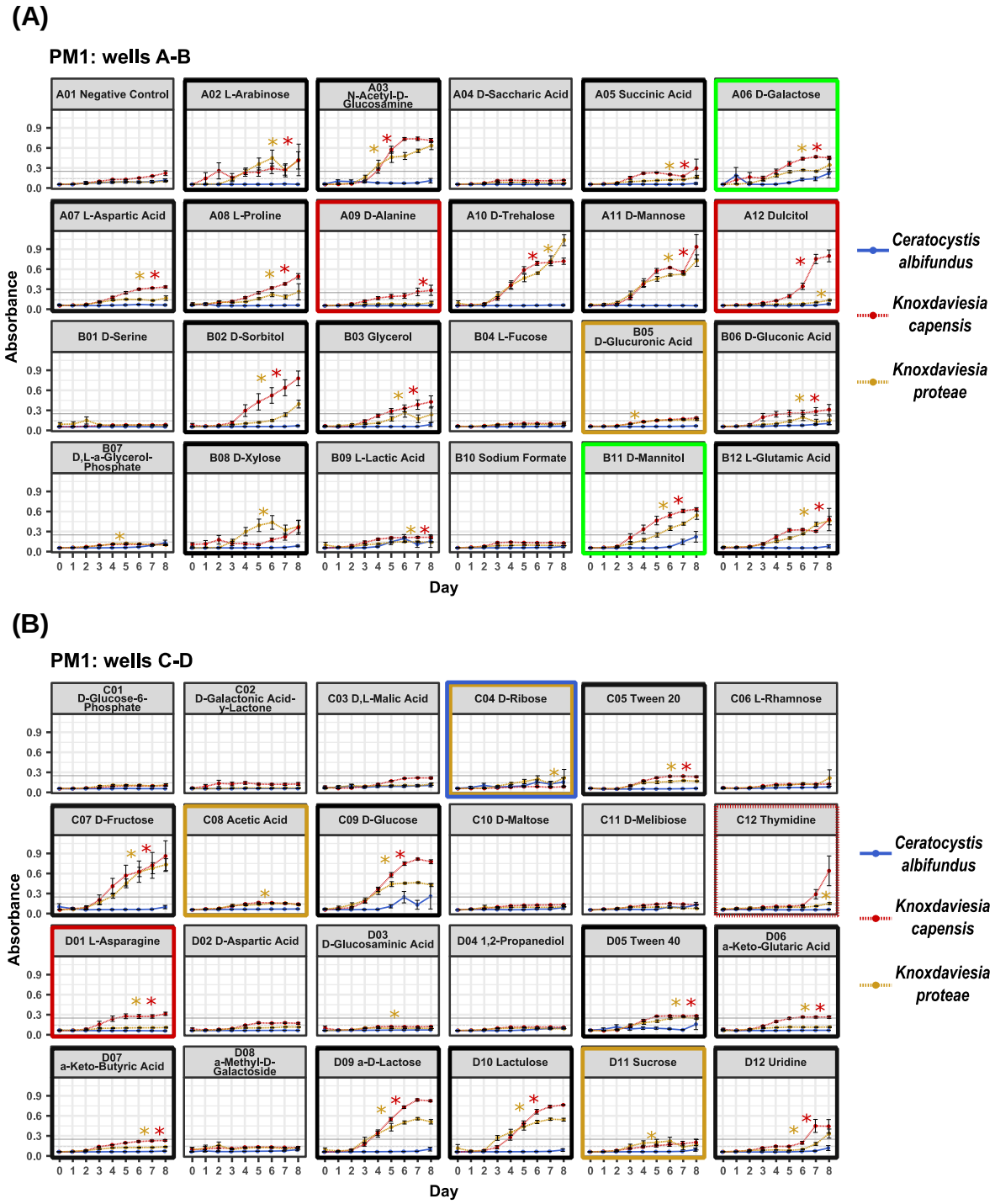
Supplementary File 4: Aylward *et al.* Contrasting carbon metabolism in saprotrophic and pathogenic Microascalean fungi from *Protea* trees

Figure S1. Growth curves of *Knoxdaviesia capensis*, *K. proteae* and *C. albifundus* on all PM1 substrates. The 96 well plate is shown in four separate blocks for clarity: (A) wells A-B, (B) wells C-D, (C) wells E-F, (D) wells G-H.



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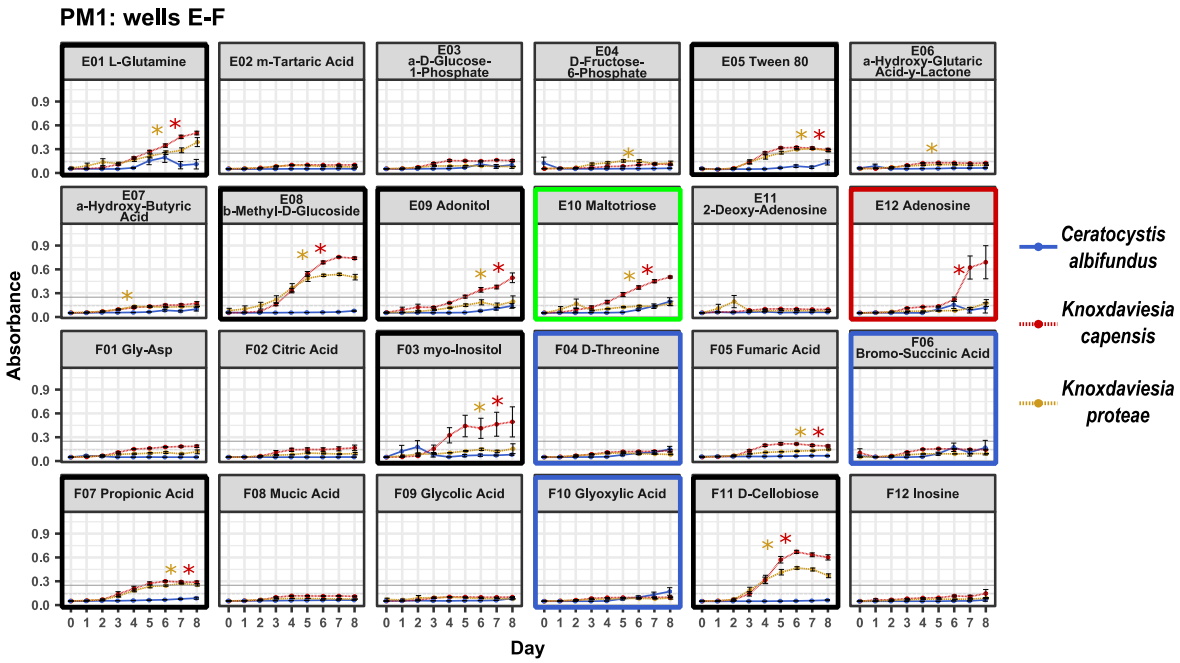
(C)



(D)

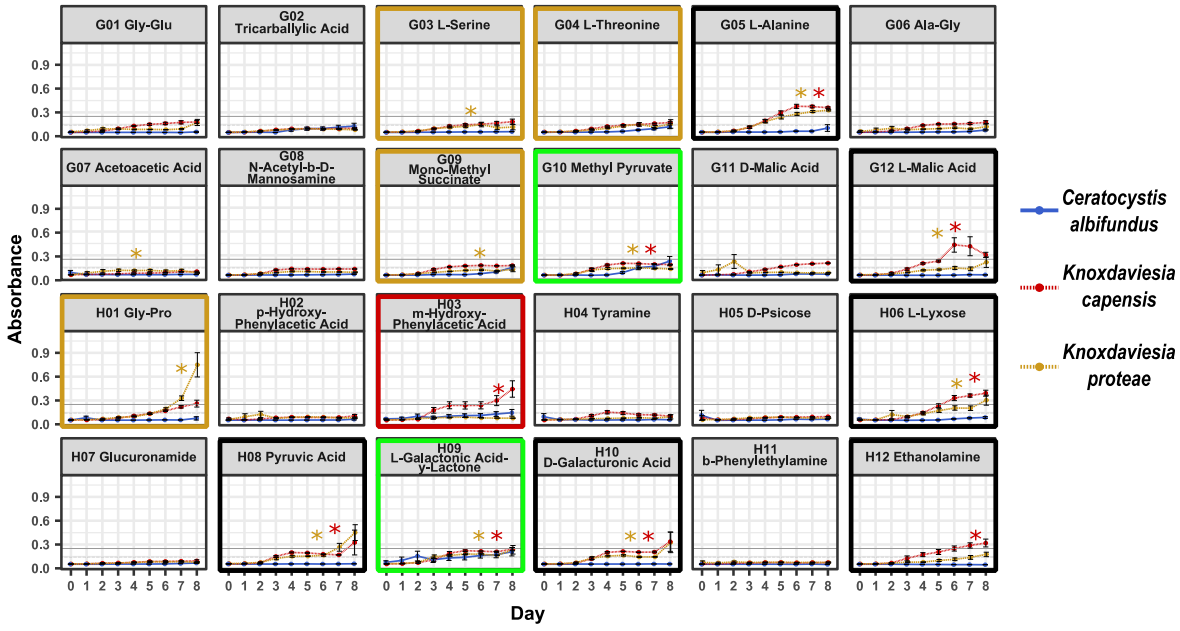


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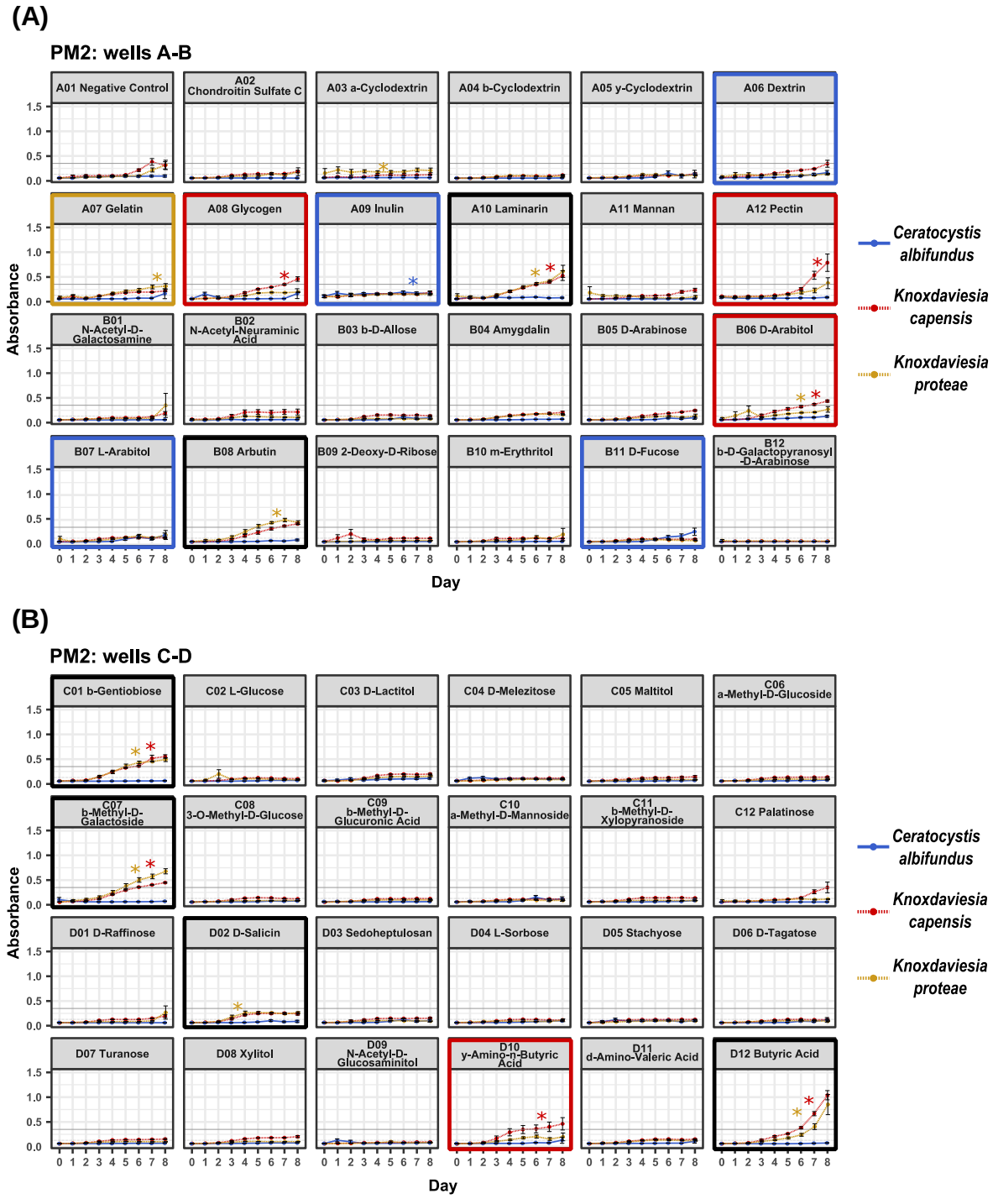
Figure S2. Growth curves of *Knoxdaviesia capensis*, *K. proteae* and *C. albifundus* on all PM2 substrates. The 96 well plate is shown in four separate blocks for clarity: (A) wells A-B, (B) wells C-D, (C) wells E-F, (D) wells G-H.



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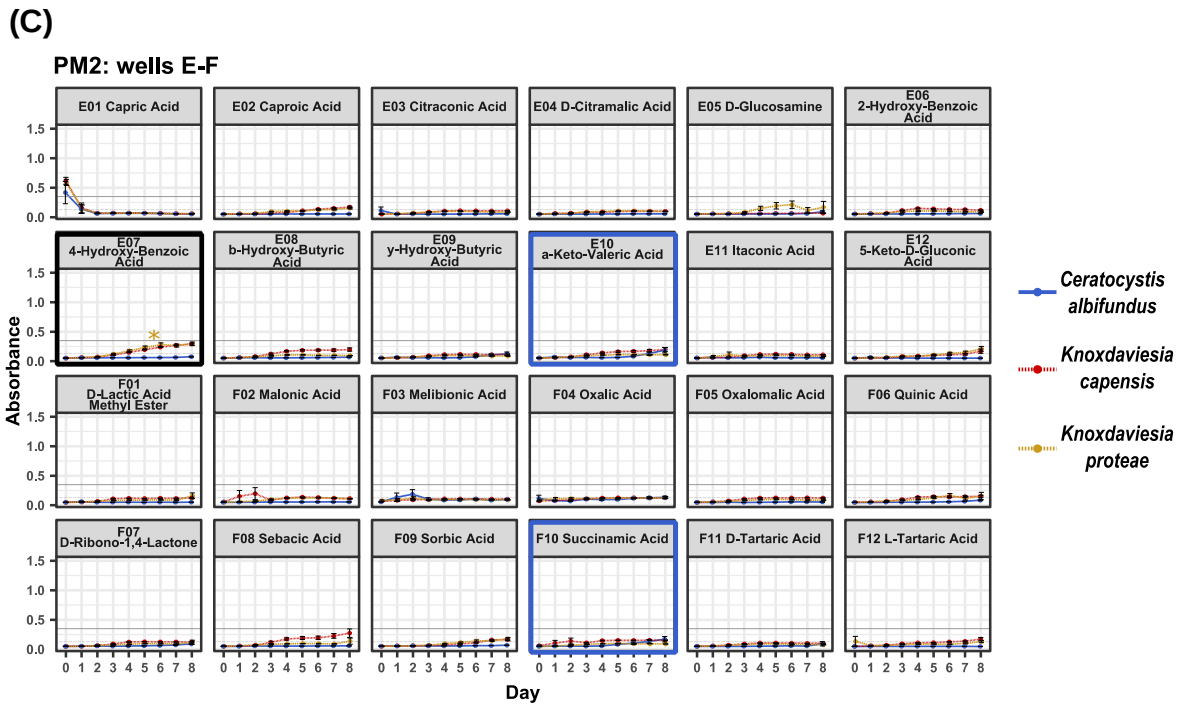

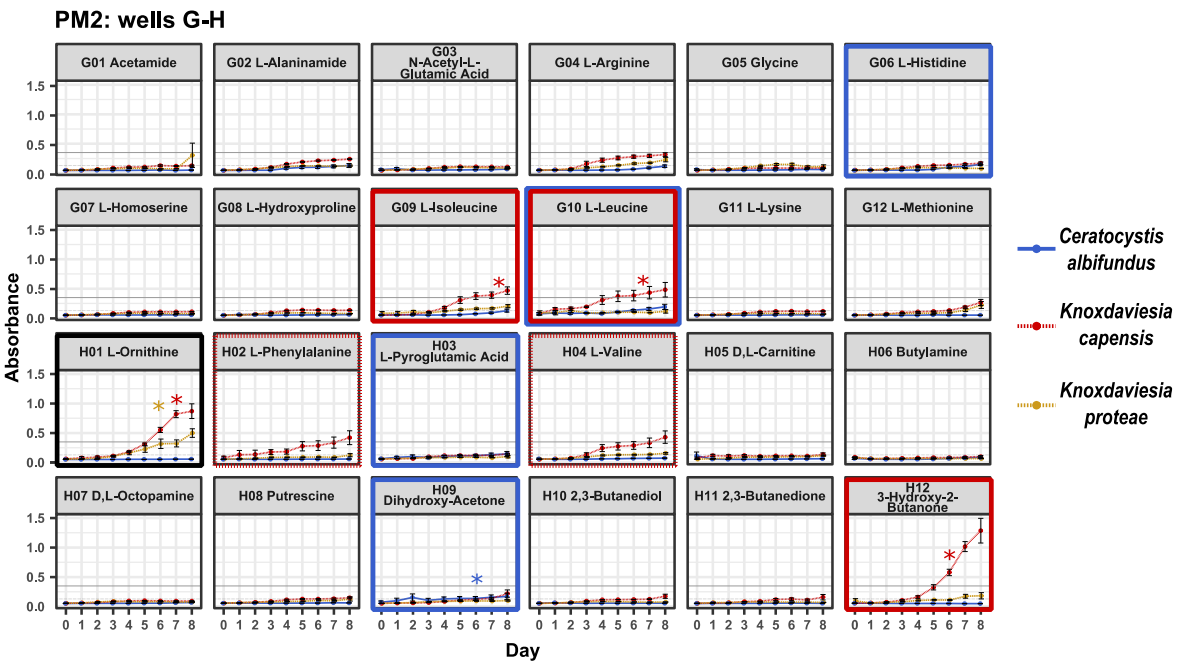

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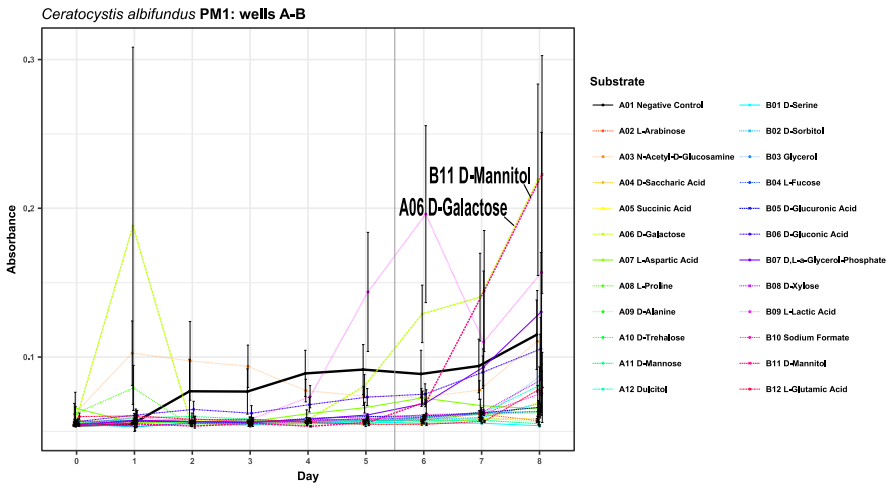
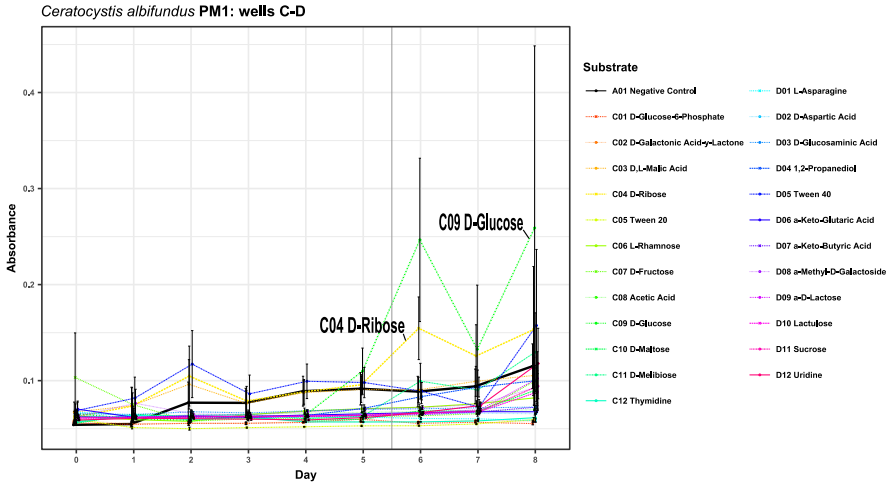
Figure S3. *Ceratocystis albifundus* growth curves for all PM1 (A-D) and PM2 (E-H) substrates. The thick black curve is the negative control. The names of active and ambiguous substrates are indicated on the plot.

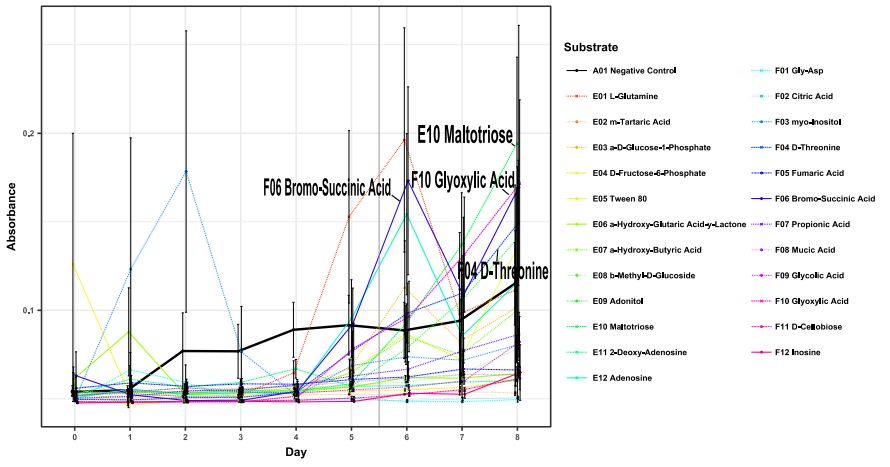
(A)



(B)



(C)



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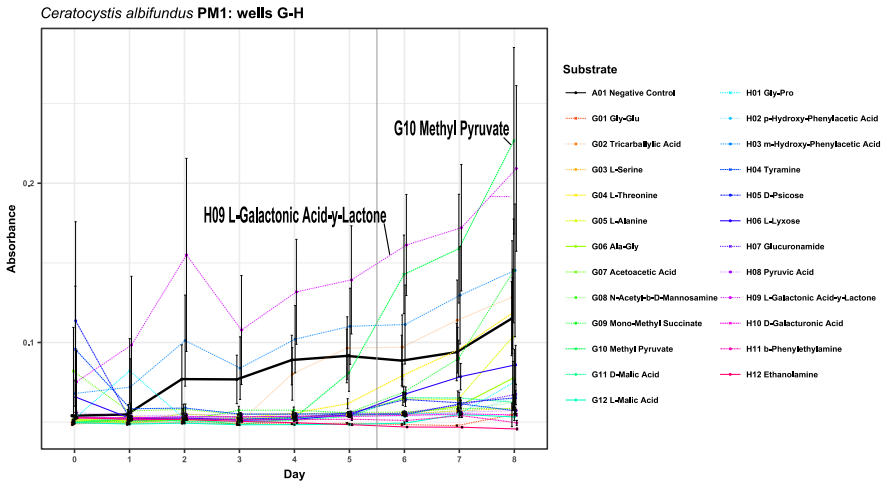
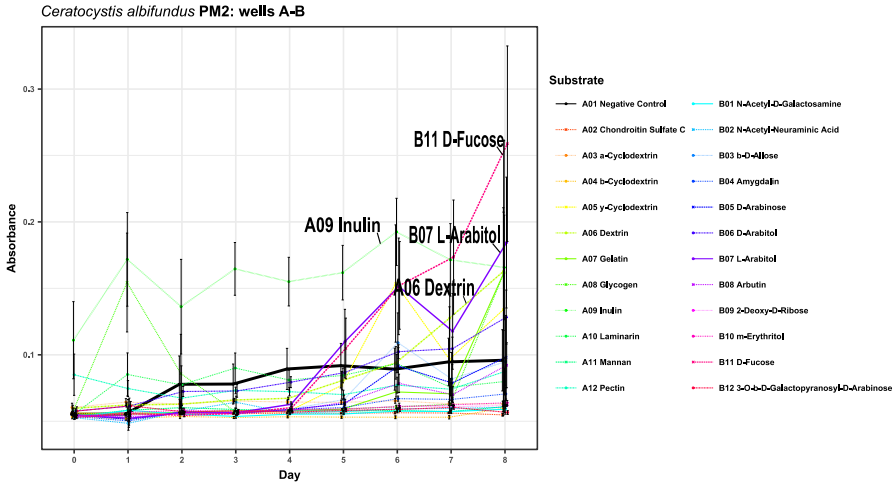
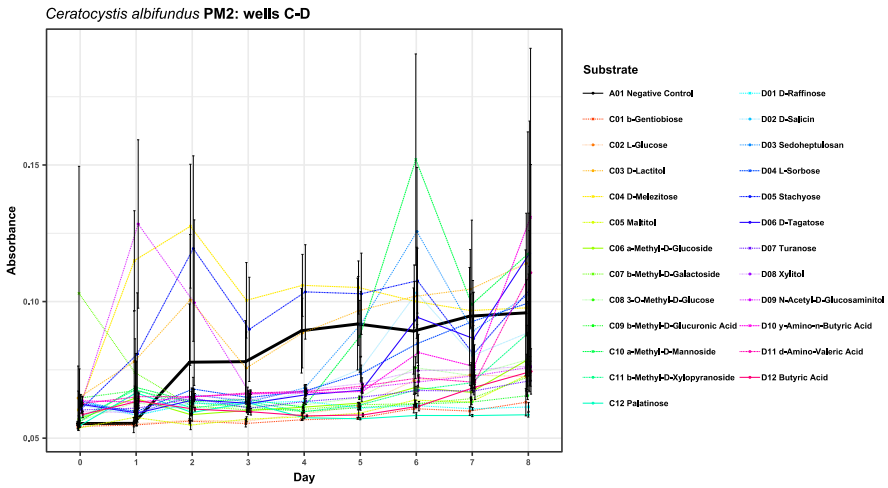
(D)



(E)



(F)



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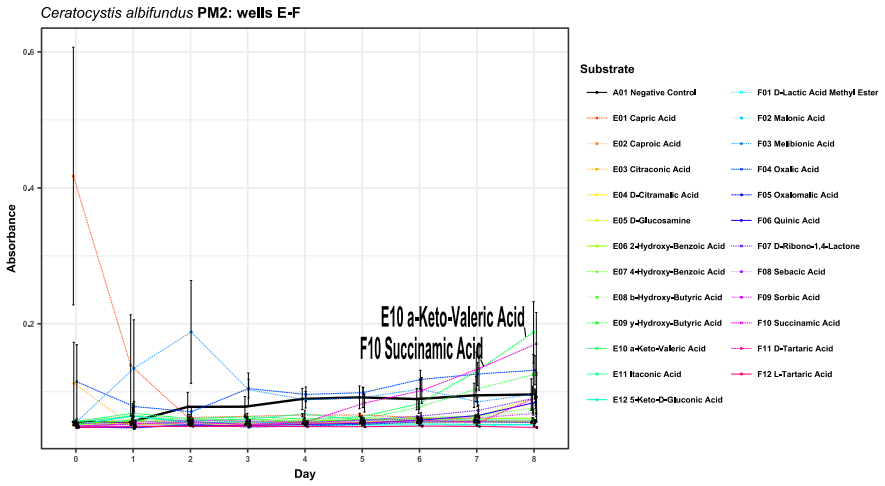
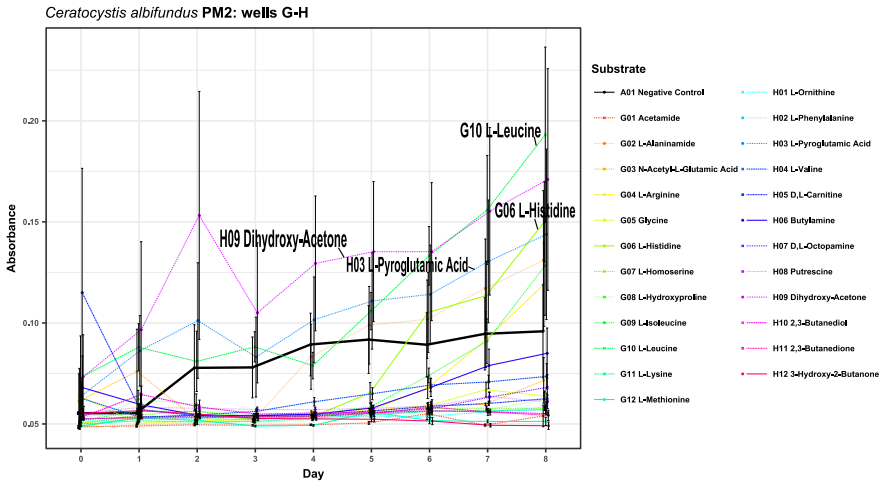
(G)



(H)



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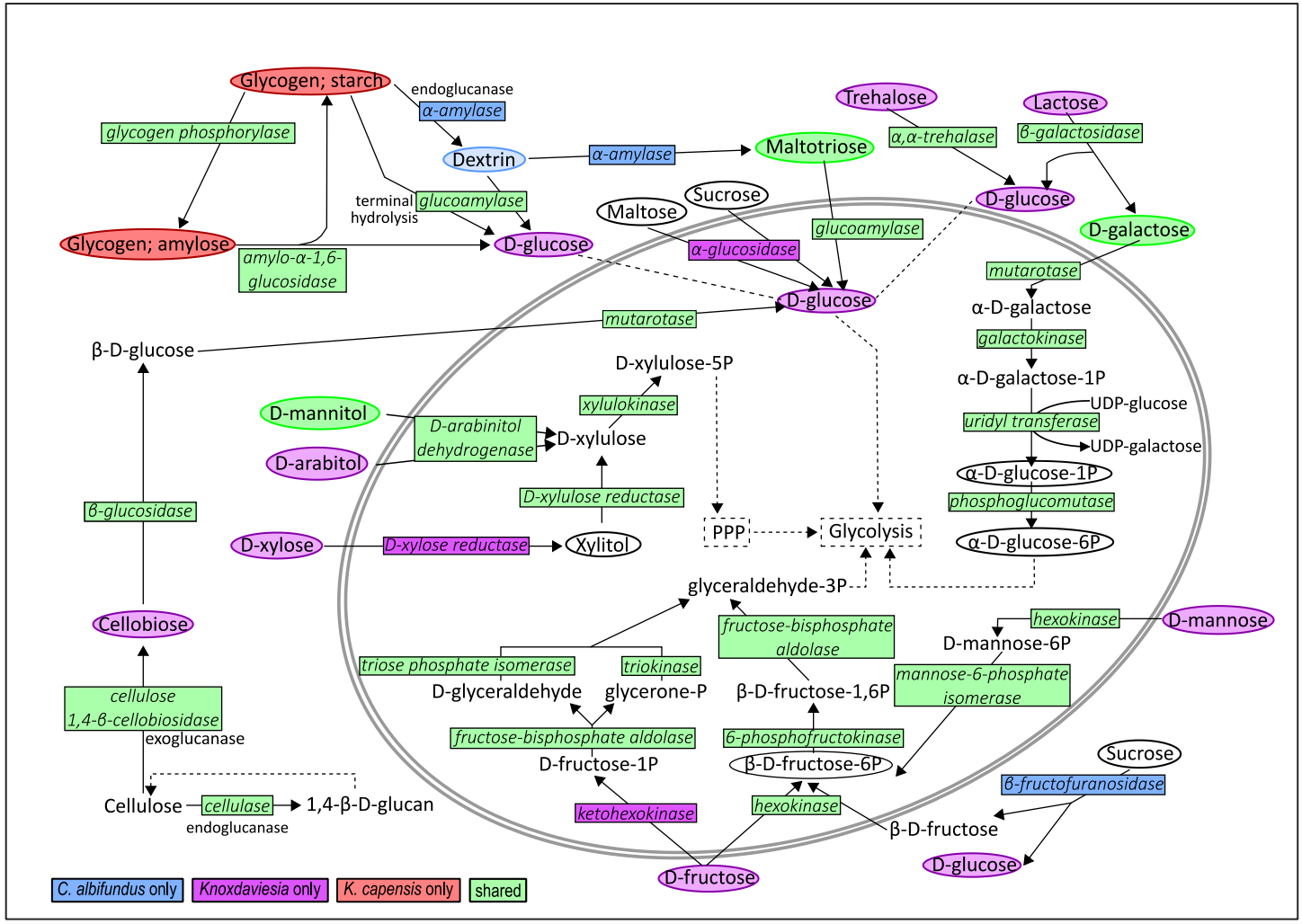

Figure S4. Carbohydrate utilization pathways in *Knoxdaviesia capensis*, *K. proteae* and *Ceratocystis albifundus*. Substrates tested in the PM assays are circled and coloured according to usage: used by all (green), used by none (white), used by both *Knoxdaviesia* species (purple), used by *K. capensis*

only (red) and used by *C. albifundus* only (blue). The same colouring scheme applies to the presence of enzymes (boxed). The grey double-lined oval represents the fungal cell.

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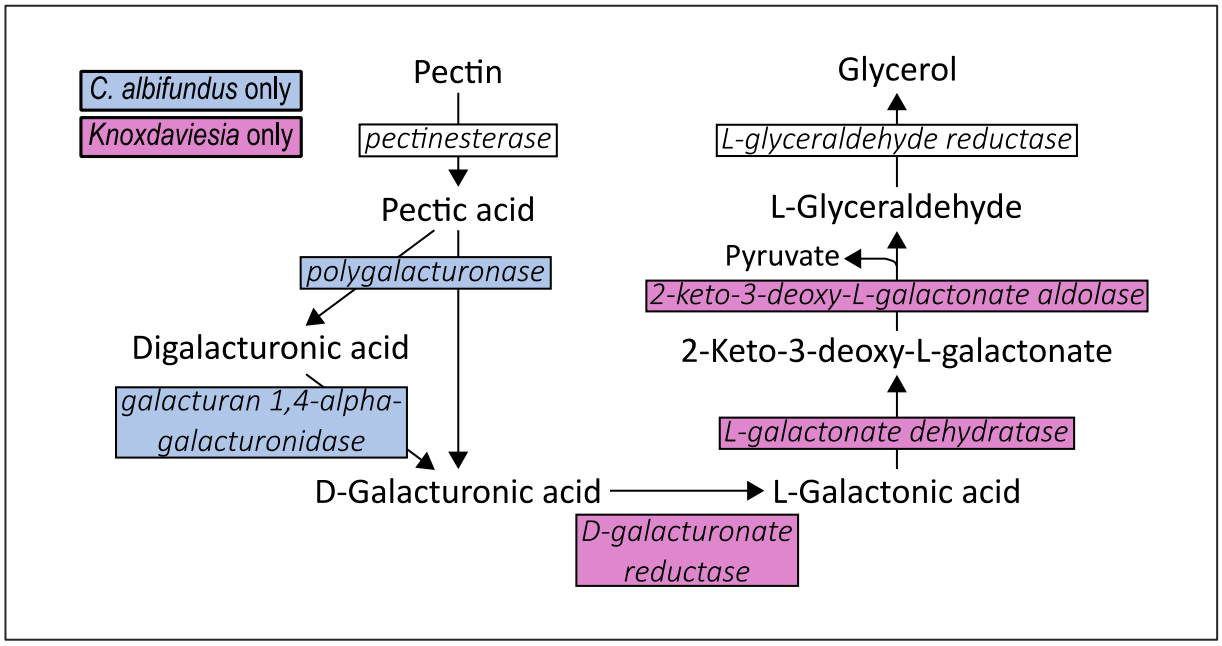

Figure S5. Predicted enzymes associated with pectin backbone (homogalacturonan) degradation in *Ceratocystis albifundus* and *Knoxdaviesia*. None of the species are apparently able to complete the pathway.