

Copper tolerance and transcriptomic response after prolonged Cu²⁺ exposure in the Antarctic psychrophile *Rhodoglobus galactosidasius* strain CPHL_1^T

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Supplementary Fig. S7 Global transcriptional patterns of representative differentially expressed genes (DEGs) between control and copper-exposed conditions. The heatmap displays variance-stabilized expression values obtained from DESeq2, subsequently standardised for each gene using Z-score normalisation. Only statistically significant annotated DEGs (adjusted $p < 0.05$, $|\log_2$ fold change| > 1) are shown. Genes were grouped in four categories (regulatory, cellular processes, metabolic, other) according to their Cluster of Orthologous Genes (COG) functional group, with up to ten representative genes selected per category based on the magnitude of differential transcript abundance and reproducibility among biological replicates

