

Table 6 Genes affected most in expression: 6h planktonic versus biofilm cells

N315 ORF	plankt. vs. biofilm fold change	Name	Product	SD	CV
<u>Secreted proteins:</u>					
SA1637	11,63	<i>ludD</i>	leukotoxin, LukD	0,297	2,548
SA0383	8,13	<i>set7</i>	exotoxin 7	0,366	4,489
SA1007	4,95		Alpha-Hemolysin precursor	0,284	5,726
SA1629	4,67	<i>spIC</i>	serine protease SpIC	0,149	3,196
SA0389	4,55	<i>set13</i>	exotoxin 13	0,194	4,28
SA0357	4,02		hypothetical protein, similar to exotoxin 2	0,26	6,487
SA0387	3,76	<i>set11</i>	exotoxin 11	0,067	1,774
SA1813	3,61		hypothetical protein, similar to leukocidin chain lukM precursor	0,117	3,236
SA0384	3,52	<i>set8</i>	exotoxin 8	0,099	2,81
SA0382	3,39	<i>set6</i>	exotoxin 6	0,228	6,704
<u>Cell-wall associated:</u>					
SA0744	3,86	<i>ssp</i>	extracellular ECM and plasma binding protein	0,229	5,94
SA2455	3,68		capsular polysaccharide biosynthesis, capC	0,261	7,109
<u>Transporter:</u>					
SA0851	6,62		oligopeptide ABC transporter ATP-binding protein homologue	0,125	1,89
SA0852	4,83	<i>appF</i>	oligopeptide transport system ATP-binding protein AppF homologue	0,262	5,413
SA0168	4,81		hypothetical protein, similar to probable permease of ABC transporter	0,253	5,259
SA0853	4,74	<i>oppB</i>	probable oligopeptide transport system permease protein OppB	0,133	2,881
SA0850	4,35		hypothetical protein, similar to oligopeptide ABC transporter oligopeptide-binding protein	0,086	1,986
SA1042	4,35	<i>pyrP</i>	uracil permease	0,068	1,986
SA1992	4,00	<i>lacE</i>	PTS system, lactose-specific IIBC component	0,058	1,451
SA2081	3,61		hypothetical protein, similar to urea transporter	0,165	4,575
SA2492	3,60	<i>vraD</i>	hypothetical protein, similar to ABC transporter	0,141	3,917
SA0303	3,50		hypothetical protein, similar to sodium-coupled permease	0,287	8,199
SA0135	3,34		hypothetical protein, similar to phosphonates transport permease	0,188	5,61
<u>Physiological Proteins:</u>					
SA1865	10,20	<i>leuD</i>	3-isopropylmalate dehydratase small subunit	0,255	2,495
SA2472	8,93		hypothetical protein, similar to ATP phosphoribosyltransferase regulatory subunit	0,323	3,627
SA2186	5,75	<i>narF</i>	uroporphyrin-III C-methyl transferase	0,224	3,899
SA1045	5,99	<i>pyrA</i>	carbamoyl-phosphate synthase small chain	0,267	4,455
SA1047	5,46	<i>pyrF</i>	orotidine-5-phosphate decarboxylase	0,07	1,29
SA1044	5,38	<i>pyrC</i>	dihydroorotase	0,093	1,73
SA1555	5,26	<i>acuA</i>	acetoin dehydrogenase homolog	0,218	4,136
SA1995	5,18	<i>lacC</i>	tagatose-6-phosphate kinase	0,097	1,861
SA1996	5,15	<i>lacB</i>	galactose-6-phosphate isomerase LacB subunit	0,338	6,538
SA2121	4,88	<i>hutI</i>	imidazolonepropionase	0,05	1,019
SA1043	4,88	<i>pyrB</i>	aspartate transcarbamoylase chain A	0,288	5,92
SA1895	4,81	<i>thiM</i>	hydroxyethyl thiazole kinase	0,13	2,699
SA1896	4,81	<i>thiD</i>	phosphomethylpyrimidine kinase	0,179	3,715
SA1048	4,69	<i>pyrE</i>	orotate phosphoribosyltransferase	0,234	4,976
SA0211	4,44		hypothetical protein, similar to NADH-dependent dehydrogenase	0,398	8,966
SA1994	4,41	<i>lacD</i>	tagatose 1,6-diphosphate aldolase	0,312	7,083
SA2213	4,24	<i>bioB</i>	biotin synthase	0,185	4,364
SA0091	4,20	<i>plc</i>	1-phosphatidylinositol phosphodiesterase precursor	0,172	4,076
SA1858	4,15	<i>ilvD</i>	dihydroxy-acid dehydratase	0,307	7,399
SA1046	4,08	<i>pyrAB</i>	carbamoyl-phosphate synthase large chain	0,098	2,389
SA2471	3,86	<i>hisG</i>	ATP phosphoribosyltransferase	0,134	3,461
SA2185	3,85	<i>narG</i>	respiratory nitrate reductase alpha chain	0,269	6,996
SA0224	3,57		hypothetical protein, similar to 3-hydroxyacyl-CoA dehydrogenase	0,126	3,533
SA0176	3,50		hypothetical protein, similar to N-acetylglutamate 5-phosphotransferase	0,212	6,066
SA1204	3,48	<i>trpB</i>	tryptophan synthase beta chain	0,23	6,601
SA1412	3,44	<i>hemN</i>	oxygen-independent coproporphyrinogen oxidase III	0,254	7,391
SA2470	3,42		hypothetical protein, similar to histidinol dehydrogenase	0,145	4,237
SA0304	3,41	<i>nanA</i>	N-acetylneuraminase lyase subunit	0,224	6,568
SA0124	3,37		hypothetical protein, similar to glycosyltransferase TaaA	0,232	6,883
SA0223	3,36		acetyl-CoA acetyltransferase homologue	0,19	5,653
SA2327	3,36		hypothetical protein, similar to pyruvate oxidase	0,169	5,054
<u>Other proteins:</u>					
SA1897	6,33		hypothetical protein, similar to transcriptional activator TenA	0,386	6,104
SA0356	5,13		truncated integrase	0,209	4,074
SA1820	4,78		hypothetical protein, similar to bacteriophage terminase small subunit	0,261	5,438
SA1842	4,46	<i>argB</i>	accessory gene regulator B	0,222	4,981
SA2433	4,42		hypothetical protein, similar to transcription antiterminator BglG family	0,295	6,681
SA1760	4,07		holin homolog	0,209	5,139
SA2123	3,79		hypothetical protein, similar to transcription regulator LysR family	0,068	1,803
SA1810	3,75	<i>int</i>	integrase	0,228	6,064

SA2447	3,75		hypothetical protein, similar to streptococcal hemagglutinin protein	0,248	6,622
SA0235	3,68		hypothetical protein, similar to BglG antiterminator family	0,149	4,05
SA0429	3,46	<i>gltC</i>	transcription activator of glutamate synthase operon	0,312	9,012
SA2465	3,40	<i>hisF</i>	cyclase-like protein hisF	0,152	4,456
<u>Hypothetical proteins:</u>					
SA1755	7,52		hypothetical protein	0,216	2,881
SA0556	5,95		conserved hypothetical protein	0,019	0,312
SA1370	5,85		hypothetical protein	0,206	3,529
SA0093	5,56		hypothetical protein	0,48	8,625
SA0184	5,38		conserved hypothetical protein	0,191	3,553
SA0185	5,29		conserved hypothetical protein	0,438	8,276
SA0301	5,21		conserved hypothetical protein	0,371	7,134
SA1616	5,18		hypothetical protein	0,159	3,071
SA2478	4,74		conserved hypothetical protein	0,247	5,208
SA1619	4,57		hypothetical protein	0,305	6,668
SA1766	4,52		hypothetical protein	0,186	4,103
SA1621	4,24		hypothetical protein	0,215	5,084
SA0358	4,15		conserved hypothetical protein	0,169	4,082
SA2273	3,94		hypothetical protein	0,078	1,997
SA0887	3,92		conserved hypothetical protein	0,075	1,912
SA0139	3,77		hypothetical protein	0,094	2,503
SA0043	3,69		conserved hypothetical protein	0,081	2,184
SA0631	3,68		hypothetical protein	0,19	5,166
SA2445	3,48		hypothetical protein	0,331	9,497
SA1788	3,37		hypothetical protein	0,269	7,99

Table 7 Genes affected most in expression: 8h planktonic versus biofilm cells

N315 ORF	plankt. vs. biofilm fold change	Name	Product	SD	CV
<u>Secreted Proteins:</u>					
SA0383	8,475	<i>set7</i>	exotoxin 7	0,252	2,96
SA0357	7,874		hypothetical protein, similar to exotoxin 2	0,392	4,992
SA1631	7,519	<i>spIA</i>	serine protease SpIA	0,649	8,632
SA1628	6,897	<i>spID</i>	serine protease SpID	0,368	5,351
SA1812	5,848		hypothetical protein, similar to synergohymenotropic toxin precursor - Staphylococcus intermedius	0,37	6,31
SA1638	5,348	<i>lukE</i>	leukotoxin LukE	0,24	4,488
SA0386	5,263	<i>set10</i>	exotoxin 10	0,109	2,062
SA1633	5,181		probable beta-lactamase	0,254	4,921
SA0390	4,975	<i>set14</i>	exotoxin 14	0,208	4,183
SA1011	4,762		hypothetical protein, similar to exotoxin 3	0,177	3,717
SA0387	4,651	<i>set11</i>	exotoxin 11	0,174	3,734
SA1629	4,098	<i>spIC</i>	serine protease SpIC	0,134	3,288
SA1637	4,082	<i>lukD</i>	leukotoxin, LukD	0,247	6,052
SA0382	4,000	<i>set6</i>	exotoxin 6	0,519	13,004
SA0384	3,876	<i>set8</i>	exotoxin 8	0,333	8,592
SA1009	3,717		hypothetical protein, similar to exotoxin 1	0,102	2,733
SA1010	3,534		hypothetical protein, similar to exotoxin 4	0,233	6,577
<u>Cell-wall associated proteins:</u>					
SA0147	10,417	<i>capD</i>	capsular polysaccharide synthesis enzyme Cap5D	0,643	6,195
SA0745	8,772		hypothetical protein, similar to extracellular matrix and plasma binding	0,511	5,819
SA0146	5,650	<i>capC</i>	capsular polysaccharide synthesis enzyme Cap8C	0,395	6,976
SA0150	5,000	<i>capG</i>	capsular polysaccharide synthesis enzyme Cap5G	0,124	2,469
SA0148	4,695	<i>capE</i>	capsular polysaccharide synthesis enzyme Cap8E	0,111	2,366
SA2455	4,587	<i>capC</i>	capsular polysaccharide biosynthesis, capC	0,48	10,467
SA0149	4,484	<i>capF</i>	capsular polysaccharide synthesis enzyme Cap5F	0,244	5,458
SA0152	4,292	<i>capI</i>	capsular polysaccharide synthesis enzyme Cap5I	0,31	7,228
SA0520	4,000	<i>sdrD</i>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	0,056	1,397
SA0157	3,788	<i>capN</i>	capsular polysaccharide synthesis enzyme Cap5N	0,259	6,851
<u>Transporter:</u>					
SA0850	10,417		hypothetical protein, similar to oligopeptide ABC transporter oligopeptide-binding protein	0,275	2,638
SA0137	8,850		hypothetical protein, similar to transport system protein	0,179	2,024
SA0237	8,621		hypothetical protein, similar to PTS, galactitol-specific IIB component	0,139	1,607
SA0206	8,264	<i>msmX</i>	multiple sugar-binding transport ATP-binding protein	0,529	6,402
SA1992	7,353	<i>lacE</i>	PTS system, lactose-specific IIBC component	0,271	3,678
SA0135	6,452		hypothetical protein, similar to phosphonates transport permease	0,43	6,66
SA0238	6,211	<i>gatC</i>	probable PTS galactitol-specific enzyme IIC component	0,273	4,397
SA0136	5,848		hypothetical protein, similar to phosphonates transport permease	0,055	0,936
SA0851	5,714		oligopeptide ABC transporter ATP-binding protein homologue	0,242	4,224
SA0166	5,618		hypothetical protein, similar to nitrate transporter	0,344	6,12
SA0318	5,155		hypothetical protein, similar to transport protein SgaT	0,356	6,893
SA0853	4,425	<i>oppB</i>	probable oligopeptide transport system permease protein OppB	0,132	2,996
SA0214	4,016	<i>uhpT</i>	hexose phosphate transport protein	0,243	6,055
SA1881	3,984	<i>kdpA</i>	probable potassium-transporting ATPase A chain	0,514	12,903
SA2492	3,817	<i>vraD</i>	hypothetical protein, similar to ABC transporter	0,133	3,477
SA0325	3,774	<i>glpT</i>	glycerol-3-phosphate transporter	0,256	6,782
SA0138	3,759		hypothetical protein, similar to alkylphosphonate ABC transporter	0,241	6,409
SA0891	3,717		hypothetical protein, similar to ferrichrome ABC transporter	0,19	5,1
SA2476	3,534		hypothetical protein, similar to cation ABC transporter (ATP-binding protein)	0,248	7,016
SA2149	3,460		hypothetical protein, similar to ABC transporter, ATP-binding protein	0,076	2,204
SA1848	3,436	<i>nrgA</i>	probable ammonium transporter	0,284	8,251
<u>Physiological proteins:</u>					
SA2427	9,901	<i>arcB</i>	ornithine transcarbamoylase	0,444	4,503
SA0304	9,346	<i>nanA</i>	N-acetylneuraminatase lyase subunit	0,445	4,74
SA1555	8,197	<i>acuA</i>	acetoin dehydrogenase homolog	0,432	5,297
SA2188	8,065	<i>nasD</i>	nitrite reductase	0,444	5,491
SA1864	7,576	<i>leuC</i>	3-isopropylmalate dehydratase large subunit	0,586	7,703
SA1858	7,519	<i>ilvD</i>	dihydroxy-acid dehydratase	0,224	2,985
SA2397	7,463		hypothetical protein, similar to pyridoxal-phosphate dependent aminotransferase	0,408	5,491
SA2464	7,407	<i>hisI</i>	histidine biosynthesis bifunctional protein HisIE	0,366	2,571
SA0837	7,353		hypothetical protein, similar to 2-isopropylmalate synthase	0,19	2,571
SA2472	6,993		hypothetical protein, similar to ATP phosphoribosyltransferase regulatory subunit	0,279	3,987
SA2184	6,897	<i>narH</i>	nitrate reductase beta chain narH	0,083	1,205
SA1271	6,757		threonine deaminase IlvA homolog	0,532	7,882
SA0171	6,494	<i>fdh</i>	NAD-dependent formate dehydrogenase	0,309	4,763

SA2469	6,098		hypothetical protein, similar to histidinol-phosphate transaminase	0,258	4,224
SA0124	5,988		hypothetical protein, similar to glycosyltransferase TaaA	0,14	2,345
SA1968	5,882	<i>arg</i>	arginase	0,222	3,777
SA2467	5,618	<i>hisH</i>	amidotransferase hisH	0,143	2,538
SA2468	5,556	<i>hisB</i>	imidazoleglycerol-phosphate dehydratase	0,23	4,15
SA2003	5,464	<i>hysA</i>	hyaluronate lyase precursor	0,128	2,335
SA1757	5,405	<i>(lytA)</i>	truncated amidase	0,223	4,121
SA0305	5,376		hypothetical protein, similar to glucokinase	0,345	6,404
SA0346	5,348		hypothetical protein, similar to cystathionine beta-lyase	0,141	2,636
SAS029	5,291		hypothetical protein, similar to lactococcin 972	0,19	3,593
SA1865	5,291	<i>leuD</i>	3-isopropylmalate dehydratase small subunit	0,267	5,052
SA0211	5,181		hypothetical protein, similar to NADH-dependent dehydrogenase	0,424	8,196
SA1964	5,155	<i>fmtB</i>	FmtB protein	0,12	2,33
SA1860	5,102		hypothetical protein, similar to acetolactate synthase small subunit	0,252	4,943
SA2122	5,000	<i>hutU</i>	urocanate hydratase	0,199	3,979
SA1090	4,525	<i>lytN</i>	LytN protein	0,266	5,879
SA0162	4,444	<i>aldA</i>	aldehyde dehydrogenase homologue	0,222	4,984
SA2164	4,348		hypothetical protein, similar to phage infection protein precursor	0,211	4,855
SA0224	4,329		hypothetical protein, similar to 3-hydroxyacyl-CoA dehydrogenase	0,202	4,668
SA0918	4,292	<i>purC</i>	phosphoribosylaminoimidazolesuccinocarboxamide synthetase homolog	0,17	3,968
SA2463	4,255	<i>lip</i>	triacylglycerol lipase precursor	0,086	2,013
SA1269	4,184		Blt-like protein	0,16	3,814
SA2185	4,115	<i>narG</i>	respiratory nitrate reductase alpha chain	0,231	5,599
SA1204	4,082	<i>trpB</i>	tryptophan synthase beta chain	0,199	6,055
SA1813	4,049		hypothetical protein, similar to leukocidin chain lukM precursor	0,158	3,899
SA2420	3,953	<i>phoB</i>	alkaline phosphatase III precursor	0,13	3,3
SA2121	3,745	<i>hutL</i>	imidazolonepropionase	0,223	5,953
SA1994	3,676	<i>lacD</i>	tagatose 1,6-diphosphate aldolase	0,01	0,272
SA0186	3,650		hypothetical protein, similar to sucrose phosphotransferase enzyme II	0,272	7,438
SA2176	3,623	<i>nark</i>	nitrite extrusion protein	0,185	5,117
SA0303	3,610		hypothetical protein, similar to sodium-coupled permease	0,195	5,412
SA2189	3,610		hypothetical protein, similar to NirR	0,085	2,342
SA0177	3,509	<i>argJ</i>	arginine biosynthesis bifunctional protein homologue	0,224	6,391
SA1995	3,448	<i>lacC</i>	tagatose-6-phosphate kinase	0,192	5,564
SA1202	3,425	<i>trpC</i>	indole-3-glycerol phosphate synthase	0,08	2,338
SA0562	3,413	<i>adh1</i>	alcohol dehydrogenase I	0,183	5,352
SA0091	3,378	<i>plc</i>	1-phosphatidylinositol phosphodiesterase precursor	0,09	2,667
SA1585	3,367		proline dehydrogenase homologue	0,295	8,785
SA0119	3,344		hypothetical protein, similar to diaminopimelate decarboxylase	0,222	6,614
<u>Other proteins:</u>					
SA1820	12,195		hypothetical protein, similar to bacteriophage terminase small subunit	0,159	1,299
SA0187	10,526		hypothetical protein, similar to transcription regulator	0,811	7,701
SA0705	10,417		hypothetical protein, similar to comF operon protein 1	0,428	4,109
SA0836	6,803		hypothetical protein, similar to transcription regulator LysR family	0,364	5,36
SA0379	6,369		probable transposase	0,376	5,893
SA0235	5,435		hypothetical protein, similar to BglG antiterminator family	0,175	3,218
SA1092	5,076		hypothetical protein, similar to DNA processing Smf protein	0,244	4,823
SA0321	4,149		hypothetical protein, similar to transcription antiterminator BglG family	0,331	7,991
SA2006	3,861		hypothetical protein, similar to MHC class II analog	0,12	3,095
SA1883	3,521	<i>kdpE</i>	KDP operon transcriptional regulatory protein KdpE	0,141	4,009
SA0858	3,344		hypothetical protein, similar to transcription factor	0,034	1,011
<u>Hypothetical proteins:</u>					
SA0396	17,857		hypothetical protein	0,532	2,987
SA0043	11,364		conserved hypothetical protein	0,377	3,333
SA1765	10,870		hypothetical protein	0,406	3,744
SA2256	10,204		conserved hypothetical protein	0,535	5,242
SA0575	9,709		hypothetical protein	0,212	2,184
SA0400	9,709		hypothetical protein	0,532	5,456
SA0301	7,937		conserved hypothetical protein	0,152	1,91
SA0185	7,634		conserved hypothetical protein	0,258	3,384
SA2273	6,993		hypothetical protein	0,504	7,209
SA2269	6,667		hypothetical protein	0,46	6,896
SA0394	5,848		hypothetical protein	0,349	5,971
SA0840	5,464		conserved hypothetical protein	0,053	0,969
SA0976	5,000		conserved hypothetical protein	0,215	4,3
SA2443	4,878		hypothetical protein	0,262	5,362
SA2370	4,831		conserved hypothetical protein	0,171	3,542
SA2445	4,608		hypothetical protein	0,206	4,475
SA0333	4,545		conserved hypothetical protein	0,177	3,901
SA1014	4,444		conserved hypothetical protein	0,189	4,256
SA2374	4,386		conserved hypothetical protein	0,371	8,466
SA1755	4,237		hypothetical protein	0,204	4,798
SA0888	4,219		conserved hypothetical protein	0,274	6,498
SA0887	4,184		conserved hypothetical protein	0,185	4,429
SA0139	4,115		hypothetical protein	0,039	0,938

SA2283	4,016	conserved hypothetical protein	0,221	5,517
SA2313	3,861	conserved hypothetical protein	0,292	7,553
SA1621	3,745	hypothetical protein	0,03	0,791
SA2380	3,690	conserved hypothetical protein	0,224	6,089
SA0631	3,623	hypothetical protein	0,143	3,949
SA0093	3,584	hypothetical protein	0,15	4,19
SA2475	3,571	conserved hypothetical protein	0,225	6,284
SA1756	3,571	truncated amidase	0,188	5,273
SA1598	3,559	hypothetical protein	0,276	7,734
SA2274	3,484	hypothetical protein	0,185	5,316
SA2362	3,436	conserved hypothetical protein	0,076	2,202
SA1706	3,425	hypothetical protein	0,253	7,373
SA1764	3,401	hypothetical protein	0,251	7,384
SA0710	3,367	conserved hypothetical protein	0,275	8,172
SA1415	3,311	conserved hypothetical protein	0,16	4,817

Table 8 Genes affected most in expression: 16h planktonic versus biofilm cells

N315 ORF	plankt. vs. biofilm fold change	Name	Product	SD	VC
<u>Secreted proteins:</u>					
SA0383	5,263	<i>set7</i>	exotoxin 7	0,332	6,308
SA0390	4,902	<i>set14</i>	exotoxin 14	0,237	4,829
SA1725	3,663		Staphopain, Cysteine Proteinase	0,38	10
SA1629	3,484	<i>spIC</i>	serine protease SpIC	0,424	12,162
<u>Transporter:</u>					
SA0891	3,846		hypothetical protein, similar to ferrichrome ABC transporter	0,117	3,044
SA0325	3,802	<i>glpT</i>	glycerol-3-phosphate transporter	0,109	2,878
SA0198	3,378	<i>oppF</i>	oligopeptide transport ATP-binding protein	0,202	5,999
<u>Physiological proteins:</u>					
SA2003	4,975	<i>hysA</i>	hyaluronate lyase precursor	0,125	2,499
SA1865	3,937	<i>leuD</i>	3-isopropylmalate dehydratase small subunit	0,259	6,587
SA2470	3,846		hypothetical protein, similar to histidinol dehydrogenase	0,441	11,476
SA2184	3,636	<i>narH</i>	nitrate reductase beta chain	0,144	3,969
SA1166	3,521	<i>thrB</i>	homoserine kinase homolog	0,184	5,224
SA2468	3,39	<i>hisB</i>	imidazoleglycerol-phosphate dehydratase	0,165	4,864
<u>Other proteins:</u>					
SA1820	4,184		hypothetical protein, similar to bacteriophage terminase small subunit	0,148	3,538
SA1371	3,534		hypothetical protein, similar to competence protein	0,171	4,848
SA2379	3,311		hypothetical protein, similar to transcriptional regulator tetR-family	0,248	7,507
<u>Hypothetical proteins:</u>					
SA0888	5,952		conserved hypothetical protein	0,101	1,696
SA1415	5,65		conserved hypothetical protein	0,405	7,167
SA2281	4,167		hypothetical protein	0,147	3,532
SA0535	4,149		hypothetical protein	0,214	5,165
SA1823	4		hypothetical protein	0,292	7,307
SA2283	3,952		conserved hypothetical protein	0,317	8,037
SA0139	3,846		hypothetical protein	0,073	1,901
SA0446	3,831		conserved hypothetical protein	0,271	7,059
SA0402	3,817		hypothetical protein	0,225	5,882
SA0976	3,802		conserved hypothetical protein	0,221	5,864
SA2225	3,636		conserved hypothetical protein	0,025	0,693
SA0403	3,534		hypothetical protein	0,091	2,578
SA0919	3,509		conserved hypothetical protein	0,136	3,874
SA0323	3,484		conserved hypothetical protein	0,19	5,461

Table 9 Genes affected most in expression: 24h planktonic versus biofilm cells

N315 ORF	plankt. vs. biofilm fold change	Name	Product	SD	CV
SA2303	2,865		<u>Cell-wall associated:</u> hypothetical protein, similar to membrane spanning protein	0,066	2,303
SA0166	6,024		<u>Transporter:</u> hypothetical protein, similar to nitrate transporter	0,274	4,556
SA0850	3,058		hypothetical protein, similar to oligopeptide ABC transporter oligopeptide-binding protein	0,234	7,636
SA0325	2,915	<i>glpT</i>	glycerol-3-phosphate transporter	0,116	3,992
SA2492	2,890	<i>vraD</i>	hypothetical protein, similar to ABC transporter	0,365	12,655
SA1226	3,300	<i>asd</i>	<u>Physiological proteins:</u> aspartate semialdehyde dehydrogenase	0,019	0,565
SA1145	3,300		hypothetical protein, similar to host factor-1	0,395	11,96
SA1228	3,195	<i>dapB</i>	dihydrodipicolinate reductase	0,105	3,297
SA2214	3,145	<i>bioA</i>	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	0,342	10,879
SA1554	3,096	<i>acsA</i>	acetyl-CoA synthetase	0,118	3,81
SA2288	3,040	<i>gtaB</i>	UTP-glucose-1-phosphate uridyltransferase	0,314	10,322
SA1165	2,967	<i>thrC</i>	threonine synthase	0,269	9,071
SA0916	2,933		hypothetical protein, similar to phosphoribosylaminoimidazole carboxylase PurE	0,231	7,866
SA2468	2,890	<i>hisB</i>	imidazoleglycerol-phosphate dehydratase	0,43	14,855
SA1862	2,857	<i>leuA</i>	2-isopropylmalate synthase	0,287	10,052
SA2478	5,000		<u>Hypothetical proteins:</u> conserved hypothetical protein	0,607	12,127
SA0301	4,566		conserved hypothetical protein	0,132	2,892
SA1755	3,484		hypothetical protein	0,335	9,613
SA0839	3,175		hypothetical protein	0,27	8,503
SA0630	3,040		conserved hypothetical protein	0,252	8,293

Table 10 Genes affected most in expression: 48h planktonic versus biofilm cells

N315 ORF	plankt. vs. biofilm fold change	Name	Product	SD	CV
SA0216	3,322		<u>Cell-wall associated:</u> hypothetical protein, similar to two-component sensor histidine kinase	0,239	7,194
SA2114	3,356	<i>glvC</i>	<u>Transporter:</u> PTS system, arbutin-like IIBC component	0,175	5,229
SA1166	5	<i>thrB</i>	<u>Physiological proteins:</u> homoserine kinase homolog	0,276	X
SA1963	4,4052	<i>mtlD</i>	mannitol-1-phosphate 5-dehydrogenase	0,33	X
SA1994	3,745	<i>lacD</i>	tagatose 1,6-diphosphate aldolase	0,157	4,175
SA0916	3,663		hypothetical protein, similar to phosphoribosylaminoimidazole carboxylase PurE	0,214	5,834
SA1865	3,509	<i>leuD</i>	3-isopropylmalate dehydratase small subunit	0,25	7,121
SA2435	3,425	<i>pmi</i>	mannose-6-phosphate isomerase	0,299	8,725
SA0373	3,311	<i>xprT</i>	xanthine phosphoribosyltransferase	0,191	5,763
SA1810	3,861	<i>int</i>	<u>Other proteins:</u> integrase	0,241	6,228
SA0104	3,247		hypothetical protein, similar to transcription regulator GntR family	0,367	11,301
SA0770	3,922		<u>Hypothetical proteins:</u> conserved hypothetical protein	0,37	9,428
SA0203	3,907		hypothetical protein	0,023	0,602
SA0095	3,344		hypothetical protein	0,121	3,616