

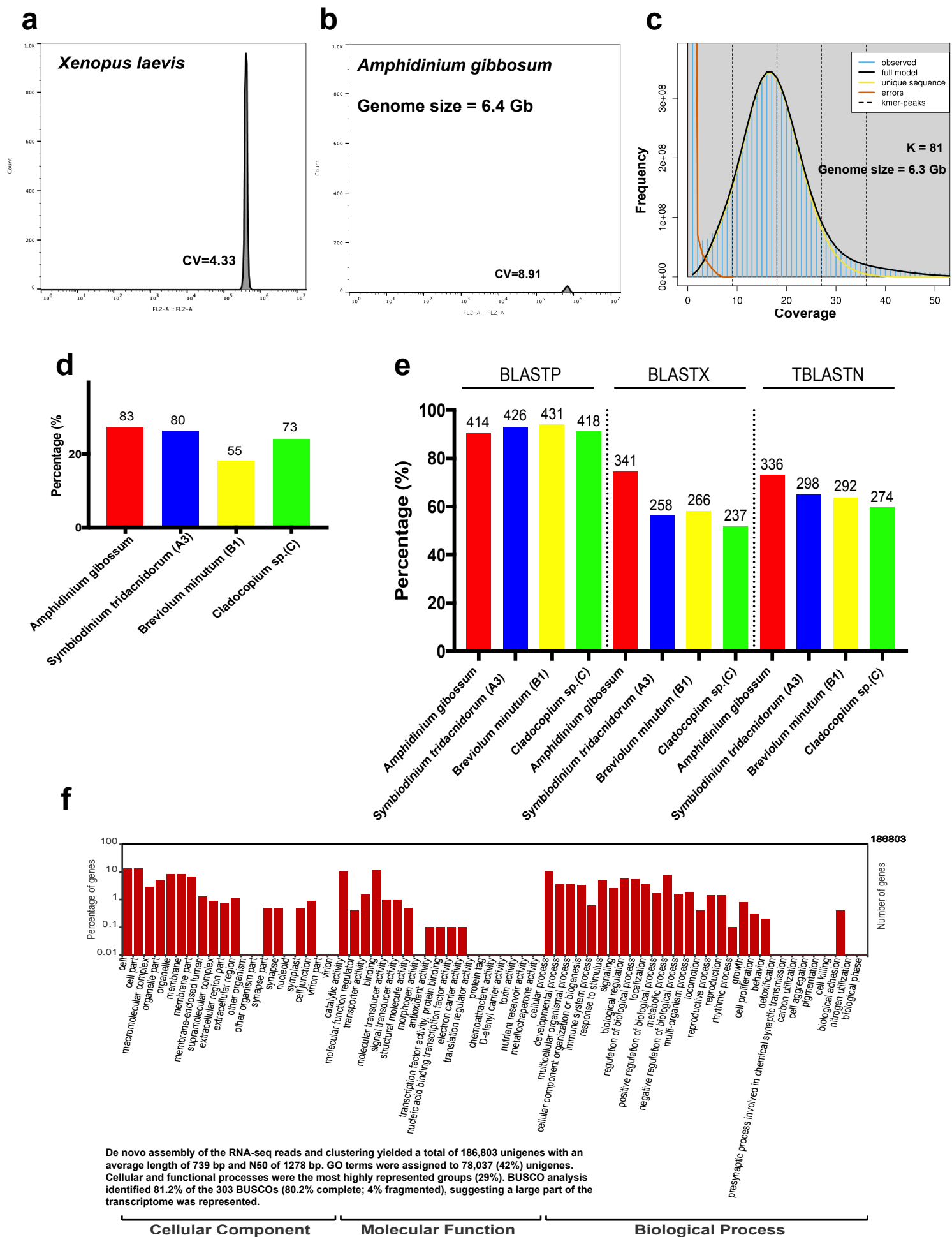
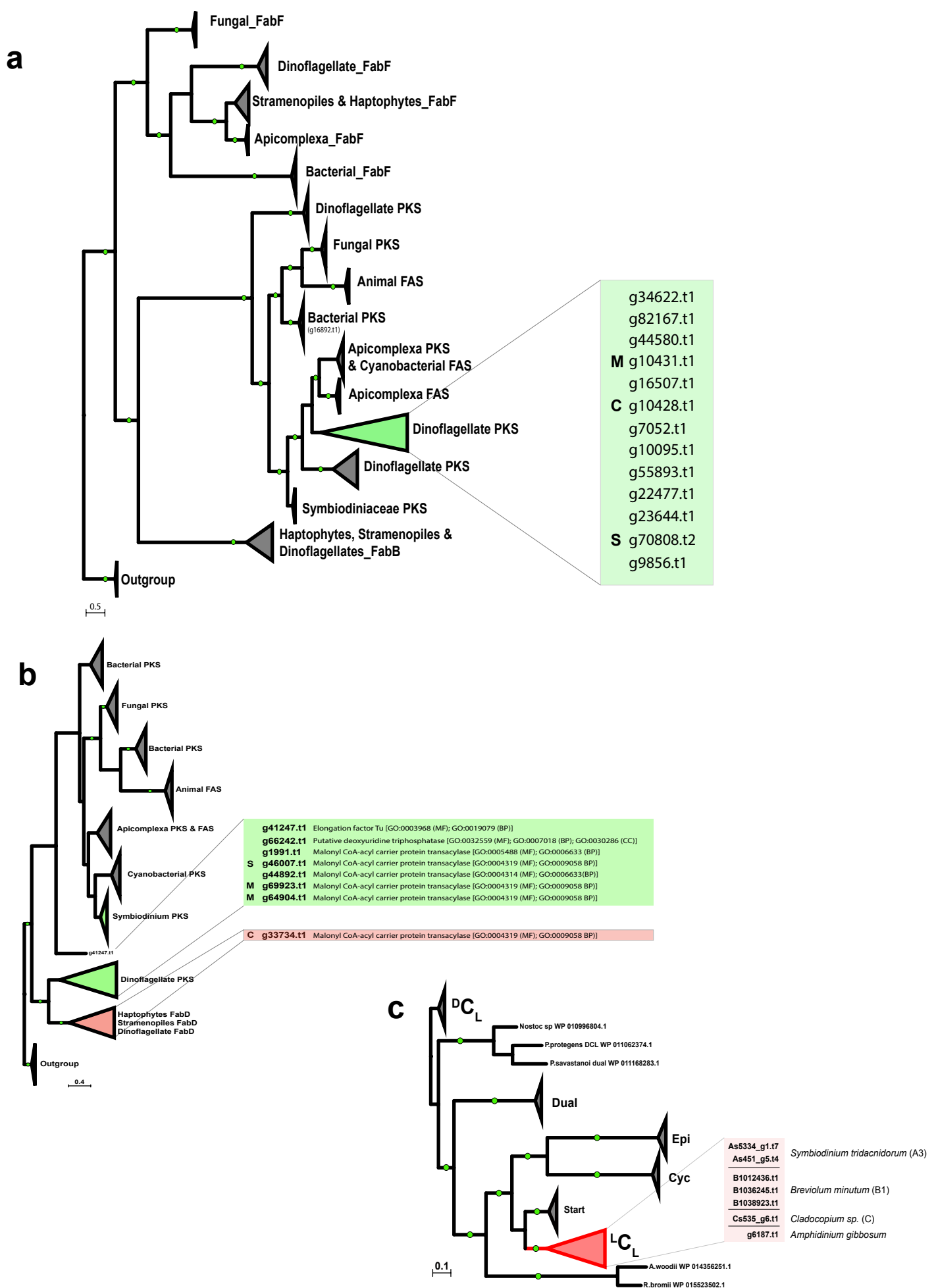


Fig. S1. Genome and transcriptome features of *A. gibbosum*. (a) FACS analysis of 3.1 Gb *Xenopus laevis* genome, (b) *A. gibbosum* haploid genome is approximately 6.4 Gb in size, which matches (c) Genomescope estimation at $k = 81$. CV is the Coefficient of Variation. (d) Recovery of 303 BUSCO genes in *Amphidinium gibbosum*, and (e) recovery of 458 CEGMA genes based on several BLAST analyses using BLASTP for predicted proteins and genome scaffolds for BLASTX and TBLASTN, respectively. (f) Gene annotation of *A.gibbosum* unigenes using gene ontology (GO).



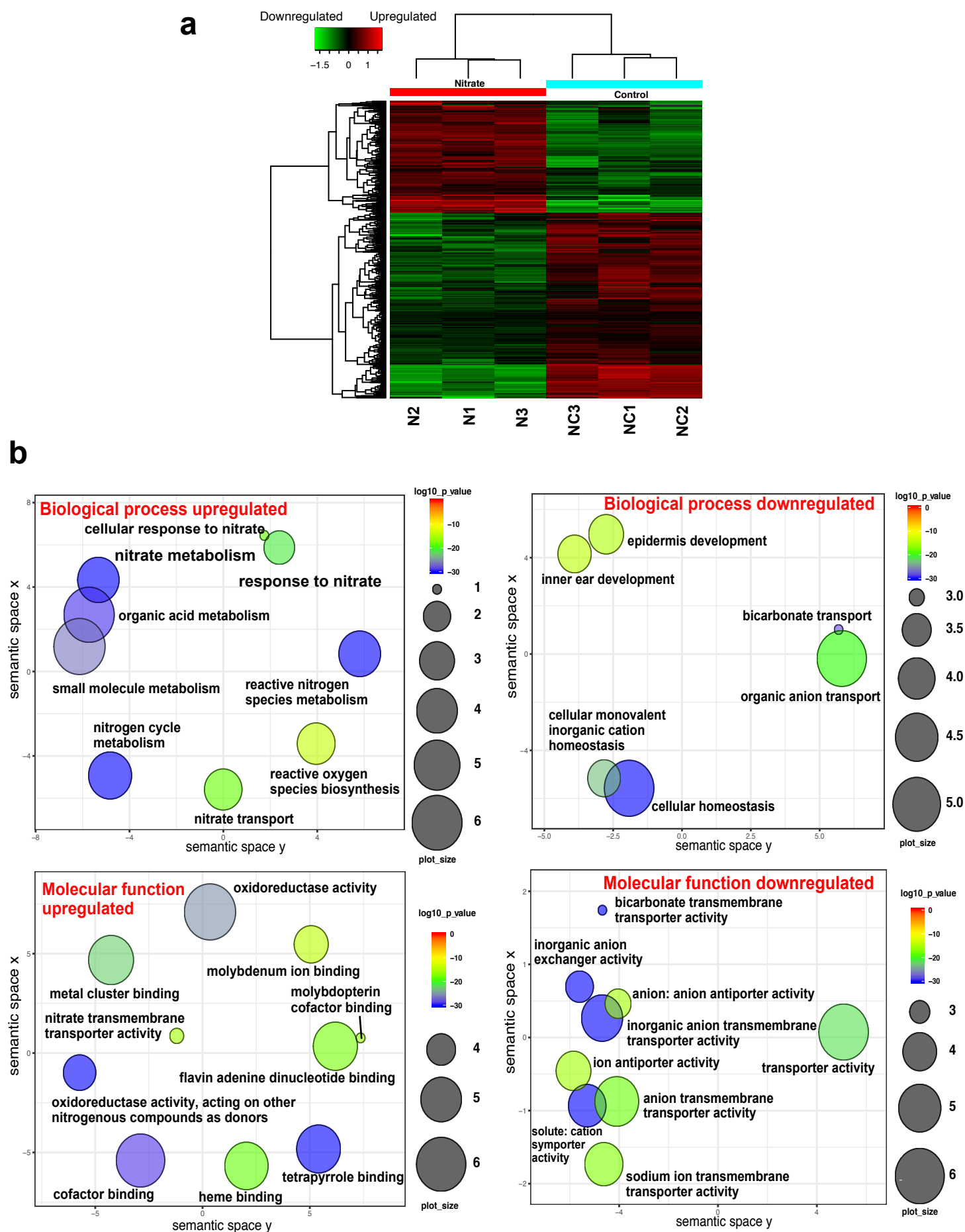


Fig. S4. (a) Global expression profile of differentially expressed genes under nitrogen starvation ($q\text{-value} < 0.001$ and $|\log_2(\text{FC})| > 1$). (b) Functional enrichment of GO-terms analyzed with topGO and summarized with REVIGO showing top 10 hits in nitrogen starvation. Scatterplots summarize the GO terms based on semantic similarities. Similar GO terms remain in close proximity together. Bubble color represent $p < 0.001$ while circle size shows the frequency of the GO term.

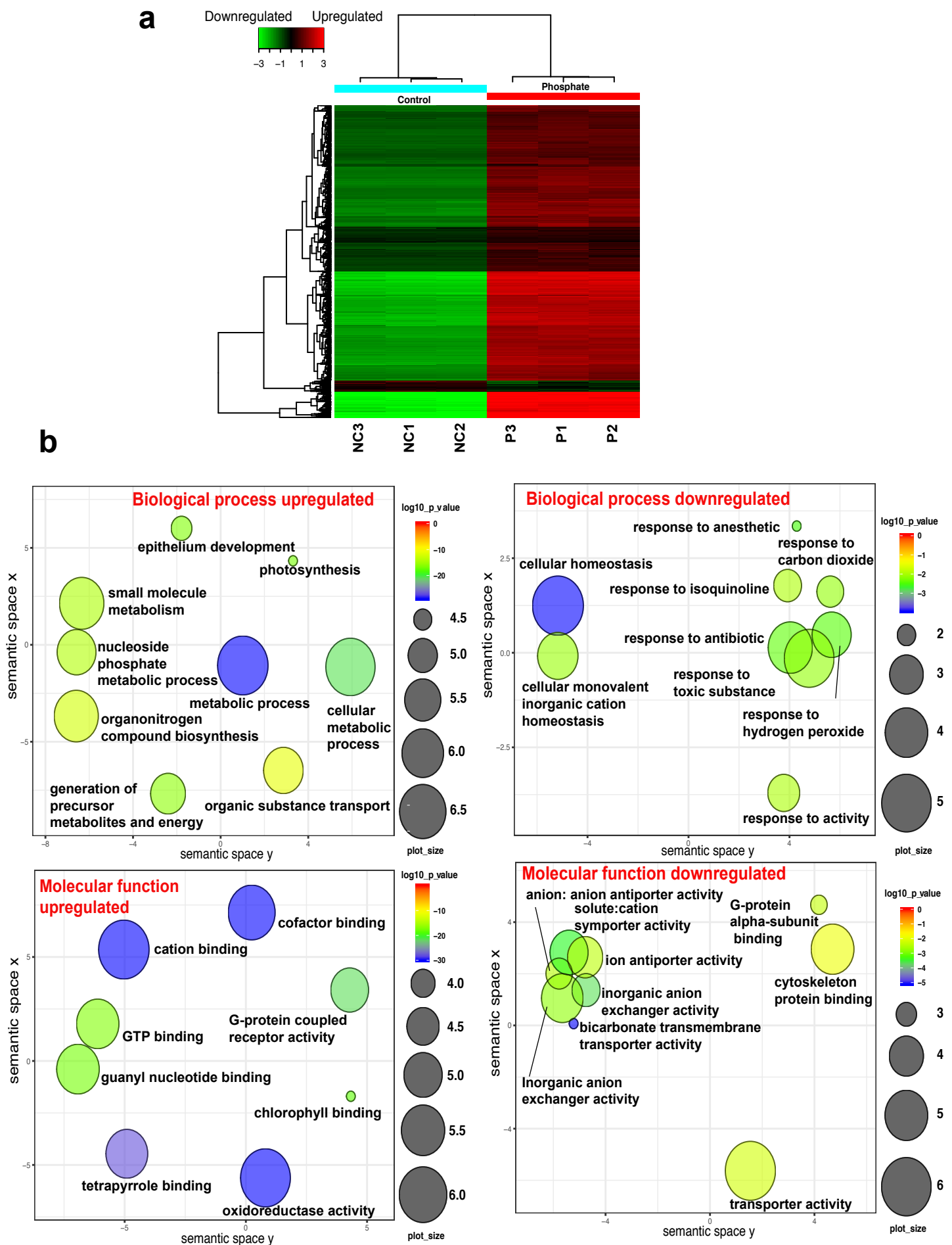


Fig. S5. (a) Global expression profile of differentially expressed genes under phosphate starvation ($q\text{-value} < 0.001$ and $|\log_2(\text{FC})| > 2$). (b) Functional enrichment of GO-terms analyzed with topGO and summarized with REVIGO for phosphate starvation showing top 10 hits. Scatterplots summarize the GO terms based on semantic similarities; Similar GO terms remain in close proximity together. Bubble color represents $p < 0.001$ while circle size shows the frequency of the GO term.

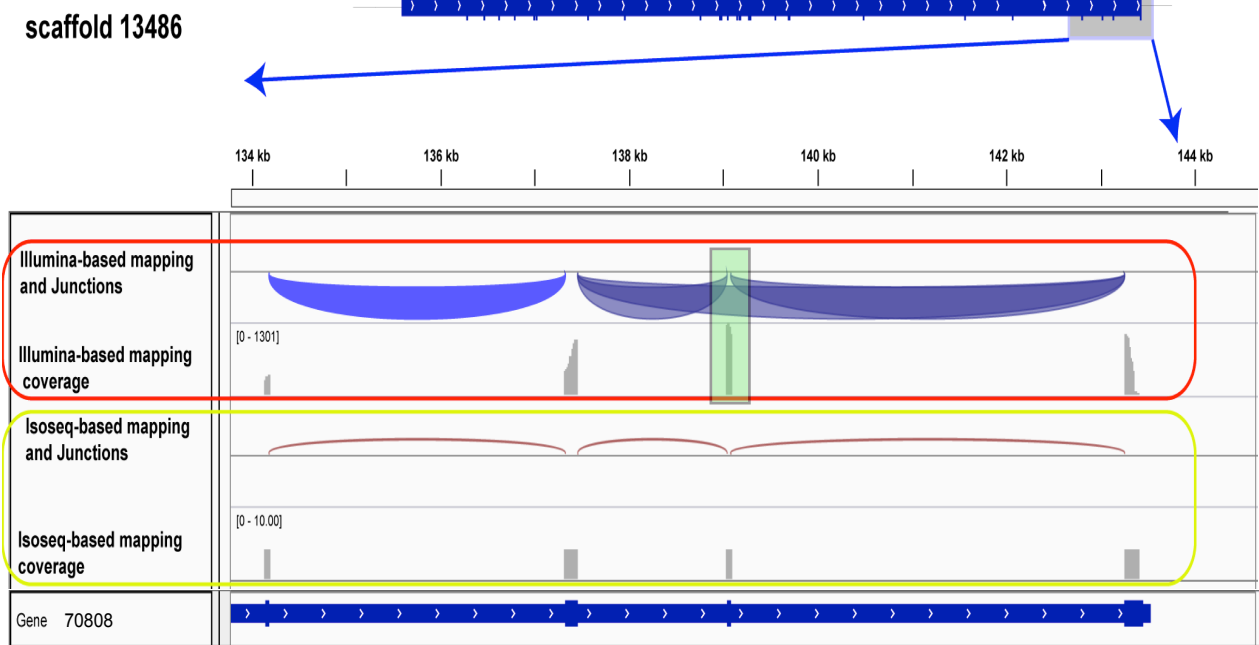
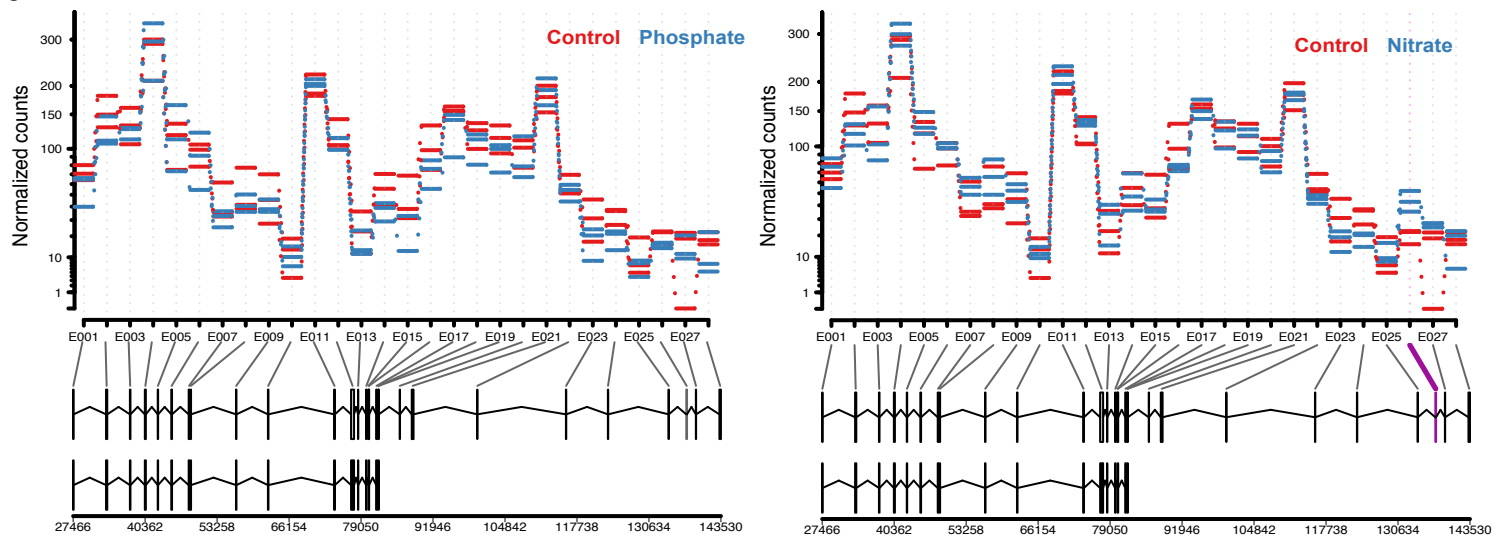
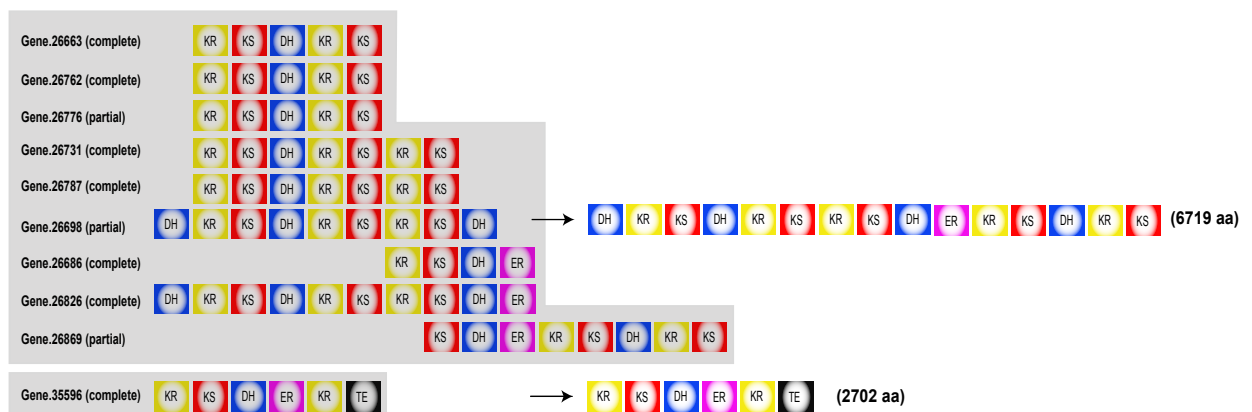
a**b****c**

Fig. S8. (a) Plot showing mapping of Illumina and Isoseq reads to g70808 and the presence of exons. Illumina reads mapping are depicted in red box while Isoseq reads mapping are in yellow box. Reads show evidence of skipped exon (shown in green box). Isoseq read coverage is too low to show such skipped exon event. (b). Gene models showing alternative splicing in g70808. Plots show counts after being normalized in each replicate of phosphate and nitrogen starvation experiment. Significant differentially expressed exons are coloured in magenta ($p.adjust < 0.05$). (c) PKS transcripts recovered from Iso-Seq showing evidence of expression of multifunctional PKS transcripts. Length are expressed in amino acids. (KS, ketosynthase; KR, ketoreductase, DH; dehydratase, ER, enoylreductase; TE, thioesterase).

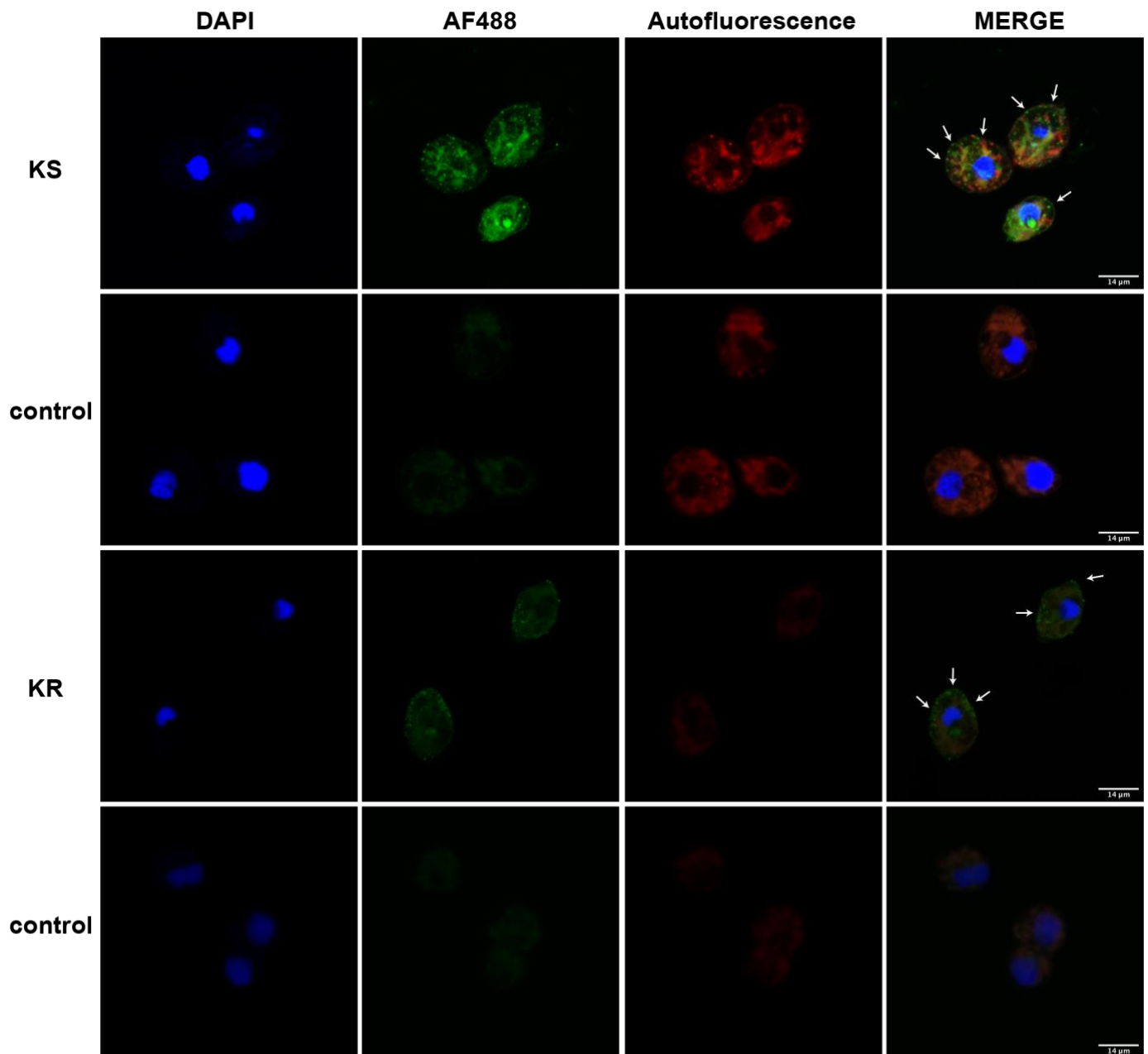


Fig. S9. Immunofluorescent staining of Amphidinium with anti-KS and anti-KR antibodies. Confocal images (63x) of antibodies show localization of KS and KR proteins indicated with white arrows. Nuclei are stained blue with DAPI. KS proteins are in green, and merged images of nuclei and KS and KR protein staining, respectively. Scale bars are 14 μm in the panels.

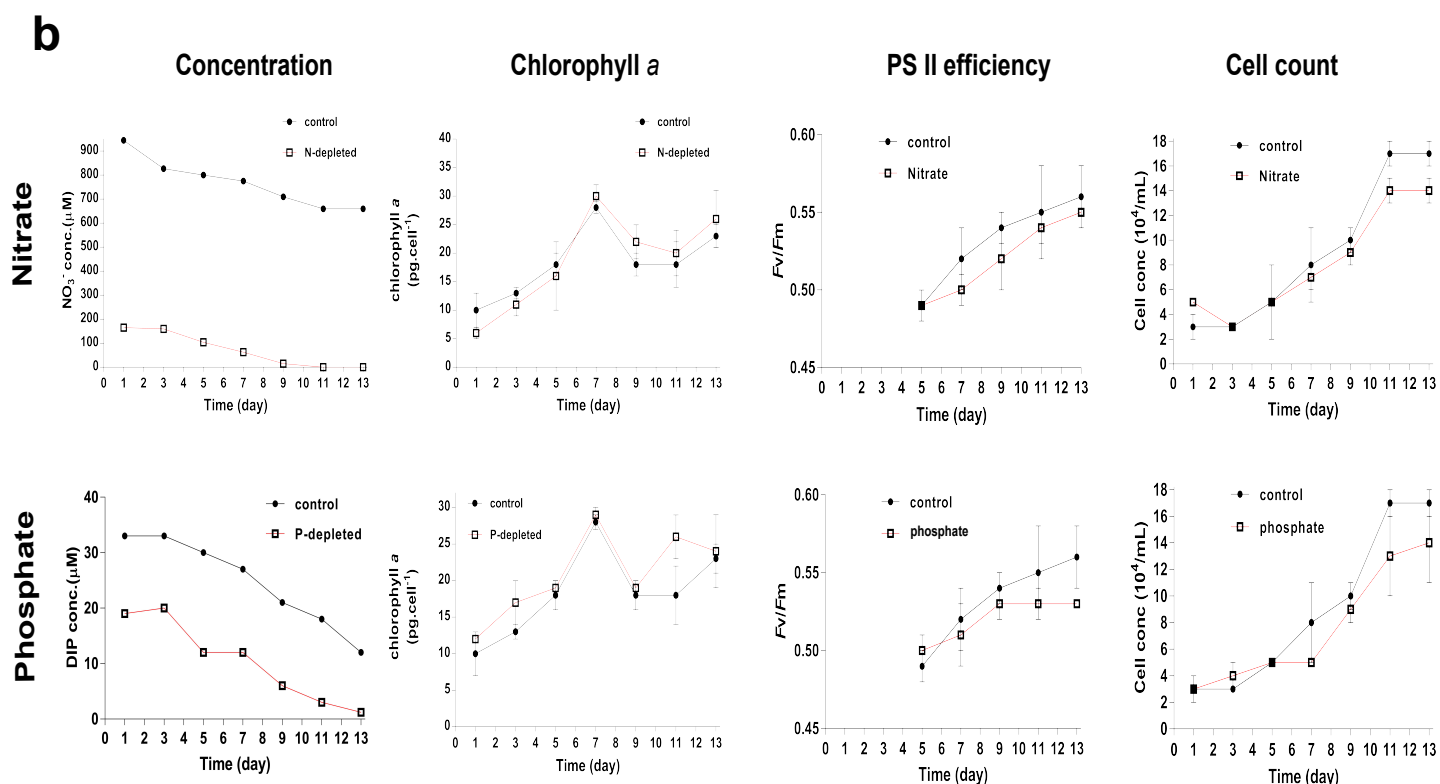
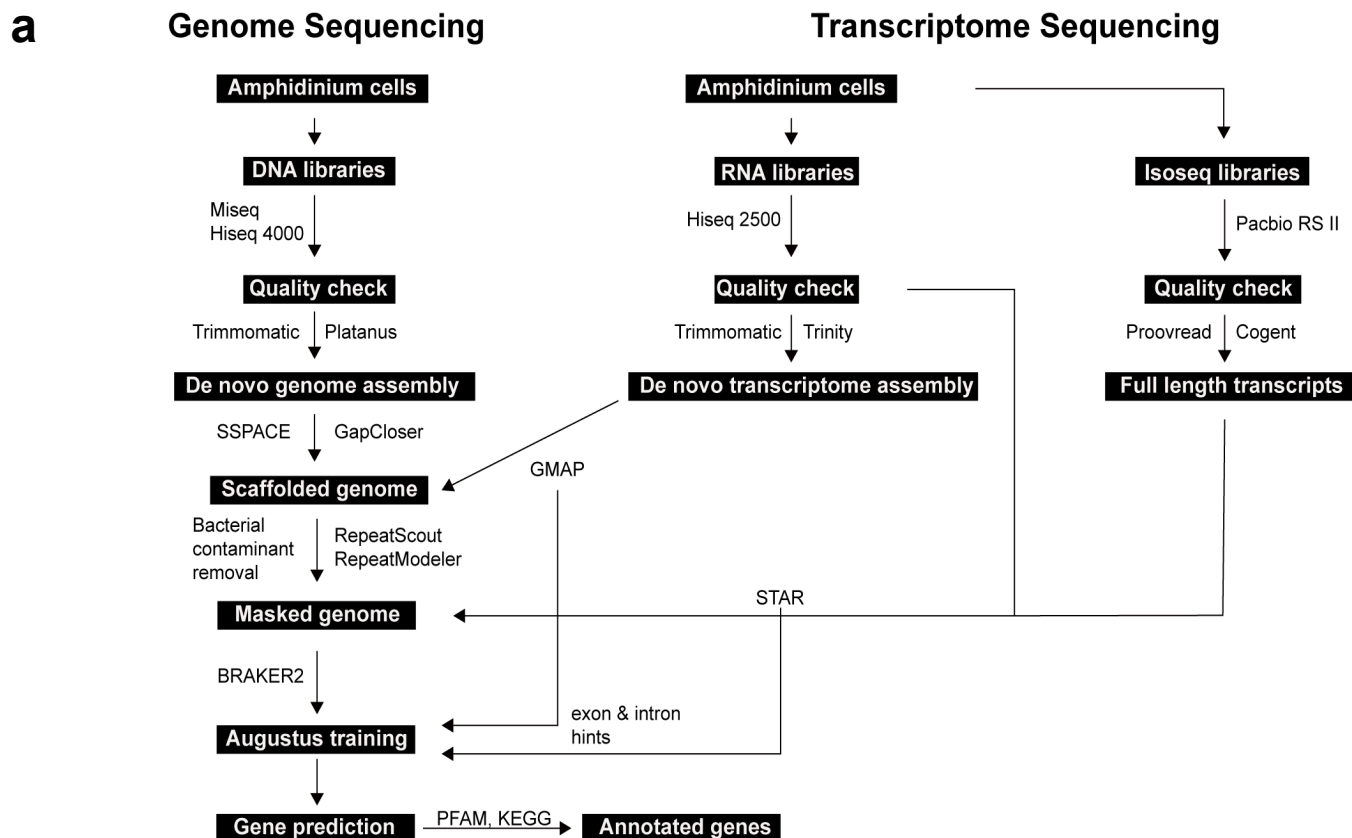


Fig. S10. (a) Genome and transcriptome assemblies' workflow for *Amphidinium gibbosum*.

(b) Physiological parameters of *Amphidinium gibbosum* under nitrate and phosphate starvation conditions. Results are mean ± SE of 3 replicates (except for nitrate/phosphate concentration).