

1 **Supplementary Figures and Tables**

2 **Fig. S1.** Alignment of Genomic Islands (GIs) (marked by the region between green arrows) described in *A.*  
3 *baumannii* LAC-4 [11] with those in *A. baumannii* AB030. Twelve different GIs have been described *A.*  
4 *baumannii* LAC-4: GI1 (a), GI2 (b), GI3 (c), GI4 (d), GI5 (e), GI6 (f), GI7 (g), GI8 (h), GI9 (i), GI10 (j), GI11 (k),  
5 and GI12 (l). Genes of interest are listed in red font, genes that are similar in both strains are listed in black  
6 font, and genes that are found in only one of the two strains are listed in gray font.

7 **Fig. S2.** Insertion Sequence (IS regions) in AB030 and LAC-4 genomes as predicted by ISfinder. Presence of  
8 the IS region is indicated by red and the absence by blue.

9 **Fig. S3.** Presence of *bla*<sub>OXA</sub> in *A. baumannii* AB030 and LAC-4 (a) and alignment of each of the three genes  
10 with published sequences of *bla*<sub>OXA-65</sub> and *bla*<sub>OXA-68</sub> [39] (b).

11 **Fig. S4.** Presence of *bla*<sub>ADC</sub> in *A. baumannii* AB030 and LAC-4.

12 **Fig. S5.** Presence of aminoglycoside phosphotransferase (APH) encoding genes, *APH(3'')*-Ib and *APH(6)*-  
13 Id in *A. baumannii* AB030 and LAC-4.

14 **Fig. S6.** Catalase activity of AB030 and LAC-4, in comparison to ATCC 17978. Catalase activity toward  
15 H<sub>2</sub>O<sub>2</sub> in overnight cultures was determined using a Clark oxygen electrode connected to a Gilson oxygraph.  
16 Values were normalized to the dry weight of bacteria. Results represent data from two independent  
17 experiments. Statistical analysis was carried out using the two-way analysis of variance (ANOVA).  
18

Fig. S1a

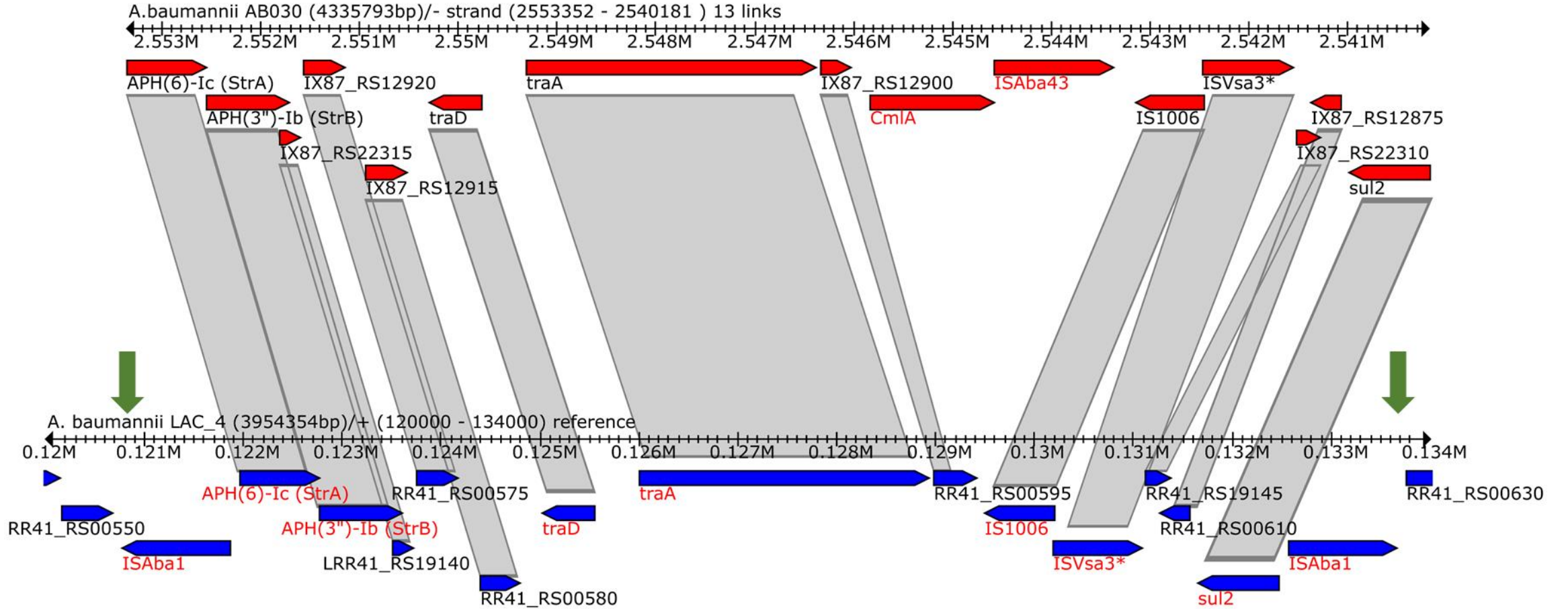


Fig. S1b

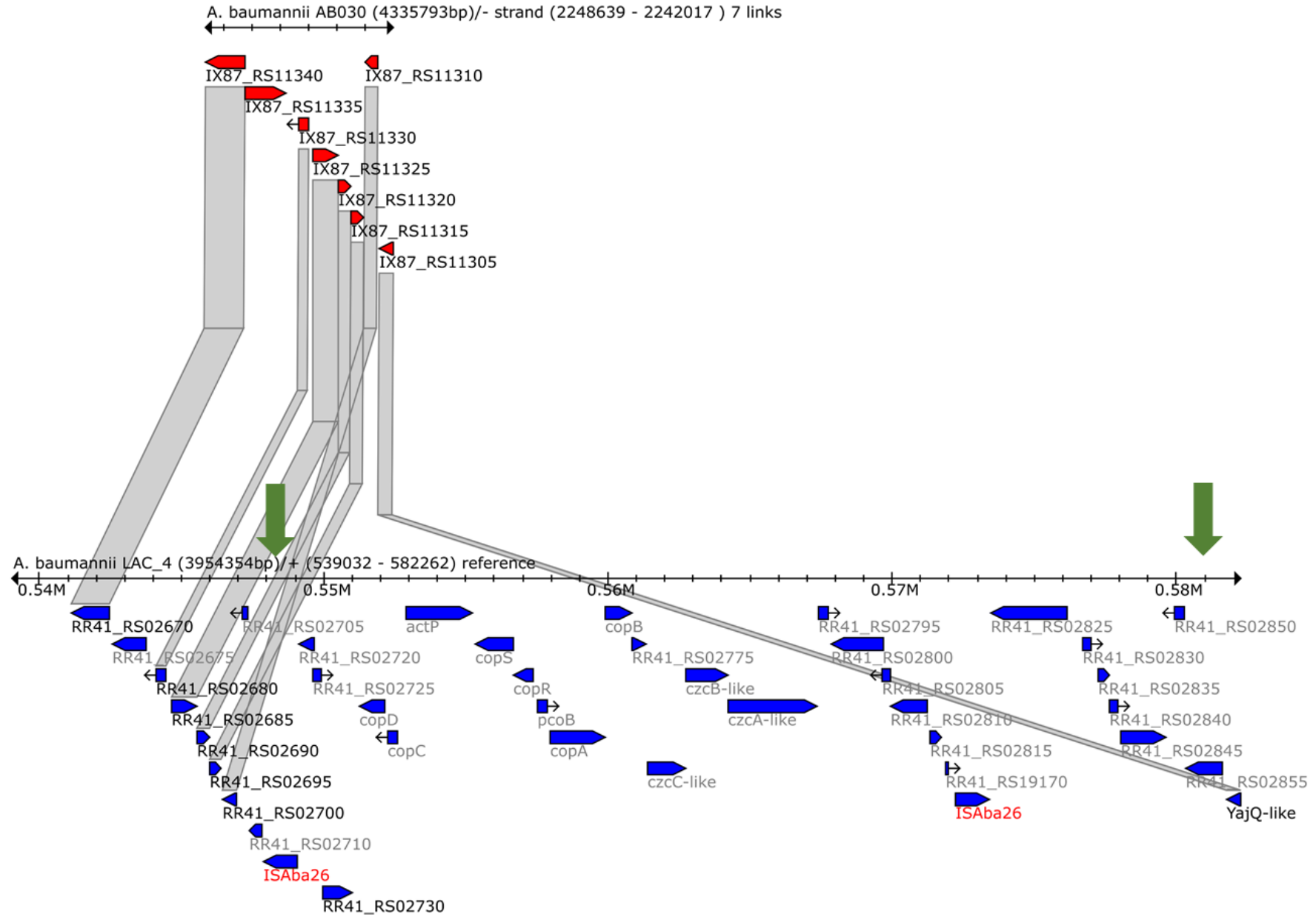


Fig. S1c

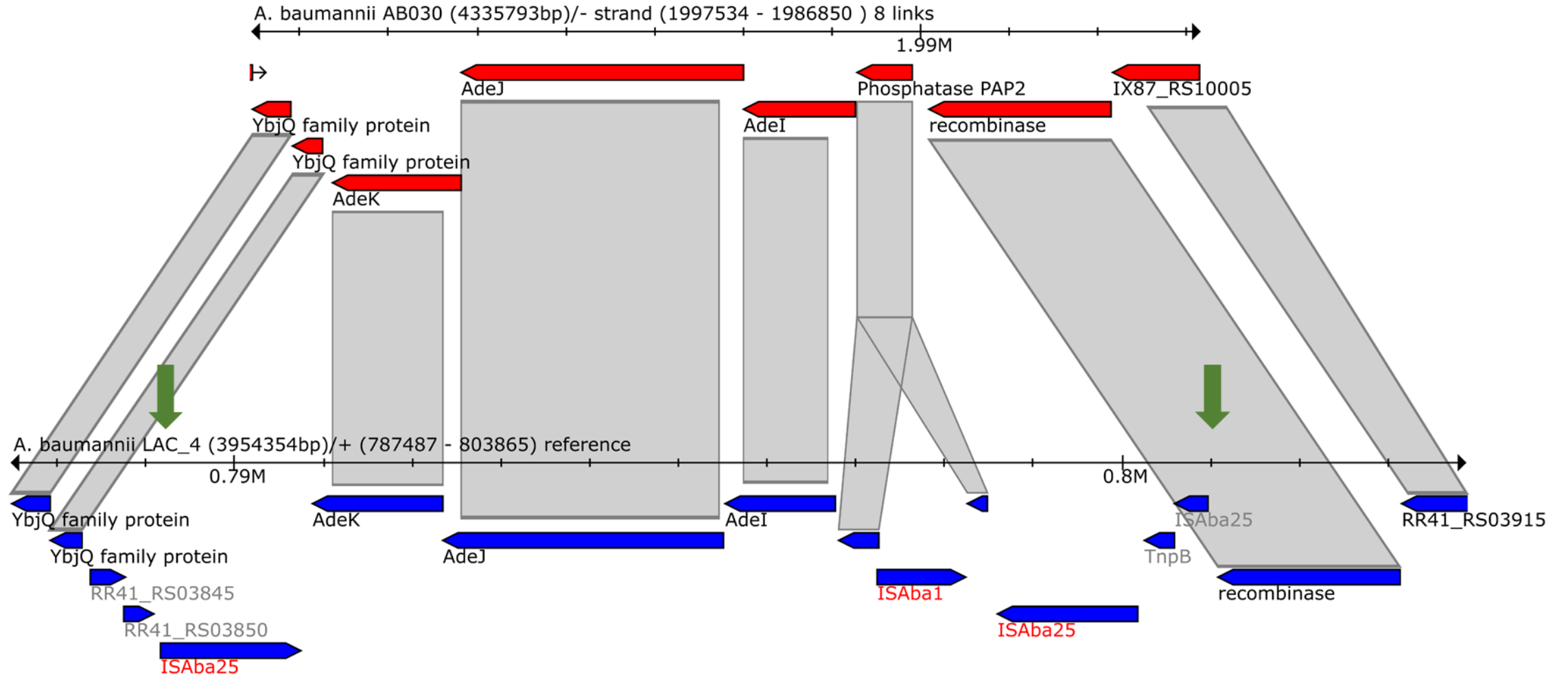


Fig. S1d

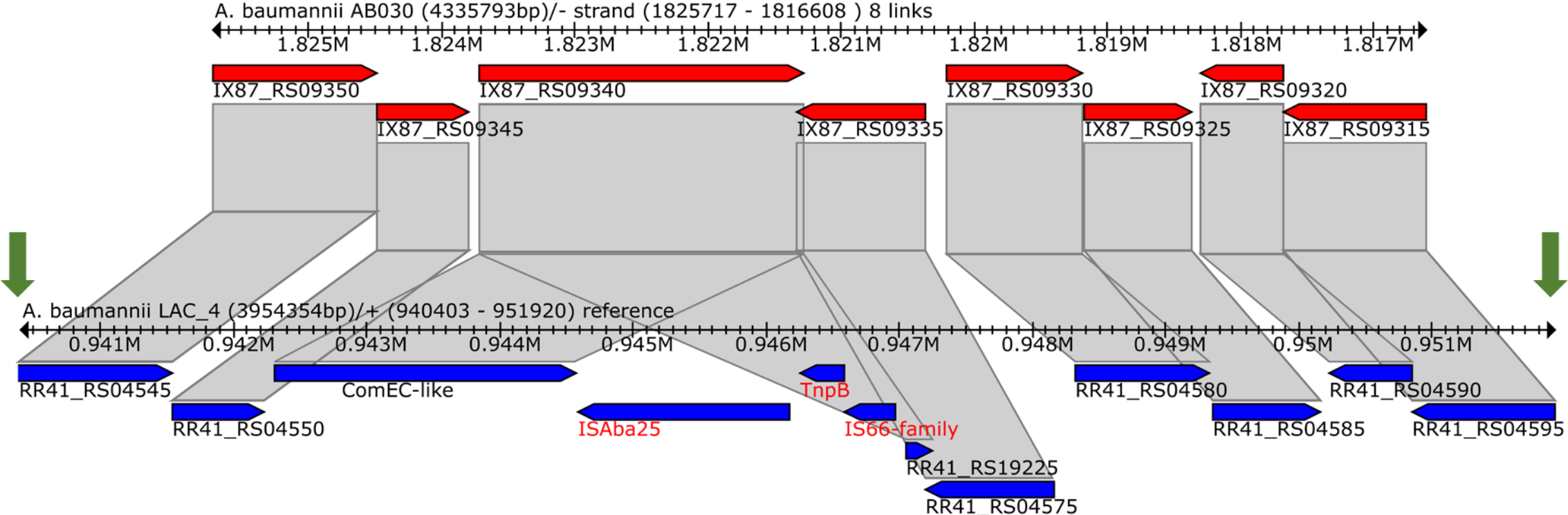


Fig. S1e

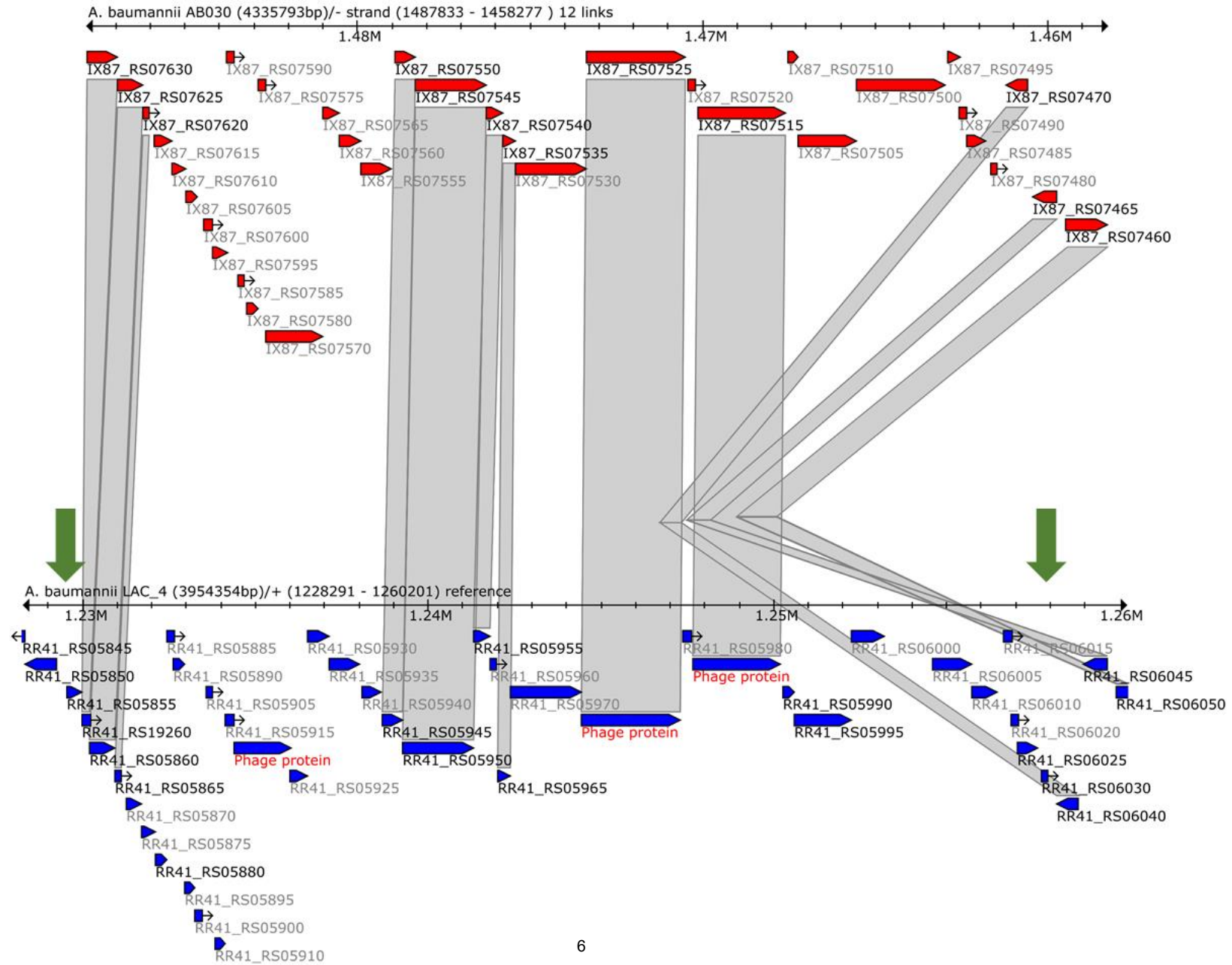


Fig. S1f

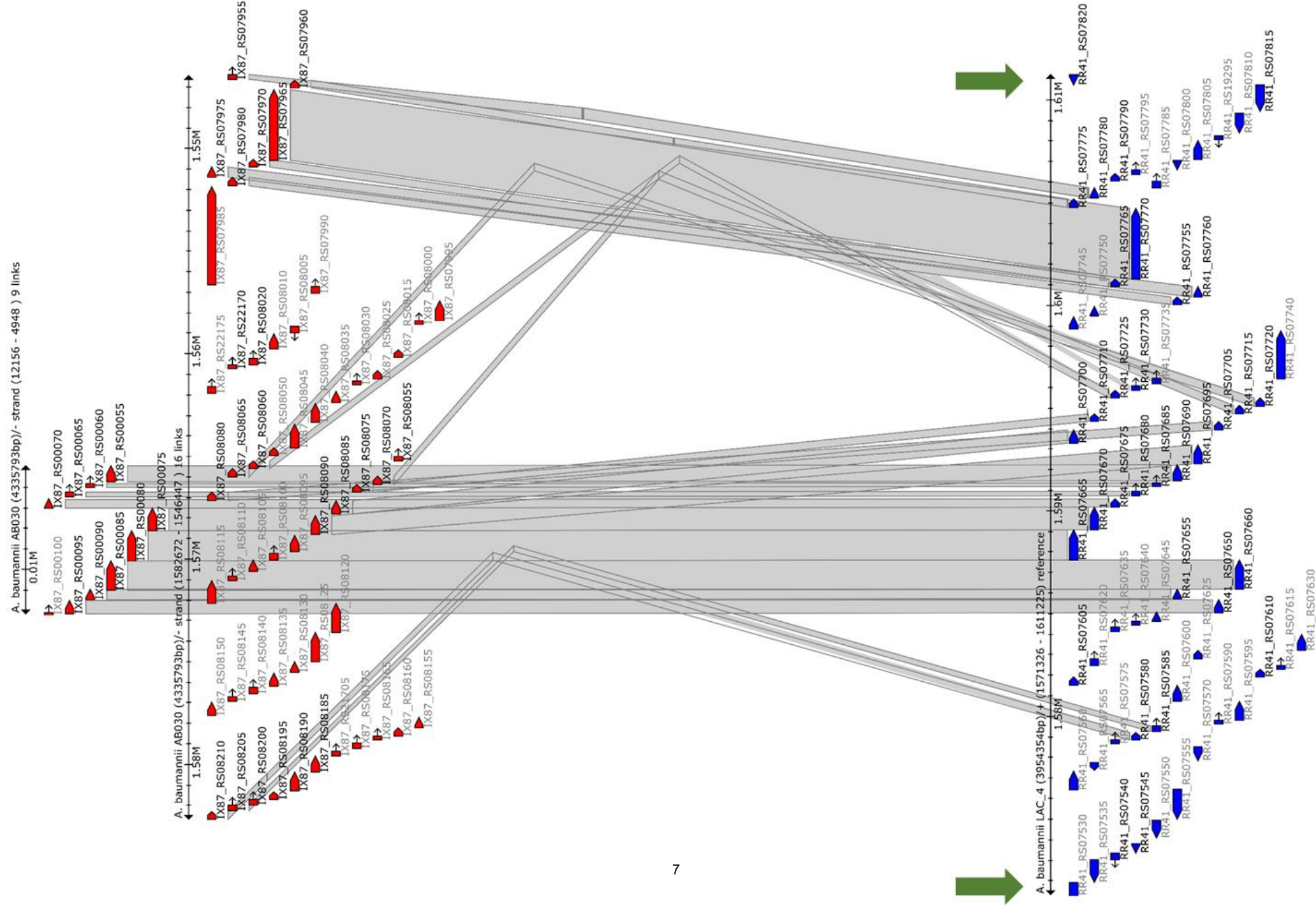


Fig. S1g

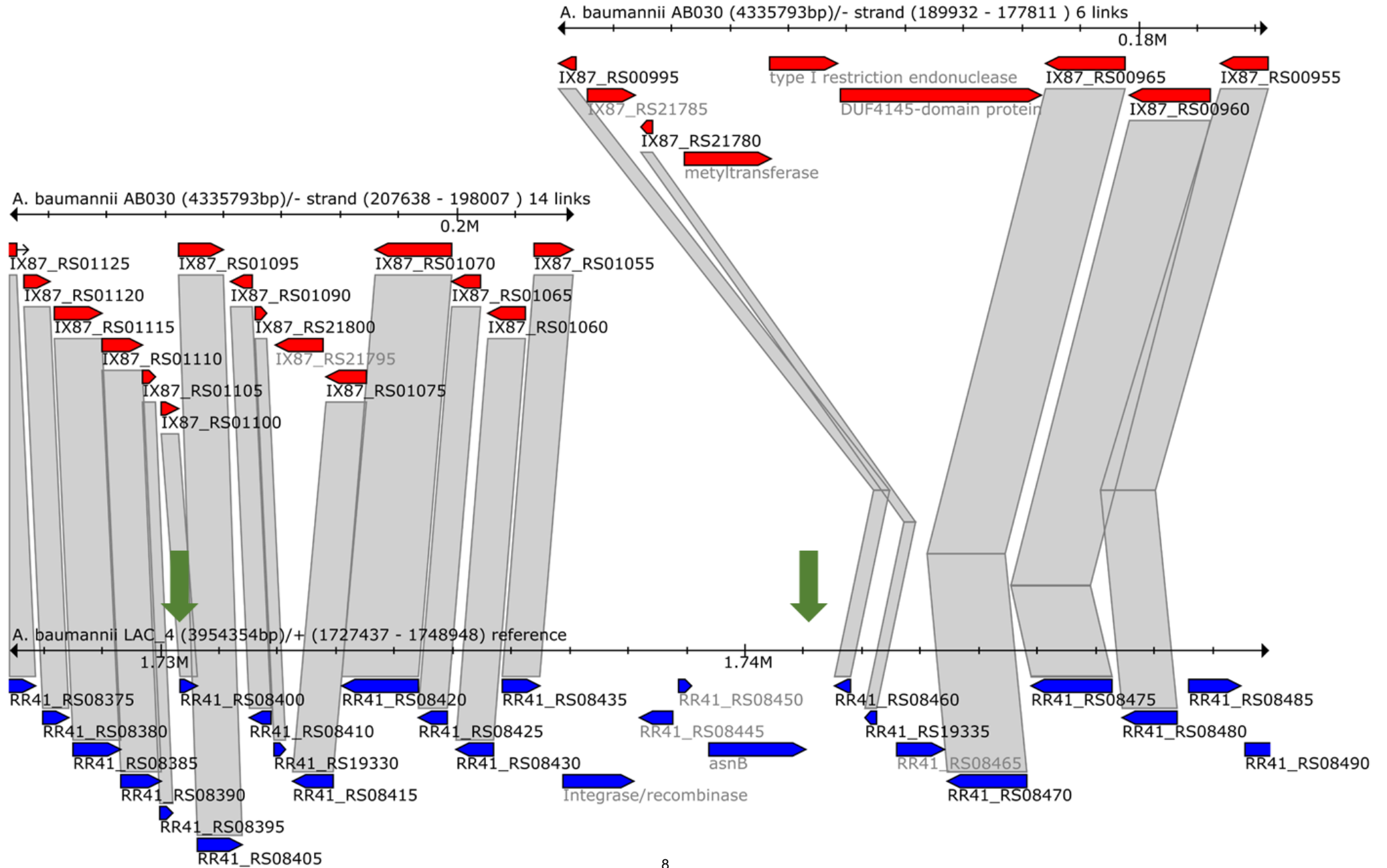




Fig. S1h

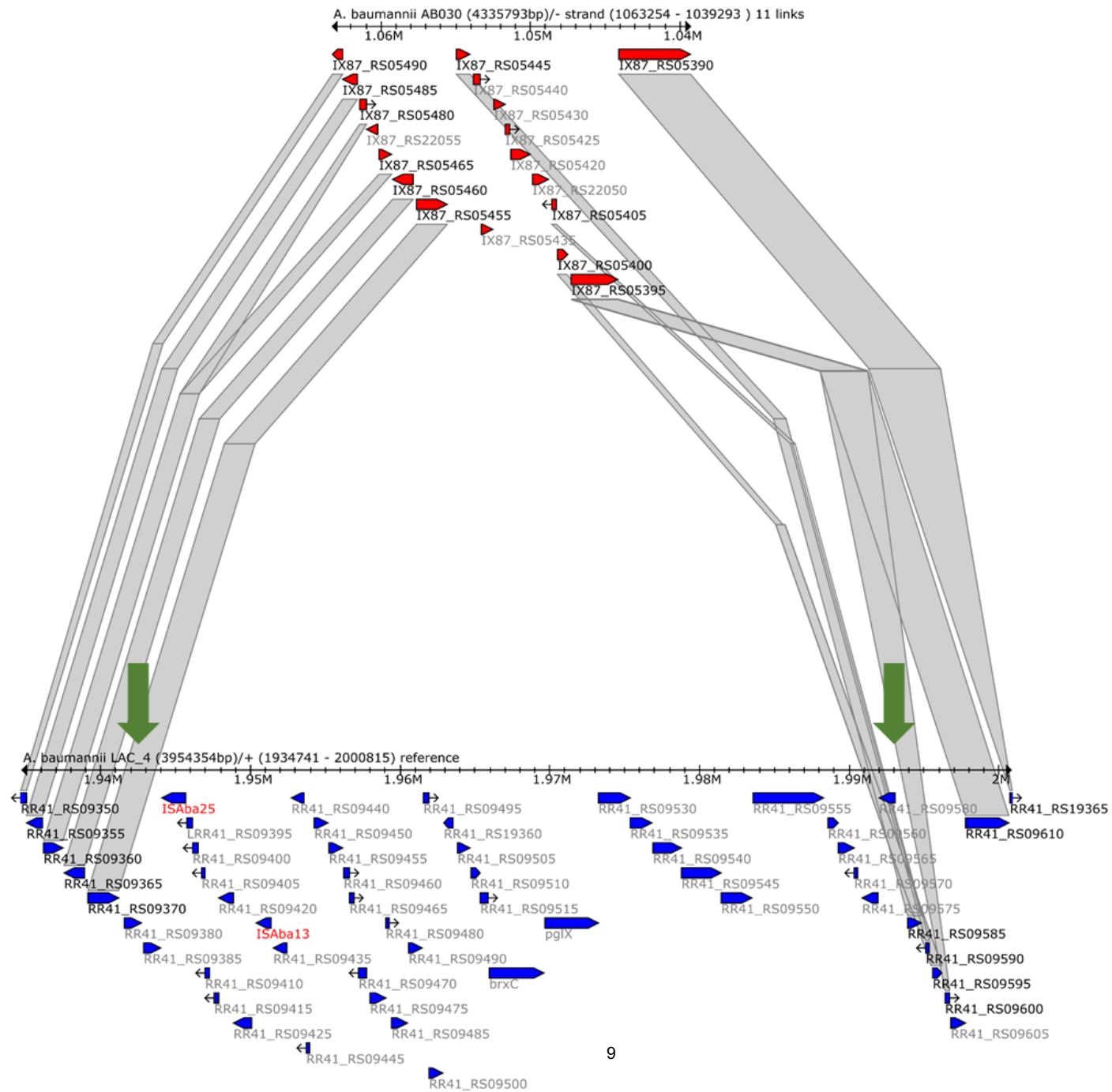


Fig. S1i

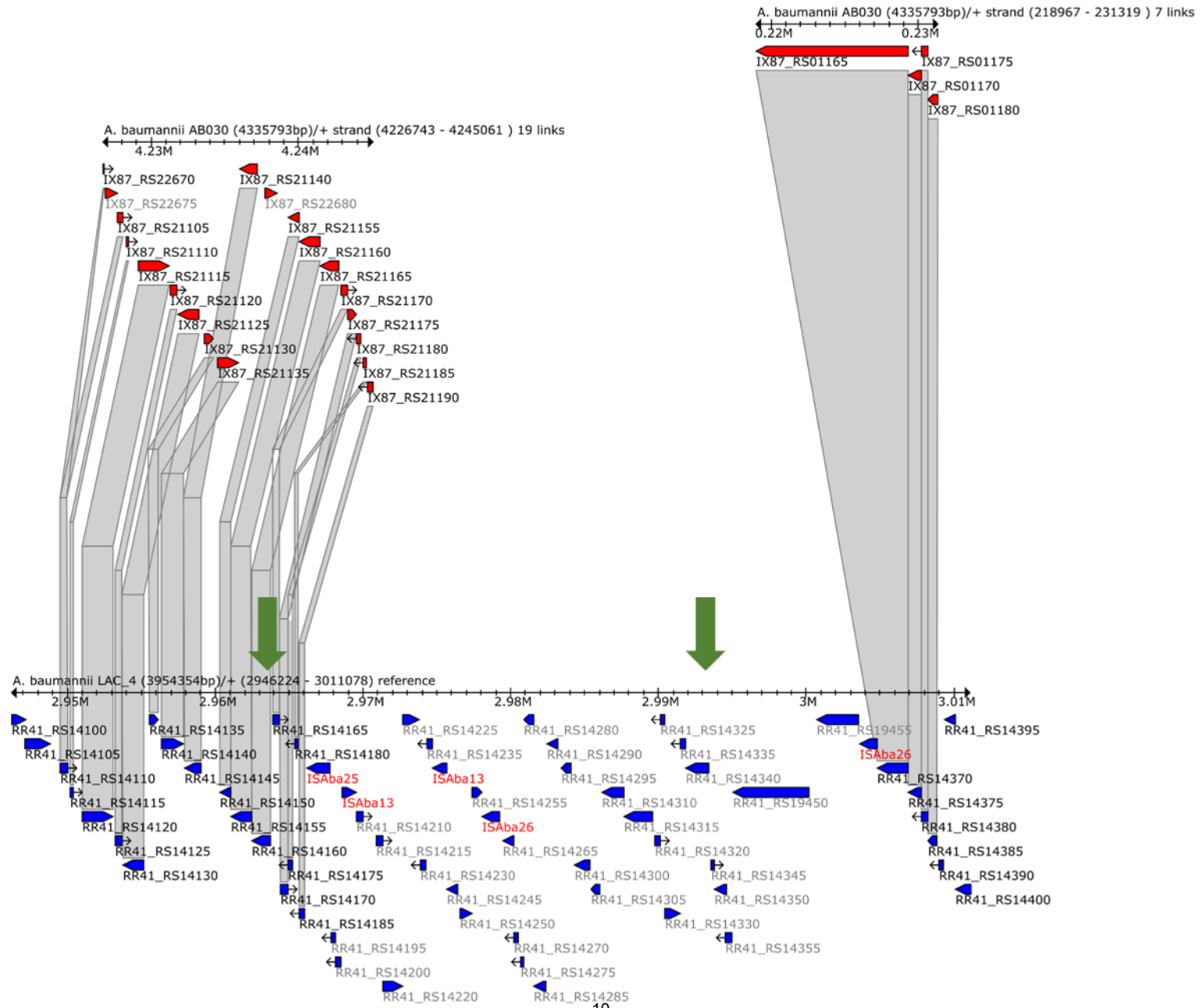


Fig. S1j

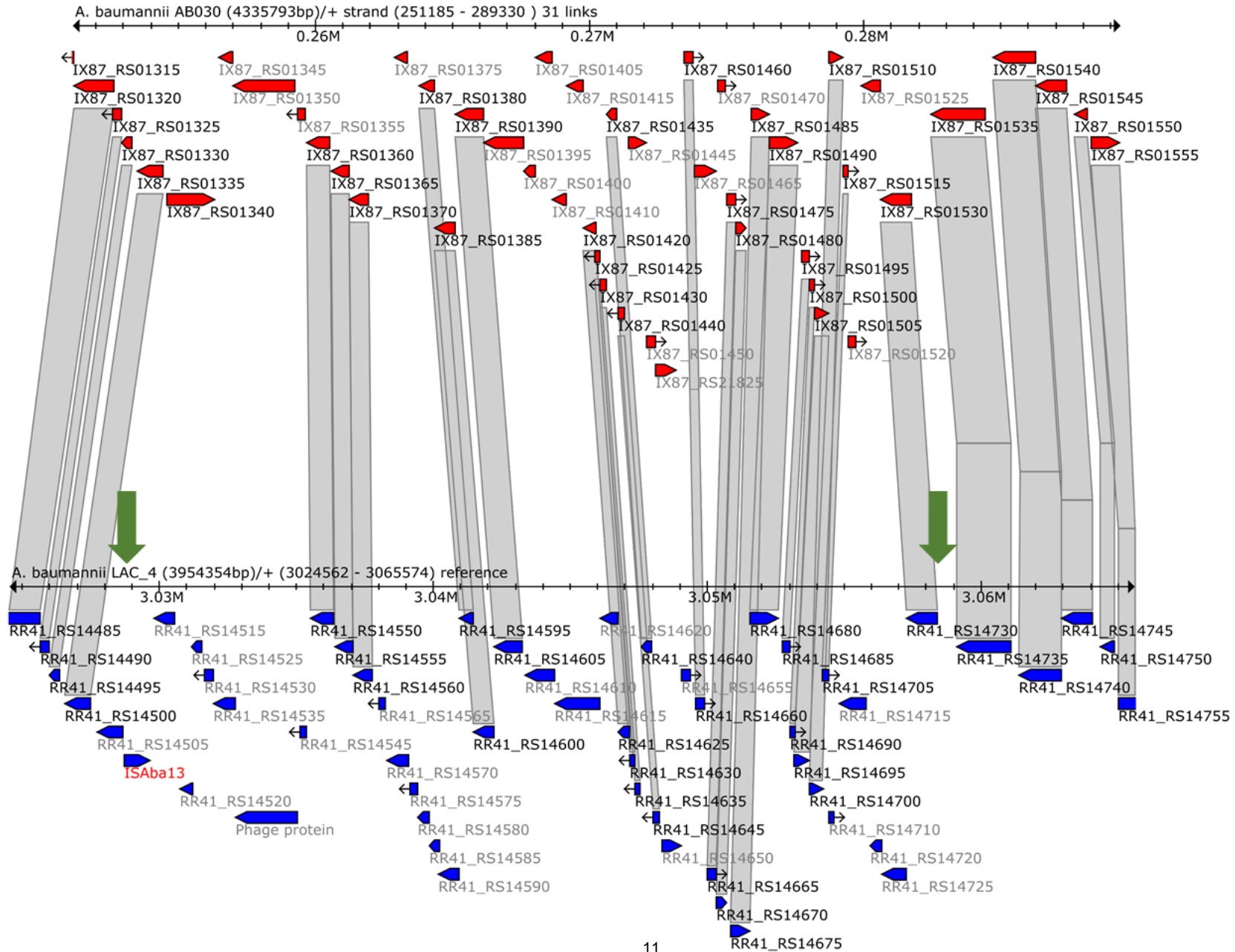


Fig. S1k

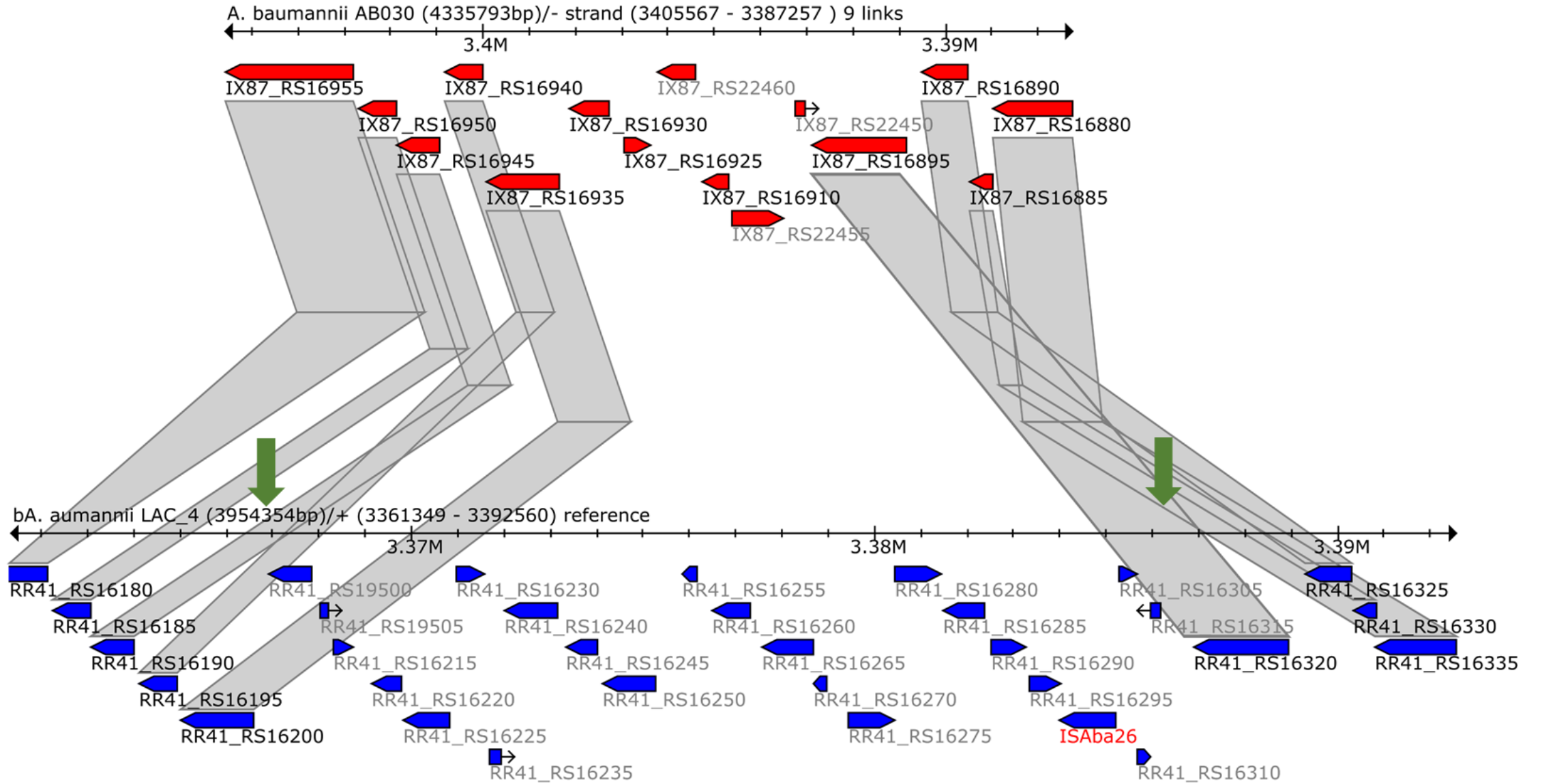


Fig. S11

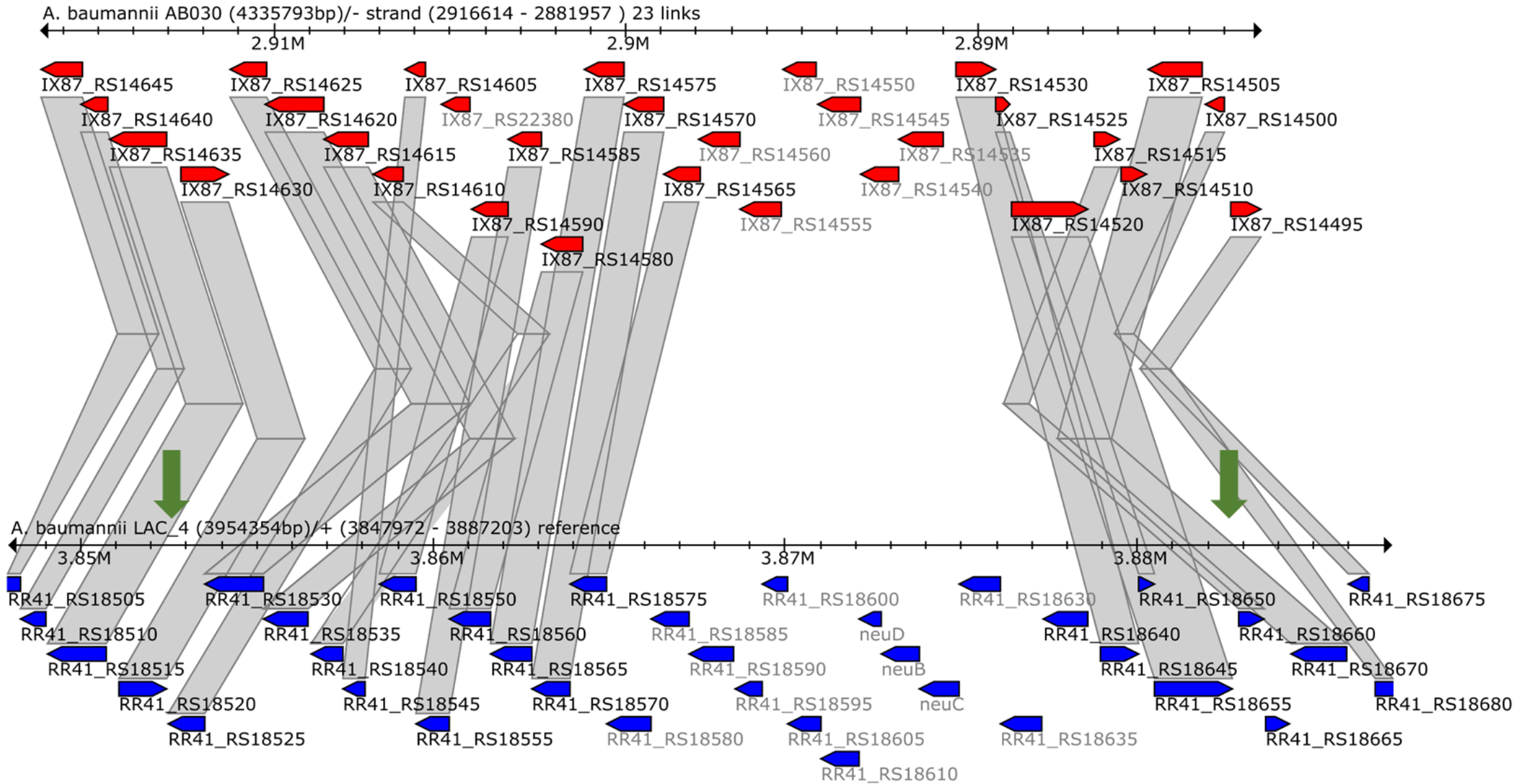
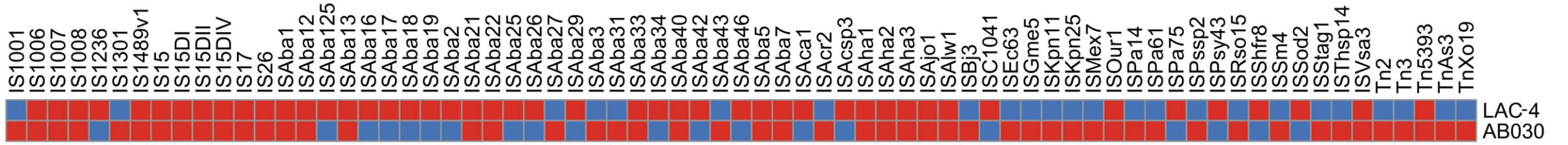
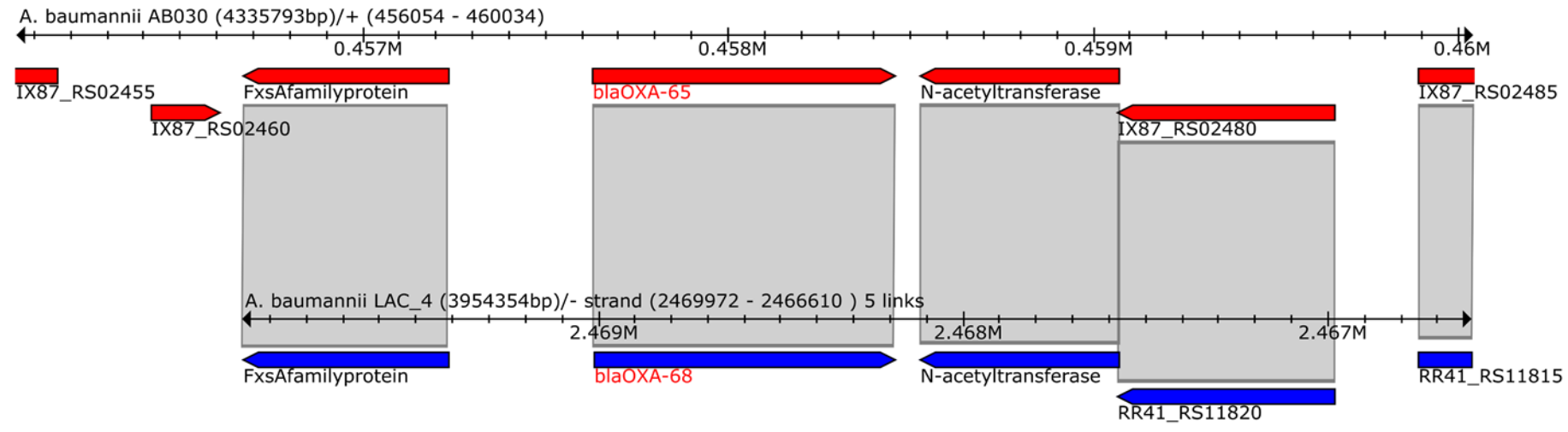


Fig. S2



a.



b.

		10	20	30	40	50	60	70	80	90	100
OXA-65	1	MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKA	EKIKNLFNEAHTTGV	LVIQQG	QTQQSYGNDLARASTEYVVPASTFKMLNALIGLEHHKATTTTE						100
OXA-65_AB030	1	.....									
OXA-68	1	.....S.....									
OXA-68_LAC-4	1	.....S.....									
		110	120	130	140	150	160	170	180	190	200
OXA-65	101	VFKWDGKKRLFP	EWKDMTLDGAMKASAI	PVYQDLARRIGLE	LMSEVKRVGYGNADIGTQVDNFWLVG	PLKITPQQE	EAQFAYKLAN	KTL	LPFSQKVQDEV		200
OXA-65_AB030	101	.....									
OXA-68	101	.....Q.....	.....N.....	.....N.....						.....E.....	200
OXA-68_LAC-4	101	.....Q.....	.....N.....	.....N.....						.....E.....	200
		210	220	230	240	250	260	270			
OXA-65	201	QSMLFIEEKNGNKIYAKSGW	GDVNPQVGWLTGWVV	QPQGNIVAFSLNLEM	KKGIPSSVRKEITYKSLEQLGIL*						275
OXA-65_AB030	201	.....*									
OXA-68	201	.....*									
OXA-68_LAC-4	201	.....*									

Fig. S4

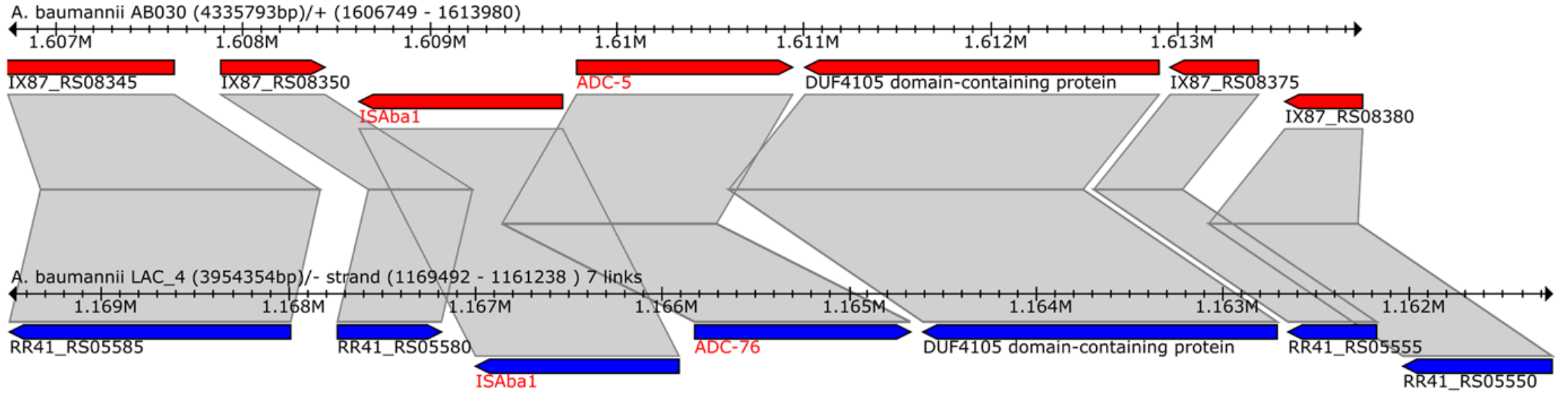




Fig. S5

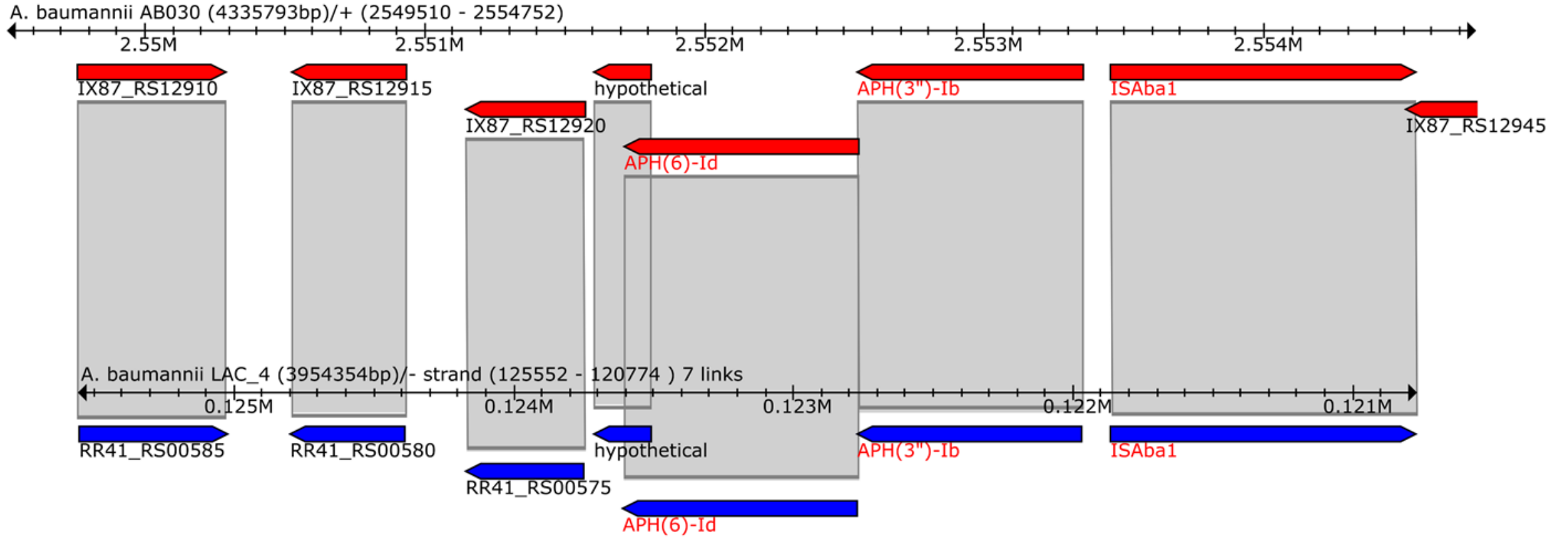
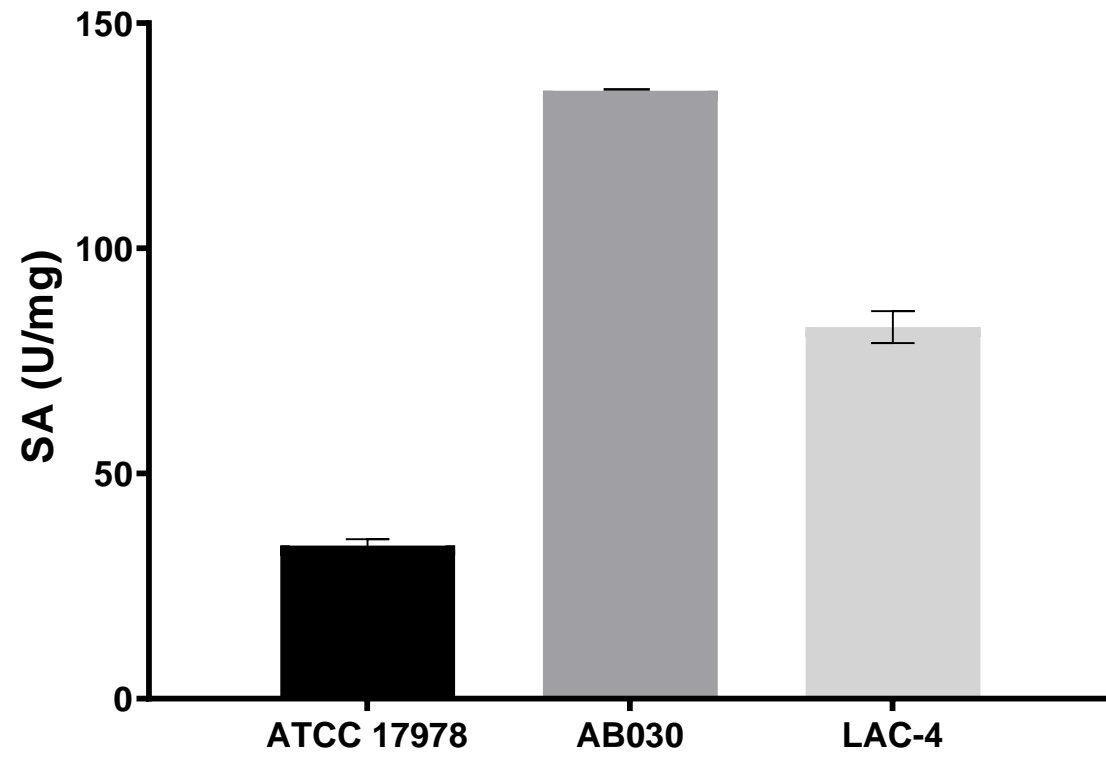


Fig. S6



19 **Table S1.** Predicted Genomic Islands present in AB030 as identified by Islandviewer.

Island no.	Island start	Island end	Length	In LAC-4 genome		
				Query coverage	E-value	Identity
1	190685	202245	11560	38%	0	99.98%
2	268005	281740	13735	57%	0	95.69%
3*	324734	335547	10813	100%	0	99.59%
4	362940	404411	41471	24%	0	99.20%
5	476867	482761	5894	70%	0	98.84%
6	765527	804448	38921	55%	0	96.33%
7	833867	843701	9834	100%	0	97.59%
8	1032352	1039273	6921	79%	0	99.13%
9	1091422	1113975	22553	64%	0	94.74%
10	1142438	1147839	5401	47%	0	98.28%
11	1181466	1191022	9556	86%	0	98.34%
12	1487849	1496718	8869	4%	2.00E-168	90.93%
13	1546090	1563347	17257	41%	0	91.52%
14	1926318	1973925	47607	61%	0	99.38%
15	2049753	2059704	9951	12%	0	94.81%
16	2202807	2211488	8681	33%	0	99.12%
17*	2458526	2467319	8793	8%	0	99.87%
18*	2538454	2578240	39786	53%	0	99.82%
19	2658176	2665482	7306	37%	0	96.55%
20	2959816	2973667	13851	0%	0	0.00%
21	3536698	3579918	43220	66%	0	99.37%
22	3661157	3698129	36972	0%	0	0.00%
23	3855311	3859508	4197	0%	0	0.00%
24	3904427	3951898	47471	17%	0	91.59%
25	3987855	3995562	7707	15%	0	93.26%
26	4062202	4067925	5723	0%	0	0.00%
27	4305821	4328706	22885	53%	0	94.22%

20 \*identified as resistance islands

21

22 **Table S2.** Predictions for the presence of phage sequences in the genomes of AB030 and LAC-4.

Phage sequences in AB030													
Region	Length	Completeness (score)	Specific keyword	Position	Total proteins	Phage proteins	Hypothetical protein	Phage + Hypothetical protein	Phage species	GC	In LAC-4 genome		
											Query coverage	E-value	Identity
1	28.6Kb	incomplete(60)	capsid, head	685-29364	54	37	15	96.20%	6	39.35%	53%	0	93.17%
2	16Kb	incomplete(60)	transposase, plate	195334-211374	19	11	8	100%	6	34.70%	80%	0	99.96%
3	9Kb	incomplete(30)	tail, transposase	241417-250505	11	7	4	100%	5	39.72%	91%	0	97.94%
4	23.1Kb	incomplete(40)	plate, transposase, integrase	263065-286249	32	17	12	90.60%	14	37.84%	74%	0	97.29%
5	53.8Kb	intact(150)	integrase, lysin, tail, head, portal	341980-395833	51	32	19	100%	21	40.15%	28%	0	98.47%
6	6.4Kb	incomplete(60)	transposase, head	576125-582561	9	7	0	77.70%	4	38.90%	75%	0	97.66%
7	49.1Kb	questionable(84)	integrase, tail, capsid, head	908821-957987	72	61	10	98.60%	16	39.85%	56%	0	88.57%
8	61.8Kb	intact(150)	integrase, transposase, tail, capsid, head	1086365-1148174	77	56	19	97.40%	17	38.82%	60%	0	93.73%
9	38.1Kb	questionable(90)	tail, capsid, head, plate	1461384-1499530	43	26	16	97.60%	17	40.81%	62%	0	95.65%
10	50.1Kb	intact(106)	integrase, tail, capsid, head, transposase	1544078-1594217	73	62	10	98.60%	12	39.29%	46%	0	91.50%
11	23.3Kb	incomplete(50)	tail, capsid, head	2036334-2059704	35	24	11	100%	13	41.75%	45%	0	95.65%
12	27Kb	intact(100)	head, portal, tail	3672382-3699422	31	24	7	100%	15	40.72%	6%	0	78.91%
13	43.2Kb	intact(150)	transposase, portal, head, tail, plate	4187963-4231200	56	41	14	98.20%	25	38.27%	12%	0	97.82%
14	17.6Kb	incomplete(30)	tail	4318067-4335678	20	19	1	100%	3	40.83%	58%	0	94.29%

23

24

Phage sequences in LAC-4													
Region	Length	Completeness (score)	Specific keyword	Position	Total protein	Phage protein	Hypothetical protein	Phage + Hypothetical protein	Phage species	GC	In AB030 genome		
											Query coverage	E-value	Identity
1	10.3Kb	incomplete(50)	transposase, head	941541-951920	11	9	0	81.80%	7	40.44%	76%	0	99.28%
2	31.2Kb	questionable(80)	head, capsid, tail	1226738-1258017	29	18	9	93.10%	13	40.63%	80%	0	95.65
3	41.5Kb	intact(100)	transposase, integrase, head, capsid, tail	1569705-1611225	62	47	12	95.10%	12	38.64%	66%	0	93.17%
4	22.1Kb	incomplete(50)	plate, transposase, integrase, lysin	1716956-1739082	12	9	3	100%	8	36.31%	85%	0	99.11%
5	10Kb	incomplete(60)	integrase, transposase	1941409-1951435	11	6	1	63.60%	3	39.55%	8%	4.00E-68	82.88%
6	29.8Kb	incomplete(20)	integrase	3028581-3058412	31	17	11	90.30%	12	35.66%	58%	0	95.64%

25

26

27 **Table S3.** Antibiotic susceptibility ( $\mu\text{g/mL}$ ) assay of AB030 and LAC-4. Different classes of antibiotics were  
 28 tested against AB030 and LAC-4 via broth dilution method. MIC values indicating resistance according to  
 29 the CLSI guidelines are shown in bold.

	AMK	GEN	CHL	CRO	CIP	LVX	IPM	MEM	FEP	TGC
AB030	<b>64</b>	<b>&gt;32</b>	1	<b>&gt;64</b>	<b>&gt;16</b>	<b>16</b>	<b>&gt;32</b>	<b>&gt;32</b>	<b>&gt;64</b>	<b>&gt;16</b>
LAC-4	32	<b>16</b>	1	<b><math>\geq 256</math></b>	<b>16</b>	$\leq 2$	$\leq 2$	4	16	$\leq 0.25$

30 AMK Amikacin; FEP Cefepime; CHL Chloramphenicol; CRO Ceftriaxone; CIP Ciprofloxacin; IPM  
 31 Imipenem; GEN Gentamicin; LVX Levofloxacin; MEM Meropenem; TGC Tigecycline

32

**Table S4.** Presence of virulence genes in AB030 and LAC-4.

Category	Virulence factors	Related genes	LAC-4	AB030
Adherence	Outer membrane protein	<i>ompA</i>	RR41_RS03275	IX87_RS10825
Biofilm formation	PNAG (Polysaccharide poly-N-acetylglucosamine)	<i>pgaD</i>	RR41_RS06830	IX87_RS06615
		<i>pgaC</i>	RR41_RS06825	IX87_RS06620
		<i>pgaB</i>	RR41_RS06820	IX87_RS06625
		<i>pgaA</i>	RR41_RS06815	IX87_RS06630
	Csu pili	<i>csuE</i>	-	IX87_RS06890
		<i>csuD</i>	-	IX87_RS06895
		<i>csuC</i>	-	IX87_RS06900
		<i>csuB</i>	-	IX87_RS06905
		<i>csuA</i>	-	IX87_RS06910
		<i>csuA/B</i>	-	IX87_RS06915
	AdeFGH efflux pump/transport autoinducer	<i>adeF</i>	RR41_RS06070	IX87_RS07440
		<i>adeG</i>	RR41_RS06065	IX87_RS07445
		<i>adeH</i>	RR41_RS06060	IX87_RS07450
Biofilm-associated protein	<i>bap</i>	-	IX87_RS22220*	
Enzyme	Phospholipase C	<i>plc</i>	RR41_RS07450	IX87_RS14485; IX87_RS06060
	Phospholipase D	<i>plcD</i>	RR41_RS02620	IX87_RS11390
Immune evasion	Capsule	Undetermined	RR41_RS18545; RR41_RS18560; RR41_RS18650; RR41_RS18550; RR41_RS18525; RR41_RS18540; RR41_RS18635; RR41_RS18565; RR41_RS18645; RR41_RS18530; RR41_RS18640; RR41_RS18655; RR41_RS18570; RR41_RS18520; RR41_RS18625; RR41_RS18620;	IX87_RS14615; IX87_RS14605; IX87_RS14580; IX87_RS14590; IX87_RS14625; IX87_RS14610; IX87_RS14575; IX87_RS14520; IX87_RS14620; IX87_RS14560; IX87_RS14570; IX87_RS14630; IX87_RS14555; IX87_RS14565; IX87_RS14545; IX87_RS14535;

			RR41_RS18630; RR41_RS18575; RR41_RS18535; RR41_RS18610; RR41_RS18615	IX87_RS14585; IX87_RS14530; IX87_RS14540; IX87_RS14550; IX87_RS14525
	LPS	<i>lpsB</i>	RR41_RS16825	IX87_RS16395
		<i>lpxL</i>	RR41_RS16820	IX87_RS16400
		<i>lpxB</i>	RR41_RS12535	IX87_RS18825
		<i>lpxA</i>	RR41_RS08095	IX87_RS21220
		<i>lpxD</i>	RR41_RS08085	IX87_RS21230
		<i>lpxM</i>	RR41_RS04575	IX87_RS09335
		<i>lpxC</i>	RR41_RS00855	IX87_RS13380
Iron uptake	Heme utilization	Undetermined	RR41_RS08485	IX87_RS00950
		Undetermined	RR41_RS08490	IX87_RS00945
		Undetermined	RR41_RS08495	IX87_RS00940
		Undetermined	RR41_RS08500	IX87_RS00935
		Undetermined	RR41_RS08505	IX87_RS00930
		Undetermined	RR41_RS08510	IX87_RS00925
		Undetermined	RR41_RS08515	IX87_RS00920
		hemO	RR41_RS08520	IX87_RS00915
		Undetermined	RR41_RS08525	IX87_RS00910
		Undetermined	RR41_RS08530	IX87_RS00905
	Acinetobactin	<i>basJ</i>	RR41_RS05535	IX87_RS08395
		<i>basI</i>	RR41_RS05530	IX87_RS08400
		<i>basH</i>	RR41_RS05525	IX87_RS08405
		<i>barB</i>	RR41_RS05520	IX87_RS08410
		<i>barA</i>	RR41_RS05515	IX87_RS08415
		<i>basG</i>	RR41_RS05505	IX87_RS08425
		<i>basF</i>	RR41_RS05500	IX87_RS08430
		<i>entE</i>	RR41_RS05495	IX87_RS08435
		<i>basD</i>	RR41_RS05490	IX87_RS08440
		<i>basC</i>	RR41_RS05485	IX87_RS08445
		<i>bauA</i>	RR41_RS05480	IX87_RS08450
		<i>bauB</i>	RR41_RS05475	IX87_RS08455
		<i>bauE</i>	RR41_RS05470	IX87_RS08460
		<i>bauC</i>	RR41_RS05465	IX87_RS08465
		<i>bauD</i>	RR41_RS05460	IX87_RS08470

		<i>basB</i>	RR41_RS05455	IX87_RS08475
		<i>basA</i>	RR41_RS05450	IX87_RS08480
		<i>bauF</i>	RR41_RS05445	IX87_RS08485
Regulation	Quorum sensing	<i>abaI</i>	-	IX87_RS14815
		<i>abaR</i>	-	IX87_RS14825
	Two-component system	<i>bfmR</i>	RR41_RS15530	IX87_RS17690
		<i>bfmS</i>	RR41_RS15525	IX87_RS17695
Serum resistance	PbpG	<i>pbpG</i>	RR41_RS17785	IX87_RS15425
Stress adaptation	Catalase	<i>katA</i>	-	IX87_RS20175

\*detected using BLASTn.