**Table S1 Differences in protein abundance associated with pathogenesis, antimicrobial activity and cell wall synthesis**

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| --- | --- | --- | --- | --- |
| Gene name | Fold change  (MSSA/MRSA) | BP | CC | MF |
| *entC2* | 2.70 | pathogenesis | extracellular region | metal ion binding |
| *SH1743* | 2.60 | pathogenesis  defense response to bacterium | extracellular region | - |
| *cap5A* | 2.40 | Pathogenesis  proton transport  lipopolysaccharide biosynthetic process | integral component of membrane | nucleotide binding  transporter activity  sugar efflux transmembrane |
| *hld* | 2.50 | pathogenesis | - | - |
| *kdpC* | 2.40 | potassium ion transmembrane transport | integral component of plasma membrane | potassium-transporting ATPase activity |
| *mraY* | 2.20 | cell cycle  cell division  cell wall organization  regulation of cell shape | plasma membrane | UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelyl-D-alanyl-D-alanine:undecaprenyl-phosphate transferase activity |
| *mscL* | 2.00 | ion transmembrane transport  cellular water homeostasis | plasma membrane  integral component of membrane | mechanically-gated ion channel activity |
| *isaB* | 0.50 | pathogenesis | extracellular region | - |
| *sarS* | 0.50 | pathogenesis  regulation of transcription | cytoplasm | DNA binding  DNA binding transcription factor activity |
| *ebh* | 0.50 | pathogenesis | plasma membrane  integral component of membrane | - |
| *mutS2* | 0.50 | mismatch repair  negative regulation of DNA recombination nucleic acid phosphodiester bond hydrolysis | - | endonuclease activity  mismatched DNA binding |
| *tpiA* | 0.45 | Pathogenesis  pentose-phosphate shunt | cytoplasm | triose-phosphate isomerase activity |
| *spa* | 0.45 | pathogenesis | cell wall  Membrane,  extracellular region | IgG binding |
| *sbi* | 0.45 | pathogenesis | extracellular region | IgG binding |
| *eno* | 0.45 | pathogenesis | cell surface  phosphopyruvate hydratase complex | magnesium ion binding |
| *rot* | 0.44 | pathogenesis  regulation of transcription, DNA-templated | integral component of membrane | DNA binding transcription factor activity |
| *dltC* | 0.44 | cell wall organization  regulation of cell shape  lipoteichoic acid biosynthetic process | - | D-alanyl carrier activity  teichoic acid D-alanylation  D-alanine [D-alanyl carrier protein] ligase activity |
| *ermA* | 0.43 | rRNA methylation  response to antibiotic | - | RNA binding  23S rRNA (adenine(2085)-N(6))-dimethyltransferase activity |
| *clpL* | 0.40 | Proteolysis  pathogenesis | - | peptidase activity |
| *mutL* | 0.38 | Mismatch repair | mismatch repair complex | ATP binding  ATPase activity  mismatched DNA binding  single-stranded DNA binding |
| *plsX* | 0.35 | fatty acid biosynthetic | cytoplasm | transferase activity, transferring acyl groups other than amino-acyl groups |
| *msrA2* | 0.33 | protein repair  oxidation-reduction  cellular protein modification process | - | peptide-methionine (S)-S-oxide reductase activity |
| *msrB* | 0.30 | protein repair  oxidation-reduction process  response to oxidative stress | - | peptide-methionine (R)-S-oxide reductase activity |
| *clfA* | 0.30 | cell wall  membrane  extracellular region | cell adhesion  pathogenesis | - |
| *sspB* | 0.25 | proteolysis | extracellular region  integral component of membrane | cysteine-type peptidase |
| *tetM* | 0.25 | response to antibiotic | - | translation elongation factor activity  GTP binding |
| *trxA* | 0.4 | protein folding  cellular response to oxidative stress | cytoplasm | oxidoreductase activity |
| *bsaA* | 0.4 | oxidation-reduction process  response to oxidative stress  cellular oxidant detoxification | - | glutathione peroxidase activity |
| *sar* | 0.46 | response to oxidative stress | - | - |