

Supplementary Table S1: Full list of differentially regulated genes with their respective expression ratio expressed in log₂, false discovery rate (FDR), annotation, and pathway.

Gene	Expression ratio(log ₂)	FDR	Protein/ortholog	Pathway
<i>butA</i>	1.71	2.36E-14	Acetoin reductase	Butanoate metabolism
<i>metE</i>	2.23	3.03E-13	5-methyltetrahydropteroyltriglutamate- Homocysteine methyltransferase	Cysteine and methionine metabolism
<i>gltB</i>	1.92	4.08E-16	Glutamate synthase large subunit	Alanine, aspartate and glutamate metabolism
<i>gltD</i>	1.84	1.10E-14	NADH-glutamate synthase small subunit	Nitrogen metabolism
<i>oppB</i>	1.65	3.58E-13	Oligopeptide transport system permease protein	Beta-Lactam resistance
<i>oppC</i>	1.73	1.21E-12	Oligopeptide transport system permease protein	ABC transporters
<i>oppD</i>	1.70	6.86E-14	Oligopeptide transport system ATP-binding protein	
<i>oppF</i>	1.64	1.73E-12	Oligopeptide transport system ATP-binding protein	
<i>oppA</i>	1.67	1.04E-13	Similar to peptide binding protein	
<i>dhoM</i>	2.63	2.94E-14	Homoserine dehydrogenase	Glycine, serine and threonine metabolism
<i>thrC</i>	2.17	3.24E-13	Threonine synthase	
<i>thrB</i>	2.27	7.45E-14	Homoserine kinase homolog	
<i>citC</i>	1.99	2.12E-14	Isocitrate dehydrogenase	Citrate cycle
<i>citZ</i>	2.01	4.13E-15	Citrate synthase II	Glutathione metabolism
<i>serA</i>	1.67	1.38E-11	D-3-phosphoglycerate dehydrogenase	Glycine, serine and threonine metabolism
<i>vraS</i>	2.33	6.29E-14	Two-component sensor histidine kinase	Two-component system
<i>vraR</i>	2.29	9.77E-14	Two-component response regulator	
<i>ilvD</i>	3.49	7.03E-13	Dihydroxy-acid dehydratase	Valine, leucine and isoleucine biosynthesis
<i>ilvB</i>	3.33	1.63E-13	Acetolactate synthase large subunit	
<i>ilvC</i>	5.21	6.60E-14	Alpha-keto-beta-hydroxylacil reductoisomerase	
<i>leuA</i>	4.53	9.77E-14	2-isopropylmalate synthase	
<i>leuB</i>	4.30	5.27E-14	3-isopropylmalate dehydrogenase	
<i>leuC</i>	4.02	1.66E-14	3-isopropylmalate dehydratase large subunit	
<i>leuD</i>	3.71	5.62E-13	3-isopropylmalate dehydratase small subunit	
<i>ilvA</i>	3.17	9.56E-14	Threonine dehydratase	
<i>fbp</i>	1.79	9.86E-14	Fructose-bisphosphatase	Glycolysis /Gluconeogenesis
<i>geh</i>	-1.68	9.56E-14	Glycerol ester hydrolase	Triacylglycerol degradation
<i>saeS</i>	-1.96	2.33E-16	Histidine protein kinase	Two-component system
<i>saeR</i>	-2.01	4.13E-15	Response regulator	
<i>saeP</i>	-2.07	1.06E-13	Hypothetical protein	
<i>saeQ</i>	-3.15	5.93E-17	Hypothetical protein	
<i>qoxC</i>	-1.73	5.24E-15	Quinol oxidase polypeptide III	Oxidative phosphorylation
<i>qoxB</i>	-1.87	9.77E-14	Quinol oxidase polypeptide I	
<i>qoxD</i>	-1.75	2.98E-12	Putative quinol oxidase polypeptide IV QoxD	
<i>sbi</i>	-2.77	9.85E-14	IgG-binding protein	Staphylococcus aureus infection
<i>ispD</i>	1.72	3.82E-10	Similar to 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	Terpenoid backbone biosynthesis
<i>prfB</i>	2.45	3.76E-12	Peptide chain release factor 2	Macromolecule metabolism
<i>pgi</i>	1.06	4.26E-13	Glucose-6-phosphate isomerase A	Glycolysis / Gluconeogenesis
<i>folD</i>	1.10	1.68E-11	FolD bifunctional protein	One carbon pool by folate Metabolic pathways Microbial metabolism in diverse environments Carbon metabolism
<i>kata</i>	1.22	5.13E-10	Catalase	Tryptophan metabolism
<i>rmpG</i>	1.11	6.91E-08	50S ribosomal protein L33	Ribosome
<i>rpsN</i>	1.06	1.05E-11	30S ribosomal protein S14 homolog	
<i>trpC</i>	2.00	2.26E-08	Indole-3-glycerol phosphate synthase	Tryptophan biosynthesis
<i>trpF</i>	1.87	9.38E-07	Phosphoriborylanthranilate isomerase	
<i>trpB</i>	1.60	3.05E-07	Tryptophan synthase beta chain	
<i>pstB</i>	1.53	4.93E-09	Phosphate ABC transporter	ABC transporters
<i>ctpA</i>	1.49	3.21E-14	Probable carboxy-terminal processing proteinase	ABC transporters
<i>malA</i>	1.48	6.17E-12	Alpha-D-1,4-glucosidase	Galactose metabolism
<i>malR</i>	1.27	2.05E-10	Maltose operon transcriptional repressor	Starch and sucrose metabolism
<i>fhs</i>	1.30	9.56E-14	Formyltetrahydrofolate synthetase	One carbon pool by folate
<i>prsA</i>	1.77	1.11E-13	Peptidyl-prolyl cis/trans isomerase	
<i>arg</i>	1.32	5.62E-11	Arginase	Arginine and proline metabolism
<i>lacE</i>	1.07	3.00E-09	PTS system lactose-specific IIBC component PTS system	Galactose metabolism
<i>lacF</i>	1.19	1.83E-06	lactose-specific IIA component	Phosphotransferase system (PTS)
<i>lacD</i>	1.13	3.85E-08	Tagatose 1,6-diphosphate aldolase	
<i>lacC</i>	1.25	4.60E-08	Tagatose-6-phosphate kinase	
<i>rocA</i>	1.81	4.47E-11	1-pyrroline-5-carboxylate dehydrogenase	Alanine, aspartate and glutamate metabolism Arginine and proline metabolism
<i>isaB</i>	1.33	3.80E-11	Immunodominant antigen B	
<i>coa</i>	-1.19	4.95E-13	Amino acid permease	Triacylglycerol degradation
<i>rpsF</i>	-1.23	4.26E-08	30S ribosomal protein S6	Ribosome
<i>ssb</i>	-1.28	7.11E-11	Single-strand DNA-binding protein of phage phi PVL	DNA replication
<i>rpsR</i>	-1.31	4.95E-13	30S ribosomal protein S18	Mismatch repair Homologous recombination
<i>nupC</i>	-1.32	9.77E-13	Pyrimidine nucleoside transport protein	

<i>rplA</i>	-1.09	1.71E-10	50S ribosomal protein L1	Ribosome
<i>rplJ</i>	-1.41	4.92E-15	50S ribosomal protein L10	
<i>rplL</i>	-1.33	7.28E-12	50S ribosomal protein L7/L12	
<i>sdrE</i>	-1.22	9.94E-13	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	Staphylococcus aureus infection
<i>nuc</i>	-2.17	2.22E-12	Staphylococcal nuclease	Staphylococcal nuclease
<i>potA</i>	-1.51	8.55E-12	Spermidine/putrescine ABC transporter	ABC transporters
<i>potB</i>	-1.57	6.75E-13	Spermidine/putrescine ABC transporter	
<i>potC</i>	-1.49	4.93E-12	Spermidine/putrescine ABC transporter	
<i>potD</i>	-1.35	3.24E-13	Spermidine/putrescine-binding protein precursor	
<i>rpsP</i>	-1.21	6.21E-11	30S ribosomal protein S16	Ribosome
<i>rimM</i>	-1.26	3.94E-12	Probable 16S rRNA processing protein	Ribosome
<i>trmD</i>	-1.28	1.04E-13	tRNA-methyltransferase	
<i>rplS</i>	-1.59	7.84E-12	50S ribosomal protein L19	Ribosome
<i>rpmA</i>	-1.08	8.07E-13	50S ribosomal protein L27	Ribosome
<i>rplT</i>	-1.25	2.15E-12	50S ribosomal protein L20	Ribosome
<i>infC</i>	-1.12	4.41E-12	Translation initiation factor IF-3	
<i>ThiI</i>	-1.13	1.43E-10	Probable thiamine biosynthesis protein	Thiamine metabolism
<i>rpsD</i>	-1.31	5.35E-12	30S ribosomal protein S4	Ribosome
<i>yent2</i>	-1.06	6.89E-05	Enterotoxin	Staphylococcus aureus infection
<i>sei</i>	-1.42	5.43E-08	Enterotoxin	
<i>sem</i>	-1.13	3.14E-06	Enterotoxin	
<i>seo</i>	-1.55	2.72E-10	Enterotoxin	
<i>tnp</i>	-1.70	6.02E-05	Transposase	
<i>hly</i>	-1.66	2.82E-13	Truncated beta-hemolysin	Defence mechanisms Virulence factors
<i>czrA</i>	-1.67	1.71E-09	Repressor protein	
<i>czrB</i>	-1.49	2.85E-10	Cation-efflux system membrane protein	
<i>rpsL</i>	-1.73	1.33E-12	30S ribosomal protein S9	Ribosome
<i>rplM</i>	-1.60	4.73E-10	50S ribosomal protein L13	
<i>rplF</i>	-1.16	1.53E-09	50S ribosomal protein L6	
<i>fnbB</i>	-1.37	9.08E-12	Fibronectin-binding protein	Bacterial invasion of epithelial cells