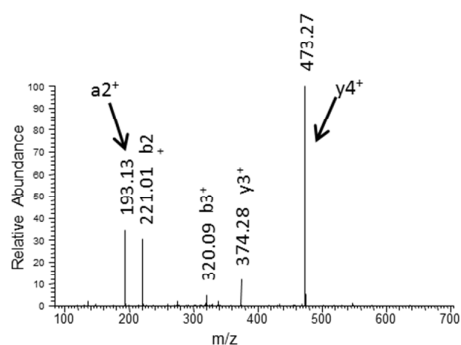


SUPPORTING INFORMATION

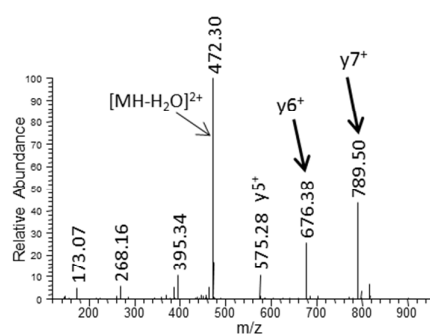
Figure S-1. Selection of monitored transitions for the SRM-based method for phage T4.

Precursor ions (a) GYVNIK ($m/z=347.2$, SOC protein), (b) AAYSTVYEENQR ($m/z=716.1$, SOC protein), (c) ATLSEVIK ($m/z=481.4$, IPI* protein) and (d) GTVYLGDGWSAK ($m/z=327.5$, IPI* protein) were submitted to CID (35%). Two product ions (shown by an arrow) among intense signal in CID spectra were selected for implementation of the SRM method.

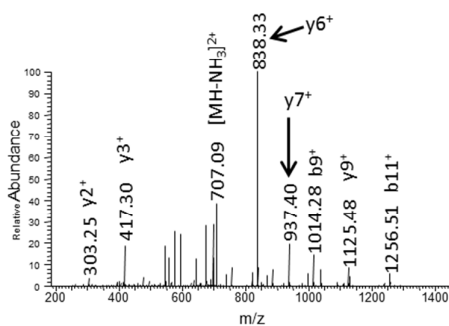
a)GYVNIK: monoisotopic precursor ion 347.2 (+2)



c)ATLSEVIK: monoisotopic precursor ion 481.3 (+2)



b)AAYSTVYEENQR: monoisotopic precursor ion 715.8 (+2)



d)GTVYLGDGWSAK: monoisotopic precursor ion 627.3 (+2)

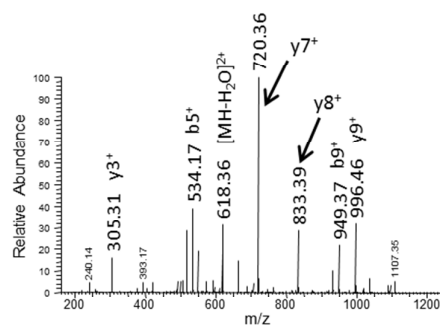
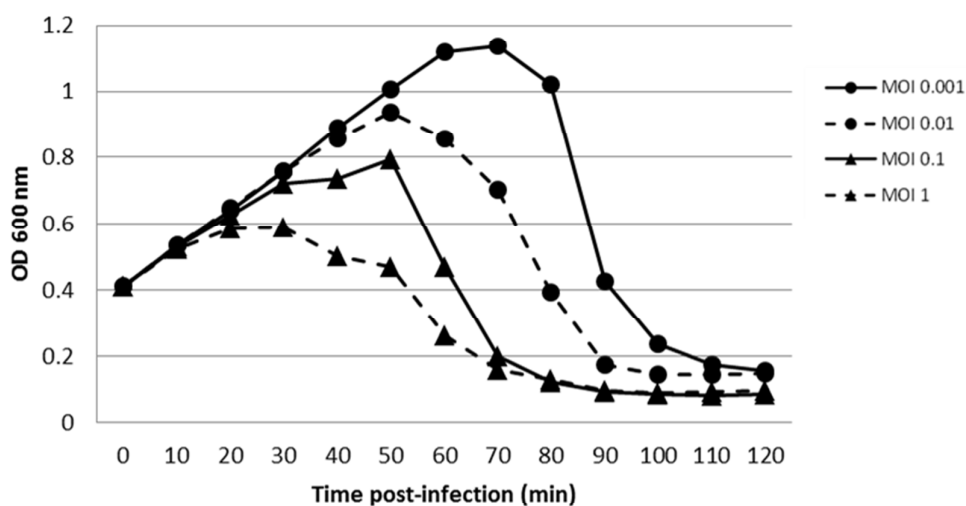


Figure S-2. Impact of the multiplicity of infection (MOI, ratio of phages to bacteria) on lysis curves for *E. coli* infected by T4 and *B. subtilis* infected by phage SSP1.

Optical density ($\lambda=600\text{nm}$) measurements were made to monitor lysis curves of (a) 10^8 CFU/mL of *E. coli* and (b) 10^8 cfu/mL of *B. subtilis* infected by phage T4 and SPP1, respectively, at MOIs of 0.001 (circles and full lines), 0.01 (circles and dotted lines), 0.1 (triangle and full lines) and 1 (triangle and dotted lines). The y-axis is centered on the starting point of infection.

a) *E. coli* (10^8 CFU/mL) lysis upon T4 infection



b) *B. subtilis* (10^8 CFU/mL) lysis upon SPP1 infection

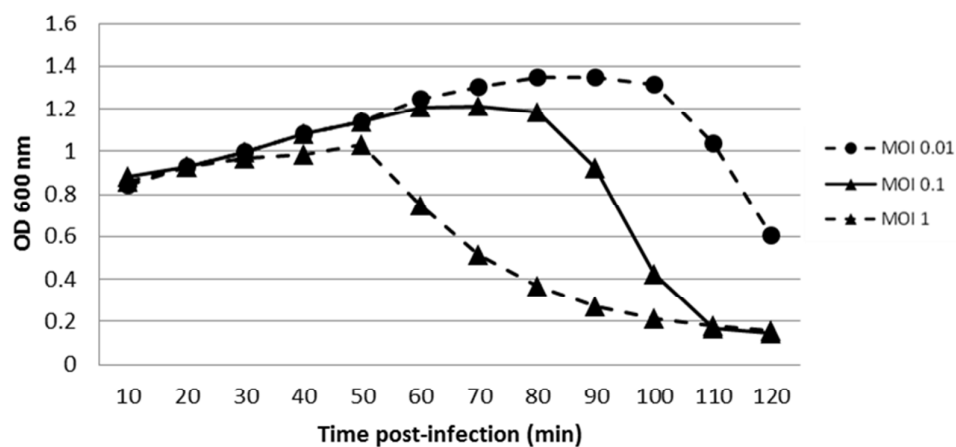


Table S-1. Proteins identified using bottom-up analysis of trypsin digests of T4-infected *E. coli* after 25 min of infection (37°C, rich medium and aeration). The dataset was compared with a database of T4 proteins using the Mascot algorithm. Results are presented according to the UniProt accession number of the identified protein, presence in T4 viral particles (structural=S, displayed in green; non-structural=NS, displayed in black), copy number in viral particles or in proheads (for the scaffolding protein gp22) when known, molecular mass, Mascot score, number of identified peptides (#Peptides), and sequence coverage of protein (SC).

Row	Accession	Protein	Family [S/NS]	Copy number	MW [kDa]	Scores	#Peptides	SC [%]
1	P04535	Major capsid protein OS=Enterobacteria phage T4 GN=23 PE=1 SV=2	S	960	56	1373.4	21	48.4
2	P03695	Single-stranded DNA-binding protein OS=Enterobacteria phage T4 GN=32 PE=1 SV=1	NS	nd	33.5	939.9	12	63.8
3	P19896	Head vertex protein Gp24 OS=Enterobacteria phage T4 GN=24 PE=1 SV=2	S	55	47	866.8	12	38.4
4	P12726	NAD--protein ADP-ribosyltransferase OS=Enterobacteria phage T4 GN=alt PE=4 SV=2	S	40	75.8	838.4	13	30.9
5	P13332	Tail sheath protein Gp18 OS=Enterobacteria phage T4 GN=18 PE=1 SV=5	S	144	71.3	823.7	13	31.6
6	P04529	Recombination and repair protein OS=Enterobacteria phage T4 GN=UVSX PE=1 SV=2	NS	nd	44	585.4	6	28.4
7	P13302	Internal protein III OS=Enterobacteria phage T4 GN=ipi3 PE=1 SV=1	S	~370	21.7	559.2	7	39.4
8	P04519	DNA alpha-glucosyltransferase OS=Enterobacteria phage T4 GN=agt PE=1 SV=1	NS	nd	46.7	520.4	11	39.2
9	P04547	DNA beta-glucosyltransferase OS=Enterobacteria phage T4 GN=bgt PE=1 SV=1	NS	nd	40.6	430.5	5	22.2
10	P03719	Internal protein II OS=Enterobacteria phage T4 GN=ipi2 PE=1 SV=2	S	~360	11.1	419.4	7	70
11	Q01437	Transcription regulatory protein motB OS=Enterobacteria phage T4 GN=motB PE=4 SV=1	NS	nd	18.2	396.3	5	35.2
12	P11156	Ribonucleoside-diphosphate reductase subunit beta OS=Enterobacteria phage T4 GN=NRDB PE=3 SV=2	NS	nd	45.3	385.8	5	17
13	P13316	Autonomous glycy radical cofactor OS=Enterobacteria phage T4 GN=grcA PE=3 SV=1	NS	nd	13.8	357.7	6	52.5
14	P39224	Uncharacterized 22.0 kDa protein in e-segB intergenic region OS=Enterobacteria phage T4 GN=y06Q PE=4 SV=1	NS	nd	22	356.7	4	34
15	P00971	RNA ligase OS=Enterobacteria phage T4 GN=63 PE=1 SV=1	NS	nd	43.5	320.2	6	20.6
16	P03718	Internal protein I OS=Enterobacteria phage T4 GN=ipi1 PE=1 SV=1	S	~360	10.2	282.9	4	51.6
17	P18058	Protein inh OS=Enterobacteria phage T4 GN=inh PE=4 SV=2	NS	nd	25.6	266.9	4	37.2
18	P03744	Long tail fiber protein p37 OS=Enterobacteria phage T4 GN=37 PE=1 SV=1	S	18	109.2	259.8	2	4.3
19	P32277	RNA ligase 2 OS=Enterobacteria phage T4 GN=Y10A PE=1 SV=1	NS	nd	37.6	258.5	4	19.8
20	P03715	Small outer capsid protein OS=Enterobacteria phage T4 GN=soc PE=1 SV=1	S	870	9.1	233.1	3	47.5
21	P04534	Major prohead-scaffolding core protein Gp22 OS=Enterobacteria phage T4 GN=22 PE=1 SV=2	NS	576*/115	29.9	215.6	3	18.6
22	P32282	Ribonucleoside-diphosphate reductase subunit alpha OS=Enterobacteria phage T4 GN=NRDA PE=3 SV=1	NS	nd	85.9	213.7	3	4.9
23	P69702	Translation repressor protein OS=Enterobacteria phage T4 GN=regA PE=1 SV=1	NS	nd	14.6	211.8	3	27.9
24	P13320	Double-stranded DNA-binding protein OS=Enterobacteria phage T4 GN=dsbA PE=1 SV=1	NS	nd	10.4	208.6	2	32.6
25	P17308	Uncharacterized 11.5 kDa protein in Gp31-cd intergenic region OS=Enterobacteria phage T4 GN=y13B PE=4 SV=1	NS	nd	11.5	207	4	39.2
26	P17309	Protein rIII OS=Enterobacteria phage T4 GN=rIII PE=1 SV=2	NS	nd	9.3	199.8	4	32.9
27	Q01438	Protein comC-alpha OS=Enterobacteria phage T4 GN=comCA PE=4 SV=1	NS	nd	16.7	198.6	3	29.1
28	P00471	Thymidylate synthase OS=Enterobacteria phage T4 GN=TD PE=1 SV=1	NS	3	33.1	195.9	3	15.7
29	P18056	Highly immunogenic outer capsid protein OS=Enterobacteria phage T4 GN=hoc PE=4 SV=1	S	155	40.4	195.7	3	10.4
30	P13333	Tail tube protein Gp19 OS=Enterobacteria phage T4 GN=19 PE=1 SV=1	S	144	18.5	148.8	3	22.7
31	P17313	Capsid assembly protein Gp31 OS=Enterobacteria phage T4 GN=31 PE=1 SV=1	NS	nd	12.1	144.4	2	59.5
32	P07879	15 kDa RNA polymerase-binding protein OS=Enterobacteria phage T4 GN=rpBA PE=1 SV=2	NS	nd	14.7	135.6	2	20.9
33	P13326	Uncharacterized 12.4 kDa protein in mobB-Gp55 intergenic region OS=Enterobacteria phage T4 GN=y03H PE=4 SV=1	NS	nd	12.4	132.2	3	41.9
34	sp P04525	DNA polymerase processivity component OS=Enterobacteria phage T4 GN=45 PE=1 SV=3	NS	nd	24.8	116	2	17.5
35	sp P09176	DNA topoisomerase large subunit OS=Enterobacteria phage T4 GN=39 PE=1 SV=2	NS	nd	57.9	115.4	1	3.1
36	sp P07082	Uncharacterized 12.7 kDa protein in Gp55-nrdG intergenic region OS=Enterobacteria phage T4 GN=y04B PE=4 SV=1	NS	nd	12.7	114	1	13

Table S-1. Continuation

37	sp P39255	Uncharacterized 39.0 kDa protein in nrdC-mobD intergenic region OS=Enterobacteria phage T4 GN=y04P PE=4 SV=	NS	nd	39	112	1	9
38	sp P13334	Structural protein of head OS=Enterobacteria phage T4 GN=20 PE=4 SV=2	S	12	61	109.2	2	5.5
39	sp P39256	Uncharacterized 39.7 kDa protein in nrdC-mobD intergenic region OS=Enterobacteria phage T4 GN=y05A PE=4 SV=	NS	nd	39.6	106.1	2	5
40	sp P39415	Uncharacterized 13.8 kDa protein in motB-dexA intergenic region OS=Enterobacteria phage T4 GN=y00E PE=4 SV=	NS	nd	13.8	104.8	1	24.4
41	sp P32267	10 kDa anti-sigma factor OS=Enterobacteria phage T4 GN=asiA PE=1 SV=1	NS	nd	10.6	100.8	1	16.7
42	sp P07065	DNA topoisomerase medium subunit OS=Enterobacteria phage T4 GN=52 PE=3 SV=2	NS	nd	50.5	98.4	1	2.7
43	sp P04537	Recombination protein uvsY OS=Enterobacteria phage T4 GN=uvsY PE=4 SV=3	NS	nd	15.8	94.3	1	16.8
44	sp P39262	dCTP pyrophosphatase OS=Enterobacteria phage T4 GN=56 PE=4 SV=1	NS	nd	20.4	90.2	2	18.7
45	sp P08773	Deoxycytidylate 5-hydroxymethyltransferase OS=Enterobacteria phage T4 GN=42 PE=1 SV=1	NS	nd	28.5	85	1	4.9
46	sp P06855	Polynucleotide kinase OS=Enterobacteria phage T4 GN=pseT PE=1 SV=1	NS	nd	34.6	82.2	1	4
47	sp P04531	Deoxynucleotide monophosphate kinase OS=Enterobacteria phage T4 GN=1 PE=1 SV=1	NS	nd	27.3	79.3	1	7.1
48	sp P39242	Uncharacterized 38.9 kDa protein in nrdC-mobD intergenic region OS=Enterobacteria phage T4 GN=y05G PE=4 SV=	NS	nd	38.9	76.1	1	6.5
49	sp P13314	Uncharacterized 10.2 kDa protein in regB-denV intergenic region OS=Enterobacteria phage T4 GN=y06G PE=4 SV=	NS	nd	10.2	72.1	1	29.5
50	sp Q02408	Uncharacterized 14.1 kDa protein in Gp30-rIII intergenic region OS=Enterobacteria phage T4 GN=y12L PE=4 SV=1	NS	nd	14.1	70.8	1	15.7
51	sp P03691	Protein rIIb OS=Enterobacteria phage T4 GN=rIIb PE=4 SV=3	NS	nd	35.5	67.8	1	6.7
52	sp P13305	Uncharacterized 8.3 kDa protein in ri-tk intergenic region OS=Enterobacteria phage T4 GN=y05Q PE=4 SV=1	NS	nd	8.3	67.2	1	18.6
53	sp P04522	Exonuclease subunit 2 OS=Enterobacteria phage T4 GN=46 PE=4 SV=2	NS	nd	63.6	62.8	1	2.9
54	sp P32275	Uncharacterized 32.4 kDa protein in Gp30-rIII intergenic region OS=Enterobacteria phage T4 GN=y12F PE=4 SV=1	NS	nd	32.4	58.8	1	8.3
55	sp P04418	Endonuclease V OS=Enterobacteria phage T4 GN=denV PE=1 SV=1	NS	nd	16.1	56.5	1	13.8
56	sp P04538	17 kDa prohead core protein OS=Enterobacteria phage T4 GN=68 PE=4 SV=1	NS	240*	15.9	56.4	1	7.1
57	sp P13303	Uncharacterized 14.6 kDa protein in mobD-ri intergenic region OS=Enterobacteria phage T4 GN=y05O PE=4 SV=3	NS	nd	14.6	53.4	1	16.4
58	sp P10930	Short tail fiber protein OS=Enterobacteria phage T4 GN=12 PE=1 SV=3	S	18	56.2	53	1	1.7
59	sp P15556	Nuclear disruption protein OS=Enterobacteria phage T4 GN=ndd PE=4 SV=2	NS	nd	16.9	52	1	4.6
60	sp P32280	Uncharacterized 10.1 kDa protein in nrdA-td intergenic region OS=Enterobacteria phage T4 GN=y14B PE=4 SV=1	NS	nd	10.1	49.3	1	9.2
61	sp P17310	Uncharacterized 11.1 kDa protein in Gp30-rIII intergenic region OS=Enterobacteria phage T4 GN=y13A PE=4 SV=1	NS	nd	11.1	44.9	1	7.2
62	sp P00970	DNA ligase OS=Enterobacteria phage T4 GN=30 PE=3 SV=1	NS	nd	55.3	43.8	1	3.9
63	sp P39254	Uncharacterized 36.3 kDa protein in nrdC-mobD intergenic region OS=Enterobacteria phage T4 GN=y04O PE=4 SV=	NS	nd	36.3	42.8	1	5.8
64	sp P39507	Uncharacterized 14.7 kDa protein in frd-Gp32 intergenic region OS=Enterobacteria phage T4 GN=y14D PE=4 SV=3	NS	nd	14.7	41	1	14.1
65	sp P03690	Protein rIIa OS=Enterobacteria phage T4 GN=rIIa PE=4 SV=2	NS	nd	82.8	38.8	1	1.1
66	sp P13319	Ribonuclease H OS=Enterobacteria phage T4 GN=rnh PE=1 SV=1	NS	nd	35.5	35.2	1	3.3
67	sp P04382	Dihydrofolate reductase OS=Enterobacteria phage T4 GN=frd PE=1 SV=1	NS	6	21.7	35.2	1	10.4
68	sp P18771	Large tail fiber protein p34 OS=Enterobacteria phage T4 GN=34 PE=4 SV=2	S	18	140.3	30.2	1	0.9

Table S-2. Details of protein identification using bottom-up analysis of trypsin digests of SPP1-infected *B. subtilis* after 25 min of infection (37°C, rich medium and aeration). The analysis against a database of SPP1 proteins and table listing display was made as in Table S-1.

Row	Accession	Protein	Family [S/NS]	Copy number	MW [kDa]	Scores	#Peptides	SC [%]
1	tr Q38578 Q38578_BPSPP	8 protein OS=Bacillus phage SPP1 GN=8 PE=4 SV=1	NS		43.7	1131.4	15	48.4
2	tr Q38580 Q38580_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 GN=11 PE=4 SV=1	NS	180-300	23.4	1007.3	17	67.8
3	tr Q38143 Q38143_BPSPP	35 protein OS=Bacillus phage SPP1 GN=35 PE=4 SV=1	NS		32	780.8	11	58.2
4	tr Q38579 Q38579_BPSPP	9 protein OS=Bacillus phage SPP1 GN=9 PE=4 SV=1	S		12.6	565.5	9	70.5
5	tr O48471 O48471_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		29.9	535.5	8	33.6
6	tr O48466 O48466_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		6.1	261.4	4	70.4
7	tr O48453 O48453_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		20.9	219.6	3	14.5
8	tr Q38142 Q38142_BPSPP	B.subtilis phage SPP1 DNA sequence coding for products required for replication initiation...	NS		11.1	168.7	3	35.4
9	tr Q38581 Q38581_BPSPP	12 protein OS=Bacillus phage SPP1 GN=12 PE=4 SV=1	S	180	6.6	161.7	2	46.9
10	tr Q0PDK8 Q0PDK8_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		34.7	158.2	2	6.6
11	tr Q76QF2 Q76QF2_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		16	149	2	20.6
12	tr O48469 O48469_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		8.4	141	2	22.4
13	tr Q38082 Q38082_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		9.5	138.3	2	30
14	tr O48468 O48468_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=1 SV=1	NS		5.8	114	1	29.4
15	tr O48490 O48490_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		35.9	100	1	4.5
16	tr Q38141 Q38141_BPSPP	B.subtilis phage SPP1 DNA sequence coding for products required for replication initiation...	NS		9.8	99	2	35.7
17	tr Q38582 Q38582_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 GN=13 PE=1 SV=1	S	420	35.3	98.3	2	4
18	tr Q38079 Q38079_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		6.8	75.4	2	47.4
19	tr Q38583 Q38583_BPSPP	14 protein OS=Bacillus phage SPP1 GN=14 PE=4 SV=1			6.7	72.6	1	19
20	tr Q9T0R1 Q9T0R1_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		14	71.5	1	10.7
21	sp Q38441 YOR5_BPSPP	Uncharacterized 10.3 kDa protein in GP2-GP6 intergenic region OS=Bacillus phage SPP1 PE=4 SV=1			10.3	63.6	1	19.1
22	tr O48476 O48476_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		12	54.6	1	21
23	tr Q38138 Q38138_BPSPP	B.subtilis phage SPP1 DNA sequence coding for products required for replication initiation...	NS		6.3	52.8	1	19.2
24	tr O48497 O48497_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		6.1	48.2	1	18.5
25	tr O48477 O48477_BPSPP	Bacteriophage SPP1 complete nucleotide sequence OS=Bacillus phage SPP1 PE=4 SV=1	NS		12.3	43.7	1	21
26	tr Q38151 Q38151_BPSPP	39 protein OS=Bacillus phage SPP1 GN=39 PE=1 SV=1	NS		14.6	33.8	1	15.1

Table S-3. Mass spectrometer parameters for SRM detection of SPP1 and T4 peptides (including their transitions T1 and T2) and their corresponding isotopically labeled form.

Phage	Protein marker	Peptide sequence	Observed precursor ion (m/z)	Observed fragment ion T1 (m/z)	Observed fragment ion T2 (m/z)	Collision energy T1/T2 (eV)
T4	Internal protein I (IPI)	GTVYLGDGWSAK	627.5 (z=2)	720.2 (y_7^+)	833.3 (y_8^+)	22/22
		GTVYLGDGWSAK[$^{13}C_6^{15}N_2$]	631.5 (z=2)	728.2 (y_7^+)	841.3 (y_8^+)	22/22
		ATLTSEVIK	481.4 (z=2)	676.3 (y_6^+)	789.3 (y_7^+)	18/18
		ATLTSEVIK[$^{13}C_6^{15}N_2$]	485.4 (z=2)	684.3 (y_6^+)	797.3 (y_7^+)	18/18
	Small outer capsid (SOC)	GYVNIK	347.2 (z=2)	473.3 (y_4^+)	193.1 (a_2^+)	15/15
		GYV[$^{13}C_5^{15}N$]NIK	350.2 (z=2)	479.3 (y_4^+)	193.1 (a_2^+)	15/15
		AAYSTVYEENQR	716.1 (z=2)	838.2 (y_6^+)	937.2 (y_7^+)	25/25
		AAYSTVYEENQR[$^{13}C_6^{15}N_4$]	721.1 (z=2)	848.2 (y_6^+)	947.2 (y_7^+)	25/25
SPP1	Coat protein (gp13)	NALGSQDILINR	657.3 (z=2)	1015.8 (y_9^+)	298.9 (b_3^+)	35/39
		NALGSQDILINR[$^{13}C_6^{15}N_4$]	662.3 (z=2)	1025.8 (y_9^+)	298.9 (b_3^+)	35/39
	Scaffolding protein (gp11)	GADLGGLPTK	464.6 (z=2)	572.3 (y_6^+)	345.0 (y_3^+)	24/35
		GADLGGLPTK[$^{13}C_6^{15}N_2$]	468.6 (z=2)	580.3 (y_6^+)	353.0 (y_3^+)	24/35
		LVDISDGSFIPK	645.8 (z=2)	328.1 (b_3^+)	244.0 (y_2^+)	35/34
		LVDISDGSFIPK[$^{13}C_6^{15}N_2$]	649.8 (z=2)	328.1 (b_3^+)	252.0 (y_2^+)	35/34