

Table S3: List of the exclusively downregulated proteins in *S. aureus* biofilm in comparison to planktonic culture (fold change >-2, p <0.05). * CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Names	Fold Change	Protein Pathways	Subcellular Localisation
AIO21667.1	delta-hemolysin	hld SA1841.1 SAS065	-34.02	Quorum sensing	Cytoplasmic
	spermidine/putrescine				
AIO20700.1	ABC transporter substrate-binding protein	potD	-22.04	ABC transporters	Unknown
AIO20763.1	alpha-hemolysin	SA1007	-13.83		Extracellular
AIO22369.1	phosphodiesterase	hlb SACOL2003	-12.33		Extracellular
OOC90902.1	calcium-binding protein	SACOL1846	-11.77		Unknown
AIO20644.1	cysteine protease	sspB SACOL1056	-11.44		Extracellular
AIO22207.1	transglycosylase	isaA SACOL2584	-10.14		Extracellular
AIO20556.1	hypothetical protein KQ76_04470	SA0841	-9.46		CM*
AIO19942.1	peptidase M23	lytM SACOL0263	-9.30		Extracellular
AIO20056.1	hypothetical protein KQ76_01725		-8.47		CM
AIO20660.1	chitinase	SA0914	-8.44		Unknown
AIO19870.1	peptidase M23	SA0205	-8.28		Extracellular

AIO21024.1	cold-shock protein	cspA SA1234	-8.08		Cytoplasmic
AIO19947.1	staphyloxanthin biosynthesis protein	SACOL0270	-7.54		Extracellular
AIO21349.1	DNA-3-methyladenine glycosylase	tag	-7.16	Base excision repair	Unknown
AIO21509.1	serine protease	splC SACOL1867	-6.98		Extracellular
AIO20463.1	thermonuclease	nuc SACOL0860	-6.97		Extracellular
AIO20332.1	peptidase M23B	SA0620	-6.86		Cell wall
AIO20645.1	glutamyl endopeptidase	sspA SACOL1057	-6.52	Quorum sensing	Extracellular
AIO20716.1	SCP-like extracellular protein	SA0967	-6.49		Unknown
AIO19770.1	1-phosphatidylinositol phosphodiesterase	plc	-5.85	Inositol phosphate metabolism	Extracellular
AIO20387.1	glycerol phosphate lipoteichoic acid synthase	ltaS SA0674	-5.84	Metabolic pathways, Glycerolipid metabolism	CM
AIO22290.1	N-acetylmuramoyl-L-alanine amidase	SACOL2666	-5.80		Extracellular
AIO21492.1	hypothetical protein KQ76_09365	SACOL1852	-5.35		Unknown

AIO20326.1	response regulator GraR	graR SACOL0716	-5.34	Two-component system, Cationic antimicrobial peptide (CAMP)	Cytoplasmic resistance
AIO21221.1	acetyl-CoA carboxylase	accB	-5.16	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Pyruvate metabolism, Carbon metabolism, Fatty acid metabolism, Propanoate metabolism, Fatty acid biosynthesis	Cytoplasmic
AIO19779.1	peptidoglycan-binding protein LysM	spa SACOL0095	-4.71	<i>Staphylococcus aureus</i> infection	Cell wall
AIO20739.1	ribonuclease HIII	rnhC SACOL1150	-4.61	DNA replication	Unknown
AIO20228.1	hydrolase	sdrD SA0520	-4.49	<i>Staphylococcus aureus</i> infection	Cell wall
AIO20762.1	hypothetical protein KQ76_05550	SA1005	-4.44		Unknown
AIO20126.1	N-acetylmuramoyl-L-alanine amidase	sle1 aaa SA0423	-4.42		Cell wall
AIO20637.1	acetyltransferase	SA0893	-4.41		Cytoplasmic
AIO21273.1	molecular chaperone DnaJ	dnaJ SA1408	-4.24		Cytoplasmic

AIO20577.1	competence negative regulator MecA	mecA SA0857	-4.19		Cytoplasmic
AIO20418.1	ABC transporter	SACOL0811	-4.18		Cytoplasmic
AIO21353.1	delta-aminolevulinic acid dehydratase	hemB SA1492	-4.18	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Porphyrin and chlorophyll metabolism	Cytoplasmic
AIO21508.1	serine protease	splE SACOL1865	-4.18	Quorum sensing	Extracellular
AIO19905.1	nucleoside hydrolase	SACOL0225	-4.17		Cytoplasmic
AIO20630.1	hypothetical protein KQ76_04865	SACOL1575	-4.12		Unknown
AIO19987.1	lipase	lip2 geh SA0309	-4.12	Metabolic pathways, Glycerolipid metabolism	Extracellular
AIO20479.1	arsenate reductase	SA0759	-4.06		Cytoplasmic
AIO20651.1	mannosyl-glycoprotein endo-beta-N-acetylglucosamidase	atl nag SACOL1062	-4.01		Extracellular
AIO21549.1	Fur family transcriptional regulator	perR SACOL1919	-4.00		Cytoplasmic

AIO22042.1	glutathione S-transferase	SACOL2402	-3.94		Unknown
AIO21406.1	Free methionine-(R)-sulfoxide reductase	SACOL1768	-3.85	Cysteine and methionine metabolism	Cytoplasmic
AIO20229.1	bis(5'-nucleosyl)-tetraphosphatase	sdrE SACOL0610	-3.82	<i>Staphylococcus aureus</i> infection	Cell wall
AIO22060.1	gamma-hemolysin subunit A	hlgC SA2208	-3.79	<i>Staphylococcus aureus</i> infection	Extracellular
AIO20738.1	phenylalanyl-tRNA synthase subunit beta	pheT SA0986	-3.75	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO21601.1	cysteine protease	sspP scpA SA1725	-3.73		Extracellular
AIO20874.1	50S ribosomal protein L7	SA1111	-3.73		Unknown
AIO21505.1	serine protease	splF SA1627	-3.71	Quorum sensing	Extracellular
AIO22081.1	sodium:proton antiporter	SA2228	-3.68		CM
AIO20884.1	zinc protease	SA1121	-3.66		Cytoplasmic
AIO20093.1	superantigen-like protein	set11	-3.63	<i>Staphylococcus aureus</i> infection	Extracellular
AIO21182.1	transcriptional regulator	srrA SA1323	-3.63	Two-component system	Cytoplasmic
AIO20960.1	secretion protein	SACOL1373	-3.63		Unknown
AIO22350.1	peptidase		-3.61		Extracellular
AIO21805.1	uridylyltransferase	SA1974	-3.60		Cytoplasmic
AIO21491.1	hypothetical protein KQ76_09360	SACOL1851	-3.58		Cytoplasmic

AIO20144.1	hypothetical KQ76_02220	protein	SA0441	-3.57		Unknown
AIO21160.1	single-stranded binding protein	DNA- ssb		-3.53	Homologous recombination, Mismatch repair, DNA replication	Unknown
AIO22099.1	peptidase M28		SA2244	-3.47		Cytoplasmic
AIO22349.1	hypothetical KQ76_14165	protein		-3.46		Unknown
AIO20756.1	formyl peptide receptor- like 1 inhibitory protein		flr SA1001	-3.39	<i>Staphylococcus aureus</i> infection	Unknown
AIO20951.1	HAD family hydrolase		SA1167	-3.34		Cytoplasmic
AIO22292.1	adhesin		sasF SACOL2668	-3.28		Cell wall
AIO19988.1	alpha/beta hydrolase		SACOL0391	-3.27		Cytoplasmic
AIO20737.1	phenylalanine--tRNA ligase		pheS SA0985	-3.27	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO21246.1	penicillin-binding protein	pbp3		-3.24	Metabolic pathways, beta-Lactam resistance, Peptidoglycan biosynthesis	CM
OOC94232.1	aureolysin		aur SACOL2659	-3.22	<i>Staphylococcus aureus</i> infection, Cationic antimicrobial peptide (CAMP) resistance	Extracellular
AIO21853.1	50S ribosomal protein L17	rplQ	SA2022	-3.19	Ribosome	Cytoplasmic

AIO21391.1	oligoribonuclease	SA1526	-3.17	Metabolic pathways, Microbial metabolism in diverse environments, Sulfur metabolism	Cytoplasmic
AIO21842.1	toxin	SACOL2197	-3.14		CM
AIO22206.1	acetyltransferase	oatA SA2354	-3.12		CM
AIO21365.1	50S ribosomal protein L20	rplT SA1502	-3.09	Ribosome	Cytoplasmic
AIO21565.1	hypothetical protein KQ76_09970	SAS054	-3.08		Cytoplasmic
AIO22160.1	lactate dehydrogenase	ldhD SACOL2535	ddh -3.04	Pyruvate metabolism, Microbial metabolism in diverse environments	Cytoplasmic
AIO20515.1	hypothetical protein KQ76_04260	SACOL0943	-3.00		Cytoplasmic
OOC94758.1	alpha/beta hydrolase	SA1990	-2.98		Unknown
AIO22074.1	glycerate kinase	SA2220	-2.97	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of antibiotics, Glycerolipid metabolism, Glyoxylate and dicarboxylate metabolism, Glycine, serine and threonine metabolism	Cytoplasmic
AIO21275.1	heat shock protein GrpE	grpE SA1410	-2.97		Cytoplasmic

AIO22275.1	clumping factor B	clfB SA2423	-2.96	<i>Staphylococcus aureus</i> infection	Cell wall
AIO20071.1	NADPH-dependent oxidoreductase	nfrA SACOL0453	-2.92	Metabolic pathways, Riboflavin metabolism	Cytoplasmic
AIO22317.1	lipase	lip1 SA2463	-2.89	Metabolic pathways, Glycerolipid metabolism	Extracellular
AIO19780.1	MarR family transcriptional regulator	sarS sarH1 SA0108	-2.87		Cytoplasmic
AIO21530.1	peptidylprolyl isomerase	prsA SA1659	-2.86		CM
AIO21602.1	staphostatin A	SA1726	-2.86		Unknown
AIO20100.1	hypothetical protein KQ76_01960	SA0395	-2.85		Unknown
AIO20776.1	phenol soluble modulins	SACOL1186	-2.85	Quorum sensing	Unknown
AIO20863.1	elongation factor Ts	tsf SACOL1276	-2.82		Cytoplasmic
OOC93971.1	phosphoglucomutase	pgcA SA2279	-2.81	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Purine metabolism, Amino sugar and nucleotide sugar metabolism, Starch and sucrose metabolism, Streptomycin	Cytoplasmic

					biosynthesis, Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Galactose metabolism	
AIO21506.1	serine protease	splE	SACOL1865	-2.81		Extracellular
AIO20279.1	hypothetical protein KQ76_03005		SA0570	-2.80		Unknown
AIO21343.1	membrane protein		SA1476	-2.76		Unknown
AIO20368.1	PTS fructose transporter subunit IIC	fruA		-2.73	Metabolic pathways, Microbial metabolism in diverse environments, Fructose and mannose metabolism, Phosphotransferase system (PTS)	CM
AIO20534.1	glycerophosphodiester phosphodiesterase	glpQ		-2.73	Glycerophospholipid metabolism	Unknown
AIO20049.1	pathogenicity island protein		SA1824	-2.72		Unknown
AIO21274.1	molecular chaperone DnaK	dnaK	SA1409	-2.68	RNA degradation	Cytoplasmic
AIO21449.1	leucyl-tRNA synthetase	leuS	SA1579	-2.67	Aminoacyl-tRNA biosynthesis	Cytoplasmic

AIO21282.1	competence protein ComE	comEB	-2.67	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO21436.1	peptidase M28	SA1566	-2.66		Cytoplasmic
AIO20170.1	hypothetical protein KQ76_02355	SA0464	-2.65		Cytoplasmic
AIO21073.1	hypothetical protein KQ76_07205	SACOL1491	-2.65		Unknown
AIO21788.1	HAD family hydrolase	SA1957	-2.64		Cytoplasmic
AIO22136.1	fibronectin-binding protein	fnbA SA2291	-2.60	Bacterial invasion of epithelial cells	Cell wall
AIO21371.1	primosomal protein DnaI	dnaI	-2.59		Cytoplasmic
AIO20579.1	oligopeptidase PepB	SA0859	-2.58		Cytoplasmic
AIO20152.1	methionine--tRNA ligase	metG SA0448	-2.58	Selenocompound metabolism, Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO20286.1	recombinase	SA0577	-2.58		Cytoplasmic
OOC92415.1	sphingomyelin phosphodiesterase	hlb SACOL2003	-2.56	Quorum sensing, Metabolic pathways, Inositol phosphate metabolism, Glycerophospholipid metabolism, Biosynthesis of secondary metabolites	Extracellular
AIO20439.1	Clp protease	clpP SA0723	-2.55		Cytoplasmic

AIO21970.1	ribose 5-phosphate isomerase	rpiA SA2127	-2.54	Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Pentose phosphate pathway	Cytoplasmic
AIO20435.1	thioredoxin reductase	trxB SA0719	-2.54	Selenocompound metabolism	Cytoplasmic
AIO21298.1	acetyl-CoA carboxylase biotin carboxylase subunit	SA1434	-2.52	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Pyruvate metabolism, Carbon metabolism, Fatty acid metabolism, Propanoate metabolism, Fatty acid biosynthesis	Cytoplasmic
AIO21363.1	DNA mismatch repair protein MutT	SA1501	-2.50		Cytoplasmic
AIO20575.1	tryptophanyl-tRNA synthetase	trpS SA0855	-2.50	Aminoacyl-tRNA biosynthesis	Cytoplasmic

AIO21606.1	nicotinate phosphoribosyltransferase	SA1729	-2.49	Metabolic pathways, Nicotinate and nicotinamide metabolism	Cytoplasmic
AIO22387.1	replication-associated protein (plasmid)	SAP031	-2.49		Unknown
AIO20282.1	transcriptional regulator	sarA SA0573	-2.48		Cytoplasmic
AIO20202.1	antitermination protein NusG	nusG SA0494	-2.48		Cytoplasmic
AIO21595.1	lipoprotein	SA1719	-2.46		Unknown
AIO22291.1	isochorismatase	SA2438	-2.45		Unknown
AIO21531.1	3'-5' exonuclease	cbfI	-2.44		Cytoplasmic
AIO20398.1	7-cyano-7-deazaguanine reductase	queF SA0683	-2.44	Metabolic pathways, Folate biosynthesis	Cytoplasmic
AIO21033.1	hypothetical protein KQ76_06965	SA1242	-2.44		Unknown
AIO19802.1	cell wall surface anchor family protein	sasD SACOL0119	-2.43		Cell wall
AIO21623.1	thioredoxin	SA1743	-2.41		Unknown
AIO20231.1	glycosyl transferase family 1	SACOL0612	-2.41		Cytoplasmic
AIO20885.1	zinc protease	SACOL1298	-2.40		Unknown

AIO21583.1	ferritin	ftnA SA1709	-2.39		Cytoplasmic
AIO22235.1	3-methyl-2-oxobutanoate hydroxymethyltransferase	panB SA2392	-2.37	Metabolic pathways, Biosynthesis of secondary metabolites, Pantothenate and CoA biosynthesis	Unknown
AIO20406.1	iron ABC transporter substrate-binding protein	SA0691	-2.37	ABC transporters	CM
AIO20712.1	pyruvate carboxylase	pyc SACOL1123	-2.35	Metabolic pathways, Pyruvate metabolism, Microbial metabolism in diverse environments, Biosynthesis of amino acids, Carbon metabolism, Citrate cycle (TCA cycle)	Cytoplasmic
AIO22158.1	glyoxalase	SA2310	-2.35	Metabolic pathways, Microbial metabolism in diverse environments, Benzoate degradation, Xylene degradation, Degradation of aromatic compounds	Unknown
AIO20704.1	hypothetical KQ76_05255	protein SA0957	-2.34		Cytoplasmic

AIO21607.1	nitric oxide synthase	nos SA1730	-2.34	Metabolic pathways, Biosynthesis of secondary metabolites, Arginine biosynthesis, Arginine and proline metabolism	Cytoplasmic
AIO22191.1	TetR family transcriptional regulator	SA2340	-2.33		Cytoplasmic
AIO22006.1	acetyltransferase	SA2159	-2.33		Cytoplasmic
AIO20913.1	glutamine synthetase	glnA SACOL1329	-2.32	Metabolic pathways, Two-component system, Biosynthesis of amino acids, Glyoxylate and dicarboxylate metabolism, Arginine biosynthesis, Microbial metabolism in diverse environments, Alanine, aspartate and glutamate metabolism, Nitrogen metabolism	Cytoplasmic
AIO20225.1	HAD family hydrolase	SA0517	-2.32		Cytoplasmic
AIO22285.1	hypothetical protein KQ76_13835	SACOL2661	-2.31		Extracellular
AIO19949.1	type VII secretion protein EsaA	esaA SA0272	-2.29		CM
AIO21929.1	transcriptional regulator	SA2091	-2.28		Unknown

AIO21020.1	hydrolase	SACOL1433	-2.28		Cytoplasmic
AIO21157.1	replication protein		-2.28		Cytoplasmic
AIO22336.1	pyrrolidone-carboxylate peptidase	pcp SACOL2714	-2.27		Cytoplasmic
AIO22054.1	phosphoglyceromutase	gpmA SA2204	-2.24	Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Methane metabolism, Glycolysis / Gluconeogenesis, Glycine, serine and threonine metabolism	Unknown
OOC89529.1	dUTP pyrophosphatase	dut SACOL0357	-2.23	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO21679.1	ABC transporter ATP- binding protein	vga	-2.23		Cytoplasmic
AIO21204.1	hypothetical protein KQ76_07895	SACOL1555	-2.22		Cytoplasmic

AIO21459.1	riboflavin synthase subunit alpha	ribE SACOL1819	-2.22	Metabolic pathways, Riboflavin metabolism, Biosynthesis of secondary metabolites	
AIO20749.1	succinate dehydrogenase	sdhB	-2.21	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Carbon metabolism, Citrate cycle (TCA cycle), Oxidative phosphorylation, Butanoate metabolism	Cytoplasmic
AIO20507.1	alanine-phosphoribitol ligase	dltA SACOL0935	-2.20	Two-component system, Cationic antimicrobial peptide (CAMP) resistance, D-Alanine metabolism, <i>Staphylococcus aureus</i> infection	Cytoplasmic
AIO21007.1	oligoendopeptidase F	SA1216	-2.19		Cytoplasmic
AIO21222.1	elongation factor P	efp SA1359	-2.19		Cytoplasmic
AIO22338.1	adhesin		-2.18		Cell wall

AIO20422.1	sigma-54 modulation protein	hpf SA0707	-2.16		Cytoplasmic
AIO20857.1	ATP-dependent protease subunit HslV	hslV clpQ SA1096	-2.16		Cytoplasmic
AIO21536.1	Cro/CI family transcriptional regulator	SA1665	-2.15		Cytoplasmic
AIO20783.1	penicillin-binding protein	pbpA	-2.15	Metabolic pathways, beta-Lactam resistance, Peptidoglycan biosynthesis	CM
AIO20880.1	polynucleotide phosphorylase	pnp pnpA SA1117	-2.14	Purine metabolism, Pyrimidine metabolism, RNA degradation	Cytoplasmic
AIO19900.1	nitric oxide dioxygenase	SA0231	-2.14		Cytoplasmic
AIO21401.1	peroxidase	tpx SACOL1762	-2.14		Unknown
AIO20237.1	6-phospho 3-hexuloisomerase	SA0529	-2.13	Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of amino acids, Pentose phosphate pathway, Methane metabolism	Unknown
AIO21562.1	RecX family transcriptional regulator	recX SA1690	-2.13		Cytoplasmic

AIO21223.1	peptidase M24	SACOL1588	-2.12		Cytoplasmic
AIO21854.1	DNA-directed RNA polymerase subunit alpha	rpoA SA2023	-2.12	Metabolic pathways, Purine metabolism, Pyrimidine metabolism, RNA polymerase	Cytoplasmic
AIO20194.1	glutamyl-tRNA synthetase	gltX SA0486	-2.11	Metabolic pathways, Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO20273.1	arginine--tRNA ligase	argS SACOL0663	-2.11	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO21926.1	MarR family transcriptional regulator	sarR SA2089	-2.10		Cytoplasmic
AIO20259.1	dihydrolipoamide dehydrogenase	SA0551	-2.09		Cytoplasmic
AIO20623.1	conjugal transfer protein	SACOL1582	-2.08		Unknown
AIO22143.1	hypothetical protein KQ76_13105	SACOL2519	-2.08		Cytoplasmic
AIO21116.1	gamma-hemolysin subunit A	hlgC SA2208	-2.06		Extracellular
AIO21055.1	membrane protein	SA1265	-2.06		CM
AIO21194.1	ribonuclease Z	rnz SACOL1548	-2.06		Cytoplasmic
AIO20555.1	phosphatidylethanolamine-binding protein	SACOL0984	-2.06		Unknown

					Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of antibiotics, Glycolysis / Gluconeogenesis, Butanoate metabolism, Pyruvate metabolism, Citrate cycle (TCA cycle)	
AIO20895.1	2-oxoglutarate oxidoreductase alpha	ferredoxin subunit	SA1131	-2.06		Cytoplasmic
AIO20402.1	ribonucleotide-diphosphate subunit beta	reductase	nrdF	-2.06	Metabolic pathways, Purine metabolism, Pyrimidine metabolism	Cytoplasmic
AIO19739.1	50S ribosomal protein L9		rpII SA0014	-2.05	Ribosome	Cytoplasmic
AIO20584.1	GTP pyrophosphokinase		SA0864	-2.04	Purine metabolism	Cytoplasmic
AIO21458.1	GTP cyclohydrolase		ribBA SACOL1818	-2.04	Metabolic pathways, Riboflavin metabolism, Biosynthesis of secondary metabolites, Folate biosynthesis	Cytoplasmic
AIO20455.1	hypothetical KQ76_03935	protein	SACOL0851	-2.04		Unknown

AIO20695.1	hypothetical KQ76_05210	protein	SA0947	-2.04		Unknown
AIO20687.1	hypothetical KQ76_05170	protein	SA0941	-2.04		Cytoplasmic
AIO20819.1	16S methyltransferase	rRNA	SA1060	-2.03		Cytoplasmic
AIO20413.1	peptidase T		pepT SA0698	-2.03		Cytoplasmic
AIO20838.1	cell division protein FtsY		ftsY SACOL1251	-2.03	Quorum sensing, Protein export, Bacterial secretion system	CM
AIO21057.1	ribonuclease H		SACOL1471	-2.03	DNA replication	Cell wall
OOC91307.1	hypothetical BWO94_08325	protein	SA1008	-2.02		Unknown
AIO20835.1	acyl carrier protein		acpP SA1075	hmrB -2.01		Cytoplasmic