

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

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Supplementary Table S2 Alignment performance metrics across samples. Overall mapping rates (from HISAT2, v2.2.2) and proportions of reads (from featureCounts, Subread package, v2.0.3) assigned to coding sequences (CDS), rRNA, tRNA, and unannotated regions are reported. The unannotated fraction is relative to CDS annotation only. Rep: replicate

ID	Description	Alignment rate (%)	Reads assigned to CDS (%)	Reads assigned to rRNA (%)	Reads assigned to tRNA (%)	Reads unannotated (%)
B_1	Control rep. 1	92.6	46.4	0.3	0.1	7.4
B_2	Control rep. 2	93.2	44.6	0.2	0.0	6.8
B_3	Control rep. 3	91.3	41.7	0.1	0.0	8.7
Cu_1	Cu-exposed rep. 1	88.2	25.0	0.1	0.3	11.8
Cu_2	Cu-exposed rep. 2	68.9	22.1	0.1	0.4	31.2
Cu_3	Cu-exposed rep. 3	91.6	38.0	0.1	0.1	8.2