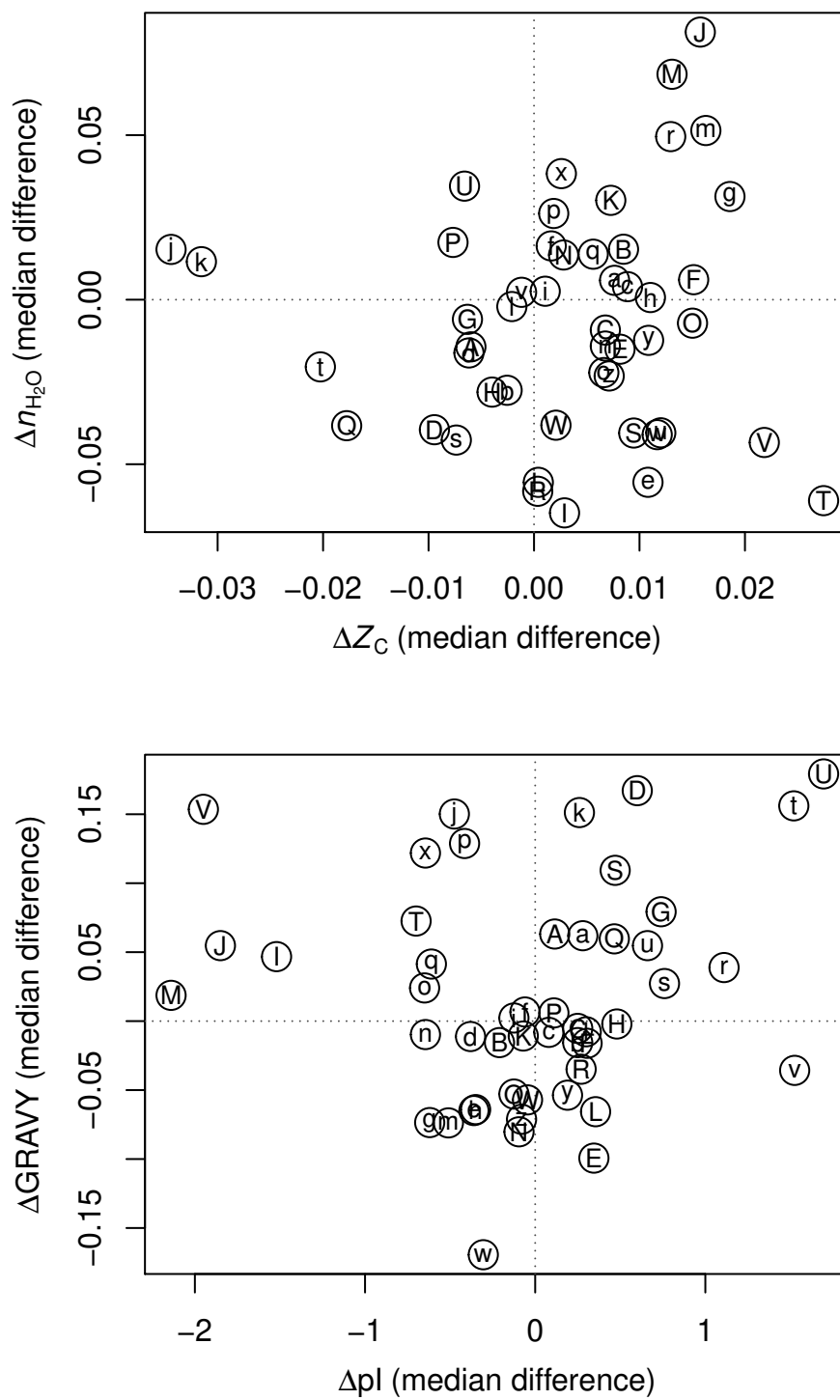


Figure S1: Analysis of bacterial transcriptomics data for hyperosmotic stress



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., Sergeyenkov, 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 microarrays, *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.