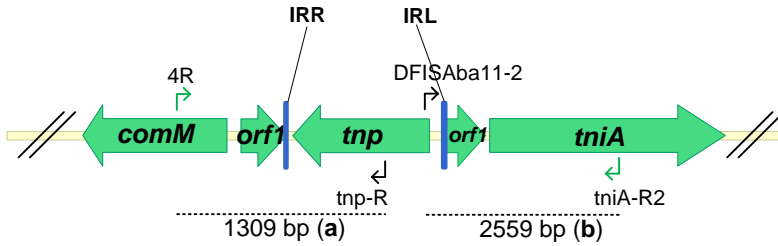
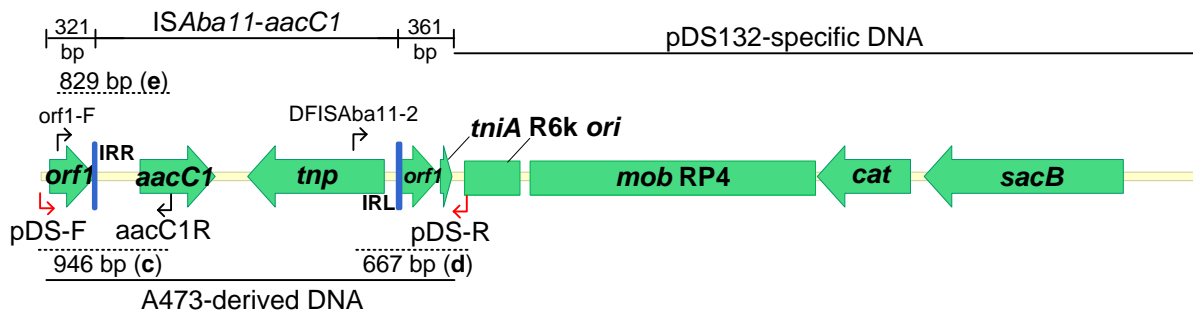


A ATCC 17978 IS*Aba11* context



B pDSISAba11Gm



C

Outcome	No. of colonies	Expected PCR results							
		<i>sacB</i>	<i>aacC1</i>	<i>tnp</i> _{ISAba11}	<i>oxa51-like</i>	a	b	c	d
5'- <i>orf1</i> single-HR	19	+	+	+	+	+	-	+	+
3'- <i>orf1</i> single-HR	1	+	+	+	+	-	+	+	+
Transposition into <i>orf1</i> or double-HR	0	-	+	+	+	+	+	+	+
None of the above	8	+	+	+	+	-	-	+	+
Controls									
A424		-	-	-	+	-	-	-	-
A473		-	ND	+	+	-	+	-	-
S17.1λpir/pDSISAba11Gm		+	+	+	-	-	-	+	+
PCR negative control		-	-	-	-	-	-	-	-

Fig. S1. Schematic drawings of the IS*Aba11*-bearing locus in *Acinetobacter baumannii* strain ATCC 17978 and the plasmid pDSISAba11Gm and PCR analysis data on 28 further gentamicin resistant colonies. (A) Genetic context of the IS*Aba11* element in *A. baumannii* strain ATCC 17978 showing its location within a Tn*AbaR orf1* gene. **(B)** Linearized map of pDSISAba11Gm showing the extent of A473-derived DNA. The short 321 bp and 361 bp sequences flanking IS*Aba11* offer the potential for targeted homologous recombination with matching sequences in *A. baumannii* A424. **(C)** Results of PCR analysis on 28 gentamicin resistant colonies obtained following transfer of pDSISAba11Gm into *A. baumannii* A424 during a subsequent conjugation experiment. Primers used for the PCR assays were as follows: *sacB*, *sacB-F/sacB-R*; *aacC1*, *aacC1F/aacC1R*; *tnp*_{ISAba11}, *tnp-F/tnp-R*; *oxa51-like*, *oxa51a/oxa51b*. Primers shown in red are specific for pDS132 only. Results shown were obtained with limiting amounts of template DNA. When excess template DNA was used, weak amplicon-a and amplicon-b bands were frequently observed for colonies that otherwise tested negative suggesting low frequency presence of genomes within the population sampled exhibiting alternative recombination patterns. This would be consistent with spontaneous low frequency excision and reintegration of pDSISAba11Gm.

IS Name	IS family	Host strain	Phylum	IS length	TIR	DR	Tnp length	Score	e-value	Identities	IRL	Motif
ISAbal1	ISAbal1	<i>A. baumannii</i> ATCC 17978	Proteobacteria	1101	13	5	325	1547	0.0	320/320 100%	taggacttacgca	HHEK
ISAcma22	ISAbal1	<i>A. marina</i> MBIC11017	Cyanobacteria	1251	22/2	5	350	785	1e-100	158/313 45%	tagaggttacgcattgacagaa	
ISAcma42	ISAbal1	<i>A. marina</i> MBIC11017	Cyanobacteria	1140	18/1	5	308	556	1e-66	116/295 36%	caggactaacgcattgaca	
ISPna6	ISAbal1	<i>P. naphthalenivorans</i> CJ2 pPNAP04	Proteobacteria	1134	22/1	0	326	885	3e-116	162/319 49%	aactt taggacttacgcattga	
ISCysp21	ISAbal1	<i>Cyanothece</i> sp. PCC 8801 pP880101	Cyanobacteria	1139	19	0	321	730	6e-93	145/316 44%	taggacttacgcattgaca	HEK
		<i>Cyanothece</i> sp. PCC 7424 pP742402	Cyanobacteria	1139	23/1	0	306	649	7e-81	129/293 44%	t taggagatacgcattgacagaa	
		<i>Cyanothece</i> sp. PCC 7822 pP782201	Cyanobacteria	1151	23/4	0	308	648	2e-80	128/305 42%	taggagatacgcattgacagaatga	
		<i>Crocospaera watsonii</i> WH 8501 A	Cyanobacteria	1136	20/2	0	322	636	9e-79	132/320 41%	t tagagagtttcgcattgacagaa	
		<i>Crocospaera watsonii</i> WH 8501 B	Cyanobacteria	1138	21/2	0	271	619	2e-76	106/267 41%	t taggagtttcgcattgacaaaa	EHEK
ISMhu9	IS701	<i>Methanospirillum hungatei</i> JF-1	Euryarchaeota	1085	15	3	328	472	5e-54	118/330 36%	a taggagttacgcag	
		<i>Meiothermus silvanus</i> DSM 9946	Deinococcus-Thermus	1092	16/1	5	343	467	5e-53	106/267 40%	taggagttacgcagttg	
		<i>Legionella pneumophila</i> str. Lens	Proteobacteria	1070	17/1	3	331	425	5e-47	96/300 32%	tgacctat tacggtt	
		<i>Gemmata obscuriglobus</i> UQM 2246	Planctomycetes	1068	13/3	1	327	355	2e-37	89/284 34%	c taggacttacgtagttg	EK
		<i>Chloroflexus aurantiacus</i> J-10-f1	Chloroflexi	1306	27/4	4	337	303	3e-29	90/296 30%	aggagttacgcagtt	
ISPlag1	IS701	<i>Planktothrix agardhii</i> NIVA-CYA	Cyanobacteria	1060	18/1	2	332	326	1e-32	93/308 30%	aggacttacgcaggcacagtatatatagtg	
		<i>Spirosoma linguale</i> DSM 74 pSLIN01	Bacteroidetes	1084	15	3	339	282	3e-26	94/312 30%	tatat taggacttacgca	
		<i>Synechococcus</i> sp. PCC 7335	Cyanobacteria	1118	15	1	358	269	3e-24	74/290 26%	a taggacttacgcag	
		<i>Parachlamydia acanthamoebae</i> UV7	Chlamydiae	1187	12/1	5	255	263	6e-24	70/227 31%	actcacc tacgcaaaa	
		<i>Salinibacter ruber</i> M8 pSR84	Bacteroidetes	1283	13/1	5	243	259	4e-23	78/293 27%	taggacttacgca	
		<i>Roseiflexus castenholzii</i> DSM 13941	Chloroflexi	1090	13	0	348	234	9e-19	87/328 27%	actcacc tacgcag	
		<i>Methylobacterium album</i> BG8	Proteobacteria	1251	16/1	1	356	221	1e-17	75/311 24%	caggacttacgca	
		<i>Methylobacter tundripaludum</i> SV96	Proteobacteria	1283	14/1	0	243	184	4e-13	87/271 35%	cttattaactgatg tacgcag	
		<i>Rhodothermus marinus</i> SG0.5JP17-172	Bacteroidetes	891	11	0	186	160	3e-10	44/132 33%	taggacttacgca	
		<i>Methanosarcina barkeri</i> str. Fusaro	Euryarchaeota	1090	20/2	1	351	312	7e-32	71/175 41%	taggacttacgca (IRR missing)	
		<i>Methanosarcina acetivorans</i> C2A	Euryarchaeota	NK	NK	NK	195	264	3e-25	59/135 44%	t taggacttacgca (IRR missing)	
		<i>Legionella longbeachae</i> D-4968	Proteobacteria	NK	NK	NK	166	366	1e-38	92/263 35%	NK	
		<i>Legionella longbeachae</i> NSW150	Proteobacteria	NK	NK	NK	324	359	2e-37	97/285 34%	NK	

Fig. S2. List of putative insertion sequence elements encoding BlastP homologs of Tnp_{ISAbal1}, which possess as a minimum the EK residues of the ISAbal1 family HHEK motif. Features of these elements and associated transposases are as indicated. Score, e-value and identities data refer to results of BlastP analysis against Tnp_{ISAbal1}. Only elements which have been archived in ISfinder carry assigned names and families. Bases shown in bold within the identified IRL sequences are conserved in the majority of sequences. NK, not known.