

**Supplementary Table 2: Fold change and cluster membership of MIT9313 genes that are differentially expressed in response to changing iron availability.**

Gene	Description	Cluster°	0	16	28	53	R*
P9313_01131 (PMT0107)	conserved hypothetical protein	14	-0.19	0.45	0.06	<b>-1.24</b>	0.01
P9313_01141 (PMT0108)	ABC transporter, ATP binding protein	13	0.04	0.27	-0.20	<b>-1.02</b>	-0.24
P9313_01161 (PMT0110)	conserved hypothetical protein	13	-0.33	0.37	-0.14	<b>-1.64</b>	-0.02
P9313_01731	conserved hypothetical protein	10	-0.09	0.86	0.31	<b>-1.51</b>	-0.30
P9313_01981	conserved hypothetical protein	19	0.06	1.71	0.68	-0.05	<b>-1.28</b>
P9313_02141		20	-0.54	<b>1.55</b>	0.41	0.33	0.37
P9313_02281		19	0.14	<b>1.65</b>	0.46	0.07	-0.50
P9313_02851		18	0.25	0.69	0.29	<b>-1.33</b>	-0.38
P9313_03041		17	-0.24	-0.40	-0.62	<b>-1.03</b>	<b>2.00</b>
P9313_03111		26	0.24	-0.39	1.18	<b>1.10</b>	-0.24
P9313_03341 (PMT0283) <sup>††</sup>	glycyl-tRNA synthetase, alpha subunit ( <i>glyQ</i> )	4	-0.11	<b>1.95</b>	<b>1.83</b>	<b>1.89</b>	<b>-1.71</b>
P9313_03361 (PMT0284)	possible porin ( <i>som</i> )	2	-0.19	0.32	0.27	<b>1.51</b>	<b>-1.75</b>
P9313_03371 (PMT0285)	possible Peptidase family M20/M25/M40	3	-0.05	0.52	0.14	<b>1.35</b>	<b>-1.93</b>
P9313_03381 (PMT0286)	uncharacterized iron-regulated protein ( <i>piuC</i> )	4	0.02	1.11	0.74	<b>1.18</b>	<b>-0.99</b>
P9313_03391 (PMT0287) <sup>††</sup>	putative iron ABC transporter, substrate binding protein ( <i>futA1</i> )	4	-0.26	1.19	0.81	<b>2.03</b>	<b>-2.72</b>
P9313_03491		14	0.07	-0.38	0.06	<b>-1.03</b>	0.28
P9313_03641 (PMT0303)	possible Kelch motif	38	0.35	0.41	0.70	<b>1.22</b>	<b>-1.01</b>
P9313_03841	conserved hypothetical protein	30	-0.50	<b>-1.36</b>	-0.45	<b>-0.64</b>	0.69
P9313_03941 (PMT0328)	possible bromodomain adjacent to zinc finger domain, 2B...	13	-0.17	0.10	-0.16	<b>-1.13</b>	-0.11
P9313_05621 (PMT0477)	hypothetical	8	0.02	<b>1.07</b>	0.10	0.12	0.04
P9313_05661	conserved hypothetical protein	17	-0.52	0.28	-0.19	<b>-1.23</b>	0.08
P9313_05761		8	-0.10	0.93	0.26	<b>1.07</b>	0.19
P9313_05891		4	-0.09	<b>1.57</b>	<b>1.89</b>	<b>3.59</b>	<b>-3.72</b>

P9313_05901 (PMT0496)	light-harvesting complex protein ( <i>pcbB</i> )	4	-0.13	<b>2.04</b>	<b>2.38</b>	<b>3.78</b>	<b>-3.70</b>
P9313_05911	conserved hypothetical protein	2	-0.15	0.06	1.09	<b>1.43</b>	<b>-1.49</b>
P9313_05921		4	-0.09	1.77	1.79	<b>2.02</b>	<b>-1.25</b>
P9313_05941 (PMT0498)	possible Gram-negative pili assembly chaperone	30	-0.11	<b>-1.74</b>	<b>-2.07</b>	<b>-1.96</b>	<b>2.87</b>
P9313_05951 (PMT0499) <sup>‡†</sup>	ferritin	23	-0.05	<b>1.20</b>	0.54	0.44	-0.12
P9313_06081 (PMT0510) <sup>‡†</sup>	GCN5-related N-acetyltransferase ( <i>rimI</i> )	30	-0.06	<b>-1.92</b>	<b>-2.05</b>	<b>-1.61</b>	<b>1.28</b>
P9313_06881	conserved hypothetical protein	38	-0.04	0.75	1.04	<b>1.06</b>	-0.28
P9313_08511 (PMT0722) <sup>‡†</sup>	putative pantetheine-phosphate adenylyltransferase ( <i>coAD</i> )	2	-0.11	0.34	0.53	<b>1.10</b>	<b>-1.10</b>
P9313_08731		4	0.05	0.94	0.43	<b>0.87</b>	<b>-1.01</b>
P9313_09371 (PMT0801) <sup>‡†</sup>	flavodoxin ( <i>isiB</i> )	4	0.09	<b>1.81</b>	<b>1.79</b>	<b>3.19</b>	<b>-2.96</b>
P9313_09501	conserved hypothetical protein	14	0.16	-0.18	0.38	<b>-2.46</b>	-0.14
P9313_09581 (PMT0820)	conserved hypothetical protein	23	-0.03	<b>1.25</b>	0.40	0.40	-0.10
P9313_09691		1	-0.20	0.40	-0.16	<b>1.11</b>	-0.18
P9313_09901		4	-0.17	0.62	0.44	<b>1.39</b>	-0.51
P9313_09911 (PMT0842)	pyrimidine dimer DNA glycosylase	4	-0.07	<b>1.73</b>	<b>1.98</b>	<b>2.71</b>	<b>-2.91</b>
P9313_10101 (PMT0855) <sup>‡†</sup>	isochorismatase hydrolase family	4	-0.23	0.84	0.56	0.40	<b>-1.32</b>
P9313_10111 (PMT0856)	possible large-conductance mechanosensitive channel ( <i>mscL</i> )	4	-0.10	0.20	0.82	<b>1.02</b>	<b>-1.57</b>
P9313_10171 (PMT0861)	uncharacterized protein conserved in bacteria	3	0.22	-0.21	0.17	<b>0.81</b>	<b>-1.10</b>
P9313_10181 (PMT0862) <sup>‡†</sup>	predicted Fe-S oxidoreductases	4	-0.14	0.99	1.00	<b>1.03</b>	<b>-1.21</b>
P9313_10851	conserved hypothetical protein	4	0.17	0.58	0.83	<b>0.64</b>	<b>-1.40</b>
P9313_10901 (PMT0911)	hypothetical	4	-0.03	<b>1.04</b>	0.50	<b>0.58</b>	-0.66
P9313_10911	conserved hypothetical protein	2	-0.56	-0.22	0.99	<b>1.52</b>	<b>-0.97</b>
P9313_10981 (PMT0916)	hypothetical	18	-0.38	0.54	-0.40	<b>-1.22</b>	-0.07
P9313_11171		14	-0.01	-0.69	-0.25	<b>-1.97</b>	-0.40
P9313_11641		3	1.22	-0.03	0.14	<b>1.55</b>	-0.23
P9313_12191		4	-0.17	0.26	0.61	0.88	<b>-1.07</b>

P9313_12361	conserved hypothetical protein	4	0.29	0.54	0.81	<b>1.28</b>	-0.60
P9313_12371 (PMT0992)	possible high light inducible protein ( <i>hli7</i> )	4	-0.16	0.61	-0.07	<b>1.08</b>	<b>-2.78</b>
P9313_12381		2	0.09	0.15	0.87	<b>1.38</b>	-0.90
P9313_12581	conserved hypothetical protein	2	-0.03	0.26	0.88	<b>1.43</b>	-0.13
P9313_12771		38	-0.07	0.06	<b>1.10</b>	0.53	-0.51
P9313_12781 (PMT1018)	hypothetical	4	-0.07	0.60	0.41	<b>1.39</b>	<b>-0.87</b>
P9313_12801		4	-0.21	<b>5.53</b>	<b>4.01</b>	<b>6.14</b>	<b>-6.38</b>
P9313_12851 (PMT1019)	conserved hypothetical protein	38	0.23	0.11	0.60	<b>1.16</b>	<b>-0.85</b>
P9313_13161	Conserved hypothetical protein	8	0.06	<b>1.69</b>	-0.23	0.14	-0.94
P9313_13251	Conserved hypothetical protein	35	0.65	0.17	-0.10	<b>1.14</b>	0.12
P9313_13381		18	0.15	<b>1.54</b>	-0.09	-0.45	-0.21
P9313_13611		26	0.06	-0.56	0.53	<b>1.23</b>	-0.38
P9313_14621 (PMT1152)	possible high light inducible protein ( <i>hli9</i> )	3	-0.16	0.05	-0.34	0.55	<b>-1.29</b>
P9313_14641 (PMT1154) <sup>‡†</sup>	possible high light inducible protein ( <i>hli8</i> )	3	0.00	-0.18	-0.40	0.30	<b>-1.45</b>
P9313_14861	cytochrome b6-F complex subunit VII	30	0.12	<b>-1.31</b>	-0.65	-0.53	0.48
P9313_14961 (PMT1181) <sup>‡†</sup>	maf-like protein	30	-0.13	-0.87	-0.53	<b>-1.04</b>	<b>0.86</b>
P9313_15141	conserved hypothetical protein	17	-0.67	-0.59	-0.47	<b>-1.30</b>	0.61
	conserved hypothetical protein (with homology to nitrogen regulatory protein P-II)	17	-0.06	-0.35	-0.53	<b>-1.40</b>	0.37
P9313_15331 (PMT1212) <sup>‡†</sup>	possible photosystem I reaction centre subunit XII ( <i>psaM</i> )	30	0.14	-0.87	-0.41	<b>-1.12</b>	<b>0.92</b>
P9313_15411 (PMT1220)		4	0.29	0.97	0.98	<b>1.77</b>	<b>-1.43</b>
P9313_16111 (PMT1277)	hypothetical	2	0.11	0.02	1.39	<b>1.95</b>	<b>-2.18</b>
P9313_16231	conserved hypothetical protein	3	0.41	0.09	-0.15	<b>1.24</b>	<b>-0.94</b>
P9313_16241	conserved hypothetical protein	4	0.19	0.65	<b>1.71</b>	<b>1.92</b>	<b>-2.25</b>
P9313_16251 (PMT1288)	conserved hypothetical	30	-0.18	<b>-1.44</b>	-0.78	<b>-0.99</b>	<b>0.81</b>
P9313_16611	guanylate kinase ( <i>gmk</i> )	17	0.06	-0.76	-0.62	<b>-1.23</b>	0.52
P9313_17651	conserved hypothetical protein	30	-0.17	-1.17	-1.06	<b>-1.17</b>	<b>0.98</b>
P9313_18001		35	0.15	<b>-1.63</b>	-0.30	-0.01	0.51
P9313_18021							

P9313_18041 (PMT1429) <sup>††</sup>	2Fe-2S Ferredoxin:Ferredoxin ( <i>petF</i> )	30	0.01	-1.02	-0.71	<b>-0.84</b>	<b>1.27</b>
P9313_18941 <sup>†</sup>	conserved hypothetical protein	30	-0.09	-0.98	-0.75	<b>-1.40</b>	0.79
P9313_19161	conserved hypothetical protein	38	0.57	0.93	1.19	<b>2.13</b>	<b>-1.07</b>
P9313_19261	conserved hypothetical protein	18	-0.33	1.23	-0.10	<b>-1.17</b>	-0.59
P9313_19501	conserved hypothetical protein	2	-0.05	-0.15	0.24	<b>1.43</b>	-0.53
P9313_19551 (PMT1554) <sup>††</sup>	pentapeptide repeats	4	-0.31	<b>2.52</b>	<b>2.49</b>	<b>4.50</b>	<b>-4.29</b>
P9313_19831 (PMT1570)	conserved hypothetical protein	13	0.32	0.03	-0.25	<b>-1.09</b>	0.01
P9313_19851 (PMT1572)	conserved hypothetical protein	27	0.06	-0.81	-0.11	<b>-1.50</b>	0.48
P9313_19981	conserved hypothetical protein	3	0.90	0.70	-0.38	<b>1.06</b>	-0.22
P9313_20721	conserved hypothetical protein	3	0.86	0.33	0.20	<b>1.19</b>	-0.13
P9313_20761		3	-0.03	-0.80	0.04	0.55	<b>-1.23</b>
P9313_21301	conserved hypothetical protein	38	-0.78	0.46	0.64	<b>1.03</b>	<b>-1.52</b>
P9313_21331		17	-0.12	-0.28	-0.58	<b>-1.04</b>	<b>1.21</b>
P9313_21571		13	-0.03	0.31	-0.41	<b>-1.32</b>	0.21
P9313_21601		39	0.09	-0.05	0.80	<b>-1.06</b>	-0.19
P9313_22121	conserved hypothetical protein	16	0.07	-0.70	-0.83	<b>-1.29</b>	0.45
P9313_22981	conserved hypothetical protein	16	0.37	-0.05	-0.24	<b>-1.16</b>	0.79
P9313_23111 (PMT1827)	hypothetical	17	-0.16	-0.04	-0.33	<b>-1.06</b>	0.35
P9313_23481		4	0.03	0.66	0.26	<b>1.39</b>	<b>-0.77</b>
P9313_24261 (PMT1927)	putative glycosyl transferase, group 1	27	-0.24	<b>-1.20</b>	-0.05	-0.43	0.04
P9313_24921	conserved hypothetical protein	35	0.29	<b>-1.94</b>	-0.88	0.11	0.34
P9313_25471		13	-0.26	0.15	-0.33	<b>-1.38</b>	0.03
P9313_28041		17	-0.18	-0.59	-0.48	<b>-1.09</b>	<b>1.17</b>
P9313_28051	conserved hypothetical protein	17	-0.11	<b>-1.09</b>	<b>-0.77</b>	<b>-1.39</b>	<b>1.62</b>
P9313_28071	conserved hypothetical protein	17	0.11	-0.44	-0.57	<b>-1.45</b>	0.59
P9313_28081 (PMT2240)	formate and nitrite transporters	30	-0.31	-0.96	-0.66	<b>-1.04</b>	<b>1.00</b>
PMT_ffs		35	0.04	<b>-2.02</b>	-0.09	1.01	-0.25
tRNA-Ala2		3	0.44	0.44	0.10	<b>1.91</b>	-0.81
tRNA-Arg2		3	0.45	-0.02	0.24	<b>1.28</b>	-0.62
tRNA-Asn1		35	-0.16	<b>-2.62</b>	-0.74	-0.13	-0.26

tRNA-Glu1		2	-0.09	-0.06	0.06	<b>1.02</b>	-0.46
tRNA-Leu1		35	-0.40	<b>-1.25</b>	-0.63	-0.52	-0.72
tRNA-Thr3		3	0.28	-0.02	0.12	<b>1.63</b>	-0.98
ncRNA_Yfr2-5_1		1	-0.03	0.62	<b>-1.20</b>	<b>2.01</b>	-0.74
ncRNA_Yfr7		2	0.15	-0.18	-0.36	<b>1.14</b>	-0.32

- All values indicate  $\log_2(-\text{Fe}/+\text{Fe})$  with the exception of R where values are  $\log_2(\text{experimental treatment after iron addition/experimental treatment before iron rescue})$ .
- 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).