

Supplementary Table S1a

OS02g48720	Poisson Coefficient	Std. Error	z value	Pr(> z)
Dry	100	0	0	0
Nit	74.22	32.29	-0.798	0.425
Air	47.39	34.98	-1.504	0.133

Supplementary Table S1b

Os05g23720	Poisson Coefficient	Std. Error	z value	Pr(> z)
Dry	100	0	0	0
Nit	83.75	32.99	-0.493	0.622
Air	56.92	35.63	-1.209	0.227

Supplementary Table S1c

Os02g52860/ Os06g10810	Poisson Coefficient	Std. Error	z value	Pr(> z)
Dry	100	0	0	0
Nit	54.8	48.35	-0.935	0.3499
Air	-70.47	76.87	-2.218	0.0266*

Supplementary Table S1d

Os05g11780	Poisson Coefficient	Std. Error	z value	Pr(> z)
Dry	100	0	0	0
Nit	135.67	49.28	0.724	0.469
Air	100	53.45	-4.2E-11	1

Supplementary Table S1e

Os11g48040	Poisson Coefficient	Std. Error	z value	Pr(> z)
Dry	100	0	0	0
Nit	151.08	73.03	0.699	0.484
Air	-9.9	115.5	-0.951	0.341

Supplementary Table S1f

Os10g42299	Poisson Coefficient	Std. Error	z value	Pr(> z)
Dry	100	0	0	0
Nit	0	0	0.002	0.998
Air	0	0	0.002	0.998

Poisson regression analysis of spectral counting data from dry seed, aerobic and anaerobically germinated seed. Each table is headed by the gene locus number for each protein. Poisson Coefficient, coefficient of a Poisson regression equation – $\log(E(Y))=a+bx$; Std. Error, standard error; z value, standard score of Poisson distribution; $Pr(>|z|)$, probability of a value being $>+z$ or $<-z$.

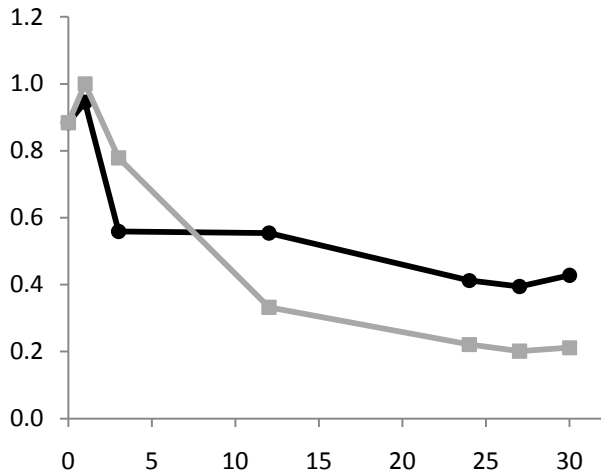
Supplementary Table S2

Os10g42299	Relative Abundance	Std. Error	T-test P=
Dry	0.23	0.03	0
Nit	0.68	0.04	0.001*
Air	0.09	0.02	0.03*

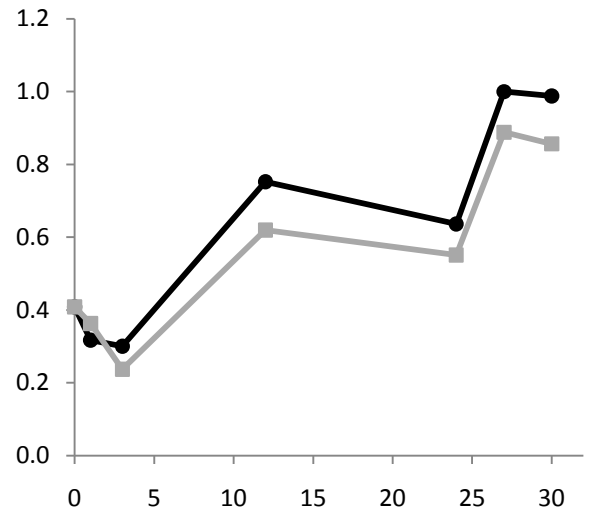
Student T-Test of QQQ data from dry seed, aerobic and anaerobically germinated seed for Os10g42299. Relative abundance, relative peak area; Std. Error, standard error; T-test P=probability of a value being $>+2\sigma$ or $<-2\sigma$.

Supplementary Figure S1

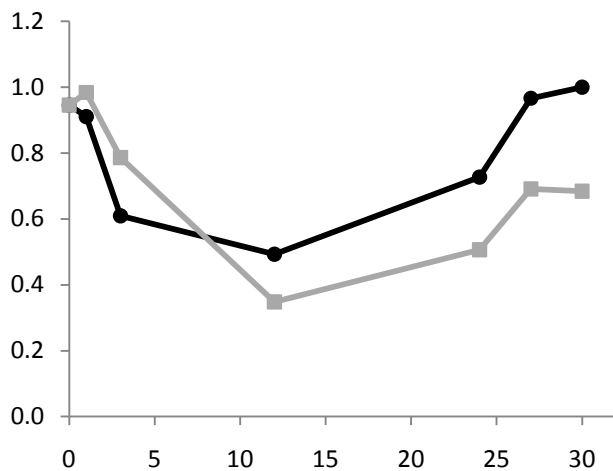
Arginase (Os04g01590)



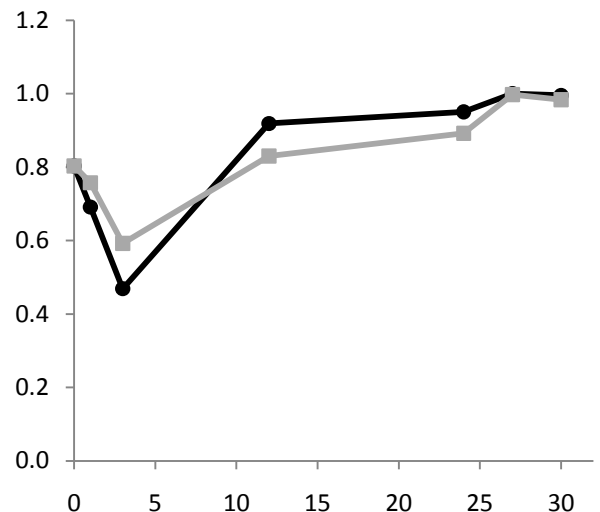
Carbamoyl-phosphate synthase large chain (Os01g38970)



Ornithine carbamoyltransferase (Os02g47590)



Argininosuccinate lyase (Os03g19280)



Changes in transcript abundance for genes of components of the Urea cycle from rice. Microarray data was extracted from supplemental data obtained from Narsai et al. (2009) over the time course of 0-30 hours post-imbibition. Rice seeds were germinated and embryos were rapidly dissected and grown in the same facilities and manner as described for this publication. Transcript abundance is shown relative to the highest hybridisation fluorescence for each gene across the time course under both aerobic and anaerobic conditions (mean fluorescence, n=3).