

Table S1: Functional classification of the significantly upregulated common proteins between hydrated biofilm and DSB compared with planktonic culture (p <0.05). *FC denotes fold change; ** CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Name	Hydrated biofilm (FC)*	DSB (FC)*	Protein Pathways	Subcellular Localization
AIO22223.1	type II secretion protein	SA2371	3.59	2.46		Unknown
AIO21382.1	isocitrate dehydrogenase	icd citC SA1517	3.06	2.17	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of amino acids, Biosynthesis of antibiotics, Microbial metabolism in diverse environments, Carbon metabolism, 2-Oxocarboxylic acid metabolism, Glutathione metabolism, Citrate cycle (TCA cycle)	Cytoplasmic
AIO20590.1	membrane protein	SA0870	2.62	2.04		CM**
AIO22305.1	hypothetical protein KQ76_13935	SA2451	5.52	4.40		Unknown
OOC90965.1	glutamine ABC transporter ATP-binding protein	SA1674	2.83	2.30		CM
AIO20668.1	phosphoribosylformylglycin amidine synthase	purL SACOL107 8	2.45	2.03	Metabolic pathways, Biosynthesis of secondary metabolites, Purine metabolism, Biosynthesis of antibiotics	Cytoplasmic
AIO20812.1	DNA-directed RNA polymerase subunit omega	rpoZ SA1053	3.74	3.16	Metabolic pathways, Pyrimidine metabolism, Purine metabolism, RNA polymerase,	Cytoplasmic

AIO20535.1	argininosuccinate lyase	argH SA0821	2.43	2.06	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of amino acids, Biosynthesis of antibiotics, Alanine, aspartate and glutamate metabolism, Arginine biosynthesis	Cytoplasmic
AIO20780.1	cell division protein MraZ	mraZ SA1021	2.58	2.21		Cytoplasmic
AIO19852.1	branched-chain amino acid transporter II carrier protein	SA0180	3.81	3.27		CM
AIO20178.1	dihydropteroate synthase	folP SA0472	3.28	2.81	Metabolic pathways, Folate biosynthesis	CM
AIO20178.1	dihydropteroate synthase	folP SA0472	3.28	2.81	Metabolic pathways, Folate biosynthesis	Cytoplasmic
AIO21773.1	membrane protein	SA1937	3.20	2.82		CM
AIO21226.1	octanoyltransferase	lipM SA1363	2.68	2.38	Metabolic pathways, Lipoic acid metabolism	Cytoplasmic
AIO20979.1	sodium:alanine symporter	alsT	2.67	2.42		CM
AIO20958.1	guanosine 5'- monophosphate oxidoreductase	guaC SACOL137 1	3.28	2.97	Purine metabolism	Cytoplasmic
AIO21819.1	hypothetical protein KQ76_11385	SA1986	3.27	2.96		CM
AIO22040.1	formate/nitrite transporter	SACOL240 1	2.56	2.33		CM
AIO21727.1	membrane protein	yidC SA1893	2.46	2.27	Protein export, Bacterial secretion system, Quorum sensing	CM
AIO21864.1	50S ribosomal protein L18	rplR SA2032	2.33	2.19	Ribosome	Cytoplasmic

AIO19795.1	acetoin reductase	butA SA0122	2.49	2.35	Butanoate metabolism	Cytoplasmic
AIO22226.1	fructosamine kinase	SA2374	2.71	2.55		Cytoplasmic
AIO21765.1	CTP synthetase	pyrG ctrA SA1929	2.32	2.24	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO21934.1	octopine dehydrogenase	SA2095	2.20	2.13		Cytoplasmic
AIO20806.1	orotidine 5'-phosphate decarboxylase	pyrF SA1047	2.54	2.49	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO21333.1	ATP-dependent DNA helicase RuvB	ruvB SACOL169 6	2.55	2.50	Homologous recombination	Cytoplasmic 9.98
AIO21826.1	PTS system lactose-specific transporter subunit IIA	lacF SA1993	2.36	2.32	Metabolic pathways, Galactose metabolism, Phosphotransferase system (PTS)	Cytoplasmic 10.01

AIO20163.1	ribose-phosphate pyrophosphokinase	prs SA0458	2.81	2.79	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of amino acids, Biosynthesis of antibiotics, Purine metabolism, Microbial metabolism in diverse environments, Carbon metabolism, Pentose phosphate pathway	Cytoplasmic
AIO21316.1	hypothetical protein KQ76_08470	SAS049	2.21	2.21		Unknown
AIO21860.1	preprotein translocase subunit SecY	secY SA2028	2.15	2.16	Protein export, Bacterial secretion system, Quorum sensing	CM
AIO21768.1	pantothenate kinase	coaW SA1932	2.01	2.03	Metabolic pathways, Pantothenate and CoA biosynthesis	Unknown
AIO20718.1	glycerophosphodiester phosphodiesterase	SA0969	2.38	2.45	Glycerophospholipid metabolism	Cytoplasmic
AIO21539.1	pseudouridine synthase	SA1668	2.50	2.58		Cytoplasmic
AIO20864.1	uridylate kinase	pyrH smbA SA1101	2.07	2.20	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO20697.1	spermidine/putrescine ABC transporter ATP-binding protein	potA SA0950	2.30	2.46	ABC transporters	CM
AIO21307.1	hypothetical protein KQ76_08425	SA1443	2.10	2.26		Cytoplasmic
AIO21769.1	hypothetical protein KQ76_11075	SA1933	2.10	2.26		Cytoplasmic

AIO20807.1	orotate phosphoribosyltransferase	pyrE SA1048	2.13	2.30	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO21210.1	2-oxoisovalerate dehydrogenase	SACOL156 1	3.11	3.36	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Propanoate metabolism, Valine, leucine and isoleucine degradation	Cytoplasmic
AIO21335.1	ACT domain-containing protein	SA1469	3.27	3.59	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of amino acids, Biosynthesis of antibiotics, Phenylalanine, tyrosine and tryptophan biosynthesis	Cytoplasmic
AIO22278.1	amino acid APC transporter	arcD	2.23	2.47		CM
AIO20787.1	cell division protein FtsA	ftsA SA1028	2.94	3.29		Cytoplasmic
AIO21825.1	PTS system lactose-specific transporter subunits IICB	lacE SACOL218 1	2.27	2.54	Metabolic pathways, Phosphotransferase system (PTS), Galactose metabolism	CM
AIO21878.1	50S ribosomal protein L23	rplW SA2045	2.15	2.41	Ribosome	Cytoplasmic
AIO20778.1	hypothetical protein KQ76_05635	SA1019	2.41	2.71		Unknown
AIO21910.1	molybdenum ABC transporter permease	modB	2.57	2.93	ABC transporters	CM
AIO21879.1	50S ribosomal protein L4	rplD SA2046	2.03	2.33	Ribosome	Unknown
AIO20968.1	exonuclease	sbcD SA1180	2.36	2.73		Cytoplasmic

AIO22176.1	PTS system glucose-specific transporter subunit IICBA	glcB SACOL255 2	2.07	2.40	Phosphotransferase system (PTS), Amino sugar and nucleotide sugar metabolism, Glycolysis / Gluconeogenesis	CM
AIO22234.1	pantoate--beta-alanine ligase	panC SACOL261 4	2.91	3.42	Metabolic pathways, Biosynthesis of secondary metabolites, Pantothenate and CoA biosynthesis, beta-Alanine metabolism	Cytoplasmic
AIO21337.1	50S ribosomal protein L27	rpmA SA1471	2.64	3.12	Ribosome	Cytoplasmic
AIO20205.1	50S ribosomal protein L10	rplJ SA0497	2.16	2.69	Ribosome	Cytoplasmic
AIO20817.1	peptide deformylase	SA1058	2.10	2.66		Cytoplasmic
AIO19749.1	hypothetical protein KQ76_00135		2.73	3.48		Cytoplasmic
AIO20985.1	LytR family transcriptional regulator	msrR SA1195	2.13	2.75		CM
AIO21707.1	4'-phosphopantetheinyl transferase	acpS dpj SA1875	2.37	3.18	Pantothenate and CoA biosynthesis	
OOC94735.1	hypothetical protein BWO94_01050		3.63	4.91		Unknown
AIO20937.1	hypothetical protein KQ76_06475	SAS040	2.84	3.94		Unknown
AIO20620.1	hypothetical protein KQ76_04815	SACOL158 5	2.20	3.15		Unknown
AIO20395.1	lipid kinase	SACOL078 7	2.05	3.03		Unknown
AIO21848.1	50S ribosomal protein L13	rplM SA2017	2.14	3.28	Ribosome	Unknown

Table S2: Functional classification of the significantly downregulated common proteins between hydrated biofilm and DSB compared with planktonic culture (p <0.05). *FC denotes fold change; ** CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Name	Hydrated biofilm (FC)*	DSB (FC)*	Protein Pathways	Subcellular Localization
AIO20700.1	spermidine/putrescine ABC transporter substrate- binding protein	potD	0.08	0.04	ABC transporters	Unknown
AIO22060.1	gamma-hemolysin subunit A	hlgC SA2208	0.35	0.22	<i>Staphylococcus aureus</i> infection	Extracellular
AIO20660.1	chitinase	SA0914	0.09	0.06		Unknown
AIO20463.1	thermonuclease	nuc SACOL0860	0.16	0.12		Extracellular
AIO21509.1	serine protease	spIC SACOL1867	0.28	0.20		Extracellular
AIO20279.1	hypothetical protein KQ76_03005	SA0570	0.48	0.36	Metabolic pathways, Glycerolipid metabolism	Unknown
AIO19987.1	lipase	lip2 geh SA0309	0.14	0.10		Extracellular
AIO20583.1	hypothetical protein KQ76_04610	SACOL1009	0.46	0.35		CM**
AIO20651.1	mannosyl-glycoprotein endo-beta-N- acetylglucosamidase	atl nag SACOL1062	0.24	0.18	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Porphyrin and chlorophyll metabolism	Extracellular
AIO21353.1	delta-aminolevulinic acid dehydratase	hemB SA1492	0.27	0.21		Cytoplasmic

AIO20960.1	secretion protein	SACOL1373	0.47	0.37		Unknown
AIO21128.1	hypothetical protein KQ76_07495		0.35	0.28		Cytoplasmic
OOC94758.1	alpha/beta hydrolase	SA1990	0.33	0.26		Unknown
AIO20644.1	cysteine protease	sspB SACOL1056	0.11	0.09		Extracellular
AIO19870.1	peptidase M23	SA0205	0.19	0.16		Extracellular
AIO20093.1	superantigen-like protein	set11	0.33	0.28	<i>Staphylococcus aureus</i> infection	Extracellular
AIO20534.1	glycerophosphodiester phosphodiesterase	glpQ	0.22	0.18		Unknown
AIO20738.1	phenylalanyl-tRNA synthase subunit beta	pheT SA0986	0.38	0.33	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO22292.1	adhesin	sasF SACOL2668	0.43	0.37		Cellwall
AIO21549.1	Fur family transcriptional regulator	perR SACOL1919	0.48	0.42		Cytoplasmic
AIO21667.1	delta-hemolysin	hld SA1841.1 SAS065	0.03	0.03	Quorum sensing	Unknown
AIO20100.1	hypothetical protein KQ76_01960	SA0395	0.14	0.12		Unknown
AIO20951.1	HAD family hydrolase	SA1167	0.43	0.37		Cytoplasmic
AIO20623.1	conjugal transfer protein	SACOL1582	0.42	0.37		Unknown
AIO22349.1	hypothetical protein KQ76_14165		0.30	0.27		Unknown
AIO20056.1	hypothetical protein KQ76_01725		0.10	0.09		CM

AIO21298.1	acetyl-CoA carboxylase biotin carboxylase subunit	SA1434	0.41	0.36	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Carbon metabolism, Fatty acid metabolism, Propanoate metabolism, Pyruvate metabolism, Fatty acid biosynthesis	Cytoplasmic
AIO19780.1	MarR family transcriptional regulator	sarS sarH1 SA0108	0.45	0.40		Cytoplasmic
AIO20712.1	pyruvate carboxylase	pyc SACOL1123	0.50	0.45	Metabolic pathways, Pyruvate metabolism, Microbial metabolism in diverse environments, Biosynthesis of amino acids, Citrate cycle (TCA cycle), Carbon metabolism	Cytoplasmic
AIO19770.1	1-phosphatidylinositol phosphodiesterase	plc	0.19	0.17	Inositol phosphate metabolism	Extracellular
AIO22290.1	N-acetylmuramoyl-L- alanine amidase	SACOL2666	0.14	0.12		Extracellular
AIO20332.1	peptidase M23B	SA0620	0.14	0.13		Cell wall
AIO20756.1	formyl peptide receptor- like 1 inhibitory protein	flr SA1001	0.35	0.32	<i>Staphylococcus aureus</i> infection	Unknown
AIO21349.1	DNA-3-methyladenine glycosylase	tag	0.40	0.36	Base excision repair	Unknown
AIO21997.1	LytTR family transcriptional regulator	SA2153	0.43	0.40		Unknown

AIO21607.1	nitric oxide synthase	nos SA1730	0.44	0.40	Metabolic pathways, Biosynthesis of secondary metabolites, Arginine biosynthesis, Arginine and proline metabolism	Cytoplasmic
AIO20419.1	DegV domain-containing protein	SACOL0812	0.49	0.45		Cytoplasmic
AIO21983.1	esterase	SA2140	0.48	0.44		Cytoplasmic
AIO22180.1	LysR family transcriptional regulator	SA2330	0.34	0.32		Cytoplasmic
AIO20126.1	N-acetylmuramoyl-L-alanine amidase	sle1 aaa SA0423	0.29	0.27		Cellwall
AIO21449.1	leucyl-tRNA synthetase	leuS SA1579	0.36	0.34	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO20739.1	ribonuclease HIII	rnhC SACOL1150	0.22	0.20	DNA replication	Unknown
AIO20704.1	hypothetical protein KQ76_05255	SA0957	0.49	0.46		Cytoplasmic
AIO20387.1	glycerol phosphate lipoteichoic acid synthase	ltaS SA0674	0.15	0.14	Metabolic pathways, Glycerolipid metabolism	CM
OOC91307.1	hypothetical protein BWO94_08325	SA1008	0.50	0.47		Unknown
AIO21583.1	ferritin	ftnA SA1709	0.44	0.42		Cytoplasmic
AIO21618.1	hypothetical protein KQ76_10250	SAS056	0.46	0.44		
AIO19947.1	staphyloxanthin biosynthesis protein	SACOL0270	0.13	0.12		Extracellular
AIO21246.1	penicillin-binding protein	pbp3	0.36	0.35	Metabolic pathways, beta-Lactam resistance, Peptidoglycan biosynthesis	CM
AIO20202.1	antitermination protein NusG	nusG SA0494	0.46	0.44		Cytoplasmic

OOC94232.1	aureolysin	aur SACOL2659	0.32	0.30	<i>Staphylococcus aureus</i> infection, Cationic antimicrobial peptide (CAMP) resistance	Extracellular
AIO19779.1	peptigoglycan-binding protein LysM	spa SACOL0095	0.16	0.15	<i>Staphylococcus aureus</i> infection	Cellwall
AIO20863.1	elongation factor Ts	tsf SACOL1276	0.36	0.35		Cytoplasmic
AIO22317.1	lipase	lip1 SA2463	0.20	0.19	Metabolic pathways, Glycerolipid metabolism	Extracellular
AIO22350.1	peptidase		0.13	0.12		Extracellular
AIO20885.1	zinc protease	SACOL1298	0.46	0.44		Unknown
AIO20273.1	arginine-tRNA ligase	argS SACOL0663	0.48	0.47	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO21182.1	transcriptional regulator	srrA SA1323	0.33	0.32	Two-component system	Cytoplasmic
AIO20196.1	cysteinyl-tRNA synthetase	cysS SACOL0576	0.41	0.40	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO20645.1	glutamyl endopeptidase	sspA SACOL1057	0.15	0.15	Quorum sensing	Extracellular
AIO20455.1	hypothetical protein KQ76_03935	SACOL0851	0.42	0.41		Unknown
AIO22160.1	lactate dehydrogenase	ldhD ddh SACOL2535	0.29	0.29	Pyruvate metabolism, Microbial metabolism in diverse environments	Cytoplasmic
AIO21406.1	Free methionine-(R)- sulfoxide reductase	SACOL1768	0.26	0.25	Cysteine and methionine metabolism	Cytoplasmic
AIO22099.1	peptidase M28	SA2244	0.32	0.31		Cytoplasmic
AIO20194.1	glutamyl-tRNA synthetase	gltX SA0486	0.39	0.39	Metabolic pathways, Aminoacyl- tRNA biosynthesis	Cytoplasmic
AIO22275.1	clumping factor B	clfB SA2423	0.33	0.33	<i>Staphylococcus aureus</i> infection	Cellwall
AIO21805.1	uridylyltransferase	SA1974	0.36	0.36		Cytoplasmic

OOC93971.1	phosphoglucomutase	pgcA SA2279	0.41	0.41	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Purine metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Glycerophospholipid metabolism, Pentose phosphate pathway, Amino sugar and nucleotide sugar metabolism, Streptomycin biosynthesis, Starch and sucrose metabolism	Cytoplasmic
OOC94101.1	DUF2648 domain-containing protein	SACOL2649	0.50	0.51		Unknown
AIO19942.1	peptidase M23	lytM SACOL0263	0.12	0.12		Extracellular
AIO21492.1	hypothetical protein KQ76_09365	SACOL1852	0.16	0.16		Unknown
AIO19900.1	nitric oxide dioxygenase	SA0231	0.34	0.35		Cytoplasmic
AIO21508.1	serine protease	spIE SACOL1865	0.40	0.41		Extracellular
AIO20228.1	hydrolase	sdrD SA0520	0.22	0.22	<i>Staphylococcus aureus</i> infection	Cellwall
AIO20556.1	hypothetical protein KQ76_04470	SA0841	0.08	0.08		CM
AIO22338.1	adhesin		0.46	0.47		Cellwall
OOC90902.1	calcium-binding protein	SACOL1846	0.05	0.05		Unknown
AAX11326.1	enterotoxin type Gv precursor	entG seg SA1642	0.40	0.41	<i>Staphylococcus aureus</i> infection	Extracellular
AIO22285.1	hypothetical protein KQ76_13835	SACOL2661	0.37	0.39		Extracellular

AIO20759.1	fibrinogen-binding protein	SA1004	0.47	0.50	<i>Staphylococcus aureus</i> infection	Unknown
AIO22081.1	sodium:proton antiporter	SA2228	0.21	0.22		CM
AIO22369.1	phosphodiesterase	hlb SACOL2003	0.12	0.12	Metabolic pathways, Quorum sensing, Biosynthesis of secondary metabolites	Extracellular
AIO22017.1	hypothetical protein KQ76_12415	SA2168	0.39	0.42		Unknown
AIO21033.1	hypothetical protein KQ76_06965	SA1242	0.46	0.49		Unknown
AIO20783.1	penicillin-binding protein	pbpA	0.39	0.42	Metabolic pathways, beta-Lactam resistance, Peptidoglycan biosynthesis	CM
AIO21282.1	competence protein ComE	comEB	0.41	0.44	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO20229.1	bis(5'-nucleosyl)-tetraphosphatase	sdrE SACOL0610	0.26	0.28	<i>Staphylococcus aureus</i> infection	Cellwall
AIO21274.1	molecular chaperone DnaK	dnaK SA1409	0.43	0.47	RNA degradation	Cytoplasmic
AIO22174.1	thioredoxin	SA2324	0.42	0.47		Cytoplasmic
AIO20145.1	DNA polymerase III subunit delta'	SACOL0526	0.31	0.34	Metabolic pathways, DNA replication, Pyrimidine metabolism, Purine metabolism, Homologous recombination, Mismatch repair	Cytoplasmic
AIO20763.1	alpha-hemolysin	SA1007	0.06	0.06		Extracellular
AIO20737.1	phenylalanine--tRNA ligase	pheS SA0985	0.35	0.39	Aminoacyl-tRNA biosynthesis	Cytoplasmic
AIO21788.1	HAD family hydrolase	SA1957	0.30	0.34		Cytoplasmic
AIO20874.1	50S ribosomal protein L7	SA1111	0.34	0.38		Unknown

AIO21867.1	30S ribosomal protein S14	rpsZ rpsN1 SA2034.1 SAS079	0.26	0.29	Ribosome	Cytoplasmic
AIO20189.1	excinuclease ABC subunit B	SA0481	0.36	0.40		Cytoplasmic
OOC92415.1	sphingomyelin phosphodiesterase	hlb SACOL2003	0.33	0.37	Glycerophospholipid metabolism, Inositol phosphate metabolism	Extracellular
AIO21275.1	heat shock protein GrpE	grpE SA1410	0.36	0.41		Cytoplasmic
AIO20225.1	HAD family hydrolase	SA0517	0.42	0.48		Cytoplasmic
AIO20637.1	acetyltransferase	SA0893	0.17	0.20		Cytoplasmic
AIO22130.1	DNA mismatch repair protein MutT	SACOL2500	0.41	0.47		Unknown
AIO20418.1	ABC transporter	SACOL0811	0.27	0.31		Cytoplasmic
AIO21842.1	toxin	SACOL2197	0.40	0.46		CM
AIO22387.1	replication-associated protein (plasmid)	SAP031	0.41	0.48		Unknown
AIO20884.1	zinc protease	SA1121	0.29	0.34		Cytoplasmic
AIO22136.1	fibronectin-binding protein	fnbA SA2291	0.23	0.26	Bacterial invasion of epithelial cells	Cellwall
AIO20222.1	deoxycytidine kinase	SA0514	0.43	0.50	Metabolic pathways, Purine metabolism, Pyrimidine metabolism	Cytoplasmic
AIO21273.1	molecular chaperone DnaJ	dnaJ SA1408	0.21	0.24		Cytoplasmic
AIO22207.1	transglycosylase	isaA SACOL2584	0.11	0.14		Extracellular

AIO19907.1	PTS sugar transporter subunit IIA	SA0236	0.24	0.29	Metabolic pathways, Galactose metabolism, Phosphotransferase system (PTS)	Cytoplasmic
AIO20259.1	dihydrolipoamide dehydrogenase	SA0551	0.42	0.51		Cytoplasmic
AIO21343.1	membrane protein	SA1476	0.30	0.37		Unknown
AIO20071.1	NADPH-dependent oxidoreductase	nfrA SACOL0453	0.26	0.32	Metabolic pathways, Riboflavin metabolism	Cytoplasmic
AIO21601.1	cysteine protease	sspP scpA SA1725	0.23	0.29		Extracellular
AIO20406.1	iron ABC transporter substrate-binding protein	SA0691	0.35	0.44	ABC transporters	CM
AIO20716.1	SCP-like extracellular protein	SA0967	0.17	0.22		Unknown
AIO21889.1	hypothetical protein KQ76_11750	SAS081	0.34	0.44		Cytoplasmic
AIO21919.1	urease subunit gamma	ureA SA2082	0.35	0.45	Metabolic pathways, Microbial metabolism in diverse environments, Purine metabolism, Arginine biosynthesis	Cytoplasmic
AIO19988.1	alpha/beta hydrolase	SACOL0391	0.32	0.42		Cytoplasmic
AIO22336.1	pyrrolidone-carboxylate peptidase	pcp SACOL2714	0.32	0.41		Cytoplasmic
AIO22042.1	glutathione S-transferase	SACOL2402	0.29	0.40		Unknown
AIO21116.1	gamma-hemolysin subunit A	hlgC SA2208	0.35	0.48		Extracellular

AIO22074.1	glycerate kinase	SA2220	0.24	0.34	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of antibiotics, Glycerolipid metabolism, lyoxylate and dicarboxylate metabolism, Glycine, serine and threonine metabolism	Cytoplasmic
AIO21505.1	serine protease	spIF SA1627	0.25	0.35	Quorum sensing	Extracellular
AIO20749.1	succinate dehydrogenase	sdhB	0.28	0.41	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Carbon metabolism, Citrate cycle (TCA cycle), Butanoate metabolism, Oxidative phosphorylation	Cytoplasmic
AIO21157.1	replication protein		0.31	0.47		Cytoplasmic
AIO21221.1	acetyl-CoA carboxylase	accB	0.23	0.40	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Carbon metabolism, Fatty acid metabolism, Propanoate metabolism, Pyruvate metabolism, Fatty acid biosynthesis	Cytoplasmic

Table S3: The list of significantly upregulated proteins in hydrated biofilm in comparison to DSB (p<0.05). * CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Name	Fold Change	Protein Pathways	Subcellular Localization
AIO21660.1	DNA-binding protein		2.968		Cytoplasmic
AIO20800.1	phosphoribosyl transferase	pyrR SA1041	2.527	Metabolic pathways, Pyrimidine metabolism	Cytoplasmic
AIO22003.1	L-lactate permease	SACOL2363	2.495		CM*
AIO20486.1	hypothetical protein KQ76_04110	SA0772	2.359		Unknown
AIO21982.1	hypothetical protein KQ76_12230	SACOL2344	2.319		Cytoplasmic
AIO20657.1	cytochrome C oxidase subunit III	qoxC SA0911	2.312	Metabolic pathways, Oxidative phosphorylation	CM
AIO22274.1	tributylin esterase	SA2422	2.304		Unknown
AIO21564.1	general stress protein	SA1692	2.294		Cytoplasmic

AIO20599.1	peptide chain release factor 3	prfC SACOL1025	2.272		Cytoplasmic
AIO20680.1	hypothetical protein KQ76_05130	SA0933	2.177		Unknown
AIO21790.1	glucosamine--fructose-6-phosphate aminotransferase	glmS SACOL2145	2.130	Metabolic pathways, Biosynthesis of antibiotics, Alanine, aspartate and glutamate metabolism, Amino sugar and nucleotide sugar metabolism	Cytoplasmic
AIO21830.1	galactose-6-phosphate isomerase	lacA SA1997	2.127	Metabolic pathways, Galactose metabolism	Unknown
AIO22037.1	nitrite reductase	nasD	2.078	Microbial metabolism in diverse environments, Nitrogen metabolism	Cytoplasmic
AIO21798.1	arginase	arg SA1968	2.039	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Arginine biosynthesis, Arginine and proline metabolism	Cytoplasmic

AIO20370.1	transporter associated domain protein	SA0657	2.038		CM
AIO21892.1	aminoacyltransferase	femX fmhB SA2057	2.026	Metabolic pathways, Peptidoglycan biosynthesis	Cytoplasmic
AIO21786.1	lytic regulatory protein	truncated-SA	2.024		CM
OOC91313.1	5- (carboxyamino)imidazole ribonucleotide mutase	purE SA0916	2.007	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Purine metabolism	CM
AIO20536.1	argininosuccinate synthase	argG SA0822	2.006	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Arginine biosynthesis, Alanine, aspartate and glutamate metabolism	Cytoplasmic

AIO20949.1	threonine synthase	thrC SACOL1363	2.004	Metabolic pathways, Biosynthesis of secondary metabolites, Microbial metabolism in diverse environments, Glycine, serine and threonine metabolism, Vitamin B6 metabolism, Biosynthesis of amino acids	Cytoplasmic
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Table S4: The list of significantly upregulated proteins in DSB in comparison to hydrated biofilm (p<0.05). * CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Name	Fold Change	Protein Pathways	Subcellular Localization
OOC91425.1	serine acetyltransferase	cysE SA0487	2.322	Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Cysteine and methionine metabolism, Sulfur metabolism, Biosynthesis of amino acids, Carbon metabolism	Cytoplasmic
AIO21414.1	PTS glucose transporter subunit IIBC	ptaA	2.318	Amino sugar and nucleotide sugar metabolism, Phosphotransferase system (PTS)	CM*
AIO21824.1	6-phospho-beta-galactosidase	lacG SA1991	2.196	Metabolic pathways, Galactose metabolism	Cytoplasmic
AIO21431.1	UDP-N-acetylmuramate--alanine ligase	murC SACOL1790	2.174	Metabolic pathways, D-Glutamine and D-glutamate metabolism, Peptidoglycan biosynthesis	Cytoplasmic

AIO20705.1	inositol monophosphatase	SACOL1116	2.128	Metabolic pathways, Streptomycin biosynthesis, Inositol phosphate metabolism	Cytoplasmic
AIO20408.1	UDP-N-acetylenolpyruvoylglucosamine reductase	murB SA0693	2.122	Metabolic pathways, Amino sugar and nucleotide sugar metabolism, Peptidoglycan biosynthesis	Cytoplasmic
AIO22036.1	nitrite reductase	nasE	2.091	Microbial metabolism in diverse environments, Nitrogen metabolism	Cytoplasmic
AIO20589.1	enoyl-ACP reductase	fabI	2.086	Metabolic pathways, Biotin metabolism, Fatty acid biosynthesis and metabolism, Biosynthesis of antibiotics	CM
AIO20891.1	recombinase RecA	recA SA1128	2.036	Homologous recombination	Cytoplasmic
AIO20673.1	phosphoribosylamine-glycine ligase	purD SA0926	2.011	Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Purine metabolism	Cytoplasmic

Table S5: The list of significantly downregulated proteins in hydrated biofilm in comparison to DSB (p<0.05). * CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Name	Fold Change	Protein Pathways	Subcellular Localization
AIO22143.1	hypothetical protein KQ76_13105	SACOL2519	0.303		Cytoplasmic
AIO20170.1	hypothetical protein KQ76_02355	SA0464	0.427		Cytoplasmic
OOC90925.1	serine protease splA	splB SA1630	0.431		Cytoplasmic
AIO19949.1	type VII secretion protein EsaA	esaA SA0272	0.432		CM*
AIO21302.1	transcription elongation factor GreA	greA SA1438	0.435		Cytoplasmic
AIO20865.1	ribosome recycling factor	frr SA1102	0.435		Cytoplasmic
AIO21853.1	50S ribosomal protein L17	rplQ SA2022	0.436	Ribosome	Cytoplasmic
AIO21993.1	hemin ABC transporter ATP-binding protein	hrtA SA2149	0.448	ABC transporters	CM

AIO20742.1	DNA polymerase	SA0990	0.451		Cytoplasmic
AIO19898.1	uroporphyrin-III methyltransferase	SA0230	0.453		Unknown
AIO20835.1	acyl carrier protein	acpP hmrB SA1075	0.473		Cytoplasmic
AIO20893.1	hypothetical protein KQ76_06215	SACOL1306	0.480		Cytoplasmic
AIO20478.1	thioredoxin	SA0758	0.484		Cytoplasmic
AIO22260.1	sulfite reductase [NADPH] flavoprotein alpha- component	SA2413	0.486	Metabolic pathways, Microbial metabolism in diverse environments, Sulfur metabolism	CM
AIO20838.1	cell division protein FtsY	ftsY SACOL1251	0.486	Protein export, Bacterial secretion system, Quorum sensing	CM
AIO19963.1	QueA protein	SACOL0282	0.489		Cytoplasmic
AIO20555.1	phosphatidylethanolamine- binding protein	SACOL0984	0.491		Unknown
AIO20584.1	GTP pyrophosphokinase	SA0864	0.496	Purine metabolism	Cytoplasmic

AIO20515.1	hypothetical protein KQ76_04260	SACOL0943	0.497		Cytoplasmic
AIO21475.1	glyoxal reductase	SA1606	0.499		Cytoplasmic
AIO20687.1	hypothetical protein KQ76_05170	SA0941	0.501		Cytoplasmic
AIO21223.1	peptidase M24	SACOL1588	0.505		Cytoplasmic
AIO22050.1	amino acid ABC transporter substrate- binding protein	SACOL2412	0.508	ABC transporters	Unknown
AIO21432.1	cell division protein FtsK	SA1562	0.510		CM

Table S6: The list of significantly downregulated proteins in DSB in comparison to hydrated biofilm (p<0.05). * CM denotes Cytoplasmic Membrane.

Accession ID	Protein Name	Gene Name	Fold Change	Protein Pathways	Subcellular Localization
AIO20286.1	recombinase	SA0577	0.388		Cytoplasmic
AIO20702.1	membrane protein	SACOL1113	0.409		CM*
AIO21531.1	3'-5' exonuclease	cbf1	0.441		Cytoplasmic
AIO20231.1	glycosyl transferase family 1	SACOL0612	0.463		Cytoplasmic
AIO21551.1	thiol peroxidase	SA1680	0.467		Cell-wall
AIO20579.1	oligopeptidase PepB	SA0859	0.477		Cytoplasmic
AIO21461.1	pyridine nucleotide-disulfide oxidoreductase	SACOL1821	0.493		Cytoplasmic
AIO20197.1	ribonuclease III	mrnC SA0489	0.496		Cytoplasmic

AIO21408.1	glycerophosphodiester phosphodiesterase	SACOL1770	0.497	Glycerophospholipid metabolism	Cytoplasmic
AIO21699.1	RNA polymerase sigma factor SigB	sigB	0.509		Cytoplasmic
AIO20740.1	cell division protein ZapA	SA0988	0.509		Cytoplasmic

Table S7: Relative correlation of selected qPCR gene expression data to TMT protein expression data (exclusive and common) in hydrated biofilm and DSB compared with planktonic. *FC denotes fold change.

Accession ID	Protein Name	Gene Name	TMT		RT-qPCR	
			Hydrated biofilm (FC)*	DSB (FC)*	Hydrated biofilm (FC)*	DSB (FC)*
AIO21431.1	UDP-N-acetylmuramate--alanine ligase	<i>MurC</i>		2.174		0.206
AIO20408.1	UDP-N-acetylenolpyruvoylglucosamine reductase	<i>MurB</i>		2.122		0.668
AIO20645.1	glutamyl endopeptidase	<i>SspA</i>	0.149	0.144	0.104	0.083
AIO20163.1	ribose-phosphate pyrophosphokinase	<i>Prs</i>	2.814	2.785	3.94	0.632
AIO20712.1	pyruvate carboxylase	<i>Pyc</i>		0.448		0.837
AIO20749.1	Succinate dehydrogenase	<i>SdhB</i>	0.283	0.406	3.30	1.313

Table S8: Primers used in this study

Gene name	Primer name	Primer sequence (5'-3')	Position in gene	PCR (bp)	size	Ta (°C)
<i>16s rRNA</i>	Staphy_16sF	GGCGAAGGCGRCTTTCTGG	704-720	95bp		55
	Staphy_16sR	CGTTTACGGCGTGGACT	782-798			
<i>MucC</i>	murC F	TAATTGGTGATGGCACAGG	395-506	112		50
	murC R	GTCATAATTGCGTAATCAGG				
<i>MurB</i>	murB F	AGGTGGTAATGCCGACTTT	99-253	155		55
	murB R	TAATTACAATGCCGCGAATA				
<i>SspA</i>	sspA F	CAGCGACACTTGTGAGTTC	53-130	109		55
	sspA R	TCTGCGTTTGTGTGGAT				
<i>Prs</i>	prs F	TCAGGACCGGCTAAAGAAC	784-918	55		55
	prs R	AGCTTGTGCGATTAAACCAG				

<i>Pyc</i>	pyc F	TCGTACAACGGCTATCAAGG			
	pyc R	AATCATTAGCGGGAAACCAG	366-480	60	60
<i>SdhB</i>	sdhB F	GCCACGTATGCCAGAGAAA			
	sdhB R	CGAACTTGCGAGATTGCTT	462-599	60	60
