

Table S1. List of Q33 and BM13 (respectively) putative open reading frames and their predicted functions or highest phage homologues

Q33							
Orf no.	Start position	Stop position	Size (aa)	Mol. Wt. (kDa)	Putative Function	Highest BlastP phage hit*	% identity (aa)
1	390	614	74	8.5	cro	P335 cro	100 (74)
2	641	859	72	8.1		<i>L. lactis</i> MG1363 prophage protein	92 (72)
3	869	1609	246	28.4	Anti-repressor	Phage regulatory protein <i>Bacillus</i> sp., putative anti-repressor	41 (237)
4	1621	1836	71	8.3		bIL285/bIL286 Orf11, hypothetical protein	100 (71)
5	1951	2346	131	14.9		ul36 Orf131, hypothetical protein	100 (131)
6	2355	3113	252	28.8	sak	ul36 Sak, single-strand annealing protein	100 (252)
7	3106	3564	152	16.9	SSB	TP901-1, single-strand DNA binding prot.	87 (152)
8	3734	4516	260	29.3	Replication protein	bIL285/ul36 DNA replication protein	99 (260)
9	4516	5241	241	27.2	Topoisomerase	bIL285 Orf17 topoisomerase	99 (241)
10	5238	5627	129	15.7	Resolvase	bIL285 RusA, Holliday junction resolvase	100 (129)
11	5630	5773	47	5.3		Ul36 Orf129, hypothetical, pseudogene	100 (937)
12	6224	5874	116	13.3		<i>L. lactis</i> KF147 integrase, pseudogene	95 (84)
13	6585	6286	99	11.3		<i>S. parauberis</i> DNA-binding protein	41 (97)
14	6820	6921	63	7.5		<i>S. suis</i> repressor-related protein, cro	52 (63)
15	7140	7814	224	26.0		<i>L. lactis</i> KF147 phage regulatory protein	97 (219)
16	7894	9588	564	64.7		<i>L. garvieae</i> phage protein, hypothetical	53 (558)
17	10054	10260	69	7.5		hypothetical	
18	10376	10582	68	8.3		ul36 Orf68a, hypothetical	99 (68)
19	10591	10701	40	4.8		hypothetical	
20	10736	10915	62	7.3		Tuc2009 Orf21, hypothetical	98 (59)
21	10905	11474	189	22.5		Q30, hypothetical	98 (186)
22	11484	11756	90	10.5		bIL285 Orf26, hypothetical	98 (90)
23	11759	12019	102	12.3		<i>L. garvieae</i> phage protein, hypothetical	85 (71)
24	12016	12381	121	14.0		Ul36.t1k1, hypothetical	100 (121)
25	12378	12800	140	15.4	dUTPase	phiLC3 Orf141 dUTPase	99 (136)
26	12889	13134	81	8.9		P335, hypothetical	98 (81)
27	13181	13423	80	9.4		Phi31.1 Orf80, hypothetical	99 (80)
28	13420	13614	64	7.7		bIL286 Orf33	95 (64)
29	13761	13949	62	7.3		ul36.k1t1, hypothetical	79 (52)
30	13946	14404	152	18.1		hypothetical	
31	14567	14965	132	14.8		hypothetical	
32	14955	16196	413	46.9	Terminase	<i>E. faecalis phage</i> phiFL4A, terminase large subunit	66 (410)
33	16196	17551	455	51.9	Portal	<i>E. faecalis phage</i> phiFL4A, portal protein	55 (452)
34	17626	18621	331	37.3	Capsid protein	<i>E. faecalis phage</i> phiFL4A gp35, capsid	48 (275)
35	18791	18925	44			hypothetical	
36	19067	19669	200	23.1	Scaffolding protein	<i>C. perfringens</i> phage minor structural protein, possible scaffolding protein	36 (174)
37	19681	19929	82	8.7		hypothetical	
38	19945	20841	298	32.1	Major Capsid protein	<i>S. suis</i> major capsid protein	57 (291)
39	20977	21543	188	21.5		<i>E. faecalis</i> phiFL4A gp41, hypothetical	50 (188)
40	21545	21865	106	12.1	Head-tail connector	<i>E. faecalis phage</i> phiFL4A gp42	52 (105)
41	21870	22289	139	15.3		<i>E. faecalis phage</i> phiFL4A gp43, possible activator of gpU (gpZ)	53 (135)
42	22289	22660	123	14.7		<i>E. faecalis phage</i> phiFL4A gp44, possible tail terminator (gpU)	39 (122)
43	22660	23508	282	29.7	Major tail protein	<i>E. faecalis phage</i> phiFL4A gp45,	46 (199)
44a	23533	23880	115	12.7		<i>E. faecalis phage</i> phiFL4A, chaperone gpG	36 (143)
44b	23856	24209	76	9.1	chaperone gpT	Programmed frame shift, fused to orf44a,	
45	24209	26488	759	79.9	Tail tape measure	<i>Bifidobacterium catenulatum</i> phage tape measure protein	41 (582)
46	26491	27363	290	32.3	Tail structural protein	<i>E. faecalis phage</i> phiFL4A tail protein gp49	42 (291)
47	27365	28480	371	42.0		<i>E. faecalis phage</i> phiFL4A gp50	45 (365)
48	28477	29505	342	37.7	Baseplate component	Tuc2009 BppL, receptor binding protein	73 (159)
49	29519	29743	74	8.6		Hypothetical phi31	100 (74)
50	29757	30044	95	10.56	Holin	BK5-T holin	100 (95)
51	30044	30823	259	28.0	Endolysin	Phi31 lysin	99 (259)
52	30937	31101	54	6.4		Tuc2009_56	93 (43)

BM13							
Orf no.	Start	Stop	Size (aa)	MW (kDa)	Predicted function	Highest BlastP phage hit	% identity (aa)
1	127	351	74	8.5	Cro-Like repressor	ORF2 4268	99 (74)
2	378	1094	238	27.7	Anti-repressor	ORF3 4268	98 (237)
3	1108	1302	64	7.2			
4	1314	1952	212	24.6			
5	2127	2369	80	9.1	Repressor	ORF1531 <i>L. lactis</i> KF147 prophage	64 (184)
6	2382	2702	106	11.9		ORF7 bIL309	95 (79)
7	2712	3452	246	28.4	Regulatory protein	ORF1878 <i>L. lactis</i> CV56 prophage	81 (101)
8	3465	3659	64	7.3		ORF0737 <i>S. aureus</i> 21305 prophage	39 (240)
9	3704	3940	78	9.1		ORF1876 <i>L. lactis</i> CV56 prophage	97 (64)
10	4038	4434	131	14.9		ORF10 ul36	99 (77)
11	4443	4958	171	19.3	Sak	ORF13 <i>L. lactis</i> phage bIL286	99 (131)
12	4972	5523	183	21.0	SSB	ORF163 ul36.13	97 (130)
13	5672	6391	239	27.9	DNA rep protein	ORF183 ul36.13	97 (183)
14	6401	7291	296	34.2	Helicase	ORF11 r1t	98 (244)
15	7300	7464	54	6.4		ORF12 r1t	99 (296)
16	7454	7843	129	15.7	Resolvase	ORF13 r1t	94 (54)
17	7846	8085	79	9.5		ORF18 bIL285	99 (129)
18	8196	8402	68	8.3		ORF18 ul36	96 (79)
19	8557	8736	59	6.9		ORF19 ul36	99 (68)
20	8726	9295	189	22.4		ORF19 Tuc2009	98 (59)
21	9305	9577	90	10.4		ORF18 r1t	93 (189)
22	9574	10122	182	21.3		ORF26 bIL285	97 (90)
23	10122	10694	190	8.5	HNH endonuclease	ORF0996 <i>L. lactis</i> CV56 prophage	55 (230)
24	10691	11110	139	15.4	dUTPase	ORF11 <i>S. gordonii</i> phage PH15	44 (185)
25	11183	11335	50	5.8		ORF17 P335	95 (139)
26	11340	11882	180	20.5		ORF18 P335	97 (38)
27	11909	12601	230	26.4		ORF25 ul36	62 (78)
28	12598	12843	81	9.6		ORF230 phi31.1	100 (230)
29	12840	13040	66	8.1		ORF80 phi31.1	99 (68)
30	13048	13233	61	6.9		ORF66 phi31.1	100 (66)
31	13237	13449	70	8.4		ORF1855 <i>L. lactis</i> CV56 prophage	100 (61)
32	13527	13937	136	16.3	Transcriptional activator	hypothetical	
33	14089	14499	136	15.4		ORF1117 <i>L. garvieae</i> ATCC 49156 prophage	49 (79)
34	14489	15730	413	46.9	Terminase large subunit	hypothetical	
35	15730	17151	473	54.2	Portal	<i>E. faecalis</i> phage phiFL4A large terminase subunit	66 (410)
36	17156	18205	349	39.6	Minor head protein	<i>E. faecalis</i> phage phiFL4A, portal protein	54 (468)
37	18181	18317	44	5.2		<i>E. faecalis</i> phage phiFL4A gp35, capsid protein	48 (275)
38	18459	19061	200	23.1	Scaffold structural protein	ORF34 TP901-1	76 (38)
39	19073	19315	80	8.8		hypothetical	
40	19331	20227	298	32.2	Major capsid protein	ORF2124 <i>S. dysgalactis</i> SK1249 prophage	57 (165)
41	20363	20929	188	21.5	Structural protein	<i>E. faecalis</i> phage phiFL4A gp41	94 (189)
42	20931	21251	106	12.1	Structural protein	<i>E. faecalis</i> phage phiFL4A gp42	52 (105)
43	21256	21675	139	15.3	Structural protein	<i>E. faecalis</i> phage phiFL4A gp43, possible activator of gpU (gpZ)	53 (135)
44	21675	22046	123	14.7	Structural protein	<i>E. faecalis</i> phage phiFL4A gp44, possible tail terminator	39 (122)
45	22046	22894	282	29.8	Major tail protein	<i>E. faecalis</i> phage phiFL4A gp45	46 (199)
46a	22919	23266	115	12.8		<i>E. faecalis</i> phage phiFL4A gp46	36 (143)
46b	23365	23595	76	9.1		<i>E. faecalis</i> phage phiFL4A gp47, possible programmed frame shift, fused to orf46a	50 (72)
47	23595	25796	733	76.9	Tape measure protein	ORF1646 <i>B. bifidum</i> BGN4 prophage	37 (722)
48	25799	26671	290	32.3	Tail protein	gp49, <i>E. faecalis</i> phage phiFL4A tail prot.	41 (291)
49	26673	27788	371	42.0	Structural protein	<i>E. faecalis</i> phage phiFL4A gp50	43 (365)
50	27785	28813	342	37.6	Base plate	ORF343 phiLC3	43 (238)
51	28827	29129	100	11.8		ORF56 ul36	94 (100)
52	29119	29343	74	8.1	Holin	ORF57 ul36	96 (74)
53	29340	30629	429	46.4	Endolysin	ORF58 M1 ul36	96 (429)
54	30705	30905	66	7.7		ORF50 r1t	98 (42)

*Phage hits represented are lactococcal phages unless otherwise indicated