

Supplementary Information

Isolation of a Non-genomic Origin Fluoroquinolone Responsive Regulatory Element Using a Combinatorial Bioengineering Approach.

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Supplementary Table 1.

Bacterial strains used in the study.

Genotype and description of each strain as acquired from EcoCyc (<http://ecocyc.org/>).

Strains	Genotype and description
<i>E.coli</i> DH5α	F ⁻ , <i>deoR</i> , <i>endA1</i> , <i>gyrA96</i> , <i>hsdR17</i> (rK ⁻ /mK ⁺), <i>recA1</i> , <i>phoA</i> , <i>relA1</i> , <i>thi-1</i> , Δ(<i>lacZYA-argF</i>), U169Φ80dlacZΔM15λ ⁻ , <i>supE44</i>
<i>E. coli</i> MG1655	F λ ilvG- rfb-50 rph-1
<i>E. coli</i> RFM443	(<i>rpsL</i> <i>galK2</i> Δ <i>lac74</i>) streptomycin resistant
<i>E. coli</i> BW25113 (Wild type)	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i>
<i>E. coli</i> BW25113 Δ <i>cra</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>cra</i> (deletion mutant of Catabolite repressor activator)
<i>E. coli</i> BW25113 Δ <i>cueR</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>cueR</i> (deletion mutant of Cu efflux regulator)
<i>E. coli</i> BW25113 Δ <i>dksA</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>dksA</i> (deletion mutant of
<i>E. coli</i> BW25113 Δ <i>yaiA</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>yaiA</i> (deletion mutant of OxyR-dependent induction of expression by hydrogen peroxide)
<i>E. coli</i> BW25113 Δ <i>ykgD</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>ykgD</i> (deletion mutant of redox-sensitive transcriptional activator)
<i>E. coli</i> BW25113 Δ <i>nhaR</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>nhaR</i> (deletion mutant of "Na ⁺ /H ⁺ antiporter Regulator)
<i>E. coli</i> BW25113 Δ <i>atoC</i>	F-, Δ(<i>araD-araB</i>)567, Δ <i>lacZ4787</i> (:: <i>rrnB-3</i>), λ ⁻ , <i>rph-1</i> , Δ(<i>rhaD-rhaB</i>)568, <i>hsdR514</i> , Δ <i>atoC</i> (deletion mutant of antizyme protein inhibitor of

	ornithine decarboxylase)
<i>E. coli</i> BW25113 $\Delta fadR$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta fadR$ (deletion mutant of Fatty acid degradation Regulon)
<i>E. coli</i> BW25113 Δacr	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , Δacr (deletion mutant of acr gene involved with Acridine transport)
<i>E. coli</i> BW25113 $\Delta mprA$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta mprA$ (deletion mutant of multidrug resistance regulator)
<i>E. coli</i> BW25113 Δfur	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , Δfur (deletion mutant of Ferric Uptake Regulation)
<i>E. coli</i> BW25113 $\Delta recA$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta recA$ (deletion mutant of Recombination protein A)
<i>E. coli</i> BW25113 $\Delta cusR$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta cusR$ (deletion mutant of Cu-sensing regulator)
<i>E. coli</i> BW25113 Δlrp	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , Δlrp (deletion mutant of Leucine-responsive regulatory protein)
<i>E. coli</i> BW25113 Δfis	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , Δfis (deletion mutant of factor for inversion stimulation)
<i>E. coli</i> BW25113 $\Delta arcA$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta arcA$ (deletion mutant of dual transcriptional regulator for Anoxic redox control)
<i>E. coli</i> BW25113 Δfnr	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , Δfnr (deletion mutant of primary transcriptional regulator, FNR activates genes involved in anaerobic metabolism and represses genes involved in aerobic metabolism)
<i>E. coli</i> BW25113 Δhu	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , Δhu (deletion mutant of The HU protein is a small DNA-binding protein that is considered a global regulatory protein and shares properties with histones, which play an important role in nucleoid organization and regulation).
<i>E. coli</i> BW25113 $\Delta sodA$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta sodA$ (deletion mutant of superoxide dismutases)
<i>E. coli</i> BW25113 $\Delta stpA$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta stpA$ (deletion mutant of StpA protein Suppressor of <i>td</i> phenotype A," is a nucleoid-associated multifunctional protein that acts as a transcriptional repressor, in chromosomal DNA packaging, and as a chaperone
<i>E. coli</i> BW25113 $\Delta oxyR$	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$, <i>hsdR514</i> , $\Delta oxyR$ (deletion mutant of oxidative stress regulator)
<i>E. coli</i> BW25113 Δhns	<i>F</i> -, $\Delta(araD-araB)567$, $\Delta lacZ4787(:rrnB-3)$, λ^- , <i>rph-1</i> , $\Delta(rhaD-rhaB)568$,

	<i>hsdR514</i> , <i>Δhns</i> (deletion mutant of Histone-like nucleoid structuring protein)
<i>E. coli</i> BW25113 <i>Δcrp</i>	<i>F</i> -, <i>Δ(araD-araB)567</i> , <i>ΔlacZ4787(:rrnB-3)</i> , <i>λ</i> -, <i>rph-1</i> , <i>Δ(rhaD-rhaB)568</i> , <i>hsdR514</i> , <i>Δcrp</i> (deletion mutant of cAMP receptor protein)
<i>E. coli</i> BW25113 <i>ΔmarA</i>	<i>F</i> -, <i>Δ(araD-araB)567</i> , <i>ΔlacZ4787(:rrnB-3)</i> , <i>λ</i> -, <i>rph-1</i> , <i>Δ(rhaD-rhaB)568</i> , <i>hsdR514</i> , <i>ΔmarA</i> (deletion mutant of multiple antibiotic resistance regulatory protein)
<i>E. coli</i> BW25113 <i>ΔbaeR</i>	<i>F</i> -, <i>Δ(araD-araB)567</i> , <i>ΔlacZ4787(:rrnB-3)</i> , <i>λ</i> -, <i>rph-1</i> , <i>Δ(rhaD-rhaB)568</i> , <i>hsdR514</i> , <i>ΔbaeR</i> (deletion mutant of bacterial adaptive response)
<i>E. coli</i> BW25113 <i>ΔcpxR</i>	<i>F</i> -, <i>Δ(araD-araB)567</i> , <i>ΔlacZ4787(:rrnB-3)</i> , <i>λ</i> -, <i>rph-1</i> , <i>Δ(rhaD-rhaB)568</i> , <i>hsdR514</i> , <i>ΔcpxR</i> (deletion mutant of conjugative plasmid gene expression regulatory protein)

Supplementary Table 2.

Plasmids used in the study

Plasmid Name	Description/Resistance	References
<i>pNYL-MCS11</i>	Plasmid derived from pZE21	2, 3
<i>pNYL-GFP</i>	GFP gene was amplified from pPROBE-TT'-GFP and was cloned in <i>pNYL-MCS11</i> plasmid vector on BamHI restriction site.	This study
<i>pNYL-ibsC</i>	Genetic locus coding for toxic peptide <i>ibsC</i> was amplified from <i>E. coli</i> genome and cloned in <i>pNYL-MCS11</i> vector at BamHI restriction site	This study
<i>pNal::ibsC</i>	Reporter plasmid containing FQ responsive regulating element fused with gene encoding toxic peptide <i>IbsC</i> . Vector backbone codes for kanamycin resistance.	This study
<i>pNal::GFP</i>	Reporter plasmid containing FQ responsive promoter fused with GFP.	This study
<i>pRx::ibsC</i>	Control plasmid containing <i>pNYL-MCS</i> backbone without FQ responsive promoter sequences.	This study
<i>pNal::ibsC-amp</i>	From vector backbone of <i>pNal::ibsC</i> , kanamycin resistant selection marker gene was replaced by ampicillin resistant gene	This study
<i>pRx::ibsC-amp</i>	From vector backbone of <i>pRx::ibsC</i> , kanamycin resistant selection marker gene was replaced by ampicillin resistant gene.	This study

Supplementary Figure S1.

Alignment of promoter regions of representative prokaryotic stress responsive genes using ClustalW2 online bioinformatics program.

Supplementary Figure S2. Schematic representation of cloning and screening of combinatorial oligonucleotide library.

A) Commercially synthesized single stranded combinatorial oligonucleotide library were converted in to double stranded DNA fragment and double digested with *XhoI* and *HindIII*. Double digested library were ligated with *XhoI-HindIII* digested fragment of pNYL-ibsC/GFP plasmid vector and transformed in *E. coli* RFM443 (Details are available in material and method section). B) To screen the inducible regulatory elements, a live and dead screening strategy has been adopted. Bacterial colonies were selected from the transformed plate and inoculated individually into 96 well plate containing 200 μ l LB broth. The grown cultures were then replica plated on a 96 well plate which contained various toxicants including DNA damaging [fluoroquinolones, mitomycin C], protein damaging [ethanol] and heavy metals [sodium arsenite, cadmium chloride, lead chloride] at sub-lethal concentrations and absorbance after incubation was measured at 600 nm. C) The presence of toxicants induces the expression of the toxic peptide IbsC which leads to the killing of the bacterial cells. The IbsC toxic peptide based reporter system selectively screens out the clones harboring functional combinatorial promoters against leaky and constitutive promoters.

Supplementary Figure S3.

E. coli BL21 DE3 strain harboring pET28a-hns was induced with 1mM IPTG Analysis of the purified H-NS protein on 12.5% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE).

Supplementary Figure S4.

Nucleotide sequence of clones representing constitutive promoters (a,b,c,d,e,f,g and h) covering a wide range of GFP fluorescence intensity.

Supplementary Figure S5.

Multiple sequence alignment of FQ-responsive regulatory element with the selected stress promoters from *E. coli* genome. FQ-responsive regulatory element displayed no homology with stress promoter sequences encoded in *E. coli* genome.

Supplementary Figure S6.

Response of FQ responsive promoter in bacterial host lacking efflux pump *tolC* gene and wild type *E. coli* strain in the presence of nalidixic acid. A-B) Wild type $\Delta tolC$ bacterial strains harboring *pNal::ibsC-amp* (test) and *pRx::ibsC-amp* (control) plasmid was induced with nalidixic acid.

Supplementary Figure S7.

Growth pattern of various stress regulator gene knock out strains of *E. coli* harboring *pNal::ibsC-amp* and *pRx::ibsC-amp* fusion system. The growth assays were carried out in duplicate for the *E. coli* mutant strain harboring *pNal::ibsC-amp* plasmid (test) and *pRx::ibsC-amp* plasmid (control).

Supplementary Figure S8. *In-silico* DNA curvature analysis of FQ responsive (Nal) promoter and their mutant variants at spacer region ('all A' and 'all T').

Figure S1



Figure S2

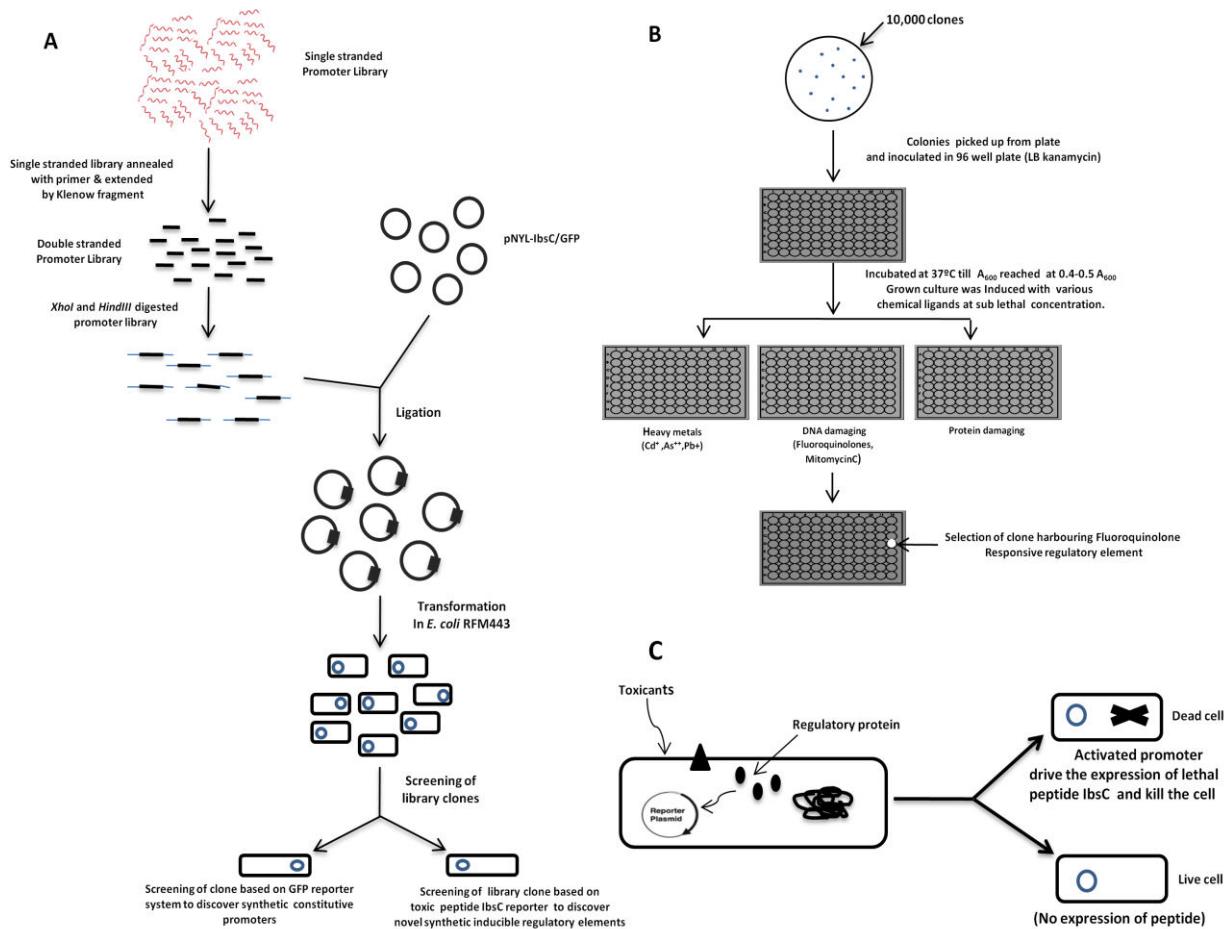
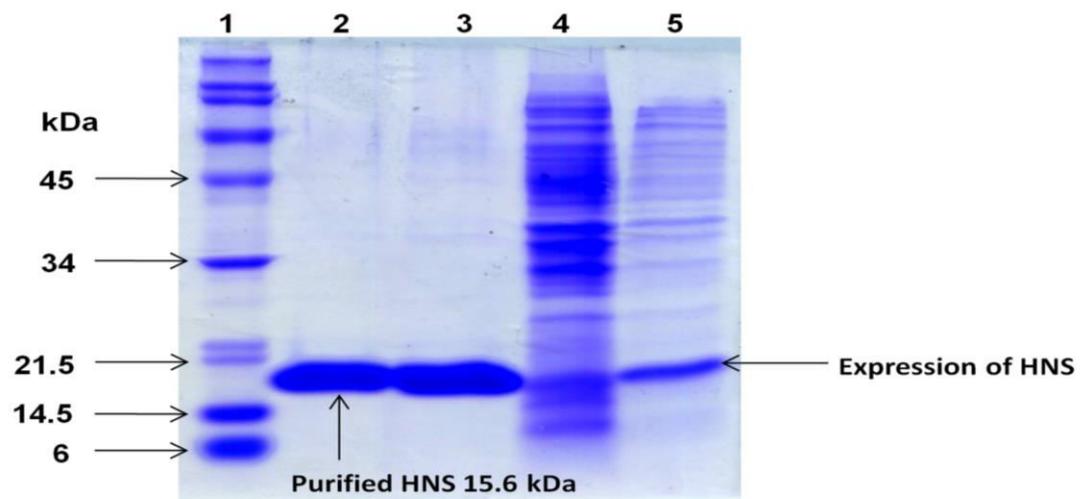


Figure S3



Lane-1 Broad range protein marker

Lane-2 Purified fraction1

Lane-3 Purified fraction2

Lane-4 Uninduced

Lane-5 *pET28a-hns* cellular extract induced with 0.5 mM IPTG

Figure S4

Clone-a

CTTTGTTACGTCTCCCTCGAGATCAGTCAAATACAGCGCAACTCGAAAAAGGGGGAGTTCCAACAATCCAGGCAGTCATAT
CTAAGCTTAGATATGACGCCAGCTTATTCCGAGCCTGAGGGTTTTCGGGTTGTCCTCTAATGACTGATCTCGAGATCAAGT
CATAAAAGTGAACCATCAAAAAGGCGCAGCCTCAGATTATCACCGGGGTCTATCTAAGCTTAGATATGACACCCCCTGTTGGT
GGGACCTACTCCCTTTAGAGTTGACGTCAAATTGACTTGATCTCGAGATCAAGTCATTATAGTGGCAACTATGAAAATACGA
CTGGTCGACCAACCGGCAGTCATATCTAAGCTTGATATCGAATTCTGCAGCCCCGGGATCCATAAGGAGGAAAACATATG
AGTAAAGGAGAAGAACTTTCACTGGAGT

Clone -b

TGGTTTTTATCTTCCCTCGAGATCAGTCATTCCCGTAAACCACGAAAATAACAGGTTCGTATAAACGCGCGTCATA
TCTAAGCTTAGATATGACGCCGGTAAATCTGAAAGTGCATTTCAGTTCGCCAGGTATGACTTGATCTCGAGATCAAG
TCATATTAACAAACCCGGAAAAGAGCAATGGTCAAACATCCGGGGCCTCATATCTAAGCTTAGATATGACCCCCCAGGTTAG
TCAGACACCCCCCCTTTGTGGTAAAGCGTTGACTTGATCTCGAGATCAAGTCATATGCCAAACACTAAAAAATCGC
GCATATCGAATTAAAGGTAAAGTCATATCTAAGCTTGATATCGAATTCTGCAGCCCCGGGATCCATAAGGAGGAAAACATATG
GAGTAAAGGAGAAGAACTTTCACTGGAGA

Clone- c

TGCATACATTATCTTCCCTCGAGATCAGTCAAATCCTGGCAACAATGCAAAAGTCTCGCATCGGACTAACATGCGCGGCAT
ACTAAGCTTAGATATGACGCCAGGAATGTCAGTGTCCGTTTCCGGGTTCACACCCATTGACTTGATCTCGAGATCAA
GTCATATAGCAGTGAACAAAGTAAAAAGGGAACCGTGCCTACCAAACGGCTGGTCAATCTAAGCTTAGATATGACGCCGTGGTAA
GTGGACCTGGGACCTTTAGTTGTCAGCCACAAATGACTTGATCTCGAGATCAAGTCATTACTCTCAACCCCTCAAACATCC
TAGGGTTCGGACATAAGCTCGGTCTATCTAAGCTTAGATATGACGAGCAGTTGTCAGACACGTGGCCTTTACTTGTGTTG
CAGGTAAATGACTTGATCTCGAGATCAAGTCATAACTCGGAAACACGCAAAAGAGCGTGGTCGAAAAACCGCGAGTCATA
TCTAAGCTTGATATCGAA

Clone-d

GTCGGGGGGTTTTATTCTTCTCGAGATCAGTCATTCTTATAAAACTCATAAAATGAACTATTCTAACTAAAGATAAGGTCAAT
ACTAAGCTTAGATATGACTCCCGTAAATCCGACCCGGGCATTGATAGTTACGGGAAATGACTTGATCTCGAGATCAA
GTCATTAAAGACAAACCTTAAAGCGTATGGCTCGCACAACCGGGCGGTCTATCTAAGCTTGATATCGAATTCTGCAGC
CCGGGGGATCCATAAGGAGGAAAACATATGAGTAAAGGAGAAGAACTTTCACTGGAGTTGCCAATTCTGTTGAATTAGATGGTGA
TGTAAATGGGACAAATTCTGTCAGTGGAGAGGGT

Clone- e

TAGGGTTTTGTCTTACTCGAGATCAGTCAAATCGCGCACCAAAAAAGGGGTGCCGGTCCAATTACCTCCCGTCATATCTA
AGCTTAGATATGACCCCTAGGAATGTCAGACCAGGGCTCTTTATTGTTGAATATGACTTGATCTCGAGATCAAGTCAA
TTGCGGCTCAACCAGGAAAAGCGAGCAAGTCGGATCTCAGAGTGTCTATCTAAGCTTGATATCGAATTCTGCAGCCGGG
GGATCCATAAGGAGGAAAACATATGAGTAAAGGAGAAGAACTTTCACTGGAGTTGCCAATTCTGTTGAATTAGATGGTGA
TGTAAATGGGACAAATTCTGTCAGTGGAGAGGGT

Clone f

CGGGGTTTCGTTCTTACTCGAGATCAGTCATTGTTGCAACCCCGAAAAAGCAGCCGGCTCATACTATACGCACGGTCATAT
CTAAGCTTAGATATGACGCCACATTAAGTGGAGAGACCGCGCTTTGAGAGTTGCGGGGAAATGACTTGATCTCGAGATCAAG
TCATTGTCGTCAACTACAAAAAGTCGCTTGCATTCAGGCTCATATCTAAGCTTGATATCGAATTCTGCAGCCGG
GGGGGATCCATAAGGAGGAAAACATATGAGTAAAGGAGAAGAACTTTCACTGGAGTTGCCAATTCTGTTGAATTAGATGG
TGTAAATGGGACAAATTCTGTCAGTGGAGAGGGT

Clone g

TTGGTTTCGTTACTCGAGATCAGTCATAGGAGCGAACCAAAAAAGGTGCCGTCCAATTCCCGGGGTCAATATCT
AAGCTTGATATCGAATTCTGCAGCCGGGGATCCATAAGGAGGAAAACATATGAGTAAAGGA

Clone-h

CGGGGGTTTCGTTACTCGAGATCAGGTCAATTGTTGAACTATTAAGGAGGAAATCCGACGTCAGACGTTTCGTTGCAACATATGACTTGATCTCGAGATCA
TATCTAAGCTTAGATATGACCCCGGGAAAATCCGACGTCAGACGTTTCGTTGCAACATATGACTTGATCTCGAGATCA
AGTCAGGGTACCCCTTATGATTCTACTCGCTCTATAACATCAGAGTGTCTATCTAAGCTTGATATCGAATTCTGCAGCCGG
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Figure S5

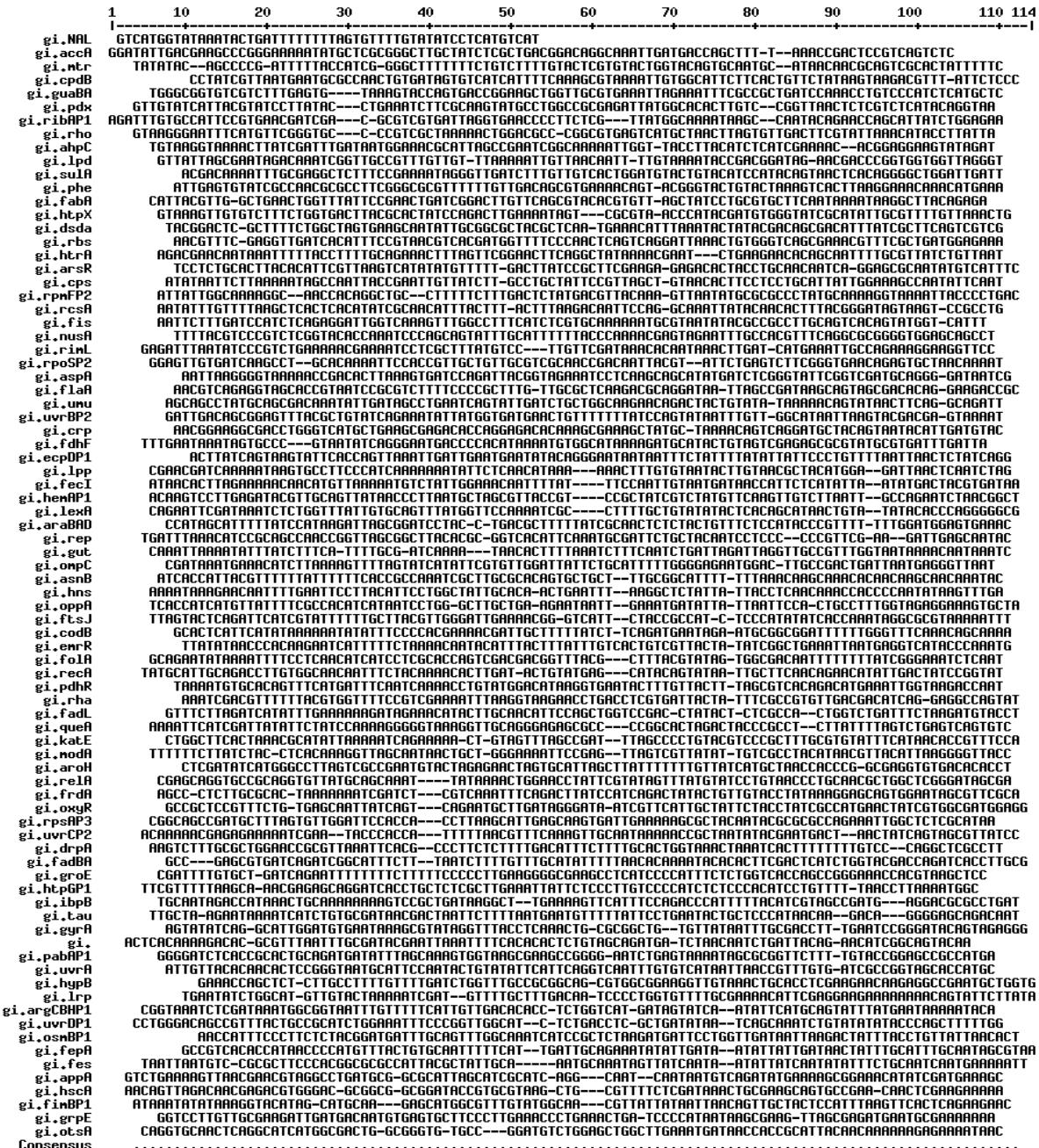


Figure S6

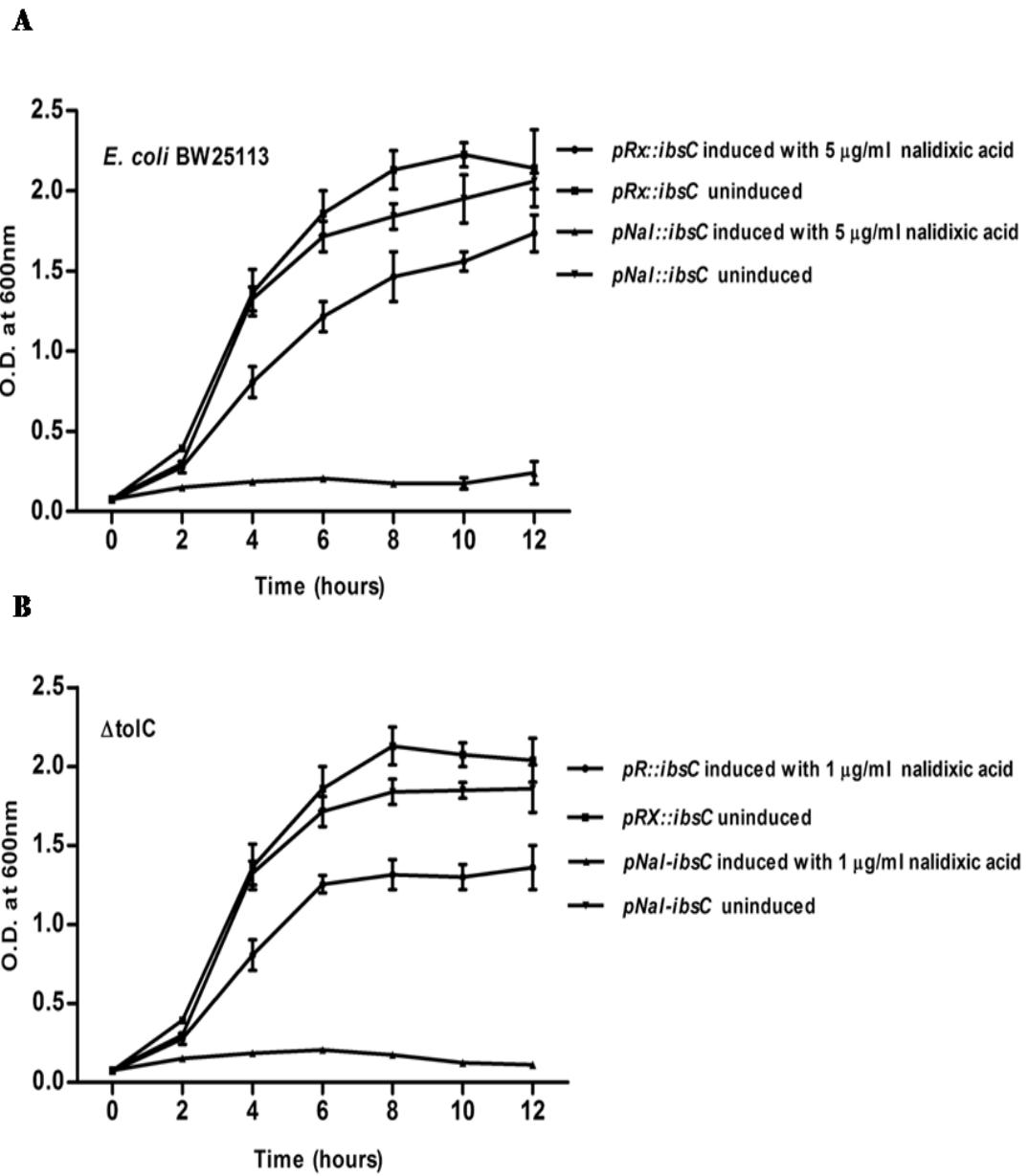


Figure S7

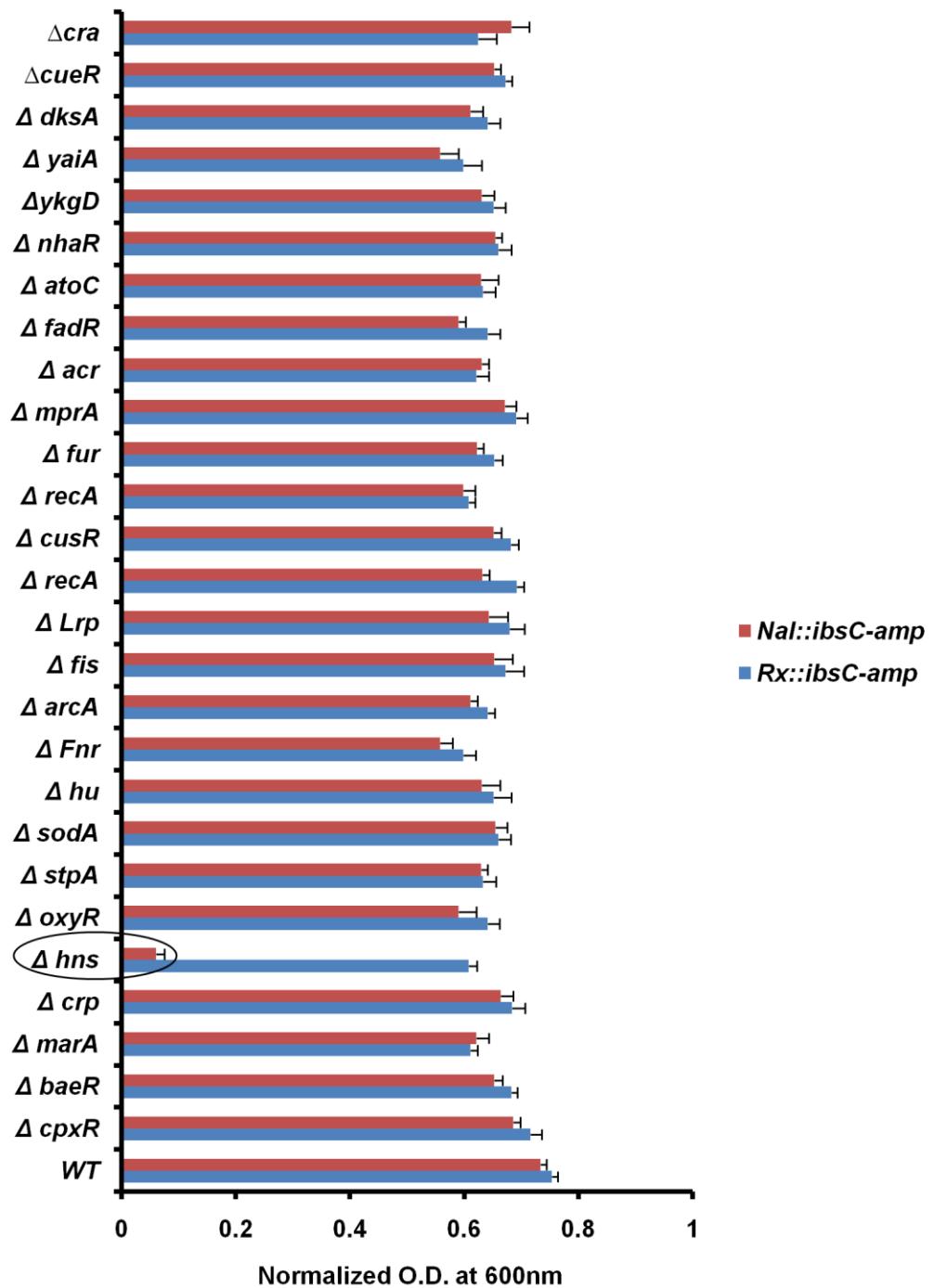


Figure S8

