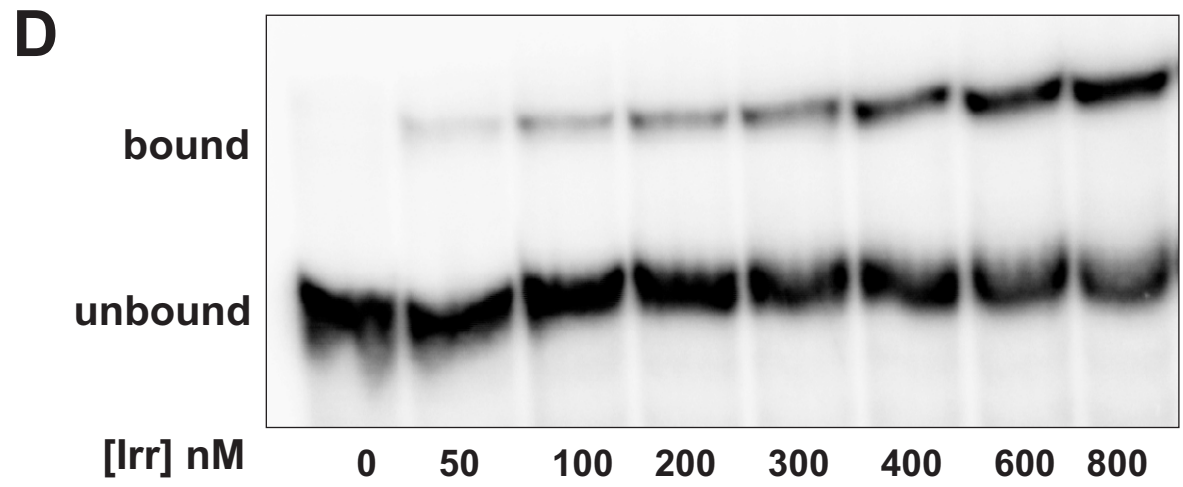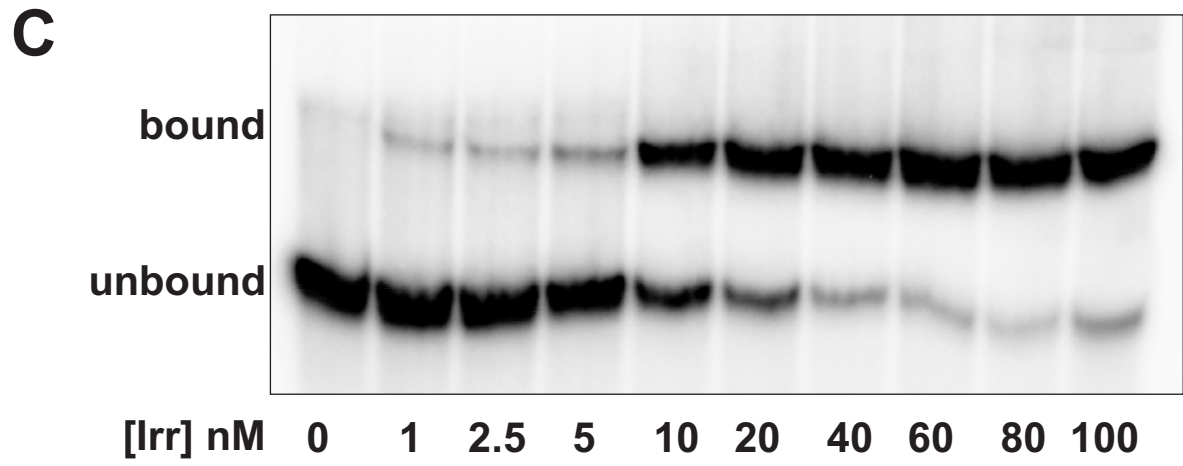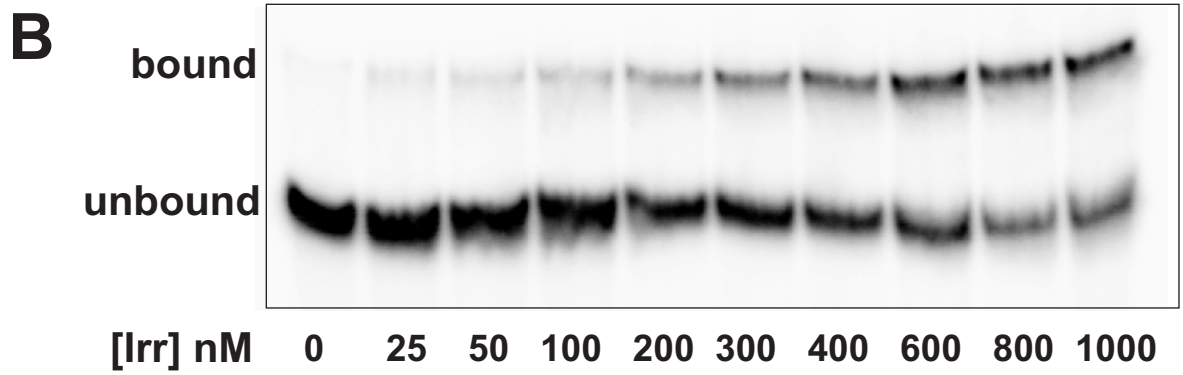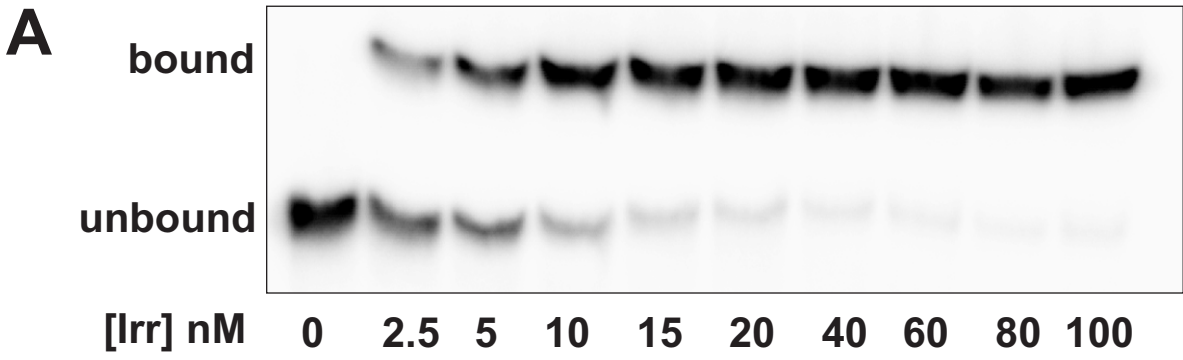SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Promoter sequences within genes described in this study for EMSA analysis and for construction of genomic mutants. The sequences contain the 21 nt ICE motif (shaded) flanked on each side by 12 nucleotides within each promoter. The underlined nucleotides represent substitutions made in oligonucleotides for EMSA or in the genome of mutant strains. P$_{bfr}$/ICE$_{fhuE}$ denotes the *bfr* promoter sequence that contains the ICE motif of *fhuE*. The other heterologous promoter designations follow the same rule.

Figure S2. EMSA analysis of promoter sequences used to generate the binding curves show in Figure 2 of the main text. EMSA was carried out by titrating 0.1 nM radiolabeled promoter sequence DNA from (A) *bfr*, (B) P$_{bfr}$/ICE$_{fhuE}$, (C) P$_{fhuE}$/ICE$_{bfr}$ and (D) *fhuE* with increasing concentrations of purified Irr. Bound and unbound DNA was resolved on a 5% non-denaturing polyacrylamide gel and visualized by autoradiography. Autoradiographs were scanned, and bands were quantified to determine bound and unbound DNA.

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bfr               GATCCTAAACCGAATTTAGAACGCTTCTAAATGAGTTTACGGAAG
fhuE               GCATGGGCTCCGGATTTGGAATCCTTCTAGACGAACACGATCGAT
P_bfr/ICE_fhuE    GATCCTAAACCGGATTTGGAATCCTTCTAGACGAGTTTACGGAAG
P_fhuE/ICE_bfr     GCATGGGCTCCGAATTTAGAACGCTTCTAAATGAACACGATCGAT
blr7895           GGCGGCCTATATAATTTAGAATCATTCTAAACTAGTGGGACAGGG
bll7968           CGCGTCCATCCGCGCTTAGAACCATTCAACACTAGAGGGATTCAA
P_7985/ICE_7968   GGCGGCCTATATCGCTTAGAACCATTCAACACTAGTGGGACAGGG
P_7968/ICE_7895   CGCGTCCATCCGAATTTAGAATCATTCTAAACTAGAGGGATTCAA
leuC              CCCTGCTATATATTCTTGGAATGTTTCCAGATCTGACCAGTCTCG
hemB              ACCATGCGAGCTGGTATAAGAATAATTCCAGCCGGAGGAAGAGTG
```

Figure S1

A

bound

unbound

[Irr] nM   0   2.5   5   10   15   20   40   60   80   100

B

bound

unbound

[Irr] nM   0   25   50   100   200   300   400   600   800   1000

C

bound

unbound

[Irr] nM   0   1   2.5   5   10   20   40   60   80   100

D

bound

unbound

[Irr] nM   0   50   100   200   300   400   600   800

Figure S2