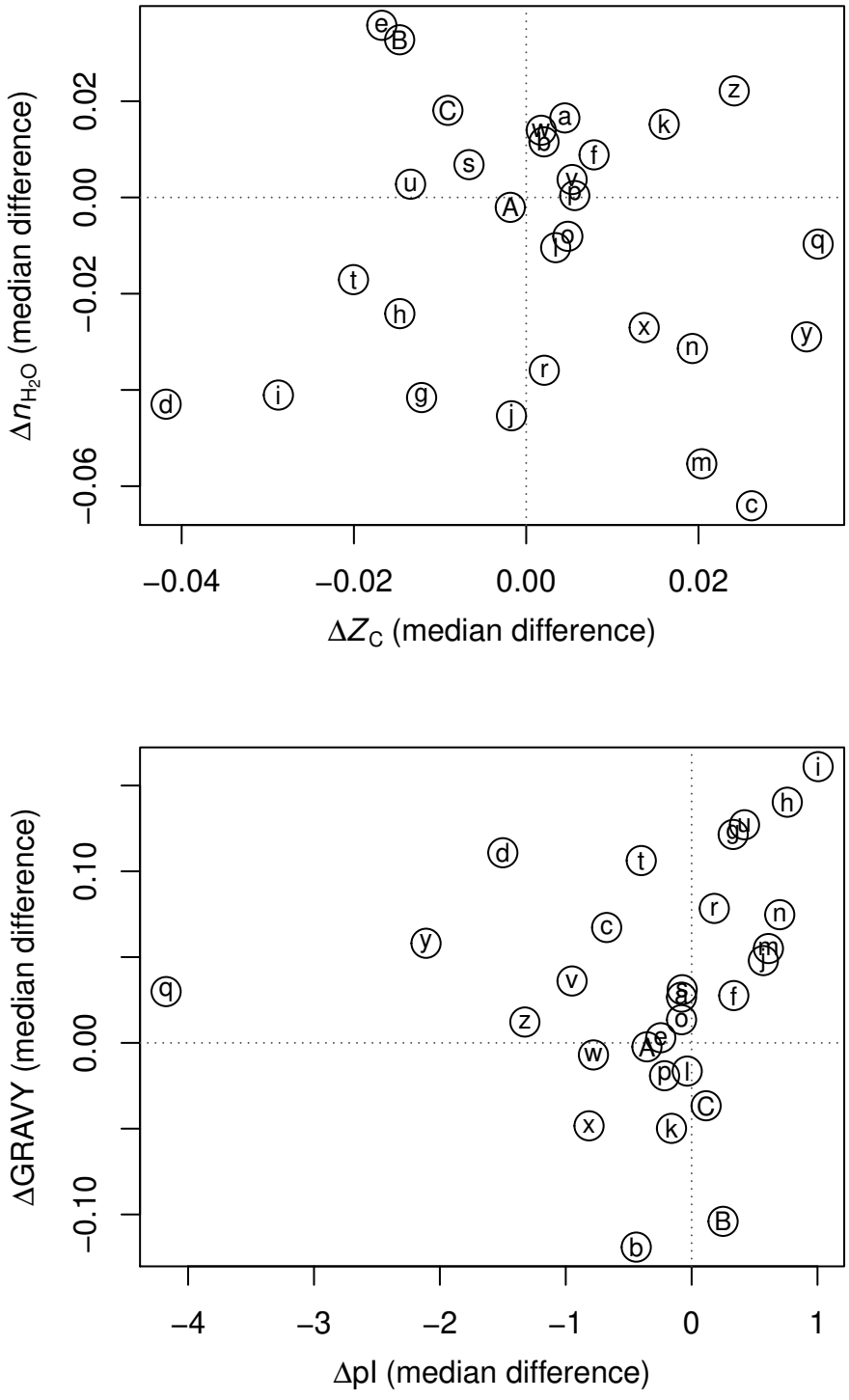
Figure S2: Analysis of bacterial proteomics data for hyperosmotic stress



Set	Reference	Description	Down	Up
a	PNWB09	*Synechocystis* sp. PCC6803 in 6% w/v NaCl vs no added salt	77	55
b	FTR+10	*Corynebacterium glutamicum* in 750 mM NaCl vs control medium	27	65
c	LPK+13	*Lactobacillus johnsonii* with vs without 0.1-0.3% bile salt	123	88
d	QHT+13	*Synechocystis* sp. PCC 6803 Protein in 4% w/v vs 0% added NaCl for 24 h	42	26
e	QHT+13	*Synechocystis* sp. PCC 6803 Protein in 4% w/v vs 0% added NaCl for 48 h	46	62
f	ADW+14	*Bifidobacterium longum* BBMN68 Protein with vs without 0.75 g/l ox bile	20	24
g	KKG+14	*Escherichia coli* Protein in NaCl (0.967 aw) vs control for immediate	30	158
h	KKG+14	*Escherichia coli* Protein in NaCl (0.967 aw) vs control for 30 min	21	162
i	KKG+14	*Escherichia coli* Protein in NaCl (0.967 aw) vs control for 80 min	37	126
j	KKG+14	*Escherichia coli* Protein in NaCl (0.967 aw) vs control for 310 min	12	399
k	PBP+14	*Listeria monocytogenes* in 3% NaCl vs control at 4.C	54	86
l	PBP+14	*Listeria monocytogenes* in 3% NaCl vs control at 37.C	60	25
m	KLB+15	*Caulobacter crescentus* Protein in 200 mM sucrose vs M2 minimal salts medium	33	33
n	KLB+15	*Caulobacter crescentus* Protein in 40/50 mM NaCl vs M2 minimal salts medium	33	27
o	SKV+16	*Escherichia coli* in Glucose vs LB	743	282
p	SKV+16	*Escherichia coli* in Osmotic.stress.glucose vs LB	978	343
q	KAK+17	*Lactobacillus fermentum* with vs without 1.2% w/v bile salts	106	81
r	LYS+17	*Lactobacillus salivarius* LI01 with vs without 0.15% ox bile	177	205
s	KSK+18	*Acidihalobacter prosperus* DSM 14174 30 g/L / 5 g/L NaCl	292	316
t	LJC+18	*Listeria monocytogenes* wt in 0.5 M NaCl vs control medium	65	66
u	LJC+18	*Listeria monocytogenes* mutant in 0.5 M NaCl vs control medium	37	30
v	TSC18	*Caulobacter crescentus* WT in 300 mM sucrose vs control	91	28
w	TSC18	*Caulobacter crescentus* GsrN in 300 mM sucrose vs control	99	107
x	LWS+19	*Lactobacillus plantarum* FS5-5 in 6-8% w/v vs 0% NaCl	72	46
y	MGF+19	*Staphylococcus aureus* in 10% vs 0% NaCl	88	58
z	MGF+19	*Staphylococcus aureus* in 20% vs 0% NaCl	184	99
A	AST+20	*Lactobacillus fermentum* with vs without 0.3% to 1.5% w/v bile salts	368	378
B	GBR+20	*Propionibacterium freudenreichii* CIRM129 in NaCl vs MMO	90	74
C	GBR+20	*Propionibacterium freudenreichii* CIRM1025 in NaCl vs MMO	64	78

a. Additional file 3: Table S2 of Pandhal et al. (2009). **b**. Supplementary Table 8 of Fränzel et al. (2010). Only proteins with consistent expression ratios (all > 1 or all < 1) at each time point (15, 60, and 180 min.) were included. **c**. Supporting Information Table 1 of Lee et al. (2013) (sheets "Up-Down Proteins" and "Unknown function"). **d**. **e**. Supplementary Tables S3A and S3B of Qiao et al. (2013). **f**. Table 1 (proteins) and supplemental Table S2 (genes) of An et al. (2014). **g**. **h**. **i**. **j**. Supporting Information Table S2 of Kocharunchitt et al. (2014). **k**. **l**. Additional file Table S2 of Kohler et al. (2015). **m**. **n**. Supplementary Table S6 of Schmidt et al. (2016), filtered to include proteins with fold change > 2 or < 0.5 for the ratios Glucose / LB (lysogeny broth) or Osmotic-stress glucose / LB. **o**. Supplementary Table 1 (sheets "0.76 fold down regulated" and "1.3 fold up regulated") of Kaur et al. (2017). **p**. Supplemental Table S-2 of Lv et al. (2017), filtered to include proteins with $\log_2$ fold change > 1 or < -1 and *p*-value < 0.05. **q**. Supplementary Table 1 of Khaleque et al. (2018) (amino acid compositions computed from protein sequences in the list of gene annotations). **r**. **s**. Tables S1–S6 of Lee et al. (2018). For each of the wild-type and Δ*sigB* mutant, only proteins that were identified in multicellular vesicles in a single condition (0.5 M salt stress or without salt stress) were included. **t**. **u**. Extracted from proteinGroups.txt in PRIDE project PXD010072/MaxQuantOutput.tar.gz (Tien et al., 2018), filtered to include proteins with non-zero LFQ intensity values for all replicates in each experiment; the medians of these values were used to compute fold changes; proteins with fold change > 1.5 or < 2/3 were kept. **v**. Table 2 of Li et al. (2019). **w**. **x**. Supplementary Tables S4 and S5 of Ming et al. (2019), filtered to include proteins with fold change >= 2 or <= 0.5. **y**. Supplementary Table 1 (sheets ">2.0 Fold" and "< 0.5 Fold") of Ali et al. (2020). **z**. **A**. Supplementary Table 1 of Gaucher et al. (2020) (column "MMO+NaCl/MMO" for CIRM129 and CIRM1025).

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