

Figure S1. Microbial growth curves of the enrichments on pretreated *A. donax* in different culture media.

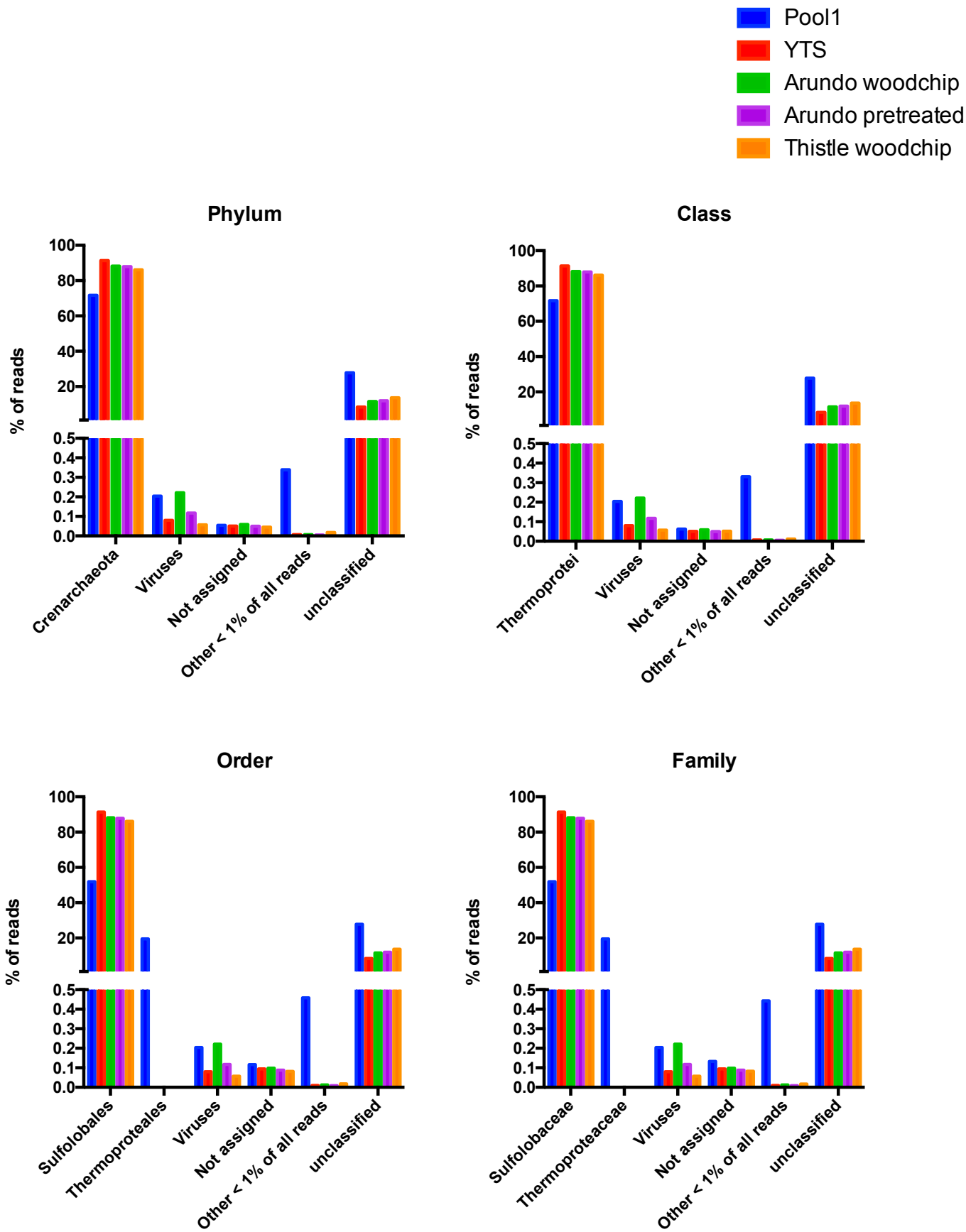


Figure S2. Taxonomic annotation at the level of phylum, class, order, and family.

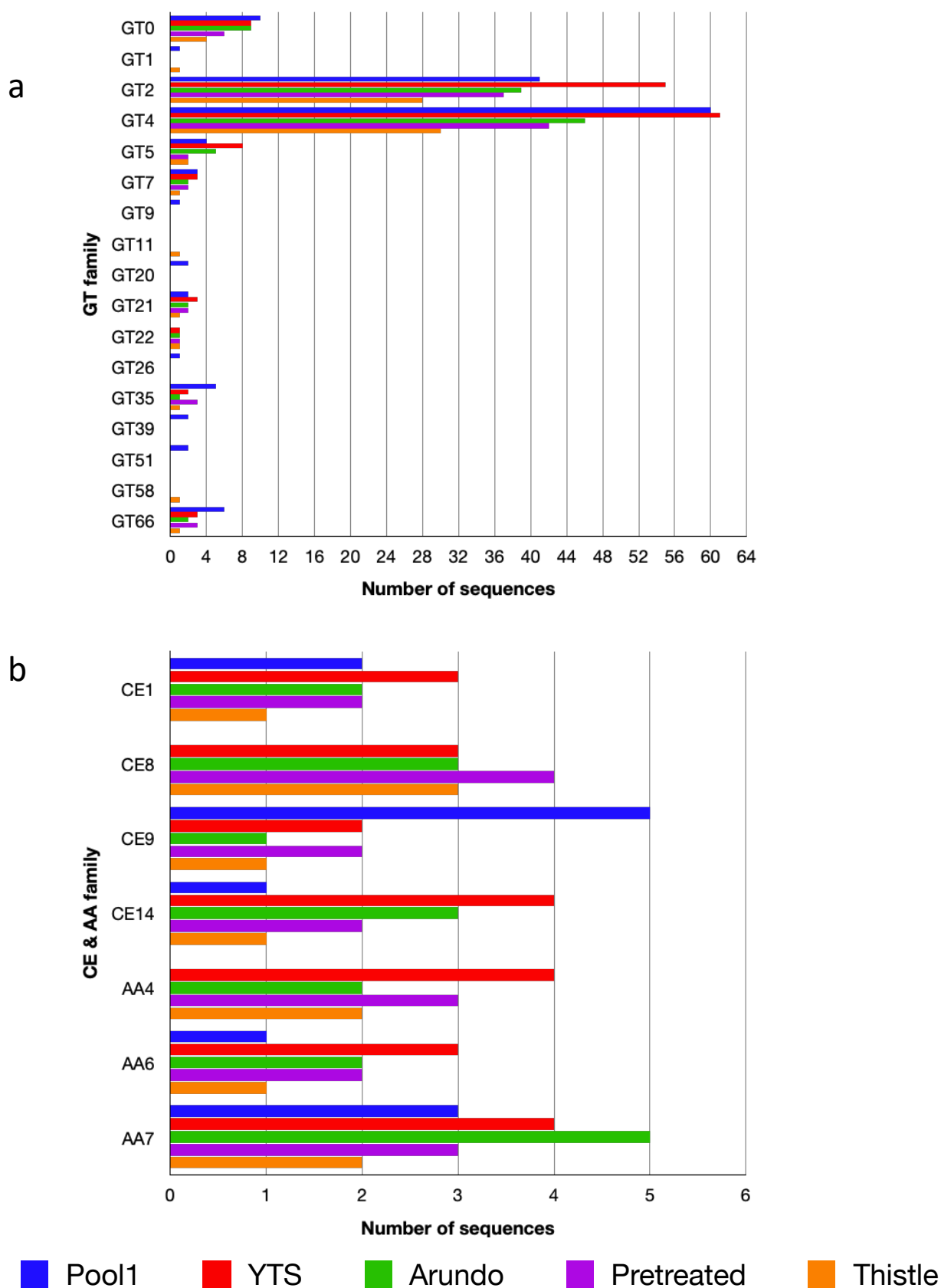
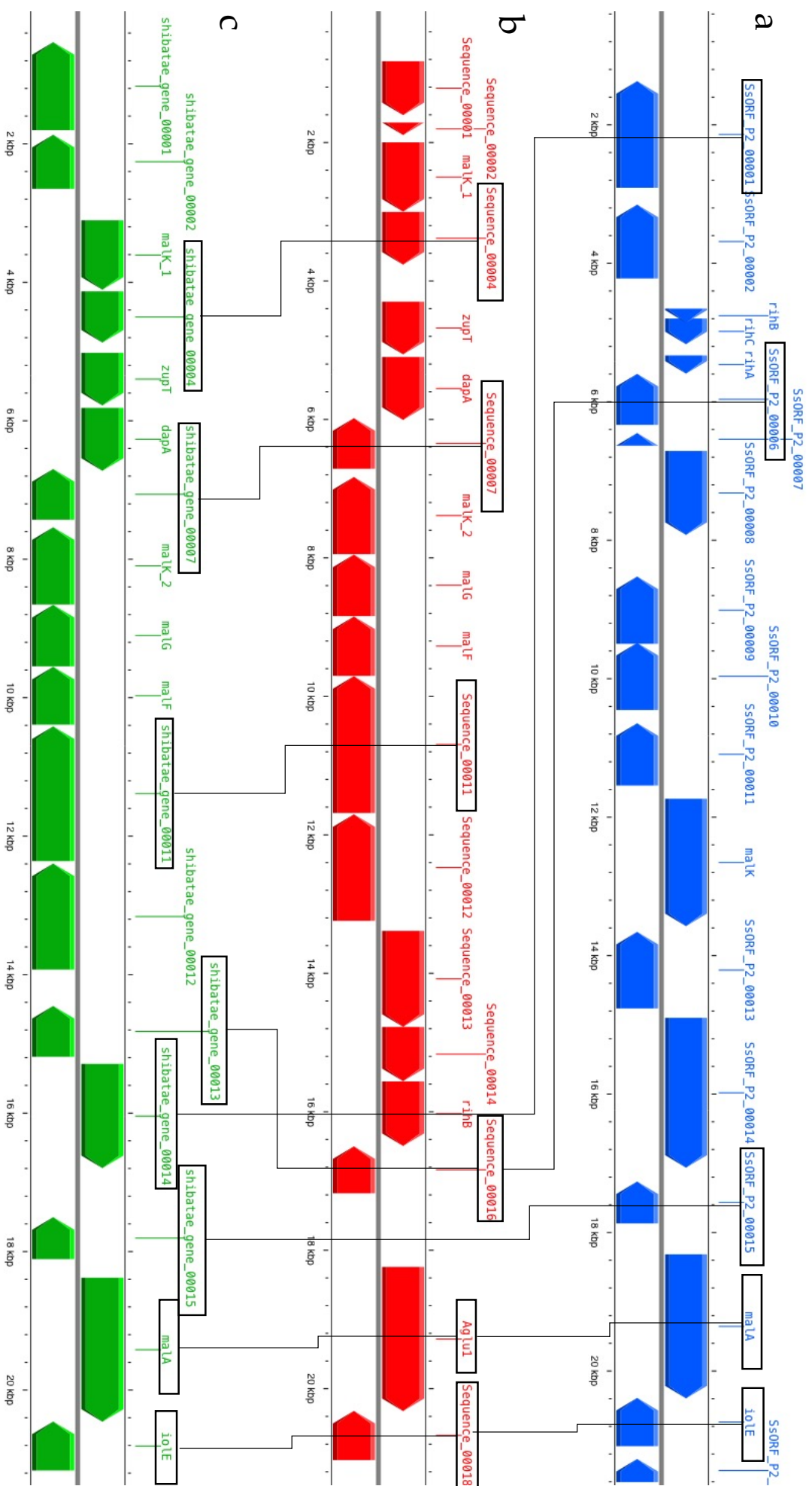


Figure S3. Distribution among the samples of the (a) glycosyltransferase, (b) carbohydrate esterases and auxiliary activities. The number of sequences assigned to each family from Pool1 and the four enrichments is displayed.



 *Saccharolobus solfataricus* P2

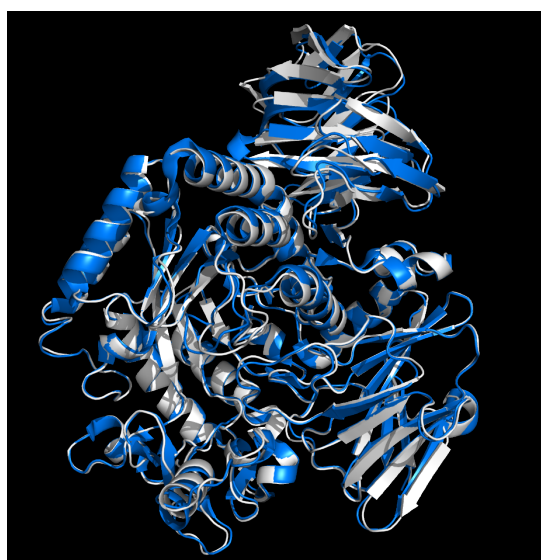
 Contig *Aglu1*

 *Saccharolobus shibatae*

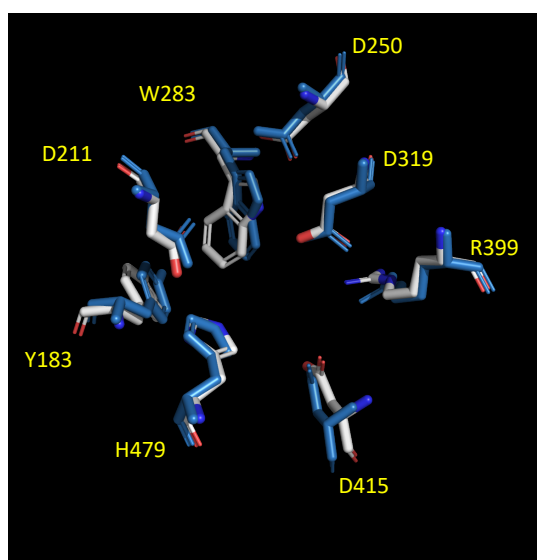
Figure S4. Genomic environments of *S. solfataricus* P2 *malA* (a), the contig containing *aglu1* gene (b) and *S. shibatae* *malA* (c). Callouts and connectors indicate homologous unannotated ORFs with amino acid identity $\geq 80\%$



(a)



(b)



(c)

Figure S6 . a) Different domains and subdomains of *S. solfataricus* MalA 3D structure (PDB ID 2G3M). The different colours indicate the domains N (blue), A (red), C (yellow), D (orange), and subdomains B (green) and B' (purple). b) Overall superimposition of *S. solfataricus* MalA (blue) and Aglu1 model (white). c) Close-up of the superimposed aminoacid residues in the active sites of the Aglu1 model (white) and MalA (blue).

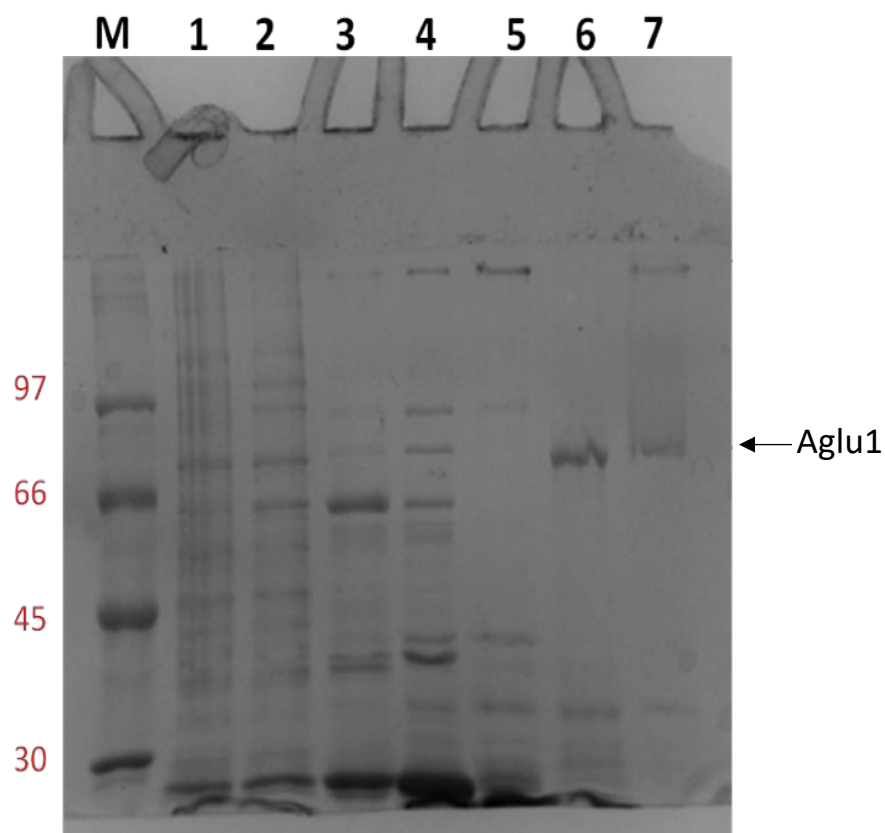


Figure S7 Purification steps of Aglu1. Lane M, molecular weight markers, lane 1) crude extract (7 μ g); lanes 2–5) heat treatment at 50 °C (7 μ g), 60 °C (10 μ g), 70 °C (10 μ g) and 80 °C (10 μ g) respectively; lane 6, Q-Sepharose 16/10 (5 μ g); lane 7, Phenyl Sepharose 26/10 (3 μ g).

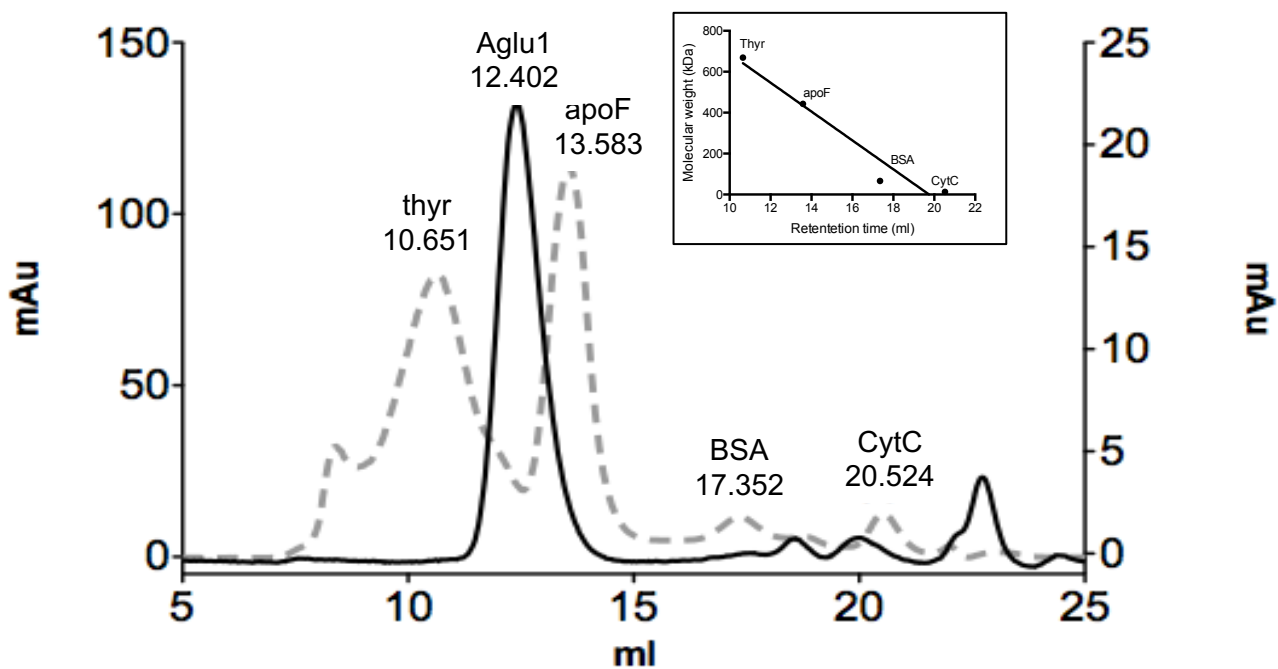


Figure S8. Elution profile of Aglu1 and molecular weight markers. Inset: graph of the calibration line obtained by plotting the retention time and the molecular weight.

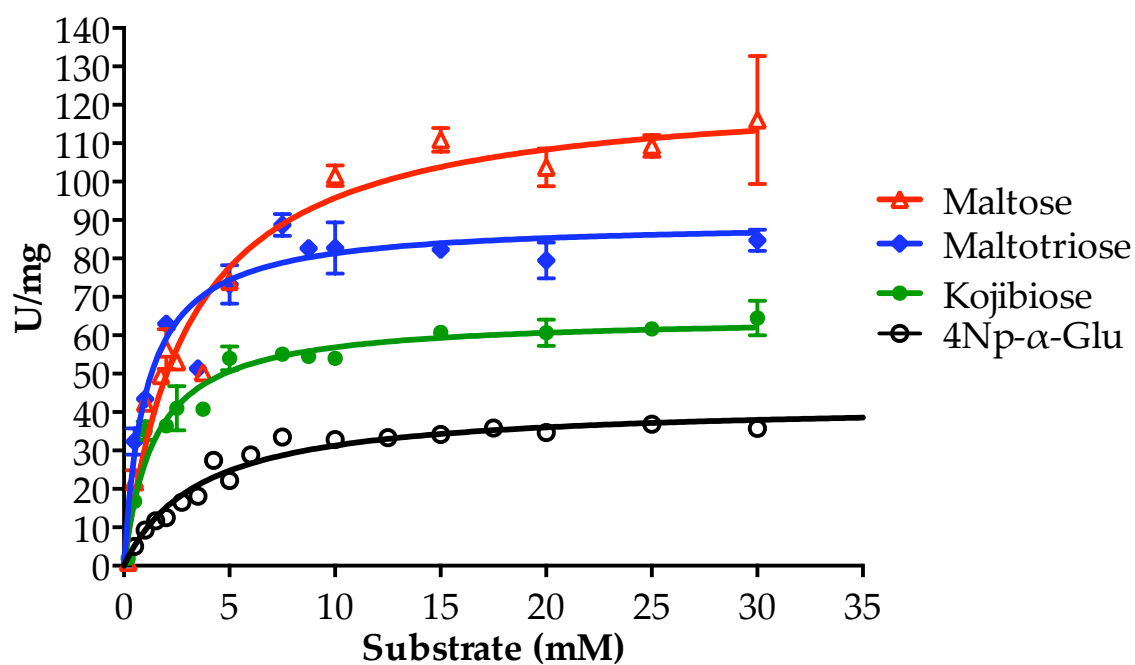


Figure S9. Kinetic curves of Aglu1 on, Maltose, Maltotriose, Kojibiose and 4Np- α -Glu.

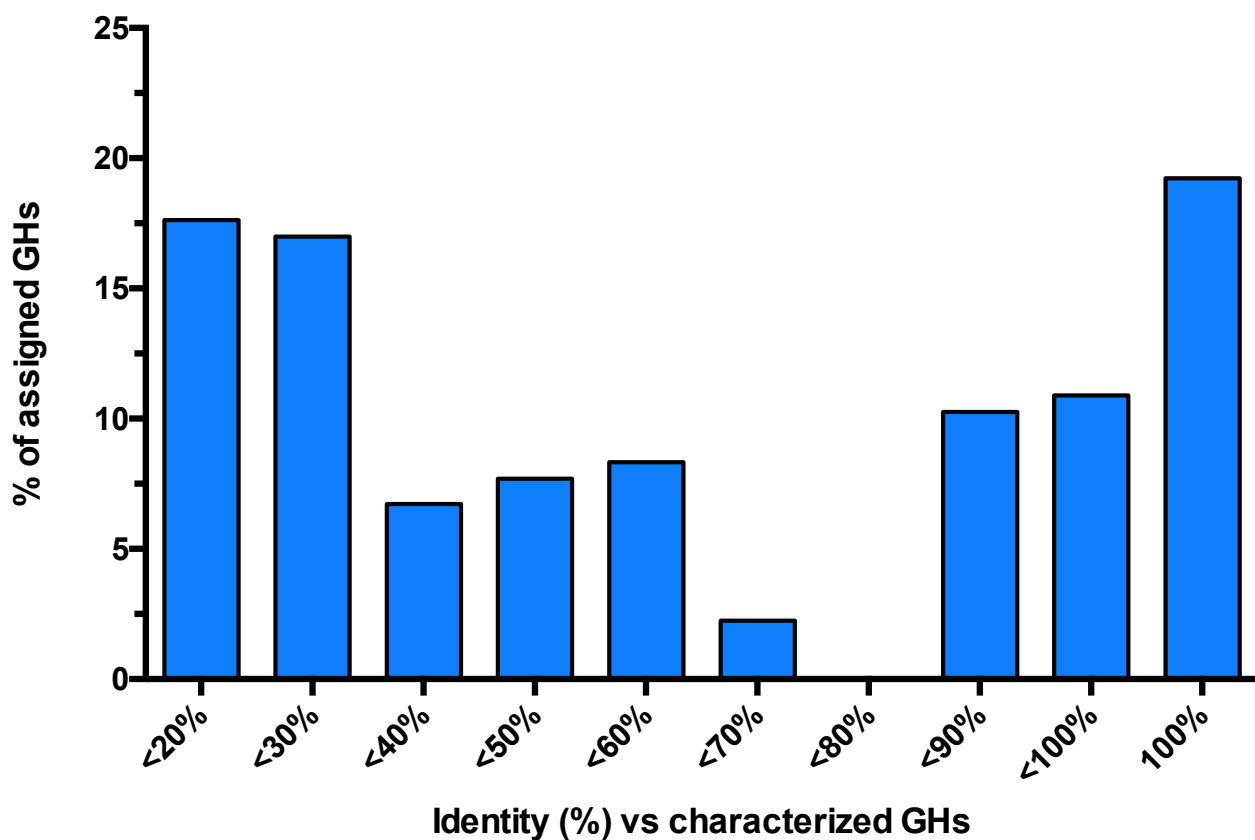


Figure S10. Percentage of the assigned GHs in the samples against the GHs characterized from www.cazy.org