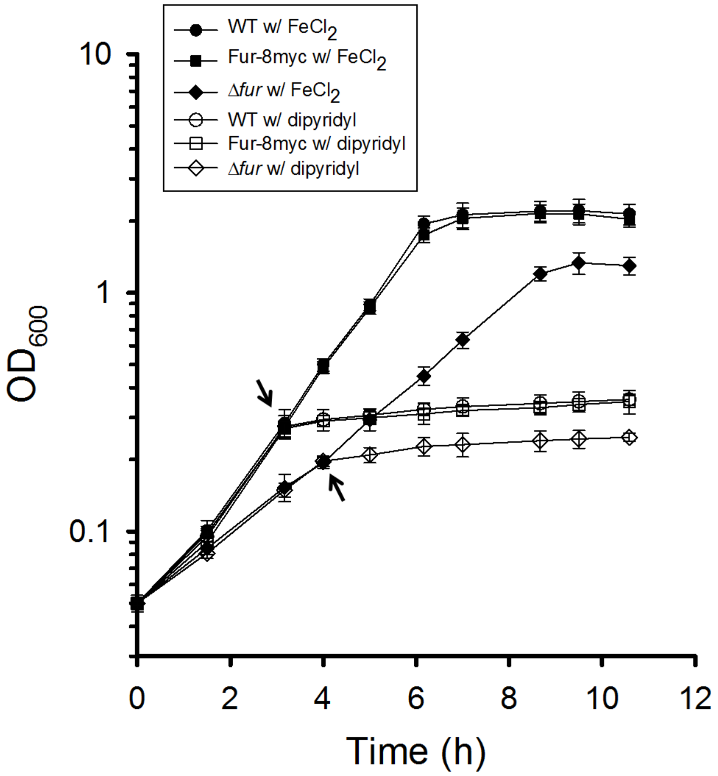
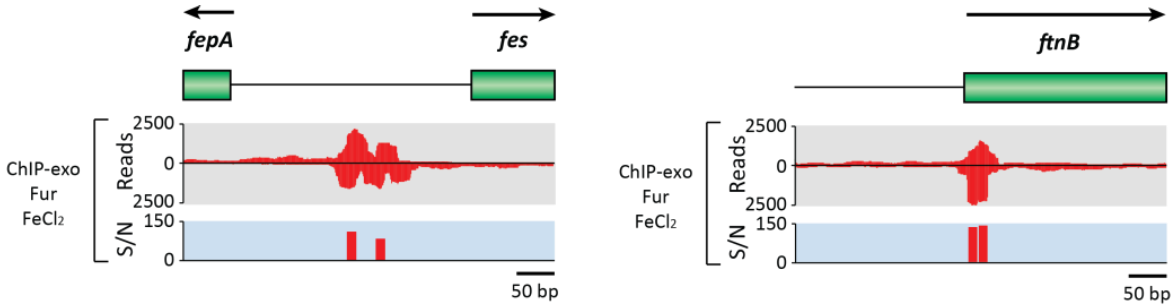
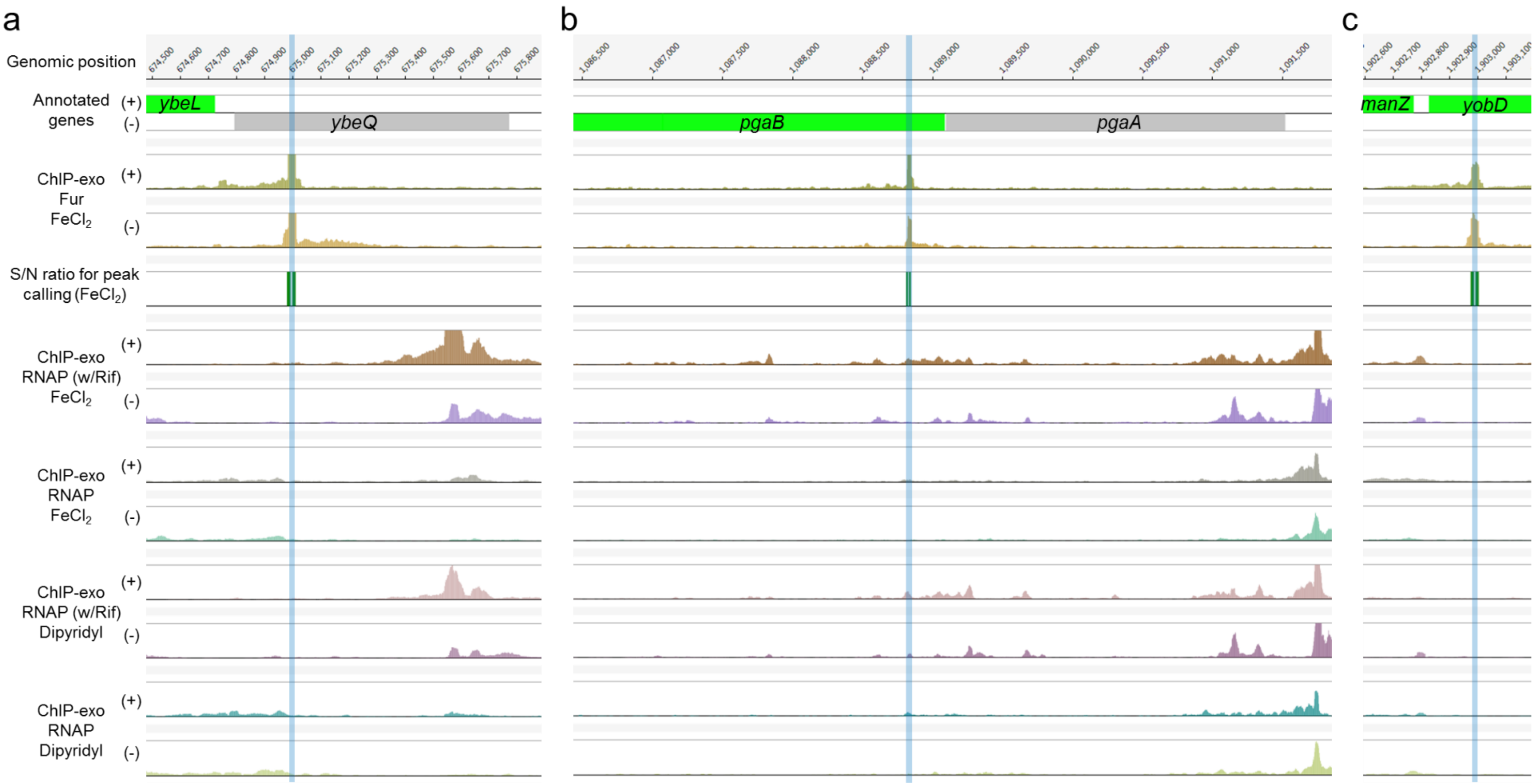
Supplementary Figures



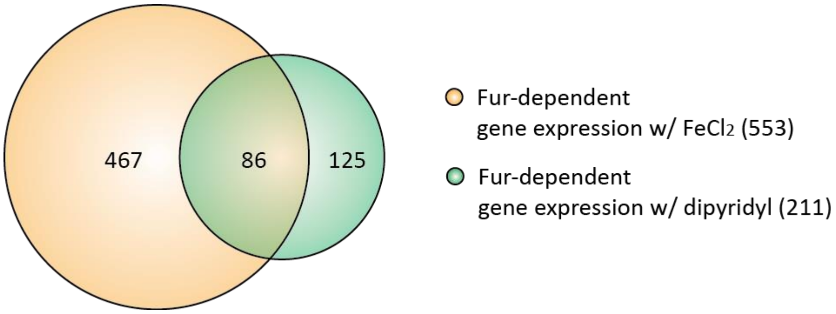
Supplementary Figure 1. Growth profiles of *E. coli* strains used in this study in response to iron availability. Doubling times of WT (K-12 MG1655), Fur-8myc, and Δ*fur* strains were 66.01 min^{-1}, 67.29 min^{-1}, and 113.63 min^{-1}, respectively. The arrows indicate the time when dipyridyl was added into the media. The error bar indicates standard deviation of triplicate experiments.



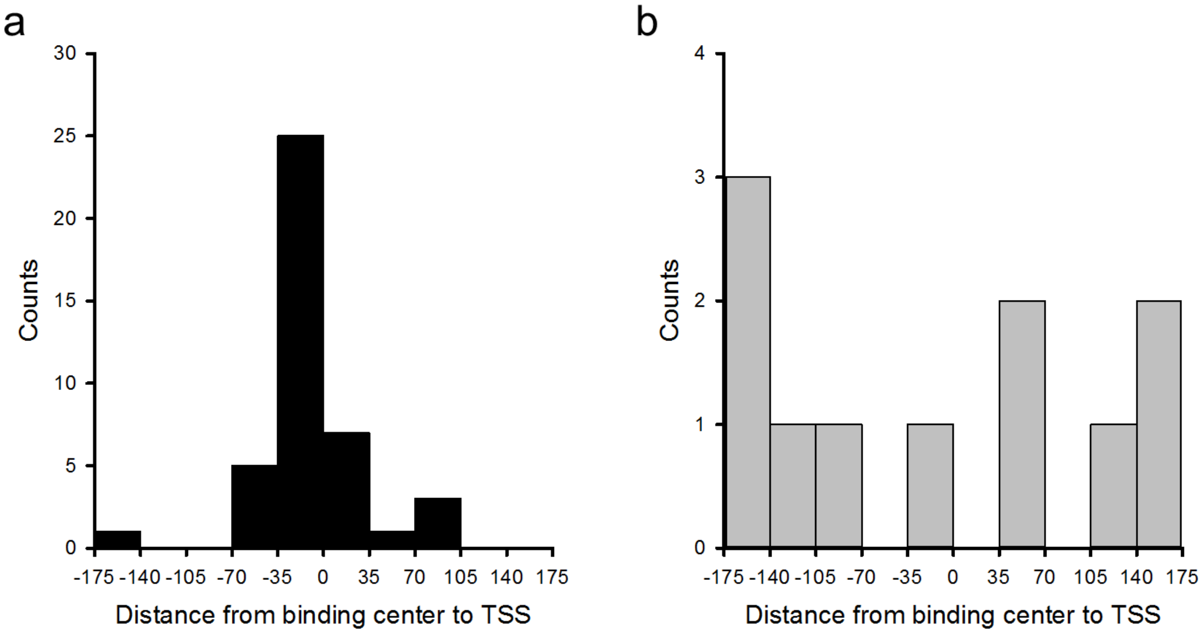
Supplementary Figure 2. Zoom-in examples of Fur bindings identified by ChIP-exo. The high-resolution of ChIP-exo method enabled us to separate binding peaks in divergent promoter regions between *fepA* and *fes* as well as identify multiple biding peaks for *ftnB*. Arrows indicate the direction of transcription of each gene.



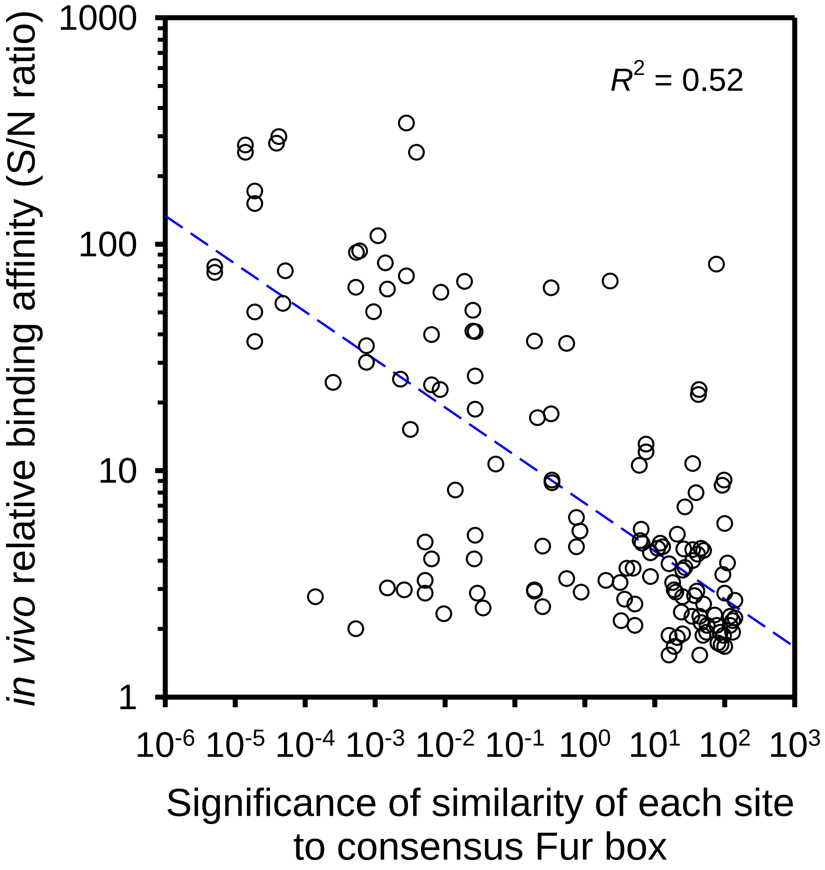
Supplementary Figure 3. Zoom-in examples of RNAP-binding profiles where Fur binds to non-regulatory regions. From ChIP-exo analysis of RNAP under both static (with rifampicin that blocks transcription elongation) and dynamic (without rifampicin) conditions, we could confirm that bindings of Fur on the annotated non-regulatory regions were not related with active transcription events under both iron-replete ($FeCl_2$) and starvation (dipyridyl) conditions. The shaded blue lines indicate where Fur binds. The data were visualized by using MetaScope (http://systemsbiology.ucsd.edu/Downloads/MetaScope).



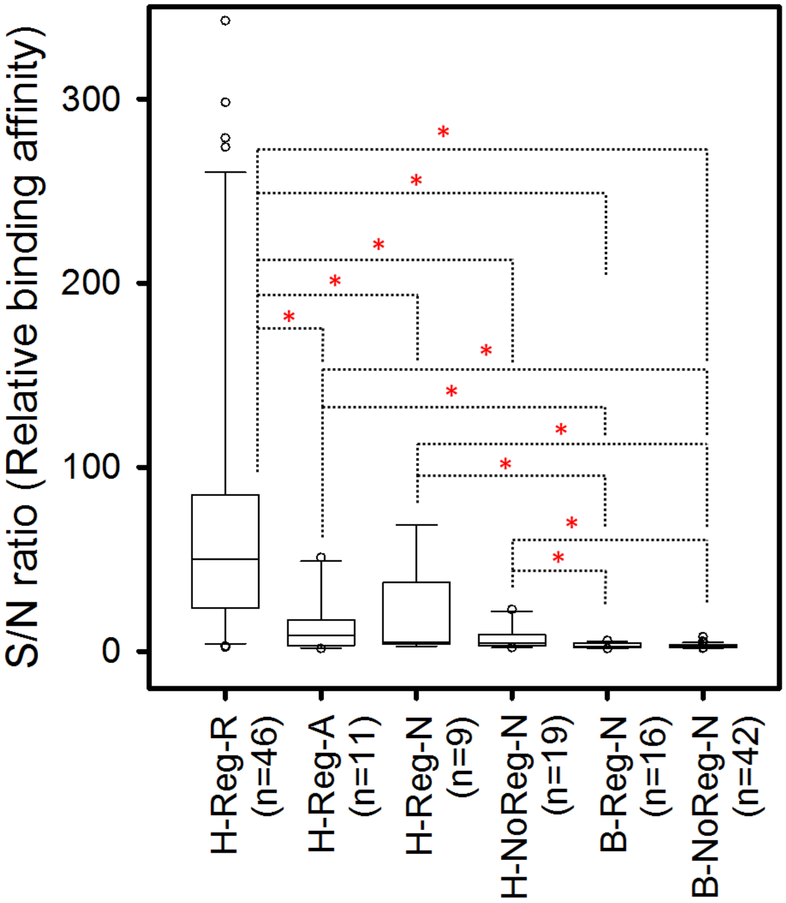
Supplementary Figure 4. Fur-dependent transcriptome in response to iron availability. Transcription level was compared between wild-type and Δ*fur* mutant under both iron-replete ($FeCl_2$) and starvation (dipyridyl) conditions.



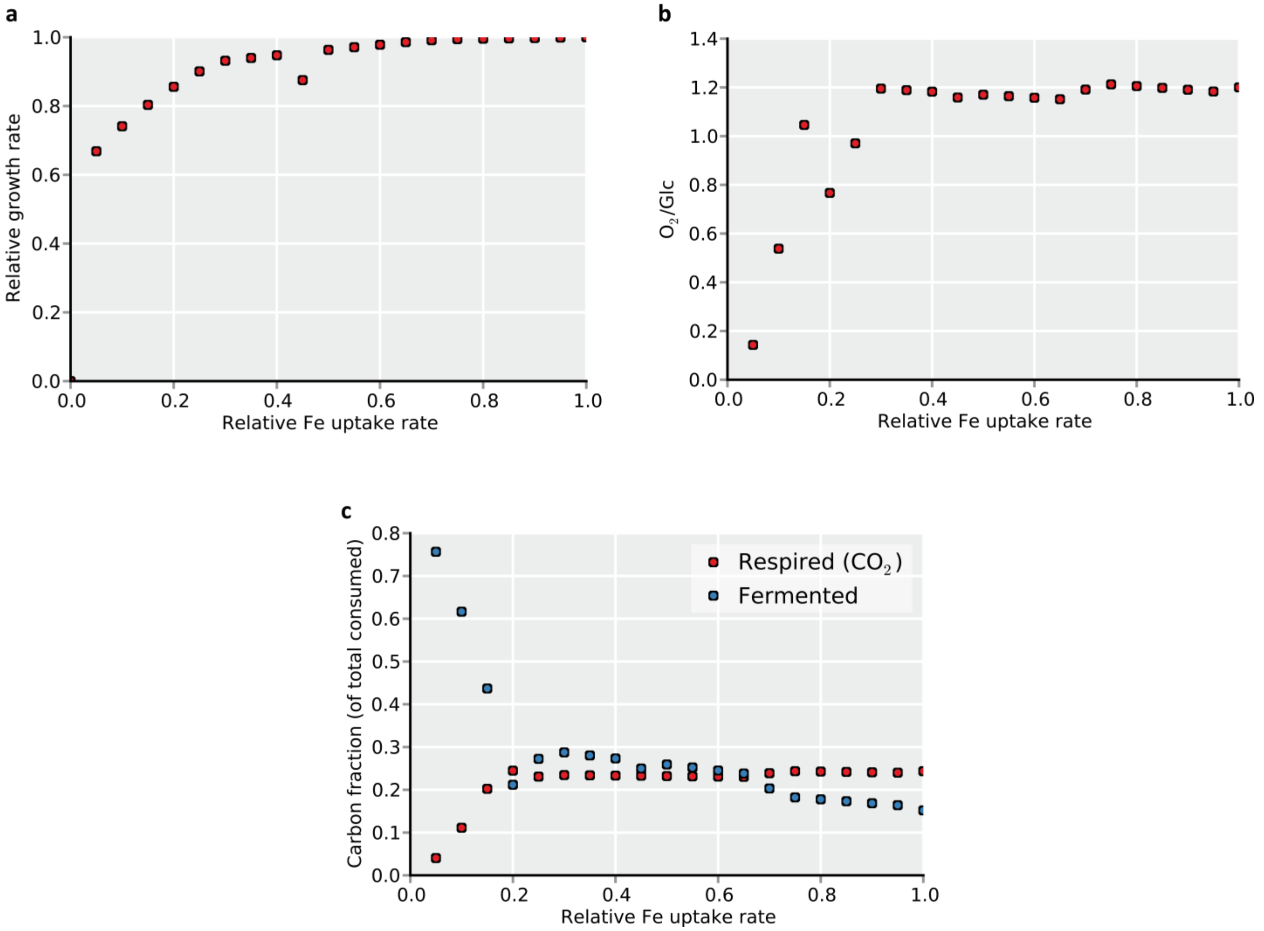
Supplementary Figure 5. Relative distance of Fur binding center to transcription start site (TSS). We calculated distance of Fur binding center to TSS of each gene in case of (a) repression and (b) activation.



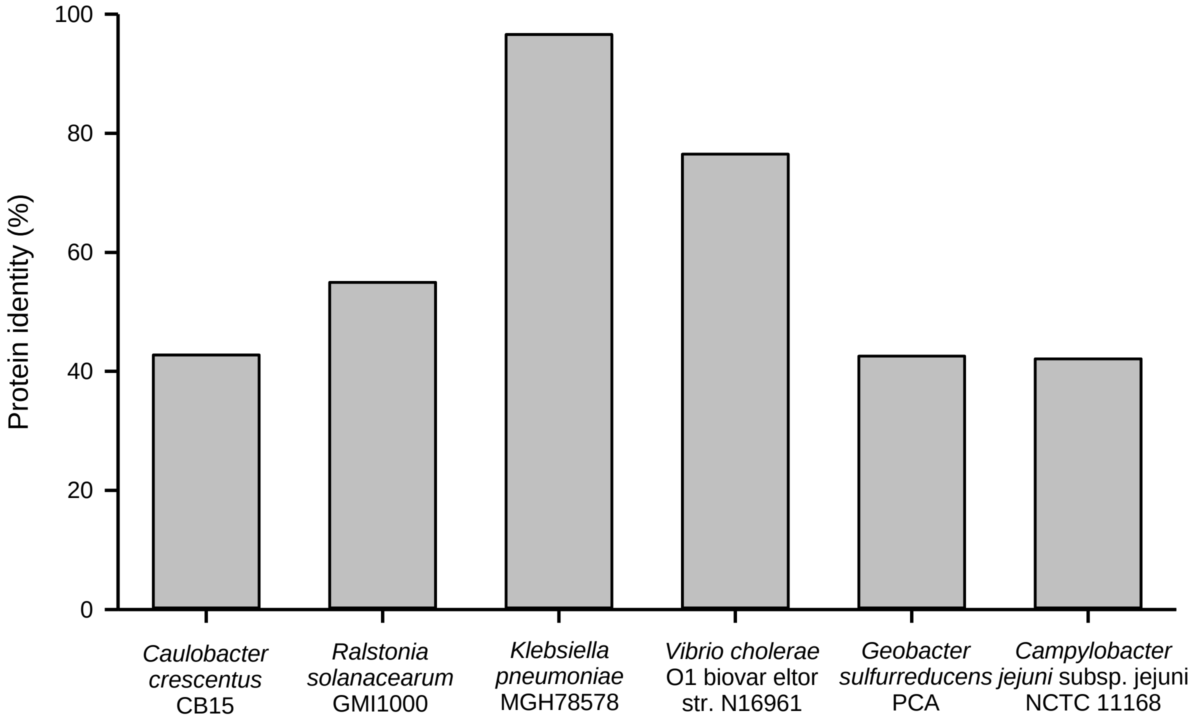
Supplementary Figure 6. Relationship between sequence similarity to consensus Fur box and *in vivo* relative binding affinity. The signal-to-noise (S/N) ratio of each Fur-binding peak was assigned to *in vivo* relative binding affinity of each site. The significance of similarity of each site to consensus Fur box was represented by statistical significance (*P*-value) computed from the match score of the site with the position specific scoring matrix for the motif. The more different the binding sequence was from the consensus Fur box, the lower the *in vivo* relative binding affinity was.



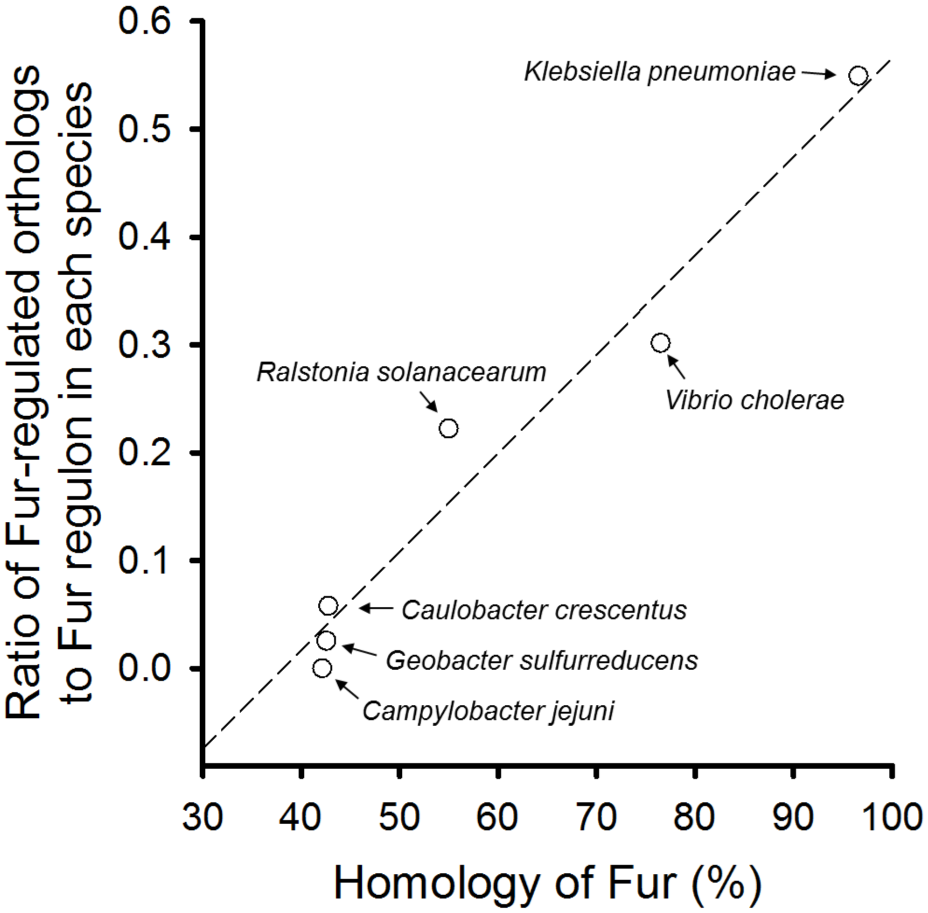
Supplementary Figure 7. Fur occupancy level of depending on Fur binding modes (with or without iron), binding location (regulatory or non-regulatory region), and change of transcript level (repression, activation, or no change in transcript). Each category has 46 binding peaks in *holo*-Fur repression (H-Reg-R), 11 binding peaks in *holo*-Fur activation (H-Reg-A), 9 holo-Fur binding peaks in regulatory regions but no change in transcript level (H-Reg-N), 19 holo-Fur binding peaks in non-regulatory regions (H-NoReg-N), 16 binding peaks regardless of iron availability in regulatory regions but no change in transcript (B-Reg-N), and 42 binding peaks regardless of iron availability in non-regulatory regions (B-NoReg-N). Signal-to-noise (S/N) ratio of each Fur-binding peak in ChIP-exo data was used to indicate a relative binding affinity. Red asterisk (*) indicates *P-value* < 0.01. The plot is median-quartile boxplots with decile error bars.



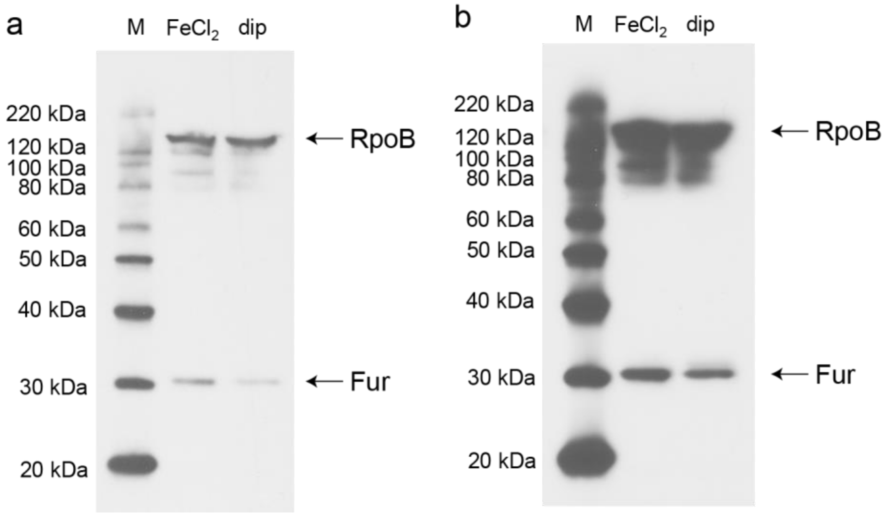
Supplementary Figure 8. ME-model simulation results as a function of the iron uptake rate. From ME-model simulation, we predicted (a) relative growth rate, (b) O_2 uptake rate relative to glucose uptake, and (c) fraction of carbon secretion in response to different iron uptake rate. As iron is scarce, both growth rate and O_2 uptake rate are decreased. However, the fraction of fermented carbon dramatically increases while that of respired carbon decreases, indicating metabolism shifts towards fermentative pathways.



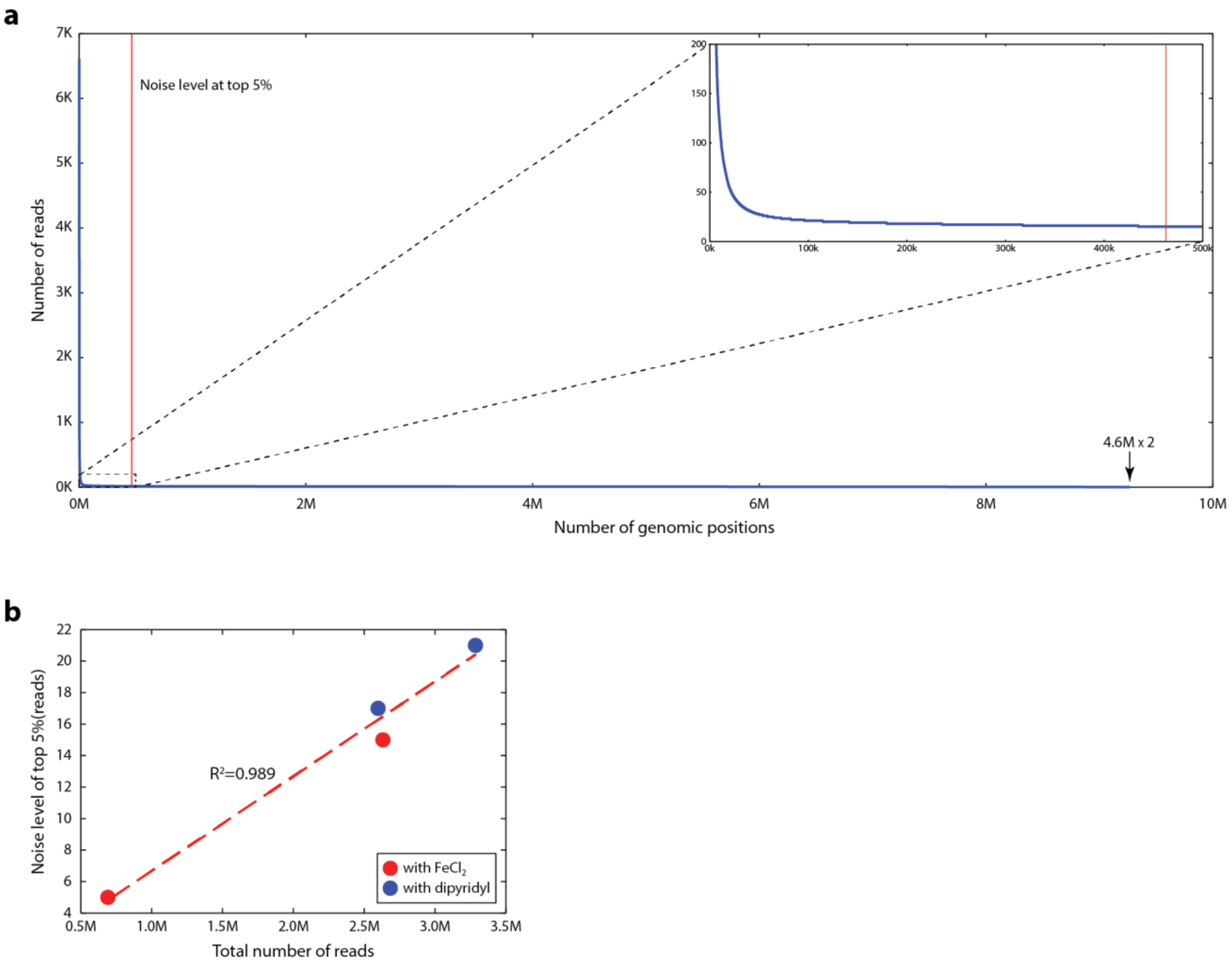
Supplementary Figure 9. Homology of Fur in each species compared to that in *E. coli* K-12 MG1655. *Caulobacter crescentus* (α-proteobacteria), *Ralstonia solanacearum* (β-proteobacteria), *Klebsiella pneumonia* (γ-proteobacteria), *Vibrio cholerae* (γ-proteobacteria), *Geobacter sulfurreducens* (δ-proteobacteria), and *Campylobacter jejuni* (ε-proteobacteria) were analyzed.



Supplementary Figure 10. The relationship between conservation of Fur and Fur-regulated orthologs. The ratio of Fur-regulated orthologs to the known Fur regulon in each species was linearly correlated with the degree of conservation of Fur ($R^2 = 0.95$).



Supplementary Figure 11. Western blot analysis. The *E. coli* strain harboring Fur-8myc was grown under iron-replete ($FeCl_2$) and iron starvation (Dipyridyl, dip) conditions. Antibodies that specifically recognize RpoB subunit of RNAP and myc-tag for Fur were used after separating membranes into two pieces. They were exposed together to generate blot image. The exposure time is (a) 1 sec and (b) 5 sec. The M lane indicates molecular marker (MagicMark^{TM} XP Standard, Life Technologies).



Supplementary Figure 12. Noise level setting for ChIP-exo analysis. (**a**) Noise level (reads) at top 5% (red line) resembles background level in plateau. (**b**) Noise level of top 5% (reads) from each ChIP-exo replicates across conditions was correlated with the total number of reads.

Supplementary Tables

Supplementary Table 1. Confirmation of previously characterized Fur-binding sites

Number	Transcription Unit	Decision
1	*fhuACDB*	Yes
2	*fepA-entD*	Yes
3	*fes-ybdZ-entF-fepE*	Yes
4	*fepD-fepG-fepC*	Yes
5	*entS*	Yes
6	*fepB*	Yes
7	*entCEBAH*	Yes
8	*fur*	No
9	*gpmA*	Yes
10	*pyrC*	No
11	*oppABCDF*	No
12	*tonB*	Yes
13	*nohA-ydfN*	No
14	*sufABCDSE*	Yes
15	*ftnA*	Yes
16	*cirA*	Yes
17	*mntH*	Yes
18	*hmp*	No
19	*exbBD*	Yes
20	*garPLRK*	No
21	*gspCDEFGHIJKLMO*	No
22	*ryhB*	Yes
23	*sodA*	Yes
24	*fecABCDE*	Yes
25	*fecIR*	Yes
26	*fhuF*	Yes
27	*yjjZ*	Yes
	Total	20/27 (74%)

Supplementary Table 2. Genes directly regulated by Fur in response to iron availability.

Number	bnum	Gene	Regulatory Mode	Cog[a]	Description
1	b0150	*fhuA*	HR	P	ferrichrome outer membrane transporter
2	b0151	*fhuC*	HR	H,P	iron-hydroxamate transporter subunit
3	b0152	*fhuD*	HR	P	iron-hydroxamate transporter subunit
4	b0153	*fhuB*	HR	P	fused iron-hydroxamate transporter subunits of ABC superfamily
5	b0273	*argF*	HA	E	ornithine carbamoyltransferase 2
6	b0272	*yagI*	HA	K	predicted DNA-binding transcriptional regulator
7	b0468	*ybaN*	HR	S	inner membrane protein
8	b0474	*adk*	HA	F	adenylate kinase
9	b0584	*fepA*	HR	P	iron-enterobactin outer membrane transporter
10	b0583	*entD*	HR	Q	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex
11	b0585	*fes*	HR	P	Enterochelin esterase
12	b4511	*ybdZ*	HR	S	stimulator of EntF adenylation activity, MbtH-like
13	b0586	*entF*	HR	Q	Enterobactin synthase component F
14	b0587	*fepE*	HR	M	Ferric enterobactin transport protein
15	b0590	*fepD*	HR	P	iron-enterobactin transporter subunit
16	b0589	*fepG*	HR	P	iron-enterobactin transporter subunit
17	b0588	*fepC*	HR	H,P	iron-enterobactin transporter subunit
18	b0591	*entS*	HR	-	enterobactin exporter
19	b0592	*fepB*	HR	P	iron-enterobactin transporter subunit
20	b0593	*entC*	HR	H,Q	isochorismate synthase 1
21	b0594	*entE*	HR	Q	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex
22	b0595	*entB*	HR	Q	isochorismatase
23	b0596	*entA*	HR	I,Q,R	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
24	b0597	*entH*	HR	Q	thioesterase required for efficient enterobactin production
25	b0755	*gpmA*	HR	G	phosphoglyceromutase 1
26	b0805	*fiu*	HR	P	catecholate siderophore receptor Fiu

27	b0804	*ybiX*	HR	S	conserved protein, Fe(II)-dependent oxygenase superfamily
28	b1017	*efeU_2*	HR	-	pseudogene
29	b1018	*efeO*	HR	P	Iron uptake system component EfeO
30	b1019	*efeB*	HR	P	Deferrochelatase/peroxidase EfeB
31	b1102	*fhuE*	HR	P	ferric-rhodotorulic acid outer membrane transporter
32	b1164	*ycgZ*	AA	-	RcsB connector protein for regulation of biofilm and acid-resistance
33	b1165	*ymgA*	AA	-	RcsB connector protein for regulation of biofilm
34	b1166	*ariR*	AA	-	RcsB connector protein for regulation of biofilm and acid-resistance
35	b1167	*ymgC*	AA	-	predicted protein
36	b1252	*tonB*	HR	M	membrane spanning protein in TonB-ExbB-ExbD transport complex
37	b1267	*acnA*	HA	C	aconitate hydratase 1
38	b1452	*yncE*	HR	S	ATP-binding protein
39	b1478	*adhP*	HR	R	ethanol-active dehydrogenase/acetaldehyde-active reductase
40	b1496	*yddA*	HR	R	Inner membrane ABC transporter ATP-binding protein
41	b1495	*yddB*	HR	P	putative porin protein
42	b1586	*ynfD*	HR	-	lipoprotein
43	b1684	*sufA*	HR	S	Fe-S cluster assembly protein
44	b1683	*sufB*	HR	O	component of SufBCD Fe-S cluster assembly scaffold
45	b1682	*sufC*	HR	O	SufBCD Fe-S cluster assembly scaffold protein
46	b1681	*sufD*	HR	O	component of SufBCD Fe-S cluster assembly scaffold
47	b1680	*sufS*	HR	E	cysteine desulfurase
48	b1679	*sufE*	HR	R	sulfur acceptor protein
49	b1705	*ydiE*	HR	P	hemin uptake protein HemP homolog
50	b1902	*ftnB*	HA	P	ferritin B
51	b1905	*ftnA*	HA	P	ferritin iron storage protein
52	b1995	*yoeA*	HR	-	pseudogene
53	b2155	*cirA*	HR	P	catecholate siderophore receptor CirA
54	b2211	*yojI*	HR	P,Q	fused ABC transporter permease and ATP-binding components
55	b2392	*mntH*	HR	P	manganese/divalent cation transporter
56	b2673	*nrdH*	HR	O	hydrogen donor for NrdEF electron transport system
57	b2674	*nrdI*	HR	F	flavodoxin required for NrdEF cluster assembly

58	b2675	*nrdE*	HR	F	ribonucleoside-diphosphate reductase 2, alpha subunit
59	b2676	*nrdF*	HR	F	ribonucleoside-diphosphate reductase 2, beta subunit
60	b2997	*hybO*	HA	C	hydrogenase 2, small subunit
61	b2996	*hybA*	HA	C	hydrogenase 2 4Fe-4S ferredoxin-type component
62	b3006	*exbB*	HR	U	membrane spanning protein in TonB-ExbB-ExbD complex
63	b3005	*exbD*	HR	U	membrane spanning protein in TonB-ExbB-ExbD complex
64	b3070	*yqjH*	HR	P	predicted siderophore interacting protein
65	b3408	*feoA*	HR	P	ferrous iron transporter
66	b3409	*feoB*	HR	P	fused ferrous iron transporter
67	b3410	*feoC*	HR	K	predicted DNA-binding transcriptional regulator
68	b4451	*ryhB*	HR	-	sRNA antisense regulator mediating positive Fur regulon response, Hfq-dependent
69	b3928	*zapB*	HA	S	FtsZ stabilizer
70	b4291	*fecA*	HR	P	ferric citrate outer membrane transporter
71	b4290	*fecB*	HR	P	iron-dicitrate transporter subunit
72	b4289	*fecC*	HR	P	iron-dicitrate transporter subunit
73	b4288	*fecD*	HR	P	iron-dicitrate transporter subunit
74	b4287	*fecE*	HR	H,P	iron-dicitrate transporter subunit
75	b4293	*fecI*	HR	K	RNA polymerase, sigma 19 factor
76	b4292	*fecR*	HR	T,P	transmembrane signal transducer for ferric citrate transport
77	b4322	*uxuA*	HA	G	mannonate hydrolase
78	b4323	*uxuB*	HA	G	D-mannonate oxidoreductase
79	b4342	*yjiT*	HA	-	pseudogene
80	b4367	*fhuF*	HR	R	ferric iron reductase involved in ferric hydroximate transport
81	b4567	*yjjZ*	HR	-	predicted protein

[a] “-” indicates genes that are not classified in Cog.

Supplementary Table 3. Other transcription factors known to regulate direct Fur regulon (81 genes).

TF	# of bindings	Target genes
crp	16	*fepA/entD/entC/entE/entB/entA/fiu/acnA/cirA/fecA/fecB/fecC/fecD/fecE/uxuA/uxuB*
oxyR	10	*sufA/sufB/sufC/sufD/sufS/sufE/mntH/uxuA/uxuB/fhuF*
nsrR	6	*sufA/sufB/sufC/sufD/sufS/sufE*
iscR	6	*sufA/sufB/sufC/sufD/sufS/sufE*
ihfB	6	*sufA/sufB/sufC/sufD/sufS/sufE*
ihfA	6	*sufA/sufB/sufC/sufD/sufS/sufE*
pdhR	5	*fecA/fecB/fecC/fecD/fecE*
fnr	4	*fes/entF/acnA/feoB*
arcA	3	*acnA/hybO/hybA*
uxuR	2	*uxuA/uxuB*
nrdR	2	*nrdE/nrdF*
narL	2	*hybO/hybA*
hns	2	*fes/entF*
fnrS	2	*gpmA/adhP*
exuR	2	*uxuA/uxuB*
soxS	1	*acnA*
rutR	1	*fepB*
rob	1	*acnA*
nagC	1	*feoB*
mntR	1	*mntH*
marA	1	*acnA*
fruR	1	*acnA*
argR	1	*argF*

Supplementary Table 4. Sequence bound by *apo*-Fur for the activation of *ycgZ-ymgA-ariR-ymgC* operon.

Peak	**ChIP-exo Start**	**ChIP-exo End**	**Sequence**
P38 (*ycgZ-ymgA-ariR-ymgC*)	1214895	1214907	TATATGCATTAG

Supplementary Table 5. The transporter and utilization genes regulated by Fur without iron in other pathogenic species.

Strains	Name	Regulatory Mode	Description	Ref
C. jejuni	*Cj1364*	AR	fumarate hydratase	(6)
C. jejuni	*Cj1345c*	AA	putative periplasmic protein	(6)
H. pylori	*pfr*	AR	prokaryotic ferritin	(1)
H. pylori	*sodB*	AR	Fe-containing superoxide dismutase	(1)
H. pylori	cytochrome c_{553}	AR	transferring electrons from cytochrome reductase to a cbb3-type terminal oxidase	(5)
H. pylori	*hydA*	AR	quinone-reactive Ni/Fe hydrogenase	(5)
S. aureus	*norA*	AA	efflux transporter	(7)

Supplementary Table 6. The lists of functional groups that significantly overlap with DEGs due to *fur* deletion under iron-replete condition.

Group[a]	*p*-value[b]	# of target genes in group	# of total genes in group
Fur_REPRESSION_regulon_db	4.21E-35	68	114
ArcA_REPRESSION_regulon_db	3.04E-22	56	118
Fur_ACTIVATION_regulon_db	1.87E-14	18	21
FNR_REPRESSION_regulon_db	2.63E-10	39	114
IscR_ACTIVATION_regulon_db	5.55E-09	10	11
IHF_REPRESSION_regulon_db	1.08E-07	29	87
NarL_ACTIVATION_regulon_db	4.31E-07	18	42
FNR_ACTIVATION_regulon_db	9.15E-07	47	194
CusR_ACTIVATION_regulon_db	2.88E-06	6	6
Zur_REPRESSION_regulon_db	2.88E-06	6	6
ArgR_REPRESSION_regulon_db	4.02E-06	14	31
Fis_ACTIVATION_regulon_db	6.69E-06	22	68
BirA_REPRESSION_regulon_db	2.43E-05	5	5
CueR_REPRESSION_regulon_db	2.43E-05	5	5
PdhR_ACTIVATION_regulon_db	2.43E-05	5	5
YjiE_REPRESSION_regulon_db	2.43E-05	5	5
GadW_REPRESSION_regulon_db	2.96E-05	7	10
IHF_ACTIVATION_regulon_db	4.22E-05	37	160
OxyR_ACTIVATION_regulon_db	5.76E-05	10	21
GadX_ACTIVATION_regulon_db	6.05E-05	11	25
AdiY_ACTIVATION_regulon_db	6.52E-05	6	8
GlcC_ACTIVATION_regulon_db	0.000131	5	6
IscR_REPRESSION_regulon_db	0.000235	9	20
OxyR_REPRESSION_regulon_db	0.000395	6	10
GadE_ACTIVATION_regulon_db	0.000475	12	35
MarA_ACTIVATION_regulon_db	0.00134	10	29
Lrp_REPRESSION_regulon_db	0.001413	11	34
SoxS_ACTIVATION_regulon_db	0.001413	11	34
CRP_ACTIVATION_regulon_db	0.001464	68	403
HdfR_ACTIVATION_regulon_db	0.001712	3	3
DcuR_ACTIVATION_regulon_db	0.00202	5	9
Nac_REPRESSION_regulon_db	0.00202	5	9
NrdR_REPRESSION_regulon_db	0.00202	5	9
ModE_ACTIVATION_regulon_db	0.002376	10	31
GatR_REPRESSION_regulon_db	0.002507	4	6
GadW_ACTIVATION_regulon_db	0.003645	5	10
LexA_REPRESSION_regulon_db	0.004285	14	55
ModE_REPRESSION_regulon_db	0.005553	6	15

MqsA_REPRESSION_regulon_db	0.006234	3	4
OmpR_REPRESSION_regulon_db	0.009598	4	8

[a] The functional groups were assigned based on the regulonDB[10] database.

[b] The hypergeometric *p*-value cutoff was < 0.01.

Supplementary Table 7. The lists of functional groups that significantly overlap with DEGs due to *fur* deletion under iron starvation condition.

Group[a]	*p*-value[b]	# of target genes in group	# of total genes in group
MetJ_REPRESSION_regulon_db	2.45E-12	11	15
GadE_ACTIVATION_regulon_db	1.18E-11	15	35
GadW_REPRESSION_regulon_db	9.35E-10	8	10
Lrp_REPRESSION_regulon_db	1.63E-09	13	34
GatR_REPRESSION_regulon_db	1.07E-08	6	6
Fur_REPRESSION_regulon_db	5.03E-08	21	114
GadW_ACTIVATION_regulon_db	5.22E-08	7	10
ArgR_REPRESSION_regulon_db	7.73E-08	11	31
GadX_ACTIVATION_regulon_db	8.16E-08	10	25
H-NS_REPRESSION_regulon_db	1.68E-06	18	106
ArcA_REPRESSION_regulon_db	1.98E-06	19	118
YjiE_ACTIVATION_regulon_db	1.14E-05	5	8
ArgR_ACTIVATION_regulon_db	2.38E-05	4	5
PurR_REPRESSION_regulon_db	6.88E-05	8	31
FNR_REPRESSION_regulon_db	7.63E-05	16	114
GcvA_ACTIVATION_regulon_db	0.000105434	3	3
AdiY_ACTIVATION_regulon_db	0.000296818	4	8
GcvA_REPRESSION_regulon_db	0.000406934	3	4
ModE_REPRESSION_regulon_db	0.000466248	5	15
NrdR_REPRESSION_regulon_db	0.00051448	4	9
IscR_ACTIVATION_regulon_db	0.001249676	4	11
FliZ_REPRESSION_regulon_db	0.001545033	5	19
RutR_ACTIVATION_regulon_db	0.002242304	2	2
SoxR_ACTIVATION_regulon_db	0.002242304	2	2
Fur_ACTIVATION_regulon_db	0.002501929	5	21
MarA_REPRESSION_regulon_db	0.003200328	3	7
NsrR_REPRESSION_regulon_db	0.004987506	10	82
PepA_REPRESSION_regulon_db	0.006516043	2	3
TorR_REPRESSION_regulon_db	0.006516043	2	3
YdeO_ACTIVATION_regulon_db	0.006516043	2	3
IHF_REPRESSION_regulon_db	0.007591188	10	87
LeuO_ACTIVATION_regulon_db	0.008919028	4	18

[a] The functional groups were assigned based on the regulonDB[10] database.

[b] The hypergeometric *p*-value cutoff was < 0.01.

Supplementary Table 8. The lists of orthologs for direct Fur regulon in *E. coli* K-12 MG1655.

E.coli K-12 MG1655 Fur regulon	*Caulobacter crescentus* CB15	*Ralstonia solanacearum* GMI1000	*Klebsiella pneumoniae* MGH78578	*Vibrio cholerae* O1 biovar eltor str. N16961	*Geobacter sulfurreducens* PCA	*Campylobacter jejuni* subsp. jejuni NCTC 11168
fhuA	CC1778	**RS00173**	**KPN_00165**	**VC0200**		
fhuC			**KPN_00166**	**VC0201**		Cj1354
fhuD			**KPN_00167**	**VC0202**		
fhuB			**KPN_00168**	**VC0203**		
argF			KPN_04659			
yagI		RS03973			GSU0514	
ybaN			KPN_00450	VC1052	GSU0917	
adk	CC1269	RSc2533	KPN_00456	VC0986	GSU2836	
fepA			**KPN_01244**			
entD			**KPN_00601**	VC0780		
fes			KPN_00603			
ybdZ		RS05513	KPN_00604			
entF		RS05860	KPN_00605	**VC2209**		Cj1307
fepE						
fepD			**KPN_00608**	**VC0777**		
fepG			**KPN_00607**	**VC0778**		
fepC		RS02720	**KPN_00606**	VC0779		
entS	CC0403	RS05067	**KPN_00609**		GSU0752	
fepB			**KPN_00610**	**VC0776**		
entC			**KPN_00611**	**VC0773**		
entE			**KPN_00612**	**VC0772**		
entB			**KPN_00613**	**VC0771**		
entA			**KPN_00614**	**VC0774**		
entH			**KPN_00615**		GSU1128	
gpmA	CC2261	RSc0353	**KPN_00768**		GSU1612	
fiu	**CC0028**	**RS02469**	**KPN_01250**			
ybiX	**CC0027**		**KPN_01249**			
efeU_2						
efeO			**KPN_01046**			
efeB			**KPN_01047**			
fhuE						
ycgZ						
ymgA						
ariR						
ymgC						
tonB			KPN_02186	**VC1544**		
acnA	CC3667	RSc2003	KPN_01272	VC1338	GSU0846	
yncE			**KPN_01908**			
adhP		RSc3130	KPN_01853		GSU0573	
yddA		RS04444				
yddB						
ynfD			KPN_01581			
sufA			**KPN_02141**			
sufB	CC1864		**KPN_02140**			
sufC	CC1862		**KPN_02139**			
sufD	CC1861		**KPN_02138**			
sufS	CC1860		**KPN_02137**	VC2309	GSU1868	

sufE	CC1061		**KPN_02136**			
ydiE			**KPN_02163**			
ftnB			KPN_02397			
ftnA			**KPN_02402**	VC0078	GSU1307	
yoeA						
cirA		**RS03722**	**KPN_02593**	**VC0475**	GSU1445	Cj0755
yojI		RS03729	KPN_02632			
mntH		RS00399	**KPN_02743**			
nrdH			KPN_03004			
nrdI			KPN_03005			
nrdE	CC3492		KPN_03006		GSU1871	
nrdF			KPN_03007			
hybO					**GSU0782**	
hybA					**GSU0783**	
exbB	CC2336		**KPN_03426**			Cj0179
exbD	CC2335	**RSc1965**	**KPN_03425**		GSU0027	Cj0180
yqjH		RS03709	**KPN_03499**	**VC2210**		
feoA			**KPN_03778**	**VC2078**		
feoB	**CC0712**	**RSp0251**	**KPN_03779**	**VC2077**	**GSU3268**	Cj1398
feoC			**KPN_03780**			
ryhB						
zapB			KPN_04009	VC2686		
fecA	**CC0139**			**VCA0064**		
fecB				**VCA0227**		Cj1355
fecC						
fecD			KPN_02102			
fecE						
fecI	CC2707	RSp0849			GSU0721	
fecR	CC2708	**RS00175**				
uxuA			KPN_02604			
uxuB	CC1487					
yjiT						
fhuF			**KPN_04821**			
yjjZ			KPN_04823			

Bold text indicates orthologous genes that have been identified as Fur regulon in each species.