

Supplementary data

Targeting virulence regulation to disarm *Acinetobacter baumannii* pathogenesis

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Supplementary Figures

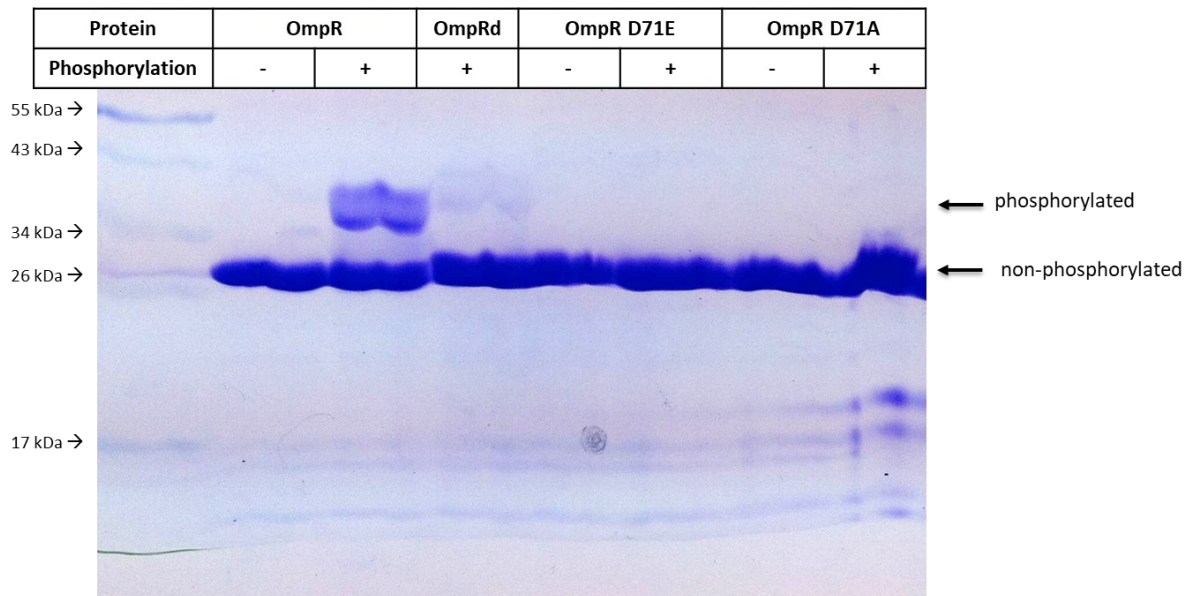


Figure S1: Phosphorylation of OmpR variants.

The OmpR variants from *A. baumannii* were phosphorylated *in vitro* and the phosphorylation was analyzed using Phos-tag SDS gel. Protein retention is significant of protein phosphorylation. Denatured OmpR (OmpRd, 5 min at 95°C) was used as control.

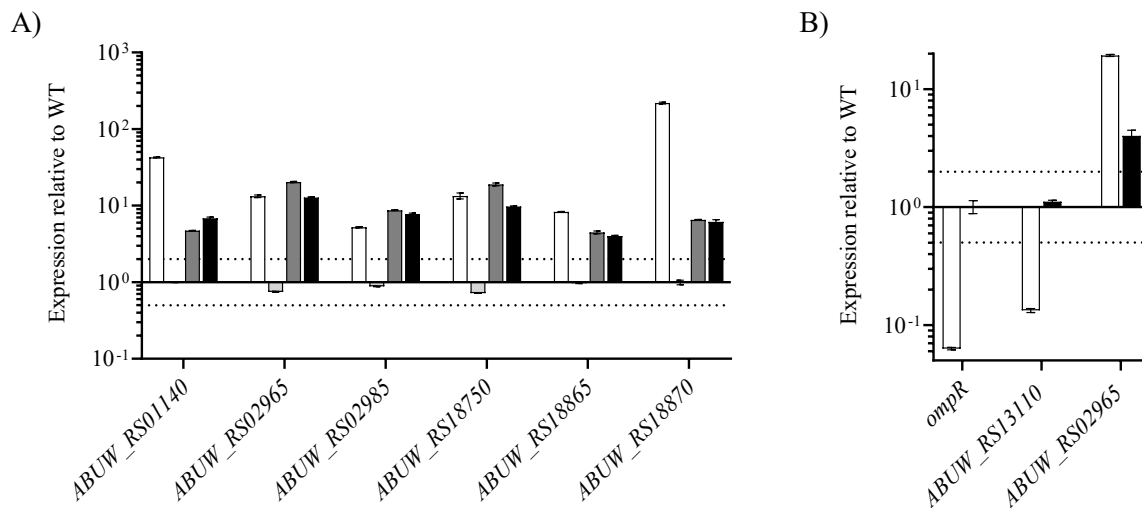


Figure S2: Confirmation of OmpR regulated genes using qRT-PCR on the chromosomal mutants and the complemented strain.

A) The transcript levels of OmpR upregulated genes encoding small hypothetical protein were determined in *A. baumannii* AB5075 wildtype, AB5075 $\Delta ompR$ (white), AB5075 OmpR D71E (light grey), AB5075 OmpR D71A (dark grey) and AB5075 OmpR R198L (black) mutants by quantitative real-time PCR and the expression level was normalized to the expression of the AB5075 wildtype strain (means \pm SEM of 2 technical replicates). B) The transcript levels of *ompR*, ABUW_RS13110 and ABUW_RS02965 were determined in *A. baumannii* AB5075 wildtype, AB5075 $\Delta ompR$ (white) and AB5075 OmpR complemented (black) strains by quantitative real-time PCR and the expression level was normalized to the expression of the AB5075 wildtype strain (means \pm SEM of 2 technical replicates). Horizontal dotted lines depict a 2-fold up- or downregulation.

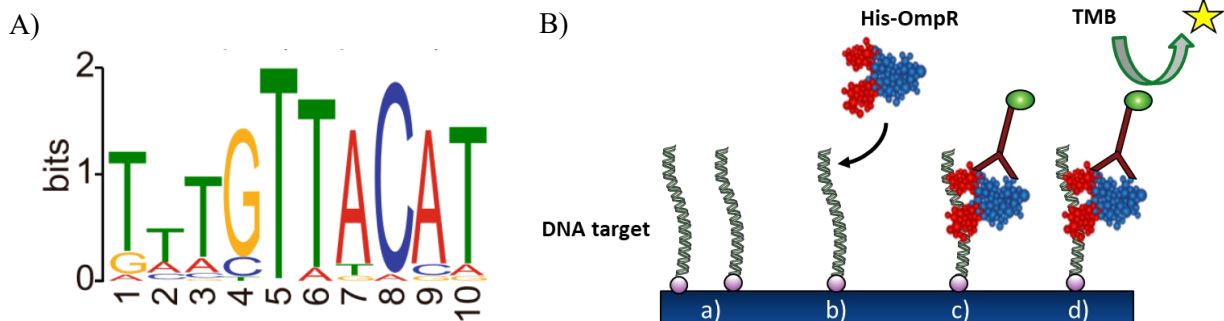


Figure S3: OmpR DNA binding motif and method to study OmpR-DNA binding *in vitro*.

(A) *E. coli* OmpR DNA binding Weblogo determined by Seo et al [18] (B) DNA binding enzyme-linked immunosorbent (D-ELISA) sandwich method to quantify OmpR-DNA binding: a) coating of D-ELISA plate with streptavidin followed by immobilization of biotinylated oligonucleotides, b) OmpR His-tag protein binding to immobilized oligonucleotides, c) anti-His-HRP antibody binding to bound OmpR and d) HRP-based enzymatic quantification of bound OmpR.

ABUW_RS02965 AGCAATTGACCTAGCTTGAAAAATGCTAA**TGGTAGCACAG**GATACAGATTCTTCATATTTTCTTTATAGTCATTACAAACAATATCAATCAAAGCCATTTTATTCATGGTTTCTCCTTGACTCTCTTAATCTAGCTTCAGATCAAGATAAAAAGGAATACTCCATG
ABUW_RS02965_A TTGAAAAATGCTAA**TGGTAGCACAG**GATACAGATTCTTCATATTTT
ABUW_RS02965_B TTTTCTTTATAGTCATTACAAACAATATCAATCAAAGCCATTTT
ABUW_RS02965_C TTTTATTCATGGTTTCTCCTTGACTCTCTTAATCTAGCTTCAGATCAAGAT

ABUW_RS07785 TAGGTCGATTTAGTACAAAAAAGGAGCTGATTATTAGCTCCTTTTATTCTAATGAGAA**TGGTACATA**ATTTAATTGTTAAAAATAAAATTAATCATGTTTATTCTAATAAAATGAAAAATAAATAACGCTAGATATTAAGAAGATTTGTTTTAAAA
 TATTTGTATGAACCTAAAAATAATTAAGAACAATGGGTATTTTATATGGAATTTAAAAATG

ABUW_RS02985 AAGCACTCTCATTTTTACTCTATATTTTGC**ATTGTAACCA**ACAACGAAAAGAAAACTCTCCATTGTTTCTTCATCTTTATTATCTAATCTTTAAGTCATCTTAAACAAACATTAAGGGTTTTAACCAATG

ABUW_RS13110 ATAAATTAAGTCTATTTTAACTTAAATTTGGTTTTTTTAAAAATTTATGTGACGATTTTGCAAATTTAAAAATGAATAATTTAT**AGTGAAGCTT**GAGTTCATTTTTATTAATGATTTGATTTTAAAAATAAAAAATTTGTAATATTTCTTGTACAACGATTTT
 GTCGACAATACAGGATTGTTTTGACATATTTGCCTAGCGTAATCAATAGAGTTTTTTGCCTAATG

Figure S4: Sequence of the intergenic region upstream of the OmpR-regulated genes.

The intergenic region upstream of *ABUW_RS02965* has been divided in three to design the oligo *ABUW_RS02965_A*, *ABUW_RS02965_B* and *ABUW_RS02965_C* for D-ELISA assay with OmpR_{ABA} (Figure 4E). The start codon is underlined and the OmpR DNA binding sequence motifs identified with the MEME suite are highlighted in red (Figure 4D). The motifs for *ABUW_RS02985* and *ABUW_RS13110* were identified on the minus strand.

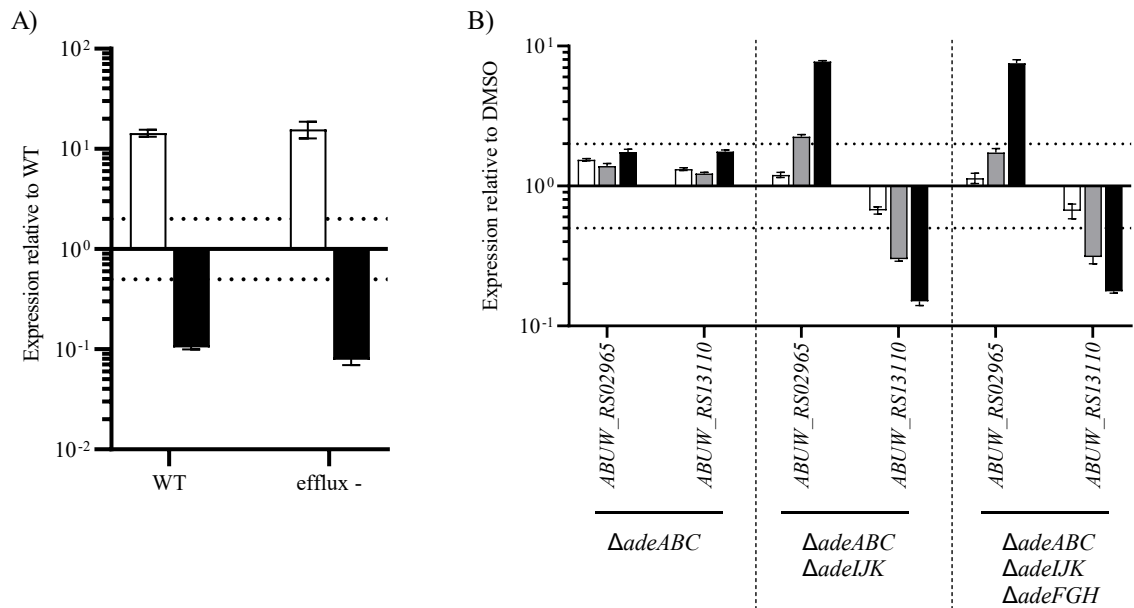


Figure S5: OmpR-regulated genes in the AYE efflux depleted mutant using qRT-PCR.

A) The transcript levels of *ABUW_RS02965* (white) and *ABUW_RS13110* (black) were determined in the $\Delta ompR$ mutants of the *A. baumannii* AYE wildtype and efflux depleted ($\Delta adeABC \Delta adeFGH \Delta adeIJK$) mutant and normalized to the transcript levels of their respective wildtype strains (mean \pm SEM of 2 technical replicates). B) The transcript levels of *ABUW_RS02965* and *ABUW_RS13110* were determined in the single ($\Delta adeABC$), double ($\Delta adeABC \Delta adeIJK$) and triple ($\Delta adeABC \Delta adeFGH \Delta adeIJK$) efflux deletion mutant of *A. baumannii* AYE in the presence of VSIS_039 at 20 μ M (white), 40 μ M (grey) and 80 μ M (black). The transcripts levels were normalized to those of the DMSO control (mean \pm SEM of 2 technical replicates). Horizontal dotted lines depict a 2-fold up- or downregulation.

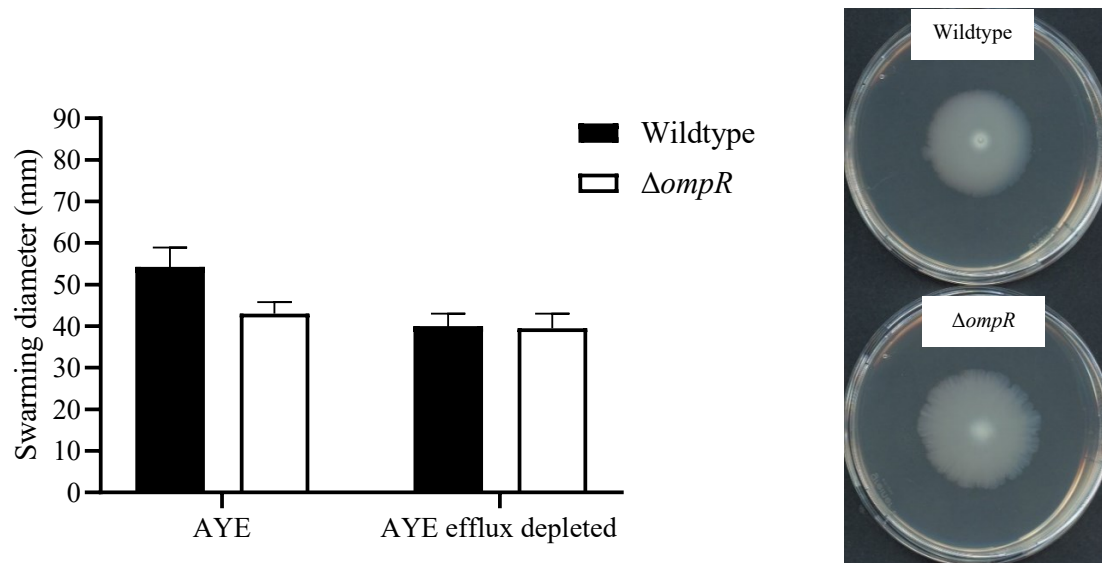


Figure S6: Swarming motility of *A. baumannii* AYE wildtype and *ompR* deleted ($\Delta ompR$) strains. Swarming motility was evaluated for the wildtype / $\Delta ompR$ pair of strains of AYE and AYE efflux depleted strain ($\Delta adeABC\Delta adeIJK\Delta adeFGH$). The graph reports the swarming diameter while the picture illustrates the swarming of the *A. baumannii* efflux depleted AYE wildtype (up) and $\Delta ompR$ (down) strains (mean \pm SEM of at least 2 replicates).

Supplementary Tables

Table S1: List of the 65 downregulated genes in $\Delta ompR$ ($<-2 \log_2$ fold change, $\Delta ompR/WT$) and 71 upregulated genes in $\Delta ompR$ ($>2 \log_2$ fold change, $\Delta ompR/WT$).

ID	\log_2 FoldChange ($\Delta ompR/WT$)	Product
ABUW_RS08030	-5.152963056	TetR family transcriptional regulator
ABUW_RS11870	-4.368892816	hypothetical protein
ABUW_RS12725	-4.305329643	hypothetical protein
ABUW_RS07965	-4.24527092	pilus assembly protein
ABUW_RS07960	-3.949138706	hypothetical protein
ABUW_RS18635	-3.79767744	UDP-N-acetyl-D-mannosamine dehydrogenase
ABUW_RS07145	-3.705203924	hypothetical protein
ABUW_RS07970	-3.698264692	fimbrial protein
ABUW_RS01495	-3.552227695	prepilin-type cleavage/methylation domain-containing protein
ABUW_RS13690	-3.354991113	TetR family transcriptional regulator
ABUW_RS03355	-3.354416154	hybrid sensor histidine kinase/response regulator
ABUW_RS11875	-3.227852494	hypothetical protein
ABUW_RS01430	-3.199573033	membrane protein
ABUW_RS09450	-3.191789235	ribose-phosphate pyrophosphokinase
ABUW_RS13040	-3.179126428	hypothetical protein
ABUW_RS10420	-3.144814662	hypothetical protein
ABUW_RS15455	-3.03176635	hypothetical protein
ABUW_RS13110	-3.01221703	transporter MatE
ABUW_RS09455	-2.98832666	nicotinate phosphoribosyltransferase
ABUW_RS07975	-2.905653226	hypothetical protein
ABUW_RS07785	-2.888583284	hypothetical protein
ABUW_RS13815	-2.887412345	hypothetical protein
ABUW_RS18630	-2.835136126	polysaccharide biosynthesis protein
ABUW_RS07255	-2.828869248	protein CsuA
ABUW_RS03350	-2.808936997	chemotaxis protein
ABUW_RS01440	-2.792972915	hypothetical protein
ABUW_RS06270	-2.743514067	hypothetical protein
ABUW_RS11790	-2.725242202	amino acid ABC transporter permease
ABUW_RS01290	-2.703419778	hypothetical protein
ABUW_RS03345	-2.667668241	twitching motility protein PilT
ABUW_RS07800	-2.661221571	membrane protein
ABUW_RS01435	-2.650341865	hypothetical protein
ABUW_RS14740	-2.573108743	hemerythrin
ABUW_RS03335	-2.45451199	response regulator
ABUW_RS17270	-2.451241573	type IV-A pilus assembly ATPase PilB
ABUW_RS17275	-2.448651293	type II secretion system protein F
ABUW_RS00895	-2.447969798	hypothetical protein
ABUW_RS06590	-2.431786046	type II secretion system protein E
ABUW_RS09960	-2.390032425	hypothetical protein
ABUW_RS07250	-2.386735092	protein CsuA/B

ABUW_RS08615	-2.384859643	hypothetical protein
ABUW_RS03360	-2.348787548	hypothetical protein
ABUW_RS00795	-2.347192551	MBL fold metallo-hydrolase
ABUW_RS16790	-2.287666781	hypothetical protein
ABUW_RS01465	-2.282931643	glutamate synthase large subunit
ABUW_RS02875	-2.272260195	two-component sensor histidine kinase
ABUW_RS01550	-2.26632454	pilus assembly protein PilW
ABUW_RS14710	-2.262323809	twitching motility protein PilT
ABUW_RS01425	-2.231965395	pilus assembly protein PilM
ABUW_RS03365	-2.21954724	coproporphyrinogen III oxidase
ABUW_RS14715	-2.211650472	twitching motility protein PilT
ABUW_RS05525	-2.208639151	hypothetical protein
ABUW_RS11235	-2.195499967	ferrous iron transporter B
ABUW_RS13105	-2.191786023	hypothetical protein
ABUW_RS09530	-2.181595516	TetR family transcriptional regulator
ABUW_RS01555	-2.167614921	hypothetical protein
ABUW_RS18625	-2.16215534	hypothetical protein
ABUW_RS18640	-2.161371559	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
ABUW_RS17370	-2.157315431	peptidoglycan hydrolase
ABUW_RS13035	-2.115209735	hypothetical protein
ABUW_RS11850	-2.095210977	NAD(P)-dependent oxidoreductase
ABUW_RS01445	-2.069233992	membrane protein
ABUW_RS07980	-2.041806136	glutathione S-transferase
ABUW_RS11425	-2.008071889	tautomerase
ABUW_RS01275	-2.00763149	fatty acyl-CoA reductase
ABUW_RS15165	2.002104113	trehalose-6-phosphate synthase
ABUW_RS04980	2.005017416	hypothetical protein
ABUW_RS11915	2.006015486	SAM-dependent methyltransferase
ABUW_RS07905	2.02022884	ethanolamine permease
ABUW_RS08920	2.044784618	3-oxoadipyl-CoA thiolase
ABUW_RS11925	2.052534622	TetR family transcriptional regulator
ABUW_RS14335	2.07063006	(2Fe-2S)-binding protein
ABUW_RS12645	2.07683365	acetyl/propionyl-CoA carboxylase subunit alpha
ABUW_RS09050	2.110067963	hypothetical protein
ABUW_RS07625	2.111922975	luciferase family oxidoreductase
ABUW_RS03655	2.114704215	hypothetical protein
ABUW_RS03690	2.115251333	DNA replication protein DnaD
ABUW_RS11950	2.143126695	hydroxymethylglutaryl-CoA lyase
ABUW_RS09360	2.149858781	hydrolase
ABUW_RS03205	2.152831275	RNA-splicing ligase RtcB
ABUW_RS05450	2.154458373	aromatic amino acid transporter AroP
ABUW_RS13610	2.180757921	gamma-aminobutyraldehyde dehydrogenase
ABUW_RS09260	2.197897889	sorbosone dehydrogenase
ABUW_RS09060	2.204598518	(2Fe-2S)-binding protein
ABUW_RS08205	2.215393814	lactonase
ABUW_RS11920	2.231187048	fatty acid--CoA ligase
ABUW_RS02945	2.251007273	hypothetical protein

ABUW_RS11940	2.253834891	enoyl-CoA hydratase
ABUW_RS15140	2.27409912	malonyl-[acyl-carrier protein] O-methyltransferase BioC
ABUW_RS09065	2.275172651	aromatic-ring-hydroxylating dioxygenase subunit beta
ABUW_RS11945	2.275395335	3-methylcrotonyl-CoA carboxylase subunit alpha
ABUW_RS08915	2.310124094	3-oxoadipate CoA-transferase subunit B
ABUW_RS12665	2.319789099	hypothetical protein
ABUW_RS12650	2.406656548	allophanate hydrolase
ABUW_RS11935	2.416654319	methylcrotonoyl-CoA carboxylase
ABUW_RS15145	2.425254961	8-amino-7-oxononanoate synthase
ABUW_RS17915	2.42534756	ATPase
ABUW_RS12660	2.454310317	hypothetical protein
ABUW_RS14330	2.470163045	hypothetical protein
ABUW_RS03685	2.504196589	hypothetical protein
ABUW_RS15150	2.525208161	adenosylmethionine--8-amino-7-oxononanoate aminotransferase BioA
ABUW_RS11930	2.528314598	isovaleryl-CoA dehydrogenase
ABUW_RS19690	2.549252604	hypothetical protein
ABUW_RS00325	2.5730652	4-hydroxyphenylpyruvate dioxygenase
ABUW_RS08910	2.575615162	3-oxoadipate CoA-transferase subunit A
ABUW_RS04555	2.616247733	ABC transporter substrate-binding protein
ABUW_RS08055	2.625805749	hypothetical protein
ABUW_RS01745	2.628652304	hypothetical protein
ABUW_RS07295	2.675155384	proline/betaine transporter
ABUW_RS05445	2.689329246	pyruvate decarboxylase
ABUW_RS12655	2.695847506	DUF1445 domain-containing protein
ABUW_RS11470	2.707164847	glutamate symport protein
ABUW_RS18865	2.739894706	hypothetical protein
ABUW_RS09045	2.743885166	acyl-CoA dehydrogenase
ABUW_RS07640	2.825507594	hypothetical protein
ABUW_RS13855	2.889418797	amino-acid transporter Mb2008
ABUW_RS09040	2.903434927	Glu-tRNA amidotransferase
ABUW_RS07910	2.972202959	aldehyde dehydrogenase
ABUW_RS10360	3.120148412	lipoyl synthase
ABUW_RS10340	3.331455667	dihydrolipoyl dehydrogenase
ABUW_RS00825	3.394383298	outer membrane protein
ABUW_RS15475	3.503486865	hypothetical protein
ABUW_RS02985	3.673087414	hypothetical protein
ABUW_RS01270	3.746149042	sulfate permease
ABUW_RS06025	3.783910616	membrane protein
ABUW_RS07925	4.027868667	alcohol dehydrogenase
ABUW_RS07950	4.186229554	hypothetical protein
ABUW_RS18750	4.279546979	hypothetical protein
ABUW_RS10345	4.313013618	diaminohydroxyphosphoribosylaminopyrimidine deaminase
ABUW_RS07630	4.328430911	hypothetical protein
ABUW_RS01140	4.375161033	hypothetical protein
ABUW_RS10355	4.750588843	ABC transporter substrate-binding protein
ABUW_RS10350	4.809402495	pyruvate dehydrogenase subunit beta

ABUW_RS02965	5.333078805	hypothetical protein
ABUW_RS14395	5.540563984	hypothetical protein
ABUW_RS18870	6.084762391	hypothetical protein

Table S2: List of the 19 OmpR-activated candidate genes and 12 OmpR-repressed candidate genes potentially relevant for *A. baumannii* pathogenesis.

ID	log2FoldChange ($\Delta ompR/WT$)	Read Ratio (<i>G. mellonella</i> /LB) ¹	Product
ABUW_RS08030	-5.152963056	0.043739863	TetR family transcriptional regulator
ABUW_RS11870	-4.368892816	0.058780238	hypothetical protein
ABUW_RS07965	-4.24527092	0.052994378	pilus assembly protein
ABUW_RS18635	-3.79767744	0.053481349	UDP-N-acetyl-D-mannosamine dehydrogenase
ABUW_RS07145	-3.705203924	0.054538365	hypothetical protein
ABUW_RS07970	-3.698264692	0.139174375	fimbrial protein
ABUW_RS11875	-3.227852494	0.195565828	hypothetical protein
ABUW_RS13040	-3.179126428	0.184394736	hypothetical protein
ABUW_RS13110	-3.01221703	0.141217409	transporter MatE
ABUW_RS07975	-2.905653226	0.120654172	hypothetical protein
ABUW_RS07785	-2.888583284	0	hypothetical protein
ABUW_RS09960	-2.390032425	0.132031752	hypothetical protein
ABUW_RS03365	-2.21954724	0.190465744	coproporphyrinogen III oxidase
ABUW_RS11235	-2.195499967	0.158606732	ferrous iron transporter B
ABUW_RS09530	-2.181595516	0.14107257	TetR family transcriptional regulator
ABUW_RS18625	-2.16215534	0.08692852	hypothetical protein
ABUW_RS13035	-2.115209735	0.004379322	hypothetical protein
ABUW_RS11850	-2.095210977	0.121539888	NAD(P)-dependent oxidoreductase
ABUW_RS11425	-2.008071889	0.008644153	tautomerase
ABUW_RS04980	2.005017416	1.085639579	hypothetical protein
ABUW_RS11925	2.052534622	0.934376763	TetR family transcriptional regulator
ABUW_RS15140	2.27409912	0.968768335	malonyl-[acyl-carrier protein] O-methyltransferase BioC
ABUW_RS15150	2.525208161	1.53242563	adenosylmethionine--8-amino-7-oxononanoate aminotransferase BioA
ABUW_RS00325	2.5730652	1.125844462	4-hydroxyphenylpyruvate dioxygenase
ABUW_RS01745	2.628652304	1.162884654	hypothetical protein
ABUW_RS18865	2.739894706	2.040619566	hypothetical protein
ABUW_RS02985	3.673087414	1.582951167	hypothetical protein
ABUW_RS18750	4.279546979	1.001278226	hypothetical protein
ABUW_RS01140	4.375161033	1.509661043	hypothetical protein
ABUW_RS02965	5.333078805	0.991747211	hypothetical protein
ABUW_RS18870	6.084762391	1.271610231	hypothetical protein

¹ Values derived from Gebhardt, M. J. et al. 2015 [1]

Table S3: Overview of the *A. baumannii* strains used in this study.

Strain	Description				Reference
	ST	Origin	Source	Year	
AB5075	1	USA	osteomyelitis	2008	[2]
AB5075 $\Delta ompR$	<i>ompR</i> deletion in the AB5075 strain				this study
AB5075 <i>OmpR</i> complemented	chromosomal insertion of <i>ompR</i> in the AB5075 $\Delta ompR$ strain				this study
AB5075 <i>OmpR</i> D71A	chromosomal mutagenesis to introduce <i>OmpR</i> D71A in AB5075				this study
AB5075 <i>OmpR</i> D71E	chromosomal mutagenesis to introduce <i>OmpR</i> D71E in AB5075				this study
AB5075 <i>OmpR</i> R198L	chromosomal mutagenesis to introduce <i>OmpR</i> R198L in AB5075				this study
AYE	1	France	urinary tract sample	2001	[3]
AYE $\Delta ompR$	<i>ompR</i> deletion in the AYE strain				this study
AYE $\Delta adeABC$	<i>adeABC</i> efflux pump deletion in the AYE strain				this study
AYE $\Delta adeABC\Delta adeIJK$	<i>adeIJK</i> efflux pump deletion in the AYE $\Delta adeABC$ strain				this study
AYE $\Delta adeABC\Delta adeIJK\Delta adeFGH$	<i>adeFGH</i> efflux pump deletion in the AYE $\Delta adeABC\Delta adeIJK$ strain				this study
HUMC1	2	USA	blood isolate	2009	[4]
HUMC1 $\Delta ompR$	<i>ompR</i> deletion in the HUMC1 strain				this study
LAC-4	10	USA	clinical outbreak	1997	[5]
LAC-4 $\Delta ompR$	<i>ompR</i> deletion in the LAC-4 strain				this study
ATCC-17978	77	France	fatal meningitis	1951	[6]
ATCC-17978 $\Delta ompR$	<i>ompR</i> deletion in the ATCC-17978 strain				this study
BV191	2	China	respiratory endotracheal aspirate	2013	[7]
BV191 $\Delta ompR$	<i>ompR</i> deletion in the BV191 strain				this study

Table S4: Primers used in this study.

Name	Sequence	Description
Genetic engineering		
<i>ompR</i> deletion		
oVT170	tgaggcctctcgaggaattcGCGGATGGCAGCTTCTAC	<i>ompR</i> -up F
oVT171	aacaacacgagctcGATGTACTCCCTTTTAAAGTCATAATTTATATATTATTG	<i>ompR</i> -up R
oVT172	gagtacatcgagctcGTGTTTGTTCGGATGGTG	<i>ompR</i> -down F
oVT173	aggatccccgggtaccATTCGTTGGCAGCATTTTG	<i>ompR</i> -down R
oVT179	ACCTTTTCACGGCGCTCATA	<i>ompR</i> deletion verification F
oVT180	TCCCCTAGCATGATTCGTC	<i>ompR</i> deletion verification R
<i>ompR</i> chromosomal complementation		
oVT425	caggggagaattgaggcctctcgagTATCGTCAAGCTCAGCGC	<i>ponA</i> -up F
oVT426	gtaccgagctcgaattcATCTCCAGAACGTCGTATGC	<i>ponA</i> -up R
oVT427	ggagatgcctgaattcagctcggtagccgggactagtgagctcctagagcctgcagCACCTCCAGCG ATGAAAC	<i>rrm</i> -down F
oVT428	ctatcaacagggagtccaagagtcgacctggTGTGGCGAGGGCTATTAC	<i>rrm</i> -down R
oVT630	catacgacgttctggagatgaattcTCGTGTTGATCCCACAAG	<i>ompR</i> complementation F
oVT631	tcacgtctggagtgctgcagGCAACGTAGTCGGTAAAGG	<i>ompR</i> complementation R
oVT430	TGCTCTGAGACAACGACG	complementation verification F
oVT431	GTGTGAACAGGGCCATAGCT	complementation verification R
<i>ompR</i> allelic exchange		
oVT634	agaattgaggcctctcgaggaattcTGGGCCTTTAAGCTAGCC	<i>ompR</i> -D71 F
oVT635	tctagaggatccccgggtaccTTGCGGTGGTATTGGCTC	<i>ompR</i> -D71 R
oVT636	CTTATCGTGCTCGAGTTTATGTTGCCCG	<i>ompR</i> -D71E mutagenesis F
oVT637	CGGGCAACATAAACTCGAGCAGCATAAG	<i>ompR</i> -D71E mutagenesis R
oVT638	CTTATCGTGCTAGCCTTTATGTTGCCCG	<i>ompR</i> -D71A mutagenesis F
oVT639	CGGGCAACATAAAAGGCTAGCAGCATAAG	<i>ompR</i> -D71A mutagenesis R
oVT642	agaattgaggcctctcgaggaattcTACTGAGGGCTTGTGGC	<i>ompR</i> -R198 F
oVT643	tctagaggatccccgggtaccCAACCCAGCCTACCAGTAG	<i>ompR</i> -R198 R
oVT644	CGTGAACCTTTAACTCTAGACAAGCTCATGAAC	<i>ompR</i> -R198L mutagenesis F
oVT645	GTTTCATGAGCTTGTCTAGAGTTAAAGGTTACG	<i>ompR</i> -R198L mutagenesis R
Efflux pump deletions		
oCK558	ggaatteGTCAGCGTCAGATTAAGCAAG	<i>adeABC</i> -up F
oCK559	cccgggCCAAACCTAGTGAGTTTTTGATG	<i>adeABC</i> -up R
oCK560	ACTCACTAGGTTTGGcccgggGCTGATAGAGGTATTCCAAATC	<i>adeABC</i> -down F
oCK561	gctctagaGCGTGAAGATTACCATTGCAGC	<i>adeABC</i> -down R
oCK564	GGCCAGCTCATTACTATTCC	<i>adeABC</i> deletion verification F
oCK565	GGCATCGTCGACAATAATCC	<i>adeABC</i> deletion verification R
oCK584	aggcctgaattcGGCAAGTACACTTTCAACGG	<i>adeIJK</i> -up F
oCK585	cccgggGACATCATTGTTCCACCTCG	<i>adeIJK</i> -up R
oCK586	CGAGGTGGAACAATGATGTCCCCGGGTGGTACATCAACCATCTAGTG	<i>adeIJK</i> -down F
oCK587	cgggatccgggtaccGGCCTAACTGATCACTTGTG	<i>adeIJK</i> -down R
oCK590	CAACAGGTGCTAACGCACTC	<i>adeIJK</i> deletion verification F
oCK591	AAAGTGCCGGTGTGAACGTC	<i>adeIJK</i> deletion verification R
oCK627	agaattgaggcctctcgaggaattcAGCGGTTGCACACTGAAAG	<i>adeFGH</i> -up F
oCK628	ttgtcccgggGAGGTGCTCCTAGTTATTGG	<i>adeFGH</i> -up R
oCK629	ggagcacctcccgggACAAATTATTTGCATATACAGGG	<i>adeFGH</i> -down F
oCK630	ccgcaagcttctgcaggtcctGACATCGCGGACAAAAGTTGG	<i>adeFGH</i> -down R
oCK633	GAAGATGTACAGCGCTTAGG	<i>adeFGH</i> deletion verification F
oCK635	AGCTCCTTCATTGTGCTACG	<i>AdeFGH</i> deletion verification R
qRT-PCR		
oVT572	TGCGATGGCCGATTCAAATC	<i>ABUW_RS02965</i> F
oVT573	TCATTGCGGTGGTCATAACG	<i>ABUW_RS02965</i> R
oVT683	ATGGGTAGTTTGGCTGCTTG	<i>ABUW_RS02985</i> F
oVT684	CACGGTGTTCATACGATGGTG	<i>ABUW_RS02985</i> R
oVT661	TTATCAGCAGAAGACGGGAATAC	<i>ABUW_RS07785</i> F
oVT662	CCCAACGCTCAGCATTAACTC	<i>ABUW_RS07785</i> R
oVT582	TGATTCCGGCAGAGGTAATAGG	<i>ABUW_RS13110</i> F
oVT583	ATAAAGCCCGCACTCATCAG	<i>ABUW_RS13110</i> R
oVT687	TATGGCTGCTTTGGCTGAAC	<i>ABUW_RS01140</i> F
oVT688	TCCGCTATTGACCAAATCGC	<i>ABUW_RS01140</i> R
oVT697	ATCGCAACAACAGCAATGGC	<i>ABUW_RS18750</i> F
oVT698	TGGATGCTGGTATTGATGCG	<i>ABUW_RS18750</i> R

oVT681	TAGTGAGTGGGAACGCAAAC	<i>ABUW_RS18865</i> F
oVT682	TCACGACGATCCTTTTGCTG	<i>ABUW_RS18865</i> R
oVT689	ACAGCTGTTGGTTGTGCATC	<i>ABUW_RS18870</i> F
oVT690	ACACCAACACCAGCTTGTAC	<i>ABUW_RS18870</i> R
oBV79	GAGTCTAATGGCGGTGGT	<i>rpoD</i> F
oBV80	ATTGCTTCATCTGCTGGT	<i>rpoD</i> R
D-ELISA		
oCK430	CCCCTTTACTTTTGGTTACATATTC	F1aF1b F 5' biotinylated
oVT279	GGGGAATATGTAACCAAAAGTAAAGGGG	F1aF1b R
oVL147	TTGAAAAATGCTAATGGTAGCACAGATACAGATTCTTCATATTTT	<i>ABUW_RS02965 A</i> F 5' biotinylated
oVL148	AAAAATATGAAGAATCTGTATCTGTGCTACCATTAGCATTTTTCAA	<i>ABUW_RS02965 A</i> R
oVL149	TTTTCTTTATAGTCATTACAAACAATATCAATCAAAGCCATTTT	<i>ABUW_RS02965 B</i> F 5' biotinylated
oVL150	AAAATGGCTTTGATTGATATTGTTTGTAATGACTATAAAGAAAA	<i>ABUW_RS02965 B</i> R
oVL151	TTTTATTCATGGTTTCTCCTTGACTCTCTTAATCTAGCTTCAGATCA AGAT	<i>ABUW_RS02965 C</i> F 5' biotinylated
oVL152	ATCTTGATCTGAAGCTAGATTAAGAGAGAGTCAAGGAGAAACCATGA ATAAAA	<i>ABUW_RS02965 C</i> R
-	ATTTGTATTTAATATTTTAAACATAAA	SarA binding site F 5' biotinylated
-	TTTATGTTAAAATATTAATACAAAT	SarA binding site R

Table S5. Crystallographic data-collection and refinement statistics

PDB entry	6ZWT
Beamline	SLS (PXIII)
wavelength (Å)	1.00003
no. of images	720
exposure time (s)	0.1
oscillation range (deg)	0.5
transmission (%)	100
Detector	PILATUS 2M
space group	<i>P1</i>
<i>a</i> , <i>b</i> , <i>c</i> (Å)	48.5, 49.7, 52.7
α , β , γ (deg)	90.1, 99.0, 103.9
resolution (Å)	48.2–2.2 (2.3–2.2)
R_{merge} (%)	15.4 (85.3)
$I/\sigma(I)$	6.1 (1.5)
completeness (%)	98.1 (97.3)
Redundancy	3.6 (3.7)
$CC_{1/2}$	98.8 (73.5)
resolution (Å)	48.2–2.2
no. of unique reflections	23437 (1999)
R_{work} , R_{free}	24.2, 27.3
no. of atoms	
Protein	3259
other ligands	34
Water	37
<i>B</i> factor (Å²)	
Protein	35.2
other ligands	47.5
Water	25.1
root-mean-square deviation	
bond lengths (Å)	0.009
bond angles (deg)	1.6
Ramachandran plot (%)	
residues in most favorable regions	94.6
residues in additional allowed regions	5.2

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