SUPPLEMENTAL TABLE 1: DIFFERENTIALLY EXPRESSED OPEN-READING FRAMES ORGANIZED BY CLUSTERS OF ORTHOLOGOUS GROUPS

ANIMO ACID TRANSPORT AND METABOLISM

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0171	patB	1.09	1.83	hemolysin-related protein
DVU0291	potA	-0.88	1.49	ABC transporter, ATP-binding protein
DVU0388		0.63	1.12	amino acid ABC transporter, ATP-binding protein
DVU0462		1.10	1.72	chorismate mutase/prephenate dehydratase
DVU0463	aroA	0.75	1.19	3-phosphoshikimate 1-carboxyvinyltransferase
DVU0464		0.90	1.55	prephenate dehydrogenase
DVU0551	livF	-0.69	1.03	high-affinity branched-chain amino acid ABC transporter ATP-binding protein
DVU0626	ilvN-1	-0.69	1.21	acetolactate synthase, small subunit
DVU0671		0.86	1.39	conserved hypothetical protein
DVU0716	livF	-0.97	1.61	branched-chain amino acid ABC transporter, ATP-binding protein
DVU0738		-0.61	1.06	substrate-binding protein, putative
DVU0841		0.64	1.14	aspartate aminotransferase, putative
DVU1388		-0.92	1.41	conserved hypothetical protein
DVU1665	aroQ	-0.59	1.02	3-dehydroquinate dehydratase, type II
DVU1766	aspA	0.74	1.02	aspartate ammonia-lyase, putative
DVU1821	gltB	-0.78	1.30	glutamate synthase, large subunit
DVU1823	gltB-1	-0.77	1.11	glutamate synthase, iron-sulfur cluster-binding subunit, putative
DVU1878	ltaE	0.94	1.42	threonine aldolase, low-specificity
DVU2204	tnaA	-0.83	1.02	tryptophanase
DVU2297		-2.48	3.69	glycine/betaine/L-proline ABC transporter, periplasmic-binding protein
DVU2298	opuBB	-1.99	2.84	glycine/betaine/L-proline ABC transporter, permease protein
DVU2299	proV	-2.22	2.90	glycine/betaine/L-proline ABC transporter, ATP binding protein
DVU2340		-0.80	1.29	amino acid ABC transporter, permease protein, His/Glu/Gln/Arg/opine
DVU2342		-1.31	1.45	amino acid ABC transporter, periplasmic amino acid-binding protein
DVU2343	glnQ	-0.83	1.15	amino acid ABC transporter, ATP-binding protein
DVU2384		-2.44	2.50	ABC transporter, periplasmic substrate-binding protein
DVU2476	gltA	0.77	1.19	glutamate synthase, small subunit
DVU2540		1.06	1.26	lyase, putative
DVU2575		-0.63	1.05	peptidase, M20/M25/M40 family
DVU2741	livG	1.01	1.33	high-affinity branched chain amino acid ABC transporter, ATP-binding
DVU3121		-0.68	1.05	aminotransferase, class V
DVUA0063		1.68	1.59	Orn/DAP/Arg family decarboxylase

CARBOHYDRATE TRANSPORT AND METABOLISM

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0342		0.76	1.28	NAD-dependent epimerase/dehydratase family protein
DVU0343		0.56	1.01	HPCH/HPAI aldolase family protein
DVU0565	gap-1	-0.79	1.22	glyceraldehyde 3-phosphate dehydrogenase
DVU0632		0.75	1.33	cupin family protein
DVU2349		-0.82	1.51	carbohydrate phosphorylase family protein
DVU2822		0.74	1.02	TRAP dicarboxylate family transporter
DVU2935	gpm	-0.88	1.57	phosphoglycerate mutase
DVU3162		0.76	1.02	ABC transporter, periplasmic substrate-binding protein
DVU3214		0.68	1.14	phosphoenolpyruvate synthase-related protein
DVU3373	ilvD	0.93	1.73	dihydroxy-acid dehydratase
DVUA0096		1.99	1.00	major facilitator superfamily protein

CELL CYCLE CONTROL, CELL DIVISION, CHROMOSOME PARTITIONING

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU2109	mrp	-3.20	4.66	MTH1175-like domain family protein
DVU2330		-0.84	1.57	MRP family protein
DVU3374		0.69	1.25	permease, putative

CELL MOTILITY

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0049		1.08	1.88	OmpA family protein
DVU0302		-1.77	2.26	chemotaxis protein CheX, putative
DVU0312	fliG	0.77	1.22	flagellar motor switch protein FliG
DVU0315	flgC	2.82	4.30	flagellar basal-body rod protein FlgC
DVU0316	flgB	2.68	3.94	flagellar basal-body rod protein FlgB
DVU0520		0.60	1.10	flagellar hook-associated protein FlgL, putative
DVU0591	mcpD	-0.75	1.34	methyl-accepting chemotaxis protein
DVU0592	cheW-1	-0.92	1.60	chemotaxis protein CheW
DVU0806		-2.59	-3.01	chemotaxis protein CheY, putative
DVU1441	flaB1	0.68	1.23	flagellin
DVU1592		-1.47	2.51	arginine N-succinyltransferase, beta subunit, putative
DVU1594	cheA-1	-1.63	2.63	chemotaxis protein CheA
DVU1595	cheR-1	-0.79	1.45	chemotaxis protein methyltransferase
DVU1596	cheB-1	-1.00	1.85	protein-glutamate methylesterase CheB
DVU2074		-0.71	1.03	chemotaxis protein CheW
DVU2076	cheR-2	-0.65	1.08	chemotaxis protein methyltransferase
DVU2078	cheB-2	-0.74	1.23	protein-glutamate methylesterase CheB
DVU2444	flaB3	2.26	3.95	flagellin
DVU2585		-0.61	1.10	methyl-accepting chemotaxis protein
DVU2738		-0.94	1.44	methyl-accepting chemotaxis protein

CELL WALL/MEMBRANE/ENVELOPE BIOGENESIS

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0150		7.35	12.21	membrane protein, putative
DVU0437		0.81	1.25	efflux transporter, RND family, MFP subunit
DVU0677		-0.57	1.01	transglycosylase domain protein
DVU0698	rfbC	-1.19	2.19	dTDP-4-dehydrorhamnose 3,5-epimerase
DVU0925	rfbA	-0.90	1.60	glucose-1-phosphate thymidylyltransferase
DVU1214		0.60	1.07	dolichyl-phosphate-mannose-protein mannosyltransferase family protein
DVU1668	lolA	-0.62	1.05	outer membrane lipoprotein carrier protein, putative
DVU1892		-0.70	1.29	glycosyl transferase, group 2 family protein
DVU2336		0.81	1.26	carboxyl-terminal protease
DVU2371	amiA	-0.57	1.05	N-acetylmuramoyl-L-alanine amidase, putative
DVU2390		-2.34	3.23	TonB domain protein
DVU2655	dacA	0.75	1.17	D-alanyl-D-alanine carboxypeptidase family protein
DVU3013	dmt	0.61	1.04	glycosyl transferase, group 2 family protein
DVU3104	pal	0.78	1.36	peptidoglycan-associated lipoprotein, putative
DVU3246		-0.69	1.08	RND efflux system, outer membrane protein, NodT family
DVU3247		-0.90	1.12	efflux transporter, RND family, MFP subunit
DVUA0048		4.25	2.35	exopolysaccharide production protein, putative

COENZYME TRANSPORT AND METABOLISM

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0100		-0.64	1.07	TonB-dependent receptor

DVU0323	folD	0.58	1.06	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase
DVU0607	ahcY	-0.75	1.33	adenosylhomocysteinase
DVU0650		-2.56	2.85	chelatase, putative
DVU0745		-1.83	1.29	ABC transporter, periplasmic substrate-binding protein
DVU0951	moeA-2	-0.79	1.33	molybdopterin biosynthesis MoeA protein, putative
DVU1411	thiC	1.52	2.54	thiamine biosynthesis protein ThiC
DVU1765	thiH	1.17	1.12	thiH protein, putative
DVU2448	panC	-0.57	1.02	pantoate--beta-alanine ligase
DVU2449	metK	-0.84	1.51	S-adenosylmethionine synthetase
DVU2558	bioB	0.78	1.27	biotin synthase
DVU2564	bioF	-0.63	1.04	8-amino-7-oxononanoate synthase
DVU2798		-0.76	1.27	ApbE family protein
DVU2882	folC	-1.27	2.09	folylpolyglutamate synthase
DVU3279	cobT	-0.61	1.05	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
DVU3293		-0.75	1.19	thiamine pyrophosphate-requiring enzyme

DEFENSE MECHANISMS

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0126	b3486	1.25	1.52	ABC transporter, ATP-binding protein
DVU1017	rtxB	-0.76	1.28	ABC transporter, ATP-binding protein/permease protein
DVU1018	rtxD	-0.59	1.00	type I secretion membrane fusion protein, HlyD family
DVU2294		0.85	1.06	femAB family protein
DVU2380	atpX	-3.02	4.75	ABC transporter, ATP-binding protein
DVU2437		-1.06	1.62	ABC transporter, permease protein
DVU3248		-0.92	1.39	AcrB/AcrD/AcrF family protein
DVUA0023		2.60	1.37	ABC transporter, permease protein, putative

ENERGY PRODUCTION AND CONSERVATION

Gene #	*ID*	*log_2R*	*Absolute Z-score*	*Annotation*
DVU0019	ngr	0.82	1.39	nigerythrin
DVU0080	fumC	-0.63	1.04	fumarate hydratase, class II
DVU0172	phsB	0.67	1.06	thiosulfate reductase (phsB)
DVU0173	phsA	2.08	3.41	thiosulfate reductase
DVU0253		-1.21	1.97	oxidoreductase, FAD/iron-sulfur cluster-binding domain protein
DVU0381	nhaC-1	0.87	1.21	Na+/H+ antiporter NhaC
DVU0402	dsrA	0.94	1.56	dissimilatory sulfite reductase alpha subunit
DVU0403	dvsB	0.81	1.19	dissimilatory sulfite reductase beta subunit
DVU0531	hmcF	1.93	2.76	HmcF, 52.7 kd protein in hmc operon
DVU0534	hmcC	1.53	2.31	HmcC, 43.2 kd protein in hmc operon
DVU0535	hmcB	1.83	2.62	40.1 kd protein in hmc operon (HmcB)
DVU0627	ptB	-0.64	1.03	phosphotransbutyrylase
DVU0692		0.93	1.62	molybdopterin oxidoreductase, transmembrane subunit, putative
DVU0693	narH	0.77	1.24	molybdopterin oxidoreductase, iron-sulfur cluster-binding subunit, putative (TIGR), containing cytochrome c heme-binding site
DVU0694		0.98	1.73	molybdopterin oxidoreductase, molybdopterin-binding subunit, putative
DVU0701	glcB	-0.80	1.45	malate synthase G
DVU0774	atpC	0.74	1.21	ATP synthase, F1 epsilon subunit
DVU0775	atpD	0.92	1.53	ATP synthase, F1 beta subunit
DVU0778	atpH	0.85	1.33	ATP synthase, F1 delta subunit
DVU0847	ApsA	1.21	1.20	adenylyl-sulphate reductase, alpha subunit
DVU0849	QmoB	0.92	1.27	Quinone-interacting membrane-bound oxidoreductase
DVU0917	atpE	0.95	1.60	ATP synthase F0, C subunit
DVU0918	atpB	0.81	1.29	ATP synthase F0, A subunit
DVU1179	aor	1.93	1.91	aldehyde:ferredoxin oxidoreductase, tungsten-containing
DVU1423	lpdA	1.01	1.35	2-oxoglutarate dehydrogenase, E3 component, lipoamide dehydrogenase
DVU1636	ppaC	1.38	1.82	inorganic pyrophosphatase, manganese-dependent

DVU1770	hydB	2.06	1.54	periplasmic [Fe] hydrogenase, small subunit
DVU1782		-0.67	1.18	iron-sulfur cluster-binding protein
DVU1812	coxB	-0.69	1.17	cytochrome c oxidase, subunit II, putative
DVU1815		-0.71	1.24	cytochrome c oxidase, subunit I, putative
DVU1921	hynB-1	0.95	1.03	periplasmic [NiFe] hydrogenase, small subunit, isozyme 1
DVU1922	hynA-1	0.96	1.09	periplasmic [NiFe] hydrogenase, large subunit, isozyme 1
DVU1974		-0.61	1.04	pyridine nucleotide-disulfide oxidoreductase
DVU2042	hdrA	1.42	2.03	heterodisulfide reductase, A subunit
DVU2103		-1.09	1.81	iron-sulfur cluster-binding/ATPase domain protein
DVU2201	b3011	-1.00	1.82	alcohol dehydrogenase, iron-containing
DVU2272		0.90	1.55	formate acetyltransferase, putative
DVU2285		1.37	1.92	L-lactate permease family protein
DVU2286		1.59	2.49	hydrogenase, CooM subunit, putative
DVU2288		1.67	2.56	hydrogenase, CooL subunit, putative
DVU2289	b2488	1.45	2.38	hydrogenase, CooX subunit, putative
DVU2290		1.73	2.77	hydrogenase, CooU subunit, putative
DVU2291		1.27	2.07	carbon monoxide-induced hydrogenase CooH, putative
DVU2293	cooF	1.13	1.74	iron-sulfur protein CooF
DVU2318	rbr2	-1.09	1.36	rubrerythrin, putative
DVU2399		1.03	1.43	hydrogenase, putative
DVU2401		1.02	1.27	hydrogenase, iron-sulfur cluster-binding subunit, putative
DVU2403	hdrB	1.10	1.62	heterodisulfide reductase, B subunit
DVU2405		2.94	3.51	alcohol dehydrogenase, iron-containing
DVU2422		-0.93	1.61	nitroreductase family protein
DVU2451		0.81	1.13	L-lactate permease family protein
DVU2481	fdoH	-0.63	1.15	formate dehydrogenase, beta subunit, putative
DVU2680	fld	-5.19	6.67	flavodoxin, iron-repressed
DVU2683		0.63	1.08	L-lactate permease family protein
DVU2793		-0.59	1.05	electron transport complex protein RnfD, putative
DVU2794		-0.63	1.16	NADH:quinone oxidoreductase subunit RnfG
DVU3025	por	1.96	2.51	pyruvate-ferredoxin oxidoreductase
DVU3026		1.17	1.98	L-lactate permease family protein
DVU3041		-0.89	1.56	cytochrome c553
DVU3094	rbr	-1.15	1.44	rubrerythrin
DVU3134	glpK	-0.78	1.07	glycerol kinase

FUNCTION UNKNOWN

Gene #	*ID*	*log$_2$R*	*Absolute Z-score*	*Annotation*
DVU0077		-0.65	1.03	conserved hypothetical protein
DVU0147		5.76	9.79	lipoprotein, putative
DVU0186		-1.57	2.61	conserved hypothetical protein
DVU0308		1.72	2.39	membrane protein, putative
DVU0359		1.56	1.28	HesB-like domain
DVU0439		0.59	1.03	YCII-related domain protein
DVU0522	yviF	0.58	1.00	conserved hypothetical protein
DVU0573	creA	-0.78	1.33	creA protein
DVU0595		-0.60	1.07	conserved hypothetical protein
DVU0859		0.76	1.29	hypothetical protein
DVU0912		0.69	1.18	conserved domain protein
DVU0915		0.58	1.06	conserved hypothetical protein
DVU0943		1.12	1.91	membrane protein, putative
DVU1019		-0.61	1.10	conserved domain protein
DVU1087		-1.40	2.48	conserved hypothetical protein
DVU1239		0.79	1.36	membrane protein, putative
DVU1545		2.03	3.68	hemolysin-type calcium-binding repeat/calx-beta domain protein
DVU1601		-0.77	1.30	ATP-dependent Clp protease adaptor protein ClpS
DVU1618		-0.73	1.33	iojap-related protein
DVU1781		-1.27	2.19	conserved hypothetical protein
DVU1969		-0.77	1.20	hypothetical protein

DVU2108		-3.47	4.99	MTH1175-like domain family protein
DVU2259		-0.66	1.16	conserved hypothetical protein TIGR01033
DVU2398		1.39	1.77	conserved hypothetical protein
DVU2590		-0.67	1.10	sensory box protein
DVU2672		-1.08	1.89	membrane protein, putative
DVUA0061		1.51	1.36	membrane protein, putative

GENERAL FUNCTION PREDICTION ONLY

Gene #	*ID*	$\log_2 R$	*Absolute Z-score*	*Annotation*
DVU0132		0.83	1.38	membrane protein, putative
DVU0189		4.07	5.93	phage/plasmid primase, P4 family
DVU0197		2.52	3.87	phage portal protein, lambda family
DVU0338		0.82	1.39	hydrolase, haloacid dehalogenase-like family
DVU0367		-0.57	1.01	Ser/Thr protein phosphatase family protein
DVU0770		0.97	1.44	membrane protein, putative
DVU0886		-0.80	1.34	thioesterase family protein
DVU1062		-0.66	1.09	conserved hypothetical protein
DVU1258	glnN	1.13	1.74	glutamine synthetase, type III
DVU1294		0.71	1.07	conserved hypothetical protein
DVU1529		-1.08	1.92	decarboxylase family protein
DVU1664		-1.07	1.82	GTP-binding protein
DVU1768		1.15	1.61	GTP-binding protein
DVU1769	hydA	2.23	1.86	periplasmic [Fe] hydrogenase, large subunit
DVU1824		-0.61	1.04	conserved hypothetical protein
DVU1968		-0.62	1.09	oxidoreductase, putative
DVU2024		0.77	1.29	conserved hypothetical protein
DVU2058		0.88	1.27	HDIG domain protein
DVU2292	hypA	1.07	1.64	hydrogenase nickel insertion protein HypA
DVU2379	pqqL	-2.78	-4.19	peptidase, M16 family, putative
DVU2386	oppC	-1.05	1.46	ABC transporter, permease protein
DVU2421	dmpI	-1.04	1.83	4-oxalocrotonate tautomerase family protein
DVU2568	cpsA	-0.98	1.57	peptidase, M20/M25/M40 family
DVU2671		-0.67	1.18	HDIG/HD/KH domain protein
DVU2783		0.62	1.03	membrane protein, putative
DVU2838		-0.76	1.12	conserved hypothetical protein
DVU3295		-0.77	1.33	hemolysin III
DVUA0129	cas3	1.34	1.03	CRISPR-associated helicase Cas3 domain protein

INORGANIC ION TRANSPORT AND METABOLISM

Gene #	*ID*	$\log_2 R$	*Absolute Z-score*	*Annotation*
DVU0053		-0.85	1.43	sulfate permease, putative
DVU0164		-1.30	1.61	cation efflux family protein
DVU0177	modA	-1.95	1.85	molybdenum ABC transporter, periplasmic molybdenum-binding protein
DVU0180	modC	-1.10	1.23	ATP-binding component of molybdate ABC transporter
DVU0181	modB	-1.33	1.64	molybdenum ABC transporter, permease protein
DVU0647		-0.94	1.44	iron compound ABC transporter, periplasmic iron compount-binding protein, putative
DVU0648	fepC	-0.87	1.40	iron compound ABC transporter, ATP-binding protein
DVU0949		-0.86	1.38	conserved domain protein
DVU1058	nikM	-0.61	1.09	component of nickel ABC transport system
DVU1085	phoU	-0.70	1.18	phosphate transport system protein PhoU
DVU1295	sat	0.75	1.17	sulfate adenylyltransferase
DVU1340	zur	-0.70	1.00	Zinc uptake transcriptional regulator ZUR (Fur family)
DVU1342	znuB	-1.19	1.89	ATPase component of zinc ABC transporter
DVU1343	znuA	-1.19	1.56	periplasmic component of zinc ABC transporter
DVU2306		0.89	1.13	phosphate transporter family protein

DVU2324		-0.87	1.27	copper-translocating P-type ATPase
DVU2325	merP	-0.90	1.58	mercuric transport protein periplasmic component
DVU2462		-0.78	1.17	oligopeptide ABC transporter, permease protein
DVU2571	feoB	-4.71	6.36	ferrous iron transport protein B
DVU2572	feoA	-4.60	7.26	ferrous iron transport protein A
DVU2574	feoA	-2.00	2.59	ferrous iron transporter component feoA
DVU2617		-0.83	1.16	sodium/calcium exchanger family protein
DVU2752		1.84	1.92	rhodanese-like domain protein
DVU2776	dsrC	0.75	1.12	dissimilatory sulfite reductase, gamma subunit
DVU2800		-0.76	1.24	heavy metal translocating P-type ATPase
DVU3095	PerR	-0.79	1.04	peroxide-responsive regulator PerR
DVU3330		-4.66	6.70	hypothetical iron-regulated P-type ATPase
DVU3332		-2.15	3.38	heavy metal translocating P-type ATPase

INTRACELLULAR TRAFFICKING, SECRTION AND VESICULAR TRANSPORT

Gene #	*ID*	log_2R	*Absolute Z-score*	*Annotation*
DVU1013		-1.01	1.37	type I secretion outer membrane protein, TolC family
DVU1262	pilT-1	-0.99	1.62	twitching motility protein PilT
DVU1263	pppA	-1.06	1.71	type IV prepilin-like proteins leader peptidase
DVU2117		-1.20	1.90	membrane protein, putative
DVU2118		-0.88	1.16	conserved hypothetical protein
DVU2119	cpaC	-1.23	1.73	type II/III secretion system protein
DVU2124		-0.84	1.20	conserved hypothetical protein
DVU2388	tolQ-1	-1.34	2.14	tolQ protein
DVU2389	tolR	-2.00	2.50	biopolymer transport protein, ExbD/TolR family
DVU2871		1.46	1.53	minor capsid protein C
DVU2922	secE	0.78	1.21	preprotein translocase, SecE subunit
DVU3097		0.71	1.33	outer membrane efflux protein
DVUA0103	invX	1.35	1.13	type III secretion protein, HrpO family
DVUA0119	sctN	1.20	1.01	type III secretion system ATPase

LIPID TRANSPORT AND METABOLISM

Gene #	*ID*	log_2R	*Absolute Z-score*	*Annotation*
DVU1344	ispG	-0.65	1.16	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
DVU1846	pgsA	-0.73	1.21	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
DVU2250		-0.59	1.02	AMP-binding protein

NUCLEOTIDE TRANSPORT AND METABOLISM

Gene #	*ID*	log_2R	*Absolute Z-score*	*Annotation*
DVU1528		-0.83	1.50	cytidine/deoxycytidylate deaminase family protein
DVU1588	hpt	-0.59	1.03	hypoxanthine phosphoribosyltransferase
DVU2947		-0.68	1.17	anaerobic ribonucleoside-triphosphate reductase, putative

POSTRANSLATIONAL MODIFICATION, PROTEIN TURNOVER, CHAPERONES

Gene #	*ID*	log_2R	*Absolute Z-score*	*Annotation*
DVU0684	hflK	-0.84	1.50	hflK protein, putative
DVU0812	grpE	0.94	1.66	heat shock protein GrpE
DVU1228	tpX	-0.65	1.09	thiol peroxidase
DVU1334	tig	-0.81	1.42	trigger factor
DVU1337	lon	-0.59	1.06	ATP-dependent protease La
DVU1602	clpA	-0.84	1.52	ATP-dependent Clp protease, ATP-binding subunit ClpA
DVU1811		-0.85	1.39	protoheme IX farnesyltransferase, putative
DVU1849	pcm	-0.99	1.73	protein-L-isoaspartate O-methyltransferase

DVU1873	ppiB-2	-0.72	1.32	peptidyl-prolyl cis-trans isomerase B
DVU1874	clpB	-0.74	1.33	ATP-dependent Clp protease, ATP-binding subunit ClpB
DVU1876	dnaJ	-0.66	1.05	dnaJ protein, putative
DVU1976	groEL	-0.63	1.09	chaperonin, 60 kDa
DVU1977	groES	-0.73	1.27	chaperonin, 10 kDa
DVU2019		1.16	1.00	conserved hypothetical protein
DVU2247	ahpC	-2.70	3.64	alkyl hydroperoxide reductase C
DVU2271	pflA	-0.95	1.04	pyruvate formate-lyase activating enzyme, putative
DVU2407		0.86	1.24	conserved hypothetical protein
DVU2441	hspC	-2.33	3.67	heat shock protein, Hsp20 family
DVU2442		-2.25	3.32	heat shock protein, Hsp20 family
DVU3282		-1.24	1.96	ADP-ribosylglycohydrolase family protein

REPLICATION, RECOMBINATION AND REPAIR

Gene #	*ID*	*$\log_2 R$*	*Absolute Z-score*	*Annotation*
DVU0004	gyrA	-0.68	1.17	DNA gyrase, A subunit
DVU0070	yhaO	2.80	2.95	Ser/Thr protein phosphatase family protein
DVU1757		-0.90	1.50	site-specific recombinase, phage integrase family
DVU1795	hup-3	0.77	1.18	DNA-binding protein HU
DVU1899		0.73	1.17	DNA repair protein RecO, putative
DVU2197		-0.83	1.42	site-specific recombinase, phage integrase family

SECONDARY METABOLITES BIOSYNTHESIS, TRANSPORT AND CATABOLISM

Gene #	*ID*	*$\log_2 R$*	*Absolute Z-score*	*Annotation*
DVU0026		0.66	1.10	conserved hypothetical protein

SIGNAL TRANSDUCTION MECHANISMS

Gene #	*ID*	*$\log_2 R$*	*Absolute Z-score*	*Annotation*
DVU0089		-0.86	1.23	conserved hypothetical protein
DVU0144	rfaE	1.85	2.78	cytidyltransferase-related protein
DVU0145		5.61	10.29	response regulator
DVU0261		-0.62	1.02	universal stress protein family
DVU0344		3.00	4.70	methyl-accepting chemotaxis protein
DVU0423		-0.92	1.48	universal stress protein family
DVU0598		2.11	2.77	carbon starvation protein A, putative
DVU0599		1.65	2.82	carbon starvation protein A, putative
DVU0608		-1.23	1.47	methyl-accepting chemotaxis protein
DVU0622		1.09	1.55	sensor histidine kinase/response regulator
DVU0666		0.97	1.66	HD domain protein
DVU0668		-0.99	1.70	methyl-accepting chemotaxis protein
DVU0700		-0.66	1.08	methyl-accepting chemotaxis protein
DVU0722		-0.71	1.11	response regulator
DVU0763	gdp	-1.91	3.08	GGDEF domain protein
DVU1020		-0.98	1.68	HD domain/sensory box protein
DVU1747		-0.70	1.18	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein
DVU2067		1.11	1.53	GGDEF domain protein
DVU2114	atoC	-1.30	2.05	sigma-54 dependent transcriptional regulator/response regulator
DVU2394	ntrC1	0.92	1.23	sigma-54 dependent transcriptional regulator/response regulator
DVU2615		-0.90	1.45	bacterial extracellular solute-binding protein, family 3
DVU2675		-1.26	1.88	DNA-binding response regulator, LuxR family
DVU2679		-1.05	1.75	sensory box histidine kinase/response regulator
DVU2954		-0.69	1.12	GGDEF domain protein
DVU3021		-2.66	3.18	HDIG domain protein
DVU3023	atoC	1.15	1.47	sigma-54 dependent DNA-binding response regulator

DVU3035		-1.72	2.58	methyl-accepting chemotaxis protein, putative
DVU3266		-2.17	2.81	conserved hypothetical protein
DVU3269		-0.98	1.68	sensory box histidine kinase/response regulator

TRANSCRIPTION

Gene #	*ID*	log_2R	*Absolute Z-score*	*Annotation*
DVU0529	rrf2	1.64	2.41	Rrf2 protein
DVU0530	rrf1	2.06	2.78	Rrf1 protein
DVU0682		1.49	1.92	DNA-binding protein, putative
DVU1571	rho	-0.96	1.70	transcription termination factor Rho
DVU1645		-0.75	1.11	transcriptional regulator, ArsR family
DVU1690		-0.69	1.08	transcriptional regulator, TetR family
DVU1760		1.65	2.23	transcriptional regulator, TetR family
DVU2111		-0.56	1.03	transcriptional regulator, LysR family
DVU2246		-0.69	1.28	S1 RNA binding domain protein
DVU2364		0.96	1.34	aminotransferase, classes I and II
DVU2378	foxR	-3.50	5.75	transcriptional regulator, AraC family
DVU2423		-1.00	1.57	transcriptional regulator, putative
DVU2686		-0.81	1.53	peptidase, S24 family
DVU2799		-0.96	1.66	transcriptional regulator, MarR family
DVU2827		-1.02	1.61	sigma-54 dependent transcriptional regulator
DVU2923	nusG	0.71	1.17	transcription antitermination protein NusG
DVU2988	pspA	-0.95	1.55	phage shock protein A
DVU3080		-1.25	1.48	transcriptional regulator, putative
DVU3131		-1.07	1.36	transcriptional regulator, putative
DVU3245	greA	-0.96	1.57	transcription elongation factor GreA
DVUA0086		2.05	1.59	response regulator

TRANSLATION, RIBOSOMAL STRUCTURE AND BIOGENESIS

Gene #	*ID*	log_2R	*Absolute Z-score*	*Annotation*
DVU0500	selB	-0.64	1.07	selenocysteine-specific translation elongation factor
DVU0958	rplI	0.63	1.12	ribosomal protein L9
DVU1248	argS	-0.59	1.09	arginyl-tRNA synthetase
DVU1315	rplE	0.74	1.32	ribosomal protein L5
DVU1322	rplO	0.67	1.10	ribosomal protein L15
DVU1666	efp	-0.83	1.42	translation elongation factor P
DVU2518	rplM	-0.62	1.10	ribosomal protein L13
DVU2536	rpmI	-0.61	1.07	ribosomal protein L35
DVU2920	tuf	0.59	1.04	translation elongation factor Tu
DVU2921	rpmG	0.84	1.44	ribosomal protein L33
DVU2927	rplL	0.68	1.22	ribosomal protein L7/L12

SUPPLEMENTAL TABLE 2: TOP 30 UP- AND DOWN-REGULATED OPEN READING FRAMES

UP-REGULATED

Gene #	ID	$\log_2 R$	Z-score	Annotation
DVU0150		7.35	12.21	membrane protein, putative
DVU0147		5.76	9.79	lipoprotein, putative
DVU0145		5.61	10.29	response regulator
DVUA0048		4.25	2.35	exopolysaccharide production protein, putative
DVU0189		4.07	5.93	phage/plasmid primase, P4 family
DVU0146		3.46	5.94	hypothetical protein
DVU2652		3.07	4.67	hypothetical protein
DVU0344		3.00	4.70	methyl-accepting chemotaxis protein
DVU2405		2.94	3.51	alcohol dehydrogenase, iron-containing
DVU0315	flgC	2.82	4.30	flagellar basal-body rod protein FlgC
DVU0070	yhaO	2.80	2.95	Ser/Thr protein phosphatase family protein
DVU0316	flgB	2.68	3.94	flagellar basal-body rod protein FlgB
DVUA0023		2.60	1.37	ABC transporter, permease protein, putative
DVU2445		2.58	4.42	hypothetical protein
DVU0197		2.52	3.87	phage portal protein, lambda family
DVU2444	flaB3	2.26	3.95	flagellin
DVU1769	hydA	2.23	1.86	periplasmic [Fe] hydrogenase, large subunit
DVU0536	hmcA	2.22	2.85	high-molecular weight cytochrome c
DVUA0085		2.18	1.38	conserved hypothetical protein
DVU0598		2.11	2.77	carbon starvation protein A, putative
DVU0644		2.11	3.00	hypothetical protein
DVU0173	phsA	2.08	3.41	thiosulfate reductase
DVU0530	rrf1	2.06	2.89	Rrf1 protein
DVU1770	hydB	2.06	1.54	periplasmic [Fe] hydrogenase, small subunit
DVUA0086		2.05	1.59	response regulator
DVU1545		2.03	3.68	hemolysin-type calcium-binding repeat/calx-beta domain protein
DVUA0096		1.99	1.00	major facilitator superfamily protein
DVU3025	por	1.96	2.51	pyruvate-ferredoxin oxidoreductase
DVU1178		1.94	1.93	hypothetical protein
DVU0531	hmcF	1.93	2.76	HmcF, 52.7 kd protein in hmc operon

DOWN-REGULATED

Gene #	ID	$\log_2 R$	Z-score	Annotation
DVU2681		-5.33	7.58	hypothetical protein
DVU0303		-5.29	5.10	hypothetical protein
DVU2680	fld	-5.19	6.67	flavodoxin, iron-repressed
DVU0273		-4.97	7.89	conserved hypothetical protein
DVU2571	feoB	-4.71	6.36	ferrous iron transport protein B
DVU3330		-4.66	6.70	hypothetical iron-regulated P-type ATPase
DVU2572	feoA	-4.60	7.26	ferrous iron transport protein A
DVU2383		-4.37	6.14	tonB dependent receptor domain protein
DVU3331		-3.89	5.51	hypothetical protein

DVU0304		-3.67	2.44	hypothetical protein
DVU2381		-3.67	5.37	conserved hypothetical protein
DVU2378	foxR	-3.50	5.75	transcriptional regulator, AraC family
DVU2108		-3.47	4.99	MTH1175-like domain family protein
DVU2109	mrp	-3.20	4.66	MTH1175-like domain family protein
DVU3333		-3.11	5.06	hypothetical protein
DVU2380	atpX	-3.02	4.75	ABC transporter, ATP-binding protein
DVU3329		-3.00	5.08	hypothetical protein
DVU2573		-2.91	4.83	hypothetical protein
DVU0822		-2.89	2.21	hypothetical protein
DVU2379	pqqL	-2.78	4.19	peptidase, M16 family, putative
DVU2382		-2.74	4.35	conserved domain protein
DVU0805		-2.73	3.21	hypothetical protein
DVU2247	ahpC	-2.70	3.64	alkyl hydroperoxide reductase C
DVU3021		-2.66	3.18	HDIG domain protein
DVU0806		-2.59	3.01	chemotaxis protein CheY, putative
DVU0650		-2.56	2.85	chelatase, putative
DVU0821		-2.53	2.05	conserved hypothetical protein
DVU2297		-2.48	3.69	glycine/betaine/L-proline ABC transporter, periplasmic-binding protein
DVU2384		-2.44	2.50	ABC transporter, periplasmic substrate-binding protein
DVU2390		-2.34	3.23	TonB domain protein