

Supplementary table 2. Cu-binding motifs in the differentially expressed proteins.

Protein name	Gene name	Cu-binding motifs
tyrosyl-tRNA synthetase	<i>tyrS</i>	H(x) ₂ H M(X) ₀ H
hypothetical protein SPD_0547	<i>SPD_0547</i>	H(X) _{4,5,10} H H(X) ₉ M M(X) _{7,8} H H(X) ₃ C C(X) ₂ H
catabolite control protein A	<i>ccpA</i>	M(X) _{0,2,5,7} H
glutamate dehydrogenase	<i>gdhA</i>	M(X) ₅ H C(X) ₉ H
aromatic amino acid aminotransferase	<i>araT</i>	H(X) _{1,5,9} M M(X) ₂ H
inosine 5'-monophosphate dehydrogenase	<i>guaB</i>	H(X) ₁ H H(X) _{0,2,7,8} M M(X) _{8,10} H
lactate oxidase	<i>lctO</i>	H(X) _{4,5} H H(X) _{1,8} M M(X) _{5,9} H H(X) _{2,8} C
recombinase A	<i>recA</i>	H(X) _{6,7} M M(X) ₁₂ M
aminopeptidase C	<i>pepC</i>	H(X) ₁ M M(X) _{1,8} H
glucosamine-1-phosphate acetyltransferase	<i>glmU</i>	H(X) _{0,1,2,9,11} H H(X) _{0,2,3,6} M M(X) _{2,5,7,8,10} H H(X) ₆ C M(X) ₈ M
acetyl-CoA carboxylase biotin carboxylase subunit	<i>accC</i>	H(X) _{1,2,4,9,11} H H(X) _{1,3,4,8,10} M M(X) _{6,7,9,10} H H(X) _{3,5,8,10} C M(X) ₁₂ M
glutamyl aminopeptidase PepA	<i>pepA</i>	H(X) _{1,11} H H(X) _{0,5,6,7,9} M C(X) _{4,6} H
threonyl-tRNA synthetase	<i>thrS</i>	H(X) _{0,1,2,3,5,6,7,8,9,10,11,12} H H(X) _{3,4,6,7,8,10} M M(X) _{0,1,3,4,5,8,10} H C(X) _{2,3,9} H M(X) _{8,12} M
GTP-binding protein EngA	<i>engA</i>	H(X) _{1,4,5,10} M M(X) _{0,4} H
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	<i>murA-2</i>	H(X) _{2,5,8,9} H H(X) _{2,3,4,5,6,10} M M(X) _{2,5,10} H H(X) ₈ C C(X) ₉ H M(X) _{8,12} M
pneumolysin	<i>ply</i>	H(X) ₁ M M(X) _{7,9} H
cell division protein DivIVA	<i>divIVA</i>	H(X) ₇ H M(X) ₈ M
hypothetical protein SPD_0310	<i>SPD_0310</i>	H(X) _{0,8,11} H H(X) _{5,9} M M(X) _{1,4} H M(X) ₈ M
UDP-N-acetylmuramate--L-alanine ligase	<i>murC</i>	H(X) _{0,3,4,6,9,10,11} H H(X) _{1,2,6,7,8,9} M M(X) _{1,2,4,5,6,7} H
3-oxoacyl-(acyl carrier protein) synthase II	<i>fabF</i>	H(X) _{4,5} H H(X) _{0,4,9} M M(X) _{1,3,7} H C(X) ₃ H M(X) ₈ M
metallo-beta-lactamase domain-containing protein	<i>SPD_0130</i>	H(X) _{1,2,3,4,6,8,10,12} H H(X) _{1,4,8} M M(X) _{2,3,10} H H(X) _{7,11} C
adenylosuccinate synthetase	<i>purA</i>	H(X) _{5,11} H M(X) ₁ H
PTS system mannose-specific transporter subunit IIAB	<i>manL</i>	H(X) ₇ H H(X) ₄ M M(X) _{1,8} H
thiamine biosynthesis protein ThiI	<i>thiI</i>	M(X) ₁₀ H
capsular polysaccharide biosynthesis protein	<i>SPD_1619</i>	H(X) _{3,9} H H(X) _{6,9} M M(X) _{9,10} H C(X) ₄ H
Cof family protein/peptidyl-prolyl cis-trans isomerase	<i>SPD_1367</i>	H(X) _{1,4,10} H H(X) _{6,7,8,9,10} M M(X) _{3,5,10} H
CTP synthetase	<i>pyrG</i>	H(X) _{1,8,10} H H(X) ₉ M M(X) _{2,4,6,9} H C(X) ₂ H M(X) ₈ M
sugar ABC transporter ATP-binding protein	<i>SPD_0740</i>	H(X) _{1,5,6,10} H H(X) _{1,3,5,7,8} M M(X) _{1,3} H
enoyl-CoA hydratase	<i>SPD_0378</i>	H(X) ₂ M M(X) ₁ H H(X) ₃ C M(X) ₁₂ M
lysyl-tRNA synthetase	<i>lysS</i>	H(X) _{0,2,5,12} H H(X) _{0,6,7,8} M M(X) _{3,8} H
glyceraldehyde-3-phosphate dehydrogenase	<i>gapN</i>	M(X) ₈ M
ATP-dependent Clp protease ATP-binding subunit ClpE	<i>clpE</i>	H(X) _{0,4,7} H H(X) _{0,3,5} M M(X) _{0,2,6} H M(X) ₈ M C(X) ₂ C

ribonucleotide-diphosphate reductase subunit alpha	<i>nrdE</i>	$H(X)_{5,8,9}H$ $H(X)_{6,10}M$ $M(X)_{1,2,3}H$ $M(X)_{12}M$ $C(X)_2C$
phosphoglucosamine mutase	<i>glmM</i>	$H(X)_3M$ $M(X)_{4,5}H$
metallo-beta-lactamase superfamily protein	<i>SPD_0533</i>	$H(X)_{1,3}H$ $H(X)_{4,8,9}M$ $M(X)_{4,5}H$
ribose-phosphate pyrophosphokinase	<i>prs2</i>	$H(X)_{1,6}M$ $M(X)_9H$ $H(X)_{1,10}C$
manganese-dependent inorganic pyrophosphatase	<i>ppaC</i>	$H(X)_0H$ $M(X)_{3,7}H$
DNA-directed RNA polymerase subunit alpha	<i>rpoA</i>	$H(X)_{9,10}M$ $C(X)_9H$
proline dipeptidase PepQ	<i>pepQ</i>	$H(X)_{3,6,10}H$ $H(X)_{3,5,7,10}M$ $M(X)_{2,10}H$ $M(X)_{8,12}M$
amino acid ABC transporter ATP-binding protein	<i>glnQ</i>	$H(X)_3H$ $H(X)_1M$ $M(X)_4H$