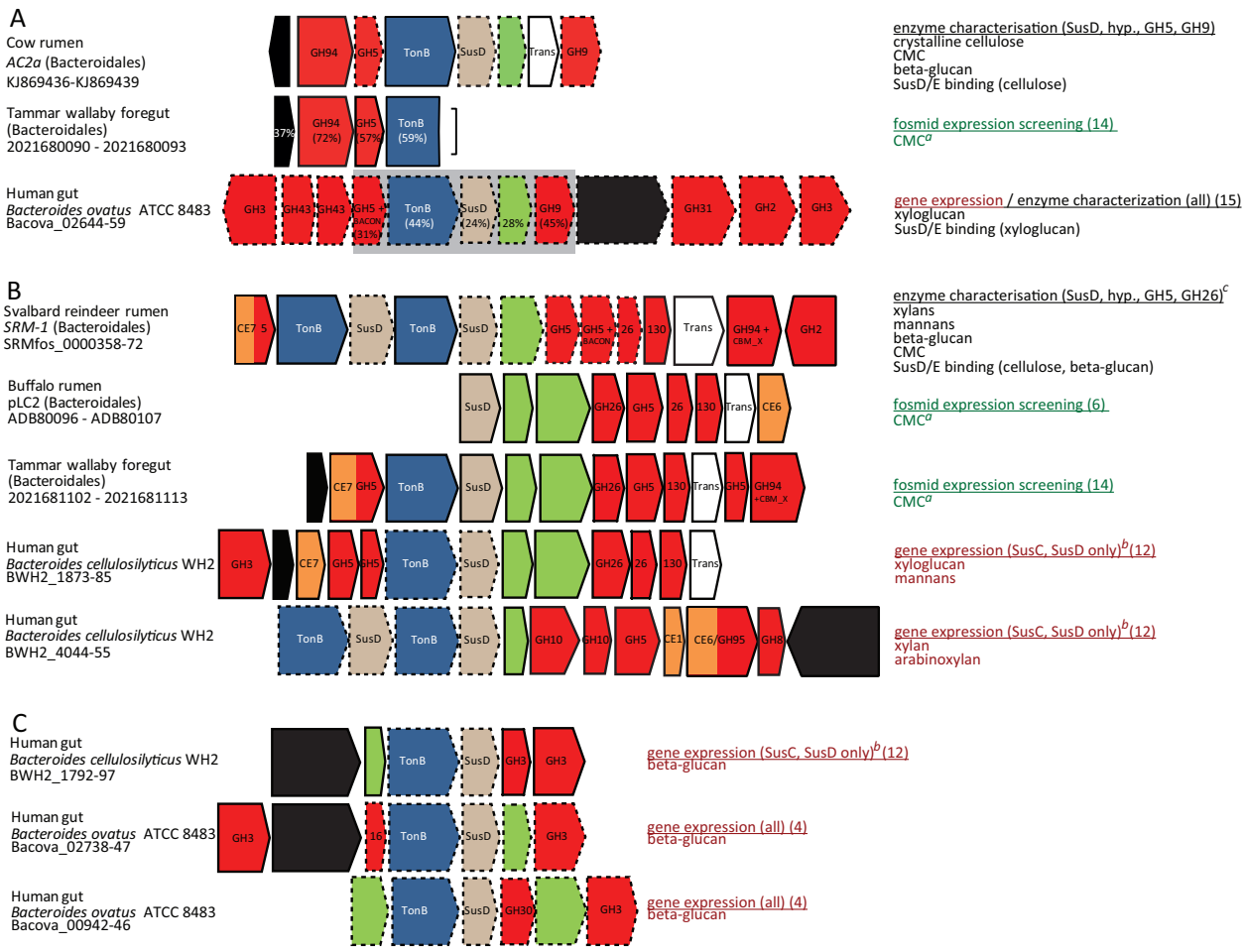

Fig. S1. Identification of partially homologous/syntenic PULs encoding GH5 and/or GH9 representatives. Genomic comparisons of the *AC2a* PUL were made with publicly-available metagenomes, Bacteroidetes genomes and previously characterised PULs that encode either a GH5 or GH9 representative. **a.** Sequence homology and synteny was observed with a partial metagenomic fragment (bracket indicates fosmid terminus) derived from the Tammar wallaby foregut and the "core" region (indicated by grey box) of a xyloglucan PUL from a human gut bacterium. Sequence identity is indicated as a percentage in parentheses. **b.** PULs that encode GH5 and/or GH9 representatives; these PULs all act on hemicellulose and there is no synteny. **c.** Example of previously characterised barley beta-glucan PULs (gene expression) which have been shown to encode a GH3 (β-(1-3)-glucosidase) or a GH16 (β-(1,3)-glucanase) and no GH5 and/or GH9 representatives. Text boxes to the left indicate the source of the PUL and the gene locus/accession number. Text boxes to the right provide a characterisation summary, including a listing of substrates for which activity has been demonstrated or inferred: black print, biochemical characterisation; red print, inferred from gene expression only; green print, fosmid screening. Green ORFs indicate SusE/F-positioned and other hypothetical proteins. Black ORFs indicate putative transcriptional regulators. "Trans" indicates an inner membrane sugar transporter. Dashed lines indicate genes the products of which have been characterized. References from main text are indicated in parentheses.

[a] only CMC hydrolysis tested.

[b] only SusC and SusD gene expression analysed.

[c] A.K. Mackenzie, A.E. Naas, J. Mravec, S. Kracun, J. Schückel, J. Fangel, J.W. Agger, W.G.T. Willats, V.G.H. Eijsink and P.B. Pope, submitted for publication, 2014.