Supplementary Table S3. Proteins differently expressed in stationary phase $\Delta tonB_m$ strain compared to wild-type

gene	protein	function	localization	$\Delta tonB_m$/wt
		Transport and secretion		
PP_0268*	**OprQ**	porin (OprD family porin)	OM	0.49
PP_0883*	**OpdP**	porin (OprD family porin)	OM	0.38
PP_0861	PP_0861	outer membrane ferric siderophore receptor	OM	2.38[i]
PP_2817[a]	MexC	multidrug efflux RND membrane fusion protein	IM	0.05
PP_2818[a]	MexD	multidrug efflux RND transporter	IM	0.01[i]
PP_2819[a]	OprJ	outer membrane protein	OM	0.01[i]
PP_3271	PhaK	porin (OprD family porin)	OM	0.11[i]
PP_3390	PP_3390	porin	OM	0.31[i]
PP_4519*	**TolC**	TolC family type I secretion outer membrane protein	OM	0.32
		Signalling and transcription regulation		
PP_3286	PhaN	PaaX family transcriptional regulator	C	3.57[i]
PP_2901	PvdQ	acyl-homoserine lactone acylase	P	0.37[i]
		Hypothetical and unknown function		
PP_0765*	PP_0765	hypothetical protein	OM	0.17
PP_2170	PP_2170	chorismate mutase	Unknown	0.18[i]
PP_4978*	**PP_4978**	hypothetical protein	IM	6.25[i]
PP_5298	PP_5298	glutamine amidotransferase	Unknown	2.39[i]

Gene and protein name in bold indicates that the protein was differentially expressed in $ZnSO_4$ treated *colR*-deficient strain as well.

[a] indicates that the genes are in the same operon.

* indicates that the protein is differently expressed also in exponentially growing $\Delta tonB_m$ strain compared to wild-type.

[i] marks that all the expression values of one strain that were used to calculate the $\Delta tonB_m$/wt difference were imputed.

Grey values represent ON-OFF differences that are not statistically significant.

Supplementary Table S4. Proteins differently expressed in exponentially growing $\Delta tonB_m$ strain compared to wild-type

gene	protein	function	localization	$\Delta tonB_m$/wt
		Transport and secretion		
PP_0101[U]	PP_0101	sulfate transporter	IM	26.23[i]
PP_0268	**OprQ**	porin	OM	0.44
PP_0504	**OprG**	OmpW family protein	OM	0.32
PP_0773[U]	**PP_0773**	OmpA/MotB domain-containing protein	OM	3.91
PP_0882[a]	**DppA**	peptide ABC transporter substrate-binding protein	P	0.46
PP_0883[a]	**PP_0883**	porin	OM	0.41
PP_1141[U]	**BraC**	ABC transporter substrate-binding protein	P	0.48
PP_1378	**PcaT**	metabolite/H+ symporter	IM	+/-[o]
PP_1400	KgtP	metabolite/H+ symporter	IM	0.21
PP_1445	OprB-II	carbohydrate-selective porin	OM	0.41[i]
PP_2659	PstB1	phosphate ABC transporter ATP-binding protein	IM	4.65[i]
PP_3088[b]	**TssA1**	K1-T6SS core component	C	3.28
PP_3089[b]	Hcp1	K1-T6SS core component	Extracellular	2.41
PP_3091[b]	**TssM1**	K1-T6SS core component	IM	16.27
PP_3093[b]	**TssK1**	K1-T6SS core component	C	7.02
PP_3092[b]	**TssL**	K1-T6SS core component	C	8.89
PP_3094[b]	**TssJ1**	K1-T6SS core component	IM	2.86
PP_3095[b]	**ClpV1**	K1-T6SS core component, ATPase	C	5.04
PP_3097[Ub]	**TssF1**	K1-T6SS core component	C	6.07
PP_3099[b]	**TssC1**	K1-T6SS core component	C	4.89
PP_3100[b]	**TssB1**	K1-T6SS core component	C	5.18
PP_3155	PP_3155	ferric siderophore receptor	OM	0.26
PP_4217	FpvA	ferripyoverdine receptor	OM	0.27
PP_4519	**TolC**	TolC family type I secretion outer membrane protein	OM	0.50
PP_4613	FecA	iron(III) dicitrate receptor	OM	0.34
PP_4735[c]	LctP	L-lactate transport	IM	0.46
PP_4838	**OprC**	TonB-dependent copper receptor	OM	0.47
PP_4864	BraF	amino acid ABC transporter ATP-binding protein	IM	6.69[i]
PP_5329	PstS	phosphate ABC transporter substrate-binding protein	IM	3.52
		Stress and defence response		
PP_0089[U]	**OsmC**	OsmC family protein	C	3.52[i]
PP_0235	LsfA	peroxidase	C	3.30
PP_0946[d]	**SodA**	superoxide dismutase	P	12.84
PP_1277[U]	**AlgA**	mannose-1-phosphate guanylyltransferase	C	6.93[i]
PP_1286[Ue]	**Alg44**	long-chain fatty acid-CoA ligase	P	2.94[i]
PP_1288[Ue]	**AlgD**	GDP-mannose 6-dehydrogenase	C	26.32[i]
PP_1502[f]	**LptF**	OmpA/MotB domain-containing protein	OM	7.14
PP_1749[Ug]	**PP_1749**	acetyltransferase	C	2.89[i]
PP_3822	PP_3822	cytochrome c family protein	P	0.15
PP_4812[U]	PP_4812	3-methyladenine DNA glycosylase	C	2.46
PP_4855[U]	**OsmE**	Osmotically-inducible lipoprotein	OM	4.80[i]
PP_5151	CarP	SdiA-regulated domain-containing protein	C	15.78[i]
PP_5288[U]	**AlgC**	phosphomannomutase	C	2.86
		Cell envelope homeostasis		
PP_3135	WapB	1,2-glucosyltransferase	C	6.41

PP_4032[U]	**PP_4032**	outer membrane lipoprotein Blc	OM	3.41
PP_5037[h]	**PP_5037**	outer membrane lipoprotein Blc	OM	6.40
		Signalling and transcription regulation		
PP_0185[U]	PprA	LytTR family two component transcriptional regulator	C	5.32
PP_0216[U]	**PP_0216**	PAS/PAC sensor containing diguanylate cyclase	C	5.22[i]
PP_0769	PP_0769	histidine kinase	C	0.47
PP_1652	PfeS-II	histidine kinase	IM	2.91[i]
PP_2347	CarR	two component transcriptional regulator	C	4.38
PP_2900	PP_2900	probable Fur like regulator	C	2.65
PP_3631[U]	**HtrG**	putative signal transduction protein	Unknown	7.10
PP_4224	PP_4224	membrane sensor signal transduction histidine kinase	IM	10.24[i]
PP_4470[U]	**AmrZ**	alginate biosynthesis regulator AlgZ	C	5.83
PP_5320	PhoB	transcriptional regulator	C	7.01
		Amino acid and protein metabolism		
PP_0675	GdhA	glutamate dehydrogenase	Unknown	2.20
PP_0988[U]	GcvP1	glycine dehydrogenase	C	0.28
PP_1750[Ug]	**AsnB**	asparagine synthetase	C	3.25[i]
PP_3664	PssA-1	phosphatidylserine synthase	C	2.12
PP_3796	**PvdA**	L-ornithine 5-oxygenase PvdA	C	4.77
PP_4209	PvdR	ABC transporter permease	IM	4.84[i]
PP_4213	PvdM	dipeptidase	Unknown	2.40
PP_4216	**PvdE**	cyclic peptide transporter	IM	6.75
PP_4218[i]	**PP_4218**	lipase/esterase	C	2.82
PP_4219[i]	**PvdD**	non-ribosomal peptide synthetase	Unknown	4.33
PP_4220[j]	**PvdJ**	non-ribosomal peptide synthetase	Unknown	3.09
PP_4221[j]	**PvdI**	non-ribosomal peptide synthetase	Unknown	6.24
PP_4222	**SyrP**	aspartyl hydroxylase	C	5.68
PP_4223	**PvdH**	diaminobutyrate-2-oxoglutarate aminotransferase	C	4.82
PP_4243	**PvdL**	peptide synthase PvdL	Unknown	5.50
PP_4245	PvdY	siderophore biosynthesis protein	C	4.69
PP_4621	HmgA	homogentisate 1,2-dioxygenase	Unknown	2.04
		Metabolism		
PP_0100[U]	**CynT**	carbonate dehydratase	C	5.33
PP_0236[k]	SsuE	NAD(P)H-dependent FMN reductase	Unknown	2.64[i]
PP_0238[k]	SsuD	alkanesulfonate monooxygenase	C	12.49[i]
PP_0543	EutB	ethanolamine ammonia-lyase subunit alpha	C	3.50
PP_0944[d]	**FumC-1**	fumarate hydratase	C	18.60
PP_1755	FumC-2	fumarate hydratase	C	2.50
PP_2136[U]	FadB	multifunctional fatty acid oxidation complex subunit	C	2.71
PP_2137	FadA	3-ketoacyl-CoA thiolase	C	2.56
PP_2168[U]	Tal	transaldolase B	Unknown	2.073
PP_2437	PP_2437	acyl-CoA dehydrogenase	C	10.36[i]
PP_3443	PP_3443	glyceraldehyde-3-phosphate dehydrogenase	C	2.14
PP_4043	GntZ	6-phosphogluconate dehydrogenase	C	2.16
PP_4058	GlgB	glycogen branching protein	C	2.01
PP_4060	GlgE	alpha-amylase	C	4.53
PP_4264	HemN	coproporphyrinogen III oxidase	C	0.24
PP_4736[l]	LldD	L-lactate dehydrogenase	C	0.39
PP_4737[l]	Dld2	D-lactate dehydrogenase	C	0.12
PP_4870	PP_4870	azurin	P	0.36

PP_5041	GlgP	glycogen/starch/alpha-glucan phosphorylase	C	2.84
PP_5210	PP_5210	zinc-containing alcohol dehydrogenase	C	6.60[i]
PP_5222	CyaA	adenylate cyclase	C	2.61[i]
PP_5365	PP_5365	cyclopropane-fatty-acyl-phospholipid synthase	C	2.55
		Chemotaxis and motility		
PP_1087	**MotY**	Flagellar proteiin MotY precursor signature	OM	0.50
PP_4377	**FlaG**	flagellin	Unknown	0.44
		Hypothetical and unknown function		
PP_0052	PP_0052	beta-lactamase domain-containing protein	C	3.21
PP_0085	**PP_0085**	hypothetical protein	Unknown	11.86[i]
PP_0128	PP_0128	hypothetical protein	C	2.26[i]
PP_0255	PP_0255	hypothetical protein	IM	8.40
PP_0541	PP_0541	acetyltransferase	C	2.35
PP_0765	PP_0765	hypothetical protein	OM	0.31
PP_0837[U]	**YcfJ**	hypothetical protein	OM	5.42
PP_0886	**PP_0886**	hypothetical protein	P	3.38
PP_0903[U]	**PP_0903**	type 11 methyltransferase	C	11.37[i]
PP_0945[d]	PP_0945	hypothetical protein	C	18.79
PP_1291	PP_1291	PhoH family protein	C	4.07
PP_1478[U]	PP_1478	NADH:flavin oxidoreductase	C	2.27
PP_1487[U]	PP_1487	hypothetical protein	IM	2.43
PP_1503[Uf]	**PP_1503**	hypothetical protein	Unknown	6.10
PP_1659	**PP_1659**	hypothetical protein	P	0.29
PP_1838	PP_1838	hypothetical protein	IM	2.26
PP_2059	**PP_2059**	CsbD family protein	Unknown	12.59[i]
PP_2103	PP_2103	hypothetical protein	Unknown	2.22[i]
PP_2132	PP_2132	universal stress protein	C	2.23
PP_2172[U]	PP_2172	hypothetical protein	Extracellular	2.21
PP_2306[Um]	PP_2306	lipoprotein	Unknown	2.66
PP_2307[m]	PP_2307	CHAD domain-containing protein	C	2.85
PP_2356	PP_2356	phytochrome family protein	IM	2.12
PP_2891	**PP_2891**	acetyltransferase	IM	3.12[i]
PP_3824	**PP_3824**	hypothetical protein	Unknown	3.25
PP_3930	PP_3930	hypothetical protein	IM	4.05
PP_4920[U]	**PP_4920**	lipoprotein	Unknown	3.14
PP_4978	**PP_4978**	hypothetical protein	IM	8.93
PP_5038[Uh]	**PP_5038**	hypothetical protein	Unknown	53.06[i]
PP_5252	PP_5252	amidohydrolase	Unknown	2.01

Gene and protein name in bold indicates that the protein was differentially expressed in $ZnSO_4$ treated *colR*-deficient strain as well.

[a-m] indicates that the genes are in the same operon.

[U] shows that the gene belongs to AlgU regulon.

[i] marks that all the expression values of one strain that were used to calculate the $\Delta tonB_m$/wt difference were imputed. Grey values represent ON-OFF differences that are not statistically significant.

[o] +/- indicates that protein was detected in $\Delta tonB_m$ but not in wt. $\Delta tonB_m$/wt ratio is not presented because imputation of missing values for wild-type resulted in higher values than determined for $\Delta tonB_m$.

Supplementary Table S5. Oligonucleotides

Name	Sequence (5'-3')[a]	Use
4994Bam	aaggatcctggaaaccctgacc	construction of pEMG/*ΔtonB*$_m$
4994pikk	agttactggacaaacggtcccaggtatccagcaaccgca	construction of pEMG/*ΔtonB*$_m$
4994del	ggaccgtttgtccagtaact	construction of pEMG/*ΔtonB*$_m$
4994Eco	aagaattcagccaggcgttgtcgg	construction of pEMG/*ΔtonB*$_m$
1898Xba	cgtctagagcagtaatgaccgttcc	construction of pEMG/*ΔpocA* and pEMG/*ΔpocAB*
pocAuus	gcagcatcatccaaccacc	construction of pEMG/*ΔpocA* and pEMG/*ΔpocAB*
pocA-pikk-uus	ggtggttggatgatgctgccgatcaagctggtggaagt	construction of pEMG/*ΔpocA*
1899Eco	ccgaattcgcacaggatcaggtctag	construction of pEMG/*ΔpocA*
1898Xba	cgtctagagcagtaatgaccgttcc	construction of pEMG/*ΔpocB*
1899algus	Aacttcacgccttgcctcc	construction of pEMG/*ΔpocB*
1899stop_pikk	ggaggcaaggcgtgaagttagggcacgccttgatggct	construction of pEMG/*ΔpocB*
1899Eco	ccgaattcgcacaggatcaggtctag	construction of pEMG/*ΔpocB* and pEMG/*ΔpocAB*
pocBstop-uus	ggtggttggatgatgctgcagggcacgccttgatggc	construction of pEMG/*ΔpocAB*
XbaIflhF	attctagaagctgaccacagagtc	construction of pEMG/*ΔflhF*
flhFpikk	gatatgcgtcaggccatgttcgctgatctctatca	construction of pEMG/*ΔflhF*
flhFalgus	Catggcctgacgcatatc	construction of pEMG/*ΔflhF*
flhFEcoRI	atgaattcggccacgaagaggt	construction of pEMG/*ΔflhF*
del_CDJEco	aggaattccagataaaaccgcaggt	construction of pEMG/*ΔmexCD-oprJ*
del_CDJ_pikk	ggaggctgtttcagcccttatcgaacctgtcttg	construction of pEMG/*ΔmexCD-oprJ*
del_CDJ	aagggctgaaacagcctcc	construction of pEMG/*ΔmexCD-oprJ*
del_CDJXba	attctagaaagctatggggaccagg	construction of pEMG/*ΔmexCD-oprJ*
2820Eco	aagaattcgacggtggctcgcgta	construction of pEMG/*ΔnfxB*
2820del	tgcaaacgctggagctgctt	construction of pEMG/*ΔnfxB*
2820pikk	aagcagctccagcgtttgcatcagaagattccacac	construction of pEMG/*ΔnfxB*
2820Sac	aagagctcaagggcctcgaccaga	construction of pEMG/*ΔnfxB*
oprB-1ees	cagggtaccatctgccagtgcagtct	verification of *oprB1* deficiency
oprB-1lopp	tggtctagagctcttgttgtttgagat	verification of *oprB1* deficiency
prtac	aattaatcatcggctcgtataa	arbitrary PCR; verification of P_{tac}-*tonB*$_m$
Arb6	ggccacgcgtcgactagtacnnnnnnnnnnacgcc	arbitrary PCR
OEint	Acttgtgtataagagtcag	arbitrary PCR
Arb2	ggccacgcgtcgactagtac	arbitrary PCR
4994alg	ccaagcttattcgactgagctgctgcc	construction of pBRlacItac/*tonB*$_m$
4994lopp	tcctctagatactccacaggcttcagc	construction of pBRlacItac/*tonB*$_m$
flhFEco	aaagaattcaagcaagtcaccatcgttg	construction of pKTlacItac/*flhF-gfp*
flhFXho	aaactcgagacccgctcgccgtgggttgt	construction of pKTlacItac/*flhF-gfp*

[a] The sites of restriction enzymes used in cloning are underlined.