

Additional data file 7. List of genes differentially expressed in pharyngeal cell-adherent pneumococci vs. culture medium control pneumococci. Numbers in bold type represent genes that met the criteria of being both statistically differentially expressed and having a ratio of ≥ 2 or ≤ 0.5 in both strains. This gene list was supplemented with genes that did not meet the fold threshold value but appeared to be co-regulated as part of an operon. NA indicates data points that were removed after analysis with Spotfinder. X indicates genes that did not meet the criteria established for microarray analysis in MeV (see methods).

Locus	Common Name	Gene Symbol	Fold increase or decrease		Function
			TIGR4 adherent/ control	G54 adherent/ control	
SP_0014	Transcriptional regulator ComX1	<i>comX1</i>	X		2.9 Cellular processes/pathogenesis/Regulatory function
SP_0018	Hypothetical protein		1.7		3.3 Hypothetical proteins
SP_0019	Adenylosuccinate synthetase	<i>purA</i>	1.0		1.7 Purines, pyrimidines, nucleosides, and nucleotides
SP_0020	Cytidine-deoxycytidylate deaminase family protein		1.3		2.5 Unknown protein
SP_0024	Conserved hypothetical protein		2.6		0.9 Hypothetical proteins
SP_0025	Hypothetical protein		2.7		1.1 Hypothetical proteins
SP_0026	Hypothetical protein		2.2		X Hypothetical proteins
SP_0042	Transport atp-binding protein ComA	<i>comA</i>	X		2.4 Cellular processes/pathogenesis/Transport and binding proteins
SP_0043	Transport protein	<i>comB</i>	X		2.6 Cellular processes/pathogenesis/Transport and binding proteins
SP_0044	Phosphoribosylaminoimidazole-succinocarboxamide synthase	<i>purC</i>	0.2		0.6 Cellular processes/pathogenesis
SP_0045	Phosphoribosylformylglycinamide synthase II	<i>purL</i>	0.2		0.4 Cellular processes/pathogenesis/Purines, pyrimidines, nucleosides, and nucleotides
SP_0046	Amidophosphoribosyltransferase		0.4		0.4 Purines, pyrimidines, nucleosides, and nucleotides
SP_0047	Phosphoribosylformylglycinamide cyclo-ligase		0.4		0.5 Purines, pyrimidines, nucleosides, and nucleotides
SP_0048	Phosphoribosylglycinamide formyltransferase		0.5		0.4 Purines, pyrimidines, nucleosides, and nucleotides
SP_0049	Vanz protein, putative		0.6		0.5 Unknown protein
SP_0050	Phosphoribosylaminoimidazolecarboxamide formyltransferase-imp cyclohydrolase	<i>purH</i>	0.5		0.4 Purines, pyrimidines, nucleosides, and nucleotides
SP_0051	Phosphoribosylamine-glycine ligase		0.3		0.4 Purines, pyrimidines, nucleosides, and nucleotides
SP_0052	Hypothetical protein		0.3		0.4 Hypothetical proteins
SP_0053	Phosphoribosylaminoimidazole carboxylase, catalytic subunit	<i>purE</i>	0.4		0.5 Cellular processes/pathogenesis/Purines, pyrimidines, nucleosides, and nucleotides
SP_0054	Phosphoribosylaminoimidazole carboxylase, ATPase subunit		0.4		0.4 Cellular processes/pathogenesis/Purines, pyrimidines, nucleosides, and nucleotides
SP_0071	Zinc metalloprotease ZmpC	<i>zmpC</i>	0.6		0.4 Cellular processes/pathogenesis/Protein fate
SP_0083	DNA-binding response regulator		0.5		1.0 Signal transduction
SP_0084	Sensor histidine kinase		0.4		0.8 Signal transduction
SP_0099	Hypothetical protein		2.2		1.2 Hypothetical proteins
SP_0100	Conserved hypothetical protein		2.2		1.4 Hypothetical proteins
SP_0101	Putative transporter		1.4		1.9 Transport and binding proteins
SP_0103	Putative capsular polysaccharide biosynthesis protein		1.6		2.4 Cell envelope
SP_0107	LysM domain protein		1.4		2.7 Cell envelope
SP_0110	Bacteriocin-associated integral membrane protein		0.8		0.6 Cellular processes/pathogenesis
SP_0111	Putative amino acid ABC transporter, ATP-binding protein		1.1		0.6 Transport and binding proteins
SP_0115	Hypothetical protein		0.8		0.7 Hypothetical proteins
SP_0124	Hypothetical protein		X		3.3 Hypothetical proteins
SP_0126	Hypothetical protein		X		1.9 Hypothetical proteins
SP_0139	Conserved domain protein		2.3		0.4 Hypothetical proteins
SP_0140	Udp-glucose 6-dehydrogenase, authentic frameshift	<i>ugd</i>	X		0.4 Cell envelope
SP_0142	Hypothetical protein		1.3		0.7 Hypothetical proteins
SP_0143	Conserved domain protein		1.3		0.6 Hypothetical proteins
SP_0144	Hypothetical protein		1.8		0.6 Hypothetical proteins
SP_0145	Conserved hypothetical protein		1.6		0.7 Hypothetical proteins
SP_0146	Conserved hypothetical protein		1.3		0.7 Hypothetical proteins
SP_0147	Hypothetical protein		1.4		0.6 Hypothetical proteins
SP_0148	ABC transporter, substrate-binding protein		0.4		0.7 Transport and binding proteins
SP_0149	Lipoprotein		X		0.6 Cell envelope
SP_0158	Nrdi family protein		1.8		1.5 Unknown protein
SP_0159	Conserved hypothetical protein		0.7		0.3 Hypothetical proteins
SP_0169	Lactose phosphotransferase system repressor, degenerate		2.1		NA Disrupted reading frame
SP_0170	Hypothetical protein		2.1		NA Hypothetical proteins
SP_0181	Conserved hypothetical protein		2.3		1.3 Hypothetical proteins
SP_0267	N5,n10-methylenetetrahydromethanopterin reductase homolog.		0.3		X Unknown protein
SP_0282	PTS system, mannose-specific ID component	<i>manM</i>	1.0		0.5 Transport and binding proteins/Signal transduction
SP_0283	PTS system, mannose-specific IIC component		0.8		0.5 Transport and binding proteins/Signal transduction
SP_0284	PTS system, mannose-specific IIB components	<i>manL</i>	0.8		0.3 Transport and binding proteins/Signal transduction
SP_0285	Alcohol dehydrogenase, propanol-preferring		0.4		0.3 Energy metabolism
SP_0287	Xanthine-uracil permease family protein		0.2		0.4 Transport and binding proteins
SP_0288	Conserved hypothetical protein		0.4		0.4 Hypothetical proteins
SP_0289	Dihydropterate synthase		0.6		0.6 Biosynthesis of cofactors, prosthetic groups, and carriers/Cellular processes/pathogenesis/Energy metabolism
SP_0290	Dihydrofolate synthetase.		0.7		0.5 Biosynthesis of cofactors, prosthetic groups, and carriers
SP_0291	GTP cyclohydrolase I		0.7		0.6 Biosynthesis of cofactors, prosthetic groups, and carriers
SP_0292	Bifunctional folate synthesis protein		0.6		0.5 Biosynthesis of cofactors, prosthetic groups, and carriers
SP_0366	Oligopeptide-binding protein alia precursor (exported protein 1)		1.0		0.3 Transport and binding proteins
SP_0371	Conserved hypothetical protein		2.0		X Hypothetical proteins
SP_0375	6-phosphogluconate dehydrogenase, decarboxylating		0.5		0.6 Energy metabolism
SP_0409	Conserved hypothetical protein		0.6		0.4 Hypothetical proteins
SP_0415	Enoyl-coa hydratase	<i>phaB</i>	1.5		0.4 Fatty acid and phospholipid metabolism
SP_0416	Transcriptional regulator, MarR family	<i>marR</i>	1.7		X Regulatory function
SP_0417	3-oxoacyl-(acyl-carrier-protein) synthase III		1.6		1.0 Fatty acid and phospholipid metabolism
SP_0418	Acyl carrier protein		1.8		0.9 Fatty acid and phospholipid metabolism
SP_0419	Enoyl-(acyl-carrier-protein) reductase	<i>fabK</i>	1.4		0.4 Fatty acid and phospholipid metabolism
SP_0420	Malonyl coa-acyl carrier protein transacylase		1.9		0.6 Fatty acid and phospholipid metabolism
SP_0421	3-oxoacyl-(acyl-carrier-protein) reductase		2.7		0.7 Fatty acid and phospholipid metabolism
SP_0422	3-oxoacyl-(acyl-carrier-protein) synthase II	<i>fabF</i>	2.4		0.7 Fatty acid and phospholipid metabolism
SP_0423	Acetyl-CoA carboxylase, biotin carboxyl carrier protein		3.6		0.9 Fatty acid and phospholipid metabolism
SP_0424	Similar to hydroxymyristoyl-(acyl carrier protein) dehydratase.		3.6		1.0 Fatty acid and phospholipid metabolism
SP_0425	Acetyl-coa carboxylase, biotin carboxylase		4.2		1.1 Fatty acid and phospholipid metabolism
SP_0426	Acetyl-coa carboxylase, carboxyl transferase subunit beta	<i>accD</i>	5.5		1.4 Fatty acid and phospholipid metabolism
SP_0427	Acetyl-coa carboxylase, carboxyl transferase subunit alpha	<i>accA</i>	2.5		1.6 Fatty acid and phospholipid metabolism
SP_0429	Hypothetical protein		X		2.8 Hypothetical proteins
SP_0430	Hypothetical protein		X		4.1 Hypothetical proteins
SP_0445	Acetolactate synthase, large subunit, biosynthetic type	<i>ilvB</i>	0.8		0.4 Amino acid biosynthesis
SP_0446	Acetolactate synthase, small subunit	<i>ilvN</i>	0.6		0.2 Amino acid biosynthesis
SP_0447	Ketol-acid reductoisomerase	<i>ilvC</i>	0.7		0.2 Amino acid biosynthesis
SP_0448	Hypothetical protein		0.8		0.2 Hypothetical proteins
SP_0449	Hypothetical protein		0.8		0.2 Hypothetical proteins
SP_0450	Threonine dehydratase	<i>ilvA</i>	1.0		0.4 Amino acid biosynthesis
SP_0461	Transcriptional regulator, putative		2.1		NA Cellular processes/pathogenesis/Regulatory function
SP_0462	Cell wall surface anchor family protein		2.6		NA Cell envelope/Cellular processes/pathogenesis
SP_0463	Cell wall surface anchor family protein		1.9		NA Cell envelope/Cellular processes/pathogenesis
SP_0464	Cell wall surface anchor family protein		2.1		NA Cell envelope/Cellular processes/pathogenesis
SP_0466	Sortase, putative		2.0		NA Cell envelope/Cellular processes/pathogenesis/Protein fate
SP_0467	Sortase, putative		2.3		NA Cell envelope/Cellular processes/pathogenesis/Protein fate
SP_0468	Sortase, putative		2.2		NA Cell envelope/Cellular processes/pathogenesis/Protein fate
SP_0494	Ctp synthetase.		1.2		2.2 Purines, pyrimidines, nucleosides, and nucleotides
SP_0496	Na/Pi cotransporter II-related protein		1.3		1.7 Unknown protein

Locus	Common Name	Gene Symbol	Fold increase or decrease		Function
			TIGR4 adherent/ control	G54 adherent/ control	
SP_0528	Peptide pheromone BlpC	<i>blpC</i>	X	X	0.5 Cellular processes/pathogenesis/Transcription
SP_0529	Transport protein BlpB	<i>blpB</i>	X	X	0.4 Cellular processes/pathogenesis/Transport and binding proteins
SP_0530	Transport ATP-binding protein ComA	<i>comA</i>	X	X	0.4 Disrupted reading frame
SP_0535	Hypothetical protein		X	X	0.8 Hypothetical proteins
SP_0539	Bacteriocin BlpM	<i>blpM</i>	X	X	0.5 Cellular processes/pathogenesis
SP_0540	BlpN protein	<i>blpN</i>	X	X	0.5 Cellular processes/pathogenesis
SP_0541	Bacteriocin BlpO	<i>blpO</i>	1.1	X	0.6 Cellular processes/pathogenesis
SP_0543	Hypothetical protein		X	X	0.6 Hypothetical proteins
SP_0544	Immunity protein BlpX	<i>blpX</i>	X	X	0.6 Cellular processes/pathogenesis
SP_0545	Immunity protein BlpY	<i>blpY</i>	X	X	0.7 Cellular processes/pathogenesis
SP_0607	Amino acid abc transporter, permease protein		X	X	2.5 Transport and binding proteins
SP_0608	ABC transporter membrane-spanning permease	<i>glnP</i>	1.4	X	1.7 Transport and binding proteins
SP_0609	Amino acid ABC transporter, amino acid-binding protein		X	X	2.0 Cellular processes/pathogenesis/Transport and binding proteins
SP_0610	Amino acid ABC transporter, ATP-binding protein		1.3	X	1.8 Transport and binding proteins
SP_0617	Conserved domain protein		1.5	X	3.6 Hypothetical proteins
SP_0626	Branched-chain amino acid transport system II carrier protein	<i>bmQ</i>	1.0	X	2.1 Transport and binding proteins
SP_0685	Hypothetical protein		X	X	0.5 Hypothetical proteins
SP_0686	Bacteriocin-associated integral membrane protein		X	X	0.4 Cellular processes/pathogenesis
SP_0696	Hypothetical protein		2.1	X	NA Hypothetical proteins
SP_0697	Abc transporter, atp-binding protein, authentic point mutation		1.8	X	NA Transport and binding proteins
SP_0701	Orotidine 5'-phosphate decarboxylase		1.0	X	2.2 Purines, pyrimidines, nucleosides, and nucleotides
SP_0702	Orotate phosphoribosyltransferase PyrE		X	X	2.0 Purines, pyrimidines, nucleosides, and nucleotides
SP_0726	Phosphomethylpyrimidine kinase		0.3	X	1.1 Biosynthesis of cofactors, prosthetic groups, and carriers
SP_0730	Pyruvate oxidase		0.3	X	0.6 Cellular processes/pathogenesis/Energy metabolism
SP_0737	Sodium-dependent transporter		2.4	X	X Cellular processes/pathogenesis/Transport and binding proteins
SP_0738	Conserved domain protein		2.0	X	X Hypothetical proteins
SP_0753	Branched-chain amino acid ABC transporter, ATP-binding protein.		1.3	X	0.5 Transport and binding proteins
SP_0766	Manganese co-factored superoxide dismutase.		0.3	X	0.5 Cellular processes/pathogenesis
SP_0784	Glutathione reductase		0.1	X	0.4 Biosynthesis of cofactors, prosthetic groups, and carriers/Cellular pr
SP_0786	ABC transporter ATP-binding protein - unknown substrate		0.8	X	2.9 Transport and binding proteins
SP_0798	Dna-binding response regulator ciar	<i>ciaR</i>	1.2	X	2.9 Regulatory function/Signal transduction
SP_0799	Sensor histidine kinase CiaH	<i>ciaH</i>	1.3	X	3.1 Regulatory function/Signal transduction
SP_0820	ATP-dependent Clp protease, ATP-binding subunit ClpE	<i>clpE</i>	0.4	X	0.9 Cellular processes/pathogenesis/Protein fate
SP_0845	Lipoprotein		0.5	X	0.4 Cell envelope
SP_0856	Branched-chain amino acid aminotransferase	<i>ilvE</i>	1.3	X	0.5 Amino acid biosynthesis
SP_0857	Oligopeptide-binding protein, internal deletion, authentic point mutation		1.3	X	0.5 Disrupted reading frame
SP_0858	Membrane protein		1.3	X	0.5 Cell envelope
SP_0860	Pyroldone-carboxylate peptidase		1.4	X	0.5 Protein fate
SP_0867	ABC transporter, ATP-binding protein		0.3	X	0.7 Transport and binding proteins
SP_0868	Conserved hypothetical protein		0.3	X	0.5 Hypothetical proteins
SP_0869	YurW protein		0.3	X	0.5 Unknown protein
SP_0870	NiU family protein		0.3	X	0.5 Unknown protein
SP_0879	Hypothetical protein		2.0	X	3.9 Hypothetical proteins
SP_0999	Cytochrome c-type biogenesis protein CcdA	<i>ccdA</i>	0.3	X	0.6 Energy metabolism
SP_1000	Thioredoxin family protein		0.2	X	0.4 Energy metabolism
SP_1003	Conserved hypothetical protein	<i>phtD</i>	0.8	X	3.9 Hypothetical proteins
SP_1004	Hypothetical protein.		X	X	2.0 Hypothetical proteins
SP_1014	Dihydrodipicolinate synthase	<i>dapA</i>	1.0	X	0.4 Amino acid biosynthesis
SP_1027	Conserved hypothetical protein		1.7	X	6.0 Hypothetical proteins
SP_1045	Conserved hypothetical protein		0.4	X	0.9 Hypothetical proteins
SP_1128	Phosphopyruvate hydratase	<i>eno</i>	0.4	X	0.8 Energy metabolism
SP_1154	Immunoglobulin A1 peptase		0.5	X	NA Cellular processes/pathogenesis/Protein fate
SP_1174	Conserved domain protein		X	X	3.3 Hypothetical proteins
SP_1175	Conserved domain protein		1.1	X	2.9 Hypothetical proteins
SP_1226	Histidine kinase		0.5	X	0.9 Signal transduction
SP_1227	DNA-binding response regulator		0.5	X	0.9 Signal transduction
SP_1228	YfhQ protein		0.3	X	0.9 DNA metabolism
SP_1229	Formate-tetrahydrofolate ligase		0.3	X	0.9 Central intermediary metabolism
SP_1230	Conserved hypothetical protein		0.5	X	1.2 Hypothetical proteins
SP_1231	Flavoprotein		0.5	X	1.3 Unknown protein
SP_1241	Amino acid ABC transporter, amino acid-binding protein/permease protein		1.6	X	2.7 Transport and binding proteins
SP_1242	Amino acid ABC transporter, ATP-binding protein		0.5	X	2.7 Transport and binding proteins
SP_1252	Hypothetical protein		X	X	1.5 Hypothetical proteins
SP_1253	Hypothetical protein		X	X	1.9 Hypothetical proteins
SP_1254	Hypothetical protein		X	X	1.9 Hypothetical proteins
SP_1255	Putative 3-isopropylmalate dehydratase, small subunit		X	X	2.1 Amino acid biosynthesis
SP_1256	Conserved hypothetical protein		X	X	1.9 Hypothetical proteins
SP_1257	3-isopropylmalate dehydrogenase, authentic point mutation	<i>leuB</i>	X	X	1.4 Amino acid biosynthesis
SP_1258	Putative 2-isopropylmalate synthase		X	X	1.9 Amino acid biosynthesis
SP_1259	Conserved hypothetical protein		X	X	1.7 Hypothetical proteins
SP_1260	Copper homeostasis protein, CutC	<i>cutC</i>	1.2	X	1.8 Transport and binding proteins
SP_1261	Conserved hypothetical protein		1.5	X	2.3 Hypothetical proteins
SP_1266	DNA processing protein DprA, putative		X	X	3.6 Cellular processes/pathogenesis
SP_1267	LicC protein	<i>licC</i>	4.0	X	3.4 Cell envelope
SP_1268	LicB	<i>licB</i>	4.0	X	3.2 Cell envelope
SP_1269	Choline kinase.		3.1	X	3.6 Cell envelope
SP_1270	Alcohol dehydrogenase, zinc-containing		3.1	X	3.6 Cell envelope/Energy metabolism
SP_1271	Putative 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase		2.1	X	2.9 Biosynthesis of cofactors, prosthetic groups, and carriers
SP_1272	Repeating unit transporter.		1.6	X	1.9 Cell envelope
SP_1273	LicD1	<i>licD1</i>	1.3	X	1.7 Cell envelope
SP_1274	LicD2protein	<i>licD2</i>	1.4	X	2.0 Cell envelope
SP_1275	Carbamoyl-phosphate synthase, large subunit	<i>carB</i>	0.5	X	1.4 Purines, pyrimidines, nucleosides, and nucleotides
SP_1276	Carbamoyl-phosphate synthase, small subunit		0.6	X	1.1 Purines, pyrimidines, nucleosides, and nucleotides
SP_1277	Aspartate carbamoyltransferase		0.5	X	1.1 Purines, pyrimidines, nucleosides, and nucleotides
SP_1294	CrcB protein	<i>crcB</i>	2.0	X	1.1 Unknown protein
SP_1295	CrcB protein	<i>crcB</i>	1.8	X	1.1 Unknown protein
SP_1296	Putative chorismate mutase		1.9	X	1.2 Amino acid biosynthesis
SP_1357	ABC transporter, permease/ATP-binding protein		0.9	X	0.4 Transport and binding proteins
SP_1358	ABC transporter, ATP-binding protein.		0.7	X	0.3 Transport and binding proteins
SP_1359	Peptide methionine sulfoxide reductase		0.7	X	0.5 Cell envelope/Cellular processes/pathogenesis/Protein fate
SP_1360	Homoserine kinase		0.5	X	0.5 Amino acid biosynthesis
SP_1361	Homoserine dehydrogenase		0.6	X	0.4 Amino acid biosynthesis
SP_1429	Peptidase, U32 family		2.1	X	2.5 Protein fate
SP_1460	Probable amino-acid ATP transporter ATP-binding protein YckI.		0.6	X	0.6 Transport and binding proteins
SP_1461	Amino acid ABC transporter, permease protein		0.6	X	0.6 Transport and binding proteins
SP_1463	Methylated-dna-protein-cysteine s- methyltransferase		0.6	X	0.6 DNA metabolism
SP_1464	Acetyltransferase, GNAT family		0.5	X	0.5 Unknown protein

Locus	Common Name	Gene Symbol	Fold increase or decrease		Function
			TIGR4 adherent/ control	G54 adherent/ control	
SP_1465	Hypothetical protein		0.7	0.3	Hypothetical proteins
SP_1499	Bacteriocin transport accessory protein		0.2	0.5	Cellular processes/pathogenesis/Transport and binding proteins
SP_1546	Hypothetical protein		0.1	0.4	Hypothetical proteins
SP_1550	Glutathione S-transferase family protein		1.1	0.3	Central intermediary metabolism
SP_1551	P-type ATPase - calcium transporter	<i>pacL</i>	0.9	0.3	Transport and binding proteins
SP_1572	Surface located protein.		1.1	2.2	Transport and binding proteins
SP_1586	Autoaggregation-mediating protein		0.4	0.4	Transcription
SP_1587	Oxalate-formate antiporter (OxIT-2).		0.2	0.2	Transport and binding proteins
SP_1588	Oxidoreductase, pyridine nucleotide-disulfide, class I		0.1	0.2	Unknown protein
SP_1596	Is3-spn1, hypothetical protein, interruption		1.0	0.5	Disrupted reading frame
SP_1600	Putative membrane protein		2.0	2.0	Hypothetical proteins
SP_1601	Conserved hypothetical protein		2.0	2.0	Hypothetical proteins
SP_1602	Required for expression of the phosphonate utilization phenotype in <i>E. coli</i>	<i>phnA</i>	2.5	2.1	Transport and binding proteins
SP_1648	Manganese ABC transporter, ATP-binding protein	<i>psaB</i>	2.8	2.8	Transport and binding proteins
SP_1649	Manganese ABC transporter, permease protein, putative, authentic frameshift	<i>psaC</i>	2.4	2.8	Transport and binding proteins
SP_1650	Manganese abc transporter, manganese-binding adhesion liprotein		2.0	2.5	Cellular processes/pathogenesis/Transport and binding proteins
SP_1651	Thiol peroxidase		0.3	0.3	Cellular processes/pathogenesis
SP_1653	ABC transporter, ATP-binding protein.		0.9	0.5	Transport and binding proteins
SP_1654	Conserved hypothetical protein		X	0.3	Hypothetical proteins
SP_1695	Xylan esterase 1		X	0.3	Energy metabolism
SP_1696	Hypothetical protein		1.1	2.5	Hypothetical proteins
SP_1708	Hypothetical protein		2.2	0.8	Hypothetical proteins
SP_1714	transcriptional regulator, GntR family		1.4	2.0	Regulatory function
SP_1715	ABC transporter, ATP-binding protein		1.1	2.2	Transport and binding proteins
SP_1716	Conserved hypothetical protein		X	2.7	Hypothetical proteins
SP_1717	ABC transporter, ATP-binding protein		X	3.0	Transport and binding proteins
SP_1754	Conserved hypothetical protein		1.8	1.5	Hypothetical proteins
SP_1758	Glycosyl transferase, group 1		2.2	NA	Cell envelope
SP_1761	Hypothetical protein		1.9	NA	Hypothetical proteins
SP_1762	Hypothetical protein		2.1	NA	Hypothetical proteins
SP_1770	Glycosyl transferase, family 8		2.2	NA	Cell envelope
SP_1771	Glycosyl transferase, family 2-glycosyl transferase family 8		1.8	NA	Cell envelope
SP_1774	Transcriptional regulator, putative		0.5	0.5	Regulatory function
SP_1775	Hypothetical protein		0.2	0.4	Hypothetical proteins
SP_1776	Thioredoxin reductase	<i>trxA</i>	0.2	0.3	Energy metabolism
SP_1778	Water channel protein.		0.5	0.7	Transport and binding proteins
SP_1811	Tryptophan synthase, alpha subunit		1.9	0.7	Amino acid biosynthesis
SP_1813	N-(5'-phosphoribosyl)-anthranilate isomerase		2.0	2.0	Amino acid biosynthesis
SP_1814	Indole-3-glycerol phosphate synthase		1.8	1.8	Amino acid biosynthesis
SP_1845	Exodeoxyribonuclease		0.4	0.7	DNA metabolism
SP_1848	Xanthine permease		0.3	X	Transport and binding proteins
SP_1853	Galactokinase	<i>galK</i>	1.1	0.3	Energy metabolism
SP_1855	Dehydrogenase		6.0	1.0	Energy metabolism
SP_1856	Transcriptional regulator, MerR family		7.6	1.1	Regulatory function
SP_1857	Cation efflux system protein		14.4	X	Transport and binding proteins
SP_1860	Choline transporter	<i>proWX</i>	0.2	0.5	Transport and binding proteins
SP_1861	ABC transporter ATP-binding protein - choline transporter	<i>proV</i>	0.2	0.5	Transport and binding proteins
SP_1862	Hypothetical protein		0.2	0.4	Hypothetical proteins
SP_1872	Ferric anguibactin-binding protein precursor fatb of <i>V. anguillarum</i>		X	0.3	Transport and binding proteins
SP_1887	Oligopeptide transport ATP-binding protein AmiF	<i>amiF</i>	1.0	0.5	Transport and binding proteins
SP_1888	Oligopeptide ABC transporter, ATP-binding protein AmiE	<i>amiE</i>	1.0	0.5	Transport and binding proteins
SP_1889	Oligopeptide abc transporter, permease protein AmiD	<i>amiD</i>	1.0	0.5	Cellular processes/pathogenesis/Transport and binding proteins
SP_1890	Oligopeptide transport system permease protein AmiC	<i>amiC</i>	1.0	0.5	Transport and binding proteins
SP_1891	Oligopeptide-binding protein AmiA precursor.	<i>amiA</i>	0.5	0.5	Cellular processes/pathogenesis/Transport and binding proteins
SP_1893	Hypothetical protein		1.2	1.4	Hypothetical proteins
SP_1906	Chaperonin, 60 kDa		0.3	1.1	Protein fate
SP_1907	Chaperonin, 10 kDa		0.4	1.2	Protein fate
SP_1908	Single-strand binding protein (ssb) (helix-destabilizing protein).		X	3.5	Cellular processes/pathogenesis/DNA metabolism
SP_1922	Conserved hypothetical protein		2.3	1.0	Hypothetical proteins
SP_1923	Pneumolysin	<i>ply</i>	3.0	0.5	Cellular processes/pathogenesis
SP_1924	Hypothetical protein		2.6	0.4	Hypothetical proteins
SP_1925	Hypothetical protein		2.3	0.4	Hypothetical proteins
SP_1926	Hypothetical protein		1.7	0.4	Hypothetical proteins
SP_1945	Hypothetical protein		X	4.0	Hypothetical proteins
SP_1954	Serine protease, subtilase family, authentic frameshift		0.5	NA	Protein fate
SP_1986	Hypothetical protein		1.1	3.6	Hypothetical proteins
SP_1987	ABC transporter, ATP-binding protein		0.9	3.8	Transport and binding proteins
SP_1988	Bacteriocin-associated integral membrane protein		0.9	4.0	Cellular processes/pathogenesis
SP_2026	Alcohol-acetaldehyde dehydrogenase		X	0.4	Energy metabolism
SP_2044	Acetate kinase		0.6	0.5	Energy metabolism
SP_2053	Competence protein		X	3.3	Cellular processes/pathogenesis
SP_2054	Hypothetical protein		0.3	1.3	Hypothetical proteins
SP_2055	Alcohol dehydrogenase		0.4	0.4	Energy metabolism
SP_2108	Maltose-maltodextrin-binding protein precursor		0.7	0.4	Transport and binding proteins
SP_2109	Maltodextrin transport system permease protein MalC	<i>malC</i>	0.9	0.6	Transport and binding proteins
SP_2110	Maltodextrin ABC transporter, permease protein	<i>malD</i>	2.5	0.6	Transport and binding proteins
SP_2125	Conserved hypothetical protein		1.3	0.4	Hypothetical proteins
SP_2136	PcpA	<i>pcpA</i>	0.5	2.4	Cell envelope/Cellular processes/pathogenesis
SP_2169	Zinc ABC transporter, zinc-binding lipoprotein		1.3	1.8	Cellular processes/pathogenesis/Transport and binding proteins
SP_2170	Zinc ABC transporter, permease protein	<i>adcB</i>	1.5	2.8	Cellular processes/pathogenesis/Transport and binding proteins
SP_2171	Zinc abc transporter, atp-binding protein	<i>adcC</i>	1.4	2.6	Cellular processes/pathogenesis/Transport and binding proteins
SP_2172	Adc operon repressor AdcR	<i>adcR</i>	1.6	2.4	Cellular processes/pathogenesis/Regulatory function
SP_2173	Extramembranal protein		1.5	2.9	Cell envelope
SP_2174	D-alanyl carrier protein	<i>dlc</i>	1.7	2.7	Cell envelope
SP_2175	Integral membrane protein	<i>dlcB</i>	1.3	2.4	Cell envelope/Transport and binding proteins
SP_2176	D-alanine-activating enzyme	<i>dlcA</i>	1.4	2.5	Cell envelope
SP_2177	Hypothetical protein		1.2	2.3	Hypothetical proteins
SP_2187	Conserved domain protein		0.3	0.9	Hypothetical proteins
SP_2188	Chaperonin, 33 kDa		0.5	1.3	Protein fate
SP_2189	TIM-barrel protein, putative, NifR3 family		0.5	1.1	Unknown protein
SP_2197	ABC transporter, substrate-binding protein, putative		0.4	0.4	Transport and binding proteins
SP_2198	ABC transporter, permease protein		0.5	X	Transport and binding proteins
SP_2199	Conserved hypothetical protein		0.4	0.5	Hypothetical proteins
SP_2235	Response regulator come.	<i>comE</i>	X	2.8	Cellular processes/pathogenesis/Regulatory function/Signal transduction
SP_2236	Putative sensor histidine kinase comD	<i>comD</i>	2.3	3.1	Cellular processes/pathogenesis/Regulatory function/Signal transduction
SP_2237	Competence stimulating peptide precursor (CSP)	<i>comC</i>	1.3	3.1	Cellular processes/pathogenesis
SP_2239	HtrA protein	<i>htrA</i>	1.2	4.6	Protein fate
SP_2240	SpspoJ protein		1.4	4.3	Cellular processes/pathogenesis

* "NA" indicates data points that were removed after analysis with spotfinder. "X" indicates genes that do not meet the criteria established for microarray analysis in MeV (see experimental procedures)