

Supplementary legends

Supplementary Figure 1. Sequence alignments among *E. faecalis* members and archetypes involved in Zn homeostasis in different bacterial species (Id code Supplementary Table 1). Asterisks indicate conserved residues involved in Zn binding, black: identical residues, grey: similar residues.

Supplementary Figure 2. Effect of Zn, TPEN and Cu supplementation on *E. faecalis* growth. Cellular growth curves at increasing concentration of ZnCl₂ (A), TPEN (B) and CuSO₄ (C). Error bars = standard deviation (SD) values. Asterisks = significant differences. (Mann-Whitney test, p<0.05).

Supplementary Figure 3. Relative mRNA abundance of *fieF* exposed to Zn, TPEN and Cu in **A.** WT and **B.** Δ *zur* strains. Light grey bars indicate the fold change (log₂) in transcript abundance between WT and Δ *zur* strains growing in the control media. Black, white and dark grey bars indicate fold changes in transcript abundance between Δ *zur* strain exposed to 0.5 mM ZnCl₂, 5 μ M TPEN or 0.5 mM CuSO₄ and the Δ *zur* growing in control media (REST test, p<0.05).

Supplementary Figure 4. Effect of Zn and Cu supplementation on WT and Δ *zur* growth. Cellular growth curves at increasing concentration of ZnCl₂ (A) or CuSO₄ (B). Error bars = standard deviation (SD) values. Asterisks = significant differences. (Mann-Whitney test, p<0.05).

Supplementary Table 1. Proteins involved in bacterial zinc homeostasis

Supplementary Table 2. Predicted transcriptional regulatory network activated by zinc in *E. faecalis*.

Supplementary Table 3. Gene-specific primers used in qPCR and Δ *zur* mutant construction.