

Table S5. Microarray results for genes in *E. coli* NC101 upregulated with decreased iron availability

E. coli NC101 was cultured in minimal media with 0, 5 or 50 mM added iron for 1 hour. The table below lists genes that are significantly upregulated great than 1.5 fold with decreased iron ($p < 0.1$, pairwise comparisons by one-way ANOVA).

Gene Symbol	Fold change			Gene description
	0 vs 5 μ M	0 vs 50 μ M	5 vs 50 μ M	
ybdZ	3.63	17.22	4.75	hypothetical protein
chuT	4.91	11.64	2.37	putative periplasmic binding protein
cirZ	6.46	11.52	1.78	colicin I receptor; catecholate siderophore receptor CirA
fes	3.36	11.28	3.36	enterobactin/ferric enterobactin esterase
entH	3.35	11.07	3.31	thioesterase required for efficient enterobactin production
c4310	5.96	11.03	1.85	hypothetical protein
chuW	5.00	10.63	2.13	coproporphyrinogen III oxidase
fhuE	7.39	10.46	1.42	ferric-rhodotorulic acid outer membrane transporter
chuA	6.49	10.45	1.61	Outer membrane heme/hemoglobin receptor
fhuF	3.52	10.26	2.92	ferric iron reductase involved in ferric hydroxamate transport
entB	3.11	9.85	3.17	2,3-dihydro-2,3-dihydroxybenzoate synthetase; isochorismatase
entE	3.03	8.69	2.87	enterobactin synthase subunit E
entA	2.89	8.40	2.91	2,3-dihydroxybenzoate-2,3-dehydrogenase
sitA	2.85	7.50	2.63	SitA protein
chuX	3.92	7.40	1.89	hypothetical protein; ShuX-like protein
ybiL	5.41	7.39	1.37	catecholate siderophore receptor Fiu
c0670	4.66	7.00	1.50	hypothetical protein
entF	2.93	6.79	2.32	enterobactin synthase subunit F
ycdO	1.77	6.75	3.82	hypothetical protein; inactive ferrous ion transporter EfeUOB
sitC	3.41	6.73	1.97	SitC protein
chuY	3.95	6.73	1.70	hypothetical protein
fes	3.23	6.12	1.89	enterobactin/ferric enterobactin esterase
sitB	2.74	5.45	1.99	SitB protein
ycdB	1.91	5.23	2.74	hypothetical protein
yncE	2.22	4.77	2.15	putative receptor; hypothetical protein
fepB	2.46	4.77	1.93	iron-enterobactin transporter periplasmic binding protein; iron-enterobactin transporter subunit
ycdO	1.78	4.61	2.59	hypothetical protein
c2423	2.85	3.66	1.28	putative AraC type regulator
tonB	1.78	3.63	2.04	transport protein TonB; membrane spanning protein in TonB-ExbB-ExbD transport complex
fhuA	1.49	3.09	2.08	ferrichrome outer membrane transporter
exbB	1.91	2.91	1.52	biopolymer transport protein ExbB; membrane spanning protein in TonB-ExbB-ExbD complex
yqjH	1.66	2.82	1.70	predicted siderophore interacting protein
bfd	1.57	2.55	1.63	bacterioferritin-associated ferredoxin
exbD	1.64	2.53	1.54	biopolymer transport protein ExbD; membrane spanning protein in TonB-ExbB-ExbD complex
pabB	1.11	1.97	1.77	para-aminobenzoate synthase component I; aminodeoxychorismate synthase, subunit I
sufS	1.57	1.90	1.21	bifunctional cysteine desulfurase/selenocysteine lyase; cysteine desulfurase, stimulated by SufE; selenocysteine lyase, PLP-dependent
sodA	1.16	1.56	1.34	superoxide dismutase, Mn
pncA	1.09	1.67	1.54	nicotinamidase/pyrazinamidase
bioB	1.06	1.64	1.55	biotin synthase
mltA	1.17	1.96	1.67	murein transglycosylase A; membrane-bound lytic murein transglycosylase A
yebU	1.02	1.68	1.64	16S rRNA m(5)C1407 methyltransferase, SAM-dependent; rRNA (cytosine-C(5)-)-methyltransferase RsmF
yebT	1.09	1.59	1.47	hypothetical protein
yciR	1.06	1.59	1.51	RNase II stability modulator; cyclic-di-GMP
flk	1.07	1.55	1.45	flagella biosynthesis regulator; predicted flagella assembly protein
holE	1.05	1.55	1.47	DNA polymerase III subunit theta