Supplementary Materials: A Functional ClpXP Protease is Required for Induction of the Accessory Toxin Genes, *tst, sed,* and *sec*

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Table S1. Significantly differentially expressed* genes between RN4282 wild-type and RN4282 expressing the ClpXI265E variant.

Pan Gene id [A]	Pan Gene Symbol [B]	Fold Change[C]	p_{adj}	Product
SAUPAN006313000	betA	**32.5**	6.70×10^{-55}	oxygen-dependent choline dehydrogenase
SAUPAN006314000	betB	**31.8**	1.79×10^{-73}	betaine–aldehyde dehydrogenase
SAUPAN001141000	lrgA	**11.9**	2.27×10^{-12}	antiholin-like protein LrgA
SAUPAN006063000	SAUSA300_2423	**10.9**	3.49×10^{-2}	hypothetical protein
SAUPAN005063000	SAUSA300_1937	**8.5**	1.34×10^{-3}	Sa3int prophage protein
SAUPAN001142000	lrgB	**8.3**	1.75×10^{-16}	antiholin-like protein LrgB
SAUPAN005056000	NWMN_1891	**7.1**	9.11×10^{-6}	Sa3int prophage protein
SAUPAN005055000	SAUSA300_1934	**6.4**	1.17×10^{-8}	Sa3int prophage encoded protein(tail protein)
SAUPAN000943000	sasD	**5.8**	3.49×10^{-6}	LPXTG cell wall anchor domain
SAUPAN006110000	**sarU**	**5.8**	5.91×10^{-14}	Transcriptional regulator
SAUPAN005244000	ear	**5.7**	1.94×10^{-7}	**SaPI1 encoded protin Ear,**
SAUPAN005623000	SAUSA300_2164	**5.4**	2.86×10^{-7}	Conserved protein. Signal peptide.
SAUPAN005361000	SAUSA300_2041	**5.0**	2.72×10^{-10}	hypothetical protein
NWMN_RS10890	NWMN_RS10890	**5.0**	3.30×10^{-5}	Hypothetical Sa3int prophage protein
SAUPAN005899000	SAUSA300_2325	**5.0**	6.27×10^{-14}	putative type II DNA modification enzyme
JKDJBECI_01742	-	**5.0**	2.77×10^{-9}	tRNA-Arg(ccg)
SAUPAN005138000	SAUSA300_1938	**4.9**	4.82×10^{-6}	Sa3int prophage protein. putative capsid protein
SAUPAN001245000	gehB	**4.8**	6.17×10^{-18}	lipase
SAUPAN006318000	cudT	**4.6**	3.10×10^{-11}	choline transporter BetT
SAUPAN002480000	SAUSA300_0602	**4.5**	7.57×10^{-12}	hypothetical protein
SAUPAN005928000	narG	**4.4**	4.32×10^{-3}	nitrate reductase subunit alpha
SAUPAN005933000	nirR	**4.4**	1.45×10^{-2}	nitrite reductase transcriptional regulator NirR
SAUPAN002548000	**sarX** (SAUSA300_0654)	**4.1**	4.06×10^{-13}	MarR family transcriptional regulator
SAUPAN005061000	SAUSA300_1936	**4.1**	4.15×10^{-2}	conserved hypothetical phage protein
SAUSA300_RS10655	-	**4.0**	3.45×10^{-2}	hypothetical protein
SAUSA300_RS05270	-	**3.9**	1.06×10^{-5}	hypothetical protein
SAUPAN005046000	SAUSA300_1929	**3.9**	1.59×10^{-3}	Sa3int prophage encoded protein (tail component)
JKDJBECI_02004	-	**3.9**	8.40×10^{-3}	tRNA-Ile(gat)
SAUPAN001175000	esxA	**3.7**	1.21×10^{-8}	T7SS EsxA

SAUPAN002816000	ohr (SAUSA300_0786)	**3.7**	1.94×10^{-3}	Putative organic hydroperoxide reductase
SAUPAN005052000	SAUSA300_1932	**3.7**	2.21×10^{-2}	Sa3int prophage encoded protein
SAUSA300_RS10625	-	**3.7**	1.99×10^{-2}	Sa3int prophage encoded protein
SAUPAN001863000	ulaA	**3.7**	4.55×10^{-8}	PTS ascorbate transporter subunit IIC.
SAUPAN006030000	cntK	**3.6**	4.87×10^{-5}	Histidine isomerase
SAUSA300_RS10500	-	**3.5**	3.17×10^{-4}	MAP domain-containing protein
SAUPAN003448000	mraZ	**3.5**	7.81×10^{-9}	division/cell wall cluster transcriptional repressor
SAUPAN003164000	**spxA**	**3.5**	9.11×10^{-14}	regulatory protein Spx
SAUPAN002481000	SAUSA300_0603	**3.5**	5.24×10^{-6}	hypothetical membrane protein
SAUPAN000662000	SAUSA300_1941	**3.4**	5.56×10^{-3}	Sa3int prophage encoded protein (terminase)
SAUPAN003449000	mraW	**3.3**	1.46×10^{-5}	Putative S-adenosyl-methyltransferase
SAUPAN005389000	SAUSA300_2056	**3.3**	2.53×10^{-4}	conserved membrane protein
SAUPAN005245000	tst	**3.2**	1.13×10^{-3}	**toxic shock syndrome toxin-1 TSST-1**
SAUPAN002802000	cspC	**3.2**	3.82×10^{-3}	cold-shock protein
SAUPAN003211000	**comK1**	**3.2**	1.27×10^{-6}	ComK competence transcription factor
SAUPAN005139000	SAUSA300_1939	**3.2**	9.72×10^{-5}	Sa3int prophage encoded protein
SAUPAN000910000	**sarS**	**3.1**	2.14×10^{-7}	Virulence regulator
SAUPAN004572000	epiG	**3.1**	9.94×10^{-8}	antibiotic epidermin immunity protein F,
SAUPAN004573000	epiE	**3.0**	9.35×10^{-7}	lantibiotic epidermin immunity protein F.
SAUPAN004574000	epiF	**3.0**	1.41×10^{-4}	bacitracin ABC transporter ATP-binding protein
SAUPAN004575000	epiP	**3.0**	3.24×10^{-5}	lantibiotic epidermin. protease EpiP
SAUPAN004939000	SAUSA300_1890	**3.0**	1.31×10^{-4}	Cysteine protease. staphopain
SAUPAN004396000	fhs	**3.0**	1.27×10^{-6}	formate—tetrahydrofolate ligase
SAUPAN004585000	epiA	**3.0**	5.98×10^{-5}	lantibiotic epidermin
SAUPAN003450000	ftsL	**3.0**	1.42×10^{-4}	cell division protein FtsL
SAUPAN001228000	SAUSA300_0307	**3.0**	8.15×10^{-6}	5'-nucleotidase. lipoprotein e(P4) family
SAUSA300_RS10495	-	**2.9**	3.04×10^{-3}	MAP domain-containing protein
SAUPAN004024000	**srrB**	**2.9**	2.67×10^{-5}	two-component sensor histidine kinase
JKDJBECI_00383	-	**2.9**	1.94×10^{-7}	hypothetical protein
SAUPAN003637000	SAUSA300_1205	**2.9**	3.77×10^{-2}	hypothetical protein
SAUPAN002374000	SAUSA300_0575	**2.9**	2.07×10^{-7}	hypothetical protein
SAUPAN005018000	scn	**2.8**	6.20×10^{-4}	staphylococcal complement inhibitor SCIN
SAUPAN002347000	hxlA	**2.8**	1.15×10^{-4}	putative hexulose–6-phosphate synthase.

SAUSA300_RS13715	-	**2.8**	1.10×10^{-5}	hypothetical membrane protein
SAUPAN006035000	SAUSA300_2416	**2.8**	3.08×10^{-6}	glucose 1-dehydrogenase−like protein
SAUPAN002348000	hxlB	**2.8**	3.51×10^{-5}	6-phospho-3-hexuloisomerase.
SAUPAN002823000	SAUSA300_0793	**2.8**	1.10×10^{-4}	conserved protein.
SAUPAN001865000	SAUSA300_0332	**2.8**	3.31×10^{-3}	Putative PTS transporter.
SAUPAN004576000	epiD	**2.6**	3.48×10^{-2}	lantibiotic epidermin biosynthesis protein EpiD
SAUPAN005023000	sak	**2.6**	1.17×10^{-3}	Sa3int prophage encoded staphylokinase
SAUPAN001971000	SAUSA300_0372	**2.6**	1.36×10^{-2}	conserved protein
SAUPAN004358000	SAUSA300_1653	**2.6**	2.58×10^{-3}	metal-dependent hydrolase
SAUSA300_RS10645	-	**2.5**	3.77×10^{-3}	Sa3int prophage encoded protein
SAUPAN003698000	thrD	**2.5**	8.22×10^{-5}	aspartate kinase
SAUPAN006490000	rnpA	**2.5**	3.67×10^{-4}	ribonuclease P protein component
SAUPAN006028000	SAUSA300_2412	**2.5**	5.06×10^{-3}	conserved protein.
SAUSA300_RS14095	-	**2.5**	3.55×10^{-5}	hypothetical protein
SAUPAN005951000	SAUSA300_2361	**2.5**	1.08×10^{-5}	hypothetical protein
SAUPAN001864000	SAUSA300_0331	**2.5**	5.06×10^{-3}	Putative PTS transporter.
SAUPAN004025000	**srrA**	**2.5**	1.28×10^{-4}	DNA-binding response regulator
SAUPAN006464000	SAUSA300_2632	**2.5**	1.31×10^{-3}	Conserved membrane protein
SAUPAN003129000	-	**2.5**	3.78×10^{-4}	Membrane protein
SAUPAN005949000	mdeA/SAUSA300_2360	**2.4**	3.08×10^{-6}	Putative efflux pump
SAUPAN000942000	sodM	**2.4**	1.32×10^{-3}	Superoxide dismutase [Mn/Fe] 2
SAUPAN001005000	SAUSA300_0171	**2.4**	1.93×10^{-3}	putative cation transporter
SAUPAN006029000	cntL	**2.4**	3.09×10^{-2}	Staphylopine biosynthesis
SAUPAN002813000	SAUSA300_0785	**2.4**	1.54×10^{-2}	N-acetyltransferase
SAUPAN006197000	cidB	**2.4**	4.94×10^{-4}	holin-like protein CidB
SAUSA300_RS10345	-	**2.4**	1.63×10^{-2}	staphostatin A
SAUPAN003631000	SAUSA300_1203	**2.4**	1.93×10^{-2}	hypothetical protein
SAUPAN005239000	SAUSA300_1980	**2.4**	1.89×10^{-3}	N-acetyltransferase
JKDJBECI_00385	-	**2.4**	2.62×10^{-5}	hypothetical protein
SAUPAN003126000	SAUSA300_0884	**2.4**	6.42×10^{-3}	hypothetical protein
SAUPAN005281000	**agrA**	**2.3**	3.71×10^{-6}	DNA-binding response regulator
SAUPAN002892000	SAUSA300_0816	**2.3**	1.34×10^{-3}	Conserved protein of unknown function
SAUPAN005048000	-	**2.3**	2.36×10^{-3}	Sa3int prophage protein
SAUPAN006033000	SAUSA300_2415	**2.3**	1.26×10^{-3}	hypothetical protein
SAUPAN002822000	SAUSA300_0792	**2.3**	1.36×10^{-2}	hypothetical protein
JKDJBECI_00384	-	**2.3**	1.14×10^{-4}	hypothetical protein
SAUPAN005192000	lukH	**2.3**	4.28×10^{-2}	succinyl-diaminopimelate desuccinylase
SAUPAN000037000	adsA	**2.3**	1.30×10^{-5}	AdsA nucleotidase
SAUPAN005279000	**agrC**	**2.3**	8.37×10^{-6}	Qurum sensing
SAUPAN003133000	opp-3B	**2.3**	3.67×10^{-4}	ABC transporter permease
SAUPAN005496000	mtlR/SAUSA300_2106	**2.3**	9.14×10^{-3}	conseved protein
SAUPAN002835000	SAUSA300_0794	**2.3**	1.09×10^{-2}	topiosmerase.
SAUPAN005897000	scrA	**2.3**	3.54×10^{-3}	PTS sucrose transporter subunit IIBC

SAUPAN005275000	**agrB**	**2.3**	1.56×10^{-5}	accessory gene regulator AgrB
SAUPAN005498000	mtlA	**2.3**	5.88×10^{-4}	mannitol-specific phosphotransferase
SAUSA300_RS10880	-	**2.2**	9.14×10^{-3}	hypothetical protein
SAUPAN001008000	SAUSA300_0172	**2.2**	3.51×10^{-2}	conserved hypothetical protein
SAUPAN003654000	SAUSA300_1210	**2.2**	3.97×10^{-3}	hypothetical protein
SAUPAN005883000	SAUSA300_2315	**2.2**	1.35×10^{-2}	Conserved secreted protein
SAUPAN001034000	murQ	**2.2**	3.31×10^{-3}	N-acetylmuramic acid 6-phosphate etherase
SAUPAN005388000	murA	**2.2**	1.49×10^{-3}	peptidoglycan biosynthesis
SAUPAN002836000	SAUSA300_0795	**2.2**	3.35×10^{-2}	Putative thiol reductase thioredoxin.
SAUPAN002669000	SAUSA300_0739	**2.2**	1.89×10^{-3}	Putative autolysin (CHAP and LysM domain)
SAUSA300_RS03975	prf2	**2.2**	1.28×10^{-4}	peptide chain release factor 2
SAUPAN005915000	narK	**2.2**	1.43×10^{-2}	nitrite extrusion protein
SAUPAN005580000	amaP/SAUSA300_2144	**2.2**	4.70×10^{-3}	hypothetical protein
SAUPAN000894000	norC	**2.2**	8.58×10^{-3}	Efflux pump NorC
SAUPAN006196000	cidC	**2.1**	3.25×10^{-4}	pyruvate oxidase
SAUPAN006107000	sasG	**2.1**	1.56×10^{-4}	LPXTG-motif cell wall anchor
SAUSA300_RS09325	-	**2.1**	3.10×10^{-4}	MarR family transcriptional regulator
SAUPAN003251000	sspA	**2.1**	2.73×10^{-4}	V8 serine protease.
SAUPAN004030000	xerD	**2.1**	6.65×10^{-4}	tyrosine recombinase XerD
SAUPAN001012000	ssuC/SAUSA300_0176	**2.1**	1.08×10^{-1}	ABC transporter permease.
SAUPAN005440000	manA	**2.1**	1.28×10^{-4}	mannose–6-phosphate isomerase.
SAUPAN003692000	SAUSA300_1221	**2.1**	1.19×10^{-2}	conserved protein
SAUPAN004317000	phoP	**2.1**	1.58×10^{-3}	DNA-binding response regulator
SAUPAN001862000	SAUSA300_0329	**2.1**	1.67×10^{-2}	putative oxidoreductase
SAUPAN004046000	SAUSA300_1458	**2.1**	1.93×10^{-3}	conserved protein
SAUPAN002570000	**mgrA**	**2.1**	3.17×10^{-4}	MarR family transcriptional regulator
SAUPAN003936000	engA	**2.1**	2.70×10^{-4}	ribosome–associated GTPase EngA
SAUPAN003057000	SAUSA300_0858	**2.1**	1.34×10^{-4}	conserved protein
SAUPAN003134000	oppC	**2.1**	8.97×10^{-3}	oligopeptide ABC transporter permease
SAUPAN001123000	tarI/SAUSA300_0245	**2.1**	5.71×10^{-4}	TarI
SAUPAN003451000	pbpA	**2.1**	2.29×10^{-2}	penicillin-binding protein 1
SAUPAN003135000	oppD	**2.1**	1.31×10^{-2}	ABC transporter ATP-binding protein.
SAUPAN005276000	**agrD**	**2.1**	1.36×10^{-2}	cyclic lactone autoinducer peptide
SAUPAN005500000	mtlD	**2.0**	3.00×10^{-3}	mannitol-1-phosphate 5-dehydrogenase
SAUPAN005274000	**Hld/RNAIII**	**2.0**	8.80×10^{-3}	delta-hemolysin/RNAIII
SAUPAN005578000	asp23	**2.0**	4.94×10^{-3}	Asp23 envelope stress response protein
SAUPAN005387000	fabZ	**2.0**	7.46×10^{-3}	fatty acid biosynthesis
SAUPAN006489000	trmE	**2.0**	1.13×10^{-3}	tRNA modification GTPase TrmE
SAUPAN002232000	SAUSA300_0471/veg	**2.0**	9.89×10^{-3}	hypothetical protein

SAUPAN003935000	gpsA	**2.0**	5.22×10^{-4}	glycerol-3-phosphate dehydrogenase (NAD(P)(+))
SAUPAN003803000	SAUSA300_1284/cvfB	**2.0**	3.15×10^{-3}	S1 RNA binding domain-containing protein
SAUPAN005439000	SAUSA300_2095	**2.0**	9.03×10^{-4}	conserved protein
SAUPAN001900000	metE	**2.0**	1.89×10^{-3}	homocysteine methyltransferase
SAUPAN002714000	rnr	**2.0**	3.76×10^{-3}	ribonuclease R
SAUPAN001013000	SAUSA300_0177	**2.0**	4.00×10^{-2}	conserved protein.
SAUPAN003808000	dapA	**2.0**	3.62×10^{-2}	4-hydroxy-tetrahydrodipicolinate synthase
SAUPAN004316000	phoR	**2.0**	4.41×10^{-3}	sensor histidine kinase
JKDJBECI_00373	-	**2.0**	6.47×10^{-3}	hypothetical protein
SAUPAN003249000	sspC	**2.0**	1.70×10^{-3}	staphostatin B
SAUPAN006210000	clpL	**2.0**	1.88×10^{-2}	ATP-dependent chaperone ClpL
SAUPAN005803000	glvC	**2.0**	1.32×10^{-3}	PTS alpha-glucoside transporter subunit IIBC
SAUPAN003746000	glcT	**0.5**	3.77×10^{-3}	protein GlcT
SAUPAN002314000	rpoB	**0.5**	3.77×10^{-3}	DNA-directed RNA polymerase subunit beta
SAUPAN006189000	-	**0.5**	2.97×10^{-2}	alpha/beta hydrolase
SAUPAN006326000	cysJ	**0.5**	1.56×10^{-2}	(NADPH) flavoprotein subunit
SAUPAN001981000	ahpF	**0.5**	1.51×10^{-2}	alkyl hydroperoxide reductase subunit F
SAUPAN002328000	-	**0.5**	1.93×10^{-2}	HAD family hydrolase
SAUPAN003440000	psmβ1	**0.5**	3.96×10^{-2}	PSM β1
SAUPAN000975000	capB	**0.5**	3.35×10^{-2}	capsular polysaccharide biosynthesis protein Cap5B
SAUPAN003392000	-	**0.5**	2.60×10^{-2}	metal-dependent phosphodiesterase
SAUPAN005723000	-	**0.5**	2.63×10^{-2}	MFS transporter
SAUPAN004195000	-	**0.5**	1.15×10^{-2}	hypothetical protein
SAUPAN006293000	panB	**0.5**	1.24×10^{-2}	hydroxymethyltransferase
SAUPAN005704000	-	**0.5**	5.46×10^{-3}	hypothetical protein
SAUPAN000035000	walI	**0.5**	8.12×10^{-3}	hypothetical protein
SAUPAN006202000	-	**0.5**	1.41×10^{-2}	CHAP domain-containing protein
SAUPAN005444000	czrB	**0.5**	3.45×10^{-2}	cation transporter
SAUPAN002315000	rpoC	**0.5**	1.32×10^{-3}	DNA-directed RNA polymerase subunit beta'
SAUPAN005301000	tsaE	**0.5**	7.48×10^{-3}	tRNA (adenosine(37)-N6)-TsaE
SAUPAN000935000	galE	**0.5**	3.75×10^{-2}	NAD-dependent dehydratase
SAUPAN002502000	-	**0.5**	8.94×10^{-3}	sodium:proton antiporter
SAUPAN002164000	mpsB	**0.5**	3.87×10^{-3}	hypothetical protein
SAUPAN003241000	-	**0.5**	1.44×10^{-2}	acetyltransferase
SAUPAN006136000	-	**0.5**	1.41×10^{-2}	hypothetical protein
SAUPAN006109000	**sarT**	**0.5**	1.57×10^{-2}	transcriptional regulator
SAUPAN005268000	sdrH	**0.5**	7.94×10^{-3}	hypothetical protein
SAUPAN005300000	tsaB	**0.5**	1.37×10^{-2}	tRNA threonylcarbamoyltransferase c
SAUPAN006292000	panC	**0.5**	4.94×10^{-3}	pantoate—beta-alanine ligase

SAUPAN001869000	mepA	**0.5**	4.55×10^{-2}	multidrug efflux MATE transporter MepA
SAUPAN002252000	ftsH	**0.5**	3.86×10^{-4}	zinc metalloprotease
SAUPAN004943000	-	**0.5**	3.58×10^{-2}	NETI motif-containing protein
SAUPAN001098000	prsS	**0.5**	8.31×10^{-3}	PrsW family intramembrane metalloprotease
SAUPAN006448000	-	**0.5**	1.93×10^{-2}	hypothetical protein
SAUPAN006325000	-	**0.5**	2.02×10^{-2}	precorrin-2 dehydrogenase
SAUPAN001173000	-	**0.5**	2.60×10^{-2}	DUF5080 domain-containing protein
SAUPAN002321000	-	**0.5**	2.66×10^{-2}	N-acetyl-L,L-diaminopimelate deacetylase
SAUPAN005993000	-	**0.5**	2.63×10^{-3}	NAD(P)-dependent oxidoreductase
SAUPAN003787000	opp-2B	**0.5**	1.94×10^{-3}	peptide ABC transporter permease
SAUPAN001984000	nfrA	**0.5**	8.31×10^{-3}	NADPH-dependent oxidoreductase
SAUPAN003331000	mntH	**0.5**	7.37×10^{-3}	divalent metal cation transporter
SAUPAN002533000	-	**0.5**	1.41×10^{-2}	alpha/beta hydrolase
SAUPAN000387000	-	**0.5**	1.70×10^{-3}	LysR family transcriptional regulator
SAUPAN002101000	-	**0.5**	2.24×10^{-3}	membrane protein
SAUPAN002183000	-	**0.5**	3.23×10^{-2}	hypothetical protein
SAUPAN006233000	-	**0.5**	3.79×10^{-2}	N-acetyltransferase
SAUPAN004501000	metK	**0.5**	3.00×10^{-3}	S-adenosylmethionine synthase
SAUPAN006457000	rarD	**0.5**	7.64×10^{-4}	protein RarD
SAUPAN005501000	fmtB	**0.5**	7.48×10^{-3}	hypothetical protein
SAUPAN003171000	pepF	**0.5**	2.37×10^{-3}	oligoendopeptidase F
SAUPAN004277000	tag	**0.5**	1.13×10^{-3}	DNA-3-methyladenine glycosylase I
SAUPAN003441000	psmβ2	**0.5**	1.31×10^{-3}	hemolytic protein
SAUPAN005722000	-	**0.5**	3.43×10^{-2}	MarR family transcriptional regulator
SAUPAN002102000	-	**0.5**	4.61×10^{-3}	NAD(P)-dependent oxidoreductase
SAUPAN001102000	opp-5A	**0.5**	5.22×10^{-4}	nickel ABC transporter substrate–binding protein
SAUPAN006159000	fbp	**0.5**	8.53×10^{-3}	fructose 1,6-bisphosphatase
SAUPAN000148000	-	**0.4**	3.18×10^{-3}	hypothetical protein
SAUPAN003257000	-	**0.4**	4.62×10^{-4}	acyltransferase
SAUPAN005997000	opuCD	**0.4**	6.78×10^{-4}	amino acid ABC transporter permease
SAUPAN000938000	-	**0.4**	3.31×10^{-3}	transferase
SAUPAN005998000	opuCC	**0.4**	4.44×10^{-4}	amino acid transporter
SAUPAN005608000	-	**0.4**	7.79×10^{-3}	MerR family transcriptional regulator
SAUPAN006191000	-	**0.4**	1.93×10^{-3}	acyl-CoA thioester hydrolase
SAUPAN005606000	-	**0.4**	1.56×10^{-3}	aldo/keto reductase
SAUPAN001171000	-	**0.4**	3.43×10^{-2}	DUF5079 domain-containing protein
SAUPAN003058000	-	**0.4**	1.32×10^{-3}	NADH-dependent flavin oxidoreductase

SAUPAN000902000	-	**0.4**	1.93×10^{-2}	oleate hydratase
SAUPAN002142000	lpl3	**0.4**	4.70×10^{-2}	tandem-type lipoprotein
SAUPAN005375000	thiD	**0.4**	3.77×10^{-3}	kinase/phosphomethylpyrimidine kinase
SAUPAN002631000	nrdF	**0.4**	3.58×10^{-3}	ribonucleotide−diphosphate reductase subunit beta
SAUPAN006437000	-	**0.4**	3.95×10^{-6}	polysaccharide deacetylase
SAUPAN000902000	-	**0.4**	7.88×10^{-3}	oleate hydratase
SAUPAN003593000	-	**0.4**	1.26×10^{-3}	2-oxoacid ferredoxin oxidoreductase subunit beta
SAUPAN002282000	-	**0.4**	8.80×10^{-4}	PLP-dependent aminotransferase family protein
SAUPAN006177000	-	**0.4**	3.24×10^{-5}	peptide ABC transporter permease
SAUPAN005741000	fdhD	**0.4**	1.80×10^{-4}	sulfurtransferase FdhD
SAUPAN003757000	-	**0.4**	3.21×10^{-5}	DNA repair protein MucB
SAUPAN006190000	-	**0.4**	9.72×10^{-5}	thiol reductase thioredoxin
SAUPAN006420000	gehA	**0.4**	2.75×10^{-3}	Lipase 1
SAUPAN005767000	ssaA	**0.4**	4.51×10^{-6}	CHAP domain-containing protein
SAUPAN005934000	-	**0.4**	1.25×10^{-4}	N-acetyltransferase
SAUPAN001163000	lytM	**0.4**	7.59×10^{-4}	glycyl-glycine endopeptidase LytM
SAUPAN003592000	-	**0.4**	7.10×10^{-4}	2-oxoglutarate ferredoxin oxidoreductase
SAUPAN003680000	-	**0.4**	2.69×10^{-5}	low specificity L-threonine aldolase
SAUPAN003201000	-	**0.3**	4.55×10^{-9}	membrane protein
SAUPAN006322000	nrdD	**0.3**	1.98×10^{-2}	anaerobic ribonucleoside−triphosphate reductase
SAUPAN005999000	opuCB	**0.3**	2.71×10^{-3}	choline ABC transporter permease
SAUPAN006408000	cap1B	**0.3**	2.87×10^{-3}	capsular polysaccharide biosynthesis protein Cap5B
SAUPAN003815000	msa	**0.3**	5.43×10^{-6}	protein msa
SAUPAN006409000	cap1A	**0.3**	3.70×10^{-2}	capsular polysaccharide biosynthesis protein CapA
SAUPAN006176000	-	**0.3**	8.40×10^{-4}	peptide ABC transporter ATP-binding protein
SAUPAN006459000	nixA	**0.3**	1.27×10^{-6}	nickel transporter NixA
SAUPAN005381000	sceD	**0.3**	8.80×10^{-4}	transglycosylase SceD
SAUPAN006218000	-	**0.3**	2.16×10^{-5}	maltose O-acetyltransferase
SAUPAN006000000	opuCA	**0.3**	1.21×10^{-8}	glycine/betaine ABC transporter ATP-binding protein
SAUPAN006366000	argR	**0.3**	1.55×10^{-5}	ArgR family transcriptional regulator
SAUSA300_RS06715	-	**0.2**	1.10×10^{-5}	hypothetical protein
SAUPAN006321000	nrdG	**0.2**	1.62×10^{-5}	anaerobic ribonucleoside−triphosphate reductase activating
NWMN_RS11100	-	**0.2**	1.04×10^{-16}	hypothetical protein
SAUPAN005772000	-	**0.2**	1.18×10^{-6}	CHAP domain-containing protein

SAUPAN005759000	ureD	**0.2**	9.35×10^{-26}	urease accessory protein
SAUPAN005756000	ureE	**0.2**	8.85×10^{-23}	urease accessory protein UreE
SAUPAN005758000	ureG	**0.2**	2.88×10^{-23}	urease accessory protein UreG
SAUPAN005757000	ureF	**0.2**	2.23×10^{-26}	urease accessory protein UreF
SAUPAN005755000	ureC	**0.2**	1.72×10^{-21}	urease subunit alpha
SAUPAN005753000	ureA	**0.2**	3.77×10^{-16}	urease subunit gamma
SAUPAN005754000	ureB	**0.2**	3.52×10^{-21}	urease subunit beta
SAUPAN005752000	-	**0.1**	3.08×10^{-18}	urea transporter
NWMN_RS10980	-	**0.0**	6.24×10^{-27}	hypothetical protein
SAUPAN005109000	-	**0.0**	4.93×10^{-26}	hypothetical protein

* Genes were considered differentially expressed if they showed a ≥2-fold change in expression with $p_{adj} < 0.05$. [A]: RN8242 genes were annotated using the AureoWiki database (http://aureowiki.med.uni-greifswald.de) using preferentially the pan-genome gene id and otherwise with identifiers corresponding to the strain-specific gene to which they map. Open reading frames in the RN4282 genome that could not be assigned to any of the five strains in Aureowiki (NCTC 8325, COL. Newman, USA300_FPR3757, and N315) were annotated using a prokka-generated identifier and reported as hypothetical proteins. [B]: Genes encoding known transcriptional regulators of virulence genes are shown in bold. In case no pan genome symbol was provided in AureoWiki, the gene annotations for the S. aureus model strain USA300_FPR3757 were used. [C]: Fold changes in RN4282 wild type/RN4282clpXI265E are shown (genes expressed >2 fold more in wild-type cells are listed in the top of the table (shaded pink). Genes expressed >2 fold more in RN4282clpXI265E cells are listed in the bottom of the table shaded green).