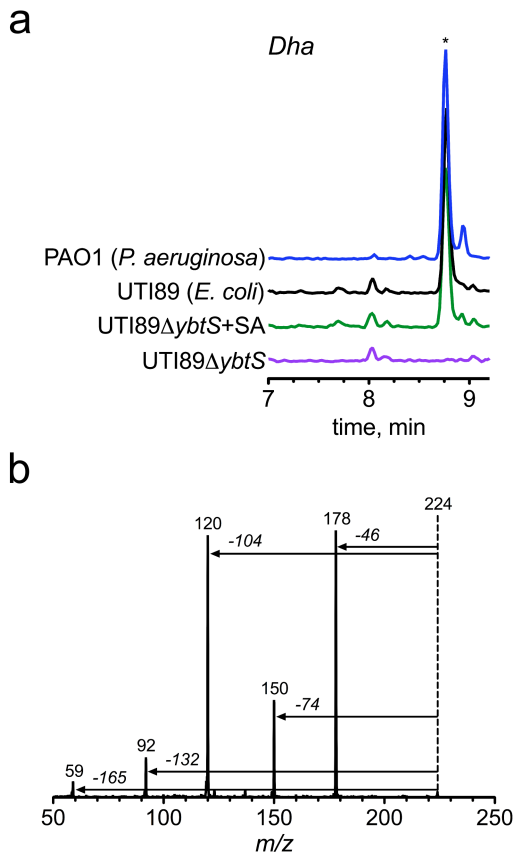
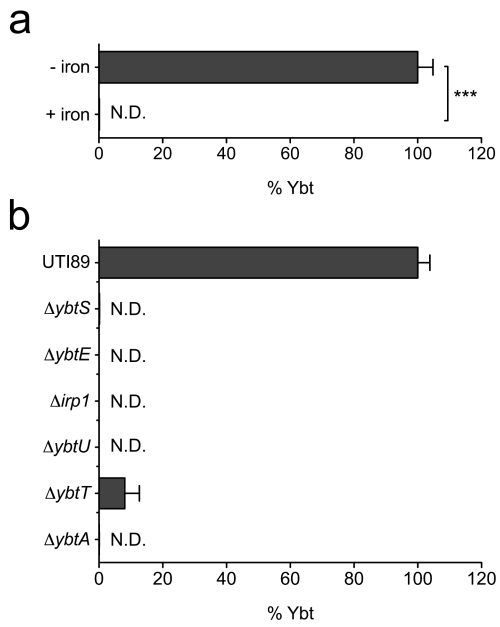
SUPPLEMENTAL FIGURES

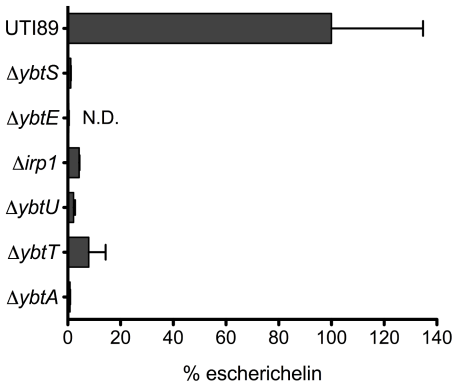


Supplemental Figure 1. The molecular feature with *m/z* 224 is dihydroaeruginoic acid (Dha)
(a) UTI89, UTI89Δ*ybtS*, and *P. aeruginosa* strain PAO1 were grown under iron-restricted conditions and the supernatants were analyzed by positive ion LC-MS. Extracted ion chromatograms show that the molecular feature with *m/z* 224 found in UTI89 co-elutes with Dha from a pyochelin-producing strain of *P. aeruginosa*. It is absent when the salicylate synthase (YbtS) is deleted from the genome and restored when UTI89Δ*ybtS* is chemically complemented with salicylate in the medium. (b) MS/MS spectrum of the molecular feature with *m/z* 224 in PAO1 supernatants, which is consistent with fragments observed in a previous study of Dha (31).



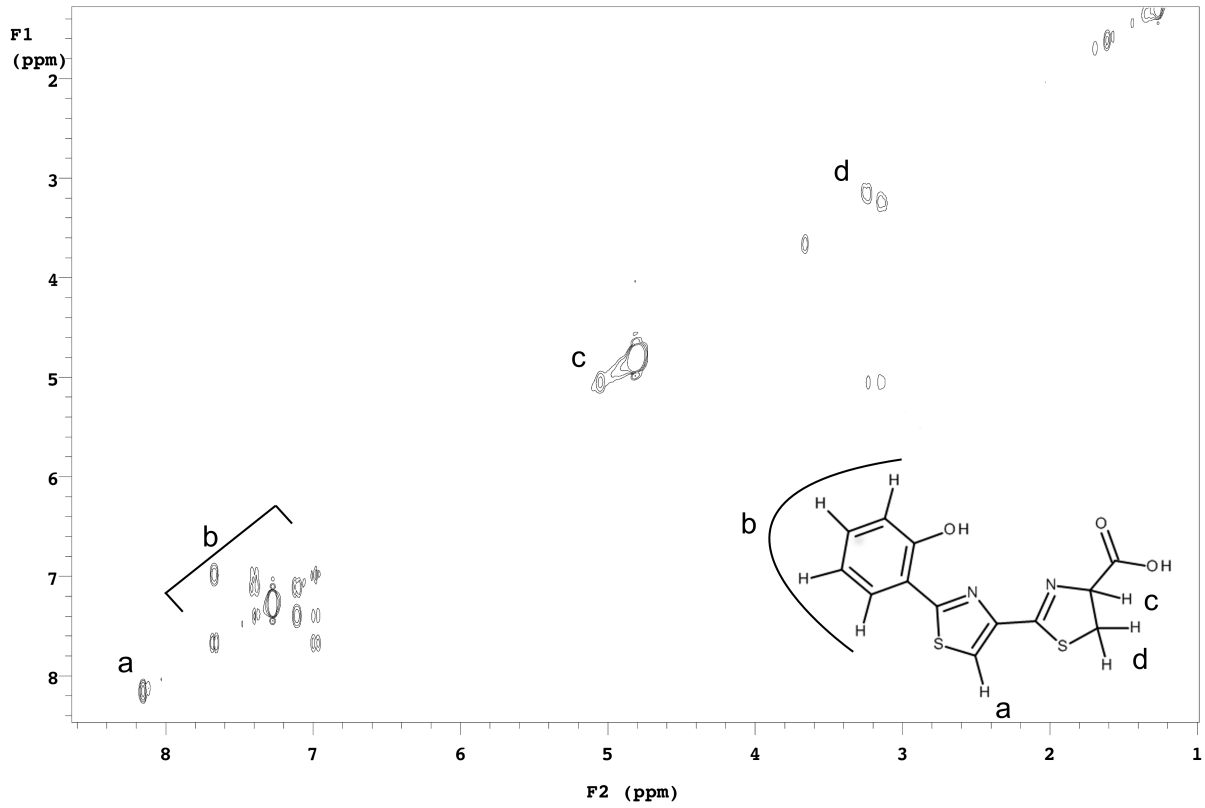
Supplemental Figure 2. Extracellular Ybt levels are repressed in the presence of iron and abolished in strains lacking biosynthetic genes and the transcription factor YbtA

Fe(III)-Ybt levels in culture supernatants were quantified by LC-MS/MS relative to a ^{13}C-internal standard. (a) UTI89 grown in complete M63 medium with or without 16.2 mg/L $FeCl_3$. Mean of n = 3 replicates with standard deviation plotted, unpaired t-test ***$p < 0.001$. (b) Isogenic mutants of UTI89 grown in iron restricted minimal medium. Mean of n = 4 replicates with standard deviation plotted.

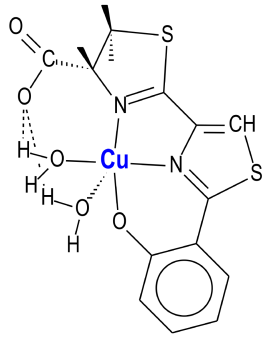


Supplemental Figure 3. Intracellular escherichelin levels mimic the extracellular escherichelin levels in *Yersinia* HPI mutants

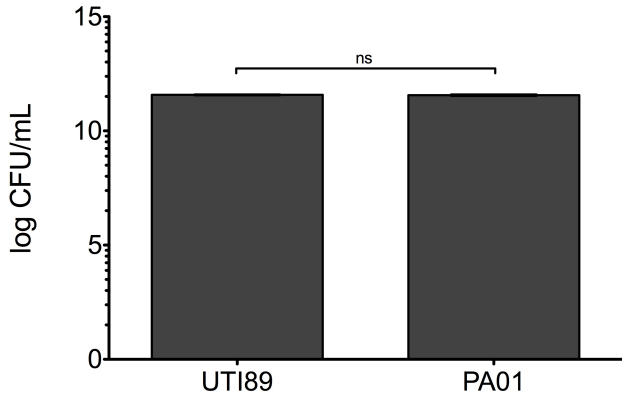
Escherichelin levels in cellular extracts were quantified by LC-MS/MS relative to a ^{13}C-escherichelin internal standard. Mean of n = 3 replicates with standard deviation plotted.



Supplemental Figure 4. Characterization of purified escherichelin by ^{1}H-NMR
^{1}H-COSY of purified escherichelin and the assignments of the proton chemical shifts on the escherichelin structure (inset).

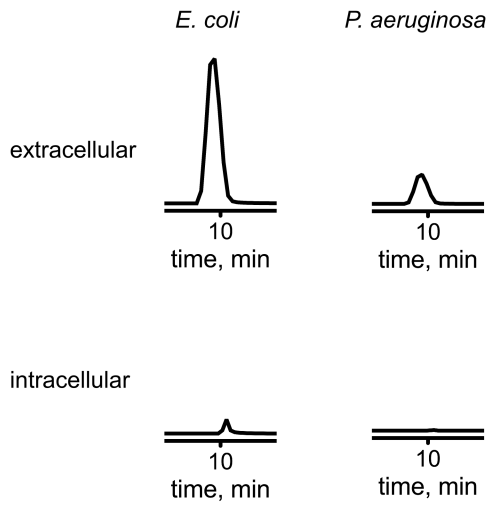


Supplemental Figure 5. Density functional theory (DFT) calculation of escherichelin bound to Cu(II)
The simulation predicts a stable complex in solution with square planar geometry.



Supplemental Figure 6. *E. coli* UTI89 and *P. aeruginosa* PA01 grow equivalently in iron-restricted medium

UTI89 and PA01 were grown for 18 hours in complete M63 medium supplemented with 1% casamino acids and bacterial growth was assessed by quantifying colony forming units per mL (CFU/mL). Mean of n = 3 with standard deviation plotted. p = 0.56, unpaired t-test.



Supplemental Figure 7. Intracellular escherichelin levels mimic the extracellular escherichelin levels in *E. coli* and *P. aeruginosa*

LC-MS/MS chromatograms are displayed for extracellular escherichelin (top) and intracellular escherichelin (bottom) from *E. coli* (UTI89, left) and *P. aeruginosa* (PA01, right) supernatants after growth in iron-restricted medium. Chromatograms are identically scaled. The extracellular escherichelin data is reproduced for comparison from Figure 4.