

A global *Staphylococcus aureus* proteome resource applicable for the *in vivo* characterization of host-pathogen interactions

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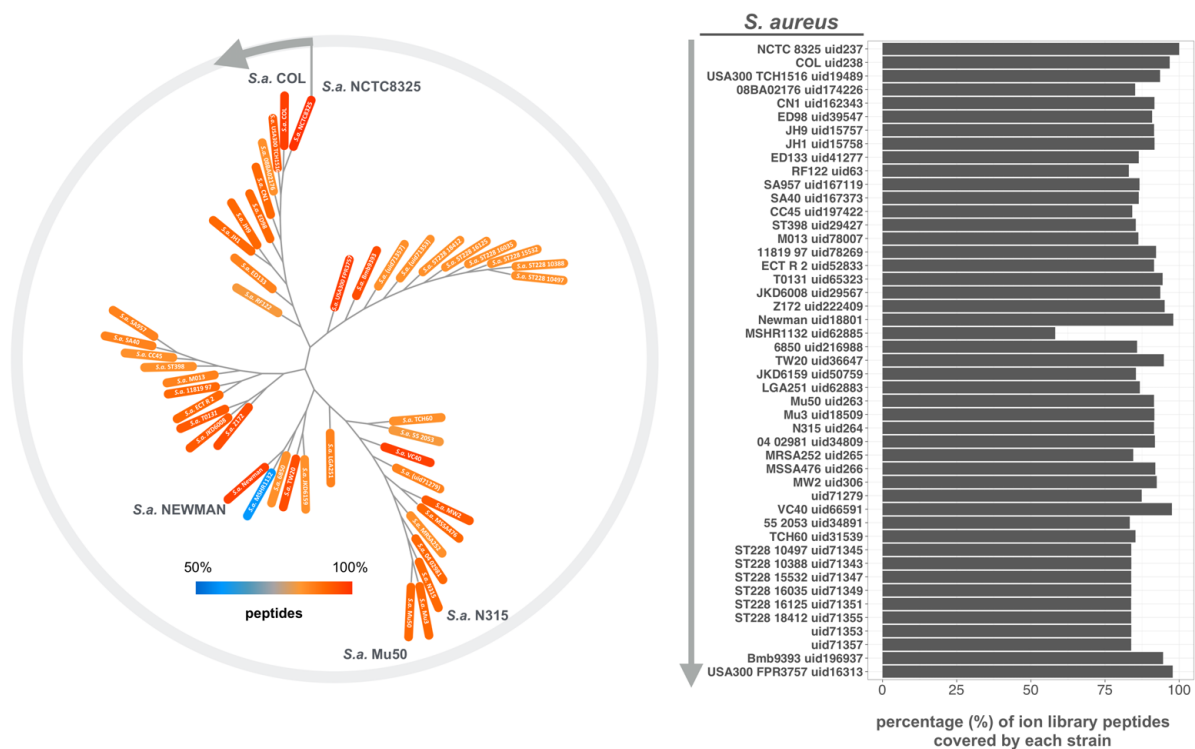
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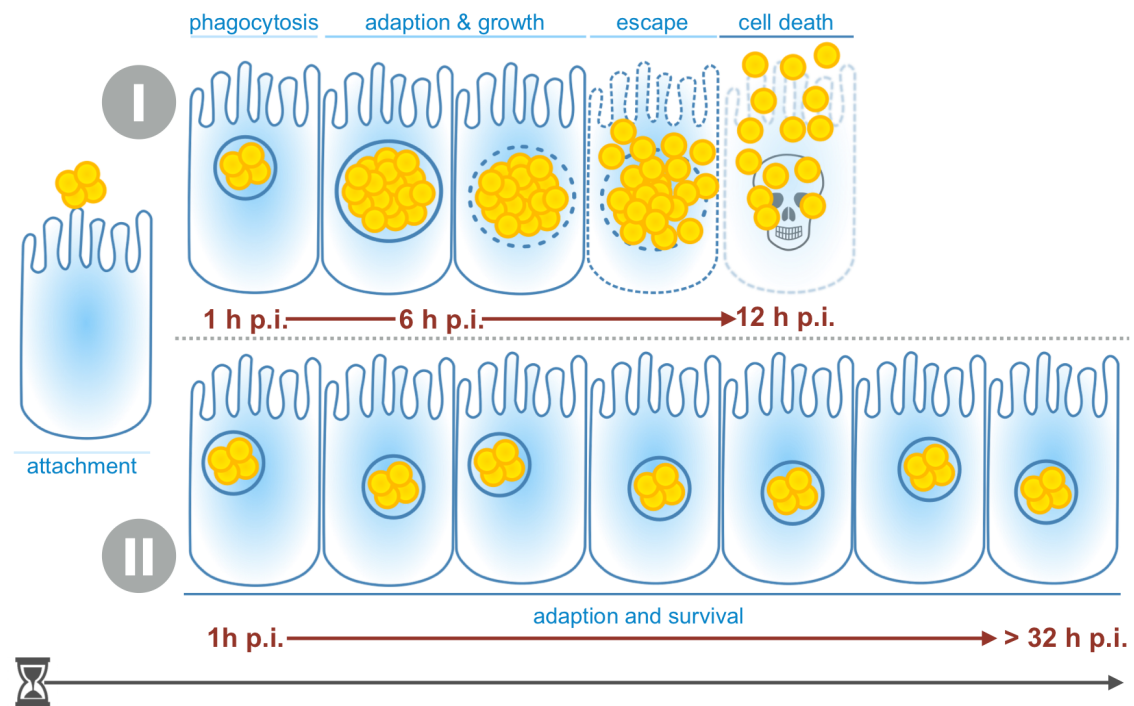
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1 Supplemental Figures



Supplemental Figure 1: Coverage of the generated ion library over various *S. aureus* strains.

Comparison of *S. aureus* strains on the proteome level. The proteome-based, unrooted, and unscaled phylogenetic tree of 46 different *S. aureus* strains visualizes the relationship of the strains on the proteome level. The color displays the percentage of peptides covered from the ion library for each strain. More intense orange indicates a higher coverage of the ion library. The dark grey arrow indicates the reading direction of the quantitative data presented in the bar plot (left side of the figure) from the top to the bottom.



Supplemental Figure 2: Model of *S. aureus* infection and re-infection of host cells. The scheme displays the suggested *S. aureus* host cell infection and proposes two cell populations during infection deduced from the life cell imaging movie (Supplemental Movie S1). (I. Growing, host cell killing and escaping bacteria and possible re-infection of host cells; II. Bacteria survive in the intracellular milieu)

2 Supplemental Results & Discussion

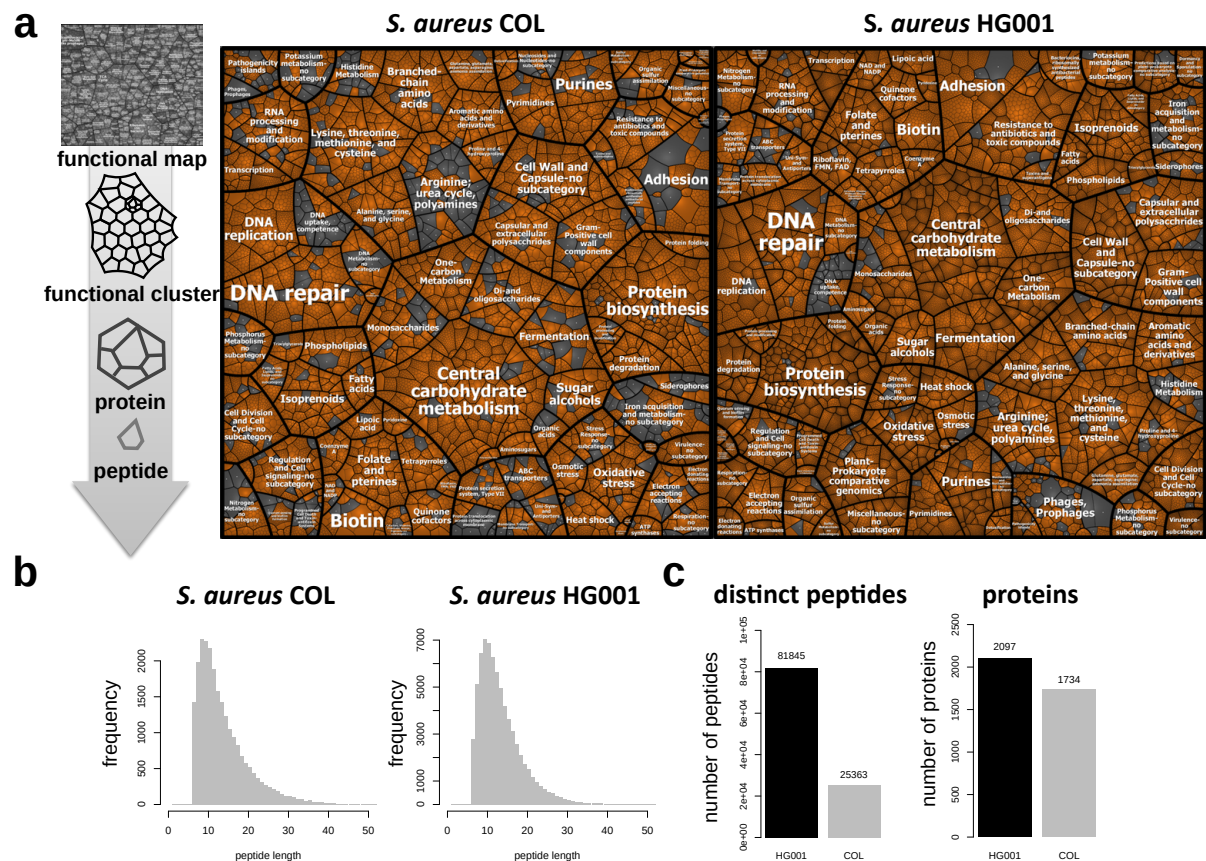
2.1 The *Staphylococcus aureus* PeptideAtlas as a prerequisite for novel analyses of host-pathogen interactions

PeptideAtlas is a well-known, publicly available resource for proteome data¹. Shotgun MS data from different experiments are processed with the Trans-Proteomic-Pipeline (TPP)² in a highly stringent analysis and results are presented to the community as PeptideAtlas builds to support experiment planning, data mining and the selection of proteotypic peptides for targeted MS approaches. Here, we generated the first *S. aureus* PeptideAtlas from previously published³ and newly acquired *S. aureus* MS DDA data sets. To analyze the proteome of the human pathogen *S. aureus* HG001, a derivative of strain NCTC8325, we first fractionated extensively the lysate and then acquired DDA-MS data³. To increase the proteome coverage, we performed several additional measurements from membrane fractionated samples, intra- and extracellular proteome preparations from cells growing under iron limitation, and recombinant *S. aureus* proteins. Furthermore, data sets of extracellular proteins from *S. aureus* HG001 wild type and its isogenic $\Delta sigB$ mutant in different media and from a time kinetics study of GFP-expressing *S. aureus* HG001 pMV158⁴ internalized by A549 cells were included to build a comprehensive *S. aureus* PeptideAtlas. After combining all data and applying strict thresholds to include only the most reliable peptide identifications and inferred proteins, we achieved the detection of 2097 proteins representing $\sim 3/4$ of the theoretical proteome. We combined all datasets (Supplementary Table S1A) and created a comprehensive *S. aureus* proteome repository which can be accessed by the research community to explore the observed peptides per protein, their spectra and related information at <http://www.peptideatlas.org>.

We analyzed not only *S. aureus* HG001, but also data from a different only *S. aureus* strain named COL. The proteome of *S. aureus* COL was extensively characterized in a previous study using subproteomic fractions of cytosolic proteins, membrane-bound proteins, cell surface-associated proteins, and extracellular proteins⁵ (Supplementary Table S1A), resulting in the identification of 65% of the annotated proteome and we generated a separate PeptideAtlas build for this strain.

To assist in the physiological interpretation of proteomic data, we provide Voronoi-like treemaps⁶ data display to provide a functionally sorted representation of the *S. aureus*

proteome in the PeptideAtlas (Supplemental Figure 3). The *S. aureus* HG001 PeptideAtlas is the most comprehensive resource where most proteins are represented by at least three peptides (median = 24; mean = 39) with 90 proteins covered by two peptides and only 126 by a single peptide. The *S. aureus* COL build likewise covers most of the proteins with at least three peptides (median = 12; mean = 17), 127 proteins with two, and 200 proteins with one peptide.



Supplemental Figure 3: Functional annotation coverage and comprehensiveness of the *S. aureus* PeptideAtlas.

(a) The Voronoi-like treemaps describe the number of identified peptides per annotated protein (orange) represented by the polygons, which also can be accessed via the *S. aureus* PeptideAtlas (www.peptidatlas.org).

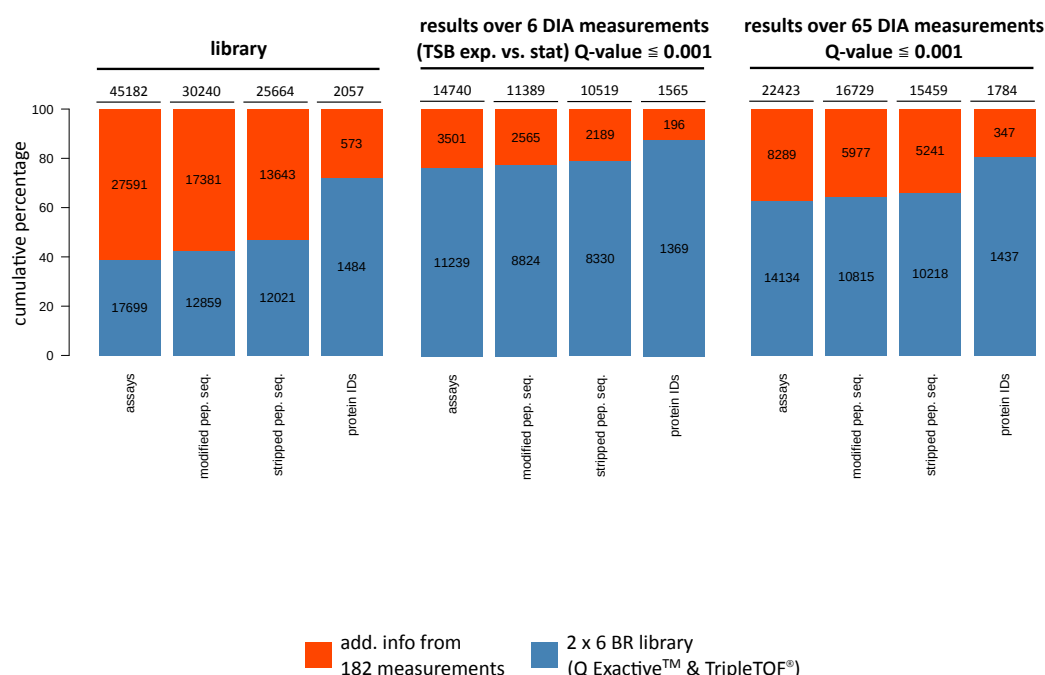
(b) Displayed are the histograms of the identified peptide length count in the *S. aureus* HG001 and *S. aureus* COL PeptideAtlas build.

(c) The barplots visualize the distinct identified peptide and protein count in the *S. aureus* HG001 and *S. aureus* COL PeptideAtlas build.

2.2 Library size for bacterial sample analysis

In order to test if the addition of strongly different sample sets and proteome fractionation is beneficial for the library generation for a comprehensive coverage of the proteome in our bacterial setting a library comparison was carried out between a standard library (12 measurements of one sample pool [mixture of *S. aureus* grown in TSB; exp. and stat. phase]) and a comprehensive library containing strongly different sample sets and proteome fractionation (Supplemental Table S1A).

The analysis of *S. aureus* tryptic soy broth (TSB) exponential and stationary phase samples measured in DIA mode and analyzed with both libraries (standard & comprehensive) revealed an assay surplus of 24% when the comprehensive ion library including non-iRT data was used, which resulted in an increase in the number of proteins identified of 12% when compared to the analysis using the basic ion library generated from just 12 DDA data sets. As a result, the quantification was now based on more data-points, which also proved to be more robust. The



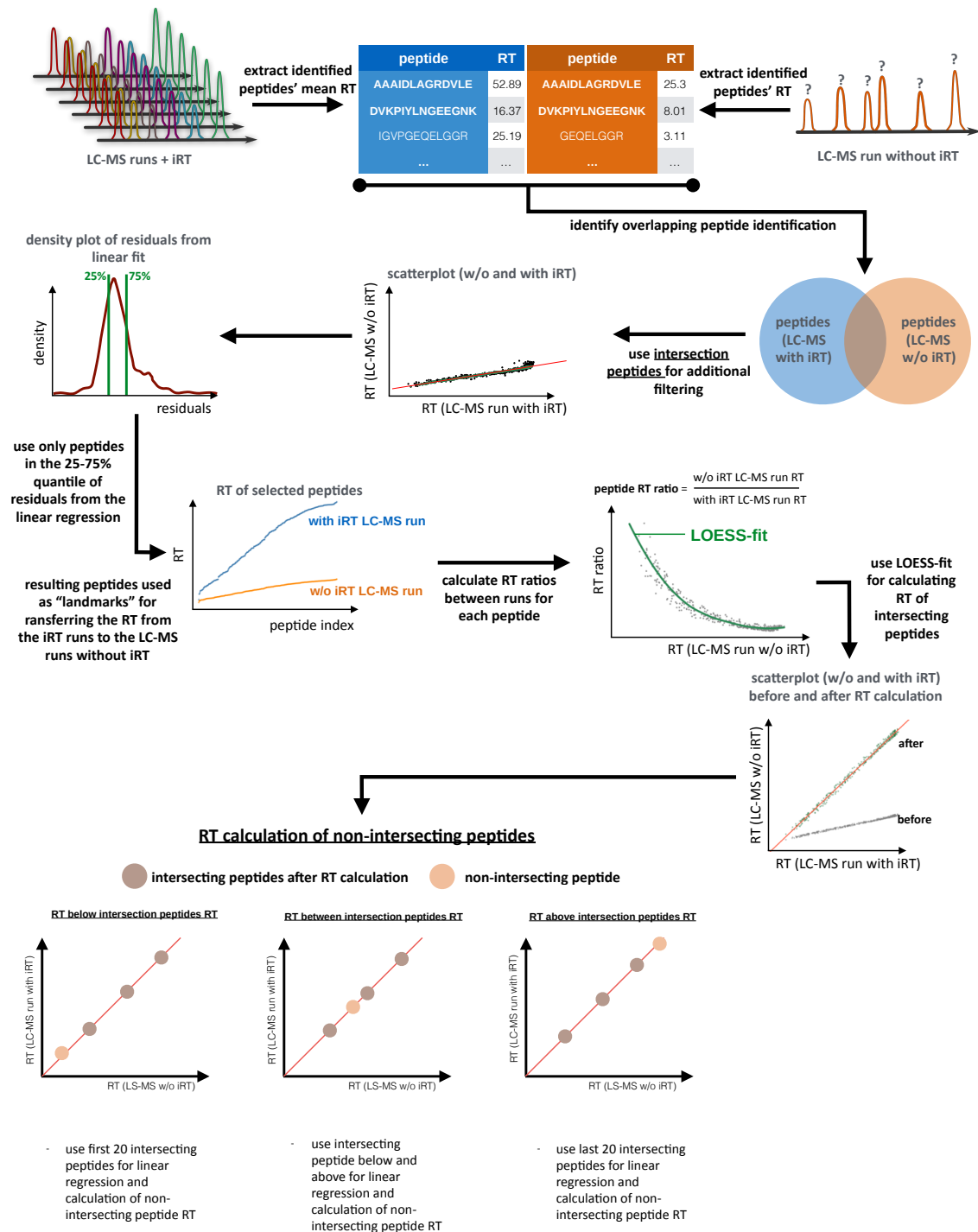
Supplemental Figure 8: Library size for data analysis.

The gain of information in the *S. aureus* ion library was shown when fractionated samples and diverse sample types (N=182) were added to a small sample set of 12 replicates measured with iRT spike-in peptides (reflecting a default ion library build). The cumulative percentage depicts the 100% scaling for each parameter. Absolute numbers are displayed in the bars.

analysis of 65 different DIA runs (Supplemental Table S1B) showed an assay surplus of approximately 37% resulting in the identification of approximately 19% more proteins (Supplemental Figure 8) when use of the expanded ion library is compared with that of the basic library. Therefore, we conclude that a larger ion library is beneficial for the investigation of organisms with a highly variable proteome available under different growth conditions.

2.3 Retention time alignment of LC-MS runs and transfer of iRT to runs without iRT peptides

A previously published dataset of our group³ contains high resolution mass spectrometric data of highly fractionated *S. aureus* HG001 proteins (e. g. SCX or off-gel IEF fractionation). The dataset consists of measurements with different liquid chromatography (LC) gradients such as 30 min, 100 min and 120 min linear LC gradient. In order to benefit from the iRT prediction algorithm implemented in data-independent acquisition (DIA) data analysis tools like SpectronautTM ⁷, all previously described high-accurate MS analysis runs³ were – based on peptide identification – separately aligned to a reference set of 6 sample replicates with spiked-in iRT peptides⁸ measured using a Q ExactiveTM (Supplemental Figure 6). The retention time (RT) values for each of the peptides in the measurements with spiked-in iRT peptides were combined by using the average over the iRT resulting in a master list of peptides and corresponding iRT values. This list was compared with a peptide list of each sample measured without iRT peptide spike-in. The intersecting peptides of this comparison were incorporated in a linear regression (RT LC-MS without iRT peptides vs. RT LC-MS with iRT peptides). Afterwards, the resulting residuals of the linear regression were used to filter for those peptides exhibiting a residual in the 25 to 75% quantile range over all residuals. This filtering step was performed in order to remove outliers or LC gradient anomalies and resulted in a filtered peptide list (“landmark peptides”). The “landmark peptide” list was used to calculate a RT ratio (RT LC-MS without iRT peptides vs. RT LC-MS with iRT peptides), which was subsequently utilized for a non-parametric regression (locally weighted scatterplot smoothing - LOESS⁹), which is beneficial for the alignment of non-linear LC shifts¹⁰. The resulting curve-fitted values were used to transfer the iRT values from the LC-MS run with iRT peptides to the run without iRT peptides. New iRT values for peptides, which were not included in the



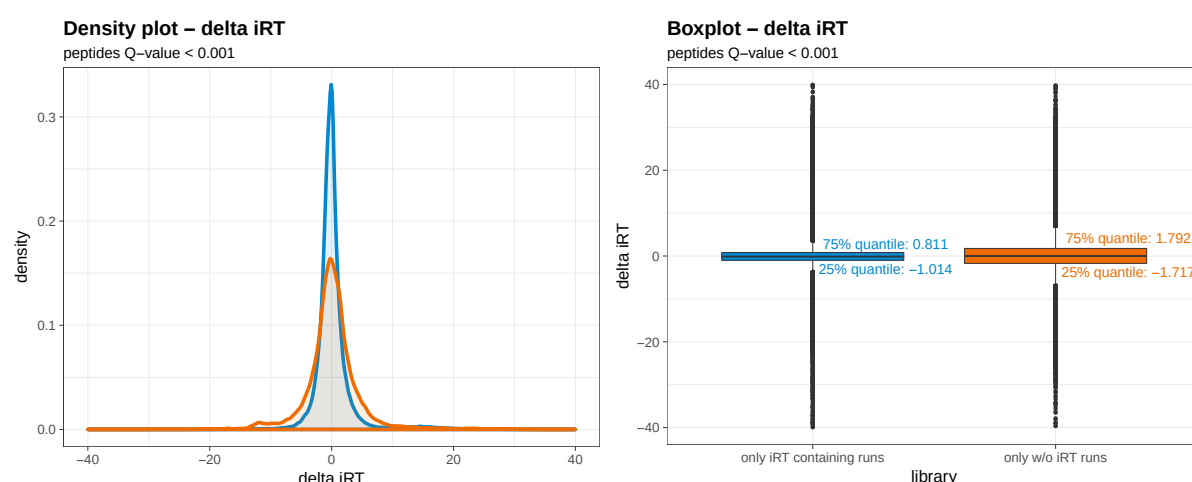
RT = retention time

Supplemental Figure 6: Schematic representation of the iRT transferring to LC-MS runs without iRT peptides spiked-in.

“landmark peptide” list, were interpolated using a linear regression along the non-parametric regression. Briefly, for peptides with an RT value smaller than the RT values in the “landmark peptide” list, the first 20 intersecting peptides with the smallest RT values were used for a

linear regression and calculation of the non-intersecting peptide's RT. For peptides with RT values in the range of the "landmark peptide" list peptides' RT, the adjacent peptides with smaller and higher RT values from the "landmark peptide" list were used for a linear regression and calculation of a non-intersecting peptide's RT. For peptides with RT values higher than the "landmark peptide" list peptides' RT, the 20 intersecting peptides with the highest RT values were used for a linear regression and calculation of non-intersecting peptide's RT.

To verify the quality of the alignment as well as the iRT transfer calculations an analysis over 65 different DIA-MS runs (Supplemental Table S1B) was performed. This analysis was based upon two different ion libraries: i) a library containing only peptides from iRT peptide-containing LC-MS runs and ii) a library containing only peptides for which the iRT value was generated by alignment and transfer of the iRT values (Supplemental Figure 7).



Supplemental Figure 7: Delta iRT of DIA analysis from 65 different DIA runs. The density plot and the corresponding boxplot are depicting the delta iRT from all peptides identified with a Q-value below 0.001. The blue colored curve/box represents the delta iRT of peptides identified with a library comprising only peptides from iRT LC-MS runs as basis. The orange colored curve/box depicts the delta iRT of peptides identified with a library including only peptides where the iRT was generated by alignment and transferring of the iRT. The 25% or 75% quantile of iRT were labeled in the boxplot.

The delta iRT values, which represent the difference between the anticipated iRT value to the empirical iRT value were reported. The distribution of delta iRT values within a 25% to 75% quantile from ca. -1 to 0.8 delta iRT for the identifications (Q-value < 0.001) using the library containing only peptides detected in LC-MS runs with iRT peptides revealed only a minor variation. The comparison to the analysis with the library containing only aligned peptides

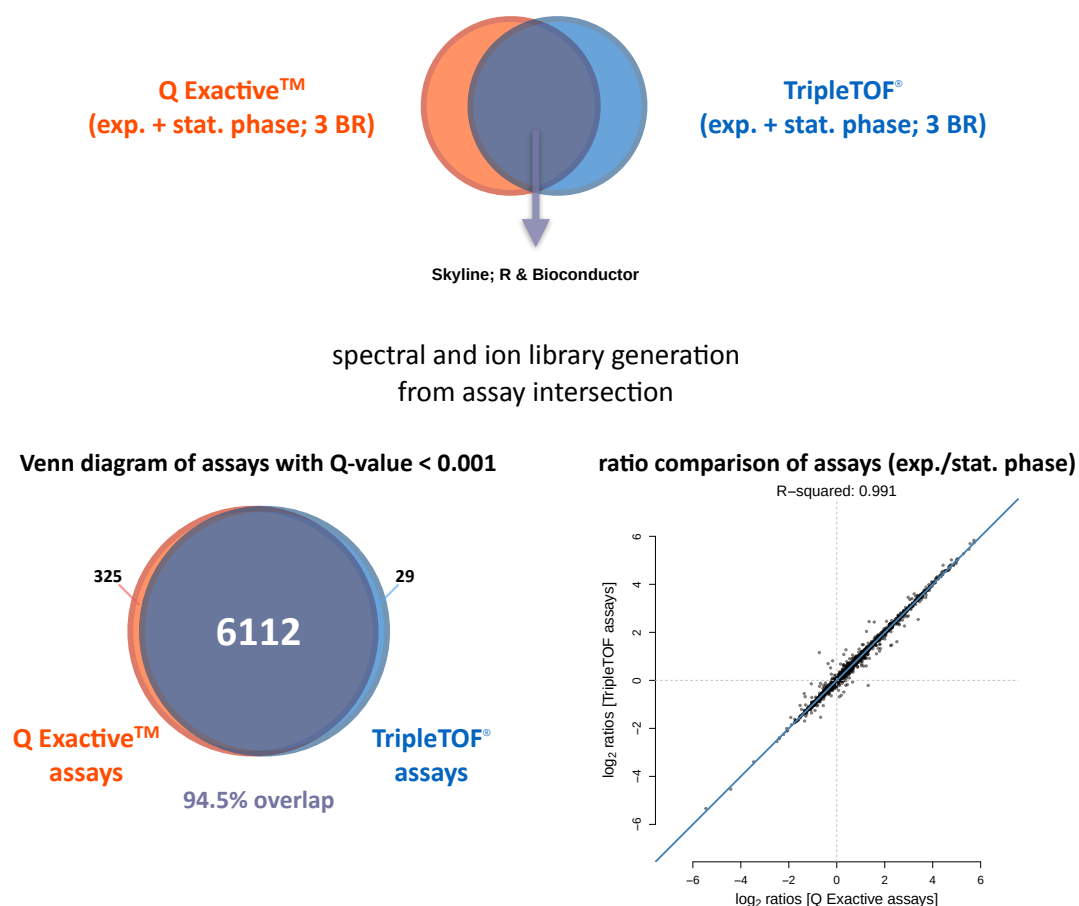
revealed delta iRT values from ca. -1.7 to 1.8 within the 25% to 75% quantile. This slightly higher delta iRT value deviation is still in an acceptable range for the data analysis isolation window during a DIA-MS analysis.

2.4 Cross-device usability of DIA-MS assays generated with SCIEX

TripleTOF® 5600⁺ and Thermo Q Exactive™

The basic ion library was generated with SpecL¹¹ by analyzing six DDA runs derived from a Q Exactive™ and six DDA runs derived from a TripleTOF® 5600⁺ instrument. Samples analyzed on both instruments were equalized with spiked-in indexed retention time (iRT)⁸ peptides and converted to an empirical retention time, iRT, which represents a “fixed number relative to a standard set of reference iRT-peptides that can be transferred across laboratories and chromatographic systems”⁸. The major differences between the TripleTOF® 5600⁺ and Q Exactive™ instruments are the mass detection and the fragmentation mode. TripleTOF® 5600⁺ data are collected with CID fragmentation (collision-induced dissociation) and Q Exactive™ data with HCD (higher-energy C-trap dissociation) fragmentation.

In order to test i) if an ion library generated with a Q Exactive™ instrument is also suitable for DIA (data-independent acquisition) data analysis of data collected on a TripleTOF® 5600⁺ instrument, ii) if we can merge the MS information obtained from both instruments in one fragment ion spectral library for data analysis purposes, and iii) if the generated assays in the fragment ion spectral library can be used to analyze data acquired on both MS devices, we measured the same sample with both instruments in DIA mode, analyzed the data with the same fragment ion spectral library and compared the results.



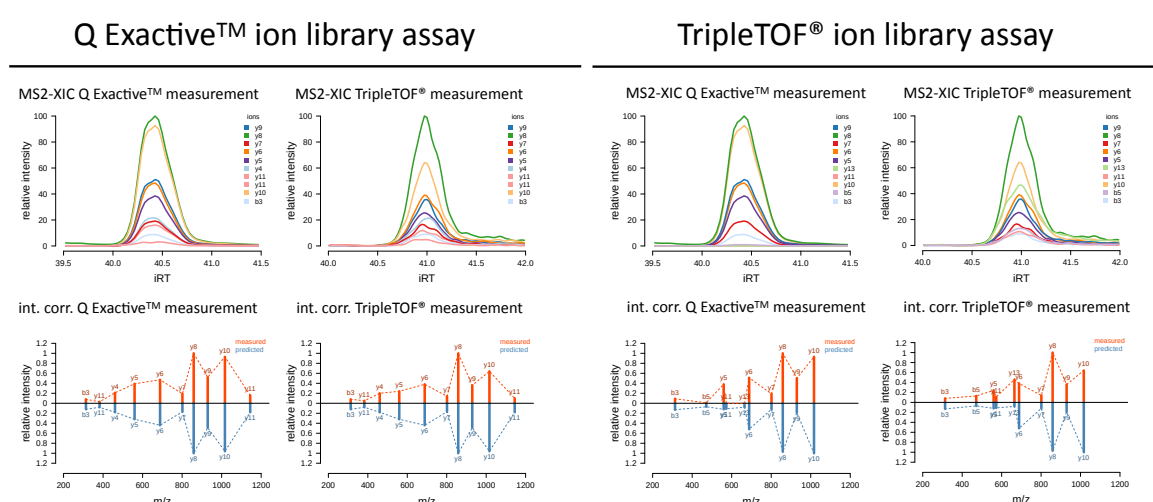
Supplemental Figure 4: Cross-device usability of DIA-MS assays. To determine whether assays derived from a Q ExactiveTM or a TripleTOF[®] instrument can be used for cross-device DIA-MS data analysis, an intersection-based assay ion library was generated. *S. aureus* HG001 TSB exponential and stationary phase samples (3 BR each) were analyzed with the redundant ion library, resulting in a large overlap (>94%) of extracted ion chromatograms (Q-value cut off < 0.001; Venn diagram) and peptide abundance patterns regardless of the origin of the assay (scatter plot).

The ion library used for this approach consisted of six DDA runs from TripleTOF[®] 5600⁺ and six Q ExactiveTM DDA measurements from the same sample. To elucidate the potential cross-platform usage of an assay, a combined intersection ion library – this means overlapping assays derived from the Q ExactiveTM and TripleTOF[®] 5600⁺ instruments – was used for the analysis of the DIA measurements with both devices (TripleTOF[®] 5600⁺ and Q ExactiveTM). If an assay was only found in either the Q ExactiveTM or the TripleTOF[®] 5600⁺ measurement the assay was neglected. This resulted in a fragment ion spectral library consisting of 13,392 assays (6,696 from Q ExactiveTM and 6,696 from TripleTOF[®] 5600⁺) containing the exact same number of assays generated by both devices in order to eliminate a possible bias of the

comparative down-stream analysis due to a higher number of assays being derived from one device (Supplemental Figure 4).

Strikingly, the cross-assay usage evaluation was successful in most of the cases tested with Q Exactive™ DIA and TripleTOF® 5600+ measurements (Supplemental Figure 4). The majority of the assays (>94%) was identified even if an assay was generated on the other instrument (Supplemental Figure 4). Additionally, the assays were not only identified on one instrument while being generated by the other, but also yielded highly comparable quantitative ratio data on both devices (Supplemental Figure 4). An analysis of the assay total peak area (TPA) of growing and non-growing cells measured with the Q Exactive™ in DIA-mode and analyzed with assays derived from Q Exactive™ DIA and TripleTOF® 5600+ revealed a high correlation between both assay fractions (0.991 R-squared) (Supplemental Figure 4).

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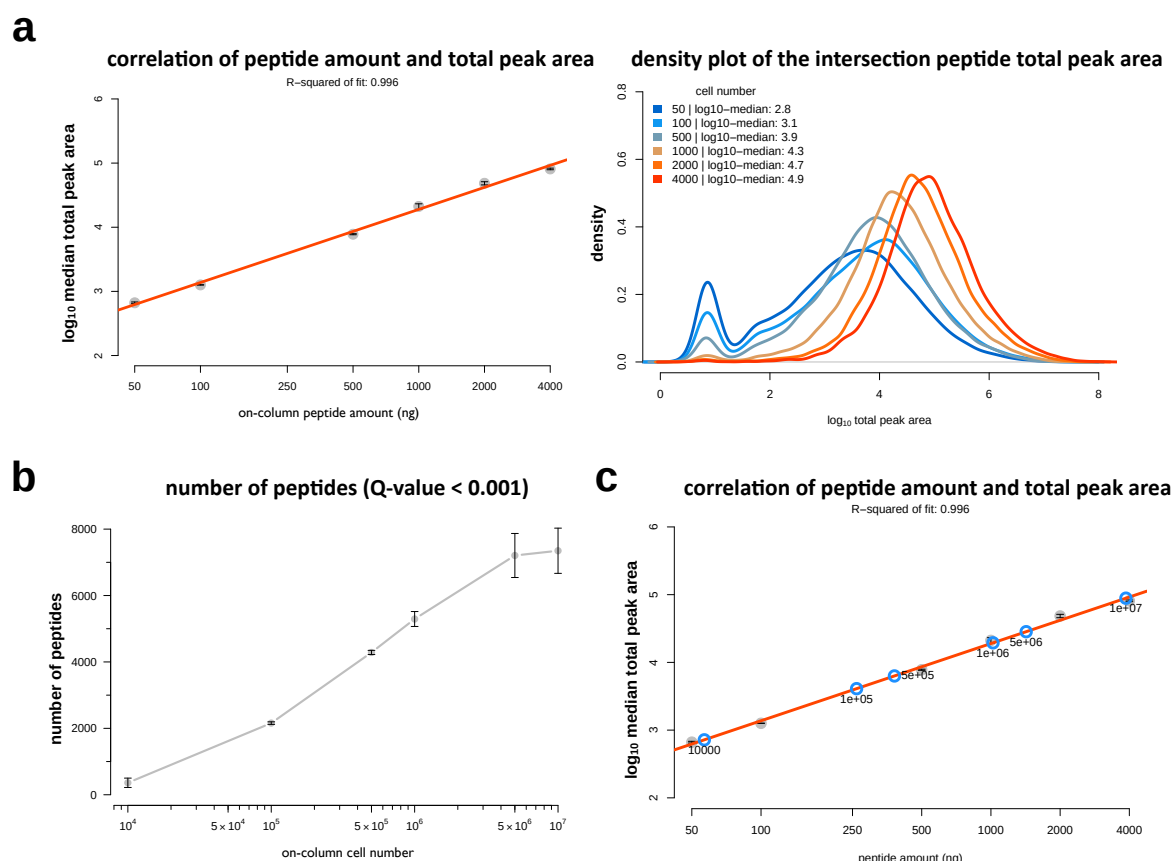


and HCD devices were similar, based on the calculation and comparison of cross-correlation scores. In agreement with de Graaf *et al.* we have concluded that cross-device assays can be used for the data analysis of DIA experiments in the future and might be highly beneficial for the proteomics community.

In summary, our data indicated that a DIA approach and analysis with the generated ion library can be performed on both MS instruments and that the obtained results are well-suited for correlation and lab comparison, underlining the benefit of an ion library for the community.

2.5 Dynamic range of DIA measurements of *S. aureus* protein samples

The dynamic range of the DIA method was tested by an on-column loading amount series with a digested complex cytosolic *S. aureus* proteome sample, which was measured on a Q ExactiveTM instrument and analyzed via SpectronautTM (Supplemental Figure 9).



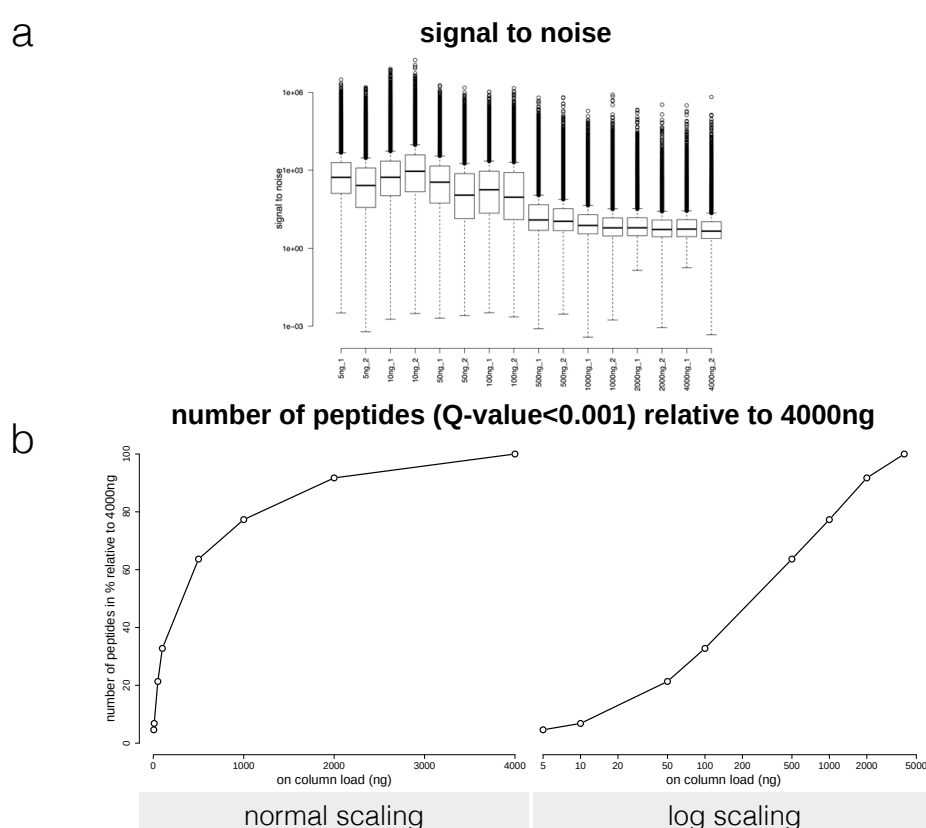
Supplemental Figure 9: Dynamic range of DIA-MS analyses.

(a) Relationship between on-column peptide load and total peak area. The median total peak area over the concentration series (50 to 4,000ng) is plotted. The linear regression indicates the linear range of the method. The kernel density plot over the concentration series depicts the distribution of the total peak area signals.

(b) Relationship between on-column cell number and the number of identified peptides. The number of peptides is depicted in relation to the number of cells digested and loaded on-column for analysis in the mass spectrometer.

(c) Relationship between on-column cell number total peak and peptide load and total peak area. Based on the linear fit (orange line) over the median total peak area of the individual on-column protein amount measurements (grey dots); the cell number measurements were displayed based on their median assay total peak area (open blue circles).

The median total peak areas were used for the estimation of the linear dynamic range. A linear range was obtained from 50 ng to 4,000 ng on-column loads on a 50 cm column. This observation implies that samples with a peptide amount far below 50 ng (e.g. 5 ng and 10 ng) are not feasible for the analysis due to the device-specific detection limits, as shown in earlier data-dependent experiments^{13,14}. An on-column load of around 1,000 ng was a good point of reference for analysis, since higher on-column amounts resulted in the saturation of information gain. Furthermore, on-column loads of 1,000 ng and more displayed a lower number of identified signals due to background interference in comparison to on-column loads of less than 1,000 ng (Supplemental Figure 9, Supplemental Figure 10).



Supplemental Figure 10: Quality control of DIA-MS analyses.

(a) Signal-to-noise boxplot over measurements.

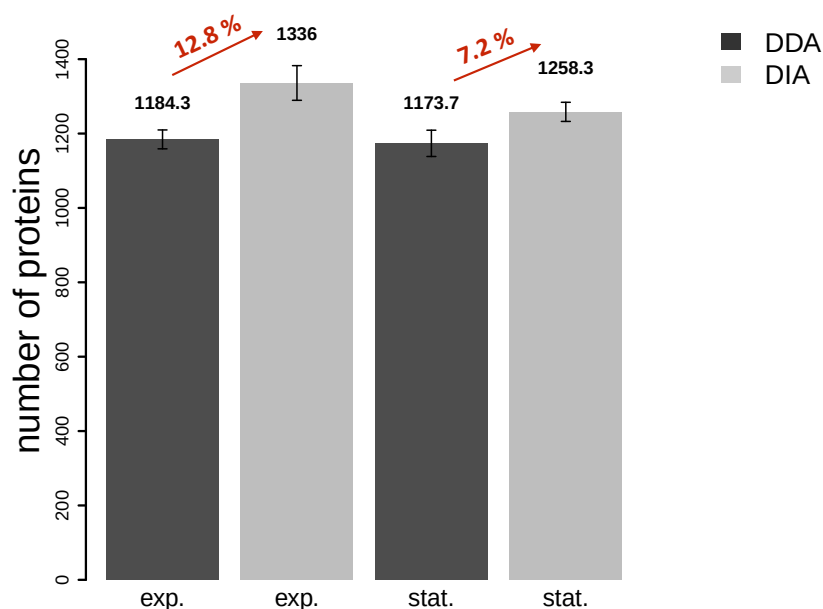
(b) Percentage of number of proteins or peptides identified in the whole column load series normalized to a 4,000 ng column load as maximum value.

Over the last 15 years, systems biology approaches have become the focus of research¹⁵. Systems biologists model complex biological processes *in silico* based on wet lab data. Here, a key element for the understanding of the functions of organisms is understanding the

complex interplay of the proteins inside a cell. Therefore, knowledge of the absolute number of proteins per cell is the essential basis for the calculations and for modeling of such interactions. For absolute protein quantification, the adjustment of recorded quantitative data to cell number data is an important criterion, rendering very crucial the determination of cell numbers for robust DIA analysis. A series of peptide extracts resulting from different *S. aureus* cell numbers was analyzed in a Q ExactiveTM mass spectrometer (Supplemental Figure 9b, c). To date, very low cell numbers such as 1×10^2 to 1×10^4 have not been feasible for a global MS-based analysis, while meaningful proteome analyses on a Q ExactiveTM mass spectrometer have been accomplished with cell numbers of approximately 1×10^5 or 1×10^6 (and higher).

2.6 Benchmarking DIA measurements of growing and non-growing cell samples of *S. aureus*

In order to extensively benchmark the method and the generated *S. aureus* DIA assay fragment ion library, we used the well-known model of growing and non-growing *S. aureus*

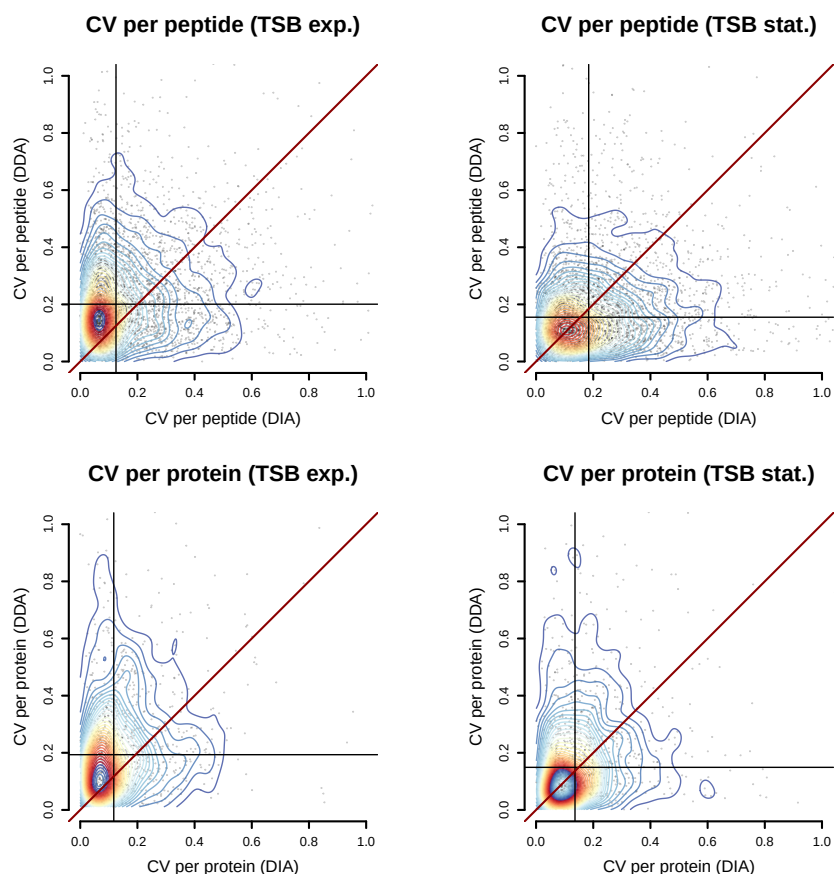


Supplemental Figure 11: Direct comparison of DIA-MS and DDA-MS measurement; Protein identification per sample.

Three biological replicates of *S. aureus* grown in TSB media at exponential (exp.) and at stationary (stat.) phase were used to calculate the number of protein identifications per sample in DDA-MS (black bars) as well as in DIA-MS (grey bars) analysis.

HG001 cells in the most frequently used complex medium for *S. aureus*, TSB (tryptic soy broth).

In direct comparison DIA-MS performs better in terms of protein identifications per sample and coefficient of variation of protein quantification compared to DDA-MS (Supplemental Figure 11, 12).

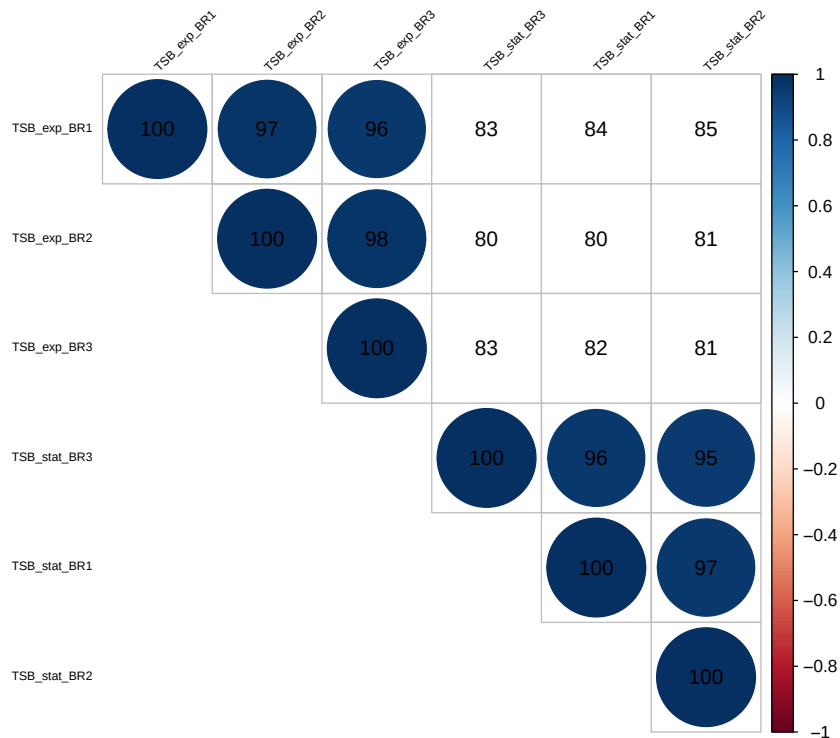


Supplemental Figure 12: Direct comparison of DIA-MS and DDA-MS measurement; Coefficient of variation over growth phases.

The coefficient of variation (CV) is scattered. The two-dimensional kernel density is plotted via colored line shapes. A more reddish color depicts a high point density and a more bluish color displays a low point density. The vertical or horizontal black lines indicate the median of the y-axis or x-axis data.

The goal was to obtain large magnitudes of changes in proteomes changes and to be able to compare the results with literature data^{5,16,17}.

The biological replicate correlation rank coefficient (Spearman correlation) for each biological state ranged from 0.95 to 0.98 (Supplemental Figure 13), showing a good reproducibility of the cultivation and DIA method itself.



Supplemental Figure 13: Spearman correlation plot based on complete observations of the total peak area of the assays.

Three biological replicates (BR) of TSB exponential (exp.) and stationary (stat.) phase samples are displayed.

We were able to identify 1,565 proteins over all six samples of the experiment and to quantify 398 significant (Benjamini-Hochberg-adjusted p-value < 0.05) protein abundance changes (Supplemental Figure 14a) with an absolute fold-change of at least 1.5 comparing exponentially growing with stationary phase cells. The data is provided in Supplemental Table S3.

The findings greatly overlap (ca. 82% [517 proteins without changes out of 630 detected in both studies]) with previously generated data⁵ in BioExpress® medium (Supplemental Figure 14c), a medium which is similar to TSB. The comparison with the mass spectrometry based publication of Becher and co-workers⁵ with cells grown in Bioexpress® medium was favored over the 2D gel-based approach of Kohler and co-workers¹⁶ with cells grown in TSB medium, because of a higher coverage of cytoplasmic proteins and a more robust protein quantification via ¹⁵N/¹⁴N labeling approach.

During the growth in glucose-rich complex media like TSB *S. aureus* utilizes glucose as its primary carbon source, which is rapidly consumed until entry into the stationary phase^{16,18}.

Glucose is preferentially metabolized via glycolysis, and acetate is produced and secreted as an overflow metabolite. As already reported by Kohler et al., 2005¹⁶, glycolytic enzymes are highly abundant, and the TCC enzymes are repressed during the exponential growth phase^{5,16}. The TCC enzymes (e.g. CitB, CitC, SucA/B, SucC/D, SdhA/B) were found to be strongly increased in their amount in the stationary growth phase^{5,16,19} when glucose has been completely consumed. Glycolytic enzymes were decreased^{5,16,19,20}, whereas gluconeogenic enzymes (e.g. GapB, PckA) were found in elevated amounts^{5,16}.

Proteins involved in the transcription process such as the RNA polymerase subunits (RpoA, RpoB, RpoC, RpoE) and transcription factors like GreA and Rho were found in approx. 2-fold diminished amounts in the stationary growth phase as compared to the exponential growth phase. Furthermore, ribosomal proteins were found at a strongly reduced level in abundance in the non-growing/stationary phase cells^{5,20}, as well as ribosomal-associated factors such as the ribosome recycling factor Frr.

In addition, enzymes involved in cell wall biosynthesis (e.g. MurA, MurZ) and lipid synthesis (e.g. FabI, FabD) were also found in decreased amounts in the stationary phase. Furthermore, the initial and PurR-controlled part of the purine synthesis pathway was up-regulated (e.g. PurH, PurS, PurC, PurF, PurD), and exit enzymes of that pathway, which are central for important building blocks of the cell (e.g. Gmk, Hpt, Adk, NrdE, NrdF), were strongly diminished. For example, the nucleotide reductase, which has been described as highly unstable during the stationary phase²⁰, was diminished drastically in the stationary phase. On the other hand, Ndk, a nucleotide kinase, was up-regulated in the stationary phase, presumably to maintain the nucleotide triphosphate (NTP) pool for setting up the basic RNA synthesis. Regulating the pool of NTPs in the cell can alter translation, subsequently leading to cell reprogramming/adaption²¹. Arginine metabolism was modulated as indicated by the up-regulation of RocA, RocD, and RocF in the stationary phase.

Finally, histidine degradation enzymes (e.g. HutI, HutU, and HutG) were also found up-regulated in the stationary growth phase. Enzymes involved in one-carbon metabolism such as Fhs (formate-tetrahydrofolate-ligase), Fld (tetra-hydrofolate dehydrogenase), and SAOUHSC_01650 (5-formyltetrahydrofolate cyclo-ligase) and RibAB (riboflavin synthase) were found in increased amounts.

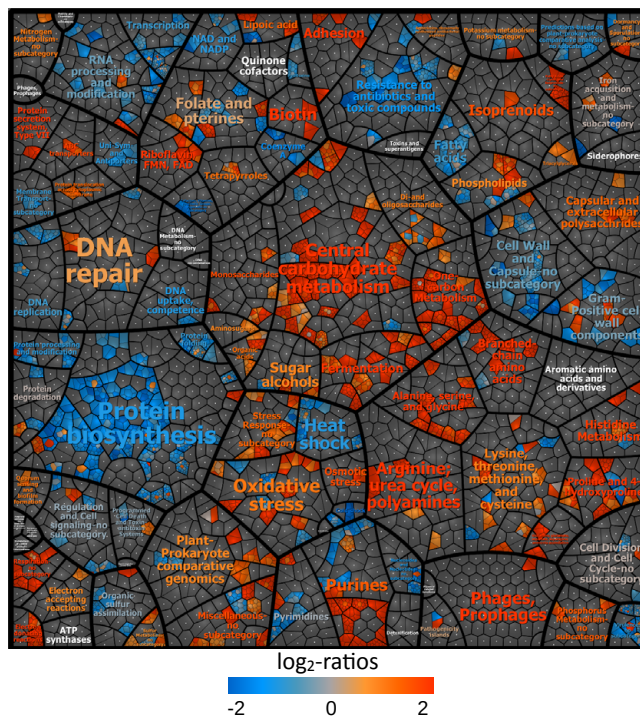
In addition to the CcpA (regulator of carbon catabolite control) regulated proteins like HutI-HutU-HutG and RocA-RocD-RocF, the FadA, FadB, FadD and FadE proteins, which are important for the fatty acid metabolism were found up-regulated in the stationary phase.

The ribosomal subunit interface protein, saHPF, *S. aureus* hibernation promoting factor²², was found in a highly increased amount in the stationary phase. In a previous study²² an increased formation of 100 S ribosomes with increasing amounts of HPF was observed. 100 S ribosomes are known to form “holding” ribosomes, which are decreased in their translational activity²³. Interestingly, one ribosomal protein, RpsA (30S ribosomal protein S1), was found in an increased amount in the stationary phase. In other organisms S1 is essential for translation initiation, enabling the ribosome to dynamically initiate translation from a large set of mRNAs with diverse structural features^{24,25}.

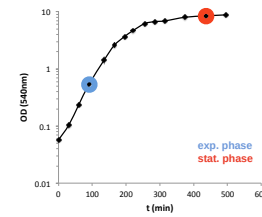
Furthermore, several important regulators could be detected in altered amounts, including the SigB-dependent SpoVG²⁶ and virulence associated regulators like ArlR²⁷ and Rot²⁸. WalR²⁹, a part of a two-component system and regulator for the cell wall metabolism was found in approx. 2fold increased amount in non-growing cells. The global effector of stress tolerance and biofilm formation³⁰, SpxA, was present in a 4fold higher amount in the stationary phase. Similar tendencies were recorded for other regulators like PhoP, IcaR, CtsR and SAOUHSC_02589, whereas MsrR, the cell envelope stress sensing regulatory protein³¹, was detected in ~1.7-fold decreased amount.

By representing the most comprehensive insight to date into growing and non-growing *S. aureus* cells in the complex medium TSB, the data from the present study can be considered as nearly complete knowledge of *S. aureus* under standard laboratory *in vitro* growth conditions.

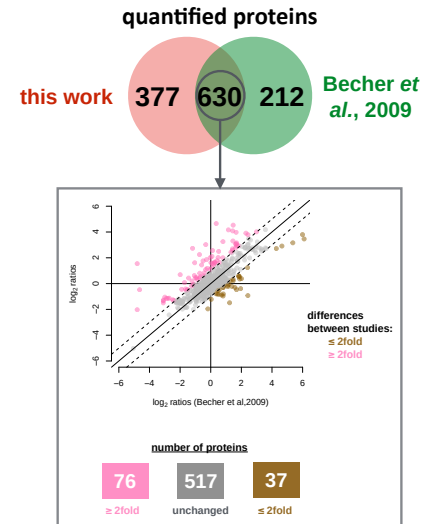
a



b



c



Supplemental Figure 14: DIA-MS analyses of *in vitro* shaking flask experiments with *S. aureus* HG001 cultivated in the rich medium TSB.

(a) Voronoi-like treemap comparing the proteome of exponentially growing and stationary phase *S. aureus* cells. A Voronoi-like treemap depicts the $\log_2$ -ratio of the peptide level between stationary and exponentially growing cells. Orange indicates an increased amount in the stationary phase and blue represents proteins which are found diminished in the stationary phase.

(b) Growth curve of *S. aureus* growing in TSB complex media. The exponential and stationary phase samples are marked by blue and orange circles in the growth curve.

(c) Comparison of protein abundance changes in growing and non-growing cells quantified via mass spectrometry in the present study and in a previously published study⁵. The Venn-diagram displays the differences and the intersection in protein identifications. The scatter plot reflects the quantitative ratios of the identification interaction. Proteins with a ratio variation below or above two-fold between the studies were colored pink (≥ 2 -fold) or brown (≤ 2 -fold).

3 Supplemental Material and Methods

3.1 Bacterial growth, optimized GFP strain construction, media and protein preparation, tryptic digestion, and peptide purification for samples subjected to DDA MS analysis and used for the generation of an *S. aureus* PeptideAtlas or a DIA library

3.1.1 Intra- and extracellular proteins from *S. aureus* HG001 pMV158GFP after iron limitation by 2,2'-bipyridyl and under control conditions

For the iron restricted cultivation *S. aureus* HG001 pMV158GFP was pre-cultured over night at 37°C in an adapted prokaryotic minimal essential medium (pMEM)^{32,33} supplemented with 0.01% (w/v) yeast extract and 20 µg/ml tetracycline. The main cultures in pMEM supplemented with 600 µM 2,2'-bipyridyl to restrict the iron availability and in unsupplemented pMEM as control were inoculated from exponentially growing overnight cultures. Bacterial cell samples were taken in the exponential growth phase ($OD_{600\text{ nm}} = 0.3$) and 4 h after entry into the stationary growth phase. Extracellular proteins were prepared from sterile-filtrated culture supernatants by precipitation using a final concentration of 10% (v/v) trichloroacetic acid (TCA). Precipitated protein samples were washed four times with 80% (v/v) acetone and once with 100% (v/v) acetone and then dissolved in 50 mM ammonium bicarbonate (ABC)/0.1% (w/v) RapiGest® (Waters) by ultrasonication. Non-soluble contaminants were removed by centrifugation, and the protein concentration was determined using a Micro BCA™ Protein Assay Kit (Pierce). For the DDA MS analysis 2 µg of each extracellular proteome sample were digested with trypsin (1:25), the resulting peptides were purified using ZipTip_{µ-C18} pipette tips (Millipore, Schwalbach, Germany), and 1000 ng were subjected to LC-MS/MS. The mass spectrometric measurement of the intracellular proteome was performed using 2×10^8 cells treated with lysostaphin followed by tryptic digestion and peptide purification using ZipTip_{C18} pipette tips (Millipore, Schwalbach, Germany).

3.1.2 Intra- and extracellular proteins from *S. aureus* HG001 growing in TSB at different growth phases

S. aureus HG001 was cultivated in tryptic soy broth (TSB) medium for DDA-MS analyses using QTOF (Agilent) and LTQ XL Orbitrap (Thermo) instruments. Bacteria and culture supernatants were harvested by centrifugation during exponential growth, at entry into stationary phase (t_0), and 4 h after t_0 . Protein samples from bacterial cells and from culture supernatants were prepared as previously described³. Equal amounts of protein from each of the three sampling points were mixed in order to obtain a single sample of intracellular proteins and another single sample of extracellular proteins. Protein samples were reduced, alkylated, tryptically digested, and purified using C18 columns as previously described³. Peptides resulting from the sample of intracellular proteins were subjected to fractionation according to the peptides' *pI* using an Agilent OFFGEL 3100 Fractionator system (Agilent Technologies, Santa Clara, CA, USA) and afterwards C18-purified as previously described³.

3.1.3 Membrane proteins from *S. aureus* HG001 growing in TSB at different growth phases

The membrane fraction preparation was performed as described previously³⁴. Briefly, cells were grown in TSB, and the same amount of cells was harvested during the exponential growth phase ($OD_{540nm}=1$) and after 4 h of the stationary phase (2,000 OD-units each). The pellets were washed with 5 ml TBS buffer (50 mM Tris, 150 mM NaCl, pH 8.0), mixed together, resuspended in lysis buffer (20 mM Tris, 10 mM $MgCl_2$, 1 mM $CaCl_2$, pH 7.5) containing cOmplete protease inhibitor (Roche), and disrupted by using a FastPrep® instrument (Thermo-Fisher). Addition of 200 U/ml DNase and 10 U/ml RNase followed by 20 min incubation at 37°C resulted in nucleic acid degradation. Centrifugation (8000 x g, 4°C, 10 min) separated cell debris and non-disrupted cells from the soluble proteins. The supernatant was used for ultra-centrifugation (100,000 x g, 4°C, 60 min), the pellet was washed with 6 ml ice-cold salt buffer (20 mM Tris, 1 M NaCl, pH 7.5) containing cOmplete protease inhibitor, followed by 1 h incubation at 4°C in an overhead shaker. A second ultra-centrifugation (100,000 x g, 4°C, 60 min) was then performed. Next, the pellet was washed with 6 ml ice-cold carbonate buffer (100 mM Na_2CO_3 , 100 mM NaCl, pH 11) containing cOmplete protease inhibitor, followed by 1 h incubation at 4°C in an over-head shaker and subsequent ultra-centrifugation (100000 x g, 4°C, 60 min). The pellet was dissolved in 10% SDS, and protein concentration was determined using a Micro BCA™ Protein Assay Kit (Pierce). 20 µg of protein were used for a short gel-based separation, followed by an in-gel tryptic digestion³⁵ and ZipTip® peptide purification. Finally, iRT peptides (Biognosys) were added to the sample, which was subsequently analyzed using a Q Exactive™ mass spectrometer (Thermo-Fisher).

3.1.4 Intra- and extracellular proteins from *S. aureus* HG001 and its isogenic $\Delta sigB$ mutant

The preparation of the extracellular protein extracts of *S. aureus* HG001 and its isogenic $\Delta sigB$ mutant³⁶ was performed by removing the cells from the culture medium (TSB: exponential growth phase; 10 h into the stationary growth phase, and at 24 h; in the late stationary growth phase; or pMEM: exponential growth phase; 5 h into the stationary growth phase; and at 19 h in the late stationary growth phase) by centrifugation (15,557 x g, 4°C, 10 min). Extracellular proteins were precipitated according to Ziebandt et al.³⁷ with 10% w/v TCA overnight at 4°C with subsequent centrifugation (15,557 x g, 4°C, 1 h). The pellets were washed several times at room temperature with 70% ethanol and purified with 100% ethanol. Afterwards, the pellets were resolved in UT buffer (8 M urea, 2 M thiourea), and the protein concentration was determined with a Bradford-assay³⁸ according to the manufacturer's guide (Bio-Rad Laboratories GmbH, Munich, Germany). For gelfree analysis 2 µg of protein was diluted with 20 mM ABC to a final concentration of 0.8 M urea and 0.2 M thiourea followed by reduction with a final concentration of 2.5 mM dithiothreitol (final concentration)(GE Healthcare, Munich, Germany) in 20 mM ABC for 60 min at 60°C and alkylation with iodacetamide (Sigma) in 20 mM ammonium bicarbonate (final concentration 10 mM) for 30 min at 37°C in the dark. The samples were predigested with Lys C (Sigma) in an enzyme to substrate ratio of 1:100 for 3 h before trypsin (Promega, Madison, WI, USA) digestion at a ratio of 1:25 over night at 37°C was carried out. Thereafter, the digestion was stopped by adding 1% v/v purified acetic acid (Sigma), and the samples were purified using ZipTip_{µ-C18} columns (Millipore, Schwalbach, Germany). The eluates were used for LC-MS/MS analysis using a nano-HPLC-ESI-LTQ-FT instrument (Thermo Fisher Electron, Bremen, Germany).

3.1.5 Generation of S9 and *S. aureus* extract mixtures

S. aureus was grown in pMEM medium supplemented with 0.01% (w/v) yeast until mid-exponential phase ($OD_{600nm}=0.4$). The cells were harvested via centrifugation (20000 x g, 4°C, 5 min) and the pellet was washed twice in ice-cold PBS. The cells were re-suspended in 250 µl 20 mM ABC (ammonium bicarbonate) and were disrupted using liquid nitrogen and a bead mill (2min, 2600 rpm). The cell debris was removed by centrifugation (20000 x g, 4°C, 30 min). The protein concentration was determined using a Micro BCA™ Protein Assay Kit (Pierce). The protein concentration was adjusted to 1 µg/µl with 50 mM ABC. The S9 protein extract was generated by harvesting one confluent cell culture dish (diameter 10 cm). Cells were washed twice with PBS, scraped in 1 ml of PBS, pelleted by centrifugation (600 x g, 4°C, 5 min) and flash-frozen with liquid nitrogen and stored at -80°C. The cells were re-suspended in 250 µl 20 mM ABC and were disrupted using liquid nitrogen and a bead mill (2 min, 2600 rpm). The cell debris was removed by centrifugation (20000 x g, 4°C, 10 min). The protein

concentration was determined using a Micro BCA™ Protein Assay Kit (Pierce). The protein concentration was adjusted to 1 µg/µl with 50 mM ABC. Mixtures (100%, 50%, 25%, 10%, 5%, 0% of *S. aureus* protein) were generated using both extracts to a total protein content of 4 µg. The mixtures were digested using trypsin followed by ZipTip® peptide purification. The peptide mixtures were measured in DDA-MS and DIA-MS mode in a Q Exactive™.

3.1.6 Construction of *S. aureus* HG001 carrying optimized GFP

For the codon usage optimization of the GFPmut2 protein the web server OPTIMIZER³⁹ was used. To do so, the codon usage was optimized employing the codon usage of ribosomal proteins of *S. aureus* NCTC8325 and the guided random method, which is a Monte Carlo algorithm that selects codons at random, based on the frequencies of use of each codon in the reference set. The optimized sequence was synthesized by the company GenScript (Piscataway, NJ, USA) and replaced the initial sequence in plasmid pJL-sar-GFP⁴⁰ resulting in pJL-sar-GFPopt.

3.2 Mass spectrometric data acquisition using different LC instruments, MS devices, and acquisition methods

3.2.1 Mass spectrometric acquisition of TripleTOF DDA and SWATH data

S. aureus tryptic digests were analyzed on a TripleTOF® 5600⁺ mass spectrometer (Sciex, Framingham, MA, USA) equipped with an Eksigent ekspert™ nanoLC 425 and cHiPLC® system in trap-elute configuration. Samples were loaded on a cHiPLC column (75 µm x 15 cm ChromXP C18-CL, 3 µm, 120 Å) and washed for 30 min at 0.5 µl/min. Chromatographic separation was performed on a nano cHiPLC column (75 µm x 15 cm ChromXP C18-CL, 3 µm, 120 Å) using a gradient from 2-25% acetonitrile / 0.1% formic acid (v/v) for 180 min at a flow rate of 300 nL/min. Spectra were acquired in data-dependent mode in the mass range m/z 400-1250 with a 250 ms accumulation time. The 20 most intense ions with charge states 2-4 were selected for fragmentation with rolling collision energy and a collision energy spread of +/-5V. MS/MS spectra were collected in the range of m/z 100-2,000 with a 150 ms accumulation time upon a threshold of 100 cps. SWATH-MS data were collected with the MS/MS^{ALL} SWATH™ Acquisition method where Q1 was scanned from 400-1,200 Da and MS/MS acquired from 300-1500 Da. The Q1 transmission window was set at 26 Da wide with a 1 Da overlap with the previous window, 32 steps were used with a 100 ms MS/MS accumulation time for a total cycle time of 3.2 s. Further, samples were analyzed under slightly modified conditions by loading the cellular protein

lysate on a cHiPLC trap (200 μm x 500 μm ChromXP C18-CL, 3 μm , 120 $\text{\AA}$) followed by a 10 min wash step at 2 $\mu\text{l}/\text{min}$ and an elution gradient from 3-35% acetonitrile / 0.1% formic acid (v/v) for 120 min on a nano cHiPLC column (75 μm x 15 cm ChromXP C18-CL, 3 μm , 120 $\text{\AA}$). MS/MS spectra in DDA mode were collected in the range of m/z 100-1,500 with a 150 ms accumulation time, and MS/MS in SWATH mode were acquired from m/z 100-2,000. All other parameters were set as described above.

3.2.2 Mass spectrometric acquisition of nano-HPLC-ESI-LTQ-FT data

Peptides were separated on a nanoAcquity UPLC reversed-phase column (BEH130, C18, 100 μm x 100 mm, Waters Corporation, Milford, USA) operated on a nanoAcquity UPLC system (Waters) using a gradient from 2% to 30% acetonitrile within 60 min at a flow rate of 400 nL/min. MS/MS data were recorded in a data-dependent mode for precursor ions with charge 2 or 3 using an LTQ-FT instrument (Thermo-Fisher Electron, Bremen, Germany). After a survey scan in the FT (scan m/z 300-1500 Da, resolution 50,000), MS/MS in the linear ion trap was triggered on the five most intensive ions exceeding a minimum threshold of 1,000. Target ions already selected for fragmentation were dynamically excluded for 90 s.

3.2.3 Mass spectrometric data-dependent-acquisition (DDA) analyses using a Q

ExactiveTM instrument

MS analyses were performed with an on-line coupled UltiMate 3000RSLC system (Thermo-Fisher Scientific, Idstein, Germany) connected to a Q ExactiveTM Orbitrap-MS (Thermo-Fisher Scientific Inc.). For LC-separation peptides were enriched on an Acclaim PepMap 100, 100 μm x 2 cm, nanoViper C18, 5 μm , 100 $\text{\AA}$ pre-column (Thermo-Fisher Scientific Inc.) and separated using an Accucore 150-C18 with a column length of 25 cm respectively 50 cm (150 $\text{\AA}$, 2.6 μm , Thermo Fisher Scientific Inc.) and a temperature of 40°C. For separation, a 120 min gradient was used with a solvent mixture of buffer A (5% acetonitrile (ACN) in water with 0.1% acetic acid) and increasing percentages of buffer B (ACN with 0.1% acetic acid): 2% for 10 min, 2–25% for 120 min, 25–40% for 5 min, 40–90% for 2 min, and 90% for 5 min. Peptides were eluted with a flow rate of 300 nL/min for the 25 cm column and 200 nL/min for the 50 cm column. Full-scan MS was carried out using a mass range of m/z 300 to 1,650. Data were acquired in a data-dependent strategy in profile mode with a resolution of 70,000 for MS at m/z 400 and 17,500 for MS/MS and a positive polarity. The method used allowed sequential isolation of the top ten most intense ions for fragmentation using high-energy collisional dissociation (HCD) with dynamic exclusion for 30 s and disabled early expiration. An intensity threshold of 8.3×10^4 was applied with an isolation width of 3 m/z , normalized collision energy of 27.5 eV, and a starting mass of m/z 100. The charge state screening and monoisotopic precursor selection rejected +1 and +7, +8, and >+8 charged ions.

3.2.4 Mass spectrometric data-independent-acquisition (DIA) analyses using a Q Exactive™ instrument

LC-MS/MS analysis was performed on a Dionex UltiMate 3000 RSLC (Thermo-Fisher Scientific, Idstein, Germany) coupled to a QExactive mass spectrometer (Thermo Fisher Scientific, Waltham, MA, USA). The protein lysate digest was enriched on a 2 cm x 100 µm Acclaim PepMap 100 trap column (100 Å pore size, 5 µm C18 particles, Thermo-Fisher Scientific) and separated on a 50 cm x 75 µm Accucore 150-C18 analytical column (150 Å pore size, 2.6 µm particles, Thermo-Fisher Scientific) with a flow rate of 200 nl/min or a 25 cm x 75 µm Accucore 150-C18 analytical column (150 Å pore size, 2.6 µm particles, Thermo Fisher Scientific) with a flow rate of 300 nl/min at a constant temperature of 40°C. Reversed-phase chromatography was performed with a binary buffer system consisting of 0.1% acetic acid, 5% ACN in water (buffer A) and 100% ACN in 0.1% acetic acid (buffer B). The peptides were separated by applying a linear gradient from 2% to 25% buffer B over a time of 120 min and 180 min for the 25 cm and the 50 cm analytical column, respectively. Eluting peptides were ionized using the chip-based TriVersa NanoMate ion source (Advion Biosciences, Norwich, UK). For the data-independent mode the parameters from Bruderer et. al, 2013 were used⁴¹.

3.3 Data processing for *S. aureus* PeptideAtlas construction, *S. aureus* and S9 cell ion library building, and DIA data analysis

3.3.1 Data processing for *S. aureus* PeptideAtlas construction

MS native data files in different proprietary formats were converted to mzXML or mzML using ProteoWizard 3.0.7364 msConvert⁴². MS/MS spectra were searched with Comet (2013.01 rev. 0)⁴³ against a reference database derived from NCBI (NCBI database year: 2014) comprising 2,891 *S. aureus* proteins. Common contaminants listed in the common repository of adventitious proteins (cRAP) and a sequence-shuffled decoy counterpart were appended to the database. For all data the parent mass error was set to ± 50 ppm and fragment mass error to 0.01 Da, and peptides were allowed to be semi-tryptic with up to two internal cleavage sites. The search parameters included either a fixed modification of +57.021464 for carbamidomethylated cysteine for reduced and alkylated samples or none for un-alkylated samples, and a variable modification of +15.9949 for oxidized methionine. For the SILAC host-pathogen internalization assay experiments, the variable modifications of +8.014199 at lysine and +10.008269 at arginine were searched. The search results were processed with the Trans-Proteomic Pipeline (TPP, version 4.6)⁴⁴ including PeptideProphet, iProphet, and ProteinProphet⁴⁵⁻⁴⁸.

Peptide spectrum matches (PSM) derived from the database search were analyzed with PeptideProphet to assign each PSM a probability of being correct. The accurate mass binning model and the non-parametric model were used in the PeptideProphet analysis. Decoy hits were reported with a probability based on the model learned. PeptideProphet results were further processed with iProphet to refine the PSM-level probabilities and compute peptide-level probabilities based on corroborating information from the ensemble of identifications⁴⁸. Finally, ProteinProphet was applied to obtain probabilities on the protein level based on the input peptide-level probabilities. A uniform PSM-level FDR threshold was applied to each experiment in order to achieve a protein-level FDR of approximately 1%. Data filtered at this threshold were assessed with MAYU⁴⁹ to calculate a decoy-based FDR at the PSM level (0.01%), peptide level (0.02%) and protein level (1.1%) for the *S. aureus* PeptideAtlas. The build named *S. aureus* HG001 2015-12 is available at www.peptideatlas.org. The *S. aureus* COL PeptideAtlas (*S. aureus* COL 2013-10, 0.04% peptide FDR, 0.22% protein FDR) is available as separate build.

3.3.2 Building an *S. aureus* fragment ion spectral library for DIA data analysis

MS native data files in different proprietary formats were converted to mzXML or mzML using ProteoWizard 3.0.7364 msconvert⁴². MS/MS spectra were searched with Comet (2014.02 rev. 0)⁴³ against a *S. aureus* NCTC8325 database comprising 2,891 proteins as described above for the *S. aureus* PeptideAtlas construction.

In addition to other essential information for building an ion library with the aim to analyze DIA data the retention time is a crucial factor. Therefore, all previously described high-accurate MS analysis runs³ were separately aligned to a reference measurement set of six sample replicates with spiked-in iRT peptides.

For this purpose, the individual Comet-searched iProphet results were converted to a blib file (BiblioSpec algorithm description⁵⁰) using ProteoWizard 3.0.7364⁴² (iProphet cut-off score = 0.9). The resulting peptide error ranged from 0.0004 to 0.0053 with a median error of 0.003 for all files. The non-redundant blib files were used to generate a library using R⁵¹ version 3.2.3 and the bioconductor package specL (1.5.2)¹¹ [parameter: max MZ error: 0.01 Da; TopN: 10; fragment ion *m/z* range: 300 - 2000; fragment ion type: b,y].

After generating the fragment ion spectral library, the peptide intersection of the ion library and the reference measurement set was compared for each file and used for retention time fitting. First, a linear regression of the sample retention time was carried out, and peptides with residuals between the 25% and the 75% quantile over all residuals were used for further analysis. Second, the ratio between the retention time of the intersecting reference set and the sample set was calculated and

used for performing a Loess fit model. Third, the fitted retention time values were used to calculate the adjusted retention time of the non-intersecting and quantile-filtered peptides.

The resulting aligned single-search ion library was filtered for 6-10 transitions per assay and peptides with two tryptic termini to obtain a robust ion library for the DIA data analysis. Redundant assays targeting the same peptide entries were filtered for the fusion of the single-search files: First, if the assays possessed equal numbers of transitions, the assay with the lowest m/z error was used and, second, if they did not possess the same number of transitions, the assay with the highest transition number was used. Furthermore, if an assay was found in both the iRT measurements and the non-iRT measurements and got a higher number of transitions or a lower m/z error in the non-iRT run, all the mass and charge information was used from the non-iRT run, and the retention time was used from the iRT run because it was empirically determined.

3.3.3 Building an S9 human cell line fragment ion spectral library for DIA data analysis

Nine measurements of S9 human cell line protein extract with spiked-in iRT peptides were searched against the human UniProt canonical database (last modified 10th of May 2015). Common contaminants listed in the common repository of adventitious proteins (cRAP), iRT peptides, and a sequence-shuffled decoy counterpart were appended to the database. For the search the parent mass error was set to ± 50 ppm and peptides were allowed to be semitryptic with up to two internal cleavage sites. The search parameters included a fixed modification of +57.021464 for carbamidomethylated cysteine and a variable modification of +15.9949 for oxidized methionine. Downstream processing of the data was performed as described above for the *S. aureus* PeptideAtlas construction.

The individual Comet searched iProphet results were converted to a blib file using ProteoWizard 3.0.7364⁴² (cut-off score = 0.9). The non-redundant blib files were used to generate a library using the bioconductor package specL (1.5.2)¹¹ [parameter: max MZ error: 0.01 Da; TopN: 10; fragment ion m/z range: 300-2,000; fragment ion type: b,y]. The final library was filtered for 6-10 transitions and the lowest fragment mass error.

3.3.4 DIA data analysis

The data analysis was performed using SpectronautTM (v7.0.8065.3.13226 academic+)⁵². For TripleTOF[®] and Q ExactiveTM-derived assay comparison TSB exponential (exp.) and stationary (stat.) phase DIA measured samples were analyzed using SpectronautTM (iRT factor = 1; interference correction = TRUE). The resulting data were used to plot the ratios of mean total peak areas (stat. / exp.) of assays (Q-value cut-off < 0.001) without missing values. The R-squared regression coefficient was calculated using the linear fit model on scattered data.

For the Spectronaut™ analysis the data was extracted with the settings as shown in Supplemental Table S2.

Only highly significant assays (Q-value < 0.001) were used for the analysis. The intensity of the samples was normalized on the assay ratio basis against the control. Ratios for each assay were calculated by generating the pairwise ratios from the experimental conditions versus the control in all combinations based on the replicates in each experiment. The obtained values were tested protein-wise using the Wilcoxon rank sum test against an absolute fold change of 1.5. The p-value was subsequently adjusted for multiple testing using Benjamini and Hochberg's method⁵³, and proteins with a p-value below 0.05 were assumed to be significantly regulated. The peptide and protein ratios were determined by using the median over the corresponding assay ratios.

The protein annotation and symbols used were from aureowiki (http://aureowiki.med.uni-greifswald.de/Main_Page).

3.3.5 DDA data analysis of S9 and *S. aureus* extract mixtures and TSB exponential and stationary phase samples

The DDA data analysis of the S9 and *S. aureus* proteome mixtures was performed using MaxQuant (v1.5.3.30) and a combined FASTA file containing human (www.uniprot.org / June 2015) and *S. aureus* (described above) proteins. The DDA data analysis of the TSB exponential and stationary phase samples was performed using MaxQuant (v1.5.3.30) and an *S. aureus* FASTA (described above).

For all data the first search mass error was set to ± 20 ppm and the main search mass error ± 4.5 ppm, and peptides were allowed to be full-tryptic with up to two internal cleavage sites. The search parameters included a variable modification of +15.9949 for oxidized methionine. Peptide false-discovery rate (FDR) was set to 0.001 and protein was set to a FDR of 0.01. The peptide and protein intensity data was used for median-median normalization over all samples. Followed by filtering for peptides uniquely belonging to *S. aureus*. For the DDA data analysis of the S9 and *S. aureus* proteome mixtures the two technical replicates were aggregated using the mean. The peptide intensities were 100 percent normalized to the pure (100%) *S. aureus* sample for each peptide.

3.3.6 DIA data analysis of S9 and *S. aureus* extract mixtures

The DIA data analysis of the S9 and *S. aureus* proteome mixtures was performed using Spectronaut™ and the S9 and *S. aureus* ion library (section 2.3.2 and 2.3.3). The analysis was performed using a Q-value of 0.001. The ion total peak was summed up for each peptide to obtain the peptide intensities. The peptide intensity data was used for median-median normalization over all samples. Followed by filtering for peptides uniquely belonging to *S. aureus*. The two technical replicates were aggregated

using the mean. The peptide intensities were 100 percent normalized to the pure (100%) *S. aureus* sample for each peptide.

3.3.7 R-packages used for the analysis and plotting

Package	Author	Title	Version
<i>BiocParallel</i>	Bioconductor Package Maintainer, Martin Morgan, Valerie Obenchain, Michel Lang, Ryan Thompson	Bioconductor facilities for parallel evaluation	v1.2.22
<i>data.table</i>	M. Dowle, A. Srinivasan, T. Short, S. Lianoglou; with contributions from R. Saporta, E. Antonyan	Extension of Data.frame	v1.9.6
<i>gplots</i>	Gregory R. Warnes, Ben Bolker, Lodewijk Bonebakker, Robert Gentleman, Wolfgang Huber, Andy Liaw, Thomas Lumley, Martin Maechler, Arni Magnusson, Steffen Moeller, Marc Schwartz, Bill Venables	Various R Programming Tools for Plotting Data	v2.17.0
<i>ggplot2</i>	Hadley Wickham	ggplot2: Elegant Graphics for Data Analysis	v2.2.1
<i>made4</i>	Aedin Culhane	Multivariate analysis of microarray data using ADE4	v1.42.0
<i>MASS</i>	Brian Ripley, Bill Venables, Douglas M. Bates, Kurt Hornik, Albrecht Gebhardt, David Firth	Support Functions and Datasets for Venables and Ripley's MASS	v7.3-45
<i>micropan</i>	Lars Snipen and Kristian Hovde Liland	micropan: Microbial Pan-Genome Analysis	1.0
<i>plotrix</i>	Jim Lemon, Ben Bolker, Sander Oom, Eduardo Klein, Barry Rowlingson, Hadley Wickham, Anupam Tyagi, Olivier Etteradossi, Gabor Grothendieck, Michael Toews, John Kane, Rolf Turner, Carl Witthoft, Julian Stander, Thomas Petzoldt, Remko Duursma, Elisa Biancotto, Ofir Levy, Christophe Dutang, Peter Solymos, Robby Engelmann, Michael Hecker, Felix Steinbeck, Hans Borchers, Henrik Singmann, Ted Toal, Derek Ogle	Various Plotting Functions	v3.6-1

<i>protViz</i>	Christian Panse, Jonas Grossmann, Simon Barkow-Oesterreicher	Visualizing and Analyzing Mass Spectrometry Related Data inProteomics	v0.2.9
<i>RColorBrewer</i>	Erich Neuwirth	ColorBrewer Palettes	v1.1-2
<i>reshape</i>	Hadley Wickham	Flexibly reshape data.	v0.8.5
<i>scales</i>	Hadley Wickham, RStudio	Scale Functions for Visualization	v0.3.0
<i>seqinr</i>	Delphine Charif, Jean R. Lobry, Anamaria Necsulea, Leonor Palmeira, Simon Penel, Guy Perriere	Biological Sequences Retrieval and Analysis	v3.1-3
<i>sfsmisc</i>	Martin Maechler <i>et al.</i>	Utilities from "Seminar für Statistik" ETH Zurich	v1.0-29
<i>specL</i>	Christian Trachsel, Christian Panse, Jonas Grossmann, Witold E. Wolski	specL - Prepare Peptide Spectrum Matches for Use in Targeted Proteomics	v1.5.2
<i>stringi</i>	Marek Gagolewski, Bartek Tartanus , IBM and other contributors, Unicode, Inc.	Character String Processing Facilities	v1.0-1
<i>stringr</i>	Hadley Wickham, RStudio	Simple, Consistent Wrappers for Common String Operations	v1.0.0

4 Supplemental legends

Supplemental Movie S1:

Live-cell imaging movie showing *S. aureus* behavior during infection of S9 human bronchial epithelial cells over time. Human S9 cells are displayed in the Nomarski Differential Interference Contrast (DIC) in transmitted-light channel (greyish), and the intracellular GFP-labeled *S. aureus* cells are shown in green.

5 Supplemental references

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6 Supplemental tables

Supplemental Table S1 (page: 41-45):

Overview of the DDA measurements (a) used for the PeptideAtlas and ion library generation and of the DIA measurements (b) used for the analysis of biological samples.

Supplemental Table S2 (page: 46):

Parameters used for the SpectronautTM (Biognosys, Schlieren/Zurich, Switzerland) DIA analysis.

Supplemental Table S3 (page: 47-50):

Significantly regulated proteins (Benjamini-Hochberg corrected p-value < 0.05; absolute fold-change > 1.5) on comparing exponential and stationary growth phase of *S. aureus* HG001 cells grown in tryptic soy broth. Orange depicts up-regulation, blue visualizes down-regulation in the stationary phase. In addition the table contains also ratios from exponential and stationary growth phase of *S. aureus* COL cells grown in BioExpress medium extracted from Becher et al., 2009⁵.

Supplemental Table S4 (page: 51-57):

Significantly regulated proteins (Benjamini-Hochberg corrected p-value < 0.05; absolute fold-change > 1.5) of the S9 human bronchial epithelial cell infection model. Orange depicts up-regulation, blue visualizes down-regulation in host-cell-internalized *S. aureus* as compared to the non-adherent cell control.

Supplemental Table S5 (page: 58-64):

Comparison of intracellularly growing cells (8h post-infection) versus non-adherent control and intracellularly growing cells to 24h or 32h post-infection.

Significantly regulated proteins (Benjamini-Hochberg corrected p-value < 0.05; absolute fold-change > 1.5) of the S9 human bronchial epithelial cell infection model. Orange depicts up-regulation, blue visualizes down-regulation in host-cell-internalized *S. aureus* as compared to the non-adherent cell control.

Supplemental Table S6 (page: 65-77):

Proteins detected in samples of the murine pneumonia infection model and S9 cell infection model (at least 2 peptides per protein and in one sample). The log₂-ratios against the individual control (murine pneumonia model = pre-infection; S9 cell infection model = non-adherent bacteria after 1 h) were colored using a blue to orange color space. Bluish color indicates a lower and orange color indicates a higher level as compared to the control. The colored arrows display the median tendency. For example, if the arrow points “up” the median of the 8, 24, 32 h p.i. samples is more than 1.5-fold higher as compared to the control.

Supplemental Table S7 (page: 78):

List of recombinant *S. aureus* proteins measured for incorporation into the ion library.

Supplemental Table S1A: Data sets used for the generation of *S. aureus* PeptideAtlas (DDA samples)

<i>S. aureus</i> strain	sample material and cultivation conditions	sampling points	biological replicates	fractionation	MS instrument type	number of raw files	used for DIA library	reference
HG001, HG001 $\Delta sigB$	culture supernatants from rich medium TSB, culture supernatants from minimal medium pMEM	exponential growth, stationary growth (TSB:10 h; pMEM: 5 h), late stationary growth (TSB: 24 h, pMEM: 19 h)	4	non-fractionated	ESI-LTQ-FT	48	NO	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	3	non-fractionated off-gel electrophoresis/pI (peptides) SCX (peptides)	Q Exactive™	3 120 21	YES	Depke, Michalik et al. Proteomics, 2015
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	non-fractionated	Q Exactive™	6	YES	this paper

HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	non-fractionated	TripleTOF®	12	YES	this paper
HG001	extracellular and intracellular proteome from unstressed cells growing in pMEM and from cells during iron limitation by adding 2,2'-bipyridyl	exponential and stationary growth phase; intracellular and extracellular proteome	3	non-fractionated	Q Exactive™	24	YES	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	membrane fraction	Q Exactive™	4	YES	this paper
HG001	purified recombinant proteins; overexpressed and purified His-tagged <i>S. aureus</i> proteins in <i>E. coli</i> SCS1	-		non-fractionated	Q Exactive™	4	YES	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	off-gel electrophoresis/pI (peptides)	QTOF	24	NO	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	off-gel electrophoresis/pI (peptides)	LTQ XL Orbitrap	24	NO	this paper

		stationary growth phase						
HG001	culture supernatants from rich medium TSB	extracellular proteome; mixed sample from supernatants of exponential growth, entry into stationary growth phase, and stationary growth phase	1	non-fractionated	QTOF	1	NO	this paper
HG001	culture supernatants from rich medium TSB	extracellular proteome; mixed sample from supernatants of exponential growth, entry into stationary growth phase, and stationary growth phase	1 (measured in 2 technical replicates)	non-fractionated	LTQ XL Orbitrap	2	NO	this paper
HG001 pMV158-GFP	internalized bacteria from cell culture infection model using human alveolar A549 cells and corresponding control cells	1.5 h, 2.5 h, 3.5 h, 4.5 h, 5.5 h, and 6.5 h after internalization into A549 cells; 1 h extracellular non-adherent bacteria; 1.5 h medium control; ¹³ C SILAC control	3	non-fractionated	Orbitrap Velos	27	NO	Surmann et al. J Prot, 2015
COL	bacteria from cultivation in BioExpress® 1000 medium and culture supernatants	exponential growth, stationary growth (5 h)	4	cell surface proteins, 1D gel (proteins) cytosolic proteins, 1D gel (proteins) extracellular proteins, 1D gel (proteins)	LTQ-Orbitrap	40 100 44	NO	Becher et al. PLoS One, 2009

Supplemental Table S1B: samples generated for DIA analysis

<i>S. aureus</i> strain	sample material and cultivation conditions	sampling points	biological replicates	fractionation	MS instrument type	number of raw files	reference
HG001	bacteria from cultivation in rich medium TSB	exponential growth, stationary growth (4 h)	3	non-fractionated	Q Exactive™	6	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	non-fractionated	Q Exactive™	3	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase	1	non-fractionated	TripleTOF®	3	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase 5ng, 10ng, 50ng, 100ng, 500ng, 1000ng, 2000ng, 4000ng on-column load	1 (measured in 2 technical replicates)	non-fractionated	Q Exactive™	16	this paper
HG001	bacteria from cultivation in rich medium TSB	mixed sample from exponential growth, entry into stationary growth phase, and stationary growth phase on-column load of peptides from 1E4, 1E5, 5E5, 1E6, 5E6, 1E7 <i>S. aureus</i> cells	1 (measured in 2 technical replicates)	non-fractionated	Q Exactive™	12	this paper
HG001	S9 cell line infection experiment	OD=0.4 in pMEM, non-adherent <i>S. aureus</i> cells, S9 internalized <i>S. aureus</i> 8 h, 24 h, 32 h p.i.	3 or 4	non-fractionated	Q Exactive™	19	this paper

HG001	murine infection model	pre-infection <i>S.aureus</i> cells, <i>S.aureus</i> from lavage preparation 8 h, 24 h, 32 h p.i.	3, finally combined to one sample	non-fractionated	Q Exactive™	6	this paper
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Supplemental table S2: Spectronaut™ parameters

peak detection	XIC extraction window: dynamic window correction factor = 1
identification	dynamic score refinement = TRUE processing base entity = RUN generate decoys = TRUE decoy generation method = workflow specific decoy generator include MS1 scoring = TRUE
calibration strategy	iRT calibration strategy: linear iRT calibration
quantification	interference correction: TRUE cross run normalization: FALSE

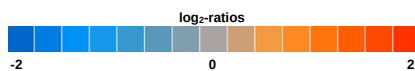
supplemental table S3: Significant regulated proteins in comparison of TSB exponentially and stationary phase *S. aureus*

locus tag	protein symbol	description	theSEED functional category	median fold-change	median fold-change (direction)	median ratio over assays (TSB stat./exp.)	IQR	p-value BH adjusted	log2 median ratio over Becher et al., 2009	log2 ratio Becher et al., 2009	locus tag (COL)
SAOUHSC_00487	HspD	Hsp33-like chaperonin	Adhesion	2.38	down	0.44	0.180	1.68E-08	-1.59	n.d.	SACOL0556
SAOUHSC_00544	SdcC	sdcC protein	Adhesion	6.70	up	6.70	3.851	4.04E-02	2.74	n.d.	SACOL0608
SAOUHSC_00812	CfA	clumping factor	Adhesion	17.79	up	17.79	14.242	1.56E-05	4.15	n.d.	SACOL0856
SAOUHSC_01501	ElpS	elastin binding protein	Adhesion	3.56	up	3.56	1.194	6.22E-27	1.83	n.d.	SACOL1532
SAOUHSC_02990	SraP	hypothetical protein	Adhesion	7.90	up	7.90	8.565	1.12E-04	2.98	n.d.	SACOL2676
SAOUHSC_01633	GcvPA	glycine dehydrogenase subunit 1	Alanine, serine, and glycine	3.34	up	3.34	1.257	5.85E-14	1.74	1.74	SACOL1594
SAOUHSC_01634	GcvT	glycine cleavage system aminomethyltransferase T	Alanine, serine, and glycine	4.46	up	4.46	2.428	1.21E-12	2.16	1.83	SACOL1595
SAOUHSC_00532	Kbl	2-amino-3-ketobutyrate coenzyme A ligase	Alanine, serine, and glycine;Lysine, threonine, and cysteine	4.01	up	4.01	1.622	1.58E-18	2.00	1.71	SACOL0596
SAOUHSC_00535		hypothetical protein	Alanine, serine, and glycine;Lysine, threonine, and cysteine	5.09	up	5.09	2.347	4.06E-08	2.35	1.83	SACOL0599
SAOUHSC_02564	UreG	urease accessory protein UreG	Arginine; urea cycle, polyamines	1.68	up	1.68	0.527	2.71E-02	0.75	-0.10	SACOL2285
SAOUHSC_00894	RccD	ornithine-oxo-acid transaminase	Arginine; urea cycle, polyamines;Proline and 4-hydroxyproline	14.02	up	14.02	11.229	4.54E-10	3.81	n.d.	SACOL0960
SAOUHSC_01809	AccD	acetyl-CoA carboxylase subunit beta	Bacteriocins, ribosomally synthesized antibacterial peptides;Fatty acids	1.80	down	0.55	0.262	5.05E-04	-0.85	-0.69	SACOL1748
SAOUHSC_01014	PurF	amidophosphoribosyltransferase	Bacteriocins, ribosomally synthesized antibacterial peptides;Purines	6.51	up	6.51	6.903	8.55E-10	2.70	1.30	SACOL1079
SAOUHSC_00198	FatE	hypothetical protein	Biotin	20.18	up	20.18	1.647	4.04E-02	4.34	n.d.	SACOL0214
SAOUHSC_00195	FatA	acetyl-CoA acetyltransferase	Biotin;Branched-chain amino acids;Fatty Acids, Lipids, and isoprenoids - no subcategory;One-carbon Metabolism	49.41	up	49.41	9.988	4.04E-02	5.63	n.d.	SACOL0211
SAOUHSC_02589		hypothetical protein	Capsular and extracellular polysaccharides	3.35	up	3.35	1.497	4.04E-02	1.75	n.d.	SACOL2081
SAOUHSC_01462	GpiB	hypothetical protein	Cell Division and Cell Cycle - no subcategory	3.05	up	3.05	1.080	5.82E-12	1.61	0.25	SACOL1484
SAOUHSC_02337	MurA1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell Wall and Capsule - no subcategory	2.22	down	0.45	0.148	1.16E-22	-1.15	-0.61	SACOL2092
SAOUHSC_02365	MurA2	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell Wall and Capsule - no subcategory	1.61	down	0.62	0.177	2.27E-02	-0.69	-0.43	SACOL1266
SAOUHSC_01373	FemA	methicillin resistance factor, FemA	Cell Wall and Capsule - no subcategory;Resistance to antibiotics and toxic compounds	2.48	down	0.40	0.185	8.24E-13	-1.31	n.d.	SACOL1410
SAOUHSC_00153		indolepyruvate decarboxylase	Central carbohydrate metabolism	4.02	up	4.02	1.141	4.24E-13	2.01	-0.03	SACOL0173
SAOUHSC_01064	PycA	pyruvate carboxylase	Central carbohydrate metabolism	2.60	up	2.60	1.047	5.64E-48	1.38	0.42	SACOL1123
SAOUHSC_01418	SucA	2-oxoglutarate dehydrogenase E1 component	Central carbohydrate metabolism	8.24	up	8.24	6.819	1.44E-11	3.04	1.44	SACOL1449
SAOUHSC_01801	CitC	isocitrate dehydrogenase	Central carbohydrate metabolism	8.03	up	8.03	0.505	3.15E-17	3.01	2.42	SACOL1741
SAOUHSC_01818	AluG	alanine dehydrogenase	Central carbohydrate metabolism	6.78	up	6.78	5.716	4.24E-13	2.76	1.57	SACOL1758
SAOUHSC_01846	AcS	acetyl-CoA synthetase	Central carbohydrate metabolism	14.17	up	14.17	5.024	1.56E-05	3.82	0.43	SACOL1783
SAOUHSC_01183	FumC	fumarate hydratase	Central carbohydrate metabolism	6.21	up	6.21	3.311	1.88E-14	2.64	2.74	SACOL1508
SAOUHSC_02647	MqoA	malate:quinone oxidoreductase	Central carbohydrate metabolism	9.56	up	9.56	4.919	1.87E-09	3.26	0.80	SACOL2362
SAOUHSC_02703	GpmA	phosphoglyceromutase	Central carbohydrate metabolism	5.34	up	5.34	2.378	2.71E-15	2.42	1.70	SACOL2415
SAOUHSC_01416	SucB	dihydroipsoamide succinyltransferase	Central carbohydrate metabolism;Lipoic acid	10.70	up	10.70	24.419	6.60E-14	2.42	2.47	SACOL1448
SAOUHSC_01216	SucC	succinyl-CoA synthetase subunit beta	Central carbohydrate metabolism;One-carbon Metabolism	7.07	up	7.07	5.345	4.07E-24	2.82	2.35	SACOL1262
SAOUHSC_01218	SucD	succinyl-CoA synthetase subunit alpha	Central carbohydrate metabolism;One-carbon Metabolism	6.80	up	6.80	3.829	2.18E-10	2.77	2.23	SACOL1263
SAOUHSC_01910	PckA	phosphoenolpyruvate carboxykinase	Central carbohydrate metabolism;One-carbon Metabolism	11.75	up	11.75	3.896	8.80E-11	2.56	n.d.	SACOL1338
SAOUHSC_00866		D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing	Central carbohydrate metabolism;Organic acids	1.71	up	1.71	0.540	8.37E-03	0.77	-0.13	SACOL2932
SAOUHSC_02577		D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing	Central carbohydrate metabolism;Organic acids	4.44	up	4.44	1.415	5.95E-19	2.35	2.07	SACOL2786
SAOUHSC_00795	GdhA	glyoxaldehyde 3-phosphate dehydrogenase, type I	Central carbohydrate metabolism;Oxidative stress;Pyridoxine	1.75	down	0.57	0.180	5.98E-07	-0.81	-0.10	SACOL2038
SAOUHSC_01012	AlaA	alanine dehydrogenase	Central carbohydrate metabolism;Phospholipids	4.54	up	4.54	0.514	4.04E-02	2.27	0.26	SACOL0154
SAOUHSC_01142	AlaH	alpha-aldehyde dehydrogenase	Central carbohydrate metabolism;Phospholipids	3.77	up	3.77	1.175	7.30E-16	1.45	1.10	SACOL1584
SAOUHSC_01075	CsdD	phosphoglutathione adenylyltransferase	Cysteine A	2.28	down	0.44	0.166	2.15E-16	-1.17	-0.78	SACOL1114
SAOUHSC_02918	PacC	penicillin-beta-lactamase ligase	Cysteine A	3.88	down	0.36	0.088	1.15E-12	-1.59	-0.19	SACOL1214
SAOUHSC_01824	ThiI	thiamine biosynthesis protein ThiI	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	3.65	down	0.27	0.061	1.52E-07	-1.57	-0.58	SACOL1764
SAOUHSC_00819	CysC	hypothetical protein	Cold shock	4.78	down	0.21	0.113	1.06E-07	-3.16	n.d.	SACOL0861
SAOUHSC_00437	TspP	hypothetical protein	Di- and oligosaccharides	2.58	up	2.58	0.750	5.79E-03	1.32	n.d.	SACOL0516
SAOUHSC_02848	GliB	PTS system glucose-specific transporter subunit IABC	Di- and oligosaccharides	2.08	up	2.08	1.011	8.38E-08	1.06	n.d.	SACOL2352
SAOUHSC_00776	UvrE	endonuclease ABC, B subunit	DNA repair	2.38	up	2.38	2.155	1.22E-04	1.25	0.87	SACOL0823
SAOUHSC_00779	UvrB2	endonuclease ABC subunit B	DNA repair	2.09	up	2.09	0.637	3.43E-10	1.18	n.d.	SACOL1583
SAOUHSC_01658	Nfo	endonuclease IV	DNA repair	1.85	down	0.54	0.163	1.51E-03	-0.69	-0.50	SACOL1554
SAOUHSC_02123	PckA	ATP-dependent DNA helicase PckA	DNA repair	1.99	down	0.50	0.219	3.11E-05	-0.99	-1.44	SACOL1566
SAOUHSC_02861		methylated DNA-protein-cysteine methyltransferase	DNA repair	3.73	up	3.73	1.541	3.00E-05	1.89	1.41	SACOL2562
SAOUHSC_01241	PicC	DNA polymerase III PicC	DNA replication	1.21	down	0.55	0.215	1.80E-04	-0.55	-0.89	SACOL1283
SAOUHSC_01351	ParE	DNA topoisomerase IV subunit B	DNA replication;Resistance to antibiotics and toxic compounds	1.89	down	0.53	0.164	5.79E-19	-0.72	n.d.	SACOL1580
SAOUHSC_01352	ParC	DNA topoisomerase IV subunit A	DNA replication;Resistance to antibiotics and toxic compounds	1.65	down	0.60	0.194	3.80E-04	-0.54	-0.89	SACOL1589
SAOUHSC_02517	TspB	DNA topoisomerase II	DNA uptake, competence	2.10	down	0.48	0.159	6.70E-12	-1.07	n.d.	SACOL2243
SAOUHSC_00469	SpoVG	regulatory protein SpoVG	Dormancy and Sporulation - no subcategory	6.59	up	6.59	4.374	4.22E-06	3.10	n.d.	SACOL0541
SAOUHSC_00883		hypothetical protein	Dormancy and Sporulation - no subcategory	2.19	down	0.46	0.142	1.56E-05	-1.13	-0.71	SACOL0552
SAOUHSC_00875		hypothetical protein	Electron donating reactions	3.05	up	3.05	1.427	0.04E-13	1.61	n.d.	SACOL0941
SAOUHSC_01104	SdhA	succinate dehydrogenase flavoprotein subunit	Electron donating reactions;Central carbohydrate metabolism;One-carbon Metabolism	9.43	up	9.43	7.235	7.36E-16	3.14	3.04	SACOL1159
SAOUHSC_01105	SdhB	succinate dehydrogenase iron-sulfur subunit	Electron donating reactions;Central carbohydrate metabolism	7.26	up	7.26	1.578	8.06E-04	2.86	2.91	SACOL1160
SAOUHSC_00920	FabH	3-oxoacyl (acyl carrier protein) synthase III	Fatty acids	1.76	down	0.57	0.166	3.34E-06	-0.81	-0.85	SACOL0987
SAOUHSC_00947	FabI	enoyl (acyl carrier protein) reductase	Fatty acids	1.94	down	0.52	0.278	1.74E-03	-0.56	-0.06	SACOL1016
SAOUHSC_01198	FabD	malonyl-CoA-acyl carrier protein transacylase	Fatty acids	2.00	down	0.50	0.125	5.34E-11	-1.00	-0.80	SACOL1244
SAOUHSC_01199	FabG	3-oxoacyl (acyl-carrier-protein) reductase	Fatty acids	1.76	down	0.57	0.209	5.61E-08	-0.81	-0.94	SACOL1245
SAOUHSC_01623	AccC	acetyl-CoA carboxylase biotin carboxylase subunit	Fatty acids;Miscellaneous - no subcategory	1.76	down	0.57	0.217	1.28E-02	-0.82	-0.37	SACOL1571
SAOUHSC_00086	BuA	acetoin reductase	Fermentation	18.03	up	18.03	0.075	4.24E-13	4.17	1.15	SACOL0111
SAOUHSC_00206	Ldh1	L-lactate dehydrogenase	Fermentation	2.92	up	2.92	2.320	1.51E-11	1.54	4.40	SACOL0222
SAOUHSC_02922	Ldh2	L-lactate dehydrogenase	Fermentation	1.98	up	1.98	0.036	1.96E-08	0.96	0.88	SACOL2618
SAOUHSC_00196	FadB	hypothetical protein	Fermentation;Branched-chain amino acids;Fatty Acids, Lipids, and isoprenoids - no subcategory	27.52	up	27.52	7.802	2.81E-12	4.76	n.d.	SACOL0212
SAOUHSC_02468	BuB	acetylaldehyde synthase	Fermentation;Organic acids;Programmed Cell Death and Toxin-antitoxin Systems	2.03	up	2.03	0.955	2.22E-09	1.02	n.d.	SACOL2199
SAOUHSC_00608	Adh	alcohol dehydrogenase	Fermentation;Phospholipids	3.88	up	3.88	1.086	1.57E-03	1.96	n.d.	SACOL0660
SAOUHSC_00187	PFB	formate acetyltransferase	Fermentation;Respiration - no subcategory	7.11	up	7.11	5.947	3.00E-05	2.83	n.d.	SACOL0204
SAOUHSC_02542	MoaA	molybdopterin biosynthesis protein moaA	Folate and pterines	2.93	up	2.93	0.799	6.23E-10	1.55	0.09	SACOL2266
SAOUHSC_02544	MoaB	molybdopterin precursor biosynthesis moaB	Folate and pterines	2.05	up	2.05	0.581	1.49E-08	1.04	0.25	SACOL2268
SAOUHSC_02549	MoaK	molybdenum ABC transporter periplasmic molybdate-binding protein	Folate and pterines	3.02	up	3.02	1.417	7.68E-11	1.39	n.d.	SACOL2272
SAOUHSC_02360	Tdk	thymidine kinase	Folate and pterines;Pyrimidines	2.41	down	0.42	0.074	7.75E-08	-1.27	-0.97	SACOL2111
SAOUHSC_00549	FolE2	putative CTP cyclohydrolase	Folate and pterines;RNA processing and modification	1.79	down	0.56	0.211	3.18E-03	-0.84	n.d.	SACOL0613
SAOUHSC_00885	GudB	glutamate dehydrogenase, NAD-specific	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	9.85	up	9.86	4.401	1.56E-05	3.30	1.45	SACOL0961
SAOUHSC_00222	TatC	tagB protein	Gram-Positive cell wall components	3.42	up	3.42	1.183	6.28E-06	1.77	0.41	SACOL2038
SAOUHSC_00548		hypothetical protein	Gram-Positive cell wall components	2.42	up	2.42	0.724	1.88E-11	1.28	n.d.	SACOL0612
SAOUHSC_00641	TagH	teichoic acids export protein ATP-binding subunit	Gram-Positive cell wall components	2.76	down	0.36	0.081	4.06E-08	-1.47	n.d.	SACOL0904
SAOUHSC_00642	TagG	teichoic acid biosynthesis protein	Gram-Positive cell wall components	1.99	down	0.50	0.220	4.43E-04	-0.59	n.d.	SACOL0695
SAOUHSC_00728	LtaS	hypothetical protein	Gram-Positive cell wall components	4.66	down	0.21	0.085	2.91E-07	-2.22	n.d.	SACOL0778
SAOUHSC_01871		polysaccharide biosynthesis protein	Gram-Positive cell wall components	1.82	down	0.55	0.117	2.32E-02	-0.67	n.d.	SACOL1804
SAOUHSC_00870	DltB	dltB protein	Gram-Positive cell wall components;Resistance to antibiotics and toxic compounds	2.31	down	0.43	0.153	5.79E-03	-1.21	n.d.	SACOL0936
SAOUHSC_00871	DltC	D-alanine-poly(phosphoribitol) ligase subunit 2	Gram-Positive cell wall components;Resistance to antibiotics and toxic compounds	1.93	down	0.52	0.218	6.25E-03	-0.95	n.d.	SACOL0937
SAOUHSC_01681	PrmA	ribosomal protein L11 methyltransferase	Heat shock;Protein biosynthesis	2.09	down	0.48	0.235	2.82E-02	-1.06	-1.52	SACOL1435
SAOUHSC_01683	DnaK	molecular chaperone DnaK	Heat shock;Protein folding	1.66	down	0.60	0.191	1.95E-08	-0.71	-0.52	SACOL1637
SAOUHSC_02606	HutI	imidazolepropionase	Histidine Metabolism	13.91	up	13.91	1.034	4.04E-02	3.80	1.19	SACOL2123
SAOUHSC_02607	HutU	uracinate hydratase	Histidine Metabolism	11.00	up	11.00	4.789	8.06E-04	3.46	6.10	SACOL2124
SAOUHSC_01738	HisG	histidinyl-RNA synthetase	Histidine Metabolism;Organic sulfur assimilation;Regulation and Cell signaling - no subcategory	1.82	down	0.55	0.166	3.31E-03	-0.86	-0.92	SACOL1486
SAOUHSC_00020	WurR	two-component response regulator	Iron acquisition and metabolism - no subcategory	2.35	up	2.35	0.665	2.91E-10	1.21	0.42	SACOL0019
SAOUHSC_00130	Iud	heme-degrading monooxygenase Iud	Iron acquisition and metabolism - no subcategory	2.76	up	2.76	0.758	1.19E-03	1.46	-0.59	SACOL0152
SAOUHSC_00749	SstD	hypothetical protein	Iron acquisition and metabolism - no subcategory	4.82	down	0.21	0.091	1.88E-11	-3.21	n.d.	SACOL0759
SAOUHSC_01632	GcvPB	glycine dehydrogenase subunit 2	Lipoic acid;Alanine, serine, and glycine	3.64	up	3.64	2.012	2.61E-11	1.96	n.d.	SACOL1593
SAOUHSC_00861	LipA	lipoyl synthase	Lipoic acid;Plant-Prokaryote comparative genomics	3.94	down	0.25	0.097	6.41E-09	-1.94	-1.85	SACOL0927
SAOUHSC_00842	MethL	ABC transporter ATP-binding protein	Lysine, threonine, methionine, and cysteine	2.22	up	2.22	0.916	2.28E-05</			

locus tag	protein symbol	description	theSEED functional category	median fold-change	median fold-change (direction)	median ratio over assays (TSB stat. / exp.)	IQR	p-value BH adjusted	log2 median ratio over assays (TSB stat. / exp.)	log2 ratio Becher et al., 2009	locus tag (COL)
SAOHSC_02122	LigA	DNA ligase, NAD-dependent	NAD and NADP, DNA repair	1.75	down	0.57	0.164	1.66E-05	-0.80	n.d.	SACOL1965
SAOHSC_00229	ScdA	cell wall biosynthesis protein ScdA	Nitrogen Metabolism - no subcategory; Stress Response - no subcategory	1.99	up	1.99	0.843	1.52E-04	0.99	n.d.	SACOL0244
SAOHSC_00743	NrIF	ribonucleotide-diphosphate reductase subunit beta	Nucleosides and Nucleotides - no subcategory	3.07	down	0.33	0.181	2.27E-11	-1.62	n.d.	SACOL0793
SAOHSC_00742	NrIF	ribonucleotide-diphosphate reductase subunit alpha	Nucleosides and Nucleotides - no subcategory; Oxidative stress	2.30	down	0.43	0.232	1.58E-18	-1.20	-1.37	SACOL0792
SAOHSC_02828		hypothetical protein	One-carbon Metabolism	2.03	up	2.03	0.547	5.56E-07	1.02	1.19	SACOL0233
SAOHSC_00552	HagB	hypothetical protein	One-carbon Metabolism; Aminoacids; Capsular and extracellular polysaccharides; Cell Wall and Capsule - no subcategory	1.87	up	1.87	0.493	1.79E-05	0.90	0.80	SACOL0616
SAOHSC_01007	FuID	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-	One-carbon Metabolism; Folate and pterines	7.63	up	7.63	3.883	7.42E-20	2.89	1.84	SACOL1072
SAOHSC_01802	Ciz2	hypothetical protein	One-carbon Metabolism; Respiration - no subcategory; Central carbohydrate metabolism	5.24	up	5.24	2.981	1.57E-03	2.39	2.95	SACOL1742
SAOHSC_00967	RyP	hypothetical protein	Organic sulfur assimilation	5.02	up	5.02	1.557	8.06E-04	2.26	n.d.	SACOL0954
SAOHSC_00873	NfU	hypothetical protein	Organic sulfur assimilation	2.11	down	0.47	0.149	8.01E-08	-1.04	n.d.	SACOL0939
SAOHSC_01735	Asp5	hypothetical protein	Organic sulfur assimilation	2.00	down	0.50	0.118	5.74E-10	-1.00	-1.13	SACOL1683
SAOHSC_01737	Asp5	aspartyl-tRNA synthetase	Organic sulfur assimilation	2.96	down	0.49	0.155	4.56E-16	-1.04	-1.13	SACOL1685
SAOHSC_00993	BetB	betaine aldehyde dehydrogenase	Osmotic stress	3.05	up	3.05	1.451	4.06E-08	1.61	-1.05	SACOL2628
SAOHSC_00757	Pcp1	peptidase 1	Oxidative stress	1.36	up	1.36	0.751	4.00E-07	0.64	0.44	SACOL0805
SAOHSC_01337	GskA	glyceraldehyde 3-phosphate dehydrogenase 2	Oxidative stress	23.09	up	23.09	14.209	4.24E-13	4.52	1.47	SACOL1558
SAOHSC_02181	Dps	hypothetical protein	Oxidative stress	3.22	up	3.22	2.024	2.94E-09	1.69	0.84	SACOL1231
SAOHSC_01794	GcpB	glyceraledehyde 3-phosphate dehydrogenase 2	Oxidative stress; Central carbohydrate metabolism	5.69	up	5.69	1.547	1.56E-05	2.15	3.30	SACOL1774
SAOHSC_00204	Hspg	globin domain-containing protein	Oxidative stress; Stress Response - no subcategory	3.38	up	3.38	1.933	7.75E-08	1.76	-0.58	SACOL0220
SAOHSC_00436	MecT2	ABC transporter substrate binding protein	Pathogenicity islands; Cytine, Threonine, methionine, and cysteine	3.63	up	3.63	2.181	4.99E-02	1.86	n.d.	SACOL0906
SAOHSC_01239		hypothetical protein	Periplasmic Stress; Regulation and Cell signaling - no subcategory	2.23	down	0.44	0.110	1.73E-04	-1.09	n.d.	SACOL1281
SAOHSC_02071		single-strand DNA-binding protein	Phages, Prophages	4.30	up	4.30	1.209	1.56E-06	2.10	n.d.	
SAOHSC_01193	FakA	hypothetical protein	Phospholipids	1.64	down	0.62	0.283	2.15E-02	-0.71	-0.46	SACOL1240
SAOHSC_01197	FlxX	putative glycerol-3-phosphate acyltransferase FlxX	Phospholipids	1.76	down	0.57	0.259	3.78E-02	-0.81	-0.78	SACOL1243
SAOHSC_02363		alkaliye dehydrogenase	Phospholipids; Central carbohydrate metabolism	3.26	up	3.26	1.812	1.09E-10	1.79	1.36	SACOL1241
SAOHSC_01672	YnfY	hypothetical protein	Phosphorus Metabolism - no subcategory	1.61	up	1.61	0.501	3.91E-02	0.68	0.55	SACOL1627
SAOHSC_00047	PhoP	alkaline phosphatase synthesis transcriptional regulatory protein	Phosphorus Metabolism - no subcategory	2.79	up	2.79	1.509	8.06E-04	1.48	1.01	SACOL1740
SAOHSC_00220	TarT	2-C-methyl-D-erythritol 4-phosphate cyclhydratransferase	Plant-Prokaryotic comparative genomics; Gram-Positive cell wall components; Isoprenoids	3.01	up	3.01	1.165	2.15E-02	1.19	0.25	SACOL0236
SAOHSC_01016		phosphoribosyl/cyrimidine formyltransferase	Potassium metabolism - no subcategory; Purines	6.90	up	6.90	4.597	5.79E-03	2.79	2.71	SACOL1081
SAOHSC_00801	SecG	peptidome translocase subunit SecG	Programmed Cell Death and Toxin-antitoxin Systems	1.78	down	0.56	0.261	5.37E-03	-0.63	n.d.	SACOL0944
SAOHSC_01597	ProC	pyrroline-5-carboxylate reductase	Proline and 4-hydroxyproline	2.35	up	2.35	1.345	9.04E-06	1.24	2.41	SACOL1546
SAOHSC_00409	RocF	arginase	Proline and 4-hydroxyproline; Arginine, urea cycle, polyamines	7.45	up	7.45	1.518	4.04E-02	2.90	4.65	SACOL2154
SAOHSC_00869	RocA	L-pyrroline-5-carboxylate dehydrogenase	Proline and 4-hydroxyproline; Arginine, urea cycle, polyamines	6.94	up	6.94	3.654	6.23E-10	3.16	1.36	SACOL2569
SAOHSC_01695	RocS	hypothetical protein	Proline and 4-hydroxyproline; NAD and NADP	2.58	down	0.39	0.134	7.28E-06	-1.37	-1.85	SACOL1548
SAOHSC_00017	RplI	50S ribosomal protein L9	Protein biogenesis	3.18	down	0.31	0.071	2.91E-07	-0.67	-0.99	SACOL0015
SAOHSC_00346	YnfF	GTP-dependent nucleic acid-binding protein EngD	Protein biogenesis	1.96	down	0.51	0.131	8.28E-18	-0.57	-0.31	SACOL0435
SAOHSC_00348	RplF	30S ribosomal protein S6	Protein biogenesis	2.57	down	0.39	0.252	3.87E-05	-1.36	n.d.	SACOL0437
SAOHSC_00463	RumV	hypothetical protein	Protein biogenesis	2.33	down	0.43	0.093	5.79E-03	-1.22	n.d.	SACOL0535
SAOHSC_00464	KagA	dimethyladenosine transferase	Protein biogenesis	1.74	down	0.57	0.198	8.59E-03	-0.80	-1.02	SACOL0536
SAOHSC_00474	RplV	50S ribosomal protein L25/general stress protein Ciz	Protein biogenesis	2.69	down	0.37	0.112	2.81E-09	-1.43	-1.34	SACOL0545
SAOHSC_00518	RplK	50S ribosomal protein L11	Protein biogenesis	3.01	down	0.33	0.156	3.37E-10	-1.59	n.d.	SACOL0583
SAOHSC_00519	RplA	50S ribosomal protein L1	Protein biogenesis	2.83	down	0.35	0.178	4.37E-16	-1.50	-1.10	SACOL0584
SAOHSC_00520	RplI	50S ribosomal protein L10	Protein biogenesis	2.27	down	0.44	0.264	2.64E-05	-1.18	n.d.	SACOL0585
SAOHSC_00521	RplL	50S ribosomal protein L7/L12	Protein biogenesis	2.35	down	0.43	0.164	3.99E-11	-1.23	-1.43	SACOL0586
SAOHSC_00767	SamPF	Staphylococcus aureus hibernation promoting factor	Protein biogenesis	25.28	up	25.28	24.916	2.18E-10	4.46	0.36	SACOL0815
SAOHSC_01058	TypA	GTP-binding protein TypA	Protein biogenesis	2.70	down	0.37	0.161	2.05E-15	-1.43	n.d.	SACOL1118
SAOHSC_01028	RplP	30S ribosomal protein S16	Protein biogenesis	2.19	down	0.46	0.084	3.97E-07	-1.13	-1.71	SACOL1254
SAOHSC_01211	RplS	50S ribosomal protein L19	Protein biogenesis	2.95	down	0.34	0.132	3.98E-11	-1.56	-1.80	SACOL1257
SAOHSC_01232	RplB	30S ribosomal protein S2	Protein biogenesis	2.45	down	0.41	0.166	9.44E-18	-1.29	-1.09	SACOL1274
SAOHSC_01234	Tsf	elongation factor Ts	Protein biogenesis	1.80	down	0.56	0.236	2.04E-09	-0.85	n.d.	SACOL1276
SAOHSC_01236	Frr	ribosome recycling factor	Protein biogenesis	1.94	down	0.52	0.156	7.59E-06	-0.95	-0.43	SACOL1278
SAOHSC_01493	RplA	30S ribosomal protein S1	Protein biogenesis	3.07	up	3.07	0.842	4.61E-41	1.62	0.02	SACOL1516
SAOHSC_01678	RplU	30S ribosomal protein S21	Protein biogenesis	4.03	down	0.25	0.036	2.15E-06	-2.01	-4.80	SACOL1632
SAOHSC_01689	RplT	30S ribosomal protein S20	Protein biogenesis	2.23	down	0.45	0.093	5.40E-09	-1.15	-1.89	SACOL1642
SAOHSC_01700		GTP-binding protein YghH	Protein biogenesis	1.92	down	0.52	0.305	5.21E-05	-0.94	n.d.	SACOL1653
SAOHSC_01755	RplM	50S ribosomal protein L27	Protein biogenesis	3.64	down	0.27	0.160	6.74E-07	-1.86	-1.10	SACOL1700
SAOHSC_01757	RplU	50S ribosomal protein L21	Protein biogenesis	2.51	down	0.40	0.140	1.70E-10	-1.33	-1.10	SACOL1702
SAOHSC_01829	RplD	30S ribosomal protein S4	Protein biogenesis	2.47	down	0.40	0.412	1.98E-10	-1.30	n.d.	SACOL1769
SAOHSC_02361	RplM2	50S ribosomal protein L31 type B	Protein biogenesis	3.63	down	0.28	0.175	2.71E-08	-1.86	-1.15	SACOL1212
SAOHSC_02477	RplS	30S ribosomal protein S9	Protein biogenesis	2.39	down	0.42	0.236	1.49E-05	-1.56	n.d.	SACOL1206
SAOHSC_02478	RplM	50S ribosomal protein L13	Protein biogenesis	2.87	down	0.35	0.124	3.43E-15	-1.52	n.d.	SACOL1207
SAOHSC_02484	RplQ	50S ribosomal protein L17	Protein biogenesis	2.30	down	0.44	0.098	1.56E-08	-1.12	-1.76	SACOL1212
SAOHSC_02485	RplK	30S ribosomal protein S11	Protein biogenesis	2.18	down	0.46	0.188	2.10E-05	-1.10	-1.80	SACOL1214
SAOHSC_02487	RplM	30S ribosomal protein S13	Protein biogenesis	2.60	down	0.38	0.172	1.26E-11	-1.38	-1.09	SACOL1215
SAOHSC_02492	RplD	50S ribosomal protein L15	Protein biogenesis	2.62	down	0.38	0.165	3.35E-17	-1.39	n.d.	SACOL1220
SAOHSC_02493	RplM0	50S ribosomal protein L30	Protein biogenesis	2.63	down	0.38	0.132	8.97E-09	-1.39	-1.85	SACOL1221
SAOHSC_02495	RplR	50S ribosomal protein L18	Protein biogenesis	2.55	down	0.39	0.246	8.52E-03	-1.35	-1.05	SACOL1223
SAOHSC_02496	RplF	50S ribosomal protein L6	Protein biogenesis	2.56	down	0.39	0.166	9.17E-17	-1.35	-1.05	SACOL1224
SAOHSC_02498	RplH	30S ribosomal protein S8	Protein biogenesis	2.47	down	0.40	0.135	7.77E-08	-1.30	n.d.	SACOL1225
SAOHSC_02500	RplI	50S ribosomal protein L5	Protein biogenesis	2.28	down	0.44	0.329	9.21E-11	-1.19	-1.10	SACOL1227
SAOHSC_02503	RplQ	30S ribosomal protein S17	Protein biogenesis	2.39	down	0.42	0.173	9.17E-04	-1.26	-1.10	SACOL1230
SAOHSC_02504	RplM	50S ribosomal protein L29	Protein biogenesis	2.87	down	0.35	0.090	6.21E-10	-1.52	-1.05	SACOL1231
SAOHSC_02505	RplP	50S ribosomal protein L16	Protein biogenesis	2.80	down	0.36	0.255	1.58E-07	-1.49	-1.09	SACOL1232
SAOHSC_02506	RplC	30S ribosomal protein S3	Protein biogenesis	2.38	down	0.42	0.151	1.15E-17	-1.25	-1.46	SACOL1233
SAOHSC_02507	RplV	50S ribosomal protein L22	Protein biogenesis	2.73	down	0.37	0.178	7.68E-11	-1.45	-1.28	SACOL1234
SAOHSC_02508	RplS	30S ribosomal protein S19	Protein biogenesis	2.80	down	0.36	0.141	2.62E-02	-1.46	-1.41	SACOL1235
SAOHSC_02509	RplH	50S ribosomal protein L2	Protein biogenesis	2.62	down	0.38	0.126	3.41E-07	-1.49	-1.28	SACOL1236
SAOHSC_02510	RplV	50S ribosomal protein L23	Protein biogenesis	2.82	down	0.49	0.353	1.96E-02	-1.82	-1.49	SACOL1237
SAOHSC_02511	RplD	50S ribosomal protein L4	Protein biogenesis	2.97	down	0.34	0.100	7.05E-13	-1.57	-1.44	SACOL1238
SAOHSC_02512	RplC	50S ribosomal protein L3	Protein biogenesis	2.72	down	0.38	0.188	2.95E-14	-1.54	-1.85	SACOL1239
SAOHSC_02553		RNA modification GTPase TrmE	Protein biogenesis	1.92	down	0.52	0.124	8.59E-05	-0.94	-0.49	SACOL2738
SAOHSC_01189	Fmt	methyl-7RNA formyltransferase	Protein biogenesis; Folate and pterines	1.63	down	0.61	0.155	2.63E-04	-0.70	-0.82	SACOL1218
SAOHSC_01608	LagA	GTP-binding protein LagA	Protein biogenesis; Heat shock; Tetraarylates	2.34	down	0.47	0.172	5.95E-14	-1.19	-0.25	SACOL1641
SAOHSC_00529	FusA	elongation factor G	Protein biogenesis; Virulence - no subcategory	1.72	down	0.58	0.264	3.43E-05	-0.78	-0.82	SACOL0949
SAOHSC_01626	PcpD2	proline dipeptidase	Protein degradation	2.08	up	2.08	0.720	6.06E-14	1.05	0.54	SACOL1588
SAOHSC_01778	CpxI	ATP-dependent protease ATP-binding subunit CpxI	Protein degradation	2.16	down	0.46	0.145	2.30E-12	-1.11	-1.10	SACOL1771
SAOHSC_02255	GroES	co-chaperonin GroES	Protein folding	1.60	down	0.63	0.153	2.34E-02	-0.67	-0.10	SACOL1617
SAOHSC_01841	DnaI	chaperone protein DnaI	Protein folding; Heat shock	2.12	down	0.47	0.176	5.71E-09	-1.08	-0.69	SACOL1636
SAOHSC_01584	GroE	heat shock protein GroE	Protein folding; Heat shock	2.55	down	0.39	0.187	3.81E-16	-1.35	-0.80	SACOL1638
SAOHSC_00903	SpaB	signal peptidase II	Protein processing and modification	1.75	down	0.57	0.188	4.04E-05	-0.81	0.82	SACOL0969
SAOHSC_02484	RplK	30S ribosomal protein S5	Protein processing and modification; Protein biogenesis	2.44	down	0.41	0.189	6.43E-12	-1.29	-1.10	SACOL1232
SAOHSC_00527	RplS	30S ribosomal protein S12	Protein processing and modification; Virulence - no subcategory; Protein biogenesis	2.79	down	0.36	0.180	1.68E-07	-1.48	-1.16	SACOL0591
SAOHSC_00527	FxaA	hypothetical protein	Protein secretion system, Type VII	6.64	up	6.64	2.614	1.26E-10	2.75	-1.19	SACOL0271
SAOHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	Purines	2.63	down	0.38	0.163	2.77E-12	-1.46	-0.94	SACOL0554
SAOHSC_00539		hypothetical protein	Purines	2.55	down	0.39	0.092	5.98E-09	-1.35	-1.34	SACOL0603
SAOHSC_01009	PurC	phosphoribosylaminoimidazole carboxylase ATPase subunit	Purines	5.93	up	5.93	5.033	4.24E-13	2.57	3.89	SACOL1074
SAOHSC_01010	PurC	phosphoribosylaminoimidazole succinocarboxamide synthase	Purines	6.57	up	6.57	5.482	6.26E-15	2.72	1.62	SACOL1075
SAOHSC_01011	PurS	phosphoribosylformyl/cyrimidine synthase, PurS protein	Purines	6.13	up	6.13	4.284	6.23E			

locus tag	protein symbol	description	theSEED functional category	median fold-change	median fold-change (direction)	median ratio over assays (TSB stat./exp.)	IQR	p-value BH adjusted	log2 median ratio over assays (TSB stat./exp.)	log2 ratio Becher et al., 2009	locus tag (COL)
SAOUHSC_01715	Urk	uridine kinase	Pyrimidines	2.52	down	0.34	0.070	5.49E-12	-1.51	n.d.	SACOL1666
SAOUHSC_02377	Pdp	pyrimidine-nucleoside phosphorylase	Pyrimidines/Monosaccharides	6.53	up	6.83	3.335	5.54E-14	2.79	3.14	SACOL2128
SAOUHSC_03001	IcaR	ica operon transcriptional regulator IcaR	Quorum sensing and biofilm formation	1.86	up	1.86	0.485	5.12E-04	0.89	0.74	SACOL2688
SAOUHSC_01361	MurK	transcriptional regulator	Regulation and Cell signaling - no subcategory	1.65	down	0.63	0.194	8.12E-03	-0.72	n.d.	SACOL1398
SAOUHSC_06201	Opp-5A	hypothetical protein	Regulation and Cell signaling - no subcategory;ABC Transporters	3.02	up	3.02	1.761	5.27E-03	1.59	n.d.	SACOL0217
SAOUHSC_01379		hypothetical protein	Resistance to antibiotics and toxic compounds	32.88	down	0.03	0.005	4.06E-08	-5.04	-5.06	SACOL1504
SAOUHSC_02630		hypothetical protein	Resistance to antibiotics and toxic compounds	2.23	down	0.45	0.119	1.54E-02	-1.16	n.d.	SACOL2348
SAOUHSC_01467	Pbp2	penicillin-binding protein 2	Resistance to antibiotics and toxic compounds;Cell Division and Cell Cycle - no subcategory;Cell Wall and Capsule - no subcategory	1.72	down	0.58	0.158	6.19E-16	-0.78	0.35	SACOL1490
SAOUHSC_00846	Pbp4	penicillin-binding protein 4	Resistance to antibiotics and toxic compounds;Cell Wall and Capsule - no subcategory	3.98	down	0.25	0.142	4.41E-04	-1.59	n.d.	SACOL0599
SAOUHSC_02873	CtpA	cation transporter E1-E2 family ATPase	Resistance to antibiotics and toxic compounds;Electron accepting reactions	1.71	up	1.71	0.679	4.09E-05	0.77	n.d.	SACOL2572
SAOUHSC_01644		hypothetical protein	Resistance to antibiotics and toxic compounds;Potassium metabolism - no subcategory;Oxidative stress;Central carbohydrate metabolism	1.89	down	0.53	0.089	3.43E-10	-0.92	n.d.	SACOL1602
SAOUHSC_02561		hypothetical protein	Respiration - no subcategory	4.05	up	4.05	1.768	5.79E-03	2.22	n.d.	SACOL2300
SAOUHSC_02582	FdhA	formate dehydrogenase subunit alpha	Respiration - no subcategory	6.42	up	6.42	3.762	4.24E-13	3.07	1.82	SACOL1261
SAOUHSC_01347	Cdh	acetate hydratase	Respiration - no subcategory;One carbon Metabolism;Central carbohydrate metabolism	5.18	up	5.18	2.893	2.94E-10	2.19	1.39	SACOL1385
SAOUHSC_01885	RdhA	6,7-dimethyl-8-ribitylsuccinate synthase	Respiration - no subcategory;One carbon Metabolism;Central carbohydrate metabolism	6.05	up	6.08	7.291	5.98E-09	3.01	-0.33	SACOL1817
SAOUHSC_01889	RdhB	ribulose biphosphatase protein RdhB	Respiration - no subcategory	3.64	up	3.64	3.366	8.33E-04	1.86	-0.28	SACOL1930
SAOUHSC_00739	QueF	7-cyste 7-deoxyquinate reductase	RNA processing and modification	2.04	down	0.49	0.103	4.06E-08	-1.05	-1.09	SACOL0789
SAOUHSC_00951		hypothetical protein	RNA processing and modification	10.33	up	10.33	5.719	6.21E-10	3.26	1.40	SACOL1020
SAOUHSC_01095	RnhC	ribonuclease HII	RNA processing and modification	2.77	down	0.36	0.133	1.10E-02	-1.47	n.d.	SACOL1150
SAOUHSC_01659		hypothetical protein	RNA processing and modification	1.84	down	0.34	0.190	6.76E-04	-0.86	-0.46	SACOL1515
SAOUHSC_01749	QueA	5-adenosylmethionine-11thA ribosyltransferase isomerase	RNA processing and modification	1.64	down	0.61	0.148	4.87E-02	-0.71	-1.52	SACOL1495
SAOUHSC_02097		hypothetical protein	RNA processing and modification	3.34	up	3.34	3.330	1.29E-08	1.23	n.d.	SACOL1941
SAOUHSC_02316	CdhA	CDAD-box ATP dependent DNA helicase	RNA processing and modification	2.82	down	0.36	0.173	1.82E-29	-1.49	-1.22	SACOL2072
SAOUHSC_02279		hypothetical protein	RNA processing and modification;Cell Division and Cell Cycle - no subcategory;Cell Wall and Capsule - no subcategory;Protein biosynthesis	1.63	down	0.62	0.109	1.34E-02	-0.68	n.d.	SACOL2040
SAOUHSC_01269	MutB	(dimethylallyl)adenosine RNA methylthiotransferase	RNA processing and modification;Protein processing and modification	2.06	down	0.48	0.181	5.83E-04	-1.04	0.39	SACOL1312
SAOUHSC_01055		isotail monophosphatase family protein	Stress Response - no subcategory	2.05	up	2.05	0.962	6.77E-05	1.04	n.d.	SACOL1116
SAOUHSC_01413		hypothetical protein	Stress Response - no subcategory	1.73	down	0.58	0.199	3.97E-05	-0.79	n.d.	SACOL1445
SAOUHSC_01814	UspA2	hypothetical protein	Stress Response - no subcategory	2.08	up	2.08	0.644	1.33E-11	1.06	0.82	SACOL1793
SAOUHSC_01819	UspA1	hypothetical protein	Stress Response - no subcategory	15.59	up	15.59	6.018	1.87E-09	3.36	1.66	SACOL1759
SAOUHSC_02402	MitA	PTS system mannitol-specific transporter subunit IIA	Sugar alcohols	3.30	up	3.30	3.647	7.03E-08	1.72	1.76	SACOL2148
SAOUHSC_02403	MitD	mannitol-1-phosphate 5-dehydrogenase	Sugar alcohols	3.42	up	3.42	1.709	2.13E-11	1.77	1.71	SACOL2149
SAOUHSC_01276	GlpK	glycerol kinase	Sugar alcohols;Phospholipids;Central carbohydrate metabolism	1.90	down	0.53	0.161	1.15E-12	-0.99	2.43	SACOL1320
SAOUHSC_00864	AlhF	alkyl hydroperoxide reductase subunit F	Sulfur Metabolism - no subcategory	1.68	up	1.68	0.532	7.75E-08	0.75	0.76	SACOL0451
SAOUHSC_00865	AlhG	alkyl hydroperoxide reductase subunit C	Sulfur Metabolism - no subcategory	2.40	up	2.40	1.339	1.70E-18	1.27	0.86	SACOL0452
SAOUHSC_01999		bacterioferritin coregulatory protein	Sulfur Metabolism - no subcategory	2.60	up	2.60	0.477	2.49E-09	1.38	0.81	SACOL1921
SAOUHSC_01499		hypothetical protein	Sulfur Metabolism - no subcategory;Pyrimidines	1.98	down	0.51	0.239	1.99E-03	-0.98	-0.48	SACOL1520
SAOUHSC_00573	HemG	putative heme peroxidase	Tetrapyrroles	2.15	up	2.15	0.910	4.06E-08	1.10	n.d.	SACOL0633
SAOUHSC_02000	GlaB	glutamate-1-semialdehyde aminotransferase	Tetrapyrroles	2.27	up	2.27	1.690	1.58E-16	1.18	-0.23	SACOL1932
SAOUHSC_01145		hypothetical protein	Transcription	1.73	down	0.58	0.102	4.25E-05	-0.79	-0.92	SACOL1287
SAOUHSC_01714	GraA	transcription elongation factor GraA	Transcription	1.78	down	0.56	0.267	8.14E-03	-0.83	-0.92	SACOL1665
SAOUHSC_02362	Rho	transcription termination factor Rho	Transcription	1.63	down	0.61	0.206	5.57E-03	-0.71	-1.02	SACOL2113
SAOUHSC_02369	RpoJ	DNA-directed RNA polymerase subunit delta	Transcription	2.22	down	0.45	0.219	9.28E-10	-1.15	-0.92	SACOL2120
SAOUHSC_02485	RpoA	DNA-directed RNA polymerase subunit alpha	Transcription	1.95	down	0.51	0.301	1.66E-10	-0.97	-1.07	SACOL2213
SAOUHSC_00524	RpoB	DNA-directed RNA polymerase subunit beta	Transcription;Virulence - no subcategory	1.85	down	0.54	0.249	2.68E-18	-0.89	-0.92	SACOL0588
SAOUHSC_01279		hydrolase alpha/beta fold domain-containing protein	Triclycylporols	2.22	up	2.22	0.415	1.12E-04	1.15	n.d.	SACOL1322
SAOUHSC_00886	MnhD	putative monovalent cation/H+ antiporter subunit D	Uni- Sym- and Antiporters	1.79	down	0.56	0.129	2.50E-03	-0.84	n.d.	SACOL0952
SAOUHSC_00889	MnhA	monovalent cation/H+ antiporter subunit A	Uni- Sym- and Antiporters	2.14	down	0.47	0.080	2.15E-06	-1.10	n.d.	SACOL0955
SAOUHSC_00528	RpsG	30S ribosomal protein S7	Virulence - no subcategory;Protein biosynthesis	2.55	down	0.39	0.150	3.18E-10	-1.35	-1.28	SACOL0592
SAOUHSC_01784	RpsT	50S ribosomal protein L20	Virulence - no subcategory;Protein biosynthesis	2.55	down	0.39	0.118	4.15E-02	-1.35	-1.94	SACOL1725
SAOUHSC_01785	RpsM	50S ribosomal protein L35	Virulence - no subcategory;Protein biosynthesis	4.81	down	0.21	0.120	5.79E-03	-2.17	-1.76	SACOL1726
SAOUHSC_00525	RpoC	DNA-directed RNA polymerase subunit beta	Virulence - no subcategory;Transcription	1.62	down	0.62	0.275	7.31E-03	-0.70	-0.85	SACOL0589
SAOUHSC_00039		hypothetical protein	Virulence - no subcategory;Transcription	3.59	down	0.28	0.092	4.56E-03	-1.64	-1.67	SACOL0067
SAOUHSC_00044		hypothetical protein		2.00	up	2.00	1.873	3.41E-02	1.00	0.85	SACOL0072
SAOUHSC_00135		hypothetical protein		2.25	up	2.25	1.263	6.23E-09	1.17	1.04	SACOL0157
SAOUHSC_00182		hypothetical protein		4.11	down	0.24	0.176	8.06E-04	-2.04	n.d.	SACOL0199
SAOUHSC_00197	FadD	hypothetical protein		26.05	up	26.05	10.794	2.91E-07	4.70	n.d.	SACOL0213
SAOUHSC_00200	PriS	hypothetical protein		1.96	down	0.51	0.173	5.37E-03	-0.97	n.d.	SACOL0216
SAOUHSC_00284		5-nucleotidase		8.55	up	8.55	3.759	8.06E-04	3.10	n.d.	SACOL0303
SAOUHSC_00290	PibA	hypothetical protein		5.34	down	0.19	0.126	5.79E-03	-2.62	n.d.	SACOL0307
SAOUHSC_00301		hypothetical protein		1.79	down	0.56	0.226	2.36E-02	-0.84	n.d.	SACOL0391
SAOUHSC_00309		hypothetical protein		4.29	up	4.29	2.198	8.96E-10	2.10	0.08	SACOL0399
SAOUHSC_00330		hypothetical protein		1.89	down	0.53	0.193	4.98E-02	-0.92	n.d.	SACOL0419
SAOUHSC_00356		hypothetical protein		3.93	up	3.93	2.933	4.06E-08	1.97	2.55	SACOL0444
SAOUHSC_00366	NthA	NAD(P)H-flavin oxidoreductase		2.07	up	2.07	0.588	8.39E-03	1.05	0.51	SACOL0453
SAOUHSC_00371		hypothetical protein		15.05	up	15.05	10.725	1.15E-12	3.95	2.30	SACOL0457
SAOUHSC_00405		hypothetical protein		2.59	up	2.59	1.190	8.06E-04	1.37	1.14	SACOL0486
SAOUHSC_00486	FtsH	hypothetical protein		1.87	down	0.54	0.311	8.62E-09	-0.90	0.70	SACOL0555
SAOUHSC_00502	CtsB	hypothetical protein		1.95	up	1.95	1.312	4.93E-02	0.96	n.d.	SACOL0567
SAOUHSC_00533	HchA	Chaperone protein HchA		1.89	up	1.89	1.168	2.26E-05	0.91	0.62	SACOL0597
SAOUHSC_00538		haloacid dehalogenase-like hydrolase		2.36	up	2.36	0.440	1.11E-09	1.24	n.d.	SACOL0602
SAOUHSC_00603		hypothetical protein		1.70	up	1.70	1.005	1.78E-04	0.79	1.21	SACOL0655
SAOUHSC_00607		hypothetical protein		2.33	down	0.43	0.097	8.06E-04	-1.21	-0.47	SACOL0659
SAOUHSC_00634	MecC	ABC transporter substrate-binding protein		3.13	up	3.13	0.961	7.59E-14	1.64	n.d.	SACOL0688
SAOUHSC_00637	MecA	hypothetical protein		2.25	up	2.25	0.602	9.10E-06	1.17	n.d.	SACOL0690
SAOUHSC_00647	AlcA	hypothetical protein		4.02	up	4.02	2.140	1.87E-12	2.86	n.d.	SACOL0700
SAOUHSC_00652	PhuA	iron compound ABC transporter ATP-binding protein		5.36	down	0.19	0.160	7.00E-08	-2.62	-2.75	SACOL0704
SAOUHSC_00663		hypothetical protein		1.19	up	1.19	0.533	2.01E-07	0.85	0.40	SACOL0714
SAOUHSC_00666		hypothetical protein		2.11	up	2.11	0.755	1.36E-08	1.11	-0.33	SACOL0738
SAOUHSC_00788		hypothetical protein		4.01	up	4.01	1.752	9.06E-04	2.00	0.79	SACOL0831
SAOUHSC_00792		hypothetical protein		3.40	up	3.40	1.309	1.29E-07	1.77	1.17	SACOL0834
SAOUHSC_00838		hypothetical protein		2.54	up	2.54	1.420	1.66E-09	1.34	0.57	SACOL0879
SAOUHSC_00862		hypothetical protein		2.83	down	0.49	0.305	5.20E-03	-1.02	-1.07	SACOL0908
SAOUHSC_00994	SpvA	transcriptional regulator SpvA		4.06	up	4.06	4.437	1.19E-12	2.82	0.48	SACOL1002
SAOUHSC_00964		hypothetical protein		2.15	down	0.46	0.213	7.33E-04	-1.15	n.d.	SACOL1035
SAOUHSC_01037		hypothetical protein		4.80	up	4.80	3.252	8.55E-10	2.26	-0.73	SACOL1090
SAOUHSC_01039		hypothetical protein		1.62	down	0.62	0.209	3.35E-02	-0.79	n.d.	SACOL1101
SAOUHSC_01138		hypothetical protein		9.25	up	9.25	3.487	1.56E-05	3.21	n.d.	SACOL1189
SAOUHSC_01154	SeqF	hypothetical protein		2.78	down	0.36	0.255	2.79E-05	-1.47	1.23	SACOL1202
SAOUHSC_01184	Sun	sun protein		2.55	down	0.39	0.120	1.16E-08	-1.35	-0.97	SACOL1229
SAOUHSC_01185		ribosomal RNA large subunit methyltransferase N		7.06	down	0.14	0.029	8.06E-04	-2.62	n.d.	SACOL1330
SAOUHSC_01186	Spa1	hypothetical protein		1.64	down	0.61	0.125	7.91E-03	-0.72	-0.28	SACOL1331
SAOUHSC_01187	PhuB	hypothetical protein		1.64	down	0.61	0.194	7.92E-04	-0.71	n.d.	SACOL1332
SAOUHSC_01222	TopA	DNA topoisomerase I		2.67	down	0.38	0.154	1.15E-12	-1.41	-0.53	SACOL1367
SAOUHSC_01223	Gid	tRNA (Lysyl-5)-methyltransferase Gid		2.44	down	0.41	0.129	1.53E-24	-1.29	n.d.	SACOL1368
SAOUHSC_01235	PyriH	uridylate kinase		1.71	down	0.59	0.181	1.07E-05	-0.77	n.d.	SACOL1377
SAOUHSC_01256		hypothetical protein		1.78	down	0.56	0.240	3.57E-02	-0.83	-1.28	SACOL1398
SAOUHSC_01264		hypothetical protein		3.55	up	3.55	4.256	1.17E-04	1.83	n.d.	SACOL1306
SAOUHSC_01284		hypothetical protein		2.40	down	0.42	0.173	7.22E-11	-1.26	n.d.	SACOL1327
SAOUHSC_01317		hypothetical protein		1.62	up	1.62	0.549	2.06E-02	0.69	n.d.	SACOL1358
SAOUHSC_01336		hypothetical protein		2.02	down	0.49	0.165	1.09E-03	-1.02	n.d.	SACOL1376
SAOUHSC_01349		hypothetical protein		2.18	up	2.18	0.546	2.98E-07	1.12	0.93	SACOL1387
SAOUHSC_0139											

locus tag	protein symbol	description	theSEED functional category	median fold-change	median fold-change (direction)	median ratio over assays (TSB stat. /exp.)	IQR	p-value BH adjusted	log2 median ratio over assays (TSB stat. /exp.)	log2 ratio Becher et al., 2009	locus tag (COL)
SAOUHSC_01606		peptidase T		3.12	up	3.12	1.037	5.39E-11	1.69	0.93	SACOL1555
SAOUHSC_01661		hypothetical protein		3.54	down	0.28	0.100	4.06E-08	-1.81	-1.55	SACOL1617
SAOUHSC_01664		hypothetical protein		1.86	up	1.86	0.842	1.58E-06	0.89	n.d.	SACOL1620
SAOUHSC_01675		hypothetical protein		1.89	up	1.89	0.558	1.42E-04	0.94	n.d.	SACOL1629
SAOUHSC_01676		hypothetical protein		1.65	up	1.65	0.550	2.62E-09	0.75	0.11	SACOL1630
SAOUHSC_01718		hypothetical protein		2.05	down	0.49	0.070	4.04E-02	-1.04	n.d.	SACOL1669
SAOUHSC_01721		hypothetical protein		1.64	up	1.64	0.161	9.68E-03	0.72	-0.89	SACOL1672
SAOUHSC_01729		hypothetical protein		6.99	up	6.99	4.362	5.98E-09	2.80	n.d.	SACOL1679
SAOUHSC_01730	C80	hypothetical protein		2.10	up	2.10	0.865	1.49E-06	1.07	n.d.	SACOL1680
SAOUHSC_01779	Tig	trigger factor		1.95	down	0.51	0.159	1.55E-18	-0.56	-0.53	SACOL1722
SAOUHSC_01786	ntfC	translation initiation factor IF-3		2.80	down	0.36	0.169	1.88E-11	-1.48	-1.05	SACOL1727
SAOUHSC_01816	PtpQ	hypothetical protein		1.87	up	1.87	0.800	5.03E-03	0.90	0.94	SACOL1756
SAOUHSC_01839	TyrS	tyrosyl-tRNA synthetase		1.71	down	0.58	0.222	5.21E-05	-0.78	-0.61	SACOL1778
SAOUHSC_01854		hypothetical protein		5.13	up	5.13	1.426	9.87E-04	1.85	0.89	SACOL1786
SAOUHSC_01855		hypothetical protein		3.78	up	3.78	1.094	9.74E-17	1.48	0.21	SACOL1789
SAOUHSC_01860		hypothetical protein		1.72	up	1.72	0.960	1.63E-05	0.78	0.32	SACOL1794
SAOUHSC_01868		lipidase PspV		2.15	up	2.15	1.244	1.91E-22	1.11	-0.03	SACOL1801
SAOUHSC_01869		hypothetical protein		5.89	up	5.89	3.710	1.98E-14	1.56	0.12	SACOL1802
SAOUHSC_01879	Rat	virulence factor regulator protein		3.23	down	0.31	0.368	3.78E-03	-1.06	n.d.	SACOL1813
SAOUHSC_01968	Hic	hypothetical protein		1.88	up	1.88	0.542	0.75E-07	0.85	n.d.	SACOL1894
SAOUHSC_01969		hypothetical protein		2.40	up	2.40	0.971	7.37E-11	1.26	n.d.	SACOL1895
SAOUHSC_01978		hypothetical protein		1.86	down	0.54	0.083	5.79E-03	-0.69	n.d.	SACOL1903
SAOUHSC_01987		hypothetical protein		2.59	up	2.59	1.938	7.99E-14	1.37	1.18	SACOL1912
SAOUHSC_01998		hypothetical protein		2.32	up	2.32	0.940	2.64E-06	1.21	n.d.	SACOL1920
SAOUHSC_02013		hypothetical protein		7.37	up	7.37	5.034	9.67E-12	2.88	1.84	SACOL1933
SAOUHSC_02106		hypothetical protein		2.31	down	0.43	0.266	6.17E-04	-1.19	0.03	SACOL1950
SAOUHSC_02107		UDP-N-acetylmuramyl triphosphate synthetase		2.31	down	0.43	0.195	3.28E-15	-1.21	-0.36	SACOL1951
SAOUHSC_02145		hypothetical protein		4.57	up	4.57	2.280	2.91E-07	2.19	n.d.	SACOL1987
SAOUHSC_02150		hypothetical protein		3.32	up	3.32	1.523	4.24E-13	1.73	1.77	SACOL1992
SAOUHSC_02152	PntC	ABC transporter ATP-binding protein		4.55	up	4.55	2.071	1.56E-10	2.19	n.d.	SACOL1994
SAOUHSC_02154	PntA	ABC transporter ATP-binding protein		2.82	up	2.82	3.090	1.69E-02	1.50	n.d.	SACOL1996
SAOUHSC_02218		hypothetical protein		3.11	up	3.11	1.365	5.65E-07	1.64	n.d.	
SAOUHSC_02387		hypothetical protein		5.84	up	5.84	2.904	2.38E-10	2.55	1.42	SACOL2136
SAOUHSC_02425		hypothetical protein		18.01	up	18.01	66.272	5.79E-03	4.17	3.57	SACOL2163
SAOUHSC_02441	Asp23	alkaline shock protein 23		8.41	up	8.41	8.100	1.70E-18	3.07	1.68	SACOL2173
SAOUHSC_02442		hypothetical protein		20.98	up	20.98	11.256	1.12E-04	4.39	n.d.	SACOL2174
SAOUHSC_02443	AmuP	hypothetical protein		13.86	up	13.86	11.184	4.06E-08	3.79	2.44	SACOL2175
SAOUHSC_02445		hypothetical protein		2.13	up	2.13	0.929	1.16E-06	1.09	1.12	SACOL2177
SAOUHSC_02519		hypothetical protein		2.34	up	2.34	0.653	4.06E-08	1.23	1.71	SACOL2245
SAOUHSC_02554	FhuD2	hypothetical protein		4.01	down	0.25	0.064	1.51E-11	-2.09	-1.13	SACOL2277
SAOUHSC_02568		hypothetical protein		2.03	up	2.03	1.188	1.30E-03	1.02	0.70	SACOL2288
SAOUHSC_02574		hypothetical protein		1.95	down	0.51	0.409	9.87E-03	-0.56	0.81	SACOL2293
SAOUHSC_02585		hypothetical protein		2.04	up	2.04	1.718	1.57E-03	1.03	n.d.	SACOL2304
SAOUHSC_02604		hypothetical protein		17.04	up	17.04	11.282	1.26E-10	4.09	1.43	SACOL2321
SAOUHSC_02611	LysA	hypothetical protein		1.84	down	0.54	0.103	8.06E-04	-0.88	n.d.	SACOL2328
SAOUHSC_02650		hypothetical protein		9.33	up	9.33	5.188	2.91E-07	3.22	n.d.	SACOL2365
SAOUHSC_02665		hypothetical protein		7.28	up	7.28	4.355	3.14E-09	2.86	1.63	SACOL2379
SAOUHSC_02670		hypothetical protein		2.41	up	2.41	0.993	1.12E-04	1.27	1.30	SACOL2385
SAOUHSC_02690		hypothetical protein		2.00	down	0.50	0.150	1.56E-06	-1.00	n.d.	SACOL2403
SAOUHSC_02724		hypothetical protein		3.05	up	3.05	1.292	1.28E-11	1.61	n.d.	SACOL2436
SAOUHSC_02731		hypothetical protein		1.84	down	0.54	0.210	7.32E-03	-0.88	n.d.	SACOL2442
SAOUHSC_02737		epimerase/dehydratase		1.97	down	0.51	0.201	1.14E-02	-0.59	-0.28	SACOL2446
SAOUHSC_02774		hypothetical protein		7.68	up	7.68	5.771	7.75E-08	2.94	n.d.	SACOL2484
SAOUHSC_02778		hypothetical protein		3.95	up	3.95	1.572	5.98E-09	1.98	1.41	SACOL2488
SAOUHSC_02820		hypothetical protein		2.26	up	2.26	1.608	9.45E-03	1.17	n.d.	SACOL2525
SAOUHSC_02827		hypothetical protein		2.76	up	2.76	1.529	6.45E-04	1.46	1.32	SACOL2532
SAOUHSC_02829	Fip	NAD(P)H-flavin oxidoreductase		2.84	up	2.84	0.912	1.47E-13	1.50	n.d.	SACOL2534
SAOUHSC_02844		hypothetical protein		1.96	up	1.96	0.644	7.75E-08	0.97	n.d.	SACOL2549
SAOUHSC_02862	CtpL	ATP-dependent Ctp protease, ATP-binding subunit CtpC		16.08	up	16.08	13.824	1.56E-05	4.01	2.89	SACOL2563
SAOUHSC_02866		hypothetical protein		2.70	down	0.37	0.134	1.92E-08	-1.43	n.d.	SACOL2566
SAOUHSC_02887	IisA	immunodominant antigen A		2.44	down	0.41	0.275	3.20E-06	-1.29	-1.05	SACOL2584
SAOUHSC_02899		hypothetical protein		6.41	up	6.41	3.288	4.06E-08	2.68	1.42	SACOL2596
SAOUHSC_02900		hypothetical protein		7.57	up	7.57	6.903	4.24E-13	2.92	1.70	SACOL2597
SAOUHSC_02929		acetyl-CoA synthetase		1.78	up	1.78	0.814	7.75E-08	0.83	0.48	SACOL2624
SAOUHSC_02972	IisB	immunodominant antigen B		17.74	up	17.74	4.885	1.12E-04	4.25	n.d.	SACOL2660
SAOUHSC_02978		phage infection protein		1.78	down	0.56	0.185	3.84E-06	-0.81	n.d.	SACOL2665
SAOUHSC_02979		N-acetylmuramoyl-L-alanine amidase		3.10	up	3.10	1.197	5.79E-03	1.63	n.d.	SACOL2666
SAOUHSC_02980		hypothetical protein		2.07	up	2.07	0.863	1.14E-06	1.06	0.18	SACOL2667
SAOUHSC_03022		hypothetical protein		3.56	up	3.56	1.883	5.85E-14	1.89	2.51	SACOL2711
SAOUHSC_03052	GidA	tRNA uridine 5-carboxymethylaminoethyl modification enzyme GidA		2.23	down	0.45	0.174	4.25E-09	-1.24	-1.37	SACOL2737



supplemental table S4: significant regulated proteins in comparison of non-adherent and S9 infection with *S. aureus* (cell culture OD=0.4, 8h p.i., 24h p.i. and 32h p.i.)

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8-24 and 32h ratio; median fold-change OD=0.4	median fold-change (direction) OD=0.4	median ratio over assays against non-ad. OD=0.4	p-value BH adjusted OD=0.4	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.	
SAOUHSC_00924	Opp-1C	hypothetical protein	ABC transporters	0.41	1.53	1.81	1.78	▲	1.33	up	1.00E+00	2.893	up	2.893	1.67E-08	3.502	up	3.502	4.58E-08	
SAOUHSC_00925	Opp-1D	hypothetical protein	ABC transporters	0.08	0.75	1.46	1.39	▲	1.06	up	1.00E+00	1.677	up	1.677	7.49E-03	2.743	up	2.743	4.87E-09	
SAOUHSC_00936	Opp-3F	oligopeptide ABC transporter ATP-binding protein	ABC transporters	0.36	0.73	0.95	1.63	▲	1.28	up	1.28	1.00E+00	1.654	up	1.937	4.57E-05	2.044	up	2.044	6.15E-07
SAOUHSC_02767	Opp-1A	peptide ABC transporter peptide-binding protein	ABC transporters;Motility and Chemotaxis - no subcategory	2.56	0.19	-0.05	0.22	▼	4.46	down	0.22	4.155E-05	1.143	up	1.143	1.00E+00	1.036	down	0.965	1.00E+00
SAOUHSC_00927	Opp-3A	oligopeptide ABC transporter substrate-binding protein	ABC transporters;Regulation and Cell signaling - no subcategory	0.35	0.33	1.08	1.59	▲	1.28	up	1.28	1.00E+00	1.256	up	1.256	1.00E+00	2.114	up	2.114	1.61E-08
SAOUHSC_00069	Ssa	protein A	Adhesion	0.56	-0.90	-0.79	-2.51	▼	1.47	up	1.47	2.89E-01	14.941	down	0.067	1.00E-12	1.723	down	0.579	9.43E-01
SAOUHSC_00487	HuO	Hsp33-like chaperonin	Adhesion	0.23	-0.15	-0.97	-0.85	▼	1.17	up	1.17	1.00E+00	1.112	down	0.899	1.00E+00	1.966	down	0.509	2.17E-03
SAOUHSC_00544	SdC	sdrC protein	Adhesion	1.07	-0.93	n.d.	n.d.	▼	2.10	down	0.48	1.309E-02	1.901	down	0.526	2.70E-02				
SAOUHSC_02963	CIB	clumping factor B	Adhesion	-1.25	-1.78	-3.44	-3.74	▼	2.38	down	0.42	2.41E-17	3.433	down	0.291	4.65E-26	10.882	down	0.092	6.27E-08
SAOUHSC_01634	GcVT	glycine cleavage system aminomethyltransferase T	Alanine, serine, and glycine	-0.49	0.27	0.60	0.81	▲	1.40	down	0.71	1.00E+00	1.208	up	1.208	1.00E+00	1.513	up	1.513	4.01E-02
SAOUHSC_02305	Alr	alanine racemase	Alanine, serine, and glycine;Central carbohydrate metabolism;RNA processing and modification	0.16	-0.32	-1.20	-0.89	▼	1.12	down	0.89	1.00E+00	1.252	down	0.798	1.00E+00	2.303	down	0.494	5.47E-04
SAOUHSC_00308		hypothetical protein	Alanine, serine, and glycine;Lipic acid;Plant Prokaryote comparative genomics;Central carbohydrate metabolism	0.27	1.50	1.32	1.51	▲	1.21	down	0.83	1.00E+00	2.819	up	2.819	1.02E-04	2.501	up	2.501	8.57E-01
SAOUHSC_00532	Kxi	2-amino-3-ketobutyrate coenzyme A ligase	Alanine, serine, and glycine;cysteine, threonine, methionine, and cysteine	0.07	0.42	0.39	0.79	▼	1.05	up	1.05	1.00E+00	1.341	up	1.341	1.00E+00	1.313	up	1.313	1.00E+00
SAOUHSC_00535		hypothetical protein	Alanine, serine, and glycine;cysteine, threonine, methionine, and cysteine	0.24	0.78	1.30	1.63	▲	1.18	down	0.85	1.00E+00	1.723	up	1.723	7.58E-03	2.469	up	2.469	5.09E-09
SAOUHSC_00009	SerS	seryl-tRNA synthetase	Alanine, serine, and glycine;Protein biosynthesis	0.25	0.69	0.15	0.16	▼	1.19	up	1.19	1.00E+00	1.617	up	1.112	1.00E+00	1.114	up	1.114	1.00E+00
SAOUHSC_01833	SerA	D-3-phosphoglycerate dehydrogenase	Alanine, serine, and glycine;Pyridoxine	0.03	1.22	1.87	1.61	▲	1.02	up	1.02	1.00E+00	2.331	up	2.331	4.02E-12	3.662	up	3.662	3.68E-14
SAOUHSC_01045		hypothetical protein	Arginine; urea cycle; polyamines	-0.01	-1.51	n.d.	-0.30	▼	1.01	down	0.99	1.00E+00	2.856	down	0.350	1.40E-04	1.227	down	0.815	1.00E+00
SAOUHSC_01046	PutA	ABC transporter	Arginine; urea cycle; polyamines	-0.94	-1.57	-0.75	-0.84	▼	1.92	down	0.52	1.68E-04	2.970	down	0.337	2.71E-07	1.653	down	0.805	1.00E+00
SAOUHSC_01047	PutB	spermidine/putrescine ABC transporter permease	Arginine; urea cycle; polyamines	-1.01	-1.89	n.d.	-0.99	▼	2.01	down	0.50	4.40E-03	3.228	down	0.310	2.27E-02	1.867	down	0.536	2.98E-01
SAOUHSC_01048	PutD	spermidine/putrescine ABC transporter spermidine/putrescine-binding protein	Arginine; urea cycle; polyamines	-1.27	-1.74	n.d.	-1.44	▼	2.42	down	0.41	1.43E-01	3.341	down	0.299	2.01E-05	2.705	down	0.370	3.75E-01
SAOUHSC_01617	ArgH	arginine repressor	Arginine; urea cycle; polyamines	0.21	0.79	0.45	0.58	▲	1.18	up	1.18	1.00E+00	1.731	up	1.731	1.79E-02	1.365	up	1.365	1.00E+00
SAOUHSC_02244		succinyl-diaminopelate desuccinylase	Arginine; urea cycle; polyamines	-1.15	-2.17	-3.03	-2.13	▲	2.22	up	2.22	4.75E-01	4.505	up	4.505	4.92E-01	4.085	up	4.085	4.43E-02
SAOUHSC_00076	ShnB	ornithine cyclodeaminase	Arginine; urea cycle; polyamines;Lysine, threonine, methionine, and cysteine;Proline and 4-hydroxyproline;Siderophores	2.99	2.02	2.41	2.30	▲	7.96	down	0.13	5.917E-01	4.050	up	4.050	1.86E-10	5.305	up	5.305	1.82E-13
SAOUHSC_00894	BoxD	ornithine-oxo acid transaminase	Arginine; urea cycle; polyamines;Proline and 4-hydroxyproline	0.58	1.59	2.64	2.81	▲	1.50	up	1.50	1.00E+00	3.002	up	3.002	1.24E-23	6.205	up	6.205	5.49E-17
SAOUHSC_00899	ArgG	argininosuccinate synthase	Arginine; urea cycle; polyamines;Proline and 4-hydroxyproline;Miscellaneous - no subcategory	0.95	0.89	1.66	1.34	▲	1.93	down	0.52	1.00E+00	1.850	up	1.850	8.80E-03	3.161	up	3.161	2.83E-03
SAOUHSC_00733	HicC	histidinol-phosphate aminotransferase	Aromatic amino acids and derivatives	0.53	1.41	1.49	1.46	▲	1.44	up	1.44	1.00E+00	2.652	up	2.652	1.98E-04	2.811	up	2.811	6.72E-05
SAOUHSC_00724		chorismate dioxygenase	Aromatic amino acids and derivatives;Folate and pterines	-0.06	0.94	2.70	0.40	▲	1.04	down	0.96	1.00E+00	1.921	up	1.921	1.54E-01	6.480	up	6.480	2.10E-02
SAOUHSC_00514	PurF	amidophosphoribosyltransferase	Bacteriocins, ribosomally synthesized antibacterial peptides;Purines	-0.07	0.54	-1.00	-0.81	▼	1.05	down	0.95	1.00E+00	1.451	up	1.451	1.00E+00	2.006	down	0.498	1.04E-07
SAOUHSC_00146	AusA	hypothetical protein	Biotin	-0.63	1.85	2.15	2.22	▲	1.55	down	0.65	1.00E+00	3.600	up	3.600	5.87E-21	4.429	up	4.429	7.66E-11
SAOUHSC_02713	BioF	hypothetical protein	Biotin	1.29	1.22	0.14	-0.08	▼	2.44	up	2.44	2.308E-07	2.494	up	2.494	8.55E-08	1.100	down	0.909	1.02E+00
SAOUHSC_02714	BioB	biotin synthase	Biotin	1.45	0.57	2.17	-1.94	▼	2.74	up	2.74	9.08E-16	1.485	up	1.485	1.00E+00	4.495	down	0.222	1.11E-05
SAOUHSC_02715	BioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Biotin	1.07	0.89	0.94	0.36	▲	2.10	up	2.10	6.29E-01	1.853	up	1.853	2.38E-05	1.560	up	1.560	4.34E-01
SAOUHSC_02716	BioD	dehydrobiotin synthase	Biotin	1.06	0.72	-0.11	-0.37	▼	2.09	up	2.09	7.26E-05	1.650	up	1.650	1.49E-01	1.077	down	0.928	1.00E+00
SAOUHSC_00336	Thi	acetyl-CoA acetyltransferase	Biotin;Fermentation;Isoprenoids;Fatty Acids, Lipids, and Isoprenoids - no subcategory;One-carbon Metabolism;Branched-chain amino acids	-0.14	0.81	-0.11	-0.18	▼	1.10	down	0.91	1.00E+00	1.757	up	1.757	1.00E+00	1.082	down	0.924	1.00E+00
SAOUHSC_02284	IvC	ketol acid reductoisomerase	Branched-chain amino acids;Coenzyme A	0.54	1.18	2.39	2.28	▲	1.45	up	1.45	1.00E+00	2.273	up	2.273	8.81E-07	5.239	up	5.239	9.09E-10
SAOUHSC_02589		hypothetical protein	Capsular and extracellular polysaccharides	0.45	0.27	0.84	0.75	▲	1.37	up	1.37	1.00E+00	1.206	up	1.206	1.00E+00	1.560	up	1.560	1.00E+00
SAOUHSC_01589	ScpA	hypothetical protein	Cell Division and Cell Cycle - no subcategory	-1.41	-1.35	n.d.	1.34	▼	2.66	down	0.38	1.00E+00	2.546	down	0.393	4.98E-03	2.261	down	0.442	4.02E-02
SAOUHSC_02012	SgtB	glycosyltransferase	Cell Wall and Capsule - no subcategory	-0.48	2.06	1.48	1.21	▲	1.39	down	0.72	1.00E+00	4.372	up	4.372	7.71E-18	2.781	up	2.781	6.48E-10
SAOUHSC_02318	Ddl	D-alanyl-alanine synthetase A	Cell Wall and Capsule - no subcategory	0.15	0.60	0.57	0.45	▼	1.11	up	1.11	1.00E+00	1.519	up	1.519	4.19E-02	1.487	up	1.487	2.89E-01
SAOUHSC_02365	MurA2	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell Wall and Capsule - no subcategory	-0.05	1.27	0.29	0.26	▼	1.04	down	0.96	1.00E+00	2.405	up	2.405	7.03E-22	1.223	up	1.223	1.00E+00
SAOUHSC_00994	Atl	bifunctional autolysin	Cell Wall and Capsule - no subcategory;Regulation and Cell signaling - no subcategory;Adhesion;Quorum sensing and biofilm formation	0.64	-1.29	-1.95	-2.57	▼	1.56	up	1.56	1.677E-07	2.440	down	0.410	2.14E-37	3.865	down	0.259	1.82E-24
SAOUHSC_00153		indolepyruvate decarboxylase	Central carbohydrate metabolism	0.30	-0.46	0.74	0.85	▲	1.23	up	1.23	1.00E+00	1.377	down	0.726	1.00E+00	1.669	up	1.669	4.70E-01
SAOUHSC_00655		dihydroxyacetone kinase subunit DhK	Central carbohydrate metabolism	0.92	2.06	4.32	4.47	▲	1.90	up	1.90	4.074E-02	7.468	up	7.468	5.63E-08	19.910	up	19.910	5.78E-06
SAOUHSC_00797	TpiA	triosephosphate isomerase	Central carbohydrate metabolism	0.86	0.05	-0.34	-0.32	▼	1.81	up	1.81	6.61E-08	1.035	up	1.035	1.00E+00	1.265	down	0.791	1.00E+00
SAOUHSC_01337	Thi	transketolase	Central carbohydrate metabolism	0.37	0.83	0.14	0.31	▼	1.29	up	1.29	1.00E+00	1.777	up	1.777	3.38E-16	1.099	up	1.099	1.00E+00
SAOUHSC_01418	SucA	2-oxoglutarate dehydrogenase E3 component	Central carbohydrate metabolism	-0.35	0.45	1.24	1.54	▲	1.27	down	0.79	1.00E+00	1.367	up	1.367	1.00E+00	2.364	up	2.364	1.70E-22
SAOUHSC_01710		acetyl-CoA carboxylase, biotin carboxyl carrier protein	Central carbohydrate metabolism	0.45	0.08	0.88	1.04	▲	1.37	up	1.37	1.00E+00	1.057	up	1.057	1.00E+00	1.838	up	1.838	2.78E-01
SAOUHSC_01801	CIC	isocitrate dehydrogenase	Central carbohydrate metabolism	0.25	0.77	2.02	2.45	▲	1.19	up	1.19	1.00E+00	1.701	up	1.701	1.00E-04	4.048	up	4.048	4.62E-32
SAOUHSC_01818	AlaZ	alanine dehydrogenase	Central carbohydrate metabolism	0.09	0.36	1.09	1.44	▲	1.06	up	1.06	1.00E+00	1.287	up	1.287	1.00E+00	2.122	up	2.122	2.71E-12
SAOUHSC_01867	Dat	D-alanine aminotransferase	Central carbohydrate metabolism	0.30	0.90	0.41	0.39	▼	1.23	up	1.23	1.00E+00	1.869	up	1.869	1.49E-11	1.332	up	1.332	1.00E+00
SAOUHSC_01983	FumC	fumarate hydratase	Central carbohydrate metabolism	0.24	0.77	1.35	1.45	▲	1.18	up	1.18	1.00E+00	1.700	up	1.700	1.35E-02	2.550	up	2.550	1.78E-12
SAOUHSC_02647	Mqo1	malate quinone oxidoreductase	Central carbohydrate metabolism	-0.18	0.16	1.01	1.05	▲	1.13	down	0.88	1.00E+00	1.116	up	1.116	1.00E+00	2.014	up	2.014	6.51E-05
SAOUHSC_00963		lipoyltransferase and lipoyate-protein ligase	Central carbohydrate metabolism;Alanine, serine, and glycine;Plant Prokaryote comparative genomics;Lipic acid	0.18	1.02	0.38	0.58	▲	1.13	up	1.13	1.00E+00	2.034	up	2.034	8.84E-06	1.304	up	1.304	1.00E+00
SAOUHSC_00536	IvE	branched-chain amino acid aminotransferase	Central carbohydrate metabolism;Branched-chain amino acids;Alanine, serine, and glycine	0.75	1.27	0.82	0.98	▲	1.69	up	1.69	9.942E-06	2.419	up	2.419	9.31E-35	1.766	up	1.766	6.72E-07
SAOUHSC_00574	EutD	phosphotransacetylase	Central carbohydrate metabolism;Fermentation	0.31	0.67	0.11	0.21	▼	1.26	up	1.26	1.00E+00	1.588	up	1.588	4.65E-02	1.079	up	1.079	1.00E+00
SAOUHSC_01416	SucB	dihydrolipoamide succinyltransferase	Central carbohydrate metabolism;Lipic acid	-0.44	0.64	1.82	1.82	▲	1.36	down	0.74	1.00E+00	1.561	up	1.561	1.26E-01	3.052	up	3.052	1.45E-13
SAOUHSC_00553	HuA	hypothetical protein	Central carbohydrate metabolism;One-carbon Metabolism	1.08	0.38	-0.07	-0.12													

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8,24 and 32h ratio; median tendence - 1.3K cutoff	median fold-change OD=4	median fold-change (direction) OD=4	median fold-change (direction) 8h p.i.	median fold-change (direction) 24h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted OD=4	median fold-change (direction) 8h p.i.	median fold-change (direction) 24h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.	
SAOUSHC_02143		hypothetical protein	Central carbohydrate metabolism;One-carbon Metabolism	0.53	0.79	0.54	0.66	▲	1.45	up	1.45	9.25E-02	1.732	up	1.732	2.07E-04	1.457	up	1.457	1.00E+00	1.578	up	1.578	5.67E-01
SAOUSHC_02577		D isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein	Central carbohydrate metabolism;Organic acids	0.32	1.12	1.01	2.18	▲	1.25	up	1.25	1.00E+00	2.181	up	2.181	6.74E-23	4.019	up	4.019	1.14E-27	4.518	up	4.518	3.62E-18
SAOUSHC_02142	AlcH	aldehyde dehydrogenase	Central carbohydrate metabolism;Phospholipids	0.12	0.67	1.20	1.45	▲	1.09	up	1.09	1.00E+00	1.592	up	1.592	1.25E-02	2.296	up	2.296	8.39E-14	2.701	up	2.701	2.20E-25
SAOUSHC_02849	CuKc	pyruvate oxidase	Central carbohydrate metabolism;Programmed Cell Death and Toxic-antitoxin Systems	0.19	-1.07	-0.48	0.32	▼	1.14	up	1.14	1.00E+00	2.092	down	0.478	1.72E-11	1.398	down	0.715	1.00E+00	1.252	down	0.799	1.00E+00
SAOUSHC_00879	AmpA	cytosol aminopeptidase	Central carbohydrate metabolism;Protein degradation	1.23	-0.34	0.12	0.37	▼	2.35	down	0.43	3.30E-03	1.264	down	0.791	1.00E+00	1.087	up	1.087	1.00E+00	1.296	up	1.296	1.00E+00
SAOUSHC_02918	PuKc	panthoate-beta-alanine ligase	Cofactors A	-0.34	-0.42	-1.28	-1.41	▼	1.26	down	0.79	1.00E+00	1.340	down	0.247	1.00E+00	2.436	down	0.410	4.43E-02	2.658	down	0.376	1.98E-05
SAOUSHC_01834	ThiI	thiamine biosynthesis protein ThiI	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	-0.95	-0.56	-0.32	-0.47	▼	1.94	down	0.52	1.07E-05	1.470	down	0.680	1.00E+00	1.250	down	0.800	1.00E+00	1.390	down	0.720	1.00E+00
SAOUSHC_02329	ThiM	hydroxyethylthiazole kinase	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	0.59	2.72	2.35	2.59	▲	1.50	up	1.50	1.00E+00	6.581	up	6.581	2.13E-07	5.113	up	5.113	4.02E-05	6.006	up	6.006	2.61E-06
SAOUSHC_02330	ThiO2	phosphomethylpyrimidine kinase	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	0.42	1.40	2.55	2.50	▲	1.34	up	1.34	1.00E+00	2.647	up	2.647	3.45E-03	5.868	up	5.868	4.86E-01	4.933	up	4.933	2.59E-01
SAOUSHC_00819	CuKc	hypothetical protein	Cold shock	-0.63	0.05	-1.20	-1.27	▼	1.55	down	0.64	1.00E+00	1.036	up	1.036	1.00E+00	2.296	down	0.436	4.21E-02	2.414	down	0.414	2.45E-03
SAOUSHC_01403	CuKc	cold shock protein	Cold shock	0.35	2.14	1.96	2.15	▲	1.27	up	1.27	1.00E+00	4.410	up	4.410	1.02E-02	3.862	up	3.862	2.74E-01	4.426	up	4.426	1.11E-03
SAOUSHC_03045	CuKc	cold shock protein	Cold shock	-0.41	-0.20	-2.18	-2.16	▼	1.32	down	0.75	1.00E+00	1.148	down	0.871	1.00E+00	4.529	down	0.221	1.89E-03	4.463	down	0.224	6.08E-06
SAOUSHC_01430	Crr	phosphotransferase system enzyme IIA	Di- and oligosaccharides	0.59	2.32	1.47	1.39	▲	1.51	up	1.51	1.00E+00	4.985	up	4.985	8.59E-22	2.778	up	2.778	1.78E-12	3.008	up	3.008	1.34E-16
SAOUSHC_02848	GxKb	PTS system glucose-specific transporter subunit IIAIC	Di- and oligosaccharides	-0.08	0.50	0.79	0.82	▲	1.05	down	0.95	1.00E+00	1.412	up	1.412	1.00E+00	1.730	up	1.730	8.23E-04	1.763	up	1.763	3.79E-06
SAOUSHC_00340	Sib	bacteriophage U54c single-stranded DNA binding protein	DNA repair	-0.28	-0.87	-0.92	-0.53	▼	1.21	down	0.83	1.00E+00	1.833	down	0.546	4.96E-03	1.896	down	0.527	1.66E-01	1.449	down	0.690	1.00E+00
SAOUSHC_02123	PuKc	ATP-dependent DNA helicase PuKc	DNA repair	-0.51	-0.46	-0.74	-0.88	▼	1.44	down	0.69	1.00E+00	1.372	down	0.720	1.00E+00	1.676	down	0.597	2.10E-01	1.841	down	0.543	1.12E-08
SAOUSHC_01454		hypothetical protein	DNA repair;DNA replication	0.80	-0.60	-1.04	-1.22	▼	1.74	down	0.58	4.29E-02	1.511	down	0.642	1.00E+00	2.063	down	0.485	4.82E-04	2.330	down	0.429	2.95E-06
SAOUSHC_01241	PuKc	DNA polymerase III PuKc	DNA replication	-0.45	-0.01	-0.68	-0.84	▼	1.37	down	0.73	1.00E+00	1.006	down	0.894	1.00E+00	1.604	down	0.623	1.00E+00	1.788	down	0.539	1.59E-02
SAOUSHC_01351	ParE	DNA topoisomerase IV subunit B	DNA replication;Resistance to antibiotics and toxic compounds	0.36	-0.74	-0.96	-0.82	▼	1.28	down	0.78	1.00E+00	1.666	down	0.600	9.67E-02	1.949	down	0.513	1.11E-03	1.771	down	0.565	2.19E-04
SAOUSHC_01352	ParC	DNA topoisomerase IV subunit A	DNA replication;Resistance to antibiotics and toxic compounds	0.32	-0.33	-0.77	-0.65	▼	1.24	down	0.80	1.00E+00	1.255	down	0.797	1.00E+00	1.700	down	0.588	1.41E-02	1.574	down	0.635	1.00E+00
SAOUSHC_00935	TrtA	adaptor protein	DNA uptake, competence	0.46	-1.00	n.d.	n.d.	▼	1.38	up	1.38	1.00E+00	1.998	down	0.501	9.45E-05								
SAOUSHC_02517	ToxB	DNA topoisomerase III	DNA uptake, competence	-0.14	-1.04	-1.28	-1.57	▼	1.10	down	0.91	1.00E+00	2.055	down	0.487	3.38E-09	2.430	down	0.411	4.86E-01	3.405	down	0.294	1.44E-01
SAOUSHC_00409	SpvG	regulatory protein SpvG	Dormancy and Sporulation - no subcategory	0.11	-0.80	-0.64	-0.09	▼	1.08	up	1.08	1.00E+00	1.739	down	0.575	3.10E-03	1.557	down	0.642	1.00E+00	1.067	down	0.937	1.00E+00
SAOUSHC_00481		hypothetical protein	Dormancy and Sporulation - no subcategory;Heat shock	0.81	0.52	0.60	0.07	▼	1.88	up	1.88	1.167E-02	1.431	up	1.431	1.00E+00	1.042	down	1.042	1.00E+00	1.051	down	0.952	1.00E+00
SAOUSHC_01031	CydA	cytochrome b ubiquinol oxidase subunit I	Electron accepting reactions	-1.80	0.88	0.57	0.48	▼	3.49	down	0.29	7.67E-04	1.845	up	1.845	9.58E-04	1.479	up	1.479	4.57E-01	1.395	up	1.395	5.37E-01
SAOUSHC_01032	CyB	cytochrome b ubiquinol oxidase subunit II	Electron accepting reactions	-1.38	1.23	1.15	0.76	▲	2.61	down	0.38	4.45E-03	2.339	up	2.339	4.07E-02	2.223	up	2.223	9.92E-02	1.692	up	1.692	1.01E-01
SAOUSHC_01104	SdHA	succinate dehydrogenase flavoprotein subunit	Electron donating reactions;Central carbohydrate metabolism;One-carbon Metabolism	0.24	0.10	1.11	1.24	▲	1.18	up	1.18	1.00E+00	1.069	up	1.069	1.00E+00	2.187	up	2.187	1.45E-13	2.362	up	2.362	1.53E-26
SAOUSHC_01105	SdHb	succinate dehydrogenase iron-sulfur subunit	Electron donating reactions;One-carbon Metabolism;Central carbohydrate metabolism	0.08	-0.34	0.48	0.69	▼	1.06	up	1.06	1.00E+00	1.269	down	0.788	1.00E+00	1.393	up	1.393	1.00E+00	1.618	up	1.618	1.59E-02
SAOUSHC_00920	FabH	3-oxoacyl (acyl carrier protein) synthase II	Fatty acids	-1.39	-0.86	-0.96	-0.77	▼	2.63	down	0.38	4.29E-13	1.809	down	0.553	4.13E-05	1.943	down	0.515	1.85E-05	1.708	down	0.585	1.65E-03
SAOUSHC_00921	FabF	3-oxoacyl-synthase	Fatty acids	-0.92	-0.52	-0.61	-0.37	▼	1.89	down	0.53	1.156E-07	1.435	down	0.657	1.00E+00	1.529	down	0.654	1.00E+00	1.290	down	0.775	1.00E+00
SAOUSHC_00086	BuA	acetyl reductase	Fermentation	0.82	2.20	3.34	3.68	▲	1.76	up	1.76	3.457E-03	4.897	up	4.897	4.32E-16	10.129	up	10.129	9.74E-13	12.818	up	12.818	3.65E-17
SAOUSHC_00206	Ldh1	L-lactate dehydrogenase	Fermentation	-1.15	-0.25	-2.09	-2.97	▼	2.22	down	0.45	9.10E-03	1.193	down	0.838	1.00E+00	1.024	down	0.235	1.77E-07	7.290	down	0.137	1.47E-02
SAOUSHC_02922	Ldh2	L-lactate dehydrogenase	Fermentation	0.51	0.89	0.25	0.35	▼	1.43	up	1.43	1.00E+00	1.860	up	1.860	1.18E-05	1.188	up	1.188	1.00E+00	1.272	up	1.272	1.00E+00
SAOUSHC_00608	Ash	alcohol dehydrogenase	Fermentation;Phospholipids	-1.11	0.89	-0.40	-0.54	▼	2.16	down	0.46	6.07E-10	1.859	up	1.859	7.87E-06	1.319	down	0.758	1.00E+00	1.458	down	0.686	1.00E+00
SAOUSHC_00187	PfHb	formate acetyltransferase	Fermentation;Degradation - no subcategory	2.10	2.07	1.19	0.75	▲	4.57	down	0.22	4.75E-01	4.198	up	4.198	2.31E-17	2.288	up	2.288	5.10E-07	1.677	up	1.677	3.90E-03
SAOUSHC_01434	DHA	dihydrofolate reductase	Folate and pterines	0.49	0.72	0.99	1.08	▲	1.40	up	1.40	1.00E+00	1.652	up	1.652	7.97E-01	1.981	up	1.981	1.75E-04	2.042	up	2.042	2.33E-05
SAOUSHC_02360	Tdk	thymidine kinase	Folate and pterines;Pyrimidines	-0.32	-0.36	-0.86	-0.71	▼	1.25	down	0.80	1.00E+00	1.285	down	0.778	1.00E+00	1.814	down	0.551	1.52E-02	1.635	down	0.612	3.72E-01
SAOUSHC_00549	FolE2	putative GTP cyclohydrolase	Folate and pterines;RNA processing and modification	0.87	-0.27	-0.40	-0.01	▼	1.83	up	1.83	1.064E-03	1.206	down	0.829	1.00E+00	1.316	down	0.760	1.00E+00	1.004	down	0.596	1.00E+00
SAOUSHC_00895	GusB	glutamate dehydrogenase, NAD-specific	Glutamine, glutamate, aspartate, asparagine, ammonia assimilation	0.36	1.13	1.76	2.09	▲	1.28	down	0.78	1.00E+00	2.182	up	2.182	3.70E-24	3.380	up	3.380	6.76E-25	4.267	up	4.267	1.19E-18
SAOUSHC_00640	TagA	teichoic acid biosynthesis protein	Gram-Positive cell wall components	-1.50	0.02	-0.77	-1.18	▼	3.00	down	0.33	2.07E-02	1.015	up	1.015	1.00E+00	1.703	down	0.587	1.00E+00	1.134	down	0.882	1.00E+00
SAOUSHC_00728	LtaS	hypothetical protein	Gram-Positive cell wall components	0.19	0.97	0.96	0.91	▲	1.14	up	1.14	1.00E+00	1.965	up	1.965	2.93E-03	1.944	up	1.944	2.27E-02	1.877	up	1.877	2.78E-02
SAOUSHC_00973	TpM	hypothetical protein	Gram-Positive cell wall components	-0.50	-1.55	-0.46	-0.41	▼	1.41	down	0.71	1.00E+00	2.921	down	0.342	1.61E-04	1.380	down	0.725	1.00E+00	1.329	down	0.753	1.00E+00
SAOUSHC_00974		glycosyl transferase, group 1	Gram-Positive cell wall components	-0.13	-1.15	-0.18	-0.16	▼	1.09	down	0.91	1.00E+00	2.219	down	0.451	8.30E-07	1.133	down	0.882	1.00E+00	1.119	down	0.894	1.00E+00
SAOUSHC_02649		hypothetical protein	Gram-Positive cell wall components	0.03	1.26	n.d.	1.07	▲	1.02	up	1.02	1.00E+00	2.395	up	2.395	2.32E-06					2.093	up	2.093	8.01E-01
SAOUSHC_00225	TarI	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	Gram-Positive cell wall components;Plant Prokaryote comparative genomics;Isoprenoids	0.76	0.37	0.44	0.62	▼	1.70	up	1.70	7.67E-04	1.296	up	1.296	1.00E+00	1.357	up	1.357	1.00E+00	1.536	up	1.536	2.25E-01
SAOUSHC_00872	DND	extramembranal protein	Gram-Positive cell wall components;Resistance to antibiotics and toxic compounds	-0.60	-1.20	-0.44	-0.40	▼	1.52	down	0.66	1.00E+00	2.289	down	0.437	1.83E-10	1.359	down	0.736	1.00E+00	1.316	down	0.760	1.00E+00
SAOUSHC_01679	MuB	hypothetical protein	Heat shock;Protein processing and modification;RNA processing and modification	-0.23	-1.36	n.d.	n.d.	▼	1.17	down	0.85	1.00E+00	2.564	down	0.390	3.84E-04								
SAOUSHC_01738	HisS	histidyl-tRNA synthetase	Histidine Metabolism;Organic sulfur assimilation;Regulation and Cell signalling - no subcategory	-0.16	-0.50	-1.03	-0.89	▼	1.11	down	0.90	1.00E+00	1.417	down	0.706	1.00E+00	2.035	down	0.491	2.20E-04	1.847	down	0.541	1.51E-04
SAOUSHC_00020	WalR	two-component response regulator	Iron acquisition and metabolism - no subcategory	0.42	0.78	0.70	0.85	▲	1.34	up	1.34	1.00E+00	1.713	up	1.71									

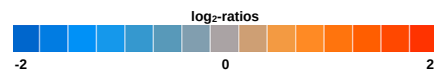
locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8,24 and 32h ratio; median tendence - 1.3K cutoff	median fold-change OD=0.4	median fold-change (direction) OD=0.4	median ratio over assays against non-ad. OD=0.4	p-value BH adjusted OD=0.4	median fold-change 8h p.i.	median fold-change (direction) 8h p.i.	median ratio over assays against non-ad. 8h p.i.	p-value BH adjusted 8h p.i.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.
SAOHS_C01395	Acd	aspartate semialdehyde dehydrogenase	Lysine, threonine, methionine, and cysteine	0.51	1.31	3.45	3.51	▲	1.43	up	1.43	1.00E+00	9.921	up	9.921	2.55E-28	10.934	up	10.934	1.73E-20	11.424	up	11.424	1.15E-26
SAOHS_C01396	DapA	dihydrodipicolinate synthase	Lysine, threonine, methionine, and cysteine	1.08	4.02	1.74	4.08	▲	2.12	up	2.12	3.89E-01	16.229	up	16.229	2.10E-09	13.404	up	13.404	4.41E-07	16.900	up	16.900	3.62E-09
SAOHS_C01397	DapB	dihydrodipicolinate reductase	Lysine, threonine, methionine, and cysteine	-0.08	1.76	2.32	2.94	▲	1.06	down	0.95	1.55E-02	3.380	down	3.380	1.55E-02	5.011	up	5.011	6.76E-03	5.048	up	5.048	4.75E-04
SAOHS_C01398	DapD	2,3,4,5-tetrahydrodipyrone-2-carboxylate N-succinyltransferase	Lysine, threonine, methionine, and cysteine	0.80	3.97	1.69	3.89	▲	1.74	up	1.74	4.01E-01	15.649	up	15.649	1.81E-10	12.945	up	12.945	1.23E-12	14.779	up	14.779	1.34E-09
SAOHS_C01399	hypothetical protein	hypothetical protein	Lysine, threonine, methionine, and cysteine	0.45	2.60	2.87	2.81	▲	1.37	up	1.37	1.00E+00	6.065	up	6.065	1.65E-14	7.291	up	7.291	1.99E-09	7.610	up	7.610	3.81E-14
SAOHS_C01401	LysA	diaminopimelate decarboxylase	Lysine, threonine, methionine, and cysteine	0.83	1.45	1.21	1.25	▲	1.78	up	1.78	1.76E-05	2.734	up	2.734	5.87E-21	2.340	up	2.340	9.04E-11	2.380	up	2.380	1.71E-15
SAOHS_C02947	CysK	sulfite reductase (NADPH) flavoprotein alpha component	Lysine, threonine, methionine, and cysteine	0.10	0.47	1.05	0.77	▲	1.07	up	1.07	1.00E+00	1.385	up	1.385	1.00E+00	2.065	up	2.065	5.49E-06	1.703	up	1.703	3.53E-03
SAOHS_C02947	hypothetical protein	hypothetical protein	Miscellaneous - no subcategory	0.89	0.26	1.29	1.69	▲	1.85	up	1.85	1.67E-04	1.195	up	1.195	1.00E+00	2.452	up	2.452	7.07E-09	3.223	up	3.223	1.95E-16
SAOHS_C02624	AccB	acetyl-CoA carboxylase, biotin carboxyl carrier protein	Miscellaneous - no subcategory;Fatty acids	-0.25	-0.17	-0.25	-0.26	▼	1.28	down	0.78	1.00E+00	1.128	down	0.887	1.00E+00	2.072	down	0.482	4.38E-03	1.656	down	0.550	6.79E-01
SAOHS_C01018	PurD	phosphoribosylamine-glycine ligase	Miscellaneous - no subcategory;Purines	-0.29	0.03	-1.40	-1.51	▼	1.22	down	0.82	1.00E+00	1.018	down	1.018	1.00E+00	2.642	down	0.378	6.11E-14	2.161	down	0.463	1.50E-11
SAOHS_C00101	DeoB	phosphopentomutase	Monosaccharides	0.45	0.35	0.30	0.77	—	1.37	up	1.37	1.00E+00	1.277	up	1.277	1.00E+00	1.230	up	1.230	1.00E+00	1.710	up	1.710	5.58E-03
SAOHS_C00239	RbsK	ribokinase	Monosaccharides	0.37	1.04	1.85	1.78	▲	1.29	up	1.29	1.00E+00	2.054	up	2.054	5.12E-02	57.531	up	57.531	1.00E+00	3.427	up	3.427	4.02E-02
SAOHS_C00708	FruA	fructose specific permease	Monosaccharides	-1.80	-0.84	-0.46	-0.35	—	3.48	down	0.29	1.77E-15	1.795	down	0.557	2.24E-03	1.374	down	0.728	1.00E+00	1.274	down	0.785	1.00E+00
SAOHS_C01907	hypothetical protein	hypothetical protein	Monosaccharides	0.11	1.41	1.95	2.08	▲	1.08	up	1.08	1.00E+00	2.653	up	2.653	3.66E-13	3.868	up	3.868	8.10E-10	4.226	up	4.226	4.77E-13
SAOHS_C02793	hypothetical protein	hypothetical protein	Monosaccharides;Cell Wall and Capsule - no subcategory;Capsular and extracellular polysaccharides	0.10	0.91	0.21	0.42	—	1.07	up	1.07	1.00E+00	1.883	up	1.883	1.62E-08	1.158	up	1.158	1.00E+00	1.334	up	1.334	1.00E+00
SAOHS_C01901	Tal	putative transaldolase	Monosaccharides;Central carbohydrate metabolism	0.63	0.74	0.25	0.15	—	1.55	up	1.55	9.37E-01	1.671	up	1.671	1.13E-02	1.188	up	1.188	1.00E+00	1.106	up	1.106	1.00E+00
SAOHS_C00501	NucC	hypothetical protein	Monosaccharides;Purines	-1.10	-0.21	-0.12	0.15	—	2.14	down	0.47	2.17E-06	1.158	down	0.864	1.00E+00	1.089	down	0.919	1.00E+00	1.110	down	0.901	1.00E+00
SAOHS_C01287	GlnA	glutamine synthetase, type I	Nitrogen Metabolism - no subcategory;Glutamine, glutamate, aspartate, asparagine; ammonia assimilation;Cell Wall and Capsule - no subcategory	0.64	-0.02	-0.09	0.17	—	1.56	up	1.56	1.44E-02	1.014	down	0.987	1.00E+00	1.063	down	0.941	1.00E+00	1.124	down	1.124	1.00E+00
SAOHS_C00229	ScdA	cell wall biosynthesis protein ScdA	Nitrogen Metabolism - no subcategory;Stress Response - no subcategory	-0.55	1.12	-0.42	-0.30	—	1.46	down	0.68	1.00E+00	2.488	up	2.488	1.61E-03	1.340	down	0.746	1.00E+00	1.228	down	0.814	1.00E+00
SAOHS_C00743	NrdF	ribonucleotide diphosphate reductase subunit beta	Nucleosides and Nucleotides - no subcategory	0.80	-0.53	-1.29	-1.32	▼	1.74	up	1.74	4.28E-04	1.442	down	0.693	1.00E+00	2.451	down	0.408	1.02E-04	2.489	down	0.402	3.85E-08
SAOHS_C01587	Rub	ribosomal large subunit pseudouridine synthase B	Nucleosides and Nucleotides - no subcategory;Cell Division and Cell Cycle - no subcategory	-0.22	-0.38	0.79	0.74	▼	1.16	down	0.86	1.00E+00	1.300	down	0.769	1.00E+00	1.982	down	0.504	3.31E-05	1.665	down	0.601	2.68E-01
SAOHS_C00742	NrdE	ribonucleotide diphosphate reductase subunit alpha	Nucleosides and Nucleotides - no subcategory;Oxidative stress	0.59	-0.97	-1.86	-1.94	▼	1.50	up	1.50	1.00E+00	1.963	down	0.509	1.59E-18	3.681	down	0.272	2.68E-26	3.841	down	0.240	6.47E-37
SAOHS_C02828	hypothetical protein	hypothetical protein	One-carbon Metabolism	0.37	0.13	1.81	1.81	▲	1.30	up	1.30	1.00E+00	1.091	up	1.091	1.00E+00	3.510	up	3.510	3.28E-01	3.100	up	3.100	1.00E-02
SAOHS_C00512	NagB	hypothetical protein	One-carbon Metabolism;Aminoglycans;Capsular and extracellular polysaccharides;Cell Wall and Capsule - no subcategory	0.41	1.43	0.92	0.91	▲	1.33	up	1.33	1.00E+00	2.694	up	2.694	7.13E-13	1.887	up	1.887	3.72E-03	1.880	up	1.880	2.88E-01
SAOHS_C00900	Pgi	glucose-6-phosphate isomerase	One-carbon Metabolism;Central carbohydrate metabolism	-0.05	0.80	-0.10	0.09	—	1.03	down	0.97	1.00E+00	1.738	up	1.738	8.08E-06	1.071	down	0.934	1.00E+00	1.065	up	1.065	1.00E+00
SAOHS_C01599	Znf	glucose-6-phosphate 1-dehydrogenase	One-carbon Metabolism;Central carbohydrate metabolism;Fermentation	0.19	0.73	0.15	0.10	—	1.14	up	1.14	1.00E+00	1.656	up	1.656	1.57E-03	1.111	up	1.111	1.00E+00	1.072	up	1.072	1.00E+00
SAOHS_C01007	FoD	bifunctional 5,10-methylene tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	One-carbon Metabolism;Folate and pterines	0.39	0.73	0.41	0.61	▲	1.31	up	1.31	1.00E+00	1.654	up	1.654	4.49E-03	1.332	up	1.332	1.00E+00	1.531	up	1.531	3.65E-01
SAOHS_C00731	ABC transporter	ABC transporter	Osmotic stress	-0.34	0.73	0.12	0.04	—	1.27	down	0.79	1.00E+00	1.656	up	1.656	1.15E-02	1.084	up	1.084	1.00E+00	1.029	up	1.029	1.00E+00
SAOHS_C02744	OpuA	amino acid ABC transporter ATP-binding protein	Osmotic stress	0.74	0.90	1.17	1.38	▲	1.68	up	1.68	4.23E-01	1.871	up	1.871	8.35E-02	2.248	up	2.248	3.69E-03	2.599	up	2.599	2.93E-06
SAOHS_C02932	BeaA	choline dehydrogenase	Osmotic stress	0.42	-1.50	-0.77	-0.51	▼	1.34	up	1.34	1.00E+00	2.838	down	0.352	1.05E-05	1.711	down	0.584	8.20E-03	1.424	down	0.702	1.00E+00
SAOHS_C02933	BeaB	betaine aldehyde dehydrogenase	Osmotic stress	0.91	-0.95	-0.33	0.13	—	1.88	up	1.88	3.25E-10	1.935	down	0.517	3.58E-04	1.261	down	0.793	1.02E+00	1.091	up	1.091	1.00E+00
SAOHS_C00851	OsmC	hypothetical protein	Oxidative stress	1.06	-0.80	0.06	n.d.	—	2.08	up	2.08	7.67E-04	1.231	down	0.812	1.00E+00	1.044	up	1.044	1.00E+00				
SAOHS_C01282	BlaA	glutathione peroxidase	Oxidative stress	0.47	0.86	0.51	0.73	▲	1.39	up	1.39	1.00E+00	1.820	up	1.820	1.58E-05	1.425	up	1.425	1.00E+00	1.657	up	1.657	2.49E-02
SAOHS_C01327	KatA	catalase	Oxidative stress	0.82	0.22	0.88	1.42	▲	1.77	up	1.77	3.28E-06	1.164	up	1.164	1.00E+00	1.841	up	1.841	4.41E-07	2.674	up	2.674	1.05E-25
SAOHS_C02381	Dps	hypothetical protein	Oxidative stress	0.20	0.26	1.70	2.55	▲	1.15	up	1.15	1.00E+00	1.195	up	1.195	1.00E+00	3.250	up	3.250	2.68E-05	5.759	up	5.759	2.87E-13
SAOHS_C01794	GsdB	glyceraldehyde 3-phosphate dehydrogenase 2	Oxidative stress;Central carbohydrate metabolism	-0.38	0.75	0.68	1.44	▲	1.30	down	0.77	1.00E+00	1.679	up	1.679	9.24E-02	1.599	up	1.599	9.21E-01	2.716	up	2.716	9.03E-04
SAOHS_C01653	SodA	superoxide dismutase, Mn	Oxidative stress;Nitrogen Metabolism - no subcategory	0.51	1.57	1.84	1.99	▲	1.42	up	1.42	1.00E+00	2.961	up	2.961	6.44E-08	3.584	up	3.584	4.10E-08	3.962	up	3.962	7.00E-13
SAOHS_C00204	Hmp	globin domain-containing protein	Oxidative stress;Stress Response - no subcategory	-0.86	1.48	-0.08	0.07	—	1.81	down	0.55	2.50E-01	2.790	down	2.790	4.48E-18	1.060	down	0.943	1.00E+00	1.053	up	1.053	1.00E+00
SAOHS_C04262	MenQ2	ABC transporter substrate-binding protein	Pathogenicity Islands;Lysine, threonine, methionine, and cysteine	0.21	0.02	1.31	1.17	▲	1.18	up	1.18	1.00E+00	1.015	up	1.015	1.00E+00	2.514	up	2.514	1.13E-02	2.253	up	2.253	9.88E-01
SAOHS_C00844	MenQ1	hypothetical protein	Pathogenicity Islands;Lysine, threonine, methionine, and cysteine	0.54	0.03	0.79	0.90	▲	1.46	up	1.46	1.00E+00	1.024	up	1.024	1.00E+00	1.733	up	1.733	5.32E-03	1.873	up	1.873	6.16E-06
SAOHS_C01239	hypothetical protein	hypothetical protein	Periplasmic Stress;Regulation and Cell signaling - no subcategory	-0.15	0.62	-0.46	-0.73	▼	1.11	down	0.90	1.00E+00	1.012	up	1.012	1.00E+00	1.584	down	0.831	1.02E+00	1.658	down	0.603	1.06E-02
SAOHS_C02363	aldhA	aldehyde dehydrogenase	Phospholipids;Central carbohydrate metabolism	0.85	0.01	0.62	0.81	▲	1.81	up	1.81	5.99E-05	1.010	up	1.010	1.00E+00	1.534	up	1.534	9.92E-02	1.753	up	1.753	5.86E-05
SAOHS_C01800	PhoP	alkaline phosphatase synthesis/transcriptional regulatory protein	Phosphorus Metabolism - no subcategory	-0.14	0.81	1.64	1.92	▲	1.10	down	0.91	1.00E+00	1.749	up	1.749	8.80E-03	3.120	up	3.120	3.32E-09	3.794	up	3.794	5.87E-14
SAOHS_C00220	TarT	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	Plant-Prokaryote comparative genomics;Gram-Positive cell wall components;Isoprenoids	0.69	1.11	1.22	1.04	▲	1.61	up	1.61	2.48E-01	2.163	up	2.163	2.94E-03	2.331	up	2.331	1.73E-02	2.052	up	2.052	2.98E-02
SAOHS_C02627	hypothetical protein	hypothetical protein	Polysaccharides	-1.19	-0.07	0.19	0.24	—	2.28	down	0.44	4.03E-04	1.051	down	0.912	1.00E+00	1.144	up	1.144	1.02E+00	1.182	up	1.182	1.00E+00
SAOHS_C01874	hypothetical protein	hypothetical protein	Potassium metabolism - no subcategory;Oxidative stress	-1.11	0.46	-0.09	0.42	—	2.16	up	2.16	2.37E-04	1.376	up	1.376	1.00E+00	1.064	down	0.940	1.00E+00	1.339	up	1.339	1.00E+00
SAOHS_C02303	Mauf	hypothetical protein	Programmed Cell Death and Twin-antitoxin Systems	-0.43	-0.43	-1.49	-0.82	▼	1.35	down	0.74	1.00E+00	1.345	down	0.743	1.00E+00	2.801	down	0.357	3.60E-03	1.726	down	0.567	3.72E-01
SAOHS_C01597	ProC	pyrroline-5-carboxylate reductase	Proline and 4-hydroxyproline	0.84	0.83	1.10	1.02	▲	1.80	up	1.80	2.74E-												

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8,24 and 32h ratio: median tendence - 1.5% cutoff	median fold-change (direction) OD=0.4	median fold-change (direction) 8h p.i.	median fold-change (direction) 24h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 8h p.i.	p-value BH adjusted OD=0.4	median fold-change (direction) 8h p.i.	median fold-change (direction) 24h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change (direction) 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.				
SAOUHSC_01757	RplU	50S ribosomal protein L21	Protein biosynthesis	-0.35	-0.95	-1.22	-1.54	▼	1.28	down			0.517	1.00E+00	1.933	down		0.428	1.34E+11	2.206	down	0.453	1.19E+11				
SAOUHSC_01829	RplD	30S ribosomal protein S4	Protein biosynthesis	-0.50	-0.84	-0.90	-1.12	▼	1.42	down			0.559	3.36E-02	1.789	down		0.537	4.02E-01	2.167	down	0.461	2.65E-06				
SAOUHSC_02361	RpmE2	50S ribosomal protein L31 type B	Protein biosynthesis	-0.01	-0.81	-1.19	-1.14	▼	1.02	down			0.569	2.54E-01	1.759	down		0.487	1.47E-04	2.197	down	0.455	1.05E-07				
SAOUHSC_02477	RplJ	30S ribosomal protein S9	Protein biosynthesis	-0.41	-0.80	-1.23	-1.38	▼	1.33	down			0.660	1.00E+00	1.514	down		0.428	5.10E-06	2.609	down	0.381	1.37E-08				
SAOUHSC_02486	RplK	30S ribosomal protein S11	Protein biosynthesis	-0.37	-0.98	-1.09	-1.79	▼	1.29	down			0.777	1.00E+00	1.973	down		0.332	4.91E-08	3.455	down	0.289	6.59E-12				
SAOUHSC_02487	RplM	30S ribosomal protein S13	Protein biosynthesis	-0.33	-1.10	-1.22	-1.29	▼	1.26	down			0.79	1.00E+00	2.150	down		0.465	2.58E-06	2.333	down	0.429	2.00E-06				
SAOUHSC_02492	RplO	52S ribosomal protein L15	Protein biosynthesis	-0.22	-1.00	-1.31	-1.38	▼	1.16	down			0.86	1.00E+00	2.000	down		0.500	6.23E-04	2.522	down	0.397	1.96E-05				
SAOUHSC_02495	RplR	52S ribosomal protein L18	Protein biosynthesis	-0.63	-0.63	-0.95	-0.93	▼	1.02	down			0.98	1.00E+00	1.525	down		0.656	8.30E-01	1.936	down	0.517	4.93E-03				
SAOUHSC_02509	RplQ	30S ribosomal protein S17	Protein biosynthesis	-0.33	-0.56	-1.41	-1.54	▼	1.26	up			1.26	1.00E+00	1.478	down		0.676	1.00E+00	2.916	down	0.376	5.13E-03				
SAOUHSC_02504	RpmC	50S ribosomal protein L29	Protein biosynthesis	0.07	-0.77	-1.30	-1.31	▼	1.05	up			1.05	1.00E+00	1.705	down		0.587	1.00E+00	2.295	down	0.496	1.31E-03				
SAOUHSC_02505	RplP	30S ribosomal protein L16	Protein biosynthesis	-0.60	-1.07	-1.50	-1.37	▼	1.51	down			0.66	1.00E+00	2.104	down		0.475	1.21E-01	2.837	down	0.352	3.73E-06				
SAOUHSC_02506	RplC	30S ribosomal protein S3	Protein biosynthesis	-0.18	-0.97	-0.70	-0.80	▼	1.13	down			0.89	1.00E+00	1.955	down		0.615	9.70E-01	1.741	down	0.574	1.05E-04				
SAOUHSC_02507	RplV	30S ribosomal protein L22	Protein biosynthesis	-0.36	-0.77	-0.77	-0.96	▼	1.29	down			0.78	1.00E+00	1.701	down		0.586	8.57E-01	1.948	down	0.513	9.77E-04				
SAOUHSC_02508	RplS	30S ribosomal protein S19	Protein biosynthesis	-0.32	-0.89	-1.76	-2.04	▼	1.25	down			0.80	1.00E+00	1.848	down		0.541	6.39E-01	3.456	down	0.289	5.04E-02				
SAOUHSC_02509	RplB	50S ribosomal protein L2	Protein biosynthesis	-0.30	-0.84	-1.04	-1.05	▼	1.23	down			0.81	1.00E+00	1.789	down		0.559	1.69E-01	2.061	down	0.485	6.28E-04				
SAOUHSC_02511	RplD	50S ribosomal protein L4	Protein biosynthesis	-0.29	-0.85	-1.42	-1.30	▼	1.23	down			0.82	1.00E+00	1.802	down		0.555	1.52E-02	2.677	down	0.374	1.66E-05				
SAOUHSC_03038	Dnf	peptide deformylase	Protein biosynthesis;Central carbohydrate metabolism	0.74	-0.04	-0.30	-0.01	—	1.67	up	1.67		2.644E-01	1.025	down		0.975	1.00E+00	1.068	down	0.936	1.00E+00	1.006	down	0.994	1.00E+00	
SAOUHSC_03037	OtxF	rRNA large subunit methyltransferase	Protein biosynthesis;NAD and NADP	-0.11	0.45	0.40	0.89	▲	1.08	down			0.93	1.00E+00	1.370	up		1.519	1.00E+00	1.519	up	1.519	1.00E+00	1.860	up	1.860	8.00E-03
SAOUHSC_03034		ribosomal protein-serine acetyltransferase	Protein biosynthesis;Protein processing and modification	0.74	1.01	2.04	2.30	▲	1.67	up	1.67		1.67	1.00E+00	2.018	up	2.018	4.09E-03	4.122	up	4.122	9.58E-04	4.924	up	4.924	3.47E-05	
SAOUHSC_01626	PepQ2	proline dipeptidase	Protein degradation	0.81	0.87	0.29	0.55	—	1.76	up	1.76		2.494E-04	1.824	up	1.824	1.20E-06	1.219	up	1.219	1.00E+00	1.464	up	1.464	7.33E-01		
SAOUHSC_01778	CpxX	ATP-dependent protease ATP-binding subunit CpxX	Protein degradation	-0.24	-0.72	-1.53	-1.66	▼	1.18	down			0.85	1.00E+00	1.642	down		0.609	2.65E-01	2.880	down	0.347	4.86E-11	3.164	down	0.316	1.12E-17
SAOUHSC_01861		hypothetical protein	Protein degradation	-0.35	-0.95	n.d.	n.d.	—	1.27	up			1.27	1.00E+00	1.937	down		0.516	2.95E-02								
SAOUHSC_02102	Map	methionine aminopeptidase	Protein degradation;Protein biosynthesis	0.69	0.03	-0.03	-0.16	—	1.62	up	1.62		3.391E-02	1.023	up	1.023	1.00E+00	1.021	down	0.979	1.00E+00	1.115	down	0.897	1.00E+00		
SAOUHSC_01972	PrsA	protein export protein PrsA	Protein folding	0.05	2.10	1.78	1.37	▲	1.03	up	1.03		1.03	1.00E+00	4.556	up	4.556	7.89E-25	3.429	up	3.429	9.86E-18	2.591	up	2.591	3.25E-15	
SAOUHSC_00912	CipB	ATP-dependent CIP protease, ATP-binding subunit CipB	Protein folding;Protein degradation	0.01	-0.75	1.10	1.79	▲	1.01	up	1.01		1.01	1.00E+00	1.687	down		0.593	2.86E-02	3.148	up	2.138	3.33E-28	3.461	up	3.461	5.55E-78
SAOUHSC_01360	MurA1	methionine sulfide reductase A	Protein processing and modification	0.52	1.08	1.02	0.99	▲	1.43	up	1.43		1.43	1.00E+00	2.112	up	2.112	4.86E-04	2.027	up	2.027	1.64E-01	1.988	up	1.988	4.52E-03	
SAOUHSC_01431	MurB	methionine sulfide reductase B	Protein processing and modification	0.50	2.69	1.85	1.89	▲	1.42	up	1.42		1.42	1.00E+00	6.467	up	6.467	9.68E-12	3.595	up	3.595	9.72E-09	3.694	up	3.694	8.04E-10	
SAOUHSC_01432	MurA2	methionine sulfide reductase A	Protein processing and modification	0.27	2.17	1.45	1.53	▲	1.20	up	1.20		1.20	1.00E+00	5.945	up	5.945	4.50E-14	3.146	up	3.146	1.87E-09	2.888	up	2.888	3.67E-12	
SAOUHSC_02494	RplK	30S ribosomal protein S5	Protein processing and modification;Protein biosynthesis	-0.01	-0.40	-1.11	-1.28	▼	1.01	down			0.99	1.00E+00	1.520	down		0.658	1.00E+00	2.159	down	0.463	1.73E-02	2.426	down	0.412	2.14E-03
SAOUHSC_00257	EsaK	hypothetical protein	Protein secretion system, Type VII	0.16	0.31	0.67	-1.36	▲	1.12	up	1.12		1.12	1.00E+00	1.239	up	1.239	1.00E+00	1.593	up	1.593	1.76E-01	2.241	up	2.241	7.73E-04	
SAOUHSC_00372	Xpt	xanthine phosphoribosyltransferase	Purines	-0.03	-0.37	-1.04	-0.85	▼	1.02	down			0.98	1.00E+00	1.290	down		0.775	1.00E+00	2.020	down	0.495	7.95E-05	1.841	down	0.543	1.70E-03
SAOUHSC_00374	GuaB	inosine 5-monophosphate dehydrogenase	Purines	-0.05	-0.23	-0.96	-0.78	▼	1.04	down			0.96	1.00E+00	1.176	down		0.850	1.00E+00	1.939	down	0.516	6.86E-06	1.679	down	0.596	8.42E-03
SAOUHSC_01010	PurC	phosphoribosylaminoimidazole succinocarboxamide synthase	Purines	-0.01	0.39	-0.97	-0.69	▼	1.00	down			1.00	1.00E+00	1.309	up	1.309	1.00E+00	1.955	down	0.512	6.71E-08	1.610	down	0.621	2.26E-01	
SAOUHSC_01011	PurS	phosphoribosylformylglycinamide synthase, PurS protein	Purines	0.27	0.73	-0.84	-0.71	▼	1.21	up	1.21		1.21	1.00E+00	1.658	up	1.658	2.91E-03	1.795	down	0.557	5.96E-02	1.635	down	0.611	1.00E+00	
SAOUHSC_01012	PurQ	phosphoribosylformylglycinamide synthase I	Purines	0.14	0.54	-0.84	-0.71	▼	1.10	up	1.10		1.10	1.00E+00	1.450	up	1.450	7.30E-01	1.791	down	0.558	1.22E-02	1.633	down	0.613	2.74E-01	
SAOUHSC_01015	PurM	phosphoribosylaminoimidazole synthase	Purines	0.09	0.63	-0.56	-0.34	—	1.07	up	1.07		1.07	1.00E+00	1.542	up	1.542	1.61E-02	1.478	down	0.677	1.00E+00	1.269	down	0.788	1.00E+00	
SAOUHSC_01017	PurH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Purines	-0.58	-0.17	-0.97	-0.91	▼	1.49	down			0.67	1.00E+00	1.123	down		0.890	1.00E+00	1.959	down	0.510	7.29E-03	1.878	down	0.532	5.07E-10
SAOUHSC_01130	GuaC	guanosine 5-monophosphate oxidoreductase	Purines	-0.63	-0.62	-0.86	-0.67	▼	1.55	down			0.65	8.267E-01	1.534	down		0.652	1.00E+00	1.816	down	0.551	2.32E-04	1.591	down	0.628	4.29E-01
SAOUHSC_01485	Ndk	nucleoside diphosphate kinase	Purines;Pyrimidines	0.42	0.28	1.11	1.12	▲	1.34	up	1.34		1.34	1.00E+00	1.215	up	1.215	1.00E+00	2.165	up	2.165	4.79E-04	2.171	up	2.171	2.74E-06	
SAOUHSC_01170	CarB	carbamoyl phosphate synthase large subunit	Pyrimidines	-0.78	-0.81	-0.88	-0.66	▼	1.71	down	0.58		9.771E-06	1.705	down	0.570	6.33E-10	1.835	down	0.545	3.37E-05	1.579	down	0.633	1.00E+00		
SAOUHSC_02377	Pdp	pyrimidine nucleoside phosphorylase	Pyrimidines;Monosaccharides	-0.16	1.14	1.87	2.30	▲	1.12	down			0.89	1.00E+00	2.205	up	2.205	4.16E-32	3.647	up	3.647	2.58E-30	4.291	up	4.291	2.23E-44	
SAOUHSC_00940		hypothetical protein	Regulation and Cell signaling - no subcategory	0.32	1.04	n.d.	n.d.	▲	1.25	up	1.25		1.25	1.00E+00	2.051	up	2.051	1.22E-04									
SAOUHSC_01361	MurK	transcriptional regulator	Regulation and Cell signaling - no subcategory	-0.53	0.84	0.21	-0.34	—	1.45	down			0.69	1.00E+00	1.795	up	1.795	2.89E-05	1.157	up	1.157	1.00E+00	1.264	down	0.791	1.00E+00	
SAOUHSC_02581		transcriptional regulator	Regulation and Cell signaling - no subcategory	0.27	2.11	1.39	1.43	▲	1.21	down			0.83	1.00E+00	4.315	up	4.315	6.02E-18	2.925	up	2.925	5.94E-11	2.690	up	2.690	6.64E-15	
SAOUHSC_00201	Opp-5A	hypothetical protein	Regulation and Cell signaling - no subcategory;ABC transporters	-0.05	1.62	n.d.	0.39	▲	1.04	down			0.97	1.00E+00	3.077	up	3.077	2.99E-10					1.310	up	1.310	1.00E+00	
SAOUHSC_01979		hypothetical protein	Resistance to antibiotics and toxic compounds	-0.43	-0.92	-2.13	-2.71	▼	1.34	down			0.74	1.00E+00	1.894	down		0.528	2.70E-06	5.038	down	0.398	3.11E-11	6.538	down	0.153	1.82E-11

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8,24 and 32h ratio; median tendence - 1.5K cutoff	median fold-change OD=0.4	median fold-change (direction) OD=0.4	median ratio over assays against non-ad. OD=0.4	p-value BH adjusted OD=0.4	median fold-change 8h p.i.	median fold-change (direction) 8h p.i.	median ratio over assays against non-ad. 8h p.i.	p-value BH adjusted 8h p.i.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.
SAOUSHC_01055		inositol monophosphatase family protein	Stress Response - no subcategory	-0.01	0.15	0.89	0.67	▲	1.01	down	0.99	1.00E+00	1.109	up	1.109	1.00E+00	1.851	up	1.851	3.57E-02	1.592	up	1.592	3.88E-01
SAOUSHC_01814	UspA2	hypothetical protein	Stress Response - no subcategory	0.08	0.37	0.54	0.75	–	1.06	up	1.06	1.00E+00	1.288	up	1.288	1.00E+00	1.453	up	1.453	1.00E+00	1.680	up	1.680	3.20E-04
SAOUSHC_01819	UspA1	hypothetical protein	Stress Response - no subcategory	0.30	1.46	2.61	1.98	▲	1.23	up	1.23	1.00E+00	2.745	up	2.745	1.00E+00	6.120	up	6.120	6.82E-19	8.468	up	8.468	4.61E-25
SAOUSHC_02299	RibW	serine protein kinase RibW	Stress Response - no subcategory	0.28	-0.57	0.92	0.53	–	1.21	up	1.21	1.00E+00	1.480	down	0.676	1.00E+00	1.893	down	0.528	8.18E-03	1.449	down	0.690	1.00E+00
SAOUSHC_02430	HraA	ABC transporter periplasmic binding protein	Stress Response - no subcategory;Iron acquisition and metabolism - no subcategory	-1.87	-0.05	0.10	0.26	–	3.64	down	0.27	1.577E-12	1.036	down	0.965	1.00E+00	1.073	up	1.073	1.00E+00	1.196	up	1.196	1.00E+00
SAOUSHC_02298	SigB	RNA polymerase sigma factor SigB	Stress Response - no subcategory;Transcription;Quorum sensing and biofilm formation;Resistance to antibiotics and toxic compounds	0.42	-0.54	0.98	0.77	▼	1.34	up	1.34	1.00E+00	1.449	down	0.690	1.00E+00	1.978	down	0.506	2.74E-02	1.706	down	0.585	1.77E-01
SAOUSHC_02402	MSA	PTS system mannitol-specific transporter subunit IIA	Sugar alcohols	0.91	-0.64	0.13	0.36	–	1.88	up	1.88	1.474E-06	3.555	down	0.643	1.00E+00	1.097	up	1.097	1.00E+00	1.284	up	1.284	1.00E+00
SAOUSHC_02403	MIO	mannitol-1-phosphate 5-dehydrogenase	Sugar alcohols	0.87	-0.38	0.23	0.51	–	1.83	up	1.83	1.474E-06	1.299	down	0.770	1.00E+00	1.169	up	1.169	1.00E+00	1.426	up	1.426	1.00E+00
SAOUSHC_01276	GlpK	glycerol kinase	Sugar alcohols;Phospholipids;Central carbohydrate metabolism	0.19	0.82	0.80	0.84	▲	1.14	up	1.14	1.00E+00	1.761	up	1.761	3.09E-05	1.737	up	1.737	6.28E-04	1.793	up	1.793	1.57E-06
SAOUSHC_00364	AhpF	alkyl hydroperoxide reductase subunit F	Sulfur Metabolism - no subcategory	1.03	0.16	0.85	1.04	▲	2.04	up	2.04	1.697E-17	1.116	up	1.116	1.00E+00	1.803	up	1.803	5.72E-07	2.062	up	2.062	1.05E-16
SAOUSHC_00365	AhpC	alkyl hydroperoxide reductase subunit C	Sulfur Metabolism - no subcategory	1.00	-0.07	1.09	1.34	▲	2.00	up	2.00	5.273E-10	1.053	down	0.950	1.00E+00	2.125	up	2.125	4.10E-08	2.525	up	2.525	4.83E-13
SAOUSHC_01822	Tpx	thiol peroxidase	Sulfur Metabolism - no subcategory	0.71	0.58	0.49	0.72	▲	1.63	up	1.63	2.644E-03	1.492	up	1.492	2.20E-01	1.409	up	1.409	1.00E+00	1.644	up	1.644	1.58E-02
SAOUSHC_01999		bacterioferritin comigratory protein	Sulfur Metabolism - no subcategory	0.87	1.07	1.04	1.31	▲	1.83	up	1.83	1.573E-01	2.096	up	2.096	5.78E-04	2.056	up	2.056	3.72E-03	2.481	up	2.481	4.49E-05
SAOUSHC_01177	RpoZ	DNA-directed RNA polymerase subunit omega	Transcription	-0.22	-0.45	1.01	0.96	▼	1.17	down	0.86	1.00E+00	1.364	down	0.733	1.00E+00	2.016	down	0.496	1.01E-02	1.947	down	0.514	9.62E-04
SAOUSHC_02342	Rho	transcription termination factor Rho	Transcription	0.82	0.05	0.16	0.30	–	1.76	down	0.57	1.016E-04	1.035	up	1.035	1.00E+00	1.120	down	0.893	1.03E+00	1.235	down	0.810	1.00E+00
SAOUSHC_02485	RpoA	DNA-directed RNA polymerase subunit alpha	Transcription	-0.45	-0.57	-0.85	-0.65	▼	1.40	down	0.71	1.00E+00	1.488	down	0.672	1.00E+00	1.801	down	0.555	4.34E-03	1.565	down	0.639	6.26E-01
SAOUSHC_00625	MhrA2	putative monovalent cation/He antiporter subunit A	Uni- Sym- and Antiporters	-0.34	-1.24	-0.90	-1.08	▼	1.26	down	0.79	1.00E+00	2.368	down	0.422	4.61E-02	1.872	down	0.534	1.00E+00	2.110	down	0.474	3.18E-01
SAOUSHC_00528	RpoG	30S ribosomal protein S7	Vinulence - no subcategory;Protein biosynthesis	-0.20	-1.01	-1.70	-1.59	▼	1.15	down	0.87	1.00E+00	2.008	down	0.498	1.17E-02	3.244	down	0.308	1.06E-08	3.802	down	0.263	7.88E-17
SAOUSHC_01784	RplT	50S ribosomal protein L20	Vinulence - no subcategory;Protein biosynthesis	-0.15	-0.58	-1.06	-0.97	▼	1.11	down	0.90	1.00E+00	1.491	down	0.671	1.00E+00	2.089	down	0.479	8.20E-03	1.962	down	0.510	8.10E-03
SAOUSHC_00044		hypothetical protein		0.01	1.05	0.56	0.82	▲	1.00	up	1.00	1.00E+00	2.064	up	2.064	2.30E-02	1.477	up	1.477	1.00E+00	1.770	up	1.770	5.67E-01
SAOUSHC_00070	SarS	accessory regulator-like protein		0.29	-2.05	-0.89	-0.65	▼	1.22	up	1.22	1.00E+00	4.132	down	0.242	3.90E-09	1.856	down	0.539	2.75E-01	1.569	down	0.637	7.61E-01
SAOUSHC_00164		hypothetical protein		0.87	1.11	1.56	1.98	▲	1.82	up	1.82	1.00E+00	2.476	up	2.476	4.81E-02	2.958	up	2.958	5.45E-02	3.952	up	3.952	9.03E-04
SAOUSHC_00253		hypothetical protein		-1.38	-2.51	-1.55	-1.13	▼	2.60	down	0.38	3.47E-05	5.689	down	0.176	2.58E-04	2.927	down	0.342	1.89E-03	2.191	down	0.456	1.74E-04
SAOUSHC_00285		hypothetical protein		-0.26	-1.47	-0.68	-0.38	▼	1.20	down	0.83	1.00E+00	2.763	down	0.362	1.48E-06	1.603	down	0.624	1.00E+00	1.211	down	0.826	1.00E+00
SAOUSHC_00356		hypothetical protein		0.92	-1.85	-1.11	0.02	▼	1.89	up	1.89	2.605E-07	3.608	down	0.277	6.88E-09	2.186	down	0.457	2.10E-02	1.766	down	0.566	4.55E-01
SAOUSHC_00371		hypothetical protein		0.57	3.29	3.73	3.95	▲	1.49	up	1.49	1.00E+00	3.439	up	1.439	5.56E-16	6.614	up	6.614	1.79E-12	7.540	up	7.540	7.35E-17
SAOUSHC_00427	Sir1	autolysin		-0.34	-1.18	-1.96	-2.45	▼	1.26	down	0.79	1.00E+00	2.266	down	0.441	5.91E-03	3.973	down	0.252	8.16E-02	5.474	down	0.183	2.59E-01
SAOUSHC_00428		hypothetical protein		-0.08	-2.89	-1.87	-1.80	▲	1.06	down	0.95	1.00E+00	6.027	up	6.027	2.15E-11	3.654	up	3.654	5.17E-06	3.035	up	3.035	2.17E-06
SAOUSHC_00502	CisR	hypothetical protein		-0.25	0.29	1.51	1.69	▲	1.19	down	0.84	1.00E+00	1.219	up	1.219	1.00E+00	2.838	up	2.838	8.10E-10	3.220	up	3.220	4.99E-10
SAOUSHC_00533	HcrA	chaperone protein HcrA		0.78	-0.08	-0.13	-0.02	–	1.72	up	1.72	1.399E-03	1.058	down	0.945	1.00E+00	1.093	down	0.915	1.00E+00	1.014	down	0.996	1.00E+00
SAOUSHC_00538		halocacid dehalogenase-like hydrolase		0.63	1.33	0.64	0.75	▲	1.55	up	1.55	1.00E+00	2.522	up	1.564	1.49E-11	1.564	up	1.564	9.38E-01	1.684	up	1.684	2.48E-01
SAOUSHC_00569		hypothetical protein		-0.06	-1.13	-1.29	-0.49	▼	1.04	down	0.96	1.00E+00	2.181	down	0.458	2.35E-03	2.448	down	0.408	2.51E-01	1.400	down	0.714	1.00E+00
SAOUSHC_00603		hypothetical protein		0.37	0.90	0.81	0.67	▲	1.30	up	1.30	1.00E+00	1.868	up	1.868	1.65E-02	1.757	up	1.757	5.35E-01	1.592	up	1.592	1.00E+00
SAOUSHC_00634	MecC	ABC transporter substrate-binding protein		-0.56	-1.94	-2.68	-3.14	▲	1.47	down	0.68	1.00E+00	3.831	down	0.261	1.15E-38	6.422	down	0.156	1.04E-12	8.805	down	0.114	3.38E-18
SAOUSHC_00637	MhrA	hypothetical protein		-0.46	-0.85	-0.82	-0.88	▼	1.37	down	0.73	1.00E+00	1.802	down	0.555	2.45E-01	1.770	down	0.565	2.14E-01	1.842	down	0.543	5.88E-04
SAOUSHC_00647	AbcA	hypothetical protein		0.38	0.29	1.38	1.45	▲	1.22	up	1.22	1.00E+00	1.223	up	1.223	1.00E+00	2.609	up	2.609	4.87E-26	2.724	up	2.724	8.77E-38
SAOUSHC_00652	RhaA	iron compound ABC transporter ATP-binding protein		2.08	0.01	0.50	0.77	–	4.18	down	0.24	1.317E-11	1.009	up	1.009	1.00E+00	1.415	down	0.707	1.00E+00	1.701	down	0.588	1.23E-02
SAOUSHC_00659		hypothetical protein		0.54	1.58	1.54	1.76	▲	1.45	up	1.45	1.00E+00	2.927	up	2.927	1.84E-02	2.914	up	2.914	1.35E-01	3.430	up	3.430	1.19E-01
SAOUSHC_00694	MprA	hypothetical protein		0.35	0.83	0.00	-0.01	–	1.28	up	1.28	1.00E+00	1.776	up	1.776	1.75E-04	1.003	up	1.003	1.00E+00	1.007	down	0.993	1.00E+00
SAOUSHC_00714	SaeS	sensor histidine kinase SaeS		0.95	1.31	0.47	0.12	–	1.94	down	0.52	1.961E-02	2.476	up	2.476	6.18E-14	1.382	up	1.382	1.00E+00	1.086	up	1.086	1.00E+00
SAOUSHC_00715	SaeR	response regulator		-0.26	1.78	1.12	0.82	▲	1.20	down	0.83	1.00E+00	3.441	up	3.441	6.44E-10	2.177	up	2.177	2.38E-02	1.760	up	1.760	1.71E-01
SAOUSHC_00717	SaeP	hypothetical protein		-1.74	2.10	2.97	1.24	▲	3.35	down	0.30	4.323E-01	5.661	up	5.661	7.59E-07	7.828	up	7.828	4.86E-01	2.369	up	2.369	2.12E-02
SAOUSHC_00736		hypothetical protein		0.90	-0.22	0.81	0.95	▲	1.86	up	1.86	1.854E-01	1.165	down	0.858	1.00E+00	1.753	up	1.753	2.78E-01	1.932	up	1.932	2.10E-02
SAOUSHC_00754		hypothetical protein		-0.09	-0.90	-1.04	-1.26	▼	1.06	down	0.94	1.00E+00	1.870	down	0.535	8.52E-04	2.051	down	0.488	9.92E-02	2.393	down	0.418	1.70E-03
SAOUSHC_00763		hypothetical protein		0.59	1.93	n.d.	n.d.	▲	1.50	up	1.50	1.00E+00	2.510	up	2.510	1.22E-02								
SAOUSHC_00833		hypothetical protein		-0.94	0.91	0.38	0.43	–	1.92	down	0.52	6.761E-02	1.885	up	1.885	3.88E-03	1.301	up	1.301	1.00E+00	1.347	up	1.347	1.00E+00
SAOUSHC_00834		thioredoxin		0.88	1.62	0.38	0.36	–	1.58	up	1.58	1.00E+00	2.030	up	2.030	3.09E-06	1.304	up	1.304	1.00E+00	1.279	up	1.279	1.00E+00
SAOUSHC_00850	SufU	hypothetical protein		0.88	-0.33	-0.17	0.02	–	1.98	up	1.98	4.002E-03	1.253	down	0.798	1.00E+00	1.122	down	0.891	1.00E+00	1.015	up	1.015	1.00E+00
SAOUSHC_00863		hypothetical protein		0.63	1.07	0.27	0.26	–	1.55	up	1.55	5.831E-01	2.093	up	2.093	1.23E-04	1.210	up	1.210	1.00E+00	1.198	up	1.198	1.00E+00
SAOUSHC_00865		hypothetical protein		0.39	0.83	0.38	0.47	–	1.31	up	1.31	1.00E+00	1.782	up	1.782	1.43E-04	1.299	up	1.299	1.00E+00				

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8,24 and 32h ratio: median tendence - 1.5K cutoff	median fold-change OD=0.4	median fold-change (direction) OD=0.4	median ratio over assays against non-ad. 8h p.i.	p-value BH adjusted OD=0.4	median fold-change 8h p.i.	median fold-change (direction) 8h p.i.	median ratio over assays against non-ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non-ad. 32h p.i.	p-value BH adjusted 32h p.i.
SAOHS_C01429		hypothetical protein		-0.52	1.60	-0.19	-0.49	—	1.43	down	0.70	1.00E+00	3.041	up	3.041	2.01E-05	1.139	down	0.878	1.00E+00	1.405	down	0.712	1.00E+00
SAOHS_C01438		hypothetical protein		0.66	0.91	0.12	0.28	—	1.58	up	1.58	3.07E-01	1.874	up	1.874	1.51E-03	1.086	up	1.086	1.00E+00	1.213	up	1.213	1.00E+00
SAOHS_C01575		heli-turn-heli domain-containing protein		0.65	0.96	1.09	1.16	▲	1.57	up	1.57	1.00E+00	1.945	up	1.945	1.15E-06	2.128	up	2.128	3.19E-04	2.236	up	2.236	1.17E-08
SAOHS_C01606		peptidase T		0.51	0.79	1.00	1.17	▲	1.42	up	1.42	1.00E+00	1.732	up	1.732	9.24E-02	1.994	up	1.994	2.21E-03	2.248	up	2.248	3.81E-07
SAOHS_C01665		CRS domain-containing protein		-0.03	0.26	n.d.	0.83	—	1.02	down	0.98	1.00E+00	1.200	up	1.200	1.00E+00	1.777	up	1.777	2.25E-02	1.777	up	1.777	2.25E-02
SAOHS_C01666	GlyS	glycyl-tRNA synthetase		0.66	-0.07	-0.17	-0.01	—	1.58	up	1.58	3.91E-03	1.047	down	0.955	1.00E+00	1.123	down	0.891	1.00E+00	1.004	down	0.996	1.00E+00
SAOHS_C01701		hypothetical protein		-1.42	-1.01	-0.51	-1.50	▼	2.68	down	0.37	1.749E-07	2.017	down	0.496	1.70E-04	1.425	down	0.702	1.00E+00	2.870	down	0.348	2.46E-04
SAOHS_C01708		Lamb/ncf family protein		0.53	0.26	0.67	1.04	▲	1.44	up	1.44	1.00E+00	1.195	up	1.195	1.00E+00	1.586	up	1.586	7.60E-01	2.055	up	2.055	9.88E-03
SAOHS_C01716		hypothetical protein		-0.70	-1.57	n.d.	-1.07	▼	1.63	down	0.62	1.00E+00	2.967	down	0.337	3.81E-05					4.209	down	0.238	2.59E-01
SAOHS_C01717		hypothetical protein		0.50	-1.38	-1.51	-2.35	▼	1.41	down	0.71	1.00E+00	2.607	down	0.384	1.34E-07	2.852	down	0.351	2.74E-01	4.765	down	0.210	2.59E-01
SAOHS_C01720		Holliday junction resolvase-like protein		0.36	0.87	0.23	0.28	—	1.28	up	1.28	1.00E+00	1.822	up	1.822	1.58E-02	1.177	up	1.177	1.00E+00	1.217	up	1.217	1.00E+00
SAOHS_C01721		hypothetical protein		0.57	0.88	0.34	0.75	▲	1.48	up	1.48	1.00E+00	1.842	up	1.842	1.35E-02	1.265	up	1.265	1.00E+00	1.679	up	1.679	2.86E-01
SAOHS_C01729		hypothetical protein		2.17	-0.03	0.42	-0.36	—	4.49	up	4.49	3.19E-03	1.019	up	0.981	1.00E+00	1.333	up	1.333	1.00E+00	1.280	down	0.781	1.00E+00
SAOHS_C01730	CuSD	hypothetical protein		0.49	-0.90	-0.61	-0.33	▼	1.40	up	1.40	1.00E+00	1.864	down	0.536	1.51E-03	1.525	down	0.656	1.00E+00	1.258	down	0.795	1.00E+00
SAOHS_C01761		hypothetical protein		-0.24	3.61	2.26	3.11	▲	1.18	down	0.85	1.00E+00	8.072	up	0.072	5.63E-08	4.799	up	4.799	1.43E-04	2.851	up	2.851	1.59E-04
SAOHS_C01782		hypothetical protein		0.51	0.83	0.28	0.21	—	1.42	up	1.42	1.00E+00	1.782	up	1.782	6.21E-04	1.210	up	1.210	1.00E+00	1.169	up	1.169	1.00E+00
SAOHS_C01786	hIFC	translation initiation factor F-3		0.33	-1.00	-1.15	-0.90	▼	1.26	down	0.79	1.00E+00	2.028	down	0.493	7.09E-07	2.225	down	0.449	1.27E-05	1.872	down	0.534	2.42E-04
SAOHS_C01787	LysP	hypothetical protein		-0.65	1.92	1.59	1.18	▲	1.57	down	0.64	1.00E+00	3.777	up	3.777	1.67E-09	3.020	up	3.020	4.81E-08	2.263	up	2.263	6.17E-07
SAOHS_C01816	PepQ	hypothetical protein		0.14	1.67	0.94	1.07	▲	1.10	up	1.10	1.00E+00	3.181	up	3.181	1.42E-13	1.924	up	1.924	1.26E-04	2.097	up	2.097	1.01E-06
SAOHS_C01828		GAF domain-containing protein		0.74	0.98	0.70	0.66	▲	1.67	up	1.67	9.93E-02	1.972	up	1.972	1.46E-04	1.625	up	1.625	4.66E-01	1.579	up	1.579	5.80E-01
SAOHS_C01838		hypothetical protein		-0.29	2.46	1.24	0.61	▲	1.23	down	0.82	1.00E+00	5.495	up	5.495	9.42E-30	2.354	up	2.354	4.03E-11	1.528	up	1.528	1.05E-01
SAOHS_C01868		dipeptidase PepV		0.52	1.19	0.55	0.74	▲	1.43	up	1.43	1.00E+00	2.287	up	2.287	2.02E-02	1.460	up	1.460	1.00E+00	1.673	up	1.673	5.17E-04
SAOHS_C01877		hypothetical protein		-0.29	-1.11	n.d.	n.d.	▼	1.22	down	0.82	1.00E+00	2.160	down	0.463	3.55E-02								
SAOHS_C01878		hypothetical protein		0.39	0.96	0.95	0.63	▲	1.31	up	1.31	1.00E+00	1.940	up	1.940	1.22E-02	1.932	up	1.932	6.76E-02	1.551	up	1.551	4.53E-01
SAOHS_C01879	Rut	virulence factor regulator protein		-0.87	-1.49	-1.59	-0.92	▼	1.82	down	0.55	5.95E-01	2.805	down	0.357	2.36E-05	3.012	down	0.332	4.74E-02	1.886	down	0.530	1.34E-02
SAOHS_C01957		hypothetical protein		-0.29	0.13	1.12	0.89	▲	1.22	down	0.82	1.00E+00	1.096	up	1.096	1.00E+00	2.181	up	2.181	1.00E+00	1.844	up	1.844	8.71E-01
SAOHS_C01964	TRAP	hypothetical protein		0.89	0.90	0.71	0.78	▲	1.62	up	1.62	1.08E-02	1.867	up	1.867	4.01E-04	1.631	up	1.831	1.05E-01	1.723	up	1.723	2.34E-02
SAOHS_C01968	Hlt	hypothetical protein		0.74	0.81	1.13	1.46	▲	1.67	up	1.67	1.84E-01	1.758	up	1.758	2.67E-03	2.191	up	2.191	5.89E-07	2.742	up	2.742	3.69E-11
SAOHS_C01977		hypothetical protein		0.67	0.48	0.17	0.56	—	1.59	up	1.59	2.18E-02	1.391	up	1.391	1.00E+00	1.127	up	1.127	1.00E+00	1.470	up	1.470	8.11E-01
SAOHS_C01987		hypothetical protein		0.87	0.35	0.52	0.49	—	1.82	up	1.82	1.15E-07	1.272	up	1.272	1.00E+00	1.437	up	1.437	1.00E+00	1.408	up	1.408	1.00E+00
SAOHS_C01998		hypothetical protein		0.06	0.21	0.99	1.06	▲	1.04	up	1.04	1.00E+00	1.159	up	1.159	1.00E+00	1.984	up	1.984	3.59E-02	2.079	up	2.079	1.41E-01
SAOHS_C02013		hypothetical protein		1.17	-0.68	0.45	0.82	—	2.25	up	2.25	3.02E-08	1.606	down	0.622	1.07E-01	1.361	up	1.361	1.00E+00	1.760	up	1.760	3.23E-04
SAOHS_C02096		hypothetical protein		-0.24	1.33	n.d.	0.28	▲	1.18	down	0.85	1.00E+00	2.512	up	2.512	4.34E-02					1.214	up	1.214	1.00E+00
SAOHS_C02098	VraR	DNA-binding response regulator VraR		0.62	2.09	1.26	1.16	▲	1.53	up	1.53	6.39E-01	4.270	up	4.270	5.39E-25	2.387	up	2.387	1.02E-09	2.240	up	2.240	4.18E-10
SAOHS_C02099	VraS	histidine kinase		-0.45	1.54	1.08	0.89	▲	1.37	down	0.73	1.00E+00	2.900	up	2.900	1.53E-09	2.116	up	2.116	7.53E-05	1.614	up	1.614	2.10E-02
SAOHS_C02100	VraT	hypothetical protein		0.36	1.47	0.65	0.61	▲	1.20	up	1.20	1.00E+00	2.777	up	2.777	4.69E-05	1.570	up	1.570	8.29E-01	1.883	up	1.883	6.65E-01
SAOHS_C02150		hypothetical protein		0.95	1.19	1.54	1.83	▲	1.93	up	1.93	1.15E-07	2.286	up	2.286	3.79E-10	2.902	up	2.902	4.37E-09	3.548	up	3.548	2.83E-17
SAOHS_C02151	PntD	hypothetical protein		1.02	1.78	2.44	2.47	▲	2.02	up	2.02	5.37E-01	3.430	up	3.430	1.81E-03	6.185	up	6.185	2.36E-02	5.536	up	5.536	1.70E-03
SAOHS_C02152	PntC	ABC transporter ATP-binding protein		0.39	1.15	1.84	1.98	▲	1.31	up	1.31	1.00E+00	2.213	up	2.213	4.50E-14	3.578	up	3.578	2.89E-16	3.952	up	3.952	4.95E-23
SAOHS_C02155		hypothetical protein		0.51	1.80	n.d.	n.d.	▲	1.42	up	1.42	1.00E+00	3.480	up	3.480	4.25E-02								
SAOHS_C02235		repressor		0.12	0.80	0.64	0.55	▲	1.09	up	1.09	1.00E+00	1.740	up	1.740	3.32E-02	1.559	up	1.559	5.80E-01	1.465	up	1.465	1.00E+00
SAOHS_C02243	LuH	hypothetical protein		n.d.	4.08	3.46	2.62	▲					16.943	up	16.943	1.81E-03	10.978	up	10.978	1.27E-02	6.127	up	6.127	4.02E-02
SAOHS_C02259		hypothetical protein		0.27	0.84	0.04	0.76	▲	1.21	up	1.21	1.00E+00	1.791	up	1.791	1.46E-02	1.029	up	1.029	1.00E+00	1.688	up	1.688	4.16E-01
SAOHS_C02264	AprC	accessory gene regulator protein C		0.48	0.13	1.28	1.07	▲	1.40	up	1.40	1.00E+00	1.094	up	1.094	1.00E+00	2.437	up	2.437	1.30E-03	2.105	up	2.105	3.91E-03
SAOHS_C02265	AprA	accessory gene regulator protein A		0.28	1.13	2.20	2.21	▲	1.21	up	1.21	1.00E+00	2.181	up	2.181	4.23E-09	4.597	up	4.597	3.91E-10	4.625	up	4.625	1.82E-11
SAOHS_C02315	KdpE	DNA-binding response regulator		-0.06	-1.90	-0.06	0.25	—	1.04	down	0.96	1.00E+00	3.736	down	0.268	3.81E-05	1.041	down	0.960	1.00E+00	1.187	up	1.187	1.00E+00
SAOHS_C02364		hypothetical protein		0.16	1.10	n.d.	0.47	▲	1.12	up	1.12	1.00E+00	2.148	up	2.148	6.88E-03					1.384	up	1.384	1.00E+00
SAOHS_C02367		hypothetical protein		0.53	0.51	3.96	3.18	▲	1.44	up	1.44	1.00E+00	1.422	up	1.422	7.37E-01	2.084	up	2.084	9.68E-03	2.269	up	2.269	5.49E-04
SAOHS_C02372		hypothetical protein		0.06	-0.05	-1.49	-1.06	▼	1.04	up	1.04	1.00E+00	1.033	down	0.968	1.00E+00	2.804	down	0.357	9.92E-02	3.157	down	0.317	2.12E-02
SAOHS_C02382		hypothetical protein		-0.14	0.82	0.15	0.50	—	1.10	down	0.91	1.00E+00	1.771	up	1.771	2.44E-02	1.113	up	1.113	1.00E+00	1.417	up	1.417	1.00E+00
SAOHS_C02387		hypothetical protein		0.88	-0.45	0.42	0.73	—	1.84	up	1.84	3.67E-03	1.368	down	0.731	1.00E+00	1.338	up	1.338	1.00E+00	1.653	up	1.653	8.85E-01
SAOHS_C02425		hypothetical protein		0.79	2.12	3.78	4.30	▲	1.73	up	1.73	6.66E-01	6.166	up	6.166	2.15E-11	13.783	up	13.783	2.27E-07	17.120	up	17.120	1.82E-11
SAOHS_C02441	Atp23	alkaline shock protein 23		0.55																				

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio 8h p.i.	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 8,24 and 32h ratio; median tendence - 1.5K cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assays against non-ad. OD=0.4	p-value BH adjusted OD=0.4	median fold-change 8h p.i.	median fold-change (direction) 8h p.i.	median ratio over assays against non- ad. 8h p.i.	p-value BH adjusted 8h p.i.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against non- ad. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against non- ad. 32h p.i.	p-value BH adjusted 32h p.i.
SAOUHSC_02668		hypothetical protein		-0.48	-0.39	-1.15	-1.34	▼	1.39	down	0.72	1.00E+00	1.308	down	0.764	1.00E+00	2.221	down	0.450	6.39E-04	2.528	down	0.396	1.47E-06
SAOUHSC_02669	SarZ	hypothetical protein		-0.31	-0.79	0.91	0.94	▲	1.24	down	0.80	1.00E+00	1.731	up	1.731	6.10E-02	1.881	up	1.881	2.78E-01	1.916	up	1.916	1.03E-01
SAOUHSC_02690		hypothetical protein		-0.77	-0.87	0.01	-0.57	—	1.71	down	0.59	1.00E+00	1.825	down	0.548	4.98E-03	1.007	up	1.007	1.00E+00	1.481	down	0.675	1.00E+00
SAOUHSC_02700	MduA	hypothetical protein		-0.31	-1.42	-1.09	-1.23	▼	1.24	down	0.81	1.00E+00	2.667	down	0.375	2.27E-02	2.130	down	0.469	6.87E-01	2.339	down	0.428	4.58E-01
SAOUHSC_02724		hypothetical protein		0.59	2.46	2.08	2.89	▲	1.51	up	1.51	1.00E+00	5.508	up	5.508	1.03E-10	4.250	up	4.250	5.94E-11	4.085	up	4.085	1.07E-09
SAOUHSC_02747		hypothetical protein		0.46	1.22	0.59	0.79	▲	1.37	up	1.37	1.00E+00	2.332	up	2.332	3.64E-09	1.506	up	1.506	1.00E+00	1.733	up	1.733	4.77E-02
SAOUHSC_02759		hypothetical protein		-0.32	0.40	0.52	0.81	—	1.25	down	0.80	1.00E+00	1.317	up	1.317	1.00E+00	1.439	up	1.439	9.89E-01	1.751	up	1.751	2.67E-03
SAOUHSC_02774		hypothetical protein		1.52	-0.61	2.72	0.73	▲	2.86	up	2.86	2.797E-05	1.527	down	0.655	1.00E+00	6.604	up	6.604	4.80E-01	1.658	up	1.658	9.59E-02
SAOUHSC_02811	RelP	hypothetical protein		-0.28	1.10	-0.16	-0.06	—	1.22	down	0.82	1.00E+00	2.147	up	2.147	2.86E-09	1.118	down	0.894	1.00E+00	1.043	down	0.959	1.00E+00
SAOUHSC_02820		hypothetical protein		-0.56	-2.08	-0.99	-0.69	▼	1.47	down	0.68	1.00E+00	4.222	down	0.237	1.23E-07	1.992	down	0.502	8.74E-01	1.610	down	0.621	8.13E-01
SAOUHSC_02827		hypothetical protein		0.92	0.25	0.56	0.68	—	1.90	up	1.90	1.348E-02	1.188	up	1.188	1.00E+00	1.475	up	1.475	1.00E+00	1.597	up	1.597	7.76E-01
SAOUHSC_02829	Frp	NAD(P)H-flavin oxidoreductase		0.45	-0.04	1.41	1.65	▲	1.37	up	1.37	1.00E+00	1.028	down	0.973	1.00E+00	2.657	up	2.657	5.06E-07	3.141	up	3.141	2.10E-12
SAOUHSC_02844		hypothetical protein		0.15	0.66	0.91	0.90	▲	1.11	up	1.11	1.00E+00	1.576	up	1.576	5.03E-02	1.881	up	1.881	5.53E-05	1.868	up	1.868	3.47E-05
SAOUHSC_02846		hypothetical protein		0.22	1.38	0.67	0.53	▲	1.17	up	1.17	1.00E+00	2.598	up	2.598	1.40E-04	1.586	up	1.586	1.00E+00	1.446	up	1.446	1.00E+00
SAOUHSC_02862	CtpC	ATP-dependent Ctp protease, ATP-binding subunit CtpC		0.53	1.09	1.15	1.52	▲	1.44	up	1.44	1.00E+00	2.129	up	2.129	1.60E-11	2.225	up	2.225	5.38E-10	2.871	up	2.871	9.66E-23
SAOUHSC_02866		hypothetical protein		0.06	-2.10	n.d.	-0.86	▼	1.05	up	1.05	1.00E+00	4.290	down	0.233	7.59E-07					1.816	down	0.551	7.30E-02
SAOUHSC_02886		hypothetical protein		-0.20	-1.67	n.d.	n.d.	▼	1.15	down	0.87	1.00E+00	3.175	down	0.315	2.59E-04								
SAOUHSC_02887	IraK	Immunodominant antigen A		0.92	0.38	1.32	0.80	▲	1.90	up	1.90	3.320E-03	1.298	up	1.298	1.00E+00	2.490	up	2.490	2.02E-05	1.745	up	1.745	3.63E-03
SAOUHSC_02900		hypothetical protein		0.92	-0.30	0.71	0.92	▲	1.89	up	1.89	6.014E-09	1.234	down	0.810	1.00E+00	1.635	up	1.635	3.28E-01	1.896	up	1.896	9.54E-06
SAOUHSC_02910		hypothetical protein		0.25	1.12	0.87	0.68	▲	1.19	up	1.19	1.00E+00	2.166	up	2.166	2.24E-05	1.831	up	1.831	1.00E+00	1.607	up	1.607	9.89E-01
SAOUHSC_02972	IraB	Immunodominant antigen B		-0.56	2.44	3.68	3.95	▲	1.47	down	0.68	1.00E+00	5.421	up	5.421	4.25E-02	12.840	up	12.840	8.16E-02	14.908	up	14.908	2.12E-02
SAOUHSC_02978		phage infection protein		-0.26	-0.73	-1.03	-0.93	▼	1.20	down	0.84	1.00E+00	1.656	down	0.604	1.21E-01	2.044	down	0.489	2.03E-06	1.909	down	0.524	1.37E-06
SAOUHSC_02980		hypothetical protein		0.39	0.92	0.75	0.83	▲	1.31	up	1.31	1.00E+00	1.891	up	1.891	1.22E-04	1.677	up	1.677	5.50E-02	1.778	up	1.778	3.50E-04
SAOUHSC_03002		hypothetical protein		0.64	-0.49	0.61	0.92	▲	1.56	up	1.56	1.00E+00	1.612	down	0.620	1.00E+00	1.525	up	1.525	1.00E+00	1.895	up	1.895	2.20E-03
SAOUHSC_03024		hypothetical protein		0.32	-0.18	-1.06	-1.56	▼	1.25	up	1.25	1.00E+00	1.134	down	0.882	1.00E+00	2.079	down	0.481	2.10E-02	2.937	down	0.340	2.59E-01
SAOUHSC_03034		hypothetical protein		1.10	1.62	2.46	2.46	▲	2.15	up	2.15	7.437E-03	3.067	up	3.067	4.32E-07	5.453	up	5.453	1.58E-06	5.442	up	5.442	3.62E-09



supplemental table S5: significant regulated proteins in comparison of 8h p.i. and S9 infection with *S. aureus* (cell culture OD=0.4, non-ad., 24h p.i. and 32h p.i.)

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio; median tendence 1.5k cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assay against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change (direction) non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold change 24h p.i.	median fold change (direction) 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold change 32h p.i.	median fold change (direction) 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SA0UHC_00924	Opp-3C	hypothetical protein	ABC transporters	-0.90	-1.53	0.32	0.09	-	1.87	down	0.53	7.646E-02	2.89	down	0.35	5.480E-07	1.25	up	1.25	1.000E+00	1.07	up	1.07	1.000E+00
SA0UHC_02767	Opp-1A	peptide ABC transporter peptide-binding protein	ABC transporters;Motility and Chemotaxis - no subcategory	-2.09	-0.19	-0.16	0.04	-	4.24	down	0.24	1.400E-06	1.14	down	0.87	1.000E+00	1.12	down	0.89	1.000E+00	1.03	up	1.03	1.000E+00
SA0UHC_00920	Opp-5A	hypothetical protein	ABC transporters;Regulation and Cell signaling - no subcategory	-1.74	-1.62	n.d.	-1.22	▼	3.35	down	0.30	1.050E-09	3.08	down	0.32	4.030E-07				2.33	down	0.43	3.074E-01	
SA0UHC_00927	Opp-3A	oligopeptide ABC transporter substrate-binding protein	ABC transporters;Regulation and Cell signaling - no subcategory	0.08	-0.32	0.82	0.82	▲	1.06	up	1.06	1.000E+00	1.26	down	0.80	1.000E+00	1.76	up	1.76	5.349E-02	1.83	up	1.83	2.063E-04
SA0UHC_00909	Ssa	protein A	Adhesion	4.96	3.90	3.28	1.42	▲	31.15	up	31.15	2.540E-13	14.94	up	14.94	6.940E-13	2.60	up	2.60	4.987E-03	2.66	up	2.66	5.720E-09
SA0UHC_00544	SdC	sdC protein	Adhesion	-0.07	0.93	n.d.	n.d.	-	1.05	down	0.96	1.000E+00	1.90	up	1.90	4.674E-03								
SA0UHC_00812	Cla	clumping factor	Adhesion	1.09	0.58	0.43	0.80	▲	2.13	up	2.13	6.290E-17	1.49	up	1.49	5.871E-01	1.34	up	1.34	1.000E+00	1.74	up	1.74	1.300E-08
SA0UHC_02161	Eap1 Msp	MHC class II analog protein	Adhesion	n.d.	n.d.	0.95	-0.24	*									1.94	up	1.94	1.719E-04	1.18	down	0.85	1.000E+00
SA0UHC_02963	Cfb	clumping factor B	Adhesion	0.53	1.79	1.31	1.48	▼	1.44	up	1.44	1.000E+00	3.43	up	3.43	1.650E-26	2.51	down	0.40	9.470E-08	3.67	down	0.27	9.390E-06
SA0UHC_01633	GcvRk	glycine dehydrogenase subunit 1	Alanine, serine, and glycine	-0.82	-0.34	0.17	0.27	-	1.76	down	0.57	1.248E-02	1.27	down	0.79	1.000E+00	1.13	up	1.13	1.000E+00	1.21	up	1.21	1.000E+00
SA0UHC_01634	GcvT	glycine cleavage system aminomethyltransferase T	Alanine, serine, and glycine	0.90	-0.27	0.29	0.45	-	1.87	down	0.53	1.629E-04	1.21	down	0.83	1.000E+00	1.23	up	1.23	1.000E+00	1.37	up	1.37	1.000E+00
SA0UHC_01832		hypothetical protein	Alanine, serine, and glycine	-1.77	-0.52	-0.33	-0.15	-	3.40	down	0.29	6.820E-05	1.43	down	0.70	1.000E+00	1.25	down	0.80	1.000E+00	1.11	down	0.90	1.000E+00
SA0UHC_00536	IleE	branched-chain amino acid aminotransferase	Alanine, serine, and glycine;Branched chain amino acids;Central carbohydrate metabolism	-0.48	-1.27	-0.48	-0.36	*	1.39	down	0.72	1.000E+00	2.42	down	0.41	7.900E-22	1.39	down	0.72	1.000E+00	1.28	down	0.78	1.000E+00
SA0UHC_00308		hypothetical protein	Alanine, serine, and glycine;Central carbohydrate metabolism;Lipic acid;Plant-Prokaryote comparative genomics	-1.50	-1.50	-0.34	-0.16	-	2.82	down	0.35	9.990E-08	2.82	down	0.35	1.171E-03	1.27	down	0.79	1.000E+00	1.11	down	0.90	1.000E+00
SA0UHC_01662	GcvPB	glycine dehydrogenase subunit 2	Alanine, serine, and glycine;Lipic acid	-0.84	-0.36	0.25	0.42	-	1.79	down	0.56	1.407E-02	1.28	down	0.78	1.000E+00	1.19	up	1.19	1.000E+00	1.34	up	1.34	1.000E+00
SA0UHC_00535		hypothetical protein	Alanine, serine, and glycine;Lipic acid;threonine, methionine, and cysteine	-1.02	-0.78	0.64	0.81	▲	2.02	down	0.49	8.810E-05	1.72	down	0.58	1.626E-01	1.56	up	1.56	5.271E-01	1.75	up	1.75	2.090E-04
SA0UHC_01833	SerA	D-3-phosphoglycerate dehydrogenase	Alanine, serine, and glycine;Pyridoxine;Miscellaneous - no subcategory	-1.37	-1.22	0.61	0.37	*	2.59	down	0.39	4.370E-11	2.33	down	0.43	7.130E-09	1.53	up	1.53	4.613E-01	1.29	up	1.29	1.000E+00
SA0UHC_00552	NagB	hypothetical protein	Aminoglycoside;One-carbon Metabolism;Capsular and extracellular polysaccharides;Cell Wall and Capsule - no subcategory	-1.01	-1.43	-0.44	-0.64	*	2.01	down	0.50	6.300E-09	2.69	down	0.37	4.200E-11	1.36	down	0.74	1.000E+00	1.56	down	0.64	1.000E+00
SA0UHC_01046	PutA	ABC transporter	Arginine; urea cycle, polyamines	0.51	1.57	0.62	0.84	▲	1.42	up	1.42	1.000E+00	2.97	up	2.97	4.700E-10	1.54	up	1.54	5.207E-01	1.79	up	1.79	8.540E-05
SA0UHC_01049	PutD	spemidine/putrescine ABC transporter spemidine/putrescine-binding protein	Arginine; urea cycle, polyamines	0.65	1.74	n.d.	0.98	▲	1.57	up	1.57	1.000E+00	3.34	up	3.34	1.800E-05				1.97	up	1.97	1.000E+00	
SA0UHC_00076	Shb	ornithine cyclodeaminase	Arginine; urea cycle, polyamines;Lipine, threonine, methionine, and cysteine;Proline and 4-hydroxyproline;Siderophores	-5.29	-2.02	0.35	0.07	*	39.08	down	0.03	2.891E-01	4.05	down	0.25	2.510E-09	1.27	up	1.27	1.000E+00	1.05	up	1.05	1.000E+00
SA0UHC_00894	RodD	ornithine-oxo acid transaminase	Arginine; urea cycle, polyamines;Proline and 4-hydroxyproline	-1.07	-1.59	0.96	1.24	▲	2.10	down	0.48	2.900E-21	3.00	down	0.33	1.510E-23	1.95	up	1.95	6.200E-14	2.36	up	2.36	4.050E-34
SA0UHC_02869	RocA	1-pyrroline-5-carboxylate dehydrogenase	Arginine; urea cycle, polyamines;Proline and 4-hydroxyproline	-3.43	-3.89	1.25	1.50	▲	10.79	down	0.09	2.390E-18	14.79	down	0.07	1.390E-12	2.39	up	2.39	3.930E-41	2.83	up	2.83	3.670E-57
SA0UHC_02409	RocC	arginase	Arginine; urea cycle, polyamines;Proline and 4-hydroxyproline;Plant-Prokaryote comparative genomics	-1.06	-0.89	1.03	0.95	▲	2.09	down	0.48	1.679E-03	1.85	down	0.54	9.251E-02	2.04	up	2.04	7.160E-03	1.94	up	1.94	7.060E-08
SA0UHC_00733	HicC	histidinol-phosphate aminotransferase	Aromatic amino acids and derivatives	-1.01	-1.41	0.22	0.22	-	2.02	down	0.50	5.888E-04	2.65	down	0.38	3.052E-03	1.07	up	1.17	1.000E+00	1.17	up	1.17	1.000E+00
SA0UHC_02343	AtpG	RF1 ATP synthase subunit gamma	ATP synthases	-0.67	-0.17	-0.54	-0.42	-	1.59	down	0.63	4.381E-02	1.12	down	0.89	1.000E+00	1.46	down	0.69	1.000E+00	1.33	down	0.75	1.000E+00
SA0UHC_00144	AuxA	hypothetical protein	Biotin	-2.64	-1.85	0.34	0.38	-	6.25	down	0.16	2.980E-12	3.60	down	0.28	3.200E-18	1.26	up	1.26	1.000E+00	1.30	up	1.30	1.000E+00
SA0UHC_02713	BioF	hypothetical protein	Biotin	-0.09	-1.32	-1.46	-1.16	▼	1.07	down	0.94	1.000E+00	2.49	down	0.40	3.040E-07	2.76	down	0.36	6.720E-02	2.23	down	0.45	1.880E-03
SA0UHC_02714	BioB	biotin synthase	Biotin	0.83	-0.57	3.36	2.56	▼	1.78	up	1.78	1.900E-06	1.49	down	0.67	1.000E+00	7.25	down	0.14	1.680E-05	7.74	down	0.13	9.390E-06
SA0UHC_02715	BioA	adenosylmethionine-8-amin-7-oxononanoate aminotransferase	Biotin	0.08	-0.89	-0.38	-0.43	*	1.06	up	1.06	1.000E+00	1.85	down	0.54	6.609E-03	1.31	down	0.77	1.000E+00	1.55	down	0.65	1.000E+00
SA0UHC_02716	BioD	dethiobiotin synthase	Biotin	0.51	-0.72	-0.94	-1.10	▼	1.42	up	1.42	1.000E+00	1.65	down	0.61	9.487E-01	1.79	down	0.56	1.053E-03	2.15	down	0.47	1.200E-11
SA0UHC_02394	IleC	ketol acid reductoisomerase	Branched-chain amino acids;Coenzyme A	-0.77	-1.18	0.88	0.82	▲	1.71	down	0.58	7.483E-01	2.27	down	0.44	8.960E-04	1.83	up	1.83	5.350E-05	1.83	up	1.83	2.040E-07
SA0UHC_02282	IleB	acetylactate synthase large subunit	Branched-chain amino acids;Fermentation	-1.61	-2.05	0.34	0.56	-	3.05	down	0.33	3.480E-05	5.11	down	0.20	1.179E-02	1.26	up	1.26	1.000E+00	1.47	up	1.47	1.000E+00
SA0UHC_00196	IleH	hypothetical protein	Branched-chain amino acids;Fermentation;Fatty Acids, Lipids, and isoprenoids - no subcategory	n.d.	n.d.	1.71	2.03	▲									3.31	up	3.31	2.590E-63	4.08	up	4.08	5.900E-90
SA0UHC_00336	Thi	acetyl CoA acetyltransferase	Branched-chain amino acids;Fermentation;One-carbon Metabolism;Biotin;Fatty Acids, Lipids, and isoprenoids - no subcategory;Isoprenoids	-1.00	-0.81	-1.01	-1.00	▼	1.99	down	0.50	7.540E-17	1.76	down	0.57	2.035E-01	2.01	down	0.50	1.180E-09	1.99	down	0.50	1.430E-11
SA0UHC_00195	FadA	acetyl CoA acetyltransferase	Branched-chain amino acids;One-carbon Metabolism;Biotin;Fatty Acids, Lipids, and isoprenoids - no subcategory	n.d.	n.d.	1.81	1.72	▲									3.06	up	3.06	1.720E-12	3.30	up	3.30	4.790E-20
SA0UHC_00158		PTS system protein	Capsular and extracellular polysaccharides	n.d.	n.d.	1.45	1.89	▲									2.73	up	2.73	1.300E-08	3.49	up	3.49	6.900E-13
SA0UHC_01204	Snc	SMC domain-containing protein	Cell Division and Cell Cycle - no subcategory	0.01	0.68	-0.08	0.10	-	1.01	up	1.01	1.000E+00	1.58	up	1.58	1.960E-04	1.06	down	0.95	1.000E+00	1.07	up	1.07	1.000E+00
SA0UHC_01827	EvaK	septation ring formation regulator EvaK	Cell Division and Cell Cycle - no subcategory	0.43	0.63	0.47	0.80	-	1.34	up	1.34	1.000E+00	1.54	up	1.54	1.560E-02	1.38	up	1.38	1.000E+00	1.51	up	1.51	1.589E-01
SA0UHC_01652	Phb3	penicillin-binding protein 3	Cell Division and Cell Cycle - no subcategory;Cell Wall and Capsule - no subcategory	-0.26	-0.00	-0.68	-0.77	▼	1.20	down	0.83	1.000E+00	1.00	down	1.00	1.000E+00	1.60	down	0.62	6.517E-01	1.70	down	0.59	4.007E-03
SA0UHC_00912	SgB	glycosyltransferase	Cell Wall and Capsule - no subcategory	-2.69	-2.06	0.63	-1.00	▼	5.61	down	0.18	1.430E-14	4.17	down	0.24	9.520E-18	1.55	down	0.64	1.000E+00	2.01	down	0.50	5.110E-08
SA0UHC_02365	MurG2	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell Wall and Capsule - no subcategory	-1.33	-1.27	-0.93	-0.81	▼	2.52	down	0.40	3.460E-20	2.40	down	0.42	2.580E-12	1.90	down	0.53	2.514E-03	1.75	down	0.57	5.320E-07
SA0UHC_00994	Ati	bifunctional autolysin	Cell Wall and Capsule - no subcategory;Quorum sensing and biofilm formation;Regulation and Cell signaling - no subcategory;Adhesion	1.98	1.21	-0.51	-0.96	▼	3.88	up	3.88	2.590E-96	2.44	up	2.44	3.840E-61	1.42	down	0.70	1.000E+00	1.94	down	0.51	9.970E-06
SA0UHC_00153		indolepyruvate decarboxylase	Central carbohydrate metabolism	0.81	0.46	1.13	1.38	▲	1.76	up	1.76	1.120E-01	1.38	up	1.38	9.618E-01	2.18	up	2.18	3.840E-09	2.60	up	2.60	1.250E-15
SA0UHC_00655		dihydroxyacetone kinase subunit Dhak	Central carbohydrate metabolism	-2.02	-2.80	0.95	1.46	▲	4.06	down	0.25	6.170E-07	7.47	down	0.13	5.370E-08	1.93	up	1.93	1.469E-04	2.75	up	2.75	5.700E-10
SA0UHC_00656		hypothetical protein	Central carbohydrate metabolism	-1.10	-1.94	1.21	1.21	▲	2.14	down	0.47	9.488E-01	3.58	down	0.28	9.458E-01	2.32	up	2.32	1.680E-05	2.31	up	2.31	8.250E-12
SA0UHC_00658		phosphotransferase mannosase-specific family component IIA	Central carbohydrate metabolism	n.d.	-1.86	0.38	0.98	▲					3.62	down	0.28	5.235E-01	1.30	up	1.30	1.000E+00	1.97	up	1.97	5.722E-04
SA0UHC_00797	TgiA	triosephosphate isomerase	Central carbohydrate metabolism	0.86	-0.05	-0.44	-0.41	-	1.58	up	1.58	9.470E-01	1.04	down	0.97	1.000E+00	1.36	down	0.74	1.000E+00	1.32	down	0.75	

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio: median tendence - 1.5% cutoff	median fold- change [direction] OD=0.4	median fold- change [direction] OD=0.4	median ratio over assays against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change [direction] non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold-change 24h p.i.	median fold-change [direction] 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change [direction] 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SAOUHSC_01820	ActA	acetate kinase	Central carbohydrate metabolism;Fermentation	0.09	0.60	-0.17	-0.03	-	1.07	up	1.07	1.00E+00	1.51	up	1.51	3.114E-02	1.12	down	0.89	1.00E+00	1.02	down	0.98	1.00E+00
SAOUHSC_01416	SucB	dihydrolipoamide succinyltransferase	Central carbohydrate metabolism;Lipoic acid	-1.09	-0.44	0.94	1.20	▲	2.13	down	0.47	1.13E-08	1.56	down	0.64	1.13E+00	1.92	up	1.92	5.830E-10	2.30	up	2.30	5.420E-19
SAOUHSC_01807	PhaA	6-phosphofructokinase	Central carbohydrate metabolism;Monosaccharides	-0.37	-0.59	-0.67	-0.74	▼	1.29	down	0.78	1.00E+00	1.51	down	0.66	1.00E+00	1.60	down	0.63	2.397E-02	1.67	down	0.60	1.379E-02
SAOUHSC_00900	Pgi	glucose 6-phosphate isomerase	Central carbohydrate metabolism;One-carbon Metabolism	-0.85	-0.80	-0.78	-0.72	▼	1.81	down	0.55	1.867E-04	1.74	down	0.58	3.871E-01	1.71	down	0.58	9.680E-05	1.64	down	0.61	8.378E-02
SAOUHSC_01216	SucC	succinyl-CoA synthetase subunit beta	Central carbohydrate metabolism;One-carbon Metabolism	-0.20	-0.13	0.84	0.98	▲	1.14	down	0.87	1.00E+00	1.10	down	0.91	1.00E+00	1.79	up	1.79	2.020E-09	1.97	up	1.97	8.540E-28
SAOUHSC_01218	SucD	succinyl-CoA synthetase subunit alpha	Central carbohydrate metabolism;One-carbon Metabolism	-0.13	-0.20	0.76	1.11	▲	1.09	down	0.91	1.00E+00	1.15	down	0.87	1.00E+00	1.69	up	1.69	1.090E-05	2.16	up	2.16	6.370E-18
SAOUHSC_01910	PckA	phosphoenolpyruvate carboxylase	Central carbohydrate metabolism;One-carbon Metabolism	-2.10	-2.45	1.37	1.72	▲	4.28	down	0.23	2.140E-05	5.47	down	0.18	7.070E-07	2.59	up	2.59	7.840E-20	3.29	up	3.29	1.170E-32
SAOUHSC_01104	SdhA	succinate dehydrogenase flavoprotein subunit	Central carbohydrate metabolism;One-carbon Metabolism;Electron donating reactions	0.13	-0.10	0.97	1.24	▲	1.10	up	1.10	1.00E+00	1.07	down	0.94	1.00E+00	1.96	up	1.96	6.200E-14	2.36	up	2.36	4.630E-25
SAOUHSC_01105	SdhB	succinate dehydrogenase iron-sulfur subunit	Central carbohydrate metabolism;One-carbon Metabolism;Electron donating reactions	0.37	0.34	0.72	0.94	▲	1.29	up	1.29	1.00E+00	1.27	up	1.27	1.00E+00	1.64	up	1.64	5.080E-03	1.92	up	1.92	1.760E-12
SAOUHSC_01347	CisB	aconitate hydratase	Central carbohydrate metabolism;One-carbon Metabolism;Respiration - no subcategory	1.16	0.11	0.64	0.97	▲	2.24	up	2.24	5.930E-60	1.24	up	1.24	1.00E+00	1.56	up	1.56	3.913E-02	1.96	up	1.96	1.260E-53
SAOUHSC_02577		D isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein	Central carbohydrate metabolism;Organic acids	-0.78	-1.12	0.92	1.60	▲	1.72	down	0.58	1.338E-01	2.18	down	0.46	1.690E-15	1.89	up	1.89	1.060E-17	2.01	up	2.01	2.580E-27
SAOUHSC_01794	GapB	glyceraldehyde 3-phosphate dehydrogenase 2	Central carbohydrate metabolism;Oxidative stress	-1.27	-0.75	-0.38	0.71	-	2.40	down	0.42	9.741E-04	1.68	down	0.60	5.139E-01	1.30	down	0.77	1.00E+00	1.63	up	1.63	5.467E-01
SAOUHSC_00112	AlaA	aldehyde dehydrogenase	Central carbohydrate metabolism;Phospholipids	-1.51	n.d.	1.14	1.42	▲	2.89	down	0.35	4.280E-02					2.20	up	2.20	2.580E-07	2.68	up	2.68	1.450E-12
SAOUHSC_02142	AlaH	aldehyde dehydrogenase	Central carbohydrate metabolism;Phospholipids	-0.64	-0.67	0.52	0.71	▲	1.55	down	0.64	1.00E+00	1.59	down	0.63	1.00E+00	1.43	up	1.43	1.00E+00	1.64	up	1.64	9.920E-07
SAOUHSC_02363		aldehyde dehydrogenase	Central carbohydrate metabolism;Phospholipids	-0.82	-0.01	0.60	0.72	▲	1.77	up	1.77	5.030E-08	1.01	down	0.99	1.00E+00	1.52	up	1.52	2.349E-01	1.65	up	1.65	3.800E-07
SAOUHSC_01038	Def	peptide deformylase	Central carbohydrate metabolism;Plant;Prokaryote comparative genomics;Protein biosynthesis	0.77	0.04	-0.28	-0.07	-	1.70	up	1.70	6.378E-04	1.03	up	1.03	1.00E+00	1.21	down	0.82	1.00E+00	1.05	down	0.95	1.00E+00
SAOUHSC_02849	CdcC	pyruvate oxidase	Central carbohydrate metabolism;Programmed Cell Death and Toxin-antitoxin Systems	1.18	1.07	0.51	0.71	▲	2.26	up	2.26	8.420E-25	2.09	up	2.09	1.110E-16	1.44	up	1.44	1.00E+00	1.64	up	1.64	4.533E-04
SAOUHSC_00879	AmpA	cytosol aminopeptidase	Central carbohydrate metabolism;Protein degradation	-0.97	0.34	0.58	0.71	▲	1.95	down	0.51	4.429E-01	1.26	up	1.26	1.00E+00	1.51	up	1.51	1.00E+00	1.64	up	1.64	1.870E-01
SAOUHSC_02918	PanC	pantoate-beta-alanine ligase	Coenzyme A	-0.01	0.42	-0.89	-0.92	▼	1.00	down	1.00	1.00E+00	1.34	up	1.34	1.00E+00	1.86	down			1.89	down	0.53	3.056E-03
SAOUHSC_02919	PanB	3-methyl-2-oxobutanate hydroxymethyltransferase	Coenzyme A;Folate and pterines	-0.50	-0.27	-0.81	-0.94	▼	1.41	down	0.71	1.00E+00	1.21	down	0.83	1.00E+00	1.76	down	0.57	2.670E-03	1.92	down	0.52	5.792E-04
SAOUHSC_02329	ThiM	hydroxyethylthiazole kinase	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	-3.09	-2.92	-0.29	-0.21	-	4.25	down	0.24	9.310E-06	6.58	down	0.15	2.030E-07	1.22	down	0.82	1.00E+00	1.16	down	0.86	1.00E+00
SAOUHSC_02330	ThiO2	phosphomethylpyrimidine kinase	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	-1.75	-1.40	-0.03	-0.11	-	3.37	down	0.30	1.690E-03	2.65	down	0.38	3.624E-03	1.02	down	0.98	1.00E+00	1.08	down	0.93	1.00E+00
SAOUHSC_02331	ThiA	hypothetical protein	Cofactors, Vitamins, Prosthetic Groups, Pigments - no subcategory	-1.79	-2.11	-0.27	-0.06	-	3.46	down	0.29	1.830E-05	4.36	down	0.23	2.430E-02	1.21	down	0.83	1.00E+00	1.04	down	0.96	1.00E+00
SAOUHSC_00819	CspC	hypothetical protein	Cold shock	-0.73	-0.05	-1.32	-1.41	▼	1.65	down	0.60	5.407E-01	1.04	down	0.97	1.00E+00	2.49	down	0.40	3.800E-09	2.65	down	0.38	1.040E-14
SAOUHSC_03045	CspB	cold shock protein	Cold shock	-0.19	0.20	-2.05	-2.19	▼	1.14	down	0.88	1.00E+00	1.15	up	1.15	1.00E+00	4.15	down	0.24	2.971E-03	4.57	down	0.22	3.000E-05
SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA	Di- and oligosaccharides	-1.74	-2.32	-0.82	-0.87	▼	3.35	down	0.30	6.770E-21	4.58	down	0.20	5.590E-22	1.77	down	0.57	3.626E-03	1.82	down	0.55	5.040E-05
SAOUHSC_00462	HsdR	HsdR family type I site-specific deoxyribonuclease	DNA Metabolism - no subcategory	0.23	0.75	n.d.	0.51	-	1.17	up	1.17	1.00E+00	1.68	up	1.68	1.554E-02					1.42	up	1.42	1.00E+00
SAOUHSC_02049	Sib	bacteriophage L54g, single-stranded DNA binding protein	DNA repair	0.62	0.87	-0.02	0.34	-	1.53	up	1.53	3.012E-01	1.83	up	1.83	2.599E-04	1.01	down	0.99	1.00E+00	1.26	up	1.26	1.00E+00
SAOUHSC_01768	Tag	hypothetical protein	DNA repair	-0.27	-0.29	-0.99	-0.42	▼	1.21	up	1.21	1.00E+00	2.22	down	0.82	1.00E+00	1.99	down	0.50	3.633E-02	1.34	down	0.75	1.00E+00
SAOUHSC_01241	PoiC	DNA polymerase III PoiC	DNA replication	-0.40	0.01	-0.69	-0.80	▼	1.32	down	0.76	1.00E+00	1.01	down	1.01	1.00E+00	1.61	down	0.62	5.703E-01	1.74	down	0.57	1.450E-02
SAOUHSC_01351	ParE	DNA topoisomerase IV subunit B	DNA replication;Resistance to antibiotics and toxic compounds	0.34	0.74	-0.16	-0.11	-	1.27	up	1.27	1.00E+00	1.67	up	1.67	3.100E-07	1.12	down	0.90	1.00E+00	1.08	down	0.92	1.00E+00
SAOUHSC_00935	TrfA	adaptor protein	DNA uptake, competence	1.38	1.00	n.d.	n.d.	-	2.60	up	2.60	5.640E-11	2.00	down	2.00	5.070E-06								
SAOUHSC_02517	TspB	DNA topoisomerase II	DNA uptake, competence	0.83	1.04	0.36	-0.26	-	1.78	up	1.78	6.270E-08	2.06	up	2.06	1.550E-12	1.29	down	0.78	1.00E+00	1.20	down	0.84	1.00E+00
SAOUHSC_00469	SpoVG	regulatory protein SpoVG	Dormancy and Sporulation - no subcategory	1.02	0.80	0.21	0.83	-	2.03	up	2.03	1.950E-05	1.74	up	1.74	1.340E-05	1.15	up	1.15	1.00E+00	1.78	up	1.78	6.970E-05
SAOUHSC_01031	CydA	cytochrome d ubiquinol oxidase subunit I	Electron accepting reactions	-2.84	-0.88	-0.49	-0.65	-	7.15	down	0.14	9.370E-09	1.84	down	0.54	3.556E-02	1.40	down	0.71	1.00E+00	1.57	down	0.64	1.00E+00
SAOUHSC_01032	CydB	cytochrome d ubiquinol oxidase subunit II	Electron accepting reactions	-2.72	-1.23	-0.39	-0.68	-	6.57	down	0.15	7.290E-07	2.34	down	0.43	3.340E-06	1.31	down	0.76	1.00E+00	1.60	down	0.63	2.947E-01
SAOUHSC_00835		hypothetical protein	Electron accepting reactions;Resistance to antibiotics and toxic compounds	-0.80	-1.41	-0.42	-0.16	-	1.74	down	0.58	1.880E-03	2.66	down	0.38	1.540E-08	1.34	down	0.75	1.00E+00	1.12	down	0.90	1.00E+00
SAOUHSC_02873	CopA	cation transporter E1-E2 family ATPase	Electron accepting reactions;Resistance to antibiotics and toxic compounds	-1.52	-1.42	-0.37	-0.33	-	2.87	down	0.35	3.00E-14	2.68	down	0.37	1.720E-11	1.30	down	0.77	1.00E+00	1.26	down	0.80	1.00E+00
SAOUHSC_00875		hypothetical protein	Electron donating reactions	-0.68	0.44	0.33	0.52	-	1.60	up	1.60	5.811E-04	1.36	up	1.36	1.00E+00	1.26	up	1.26	1.00E+00	1.43	up	1.43	1.00E+00
SAOUHSC_00920	FadH	3-oxoacyl (acyl carrier protein) synthase III	Fatty acids	-0.57	0.86	-0.12	0.30	-	1.49	down	0.67	1.00E+00	1.81	up	1.81	2.470E-09	1.09	down	0.92	1.00E+00	1.07	up	1.07	1.00E+00
SAOUHSC_01624	AccB	acetyl-CoA carboxylase, biotin carboxyl carrier protein	Fatty acids;Miscellaneous - no subcategory	-0.11	0.17	0.84	0.55	▼	1.08	down	0.93	1.00E+00	1.13	up	1.13	1.00E+00	1.80	down	0.56	1.453E-03	1.47	down	0.68	1.00E+00
SAOUHSC_00086	BucA	acetoin reductase	Fermentation	-1.45	-2.29	-0.91	-1.16	▲	2.73	down	0.37	2.890E-12	4.90	down	0.20	1.710E-15	1.90	up	1.90	1.760E-07	2.24	up	2.24	7.200E-20
SAOUHSC_00206	LdhI	L-lactate dehydrogenase	Fermentation	-0.92	0.25	-1.68	-2.37	▼	1.90	down	0.53	1.010E-07	1.19	up	1.19	1.00E+00	3.20	down	0.31	2.960E-12	4.82	down	0.21	4.883E-04
SAOUHSC_00608	AldH	alcohol dehydrogenase	Fermentation;Phospholipids	-2.04	-0.89	-1.68	-1.99	▼	4.11	down	0.24	3.95E-11	1.86	down	0.54	1.389E-03	3.20	down	0.31	3.633E-02	3.70	down	0.27	3.074E-01
SAOUHSC_00187	PFB	formate acetyltransferase	Fermentation;Respiration - no subcategory	-4.83	-2.97	-0.89	-1.29	▼	21.59	down	0.05	2.237E-02	4.20	down	0.24	2.690E-17	1.86	down	0.54	2.315E-02	2.45	down	0.41	1.050E-09
SAOUHSC_02549	ModA	molybdenum ABC transporter periplasmic molybdate-binding protein	Folate and pterines	0.13	0.40	0.58	0.78	▲	1.09	up	1.09	1.00E+00	1.32	up	1.32	1.00E+00	1.50	up	1.49	1.00E+00	1.71	up	1.71	1.901E-03
SAOUHSC_01435	ThyA	thymidylate synthase	Folate and pterines;Pyrimidines	0.89	0.24	0.10	0.10	-	1.85	up	1.85	4.556E-02	1.18	up	1.18	1.00E+00	1.07	up	1.07	1.00E+00	1.07	up	1.07	1.00E+00
SAOUHSC_00878	RbaA	riboflavin biosynthesis protein	Folate and pterines;Riboflavin, FMN, FAD	0.78	0.14	-0.12	-0.12	-	1.71	up	1.71	3.980E-02	1.10	up	1.10	1.00E+00	1.08	down	0.92	1.00E+00	1.09	down	0.92	1.00E+00
SAOUHSC_00549	PoiE2	putative GTP cyclohydrolase	Folate and pterines;DNA processing and modification	0.82	0.27	-0.18	0.25	-	1.77	up	1.77	0.002E-04												

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio: median tendency -1.5% cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assays against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change (direction) non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SAOUSHC_00130	IsdI	heme-degrading monooxygenase IsdI	Iron acquisition and metabolism - no subcategory	-1.54	-1.46	0.67	0.99	▲	2.91	down	0.34	4.110E-05	2.78	down	0.36	2.460E-07	1.59	up	1.59	6.923E-01	1.99	up	1.99	6.530E-40
SAOUSHC_00749	SidD	hypothetical protein	Iron acquisition and metabolism - no subcategory	-1.95	0.27	-0.88	-0.96	▼	3.87	down	0.26	6.65E-14	1.20	down	1.20	1.000E+00	1.84	down	0.54	2.052E-02	1.98	down	0.51	7.760E-06
SAOUSHC_02434		hypothetical protein	Iron acquisition and metabolism - no subcategory	-2.52	-1.57	-0.03	-0.37	-	4.98	down	0.20	2.070E-09	2.96	down	0.34	2.400E-09	1.02	down	0.98	1.000E+00	1.29	down	0.77	1.000E+00
SAOUSHC_02436		hypothetical protein	Iron acquisition and metabolism - no subcategory	-1.48	-1.02	-0.30	-0.45	-	2.79	down	0.36	5.160E-15	2.03	down	0.49	1.830E-07	1.23	down	0.81	1.000E+00	1.37	down	0.73	1.000E+00
SAOUSHC_02430	HfuA	ABC transporter periplasmic binding protein	Iron acquisition and metabolism - no subcategory;Stress Response - no subcategory	-1.81	0.05	0.15	0.28	-	3.52	down	0.28	2.030E-10	1.04	up	1.04	1.000E+00	1.11	up	1.11	1.000E+00	1.21	up	1.21	1.000E+00
SAOUSHC_02860	MhuS	HMG CoA synthase	Iso prenoids	0.71	-1.06	-0.66	-0.62	▼	1.64	down	0.61	6.893E-02	2.09	down	0.48	1.091E-04	1.58	down	0.63	1.000E+00	1.54	down	0.65	1.000E+00
SAOUSHC_02877	CrtN	squalene synthase	Iso prenoids	1.29	1.34	n.d.	0.87	▲	2.45	up	2.45	9.940E-05	2.54	up	2.54	1.226E-03					1.83	down	1.83	2.589E-01
SAOUSHC_00861	LipA	lipoyl synthase	Lipoic acid	0.64	1.42	-1.04	-1.07	▼	1.56	up	1.56	2.729E-01	2.67	up	2.67	5.790E-15	2.05	down	0.49	3.867E-04	2.10	down	0.48	5.700E-08
SAOUSHC_00842	MetN1	ABC transporter ATP-binding protein	Lysine, threonine, methionine, and cysteine	0.29	-0.20	0.83	0.99	▲	1.22	up	1.22	1.000E+00	1.15	down	0.87	1.000E+00	1.78	up	1.78	4.002E-04	1.99	up	1.99	1.533E-04
SAOUSHC_00989		hypothetical protein	Lysine, threonine, methionine, and cysteine	0.88	-0.39	0.20	-0.16	-	1.85	down	0.54	5.986E-04	1.31	down	0.76	1.000E+00	1.15	up	1.15	1.000E+00	1.12	down	0.89	1.000E+00
SAOUSHC_01395	Aud	aspartate semialdehyde dehydrogenase	Lysine, threonine, methionine, and cysteine	-2.67	-1.31	0.15	0.25	-	6.35	down	0.16	7.860E-18	9.92	down	0.10	7.550E-21	1.11	up	1.11	1.000E+00	1.19	up	1.19	1.000E+00
SAOUSHC_01396	DapA	dihydrodipicolinate synthase	Lysine, threonine, methionine, and cysteine	-1.11	-1.02	-0.05	0.18	-	8.61	down	0.12	6.580E-14	16.23	down	0.06	2.270E-09	1.04	down	0.96	1.000E+00	1.13	up	1.13	1.000E+00
SAOUSHC_01398	DapD	2,3,4,5-tetrahydroxyline-2-carboxylate N-succinyltransferase	Lysine, threonine, methionine, and cysteine	-2.89	-1.97	-0.02	0.14	-	7.39	down	0.14	2.370E-12	15.65	down	0.06	1.990E-10	1.02	down	0.98	1.000E+00	1.11	up	1.11	1.000E+00
SAOUSHC_01399		hypothetical protein	Lysine, threonine, methionine, and cysteine	-2.15	-2.90	0.04	0.16	-	4.42	down	0.23	4.750E-16	6.06	down	0.16	3.680E-14	1.03	up	1.03	1.000E+00	1.12	up	1.12	1.000E+00
SAOUSHC_01400	AroJ	alanine racemase	Lysine, threonine, methionine, and cysteine	-2.06	-0.49	-0.40	-0.52	▼	4.10	down	0.24	4.280E-02	1.41	down	0.71	1.000E+00	1.51	down	0.66	1.000E+00	1.43	down	0.70	1.000E+00
SAOUSHC_01401	LysA	diaminopimelate decarboxylase	Lysine, threonine, methionine, and cysteine	-0.53	-1.45	-0.32	-0.25	-	1.44	down	0.69	1.000E+00	2.73	down	0.37	1.970E-12	1.25	down	0.80	1.000E+00	1.19	down	0.84	1.000E+00
SAOUSHC_00426	MerG2	ABC transporter substrate-binding protein	Lysine, threonine, methionine, and cysteine;Pathogenicity islands	0.10	-0.02	1.21	1.25	▲	1.08	up	1.08	1.000E+00	1.01	down	0.99	1.000E+00	2.31	up	2.31	7.810E-06	2.31	up	2.31	7.800E-06
SAOUSHC_00844	MerG1	hypothetical protein	Lysine, threonine, methionine, and cysteine;Pathogenicity islands	0.49	-0.03	0.72	0.84	▲	1.41	up	1.41	1.000E+00	1.02	down	0.98	1.000E+00	1.65	up	1.65	1.940E-02	1.79	up	1.79	4.320E-06
SAOUSHC_01828		GAF domain-containing protein	Miscellaneous - no subcategory	0.19	-0.98	-0.46	-0.50	-	1.14	down	0.88	1.000E+00	1.97	down	0.51	1.795E-02	1.37	down	0.73	1.000E+00	1.42	down	0.71	1.000E+00
SAOUSHC_02425		hypothetical protein	Miscellaneous - no subcategory	-2.03	-2.62	1.06	1.44	▲	4.08	down	0.25	3.710E-09	6.15	down	0.16	2.460E-11	2.08	up	2.08	1.851E-04	2.71	up	2.71	5.630E-09
SAOUSHC_02447		hypothetical protein	Miscellaneous - no subcategory	0.71	-0.26	1.12	1.47	▲	1.64	up	1.64	4.330E-02	1.20	down	0.84	1.000E+00	2.18	up	2.18	8.590E-11	2.77	up	2.77	1.120E-19
SAOUSHC_02754		ABC transporter ATP-binding protein	Miscellaneous - no subcategory	0.83	1.45	n.d.	n.d.	-	1.91	up	1.91	4.581E-02	2.74	up	2.74	5.711E-02								
SAOUSHC_01018	PurD	phosphoribosylamine-glycine ligase	Miscellaneous - no subcategory;Purines	-0.27	-0.03	-1.37	-1.30	▼	1.21	down	0.83	1.000E+00	1.02	down	0.98	1.000E+00	2.58	down	0.39	1.590E-15	2.14	down	0.47	6.070E-30
SAOUSHC_00721	QueC	Miscellaneous - no subcategory;RNA processing and modification	Miscellaneous - no subcategory;RNA processing and modification	1.97	1.23	0.96	1.13	▲	3.92	up	3.92	5.220E-08	2.34	up	2.34	4.412E-04	1.94	up	1.94	1.515E-02	2.19	up	2.19	2.597E-04
SAOUSHC_00364	AhpF	alkyl hydroperoxide reductase subunit F	Miscellaneous - no subcategory;Sulfur Metabolism - no subcategory	0.96	-0.16	0.68	0.86	▲	1.95	up	1.95	8.170E-27	1.12	down	0.90	1.000E+00	1.60	up	1.60	2.514E-03	1.82	up	1.82	2.100E-30
SAOUSHC_00365	AhpC	alkyl hydroperoxide reductase subunit C	Miscellaneous - no subcategory;Sulfur Metabolism - no subcategory	1.02	0.07	1.08	1.17	▲	2.03	up	2.03	4.470E-17	1.05	up	1.05	1.000E+00	2.11	up	2.11	9.270E-17	2.42	up	2.42	1.070E-30
SAOUSHC_00239	RbuK	ribulase	Monosaccharides	0.36	-1.03	-0.76	-2.54	▲	1.28	down	0.78	1.000E+00	2.04	down	0.49	1.000E+00	1.69	down	0.59	1.000E+00	5.70	up	5.70	8.070E-04
SAOUSHC_00708	FruA	fructose specific permease	Monosaccharides	-0.69	0.84	0.38	0.49	-	1.61	down	0.62	2.882E-01	1.79	up	1.79	3.740E-07	1.30	up	1.30	1.000E+00	1.40	up	1.40	1.000E+00
SAOUSHC_01507		hypothetical protein	Monosaccharides	-1.11	-1.41	0.46	0.63	-	2.16	down	0.46	1.530E-05	2.65	down	0.38	1.990E-10	1.38	up	1.38	1.000E+00	1.55	up	1.55	1.593E-01
SAOUSHC_02809	GntR	glucanate operon transcriptional repressor	Monosaccharides	-1.07	n.d.	1.05	0.85	▲	2.09	down	0.48	2.895E-01	2.06	down	0.26	6.530E-01	1.80	up	1.80	5.907E-04				
SAOUSHC_02793		hypothetical protein	Monosaccharides;Capsular and extracellular polysaccharides;Cell Wall and Capsule - no subcategory;Plant-Prokaryote comparative genomics	0.79	-0.91	-0.70	-0.52	▼	1.73	down	0.58	9.370E-09	1.88	down	0.53	1.385E-02	1.62	down	0.62	6.003E-01	1.44	down	0.70	1.000E+00
SAOUSHC_00501	NucC	hypothetical protein	Monosaccharides;Purines	0.83	0.21	0.30	-0.01	-	1.78	down	0.56	4.402E-04	1.16	up	1.16	1.000E+00	1.07	up	1.07	1.000E+00	1.01	down	0.99	1.000E+00
SAOUSHC_02377	Ptp	pyrimidine nucleoside phosphorylase	Monosaccharides;Pyrimidines	-1.32	-1.14	0.84	0.89	▲	2.50	down	0.40	1.160E-28	2.21	down	0.45	1.400E-25	1.56	up	1.56	2.815E-03	1.85	up	1.85	1.770E-32
SAOUSHC_02133		nicotinate phosphoribosyltransferase	NAD and NADP;Oxidative stress	0.33	-0.18	-0.81	-0.69	▼	1.26	down	0.80	1.000E+00	1.13	down	0.88	1.000E+00	1.75	down	0.57	1.852E-04	1.62	down	0.62	5.871E-01
SAOUSHC_00093	SodM	superoxide dismutase	Nitrogen Metabolism - no subcategory;Oxidative stress	0.47	-0.16	0.80	1.00	▲	1.39	up	1.39	1.000E+00	1.12	down	0.89	1.000E+00	1.74	up	1.74	2.921E-01	1.99	up	1.99	3.802E-02
SAOUSHC_01653	SodA	superoxide dismutase, Mn	Nitrogen Metabolism - no subcategory;Oxidative stress	-1.02	-1.57	-0.58	-0.84	▲	2.03	down	0.49	1.610E-09	2.96	down	0.34	1.510E-07	1.49	up	1.49	4.708E-01	1.79	up	1.79	1.740E-05
SAOUSHC_00229	ScdA	cell wall biosynthesis protein ScdA	Nitrogen Metabolism - no subcategory;Stress Response - no subcategory	-2.00	-1.32	-1.35	-1.38	▼	4.00	down	0.25	1.282E-04	2.49	down	0.40	2.820E-01	2.54	down	0.39	2.971E-03	2.42	down	0.41	2.493E-02
SAOUSHC_00743	NrdF	ribonucleotide diphosphate reductase subunit beta	Nucleosides and Nucleotides - no subcategory	1.31	0.53	-0.76	-0.79	▼	2.48	up	2.48	3.480E-26	1.44	up	1.44	2.977E-01	1.69	down	0.59	1.770E-01	1.73	down	0.58	6.490E-07
SAOUSHC_00742	NrdE	ribonucleotide diphosphate reductase subunit alpha	Nucleosides and Nucleotides - no subcategory;Oxidative stress	1.37	0.97	-0.81	-0.78	▼	2.96	up	2.96	2.550E-71	1.96	up	1.96	2.180E-03	1.75	down	0.57	2.121E-04	1.72	down	0.58	7.720E-11
SAOUSHC_00367	TcyP	hypothetical protein	Organic sulfur assimilation	n.d.	-1.64	2.02	2.37	▲					3.13	down	0.32	2.938E-01	4.04	up	4.04	2.549E-08	5.18	up	5.18	1.820E-11
SAOUSHC_00731	ABC transporter	Osmotic stress	Osmotic stress	-1.09	-0.73	-0.46	-0.65	-	2.13	down	0.47	1.530E-08	1.66	down	0.60	1.000E+00	1.38	down	0.73	1.000E+00	1.57	down	0.64	4.808E-01
SAOUSHC_00732	OpuAB	amino acid ABC transporter permease	Osmotic stress	-1.24	-0.48	-0.38	-0.54	-	2.36	down	0.42	9.590E-11	1.40	down	0.71	1.000E+00	1.30	down	0.77	1.000E+00	1.45	down	0.69	1.000E+00
SAOUSHC_02932	BetA	choline dehydrogenase	Osmotic stress	1.86	1.50	0.72	0.77	▲	3.63	down	3.63	1.480E-05	2.84	up	2.84	9.840E-06	1.64	up	1.64	3.180E-01	1.71	up	1.71	1.850E-01
SAOUSHC_02933	BetB	betaine aldehyde dehydrogenase	Osmotic stress	1.84	0.95	0.67	0.93	▲	3.83	up	3.83	1.400E-13	1.93	up	1.93	3.570E-06	1.59	up	1.59	1.000E+00	1.90	up	1.90	2.150E-07
SAOUSHC_00831	OsmC	hypothetical protein	Oxidative stress	1.36	0.30	0.41	n.d.	-	2.57	up	2.57	1.282E-04	1.23	up	1.23	1.000E+00	1.33	up	1.33	1.000E+00				
SAOUSHC_01282	BsaA	glutathione peroxidase	Oxidative stress	-0.39	-0.86	-0.55	-0.12	-	1.31	down	0.76	1.000E+00	1.82	down	0.55	1.518E-02	1.46	down	0.69	1.000E+00	1.09	down	0.92	1.000E+00
SAOUSHC_01337	KdsA	catalase	Oxidative stress	0.52	-0.22	0.78	1.12	▲	1.44	up	1.44	1.000E+00	1.16	down	0.86	1.000E+00	1.72	up	1.72	2.971E-03	2.32	up	2.32	1.050E-33
SAOUSHC_02381	Dps	hypothetical protein	Oxidative stress	0.09	-0.25	-1.46	-2.36	▲	1.06	up	1.06	1.000E+00	1.19	down	0.84	1.000E+00	3.15	up	3.15	3.490E-07	4.55	up	4.55	9.270E-14
SAOUSHC_00204	Hmp	globin domain-containing protein	Oxidative stress;Stress Response - no subcategory	-2.25	-1.46	-1.44	-1.31	▼	4.76	down	0.21													

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio: median tendence - 1.5% cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assays against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change (direction) non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SAOHS_00348	RplJ	30S ribosomal protein S6	Protein biogenesis	0.39	0.79	-0.20	0.07	-	1.31	up	1.31	1.00E+00	1.73	up	1.73	1.680E-04	1.14	down	0.87	1.00E+00	1.05	up	1.05	1.00E+00
SAOHS_00474	RplY	50S ribosomal protein L25/general stress protein Ctc	Protein biogenesis	0.89	0.19	-0.22	-0.03	-	1.85	down	1.85	2.82E-11	1.14	up	1.14	1.00E+00	1.17	down	0.86	1.00E+00	1.02	down	0.98	1.00E+00
SAOHS_00518	RplK	50S ribosomal protein L11	Protein biogenesis	0.86	0.82	0.52	-0.48	-	1.82	up	1.82	3.24E-06	1.77	up	1.77	5.790E-05	1.44	down	0.70	1.00E+00	1.40	down	0.72	1.00E+00
SAOHS_00519	RplA	50S ribosomal protein L1	Protein biogenesis	0.78	1.04	-0.20	0.04	-	1.72	up	1.72	3.18E-05	2.05	down	2.05	2.40E-09	1.15	down	0.70	1.00E+00	1.03	up	1.03	1.00E+00
SAOHS_00767	SaHPF	hypothetical protein	Protein biogenesis	-0.67	-1.40	0.98	1.26	▲	1.59	down	0.63	1.00E+00	2.63	down	0.38	1.06E-06	1.97	up	1.97	3.030E-09	2.40	up	2.40	1.36E-17
SAOHS_01058	TypA	GTP-binding protein TypA	Protein biogenesis	0.24	0.99	0.28	0.40	-	1.18	up	1.18	1.00E+00	1.98	up	1.98	1.99E-25	1.21	up	1.21	1.00E+00	1.32	up	1.32	1.00E+00
SAOHS_01092	Pha5	phenylalanyl-tRNA synthetase subunit alpha	Protein biogenesis	0.85	1.00	0.07	0.23	-	1.80	up	1.80	4.84E-07	1.99	up	1.99	2.98E-12	1.05	up	1.05	1.00E+00	1.18	up	1.18	1.00E+00
SAOHS_01093	PhaT	phenylalanyl-tRNA synthetase subunit beta	Protein biogenesis	0.54	0.90	-0.06	0.09	-	1.46	up	1.46	1.00E+00	1.86	up	1.86	4.88E-23	1.04	down	0.96	1.00E+00	1.07	up	1.07	1.00E+00
SAOHS_01163		hypothetical protein	Protein biogenesis	0.47	0.66	0.34	0.33	-	1.38	up	1.38	1.00E+00	1.58	up	1.58	2.22E-02	1.27	up	1.27	1.00E+00	1.26	up	1.26	1.00E+00
SAOHS_01211	RplS	50S ribosomal protein L19	Protein biogenesis	0.45	0.71	-0.21	-0.09	-	1.36	up	1.36	1.00E+00	1.63	up	1.63	3.48E-03	1.15	down	0.87	1.00E+00	1.06	down	0.94	1.00E+00
SAOHS_01232	RplB	30S ribosomal protein S2	Protein biogenesis	0.54	0.64	-0.10	0.03	-	1.45	up	1.45	5.44E-01	1.55	up	1.55	1.79E-02	1.07	down	0.93	1.00E+00	1.02	down	0.98	1.00E+00
SAOHS_01234	Tyf	elongation factor Tl	Protein biogenesis	0.61	0.06	-0.21	-0.02	-	1.53	up	1.53	1.60E-03	1.04	up	1.04	1.00E+00	1.15	down	0.87	1.00E+00	1.01	up	1.01	1.00E+00
SAOHS_01678	RplU	30S ribosomal protein S21	Protein biogenesis	0.50	0.82	-1.30	-0.94	▼	1.41	up	1.41	8.37E-01	1.77	up	1.77	5.23E-02	2.45	down	0.41	5.53E-03	1.92	down	0.52	3.26E-02
SAOHS_01755	RpmA	50S ribosomal protein L27	Protein biogenesis	1.02	0.71	-0.61	-0.47	-	2.02	up	2.02	5.70E-07	1.64	up	1.64	1.59E-01	1.53	down	0.65	1.00E+00	1.38	down	0.72	1.00E+00
SAOHS_01757	RplU	30S ribosomal protein L21	Protein biogenesis	0.56	0.95	-0.28	-0.20	-	1.48	up	1.48	1.00E+00	1.93	up	1.93	3.60E-10	1.21	down	0.82	1.00E+00	1.15	down	0.87	1.00E+00
SAOHS_01829	RplD	30S ribosomal protein S4	Protein biogenesis	0.34	0.84	-0.05	-0.24	-	1.27	up	1.27	1.00E+00	1.79	up	1.79	5.05E-09	1.04	down	0.96	1.00E+00	1.19	down	0.84	1.00E+00
SAOHS_02361	RpmE2	50S ribosomal protein L31 type B	Protein biogenesis	0.80	0.81	-0.44	-0.31	-	1.75	up	1.75	1.13E-02	1.76	up	1.76	1.304E-02	1.36	down	0.74	1.00E+00	1.24	down	0.81	1.00E+00
SAOHS_02486	RplK	30S ribosomal protein S11	Protein biogenesis	0.61	0.98	-0.53	-0.74	▼	1.53	up	1.53	4.43E-01	1.97	up	1.97	1.47E-06	1.44	down	0.69	1.00E+00	1.67	down	0.60	1.39E-02
SAOHS_02487	RplM	30S ribosomal protein S13	Protein biogenesis	0.75	1.10	-0.10	-0.12	-	1.68	up	1.68	5.11E-02	2.15	up	2.15	1.42E-09	1.07	down	0.93	1.00E+00	1.08	down	0.92	1.00E+00
SAOHS_02492	RplO	50S ribosomal protein L15	Protein biogenesis	0.82	1.00	-0.41	-0.33	-	1.77	up	1.77	4.91E-06	2.00	up	2.00	1.18E-09	1.35	down	0.74	1.00E+00	1.26	down	0.80	1.00E+00
SAOHS_02493	RpmD	50S ribosomal protein L30	Protein biogenesis	0.73	0.32	-0.38	-0.19	-	1.66	up	1.66	8.76E-01	1.25	up	1.25	1.00E+00	1.31	down	0.77	1.00E+00	1.14	down	0.88	1.00E+00
SAOHS_02496	RplF	50S ribosomal protein L6	Protein biogenesis	0.67	0.53	-0.09	-0.10	-	1.59	up	1.59	6.65E-03	1.45	up	1.45	3.81E-01	1.07	down	0.94	1.00E+00	1.07	down	0.93	1.00E+00
SAOHS_02508	RplE	50S ribosomal protein L5	Protein biogenesis	0.39	0.57	0.03	0.04	-	1.31	up	1.31	1.00E+00	1.48	up	1.48	1.419E-02	1.02	up	1.02	1.00E+00	1.03	up	1.03	1.00E+00
SAOHS_02504	RpmC	50S ribosomal protein L29	Protein biogenesis	0.81	0.77	-0.42	-0.36	-	1.75	up	1.75	1.88E-02	1.71	up	1.71	7.54E-02	1.34	down	0.75	1.00E+00	1.28	down	0.78	1.00E+00
SAOHS_02505	RplP	50S ribosomal protein L16	Protein biogenesis	0.41	1.07	-0.58	-0.36	-	1.33	up	1.33	1.00E+00	2.10	up	2.10	8.20E-06	1.50	down	0.67	1.00E+00	1.28	down	0.78	1.00E+00
SAOHS_02506	RplC	30S ribosomal protein S3	Protein biogenesis	0.76	0.97	0.19	0.10	-	1.69	up	1.69	7.10E-06	1.96	up	1.96	6.31E-11	1.14	up	1.14	1.00E+00	1.07	up	1.07	1.00E+00
SAOHS_02507	RplV	50S ribosomal protein L22	Protein biogenesis	0.47	0.77	-0.08	-0.35	-	1.39	up	1.39	8.81E-01	1.70	up	1.70	7.77E-03	1.05	down	0.95	1.00E+00	1.28	down	0.78	1.00E+00
SAOHS_02508	RplS	30S ribosomal protein S19	Protein biogenesis	0.51	0.89	-0.52	-0.90	▼	1.43	up	1.43	1.00E+00	1.85	up	1.85	1.48E-02	1.43	down	0.70	1.00E+00	1.86	down	0.54	6.33E-02
SAOHS_02509	RplB	50S ribosomal protein L2	Protein biogenesis	0.51	0.84	-0.24	-0.28	-	1.43	up	1.43	1.00E+00	1.79	up	1.79	3.53E-07	1.18	down	0.85	1.00E+00	1.21	down	0.82	1.00E+00
SAOHS_02511	RplD	50S ribosomal protein L4	Protein biogenesis	0.71	0.85	-0.52	-0.17	-	1.63	up	1.63	9.13E-03	1.80	up	1.80	5.08E-06	1.43	down	0.70	1.00E+00	1.12	down	0.89	1.00E+00
SAOHS_00324		ribosomal protein-serine acetyltransferase	Protein biogenesis/Protein processing and modification	-0.44	-1.01	0.89	1.01	▲	1.35	down	0.74	1.00E+00	2.02	down	0.50	2.25E-02	1.85	up	1.85	3.85E-02	2.02	up	2.02	2.53E-06
SAOHS_00527	RplL	30S ribosomal protein S12	Protein biogenesis/Protein processing and modification/Vulence - no subcategory	1.16	0.76	-0.01	-0.27	-	2.23	up	2.23	6.96E-07	1.70	up	1.70	1.79E-01	1.01	down	0.99	1.00E+00	1.21	down	0.83	1.00E+00
SAOHS_00528	RplG	30S ribosomal protein S7	Protein biogenesis/Vulence - no subcategory	0.66	1.01	-0.70	-0.79	▼	1.58	up	1.58	3.64E-02	2.01	up	2.01	1.08E-09	1.63	down	0.61	6.00E-01	1.72	down	0.58	4.32E-06
SAOHS_00248	LytM	peptidoglycan hydrolase	Protein degradation	2.13	1.02	n.d.	n.d.	-	4.37	up	4.37	4.91E-06	2.02	up	2.02	1.74E-02								
SAOHS_00505	CtpC	endopeptidase	Protein degradation	0.63	0.48	0.26	0.88	-	1.55	up	1.55	1.33E-02	1.39	up	1.39	5.45E-01	1.20	up	1.20	1.00E+00	1.60	up	1.60	1.84E-08
SAOHS_01178	CtpK	ATP-dependent protease ATP-binding subunit CtpK	Protein degradation	0.46	0.72	0.81	-0.96	▼	1.38	up	1.38	1.00E+00	1.64	up	1.64	2.60E-06	1.77	down	0.56	8.17E-05	1.95	down	0.51	3.41E-09
SAOHS_01861		hypothetical protein	Protein degradation	1.35	0.95	n.d.	n.d.	-	2.55	up	2.55	3.79E-06	1.94	up	1.94	7.87E-03								
SAOHS_00912	CtpB	ATP-dependent Ctp protease, ATP-binding subunit CtpB	Protein degradation/Protein folding	0.72	0.75	3.84	-2.80	▲	1.65	up	1.65	1.89E-06	1.69	up	1.69	9.59E-09	3.58	up	3.58	4.46E-43	6.08	up	6.08	4.14E-06
SAOHS_01683	DnaK	molecular chaperone DnaK	Protein folding/Heat shock	0.61	0.87	0.44	-0.30	-	1.52	up	1.52	8.94E-02	1.29	up	1.29	1.00E+00	1.36	up	1.36	1.00E+00	1.63	up	1.63	1.68E-04
SAOHS_01431	MtrB	methionine sulfide reductase B	Protein processing and modification	-2.18	-2.69	-0.70	-0.81	▼	4.54	down	0.22	7.60E-08	6.47	down	0.15	6.84E-10	1.63	down	0.61	1.00E+00	1.75	down	0.47	4.77E-09
SAOHS_01432	MtrA2	methionine sulfide reductase A	Protein processing and modification	-2.52	-2.67	-0.82	-0.95	▼	5.00	down	0.20	2.14E-11	5.94	down	0.17	1.66E-11	1.77	down	0.57	8.88E-01	1.93	down	0.52	1.94E-05
SAOHS_01269	MiaB	(dimethylallyl)adenosine RNA methyltransferase	Protein processing and modification/RNA processing and modification	1.21	1.29	1.96	-1.51	▼	2.31	up	2.31	2.30E-10	2.44	up	2.44	1.14E-11	2.94	down	0.34	3.92E-01	2.85	down	0.35	2.49E-02
SAOHS_01679	MraB	hypothetical protein	Protein processing and modification/RNA processing and modification/Heat shock	1.17	1.38	n.d.	n.d.	-	2.25	up	2.25	2.09E-03	2.57	up	2.57	3.84E-04								
SAOHS_00257	EsaK	hypothetical protein	Protein secretion system, Type VII	0.16	-0.31	0.82	0.81	▲	1.12	down	0.90	1.00E+00	1.24	down	0.81	1.00E+00	1.54	up	1.54	1.00E+00	1.75	up	1.75	1.77E-02
SAOHS_01972	PrsA	protein export protein PrsA	Protein translocation across cytoplasmic membrane/Plant-Prokaryote comparative genomics/Protein folding	-2.16	-2.19	-0.37	-0.76	▼	4.47	down	0.22	4.15E-16	4.56	down	0.22	4.42E-19	1.29	down	0.78	1.00E+00	1.69	down	0.59	2.41E-01
SAOHS_01008	PurE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	Purines	-0.64	-0.46	-1.08	-0.74	▼	1.56	down	0.64	1.00E+00	1.38	down	0.73	1.00E+00	2.11	down	0.47	2.14E-02	1.67	down	0.60	5.88E-01
SAOHS_01009	PurK	phosphoribosylaminoimidazole carboxylase ATPase subunit	Purines	-0.55	-0.34	-1.13	-0.96	▼	1.46	down	0.68	1.00E+00	1.26	down	0.79	1.00E+00	2.19	down	0.46	2.89E-06	1.94	down	0.51	3.98E-07
SAOHS_01010	PurC	phosphoribosylaminoimidazole succinocarboxamide synthase	Purines	-0.38	-0.39	-1.26	-1.02	▼	1.30	down	0.77	1.00E+00	1.31	down	0.76	1.00E+00	2.39	down	0.42	2.31E-20	2.03	down	0.49	4.74E-19
SAOHS_01011	PurS	phosphoribosylformylglycinamide synthase, PurS protein	Purines	-0.45	-0.73	-1.30	-1.21	▼	1.37	down	0.73	1.00E+00	1.66	down	0.60	2.65E-01	2.83	down	0.35	2.23E-12	2.31	down	0.43	5.08E-15
SAOHS_01012	PurQ	phosphoribosylformylglycinamide synthase I	Purines	-0.48	-0.54	-1.40	-1.27	▼	1.40	down	0.72	1.00E+00	1.45	down	0.69	1.00E+00	2.64	down	0.38	1.16E-12	2			

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio: median tendence - 1.5% cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assays against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change (direction) non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SAOUSHC_00940		hypothetical protein	Regulation and Cell signaling - no subcategory	-0.81	-1.04	n.d.	n.d.	-	1.75	down	0.57	1.000E+00	2.05	down	0.49	5.122E-03								
SAOUSHC_01361	MurK	transcriptional regulator	Regulation and Cell signaling - no subcategory	-1.20	-0.84	-0.71	-1.03	▼	2.30	down	0.43	2.18E-10	1.79	down	0.56	2.137E-02	1.66	down	0.60	1.000E+00	2.05	down	0.49	2.310E-05
SAOUSHC_00998	FntA	fnt protein	Regulation and Cell signaling - no subcategoryResistance to antibiotics and toxic compounds	-2.24	-1.34	-0.48	-1.01	▼	4.73	down	0.21	1.310E-09	2.52	down	0.40	2.710E-05	1.39	down	0.72	1.000E+00	2.02	down	0.50	1.400E-03
SAOUSHC_01979		hypothetical protein	Resistance to antibiotics and toxic compounds	0.85	0.09	-1.38	-1.74	▼	1.57	up	1.57	5.967E-01	1.89	up	1.89	2.760E-07	2.59	down	0.39	4.000E-11	3.38	down	0.30	1.820E-11
SAOUSHC_02630		hypothetical protein	Resistance to antibiotics and toxic compounds	0.01	1.57	-0.52	-0.28	-	1.01	up	1.01	1.000E+00	2.97	up	2.97	4.674E-03	1.43	down	0.70	1.000E+00	1.22	down	0.82	1.000E+00
SAOUSHC_02635	TcaA	hypothetical protein	Resistance to antibiotics and toxic compounds	-1.95	-0.76	-0.25	-0.45	-	2.54	down	0.39	1.889E-04	1.69	down	0.59	1.608E-02	1.19	down	0.84	1.000E+00	1.37	down	0.73	1.000E+00
SAOUSHC_02582	FdhA	formate dehydrogenase subunit alpha	Respiration - no subcategory	1.83	1.37	0.40	0.78	▲	3.56	up	3.56	1.430E-12	2.58	down	2.58	5.440E-11	1.32	up	1.32	1.000E+00	1.72	up	1.72	3.717E-02
SAOUSHC_01889	RibD	riboflavin biosynthesis protein RibD	Riboflavin, FMN, FAD	1.37	1.24	n.d.	1.01	▲	2.58	up	2.58	2.237E-02	2.36	up	2.36	9.459E-01					2.02	up	2.02	3.074E-01
SAOUSHC_00719	QueE	hypothetical protein	RNA processing and modification	1.77	1.75	0.21	1.08	▲	3.42	up	3.42	2.237E-02	3.36	up	3.36	8.621E-02	1.16	up	1.16	1.000E+00	2.12	up	2.12	1.000E+00
SAOUSHC_00951		hypothetical protein	RNA processing and modification	-0.84	-1.11	-1.28	-1.53	▲	1.79	down	0.56	8.121E-02	2.16	down	0.46	2.290E-06	2.42	up	2.42	1.560E-13	2.88	up	2.88	7.740E-23
SAOUSHC_01659		hypothetical protein	RNA processing and modification	0.17	0.72	0.02	0.18	-	1.12	up	1.12	1.000E+00	1.65	up	1.65	3.534E-02	1.02	up	1.02	1.000E+00	1.14	up	1.14	1.000E+00
SAOUSHC_02097		hypothetical protein	RNA processing and modification	1.60	1.11	0.16	0.55	-	3.03	up	3.03	1.050E-12	2.16	up	2.16	4.680E-07	1.12	up	1.12	1.000E+00	1.47	up	1.47	1.000E+00
SAOUSHC_02316	CtIA	DEAD-box ATP-dependent DNA helicase	RNA processing and modification	0.37	1.07	0.08	0.20	-	1.30	up	1.30	1.000E+00	2.11	up	2.11	3.310E-36	1.06	up	1.06	1.000E+00	1.15	up	1.15	1.000E+00
SAOUSHC_00074	SrA	periplasmic binding protein	Siderophores	-2.49	-0.12	-0.21	-0.30	-	5.62	down	0.18	9.430E-15	1.09	down	0.92	1.000E+00	1.18	down	0.85	1.000E+00	1.23	down	0.81	1.000E+00
SAOUSHC_00075	SrBA	hypothetical protein	Siderophores	n.d.	-2.20	0.17	-0.71	-					4.61	down	0.22	7.070E-07	1.13	up	1.13	1.000E+00	1.63	down	0.61	1.000E+00
SAOUSHC_00077	SrBC	hypothetical protein	Siderophores	n.d.	-2.15	-0.39	-0.90	▼					4.38	down	0.23	1.860E-05	1.31	down	0.76	1.000E+00	1.86	down	0.54	2.287E-02
SAOUSHC_00079	SrBE	hypothetical protein	Siderophores	n.d.	-1.91	0.35	-0.22	-					3.80	down	0.26	3.360E-10	1.27	up	1.27	1.000E+00	1.16	down	0.86	1.000E+00
SAOUSHC_00080	SrBF	hypothetical protein	Siderophores	n.d.	-1.40	-0.10	-0.34	-					3.07	down	0.33	6.204E-04	1.07	down	0.94	1.000E+00	1.26	down	0.79	1.000E+00
SAOUSHC_01819	UspA1	hypothetical protein	Stress Response - no subcategory	-1.13	-1.46	1.23	1.54	▲	2.19	down	0.46	4.110E-12	2.74	down	0.36	6.430E-21	2.35	up	2.35	6.130E-19	2.91	up	2.91	1.170E-32
SAOUSHC_02299	RibW	serine-protein kinase RibW	Stress Response - no subcategory	0.86	0.57	-0.24	0.04	-	1.81	up	1.81	5.210E-09	1.48	up	1.48	1.820E-02	1.18	up	1.48	1.000E+00	1.03	up	1.03	1.000E+00
SAOUSHC_02300	RibV	STAS domain-containing protein	Stress Response - no subcategory	0.87	0.42	-0.01	0.20	-	1.82	up	1.82	1.960E-04	1.34	up	1.34	1.000E+00	1.01	down	0.99	1.000E+00	1.15	up	1.15	1.000E+00
SAOUSHC_02402	MSA	PTS system mannitol-specific transporter subunit IIA	Sugar alcohols	1.49	0.64	0.58	1.04	▲	2.81	up	2.81	9.470E-12	1.56	up	1.56	2.191E-01	1.50	up	1.50	1.000E+00	2.06	up	2.06	1.000E-07
SAOUSHC_02403	MSD	mannitol-1-phosphate 5-dehydrogenase	Sugar alcohols	1.34	0.18	0.74	1.06	▲	2.53	up	2.53	1.020E-15	1.30	up	1.30	1.000E+00	1.67	up	1.67	9.794E-02	2.08	up	2.08	1.070E-08
SAOUSHC_01278	GldD	aerobic glycerol-3-phosphate dehydrogenase	Sugar alcohols,Phospholipids,Electron donating reactions	0.20	0.33	0.63	0.90	▲	1.15	up	1.15	1.000E+00	1.26	up	1.26	1.000E+00	1.55	up	1.55	3.442E-03	1.86	up	1.86	1.020E-28
SAOUSHC_00833		hypothetical protein	Tetrazepines	-1.80	-0.91	-0.55	-0.29	-	3.49	down	0.29	1.420E-09	1.88	down	0.53	6.912E-02	1.46	down	0.68	1.000E+00	1.22	down	0.82	1.000E+00
SAOUSHC_01960	HemY	protoporphyrinogen oxidase	Tetrazepines	0.37	0.48	0.62	1.02	▲	1.29	up	1.29	1.000E+00	1.40	up	1.40	1.000E+00	1.53	up	1.53	8.973E-01	2.02	up	2.02	3.602E-02
SAOUSHC_02747		hypothetical protein	Tetrazepines	-0.74	-1.22	-0.66	-0.41	-	1.67	down	0.60	2.165E-02	2.33	down	0.43	1.180E-06	1.58	down	0.63	8.363E-01	1.33	down	0.75	1.000E+00
SAOUSHC_01121	Ha	alpha-hemolysin	Toxins and superantigens	n.d.	n.d.	n.d.	1.85	▲					2.04	down	0.49	5.235E-01			3.28	2.397E-02	3.61	up	3.61	4.063E-03
SAOUSHC_02206	Sli	immunoglobulin G-binding protein Sli	Toxins and superantigens	n.d.	-1.03	0.43	-2.86	▲							10.77	9.550E-13			10.77	9.550E-13	7.76	up	7.76	4.650E-09
SAOUSHC_01754	GreA	transcription elongation factor GreA	Transcription	0.22	-0.49	-0.75	-0.58	▼	1.16	up	1.16	1.000E+00	1.41	down	0.71	1.000E+00	1.68	down	0.59	1.277E-02	1.49	down	0.67	1.000E+00
SAOUSHC_02362	Rho	transcription termination factor Rho	Transcription	-0.85	-0.05	-0.17	-0.37	-	1.81	down	0.55	1.650E-06	1.04	down	0.97	1.000E+00	1.13	down	0.89	1.000E+00	1.29	down	0.77	1.000E+00
SAOUSHC_01732	CysR	hypothetical protein	Transcription,Stress Response - no subcategoryOrganic sulfur assimilation	-0.59	-0.80	-0.59	-0.78	▼	1.50	down	0.67	1.000E+00	1.74	down	0.57	1.000E+00	1.50	down	0.67	1.000E+00	1.72	down	0.58	1.558E-02
SAOUSHC_00906	Lip	lipase	Triacylglycerids	-0.42	n.d.	1.16	-1.62	▲	1.34	down	0.75	1.000E+00					2.24	up	2.24	1.000E+00	3.06	up	3.06	2.491E-02
SAOUSHC_00625	MnhA2	putative monovalent cation/H+ antiporter subunit A	Uni- Sym- and Antiporters	1.00	1.24	0.72	0.20	-	2.00	up	2.00	1.237E-02	2.37	up	2.37	1.286E-03	1.64	up	1.64	1.000E+00	1.15	up	1.15	1.000E+00
SAOUSHC_00014		hypothetical protein		-1.27	0.05	-0.11	-0.30	-	2.41	down	0.41	1.478E-02	1.04	up	1.04	1.000E+00	1.08	down	0.93	1.000E+00	1.23	down	0.81	1.000E+00
SAOUSHC_00070	SarS	accessory regulator-like protein		2.35	2.05	1.20	1.31	▲	5.09	up	5.09	7.710E-09	4.13	up	4.13	3.990E-09	2.30	up	2.30	9.113E-04	2.52	up	2.52	3.490E-09
SAOUSHC_00135		hypothetical protein		-0.24	-0.42	n.d.	0.94	▲	1.18	down	0.84	1.000E+00	1.34	down	0.75	1.000E+00					1.92	up	1.92	4.759E-02
SAOUSHC_00173	AcpD	acetyl-CoA synthetase		1.36	1.07	1.03	1.61	▲	2.95	up	2.95	6.310E-03	2.10	up	2.10	6.081E-02	2.05	up	2.05	1.000E+00	3.06	up	3.06	4.883E-04
SAOUSHC_00182		hypothetical protein		-1.71	0.07	0.53	-0.28	-	3.27	down	0.31	1.798E-02	1.05	up	1.05	1.000E+00	1.45	up	1.45	1.000E+00	1.21	down	0.82	1.000E+00
SAOUSHC_00197	FadD	hypothetical protein		n.d.	n.d.	1.08	2.06	▲							3.21	up	3.21	1.660E-22			4.18	up	4.18	1.070E-31
SAOUSHC_00198	FadE	hypothetical protein		n.d.	n.d.	1.51	1.85	▲							2.85	up	2.85	5.620E-11			3.61	up	3.61	3.470E-17
SAOUSHC_00199	FadX	hypothetical protein		n.d.	n.d.	1.52	1.46	▲							2.75	up	2.75	1.250E-01			2.75	up	2.75	1.800E-03
SAOUSHC_00221	TarT	alcohol dehydrogenase, zinc-containing		-1.44	-0.38	0.00	0.05	-	2.72	down	0.37	4.333E-03	1.30	down	0.77	1.000E+00	1.00	up	1.00	1.000E+00	1.03	up	1.03	1.000E+00
SAOUSHC_00244		hypothetical protein		-0.20	-0.21	0.69	0.97	▲	1.15	down	0.87	1.000E+00	1.16	up	1.16	1.000E+00	1.62	up	1.62	1.000E+00	1.95	up	1.95	4.759E-02
SAOUSHC_00253		hypothetical protein		0.95	2.31	1.18	1.20	▲	1.93	up	1.93	1.974E-02	5.69	up	5.69	1.800E-08	2.27	up	2.27	1.794E-02	2.29	up	2.29	9.390E-06
SAOUSHC_00285		hypothetical protein		1.16	1.67	1.06	0.98	▲	2.23	up	2.23	1.327E-04	2.77	up	2.77	6.430E-07	2.08	up	2.08	1.109E-01	1.97	up	1.97	5.907E-04
SAOUSHC_00311		hypothetical protein		-5.31	n.d.	0.92	0.99	▲	39.66	down	0.03	5.373E-01			1.89	up	1.89	1.601E-01			1.98	up	1.98	9.130E-04
SAOUSHC_00319		hypothetical protein		0.48	0.24	0.60	0.76	▲	1.40	up	1.40	1.000E+00	1.18	up	1.18	1.000E+00	1.52	up	1.52	1.000E+00	1.69	up	1.69	1.173E-02
SAOUSHC_00356		hypothetical protein		2.61	1.85	0.61	1.01	▲	6.11	up	6.11	8.120E-17	3.61	up	3.61	4.560E-14	1.53	up	1.53	2.754E-01	2.02	up	2.02	1.230E-07
SAOUSHC_00357		hypothetical protein		-0.30	-0.69	-0.88	-1.17	▼	1.23	down	0.81	1.000E+00	1.62	down	0.62	8.293E-01	1.84	down	0.54	4.613E-01	2.25	down	0.44	2.641E-02
SAOUSHC_00362		hypothetical protein		-0.28	-0.49	-0.56	-1.04	▼	1.21	down	0.82	1.000E+00	1.41	down	0.71	1.000E+00	1.48	down	0.68	1.000E+00	2.05	down	0.49	9.480E-06
SAOUSHC_00371		hypothetical protein		-1.14	-1.78	0.98	1.19	▲	2.20	down	0.46	3.610E-12	3.44	down	0.29	2.040E-15	1.98	up	1					

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio: median tendence - 1.5% cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assays against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change (direction) non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SAOHS_C0069		hypothetical protein		-1.34	-1.43	-0.32	-0.17	-	2.53	down	0.40	9.310E-06	2.69	down	0.37	2.396E-02	1.43	down	0.70	1.000E+00	1.13	down	0.89	1.000E+00
SAOHS_C0064	MgR	hypothetical protein		-0.40	-0.83	-0.85	-0.76	▼	1.32	down	0.76	2.272E-01	1.78	down	0.56	2.272E-01	1.80	down	0.56	1.290E-05	1.70	down	0.59	2.958E-03
SAOHS_C00714	SaeS	sensor histidine kinase SaeS		-2.47	-1.31	-0.76	-1.14	▼	5.55	down	0.18	1.670E-12	2.48	down	0.40	3.380E-12	1.69	down	0.59	6.424E-01	2.20	down	0.45	6.500E-09
SAOHS_C00715	SaeR	response regulator		-1.88	-1.78	-0.83	-0.99	▼	3.68	down	0.27	2.568E-10	3.44	down	0.29	7.700E-10	1.78	down	0.56	2.492E-04	1.98	down	0.51	3.740E-11
SAOHS_C00717	SaeP	hypothetical protein		-4.35	-2.50	0.21	-0.76	-	21.02	down	0.05	1.282E-04	5.66	down	0.18	1.705E-04	1.16	up	1.16	1.000E+00	1.69	down	0.59	1.000E+00
SAOHS_C00736		hypothetical protein		1.00	0.22	1.33	1.25	▲	1.99	up	1.99	6.637E-03	1.17	up	1.17	1.000E+00	2.52	up	2.52	1.074E-02	2.38	up	2.38	4.050E-09
SAOHS_C00754		hypothetical protein		0.97	0.90	-0.14	-0.28	-	1.95	up	1.95	8.910E-05	1.87	up	1.87	3.830E-04	1.10	down	0.91	1.000E+00	1.21	down	0.82	1.000E+00
SAOHS_C00792		hypothetical protein		0.79	0.56	0.65	0.86	▲	1.73	up	1.73	2.992E-07	1.48	up	1.48	7.493E-01	1.57	up	1.57	3.918E-01	1.82	up	1.82	1.240E-09
SAOHS_C00834		thioredoxin		-0.37	-1.02	-0.70	-0.65	▼	1.29	down	0.77	1.000E+00	2.03	down	0.49	2.598E-04	1.62	down	0.62	3.798E-01	1.56	down	0.64	5.517E-01
SAOHS_C00850	SuR	hypothetical protein		1.33	0.33	0.28	0.40	-	2.51	up	2.51	1.689E-12	1.25	up	1.25	1.000E+00	1.21	up	1.21	1.000E+00	1.32	up	1.32	1.000E+00
SAOHS_C00863		hypothetical protein		-0.31	-1.07	-0.66	-0.83	▼	1.24	down	0.81	1.000E+00	2.09	down	0.48	1.205E-02	1.59	down	0.63	1.000E+00	1.78	down	0.56	1.339E-02
SAOHS_C00934	SpxA	transcriptional regulator Spx		-0.05	-1.25	-0.40	-0.45	-	1.03	down	0.97	1.000E+00	2.38	down	0.42	1.030E-12	1.32	down	0.76	1.000E+00	1.57	down	0.64	2.457E-01
SAOHS_C00972		hypothetical protein		1.36	0.90	0.37	0.80	▲	2.56	up	2.56	7.870E-09	1.87	up	1.87	2.160E-05	1.30	up	1.30	1.000E+00	1.74	up	1.74	3.668E-03
SAOHS_C01050		hypothetical protein		0.76	0.64	-0.16	-0.08	-	1.70	up	1.70	2.961E-03	1.56	up	1.56	3.741E-02	1.12	down	0.90	1.000E+00	1.06	down	0.95	1.000E+00
SAOHS_C01138		hypothetical protein		0.01	-0.76	1.02	1.31	▲	1.01	up	1.01	1.000E+00	1.69	down	0.59	9.545E-01	2.03	up	2.03	8.980E-07	2.35	up	2.35	9.480E-10
SAOHS_C01154	SepF	hypothetical protein		0.07	-0.04	-1.32	-1.31	▼	1.05	up	1.05	1.000E+00	1.03	down	0.97	1.000E+00	2.49	down	0.40	2.032E-09	2.52	down	0.40	3.630E-13
SAOHS_C01185		ribosomal RNA large subunit methyltransferase N		1.39	2.13	-0.52	-0.66	-	2.62	up	2.62	3.680E-11	4.08	up	4.08	2.890E-12	1.43	down	0.70	1.000E+00	1.58	down	0.63	4.540E-01
SAOHS_C01222	TopA	DNA topoisomerase I		0.62	0.80	-0.07	0.07	-	1.54	up	1.54	3.958E-01	1.75	up	1.75	4.130E-06	1.05	down	0.95	1.000E+00	1.05	up	1.05	1.000E+00
SAOHS_C01263	RnyI cvtA	phosphodiesterase		0.70	0.60	0.14	0.09	-	1.63	up	1.63	3.662E-03	1.51	up	1.51	1.721E-01	1.10	up	1.10	1.000E+00	1.06	up	1.06	1.000E+00
SAOHS_C01264		hypothetical protein		0.97	0.17	-0.37	-0.23	-	1.95	up	1.95	3.304E-03	1.13	up	1.13	1.000E+00	1.29	down	0.76	1.000E+00	1.18	down	0.85	1.000E+00
SAOHS_C01265		hypothetical protein		0.69	0.51	0.41	0.45	-	1.61	up	1.61	2.058E-02	1.43	up	1.43	3.776E-01	1.33	up	1.33	1.000E+00	1.36	up	1.36	1.000E+00
SAOHS_C01324		hypothetical protein		-1.59	-1.28	-0.13	-0.28	-	3.00	down	0.33	3.820E-10	2.43	down	0.41	7.070E-07	1.09	down	0.92	1.000E+00	1.22	down	0.82	1.000E+00
SAOHS_C01349		hypothetical protein		-0.84	-1.48	-0.66	-0.59	▼	1.79	down	0.56	8.760E-06	2.80	down	0.36	8.990E-11	1.58	down	0.63	4.846E-01	1.50	down	0.66	1.000E+00
SAOHS_C01354	Akt	sodium/calcine symporter family protein		0.64	0.85	0.54	0.58	-	1.56	up	1.56	8.575E-01	1.80	up	1.80	6.070E-03	1.46	up	1.46	1.000E+00	1.49	up	1.49	1.000E+00
SAOHS_C01392		ABC transporter ATP-binding protein		0.51	0.77	-0.06	0.11	-	1.43	up	1.43	1.000E+00	1.70	up	1.70	3.580E-09	1.04	down	0.96	1.000E+00	1.08	up	1.08	1.000E+00
SAOHS_C01415		hypothetical protein		-0.10	-0.70	0.36	0.86	-	1.07	down	0.93	1.000E+00	1.63	down	0.61	1.000E+00	1.29	up	1.29	1.000E+00	1.58	up	1.58	9.400E-04
SAOHS_C01419	ArS	hypothetical protein		-0.76	-0.39	0.90	n.d.	▲	1.69	down	0.59	3.508E-02	1.31	down	0.77	1.000E+00	1.86	up	1.86	3.929E-01				
SAOHS_C01425		hypothetical protein		0.91	-0.12	-0.19	0.16	-	1.89	up	1.89	1.438E-03	1.09	down	0.92	1.000E+00	1.14	down	0.88	1.000E+00	1.12	up	1.12	1.000E+00
SAOHS_C01427	CtpA	hypothetical protein		-1.00	-0.81	-0.49	-0.78	▼	2.00	down	0.50	2.388E-09	1.76	down	0.57	3.651E-04	1.41	down	0.71	1.000E+00	1.72	down	0.58	4.430E-02
SAOHS_C01429		hypothetical protein		-2.02	-1.80	-1.87	-2.23	▼	4.06	down	0.25	1.068E-03	3.04	down	0.33	3.860E-05	3.65	down	0.27	2.971E-03	4.70	down	0.21	2.493E-02
SAOHS_C01476		hypothetical protein		-0.01	-0.46	-1.29	-1.51	▼	1.01	down	0.99	1.000E+00	1.37	down	0.73	1.000E+00	2.45	down	0.41	3.923E-01	2.84	down	0.35	2.493E-02
SAOHS_C01610		hypothetical protein		-0.20	-0.01	-0.89	-1.06	▼	1.15	down	0.87	1.000E+00	1.01	down	0.99	1.000E+00	1.86	down	0.54	1.923E-01	2.08	down	0.48	2.460E-06
SAOHS_C01627		hypothetical protein		-0.50	-0.09	-0.54	-0.74	▼	1.42	down	0.71	1.000E+00	1.07	down	0.94	1.000E+00	1.46	down	0.69	1.000E+00	1.67	down	0.60	2.665E-04
SAOHS_C01666	GlyS	glycyl-tRNA synthetase		0.75	0.07	-0.05	0.04	-	1.68	up	1.68	7.360E-10	1.05	up	1.05	1.000E+00	1.04	down	0.96	1.000E+00	1.03	up	1.03	1.000E+00
SAOHS_C01718		hypothetical protein		0.82	1.57	n.d.	0.57	-	1.76	up	1.76	7.455E-02	2.97	up	2.97	3.560E-05					1.49	down	0.67	1.000E+00
SAOHS_C01717		hypothetical protein		1.08	1.38	-0.41	-0.79	▼	2.11	up	2.11	1.180E-02	2.61	up	2.61	2.450E-08	1.52	down	0.66	1.000E+00	1.73	down	0.58	1.000E+00
SAOHS_C01729		hypothetical protein		2.32	0.08	0.45	-0.21	-	4.98	up	4.98	5.934E-04	1.06	up	1.06	1.000E+00	1.37	up	1.37	1.000E+00	1.16	down	0.87	1.000E+00
SAOHS_C01730	CBD	hypothetical protein		1.75	0.90	0.53	0.59	-	3.45	up	3.45	2.640E-06	1.87	up	1.87	1.963E-03	1.45	up	1.45	1.000E+00	1.50	up	1.50	1.000E+00
SAOHS_C01761		hypothetical protein		-2.40	-1.01	-0.82	-1.46	▼	7.88	down	0.13	9.310E-06	8.07	down	0.12	5.370E-08	1.77	down	0.56	1.885E-02	2.79	down	0.36	9.390E-06
SAOHS_C01786	IntC	translational initiation factor IF-3		0.61	1.02	-0.08	0.04	-	1.52	up	1.52	2.629E-01	2.03	up	2.03	1.700E-09	1.06	down	0.94	1.000E+00	1.03	up	1.03	1.000E+00
SAOHS_C01787	LysP	hypothetical protein		-2.66	-1.50	-0.50	-0.86	▼	6.33	down	0.16	9.310E-06	3.78	down	0.26	3.740E-09	1.41	down	0.71	1.000E+00	1.81	down	0.55	4.834E-02
SAOHS_C01816	PepQ	hypothetical protein		-1.49	-1.67	-0.69	-0.60	▼	2.81	down	0.36	6.790E-16	3.18	down	0.31	4.500E-13	1.61	down	0.62	1.000E+00	1.52	down	0.66	1.000E+00
SAOHS_C01838		hypothetical protein		-2.93	-2.46	-1.57	-1.95	▼	7.55	down	0.13	8.870E-23	5.50	down	0.18	3.980E-28	2.96	down	0.34	2.480E-06	3.86	down	0.26	3.900E-21
SAOHS_C01854		hypothetical protein		0.73	0.45	0.27	0.44	-	1.66	up	1.66	3.050E-06	1.37	up	1.37	1.000E+00	1.21	up	1.21	1.000E+00	1.35	up	1.35	1.000E+00
SAOHS_C01863		hypothetical protein		-0.80	-0.46	0.15	0.41	-	1.74	down	0.58	3.024E-02	1.37	down	0.73	1.000E+00	1.11	up	1.11	1.000E+00	1.33	down	0.75	1.000E+00
SAOHS_C01868		dipeptidase PepV		-0.71	-1.19	-0.72	-0.54	▼	1.63	down	0.61	7.027E-02	2.29	down	0.44	3.440E-17	1.64	down	0.61	1.000E+00	1.46	down	0.69	1.000E+00
SAOHS_C01869		hypothetical protein		0.69	0.10	0.11	0.38	-	1.62	up	1.62	2.162E-01	1.07	up	1.07	1.000E+00	1.08	up	1.08	1.000E+00	1.30	up	1.30	1.000E+00
SAOHS_C01877		hypothetical protein		0.72	1.11	n.d.	n.d.	-	1.65	up	1.65	4.365E-01	2.16	up	2.16	1.802E-03								
SAOHS_C01879	Rut	virulence factor regulator protein		0.52	1.49	0.46	0.47	-	1.44	up	1.44	1.000E+00	2.80	up	2.80	1.700E-08	1.38	up	1.38	1.000E+00	1.39	up	1.39	1.000E+00
SAOHS_C01978		hypothetical protein		0.81	0.73	0.39	0.43	-	1.75	up	1.75	8.980E-03	1.66	up	1.66	1.278E-02	1.31	up	1.31	1.000E+00	1.35	up	1.35	1.000E+00
SAOHS_C02013		hypothetical protein		1.84	0.68	1.36	1.50	▲	3.59	up	3.59	8.080E-14	1.61	up	1.61	1.676E-02	2.23	up	2.23	2.940E-08	2.83	up	2.83	5.090E-14
SAOHS_C02096		hypothetical protein		-1.50	-1.32	n.d.	-1.08	▼	2.82	down	0.35	1.690E-03	2.50											

The comparison of the early intracellular phase sample (8h p.i.) and late intracellular phase samples (24h and 32h p.i.) revealed proteins that were not significantly altered in their amount by using the non-adherent control as point of reference, because proteins were not detected in the non-adherent control sample or proteins were altered by opposing changes (early phase / late phase).

locus tag	protein symbol	description	theSEED functional category	log2 ratio OD=0.4	log2 ratio non- adherent	log2 ratio 24h p.i.	log2 ratio 32h p.i.	median over 24 and 32h ratio: median tendence - 1.5% cutoff	median fold- change OD=0.4	median fold- change (direction) OD=0.4	median ratio over assays against 8h p.i. OD=0.4	p-value BH adjusted OD=0.4	median fold-change non-ad.	median fold-change (direction) non-ad.	median ratio over assays against 8h p.i. non-ad.	p-value BH adjusted non-ad.	median fold-change 24h p.i.	median fold-change (direction) 24h p.i.	median ratio over assays against 8h p.i. 24h p.i.	p-value BH adjusted 24h p.i.	median fold-change 32h p.i.	median fold-change (direction) 32h p.i.	median ratio over assays against 8h p.i. 32h p.i.	p-value BH adjusted 32h p.i.
SAOUMSC_02364		hypothetical protein		-1.93	-1.10	n.d.	-0.88	▼	2.05	down	0.49	1.021E-02	2.15	down	0.47	6.363E-01					1.84	down	0.54	1.000E+00
SAOUMSC_02372		hypothetical protein		-0.20	0.05	-1.55	-1.76	▼	1.15	down	0.87	1.000E+00	1.03	up	1.03	1.000E+00	2.92	down	0.34	9.645E-02	3.24	down	0.31	2.493E-02
SAOUMSC_02382		hypothetical protein		-0.82	-0.82	-0.39	-0.12	-	1.76	down	0.57	4.460E-02	1.77	down	0.56	4.936E-01	1.31	down	0.76	1.000E+00	1.09	down	0.92	1.000E+00
SAOUMSC_02387		hypothetical protein		1.37	0.45	0.78	1.09	▲	2.58	up	2.58	4.250E-07	1.37	up	1.37	1.000E+00	1.72	up	1.72	1.882E-01	2.13	up	2.13	1.950E-06
SAOUMSC_02420	SdrM	hypothetical protein		-0.28	0.01	0.79	0.90	▲	1.22	down	0.82	1.000E+00	1.01	up	1.01	1.000E+00	1.72	up	1.72	1.503E-01	1.87	up	1.87	3.875E-03
SAOUMSC_02441	Asp23	alkaline shock protein 23		1.33	0.84	1.11	1.52	▲	2.51	up	2.51	3.660E-09	1.79	up	1.79	4.384E-03	2.15	up	2.15	3.830E-06	2.86	up	2.86	3.500E-14
SAOUMSC_02442		hypothetical protein		1.00	0.46	1.13	1.19	▲	2.00	up	2.00	6.297E-03	1.37	up	1.37	1.000E+00	2.18	up	2.18	7.280E-02	2.28	up	2.28	2.380E-05
SAOUMSC_02443	AmaP	hypothetical protein		1.75	1.38	1.30	1.67	▲	3.37	up	3.37	4.500E-12	2.60	up	2.60	5.410E-10	2.47	up	2.47	4.000E-11	3.17	up	3.17	2.160E-09
SAOUMSC_02448		hypothetical protein		-0.60	-0.14	0.36	-0.97	▼	1.51	down	0.66	1.000E+00	1.10	down	0.91	1.000E+00	1.82	down	0.55	6.063E-02	1.83	down	0.55	7.128E-03
SAOUMSC_02554	PhiD2	hypothetical protein		1.95	-0.21	-0.46	-0.64	-	3.87	down	0.26	5.250E-36	1.16	down	0.86	1.000E+00	1.37	down	0.73	1.000E+00	1.56	down	0.64	1.000E+00
SAOUMSC_02566	SarK	hypothetical protein		0.75	0.05	-0.24	-0.14	-	1.68	down	0.60	2.960E-03	1.04	up	1.04	1.000E+00	1.18	down	0.85	1.000E+00	1.10	down	0.91	1.000E+00
SAOUMSC_02568		hypothetical protein		-0.62	-1.46	0.25	0.39	-	1.54	down	0.65	1.000E+00	2.79	down	0.36	3.150E-09	1.19	down	0.84	1.000E+00	1.14	up	1.14	1.000E+00
SAOUMSC_02571	SiaA	secretory antigen		0.25	0.74	2.54	1.86	▲	1.19	up	1.19	1.000E+00	1.67	up	1.67	3.794E-01	5.80	up	5.80	6.500E-11	3.63	up	3.63	2.940E-09
SAOUMSC_02604		hypothetical protein		1.72	0.88	1.05	1.23	▲	3.30	up	3.30	2.420E-13	1.84	up	1.84	1.935E-02	2.08	up	2.08	1.730E-05	2.35	up	2.35	1.270E-08
SAOUMSC_02619		hypothetical protein		0.64	1.17	n.d.	0.82	▲	1.56	up	1.56	1.000E+00	2.25	up	2.25	1.058E-02					1.77	up	1.77	1.000E+00
SAOUMSC_02650		hypothetical protein		0.41	0.00	0.51	0.89	▲	1.33	up	1.33	1.000E+00	1.00	up	1.00	1.000E+00	1.42	up	1.42	1.000E+00	1.91	up	1.91	7.430E-05
SAOUMSC_02665		hypothetical protein		1.54	0.58	0.98	1.08	▲	2.90	up	2.90	4.370E-11	1.49	up	1.49	2.825E-01	1.97	up	1.97	7.140E-06	2.12	up	2.12	1.390E-08
SAOUMSC_02668		hypothetical protein		-0.21	0.39	-0.78	-1.06	▼	1.17	down	0.85	1.000E+00	1.31	up	1.31	1.000E+00	1.72	down	0.58	6.578E-03	2.09	down	0.48	1.500E-06
SAOUMSC_02669	SarZ	hypothetical protein		-0.98	-0.78	-0.37	-0.26	-	1.97	down	0.51	4.700E-07	1.72	down	0.58	1.000E+00	1.30	down	0.77	1.000E+00	1.20	down	0.83	1.000E+00
SAOUMSC_02690		hypothetical protein		0.12	0.87	0.65	0.50	-	1.09	up	1.09	1.000E+00	1.83	up	1.83	2.474E-04	1.56	up	1.56	1.000E+00	1.42	up	1.42	1.000E+00
SAOUMSC_02734		hypothetical protein		1.81	-2.46	-0.23	-0.47	-	3.51	down	0.28	1.030E-10	5.49	down	0.18	7.720E-08	1.17	down	0.85	1.000E+00	1.39	down	0.72	1.000E+00
SAOUMSC_02727		hypothetical protein		1.19	-0.49	-0.16	-0.25	-	2.28	down	0.44	1.400E-08	1.40	down	0.71	1.000E+00	1.11	down	0.90	1.000E+00	1.19	down	0.84	1.000E+00
SAOUMSC_02761		hypothetical protein		0.89	-0.57	-0.49	-0.86	▼	1.86	down	0.54	1.629E-04	1.49	down	0.67	1.000E+00	1.41	down	0.71	1.000E+00	1.82	down	0.55	1.820E-09
SAOUMSC_02811	RaIP	hypothetical protein		1.38	-1.10	-1.22	-1.21	▼	2.61	down	0.38	7.650E-08	2.15	down	0.47	5.370E-08	2.33	down	0.43	5.316E-02	2.32	down	0.43	1.054E-03
SAOUMSC_02820		hypothetical protein		1.45	2.08	0.88	0.91	▲	2.72	up	2.72	4.660E-06	4.22	up	4.22	1.850E-10	1.84	up	1.84	7.752E-02	1.87	up	1.87	3.654E-04
SAOUMSC_02829	Frp	NAD(P)H flavin oxidoreductase		0.70	0.04	1.42	1.67	▲	1.62	up	1.62	2.438E-01	1.03	up	1.03	1.000E+00	2.67	up	2.67	3.126E-09	3.19	up	3.19	9.180E-16
SAOUMSC_02846		hypothetical protein		-1.26	-1.38	0.56	-0.96	-	2.40	down	0.42	5.220E-08	2.60	down	0.38	2.426E-02	1.47	up	1.47	1.000E+00	1.95	down	0.51	1.526E-01
SAOUMSC_02862	CipL	ATP-dependent Cip protease, ATP-binding subunit CipC		-0.46	-1.09	0.21	0.46	-	1.38	down	0.73	1.000E+00	2.13	down	0.47	1.019E-02	1.15	up	1.15	1.000E+00	1.38	up	1.38	1.000E+00
SAOUMSC_02866		hypothetical protein		2.01	2.10	n.d.	0.96	▲	4.03	up	4.03	7.290E-07	4.29	up	4.29	7.070E-07					1.95	up	1.95	1.327E-04
SAOUMSC_02886		hypothetical protein		1.73	1.67	n.d.	n.d.	-	3.33	up	3.33	3.273E-03	3.17	up	3.17	2.617E-04								
SAOUMSC_02887	IsaA	immunodominant antigen A		0.50	-0.38	0.81	0.59	▲	1.41	up	1.41	1.000E+00	1.30	down	0.77	1.000E+00	1.75	up	1.75	2.490E-03	1.50	up	1.50	1.000E+00
SAOUMSC_02899		hypothetical protein		0.54	0.19	0.72	0.90	▲	1.46	up	1.46	1.000E+00	1.14	up	1.14	1.000E+00	1.65	up	1.65	2.744E-02	1.86	up	1.86	1.050E-09
SAOUMSC_02900		hypothetical protein		1.15	0.30	0.91	1.16	▲	2.22	up	2.22	7.390E-15	1.23	up	1.23	1.000E+00	1.88	up	1.88	3.986E-09	2.23	up	2.23	1.796E-15
SAOUMSC_02910		hypothetical protein		-0.94	-1.11	-0.85	-0.84	▼	1.92	down	0.52	1.520E-01	2.16	down	0.46	3.441E-03	1.57	down	0.64	1.000E+00	1.10	down	1.10	1.000E+00
SAOUMSC_02940		precursor 2 dehydrogenase		-0.78	-0.50	n.d.	0.34	-	1.72	down	0.58	3.743E-02	1.42	down	0.71	1.000E+00					1.10	up	1.10	1.000E+00
SAOUMSC_02955	NusS	nitro susceptibility-associated sensor histidine kinase		-0.95	-0.25	n.d.	-0.68	▼	1.93	down	0.52	4.280E-02	1.19	down	0.84	1.000E+00					1.60	down	0.62	1.000E+00
SAOUMSC_02961		hypothetical protein		-0.90	-0.68	-0.08	-0.24	-	1.87	down	0.53	1.304E-02	1.60	down	0.62	1.000E+00	1.05	down	0.95	1.000E+00	1.18	down	0.85	1.000E+00
SAOUMSC_02972	IsaB	immunodominant antigen B		-1.05	-2.44	1.24	1.53	▲	8.51	down	0.12	1.690E-03	5.42	down	0.18	4.633E-02	2.36	up	2.36	3.410E-06	2.88	up	2.88	1.020E-12
SAOUMSC_02978		phage infection protein		0.45	0.73	0.33	-0.29	-	1.37	up	1.37	1.000E+00	1.66	up	1.66	1.350E-07	1.26	down	0.80	1.000E+00	1.23	down	0.82	1.000E+00
SAOUMSC_02979		N-acetylmuramoyl-L-alanine amidase		-0.12	0.53	1.36	0.82	▲	1.08	down	0.92	1.000E+00	1.44	up	1.44	1.000E+00	2.57	up	2.57	2.013E-02	1.76	up	1.76	2.076E-01
SAOUMSC_03022		hypothetical protein		1.09	0.69	1.37	1.65	▲	2.12	up	2.12	3.540E-06	1.61	up	1.61	3.547E-01	2.58	up	2.58	1.469E-04	3.13	up	3.13	3.470E-12
SAOUMSC_03034		hypothetical protein		-0.41	-1.62	0.80	0.80	▲	1.32	down	0.76	1.000E+00	3.07	down	0.33	8.400E-07	1.74	up	1.74	5.051E-02	1.74	up	1.74	8.000E-06



supplemental table S6: Detected proteins with at least 2 peptides: murine pneumonia model and S9 cell line infection model (log2 ratios to controls [non-adherent or pre-infection])

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_00069	Spa	protein A	Adhesion	0.56	-3.90	-0.79	-2.21	-5.33	-3.44	n.d.	▼	▼
SAOUHSC_00487	HslO	Hsp33-like chaperonin	Adhesion	0.23	-0.15	-0.97	-0.85	-0.26	-0.82	-0.69	▼	▼
SAOUHSC_01501	EbpS	elastin binding protein	Adhesion	0.12	0.47	0.47	0.62	-0.37	-0.30	-0.34	—	—
SAOUHSC_02161	Eap I map	MHC class II analog protein	Adhesion	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	2.50	n.d.	▲
SAOUHSC_02982		hypothetical protein	Adhesion	0.40	0.16	-1.35	2.91	n.d.	n.d.	1.03	—	▲
SAOUHSC_00836	GcvH	glycine cleavage system protein H	Alanine, serine, and glycine;Alanine, serine, and glycine	0.32	0.23	0.51	0.70	0.80	2.23	2.20	—	▲
SAOUHSC_01633	GcvPA	glycine dehydrogenase subunit 1	Alanine, serine, and glycine;Alanine, serine, and glycine	-0.57	0.34	0.55	0.61	-0.36	-0.10	0.42	—	—
SAOUHSC_01634	GcvT	glycine cleavage system aminomethyltransferase T	Alanine, serine, and glycine;Alanine, serine, and glycine	-0.49	0.27	0.60	0.81	0.24	0.31	0.29	▲	—
SAOUHSC_02354	GlyA	serine hydroxymethyltransferase	Alanine, serine, and glycine;Alanine, serine, and glycine;Folate and pterines;One-carbon Metabolism;Stress Response - no subcategory;Alanine, serine, and glycine;Alanine, serine, and glycine	-0.39	0.11	-0.16	-0.21	0.61	0.06	-0.29	—	—
SAOUHSC_02305	Alr	alanine racemase	Alanine, serine, and glycine;Central carbohydrate metabolism;RNA processing and modification	-0.16	-0.32	-1.20	-0.89	1.19	3.52	3.88	▼	▲
SAOUHSC_00532	Kbl	2-amino-3-ketobutyrate coenzyme A ligase	Alanine, serine, and glycine;Lysine, threonine, methionine, and cysteine;Alanine, serine, and glycine	0.07	0.42	0.39	0.79	-0.03	-0.14	0.23	—	—
SAOUHSC_00009	SerS	seryl-tRNA synthetase	Alanine, serine, and glycine;Protein biosynthesis	0.25	0.69	0.15	0.16	-0.96	-0.27	-0.77	—	▼
SAOUHSC_01617	ArgR	arginine repressor	Arginine; urea cycle, polyamines;Arginine; urea cycle, polyamines;Arginine; urea cycle, polyamines	0.23	0.79	0.45	0.58	-1.13	-0.40	-0.48	▲	—
SAOUHSC_00894	RocD	ornithine--oxo-acid transaminase	Arginine; urea cycle, polyamines;Arginine; urea cycle, polyamines;Proline and 4-hydroxyproline	0.58	1.59	2.64	2.91	0.25	0.89	1.18	▲	▲
SAOUHSC_01702	MtnN	MTA/SAH nucleosidase	Arginine; urea cycle, polyamines;Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.45	0.30	-0.30	-0.09	-0.91	1.16	-0.75	—	▼
SAOUHSC_01483	AroC	chorismate synthase	Aromatic amino acids and derivatives;Aromatic amino acids and derivatives	0.11	-0.08	0.00	-0.01	-0.07	0.08	-0.79	—	—
SAOUHSC_01852	AroA2	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase	Aromatic amino acids and derivatives;Aromatic amino acids and derivatives;Aromatic amino acids and derivatives	0.35	0.39	0.17	0.31	-0.39	-0.36	-0.33	—	—
SAOUHSC_02340	AtpC	FOF1 ATP synthase subunit epsilon	ATP synthases	-0.19	0.25	-0.27	-0.32	0.89	0.70	1.20	—	▲
SAOUHSC_02341	AtpD	FOF1 ATP synthase subunit beta	ATP synthases	-0.49	0.28	-0.12	-0.21	-0.31	-0.05	-0.69	—	—
SAOUHSC_02343	AtpG	FOF1 ATP synthase subunit gamma	ATP synthases	-0.55	0.17	-0.34	-0.26	0.01	0.07	0.00	—	—
SAOUHSC_02345	AtpA	FOF1 ATP synthase subunit alpha	ATP synthases	-0.47	0.18	-0.26	-0.41	-0.15	-0.10	-0.28	—	—
SAOUHSC_02346	AtpH	FOF1 ATP synthase subunit delta	ATP synthases	-0.18	0.39	-0.17	-0.22	-1.01	-0.91	-1.20	—	▼
SAOUHSC_02347	AtpF	FOF1 ATP synthase subunit B	ATP synthases	-0.43	0.35	0.40	-0.06	-0.41	-0.29	-0.39	—	—
SAOUHSC_01809	AccD	acetyl-CoA carboxylase subunit beta	Bacteriocins, ribosomally synthesized antibacterial peptides;Fatty acids	0.06	-0.28	-0.43	-0.39	1.59	0.03	-0.26	—	—
SAOUHSC_01014	PurF	amidophosphoribosyltransferase	Bacteriocins, ribosomally synthesized antibacterial peptides;Purines	-0.07	0.54	-1.00	-0.81	-0.23	0.51	1.02	▼	—
SAOUHSC_02714	BioB	biotin synthase	Biotin	1.45	0.57	-2.17	-1.84	-2.89	-1.90	-2.63	▼	▼
SAOUHSC_02715	BioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Biotin	1.07	0.89	0.64	0.36	-0.27	-0.08	-0.18	▲	—
SAOUHSC_02716	BioD	dethiobiotin synthase	Biotin	1.06	0.72	-0.11	-0.37	0.03	-2.46	n.d.	—	▼
SAOUHSC_00336	Thi	acetyl-CoA acetyltransferase	Biotin;Fermentation;Isoprenoids;Isoprenoids;Fatty Acids, Lipids, and Isoprenoids - no subcategory;One-carbon Metabolism;Fermentation;Branched-chain amino acids	-0.14	0.81	-0.11	-0.18	-0.33	-0.23	0.06	—	—
SAOUHSC_01612	BfmBAB	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	Branched-chain amino acids;Central carbohydrate metabolism;Branched-chain amino acids	-0.34	-0.08	-0.22	-0.23	0.21	0.22	0.08	—	—
SAOUHSC_01613	BfmBAA	2-oxoisovalerate dehydrogenase, E1 component subunit alpha	Branched-chain amino acids;Central carbohydrate metabolism;Branched-chain amino acids	-0.43	-0.19	-0.65	-0.58	-0.35	-0.18	-0.83	▼	—
SAOUHSC_00471	GlmU	bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase	Capsular and extracellular polysacchrides;Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory	-0.30	-0.02	-0.73	-0.62	-1.24	0.04	1.01	▼	—
SAOUHSC_02399	GlmS	glucosamine-fructose-6-phosphate aminotransferase	Capsular and extracellular polysacchrides;Cell Wall and Capsule - no subcategory;One-carbon Metabolism	-0.16	-0.38	-0.47	-0.51	0.55	0.18	1.18	—	—
SAOUHSC_01149	FtsA	cell division protein	Cell Division and Cell Cycle - no subcategory	0.25	0.23	0.07	0.15	-0.21	-0.28	-0.16	—	—
SAOUHSC_01150	FtsZ	cell division protein FtsZ	Cell Division and Cell Cycle - no subcategory	0.13	0.02	-0.28	-0.34	0.06	0.19	0.03	—	—
SAOUHSC_01158		hypothetical protein	Cell Division and Cell Cycle - no subcategory	0.30	0.07	0.07	0.32	0.10	-0.48	-0.31	—	—
SAOUHSC_01253	FtsK	hypothetical protein	Cell Division and Cell Cycle - no subcategory	-0.34	-0.30	-0.41	-0.30	4.05	-0.06	n.d.	—	▲
SAOUHSC_01460		hypothetical protein	Cell Division and Cell Cycle - no subcategory	-0.02	-0.15	-0.40	-0.16	0.12	-0.09	0.87	—	—
SAOUHSC_01462	GpsB	hypothetical protein	Cell Division and Cell Cycle - no subcategory	0.44	0.32	0.04	0.18	-0.83	-0.48	-0.49	—	—
SAOUHSC_01827	EzrA	septation ring formation regulator EzrA	Cell Division and Cell Cycle - no subcategory	-0.32	-0.63	-0.20	-0.08	0.16	-0.41	0.03	—	—
SAOUHSC_03049		hypothetical protein	Cell Division and Cell Cycle - no subcategory;Cell Division and Cell Cycle - no subcategory	0.07	0.25	-0.22	-0.16	-0.45	-0.30	-0.09	—	—
SAOUHSC_01205	FtsY	signal recognition particle-docking protein FtsY	Cell Division and Cell Cycle - no subcategory;Protein biosynthesis	0.21	0.14	-0.02	0.23	n.d.	-0.39	0.04	—	—
SAOUHSC_01424	MurG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	Cell Wall and Capsule - no subcategory	0.03	-0.63	-0.15	-0.10	0.67	0.17	-0.24	—	—
SAOUHSC_00752	MurB	UDP-N-acetylenolpyruvoylglucosamine reductase	Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory	0.37	0.09	0.10	-0.02	-0.67	-0.16	-0.14	—	—
SAOUHSC_02318	Ddl	D-alanyl-alanine synthetase A	Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory	0.15	0.60	0.57	0.45	-1.45	-0.54	0.67	—	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_02337	MurA1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory	-0.17	-0.39	-0.56	-0.56	-0.54	-0.41	-0.44	—	—
SAOUHSC_02365	MurA2	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory	-0.05	1.27	0.29	0.26	n.d.	0.69	1.06	—	▲
SAOUHSC_02423		UDP-N-acetylglucosamine pyrophosphorylase	Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory	0.45	0.57	0.17	0.36	0.25	-0.27	-0.04	—	—
SAOUHSC_02317	MurF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	Cell Wall and Capsule - no subcategory;Cell Wall and Capsule - no subcategory;Resistance to antibiotics and toxic compounds	-0.04	0.22	-0.18	-0.24	-1.78	0.37	-0.87	—	▼
SAOUHSC_01373	FemA	methicillin resistance factor, FemA	Cell Wall and Capsule - no subcategory;Resistance to antibiotics and toxic compounds	-0.28	-0.56	-0.66	-0.62	-0.14	0.02	0.36	▼	—
SAOUHSC_01374	FemB	methicillin resistance factor	Cell Wall and Capsule - no subcategory;Resistance to antibiotics and toxic compounds	-0.27	-0.29	-0.25	-0.46	0.56	0.21	-0.11	—	—
SAOUHSC_02405	GlmM	phosphoglucosamine mutase	Cell Wall and Capsule - no subcategory;Resistance to antibiotics and toxic compounds;Capsular and extracellular polysacchrides	0.43	0.02	-0.11	-0.01	-0.58	-0.56	-0.44	—	—
SAOUHSC_00796	Pgk	phosphoglycerate kinase	Central carbohydrate metabolism	0.21	-0.09	-0.49	-0.40	0.01	-0.17	-0.33	—	—
SAOUHSC_00798	Pgm	phosphoglyceromutase	Central carbohydrate metabolism	-0.36	-0.30	-0.91	-0.74	-0.30	-0.28	-0.35	▼	—
SAOUHSC_01064	PycA	pyruvate carboxylase	Central carbohydrate metabolism	-0.21	0.42	0.07	0.06	0.28	0.37	0.61	—	—
SAOUHSC_01337	Tkt	transketolase	Central carbohydrate metabolism	0.37	0.83	0.14	0.31	-0.30	-0.37	-0.27	—	—
SAOUHSC_01646	Gik	glucokinase	Central carbohydrate metabolism	0.25	0.35	-0.01	-0.00	1.44	-0.73	-0.78	—	▼
SAOUHSC_01801	CitC	isocitrate dehydrogenase	Central carbohydrate metabolism	0.25	0.77	2.02	2.45	0.86	0.18	1.03	▲	▲
SAOUHSC_01810		NADP-dependent malic enzyme	Central carbohydrate metabolism	0.13	-0.29	-0.26	-0.12	0.63	-0.29	-0.45	—	—
SAOUHSC_01818	Ald2	alanine dehydrogenase	Central carbohydrate metabolism	0.09	0.36	1.09	1.44	-0.54	0.98	n.d.	▲	—
SAOUHSC_01867	Dat	D-alanine aminotransferase	Central carbohydrate metabolism	0.30	0.90	0.41	0.39	0.40	0.40	-0.20	—	—
SAOUHSC_01983	FumC	fumarate hydratase	Central carbohydrate metabolism	0.24	0.77	1.35	1.45	1.12	1.25	1.30	▲	▲
SAOUHSC_02647	Mqo1	malate:quinone oxidoreductase	Central carbohydrate metabolism	-0.18	0.16	1.01	1.05	1.49	1.14	-0.30	▲	▲
SAOUHSC_02703	GpmA	phosphoglyceromutase	Central carbohydrate metabolism	0.41	0.32	-0.26	0.04	0.37	0.37	0.23	—	—
SAOUHSC_02927	Lqo	malate:quinone oxidoreductase	Central carbohydrate metabolism	-0.20	0.26	0.20	0.25	-0.02	-0.01	-0.57	—	—
SAOUHSC_01611	BmfBB	2-oxoisovalerate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	Central carbohydrate metabolism;Branched-chain amino acids;Branched-chain amino acids;Lipoic acid	-0.19	0.04	-0.25	-0.09	-0.13	0.39	n.d.	—	—
SAOUHSC_00536	IlvE	branched-chain amino acid aminotransferase	Central carbohydrate metabolism;Branched-chain amino acids;Central carbohydrate metabolism;Branched-chain amino acids;Branched-chain amino acids;Alanine, serine, and glycine;Branched-chain amino acids	0.75	1.27	0.82	0.98	0.15	-0.08	0.49	▲	—
SAOUHSC_00797	TpiA	triosephosphate isomerase	Central carbohydrate metabolism;Central carbohydrate metabolism	0.86	0.05	-0.34	-0.32	-0.22	-0.66	-0.78	—	▼
SAOUHSC_01040	PdhA	pyruvate dehydrogenase complex, E1 component subunit alpha	Central carbohydrate metabolism;Central carbohydrate metabolism	-0.55	-0.07	-0.57	-0.52	-0.43	-1.15	-1.68	—	▼
SAOUHSC_01041	PdhB	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit	Central carbohydrate metabolism;Central carbohydrate metabolism	-0.54	-0.20	-0.44	-0.49	-0.04	0.78	-0.26	—	—
SAOUHSC_01418	SucA	2-oxoglutarate dehydrogenase E1 component	Central carbohydrate metabolism;Central carbohydrate metabolism	-0.35	0.45	1.24	1.54	n.d.	2.92	1.78	▲	▲
SAOUHSC_01043	PdhD	dihydrolipoamide dehydrogenase	Central carbohydrate metabolism;Central carbohydrate metabolism;Central carbohydrate metabolism	-0.60	-0.12	-0.75	-0.55	-0.19	-0.20	-0.26	—	—
SAOUHSC_01218	SucD	succinyl-CoA synthetase subunit alpha	Central carbohydrate metabolism;Central carbohydrate metabolism;One-carbon Metabolism	0.16	0.20	1.01	1.27	-1.12	0.04	-0.15	▲	—
SAOUHSC_00574	EutD	phosphotransacetylase	Central carbohydrate metabolism;Fermentation;Fermentation	0.33	0.67	0.11	0.21	-0.44	-0.57	-0.60	—	—
SAOUHSC_01416	SucB	dihydrolipoamide succinyltransferase	Central carbohydrate metabolism;Lipoic acid;Central carbohydrate metabolism	-0.44	0.64	1.61	1.86	1.43	2.32	1.52	▲	▲
SAOUHSC_00553	HxlA	hypothetical protein	Central carbohydrate metabolism;One-carbon Metabolism	1.08	0.38	-0.07	0.12	-0.66	-0.59	-1.22	—	▼
SAOUHSC_02143		hypothetical protein	Central carbohydrate metabolism;One-carbon Metabolism	0.53	0.79	0.54	0.66	0.41	0.42	0.26	▲	—
SAOUHSC_01216	SucC	succinyl-CoA synthetase subunit beta	Central carbohydrate metabolism;One-carbon Metabolism;Central carbohydrate metabolism	-0.04	0.13	1.01	1.11	-0.39	-0.01	-0.60	▲	—
SAOUHSC_00866		D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein	Central carbohydrate metabolism;Organic acids	0.19	0.36	0.30	0.31	0.79	2.93	2.55	—	▲
SAOUHSC_02577		D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein	Central carbohydrate metabolism;Organic acids	0.32	1.12	2.01	2.18	0.51	1.12	0.49	▲	—
SAOUHSC_01806	PykA	pyruvate kinase	Central carbohydrate metabolism;Organic acids;Central carbohydrate metabolism;Fermentation	0.06	0.36	-0.15	-0.18	-0.64	0.06	-0.38	—	—
SAOUHSC_00795	GapA	glyceraldehyde 3-phosphate dehydrogenase, type I	Central carbohydrate metabolism;Oxidative stress;Oxidative stress;Pyridoxine	0.38	-0.07	-0.59	-0.43	4.40	4.32	4.02	—	▲
SAOUHSC_02142	AldH	aldehyde dehydrogenase	Central carbohydrate metabolism;Phospholipids;Central carbohydrate metabolism	0.12	0.67	1.20	1.43	-1.40	-0.40	-0.13	▲	—
SAOUHSC_02849	CidC	pyruvate oxidase	Central carbohydrate metabolism;Programmed Cell Death and Toxin-antitoxin Systems	0.19	-1.07	-0.48	-0.32	-0.68	-0.04	-0.51	—	—
SAOUHSC_01178	CoaBC	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	Coenzyme A	-0.32	-0.15	-0.19	-0.28	n.d.	-0.03	0.78	—	—
SAOUHSC_02918	PanC	pantoate--beta-alanine ligase	Coenzyme A	-0.34	-0.42	-1.28	-1.41	n.d.	1.63	0.77	▼	▲
SAOUHSC_02919	PanB	3-methyl-2-oxobutanoate hydroxymethyltransferase	Coenzyme A	-0.04	0.27	-0.71	-0.64	-0.86	-0.30	-1.02	▼	▼
SAOUHSC_00819	CspC	hypothetical protein	Cold shock	-0.63	0.05	-1.20	-1.27	0.57	-0.23	-1.13	▼	—
SAOUHSC_01403	CspA	cold shock protein	Cold shock	0.35	2.14	1.95	2.15	3.79	3.02	2.95	▲	▲
SAOUHSC_02791		pyrophosphohydrolase	Detoxification	0.57	0.68	0.29	0.50	-0.55	-0.76	n.d.	—	▼
SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr) deacylase	Detoxification;Regulation and Cell signaling - no subcategory;Organic sulfur assimilation	0.84	0.21	0.20	0.17	-0.73	0.03	n.d.	—	—
SAOUHSC_00155	GlcA	PTS system glucose-specific protein	Di- and oligosaccharides	-0.64	-0.31	-0.17	-0.15	0.13	-0.34	-1.14	—	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA	Di- and oligosaccharides	0.59	2.32	1.47	1.59	0.17	-0.52	-0.58	▲	—
SAOUHSC_02268	ScrB	sucrose-6-phosphate hydrolase	Di- and oligosaccharides	0.23	0.35	0.05	0.16	0.53	-0.15	n.d.	—	—
SAOUHSC_02848	GlcB	PTS system glucose-specific transporter subunit IIB/C	Di- and oligosaccharides	-0.08	0.50	0.79	0.82	-0.75	0.60	0.47	▲	—
SAOUHSC_01490	Hup	DNA-binding protein HU	DNA Metabolism - no subcategory	0.21	-0.05	-0.01	-0.04	-0.80	0.21	0.74	—	—
SAOUHSC_01472	DinG	DnaQ family exonuclease/DinG family helicase	DNA repair	-0.06	0.23	-0.02	0.05	3.60	0.30	1.88	—	▲
SAOUHSC_01620	XseA	exodeoxyribonuclease VII large subunit	DNA repair	-0.23	-0.26	-0.34	0.09	n.d.	0.12	n.d.	—	—
SAOUHSC_01975		hypothetical protein	DNA repair	-0.48	-0.41	-0.58	-0.58	0.54	0.41	0.06	▼	—
SAOUHSC_02123	PcrA	ATP-dependent DNA helicase PcrA	DNA repair	-0.53	-0.46	-0.74	-0.88	n.d.	-0.22	1.73	▼	▲
SAOUHSC_01262	RecA	recombinase A	DNA repair;DNA repair;Plant-Prokaryote comparative genomics;DNA replication;DNA repair	-0.34	-0.61	-0.61	-0.54	0.16	-0.03	-0.34	▼	—
SAOUHSC_01615	RecN	DNA repair protein RecN	DNA repair;DNA replication	-0.26	0.40	0.23	0.17	-0.34	1.46	0.14	—	—
SAOUHSC_00001	DnaA	chromosomal replication initiation protein	DNA replication	-0.46	-0.24	-0.03	-0.19	n.d.	0.82	-0.16	—	—
SAOUHSC_00002	DnaN	DNA polymerase III subunit beta	DNA replication	-0.04	0.50	0.48	0.52	0.63	-0.09	-0.09	—	—
SAOUHSC_01241	PolC	DNA polymerase III PolC	DNA replication	-0.45	-0.01	-0.68	-0.84	0.28	-0.07	n.d.	▼	—
SAOUHSC_01791	DnaI	primosomal protein DnaI	DNA replication	0.09	0.03	0.40	0.37	n.d.	n.d.	0.53	—	—
SAOUHSC_01797	PolA	DNA polymerase I	DNA replication;DNA repair	-0.15	0.29	-0.11	0.06	-1.00	-0.18	-0.63	—	▼
SAOUHSC_00442	DnaX	DNA polymerase III subunits gamma and tau	DNA replication;DNA uptake, competence	-0.26	-0.03	-0.48	-0.53	-0.93	-0.11	1.20	—	—
SAOUHSC_00005	GyrB	DNA gyrase, B subunit	DNA replication;Resistance to antibiotics and toxic compounds	-0.37	-0.07	-0.41	-0.33	2.98	-0.73	0.37	—	—
SAOUHSC_00006	GyrA	DNA gyrase, A subunit	DNA replication;Resistance to antibiotics and toxic compounds	-0.48	-0.11	-0.38	-0.37	0.50	-0.06	0.26	—	—
SAOUHSC_01351	ParE	DNA topoisomerase IV subunit B	DNA replication;Resistance to antibiotics and toxic compounds	-0.36	-0.74	-0.96	-0.82	0.85	0.02	0.78	▼	▲
SAOUHSC_01352	ParC	DNA topoisomerase IV subunit A	DNA replication;Resistance to antibiotics and toxic compounds	-0.32	-0.33	-0.77	-0.65	1.44	-0.01	n.d.	▼	▲
SAOUHSC_02517	TopB	DNA topoisomerase III	DNA uptake, competence	-0.14	-1.04	-1.28	-1.77	n.d.	-0.61	6.00	▼	▲
SAOUHSC_00444		hypothetical protein	DNA uptake, competence;DNA repair	-0.24	0.35	-0.29	-0.37	1.76	1.94	2.17	—	▲
SAOUHSC_00469	SpoVG	regulatory protein SpoVG	Dormancy and Sporulation - no subcategory	0.11	-0.80	-0.64	-0.09	-0.33	-0.80	-0.61	▼	▼
SAOUHSC_00483		hypothetical protein	Dormancy and Sporulation - no subcategory	-0.20	-0.47	-0.60	-0.84	0.16	-0.40	-0.42	▼	—
SAOUHSC_00480		hypothetical protein	Dormancy and Sporulation - no subcategory;Detoxification	-0.03	0.19	-0.51	-0.51	-1.26	-0.77	5.62	—	▼
SAOUHSC_00477	Mfd	transcription-repair coupling factor	Dormancy and Sporulation - no subcategory;DNA replication;Transcription	-0.04	-0.21	0.05	-0.13	n.d.	0.70	n.d.	—	▲
SAOUHSC_00481		hypothetical protein	Dormancy and Sporulation - no subcategory;Heat shock	0.91	0.52	0.06	-0.07	-0.48	-0.82	-0.92	—	▼
SAOUHSC_01002	QoxA	quinol oxidase AA3 subunit II	Electron accepting reactions	-0.48	-0.46	-0.26	-0.23	-0.41	-1.03	0.06	—	—
SAOUHSC_00875		hypothetical protein	Electron donating reactions	0.27	-0.44	-0.11	0.16	-0.83	-0.07	-0.10	—	—
SAOUHSC_00878	Ndh2	hypothetical protein	Electron donating reactions	-0.18	-0.28	-0.28	-0.29	0.77	0.55	0.30	—	—
SAOUHSC_01104	SdhA	succinate dehydrogenase flavoprotein subunit	Electron donating reactions;Central carbohydrate metabolism;One-carbon Metabolism	0.24	0.10	1.13	1.24	0.44	0.69	0.26	▲	—
SAOUHSC_00920	FabH	3-oxoacyl-(acyl carrier protein) synthase III	Fatty acids	-1.39	-0.86	-0.96	-0.77	n.d.	-0.89	-1.49	▼	▼
SAOUHSC_00921	FabF	3-oxoacyl- synthase	Fatty acids	-0.92	-0.52	-0.61	-0.37	0.04	-0.16	-0.52	—	—
SAOUHSC_00947	FabI	enoyl-(acyl carrier protein) reductase	Fatty acids	-0.13	-0.01	-0.32	-0.29	-0.49	0.03	-0.47	—	—
SAOUHSC_01198	FabD	malonyl CoA-acyl carrier protein transacylase	Fatty acids	-0.59	-0.26	-0.57	-0.26	-0.40	-0.18	-0.73	—	—
SAOUHSC_01199	FabG	3-oxoacyl-(acyl-carrier-protein) reductase	Fatty acids	-0.24	-0.15	-0.29	-0.08	0.51	-0.36	-0.95	—	—
SAOUHSC_01808	AccA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	Fatty acids	0.01	-0.19	-0.13	-0.27	n.d.	0.02	n.d.	—	—
SAOUHSC_01623	AccC	acetyl-CoA carboxylase biotin carboxylase subunit	Fatty acids;Miscellaneous - no subcategory	-0.07	0.09	-0.51	-0.36	0.17	-0.54	1.00	—	—
SAOUHSC_00086	ButA	acetoin reductase	Fermentation	0.82	2.29	3.34	3.68	3.11	2.73	3.09	▲	▲
SAOUHSC_00206	Ldh1	L-lactate dehydrogenase	Fermentation;Fermentation	-1.15	-0.25	-2.09	-2.87	0.44	0.64	0.61	▼	▲
SAOUHSC_02830	Ddh	D-lactate dehydrogenase	Fermentation;Fermentation	0.59	0.31	-0.19	-0.19	0.59	-0.16	-0.53	—	—
SAOUHSC_02922	Ldh2	L-lactate dehydrogenase	Fermentation;Fermentation	0.51	0.89	0.25	0.35	-0.13	-0.04	-0.02	—	—
SAOUHSC_01820	AckA	acetate kinase	Fermentation;Fermentation;Central carbohydrate metabolism	-0.45	-0.60	-0.73	-0.64	-0.44	-0.05	-0.58	▼	—
SAOUHSC_00608	Adh	alcohol dehydrogenase	Fermentation;Fermentation;Phospholipids	-1.11	0.89	-0.40	-0.54	1.10	0.69	n.d.	—	▲
SAOUHSC_00187	PflB	formate acetyltransferase	Fermentation;Fermentation;Respiration - no subcategory	-2.19	2.07	1.19	0.75	1.12	1.65	1.12	▲	▲
SAOUHSC_02544	MoaB	molybdopterin precursor biosynthesis moaB	Folate and pterines	0.31	0.37	0.51	0.69	0.81	0.43	0.37	—	—
SAOUHSC_00549	FolE2	putative GTP cyclohydrolase	Folate and pterines;RNA processing and modification	0.87	-0.27	-0.40	-0.01	0.70	0.39	0.67	—	▲
SAOUHSC_01497	AnsA	L-asparaginase	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	0.03	0.08	-0.49	-0.35	1.24	0.23	n.d.	—	▲

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				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_01106	MurI	glutamate racemase	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation;Cell Wall and Capsule - no subcategory	-0.18	0.10	-0.26	-0.16	n.d.	0.91	-0.78	—	—
SAOUHSC_00895	GudB	glutamate dehydrogenase, NAD-specific	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation;Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	-0.36	1.13	1.76	2.09	3.19	0.94	2.06	▲	▲
SAOUHSC_00223	TarF	teichoic acid biosynthesis protein F	Gram-Positive cell wall components	0.03	-0.12	0.12	-0.06	-0.31	2.19	-1.53	—	—
SAOUHSC_00641	TagH	teichoic acids export protein ATP-binding subunit	Gram-Positive cell wall components	-0.57	-0.63	-0.75	-0.74	0.17	n.d.	-1.63	▼	▼
SAOUHSC_00974		glycosyl transferase, group 1	Gram-Positive cell wall components	-0.13	-1.15	-0.18	-0.16	n.d.	1.57	n.d.	—	▲
SAOUHSC_00872	DltD	extramembranal protein	Gram-Positive cell wall components;Gram-Positive cell wall components;Resistance to antibiotics and toxic compounds	-0.60	-1.20	-0.44	-0.40	-0.25	-0.49	n.d.	—	—
SAOUHSC_00225	TarI	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Gram-Positive cell wall components;Plant-Prokaryote comparative genomics;Isoprenoids	0.76	0.37	0.44	0.62	-0.53	-0.28	-0.43	—	—
SAOUHSC_01683	DnaK	molecular chaperone DnaK	Heat shock;Protein folding	0.20	-0.37	-0.01	0.30	0.01	0.22	0.10	—	—
SAOUHSC_02610	HutG	formimidoylglutamate	Histidine Metabolism	0.49	-0.05	n.d.	0.56	1.09	-0.69	n.d.	—	—
SAOUHSC_01738	HisS	histidyl-tRNA synthetase	Histidine Metabolism;Organic sulfur assimilation;Regulation and Cell signaling - no subcategory	-0.16	-0.50	-1.03	-0.89	-1.20	-0.87	-1.08	▼	▼
SAOUHSC_00749	SstD	hypothetical protein	Iron acquisition and metabolism - no subcategory;Iron acquisition and metabolism - no subcategory	-2.15	-0.27	-0.81	-1.18	-0.21	n.d.	n.d.	▼	—
SAOUHSC_00579	MvaK2	phosphomevalonate kinase	Isoprenoids;Isoprenoids	-0.17	0.08	0.07	0.00	-1.30	0.37	1.18	—	—
SAOUHSC_02859	MvaA	hydroxymethylglutaryl-CoA reductase, degradative	Isoprenoids;Isoprenoids	-0.17	-0.26	-0.36	-0.11	n.d.	2.61	0.21	—	▲
SAOUHSC_02860	MvaS	HMG-CoA synthase	Isoprenoids;Isoprenoids	0.35	1.06	0.40	0.45	-0.02	0.16	0.01	—	—
SAOUHSC_01042	PdhC	branched-chain alpha-keto acid dehydrogenase subunit E2	Lipoic acid;Central carbohydrate metabolism;Central carbohydrate metabolism	-0.41	-0.06	-0.40	-0.31	0.78	0.08	0.32	—	—
SAOUHSC_00348	MetE	5-methyltetrahydropteroylglutamate-homocysteine S-methyltransferase	Lysine, threonine, methionine, and cysteine	0.47	0.69	0.79	1.21	n.d.	2.73	3.10	▲	▲
SAOUHSC_01321	ThrC	threonine synthase	Lysine, threonine, methionine, and cysteine	0.98	0.91	1.19	1.11	1.44	1.57	2.25	▲	▲
SAOUHSC_01398	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	Lysine, threonine, methionine, and cysteine	0.80	3.97	3.69	3.89	n.d.	2.09	n.d.	▲	▲
SAOUHSC_01401	LysA	diaminopimelate decarboxylase	Lysine, threonine, methionine, and cysteine	0.83	1.45	1.23	1.25	-0.62	0.26	0.09	▲	—
SAOUHSC_00488	CysK	hypothetical protein	Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.38	0.55	0.66	0.76	-0.73	-0.49	0.14	▲	—
SAOUHSC_01320	Hom	homoserine dehydrogenase	Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.75	0.64	1.11	1.20	1.64	1.64	1.81	▲	▲
SAOUHSC_01395	Asd	aspartate semialdehyde dehydrogenase	Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.51	3.31	3.45	3.51	1.63	1.44	2.06	▲	▲
SAOUHSC_01909	MetK	S-adenosylmethionine synthetase	Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.24	-0.29	-0.04	-0.07	0.32	-0.22	0.08	—	—
SAOUHSC_02579		hypothetical protein	Metabolism of Aromatic Compounds - no subcategory;Metabolism of central aromatic intermediates;Peripheral pathways for catabolism of aromatic compounds	-0.33	-0.28	-0.14	-0.38	0.23	-0.16	n.d.	—	—
SAOUHSC_00906		hypothetical protein	Metabolism of central aromatic intermediates;Metabolism of Aromatic Compounds - no subcategory	0.64	0.65	0.41	0.55	0.49	0.30	0.52	—	—
SAOUHSC_01845	Fhs	formate-tetrahydrofolate ligase	Miscellaneous - no subcategory;One-carbon Metabolism;One-carbon Metabolism;Folate and pterines	-0.18	0.48	0.30	0.52	-0.33	0.11	-0.27	—	—
SAOUHSC_01018	PurD	phosphoribosylamine-glycine ligase	Miscellaneous - no subcategory;Purines	-0.29	0.03	-1.40	-1.11	-0.21	-0.29	-0.00	▼	—
SAOUHSC_02368	PyrG	CTP synthetase	Miscellaneous - no subcategory;Pyrimidines	-0.07	-0.55	-0.46	-0.40	-1.00	-0.45	-0.16	—	—
SAOUHSC_00101	DcoB	phosphopentomutase	Monosaccharides	0.45	0.35	0.30	0.77	0.14	0.05	-0.14	—	—
SAOUHSC_01907		hypothetical protein	Monosaccharides	0.11	1.41	1.95	2.08	n.d.	0.36	3.60	▲	▲
SAOUHSC_02793		hypothetical protein	Monosaccharides;Cell Wall and Capsule - no subcategory;Capsular and extracellular polysacchrides	0.10	0.91	0.21	0.42	n.d.	-0.18	n.d.	—	—
SAOUHSC_01807	PfkA	6-phosphofructokinase	Monosaccharides;Central carbohydrate metabolism	0.10	0.59	-0.04	-0.15	0.48	0.07	-0.45	—	—
SAOUHSC_01901	Tal	putative transaldolase	Monosaccharides;Central carbohydrate metabolism	0.63	0.74	0.25	0.15	-0.21	-0.43	-0.64	—	—
SAOUHSC_01028	PtsH	phosphocarrier protein HPr	Monosaccharides;Regulation and Cell signaling - no subcategory;Sugar alcohols	0.49	0.64	-0.02	-0.01	1.07	0.80	0.78	—	▲
SAOUHSC_01029	PtsI	phosphoenolpyruvate-protein phosphotransferase	Monosaccharides;Sugar alcohols	0.03	0.39	-0.25	-0.13	-0.80	-0.58	-0.77	—	▼
SAOUHSC_02132	NadE	NAD synthetase	NAD and NADP	0.53	0.70	0.07	0.41	0.33	-0.22	1.08	—	—
SAOUHSC_02122	LigA	DNA ligase, NAD-dependent	NAD and NADP;DNA repair	-0.11	0.05	0.01	-0.28	0.28	-0.28	0.04	—	—
SAOUHSC_01287	GlnA	glutamine synthetase, type I	Nitrogen Metabolism - no subcategory;Glutamine, glutamate, aspartate, asparagine; ammonia assimilation;Cell Wall and Capsule - no subcategory;Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	0.64	-0.02	-0.09	0.17	0.64	0.17	-0.01	—	—
SAOUHSC_00743	NrdF	ribonucleotide-diphosphate reductase subunit beta	Nucleosides and Nucleotides - no subcategory	0.80	-0.53	-1.29	-1.32	-1.20	-1.36	-1.53	▼	▼
SAOUHSC_01587	RluB	ribosomal large subunit pseudouridine synthase B	Nucleosides and Nucleotides - no subcategory;Cell Division and Cell Cycle - no subcategory	-0.22	-0.38	-0.99	-0.74	-0.47	-0.58	0.09	▼	—
SAOUHSC_00742	NrdE	ribonucleotide-diphosphate reductase subunit alpha	Nucleosides and Nucleotides - no subcategory;Oxidative stress	0.59	-0.97	-1.88	-1.94	-2.50	-2.12	-1.43	▼	▼
SAOUHSC_02828		hypothetical protein	One-carbon Metabolism	0.37	0.13	1.81	1.63	n.d.	1.36	1.40	▲	▲
SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase	One-carbon Metabolism;Central carbohydrate metabolism	-0.05	0.80	-0.10	0.09	0.25	2.15	2.40	—	▲
SAOUHSC_02366	FbaA	fructose-bisphosphate aldolase	One-carbon Metabolism;Central carbohydrate metabolism	0.04	0.52	-0.17	-0.10	-0.11	0.14	-0.15	—	—
SAOUHSC_02926	FdaB	fructose-1,6-bisphosphate aldolase	One-carbon Metabolism;Central carbohydrate metabolism	0.18	0.18	-0.08	0.23	-0.64	-0.41	-0.62	—	▼
SAOUHSC_00799	Eno	phosphopyruvate hydratase	One-carbon Metabolism;Central carbohydrate metabolism;Central carbohydrate metabolism	0.18	0.13	-0.23	-0.15	0.31	0.07	0.29	—	—
SAOUHSC_01599	Zwf	glucose-6-phosphate 1-dehydrogenase	One-carbon Metabolism;Central carbohydrate metabolism;Fermentation;Central carbohydrate metabolism	0.19	0.73	0.15	0.10	-0.49	-0.60	-0.26	—	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase	One-carbon Metabolism;Central carbohydrate metabolism;Monosaccharides	0.12	0.48	-0.15	0.02	-0.34	0.05	0.29	—	—
SAOUHSC_01007	FolD	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	One-carbon Metabolism;One-carbon Metabolism;Folate and pterines	0.39	0.73	0.41	0.61	0.20	0.28	-0.23	▲	—
SAOUHSC_01735		hypothetical protein	Organic sulfur assimilation	0.19	-0.08	-0.20	-0.02	n.d.	-0.13	0.36	—	—
SAOUHSC_01737	AspS	aspartyl-tRNA synthetase	Organic sulfur assimilation	0.03	-0.26	-0.40	-0.48	-0.16	-0.33	-0.27	—	—
SAOUHSC_02699	TcyA	hypothetical protein	Organic sulfur assimilation	-0.06	-0.08	0.25	0.31	0.01	-1.15	n.d.	—	—
SAOUHSC_00849	SufS	aminotransferase	Organic sulfur assimilation;Alanine, serine, and glycine	0.49	0.07	0.34	0.62	-0.49	-0.05	n.d.	—	—
SAOUHSC_00851	SufB	hypothetical protein	Organic sulfur assimilation;Phages, Prophages	0.16	-0.25	-0.25	-0.18	-0.80	-1.74	-1.20	—	▼
SAOUHSC_01346	OpuD1	glycine betaine transporter	Osmotic stress	0.02	-0.21	-0.10	-0.38	-0.29	-0.70	-1.22	—	▼
SAOUHSC_02932	BetA	choline dehydrogenase	Osmotic stress	0.42	-1.50	-0.77	-0.51	n.d.	n.d.	1.95	▼	▲
SAOUHSC_00757	PepT	peptidase T	Oxidative stress	0.04	0.40	0.26	0.47	-0.32	0.14	-0.17	—	—
SAOUHSC_00831	OsmC	hypothetical protein	Oxidative stress	1.06	-0.30	0.06	n.d.	4.34	0.72	0.58	—	▲
SAOUHSC_01282	BsaA	glutathione peroxidase	Oxidative stress	0.47	0.86	0.51	0.73	n.d.	n.d.	1.64	▲	▲
SAOUHSC_01592	Fur	transcriptional regulator, Fur	Oxidative stress	0.56	0.23	0.21	0.05	n.d.	0.83	-0.02	—	—
SAOUHSC_02273	Rex	redox-sensing transcriptional repressor Rex	Oxidative stress	0.06	0.06	0.09	-0.04	0.17	-0.05	-0.52	—	—
SAOUHSC_02381	Dps	hypothetical protein	Oxidative stress	0.20	0.26	1.70	2.53	-0.87	2.88	0.14	▲	—
SAOUHSC_02133		nicotinate phosphoribosyltransferase	Oxidative stress;NAD and NADP	-0.14	0.18	-0.66	-0.57	0.33	0.10	0.18	—	—
SAOUHSC_01327	KatA	catalase	Oxidative stress;Oxidative stress	0.82	0.22	0.88	1.42	2.71	1.36	1.90	▲	▲
SAOUHSC_00093	SodM	superoxide dismutase	Oxidative stress;Oxidative stress;Nitrogen Metabolism - no subcategory	0.26	0.16	1.10	0.29	0.92	2.76	2.71	—	▲
SAOUHSC_01653	SodA	superoxide dismutase, Mn	Oxidative stress;Oxidative stress;Nitrogen Metabolism - no subcategory	0.51	1.57	1.84	1.99	0.34	1.92	1.99	▲	▲
SAOUHSC_01630		hypothetical protein	Oxidative stress;Potassium metabolism - no subcategory	-0.04	-0.41	-0.91	-0.67	-1.24	n.d.	-1.60	▼	▼
SAOUHSC_01249	RibC	riboflavin biosynthesis protein RibF	Oxidative stress;Riboflavin, FMN, FAD;Riboflavin, FMN, FAD	0.29	-0.07	-0.45	-0.40	-0.11	-0.80	-0.32	—	—
SAOUHSC_00204	Hmp	globin domain-containing protein	Oxidative stress;Stress Response - no subcategory;Stress Response - no subcategory	-0.86	1.48	-0.08	0.07	0.52	-0.93	-0.05	—	—
SAOUHSC_00426	MetQ2	ABC transporter substrate-binding protein	Pathogenicity islands;Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.23	0.02	1.33	1.17	n.d.	0.99	1.52	▲	▲
SAOUHSC_00844	MetQ1	hypothetical protein	Pathogenicity islands;Lysine, threonine, methionine, and cysteine;Lysine, threonine, methionine, and cysteine	0.54	0.03	0.79	0.90	0.67	0.50	1.10	▲	▲
SAOUHSC_02254	GroEL	chaperonin GroEL	Pathogenicity islands;Protein folding	0.09	-0.36	-0.57	-0.50	0.04	0.04	0.23	—	—
SAOUHSC_02071		single-strand DNA-binding protein	Phages, Prophages	n.d.	n.d.	n.d.	n.d.	3.18	2.78	4.15	n.d.	▲
SAOUHSC_02080		bacteriophage L54a, antirepressor	Phages, Prophages	n.d.	n.d.	n.d.	n.d.	4.10	3.54	3.34	n.d.	▲
SAOUHSC_01193	FakA	hypothetical protein	Phospholipids	-0.12	-0.33	-0.65	-0.38	-0.15	0.05	-0.10	—	—
SAOUHSC_01197	PlsX	putative glycerol-3-phosphate acyltransferase PlsX	Phospholipids	-0.39	-0.16	-0.39	-0.29	-1.25	-0.94	n.d.	—	▼
SAOUHSC_01310	Cls1	cardiolipin synthetase	Phospholipids	-0.51	-0.27	-0.28	-0.08	n.d.	-0.26	-0.05	—	—
SAOUHSC_02363		aldehyde dehydrogenase	Phospholipids;Central carbohydrate metabolism;Central carbohydrate metabolism	0.85	0.01	0.62	0.81	-0.48	-0.20	0.25	▲	—
SAOUHSC_01278	GlpD	aerobic glycerol-3-phosphate dehydrogenase	Phospholipids;Electron donating reactions;Sugar alcohols	-0.13	-0.33	0.38	0.55	1.13	0.94	1.39	—	▲
SAOUHSC_01201	AcP	acyl carrier protein	Phospholipids;Resistance to antibiotics and toxic compounds;Fatty acids	0.77	0.04	0.06	0.23	-0.51	-1.03	-0.99	—	▼
SAOUHSC_01491	GpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	Phospholipids;Sugar alcohols;Oxidative stress	-0.50	-0.31	-0.52	-0.42	8.22	0.34	0.97	—	▲
SAOUHSC_00060		hypothetical protein	Phosphorus Metabolism - no subcategory	-0.44	0.06	0.22	0.20	1.80	1.31	n.d.	—	▲
SAOUHSC_01672	YbeY	hypothetical protein	Phosphorus Metabolism - no subcategory	0.23	0.76	0.27	0.51	0.41	-0.39	n.d.	—	—
SAOUHSC_02140	PpaC	putative manganese-dependent inorganic pyrophosphatase	Phosphorus Metabolism - no subcategory	0.20	0.06	-0.28	-0.17	-0.52	-0.22	-0.02	—	—
SAOUHSC_00511	CysS	cysteinyI-tRNA synthetase	Plant-Prokaryote comparative genomics	0.36	0.23	0.12	0.26	0.02	-0.15	-0.10	—	—
SAOUHSC_00513		hypothetical protein	Plant-Prokaryote comparative genomics	-0.18	-0.06	-0.39	-0.38	-0.57	-0.57	n.d.	—	—
SAOUHSC_01261	CinA	competence-damage inducible protein cinA	Plant-Prokaryote comparative genomics;Riboflavin, FMN, FAD	-0.35	0.08	-0.08	-0.56	1.17	-0.06	n.d.	—	—
SAOUHSC_01034	TrkA	hypothetical protein	Potassium metabolism - no subcategory;Potassium metabolism - no subcategory;Potassium metabolism - no subcategory	-0.52	0.16	-0.27	-0.16	n.d.	1.93	1.84	—	▲
SAOUHSC_01016	PurN	phosphoribosylglycinamide formyltransferase	Potassium metabolism - no subcategory;Purines	-0.57	0.58	-0.48	-0.56	n.d.	n.d.	0.52	—	—
SAOUHSC_02158		hypothetical protein	Proline and 4-hydroxyproline;Lysine, threonine, methionine, and cysteine;Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	0.00	0.26	-0.15	-0.17	-0.99	-0.18	n.d.	—	▼
SAOUHSC_02869	RocA	1-pyrroline-5-carboxylate dehydrogenase	Proline and 4-hydroxyproline;Proline and 4-hydroxyproline;Arginine; urea cycle, polyamines	0.32	3.89	5.03	5.22	n.d.	2.26	2.79	▲	▲
SAOUHSC_01597	ProC	pyrroline-5-carboxylate reductase	Proline and 4-hydroxyproline;Proline and 4-hydroxyproline;Proline and 4-hydroxyproline;Proline and 4-hydroxyproline	0.84	0.83	1.10	1.02	2.16	-0.08	1.32	▲	▲
SAOUHSC_00346	YchF	GTP-dependent nucleic acid-binding protein EngD	Protein biosynthesis	0.43	0.26	0.16	0.07	-0.29	-0.32	-0.48	—	—
SAOUHSC_00348	RpsF	30S ribosomal protein S6	Protein biosynthesis	-0.38	-0.79	-0.99	-0.76	0.01	0.76	2.01	▼	▲

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SAOUHSC_00474	RplY	50S ribosomal protein L25/general stress protein Ctc	Protein biosynthesis	0.62	-0.19	-0.47	-0.24	-0.67	-0.52	-0.95	—	▼
SAOUHSC_00518	RplK	50S ribosomal protein L11	Protein biosynthesis	-0.01	-0.82	-1.28	-1.31	-0.24	-1.24	-1.51	▼	▼
SAOUHSC_00519	RplA	50S ribosomal protein L1	Protein biosynthesis	-0.21	-1.04	-1.14	-0.97	0.04	0.21	0.23	▼	—
SAOUHSC_00520	RplJ	50S ribosomal protein L10	Protein biosynthesis	-0.22	-0.53	-0.77	-0.59	-0.38	-0.31	-0.73	▼	—
SAOUHSC_00521	RplL	50S ribosomal protein L7/L12	Protein biosynthesis	0.07	-0.45	-0.61	-0.57	2.56	1.49	0.87	—	▲
SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	Protein biosynthesis	0.35	0.16	-0.08	-0.02	-0.31	0.06	-0.05	—	—
SAOUHSC_00767	SaHPF	Staphylococcus aureus hibernation promoting factor	Protein biosynthesis	0.89	1.40	2.42	2.80	1.78	2.69	1.99	▲	▲
SAOUHSC_00933	TrpS	tryptophanyl-tRNA synthetase	Protein biosynthesis	0.23	0.24	0.08	0.26	-0.27	0.56	0.81	—	—
SAOUHSC_00956	PrfC	peptide chain release factor 3	Protein biosynthesis	-0.33	-0.31	-0.03	-0.24	0.27	1.36	2.17	—	▲
SAOUHSC_01058	TypA	GTP-binding protein TypA	Protein biosynthesis	-0.70	-0.99	-0.68	-0.52	0.08	-0.17	0.06	▼	—
SAOUHSC_01092	PheS	phenylalanyl-tRNA synthetase subunit alpha	Protein biosynthesis	-0.03	-1.00	-0.87	-0.81	-0.79	-0.25	-1.09	▼	▼
SAOUHSC_01093	PheT	phenylalanyl-tRNA synthetase subunit beta	Protein biosynthesis	-0.36	-0.90	-0.96	-0.79	-0.05	0.35	-0.32	▼	—
SAOUHSC_01163		hypothetical protein	Protein biosynthesis	-0.20	-0.66	-0.19	-0.18	-0.30	n.d.	-0.47	—	—
SAOUHSC_01208	RpsP	30S ribosomal protein S16	Protein biosynthesis	0.40	0.03	-0.38	-0.39	-0.47	-0.75	-1.06	—	▼
SAOUHSC_01211	RplS	50S ribosomal protein L19	Protein biosynthesis	-0.18	-0.71	-0.78	-0.74	0.99	1.41	0.17	▼	▲
SAOUHSC_01214	RbgA	ribosomal biogenesis GTPase	Protein biosynthesis	-0.11	-0.26	-0.02	0.09	n.d.	-0.23	-0.17	—	—
SAOUHSC_01232	RpsB	30S ribosomal protein S2	Protein biosynthesis	-0.10	-0.64	-0.84	-0.77	0.51	-0.06	-0.60	▼	—
SAOUHSC_01234	Tsf	elongation factor Ts	Protein biosynthesis	0.63	-0.06	-0.20	0.02	0.09	0.03	-0.18	—	—
SAOUHSC_01236	Frr	ribosome recycling factor	Protein biosynthesis	0.55	-0.16	-0.25	-0.14	-0.42	-0.55	-0.70	—	—
SAOUHSC_01471	AsnC	asparaginyl-tRNA synthetase	Protein biosynthesis	-0.01	0.25	-0.18	-0.04	-0.21	0.10	0.14	—	—
SAOUHSC_01492	EngA	GTP-binding protein EngA	Protein biosynthesis	-0.37	-0.40	-0.35	-0.27	-0.25	-0.92	-0.55	—	—
SAOUHSC_01493	RpsA	30S ribosomal protein S1	Protein biosynthesis	0.34	0.53	0.34	0.46	-0.09	0.03	0.03	—	—
SAOUHSC_01625	Efp	elongation factor P	Protein biosynthesis	0.57	0.35	-0.31	-0.05	-1.08	0.52	-0.72	—	▼
SAOUHSC_01668	Era	GTP-binding protein Era	Protein biosynthesis	-0.25	0.21	0.28	0.22	n.d.	-1.59	-2.26	—	▼
SAOUHSC_01678	RpsU	30S ribosomal protein S21	Protein biosynthesis	-0.30	-0.82	-1.85	-1.53	-1.69	-0.98	-0.66	▼	▼
SAOUHSC_01722	AlaS	alanyl-tRNA synthetase	Protein biosynthesis	-0.02	-0.14	-0.61	-0.33	0.05	-0.28	-0.05	—	—
SAOUHSC_01753	OlgE	GTPase OlgE	Protein biosynthesis	-0.12	-0.37	-0.05	0.06	0.26	-0.48	-1.08	—	—
SAOUHSC_01755	RpmA	50S ribosomal protein L27	Protein biosynthesis	0.43	-0.71	-1.25	-1.12	-1.55	-0.90	-1.33	▼	▼
SAOUHSC_01757	RplU	50S ribosomal protein L21	Protein biosynthesis	-0.35	-0.95	-1.22	-1.14	-0.18	-0.46	-0.74	▼	—
SAOUHSC_01788	ThrS	threonyl-tRNA synthetase	Protein biosynthesis	0.11	0.01	-0.43	-0.45	-0.17	-0.08	-0.22	—	—
SAOUHSC_01829	RpsD	30S ribosomal protein S4	Protein biosynthesis	-0.50	-0.84	-0.90	-1.12	-0.03	0.13	-0.21	▼	—
SAOUHSC_01982		ribosomal large subunit pseudouridine synthase D	Protein biosynthesis	-0.27	-0.02	-0.40	-0.39	0.11	0.45	n.d.	—	—
SAOUHSC_02116	GatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	Protein biosynthesis	0.29	0.27	-0.05	-0.03	-0.24	-0.23	-0.26	—	—
SAOUHSC_02117	GatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	Protein biosynthesis	0.29	0.17	0.09	0.03	-0.42	-0.39	-0.26	—	—
SAOUHSC_02361	RpmE2	50S ribosomal protein L31 type B	Protein biosynthesis	-0.03	-0.81	-1.19	-1.14	-0.36	-1.60	-0.32	▼	—
SAOUHSC_02477	RplI	30S ribosomal protein S9	Protein biosynthesis	-0.41	-0.60	-1.23	-1.38	-0.97	-0.88	-1.06	▼	▼
SAOUHSC_02478	RplM	50S ribosomal protein L13	Protein biosynthesis	0.13	-0.42	-0.59	-0.52	0.93	0.35	0.80	—	▲
SAOUHSC_02484	RplQ	50S ribosomal protein L17	Protein biosynthesis	0.48	-0.34	-0.23	-0.33	0.37	-0.01	-0.36	—	—
SAOUHSC_02486	RpsK	30S ribosomal protein S11	Protein biosynthesis	-0.37	-0.98	-1.59	-1.79	-0.79	-0.78	-1.11	▼	▼
SAOUHSC_02487	RpsM	30S ribosomal protein S13	Protein biosynthesis	-0.33	-1.10	-1.22	-1.29	0.03	0.24	-0.04	▼	—
SAOUHSC_02489	InfA	translation initiation factor IF-1	Protein biosynthesis	0.28	-0.02	0.01	0.02	-0.67	-2.24	-2.64	—	▼
SAOUHSC_02492	RplO	50S ribosomal protein L15	Protein biosynthesis	-0.22	-1.00	-1.33	-1.38	-0.69	-1.06	-2.19	▼	▼
SAOUHSC_02493	RpmD	50S ribosomal protein L30	Protein biosynthesis	0.51	-0.32	-0.73	-0.53	-0.55	-2.84	-3.21	—	▼
SAOUHSC_02495	RplR	50S ribosomal protein L18	Protein biosynthesis	-0.03	-0.61	-0.95	-0.93	0.43	-0.98	-1.40	▼	▼
SAOUHSC_02496	RplF	50S ribosomal protein L6	Protein biosynthesis	0.13	-0.53	-0.65	-0.63	0.01	-0.36	0.51	▼	—
SAOUHSC_02498	RpsH	30S ribosomal protein S8	Protein biosynthesis	0.36	-0.22	-0.86	-0.82	-0.16	-0.47	-0.75	▼	—
SAOUHSC_02500	RplE	50S ribosomal protein L5	Protein biosynthesis	-0.08	-0.57	-0.47	-0.55	-0.05	0.75	0.29	—	—
SAOUHSC_02503	RpsQ	30S ribosomal protein S17	Protein biosynthesis	0.33	-0.56	-1.41	-1.54	-0.10	1.62	-0.41	▼	—

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SAOUHSC_02504	RpmC	50S ribosomal protein L29	Protein biosynthesis	0.07	-0.77	-1.20	-1.11	-0.15	-0.57	-0.89	▼	—
SAOUHSC_02505	RplP	50S ribosomal protein L16	Protein biosynthesis	-0.60	-1.07	-1.50	-1.37	1.49	3.47	1.21	▼	▲
SAOUHSC_02506	RpsC	30S ribosomal protein S3	Protein biosynthesis	-0.18	-0.97	-0.70	-0.80	-0.68	-0.15	-0.34	▼	—
SAOUHSC_02507	RplV	50S ribosomal protein L22	Protein biosynthesis	-0.36	-0.77	-0.77	-0.96	-0.78	-0.53	-0.68	▼	▼
SAOUHSC_02509	RplB	50S ribosomal protein L2	Protein biosynthesis	-0.30	-0.84	-1.04	-1.05	1.12	-0.10	-0.19	▼	—
SAOUHSC_02510	RplW	50S ribosomal protein L23	Protein biosynthesis	-0.05	-0.55	-0.81	-0.67	-4.25	-1.47	0.70	▼	▼
SAOUHSC_02511	RplD	50S ribosomal protein L4	Protein biosynthesis	-0.29	-0.85	-1.42	-1.10	-0.15	-0.54	-0.68	▼	—
SAOUHSC_02512	RplC	50S ribosomal protein L3	Protein biosynthesis	-0.46	-0.70	-1.24	-0.75	0.47	0.67	0.27	▼	—
SAOUHSC_01207	Ffh	signal recognition particle protein	Protein biosynthesis;Cell Division and Cell Cycle - no subcategory	-0.13	-0.47	-0.61	-0.53	-0.43	-0.22	-0.16	—	—
SAOUHSC_01038	Def	peptide deformylase	Protein biosynthesis;Central carbohydrate metabolism	0.74	-0.04	-0.10	-0.01	-0.42	0.28	0.36	—	—
SAOUHSC_01183	Fmt	methionyl-tRNA formyltransferase	Protein biosynthesis;Folate and pterines	0.28	-0.01	0.09	0.25	-0.37	-0.51	-1.03	—	—
SAOUHSC_01688	LepA	GTP-binding protein LepA	Protein biosynthesis;Heat shock;Tetrapyrroles;Protein biosynthesis	-0.38	-0.26	-0.52	-0.47	-0.52	-0.56	n.d.	—	—
SAOUHSC_02359	PrfA	peptide chain release factor 1	Protein biosynthesis;Oxidative stress	0.07	0.06	-0.34	-0.21	0.23	-0.64	0.72	—	—
SAOUHSC_01246	InfB	translation initiation factor IF-2	Protein biosynthesis;Protein biosynthesis	0.15	-0.07	0.44	0.54	0.18	0.02	-0.04	—	—
SAOUHSC_00529	FusA	elongation factor G	Protein biosynthesis;Protein biosynthesis;Virulence - no subcategory;Protein biosynthesis	-0.06	-0.27	-0.37	-0.16	-0.23	-0.36	-0.48	—	—
SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	Protein biosynthesis;Tetrapyrroles	0.29	0.10	-0.24	-0.01	0.05	-0.41	-0.14	—	—
SAOUHSC_00505	ClpC	endopeptidase	Protein degradation	0.15	-0.48	-0.19	0.22	0.04	-0.10	0.17	—	—
SAOUHSC_01626	PepQ2	proline dipeptidase	Protein degradation	0.81	0.87	0.29	0.55	0.67	-0.10	0.99	—	▲
SAOUHSC_02092	AmpS	aminopeptidase PepS	Protein degradation	0.47	0.04	-0.00	0.03	0.06	0.04	0.29	—	—
SAOUHSC_02102	Map	methionine aminopeptidase	Protein degradation;Protein biosynthesis	0.69	0.03	-0.03	-0.16	-0.54	-1.34	-1.28	—	▼
SAOUHSC_01226	HslU	ATP-dependent protease ATP-binding subunit HslU	Protein degradation;Protein degradation	-0.14	-0.05	0.15	-0.02	0.90	1.09	0.48	—	▲
SAOUHSC_01778	ClpX	ATP-dependent protease ATP-binding subunit ClpX	Protein degradation;Protein degradation	-0.24	-0.72	-1.53	-1.66	-0.38	-0.65	-1.17	▼	▼
SAOUHSC_00790	ClpP	ATP-dependent Clp protease proteolytic subunit	Protein degradation;Protein degradation;Regulation and Cell signaling - no subcategory	0.07	-0.13	-0.16	-0.03	-0.60	-0.81	-0.87	—	▼
SAOUHSC_01972	PrsA	protein export protein PrsA	Protein folding	0.05	2.19	1.78	1.37	-0.58	-3.11	n.d.	▲	▼
SAOUHSC_02255	GroES	co-chaperonin GroES	Protein folding	0.45	-0.08	0.02	-0.20	0.69	0.43	0.37	—	—
SAOUHSC_01682	DnaJ	chaperone protein DnaJ	Protein folding;Heat shock	-0.08	-0.45	-0.60	-0.44	n.d.	0.17	-0.33	—	—
SAOUHSC_01684	GrpE	heat shock protein GrpE	Protein folding;Heat shock	0.34	-0.30	-0.39	-0.36	-0.13	0.01	-0.34	—	—
SAOUHSC_00912	ClpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	Protein folding;Protein degradation	0.01	-0.75	1.10	1.79	0.70	1.22	1.80	▲	▲
SAOUHSC_00903	SpsB	Signal peptidase IB	Protein processing and modification	-0.20	0.54	0.12	0.01	-0.50	-1.03	-1.28	—	▼
SAOUHSC_01432	MsrA2	methionine sulfoxide reductase A	Protein processing and modification	0.27	2.57	1.65	1.53	1.18	0.54	0.48	▲	—
SAOUHSC_02494	RpsE	30S ribosomal protein S5	Protein processing and modification;Protein biosynthesis	-0.01	-0.60	-1.11	-1.28	0.11	-0.16	-0.19	▼	—
SAOUHSC_00527	RpsL	30S ribosomal protein S12	Protein processing and modification;Virulence - no subcategory;Protein biosynthesis	0.46	-0.76	-0.76	-1.02	-0.77	-0.59	-1.20	▼	▼
SAOUHSC_00257	ExsA	hypothetical protein	Protein secretion system, Type VII	0.16	0.31	0.67	1.16	0.68	0.43	1.05	▲	▲
SAOUHSC_00374	GuaB	inosine-5-monophosphate dehydrogenase	Purines	-0.05	-0.23	-0.96	-0.75	0.21	-0.20	0.36	▼	—
SAOUHSC_00467	PurR	pur operon repressor	Purines	-0.20	0.20	0.13	0.17	0.63	1.16	0.16	—	▲
SAOUHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	Purines	0.06	-0.23	-0.18	-0.08	-0.26	-0.56	-0.87	—	—
SAOUHSC_00539		hypothetical protein	Purines	0.30	-0.41	-0.60	-0.38	-0.17	-0.63	1.77	—	—
SAOUHSC_01008	PurE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	Purines	0.02	0.46	-0.65	-0.31	-0.78	-0.39	-1.12	—	▼
SAOUHSC_01009	PurK	phosphoribosylaminoimidazole carboxylase ATPase subunit	Purines	-0.21	0.34	-0.77	-0.70	-0.52	0.09	-0.58	▼	—
SAOUHSC_01010	PurC	phosphoribosylaminoimidazole-succinocarboxamide synthase	Purines	-0.01	0.39	-0.97	-0.69	0.20	0.42	0.17	▼	—
SAOUHSC_01011	PurS	phosphoribosylformylglycinamide synthase, PurS protein	Purines	0.27	0.73	-0.84	-0.71	1.17	0.27	-0.05	▼	—
SAOUHSC_01012	PurQ	phosphoribosylformylglycinamide synthase I	Purines	0.14	0.54	-0.84	-0.71	-0.80	-0.49	-0.86	▼	▼
SAOUHSC_01013	PurL	phosphoribosylformylglycinamide synthase II	Purines	-0.09	0.49	-0.31	-0.37	0.09	-0.10	-0.22	—	—
SAOUHSC_01015	PurM	phosphoribosylaminoimidazole synthetase	Purines	0.09	0.63	-0.56	-0.34	n.d.	0.10	0.22	—	—
SAOUHSC_01017	PurH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Purines	-0.58	-0.17	-0.97	-0.91	-0.68	-0.02	-0.05	▼	—
SAOUHSC_01330	GuaC	guanosine 5-monophosphate oxidoreductase	Purines	-0.63	-0.62	-0.86	-0.67	0.50	-0.37	0.50	▼	—
SAOUHSC_02490	Adk	adenylate kinase	Purines	0.36	0.02	-0.15	0.01	-1.61	0.21	-0.78	—	▼
SAOUHSC_00472	Prs	ribose-phosphate pyrophosphokinase	Purines;Central carbohydrate metabolism	-0.59	-0.01	-0.45	-0.41	0.40	-0.09	0.00	—	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_00019	PurA	adenylosuccinate synthetase	Purines;Histidine Metabolism;Miscellaneous - no subcategory	0.07	0.04	-0.40	-0.27	0.38	0.05	-0.20	—	—
SAOUHSC_00375	GuaA	GMP synthase	Purines;Pathogenicity islands	0.31	0.29	-0.58	-0.36	-0.17	-0.15	-0.17	—	—
SAOUHSC_00372	Xpt	xanthine phosphoribosyltransferase	Purines;Purines	-0.03	-0.37	-1.01	-0.88	0.13	0.37	0.27	▼	—
SAOUHSC_02126	PurB	adenylosuccinate lyase	Purines;Purines	0.01	-0.30	-0.62	-0.48	-0.61	-0.02	-0.44	—	—
SAOUHSC_01485	Ndk	nucleoside diphosphate kinase	Purines;Pyrimidines	0.42	0.28	1.11	1.12	0.19	-0.24	n.d.	▲	—
SAOUHSC_01743	Apt	adenine phosphoribosyltransferase	Purines;Regulation and Cell signaling - no subcategory;Regulation and Cell signaling - no subcategory	0.44	-0.35	0.41	0.37	n.d.	0.42	0.37	—	—
SAOUHSC_00499	PdxS	pyridoxal biosynthesis lyase PdxS	Pyridoxine	-0.41	-0.02	-0.43	-0.31	n.d.	0.99	0.41	—	▲
SAOUHSC_00451	Tmk	thymidylate kinase	Pyrimidines	0.20	0.40	-0.11	0.12	n.d.	0.36	n.d.	—	—
SAOUHSC_01166	PyrB	aspartate carbamoyltransferase catalytic subunit	Pyrimidines	-0.71	-0.87	-0.72	-0.57	n.d.	-0.42	n.d.	▼	—
SAOUHSC_01168	PyrC	dihydroorotase	Pyrimidines	-0.14	-0.03	0.01	0.06	0.22	-1.57	-0.99	—	▼
SAOUHSC_01169	CarA	carbamoyl phosphate synthase small subunit	Pyrimidines	-0.86	-0.76	-0.52	-0.42	n.d.	0.21	1.44	—	▲
SAOUHSC_01170	CarB	carbamoyl phosphate synthase large subunit	Pyrimidines	-0.78	-0.81	-0.88	-0.66	-0.61	-0.41	-0.67	▼	▼
SAOUHSC_01172	PyrE	orotate phosphoribosyltransferase	Pyrimidines	0.01	-0.31	-0.48	-0.18	-0.70	0.73	0.65	—	▲
SAOUHSC_01496	Cmk	cytidylate kinase	Pyrimidines	0.24	-0.38	-0.51	-0.37	0.96	-0.09	-0.14	—	—
SAOUHSC_01715	Udk	uridine kinase	Pyrimidines	-0.25	-0.19	-0.58	-0.61	-0.49	-0.58	-0.90	▼	▼
SAOUHSC_02377	Pdp	pyrimidine-nucleoside phosphorylase	Pyrimidines;Monosaccharides	-0.16	1.14	1.87	2.10	1.84	2.08	1.65	▲	▲
SAOUHSC_01164	PyrR	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	Pyrimidines;Pyrimidines	0.08	-0.01	0.13	0.07	-0.24	-0.14	-0.00	—	—
SAOUHSC_02353	Upp	uracil phosphoribosyltransferase	Pyrimidines;Pyrimidines	-0.01	0.01	-0.03	-0.02	0.22	0.22	-0.39	—	—
SAOUHSC_00785	TrxB	thioredoxin reductase	Pyrimidines;Sulfur Metabolism - no subcategory	0.28	0.22	0.03	0.24	0.08	0.02	0.19	—	—
SAOUHSC_00980	MenA	1,4-dihydroxy-2-naphthoate octaprenyltransferase	Quinone cofactors;Quinone cofactors	-0.41	-0.32	-0.48	-0.59	0.98	1.71	n.d.	—	▲
SAOUHSC_00985	MenB	naphthoate synthase	Quinone cofactors;Quinone cofactors	0.27	0.20	-0.06	0.09	0.04	0.30	0.06	—	—
SAOUHSC_01487	UbiE	ubiquinone/menaquinone biosynthesis methyltransferase	Quinone cofactors;Quinone cofactors	-0.44	-0.14	-0.40	-0.57	n.d.	1.21	-0.74	—	—
SAOUHSC_00620	SarA	accessory regulator A	Quorum sensing and biofilm formation	0.25	0.08	-0.25	-0.39	1.88	1.25	1.37	—	▲
SAOUHSC_01850	CcpA	catabolite control protein A	Regulation and Cell signaling - no subcategory	0.11	0.33	0.32	0.27	0.33	0.18	-0.09	—	—
SAOUHSC_02374	HmrA	aminobenzoyl-glutamate utilization protein B	Resistance to antibiotics and toxic compounds	0.28	-0.32	-0.63	-0.16	n.d.	1.13	1.61	—	▲
SAOUHSC_02525		hypothetical protein	Resistance to antibiotics and toxic compounds	-0.14	-0.21	-0.31	-0.28	n.d.	-0.57	4.95	—	▲
SAOUHSC_01467	Pbp2	penicillin-binding protein 2	Resistance to antibiotics and toxic compounds;Cell Division and Cell Cycle - no subcategory;Cell Wall and Capsule - no subcategory	-0.20	-0.14	-0.45	-0.42	-1.41	n.d.	n.d.	—	▼
SAOUHSC_00954	MurE	UDP-N-acetylmuramoylalanyl-D-glutamate—L-lysine ligase	Resistance to antibiotics and toxic compounds;Cell Wall and Capsule - no subcategory	-0.24	-0.38	-0.77	-0.62	n.d.	1.24	n.d.	▼	▲
SAOUHSC_02527	FmhB	FmhB protein	Resistance to antibiotics and toxic compounds;Cell Wall and Capsule - no subcategory	-0.31	-0.23	-0.47	-0.52	n.d.	-0.14	-0.12	—	—
SAOUHSC_00869	DltA	D-alanine-poly(phosphoribitol) ligase subunit 1	Resistance to antibiotics and toxic compounds;Gram-Positive cell wall components;Gram-Positive cell wall components	0.32	-0.58	-0.54	-0.23	0.11	-0.23	-0.43	—	—
SAOUHSC_02582	FdhA	formate dehydrogenase subunit alpha	Respiration - no subcategory	0.38	-1.37	-1.06	-0.62	0.72	n.d.	-0.40	▼	—
SAOUHSC_01347	CitB	aconitate hydratase	Respiration - no subcategory;One-carbon Metabolism;Central carbohydrate metabolism	0.83	-0.31	0.25	0.69	0.35	0.32	0.49	—	—
SAOUHSC_01961	HemH	ferrochelatase	Respiration - no subcategory;Tetrapyrroles	0.07	0.21	0.53	0.59	-0.33	-0.22	-0.24	—	—
SAOUHSC_01248	TruB	tRNA pseudouridine synthase B	Riboflavin, FMN, FAD;RNA processing and modification	0.15	-0.42	-0.28	-0.10	0.39	0.01	0.53	—	—
SAOUHSC_00803	Rnr	ribonuclease R	RNA processing and modification	-0.38	-0.46	-0.32	-0.17	-0.37	-0.47	n.d.	—	—
SAOUHSC_00951		hypothetical protein	RNA processing and modification	0.30	1.11	2.45	2.54	0.83	1.14	1.64	▲	▲
SAOUHSC_01659		hypothetical protein	RNA processing and modification	-0.42	-0.72	-0.41	-0.43	-0.28	-0.29	-0.17	—	—
SAOUHSC_01748	Tgt	queuine tRNA-ribosyltransferase	RNA processing and modification	-0.34	-0.34	-0.36	-0.34	n.d.	-1.22	-0.84	—	▼
SAOUHSC_01749	QueA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	RNA processing and modification	-0.12	-0.25	-0.52	-0.90	n.d.	-0.43	n.d.	—	—
SAOUHSC_02097		hypothetical protein	RNA processing and modification	0.32	-1.11	-0.99	-0.72	0.11	0.27	0.19	▼	—
SAOUHSC_02316	CshA	DEAD-box ATP dependent DNA helicase	RNA processing and modification	-0.67	-1.07	-0.99	-0.90	-0.33	-0.38	-0.51	▼	—
SAOUHSC_00721	QueC	hypothetical protein	RNA processing and modification;Miscellaneous - no subcategory	0.79	-1.23	-0.37	-0.24	0.28	0.51	n.d.	—	—
SAOUHSC_01247	RbfA	ribosome-binding factor A	RNA processing and modification;Protein biosynthesis	0.34	0.75	0.28	0.51	n.d.	-0.09	n.d.	—	—
SAOUHSC_00074	SirA	periplasmic binding protein	Siderophores	-2.39	0.12	-0.03	-0.15	0.02	-1.76	n.d.	—	▼
SAOUHSC_01742	RelA	GTP pyrophosphokinase	Signal transduction in Eukaryotes;Regulation and Cell signaling - no subcategory	0.01	-0.23	-0.12	0.00	1.05	0.32	0.67	—	▲
SAOUHSC_01413		hypothetical protein	Stress Response - no subcategory	0.10	0.03	-0.41	-0.59	-0.45	-0.10	-0.81	—	—
SAOUHSC_01814	UspA2	hypothetical protein	Stress Response - no subcategory	0.08	0.37	0.54	0.75	0.70	1.08	1.36	—	▲

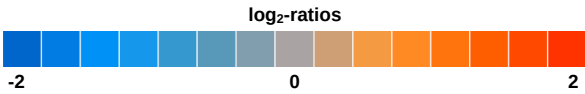
locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_01819	UspA1	hypothetical protein	Stress Response - no subcategory	0.30	1.46	2.61	3.08	3.39	2.90	2.99	▲	▲
SAOUHSC_02299	RsbW	serine-protein kinase RsbW	Stress Response - no subcategory	0.28	-0.57	-0.92	-0.53	-0.37	-0.42	-0.97	—	—
SAOUHSC_02300	RsbV	STAS domain-containing protein	Stress Response - no subcategory	0.46	-0.42	-0.41	-0.16	-0.27	-0.03	-0.06	—	—
SAOUHSC_02301	RsbU	sigmaB regulation protein RsbU	Stress Response - no subcategory	0.25	-0.28	-0.26	-0.08	0.57	0.20	n.d.	—	—
SAOUHSC_02302		sigmaB regulation protein RsbU	Stress Response - no subcategory	0.59	0.21	0.22	0.08	-0.10	0.20	0.78	—	—
SAOUHSC_02430	HtsA	ABC transporter periplasmic binding protein	Stress Response - no subcategory;Iron acquisition and metabolism - no subcategory	-1.87	-0.05	0.10	0.26	-0.03	-0.64	-0.21	—	—
SAOUHSC_02298	SigB	RNA polymerase sigma factor SigB	Stress Response - no subcategory;Transcription;Quorum sensing and biofilm formation;Resistance to antibiotics and toxic compounds	0.42	-0.54	-0.98	-0.77	n.d.	-0.78	0.52	▼	—
SAOUHSC_01071		glycerophosphoryl diester phosphodiesterase	Sugar alcohols	-0.01	0.35	0.55	0.48	n.d.	0.78	n.d.	—	▲
SAOUHSC_02402	MitA	PTS system mannitol-specific transporter subunit IIA	Sugar alcohols	0.91	-0.64	0.13	0.36	2.20	1.94	2.40	—	▲
SAOUHSC_02403	MitD	mannitol-1-phosphate 5-dehydrogenase	Sugar alcohols	0.87	-0.38	0.23	0.51	0.14	0.71	0.67	—	▲
SAOUHSC_01276	GlpK	glycerol kinase	Sugar alcohols;Phospholipids;Central carbohydrate metabolism	0.19	0.82	0.80	0.84	0.14	0.13	0.29	▲	—
SAOUHSC_00781	HprK	HPr kinase/phosphorylase	Sugar alcohols;Regulation and Cell signaling - no subcategory	-0.06	0.29	-0.22	-0.17	n.d.	0.74	0.61	—	▲
SAOUHSC_00364	AhpF	alkyl hydroperoxide reductase subunit F	Sulfur Metabolism - no subcategory	1.03	0.16	0.85	1.04	-0.04	-0.01	0.08	▲	—
SAOUHSC_00365	AhpC	alkyl hydroperoxide reductase subunit C	Sulfur Metabolism - no subcategory	1.00	-0.07	1.09	1.34	0.08	-0.77	-0.90	▲	▼
SAOUHSC_01822	Tpx	thiol peroxidase	Sulfur Metabolism - no subcategory	0.71	0.58	0.49	0.72	0.76	0.53	0.22	—	—
SAOUHSC_01999		bacterioferritin comigratory protein	Sulfur Metabolism - no subcategory	0.87	1.07	1.04	1.31	-0.24	0.23	1.19	▲	—
SAOUHSC_00573	HemQ	putative heme peroxidase	Tetrapyrroles	0.14	0.53	0.11	0.35	0.36	0.05	0.42	—	—
SAOUHSC_01771	HemL	glutamate-1-semialdehyde aminotransferase	Tetrapyrroles	0.21	0.02	-0.31	-0.13	-0.03	-0.26	-0.35	—	—
SAOUHSC_01772	HemB	delta-aminolevulinic acid dehydratase	Tetrapyrroles	0.05	0.06	-0.29	0.03	2.89	2.67	2.54	—	▲
SAOUHSC_01774	HemC	porphobilinogen deaminase	Tetrapyrroles	0.25	0.20	-0.08	0.17	n.d.	-0.79	n.d.	—	▼
SAOUHSC_01962	HemE	uroporphyrinogen decarboxylase	Tetrapyrroles	0.20	-0.24	-0.05	-0.08	-1.41	1.21	n.d.	—	—
SAOUHSC_02000	GsaB	glutamate-1-semialdehyde aminotransferase	Tetrapyrroles	0.48	0.44	0.42	0.67	-0.60	-0.14	-0.97	—	▼
SAOUHSC_00517	NusG	transcription antitermination protein	Transcription	0.04	0.01	-0.36	-0.39	-0.37	-0.52	-0.57	—	—
SAOUHSC_01177	RpoZ	DNA-directed RNA polymerase subunit omega	Transcription	-0.22	-0.45	-1.01	-0.96	n.d.	-2.09	n.d.	▼	▼
SAOUHSC_01243	NusA	transcription elongation factor NusA	Transcription	0.06	0.02	-0.19	-0.07	-0.10	-0.29	-0.48	—	—
SAOUHSC_01621	NusB	transcription antitermination protein NusB	Transcription	0.10	0.12	-0.66	-0.39	-0.40	-0.51	-0.30	—	—
SAOUHSC_01662	SigA	RNA polymerase sigma factor RpoD	Transcription	-0.13	-0.22	-0.60	-0.31	-1.09	0.17	-0.27	—	—
SAOUHSC_01714	GreA	transcription elongation factor GreA	Transcription	0.70	0.49	-0.34	-0.08	-0.06	-0.55	-0.80	—	—
SAOUHSC_02362	Rho	transcription termination factor Rho	Transcription	-0.82	0.05	-0.16	-0.30	n.d.	-1.45	-1.48	—	▼
SAOUHSC_02369	RpoE	DNA-directed RNA polymerase subunit delta	Transcription	-0.05	-0.24	-0.83	-0.74	-0.42	-0.36	-0.40	▼	—
SAOUHSC_02485	RpoA	DNA-directed RNA polymerase subunit alpha	Transcription	-0.49	-0.57	-0.85	-0.65	-0.03	0.35	-0.03	▼	—
SAOUHSC_00524	RpoB	DNA-directed RNA polymerase subunit beta	Transcription;Virulence - no subcategory	-0.29	-0.43	-0.59	-0.53	-0.31	-0.13	-0.14	—	—
SAOUHSC_00886	MnhD	putative monovalent cation/H+ antiporter subunit D	Uni- Sym- and Antiporters	-0.47	-0.18	-0.82	-0.83	n.d.	0.36	n.d.	▼	—
SAOUHSC_00528	RpsG	30S ribosomal protein S7	Virulence - no subcategory;Protein biosynthesis	-0.20	-1.01	-1.70	-1.93	-0.40	-0.27	-0.43	▼	—
SAOUHSC_00530	Tuf	elongation factor Tu	Virulence - no subcategory;Protein biosynthesis;Protein biosynthesis	-0.24	-0.22	-0.31	-0.34	-0.25	-0.10	-0.30	—	—
SAOUHSC_00525	RpoC	DNA-directed RNA polymerase subunit beta	Virulence - no subcategory;Transcription	-0.31	-0.35	-0.51	-0.49	-0.47	-0.07	-0.52	—	—
SAOUHSC_00015		hypothetical protein		-0.09	-0.25	0.33	0.25	1.29	0.67	n.d.	—	▲
SAOUHSC_00070	SarS	accessory regulator-like protein		0.29	-2.05	-0.89	-0.65	n.d.	-1.77	-0.18	▼	▼
SAOUHSC_00228	TarS	hypothetical protein		-0.36	0.03	-0.42	-0.33	-1.42	-1.01	0.44	—	▼
SAOUHSC_00356		hypothetical protein		0.92	-1.85	-1.13	-0.82	-0.60	-1.04	-1.81	▼	▼
SAOUHSC_00369		hypothetical protein		-0.18	-0.06	-0.36	-0.35	0.25	-0.29	-0.70	—	—
SAOUHSC_00371		hypothetical protein		0.57	1.78	2.73	2.91	1.29	1.60	1.61	▲	▲
SAOUHSC_00417		hypothetical protein		0.22	0.54	0.53	0.55	n.d.	n.d.	-0.26	—	—
SAOUHSC_00461	MetS	methionyl-tRNA synthetase		-0.08	0.06	-0.60	-0.49	-0.39	-0.21	-0.53	—	—
SAOUHSC_00486	PtsH	hypothetical protein		0.16	-0.40	-0.30	-0.33	-0.53	-0.20	-0.38	—	—
SAOUHSC_00493	LysS	lysyl-tRNA synthetase		0.18	0.04	-0.18	-0.09	-0.34	0.28	-0.05	—	—
SAOUHSC_00533	HchA	chaperone protein HchA		0.78	-0.08	-0.13	-0.02	-0.04	-0.23	0.58	—	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_00542		hypothetical protein		0.11	-0.02	0.19	0.22	-0.52	0.16	0.11	—	—
SAOUHSC_00562	ThiD1	phosphomethylpyrimidine kinase		0.08	0.21	-0.23	-0.10	0.22	-0.01	-0.06	—	—
SAOUHSC_00605		hypothetical protein		0.08	-0.32	-0.21	-0.38	0.64	-0.47	1.02	—	▲
SAOUHSC_00616		hypothetical protein		0.28	0.00	0.56	0.40	-0.18	0.22	-0.05	—	—
SAOUHSC_00634	MntC	ABC transporter substrate-binding protein		-0.56	-1.94	-2.68	-3.14	-2.51	-3.14	n.d.	▼	▼
SAOUHSC_00637	MntA	hypothetical protein		-0.46	-0.85	-0.82	-0.88	-0.33	-0.66	-0.46	▼	—
SAOUHSC_00638	MntR	hypothetical protein		0.08	0.30	-0.04	0.17	n.d.	2.90	1.15	—	▲
SAOUHSC_00647	AbcA	hypothetical protein		0.28	0.29	1.38	1.45	n.d.	0.79	-0.26	▲	—
SAOUHSC_00669		hypothetical protein		-0.29	-0.52	-0.20	-0.04	0.65	0.89	-0.51	—	▲
SAOUHSC_00675		hypothetical protein		0.62	0.67	0.18	0.35	-0.48	0.05	0.12	—	—
SAOUHSC_00686		hypothetical protein		0.10	-0.09	-0.32	-0.29	-0.72	-0.28	-0.87	—	▼
SAOUHSC_00690		hypothetical protein		n.d.	n.d.	n.d.	n.d.	0.09	-0.06	-0.01	n.d.	—
SAOUHSC_00694	MgrA	hypothetical protein		0.35	0.83	0.00	-0.01	-0.10	-0.06	-0.09	—	—
SAOUHSC_00755		hypothetical protein		0.93	-0.11	-0.22	-0.11	n.d.	-0.53	-1.06	—	▼
SAOUHSC_00769	SecA	preprotein translocase subunit SecA		-0.23	-0.43	-0.15	-0.23	-0.18	0.03	0.21	—	—
SAOUHSC_00787		hypothetical protein		-0.01	0.29	-0.08	-0.05	-0.53	0.18	n.d.	—	—
SAOUHSC_00792		hypothetical protein		0.28	-0.56	0.23	0.46	3.81	3.04	-0.20	—	▲
SAOUHSC_00794	GapR	glycolytic operon regulator		-0.39	-0.66	-1.05	-1.07	4.64	n.d.	n.d.	▼	▲
SAOUHSC_00847	SufC	ABC transporter ATP-binding protein		0.28	-0.25	-0.02	0.07	-0.08	-0.36	-0.57	—	—
SAOUHSC_00848	SufD	hypothetical protein		0.31	-0.24	0.01	0.12	-0.33	0.24	-0.33	—	—
SAOUHSC_00850	SufU	hypothetical protein		0.98	-0.33	-0.17	0.02	-0.86	-0.92	n.d.	—	▼
SAOUHSC_00865		hypothetical protein		0.39	0.83	0.38	0.47	-0.20	-0.32	-0.06	—	—
SAOUHSC_00908	Cdr	coenzyme A disulfide reductase		-0.31	0.06	-0.17	-0.03	n.d.	1.03	0.88	—	▲
SAOUHSC_00909		hypothetical protein		-0.30	-0.01	-0.39	-0.36	0.53	-0.34	0.63	—	—
SAOUHSC_00934	SpxA	transcriptional regulator Spx		1.19	1.25	0.66	0.57	0.97	0.75	1.49	▲	▲
SAOUHSC_00937	PepF	oligoendopeptidase F		0.20	0.29	-0.15	-0.18	-0.69	-0.19	-0.21	—	—
SAOUHSC_00958	HtrA	serine protease HtrA		-0.49	-0.32	-0.22	-1.42	-0.24	0.42	0.28	—	—
SAOUHSC_00972		hypothetical protein		0.26	-0.90	-0.63	-0.32	-0.17	-0.03	-0.49	▼	—
SAOUHSC_01035	RnjA	hypothetical protein		0.02	-0.19	-0.01	0.12	0.54	-0.11	0.43	—	—
SAOUHSC_01036	RpoY	hypothetical protein		0.71	0.30	0.13	0.48	1.81	1.08	1.90	—	▲
SAOUHSC_01039		hypothetical protein		0.27	-0.01	-0.21	-0.27	-0.25	-1.90	-1.72	—	▼
SAOUHSC_01050		hypothetical protein		0.05	-0.64	-0.77	-0.75	-0.18	-0.42	-0.60	▼	—
SAOUHSC_01054		hypothetical protein		0.48	0.82	0.66	0.60	-0.14	-0.06	-0.42	▲	—
SAOUHSC_01061		hypothetical protein		0.21	0.56	0.76	0.58	-0.17	0.80	-0.13	—	—
SAOUHSC_01091		hypothetical protein		-0.40	0.06	-0.54	-0.64	-1.27	-1.95	n.d.	—	▼
SAOUHSC_01100	TrxA	thioredoxin		0.57	0.46	0.44	0.52	-0.34	-0.87	-0.52	—	—
SAOUHSC_01138		hypothetical protein		0.76	0.76	1.88	2.07	1.35	1.68	0.80	▲	▲
SAOUHSC_01143	MraW	S-adenosyl-methyltransferase MraW		-0.35	0.07	0.07	-0.10	-0.23	-0.14	-0.44	—	—
SAOUHSC_01159	IleS	isoleucyl-tRNA synthetase		0.05	-0.27	-0.54	-0.40	0.01	-0.08	-0.06	—	—
SAOUHSC_01186	Stp1	hypothetical protein		0.06	0.26	0.05	0.18	-0.47	0.66	n.d.	—	—
SAOUHSC_01187	PknB	hypothetical protein		-0.24	-0.38	-0.20	-0.37	2.30	-1.61	n.d.	—	—
SAOUHSC_01192		hypothetical protein		0.06	-0.52	-0.13	-0.17	-0.19	-0.69	0.18	—	—
SAOUHSC_01222	TopA	DNA topoisomerase I		-0.15	-0.80	-0.88	-0.81	-1.22	-0.97	n.d.	▼	▼
SAOUHSC_01223	Gid	tRNA (uracil-5)-methyltransferase Gid		-0.10	-0.47	-0.48	-0.34	0.35	0.28	0.22	—	—
SAOUHSC_01228	CodY	transcriptional repressor CodY		0.33	0.44	0.21	0.47	0.26	-0.16	-0.29	—	—
SAOUHSC_01235	PyrH	uridylyate kinase		-0.18	-0.55	-0.49	-0.51	0.03	-0.20	-0.16	—	—
SAOUHSC_01240	ProS	prolyl-tRNA synthetase		-0.01	0.22	-0.22	-0.26	-0.34	-0.52	-0.16	—	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_01251	PnpA	polynucleotide phosphorylase/polyadenylase		-0.21	-0.71	-0.74	-0.66	0.01	-0.25	-0.19	▼	—
SAOUHSC_01252	RnjB	hypothetical protein		0.05	-0.68	-0.57	-0.58	-0.35	-0.39	-0.36	▼	—
SAOUHSC_01256		hypothetical protein		0.11	-0.20	-0.52	-0.32	n.d.	1.33	0.05	—	▲
SAOUHSC_01263	RnyI cvfA	phosphodiesterase		0.10	-0.60	-0.46	-0.45	-0.92	-0.72	-0.47	—	▼
SAOUHSC_01264		hypothetical protein		0.81	-0.17	-0.56	-0.39	-1.43	-0.98	-0.11	—	▼
SAOUHSC_01265		hypothetical protein		0.03	-0.51	-0.06	-0.03	n.d.	0.82	0.49	—	▲
SAOUHSC_01284		hypothetical protein		0.07	0.14	0.04	-0.03	n.d.	-0.24	n.d.	—	—
SAOUHSC_01317		hypothetical protein		0.02	0.63	0.32	0.21	-0.37	-0.58	n.d.	—	—
SAOUHSC_01323		hypothetical protein		0.40	0.61	0.14	0.55	-0.18	0.06	-0.47	—	—
SAOUHSC_01336		hypothetical protein		0.51	0.19	-0.69	-0.68	6.41	-1.06	-1.38	▼	▼
SAOUHSC_01349		hypothetical protein		0.59	1.48	0.65	0.93	n.d.	-0.84	n.d.	▲	▼
SAOUHSC_01354	AlsT	sodium:alanine symporter family protein		-0.18	-0.85	-0.20	-0.39	1.16	-0.28	n.d.	—	—
SAOUHSC_01383		hypothetical protein		0.30	0.69	0.25	0.22	-1.38	-1.71	n.d.	—	▼
SAOUHSC_01391	Cvf8	hypothetical protein		-0.30	-0.34	-0.71	-0.49	n.d.	-0.42	-0.02	—	—
SAOUHSC_01392		ABC transporter ATP-binding protein		-0.19	-0.77	-0.73	-0.64	-0.03	-0.31	-0.54	▼	—
SAOUHSC_01408		hypothetical protein		0.41	0.74	0.32	0.29	n.d.	-1.18	n.d.	—	▼
SAOUHSC_01414		hypothetical protein		0.07	0.12	0.31	-0.04	-0.52	0.63	n.d.	—	—
SAOUHSC_01415		hypothetical protein		0.48	0.70	1.05	1.29	0.20	0.11	0.31	▲	—
SAOUHSC_01433	Fak82	hypothetical protein		0.20	0.24	0.17	0.47	-0.77	-0.04	-1.06	—	▼
SAOUHSC_01436		hypothetical protein		0.38	-0.11	-0.09	-0.12	-0.48	-0.59	-0.91	—	▼
SAOUHSC_01455		hypothetical protein		0.19	-0.03	-0.18	-0.16	0.49	0.32	0.40	—	—
SAOUHSC_01575		helix-turn-helix domain-containing protein		0.65	0.96	1.09	1.16	n.d.	0.92	n.d.	▲	▲
SAOUHSC_01586	SrrA	DNA-binding response regulator		0.41	0.47	0.26	0.42	0.50	-0.70	-1.27	—	▼
SAOUHSC_01604		hypothetical protein		0.44	0.50	-0.25	0.01	n.d.	-0.39	0.86	—	—
SAOUHSC_01606		peptidase T		0.51	0.79	1.00	1.17	-0.93	n.d.	3.41	▲	▲
SAOUHSC_01610		hypothetical protein		-0.09	0.01	-0.62	-0.80	n.d.	0.20	n.d.	▼	—
SAOUHSC_01661		hypothetical protein		0.37	-0.10	-0.43	-0.12	n.d.	1.08	n.d.	—	▲
SAOUHSC_01666	GlyS	glycyl-tRNA synthetase		0.66	-0.07	-0.17	-0.01	-0.39	-1.17	-0.36	—	—
SAOUHSC_01676		hypothetical protein		-0.26	0.26	0.32	0.21	-0.52	-0.72	-0.36	—	—
SAOUHSC_01698		hypothetical protein		0.08	-0.36	-0.82	-0.27	-0.39	-0.13	0.48	—	—
SAOUHSC_01729		hypothetical protein		n.d.	n.d.	n.d.	n.d.	0.26	-1.99	n.d.	n.d.	▼
SAOUHSC_01746	SecF	bifunctional preprotein translocase subunit SecD/SecE		-0.55	-0.23	-0.04	-0.11	-0.36	-0.77	-0.78	—	▼
SAOUHSC_01767	ValS	valyl-tRNA synthetase		0.29	-0.10	-0.31	-0.06	-0.27	-0.25	-0.15	—	—
SAOUHSC_01779	Tlg	trigger factor		0.34	0.15	-0.14	-0.12	-0.04	0.03	-0.13	—	—
SAOUHSC_01782		hypothetical protein		0.51	0.83	0.28	0.23	-0.50	-1.22	n.d.	—	▼
SAOUHSC_01786	InfC	translation initiation factor IF-3		-0.33	-1.02	-1.15	-0.90	-0.33	0.14	-0.62	▼	—
SAOUHSC_01815		metal-dependent hydrolase		-0.41	-0.98	n.d.	0.58	-0.24	0.35	1.06	—	—
SAOUHSC_01816	PepQ	hypothetical protein		0.14	1.67	0.94	1.07	n.d.	n.d.	-0.54	▲	—
SAOUHSC_01839	TyrS	tyrosyl-tRNA synthetase		0.34	-0.07	-0.26	-0.13	-0.15	0.17	0.14	—	—
SAOUHSC_01854		hypothetical protein		0.24	-0.45	-0.11	0.10	0.85	-0.14	0.11	—	—
SAOUHSC_01855		hypothetical protein		-0.04	-0.38	0.29	0.30	0.26	-0.01	0.17	—	—
SAOUHSC_01858		hypothetical protein		0.33	-0.06	-0.13	-0.14	0.09	-0.33	-0.24	—	—
SAOUHSC_01860		hypothetical protein		0.66	0.68	0.68	0.69	-0.24	-0.37	-0.56	▲	—
SAOUHSC_01868		dipeptidase PepV		0.52	1.19	0.55	0.74	-0.02	0.04	-0.06	▲	—
SAOUHSC_01869		hypothetical protein		0.63	-0.10	0.15	0.28	-0.43	-0.70	-0.93	—	▼
SAOUHSC_01875	LeuS	leucyl-tRNA synthetase		0.47	0.43	-0.14	-0.01	-0.49	-0.47	-0.36	—	—
SAOUHSC_01895		hypothetical protein		-0.31	-0.31	-0.82	-0.95	0.33	n.d.	n.d.	▼	—

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
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SAOUHSC_01908		hypothetical protein		-0.11	-0.23	-0.08	-0.16	n.d.	0.98	2.84	—	▲
SAOUHSC_01964	TRAP	hypothetical protein		0.69	0.90	0.71	0.78	0.51	0.66	0.99	▲	▲
SAOUHSC_01968	Hit	hypothetical protein		0.74	0.81	1.13	1.46	0.48	0.44	0.80	▲	—
SAOUHSC_01969		hypothetical protein		-0.14	-0.01	0.01	0.40	1.19	0.64	1.03	—	▲
SAOUHSC_01973	Cbf1	3-5 exoribonuclease YhaM		-0.41	-0.47	-0.36	-0.55	n.d.	0.48	0.23	—	—
SAOUHSC_01974		hypothetical protein		-0.36	-0.20	-0.12	-0.04	0.25	0.28	1.15	—	—
SAOUHSC_01977		hypothetical protein		0.67	0.48	0.17	0.56	-0.08	-0.36	-0.62	—	—
SAOUHSC_01987		hypothetical protein		0.87	0.35	0.52	0.49	0.66	0.39	1.27	—	▲
SAOUHSC_02013		hypothetical protein		1.17	-0.68	0.45	0.82	0.84	1.19	0.88	—	▲
SAOUHSC_02073		hypothetical protein		n.d.	n.d.	n.d.	n.d.	2.53	n.d.	3.38	n.d.	▲
SAOUHSC_02098	VraR	DNA-binding response regulator VraR		0.62	2.09	1.26	1.16	0.42	1.26	3.60	▲	▲
SAOUHSC_02107		UDP-N-acetylmuramyl tripeptide synthetase		-0.41	-0.41	-0.47	-0.47	0.13	0.06	0.67	—	—
SAOUHSC_02108	FtnA	ferritin		0.54	-0.77	-0.05	0.18	0.23	-0.24	0.14	—	—
SAOUHSC_02114		putative lipid kinase		0.41	0.16	-0.27	0.07	-0.28	0.48	0.51	—	—
SAOUHSC_02145		hypothetical protein		0.56	-0.20	n.d.	0.83	-0.08	-0.55	-0.11	—	—
SAOUHSC_02150		hypothetical protein		0.95	1.19	1.54	1.83	-0.35	-0.14	-0.54	▲	—
SAOUHSC_02152	PmtC	ABC transporter ATP-binding protein		0.39	1.15	1.84	1.98	n.d.	0.52	-0.18	▲	—
SAOUHSC_02218		hypothetical protein		0.22	0.25	0.20	0.55	-0.43	-0.11	-0.06	—	—
SAOUHSC_02297		S1 RNA-binding domain-containing protein		-0.17	0.02	-0.48	-0.50	-0.44	-0.49	-0.40	—	—
SAOUHSC_02370		hypothetical protein		0.06	-0.17	-0.41	-0.43	n.d.	1.18	2.23	—	▲
SAOUHSC_02372		hypothetical protein		0.06	-0.05	-1.49	-1.66	n.d.	0.69	1.53	▼	▲
SAOUHSC_02373		hypothetical protein		0.58	-0.08	0.02	0.03	n.d.	2.72	n.d.	—	▲
SAOUHSC_02383		hypothetical protein		-0.02	-0.42	-0.58	-0.57	0.60	0.19	-0.78	—	—
SAOUHSC_02387		hypothetical protein		0.88	-0.45	0.42	0.73	0.46	0.12	0.17	—	—
SAOUHSC_02441	Asp23	alkaline shock protein 23		0.55	-0.84	0.29	0.78	0.70	0.33	0.43	—	—
SAOUHSC_02442		hypothetical protein		0.47	-0.46	0.57	0.76	n.d.	0.04	n.d.	—	—
SAOUHSC_02443	AmaP	hypothetical protein		0.34	-1.38	-0.24	0.17	1.96	0.61	1.15	—	▲
SAOUHSC_02460		hypothetical protein		0.53	0.82	0.21	0.26	0.41	0.30	-0.40	—	—
SAOUHSC_02491	SecY	preprotein translocase subunit SecY		-0.21	-0.66	-0.54	-0.56	-0.24	-0.38	n.d.	—	—
SAOUHSC_02554	FhuD2	hypothetical protein		-1.70	0.21	-0.28	-0.41	-0.90	-1.49	-1.56	—	▼
SAOUHSC_02566	SarR	hypothetical protein		-0.76	-0.05	-0.34	-0.25	3.71	0.33	0.05	—	—
SAOUHSC_02574		hypothetical protein		0.06	-0.22	-0.19	-0.10	-0.16	0.42	-0.04	—	—
SAOUHSC_02611	LyrA	hypothetical protein		0.24	-0.02	-0.42	-0.49	-1.05	-0.46	n.d.	—	▼
SAOUHSC_02666		hypothetical protein		-0.13	-0.21	-0.52	-0.42	n.d.	-1.06	n.d.	—	▼
SAOUHSC_02724		hypothetical protein		0.59	2.46	2.09	2.03	2.17	n.d.	n.d.	▲	▲
SAOUHSC_02747		hypothetical protein		0.46	1.22	0.59	0.79	n.d.	0.23	n.d.	▲	—
SAOUHSC_02820		hypothetical protein		-0.56	-2.08	-0.99	-0.69	0.12	0.36	0.56	▼	—
SAOUHSC_02829	Frp	NAD(P)H:Flavin oxidoreductase		0.45	-0.04	1.41	1.65	1.11	-0.11	0.30	▲	—
SAOUHSC_02844		hypothetical protein		0.15	0.66	0.91	0.90	0.35	0.36	n.d.	▲	—
SAOUHSC_02862	ClpL	ATP-dependent Clp protease, ATP-binding subunit ClpC		0.53	1.09	1.15	1.52	0.37	-0.08	-0.34	▲	—
SAOUHSC_02895		hypothetical protein		-0.11	-0.59	-0.24	-0.06	n.d.	0.69	n.d.	—	▲
SAOUHSC_02900		hypothetical protein		0.92	-0.30	0.71	0.92	-0.44	-0.93	-2.43	▲	▼
SAOUHSC_02929		acetyl-CoA synthetase		0.24	0.20	-0.14	-0.05	0.11	0.16	-0.04	—	—
SAOUHSC_02972	IsaB	immunodominant antigen B		-0.56	2.44	3.68	3.90	2.35	n.d.	n.d.	▲	▲
SAOUHSC_02978		phage infection protein		-0.26	-0.73	-1.03	-0.93	1.24	0.77	n.d.	▼	▲
SAOUHSC_02980		hypothetical protein		0.39	0.92	0.75	0.83	n.d.	-0.45	0.78	▲	—
SAOUHSC_03022		hypothetical protein		0.64	-0.69	0.61	0.92	0.99	1.04	0.56	▲	▲

locus tag	protein symbol	description	theSEED functional category	S9 cell line infection model				murine pneumonia model			median over 8,24 and 32h ratio	
				exp.	8h	24h	32h	8h	24h	32h	median tendence (S9) - 1.5fc cutoff	median tendence (mice) - 1.5fc cutoff
SAOUHSC_03052	GidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA		-0.27	-0.32	-0.55	-0.64	n.d.	1.18	0.09	—	▲



supplemental table S7:

locus	<i>S. aureus</i> strain	gene	description	localization (PSORT)	molar weight [Da] [μg/μmol] Uniprot	protein mix
SA0393	N315	<i>set15</i>	superantigen-like protein SET15	extracellular	25440	mix 2
SA0506	N315	<i>tuf</i>	elongation factor Tu	cytoplasmic membrane	43104	mix 2
SA1063	N315	<i>prkC</i>	protein kinase	extracellular	74377	mix 2
SA1646	N315	<i>sei</i>	staphylococcal enterotoxin I	extracellular	27864	mix 2
SA1648	N315	<i>seo</i>	staphylococcal enterotoxin O	extracellular	29836	mix 2
SA1816	N315	<i>sel</i>	staphylococcal enterotoxin L	extracellular	27496	mix 2
SA1819	N315	<i>tsst-1</i>	toxic shock syndrome toxin-1	extracellular	26393	mix 2
SA06159_01007	JKD6159	<i>efb</i>	extracellular fibrinogen binding protein	extracellular	12597	mix 2
SAB0363	RF122	<i>sec</i>	staphylococcal enterotoxin C	extracellular	31267	mix 2
SACOL0886	COL	<i>sek</i>	staphylococcal enterotoxin K	extracellular	27727	mix 2
SACOL0887	COL	<i>seq</i>	staphylococcal enterotoxin Q	extracellular	28185	mix 2
SACOL0908	COL	<i>SACOL0908</i>	hypothetical protein	unknown	20346	mix 2
SACOL1722	COL	<i>tig</i>	trigger factor	cytoplasmic	48609	mix 2
SACOL1802	COL	<i>SACOL1802</i>	hypothetical protein	unknown	15734	mix 2
SACOL2197	COL	<i>SACOL2197</i>	surface protein	cytoplasmic membrane	15448	mix 2
SAKOR_01991	CN1	<i>fhvD2</i>	ferrichrome-binding protein	non available	34843	mix 2
SAOUHSC_00051	NCTC8325/HG001	<i>plc</i>	phosphatidylinositol phosphodiesterase precursor, putative	extracellular	37087	mix 1
SAOUHSC_00081	NCTC8325/HG001	<i>SAOUHSC_00081</i>	aldolase	cytoplasmic	28588	mix 2
SAOUHSC_00192	NCTC8325/HG001	<i>coa</i>	coagulase	extracellular	71718	mix 1
SAOUHSC_00196	NCTC8325/HG001	<i>SAOUHSC_00196</i>	3-hydroxyacyl-CoA dehydrogenase protein	unknown	84608	mix 1
SAOUHSC_00257	NCTC8325/HG001	<i>SAOUHSC_00257</i>	ESAT-6 family virulence protein	extracellular	11036	mix 1
SAOUHSC_00300	NCTC8325/HG001	<i>geh</i>	lipase precursor	extracellular	76418	mix 1
SAOUHSC_00383	NCTC8325/HG001	<i>set6</i>	superantigen-like protein	extracellular	25647	mix 1
SAOUHSC_00384	NCTC8325/HG001	<i>set7</i>	superantigen-like protein	extracellular	26500	mix 1
SAOUHSC_00386	NCTC8325/HG001	<i>set8</i>	superantigen-like protein	extracellular	40181	mix 1
SAOUHSC_00389	NCTC8325/HG001	<i>SAOUHSC_00389</i>	superantigen-like protein	extracellular	34072	mix 1
SAOUHSC_00390	NCTC8325/HG001	<i>set10</i>	superantigen-like protein 5	extracellular	27170	mix 1
SAOUHSC_00391	NCTC8325/HG001	<i>SAOUHSC_00391</i>	superantigen-like protein	extracellular	26656	mix 1
SAOUHSC_00392	NCTC8325/HG001	<i>set11</i>	superantigen-like protein 7	extracellular	26168	mix 1
SAOUHSC_00393	NCTC8325/HG001	<i>SAOUHSC_00393</i>	superantigen-like protein	extracellular	26875	mix 1
SAOUHSC_00394	NCTC8325/HG001	<i>SAOUHSC_00394</i>	superantigen-like protein	extracellular	26676	mix 1
SAOUHSC_00399	NCTC8325/HG001	<i>set15</i>	superantigen-like protein	extracellular	25366	mix 1
SAOUHSC_00401	NCTC8325/HG001	<i>SAOUHSC_00401</i>	hypothetical protein SAOUHSC_00401	unknown	11302	mix 2
SAOUHSC_00427	NCTC8325/HG001	<i>aaa/sle1</i>	autolysin precursor, putative	cell wall	35836	mix 2
SAOUHSC_00749	NCTC8325/HG001	<i>SAUSA300_0721</i>	transferrin receptor	cytoplasmic membrane	37854	mix 2
SAOUHSC_00795	NCTC8325/HG001	<i>SAOUHSC_00795</i>	glyceraldehyde-3-phosphate dehydrogenase, type I	cytoplasmic	36281	mix 2
SAOUHSC_00897	NCTC8325/HG001	<i>glpQ</i>	glycerophosphoryl diester phosphodiesterase	extracellular	35311	mix 1
SAOUHSC_00918	NCTC8325/HG001	<i>SAOUHSC_00918</i>	truncated MHC class II analog protein	cytoplasmic membrane	15838	mix 2
SAOUHSC_01082	NCTC8325/HG001	<i>isdC</i>	LPXTG cell wall surface anchor protein	unknown	24855	mix 2
SAOUHSC_01114	NCTC8325/HG001	<i>fib</i>	fibrinogen-binding protein	extracellular	18765	mix 1
SAOUHSC_01115	NCTC8325/HG001	<i>SAOUHSC_01115</i>	fibrinogen-binding protein precursor-like protein	unknown	13114	mix 2
SAOUHSC_01121	NCTC8325/HG001	<i>hly</i>	alpha-hemolysin precursor	extracellular	35973	mix 1
SAOUHSC_01653	NCTC8325/HG001	<i>sodA2</i>	superoxide dismutase, Mn, putative	extracellular	22711	mix 1
SAOUHSC_01683	NCTC8325/HG001	<i>dnaK</i>	DNAK protein, putative	cytoplasmic	66361	mix 1
SAOUHSC_01714	NCTC8325/HG001	<i>SAOUHSC_01714</i>	transcription elongation factor GreA	cytoplasmic	17743	mix 2
SAOUHSC_01935	NCTC8325/HG001	<i>spiF</i>	serine protease SpiF, putative	extracellular	25655	mix 1
SAOUHSC_01936	NCTC8325/HG001	<i>spiE</i>	serine protease SpiE	extracellular	25679	mix 2
SAOUHSC_01938	NCTC8325/HG001	<i>spiD</i>	serine protease SpiD	extracellular	25678	mix 2
SAOUHSC_01939	NCTC8325/HG001	<i>spiC</i>	serine protease SpiC	extracellular	26098	mix 2
SAOUHSC_01942	NCTC8325/HG001	<i>spiA</i>	serine protease SpiA	extracellular	25549	mix 2
SAOUHSC_01972	NCTC8325/HG001	<i>prfA</i>	protein export protein PrfA, putative	cytoplasmic membrane	35638	mix 1
SAOUHSC_02003	NCTC8325/HG001	<i>grfA</i>	γ transporter, ATP-binding/permease protein, putative	cytoplasmic membrane	64863	mix 2
SAOUHSC_02169	NCTC8325/HG001	<i>chp</i>	chemotaxis-inhibiting protein CHIPS	unknown	17040	mix 1
SAOUHSC_02171	NCTC8325/HG001	<i>sak</i>	staphylokinase precursor, putative	extracellular	18504	mix 1
SAOUHSC_02254	NCTC8325/HG001	<i>groEL</i>	chaperonin, 60 kDa, GrpEL, putative	cytoplasmic	57630	mix 1
SAOUHSC_02257	NCTC8325/HG001	<i>sdrH</i>	sdrH protein	unknown	46620	mix 2
SAOUHSC_02260	NCTC8325/HG001	<i>hld</i>	hemolysin D	extracellular	2979	mix 2
SAOUHSC_02466	NCTC8325/HG001	<i>SAOUHSC_02466</i>	truncated MHC class II analog protein	cytoplasmic membrane	15448	mix 1
SAOUHSC_02708	NCTC8325/HG001	<i>hlgA</i>	gamma-hemolysin h-gamma-ii subunit, putative	extracellular	34956	mix 2
SAOUHSC_02710	NCTC8325/HG001	<i>hlgB</i>	leukocidin f subunit precursor	extracellular	36711	mix 2
SAOUHSC_02802	NCTC8325/HG001	<i>fnbpB</i>	fibronectin binding protein B, putative	cell wall	101025	mix 2
SAOUHSC_02803	NCTC8325/HG001	<i>fnbA</i>	fibronectin binding protein A	cell wall	111780	mix 2
SAOUHSC_02887	NCTC8325/HG001	<i>isaA</i>	immunodominant antigen A, putative	extracellular	24203	mix 1
SAOUHSC_02972	NCTC8325/HG001	<i>isaB</i>	immunodominant antigen B	extracellular	19370	mix 1
SAOUHSC_03006	NCTC8325/HG001	<i>lip</i>	lipase	extracellular	76675	mix 1
SAP057A_011	plasmid SAP057A	<i>sspA</i>	serine proteinase SspA	non available	30765	mix 2
SAR0567	MRSA252	<i>bbp</i>	bone sialoprotein-binding protein	non available	123326	mix 2
SAUSA300_1065	USA300_FPR3757	<i>eta</i>	exfoliative toxin A	cytoplasmic membrane	35310	mix 2
SAUSA300_1381	USA300_FPR3757	<i>lukF-PV</i>	Pantaoon-Valentin-leukocidin, LukF-PV	extracellular	36962	mix 2
SAUSA300_1382	USA300_FPR3757	<i>lukS-PV</i>	Pantaoon-Valentin-leukocidin, LukS-PV	extracellular	35313	mix 2
SAUSA300_1982	USA300_FPR3757	<i>groES</i>	chaperonin, GroES	cytoplasmic	57630	mix 2
SAUSA300_2296	USA300_FPR3757	<i>SAUSA300_2296</i>	esterase-like protein	cytoplasmic	35545	mix 2
USA300HOU_1167	USA300_TCH1516	<i>fabG</i>	3-oxoacyl-[acyl-carrier-protein] reductase	cytoplasmic	26146	mix 2