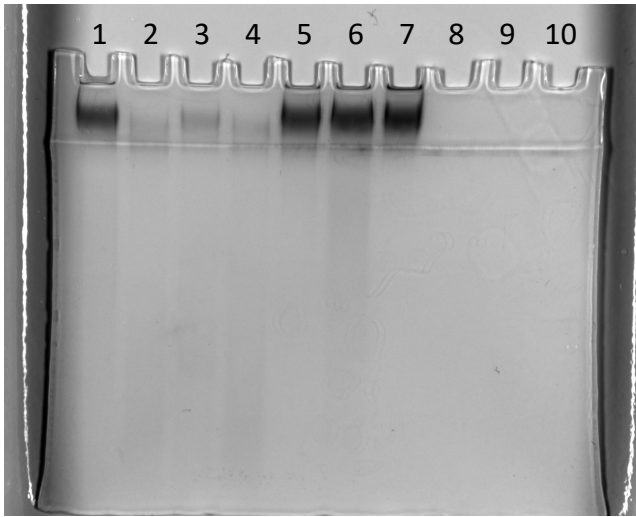


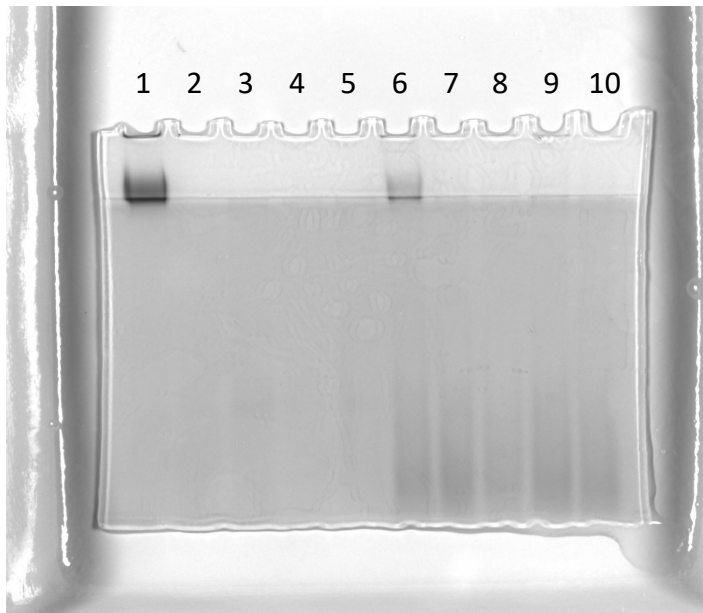
**Figure S1.** Maximum likelihood tree of *wzi* nucleotide sequences from 109 *A. baumannii* genome assemblies. Tree is based on 1000 replicate trees constructed using RAxML v 8.0.0 with the GTRGAMMA model and visualised in iTOL. Bootstrap values are not shown. Tree scale is below. Major phylogeny clades indicating *wzi* types are coloured differently. Assembly accession numbers are listed in Supplementary Table S1.

Type4	MFLRKTL <sup>S</sup> IALLATASSAVFAQGLVLNDDLR <sup>T</sup> DLNWL <sup>N</sup> QQGVINIST <sup>S</sup> TWPLSGDEIQ <sup>R</sup>	60
Type1	MFLRKTL <sup>S</sup> IALLATASSAVFAQGLVLNDDLR <sup>T</sup> DLNWL <sup>N</sup> QQGVISIST <sup>S</sup> TWPLSGDEIQ <sup>R</sup>	60
Type2	MFLRKTL <sup>S</sup> IALLATASSAVFAQGLVLNDDLR <sup>T</sup> DLNWL <sup>N</sup> QQGVINIST <sup>S</sup> TWPLSGDEIQ <sup>R</sup>	60
Type3	MFLRKTL <sup>S</sup> IALLATASSAVFAQGLVLNDDLR <sup>T</sup> DLNWL <sup>N</sup> QQGVINIST <sup>S</sup> TWPLSGDEIQ <sup>R</sup>	60
	<b>Loop 1</b>	
Type4	ALSQAKVTHPAQQKVINSVLNALKADND <sup>T</sup> VKVGAF <b>AETDIKNI</b> PQAFGDNQKSQYQGSLE	120
Type1	ALSQAKVTHPAQQKVINSVLNALKADND <sup>T</sup> VKVGAF <b>AETDIKNI</b> PQAFGDNQKAQYQGSLE	120
Type2	ALSQAKVTHPAQQKVINSVLNALKADND <sup>T</sup> VKVGAF <b>AESDIKNI</b> PQAFGDNQKSQYQGSLE	120
Type3	ALSQAKVTHPAQQKVINSVLNALKADND <sup>T</sup> VKVGAF <b>AETDIKNI</b> PQAFGDNQKSQYQGSLE	120
	<b>Loop 2</b>	<b>Loop 3</b>
Type4	FNAGGENWDAKIRVNAEK <b>DPQIDSGHDV</b> NEGSYVAGKLNQWL <b>VAGQIP</b> TWWGPGHDGS	180
Type1	FNAGGENWDAKIRVNAEK <b>DPQIDSGHDV</b> NEGSYVAGKLNQW <b>IVAGQIP</b> TWWGPGHDGS	180
Type2	FNAGGENWDAKIRVNAEK <b>DPQIDSGHDV</b> NEGSYVAGKLNQW <b>IVAGQIP</b> TWWGPGHDGS	180
Type3	FNAGGENWDAKIRVNAEK <b>DPQIDSGHDV</b> NEGSYVAGKLNQWL <b>VAGQIP</b> TWWGPGHDGS	180
	<b>Loop 4</b>	
Type4	<b>LIRGDASRPV</b> YGV <sup>T</sup> MQRAVQDAFENK <sup>W</sup> LSWIGPWQYQ <b>L</b> FAGQ <b>LDDYKAV</b> PHAKLLGMRVT	240
Type1	<b>LIRGDASRPV</b> YGV <sup>T</sup> AQRAVQNAFET <sup>K</sup> WLSWIGPWQYQAFAGQ <b>LDDYKAV</b> PDAKLI <sup>G</sup> LRVT	240
Type2	<b>LIRGDASRPV</b> YGV <sup>T</sup> AQRAVQNAFET <sup>K</sup> WLSWIGPWQYQAFAGQ <b>LDDYKAV</b> PDAKLI <sup>G</sup> LRLT	240
Type3	<b>LIRGDASRPV</b> YGV <sup>T</sup> AQRAVQNAFET <sup>K</sup> WLSWIGPWQYQAFAGQ <b>LDDYKAV</b> PHAKLL <sup>G</sup> LRLT	240
	<b>Loop 5</b>	
Type4	ARVP <b>PALEIGASRAIQIGDGPDSFKAYW</b> NAVIGK <b>DN</b> GC <b>TENS</b> CVGEDNAS <b>N</b> QLAGFDA	300
Type1	AQPLPYIELGASRAIQ <b>WGDGRPELS</b> SLWDAFVGNK----DNGGT <b>GE</b> PDPS <b>N</b> QIAGFDG	296
Type2	AQPLPYLELGASRTIQ <b>WGDGRSE</b> SF <b>SS</b> LWDAIK <b>GN</b> ----NVYGD <b>TEN</b> PS <b>N</b> QLAGFDG	295
Type3	ARPLPYLELGASRTLQ <b>WGEGRSE</b> SWD <b>SL</b> WNAIK <b>GN</b> ----NVYD <b>S</b> -DEDR <b>S</b> NQIAGFDA	295
	<b>Loop 5</b>	
Type4	RLQLQPLFNIPVSVYGYIG <b>DEAGGLPSK</b> KMYLAGADYSSMINMPYQIYA <b>E</b> WAD <b>TRTN</b>	360
Type1	RLLQPLFQVPVSLYGYV <b>GEDEAGGLPSK</b> KMYLAGVDYSSSYNNMPYQLYA <b>E</b> WAD <b>TRTN</b>	356
Type2	RLLQPLLNIPVSLYGYV <b>GEDEAGYLP</b> SKKMYLAGVDYSSSYNDMPYQLYA <b>E</b> WAD <b>TRTN</b>	355
Type3	RLNLQSLINAPVGIYGYV <b>GEDEAGLLP</b> SKKMYLAGVDYSSSYNNMPYQLYA <b>E</b> WAD <b>TRTN</b>	355
	<b>Loop 7</b>	
Type4	<b>GD</b> IRGISY <b>NH</b> HQYTDGY <b>YQHGYPLGHAMGGD</b> QMYSVGGDIRFDV <b>M</b> NRLS <b>G</b> RAMV <b>V</b> KV <b>NQ</b>	420
Type1	<b>GD</b> VRGISY <b>AH</b> STYKDGYY <b>QHGYPLGHAMGGD</b> QMYSVGGDIRFDV <b>M</b> NRLS <b>G</b> RAMV <b>V</b> KV <b>NQ</b>	416
Type2	<b>GD</b> VKISY <b>TH</b> SVYKDGYY <b>QHGFPLGHAMGGD</b> QMYSVGGDIRFDV <b>M</b> NRLS <b>G</b> RAMV <b>V</b> KV <b>NQ</b>	415
Type3	<b>ND</b> VKGISY <b>NH</b> YVYKDGYY <b>QHGFPLGHAMGGD</b> QMYSVGGDIRFDV <b>M</b> NRLS <b>G</b> RAMV <b>V</b> KV <b>NQ</b>	415
	<b>Loop 8</b>	<b>Loop 9</b>
Type4	<b>SNLAIN</b> KAFPKDYEIKALD <b>L</b> TWTHFIK <b>P</b> DLPLKINGW <b>VSDS</b> LE <b>G</b> NDAGASIGIEI <b>P</b> LER	480
Type1	<b>SNLAIN</b> KAFPKDDEIKALD <b>L</b> TWTHFIK <b>P</b> DLPLKINGW <b>VSDS</b> LE <b>G</b> NDAGASIGIEI <b>P</b> LER	476
Type2	<b>SNLAIN</b> KAFPKDDEIKALD <b>L</b> TWTHYIK <b>P</b> DLPLKINGW <b>VSDS</b> LE <b>G</b> NDAGASIGIEI <b>P</b> LER	475
Type3	<b>SNLAIN</b> KAFPKDDEIKALD <b>L</b> TWTHYIK <b>P</b> DLPLKINGW <b>VSDS</b> LE <b>G</b> NDAGASIGIEI <b>P</b> LER	475
Type4	KMFGF 485	
Type1	KMFGF 481	
Type2	KMFGF 480	
Type3	----- 480	

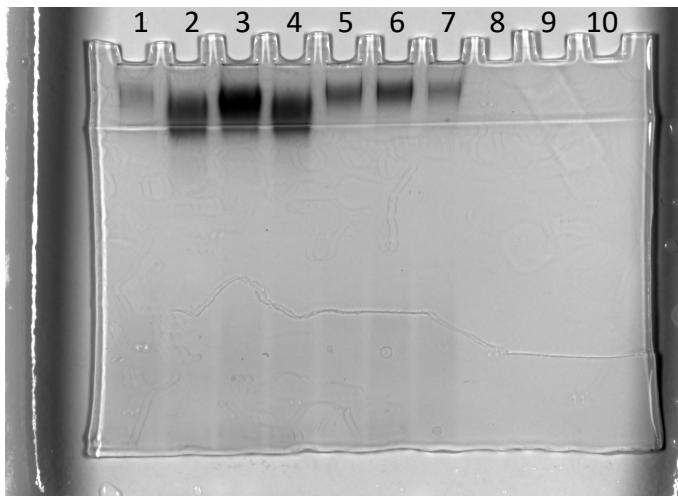
**Figure S2.** Multiple sequence alignment of the four main Wzi sequence types. Alignment constructed by CLUSTAL Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Representative types are: Type 1 = AB5075-UW (ABUW\_2898 in CP008706.1), type 2 = ATCC17978 (AUO97\_12210 in CP018664.1), type 3 = ACICU (DMO12\_03033 in CP031380.1), type 4 = LAC4 (BBX32\_12830 in CP018677.1). Bold face indicates loops identified by structural comparison to *E. coli* K30 Wzi in Fig. 7, with red indicating loops identified in *E. coli* that may interact with the CPS.



Gel 1	
Lane	Sample
1	AB5075 WT, attached CPS, 6 OD equiv.
2	<i>wzi</i> ::T26-1, attached CPS, 6 OD equiv.
3	<i>wzi</i> ::T26-2, attached CPS, 6 OD equiv.
4	<i>wzi</i> ::T26-3, attached CPS, 6 OD equiv.
5	<i>wzi</i> ::T26 -1 attTn7- <i>wzi</i> , attached CPS, 6 OD equiv.
6	<i>wzi</i> ::T26 -2 attTn7- <i>wzi</i> , attached CPS, 6 OD equiv.
7	<i>wzi</i> ::T26 -3 attTn7- <i>wzi</i> , attached CPS, 6 OD equiv.
8	Blank
9	Blank
10	Blank



Gel 2	
Lane	Sample
1	AB5075 WT, attached CPS, 6 OD equiv.
2	Other sample
3	<i>itrA1</i> ::T26, attached CPS, 6 OD equiv.
4	Other sample
5	Other sample
6	AB5075 WT, shed CPS, 6 OD equiv.
7	Other sample
8	<i>itrA1</i> ::T26, shed CPS, 6 OD equiv.
9	Other sample
10	Other sample



Gel 3	
Lane	Sample
1	AB5075 WT, shed CPS, 6 OD equiv.
2	<i>wzi</i> ::T26-1, shed CPS, 6 OD equiv.
3	<i>wzi</i> ::T26-2, shed CPS, 6 OD equiv.
4	<i>wzi</i> ::T26-3, shed CPS, 6 OD equiv.
5	<i>wzi</i> ::T26 -1 attTn7- <i>wzi</i> , shed CPS, 6 OD equiv.
6	<i>wzi</i> ::T26 -2 attTn7- <i>wzi</i> , shed CPS, 6 OD equiv.
7	<i>wzi</i> ::T26 -3 attTn7- <i>wzi</i> , shed CPS, 6 OD equiv.
8	Blank
9	Blank
10	Blank

**Figure S3.** Original uncropped SDS-PAGE gels shown in Fig. 2. Samples for each lane are indicated in the adjacent tables. Yellow highlighted lanes are sample shown in Fig. 2.