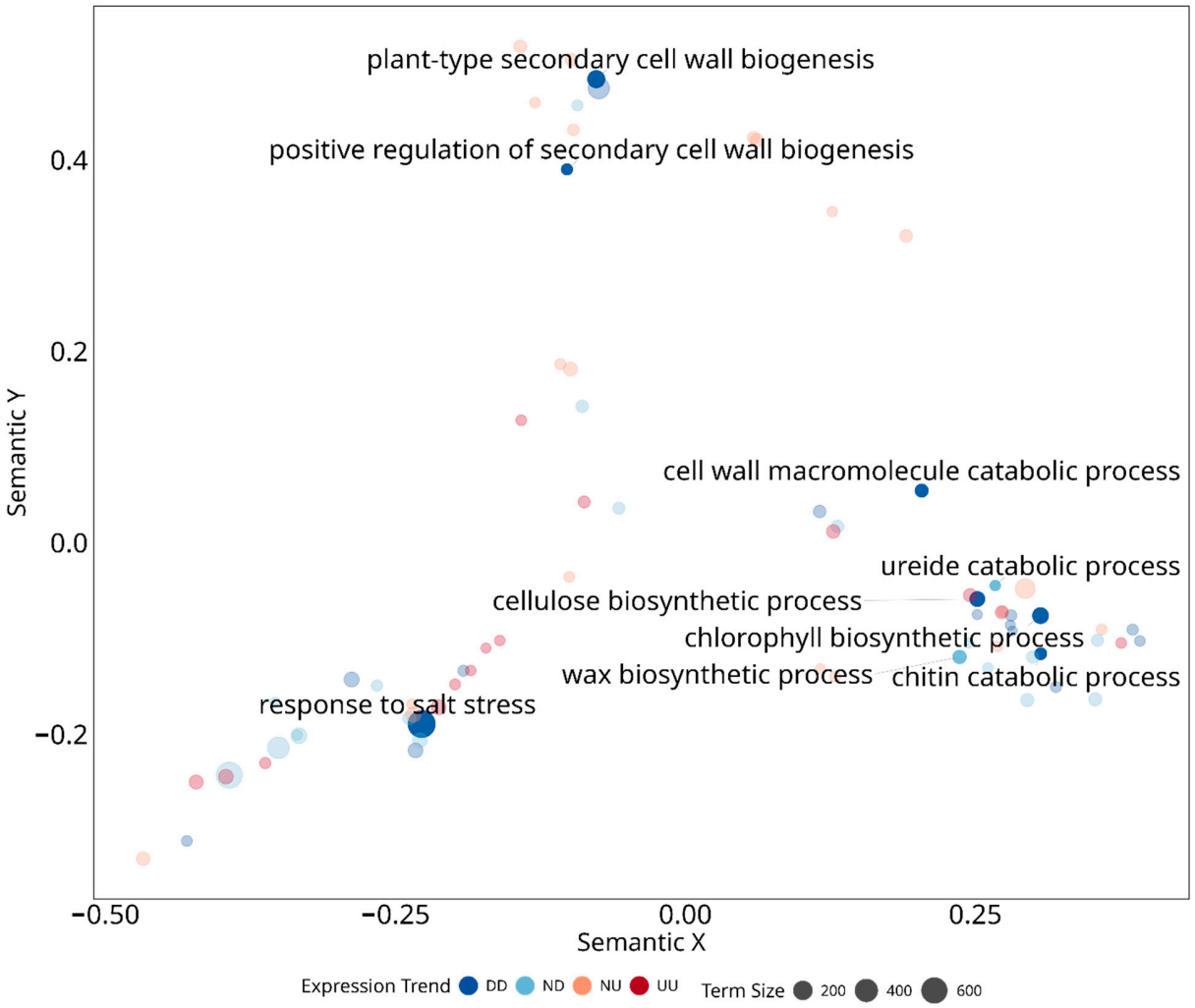

Supplementary Figure S4. Semantic space reduction of enriched Gene Ontology (GO) biological processes across desiccation-response trends, calculated on the Unreported orthogroups only (the orthogroups without a report of a role of the gene family in desiccation; Section 4.8). Multidimensional scaling plot displaying top-ranked enriched GO terms clustered by semantic similarity across the four expression trends: consistently down-regulated (DD), down-regulated during desiccation (ND), up-regulated during desiccation (NU), and consistently up-regulated (UU). Circle size corresponds to the number of annotated genes per GO term (Term Size). Spatial proximity reflects functional similarity along the semantic axes (Semantic X and Y). Labels show the representative (parent) term of each semantic cluster (rrvgo); terms grouped under a parent are not labelled separately. The full list of enriched terms and their cluster assignments is given in Supplementary Table S8. The enrichment is exploratory (nominal weight01 p-values; few terms remain significant after Benjamini–Hochberg adjustment, Supplementary Table S9) and hypothesis-generating.