Highly flexible metabolism of the marine euglenozoan protist *Diplonema papillatum*

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Additional file 1: Fig. S1-S5

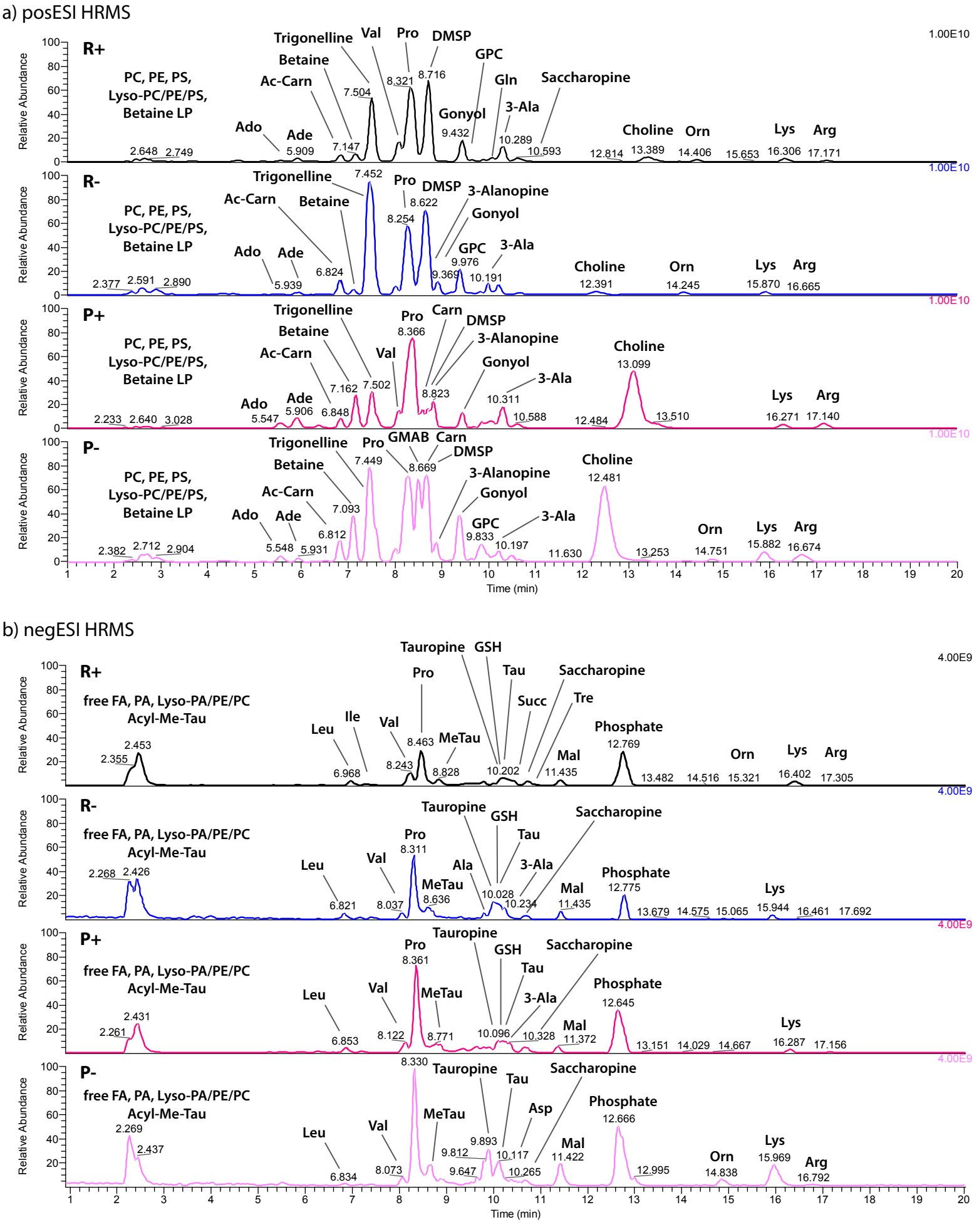
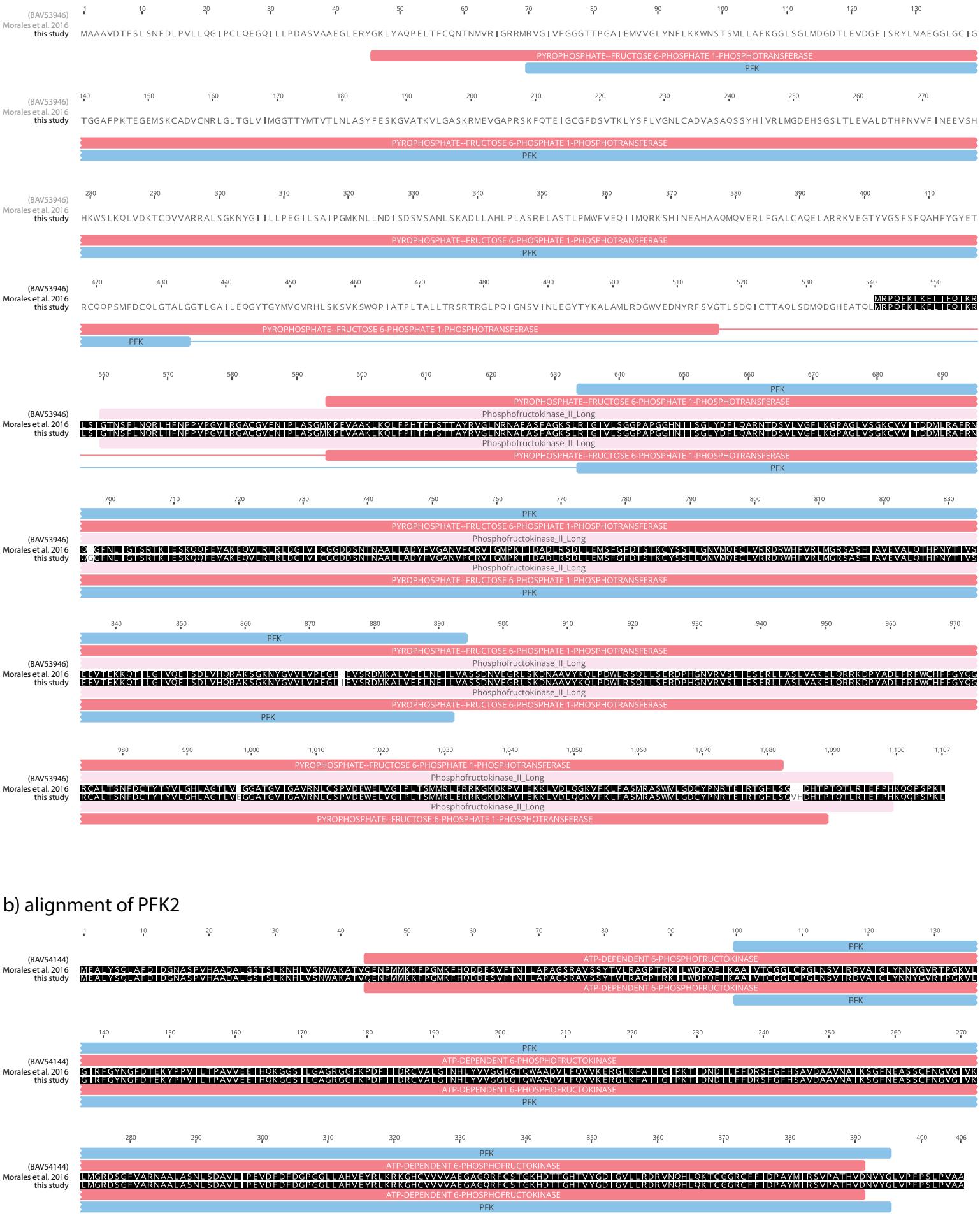


Fig. S1. LC-HRMS metabolic profiles. Characteristic (**a**) posESI HRMS and (**b**) negESI HRMS metabolic signatures for the *D. papillatum* cell extracts grown in rich normoxic (R+), rich hypoxic (R-), nutrient poor normoxic (P+), and nutrient poor hypoxic (P-) conditions. 3-Ala, 3-alanine; Ac-Carn, acylcarnitine; Acyl-Me-Tau, acyl-methyl-taurines (taurates); Ade, adenine; Ado, adenosine; Ala, alanine; Arg, arginine; Arg, arginine; DMSP, 3-dimethylsulfoniopropionate; FA, fatty acid; GMAB, glycerolmethyl-3-alanine betaine; Gln, glutamine; GPC, glycerophosphocholine; GSH, glutathione; HRMS, high resolution mass spectrometry; Ile, isoleucine; Betaine LP, betaine-lipids; Lys, lysine; Mal, malate; MeTau, N-methyltaurine; negESI, negative electrospray ionization; Orn, ornithine; PA, phosphatidic acid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; Pro, proline; posESI, positive electrospray ionization; PS, phosphatidylserine; Tau, taurine; Tre, trehalose; Val, valine.

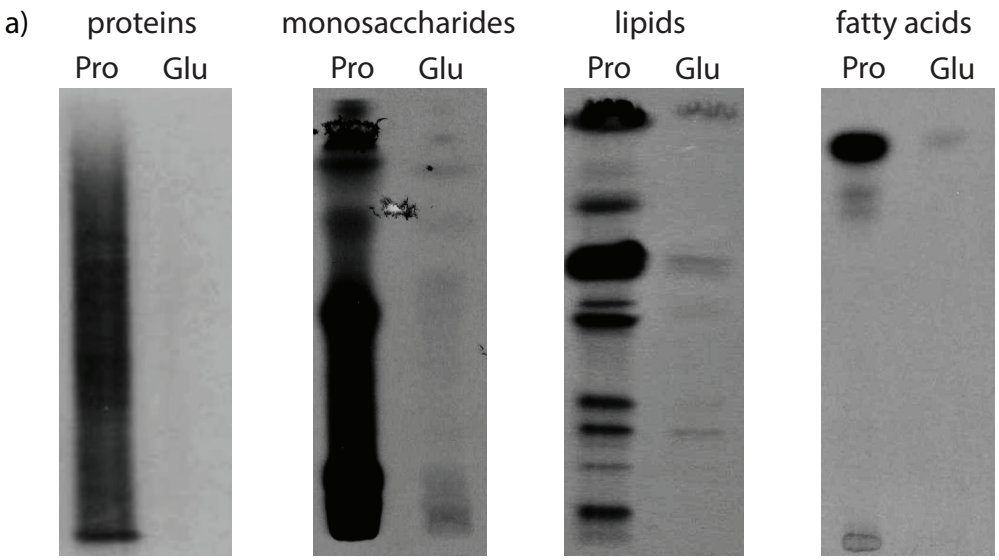
a) alignment of PFK1

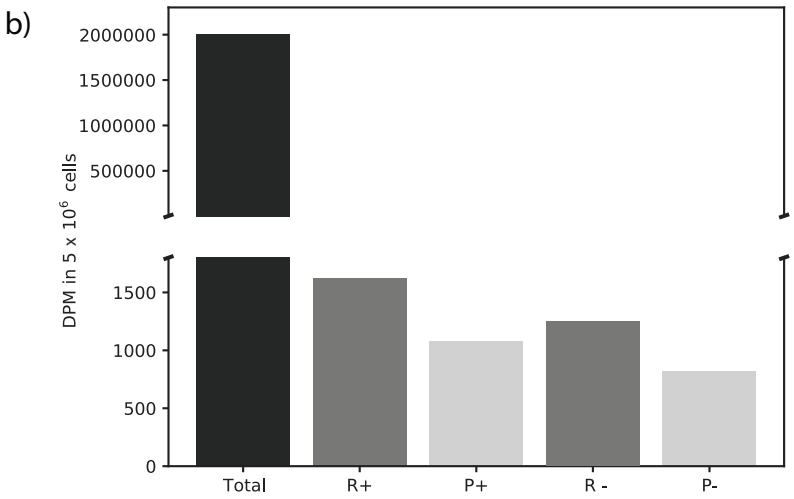


b) alignment of PFK2

c) sequence of PFP

Fig. S2. Sequences of phosphofructokinase (PFK) and pyrophosphate-fructose phosphotransferase (PFP). (**a**) Alignment of PFK1 shows that the sequence previously identified [13] was truncated at its N-terminus. Moreover, predicted protein domains classify it as PFP rather than PFK. (**b**) Alignment of PFK2 identified in this and previous study [13]. (**c**) Sequence of PFP identified only in this study. Color boxes correspond to predicted protein domains as in different databases as explained in graphical legend.





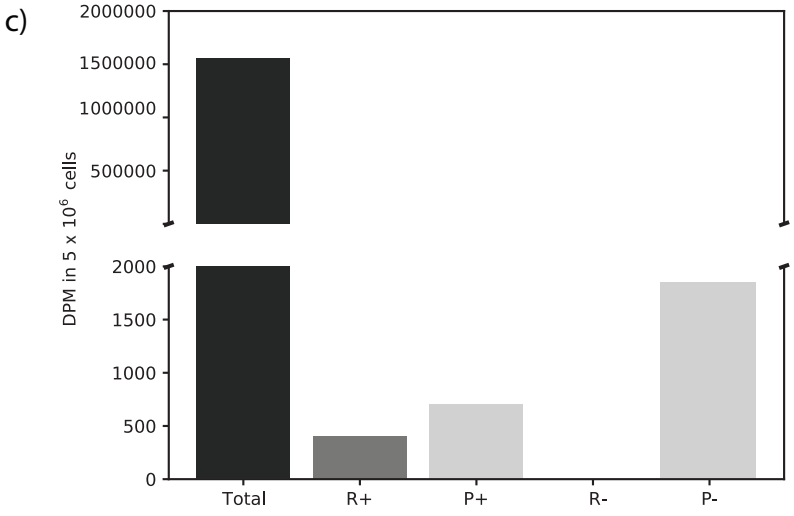


Fig. S3. ^{14}C-proline (Pro) and ^{14}C-glucose (Glu) uptake in D. papillatum. (**a**) Cultures of 5 x 10^6 cells were fed with ^{14}C-Pro and ^{14}C-Glu in the poor medium under aerobic conditions. Shown are autoradiograms of separated proteins, monosaccharides, lipids, and fatty acids. (**b**) Cells were cultivated for 24 h in the presence of radioactive glucose in rich (R) and poor (P) medium under aerobic (+) and hypoxic (-) conditions. (**c**) Cells were placed into sea salt solution supplemented with radioactive glucose and cultured for 12 h. The amount of isotope was determined with scintillation counter as disintegrations per minute (DPM) in 1 ml of growth medium containing 5 x 10^6 cells and cellular lysates.

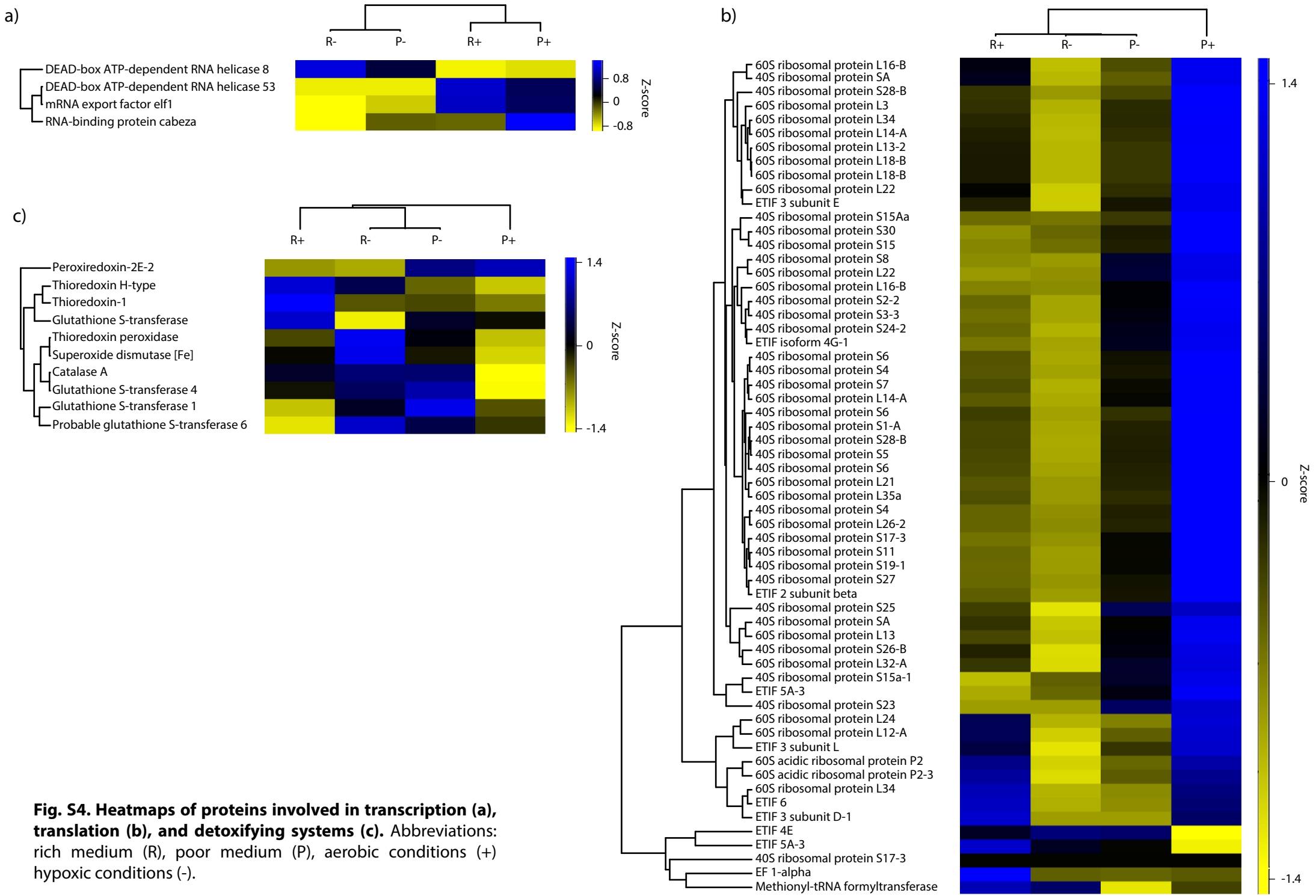


Fig. S4. Heatmaps of proteins involved in transcription (a), translation (b), and detoxifying systems (c). Abbreviations: rich medium (R), poor medium (P), aerobic conditions (+) hypoxic conditions (-).

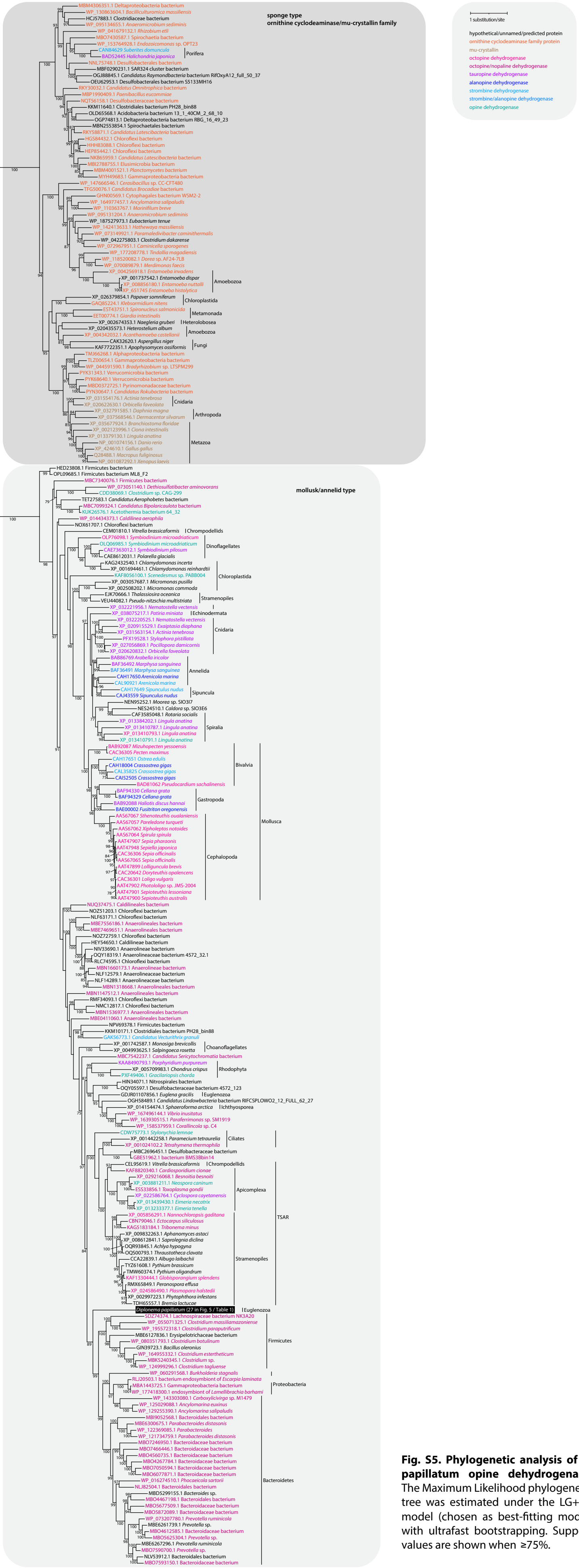


Fig. S5. Phylogenetic analysis of D. papillatum opine dehydrogenase. The Maximum Likelihood phylogenetic tree was estimated under the LG+G4 model (chosen as best-fitting model) with ultrafast bootstrapping. Support values are shown when ≥75%.