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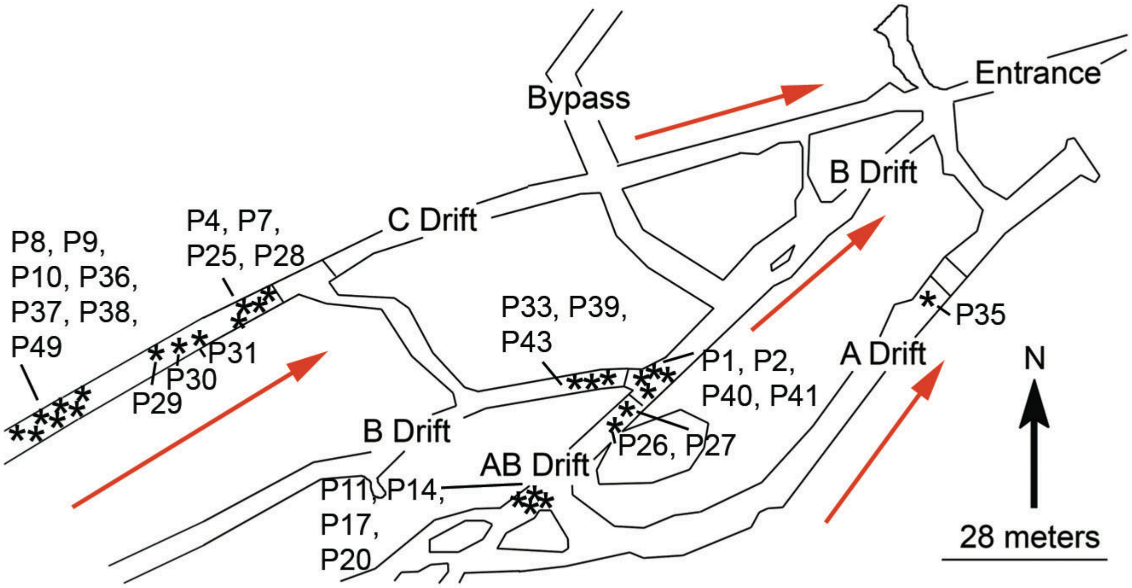
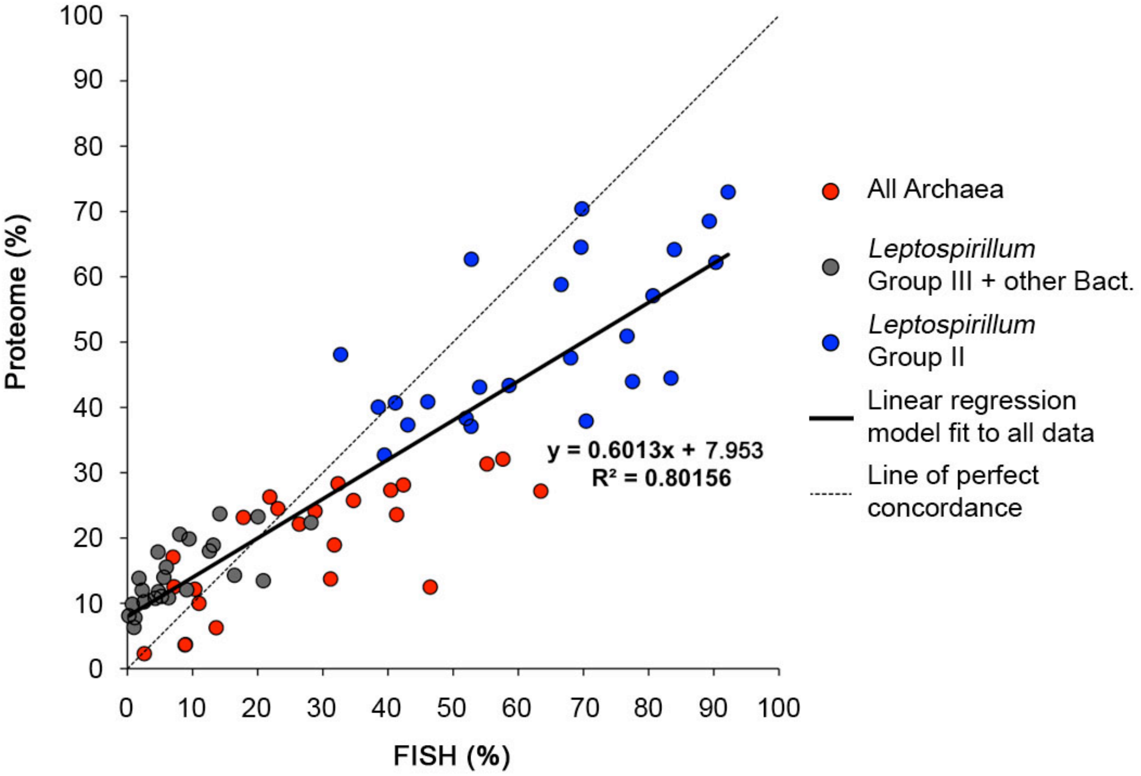
Figure S1



Map of Richmond Mine. Asterisks note collection sites for each sample and red arrows represent the direction of flow through the mine.

Figure S2



Pair-wise Scatter Plot of FISH Relative Abundance Data Versus Proteomic Relative Abundance Data Proteomic relative abundance data is based on the percentage of total proteins identified in a given sample summed for an organism (e.g summed NSAF values for *Leptospirillum* Group II) or across an organismal group (e.g. summed NSAF values for all Archaea). Dashed line of perfect concordance represents a 1:1 fit of the two data sets to each other.

Figure S3A

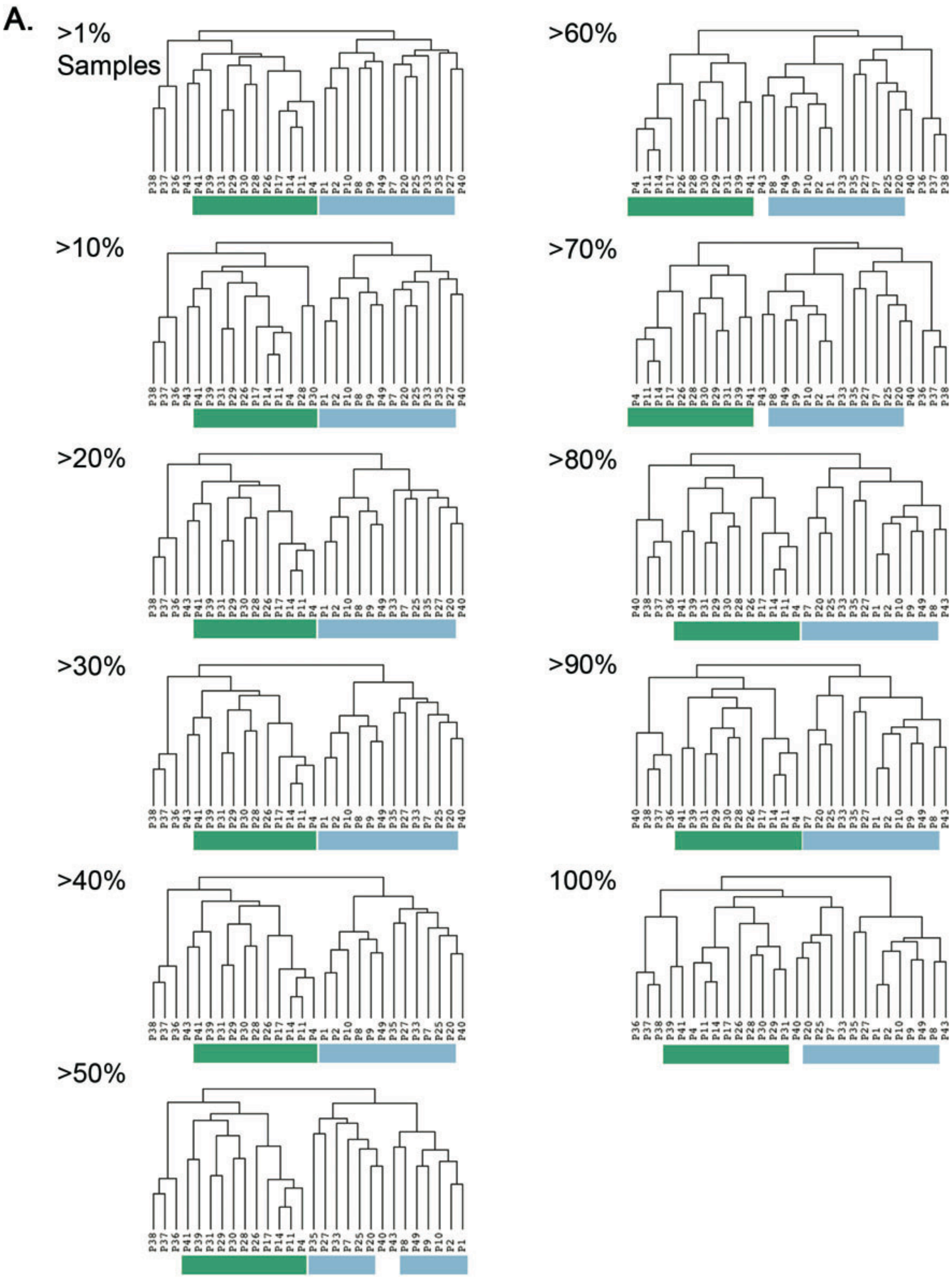
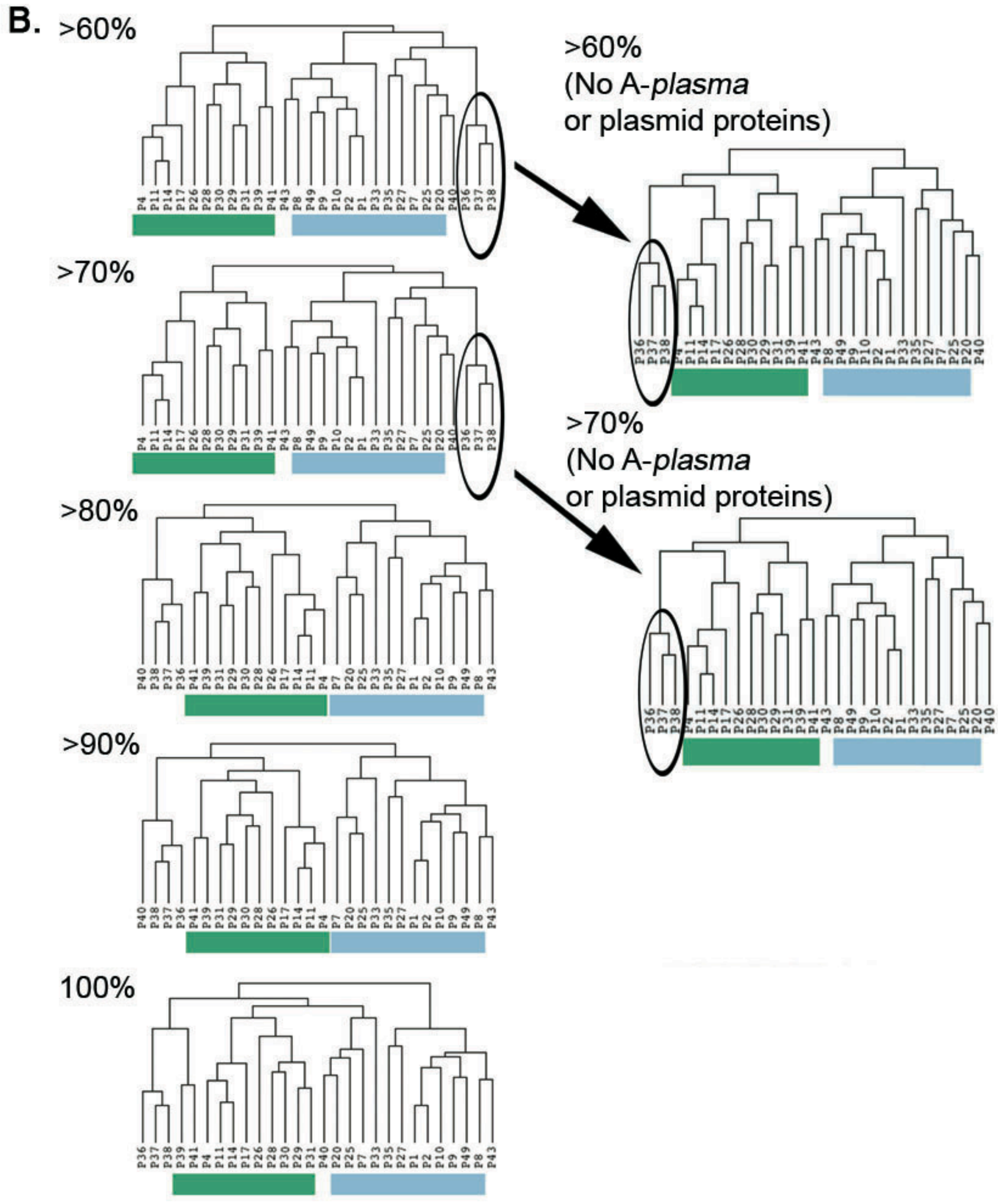
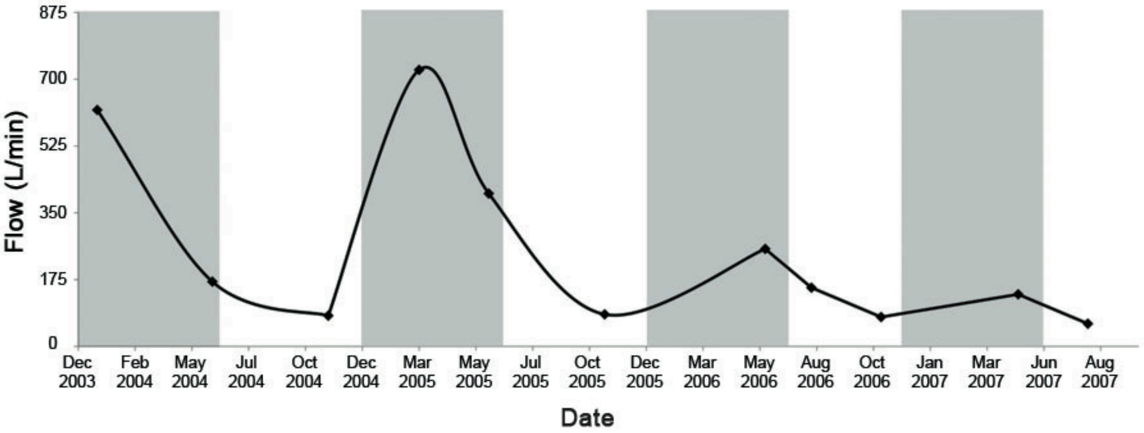


Figure S3B



Hierarchical Clustering of Samples Using Defined Subsets of Proteins From Whole-community Proteomes A. Un-centered, average linkage clustering of proteome samples based on Pearson correlation metric using subsets of protein abundance data. ***B.*** Un-centered, average linkage clustering of proteome samples based on Pearson correlation metric using subsets of protein abundance data that do not include proteins from the plasmid or A-*plasma* category. When A-*plasma* and plasmid proteins are removed from the analysis the inconsistent samples (P36, P37 and P38) group back with the green expression group.

Figure S4



Values of Flow Across all Sampling Dates Values represent total outflow of the AMD solution on the day of sampling and are consistently highest during the rainy months of the year (Dec. – Jun. represented by shaded rectangles), reflecting seasonal precipitation rates.

Table S1. Environmental Data Collected for Each Biofilm Sample*

Sample	Full name	Site	Flow (L/min)	pH	Temp (°C)	Cond (mS/cm)	Fe^{2+}(M)	FeT (M)	Cu (mM)	As (mM)	Zn (mM)
P1	ABmuckGS2 Nov06	1.50	83.3	0.84	43.0	85.1	0.278	0.328	1.06	0.39	27.44
P2	ABmuck friable Nov06	1.50	83.3	0.84	43.0	85.1	0.278	0.328	1.06	0.39	27.44
P4	C10m GS1 Nov2006	2.50	83.3	1.01	39.5	56.3	0.145	0.218	1.98	0.32	18.50
P7	C10m GS2 Nov2006	2.50	83.3	1.01	39.5	56.3	0.145	0.218	1.98	0.32	18.50
P8	C75m GS1 Nov2006	3.00	83.3	1.18	42.7	49.2	0.131	0.175	1.75	0.28	14.78
P9	C75m GS1 Aug2006	3.00	166.6	1.00	43.0	57.9	0.226	0.283	2.57	0.31	16.74
P10	C75m GS1 Jun2006	3.00	276.3	0.70	43.0	70.5	0.263	0.303	4.12	0.37	21.17
P11	AB drift GS0 Jun2006	1.25	276.3	0.72	36.0	**ND**	0.238	0.285	**ND**	**ND**	ND
P14	AB drift GS1 Jun2006	1.25	276.3	0.72	36.0	**ND**	0.238	0.285	**ND**	**ND**	ND
P17	AB drift GS1.5 Jun2006	1.25	276.3	0.72	36.0	**ND**	0.238	0.285	**ND**	**ND**	ND
P20	AB drift GS2*** Jun2006	1.25	276.3	0.72	36.0	**ND**	0.238	0.285	**ND**	**ND**	ND
P25	C drift +8m GS1 Rep3 Aug06	2.50	166.6	0.92	39.3	65.2	0.227	0.281	2.80	0.37	20.79
P26	AB end GS0 Jan04	1.25	670.0	1.07	43.3	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P27	AB front GS3 Jun04	1.25	183.6	0.99	39.0	48.5	**ND**	**ND**	**ND**	**ND**	**ND**
P28	C drift +8m GS1-2 Nov2005	2.50	90.8	0.50	40.0	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P29	UBC level1 Nov2004	2.50	87.1	**ND**	41.0	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P30	UBC level2 Nov2004	2.50	87.1	**ND**	41.0	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P31	UBC level3 Nov2004	2.50	87.1	**ND**	41.0	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P33	B drift +5m level 1-2 Mar2005	1.75	783.6	0.93	42.0	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P35	UBA Jun05	-3.00	433.2	1.10	41.0	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P36	C75m GS1 May07	3.00	147.6	1.17	44.4	43.5	0.093	0.122	1.54	0.24	9.83
P37	C75m GS1.5 May07	3.00	147.6	1.17	44.4	43.5	0.093	0.122	1.54	0.24	9.83
P38	C75m GS1 cell-like May07	3.00	147.6	1.17	44.4	43.5	0.093	0.122	1.54	0.24	9.83
P39	B+1m GS1 May07	1.75	147.6	0.99	46.0	58.9	0.140	0.165	0.45	0.26	12.30
P40	ABmuck GS2 May07	1.50	147.6	1.00	41.0	55.8	0.136	0.156	0.49	0.27	12.91
P41	ABmuck GS1(patchy) Aug07	1.50	64.4	0.83	37.1	75.3	0.181	0.224	0.47	0.36	20.03
P43	B+1m GS1- Aug07	1.75	64.4	0.87	43.0	81.0	0.200	0.221	0.45	0.34	19.65
P49	C75m GS1+ cell-like Aug2007	3.00	64.4	1.12	40.2	48.8	0.118	0.131	1.21	0.28	12.64
Average		-	196	0.93	40.9	60.3	0.185	0.227	1.56	0.31	17.02
Standard Deviation		-	176	0.18	2.8	14.4	0.064	0.072	1.00	0.05	5.70

Table S1. Continued

Sample	Ca (mM)	SO_4^{2-}(M)	NO_3^- (nM)	NO_2^- (nM)	CS
P1	5.42	0.298	120	15	22.82
P2	5.42	0.252	120	15	17.70
P4	6.89	0.252	69	22	1.00
P7	6.89	0.252	69	22	17.90
P8	6.81	0.350	155	28	18.06
P9	6.97	0.352	104	< 5	18.16
P10	7.22	0.361	342	24	17.81
P11	ND	0.522	**ND**	**ND**	1.93
P14	ND	0.636	**ND**	**ND**	6.27
P17	ND	0.417	**ND**	**ND**	6.27
P20	ND	0.417	**ND**	**ND**	17.55
P25	7.09	0.529	48	< 5	4.24
P26	**ND**	0.454	**ND**	**ND**	1.45
P27	**ND**	**ND**	**ND**	**ND**	22.82
P28	**ND**	**ND**	**ND**	**ND**	**ND**
P29	**ND**	**ND**	**ND**	**ND**	6.16
P30	**ND**	**ND**	**ND**	**ND**	4.14
P31	**ND**	0.619	**ND**	**ND**	22.81
P33	**ND**	0.616	**ND**	**ND**	22.81
P35	**ND**	0.616	**ND**	**ND**	**ND**
P36	8.55	**ND**	1680	< 5	1.93
P37	8.55	**ND**	1680	< 5	**ND**
P38	8.55	**ND**	1680	10	**ND**
P39	7.36	**ND**	**ND**	**ND**	4.24
P40	7.95	**ND**	420	10	17.66
P41	6.59	**ND**	190	10	1.45
P43	6.39	**ND**	**ND**	20	18.16
P49	7.82	**ND**	210	< 10	17.81
AVG	7.15	0.434	492	18	-
STDEV	0.97	0.141	652	7	-

*** Values and abbreviations are reported as follows:**

Site - Quantitative measure of collection site based on sampling location within the mine (See materials and methods - sample collection and metadata measurements subsection)

Flow - Solution discharge rates from the mine on the day of each sample's collection

pH - in situ pH

Temp - Temperature

Cond - Conductivity

Fe^{2+} - Iron (II) concentration

FeT - Iron (II) + Iron (III) concentration

Cu - Copper concentration

As - Arsenic concentration

Zn - Zinc concentration

Ca - Calcium concentration

SO_4^{2-} - sulfate concentration

NO_3^- - Nitrate concentration

NO_2^- - Nitrite concentration

CS - Quantitative measure of community structure based on the branch lengths from the clustering of FISH data in Figure 1B

ND - Not Determined

Table S2. Community Structure Data Based on FISH Data

Sample	**Archaea (%)**	***Lepto*. Gp. III (%)**	***Lepto.* Gp. II (%)**	***Lepto*. Gp II strains (UBA%/5-way%)**
P1[a,b]	32.32	9.10	58.58	(10.31/48.27)
P2[a]	63.45	1.15	32.72	(31.11/1.61)
P4	10.98	4.27	83.94	(83.41/0.53)
P7[a]	41.32	12.59	46.1	(38.81/7.29)
P8[a]	34.69	13.18	51.98	(51.98/0.01)
P9[a]	42.36	4.76	52.75	(51.51/1.24)
P10[a]	57.63	1.00	41.12	(40.61/0.51)
P11	2.59	5.22	92.2	(89.38/2.82)
P14	8.84	20.86	69.76	(49.99/19.77)
P17	13.62	16.43	69.61	(55.63/13.99)
P20[a,b]	40.42	20.04	39.44	(14.82/24.63)
P25[a]	17.79	4.69	77.52	(75.79/1.73)
P26	8.92	1.77	89.31	(89.18/0.13)
P27[a,b]	31.76	14.18	54.06	(6.02/48.04)
P28	**ND**[c]	**ND**	**ND**	**ND**
P29	10.35	5.97	80.67	(48.92/31.75)
P30	26.38	5.59	68.03	(57.10/10.93)
P31[b]	31.18	2.26	66.56	(4.16/62.40)
P33[a,b]	21.85	8.04	70.41	(14.22/56.19)
P35[a]	**ND**	**ND**	**ND**	**ND**
P36	7.00	9.46	83.43	(83.43/0.00)
P37	**ND**	**ND**	**ND**	**ND**
P38	**ND**	**ND**	**ND**	**ND**
P39	23.11	0.21	76.69	(76.69/0.00)
P40	28.79	28.18	43.03	(41.59/1.44)
P41	7.14	2.55	90.31	(88.79/1.52)
P43	46.47	0.74	52.78	(52.71/0.08)
P49[a]	55.19	6.31	38.5	(38.50/0.00)

[a] Designated as high developmental stage samples.

[b] Have a greater percentage of counted cells from the 5-way strain of *Leptospirillum* Group II than the UBA strain.

[c] Not Determined

Table S3. Proteome Composition Data Using Species-assigned Protein Counts

Organism	P1	P2	P4	P7	P8	P9	P10	P11	P14	P17	P20	P25	P26	P27	P28
Lepto. Gp. II	1006	1097	1187	1069	1149	1083	993	1210	1166	1061	900	1012	1223	922	1085
Unassigned	372	363	269	435	505	599	453	222	198	232	446	339	231	293	373
Lepto. Gp. III	257	154	172	438	543	324	135	152	202	213	610	383	221	488	225
G-*plasma*	413	344	86	300	309	244	435	9	28	58	320	245	25	249	292
A-*plasma*	49	118	52	125	287	401	178	5	9	16	92	57	16	23	110
Ferro. Type II	74	59	14	72	58	63	48	4	5	9	143	116	5	46	39
E-*plasma*	44	40	12	51	43	48	54	5	6	8	44	31	8	22	43
Ferro. Type I	54	40	11	41	40	39	33	5	7	6	131	68	7	54	28
Plasmid	5	22	6	24	4	61	52	3	6	11	13	5	15	11	11
I-*plasma*	17	15	9	17	20	22	27	5	2	4	19	12	3	7	18
Actino. 2	13	10	13	15	13	9	9	14	8	9	13	12	10	6	10
Actino. 1	8	7	10	10	9	9	8	11	8	9	12	12	7	8	10
ARMAN2	6	4	1	11	15	4	8	5	3	2	3	4	2	4	6
Firmicutes sp.	2	7	4	8	2	2	2	6	5	4	5	4	9	5	3
Virus	0	1	4	0	1	11	5	2	3	2	1	2	3	1	1
Total	**2320**	**2281**	**1850**	**2616**	**2998**	**2919**	**2440**	**1658**	**1656**	**1644**	**2752**	**2302**	**1785**	**2139**	**2254**

Table S3. Continued

Organism	P29	P30	P31	P33	P35	P36	P37	P38	P39	P40	P41	P43	P49	Total	AVG	STDEV
Lepto. Gp. II	1014	1045	994	1139	1070	1037	950	890	1000	788	1052	1270	878	1684	1046	113
Unassigned	265	354	256	445	386	388	298	349	323	318	245	295	366	1350	344	94
Lepto. Gp. III	257	284	178	588	675	442	263	305	132	456	149	168	216	976	308	160
G-*plasma*	102	264	151	345	60	119	95	115	255	328	127	138	266	639	204	124
A-*plasma*	33	129	27	46	66	196	228	243	117	89	37	51	203	509	107	97
Ferro. Type II	37	25	18	132	19	21	15	21	31	28	12	20	32	259	42	37
E-*plasma*	15	32	19	50	144	29	22	31	36	28	13	20	107	231	36	30
Ferro. Type I	19	19	12	192	9	16	9	21	27	19	16	13	21	248	34	40
Plasmid	2	3	1	8	36	43	27	31	0	21	2	5	21	86	16	16
I-*plasma*	9	13	4	21	14	15	12	14	12	14	7	10	18	90	13	6
Actino. 2	9	10	11	14	14	9	6	6	12	6	11	17	11	45	11	3
Actino. 1	7	7	11	11	11	9	5	6	11	9	9	11	8	45	9	2
ARMAN2	1	4	1	4	14	2	5	8	3	3	0	1	40	71	6	8
Firmicutes sp.	3	6	3	5	5	3	2	3	4	1	4	4	3	30	4	2
Virus	3	1	4	5	4	2	1	2	1	3	7	3	2	33	3	2
Total	**1776**	**2196**	**1690**	**3005**	**2527**	**2331**	**1938**	**2045**	**1964**	**2111**	**1691**	**2026**	**2192**	**6296**	**2182**	**411**

Table S4. ***Leptospirillum*** **Group II Proteins Demonstrating Significant Abundance Differences Between Biofilm Developmental Stages**

Protein ID	d-score	*Q*-value	Expression Ratio (LowDS/HighDS)	Annotation
Amino Acid Biosynthesis				
UBAL2_80620197	3.47	0.004	0.378	Amino-acid N-acetyltransferase (EC 2.3.1.1)
UBAL2_85240200	3.85	0.002	0.467	Aspartate aminotransferase (EC 2.6.1.17)
UBAL2_82410602	2.57	0.019	0.476	Alanine racemase (EC 5.1.1.1)
UBAL2_80620363	3.00	0.009	0.524	Histidinol-phosphate aminotransferase (EC 2.6.1.9)
UBAL2_85240093	4.55	0.001	0.538	GTP pyrophosphokinase (EC 2.7.6.5)
UBAL2_81350085	3.19	0.007	0.539	Prephenate dehydrogenase (EC 1.3.1.12)
UBAL2_82410105	2.78	0.014	0.561	Cystathionine gamma-synthase (EC 2.5.1.48)
UBAL2_80490024	3.11	0.008	0.595	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)
UBAL2_82410230	3.67	0.003	0.610	Glycine dehydrogenase (Decarboxylating) subunit 1 (EC 1.4.4.2)
UBAL2_80620364	4.84	0.000	0.638	Histidinol dehydrogenase (EC 1.1.1.23) (HDH)
UBAL2_80490236	3.20	0.007	0.643	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)
UBAL2_82410307	4.13	0.001	0.643	Branched-chain amino acid aminotransferase (EC 2.6.1.42)
UBAL2_82410631	4.39	0.001	0.666	Acetylornithine aminotransferase (EC 2.6.1.11)
UBAL2_81350083	4.73	0.001	0.670	Prephenate dehydratase (EC 4.2.1.51)
UBAL2_82410317	2.66	0.017	0.671	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)
UBAL2_85240207	5.53	0.000	0.672	2-isopropylmalate synthase (EC 2.3.3.13)
UBAL2_85240183	4.36	0.001	0.675	Aspartate aminotransferase (EC 2.6.1.1)
UBAL2_82410621	2.12	0.042	0.685	Putative Ppx/GppA phosphatase family protein
UBAL2_82410182	6.19	0.000	0.686	Aspartate aminotransferase (EC 2.6.1.1)
UBAL2_80490034	6.36	0.000	0.688	Glutamate synthase, small subunit (EC 1.4.1.13)
UBAL2_82410633	5.35	0.000	0.695	Argininosuccinate synthase (EC 6.3.4.5)
UBAL2_81350079	2.07	0.045	0.703	Glycine oxidase (ThiO)
UBAL2_82410247	4.81	0.001	0.709	Diaminopimelate epimerase (EC 5.1.1.7)
UBAL2_82410596	3.85	0.002	0.712	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)
UBAL2_79310335	2.66	0.017	0.718	Glutamate decarboxylase (EC 4.1.1.15)
UBAL2_81350101	4.97	0.000	0.724	Glutamate synthase [NADPH] large subunit (EC 1.4.1.13)
UBAL2_80270006	4.25	0.001	0.730	Spermidine synthase (EC 2.5.1.16)
UBAL2_82410318	2.23	0.035	0.733	Glutamate 5-kinase (EC 2.7.2.11)
UBAL2_79310071	3.50	0.004	0.740	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)
UBAL2_80490151	2.77	0.014	0.748	Dihydroxy-acid dehydratase (EC 4.2.1.9)

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_82410616	4.76	0.001	0.749	Glycine hydroxymethyltransferase (EC 2.1.2.1)
UBAL2_82410232	2.88	0.012	0.752	Glycine cleavage system T protein (EC 2.1.2.10)
UBAL2_82410229	4.20	0.001	0.753	Glycine dehydrogenase (Decarboxylating) subunit 2 (EC 1.4.4.2)
UBAL2_82410567	3.57	0.003	0.758	Putative aminomethyltransferase
UBAL2_80620359	2.85	0.012	0.760	Histidine biosynthesis protein (HisF) (EC 5.3.1.16)
UBAL2_82410450	4.46	0.001	0.761	Acetolactate synthase, large subunit (EC 2.2.1.6)
UBAL2_80490027	4.19	0.001	0.762	Tryptophan synthase, beta subunit (EC 4.2.1.20)
UBAL2_85240202	4.09	0.001	0.774	Homoserine dehydrogenase (EC 1.1.1.3)
UBAL2_79310208	3.37	0.005	0.774	Adenosylhomocysteinase (EC 3.3.1.1)
UBAL2_79310343	3.21	0.007	0.776	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
UBAL2_86920006	3.97	0.002	0.782	Dihydroxy-acid dehydratase (EC 4.2.1.9)
UBAL2_81350042	3.38	0.005	0.782	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)
UBAL2_81350062	6.85	0.000	0.783	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
UBAL2_80490070	3.88	0.002	0.785	Glutamine synthetase, type I (EC 6.3.1.2)
UBAL2_79310227	2.44	0.024	0.792	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)
UBAL2_85240203	3.30	0.006	0.800	Threonine synthase (EC 4.2.3.1)
UBAL2_81350063	3.78	0.002	0.812	Serine--glyoxylate transaminase (EC 2.6.1.45)
UBAL2_80270041	2.59	0.019	0.817	3-dehydroquinate synthetase (EC 4.2.3.4)
UBAL2_82410006	2.83	0.013	0.817	Cysteine desulfurase (EC 2.8.1.7)
UBAL2_79310204	2.99	0.010	0.817	Threonine synthase (EC 4.2.3.1)
UBAL2_79310206	1.97	0.052	0.851	Cysteine synthase (EC 2.5.1.47)
UBAL2_82410456	3.21	0.007	0.862	3-isopropylmalate dehydrogenase (EC 1.1.1.85)
UBAL2_81350084	3.48	0.004	0.866	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 2 (EC 2.5.1.54)
UBAL2_82410452	3.06	0.008	0.869	Acetohydroxy acid isomeroreductase (EC 1.1.1.86)
UBAL2_82410637	2.58	0.019	0.879	Dihydrodipicolinate synthase (EC 4.2.1.52)
UBAL2_81350093	2.49	0.022	0.898	Putative methylenetetrahydrofolate reductase
UBAL2_80270007	-6.32	0.000	5.003	Putative S-adenosylmethionine decarboxylase
UBAL2_80490025	-2.61	0.018	8.360	Indole-3-glycerol phosphate synthase (EC 4.1.1.48)
UBAL2_80620013	-3.97	0.002	Inf	Lysine 2,3-aminomutase
Cell Division				
UBAL2_79310231	2.69	0.016	0.799	Cell division protein (FtsA)
UBAL2_82410495	-4.61	0.001	1.274	ParB-like partition protein

Table S4. Continued

Protein ID	d-score	*Q*-value	Expression Ratio (LowDS/HighDS)	Annotation
UBAL2_82410492	-2.79	0.013	Inf	Glucose-inhibited division protein A
Cell Wall, Membrane, and EPS Biosynthesis				
UBAL2_79310234	2.25	0.033	Inf	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)
UBAL2_79310299	1.90	0.058	Inf	Probable glycosyl transferase, family 2
UBAL2_85240155	2.32	0.029	Inf	Lipopolysaccharide heptosyltransferase II
CGL2_11284049	2.88	0.012	0.101	Putative glycosyl transferase, family 2
UBAL2_80620336	4.34	0.001	0.239	Predicted membrane protein
UBAL2_81350078	5.11	0.000	0.360	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)
UBAL2_79310201	5.33	0.000	0.509	Putative molybdopterin biosynthesis protein
UBAL2_79310264	2.45	0.023	0.520	Glucosamine--fructose-6-phosphate aminotransferase (EC 2.6.1.16)
UBAL2_80620158	4.48	0.001	0.624	Glucosamine--fructose-6-phosphate aminotransferase (EC 2.6.1.16)
UBAL2_80620137	4.43	0.001	0.632	Phosphoglucosamine mutase (EC 5.4.2.10)
UBAL2_86920076	4.71	0.001	0.640	ADP-L-glycero-D-mannoheptose-6-epimerase (EC 5.1.3.20)
UBAL2_82410340	4.64	0.001	0.654	Acetyl-CoA synthetase (EC 6.2.1.1)
UBAL2_86920038	4.84	0.000	0.655	Acetyl-CoA carboxylase, biotin carboxylase (EC 6.3.4.14)
UBAL2_79310197	3.01	0.009	0.706	UDP-glucose 4-epimerase (EC 5.1.3.2)
UBAL2_80620228	2.28	0.031	0.725	Fatty acid/phospholipid synthesis protein (PlsX)
UBAL2_80620233	2.18	0.038	0.731	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)
UBAL2_79310341	2.22	0.035	0.740	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)
UBAL2_79310261	2.90	0.011	0.768	UDP-glucose 4-epimerase (EC 5.1.3.2)
UBAL2_80490100	2.03	0.048	0.775	3-deoxy-D-manno-octulosonate cytidylyltransferase (EC 2.7.7.38)
UBAL2_80620223	3.85	0.002	0.776	3-oxoacyl-(Acyl-carrier-protein) synthase II (EC 2.3.1.41)
UBAL2_79310269	2.79	0.013	0.789	UDP-galactopyranose mutase (EC 5.4.99.9)
UBAL2_79310263	2.54	0.020	0.790	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)
UBAL2_82410583	4.58	0.001	0.797	Putative cell shape determining protein (MreB/Mrl)
UBAL2_80620224	2.54	0.020	0.827	Acyl carrier protein (ACP)
UBAL2_80620231	2.08	0.045	0.869	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC 1.17.4.3)
UBAL2_79310181	-3.08	0.008	2.638	Putative lytic transglycosylase
UBAL2_79310186	-5.57	0.000	2.830	Probable outer membrane lipoprotein carrier protein
UBAL2_82410526	-3.18	0.007	8.235	Cytidylyltransferase family protein
Carbohydrate Biosynthesis				
UBAL2_80490092	2.30	0.030	Inf	Putative glycoside hydrolase, family 15

Table S4. Continued

Protein ID	d-score	*Q*-value	Expression Ratio (LowDS/HighDS)	Annotation
UBAL2_80620329	2.98	0.010	0.147	Glycogen debranching enzyme (GlgX) (EC 3.2.1.68)
UBAL2_79310287	2.43	0.024	0.177	Putative glycosyl transferase, group 1
UBAL2_81350026	3.43	0.005	0.361	Glycogen synthase (EC 2.4.1.21)
UBAL2_85240240	2.86	0.012	0.467	Glycogen phosphorylase (EC 2.4.1.1)
UBAL2_79310106	3.88	0.002	0.495	Glucose-6-phosphate isomerase (EC 5.3.1.9)
UBAL2_82410564	5.39	0.000	0.513	Putative glycoside hydrolase, family 57
UBAL2_85240236	3.76	0.003	0.551	Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)
UBAL2_79310321	4.73	0.001	0.553	Probable alpha amylase
UBAL2_82410560	2.33	0.028	0.578	Putative glycoside hydrolase, family 57
UBAL2_82410561	6.50	0.000	0.579	4-alpha-glucanotransferase (EC 2.4.1.25)
UBAL2_85240174	5.31	0.000	0.586	Putative glycosyl transferase, family 9
UBAL2_82410559	6.47	0.000	0.627	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)
UBAL2_82410562	6.07	0.000	0.655	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)
UBAL2_86920155	6.84	0.000	0.663	Transketolase (EC 2.2.1.1)
UBAL2_80620201	4.86	0.000	0.678	Glucose-6-phosphate dehydrogenase (EC 1.1.1.49)
UBAL2_86920154	7.49	0.000	0.696	Transaldolase
UBAL2_82410373	4.99	0.000	0.707	Phosphoglycerate kinase (EC 2.7.2.3)
UBAL2_80620124	2.88	0.012	0.710	Putative alcohol dehydrogenase
UBAL2_80490185	3.43	0.005	0.722	Transaldolase
UBAL2_79310364	3.94	0.002	0.730	Putative NAD-binding 6-phosphogluconate dehydrogenase
UBAL2_80490184	3.88	0.002	0.733	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
UBAL2_80270054	2.48	0.022	0.738	Putative carbohydrate kinase, PfkB family
UBAL2_85240241	3.68	0.003	0.744	Phosphoglucomutase, alpha-D-glucose phosphate-specific (EC 5.4.2.2)
UBAL2_80620194	5.17	0.000	0.761	Phosphoenolpyruvate synthase (EC 2.7.9.2)
UBAL2_82410114	2.45	0.023	0.763	Putative glycosyl hydrolase, BNR repeat
UBAL2_80620202	4.78	0.001	0.764	6-phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44)
UBAL2_82410277	3.94	0.002	0.775	Probable glycosyl transferase family protein
UBAL2_80490186	2.52	0.021	0.775	Transketolase (EC 2.2.1.1)
UBAL2_82410372	2.82	0.013	0.799	Triosephosphate isomerase (EC 5.3.1.1)
UBAL2_80620149	2.89	0.012	0.800	Enolase (EC 4.2.1.11)
UBAL2_79310084	2.50	0.022	0.800	Phosphomannomutase (EC 5.4.2.8)
UBAL2_82410374	4.48	0.001	0.805	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_79310322	2.73	0.015	0.816	Putative alpha amylase, catalytic region
UBAL2_86920157	2.51	0.021	0.817	Glucokinase (EC 2.7.1.2)
UBAL2_86920153	3.70	0.003	0.817	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
UBAL2_82410467	2.62	0.018	0.851	Ribulose-bisphosphate carboxylase (EC 4.1.1.39)
UBAL2_85240237	2.16	0.039	0.867	Fructose-bisphosphate aldolase (EC 4.1.2.13)
UBAL2_80490099	3.40	0.005	0.881	Carbohydrate kinase, PfkB
UBAL2_82410705	2.21	0.036	0.884	Fructose-1,6-bisphosphatase (EC 3.1.3.11)
UBAL2_82410509	-2.88	0.012	1.370	Inositol monophosphatase (EC 3.1.3.25)
Cofactor Biosynthesis				
UBAL2_86920025	2.50	0.022	0.275	8-amino-7-oxononanoate synthase (EC 2.3.1.47)
UBAL2_80490030	2.68	0.016	0.487	Folylpolyglutamate synthase (EC 6.3.2.17)
UBAL2_82410623	2.15	0.040	0.514	Ubiquinone/menaquinone biosynthesis methyltransferase
UBAL2_82410545	4.87	0.000	0.611	L-aspartate oxidase (EC 1.4.3.16)
UBAL2_85240114	2.68	0.016	0.629	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
UBAL2_86920176	4.98	0.000	0.646	Protoporphyrinogen oxidase (EC 1.3.3.4)
UBAL2_79310171	5.20	0.000	0.648	Deoxyxylulose-5-phosphate synthase (EC 2.2.1.7)
UBAL2_85240217	5.98	0.000	0.659	NAD+ synthase (EC 6.3.5.1)
UBAL2_79310212	7.32	0.000	0.683	Oxygen-independent coproporphyrinogen III oxidase
UBAL2_82410326	2.26	0.033	0.698	Probable 6-pyruvoyl tetrahydrobiopterin synthase family protein
UBAL2_82410483	2.15	0.040	0.709	Cobalamin biosynthesis protein (CbiD)
UBAL2_82410528	4.19	0.001	0.717	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)
UBAL2_85240124	5.04	0.000	0.735	Putative precorrin-8X methylmutase (CbiC)
UBAL2_79310213	1.98	0.051	0.760	Uroporphyrinogen decarboxylase (EC 4.1.1.37)
UBAL2_79310209	2.39	0.025	0.772	S-adenosylmethionine synthetase (EC 2.5.1.6)
UBAL2_82410482	2.55	0.020	0.775	Precorrin-6B methylase 2
UBAL2_80620019	2.80	0.013	0.836	Porphobilinogen synthase (EC 4.2.1.24)
UBAL2_85240218	2.34	0.028	0.849	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II
UBAL2_81350092	1.94	0.053	0.884	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)
UBAL2_79310189	2.03	0.048	0.896	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)
UBAL2_80620017	1.95	0.052	0.905	Porphobilinogen deaminase (EC 2.5.1.61)
UBAL2_79310039	-2.70	0.016	1.367	Putative pyridoxal phosphate biosynthesis protein
UBAL2_82410380	-2.66	0.017	2.014	Siroheme synthase, N-terminal

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_80270018	-3.81	0.002	7.327	Aminodeoxychorismate lyase
Core Metabolism				
UBAL2_79310158	2.60	0.018	Inf	Putative NADH dehydrogenase (ubiquinone), H subunit
UBAL2_85240244	4.48	0.001	0.146	Probable cytochrome c oxidase, subunit I
UBAL2_82410394	2.33	0.028	0.182	Putative sulfide-quinone reductase
UBAL2_80490035	1.98	0.051	0.190	Putative cytochrome b/b6, N-terminal
UBAL2_80490121	5.99	0.000	0.237	Putative cytochrome c oxidase, subunit I
UBAL2_82410389	4.54	0.001	0.502	Putative UbiE/COQ5 methyltransferase
UBAL2_80620132	4.62	0.001	0.510	NADH dehydrogenase (Quinone) (EC 1.6.99.5)
UBAL2_79310250	2.06	0.046	0.555	Probable ferredoxin
UBAL2_82410286	2.33	0.028	0.603	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)
UBAL2_82410149	4.00	0.002	0.649	Protein of unknown function
UBAL2_81350053	4.17	0.001	0.651	NADH dehydrogenase, subunit F (EC 1.6.99.5)
UBAL2_79310157	4.36	0.001	0.652	NADH dehydrogenase, chain I (EC 1.6.99.3)
UBAL2_79310163	4.41	0.001	0.679	NADH dehydrogenase (ubiquinone), D subunit (EC 1.6.5.3)
UBAL2_79310161	3.40	0.005	0.683	NADH dehydrogenase (quinone) (EC 1.6.99.5)
UBAL2_79310159	5.91	0.000	0.713	NADH dehydrogenase (quinone), chain G (EC 1.6.99.5)
UBAL2_82410531	3.78	0.002	0.731	Pyruvate synthase alpha subunit (EC 1.2.7.1)
UBAL2_85240238	2.23	0.035	0.750	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)
UBAL2_81350018	3.59	0.003	0.767	NADH dehydrogenase (Quinone) (EC 1.6.99.5)
UBAL2_79310253	2.92	0.011	0.785	Aconitate hydratase (EC 4.2.1.3)
UBAL2_86920055	2.45	0.023	0.798	Putative oxidoreductase FAD/NAD(P)-binding
UBAL2_79310255	4.87	0.000	0.807	Succinyl-CoA synthetase, alpha subunit (EC 6.2.1.5)
UBAL2_82410537	4.08	0.001	0.817	Pyruvate synthase alpha chain (EC 1.2.7.1)
UBAL2_79310256	3.30	0.006	0.818	Succinyl-CoA synthetase, beta subunit (EC 6.2.1.5)
UBAL2_82410359	2.39	0.025	0.825	ATP synthase F1, alpha subunit (EC 3.6.3.15)
UBAL2_79310249	3.38	0.005	0.841	L-aspartate oxidase (EC 1.4.3.16)
UBAL2_79310247	3.11	0.008	0.859	Succinyl-CoA synthetase, alpha subunit (EC 6.2.1.5)
UBAL2_79310162	2.28	0.031	0.861	Putative NADH dehydrogenase (ubiquinone), E subunit
UBAL2_82410357	5.31	0.000	0.870	ATP synthase F1, beta subunit (EC 3.6.3.15)
UBAL2_79310248	2.70	0.016	0.890	Succinyl-CoA synthetase, beta subunit (EC 6.2.1.5)
UBAL2_82410360	-2.70	0.016	1.225	Putative ATP synthase F1, delta subunit

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
General Functions				
UBAL2_80620251	2.53	0.020	0.100	Putative amine oxidase
UBAL2_82410657	3.97	0.002	0.183	Putative SAM-dependent methyltransferase
UBAL2_80620181	2.37	0.026	0.420	Putative acetyltransferase
UBAL2_82410660	2.59	0.019	0.437	Probable heptosyltransferase family protein
UBAL2_82410225	3.70	0.003	0.651	Probable metal dependent phosphohydrolase
UBAL2_79310176	3.32	0.006	0.651	Metal dependent phosphohydrolase
UBAL2_82410593	4.99	0.000	0.673	Putative cobalamin B12-binding/Radical SAM family protein
UBAL2_82410624	3.49	0.004	0.697	Putative radical SAM family protein
UBAL2_79310184	2.54	0.020	0.703	Metallo-beta-lactamase family protein
UBAL2_79310357	4.39	0.001	0.721	Putative NAD-dependent epimerase/dehydratase
UBAL2_79310217	2.73	0.015	0.726	Putative radical SAM family protein
UBAL2_80490380	3.56	0.003	0.728	Aldo/keto reductase (EC 1.1.1.91)
UBAL2_82410519	3.15	0.008	0.731	Putative aminoglycoside phosphotransferase
UBAL2_80620344	3.31	0.006	0.731	Probable phosphohydrolase
UBAL2_80490077	3.28	0.006	0.748	Probable AAA ATPase superfamily
UBAL2_86920129	3.16	0.007	0.757	Putative flavoprotein reductase
UBAL2_82410348	3.36	0.005	0.781	Putative outer membrane protein
UBAL2_82410244	2.43	0.024	0.782	NHL repeat domain protein
UBAL2_82410158	3.49	0.004	0.792	Putative carbon-nitrogen hydrolase
UBAL2_79310320	3.09	0.008	0.799	Zinc-containing alcohol dehydrogenase superfamily (EC 1.1.1.255)
UBAL2_82410395	2.25	0.033	0.803	Carbonic anhydrase
UBAL2_82410701	2.07	0.045	0.851	Aldehyde dehydrogenase (EC 1.2.1.3)
UBAL2_85240121	2.74	0.015	0.867	Aldo/keto reductase (EC 1.1.1.65)
UBAL2_82410556	4.47	0.001	0.885	Probable O-methyltransferase family protein
UBAL2_82410341	-2.70	0.016	1.159	Putative glyoxalase (GloA)
UBAL2_82410575	-3.93	0.002	2.989	Putative carboxylesterase
UBAL2_80490014	-2.86	0.012	Inf	Probable iron-sulfur protein
Mobile Genetic Elements				
UBAL2_80620072	2.69	0.016	0.591	Probable mobilization protein (MobD)
UBAL2_85240068	-2.55	0.020	2.246	Probable transposase
UBAL2_79310397	-2.58	0.019	2.315	Probable transposase

Table S4. Continued

Protein ID	d-score	*Q*-value	Expression Ratio (LowDS/HighDS)	Annotation
UBAL2_82410476	-2.97	0.010	3.223	Probable transposase
UBAL2_82410177	-3.00	0.009	3.306	Transposase
UBAL2_80620047	-3.13	0.008	3.898	Putative transposase
UBAL2_80620297	-3.13	0.008	3.898	Probable transposase
UBAL2_80490418	-3.17	0.007	4.014	Putative transposase
UBAL2_80490302	-3.17	0.007	4.014	Probable transposase
Motility, Chemotaxis and Signalling				
UBAL2_79040006	2.06	0.046	0.136	flagellar biosynthesis protein FlhF
UBAL2_79310198	2.71	0.016	0.138	Putative multi-sensor signal transduction histidine kinase
UBAL2_82410640	2.61	0.018	0.147	Putative flagellar basal body rod protein
UBAL2_82410197	3.09	0.008	0.163	Protein-glutamate methylesterase (CheB) (EC 3.1.1.61)
UBAL2_82410221	3.00	0.009	0.183	Putative PAS/PAC sensor signal transduction histidine kinase
UBAL2_82410335	5.64	0.000	0.242	Putative diguanylate cyclase/phosphodiesterase
UBAL2_80490108	3.48	0.004	0.243	Putative periplasmic sensor signal transduction histidine kinase
UBAL2_79310367	3.23	0.007	0.279	Putative osmosensitive K+ channel signal transduction histidine kinase
UBAL2_79310190	1.97	0.051	0.339	Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)
UBAL2_80620131	2.61	0.018	0.342	Diguanylate cyclase with GAF sensor
UBAL2_82410391	3.60	0.003	0.550	Putatative diguanylate phosphodiesterase
UBAL2_82410396	3.01	0.009	0.611	Diguanylate cyclase
UBAL2_82410196	4.61	0.001	0.656	Putative methyl-accepting chemotaxis sensory transducer
UBAL2_80490147	3.44	0.004	0.676	Multi-sensor signal transduction histidine kinase
UBAL2_85240169	2.95	0.010	0.689	Putative PilT protein-like
UBAL2_80620198	4.77	0.001	0.692	Methyl-accepting chemotaxis sensory transducer
UBAL2_82410198	4.35	0.001	0.724	Putative signal transduction histidine kinase (CheA)
UBAL2_82410195	4.21	0.001	0.735	Putative chemotaxis protein (CheW)
UBAL2_82410199	3.28	0.006	0.778	Putative response regulator receiver protein (CheY)
UBAL2_81350098	3.21	0.007	0.820	Putative methyl-accepting chemotaxis sensory transducer
UBAL2_80270042	1.90	0.058	0.881	Putative GAF sensor protein
CGL2_11278042	-2.55	0.020	2.146	Putative methyl-accepting chemotaxis protein
Nucleotide Biosynthesis				
UBAL2_86920073	3.57	0.003	0.485	Amidophosphoribosyltransferase (EC 2.4.2.14)
UBAL2_80490057	4.81	0.001	0.493	Aspartate carbamoyltransferase (EC 2.1.3.2)

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_80490058	4.25	0.001	0.583	Dihydroorotase (EC 3.5.2.3)
UBAL2_86920072	3.43	0.005	0.587	Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3)
UBAL2_80490061	5.15	0.000	0.646	Carbamoyl-phosphate synthase, large subunit (EC 6.3.5.5)
UBAL2_80620237	5.63	0.000	0.736	Formate--tetrahydrofolate ligase (EC 6.3.4.3)
UBAL2_82410054	4.37	0.001	0.742	Ribonucleotide reductase (EC 1.17.4.1)
UBAL2_80490101	3.56	0.004	0.760	CTP synthase (EC 6.3.4.2)
UBAL2_86920143	4.62	0.001	0.768	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
UBAL2_80490075	4.65	0.001	0.770	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)
UBAL2_82410688	3.41	0.005	0.786	Adenylosuccinate synthase (EC 6.3.4.4)
UBAL2_80270053	2.38	0.026	0.842	Methylthioadenosine phosphorylase (EC 2.4.2.28)
UBAL2_82410600	2.59	0.019	0.845	Uridylate kinase
UBAL2_85240223	2.42	0.024	0.871	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)
UBAL2_85240177	3.16	0.007	0.871	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)
UBAL2_85240222	2.01	0.049	0.877	Adenylosuccinate lyase (EC 4.3.2.2)
UBAL2_82410161	-3.49	0.004	1.887	Deoxyuridine-triphosphatase (EC 3.6.1.23)
Protein Processing				
UBAL2_82410071	3.92	0.002	Inf	Putative proteasome component
UBAL2_82410301	2.29	0.031	0.625	ATP-dependent protease La (EC 3.4.21.53)
UBAL2_80620009	4.04	0.002	0.646	Putative proteasome component
UBAL2_79310010	3.85	0.002	0.697	Peptidase S49 (SppA)
UBAL2_80490087	5.32	0.000	0.713	ATP-dependent protease La (EC 3.4.21.53)
UBAL2_80620023	6.41	0.000	0.716	Peptidase M41, FtsH (EC 3.6.4.6)
UBAL2_80620010	1.95	0.052	0.721	Putative AAA-family ATPase
UBAL2_82410092	5.02	0.000	0.729	Aminopeptidase N (EC 3.4.11.2)
UBAL2_82410075	3.06	0.009	0.733	Putative proteasome component
UBAL2_82410555	2.29	0.031	0.745	Putative Xaa-Pro aminopeptidase
UBAL2_79310040	2.29	0.031	0.752	Processing peptidase (EC 3.4.24.64)
UBAL2_80620247	4.24	0.001	0.764	Putative peptidase U62, modulator of DNA gyrase
UBAL2_86920150	4.06	0.002	0.823	Peptidase S14, ClpP (EC 3.4.21.92)
UBAL2_85240109	1.94	0.053	0.870	Chaperone DnaJ
DNA Replication				
CGL2_11386018	2.65	0.017	Inf	DNA methyltransferase/helicase

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_79310067	2.10	0.043	0.093	Excinuclease ABC, C subunit (UvrC)
UBAL2_80620177	2.27	0.032	0.109	DNA polymerase III, delta' subunit (EC 2.7.7.7)
UBAL2_80270051	6.26	0.000	0.260	DNA mismatch repair protein MutL
UBAL2_85240275	2.17	0.039	0.275	DNA polymerase III, alpha subunit (EC 2.7.7.7)
UBAL2_85240276	2.61	0.018	0.290	Putative UvrD/rep helicase
UBAL2_79310423	4.53	0.001	0.339	Putative helicase
UBAL2_79310424	4.32	0.001	0.362	Putative helicase
UBAL2_80620156	1.88	0.060	0.464	Putative ATP-dependent DNA helicase, UvrD/REP family
UBAL2_82410449	2.91	0.011	0.520	Chromosomal replication initiator protein (DnaA)
UBAL2_79310187	3.21	0.007	0.556	Excinuclease ABC, A subunit (UvrA)
UBAL2_86920007	2.64	0.017	0.588	Putative DNA recombination protein, RmuC family
UBAL2_80490081	2.91	0.011	0.602	DNA ligase (EC 6.5.1.1)
UBAL2_82410447	3.48	0.004	0.724	DNA gyrase, B subunit (EC 5.99.1.3)
UBAL2_82410446	3.35	0.005	0.758	DNA gyrase, A subunit
UBAL2_82410448	3.76	0.003	0.763	DNA polymerase III, beta chain (EC 2.7.7.7)
UBAL2_82410550	-2.95	0.010	1.314	Putative histone-like DNA-binding protein
UBAL2_79310173	-2.58	0.019	1.401	Exodeoxyribonuclease VII small subunit
UBAL2_82410122	-3.34	0.005	2.679	Probable crossover junction endodeoxyribonuclease (RuvC)
Ribosome Biosynthesis				
UBAL2_86920086	1.94	0.053	0.882	Ribosomal protein S4 and related proteins
UBAL2_82410488	-2.66	0.017	1.154	Ribosomal protein L9
UBAL2_86920109	-5.39	0.000	1.223	Ribosomal protein L23
UBAL2_82410041	-2.88	0.012	1.227	Ribosomal protein S20
UBAL2_79310043	-3.39	0.005	1.253	Ribosomal protein S15
UBAL2_86920094	-4.10	0.001	1.263	Ribosomal protein L30
UBAL2_82410320	-3.91	0.002	1.271	Ribosomal protein L27
UBAL2_86920107	-5.51	0.000	1.280	Ribosomal protein S19
UBAL2_86920097	-3.89	0.002	1.309	Ribosomal protein L6P/L9E
UBAL2_79310008	-2.62	0.018	1.316	Ribosomal protein S16
UBAL2_86920102	-4.11	0.001	1.382	Ribosomal protein S17
UBAL2_86920116	-4.33	0.001	1.390	Ribosomal protein S12
UBAL2_86920125a	-5.56	0.000	2.208	Ribosomal protein L33

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_82410332	-4.03	0.002	4.360	Ribosomal protein L35
Stress Defense				
UBAL2_82410433	3.01	0.009	0.315	CRISPR-associated helicase (Cas3)
UBAL2_79310219	3.46	0.004	0.415	Dihydroflavonol 4-reductase (EC 1.1.1.219)
UBAL2_79310333	1.87	0.061	0.538	Malto-oligosyltrehalose synthase (EC 5.4.99.15)
UBAL2_79310331	2.36	0.027	0.561	Trehalose synthase (EC 5.4.99.16)
UBAL2_82410566	3.14	0.008	0.564	Putative acriflavin resistance protein
UBAL2_79310093	2.71	0.016	0.574	Putative metallo-beta-lactamase family protein
UBAL2_82410432	4.23	0.001	0.606	CRISPR-ssociated protein (Cse1)
UBAL2_82410427	1.96	0.052	0.645	CRISPR associated protein (Cse3)
UBAL2_82410430	2.26	0.033	0.696	CRISPR associated protein (Cse4)
UBAL2_80620172	3.33	0.006	0.821	Putative alkyl hydroperoxide reducatase
UBAL2_82410346	2.10	0.043	0.904	Carboxymethylenebutenolidase (EC 3.1.1.45)
UBAL2_82410298a	-2.79	0.013	1.092	Probable OmpA family protein
UBAL2_82410524	-2.69	0.016	1.198	Probable peptidil-prolyl cis-trans isomerase
UBAL2_85240107	-2.57	0.019	1.201	Putative GrpE protein
UBAL2_79310073	-3.46	0.004	1.495	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
UBAL2_80490086	-2.68	0.016	1.601	Putative heat shock protein (Hsp20)
UBAL2_79310363	-3.08	0.008	1.875	Putative peroxiredoxin
UBAL2_85240216	-4.19	0.001	3.097	Putative thioredoxin family protein
UBAL2_82410522	-7.55	0.000	4.252	Putative peptidyl-prolyl cis-trans isomerase
UBAL2_82410276	-2.87	0.012	4.808	MazG family protein
UBAL2_82410610	-4.08	0.001	14.029	Putative thioredoxin family protein
UBAL2_80620111	-2.86	0.012	Inf	RelB antitoxin
Transcription				
UBAL2_80270023	2.64	0.017	0.181	Transcriptional acitvator, Baf family
UBAL2_79310315	4.02	0.002	0.421	Response regulator receiver modulated metal dependent phosphohydrolase
UBAL2_82410525	3.02	0.009	0.429	Transcription-repair coupling factor
UBAL2_86920062	3.93	0.002	0.578	Putative transcriptional regulator, LysR family
UBAL2_80490146	3.69	0.003	0.596	Two component, sigma54 specific, transcriptional regulator, Fis family
UBAL2_86920040	5.28	0.000	0.599	Response regulator receiver (diguanylate cyclase/phosphodiesterase)
UBAL2_80270035	3.23	0.007	0.630	RNA polymerase, sigma 54 subunit, RpoN

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_80490110	4.00	0.002	0.730	Two component, sigma54 specific, transcriptional regulator, Fis family
UBAL2_86920117	5.66	0.000	0.734	DNA-directed RNA polymerase, beta' subunit (EC 2.7.7.6)
UBAL2_86920119	5.41	0.000	0.764	DNA-directed RNA polymerase, beta subunit (EC 2.7.7.6)
UBAL2_82410671	2.66	0.017	0.799	Transcriptional regulator, NifA, Fis Family
UBAL2_82410588	3.63	0.003	0.828	Ribonucleases G and E
UBAL2_79310054	2.59	0.019	0.842	Putative response regulator receiver protein
UBAL2_79310048	2.22	0.035	0.901	Transcription termination factor (NusA)
UBAL2_86920032	-2.61	0.018	1.113	Putative DNA-directed RNA polymerase, omega subunit
UBAL2_81350051	-3.10	0.008	1.278	Putative transcriptional regulators, TraR/DksA family
UBAL2_79310148	-2.66	0.017	1.436	Putative nitrogen regulatory protein P-II
UBAL2_80620349a	-4.03	0.002	1.775	Putative ribonuclease H
UBAL2_82410250	-2.51	0.021	1.776	Putative transcriptional regulators, TraR/DksA family
UBAL2_79310089	-2.74	0.015	1.957	Transcriptional regulator, BadM/Rrf2 family
UBAL2_81350107	-2.71	0.016	1.965	Putative bacterial regulatory protein, MerR family
UBAL2_85240220	-3.30	0.006	3.624	Transcription antitermination factor (NusB)
UBAL2_80620137a	-3.36	0.005	6.025	Putative transcriptional regulator, BadM/Rrf2 family
Translation				
UBAL2_80490097	4.70	0.001	0.490	GTP-binding protein (lepA)
UBAL2_80270014	4.46	0.001	0.499	Alanyl-tRNA synthetase (EC 6.1.1.7)
UBAL2_82410516	3.12	0.008	0.559	Isoleucyl-tRNA synthetase (EC 6.1.1.5)
UBAL2_81350061	2.57	0.019	0.614	Histidyl-tRNA lygase (EC 6.1.1.21)
UBAL2_86920132	2.40	0.025	0.626	RNA modification enzyme, MiaB family
UBAL2_80620152	5.97	0.000	0.628	Glutamyl-tRNA(Gln) amidotransferase B subunit
UBAL2_82410267	3.75	0.003	0.660	Peptide chain release factor 3
UBAL2_85240087	6.06	0.000	0.697	Arginyl-tRNA synthetase (EC 6.1.1.19)
UBAL2_80620230	4.31	0.001	0.699	Prolyl-tRNA synthetase (EC 6.1.1.15)
UBAL2_80490071	4.86	0.000	0.703	Aspartyl-tRNA synthetase (EC 6.1.1.12)
UBAL2_82410334	5.07	0.000	0.711	Threonyl-tRNA synthetase (EC 6.1.1.3)
UBAL2_86920019	4.65	0.001	0.721	Glycyl-tRNA synthetase, beta subunit (EC 6.1.1.14)
UBAL2_86920113	5.40	0.000	0.743	Translation elongation factor Tu (EC 2.7.7.4)
UBAL2_86920126	5.37	0.000	0.744	Translation elongation factor Tu (EC 2.7.7.4)
UBAL2_82410543	4.05	0.002	0.746	Glutamyl-tRNA synthetase (EC 6.1.1.17)

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_79310074	3.81	0.002	0.750	GTP-binding protein (TypA)
UBAL2_80620179	3.87	0.002	0.764	Methionyl-tRNA synthetase (EC 6.1.1.10)
UBAL2_80270019	3.68	0.003	0.768	Valyl-tRNA synthetase (EC 6.1.1.9)
UBAL2_80490093	3.01	0.009	0.769	Histidyl-tRNA synthetase (EC 6.1.1.21)
UBAL2_79310047	4.17	0.001	0.770	Translation initiation factor IF-2
UBAL2_85240214	4.18	0.001	0.771	Cysteinyl-tRNA synthetase, class Ia (EC 6.1.1.16)
UBAL2_86920140	3.10	0.008	0.781	GTP binding protein
UBAL2_80620153	4.44	0.001	0.788	Glutamyl-tRNA(Gln) amidotransferase A subunit / Amidase (EC 3.5.1.4)
UBAL2_82410038	2.59	0.019	0.800	Leucyl-tRNA synthetase (EC 6.1.1.4)
UBAL2_86920114	5.22	0.000	0.802	Translation elongation factor G
UBAL2_85240188	4.03	0.002	0.802	Translation initiation factor (EC 5.3.1.23)
UBAL2_82410329	2.74	0.015	0.806	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
UBAL2_79310042	2.66	0.017	0.857	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)
UBAL2_82410330	2.66	0.017	0.870	Phenylalanyl-tRNA synthetase beta chain
UBAL2_82410599	-5.53	0.000	1.224	Elongation factor Ts (EF-Ts)
UBAL2_86920141	-3.26	0.006	1.244	Peptidyl-tRNA hydrolase (EC 3.1.1.29)
UBAL2_86920089	-2.52	0.021	1.327	Translation initiation factor 1 (IF-1)
UBAL2_80620155	-2.95	0.010	2.046	Glutamyl-tRNA(Gln) amidotransferase, C subunit
UBAL2_79310005	-2.76	0.014	5.066	tRNA (guanine-N(1)-)-methyltransferase (EC 2.1.1.31)
Transport and Secretion				
UBAL2_79310129	2.43	0.024	0.133	General secretion pathway protein E
CGL2_11277178	1.99	0.051	0.203	TolQ
UBAL2_85240089	2.93	0.011	0.504	Preprotein translocase, YajC subunit
UBAL2_81350095	2.78	0.014	0.535	Probable cation transport protein
UBAL2_79310378	2.34	0.028	0.652	Putative amino acid permease
UBAL2_82410696	3.52	0.004	0.653	Phosphate import ATP-binding protein (PstB) (EC 3.6.3.27)
UBAL2_79310167	7.45	0.000	0.670	Preprotein translocase SecA subunit
UBAL2_82410693	3.83	0.002	0.785	Periplasmic phosphate binding protein
UBAL2_82410569	2.44	0.023	0.817	Probable secretion protein HlyD
UBAL2_82410570	2.26	0.032	0.823	Putative outer membrane efflux protein
UBAL2_82410667	-3.32	0.006	1.910	ABC transporter, ATP-binding protein (EC 3.6.3.25)

Table S4. Continued

Protein ID	d-score	*Q*-value	Expression Ratio (LowDS/HighDS)	Annotation
Unknown Function				
CGL2_11276035	1.91	0.057	Inf	Conserved hypothetical protein
UBAL2_79310229	2.34	0.027	Inf	Conserved hypothetical protein
UBAL2_80620026	2.01	0.049	0.104	Conserved protein of unknown function
UBAL2_82410659	4.44	0.001	0.214	Conserved hypothetical protein
UBAL2_82410116	6.25	0.000	0.277	Hypothetical protein
UBAL2_79310354	2.71	0.016	0.281	Protein of unknown function
UBAL2_82410002	7.19	0.000	0.347	Protein of unknown function
UBAL2_80490114	3.38	0.005	0.352	Conserved protein of unknown function
CGL2_11277179	2.60	0.019	0.362	Protein of unknown function
UBAL2_82410674	3.97	0.002	0.366	Conserved protein of unknown function
UBAL2_80620160	4.45	0.001	0.394	Conserved protein of unknown function
UBAL2_80620005	4.55	0.001	0.416	Conserved protein of unknown function
UBAL2_79310021	2.51	0.021	0.420	Protein of unknown function
UBAL2_79310377	4.49	0.001	0.433	Conserved protein of unknown function
UBAL2_80620288	4.54	0.001	0.452	Conserved protein of unknown function
UBAL2_80620139	1.91	0.057	0.455	Hypothetical protein
CGL2_11277198	1.93	0.054	0.478	Protein of unknown function
UBAL2_82410690	3.02	0.009	0.505	Protein of unknown function
UBAL2_80490238	1.95	0.052	0.505	Conserved protein of unknown function
UBAL2_82410574	2.87	0.012	0.556	Conserved protein of unknown function
UBAL2_80490237	2.67	0.017	0.566	Probable alpha/beta fold family protein
UBAL2_82410507	7.34	0.000	0.567	Conserved protein of unknown function
UBAL2_80490235	2.97	0.010	0.578	Conserved protein of unknown function
UBAL2_82410103	2.90	0.011	0.594	Protein of unknown function
UBAL2_79310383	2.34	0.027	0.608	Conserved protein of unknown function
UBAL2_80490148	2.74	0.015	0.624	Conserved protein of unknown function
UBAL2_82410126	3.73	0.003	0.643	Conserved protein of unknown function
UBAL2_82410050a	3.59	0.003	0.657	Hypothetical protein
UBAL2_79310225	1.93	0.053	0.695	Protein of unknown function
UBAL2_82410016	4.89	0.000	0.718	Conserved protein of unknown function
UBAL2_85240039a	2.01	0.049	0.749	Conserved hypothetical protein

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
CGL2_11172038	2.01	0.049	0.749	Conserved hypothetical protein
UBAL2_82410076	4.77	0.001	0.776	Vesicle-fusing ATPase (EC 3.6.4.6)
UBAL2_79310142	1.93	0.054	0.781	Conserved protein of unknown function
UBAL2_80270056	3.78	0.002	0.783	Conserved protein of unknown function
UBAL2_85240239	3.20	0.007	0.785	Conserved protein of unknown function
UBAL2_82410078	3.76	0.003	0.830	Putative band 7 family protein
UBAL2_86920044	3.14	0.008	0.836	Protein of unknown function
UBAL2_82410107	1.87	0.062	0.868	Conserved protein of unknown function
UBAL2_86920128	1.98	0.051	0.918	Protein of unknown function
UBAL2_80620157	2.88	0.012	0.920	Protein of unknown function
UBAL2_82410689	-2.49	0.022	1.176	Conserved protein of unknown function
UBAL2_85240165	-3.16	0.007	1.280	Protein of unknown function
UBAL2_82410240	-3.86	0.002	1.298	Protein of unknown function
UBAL2_80620355	-4.73	0.001	1.328	Conserved protein of unknown function
UBAL2_82410239	-3.71	0.003	1.399	Putative rhodanese-like domain protein
UBAL2_85240269	-2.68	0.016	1.597	Protein of unknown function
UBAL2_85240201	-2.82	0.013	1.741	Protein of unknown function
UBAL2_82410080	-2.71	0.016	1.770	Protein of unknown function
UBAL2_82410501	-4.27	0.001	1.845	Conserved protein of unknown function
UBAL2_79310096	-3.35	0.005	1.875	Putative Kelch domain-containing protein
UBAL2_80620241	-3.71	0.003	2.028	Protein of unknown function
UBAL2_86920030	-3.63	0.003	2.096	Conserved protein of unknown function
UBAL2_82410472	-3.23	0.007	2.201	Protein of unknown function
UBAL2_80270038	-3.42	0.005	2.263	Protein of unknown function
UBAL2_86920135	-3.91	0.002	2.294	Protein of unknown function
UBAL2_82410392	-2.76	0.014	2.369	Conserved protein of unknown function
UBAL2_82410024	-4.38	0.001	2.385	Protein of unknown function
UBAL2_82410259	-3.51	0.004	2.417	Conserved protein of unknown function
UBAL2_80490135	-3.07	0.008	2.571	Protein of unknown function
UBAL2_82410012	-2.81	0.013	2.750	Conserved protein of unknown function
UBAL2_82410227	-3.50	0.004	2.861	Protein of unknown function
UBAL2_80620008	-2.56	0.020	2.985	Hypothetical protein

Table S4. Continued

Protein ID	**d-score**	***Q*-value**	**Expression Ratio (LowDS/HighDS)**	**Annotation**
UBAL2_82410530	-2.65	0.017	3.224	Hypothetical protein
UBAL2_85240162	-5.01	0.000	3.341	Protein of unknown function
UBAL2_79310051	-2.55	0.020	3.517	Protein of unknown function
UBAL2_80270055	-2.90	0.011	3.844	Putative TPR-domain containing protein
UBAL2_81350014	-2.58	0.019	5.015	Protein of unknown function
UBAL2_79310390	-2.74	0.015	5.474	Protein of unknown function
UBAL2_79310338	-2.78	0.014	5.569	Conserved protein of unknown function
UBAL2_80490395	-3.43	0.005	7.373	Conserved protein of unknown function
UBAL2_80490042a	-3.95	0.002	13.303	Hypothetical protein
UBAL2_80490393	-2.66	0.017	Inf	Hypothetical protein
UBAL2_80490048	-3.35	0.005	Inf	Protein of unknown function
UBAL2_82410387a	-3.06	0.009	Inf	Hypothetical protein
UBAL2_82410046	-2.77	0.014	Inf	Hypothetical protein
UBAL2_82410473	-3.27	0.006	Inf	Conserved protein of unknown function

Table S5a. Data for a Subset of Lipid Metabolism Proteins Whose Abundances are Strongly Correlated with Temperature

Protein ID	**r** [a]	**d-score** [b]	***Q-value*** [c]	**Annotation**
UBA_LeptoII_Scaffold_8135_GENE_56	-0.6	-4.24	0	Cold shock protein
UBA_LeptoII_Scaffold_8241_GENE_482	0.64	3.67	0	Precorrin-6B methylase 2
UBA_LeptoII_Scaffold_8692_GENE_33	0.62	3.78	0	DNA/pantothenate metabolism flavoprotein
UBA_LeptoII_Scaffold_8062_GENE_228	0.59	3.84	0	Fatty acid/phospholipid synthesis protein, PlsX
UBA_LeptoII_Scaffold_8241_GENE_482a	0.56	3.42	0	Precorrin-6Y C5_15-methyltransferase
UBA_LeptoII_Scaffold_8049_GENE_102	0.56	2.88	0.029	2-Dehydro-3-deoxyphosphooctonate aldolase
UBA_LeptoII_Scaffold_8692_GENE_144	0.55	2.9	0.029	GHMP kinase
UBA_LeptoII_Scaffold_8524_GENE_131	0.51	2.36	0.068	UDP-N-acetylglucosamine acyltransferase
UBA_LeptoII_Scaffold_8062_GENE_227	0.5	2.54	0.058	3-oxoacyl-(Acyl-carrier-protein) synthase III
UBA_LeptoII_Scaffold_8692_GENE_48	0.49	2.24	0.083	DegT/DnrJ/EryC1/StrS aminotransferase
UBA_LeptoII_Scaffold_8692_GENE_15	0.44	2.57	0.058	Cobalt-precorrin-2 C(20)-methyltransferase
UBA_LeptoII_R_Cont_7197_GENE_1	0.82	ND [d]	ND	Fatty acid phospholipid biosynthesis enzyme

[a] r-values represent the pearson or spearman rank correlation coefficient between a given protein's abundance and measurements for each environmental variable.

[b] A d-score is the *T*-statistic determined by SAM (Tusher *et al,* 2001)

[c] A *Q*-value is the lowest FDR at which that gene is called significant (analogous to a p-value, Tusher *et al*, 2001).

[d] Not determined

Table S5b. Data for a Subset of Ribosomal Proteins whose Abundances are Strongly Correlated with Nitrate Concentrations

Protein ID	r	d-score	*Q*-value	Annotation
UBA_LeptoII_Scaffold_8241_GENE_594	0.87	3.25	0	Ribosomal protein L13
UBA_LeptoII_Scaffold_8692_GENE_86	0.87	3.25	0	Ribosomal protein S4
UBA_LeptoII_Scaffold_7931_GENE_4	0.85	3.02	0	Ribosomal protein L19
UBA_LeptoII_Scaffold_8692_GENE_102	0.84	2.95	0	Ribosomal protein S17
UBA_LeptoII_Scaffold_8241_GENE_332	0.78	2.52	0	Ribosomal protein L35
UBA_LeptoII_Scaffold_8062_GENE_370	0.74	2.34	0	Ribosomal protein L31
UBA_LeptoII_Scaffold_8692_GENE_97	0.73	2.25	0.014	Ribosomal protein L6P/L9E
UBA_LeptoII_Scaffold_8692_GENE_87	0.73	2.24	0.014	Ribosomal protein S11
UBA_LeptoII_Scaffold_8241_GENE_595	0.71	2.17	0.014	Ribosomal protein S9
UBA_LeptoII_Scaffold_8692_GENE_105	0.71	2.16	0.014	Ribosomal protein S3
UBA_LeptoII_Scaffold_8692_GENE_106	0.71	2.16	0.014	Ribosomal protein L22
UBA_LeptoII_Scaffold_8692_GENE_100	0.71	2.15	0.014	Ribosomal protein L24
UBA_LeptoII_Scaffold_8692_GENE_99	0.71	2.14	0.014	Ribosomal protein L5
UBA_LeptoII_Scaffold_8062_GENE_356	0.69	2.09	0.014	Ribosomal protein S21
UBA_LeptoII_Scaffold_8027_GENE_36	0.66	1.94	0.033	Ribosomal protein S30EA
UBA_LeptoII_Scaffold_8692_GENE_88a	0.67	1.93	0.033	Ribosomal protein L36
UBA_LeptoII_Scaffold_8692_GENE_109	0.64	1.86	0.04	Ribosomal protein L23
UBA_LeptoII_Scaffold_8692_GENE_122	0.64	1.86	0.04	Ribosomal protein L1
UBA_LeptoII_Scaffold_8692_GENE_139	0.63	1.82	0.056	Ribosomal protein S6
UBA_LeptoII_Scaffold_8692_GENE_95	0.62	1.77	0.068	Ribosomal protein S5
UBA_LeptoII_Scaffold_8692_GENE_94	0.58	1.61	0.093	Ribosomal protein L30
UBA_LeptoII_Scaffold_8692_GENE_116	0.58	1.59	0.093	Ribosomal protein S12

Table S5c. Data for a Subset of Protein Processing Proteins whose Abundances are Strongly Correlated with Sulfate Concentrations

Protein ID	r	d-score	*Q*-value	Annotation
UBA_LeptoII_Scaffold_8241_GENE_301	0.76	4.67	0	ATP-dependent protease La
UBA_LeptoII_Scaffold_8692_GENE_149	0.66	3.44	0.015	ClpX ATPase regulatory subunit
UBA_LeptoII_Scaffold_8062_GENE_339	0.68	2.87	0.036	Putative peptidase C26
UBA_LeptoII_Scaffold_8241_GENE_121	0.54	2.8	0.036	Peptidase S1C
UBA_LeptoII_Scaffold_8241_GENE_92	0.55	2.4	0.049	Aminopeptidase N
UBA_LeptoII_Scaffold_8062_GENE_9	0.55	2.39	0.049	Putative proteasome component
UBA_LeptoII_Scaffold_8241_GENE_75	0.54	2.33	0.049	Putative proteasome component
UBA_LeptoII_Scaffold_8049_GENE_87	0.5	2.21	0.077	ATP-dependent protease La
UBA_LeptoII_Scaffold_8062_GENE_247	0.5	2.17	0.077	Putative peptidase
UBA_LeptoII_Scaffold_8524_GENE_82	0.53	2.07	0.077	Putative ATP-dependent Clp protease
UBA_LeptoII_Scaffold_8062_GENE_10	0.52	2.06	0.077	Putative AAA-family ATPase

Table S5d. Data for a Subset of Biosynthesis Proteins whose Abundances are Strongly Correlated with Calcium Concentrations

Protein ID	r	d-score	*Q*-value	Annotation
UBA_LeptoII_Scaffold_8524_GENE_127	-0.71	-3.04	0.017	Putative bacterial surface antigen
UBA_LeptoII_Scaffold_7931_GENE_236	-0.69	-2.09	0.063	N-acetylglucosaminyltransferase
UBA_LeptoII_Scaffold_8524_GENE_134	-0.67	-2.8	0.027	Lipid A disaccharide synthase
UBA_LeptoII_Scaffold_8241_GENE_6	-0.65	-4.54	0	Cysteine desulfurase
UBA_LeptoII_Scaffold_7931_GENE_342	-0.64	-1.98	0.063	DTDP-glucose 4_6-dehydratase
UBA_LeptoII_Scaffold_8027_GENE_5	-0.64	-2.83	0.027	Arginine decarboxylase
UBA_LeptoII_Scaffold_8027_GENE_41	-0.62	-2.64	0.027	3-dehydroquinate synthetase
UBA_LeptoII_Scaffold_8049_GENE_22	-0.6	-2.47	0.041	Anthranilate synthase component I
UBA_LeptoII_Scaffold_7931_GENE_38	-0.59	-2.08	0.063	Holo-[acyl-carrier-protein] synthase
UBA_LeptoII_Scaffold_8062_GENE_340	-0.58	-1.84	0.063	Glutamate racemase
UBA_LeptoII_Scaffold_8049_GENE_100	-0.57	-1.96	0.063	CMP-KDO synthetase
UBA_LeptoII_Scaffold_8692_GENE_82	-0.57	-1.86	0.063	DTDP-4-dehydrorhamnose reductase
UBA_LeptoII_Scaffold_7931_GENE_84	-0.51	-2.18	0.063	Phosphomannomutase

Table S6. Tests of Concordance Between Proteome Sample Technical Replicates. R^2 Values of Linear Regressions are Reported for Paired Combinations of NSAF Values from Technical Replicates (TechRep)

Sample	TechRep1 vs. TechRep2	TechRep1 vs. TechRep3	TechRep2 vs. TechRep3	AVERAGE	STDEV
P1	0.938	0.968	0.955	0.953	0.015
P2	0.989	0.970	0.977	0.979	0.010
P4	0.993	0.972	0.963	0.976	0.016
P7	0.977	0.951	0.911	0.946	0.033
P8	0.969	0.973	0.966	0.969	0.004
P9	0.960	0.938	0.952	0.950	0.011
P10	0.960	0.976	0.978	0.971	0.010
P11	0.986	0.933	0.929	0.949	0.032
P14	0.958	0.992	0.965	0.972	0.018
P17	0.979	0.992	0.986	0.986	0.006
P20	0.983	0.989	0.990	0.988	0.004
P25	0.994	0.993	0.992	0.993	0.001
P26	0.968	0.926	0.893	0.929	0.037
P27	0.978	0.982	0.988	0.982	0.005
P28	0.947	0.954	0.980	0.961	0.017
P29	0.974	0.962	0.988	0.975	0.013
P30	0.967	0.963	0.981	0.970	0.010
P31	0.982	0.984	0.995	0.987	0.007
P33	0.975	0.972	0.972	0.973	0.001
P35	0.976	0.984	0.981	0.980	0.004
P36	0.987	0.993	0.987	0.989	0.003
P37	0.995	0.990	0.991	0.992	0.003
P38	0.991	0.993	0.984	0.989	0.004
P39	0.990	0.987	0.992	0.990	0.003
P40	0.989	0.982	0.979	0.983	0.005
P41	0.991	0.989	0.988	0.989	0.001
P43	0.982	0.985	0.990	0.986	0.004
P49	0.963	0.970	0.952	0.962	0.009
AVERAGE	-	-	-	**0.974**	**0.010**