

Supplemental information:

	U_t1	U_t2	Genes	U_t1	U_t2	stddev U_t1	stddev U_t2	func tion
1			SO4484 cytochrome c-type protein Shp	32.0	22.6	0.3	0.4	cyt
2			SO4126 hypothetical protein	16.0	17.1	1	0.3	hyp
3			SO1925 HlyD family secretion protein	24.3	7.0	1.7	0.2	sec
4			SO3364 conserved hypothetical protein	10.6	19.7	0.5	0.2	hyp
5			SO1808 phage shock protein B (pspB)	2.1	24.3	0	0.4	me
6			SO4483 cytochrome b, putative	9.8	14.9	0.8	0.4	cyt
7			SO1809 phage shock protein C (pspC)	3.7	19.7	0.8	0.5	me
8			SO3840 RNA polymerase sigma-70 factor, ECF subfamily	17.1	4.3	0.3	0.3	str
9			SO4485 diheme cytochrome c	8.0	12.1	0.6	0.2	cyt
10			SO2746 conserved hypothetical protein	8.0	8.0	1.2	0.4	hyp
11			SO2884 conserved hypothetical protein	13.0	2.3	0.8	0.2	hyp
12			SO0150 lipoprotein, putative	9.2	6.1	1	0.6	me
13			SO0637 conserved hypothetical protein	10.6	4.0	0.8	0.3	hyp
14			SO2883 conserved hypothetical protein	12.1	2.1	1.2	0.2	hyp
15			SO4476 spheroplast protein γ precursor, putative	4.6	9.2	0.1	0.5	me
16			SO2007 conserved hypothetical protein	5.7	8.0	0.6	0.3	hyp
17			SO3577 clpB protein (clpB)	5.7	8.0	0.8	0.4	str
18			SO0970 fumarate reductase flavoprotein subunit	3.5	9.8	0.8	0.5	cyt
19			SO1428 outer membrane protein	2.3	10.6	1.1	0.6	sec
20			SO3842 conserved hypothetical protein	7.0	5.3	0.1	0.3	hyp
21			SO3942 serine protease, HtrA/DegQ/DegS family	4.9	7.0	0.4	0.3	str
22			SO1611 hypothetical protein	6.5	5.3	1.9	0.5	hyp
23			SO1357 ribosomal protein S16 (rpsP)	2.1	9.2	0.2	0.4	tr
24			SO1337 hypothetical protein	7.5	3.7	0.7	0.2	hyp
25			SO1431 conserved hypothetical protein	4.6	6.5	0.2	0.3	hyp
26			SO2750 tolR protein (tolR)	5.7	5.3	0.2	0.4	sec
27			SO4321 OmpA family protein	6.5	4.3	0.4	0.4	sec
28			SO2625 translation initiation factor IF-1 (InfA)	4.3	6.5	0.6	0.2	tr
29			SO0704 chaperonin GroEL (groEL)	3.0	7.5	0.7	0.5	str
30			SO4162 ATP-dependent protease HslV (hslV)	4.3	6.1	0.6	0.5	str
31			SO1429 anaerobic dimethyl sulfoxide reductase, A subunit (dmsA-1)	3.7	6.5	0.6	0.2	cyt
32			SO3286 cytochrome d ubiquinol oxidase, subunit I (cydA)	6.1	4.0	0.4	0.3	cyt
33			SO4053 methyl-accepting chemotaxis protein	7.0	3.0	0.5	0.5	mot
34			SO3617 hypothetical protein	2.3	7.5	0.5	0.2	hyp
35			SO2017 conserved hypothetical protein	2.1	7.5	0.8	0.3	hyp
36			SO0162 phosphoenolpyruvate carboxykinase (ATP)	8.0	ND	1		nrg
37			SO1776 outer membrane protein precursor MtrB (mtrB)	3.2	5.7	0.8	0.4	sec
38			SO2604 conserved hypothetical protein	5.7	3.0	0.5	0.2	hyp
39			SO2016 heat shock protein HtpG (htpG)	3.0	5.7	0.5	0.9	str
40			SO1126 chaperone protein DnaJ (dnaJ)	2.1	6.5	0.3	0.3	str
41			SO3236 flagellin FlaG (flaG)	3.7	4.9	0.1	0.8	mot
42			SO0244 ribosomal protein S14 (rpsN)	2.8	5.7	0.8	0.2	tr
43			SO3417 peptidyl-prolyl cis-trans isomerase SlyD (slyD)	5.3	3.2	0.3	0.5	str
44			SO0260 heme exporter protein CcmD (ccmD)	4.6	3.7	0.3	0.6	cyt
45			SO1445 transcriptional regulator, CopG family	3.7	4.3	0.8	0.5	tr
46			SO4320 agglutination protein (aggA)	5.3	2.6	0.9	0.6	me
47			SO3765 conserved hypothetical protein	3.5	4.3	0.7	0.3	hyp
48			SO4520 oxygen-independent coproporphyrinogen II	5.7	2.1	0.2	0.6	cyt
49			SO1111 bacterioferritin subunit 2 (bfr2)	4.9	2.8	0.9	0.3	cyt
50			SO4649 conserved hypothetical protein	1.9	5.7	0.2	0.2	hyp

SI Table 1. Genes upregulated ($\geq 3x$) during U(VI) reduction after 6 and 11 hours (T1 and T2). The brighter the red color is, the greater the fold upregulation. The average fold upregulation for both time points and standard deviations are shown on the right. ND refers to no data. Genes included in this list were upregulated $\geq 3x$ at either or both time points. The genes are listed in order of decreasing upregulation at either time point. The functions listed correspond to: cyt: cytochrome and heme synthesis; hyp: hypothetical; sec: secretion; me: membrane; str: stress; tr: transcription and translation; mot: motility; nrg: energy production; un: unknown.

51	SO0233	ribosomal protein L23 (rplW)	1.0	6.5	0.5	0.2	tr
52	SO4646	hypothetical protein	3.7	3.7	1.2	0.4	hyp
53	SO1798	peptidyl-prolyl cis-trans isomerase D (ppiD)	2.0	5.3	0.1	0.1	str
54	SO1777	decaheme cytochrome c MtrA (mtrA)	4.0	3.0	0.1	0.5	cyt
55	SO3426	carbon storage regulator (csrA)	3.5	3.5	0.6	0.4	nrg
56	SOA0040	hypothetical protein	3.2	3.7	0.1	0.2	hyp
57	SO1582	conserved hypothetical protein	3.2	3.7	0.6	1.1	hyp
58	SO0222	ribosomal protein L10 (rplJ)	3.2	3.7	0.2	0.2	tr
59	SO3682	hypothetical protein	4.3	2.5	0.3	0.1	hyp
60	SO4129	SPFH domain/Band 7 family protein	2.8	4.0	0.8	0.2	me
61	SO0662	conserved hypothetical protein	4.0	2.8	0.3	0.2	hyp
62	SO0493	hypothetical protein	3.5	3.2	0.2	1.1	hyp
63	SO1497	hypothetical protein	3.5	3.2	0.5	0.9	hyp
64	SO3888	conserved hypothetical protein	3.5	3.2	0.8	0.4	hyp
65	SO4247	ribosomal protein L28 (rpmB)	2.6	4.0	0.4	0.4	tr
66	SO1778	decaheme cytochrome c (omcB) or (mtrC)	4.9	1.6	0.2	0.6	cyt
67	SO1274	conserved hypothetical protein	3.2	3.2	0.3	0.2	hyp
68	SO1490	alcohol dehydrogenase II (adhB)	3.2	3.2	0.6	0.1	nrg
69	SO1998	conserved hypothetical protein	1.7	4.6	0.2	0.2	hyp
70	SO2403	cytidylate kinase (cmk)	3.5	2.8	0.7	0.4	tr
71	SO1112	bacterioferritin subunit 1 (bfr1)	2.3	4.0	0.7	0.3	cyt
72	SO1919	hypothetical protein	2.3	4.0	0	0.9	hyp
73	SO3787	hypothetical protein	4.3	1.9	0.4	0.3	hyp
74	SO3000	conserved hypothetical protein	1.9	4.3	0.5	0.4	hyp
75	SO3430	recA protein (recA)	3.2	3.0	0.5	0.5	str
76	SO0238	ribosomal protein L16 (rplP)	2.1	4.0	0.8	0.2	tr
77	SO3764	conserved hypothetical protein	2.1	4.0	0.3	0.2	hyp
78	SO1577	glutathione S-transferase family protein	2.5	3.5	0.6	0.1	str
79	SO1746	conserved hypothetical protein	2.0	4.0	0.2	0.7	hyp
80	SO4564	TonB2 protein, putative	4.3	1.7	0.6	0.3	me
81	SO1175	conserved hypothetical protein	2.5	3.5	0.8	0.5	hyp
82	SO2913	pyruvate formate-lyase 1 activating enzyme (pflA)	4.3	1.6	0.5	0.4	nrg
83	SO4326	transcriptional regulator, TetR family	1.9	4.0	0.6	0.3	tr
84	SO2074	ATP phosphoribosyltransferase (hisG)	4.3	1.6	0.4	0.3	tr
85	SO0203	hypothetical protein	2.3	3.5	0.6	0.5	hyp
86	SO1359	tRNA (guanine-N1)-methyltransferase (trmD)	2.6	3.2	0.6	0.2	tr
87	SO0466	hypothetical protein	2.1	3.7	0.9	0.5	hyp
88	SO1361	phospho-2-dehydro-3-deoxyheptonate aldolase, tyr sens.	2.1	3.7	0.6	0.2	tr
89	SO1097	conserved hypothetical protein	2.3	3.5	0.8	0.2	hyp
90	SO1427	decaheme cytochrome c	4.0	1.7	0.6	0.4	cyt
91	SO1430	anaerobic dimethyl sulfoxide reductase, B subunit (dmsB-1)	3.2	2.5	0.5	0.3	cyt
92	SO4406	thioredoxin 1 (trxA)	2.1	3.5	0.6	0.2	cyt
93	SO1989	chemotaxis protein CheV (cheV-1)	3.7	1.9	0.8	0.2	mot
94	SO1473	SsrA-binding protein (smpB)	2.1	3.5	0.2	0.5	tr
95	SO3285	cytochrome d ubiquinol oxidase, subunit II (cydB)	4.6	ND	0.3		cyt
96	SO1779	decaheme cytochrome c (omcA)	2.8	2.8	0.4	0.6	cyt
97	SO0225	DNA-directed RNA polymerase, beta subunit (rpoC)	2.6	3.0	0.6	0.8	str
98	SO1538	isocitrate dehydrogenase, NAD-dependent	3.0	2.6	1.1	0.3	nrg
99	SO2402	ribosomal protein S1 (rpsA)	2.5	3.0	0.4	0.3	tr
100	SO2248	L-serine dehydratase 1 (sdaA)	2.3	3.2	0.1	0.1	tr
101	SO3718	thiol:disulfide interchange protein, DsbA family	4.3	ND	0.4		me
102	SO4736	hypothetical protein	ND	4.3		0.1	hyp
103	SO0021	fatty oxidation complex, alpha subunit (fadB)	3.2	2.0	0.5	0.1	nrg
104	SO3314	fimbrial biogenesis and twitching motility protein, putative	3.7	1.5	0.8	0.4	mot
105	SO0490	transcriptional regulator	4.0	ND	0.4		tr
106	SO2882	conserved hypothetical protein	3.5	1.5	0.8	0.3	hyp
107	SO3387	hypothetical protein	3.2	1.6	0.3	0.5	hyp
108	SO3929	primosomal replication protein n (priB)	ND	3.7		0.2	tr
109	SO4667	GTP-binding protein EngB (engB)	ND	3.7		0.1	nrg
110	SO3088	fatty oxidation complex, alpha subunit	ND	3.7		0.4	nrg
111	SOA0122	conserved hypothetical protein	3.2	1.4	0.4	0.3	hyp
112	SO3467	3,4 dihydroxy-2-butanone 4-phos. synth./GTP cyclohydrolase	3.0	1.6	0.3	0.2	nrg
113	SO1170	iojap domain protein	ND	3.5		0.3	un
114	SO3786	hypothetical protein	3.5	ND	0.2		hyp
115	SO4510	formate dehydrogenase, iron-sulfur subunit (fdhB-1)	ND	3.5		0.9	cyt
116	SO4315	hemX protein (hemX)	3.2	1.2	0.9	0.4	cyt
117	SO4604	conserved hypothetical protein	3.2	1.2	0.8	0.4	hyp
118	SO0433	regulator of sigma D (rsd)	3.0	1.2	0.5	0.2	tr
119	SO2439	srpA-related protein	3.2	ND	0.5		str
120	SO4055	aspartokinase II/homoserine dehydrog., met.-sens.	3.2	ND	0.5		tr
121	SO2373	drug resistance transporter, Bcr/CflA family protein	3.7	ND	0.6		sec

SI Table 1 continued.

	Cr_t1	Cr_t2	Genes	Cr_t1	Cr_t2	stddev Cr_t1	stddev Cr_t2	func ion
1			SO4484 cytochrome c-type protein Shp	12.1	16.0	0.7	0.5	cyt
2			SO4483 cytochrome b, putative	12.9	8.8	0.8	0.3	cyt
3			SO4485 diheme cytochrome c	7.7	11.4	0.5	0.3	cyt
4			SO4055 aspartokinase II/homoserine dehydrogenase, met.-sens.	9.3	7.4	0.7	0.3	tr
5			SO3718 thiol:disulfide interchange protein, Dsb	5.6	8.0	0.5	0.2	me
6			SO0518 outer membrane efflux family protein, putative	4.2	9.0	0.6	0.2	det
7			SO0519 cation efflux protein, putative	4.5	7.8	0.8	0.3	det
8			SOA0154 heavy metal efflux protein, putative	4.7	7.3	0.5	0.3	det
9			SO4477 transcriptional regulatory protein CpxR	ND	10.6		0.2	me
10			SO4593 hypothetical protein	10.0	ND	0.3		hyp
11			SO0820 HlyD family secretion protein	ND	9.8		0.2	sec
12			SO4476 spheroplast protein y precursor, putative	3.3	7.3	0.3	0.2	me
13			SO4716 acetyltransferase, GNAT family	7.3	3.3	0.5	0.4	nrg
14			SO1111 bacterioferritin subunit 2 (bfr2)	4.8	4.9	0.6	0.3	cyt
15			SO4592 hypothetical protein	4.6	5.1	1.1	0.2	hyp
16			SO0817 transcriptional activator protein MetR (metR)	5.8	3.8	0.7	0.1	tr
17			SO0970 fumarate reductase, flavoprotein subunit precursor	5.6	4.0	0.4	0.2	cyt
18			SO4746 ATP synthase F1, epsilon subunit (atpC)	ND	8.3		0.1	nrg
19			SO0520 heavy metal efflux pump, CzCA family	ND	7.7		0.1	det
20			SO3846 conserved hypothetical protein	3.7	4.8	0.8	0.1	hyp
21			SO3286 cytochrome d ubiquinol oxidase, subunit	3.8	4.4	0.5	0.1	cyt
22			SO4056 cystathionine gamma-synthase (metB)	3.5	4.5	0.7	0.0	tr
23			SO4558 hypothetical protein	4.2	3.7	0.5	0.2	hyp
24			SO2824 carbon starvation protein A, authentic point mutation	3.2	4.6	0.8	0.2	nrg
25			SO0704 chaperonin GroEL (groEL)	3.9	3.9	0.7	0.6	str
26			SO1776 outer membrane protein precursor MtrB (mtrB)	2.3	5.5	0.4	0.3	me
27			SO2007 conserved hypothetical protein	ND	6.8		0.3	hyp
28			SO4487 DNA-binding response regulator	3.1	4.3	0.5	0.3	tr
29			SO0958 alkyl hydroperoxide reductase, C subunit	4.0	3.3	0.6	0.2	str
30			SO0259 cytochrome c biogenesis protein CcmE (ccmE)	2.0	5.2	0.4	0.3	cyt
31			SO1357 ribosomal protein S16 (rpsP)	3.2	3.9	0.5	0.3	tr
32			SO4054 5,10-methylenetetrahydrofolate reductase	2.6	4.4	0.7	0.2	tr
33			SO1777 decaheme cytochrome c MtrA (mtrA)	2.4	4.5	0.6	0.3	cyt
34			SO4428 DNA-binding response regulator	2.1	4.6	0.6	0.2	tr
35			SO4028 single-strand binding protein (ssb)	4.1	2.3	0.4	0.2	tr
36			SO2884 conserved hypothetical protein	3.7	2.7	0.1	0.0	hyp
37			SO1087 conserved hypothetical protein	3.4	2.9	0.8	0.1	hyp
38			SO0276 acetylglutamate kinase (argB)	3.4	2.9	0.7	0.3	tr
39			SO2895 pyridoxamine 5'-phosphate oxidase (pdxH)	3.2	3.0	1.0	0.1	tr
40			SO3417 peptidyl-prolyl cis-trans isomerase SlyD	2.2	4.0	0.2	0.1	str
41			SO4053 methyl-accepting chemotaxis protein	ND	5.2		0.1	mot
42			SO0293 phosphoglycolate phosphatase (gph)	3.2	2.9	1.3	0.2	nrg
43			SO1917 multidrug resistance protein, putative	3.2	2.8	0.5	0.3	sec
44			SO4594 hypothetical protein	2.7	3.2	0.4	0.4	hyp
45			SO4520 oxygen-independent coproporphyrinogen II	2.8	3.1		0.7	cyt
46			SO3888 conserved hypothetical protein	ND	4.7		0.2	hyp
47			SO1127 hypothetical protein	ND	4.7		0.3	hyp
48			SO1779 decaheme cytochrome c (omcA)	2.9	2.7	0.6	0.4	cyt
49			SO1317 hypothetical protein	ND	4.5		0.5	hyp
50			SO2683 hypothetical protein	2.0	3.5	0.3	0.2	hyp
51			SO2407 conserved hypothetical protein	ND	4.4		0.3	hyp
52			SO0325 dsrE-related protein	4.4	ND	0.5		nrg
53			SO4057 met repressor (metJ)	ND	4.3		0.3	tr
54			SO1095 O-acetylhomoserine (thiol)-lyase, putative	2.0	3.3		0.5	tr
55			SO0263 heme exporter protein CcmA (ccmA)	2.0	3.3	0.3	0.1	cyt
56			SO3560 peptidase, M16 family	4.2	ND	1.1		tr
57			SO0324 conserved hypothetical protein	4.2	ND	0.8		hyp
58			SO4750 ATP synthase F1, delta subunit (atpH)	ND	4.2		0.1	tr
59			SO4649 conserved hypothetical protein	3.1	2.1	0.1	0.5	hyp
60			SO1430 anaerobic DMSO reductase, B subunit (dmsB-1)	ND	4.1		0.1	cyt
61			SO2883 conserved hypothetical protein	2.4	2.7	1.1	0.0	hyp
62			SO1287 conserved hypothetical protein	ND	4.1		0.3	hyp
63			SO1126 chaperone protein DnaJ (dnaJ)	ND	4.1		0.5	str
64			SO3842 conserved hypothetical protein	ND	4.0		0.2	hyp
65			SO1778 decaheme cytochrome c (omcB) or (mtrC)	2.4	2.6	0.5	0.1	cyt
66			SO3395 hypothetical protein	ND	3.9		0.2	hyp
67			SO4620 fumarate reductase, flavoprotein subunit precursor	ND	3.7		0.1	cyt
68			SO1274 conserved hypothetical protein	3.7	ND	0.4		hyp
69			SO1358 16S rRNA processing protein RimM (rimM)	ND	3.7		0.4	tr
70			SO2806 conserved hypothetical protein	3.7	ND	0.8		hyp
71			SO2016 heat shock protein HtpG (htpG)	ND	3.7		0.3	str
72			SO1605 lipoprotein, putative	ND	3.6		0.4	me
73			SO4403 hypothetical protein	ND	3.6		0.2	hyp
74			SO3940 ribosomal protein L13 (rplM)	ND	3.6		0.1	tr
75			SOA0060 acetyltransferase, GNAT family	ND	3.5	0.3	0.3	nrg
76			SO3066 conserved hypothetical protein	ND	3.5		0.2	hyp
77			SO3285 cytochrome d ubiquinol oxidase, subunit II (cydB)	ND	3.4		0.2	cyt
78			SO0065 molybdenum cofactor biosynthesis protein	ND	3.4		0.3	tr
79			SO3284 conserved hypothetical protein	ND	3.4		0.5	hyp
80			SO1429 anaerobic dimethyl sulfoxide reductase, A subunit (dmsA-1)	2.3	2.0	0.2	0.4	cyt
81			SO4157 DNA-binding response regulator	3.2	ND	0.7		tr
82			SO2419 2,4-dienoyl-CoA reductase, putative	3.2	ND	0.7		nrg
83			SO1112 bacterioferritin subunit 1 (bfr1)	ND	2.7		0.2	cyt

SI Table 2. Genes upregulated ($\geq 3x$) during Cr(VI) reduction after 14 and 34 minutes

(T1 and T2). The brighter the red color is, the greater the fold upregulation. The fold upregulation for both time points is shown on the right. ND refers to no data. Genes included in this list were upregulated $\geq 3x$ at either or both time points. The genes are listed in order of decreasing upregulation at either time point. The functions listed correspond to: cyt: cytochrome and heme synthesis; hyp: hypothetical; sec: secretion; me: membrane; str: stress; tr: transcription and translation; mot: motility; nrg: energy production.