Supplementary information

Table S1. Metatransciptomic changes of selected marker genes in samples from *Trichodesmium* bloom and crash. Metatranscriptomic samples were obtained from the *Trichodesmium* bloom on day 23 at three successive time points [(T_0, T_8 and T_{22}, representing time from surface bloom (h)]. Columns of the table provide the respective locus_tag in the *T. erythraeum* genome, the gene name and annotation, the expected fold-change calculated from the results of ASC (see methods section), the posterior probabilities for these fold-changes as calculated by ASC (significant if $P > 0.98$, in bold), and the reads per million reads (RPM) for each time point.

	Locus_tag	Symbol	Annotation	Fold-change (from ASC)			Posterior probabilities (P) from ASC						Reads per Million reads		
				(T8/T0)	(T22/T8)	(T22/T0)	P(T0/T8>2)	P(T8/T0>2)	P(T8/T22>2)	P(T22/T8>2)	P(T22/T0>2)	P(T0/T22>2)	T0	T8	T22
Gas Vesicle Protein (Gvp) formation	Tery_2322	gvpA	Gas vesicle synthesis protein- GvpA	0.53	NA	0.27	0.43	0.00	NA	NA	0.00	0.81	8	0	0
	Tery_2323	gvpA	Gas vesicle synthesis protein- GvpA	0.41	NA	0.20	0.73	0.00	NA	NA	0.00	0.93	15	0	0
	Tery_2324	gvpA	Gas vesicle synthesis protein- GvpA	0.12	4.09	0.48	**1.00**	0.00	0.00	**1.00**	0.00	0.97	5042	603	3009
	Tery_2325	gvpA	Gas vesicle synthesis protein- GvpA	0.12	2.12	0.26	**1.00**	0.00	0.00	0.79	0.00	**1.00**	4022	497	1285
	Tery_2329	gvpN	Gas vesicle protein- GvpN	0.58	0.45	0.26	0.00	0.00	0.91	0.00	0.00	**1.00**	1964	1198	653
	Tery_2330	gvpA	Gas vesicle synthesis protein- GvpA	0.08	2.54	0.13	**1.00**	0.00	0.00	0.78	0.00	**1.00**	444	19	71
	Tery_2332	gvpK	Gas vesicle protein- GvpK	0.21	0.70	0.15	**1.00**	0.00	0.01	0.00	0.00	**1.00**	1408	306	257
	Tery_2334	gvpN	Gas vesicle protein- GvpN	1.37	0.04	0.05	0.00	0.00	**1.00**	0.00	0.00	**1.00**	464	674	19
	Tery_2335	gvpA	Gas vesicle synthesis protein- GvpA	0.67	0.41	0.27	0.00	0.00	0.90	0.00	0.00	**1.00**	479	335	164
	Tery_2338	gvpG	Gas vesicle protein- GvpG	1.11	0.26	0.28	0.00	0.00	**1.00**	0.00	0.00	**1.00**	431	505	152
	Tery_2339	gvpL/gvpF	Gas vesicle synthesis protein- GvpLGvpF	2.05	0.33	0.67	0.00	0.85	**1.00**	0.00	0.00	0.00	1608	3473	1371
	Tery_2340	gvpL/gvpF	Gas vesicle synthesis protein- GvpLGvpF	0.24	2.17	0.39	**1.00**	0.00	0.00	0.59	0.00	0.85	102	15	50
Phosphonate transporters and metabolism	Tery_0365	phnC	Phosphonate transport	3.29	1.18	4.59	0.00	**1.00**	0.00	0.01	**1.00**	0.00	16	72	105
	Tery_0366	phnD	Phosphonate transport	1.99	0.27	0.53	0.00	0.48	**1.00**	0.00	0.00	0.36	193	412	130
	Tery_0367	phnE	Phosphonate transport	0.62	1.93	1.18	0.06	0.00	0.00	0.42	0.00	0.00	126	79	192
	Tery_4993	phnD	Phosphonate transport	1.44	1.19	1.77	0.00	0.01	0.00	0.00	0.23	0.00	61	97	142
	Tery_4994	phnC	Phosphonate transport	0.87	7.90	7.71	0.00	0.00	0.00	**1.00**	**1.00**	0.00	34	30	344
	Tery_4995	phnE	Phosphonate transport	1.78	4.49	9.34	0.00	0.26	0.00	**1.00**	**1.00**	0.00	25	54	319
	Tery_4996	phnE	Phosphonate transport	5.18	0.40	2.19	0.00	**1.00**	0.85	0.00	0.67	0.00	26	166	77
	Tery_4997	phnG	Membrane associated C-P lyase	0.39	2.97	0.68	0.79	0.00	0.00	0.75	0.00	0.22	17	0	15
	Tery_4998	phnH	Phosphonate metabolism	1.16	2.70	4.04	0.00	0.03	0.00	0.82	**0.99**	0.00	10	14	59
	Tery_4999	phnI	Phosphonate metabolism	2.06	1.77	4.58	0.00	0.56	0.00	0.33	**1.00**	0.00	12	35	80
	Tery_5000	phnJ	Membrane associated C-P lyase	2.93	0.91	3.24	0.00	0.96	0.02	0.00	0.95	0.00	11	47	53
	Tery_5001	phnK	C-P lyase system	2.50	0.97	2.92	0.00	0.83	0.02	0.01	0.89	0.00	11	39	46
	Tery_5002	phnL	C-P lyase system	3.36	2.09	9.25	0.00	**0.99**	0.00	0.58	**1.00**	0.00	11	55	149
	Tery_5003	phnM	Membrane associated C-P lyase	0.84	3.94	3.87	0.04	0.00	0.00	**0.98**	**0.99**	0.00	13	11	74
Inorganic P transporters	Tery_3534	sphX	Phosphate bindig protein (regulated by P supply)	2.57	0.57	1.47	0.00	**0.99**	0.22	0.00	0.02	0.00	71	202	136
	Tery_3537	pstS	Phosphate bindig protein	0.39	4.97	1.77	0.87	0.00	0.00	**1.00**	0.23	0.00	62	19	146
	Tery_3539	pstS	Phosphate transport system permease protein 2	0.68	1.01	0.66	0.04	0.00	0.01	0.00	0.00	0.12	69	47	59
	Tery_3540	pstB	Inorganic P transporter	0.57	0.69	0.38	0.12	0.00	0.08	0.00	0.00	0.92	162	94	77
	Tery_3583	pstC	Inorganic P transporter	2.17	1.34	3.25	0.00	0.68	0.00	0.03	**0.99**	0.00	25	66	111
Degradation of organic P sources	Tery_3467	phoA	Alkaline phosphatase	1.47	2.58	3.86	0.00	0.00	0.00	**1.00**	**1.00**	0.00	179	279	885
	Tery_3845	phoX	Alkaline phosphatase	0.79	0.87	0.68	0.00	0.00	0.00	0.00	0.00	0.01	223	184	195
Arsenate	Tery_0013	arsA	arsenite-activated ATPase ArsA	0.90	0.43	0.39	0.00	0.00	**0.98**	0.00	0.00	**1.00**	1556	1466	768
	Tery_0875	arsA	arsenite-activated ATPase ArsA	0.87	0.87	0.75	0.00	0.00	0.00	0.00	0.00	0.01	151	137	146
	Tery_2327	arsA	arsenite-activated ATPase ArsA	0.30	0.61	0.18	**1.00**	0.00	0.05	0.00	0.00	**1.00**	1275	397	291
***Trichodesmium* Fe acquisition, storage, regulation ans quota reduction genes. (Gene list from Chappell and Webb 2009)**	Tery_1560	tonB	TonB family protein	2.38	0.37	0.88	0.00	**1.00**	**1.00**	0.00	0.00	0.00	979	2459	1096
	Tery_1666	fldA	Flavodoxin FldA	0.39	1.02	0.40	**1.00**	0.00	0.00	0.00	0.00	**1.00**	1535	629	777
	Tery_1667	isiA	iron-stress induced protein A, photosystem antenna protein-like, isiA	1.72	1.15	2.06	0.00	0.13	0.00	0.00	0.57	0.00	55	105	149
	Tery_1953	fur	Ferric uptake regulator	1.81	0.86	1.67	0.00	0.31	0.03	0.00	0.27	0.00	20	44	46
	Tery_1958	fur	Ferric uptake regulator	0.42	0.26	0.09	0.88	0.00	0.95	0.00	0.00	**1.00**	127	50	9
	Tery_2559	flavodoxin	Flavodoxin	0.15	2.97	0.38	**1.00**	0.00	0.00	**0.99**	0.00	0.99	541	69	263
	Tery_2787	dps	Ferritin and Dps	2.12	0.24	0.29	0.00	0.60	0.92	0.00	0.00	0.78	7	25	0
	Tery_2878	feoB	ferrous iron transport protein B	1.09	1.121	1.23	0.00	0.00	0.00	0.00	0.00	0.00	81	94	130
	Tery_2879	feoA	ferrous iron transport protein A	0.38	NA	0.19	0.79	0.00	NA	NA	0.00	0.95	17	0	0
	Tery_3222	futC	iron(III) ABC transporter, ATP-binding protein	1.08	1.79	1.96	0.00	0.00	0.00	0.18	0.41	0.00	152	174	384
	Tery_3223	futB	iron(III) ABC transporter, permease protein	2.70	1.70	5.02	0.00	**0.99**	0.00	0.15	**1.00**	0.00	38	120	254
	Tery_3377	idiA	idiA	3.27	0.37	1.23	0.00	**1.00**	**1.00**	0.00	0.00	0.00	413	1434	647
	Tery_3404	fur	Ferric uptake regulator	0.28	1.01	0.26	**1.00**	0.00	0.00	0.00	0.00	**1.00**	221	57	71
	Tery_3943	Periplasmic binding protein	Periplasmic binding protein	0.82	0.88	0.71	0.00	0.00	0.01	0.00	0.00	0.04	88	75	80
	Tery_4282	dpsA	Ferritin and Dps	1.21	0.22	0.26	0.00	0.00	**1.00**	0.00	0.00	**1.00**	491	625	158
	Tery_4448	motA/exbB	MotA/TolQ/ExbB proton channel	0.70	1.89	1.31	0.03	0.00	0.00	0.40	0.01	0.00	57	40	99
	Tery_4449	exbD	Biopolymer transport protein ExbD/TolR	2.02	1.37	3.39	0.00	0.52	0.00	0.09	**0.97**	0.00	12	33	59
Metacaspases genes	Tery_0382	TeMC8	Putative Chase2 sensor protein, metacaspase	3.25	1.04	3.49	0.00	**1.00**	0.00	0.00	**1.00**	0.00	90	322	409
	Tery_1841	TeMC7	Peptidase C14,C caspase catalytic subunit p20, metacaspase	2.60	1.11	2.92	0.00	**1.00**	0.00	0.00	**1.00**	0.00	442	1219	1647
	Tery_2963	TeMC12	Hypothetical protein	0.64	NA	0.41	0.25	0.00	NA	NA	0.01	0.63	5	0	0
	Tery_2058	TeMC6	Peptidase C14,C caspase catalytic subunit p20, metacaspase	2.91	0.44	1.28	0.00	**1.00**	0.76	0.00	0.01	0.00	61	199	102
	Tery_2077	TeMC1	Hypothetical protein, metacaspase	5.31	1.08	5.91	0.00	**1.00**	0.00	0.00	**1.00**	0.00	129	747	981
	Tery_2158	TeMC11	Hypothetical+protein	2.60	1.39	3.89	0.00	**0.98**	0.00	0.01	**1.00**	0.00	41	124	214
	Tery_2471	TeMC4	Peptidase C14,C caspase catalytic subunit p20, metacaspase	2.38	1.78	4.30	0.00	**1.00**	0.00	0.04	**1.00**	0.00	266	675	1461
	Tery_2624	TeMC10	Peptidase C14,C caspase catalytic subunit p20, metacaspase	1.46	2.07	3.19	0.00	0.01	0.00	0.58	**1.00**	0.00	58	94	245
	Tery_2689	TeMC2	Hypothetical protein, metacaspase	1.98	1.12	2.27	0.00	0.46	0.00	0.00	0.88	0.00	118	253	347
	Tery_2760	TeMC5	Peptidase C14,C caspase catalytic subunit p20, metacaspase	1.84	1.49	2.90	0.00	0.27	0.00	0.04	**0.99**	0.00	49	102	189
	Tery_3869	TeMC3	WD-40 repeat containing protein, metacaspase	2.79	2.21	6.24	0.00	**1.00**	0.00	**0.97**	**1.00**	0.00	300	889	2390
	Tery_4625	TeMC9	WD-40 repeat-containing protein, metacaspase	2.82	1.54	4.36	0.00	**1.00**	0.00	0.00	**1.00**	0.00	507	1516	2826