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A partial proteome reference map of *Tetragenococcus halophilus* and comparative proteomic and physiological analysis under salt stress

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Fig. S1 Representation of 2D gel separation of the *T. halophilus* proteome according to the predicted pI and molecular weights.

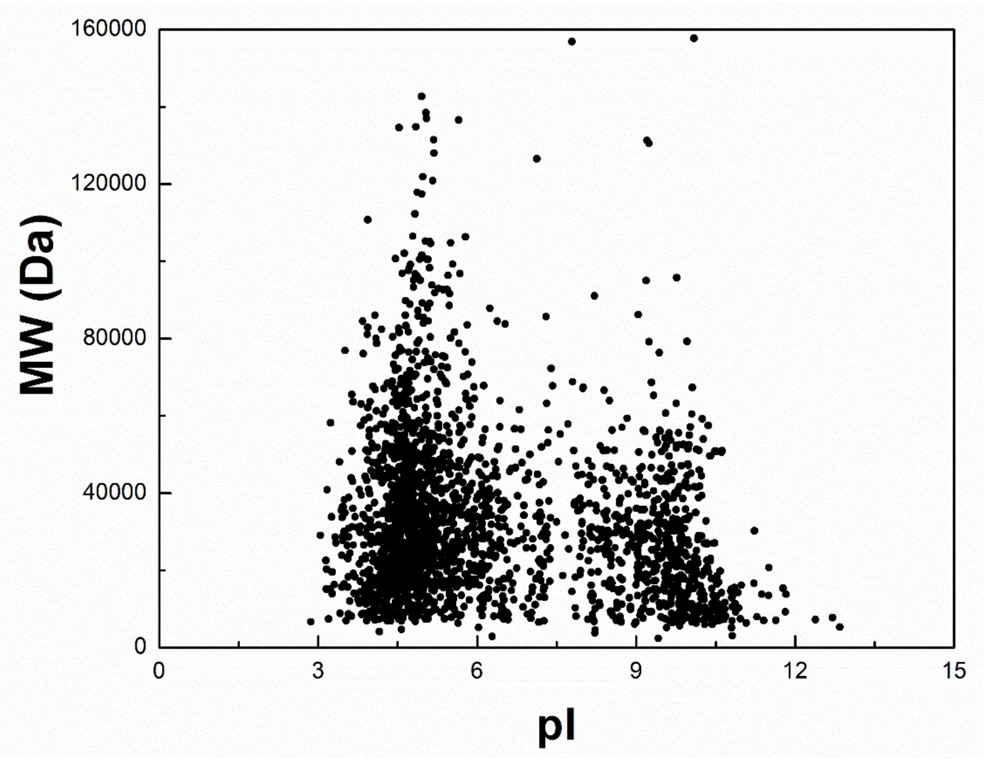

Fig. S2 Two-dimensional electrophoresis gels of the whole cytoplasm proteins of T. halophilus treated by different NaCl contents. (A) 0% NaCl; (B) 12% NaCl.

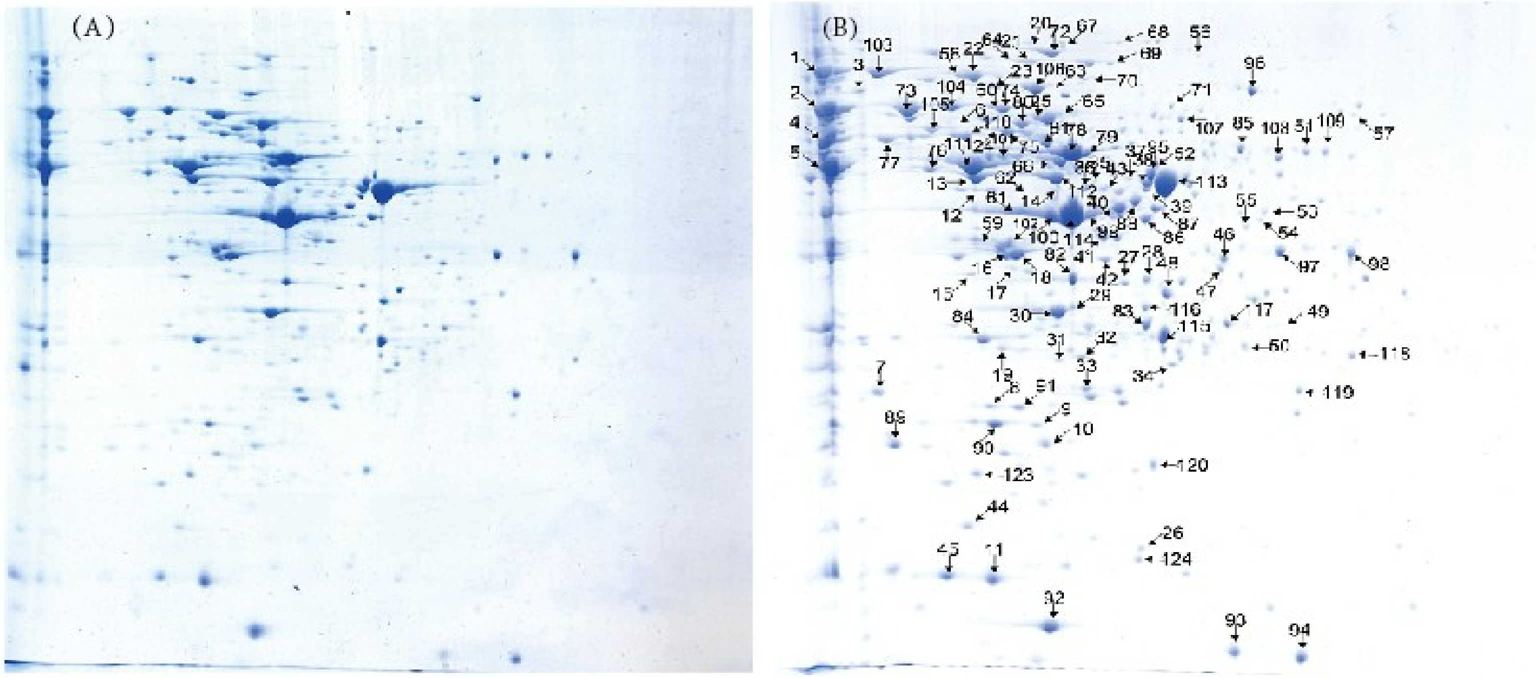

Table S1 Primers for quantitative real-time polymerase chain reaction.

Gene	**Forward primer sequence**	**Reverse primer sequence**	**Amplicon size (bp)**
pfk	GAACCTTCCTTTATTCAGCACG	ATGATAAGAGCCATCGCCAC	128
Ldh	TTCACAGTTTACTGCTTGGTCG	AAATCAACGGGACGCTCTT	81
AtpD	CACTGCTGGATAGATTCCTTGC	GCTTTTGCCCACTTAGATGCTA	72
Dnak	GTTTTAGAAGGCGGCGAAT	AATGCTACAGCAGAAGGTGTTG	74
GroEL	CACCAGTAGAATCAAAAGAAGCG	CCGTCGTTACCAACTTTATCCAT	109
opuAA	TCACCCACGATTTGAACGA	ACATTTGGACCATCTGCTTCTAC	223
16S rRNA	CCTACGGGAGGCAGCAG	ATTACCGCGGCTGCTGG	169

Table S2 List of proteins on the pI 4-7 gel identified by MALDI-MS/MS analysis

Number	Protein description	Accession	*M*r	p*I*	Gene	Locus names	Sequence coverage (%)^a	Function
1	chaperone protein DnaK	gi|352517474	66743.42969	4.38	dnaK	TEH_13000	14.60	O
2	60 kDa chaperonin	gi|352517299	57740.67969	4.47	groEL	TEH_11250	45.60	O
3	trigger factor	gi|352517651	47913.51953	4.31	tig	TEH_14770	35.60	O
4	30S ribosomal protein S1	gi|352518176	44195.5	4.42	rpsA	TEH_20020	74.65	R
6	glycerol kinase	gi|352517828	56131.64063	4.57	glpK	TEH_16450	69.73	C
7	putative C56 family peptidase	gi|352516269	18127.0293	4.37		TEH_00950	32.50	S
8	hypothetical protein TEH_10060	gi|352517180	19031.71094	4.83		TEH_10060	29.51	S
9	ribosome recycling factor	gi|352518139	20910.75977	4.81	frr	TEH_19650	71.29	J
10	single-stranded DNA-binding protein	gi|352516181	18864.31055	4.76	ssb	TEH_00080	68.45	L
11	putative organic hydroperoxide resistance protein	gi|352516281	15119.37988	4.68	ohr	TEH_01070	48.52	V
12	hypothetical protein TEH_16460	gi|352517820	42055.89844	4.64		TEH_16460	36.21	S
13	acetate kinase	gi|352516418	44074.17969	4.64	ackA	TEH_02440	51.90	C
14	D-alanine--D-alanine ligase	gi|352516351	40276.32031	4.87	ddl	TEH_01770	61.09	M
15	hypothetical protein TEH_24600	gi|352518634	26725.05078	4.57		TEH_24600	39.80	S
16	mannose/glucose-specific phosphotransferase system enzyme IIAB component	gi|352516905	36192.32813	4.68	manL	TEH_07310	42.80	G
17	glucokinase	gi|352518161	34602.42188	4.76	glk	TEH_19870	79.84	G
18	L-lactate dehydrogenase	gi|352518632	35041.83984	4.72	ldh	TEH_24580	72.60	C

19	putative DeoR family transcriptional regulator	gi|352517328	75705.15625	5.49		TEH_11540	50.21	K
20	polynucleotide phosphorylase	gi|352516734	77872.92969	4.79	pnpA	TEH_05600	41.01	J
21	transketolase	gi|352517519	72335.64844	4.77	tkt	TEH_13450	45.89	G
22	phosphoenolpyruvate-protein phosphotransferase	gi|352518123	63700.78125	4.68	ptsI	TEH_19490	77.39	G
23	hypothetical protein TEH_17340	gi|352517908	58237.25	4.67		TEH_17340	32.90	S
24	NADH peroxidase	gi|352516444	49935.30078	4.67	npr	TEH_02700	75.70	C
25	betaine aldehyde dehydrogenase	gi|352516633	53424.14063	4.85	gbsA	TEH_04590	45.90	E
26	hypothetical protein TEH_19530	gi|352518127	11891.17969	4.77		TEH_19530	31.02	S
27	hypothetical protein TEH_01480	gi|352516322	31027.15039	5		TEH_01480	29.78	S
28	putative aldo-keto reductase	gi|352517884	30644.68945	4.93		TEH_17100	19.04	Q
29	fructose-bisphosphate aldolase	gi|352517161	31482.67969	4.84	fba	TEH_09870	65.89	G
30	fructose-bisphosphate aldolase	gi|352517161	31482.67969	4.84	fba	TEH_09870	65.89	G
31	putative hydrolase	gi|352518095	26749.46094	5.31		TEH_19210	69.72	S
32	hypothetical protein TEH_07030	gi|352516877	22900.33008	4.9		TEH_07030	29.83	S
33	dihydroxyacetone kinase nucleotide-binding subunit DhaL	gi|352516447	21888.09961	5.36	dhaL	TEH_02730	31.02	T
34	putative ribosome-associated protein	gi|352517920	21275.89063	5.21		TEH_17460	41.02	J
35	putative tRNA uridine-sulfurtransferase	gi|352518309	41922.57813	4.97		TEH_21350	42.12	J
36	putative tRNA uridine-sulfurtransferase	gi|352518309	41922.57813	4.97		TEH_21350	42.12	J
37	alcohol dehydrogenase	gi|352516634	43324.55078	5.04	adh	TEH_04600	67.92	C

38	alcohol dehydrogenase	gi|352516634	43324.55078	5.04	adh	TEH_04600	81.07	C
39	putative RNA methyltransferase	gi|352517636	52304.58984	8.18		TEH_14620	38.48	J
40	S-adenosylmethionine-tRNA ribosyltransferase-isomerase	gi|352516385	38594.66016	4.96	queA	TEH_02110	23.10	J
41	oxidoreductase	gi|352517258	31532.75	4.84		TEH_10840	35.75	C
42	aldo-keto reductase	gi|352516538	31997.21094	5.02		TEH_03640	31.03	Q
44	UspA family protein	gi|352518338	17457.93945	4.65		TEH_21640	70.01	T
45	iron-binding protein	gi|352518683	17759.57031	4.52		TEH_25090	45.92	P
46	glycerol-3-phosphate dehydrogenase	gi|352517896	36444.80859	5.44	gpsA	TEH_17220	29.96	C
47	N-acetylmuramic acid 6-phosphate etherase	gi|352518617	32040.61914	5.37	murQ	TEH_24430	34.58	M
48	cysteine synthase CysK	gi|352516768	32563.83008	5.15	cysK	TEH_05940	71.29	E
50	putative phosphopantothenoylcysteine synthetase	gi|352518051	27529.33008	5.7	coaB	TEH_18770	30.82	H
51	NAD(P)-dependent glutamate dehydrogenase	gi|352516993	50173.28125	5.64	gdh	TEH_08190	43.05	R
52	L-lactate oxidase	gi|352518714	41563.91016	5.15	lctO	TEH_25400	40.82	C
53	tryptophanyl-tRNA synthetase	gi|352517495	37431.12109	5.54	trpS	TEH_13210	71.07	J
54	acyl-ACP--phosphate acyltransferase	gi|352518404	35799.76953	5.5	plsX	TEH_22300	42.86	I
55	hypothetical protein TEH_01650	gi|352516339	37519.07031	5.44		TEH_01650	31.07	S
56	pyruvate formate-lyase	gi|352517732	85601.42188	5.22	pflB	TEH_15580	63.20	S
57	formate--tetrahydrofolate ligase	gi|352517552	59667.39844	5.69	fhs	TEH_13780	51.02	H
58	phosphoenolpyruvate-protein	gi|352518123	63700.78125	4.68	ptsI	TEH_19490	73.21	G

	phosphotransferase							
59	thioredoxin reductase	gi|352516438	34426.03125	4.67	trxB	TEH_02640	45.91	O
60	citrate lyase alpha subunit	gi|352516973	54957.89844	4.77	citF	TEH_07990	54.92	C
62	glycerol dehydrogenase	gi|352516658	41312.78906	4.76	gldA	TEH_04840	67.29	C
63	pyruvate kinase	gi|352517072	63307.32031	4.81	pyk	TEH_08980	69.75	G
64	transketolase	gi|352517519	72335.64844	4.77	tkt	TEH_13450	28.38	G
65	betaine aldehyde dehydrogenase	gi|352516633	53424.14063	4.85	gbsA	TEH_04590	55.48	E
66	alcohol dehydrogenase	gi|352518466	44039.91016	4.92		TEH_22920	52.49	C
67	phenylalanyl-tRNA synthetase beta chain	gi|352517494	90094.24219	4.89	pheT	TEH_13200	65.82	J
68	leucyl-tRNA synthetase	gi|352516280	91705.14063	5.02	leuS	TEH_01060	41.05	J
69	GTP-binding protein TypA	gi|352517697	68540.15625	4.95	typA	TEH_15230	66.19	D
70	glucosamine-6-phosphate synthase	gi|352517655	66188.8125	4.94	glmS	TEH_14810	73.92	G
71	nicotinate phosphoribosyltransferase	gi|352517301	55510.94141	5.21	pncB	TEH_11270	70.01	H
72	elongation factor G	gi|352518461	77058.27344	4.83	fusA	TEH_22870	45.91	S
73	60 kDa chaperonin	gi|352517299	57740.67969	4.47	groL	TEH_11250	67,21	O
74	citrate lyase alpha subunit	gi|352516973	54957.89844	4.77	citF	TEH_07990	54.37	C
75	NADH peroxidase	gi|352516444	49935.30078	4.67	npr	TEH_02700	42.48	C
76	putative oxidoreductase	gi|352517589	44542.26953	4.54		TEH_14150	19.54	C
77	30S ribosomal protein S1	gi|352518176	44195.5	4.42	rpsA	TEH_20020	49.58	J
78	elongation factor Tu	gi|352518460	43469.80078	4.82	tuf	TEH_22860	68.72	J
79	elongation factor Tu	gi|352518460	43469.80078	4.82	tuf	TEH_22860	68.72	J

80	dihydrolipoamide dehydrogenase	gi|352517700	49358.35938	4.77	lpd	TEH_15260	64.21	C
81	glycine betaine ABC transporter ATP-binding protein	gi|352518036	47005.07031	4.83	opuAA	TEH_18620	81.01	M
82	aldo-keto reductase	gi|352516193	34397.17188	4.91		TEH_00190	67.02	Q
83	pyridoxal kinase	gi|352518458	29882.96094	5.1	pdxK	TEH_22840	56.87	H
84	triose-phosphate isomerase	gi|352517947	27490.80078	4.75	tpiA	TEH_17730	53.82	G
85	putative NADH dehydrogenase	gi|352518640	44569.46094	5.31		TEH_24660	61.76	C
86	catabolite control protein A	gi|352517890	36383.98828	5.17	ccpA	TEH_17160	56.82	T
87	putative 6-phosphogluconolactonase	gi|352516729	37728.51953	5.14	pgl	TEH_05550	61.29	G
88	pyruvate dehydrogenase E1 component alpha subunit	gi|352517703	41213.78906	5.03	pdhA	TEH_15290	88.21	C
89	small heat shock protein	gi|352516333	16030.65039	4.43		TEH_01590	92.10	O
90	hypothetical protein TEH_24310	gi|352518605	19537.85938	4.73		TEH_24310	56.88	S
91	hypothetical protein TEH_10060	gi|352517180	19031.71094	4.83		TEH_10060	21.86	S
92	phosphocarrier protein HPr	gi|352518124	9301.650391	4.88	ptsH	TEH_19500	81.76	G
93	acylphosphatase	gi|352517859	9924.990234	5.45	acyP	TEH_16850	75.45	C
94	50S ribosomal protein L31 type B	gi|352517164	9974.75	5.54	rpmE2	TEH_09900	68.50	R
95	alanine dehydrogenase	gi|352518048	39665.58984	5.02	ald	TEH_18740	58.88	E
96	hypothetical protein TEH_23400	gi|352518514	64126.66016	5.4		TEH_23400	54.78	S
97	6-phosphofructokinase	gi|352517071	34427.62891	5.51	pfk	TEH_08970	78.90	G
98	putative 2-dehydropantoate 2-reductase	gi|352517755	34262.53125	5.63		TEH_15810	42.18	S

99	glyceraldehyde-3-phosphate dehydrogenase	gi|352517949	35758.14063	4.79	gap	TEH_17750	78.90	G
100	glyceraldehyde-3-phosphate dehydrogenase	gi|352517949	35758.14063	4.79	gap	TEH_17750	51.20	G
101	aminopeptidase PepC	gi|352517119	50155.57031	4.71	pepC	TEH_09450	61.04	E
102	citrate lyase beta subunit	gi|352516972	32347.69922	4.71	citE	TEH_07980	62.01	G
103	chaperone protein DnaK	gi|352517474	66743.42969	4.38	dnaK	TEH_13000	78.91	O
104	dipeptidase PepV	gi|352516420	51963.28906	4.56	pepV	TEH_02460	49.01	E
105	ATP synthase beta subunit	gi|352517934	50876.73047	4.52	atpD	TEH_17600	78.52	C
106	pyruvate kinase	gi|352517072	63307.32031	4.81	pyk	TEH_08980	72.45	G
107	glutamyl-tRNA synthetase	gi|352516197	55194.92969	5.22	gltX	TEH_00230	19.95	J
108	adenylosuccinate synthetase	gi|352516187	48127.51172	5.52	purA	TEH_00140	52.21	F
109	serine hydroxymethyltransferase	gi|352516340	44895	5.58	glyA	TEH_01660	65.14	E
110	cell division protein FtsZ	gi|352516934	44197.46094	4.61	ftsZ	TEH_07600	67.82	D
111	enolase	gi|352517946	46628.55859	4.58	eno	TEH_17720	86.21	G
112	phosphoglycerate kinase	gi|352517948	42176.76172	4.91	pgk	TEH_17740	82.52	G
113	alcohol dehydrogenase	gi|352516634	43324.55078	5.04	adh	TEH_04600	71.24	C
114	glyceraldehyde-3-phosphate dehydrogenase	gi|352517949	35758.14063	4.79	gap	TEH_17750	69.52	G
115	phosphoglycerate mutase	gi|352518465	25426.99023	5.15	gpm	TEH_22910	61.23	G
116	putative ribulosamine/erythrulosamine 3-kinase	gi|352516518	32736.13086	5.16		TEH_03440	51.36	S
117	ribose-5-phosphate isomerase A	gi|352518464	24621.07031	5.37	rpiA	TEH_22900	31.50	G
118	putative ferredoxin	gi|352516835	47451.01172	5.3		TEH_06610	30.11	C

119	putative phosphopantothenoylcysteine decarboxylase	gi|352518052	19870.49023	5.56	coaC	TEH_18780	19.21	H
120	peptide methionine sulfoxide reductase MsrA	gi|352517759	20019.65039	5.15	msrA	TEH_15850	23.56	O
121	single-stranded DNA-binding protein	gi|352516181	18864.31055	4.76	ssb	TEH_00080	56.42	L
122	superoxide dismutase	gi|352517775	22700.05078	5.06	sodA	TEH_16010	61.32	P
123	hypothetical protein TEH_19940	gi|352518168	17557.5293	4.6		TEH_19940	28.60	S
124	CTP--glycerol-3-phosphate cytidylyltransferase	gi|352517773	15603.9502	5.08	tagD	TEH_15990	43.50	M

[a] the percentage of amino acid coverage (peptides observed/theoretical value from sequence data) is shown.