Explanation of Excel files containing reevaulated microarray data from Ehira & Ohmori 2006 [Molec Microbiol 59:1692-1703]

Files

- Ehira-Ohmori2006-raw.xls
  Each line in the file represents the results from microarray experiments by Ehira and Ohmori on the cyanobacterium *Anabaena* PCC 7120 subjected to nitrogen deprivation. The light columns represent experiments in which DNA from the +N condition was labeled with Cy3 and DNA from the –N condition was labeled with Cy5.

- Ehira-Ohmori2006-processed.xls
  The raw data was processed as described elsewhere in this web site. The lines are sorted by physical position of genes on the chromosome of *Anabaena*. Ehira and Ohmori considered only chromosomal genes.

- Ehira-Ohmori2006-classes.xls
  Same data as in the previous file, but organized by functional categories. Be warned that in some cases the organization is incomplete.

Explanation of columns in processed and classes spreadsheets

	Column	Explanation
A	Gene	Name of gene
B	Order	Numerical part of name (to order by physical position)
C	Name	Short functional name of gene (if known)
D	Description	Annotation of gene
E	KEGG	Kyoto Encyclopedia of Genes and Genomes categories for gene
F	EC	Enzyme Commission number
G	Het-core	T if orthologs found in all heterocystous cyanobacteria and nowhere else
H	Fil-core	T if orthologs found in all filamentous cyanobacteria and nowhere else
I	N2-core	T if orthologs fouind in all N-fixing cyanobacteria and nowhere else
J	Avar	T if orthologs found in *Anabaena variabilis*
K	Np orthologs	Name of orthologs in *Nostoc punctiforme*
L	Upstream	Nucleotides between gene and upstream gene
M	Hr	3 hours after removal of nitrogen
N	DiscardC3	T if control (+N) measurements do not pass threshold criterion at 3 hrs
O	N-C3	The number control measurements that pass threshold criterion at 3 hrs
P	C-mean3	Mean of all control (+N) chips at 3 hrs for this gene
Q	C-SD3	Standard deviation of all control (+N) chips at 3 hrs for this gene
R	DiscardT3	T if test (-N) measurements do not pass threshold criterion at 3 hrs
S	N-T3	The number of test measurements that pass threshold criterion at 3 hrs
T	T-mean3	Mean of all test (-N) chips at 3 hrs for this gene
U	T-SD3	Standard deviation of all test (-N) chips at 3 hrs for this gene
V	Discard3	T if either control or test measurements do not pass threshold criterion
W	LogR3	Log base 2 of T-mean3 / C-mean3
X	T-score3	Score from paired T-test at 3 hrs
Y	Sig?3	T if $p < 0.01$ from T-test at 3 hrs
Z	Hr	8 hours after removal of nitrogen
AA	DiscardC8	T if control (+N) measurements do not pass threshold criterion at 8 hrs

AB	N-C8	The number control measurements that pass threshold criterion at 8 hrs
AC	C-mean8	Mean of all control (+N) chips at 8 hrs for this gene
AD	C-SD8	Standard deviation of all control (+N) chips at 8 hrs for this gene
AE	DiscardT8	T if test (-N) measurements do not pass threshold criterion at 8 hrs
AF	N-T8	The number of test measurements that pass threshold criterion at 8 hrs
AG	T-mean8	Mean of all test (-N) chips at 8 hrs for this gene
AH	T-SD8	Standard deviation of all test (-N) chips at 8 hrs for this gene
AI	Discard8	T if either control or test measurements do not pass threshold criterion
AJ	LogR8	Log base 2 of T-mean8 / C-mean8
AK	T-score8	Score from paired T-test at 8 hrs
AL	Sig?8	T if $p < 0.01$ from T-test at 8 hrs
AM	Hr	24 hours after removal of nitrogen
AN	DiscardC3	T if control (+N) measurements do not pass threshold criterion at 24 hrs
AO	N-C3	The number control measurements that pass threshold criterion at 24 hrs
AP	C-mean3	Mean of all control (+N) chips at 24 hrs for this gene
AQ	C-SD3	Standard deviation of all control (+N) chips at 24 hrs for this gene
AR	DiscardT3	T if test (-N) measurements do not pass threshold criterion at 24 hrs
AS	N-T3	The number of test measurements that pass threshold criterion at 24 hrs
AT	T-mean3	Mean of all test (-N) chips at 24 hrs for this gene
AU	T-SD3	Standard deviation of all test (-N) chips at 24 hrs for this gene
AV	Discard3	T if either control or test measurements do not pass threshold criterion
AW	LogR3	Log base 2 of T-mean24 / C-mean24
AX	T-score3	Score from paired T-test at 24 hrs
AY	Sig?3	T if $p < 0.01$ from T-test at 24 hrs
AZ	LogRatioH	Log base 2 of T-mean in heterocysts / C-mean (per Ehira et al 2003)
BA	Avg C	Average of C-mean measurements
BB	Peak	Greatest of T-mean measurements
	All data below from Ehira and Ohmori (2006) Tables S1-S3, without renormalization	
BC	T3n	Log_2 (mean) in wild-type *Anabaena* at 3 hrs
BD	T3SD	Standard deviation in wild-type *Anabaena* at 3 hrs
BE	Nrr3	Log_2 (mean) in *nrrA⁻* mutant at 3 hrs
BF	Nrr3-SD	Standard deviation in *nrrA⁻* mutant at 3 hrs
BG	Nrr3-P	p value resulting from t-test comparing wild-type to *nrrA⁻* mutant at 3 hrs
BH	Nrr:wt3	
BI	T3n	
BJ	T3SD	
BK	Nrr3	
BL	Nrr3-SD	
BM	Nrr3-P	
BN	Nrr:wt3	
BO	T3n	
BP	T3SD	
BQ	Nrr3	
BR	Nrr3-SD	
BS	Nrr3-P	
BT	Nrr:wt3	