

Supplementary Table 1: Fold change and cluster membership of MED4 genes that are differentially expressed in response to changing iron availability.

Gene	Description	Cluster [°]	0	12	24	48	R*
PMED4_00651 (PMM0063)	conserved hypothetical protein	19	-0.08	0.62	0.81	0.91	-1.53
PMED4_00941 (PMM1805)	conserved hypothetical protein	9	-0.09	-0.69	-0.69	-0.77	1.79
PMED4_02321 (PMM0227)	ATP-sulfurylase (<i>cysD</i>)	9	-0.16	-0.33	-0.74	-0.81	1.11
PMED4_03261 (PMM1808)	conserved hypothetical protein	13	-0.20	0.98	1.15	0.06	-0.32
PMED4_03441 (PMM1811)	conserved hypothetical protein	9	-0.31	-0.74	-0.73	-0.92	1.62
PMED4_03461 (PMM0336)	conserved hypothetical (with homology to plastoquinol terminal oxidase)	19	-0.05	1.01	0.97	1.14	-2.52
PMED4_03462		9	0.43	-0.51	-0.07	-0.34	1.49
PMED4_03481 (PMM0337) ^{††}	conserved hypothetical protein	19	-0.05	0.66	1.04	0.79	-1.70
PMED4_03531 (PMM1815)	conserved hypotheical protein	19	0.34	0.85	0.83	1.16	-1.21
PMED4_03591 (PMM1873)	protein family PM-16	7	-0.07	-0.01	-1.59	-0.61	0.75
PMED4_03621 (PMM0345) [‡]	putative bacterioferritin comigratory protein	19	-0.10	0.31	0.82	1.44	-1.47
PMED4_03691 (PMM1820)	conserved hypothetical protein	6	0.12	-1.02	-0.35	-1.05	2.09
PMED4_03841 (PMM1826)	conserved hypothetical protein	9	0.31	-0.76	-0.79	-0.92	1.76
PMED4_03871 (PMM0362)	hypothetical	19	-0.04	1.49	2.65	3.40	-4.06
PMED4_03901 (PMM1828)	conserved hypothetical protein	19	-0.10	0.46	0.93	1.51	-1.18
PMED4_03961 (PMM1829)	conserved hypothetical protein	19	-0.23	0.64	0.71	0.87	-1.81
PMED4_03962		19	-0.32	0.86	0.86	1.16	-1.22
PMED4_03963		19	-0.18	1.02	1.24	1.51	-1.97
PMED4_03964		19	-0.24	0.76	0.92	1.18	-1.78
PMED4_03965		19	-0.03	0.64	1.15	1.19	-1.37
PMED4_03971 (PMM1830)	conserved hypothetical protein	13	0.18	1.22	0.66	0.71	-1.38
PMED4_03981 (PMM1831)	conserved hypothetical protein	19	0.18	1.01	0.79	1.10	-1.07
PMED4_03991 (PMM1832)	conserved hypothetical protein	19	0.39	1.07	0.89	1.21	-1.22
PMED4_04001 (PMM1833)	conserved hypothetical protein	19	-0.05	0.58	0.65	0.69	-1.19
PMED4_04031 (PMM0370)	putative cyanate ABC transporter, substrate binding protein	19	0.00	0.29	0.56	0.75	-1.10

PMED4_05091 (PMM0461) ^{††}	Cytochrome f (<i>petA</i>)	3	0.06	-0.10	-0.69	-1.06	0.86
PMED4_05101 (PMM0462) ^{††}	Rieske iron-sulfur protein (<i>petC</i>)	3	-0.20	-0.35	-0.71	-1.01	0.88
PMED4_05111 (PMM0463)	conserved hypothetical protein	19	0.11	1.25	1.44	1.71	-2.04
PMED4_05451 (PMM0496)	Putative principal RNA polymerase sigma factor (<i>sigA, rpoD</i>)	19	-0.51	0.02	0.37	0.62	-1.13
PMED4_06311 (PMM0582) ^{††}	Nucleoside-diphosphate-sugar epimerases	3	-0.23	-0.31	-0.52	-0.51	1.14
PMED4_06971 (PMM0647)	conserved hypothetical protein	19	-0.16	0.40	0.45	0.66	-1.24
PMED4_07081 (PMM1854)	conserved hypothetical protein	19	0.07	0.56	0.56	1.02	-0.87
PMED4_07131 (PMM1856)	conserved hypothetical protein	9	-0.52	-0.95	-0.89	-1.14	1.95
PMED4_07481 (PMM1864)	conserved hypothetical protein	19	0.00	0.80	0.82	1.42	-1.34
PMED4_07522		9	-0.22	-0.63	-0.26	-0.58	1.75
PMED4_07531 (PMM1868)	conserved hypothetical protein	9	-0.15	-0.09	0.07	-0.27	1.87
PMED4_07571 (PMM1870)	conserved hypothetical protein	16	0.10	0.28	0.46	1.33	-0.56
PMED4_07691 (PMM1874)	conserved hypothetical protein	19	0.45	0.81	0.90	1.50	-1.27
PMED4_07741 (PMM0702)	possible DUP family	19	-0.14	0.75	0.68	1.12	-1.19
PMED4_07751 (PMM1876)	conserved hypothetical protein	19	-0.24	0.44	0.53	0.98	-1.14
PMED4_07791 (PMM0705) [‡]	two-component response regulator, phosphate (<i>phoB</i>)	3	-0.06	-0.32	-0.48	-1.01	0.43
PMED4_08081 (PMM0731)	possible COMC family	13	0.06	0.54	0.19	0.35	-1.02
PMED4_08161 (PMM1885)	conserved hypothetical protein	22	0.74	-2.28	-0.14	0.51	-0.12
PMED4_08531 (PMM0768) ^{††}	glutamyl-tRNA reductase (<i>hemA</i>)	9	0.00	-0.41	-0.72	-0.82	1.18
PMED4_08911 (PMM0805)	Hypothetical (with homology to a Gram-negative pili assembly chaperone)	19	0.09	1.74	1.80	2.01	-3.66
PMED4_08921 (PMM0806) ^{††}	Bacterial regulatory proteins, Crp family	19	0.22	1.24	1.51	1.73	-3.54
PMED4_09091 (PMM0817)	possible high light inducible protein (<i>hli7</i>)	19	0.31	0.71	0.95	1.23	-1.29
PMED4_09101 (PMM0818)	possible high light inducible protein (<i>hli6</i>)	19	0.16	0.68	0.91	1.06	-1.23
PMED4_09321 (PMM0838)	possible Nucleoside diphosphate kinase	19	0.12	0.08	0.49	0.69	-1.11
PMED4_09651 (PMM1910)	conserved hypothetical protein	16	-0.10	1.02	1.02	1.71	-0.79
PMED4_09701 (PMM0861)	possible Virion host shutoff protein	19	0.05	0.82	0.72	0.93	-1.19
PMED4_09841 (PMM1915)	conserved hypothetical protein	19	-0.18	0.81	0.71	1.24	-1.44

PMED4_10041 (PMM0893) ^{††}	possible GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase (<i>ribB</i>)	19	-0.02	0.55	0.64	1.21	-1.12	
PMED4_10701 (PMM0958)	conserved hypothetical	19	-0.02	0.26	0.88	1.14	-1.03	
PMED4_11021 (PMM1925)	conserved hypothetical protein	9	0.06	-0.55	-0.39	-0.44	1.05	
PMED4_11221 (PMM1931)	conserved hypothetical protein	9	-0.27	-0.59	-0.28	-0.43	1.09	
PMED4_11251 (PMM1000)	conserved hypothetical protein	3	-0.07	-0.30	-0.53	-0.92	1.30	
PMED4_11391 (PMM1935)	conserved hypothetical protein	9	0.13	-0.20	-0.36	-0.59	1.30	
PMED4_11531 (PMM1940)	conserved hypothetical protein	19	-0.01	0.52	0.79	1.18	-1.04	
PMED4_11691 (PMM1949)	conserved hypothetical protein	3	-0.47	-0.52	-0.63	-0.85	2.18	
PMED4_11701 (PMM1028)	conserved hypothetical (with homology to a Carboxylesterase)	9	0.20	-0.42	-0.32	-0.61	1.94	
PMED4_11751 (PMM1032)	ABC transporter, substrate binding protein, possibly Mn (<i>iraI</i>)	19	-0.16	0.69	0.95	0.86	-1.88	
PMED4_11781 (PMM1951)	conserved hypothetical protein	3	-0.51	-0.81	-0.69	-1.29	2.43	
PMED4_11861 (PMM1041)	conserved hypothetical protein (with homology to a Hemagglutinin neuraminidase)	19	0.01	0.60	0.44	1.03	-1.38	
PMED4_12641 (PMM1118)	possible high light inducible protein (<i>hli4</i>)	19	0.38	0.92	0.96	1.10	-1.33	
PMED4_12832		19	-0.36	0.09	0.47	0.56	-1.04	
PMED4_12871 (PMM1961)	conserved hypothetical protein	9	-0.13	-0.99	-0.39	-0.77	1.64	
PMED4_12891 (PMM1135) ^{††}	possible high light inducible protein (<i>hli14</i>)	19	0.45	0.94	1.12	1.55	-1.46	
PMED4_13281 (PMM1164) ^{††}	putative iron ABC transporter, substrate binding protein (<i>afuA</i>)	19	0.00	1.47	1.59	1.68	-3.63	
PMED4_13351 (PMM1170) ^{††}	conserved hypothetical protein	19	-0.14	0.61	0.82	0.87	-1.04	
PMED4_13361 (PMM1171) ^{††}	flavodoxin (<i>isiB</i>)	19	0.00	1.23	1.56	1.84	-1.96	
PMED4_13941 (PMM1229)	dehydrogenase, E1 component	9	0.09	-0.17	-0.41	-0.43	1.04	
PMED4_14491 (PMM1283) ^{††}	Integral membrane protein, interacts with FtsH	19	0.13	0.55	0.85	0.84	-1.07	
PMED4_14671 (PMM1973)	conserved hypothetical protein	19	0.39	1.38	1.03	1.11	-1.28	

PMED4_15201 (PMM1352) ^{††}	ferredoxin (<i>petF</i>)	6	0.26	-1.06	-0.73	-1.09	1.64
PMED4_15351 (PMM1365)	possible MATH domain	13	0.41	1.12	0.59	0.80	-1.02
PMED4_15431 (PMM1979)	conserved hypothetical protein	13	0.07	0.30	0.34	0.19	-1.03
PMED4_15442		9	-0.24	-0.77	-0.60	-0.77	1.26
	conserved hypothetical protein (with homology to predicted protein family PM-23)	19	0.13	0.73	0.63	1.04	-0.99
PMED4_15451 (PMM1980)		19	0.32	0.56	0.97	1.11	-1.11
PMED4_15481 (PMM1982)	conserved hypothetical protein	19	0.36	0.74	0.58	1.08	-0.85
PMED4_15491 (PMM1983)		19	0.14	1.10	1.03	1.07	-0.42
PMED4_15531 (PMM1986)	conserved hypothetical protein						
	possible Type I restriction modification DNA s	9	-0.09	-0.84	-0.67	-1.30	2.08
PMED4_15541 (PMM1374)		9	-0.14	-0.53	-0.69	-0.48	1.17
PMED4_15611 (PMM1989)	conserved hypothetical protein	9	-0.30	-0.59	-0.77	-0.87	2.22
PMED4_15621 (PMM1990)		9	0.12	-0.59	-0.59	-0.96	2.20
PMED4_15631 (PMM1991)	conserved hypothetical protein	9	0.03	-0.29	-0.38	-0.49	1.33
PMED4_15641 (PMM1379)	putative dape gene and orf2	9	-0.36	-0.39	-0.71	-0.68	1.09
PMED4_15651 (PMM1992)		3	0.06	-0.82	-1.06	-1.47	1.96
PMED4_15652		9	0.30	-0.26	-0.87	-1.02	1.28
PMED4_15701 (PMM1994)	conserved hypothetical protein	9	-0.25	-0.03	0.75	0.98	-1.48
PMED4_15751 (PMM1996)		9	-0.20	-0.45	-0.17	-0.04	1.14
PMED4_15762		9	-0.57	-0.48	-0.04	-0.08	1.02
PMED4_15771 (PMM1998)	conserved hypothetical protein	9	-0.31	0.24	1.54	2.09	-1.55
PMED4_15781 (PMM1999)		1	0.02	-0.68	-1.52	-1.16	0.22
PMED4_15801 (PMM2001)	possible Helix-turn-helix protein, copG family	13	-0.01	0.49	0.20	0.32	-1.36
PMED4_15871 (PMM1391)		19	0.51	0.33	0.54	1.03	-0.92
PMED4_15921 (PMM2004)	conserved hypothetical protein (with homology to protein family PM-15)	19	0.21	0.56	0.85	0.98	-1.16
PMED4_15931 (PMM1396)	possible high light inducible protein (<i>hli9</i>)	19	0.28	0.68	0.93	1.17	-1.32
PMED4_15941 (PMM1397)	possible high light inducible protein (<i>hli8</i>)						

PMED4_15971 (PMM1400)	possible Hemagglutinin-neuraminidase	19	0.23	1.42	1.40	1.71	-2.37
PMED4_15981 (PMM2005)	conserved hypothetical protein	19	0.51	1.37	1.47	1.83	-2.07
PMED4_16011 (PMM1402)	Conserved hypothetical protein	3	-0.23	-0.32	-0.62	-0.79	1.24
PMED4_16051 (PMM1404) [‡]	possible high light inducible protein (<i>hlh5</i>)	19	0.46	0.65	0.84	1.00	-1.12
PMED4_16131 (PMM2010)	hypothetical protein	13	-0.09	0.41	0.12	0.12	-1.06
PMED4_16161 (PMM2012)	conserved hypothetical protein	9	0.06	-0.45	-0.95	-1.22	1.82
PMED4_16171 (PMM1412)	conserved hypothetical protein	19	-0.04	1.13	1.67	2.08	-2.29
PMED4_16221 (PMM2013)	conserved hypothetical protein	19	-0.08	1.20	1.01	1.11	-1.77
	possible Uncharacterized protein family UPF003	19	-0.23	0.74	0.79	1.15	-1.41
PMED4_16311 (PMM1424)	ATP synthase, Epsilon subunit (<i>atpC</i>)	9	-0.08	-0.24	-0.66	-0.70	1.10
PMED4_16481 (PMM1439) ^{‡‡}	Photosystem I Psal protein (subunit XI) (<i>psal</i>)	3	-0.30	-0.46	-0.67	-1.11	1.34
PMED4_17291 (PMM1519) ^{‡‡}	photosystem I subunit VIII (<i>psaI</i>)	3	-0.25	-0.37	-0.53	-0.80	1.11
PMED4_17301 (PMM1520) [‡]	putative photosystem I assembly related protein Ycf37	3	-0.21	-0.15	-0.52	-0.64	1.10
PMED4_asRNA_04601		19	0.54	-0.79	1.84	1.48	-0.56
PMED4_asRNA_07401		19	-0.22	0.21	0.82	1.23	-1.13
PMED4_ncRNA_Yfr10		3	0.02	-0.10	0.04	-0.70	1.61
PMED4_ncRNA_Yfr11		3	-0.63	-0.69	-0.78	-1.16	1.83
PMED4_ncRNA_Yfr16		9	-0.03	-1.27	-1.15	-0.75	1.58
PMED4_ncRNA_Yfr19		9	0.19	-0.29	-0.36	-0.41	1.14
PMED4_ncRNA_Yfr2		16	0.03	0.14	0.79	1.71	-0.27
PMED4_ncRNA_Yfr20		19	0.45	1.01	0.97	1.56	-2.21
PMED4_ncRNA_Yfr4		16	0.32	0.20	0.80	1.50	-0.12
PMED4_ncRNA_Yfr8		9	0.09	-0.55	-0.46	-0.43	1.70
PMED4_pseudo_3		3	-0.20	-0.28	-0.43	-0.58	1.72
PMED4_pseudo_6		4	-0.26	-0.83	-0.05	-0.54	1.61
PMM_tRNA-Ser2		19	0.13	0.29	1.19	1.36	-0.28

- All values indicate $\log_2(-\text{Fe}/+\text{Fe})$ with the exception of R where values are $\log_2(\text{experimental treatment after iron addition}/\text{experimental treatment before iron rescue})$.
 - Values in bold print have q-values<0.01. Values in red bold print have q-values<0.01 and $\log_2(\text{fold change})$ greater than 1 or less than -1.
- * Following iron addition to experimental treatment (R) – See Methods.
- Hierarchical clustering. Gene expression profiles of each cluster shown in Figure 3.
- † *Prochlorococcus* core gene.
- ‡ MED4-MIT9313 shared gene (bi-directional ortholog of MED4 and MIT9313).