

Additional file 8: All reverse-transcription qPCR and growth tests of *S. bryantii* TF1-3 grown in mixtures of two polysaccharides that are presented in a heatmap (Fig. 4). Left graphs show relative normalized expression of *susC*-like genes of designated PULs over time relative to quantity of transcripts on glucose (time 0) in the mixture of two polysaccharides present in equal concentrations (0.15% each). Values are written at the bottom of each bar. The expression of *susC*-like genes was measured with qPCR. Right graphs show growth of *S. bryantii* TF1-3 in each of the two polysaccharides (0.15%) and in the mixture of both (0.3% - each 0.15%). Data are averages and standard errors of two biological replicates. Substrates used: starch, galactomannan (GalM), glucomannan (GlcM), xyloglucan (XG), beechwood xylan (BX), arabinoxylan (AX), arabinan (ARA).







