Supplemental Table 1. Open Reading Frames deduced from Ldl1 and their predicted proteins

Gene	Start	End	Length (aa)	kDa	Strand	RBS/Start Codon[a]	Predicted Function	Representative similarity to proteins in database[b]	Identity (aa)	e-value
1	101	547	149	16.39	+	aa**agagg**taaaaa**atg**				
2	706	1077	124	13.64	+	at**aggagg**tatacaaaa**atg**	DNA repair protein family protein	DNA repair protein RadC [Enterococcus faecium C1904]	28% (32)	2.00E-04
3	1092	1418	109	11.99	+	**a**t**g**aaaggaaaaaa**atg**				
4	1436	1765	110	12.1	+	c**aggagg**ttttaaa**atg**				
5	3220	3339	40	4.4	+	tgaa**aggaga**acaaac**atg**				
6	3419	3805	129	14.19	+	a**aa**ct**gagg**ttaaa**atg**				
7	3811	3996	62	6.82	+	tt**agaaag**t**g**tgattatt**gtg**				
8	4011	4166	52	5.72	+	at**aggaag**t**g**tagtaatc**atg**				
9	4168	4938	257	28.27	+	cg**a**t**gg**t**aag**taac**atg**		fatty acid/phospholipid synthesis [Lactobacillus phage ATCC 8014-B2]	27% (52)	0.02
10	5439	5852	138	15.18	+	**gaga**t**gg**tttaaa**atg**	HNH endonuclease	HNH endonuclease [Lactobacillus phage ATCC 8014-B2]	54% (71)	9.00E-46
11	5978	6385	136	14.96	+	tcaa**aggaga**ttctgac**ttg**	terminase small subunit	terminase small subunit [Lactobacillus phage ATCC 8014-B2]	35% (47)	9.00E-20
12	6372	8132	587	64.57	+	agcctt**aa**t**gaa**t**g**acg**atg**	phage large subunit	terminase large subunit [Lactobacillus phage ATCC 8014-B2]	74% (336)	0.00E+00
13	8145	9626	494	54.34	+	gaa**agaagg**tgtt**ttg**	portal	portal protein [Lactobacillus phage ATCC 8014-B2]	45% (168)	7.00E-101
14	9616	10770	385	42.35	+	t**aggaag**tgaacaagaagaaa**gtg**	prohead protease	major capsid protein [Lactobacillus phage ATCC 8014-B2] (PROTEASE DOMAIN)	52% (100)	3.00E-48
15	10770	12041	424	46.64	+	ga**aggagc**tgttccatta**gtg**	phage major capsid	major capsid protein [Lactobacillus phage ATCC 8014-B2]	34% (148)	4.00E-63
16	12200	12835	212	23.32	+	gaa**agaagc**atagaaaat**atg**	HNH endonuclease	putative HNH homing endonuclease [Lactobacillus phage phiJL-1]	52% (100)	8.00E-47
17	12884	13195	104	11.44	+	agaa**aggagaag**aggcttt**ttg**		hypothetical protein 8014-B2_0026	39% (25)	7.00E-05
18	13198	13578	127	13.97	+	a**agaa**c**gg**aaatctgaca**atg**	head-tail adaptor	head-tail adaptor [Lactobacillus phage ATCC 8014-B2]	41% (77)	1.00E-25
19	13571	14056	162	17.82	+	atcc**agaagg**aaagg**gtg**	head-tail-joining protein	head-tail joining protein [Lactobacillus phage ATCC 8014-B2]	59% (17)	4.00E-04
20	14060	14515	152	16.72	+	ctt**ggagg**taatat**atg**	tail protein	tail protein [Lactobacillus phage ATCC 8014-B2]	37% (36)	6.00E-10
21	14535	15182	216	23.76	+	a**a**t**ggagaa**tataatat**atg**	major tail protein	major tail protein [Lactobacillus phage ATCC 8014-B2]	40% (79)	3.00E-40
22	15271	15883	204	24.1	+	aga**aagag**t**g**ttataatatt**atg**		conserved hypothetical protein [Lactobacillus paracasei subsp. paracasei ATCC 25302]	22% (23)	3.30E-02
23	15936	23819	2628	289.08	+	gaa**agag**t**agg**aatatatat**atg**	tape measure protein	SLT domain protein [Lactobacillus pasteurii CRBIP 24.76]	54% (308)	0
24	23888	26443	852	93.72	+	ga**agaaagg**aaattaacac**atg**	distal tail protein	hypothetical protein HMPREF9024_01543 [Pediococcus acidilactici 7_4]	35% (144)	1.00E-43
25	26466	28958	831	91.41	+	t**agaaagg**aattctccattat**atg**	Tal-like protein	hypothetical protein PEPE_0991 [Pediococcus pentosaceus ATCC 25745]	36% (298)	2.00E-158

26	28955	30541	529	58.19	+	taa**aggag**t**g**ataccaga**atg**	adsorption protein	adsorption protein [Lactobacillus delbrueckii subsp. bulgaricus ND02]	41% (101)	1.00E-36
27	30519	34190	1224	134.64	+	attt**ga**cc**a**t**a**tc**ga**aaa**atg**	adsorption protein	minor structural protein gp58 [Lactobacillus phage LL-H]		
28	34208	34675	156	17.16	+	aa**aggaga**actaatc**atg**		hypothetical protein [Lactobacillus phage LL-H]	74% (73)	5.00E-42
29	34686	34844	53	5.83	+	aat**aggaga**agcact**atg**				
30	34930	35283	118	12.98	+	ag**aagagg**ataatcttt**atg**		ORF 109 [Lactobacillus phage mv4]	31% (30)	3.00E-04
31	35296	35712	139	15.29	+	a**a**ta**gagg**aaaaaaatt**atg**		holin [Lactobacillus jensenii SJ-7A-US]	32% (39)	6.00E-07
32	35734	36045	104	11.44	+	a**agg**aaaaa**agg**gtta**atg**		GAF sensor hybrid histidine kinase [Methylobacterium sp. 4-46]	43% (29)	2.30E-02
33	36029	36463	145	15.95	+	**aagagg**ttaaatgaat**atg**	holin	holin [Lactobacillus phage phiPYB5]	50% (61)	2.00E-31
34	36477	37733	419	46.09	+	aa**aggag**tattaata**gtg**	lysin	lysin [Lactobacillus delbrueckii subsp. bulgaricus ND02]	58% (180)	2.00E-106
35	37811	38788	326	35.86	+	aagaa**agagg**aaact**atg**	recombinase/integrase	recombinase/integrase [Lactobacillus phage ATCC 8014-B2]	53% (171)	8.00E-118
36	38865	39710	282	31.02	-	caagaa**aggagag**ttta**tg**	HNH endonuclease	putative endonuclease [Lactobacillus phage phiAT3]	41% (104)	4.00E-54
37	39832	43569	1246	137.06	-	a**aggagg**ataaaac**aagg**tacaa**atg**	DNA polymerase	putative DNA polymerase [Bacillus subtilis subsp. natto]	41% (508)	0.00E+00
38	43721	43918	66	7.26	-	ta**agaaagg**acaaat**atg**				
39	44015	44677	221	24.31	-	gtgaaaggtgaaatataaaaagt**atg**	HNH endonuclease	putative HNH homing endonuclease [Lactobacillus phage phiJL-1]	48% (94)	1.00E-46
40	44775	45431	219	24.09	-	ta**aggaga**atgaccaac**atg**		hypothetical protein KQS_07715 [Flavobacterium indicum GPTSA100-9]	29% (124)	1.10E+00
41	45415	46197	261	28.71	-	ta**aggaag**cgagagt**ttg**	thymidine kinase	thymidine kinase [Eubacterium yurii subsp. margaretiae ATCC 43715]	33% (78)	1.00E-25
42	46218	46874	219	24.09	-	aa**aggaga**aagattt**ttg**	extracellular transglycosylase	extracellular transglycosylase, with LysM peptidoglycan binding domain [Lactobacillus pentosus KCA1]	(37% (86)	2.00E-28
43	47269	47898	210	23.1	-	aa**aggaga**aaaacatagtggt**atg**	phage-related HNH endonuclease	putative HNH homing endonuclease [Lactobacillus phage phiJL-1]	52% (98)	1.00E-52
44	48029	48355	109	11.99	-	ttga**aggaga**ctggttcta**atg**	growth inhibitor	growth inhibitor [Xenococcus sp. PCC 7305] >gb|ELS03630.1|	31% (32)	2.00E-05
45	48355	50211	619	68.09	-	agaa**agagaaag**attct**atg**	single-stranded-dna-specific exonuclease	single-stranded-DNA exonuclease [Lactobacillus phage ATCC 8014-B2]	33% (194)	7.00E-68
46	50208	51236	343	37.73	-	a**agaagg**taatttt**gtg**	DNA primase	DNA primase [Lactobacillus phage ATCC 8014-B2]	43% (122)	3.00E-71
47	51249	51866	206	22.66	-	**aggag**tacataaaagc**atg**	HNH homing endonuclease	putative endonuclease [Lactobacillus phage phiAT3]	44% (82)	4.00E-44
48	51889	53481	531	58.41	-	attt**gggaga**tttagatta**atg**	DNA helicase	DNA helicase [Lactobacillus phage ATCC 8014-B2]	48% (247)	6.00E-153
49	53481	53834	118	12.98	-	gtt**ggaaagg**aaaaatca**atg**		hypothetical protein 8014-B2_0085 [Lactobacillus phage ATCC 8014-B2]	35% (42)	2.00E-11
50	53931	54308	126	13.86	-	aag**aaagaga**caattaaa**gtg**				
51	54332	55051	240	26.4	-	t**agaaagg**aaacct**atg**	deoxynucleoside kinase	deoxyguanosine kinase [Lactobacillus phage ATCC 8014-B2]	50% (115)	1.00E-73
52	55063	55815	251	27.61	-	agcac**a**c**gagg**acttctg**atg**		hypothetical protein Pnap_2274 [Polaromonas naphthalenivorans CJ2]	25% (43)	6.00E+04

53	55815	56315	167	18.37	-	aatag**aggagg**aatt**atg**	phosphatidylglycerophosphatase a	phosphatidylglycerophosphatase A [Lactobacillus reuteri]	41% (67)	2.00E-39
54	56329	56550	74	8.14	-	att**gaaaggg**cattttatatt**atg**				
55	56656	57297	214	23.54	-	agaa**aggaga**taataatctt**atg**	HNH endonuclease	putative HNH homing endonuclease [Lactobacillus phage phiJL-1]	59% (85)	2.00E-39
56	57436	58524	363	39.93	-	agaagaa**agaa**c**aagg**aaaacaaat**atg**	ATP binding cassette transporter	ABC superfamily ATP binding cassette transporter, binding protein [Lactobacillus delbrueckii subsp. lactis DSM 20072]	50 & (180)	8.00E-110
57	58627	58800	58	6.38	-	ag**aagagg**aaaacta**atg**				
58	58800	58970	57	6.27	-	ta**gaaag**taaatgacaaatgg				
59	58974	59234	87	9.57	-	atgc**gggag**c**g**gtttatta**atg**				
60	59234	59701	156	17.16	-	aaga**aagagag**atttatatt**atg**	nucleoside deoxyribosyltransferase	Nucleoside deoxyribosyltransferase [Lactobacillus hominis CRBIP 24.179]	70% (108)	5.00E-77
61	59758	60081	108	11.88	-	ctgatta**aggga**cgac**atg**				
62	60091	60342	84	9.24	-	**aag**ta**aag**tacatattc**atg**				
63	60394	60666	91	10.01	-	t**ag**t**ga**t**a**caaattg**atg**				
64	60692	60805	38	4.18	-	gcac**agga**t**ga**aaaata**atg**		hypothetical protein LDBND_1222 [Lactobacillus delbrueckii subsp. bulgaricus ND02]	50% (13)	0.046
65	60805	61011	69	7.59	-	aa**atggagg**tatttaata**gtg**				
66	61112	62380	423	46.53	-	gaagatt**aaaaagg**ttactgga**atg**	putatve DNA repair enzyme	DNA polymerase [Lactobacillus phage ATCC 8014-B2]	37% (159)	5.00E-77
67	62480	63139	220	24.2	-	t**a**c**gaaagg**aaatcgttatt**atg**	phage antirepressor protein	phage-related antirepressor [Lactobacillus phage Sha1]	51% (98)	1.00E-52
68	63217	64305	363	39.93	-	tta**a**c**ggagg**aaaacct**gtg**	atp gtp binding protein	ATP/GTP binding protein [Lactobacillus phage ATCC 8014-B2]	45% (160)	1.00E-91
69	64406	65185	260	28.6	-	ta**agaa**c**agg**ataaaatatact**atg**	phage antirepressor protein	putative antirepressor [Lactobacillus phage c5]	65% (165)	2.00E-111
70	65460	66386	309	33.99	-	ttt**ag**t**gagg**taaaacact**atg**	replication related protein	replication protein [Lactobacillus phage ATCC 8014-B2]	32% (104)	6.00E-35
71	67596	67802	69	7.59	-	ta**a**t**gg**t**gg**ttaattaaat**atg**				
72	67805	68014	70	7.7	-	ac**agaaagag**tgatagt**atg**				
73	68011	68874	288	31.68	-	aa**agaggag**cataaaaa**atg**	HNH endonuclease	putative endonuclease [Lactobacillus phage phiAT3]	45% (93)	9.00E-47
74	68871	69224	118	12.98	-	tgatt**ggaaaga**agcact**atg**		hypothetical protein PAV_5c03930 [Paenibacillus alvei DSM 29]	30% (25)	0.082
75	69221	69670	150	16.5	-	att**agaaag**c**gag**atttttaaa**ttg**		conserved hypothetical protein [Enterococcus faecalis T1]	46% (67)	3.00E-30
76	69762	70514	251	27.61	-	ttgaa**agagaga**actaaa**atg**	phage antirepressor protein	Ant [Lactobacillus phage mv4]	74% (183)	8.00E-131
77	70516	71175	220	24.2	-	agaac**gggaagg**tttat**gtg**	phage antirepressor protein	prophage antirepressor [Leuconostoc mesenteroides subsp. cremoris ATCC 19254]	64% (144)	2.00E-93
78	71206	71313	36	3.96	-	agcaa**aaagg**acaaaatc**atg**	putative truncated antirepressor	putative antirepressor II [Lactobacillus phage JCL1032]	74% (31)	5.00E-10
79	71330	72112	261	28.71	-	a**a**t**ggaagg**aaatcgtgtt**atg**	phage antirepressor protein	prophage antirepressor [Lactobacillus phage AQ113]	67% (174)	5.00E-123