

Suppl. Table S1. The RirA regulon in alpha-proteobacteria

Locus ID	Operon	Position	Score	RirA-box	Function
<i>Sinerhizobium meliloti</i>					
<i>SMc01657</i>	<i>fhuA2-fhuF-irp6A2</i>	-94	5.34	CATGACTtaAAaAGTCATG	ferrichrome iron receptor, ferric iron reductase, Ferrisiderophore-binding protein
		-51	4.01	CATGAgTgaTtagcTCacc	
<i>SMA2412</i>	<i>rhrA</i>	-107	4.88	CAaGACTATTtaAGTCATG	transcriptional activator of rhizobactin biosynthesis and transport
<i>SMA2414</i>	<i>rhtA-iucB(vbsA)</i>	-80	4.88	CATGACTtaAATAGTCtTG	rhizobactin receptor, siderophore biosynthesis
<i>SMc01747</i>	<i>hmuPSTUV</i>	-134	4.82	tATGAgTAaTgaAGTCAaG	hemin ABC transporter
<i>SMc01514</i>	<i>SMc01514-tonB</i>	-114	4.82	CtTGACTtcAtTAcTCATa	hypothetical protein, iron transport component TonB
<i>SMc02889</i>	<i>rhtX2 - viuA</i>	-65	4.77	CcTGAaTgcAATAGTCAaG	ferrisiderophore permease and receptor
<i>SMc00529</i>	<i>sufS2-sufBCDS1XA</i>	-164	4.74	CtTGACTAaAccAGTCAgc	Fe-S cluster assembly
<i>SMc04203</i>	<i>fecl-fecR</i>	-171	4.68	CATGAtTATctcAaTCAac	iron transport sigma factor and sensor
<i>SMb21432</i>	<i>irp6A1-irp6BC</i>	-58	4.68	gtTGACcggTAaAGTCATG	ferrisiderophore ABC transporter
<i>SMc00045</i>	<i>cycF-cycG</i>	-183	4.57	gATGAgTtcTATAtTCATa	cytochrome c-556, diheme cytochrome c-type [heme]
<i>SMA2337</i>	<i>rhtX-rhbABCDEF</i>	-60	4.47	gATGACggcAAcAcTCATG	rhizobactin siderophore transporter, and biosynthesis genes
<i>SMc00592</i>		-54	4.37	CtTGACgATcAaAGTCAgc	similar to AMP-dependent synthetase / ligase:Acyltransferase 3
<i>SMc02726</i>	<i>shmR</i>	-140	4.26	atTGACaATcAcAcTCATG	hemin receptor
		-53	3.84	CtTGAgTtcgcccgcTCAac	
<i>SMc02727</i>		-89	3.84	gtTGAgcggcgaAcTCAaG	hypothetical protein
		-2	4.26	CATGAgTgTgATtGTCAat	
<i>SMc04205</i>	<i>hmuR</i>	-120	4.26	tATGACatccgTttTCAaG	heme receptor
<i>SMc02085</i>	<i>exbB-exbD</i>	-182	4.20	CtTGAtTATTgTAcTCcac	components for TonB-dependent iron transporters
<i>SMc01611</i>	<i>fhuA1</i>	-86	4.08	gtTGAtctagAcAcTCATc	ferrichrome iron receptor
		-62	4.19	gtTGACagTAccgGTCACG	
<i>SMA1746</i>	<i>fepBDGC-mxcB</i>	-178	4.09	CATGAaagcTtcgctCAac	ferrierobactin ABC transporter, siderophore-interacting protein
<i>SMA1747</i>	<i>fhuA3</i>	-103	4.09	gtTGAgcgaAgcttTCATG	ferrichrome iron receptor
<i>SMA1749</i>	<i>araX1</i>	-115	4.01	aATGAgAATAcgAGTCAac	siderophore uptake AraC-type regulator
<i>SMc00784</i>	<i>fbpA</i>	-46	3.97	tATGAtTgactaAGTtAaG	ABC-type Fe ³⁺ transport system, periplasmic component
<i>SMc00785</i>	<i>rirA</i>	-172	3.97	CtTaACTtagtcAaTCATa	iron-responsive regulator RirA
<i>SMc03787</i>	<i>bfd-bfr</i>	-67	3.79	gtTGACggcAAatGTCcTc	bacterioferritin ferredoxin, bacterioferritin
Expression data: RirA-repressed genes (Chao et al., 2006)					
<i>Mesorhizobium loti</i>					
<i>msl1154</i>	<i>hmuPSTUV</i>	-82	5.06	CATGAtTATTcaAGTCAaG	hemin ABC transporter
<i>mlr1155</i>	<i>hmuR-SMc01514</i>	-84	5.06	CtTGACTtgAATAaTCATG	heme receptor, hypothetical protein
<i>mlI4168</i>	<i>exbB-exbD-tonB</i>	-83	4.99	gtTGACTgTTgcAGTCATc	components for TonB-dependent iron transporters
		-58	4.89	gtTGACTtgTATAcTCATG	
<i>mlr3495</i>	<i>fbpABC</i>	-68	4.80	gtTGACTATTcgtGTCATG	ferric cations ABC transporter
<i>mlI6832</i>		-260	4.74	CtTGAaTAaAtctaTCAaG	hypothetical protein
<i>mlI5668</i>		-57	4.72	CtTGACTAaAAaAcTCAcc	transcriptional regulator, ArsR family
<i>mlI0429</i>		-318	4.60	CATGAtTcaAAaAcTCAac	hypothetical protein
<i>mlr1147</i>	<i>rirA</i>	-173	4.46	gtTGACgAgAATaTTCATc	iron-responsive regulator RirA
<i>mlr5523</i>	<i>irpA-bfd-bfr</i>	-257	3.89	gtTGACTtcTgTAGTttaG	iron-regulated protein A, bacterioferritin ferredoxin, bacterioferritin

Mesorhizobium sp. BNC1

MBNC03002200	<i>hmuPTUV</i>	-84	4.86	gtTGAtTATTgatGTCAaG	hemin ABC transport system
MBNC03002201	<i>hmuR-SMc01514-exbBD-tonB</i>	-172	4.86	CtTGACatcAATAaTCAac	Fe receptor, conserved protein, TonB-dependent transporter components
MBNC03003078	<i>bfd-bfr</i>	-183	4.79	CATGACctTgAaAGTCAaG	bacterioferritin ferredoxin, bacterioferritin
MBNC03004224	<i>fhuA-rhtX-mxcB</i>	-148	4.78	gtTGACatTgATAaTCATG	ferrichrome iron receptor, MFS permease, siderophore-interacting protein
MBNC03004482	<i>chpA -X- ftr -COG0348</i>	-183	4.70	gtTGACctTTcaAGTCATG	involved in high-affinity Fe transport, High-affinity Fe permease, Polyferredoxin
MBNC03003400	<i>fbpAB</i>	-154	<u>4.19</u>	CtTGACTAcTATAGTttaG	ferric cations ABC transporter
MBNC03003363	<i>fecB</i>	-75	<u>4.09</u>	ggTGAtgtTgAcAGTCAaG	iron(III) dicitrate-binding protein
		-29	<u>4.06</u>	tcTGACcATgctTtGTCAaG	
MBNC03003364	<i>fecCDE</i>	-91	<u>4.06</u>	CtTGACaAgcATgGTCAga	iron(III) dicitrate ABC transporter, permease subunits, ATPase
		-45	<u>4.09</u>	CtTGACTgTcAacaTCacc	
MBNC03002196	<i>rirA</i>	-136	<u>3.60</u>	CtgGACctaTAgcGTCATc	iron-responsive regulator RirA

Rhizobium leguminosarum

pRL120322	<i>fhuA1-fhuF</i>	-19	5.10	gATGACTAaAATAaTCATc	ferrichrome iron receptor, ferric iron reductase
RL4584	<i>fbpABC</i>	-25	4.75	tATGAaataTtTAGTCAaG	ferric cations ABC transporter
pRL100314		6	4.72	CATGACaAgAgcAcTCAaG	hypothetical protein
RL3522	<i>shmR</i>	-178	4.71	CATGAtagaTATAtTCAac	hemin receptor
		-142	4.60	gtTGACaATgctTAcTCATG	
RL3695	<i>SMc01514-tonB</i>	-114	4.71	CtTGACTtTctTAcTCATa	conserved protein, iron transport component TonB
RL3696	<i>hmuPSTUV</i>	-81	4.71	tATGAgTAagAaAGTCAaG	hemin ABC transporter
RL2713	<i>irp6ABC</i>	-66	4.68	CtTGATtcaTtaAGTCATa	ferrisiderophore ABC transporter
RL2583	<i>sufS2-sufBCDS1XA</i>	-164	4.63	CtTGACTAgTgTtGTCAgc	Fe-S cluster assembly
pRL120319	<i>rpol</i>	-134	<u>4.28</u>	CtTGACTccTgTtaTCacc	iron transport sigma factor
pRL120320	<i>vbsC</i>	-48	<u>4.28</u>	ggTGAtaAcAggAGTCAaG	vicibactin biosynthesis
pRL100328	<i>fhuCDB</i>	-63	<u>4.09</u>	gtTGAtTgcccgtctTCATc	ferrichrome iron transporter
pRL120713	<i>btuFCD</i>	-290	<u>4.01</u>	gtTGAtTtgTtTgGTCTTG	siderophore ABC transporter (SBP, permease) similar to B12 ABC transporter
pRL100325	<i>fhuA2</i>	-96	<u>4.00</u>	gtTGACTccAATtcTCcTG	ferrichrome iron receptor
001_4255	<i>fumC</i>	-120	<u>4.00</u>	CATGACTtccgattTCAat	fumarate hydratase C
RL0777	<i>rirA</i>	-86	<u>3.80</u>	gcTGAaTgCGAattTCATa	iron-responsive regulator RirA
pRL120315	<i>vbsGSO</i>	-88	<u>3.98</u>	gAaGAaaAaAATtcTCATc	vicibactin biosynthesis
pRL120316	<i>vbsADL</i>	-124	<u>3.98</u>	gATGAgAATTtTtTCTcTc	vicibactin biosynthesis
RL4696-RL4695	<i>bfd-bfr</i>	-128	<u>3.59</u>	CtTGACagccAccaTCTcTc	bacterioferritin ferredoxin, bacterioferritin
		-97	<u>3.56</u>	CACGAtagTcAgtGTCATG	

Experimental data: Fe-RirA-repressed operons (Yeoman et al., 2004; Todd et al., 2002; 2006)**Rhizobium etli**

RHE_CH03076	<i>shmR</i>	-142	4.96	gtTGACaAcAgaAGTCATG	hemin receptor
RHE_CH03266	<i>Smc01514-exbBD-tonB</i>	-117	4.71	CtTGACTtTctTAcTCATa	conserved protein, components of TonB-dependent transporters
RHE_CH03267	<i>hmuPSTUV</i>	-79	4.71	tATGAgTAagAaAGTCAaG	hemin ABC transporter
RHE_CH04056	<i>fbpABC</i>	-69	4.66	CtTGAaataggTAGTCAaG	ferric cations ABC transporter
RHE_CH02254	<i>sufS2-sufBCDS1XA</i>	-237	<u>4.56</u>	CtTGACTAacgTtGTCAgc	Fe-S cluster assembly
RHE_CH02383	<i>fumC</i>	-120	<u>4.11</u>	CATGACTgTgATcaTCAat	fumarate hydratase C
RHE_CH00735	<i>rirA</i>	-88	<u>3.8</u>	gcTGAaTgCGAattTCATa	iron-responsive regulator RirA

Agrobacterium tumefaciens

AGR_L_2869	<i>fecI1</i>	-132	5.04	CtTGAtaATAATtGTCATG	iron transport sigma factor and sensor
AGR_C_616	<i>sssA</i>	-108	4.87	CtTGAAaTgTAATtATCATG	hypothetical Fe-S scaffold protein
AGR_pAT_635	<i>mocC</i>	-2	4.80	CATGAaTATTAcAGTCAcc	myo-inositol 2-dehydrogenase
AGR_C_720	<i>araX</i>	-42	4.75	CATGAaTAgaTtTtaTCATG	siderophore uptake AraC-type regulator
AGR_L_309	<i>exsA</i>	-217	4.73	CATGACatcAtcAtTCATc	ATP-binding transport protein (EPS I biosynthesis)
AGR_C_1984		0	4.72	CATGACTATcgatcTCAaG	short chain dehydrogenase
AGR_L_2862	<i>irp6AABC</i>	-63	4.68	CtTGACTAgTAcAGTCAga	ferrisiderophore ABC transporter
AGR_C_4156	<i>shmR</i>	-105	4.76	CATGAtTcaAAaAGTCATa	hemin receptor
		-78	4.52	gtTGACagTgATcGTCATG	
AGR_C_344	<i>rirA</i>	-145	4.62	CtTGACTtgTtTgtTCATG	iron-responsive regulator RirA
AGR_C_346	<i>fbpA2</i>	-2	4.62	CATGAacAaAcaAGTCAaG	ferric cations ABC transporter
AGR_L_2323	<i>AGR_L_2323-2304-viuA-fecBCI</i>	-173	4.54	CtTGAAaTcgctTAGTCAaG	siderophore biosynthesis, iron (III) dicitrate ABC transporter
AGR_L_2326	<i>AGR_L_2326-2334</i>	-107	4.54	CtTGACTAagcgAtTCAaG	siderophore biosynthesis cluster
AGR_L_2875	<i>hmuR</i>	-270	4.44	gtTGAgTAaTccgGTCAaG	heme receptor
AGR_C_5028	<i>bfd-bfr</i>	-70	4.39	CtTGACatTTActGTCcTG	bacterioferritin ferredoxin, bacterioferritin
AGR_C_3350	<i>sufS2-sufBCDS1XA</i>	0	4.26	CtTGACgAactgtGTCATc	Fe-S cluster assembly
AGR_L_1661	<i>fhuADBC</i>	-61	4.24	gATGACTtaAATtcTCcaG	ferrichrome iron receptor, ABC transporter
AGR_C_715	<i>fbpAB</i>	-28	4.21	CtTGAtTtgcgccGTCATG	ferric cations ABC transporter
AGR_C_718	<i>fhuA2</i>	-29	4.05	CcTGAtgtaAAcAcTCATc	ferrichrome iron receptor
AGR_C_4467	<i>hmuTUV</i>	-22	3.58	CATGtgcAaAaAcTCAaG	hemin ABC transporter
AGR_pAT_442	<i>fecI1R2-fhuA3-fepB-mxcB-fepDC</i>	-396	4.00	gcTGAaTAcAgctaTCAaa	ferrienterobactin ABC transporter, siderophore-interacting protein
		-87	3.96	CATGAgTtTTcTtTcTctac	
AGR_L_2290	<i>fecI1R3</i>	-218	4.26	CATGAtaAaAATtGTCcTc	
AGR_C_4488	<i>fatBDCE</i>	10	3.83	gcTGACagcgAacaTCAaG	ferric anguibactin ABC transporter

Brucella melitensis

BMEI0542		-132	4.92	CATGAtTAacATAaTCATG	hypothetical protein
BMEI0543		-162	4.92	CATGAtTATgtTAaTCATG	choloylglycine hydrolase
BMEI10105	<i>OMP</i>	-262	4.85	tATGAaTgTATAGTCATc	outer membrane iron receptor
BMEI11051	<i>fumC</i>	-80	4.53	CtTGACatTTATAtTCaca	fumarate hydratase C
BMEI0365	<i>exbB-exbD-tonB</i>	-163	4.46	CATGACTtgAAgtaTCATa	components for TonB-dependent iron transporters
BMEI10077	<i>dhbCEBAD</i>	-55	4.38	CgTGACTggTtcttTCAaG	2,3-dihydroxybenzoic acid biosynthesis (brucebactin synthesis)
BMEI10584	<i>fbpAB</i>	-53	4.15	CcTGAtccaTATAcTCATG	ferric cations ABC transporter
BMEI1042	<i>sufBCDS1X</i>	-160	4.03	CtTGAaTttTaTtGgCAaa	Fe-S cluster assembly
BMEI10705	<i>bfd-bfr</i>	-344	4.00	CATGgaTATTtaAcTCATa	bacterioferritin ferredoxin, bacterioferritin
BMEI10707	<i>rirA</i>	-182	3.72	ggTGAgAaAagggttTCATa	iron-responsive regulator RirA
BMEI10607	<i>fatBDCE</i>	-88	3.49	gtTGACTATAAagcaCAgG	ferric anguibactin ABC transporter

Experimental data: Iron-responsive regulation (Bellaire et al., 2003)**Bartonella quintana**

BQ04160	<i>shmR-hmuSTUV</i>	-157	4.93	CtTGACTgcTtTtaTCATG	hemin receptor and ABC transporter
BQ04170	<i>tonB</i>	-101	4.93	CATGAtaAaAgcAGTCAaG	components for TonB-dependent iron transporters
BQ02630		-53	4.65	ttTGAaTtTTtaAtTCATG	Phage related lysozyme
BQ05940	<i>sufS2-sufBCDS1XA</i>	-76	4.40	ttTGAgTgcAtTttTCAaG	Fe-S cluster assembly

BQ02420	<i>hbpAB</i>	-261	<u>4.26</u>	CAGGACTcaTATtaTCATG	hemin binding proteins
BQ11710	<i>exbB-exbD</i>	-342	<u>4.05</u>	ttTGAtaAaAtcAaTCtTG	components for TonB-dependent iron transporters
BQ10310	<i>fatDCE</i>	-75	<u>3.74</u>	CATGAaataAAgttTtAaG	ferric anguibactin ABC transporter
BQ10300	<i>fatBDCE</i>	-35	<u>3.44</u>	gATGAtcAaAtatcTgAaa	ferric anguibactin ABC transporter

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, fecIR, irr)

Genes with other or uncertain functional roles