



Figure S1: Transcriptomics data for non-halophilic bacteria in hyperosmotic stress experiments. The plots show median differences of compositional metrics, GRAVY, and pI for proteins coded by the differentially expressed genes, i.e. median value for all up-regulated proteins minus median value for all down-regulated proteins in each dataset. Data sources, indicated by letters, are described in the following table and footnotes. Reference keys in the table, derived from the first letters of the authors' surnames and publication year, correspond to file names used for the datasets in the canprot package.

Set	Reference	Description	Down	Up
a	KSA+02	<i>Synechocystis</i> sp. PCC 6803 in 0.5 M NaCl vs control	36	62
b	KSA+02	<i>Synechocystis</i> sp. PCC 6803 in 0.5 M sorbitol vs control	32	45
c	WJ02	<i>Escherichia coli</i> in 0.4 M NaCl vs control	102	41
d	HZP+05	<i>Yersinia pestis</i> in 0.5 M NaCl vs control	13	103
e	HZP+05	<i>Yersinia pestis</i> in 0.5 M sorbitol vs control	40	103
f	LGW+05	<i>Shewanella oneidensis</i> MR-1 in 0.5 vs 0.1 M NaCl	563	541
g	SLA+05	<i>Synechocystis</i> sp. PCC 6803 in 0.5 M sorbitol vs control	27	53
h	GCP08	<i>Escherichia coli</i> in 0.5 M vs 0 M NaCl at 30 deg C	307	40
i	GCP08	<i>Escherichia coli</i> in 0.5 M vs 0 M NaCl at 43 deg C	89	144
j	SBB+09	<i>Escherichia coli</i> in 2.7 Os/kg NaCl vs control	35	26
k	SBB+09	<i>Escherichia coli</i> in 2.7 Os/kg sucrose vs control	28	37
l	HMO+10	<i>Bacillus subtilis</i> in 6% w/v NaCl vs control	417	459
m	BBWB12	<i>Listeria monocytogenes</i> strain H7858 in 6% NaCl at 2.5% lag-phase duration	18	55
n	BBWB12	<i>Listeria monocytogenes</i> strain H7858 in 6% NaCl at 5% lag-phase duration	85	134
o	BBWB12	<i>Listeria monocytogenes</i> strain H7858 in 6% NaCl at 10% lag-phase duration	136	156
p	BBWB12	<i>Listeria monocytogenes</i> strain H7858 in 6% NaCl at 20% lag-phase duration	58	44
q	LB12	<i>Synechococcus</i> sp. strain PCC 7002 in 1.5 M NaCl vs control	311	646
r	QHT+13	<i>Synechocystis</i> sp. PCC 6803 Gene in 4% w/v vs 0% added NaCl for 24 h	50	48
s	QHT+13	<i>Synechocystis</i> sp. PCC 6803 Gene in 4% w/v vs 0% added NaCl for 48 h	50	50
t	QHT+13	<i>Synechocystis</i> sp. PCC 6803 Gene in 4% w/v vs 0% added NaCl for 72 h	50	49
u	WGB+13	<i>Escherichia coli</i> in 0.3 M NaCl vs control	525	524
v	WGB+13	<i>Escherichia coli</i> in 0.6 M urea vs control	337	370
w	ADW+14	<i>Bifidobacterium longum</i> BBM68 Gene with vs without 0.75 g/l ox bile	160	76
x	KKG+14	<i>Escherichia coli</i> Gene in NaCl (0.967 aw) vs control for 30 min	15	164
y	KKG+14	<i>Escherichia coli</i> Gene in NaCl (0.967 aw) vs control for 80 min	409	727
z	KKG+14	<i>Escherichia coli</i> Gene in NaCl (0.967 aw) vs control for 310 min	319	571
A	KSM+14	<i>Bacillus subtilis</i> in 1.2 M NaCl vs control	687	642
B	KSM+14	<i>Bacillus subtilis</i> with vs without glycine betaine in 1.2 M NaCl	311	559
C	MGM+14	<i>Escherichia coli</i> in 3.5 vs 2% NaCl (with glycine betaine)	169	64
D	MGM+14	<i>Escherichia coli</i> in 4.5 vs 2% NaCl (with glycine betaine)	740	579
E	MGM+14	<i>Escherichia coli</i> in 5 vs 2% NaCl (with glycine betaine)	43	82
F	MGM+14	<i>Escherichia coli</i> in 5.5 vs 2% NaCl (with glycine betaine)	79	84
G	SLM+14	<i>Enterococcus faecalis</i> in 6.5% NaCl vs control at 5 min	113	69
H	SLM+14	<i>Enterococcus faecalis</i> in 6.5% NaCl vs control at 30 min	125	175
I	SLM+14	<i>Enterococcus faecalis</i> in 6.5% NaCl vs control at 60 min	170	172
J	FRH+15	<i>Salmonella enterica</i> in NaCl vs control for 1h h	113	60
K	FRH+15	<i>Salmonella enterica</i> in NaCl vs control for 6h h	255	149
L	FRH+15	<i>Salmonella enterica</i> in NaCl vs control for 24h h	163	60
M	FRH+15	<i>Salmonella enterica</i> in KCl vs control for 1h h	92	45
N	FRH+15	<i>Salmonella enterica</i> in KCl vs control for 6h h	349	264
O	FRH+15	<i>Salmonella enterica</i> in KCl vs control for 24h h	403	182
P	FRH+15	<i>Salmonella enterica</i> in glycerol vs control for 1h h	300	333
Q	FRH+15	<i>Salmonella enterica</i> in glycerol vs control for 6h h	261	132
R	FRH+15	<i>Salmonella enterica</i> in glycerol vs control for 24h h	164	67
S	KLB+15	<i>Caulobacter crescentus</i> Gene in 40/50 mM NaCl vs M2 minimal salts medium	209	142
T	KLB+15	<i>Caulobacter crescentus</i> Gene in 200 mM sucrose vs M2 minimal salts medium	105	96
U	HLL17	<i>Methylocystis</i> sp. strain SC2 in 0.75% NaCl vs control at 45min	105	46
V	HLL17	<i>Methylocystis</i> sp. strain SC2 in 0.75% NaCl vs control at 14h	22	75
W	MWZ+18	<i>Lactobacillus paracasei</i> L9 with vs without 0.13% ox bile	42	56

**a. b.** Tables 1–2 of Kanesaki et al. (2002). **c.** Table 1 of Weber and Jung (2002). **d. e.** Table 3 of Han et al. (2005). **f.** Table 1S of Liu et al. (2005). **g.** Tables 2–3 of Shapiguzov et al. (2005). **h. i.** [Dataset.txt](#) of Gunasekera et al. (2008). **j. k.** Table 3 of Shabala et al. (2009). **l.** Table S2 (sheet “S2\_Table\_3”) of Hahne et al. (2010). **m. n. o. p.** Table S5 of Bergholz et al. (2012), filtered to include genes with  $\log_2$  fold change  $> 1$  or  $< -1$ . **q.** Table S2 of Ludwig and Bryant (2012), filtered to include genes with  $p$ -value  $< 0.05$  and fold change  $> 2$  or  $< 0.5$ . **r. s. t.** Supplementary Tables S2A–S2F of Qiao et al. (2013). **u. v.** [Dataset.txt](#) of Withman et al. (2013), filtered to include proteins with log fold change (column “N vs K Wmean [M]” for NaCl and “U vs K Wmean [M]” for urea)  $> 1$  or  $< 1$  and  $p$ -value less than 0.05. **w.** Table S2 of An et al. (2014) **x. y. z.** Table S2 of Kocharunchitt et al. (2014) **A. B.** Tables S5–S6 of Kohlstedt et al. (2014). **C. D. E. F.** Supplemental Table S1 of Metris et al. (2014), filtered to include genes with differences of Normalized  $\ln(\text{cDNA/gDNA}) > 1$  or  $< 1$  between 2 % and higher NaCl concentration. **G. H. I.** Table S2 of Solheim et al. (2014). **J. K. L. M. N. O. P. Q. R.** Tables S1–S3 of Finn et al. (2015). **S. T.** Table S2 of Kohler et al. (2015). **U. V.** Tables S5–S8 of Han et al. (2017). **W.** Table S6 of Ma et al. (2018).

## References

- An, H., Douillard, F. P., Wang, G., Zhai, Z., Yang, J., Song, S., Cui, J., Ren, F., Luo, Y., Zhang, B. and Hao, Y.: Integrated transcriptomic and proteomic analysis of the bile stress response in a centenarian-originated probiotic *Bifidobacterium longum* BBMN68, *Molecular & Cellular Proteomics*, 13(10), 2558–2572, doi:[10.1074/mcp.M114.039156](#), 2014.
- Bergholz, T. M., Bowen, B., Wiedmann, M. and Boor, K. J.: *Listeria monocytogenes* shows temperature-dependent and -independent responses to salt stress, including responses that induce cross-protection against other stresses, *Applied and Environmental Microbiology*, 78(8), 2602–2612, doi:[10.1128/AEM.07658-11](#), 2012.
- Finn, S., Rogers, L., Händler, K., McClure, P., Amézquita, A., Hinton, J. C. D. and Fanning, S.: Exposure of *Salmonella enterica* serovar Typhimurium to three humectants used in the food industry induces different osmoadaptation systems, *Applied and Environmental Microbiology*, 81(19), 6800–6811, doi:[10.1128/AEM.01379-15](#), 2015.
- Gunasekera, T. S., Csonka, L. N. and Paliy, O.: Genome-wide transcriptional responses of *Escherichia coli* K-12 to continuous osmotic and heat stresses, *Journal of Bacteriology*, 190(10), 3712–3720, doi:[10.1128/JB.01990-07](#), 2008.
- Hahne, H., Mäder, U., Otto, A., Bonn, F., Steil, L., Bremer, E., Hecker, M. and Becher, D.: A comprehensive proteomics and transcriptomics analysis of *Bacillus subtilis* salt stress adaptation, *Journal of Bacteriology*, 192(3), 870–882, doi:[10.1128/JB.01106-09](#), 2010.
- Han, D., Link, H. and Liesack, W.: Response of *Methylocystis* sp. Strain SC2 to salt stress: Physiology, global transcriptome, and amino acid profiles, *Applied and Environmental Microbiology*, 83(20), e00866–17, doi:[10.1128/AEM.00866-17](#), 2017.
- Han, Y., Zhou, D., Pang, X., Zhang, L., Song, Y., Tong, Z., Bao, J., Dai, E., Wang, J., Guo, Z., Zhai, J., Du, Z., Wang, X., Wang, J., Huang, P. and Yang, R.: Comparative transcriptome analysis of *Yersinia pestis* in response to hyperosmotic and high-salinity stress, *Research in Microbiology*, 156(3), 403–415, doi:[10.1016/j.resmic.2004.10.004](#), 2005.
- Kanesaki, Y., Suzuki, I., Allakhverdiev, S. I., Mikami, K. and Murata, N.: Salt stress and hyperosmotic stress regulate the expression of different sets of genes in *Synechocystis* sp. PCC 6803, *Biochemical and Biophysical Research Communications*, 290(1), 339–348, doi:[10.1006/bbrc.2001.6201](#), 2002.
- Kocharunchitt, C., King, T., Gobius, K., Bowman, J. P. and Ross, T.: Global genome response of *Escherichia coli* O157:H7 Sakai during dynamic changes in growth kinetics induced by an abrupt downshift in water activity, *PLoS One*, 9(3), 1–13, doi:[10.1371/journal.pone.0090422](#), 2014.
- Kohler, C., Lourenço, R. F., Bernhardt, J., Albrecht, D., Schüler, J., Hecker, M. and Gomes, S. L.: A comprehensive genomic, transcriptomic and proteomic analysis of a hyperosmotic stress sensitive  $\alpha$ -proteobacterium, *BMC Microbiology*, 15(1), 1–15, doi:[10.1186/s12866-015-0404-x](#), 2015.
- Kohlstedt, M., Sappa, P. K., Meyer, H., Maaß, S., Zapras, A., Hoffmann, T., Becker, J., Steil, L., Hecker, M., Dijk, J. M. van, Lalk, M., Mäder, U., Stülke, J., Bremer, E., Völker, U. and Wittmann, C.: Adaptation of *Bacillus subtilis* carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: A multi-omics perspective, *Environmental Microbiology*, 16(6), 1898–1917, doi:[10.1111/1462-2920.12438](#), 2014.

- Liu, Y., Gao, W., Wang, Y., Wu, L., Liu, X., Yan, T., Alm, E., Arkin, A., Thompson, D. K., Fields, M. W. and Zhou, J.: Transcriptome analysis of *Shewanella oneidensis* MR-1 in response to elevated salt conditions, *Journal of Bacteriology*, 187(7), 2501–2507, doi:[10.1128/JB.187.7.2501-2507.2005](https://doi.org/10.1128/JB.187.7.2501-2507.2005), 2005.
- Ludwig, M. and Bryant, D.: *Synechococcus* sp. Strain PCC 7002 transcriptome: Acclimation to temperature, salinity, oxidative stress, and mixotrophic growth conditions, *Frontiers in Microbiology*, 3, 354, doi:[10.3389/fmicb.2012.00354](https://doi.org/10.3389/fmicb.2012.00354), 2012.
- Ma, X., Wang, G., Zhai, Z., Zhou, P. and Hao, Y.: Global transcriptomic analysis and function identification of malolactic enzyme pathway of *Lactobacillus paracasei* L9 in response to bile stress, *Frontiers in Microbiology*, 9, 1978, doi:[10.3389/fmicb.2018.01978](https://doi.org/10.3389/fmicb.2018.01978), 2018.
- Metris, A., George, S. M., Mulholland, F., Carter, A. T. and Baranyi, J.: Metabolic shift of *Escherichia coli* under salt stress in the presence of glycine betaine, *Applied and Environmental Microbiology*, 80(15), 4745–4756, doi:[10.1128/AEM.00599-14](https://doi.org/10.1128/AEM.00599-14), 2014.
- Qiao, J., Huang, S., Te, R., Wang, J., Chen, L. and Zhang, W.: Integrated proteomic and transcriptomic analysis reveals novel genes and regulatory mechanisms involved in salt stress responses in *Synechocystis* sp. PCC 6803, *Applied Microbiology and Biotechnology*, 97(18), 8253–8264, doi:[10.1007/s00253-013-5139-8](https://doi.org/10.1007/s00253-013-5139-8), 2013.
- Shabala, L., Bowman, J., Brown, J., Ross, T., McMeekin, T. and Shabala, S.: Ion transport and osmotic adjustment in *Escherichia coli* in response to ionic and non-ionic osmotica, *Environmental Microbiology*, 11(1), 137–148, doi:[10.1111/j.1462-2920.2008.01748.x](https://doi.org/10.1111/j.1462-2920.2008.01748.x), 2009.
- Shapiguzov, A., Lyukevich, A. A., Allakhverdiev, S. I., Sergeyenko, T. V., Suzuki, I., Murata, N. and Los, D. A.: Osmotic shrinkage of cells of *Synechocystis* sp. PCC 6803 by water efflux via aquaporins regulates osmostress-inducible gene expression, *Microbiology*, 151(2), 447–455, doi:[10.1099/mic.0.27530-0](https://doi.org/10.1099/mic.0.27530-0), 2005.
- Solheim, M., La Rosa, S. L., Mathisen, T., Snipen, L. G., Nes, I. F. and Brede, D. A.: Transcriptomic and functional analysis of NaCl-induced stress in *Enterococcus faecalis*, *PLoS One*, 9(4), 1–13, doi:[10.1371/journal.pone.0094571](https://doi.org/10.1371/journal.pone.0094571), 2014.
- Weber, A. and Jung, K.: Profiling early osmostress-dependent gene expression in *Escherichia coli* using DNA macroarrays, *Journal of Bacteriology*, 184(19), 5502–5507, doi:[10.1128/JB.184.19.5502-5507.2002](https://doi.org/10.1128/JB.184.19.5502-5507.2002), 2002.
- Withman, B., Gunasekera, T. S., Beesetty, P., Agans, R. and Paliy, O.: Transcriptional responses of uropathogenic *Escherichia coli* to increased environmental osmolality caused by salt or urea, *Infection and Immunity*, 81(1), 80–89, doi:[10.1128/IAI.01049-12](https://doi.org/10.1128/IAI.01049-12), 2013.