

Table S2: Primers used in this study

			EMSA		
Amplicon	PA number	Primer	Sequence 5'-3'	Position (from ATG)	Lenght
<i>pczR</i>	PA2523	686	GCCGGTACCACTTCGGCAACCTTCGAAGAG	-302	301
		687	GCCAGATCTGTTGCCCCCTATATAAAGTA	-1	
<i>znuB</i>	PA5501	676	CACCTCGCTGCTGATCATTC	576	190
		677	AAAACTCAGCAGGAACAGGC	765	
			RT-qPCR		
Amplicon	PA number	Primer	Sequence 5'-3'	Position (from ATG)	Lenght
<i>czcR</i>	PA2523	419	GTCATCACCCGGACGCAGATCAT	502	153
		420	GTAGCCGACGCCGCGAATGGTAT	654	
<i>czcC</i>	PA2522	czcC1	GGTCAGCATCGGCAGCAAGTACG	834	206
		czcC2	GGTCGTAGGCCTGTACCGCTTCG	1039	
<i>czcD</i>	PA0397	574	GGCGTGGCCTTCTATATCCT	285	183
		575	TCCAGACCTCCAGGTAGGC	450	
<i>cadA</i>	PA3690	1086	CATCAACGCCCTGATGAGTA	543	231
		1087	GCTTCCAGTTCCACTTGCTT	773	
<i>oprF</i>	PA1777	594	GGTTACTTCCTGACCGACGA	172	209
		595	TCGCTGTTGATGTTGGTGAT	380	
			DNA cloning		
	Amplicon	Primer	Sequence 5'-3'	Lenght	
Footprinting	<i>pczR</i> 5'FAM	1271	FAM-ACTTCGGCAACCTTCGAAGAG	353	
		857	GGTGCAGGTAGTCGGCAGTC		
	<i>pczR</i> 3'FAM	686	ACTTCGGCAACCTTCGAAGAG	353	
		1272	FAM-GGTGCAGGTAGTCGGCAGTC		
GFP fusions	<i>pczR</i> #1	686	GCC ggtacc ACTTCGGCAACCTTCGAAGAG	301	
		687	GCC gagatct GTTGCCCCCTATATAAAGTA		
	<i>pczR</i> #2	895	CGC ggtacc GGAACCACGCAACCGTTCAT	457	
		687	GCC gagatct GTTGCCCCCTATATAAAGTA		
Mutant	Δ <i>zur</i>	678	CG gaattc CATGGTCGTGCTCGTCGTG	510	
		679	caccagcgcgttgccatcaggcgtccttctggtcGTGGTCATGGGGCTGGCA		
		680	GACCAGAAGGACGCCTGA	500	
		681	CG gga tccGTAGAGTTCAGCCTGGCC		
<i>pMMB66EH-zur6HIS</i>	<i>zur</i>	731	GCC gaattc ATGTACAAGATTGCGCCC	500	
		732	GCC gga tccTCAatgatgatgatgatgGGCGTCTTCTGGTCCC		
<i>pME6001-czcRS</i>	<i>czcRS</i>	384	GGG ctcgag TCTGCTGATCGTCGTCGGCG	2963	
		385	GGG aa gcttGTTCTTCTCGCTGCCTGTTC		
<i>pGEX2T-zur</i>	<i>zur</i>	1044	GCG gga tccATGTACAAGATTGCGCCCAAGACCC	503	
		1045	GCC gaattc TCAGGCGTCTTCTGGTCCC		
			5'RACE		
		Primer	Sequence 5'-3'		
		sp1R	GCAGGCCGTCGATGCCATCG		
		sp1C	TGCCGCGCGCCGCTGGCGAT		
		sp2R	GGTGCAGGTAGTCGGCAGTC		
		sp2C	GCCGCCAGCTCGGGGTTGCT		
		sp3R	AGTCTTGACTTCATCTTCGA		