

Supplementary material:

Table 1: List of KO (KEGG Orthology) Numbers & genes of the Essential Non-human homolog metabolic proteins of *S. aureus* N315

Metabolic pathway	KO number (gene name)
Energy Metabolism	
(a) Carbonfixation pathways in prokaryotes	KO0925(ackA), KO0625(eutD)
(b) Methane metabolism	KO0925(ackA), KO1624(fbaA), KO0625(eutD)
(c) Oxidative phosphorylation	KO2109(TpF)
Carbohydrate metabolism	
(a) Pyruvate metabolism	KO0625(eutD), KO0925(ackA), K01962(accA)
(b) Propanoate metabolism	KO0925(ackA), KO065(eutD), K01962(accA)
(c) Pentose phosphate pathway	KO1839(drm), KO1624(fbaA)
(d) Fructose and Mannose metabolism	KO2768(fruA), KO2769(fruA), KO2770(fruA), KO1624(fbaA), KO2798(mtIA), KO2793, KO2794, KO2795, KO1809(pmi), KO0009(mtID)
(e) Amino sugar and Nucleotide sugar metabolism	KO1809(pmi), KO0790(murA)
(f) Glycolysis (Gluconeogenesis)	KO1624(fbaA)
Lipid metabolism	
Glycerolipid metabolism	KO3621(plsX), KO3691(plsY)
Nucleotide metabolism	
(a) Purine metabolism	KO1428(ureC), KO1839(drm), KO3040(rpoA), K02335(poIA)
Pyrimidine metabolism	KO3040(rpoA), K02335(poIA)
Amino acid metabolism	
(a) Tryptophan metabolism	KO1696(trpB)
(b) Arginine and Proline metabolism	KO1428(ureC)
(c) Lysine biosynthesis	KO1929(murF)
Metabolism of other amino acids	
Taurine and Hypotaurine metabolism	KO0925(ackA), KO0625 (eutD)
(b) D-glutamate and D-glutamine metabolism	KO1925(Mur D)
(c) D-Alanine metabolism	KO1921(ddl)
Glycan biosynthesis & metabolism	
Peptidoglycan Biosynthesis	KO1924(murC), KO1925(murD), KO6153(uppP), KO0790(murA), KO1921(ddl), KO1929(murF)
Metabolism of Terpenoids and Polyketides	
(a) Tetracycline biosynthesis	KO1962(aceA)
Membrane transport	
(a) Phosphotransferase system	KO8483(PTS I), KO2768(fruA), KO2769(fruA), KO2770(fruA), KO2763(ptsG), KO2764(ptsG), KO2765(ptsG), KO2798(mtIA), KO2793, KO2794, KO2795
(b) Bacterial secretion system	KO3070(secA), KO3076 (secY), KO3070(azi, dix)
(c) ABC transporters	KO2073
	KO3070(secA), KO3076(secY)
Protein export	
Genetic information processing	
(a) Ribosome	KO2911(rpmF), KO2864(rplJ) KO2909(rpmE2), KO2939(rplI), KO2916(rpmI), KO2990(rpsF), KO2946(rpsJ,nusE), KO2892(rplW) KO2965(rpsS), KO2982(rpsC), KO2904(rpmC), KO2961(rpsQ), KO2994(rpsH), KO2933(rplF), KO2881(rplR), KO2907(rpmD), KO2876(rplO), KO2919(rpmJ), KO2968(rpsT), KO2970(rpsU)
(b) Nucleotide excision repair	KO3703(UvrC)
(c) DNA replication	KO2337(dnaE), KO2314(dnaC),KO2316(dnaG)
(d) Homologous recombination	KO2337(dnaE), KO3626(recF)
(e) Mismatch repair	KO2337(dnaE)
(f) RNA degradation	KO3628(Rho)
(g) RNA polymerase	KO3040(rpoA)

(h)Cell-cycle Caulobacter KO3590(ftsA), KO3531(ftsZ), KO2314(dnaC), KO2313(dnaA)
Epithelial cell signaling in Helicobacter pylori infection KO1428(ureC)

Table 2: List of Essential non-human homolog membrane proteins in *S. aureus* N315 strain identified by PSORTb and Protein Families Of Membrane-bound Hypothetical Proteins identified by SVM-PROT

SN.	Accession No.	Name of Protein
1.	GI:15926360	UDP pyrophosphate phosphatase
2.	GI: 15926377	Fructose specific permease
3.	GI:15927459	Two-component sensor histidine kinase
4.	GI:15927681	F0F1 ATP synthase subunit B
5.	GI:15927652	potassium-transporting ATPase subunit A
6.	GI:15928117	PTS system, glucose-specific IIABC component
7.	GI:15927975	Respiratory nitrate reductase alpha chain
8.	GI:15927810	Preprotein translocase subunit SecY
SN.	Accession No	Protein family of Hypothetical proteins generated by svm-prot
9.	GI:15926499	Lipid-binding Protein
10.	GI:15926454	Transmembrane, Electrochemical potential-driven transporter
11.	GI:15926933	Transmembrane, Manganese-binding Protein
12.	GI:15928227	Transmembrane, Transferase
13.	GI:15927946	Electrochemical potential driven transporter
14.	GI:15927800	Transmembrane, Zinc-binding protein
15.	GI:15926141	Lipid Binding Protein