SUPPLEMENTAL DATA

Table S1. Complete Microarray Analysis of the Δ*prrF12* Mutant.

Gene ID	Function of Gene Product	WT High Fe vs. WT Low Fe[1]				Δ*prrF12* Low Fe vs WT Low			
PA0792 *prpD*	methyl-citrate dehydratase	1.4	0.6	0.6	1.5	0.7	0.3	0.4	0.5
PA0793	conserved hypothetical protein	2.5	2.3	2.6	8.0	2.6	1.1	2.5	2.6
PA0794	methyl-isocitrate dehydratase	4.9	8.6	4.9	12.1	4.3	2.1	2.8	3.7
PA0795 *prpC*	methyl-citrate synthase	9.8	4.0	3.0	3.7	3.2	0.8	2.0	1.7
PA0796 *prpB*	methyl-isocitrate lyase	4.6	3.0	2.0	3.2	3.5	1.5	2.6	2.6
PA0797	putative GntR-type regulator	1.9	1.3	1.9	1.6	2.0	1.0	1.6	2.5
PA0844 *plcH*	hemolytic phospholipase C	6.1	4.3	9.8	26.0	3.5	2.3	2.0	2.5
PA0918	cytochrome b561	9.2	5.3	7.0	7.0	13.9	5.3	6.5	11.3
PA1172 *napC*	periplasmic nitrate reductase	4.9	1.9	6.5	24.3	2.8	2.8	4.3	6.1
PA1173 *napB*	periplasmic nitrate reductase	17.1	3.0	6.5	26.0	8.0	3.7	5.3	8.0
PA1174 *napA*	periplasmic nitrate reductase	14.9	2.1	7.5	29.9	13.0	4.3	8.0	13.9
PA1175 *napD*	periplasmic nitrate reductase	4.9	0.8	2.0	17.1	5.3	2.6	1.6	3.2
PA1176 *napF*	periplasmic nitrate reductase	42.2	1.1	1.9	17.1	5.7	3.0	1.4	3.2
PA1177 *napE*	periplasmic nitrate reductase	1.7	0.9	0.7	4.9	2.5	0.9	0.5	1.1
PA1186	possible flavin-dependent	8.0	1.9	8.0	29.9	4.6	4.3	3.0	2.1
PA1562 *acnA*	aconitase A	5.3	4.6	3.7	3.5	8.6	2.5	6.5	9.8
PA1580 *gltA*	citrate synthase	3.2	2.8	2.0	0.9	0.8	0.6	0.7	0.9
PA1581 *sdhC*	succinate dehydrogenase	8.6	5.7	1.9	2.1	2.1	1.3	1.7	2.0
PA1582 *sdhD*	succinate dehydrogenase	6.1	6.1	2.0	2.5	3.2	1.3	2.0	2.5
PA1583 *sdhA*	succinate dehydrogenase	4.0	4.6	2.1	2.8	3.7	1.5	2.1	2.5
PA1584 *sdhB*	succinate dehydrogenase	2.8	3.5	1.2	2.1	4.0	1.1	1.1	1.2
PA1600	putative cytochrome C	1.4	0.9	7.0	16.0	2.1	2.0	2.5	2.3
PA1601	putative aldehyde	16.0	1.6	14.9	52.0	2.1	7.5	12.1	8.0
PA1602	probable oxidoreductase	5.7	1.0	3.7	19.7	3.2	2.8	2.8	2.0
PA1787 *acnB*	aconitase B	4.9	5.7	3.2	1.6	1.1	0.8	2.3	2.5
PA2378	probable aldehyde	11.3	3.2	3.5	3.5	5.3	2.3	3.5	7.0
PA2379	probable oxidoreductase	7.0	4.9	2.6	1.7	3.0	1.5	2.8	5.3
PA2507 *catA*	catechol degradation	5.7	7.0	32.0	32.0	5.7	2.8	3.0	3.7
PA2508 *catC*	catechol degradation	6.1	4.9	27.9	24.3	64.0	1.9	2.6	3.2
PA2509 *catB*	catechol degradation	2.3	3.2	8.0	12.1	4.6	1.1	3.5	2.5
PA2510 *catR*	LysR-type regulator	1.7	1.1	3.5	5.7	1.4	1.3	2.0	1.4
PA2511 *antR*	AraC-type regulator	168.9	6.5	8.6	22.6	104.0	13.0	4.0	4.3
PA2512 *antA*	anthranilate degradation	52.0	238.9	104.0	238.9	512.0	111.4	2.3	2.1
PA2513 *antB*	anthranilate degradation	68.6	207.9	194.0	222.9	137.2	73.5	2.6	2.3
PA2514 *antC*	anthranilate degradation	52.0	73.5	168.9	59.7	55.7	13.9	3.7	3.0
PA2682	dienelactone hydrolase	59.7	18.4	12.1	13.9	29.9	14.9	2.8	2.8
PA2916	hypothetical protein	119.4	1.2	11.3	111.4	5.3	17.1	4.3	3.5
PA2917	hypothetical protein	48.5	2.3	4.0	24.3	4.6	4.3	2.3	2.6
PA3327	probable non-ribosomal peptide	2.3	1.1	2.8	7.5	2.3	2.8	1.4	1.2
PA3328	probable FAD-dependent	2.5	1.3	2.5	13.9	2.3	2.3	1.6	1.4
PA3329	hypothetical protein	5.7	1.7	4.6	13.9	2.5	3.0	3.5	2.8
PA3330	probable short-chain	32.0	2.6	5.3	24.3	4.6	6.5	3.2	2.1
PA3331	cytochrome P450	3.7	2.5	3.7	12.1	2.8	1.9	3.5	3.0
PA3332	conserved hypothetical protein	2.5	2.6	3.5	13.0	3.0	1.9	2.3	1.9

Gene ID	Function of Gene Product	WT High Fe vs. WT Low Fe[1]				Δ*prrF12* Low Fe vs WT Low			
PA3333 *fabH2*	acetyl-CoA ACP transacetylase	1.9	2.1	4.6	17.1	3.5	2.6	3.0	2.5
PA3531 *bfrB*	bacterioferritin	168.9	24.3	9.2	26.0	3.0	0.9	0.7	0.6
PA3602	conserved hypothetical protein	4.0	3.5	3.2	10.6	18.4	6.1	4.0	4.3
PA3872 *narI*	nitrate reductase	1.2	1.1	4.3	19.7	2.0	2.3	0.9	1.9
PA3873 *narJ*	nitrate reductase assembly	1.9	0.9	4.3	12.1	2.0	1.6	1.7	1.5
PA3874 *narH*	nitrate metabolism	3.7	2.1	21.1	181.0	2.0	17.1	10.6	8.0
PA3875 *narG*	nitrate reductase	1.1	1.6	7.5	48.5	1.4	4.6	2.3	2.5
PA3876 *narK*$_1$	nitrate extrusion protein 1	2.5	1.1	3.7	32.0	2.8	3.0	1.0	0.9
PA3877 *narK*$_2$	nitrate extrusion protein 2	2.3	0.9	5.3	73.5	3.0	4.9	1.1	1.0
PA3878 *narX*	2-component sensor kinase	1.4	2.1	2.5	7.0	3.0	1.5	3.7	2.6
PA3879 *narL*	2-component response regulator	2.0	2.3	2.1	4.0	2.6	0.8	1.1	1.3
PA4236 *katA*	catalase	7.5	7.0	3.0	4.0	5.7	3.2	5.3	6.1
PA4366 *sodB*	Fe-superoxide dismutase	5.3	9.8	5.7	1.4	4.6	1.9	4.6	4.0
PA4809 *fdhE*	formate dehydrogenase	1.5	1.5	2.8	6.5	3.7	1.6	3.0	4.3
PA4810 *fdnI*	nitrate-inducible formate	34.3	4.9	9.2	13.9	16.0	6.5	18.4	24.3
PA4811 *fdnH*	nitrate-inducible formate	78.8	32.0	14.9	104.0	181.0	64.0	55.7	90.5
PA4812 *fdnG*	nitrate-inducible formate	4.0	8.0	4.9	8.6	24.3	6.5	27.9	48.5
PA4844	probable chemotaxis transducer	9.2	1.9	5.7	19.7	3.5	3.7	6.5	3.7
PA4880	probable bacterioferritin	13.0	7.5	5.3	2.3	14.9	2.1	13.9	21.1
PA5352	conserved hypothetical protein	1.6	4.3	6.1	24.3	1.1	2.0	1.5	1.6
PA5353 *glcF*	glycolate oxidase subunit	10.6	3.7	9.2	111.4	3.7	16.0	1.5	1.9
PA5354 *glcE*	glycolate oxidase subunit	0.9	4.9	8.6	97.0	2.8	7.5	2.8	2.6
PA5355 *glcD*	glycolate oxidase subunit	1.0	5.3	9.2	10.6	1.4	1.6	2.5	2.0

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[1] Ratio of expression in wild type PAO1 grown in iron-replete conditions vs. wild type PAO1 grown in iron-depleted conditions. $P < 0.0001$ for the expression ratio of each gene in each experiment as determined by GeneSpring® analysis software.

[2] Ratio of expression in the Δ*prrF12* mutant grown in iron depleted conditions vs. wild type PAO1 grown in iron depleted conditions. $P < 0.0001$ for the expression ratio of each gene in each experiment as determined by GeneSpring® analysis software.

Table S2. Complementarity between PrrF RNAs and target mRNAs

Gene/Operon | Complementarity identified between PrrF1 and target mRNA | Identified by:[1,2]

PA1562 *acnA* | LALIGN

```
PrrF1   62 UCUCCUCAUCAGGCUAAUCACGGUUUUUGACCCGGC  97
           | |||  | |||||  ||  | | |||:  | ||||
acnA    16 ACAGGUUUCGUCCG--UAAAGACUAAAGGAGUGCCG -18
```

sdhB | Target RNA

```
PrrF1  6   GGUCGCGAGAUCAGCCGGUAAGCUGAGAGACCCACGCAGUCGGACUCUUCAGAUUAUCUCCUCAUCAGGC 75
           ||||:||| || | ||||:| ||:  |     || || | |||| || :||| || :| || | ||||||
sdhB   301 CCAGUGCU-UACU-GGCCGUCCGGGCC-----GU-CGCCUGCCU-AGUGGUCGAACGGCGG-GAAGUCCG 241
```

acnB | LALIGN

```
PrrF1 42 GCAGUCGGACUCUU-CAGAUUAUCUCC-UCAUCAG  74
         || || ||  ||   || | ||| ||| |||||||
acnB  18 CGCCAUCCGAAGUUCGUGUCAUAAAGGGAGUAGUC -17
```

PA0792-PA0797 | N/A

```
None identified
```

catBCA | N/A

```
None identified; possibly regulated by PrrF via antR
```

antR | LALIGN

```
PrrF1  66 CCUCAUCAGGCUAAUCACGGUUUUUGACCCGGCA 100
          |||||||| | |     |||: :|:||| |||||
antR     9 GGAGUAGUACCA----AGCCGUGAGCUGUGCCGU -21
```

antABC | LALIGN

```
PrrF1  81 CGGUUUUUGACCCGGCACUUUGCC 104
          ||| | ||  |||||| |:||| |
antA  414 GCCCAUAAGCGGGCCGCGGAACUG 391
```

bfrB | LALIGN

```
prrF1 112 UUUUUUGCCUGCGAUUCG-GCCGGAGACGACCGU 145
          |||:||| | ||  |||: ||||:|  |  ||||
bfrB   18 AAAGAACAG-CGGAAAGUACGGCUUAGGACGGCA -15
```

katA | LALIGN

```
prrF1  50 CUCUUCAGAUUAUCUC-CUCAUCA  72
          ||||||  |||  ||| ||| |||
katA     9 GAGAAGG-UAAAUGAGAGAGGAGU -14
```

sodB | Wilderman, 2004. *PNAS*

```
PrrF1  50 CUCUUCAGAUUAUCUCCUCA--UCAGGCUAAUCACGG  34
          ||||:|  ||| | ||||||  ||||| :   | |||
sodB   -6 GAGAGG-AUAAGA-AGGAGUCCAGUCCUGACCGCGCC -40
```

Gene/Operon	Complementarity identified between PrrF1 and target mRNA	Identified by:[1,2]
PA4880	`PrrF1  50 CUCUUCA--GAUUAUCUCCUCAUCAGGCUAAUCACGG  34` `	|||	|| ||||||	||||| ||| |||` `PA4880 8 CACCAGUAGCCAAAAGAGGA--ACUCCGACUAG-GCC -26`	Wilderman, 2004. *PNAS*

napCBADFE	`PrrF1  80 CGGUUUUUGACCCGGCA-CUUUGCCGG 105`
	`          || |: ||| |||:||  || ||| ||`
	`napE    7 GCAAGUAACCGGGUCGGAGAUACGUCC -20`
		LALIGN

narIJHGK$_1$*K*$_2$*XL*	`Identified in PA3869, transcribed convergent to the nar operon:`
	`PrrF1    74 GCUAAUCACGGUUUUUGACCCGGCACUUUGCCGGGUCUUUUUUUGCCUGCGAUUCG 129`
	`            ||| ||  ||||    :| ||||||||||||   :||||||    |||||:|:|||`
	`PA3869  386 CGAGUAUGGCCA----UUAGGCCGUGAAACG---UAGAAAA----GGACGUUGAGC 342`
		Target RNA

fdnGHI,fdhE	`None identified`	N/A

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[1] LALIGN available at http://www.ch.embnet.org/software/LALIGN_form.html

[2] Target RNA available at http://snowwhite.wellesley.edu/targetRNA/