
56-80	2615.48	2615.24	0.01	YIGDAQDVAEGAAIDYSALETESVK
92-110	2037.13	2036.97	0.01	LTDESVLSGYGDPVEEAQK
120-136	1903.13	1902.99	0.01	VDNDILEEALTTTLEVK
147-174	3117.75	3117.52	0.01	IENTFTDAPDAIEDESITTTGVLFLNYK
179-189	1247.71	1247.64	0.01	LREEAAGSWTK
190-200	1158.70	1158.64	0.01	ASQLGDDLLVK
201-213	1446.86	1446.77	0.01	GAFGELLGWEIVR
217-226	971.61	971.55	0.01	LADGNALAVK
237-244	859.52	859.46	0.01	NLLAESGR
284-304	**2269.09**	**2269.25**	**0.01**	**SVETDSAPIQDFSTMTVAELKEELVTR**

Table S3 B: Peptide mass fingerprinting (MALDI-MS) of tryptic fragments of Tsh-L of A500

Fragment [aa]	MW (exp) [Da] [a]	MW (calc) [Da] [b]	Δ MW [%] [c]	Corresponding aa-sequence [d]
11-26	1807.89	1807.93	0.00	YFVAEIVDGVGEPVWK
31-56	2859.99	2860.13	0.00	WITNVSDDGSDNTEEQGDYDGDGNEK
57-85	3255.33	3255.58	0.01	TVVLGYSEAYTFEGTHDREDEAQNLIVAK
98-109	1272.62	1272.67	0.00	IEIPDTETAVGK
117-133	1613.74	1613.70	0.00	GSAGGGDATEFPAFACR
134-141	936.43	936.47	0.00	IAYDETPK
142-162	**2269.13**	**2269.16**	**0.00**	VTKP**EESPSSVTVDHDTITVK**
163-191	**2965.32**	**2965.48**	**0.01**	**VGETFTINASVLPAGASQEVTYTSSNPPK**

a. Expected molecular weight determined from the observed molecular mass of the protonated ions.

b. Molecular weight of the corresponding fragment claculated from the deduced aa sequence.

c. Difference between the expected and the calculated molecular weights.

d. Amino acid residues resulting from the frameshift are indicated in bold letters

TABLE 4. General features and database matches of predicted proteins encoded by *Listeria monocytogenes* bacteriophage A006. Gene products annotated on the complementary strand are marked with an asterisk*. gp Gene product, pI isoelectric point, MW molecular weight.

ORF	**Start**	**Stop**	**GP** (pI)	**MW** (kDa)	**Protein similarities in the database**
gp1	28	768	9.3	27.7	*Listeria innocua* lin2395 terminase small subunit, *L. monocytogenes* F6854, H7858
gp2	761	2080	5.7	50.7	*L. innocua* lin2394 terminase large subunit, *L. monocytogenes* H7858, F6854
gp3	2095	3651	5.5	58.7	*L. monocytogenes* F6854, *L. innocua* lin2393, *L. monocytogenes* H7858
gp4	3656	4696	6.2	40.7	*L. innocua* lin2392 + *L. monocytogenes* H7858, F6854, Bacteriophage A118 gp4 putative minor capsid
gp5	4792	5346	4.6	21.0	*L. monocytogenes* F6854, H7858, *L. innocua* lin2391
gp6	5369	6241	5.4	32.2	*L. innocua* lin2390 major capsid, *L. monocytogenes* H7858, F6854
gp7	6255	6392	4.2	5.4	*L. monocytogenes* H7858 + F6854, *L. innocua* lin2389
gp8	6424	6777	4.2	12.7	*L. monocytogenes* F6854, *L. innocua* lin2388, H7858
gp9	6777	7142	4.4	13.6	*L. monocytogenes* H7858, *L. innocua* lin2387
gp10	7132	7449	10.0	12.0	*L. monocytogenes* F6854 LMOf6854_2667
gp11	7446	7817	5.7	14.1	*L. monocytogenes* H7858, F6854, *L. innocua* lin2386
gp12	7822	8508	4.4	23.5	*L. innocua* lin2385, *L. monocytogenes* H7858, F6854, Bacteriophage A118 gp13 major tail protein (Tsh)
gp13	8564	8995	4.3	16.1	*L. monocytogenes* H7858, *L. innocua* lin2384, F6854
gp14	9028	9303	10.1	10.7	*L. monocytogenes* F6854 LMOf6854_2662, *L. monocytogenes* H7858 LMOh7858_2424
gp15	9308	14107	9.7	174.1	*L. monocytogenes* H7858, M23/37, Bacteriophage L54a, *L. innocua* lin2383, *L. monocytogenes* F6854 putative Tape measure protein (Tmp)
gp16	14104	15672	5.2	58.5	*L. monocytogenes* F6854, *B. cereus* phage putative tail component
gp17	15685	17847	4.6	78.8	*L. monocytogenes* F6854 phage minor structural protein
gp18	17898	18203	9.2	11.5	*L. innocua* lin2376, *L. monocytogenes* F6854
gp19	18203	18484	10.2	10.5	*L. monocytogenes* F6854 holin, *L. innocua* lin2375, lin1295
gp20	18484	19191	10.1	25.7	*L. monocytogenes* F6854 phage lysin cply2438, *L. innocua*, A500 L-Alanoyl-D-glutamate-peptidase
gp21*	20020	19232	8.7	31	*L. monocytogenes* F6854 LMOf6854_2339
gp22*	20777	20280	10.2	19.3	*L. monocytogenes* EGDe lmo2276, F6854
gp23*	21251	20802	5.4	17.3	*L. monocytogenes* F6854 gp28, *L. monocytogenes* EGDe, *L. innocua*, Bacteriophage A118 gp28
gp24*	21503	21252	4.3	9.9	
gp25*	21768	21535	4.1	9.3	*L. monocytogenes* F6854 LMOf6854_2335
gp26	22067	22300	5.0	9.4	*L. innocua* lin2372, Bacteriophage PSA Gp22, *L. monocytogenes* EGDe lmo2271, *L. monocytogenes* H7858
gp27	22297	22500	6.6	7.9	*L. innocua* lin1302, Bacteriophage PSA Gp23, *L. monocytogenes* H7858
gp28*	23910	22780	9.4	43.6	*Genobacillus sp.* G11MC15 integrase, *Bacillus halodurans* integrase, Bacteriophage phig1e, *Enterococcus faecium*
gp29*	24483	23974	4.9	19.1	
gp30*	25001	24510	5.3	19.3	*L. monocytogenes* H7858 gp35, Bacteriophage A118 gp35, *L. innocua* lin0160, *L. monocytogenes* EGDe lmo0113, F2365
gp31*	25341	25033	4.6	12.1	*L. monocytogenes* H7858 transcriptional regulator, *L. innocua* lin2422, Bacteriophage A118 putative repressor protein
gp32	25490	25741	9.8	9.5	*L. innocua* lin2421, *L. monocytogenes* H7858 putative transcriptional regulator
gp33	25745	25981	4.4	8.8	*L. innocua* gp40, lin2420
gp34	25978	26331	4.7	13.2	*L. monocytogenes* EGDe lmo2326, *L. innocua* lin0078, *L. monocytogenes* H7858, F6854, Bacteriophage A118 gp41
gp35*	26851	26309	4.4	21.3	

gp36	26915	27688	10.0	29.3	*L. innocua* lin0080 anti-repressor homolog A118, lin2418, *Streptococcus pyogenes*, orf010 Bacteriophage 77
gp37	27810	28334	5.3	19.3	*L. innocua* lin0081, *L. monocytogenes* F6854, EGDe, H7858, Bacteriophage A118 gp43
gp38	28341	28577	6.8	9.3	*Bacillus halodurans*
gp39	28685	28873	5.7	7.2	*L. innocua* lin0083, Bacteriophage A118 gp45, *L. monocytogenes* H7858, *L. innocua* lin2415, *L. monocytogenes* EGDe lmo2321, F6854
gp40	28873	28962	9.5	3.4	Bacteriophage A118 gp46
gp41	29109	30068	6.3	36.7	*L. innocua* gp47, lin0084, *L. monocytogenes* H7858, F6854, Bacteriophage A118 gp47
gp42	30068	30883	5.1	30.7	*L. innocua* putative recombinase lin2413, *L. monocytogenes* F6854, Bacteriophage A118, lin0085, H7858
gp43	30903	31835	9.3	36.8	Bacteriophage A118 gp49, *L. innocua* lin2412, *L. monocytogenes* F6854 DnaD domain protein, EGDe lmo2317, F6854, lin0086
gp44	31832	32296	9.2	18.1	Bacteriophage A118 putative methyltransferase, *Enterococcus faecalis* V583, Bacteriophage phig1e
gp45	32293	32853	4.4	21.3	Bacteriophage A118 gp51, *L. innocua* lin0089, *L. monocytogenes* EGDe lmo2315, F6854, H7858, Bacteriophage PSA Gp35
gp46	32850	32996	4.2	5.5	Bacteriophage A118 gp52, *L. innocua*
gp47	33074	33475	4.5	15.7	Bacteriophage A118 gp54
gp48	33472	33681	4.0	8.1	Bacteriophage A118 gp55, *L. innocua* lin0094, *L. monocytogenes* F6854
gp49	33678	34076	9.5	15.1	Bacteriophage A118 gp56
gp50	34082	34192	4.6	4	Bacteriophage A118 gp57
gp51	34192	34284	7.3	3.3	Bacteriophage A118 gp58
gp52	34520	34921	5.7	15.2	Bacteriophage A118 gp59, *L. monocytogenes* H7858, F6854, *L. innocua* lin0095
gp53	34918	35400	5.1	17.8	Bacteriophage A118 putative SSB protein, *L. monocytogenes* EGDe lmo2398, H7858, F6854, *L. innocua* lin0079, lin2402
gp54	35432	35737	10.6	11.7	Bacteriophage A118 gp61, *L. monocytogenes* H7858 putative response regulator, *L. innocua* lmaD, EGDe lmo0115
gp55	35734	35874	5.0	5.6	Bacteriophage A118 gp62
gp56	35840	36244	8.4	15.5	Bacteriophage A118 gp63, *L. monocytogenes* H7858, *Lactobacillus plantarum* prophage LP2 protein 24
gp57	36237	36362	10.6	4.6	Bacteriophage A118 gp64
gp58	36373	36537	4.2	6.3	Bacteriophage A118 gp65, *L. monocytogenes* EGDe
gp59	36556	36990	9.0	17.1	Bacteriophage A118 gp66, *L. innocua*, *L. monocytogenes* EGDe, F6854 transcriptional regulator, *L. innocua* lin1739 + lin1259
gp60	37036	37185	6.1	5.6	Bacteriophage A118 gp67 (100% of n-terminal 25aa)
gp61	37172	37804	4.7	25	
gp62	37885	38112	5.7	8.4	*L. innocua* lin2396, *L. monocytogenes* H7858 + F6854

TABLE 5. General features and database matches of the predicted proteins encoded by *Listeria monocytogenes* bacteriophage A500. Gene products annotated on the complementary strand are marked with an asterisk*. gp Gene product, pI isoelectric point, MW molecular weight.

ORF	**Start**	**Stop**	**GP** (pI)	**MW** (kDa)	**Protein similarities in the database**
gp1	23	65	5.1	20.0	*Listeria innocua* lin0104 terminase small subunit, Bacteriophage A118
gp2	534	1865	5.7	51.4	*L. innocua* lin0105 terminase large subunit, *L. monocytogenes* EGDe lmo2300, Bacteriophage A118, *L. monocytogenes* F6854, phage IEBH
gp3	1878	3377	4.7	56.8	Bacteriophage A118 putative portal protein, *L. innocua* lin0106, *L. monocytogenes* F6854, EGDe lmo2299
gp4	3383	4522	9.6	43.1	Baceriophage A118 gp4, *L. innocua* lin0107, *L. monocytogenes* F6854, EGDe, Bacteriophage A118 minor capsid protein
gp5	4601	5200	4.5	21.8	*L. monocytogenes* F6854 putative scaffolding protein, Bacteriophage A118, *L. innocua* lin0108, *L. monocytogenes* EGDe lmo2297, phage BCJA1c
gp6	5223	6059	4.9	29.7	*L. monocytogenes* F6854, *Lactococcus lactis* phage TP901-1; *Streptococcus pyogenes* phage 315.4 putative major head protein
gp6*	5223	6213			Cps-L
gp7	6059	6217	4.2	5.6	*L. innocua* lin0110, *L. monocytogenes* F6854, Bacteriophage A118 gp7
gp8	6219	6614	5.5	14.6	*L. innocua* lin0111, Bacteriophage A118 gp8, *L. monocytogenes* F6854, EGDe
gp9	6614	6976	5.6	13.8	*L. innocua* lin0112, *L. monocytogenes* F6854, Bacteriophage A118 gp9, *L. monocytogenes* EGDe
gp10	6976	7314	9.8	12.7	*L. innocua* lin0113, *L. monocytogenes* EGDe, Bacteriophage A118 putative minor capsid, *L. monocytogenes* F6854
gp11	7314	7721	4.2	15.1	*L. innocua* lin0114, *L. monocytogenes* EGDe, F6854, Bacteriophage A118 gp11
gp12	7724	8161	4.6	15.9	*L. innocua* lin0115, *L. monocytogenes* F6854, EGDe, Bacteriophage A118 major tail protein (Tsh)
gp13	8184	8423	4.5	8.0	*L. monocytogenes* EGDe gp13, Bacteriophage A118 gp13, *L. monocytogenes* F6854
gp14	8476	8898	4.9	16.6	*L. innocua* lin0117, *L. monocytogenes* F6854, EGDe, Bacteriophage A118 gp14
gp15	8904	9506	4.2	23.2	*L. innocua* lin0118 *L. monocytogenes* F6854, EGDe, phage phiNIH1.1_40, Bacteriophage A118 gp15 putative tail protein
gp16	9517	14883	10.1	185.6	*L. innocua* lin0019, *L. monocytogenes* EGDe lmo2287, F6854, Bacteriophage A118 gp16 putative tape measure protein (Tmp)
gp17	14880	15707	6.8	31.7	*L. innocua* lin0120 gp17, *L. monocytogenes* EGDe, F6854, Bacteriophage A118 putative tail or base plate
gp18	15722	16744	5.2	40.0	*L. innocua* lin0121, Bacteriophage A118 gp18 putative tail or base plate, *L. monocytogenes* F6854, EGDe, F2365
gp19	16745	17770	4.7	37.3	*L. innocua* lin0122, lin2380, *L. monocytogenes* H7858, EGDe, F6854, Bacteriophage A118 gp19 putative tail or base plate
gp20	16767	18834	4.8	38.9	*L. innocua* lin0123, *L. monocytogenes* H7858, *L. innocua* lin2379, lin2565 Bacteriophage PSA Gp15, Bacteriophage A118 gp20 putative tail fiber
gp21	18831	19172	4.0	12.5	*L. innocua* lin0124, lin2378, lin2564; *L. monocytogenes* H7858 gp16, Bacteriophage PSA Gp16
gp22	19173	19319	9.1	5.6	*L. innocua* lin0125, Bacteriophage PSA Gp17, *L. innocua* lin2377
gp23	19356	19721	7.7	14.4	*L. monocytogenes* H7858 + *L. innocua* gp23, Bacteriophage A118 gp23, *L. monocytogenes* F6854 + EGDe
gp24	19725	20015	9.8	10.2	*L. innocua* holin, *L. monocytogenes* H7858, Bacteriophage A118 gp24, *L. monocytogenes* F6854, EGDe
gp25	20015	20884	9.8	33.4	*L. monocytogenes* H7858 L-Alanoyl-D-glutamate-peptidase, *L. innocua*, *L. monocytogenes* F6854 cply2438, *L. innocua* lin2563, lin2374, lin1700, Bacteriophage PSA , Bacteriophage A118 gp25

gp26	21378	21929	9.8	21.1	*L. monocytogenes* EGDe lmo2277
gp27	22516	23148	9.7	22.9	*L. monocytogenes* EGDe lmo0638
gp28	23171	23353	10.3	7.3	
gp29	23596	23829	5.4	9.4	*L. innocua* lin2372, Bacteriophage PSA Gp22, *L. monocytogenes* EGDe lmo2271, H7858
gp30	23826	24032	9.7	8.1	Bacteriophage PSA Gp23, *L. monocytogenes* H7858, *L. innocua* lin1302
gp31*	25483	24281	9.9	46.2	*L. innocua* lin0071 integrase, *L. monocytogenes* F6854 putative site specific recombinase
gp32*	26289	25549	4.4	27	Bacteriophage A118 gp32, *C. perfringens* SM101 CPR_0150
gp33*	26852	26424	4.6	16.2	*L. monocytogenes* EGDe lmo2329 putative repressor protein, F6854 transcriptional regulator; *L. innocua* lin0073, lin2422 , Bacteriophage A118 gp33
gp34	27015	27236	8.7	8.2	*Moorella theramoacetica* predicted transcriptional regulator, *Lactobacillus* phage phig1e repressor protein
gp35	27250	27477	9.6	8.4	*L. innocua* lin2420, Bacteriophage A118 gp40
gp36	27489	27773	4.2	10.9	*L. innocua* lin2411, lin2603
gp37	27786	28565	8.7	30	*L. monocytogenes* EGDe lmo2324 + F6854 anti-repressor, Bacteriophage A118 gp42; *L. monocytogenes* H7858
gp38	28689	29213	5.9	19.4	*L. innocua* lin0081, *L. monocytogenes* F6854, EGDe, H7858 gp43; Bacteriophage A118 gp43
gp39	29220	29405	10	6.9	*L. innocua* lin0082, *Verminephrobacter eiseniae* EF01-2 phage transcription regulator
gp40	29422	29511	9.5	3.3	Bacteriophage A118 gp46
gp41	29504	29632	3.7	5.1	
gp42	29727	29921	5.4	7.6	*L. monocytogenes* EGDe lmo2320
gp43	29918	30394	5.2	18.2	*L. monocytogenes* EGDe lmo2319, H7858, F6854; lmo2180 EGDe; *L. innocua* lin2284, Bacteriophage PSA Gp46
gp44	30400	31059	7.6	23.8	*L. monocytogenes* EGDe lmo2318; Bacteriophage ORF020, *Staphylococcus aureus* prophage phiPV83 orf 17 and phage EW ORF021
gp45	31076	32053	5.7	37.7	*L. monocytogenes* EGDe lmo2317, F6854 putative DnaD domain protein; Bacteriophage A118 gp49; *L. innocua* lin2412
gp46	32050	32217	9.5	6.4	*L. innocua* lin0087, *Streptococcus thermophilus* phage Sfi11 gp57
gp47	32223	32516	10.4	11.6	*L. monocytogenes* F6854 LMOf6854_2692, Bacteriophage PSA Gp33
gp48	32513	32722	9.9	8.1	*L. monocytogenes* F6854 LMOf6854_2691
gp49	32719	33327	4.7	23.3	*L. monocytogenes* H7858, F6854, EGDe lmo2315, Bacteriophage A118 gp51
gp50	33324	33692	5.9	14.2	
gp51	33689	33865	4.4	6.6	
gp52	33852	34313	4.9	17.3	*L. monocytogenes* EGDe lmo2313, F6854; *L. innocua* lin0090; Bacteriophage PSA Gp37
gp53	34310	34831	4.3	20.3	
gp54	34828	35268	4.7	17.2	*L. monocytogenes* EGDe lmo2312, F6854
gp55	35265	35465	5.4	7.5	
gp56	35465	35947	4.9	17.7	Bacteriophage A118 gp60 putative SSB protein; *L. monocytogenes* EGDe lmo2308, F6854; *L. innocua* lin0097, lin2402; *L. monocytogenes* H7858
gp57	35968	36159	4.2	7.1	*L. monocytogenes* F6854, *L. innocua* lin0098; *L. monocytogenes* EGDe lmo2307; *L. innocua* lin2401
gp58	36104	36508	10.2	15.9	*L. innocua* lin0099; *L. monocytogenes* F6854, EGDe lmo2306, *L. innocua* lin2400
gp59	36512	36895	9.6	15.5	*L. monocytogenes* EGDe lmo2305, *L. innocua* lin0100; *L. monocytogenes* F6854, *L. innocua* lin2399
gp60	36888	37013	10	4.6	Bacteriophage A118 gp64
gp61	37025	37189	4.3	6.3	*L. monocytogenes* EGDe lmo2304, Bacteriophage A118 gp65
gp62	37208	37642	9.3	16.9	*L. monocytogenes* EGDe lmo2303, F6854 transcriptional regulator, *L. innocua*, Bacteriophage A118 gp66
gp63	38006	38566	5.2	21.5	*Enterococcus faecalis* V583 EF0126

gp64	38663	38848	5.1	6.8	*L. innocua* lin1734, lin1265

TABLE 6. General features and database matches of the of predicted proteins encoded by *Listeria innocua* bacteriophage B025. Gene products annotated on the complementary strand are marked with an asterisk*. gp Gene product, pI isoelectric point, MW molecular weight.

ORF	**Start**	**Stop**	**GP** (pI)	**MW** (kDa)	**Protein similarities in the database**
gp1	62	361	5.4	11.5	*Streptococcus pyogenes* SSI-1, Bacteriophage 2638A
gp2	358	2001	5.2	63.4	*Staphylococcus aureus* terminase large subunit, phage phiNM3, phage 77, Bacteriophage PSA
gp3	2013	3143	4.8	43.6	Bacteriophage 77 ORF008, *S. aureus* JH1 and SAR2063, Bacteriophage PSA putative portal protein
gp4	3140	3889	4.9	27.5	*Clostridium tetani* E88 putative scaffold protein, Bacteriophage 77, *S. pyogenes* SSI-1, *S. agalactiae* ClpP protease
gp5	3916	5067	4.9	42.4	Bacteriophage 77 Orf006, *S. aureus* SAR2061, JH9 and JH1, Bacteriophage PSA Gp5major capsid
gp6	5074	5244	10.1	6.6	
gp7	5254	5553	4.4	11.5	Bacteriophage 77 ORF042; Bacteriophage 2638A ORF036; Bacteriophage PSA Gp6
gp8	5537	5902	6.2	13.9	Bacteriophage 77 ORF033; Bacteriophage 2638A ORF027
gp9	5899	6300	10.0	14.8	Bacteriophage 3A ORF028, Bacteriophage 47 ORF028, other *S. aureus* bacteriophages
gp10	6297	6680	4.8	14.7	Bacteriophage 3A ORF029, Bacteriophage 47 ORF029, Bacteriophage 3A ORF029
gp11	6702	7289	4.6	21.1	Bacteriophage 3A ORF017, *S. aureus* phi14 family major tail protein. *S. aureus* phage phiSLT major tail protein (Tsh)
gp12	7324	7692	4.8	14.6	Bacteriophage 47 ORF033, Bacteriophage 42e ORF041, *S. aureus* protein MW1391
gp13	7743	7892	4.8	5.9	
gp14	7908	12803	10.0	174.5	*Listeria innocua* lin1716, *Leuconostoc mesenteroides* COG5283, *Lactococcus lactis* prophage pi3 tail protein, Bacteriophage B054 gp18
gp15	12830	13660	6.5	31.7	Bacteriophage 47 ORF015, Bacteriophage 42e ORF014, *L. monocytogenes* EGDe gp17, F6854, *L. innocua* lin0169
gp16	13670	15262	6.4	60.1	Bacteriophage 47 ORF006, *S. aureus* SAS0946, Bacteriophage 42e + 3A ORF004, *L. monocytogenes* EGDe lmo0123
gp17	15262	15486	4.3	8.4	
gp18	15486	17405	5.4	71.1	*Bacillus licheniformes*, *S. aureus* SAS1841
gp19	17417	18691	4.6	47.0	Bacteriophage 37 ORF005; Bacteriophage EW ORF004; *L. monocytogenes* F2365 LMOf2365_0145
gp20	18708	18983	4.2	10.4	*L. monocytogenes* EGDe, F6854; Bacteriophage A118 gp21 putative short tail fiber, Bacteriophage B054 gp27
gp21	18989	19153	4.9	6.4	Bacteriophage A118 gp22, *L. monocytogenes* F6854, EGDe; *L. innocua* lin1292, lin1706 , Bacteriophage B054 gp28
gp22	19179	19634	9.6	17.3	Bacteriophage PSA Gp17-1 *L. innocua* lin1705, lin1293, Bacteriophage B054 gp29
gp23	19601	19996	5.9	14.9	Bacteriophage PSA Gp18, *L. innocua* lin1704, lin1294, Bacteriophage B054 gp30
gp24	20009	20257	9.7	9.4	*L. innocua* lin1295 holin, Bacteriophage Tuc2009, Bacteriophage PSA holin, Bacteriophage TP901-1 + P335 Holin, Bacteriophage B054 gp32
gp25	20257	21087	10.0	31.7	*L. monocytogenes* EGDe endolysin L-alanoyl-D-glutamate peptidase, Bacteriophage A118 gp25; *L. monocytogenes* F6854
gp26	21099	21533	9.7	16.0	*L. innocua* lin0129
gp27	21942	22445	4.5	19.8	
gp28	22442	22834	8.9	15.2	
gp29	22859	23017	10.2	5.8	
gp30	23023	23175	10.2	6.1	

gp31	23229	23463	11.0	6.3	
gp32	23531	23764	5.1	9.3	Bacteriophage PSA Gp22, *L. monocytogenes* H7858, EGDe lmo2271 *L. innocua* lin2372
gp33	23761	23952	10.0	7.7	Bacteriophage PSA Gp23, *L. monocytogenes* H7858, *L. innocua* lin1302
gp34*	25301	24147	9.8	44.6	Bacteriophage PSA integrase, *L. innocua* lin2610
gp35*	26050	25436	3.8	22.3	*L. lactis* prophage pi3; *L. innocua* lin1471; Bacteriophage PSA Gp25
gp36*	26553	26101	5.3	17.9	*L. innocua* lin2608, Bacteriophage PSA Gp26; *L. monocytogenes* F2365, EGDe lmo0113, F6854
gp37*	26890	26570	5.2	12.2	Phage PSA Gp27 repressor protein, *L. innocua* lin2607, *Enterococcus faecalis* transcriptional regulator, Phage phi3396 repressor
gp38	27157	27360	9.6	7.7	Bacteriophage PSA Gp28, *L. innocua* lin2605
gp39	27362	27604	9.5	9.6	Bacteriophage PSA Gp29; *L. innocua* lin2604
gp40	27607	27792	10.0	7.5	Bacteriophage PSA Gp30
gp41	28027	28179	4.8	5.5	Bacteriophage PSA Gp31
gp42	28316	29029	4.6	27.6	*L. innocua* lin2602, lin2410, *Streptococcus pyogenes* phage SSI-1
gp43	29040	29984	9.5	36.2	*L. innocua* integrase lin2409, lin2601, lin1743, lin1254, lin0524, Bacteriophage B054 gp64
gp44	29997	30677	9.7	27.0	*L. innocua* lin2600 lin1255, lin1742, lin2408, Bacteriophage B054 gp65
gp45	30674	31237	4.4	21.8	*L. monocytogenes* H7858, Bacteriophage A118 gp51; *L. monocytogenes* EGDe lmo2315, Bacteriophage PSA Gp35
gp46	31458	31859	4.5	15.7	Bacteriophage A118 gp54
gp47	31856	32065	4.0	8.1	Bacteriophage A118 gp55, *L. monocytogenes* F6854, *L. innocua* lin0094
gp48	32066	32395	4.0	12.5	
gp49	32392	32664	4.5	10.3	
gp50	32664	32843	9.2	6.8	*L. innocua* lin2403
gp51	32840	33379	4.4	20.1	*L. monocytogenes* F6854, EGDe lmo2312
gp52	33379	33813	4.7	16.9	Bacteriophage PSA Gp40
gp53	33810	34037	9.9	9.1	Bacteriophage PSA Gp41, *L. innocua*
gp54	34076	34249	9.6	6.6	Bacteriophage PSA Gp44, *L. innocua* lin2592
gp55	34246	34629	4.6	14.2	Bacteriophage PSA Gp45
gp56	34631	35110	5.7	18.3	*L. innocua* lin2591, Bacteriophage PSA Gp46; *L. monocytogenes* EGDe lmo2319, *L. innocua* lin2284, *L. monocytogenes* F2365
gp57	35123	35815	5.1	25.9	*S. pyogenes* SSI-1 COGO593, *S. suis* ATPase, *Lactococcus* phage phi31, *L. innocua* lin2590, Bacteriophage PSA Gp47
gp58	35993	37135	6.7	43.1	*L. innocua* lin2589 putative helicase, Bacteriophage PSA Gp48, *Lactococcus* phage phi31
gp59	37158	37640	5.8	18.3	*L. innocua* lin2588, Bacteriophage PSA Gp49, Phage 858 orf38
gp60	37663	39936	5.6	87.2	*L. innocua* lin2587, Bacteriophage PSA Gp50 primase, *L. casei* phage A2
gp61	40225	40539	9.3	11.7	*L. innocua* lin2586, Bacteriophage PSA Gp51; *S. pyogenes* SSI-1
gp62	40542	41180	8.7	25.5	*L. innocua* lin2585, Bacteriophage PSA Gp52
gp63	41185	41610	9.7	16.8	Bacteriophage PSA Gp53 transcriptional activator, *L. innocua* lin2583, *Geobacillus* virus E2 RinA transcription activator
gp64	42047	42250	8.6	7.9	
gp65	42295	42609	9.5	12.8	*S. aureus* phage phiN315, Bacteriophage 77 ORF040, Bacteriophage PSA Gp54; domain: restriction endonuclease

(n)… percent identity only to n-terminal 200aa
(c)… percent identity only to c-terminal 42aa

TABLE 7. General features and database matches of predicted proteins encoded by *Listeria innocua Myovirus* B054. Gene products annotated on the complementary strand are marked with an asterisk*. gp Gene product, pI isoelectric point, MW molecular weight.

ORF	**Start**	**Stop**	**GP** (pI)	**MW** (kDa)	**Protein similarities in the database**
gp1	26	910	9.7	33.5	*Listeria innocua* lin1733, lin1266; *L. monocytogenes* F6854 small terminase subunit, *B. pumilus* ATCC7061 TerS
gp2	888	2348	5.7	56.1	*L. innocua* lin1732; *Enterococcus faecalis* V583 large terminase subunit; Bacteriophage Aaphi23
gp3	2362	3747	5.2	52.3	*L. innocua* lin1731; *E. faecalis* V583
gp4	3740	5149	8.98	52.8	*L. innocua* lin1730; *E. faecalis* V583 minor head protein
gp5	5146	5316	6.8	6.8	*L. innocua* lin1729
gp6	5365	6474	5.6	40.5	*L. innocua* lin1728; *E. faecalis* V583 EF1461
gp7	6474	6923	4.6	15.9	*L. innocua* lin1727; *E. faecalis* V583 EF1462
gp8	6944	7849	5.6	33.0	*L. innocua* lin1726; *E. faecalis* V583 EF1463
gp9	7872	8258	4.6	14.5	*L. innocua* lin1725; *E. faecalis* V583 EF1464
gp10	8270	8605	5.4	12.3	*L. innocua* lin1724; *E. faecalis* V583 EF1465
gp11	8605	9204	9.6	22.5	*L. innocua* lin1723; *E. faecalis* V583 EF1466
gp12	9204	9578	4.9	14.1	*L. innocua* lin1722; *E. faecalis* V583 EF1467
gp13	9568	10056	4.5	18.0	*L. innocua* lin1721; *E. faecalis* V583 EF1468
gp14	10061	11056	5.2	36.3	*L. innocua* lin1720; *E. faecalis* V853 EF1469
gp15	11073	11471	5.6	14.2	*L. innocua* lin1719; *E. faecalis* V583 EF1470
gp16	11524	11880	5.9	13.4	*L. innocua* lin1718; *E. faecalis* V583 EF1471
gp17	11843	12055	5.1	8.1	*L. innocua* lin1717; *E. faecalis* V583 EF1472
gp18	12057	16772	9.6	168.0	*L.. innocua* lin1716; *E. faecalis* V583 EF1473; Bacteriophage phig1e minor capsid protein, Bacteriophage B025 gp14
gp19	16778	17341	10.3	21.4	*L. innocua* lin1715; *E. faecalis* V583 LysM domain protein
gp20	17341	17706	3.7	13.9	*L. innocua* lin1714; *E. faecalis* V583 EF1475
gp21	17706	18512	9	29.6	*L. innocua* lin1713; *E. faecalis* V583 EF1476
gp22	18513	18851	4.9	12.4	*L. innocua* lin1712; *E. faecalis* V583 EF1477
gp23	18848	19210	4.2	13.9	*L. innocua* lin1711; *E. faecalis* V583 EF1478, Virus PhiCh1
gp24	19203	20354	4.6	41.5	*L. innocua* lin1710; *E. faecalis* V583 EF1479; *Salmonella enterica* serovar *typhi*
gp25	20344	20985	5.3	23.1	*L. innocua* lin1709; *E. faecalis* V583 EF1480
gp26	21006	21734	5.3	26.5	*L. innocua* lin1708, lin1290
gp27	21740	22081	4.1	13.1	*L. innocua* lin1291, lin1707 , Bacteriophage B025 gp20
gp28	22113	22238	6.3	4.7	*L. innocua* lin1292, lin1706; Bacteriophage A118 gp22, *L. monocytogenes* EGDe + F6854, Bacteriophage B025 gp21
gp29	22268	22714	9.3	16.7	*L. innocua* lin1705, lin1293; Bacteriophage PSA GP17-1, Bacteriophage B025 gp22
gp30	22690	23136	5.8	17.0	*L. innocua* lin1294, lin1704; Bacteriophage PSA GP18, Bacteriophage B025 gp23
gp31	23155	23370	8.9	7.9	*L. innocua* lin1703
gp32	23381	23638	6.4	10.0	*L. innocua* holin homolog lin1295; Bacteriophage Tuc2009 holin; *Lactococcus lactis* subsp. *cremoris* COG5546, Bacteriophage B025 gp24
gp33	23638	24603	9.4	36.3	Bacteriophage PSA Ply protein; *L. innocua* lin2374, lin2563 N-Acetylmuramoyl-L-alanine amidase (n-terminal) + L-alanoyl-D-glutamate peptidase (c-terminal); *Clostridium tetani*
gp34*	24887	24666	6.8	8.6	*L. innocua* lin1297 (gp28 A118 homolog)
gp35*	25118	24915	4.4	7.9	*L. innocua* lin1298
gp36*	25506	25132	4.5	14.5	*L. innocua* lin1299
gp37*	25912	25646	10.4	10.6	
gp38*	27463	26288	9.5	45.8	*L. innocua* lin1765 integrase, *Streptococcus pyogenes* phage 315.5

gp39*	27952	27560	6.8	13.8	
gp40*	28419	28000	6.2	16.5	*L. innocua* lin1233; *Bacillus anthracis* prophage lambda ba01 putative repressor protein
gp41*	28864	28436	8	16.6	*L. innocua* lin1234, *Bacillus cereus* ZK putative transcription regulator
gp42	29025	29210	9.3	7.3	*L. innocua* lin1235 transcriptional regulator; *E. faecalis* V583, *L. monocytogenes* EGDe lmo2328
gp43	29287	29811	5.3	20.0	*L. innocua* lin1760, lin1236, Bacteriophage A118 gp43
gp44	29826	30119	5.9	11.7	*B. pumilus* ATCC 7061 gp44
gp45	30124	30288	4.9	6.1	*L. innocua* lin1238
gp46	30438	30728	5.3	11.2	*L. innocua* lin1759, lin1239
gp47	30906	31133	9.3	9.1	*L. innocua* lin1758
gp48	31151	31492	4.7	12.6	*L. innocua* lin1757, lin1240
gp49	31479	33422	5	74.4	*L. innocua* lin1756, lin1241; *Staphylococcus aureus* MSSA476
gp50	33423	34208	5	29.7	*L. innocua* lin1755, lin1242; *Streptococcus pyogenes* M1GAS
gp51	34168	34905	8.6	28.1	*L. innocua* lin1243, lin1754; *E. faecalis* V583 EF1433
gp52	34917	35834	5.7	35.3	*L. innocua* lin1244, lin1753; Bacteriophage bIL286 replication protein; *E. faecalis* V583 DnaD domain protein
gp53	35758	36573	6.3	31.3	*L. innocua* lin1752, lin1245; Bacteriophage 55 ORF016
gp54	36570	36764	5	7.6	
gp55	36751	36957	10.5	8.2	*L. innocua* lin1751, lin1246
gp56	36958	37167	6.8	8.3	*L. innocua* lin1750, lin1247
gp57	37148	37585	9.8	16.7	*L. innocua* lin1749, lin1248; Bacteriophage LLH ORF139; *Pediococcus pentosaceus* holliday junction resolvase
gp58	37606	38226	4.2	23.8	*L. innocua* lin1748, lin1249; *E. faecalis* V583 EF2835
gp59	38267	38647	7.9	15.1	*L. innocua* lin1250, lin1747
gp60	38607	38783	5	6.9	*L. innocua* lin1251, lin1746
gp61	38795	39217	9.1	15.9	*L. innocua* lin1252, lin1745; *S. pyogenes* phage 315.3; *E. faecalis* V583
gp62	39214	40575	9.5	53.5	*L. innocua* lin1253, lin1744; *S. pyogenes* phage 315.3; *E. faecalis* V583
gp63	40588	40812	7.8	9.2	
gp64	40812	41756	8.8	36.2	*L. innocua* lin1254, lin1743, lin2409, lin2609; *Lactobacillus delbrueckii* integrase; *L. innocua* lin0524, Bacteriophage B025 gp43
gp65	41769	42449	9.6	26.9	*L. innocua* lin1255, lin1742, lin2600, lin2408; Bacteriophage EJ-1 transcriptional regulator, Bacteriophage B025 gp44
gp66	42446	42739	4.8	11.8	*L. innocua* lin1256, lin2597
gp67	42757	42897	4.0	5.4	
gp68	42884	43036	10.3	6.0	*Bacillus clausii* KSM-K16 ABC1364
gp69	43033	43284	5.4	10.1	*L. innocua* lin1741; *E. faecalis* V583 EF0509
gp70	43296	43856	9.1	21.6	*L. innocua* lin1740, lin1258
gp71	43937	44359	9.2	16.6	*L. innocua* lin1739, lin1259; *L. monocytogenes* EGDe and F6854 transcriptional regulator; Bacteriophage A118 gp66
gp72	44372	45139	7.2	29.3	*L. innocua* putative antirepressor lin1738, lin1260
gp73	45087	45257	10.6	7.0	
gp74	45270	45386	9.7	4.6	
gp75	45576	45710	8.4	5.5	
gp76	45667	45960	9.4	11.6	
gp77	45957	47294	4.9	51.1	*L. innocua* lin1737, lin1262; *Ralstonia eutropha* COG0863
gp78	47342	47539	10.1	7.8	*L. innocua* lin1736, lin1263
gp79	47670	47900	5	9.1	*L. innocua* lin1735, lin1264; *E. faecalis* V583 EF1453
gp80	47928	48152	4.2	8.7	*L. innocua* lin1734, lin1265

TABLE 8. General features and database matches of predicted proteins encoded by *Listeria monocytogenes* bacteriophage P35. gp Gene product, pI isoelectric point, MW molecular weight.

ORF	**Start**	**Stop**	**GP** (pI)	**MW** (kDa)	**Protein similarities in the database**
gp1	29	649	5.4	23.5	Bacteriophage P40 gp1
gp2	637	1959	5.3	50.7	*Bacillus subtilis* phage SPP1 terminase large subunit, *Clostridium thermocellum* COG1783, Bacteriophage P40 gp2
gp3	2008	3621	4.3	60.4	*Enterococcus faecalis* V583 portal protein, Bacteriophage phiETA, *C. novyi* NT SPP1 gp6-like protein, Bacteriophage P40 gp3
gp4	3872	4780	8.1	34.7	*E. faecalis* V583 minor head protein, *Staphylococcus* phage EW ORF012, Bacteriophage P40 gp4
gp5	4918	5499	4.6	21.6	*E. faecalis* V583 scaffold protein, Bacteriophage P40 gp5
gp6	5543	6451	4.9	32.9	*Listeria monocytogenes* H7858 Gp34 main capsid, *L. innocua* lin2390, *C. thermocellum* DSM4150 phage major capsid protein, Bacteriophage P40 gp6
gp7	6518	7054	4.1	20.4	*E. faecalis* V583 protein EF0341, Bacteriophage P40 gp7
gp8	7054	7407	5.6	13.1	*E. faecalis* V583 protein EF0342, Bacteriophage P40 gp8
gp9	7409	7834	9.5	16.1	*E. faecalis* V583 protein EF0343, *C. perfringens* phage protein HK97 gp10 family, Bacteriophage P40 gp9
gp10	7834	8298	4.5	18.2	*E. faecalis* V583 protein EF0344, Bacteriophage P40 gp10
gp11	8299	9279	4.3	35	*E. faecalis* V583 protein EF0345, *C. acetobutylicum* CAC0057, Bacteriophage P40 gp11
gp12	9363	9821	5.6	17.4	Bacteriophage P40 gp12
gp13	9875	10147	4.5	10.3	*E. faecalis* V583 peptide methionine sulfoxid reductase, Bacteriophage P40 gp13
gp14	10153	12039	10	67.9	*E. faecalis* V583 tail protein, *C. thermocellum* tail protein, Bacteriophage P40 gp14
gp15	12036	13295	4.1	46.5	Bacteriophage fOg44 hypothetical protein, Bacteriophage P40 gp15
gp16	13288	14451	8.7	43.7	*Leuconostoc mesenteroides* Lmes02000557, Bacteriophage fOg44 hypothetical protein, Bacteriophage P40 gp16
gp17	14459	15295	9.4	30.6	*Leuconostoc mesenteroides* Lmes02000556, Bacteriophage fOg44 hypothetical protein, Bacteriophage P40 gp17
gp18	15427	15876	5.9	16.6	*Streptococcus* phage Cp-1 holin protein, *C. thermocellum* holin, Bacteriophage P40 gp18
gp19	16299	16544	7.1	9.5	Bacteriophage P40 gp20
gp20	16660	16905	8.6	9.7	
gp21	16905	17117	4.6	8.5	
gp22	17119	17448	9.9	12.3	
gp23	17448	18221	4.5	28.3	
gp24	18218	18460	6.1	9.2	
gp25	18444	19067	8.5	24.1	Vibriophage VpV262 HNH DNase, Mimivirus endonuclease
gp26	19103	19261	10.2	6	
gp27	19272	19433	9.2	6.3	
gp28	19450	20325	10.2	33.1	*L. innocua* phage lysin, Bacteriophage A500 L-alanoyl-D-glutamate peptidase
gp29	20439	20834	4.8	15.8	
gp30	20884	21456	6	22.3	Bacteriophage P40 gp28
gp31	21497	22243	5.1	28.9	*Lactobacillus johnsonii* prophage Lj965 protein Ljo0298, Bacteriophage P40 gp29
gp32	22263	22958	4.9	27	Bacteriophage P40 gp30
gp33	23285	25192	6.9	73.3	*C. thermocellum* DNA polymerase elongation subunit, *C. botulinum* DNA polymerase, Bacteriophage P40 gp31
gp34	25205	27109	5.5	72.5	*C. thermocellum* ATPase, *Streptococcus thermophilus* DNA primase,

					Bacteriophage P40 gp32
gp35	27102	27341	9.5	9	
gp36	27437	27652	5	8.1	
gp37	27649	28203	5.4	21.5	
gp38	28203	28787	9.1	22.6	*Listeria innocua* lin2585, Cyanophage Syn5 gp31, Bacteriophage P40 gp35
gp39	28784	29215	7.8	16.9	
gp40	29290	29490	5.2	7.6	
gp41	29487	29957	7.6	17.6	(LP65 orf143 HNH homing endonuclease), Bacteriophage P40 gp41
gp42	29957	30172	5	8.2	
gp43	30183	30644	4.8	17.7	
gp44	30647	31012	6.2	14.4	
gp45	31005	31319	4.7	11.8	*Staphylococcus aureus* Phage K ORF17, *Enterococcus hirae* ArpR
gp46	31316	31624	4.6	11.5	
gp47	31617	31799	4	7.1	
gp48	31908	32012	7.6	3.8	
gp49	32009	32320	6.2	11.9	
gp50	32298	32465	10.2	6.7	
gp51	32449	33357	6.9	34.8	
gp52	33357	33548	8.6	7.5	
gp53	33550	34179	5.2	25	
gp54	34270	34674	5.5	15.5	
gp55	34677	35090	9.5	16.2	
gp56	35063	35326	4.7	10.3	

* identity to only c-terminal 73 amino acids of LP65 orf143

TABLE 9. General features and database matches of predicted proteins encoded by *Listeria monocytogenes* bacteriophage P40. gp Gene product, pI isoelectric point, MW molecular weight.

ORF	**Start**	**Stop**	**GP** (pI)	**MW** (kDa)	**Protein similarities in the database**
gp 1	62	781	4.7	28.9	Bacteriophage P35 gp1
gp 2	781	2073	6.0	49.7	*Clostridium thermocellum* ATCC 27405 phage terminase large subunit, Bacteriophage P35 gp2
gp 3	2322	3914	4.4	60.3	*Enterococcus faecalis* V583 portal protein, C. novyi NT portal protein, Bacteriophage P35 gp3
gp 4	3930	4841	8.7	34.7	*E. faecalis* V583 and *C. perfringens* JGS1495 minor head protein, Bacteriophage P35 gp4
gp 5	4969	5556	4.6	22.0	*C. novyi* NT scaffold protein, Bacteriophage P35 gp5
gp 6	5582	6475	5.0	32.3	*C. thermocellum* ATCC 27405 Lj928 prophage protein, *Listeria monocytogenes* str. 4b H7858 main capsid protein Gp34, Bacteriophage P35 gp6
gp 7	6543	7079	4.3	20.4	*E. faecalis* V583 protein EF0341, Bacteriophage P35 gp7
gp 8	7072	7419	5.5	13.3	*E. faecalis* V583 protein EF0342, Bacteriophage P35 gp8
gp 9	7394	7858	8.6	17.6	*E. faecalis* V583 conserved hypothetical protein TIGR01725, *C. perfringens* JGS1495 HK97 gp10 family protein, Bacteriophage P35 gp9
gp 10	7855	8322	4.9	18.3	Bacteriophage P35 gp10
gp 11	8323	9285	4.5	34.7	*E. faecalis* V583 protein EF0345, *C. acetobutylicum* ATCC 824 hypothetical protein CAC0057, Bacteriophage P35 gp11
gp 12	9371	9808	5.2	16.1	Bacteriophage P35 gp12
gp 13	9862	10125	4.7	10.2	*E. faecalis* V583 peptide methionine sulfoxide reductase, Bacteriophage P35 gp13
gp 14	10160	12046	9.6	67.7	*Streptococcus pneumoniae* SP3-BS71 unknown phage protein, *E. faecalis* V583 tail protein, *L. casei* BL23 tail tape measure protein, Bacteriophage P35 gp14
gp 15	12046	13332	4.3	47.5	*Oenococcus oeni* bacteriophage fOg44 hypothetical protein*, Bacteriophage P35 gp15
gp 16	13325	14470	7.2	43.5	*Oenococcus oeni* bacteriophage fOg44 hypothetical protein, Bacteriophage P35 gp16
gp 17	14486	15325	8.9	30.2	*Oenococcus oeni* bacteriophage fOg44 hypothetical protein*, Bacteriophage P35 gp17
gp 18	15487	15942	7.0	16.8	*Streptococcus* phage Cp-1 holin protein, Bacteriophage P35 gp18
gp 19	15947	16096	9.9	5.7	
gp 20	16305	16589	4.9	11.1	Bacteriophage P35 gp19
gp 21	16780	16968	8.2	7.7	
gp 22	16937	17314	9.9	14.4	
gp 23	17317	17457	6.2	5.3	
gp 24	17764	17916	10.1	5.9	
gp 25	17927	18082	9.6	6.0	
gp 26	18076	19110	9.7	38.4	*Bacillus licheniformis* ATCC 14580 glycoside hydrolase family 25, *B. thuringiensis* serovar *israelensis* ATCC 35646 N-acetylmuramoyl-L-alanine amidase, *B. cereus* NVH0597-99 endolysin
gp 27	19265	19627	9.3	14.3	
gp 28	19633	20256	6.6	24.2	*C. thermocellum* ATCC 27405 beta-lactamase-like protein, Bacteriophage P35 gp30
gp 29	20268	21017	5.5	28.9	*Lactobacillus johnsonii* prophage Lj965 protein Ljo0298, Bacteriophage P35 gp31
gp 30	21038	21742	5.1	36.8	Bacteriophage P35 gp32
gp 31	21827	23833	6.5	76.9	*Fusobacterium nucleatum* subsp. *polymorphum* ATCC 10953 possible DNA-directed DNA polymerase II, *C. thermocellum* ATCC 27405 phage

					DNA polymerase, Bacteriophage P35 gp33
gp 32	23846	25753	6.2	72.8	*Fusobacterium nucleatum* subsp. *polymorphum* ATCC 10953 ATP-binding protein, *C. thermocellum* ATCC 27405 DNA primase, Bacteriophage P35 gp34
gp 33	25754	25999	6.8	9.6	
gp 34	25983	26411	4.9	16.6	
gp 35	26526	27065	7.9	20.9	Bacteriophage P35 gp37
gp 36	27062	27247	8.3	7.4	
gp 37	27244	27447	9.2	8.7	
gp 38	27444	28220	5.7	29.4	*Listeria* bacteriophage P100 gp124**, Cyanophage Syn5 gp31
gp 39	28233	28673	5.1	17.0	
gp 40	28663	28857	4.6	7.3	
gp 41	28854	29384	6.0	20.5	LP65 orf143 HNH homing endonuclease***, Bacteriophage P35 gp41
gp 42	29374	29925	5.5	21.8	*L. monocytogenes* str. 4b H7858 protein gp51, A118 gp51
gp 43	29926	30135	6.1	8.0	
gp 44	30136	30540	5.8	15.6	
gp 45	30537	30707	4.5	6.8	
gp 46	30685	30843	9.6	6.3	
gp 47	30869	31150	4.7	11.3	
gp 48	31175	31447	5.1	10.4	
gp 49	31611	31886	4.4	10.9	
gp 50	31893	32024	9.8	5.4	
gp 51	32027	32227	6.1	7.4	
gp 52	32227	32376	10.0	5.8	
gp 53	32373	32588	8.7	8.3	
gp 54	32578	32829	4.4	9.7	
gp 55	32819	33103	5.0	11.2	
gp 56	33075	33371	5.8	11.6	
gp 57	33368	33652	7.0	10.9	
gp 58	33770	34501	9.5	29.6	
gp 59	34520	34702	4.7	7.2	
gp 60	34702	34896	6.8	9.3	
gp 61	34889	35059	4.5	6.7	
gp 62	35366	35524	10.0	6.1	

* identities only in the first 152 n-terminal amino acids of P40 gp 17
** identities only in a 62 c-terminal amino acids region of P40 gp 38
*** identities only in a 42 c-terminal amino acids region of P40 gp 41