

Table S1: Bacterial strains, plasmids and primers used in this study.

Strain	Description/phenotype	Reference
Recipient strains for natural transformation		
M2	<i>A. nosocomialis</i> strain M2 wild-type	(1)
M2 Rif ^R	Spontaneous <i>rpoB</i> mutant; rifampicin resistant	This study
M2 Rif ^R Δ <i>comEC</i> ::aacC4	Insertion of an apramycin resistance cassette in the <i>comEC</i> gene of the M2 Rif ^R strain; Non transformable and rifampicin resistant	This study
M2 Rif ^R Δ <i>recA</i> ::aacC4	Insertion of an apramycin resistance cassette in the <i>recA</i> gene of the M2 Rif ^R strain; Non transformable and rifampicin resistant	This study
M2 Rif ^R Δ <i>pilA</i> ::kan	Insertion of a kanamycin resistance cassette in the <i>pilA</i> gene of the M2 Rif ^R strain; Non transformable and rifampicin resistant	This study
AYE	<i>A. baumannii</i> strain AYE wild-type	(2)
AYE Rif ^R	Spontaneous <i>rpoB</i> mutant; rifampicin resistant	This study
29D2	<i>A. baumannii</i> nonclinical isolate 29D2 wild-type	(3)
29D2 Rif ^R	Spontaneous <i>rpoB</i> mutant; rifampicin resistant	This study
A118	<i>A. baumannii</i> strain A118 wild-type	(4)
A118 Rif ^R	Spontaneous <i>rpoB</i> mutant; rifampicin resistant	This study
27304	<i>A. baumannii</i> veterinary clinical isolate 27304	Resapath, ANSES
27304 Rif ^R	Spontaneous <i>rpoB</i> mutant; rifampicin resistant	This study
27024	<i>A. baumannii</i> veterinary clinical isolate 27024	Resapath, ANSES
27024 Rif ^R	Spontaneous <i>rpoB</i> mutant; rifampicin resistant	This study

Donor strains for natural transformation			
Genetic construct		Name	Primer Sequence 5' to 3'
Chromosomal modifications using overlap extension PCR			
<i>comEC::aacC4</i>	comEC_UP_F	TGGTGTGCGCTGTACTAATTACGGT	<i>Acinetobacter</i> genomic DNA; 2kb upstream of the <i>comEC</i> gene
	comEC_apra_R	GTGCCGTGCTAGTAGCACGCCCTCCCGTTCAGAGCCTGCCACTTTTC	<i>Acinetobacter</i> genomic DNA; Chimeric, middle of the <i>comEC</i> gene
	comEC_apra_F	GGCGAGCGGTCAAGCTAACGACTCGAGTACTGGATAGGCTCTGGTTGAGTA	<i>Acinetobacter</i> genomic DNA; Chimeric, middle of the <i>comEC</i> gene
	Apr_Fw	CAGGCTGGTGCCAAGCTCT	pMHL-2 (Godeux et al., 2018) ; downstream <i>aacC4</i> gene
	Apr_Rev	TCATGAGCTCAGCCAATCGACTGG	pMHL-2 (Godeux et al., 2018) ; upstream

			<i>aacC4</i> gene
	comEC_DW_R	CTTCAGTTCACGCATCAAGCTTGT	Acinetobacter genomic DNA; 2kb upstream of the <i>comEC</i> gene
<i>pilA::kan</i>	asg-145	GTTATGGCGGCGGTGGAGGTC	Acinetobacter genomic DNA ; 1kb upstream of the <i>pilA</i> gene
	asg-143	GAACACTTGAGGCGCAGAGTAAATGCTTCAGATGC	Acinetobacter genomic DNA ; Chimeric, middle of the <i>pilA</i> gene
	asg-144	CCTTCTTCACGAGGCATCAATCATTGTAGCATCG	Acinetobacter genomic DNA ; Chimeric, middle of the <i>pilA</i> gene
	kan-F	CTGCGCCTCAAGTGTTC	KanR gene cassette ; upstream the <i>kanR</i> gene
	kan-R	TGCCTCGTGAAGAAGG	KanR gene cassette ; downstream the <i>kanR</i> gene
	asg-146	AGAATACTTGATAGTGACAGGTTACAG	Acinetobacter genomic DNA ; 1kb downstream of the <i>pilA</i> gene
<i>recA::aacC4</i>	LH114_V2_recA	CTTTTCATTGCTCTCAAGATGAAC	Acinetobacter genomic DNA; 2kb upstream of the <i>recA</i> gene
	LH115_V2_recA	GGAACTTCGAAGCAGCTCCAGCCTACACAATCGTAATGCTTGCTTTATTCTCATCC	Acinetobacter genomic DNA; Chimeric: 5' of the <i>recA</i> gene and upstream of <i>aac4</i> gene
	LH116_recA_AB 5075	AACTAAGGAGGATATTCATATGGACCATGGCGACTACAGGCACAAATGGTGC	Acinetobacter genomic DNA; Chimeric: downstream of <i>aac4</i> gene and 3' of the <i>recA</i> gene
	LH117_recA_AB 5075	GTTGGTACAATGCTCGAGGTG	Acinetobacter genomic DNA; 2kb downstream of the <i>recA</i> gene
Primers for control of the transformants using colony PCR			
	comM-For	CCACAATGGAACAAGAAGATGTCT	M2 genomic DNA; 5' of the <i>comM</i> gene
	comM-Rev	TTAAGAGTGATTACCTCGATAAGA	M2 genomic DNA; 3' of the <i>comM</i> gene

	OXA23-For	GATCGGATTGGAGAACAGA	<i>bla</i> _{OXA-23} gene
	OXA23-Rev	ATTCTGACCGCATTCCAT	<i>bla</i> _{OXA-23} gene
	mlo-80	CGGATCTCGATGCTGGC	AbaR1 from AYE strain
	mlo-84	GCAACGATGTTACGCAGC	AbaR1 from AYE strain
	5'-J-Rev	ATGGAATGTAGTACTCTGACG	AbaR1 from AYE; AbaR junction
	3'-J-For	GATTCACATCATATTCAATTGCC	AbaR1 from AYE; AbaR junction

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