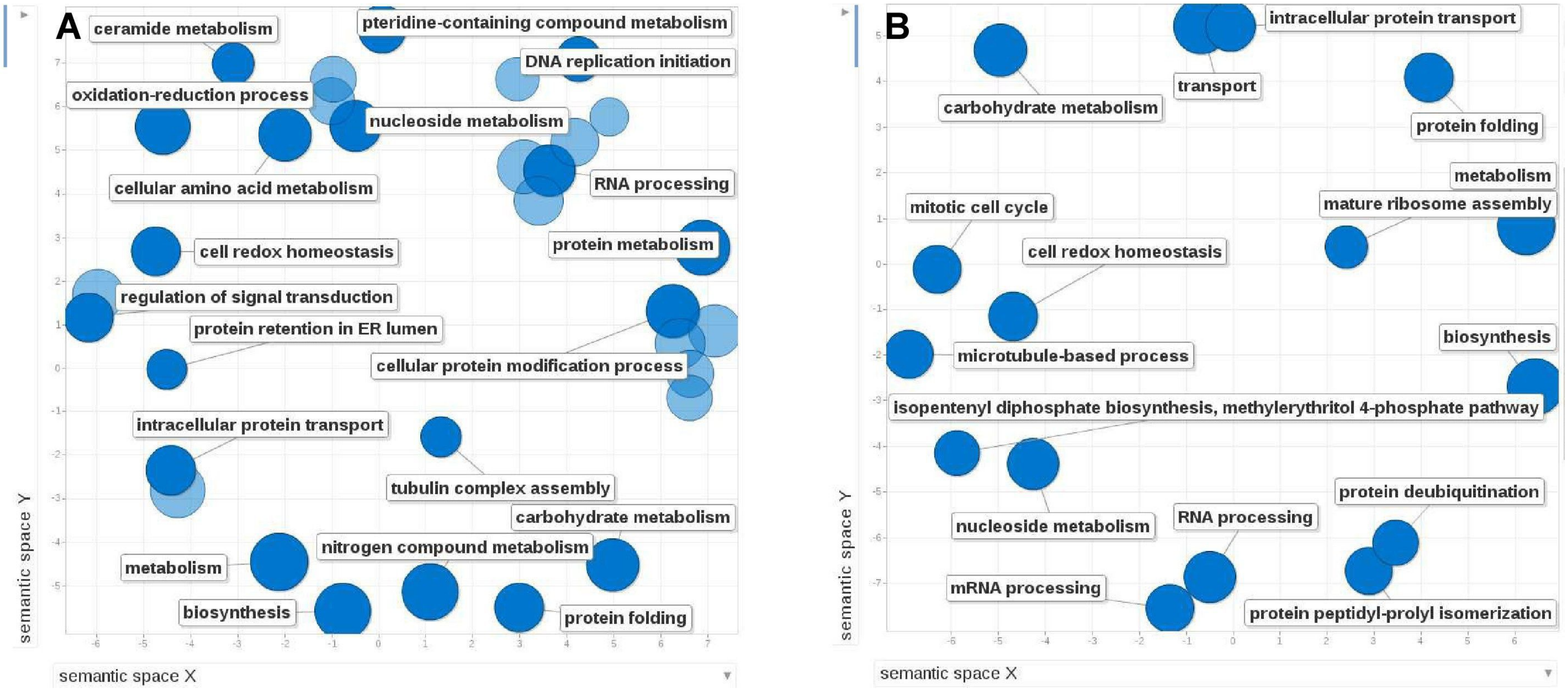

Figure S3. Results of REViGO semantic analysis of GO biological process terms. Functional enrichment of GO-terms was analyzed in the annotated transcripts with using InterProScan and summarized using REVIGO. The terms remaining after the redundancy reduction are represented as scatterplots, where the more semantically similar terms are positioned closer together. A – analysis of the proteins resulted in the phylogenetic trees, which are congruent to the phylotranscriptomic tree (Fig 2B). Light blue bubble show the process which is associated with the main one (e.g. bubble named “cellular protein modification process” is bound with four light blue bubbles “peptidyl-amino acid modification”, “protein peptidyl-prolyl isomerization”, “protein deubiquitination“ and “proteolysis”). B - analysis of the proteins, that are identical within Apocalathium complex, and the proteins resulted in the trees which incongruent to the phylotranscriptomic tree (Fig 2B).