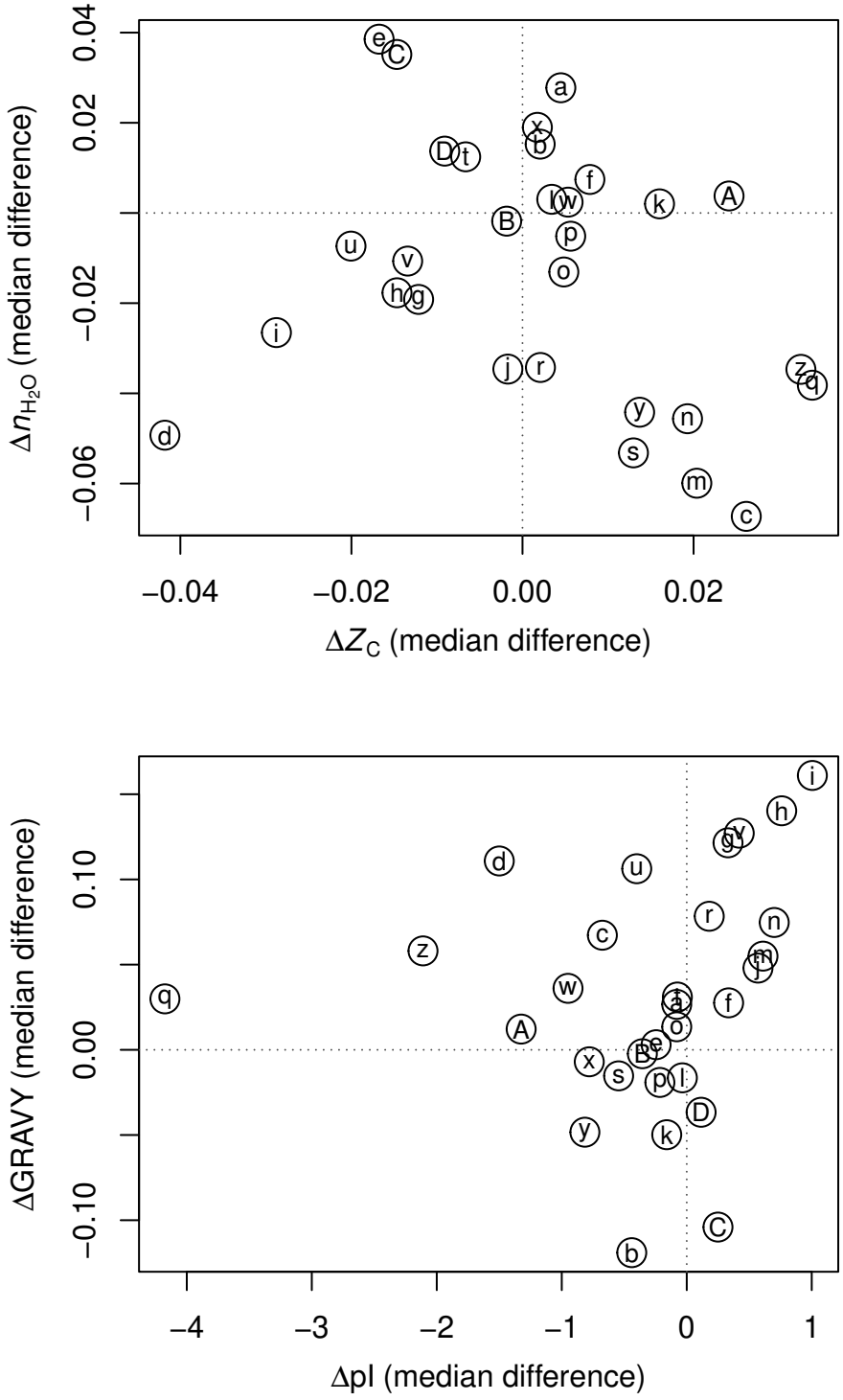

Figure S2: Proteomics data for non-halophilic bacteria in hyperosmotic stress experiments. The plots show median differences of compositional metrics, GRAVY, and pI for the differentially expressed proteins, i.e. median value for all up-regulated proteins minus median value for all down-regulated proteins 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	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	HGC+18	*Lactobacillus casei* BL23 in hyper-concentrated vs isotonic sweet whey	116	64
t	KSK+18	*Acidihalobacter prosperus* DSM 14174 30 g/L / 5 g/L NaCl	292	316
u	LJC+18	*Listeria monocytogenes* WT in 0.5 M NaCl vs control medium	65	66
v	LJC+18	*Listeria monocytogenes* mutant in 0.5 M NaCl vs control medium	37	30
w	TSC18	*Caulobacter crescentus* WT in 300 mM sucrose vs control	91	28
x	TSC18	*Caulobacter crescentus* GsrN in 300 mM sucrose vs control	99	107
y	LWS+19	*Lactobacillus plantarum* FS5-5 in 6-8% w/v vs 0% NaCl	72	46
z	MGF+19	*Staphylococcus aureus* in 10% vs 0% NaCl	88	58
A	MGF+19	*Staphylococcus aureus* in 20% vs 0% NaCl	184	99
B	AST+20	*Lactobacillus fermentum* with vs without 0.3% to 1.5% w/v bile salts	368	378
C	GBR+20	*Propionibacterium freudenreichii* CIRM129 in NaCl vs MMO	90	74
D	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**. Supporting Information Table of Pittman et al. (2014), filtered to include proteins with p-value < 0.05. **m**. **n**. Additional file Table S2 of Kohler et al. (2015). **o**. **p**. 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. **q**. Supplementary Table 1 (sheets "0.76 fold down regulated" and "1.3 fold up regulated") of Kaur et al. (2017). **r**. 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. **s**. Supplementary Figure 1 of Huang et al. (2018). **t**. Supplementary Table 1 of Khaleque et al. (2018) (amino acid compositions computed from protein sequences in the list of gene annotations). **u**. **v**. 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. **w**. **x**. 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. **y**. Table 2 of Li et al. (2019). **z**. **A**. Supplementary Tables S4 and S5 of Ming et al. (2019), filtered to include proteins with fold change >= 2 or <= 0.5. **B**. Supplementary Table 1 (sheets ">2.0 Fold" and "< 0.5 Fold") of Ali et al. (2020). **C**. **D**. Supplementary Table 1 of Gaucher et al. (2020) (column "MMO+NaCl/MMO" for CIRM129 and CIRM1025).

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