**Additional file 2 Proteins identified as differentially abundant in secretome of *S. aureus* RF122 and N305.**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Name of proteins identified in RF122 a | Spot b | *p*-value c | Fold d | Locus e | Access. f | log(E value) g | Cover. h | Mass i | NP j | PAI k | Loc. l |
| **CELLULAR PROCESSES AND SIGNALING** |
|  **Cell cycle control, cell division, chromosome partitioning** |
|  Probable transglycosylase IsaA | 22 | 4.99E-06 | 2.1 | isaA | Q2YWD9 | -19,11 | 26 | 28,2 | 4 | 0.83 | S |
|  **Cell wall/membrane/envelope biogenesis** |
|  Iron-regulated surface determinant protein B | 1, 2, 3, 4, 5, 6 | 3.93E-05 | 2.4 | isdB | Q2YX96 | -110,18 | 39 | 72,0 | 25 | 1.22 | W |
|  Lipoteichoic acid synthase | 7 | 4.53E-04 | 2.1 | ltaS | Q2YSL2 | -71,63 | 33 | 74,2 | 16 | 1.05 | C/M |
|  N-acetylmuramoyl-L-alanine amidase | 14, 16 | 7.29E-05 | 2.4 | SAB2519 | Q2YZ57 | -45,94 | 21 | 69,2 | 11 | 0.62 | S |
| **METABOLISM** |
|  **Nucleotide transport and metabolism**  |
|  Inosine-5'-monophosphate dehydrogenase | 19 | 1.05E-05 | 2.2 | guaB | Q2YVL6 | -22,08 | 13 | 52,7 | 5 | 0.20 | C |
|  **Inorganic ion transport and metabolism** |
|  Probable zinc-binding lipoprotein | 8 | 2.79E-04 | 2 | SAB2286c | Q2YW05 | -15,12 | 14 | 59,0 | 6 | 0.35 | C/M |
|  **Secondary metabolites biosynthesis, transport, and catabolism** |
|  D-alanine--poly(phosphoribitol) ligase subunit 1 | 18 | 4.14E-04 | 2.6 | dltA | Q2YWQ8 | -14,13 | 10 | 54,5 | 3 | 0.18 | C |
| **POORLY CHARACTERIZED** |
|  Glycerol ester hydrolase | 1, 2 | 9.76E-05 | 2.4 | geh | Q2YVD0 | -42,68 | 22 | 72,2 | 9 | 0.42 | S |
|  Staphylococcal enterotoxin C-bovine | 9, 10, 11, 12, 13 | 1.08E-06 | 3.8 | sec-bov | Q2YVN9 | -80,55 | 57 | 31,2 | 20 | 2.00 | S |
|  Probable exported protein | 17, 18 | 4.14E-04 | 2.6 | SAB0387 | Q2YVR3 | -15,00 | 8 | 56,3 | 4 | 0.19 | U |
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| **Additional file 2 (*continued*)** |
| Name of proteins identified in N305 a | Spot b | *p*-value c | Fold d | Locus e | Access. f | log(E value) g | Cover. h | Mass i | NP j | PAI k | Loc. l |
| **CELLULAR PROCESSES AND SIGNALING** |
|  **Post-translational modification, protein turnover, and chaperones** |
|  Foldase protein PrsA  | 40 | 4.21E-07 | 6.6 | prsA | J0L203 | -56.29 | 34 | 35.5 | 15 | 1.07 | C/M |
|  Coenzyme A disulfide reductase  | 29 | 2.21E-03 | 2 | cdr | J1EWL3 | -62.67 | 44 | 49.2 | 14 | 0.63 | C |
|  Alkyl hydroperoxide reductase subunit C  | 32, 34, 35, 36, 51, 52 | 1.28E-04 | 2 | ahpC | J1EYK8 | -19.09 | 27 | 20.9 | 3 | 0.30 | C |
|  Serine protease SplE  | 47, 48, 49 | 2.57E-04 | 3.3 | splE | J1EZ78 | -10.09 | 10 | 25.6 | 2 | 0.25 | C/M |
|  Serine protease SplF  | 48, 49 | 2.57E-04 | 3.3 | splF | J0KV93 | -56.13 | 72 | 25.6 | 15 | 1.89 | S |
|  Serine protease SplD  | 48 | 2.57E-04 | 3.3 | splD | J0L226 | -46.44 | 59 | 25.6 | 12 | 1.78 | S |
|  Serine proteinase (SplB) | 47 | 1.07E-04 | 3.2 | Newbould305\_0049 | J0UNB6 | -65.13 | 45 | 27.8 | 16 | 2.56 | S |
| **INFORMATION STORAGE AND PROCESSING** |
|  **Translation, ribosomal structure and biogenesis** |
|  Elongation factor Ts  | 36, 37, 42 | 1.51E-05 | 2 | tsf | J0KWZ6 | -91.77 | 68 | 32.4 | 21 | 1.56 | C |
| **METABOLISM** |
|  **Energy production and conversion** |
|  Pyruvate dehydrogenase E1 component alpha subunit  | 32 | 7.32E-04 | 2.4 | pdhA | J0KP28 | -8.58 | 7 | 41,3 | 2 | 0.15 | C |
|  L-lactate dehydrogenase  | 50, 51, 52 | 2.44E-04 | 2.4 | ldh | J1EXA2 | -31.90 | 22 | 34,3 | 6 | 0.54 | C |
|  **Amino acid transport and metabolism** |
|  Xaa-Pro dipeptidase-like protein | 32 | 7.32E-04 | 2.4 | Newbould305\_0180 | J0UNM4 | -9.93 | 9 | 39,5 | 3 | 0.30 | C |
|  Thimet oligopeptidase  | 25 | 1.53E-03 | 2.4 | pepB | J1EWN7 | -46.18 | 23 | 69,7 | 12 | 0.60 | C |
|  **Carbohydrate transport and metabolism** |
|  Glyceraldehyde-3-phosphate dehydrogenase  | 32, 34, 35, 36 | 4.15E-06 | 4.1 | gap | J0KSH5 | -17.63 | 22 | 36,2 | 5 | 0.46 | C |
|  Glucose-6-phosphate isomerase  | 30 | 2.18E-05 | 2.7 | pgi | J0UKP5 | -101.03 | 55 | 49,7 | 22 | 2.06 | C |
|  2,3-bisphosphoglycerate-dependent phosphoglycerate mutase  | 43, 44 | 6.54E-05 | 2.8 | gpmA | J1ET24 | -67.89 | 64 | 26,6 | 15 | 1.42 | U |
|  UTP--glucose-1-phosphate uridylyltransferase  | 32 | 7.32E-04 | 2.4 | Newbould305\_1539 | J1EUY4 | -40.81 | 35 | 44,8 | 12 | 0.75 | C |
|  Phosphoglycerate kinase  | 32, 33 | 7.32E-04 | 2.4 | pgk | J1EWC9 | -86.90 | 55 | 42,5 | 19 | 1.11 | C |
|  Enolase  | 28, 31 | 3.75E-04 | 2.3 | eno | J1EWJ2 | -104.19 | 57 | 47,0 | 20 | 1.15 | C |
|  Fructose-bisphosphate aldolase class 1  | 43 | 6.54E-05 | 2.8 | fda | J1EXA7 | -83.88 | 65 | 32,9 | 18 | 1.80 | U |

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| **Additional file 2 (*continued*)** |
| Name of proteins identified in N305 a | Spot b | *p*-value c | Fold d | Locus e | Access. f | log(E value) g | Cover. h | Mass i | NP j | PAI k | Loc. l |
|  **Lipid transport and metabolism** |
|  3-hydroxy-3-methylglutaryl CoA synthase  | 34 | 4.15E-06 | 4.1 | mvaS | J1EX99 | -26.02 | 30 | 40.9 | 9 | 0.60 | C |
|  **Inorganic ion transport and metabolism** |
|  Superoxide dismutase  | 51, 52 | 2.44E-04 | 2.4 | sodM | J0UM22 | -18,62 | 38 | 22.9 | 5 | 0.56 | S |
| **POORLY CHARACTERIZED** |
|  Alpha-hemolysin  | 39, 40, 41, 47 | 4.21E-07 | 6.6 | hla | J0KWK7 | -81.73 | 70 | 36.2 | 19 | 1.29 | S |
|  Gamma-hemolysin component C  | 40 | 4.21E-07 | 6.6 | hlgC | J1ET20 | -61.41 | 46 | 35.5 | 17 | 1.44 | S |
|  Superantigen-like protein  | 48 | 1.07E-04 | 3.2 | set11 | J1EYV1 | -20.88 | 28 | 25.7 | 5 | 0.50 | S |
|  Superantigen-like protein 7  | 46 | 1.32E-05 | 3.2 | set5 | J1EYV6 | -58.90 | 59 | 26.0 | 14 | 1.46 | S |

a Proteins of each strain are classified in COG. Names are given according to annotation of genome sequences

b Spot numbers (cf Figure 4)

c The ANOVA p-value indicates the degree of confidence of each fold change, determined by the SameSpot software on 3 biological replicates and 3 technical replicates

d The fold change is the rate of overexpression in one of the strains, determined by the SameSpot software

e Correspond to the commonly found name of the gene

f Accessions numbers are given according to references on UniProtKB [35]

g Probability of critical error in the protein identification given by the X!Tandem software [36]

h % of the protein covered with the identified peptides

i Theoretical mass as predicted from the protein sequence

j Number of identified peptides

k Protein abundance index ([1])

l Predicted localisation based on PSORTb software. S = Extracellular C = Cytoplasmic C/M = Cytoplasmic/Membrane W = Cell wall U = Unknown