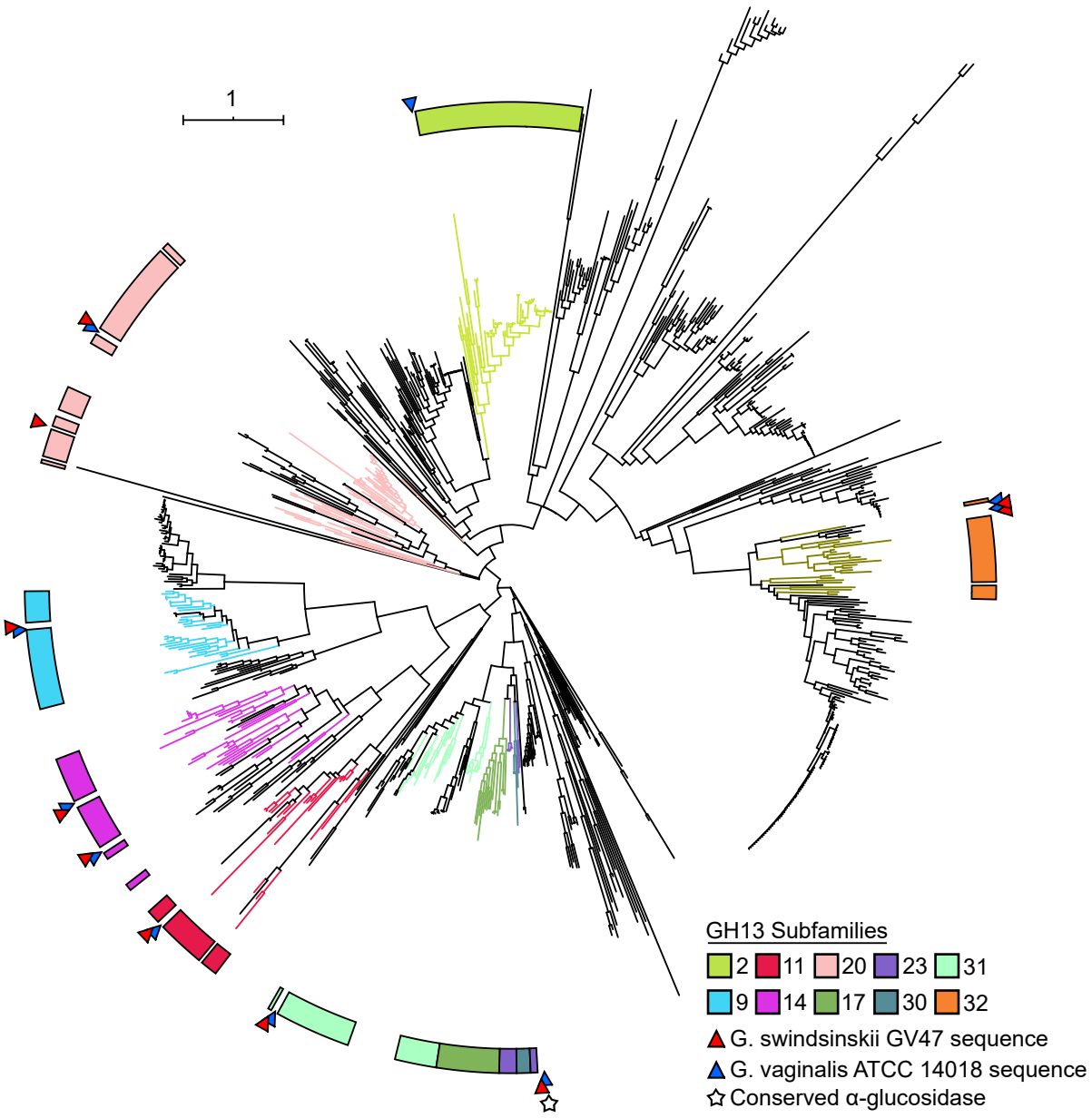


**Figure S1.** Phylogenetic tree of GH13 functionally characterized members with predicted GH13 domains from *G. swindsinskii* GV37 (red arrow) and *G. vaginalis* ATCC 14018 (blue arrow). Tree branches are coloured based on GH13 subfamily. The conserved α-glucosidase between the 26 proteomes is denoted by a white star. Trees were generated using SACCHARIS and viewed in iTOL**.**

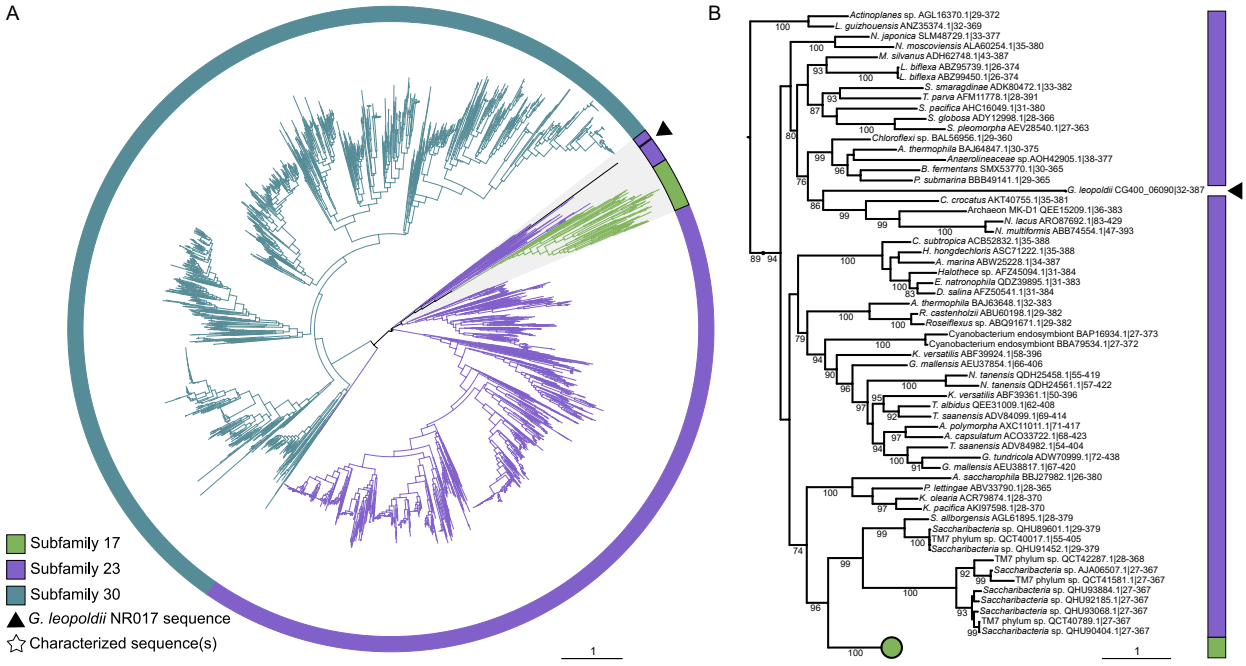


**Figure S2.** (A) Phylogenetic tree of all GH13 subfamily 17, 23 and 30 members in the CAZy database and *G. leopoldii* CG400_06090. Branch colour is based on GH13 subfamily and functionally characterized proteins are indicated with stars. The clade highlighted in grey including *G. leopoldii* CG400_06090 and its closest relatives is expanded in (B).

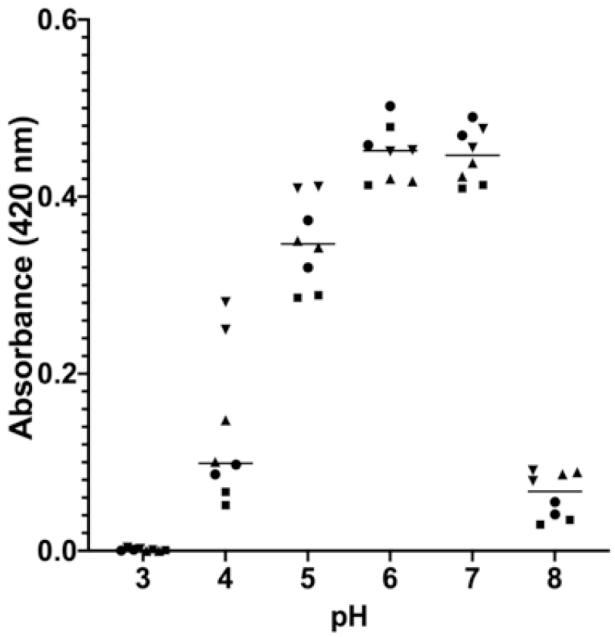


**Figure S3.** Release of 4-nitrophenol from chromogenic substrate 4-nitrophenyl-α-D-glucopyranoside at pH 3-8. Results from four independent experiments each with two technical replicates are shown. The α-glucosidase (0.8 mM) was incubated with 10 mM substrate at different pH and amount of 4-nitrophenol released in 10 minutes was measured.

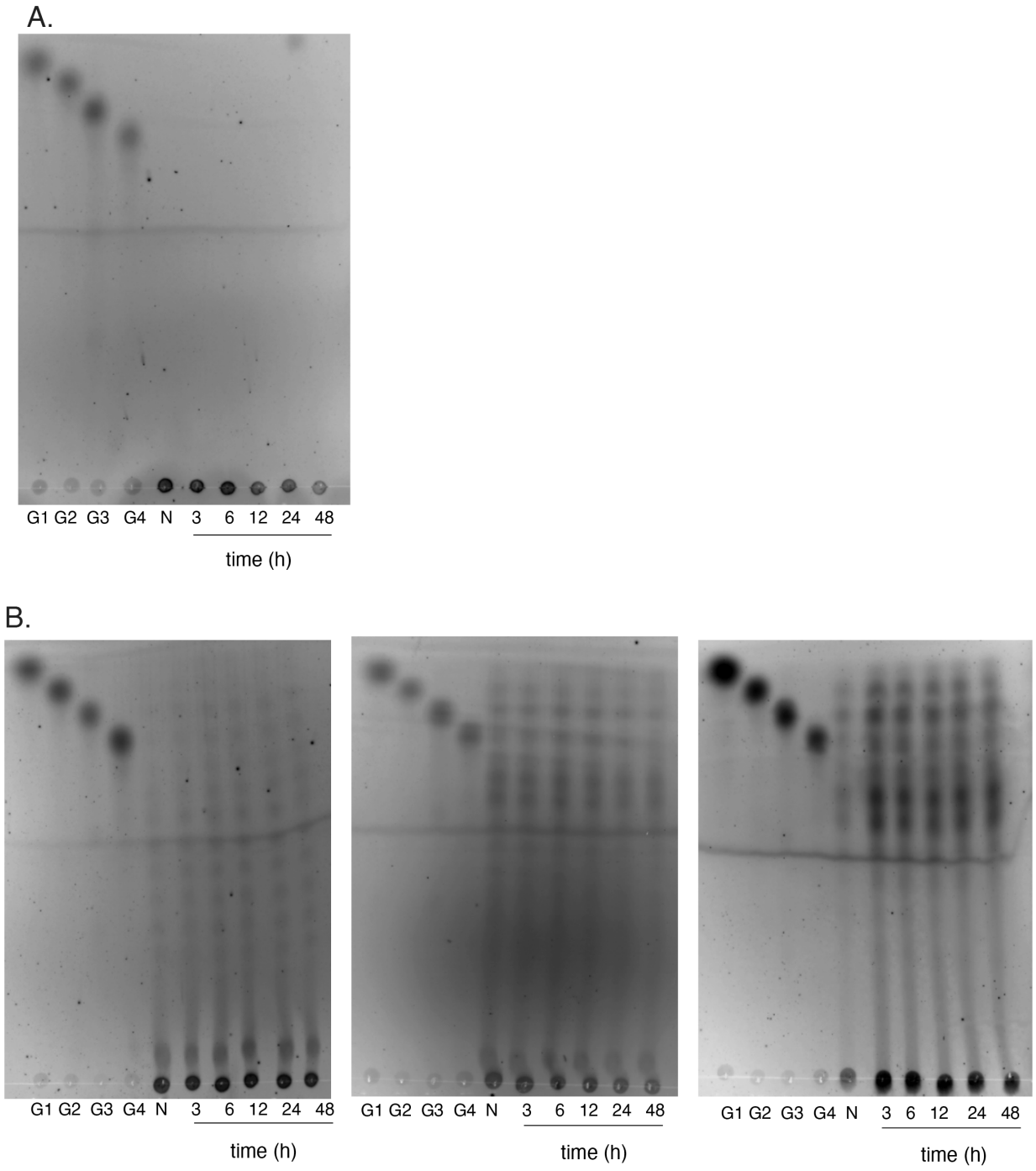


**Figure S4.** (A) TLC of products of glycogen hydrolysis by α-glucosidase enzyme. Reaction mixtures were assessed at 3 h, 6 h, 12 h, 24 h and 48 h. N = Substrate with no enzyme. (B) TLC of products hydrolysis by α-glucosidase enzyme of maltodextrins MD 4-7 (left panel), MD 13-17 (middle panel) and MD 16.5- 19.5 (right panel). Reaction mixtures were assessed at 3 h, 6 h, 12 h, 24 h and 48 h. N = Substrate with no enzyme.