

Original article

Genomic identification and characterization of prophages associated with *Citrobacter freundii* strains

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SUPPLEMENTARY MATERIALS

Supplementary Table 1. Characterization of the prophage genomes in *C. freundii* genomes

	Accession number	Strain	Genome Size(bp)	Potential phage regions in Chromosome	Number of intact Prophages	Total prophage size (bp)	Total intact prophage size (bp)	Prevalence of Total prophage in Chromosome (%)	Prevalence of Intact Phage in Chromosome (%)	Family of Intact Prophage regions*
1	CP085642.1	Cf.1	5153556	7	3	186300	113200	3.61	2.19	P(1), S(2)
2	LR134118.1	NCTC9750	4960737	6	4	173300	142100	3.49	2.86	M(2), S(1)
3	AP025035.1	RTE-E5	4901704	7	2	160600	61400	3.27	1.25	P(1), S(1)
4	CP057863.1	RHB12-C20	5359677	9	4	304000	173000	5.67	3.23	M(2), P(2), S(1)
5	CP024679.1	UMH15	5343952	11	7	415100	312200	7.77	5.84	M(4), P(2), S(1)
6	CP026045.1	FDAARGOS_61	5258481	2	1	66400	48100	1.26	0.91	S(1)
7	LR699006.1	MGYG-HGUT-02495	5258449	2	1	66400	48100	1.26	0.91	S(1)
8	CP057146.1	RHB35-C22	5112880	5	3	149400	93900	2.92	1.84	S(2), M(1)
9	CP057149.1	RHB35-C18	5112878	5	3	149400	93900	2.92	1.84	M(2), P(1)
10	CP056809.1	RHBSTW-00162	5066655	12	5	320800	164900	6.33	3.74	M(4), S(1)
11	CP057136.1	RHB36-C06	5042664	6	4	204200	188700	4.05	3.74	M(2), S(2)
12	CP085737.1	52323CZ	4989314	8	1	210500	38100	4.21	0.76	M(1)

13	CP056314.1	RHBSTW-00830	4983531	5	4	214900	176800	4.31	3.55	M(1), S(2), U(1)
14	CP033742.1	FDAARGOS_550	4969137	3	3	138900	138900	2.79	2.79	S(2), M(1)
15	CP024683.1	UMH13	4917351	9	2	197200	39900	4.01	0.81	S(1), U(1)
16	CP057868.1	RHB12-C05	4904767	10	4	295000	105800	6.01	2.16	M(2), S(1), I(1)
17	CP024672.1	HM38	4899014	5	4	171500	159400	3.5	3.25	M(2), S(2)
18	CP056395.1	RHBSTW-00589	4895815	9	4	190100	126600	3.88	0.03	M(3), U(1)
19	CP057867.1	RHB12-C12	4889917	8	3	268700	155500	5.49	3.18	S(2), M(1)
20	CP057866.1	RHB12-C18	4889497	10	4	297300	149500	6.08	3.06	S(4)
21	CP047247.1	LDL3-3	4878270	8	3	285200	131900	5.85	2.7	M(2), S(1)
22	CP056967.1	RHB41-C16	4861768	9	3	226200	88500	4.65	1.82	M(1), S(1), U(1)
23	CP038856.1	Upstream_1	4839493	6	3	177700	120600	3.67	2.49	S(2), M(1)
24	CP056244.1	RHBSTW-00923	4818023	7	2	187100	57300	3.88	1.19	M(1), U(1)
25	CP056473.1	RHBSTW-00477	4792949	6	4	188300	132400	3.93	2.76	S(3), M(1)
26	CP056597.1	RHBSTW-00334	4783420	5	2	222100	160200	4.64	3.35	M(2)
27	CP056559.1	RHBSTW-00408	4774094	3	2	106600	87300	2.23	1.83	M(2)
28	CP057353.1	RHB29-C07	4755731	7	2	181500	66500	3.82	1.39	S(1), U(1)
29	CP057258.1	RHB31-C16	4719098	7	2	137100	36600	2.91	0.78	S(1), U(1)

30	CP057506.1	RHB24-C05	4696854	5	1	109000	26800	2.32	0.57	M(1)
31	CP057509.1	RHB24-C03	4692130	5	1	109000	26800	2.32	0.57	S(1)
32	CP033744.1	FDAARGOS_549	4974986	4	4	134800	134800	2.71	2.71	M(1), S(2), U(1)
33	CP049015.1	ATCC 8090	4957773	5	4	146800	140900	2.96	2.84	M(3), S(1)
34	CP056907.1	RHBSTW-00011	5384013	7	6	338600	309500	6.29	5.75	M(4), S(2)
35	CP058318.1	M92	5338221	17	7	471100	300000	8.83	5.62	M(4), S(2), P(1)
36	CP024819.1	CRCB-101	5311319	7	3	231000	141700	4.35	2.67	M(2), S(1)
37	CP056235.1	RHBSTW-00942	5297052	15	3	348900	160300	6.59	3.03	M(2), S(1)
38	CP047269.1	N16-03880	5268984	13	9	412100	354000	7.82	6.72	M(7), S(2)
39	CP055551.1	RHBSTW-00200	5266015	3	2	120100	92500	2.28	1.76	S(2)
40	CP022151.1	705SK3	5242839	15	8	474600	363700	9.05	6.94	M(4), S(4)
41	LR881934.1	PSV	5233206	7	5	295100	274500	5.64	4.73	S(3), M(1), P(1)
42	CP057824.1	RHB14-C12	5232071	7	6	276000	261400	5.28	4.99	M(4), S(2)
43	CP047273.1	N18-04078	5216668	11	8	368300	323600	7.06	6.2	M(4), S(3), U(1)
44	CP038656.1	565	5207876	15	7	612000	322000	11.75	6.18	S(2), M(4), P(1)

45	CP056505.1	RHBSTW-00449	5205079	12	7	437900	327900	8.41	6.29	S(1), M(4), P(2)
46	CP047279.1	N18-04128	5195939	12	9	376700	355200	7.25	6.84	M(4), S(4), U(1)
47	CP024677.1	UMH16	5195086	7	4	280400	224800	5.39	4.33	S(4)
48	CP056232.1	RHBSTW-00965	5167828	10	3	293300	152800	5.68	2.96	M(1), S(2)
49	CP038658.1	680	5167642	14	7	564900	356100	10.93	6.89	S(1), M(4), P(1)
50	CP047275.1	N18-04085	5167126	10	8	368500	323700	7.13	6.26	S(3), M(4), U(1)
51	CP038653.1	154	5143118	12	4	481600	239700	9.36	4.66	M(1), S(2), P(1)
52	CP056827.1	RHBSTW-00135	5136614	4	3	213700	173200	4.16	3.37	M(2), S(1)
53	CP060659.1	MGH281C	5128186	7	6	272700	231500	5.32	4.51	S(3), M(2), U(1)
54	CP056850.1	RHBSTW-00120	5126944	11	7	327800	285600	6.39	5.57	M(4), P(1), U(2)
55	CP047307.1	L75	5125834	5	2	124500	73500	2.43	1.43	S(2)
56	CP035276.1	R17	5124258	3	3	153800	112000	3	2.19	M(2), P(1)
57	CP059427.1	CIFR51929	5107866	6	3	196900	160000	3.86	3.13	M(2), S(1)
58	CP016952.1	SL151	5096586	8	4	282700	170300	5.55	3.34	M(1), S(2), P(1)

59	CP042478.1	C50	5095110	11	2	264400	95200	5.19	1.87	M(1), S(1)
60	CP056527.1	RHBSTW-00435	5087480	11	3	283900	154500	5.58	3.04	M(2), S(1)
61	CP056622.1	RHBSTW-00310	5065503	6	3	211800	134400	4.18	2.65	M(2), S(1)
62	CP026056.1	FDAARGOS_73	5064681	13	5	383800	161500	7.56	3.19	S(2), M(2), U(1)
63	CP056653.1	RHBSTW-00214	5056951	7	4	287600	186200	5.69	3.68	M(2), S(2)
64	AP022380.1	STW0522-01	5055174	7	3	194600	106000	3.85	2.09	S(1), M(1), U(1)
65	AP022384.1	STW0522-19	5044118	7	2	194600	93100	3.86	1.85	S(2)
66	CP056595.1	RHBSTW-00342	5031983	10	2	271100	93100	5.39	1.85	M(2)
67	CP042517.1	E33	5022915	9	3	240500	107000	4.79	2.13	M(2), S(1)
68	LS992183.1	Citrobacter freundii str. U2785	5009078	8	3	284000	141500	5.67	2.82	M(1), S(2)
69	CP056852.1	RHBSTW-00119	5004623	10	5	300600	190000	6.01	3.79	S(3), M(1), U(1)
70	CP024673.1	UMH19	4996291	9	3	293300	117500	5.87	2.35	M(1), S(2)
71	CP056592.1	RHBSTW-00350	4982711	7	4	241700	178200	4.85	3.58	M(3), S(1)
72	CP085726.1	56415CZ	4976621	5	3	201200	172200	4.04	3.46	M(2), S(1)
73	CP056245.1	RHBSTW-00915	4956708	7	5	295700	249300	5.97	5.03	M(2), S(2), P(1)

74	CP040698.1	R47	4952107	5	2	132400	81200	2.67	1.64	S(2)
75	CP056644.1	RHBSTW-00267	4936735	9	5	297600	254600	6.03	5.16	M(5)
76	CP045726.1	zone4	4919686	5	4	162300	144000	3.29	2.93	M(3), S(1)
77	CP024881.1	AR_0022	4919453	7	4	226700	156500	4.61	3.18	M(2), P(1), U(1)
78	LR890181.1	MSB1_1H-sc- 2280393	4908711	4	2	210800	144000	4.29	2.93	S(2)
79	CP056839.1	RHBSTW-00126	4906122	12	5	311200	180200	6.34	3.67	M(4), S(1)
80	CP056451.1	RHBSTW-00502	4892927	8	4	271400	190000	5.55	3.88	M(3), S(1)
81	CP057864.1	RHB12-C19	4885177	4	2	159300	89100	3.26	1.82	M(1), S(1)
82	CP056333.1	RHBSTW-00714	4883072	10	7	406200	309500	8.32	6.34	M(4), S(2), U(1)
83	CP024680.1	UMH14	4859315	5	1	134400	12100	2.77	0.25	U(1)
84	CP056229.1	RHBSTW-00968	4773574	5	1	179700	63700	3.76	1.33	S(1)
85	CP007557.1	CFNIH1	5099034	11	7	379000	322400	7.43	6.32	M(3), S(3), P(1)
86	CP057746.1	RHB16-C09	4936996	7	4	237400	175700	4.81	3.56	M(3), S(1)
87	CP022273.1	18-1	5215381	12	6	392300	257700	7.52	4.94	M(3), S(3)
88	CP056910.1	RHBSTW-00006	5182470	15	6	431200	262800	8.32	5.07	M(3), S(3)
89	LS992175.1	Citrobacter freundii str. E2614	5172644	12	8	371000	286200	7.17	5.53	M(3), S(4), U(1)
90	CP016762.1	B38	5134500	7	5	432000	399900	8.41	7.79	M(3), S(2)

91	CP060650.1	MGH279	5128721	7	6	275800	234600	5.78	4.74	M(2), S(4)
92	CP060662.1	MGH281	5128689	7	6	272700	231500	5.32	4.51	M(2), S(4)
93	CP056573.1	RHBSTW-00370	5126475	10	5	297800	190800	5.81	3.72	M(2), S(3)
94	CP060654.1	MGH283	5125085	7	6	272400	231200	5.32	4.51	M(2), S(4)
95	CP056256.1	RHBSTW-00902	5108587	11	6	335800	235700	6.57	4.61	M(2), S(3), U(1)
96	CP056238.1	RHBSTW-00935	5103922	11	6	335500	235400	6.57	4.61	M(2), S(3), U(1)
97	CP070549.1	CF49969	5098771	10	5	288100	195700	5.65	3.84	M(1), S(4)
98	CP086287.1	DY2010	5092352	10	4	297300	146700	5.84	2.88	M(2), S(2)
99	CP056336.1	RHBSTW-00697	5084908	9	6	325100	259000	6.39	5.09	S(2), M(2), U(1), P(1)
100	CP055538.1	RHBSTW-00398	5067906	8	3	262600	157400	5.18	3.11	S(3)
101	CP047773.1	Cfr-13	5050163	13	3	359100	103200	7.11	2.04	M(1), U(2)
102	CP056365.1	RHBSTW-00658	5044080	7	3	196100	114200	3.89	2.26	M(2), S(1)
103	CP056466.1	RHBSTW-00486	5027895	9	3	267100	124600	5.31	2.48	M(1), S(2)
104	CP055588.1	RHBSTW-00084	5024564	10	3	285600	124600	5.68	2.48	M(1), S(2)
105	CP055247.1	ZY198	4997964	9	3	313000	148800	6.26	2.98	M(1), S(2)
106	CP054278.1	IDR1900015725- 01-02	4995557	8	3	340200	208100	6.81	4.17	M(2), S(1)

107	CP056181.1	RHBSTW-01016	4992760	10	4	320700	211100	6.42	4.23	M(1), S(2), P(1)
108	CP055421.1	RHBSTW-00862	4978770	8	3	230100	124600	4.62	2.51	M(1), S(2)
109	CP046502.1	111	4954350	8	4	281400	190200	5.68	3.84	M(4)
110	CP057319.1	RHB30-C04	4928912	7	3	233500	135900	4.74	2.76	M(1), S(2)
111	CP056515.1	RHBSTW-00444	4927085	6	4	236100	182200	4.79	3.69	M(4)
112	CP056289.1	RHBSTW-00858	4920836	6	1	151700	46300	3.08	0.94	M(1)
113	CP056293.1	RHBSTW-00857	4920836	6	1	151700	46300	3.08	0.94	M(1)
114	CP048382.1	62	4695344	5	3	190200	134300	4.05	2.86	M(1), S(2)
115	CP032184.1	AR_0116	5121015	12	4	348600	182300	6.81	3.56	M(2), S(1), P(1)
116	CP056635.1	RHBSTW-00302	5099027	13	6	431600	242300	8.46	4.75	M(5), S(1)
117	CP042524.1	E11	5088693	6	3	186100	141400	3.66	2.78	M(2), S(1)
118	CP042534.1	E51	5070767	6	3	183400	141400	3.62	2.79	M(2), S(1)
119	CP057323.1	RHB30-C03	5062205	10	6	261500	218400	5.17	4.31	M(5), S(1)
120	CP056586.1	RHBSTW-00355	5031645	12	4	378600	194600	7.59	3.67	M(3), S(1)
121	CP011657.1	CAV1741	5029496	8	4	246800	157200	4.91	3.13	M(1), S(3)
122	CP055582.1	RHBSTW-00110	5023392	10	3	285400	124600	5.68	2.48	M(1), S(2)
123	CP078020.1	CF_324	4996134	9	6	379400	321900	7.59	6.44	M(2), S(3), P(1)
124	CP054294.1	IDR1800045912- 01-00	4988401	7	4	234800	181400	4.71	3.64	M(2), S(2)

125	CP070559.1	CF50935	4984319	7	3	236900	106900	4.75	2.14	M(1), S(2)
126	CP070544.1	CF48846	4977086	6	3	225100	112300	4.52	2.56	M(2), S(1)
127	CP037734.1	CAV1857	4947788	8	3	225900	91400	4.57	1.85	M(1), S(2)
128	CP056208.1	RHBSTW-00985	4829251	6	1	161800	50300	3.35	1.04	P(1)
129	CP011612.1	CAV1321	4976908	7	4	176100	130600	3.54	2.62	M(2), S(2)
130	CP059849.1	3863	4947352	6	5	219500	201500	4.44	4.07	U(1), S(4)
131	CP092463.1	Cf7308	5108147	13	7	452900	305900	8.87	5.99	S(3), M(2), P(1), U(1)
132	CP103365.1	140542	5092216	11	6	428100	263500	8.41	5.17	M(5), S(1)
133	CP092493.1	SCLZS47	5122668	11	7	446900	324800	8.72	6.34	M(5), S(2)
134	CP066115.1	Cfr-12	4926478	6	3	198500	134300	4.03	2.73	M(2), S(1)
135	CP098330.1	59174	5197783	14	9	476300	345600	9.16	6.65	M(5), S(3), U(1)
136	LS992175.1	E2614	5172644	12	8	371000	286200	7.17	5.53	S(4), M(3), U(1)
137	CP026677.1	AR-0023	4784656	4	1	122100	41100	2.55	0.86	M(1)
138	CP048416.1	CitB	4784656	2	0	49900	0	1.04	0	null
139	CP024898.1	AR-0021	4784670	5	2	132000	72400	2.76	1.51	M(1), S(1)
140	AP026940.1	CF20-4P-1 DNA	4907659	6	2	172700	75700	3.52	1.54	M(1), S(1)
141	OW995941.1	112	5218036	12	6	399800	241700	7.66	4.63	M(4), S(1), P(1)

142	CP071265.1	MEI002	4907484	4	1	100300	34200	2.04	0.7	S(1)
143	CP097107.1	GMU8049	4997193	9	4	286900	206300	5.74	4.13	S(3), M(1)
144	OW969875.1	22	5176111	15	6	438400	367500	8.47	7.1	M(5), S(3), U(1)

*M= Myoviridae,S=Siphoviridae 42%,P= Podoviridae 4.67%, I=Inoviridae, U= Unclassified

Supplementary Table 2. List of Toxin and virulence proteins

Toxin Proteins/Virulence proteins	Clade	Strain associated prophages
MsgA	Clade 1	18-1 -1; CF49969 -3,4; M92 -5; N18-04128 -9; psv -4; RHBSTW-00310 -2; IDR1800045912-01-00 -2; RHBSTW-00355 -1; ZY198 -3; 3863 -2,4; CF20-4P-1 DNA -1,2 ; cfr-12 -3; 140542 -1; E2614 -5
	Clade 2	565 -3,4,5; 680 -3,4,5; B38 -3; C50 -2; FDAARGOS_550 -2; M92 -4; MGH281C -4; NCTC9750 -1; RHB29-C07 -1; RHBSTW-00342 -1; RHBSTW-00350 -3; RHBSTW-00502 -1,3; RHBSTW-00915 -3; RHBSTW-00965 -2; SL151 -2; AR_0021-1,2; AR_0023 -1; E2614 -4; SCLZS4 -4,6; U2785 -3
	Clade 3	18-1-2; 154 -1,2; 565 -1; ATCC 8090 -2,3; B38 -1,4; C50 -1; CF1 -1; FDAARGOS_73 -1,2; FDAARGOS_550 -1; HM38 -1,3; MGH279 -2,3; MGH281C -3; MGH283 -2,3; N18-04128 -4; NCTC9750 -2; psv -1,5; R47 -1,2; RHB12-C05 -1,3; RHB12-C20 -3; RHB14-C12 -1; RHB16-C09 -3; RHB36-C06 -1,3; RHBSTW-00120 -2,3; RHBSTW-00126 -3; RHBSTW-00267 -1,3,4; RHBSTW-00310 -1; RHBSTW-00334 -1,2; RHBSTW-00502 -2,4; RHBSTW-00697 -2,4,6; RHBSTW-00830 -1,2; RHBSTW-00915 -4; RHBSTW-00942 -1; RHBSTW-00965 -1,3; 111 -1; CAV1321 -2; CF48846 -1,2; IDR1800045912-01-00 -1; IDR1900015725-01-02 -1,3; RHB30-C04 -1; RHBSTW-00084 -1; RHBSTW-00355 -2; RHBSTW-00857 -1; RHBSTW-01016 -2; UMH13 -1; UMH19 -3; Zone4 -3; 112 -6; 59174 -5; 140542 -2; Cf7308 -7; U2785 -1; RHB29-C07 -2
Hcp	Clade 3	RHB12-C20-1
HipA	Clade 1	705SK3-7
T1SS secreted agglutinin RTX	Clade 1	62-1
	Clade 2	Cf7308-3; 59174-4; 140542-3
	Clade 3	RHBSTW-00126-4,2; RHBSTW-00267-1; RHBSTW-00334-1; B38-1; 112-3; RHB30-C04-1
Toxin HigB	Clade 1	RHBSTW-00120-1; MEI002-1; 705SK3-7
	Clade 2	U2785-3
	Clade 3	B38-1; U2785-1; N16-03880-7
Toxin Ykfl	Clade 1	N18-04128-8; 111-4
	Clade 2	E2614-8; SCLZS4-6
	Clade 3	RHBSTW-00942-3; IDR1800045912-01-00-4; 565-7; N18-04085-7; SL151-1; RHBSTW-00449-7
Toxin YeeV	Clade 3	RHB12-C19-1; RHB35-C22-1; RHBSTW-00126-4,2

Supplementary Table 3. Distribution of the prophages in different clades

<p>Clade 1</p>	<p>111 -2,4; 112 -5; 140542 -1; 18-1 -1; 22 -1,2,3,4; 3863 -1,2,3,4; 565 -2; 59174 -1,2,3,8,9; 62 -1; 680 -2; 705SK3 -7; CAV1741 -3; CAV1857 -3; CF 324 -4; CF20-4P-1 -1,2; CF49969 -2,3,4; CF50935 -2; Cf7308 -1,2,4,6; CFNIH1 -4; Cfr-12 -1,3; CIFR51929 -3; DY2010 -4; E11 -2; E2614 -1,2,3,5,7; E51 -2; IDR1800045912-01-00 -2,3; L75 -1,2; M92 -3,5; MEI002 -1; MGH279 -5; MGH281 -5; MGH281C -5; MGH283 -5; N16-03880 -2,6; N18-04078 -1,6,8; N18-04085 -1,6,8; N18-04128 -1,7,9; PSV -3,4; RHB12-C18 -2; RHB14-C12 -5; RHB30-C03 -6; RHB35-C18 -2; RHB35-C22 -2; RHB36-C06 -2; RHBSTW-00110 -2; RHBSTW-00119 -1,3; RHBSTW-00120 -1,5,6; RHBSTW-00126 -1; RHBSTW-00162 -2; RHBSTW-00214 -4; RHBSTW-00267 -2; RHBSTW-00302 -5; RHBSTW-00310 -2; RHBSTW-00355 -1; RHBSTW-00370 -3; RHBSTW-00398 -1,2; RHBSTW-00435 -1; RHBSTW-00444 -4; RHBSTW-00449 -3; RHBSTW-00714 -5; RHBSTW-00902 -6; RHBSTW-00935 -6; RHBSTW-01016 -3; SCLZS47 -1; STW0522-01 -1,3; UMH15 -2; ZY198 -3</p>
<p>Clade 2</p>	<p>111 -3; 112 -1; 140542 -3,4,5,6; 18-1 -5; 3863 -5; 56415CZ -1; 565 -3,4,5; 59174 -4; 62 -2; 680 -3,4,5; 705SK3 -3,5,8; AR 0022 -3,4; AR-0021 -1,2; AR-0023 -1; ATCC 8090 -1; B38 -2,3,5; C50 -2; CAV1321 -3; CAV1741 -2,4; CAV1857 -2; CF 324 -2,6; CF49969 -1; CF50935 -3; Cf7308 -3; Cfr-13 -2; CRCB-101 -2; DY2010 -3; E11 -1,3; E2614 -4,8; E33 -2; E51 -1,3; FDAARGOS 549 -3; FDAARGOS 550 -2; FDAARGOS 61 -1; FDAARGOS 73 -3; GMU8049 -1,3,4; HM38 -2,4; M92 -4,7; MGH279 -4; MGH281 -4; MGH281C -4; MGH283 -4; MGYG-HGUT-02495 -1; MSB1 1H-sc-2280393 -2; N16-03880 -4,8; N18-04078 -4; N18-04085 -4; N18-04128 -5; NCTC9750 -1; RHB12-C12 -1; RHB12-C18 -3; RHB12-C19 -2; RHB12-C20 -4; RHB14-C12 -3,6; RHB16-C09 -4; RHB29-C07 -1; RHB30-C03 -1; RHB30-C04 -2,3; RHB35-C18 -3; RHB35-C22 -3; RHB36-C06 -4; RHB41-C16 -3; RHBSTW-00006 -1,6; RHBSTW-00011 -3,4; RHBSTW-00084 -3; RHBSTW-00110 -3; RHBSTW-00119 -2,5; RHBSTW-00135 -1,3; RHBSTW-00162 -3,4,5; RHBSTW-00200 -1; RHBSTW-00214 -3; RHBSTW-00267 -5; RHBSTW-00302 -2,3,4,6; RHBSTW-00342 -1; RHBSTW-00350 -3; RHBSTW-00355 -4; RHBSTW-00398 -3; RHBSTW-00408 -2; RHBSTW-00435 -2; RHBSTW-00449 -2,5; RHBSTW-00477 -3,4; RHBSTW-00486 -3; RHBSTW-00502 -1; RHBSTW-00502 -3; RHBSTW-00589 -3,4; RHBSTW-00658 -2,3; RHBSTW-00697 -3; RHBSTW-00714 -6,7; RHBSTW-00830 -4; RHBSTW-00862 -3; RHBSTW-00902 -1,3; RHBSTW-00915 -3,5; RHBSTW-00923 -2; RHBSTW-00935 -1,3; RHBSTW-00942 -2; RHBSTW-00965 -2; RHBSTW-00968 -1; RTE-E5 -1; SCLZS47 -4,5,6,7; SL151 -2,4; STW0522-19 -1; U2785 -2,3; UMH15 -3,4; UMH19 -2 zone4 -2,4; ZY198 -2</p>
<p>Clade 3</p>	<p>111 -1; 112 -2,3,4,6; 140542 -2; 154 -1,2,3,4; 18-1 -2,3,4,6; 22 -5,6; 52323CZ -1; 56415CZ -2,3; 565 -1,6,7; 59174 -5,6,7; 62 -3; 680 -1,6,7; 705SK3 -1,2,4,6; AR 0022 -1,2; AR 0116 -2,1,3,4; ATCC 8090 -2,3,4; B38 -1,4; C50 -1; CAV1321 -1,2,4; CAV1741 -1; CAV1857 -1; CF 324 -1,5; cf1 -1,2,3; CF324 -3; CF48846 -1,2,3; CF49969 -5; CF50935 -1; Cf7308 -5,7; CFNIH1 -1,2,3,5,6,7 Cfr-12 -2; Cfr-13 -1,3; CIFR51929 -1,2; CRCB-101 -1,3; DY2010 -1,2; E2614 -1,2,3,4,5,6,6, 7,8; E33 -1,3; FDAARGOS 549 -1,2,4; FDAARGOS 550 -1,3; FDAARGOS 73 -1,2,4,5; GMU8049 -2; HM38 -1,3; IDR1800045912-01-00 -1,4; IDR1900015725-01-02 -1,2,3; LDL3-3 -1,2,3; M92 -1,2,6; MGH279 -1,2,3,6; MGH281 -1,2,3,6; MGH281C -1,2,3,6; MGH283 -1,2,3,6; MSB1 1H-sc-2280393 -1; N16-03880 -1,3,5,7,9; N18-04078 -2,3,5,7; N18-04085 -2,3,5,7; N18-04128 -2,3,4,6,8; NCTC9750 -2,3,4; PSV -1,2,5; R17 -1,2,3; R47 -1,2; RHB12-C05 -1,2,3,4; RHB12-C12 -2,3; RHB12-C18 -1,4; RHB12-C19 -1; RHB12-C20 -1,2,3; RHB14-C12 -1,2,4; RHB16-C09 -1,2,3; RHB24-C03 -1; RHB24-C05 -1; RHB29-C07 -2; RHB30-C03 -2,3,4,5; RHB30-C04 -1; RHB31-C16 -1,2; RHB35-C18 -1; RHB35-C22 -1; RHB36-C06 -1,3; RHB41-C16 -1,2; RHBSTW-00006 -2,3,4,5; RHBSTW-00011 -1,2,5,6; RHBSTW-00084 -1,2; RHBSTW-00110 -1; RHBSTW-00119 -4; RHBSTW-00120 -2,3,4,7; RHBSTW-00126 -2,3,4,5; RHBSTW-00135 -2; RHBSTW-00162 -1; RHBSTW-00200 -2; RHBSTW-00214 -1,2; RHBSTW-00267 -1,3,4; RHBSTW-00302 -1; RHBSTW-00310 -1,3; RHBSTW-00334 -1,2; RHBSTW-00342 -2; RHBSTW-00350 -1,2,4; RHBSTW-00355 -2,3; RHBSTW-00370 -1,2,4,5; RHBSTW-00408 -1; RHBSTW-00435 -3; RHBSTW-00444 -1,2,3; RHBSTW-00449 -1,4,6,7; RHBSTW-00477 -1,2; RHBSTW-00486 -1,2; RHBSTW-00502 -2,4; RHBSTW-00589 -1,2; RHBSTW-00658 -1; RHBSTW-00697 -1,2,4,5,6; RHBSTW-00714 -1,2,3,4; RHBSTW-00830 -1,2,3; RHBSTW-00857 -1; RHBSTW-00858 -1; RHBSTW-00862 -1,2; RHBSTW-00902 -2,4,5; RHBSTW-00915 -1,2,4; RHBSTW-00923 -1; RHBSTW-00935 -2,4,5; RHBSTW-00942 -1,3; RHBSTW-00965 -1,3; RHBSTW-00985 -1; RHBSTW-01016 -1,2,4; RTE-E5 -2; SCLZS47 -2,3; SL151 -1,3; STW0522-01 -2; STW0522-19 -2; U2785 -1; UMH13 -1,2; UMH14 -1; UMH15 -1,5,6,7; UMH16 -1,2,3,4; UMH19 -1,3; Upstream 1 -1,2,3; zone4 -1,3; ZY198 -1</p>

Supplementary Table 4. Representative prophages present in the genomes of *C. freundii*

SL	Accession number	Name	Family	Genome size kb	G+C%	No. of time identified in the host
1	NC_005857	Klebsiella phage phiKO2	Siphoviridae	51.6	51.49%	57
2	NC_031940	Salmonella phage 118970_sal3	Myoviridae	77.38	50.70%	55
3	NC_028699	Salmonella phage SEN34	Myoviridae	40.74	49.91%	33
4	NC_019704	Enterobacteria phage mEp237	Siphoviridae	44.38	51.43%	31
5	NC_021774	Salmonella phage FSL SP-004	Myoviridae	29.74	52.84%	25
6	NC_019706	Enterobacteria phage mEp043 c-1	Siphoviridae	42.78	50.79%	24
7	NC_019717	Enterobacteria phage HK225	Siphoviridae	45.37	51.96%	21
8	NC_016158	Escherichia phage HK639	Siphoviridae	49.58	52.45%	21
9	NC_001609	Enterobacteria phage P4	unclassified	11.62	49.53%	21
10	NC_048198	Erwinia phage vB_EhrS_59	Siphoviridae	47.12	50.41%	18
11	NC_019721	Enterobacterial phage mEp390	Siphoviridae	40.03	51.68%	18
12	NC_047753	Salmonella phage SEN8	Myoviridae	35.2	51.94%	17
13	NC_021070	Vibrio phage martha 12B12	Myoviridae	33.28	45.76%	17
14	NC_047854	Cronobacter phage ESSI-2	Myoviridae	28.77	55.17%	12
15	NC_003356	Enterobacteria phage phiP27	Myoviridae	42.58	49.35%	10
16	NC_028766	Mannheimia phage vB_MhM_3927AP2	Myoviridae	33.76	43.14%	10
17	NC_001317	Escherichia phage 186	Myoviridae	30.62	53.09%	10
18	NC_016761	Salmonella phage SPN1S	Podoviridae	38.68	50.16%	10
19	NC_019708	Enterobacteria phage mEp235	Siphoviridae	37.6	50.01%	9
20	NC_005882	Burkholderia cenocepacia phage BcepMu	Myoviridae	36.75	62.86%	8
21	NC_010463	Enterobacteria phage Fels-2	Myoviridae	33.69	52.49%	7
22	NC_015295	Erwinia phage phiEt88	Myoviridae	47.28	47.33%	7
23	NC_010393	Phage Gifsy-2	unclassified	45.84	51.10%	7
24	NC_049429	Enterobacter phage phiT5282H	Myoviridae	31.98	52.46%	6
25	NC_049460	Salmonella phage SI7	Myoviridae	30.16	54.36%	6
26	NC_019545	Salmonella phage SPN3UB	Siphoviridae	47.36	49.61%	6

27	NC_021857	Shigella phage SfIII	Myoviridae	41.48	49.17%	5
28	NC_013594	Escherichia phage D108	Myoviridae	37.24	51.76%	5
29	NC_029015	Salmonella phage SEN4	Myoviridae	33.51	53.36%	5
30	NC_019716	Enterobacteria phage mEp460	Siphoviridae	44.51	50.87%	5
31	NC_019720	Enterobacterial phage mEp213	Siphoviridae	44.12	50.98%	5
32	NC_003444	Enterobacteria phage SfV	Myoviridae	37.07	50.77%	4
33	NC_042128	Escherichia phage RCS47	Myoviridae	115.15	49.35%	4
34	NC_020850	Vibrio phage VBM1	Myoviridae	38.37	42.26%	4
35	NC_028701	Salmonella phage SEN5	Myoviridae	33.51	53.36%	4
36	NC_026611	Edwardsiella phage GF-2 DNA	Myoviridae	43.13	51.27%	4
37	NC_031077	Enterobacter phage Tyrion	Podoviridae	41.76	50.60%	4
38	NC_027398	Enterobacteria phage Sf101	Podoviridae	38.74	47.44%	4
39	NC_001901	Bacteriophage N15	Siphoviridae	46.38	51.17%	4
40	NC_019934	Cronobacter phage ENT39118	Siphoviridae	39.01	53.06%	4
41	NC_049342	Escherichia phage 500465-1	Myoviridae	39.18	52.65%	3
42	NC_047817	Klebsiella phage 3 LV-2017	Myoviridae	35.1	54.43%	3
43	NC_047833	Erwinia phage EtG	Myoviridae	30.41	54.14%	3
44	NC_049919	Escherichia phage SH2026Stx1	Podoviridae	61.56	49.39%	3
45	NC_011357	Stx2-converting phage 1717	Siphoviridae	62.15	50.91%	3
46	NC_048197	Erwinia phage vB_EhrS_49	Siphoviridae	46.84	50.84%	3
47	NC_019710	Enterobacteria phage HK140	Siphoviridae	40.71	49.91%	3
48	NC_005886	Burkholderia cenocepacia phage BcepB1A	Myoviridae	47.4	54.45%	2
49	NC_023006	Pseudomonas phage PPpW-3 DNA	Myoviridae	43.56	61.11%	2
50	NC_019455	Haemophilus phage SuMu	Myoviridae	37.15	41.87%	2
51	NC_005344	Enterobacteria phage Sf6	Podoviridae	39.04	47.47%	2
52	NC_049924	Stx2-converting phage Stx2a_F451 proviral DNA	Podoviridae	64.9	49.77%	2
53	NC_007804	Escherichia phage phiV10	Podoviridae	39.1	48.97%	2
54	NC_018279	Salmonella phage vB_SosS_Oslo	Siphoviridae	49.12	48.74%	2

55	NC_010392	Phage Gifsy-1	unclassified	48.49	51.10%	2
56	NC_001332	Enterobacteria phage I2-2	Inoviridae	6.74	42.72%	1
57	NC_005856	Enterobacteria phage P1	Myoviridae	94.8	47.31%	1
58	NC_022749	Shigella phage SfIV	Myoviridae	39.76	50.30%	1
59	NC_049459	Salmonella phage SW9	Myoviridae	31.12	53.01%	1
60	NC_019927	Cronobacter phage ENT47670	Siphoviridae	47.61	51.59%	1
61	NC_001416	Enterobacteria phage lambda	Siphoviridae	48.5	49.86%	1
62	NC_049926	Escherichia phage ECP1	Siphoviridae	40.47	51.01%	1
63	NC_006949	Enterobacteria phage ES18	Siphoviridae	46.9	48.59%	1
64	NC_019709	Enterobacteria phage mEpX1	Siphoviridae	41.57	49.31%	1
65	NC_010391	Salmonella phage Fels-1	unclassified	42.72	51.56%	1