

Suppl. Table S3. The Irr regulon in alpha-proteobacteria

Locus ID	Operon	Position	Score	Irr site (ICE)	Function
<i>Sinerhizobium meliloti</i>					
SMc00529	<i>sufS2-sufBCDS1XA</i>	-132	6.02	AcTTTAGAAccgTTCaAAACT	Fe-S cluster assembly
SMc01119	<i>fssA</i>	-61	5.87	AtTTTgGAAcAATTCTAAAaa	hypothetical Fe-S scaffold protein
SMc03104	<i>hemA</i>	-245	5.87	AtTTTgGAATggTTCaAAACT	heme biosynthesis
SMc00784	<i>fbpA</i>	-147	5.76	AGTTTgGAAcAATTCcAAAaa	ABC-type Fe ³⁺ transport system, periplasmic component
SMc00785	<i>rirA</i>	-73	5.76	ttTTTgGAATTgTTCcAAACT	Iron-responsive regulator RirA
SMc00359	<i>mbfA</i>	-32	5.67	taaTTAGAATTATTCTAAAgA	membrane-bound ferritin
SMc04019	<i>hemH</i>	-75	5.29	ttTTTAGAAggATTtgAAACT	ferrochelatase (haem biosynthesis)
SMc00455		-99	5.28	cGTTTcGAACTGTTcGAAAtCc	putative hemolysin III
SMc03787	<i>bfd-bfr</i>	-118	5.26	AGTTTAGAATcgcTCTAAAtgc	bacterioferritin ferredoxin, bacterioferritin
SMb21432	<i>irp6A1-irp6BC</i>	-85	5.26	tGTTTgGAAgcgTTCTAAAag	ferrisiderophore ABC transporter
SMc00402	<i>irpA</i>	-117	4.86	AacTTcaAgccgTTCTAAACT	iron-regulated protein A (<i>Vibrio</i>)
<i>Mesorhizobium loti</i>					
mlr5523	<i>irpA-bfd-bfr</i>	-245	6.70	AGTTTAGAATAAATTCTAAACT	iron-regulated protein A, bacterioferritin ferredoxin, bacterioferritin
mlr4601	<i>mbfA</i>	-36	6.63	AGTTTAGAAcAATTCTAAACT	membrane-bound ferritin
mlr0015	<i>sufS2-sufBCDS1XA</i>	-151	6.38	AGTTTAGAAcTATTcAAAACCT	Fe-S cluster assembly
mll5315	<i>fssA</i>	-49	6.04	taTTTAGAAcTATTcAAAACCT	hypothetical Fe-S scaffold protein
mlr4647		-33	5.20	AGcTTAGAAATcTTCaAAACT	cytochrome b561, homologs in beta and gamma
mll2542		-89	5.16	ttTTTAtAATgATTcAAAAGT	probable drug transporter
mlr1147	<i>rirA</i>	-140	5.10	AGTcTgGAATTgTTCcAAAggT	Iron-responsive regulator RirA
mll4333	<i>ccmABCDG</i>	-85	5.02	ttTcTgGAATAgTTCTAgACa	heme export
mlr6940	<i>katG</i>	-23	5.02	AGTcTgGAATcgtTCcAgAtT	catalase (peroxidase I)
<i>Mesorhizobium sp. BNC1</i>					
MBNC03003400	<i>fbpAB</i>	-142	6.70	AGTTTAGAATAAATTCTAAACT	ferric cations ABC transporter
MBNC03003799	<i>sufS2-sufBCDS1XA</i>	-136	6.31	AGTTTAGAAcTgTTCaAAACT	Fe-S cluster assembly
MBNC03003055	<i>mbfA</i>	-38	6.20	AGTTTAGAATTATTCTAAAtCa	membrane-bound ferritin
MBNC03003089	<i>fssA</i>	-43	5.87	AtTTTAGAATTgTTCcAAAaa	hypothetical Fe-S scaffold protein
MBNC03002826	<i>katG</i>	-37	4.95	AGTcTgGAATAgTTCTAgggT	catalase (peroxidase I)
<i>Rhizobium leguminosarum</i>					
RL2583	<i>sufS2-sufBCDS1XA</i>	-132	6.36	AGTTTAGAAcAATTCgAAACT	Fe-S cluster assembly
RL0263	<i>mbfA</i>	-35	6.06	gaTTTAGAATTATTCTAAAaT	membrane-bound ferritin
RL0777	<i>rirA</i>	-68	5.95	AtTTTgGAATTgTTCaAAACT	Iron-responsive regulator RirA
RL0400	<i>fssA</i>	-43	5.30	tcTTTtGAAgcATTCTAAAgA	hypothetical Fe-S scaffold protein
RL1432	<i>feuPQ-lipA-cycHJKL</i>	-108	5.30	AGTcgAGAAcAgTTCTAAACa	regulator, maturation of cytochrome c?
RL4379	<i>hemA1</i>	-113	5.36	taTcTgGAATcATTcAAAACCT	heme biosynthesis
RL0322	<i>irpA</i>	-205	5.24	ttcTTAaAATcATTcAAAACCT	iron-regulated protein A
RL2703	<i>fumA</i>	-55	4.91	gaTTTAGAaccggTTCcAAAtCT	fumarate hydratase class I
RL2713	<i>irp6ABC</i>	-93	4.79	AGTTTgGAAacgcTCTAAAac	ferrisiderophore ABC transporter
Experimental data: Irr/iron-regulated genes (Todd et al., 2006b)					

Rhizobium etli

RHE_CH00257	<i>mbfA</i>	-35	6.22	gGTTTAGAATTATTCTAAAAtT	membrane-bound ferritin
RHE_CH00304	<i>irpA</i>	-98	5.49	AtcTTAAaAATTATTCcAAACT	iron-regulated protein A
RHE_CH00381	<i>fssA</i>	-56	5.38	tCtTTTtGAAgAATTCTAAAga	hypothetical Fe-S scaffold protein
RHE_CH00735	<i>rirA</i>	-70	5.95	AtTTTgGAATTgTTCaAAACT	Iron-responsive regulator RirA
RHE_CH02254	<i>sufS2-sufBCDS1XA</i>	-205	6.36	AGTTTAGAAcAATTCgAAACT	Fe-S cluster assembly
RHE_CH03846	<i>hemA1</i>	-117	5.18	tGtCtGGAATcATTcAAAaa	heme biosynthesis
RHE_CH02385	<i>fumA</i>	-157	4.55	caTTTAGATcggTTCcAAAttT	fumarate hydratase class I

Agrobacterium tumefaciens

AGR_C_3350	<i>sufS2-sufBCDS1XA</i>	32	6.43	AGTTTAGAATAATTCgAAACT	Fe-S cluster assembly
AGR_C_430	<i>mbfA</i>	-80	5.24	ttgTTAGAATTATTCTAAAac	membrane-bound ferritin
		-33	6.05	taTTTAGAATTATTCTAAAaa	
AGR_C_344	<i>rirA</i>	-65	5.61	ttTcTgGAATTgTTCTAAACT	Iron-responsive regulator RirA
AGR_C_346	<i>fbpA</i>	-84	5.61	AGTTTAGAAcAATTCcAgAaa	ABC-type Fe3+ transport system, periplasmic component
AGR_L_1858	<i>irgA</i>	-78	5.65	AaTTTAGAAcTgTTCgAAAac	iron-regulated outer membrane receptor irgA
AGR_C_616	<i>fssA</i>	-57	5.64	ttTTTgGAAgAATTCTAAAAtT	hypothetical Fe-S scaffold protein
AGR_C_493	<i>irpA</i>	-40	5.45	tGTTTcaAAgCATTCTAAACT	iron-regulated protein A
AGR_L_1661	<i>fhuADBC</i>	-167	5.49	AGaTTtGAATAATTCcAAgCT	hydroxamate-dependent iron uptake
AGR_C_2495	<i>fdx</i>	-70	5.27	tGTTTAGAAcAATTCtCagaT	ferredoxin, 2fe-2S
AGR_C_5028	<i>bfd-bfr</i>	-119	5.26	AGTTTAGAAcAgTCTAgAga	bacterioferritin ferredoxin, bacterioferritin
AGR_C_4738	<i>hemA</i>	-62	5.20	ttAtTgGAATggTTCaAAAca	heme biosynthesis
AGR_C_4488	<i>fatBDCE</i>	-44	5.17	AaTTcAGAAccgTTCTAAAac	ferric anguibactin ABC transporter
AGR_L_2862	<i>irp6AABC</i>	-90	4.97	AGTTaAGAATggcTCTAAAac	ferrisiderophore ABC transporter

Brucella melitensis

BMEI0354	<i>mbfA</i>	-204	6.39	AtTTTAGAATTATTCTAAAAtT	membrane-bound ferritin
BMEI0885	<i>tpd-X-ftr1-COG0348</i>	-136	5.81	tGTTTAGAATTgaTCTAAACT	High-affinity Fe2+ transport component and permease, polyferredoxin
BMEI0707	<i>rirA</i>	-161	5.41	ttTTaAGAATgATTCTAAAgt	Iron-responsive regulator RirA
BMEI1892		-306	5.70	AGTcTAGAATAtTTCTAAACT	hypothetical cytosolic protein (cysteine-rich)
BMEI1724		-102	5.18	tCtTTTaaAgccATTCTAAAAtT	hypothetical protein
BMEI0705	<i>bfd-bfr</i>	-300	5.05	ttTTTAGAATAtTTCaAAAac	bacterioferritin ferredoxin, bacterioferritin
BMEI1042	<i>sufBCDS1X</i>	-118	4.75	AGTTTAGAgaggTTtTAAAga	Fe-S cluster assembly

Bartonella quintana

BQ11660	<i>mbfA</i>	-37	5.97	AtcTTAGAATTATTCTAAAgt	ferritin-like and TM domains
BQ01080	<i>ccmABCDG</i>	-97	5.14	ttTcTAGAAcTATTCTAgAta	heme export
BQ05950	<i>sufBCDS1XA</i>	-149	5.14	gaaTTAGAATTATTtTAAAaa	Fe-S cluster assembly

Bradyrhizobium japonicum

blr7895	<i>mbfA</i>	-39	5.95	AaTTTAGAATCATTCTAAACT	membrane-bound ferritin
bsl6680	<i>bfr</i>	-61	5.50	caTTTAGAAgCgTTCTAAAAtT	bacterioferritin
bsl6681	<i>bfd</i>	-127	5.19	AtTTTAGAgcCgTTCTAggCT	bacterioferritin ferredoxin
blI7968	<i>fhuA3-piuB</i>	-115	5.12	cGcTTAGAAcCATTcAaACT	outer membrane iron receptor, Iron-uptake factor
blr4339	<i>sufBCDS1XA</i>	-103	5.07	cGgcTtGAAcGgTTCTAAgCg	Fe-S cluster assembly
blr4504	<i>fhuA1-blr4505</i>	-170	4.90	cGTcTAGAAgGATTCcAAAAtc	outer membrane iron receptor

<i>blr3904</i>	<i>fiu-piuC-exbBD-tonB2</i>	-185	4.83	gtTTTAGAAcGAcTCcAAttT	outer membrane iron receptor, iron uptake factor, iron transporter components
		-163	4.81	AcTTTAGAAcCgTTtgAAACT	
		-140	4.98	AGaTTAGAATCgTTtTgAtCT	
<i>bll5796</i>	<i>fumA</i>	-61	4.83	AGcTTAGAAcGcTTCTAtgCc	fumarate hydratase, class I
<i>blr0512</i>	<i>sdhCDAB</i>	-267	4.79	gGcTTAGAgcCgTTcCAAtag	succinate dehydrogenase
<i>bsr6522</i>	<i>feoAB</i>	-80	4.64	AcTTTAaAATCAcTCTAAggT	ferrous iron transporter
<i>blr0778</i>	<i>katG</i>	113	4.64	gGcTTAGAgTGgTTCTAcctg	catalase (peroxidase I)
<i>bll0768</i>	<i>irr</i>	-95	4.63	cGaTTAGAAcCtcTCTAgttg	iron response regulator
<i>bll7076</i>	<i>hmuR-XX-exbBD-tonB1</i>	-166	4.62	AaTTTAcAATCgaTaTAAACT	hemin receptor
<i>blr7077</i>	<i>hmuTUV</i>	-303	4.62	AGTTTAtAtcGATTgTAAAtT	hemin ABC transporter
<i>bll3138</i>	<i>nuoEF-fdhFD-bll3134</i>	-57	4.57	AtcTTcGAATGATTcAAAAta	NAD-dependent formate dehydrogenase
<i>bll2737</i>	<i>bll2737-bll2736</i>	-51	4.56	tGaTTtGAAcagTTcCAAttT	Fe-S oxidoreductase, putative aldehyde dehydrogenase
<i>blr674</i>	<i>blr6742-blr6743-blr6744</i>	-126	4.51	AcTTcgGAAgAgTTCTAAtaa	pyridine nucleotide-disulphide oxidoreductase, ferredoxin oxidoreductase
<i>blr2933</i>		-45	4.44	tGaTTgGAATGATTtcAgACT	probable aerotaxis receptor
<i>bll4919</i>	<i>nuoABCDEFGHIJLMN</i>	-68	4.43	gGcTcAGAATaATTcAAAAtc	NADH ubiquinone oxidoreductase
<i>bll4920</i>	<i>fhuA2</i>	-120	4.43	AtgTTgGAtcGcTTCTAAgag	outer membrane iron receptor
<i>blr1720</i>	<i>hupSLCDFGHIJK-hypABFCD</i>	-82	4.43	AcTTTtGAATCgcTcCAggCT	membrane-bound uptake hydrogenase
<i>bll0466</i>	<i>acnA</i>	-134	4.41	cGgTTAGAAaGcTTCTAtAag	aconitase
<i>bll5701</i>	<i>cycB-bll5700</i>	-101	4.22	AaTTTtGAAcGATTcAAtttc	cytochrome b561, glutathione S-transferase

Expression data: Iron- and/or Irr-regulated genes (Roudolph et al., 2006 and Yang et al., 2006)

Bradyrhizobium sp. BTAi1

<i>Brad_6124</i>	<i>fhuA2-piuB2</i>	-112	4.36	gagTTtAATAATTCTAAAta	outer membrane iron receptor, Iron-uptake factor
<i>Brad_3189</i>	<i>mbfA</i>	-59	5.86	AcTTTAGAAgCgTTCTAAACa	membrane-bound ferritin
<i>Brad_5789</i>		-35	5.16	ttTTTAGAAcgtTTCTAAAtT	conserved hypothetical protein
<i>Brad_3567</i>	<i>Brad_3567 - fhuA-piuB</i>	-151	5.07	gaTTTgGAAccgTTCTAAAta	outer membrane iron receptor, Iron-uptake factor
<i>Brad_3512</i>	<i>feoAB</i>	-78	5.02	tGTTTAaAATcgcTCTAAgaT	ferrous iron transporter
<i>Brad_2353</i>		-77	4.97	AaTcTAGAAgcATTcCAAtCa	probable aerotaxis receptor
<i>Brad_4228</i>	<i>fiu-piuC-exbBD-tonB2</i>	-198	4.86	gtTTTAGAAcGATTtcAAgtT	outer membrane iron receptor, iron uptake factor, iron transporter components
<i>Brad_4228</i>		-156	4.88	ttTTTAGAATTgTTtTgAtCT	
<i>Brad_0131</i>		-106	4.80	AacTcAGAAcAgTTCaAAAaa	regulatory protein, similar to LuxR
<i>Brad_1683</i>	<i>bfd-bfr</i>	-95	4.38	AGaTTgGAATAgcTtcAAAag	bacterioferritin ferredoxin, bacterioferritin
<i>Brad_5162</i>	<i>irr</i>	-76	4.25	AGTTTAGggcgTTCTAgAtc	iron response regulator
<i>Brad_3677</i>	<i>nifHDKX</i>	-201	4.25	ccTTTtAAcGATTcAAAagc	molybdenum-iron nitrogenase
<i>Brad_1627</i>	<i>Brad_1627-1626-1625</i>	-175	4.21	gccTTgGAATggcTCTAgTCT	pyridine nucleotide-disulphide oxidoreductase, ferredoxin oxidoreductase
<i>Brad_3993</i>	<i>nuoEF-fdhFD-bll3134</i>	-62	4.14	taTcTtGAgcAATTcCAAttc	NAD-dependent formate dehydrogenase
<i>Brad_3670</i>	<i>frd-sufBCDS</i>	-109	4.13	AaTTTAGAATccTcCTtAgaa	ferredoxin, FeS cluster assembly

Rhodopseudomonas palustris CGA009

<i>RPA4303</i>	<i>mbfA</i>	-33	5.51	taTTTAGAAgCgTTCTAAACT	membrane-bound ferritin
<i>RPA4636</i>	<i>feoAB</i>	-78	5.19	ctgTTAcAATCgTTCTAAACT	ferrous iron transporter
<i>RPA1876</i>	<i>fhuA1</i>	-222	4.95	tGaTTtGAAcGATTcAAAaT	outer membrane iron receptor
<i>RPA4152</i>	<i>fbpAB</i>	-99	4.81	cGgcTgGAATagTTCTAAAtCg	ferric cations ABC transporter

RPA3600	<i>bfr</i>	-66	4.79	gaTcTAGAATtATTCTAAAtc	bacterioferritin
RPA0765	<i>RPA0765</i>	-317	4.74	gGTTTtGAAgGccTCTAAAtCg	outer membrane iron receptor
RPA1845	<i>fcuA3</i>	-266	4.73	AGcTcgGAATCgTTCTAgAtT	outer membrane iron receptor
		-129	4.43	AcaaTAGAgTCgTTCTAAgtT	
RPA3195	<i>iorAB</i>	-73	4.60	AGcTTAGAcTGgTTCgAAACa	indolepyruvate ferredoxin oxidoreductase
RPA3480	<i>fiu-piuC-exbBD-tonB3</i>	-306	4.60	ttcTTAGAATGATTtTgAtCT	outer membrane iron receptor, iron uptake factor, iron transporter components
RPA2464	<i>sufBCDS1XA</i>	-101	4.58	gtgcTtGAAcGgTTCTAAgag	Fe-S cluster assembly
RPA1224	<i>iorAB2-oorABC</i>	-51	4.47	ccTTTAcAgcagTTCTAAAtCg	indolepyruvate ferredoxin oxidoreductase, 2-oxoglutarate dehydrogenase
RPA4430	<i>RPA4430-piuB</i>	-87	4.47	ccgTTAGAcTGATTcCAAgCT	outer membrane iron receptor, iron-uptake factor
RPA2307	<i>RPA2307</i>	-207	4.46	AGAcTAGAATCtCtCaAgACT	outer membrane iron receptor
RPA2308	<i>RPA2308-2310</i>	-48	4.46	AGTcTtGAgGATTCTAgTCT	hypothetical iron siderophore ABC transporter
RPA3282	<i>fecIR-hmuR2</i>	-112	4.45	cGgcTAGAgcCAaTCTAAAtc	iron transport sigma factor and sensor, heme receptor
RPA2026	<i>fcuA1</i>	-123	4.29	tgcTAgAAcGgTTCTAgTgg	ferrichrome receptor
RPA0489	<i>fdx</i>	-26	4.21	AaaTTAGAAcCgTTCcggAgc	ferredoxin II
RPA3414	<i>fhuA2-X</i>	-115	4.18	tGTTTcGAgcaATTcCAAtCc	outer membrane iron receptor
RPA2121	<i>hmuPTUV</i>	-86	4.14	cGTTTAtAgTaATTaTAAgac	heme ABC transporter
RPA2122	<i>hemN3</i>	-267	4.14	gtcTTAtAATtAcTaTAAACg	paralog of oxygen-independent coproporphyrinogen III oxidase
RPA3840	<i>fhuA3-XX</i>	-110	4.13	gacgTAGAAcGtTTgTAAAtCg	outer membrane iron receptor
RPA2124	<i>hmuR1-XX-exbBD-tonB1</i>	-163	4.04	AagTTAtAATtgcTtTAAAtCa	heme uptake
RPA3876	<i>fumA</i>	-81	3.94	cccTTAGAggtATaCTAAAtg	fumarate hydratase class I
RPA2390	<i>rhbCF-XXX-fatBDCE-fecR</i>	-112	3.91	tGaTTgGttgaATTCTAAACT	siderophore biosynthesis, ferric anguibactin ABC transporter

***Nitrobacter winogradskyi* Nb-255**

Nwi_2475	<i>bfr</i>	-80	5.15	gaTTTAGAAgtATTCTAAAtT	bacterioferritin
Nwi_0035	<i>irr</i>	-113	4.87	AGTTTtGAgcCATTCTAgTtg	iron regulatory protein Irr
Nwi_3045	<i>fecIR-fhuA1</i>	-62	4.76	AGcTTAGAAcCAaTcCAgACa	iron sigma factor and sensor, outer membrane iron receptor
Nwi_0894	<i>fecIR-omp</i>	-226	4.66	tCtTAGAAcCAaTCTAAAtg	iron sigma factor and sensor, outer membrane iron receptor
Nwi_1340	<i>fecIR-fhuA3</i>	-55	4.6	gGTTTAGAtgCgaTCTAAAgT	iron sigma factor and sensor, outer membrane iron receptor
Nwi_2582	<i>cycA1</i>	-169	4.52	AcacTcGAATCgTTCTAAgaT	cytochrome c class I
Nwi_1204	<i>glgP</i>	-198	4.51	cGcTTAaAAaCgcTCTAAgtg	glycogen phosphorylase
Nwi_2048	<i>fecI1</i>	-139	4.45	cacTTAGAAgCtCtCCaAACT	iron transport sigma factor
Nwi_2462		-140	4.45	gGTTTAtAgcGtTTCaAAACg	hypothetical protein
Nwi_1467		-94	4.41	gagaTAGAATCATTcCAAcCg	hypothetical protein
Nwi_0773	<i>cycA1-narG</i>	-144	4.36	gtTTTctAAcGATTCTAgTCT	cytochrome c class I, nitrate reductase
Nwi_0902	<i>fecI2</i>	-88	4.36	ctcTTAaAccCATTCTAAAtc	iron transport sigma factor
Nwi_2813	<i>piuB-COG3656</i>	-128	4.35	taTTTAGAATGAacCTAAAtCT	Iron-uptake factor, hypothetical lipoprotein
Nwi_1734	<i>fecIR-omp</i>	-21	4.31	tccTAGAATCAaTCTAgAtc	iron sigma factor and sensor, outer membrane iron receptor
Nwi_2610		-81	4.3	cGgTTAGAAaagTTCaAgTtg	hypothetical protein
Nwi_0703	<i>exbBD-tonB2</i>	-474	4.26	AaTcTAGAAgGATTCTtAAgT	components for TonB-dependent iron transporters
Nwi_0700	<i>fiu-piuC</i>	-92	4.25	gGTTTAGAtgaATTCTAtAaT	outer membrane iron receptor, iron uptake factor piuC
Nwi_2883	<i>fecIR-fhuA2</i>	-196	4.19	ttcTTAaAcTCATTCTAAAta	iron sigma factor and sensor, outer membrane iron receptor

Nwi_3079	<i>fecIR-fhuA4</i>	-249	<u>4.17</u>	ttTcTAGAAcaggTCTAAAtc	iron sigma factor and sensor, outer membrane iron receptor
Nwi_1966	<i>fecI3</i>	-562	<u>4.06</u>	AcTTTgGAaccGgaTCTAAAtc	iron sigma factor
Nwi_0724	<i>fecR-fhuA5</i>	-45	<u>3.93</u>	cGcTTgAaaaCgcTCTAggaT	iron sensor, outer membrane iron receptor
Nwi_2053	<i>tonB</i>	-279	<u>3.91</u>	AcTTTcGAAgtATTcCaAgttT	component for TonB-dependent iron transporters
Nwi_2051	<i>fecIR-omp</i>	-126	<u>3.89</u>	gcaTTAGAcgCtaTCTAAACT	iron sigma factor and sensor, outer membrane iron receptor
Nwi_0242	<i>hemA</i>	-65	<u>3.86</u>	ccgcTgGAAaGgcTCTAAaaa	heme biosynthesis
Nwi_2976	<i>feoAB</i>	-197	<u>3.85</u>	AcTTTttAATCATTCcAgcaa	ferrous iron transporter

Nitrobacter hamburgensis X14

Nham_3279	<i>fiu2-piuC2</i>	-245	5.13	AaTTTAGAATCgTTtTAAAAa	outer membrane iron receptor, iron uptake factor piuC
		-152	4.31	gaTTTAGAtaGATTCaAAAAa	
Nham_3277	<i>exbBD-tonB</i>	2	5.15	tGTTTAGAAcGcTTCTAAataa	components for TonB-dependent iron transporters
Nham_3901	<i>bfr</i>	-95	5.05	gaTTTAGAAgCATTCTAAgaa	bacterioferritin
Nham_3555	<i>fhuA</i>	-177	4.96	AaTTTAGAAcGATTaaAAAatg	outer membrane iron receptor
		-124	4.27	AaTaTtGAtctATTCTAAACg	
Nham_2133	<i>feoAB</i>	-61	4.85	taTTTttAAcCATTCTAAatCT	ferrous iron transporter
Nham_1013	<i>irr</i>	-105	4.83	AGTTTgGAgcCgTTCTAgttg	iron regulatory protein Irr
Nham_3637	<i>cycA1</i>	-164	4.63	AtgcTcGAATCATTCTAAgaT	cytochrome c class I
Nham_2257		-90	4.55	cagcTAGAATCATTcCagttT	hypothetical lipoprotein
Nham_4206	<i>cycB</i>	-121	4.48	ctcTTAGAtgGATTcCAAtCa	cytochrome b561
Nham_1606	<i>piuB2</i> -COG3656	-148	4.41	AGTTTAGAgcGAacCTAAatCT	Iron-uptake factor, hypothetical lipoprotein
Nham_1610	<i>fiu1-piuC1</i>	-138	<u>4.17</u>	gagcTAGAAcCtcTgTAAACT	outer membrane iron receptor, iron uptake factor piuC
Nham_1611	<i>exbBD-tonB2</i>	-125	4.33	gtTTTAaAgaGATTCTAAaac	components for TonB-dependent iron transporters
Nham_2255	<i>fcuA1-piuB</i>	-102	4.32	gacTTAGAtcGATTCTActtc	outer membrane iron receptor, Iron-uptake factor
Nham_1436	<i>cycA2-narG</i>	-143	4.22	gcTTTctAAcGATTCTAgctCT	cytochrome c class I, nitrate reductase
Nham_4406	<i>hemA</i>	-67	<u>4.19</u>	cGgcTgGAAaGgcTCTAAaaa	heme biosynthesis

Rhodobacter sphaeroides

RSP_0850	<i>mbfA</i>	-30	5.72	AaTTTAGAATGAcTCTAAaaa	membrane-bound ferritin
RSP_2395	<i>ccpA</i>	-86	<u>4.81</u>	AGaTTAGAAAtgaTCTAAgtc	cytochrome c peroxidase

Rhodobacter capsulatus

RRC04069	<i>mbfA</i>	-28	5.55	AtgTTgGAATCATTCTAAACT	membrane-bound ferritin
RRC03475	<i>ccpA</i>	-44	5.15	tGTTTAGAAgtATTcCAAtT	cytochrome c peroxidase

Silicibacter pomeroyi

SPO3842	<i>mbfA</i>	-33	5.68	AtcTTgGAATCATTCTAAAtT	membrane-bound ferritin
SPO0382	<i>fssA</i>	-75	5.62	tcTTTAGAAcCgTTcCAAAgT	hypothetical Fe-S scaffold protein
SPO2025	<i>iscR-sufSBCD</i>	-120	5.19	AtcTTAGAATGgTTCTAAgtc	Fe-S cluster assembly
SPO0330	<i>ccpA</i>	-73	5.11	AtgTTAGAATGATTCTAAAtCg	cytochrome c peroxidase

Silicibacter sp. TM1040

TM1040_3091	<i>fssA</i>	-75	5.64	AaTTTAGAAaccATTcCAAAac	hypothetical Fe-S scaffold protein
TM1040_1240	<i>iscR-sufSBCD</i>	-118	5.61	AccTTAGAActgTTCTAAAgA	Fe-S cluster assembly
TM1040_2791	<i>katG</i>	-145	5.52	AacTTAGAATAATTCTgAACT	Catalase (peroxidase I)

Jannaschia sp. CC51

Jann_0865	<i>fssA</i>	-78	<u>4.84</u>	AcTTTAGAAcGATTcCagttc	hypothetical Fe-S scaffold protein
Jann_3276	<i>dps</i>	-124	6.11	AGTTTAGAATTATTCTAgACa	DNA-binding ferritin-like protein Dps
Jann_2366	<i>iscR-sufSBCD</i>	-136	5.14	AcccTAGAAcGATTcCAAAtT	Fe-S cluster assembly
Rhodobacterales bacterium HTCC2654					
RB2654_18613	<i>fssA</i>	-53	<u>4.81</u>	gacTTgGAAcGATTcCAAgCT	hypothetical Fe-S scaffold protein
RB2654_16991	<i>mbfA</i>	-31	5.84	AGTTTgGAATcgTTCcAAACa	membrane-bound ferritin
RB2654_13154	<i>irpA-bfd-bfr</i>	-45	5.36	tGaTTgGAAccATTcCAAAtT	iron-regulated protein A (Vibrio),bacterioferritin ferredoxin, bacterioferritin
Roseobacter sp. MED193					
MED193_04321	<i>iscR-sufSBCD</i>	-123	5.25	AtcTTAGAAcAATTCTAAAtg	Fe-S cluster assembly
MED193_04676	<i>ahpC</i>	-58	5.3	AaTTTAGAAcTATTaTAAAtg	peroxiredoxin/glutaredoxin family protein
MED193_10358	<i>fssA</i>	-76	6.22	AaTTTAGAATAATTCTAAACc	hypothetical Fe-S scaffold protein
Roseovarius sp. 217					
ROS217_20542	<i>iscR-sufSBCD</i>	-99	5.84	AccTTAGAAcTgTTCTAAAtT	Fe-S cluster assembly
ROS217_10487	<i>fssA</i>	-77	5.7	AtcTTAGAATggTTCTAAACc	hypothetical Fe-S scaffold protein
ROS217_11126	<i>mbfA</i>	-31	6.16	AGTTTAGAATTATTCTAAAg	membrane-bound ferritin
ROS217_11501	<i>ccpA</i>	-76	5.42	gaTTTAGAATggTTCcAAACg	cytochrome c peroxidase
Roseovarius nubinhibens ISM					
ISM_02850	<i>fssA</i>	-76	5.47	ttTTTAGAATcgTTCcAAAtc	hypothetical Fe-S scaffold protein
ISM_08740	<i>mbfA</i>	-38	5.76	AGTTTAGAATcATTCTAAAtg	membrane-bound ferritin
ISM_16015	<i>iscR-sufSBCD</i>	-128	6.18	AcTTTAGAAcTgTTCTAAACa	Fe-S cluster assembly
ISM_16225	<i>katG</i>	-93	<u>4.64</u>	cGcTTAGAAcGATTcCAAggc	catalase (peroxidase I)
Loktanelia vestfoldensis SKA53					
SKA53_14166	<i>mbfA</i>	-33	5.97	AGaTTAGAATcATTCTAAAta	membrane-bound ferritin
SKA53_14701	<i>fssA</i>	-77	5.8	AGTTTAGAATcgTTCcAAAtc	hypothetical Fe-S scaffold protein
SKA53_05183	<i>iscR-sufSBCD</i>	-110	5.74	AccTTAGAAggATTCTAAACT	Fe-S cluster assembly
SKA53_02751	<i>hemA</i>	-63	<u>4.14</u>	AGaTTAGAAcGATTcCagggCg	heme biosynthesis
SKA53_14466	<i>katG</i>	-84	<u>4.77</u>	AtgTTAGAAggATTCTAAgCg	catalase (peroxidase I)
Sulfitobacter sp. EE-36					
EE36_14302	<i>iscR-sufSBCD</i>	-117	5.69	AGTTTAGAAcggTTCTAAActT	Fe-S cluster assembly
EE36_14417	<i>hemA</i>	-102	<u>4.73</u>	tGaaTtGAATggcTCTAAACT	heme biosynthesis
EE36_01790	<i>dps</i>	-117	6.1	AGTTTAGAATAATTcCAAAaa	DNA-binding ferritin-like protein Dps
EE36_09510	<i>fssA</i>	-75	5.44	AacTTAGAATcgTTCcAAACc	hypothetical Fe-S scaffold protein
EE36_11399	<i>katG</i>	-111	<u>4.43</u>	ctgTTAGAAcAATTcCAgAaa	catalase (peroxidase I)
Oceanicola batsensis HTCC2597					
OB2597_06815	<i>bfr</i>	-84	5.95	ttTTTgGAATAATTCTAAAtT	bacterioferritin
OB2597_10089	<i>fssA</i>	-80	5.19	gaaTTAGAAcggTTCTAAAtc	hypothetical Fe-S scaffold protein
OB2597_01932	<i>hemA</i>	-92	<u>4.21</u>	gacTTAaAAccATTcCAAttc	heme biosynthesis
OB2597_03589	<i>iscR-sufSBCD</i>	-113	<u>4.93</u>	AccTTAGAAagATTCTAAAgc	Fe-S cluster assembly
OB2597_11886	<i>katG</i>	-64	<u>4.25</u>	gtgTTAGATgATTCTAAAgg	catalase (peroxidase I)
Pelagibacter ubique HTCC1002					
PU1002_04356	<i>rbr</i>	-76	5.74	AcaTTAaAATAATTCTAAACT	Rubrerythrin

PU1002_04361	<i>irr</i>	-23	5.88	AGTTTAGAATTATTaTAAACa	iron regulatory protein
Rhodospirillum rubrum ATCC11170					
Rru_A0038	<i>ccmCDE</i>	-161	5.46	TTTCTgGAAgAcTTCcAGAtA	heme export
Rru_A1789	<i>ccpA</i>	-97	4.61	TTcCTAGAgcAATTcCAtAt	cytochrome c peroxidase
Magnetospirillum magneticum AMB-1					
amb2822	<i>ccpA</i>	-163	5.24	gagtTAGAAgAATTCTAaAtA	cytochrome c peroxidase
Magnetospirillum magnetotacticum MS-1					
Magn03010382	<i>rbr</i>	-112	5.02	aaTCTcGAATTAaTCgAtAAA	Rubrerythrin

Color code for functional roles of genes:

Genes involved in iron uptake

Genes involved in iron storage

Genes involved in iron utilization pathways (synthesis of Fe-S, heme; iron-containing enzymes)

Transcription factors (*rirA*, *araX*, *feclR*, *irr*)

Genes with other or uncertain functional roles