

Table S1: Significant changes in protein abundance of *S. pneumoniae* D39 upon CTAB exposure

Significant* changes in protein abundance are shown in bold. On/off proteins are proteins that are exclusively identified in either stress or control samples. Arrows indicate if a protein was more or less abundant after application of CTAB in comparison to the control condition. "nc": fold change not calculable because of low identification rate. * Student's *t*-test (*p*-value= 0.01, min. fold change= 1.5).

CTAB stress ↑

locusID	protein	localization PSORTdb_3.0 [1]	protein fold change	
			<u>1 h stress</u>	<u>2 h stress</u>
SPD_0091	Unknown	Cytoplasmic	1.3	1.7
SPD_0093	Putative membrane protein PtvC	Cytoplasmic Membrane	1.6	1.0
SPD_0094	Putative membrane-associated protein PvtB	Unknown	1.8	1.1
SPD_0166	Lumazine synthase RibH	Cytoplasmic	3.5	1.6
SPD_0167	Riboflavin biosynthesis protein RibB	Cytoplasmic	2.9	1.4
SPD_0169	Riboflavin biosynthesis protein RibD	Cytoplasmic	2.6	1.9
SPD_0184	Putative lipoprotein	Extracellular	2.0	1.3
SPD_0240	Acetyltransferase	Unknown	3.9	3.0
SPD_0265	Alcohol dehydrogenase AdhA	Cytoplasmic	2.3	1.7
SPD_0308	ATP-dependent Clp protease, subunit ClpL	Cytoplasmic	14.4	7.0
SPD_0351	Sensor histidine kinase LiaS	Cytoplasmic Membrane	1.7	2.0
SPD_0372	ABC transporter	Cytoplasmic Membrane	1.6	1.7
SPD_0420	Pyruvate formate lyase PflB	Cytoplasmic	1.7	1.1
SPD_0646	Unknown	Cytoplasmic	1.6	1.4
SPD_0701	Response regulator CiaR	Cytoplasmic	1.9	1.4
SPD_0803	Unknown	Cytoplasmic Membrane	on	on
SPD_0868	Foldase PrsA	Cytoplasmic Membrane	1.8	2.1
SPD_0913	Unknown	Unknown	1.9	2.0
SPD_1262	Transcriptional regulator AraC family	Cytoplasmic	1.2	2.0

SPD_1263	ABC transporter	Cytoplasmic Membrane	8.5	11.2
SPD_1264	ABC transporter	Cytoplasmic Membrane	7.4	11.8
SPD_1265	Putative membrane protein	Cytoplasmic Membrane	on	on
SPD_1266	Putative membrane protein	Cytoplasmic Membrane	nc	on
SPD_1267	ABC transporter	Cytoplasmic Membrane	6.9	19.9
SPD_1793	Universal stress protein	Cytoplasmic	1.6	0.8
SPD_1834	Aldehyde-alcohol dehydrogenase	Cytoplasmic	2.0	1.2
SPD_1932	Alpha-1,4 glucan phosphorylase MalP	Cytoplasmic Membrane	1.9	1.8
SPD_2068	Serine protease HtrA	Extracellular	3.1	2.6

CTAB stress ↓

locusID	protein	localization PSORTdb_3.0 [1]	protein fold change	
			<u>1 h stress</u>	<u>2 h stress</u>
SPD_0095	Putative integral membrane protein PtvA	Cytoplasmic Membrane	1.0	0.4
SPD_0104	LysM domain protein	Cytoplasmic Membrane	0.5	0.3
SPD_0321	Glycosyl transferase Cps2F	Cytoplasmic Membrane	0.3	0.4
SPD_0558	Serine protease PrtA	Cellwall	0.6	0.9
SPD_0736	Pyrimidine-nucleoside phosphorylase Pdp	Cytoplasmic	1.0	0.6
SPD_0960	Glycosyl transferase CpoA	Cytoplasmic	0.6	0.6
SPD_1153	Phosphoesterase Pde2	Cytoplasmic	0.7	1.0
SPD_1211	3-dehydroquinate dehydratase I AroD	Cytoplasmic	0.9	0.6
SPD_1246	Glucosamine-6-phosphate deaminase NagB	Cytoplasmic	0.8	0.6
SPD_1250	NAD synthetase NadE	Cytoplasmic	0.9	0.6
SPD_1428	Cytidylate kinase Cmk	Cytoplasmic	0.9	0.7
SPD_1449	Unknown	Cytoplasmic	0.9	0.5
SPD_1514	ABC transporter	Cytoplasmic Membrane	0.5	0.2

SPD_1516	Putative membrane protein	Cytoplasmic Membrane	0.5	0.3
SPD_1527	Putative sodium ABC exporter	Cytoplasmic Membrane	0.7	0.6
SPD_1597	Tryptophan synthase beta chain TrpB	Cytoplasmic	0.7	0.6
SPD_1600	Anthranilate phosphoribosyltransferase TrpD	Cytoplasmic	0.7	0.5
SPD_1601	Anthranilate synthase component II TrpG	Cytoplasmic	0.5	0.5
SPD_1634	Galactokinase GalK	Cytoplasmic	off	nc
SPD_1928	Unknown	Unknown	0.6	0.4

References

1. Peabody, M.A.; Laird, M.R.; Vlasschaert, C.; Lo, R.; Brinkman, F.S. PSORTdb: expanding the bacteria and archaea protein subcellular localization database to better reflect diversity in cell envelope structures. *Nucleic Acids Res.* **2016**, *44*, D663-D668, doi:10.1093/nar/gkv1271.