**Description of Additional Supplementary Information**

* Title: **Supplementary Data 1**
* Description: **Quantitative transcriptomic data corresponding to the regulated transcripts and corresponding modules.**
* Title: **Supplementary Data 2**
* Description: **Gene Ontology term enrichment results at transcriptome, proteome and phosphoproteome level.** GO term enrichments were performed using a hypergeometric test with the full transcriptome or the full proteome as background for modules or proteome/phospho enrichment, respectively. Genes from significant child-categories were removed with a FWER threshold of 0.1 (R package GOfuncR).
* Title: **Supplementary Data 3**
* Description: **Functional annotation of transcripts using eggNOG-mapper.**
* Title: **Supplementary Data 4**
* Description: **Protein-centric analysis of *A. castellanii* encystment.**
* Title: **Supplementary Data 5**
* Description: **Phosphoproteomic analysis of *A. castellanii* encystment.**
* Title: **Supplementary Data 6**
* Description: **Phosphorylation motif analysis using rmotifx R package.**
* Title: **Supplementary Data 7**
* Description: **List of primers used in this study.**