Table S1. The list of primers used in this work. All primer sequences are in 5’-3’ orientation.

Primers for cloning TA components		Target
F_AbTRel1	CATGAGTTACGAGCTAGAGTTCTC	RelE$_{Ab}$
R_AbTRel1	GATTTATGCAACAAGCTTAAGGATG	RelE$_{Ab}$, introduces HindIII site
F_AbARel1	CATGAGAAACGTCATGAACCACA	RelB$_{Ab}$
R_AbARel1	ATTGCTTCAAGCTTACGAATAAAC	RelB$_{Ab}$, introduces HindIII site
F_AbHicT	TCTTTCTGCAGCAATTGGATACAAC	HicA$_{Ab}$, introduces PstI site
NR_AbHicT	CGTGAAAAGTCTGGATTTAGTCAAA	HicA$_{Ab}$
F_AbHicB	GGGAAATAAAAAAGCTTCTCGATTG	HicB$_{Ab}$, introduces HindIII site
R_AbHicB	CGTGAGTGCAATGTTGTATCCAAT	HicB$_{Ab}$
F_AbGPtox	CGTTGTAAGCTTTCAGGTGAGCG	GP49$_{Ab}$, introduces HindIII site
R_AbGPtox	CATGGCTTGGGATGTAGAAACAA	GP49$_{Ab}$
F_AbGPant	TTAACACAAGCTTTTAGGTCTAT	Cro$_{Ab}$, introduces HindIII site
R_AbGPant	CATGGCTAAATTAAACGATATAA	Cro$_{Ab}$
F_AbTRtox	CATGTTTTTTATGGAACAGTATTTT	DUF497$_{Ab}$
R_AbTRtox	CTTTAGCAAGCAAGCTTTGAATT	DUF497$_{Ab}$, introduces HindIII site
F_AbTRant	CATGGTTAGATACTCACACAAAGA	COG3514$_{Ab}$
R_AbTRant	GCATAAAACAACCAAGCTTAATGTT	COG3514$_{Ab}$, introduces HindIII site
F_AbGNanti	CATGCGAAAAACAGAAGTTTATCAG	HTH$_{Ab}$
R_AbGNanti	ACAAAGAAAGCTTAACTAAAAAAGA	HTH$_{Ab}$, introduces HindIII site
F_AbGnaT	CATGATTGTAAGACGAGCGACCT	GNAT$_{Ab}$
R_AbGnaT	AGTTAAAAGCTTGATTGCAGCCG	GNAT$_{Ab}$, introduces HindIII site
F_AbZetacl	CATGGTAACAAATAATTTTGAAA	Zeta$_{Ab}$
R_AbZetacl	AATTACATCTGCAGCAAATAATA	Zeta$_{Ab}$, introduces PstI site
F_AbX	CATGGAAAATCTTTATTTTTTTAAC	X$_{Ab}$
F_pBAD	TGTAACAAAGCGGGACCAAAGC	pBAD30 plasmid, behind cloning site
R_pBAD	GGCGTTTCACTTCTGAGTTCGG	pBAD30 plasmid, after cloning site
F_pUH	CAAAAAGAGTGTTGACTTGTGAGCG	pUH25-2 plasmid, behind cloning site
R_pUH	GATCTATCAACAGGAGTCCAAGCTC	pUH25-2 plasmid, after cloning site
F_pUHXba	AACAATTTCATCTAGAATTCATTAA	pUH25-2 plasmid, behind cloning, introduces XbaI site
Primers for detection and screening of TA systems in clinical *A. baumannii* isolates		
Fbau_Rel	TGTATGAACGCATGATGGATC	Screening for RelB$_{Ab}$/RelE$_{Ab}$
Rbau_Rel	AGCTTATTCTTCGGTATCTTAGG	Screening for RelB$_{Ab}$/RelE$_{Ab}$
F_HicABins	GGTAAAGTAACATTGATTTTTTCTG	Screening for HicA$_{Ab}$/HicB$_{Ab}$
R_HicABins	CATTTTGAAGCAAGCGGGTCTAA	Screening for HicA$_{Ab}$/HicB$_{Ab}$
F_GPCroIns	AATATGAAAGAGCTACGTGTTCA	Screening for GP49$_{Ab}$/Cro$_{Ab}$
R_GPCroIns	CCCATTGCTTCAACATACTTTTT	Screening for GP49$_{Ab}$/Cro$_{Ab}$
F_AbTRtox	CATGTTTTTTATGGAACAGTATTTT	Screening for DUF497$_{Ab}$/COG3514$_{Ab}$
R_DufCogins	TTGATGATTTTTTAATTCTTTTAGC	Screening for DUF497$_{Ab}$/COG3514$_{Ab}$
F_AbGNanti	CATGCGAAAAACAGAAGTTTATCAG	Screening for HTH$_{Ab}$/GNAT$_{Ab}$
R_HTHGnatins	TTTAAGAAAACAATGAAATGTCTGG	Screening for HTH$_{Ab}$/GNAT$_{Ab}$
Fbau_Zeta	TCTAGTTTGAATTCGGAAGAAA	Screening for Zeta$_{Ab}$
Rbau_Zeta	TTATCTGTCTAGTTCTACGCCA	Screening for Zeta$_{Ab}$
Fbau_Rel2	GATGAAGCCCTTAAAGAAAAATC	Screening for RelB$_{Ab}$/RelE$_{Ab}$ 2
Rbau_Rel2	GTGATGAGCAAGATAACTACCT	Screening for RelB$_{Ab}$/RelE$_{Ab}$ 2

Fbau_Yoe	TCTGTTTTAGATAAAGTAATTGAT	Screening for Phd$_{Ab}$/YoeB$_{Ab}$
Rbau_Yoe	TCGACATTGAATTATAGAGATTC	Screening for Phd$_{Ab}$/YoeB$_{Ab}$
F_YbauN	TTTCAAAGCTTCGAGCGATAGTC	Screening for RelB$_{Ab}$/YafQ$_{Ab}$
Rbau_Yaf	ATGGCTAAACGTAAGATTATCGTAA	Screening for RelB$_{Ab}$/YafQ$_{Ab}$
Primers for probes of Northern analysis		
lppF2	TATATCGAAGCGCCCTGATGGGC	*lpp* transcript
lppR2	CACGAGCTGCGTCATCTTTA	*lpp* transcript
F_tmRNA	GGGGCTGATTCTGGATTCGACG	*ssrA* transcript
R_tmRNA	TGGTGGAGCTGGCGGGAGTT	*ssrA* transcript

Table S2. The GI codes of psi-BLAST and TBLASTN input for TA search* based on the homology.

TA	toxin GI	antitoxin GI	host
AfuT2$_{\text{DSM4304}}$/AfuA2$_{\text{DSM4304}}$	11499074	11499073	*Archaeoglobus fulgidus*
AtuT1$_{\text{C58}}$/AtuA1$_{\text{C58}}$	15888171	15888172	*Agrobacterium tumefaciens*
Axe-txe	32470464	32470465	*Enterococcus faecium*
BceT1$_{\text{E33L}}$/BceA1$_{\text{E33L}}$	52141794	52141791	*Bacillus cereus*
BceT5$_{\text{E33L}}$/BceA5$_{\text{E33L}}$	52140501	52140498	*Bacillus cereus*
Ccd$_{\text{F}}$	9507756	9507755	*Plasmid F*
ccd$_{\text{O157}}$	15799733	15799732	*Escherichia coli*
chpB	157157445	157156816	*Escherichia coli*
dinJ/yafQ	16128211	16128212	*Escherichia coli*
EcoT1$_{\text{EDL933}}$/EcoA1$_{\text{EDL933}}$	15802544	15802545	*Escherichia coli*
hicAB	87081911	145693129	*Escherichia coli*
hig	21233923	21233924	*Proteus vulgaris*
hip	16129466	16129467	*Escherichia coli*
MavT1$_{\text{K10}}$/MavA1$_{\text{K10}}$	41410367	41410366	*Mycobacterium avium*
MazEF /chpA	110642923	110642924	*Escherichia coli*
mvp	13449197	13449196	*Shigella flexneri*
NeuT1$_{\text{C91}}$/NeuA1$_{\text{C91}}$	114331792	114331793	*Nitrosomonas eutropha*
NspT1$_{\text{PC7120}}$/NspA1$_{\text{PC7120}}$	17228248	17228249	*Nostoc* sp. PCC 7120
NspT2$_{\text{PC7120}}$/NspA2$_{\text{PC7120}}$	17228000	17227999	*Nostoc* sp. PCC 7120
NspT5$_{\text{PC7120}}$/NspA5$_{\text{PC7120}}$	17231114	17231113	*Nostoc* sp. PCC 7120
paaR1-paaA1-parE1	15830321	15830322	*Escherichia coli*
parDE	15829716	15829715	*Escherichia coli*
ParDE3	16126988	16126989	*Caulobacter crescentus*
parDE$_{\text{RK2}}$	168998416	168998415	Birmingham IncP-alpha plasmid
pas	30027760	30027759	*Acidithiobacillus caldus*
Pem/parD	133756559	133756558	*Escherichia coli*
pezAT	81531989	81620431	*Streptococcus pneumoniae*
phd/doc	187736902	187736903	*Escherichia coli*
prlF/yhaV	16131022	16131021	*Escherichia coli*
RelBE2	16126752	16126753	*Caulobacter crescentus*
RelBE2Spn	15901085	15901086	*Streptococcus pneumoniae*
relBE$_{\text{307}}$	10955393	10955394	*Escherichia coli*
relBE$_{\text{K-12}}$	16129522	16129523	*Escherichia coli*
RPC4130/ RPC4129	90425605	90425604	*Rhodopseudomonas palustris*
SmeT1$_{\text{1021}}$/ SmeA1$_{\text{1021}}$	15964520	15964521	*Sinorhizobium meliloti*
SpeT3$_{\text{TIGR4}}$/SpeA3$_{\text{TIGR4}}$	15900772	15900771	*Streptococcus pneumoniae*

SpyT1$_{10270}$/SpyA1$_{10270}$	94990855	94990856	*Streptococcus pyogenes*
SpyT1$_{M1}$/SpyA1$_{M1}$	15675208	15675209	*Streptococcus pyogenes*
SpyT2$_{10270}$/SpyA2$_{10270}$	94990057	94990058	*Streptococcus* phage 10270.1
stbDE	190015809	190015808	*Salmonella enterica*
vapBC	45658497	45658496	*Leptospira interrogans*
vapXD	16272398	16272399	*Haemophilus influenzae*
yafNO	16128219	16128218	*Escherichia coli*
ydcDE	16077533	16077532	*Bacillus subtilis*
yefM/yoeB	94541116	90111372	*Escherichia coli*
ygiUT (mqsRA)	16130918	16130917	*Escherichia coli*
Zeta/Epsilon/Omega	63021992	63021991	*Streptococcus pyogenes*

*Our query included TA proteins suggested as “original” TA pairs in bioinformatic research by Leplae *et al*., 2011 (1), as well as gene pairs that were validated in this research. Other TA pairs that were suggested to form unique TA families were added from references at TADB (http://bioinfo-mml.sjtu.edu.cn/TADB/browse_fam.php) (2).

Table S3. The list of *A. baumannii* DNA sequences* subjected to bioinformatic search.

Chromosomes	Plasmids	Phages
		133; Ac42; Acj9; Acj61; AP205; AB1; phiAB1; ZZ1.
ATCC17978	pAB1; pAB2.	
1656-2	ABKp1; ABKp2.	
TCDC-AB0057	p1ABTCDC0715; p2ABTCDC0715.	
AB0057	pAB0057	
AB307-0294		
ACICU	pACICU1; pACICU2	
AYE	p1ABAYE; p2ABAYE; p3ABAYE; p4ABAYE.	
MDR-TJ	pABTJ1	
MDR-ZJ06	pMDR-ZJ06	
SDF	p1ABSDF; p2ABSDF; p3ABSDF.	
TYTH-1		
	pAB120; pABIR; pAbSK-OXA-82; pABVA01; pMAC; pMMA2; pMMCU3.	

**A. baumannii* chromosomes, plasmids and *Acinetobacter* phages, which were used in this work were downloaded from NCBI database. Our bioinformatic search included completed genomes suitable for search with RASTA tool.

Table S4. The list of GI codes of validated and estimated *A. baumannii* TA systems.

Toxin	**Antitoxin**	**Chromosome/plasmid**	**Toxin GI**	**Antitoxin GI**
RelE	**RelB**	ACICU	184158489	184158490
		MDR-ZJ06	384142221	384142220
		TCDC-AB0715	345447463: 1041311-1041577	385236512
		TCDC-AB0715	345447463: 2523828-2524094	385237910
		TYTH1	407931855	407931854
		pACICU1	184159998	184159997
HicA	**HicB**	1656-2	384131513	384131514
		1656-2	384132583	384132582
		ATCC17978	126642065	126642064
		MDR-ZJ06	384143590	384143589
		ACICU	184159046	184159045
		TCDC-AB0715	345447463: 2942160-2942342	385238300
		MDR-TJ	387123027	387123028
		pABIR	169949436: 24764-24943	170780400
GP49 (HigB)	**Cro (HigA)**	pAB1	126640106	126640105
		pAB120	398359516	398359515
		pMAC	61199614	61199615
		ABKp1	384133689	384133688
		p2ABTCDC0715	385239490	385239489
		p3ABAYE	169786925	169786926
		p3ABAYE	169786931	169786930
DUF497 (SplT)	**COG3514 (SplA)**	ABKp2	384133676: 1522-1818	384133680
		p1ABTCDC0715	385239408	385239409
		p2ABAYE	169302985	169302986
		pAB0057	213155362	213155363
		pAB120	398359521	398359520
		pAB2	126373843: 5471-5767	126373843: 5760-6068
		pABIR	170780380	170780381
		pABVA01	240887309	240887310
		pMMA2	260414705	260414704
		pMMCU3	410687673	410687672

HTH (CheT)	**GNAT (CheA)**	1656-2	384131381	384131380
		AB0057	213158500	213158502
		AB307-0294	215483046	215483045
		ACICU	184158635	184158636
		ATCC17978	126642163	126642164
		AYE	169795559	169795558
		MDR-TJ	387123449	387123448
		SDF	169633281	169633280
		TCDC-AB0715	385238053	385238054
		TYTH1	407933243	407933244
		MDR-ZJ06	347594209	384141246: 2530802-2531044; 2531001-2531207;
Zeta	**X**	ABKp1	384133754	384133753
		p2ABTCDC0715	385239451	385239450
		pAbSK-OXA-82	255076963	255076961: 1442-1681
		pABTJ1	387125817-387125816	387125818
		pACICU2	184160019-184160020	183211611: 1443-1682
RelE 2	**RelB2**	p3ABAYE	169786924	169786923
		pAB2	126373843: 2549-2842	126373843: 2314-2559
YoeB	**Phd**	p1ABAYE	169302977	169302976
YafQ	**RelB**	p2ABSDF	169786858	169786859
HicA 2	**HicB 2**	SDF	169634247	169634248
HipA	**HipB**	ATCC17978	193077387	193077386
		SDF	169632029: 1806022-1806927	169633561
HipA 2	**HipB 2**	p3ABAYE	169786889: 89791-90321; 90131-91042	169786969
DUF1044	**RelB**	pABIR	170780395	170780396
GP49	**HTH**	p3ABAYE	169786952	169786953
HTH 2	**GNAT 2**	1656-2	384131976	384131977
		AB0057	213157074	213157075
		AB307-0294	215483646	215483645
		ACICU	184157878	184157879
		AYE	169796192	169796191
		MDR-TJ	387124163	387124162

MDR-ZJ06	384142966	384142967
SDF	169633695	169633694
TCDC-AB0715	385237297	385237298
TYTH1	407932590	407932591
ATCC17978	126641560	126641561

References:

1. **Leplae R, Geeraerts D, Hallez R, Guglielmini J, Drèze P, Van Melderen L.** 2011. Diversity of bacterial type II toxin-antitoxin systems: a comprehensive search and functional analysis of novel families. Nucleic Acids Res. **39**:5513-5525.

2. **Shao Y, Harrison EM, Bi D, Tai C, He X, Ou HY, Rajakumar K, Deng Z.** 2011. TADB: a web-based resource for Type 2 toxin-antitoxin loci in bacteria and archaea. Nucleic Acids Res. **39**:D606-611.