Table- S3: Microarray-based differential gene expression analysis for M1-SDH$_{\text{HBtail}}$ vs M1-WT (M1-SF370) (GSE# 15231).

ORF No.	Gene	Product	Median Log$_2$ ratio	P value
Amino acid transport and metabolism				
SPy0323	braB	putative branched-chain amino acid transport protein	2.56	0.007249
SPy1542	-	putative Xaa-His dipeptidase	-5.29	1.48E-07
SPy1544	arcB	putative ornithine transcarbamylase	-5.07	4.16E-06
SPy1547	sagP (arcA)	streptococcal antitumor protein (possible arginine deiminase)	-4.51	0.001068
SPy2189	sdhB	putative L-serine dehydratase beta subunit	-1.26	0.008149
SPy2190	sdhA	putative L-serine dehydratase alpha subunit	-2.13	0.013243
SPy0183	opuAA	putative glycine betaine/proline ABC transporter (ATP-binding protein)	2.47	6.18E-05
SPy0184	opuABC	putative glycine-betaine binding permease protein	1.65	0.001265
SPy0324	-	putative sodium/dicarboxylate symporter	2	0.000342
SPy1541	arcC	putative carbamate kinase	-4.97	8.37E-07
SPy1549	ahrC.2	putative arginine repressor	-1.59	0.045987
Carbohydrate transport and metabolism				
SPy0146	-	putative regulatory protein	-2.51	0.004096
SPy0252	-	putative sugar transporter sugar binding lipoprotein	-1.89	0.023852
SPy0854	fruB	putative fructose-1-phosphate kinase	-4.56	0.008172
SPy0855	-	putative fructose-specific enzyme II, PTS system BC component	-2.27	0.003793
SPy1057	-	hypothetical protein	-5.51	9.66E-05
SPy1058	-	putative phosphotransferase system (PTS), enzyme II component B	-5.6	0.000223
SPy1059	-	putative phospotransferase system (PTS), enzyme II, component C	-5.39	9.37E-05
SPy1060	-	putative phospotransferase system (PTS), enzyme II component D	-4.91	3.44E-05
SPy1291	glgP	putative glycogen phosphorylase	-2.64	0.037309
SPy1292	malM	putative 4-alpha-glucanotransferase	-5.13	0.003174
SPy1294	-	putative maltose/maltodextrin-binding protein	-4.07	0.006518
SPy1295	malF	putative maltose/maltodextrin ABC transport system (permease)	-3.85	0.018853
SPy1296	malG	putative maltose/maltodextrin ABC transport system (permease)	-2.25	0.02073
SPy1299	malD	putative maltodextrin transport system permease	-2.76	0.000875
SPy1301	malC	maltodextrin transport system permease	-3.57	0.000393
SPy1304	amyB	putative cyclomaltodextrinase	-4.19	0.000302
SPy1306	malX	maltose/maltodextrin-binding protein	-5.46	0.000544
SPy1373	ptsH	putative phosphotransferase system phosphohistidine-containing protein	-1.6	0.002916
SPy1399	nagB	putative N-acetylglucosamine-6-phosphate isomerase	2	0.000618
SPy1503	-	putative phosphomannomutase	-2.31	0.031433
SPy1599	-	putative beta-glucosidase	-0.98	0.024817
SPy1678	-	putative transaldolase	-1.71	0.030279
SPy1704	lacD.1	putative tagatose 1,6-diphosphate aldolase	-1.65	0.010332
SPy1707	lacB.1	putative galactose-6-phosphate isomerase	-2.84	1.49E-05
SPy1708	lacA.1	putative galactose-6-phosphate isomerase	-2.21	0.001005
SPy1709	-	putative PTS system, enzyme IIC component	-2.88	1.44E-05
SPy1711	-	putative PTS system, enzyme IIA component	-2.24	0.024784
SPy1916	lacG	putative phospho-beta-D-galactosidase	-1.65	0.000667
SPy1917	lacE	putative PTS system, lactose-specific component IIBC	-1.77	0.005795
SPy1919	lacD.2	putative tagatose 1,6-diphosphate aldolase	-1.8	0.019259
SPy1922	lacB.2	putative galactose-6-phosphate isomerase (B subunit)	-1.71	0.01556
SPy1923	lacA.2	galactosidase acetyltransferase	-2.47	0.000756
SPy1972	pulA	putative pullulanase	-1.16	0.023886
SPy1973	dexB	dextran glucosidase	-2.26	0.001396
SPy2052	-	putative PTS system, enzyme III	-1.8	0.00055

SPy2096	dexS	putative dextran glucosidase	-1.25	0.023587
SPy2097	-	putative PTS system enzyme II	-1.38	0.003626
		Cell division and chromosome partitioning		
SPy2165	-	hypothetical protein	1.55	0.004494
		Cell envelope biogenesis, outer membrane		
SPy2201	hasB	UDP-glucose 6-dehydrogenase	-4.77	1.72E-09
SPy2202	hasC	UDP-glucose pyrophosphorylase	-4.32	1.50E-08
Cell motility and secretion				
SPy1976	msmK	multiple sugar-binding ABC transport system (ATP-binding protein)	-2.17	0.025933
Coenzyme metabolism				
SPy1063	-	putative periplasmic-iron-binding protein	-2.12	0.011472
SPy1190	citX	conserved hypothetical protein	-1.01	0.026246
SPy1214	lplA	putative lipoate-protein ligase	-1.29	0.034975
DNA replication, recombination and repair				
SPy1196	-	putative integrase/recombinase	1.77	0.012592
SPy1336	-	putative transposase - IS861 associated	1.95	0.029864
SPy1415	deaD	putative ATP-dependent RNA helicase	1.32	0.001425
SPy1563	-	conserved hypothetical protein	-2.44	0.000995
Energy production and conversion				
SPy0148	ntpI	V-type Na+ -ATPase subunit I	-2.48	0.002983
SPy0149	ntpK	V-type Na+ -ATPase subunit K	-3.36	0.000355
SPy0150	ntpE	putative V-type Na+ -ATPase subunit E	-3.77	7.45E-05
SPy0151	ntpC	putative V-type Na+ -ATPase subunit C	-3.79	0.000349
SPy0154	ntpA	putative V-type Na+ -ATPase alpha subunit	-4.37	0.000169
SPy0155	ntpB	putative V-type Na+ -ATPase subunit B	-4.33	0.00093
SPy0157	ntpD	putative V-type Na+ -ATPase subunit D	-3.71	0.000102
SPy0414	lctO	putative lactate oxidase	-1.14	0.042237
SPy0739	sagB	streptolysin S associated ORF	-4.18	0.000177
SPy0755	atpB	putative proton-translocating ATPase a subunit	1.12	0.034206
SPy0757	atpH	putative proton-translocating ATPase, delta subunit	1.51	0.011097
SPy0759	atpG	putative proton-translocating ATPase, gamma subunit	1.4	0.021545
SPy1128	pta	putative phosphotransacetylase	-1.63	0.025472
SPy1849	pfl	putative pyruvate formate-lyase	-2.82	0.001851
Function unknown				
SPy0136	-	hypothetical protein	-5.42	7.69E-09
SPy0147	-	hypothetical protein	-4.55	0.000205
SPy0166	-	hypothetical protein	-2.22	0.002246
SPy0169	-	hypothetical protein	-2.92	7.95E-06
SPy0170	-	hypothetical protein	-5.58	3.55E-11
SPy0174	-	conserved hypothetical protein	-1.1	0.023672
SPy0227	-	hypothetical protein	1.46	0.025308
SPy0373	-	conserved hypothetical protein	1.3	0.031543
SPy0421	-	conserved hypothetical protein	2.01	0.000696
SPy0428	-	conserved hypothetical protein	-1.29	0.003114
SPy0430	-	hypothetical protein	-4.36	3.64E-11
SPy0431	-	hypothetical protein	-1.66	0.003665
SPy0433	-	hypothetical protein	-3.29	1.49E-05
SPy0435	-	hypothetical protein	-3.25	9.47E-07
SPy0437	-	hypothetical protein	-2.18	0.005232
SPy0740	sagC	streptolysin S associated ORF	-2.81	1.42E-05
SPy0741	-	hypothetical protein	-2.46	6.08E-05
SPy0743	-	hypothetical protein	-2.59	5.49E-06
SPy0798	-	conserved hypothetical protein	1.26	0.012063
SPy0861	-	hypothetical protein	-2.95	2.77E-07

SPy0914	-	hypothetical protein	1.11	0.016859
SPy0916	-	hypothetical protein	1.11	0.003215
SPy1017	-	hypothetical protein	1.33	0.03516
SPy1298	malA	putative maltodextrose utilization protein	-2.22	0.000682
SPy1326	-	conserved hypothetical protein	-1.03	0.017117
SPy1339	-	hypothetical protein	-1.29	0.015768
SPy1395	-	putative transcription factor	2.07	0.000347
SPy1543	-	conserved hypothetical protein	-3.61	1.40E-05
SPy1562	-	conserved hypothetical protein	-3.16	1.64E-05
SPy1564	-	conserved hypothetical protein	-1.91	0.005807
SPy1565	-	conserved hypothetical protein	-3.26	9.59E-06
SPy1566	-	conserved hypothetical protein	-1.7	0.002474
SPy1680	-	putative transcriptional regulatory protein	-1.4	0.022179
SPy1710	-	putative PTS system, enzyme IIB component	-1.97	0.002762
SPy1985	-	hypothetical protein	-1.96	0.004481
SPy2209	-	conserved hypothetical protein	1.19	0.006229
General function prediction only				
SPy0044	adhA	putative alcohol dehydrogenase I	-4.88	0.001049
SPy0207	-	putative biotin synthase	2.23	0.000258
SPy0285	-	putative ABC transporter (ATP-binding protein)	1.53	0.032121
SPy0519	-	conserved hypothetical protein	-1.55	0.008426
SPy0742	-	hypothetical protein	-2.94	1.47E-05
SPy0745	sagH	ABC transporter (ATP-binding protein) - streptolysin S associated ORF	-2.66	5.08E-05
SPy0746	-	putative ABC transporter (ATP-binding protein)	-2.68	0.000295
SPy0747	-	conserved hypothetical protein	-1.9	0.0072
SPy1113	-	putative acid phosphatase (class B)	-4.03	9.73E-05
SPy1567	-	conserved hypothetical protein	-2.21	0.001016
SPy1681	-	putative NADH peroxidase	-1.34	0.005186
SPy1736	-	conserved hypothetical protein	2.38	0.000581
SPy1737	-	conserved hypothetical protein	1.02	0.038873
SPy1751	fabK	putative trans-2-enoyl-ACP reductase II	1.95	0.001007
		Inorganic ion transport and metabolism		
SPy1424	-	putative formate dehydrogenase	-1.12	0.009066
Lipid metabolism				
SPy0374	-	conserved hypothetical protein	1.48	0.018614
SPy1718	-	putative esterase	-1.98	0.001495
SPy1743	accA	putative acetyl-CoA carboxylase alpha subunit	1.23	0.003546
SPy1744	accD	putative acetyl-CoA carboxylase beta subunit	1.88	0.015576
SPy1745	accC	putative acetyl-CoA carboxylase biotin carboxylase subunit	2.2	0.002519
SPy1746	fabZ	putative beta-hydroxyacyl-ACP dehydratase	2.19	0.017344
SPy1747	accB	putative biotoin carboxyl carrier protein	2.05	0.000841
SPy1748	fabF	putative beta-ketoacyl-ACP synthase II	1.76	0.002773
SPy1750	fabD	putative malonyl CoA-acyl carrier protein transacylase	2.05	0.000326
SPy1753	acpP	putative acyl carrier protein	2.13	0.000668
SPy1754	fabH	putative beta-ketoacyl-[ACP] synthase III	1.51	0.001933
SPy1758	phaB	putative enoyl CoA hydratase	1.63	0.001134
Nucleotide transport and metabolism				
SPy0831	pyrP	putative uracil permease	0.99	0.037869
SPy0900	pyrF	putative orotidine-5'-decarboxylase PyrF	1.16	0.041346
SPy1375	nrdE.2	putative ribonucleotide reductase alpha-chain	1.15	0.023049
SPy2206	guaB	inosine monophosphate dehydrogenase	1.15	0.01234
Phage				
SPy0660	-	hypothetical protein, phage associated	1.93	0.012448

SPy0667	-	hypothetical protein, phage associated	1.09	0.033773
SPy0967	-	conserved hypothetical protein - phage associated	1.45	0.006787
SPy0968	-	hypothetical protein	-1	0.003845
SPy0971	-	putative terminase, small subunit - phage associated	-1.49	0.002885
SPy0978	-	hypothetical protein	-1.4	0.047899
SPy0979	-	hypothetical protein	2.26	0.00205
SPy0980	-	putative antirepressor - phage associated	2	0.000203
SPy1437	-	hypothetical protein	1.94	0.007943
SPy2122	int4	putative integrase - phage associated	1.38	0.015163
SPy2129	-	hypothetical protein	1.15	0.049082
SPy2132	-	hypothetical protein	1.67	0.014003
SPy2134	-	hypothetical protein	1.71	0.020079
SPy2136	-	putative DNA primase - phage associated	1.37	0.000848
Posttranslational modification, protein turnover, chaperones				
SPy0379	pflC	putative pyruvate-formate lyase activating enzyme	-1.56	0.011661
SPy0416	prtS	putative cell envelope proteinase	-2.93	1.67E-06
SPy1557	msrA	putative peptide methionine sulfoxide reductase	1.43	0.006847
SPy1558	-	hypothetical protein	3.29	0.000235
SPy1559	ccdA	putative cytochrome C-type biogenesis protein	2.35	0.001259
Secondary metabolites biosynthesis, transport and catabolism				
SPy0229	-	putative ABC transporter, ATP-binding protein	1.06	0.002317
SPy0518	-	putative ABC transporter (ATP-binding protein)	-1.73	0.011459
SPy0744	-	putative ABC transporter (ATP-binding protein)	-2.25	0.000207
SPy1729	-	putative ABC transporter (ATP-binding protein)	-1.16	0.009304
SPy1749	fabG	putative beta-ketoacyl-ACP reductase	1.3	0.001583
Signal transduction mechanisms				
SPy1061	-	putative two-component sensor histidine kinase	-2.61	0.00324
Transcription				
SPy0037	-	hypothetical protein	-1.02	0.015531
SPy0853	-	putative transcriptional repressor	-4.1	0.001445
SPy1062	-	putative two-component response regulator	-1.83	0.00926
SPy1546	-	hypothetical protein	-5.25	6.97E-07
SPy1755	-	putative transcriptional regulator (MarR family)	1.24	0.003805
Translation, ribosomal structure and biogenesis				
SPy0071	rpmD	50S ribosomal protein L30	1	0.011878
SPy0145	-	conserved hypothetical protein	-1.56	0.001179
SPy1398	-	putative 16S pseudouridylate synthetase	1.8	0.001886
SPy1613	-	conserved protein - function unknown	-2.62	6.24E-05
Virulence genes				
SPy0165	nga	nicotine adenine dinucleotide glycohydrolase precursor	-2.35	0.001111
SPy0167	slo	streptolysin O precursor	-2.25	0.001306
SPy0436	speJ	putative exotoxin (superantigen)	-1.24	0.003544
SPy0711	speC	pyrogenic exotoxin C precursor, phage associated	1.54	0.001285
SPy0712	mf2	putative DNase (similar to mitogenic factor), phage associated	1.69	0.001229
SPy0737	epf	putative extracellular matrix binding protein	3.45	0.000494
SPy0738	sagA	streptolysin S associated protein	-3.87	3.72E-06
SPy1302	amyA	putative cyclomaltodextrin glucanotransferase	-3.44	1.65E-05
SPy1357	grab	protein GRAB (protein G-related alpha 2M-binding protein)	2.41	5.45E-05
SPy1436	mf3	putative deoxyribonuclease	1.84	9.37E-06
SPy1915	salA	lantibiotic precursor	-1.2	0.033775
SPy1979	ska	streptokinase A precursor	-1.5	0.004047
SPy1983	scl	collagen-like surface protei	-5.59	4.94E-09
SPy2016	sic	inhibitor of complement-mediated lysis	-2.13	4.76E-07
SPy2018	emm1	M protein type 1	-1.13	0.012141

SPy2039	speB	pyrogenic exotoxin B	-2.81	0.000665
SPy2043	mf	mitogenic factor	-1.83	0.001632
SPy2200	hasA	hyaluronate synthase	-4.49	1.29E-08