Supplemental Table S1. Genes differentially expressed by change in growth rate. Data from microarray analyses. Significantly regulated genes are $q<0.05$ (bold). “NA” denotes non expressed or excluded genes. *Genes statistically differences in transcription between the lowest and the higher growth rates.

			0.05/0.15		**0.4/0.15**	
ID	**Gene**	**Name**	**log$_2$**	**qVal.**	**log$_2$**	**qVal.**
Biosynthesis of cofactors, prosthetic group, carriers						
EF0051	*isp*E	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	0.43	0.44	**-1.43**	**0.01**
EF1858	*pan*D	Aspartate 1-decarboxylase	**-1.64**	**0.04**	-1.24	0.09
EF2776	*thi*E	Thiamine-phosphate pyrophosphorylase	**2.21**	**0.04**	0.73	0.62
EF2777		Hydroxyethylthiazole kinase	**1.70**	**0.04**	0.43	0.73
Cell envelope						
EF0025*		Membrane protein. putative	**-1.00**	**0.02**	**0.60**	**0.02**
EF0235		Membrane protein. putative	0.24	0.70	**1.11**	**0.04**
EF0370		Septation ring formation regulator EzrA	**-1.31**	**0.01**	**-1.44**	**0.00**
EF0490		LPX-motif cell wall anchor domain protein	**2.07**	**0.00**	**3.05**	**0.00**
EF0516		Transcriptional regulator, putative	0.58	0.49	**1.59**	**0.04**
EF0989	*mra*W	S-adenosyl-methyltransferase MraW	-0.50	0.32	**-1.14**	**0.02**
EF0991	*pbp*C	Penicillin-binding protein	-0.74	0.28	**-1.69**	**0.03**
EF1583		N-acetylmuramoyl-L-alanine amidase	-0.97	0.10	**-1.29**	**0.02**
EF1740		Penicillin-binding protein 1, putative	0.78	0.17	**1.23**	**0.02**
EF1751		Membrane protein. putative	**-1.12**	**0.02**	**-0.54**	**0.22**
EF2367		N-acetylmuramoyl-L-alanine amidase	-0.69	0.13	**-1.29**	**0.01**
EF2891		Glycosyl transferase, group 1	-0.77	0.13	**-1.02**	**0.04**
EFB0051		Membrane protein, putative	0.33	0.58	**1.34**	**0.02**
Cellular processes						
EF0439*		Immunity protein PlnM, putative	**0.50**	**0.02**	**-1.00**	**0.00**
EF0990		Cell division protein	-0.37	0.52	**-1.29**	**0.01**
EF1151		Cell division protein DivIVA	-1.19	0.17	**-1.81**	**0.03**
EF2052		Cell division protein FtsK	**-1.61**	**0.02**	**-2.42**	**0.03**
EF2387		ParA family chromosome partitioning ATPase	**-1.08**	**0.02**	**-1.51**	**0.01**
EF2739	*ahp*C	Alkyl hydroperoxide reductase	**-1.59**	**0.02**	-0.56	0.40
EFA0007		Ribosomal RNA adenine dimethylase family protein	**-0.50**	**0.18**	**-1.52**	**0.00**
EFA0042		Cell wall surface anchor signal protein	**1.16**	**0.05**	**2.33**	**0.00**
EFB0012	*prg*C	Surface protein PrgC	1.03	0.24	**1.45**	**0.03**
Conserved hypothetical protein						
EF0003		Conserved hypothetical protein	**-1.00**	**0.01**	**-0.72**	**0.04**
EF0145		Conserved hypothetical protein	**1.10**	**0.05**	**1.50**	**0.03**
EF0349		Conserved hypothetical protein	**1.63**	**0.02**	**2.40**	**0.01**
EF0350		Conserved hypothetical protein	**1.49**	**0.04**	**2.56**	**0.00**
EF0469		Conserved hypothetical protein	**-1.19**	**0.01**	**-1.16**	**0.00**
EF0486		Conserved hypothetical protein	**2.00**	**0.02**	**2.46**	**0.00**
EF0487		Conserved hypothetical protein	**2.64**	**0.02**	**1.54**	**0.03**
EF0491		Conserved hypothetical protein	**2.17**	**0.00**	**3.42**	**0.00**
EF0500		Conserved hypothetical protein	**2.50**	**0.00**	**3.67**	**0.00**
EF1026		Conserved hypothetical protein	-0.48	0.30	**-1.35**	**0.00**

EF1541*		Conserved hypothetical protein	**-1.27**	**0.02**	**0.84**	**0.23**
EF1682		Conserved hypothetical protein	**-1.39**	**0.05**	**-1.37**	**0.05**
EF1752		Conserved hypothetical protein	**-1.42**	**0.01**	**-1.08**	**0.02**
EF1753		Conserved hypothetical protein	**-1.46**	**0.03**	**-1.3**	**0.04**
EF1861		Conserved hypothetical protein	**-1.51**	**0.04**	**-1.07**	**0.12**
EF2281		Conserved hypothetical protein	-0.02	0.97	**-1.33**	**0.00**
EF2437		Conserved hypothetical protein	**-3.35**	**0.00**	**-2.55**	**0.00**
EF2604		Conserved hypothetical protein	0.62	0.35	**1.67**	**0.01**
EF2606		Conserved hypothetical protein	**-1.06**	**0.02**	**-0.85**	**0.05**
EF2770		Conserved hypothetical protein	**2.19**	**0.01**	1.05	0.27
EF2923		Conserved hypothetical protein	-0.31	0.60	**-1.37**	**0.01**
EF2965		Conserved hypothetical protein	**-1.82**	**0.00**	-0.65	0.18
EF3009		Conserved hypothetical protein	**1.18**	**0.02**	**1.63**	**0.01**
EF3115		Conserved hypothetical protein	-0.53	0.13	**-1.22**	**0.00**
EF3151		Conserved hypothetical protein	-0.58	0.24	**-1.25**	**0.01**
EFA0035		Conserved hypothetical protein	**2.36**	**0.05**	**1.93**	**0.02**
EFA0036		Conserved hypothetical protein	**1.85**	**0.03**	**3.5**	**0**
EFA0037		Conserved hypothetical protein	**2.17**	**0.03**	**1.56**	**0.02**
EFA0048		Conserved hypothetical protein	**1.99**	**0.04**	**1.26**	**0.05**
EFA0065		Conserved hypothetical protein	**-1.32**	**0.02**	**-1.77**	**0.00**
EFA0066		Conserved hypothetical protein	**-0.95**	**0.01**	**-1.53**	**0.00**
EFB0013		Conserved hypothetical protein	**1.97**	**0.02**	**2.38**	**0.01**
EFB0033		Conserved hypothetical protein	**1.82**	**0.02**	**2.69**	**0.00**
DNA metabolism						
EF0004		recF protein	**-1.32**	**0.00**	**-1.02**	**0.01**
EF0005		DNA gyrase, B subunit	**-1.06**	**0.02**	**-0.86**	**0.04**
EF0325		DNA polymerase I, putative	**1.3**	**0.03**	0.67	0.31
EF0499	*ssb*-2	Single-strand binding protein	**1.29**	**0.04**	**1.95**	**0.01**
EF0762	*uvr*B	Excinuclease ABC, subunit B	0.68	0.20	**-1.29**	**0.01**
EF1521	*dna*G	DNA primase	**-0.73**	**0.02**	**-1.68**	**0**
EF2283*		Resolvase family site-specific recombinase	**1.26**	**0.00**	**-0.356**	**0.02**
Energy metabolism						
EF0900	*ald*E	Aldehyde-alcohol dehydrogenase	**-1.30**	**0.00**	**-1.00**	**0.01**
EF0956	*mal*B/*bop*E	Beta-phosphoglucomutase	**1.20**	**0.03**	0.31	0.67
EF1109		Iron-sulfur cluster binding protein	**-2.12**	**0.03**	-1.39	0.14
EF1125		Putative L-ascorbate 6-phosphate lactonase	**-1.45**	**0.10**	**-2.54**	**0.00**
EF1211	*npr*	NADH peroxidase	**-1.10**	**0.01**	-0.65	0.09
EF1356	*lpd*A	Pyruvate dehydrogenase complex. E3 component. Lipoamide dehydrogenase	-0.38	0.53	**-1.22**	**0.02**
EF1568		Prephenate dehydratase	**-1.53**	**0.02**	-0.31	0.68
EF2058		Transport P-binding protein CydC, putative	**-1.00**	**0.03**	-0.20	0.70
EF2059		Transport P-binding protein CydD, putative	**-1.34**	**0.01**	-0.85	0.06
EF2559		Pyruvate flavodoxin/ferredoxin oxidoreductase	0.67	0.30	**-1.19**	**0.05**
EF2863		Beta-N-acetylglucosaminidase, putative	**1.28**	**0.01**	-0.17	0.75
EF3317		Oxaloacetate decarboxylase, alpha subunit	-0.02	0.96	**1.01**	**0.01**
EF3319	*cit*F	Citrate lyase, alpha subunit	-0.17	0.75	**1.00**	**0.03**

EF3321	*cid*D	Citrate lyase, gamma subunit	-0.24	0.54	**1.00**	**0.01**
EF3322	*cit*C	Citrate lyase ligase	-0.05	0.94	**1.13**	**0.02**
EF3324		Sodium ion-translocating decarboxylase, beta subunit	0.18	0.76	**1.92**	**0.00**
EF3325		Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	-0.17	0.83	**1.50**	**0.02**
Fatty acid and phospholipid metabolism						
EF0779		Glycerophosphoryl diester phosphodiesterase family protein	0.44	0.32	**1.10**	**0.01**
EF1608		Cardiolipin synthetase, putative	0.70	0.12	**1.79**	**0.00**
EF2618		Carboxylesterase precursor, putative	**-1.21**	**0.00**	**-0.99**	**0.01**
Hypothetical protein						
EF0083		Hypothetical protein	**-1.56**	**0.03**	**0.54**	**0.43**
EF0128		Hypothetical protein	**-1.05**	**0.04**	**-1.30**	**0.01**
EF0340		Hypothetical protein	1.46	0.10	**2.31**	**0.03**
EF0341		Hypothetical protein	1.49	0.07	**2.04**	**0.04**
EF0477		Hypothetical protein	-0.53	0.24	**-1.59**	**0.00**
EF0532		Hypothetical protein	-0.76	0.25	**-1.34**	**0.04**
EF0566		Hypothetical protein	-0.79	0.10	**-1.40**	**0.02**
EF0573		Hypothetical protein	**1.71**	**0.01**	NA	NA
EF0605		Hypothetical protein	-0.63	0.46	**-2.23**	**0.00**
EF0723		Hypothetical protein	0.41	0.35	**1.09**	**0.01**
EF0769		Hypothetical protein	-0.60	0.19	**-1.12**	**0.01**
EF0778		Hypothetical protein	0.66	0.22	**1.25**	**0.02**
EF0908		Hypothetical protein	0.97	0.06	**1.77**	**0.00**
EF1067		Hypothetical protein	-0.10	0.83	**-1.22**	**0.00**
EF1095		Hypothetical protein	0.57	0.49	**1.73**	**0.02**
EF1107		Hypothetical protein	**-1.76**	**0.00**	0.65	0.14
EF1262		Hypothetical protein	0.68	0.17	**1.10**	**0.02**
EF1263		Hypothetical protein	0.54	0.24	**1.11**	**0.01**
EF1309		Hypothetical protein	**-1.28**	**0.02**	-0.94	0.08
EF1315		Hypothetical protein	**-0.98**	**0.04**	0.32	0.52
EF1365		Hypothetical protein	0.76	0.14	**1.32**	**0.01**
EF1375		Hypothetical protein	**1.06**	**0.01**	**1.32**	**0.00**
EF1418		Hypothetical protein	-1.05	0.10	**-2.48**	**0.00**
EF1774		Hypothetical protein	0.40	0.43	**1.08**	**0.02**
EF1946		Hypothetical protein	-0.23	0.67	**-1.09**	**0.02**
EF1947		Hypothetical protein	-0.50	0.41	**-1.35**	**0.02**
EF2169		Hypothetical protein	0.40	0.67	**1.83**	**0.02**
EF2229		Hypothetical protein	**1.4**	**0.04**	0.63	0.44
EF2231		Hypothetical protein	**2.01**	**0.00**	0.97	0.13
EF2287		Hypothetical protein	**1.58**	**0.03**	1.17	0.16
EF2317		Hypothetical protein	0.45	0.51	**-1.47**	**0.02**
EF2366		Hypothetical protein	-0.64	0.13	**-1.39**	**0.00**
EF2368		Hypothetical protein	**-1.01**	**0.04**	**-1.18**	**0.01**
EF2466		Hypothetical protein	**1.59**	**0.01**	**1.72**	**0.00**
EF2467		Hypothetical protein	**1.23**	**0.02**	-0.43	0.42

EF2490	*cps*F	Hypothetical protein	0.23	0.69	**1.16**	**0.02**
EF2518*		Hypothetical protein	**-0.63**	**0.02**	**1.13**	**0.01**
EF2588		Hypothetical protein	-0.08	0.89	**1.16**	**0.01**
EF2619		Hypothetical protein	**-2.19**	**0.02**	**-2.91**	**0.05**
EF2707		Hypothetical protein	0.79	0.33	**2.22**	**0.02**
EF2768		Hypothetical protein	**2.40**	**0.01**	1.10	0.29
EF2967		Hypothetical protein	**2.13**	**0.04**	**3.06**	**0.01**
EF3087		Hypothetical protein	**1.92**	**0.00**	**2.46**	**0.00**
EF3088		Hypothetical protein	**1.85**	**0.00**	**2.41**	**0.00**
EF3101		Hypothetical protein	**1.15**	**0.05**	**1.61**	**0.02**
EF3247		Hypothetical protein	0.69	0.17	**1.07**	**0.03**
EF3323		Hypothetical protein	**0.5**	**0.04**	**2.32**	**0.00**
EFA0017		Hypothetical protein	**1.02**	**0.02**	**1.21**	**0.00**
EFA0029		Hypothetical protein	1.72	0.08	**1.99**	**0.01**
EFA0050		Hypothetical protein	**1.95**	**0.02**	**1.69**	**0.03**
EFA0051		Hypothetical protein	**1.9**	**0.03**	**2.12**	**0.02**
EFB0015		Hypothetical protein	**1.63**	**0.01**	**2.78**	**0.00**
Mobile and extrachromosomal element functions						
EF0125		IS256 transposase	**1.3**	**0.02**	**1.4**	**0.01**
EF0351		Structural protein	**1.59**	**0.03**	**1.99**	**0.02**
EF0355	*atl*B	Endolysin	**1.83**	**0.03**	**1.98**	**0.02**
EF2145		Integrase, phage family	**-1.5**	**0.00**	**-1.48**	**0.00**
EF2173		ISEf1, transposase	**1.51**	**0.02**	**1.39**	**0.03**
EFA0001	*tra*A-1	Replication-associated protein RepA	1.38	0.10	**1.2**	**0.04**
EFA0002	*tra*B-1	Pheromone shutdown protein TraB	1.10	0.10	**2.15**	**0.00**
EFA0003	*tra*C-1	traC protein	0.56	0.38	**1.59**	**0.01**
EFA0083	*rep*B-1	Replication-associated protein RepB	0.58	0.32	**1.25**	**0.02**
EFB0063	*prg*N	Replication control protein PrgN	1.39	0.09	**1.67**	**0.04**
Protein fate						
EF0302		Aminopeptidase C	-0.59	0.26	**-1.04**	**0.03**
EF0306		Cro/CI family transcriptional regulator	-0.71	0.11	**-1.01**	**0.02**
EF1307	*grp*E	Heat shock protein GrpE	**-1.49**	**0.03**	-0.70	0.30
EF1308	*dna*K	dnak protein	**-1.31**	**0.04**	-1.09	0.07
EF1763	*sec*A	Preprotein translocase, SecA subunit	**-1.73**	**0.04**	**-2.59**	**0.05**
EF2634	*gro*ES	Chaperonin, 10 kDa	**-1.29**	**0.02**	-0.26	0.66
Protein synthesis						
EF0206	*rpl*C	50S ribosomal protein L3	**-1.18**	**0.00**	**-0.87**	**0.02**
EF0633	*try*S-1	Tyrosyl-tRNA synthetase	-0.68	0.17	**1.19**	**0.01**
EF1694	npsP	Ribosomal protein S16	**-1.19**	**0.01**	0.05	0.95
EF2715	*rpl*L	Ribosomal protein L7/L12	**-1.23**	**0.01**	0.15	0.77
EF2716	*rpl*J	50S ribosomal protein L10	**-1.32**	**0.02**	-0.40	0.47
EF2731	*rpm*G-2	Ribosomal protein L33	**-1.08**	**0.01**	**-1.47**	**0.00**
Purines. pyrimidines. nucleosides. and nucleotides						
EF1714	*pyr*D	Dihydroorotate dehydrogenase	**-1.44**	**0.03**	-0.36	0.61
EF1715	*pyr*DII	Dihydroorotate dehydrogenase electron transfer subunit	**-1.63**	**0.02**	-0.61	0.38

EF1716	*car*B	Carbamoyl-phosphate synthase, large subunit	**-1.72**	**0.02**	-0.86	0.19
EF1717	*pyra*A	Carbamoyl-phosphate synthase, small subunit	**-1.64**	**0.04**	-0.85	0.27
EF1720		Uracil permease	**-1.39**	**0.05**	-0.48	0.50
Regulatory functions						
EF0129		Transcription regulator	-0.85	0.08	**-1.36**	**0.01**
EF0869		Cro/CI family transcriptional regulator	-0.67	0.13	**-1.06**	**0.02**
EF1297		PadR family transcriptional regulator	-1.05	0.12	**-1.84**	**0.01**
EF1306	*hrc*A	Heat-inducible transcription repressor HrcA	**-1.64**	**0.01**	-0.40	0.55
EF1357		AraC family transcriptional regulator	-0.28	0.68	**-1.64**	**0.04**
EF1579	*lex*A	LexA repressor	-0.51	0.16	**-1.10**	**0.00**
EF1709		GntR family sugar-binding transcriptional regulator	**-1.31**	**0.01**	**-0.95**	**0.05**
EF2291*		Cro/CI family transcriptional regulator	**1.16**	**0.01**	**-0.86**	**0.03**
EF2966		BglG family transcriptional antiterminator	**-1.74**	**0.00**	-0.22	0.70
EFA0071		PemK family protein	**-0.75**	**0.05**	**-1.00**	**0.01**
EFB0005.1		Transcriptional regulator, Cro/CI family	**0.99**	**0.05**	**2.02**	**0.00**
Signal transduction						
EF0406		PTS system, component	**1.74**	**0.04**	1.28	0.08
EF0958	*mak*T	PTS system component	**1.33**	**0.03**	1.20	0.08
EF1126		PTS system component	-0.64	0.53	**-2.3**	**0.02**
EF2598		PTS system component	**2.59**	**0.02**	1.80	0.06
EFA0067		PTS system. IIABC components	**1.13**	**0.02**	0.06	0.97
Transcription						
EF2617	*vac*B	Ribonuclease R	**-1.09**	**0.02**	-0.80	0.07
EF2729	*nus*G	Transcription antitermination protein NusG	**-2.24**	**0.00**	**-1.81**	**0.00**
Transport and binding proteins						
EF0022		PTS system component	0.67	0.29	**1.42**	**0.02**
EF0246		Amino acid ABC transporter, ATP-binding protein	0.49	0.36	**1.06**	**0.04**
EF0431		TRAP dicarboxylate transporter DctM subunit, putative	**2.13**	**0.02**	**1.67**	**0.04**
EF0475	*feo*A	Ferrous iron transport protein A, putative	-0.45	0.52	**-1.33**	**0.03**
EF0909		Peptide ABC transporter, permease	0.30	0.56	**1.09**	**0.02**
EF0938		Sugar ABC transporter ATP-binding protein	**-1.31**	**0.01**	-0.69	0.11
EF1027		Putative transport protein SgaT protein	NA	NA	**-2.5**	**0.02**
EF1127	*ula*A	PTS system ascorbate-specific transporter subunit IIC	-0.38	0.77	**-2.5**	**0.02**
EF1398		Molybdenum ABC transporter, permease protein	**1.4**	**0.03**	0.09	0.93
EF2232		Sugar ABC transporter, permease	**1.97**	**0.01**	1.44	0.16
EF2233		Sugar ABC transporter, permease	**1.62**	**0.01**	0.54	0.47
EF2394		ABC transporter ATP-binding protein	-0.46	0.21	**-1.00**	**0.01**
EF2650		Spermidine/putrescine ABC transporter, permease	0.35	0.53	**1.05**	**0.04**
EF2720		ABC transporter ATP-binding protein	**-1.81**	**0.00**	**-1.22**	**0.02**
EF2769		ABC transporter ATP-binding protein	**2.51**	**0.00**	0.70	0.44
EF2992		Major facilitator family transporter	**1.14**	**0.02**	0.43	0.46
EF3004		Sulfate permease family protein	0.55	0.20	**1.41**	**0.01**
EF3015		Serine/threonine transporter SstT	**0.98**	**0.05**	**1.51**	**0.01**
EF3099		Transporter accessory protein. putative	-0.13	0.93	**-3.09**	**0.03**

EF3108		Peptide ABC transporter, permease	0.08	0.87	**1.00**	**0.02**
EF3277		Cytosine permease, putative	**1.46**	**0.01**	**2.57**	**0.00**
EFA0014		Drug resistance transporter. putative	0.75	0.27	**1.78**	**0.00**
EFB0050		Toxin ABC transporter. ATP-binding/permease protein	0.02	0.98	**1.17**	**0.03**
Unknown function						
EF0468		lemA protein	**-1.37**	**0.01**	**-1.05**	**0.04**
EF0512		DNA-damage-inducible protein. putative	**-0.79**	**0.03**	**-1.11**	**0.00**
EF0796		Type 2 phosphatidic acid phosphatase family protein	1.20	0.08	**1.57**	**0.02**
EF0856		Aldo/keto reductase family protein	**-1.11**	**0.02**	**-1.00**	**0.03**
EF1025		CBS domain-containing protein	-0.64	0.24	**-1.29**	**0.01**
EF1108		Oxidoreductase, putative	**-1.62**	**0.00**	-0.84	0.07
EF1110		YkgG family protein	**-1.52**	**0.01**	-0.50	0.37
EF2214		Glyoxylase family protein	1.05	0.08	**1.28**	**0.03**
EF2436	*mur*Q	N-acetylmuramic acid-6-phosphate etherase	**-1.56**	**0.04**	**-1.49**	**0.04**
EF2577		Aspartate/ornithine carbamoyltransferase family protein	**1.04**	**0.03**	0.32	0.51
EF2738	*ahp*F	Thioredoxin reductase	**-1.43**	**0.01**	-0.96	0.06
EF2756	*din*P	DNA-damage-inducible protein P	-0.78	0.26	**-1.34**	**0.04**
EF2874		HAD superfamily hydrolase	**-1.22**	**0.04**	**-1.17**	**0.04**
EF2933		Redox-sensing transcriptional repressor Rex	-0.64	0.12	**-0.95**	**0.02**
EF3114		DAK2 domain-containing protein	-0.16	0.68	**-1.00**	**0.01**
EF3311	*gid*A	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	0.83	0.16	**1.34**	**0.02**
EFA0072		PemI family protein	**-0.95**	**0.01**	**-1.48**	**0.00**