SUPPLEMENTARY INFORMATION:

MODIFICATION OF WHEAT BRAN PARTICLE SIZE AND TISSUE COMPOSITION AFFECTS COLONISATION AND METABOLISM BY HUMAN FAECAL MICROBIOTA.

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Running Title: Impact of wheat bran structure on microbiota colonisation

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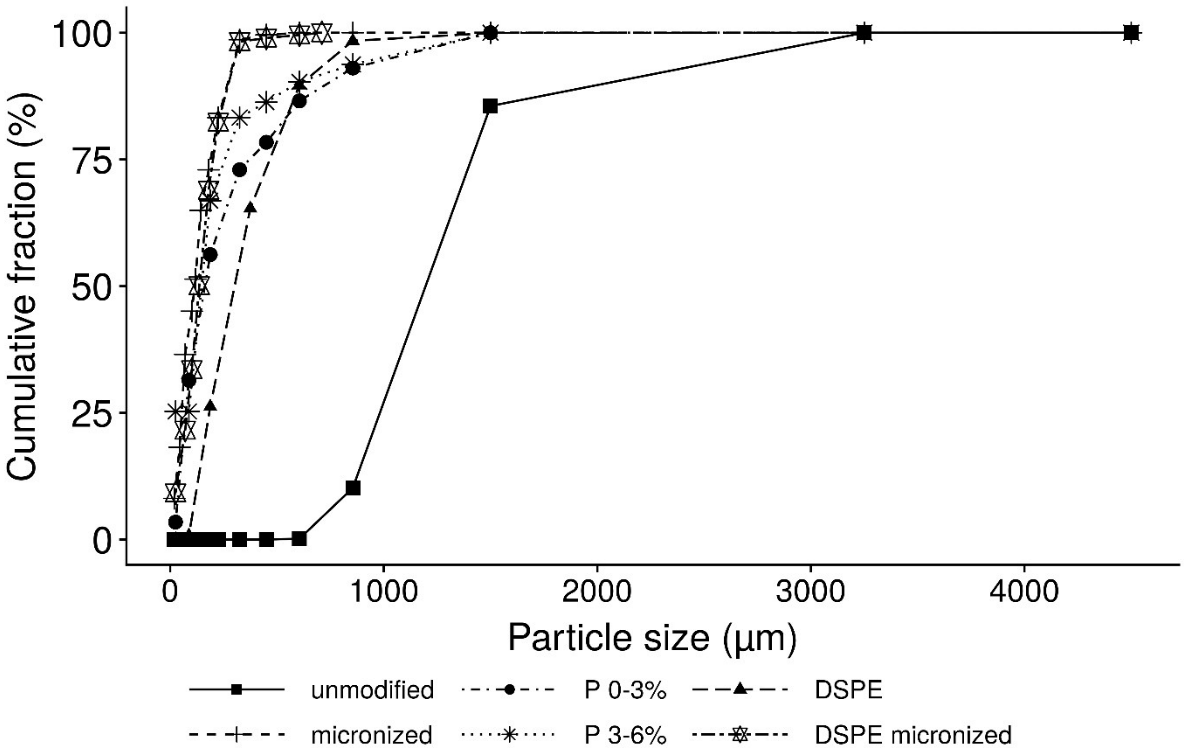

Figure S1: Wheat bran particle size distribution.

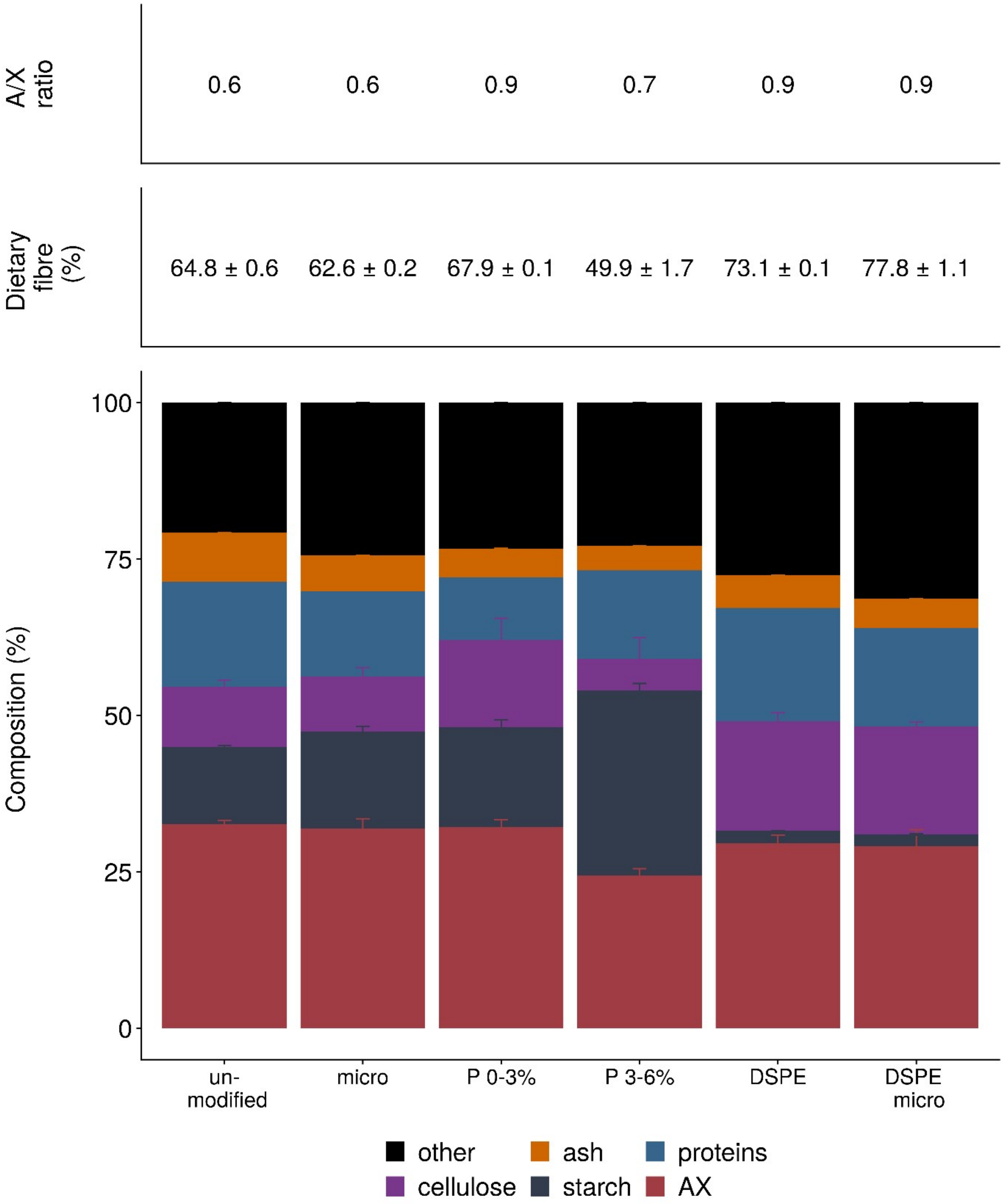

Figure S2: Chemical composition of the different wheat bran products after pre-digestion. The chemical composition was determined in triplicate (n=3), except for the dietary fibre content (n=2). Average values and standard deviations are shown.

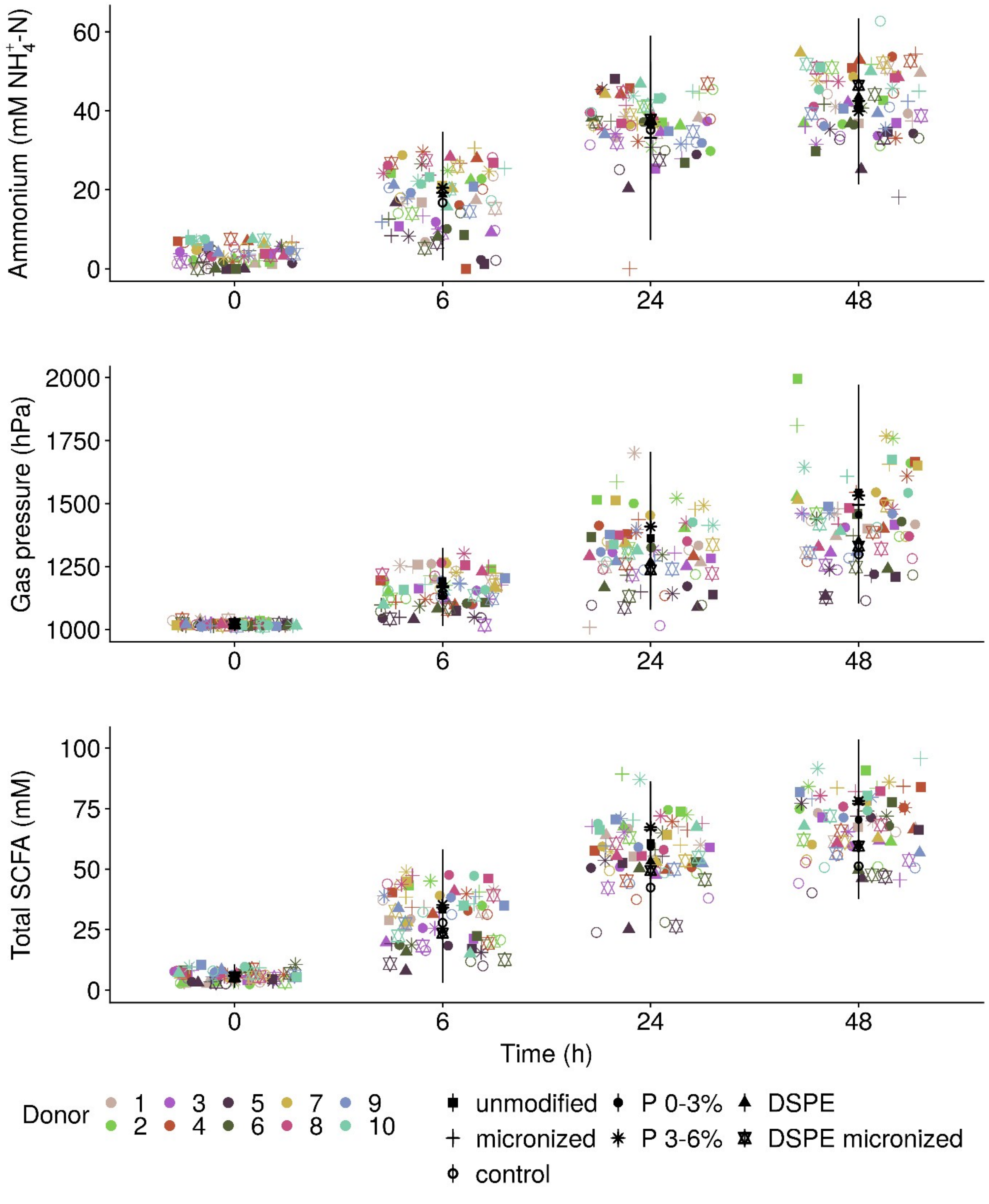

Figure S3: Effects of different wheat bran products on the gas pressure build-up and the production of fermentation metabolites after incubation with the faecal material of ten donors in a carbohydrate-low control medium over time.

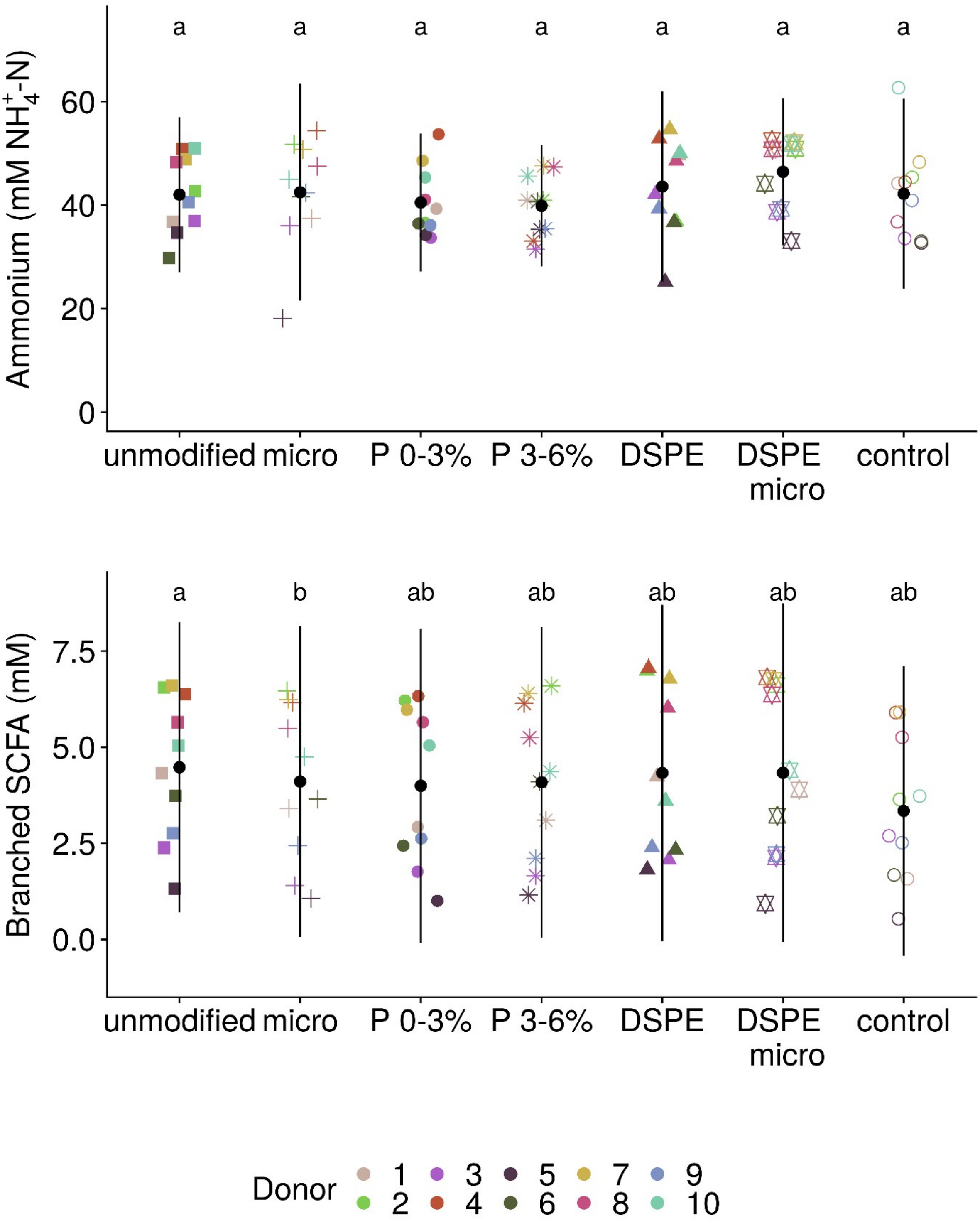

Figure S4: Effects of different wheat bran products on the markers for proteolytic fermentation activity after 48 h incubation with the faecal material of ten donors in a carbohydrate-low control medium. Statistically significant differences between the products (α=0.05), as determined by Pairwise Wilcoxon Rank Sum Tests with Holm correction, are denoted by the letters a and b. Identical letters indicate no statistical differences (p>0.05).

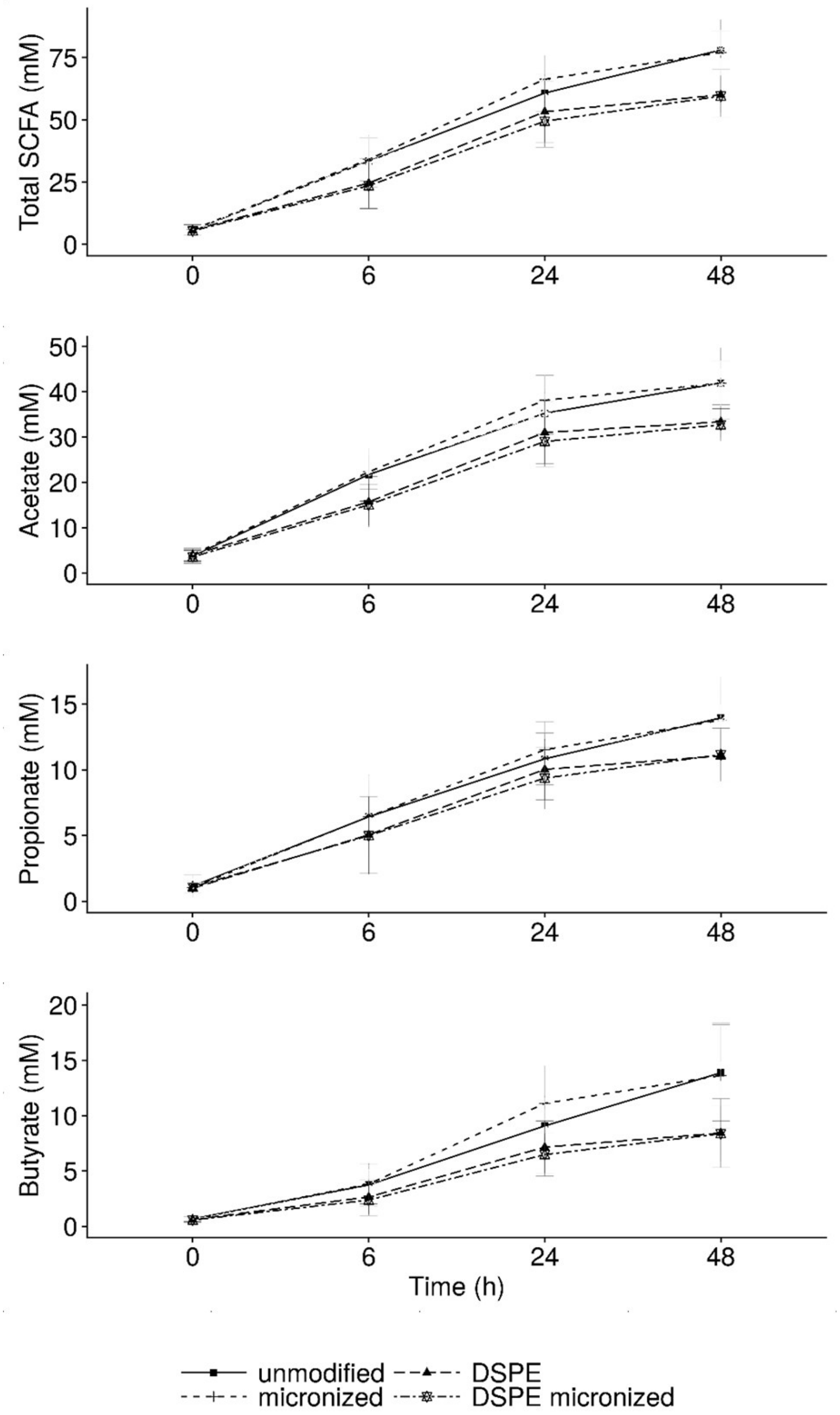

Figure S5: The rate of SCFA production averaged over ten donors in a carbohydrate-low control medium supplemented with different wheat bran products. Only the butyrate production was significantly reduced ($p<0.05$) with unmodified compared to micronized wheat bran, as assessed by Pairwise Wilcoxon Rank Sum Tests, with Holm correction.

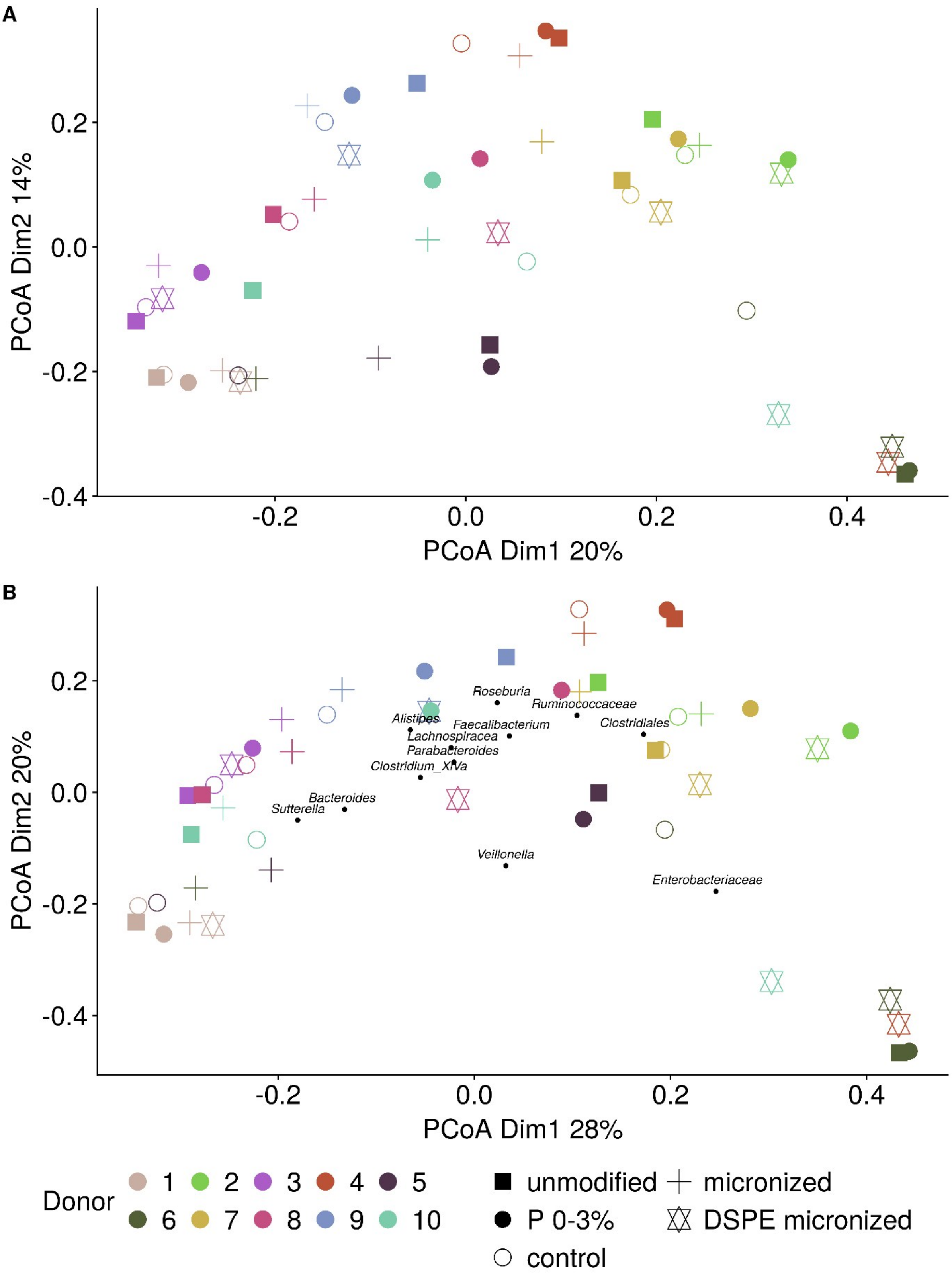

Figure S6: Principle Coordinate Analysis (PCoA) of the luminal microbial community composition at species (a) and genus level (b) after 48 h of incubation with the faecal material of ten individuals in a carbohydrate-low control medium supplemented with different wheat bran products, as determined by amplicon sequencing.

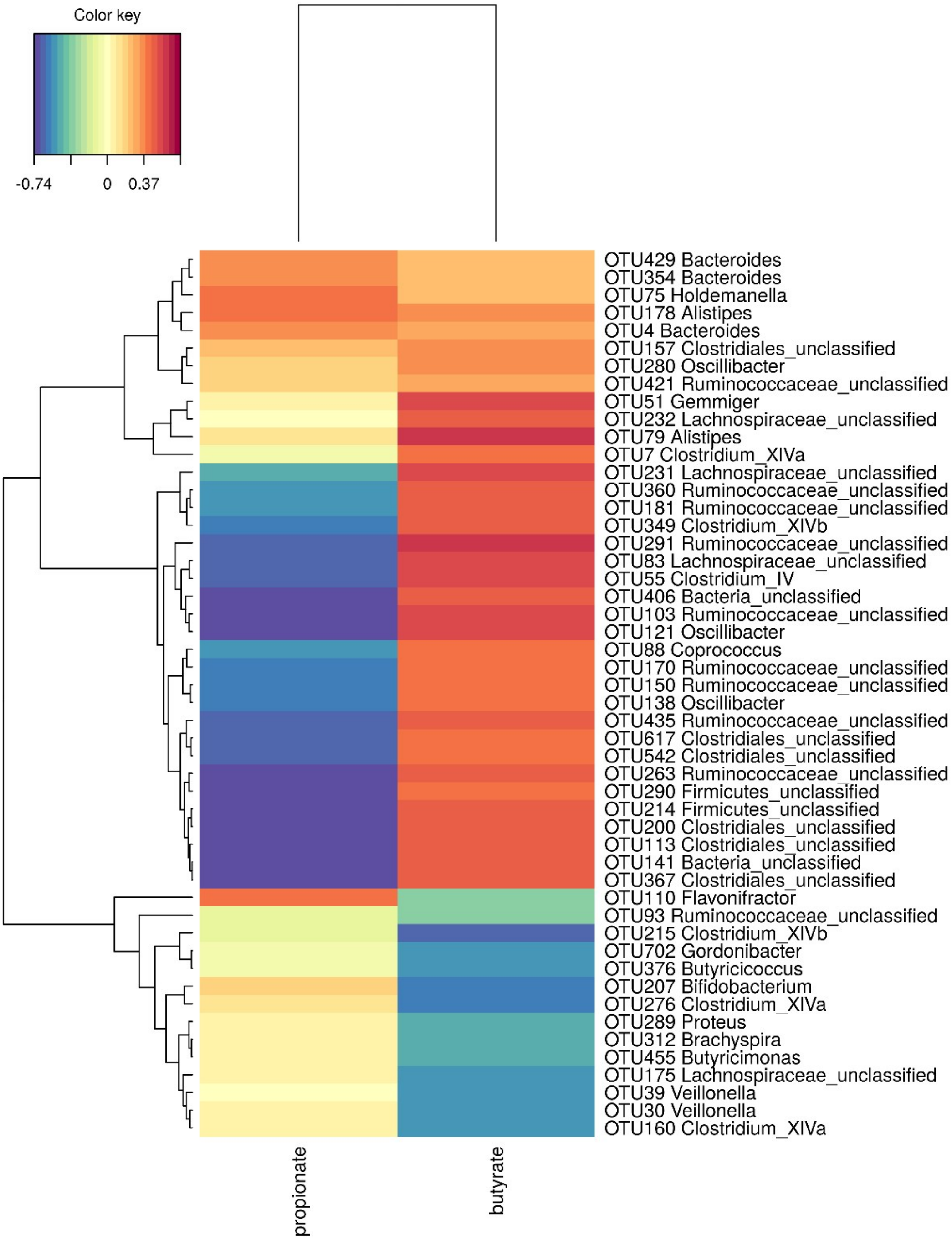

Figure S7: Heatmap representation of a sparse Partial Least Squares (sPLS) regression analysis of the luminal microbial community composition data at species level and the molar propionate and butyrate concentrations after 48 h of incubation with the faecal material of ten individuals in a carbohydrate-low control medium supplemented with different wheat bran products, as determined by amplicon sequencing.

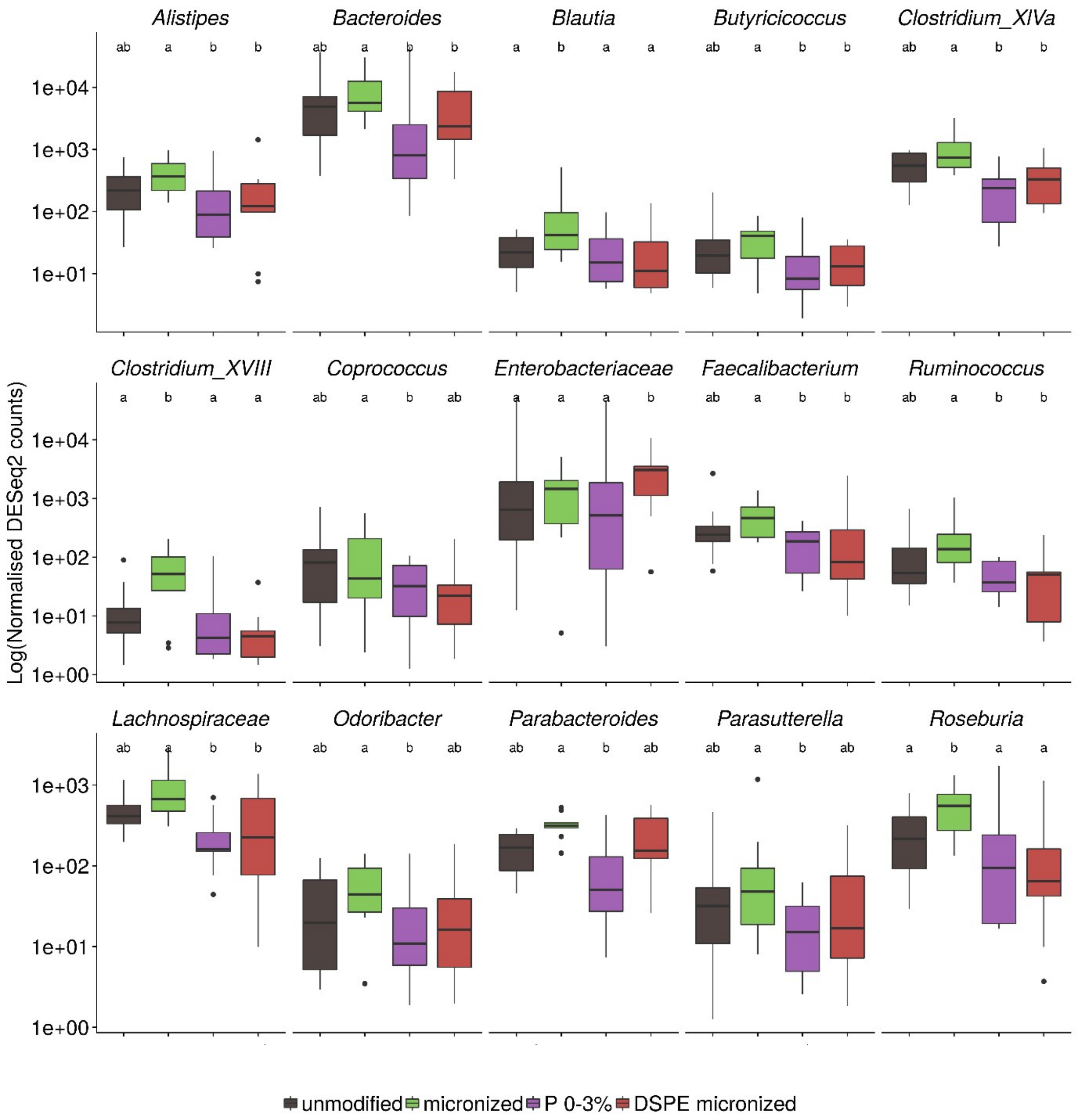

Figure S8: Wheat bran chemical modification induces significant differences (DESeq2;α=0.05) in the luminal microbial community composition at genus level after 48 h incubations with the faecal material of ten individuals in a carbohydrate-low control medium, as determined by amplicon sequencing. Pairwise significant differences, according to Walt test are denoted by the letters a and b. Identical letters indicate no statistical differences (p>0.05).

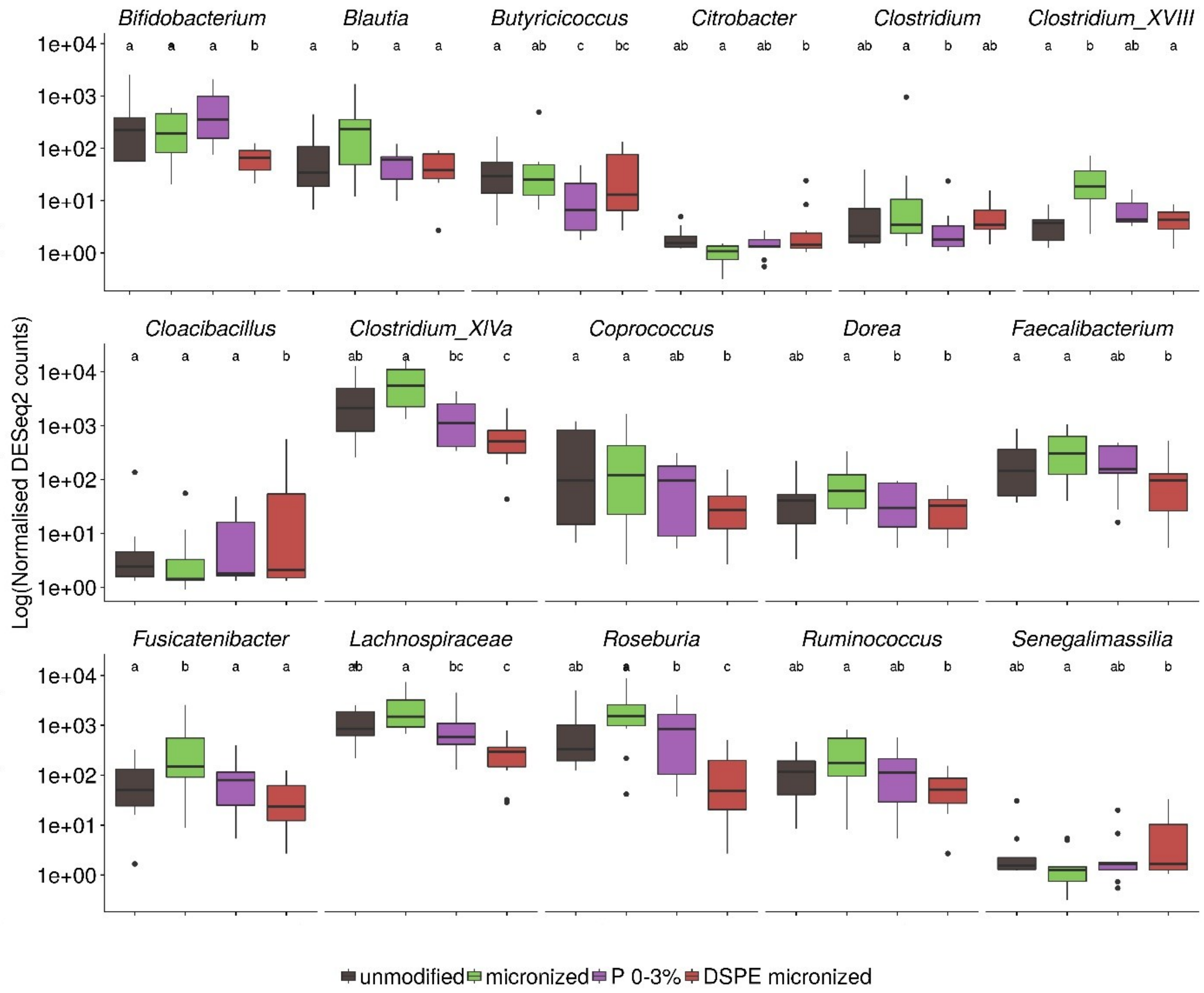

Figure S9: Wheat bran chemical modification induces significant differences (DESeq2;α=0.05) in the bran-attached microbial community composition at genus level after 48 h incubations with the faecal material of ten individuals in a carbohydrate-low control medium, as determined by amplicon sequencing. Pairwise significant differences, according to Walt test are denoted by the letters a and b. Identical letters indicate no statistical differences (p>0.05).

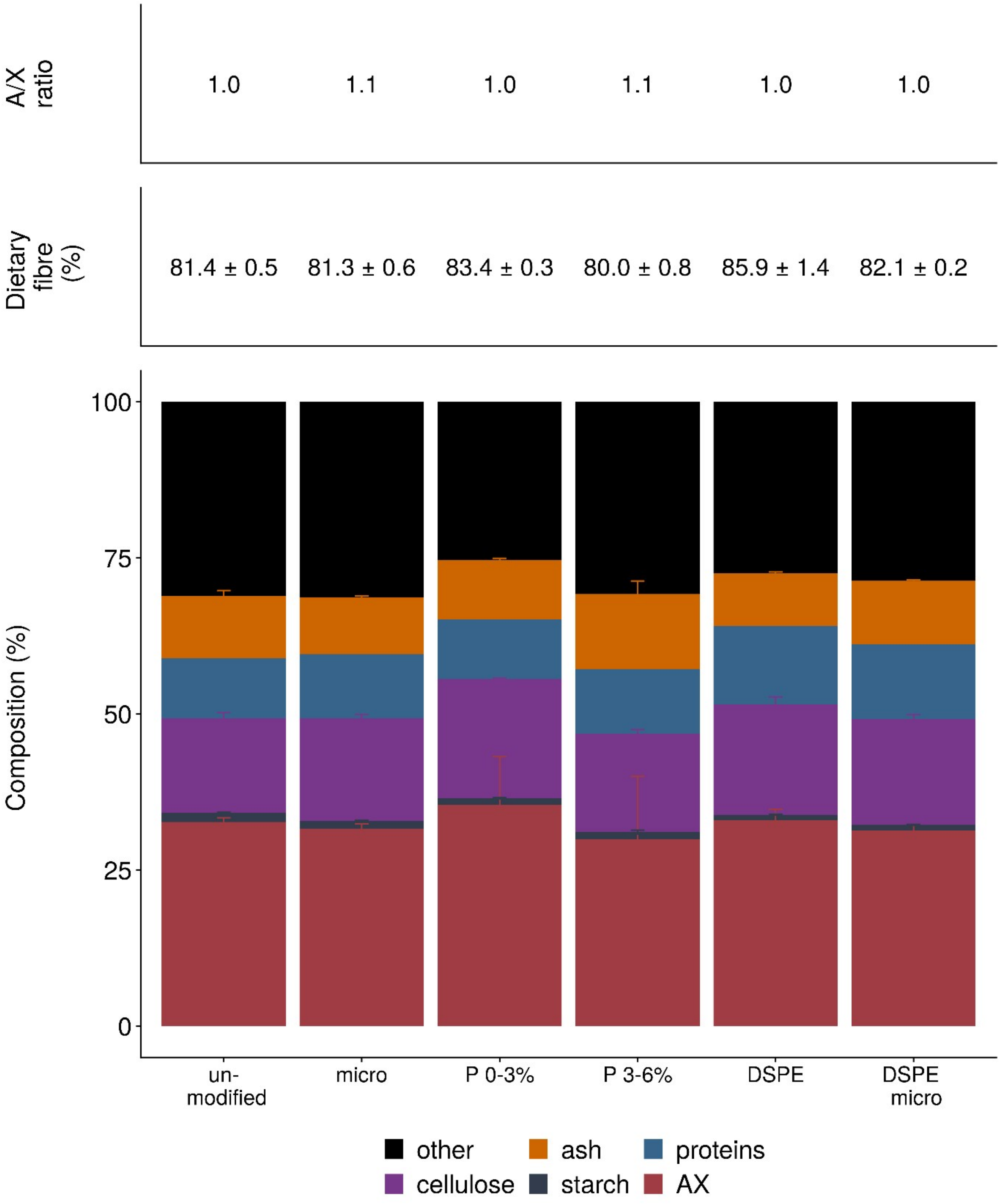

Figure S10: Chemical composition of the different wheat bran products after fermentation. The chemical composition was determined in triplicate (n=3), except for the dietary fibre content (n=2). Average values and standard deviations are shown.

Table S1: Composition of the mock community.

Strain	Phylum
Lactobacillus casei LMG 6904	*Firmicutes*
Lysinibacillus sphaericus LMG 22257	*Firmicutes*
Roseburia hominis A2-138	*Firmicutes*
Acetobacterium woodii DSM 1030	*Firmicutes*
Alcanivorax borkumensis SK2	*Proteobacteria*
Alcanivorax dieselolei KS 293	*Proteobacteria*
Cupriavidus pinatubonensis LMG 1197	*Proteobacteria*
Cupriavidus metallidurans LMG 1195	*Proteobacteria*
Pseudomonas putida LMG 24210	*Proteobacteria*
Geobacter sulfurreducens DSM 12127	*Proteobacteria*
Porphyromonas gingivalis ATCC 33277	*Bacteroidetes*
Fusobacterium nucleatum subsp. *polymorphum* ATCC 10953	*Fusobacteria*

Table S2: RDP Seqmatch and NCBI BLAST results for the 30 most abundant species in the luminal and bran environment after 48 h of incubation with the faecal material of ten individuals in a carbohydrate-low control medium containing wheat bran, as determined by amplicon sequencing. The similarity score (Sab), as calculated by RDP, and the NCBI BLAST output for the best hit and next best hit(s) is shown. The NCBI maximal score (not shown) equalled the total score for all displayed hits.

		RDP	NCBI BLAST			
		Sab	Total score	Query coverage (%)	E-value	Identity (%)
OTU1	*Escherichia fergusonii*	1	787	100	0.0	100
	Shigella sonei	1	787	100	0.0	100
	Shigella flexneri	1	787	100	0.0	100
	Escherichia coli	0.983	787	100	0.0	100
OTU2	*Bacteroides dorei*	1	778	100	0.0	100
	Bacteroides vulgatus	0.953	756	100	0.0	99
OTU3	*Bacteroides uniformis*	1	778	100	0.0	100
	Bacteroides rodentium	0.906	717	100	0.0	97
OTU4	*Bacteroides stercoris*	0.981	778	100	0.0	100
	Bacteroides intestinalis	0.893	717	100	0.0	97
OTU5	*Fusobacterium mortiferum*	0.995	747	100	0.0	100
	Fusobacterium necrogenes	0.964				
OTU6	*Bacteroides ovatus*	0.978	773	100	0.0	99
	Bacteroides xylanisolvens	0.891	730	100	0.0	98
OTU7	*Clostridium xylanolyticum*	0.857	686	100	0.0	98
	Clostridium aerotolerans	0.844	678	100	0.0	97
OTU8	*Prevotella copri*	0.93	752	100	0.0	99
	Prevotella histicola	0.69	634	100	0.0	94
OTU9	*Eubacterium rectale*	0.949	741	100	0.0	100
	Roseburia faecis	0.941	713	100	0.0	99
OTU10	*Faecalibacterium prausnitzii*	0.983	736	100	0.0	99
	Gemmiger formicilis	0.716	569	100	3.0e-162	92
OTU11	*Oscillibacter ruminantium*	0.732	612	100	5.0e-175	94
	Oscillibacter valericigenes	0.742	601	100	1.0e-171	94
OTU12	*Sutterella wadsworthensis*	1	787	100	0.0	100
	Sutterella stercoricanis	0.793	654	100	0.0	94
OTU13	*Bacteroides eggerthii*	0.983	773	100	0.0	99
	Bacteroides rodentium	0.843	706	100	0.0	97
OTU14	*Pantoea vagans*	1	787	100	0.0	100
	Pantoea brenneri	0.952	784	100	0.0	99
OTU15	*Bacteroides caccae*	0.966	767	100	0.0	99
	Bacteroides faecis	0.865	723	100	0.0	98
OTU16	*Coprococcus eutactus*	0.982	736	100	0.0	99

	Eubacterium ruminantium	0.798	641	100	0.0	96
OTU17	*Roseburia faecis*	1	743	100	0.0	100
	Roseburia intestinalis	0.949	721	100	0.0	99
OTU18	*Prevotella copri*	0.969	773	100	0.0	99
	Prevotella histicola	0.707	628	100	5.0e-180	94
OTU19	*Clostridium xylanolyticum*	0.863	654	100	0.0	96
	Clostridium celerecrescens	0.863	654	100	0.0	96
	Clostridium asparagiforme	0.86	654	100	0.0	96
	Hungatella hathewayi	0.85	665	100	0.0	97
OTU20	*Faecalibacterium prausnitzii*	0.946	725	100	0.0	99
	Gemmiger formicilis	0.732	580	1	1.0e-165	93
OTU21	*Acetivibrio ethanolgignens*	0.862	658	100	0.0	96
	Clostridium xylanolyticum	0.849	669	100	0.0	97
OTU22	*Bacteroides cellulosilyticus*	0.966	778	100	0.0	100
	Bacteroides intestinalis	0.934	756	100	0.0	99
OTU23	*Prevotella copri*	0.883	736	100	0.0	98
	Prevotella micans	0.704	590	100	2.0e-168	92
OTU24	*Bacteroides xylanisolvens*	1	778	100	0.0	100
	Bacteroides acidifaciens	0.959	756	100	0.0	99
OTU25	*Bifidobacterium faecale*		758	100	0.0	100
	Bifidobacterium adolescentis	1	758	100	0.0	100
	Bifidobacterium ruminantium	0.982	752	100	0.0	99
OTU26	*Parabacteroides merdae*	1	778	100	0.0	100
	Parabacteroides johnsonii	0.895				
OTU27	*Clostridium bolteae*	0.814	647	100	0.0	96
	Clostridium asparagiforme	0.804	636	100	0.0	95
OTU28	*Parabacteroides distasonis*	0.956	773	100	0.0	99
	Parabacteroides gordonii	0.674	610	100	2.0e-174	93
OTU29	*Bacteroides thetaiotaomicron*	1	778	100	0.0	100
	Bacteroides faecichinchillae	0.947	756	100	0.0	99
OTU30	*Veillonella dispar*	0.968	776	100	0.0	99
	Veillonella tobetsuensis	0.949	760	100	0.0	99
OTU31	*Flavonifractor plautii*	0.683	534	100	1.0e-151	91
	Pseudoflavonifractor capillosus	0.652	551	100	1.0e-156	91
	Oscillibacter ruminantium		573	100	2.0e-163	92
OTU37	*Alistipes onderdonkii*	1	778	100	0.0	100
	Alistipes shahii	0.882	717	100	0.0	97
OTU39	*Veillonella ratti*	1	787	100	0.0	100
	Veillonella seminalis	1				
	Veillonella criceti	0.879	739	100	0.0	98
OTU40	*Fusicatenibacter saccharivorans*	1	741	100	0.0	100
	Murimonas intestini	0.856	669	100	0.0	97
OTU42	*Ruminococcus faecis*	1	741	100	0.0	100
	Ruminococcus torques	0.872	682	100	0.0	97

OTU43	*Megamonas funiformis*	1	787	100	0.0	100
	Megamonas rupellensis	0.872	721	100	0.0	97
OTU44	*Bifidobacterium catenulatum*	1	754	100	0.0	100
	Bifidobacterium pseudocatenulatum	1	754	100	0.0	100
	Bifidobacterium kashiwanohense	1	754	100	0.0	100
OTU48	*Clostridium bolteae*	1	741	100	0.0	100
	Clostridium clostridioforme	0.977	741	100	0.0	100
OTU51	*Gemmiger formicilis*	1	741	100	0.0	100
	Subdoligranulum variabile	0.959	719	100	0.0	99
OTU54	*Bacteroides fragilis*	1	778	100	0.0	100
OTU55	*Eubacterium siraeum*	0.954	726	100	0.0	99
	Acetanaerobacterium elongatum	0.587	496	100	5.0e-140	89
OTU56	*Clostridium asparagiforme*	0.902	680	100	0.0	97
	Clostridium lavalense	0.887	675	100	0.0	97
OTU57	*Alistipes timonensis*	0.863	712	100	0.0	97
	Alistipes putredinis	0.846	778	100	0.0	100
OTU58	*Parasutterella excrementihominis*	1	787	100	0.0	100
	Parasutterella secunda	0.603	582	100	4.0e-166	91
OTU59	*Vallitalea pronyensis (T); FatNI3; KC876639*	0.534	468	99	1.0e-131	88
	Vallitalea guaymasensis	0.516	479	99	5.0e-135	88
	Anaerobacterium chartisolvens	0.5	486	99	3.0e-137	89
OTU61	*Ruminococcus bromii*	0.974	732	100	0.0	99
	Clostridium leptum	0.61	547	100	1.0e-155	91
OTU63	*Blautia wexlerae*	1	741	100	0.0	100
	Blautia obeum	0.895				
OTU65	*Dorea longicatena*	0.992	736	100	0.0	99
	Clostridium scindens	0.86	675	100	0.0	97
OTU66	*Anaerostipes hadrus*	1	741	100	0.0	100
	Anaerostipes butyraticus	0.897	697	100	0.0	98
OTU67	*Eubacterium xylanophilum*	0.87	689	100	0.0	97
	Clostridium populeti	0.867	680	100	0.0	97
OTU78	*Oscillibacter valericigenes*	0.778	617	100	1.0e-176	94
	Oscillibacter ruminantium	0.745	606	100	2.0e-173	94
OTU80	*Eubacterium eligens*	0.802	669	100	0.0	97
	Lactobacillus rogosae		741	100	0.0	100
OTU82	*Roseburia inulinivorans*	1	745	100	0.0	100
	Roseburia intestinalis	0.931	701	100	0.0	98
OTU83	*Eubacterium ruminantium*	0.844	686	100	0.0	98
	Coprococcus eutactus	0.803	636	100	0.0	95
OTU86	*Blautia luti*	0.987	736	100	0.0	99
	Blautia stercoris	0.926	691	100	0.0	98
OTU87	*Odoribacter splanchnicus*	0.891	765	100	0.0	99
OTU92	*Ruminococcus albus*	0.793	636	100	0.0	95
	Ruminococcus champanellensis	0.773	636	100	0.0	95

OTU104	*Dialister invisus*	1				
	Dialister propionicifaciens	0.839				
OTU106	*Blautia obeum*	1	737	100	0.0	99
	Blautia schinkii	0.926	693	100	0.0	98
OTU108	*Clostridium populeti*	0.727	614	100	1.0e-171	94
	Lachnospira multipara	0.719	614	100	1.0e-175	94
	Eubacterium eligens	0.702	625	100	6.0e-179	95
OTU117	*Clostridium spiroforme*	0.709	619	100	3.0e-177	93
	Clostridium cocleatum	0.697	608	100	6.0e-174	92
OTU132	*Cloacibacillus evryensis*	1	741	100	0.0	100
	Cloacibacillus porcorum	0.832	664	100	0.0	97
OTU137	*Blautia faecis*	1	741	100	0.0	100
	Blautia glucerasea	0.926	708	100	0.0	99
OTU139	*Alistipes shahii*	0.823	656	100	0.0	95
	Alistipes obesi		778	100	0.0	100
OTU140	*Coprococcus comes*	1	741	100	0.0	100
OTU146	*Clostridium aldenense*	0.809	664	100	0.0	97
	Clostridium amygdalinum	0.752	647	100	0.0	96
OTU158	*Hungatella hathewayi*	1	741	100	0.0	100
	Hungatella effluvii	0.931	719	100	0.0	99
OTU171	*Clostridium amygdalinum*	0.837	675	100	0.0	97
	Clostridium celerecrescens	0.855	669	100	0.0	97
OTU183	*Blautia obeum*	0.934				
	Blautia schinkii	0.926	688	100	0.0	98
	Blautia glucerasea	0.901	686	100	0.0	98
OTU185	*Clostridium hylemonae*	0.874	678	100	0.0	97
	Clostridium oroticum	0.869	680	100	0.0	97
	Hespellia porcina	0.864	691	100	0.0	98
OTU191	*Fusicatenibacter saccharivorans*	0.828	664	100	0.0	97
	Ruminococcus lactaris	0.792	649	100	0.0	96
OTU197	*Ruminococcus lactaris*	0.895	688	100	0.0	98
	Fusicatenibacter saccharivorans	0.855	680	100	0.0	97
OTU198	*Fusicatenibacter saccharivorans*	0.967	730	100	0.0	99
	Clostridium lavalense	0.831	675	100	0.0	97
OTU233	*Ruminococcus gnavus*	1	741	100	0.0	100
	Dorea longicatena	0.834	664	100	0.0	97
OTU248	*Ruminococcus lactaris*	0.817				
	Ruminococcus gauvreauii	0.817				
	Lachnobacterium bovis	0.805	651	100	0.0	96
OTU250	*Intestinimonas butyriciproducens*	1	747	100	0.0	100
	Flavonifractor plautii	0.732	625	100	6.0e-179	95
OTU261	*Murimonas intestini*	0.872	686	100	0.0	98
	Marvinbryantia formatexigens	0.798	675	100	0.0	97
OTU280	*Oscillibacter ruminantium*	0.778	617	100	1.0e-176	94

	Oscillibacter valericigenes	0.775	612	100	5.0e-175	94
OTU303	*Oscillibacter ruminantium*	0.826	634	100	0.0	95
	Oscillibacter valericigenes	0.813	601	100	1.0e-171	94
OTU383	*Ruminococcus faecis*	0.826	664	100	0.0	97
	Ruminococcus torques	0.811	660	100	0.0	96
OTU391	*Roseburia intestinalis*	0.943	719	100	0.0	99
	Roseburia hominis	0.941	713	100	0.0	99
OTU459	*Roseburia faecis*	0.852	686	100	0.0	98
	Roseburia intestinalis	0.837	665	100	0.0	97
OTU491	*Clostridium lavalense*	0.934	713	100	0.0	99
	Clostridium asparagiforme	0.916	708	100	0.0	99
OTU604	*Roseburia faecis*	0.855	675	100	0.0	97
	Roseburia intestinalis	0.829	660	100	0.0	96
OTU731	*Clostridium celerecrescens*	0.824	643	100	0.0	96
	Clostridium xylanovorans	0.822				

Table S3: Wheat bran micronization induces pairwise significant differences (DESeq2;$\alpha=0.05$) in the luminal microbial community composition at genus and species level after 48 h incubations with the faecal material of ten individuals in a carbohydrate-low control medium, as determined by amplicon sequencing.

	Taxa	**log2FC**	**p-value**
Genus	*Anaerostipes*	-1.81	0.046
	Bifidobacterium	-1.98	0.033
	Blautia	-1.44	0.011
	Clostridium XVIII	-2.25	0.001
	Roseburia	-1.49	0.046
Species	OTU6 *Bacteroides*	-2.63	0.011
	OTU9 *Roseburia*	-1.83	0.048
	OTU27 *Lachnospiraceae*	-1.90	0.014
	OTU48 *Clostridium* XIVa	-1.86	0.018
	OTU54 *Bacteroides*	-2.41	0.018
	OTU57 *Alistipes*	-1.95	0.048
	OTU117*Clostridium* XVIII	-2.18	0.015
	OTU140 *Coprococcus*	-1.66	0.015
	OTU146 *Lachnospiraceae*	-2.23	0.006

Table S4: Wheat bran chemical modification induces pairwise significant differences (DESeq2;α=0.05) in the luminal microbial community composition at species level after 48 h incubations with the faecal material of ten individuals in a carbohydrate-low control medium, as determined by amplicon sequencing.

	micronized - DSPE micronized		**micronized - P0-3%**	
Genus	**log2FC**	**p-value**	**log2FC**	**p-value**
OTU2 *Bacteroides*	2.41	0.014	3.40	$8.6\ e^{-05}$
OTU6 *Bacteroides*	2.26	0.016	3.52	$2.3\ e^{-05}$
OTU7 *Clostridium XIVa*	3.62	$1.2\ e^{-05}$	3.14	$9.7\ e^{-05}$
OTU9 *Roseburia*	2.05	0.012	2.30	0.00101
OTU17 *Roseburia*	4.03	$2.5\ e^{-08}$	3.45	$1,5\ e^{-06}$
OTU20 *Faecalibacterium*	1.77	0.028	2.27	0.00079
OTU21 *Clostridium* XIVa			2.13	0.00049
OTU26 *Parabacteroides*			2.35	0.00088
OTU27 *Lachnospiraceae*	1.78	0.012	2.03	0.00079
OTU37 *Alistipes*			2.61	0.00022
OTU40 *Fusicatenibacter*			1.73	0.00979
OTU42 *Ruminococcus*	2.16	0.009	1.61	0.02683
OTU48 *Clostridium* XIVa			2.54	0.0001
OTU54 *Bacteroides*	2.55	0.01	3.38	0.0001
OTU57 *Alistipes*	2.59	0.002	2.93	0.0001
OTU58 *Parasutterella*			2.43	0.00079
OTU61 *Ruminococcus*	2.01	0.037	2.28	0.00492
OTU65 *Dorea*	1.81	0.026	1.79	0.01168
OTU67 *Lachnospiraceae*			1.81	0.01616
OTU80 *Lachnospiraceae*	2.35	0.01	2.75	0.00039
OTU82 *Roseburia*			2.14	0.00205
OTU86 *Blautia*			1.75	0.00181
OTU87 *Odoribacter*			1.96	0.00359
OTU92 *Ruminococcus*	1.76	0.048	2.57	0.00101
OTU117 *Clostridium* XVIII	3.33	$3.9\ e^{-05}$	2.28	0.00184
OTU137 *Blautia*			1.50	0.01207
OTU139 *Alistipes*			2.47	0.00049
OTU140 *Coprococcus*	2.35	$1.2\ e^{-04}$	2.21	0.0001
OTU146 *Lachnospiraceae*	2.3	0.001	2.37	0.00021
OTU158 *Clostridium* XIVa			1.48	0.03143
OTU171 *Clostridium* XIVa			1.74	0.00417
OTU185 *Lachnospiraceae*	1.87	0.009	2.19	0.00037
OTU191 *Lachnospiraceae*	1.72	0.01	1.40	0.01446
OTU233 *Clostridium* XIVa	1.76	0.035	1.74	0.01446
OTU250 *Intestinimonas*			2.11	0.00444

Table S5: Wheat bran micronization induces pairwise significant differences (DESeq2;α=0.05) in the bran-attached microbial community composition at genus and species level after 48 h incubations with the faecal material of ten individuals in a carbohydrate-low control medium, as determined by amplicon sequencing.

	Taxa	log2FC	p-value
Genus	*Blautia*	-1.68	0.002
	Clostridium XVIII	-2.79	1.8 e^{-06}
	Fusicatenibacter	-1.96	0.004
Species	OTU17 *Roseburia*	-1.98	0.039
	OTU40 *Fusicatenibacter*	-2.19	0.005
	OTU55 *Clostridium* IV	-1.69	0.039
	OTU59 *Clostridiales*	-2.28	0.00049
	OTU86 *Blautia*	-1.69	0.039
	OTU104 *Dialister*	-1.21	0.049
	OTU106 *Blautia*	-2.47	6 e^{-05}
	OTU117 *Clostridium* XVIII	-2.68	6.3 e^{-05}
	OTU137 *Blautia*	-2.52	1.9 e^{-05}
	OTU183 *Blautia*	-1.75	0.024
	OTU198 *Fusicatenibacter*	-1.83	0.012
	OTU261 *Lachnospiraceae*	-2.28	0.001
	OTU303 *Oscillibacter*	-1.81	0.039
	OTU383 *Lachnospiraceae*	-2.10	0.009

Table S6: Wheat bran chemical modification induces pairwise significant differences (DESeq2;α=0.05) in the bran-attached microbial community composition at species level after 48 h incubations with the faecal material of ten individuals in a carbohydrate-low control medium, as determined by amplicon sequencing.

	micronized - DSPE micronized		**micronized - P0-3%**	
Taxa	**log2FC**	**p-value**	**log2FC**	**p-value**
OTU1 *Enterobacteriaceae*	-1.96	0.02415		
OTU2 *Bacteroides*	1.69	0.00397		
OTU7 *Clostridium* XIVa	5.78	$1.3\ e^{-18}$	2.94	0.0005
OTU9 *Roseburia*	4.71	$2\ e^{-09}$		
OTU10 *Faecalibacterium*	2.51	$2.2\ e^{-06}$	1.59	0.02
OTU16 *Coprococcus*	3.75	$9.5\ e^{-07}$		
OTU17 *Roseburia*	5.13	$9.5\ e^{-17}$	1.95	0.02
OTU19 *Lachnospiraceae*	3.28	0.00022		
OTU20 *Faecalibacterium*	1.68	0.00174		
OTU25 *Bifidobacterium*	2.67	0,00003		
OTU31 *Ruminococcaceae*	1.35	0.01899	1.47	0.03
OTU40 *Fusicatenibacter*	3.30	$2.6\ e^{-08}$	1.96	0.01
OTU42 *Ruminococcus*	2.61	0,00001		
OTU54 *Bacteroides*	1.85	0.00608		
OTU55 *Clostridium* IV	1.42	0.01615		
OTU56 *Clostridium* XIVa	2.66	0.00123		
OTU59 *Clostridiales*			1.94	0.001
OTU63 *Blautia*	2.38	0.00016		
OTU65 *Dorea*	2.12	0.00011	1.55	0.02
OTU66 *Anaerostipes*	1.68	0.00061		
OTU67 *Lachnospiraceae*	3.42	$8\ e^{-08}$	1.91	0.02
OTU78 *Oscillibacter*	1.07	0.03485	1.31	0.04
OTU83 *Lachnospiraceae*	2.32	0.0014		
OTU86 *Blautia*	1.71	0.00449		
OTU87 *Odoribacter*	1.38	0.00641	1.41	0.02
OTU104 *Dialister*	1.35	0.00348	1.2	0.02
OTU106 *Blautia*	2.21	0,00001	2.25	0.0002
OTU108 *Lachnospiraceae*	2.63	$1.2\ e^{-06}$		
OTU117 *Clostridium* XVIII	2.37	0,00002	1.93	0.004
OTU132 *Cloacibacillus*	-1.96	0.00894		
OTU137 *Blautia*	2.47	$3.3\ e^{-07}$	2.32	$5.0\ e^{-05}$
OTU140 *Coprococcus*	1.61	0.00014		
OTU183 *Blautia*	2.30	0.00015	1.73	0.02
OTU188 *Bacteria*	1.81	0.01615		
OTU197 *Lachnospiraceae*	1.51	0.02902		
OTU198 *Fusicatenibacter*	3.03	$6.1\ e^{-08}$	1.92	0.005

OTU248 *Lachnospiraceae*	2.00	0.00384	2.12	0.01
OTU261 *Lachnospiraceae*	2.76	$6.3\ e^{-07}$	1.5	0.02
OTU280 *Oscillibacter*	1.69	0.01044		
OTU303 *Oscillibacter*	1.83	0.00622	1.8	0.02
OTU383 *Lachnospiraceae*	3.36	$3.6\ e^{-07}$	2.08	0.005
OTU391 *Roseburia*	2.35	0.00157		
OTU459 *Roseburia*	2.41	0.00058		
OTU491 *Clostridium* XIVa	1.84	0.00341		
OTU514 *Bacteria*			-1.87	0.04
OTU591 *Lachnospiraceae*	2.11	0.00364		
OTU598 *Lachnospiraceae*	2.27	0.00087		
OTU604 *Lachnospiraceae*	2.32	0.00081		
OTU731 *Lachnospiraceae*	1.94	0.00894	2.04	0.02
OTU740 *Lachnospiraceae*	1.84	0.01117		