

Table S1

<b>Genome position</b>	<b>Gene function</b>	<b>-gp67<sup>a</sup></b>	<b>+gp67<sup>b</sup></b>	<b>fold change<sup>c</sup></b>	<b>Locus (SAUOHSC)</b>
9754		118.291	21.109	-1.723	0007
12785	trna synthesis	338.936	69.359	-1.587	***serS 00074
78526	Fe transport	320.21	51.904	-1.820	(sirA)
99487		751.303	128.28	-1.768	sodM
164124	Pyrimidine metabolism	109.03	17.41	-1.835	00152 (187)
164748	indolpuyruvate decarboxylate	139.571	21.343	-1.878	00153 (0188)
166582		628.011	93.171	-1.908	ptsG
199582	isoprenyl cystein carboxyl methyltransferase	382.718	86.026	-1.493	00182 (0220)
222778		120.479	20.511	-1.770	0200
271578		431.454	60.837	-1.959	00253 (280)
297407		285.614	47.161	-1.801	00282 (306)
341745		148.352	33.927	-1.475	00328 (0346)
342463		129.186	24.217	-1.674	00329 (347)
342787		168.878	31.855	-1.668	00330 (348)
366132		187.023	41.175	-1.513	00357 (0373)
402507		44.8496	7.0150	-1.855	00399 (set15)
500137	NTP synthesis	742.144	89.702	-2.113	pdxS
501028		841.017	116.51	-1.977	pdxT (sav0520)
536141	2-amino-3-oxobutane from acetyl coa	242.677	39.254	-1.822	00532 (550)
547607		36.7493	7.0773	-1.647	00543.1
551104		507.965	83.640	-1.804	sdrD
690241		195.406	23.006	-2.139	0707
691928	fructose permease	316.081	52.638	-1.793	00708 (FruA)
722747		1358.73	86.276	-2.757	00738 (SAV0727)
776118		3048	443.72	-1.927	00794 (gapR)
801076	cold shock	5402.94	322.97	-2.817	cspC
804681		207.55	48.308	-1.458	00827 (0824)
806086	028697 acyl transferase	352.807	59.718	-1.776	00830 (0826)
864859	pqi glucose 6-	1297.41	192.49	-1.908	***pqi

phosphate (required)					
890664		999.459	146.08	-1.923	00919 (0982)
909471		411.913	67.071	-1.815	00937 (1000)
940007		185.156	31.379	-1.775	00963 (1028)
947204		111.982	25.901	-1.464	00973 01021
990820		853.732	147.18	-1.758	(1075)
993034		579.556	64.304	-2.199	01022 1077)
1004297	mrna degradation and processing (required)	966.567	134.26	-1.974	***01036( 1089)
1006241		914.677	119.55	-2.035	01037 (def)
1028809		702.261	97.723	-1.972	01064 (pycA)
1033752	heme biosynthesis	527.373	69.373	-2.028	ctaB 01067
1034688		473.681	67.918	-1.942	(1118)
1051882	trna synthetase	281.582	53.940	-1.653	***pheS
1114346	uracil permease	372.335	32.925	-2.426	pyrP
1115681	pyrimidine biosynthesis	409.408	36.638	-2.414	pyrB 01168
1116580	Pyrimidine biosynthesis	413.906	54.705	-2.024	(pyrC)
1117856	Pyrimidine biosynthesis	430.515	85.961	-1.611	01169 (pyrAA)
1122232	Pyrimidine biosynthesis	461.721	87.618	-1.662	01172 (pyrF)
1148092		1135.87	185.42	-1.813	fapR (1228)
1148669	negative regulator of fatty acid biosynthesis	1206.48	210.10	-1.748	plsX 01252
1204422		571.444	71.310	-2.081	(1275)
1242420		1896.92	236.95	-2.080	01285 (glnR)
1242807	glutamine synthetase (required)	2175.49	290.89	-2.012	***01287 (glnA)
1249421		46.319	7.8498	-1.775	1297 01309
1253698		69.4637	10.140	-1.924	SAV1316
1268367	amino acid transporter	597.115	92.257	-1.868	1326 guaC
1272662	NTP biosynthesis	304.507	41.202	-2.000	(sav1337) 01332
1273814		458.992	76.713	-1.789	(1338)
1304208	Oxidative stress	874.423	115.66	-2.023	msrA1
1426309	tRNA synthetase	888.695	146.32	-1.804	asnS 01505
1458084		643.869	125.43	-1.636	(1485)
1545327	malonyl co-a fatty acid biosynthesis	525.605	68.133	-2.043	***01624 (accB)

(required)					
					01759
1659667	MreD	238.947	27.886	-2.148	(1648)
1798610	riboflavin biosynthesis	673.018	142.48	-1.553	ribH
1799087	riboflavin biosynthesis	602.566	124.79	-1.575	01887 (ribA)
1800279	riboflavin biosynthesis	647.036	107.00	-1.800	01888 (ribB)
1800918	riboflavin biosynthesis	654.379	115.33	-1.736	01889 (ribD)
1811161	fructose 6 phosphate aldolase	817.344	170.19	-1.569	01901 (1781)
1883879		1006.38	193.93	-1.647	01979 (1847)
1991203	trna synthesitase	953.649	201.14	-1.556	gatC
2103845		593.509	125.44	-1.554	rex 2273 (xcription reg) (2046)
2152964		248.686	53.497	-1.537	02319 (2084)
2189428		261.971	54.169	-1.576	02367 (2126)
2256513	Fe transport	477.757	96.856	-1.596	02430 (htsA)
2270735	prostoglandin dehydrogenase, putative	177.138	38.462	-1.527	02447 (2187)
2272019		83.2365	16.023	-1.648	02448 (2188)
2348592		452.331	43.248	-2.347	02554 (2284)
2357498	transcriptional regulators: GntR family	1032.03	200.06	-1.641	sarR
2370059	ribosomal protein E (required)	394.45	42.534	-2.227	***rpsE
2370857		200.504	20.811	-2.265	2580.1
2438501		146.33	33.948	-1.461	02652 (2370)
2453507		181.402	38.899	-1.540	02668 (2385)
2454270		825.607	75.899	-2.387	sarZ
2454932	protein oxidoreductase	533.963	113.27	-1.551	02670 (2387)
2477970		129.194	23.611	-1.700	02694 (2409)
2478588		86.8084	14.415	-1.795	02695 (2410)
2595325		94.3532	15.658	-1.796	02816 (2513)
2619737		92.976	15.579	-1.786	02845 (5326)
2620123	glycolosis	98.7279	11.306	-2.167	02846 ptsG
2691654	Na/SO4 symporter	2120.95	361.13	-1.770	fda (2606)

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2801301	Cold shock protein	147.207	27.530	-1.677	03030 (2694)
2813019	trna synthesis	6199.66	634.56	-2.279	cspB

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<sup>a</sup> Reads per kilobase per million total reads

<sup>b</sup> Reads per kilobase per million total reads

<sup>c</sup> =  $e^{(+gp67/-gp67)}$