

Table S2. Comparison of genes curated as essential after growth in BHI in this study compared to previous study of essentiality in *S. aureus*

| Locus | Product | Essential in BHI by TnSeq ¹ | Essential in <i>S.aureus</i> list ² |
|---------------|--|---|---|
| SAOUHSC_00022 | * hypothetical protein | | |
| SAOUHSC_00486 | * hypothetical protein | | |
| SAOUHSC_01239 | * hypothetical protein | | |
| SAOUHSC_01857 | * hypothetical protein | | |
| SAOUHSC_02383 | * hypothetical protein | | |
| SAOUHSC_00889 | * monovalent cation/H ⁺ antiporter subunit A | | |
| SAOUHSC_01263 | * phosphodiesterase | | |
| SAOUHSC_01203 | * ribonuclease III | | |
| SAOUHSC_01698 | hypothetical protein | | |
| SAOUHSC_00017 | 50S ribosomal protein L9 | | |
| SAOUHSC_00985 | naphthoate synthase | | |
| SAOUHSC_01487 | ubiquinone/menaquinone biosynthesis methyltransferase | | |
| SAOUHSC_00374 | inosine-5'-monophosphate dehydrogenase | | |
| SAOUHSC_00884 | putative monovalent cation/H ⁺ antiporter subunit F | | |
| SAOUHSC_00886 | putative monovalent cation/H ⁺ antiporter subunit D | | |
| SAOUHSC_00887 | putative monovalent cation/H ⁺ antiporter subunit C | | |
| SAOUHSC_00888 | putative monovalent cation/H ⁺ antiporter subunit B | | |
| SAOUHSC_01483 | chorismate synthase | | |
| SAOUHSC_01772 | delta-aminolevulinic acid dehydratase | | |
| SAOUHSC_01773 | uroporphyrinogen III synthase | | |
| SAOUHSC_01774 | porphobilinogen deaminase | | |
| SAOUHSC_00023 | hypothetical protein | | |
| SAOUHSC_00038 | hypothetical protein | | |
| SAOUHSC_00100 | deoxyribose-phosphate aldolase | | |
| SAOUHSC_00112 | IS200 family transposase | | |
| SAOUHSC_00275 | hypothetical protein | | |
| SAOUHSC_00396 | hypothetical protein | | |
| SAOUHSC_00453 | hypothetical protein | | |
| SAOUHSC_00473 | hypothetical protein | | |
| SAOUHSC_00481 | hypothetical protein | | |
| SAOUHSC_00526 | putative ribosomal protein L7Ae-like | | |
| SAOUHSC_00573 | putative heme peroxidase | | |
| SAOUHSC_00610 | hypothetical protein | | |
| SAOUHSC_00680 | hypothetical protein | | |
| SAOUHSC_00735 | hypothetical protein | | |
| SAOUHSC_00778 | hypothetical protein | | |
| SAOUHSC_00786 | hypothetical protein | | |
| SAOUHSC_00794 | glycolytic operon regulator | | |
| SAOUHSC_00819 | hypothetical protein | | |
| SAOUHSC_00857 | hypothetical protein | | |
| SAOUHSC_00867 | hypothetical protein | | |
| SAOUHSC_00885 | putative monovalent cation/H ⁺ antiporter subunit E | | |
| SAOUHSC_00896 | hypothetical protein | | |
| SAOUHSC_00938 | hypothetical protein | | |
| SAOUHSC_00939 | hypothetical protein | | |
| SAOUHSC_00981 | hypothetical protein | | |
| SAOUHSC_01003 | hypothetical protein | | |
| SAOUHSC_01023 | hypothetical protein | | |
| SAOUHSC_01118 | hypothetical protein | | |

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|---------------|---|--|
| SAOUHSC_01142 | cell division protein MraZ | |
| SAOUHSC_01143 | S-adenosyl-methyltransferase MraW | |
| SAOUHSC_01158 | hypothetical protein | |
| SAOUHSC_01196 | fatty acid biosynthesis transcriptional regulator | |
| SAOUHSC_01200 | hypothetical protein | |
| SAOUHSC_01224 | site-specific recombinase | |
| SAOUHSC_01230 | hypothetical protein | |
| SAOUHSC_01233 | hypothetical protein | |
| SAOUHSC_01259 | hypothetical protein | |
| SAOUHSC_01262 | recombinase A | |
| SAOUHSC_01270 | hypothetical protein | |
| SAOUHSC_01289 | hypothetical protein | |
| SAOUHSC_01293 | hypothetical protein | |
| SAOUHSC_01294 | hypothetical protein | |
| SAOUHSC_01338 | hypothetical protein | |
| SAOUHSC_01390 | putative transposase | |
| SAOUHSC_01409 | putative transposase | |
| SAOUHSC_01410 | putative transposase | |
| SAOUHSC_01441 | hypothetical protein | |
| SAOUHSC_01544 | hypothetical protein | |
| SAOUHSC_01550 | hypothetical protein | |
| SAOUHSC_01551 | hypothetical protein | |
| SAOUHSC_01554 | PV83 orf 27-like protein | |
| SAOUHSC_01555 | hypothetical protein | |
| SAOUHSC_01573 | hypothetical protein | |
| SAOUHSC_01578 | hypothetical protein | |
| SAOUHSC_01579 | hypothetical protein | |
| SAOUHSC_01580 | phi PVL ORF 30-like protein | |
| SAOUHSC_01619 | exodeoxyribonuclease VII small subunit | |
| SAOUHSC_01669 | hypothetical protein | |
| SAOUHSC_01687 | hypothetical protein | |
| SAOUHSC_01760 | hypothetical protein | |
| SAOUHSC_01776 | glutamyl-tRNA reductase | |
| SAOUHSC_01778 | ATP-dependent protease ATP-binding subunit ClpX | |
| SAOUHSC_01789 | hypothetical protein | |
| SAOUHSC_01804 | transposase | |
| SAOUHSC_01805 | putative transposase | |
| SAOUHSC_01841 | hypothetical protein | |
| SAOUHSC_01858 | hypothetical protein | |
| SAOUHSC_01859 | hypothetical protein | |
| SAOUHSC_01905 | putative transposase | |
| SAOUHSC_01906 | putative transposase | |
| SAOUHSC_01911 | IS200 family transposase | |
| SAOUHSC_01924 | hypothetical protein | |
| SAOUHSC_01961 | ferrochelatase | |
| SAOUHSC_01962 | uroporphyrinogen decarboxylase | |
| SAOUHSC_01973 | 3'-5' exoribonuclease YhaM | |
| SAOUHSC_01977 | hypothetical protein | |
| SAOUHSC_01993 | transposase | |
| SAOUHSC_02002 | hypothetical protein | |
| SAOUHSC_02017 | hypothetical protein | |
| SAOUHSC_02053 | transcriptional activator rinb-like protein | |
| SAOUHSC_02054 | hypothetical protein | |

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|---------------|--|
| SAOUHSC_02055 | hypothetical protein |
| SAOUHSC_02065 | hypothetical protein |
| SAOUHSC_02076 | phi PVL orf 38-like protein |
| SAOUHSC_02084 | phage repressor protein |
| SAOUHSC_02154 | ABC transporter ATP-binding protein |
| SAOUHSC_02164 | hypothetical protein |
| SAOUHSC_02175 | hypothetical protein |
| SAOUHSC_02183 | hypothetical protein |
| SAOUHSC_02209 | hypothetical protein |
| SAOUHSC_02214 | hypothetical protein |
| SAOUHSC_02215 | hypothetical protein |
| SAOUHSC_02219 | phi ETA orf 20-like protein |
| SAOUHSC_02224 | phi PVL orf 38-like protein |
| SAOUHSC_02235 | repressor |
| SAOUHSC_02237 | hypothetical protein |
| SAOUHSC_02238 | phi PVL ORF 30-like protein |
| SAOUHSC_02294 | hypothetical protein |
| SAOUHSC_02307 | hypothetical protein |
| SAOUHSC_02325 | hypothetical protein |
| SAOUHSC_02332 | hypothetical protein |
| SAOUHSC_02379 | deoxyribose-phosphate aldolase |
| SAOUHSC_02410 | transposase |
| SAOUHSC_02411 | hypothetical protein |
| SAOUHSC_02412 | hypothetical protein |
| SAOUHSC_02416 | hypothetical protein |
| SAOUHSC_02437 | hypothetical protein |
| SAOUHSC_02438 | hypothetical protein |
| SAOUHSC_02440 | hypothetical protein |
| SAOUHSC_02534 | hypothetical protein |
| SAOUHSC_02707 | hypothetical protein |
| SAOUHSC_02721 | hypothetical protein |
| SAOUHSC_02745 | hypothetical protein |
| SAOUHSC_02872 | hypothetical protein |
| SAOUHSC_03043 | hypothetical protein |
| SAOUHSC_01337 | transketolase |
| SAOUHSC_00350 | 30S ribosomal protein S18 |
| SAOUHSC_02366 | fructose-bisphosphate aldolase |
| SAOUHSC_00788 | hypothetical protein |
| SAOUHSC_01210 | tRNA (guanine-N(1)-)methyltransferase |
| SAOUHSC_01211 | 50S ribosomal protein L19 |
| SAOUHSC_01466 | Holliday junction-specific endonuclease |
| SAOUHSC_01661 | hypothetical protein |
| SAOUHSC_01742 | GTP pyrophosphokinase |
| SAOUHSC_01750 | Holliday junction DNA helicase RuvB |
| SAOUHSC_01751 | Holliday junction DNA helicase RuvA |
| SAOUHSC_03049 | hypothetical protein |
| SAOUHSC_03052 | tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA |
| SAOUHSC_01678 | 30S ribosomal protein S21 |
| SAOUHSC_00336 | acetyl-CoA acetyltransferase |
| SAOUHSC_00903 | Signal peptidase IB |
| SAOUHSC_01188 | hypothetical protein |
| SAOUHSC_01361 | transcriptional regulator |
| SAOUHSC_01739 | hypothetical protein |

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|---------------|--|--|--|
| SAOUHSC_01782 | hypothetical protein | | |
| SAOUHSC_02859 | hydroxymethylglutaryl-CoA reductase, degradative | | |
| SAOUHSC_03053 | tRNA modification GTPase TrmE | | |
| SAOUHSC_00645 | glycerol-3-phosphate cytidylyltransferase | | |
| SAOUHSC_00803 | ribonuclease R | | |
| SAOUHSC_00892 | hypothetical protein | | |
| SAOUHSC_01250 | 30S ribosomal protein S15 | | |
| SAOUHSC_01668 | GTP-binding protein Era | | |
| SAOUHSC_01721 | hypothetical protein | | |
| SAOUHSC_01770 | hypothetical protein | | |
| SAOUHSC_01866 | hypothetical protein | | |
| SAOUHSC_01928 | transposase family protein | | |
| SAOUHSC_02260 | delta-hemolysin | | |
| SAOUHSC_01720 | Holliday junction resolvase-like protein | | |
| SAOUHSC_01930 | hypothetical protein | | |
| SAOUHSC_02612 | ribose-5-phosphate isomerase A | | |
| SAOUHSC_02337 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | | |
| SAOUHSC_01078 | ribosomal protein L32 | | |
| SAOUHSC_01216 | succinyl-CoA synthetase subunit beta | | |
| SAOUHSC_01352 | DNA topoisomerase IV subunit A | | |
| SAOUHSC_01359 | hypothetical protein | | |
| SAOUHSC_01806 | pyruvate kinase | | |
| SAOUHSC_01979 | hypothetical protein | | |
| SAOUHSC_02575 | hypothetical protein | | |
| SAOUHSC_02805 | hypothetical protein | | |
| SAOUHSC_00575 | hypothetical protein | | |
| SAOUHSC_01208 | 30S ribosomal protein S16 | | |
| SAOUHSC_00760 | hypothetical protein | | |
| SAOUHSC_00998 | fmt protein | | |
| SAOUHSC_00003 | hypothetical protein | | |
| SAOUHSC_01038 | peptide deformylase | | |
| SAOUHSC_01040 | pyruvate dehydrogenase complex, E1 component subunit alpha | | |
| SAOUHSC_01050 | hypothetical protein | | |
| SAOUHSC_01100 | thioredoxin | | |
| SAOUHSC_01119 | hypothetical protein | | |
| SAOUHSC_01462 | hypothetical protein | | |
| SAOUHSC_01504 | ferredoxin | | |
| SAOUHSC_00474 | 50S ribosomal protein L25/general stress protein Ctc | | |
| SAOUHSC_00620 | accessory regulator A | | |
| SAOUHSC_00793 | hypothetical protein | | |
| SAOUHSC_00798 | phosphoglyceromutase | | |
| SAOUHSC_00881 | hypothetical protein | | |
| SAOUHSC_00922 | hypothetical protein | | |
| SAOUHSC_01077 | hypothetical protein | | |
| SAOUHSC_02572 | hypothetical protein | | |
| SAOUHSC_02757 | hypothetical protein | | |
| SAOUHSC_02791 | pyrophosphohydrolase | | |
| SAOUHSC_00001 | chromosomal replication initiation protein | | |
| SAOUHSC_00002 | DNA polymerase III subunit beta | | |
| SAOUHSC_00005 | DNA gyrase, B subunit | | |
| SAOUHSC_00006 | DNA gyrase, A subunit | | |
| SAOUHSC_00009 | seryl-tRNA synthetase | | |
| SAOUHSC_00015 | hypothetical protein | | |

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| SAOUHSC_00018 | replicative DNA helicase |
| SAOUHSC_00020 | two-component response regulator |
| SAOUHSC_00021 | sensory box histidine kinase VicK |
| SAOUHSC_00223 | teichoic acid biosynthesis protein F |
| SAOUHSC_00225 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase |
| SAOUHSC_00226 | hypothetical protein |
| SAOUHSC_00227 | hypothetical protein |
| SAOUHSC_00345 | hypothetical protein |
| SAOUHSC_00348 | 30S ribosomal protein S6 |
| SAOUHSC_00349 | bacteriophage L54a, single-stranded DNA binding protein |
| SAOUHSC_00375 | GMP synthase |
| SAOUHSC_00442 | DNA polymerase III subunits gamma and tau |
| SAOUHSC_00444 | hypothetical protein |
| SAOUHSC_00451 | thymidylate kinase |
| SAOUHSC_00454 | DNA polymerase III subunit delta' |
| SAOUHSC_00461 | methionyl-tRNA synthetase |
| SAOUHSC_00471 | bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamini |
| SAOUHSC_00472 | ribose-phosphate pyrophosphokinase |
| SAOUHSC_00475 | peptidyl-tRNA hydrolase |
| SAOUHSC_00482 | hypothetical protein |
| SAOUHSC_00484 | hypothetical protein |
| SAOUHSC_00489 | dihydropteroate synthase |
| SAOUHSC_00490 | dihydronicopterin aldolase |
| SAOUHSC_00491 | 2-amino-4-hydroxy-6- hydroxymethylidihydropteridine pyrophosphokinase |
| SAOUHSC_00493 | lysyl-tRNA synthetase |
| SAOUHSC_00509 | glutamyl-tRNA synthetase |
| SAOUHSC_00510 | serine acetyltransferase |
| SAOUHSC_00511 | cysteinyl-tRNA synthetase |
| SAOUHSC_00516 | preprotein translocase subunit SecE |
| SAOUHSC_00518 | 50S ribosomal protein L11 |
| SAOUHSC_00519 | 50S ribosomal protein L1 |
| SAOUHSC_00520 | 50S ribosomal protein L10 |
| SAOUHSC_00521 | 50S ribosomal protein L7/L12 |
| SAOUHSC_00524 | DNA-directed RNA polymerase subunit beta |
| SAOUHSC_00525 | DNA-directed RNA polymerase subunit beta' |
| SAOUHSC_00527 | 30S ribosomal protein S12 |
| SAOUHSC_00528 | 30S ribosomal protein S7 |
| SAOUHSC_00529 | elongation factor G |
| SAOUHSC_00530 | elongation factor Tu |
| SAOUHSC_00549 | putative GTP cyclohydrolase |
| SAOUHSC_00574 | phosphotransacetylase |
| SAOUHSC_00577 | mevalonate kinase |
| SAOUHSC_00578 | mevalonate diphosphate decarboxylase |
| SAOUHSC_00579 | phosphomevalonate kinase |
| SAOUHSC_00611 | arginyl-tRNA synthetase |
| SAOUHSC_00640 | teichoic acid biosynthesis protein |
| SAOUHSC_00641 | teichoic acids export protein ATP-binding subunit |
| SAOUHSC_00642 | teichoic acid biosynthesis protein |
| SAOUHSC_00643 | tagB protein |
| SAOUHSC_00728 | hypothetical protein |
| SAOUHSC_00741 | ribonucleotide reductase stimulatory protein |
| SAOUHSC_00742 | ribonucleotide-diphosphate reductase subunit alpha |
| SAOUHSC_00743 | ribonucleotide-diphosphate reductase subunit beta |

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| SAOUHSC_00752 | UDP-N-acetylenolpyruvoylglucosamine reductase | | |
| SAOUHSC_00762 | hypothetical protein | | |
| SAOUHSC_00769 | preprotein translocase subunit SecA | | |
| SAOUHSC_00771 | peptide chain release factor 2 | | |
| SAOUHSC_00781 | HPr kinase/phosphorylase | | |
| SAOUHSC_00785 | thioredoxin reductase | | |
| SAOUHSC_00790 | ATP-dependent Clp protease proteolytic subunit | | |
| SAOUHSC_00795 | glyceraldehyde-3-phosphate dehydrogenase, type I | | |
| SAOUHSC_00796 | phosphoglycerate kinase | | |
| SAOUHSC_00797 | triosephosphate isomerase | | |
| SAOUHSC_00799 | phosphopyruvate hydratase | | |
| SAOUHSC_00804 | SsrA-binding protein | | |
| SAOUHSC_00847 | ABC transporter ATP-binding protein | | |
| SAOUHSC_00848 | hypothetical protein | | |
| SAOUHSC_00849 | aminotransferase | | |
| SAOUHSC_00850 | hypothetical protein | | |
| SAOUHSC_00851 | hypothetical protein | | |
| SAOUHSC_00868 | hypothetical protein | | |
| SAOUHSC_00869 | D-alanine--poly(phosphoribitol) ligase subunit 1 | | |
| SAOUHSC_00870 | dltB protein | | |
| SAOUHSC_00871 | D-alanine--poly(phosphoribitol) ligase subunit 2 | | |
| SAOUHSC_00872 | extramembranal protein | | |
| SAOUHSC_00900 | glucose-6-phosphate isomerase | | |
| SAOUHSC_00920 | 3-oxoacyl-(acyl carrier protein) synthase III | | |
| SAOUHSC_00921 | 3-oxoacyl- synthase | | |
| SAOUHSC_00933 | tryptophanyl-tRNA synthetase | | |
| SAOUHSC_00934 | transcriptional regulator Spx | | |
| SAOUHSC_00943 | inorganic polyphosphate/ATP-NAD kinase | | |
| SAOUHSC_00947 | enoyl-(acyl carrier protein) reductase | | |
| SAOUHSC_00954 | UDP-N-acetyl muramoylalanyl-D-glutamate--L-lysine ligase | | |
| SAOUHSC_00957 | hypothetical protein | | |
| SAOUHSC_00980 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase | | |
| SAOUHSC_01028 | phosphocarrier protein HPr | | |
| SAOUHSC_01035 | hypothetical protein | | |
| SAOUHSC_01036 | hypothetical protein | | |
| SAOUHSC_01063 | hypothetical protein | | |
| SAOUHSC_01075 | phosphopantetheine adenylyltransferase | | |
| SAOUHSC_01092 | phenylalanyl-tRNA synthetase subunit alpha | | |
| SAOUHSC_01093 | phenylalanyl-tRNA synthetase subunit beta | | |
| SAOUHSC_01106 | glutamate racemase | | |
| SAOUHSC_01144 | cell division protein | | |
| SAOUHSC_01145 | penicillin-binding protein 1 | | |
| SAOUHSC_01146 | phospho-N-acetyl muramoyl-pentapeptide- transferase | | |
| SAOUHSC_01147 | UDP-N-acetyl muramoyl-L-alanyl-D-glutamate synthetase | | |
| SAOUHSC_01148 | cell division protein | | |
| SAOUHSC_01149 | cell division protein | | |
| SAOUHSC_01150 | cell division protein FtsZ | | |
| SAOUHSC_01154 | hypothetical protein | | |
| SAOUHSC_01159 | isoleucyl-tRNA synthetase | | |
| SAOUHSC_01176 | guanylate kinase | | |
| SAOUHSC_01178 | phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cyste | | |
| SAOUHSC_01179 | primosomal protein N | | |
| SAOUHSC_01183 | methionyl-tRNA formyltransferase | | |

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| SAOUHSC_01189 | ribulose-phosphate 3-epimerase |
| SAOUHSC_01190 | hypothetical protein |
| SAOUHSC_01191 | 50S ribosomal protein L28 |
| SAOUHSC_01197 | putative glycerol-3-phosphate acyltransferase PlsX |
| SAOUHSC_01198 | malonyl CoA-acyl carrier protein transacylase |
| SAOUHSC_01199 | 3-oxoacyl-(acyl-carrier-protein) reductase |
| SAOUHSC_01201 | acyl carrier protein |
| SAOUHSC_01205 | signal recognition particle-docking protein FtsY |
| SAOUHSC_01207 | signal recognition particle protein |
| SAOUHSC_01209 | 16S rRNA-processing protein RimM |
| SAOUHSC_01214 | ribosomal biogenesis GTPase |
| SAOUHSC_01222 | DNA topoisomerase I |
| SAOUHSC_01232 | 30S ribosomal protein S2 |
| SAOUHSC_01234 | elongation factor Ts |
| SAOUHSC_01235 | uridylate kinase |
| SAOUHSC_01236 | ribosome recycling factor |
| SAOUHSC_01237 | undecaprenyl pyrophosphate synthase |
| SAOUHSC_01238 | phosphatidate cytidylyltransferase |
| SAOUHSC_01240 | prolyl-tRNA synthetase |
| SAOUHSC_01241 | DNA polymerase III PolC |
| SAOUHSC_01243 | transcription elongation factor NusA |
| SAOUHSC_01244 | hypothetical protein |
| SAOUHSC_01245 | hypothetical protein |
| SAOUHSC_01246 | translation initiation factor IF-2 |
| SAOUHSC_01249 | riboflavin biosynthesis protein RibF |
| SAOUHSC_01252 | hypothetical protein |
| SAOUHSC_01260 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase |
| SAOUHSC_01285 | glutamine synthetase repressor |
| SAOUHSC_01287 | glutamine synthetase, type I |
| SAOUHSC_01333 | LexA repressor |
| SAOUHSC_01350 | hypothetical protein |
| SAOUHSC_01351 | DNA topoisomerase IV subunit B |
| SAOUHSC_01362 | 4-oxalocrotonate tautomerase |
| SAOUHSC_01373 | methicillin resistance factor, FemA |
| SAOUHSC_01374 | methicillin resistance factor |
| SAOUHSC_01424 | undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyl transferase |
| SAOUHSC_01434 | dihydrofolate reductase |
| SAOUHSC_01435 | thymidylate synthase |
| SAOUHSC_01467 | penicillin-binding protein 2 |
| SAOUHSC_01470 | hypothetical protein |
| SAOUHSC_01473 | BirA bifunctional protein |
| SAOUHSC_01474 | tRNA CCA-pyrophosphorylase |
| SAOUHSC_01477 | hypothetical protein |
| SAOUHSC_01490 | DNA-binding protein HU |
| SAOUHSC_01492 | GTP-binding protein EngA |
| SAOUHSC_01496 | cytidylate kinase |
| SAOUHSC_01501 | elastin binding protein |
| SAOUHSC_01592 | transcriptional regulator, Fur |
| SAOUHSC_01598 | AtsA/ElaC family protein |
| SAOUHSC_01599 | glucose-6-phosphate 1-dehydrogenase |
| SAOUHSC_01605 | 6-phosphogluconate dehydrogenase |
| SAOUHSC_01623 | acetyl-CoA carboxylase biotin carboxylase subunit |
| SAOUHSC_01624 | acetyl-CoA carboxylase, biotin carboxyl carrier protein |

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| SAOUHSC_01625 | elongation factor P | |
| SAOUHSC_01627 | hypothetical protein | |
| SAOUHSC_01662 | RNA polymerase sigma factor RpoD | |
| SAOUHSC_01663 | DNA primase | |
| SAOUHSC_01666 | glycyl-tRNA synthetase | |
| SAOUHSC_01672 | hypothetical protein | |
| SAOUHSC_01682 | chaperone protein DnaJ | |
| SAOUHSC_01683 | molecular chaperone DnaK | |
| SAOUHSC_01684 | heat shock protein GrpE | |
| SAOUHSC_01690 | DNA polymerase III subunit delta | |
| SAOUHSC_01697 | nicotinate (nicotinamide) nucleotide adenyltransferase | |
| SAOUHSC_01700 | GTP-binding protein YqeH | |
| SAOUHSC_01701 | hypothetical protein | |
| SAOUHSC_01714 | transcription elongation factor GreA | |
| SAOUHSC_01722 | alanyl-tRNA synthetase | |
| SAOUHSC_01725 | tRNA methyl transferase | |
| SAOUHSC_01726 | (5-methylaminomethyl-2-thiouridylate)- methyltransferase | |
| SAOUHSC_01727 | hypothetical protein | |
| SAOUHSC_01737 | aspartyl-tRNA synthetase | |
| SAOUHSC_01738 | histidyl-tRNA synthetase | |
| SAOUHSC_01741 | D-tyrosyl-tRNA(Tyr) deacylase | |
| SAOUHSC_01746 | bifunctional preprotein translocase subunit SecD/SecF | |
| SAOUHSC_01753 | GTPase ObgE | |
| SAOUHSC_01755 | 50S ribosomal protein L27 | |
| SAOUHSC_01756 | hypothetical protein | |
| SAOUHSC_01757 | 50S ribosomal protein L21 | |
| SAOUHSC_01766 | folylpolyglutamate synthase/dihydrofolate synthase | |
| SAOUHSC_01767 | valyl-tRNA synthetase | |
| SAOUHSC_01777 | ribosome biogenesis GTP-binding protein YsxC | |
| SAOUHSC_01784 | 50S ribosomal protein L20 | |
| SAOUHSC_01785 | 50S ribosomal protein L35 | |
| SAOUHSC_01786 | translation initiation factor IF-3 | |
| SAOUHSC_01787 | hypothetical protein | |
| SAOUHSC_01788 | threonyl-tRNA synthetase | |
| SAOUHSC_01791 | primosomal protein Dnal | |
| SAOUHSC_01792 | hypothetical protein | |
| SAOUHSC_01795 | dephospho-CoA kinase | |
| SAOUHSC_01807 | 6-phosphofructokinase | |
| SAOUHSC_01808 | acetyl-CoA carboxylase carboxyltransferase subunit alpha | |
| SAOUHSC_01809 | acetyl-CoA carboxylase subunit beta | |
| SAOUHSC_01811 | DNA polymerase III subunit alpha superfamily protein | |
| SAOUHSC_01827 | septation ring formation regulator EzrA | |
| SAOUHSC_01829 | 30S ribosomal protein S4 | |
| SAOUHSC_01837 | 1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein | |
| SAOUHSC_01839 | tyrosyl-tRNA synthetase | |
| SAOUHSC_01856 | UDP-N-acetylmuramate--L-alanine ligase | |
| SAOUHSC_01871 | polysaccharide biosynthesis protein | |
| SAOUHSC_01875 | leucyl-tRNA synthetase | |
| SAOUHSC_01908 | hypothetical protein | |
| SAOUHSC_01909 | S-adenosylmethionine synthetase | |
| SAOUHSC_02102 | methionine aminopeptidase | |
| SAOUHSC_02106 | hypothetical protein | |
| SAOUHSC_02107 | UDP-N-acetylmuramyl tripeptide synthetase | |

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| SAOUHSC_02114 | putative lipid kinase |
| SAOUHSC_02116 | aspartyl/glutamyl-tRNA amidotransferase subunit B |
| SAOUHSC_02117 | aspartyl/glutamyl-tRNA amidotransferase subunit A |
| SAOUHSC_02118 | aspartyl/glutamyl-tRNA amidotransferase subunit C |
| SAOUHSC_02122 | DNA ligase, NAD-dependent |
| SAOUHSC_02123 | ATP-dependent DNA helicase PcrA |
| SAOUHSC_02132 | NAD synthetase |
| SAOUHSC_02133 | nicotinate phosphoribosyltransferase |
| SAOUHSC_02140 | putative manganese-dependent inorganic pyrophosphatase |
| SAOUHSC_02151 | hypothetical protein |
| SAOUHSC_02152 | ABC transporter ATP-binding protein |
| SAOUHSC_02254 | chaperonin GroEL |
| SAOUHSC_02255 | co-chaperonin GroES |
| SAOUHSC_02277 | putative DNA-binding/iron metalloprotein/AP endonuclease |
| SAOUHSC_02279 | hypothetical protein |
| SAOUHSC_02280 | hypothetical protein |
| SAOUHSC_02306 | 4'-phosphopantetheinyl transferase |
| SAOUHSC_02317 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D |
| SAOUHSC_02318 | D-alanyl-alanine synthetase A |
| SAOUHSC_02327 | hypothetical protein |
| SAOUHSC_02336 | (3R)-hydroxymyristoyl-ACP dehydratase |
| SAOUHSC_02357 | hypothetical protein |
| SAOUHSC_02359 | peptide chain release factor 1 |
| SAOUHSC_02361 | 50S ribosomal protein L31 type B |
| SAOUHSC_02368 | CTP synthetase |
| SAOUHSC_02371 | pantothenate kinase |
| SAOUHSC_02399 | glucosamine--fructose-6-phosphate aminotransferase |
| SAOUHSC_02405 | phosphoglcosamine mutase |
| SAOUHSC_02407 | hypothetical protein |
| SAOUHSC_02477 | 30S ribosomal protein S9 |
| SAOUHSC_02478 | 50S ribosomal protein L13 |
| SAOUHSC_02484 | 50S ribosomal protein L17 |
| SAOUHSC_02485 | DNA-directed RNA polymerase subunit alpha |
| SAOUHSC_02486 | 30S ribosomal protein S11 |
| SAOUHSC_02487 | 30S ribosomal protein S13 |
| SAOUHSC_02488 | 50S ribosomal protein L36 |
| SAOUHSC_02489 | translation initiation factor IF-1 |
| SAOUHSC_02490 | adenylate kinase |
| SAOUHSC_02491 | preprotein translocase subunit SecY |
| SAOUHSC_02492 | 50S ribosomal protein L15 |
| SAOUHSC_02493 | 50S ribosomal protein L30 |
| SAOUHSC_02494 | 30S ribosomal protein S5 |
| SAOUHSC_02495 | 50S ribosomal protein L18 |
| SAOUHSC_02496 | 50S ribosomal protein L6 |
| SAOUHSC_02498 | 30S ribosomal protein S8 |
| SAOUHSC_02499 | 30S ribosomal protein S14 |
| SAOUHSC_02500 | 50S ribosomal protein L5 |
| SAOUHSC_02501 | 50S ribosomal protein L24 |
| SAOUHSC_02502 | 50S ribosomal protein L14 |
| SAOUHSC_02503 | 30S ribosomal protein S17 |
| SAOUHSC_02504 | 50S ribosomal protein L29 |
| SAOUHSC_02505 | 50S ribosomal protein L16 |
| SAOUHSC_02506 | 30S ribosomal protein S3 |

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| SAOUHSC_02507 | 50S ribosomal protein L22 | | |
| SAOUHSC_02508 | 30S ribosomal protein S19 | | |
| SAOUHSC_02509 | 50S ribosomal protein L2 | | |
| SAOUHSC_02510 | 50S ribosomal protein L23 | | |
| SAOUHSC_02511 | 50S ribosomal protein L4 | | |
| SAOUHSC_02512 | 50S ribosomal protein L3 | | |
| SAOUHSC_02527 | FmhB protein | | |
| SAOUHSC_02571 | secretory antigen | | |
| SAOUHSC_02623 | isopentenyl pyrophosphate isomerase | | |
| SAOUHSC_02720 | hypothetical protein | | |
| SAOUHSC_02860 | HMG-CoA synthase | | |
| SAOUHSC_03054 | ribonuclease P | | |
| SAOUHSC_03055 | 50S ribosomal protein L34 | | |

¹ Genes that met essential criteria after growth in BHI in this study

² Gene list curated as essential in *S. aureus* by Chaudhuri et al (BMC Genomics 2009)

* Selected for validation by antisense in this study

Essential genes (dark gray) or Fitness compromised genes (light gray) are shown here (white=not-essential or compromised in condition)