

Supplementary Materials

Supplementary Table S1. Primers used for the DNA cloning in this study.

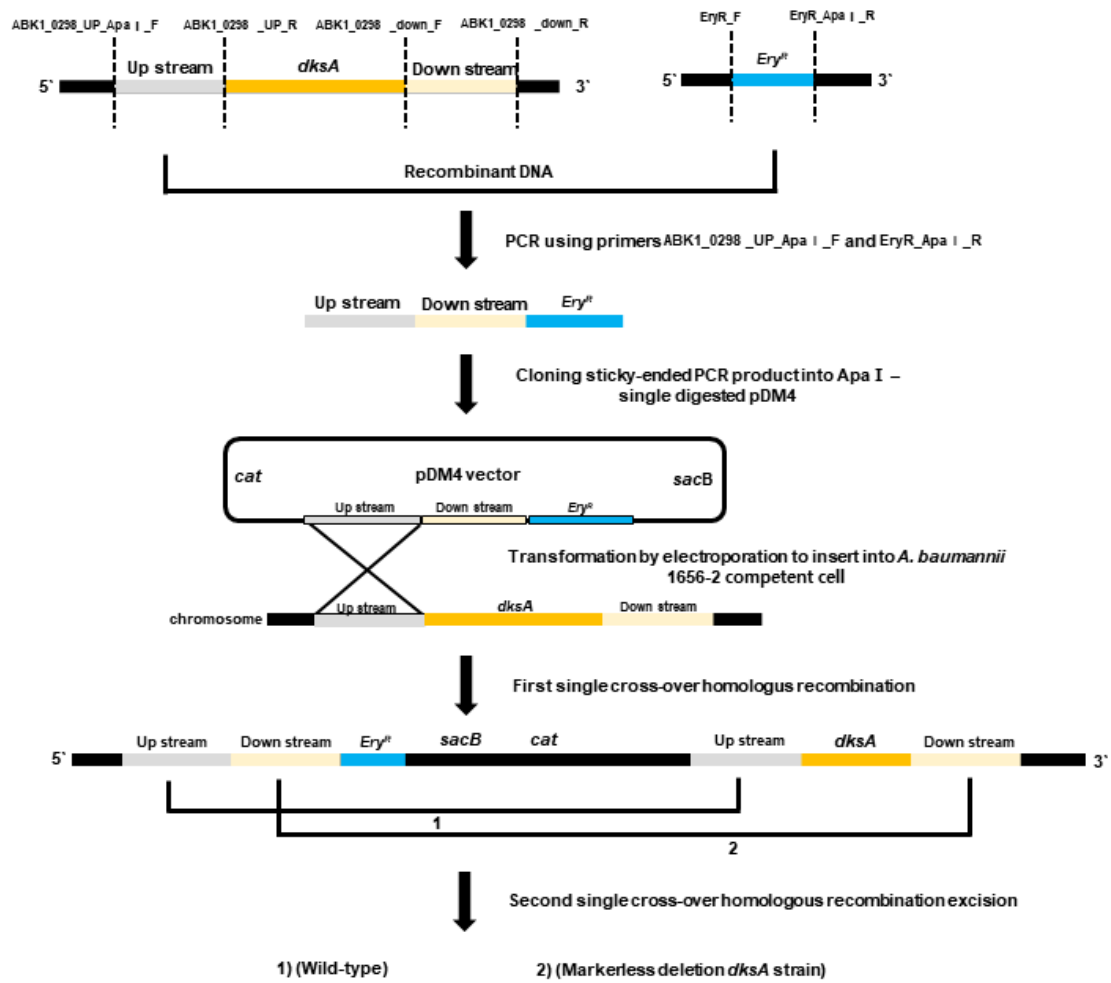
Primer	Sequence (5'→3')*
ABK1_0298_UP_ApaI_F	<u>GTTGGGCCCCCGAAGAGGTAGGACGGTGAC</u>
ABK1_0298_UP_R	<u>CTTAACCGTCACAATTACATAATAGGGCATTTCCTCATC</u> ATACACGTATTATC
ABK1_0298_down_16_F	<u>AATGCCCTATTATGTAATTGTGACGGTTAAGAATTCTC</u> CAG
ABK1_0298_down_16_R	<u>CAAGTCAGCACGAACACGAATCAA</u> ACTTCTAAACCATG AAGCGTTAT
EryR_F	TCGTGTTTCGTGCTGACTTG
EryR_ApaI_R	<u>GTTGGGCCCCGACCTCTTTAGCTCCTTGGAAGC</u>

* Underlined sequences indicate regions that are not complementary to the templates.

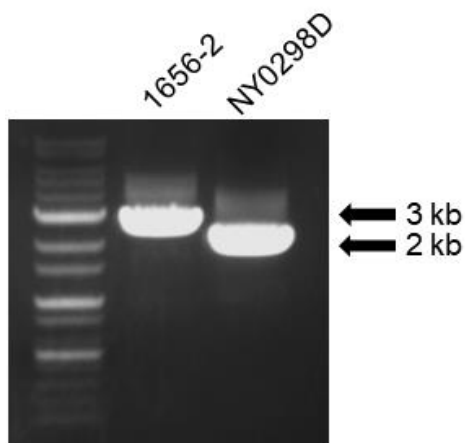
Supplementary Table S2. Primers used for qPCR in this study.

Primers	Sequence (5' to 3')	Target genes
16S rRNA-F	GCACAAGCGGTGGAGCAT	16S rRNA for ATCC 17978 and 1656-2
16S rRNA-R	CGAAGGCACCAATCCATCTC	
DksA-F	TCTTGGGTAGCACGGTCATTT	<i>dksA</i> for ATCC 17978 and 1656-2
DksA-R	GGAAGGACAGCTCGAGCATT	
AdeB-F	GCACAACCAGCATCACAGAAA	<i>adeB</i> for ATCC 17978
AdeB-R	AAAAGCAGTCTGAATCACAAATGG	
AdeB-F	CCTTGTGGCAACCCTTCATT	<i>adeB</i> for 1656-2
AdeB-R	CCTGCTTTACTGGCTGCTCAA	
AdeI-F	TGGTTATTCTACAATTCGCTCTCCTAT	<i>adeI</i> for ATCC 17978 and 1656-2
AdeI-R	CAAAGCACCCAGCCGTTACTG	
AdeJ-F	GCGGGCAGCCGTATGA	<i>adeJ</i> for ATCC 17978 and 1656-2
AdeJ-R	ACGCCGAGAATGGAACCA	
TetA-F	GGCAAAAATCATCCAACCACTT	<i>tetA</i> for ATCC 17978
TetA-R	CGTGCTAATCGGTATTGCTTGTT	
AbeM-F	GCCCAGTTCTTTTCGCCATA	<i>abeM</i> for ATCC 17978
AbeM-R	CCACTTTCTCTTGCCATTGCT	
AbeM-F	GAAGCCCAGTTCTTTTCACCATA	<i>abeM</i> for 1656-2
AbeM-R	CCACTTTCTCTTGCCATTGCT	

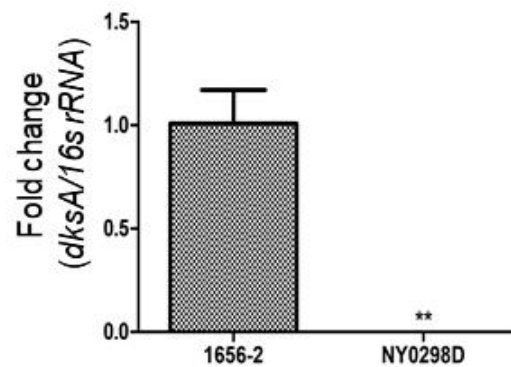
(A)



(B)



(C)



Supplementary Figure S1. Construction of the $\Delta dksA$ mutant strain. **(A)** Construction of $\Delta dksA$ mutant (NY0298D) in *A. baumannii* 1656-2. **(B)** The deletion of *dksA* in the NY0298D strain was confirmed by PCR using the primers ABK1_0298_UP_ApaI_F and ABK1_0298_down_16_R (Supplementary Table S1). The WT WT 1656-2 and NY0298D strains had amplicon sizes of 2,601 bp and 2,070 bp, respectively. **(C)** The expression of *dksA* was determined in the WT and $\Delta dksA$ mutant strains using qPCR. The data are presented as mean \pm SD of three independent experiments. ** $p < 0.005$ compared to WT strain.