

Supplementary Table 1. ICP-MS operating conditions

Element (m/z)	Mg (24), K (39), Ca (43), Mn (55), Fe (57), Cu (63), Zn (66), Rb (85)
Internal Standard Element (m/z)	Y (89)
Plasma power (W)	1200
Carrier gas flow rate (L min ⁻¹)	1.15
Sample depth	7.5
Sample flow rate (mL min ⁻¹)	0.40
Spray chamber temperature (°C)	2
Extraction lens 1 (V)	-150
Extraction lens 2 (V)	-70
Integration time per point (sec)	0.1
Point per mass	3

Supplementary Table 2. Relationship between the element concentrations in *S. Typhimurium* MA6926 (wild type, n=16) and SA123*znuA::kan*, (n=16) strains. Pearson's correlation coefficients are shown. Significant correlation coefficients (95% confidence level) are bold.

MA6926 (wild type)	Mg	K	Ca	Mn	Fe	Cu	Zn	Rb
Mg	1							
K	-0.187	1						
Ca	-0.289	0.174	1					
Mn	0.679	-0.560	-0.137	1				
Fe	0.627	-0.550	-0.229	0.772	1			
Cu	0.433	-0.591	0.029	0.837	0.563	1		
Zn	0.257	0.055	0.504	0.327	0.029	0.574	1	
Rb	-0.398	0.147	0.106	-0.429	-0.244	-0.499	-0.420	1
SA123 (<i>znuA::kan</i>)	Mg	K	Ca	Mn	Fe	Cu	Zn	Rb
Mg	1							
K	-0.075	1						
Ca	-0.184	0.613	1					
Mn	0.782	0.279	0.116	1				
Fe	0.468	-0.329	-0.206	0.404	1			
Cu	0.689	-0.054	-0.250	0.646	0.557	1		
Zn	-0.693	-0.350	0.143	-0.789	-0.164	-0.550	1	
Rb	-0.243	0.746	0.783	-0.021	-0.196	-0.321	0.029	1

Supplementary Table 3. Differentially expressed proteins *S. Typhimurium* MA6926 (wild type) and SA123znuA::kan. Table shows the SwissProt accession number, the protein name, and the measured expression ratio between the two analysed strains grown in Zn depleted and Zn supplemented medium. Yeast enolase 1 is bold and was used as internal standard.

Accession	Description	MA6926:SA123znuA::kan_Ratio Zn ²⁺ depleted medium	MA6926:SA123znuA::kan_Ratio Zn ²⁺ supplemented medium
P15717	3-isopropylmalate dehydratase large subunit 1; (a)	(a)	
P66593	30S ribosomal protein S6;	0.46	0.56
P0A1V6	Ribose-phosphate pyrophosphokinase;	0.78	(a)
P0A1V4	Adenylate kinase;	0.77	0.81
P02936	Outer membrane protein A;	1.42	1.42
P66193	50S ribosomal protein L31 type B;	(b)	(b)
P10367	Histidine biosynthesis bifunctional protein hisIE;	(b)	
P64076	Enolase;	0.73	0.64
Q9L6N1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase;	0.93	0.88
P0A251	Alkyl hydroperoxide reductase subunit C;	0.84	0.58
P02910	Histidine-binding periplasmic protein;	1.84	1.22
P63411	Acetate kinase;	0.72	0.55
P68684	30S ribosomal protein S21;	(b)	
P64052	Elongation factor Ts;	0.59	0.8
P0A2M5	Uracil phosphoribosyltransferase;	0.55	0.69
P65889	Phosphoribosylaminoimidazole-succinocarboxamide synthase;	0.67	0.87
P02906	Sulfate-binding protein;	1.22	1.16
P0A1S2	DNA-binding protein H-NS;	0.64	0.71
Q7CQ05	Autonomous glycyl radical cofactor;	0.41	0.42
O33921	Glucose-1-phosphatase;	(a)	2.46
P66955	Transaldolase B;	0.98	1.13
P23905	D-galactose-binding periplasmic protein;	(a)	2.23
P0A1R6	DNA-binding protein HU-alpha;	0.47	0.81
Q8ZRP4	2,3,4,5-tetrahydropyridine-2.6-dicarboxylate N-succinyltransferase;	0.48	0.94
Q9ZF60	Glutamate/aspartate periplasmic-binding protein;	2.59	1.2
P66541	30S ribosomal protein S2;	0.31	0.51
Q8ZQU3	Succinate dehydrogenase flavoprotein subunit;	(a)	
P0A1P6	Glutamine synthetase;	0.76	0.58
P0A1P0	Glyceraldehyde-3-phosphate dehydrogenase;	0.63	0.68
Q7CPL7	50S ribosomal protein L17;	(b)	(b)
P58661	Aspartate aminotransferase;	1.04	0.68
P67605	UPF0265 protein yeeX;	(b)	
Q8ZQT5	Protein tolB;	1.88	1.48
Q56073	Chaperone protein dnaK;	0.73	0.8
P05989	Ketol-acid reductoisomerase;	1.16	1.13
P61179	50S ribosomal protein L22;	0.28	(b)
Q7CPK0	sn-glycerol-3-phosphate-binding periplasmic protein ugpB;	(a)	(a)
P26982	Protease do;	2.34	1.48
P0A2H9	Thiol:disulfide interchange protein dsbA;	2.32	1.45
Q9L4T0	S-ribosylhomocysteine lyase;	0.74	0.69
P0A7Z7	DNA-directed RNA polymerase subunit alpha;	0.69	0.7
P26976	Non-specific acid phosphatase;	0.25	(a)
P67537	UPF0250 protein ybeD;	(b)	
P0AA28	Thioredoxin-1;	0.61	0.71
P0A7X0	30S ribosomal protein S8;	0.42	0.75
P06196	Silent protein ushA(0);		(a)
P0A7W4	30S ribosomal protein S5;	0.35	0.61
P25077	Malate dehydrogenase;	2.83	0.93
Q9L9I8	Thiamine-phosphate pyrophosphorylase;	(b)	
P60446	50S ribosomal protein L3;	0.45	0.5
P06179	Flagellin;	(a)	1.02
P66038	6,7-dimethyl-8-ribityllumazine synthase;	0.47	0.92
P66032	3,4-dihydroxy-2-butanone 4-phosphate synthase;	(b)	
P67904	30S ribosomal protein S10;	0.45	0.61
P0A2C5	D-ribose-binding periplasmic protein;	0.93	1.48
P06202	Periplasmic oligopeptide-binding protein;	4.06	1.57
Q7CR87	Chaperone surA;	2.41	1.39
P0A2B1	30S ribosomal protein S20;	(b)	
P0A1H5	Elongation factor Tu;	1.11	0.68
P0A1H3	Elongation factor G;	1.08	0.78
P53636	Superoxide dismutase [Cu-Zn] 1;	1.05	1.34
P17215	Leu/Ile/Val/Thr-binding protein;	(a)	1.73
P0A2A3	50S ribosomal protein L1;	0.48	0.62
P0A2A1	50S ribosomal protein L19;	(b)	
P66764	S-adenosylmethionine synthetase;	(a)	(a)

Accession	Description	MA6926:SA123znuA::kan_Ratio Zn ²⁺ depleted medium	MA6926:SA123znuA::kan_Ratio Zn ²⁺ supplemented medium
Q8ZRE7	UPF0345 protein yaiE;		(b)
O54297	30S ribosomal protein S4;	0.46	0.49
P0A1E3	Cysteine synthase A;	0.94	0.57
P65702	Phosphoglycerate kinase;	0.72	0.65
P69936	NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG;	0.57	1.2
P00499	ATP phosphoribosyltransferase;	(b)	
Q7CR46	Anti-adapter protein iraP;	(b)	(a)
O68926	Bacterioferritin;	(a)	
P0A1D5	10 kDa chaperonin;	0.68	0.62
P00924	Enolase 1;		
P0A1D3	60 kDa chaperonin;	0.72	0.58
Q8ZP65	Probable thiol peroxidase;	0.46	0.55
P66313	50S ribosomal protein L6;	0.47	0.59
P0A1Z2	Chaperone protein skp;	2.14	0.9
P0A9Y9	Cold shock-like protein cspC;	0.53	0.44
P41031	Thiosulfate-binding protein;	1.75	1.27
Q8ZP20	Periplasmic trehalase;	(a)	3.22
P0A2R4	DNA-directed RNA polymerase subunit beta';	(a)	
Q8ZKQ1	Autoinducer 2-binding protein lsrB;	(a)	1.51
P0A299	50S ribosomal protein L7/L12;	0.57	0.54
P0A297	50S ribosomal protein L10;	0.66	0.76
P40732	Acetylornithine/succinyldiaminopimelate aminotransferase;	(b)	
Q8ZK81	30S ribosomal protein S18;	0.23	
Q8ZK80	50S ribosomal protein L9;	0.58	0.57
P0A7K0	50S ribosomal protein L11;	0.29	0.54
Q8ZKP7	Triosephosphate isomerase;	0.53	0.75
P0A1W6	Leucine-specific-binding protein;	4.81	(a)
P0A283	Glucose-specific phosphotransferase enzyme IIA component;	0.73	0.71
P40720	Fumarate hydratase class I, aerobic;	(a)	
P20753	Peptidyl-prolyl cis-trans isomerase A;	(a)	(a)
P10372	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase;	(b)	
P10370	Histidinol dehydrogenase;	(b)	
O54296	30S ribosomal protein S11;	(b)	
P0A1F8	Aspartate-semialdehyde dehydrogenase;	(b)	
P0A1S4	DNA-binding protein stpA;	(b)	
P0A2A1	50S ribosomal protein L19;	(b)	
P0A2B3	30S ribosomal protein S7;	(b)	
P0A2C7	Spermidine/putrescine-binding periplasmic protein;	(b)	
P0A7V6	30S ribosomal protein S3;	(b)	
P0AA02	Transcription antitermination protein nusG;	(b)	
P14146	Virulence transcriptional regulatory protein phoP;	(b)	
P16657	Enoyl-[acyl-carrier-protein] reductase [NADH];	(b)	
P60726	50S ribosomal protein L4;	(b)	
P66643	30S ribosomal protein S9;	(b)	
P67617	Probable Fe(2+)-trafficking protein;	(b)	
Q8ZLM1	30S ribosomal protein S13;	(b)	
Q8ZQS2	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase;	(b)	
O54296	30S ribosomal protein S11;	(b)	
P0A1F8	Aspartate-semialdehyde dehydrogenase;	(b)	
P0A1S4	DNA-binding protein stpA;	(b)	
P0A2A1	50S ribosomal protein L19;	(b)	
P0A2B3	30S ribosomal protein S7;	(b)	
P0A2F6	Single-stranded DNA-binding protein;	(a)	
P55900	Phosphoserine aminotransferase;	(a)	
P62405	50S ribosomal protein L5;	(a)	
P65215	50S ribosomal protein L5;	(a)	
Q7CPD8	UPF0438 protein yifE;	(a)	
Q7CPL4	50S ribosomal protein L16;	(a)	
Q7CPP7	50S ribosomal protein L21;	(a)	
Q8ZL56	2,3-bisphosphoglycerate-independent phosphoglycerate mutase;	(a)	
Q8ZLD7	2,3-bisphosphoglycerate-independent phosphoglycerate mutase;	(a)	
P0A1R8	DNA-binding protein HU-beta	(b)	
P0A2C5	D-ribose-binding periplasmic protein	(b)	
P0A8B8	UPF0133 protein ybaB	(b)	
P52616	Phase 2 flagellin	(b)	
P66170	50S ribosomal protein L29	(b)	
P67091	Universal stress protein F	(b)	
Q8ZRE7	UPF0345 protein yaiE	(b)	

(a) Exclusively found in the MA6926 (wild type) strain

(b) Exclusively found in the SA123znuA::kan strain