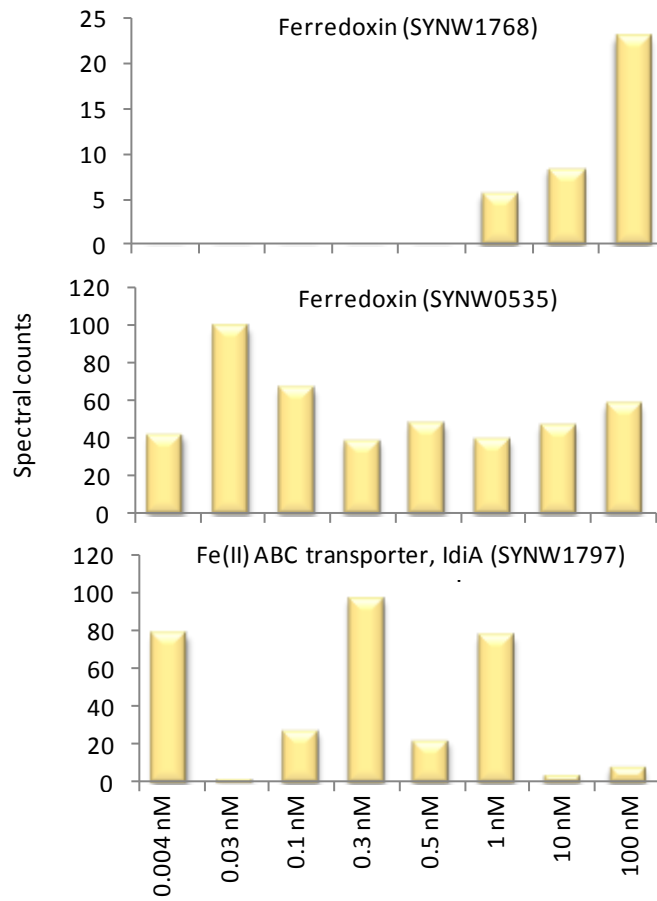


1 **Supplemental Information**

2 Figure S1: Abundance of Fe related proteins in oceanic *Synechococcus sp.* strain WH8102 in

3 response to [Fe²⁺].

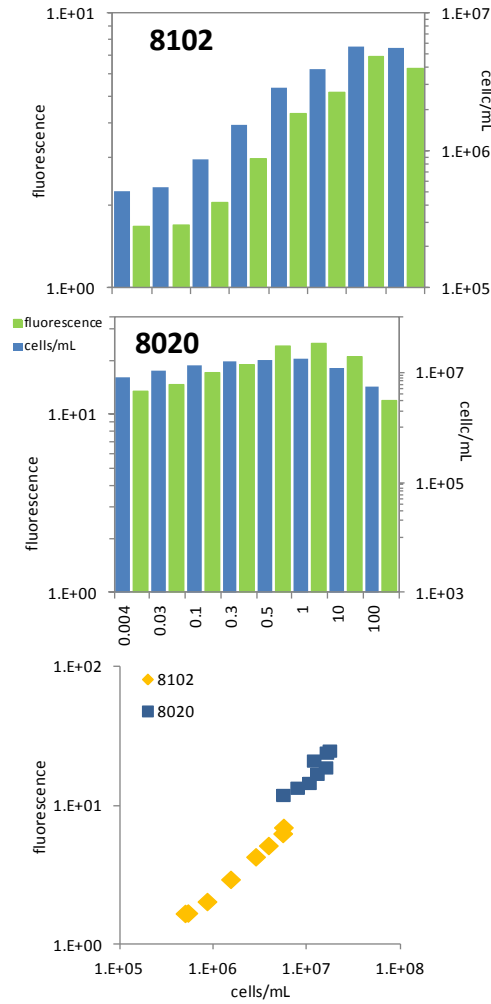
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7 Figure S2: Comparison of flow cytometry and fluorescence measurements on the final day of
8 each experiment.



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Table S1: Fe related proteins in the *Synechococcus* WH8020, WH8102, and CC9311 genomes. Proteins listed in each row represent the closest matching amino acid sequences among the three strains. Black, green, and blue text indicates that the protein in a given row is present in three, two, or one of the strain genomes respectively. This information is shown graphically in the Venn diagram in figure 3B.

WH8102		WH8020		CC9311	
ID	Protein	ID	Protein	ID	Protein
SYNW1841	Cytochrome b6/f complex subunit (Rieske iron-sulfur protein)	WB44_07765	Cytochrome b6-f complex iron-sulfur subunit PetC1 (Rieske iron sulfur protein EC 1.10.99.1)	sync_2149	cytochrome b6-f complex iron-sulfur subunit
SYNW1632	hypothetical	WB44_00870	Possible 4Fe-4S iron sulfur cluster binding protein	sync_0748	4Fe-4S iron sulfur cluster binding protein
SYNW1705	hypothetical	WB44_01950	Ferredoxin	sync_0892	ferredoxin
SYNW1277	ferredoxin		Ferredoxin	sync_1397	iron-sulfur cluster-binding protein
SYNW1768	ferredoxin	WB44_07000	Ferredoxin	sync_2017	iron-sulfur cluster-binding protein
SYNW0624	possible 3Fe-4S ferredoxin	WB44_08620	Ferredoxin	sync_2348	ferredoxin (3Fe-4S)
SYNW1981	ferredoxin	WB44_13840	Ferredoxin	sync_0535	ferredoxin (2Fe-2S)
SYNW0697	putative ferredoxin like protein	WB44_02125	Ferredoxin, 2Fe-2S	sync_0919	ferredoxin
SYNW1343	ferredoxin	WB44_02385	soluble [2Fe-2S] ferredoxin	sync_0980	ferredoxin
SYNW1274	Ferredoxin	WB44_04140	soluble [2Fe-2S] ferredoxin	sync_1394	ferredoxin (2Fe-2S)
		WB44_06700	soluble [2Fe-2S] ferredoxin	sync_1953	ferredoxin

SYNW0535	Ferredoxin	WB44_08230	soluble [2Fe-2S] ferredoxin	sync_2254	ferredoxin
SYNW0497	Ferredoxin	WB44_08440	soluble [2Fe-2S] ferredoxin	sync_2310	ferredoxin, 2Fe-2S
		WB44_10810	soluble [2Fe-2S] ferredoxin	sync_2841	ferredoxin
SYNW0521	putative ferredoxin-thioredoxin reductase, variable chain	WB44_08310	Ferredoxin-thioredoxin reductase, variable chain	sync_2274	ferredoxin-thioredoxin reductase variable chain
SYNW0318	Ferredoxin thioredoxin reductase, catalytic beta chain	WB44_09225	Ferredoxin	sync_2484	ferredoxin thioredoxin reductase, catalytic beta chain
SYNW0751	ferredoxin--NADP reductase	WB44_02485	Ferredoxin-NADP(+) reductase (EC 1.18.1.2)	sync_1003	ferredoxin--NADP reductase
SYNW2132	Ferredoxin-dependent glutamate synthase	WB44_13115	Ferredoxin-dependent glutamate synthase (EC 1.4.7.1)	sync_0387	ferredoxin-dependent glutamate synthase
SYNW2477	Ferredoxin--nitrite reductase	WB44_11090	Ferredoxin--nitrite reductase (EC 1.7.7.1)	sync_2898	ferredoxin-nitrite reductase
SYNW1095	Ferredoxin-sulfite reductase	WB44_03570	Ferredoxin--sulfite reductase (EC 1.8.7.1)	sync_1280	sulfite reductase subunit beta
		WB44_11855	Ferredoxin reductase		
SYNW1797	putative iron ABC transporter, substrate binding protein	WB44_04835	Ferric iron ABC transporter, iron-binding protein	sync_1545	ABC-type Fe ³⁺ transport system periplasmic component
SYNW1798	putative iron ABC transporter	WB44_07150	Ferric iron ABC transporter, permease protein	sync_2048	ABC-type Fe ³⁺ transport system permease component
SYNW1544	ABC transporter, ATP binding component, possibly iron transporter	WB44_06655	ABC transporter, ATP binding component, possibly iron transporter	sync_1942	ABC transporter ATP-binding protein

				sync_0682	ferrous iron transport protein A
				sync_0681	ferrous iron transport protein B
				sync_2395	iron ABC transporter ATP-binding protein
SYNW1340	ABC transporter, ATP binding domain, possibly Mn transporter	WB44_05820	ABC transporter, ATP binding domain, possibly Mn transporter	sync_1757	iron chelate ABC transporter ATP-binding protein
SYNW2366	conserved hypothetical putative integral membrane protein	WB44_10525	Mn ²⁺ and Fe ²⁺ transporter, NRAMP family	sync_2773	Mn²⁺/Fe²⁺ transporter
		WB44_04810	Ferritin	sync_1539	Ferritin
				sync_0687	Ferritin
				sync_0854	Ferritin
				sync_1077	Ferritin
				sync_0680	Ferritin
SYNW1747	ferrochelatase	WB44_06915	Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1)	sync_2000	ferrochelatase
SYNW0865	Ferric uptake regulator family	WB44_03040	Ferric uptake regulation protein FUR	sync_1167	transcriptional regulator, Fur family protein
SYNW0774	Ferric uptake regulation protein	WB44_05660	Peroxide stress regulator; Ferric uptake regulation protein; Fe ²⁺ /Zn ²⁺ uptake regulation proteins	sync_1722	transcriptional regulator, Fur family protein
SYNW2401	Ferric uptake regulator family	WB44_10775	Ferric uptake regulation protein	sync_2831	transcriptional regulator, Fur family protein

		WB44_06685	Flavodoxin 1	sync_1950	flavodoxin FldA
SYNW2368	putative flavoprotein	WB44_10555	Diflavin flavoprotein SYNW2368	sync_2780	flavodoxin:flavin reductase- likedomain-containing protein
SYNW0163	putative glycolate oxidase subunit (Fe-S)	WB44_12240	Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF	sync_0213	Fe-S oxidoreductase
				sync_2669	Iron-containing alcohol dehydrogenase
		WB44_04570	Iron-regulated protein A precursor	sync_1502	Iron-regulated protein A precursor, putative
SYNW0321	ABC transporter, membrane component	WB44_09210	Iron-sulfur cluster assembly protein SufD	sync_2481	FeS assembly protein SufD
SYNW0320	ABC transporter, ATP-binding component	WB44_09215	Iron-sulfur cluster assembly ATPase protein SufC	sync_2482	FeS assembly ATPase SufC
SYNW0319	ABC transporter, membrane component	WB44_09220	Iron-sulfur cluster assembly protein SufB	sync_2483	cysteine desulfurase activator complex subunit SufB
SYNW0317	ArsR family transcriptional regulator	WB44_09230	Iron-sulfur cluster regulator SufR	sync_2485	iron-sulfur cluster biosynthesis transcriptional regulator SufR
SYNW0712	possible sufE protein	WB44_02220	Sulfur acceptor protein SufE for iron-sulfur cluster assembly	sync_0942	Fe-S metabolism protein, SufE family protein
SYNW0007	hypothetical protein	WB44_11325	FIG01150787: hypothetical protein	sync_0007	iron-sulfur cluster binding protein, putative
SYNW2479	ABC transporter component, possibly Zn	WB44_04545	manganese/zinc/iron chelate ABC transporter (MZT) family, permease	sync_1497	manganese/zinc/iron chelate ABC transporter permease

			protein		
SYNW2480	ABC transporter,ATP binding component, possibly zinc transport	WB44_04550	ABC transporter,ATP binding component, possibly zinc transport	sync_1498	manganese/zinc/iron chelate ABC transporter ATP-binding protein
SYNW2214	hypothetical protein	WB44_09615	probable iron binding protein from the HesB_IscA_SufA family	sync_2569	iron-sulfur cluster assembly accessory protein
SYNW1990	hypothetical protein	WB44_13800	Putative heme iron utilization protein	sync_0526	hypothetical protein
		WB44_10870	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase	sync_2856	hypothetical protein

Table S2: Stoichiometric calculations of iron responsive proteins in WH8020. The quantitation is based on the average of all measurements for each peptide standard. "Low Fe" values are averages of all measurements ≤ 1 nM Fe', while "high Fe" values are averages of all measurements > 1 nM Fe'. The molecular weight and number of N atoms per protein are based on amino acid sequences for each protein.

Protein	Peptide standard target sequences	Protein molecular weight (fg / fmol)	N atoms per protein (fmol N / fmol)	Target protein abundance "Low Fe" (fmol / μ g total protein)	Target protein abundance "High Fe" (fmol / μ g total protein)	Difference in fmol between "high" and "low" treatments (fmol / μ g total protein)	Difference in fg between "high" and "low" treatments (fg / μ g total protein)	Difference in percent between "high" and "low" treatments* (%)	N content "Low Fe" (pmol N/ug total protein)	N content "High Fe" (pmol N/ug total protein)
IdiA (1196)	ADVIIIVLDAAR, LVEASGISLVQR, GLTSNVSQPYFGGDIGLIR	35907	457	7.14	0.39	6.76	242585	0.024	3.27	0.18
Ferritin (1188)	SQSNLQALDAPR, FANGDPTALLVIDNELR	20138	244	0.28	17.25	16.97	341713	0.034	0.068	4.21

Flavodoxin (1628)	DLLPGTETK, VPTDGYTFAESK	18829	149	98.88	0.038	98.84	1861086	0.19	14.73	0.0056
Ferredoxin (2042)	SGAVEQPDAMGVK, ADGFLLCVAFPCSDLR	13057	153	0.73	0.29	0.44	5745	0.00057	0.11	0.044

* Difference in percent is calculated as the difference in protein under high and low Fe conditions (in μg) divided by the total protein (in μg) multiplied by 100.

Table S3: Nutrient data from GEOTRACES cruise GT11. For samples collected via geofish, dissolved nitrate and phosphate data were selected based on the nearest sampling station to the dissolved iron sample site (less than 0.2 degrees latitude difference).

Station number	Collection method	latitude (degrees)	longitude (degrees)	nitrate (nM)	phosphate (nM)	dissolved Fe (nM)
1	Go-Flo, 30 m	39.700°N	-69.808°W	734.1	69.8	0.51
2	Go-Flo, 35 m	39.350°N	-69.541°W	83	58.2	0.54
3	Go-Flo, 28 m	38.690°N	-69.060°W	81.6	16.1	0.43
6	Go-Flo, 41 m	37.580°N	-68.437°W	22.9	16.3	0.31
8	Go-Flo, 32 m	35.420°N	-66.534°W	43.3	19.6	0.38
10	Go-Flo, 40 m	31.750°N	-64.170°W	29.77	14.5	0.42
12	Go-Flo, 41 m	29.700°N	-56.810°W	52.3	9.3	0.62
14	Go-Flo, 41 m	27.580°N	-49.630°W	45.4	7.2	0.87
16	Go-Flo, 41 m	26.136°N	-44.820°W	30	7.9	0.8
18	Go-Flo, 40 m	24.150°N	-40.210°W	81.3	11	0.54
20	Go-Flo, 41 m	22.333°N	-35.870°W	71.9	8.9	0.48
22	Go-Flo, 51 m	19.433°N	-29.380°W	27.1	9.9	0.35
24	Go-Flo, 40 m	17.400°N	-24.500°W	209.3	21.6	0.39
1	Geofish, mixed layer	39.693°N	-69.808°W	734.1	69.8	0.65
2	Geofish, mixed layer	39.350°N	-69.541°W	83.0	58.2	0.75
8	Geofish, mixed layer	35.420°N	-66.534°W	43.3	19.6	1.18
10	Geofish, mixed layer	31.750°N	-64.17°W	29.8	14.5	0.45
12	Geofish, mixed layer	29.700°N	-56.817°W	52.3	9.3	0.62
14-15	Geofish, mixed layer	27.583°N	-49.693°W	59.1	6.7	0.89
16-17	Geofish, mixed layer	26.137°N	-44.826°W	45.2	9.5	0.74
18-19	Geofish, mixed layer	24.150°N	-40.218°W	34.3	10.3	0.48
22-23	Geofish, mixed layer	19.433°N	-29.383°W	45.5	13.6	0.32
23-24	Geofish, mixed layer	17.400°N	-24.500°W	47.9	18.5	0.32

Table S4: Parallel reaction monitoring conditions for targeted natural abundance peptides and isotopically labeled peptide standards.

Protein	Peptide standard target sequences	Natural abundance mass (m/z)	Isotopically-labeled standard mass (m/z)
IdiA (1196)	ADVIIIVDAAR,	578.3402	583.3444
	LVEASGISLVQR,	636.3695	641.3737
	GLTSNVSQPYFGDIGLIR	997.5207	1002.525
Ferritin (1188)	SQSNLQALDAPR,	707.8497	712.8538
	FANGDPTALLVIDNELR	929.4889	934.493
Flavodoxin (1628)	DLLPGTETK,	487.2637	491.2708
	VPTDGYTFAESK	657.8143	661.8213
Ferredoxin (2042)	SGAVEQPDAMGVK,	644.8137	648.8208
	ADGFTLLCVAFPCSDLR	971.4635	976.4676

Table S5: global proteome data (see excel spreadsheet uploaded separately).