



Supplementary Figure 1. The MS/MS spectrum of acetylated peptides from *rpoC* and superoxide dismutase. (a) The MS/MS spectrum of an acetylated peptide from *rpoC*. The peptide sequence is TLKPEk(Ac)DGLFCEK; (b) The MS/MS spectrum of the TMT-labeled peptide sVIVVGPQLk from *rpoC*. The inset displays intensities of the reported ions at m/z 128 (mc²155-pMV261) and m/z 130 (mc²155-MS5175); (c) The MS/MS spectrum of an acetylated peptide from superoxide dismutase. The peptide sequence is GVNDAlAk(Ac)LEEAR. The inset shows the ion intensity of the same peptide from mc²155-pMV261 (solid line) and mc²155-MS5175 (dotted line). (d) The MS/MS spectrum of the TMT-labeled peptide AIWNVNVNWQDVQVR from superoxide dismutase. The inset shows intensities of the reported ions at m/z 128 (mc²155-pMV261) and m/z 130 (mc²155-MS5175).

Supplementary Table 1. Primers used in PCR and RT-PCR this work.

primer name	primer sequence
Msm5175For	CGCCGCCGGATCCTGTGCAAGTTACTGTGCTCAGCG
Msm5175Rev	CCCAAGCTTTCACCTTATCGTCGTCATCCTTGTAATCGGCCGA GCGGTTGAGCA
pMV261Rev	GGCAGTCGATCGTACGCTAG
MSMEG_5175-F	TGGCGGCACTACATGATGGC
MSMEG_5175-R	GCAGATCGTCGATGTTCTGGGT
KatG2-F	TGGAAGACCTCGGAGACGACGGAGAACG
KatG2-R	ATAAACCTCGGCCACGGCACGCAGCACC
rpoD-F	GTCCGGCGACTTCGTGT
rpoD-R	TCTTCGGCGTTGAGCAG

Supplementary Table 2. Up-regulated proteins in mc²155-MS5175 compared with mc²155-pMV261

accession	protein description	score	coverage (%)	unique peptides	peptides	mc ² 155-5175/ mc ² 155-pMV261	variability (%)	MW (kDa)	p value (BH)
A0R0H2	ABC transporter oligopeptide binding protein	93	34.6	15	15	1.5	34.8	60	0.03
A0R0H5	ABC transporter	10	7.93	2	2	1.5	7.9	58.5	0.00
A0R0H7	Acyl-CoA dehydrogenase	103	43.46	13	13	1.4	44.5	43.4	0.02
A0QS90	Alcohol dehydrogenase, class IV	158	62.08	17	17	1.9	33.4	40.2	0.01
A0R2P9	Aldo/keto reductase	26	19.71	6	6	1.6	34.2	38	0.02
A0QZ05	Aliphatic sulfonate binding protein	18	17.35	3	3	1.3	30	35.7	0.03
A0QVQ0	Alkanesulfonate monooxygenase family protein	211	64.68	21	23	1.4	25.7	41.6	0.01
A0QZ04	Alkanesulfonate monooxygenase	28	24.73	5	6	1.5	23.7	40.5	0.01
A0QQN5	Amidase, hydantoinase/carbamoylase	45	24.34	9	9	1.3	22.3	45.1	0.01
A0R5J4	Catalase	18	16.5	4	4	1.3	7.2	32.9	0.00
A0QTD6	ChaB protein	25	34.53	5	5	1.4	9.6	15.3	0.03
A0R0H6	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase-like flavin-dependent oxidoreductase	52	25.22	8	8	1.6	19.4	50.5	0.02
A0QTS9	Conserved domain protein	270	74.55	30	30	1.3	34.3	24.7	0.00
A0QVH0	Cupin 2, conserved barrel	18	31.63	3	3	3	39.5	10.9	0.04
A0QS50	Cyclopropane-fatty-acyl-phpholipid synthase	19	20.34	2	5	2.1	21.7	33.3	0.01
A0QX02	Cysteine desulfurase	380	71.01	26	26	1.3	39.8	43.9	0.00
A0R692	DNA protection during starvation protein	155	77.6	15	15	1.3	28.1	20.3	0.02
A0QNP2	Extracellular solute-binding protein, family protein 3	205	64.62	16	16	1.4	33.8	36	0.02
A0QWZ9	FeS assembly protein SufB	841	81.76	43	43	1.3	34.8	52.7	0.01
A0R0F4	Formamidase	41	21.05	6	6	1.7	32.4	44.5	0.02
A0QR33	Glutamate-1-semialdehyde 2,1-aminomutase	374	73.61	24	24	1.3	30	46.7	0.03

accession	protein description	score	coverage (%)	unique peptides	peptides	mc ² 155-5175/ mc ² 155-pMV261	variability (%)	MW (kDa)	p value (BH)
A0R5J3	Hemerythrin HHE cation binding domain subfamily protein, putative	39	68.56	7	7	1.5	15.8	21.4	0.02
A0QV17	Hemerythrin HHE cation binding region	70	68.75	12	12	1.5	32.1	21.2	0.00
A0R597	Inorganic pyrophosphatase	814	54.94	11	11	1.4	40.6	18.3	0.02
A0R713	Lactoylglutathione lyase	12	13.91	2	2	1.3	13	15.9	0.03
A0R280	Lipoprotein	47	23.38	4	4	1.5	38.7	21.6	0.02
A0QRT9	Mpr protein	24	27.44	4	4	1.5	11.9	22.9	0.04
A0R2N3	NAD-dependent protein deacylase Sir2	273	45	10	10	3.3	40.5	26.1	0.03
A0QQY0	Polyphosphate kinase 2 superfamily protein	153	64.41	20	20	1.3	21	33.8	0.01
A0QRW7	Prophage Lp1 protein 5	28	39.39	3	3	2.2	29.9	14.3	0.05
Q2YHI6	Rv1174c	26	34.82	3	3	1.8	21.5	12.1	0.02
A0QQS8	Short chain dehydrogenase	225	70.03	28	29	1.3	27.9	33.2	0.01
A0R2W6	Steroid Delta-isomerase	99	79.03	9	9	1.7	46.6	13.2	0.01
A0R5Y7	Transcriptional regulator, MarR family	56	71.18	13	13	1.7	24.7	18.7	0.02

The p values were adjusted using the Benjamini-Hochberg procedure (ref. 25).

Supplementary Table 3. Down-regulated proteins in mc²155-MS5175 compared with mc²155-pMV261

accession	protein description	score	coverage (%)	unique peptides	peptides	mc ² 155-5175/ mc ² 155-pMV261	variability (%)	MW (kDa)	p value (BH)
A0QZ83	14 kDa antigen	13	28.97	2	2	0.4	25.7	15.9	0.01
A0QTQ0	3-dehydroquinate dehydratase	30	33.1	3	3	0.6	30.5	15.6	0.04
A0R2I1	4Fe-4S ferredoxin, iron-sulfur binding protein	160	35.51	4	4	0.6	16.6	11.6	0.01
A0QV03	50S ribosomal protein L28	79	67.19	6	6	0.5	31.7	6.9	0.01
A0R2I5	50S ribosomal protein L31	194	86.67	6	6	0.5	38.2	8.3	0.00
A0QSL4	50S ribosomal protein L36	101	64.86	4	4	0.4	19.8	4.3	0.00
A0R6M2	6,7-dimethyl-8-ribityllumazine synthase	21	29.33	5	5	0.4	22.6	16.4	0.01
A0QXB1	ABC-type amino acid transport system, permease component	21	14.19	3	3	0.6	13.1	34.4	0.01
A0QXB0	ABC-type amino acid transport system, secreted component	527	85.42	14	14	0.4	41.3	30.7	0.00
A0QRS0	ABC-type transport system periplasmic substrate-binding protein	20	15.78	6	6	0.5	16.5	44.5	0.01
A0QPD1	Acetyltransferase	17	26.53	2	2	0.5	29.3	10.4	0.00
A0QT89	Anti-sigm factor, ChrR	12	19.67	2	2	0.6	8.8	13	0.02
A0R5B0	Anti-sigma factor antagonist	175	38.66	6	6	0.6	28	12	0.01
A0QTP3	Anti-sigma factor RshA	32	32.67	6	6	0.5	31.1	11.6	0.01
A0QW31	ATP/GTP-binding integral membrane protein	199	60.29	22	22	0.6	29	37.1	0.01
A0QSY5	Bifunctional protein FOLD	170	79.86	17	17	0.6	37.9	29.7	0.00
A0QXX7	Catalase-peroxidase 2	419	63.37	35	35	0.8	21.1	81.9	0.02
A0QTH0	Cationic amino acid transporter	14	3.44	2	2	0.6	22.2	52.1	0.00
A0R4P2	Conserved domain protein	25	88.89	2	2	0.3	39	7	0.00
Q3L893	Conserved domain protein	15	32.89	2	2	0.4	12.4	8.6	0.01
A0QNR0	Conserved hypothetical integral membrane protein Yrbe1a	11	12.78	3	3	0.6	14.3	27.6	0.03
A0R2B9	Conserved hypothetical membrane protein	31	27.86	4	4	0.6	22.3	21.3	0.01

accession	protein description	score	coverage (%)	unique	peptides	mc ² 155-5175/ mc ² 155-pMV261	variability (%)	MW (kDa)	p value (BH)
A0QX31	Conserved membrane protein	10	11.11	2	2	0.5	22.5	15.4	0.00
A0QS91	Conserved threonine rich protein	71	50	9	9	0.6	22	13.6	0.01
A0QQG9	Conserved transmembrane protein	27	17.08	5	5	0.6	20.8	26.1	0.01
A0QPZ9	Conserved transmembrane transport protein MmpL1	32	7.89	8	8	0.6	17	104.3	0.00
A0QT11	Cytidine deaminase	39	42.97	3	3	0.6	31.8	13.3	0.02
A0QVL8	Efflux protein	16	10.49	3	3	0.4	33.3	53.1	0.01
A0QT19	Endoribonuclease L-PSP superfamily protein	84	47.62	5	5	0.5	24.8	16.2	0.01
A0QVX3	Glutamate binding periplasmic protein	183	66.3	22	22	0.5	28	29	0.00
A0QVX1	Glutamate transporter permease protein GluD	15	13.71	2	2	0.6	16.8	32.2	0.01
A0QTS5	Glutaredoxin-like protein	66	67.07	4	4	0.6	38.8	8.6	0.03
A0QPD6	Glycosyl hydrolase family protein 3	118	56.59	15	15	0.5	37.3	39.1	0.01
A0QRC5	Glyoxalase/bleomycin resistance protein/dioxygenase	12	25.2	3	3	0.6	17.5	13.7	0.01
A0R2V1	Helix-turn-helix motif	52	36.73	5	5	0.6	29.5	16.2	0.00
A0R4K9	HIT family protein	98	67.61	7	7	0.6	24.8	15.6	0.00
A0QTR8	Hydrolase, alpha/beta fold family protein	48	37.94	6	6	0.5	19.9	27.4	0.01
A0QX83	Imidazoleglycerol-phosphate dehydratase	36	32.52	5	5	0.5	44.2	22.4	0.01
A0R269	Lipoprotein LprC	54	37.63	6	6	0.6	35.1	19.5	0.01
A0QZB3	L-lactate 2-monoxygenase	185	68.02	23	23	0.6	25.2	42.7	0.00
A0QZ03	LppI	54	26.2	4	4	0.6	42.2	23.2	0.00
A0QVQ4	LppU protein	15	43.7	4	4	0.6	16.2	14.7	0.01
A0R433	MarR-family transcriptional regulator	12	22.38	3	3	0.7	22.3	15.5	0.04
A0R4N7	MCE-family protein MCE4b	27	28.78	7	7	0.6	36.7	36.9	0.00
A0QW27	Methionine-R-sulfoxide reductase	84	64.23	11	11	0.6	41.5	15.4	0.02

accession	protein description	score	coverage (%)	unique	peptides	mc ² 155-5175/ mc ² 155-pMV261	variability (%)	MW (kDa)	p value (BH)
A0QXF9	Methyltransferase	13	20.99	3	3	0.6	10.4	27.4	0.00
A0R0C7	NAD/mycothiol-dependent formaldehyde dehydrogenase	377	81.27	23	23	0.6	21.3	38.4	0.00
A0R3S7	Non-homologous end joining protein Ku	147	58.81	18	18	0.6	20.7	35.7	0.01
A0QPX5	osmC-like protein	34	35.37	5	5	0.6	27.1	17.7	0.01
A0QSN8	PduO protein	71	39.39	4	4	0.6	19.5	13.3	0.02
A0QWK5	Peptidyl-prolyl cis-trans isomerase B PpiB	155	42.51	9	9	0.6	39.6	29.6	0.00
A0QNF6	Peptidyl-prolyl cis-trans isomerase	388	96.57	15	15	0.6	33.5	18.7	0.01
A0QWJ1	Preprotein translocase, YajC subunit	75	25.23	2	2	0.4	18.5	11.9	0.01
A0R4C5	Probable exported protein	32	25.09	6	6	0.6	36.4	28.6	0.00
A0R125	Probable serine/threonine-protein kinase PknH, putative	66	56.3	8	8	0.6	44.7	28.6	0.01
A0QX98	Prolipoprotein diacylglyceryl transferase	20	9.58	2	2	0.6	10.3	65	0.01
A0QV12	Putative conserved membrane protein	143	75.62	14	15	0.5	42.7	25.6	0.00
A0R5H3	Putative endoribonuclease L-PSP family	39	32.91	2	2	0.4	48.8	15.7	0.01
A0QPP7	Putative lipoprotein	24	19.16	3	3	0.5	19.4	25.7	0.02
A0QRB8	Putative Lsr2 protein	153	67.16	13	13	0.6	45.1	14.4	0.01
A0QZ40	Sec-independent protein translocase protein TatA	84	54.32	9	9	0.5	29.5	8.9	0.00
A0R652	Superoxide dismutase [Mn]	242	39.61	6	9	0.6	40.2	22.9	0.00
A0R1Y5	Tetratricopeptide repeat domain protein	108	59.46	13	13	0.6	32.6	31.1	0.01
A0QTP7	Transcriptional regulator WhiB	57	69.05	3	3	0.5	20.9	9.3	0.01
A0QTG3	Transcriptional regulator WhiB2	53	41.86	7	7	0.6	19.2	14.4	0.03
A0QPM3	Transcriptional regulator, MarR family	15	23.13	2	2	0.6	6.8	16.7	0.02
A0R438	Transporter, major facilitator family protein	12	5.83	2	2	0.6	24.5	53.5	0.00
A0R3H9	Type I antifreeze protein	26	43.4	5	5	0.6	19.8	10.7	0.02

accession	protein description	score	coverage (%)	unique	peptides	mc ² 155-5175/ mc ² 155-pMV261	variability (%)	MW (kDa)	p value (BH)
A0R052	Ubiquinol-cytochrome C reductase QcrB	176	24.18	13	13	0.6	37.7	60.2	0.00
A0R2V3	Universal stress protein family protein	152	50.71	13	13	0.6	41.9	30.1	0.00
A0QS40	UPF0336 protein MSMEG_1340	87	58.23	11	11	0.6	35.6	17.6	0.00
A0QQI3	Zinc finger, UBP-type	21	51	4	4	0.6	34.2	11.5	0.02

The p values were adjusted using the Benjamini-Hochberg procedure (ref. 25).