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Figure S2. Functional enrichment analysis of 125 genes responding to 0.3 μ mol m⁻² s⁻¹ UV-B independent of UVR8 and stress pathways using gene ontology (GO) analysis with respect to **A**, Biological Process and **B**, Molecular Function. The top 20 most significant categories are shown. Gene ratio represents the proportion of genes annotated to a particular GO category within the list of 125 genes. The number of genes identified by a particular biological process or molecular function is represented by "Counts". The level of significance "p.adjust" was calculated using Bonferroni corrections.