Electronic Supplemental Material for Bosch, Skovran *et al.*

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Instructions for accessing the Supplemental Data Tables and *DTASelect* filter files

Table S3, the results for ORFs associated with methanol and succinate metabolism, is contained below in this PDF document. Tables S1 and S2 were too large for the journal web server at the time of submission and are thus available on Dr. Hackett's data server at the UW College of Engineering Center for Microbial Proteomics. Table S4, the RMQ number conversion table between the 2002 RMQ numbers and the revision issued in 2007, can also be found at the same URL. For purposes of comparing the microarray results published originally by Okubo, Skovran *et al.* (2007) *Omics* 11, 325-340 and also reproduced in Tables S1-S3, it is not necessary to use the conversion table because both the array results and the proteomics are based on the 2002 RMQ numbers given in the tables. An RMQ number designates an ORF in the annotated genome. A new and complete genome annotation for *Methylobacterium extorquens* AM1 will be publicly released in latter 2008. At the time of release a new conversion table will be posted to allow the use of the present data tables with the new annotation. As genome annotation is always to some degree a work in progress, scientists interested in the latest information regarding AM1 should also consult links from the Lidstrom Lab website at the second URL given below. Reviewers and other parties interested in viewing the PDF summary tables for all 7,556 RMQ numbers, the DTASelect filter files and Table S4 should login at the following URL:

http://depts.washington.edu/mhlab/

login name: guest

password: AM1DATA

Please note that the password is case sensitive. Parties with a desire to download the entire *Methylobacterium extorquens* AM1 FileMaker Pro database, on which the PDFs are based, should contact the corresponding author at *mhackett@u.washington.edu* or Dr. Mary Lidstrom at *lidstrom@u.washington.edu*. The original *DTASelect* filter files for all AM1 proteomics data reported in this paper are also available at this URL. The Lidstrom Lab website can be found at http://depts.washington.edu/mllab/. No established public proteomic data archive at the time of submission was able to easily accommodate the scale of the raw mass spectrometry data acquired for this study. Thus, the raw data will be maintained on the corresponding author's server until such time as the mechanics of archival storage can be arranged.

Notes for Supplemental Tables S1-S3

The ORF numbers (RMQ numbers) and functional descriptors are primarily those derived from Okubo, Skovran *et al.* (2007) *Omics* 11, 325-340, with some changes and corrections. Table S1 lists all annotated ORFs by RMQ number in ascending order, including RMQ numbers for which there is no data. This table was derived from a much larger relational database of *Methylobacterium extorquens* AM1 proteomics and genomics data implemented in FileMaker Pro at the University of Washington by Dr. Fred Taub, *fredtaub@u.washington.edu*. An explanation is given below for each field in the table.

RMQ: these are the 2002 ORF numbers used in the previously published array paper cited above. A cross-reference to the RMQ numbers assigned in 2007 can be found in Table S4.

Protein Spectral Count fields

***q*-value:** this is a measure of false discovery rate that is discussed in the main text. In this study any *q*-value less than 0.01 was judged to be significant. Similarly to a *p*-value, the *q*-value is influenced by both the magnitude of the abundance change and the variance, but it is a measure of significance in terms of false discovery rate rather than false positive rate. It implicitly contains a correction for multiple hypothesis testing. See Storey and Tibshirani (2003) *PNAS* 100, 9440-9445 for a complete description of the *q*-value. As described in the main text, the spectral count *q*-value was derived from the uncorrected *p*-value associated with a *G*-test as described for proteomics data in Xia *et al.* (2007) *Inter. Jour. Mass Spectrom. 259*, 105-116. The key difference in detail in this work is that the actual value of *G* was calculated globally as G_{Total} according to the method described in Sokal and Rohlf, *Biometry*, 3rd Ed. (1995), which takes advantage of the additivity of *G* for each individual comparison, i.e. $G_{Total} = G\,(MeOH\_1, Succin\_1) + G\,(MeOH\_1, Succin\_2) + G\,(MeOH\_2, Succin\_1) + G\,(MeOH\_2, Succin\_2)$ with 2 to 4 degrees of freedom, depending on missing values for certain ORFs. Each individual value of *G* was calculated as given below:

$$G = 2\left[f_{Succin} \cdot \ln\left(\frac{f_{Succin}}{\frac{f_{Succin} + f_{MeOH}}{2}} \right) + f_{MeOH} \cdot \ln\left(\frac{f_{MeOH}}{\frac{f_{Succin} + f_{MeOH}}{2}} \right) \right]$$

Where the expectation value of equal spectral counts for *MeOH* and *Succin* assumes a null hypothesis of zero abundance change between methanol and succinate nutrient conditions:

$$\hat{f}_{MeOH} = \hat{f}_{Succin} = \frac{f_{MeOH} + f_{Succin}}{2}$$

The value of G_{Total} was then compared using R to the value of Chi-square at the appropriate degrees of freedom to derive the *p*-value, which in turn served as the input into the QVALUE R package, *see http://faculty.washington.edu/jstorey/qvalue/.* The correction for multiple hypothesis testing contained in the *q*-value is significantly less conservative in practice than other, more common corrections to the *p*-value, such as the Bonferroni method. This is a good thing for the work reported here, because the combination of spectral counting and the *G*-test as presented in Xia *et al.* (2007) *Inter. Jour. Mass Spectrom. 259*, 105-116 suffers from high false negative rates, as we have described in Xia *et al.* (2007) *Proteomics 7*, 2904-2919. In other words, the method is inherently conservative to begin with, and applying a conservative correction to eliminate an even greater number of ORFs from consideration was probably unwise for this dataset.

Log$_2$ Ratio: this is the global log$_2$ ratio of the average of the normalized total spectral count values for Methanol/Succinate, log$_2$[(MeOH_1 + MeOH_2) ÷ (Succin_1 + Succin_2)].

Log$_2$ Sum: the sum of the normalized global spectral counts for both MeOH and Succinate. This number is primarily useful for estimating the degree to which a particular ORF is represented in the dataset.

Log$_2$ MeOH: the sum of normalized spectral counts associated with a particular ORF in the methanol nutrient data.

Log$_2$ Succ: the sum of normalized spectral counts associated with a particular ORF in the succinate nutrient data.

Protein Intensity fields

***q*-value:** this is a measure of false discovery rate that is discussed in the main text. In this study any q-value less than 0.01 was judged to be significant. Similarly to a p-value, the q-value is influenced by both the magnitude of the abundance change and the variance, but in terms of false discovery rate rather than false positive rate. It implicitly contains a correction for multiple hypothesis testing. See Storey and Tibshirani (2003) as cited above. As described in the main text, the summed intensity q-value was derived from the uncorrected p-value associated with a t-test as described for proteomics data in Xia *et al.* (2007*) Inter. Jour. Mass Spectrom. 259*, 105-116. The key difference in detail in this work is that the actual value of t for the global score over n = 4 summed signal intensity comparisons was calculated as paired t according to the method described in Sokal and Rohlf (1995), which differs from that given in the citation above. This is the paired t-test that has been in common use for microarray expression data for a number of years. The equation for global t is given below ($n = 4$), where sd is standard deviation:

$$t = \frac{\{(MeOH\_1 - Succin\_1) + (MeOH\_1 - Succin\_2) + (MeOH\_2 - Succin\_1) + (MeOH\_2 - Succin\_2)\} / n}{sd / \sqrt{n}}$$

The value of paired t was calculated in R to derive the p-value, which in turn served as the input into the QVALUE R package, *see http://faculty.washington.edu/jstorey/qvalue/.* The correction for multiple hypothesis testing contained in the q-value is significantly less conservative in practice than other, more common corrections to the p-value, such as the Bonferroni method. This is a good thing for summed intensity as well, because the paired t-test was quite sensitive to the noisiness inherent in the method, yielding relatively few abundance changes relative to the spectral counts. The t-test originally presented in Xia *et al.* (2007) cited above was probably slightly too liberal, the test used here was probably too conservative. We are exploring variance shrinkage approaches to optimizing our use of the t-test as a means to find a middle ground that agrees more precisely with our intuitive ideas as experimentalists regarding significance for this type of data. The previously published t-test, that was also used to evaluate the four individual MeOH/succinate comparisons prior to calculating a global value using the equation above, was more powerful because it based n and m on the number of redundant unique peptides associated with a protein, rather than the number of comparisons, $n = 4$ comparisons versus $(m + n) \geq \sim 6$ peptides, the approximate minimum number that will allow for a call as significantly changed.

$$t = \frac{X - Y}{\sqrt{m \cdot sd_x^{\,2} + n \cdot sd_y^{\,2}}}$$

where X and Y are the summed intensities over all redundant unique peptides m and n for each state for a single protein in a two state experiment. Using this approach without modification required unrealistically low q cut-offs when applied globally, so the conventional paired t-test was used instead.

$\mathbf{Log_2}$ Ratio: this is the global $\log_2$ ratio of the average of the normalized total summed intensity values for Methanol/Succinate, $\log_2[(MeOH\_1 + MeOH\_2) \div (Succin\_1 + Succin\_2)]$.

$\mathbf{Log_2}$ Sum: the sum of the normalized global summed intensity values for both MeOH and Succinate. This number is primarily useful for estimating the degree to which a particular ORF is represented in the dataset.

$\mathbf{Log_2}$ MeOH: the sum of normalized total summed intensity for a particular ORF in the methanol nutrient data.

$\mathbf{Log_2}$ Succ: the sum of normalized total summed intensity for a particular ORF in the succinate nutrient data.

gene name: self-explanatory

Abundance Change fields

The proteomic relative abundance color codes in these two fields follow what has evolved as a standard format in Hackett's lab: **green**, an abundance ratio significantly greater than zero on a $\log_2$ scale (higher relative abundance in MeOH) at a q-value cutoff of 0.01; **red**, an abundance ratio significantly less than zero on a $\log_2$ scale (lower relative abundance in MeOH, higher in succinate); **yellow**, detected qualitatively but lacking statistical support for abundance change; **black**, no data for this ORF, a qualitative non-detect. This color scheme is the opposite of that commonly employed to code for Cy3 and Cy5 dyes in microarray false color images. This is done intentionally to emphasize the point that this is a completely different technology, thus we use green to indicate up-regulation for the ratio MeOH/succinate.

Sc: color code for global spectral counting significance.

Pi: color code for global summed signal intensity significance.

Desc: the gene functional description.

Transcription Microarray Data Fields

This data is a summary of the microarray results previously published in Okubo, Skovran *et al.* (2007) *Omics* 11, 325-340.

Log Avg Ratio: the $\log_{10}$ expression ratio of MeOH/succinate published in the original paper cited above.

$\mathbf{Log_2}$ Avg Ratio: self-explanatory. The $\log_2$ transformation allows a more intuitive direct comparison with the proteomics abundance ratios.

Avg p-value: the linear *p*-value given in the array paper cited above.

Avg Log p-value: the $\log_{10}$ *p*-value given in the array paper cited above.

SAM ∂=1.25: Significance Analysis of Microarrays score reported in the original array paper cited above. For an explanation of the SAM score, see *http://www-stat.stanford.edu/~tibs/SAM/* and the citation above from Okubo, Skovran *et al.*

Probe: key to the probes used to construct the AM1 microarray, see the citation above.

Supplemental Table S3

This table includes a global data summary for those ORFs known or suspected to be involved in the metabolism of methanol and succinate for which proteomic data was collected, as of the state of curation that existed on December 15, 2007. This is a subset of Table S1 and lists the ORFs in order of 2002 RMQ number. The field headings are explained in the notes above at the beginning of this file.

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	$\log_2$Ratio	$\log_2$Sum	$\log_2$MeOH	$\log_2$Succ	*q*-value	$\log_2$Ratio	$\log_2$Sum	$\log_2$MeOH	$\log_2$Succ		Sc	Pi	Log Avg Ratio	Log_2 Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ00003	0.001549	-0.280	8.100	6.954	7.234	0.046410	-0.560	26.988	25.179	25.700	mxcE	🔴 R	🟡 Y	-0.0578	-0.1921	0.327307	-0.5975		461c
Desc	Transcriptional regulator, Methanol utilization control regulatory protein MxcE																		
RMQ00015	0.000000	0.620	9.640	8.919	8.298	0.008291	0.750	28.054	27.010	26.255	meaA	🟢 G	🟢 G	0.1776	0.5900	0.004167	-3.0785	3.0591	978c
Desc	A mutase, Methylmalonyl-CoA mutase homolog																		
RMQ00044	0.000000	0.540	11.370	10.611	10.073	0.008236	0.620	31.021	29.909	29.288	mxaJ	🟢 G	🟢 G	0.1340	0.4451	0.141808	-2.2858	1.8792	376c
Desc	MxaJ protein																		
RMQ00079	0.999913	-0.090	6.970	5.921	6.011	0.040243	-0.420	25.780	24.063	24.481	folP	🟡 Y	🟡 Y	-0.1072	-0.3561	0.094876	-1.3991	-1.7781	708c
Desc	Dihydroxypteroate synthase (EC 2.5.1.15)																		
RMQ00403	0.999913	-0.670	4.250	2.874	3.545	0.101646	-0.650	22.705	20.792	21.400	dyr	🟡 Y	🟡 Y	-0.0087	-0.0290	0.262931	-0.6588		780c
Desc	DHFR, Dihydrofolate reductase (EC 1.5.1.3)																		
RMQ00448	0.009910	0.890	6.450	5.831	4.939	0.059325	0.780	24.313	23.287	22.565	mcmA	🟢 G	🟡 Y	0.3311	1.0999	0.000236	-7.8535	4.0739	449cn
Desc	Methylmalonyl-CoA mutase alpha subunit																		
RMQ00777	0.099668	0.310	8.890	8.035	7.727	0.038006	0.390	27.717	26.490	26.105	fhcA	🟡 Y	🟡 Y	-0.0136	-0.0451	0.529619	-0.2953		1081c
Desc	Formyltransferase/hydrolase complex, alpha subunit																		
RMQ00778	0.999913	-0.080	9.080	8.037	8.122	0.108593	0.360	27.114	25.902	25.494	fhcB	🟡 Y	🟡 Y	0.0113	0.0376	0.705538	-0.1930		474c
Desc	Formyltransferase/hydrolase complex, beta subunit																		
RMQ01050	0.000000	-1.270	10.980	9.207	10.475	0.001345	-1.950	30.793	27.863	29.808		🔴 R	🔴 R	-0.5037	-1.6732	0.000000	-15.4455	-6.5162	628
Desc	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)																		
RMQ01146	0.000000	0.510	9.870	9.097	8.591	0.032946	0.390	28.344	27.117	26.738	meaC	🟢 G	🟡 Y	0.0562	0.1866	0.279511	-0.7836		667c
Desc	mesaconyl coA hydratase																		
RMQ01208	0.630978	-0.290	7.980	6.825	7.114	0.101444	-0.390	26.035	24.334	24.766	croR	🟡 Y	🟡 Y	0.1091	0.3625	0.108393	-1.5372	1.7254	180c
Desc	cROTONASE; 3-hydroxybutyryl-CoA dehydratase																		
RMQ01238	0.999913	0.040	4.410	3.430	3.392	0.255116	-0.560	22.444	20.875	21.010	orf19	🟡 Y	🟡 Y	-0.0267	-0.0887	0.685670	-0.1681		419c
Desc	Cofactor biosynthesis, participates in tetrahydromethanopterin-linked formaldehyde oxidation, orfB117																		
RMQ01365	0.000000	-0.630	10.700	9.351	9.980	0.010307	-1.110	30.097	27.832	28.951	gap20	🔴 R	🟡 Y	-0.5961	-1.9802	0.000000	-18.5712	-9.4593	229cn
Desc	Granule associated protein																		

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ01883	0.000000	-2.360	8.740	6.126	8.483	0.034218	-3.160	28.701	24.531	27.763	pntB	●	●	-0.7559	-2.5109	0.000000	-23.4573	-15.0692	753
Desc	NADP transhydrogenase subunit beta (EC 1.6.1.2)											R	Y						
RMQ02159	0.000000	-1.540	11.160	9.188	10.730	0.003893	-1.750	30.063	27.295	29.040	pdhB	●	●	-0.3999	-1.3285	0.000000	-11.0799	-8.2296	964c
Desc	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)											R	R						
RMQ02161	0.000000	-1.190	10.310	8.589	9.783	0.000544	-1.370	29.241	26.800	28.170	pdhC	●	●	-0.4445	-1.4764	0.000000	-12.4699	-8.3222	1068c
Desc	Dihydrolipoamide acetyltransferase, component of pyruvate dehydrogenase complex (EC 2.3.1.12)											R	R						
RMQ02662	0.000000	-4.060	5.520	1.373	5.437	0.059200	-7.010	23.110	15.193	22.508	sucT1	●	●	-1.2267	-4.0750	0.000000	-30.9253	-16.9500	568
Desc	C4-dicarboxylate transport protein (permease)											R	Y						
RMQ02792	0.003134	-0.570	7.600	6.286	6.858	0.084904	-0.560	26.264	24.489	24.990	nuoB	●	●	-0.4234	-1.4065	0.000000	-10.0642	-8.3134	213c
Desc	NADH-quinone oxidoreductase chain B (EC 1.6.5.3)											R	Y						
RMQ03311	0.000000	2.450	11.940	11.695	9.247	0.002195	2.900	29.738	29.368	26.478	mtdA	●	●	0.7793	2.5887	0.000000	-23.6669	11.4528	612c
Desc	Methylenetetrahydromethanopterin/methylenetetrahydrofolate dehydrogenase											G	G						
RMQ03312	0.000000	1.880	10.400	10.056	8.179	0.001795	2.350	28.903	28.413	26.062	hpr	●	●	0.6368	2.1153	0.000000	-18.7976	6.6519	432c
Desc	Hydroxypyruvate reductase											G	G						
RMQ03407	0.999913	0.340	4.380	3.541	3.197	0.072873	0.610	21.994	20.897	20.244	orf7	●	●	0.0007	0.0024	0.636392	-0.1983		237c
Desc	Cofactor biosynthesis, (C1-, Me-S)											Y	Y						
RMQ03495	0.999913	0.090	4.670	3.717	3.624	0.255116	-0.250	22.328	20.795	20.888	fdh3B	●	●	-0.2336	-0.7759	0.459360	-0.3708	-3.4817	559c
Desc	Formate dehydrogenase beta subunit, Cytochrome-linked; formate dehydrogenase, beta subunit											Y	Y						
RMQ03496	0.999913	-0.190	3.130	2.036	2.223	0.099824	0.410	20.805	19.580	19.140	fdh3C	●	●	-0.1708	-0.5673	0.004841	-2.6436	-3.1806	505c
Desc	Formate dehydrogenase gamma subunit, Cytochrome-linked; formate dehydrogenase, gamma subunit											Y	Y						
RMQ03649	0.000005	-2.040	5.460	3.108	5.143	0.010344	-2.270	23.449	20.438	22.507	qscR	●	●	-0.0443	-0.1471	0.516364	-0.3236		413c
Desc	Serine cycle transcriptional regulator											R	Y						
RMQ03665	0.002624	1.040	6.290	5.723	4.682	0.161072	-0.100	25.336	23.805	23.897	nuoI	●	●	-0.4719	-1.5677	0.000000	-13.5404	-6.9989	66c
Desc	NADH-quinone oxidoreductase chain I (EC 1.6.5.3)											G	Y						
RMQ03831	0.000000	0.480	10.940	10.158	9.677	0.200513	0.100	30.596	29.205	29.126	phaB	●	●	-0.0192	-0.0638	0.253225	-0.8002		276c
Desc	Acetoacetyl-CoA reductase											G	Y						

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	$\log_2$Ratio	$\log_2$Sum	$\log_2$MeOH	$\log_2$Succ	*q*-value	$\log_2$Ratio	$\log_2$Sum	$\log_2$MeOH	$\log_2$Succ		Sc	Pi	Log Avg Ratio	Log_2 Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ04144	0.103952	1.070	5.510	4.946	3.875	0.184878	-0.170	25.024	23.204	23.607	mxaS	🟡	🟡	-0.0178	-0.0592	0.676291	-0.1837		341c
Desc	Methanol oxidation protein, unknown function											Y	Y						
RMQ04203	0.999913	-0.420	3.260	2.036	2.459	0.101646	-0.680	21.975	20.043	20.856	orf5	🟡	🟡	0.0057	0.0188	0.701490	-0.1581		441c
Desc	Orf5 (Archaeal)											Y	Y						
RMQ04236	0.000000	4.660	5.710	5.657	1.000	0.000031	9.880	24.531	24.434	14.578	fdh2C	🟢	🟢	0.8310	2.7605	0.000000	-21.2726	12.1072	232c
Desc	NAD-linked formate dehydrogenase gamma subunit, Molybdenum-dependent											G	G						
RMQ04256	0.045995	0.040	8.980	8.004	7.963	0.043403	0.270	27.912	26.614	26.343	mxaR	🟡	🟡	0.1072	0.3563	0.189062	-1.8018		587c
Desc	Methanol oxidation, unknown function											Y	Y						
RMQ04586	0.000000	0.300	11.060	10.206	9.903	0.041599	0.230	29.732	28.408	28.188	ibd2	🟢	🟡	0.1649	0.5479	0.020853	-3.0785	2.3292	839c
Desc	Isobutyryl-CoA dehydrogenase, Acyl-CoA dehydrogenase, medium-chain specific											G	Y						
RMQ04612	0.062390	0.880	6.150	5.528	4.644	0.006998	1.210	25.703	24.866	23.679	mxaH	🟡	🟢	0.0619	0.2057	0.385603	-0.5998		319c
Desc	Methanol oxidation, unknown function											Y	G						
RMQ04643	0.000000	-0.890	10.330	8.819	9.707	0.005062	-1.490	29.125	26.569	28.058		🔴	🔴	-0.2962	-0.9840	0.000437	-4.8302	-4.3353	1046c
Desc	Phosphoenolpyruvate (PEP) synthase, pyruvate diphosphate kinase (EC 2.7.9.1)											R	R						
RMQ04824	0.000000	0.490	10.930	10.153	9.659	0.122349	0.140	29.743	28.371	28.221	eno	🟢	🟡	-0.0262	-0.0869	0.355883	-0.5868		720c
Desc	Enolase (EC 4.2.1.11)											G	Y						
RMQ05001	0.000000	-1.450	10.450	8.551	9.997	0.000822	-1.900	29.331	26.442	28.343	pdhD	🔴	🔴	-0.5551	-1.8441	0.000000	-16.7017	-7.2334	523c
Desc	Dihydrolipoamide dehydrogenase, putative subunit of pyruvate dehydrogenase (EC 1.8.1.4)											R	R						
RMQ05266	0.706090	0.480	6.310	5.528	5.044	0.053274	0.490	25.682	24.516	24.031	mxaA	🟡	🟡	0.0780	0.2590	0.299488	-0.6013		581c
Desc	Essential for Ca2+ insertion into MDH											Y	Y						
RMQ05267	0.999913	0.390	4.790	3.976	3.585	0.101770	0.780	22.423	21.383	20.734	mxaL	🟡	🟡	0.0836	0.2777	0.173667	-0.9050		461c
Desc	Essential for Ca2+ insertion into MDH											Y	Y						
RMQ05268	0.156983	-0.040	9.010	7.992	8.034	0.204371	-0.080	28.835	27.269	27.378	mxaD	🟡	🟡	0.0864	0.2869	0.157411	-1.1321		251c
Desc	Essential for Ca2+ insertion into MDH											Y	Y						
RMQ05335	0.000000	-1.190	10.330	8.616	9.803	0.003440	-1.430	30.225	27.742	29.176	fumA	🔴	🔴	-0.5377	-1.7864	0.000000	-14.7414	-8.3561	1057c
Desc	Fumarase, Fumarate hydratase (EC 4.2.1.2)											R	R						

	Protein Spectral Count					Protein Intensity						Abundance Change		Transcription Microarray Data					
ORF	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	gene name	Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ05448	0.690172	-0.010	9.590	8.591	8.597	0.292660	0.000	28.658	27.202	27.202	epm	Y	Y	-0.0760	-0.2524	0.274924	-1.1399		181c
Desc	Epimerase, Methylmalonyl CoA epimerase (EC 5.1.99.1)																		
RMQ05670	0.000000	0.610	9.250	8.518	7.908	0.045042	0.350	28.747	27.497	27.163	mch	G	Y	0.0535	0.1776	0.312308	-0.5363		594c
Desc	N5,N10-methenyltetrahydromethanopterin cyclohydrolase (EC 3.5.4.27)																		
RMQ05674	0.999913	-0.430	2.610	1.373	1.807	0.102426	-1.720	19.158	15.193	18.079	orfY	Y	Y	0.0019	0.0062	0.665742	-0.1791		641c
Desc	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)																		
RMQ05675	0.024371	0.310	9.050	8.194	7.887	0.053077	-0.250	27.718	26.078	26.333	mtdB	Y	Y	0.0005	0.0018	0.678645	-0.1725		471c
Desc	Methylene tetrahydromethanopterin dehydrogenase (NAD+/NADP+)																		
RMQ05676	0.295782	-0.690	6.050	4.669	5.358	0.055104	-0.680	24.193	22.314	22.983	orf4	Y	Y	0.0112	0.0373	0.496385	-0.3977		589c
Desc	Tetrahydromethanopterin biosynthesis, Hypothetical 34.4 kDa protein																		
RMQ05703	0.999913	-0.290	2.530	1.373	1.664	0.038262	-2.820	18.904	15.193	18.125	sdhD	Y	Y	-0.5144	-1.7089	0.000000	-14.8547	-8.7208	209c
Desc	Succinate dehydrogenase delta subunit, Succinate dehydrogenase membrane anchor subunit																		
RMQ05704	0.999913	0.110	2.640	1.692	1.585	0.203045	0.490	18.900	17.651	17.081	sdhC	Y	Y	-0.6172	-2.0501	0.000000	-18.0968	-8.1446	41c
Desc	Succinate dehydrogenase gamma subunit, Succinate dehydrogenase cytochrome B-556 subunit																		
RMQ05964	0.000000	1.160	8.790	8.260	7.102	0.021437	1.830	29.184	28.559	26.823	mxaI	G	Y	0.2482	0.8244	0.002434	-5.5010	3.2776	204c
Desc	Methanol dehydrogenase small subunit (EC 1.1.99.8)																		
RMQ05965	0.000000	0.600	10.160	9.428	8.827	0.036336	0.300	28.873	27.569	27.275	mxaG	G	Y	-0.0421	-0.1397	0.265600	-1.5653		207c
Desc	Cytochrome c1																		
RMQ05966	0.000000	0.640	14.710	13.995	13.359	0.007563	0.950	34.851	33.902	32.963	mxaF	G	G	0.2498	0.8297	0.089257	-5.9896	2.2442	1256c
Desc	Methanol dehydrogenase large subunit (EC 1.1.99.8)																		
RMQ05969	0.000000	2.360	11.290	11.035	8.676	0.000174	2.660	30.172	29.755	27.097	ftfL	G	G	0.4472	1.4855	0.000000	-12.6017	7.8166	1300c
Desc	Formate-tetrahydrofolate ligase																		
RMQ05989	0.000000	-2.960	7.960	4.820	7.784	0.064761	-3.460	26.985	22.272	26.022	mqo	R	Y	-0.5311	-1.7644	0.000000	-15.1757	-6.8485	1021
Desc	Malate:quinine oxidoreductase (EC 1.1.99.16)																		
RMQ06009	0.000440	-0.610	8.080	6.743	7.356	0.045567	-0.510	27.158	25.339	25.848	phaC	R	Y	-0.2950	-0.9800	0.003842	-6.1631	-3.4135	871d
Desc	Poly 3-hydroxyalkanoate polymerase (EC 2.3.1.-)																		

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ06072	0.000000	-2.090	11.070	8.672	10.762	0.000365	-3.510	31.772	27.448	30.939	gap11	🔴 R	🔴 R	-0.4439	-1.4747	0.000000	-13.0196	-7.1152	290c
Desc	Granule associated protein																		
RMQ06075	0.000000	-0.600	9.170	7.835	8.439	0.001471	-0.770	27.962	25.976	26.746		🔴 R	🔴 R	-0.2042	-0.6783	0.012542	-4.0646	-2.9767	400d
Desc	3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6)/ Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit																		
RMQ06161	0.000000	-1.360	9.330	7.500	8.857	0.013006	-1.970	28.753	25.770	27.745	pdhA	🔴 R	🟡 Y	-0.4928	-1.6369	0.000000	-14.4125	-6.0517	757c
Desc	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)																		
RMQ06255	0.000000	-2.610	8.920	6.099	8.704	0.023999	-1.840	25.824	22.962	24.782		🔴 R	🟡 Y	-0.0996	-0.3309	0.116678	-1.3843		101
Desc	Pyruvate,phosphate dikinase (EC 2.7.9.1)																		
RMQ06367	0.000728	1.520	5.250	4.820	3.297	0.006416	3.440	24.400	24.091	20.942	mxaW	🟢 G	🟢 G	0.0474	0.1575	0.459603	-0.4135		681c
Desc	Methanol oxidation, unknown function																		
RMQ06481	0.999913	0.250	6.860	5.976	5.728	0.108721	0.520	25.548	24.460	23.790	mxaB	🟡 Y	🟡 Y	0.0664	0.2205	0.374058	-0.6229		627c
Desc	Transcriptional regulator, involved in methanol oxidation																		
RMQ06485	0.000000	-0.770	8.430	6.993	7.763	0.044933	-0.710	27.683	25.718	26.422	sucD	🔴 R	🟡 Y	-0.1853	-0.6155	0.033439	-2.7730	-2.6614	242
Desc	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)																		
RMQ06486	0.000002	-0.600	8.770	7.443	8.038	0.024029	-0.980	28.160	26.054	27.023	sucD	🔴 R	🟡 Y	-0.1876	-0.6231	0.009819	-2.6474	-3.0763	241
Desc	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)																		
RMQ06487	0.000000	-0.810	9.760	8.293	9.105	0.002013	-1.190	29.675	27.380	28.572	sucC	🔴 R	🔴 R	-0.2725	-0.9051	0.000048	-6.5944	-4.0590	655
Desc	Succinyl-CoA synthetase beta chain (EC 6.2.1.5)																		
RMQ06488	0.000000	-0.890	11.360	9.848	10.742	0.008236	-1.000	30.772	28.626	29.610	mdh	🔴 R	🔴 R	-0.0078	-0.0259	0.379707	-0.6137		74c
Desc	mdh, Malate dehydrogenase (EC 1.1.1.37)																		
RMQ06654	0.000000	-2.510	11.930	9.194	11.699	0.002695	-2.840	31.611	27.924	30.713	pntA	🔴 R	🔴 R	-0.8199	-2.7238	0.000000	-24.9448	-12.8487	697
Desc	NADP transhydrogenase alpha subunit (EC 1.6.1.2)																		
RMQ06958	0.000000	2.420	11.870	11.627	9.203	0.000395	3.010	31.828	31.478	28.481	mcl	🟢 G	🟢 G	0.7540	2.5049	0.000000	-21.2843	8.6860	506c
Desc	Malyl-CoA lyase (EC 4.1.3.24)																		
RMQ06988	0.000000	3.470	9.650	9.529	6.062	0.003479	4.400	29.424	29.225	24.825	mtkB	🟢 G	🟢 G	0.9416	3.1279	0.000000	-25.9938	15.6636	453c
Desc	Malate thiokinase, beta subunit																		

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ06989	0.000000	4.210	10.560	10.482	6.270	0.000174	4.410	29.347	29.150	24.776	mtkA	🟢	🟢	0.4131	1.3723	0.000000	-11.2565	5.6789	586c
Desc	Malate thiokinase, alpha subunit											G	G						
RMQ06990	0.000000	2.670	10.320	10.108	7.435	0.001593	3.540	28.557	28.279	24.804	fch	🟢	🟢	0.3522	1.1699	0.000051	-8.8739	4.0102	370c
Desc	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)											G	G						
RMQ07025	0.407858	-0.260	8.270	7.135	7.392	0.101564	-0.240	26.642	25.044	25.266	pqqG	🟡	🟡	0.0058	0.0193	0.572878	-0.3237		1061c
Desc	PQQ synthesis, ZINC PROTEASE											Y	Y						
RMQ07071	0.000000	-0.910	10.930	9.406	10.316	0.001447	-1.270	30.441	28.071	29.343		🔴	🔴	-0.3999	-1.3286	0.000000	-10.9756	-4.7010	609c
Desc	Citrate synthase (EC 4.1.3.7)											R	R						
RMQ07145	0.999913	0.040	7.950	6.966	6.929	0.289893	0.000	25.813	24.354	24.352	folC	🟡	🟡	-0.3996	-1.3276	0.000000	-11.3866	-7.1982	1024c
Desc	Dihydrofolate synthase, FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)											Y	Y						
RMQ07583	0.394553	0.440	6.880	6.086	5.649	0.012089	0.220	25.189	23.860	23.637	meaB	🟡	🟡	0.0173	0.0573	0.545718	-0.3072		488c
Desc	Essential for methylmalonyl-CoA mutase reaction											Y	Y						
RMQ07614	0.999913	0.020	3.420	2.430	2.414	0.137013	0.680	21.098	19.958	19.533	dmrA	🟡	🟡	-0.1233	-0.4096	0.154957	-1.0659	-2.0553	62c
Desc	Dihydromethanopterin reductase											Y	Y						
RMQ07639	0.000275	0.640	7.590	6.876	6.235	0.022387	0.840	26.280	25.284	24.433	meaD	🟢	🟡	0.0322	0.1068	0.310008	-0.8011		423c
Desc	Hypothetical cytosolic protein											G	Y						
RMQ07691	0.999913	-0.190	6.130	5.034	5.229	0.084622	-0.370	23.812	22.127	22.519	mxcQ	🟡	🟡	0.0293	0.0974	0.555174	-0.3194		986c
Desc	Sensor kinase, Methanol utilization control sensor protein moxY											Y	Y						
RMQ07705	0.000000	-1.480	10.500	8.577	10.053	0.002020	-1.550	29.715	27.134	28.673	maeB	🔴	🔴	-0.3942	-1.3095	0.000000	-8.3218	-7.1531	1497c
Desc	NAD-dependent malic enzyme (EC 1.1.1.39)											R	R						
RMQ07911	0.000000	1.190	7.730	7.202	6.015	0.016190	1.660	26.665	25.983	24.310	fdh1B	🟢	🟡	0.3250	1.0796	0.000001	-7.5724	5.5046	1287c
Desc	Tungsten-containing formate dehydrogenase beta subunit; NAD-dependent formate dehydrogenase beta subunit											G	Y						
RMQ07912	0.000000	1.320	7.670	7.181	5.858	0.021900	1.550	26.027	25.218	23.805	fdh1A	🟢	🟡	0.3437	1.1418	0.000002	-8.2193	4.8330	1987c
Desc	Tungsten-containing formate dehydrogenase alpha subunit; NAD-dependent formate dehydrogenase alpha subunit											G	Y						
RMQ07918	0.000000	0.510	12.320	11.550	11.040	0.000845	0.720	31.212	30.141	29.423	glyA	🟢	🟢	0.1625	0.5397	0.009093	-2.8804	2.7071	916c
Desc	Serine hydroxymethyltransferase (EC 2.1.2.1)											G	G						

	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
ORF	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ08314	0.999913	-0.090	7.010	5.966	6.055	0.042268	0.290	25.381	24.098	23.812	folE	🟡 Y	🟡 Y	-0.0372	-0.1235	0.464801	-0.5298		350c
Desc	folE, GTP synthase, GTP cyclohydrolase I (EC 3.5.4.16)																		
RMQ08757	0.343025	0.250	8.730	7.846	7.594	0.037149	0.190	27.417	26.062	25.871	fhcD	🟡 Y	🟡 Y	0.0548	0.1821	0.478368	-0.3466		421c
Desc	Formyltransferase/hydrolase complex, delta subunit																		
RMQ08759	0.000121	0.720	7.660	6.971	6.254	0.054804	0.480	26.523	25.351	24.856	fhcC	🟢 G	🟡 Y	0.0289	0.0961	0.564469	-0.2779		241c
Desc	Formyltransferase/hydrolase complex, gamma subunit																		
RMQ08763	0.891061	0.140	8.170	7.242	7.105	0.155222	0.200	26.190	24.880	24.659	mxbM	🟡 Y	🟡 Y	0.0373	0.1240	0.496879	-0.4208		294c
Desc	Transcriptional regulator, methanol oxidation																		
RMQ08765	0.056892	0.260	8.000	7.131	6.866	0.096333	0.390	26.737	25.527	25.117	pqqB	🟡 Y	🟡 Y	0.0130	0.0432	0.610677	-0.2382		473c
Desc	Coenzyme PQQ synthesis protein B																		
RMQ08766	0.000000	0.870	9.750	9.125	8.251	0.025692	0.890	28.573	27.597	26.755	pqqC|D	🟢 G	🟡 Y	0.0226	0.0752	0.334933	-0.9182		634c
Desc	Coenzyme PQQ synthesis protein C/D																		
RMQ08767	0.000000	1.360	7.750	7.274	5.919	0.000740	1.160	26.480	25.609	24.453	pqqE	🟢 G	🟢 G	0.2095	0.6960	0.002327	-4.2203	3.2674	693c
Desc	Coenzyme PQQ synthesis protein E																		
RMQ08769	0.999913	0.370	2.200	1.373	1.000	0.101548	2.240	17.893	17.548	14.578	folB	🟡 Y	🟡 Y	0.0255	0.0846	0.512143	-0.3359		61c
Desc	folB, Dihydroneopterin aldolase (EC 4.1.2.25)																		
RMQ08770	0.999913	0.180	5.920	5.005	4.824	0.005062	-0.300	23.706	22.057	22.352	folK	🟡 Y	🔴 R	-0.0869	-0.2888	0.239307	-0.6740	-1.7572	428c
Desc	2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase																		
RMQ08958	0.999913	-0.090	7.900	6.852	6.943	0.289893	0.010	26.065	24.583	24.586	fdh3A	🟡 Y	🟡 Y	-0.2023	-0.6721	0.049496	-1.5074	-3.8796	1684c
Desc	Formate dehydrogenase alpha subunit, Cytochrome-linked																		
RMQ09345	0.000000	-0.880	10.550	9.037	9.921	0.013242	-1.250	30.305	27.924	29.183	acnA	🔴 R	🟡 Y	-0.6833	-2.2699	0.000000	-20.2527	-8.6672	1746
Desc	Aconitate hydratase (EC 4.2.1.3)																		
RMQ09375	0.999913	-0.040	6.350	5.333	5.375	0.025848	-0.760	25.170	23.223	23.971	phaR	🟡 Y	🟡 Y	-0.0767	-0.2549	0.264675	-0.8997		681c
Desc	Regulator of PHB synthesis and acetyl-CoA flux																		
RMQ09543	0.000000	0.140	10.790	9.860	9.723	0.102426	0.190	29.765	28.428	28.247	pccB	🟢 G	🟡 Y	0.1697	0.5639	0.117155	-3.3004	2.1050	1337c
Desc	Propionyl-CoA carboxylase, beta subunit (EC 6.4.1.3)																		

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ09548	0.000000	0.580	10.100	9.365	8.780	0.007563	0.430	30.696	29.475	29.050	ccr	🟢	🟢	0.1788	0.5940	0.082700	-3.5915	2.3026	806c
Desc	Crotonyl-CoA reductase											G	G						
RMQ09623	0.557310	-0.750	5.570	4.144	4.891	0.037149	-1.480	25.049	22.420	23.948	nuoL	🟡	🟡	-0.2950	-0.9800	0.000000	-7.2439	-5.4546	1612c
Desc	NADH-quinone oxidoreductase chain L (EC 1.6.5.3)											Y	Y						
RMQ09624	0.999913	0.370	2.200	1.373	1.000	0.102426	-2.920	21.432	15.193	20.416	nuoJ	🟡	🟡	-0.2357	-0.7830	0.000128	-4.5641	-4.6119	241c
Desc	NADH-quinone oxidoreductase chain J (EC 1.6.5.3)											Y	Y						
RMQ09626	0.000002	-0.510	8.870	7.590	8.097	0.034390	-0.880	27.621	25.514	26.406	nuoF	🔴	🟡	-0.4136	-1.3741	0.000000	-9.7609	-8.1710	957c
Desc	NADH-quinone oxidoreductase chain F (EC 1.6.5.3)											R	Y						
RMQ09627	0.830251	-0.030	8.160	7.148	7.180	0.051608	-0.360	28.024	26.345	26.713	nuoE	🟡	🟡	-0.3457	-1.1485	0.000010	-6.2528	-6.4300	1025c
Desc	NADH-quinone oxidoreductase chain E (EC 1.6.5.3)											Y	Y						
RMQ09628	0.018092	-0.300	8.660	7.506	7.803	0.032127	-0.680	27.527	25.628	26.271	nuoD	🟡	🟡	-0.4280	-1.4218	0.000000	-12.2820	-7.5788	615c
Desc	NADH-quinone oxidoreductase chain D (EC 1.6.5.3)											Y	Y						
RMQ09629	0.999913	0.260	6.680	5.809	5.544	0.102426	-0.230	26.397	24.803	25.051	nuoC	🟡	🟡	-0.4174	-1.3864	0.000000	-11.2359	-7.4867	561c
Desc	NADH-quinone oxidoreductase chain C (EC 1.6.5.3)											Y	Y						
RMQ09630	0.999913	0.370	2.200	1.373	1.000	0.102426	-1.290	18.415	15.193	17.280	nuoA	🟡	🟡	-0.3998	-1.3281	0.000000	-10.7237	-6.1329	265c
Desc	NADH-quinone oxidoreductase chain A (EC 1.6.5.3)											Y	Y						
RMQ09677	0.999913	0.180	4.120	3.213	3.030	0.157581	-0.190	21.490	19.924	20.159	orf22	🟡	🟡	-0.0150	-0.0497	0.774735	-0.1182		401c
Desc	Orf22, Cofactor biosynthesis, OrfB120											Y	Y						
RMQ09678	0.999913	-0.270	3.100	1.956	2.223	0.090924	3.100	20.753	20.151	18.505	orf21	🟡	🟡	-0.1056	-0.3509	0.256804	-1.0151		360c
Desc	orf21, Cofactor biosynthesis, OrfB119, Cofactor biosynthesis, participates in tetrahydromethanopterin-linked formaldehyde oxidation, Cluster function: GLUTAMATE 5-KINASE / GAMMA-GLUTAMYL PHOSPHATE											Y	Y						
RMQ09680	0.024285	-0.840	6.550	5.072	5.915	0.034563	-1.030	24.920	22.792	23.804	orf9	🟡	🟡	0.0128	0.0426	0.638348	-0.2077		381c
Desc	tr|Q9FA36 orf9, Cofactor biosynthesis beta											Y	Y						
RMQ09682	0.000000	0.880	13.880	13.251	12.374	0.000086	1.350	33.123	32.330	30.981	fae	🟢	🟢	0.3611	1.1997	0.000000	-9.7325	6.4110	256c
Desc	Formaldehyde activating enzyme											G	G						
RMQ10718	0.000000	-4.410	5.850	1.373	5.781	0.000086	-7.330	23.282	15.193	22.515	fumC2	🔴	🔴	-0.6987	-2.3212	0.000000	-15.6215	-9.3137	194n
Desc	Fumarate hydratase, class II (EC 4.2.1.2)											R	R						

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ10844	0.999913	-1.060	2.740	1.111	2.170	0.100907	-2.710	21.277	18.683	20.398	pntA	● Y	● Y	-0.7232	-2.4023	0.000000	-22.3650	-10.5672	404n
Desc	NADP transhydrogenase subunit alpha (EC 1.6.1.2)																		
RMQ10950	0.000000	0.610	9.110	8.382	7.776	0.279368	-0.060	26.396	24.922	24.941	eno	● G	● Y	-0.0506	-0.1682	0.432975	-0.6756		37c
Desc	eno, Enolase (EC 4.2.1.11)																		
RMQ11484	0.000000	-0.970	9.690	8.131	9.099	0.001340	-1.430	28.965	26.464	27.896	sucB	● R	● R	-0.2248	-0.7469	0.000627	-4.7806	-3.1217	864c
Desc	Dihydrolipoamide succinyltransferase, component (E2 of 2-oxoglutarate dehydrogenase complex)																		
RMQ11485	0.000000	-1.640	10.850	8.814	10.452	0.014723	-1.700	29.197	26.436	28.150	sucA	● R	● Y	-0.3511	-1.1664	0.000000	-8.9532	-5.3321	1549c
Desc	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)																		
RMQ11528	0.999913	-0.110	6.540	5.487	5.600	0.152636	-0.400	23.994	22.322	22.616		● Y	● Y	0.2190	0.7276	0.044920	-5.8738	1.9235	1386
Desc	Pyruvate oxidase (EC 1.2.3.3)																		
RMQ11545	0.000000	-5.540	6.680	1.111	6.649	0.028381	-3.190	25.665	21.590	24.732	fumC2	● R	● Y	-0.2237	-0.7430	0.000653	-4.6976	-3.3997	721c
Desc	Fumarate hydratase, class II (EC 4.2.1.2)																		
RMQ11711	0.000571	0.170	10.620	9.705	9.536	0.014328	0.200	29.527	28.178	27.977	pccA	● G	● Y	0.1716	0.5701	0.004962	-2.8679	2.9367	739c
Desc	Propionyl-CoA carboxylase alpha subunit, Propionyl-CoA carboxylase biotin-containing subunit																		
RMQ11863	0.261203	-0.450	6.950	5.705	6.160	0.009386	-0.900	25.799	23.731	24.612	sucT2	● Y	● R	-0.3834	-1.2735	0.000000	-10.8270	-4.7049	778
Desc	C4-dicarboxylate transport protein / Na+ or H+ symporter																		
RMQ11864	0.999913	-0.270	6.710	5.574	5.841	0.178319	0.150	24.697	23.340	23.214	pqqF	● Y	● Y	0.0393	0.1307	0.507642	-0.3630		983c
Desc	pqqF, PQQ synthesis, ZINC PROTEASE (EC 3.4.99.-)																		
RMQ11866	0.000000	1.410	8.930	8.466	7.061	0.009966	1.610	28.112	27.424	25.815	gck	● G	● G	0.3376	1.1214	0.001748	-3.3714	4.2323	563c
Desc	Glycerate kinase																		
RMQ11999	0.000457	-0.690	7.310	5.931	6.617	0.008612	-1.080	27.815	25.583	26.663		● R	● R	-0.2212	-0.7348	0.008005	-4.8140	-2.9226	146
Desc	Pyruvate,phosphate dikinase (EC 2.7.9.1)																		
RMQ12088	0.000000	3.420	12.330	12.204	8.787	0.000174	4.370	31.779	31.578	27.209	sga	● G	● G	1.0458	3.4740	0.000000	-28.8913	12.5071	709c
Desc	Serine glyoxylate aminotransferase																		
RMQ12137	0.000000	-1.790	10.010	7.854	9.640	0.010633	-2.410	29.623	26.245	28.668	sdhA	● R	● Y	-0.6771	-2.2493	0.000000	-19.6844	-7.5234	1720c
Desc	Succinate dehydrogenase flavoprotein subunit, iron sulfur protein (EC 1.3.99.1)																		

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ12328	0.033522	1.060	5.850	5.286	4.223	0.014998	1.010	24.280	23.358	22.383	mxaC	●	●	0.1101	0.3659	0.184697	-1.6858		641c
Desc	Essential for Ca2+ insertion into MDH											Y	Y						
RMQ12329	0.003244	0.940	6.360	5.752	4.807	0.003491	1.610	25.244	24.556	22.966	mxaK	●	●	0.1192	0.3961	0.123333	-1.2696	1.8819	416c
Desc	Essential for Ca2+ insertion into MDH											G	G						
RMQ12330	0.999913	0.180	6.960	6.048	5.870	0.121704	0.150	25.437	24.038	23.900	mxaE	●	●	0.0757	0.2514	0.198889	-0.7225		332c
Desc	Methanol oxidation, unknown function											Y	Y						
RMQ12432	0.000011	0.480	9.230	8.453	7.973	0.010414	0.810	28.394	27.379	26.573	mcmB	●	●	0.1421	0.4720	0.019692	-2.0832	2.5574	1533c
Desc	mcmB, Methylmalonyl-CoA mutase beta subunit (EC 5.4.99.2)											G	Y						
RMQ12606	0.098679	-0.220	9.950	8.841	9.057	0.003827	-0.450	29.253	27.497	27.940	nuoG	●	●	-0.3057	-1.0156	0.000000	-7.2560	-5.6024	1033c
Desc	NADH-quinone oxidoreductase chain G (EC 1.6.5.3)											Y	R						
RMQ12669	0.000000	8.460	9.460	9.456	1.000	0.000086	13.220	27.864	27.769	14.578	fdh2A	●	●	0.9510	3.1591	0.000000	-26.6746	15.8053	1398c
Desc	NAD-linked formate dehydrogenase alpha subunit; Molybdenum-dependent formate dehydrogenase, alpha subunit											G	G						
RMQ12670	0.000000	8.110	9.110	9.108	1.000	0.000031	13.130	27.776	27.682	14.578	fdh2B	●	●	0.3144	1.0444	0.000005	-7.9256	4.2410	1103c
Desc	NAD-linked formate dehydrogenase beta subunit; Molybdenum-dependent formate dehydrogenase, beta subunit											G	G						
RMQ12744	0.000261	0.540	8.210	7.450	6.911	0.015433	0.830	27.440	26.438	25.623	mcmA	●	●	0.3290	1.0930	0.000107	-7.8906	4.0705	157cn
Desc	Methylmalonyl-CoA mutase alpha subunit (EC 5.4.99.2)											G	Y						
RMQ12876	0.000000	2.310	7.680	7.410	5.101	0.006231	4.010	26.492	26.249	22.298	ppc	●	●	0.5584	1.8549	0.000000	-16.7263	7.6305	1714c
Desc	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)											G	G						
RMQ12879	0.000604	0.770	7.220	6.558	5.790	0.090528	0.650	25.271	24.208	23.525	mxbD	●	●	0.0295	0.0980	0.294059	-0.6731		1201c
Desc	Sensor kinase											G	Y						
RMQ12882	0.999913	0.360	6.020	5.187	4.824	0.219837	-0.170	24.081	22.567	22.697	orf20	●	●	-0.0569	-0.1889	0.742998	-0.1315		1031c
Desc	Cofactor biosynthesis, participates in tetrahydromethanopterin-linked formaldehyde oxidation, C1-, Me-S), Dihydropteroate synthase											Y	Y						
RMQ08549	0.999913	0.150	2.300	1.373	1.220	0.102426	-1.550	18.860	15.193	18.245	fdh4	●	●	0.1746	0.5801	0.053324	-2.4532	2.3322	880
Desc	Formate dehydrogenase alpha chain (EC 1.2.1.2)											Y	Y						
RMQ02676											nuoM			-0.1967	-0.6534	0.003086	-3.3633	-3.4466	852c
Desc	NADH-quinone oxidoreductase chain M (EC 1.6.5.3)																		

ORF	Protein Spectral Count					Protein Intensity					gene name	Abundance Change		Transcription Microarray Data					
	q-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ	*q*-value	log$_2$Ratio	log$_2$Sum	log$_2$MeOH	log$_2$Succ		Sc	Pi	Log Avg Ratio	Log$_2$ Avg Ratio	Avg p-Value	Avg Log p-Value	SAM ∂=1.25 obs score	Probe
RMQ03664											nuoK			-0.2292	-0.7614	0.000017	-4.8289	-4.9262	329c
Desc	NADH-quinone oxidoreductase chain K (EC 1.6.5.3)																		
RMQ06655											pntA			-0.6281	-2.0867	0.000000	-19.6315	-9.3126	148n
Desc	NADP transhydrogenase alpha subunit (EC 1.6.1.2)																		
RMQ08550											fdh4			0.3406	1.1315	0.047664	-2.9209	2.8543	452
Desc	Formate dehydrogenase alpha chain, (EC 1.2.1.2)																		
RMQ09621											nuoN			-0.2828	-0.9395	0.000016	-5.8515	-5.0352	984c
Desc	NADH-quinone oxidoreductase chain N (EC 1.6.5.3)																		
RMQ09625											nuoH			-0.4111	-1.3656	0.000000	-11.3154	-5.5694	572c
Desc	NADH-quinone oxidoreductase chain H (EC 1.6.5.3)																		
RMQ10845											pntB			-0.7975	-2.6492	0.000000	-24.3814	-11.8044	71n
Desc	NADP transhydrogenase subunit beta (EC 1.6.1.2)																		
RMQ11702											phaA			-0.1023	-0.3397	0.069921	-1.3274	-1.8420	372cn
Desc	beta-ketothiolase, Acetyl-CoA acetyltransferase																		
RMQ11763											pntA			-0.7774	-2.5826	0.000000	-23.8968	-11.4705	213
Desc	NADP transhydrogenase subunit alpha (EC 1.6.1.2)																		
MELorf17											orf17			0.0251	0.0835	0.507965	-0.3881		451c
Desc	Cofactor biosynthesis, AF032114																		
RMQ15762											pqqA			0.4709	1.5643	0.000002	-13.5676	4.5710	19c
Desc	PQQ biosynthesis polypeptide, 29 amino acid peptide; putative, PQQ synthesis																		
MELfdh2D	0.000000	5.670	6.700	6.675	1.000	0.000107	11.120	25.765	25.670	14.578	fdh2D	● G	● G	0.6008	1.9957	0.000000	-15.7819	8.8664	61c
Desc	Molybdenum-dependent formate dehydrogenase																		

Notes for supplemental Figures SF1-SF4

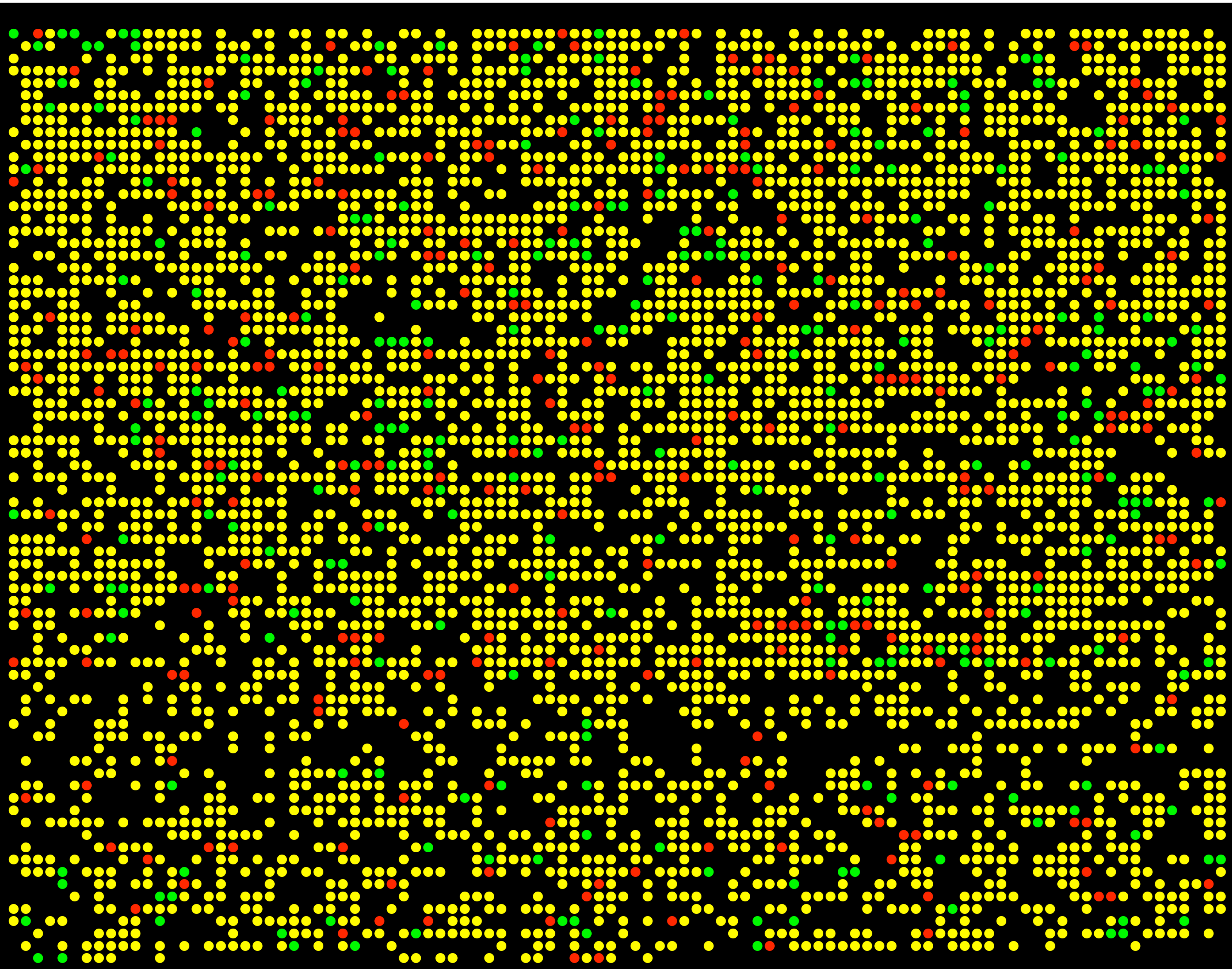
This type of figure has been referred to in our past work as a reconstructed array image and represents a computer generated global overview of the *Methylobacterium extorquens* AM1 proteomics dataset. Four such overviews are given. Unlike our previous work, there is no direct relationship implied between the physical order of the genes on their respective genetic elements and their presentation in the array images. The AM1 genome is made up of multiple genetic elements, and at this time it is not possible to illustrate with certainty in such a display which ORFs are associated with each physically distinct genetic element. Each image follows the same order as Summary Data Table S1, ascending RMQ number (2002 curation) from left to right, top to bottom, for all 7,556 entries in Table S1. The main value of the images is that they allow a quick overview of the dataset in terms of proteome coverage and the relative numbers of proteins called as changed using the two different quantitative approaches described in the paper. The color codes are the same as described in the notes for Tables S1-S3: **green**, more abundant in MeOH; **red**, more abundant in succinate; **yellow**, protein detected but without adequate statistical support for abundance change; **black**, no data for this ORF. For the proteomic data, black can mean several things: protein may have been present but was not detected, the ORF may have been annotated incorrectly, or that a protein encoding ORF exists but was not expressed under these conditions.

Figure SF1. All RMQ numbers shown according to the spectral counting results, including those that were detected qualitatively (yellow), but without adequate evidence for abundance change.

Figure SF2. All RMQ numbers showing only those with statistical support for abundance change (green and red only) by spectral counting.

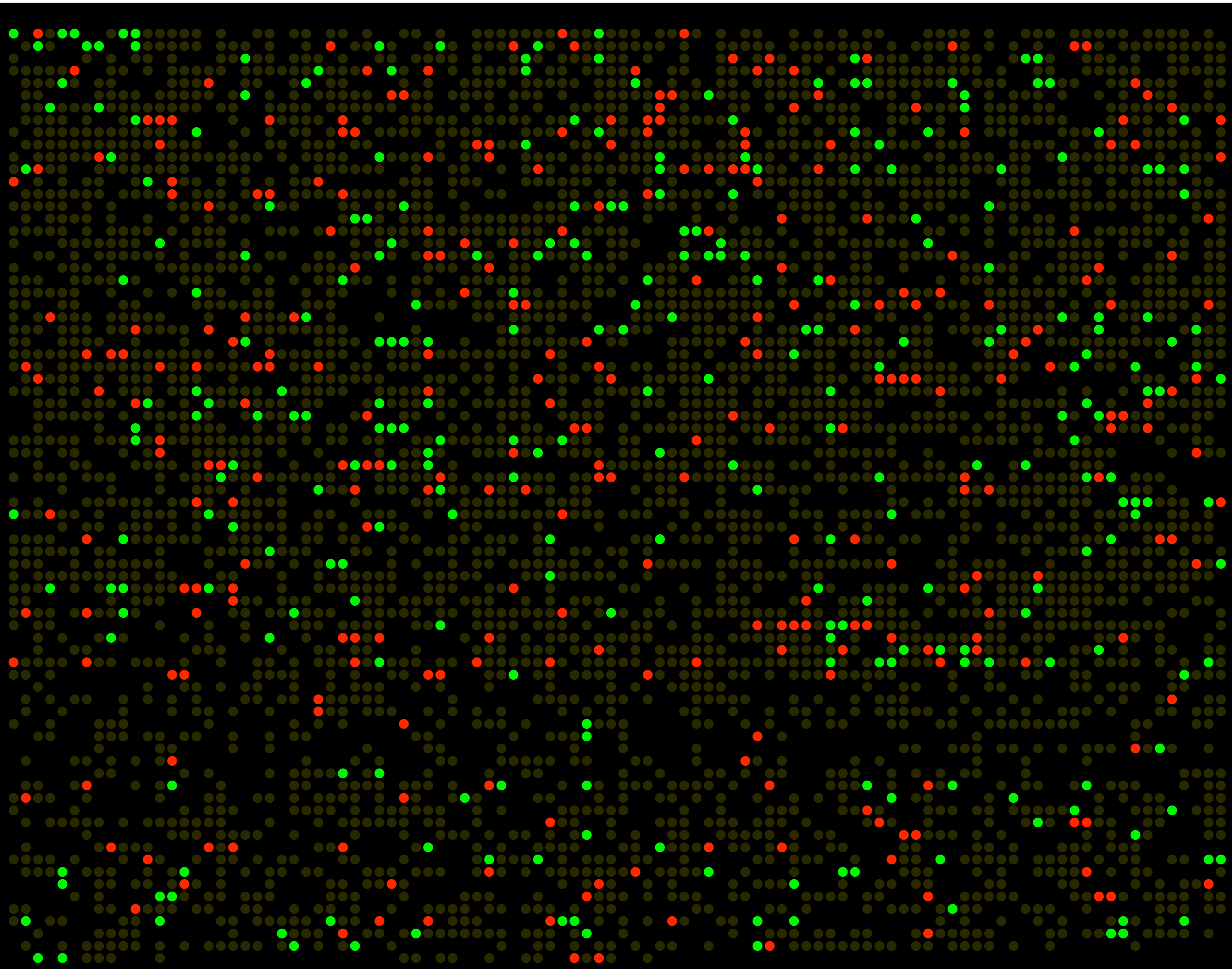
Figure SF3. All RMQ numbers shown according to the summed signal intensity results, including those that were detected qualitatively (yellow), but without adequate evidence for abundance change.

Figure SF4. All RMQ numbers showing only those with statistical support for abundance change (green and red only) by summed signal intensity.



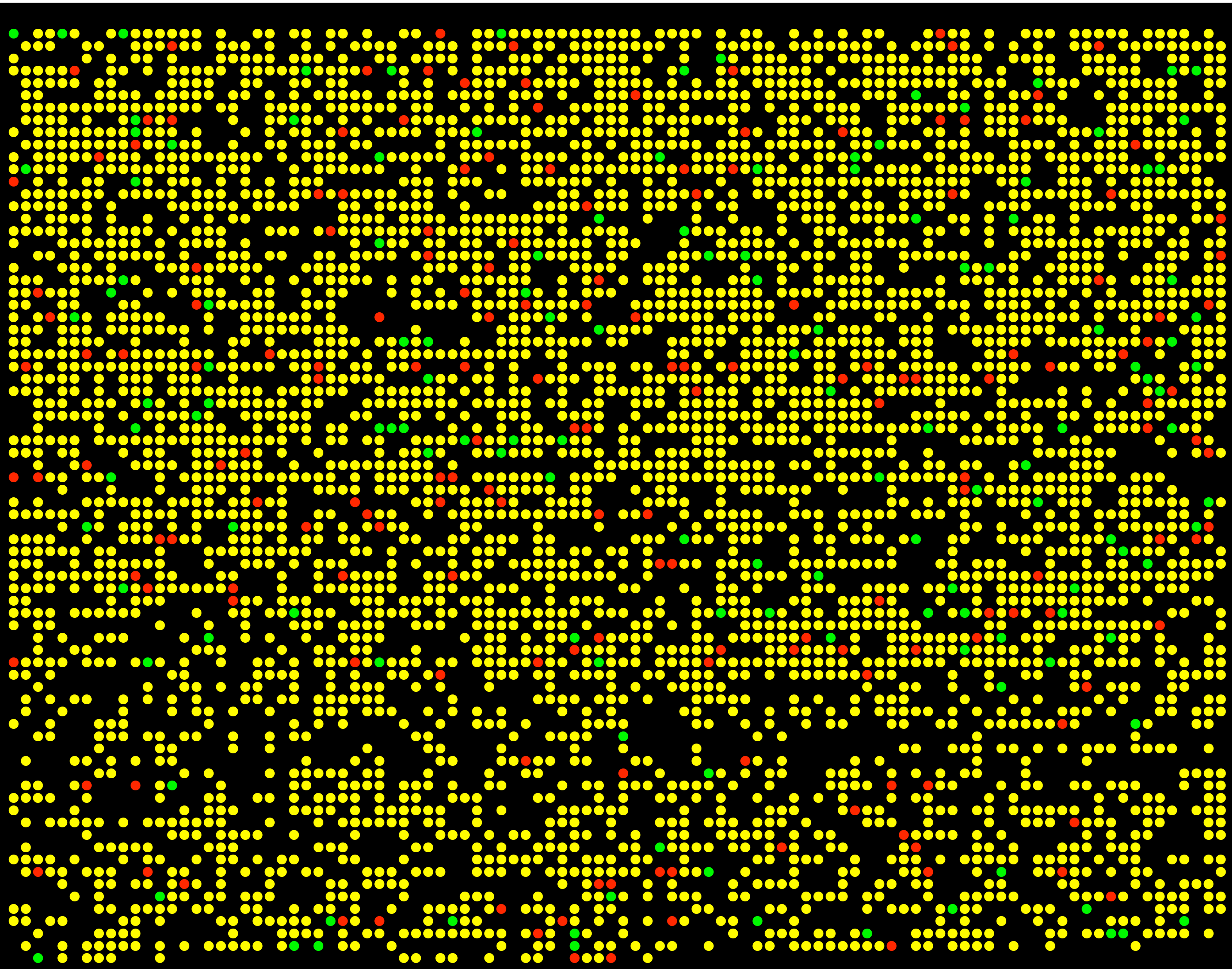
Global Spectral Counts

Supplemental Figure SF1



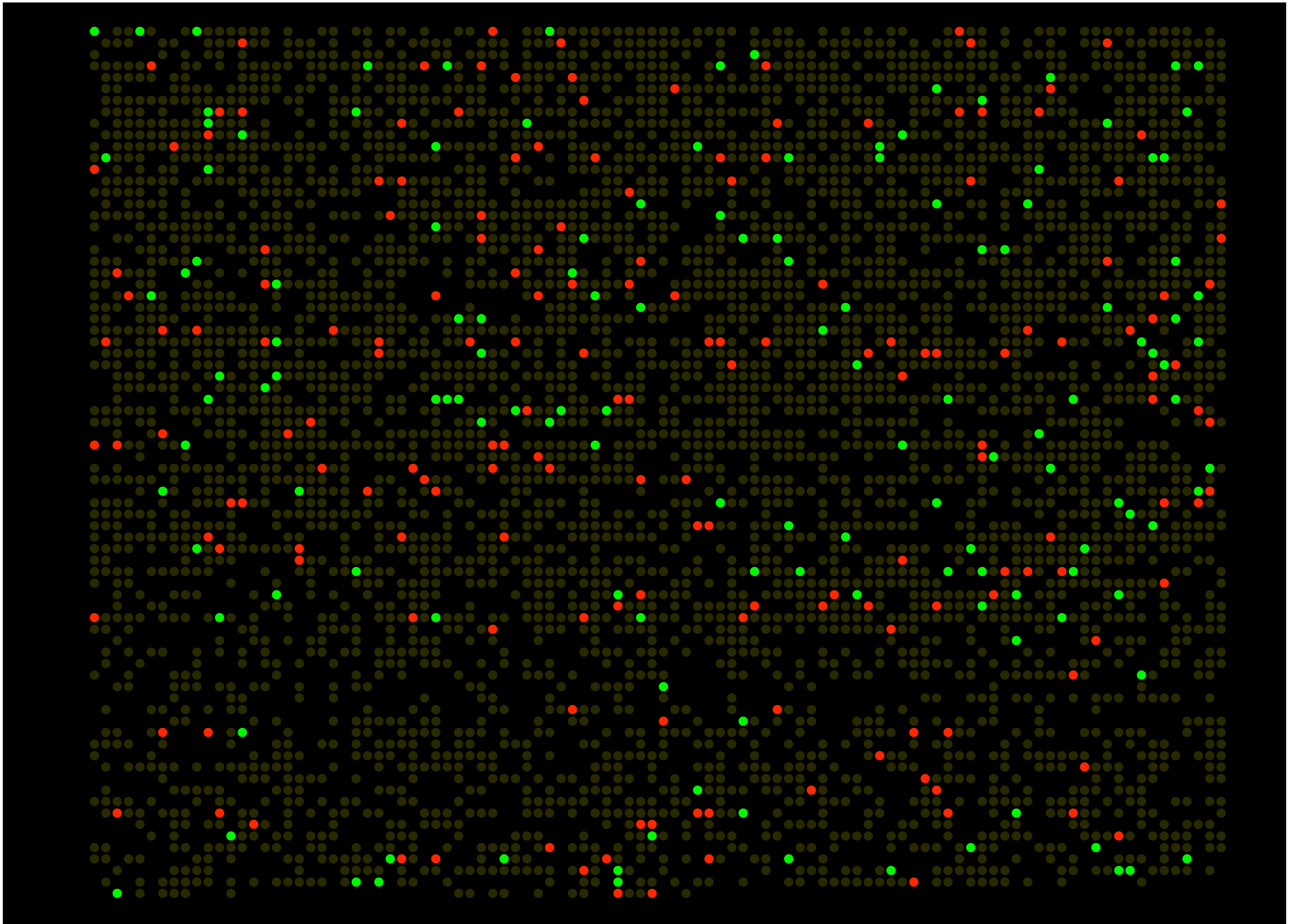
Global Spectral Counts

Supplemental Figure SF2



Global Intensity

Supplemental Figure SF3



Global Intensity

Supplemental Figure SF4

Misc. R source code used for the statistical analysis

R code for the *G*-test, calculation of G_{Total}:

```
test = read.table(file.choose(), header =T)

Protein=test$Protein

G=test$TotalG

df=test$df

for (n in 1:length(Protein)){
        pvals[n] = 1 - pchisq(G[n],df=df[n])   ## calculates p-values
        n=n+1
}

install.packages("qvalue")

library(qvalue)
## install the q-value software (computer must be connected to the internet)

qobj = qvalue(pvals)
qobj$qvalue
## calculate the q-values

q=qobj$qvalue

x=data.frame(Protein, q)

write.table (x, file = "G:\\RMQ\\ScRatios\\TotalG\\ProSc.q.txt", append =F, quote=F, row.names=F, sep="\t")
```

Normalization of the global data over all four comparisons for summed signal intensity:

Two sets of data from two biological replicates were collected for each growth condition. The sums of the signal intensities from *MeOH_1*, *MeOH_2*, *Succin_1*, and *Succin_2* were compared. *Succin_1* was chosen as the reference dataset for normalization because it had the highest value of summed signal intensity among the four datasets. The signal intensities values for the remaining three datasets were thus normalized such that the sum values of signal intensities from all four datasets became equal. The implicit assumption behind such a calculation is that the total protein expressed under each condition is about the same, an assumption that was valid for this study. This step was carried out in R. Note that the variables were given different names in the R code, mc2 = *MeOH_1*, mc3 = *MeOH_2*, sc1 = *Succin_1*, sc2 = *Succin_2*.

```
test=read.table(file.choose(), header=T) #Read in the signal intensity data.

Protein=test$Protein

mc2=test$mc2
mc3=test$mc3
sc1=test$sc1
sc2=test$sc2
sum(mc2)
sum(mc3)
sum(sc1)
sum(sc2)

max(sum(mc2), sum(mc3), sum(sc1), sum(sc2)) #Check which dataset has the highest sum value.

mc2Norm=round(mc2*(sum(sc1)/sum(mc2)),0)
mc3Norm=round(mc3*(sum(sc1)/sum(mc3)),0)
sc1Norm=sc1
sc2Norm=round(sc2*(sum(sc1)/sum(sc2)),0)

x=data.frame(Protein, mc2, mc3, sc1, sc2, mc2Norm, mc3Norm, sc1Norm, sc2Norm)

write.table (x, file = "G:\\RMQ\\PiRatios\\Total.t.test.102907\\proPi_bf_af_Norm_Oct29_07.txt", append =F, quote=F, row.names=F,
sep="\t")
```

The *p*-values and *q*-values for global intensity were subsequently calculated in R as:

```
n=4

df=n-1

pvals=2*(1-pt(abs(t),df)

library(qvalue)

qobj = qvalue(pvals)

q=qobj$qvalue
```