

Figure S1. Reproducibility of duplicate RNA-seq experiments performed in the absence (Control) or in the presence (Caspofungin) of caspofungin (concentration at 8 mg/L). The expression of genes in different RNA-seq samples was compared using normalized RPKM values calculated as follows: (# reads for the gene*10⁹)/(# total of reads*size of the gene).

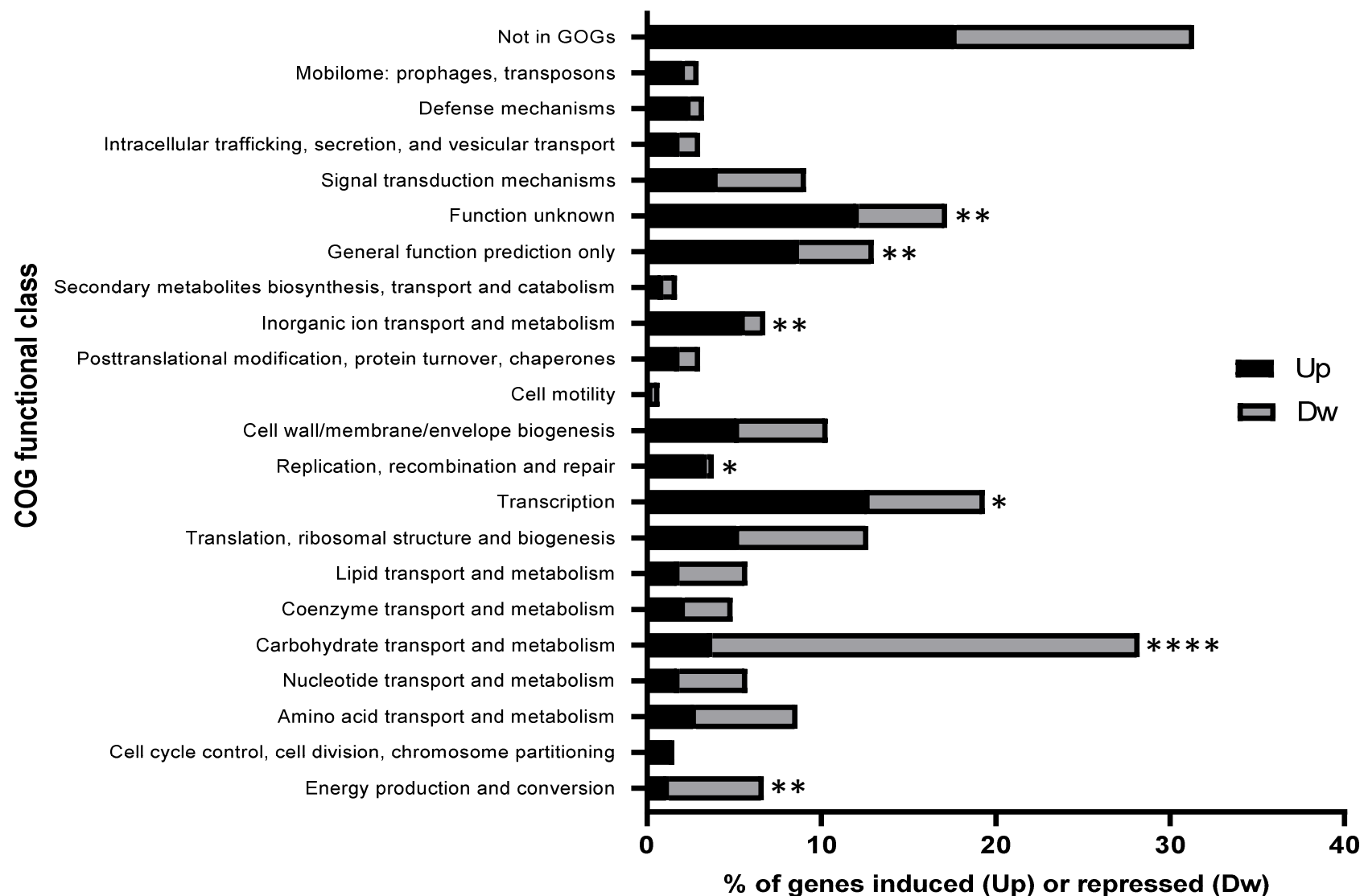


Figure S2. Classification in functional categories of the 580 genes significantly induced (n=321) or repressed (n=259) by sub-inhibitory concentration of caspofungin (8 mg/L) in *E. faecium* Aus0004. Percentages of genes with a transcript change in expression level lower or greater than 2 log₂-fold (with an adjusted p-value <0.1) are represented in white or black bars, respectively. Statistically significant differences (using Fisher's exact test) are indicated as follows: *, P<0.05; **, P<0.01; ****, P<0.0001.

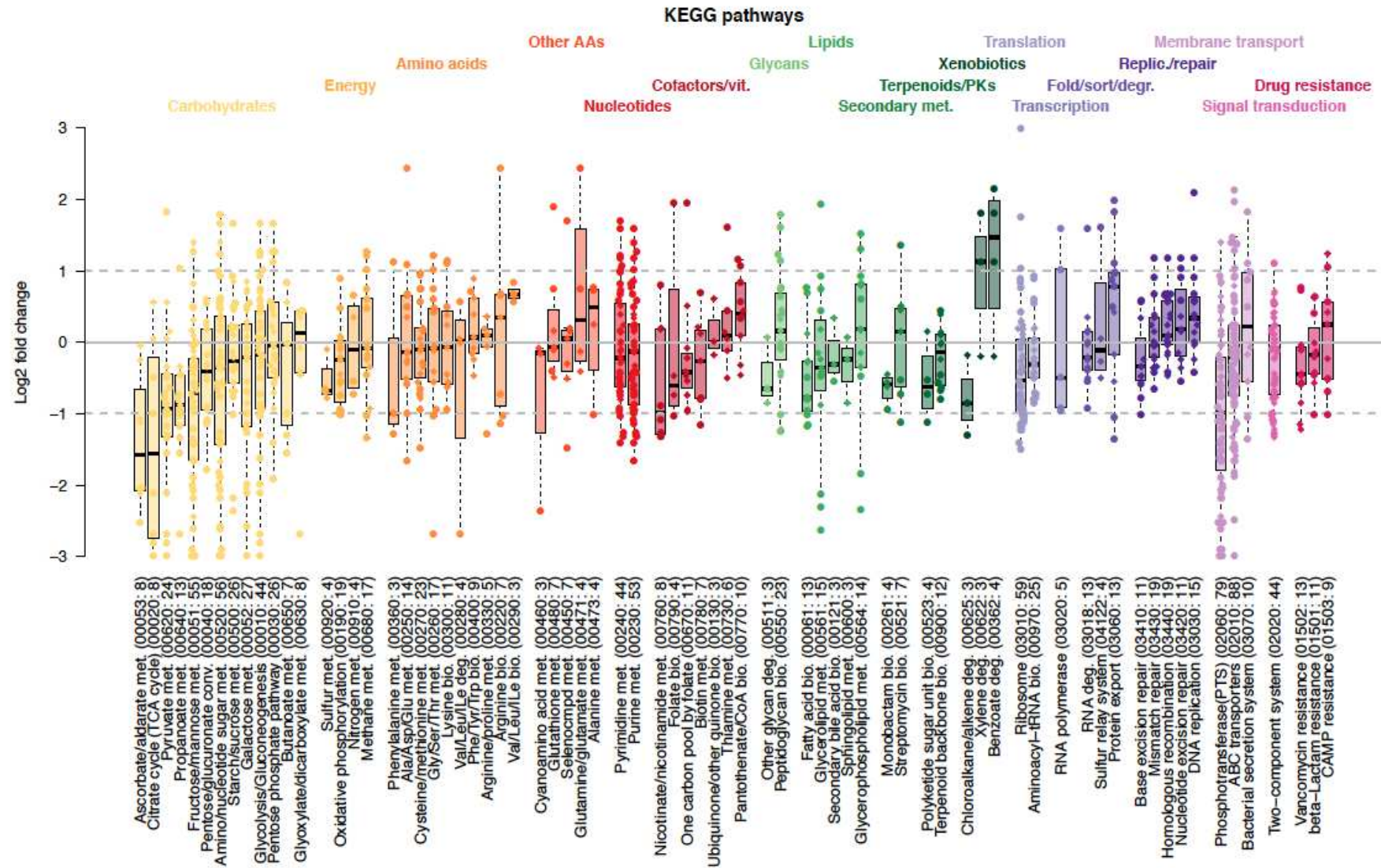


Figure S3. Representation and classification of transcripts fold changes levels of the 580 genes significantly induced (n = 321) or repressed (n = 259) by growth in the presence of caspofungin across biological pathways in *E. faecium* Aus0004, according to the KEGG pathways (available in www.kegg.jp) using the KEGGREST R library.

References

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2. **Bozdogan B, Leclercq R.** 1999. Effects of genes encoding resistance to streptogramins A and B on the activity of quinupristin-dalfopristin against *Enterococcus faecium*. *Antimicrob Agents Chemother* 43:2720-2725.
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