Supplementary material

Fig. S1: Description of novel ISs found in *A. baumannii* Ab825. The transposase gene is shown in bold and cargo genes in italics. Inverted repeats IRL and IRR are highlighted in yellow and blue, respectively.

>*ISAba*42; 1,320 bp long

GAGACTGTAAATTAAATTGTGTAATTGCCTGAATTTGCTATGTTCATATTCACAACGGAGTCAGGCAAC**ATGATGAACGAACAAAAACTAAAAGACCTTGCAGCAGAATTTGCTAAAGGAATCAAAACAGAAGACGATCTCAATCAATTCACCCGATTGTTGACTAAACTCACTGTTGAAACGGCTCTCAATGCCGAACTTACCGAACATCTCGGACATGAAAAGAATGCTCGTAAGAACGGTTCAAATGCTCGTAACGGTTATTCCAGTAAGACCGTGCTGAGCGATGATGGTGAGATTGAGATCACCACACCACGAGATCGTGATGGCACATTTGAGCCACAGCTAATTAAAAAGAATCAGACTCGTATCACGCAAATGGATAACCAAATTCTATCCCTTTATGCCAAAGGCATGACTACCCGTGAAATCGTGGCTACTTTCAAAGAAATGTACGATGCTGATGTATCGCCAACGCTTATTTCCAAGGTGACTGATGCTGTTAAGGAGCAAGTCGCTGAATGGCAAAACCGTCCGCTGGATGCACTCTATCCCATCGTCTATATGGACTGTATTGTAGTTAAAGTCCGTCATAATGGCAGTGTTATCAACAAGGCTGTATTCCTTGCCTTAGGCATTAATCTTGATGGACAGAAAGAACTGCTCGGCATGTGGATGGCTGAGAATGAAGGTGCAAAGTTCTGGCTGAATGTCCTGACTGAGCTTAAAAACCGAGGGTTGCAGGATATTCTGATCGCCTGTGTGGATGGACTAAAAGGCTTTCCTGATGCCATTAACAGCGTATACCCGCAAACCCATATCCAGCTGTGCATTATCCATATGCTGCGTAACAGCTTGAAATACGTATCATGGAAAGATTACAAGGCCGTCACTCAGGATTTAAAAACCGTTTATCAGTCACCTACTGAAGAGGCAGCCTTGATGGCCTTGGATCAATTCGCCCAAACATGGGATGACAAGTACCCACAGATCAGCAAAAGCTGGCGTACACACTGGGAGAATCTAAATACCTTCTTTGCTTATCCAGCCGAGATACGCAAAGCCATCTATACCACCAATGCGATCGAATCATTAAACAGCGTAATACGTCAGGCGATCAAAAAGCGTAAAGTCTTTCCAACGGATGATTCTGTACGTAAAGTGATTTACCTGGCAATTGATGCAGCGTCT**

AAAAAGTGGAATATGCCTATTCGCGACTGGCGTTTAGCCATGAGCCGCTTTATTATTGAATTCGGTGACCGCTTAAGCAATCACCTTTAAATTTATGAAAAGCAATTACACAAAATTATTTACAGGCTC

IR-L:GAGACTGTAAATTAAATTGTGTAATTGCCTGAATTTGCTATGTTCATATT

IR-R:GAGCCTGTAAATAATTTTGTGTAATTGCTTTTCATAAATTTAAAGGTGAT

DR length: 8 bp

>TnpA (coord: 70-1281, 403 aa)

MMNEQKLKDLAAEFAKGIKTEDDLNQFTRLLTKLTVETALNAELTEHLGHEKNARKNGSNARNGYSSKTVLSDDGEIEITTPRDRDGTFEPQLIKKNQTRITQMDNQILSLYAKGMTTREIVATFKEMYDADVSPTLISKVTDAVKEQVAEWQNRPLDALYPIVYMDCIVVKVRHNGSVINKAVFLALGINLDGQKELLGMWMAENEGAKFWLNVLTELKNRGLQDILIACVDGLKGFPDAINSVYPQTHIQLCIIHMLRNSLKYVSWKDYKAVTQDLKTVYQSPTEEAALMALDQFAQTWDDKYPQISKSWRTHWENLNTFFAYPAEIRKAIYTTNAIESLNSVIRQAIKKRKVFPTDDSVRKVIYLAIDAASKKWNMPIRDWRLAMSRFIIEFGDRLSNHL

>*ISAba*43; 2,655 bp long

GTTCTTTGCACTTTAGCGTGAAGATTGTTACGATATGGACTCATCCATGAGATAACCCGCACATGAGCGCTACCAAGAAAGCAGACAAGTAAGCCGCAGCAACCTTCGTTTTCGGTTGTTGCGGCGTTCTCAAGAACCTAGTTGCTCTGCAAGAGCGCCGCCAAATTCTTAACTTAAGGAGATGGCTTC*GTGCGCTCAAAAGATTTTTCTTGGCGGTATTCTCTTCCCGCCACGCTATTGCTGTTATCACCATTCGATTTGCTGGCGTCACTGGGCATGGATATGTACCTGCCCGTGGTGCCTTTCATGGCGGATGCACTTGGGTCCGGTGCAGGGACGATCCAGCTGACG*

*TTGACGGCATACCTGGTTTTGCTTGGAGCCGGACAGCTTCTCTTCGGCCCACTGTCGGATCGGCTGGGTCGCCGCCCCGTTTTACTTGGTGGCGGGATTGCCTATATTGCGGCTTCATTCGGCCTCACCGTAGTTTCATCGCCAGAACTTTTTCTGAGCTTCCGCGTTCTTCAGGCCTGCGGCGCTTCGGCATGTCTCGTTTCCACTTTCGCGACGGTACGCGACATCTATTCGGGCCGTGAGGAAAGCAACGTCATCTATGGCTTGCTCGGCTCTATGCTTGCGATGGTTCCTGCGATAGGCCCACTGCTAGGAGCGCTGGTCGACGCGTGGCTCGGATGGCGCGCAATCTTCGGCTTGCTAGGGATGGCAATGATAGGCGCTGTTATCGCAGCCTGGCGACTCTGGCCAGAGACTCGGCGGCACCGGACGGCAGACCTACAGTGGTCGCAGCTATTGACTCCTGTGAAACACCTGAACTTCTGGCTGTACACGCTCTGTTACAGCGCGGGGATGGGCAGCTTTTTCGTCTTTTTCTCGACCGCCCCCTGGCTAATGATGGGGAGGCAAGGGTTATCGCAACTTAGCTTCAGCTTGCTATTTGCTACAGTGGCCATCGCTATGATGGCTACAGCGCGAATCATGGGACGACTGATTCCCCGGTGGGGAAGCCTGAAGACCTTACGAGTGGGAATGGGGTGTCTGATGGCGGGAGCGCTGTTGCTCGCTGTTGGCGAGACATTGGCACCGGTCTCGGTGCTTGGCTTCATCGCCCCGATGTGGCTCGTGGGTGTTGGTATCGCCACTGCGGTATCGGTGGCACCCAATGCCGCTCTTCGAGGTTTCGATCATATCGCTGGGACCGCTACAGCAGTCTACTTCTGTTTGGGTGGACTACTGTTAGGGATTATCGGGACACTCATTATTACGCTTTTATCGACTGGTACCACCTGGCCGATCATCGCTTATTGCCTCATCCTCGCAACAGCAGTGCTTTGTCTGTCCTGCATCAATCCCAACAGACGCCATCTCAGCCAAGAAGAACATGATGCCTTGGCGCTACAAGGCACCGATAGCGCGCAATCGGTCCATGATC****ATGACTAG*****CGCTGATGTTTGGAGCCTGTTCTGGAAGGGCTTTTCGCCAGCGTCTCATGGGCTTCTAGATGAACAGACTTTGCTGATCCGTCTTACACACGACGAGGAGCATACGCCAATTTGTAGCCGATGCGATTGCCCTTGTTTCCTGGTACATGACATCAATTGGCGCCGAGTTCGCGAGTCACCAATTATGCAGTATCGCGTCGAGTTGGATGTACCTGTGCGGCGGCTGCGTTGTCCACAATGCGGTCCAACCAGAGAGCGGATCGATTGGCTACCACCGCGCTCCCGTATTACGCAATCATTGCGCAACTGGATTGAGAAATTAGTACAGATGCTGCCCGTCAGTCATGTTGCCAATCTTTTGGGCTTGCATTGGCATACAGTCAAGACTATTGACATGGAGCGGCTCAAACGTGATTTGCACGAGCCAGATCGAAGTCGATTGCGCCGCCTGATGATGGACG**

AATTCGCCTTGCACAAGGGTCATCGCTACGCCACGGTGGTCGCCTGTGCCGACACCCAGCAAGTGGTGTGGATTGGCGAGGGCCGCTCGCGTGAGGCGATCCGGCCGTTCTTCGAGTGGTTAGGCGATGCCCGGAACCAGATCGAGGCAGTGGCCATGGACATGAACTCAGCCTTCGATCTTGAAGTGAAGGCCCAGTGCCCCAACGCGGTGGTGGTCTACGACCTGTTCCATGTGGTGGCTAAGTATGGCCGCGAAGTGATGGATAGAGTGCGAGTTGATCAGGCCAATCAACTGCGAGATGACAAGGTCGCCCGCAAGGTGATCAAAAGCAGCCGTTGGATACTGTTACGCAATGCTGACAACCTTGAGCCCGAGCAGGCGGTCAAGCTGGACGAACTCCTGGCCGCCAATGCGTTCTTGACTACGGTGTACGTGCTCAAGGACCAACTTAAGACGCTATGGTTTGCGGAAAGCGAGACGACGGCCAGAAGCGCCTGGCGGGAATGGGCCGGCATGGCCCTCGGTAGCGGAATTGATGCTTTGGTACGATTTGCCAAGAAGCTGGAGCCATATATGGAGGGTATCGTTTCCAGTGCCCTCCACCGGCTGAACACCAGCGTGCTGGAGGGCATGAACAACCGGATCAAAGTCATTAAGCGGATGGCCTATGGATACCGCGACACGGACTACTTCTTCCTCAAGATCCGTGCTGCATTTCCCGGCAAAGTGCGATGAAC

IRL:GTTCTTTGCACTTTAGCGTGAAGATTGTTACGATATGGACTCATCCATGAGATAACCCGCACATG

IRR:GT*TCATCGCACTTTGCCGGGAAATGCAGCACGGATCTTGAGGAAGAAGTAGTCCGTGTCGCGGTA*

DR length: 8/10 bp

>ORF1 Chloramphenicol resistance protein drug resistance transporter, Bcr/CflA subfamily [*Acinetobacter baumannii* Ab825sp] (coord: 190-1455; 1266 bp; 421 aa)

MRSKDFSWRYSLPATLLLLSPFDLLASLGMDMYLPVVPFMADALGSGAGTIQLTLTAYL

VLLGAGQLLFGPLSDRLGRRPVLLGGGIAYIAASFGLTVVSSPELFLSFRVLQACGASACLVSTFATVRDIYSGREESNVIYGLLGSMLAMVPAIGPLLGALVDAWLGWRAIFGLLGMAMIGAVIAAWRLWPETRRHRTADLQWSQLLTPVKHLNFWLYTLCYSAGMGSFFVFFSTAPWLMMGRQGLSQLSFSLLFATVAIAMMATARIMGRLIPRWGSLKTLRVGMGCLMAGALLLAVGETLAPVSVLGFIAPMWLVGVGIATAVSVAPNAALRGFDHIAGTATAVYFCLGGLLLGIIGTLIITLLSTGTTWPIIAYCLILATAVLCLSCINPNRRHLSQEEHDALALQGTDSAQSVHDHD

>ORF2 Transposase DDE Domain [Acinetobacter baumannii Ab825sp] (coord: 1448-2653; 1206 bp; 401 aa)

MTSADVWSLFWKGFSPASHGLLDEQTLLIRLTHDEEHTPICSRCDCPCFLVHDINWRRVRESPIMQYRVELDVPVRRLRCPQCGPTRERIDWLPPRSRITQSLRNWIEKLVQMLPVSHVANLLGLHWHTVKTIDMERLKRDLHEPDRSRLRRLMMDEFALHKGHRYATVVACADTQQVVWIGEGRSREAIRPFFEWLGDARNQIEAVAMDMNSAFDLEVKAQCPNAVVVYDLFHVVAKYGREVMDRVRVDQANQLRDDKVARKVIKSSRWILLRNADNLEPEQAVKLDELLAANAFLTTVYVLKDQLKTLWFAESETTARSAWREWAGMALGSGIDALVRFAKKLEPYMEGIVSSALHRLNTSVLEGMNNRIKVIKRMAYGYRDTDYFFLKIRAAFPGKVR

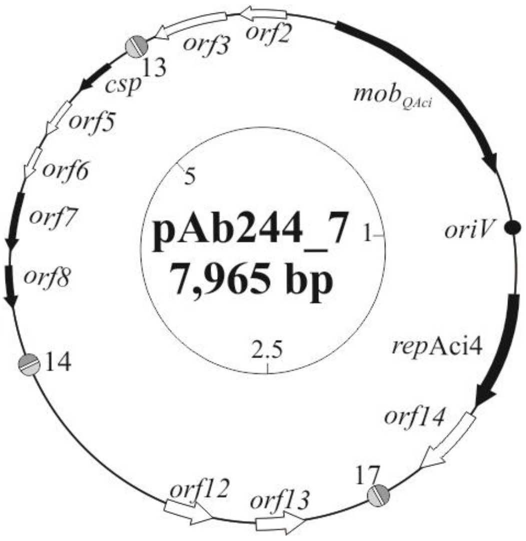

Figure S2. Organization and gene content of plasmid pAb244_7. Inferred scheme of pAb244_7 plasmid (MG520098). The ORFs and their corresponding orientations are denoted by arrows. Closed arrows correspond to genes with described functions, whereas open arrows relate to unknown functions in databases. A dark circle denotes the predicted *oriV* region, whose starting bases were arbitrarily set to 1 in the clockwise scale (innermost circle) that also indicates the corresponding kbp. XerC/D-like binding sites are shown as dark/gray ovals.

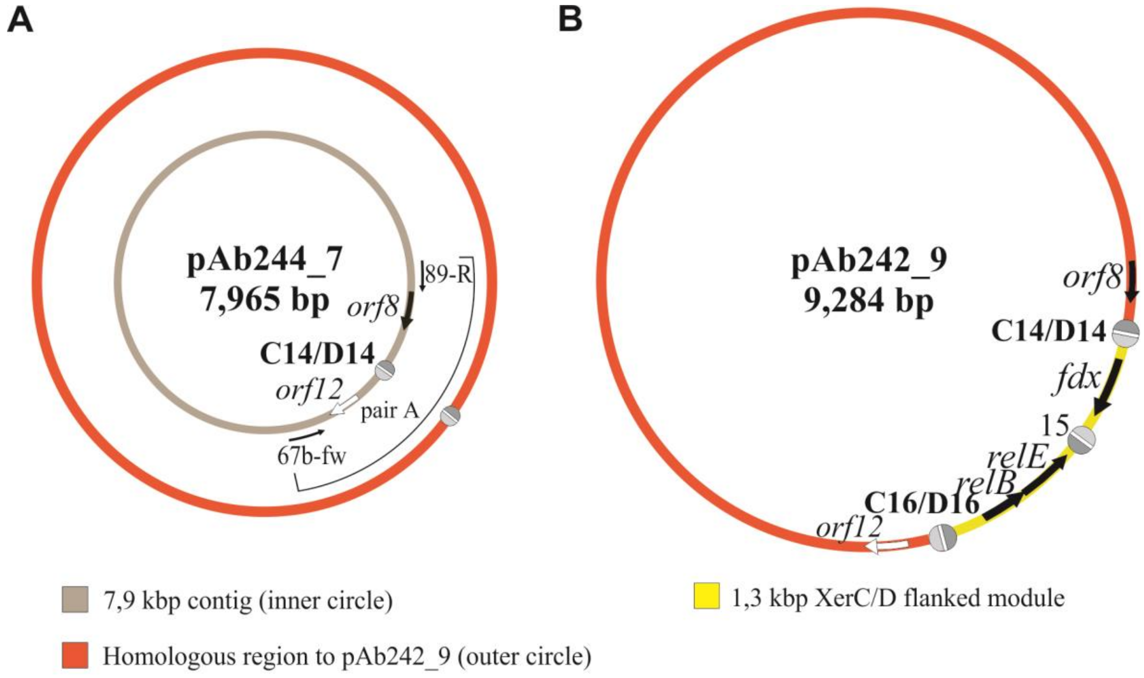

Figure S3. Schematic representation of pAb244_7 sequence inferred by comparative sequence analysis and gap closure strategy. A. The circular form of pAb244_7 (gray inner circle) was confirmed by gap closure of the contigs assembled from the pyrosequencing data. The primer pair A (67b-fw and 89-R) used for this purpose is described in Supplementary Table S1. The sequence of the corresponding amplicon was verified by sequencing analysis. Regions of homology between pAb244_7 and pAb242_9 from Ab242 [1] are indicated by the outer circle in orange. Relevant XerC/D (C/D) sites identified in these plasmids are indicated as circles (not drawn to scale), with the XerC (C) and XerD (D) recognition motifs depicted as dark gray and light gray semi-circles, respectively. The *orf8*, *orf12* genes and the XerC/D recognition site #14 (C14/D14) are shown. **B.** Representation of the pAb242_9 plasmid containing a 1.3 kbp region (depicted in yellow) flanked by XerC/D sites, which are absent from pAb244_7.

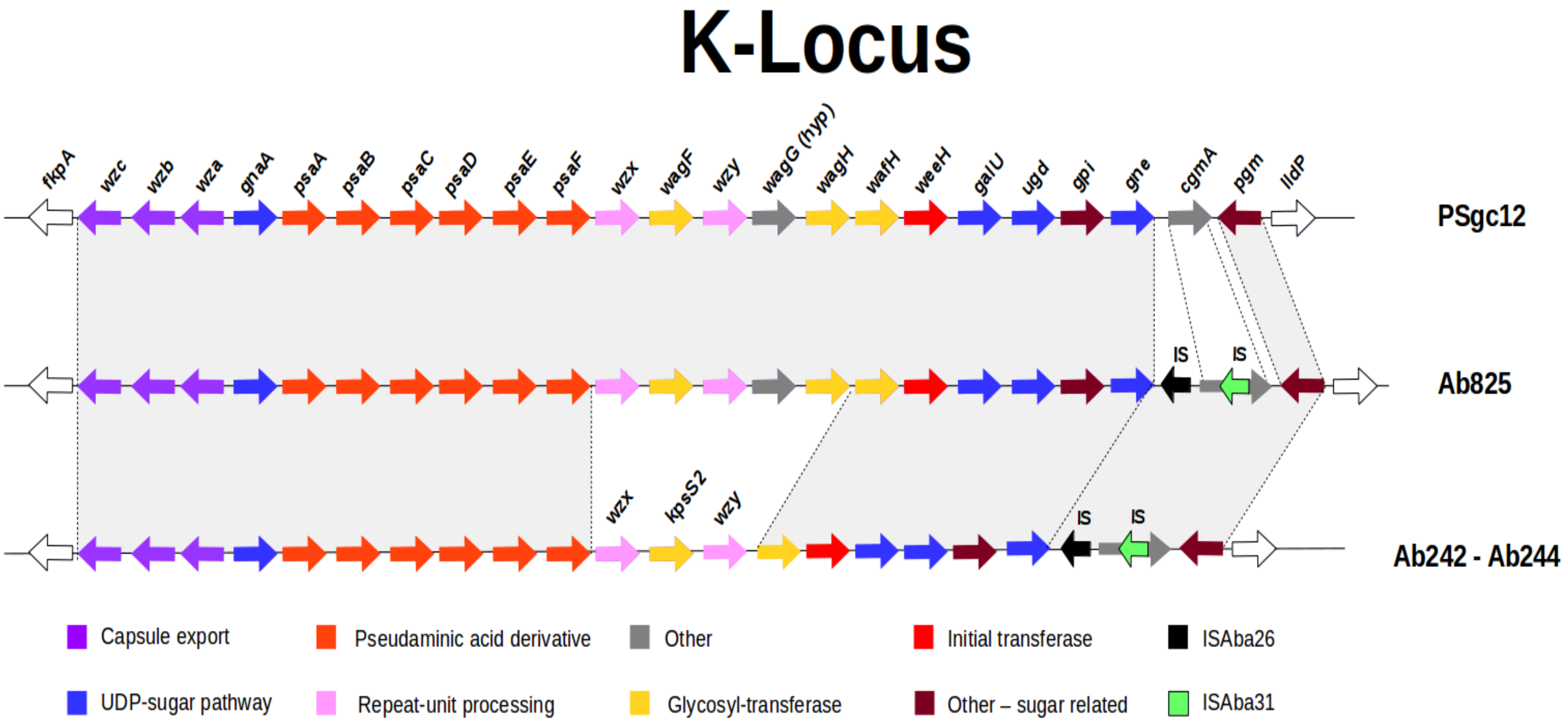

Figure S4. Genetic organization of K loci in strains under study. A novel K-locus with a similar gene composition to the PSgc12 [2] was identified. This locus is identical between strains Ab242 and Ab244, whereas in strain Ab825, the presence of two additional ORFs predicted to code for glycosyl-transferase proteins was observed. It contains a gene cluster (*psaA*-*psaF*) predicted to direct the synthesis of a pseudaminic acid derivative. Notably, the *gne* gene, which codes for a UDP-NAc-glucose-4-epimerase, is followed by an IS*Aba26* in all strains. Moreover, the *cgmA* gene is interrupted by an IS*Aba31* (see text for details). The gray-shaded background interconnecting the different structures highlights the homologous regions (nucleotide sequences ≥ 90% identity). Genes are coloured according to the code shown in the figure. The genes are not drawn to scale.

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Table S1. Oligonucleotide primers used for PCR analysis

Primer pairs		**DNA molecule**	**Annealing region coordinates**	**Sequence (5´→3´)**	**Expected product size (bp)**	**Application**	**Reference or source**
A	67b-Fw	pAb244_7	4,412-4,442	AGCGTAAAAGACCAGTTTGGCGTTAAACACG	2,616	Plasmid gap-closure (see Fig. S2)	This work
	89-R	pAb244_7	1,827-1,854	GTATCCCTGTTCCAGAACACGTTGAGCC			
B	usp-fw	Ab242/chromosome	504-522 (contig 86)	ACCGAGCATGATTCCAGTA	1,600	Confirmation of ISAba125 insertion into Tn6022	This work
	orf-rv		38,463-38,479 (contig 87)	GGTGTCCGAGCATAAGC			This work

Table S5. Antimicrobial susceptibility profiles of *A. baumannii* Ab242, Ab244 and Ab825 as determined by VITEK-2

	MIC (µg/ml) [a]		
Antimicrobial	**Ab242**	**Ab244**	**Ab825**
Ampicillin	≥32 (R)	≥32 (R)	≥32 (R)
Ampicillin/Sulbactam	16 (R)	≥32 (R)	16 (R)
Piperacillin/Tazobactam	≥128 (R)	≥128 (R)	≥128 (R)
Cefotaxime	≥64 (R)	≥64 (R)	≥64 (R)
Ceftazidime	16 (I)	≥64 (R)	≥64 (R)
Cefepime	16 (I)	32 (R)	32 (R)
Imipenem	≥16 (R)	≤ 0.5 (S)	≥16 (R)
Meropenem	≥16 (R)	≤ 0.5 (S)	≥16 (R)
Nalidixic acid	≥32 (R)	≥32 (R)	≥32 (R)
Ciprofloxacin	≥4 (R)	≥4 (R)	≥4 (R)
Amikacin	≥64 (R)	16 (R)	≥64 (R)
Sulfamethoxazole/ Trimetoprim (23.75/1.25)	≥320 (R)	≥320 (R)	≥20 (S)
Tetracycline[b]	2	4	64 (R)

[a] The antimicrobial susceptibility profiles of the strains was evaluated using the VITEK-2 System (bioMérieux) following the criteria recommended by CLSI standards. Interpretation: S: susceptible; R: resistant; I: intermediate.

[b] Determined by the macrodilution method using MH broth in accordance to CLSI recommended procedures

Table S8. Location of insertion sequences found in *A. baumannii* Ab242, Ab244 and Ab825 chromosomes^{a}.

Ab242									
IS	**IS locus tag**	**IS location**	**Locus tag(s) of the disrupted gene^{b}**	**Putative function of the disrupted gene**	**Locus tag(s) of IS flanking genes**	**Putative function of IS flanking genes**	**Metabolic pathway/Virulence Factor**	**Number of genomes with same IS location^{c}**	**Ref. genome locus Tag^{d}**
ISAba42	CJU83_05025	In	CJU83_05020 (N)	Type I secretion system-dependent protein	-	-	Ca2+-binding protein, RTX toxin-related	N/R	
ISAba43	CJU83_05970-CJU83_05975	In	CJU83_05965 (N)	PhzF-like	-	-	Phenazine biosynthesis	N/R	
ISAba31	CJU83_07630	In	CJU83_07625 (N)-CJU83_07635 (C)	Hypothetical	-	-	Ph242-B	N/R	
ISAba125	Not annotated	In	-	-	CJU83_17340/CUJ17770	UspA/Hypothetical protein	AbaR-like	N/R	
ISAba26	CJU83_18565	IR	-	-	CJU83_18560/ CJU83_18570	Gne/CgmA	K locus for capsule biosynthesis	N/R	
ISAba31	Not annotated	In	CJU83_18570	Lipoteichoic acid synthase (LTA) like domain protein CgmA	-	-	K locus for capsule biosynthesis	N/R	
Ab244									
IS	**IS locus tag**	**IS location**	**Locus tag(s) of disrupted gene^{a}**	**Putative function of disrupted gene**	**Locus tag(s) of IS flanking genes**	**Putative function of IS flanking genes**	**Metabolic pathway/Virulence Factor**	**Number of genomes with same IS location^{b}**	**Ref. genome locus Tag^{c}**
ISAba1	CVG52_05305	IR	-	-	CVG52_05300/ CVG52_05310	*bla*$_{ADC}$- beta-lactamase	Resitance to beta-lactamics	736	M3Q_2831/ M3Q_2828
ISAba42	CVG52_05065	In	CVG52_05060 (N)	Type I secretion system-dependent protein	-	-	Ca2+-binding protein, RTX toxin-related	N/R	

ISAba31	CVG52_07330	In	CVG52_07325 (N) CVG52_07335 (C)	Hypothetical protein	-	-	Ph244-B	N/R	
ISAba125	CVG52_11015	In	CVG52_11010 (pseudogene)	CinA	-	-	Competence	30	M3Q_1781
ISAba26	CVG52_18150	IR	-	-	CJU83_18145/ CJU83_18155	CgmA/Gne	K locus for capsule biosynthesis	N/R	
ISAba31	Not annotated	In	CVG52_18145	Lipoteichoic acid synthase (LTA)-like domain protein CgmA	-	-	K locus for capsule biosynthesis	N/R	
Ab825									
IS	**IS locus tag**	**IS location**	**Locus tag(s) of disrupted gene[a]**	**Putative function of disrupted gene**	**Locus tag(s) of IS flanking genes**	**Putative function of IS flanking genes**	**Metabolic pathway/Virulence Factor**	**Number of genomes with same IS location[b]**	**Ref. genome locus Tag[c]**
ISAba125	CLM70_00285	In	CLM70_00280 CLM70_00290	Sodium dependent transporter	-	-	-	N/R	
IS10R	CLM70_00700 - CLM70_00705	IR	-	-	CLM70_00695/ CLM70_00710	Acetamidase-Formamidase/ABC transporter substrate-binding protein	Variety of functions/Transport	N/R	
ISAba31	Not annotated	In	CLM70_02585 (pseudogene)	Di-guanylate cyclase (GGDEF domain)	-	-	Biofilm regulation	23	M3Q_798
ISAba1	CLM70_02870	In	CLM70_02875 (pseudogene)	Sensor histidine kinase	-	-	Transcriptional regulation	31	M3Q_3394
IS10R	Not annotated	IR	-	-	CLM70_03360/ CLM70_03605	Putative esterase or lipase (alpha/beta hydrolase fold)/DapE N-succinyl-L,L-diaminopimelate desuccinylase.	DAP	N/R	

IS10R	Not annotated	IR	CLM70_04515/ CLM70_04900	Diacylglycerolkinase/ metallohydrolase	-	-	Phospholipid metabolism/urea cycle and metabolism of amino groups	N/R	
IS10R	Not annotated	IR	-	-	CLM70_04520/ CLM70_04910	Amidohydrolase DapE/ Holliday junction DNA helicase RuvB	DAP	7	M3Q_3063 / M3Q_3064
ISAba825	CLM70_04990	In	CLM70_04985 (pseudogene)	CarO outer membrane protein	-	-	Carbapenem resistance	9	M3Q_3047
ISAba42	Not annotated	In	CLM70_04995 (pseudogene)	Type I secretion system-dependent protein	-	-	Ca2+-binding protein, RTX toxin-related	N/R	
ISAba1	Not annotated	IR	-	-	CLM70_05835/ CLM70_06100	*bla*$_{ADC}$- beta-lactamase	Resitance to beta-lactamics	736	M3Q_2831 / M3Q_2828
ISAba43	CLM70_06200/ CLM70_06205	In	CLM70_06195 (pseudogene)	PhzF	-	-	Phenazine biosynthesis	N/R	
ISAba1	Not annotated	IR	-	-	CLM70_06590 CLM70_06595	Transcriptional regulator, TetR family/Sigma-fimbriae uncharacterized paralogous subunit	Transcriptional regulation/Type I-Pili component CsuAB	184	M3Q_2687/ M3Q_2688
ISAba125	Not annotated	In	CLM70_06600 (pseudogene) CLM70_06605 (pseudogene)	CsuA	-	-	Type I-Pili component	36	M3Q_2685
IS10R	Not annotated	In	CLM70_06820 (N) CLM70_06810 (C)	Alanine racemase	-	-	Cell wall synthesis	N/R	
ISAba125	Not annotated	In	CLM70_06890 (pseudogene) CLM70_06895	Biofilm PGA synthesis deacetylase PgaB	-	-	EPS synthesis	4	M3Q_2611

ISAba42	Not annotated	IR	-	-	CLM70_07550 CLM70_07820	Phage integrase/Transcriptional regulator	-	N/R	
ISAba31	Not annotated	In	CLM70_07890(N) (pseudogene) CLM70_07915(C)	Hypothetical/Hypothetical	-	-	Ph825-B	N/R	
ISAba43	Not annotated	IR	-	-	CLM70_07925 CLM70_08175	Transcriptional regulator, TetR family/Nitrogen regulation protein NtrC	Transcriptional regulation/Gln Synthetase regulation	9	M3Q_2447 /M3Q_2448
ISAba125	Not annotated	IR	-	-	CLM70_08875 (pseudogene) CLM70_09040	Hypothetical/Hypothetical	-	N/R	
ISAba43	CLM70_09440	In	CLM70_09435 (pseudogene) CLM70_09445	Phospholipase D	-	-	Host colonization	2	M3Q_3378
ISAba125	Not annotated	In	CLM70_09885 (pseudogene) CLM70_09890 (pseudogene)	Ribonuclease D	-	-	-	17	M3Q_2071
ISAba125	Not annotated	In	CLM70_09930 (N)	Hypothetical	-	-	-	N/R	
ISAba125	Not annotated	In	CLM70_11630 (pseudogene)	CinA	-	-	Competence	30	M3Q_1781
ISAba43	CLM70_11635	In	CLM70_11640 (pseudogene; C) CLM70_11915 (N)	Cytosine, purine, uracil, thiamine, allantoin permease family protein	-	-	-	9	M3Q_1895
ISAba125	Not annotated	In	CLM70_12310 CLM70_12315	T6SS component AsaA	-	-	Type 6 secretion system	N/R	
ISAba125	Not annotated	IR	-	-	CLM70_12475 CLM70_12590	Rhs-family protein/Hypothetical	Toxin/ Hypothetical	N/R	

ISAba43	Not annotated	IR	-	-	CLM70_12480 CLM70_12595	Diguanylate cyclase-phosphodiesterase /EamA family transporter (threonine)	Biofilm regulation	6	M3Q_1620/ M3Q_1621
ISAba42	Not annotated	In	CLM70_13785(N)	Hypothetical	-	-	-	N/R	
ISAba125	Not annotated	IR	-	-	CLM70_14685 (pseudogene) CLM70_14690	SAM-dependent methyl transferase/Hypothetical	-	N/R	
ISAba125	Not annotated	In	CLM70_15390(N)	Hypothetical	-	-	-	N/R	
IS10L	Not annotated	IR	-	-	CLM70_15930 CLM70_16745	Hypothetical/DNA topoisomerase I	-	N/R	
IS10R	CLM70_17485 CLM70_17490	IR	-	-	CLM70_17480/ CLM70_17495	Predicted esterase of the alpha-beta hydrolase fold/TetC	-	N/R	
IS10L	Not annotated	IR	-	-	CLM70_17530 (pseudogene)/ CLM70_17535	LysR family transcriptional regulator/MerR family transcriptional regulator	-	N/R	
IS10R	Not annotated	In	CLM70_17780(N) (pseudogene) CLM70_17955(C)	Hypothetical	-	-	-	N/R	
ISAba43	Not annotated	In	CLM70_18160(N) (pseudogene) CLM70_18175 (C)	Hypothetical protein (DUF2236)	-	-	-	N/R	
ISAba31	CLM70_18695	In	CLM70_18700 (N) CLM70_18690 (C)	Lipoteichoic acid synthase (LTA) like domain protein CgmA	-	-	K locus for capsule biosynthesis	N/R	
ISAba26	CLM70_18705	IR	-	-	CLM70_18700/ CLM70_18710	CgmA/Gne	K locus for capsule biosynthesis	N/R	

[a] Only most relevant IS elements were considered in this Table.

[b] N and C refer to the N- and C-terminal segments of encoded proteins.

[c] According to Adams, et al. 2016

[d] *Acinetobacter baumannii* TYTH-1

In: interrupted gene; IR: intergenic region; N/R: not reported

REFERENCES

1. **Cameranesi MM, Morán-Barrio J, Limansky AS, Repizo GD, Viale AM**. Site-specific recombination at XerC/D sites mediates the formation and resolution of plasmid co-integrates carrying a blaOXA-58- and TnaphA6-resistance module in Acinetobacter baumannii. *Front Microbiol*. Epub ahead of print 2018. DOI: 10.3389/fmicb.2018.00066.
2. **Hu D, Liu B, Dijkshoorn L, Wang L, Reeves PR**. Diversity in the Major Polysaccharide Antigen of Acinetobacter Baumannii Assessed by DNA Sequencing, and Development of a Molecular Serotyping Scheme. *PLoS One* 2013;8:1–13.