TABLE S1. ORF’s and genetic features of *L. helveticus* ΦAQ113

ORF	Start	Stop	Size (aa)	pI	Putative RBS and start codon AGGAGGACAGCTATG*	Putative Predicted Function	Organism matched	Identity (%)	E-value
1	1	489	162	9.52	AGCATCAAAAGGCTGTAAAAATG	Phage terminase small subunit	*Lactobacillus vaginalis* ATCC 49540	66	6,00E-12
2	600	1232	210	10.03	CATAGAAAGGCTATGATCACATG	HNH endonuclease	*Bacteroides* sp. 3_1_33FAA	46,4	4,00E-54
3	1365	1775	136	9.10	TTGAAAGAAGGTGATTAAGATTG	Possible phage terminase large subunit B	*Lactobacillus vaginalis* ATCC 49540	82	7,00E-83
4	1929	2528	200	5.09	AAGCTCAAACACCTTCAGGAATG	Putative phage terminase large subunit B	*Lactobacillus gasseri* phage KC5a	80,4	6,00E-120
5	2479	3615	378	4.85	GAGAAACGCGAAAGGAGGCTTTG	Portal protein	*Lactobacillus gasseri* ATCC 33323	71	2,00E-111
6	3651	3986	111	9.05	AAGAAGTCTAGTGATTAATTATG	Minor head protein	*Lactobacillus johnsonii* prophage Lj771	54	7,00E-27
7	3997	4185	62	9.22	CGGAATATGACCTTTGAACAATG	Unknown protein			
8	4294	4833	179	5.01	AAAAGGTAAGGAGAATTTATATG	Phage minor structural protein GP20	*Lactobacillus gasseri* ATCC 33323	58,8	1,00E-70
9	4848	5924	358	5.01	AAATAGAGGAGATTTATTAAATG	Putative phage major capsid protein	*Lactobacillus gasseri* phageKC5a	71	2,00E-178
10	5942	6313	123	4.36	TAGCATAAGGTGGTGATTGGATG	Head-tail connector protein gp15	Bacteriophage SPP1	47,3	2,36E-08
11	6310	6492	60	9.85	AACTTCAGGAGATTACCAGAATG	Hypothetical protein Ll771_035	*Lactobacillus johnsonii* prophage Lj771	59,3	8,00E-15
13	6835	7260	141	4.54	GCTTTTAGGAATTTACTATCATG	Hypothetical protein LGAS_614	*Lactobacillus gasseri* ATCC 33323	38	4,00E-24
14	7229	7432	67	4.83	ACAAAGGAGCTTAGATTTAAATG	Hypothetical protein	*Lactobacillus gasseri* phage KC5a	37	4,00E-03
15	7436	8896	486	5.17	TTAAAGGAGGTATGTAATAAATG	Putative phage sheath tail protein	*Lactobacillus gasseri* JV-V03	50	2,00E-146
16	8908	9381	157	4.88	GTTAGATAGGAGGTAAATAAATG	Sheat tail protein	*Lactobacillus gasseri* ATCC 33323	60,6	1,00E-68
17	9393	9809	138	4.76	ATTCAGTAAGGAGAAAATAAATG	Phage XkdN-like protein	*Lactobacillus gasseri* 224-1	46	2,00E-32
19	10058	12304	748	10.08	AACTAGAAAGGAGTAATATATG	Tape measure protein	*Lactobacillus gasseri* 224-1	60,8	3,00E-140
21	12421	12894	157	5.76	GTAGTGCATTAAATCNACCTGTG	Minor tail protein gp26-like	*Lactobacillus gasseri* ATCC 33323	31	3,00E-17
22	12901	13602	233	9.84	AATCATTAAGTTAGGAAGCGATG	LysM-like protein	*Lactobacillus gasseri phage* KC5a	48	3,00E-62
23	13595	14662	355	9.58	AATGAGCGAGGTTAAAAGATATG	Phage late control gene D protein GPD	*Lactobacillus gasseri* ATCC 33323	44	2,00E-93
24	14635	14979	114	7.93	GTAAACGGCTCTATGAGTTAATG	Hypothetical protein Ll771_045	*Lactobacillus johnsonii* prophage Lj771	50,4	2,00E-35
25	15005	15418	137	3.85	AGGATAGGTGAAGACGGTTTTG	Phage protein DUF2634 superfamily	*Lactobacillus gasseri* JV-V03	57	5,00E-42
26	15408	16553	381	4.56	AAGTAGGTGGATATAGTAGATG	Baseplate J-like protein	*Lactobacillus gasseri* 224-1	62,7	1,00E-179
27	16546	17115	189	4.83	TTTAGGTGAGGTGACTATAAATG	Hypothetical protein Ll771_048	*Lactobacillus johnsonii* prophage Lj771	47,8	2,00E-52
28	17301	19031	576	5.29	TGTAAGAGGTGATTTTTAAAAGT	Hypothetical protein HMPREF0891_0013	*Lactobacillus crispatus* 214-1	51	5,00E-44
29	19047	19430	127	5.81	AATAGAAAGGGGGCGAACACATG	Hypothetical protein HMPREF0891_0014	*Lactobacillus crispatus* 214-1	40,2	3,00E-21
30	19496	20092	198	5.07	AATAGAAAGGAGCCAATAAAATG	Phage related protein	*Lactobacillus amylovorus* GRL 1112	51,6	4,00E-49
31	20106	20294	62	4.46	GCAATAAGGAGGATTAGGCTATG	Hypothetical protein LA2_05900	*Lactobacillus amylovorus* GRL 1112	88,5	3,00E-31

32	20687	20896	69	6.23	AGAAAGGAGCTGATACACTTATG	Predicted protein	*Lactobacillus crispatus* MV-3A-US	76,8	1,00E-32
33	20880	21107	75	5.07	ACGAAAGGAGTTAAATAACAATG	Predicted protein	*Lactobacillus crispatus* MV-3A-US	61,8	2,00E-23
34	21116	21505	129	4.83	GTGGGTGACTAGTCGTGTCAATG	Predicted protein	*Lactobacillus crispatus* MV-3A-US	40	7,00E-18
35	21514	22689	391	9.72	ATGCCAAAAATGGCTAAAACATG	Endolysin	*Lactobacillus helveticus* phage f-0303	88	0.0
36	22909	23610	233	4.64	AGAAATAGGGGGAAAAGAAAATG	Unknown protein			
37	23610	23939	109	9.8	TATGAATATGAAGAAATATAATG	Unknown protein			
38	23920	25089	389	9.5	AAAAATTGGAGCGTCTGCGAGTG	Hypothetical protein lmo1311	*Listeria monocytogenes* EGD-e	47,3	4,00E-118
39	25079	26380	433	9.24	CAATAGAAAGGAGTTTGCAAATG	Phosphoadenosine phosphosulfate reductase	*Akkermansia muciniphila* ATCC BAA-835	51	9,00E-160
40	26286	26876	196	9.06	AGAAAAGAGGAGAAAAGCAATTG	Co-activator of prophage gene expression	*Staphylococcus pseudintermedius* HKU10-03	81,9	3,00E-101
43	27531	27746	71	10.14	TATAGTAAGGCGTGGAAATAATG	Cro-like protein phage associated	*Lactobacillus* phage Sal2	52	3,00E-12
44	27851	28639	262	9.21	AAGTCGAAAGGAAAAATTAAATG	Prophage antirepressor	*Lactobacillus jensenii* 269-3	80,7	2,00E-152
45	28795	28974	59	6.27	TTAGACAAATAGGAGAAAAAATG	Hypothetical protein LA2_07830	*Lactobacillus amylovorus* GRL 1112	64,4	1,00E-19
46	28988	29149	53	9.57	GTACTAAGGAGGATTCAAGATG	Hypothetical protein LA2_07825	*Lactobacillus amylovorus* GRL 1112	56,6	2,00E-15
47	29195	29725	176	9.56	TAGGAGATTATAAACCAAAAATG	HNH endonuclease	*Lactobacillus rhamnosus* Lc-Nu	42,3	2,00E-34
49	29730	30101	123	3.94	AGATTGTGAGGCATAACACAATG	Prophage protein	*Lactobacillus crispatus* CTV-05	74,8	1,00E-60
50	30112	30399	95	4,97	TGGAAAGTAGGTTCTTAATAATG	Predicted protein	*Lactobacillus crispatus* MV-3A-US	29	5,00E-05
51	30399	31043	214	7.78	CAGAAATGGAGTAGAGACTAATG	ERF Recombinase	*Lactococcus lactis* phage P335	57	1,00E-35
52	31054	31890	278	9.03	AGCTATTTAGAGGGAAAACTATG	DNA replication protein	*Lactobacillus johnsonii* prophage Lj771	47	6,00E-67
53	31925	32725	266	9.24	TGTCAAAAGCAAAGCCAATCATG	DNA replication protein	*Lactobacillus crispatus* CTV-05	45,9	5,00E-83
54	32727	33083	118	7.8	TACGGACAAGAGGTACTAATATG	Putative transcriptional regulator	*Lactobacillus gasseri* phage KC5a	73	1,00E-26
56	33516	33941	141	6.27	ACAAGTAGATATTGCAGATGATG	Single-strand DNA binding protein	Temperate phage phiNIH1.1	55	9,00E-48
57	34001	34471	156	8.90	TTTTGATTTCCTTAACAATAATG	Unknown protein			
58	34490	34663	57	5.41	AATTATTCGAGGTGATATAGATG	Unknown protein			
59	34679	34969	96	5.6	ATTAAAGCAATACAGTGTGCATG	Hypothetical protein HMPREF0506_1653	*Lactobacillus crispatus* JV-V01	55	3,00E-31
60	34941	35324	127	7.79	GATCCTTGCTCGTAGAATTCATG	Phage protein - Restriction nuclease superfamily	*Lactobacillus gasseri* JV-V03	83,6	5,00E-64
61	35431	35574	47	5.08	CGTGGGAGAAGGTGGTTTAGATG	Predicted protein	*Lactobacillus crispatus* MV-3A-US	61,9	3,00E-10
63	35692	36132	146	5.93	AAAATTTATGGAGTGATTATGTG	Phage transcriptional regulator, ArpU family	*Lactobacillus gasseri* JV-V03	38	7,00E-26
62	36372	36521	49	9.95	TTGATAGGAATAAAAAAATCATG	Hypothetical protein LA2_07740	*Lactobacillus amylovorus* GRL 1112	63,6	1,00E-11

* The sequence shown includes the immediate upstraem 20 nucleotides of the putative start codon and the putative RBS sequences find with RBSfinder (Delcher et al; 1999). The nucleotides complementary to the 3' end of the 16S rRNA of L.delbruckii (3'-…………; Mikkonen et al, 1994).

A.L. Delcher, D. Harmon, S. Kasif, O. White, and S.L. Salzberg. Improved Microbial Gene Identification with Glimmer. Nucleic Acids Research, 27 (1999), 4636-4641.