Table S1. DDH *in silico* results obtained by Type Strain Genome Server for *C. rouxii* strains compared to the closest related type strain.

Strain	***C. rouxii* FRC0190^T**	***C. diphtheriae* NCTC 11397^T**	***C. belfantii* FRC0043^T**	***C. ulcerans* NCTC 7910^T**	***C. silvaticum* KL0182^T**	***C. pseudotuberculosis* ATCC 19410^T**
21395	90.9%	49.2%	45.2%	22.3%	21.8%	21.5%
58111	91.1%	49.2%	45.2%	22.2%	21.6%	21.5%
70862	92.7%	48.6%	44.9%	22.1%	21.8%	21.5%
70863	93.1%	48.6%	44.9%	22.2%	21.8%	21.5%
FRC0071	98.1%	48.6%	45.0%	22.8%	22.3%	21.7%
FRC0284	98.5%	48.6%	45.0%	22.8%	22.3%	21.7%
FRC0297	94.6%	48.7%	45.1%	22.2%	21.5%	21.5%
FRC0412	95.5%	48.6%	45.0%	22.1%	21.8%	21.4%
FRC0527	98.1%	48.7%	45.0%	23.0%	22.4%	21.7%
PC0230	90.3%	48.9%	45.0%	22.6%	22.6%	21.5%
PC0231	90.3%	48.9%	45.1%	22.6%	22.6%	21.5%
PC0226	90.3%	48.9%	45.0%	22.6%	22.6%	21.5%
PC0229	90.3%	48.9%	45.1%	22.6%	22.6%	21.5%
CS30	94.0%	48.7%	45.1%	22.1%	21.7%	21.5%

Table S2. Information about the Multilocus Sequence Typing for the *C. rouxii* strains.

Strain	Country	Host	ST	*atp*A	*dna*E	*dna*K	*fus*A	*leu*A	*odh*A	*rpo*B
FRC0190[T]	France	Human	181	37	25	53	39	36	35	17
21395	Brazil	Dog	918	37	75	113	39	112	21	17
58111	Brazil	Dog	918	37	75	113	39	112	21	17
70862	Brazil	Cat	899	37	25	91	26	61	21	17
70863	Brazil	Cat	899	37	25	91	26	61	21	17
FRC0071	France	Human	181	37	25	53	39	36	35	17
FRC0284	France	Human	181	37	25	53	39	36	35	17
FRC0297	France	Human	537	37	25	91	54	61	21	17
FRC0412	France	Dog	538	37	25	113	66	72	35	17
FRC0527	France	Human	181	37	25	53	39	36	35	17
PC0230	USA	Cat	74	20	14	31	26	22	21	17
PC0231	USA	Cat	74	20	14	31	26	22	21	17
PC0226	USA	Cat	74	20	14	31	26	22	21	17
PC0229	USA	Cat	74	20	14	31	26	22	21	17
CS30	Spain	Human	537	37	25	91	54	61	21	17

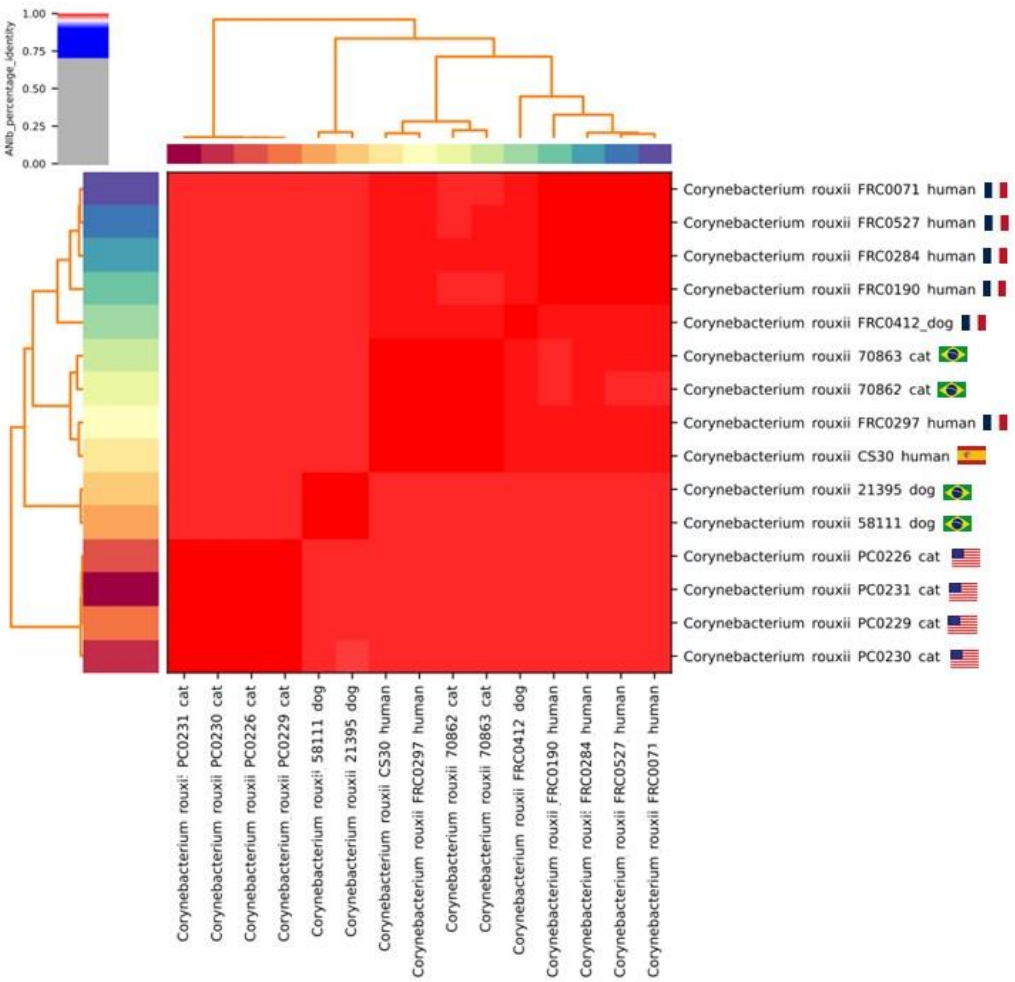

Figure S1. Heatmap representing the ANI percentage nucleotide identity of all matching regions between *C. rouxii* the genomes using PyANI v.0.2.12. The default scheme colors cells with identity > 0.95 as red, and those with < 0.95 as blue.

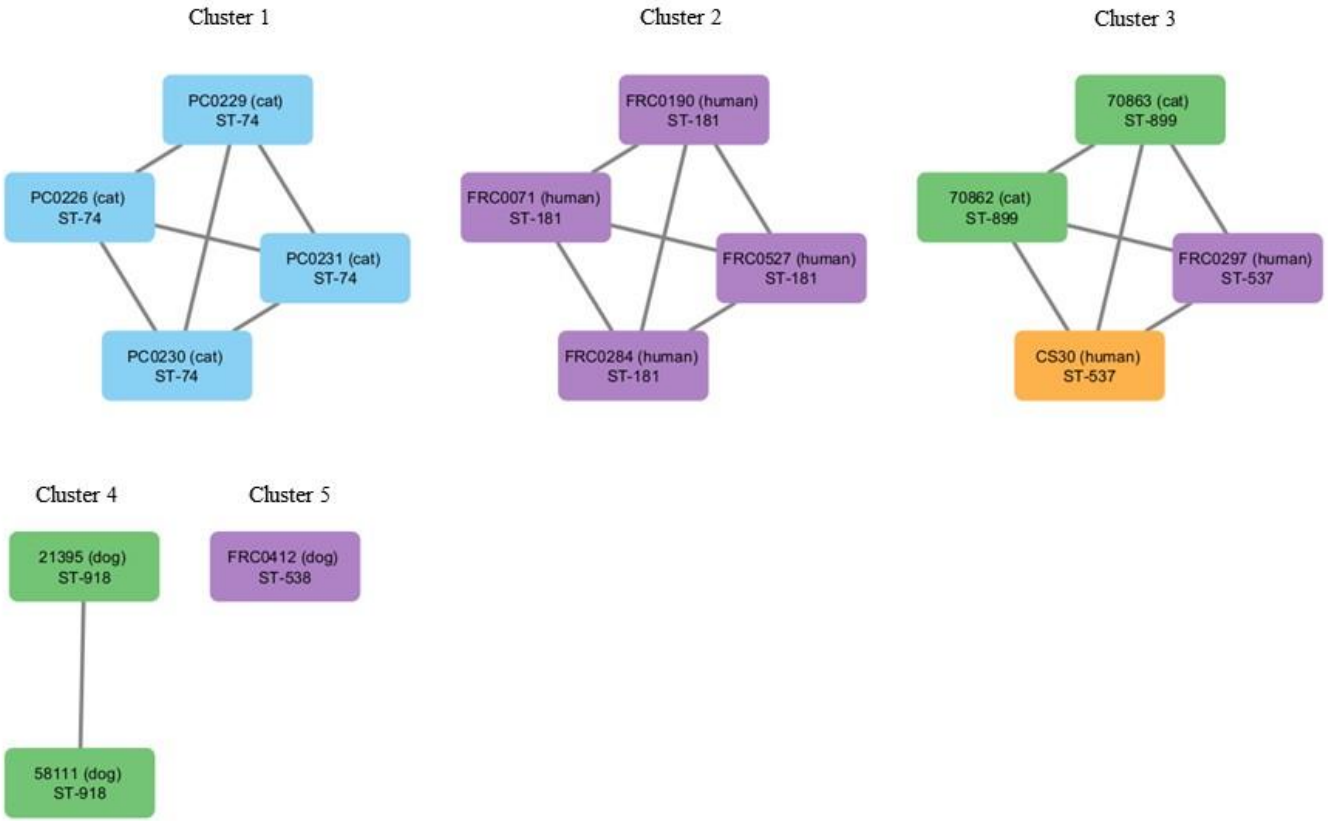

Figure S2. Clusters of *C. rouxii* strains genomes generated using PopPUNK v.2.6.0, in which the American samples are represented by blue color, Brazilian samples by green color, French samples by the purple color and Spanish samples by orange color.

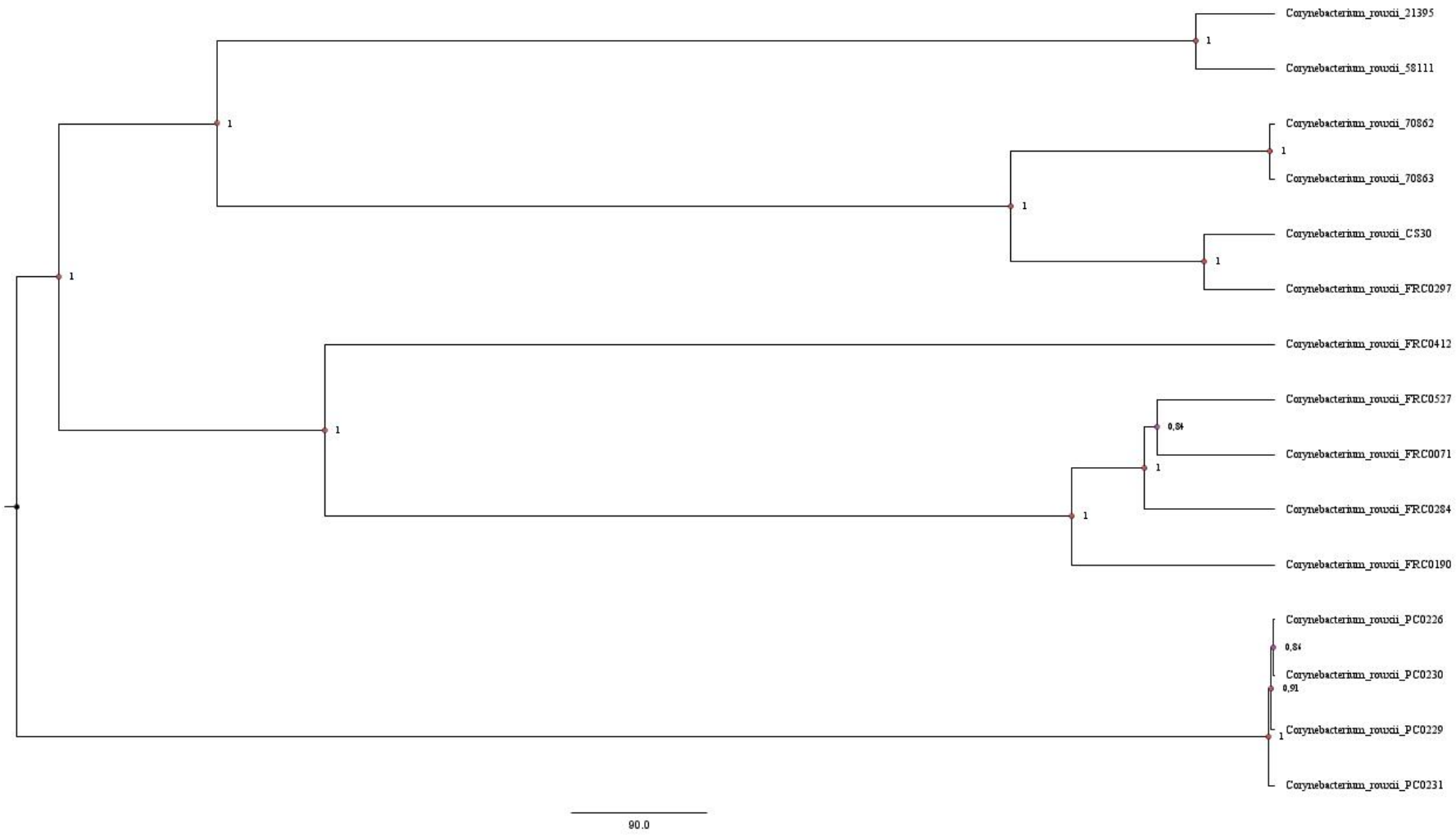

Figure S3. The wgMLST tree based on genomes from *C. rouxii* strains using PGAdb-builder.

Table S3. Information about the prophage regions found in the *C. rouxii* genomes.

Strain	Region Length (kb)	Completeness	Score	Total Proteins	Total Hypothetical Proteins	Region Position	Most Common Phage	GC%
FRC0190^{T}	34.1	Questionable	70	46	22	170752 - 204857	PHAGE_Coryne_Poushou_NC_042139	52.84
FRC0190^{T}	34.1	Incomplete	60	50	23	1280697 - 1314829	PHAGE_Coryne_Adelaide_NC_048791	53.23
FRC0190^{T}	12.5	Incomplete	10	17	4	1864480 - 1877041	PHAGE_Gordon_GMA5_NC_030907	58.10
21395	32.6	Incomplete	60	43	17	49791 - 82483	PHAGE_Coryne_Poushou_NC_042139	52.86
21395	6.2	Incomplete	40	10	4	42225 - 48497	PHAGE_Mycoba_Xeno_NC_031243	50.95
21395	6.8	Incomplete	30	8	0	100268 - 107159	PHAGE_Paenib_Tripp_NC_028930	55.19
58111	25.3	Intact	107	28	6	282040 - 307345	PHAGE_Coryne_phi673_NC_042354	53.50
58111	6.2	Incomplete	40	10	4	91876 - 98148	PHAGE_Klebsi_ST13_OXA48phi12.1_NC_049453	50.95
70862	6.8	Incomplete	30	8	0	100778 - 107670	PHAGE_Vibrio_VP58.5_NC_027981	55.20
70862	5.3	Incomplete	40	8	2	41957 - 47333	PHAGE_Vibrio_ICP3_NC_015159	55.18
70863	6.8	Incomplete	30	8	0	47746 - 54638	PHAGE_Haemop_HP1_NC_001697	55.20
70863	61.3	Questionable	80	62	27	21866 - 83174	PHAGE_Coryne_Poushou_NC_042139	53.63
70863	5.3	Incomplete	40	8	2	41957-47333	PHAGE_Rhodoc_Sleepyhead_NC_048782	55.18
FRC0071	26	Incomplete	30	28	6	131649 -157694	PHAGE_Gordon_BritBrat_NC_030942	54.81
FRC0071	10	Incomplete	40	17	6	161428 - 171483	PHAGE_Rhodoc_Sleepyhead_NC_048782	50.92
FRC0071	15.3	Incomplete	30	24	10	32868 - 48266	PHAGE_Gordon_Nyceirae_NC_031004	52.31

FRC0071	6.8	Incomplete	30	8	0	48647 - 55538	PHAGE_Gordon_Bowser_NC_030930	55.28
FRC0284	22.3	Incomplete	30	27	12	5959 - 28277	PHAGE_Gordon_Nyceirae_NC_031004	53.04
FRC0284	34	Incomplete	60	40	20	33626 - 67722	PHAGE_Coryne_Adelaide_NC_048791	53.23
FRC0284	12.5	Incomplete	10	17	4	617935 - 630495	PHAGE_Gordon_GMA5_NC_030907	58.10
FRC0284	6.8	Incomplete	30	8	0	80324-87215	PHAGE_Staphy_vB_SscM_1_NC_047767	55.28
FRC0297	6.8	Incomplete	30	8	0	100826 - 107718	PHAGE_Lactoc_phiL47_NC_023574	55.19
FRC0297	37.6	Questionable	80	14	5	95428 - 133076	PHAGE_Lactoc_TP901_1_NC_002747	55.49
FRC0412	6.8	Incomplete	30	8	0	133418 - 140310	PHAGE_Natria_PhiCh1_NC_004084	55.20
FRC0412	8.9	Incomplete	40	11	3	83381-92355	PHAGE_Sinorh_phiM9_NC_028676	54.37
FRC0412	30	Incomplete	50	32	9	1082 - 31167	PHAGE_Gordon_BritBrat_NC_030942	55.18
FRC0412	12.5	Incomplete	10	17	4	354837 - 367398	PHAGE_Gordon_GMA5_NC_030907	58.09
FRC0527	36.6	Questionable	70	48	21	18377 - 54988	PHAGE_Coryne_Poushou_NC_0421395	52.47
FRC0527	6.8	Incomplete	30	8	0	130612 - 137503	PHAGE_Natria_PhiCh1_NC_004084	55.28
FRC0527	26.1	Incomplete	30	29	6	29068 - 55174	PHAGE_Gordon_BritBrat_NC_030942	54.82
FRC0527	10.1	Incomplete	40	17	6	58909 - 69025	PHAGE_Rhodoc_Sleepyhead_NC_048782	50.92
PC0230	39.6	Questionable	80	51	21	254169 - 293862	PHAGE_Coryne_Poushou_NC_042139	52.93
PC0230	12.5	Incomplete	10	17	4	25885 - 38446	PHAGE_Gordon_GMA5_NC_030907	58.10
PC0230	12.6	Incomplete	50	22	11	484 -13089	PHAGE_Rhodoc_Sleepyhead_NC_048782	53.20

PC0230	7.9	Incomplete	40	11	3	43253 - 51183	PHAGE_Aeromo_Aes012_NC_020879	55.05
PC0230	16.5	Incomplete	40	24	7	19147 - 35745	PHAGE_Gordon_Attis_NC_041883	55.20
PC0230	31.5	Incomplete	50	36	9	124477 - 156049	PHAGE_Coryne_Poushou_NC_042139	55.63
PC0231	12.5	Incomplete	10	17	4	557244 - 569805	PHAGE_Gordon_GMA5_NC_030907	58.10
PC0231	4.1	Intact	109	7	0	1192 - 5335	PHAGE_Entero_lato_NC_001422	44.57
PC0231	7.9	Incomplete	40	11	3	83278 - 91208	PHAGE_Vibrio_ICP3_NC_015159	55.05
PC0231	16.5	Incomplete	40	24	7	19147 - 35745	PHAGE_Gordon_Attis_NC_041883	55.20
PC0231	31.5	Incomplete	50	36	9	2662 - 34234	PHAGE_Coryne_Poushou_NC_042139	55.63
PC0231	39.6	Questionable	80	51	21	254108 - 293801	PHAGE_Coryne_Poushou_NC_042139	52.93
PC0231	12.6	Incomplete	50	22	11	484 - 13089	PHAGE_Coryne_Juicebox_NC_048070	53.20
PC0226	12.6	Incomplete	50	22	11	484 - 13089	PHAGE_Rhodoc_Sleepyhead_NC_048782	53.20
PC0226	5.0	Intact	95	7	0	286 - 5384	PHAGE_Entero_lato_NC_001422	44.60
PC0226	12.5	Incomplete	10	17	4	25885 - 38446	PHAGE_Gordon_GMA5_NC_030907	58.10
PC0226	31.5	Incomplete	50	36	9	2662 - 34234	PHAGE_Coryne_Poushou_NC_042139	55.63
PC0226	7.9	Incomplete	40	11	3	83278 - 91208	PHAGE_Bacill_SPbeta_NC_001884	55.05
PC0226	16.5	Incomplete	40	24	7	1674 - 18272	PHAGE_Gordon_Attis_NC_041883	55.20
PC0226	39.6	Questionable	80	51	21	254169-293862	PHAGE_Coryne_Poushou_NC_042139	52.93
PC0229	7.9	Incomplete	40	11	3	43253 - 51183	PHAGE_Escher_80001_NC_027387	55.05

PC0229	12.6	Incomplete	50	22	11	454767 - 467383	PHAGE_Coryne_Juicebox_NC_048070	53.20
PC0229	45	Questionable	90	53	21	53795 - 98823	PHAGE_Coryne_Poushou_NC_042139	52.23
PC0229	16.5	Incomplete	40	24	7	19147 - 35745	PHAGE_Gordon_Attis_NC_041883	55.20
PC0229	12.5	Incomplete	10	17	4	444033 - 456594	PHAGE_Gordon_GMA5_NC_030907	58.10
PC0229	31.5	Incomplete	50	36	9	124477 - 156049	PHAGE_Coryne_Poushou_NC_042139	55.63

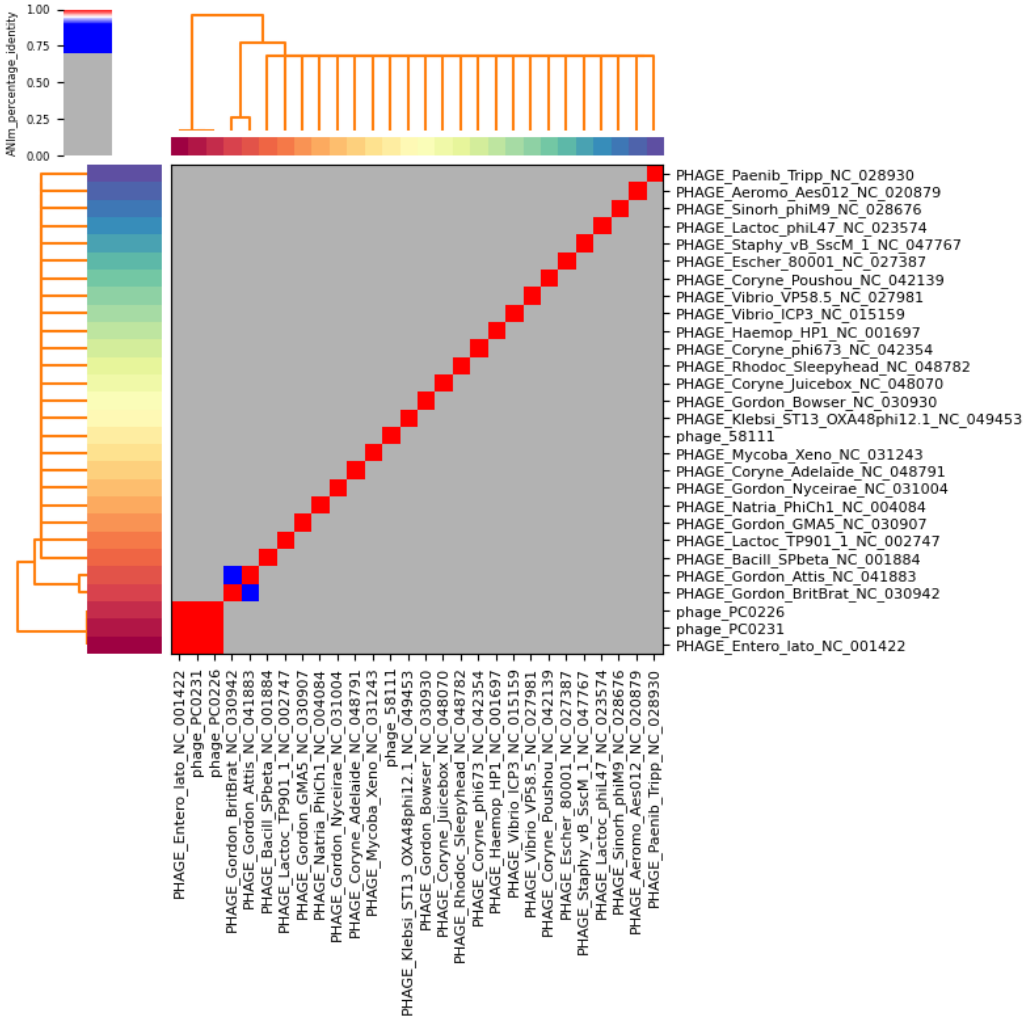

Figure S4. Heatmap representing the ANI percentage nucleotide identity of all matching regions between intact prophage regions of *C. rouxii* and the most common phages using PyANI v.0.2.12. The default scheme colors cells with identity > 0.95 as red, and those with < 0.95 as blue.

Table S4. Number of predicted IS family in each one of *C. rouxii* strain.

Strain	IS110	IS21	IS256	IS3	IS30	IS5	ISL3
FRC0190^{T}	5	1	4	19	2	1	1
21395	6	1	4	15	2	1	1
58111	6	1	4	16	2	1	1
70862	6	1	3	14	2	1	1
70863	6	1	3	14	2	1	1
FRC0071	6	1	4	17	2	1	1
FRC0284	4	1	3	17	2	1	1
FRC0297	5	1	3	11	2	1	1
FRC0412	6	1	4	18	1	1	1
FRC0527	5	1	4	13	2	1	1
PC0230	6	1	4	11	1	1	1
PC0231	7	1	3	11	1	1	1
PC0226	7	1	4	11	1	1	1
PC0229	5	1	3	12	1	1	1
CS30	6	1	3	11	2	1	1

Table S5. Hits found to spacer sequences in the CRISPRTarget databases.

Strain	Cas-Type	*cas* genes	Number of spacers	Evidence Level	CRISPRTarget		
					Spacer	IC score	Identity
FRC0190[T]	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	33	4	1	1.0	*C. diphtheriae* NCTC 13129
						0.88	*C. ulcerans* BR-AD22
						0.88	Phage *Rhodococcus* REQ3
					5	1.0	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					6	0.82	*C. ulcerans* 0102
					7	0.82	*C. ulcerans* BR-AD22
					29	1.0	*C. diphtheriae* C7 (beta)
21395	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	29	4	1	1.0	*C. ulcerans* FRC58
					2	1.0	Phage *Corynebacterium* BFK20
							C. diphtheriae PW8, C7 (beta) and CDCE 8392
					3	0.97	Prophage 166099 GID2649121
							C. diphtheriae PW8, CDC E8392, C7 (beta) and NCTC 13129
							Phage *Corynebacterium* BFK20
					4	1.0	*C. diphtheriae* C7 (beta) and NCTC13129
							Phage *Corynebacterium* BFK20
					5	1.0	Phage *Corynebacterium* LGCM
							C. pseudotuberculosis 31 to 36, 38, 39, and 48
					6	0.97	*C. diphtheriae* CDC E8392, C7 (beta), NCTC 13129
							Prophage 166106 GID2650449
							Phage *Corynebacterium* BFK20

					7	1.0	Phage *Corynebacterium* BFK20
							C. diphtheriae CDCE 8392
					9	0.85	Plasmid pPME5 *P. mendocina* S5.2
					10	0.94	Phage *Staphylococcus* phi7401PVL
							C. ulcerans 809
					16	1.0	Phage *Rhodococcus* REQ3
							C. diphtheriae ISS 3319 and C7 (beta)
					24	0.91	*C. diphtheriae* ISS 3319 and C7 (beta)
							Phage *Rhodococcus* REQ3
					27	1.0	Phage *Rhodococcus* RRH1
							C. ulcerans BR-AD22
58111	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	29	4	2	0.85	Plasmid pmE5 *P. mendocina* S5.2
					3	0.94	*C. ulcerans* 809
							Phage *Staphylococcus* phi7401PVL
					15	0.91	*C. diphtheria*e BH8
							Phage *Rhodococcus* RRH1
					17	0.91	*C. ulcerans* BR-AD22
							Phage *Rhodococcus* RRH1
					22	0.94	*C. diphtheriae* BH8
							Phage *Rhodococcus* RRH1
					23	1.0	*C. diphtheriae* NCTC13129 and B-D-16-78
							Phage *Corynebacterium* BFK20
70862	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	16	4	1	0.82	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8

					2	1.0	*C. diphtheriae* NCTC 11397 and C7 (beta)
					15	0.94	*C. ulcerans* 131001 and *210932*
							Prophage *Staphylococcus* phi7401PVL
70863	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	16	4	2	0.82	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					16	0.94	Prophage *Staphylococcus* phi7401PVL
							C. ulcerans 131001 and *210932*
FRC0071	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	29	4	2	0.82	Phage *Rhodococcus* REQ3
							C. ulcerans BR-AD22 and 0102
					3	0.95	Phage *Rhodococcus* RRH1
							C. diphtheriae 31A
						0.9	*C. ulcerans* BR-AD22
					4	1.0	Phage *Rhodococcus* RRH1
							C. diphtheriae 31A
					5	0.82	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					10	0.94	*C. diphtheriae* C7 (beta)
					20	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					21	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
FRC0297	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	17	4	9	0.94	Prophage *Staphylococcus* phi7401PVL
							C. ulcerans 131001, 210932
					12	0.94	Phage *Rhodococcus* RRH1

							C. diphtheriae BH8
					13	0.82	*C. diphtheriae* NCTC 11397 and C7 (beta)
					17	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
FRC0412	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	70	4	13	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					14	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					21	0.94	*C. diphtheriae* NCTC 11397 and C7 (beta)
					65	0.82	Phage *Rhodococcus* RRH1
							C. diphtheriae NCTC 13129
					66	0.94	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					67	1.0	Phage *Rhodococcus* RRH1
							C. diphtheriae NCTC 13129
					68	1.0	Phage *Rhodococcus* RRH1
							C. diphtheriae NCTC 13129 and BH8
					69	1.0	Phage *Rhodococcus* RRH1
							C. diphtheriae NCTC 13129 and BH8
					70	1.0	Phage *Rhodococcus* RRH1
							C. diphtheriae NCTC 13129 and BH8
FRC0527	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	22	4	6	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					20	0.88	Phage *Rhodococcus* RRH1

							C. diphtheriae BH8
					21	0.88	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
					22	0.82	Phage *Rhodococcus* RRH1
							C. diphtheriae BH8
PC0230	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	8	4	1	0.94	*C. diphtheriae* PW8, C7 (beta) and NCTC 13129
							Prophage 166106 GID2650479
							Phage *Corynebacterium* BFK20
						0.82	*C. ulcerans* FRC58
					7	0.88	Prophage *Staphylococcus* phi7401PVL
							C. ulcerans 131001, 210932
PC0231	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	7	4	1	0.91	*C. diphtheriae* PW8, CDCE 8392, C7 (beta) and NCTC 13129
							Prophage 166106 GID2650479
							Phage *Corynebacterium* BFK20
					6	0.85	Prophage *Staphylococcus* phi7401PVL
							C. ulcerans 131001, 210932
PC0226	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	8	4	1	0.94	*C. diphtheriae* PW8, CDCE 8392, C7 (beta) and NCTC 13129
							Prophage 166106 GID2650449
							Phage *Corynebacterium* BFK20
						0.82	*C. ulcerans* FRC58
					7	0.88	Prophage *Staphylococcus* phi7401PVL
							C. ulcerans 131001, 210932
PC0229	I-E	*cse1, cse2, cas7, cas5, cas6, cas1, cas2*	8	4	2	0.88	Prophage *Staphylococcus* phi7401PVL
							C. ulcerans 131001, 210932

	8	0.94	*C. diphtheriae* PW8, CDCE 8392, C7 (beta) and NCTC 13129
			Prophage 166106 GID2650449
			Phage *Corynebacterium* BFK20
		0.82	*C. ulcerans* FRC58

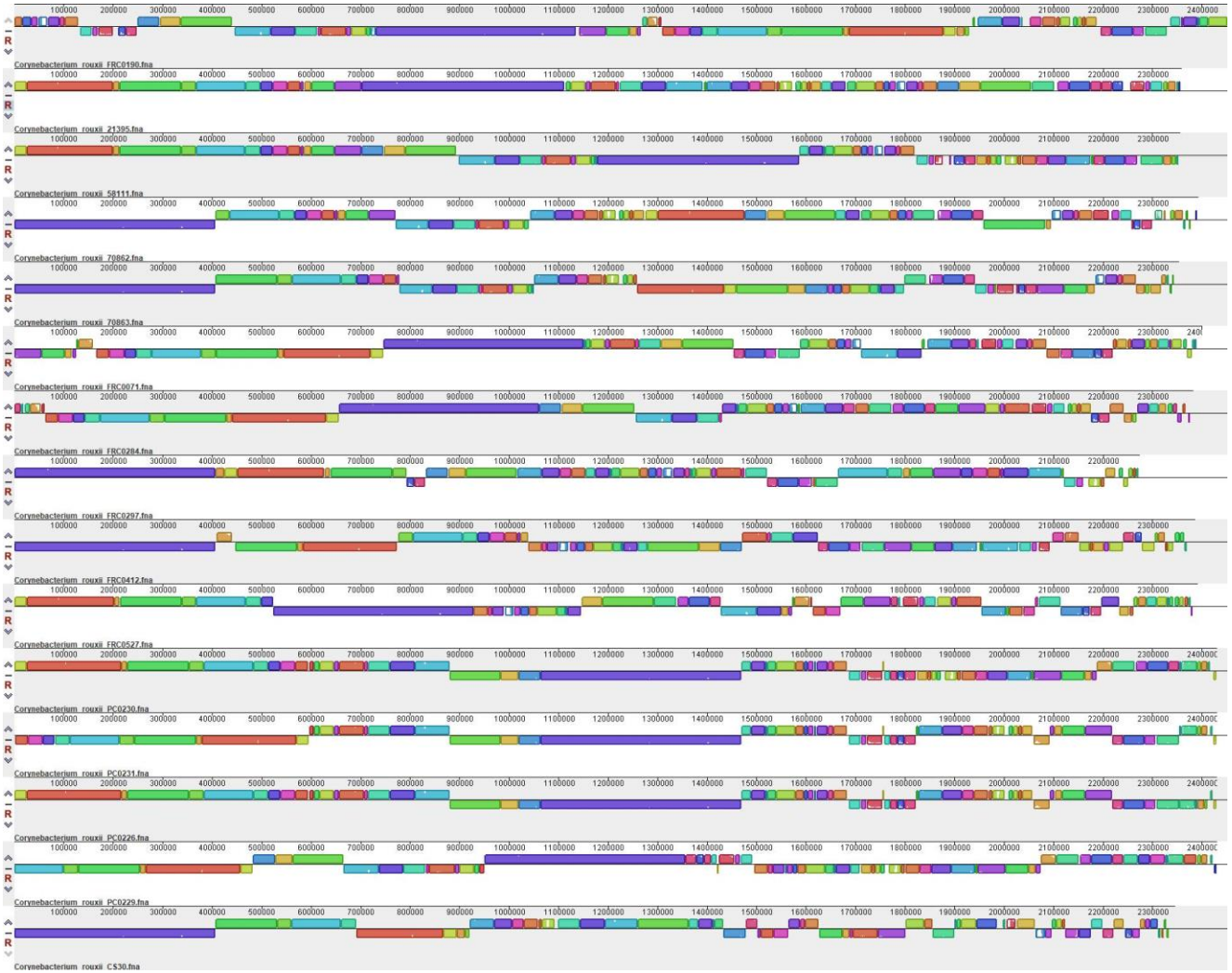

Figure S5. Gene synteny analysis using the software Mauve. Each contiguously colored region is a locally collinear block that has passed through evolution for inversions, translocations, or deletion.