

Supplementary Material

Table S1. Chemical composition of breads pre and post *in vitro* digestions.

Components	Ebindb		Eblfb1		Eblfb2	
	Pre-digestion	Post-digestion	Pre-digestion	Post-digestion	Pre-digestion	Post-digestion
Proteins ^a	10.12	1.26	8.12	1.13	9.09	1.39
Dietary fiber ^a	2.6	< 1.0	3.13	1.5	3.27	1.7
Starch ^a	NA	5.5	NA	5.8	NA	6.8
SCFA ^b						
Acetic acid	NA	173.12	NA	163.72	NA	153.42
Propionic acid	NA	42.77	NA	31.61	NA	29.78
Isobutyric acid	NA	ND	NA	ND	NA	ND
Butyric acid	NA	ND	NA	ND	NA	ND
Isovaleric acid	NA	14.05	NA	ND	NA	ND
Valeric acid	NA	17.69	NA	10.66	NA	9.82
Hexanoic acid	NA	45.96	NA	25.61	NA	26.34

^a Values are grams per 100 grams of sample.

^b Values are micrograms per liter of sample.

Table S2. Biomarkers abundances in fecal samples of 3 UC patients incubated with different bread treatments. Values are means $\pm$ standard deviation of abundances given as logarithm of total number of genomic units per stool gram analyzed in triplicate. Values within a row with different superscript letters are significantly different (p -value < 0.05).

Bacterial Markers *	Incubation control	Substrate control	Ebindb 1 g	Ebindb 2 g	Eblfb1 2 g	Eblfb1 2 g	Eblfb2 1 g	Eblfb2 2 g	Pectin 100 mg
EUB	10.48 $\pm$ 0.21 ^a	10.16 $\pm$ 0.22 ^b	10.71 $\pm$ 0.18 ^{ac}	10.80 $\pm$ 0.17 ^c	10.66 $\pm$ 0.22 ^{ac}	10.75 $\pm$ 0.15 ^{ac}	10.52 $\pm$ 0.15 ^a	10.62 $\pm$ 0.11 ^a	10.61 $\pm$ 0.37 ^{ac}
ECO	3.19 $\pm$ 0.71 ^a	3.34 $\pm$ 0.84 ^a	3.94 $\pm$ 1.12 ^a	4.56 $\pm$ 1.46 ^b	3.69 $\pm$ 0.43 ^a	3.66 $\pm$ 0.69 ^a	3.51 $\pm$ 0.87 ^a	3.53 $\pm$ 0.76 ^a	4.62 $\pm$ 1.68 ^b
FPRA	9.82 $\pm$ 0.55 ^a	8.91 $\pm$ 0.38 ^{bd}	9.05 $\pm$ 1.15 ^{cd}	8.43 $\pm$ 1.36 ^{bcd}	9.16 $\pm$ 0.31 ^{cd}	9.31 $\pm$ 0.47 ^d	8.88 $\pm$ 0.24 ^b	9.14 $\pm$ 0.52 ^{bcd}	8.77 $\pm$ 1.81 ^{a-d}
PGHI	7.52 $\pm$ 3.46 ^a	7.06 $\pm$ 3.12 ^b	7.39 $\pm$ 3.37 ^{ac}	6.72 $\pm$ 3.28 ^{bc}	7.35 $\pm$ 3.34 ^{ac}	7.01 $\pm$ 3.08 ^b	7.32 $\pm$ 3.31 ^{ac}	7.06 $\pm$ 3.13 ^{bc}	7.04 $\pm$ 3.56 ^a
PGHII	10.26 $\pm$ 0.32 ^a	9.25 $\pm$ 0.20 ^b	9.83 $\pm$ 0.41 ^d	9.60 $\pm$ 0.35 ^{cd}	9.60 $\pm$ 0.39 ^{cd}	9.44 $\pm$ 0.35 ^{bcd}	9.42 $\pm$ 0.54 ^{bcd}	9.23 $\pm$ 0.37 ^{bc}	10.39 $\pm$ 0.44 ^a
ROS	8.50 $\pm$ 0.16 ^a	6.95 $\pm$ 0.25 ^b	7.67 $\pm$ 0.46 ^{cd}	8.12 $\pm$ 0.65 ^{acd}	7.92 $\pm$ 0.65 ^d	8.23 $\pm$ 0.76 ^{ad}	7.48 $\pm$ 0.39 ^c	8.39 $\pm$ 0.50 ^{ad}	6.83 $\pm$ 0.40 ^b
AKK	4.21 $\pm$ 0.56	3.58 $\pm$ 0.47 ^a	3.97 $\pm$ 0.44	3.91 $\pm$ 0.31	4.65 $\pm$ 1.64 ^b	4.09 $\pm$ 0.39 ^b	4.01 $\pm$ 0.66	3.88 $\pm$ 0.37	3.65 $\pm$ 0.41 ^a
B46	7.97 $\pm$ 0.15 ^a	7.16 $\pm$ 0.15 ^{bd}	7.56 $\pm$ 0.29 ^c	7.22 $\pm$ 0.38 ^b	7.38 $\pm$ 0.26 ^{bc}	7.07 $\pm$ 0.23 ^d	7.24 $\pm$ 0.35 ^{bc}	6.98 $\pm$ 0.23 ^d	8.00 $\pm$ 0.48 ^a
RUM	8.97 $\pm$ 0.41	8.97 $\pm$ 0.37 ^a	9.31 $\pm$ 0.58 ^a	9.38 $\pm$ 0.78 ^a	9.29 $\pm$ 0.49 ^a	9.06 $\pm$ 0.65 ^a	9.12 $\pm$ 0.37 ^a	9.34 $\pm$ 0.84 ^a	8.54 $\pm$ 0.58 ^b
LAC	6.05 $\pm$ 1.94	5.64 $\pm$ 2.01	6.14 $\pm$ 1.94	6.72 $\pm$ 1.50	5.92 $\pm$ 1.71	6.50 $\pm$ 1.66	5.53 $\pm$ 1.83	6.00 $\pm$ 1.50	6.38 $\pm$ 1.37
FIR	10.53 $\pm$ 0.14 ^a	10.11 $\pm$ 0.09 ^b	10.44 $\pm$ 0.17 ^a	10.57 $\pm$ 0.18 ^a	10.35 $\pm$ 0.16 ^{ac}	10.54 $\pm$ 0.18 ^a	10.15 $\pm$ 0.28 ^{bc}	10.40 $\pm$ 0.15 ^a	10.52 $\pm$ 0.29 ^a
BAC	9.72 $\pm$ 0.19 ^a	9.73 $\pm$ 0.16 ^a	10.24 $\pm$ 0.24 ^b	10.35 $\pm$ 0.19 ^b	10.26 $\pm$ 0.25 ^b	10.22 $\pm$ 0.14 ^b	10.19 $\pm$ 0.17 ^b	10.16 $\pm$ 0.21 ^b	10.13 $\pm$ 0.33 ^b
XIV	8.78 $\pm$ 1.01 ^{ac}	7.46 $\pm$ 1.97 ^b	8.48 $\pm$ 0.96 ^{abc}	8.68 $\pm$ 1.56 ^c	8.36 $\pm$ 0.98 ^{abc}	8.80 $\pm$ 0.91 ^{ac}	8.27 $\pm$ 0.72 ^{abc}	8.03 $\pm$ 1.79 ^{abc}	8.21 $\pm$ 0.81 ^{ab}

* EUB, Eubacteria; ECO, *Escherichia coli*; FPRA, *F. prausnitzii*; PGHI, *F. prausnitzii* phylogroup I; PGHII, *F. prausnitzii* phylogroup II; ROS, *Roseburia* spp.; AKK, *A. muciniphila*; B46, best match BLAST *Subdoligranulum variabile*; RUM, *Ruminococcus* spp.; LAC, *Lactobacillus*; FIR, Firmicutes; BAC, Bacteroidetes; XIV, *Clostridial cluster XIV*.

Table S3. Biomarkers abundances in fecal samples of 3 CD patients incubated with different bread treatments. Values are means $\pm$ standard deviation of abundances given as logarithm of total number of genomic units per stool gram analyzed in triplicate. Values within a row with different superscript letters are significantly different (p -value < 0.05).

Bacterial markers*	Incubation control	Substrate control	Ebindb 1 g	Ebindb 2 g	Eblfb1 2 g	Eblfb1 2 g	Eblfb2 1 g	Eblfb2 2 g	Pectin 100 mg
EUB	10.49 $\pm$ 0.35 ^{a-e}	10.26 $\pm$ 0.39 ^b	10.49 $\pm$ 0.20 ^{acd}	10.79 $\pm$ 0.26 ^{ef}	10.48 $\pm$ 0.11 ^c	10.67 $\pm$ 0.15 ^{def}	10.44 $\pm$ 0.18 ^{ac}	10.63 $\pm$ 0.19 ^{adef}	10.81 $\pm$ 0.17 ^f
ECO	4.97 $\pm$ 0.70 ^{abc}	4.56 $\pm$ 0.75 ^a	4.75 $\pm$ 0.45 ^{ab}	5.21 $\pm$ 0.18 ^c	4.83 $\pm$ 0.44 ^{ab}	5.21 $\pm$ 0.17 ^c	4.73 $\pm$ 0.51 ^{ab}	5.11 $\pm$ 0.33 ^{ab}	5.00 $\pm$ 0.51 ^{ac}
FPRA	9.74 $\pm$ 0.48 ^a	9.27 $\pm$ 0.59	9.47 $\pm$ 0.43	9.73 $\pm$ 0.58	9.37 $\pm$ 0.41 ^b	9.48 $\pm$ 0.56	9.23 $\pm$ 0.40 ^b	9.49 $\pm$ 0.50	9.77 $\pm$ 0.74
PGHI	7.24 $\pm$ 2.99 ^a	7.13 $\pm$ 2.93 ^{ab}	7.03 $\pm$ 3.11 ^{ab}	7.00 $\pm$ 3.08 ^{ab}	6.71 $\pm$ 2.88 ^b	6.91 $\pm$ 3.01 ^{ab}	6.93 $\pm$ 2.79 ^b	6.81 $\pm$ 2.93 ^b	7.60 $\pm$ 3.24 ^c
PGHII	10.02 $\pm$ 0.57 ^a	9.46 $\pm$ 0.66 ^b	9.46 $\pm$ 0.56 ^{ab}	9.65 $\pm$ 0.69 ^{ab}	9.29 $\pm$ 0.41 ^{bc}	9.56 $\pm$ 0.70 ^{ab}	9.22 $\pm$ 0.41 ^b	9.49 $\pm$ 0.60 ^{bc}	9.94 $\pm$ 0.74 ^{ac}
ROS	8.24 $\pm$ 0.80 ^{acd}	7.50 $\pm$ 0.76 ^{be}	7.22 $\pm$ 0.53 ^b	8.19 $\pm$ 0.40 ^c	7.22 $\pm$ 0.77 ^b	8.64 $\pm$ 0.32 ^d	7.30 $\pm$ 0.91 ^{ab}	8.42 $\pm$ 0.76 ^{cd}	8.20 $\pm$ 0.85 ^{cde}
AKK	4.48 $\pm$ 2.42 ^a	4.33 $\pm$ 2.23	5.35 $\pm$ 2.10	5.67 $\pm$ 1.79 ^b	5.11 $\pm$ 2.04	5.27 $\pm$ 1.84	5.25 $\pm$ 2.21	5.17 $\pm$ 1.93	5.59 $\pm$ 1.78 ^b
B46	7.58 $\pm$ 0.50 ^{ad}	7.17 $\pm$ 0.56 ^{ab}	7.40 $\pm$ 0.45 ^{abd}	7.66 $\pm$ 0.58 ^{acd}	7.08 $\pm$ 0.23 ^{bc}	7.25 $\pm$ 0.56 ^{abd}	6.91 $\pm$ 0.26 ^b	7.27 $\pm$ 0.55 ^{abd}	7.72 $\pm$ 0.76 ^{cd}
RUM	8.92 $\pm$ 0.55	8.62 $\pm$ 0.37 ^a	9.13 $\pm$ 0.43	9.38 $\pm$ 0.83 ^b	9.07 $\pm$ 0.51	9.28 $\pm$ 0.69 ^b	9.01 $\pm$ 0.51	9.17 $\pm$ 0.61	9.16 $\pm$ 0.54
LAC	7.30 $\pm$ 1.53	7.14 $\pm$ 1.51	7.64 $\pm$ 1.31	7.81 $\pm$ 1.29	7.38 $\pm$ 1.07	7.62 $\pm$ 1.19	6.72 $\pm$ 1.97	7.42 $\pm$ 1.07	7.58 $\pm$ 1.24
FIR	10.53 $\pm$ 0.27 ^{abd}	10.29 $\pm$ 0.25 ^{bc}	10.42 $\pm$ 0.22 ^{ac}	10.68 $\pm$ 0.31 ^{ade}	10.32 $\pm$ 0.14 ^c	10.66 $\pm$ 0.20 ^{de}	10.39 $\pm$ 0.20 ^{ac}	10.60 $\pm$ 0.29 ^{ade}	10.76 $\pm$ 0.25 ^e
BAC	9.89 $\pm$ 0.55 ^{ab}	9.72 $\pm$ 0.48 ^b	10.02 $\pm$ 0.21 ^{acd}	10.27 $\pm$ 0.15 ^e	9.99 $\pm$ 0.11 ^c	10.17 $\pm$ 0.15 ^{de}	9.98 $\pm$ 0.23 ^{ac}	9.99 $\pm$ 0.33 ^{abd}	10.23 $\pm$ 0.12 ^e
XIV	8.62 $\pm$ 0.88	8.25 $\pm$ 0.94 ^a	8.50 $\pm$ 0.26 ^a	9.08 $\pm$ 0.55 ^b	8.45 $\pm$ 0.96 ^a	9.30 $\pm$ 0.47 ^b	8.02 $\pm$ 1.09 ^a	8.86 $\pm$ 0.75	9.25 $\pm$ 0.35 ^b

* EUB, Eubacteria; ECO, *Escherichia coli*; FPRA, *F. prausnitzii*; PHGI, *F. prausnitzii* phylogroup I; PHGII, *F. prausnitzii* phylogroup II; ROS, *Roseburia* spp.; AKK, *A. muciniphila*; B46, best match BLAST *Subdoligranulum variabile*; RUM, *Ruminococcus* spp.; LAC, *Lactobacillus*; FIR, Firmicutes; BAC, Bacteroidetes; XIV, *Clostridial cluster XIV*.

Table S4. Comparison of SFCA concentrations analyzed in fecal samples of UC patients among different treatments. Values are means $\pm$ standard deviation in micrograms per liter of three samples analyzed in triplicate (N = 9). Values within a row with different superscript letters are significantly different (p -value < 0.05).

SCFA	Substrate control	ebindb 1 g	ebindb 2 g	ebfb1 1 g	ebfb1 2 g	ebfb2 1 g	ebfb2 2 g	Pectin 100 mg
Acetic acid	489.98 $\pm$ 140.05 ^a	1426.80 $\pm$ 399.96 ^{bc}	1959.62 $\pm$ 527.45 ^d	1388.67 $\pm$ 210.47 ^{bc}	1912.90 $\pm$ 375.56 ^{cd}	1258.84 $\pm$ 263.51 ^b	1788.92 $\pm$ 450.78 ^{bcd}	2556.24 $\pm$ 1477.47 ^d
Propionic acid	353.47 $\pm$ 118.06 ^a	1036.55 $\pm$ 370.21 ^b	1593.37 $\pm$ 575.59 ^d	1021.73 $\pm$ 212.26 ^b	1478.48 $\pm$ 465.39 ^{cd}	937.32 $\pm$ 210.76 ^{be}	1373.98 $\pm$ 563.74 ^{bc}	743.48 $\pm$ 251.11 ^e
Isobutyric acid	65.01 $\pm$ 20.87	90.44 $\pm$ 58.98 ^a	64.04 $\pm$ 48.37 ^b	75.68 $\pm$ 32.42	72.08 $\pm$ 51.84	65.27 $\pm$ 17.64	57.32 $\pm$ 29.25 ^b	71.44 $\pm$ 22.27
Butyric acid	270.14 $\pm$ 54.47 ^a	1114.16 $\pm$ 743.50 ^{bce}	1667.85 $\pm$ 648.51 ^{de}	904.70 $\pm$ 371.74 ^b	1887.9 $\pm$ 794.14 ^d	907.25 $\pm$ 152.84 ^{bc}	1392.72 $\pm$ 426.78 ^{cd}	695.2 $\pm$ 194.56 ^b
Isovaleric acid	115.75 $\pm$ 43.50 ^{ac}	143.43 $\pm$ 109.47 ^{ab}	99.36 $\pm$ 83.36 ^{cd}	111.15 $\pm$ 58.00 ^{abd}	115.86 $\pm$ 89.21 ^{abd}	92.17 $\pm$ 33.56 ^{bd}	86.2 $\pm$ 45.83 ^{bd}	93.79 $\pm$ 47.03 ^{bd}
Valeric acid	94.47 $\pm$ 51.39 ^a	191.06 $\pm$ 118.90 ^{bc}	206.28 $\pm$ 127.42 ^c	180.02 $\pm$ 107.49 ^{bc}	183.08 $\pm$ 138.19 ^{bc}	156.81 $\pm$ 122.49 ^{bd}	174.73 $\pm$ 109.50 ^{bc}	136.23 $\pm$ 88.07 ^d
Hexanoic acid	24.10 $\pm$ 34.69 ^a	58.22 $\pm$ 87.14	59.52 $\pm$ 77.53 ^b	56.99 $\pm$ 84.18	38.73 $\pm$ 69.37	58.51 $\pm$ 86.54	48.10 $\pm$ 69.42 ^b	42.47 $\pm$ 57.23

Table S5. Comparison of SFCA concentrations analyzed in fecal samples of CD patients among different treatments. Values are means $\pm$ standard deviation in micrograms per liter of three CD samples analyzed in triplicate (N = 9). Values within a row with different superscript letters are significantly different (p -value < 0.05).

SCFA	Substrate control	Ebindb 1 g	Ebindb 2 g	Eblfb1 1 g	Eblfb1 2 g	Eblfb2 1 g	Eblfb2 2 g	Pectin 100 mg
Acetic acid	505.75 $\pm$ 127.58 ^a	1233.83 $\pm$ 251.25 ^b	1958.61 $\pm$ 307.89 ^c	1365.97 $\pm$ 219.94 ^b	1979.95 $\pm$ 794.72 ^c	1286.09 $\pm$ 180.43 ^b	2157.08 $\pm$ 436.36 ^c	2157.09 $\pm$ 436.36 ^c
Propionic acid	268.41 $\pm$ 121.81 ^a	729.29 $\pm$ 366.31 ^b	960.44 $\pm$ 621.04 ^{bc}	791.51 $\pm$ 475.41 ^b	1364.25 $\pm$ 563.71 ^c	816.54 $\pm$ 380.00 ^b	1308.12 $\pm$ 548.92 ^c	1308.12 $\pm$ 548.92 ^b
Isobutyric acid	55.90 $\pm$ 11.23 ^a	72.00 $\pm$ 21.50 ^b	177.86 $\pm$ 268.76 ^c	64.17 $\pm$ 10.78 ^b	69.01 $\pm$ 15.73 ^b	60.81 $\pm$ 12.92 ^{ab}	72.83 $\pm$ 16.62 ^{bc}	72.83 $\pm$ 16.62 ^{abc}
Butyric acid	270.79 $\pm$ 125.79 ^a	688.00 $\pm$ 371.99 ^b	1108.14 $\pm$ 500.98 ^c	729.38 $\pm$ 409.62 ^b	1228.04 $\pm$ 765.58 ^c	623.11 $\pm$ 337.46 ^b	1212.90 $\pm$ 621.22 ^c	1212.9 $\pm$ 621.22 ^{bc}
Isovaleric acid	99.27 $\pm$ 22.76 ^{ad}	116.45 $\pm$ 42.14 ^{bc}	140.24 $\pm$ 69.78 ^c	98.01 $\pm$ 20.14 ^{ab}	103.46 $\pm$ 28.86 ^{ab}	93.41 $\pm$ 25.41 ^{abd}	108.23 $\pm$ 33.64 ^{abc}	108.23 $\pm$ 33.64 ^d
Valeric acid	66.06 $\pm$ 22.48 ^a	115.22 $\pm$ 29.46 ^b	137.17 $\pm$ 53.03 ^b	121.67 $\pm$ 30.88 ^b	132.75 $\pm$ 85.82	119.06 $\pm$ 26.49 ^b	135.66 $\pm$ 76.59	135.65 $\pm$ 76.59 ^a
Hexanoic acid	4.72 $\pm$ 7.79 ^a	30.77 $\pm$ 46.09 ^{ab}	52.42 $\pm$ 76.31 ^{bc}	39.18 $\pm$ 57.52 ^{ab}	68.11 $\pm$ 93.68 ^c	40.59 $\pm$ 55.71 ^{ab}	59.88 $\pm$ 84.76 ^{bc}	177.16 $\pm$ 0.66 ^d

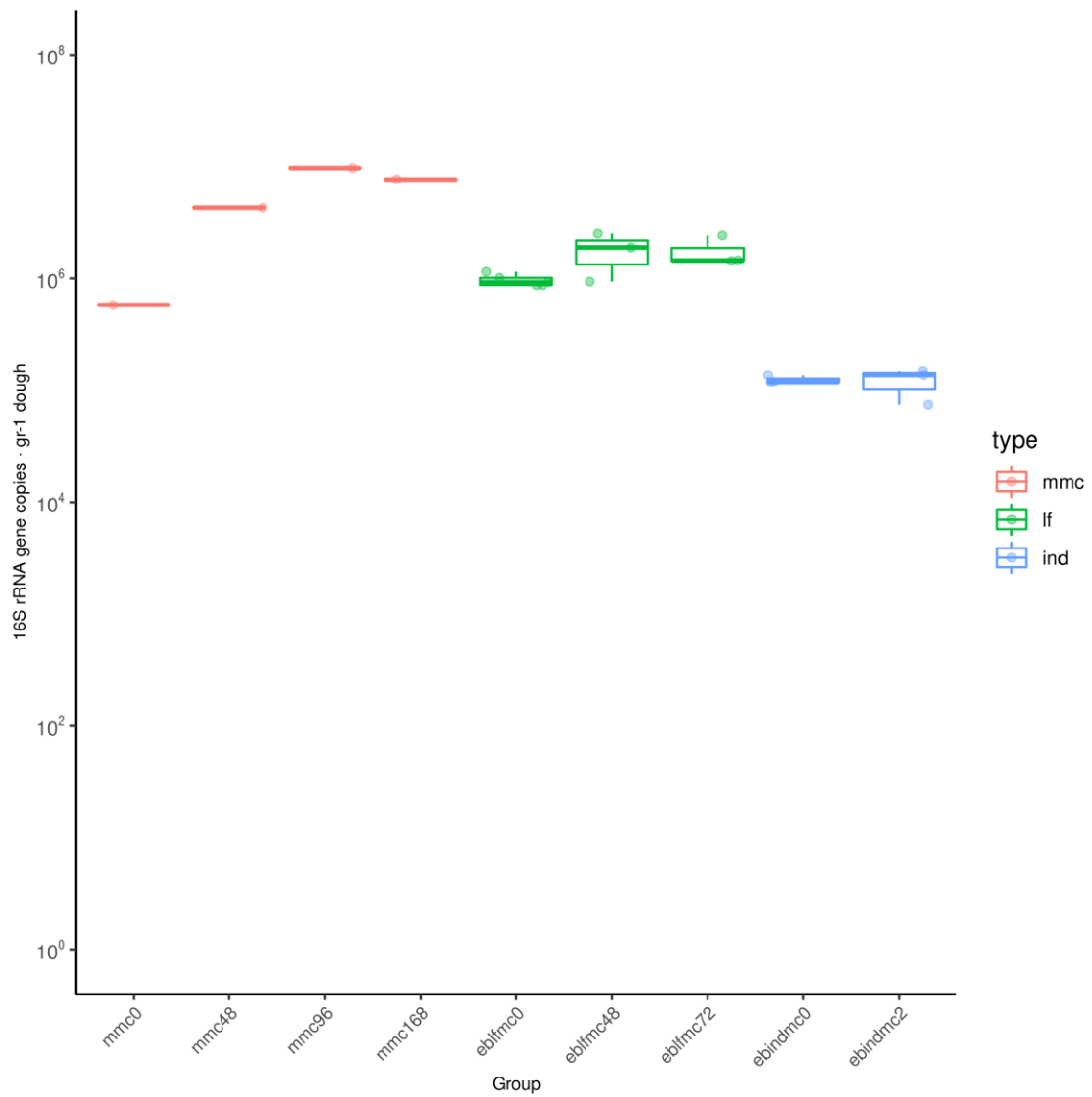


Figure S1. Representation of number of 16S rRNA gene copies per gram of the different types of bread doughs (MMC, sourdough; eblfmc, Elias-Boulangier long-fermentation raw dough; ebindmc, Elias-Boulangier industrial raw dough) at different times of fermentation.

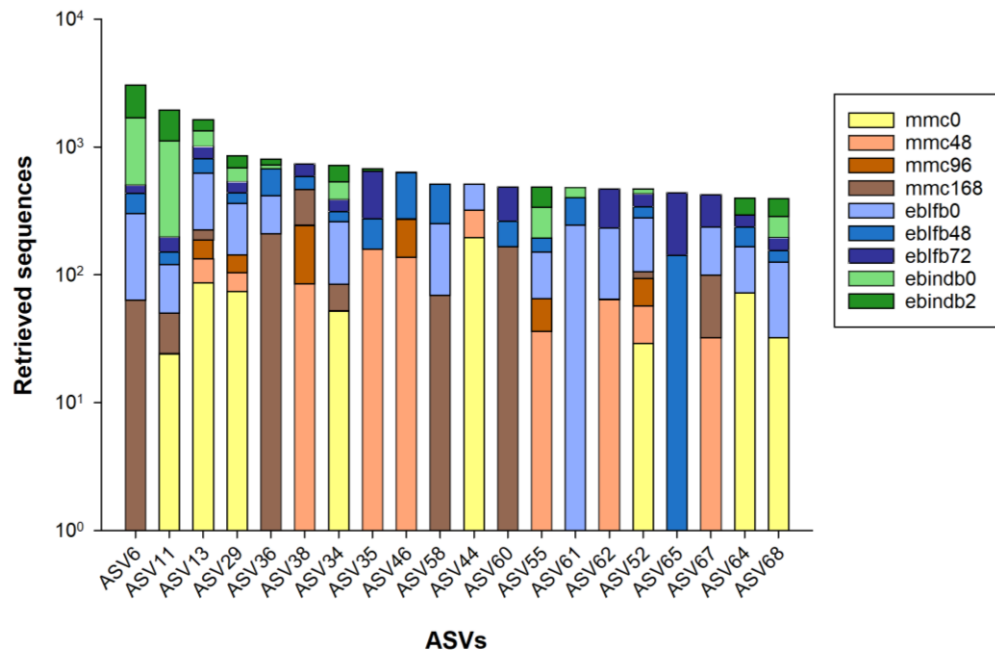


Figure S2. Rank abundance plot showing the top 20 most abundant retrieved ASVs and their abundance in samples grouped according to type of bread doughs and fermentation time for bacteria (16S rRNA gene).

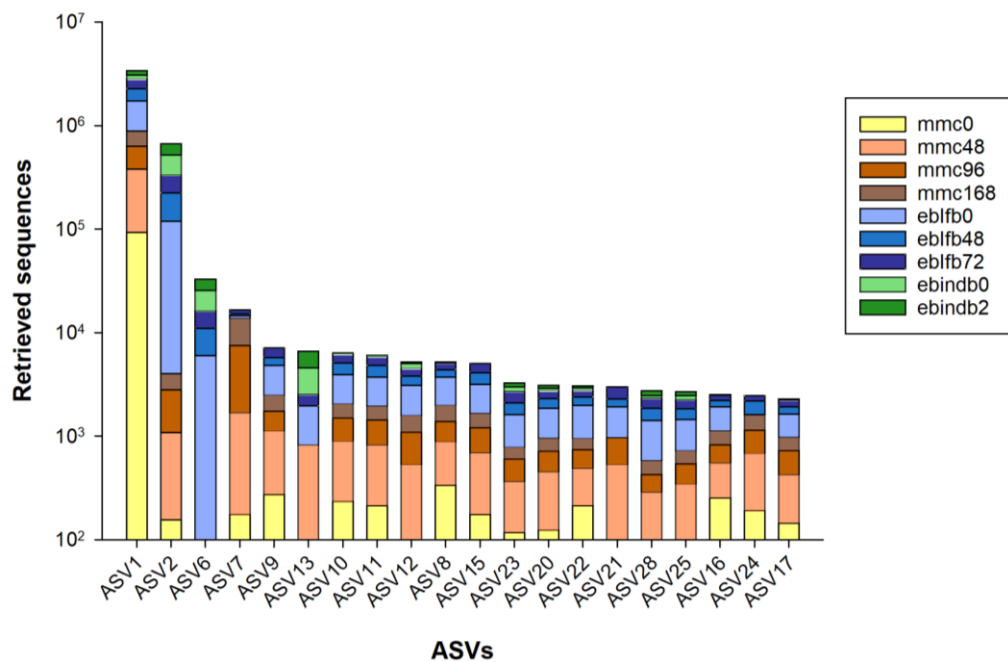


Figure S3. Rank abundance plot showing the top 20 most abundant retrieved ASVs and their abundance in samples grouped according to type of bread doughs and fermentation time for yeast (18S rRNA gene).

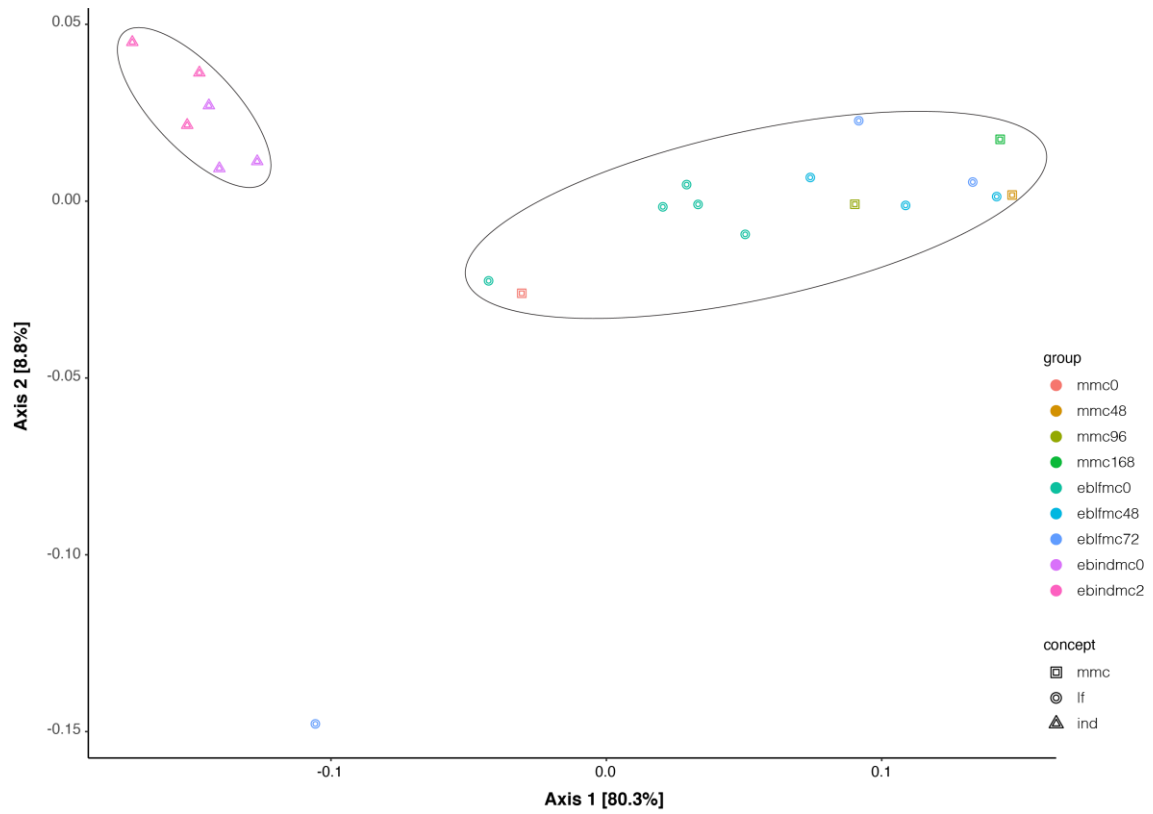


Figure S4. Principal coordinate analysis (PCOA) based on the balanced unifracc metric from the mass sequencing analyses of the different types of bread doughs (MMC, sourdough; eblfmc, Elias-Boulangier long-fermentation raw dough; ebindmc, Elias-Boulangier industrial raw dough) at different times of fermentation for bacteria (16S rRNA gene)

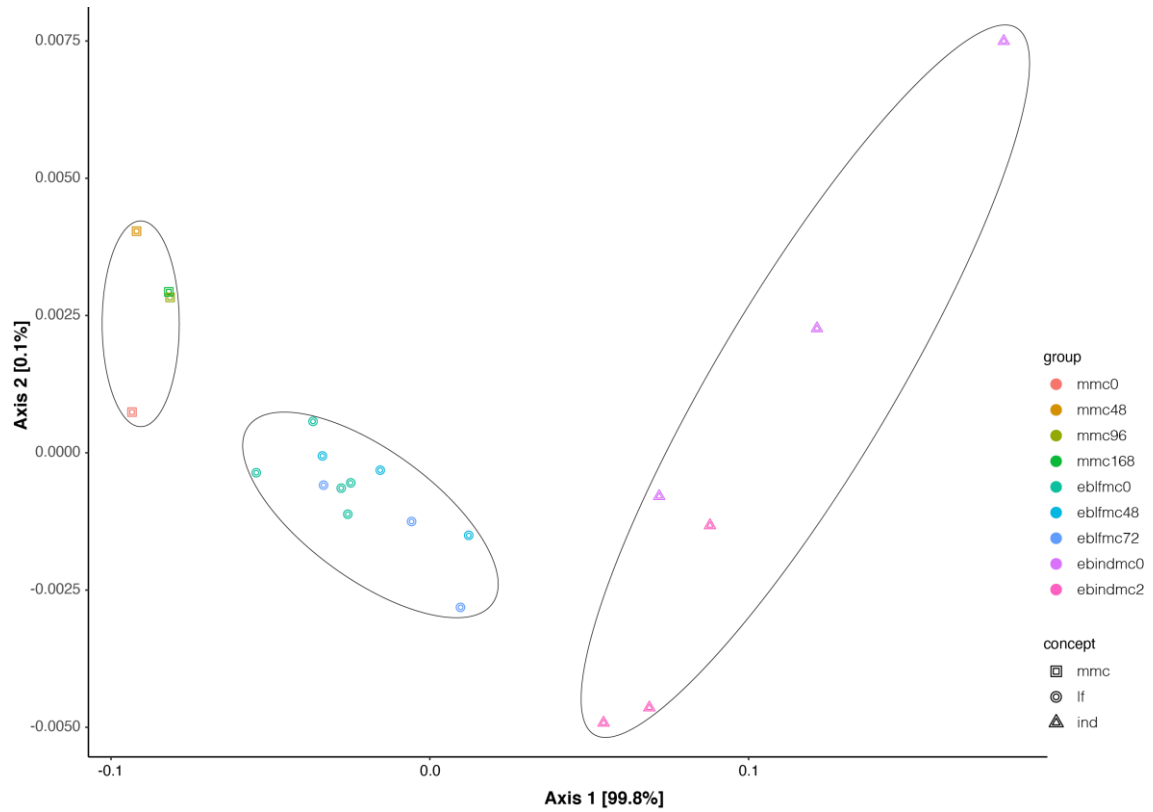


Figure S5. Principal coordinate analysis (PCOA) based on the balanced unifrac metric from the mass sequencing analyses of the different types of bread doughs (MMC, sourdough; eblfmc, Elias-Boulangier long-fermentation raw dough; ebindmc, Elias-Boulangier industrial raw dough) at different times of fermentation for yeast (18S rRNA gene).