

<i>S. aureus</i> USA300	<i>S. aureus</i> SCV	Aminoacidc Change	Annotation	Type of Mutation
T	C	STOP401R	ISL3 like element IS1181 family transposase	missense
T	A	I268N	purR	missense
G	A	R874Q	sasG	Missense
G	A	W102STOP	shikimate kinase	Nonsense

Table S1: mutations annotated by comparing *S. aureus* USA300 and its SCVs genomes.

<i>S.aureus</i> USA300 Vs <i>S.aureus</i> SCV		Unpaired t test P value	P value summary	Significantly different (P < 0.05)?	95% confidence interval	R squared (eta squared)
Regulator	<i>sarA</i>	0,5214	ns	No	-1,058 to 1,520	0,229
	<i>sigB</i>	0,7005	ns	No	-0,4126 to 0,5075	0,08971
	<i>agrA</i>	0,1483	ns	No	-2,962 to 9,757	0,7255
Virulence	<i>psmA</i>	0,844	ns	No	-1,746 to 1,574	0,02434
	<i>hla</i>	0,0878	ns	No	-0,9560 to 6,173	0,8321
	<i>hld</i>	0,097	ns	No	-1,344 to 7,353	0,8155
Surface protein	<i>sdrE</i>	0,0459	*	Yes	0,07210 to 3,155	0,9103
ROS neutralization	<i>katA</i>	0,3294	ns	No	-0,9269 to 0,4983	0,4557
	<i>sodM</i>	0,1953	ns	No	-0,2474 to 0,6450	0,6475
	<i>sodA</i>	0,2778	ns	No	-1,189 to 2,432	0,5216
Metal Ions Uptake	<i>sirC</i>	0,2554	ns	No	-3,327 to 7,178	0,5545
	<i>zur</i>	0,044	*	Yes	0,1265 to 3,717	0,9138
	<i>mntR</i>	0,0245	*	Yes	0,3277 to 1,765	0,9515
	<i>fur</i>	0,0358	*	Yes	0,4478 to 5,018	0,9298
	<i>perR</i>	0,7316	ns	No	-2,033 to 2,442	0,07206
Metabolic Pathways (TCA - Glycolysis)	<i>pdhA</i>	0,8241	ns	No	-1,769 to 1,573	0,03093
	<i>fumC</i>	0,3329	ns	No	-0,9176 to 1,683	0,445
	<i>uhpt</i>	0,0209	*	Yes	0,7451 to 3,307	0,9586

Table S2: statistical insights of gene expression levels detected through qRT-PCR