Wheat cell walls and constituent polysaccharides induce similar microbiota profiles upon *in vitro* fermentation despite different short chain fatty acid end-product levels.

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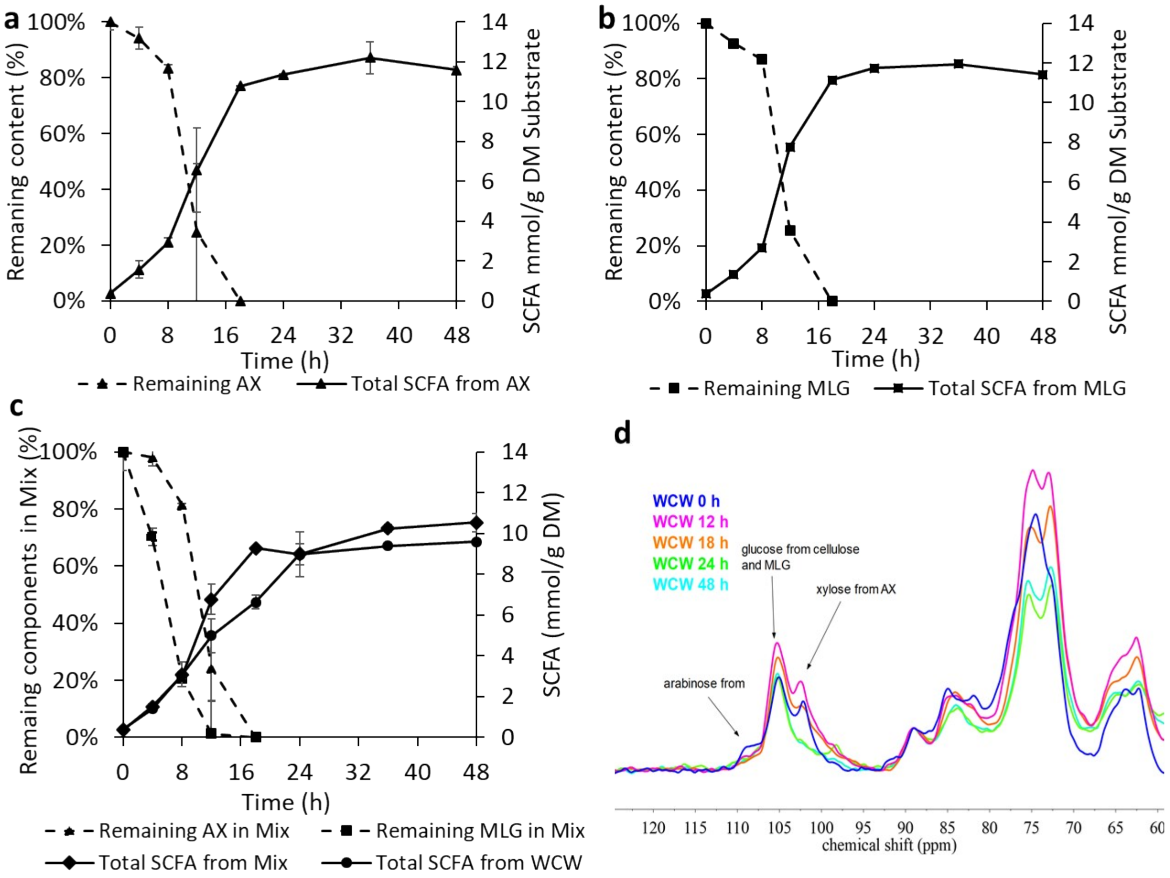
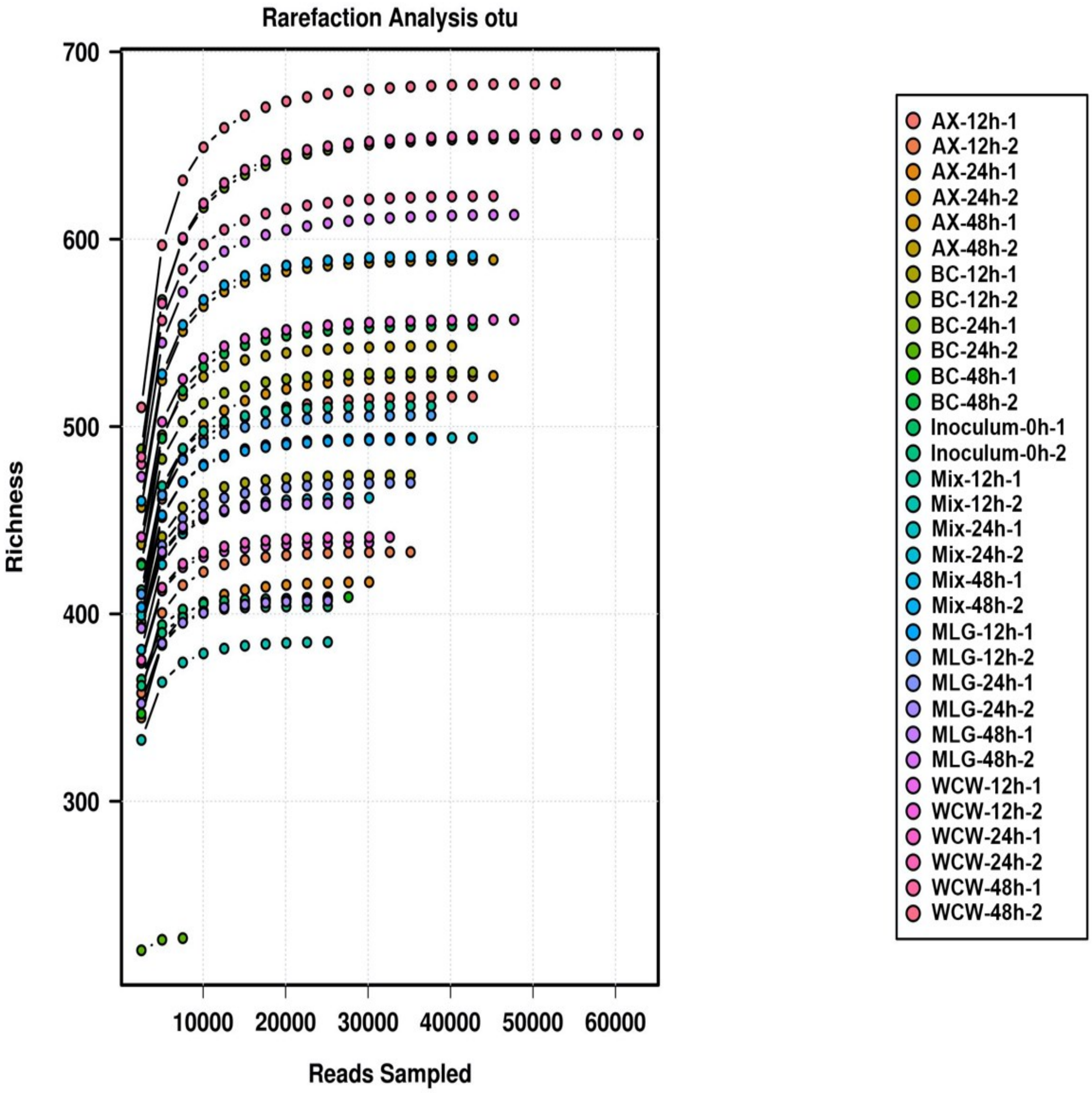
Supplementary Materials



S1. Chemical analyses for AX, MLG, Mix and WCW degradation and SCFA production a. The time course of AX degradation and total SCFA production **b**. The time course of MLG degradation and total SCFA production **c.** The time course of AX/MLG component degradation in Mix and total SCFA production of Mix and WCW **d.** CP/ MAS ^{13}C solid state NMR spectra for WCW rigid components over the fermentation time course [25].



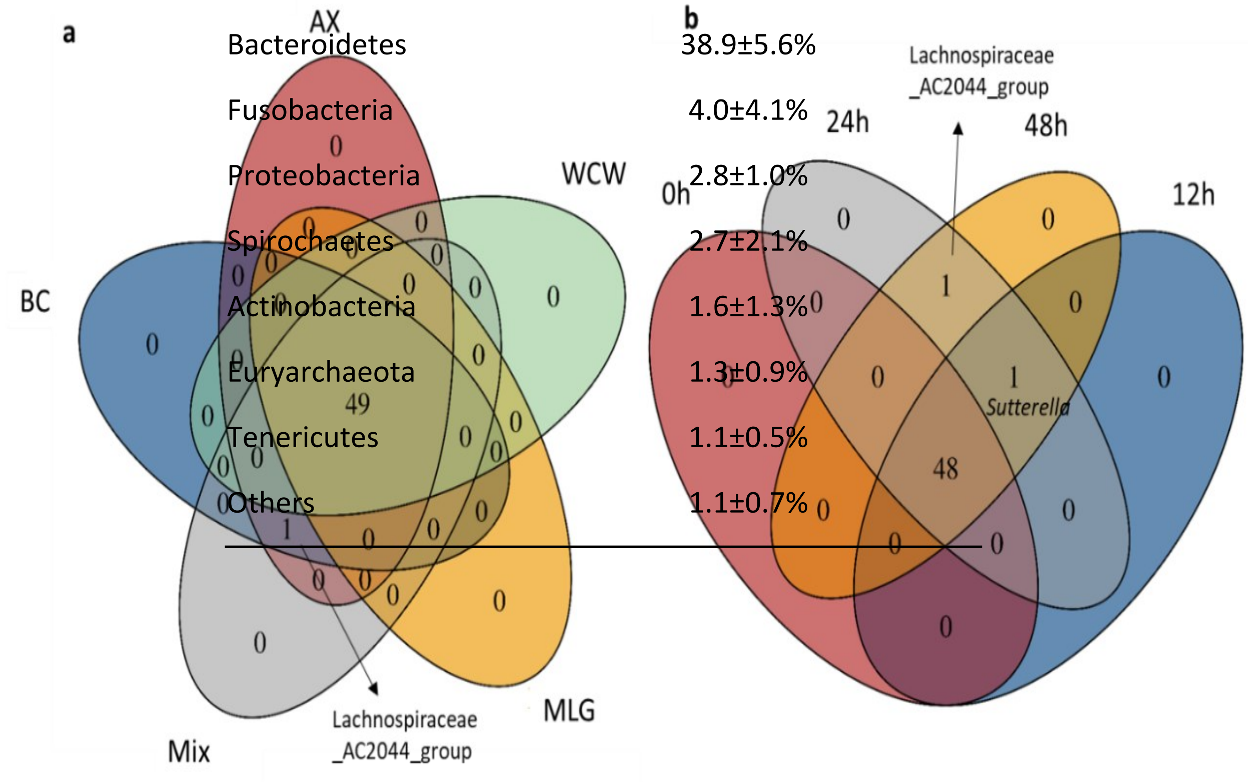
S2. A rarefaction plot for samples for 16S rRNA sequencing (n=32)

S3. Alpha diversity analysis for substrates at each time point

Samples	Richness	Evenness	Shannon Index	Simpson's Index	Chao1
Inoculum_0h	403	0.903	5.42	0.992	406
AX-12h	456	0.821	5.06	0.979	475
AX-24h	451	0.818	5.03	0.980	472
AX-48h	542	0.875	5.55	0.991	566
BC-12h	486	0.844	5.25	0.977	502
BC-24h	419	0.878	5.22	0.986	441
BC-48h	464	0.850	5.24	0.987	482
Mix-12h	436	0.853	5.20	0.984	448
Mix-24h	463	0.849	5.24	0.985	478
Mix-48h	507	0.890	5.57	0.993	525
MLG-12h	483	0.846	5.26	0.983	500
MLG-24h	428	0.853	5.19	0.982	439

MLG-48h	516	0.878	5.51	0.991	536
WCW-12h	481	0.854	5.30	0.985	498
WCW-24h	522	0.851	5.35	0.986	549
WCW-48h	619	0.881	5.71	0.993	653

S4. Proportion of each phyla across all substrates	
Firmicutes	46.4±5.0%
Bacteroidetes	38.9±5.6%
Fusobacteria	4.0±4.1%
Proteobacteria	2.8±1.0%
Spirochaetes	2.7±2.1%
Actinobacteria	1.6±1.3%
Euryarchaeota	1.3±0.9%
Tenericutes	1.1±0.5%
Others	1.1±0.7%

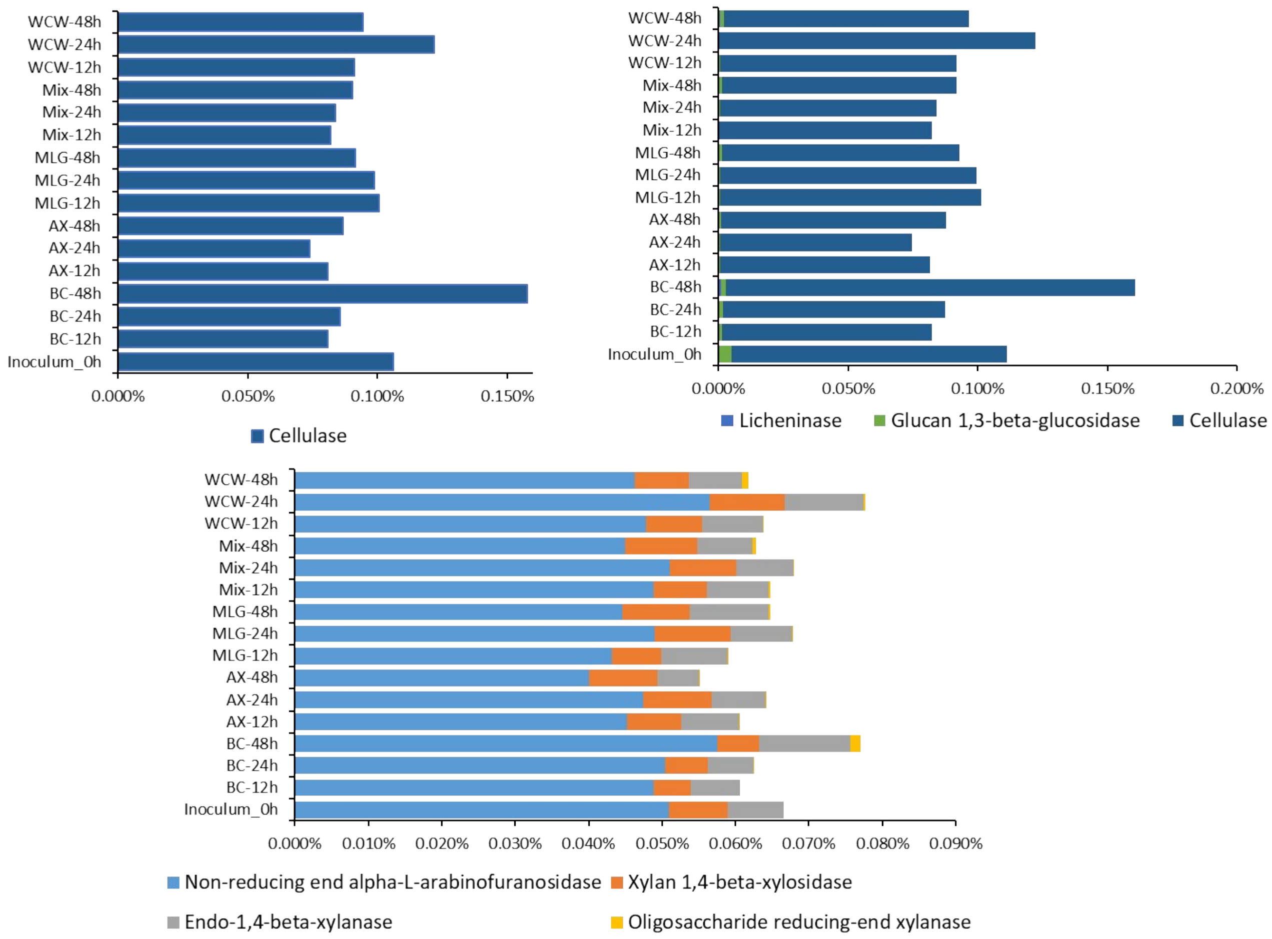


S5. Core microbiome analysis for the top 50 dominant genera a. Abundances grouped by substrates **b**. Abundances grouped by fermentation time. A genus is marked as present in the core, pan and unique groups if it was identified in at least 40% of the samples within the group.

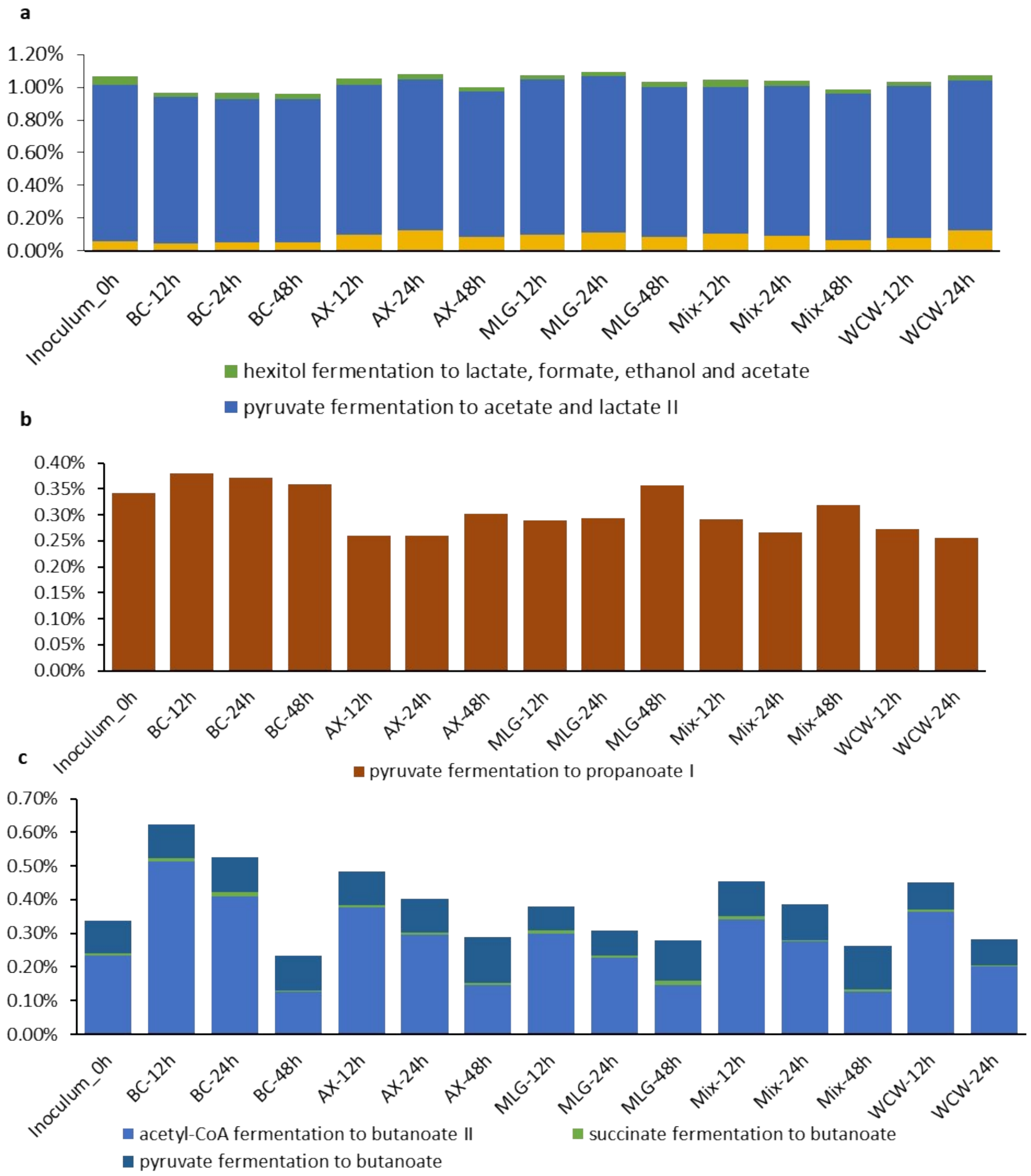
S6. SCFA production for each substrate [25]

Removal Time	0h			12h			24h			48h		
Substrate	**Ac**	**Pr**	**Bu**	**Ac**	**Pr**	**Bu**	**Ac**	**Pr**	**Bu**	**Ac**	**Pr**	**Bu**
AX	0.23^{a}	0.15^{a}	0.00^{a}	3.82^{ab}	1.94^{a}	0.35^{ab}	6.17^{a}	4.26^{a}	0.47^{a}	6.24^{a}	4.16^{a}	0.62^{a}
MLG	0.22^{a}	0.15^{a}	0.00^{a}	4.38^{a}	2.44^{a}	0.55^{ab}	6.55^{b}	3.86^{b}	0.82^{b}	6.24^{a}	3.79^{b}	0.84^{b}
Mix	0.22^{a}	0.14^{a}	0.00^{a}	4.01^{a}	1.92^{a}	0.40^{ab}	5.03^{abc}	2.98^{c}	0.48^{acd}	5.91^{ab}	3.36^{b}	0.65^{a}
WCW	0.25^{a}	0.14^{a}	0.00^{a}	2.88^{ab}	1.35^{a}	0.34^{ab}	5.05^{ab}	2.73^{c}	0.62^{c}	5.31^{b}	2.89^{c}	0.78^{bc}
BC	0.28^{a}	0.13^{a}	0.00^{a}	1.89^{b}	0.62^{a}	0.33^{b}	1.95^{d}	0.71^{d}	0.37^{d}	2.55^{d}	0.89^{e}	0.43^{d}

*Ac represents acetate; Pr represents propionate; Bu represents butyrate; Letters in the same column show significant differences ($P<0.05$).



S7. Comparison of predicted enzyme genes for degrading different polysaccharides in each substrate generated from PICRUSt2 a. Predicted enzyme genes for degrading cellulose **b.** Predicted enzyme genes for degrading MLG **c.** Predicted enzyme genes for degrading AX. Means of relative abundances are shown in the bar chart; only enzymes identified in PICRUSt2 were included.



S8. Comparison in predicted pathway genes for SCFA production generated from PICRUSt2 a. Predicted pathway genes for acetate production **b.** Predicted pathway genes for propionate production **c.** Predicted pathway genes for butyrate production *Means of relative abundances were shown in the bar chart; only pathways identified in PICRUSt2 were included.