Supplementary material

Sequencing and analysis of the phage 2 genome. Coliphage 2 lysate was provided by the Félix d'Hérelle Reference Center for Bacterial Viruses (#HER256). Phage DNA was prepared using the Lambda maxi kit (Qiagen) and sequenced at the Plateforme d'analyses génomiques de l'Université Laval using the 454 pyrosequencing method. The assembling of the different contigs was done with GS De novo Assembler with a coverage of 132X. The sequence was completed and validated by primer walking with the Sanger sequencing method. GeneMark (1) and Orf Finder (NCBI) tools were used to identify potential *orf* with at least 30 codons and with a putative RBS sequence (consensus AGGAGGT) preceding the first starting codon (AUG, GUG or CUG). Comparison of the gene products was done with BLAST (NCBI). The sequence was edited using the Bioedit software (http://www.mbio.ncsu.edu/bioedit/bioedit.html) and the genome map was done using Adobe Illustrator. To find tRNA sequences, tRNA-scan SE (2) and ARAGORN (3) servers were used.

Coliphage 2 genome characterization. Bacteriophage 2 was used as an *E. coli* O157-H7 typing phage (4) and it also infect the *E. coli* strain MG1655 (K-12) (5). Its 136,910 kb genome has a GC content of 43.6%. Nucleotide comparison of the phage 2 complete genome has reveal its close relatedness with the *E. coli* phages rv5 (GenBank # NC_011041, 92.7% identity in nucleotides) and vB_EcoM_FV3 (GenBank # NC_019517, 87.2% identity in nucleotides, (6)). Four gene clusters oriented in opposite direction have been identified (Fig. S1). Phage 2 possesses 220 open reading frames and 4 tRNA (Fig. S1). Only 23.2% of the ORFs could be associated to a putative function, which is very low, but similar to other rv5-like viruses (6).

Table S1. List of probes used for the Northern blot experiments

Probe name	Sequence[a]	Relevant characteristics
orf33_s1	GTCGGCACTATGCCAATGAATACGGTGTGGA	*orf33* of P008, detect anti-sense transcript
orf33_s2	GTCCACACCGTATTCATTGGCATAGTGCCGA	*orf33* of P008, detect sense transcript
orf36_s1	GTAGCTAAATACGTCGGAGTTACCCAGCCAG	*orf36* of P008, detect anti-sense transcript
orf36_s2	GCTGGCTGGGTAACTCCGACGTATTTAGCTA	*orf36* of P008, detect sense transcript
orf37_s1	GGGCAAACTTGGACGACACGCACAGCAAATT	*orf37* of P008, detect anti-sense transcript
orf37_s2	GAATTTGCTGTGCGTGTCGTCCAAGTTTGCC	*orf37* of P008, detect sense transcript
orf38_s1	GTGCCCTTTGACTTCGACGGAGAACAGCAAT	*orf38* of P008, detect anti-sense transcript
orf38_s2	GATTGCTGTTCTCCGTCGAAGTCAAAGGGCA	*orf38* of P008, detect sense transcript
orf39_s1	GAAAGTCGCGTACGGTTCAGCATTCTTGCCT	*orf39* of P008, detect anti-sense transcript
orf39_s2	GAGGCAAGAATGCTGAACCGTACGCGACTTT	*orf39* of P008, detect sense transcript
orf40_s1	GAAGCAACGACTTAGAGAGATCCAGCCAGCACT	*orf40* of P008, detect anti-sense transcript
orf40_s2	GAGTGCTGGCTGGATCTCTCTAAGTCGTTGCTT	*orf40* of P008, detect sense transcript
orf41_s1	GGAGCTTTCAGATACAGCACGTGAAGAACCA	*orf41* of P008, detect anti-sense transcript
orf41_s2	GTGGTTCTTCACGTGCTGTATCTGAAAGCTC	*orf41* of P008, detect sense transcript
orf45_s1	GGGCTTGGTCGTGCTGAATTTCTAGTCAGAC	*orf45* of P008, detect anti-sense transcript
orf45_s2	GGTCTGACTAGAAATTCAGCACGACCAAGCC	*orf45* of P008, detect sense transcript
orf52_s1	GGTACTTACGACAGCAGGAATACAAGAAGCG	*orf52* of P008, detect anti-sense transcript
orf52_s2	GCGCTTCTTGTATTCCTGCTGTCGTAAGTAC	*orf52* of phage P008, detect sense transcript
orf53_s1	GCGAGTTCTTACTTAATGCTGTTGAATGTGG	*orf53* of P008, detect anti-sense transcript
orf53_s2	GCCACATTCAACAGCATTAAGTAAGAACTCG	*orf53* of P008, detect sense transcript

[a] A G is added at the 5’ end of each probe to increase radiolabelling efficiency

Table S2. Analysis of the phage 2 genome. ORF annotation, proteins characterization, putative function, and comparison with the public databases.

ORF	Start position	Stop position	Size (a.a.)	MM (kDa)	pI	Putative RBS and start codon[a]	Predicted function	Best match BLASTP	E value	Size (a.a.)	ID[b]	Accession number
orf1	1983	1	660	75.8	8.3	AGGAGCGCAATAAATG	rIIA	rIIA_gp001 [Escherichia phage rv5]	0	660	649/660 (98%)	YP_002003503
orf2	2480	1980	166	19	10.0	TGGAGTTATTGTG	cell wall hydrolase SleB	SleB_gp002 [Escherichia phage rv5]	9E-121	166	165/166 (99%)	YP_002003504
orf3	2910	2530	126	14.6	4.4	AGGAGGTTGTATG	hypothetical protein	rv5_gp003 [Escherichia phage rv5]	8E-87	126	126/126 (100%)	YP_002003505
orf4	4104	2920	394	43.4	5.0	AGGACTTTTACTAATG	MoxR ATPase	MoxR ATPase_gp004 [Escherichia phage rv5]	0	394	394/394 (100%)	YP_002003506
orf5	4373	4104	89	10.8	5.4	AGGAGTAGTAGAGATG	hypothetical protein	rv5_gp005 [Escherichia phage rv5]	8E-59	89	89/89 (100%)	YP_002003507
orf6	4798	4418	126	14.8	4.3	AGGTGGACTGATAATG	hypothetical protein	rv5_gp006 [Escherichia phage rv5]	6E-88	126	125/126 (99%)	YP_002003508
orf7	5058	4801	85	9.8	4.3	AGGAGGTAGAATAATG	hypothetical protein	rv5_gp007 [Escherichia phage rv5]	2E-53	85	83/85 (98%)	YP_002003509
orf8	5414	5058	118	13.3	4.2	AGGAGACCTTACCGATG	hypothetical protein	rv5_gp008 [Escherichia phage rv5]	2E-71	118	106/109 (97%)	YP_002003510
orf9	5700	5428	90	10.2	6.2	CGGGGATTTGACTATG	hypothetical protein	rv5_gp009 [Escherichia phage rv5]	5E-60	90	89/90 (99%)	YP_002003511
orf10	6602	5703	299	33.7	5.0	AGGAGCACTCACTCATG	alpha 1-3 fucosyltransferase	putative alpha 1-3 fucosyltransferase_gp010 [Escherichia phage rv5]	0	299	299/299 (100%)	YP_002003512
orf11	6745	7722	325	37.7	4.7	ACGAGAGACAACTCATG	anti-sigma factor	anti-sigma factor_gp011 [Escherichia phage rv5]	0	311	310/311 (99%)	YP_002003513
orf12	7756	9216	486	54.9	7.1	TGGAGTTTTAATG	hypothetical protein	FV3_00012[Enterobacteria phage vB_EcoM-FV3]	0	497	477/486 (98%)	AEZ65148
orf13	9232	9489	85	9.4	4.6	AGGATGTTATTTATG	hypothetical protein	FV3_00013 [Enterobacteria phage vB_EcoM-FV3]	8E-53	89	84/85 (99%)	AEZ65149
orf14	9489	9752	87	10	4.5	AGGAGGAGTAATG	hypothetical protein	rv5_gp015 [Escherichia phage rv5]	6E-56	87	86/87 (99%)	YP_002003517
orf15	9754	9987	77	8.8	4.5	AGAGGGTTTCTAATATG	hypothetical protein	rv5_gp016 [Escherichia phage rv5]	2E-47	77	76/77 (99%)	YP_002003518
orf16	10004	10453	149	17.4	5.1	AGGAGATAGCCGTG	hypothetical protein	rv5_gp017 [Escherichia phage rv5]	2E-100	149	143/149 (96%)	YP_002003519
orf17	10450	10695	81	9.3	7.9	AGGAGCTATACCTGTTATG	hypothetical protein	rv5_gp018 [Escherichia phage rv5]	1E-53	81	81/81 (100%)	YP_002003520
orf18	10698	11264	188	21.4	5.8	TGGAGCTATAGTCATG	hypothetical protein	rv5_gp019 [Escherichia phage rv5]	1E-135	188	188/18 (100%)	YP_002003521
orf19	11322	11597	91	10.4	4.8	AGGAGAGACTGAGATG	hypothetical protein	rv5_gp020 [Escherichia phage rv5]	1E-59	91	91/91 (100%)	YP_002003522
orf20	11600	12064	154	18	4.5	AGAAGGTGTGAATATG	hypothetical protein	rv5_gp021 [Escherichia phage rv5]	2E-110	154	154/154 (100%)	YP_002003523
orf21	12070	12240	56	6.9	8.2	CGGAG*TAAGAGCCATG	hypothetical protein	rv5_gp022 [Escherichia phage rv5]	1E-32	56	56/56 (100%)	YP_002003524
orf22	12113	12262	49	5.5	9.5	TGGAAGTTATATCAAAATG	hypothetical protein	rv5_gp023 [Escherichia phage rv5]	2E-25	49	49/49 (100%)	YP_002003525
orf23	12293	12673	126	14.2	9.4	CGGAGACTGATTAAATG	hypothetical protein	rv5_gp024 [Escherichia phage rv5]	2E-87	126	126/126 (100%)	YP_002003526
orf24	12837	13244	135	15.5	5.2	AGGAGACTGCCATG	hypothetical protein	rv5_gp025 [Escherichia phage rv5]	1E-95	135	135/135 (100%)	YP_002003527
orf25	13248	13448	66	7.5	4.3	AGGAC*TGAGAAATG	hypothetical protein	rv5_gp026 [Escherichia phage rv5]	2E-40	66	66/66 (100%)	YP_002003528
orf26	19023	13498	1841	204.4	6.3	no RBS	hypothetical protein	rv5_gp027 [Escherichia phage rv5]	0	1878	1784/1833 (97%)	YP_002003529
orf27	20917	19172	581	62.5	4.8	AGGAGAAATCATG	tail fiber protein	tail fiber protein_gp28 [Escherichia phage rv5]	0	581	575/581 (99%)	YP_002003530
orf28	21193	20927	88	10	6.8	AGAGGGTAAATG	hypothetical protein	rv5_gp029 [Escherichia phage rv5]	1E-59	88	88/88 (100%)	YP_002003531
orf29	22246	21203	347	38.4	6.0	AGGAGAACGCGATG	tail fiber protein	tail fiber [Enterobacteria phage vB_EcoM-FV3]	0	347	340/347 (98%)	AEZ65166
orf30	22650	22336	104	11.9	7.0	AGGAGGTGTTGTG	hypothetical protein	rv5_gp031 [Escherichia phage rv5]	1E-67	104	103/104 (99%)	YP_002003533
orf31	23246	22662	194	22.6	4.6	CGGAGGACTAGCATG	tail fiber assembly protein	tail fiber assembly protein_gp032 [Escherichia phage rv5]	7E-139	194	192/194 (99%)	YP_002003534
orf32	24301	23261	346	38.3	5.5	AGGAGATAAAATG	tail fiber protein	tail fiber protein_gp033 [Escherichia phage rv5]	0	346	345/346 (99%)	YP_002003535
orf33	26386	24314	690	79.1	5.0	AGGAGGGTTAATG	hypothetical protein	rv5_gp034 [Escherichia phage rv5]	0	690	687/690 (99%)	YP_002003536
orf34	27072	26386	228	25.4	4.6	AGGCGGCGAGATATG	hypothetical protein	rv5_gp035 [Escherichia phage rv5]	3E-165	228	228228 (100%)	YP_002003537

orf35	28574	27084	496	54.7	4.9	CGGAGGAGTGACGTG	baseplate component	rv5_gp036 [Escherichia phage rv5]	0	496	493/496 (99%)	YP_002003538
orf36	32279	28680	1199	131.8	5.5	TGGAGGTATTAATG	tail fiber /phage host specificity	tail fiber protein_gp037 [Escherichia phage rv5]	0	1279	1068/1279 (84%)	YP_002003539
orf37	32704	32279	141	16.7	5.3	TGGGAGGTTTAATG	hypothetical protein	rv5_gp038 [Escherichia phage rv5]	1E-100	141	141/141 (100%)	YP_002003540
orf38	33255	32704	183	19.9	4.7	AGGATTTCTAAGATG	hypothetical protein	rv5_gp039 [Escherichia phage rv5]	5E-131	183	183/183 (100%)	YP_002003541
orf39	33847	33257	196	22	9.2	TGGAGGCACAATG	hypothetical protein	rv5_gp040 [Escherichia phage rv5]	2E-140	196	196/196 (100%)	YP_002003542
orf40	37765	33947	1272	139.4	5.5	AGGAGAAAGAATG	tail fiber protein	tail fiber protein_gp041 [Escherichia phage rv5]	0	1272	1242/1272 (98%)	YP_002003543
orf41	40398	37801	865	97.8	5.5	AGGAGCTATCTAAGATG	phage tail protein	rv5_gp042 [Escherichia phage rv5]	0	865	862/865 (99%)	YP_002003544
orf42	41068	40400	222	24.2	4.4	AGGAGAAATCATG	tail fiber protein	rv5_gp043 [Escherichia phage rv5]	5E-158	222	222/222 (100%)	YP_002003545
orf43	41794	41078	238	27.5	4.5	AG*AGGGCTTTCATG	hypothetical protein	rv5_gp044 [Escherichia phage rv5]	4E-175	238	238/238 (100%)	YP_002003546
orf44	42484	41807	225	24.5	4.8	AGGAGGTATAATG	baseplate protein	rv5_gp045 [Escherichia phage rv5]	8E-166	225	225/225 (100%)	YP_002003547
orf45	43488	42484	334	37	9.0	AAG*GGTTAGAATAATG	hypothetical protein	rv5_gp046 [Escherichia phage rv5]	0	334	333/334 (99%)	YP_002003548
orf46	43868	43488	126	14.8	4.6	AGG*GGAGCGTATAATG	hypothetical protein	rv5_gp047 [Escherichia phage rv5]	2E-86	126	125/126 (99%)	YP_002003549
orf47	44765	43881	294	32.8	5.4	AG*AGGTTATG	hypothetical protein	rv5_gp048 [Escherichia phage rv5]	0	294	294/294 (100%)	YP_002003550
orf48	47207	44871	778	85.6	9.8	ATGAGGAAACCATG	tape measure protein	rv5_gp049 [Escherichia phage rv5]	0	778	774/778 (99%)	YP_002003551
orf49	47631	47263	122	13.9	8.6	TGGAGGTTAACTACGGCTG	hypothetical protein	rv5_gp050 [Escherichia phage rv5]	1E-83	122	121/122 (99%)	YP_002003552
orf50	47996	47523	157	17.2	4.4	AGGATGCTATAAAATG	hypothetical protein	rv5_gp051 [Escherichia phage rv5]	1E-109	157	157/157 (100%)	YP_002003553
orf51	48632	48159	157	17.1	4.6	AGGAAGACTAGATG	structural protein	structural [Enterobacteria phage vB_EcoM-FV3]	2E-109	157	157/157 (100%)	AEZ65188
orf52	50019	48643	458	50.3	5.2	AAGAGGAAACAAATG	structural protein	structural protein_gp053 [Escherichia phage rv5]	0	458	455/458 (99%)	YP_002003555
orf53	50643	50092	183	20.4	5.1	AGGAGAAAACTGATG	hypothetical protein	rv5_gp054 [Escherichia phage rv5]	3E-130	183	180/183 (98%)	YP_002003556
orf54	51068	50643	141	15.9	5.3	AGGGGGTTGAGTG	hypothetical protein	FV3_00055[Enterobacteria phage vB_EcoM-FV3]	4E-98	141	138/141 (98%)	AEZ65191
orf55	51543	51085	152	17.2	8.7	AGTGAGGAATATAATG	hypothetical protein	rv5_gp056 [Escherichia phage rv5]	8E-109	152	151/152 (99%)	YP_002003558
orf56	52217	51597	206	23.4	4.5	ACGAGGTATTTCAAATG	hypothetical protein	rv5_gp057 [Escherichia phage rv5]	8E-143	206	203/206 (99%)	YP_002003559
orf57	53131	52277	284	31	4.5	AGGA*GTGTCCCGTG	hypothetical protein	FV3_00058[Enterobacteria phage vB_EcoM-FV3]	1E-156	271	237/284 (83%)	AEZ65194
orf58	54223	53213	336	37.9	5.8	TGGAGAAAATAATG	major head protein	major head protein_gp060 [Escherichia phage rv5]	0	336	290/331 (88%)	YP_002003562
orf59	54644	54270	124	12.8	5.6	AGG*GGAAAATAATG	head stabilization/decoration protein	Head stabilization/ decoration protein_gp061 [Escherichia phage rv5]	1E-52	129	90/123 (73%)	YP_002003563
orf60	55646	54666	326	36.9	4.6	AG*AGGGCAATGAGTAATG	hypothetical protein	rv5_gp062 [Escherichia phage rv5]	0	325	276/326 (85%)	YP_002003564
orf61	56218	55646	190	21.6	4.9	AGCAGGGCTGGTGATG	hypothetical protein	rv5_gp063 [Escherichia phage rv5]	2E-135	190	188/190 (99%)	YP_002003565
orf62	57689	56133	518	57.1	6.1	AGG*GGTAAAGCTTGTG	hypothetical protein	rv5_gp064 [Escherichia phage rv5]	0	518	517/518 (99%)	YP_002003566
orf63	58808	57792	338	38.2	5.2	no RBS	large terminase subunit	terminase large subunit [Enterobacteria phage vB_EcoM-FV3]	0	515	338/338 (100%)	AEZ65200
orf64	59467	58988	159	19	8.7	AGGAA*TGCTATATG	recombination endonuclease	recombination endonuclease VII [Segniliparus rugosus ATCC BAA-974]	3E-12	146	39/84 (46%)	ZP_10246071
orf65	60222	59794	142	16.1	7.7	GAGAGGTTAATG	Large terminase subunit	terminase large subunit [Enterobacteria phage vB_EcoM-FV3]	3E-97	515	142/142 (100%)	AEZ65200
orf66	60509	60222	95	10.4	9.2	CAGGAGGATCGATG	hypothetical protein	rv5_gp067 [Escherichia phage rv5]	5E-60	95	92/95 (97%)	YP_002003569
orf67	60904	60506	132	15.1	5.9	TGGAGCCTTAAAATG	hypothetical protein	rv5_gp068 [Escherichia phage rv5]	1E-86	132	128/132 (97%)	YP_002003570
orf68	61351	61010	113	13.3	5.7	AGGAGGTCGAGTG	hypothetical protein	rv5_gp069 [Escherichia phage rv5]	8E-58	89	89/89 (100%)	YP_002003571
orf69	62297	61959	112	13.1	4.9	TGGAGGAAACATG	hypothetical protein	rv5_gp070 [Escherichia phage rv5]	2E-74	112	112/112 (100%)	YP_002003572
orf70	62888	62646	80	9.3	4.2	ACGAGGTCTACAGGTAATG	hypothetical protein	rv5_gp071 [Escherichia phage rv5]	9E-52	80	80/80 (100%)	YP_002003573
orf71	63153	62965	62	7.1	5.0	AGGAGCGCTTAATG	hypothetical protein	rv5_gp072 [Escherichia phage rv5]	1E-36	62	61/62 (98%)	YP_002003574
orf72	63742	63164	192	22.5	6.2	AGGAGGCAGCTATG	hypothetical protein	rv5_gp073 [Escherichia phage rv5]	3E-132	192	182/192 (85%)	YP_002003575

orf73	64733	64383	116	12.8	9.2	AGGAGATATG	transcriptional regulator	transcriptional reg. gp075 [Escherichia phage rv5]	4E-78	116	115/116 (99%)	YP_002003577
orf74	65335	64781	184	21.4	6.3	ATGAGGAATGTATG	Phosphoester.	phosphoesterase gp076 [Escherichia phage rv5]	1E-132	184	180/184 (98%)	YP_002003578
orf75	65753	65343	136	15.8	6.5	CGGAGGATTGCTATG	hypothetical protein	rv5_gp077 [Escherichia phage rv5]	1E-96	136	135/136 (99%)	YP_002003579
orf76	65875	66789	304	35.3	6.5	ATGAGGAACGTATGATG	RNA ligase and tail attachment protein	RNA ligase 1 and tail attachment protein_gp078 [Escherichia phage rv5]	0	311	297/304 (98%)	YP_002003580
orf77	66786	67136	116	13.5	5.7	AGGAC*TATATGCAATG	hypothetical protein	FV3_00076 [Enterobacteria phage vB_EcoM-FV3]	6E-79	116	115/116 (99%)	AEZ65212
orf78	67145	67906	253	28.6	4.9	CTGAGGACACTTATG	Sir2-like(NAD-dependent deacetylase)	putative Sir2-like protein_gp080 [Escherichia phage rv5]	0	253	251/253 (99%)	YP_002003582
orf79	67920	68633	237	27.4	5.8	AGGAGACCTTTAATG	hypothetical protein	rv5_gp081 [Escherichia phage rv5]	1E-173	237	236/237 (99%)	YP_002003583
orf80	68676	69005	109	12.9	6.4	TTGTGGAAAGTATG	hypothetical protein	rv5_gp082 [Escherichia phage rv5]	2E-66	102	100/102 (98%)	YP_002003584
orf81	68992	69261	89	10.4	4.6	AGGAGGACTGCAATG	hypothetical protein	rv5_gp083 [Escherichia phage rv5]	2E-58	89	89/89 (100%)	YP_002003585
orf82	69261	70544	427	49.5	5.5	AAGAGGTAGAGTAATG	ATP-dependent DNA ligase	ATP-dependent DNA ligase [Enterobacteria phage vB_EcoM-FV3]	0	427	420/427 (98%)	AEZ65217
orf83	70687	71157	156	17.4	9.1	TGGAGAGTATGAAAAATG	Lysozyme/Endolysin	Lysozyme_gp085 [Escherichia phage rv5]	4E-110	156	155/156 (99%)	YP_002003587
orf84	71221	71427	68	7.6	4.9	AGGAGGGTTTAACCATG	hypothetical protein	membrane protein_gp086 [Escherichia phage rv5]	3E-42	68	68/68 (100%)	YP_002003588
orf85	71438	71902	154	17.7	8.4	ATGAGGGAGAACACGTG	HNH endonuclease	HNH endonuclease gp087 [Escherichia phage rv5]	2E-109	154	152/154 (99%)	YP_002003589
orf86	71895	72185	96	11.2	9.8	AG*AGGGTTACCTTGATG	transposase	transposase protein gp088 [Escherichia phage rv5]	5E-23	96	91/96 (95%)	YP_002003590
orf87	72245	72553	102	12	6.0	AGGAGAACTAGGTATG	hypothetical protein	FV3_00087 [Enterobacteria phage vB_EcoM-FV3]	2E-67	102	98/102 (96%)	AEZ65223
orf88	72546	73685	379	43.4	8.4	AGGAGGGTCTTTG	exodeoxyribonuclease	exodeoxyribonuclease_gp090 [Escherichia phage rv5]	0	379	378/379 (99%)	YP_002003592
orf89	73685	74017	110	12.5	4.1	TGGAGCAATTTGATG	hypothetical protein	rv5_gp091 [Escherichia phage rv5]	9E-71	110	106/109 (97%)	YP_002003593
orf90	74014	74643	209	23.3	8.3	AGGATGAGGAAGCATG	hypothetical protein	rv5_gp092 [Escherichia phage rv5]	6E-152	209	209/209 (100%)	YP_002003594
orf91	74922	75200	92	10.9	4.9	AGGC*GTTGCGCCGGATG	EndoVII packaging and recombination endonuclease	EndoVII packaging and recombination endonuclease_gp093 [Escherichia phage rv5]	1E-57	192	89/92 (97%)	YP_002003595
orf92	75139	75360	73	8.8	7.8	GAGAGATTTCTATG	hypothetical protein	rv5_gp094 [Escherichia phage rv5]	4E-47	73	72/73 (99%)	YP_002003596
orf93	75373	76356	327	38.3	6.0	AGGAATCTTAACGATG	DNA pol/ exonuclease	rv5_gp095 [Escherichia phage rv5]	0	327	326/327 (99%)	YP_002003597
orf94	76402	77220	272	30.9	5.7	TGGAGGCACTTTG	N6-adenine methyltransf.	N6-adeninemethyltransferase gp096 [Escherichia phage rv5]	0	272	268/272 (99%)	YP_002003598
orf95	77183	77641	152	17.1	10.0	TGGAGACCCGGTATG	hypothetical protein	rv5_gp097 [Escherichia phage rv5]	2E-105	152	151/152 (99%)	YP_002003599
orf96	77669	77860	63	7.2	4.1	TGGAGACCGCAATG	hypothetical protein	rv5_gp098 [Escherichia phage rv5]	5E-37	63	61/63 (97%)	YP_002003600
orf97	77860	78474	204	22.8	5.2	CGGAGGTTTTTGATG	hypothetical protein	rv5_gp099 [Escherichia phage rv5]	4E-149	204	204/204 (100%)	YP_002003601
orf98	78468	78710	80	9.4	4.3	AG*AGGCCCAAGAAGAATG	hypothetical protein	rv5_gp100 [Escherichia phage rv5]	2E-48	197	77/79 (97%)	YP_002003602
orf99	78715	79062	115	13.4	7.0	AGGGGGGCTATTGAGGTTATG	hypothetical protein	rv5_gp100 [Escherichia phage rv5]	2E-77	197	114/115 (99%)	YP_002003602
orf100	79064	79264	66	7.5	9.3	AGAAGGTATTTGAAATG	hypothetical protein	rv5_gp101 [Escherichia phage rv5]	2E-41	66	66/66 (100%)	YP_002003603
orf101	79264	80247	327	37.6	6.1	AGGAGAGCTAAATAATG	thymidylate synthase	thymidylate synthase_gp102 [Escherichia phage rv5]	0	327	324/237 (99%)	YP_002003604
orf102	80346	80807	153	17.5	7.8	TGGAGACAGATATG	hypothetical protein	rv5_gp103 [Escherichia phage rv5]	1E-106	153	151/153 (99%)	YP_002003605
orf103	80818	81048	76	9	4.1	AGGTGGTGAAGATG	hypothetical protein	FV3_00102 [Enterobacteria phage vB_EcoM-FV3]	1E-47	100	75/76 (99%)	AEZ65238
orf104	81045	83360	771	87.3	6.0	TGGAGGAAGCAAATTG	ribonucleotide triphosphate reductase	ribonucleoside triphosphate reductase alpha chain_gp105 [Escherichia phage rv5]	0	771	765/771 (99%)	YP_002003607
orf105	83399	84487	362	41.8	4.5	AG*AGGTAGAATAATG	ribonucleotide diphosphate reductase	ribonucleoside diphosphate reductase beta chain_gp106 [Escherichia phage rv5]	0	362	361/362 (99%)	YP_002003608
orf106	84491	84769	92	10.4	6.7	GGGAGTTTTAATACATG	glutaredoxin 1	glutaredoxin 1_gp107 [Escherichia phage rv5]	6E-60	92	92/92 (100%)	YP_002003609
orf107	84766	86889	707	78.9	5.7	TGGAGAGAAAAAGTG	anaerobic ribonucleoside-triphosphate	anaerobic ribonucleoside-triphosphatereductase_gp108 [Escherichia phage rv5]	0	707	701/707 (99%)	YP_002003610

							reductase					
orf108	86953	87069	38	4.5	8.2	AGGAGGTACAGTATG	hypothetical protein	Sec23 protein, putative [Entamoeba nuttalli P19]	0.32	726	16/33 (48%)	EKE37794
orf109	87066	87539	157	17.6	5.4	CGGAG*TATCTATG	anaerobic NTP reductase small subunit	anaerobic NTP reductase small subunit [Enterobacteria phage vB_EcoM-FV3]	1E-104	163	147/157 (94%)	AEZ65245
orf110	87604	87717	37	4.5	9.8	AGGAGGTGCCAAATG	hypothetical protein	FV3_00110 [Enterobacteria phage vB_EcoM-FV3]	3E-14	37	37/37 (100%)	AEZ65246
orf111	87714	88064	116	13.3	5.2	AGGGGGTGCAACAGTG	hypothetical protein	FV3_00111 [Enterobacteria phage vB_EcoM-FV3]	7E-76	116	115/116 (99%)	AEZ65247
orf112	88103	88891	262	29.6	9.2	AGGA*GTCCCAACATG	PhoH-like protein	PhoH-like protein_gp115 [Escherichia phage rv5]	0	262	262/262 (100%)	YP_002003617
orf113	88995	89306	103	12	9.1	AGGAGATAGTATG	hypothetical protein	rv5_gp116 [Escherichia phage rv5]	1E-65	103	99/103 (96%)	YP_002003618
orf114	89367	90416	349	38.5	5.1	AGGATTTCTCATG	ClpP ATP-dep. protease subunit	ClpP ATP-dependent protease subunit_gp117 [Escherichia phage rv5]	0	349	348/348 (100%)	YP_002003619
orf115	90468	91001	117	20.6	4.6	TGGAGATTTGCATG	hypothetical protein	rv5_gp118 [Escherichia phage rv5]	5E-127	177	175/177 (99%)	YP_002003620
orf116	90998	91282	94	10.2	6.2	AGGCAGATTTGAAATG	hypothetical protein	rv5_gp119 [Escherichia phage rv5]	8E-63	94	94/94 (100%)	YP_002003621
orf117	91318	91557	79	9.5	6.0	AGGGGGGTCATTTATG	hypothetical protein	rv5_gp120 [Escherichia phage rv5]	3E-51	79	79/79 (100%)	YP_002003622
orf118	91554	91952	132	14.4	4.9	AGGAGCCCAGTGTATG	hypothetical protein	rv5_gp121 [Escherichia phage rv5]	3E-86	132	127/132 (96%)	YP_002003623
orf119	91992	92225	77	8.3	5.3	AGGAGGTAGCATG	hypothetical protein	FV3_00119 [Enterobacteria phage vB_EcoM-FV3]	7E-47	77	77/77 (100%)	AEZ65255
orf120	92231	92749	172	20.2	7.7	AGGAG*TGACAGGTATG	hypothetical protein	FV3_00120 [Enterobacteria phage vB_EcoM-FV3]	1E-119	172	164/172 (95%)	AEZ65256
orf121	92751	92987	78	8.8	7.6	AGGAGATGTAATATG	hypothetical protein	FV3_00121 [Enterobacteria phage vB_EcoM-FV3]	8E-47	78	76/78 (97%)	AEZ65257
orf122	92971	93102	43	5	5.0	AGGAGGCAGATAAGAATG	hypothetical protein	FV3_00122 [Enterobacteria phage vB_EcoM-FV3]	4E-21	43	43/43 (100%)	AEZ65258
orf123	93048	93221	57	6.3	7.9	no RBS	hypothetical protein	FV3_00123 [Enterobacteria phage vB_EcoM-FV3]	2E-30	57	56/57 (98%)	AEZ65259
orf124	93208	93393	61	7.5	4.3	AGGAGACAGCAATG	hypothetical protein	rv5_gp127 [Escherichia phage rv5]	4E-36	61	60/61 (98%)	YP_002003629
orf125	93396	93851	151	17.5	9.1	AGG*GGTGACGATG	hypothetical protein	structural protein_gp128 [Escherichia phage rv5]	1E-100	151	147/151 (97%)	YP_002003630
orf126	93912	94259	115	13.2	4.8	AAGAGGTAGAGAGAATG	hypothetical protein	rv5_gp129 [Escherichia phage rv5]	2E-76	115	112/115 (97%)	YP_002003631
orf127	94256	94543	95	10.9	8.6	AGGAGGCTCAATG	hypothetical protein	rv5_gp130 [Escherichia phage rv5]	1E-59	95	91/95 (96%)	YP_002003632
orf128	94540	94740	66	7.7	4.6	AGGAG*TAGAAAATG	hypothetical protein	rv5_gp131 [Escherichia phage rv5]	2E-38	66	64/66 (97%)	YP_002003633
orf129	94760	94945	61	7.2	4.8	TGGAGGGTTTTTATG	hypothetical protein	rv5_gp132 [Escherichia phage rv5]	5E-38	61	61/61 (100%)	YP_002003634
orf130	95041	95334	97	11.2	8.5	GCGAGGCTGAATTATG	hypothetical protein	rv5_gp133 [Escherichia phage rv5]	1E-55	98	81/96 (84%)	YP_002003635
orf131	95338	95619	93	10.8	7.6	AG*AGGACTAAGTAATG	hypothetical protein	rv5_gp134 [Escherichia phage rv5]	1E-50	93	78/93 (84%)	YP_002003636
orf132	95619	95843	74	8.2	4.1	AGGAGACCGTTGATG	hypothetical protein	rv5_gp135 [Escherichia phage rv5]	2E-45	74	72/74 (97%)	YP_002003637
orf133	95833	96087	84	9.3	4.7	TGGAGGATGATCATG	hypothetical protein	rv5_gp136 [Escherichia phage rv5]	8E-53	84	82/84 (98%)	YP_002003638
orf134	96100	96498	132	15	7.9	GATGGGTAACCGTTGTG	hypothetical protein	rv5_gp137 [Escherichia phage rv5]	5E-91	132	128/132 (97%)	YP_002003639
orf135	96516	96806	96	10.7	4.3	GTGAGGTGTCACCATG	hypothetical protein	rv5_gp138 [Escherichia phage rv5]	7E-59	96	93/96 (97%)	YP_002003640
orf136	96889	97206	105	11.5	9.0	AAAAGGAACATGTTGTG	sigma 54 modulation factor	sigma 54 modulation factor_gp139 [Escherichia phage rv5]	6E-59	105	102/105 (97%)	YP_002003641
orf137	97216	97317	33	3.6	5.9	ATGAGGTGCTACAATG	hypothetical protein	rv5_gp140 [Escherichia phage rv5]	3E-13	33	32/33 (97%)	YP_002003642
orf138	97344	97613	89	9.9	4.4	AGGAGACCTCTAAATG	hypothetical protein	rv5_gp141 [Escherichia phage rv5]	1E-55	89	89/89 (100%)	YP_002003643
orf139	97709	97972	87	9.7	4.2	AGGTGATACTATATG	hypothetical protein	rv5_gp142 [Escherichia phage rv5]	2E-54	87	84/87 (97%)	YP_002003644
orf140	97977	98309	110	12.1	4.7	TGTTGGGTGAGAATATG	hypothetical protein	rv5_gp143 [Escherichia phage rv5]	3E-72	110	108/110 (98%)	YP_002003645
orf141	98309	98704	131	15	4.9	AGGAGGTGCGGTAATG	hypothetical protein	rv5_gp144 [Escherichia phage rv5]	5E-82	131	128/131 (98%)	YP_002003646
orf142	98784	99041	85	9.3	4.2	AGGAGACCGATTGATG	hypothetical protein	rv5_gp145 [Escherichia phage rv5]	1E-43	85	72/85 (85%)	YP_002003647
orf143	99042	99392	116	12.8	3.8	AGGCGCTGTAAATG	hypothetical protein	rv5_gp146 [Escherichia phage rv5]	1E-72	116	114/116 (98%)	YP_002003648
orf144	99392	99721	109	12.3	4.4	AGGAGGACGAATAATG	hypothetical protein	FV3_00144 [Enterobacteria phage vB_EcoM-FV3]	1E-71	109	107/109 (98%)	AEZ65280
orf145	99721	100008	95	10.5	4.8	TGGAGGAAGACTAATG	hypothetical protein	FV3_00145 [Enterobacteria phage vB_EcoM-FV3]	5E-59	95	90/95 (95%)	AEZ65281

orf146	100098	100361	87	10.1	8.9	AGTGAGGTGCTTGTATG	hypothetical protein	rv5_gp150 [Escherichia phage rv5]	2E-55	87	86/87 (99%)	YP_002003652
orf147	100390	100530	46	5.1	4.6	AAGAGGTGAGGAATG	hypothetical protein	rv5_gp151 [Escherichia phage rv5]	2E-23	46	45/46 (98%)	YP_002003653
orf148	100517	100768	83	9.3	4.3	AGGAGCGCAGTAATG	hypothetical protein	rv5_gp152 [Escherichia phage rv5]	4E-51	83	83/83 (100%)	YP_002003654
orf149	100797	101102	101	11.9	5.3	AGGAGACTCTTACTATG	hypothetical protein	rv5_gp153 [Escherichia phage rv5]	1E-62	101	101/101 100%)	YP_002003655
orf150	101158	101484	108	12.5	4.8	AGGAGATTTGAGATG	hypothetical protein	FV3_00150 [Enterobacteria phage vB_EcoM-FV3]	4E-69	108	104/108 (96%)	AEZ65286
orf151	101493	101792	99	11.5	5.4	GTGAGGTGGATTATG	hypothetical protein	rv5_gp155 [Escherichia phage rv5]	1E-65	99	97/99 (98%)	YP_002003657
orf152	102067	102156	29	2.9	5.8	TGGAGAATATGGAATACACAATG	hypothetical protein	no hit				
orf153	102153	102365	70	7.9	4.0	CACGGGTGGAACATG	hypothetical protein	rv5_gp157 [Escherichia phage rv5]	1E-41	101	67/70 (96%)	YP_002003659
orf154	102487	102702	71	8.0	3.8	AGGAGATTTTATG	hypothetical protein	rv5_gp158 [Escherichia phage rv5]	2E-43	93	71/71 (100%)	YP_002003660
orf155	103517	103395	40	4.1	10.3	ACGG*GGTATATG	hypothetical protein	no hit				
orf156	105715	105296	139	16.1	6.1	AAGAGGTAAAAACACCATG	hypothetical protein	rv5_gp159 [Escherichia phage rv5]	3E-94	139	134/139 (96%)	YP_002003661
orf157	106124	105861	87	10.7	8,6	AG*AGGTAAACATCATG	hypothetical protein	rv5_gp160 [Escherichia phage rv5]	1E-42	87	84/87 (97%)	YP_002003662
orf158	106457	106185	90	10.4	4.4	AGAGAGGAAAACACTGTG	hypothetical protein	rv5_gp162 [Escherichia phage rv5]	1E-56	90	86/90 (96%)	YP_002003664
orf159	106860	106669	63	7.4	6.1	AGAGCGGTAAAAATG	hypothetical protein	rv5_gp164 [Escherichia phage rv5]	1E-23	63	46/63 (73%)	YP_002003666
orf160	107007	106873	44	4.8	8.3	no RBS	hypothetical protein	FV3_00157 [Enterobacteria phage vB_EcoM-FV3]	1E-14	44	36/44 (82%)	AEZ65293
orf161	107294	107010	94	10.4	5.8	AG*AGGATGGACACAATG	hypothetical protein	rv5_gp166 [Escherichia phage rv5]	6E-60	94	92/94 (98%)	YP_002003668
orf162	107601	107386	71	8.1	9.7	GTGAGGTTGCCAAATG	hypothetical protein	FV3_00159 [Enterobacteria phage vB_EcoM-FV3]	3E-42	71	70/71 (99%)	AEZ65295
orf163	107715	107611	34	3.4	8.4	AGAGAA*TAAACACCATG	hypothetical protein	rv5_gp168 [Escherichia phage rv5]	2E-11	46	32/34 (94%)	YP_002003670
orf164	108038	107793	81	9.2	9.6	AAGAGGTAAACACCATG	hypothetical protein	Phi92_gp232 [Enterobacteria phage phi92]	8E-36	79	60/79 (76%)	CBY99661
orf165	108309	108130	59	7.0	4.4	AG*AGGATAAAAAATCATG	hypothetical protein	rv5_gp169 [Escherichia phage rv5]	1E-32	59	59/59 (100%)	YP_002003671
orf166	108619	108386	77	8.7	8.0	AGAGAGGCAAATCATCATG	hypothetical protein	rv5_gp170 [Escherichia phage rv5]	1E-48	77	75/77 (97%)	YP_002003672
orf167	108960	108676	94	10.8	4.3	AGGAGTTAAAACCATG	hypothetical protein	FV3_00164 [Enterobacteria phage vB_EcoM-FV3]	2E-58	99	89/94 (95%)	AEZ65300
orf168	109485	109186	99	11.1	4.5	AGGAG*TGATAAACATG	hypothetical protein	FV3_00165 [Enterobacteria phage vB_EcoM-FV3]	6E-55	101	87/98 (89%)	AEZ65301
orf169	109778	109578	66	7.6	8.0	AGGAGAAACAAAATG	hypothetical protein	rv5_gp174 [Escherichia phage rv5]	3E-38	66	65/66 (98%)	YP_002003676
orf170	110039	109920	39	4.5	9.5	AGG*GGAGACGATG	hypothetical protein	rv5_gp176 [Escherichia phage rv5]	6E-18	39	38/39 (97%)	YP_002003678
orf171	110281	110036	81	9.6	6.7	AGA*GGAATAGAAAATATG	hypothetical protein	rv5_gp177 [Escherichia phage rv5]	1E-35	81	68/81 (84%)	YP_002003679
orf172	110630	110259	123	14.0	7.8	AAGAGGTACATAGAATG	hypothetical protein	rv5_gp178 [Escherichia phage rv5]	7E-83	123	121/123 (98%)	YP_002003680
orf173	111075	110695	126	14.5	6.1	AAGAGGAAAACATTATG	hypothetical protein	FV3_00170 [Enterobacteria phage vB_EcoM-FV3]	3E-88	126	124/126 (98%)	AEZ65306
orf174	111790	111167	207	24.1	4.4	AGGAGAAAATATCATG	hypothetical protein	FV3_00171 [Enterobacteria phage vB_EcoM-FV3]	2E-144	207	202/207 (98%)	AEZ65307
orf175	112125	111865	86	10.3	9.9	AGGAG*TAAACACTATG	hypothetical protein	rv5_gp181 [Escherichia phage rv5]	3E-54	86	84/86 (98%)	YP_002003683
orf176	112568	112371	65	8.2	10.6	AGCAAGGGTGGGAATATATG	hypothetical protein	rv5_gp184 [Escherichia phage rv5]	4E-37	65	64/65 (98%)	YP_002003686
orf177	112912	112565	115	13	7.8	AGGAGAAAGTAACATG	hypothetical protein	rv5_gp185 [Escherichia phage rv5]	5E-75	117	110/113 (97%)	YP_002003687
orf178	113233	112988	81	9.2	8.7	AGGAGTTAAAACCATG	hypothetical protein	rv5_gp186 [Escherichia phage rv5]	2E-49	81	78/81 (96%)	YP_002003688
orf179	113664	113323	113	13.2	3.8	AGGAGAAAACACCATG	hypothetical protein	FV3_00176 [Enterobacteria phage vB_EcoM-FV3]	2E-71	113	111/113 (98%)	AEZ65312
orf180	113863	113744	39	4.4	9.8	AGGGGGGCTTAAAGATG	hypothetical protein	rv5_gp188 [Escherichia phage rv5]	2E-17	39	36/39 (92%)	YP_002003690
orf181	114339	113944	131	15	9.5	AG*AGGAAAAGCTATG	hypothetical protein	rv5_gp189 [Escherichia phage rv5]	4E-79	134	117/134 (87%)	YP_002003691
orf182	114821	114423	132	14.8	6.0	AG*AGGATAAAATCATG	hypothetical protein	rv5_gp190 [Escherichia phage rv5]	2E-87	132	127/132 (96%)	YP_002003692
orf183	115083	114886	65	7.6	10.5	AG*AGGATAAAAAATCATG	hypothetical protein	rv5_gp191 [Escherichia phage rv5]	8E-38	94	62/65 (95%)	YP_002003693
orf184	115323	115162	53	5.7	4.9	GGGAGGTACAAAAATG	hypothetical protein	FV3_00181 [Enterobacteria phage vB_EcoM-FV3]	4E-19	58	43/46 (93%)	AEZ65317
orf185	115733	115455	92	10.2	8.8	AGGAGTTCTCA	hypothetical	rv5_gp193 [Escherichia	1E-56	92	86/92	YP_002

						TTTAGAATTTTGAATG	protein	phage rv5]			(93%)	003695
orf186	116230	116069	53	6.5	10.2	AGAAAATCAGAAAATG	hypothetical protein	rv5_gp194 [Escherichia phage rv5]	1.1	70	15/32 (47%)	YP_002003696
orf187	116669	116340	109	12.7	9.4	AGG*GGACGACAAATG	hypothetical protein	rv5_gp195 [Escherichia phage rv5]	2E-74	109	108/109 (99%)	YP_002003697
orf188	116863	116666	65	7.5	9.1	AGGAGGGTGCAGATG	hypothetical protein	FV3_00185 [Enterobacteria phage vB_EcoM-FV3]	4E-36	67	63/65 (97%)	AEZ65321
orf189	117101	116856	81	8.8	4.6	AGGAGATAAAGTATG	hypothetical protein	rv5_gp198 [Escherichia phage rv5]	9E-51	81	80/81 (99%)	YP_002003700
orf190	117454	117122	110	12.4	4.8	AGTGAGTATCGTGCCATG	hypothetical protein	rv5_gp199 [Escherichia phage rv5]	7E-71	110	105/110 (95%)	YP_002003701
orf191	117656	117465	63	7.6	6.0	AGCGACGTATTATG	hypothetical protein	rv5_gp200 [Escherichia phage rv5]	8E-40	63	63/63 (100%)	YP_002003702
orf192	117914	117720	64	7.7	9.3	AGGATTTGGGAGAGAATTATG	hypothetical protein	FV3_00189 [Enterobacteria phage vB_EcoM-FV3]	3E-39	64	60/64(94%)	AEZ65325
orf193	118111	117941	56	6.2	4.8	AGAGAGGGAGCACTATG	hypothetical protein	rv5_gp203 [Escherichia phage rv5]	4E-31	56	53/55 (96%)	YP_002003705
orf194	118623	118165	152	16.8	6.6	AGGAGCTGGCATACCGTG	hypothetical protein	Tk.4 protein_gp204 [Escherichia phage rv5]	5E-88	152	124/152 (82%)	YP_002003706
orf195	119038	118613	141	16.9	4.3	CGGAGAACTAAGATG	hypothetical protein	FV3_00192[Enterobacteria phage vB_EcoM-FV3]	2E-96	141	137/141 (97%)	AEZ65328
orf196	119304	119107	65	7.7	4.3	AGGAGGCCACTGCCCATG	hypothetical protein	rv5_gp206 [Escherichia phage rv5]	6E-40	65	65/65 (100%)	YP_002003708
orf197	119817	119401	138	16	4.3	AGGAGATCTGAAAAATG	hypothetical protein	rv5_gp207 [Escherichia phage rv5]	7E-98	138	138/138 (100%)	YP_002003709
orf198	120503	119880	207	24.4	9.1	CGGTAGGTCTGCAATATG	endonuclease VII	endonuclease VII_gp208 [Escherichia phage rv5]	8E-150	207	204/207 (99%)	YP_002003710
orf199	121746	120475	423	45.8	5.5	AGGAGACAAATAATG	hypothetical protein	rv5_gp209 [Escherichia phage rv5]	0	423	421/423 (99%)	YP_002003711
orf200	122111	121746	121	13.8	4.4	CGGAGATTCCATAATG	hypothetical protein	rv5_gp210 [Escherichia phage rv5]	2E-79	121	120/121 (99%)	YP_002003712
orf201	122440	122195	81	8.6	4.1	AGGAGACCTTAAGATG	hypothetical protein	rv5_gp211 [Escherichia phage rv5]	8E-50	81	80/81 (99%)	YP_002003713
orf202	122760	122458	100	11.6	4.3	AGGAGAAGCAGCAAATG	hypothetical protein	rv5_gp212 [Escherichia phage rv5]	4E-65	100	99/100 (99%)	YP_002003714
orf203	123139	122750	129	13.8	4.1	ACGAGGAAGCGTAATG	hypothetical protein	rv5_gp213 [Escherichia phage rv5]	7E-85	129	127/129 (98%)	YP_002003715
orf204	123444	123139	101	11.6	4.4	AGGACCTAATACAATG	hypothetical protein	FV3_00200[Enterobacteria phage vB_EcoM-FV3]	6E-62	106	95/99 (96%)	AEZ65336
orf205	123729	123475	84	9.4	4.2	AGGAGACTGCCAAGATG	hypothetical protein	FV3_00201[Enterobacteria phage vB_EcoM-FV3]	7E-54	84	84/84 (100%)	AEZ65337
orf206	124177	123806	123	14.6	5.1	AGGAGGTAGGATG	hypothetical protein	FV3_00202[Enterobacteria phage vB_EcoM-FV3]	2E-82	123	119/123 (97%)	AEZ65338
orf207	124382	124188	64	7.3	5	AAGAGGGCCTATG	hypothetical protein	rv5_gp217 [Escherichia phage rv	1E-38	64	62/64 (97%)	YP_002003719
orf208	124606	124379	75	8.7	5.3	AGAAGGAGACCGATCAATG	hypothetical protein	rv5_gp218 [Escherichia phage rv5]	8E-42	75	68/75 (91%)	YP_002003720
orf209	124887	124603	94	10.7	6.5	AAGAGGAGACTTTTATG	hypothetical protein	FV3_00205[Enterobacteria phage vB_EcoM-FV3]	9E-63	94	93/94 (99%)	YP_007006376
orf210	127714	124937	925	106.7	6.9	AGGAGGAGACAGTATG	DNA polymerase	DNA pol. [Enterobacteria phage vB_EcoM-FV3]	0	809	797/808 (99%)	YP_007006380
orf211	128445	127711	244	27.6	6.7	AGGAGAACACTTTATG	HNH endonuclease	HNH endonuclease [Enterobacteria phage vB_EcoM-FV3]	2E-20	227	69/192 (36%)	YP_007006254
orf212	130582	128504	692	77.4	5.6	AGGAGCAGAATTAATG	DNA helicase/ primase	DNA replicative helicase/primase_gp225 [Escherichia phage rv5]	0	692	679/692 (98%)	YP_002003727
orf213	131366	130572	264	29.6	6.9	AGGCCCTGCCCGAAAGGGTG	hypothetical protein	rv5_gp226 [Escherichia phage rv5]	0	254	250/254 (98%)	YP_002003728
orf214	131870	131388	160	18.5	6.1	AGGAGATAGTGTTATG	hypothetical protein	rv5_gp227 [Escherichia phage rv5]	2E-100	160	155/160 (97%)	YP_002003729
orf215	132281	131883	132	14.7	4.3	GGGAGGTTTCTGATG	hypothetical protein	rv5_gp228 [Escherichia phage rv5]	1E-78	131	125/131 (95%)	YP_002003730
orf216	132586	132281	101	11.8	4.5	AAGAG*TACAATCAAATG	hypothetical protein	rv5_gp229 [Escherichia phage rv5]	1E-66	101	99/101 (98%)	YP_002003731
orf217	133925	132600	441	50	6.3	AGGAGAGCACCAAACGATG	adenine methyltransferase	putative adenine methyltransferase_gp230 [Escherichia phage rv5]	0	441	427/441 (97%)	YP_002003732
orf218	134328	133987	113	12.8	4.3	AAGAGGGGGACGTATG	hypothetical protein	rv5_gp231 [Escherichia phage rv5]	4E-76	113	112/113 (99%)	YP_002003733
orf219	135695	134325	456	51.4	7.5	AGGAGGCGTAATG	putative helicase	putative helicase_gp232 [Escherichia phage rv5]	0	456	456/456 (100%)	YP_002003734
orf220	136900	135695	401	45.8	4.8	AGGAGACCAAGATG	rIIB protector	rIIB protector_gp233 [Escherichia phage rv5]	0	401	401/401 (100%)	YP_002003735

[a] RBS consensus sequence of *E. coli* AGGAGGT.

[b] Identity = a.a. protein phage 2/a.a. protein with a hit (% identity).

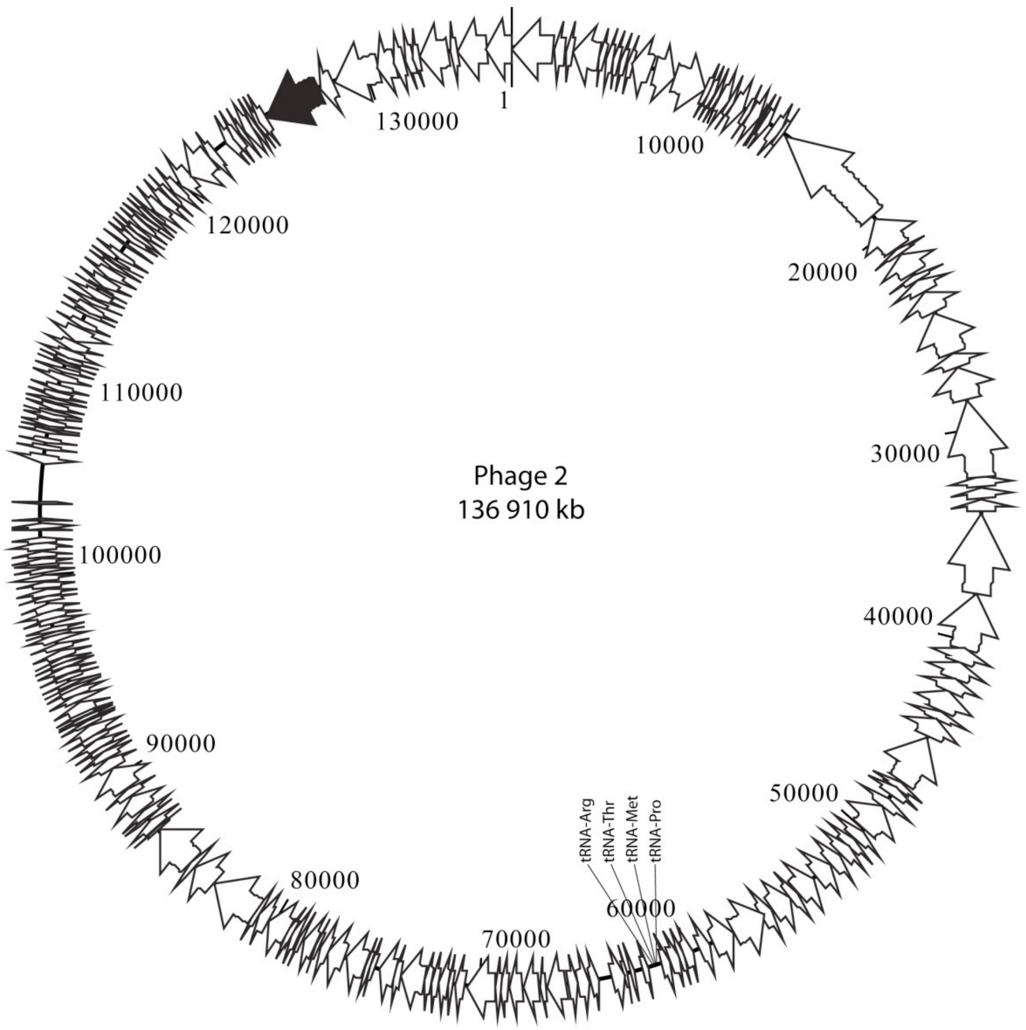

Figure S1. Genomic map of the coliphage 2 genome. Each arrow represents a putative ORF. The black arrow is gene *orf210*.

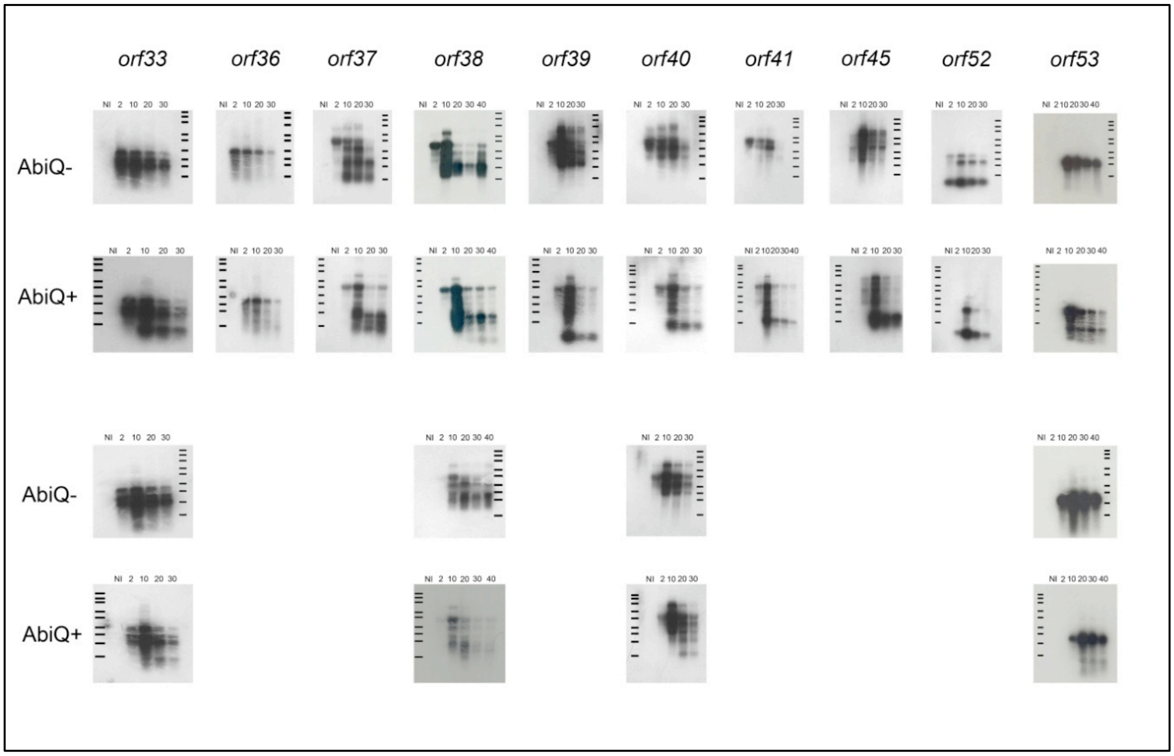

Figure S2. Northern blot results for phages P008 (Panel A) and P008-Q12 (Panel B) early- and middle-expressed genes. A time course experiment of phage-infected *L. lactis* IL1403 with or without AbiQ was performed and samples were withdrawn at time NI (Non-Infected), 2, 10, 20, 30 and 40 minutes. Total RNA was extracted with Trizol (Invitrogen) and migrated through 1% agarose-formaldehyde gels. The transfer to nylon membrane and hybridization procedure is described in Materials and Methods. The probes presented here detect the sense transcript for early-expressed (from *orf33* to *orf52*) and middle-expressed (*orf53*) genes (named _s2 in the Table S1). The ladder used is the 0.5-10 kb ladder (Invitrogen) with bands in the following order: 10, 8, 6, 4, 3, 2, 1.5, 1, and 0.5 kb.

A)

```
                      10        20        30        40        50        60        70
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|.. Similarity/Identity
P008-ORF38  MYTAEEREQIIDIVDKMSLLRQDFDGAFTWIKENVAMPFDFDGEQQFISDLKQLVKINALKFGKIYEGVLN*
bIL170-E14  ............................A......S.............................................................* 96%/97%
sk1-ORF33   ...................................S.............E.....................* 96%/97%
712-ORF33   ...L..K.............K..........R...S...................................* 92%/93%
jj50-ORF32  ...................................S...............N...................* 96%/97%
p2-ORF33    ...................................S.............E.....................* 96%/97%
```

B)

```
                      10        20        30        40
            ....|....|....|....|....|....|....|....|... Similarity/Identity
bIL170-m1   MTEEQLLFKQETLSKVDFNEFLLNAVECGLINLDTALIFKGE*
P008-orf53  ..............M...........................*  98%/98%
sk1-orf51   ..............E...........................*  98%/98%
jj50-orf46  ..............E...........................*  98%/98%
712-orf51   ..D..................................V....*  95%/95%
p2-orf46    ..............E...........................*  98%/98%
```

Figure S3. Alignments of A) ORF38 (P008) and B) M1 (bIL170) proteins with their homologues in 936 phages. The similarity and identity of the proteins was calculated using Bioedit software.

Additional references

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