

Supplementary Tables

Table S1 Number of reads identified by GraftM per substrate × time × inoculum

		Time	Bacteria	Archaea	Unclassified	
Porcine 1	Inoculum	0 h	10620	27	4	
		4 h	18513	170	2	
	WAX	8 h	19753	387	1	
		48 h	13481	274	4	
		4 h	24281	156	1	
	RAX	8 h	18327	241	3	
		48 h	15084	247	1	
		Inoculum	0 h	8896	27	0
	Porcine 2	WAX	12 h	26361	56	0
18 h			35810	44	0	
72 h			27935	39	0	
GXG		12 h	30817	97	0	
		18 h	41442	74	0	
		72 h	23458	37	1	
Human		Inoculum	0 h	29874	22	0
			4 h	36708	9	0
		WAX	8 h	33692	7	0
	48 h		33749	28	1	
	GXG	7 h	29845	3	0	
		11 h	23606	4	0	
		48 h	28414	29	1	

The numbers of Porcine 1 were the sum of two fermentation replicates, and those of Porcine 2 were the sum of three fermentation replicates. The numbers of 16s rRNA sequence in Human samples were identified from the metagenomics shotgun sequencing of pooled DNA from the three fermentation replicates.

Table S2 Relative abundance of major phyla detected in the porcine and human fecal inoculum.

Phylum	H_Inoc	P1_Inoc	P2_Inoc
Firmicutes	74.197%	35.884%	40.939%
Melainabacteria	0.003%	25.650%	16.205%
Bacteroidetes	15.450%	5.126%	10.546%
Actinobacteria	8.627%	7.915%	8.730%
Proteobacteria	1.254%	4.647%	8.237%
Tenericutes	0.107%	5.164%	6.085%
Euryarchaeota	0.074%	0.244%	0.224%
Chloroflexi	0.003%	0.141%	0.370%
Verrucomicrobia	0.224%	0.113%	0.000%
TM7	0.003%	0.028%	0.303%
Parvarchaeota	0.000%	0.009%	0.078%
WPS-2	0.000%	0.009%	0.034%
Acidobacteria	0.003%	0.009%	0.011%
Spirochaetes	0.000%	0.000%	0.022%
Elusimicrobia	0.000%	0.009%	0.011%
Others	0.054%	15.013%	8.204%

Those phyla with < 0.01% relative abundance across all the inocula were assigned to “Others”.

Table S3 Results of the core microbiome analysis of the major OTUs as grouped by each fermentation experiment (P1: Porcine 1; P2: Porcine 2; H: Human)

Taxa	Type	Details	H.abu	P1.abu	P2.abu	H.occ	P1.occ	P2.occ
<i>g__Blautia</i>	unique	H	7.629	0	0.003	1	0	0.29
<i>g__Bacteroides</i>	unique	H	7.124	0	0	1	0	0
<i>f__Ruminococcaceae</i>	unique	H	5.927	0.003	0	1	0.29	0
<i>Faecalibacterium prausnitzii</i>	unique	H	5.109	0	0	1	0	0
<i>Bacteroides plebeius</i>	unique	H	3.571	0	0	1	0	0
<i>Parabacteroides distasonis</i>	unique	H	1.604	0	0	1	0	0
<i>Bifidobacterium adolescentis</i>	pan	H&P1	1.229	0.014	0.004	1	0.86	0.29
<i>Prevotella copri</i>	core	H&P1&P2	0.094	20.126	25.759	1	1	1
<i>f__Lachnospiraceae</i>	core	H&P1&P2	30.89	0.01	0.016	1	0.57	0.71
<i>k__Bacteria</i>	core	H&P1&P2	0.043	6.857	5.93	1	1	1
<i>o__Clostridiales</i>	core	H&P1&P2	9.967	0.133	0.184	1	1	1
<i>Blautia obeum</i>	core	H&P1&P2	0.176	3.5	4.506	1	1	1
<i>Eubacterium dolichum</i>	core	H&P1&P2	0.006	3.189	3.87	0.43	1	1
<i>g__Bifidobacterium</i>	core	H&P1&P2	3.54	0.649	1.919	1	1	1
<i>g__Ruminococcus</i>	core	H&P1&P2	1.863	0.017	0.164	1	0.71	1
<i>g__Adlercreutzia</i>	core	H&P1&P2	0.06	0.634	1.294	1	1	1
<i>f__EB1017</i>	core	H&P1&P2	0.01	0.421	1.42	0.57	1	1
<i>g__Bilophila</i>	core	H&P1&P2	0.103	0.483	0.857	1	1	1
<i>Bacteroides uniformis</i>	pan	H&P2	1.913	0.001	0.004	1	0.14	0.43
<i>g__rc44</i>	pan	P1&P2	0	22.004	14.836	0	1	1
<i>o__YS2</i>	pan	P1&P2	0	12.896	11.934	0	1	1
<i>o__Bacteroidales</i>	pan	P1&P2	0	2.843	3.649	0	1	1
<i>f__Lachnospiraceae 2</i>	pan	P1&P2	0	3.514	2.323	0	1	1
<i>g__Brevibacillus</i>	pan	P1&P2	0	2.027	2.547	0	1	1
<i>g__Planomicrobium</i>	pan	P1&P2	0	2.021	1.976	0	1	1
<i>g__Bacteroides 2</i>	pan	P1&P2	0	1.877	1.793	0	1	1
<i>Rothia dentocariosa</i>	pan	P1&P2	0	1.299	1.431	0	1	1
<i>f__Aerococcaceae</i>	pan	P1&P2	0	1.533	1.164	0	1	1
<i>o__RF39</i>	pan	P1&P2	0	1.073	1.471	0	1	1
<i>g__p75a5</i>	pan	P1&P2	0	1.441	0.801	0	1	1
<i>g__Faecalibacterium</i>	pan	P1&P2	0.001	0.789	0.83	0.14	1	1
<i>Clostridium intestinale</i>	pan	P1&P2	0	0.456	0.074	0	1	1

OTUs < 2% across all the samples were not included. A bacterial group is marked as present in a sample group if it was identified in at least 40% (relation = 0.40) of the samples within the group.

Table S4 Results of the core microbiome analysis of the major OTUs as grouped by the substrates (RAX: rye arabinoxylan; WAX: wheat arabinoxylan; GXG: galactoxyloglucan) and inoculum (Inoc).

Taxa	Type	Details	Inoc.abu	RAX.abu	WAX.abu	GXG.abu	Inoc.occ	RAX.occ	WAX.occ	GXG.occ
<i>Prevotella copri</i>	core	Inoc&RAX&WAX&GXG	0.563	22.293	19.783	12.538	1	1	1	1
g__rc44	core	Inoc&RAX&WAX&GXG	2.31	24.54	13.166	9.807	0.67	1	0.67	0.5
o__YS2	core	Inoc&RAX&WAX&GXG	13.7	10.553	7.301	5.89	0.67	1	0.67	0.5
k__Bacteria	core	Inoc&RAX&WAX&GXG	7.707	5.447	3.628	2.95	1	1	1	1
o__Clostridiales	core	Inoc&RAX&WAX&GXG	3.523	0.137	3.061	5.577	1	1	1	1
<i>Blautia obeum</i>	core	Inoc&RAX&WAX&GXG	5.34	3.803	2.249	1.6	1	1	1	1
<i>Eubacterium dolichum</i>	core	Inoc&RAX&WAX&GXG	2.77	3.807	2.144	1.737	1	1	0.67	0.83
o__Bacteroidales	core	Inoc&RAX&WAX&GXG	3.487	2.857	1.891	1.565	0.67	1	0.67	0.5
g__Bifidobacterium	core	Inoc&RAX&WAX&GXG	2.61	0.487	2.024	2.54	1	1	1	1
f__Lachnospiraceae 2	core	Inoc&RAX&WAX&GXG	1.437	3.523	2.081	1.208	0.67	1	0.67	0.5
g__Brevibacillus	core	Inoc&RAX&WAX&GXG	1.17	2.48	1.476	1.298	0.67	1	0.67	0.5
g__Planomicrobium	core	Inoc&RAX&WAX&GXG	1.787	1.633	1.297	1.008	0.67	1	0.67	0.5
g__Bacteroides 2	core	Inoc&RAX&WAX&GXG	0.453	2.773	1.239	0.81	0.67	1	0.67	0.5
<i>Rothia dentocariosa</i>	core	Inoc&RAX&WAX&GXG	0.913	1.403	0.811	0.81	0.67	1	0.67	0.5
Aerococaceae	core	Inoc&RAX&WAX&GXG	3.133	1.113	0.51	0.258	0.67	1	0.67	0.5
o__RF39	core	Inoc&RAX&WAX&GXG	3.73	0.35	0.391	0.342	0.67	1	0.67	0.5
g__p75a5	core	Inoc&RAX&WAX&GXG	2.167	1.053	0.454	0.325	0.67	1	0.67	0.5
g__Ruminococcus	core	Inoc&RAX&WAX&GXG	0.88	0.027	0.372	1.373	0.67	1	0.89	1
g__Adlercreutzia	core	Inoc&RAX&WAX&GXG	0.263	0.723	0.736	0.723	1	1	1	1
f__EB1017	core	Inoc&RAX&WAX&GXG	0.64	0.46	0.442	0.947	0.67	1	0.89	0.83
g__Faecalibacterium	core	Inoc&RAX&WAX&GXG	0.167	0.88	0.623	0.432	1	1	0.67	0.5
g__Bilophila	core	Inoc&RAX&WAX&GXG	1.02	0.453	0.4	0.347	1	1	1	1
<i>Bifidobacterium adolescentis</i>	core	Inoc&RAX&WAX&GXG	0.483	0.017	0.61	0.29	0.67	1	0.67	0.67
<i>Clostridium intestinale</i>	core	Inoc&RAX&WAX&GXG	0.827	0.167	0.067	0.022	0.67	1	0.67	0.5
f__Lachnospiraceae	pan	Inoc&WAX&GXG	6.573	0.003	10.103	17.625	1	0.33	0.78	0.83
<i>Bacteroides uniformis</i>	pan	Inoc&WAX&GXG	0.27	0	0.278	1.687	0.67	0	0.56	0.67
g__Blautia	pan	Inoc&GXG	2.18	0	3.416	2.69	0.67	0	0.33	0.67
f__Ruminococaceae	pan	WAX&GXG	3.003	0.003	1.74	2.805	0.33	0.33	0.44	0.5
g__Bacteroides	unique	GXG	2.16	0	2.032	4.183	0.33	0	0.33	0.5
<i>Faecalibacterium prausnitzii</i>	unique	GXG	3.227	0	1.511	2.08	0.33	0	0.33	0.5
<i>Bacteroides plebeius</i>	unique	GXG	1.09	0	1.791	0.935	0.33	0	0.33	0.5
<i>Parabacteroides distasonis</i>	unique	GXG	0.137	0	0.129	1.61	0.33	0	0.33	0.5

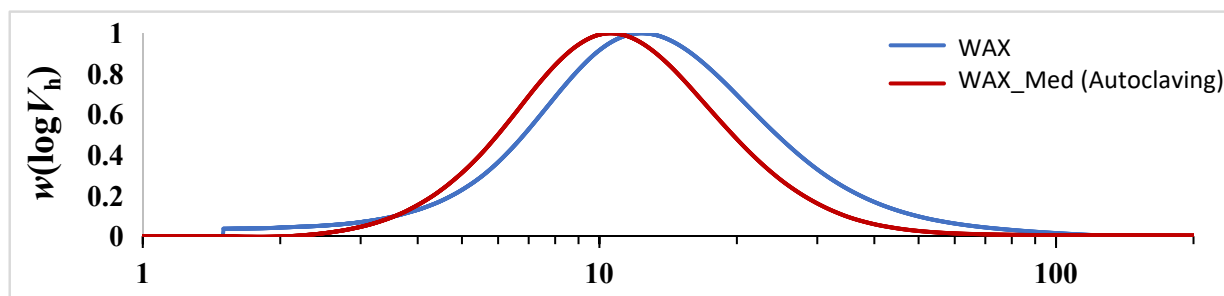
OTUs < 2% across all the samples were not included. A bacterial group is marked as present in a sample group if it was identified in at least 40% (relation = 0.40) of the samples within the group.

Supplementary Figures

a

Treatment	WAX			GXG	
	A/X ratio	Mono-Xyl	Di-Xyl	Un-Xyl	
WAX/GXG powder	0.45	0.15	0.14	0.70	Gal: Xyl: Glc 1:2.41:3.03
WAX/GXG_Med (Autoclaving)	0.47	0.17	0.15	0.68	1:2.34:2.54

b



c

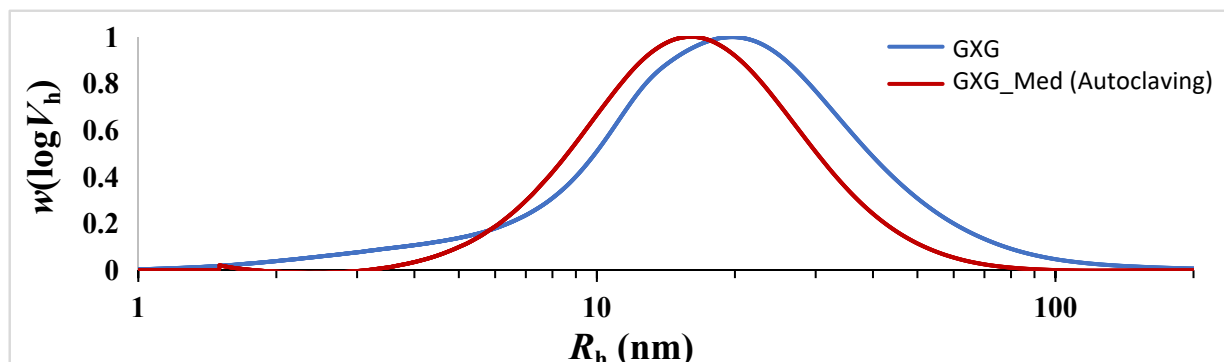


Figure S1 The effects of autoclaving on the structure of wheat arabinoxylan (WAX) and tamarind galactoxyloglucan (GXG). **(a)** ^1H NMR analysis of the WAX/GXG powder and WAX/GXG dissolved in the fermentation medium with autoclaving (WAX/GXG_Med (Autoclaving)). Molecular size distributions (as functions of the relative hydrodynamic radius R_h) of WAX **(b)** and GXG **(c)** powder and WAX/GXG_Med (Autoclaving). Distributions were normalised to the height of the maximum between 1 and 100 nm. The size exclusion chromatography (SEC) was performed according to the method described by Wang *et al.*

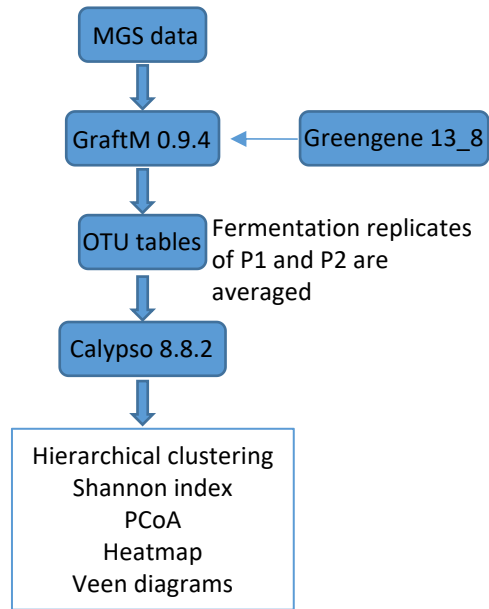


Figure S2 The bioinformatics workflow used to analyze the shotgun metagenome sequencing (MGS) data.

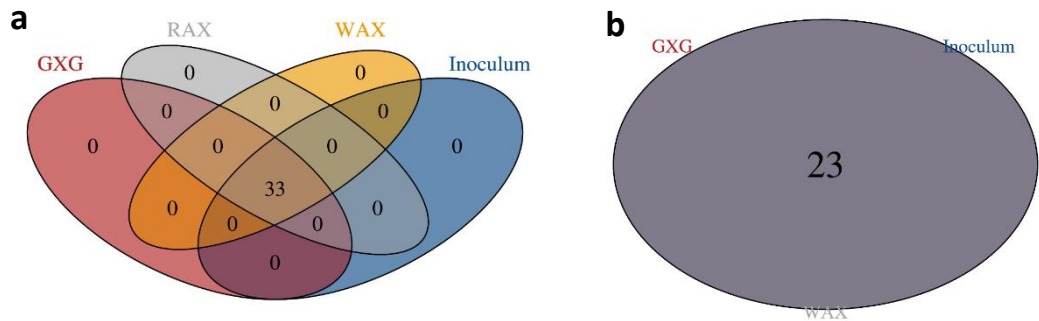


Figure S3 Venn diagrams representing the core, pan and unique OTUs as grouped by each substrate (WAX, GXG and RAX) & inoculum. The porcine (**a**) and human (**b**) fecal inoculum based samples. OTUs < 1% across all the porcine (**a**) or human (**b**) samples were not included. WAX: wheat arabinoxylan. RAX: rye arabinoxylan. GXG: galactoxyloglucan.

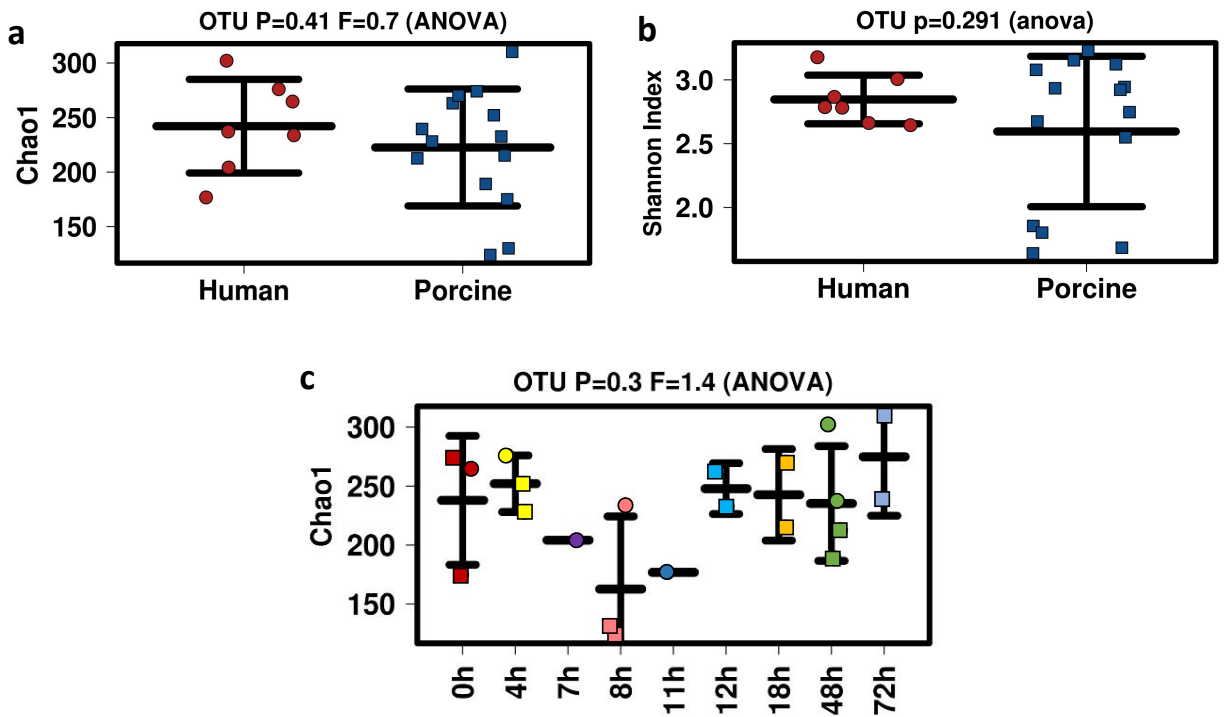


Figure S4 Microbial richness as shown by Chao1 (a) and Shannon index (b) of α -diversity as grouped by the inoculum type. (c) Chao 1 as grouped by the fermentation time. Circles represent the human samples, and squares represent the porcine samples.

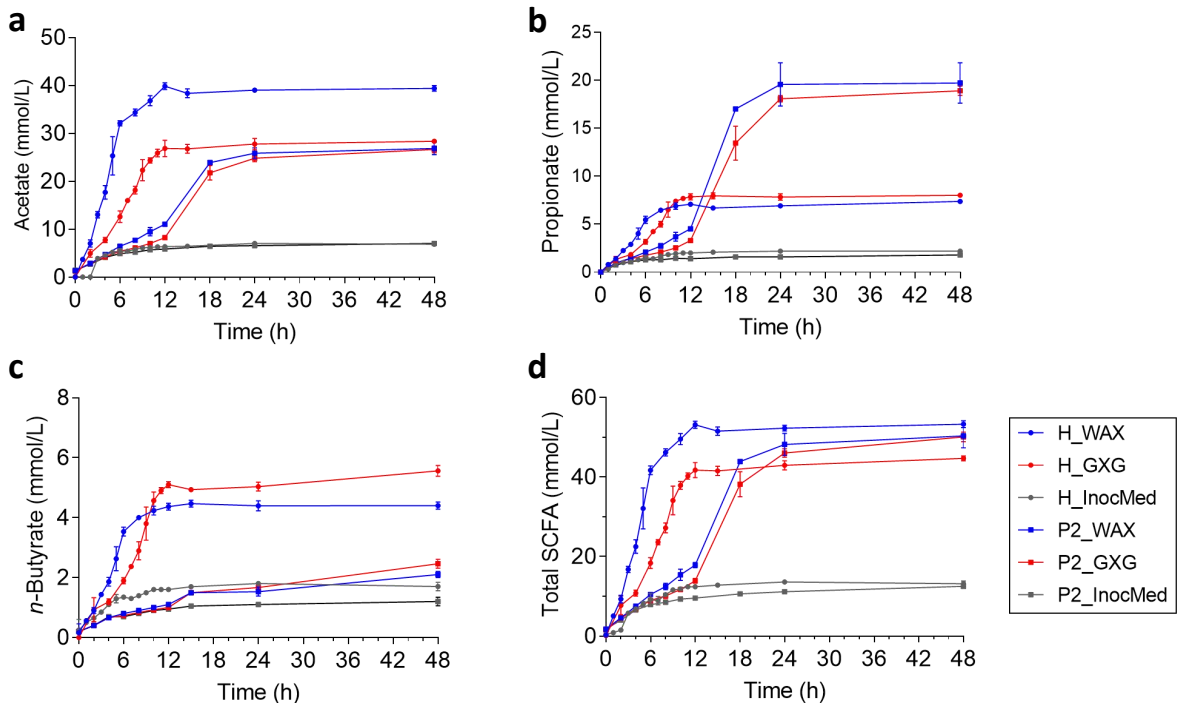


Figure S5 Short chain fatty acids (a: acetate, b: propionate, c: *n*-butyrate, d: total SCFA) generated during the fermentation of wheat arabinoxylan (WAX) and galactoxyloglucan (GXG) with a human (H) or porcine (P) fecal inoculum. InocMed was the blank that contained the inoculum and the medium but not the substrates. The concentration of the SCFA is expressed in mmol per litre of the fermentation supernatant.

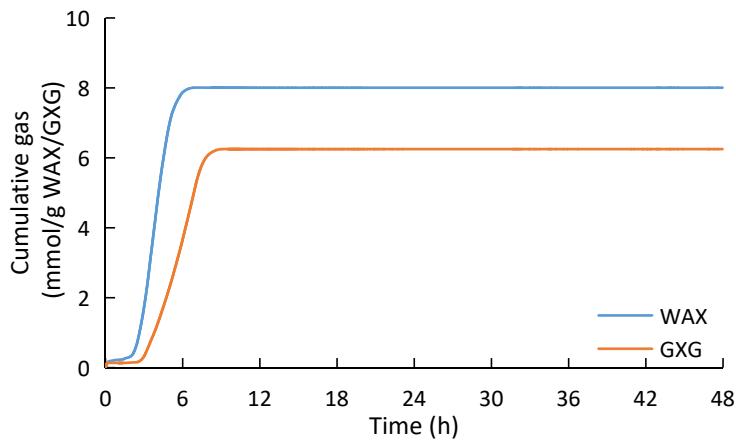


Figure S6 Cumulative gas production during fermentation of wheat arabinoxylan (WAX) and tamarind galactoxyloglucan (GXG) with a human fecal inoculum.

References

1. Wang, K., Wambugu, P. W., Zhang, B., Wu, A. C., Henry, R. J., & Gilbert, R. G., The biosynthesis, structure and gelatinization properties of starches from wild and cultivated African rice species (*Oryza barthii* and *Oryza glaberrima*), *Carbohydr. Polym.*, 2015, **129**. 92-100.