

**Table 5. Genes regulated by the FixL, FixJ, FixK, FtrA, and FtrB under hypoxia**

Gene number/annotation	$\bar{X}$ change in transcript levels (wild-type/mutant)				
	$\Delta fixL$	$\Delta fixJ$	$\Delta fixK$	$\Delta ftrA$	$\Delta ftrB$
<b><i>Energy Production and Conversion</i></b>					
CC1405 ferredoxin, putative	50.96	16.07		1.11	0.92
CC0762 cytochrome d ubiquinol oxidase subunit I CydA	11.66	8.22	24.93	1.40	1.21
CC0763 cytochrome d ubiquinol oxidase subunit II CydB	8.12	4.09	3.16	0.95	0.97
CC1402 cytochrome c oxidase, subunit CcoO	12.32	3.90	7.31	1.34	1.16
CC1401 cytochrome c oxidase, subunit CcoN	6.06	2.86	4.76	0.97	0.97
CC1403 cytochrome c oxidase, subunit CcoQ	4.53	1.03	1.33	0.95	1.01
CC1404 cytochrome c oxidase, subunit CcoP	4.56	1.88	2.21	1.16	1.14
CC1363 proton pump, putative	4.46	1.00	2.28	0.88	0.90
CC1408 cytochrome oxidase maturation protein, cbb3-type	3.72	1.40	2.51	0.97	0.99
CC2970 cytochrome c family protein	3.12	1.51	0.80	1.11	1.00
CC1406 ferredoxin, putative	2.05	1.12	2.46	1.01	0.93
CC1773 ubiquinol oxidase subunit II QoxA	0.09	0.19	0.15	1.44	0.81
CC1771 ubiquinol oxidase subunit III QoxC	0.18	0.56	0.32	0.98	0.99
CC1769 SurF1 family protein	0.29	0.67	0.47	0.99	1.00
CC1770 ubiquinol oxidase subunit IV QoxD	0.32	0.64	0.37	0.99	0.90
CC3403 cytochrome c oxidase assembly protein	0.91	0.85	0.54	1.04	1.01
CC3407 cytochrome c oxidase, subunit II CoxB	0.79	1.04	0.58	1.06	0.97
CC3406 cytochrome c oxidase, subunit I CoxA	0.73	1.00	0.61	1.19	1.11
<b><i>Coenzyme Metabolism</i></b>					
CC1411 coproporphyrinogen III oxidase HemN	20.12	4.31		1.08	0.71
CC1355 5-aminolevulinic acid synthase HemaA	3.36	3.58	0.70	0.95	0.93
CC2760 cytochrome c-type biogenesis protein CycK	2.22	1.27	1.03	1.40	0.99
CC3763 uroporphyrinogen decarboxylase HemE	1.98	1.33	0.85	1.22	0.98
CC2759 cytochrome c-type biogenesis protein CycL	1.92	1.26	0.87	0.77	0.93
CC1347 delta-aminolevulinic acid dehydratase HemB	1.75	1.08	0.93	0.88	0.95
CC2029 thiamine biosynthesis protein ThiC	0.59	0.80	1.02	0.31	0.53
<b><i>Signal Transduction</i></b>					
CC0759 sensory box histidine kinase FixL	3.01	2.34	1.38	0.89	1.08
CC0758 DNA-binding response regulator FixJ	1.56	2.68	1.49	1.07	1.09
CC0629 sensor histidine kinase, putative	2.28	1.27	1.50	0.83	0.83
CC3058 response regulator/sensor histidine kinase	1.86	1.58	1.55	0.95	0.94
CC0753 regulatory protein FixT	26.56	11.82	5.46	1.22	1.10
CC1768 sensor histidine kinase	0.33	0.66	0.61	0.92	0.94
CC1767 response regulator	0.35	0.38	0.65	0.97	0.92
<b><i>Carbohydrate and Amino Acid Transport and Metabolism</i></b>					
CC1409 outer membrane protein OmpW	29.14	4.20	17.88	1.07	1.06
CC1407 cation-transporting ATPase, E1-E2 family	8.02			1.04	0.97
CC0761 ABC transporter, ATP-binding protein CydD	2.51	1.33	1.27	0.95	1.15
CC0760 ABC transporter, ATP-binding protein CydC	2.27	1.53	1.76	1.39	1.06
CC3069 major facilitator family transporter	2.38	2.11	1.38	0.90	1.01

$\bar{X}$  change in transcript levels  
(wild-type/mutant)

Gene number/annotation	$\Delta fixL$	$\Delta fixJ$	$\Delta fixK$	$\Delta ftrA$	$\Delta ftrB$
CC1446 TRAP dicarboxylate transporter, DctP subunit family	2.35	1.39			
CC1298 myo-inositol degradation, iolC protein	0.91	1.17	1.81	1.99	0.99
CC1302 methylmalonate-semialdehyde dehydrogenase, putative	0.91	1.19	1.09	1.99	1.12
CC1314 ABC transporter, HlyB/MsbA family	0.97	1.24	1.06	1.89	1.23
CC3262 bacterioferritin bfr	1.22	0.93	0.99	1.75	1.12
CC0584 succinylornithine transaminase	1.15	1.18	0.73	1.75	1.74
CC1300 myo-inositol degradation, IolE protein	0.93	1.22	1.38	1.75	1.07
CC2534 histidinol-phosphate aminotransferase	1.40	0.66		1.73	1.60
CC1296 myo-inositol 2-dehydrogenase IdhA	1.04	1.20	1.11	1.67	1.13
CC2999 citrate lyase, beta subunit, putative	0.47	0.61	0.59	0.95	1.00
CC1760 acyl-CoA thioesterase I TesA	0.59	0.52	0.48	1.06	0.97
CC1785 efflux system protein	0.61	0.43	0.34	1.21	1.04
<b>Transcription</b>					
CC3367 transcriptional regulator, FtrA	3.71	2.28	3.46	3.61	0.88
CC0752 transcriptional regulator, FixK	2.73	1.89	2.65	1.62	1.30
CC1410 transcriptional activator, FtrB	6.16	3.81	6.59	1.05	9.12
CC2883 RNA polymerase sigma-70 factor, ECF subfamily sigU	1.21	0.58	1.22	0.54	1.03
<b>Replication, Recombination and Repair</b>					
CC0377 A/G-specific adenine glycosylase MutY	1.89	1.52	1.09	0.90	1.04
CC0008 chromosomal replication initiator protein DnaA	1.18	0.99	1.02	1.66	1.05
<b>General Function Prediction Only</b>					
CC0212 hydrolase, carbon-nitrogen family	2.12	2.61	1.24	1.04	0.96
CC1456 flagellin modification protein FlmH	4.42	1.93	3.48	1.27	1.05
CC0257 adenosylhomocysteinase achY	1.44	1.84	1.43	1.11	0.91
CC0811 metallo-beta-lactamase family protein	2.57	1.33	1.42	0.99	0.91
CC1716 ISCc2, transposase	2.11	1.08	1.36	0.89	0.99
CC0200 oxidoreductase iron/ascorbate family	2.06	1.17	1.89	1.37	1.16
CC1348 monooxygenase, flavin-binding family	1.99	1.08	1.32	1.45	1.06
CC2948 pilus subunit protein PilA	1.01	0.82	1.18	1.74	1.10
CC2538 membrane protein, putative	0.41	0.43	1.10	0.90	0.99
CC0714 membrane protein, putative	0.43	0.63	0.95	1.14	1.06
CC1761 IS30 family, transposase	0.50	0.47	0.30	1.28	0.92
CC3733 carbohydrate kinase, PfkB family	0.50	0.96	0.86	0.89	0.90
CC0335 TonB-dependent receptor	0.56	0.96	0.95	0.90	0.96
<b>Posttranslational Modification / Protein Turnover</b>					
CC0685 chaperonin, 60 kDa groEL		0.77	0.99	2.13	1.41
CC0686 chaperonin, 10 kDa groES	1.06	0.90	1.00	2.03	1.22
CC2258 heat shock protein, Hsp20 family	1.26	0.74	0.85	1.73	1.11
<b>Hypothetical Proteins</b>					
CC1400 hypothetical protein	6.74	4.47	6.14	1.06	1.16
CC2193 hypothetical protein	1.08	3.56	0.87	1.05	0.77
CC0277 hypothetical protein	6.35	2.74	6.28	1.00	0.98
CC0027 conserved hypothetical protein	3.27	2.21	1.92	0.65	0.80

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CC0845 hypothetical protein	2.43	1.92	0.85	1.26	0.96
CC2115 hypothetical protein	4.60	1.89	9.06	0.87	0.87
CC1453 hypothetical protein	6.57	1.88	3.27	1.01	1.12
CC2910 conserved hypothetical protein	2.56	1.82	1.82	1.04	1.24
CC0135 conserved hypothetical protein	1.72	1.78	1.27	0.90	1.04
CC1452 conserved hypothetical protein	13.20			1.26	1.03
CC2518 hypothetical protein	7.77	1.60	2.42	1.01	0.99
CC2831 hypothetical protein	3.38	1.49	1.28	1.13	1.04
CC1391 hypothetical protein	2.94	1.54	1.71	0.92	1.00
CC1067 hypothetical protein	2.33	1.63	1.46	1.06	1.18
CC0387 hypothetical protein	2.12	1.04	1.36	0.83	0.93
CC3115 conserved hypothetical protein	1.99	1.35	0.77	0.78	0.81
CC1450 conserved hypothetical protein	1.95	1.30	1.16	1.27	1.18
CC0209 conserved hypothetical protein	1.81	1.47	1.38	0.92	0.94
CC0730 hypothetical protein	1.74	1.40	0.84	1.37	1.16
CC0135 conserved hypothetical protein	1.72	1.78	1.27	0.90	1.04
CC1662 conserved hypothetical protein	0.95	0.98	1.74	1.01	1.00
CC0876 hypothetical protein	1.00	0.90	1.12	1.81	1.11
CC2074 hypothetical protein	0.99	0.84	0.95	1.75	1.02
CC2998 hypothetical protein	1.33	0.78	0.86	1.75	1.02
CC1784 conserved hypothetical protein	0.27	0.41	0.31	1.37	
CC1782 hypothetical protein	0.32	0.56	0.45	1.02	0.84
CC1758 conserved hypothetical protein	0.40	0.51	0.32	1.09	0.93
CC1500 conserved hypothetical protein	0.45	0.62	0.88	1.19	1.05
CC2778 hypothetical protein	0.53	0.86	0.82	1.13	1.03
CC1783 hypothetical protein	0.54	0.69	0.51	1.19	0.98
CC1234 hypothetical protein	1.04	0.70	0.50	0.75	0.91
CC0559 hypothetical protein	0.88	1.10	0.57	1.01	1.09
CC2229 conserved hypothetical protein	0.74	0.92	0.60	1.19	1.02
CC0681 hypothetical protein	1.05	1.78	0.61	0.65	1.00
CC0682 hypothetical protein	0.93	1.46	0.61	0.73	1.14
CC3263 conserved hypothetical protein	0.76	1.52	1.07	0.54	0.95
CC0421 conserved hypothetical protein	1.00	0.99		0.56	0.97
CC0669 hypothetical protein	0.66	0.47	0.75	1.09	0.53
CC2435 hypothetical protein	0.66	0.62	0.95	0.82	0.91
CC3220 hypothetical protein	0.64	0.67	0.95	0.98	0.86
CC3061 hypothetical protein	0.86	1.45	0.86	0.78	0.80
CC3060 conserved hypothetical protein	0.95	1.66	0.97	0.63	0.85
CC1325 hypothetical protein	0.64	0.67	1.01	0.96	0.96
CC3073 hypothetical protein	0.52	0.49	0.96	0.93	0.93

Values shown are averaged from four independent gene chip experiments. All genes that exhibit 1.6-fold change or greater in at least one of the mutant strains, and that meet a

statistical cutoff parameter (computed in SIGNIFICANCE ANALYSIS OF MICROARRAYS software package version 1.21) are shown. See *Materials and Methods* for a reference on our microarray methods. Genes are arranged by functional category based on their COG description. Blank values indicate missing data.