**Additional file 3 Proteins identified as differentially expressed in the total lysate by *S. aureus* RF122 and N305.**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Name of proteins identified in RF122a | Spotb | *p*-valuec | Foldd | Locuse | Access.f | log(E value)g | Cover.h | Massi | NPj | PAIk | Loc.l |
| **CELLULAR PROCESSES AND SIGNALING** |
|  **Post-translational modification, protein turnover, and chaperones** |
|  Chaperone protein DnaK | 57, 62, 63, 64, 65 | 6.30E-06 | 4.3 | dnaK | Q2YT47 | -56.49 | 33 | 66.2 | 15 | 1.00 | C |
|  Alkyl hydroperoxide reductase subunit F | 57, 58, 59 | 5.01E-05 | 4.6 | ahpF | Q2YVH8 | -63.11 | 35 | 54.5 | 11 | 1.42 | C/M |
|  Alkyl hydroperoxide reductase subunit C | 56 | 7.40E-04 | 2.5 | ahpC | Q2YVK2 | -43.00 | 65 | 20.9 | 9 | 1.80 | C |
|  Probable protease (Zinc) protein | 53 | 3.76E-05 | 2 | SAB1141 | Q2YXN7 | -7.79 | 5 | 49.9 | 2 | 0.13 | U |
| **INFORMATION STORAGE AND PROCESSING** |
|  **Translation, ribosomal structure and biogenesis** |
|  Elongation factor Ts | 55 | 8.29E-04 | 3.7 | tsf |  |  |  |  |  |  |  |
| **METABOLISM** |
|  **Energy production and conversion** |
|  Phosphotransacetylase | 56 | 7.40E-04 | 2.5 | pta | Q2YS76 | -43.29 | 42 | 34.9 | 9 | 0.83 | U |
|  ATP synthase subunit beta | 53 | 3.76E-05 | 2 | atpD | Q2YUK1 | -115.92 | 56 | 51.3 | 21 | 1.33 | C/M |
|  **Carbohydrate transport and metabolism** |
|  Enolase | 53 | 3.76E-05 | 2 | eno | Q2YSE8 | -86.66 | 52 | 47.0 | 15 | 1.20 | C |
|  Fructose-disphosphate aldolase class 1 | 60, 61 | 4.33E-04 | 6.3 | fda | Q2YWF3 | -58.15 | 55 | 32.8 | 13 | 1.40 | U |
|  **Coenzyme transport and metabolism** |
|  Coenzyme A disulfide reductase | 54 | 2.19E-09 | 16 | cdr | Q2YWW1 | -67.61 | 29 | 49.2 | 8 | 0.42 | C |
| Name of proteins identified in N305a | Spotb | *p*-valuec | Foldd | Locuse | Access. f | log(E value) g | Cover.h | Massi | NPj | PAIk | Loc.l |
| **CELLULAR PROCESSES AND SIGNALING** |  |  |  |  |  |  |  |  |  |  |  |
|  **Post-translational modification, protein turnover, and chaperones** |
|  Thioredoxin reductase | 85 | 6.52E-07 | 2.4 | trxB | J1EWC4 | -45.94 | 42 | 33.5 | 11 | 1.10 | C |

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| --- |
| **Additional file 3 (*continued*)**  |
| Name of proteins identified in N305a | Spotb | *p*-valuec | Foldd | Locuse | Access.f | log(E value)g | Cover.h | Massi | NPj | PAIk | Loc.l |
|  Protein GrpE | 88 | 9.35E-08 | 2.8 | grpE | J0KVU6 | -7.36 | 13 | 23.9 | 2 | 0.25 | C |
|  Trigger factor | 86 | 6.05E-05 | 4.4 | tig | J0KVL9 | -32.61 | 16 | 48.4 | 5 | 0.46 | C |
|  **Defense mechanisms** |
|  Alkaline shock protein 23 | 98 | 3.80E-04 | 9.8 | asp23 | J0KY19 | -7.51 | 15 | 18.6 | 2 | 0.40 | U |
| **INFORMATION STORAGE AND PROCESSING** |
|  **Translation, ribosomal structure and biogenesis** |
|  Translation initiation factor IF-2 | 66 | 9.03E-04 | 2 | infB | J1ETX7 | -18.74 | 6 | 77.7 | 3 | 0.10 | C |
|  Elongation factor Tu | 87, 93 | 1.92E-05 | 3 | tuf | J1EVM7 | -21.55 | 12 | 43.0 | 3 | 0.35 | C |
|  **Replication, recombination and repair** |
|  DNA polymerase III subunit beta | 81 | 5.46E-05 | 3.4 | dnaN | J1EXP8 | -10.55 | 8 | 41.8 | 2 | 0.10 | C |
| **METABOLISM** |
|  **Energy production and conversion** |
|  L-lactate dehydrogenase | 83 | 1.50E-04 | 4 | ldh | J1EXA2 | -68.53 | 49 | 34.3 | 11 | 1.38 | C |
|  Phosphotransacetylase | 81 | 5.46E-05 | 3.4 | eutD | J0UJS8 | -49.54 | 45 | 34.8 | 10 | 0.92 | C |
|  L-lactate dehydrogenase | 74, 84 | 8.36E-07 | 5.7 | ldh | J0UMC4 | -64.29 | 42 | 34.5 | 21 | 1.75 | C |
|  **Amino acid transport and metabolism** |
|  Ornithine cyclodeaminase protein | 77 | 5.41E-04 | 4.1 | Newbould305\_0656 | J0KU07 | -5.02 | 8 | 37.7 | 2 | 0.17 | C |
|  Branched-chain-amino-acid aminotransferase | 76 | 6.62E-04 | 3.4 | Newbould305\_1079 | J0UJN7 | -51.83 | 47 | 40.0 | 10 | 0.78 | U |
|  Branched-chain alpha-keto acid dehydrogenase subunit E2 | 67 | 1.99E-02 | 3.7 | pdhC | J0KW19 | -13.81 | 11 | 46.4 | 2 | 0.13 | C |
|  D-alanine aminotransferase | 89, 91 | 3.62E-05 | 2.6 | dat | J1EZD0 | -40.52 | 41 | 31.7 | 8 | 0.59 | C |
|  Proline dipeptidase | 78, 80 | 8.49E-07 | 8.2 | Newbould305\_2310 | J0UJ09 | -19.86 | 20 | 39.2 | 5 | 0.50 | C |
|  Oligoendopeptidase F | 66 | 9.03E-04 | 2 | Newbould305\_2157 | J1EUN3 | -29.36 | 12 | 69.1 | 5 | 0.24 | C |
|  Ornithine carbamoyltransferase | 78 | 8.49E-07 | 8.2 | arcB | J0ULD6 | -76.37 | 48 | 37.7 | 14 | 1.36 | C |
|  **Carbohydrate transport and metabolism** |
|  Triosephosphate isomerase | 94 | 6.99E-04 | 2.9 | tpiA | J0UKG7 | -20.62 | 24 | 27.2 | 4 | 0.29 | C |
|  Glyceraldehyde-3-phosphate dehydrogenase | 89 | 1.00E-03 | 4.7 | gap | J0KSH5 | -14.29 | 8 | 36.2 | 2 | 0.31 | C |
| **Additional file 3 (*continued*)**  |
| Name of proteins identified in N305 a | Spot b | *p*-valuec | Foldd | Locuse | Access.f | log(E value)g | Cover.h | Massi | NPj | PAIk | Loc.l |
|  Phosphoglycerate kinase | 79 | 4.35E-05 | 4.4 | pgk | J1EWC9 | -63.97 | 44 | 42.5 | 11 | 0.67 | C |
|  Transketolase | 67, 89 | 1.00E-03 | 4.7 | Newbould305\_2114 | J1EUC2 | -84.78 | 35 | 72.1 | 16 | 0.69 | U |
|  Putative translaldolase | 97 | 1.98E-04 | 2.5 | Newbould305\_0104 | J1EZA8 | -24.29 | 36 | 25.6 | 6 | 0.58 | C |
|  6-phosphogluconate dehydrogenase, decarboxylating | 71 | 3.51E-05 | 3.1 | gnd | J0UIZ1 | -20.99 | 10 | 51.7 | 4 | 0.26 | C |
|  **Secondary metabolites biosynthesis, transport, and catabolism** |
|  Acetoin reductase | 95 | 1.07E-04 | 4.1 | Newbould305\_0667 | J1EXV9 | -10.20 | 16 | 27.1 | 3 | 0.38 | C |
| **POORLY CHARACTERIZED** |
|  UPF0447 protein Newbould305\_1113 | 96 | 1.07E-04 | 2.2 | Newbould305\_1113 | J1EVS0 | -16.53 | 21 | 29.3 | 4 | 0.56 | U |
|  Molecular chaperone Hsp31 and glyoxalase 3 | 89, 90, 91 | 3.62E-05 | 2.6 | hchA | J1EVT7 | -32.69 | 38 | 32.0 | 8 | 1.36 | C |

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

b Spot numbers (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