Table S1. 45 significantly up-regulated *P. mirabilis* HI4320 genes as determined by SAM during iron-limiting microarray[a]

PMI no.	Gene	Description	Log$_2$ fold-change[b]
PMI0029	*exbB*	biopolymer transport protein	7.66
PMI0030	*exbD*	biopolymer transport protein	5.61
PMI0172		putative Dyp-type peroxidase	4.92
PMI0174		putative membrane protein	5.49
PMI0175		putative exported protein	5.66
PMI0176		putative exported protein	8.36
PMI0229		ABC transporter; permease protein (FecCD transport family)	4.81
PMI0231		putative citrate lyase β chain	6.45
PMI0232		putative siderophore biosynthesis protein	6.36
PMI0233		putative TonB-dependent siderophore receptor	6.04
PMI0234		putative decarboxylase	5.30
PMI0235		putative pyridoxal-phosphate dependent enzyme	4.77
PMI0331		putative ABC transporter; substrate-binding protein	6.49
PMI0409		putative TonB-dependent heme receptor	6.22
PMI0413	*nrdF*	ribonucleoside-diphosphate reductase β chain	4.88
PMI0415	*nrdI*	NrdI	4.50
PMI0416	*nrdH*	glutaredoxin-like protein	5.68
PMI0842		putative TonB-dependent receptor	7.20
PMI1026	*sitB*	iron ABC transporter; ATP-binding protein	5.49
PMI1210		PadR-family transcriptional regulator	4.67
PMI1211		hypothetical protein	4.25
PMI1355	*tonB*	TonB	4.18
PMI1413	*sufD*	subunit of cysteine desulferase; activator complex	4.29
PMI1414	*sufC*	putative ATP-dependent transporter	3.79
PMI1416	*sufA*	putative scaffold protein for iron-sulfer cluster assembly	4.65
PMI1424		putative hemin uptake protein	8.52
PMI1425	*hmuR1*	hemin receptor	5.92
PMI1426	*hmuR2*	hemin receptor	7.89
PMI1427	*hmuS*	hemin transport protein	6.96
PMI1428	*hmuT*	hemin binding periplasmic protein	5.02
PMI1430	*hmuV*	hemin transport system; ATP-binding protein	5.42
PMI1437		putative iron utilization protein	7.38
PMI1447		conserved hypothetical protein	4.83
PMI1548		putative TonB-dependent receptor	5.47
PMI1549	*ptrB*	oligopeptidase B	5.32
PMI1550		TonB-like protein	4.25
PMI1551		putative lipoprotein	6.69
PMI1945	*ireA*	putative TonB-dependent ferric siderophore receptor	6.65
PMI2497		putative membrane protein	5.92
PMI2596		putative siderophore TonB-dependent receptor	7.13
PMI2598		conserved hypothetical protein	7.93
PMI2957		putative iron ABC transporter; substrate-binding protein	6.20
PMI2930	*glpD/glyD*	aerobic glycerol-3-phosphate dehydrogenase	4.94
PMI3252	*bfd*	bacterioferritin associated ferredoxin	5.69
PMI3446		putative exported protein	3.74

[a] One-class unpaired test performed by Significance Analysis of Microarray (SAM). False Discovery Rate=0; all up-regulated genes listed are statistically significant. Genes listed in ascending order by *P. mirabilis* gene identification number (PMI no.).
[b] Log$_2$ transformation of fold-change values determined by taking ratio of transcript level of *P. mirabilis* growth in LB and LB broth treated with 15 μM Desferal averaged across all five microarray experiments.

Table S2. 43 significantly down-regulated *P. mirabilis* HI4320 genes as determined by SAM during iron-limiting microarray[a]

| PMI no.	Gene	Description	Log$_2$ fold-change[b]
PMI0031	*hybO*	hydrogenase-2 small chain precursor	3.46
PMI0033	*hybB*	hydrogenase-2 cytochrome; b subunit	3.25
PMI0034	*hybC*	hydrogenase-2 large subunit	3.18
PMI0035	*hybD*	hydrogenase-2 maturation protease	2.19
PMI0037	*hypB*	hydrogenase nickel incorporation protein	3.08
PMI0038	*hybG*	hydrogenase-2 maturation protein	3.11
PMI0039	*hypD*	hydrogenase formation protein	2.85
PMI0040	*hypE*	hydrogenase formation protein	2.73
PMI0041		putative membrane protein	2.36
PMI0042		SirA-like protein	2.34
PMI0134		putative cytoplasmic sulphur reductase	1.99
PMI0648		putative ATP-binding protein	2.08
PMI0657		probable alcohol dehydrogenase	3.94
PMI0874		conserved hypothetical protein	2.25
PMI0882	*pepT*	peptidase T	2.47
PMI1007	*ftnA*	ferritin	2.98
PMI1082		putative membrane protein	3.30
PMI1176		ABC transporter; ATP-binding protein	1.81
PMI1350	*ompW*	outer membrane protein	2.94
PMI1397	*sodB*	superoxide dismutase [Fe]	3.88
PMI1705	*dmsA*	putative dimethyl sulfoxide reductase; chain A	3.69
PMI1706	*dmsB*	anaerobic dimethyl sulfoxide reductase; chain B	3.88
PMI1740	*katA*	catalase	1.92
PMI1769		conserved hypothetical protein	2.17
PMI1800		conserved hypothetical protein	1.54
PMI1836		conserved hypothetical protein	3.02
PMI1855	*fdx*	2Fe-2S ferredoxin	1.98
PMI1898	*grcA*	autonomous glycyl radical cofactor	2.81
PMI2509		conserved hypothetical protein	3.04
PMI2724		putative regulatory protein	2.18
PMI2725		TetR-family transcriptional regulator	3.11
PMI3442		protease	2.43
PMI3443		putative lipid carrier protein	2.36
PMI3450	*nrdG*	anaerobic ribonucleoside-triphosphate reductase; activating protein	2.07
PMI3451	*nrdD*	anaerobic ribonucleoside-triphosphate reductase	2.86
PMI3582	*hybF*	probable hydrogenase nickel incorporation protein	2.41
PMI3583	*hypC*	putative hydrogenase formation protein	2.25
PMI3585	*frdD*	fumarate reductase subunit D	4.07
PMI3586	*frdC*	fumarate reductase subunit C	4.21
PMI3587	*frdB*	fumarate reductase iron-sulfur protein	3.96
PMI3588	*frdA*	fumarate reductase flavoprotein subunit	4.15
PMI3674		probable aminohydrolase	2.93
PMI3675		putative C4-dicarboxylate transporter	3.67

Table S3. Oligonucleotides used in this study.

Experiment	PMI # (Gene)	Direction[a]	Primer Name	Sequence (5' → 3')
qPCR	3280 (*rpoA*)	F	*rpoA*	GCAAATCTGGCATTGGCCCTGTTA
		R	*rpoA*	TAGGGCGCTCATCTTCTTCCGAAT
	0030 (*exbD*)	F	*exbD*	ACGATGGCCAGTGTCTTGGATTCT
		R	*exbD*	TCCCGCCTTCCTTAATGAGTCCAT
	0842	F	0842	AAGCGTGTTGCATCTCGTGAAACG
		R	0842	ATACGCTCAATCGCGGGTAAAGGA
	1027 (*sitA*)	F	*sitA*	TGCGGTCGTTGTCACTGAAGGTAT
		R	*sitA*	ATCCATGCATGTGGGTTTGGGTTG
	1425 (*hmuR1*)	F	*hmuR1*	TCTTATGGTGGTGTGATCGCAGGT
		R	*hmuR1*	TCATCAGCAATACGTATCGGGCCA
	2930 (*glpD*)	F	*glpD*	ATTGTCATCGGCGGCGGAATAAAC
		R	*glpD*	TGGCTAAGTCTTGAGCTTCCAGCA
	3252 (*bfd*)	F	*bfd*	CTGTCTGTGTCATGGTGTGAGTGA
		R	*bfd*	TGCCTACAGGTAGGATTTGACGCA
	1007 (*ftnA*)	F	ftnA	GCGCTTGGTGCGATGATAAAGGAT
		R	ftnA	CCCTAACAAAGGCATAGCACCTGT
	2596	F	2596	GGCCAATCTTCGGCCGATTTCTTT
		R	2596	ATGCTTCAGCGTGACTACTGGGTT
	2597 (*nrpX*)	F	*nrpX*	TGATGGCATGGCGGTAGAACAGAT
		R	*nrpX*	CTCCTATTTCTCCTCCGCCAACTT
	2598 (*nrpY*)	F	*nrpY*	AGCGAACCTCATTGGGAAACTCGT
		R	*nrpY*	TGGCCAGTGCCGGAACCTATATTT
	2599 (*nrpR*)	F	*nrpR*	ATCCCATGCCAGCGCAATGAATAC
		R	*nrpR*	AGTGCTGATATGGCAAGTACCCGA
	2600 (*nrpS*)	F	*nrpS*	TCCTGAAGGTGCATCTCAAGGTGT
		R	*nrpS*	TTAAGTACCGCGGCAGCAATTTGG
	2601 (*nrpU*)	F	*nrpU*	TTCCAAAGGTAGCACTCGTTCTCG
		R	*nrpU*	CCAACAATGGCTGATCGCACAACA
	2602 (*nrpT*)	F	*nrpT*	AGGCTGCCAAGCTCCTCATATTCA
		R	*nrpT*	CAGCATCACATCCACCAATGGCAA
	2603 (*nrpA*)	F	*nrpA*	TAAGTCATATTGCCGCACATCGGG
		R	*nrpA*	ACGTCGCAGATTTCCACTGCCATA
	2604 (*nrpB*)	F	*nrpB*	ACAAGCCCGTCTAAGAATAGCCGA
		R	*nrpB*	TGATGCAAGATCACCACTGCGTTG
	2605 (*nrpG*)	F	*nrpG*	GCTATCAAGAGTCATGTTACGCGA
		R	*nrpG*	GCGAGAGCAACACAATTATTTGAATG
	0229	F	0229	TGAATGCTTGGAAACTGACGGCAC
		R	0229	TATTGGGCCAACAAATGCTACCGC
	0230	F	0230	TTAACGGTCTCACTGCTTCCACGA
		R	0230	ACCACCTGCTCTGCTCGTTTAGAA
	0231 (*pbtI*)	F	*pbtI*	AAGCGTTGCTATACGCAAGAAGCC
		R	*pbtI*	AGTTTAGCGCCAAATCCAAGAGCG
	0232 (*pbtA*)	F	*pbtA*	TTTATGGCATTGCCCTTGAGGCAC
		R	*pbtA*	ATGCCGGGCCAGATATAAGGTTGA
	0233 (*pbtB*)	F	*pbtB*	TCTCCAGCAAGCGTTCCCAAAGTA
		R	*pbtB*	TGGCGTCACCGCTGATTCATCATA
	0234 (*pbtC*)	F	*pbtC*	TGGATTGCAGGCCATAGCTGTTTG
		R	*pbtC*	ACCGCAGTTAATCTTGTGGGCAAC
	0235 (*pbtD*)	F	*pbtD*	TGGCGAGAAATATGGTTGTTGCGG
		R	*pbtD*	ATAGCAGCGATTGCCAACCCAATG
	0236 (*pbtE*)	F	*pbtE*	ACGTCACTCTTTACAGCAGTCGCT
		R	*pbtE*	CGCCTCATCAATGGCTTCTGTCAT
	0237 (*pbtF*)	F	*pbtF*	TGGGCAAGATGGTTTGAAGCACAC
		R	*pbtF*	TGCGGTTAATACTGGCGTTGTTGC
	0238 (*pbtG*)	F	*pbtG*	TTAATACAGTCCGATCCGGCCACA
		R	*pbtG*	ATCAAACGTTCCTTGTTCGCTGCC
	0239 (*pbtH*)	F	*pbtH*	GCTCCGTCCTTCAGAAGAAGTCA

		R	*pbtH*	GTGTTGTCCATCTTTGGCAACGGA
Mutant design & confirmation	*pbtA::kan*		*pbtA*IBS	AAAAAAGCTTATAATTATCCTTATCATTCTGGATAGTGCGCCCAGATAGGGTG
			*pbtA*EBS1d	CAGATTGTACAAATGTGGTGATAACAGATAAGTCTGGATACTTAACTTACCTTTCTTTGT
			*pbtA*EBS2	TGAACGCAAGTTTCTAATTTCGGTTAATGATCGATAGAGGAAAGTGTCT
		F	C*pbtA::kan*	GAACTTATGGGGATACTGAAAA
		R	C*pbtA::kan*	ATGCCGGGCCAGATATAAGGTTGA
	nrpR::kan		*nrpR*IBS	AAAAAAGCTTATAATTATCCTTAAGTTACTCATTAGTGCGCCCAGATAGGGTG
			*nrpR*EBS1d	CAGATTGTACAAATGTGGTGATAACAGATAAGTCTCATTACTTAACTTACCTTTCTTTGT
			*nrpR*EBS2	TGAACGCAAGTTTCTAATTTCGATTTAACTTCGATAGAGGAAAGTGTCT
		F	C*nrpR::kan*	CTCTTGGTGGTGTTGCTTGCCAAA
		R	C*nrpR::kan*	AATGGCAGAAGAGGAGAGTCTGGT
	nrpRpbtA::kan		*nrpR*2050-IBS	AAAAAAGCTTATAATTATCCTTAATATACCTATATGTGCGCCCAGATAGGGTG
	nrpR2596::kan		*nrpR*2050-EBS1d	CAGATTGTACAAATGTGGTGATAACAGATAAGTCCTATATTGTAACTTACCTTTCTTTGT
			*nrpR*2050-EBS2	TGAACGCAAGTTTCTAATTTCGATTTATATTCGATAGAGGAAAGTGTCT
		F	C*nrpR*(2050)*::kan*	CTCTTGGTGGTGTTGCTTGCCAAA
		R	C*nrpR*(2050)*::kan*	AGTGCTGATATGGCAAGTACCCGA
	nrpR2596::kan		2596IBS	AAAAAAGCTTATAATTATCCTTAGATGACTTGAGCGTGCGCCCAGATAGGGTG
			2596EBS1d	CAGATTGTACAAATGTGGTGATAACAGATAAGTCTTGAGCGCTAACTTACCTTTCTTTGT
			2596EBS2	TGAACGCAAGTTTCTAATTTCGATTTCATCTCGATAGAGGAAAGTGTCT
		F	C*2596::kan*	TGTAGCTGCCACAGAACAGCATGA
		R	C*2596::kan*	ATGCTTCAGCGTGACTACTGGGTT
RT-PCR	0228 - 0229	F	3' 0228	AAGAGTAATAAAAGCCTCTGCAGA
		R	5' 0229	GAAACGACGAAGTATCTGTCGCTG
	0229 - 0230	F	3' 0229	TGAATGCTTGGAAACTGACGGCAC
		R	5' 0230	AACCACCTGCTCTGCTCGTTTAGA
	0230 - 0231	F	3' 0230	TTATCGCGTTAGCGCCCGTATTGA
		R	5' 0231	ACCATGCTAGCGCTCTTGGATTTG
	0231 - 0232	F	3' 0231	CAAATCCAAGAGCGCTAGCATGGT
		R	5' 0232	TGGCGGCCATCCATTGATTTAAGG
	0232 - 0233	F	3' 0232	ACTGTGATCGGCGAAGAGCTTGAA
		R	5' 0233	CCGCGCTGACGAAATCAGGAATTA
	0233 - 0234	F	3' 0233	TCCTTGCCTCGGTAAGTGTTGACT
		R	5' 0234	TTGGCGACTTCGACCATGGCATTA
	0234 - 0235	F	3' 0234	TGGATTGCAGGCCATAGCTGTTTG
		R	5' 0235	CCGATTGCAGCAGCGGTAATTGAA
	0235 - 0236	F	3' 0235	TTGCACTTGCTATGGCTGATGGTG
		R	5' 0236	ACAGCTTCTGAGCGACTGCTGTAA
	0236 - 0237	F	3' 0236	AACGTCTTCGAGTACCAACACCCT
		R	5' 0237	ATAGGTGCGATATACACGCCGGTT
	0237 - 0238	F	3' 0237	TTGCCTCTATGGTTGGCATTGCAC
		R	5' 0238	CGCGCTGTACCGGTAATTTGACAT
	0238 - 0239	F	3' 0238	TCCAGCAGCTAGCTAAGTGGATAC
		R	5' 0239	TGTTGTCCATCTTTGGCAACGGAC
	0239 - 0240	F	3' 0239	AAGGTAATATTTTCCCTTATAAAA
		R	5' 0240	TCACGCCATAATACTTCTGCAATA
	2596 - 2597	F	3' 2596	AGCCAGTGCTTCCTCCTGTATTGA
		R	5' 2597	CTCAGGCGTTCAATAAATGGAGACC
	2597 - 2598	F	3' 2597	ATTAGGCACTTGGACAGCGGAGAA
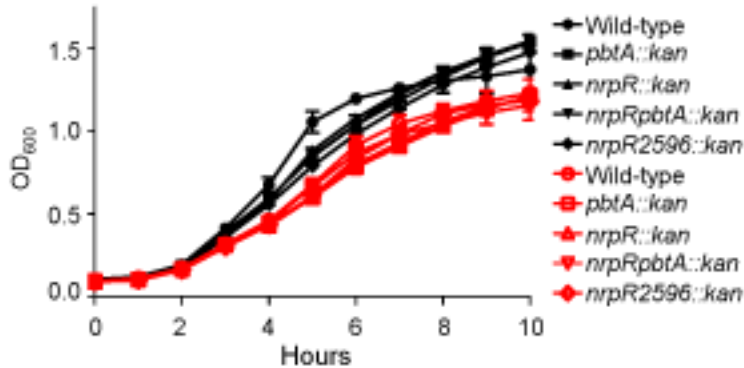
Fig. S1. Growth of *P. mirabilis* wild-type and siderophore biosynthesis mutants in LB broth alone and LB broth containing 15 µM Desferal. Growth of *P. mirablis* HI4320 wild-type, proteobactin synthetase/receptor mutant (*pbtA::kan*), yersiniabactin synthetase mutant (*nrpR::kan*), yersiniabactin synthetase and proteobactin synthetase/receptor mutant (*nrpRpbtA::kan*), yersiniabactin synthetase/receptor mutant (*nrpR2596::kan*) in LB broth alone (black symbols and lines) and in LB broth containing 15 µM Desferal (red symbols and lines).
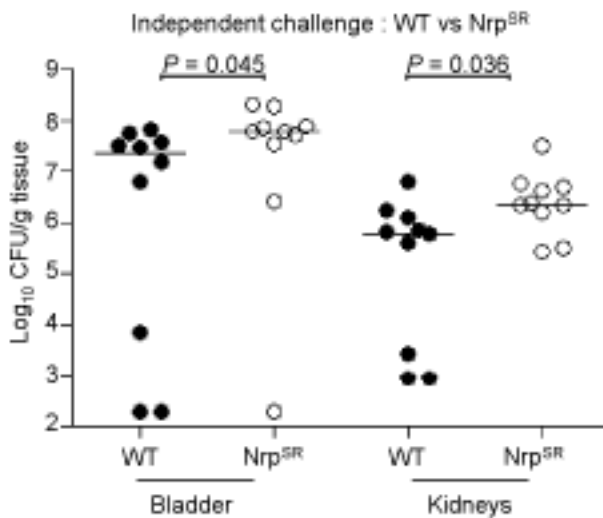
Fig. S2. Independent infection of yersiniabactin-related synthetase/receptor mutant and wild-type HI4320. Each data point represents the $\log_{10}$ CFU/g tissue collected from a single animal. The bars represent the median values of the populations. The limit of detection of this assay is 2×10^2 CFU/g. A significant difference in colonization was determined using a two-tailed Mann-Whitney test.