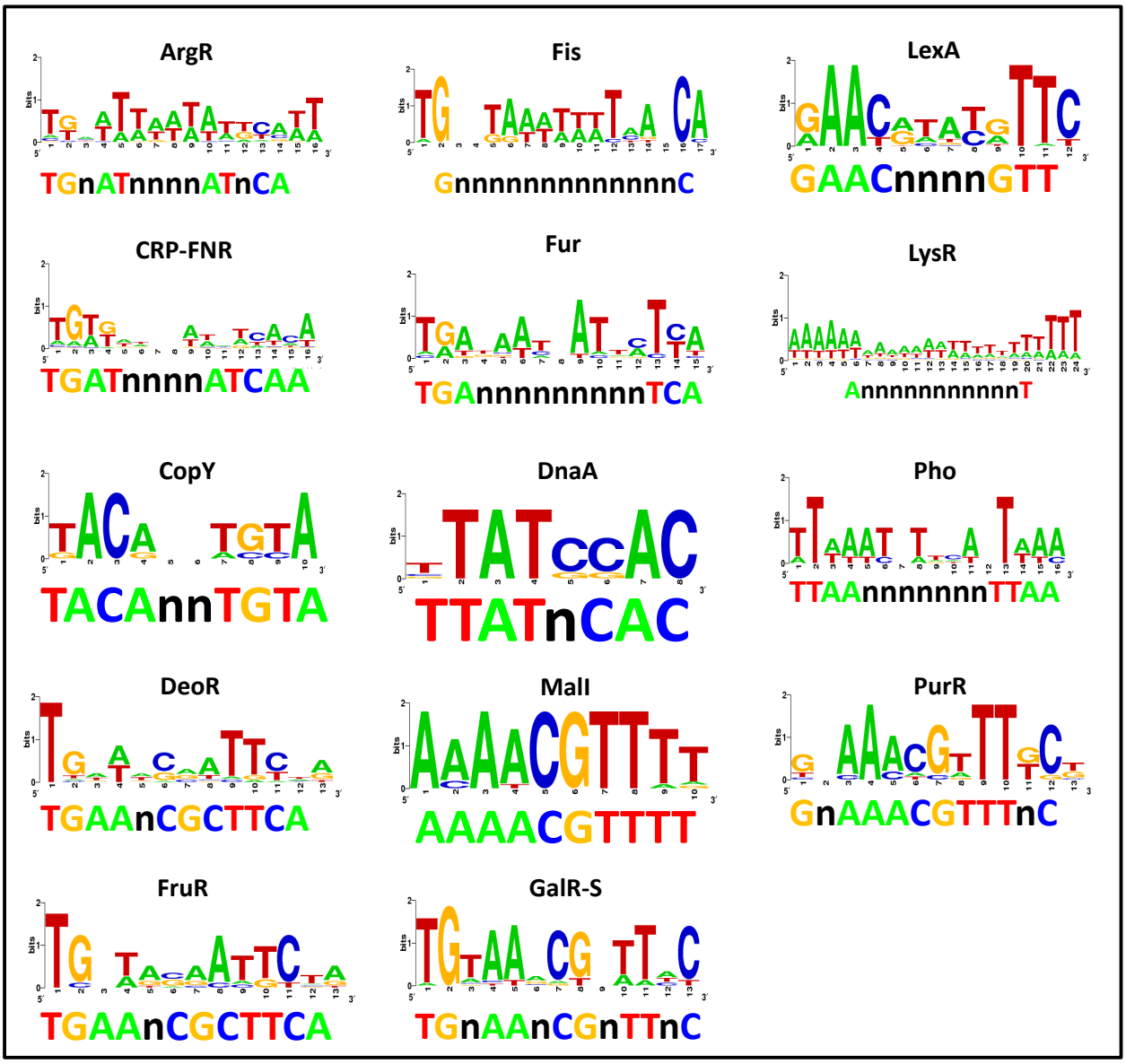
**Supplementary Figure 1.** Putative binding-site consensus logos for different regulons. The logos represent the consensus sequence generated with for the putative DNA binding-sites for each regulon. The sequence underneath the diagram represents previously reported consensus binding site for each family. Logos were generated by WebLogo algorithm using the entire set of binding site sequences identified for each *E. faecalis* transcription family.



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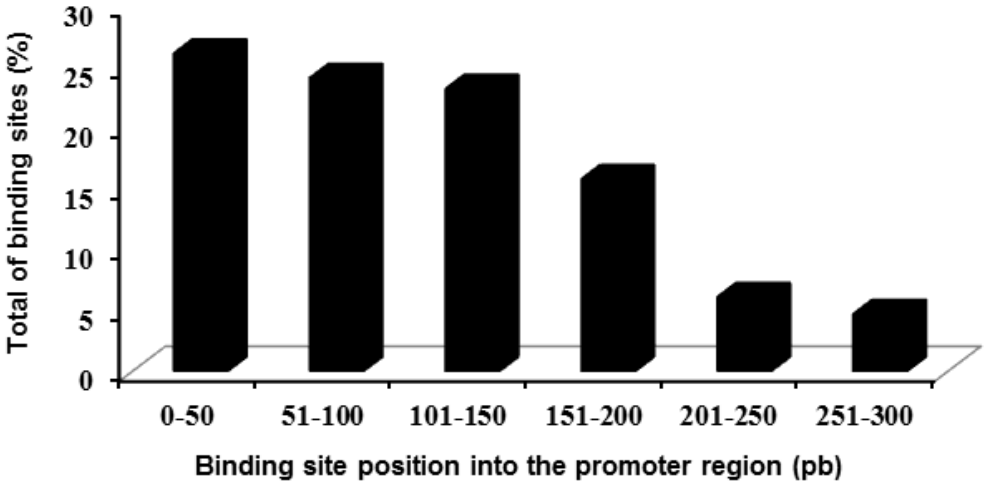
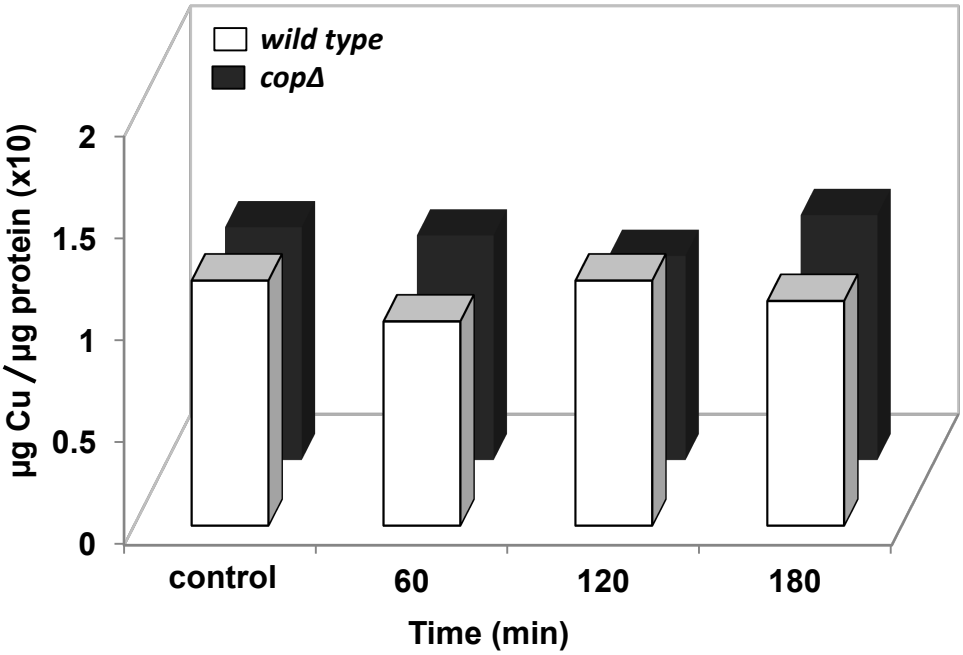
**Supplementary Figure 2.** Distribution of the position of the binding sites within the promoter region in *E. faecalis*. Bars indicate the total number of sequences contained within the promoter regions, grouped by their distance to the translational start site. Values are expressed as the percent of binding sites in each position range related to the total of binding sites within the network. (n = 629).



**Supplementary Figure 3.** Time course of intracellular copper content in *E. faecalis* wild type and *cop*Δ strains grown in basal medium. The basal concentration of copper quantified was 10 μM. No significant differences between each column were detected. ANOVA test $p < 0.05$. Control time indicated exactly the moment was the bacteria were added in the media.



**Supplementary Figure 4.** Growth curve of wild type and *cop*Δ strains exposed to different copper concentrations. White and black figures represent the wild type and *cop*Δ strains, respectively. Growing medium: Basal N (circles), 0.5 mM $CuSO_4$ (squares) and 1 mM $CuSO_4$ (triangles). Each value corresponds to the average of 3 independent biological replicates (error bars indicate standard deviation).