

Supplementary information

Table S1. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to clinical diagnosis group.

	Control (n=25)	Polyps (n=35)
Microbial families (% Abundance)		
Bifidobacteriaceae	13.05 ± 13.25	11.13 ± 11.83
Peptostreptococcaceae	6.04 ± 8.06	5.12 ± 5.30
Prevotellaceae	3.42 ± 6.29	3.86 ± 8.22
Lachnospiraceae	19.82 ± 7.29	21.98 ± 8.99
Coriobacteriaceae	6.14 ± 4.13	10.31 ± 9.05
Enterobacteriaceae	2.98 ± 5.09	1.08 ± 2.78
Bacteroidaceae	4.95 ± 6.83	4.32 ± 4.45
Ruminococcaceae	12.43 ± 4.27	11.95 ± 5.40
Veillonellaceae	1.30 ± 1.63	2.39 ± 4.83
Akkermansiaceae	0.59 ± 1.04	1.41 ± 3.50
Streptococcaceae	1.63 ± 3.31	0.87 ± 1.30
Methanobacteriaceae	1.75 ± 2.67	1.57 ± 2.73
Eggerthellaceae	3.25 ± 1.95	4.04 ± 2.13
Erysipelatoclostridiaceae	1.17 ± 1.14	1.40 ± 1.66
Erysipelotrichaceae	1.63 ± 1.97	1.50 ± 2.18
Clostridiaceae	0.78 ± 0.48	1.01 ± 0.86
Oscillospiraceae	2.64 ± 1.51	2.22 ± 1.60
Christensenellaceae	1.61 ± 1.07	1.23 ± 1.21
Eubacterium_coprostanoligenes_group	1.21 ± 0.58	1.22 ± 0.69
Others	13.59 ± 11.16	11.40 ± 9.56
SCFAs (mM)		
Acetic acid	45.97 ± 20.25	50.00 ± 28.23
Butyric acid	13.13 ± 8.72	11.75 ± 7.64
Propionic acid	13.23 ± 6.98	16.12 ± 8.94
Isobutyric acid	0.92 ± 1.04	0.92 ± 1.07
Isovaleric acid	2.01 ± 1.71	2.00 ± 1.52
Valeric acid	2.13 ± 1.56	1.55 ± 1.08
Caproic acid	0.85 ± 1.02	0.27 ± 0.55
Amino acids (mM)		
Total amino acids	48.55 ± 24.78	49.13 ± 22.44
Protein amino acids	47.46 ± 23.82	47.86 ± 21.43
Biogenic amines	0.94 ± 1.40	1.12 ± 2.03
Ammonium	28.51 ± 17.22	29.36 ± 17.36

Values are presented as mean ± standard deviation. SCFAs, short chain fatty acids.

Table S2. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to milk consumption (g/day) category in each diagnosis group.

	Control		Polyps	
	Milk<120 (n=11)	Milk≥120 (n=14)	Milk<120 (n=12)	Milk≥120 (n=23)
Microbial families (% Abundance)				
Bifidobacteriaceae	9.03 ± 11.98	16.21 ± 13.75	12.52 ± 14.58	10.40 ± 10.42
Peptostreptococcaceae	2.48 ± 2.16	8.85 ± 9.86 *	6.26 ± 7.66	4.53 ± 3.62
Prevotellaceae	2.71 ± 4.67	3.98 ± 7.45	3.82 ± 6.71	3.88 ± 9.05
Lachnospiraceae	21.51 ± 4.96	18.5 ± 8.65	18.33 ± 5.74	23.88 ± 9.86
Coriobacteriaceae	5.02 ± 5.06	7.02 ± 3.14 *	9.79 ± 10.21	10.59 ± 8.61
Enterobacteriaceae	3.85 ± 5.45	2.30 ± 4.88	2.14 ± 4.63	0.52 ± 0.56
Bacteroidaceae	8.46 ± 9.17	2.19 ± 1.69 *	2.84 ± 1.74	5.09 ± 5.22
Ruminococcaceae	12.18 ± 3.08	12.63 ± 5.12	11.73 ± 3.69	12.06 ± 6.19
Veillonellaceae	1.39 ± 2.15	1.23 ± 1.17	2.81 ± 5.46	2.17 ± 4.59
Akkermansiaceae	0.61 ± 1.13	0.58 ± 1.02	0.30 ± 0.58	1.98 ± 4.21 *
Streptococcaceae	2.07 ± 4.70	1.29 ± 1.73	0.75 ± 0.68	0.94 ± 1.54
Methanobacteriaceae	1.70 ± 3.15	1.8 ± 2.35	2.76 ± 3.72	0.94 ± 1.84
Eggerthellaceae	3.34 ± 2.45	3.18 ± 1.56	4.44 ± 2.26	3.83 ± 2.09
Erysipelatoclostridiaceae	0.94 ± 1.19	1.35 ± 1.11	1.24 ± 2.26	1.48 ± 1.30
Erysipelotrichaceae	1.35 ± 2.18	1.85 ± 1.84 *	2.20 ± 2.60	1.14 ± 1.89
Clostridiaceae	0.65 ± 0.41	0.89 ± 0.52	0.94 ± 0.80	1.05 ± 0.90
Oscillospiraceae	2.34 ± 1.04	2.87 ± 1.80	2.29 ± 1.45	2.19 ± 1.70
Christensenellaceae	1.77 ± 1.32	1.48 ± 0.86	1.25 ± 0.73	1.22 ± 1.41
Eubacterium_coprostanoligenes_group	1.10 ± 0.53	1.30 ± 0.62	1.48 ± 0.59	1.08 ± 0.72
Others	17.50 ± 12.50	10.51 ± 9.31	12.12 ± 9.28	11.03 ± 9.89
SCFAs (mM)				
Acetic acid	50.77 ± 21.68	42.20 ± 18.98	44.33 ± 24.44	52.95 ± 30.10
Butyric acid	14.44 ± 9.79	12.10 ± 8.02	11.44 ± 6.65	11.91 ± 8.25
Propionic acid	12.64 ± 5.4	13.69 ± 8.18	13.89 ± 8.84	17.29 ± 8.95
Isobutyric acid	0.61 ± 0.70	1.16 ± 1.22	1.08 ± 1.26	0.85 ± 0.97
Isovaleric acid	1.48 ± 1.14	2.43 ± 1.99	2.14 ± 1.32	1.92 ± 1.64
Valeric acid	1.79 ± 1.02	2.39 ± 1.88	1.74 ± 1.3	1.44 ± 0.96
Caproic acid	1.08 ± 1.28	0.67 ± 0.77	0.62 ± 0.83	0.09 ± 0.15
Amino acids (mM)				
Total amino acids	42.14 ± 19.91	53.58 ± 27.70	48.31 ± 16.52	49.56 ± 25.33
Protein amino acids	41.10 ± 19.50	52.46 ± 26.34	47.46 ± 15.66	48.06 ± 24.24
Biogenic amines	0.91 ± 1.39	0.97 ± 1.47	0.67 ± 1.34	1.35 ± 2.31
Ammonium	26.32 ± 15.23	30.23 ± 19.02	29.3 ± 13.25	29.39 ± 19.44

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. SCFAs, short chain fatty acids.

Table S3. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to red meat consumption (g/day) category in each diagnosis group.

	Control		Polyps	
	R.M<50 (n=14)	R.M≥50 (n=11)	R.M<50 (n=18)	R.M≥50 (n=17)
Microbial families (% Abundance)				
Bifidobacteriaceae	12.37 ± 12.26	13.92 ± 14.98	10.37 ± 10.25	11.93 ± 13.59
Peptostreptococcaceae	5.45 ± 8.60	6.80 ± 7.66	4.76 ± 4.07	5.51 ± 6.47
Prevotellaceae	2.43 ± 4.17	4.68 ± 8.32	5.4 ± 10.52	2.22 ± 4.53
Lachnospiraceae	19.10 ± 5.03	20.74 ± 9.64	23.46 ± 9.24	20.42 ± 8.70
Coriobacteriaceae	4.15 ± 2.56	8.67 ± 4.46 *	9.02 ± 8.18	11.69 ± 9.95
Enterobacteriaceae	2.66 ± 4.89	3.40 ± 5.54	0.58 ± 0.49	1.60 ± 3.95
Bacteroidaceae	7.17 ± 8.45	2.12 ± 1.88 *	5.22 ± 5.21	3.36 ± 3.36
Ruminococcaceae	12.22 ± 3.63	12.71 ± 5.14	12.80 ± 4.74	11.04 ± 6.04
Veillonellaceae	1.10 ± 1.26	1.56 ± 2.05	2.25 ± 4.17	2.54 ± 5.58
Akkermansiaceae	0.82 ± 1.18	0.31 ± 0.80 *	1.40 ± 2.56	1.41 ± 4.36
Streptococcaceae	2.36 ± 4.3	0.72 ± 0.82	0.83 ± 1.49	0.92 ± 1.12
Methanobacteriaceae	1.65 ± 2.95	1.89 ± 2.42	0.88 ± 2.19	2.29 ± 3.10
Eggerthellaceae	3.31 ± 2.37	3.18 ± 1.37	4.04 ± 1.77	4.04 ± 2.52
Erysipelatoclostridiaceae	0.87 ± 0.92	1.55 ± 1.31	0.96 ± 0.69	1.87 ± 2.22
Erysipelotrichaceae	1.43 ± 2.04	1.89 ± 1.93	1.26 ± 1.69	1.77 ± 2.64
Clostridiaceae	0.75 ± 0.48	0.83 ± 0.51	1.01 ± 1.01	1.01 ± 0.69
Oscillospiraceae	2.85 ± 1.50	2.37 ± 1.55	2.38 ± 1.50	2.06 ± 1.73
Christensenellaceae	1.62 ± 0.97	1.60 ± 1.24	1.18 ± 0.94	1.29 ± 1.47
Eubacterium_coprostanoligenes_group	1.11 ± 0.68	1.34 ± 0.40	1.29 ± 0.54	1.13 ± 0.84
Others	16.50 ± 11.89	9.75 ± 9.30	10.92 ± 7.14	11.91 ± 11.81
SCFAs (mM)				
Acetic acid	44.44 ± 20.51	47.91 ± 20.72	44.66 ± 21.14	55.65 ± 33.95
Butyric acid	12.00 ± 9.30	14.56 ± 8.13	10.44 ± 4.83	13.13 ± 9.76
Propionic acid	11.52 ± 5.46	15.40 ± 8.29	13.89 ± 6.98	18.49 ± 10.31
Isobutyric acid	0.66 ± 0.63	1.24 ± 1.38	0.91 ± 0.90	0.94 ± 1.24
Isovaleric acid	1.60 ± 0.97	2.54 ± 2.28	2.06 ± 1.47	1.93 ± 1.62
Valeric acid	1.48 ± 0.58	2.95 ± 2.02 †	1.61 ± 0.92	1.48 ± 1.25
Caproic acid	0.62 ± 0.86	1.14 ± 1.18	0.25 ± 0.59	0.29 ± 0.52
Amino acids (mM)				
Total amino acids	43.00 ± 20.40	55.60 ± 28.90	44.18 ± 21.34	54.37 ± 23.02
Protein amino acids	42.21 ± 20.08	54.13 ± 27.39	43.64 ± 20.75	52.32 ± 21.86
Biogenic amines	0.65 ± 1.05	1.32 ± 1.74	0.40 ± 0.77	1.88 ± 2.64
Ammonium	24.74 ± 11.90	33.31 ± 21.96	28.37 ± 17.11	30.41 ± 18.08

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (†) U Mann-Whitney statistically significant difference (p < 0.05) in metabolite between the two levels of consumption in the diagnosis group. R.M, red meat; SCFAs, short chain fatty acids.

Table S4. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to processed meat consumption (g/day) category in each diagnosis group.

	Control		Polyps	
	P.M<25 (n=4)	P.M≥25 (n=21)	P.M<25 (n=7)	P.M≥25 (n=28)
Microbial families (% Abundance)				
Bifidobacteriaceae	24.94 ± 12.35	10.79 ± 12.41 *	15.83 ± 13.65	9.95 ± 11.31
Peptostreptococcaceae	9.97 ± 11.73	5.30 ± 7.33	4.15 ± 3.22	5.37 ± 5.73
Prevotellaceae	3.09 ± 2.30	3.48 ± 6.83 *	4.87 ± 6.52	3.60 ± 8.68
Lachnospiraceae	15.11 ± 5.77	20.72 ± 7.31	20.14 ± 10.08	22.44 ± 8.83
Coriobacteriaceae	4.81 ± 1.67	6.39 ± 4.43	9.79 ± 7.36	10.44 ± 9.54
Enterobacteriaceae	2.62 ± 4.75	3.06 ± 5.26	0.43 ± 0.50	1.24 ± 3.09
Bacteroidaceae	2.91 ± 1.01	5.34 ± 7.41	2.57 ± 1.83	4.76 ± 4.81
Ruminococcaceae	9.99 ± 3.07	12.90 ± 4.36	10.23 ± 3.46	12.38 ± 5.76
Veillonellaceae	1.63 ± 1.36	1.24 ± 1.70	3.98 ± 8.17	1.99 ± 3.71
Akkermansiaceae	0.62 ± 1.00	0.59 ± 1.07	0.78 ± 1.32	1.56 ± 3.86
Streptococcaceae	5.12 ± 7.22	0.97 ± 1.57	0.58 ± 0.42	0.95 ± 1.44
Methanobacteriaceae	0.53 ± 0.46	1.99 ± 2.86	1.11 ± 2.32	1.68 ± 2.84
Eggerthellaceae	2.77 ± 0.77	3.34 ± 2.11	4.78 ± 2.65	3.85 ± 2.00
Erysipelatoclostridiaceae	0.46 ± 0.20	1.30 ± 1.20 *	0.52 ± 0.39	1.62 ± 1.79 *
Erysipelotrichaceae	0.91 ± 0.83	1.77 ± 2.10	1.65 ± 1.93	1.47 ± 2.27
Clostridiaceae	0.75 ± 0.41	0.79 ± 0.50	0.90 ± 0.80	1.04 ± 0.88
Oscillospiraceae	2.46 ± 0.50	2.68 ± 1.64	2.83 ± 1.62	2.07 ± 1.59
Christensenellaceae	1.54 ± 0.29	1.62 ± 1.17	1.86 ± 1.70	1.07 ± 1.03
Eubacterium_coprostanoligenes_group	1.05 ± 0.26	1.24 ± 0.62	0.94 ± 0.36	1.29 ± 0.74
Others	8.75 ± 4.64	14.51 ± 11.86	12.08 ± 7.76	11.23 ± 10.08
SCFAs (mM)				
Acetic acid	40.38 ± 30.09	47.03 ± 18.67	45.19 ± 17.95	51.20 ± 30.4
Butyric acid	13.92 ± 13.92	12.98 ± 7.88	11.65 ± 5.37	11.77 ± 8.19
Propionic acid	10.77 ± 8.13	13.70 ± 6.86	15.25 ± 7.90	16.34 ± 9.30
Isobutyric acid	0.43 ± 0.19	1.01 ± 1.12	1.34 ± 1.04	0.82 ± 1.06
Isovaleric acid	1.30 ± 0.40	2.15 ± 1.83	2.77 ± 1.74	1.80 ± 1.43
Valeric acid	1.59 ± 0.73	2.23 ± 1.67	1.87 ± 0.80	1.47 ± 1.14
Caproic acid	0.87 ± 0.89	0.84 ± 1.07	0.13 ± 0.17	0.30 ± 0.61
Amino acids (mM)				
Total amino acids	46.90 ± 10.80	48.86 ± 26.81	60.01 ± 30.34	46.41 ± 19.78
Protein amino acids	45.70 ± 9.64	47.79 ± 25.81	59.36 ± 29.56	44.98 ± 18.48
Biogenic amines	0.98 ± 1.64	0.94 ± 1.40	0.49 ± 0.80	1.28 ± 2.22
Ammonium	25.34 ± 10.42	29.11 ± 18.36	41.14 ± 26.43	26.42 ± 13.38

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. P.M, processed meat; SCFAs, short chain fatty acids.

Table S5. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to fibre consumption (g/day) category in each diagnosis group.

	Control		Polyps	
	Fibre<20 (n=9)	Fibre≥20 (n=16)	Fibre<20 (n=20)	Fibre≥20 (n=15)
Microbial families (% Abundance)				
Bifidobacteriaceae	12.41 ± 15.75	13.41 ± 12.17	11.12 ± 11.22	11.13 ± 13.01
Peptostreptococcaceae	3.16 ± 2.12	7.67 ± 9.69	4.83 ± 4.09	5.52 ± 6.73
Prevotellaceae	3.24 ± 4.88	3.52 ± 7.11	1.84 ± 4.03	6.54 ± 11.34
Lachnospiraceae	20.93 ± 5.58	19.20 ± 8.20	24.32 ± 9.78	18.86 ± 6.93
Coriobacteriaceae	4.23 ± 2.16	7.21 ± 4.63 *	11.72 ± 8.62	8.43 ± 9.55
Enterobacteriaceae	3.76 ± 5.85	2.55 ± 4.75	0.58 ± 0.65	1.74 ± 4.17
Bacteroidaceae	8.15 ± 9.86	3.15 ± 3.64	3.73 ± 3.96	5.10 ± 5.05
Ruminococcaceae	12.93 ± 4.79	12.15 ± 4.08	11.4 ± 4.25	12.67 ± 6.75
Veillonellaceae	0.78 ± 0.71	1.59 ± 1.94	1.84 ± 3.95	3.12 ± 5.88
Akkermansiaceae	0.80 ± 1.32	0.48 ± 0.88	1.25 ± 2.45	1.61 ± 4.63
Streptococcaceae	2.62 ± 5.10	1.08 ± 1.66	0.82 ± 1.03	0.95 ± 1.64
Methanobacteriaceae	1.87 ± 3.08	1.69 ± 2.52	1.74 ± 3.14	1.34 ± 2.14
Eggerthellaceae	3.13 ± 2.60	3.32 ± 1.58	4.35 ± 1.93	3.62 ± 2.38
Erysipelatoclostridiaceae	0.86 ± 0.88	1.34 ± 1.26	1.61 ± 2.05	1.12 ± 0.93
Erysipelotrichaceae	1.82 ± 2.33	1.52 ± 1.80	1.03 ± 1.46	2.14 ± 2.81
Clostridiaceae	0.70 ± 0.34	0.83 ± 0.55	1.18 ± 0.99	0.79 ± 0.60
Oscillospiraceae	2.58 ± 1.40	2.68 ± 1.62	2.38 ± 1.94	2.01 ± 1.01
Christensenellaceae	1.96 ± 1.38	1.41 ± 0.84	1.34 ± 1.32	1.08 ± 1.07
Eubacterium_coprostanoligenes_group	1.03 ± 0.43	1.32 ± 0.64	1.14 ± 0.66	1.32 ± 0.74
Others	13.04 ± 12.13	13.90 ± 10.99	11.77 ± 7.49	10.92 ± 12.06
SCFAs (mM)				
Acetic acid	51.37 ± 25.88	42.93 ± 16.47	46.87 ± 27.55	54.17 ± 29.54
Butyric acid	14.45 ± 11.19	12.39 ± 7.31	10.39 ± 6.73	13.56 ± 8.62
Propionic acid	14.23 ± 9.15	12.67 ± 5.69	15.30 ± 9.55	17.22 ± 8.24
Isobutyric acid	0.35 ± 0.28	1.23 ± 1.19 ⁺	0.65 ± 0.68	1.29 ± 1.37
Isovaleric acid	1.12 ± 0.59	2.51 ± 1.93 ⁺	1.67 ± 1.09	2.43 ± 1.91
Valeric acid	1.68 ± 0.86	2.37 ± 1.83	1.41 ± 1.13	1.73 ± 1.02
Caproic acid	1.11 ± 1.00	0.70 ± 1.04	0.28 ± 0.65	0.26 ± 0.41
Amino acids (mM)				
Total amino acids	38.51 ± 19.94	54.19 ± 26	46.43 ± 22.34	52.73 ± 22.83
Protein amino acids	37.50 ± 19.46	53.05 ± 24.75	44.93 ± 20.96	51.76 ± 22.17
Biogenic amines	0.84 ± 1.21	1.00 ± 1.54	1.35 ± 2.52	0.81 ± 1.12
Ammonium	19.83 ± 10.19	33.39 ± 18.66	28.40 ± 17.63	30.64 ± 17.51

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (⁺) U Mann-Whitney statistically significant difference (p < 0.05) in metabolite between the two levels of consumption in the diagnosis groups. SCFAs, short chain fatty acids.

Table S6. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to soluble pectin intake (g/day) category in each diagnosis group.

	Control		Polyps	
	S.P.<0.57 (n=9)	S.P.≥0.57 (n=16)	S.P.<0.57 (n=17)	S.P.≥0.57 (n=18)
Microbial families (% Abundance)				
Bifidobacteriaceae	10.37 ± 7.17	14.56 ± 15.7	10.08 ± 10.20	12.12 ± 13.42
Peptostreptococcaceae	4.70 ± 4.41	6.80 ± 9.59	5.98 ± 6.81	4.32 ± 3.34
Prevotellaceae	4.17 ± 8.47	3.00 ± 4.95	2.10 ± 4.54	5.52 ± 10.48
Lachnospiraceae	20.04 ± 8.15	19.7 ± 7.04	25.02 ± 9.17	19.11 ± 8.02
Coriobacteriaceae	6.23 ± 4.41	6.08 ± 4.11	11.04 ± 7.44	9.63 ± 10.51
Enterobacteriaceae	3.76 ± 5.91	2.55 ± 4.72	1.49 ± 3.88	0.69 ± 1.00
Bacteroidaceae	6.93 ± 10.12	3.84 ± 4.06	4.09 ± 3.57	4.54 ± 5.24
Ruminococcaceae	11.54 ± 4.02	12.94 ± 4.44	11.10 ± 4.49	12.74 ± 6.17
Veillonellaceae	1.20 ± 1.23	1.36 ± 1.86	0.90 ± 1.10	3.80 ± 6.42
Akkermansiaceae	0.50 ± 1.12	0.65 ± 1.03	1.77 ± 4.35	1.06 ± 2.53
Streptococcaceae	2.31 ± 5.06	1.26 ± 1.86	0.75 ± 1.55	0.99 ± 1.05
Methanobacteriaceae	1.30 ± 1.49	2.01 ± 3.17	1.19 ± 2.03	1.93 ± 3.27
Eggerthellaceae	3.41 ± 1.79	3.16 ± 2.09	4.33 ± 2.21	3.76 ± 2.08
Erysipelatoclostridiaceae	0.98 ± 0.82	1.27 ± 1.30	1.50 ± 2.00	1.31 ± 1.32
Erysipelotrichaceae	2.17 ± 2.62	1.33 ± 1.50	1.91 ± 2.70	1.13 ± 1.53
Clostridiaceae	0.66 ± 0.38	0.85 ± 0.53	1.12 ± 1.03	0.90 ± 0.67
Oscillospiraceae	2.85 ± 1.65	2.52 ± 1.47	1.86 ± 1.38	2.57 ± 1.75
Christensenellaceae	1.70 ± 0.99	1.55 ± 1.15	1.03 ± 1.15	1.42 ± 1.26
Eubacterium_coprostanoligenes_group	1.03 ± 0.47	1.31 ± 0.62	1.18 ± 0.70	1.25 ± 0.70
Others	14.15 ± 11.91	13.27 ± 11.11	11.58 ± 9.33	11.23 ± 10.04
SCFAs (mM)				
Acetic acid	53.17 ± 21.53	41.92 ± 18.97	54.18 ± 25.66	46.05 ± 30.66
Butyric acid	14.16 ± 11.44	12.55 ± 7.14	12.50 ± 7.45	11.04 ± 7.96
Propionic acid	13.39 ± 5.86	13.14 ± 7.72	17.37 ± 7.42	14.95 ± 10.24
Isobutyric acid	0.96 ± 1.47	0.89 ± 0.77	1.08 ± 1.32	0.78 ± 0.76
Isovaleric acid	2.13 ± 2.46	1.94 ± 1.19	2.12 ± 1.75	1.87 ± 1.31
Valeric acid	2.48 ± 2.28	1.93 ± 1.01	1.85 ± 1.26	1.26 ± 0.82
Caproic acid	10 ± 1.06	0.76 ± 1.03	0.40 ± 0.72	0.14 ± 0.28
Amino acids (mM)				
Total amino acids	42.88 ± 24.88	51.73 ± 24.95	49.89 ± 25.29	48.42 ± 20.10
Protein amino acids	41.39 ± 23.48	50.87 ± 24.06	48.76 ± 24.22	47.00 ± 19.12
Biogenic amines	1.35 ± 1.73	0.71 ± 1.18	0.96 ± 1.34	1.27 ± 2.56
Ammonium	27.19 ± 15.39	29.25 ± 18.61	29.89 ± 18.07	28.86 ± 17.17

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. S.P , soluble pectin; SCFAs, short chain fatty acids.

Table S7. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to total polyphenols intake (mg/day) category in each diagnosis group.

	Control		Polyps	
	T.P.<650 (n=2)	T.P.≥650 (n=23)	T.P.<650 (n=4)	T.P.≥650 (n=31)
Microbial families (% Abundance)				
Bifidobacteriaceae	12.33 ± 12.69	18.32 ± 19.19	11.64 ± 12	2.71 ± 0.24
Peptostreptococcaceae	6.46 ± 8.49	3.02 ± 2.68 *	4.89 ± 5.34	9 ± 3.52
Prevotellaceae	3.71 ± 6.66	1.30 ± 0.99 *	4.07 ± 8.43	0.41 ± 0.11
Lachnospiraceae	19.65 ± 7.34	21.11 ± 8.3	21.39 ± 8.91	31.73 ± 0.7
Coriobacteriaceae	5.76 ± 3.49	8.86 ± 8.02 *	10.8 ± 9.10	2.32 ± 0.25
Enterobacteriaceae	3.05 ± 5.29	2.49 ± 4.08	1.11 ± 2.86	0.62 ± 0.02
Bacteroidaceae	5.21 ± 7.26	3.03 ± 0.67 *	4.17 ± 4.48	6.79 ± 4.25
Ruminococcaceae	12.28 ± 4.30	13.56 ± 4.68	11.2 ± 4.55	24.29 ± 2.87
Veillonellaceae	1.24 ± 1.65	1.74 ± 1.78 *	2.52 ± 4.95	0.23 ± 0.03
Akkermansiaceae	0.56 ± 1.06	0.86 ± 1.09	1.47 ± 3.59	0.27 ± 0.30
Streptococcaceae	1.82 ± 3.50	0.27 ± 0.25	0.87 ± 1.34	0.91 ± 0.11
Methanobacteriaceae	1.94 ± 2.80	0.41 ± 0.42	1.64 ± 2.79	0.43 ± 0.15
Eggerthellaceae	3.23 ± 2.00	3.41 ± 1.98	3.98 ± 2.18	4.97 ± 0.83
Erysipelatoclostridiaceae	1.27 ± 1.18	0.44 ± 0.09	1.39 ± 1.71	1.64 ± 0.84
Erysipelotrichaceae	1.56 ± 1.78	2.17 ± 3.57 *	1.41 ± 2.13	2.99 ± 3.54
Clostridiaceae	0.83 ± 0.48	0.46 ± 0.37	0.99 ± 0.86	1.28 ± 0.89
Oscillospiraceae	2.63 ± 1.59	2.73 ± 0.85	2.23 ± 1.65	2.03 ± 0.47
Christensenellaceae	1.64 ± 1.10	1.4 ± 0.98	1.22 ± 1.24	1.4 ± 0.34
Eubacterium_coprostanoligenes_group	1.15 ± 0.57	1.69 ± 0.41	1.2 ± 0.70	1.49 ± 0.63
Others	31.23 ± 0.53	12.05 ± 10.26	9.04 ± 9.10	11.71 ± 9.72
SCFAs (mM)				
Acetic acid	44.99 ± 19.46	53.15 ± 29.21	49.79 ± 28.94	53.32 ± 16.16
Butyric acid	12.61 ± 8.52	16.91 ± 11.27	11.63 ± 7.83	13.71 ± 3.63
Propionic acid	13.55 ± 7.19	10.88 ± 5.66	16.23 ± 9.2	14.32 ± 0.95
Isobutyric acid	0.91 ± 1.06	0.98 ± 1.17	0.96 ± 1.08	0.28 ± 0.39
Isovaleric acid	2.00 ± 1.75	2.05 ± 1.69	2.06 ± 1.54	0.92 ± 0.75
Valeric acid	2.08 ± 1.59	2.49 ± 1.64	1.56 ± 1.11	1.31 ± 0.02
Caproic acid	0.66 ± 0.80	2.2 ± 1.67	0.28 ± 0.56	0.01 ± 0.00
Amino acids (mM)				
Total amino acids	49.21 ± 25.84	43.71 ± 17.95	49.8 ± 22.85	38.16 ± 12.82
Protein amino acids	48.14 ± 24.89	42.46 ± 16.13	48.48 ± 21.81	37.57 ± 13.34
Biogenic amines	0.91 ± 1.38	1.21 ± 1.86	1.16 ± 2.09	0.46 ± 0.48
Ammonium	27.91 ± 17.69	32.93 ± 15.49	30.28 ± 17.43	14.23 ± 5.56

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. T.P., total polyphenols; SCFAs, short chain fatty acids.

Table S8. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to flavonoids intake (mg/day) category in each diagnosis group.

	Control		Polyps	
	Flavonoids<82	Flavonoids≥82	Flavonoids<82	Flavonoids≥82
	.18 (n=9)	.18 (n=16)	.18 (n=15)	.18 (n=20)
Microbial families (% Abundance)				
Bifidobacteriaceae	14.14 ± 16.08	12.43 ± 11.9	11.57 ± 10.18	10.79 ± 13.19
Peptostreptococcaceae	4.11 ± 4.54	7.13 ± 9.46	5.50 ± 6.88	4.84 ± 3.91
Prevotellaceae	5.25 ± 9.30	2.39 ± 3.75	3.34 ± 5.88	4.25 ± 9.76
Lachnospiraceae	15.74 ± 3.98	22.12 ± 7.80	22.21 ± 10.99	21.81 ± 7.45
Coriobacteriaceae	5.50 ± 4.35	6.49 ± 4.10	13.39 ± 9.53	8.01 ± 8.16
Enterobacteriaceae	4.14 ± 7.55	2.33 ± 3.12	1.49 ± 4.15	0.77 ± 0.96
Bacteroidaceae	7.04 ± 10.13	3.78 ± 3.98	4.18 ± 3.85	4.43 ± 4.95
Ruminococcaceae	10.35 ± 2.86	13.61 ± 4.55	10.32 ± 5.12	13.16 ± 5.42
Veillonellaceae	1.32 ± 1.51	1.29 ± 1.75	2.44 ± 5.61	2.35 ± 4.31
Akkermansiaceae	0.47 ± 1.13	0.66 ± 1.02	1.87 ± 4.64	1.05 ± 2.39
Streptococcaceae	0.63 ± 0.88	2.20 ± 4.03	0.39 ± 0.41	1.23 ± 1.61
Methanobacteriaceae	1.24 ± 1.53	2.05 ± 3.15	0.77 ± 1.60	2.17 ± 3.25
Eggerthellaceae	3.38 ± 1.94	3.18 ± 2.02	4.22 ± 2.42	3.90 ± 1.95
Erysipelatoclostridiaceae	1.24 ± 0.98	1.13 ± 1.25	1.81 ± 2.17	1.09 ± 1.13
Erysipelotrichaceae	2.04 ± 2.36	1.40 ± 1.75	1.38 ± 2.59	1.60 ± 1.88
Clostridiaceae	0.80 ± 0.47	0.77 ± 0.50	1.04 ± 1.10	0.98 ± 0.65
Oscillospiraceae	2.74 ± 1.64	2.59 ± 1.49	1.82 ± 1.37	2.52 ± 1.72
Christensenellaceae	1.37 ± 1.06	1.74 ± 1.09	0.72 ± 0.48	1.61 ± 1.44
Eubacterium_coprostanoligenes_group	1.04 ± 0.50	1.31 ± 0.61	1.02 ± 0.76	1.36 ± 0.63
Others	17.46 ± 13.43	11.41 ± 9.44	10.51 ± 9.06	12.07 ± 10.10
SCFAs (mM)				
Acetic acid	43.17 ± 12.70	47.54 ± 23.72	51.58 ± 28.04	48.80 ± 29.04
Butyric acid	11.19 ± 7.56	14.22 ± 9.37	12.12 ± 8.02	11.47 ± 7.54
Propionic acid	12.37 ± 4.93	13.71 ± 8.01	17.59 ± 8.21	15.03 ± 9.50
Isobutyric acid	1.25 ± 1.48	0.73 ± 0.68	1.12 ± 1.34	0.78 ± 0.81
Isovaleric acid	2.68 ± 2.43	1.63 ± 1.04	2.21 ± 1.73	1.84 ± 1.37
Valeric acid	2.38 ± 2.19	1.98 ± 1.14	1.74 ± 1.24	1.40 ± 0.95
Caproic acid	0.89 ± 0.94	0.82 ± 1.10	0.30 ± 0.56	0.25 ± 0.56
Amino acids (mM)				
Total amino acids	56.11 ± 34.96	44.29 ± 16.65	55.61 ± 26.03	44.27 ± 18.55
Protein amino acids	54.62 ± 33.74	43.43 ± 15.89	54.00 ± 25.21	43.25 ± 17.37
Biogenic amines	1.33 ± 1.79	0.72 ± 1.14	1.41 ± 1.95	0.90 ± 2.11
Ammonium	34.31 ± 24.25	25.25 ± 11.36	34.16 ± 20.09	25.76 ± 14.48

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis (p < 0.05) of metabolites between the two consumption levels. SCFAs, short chain fatty acids.

Table S9. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to other polyphenols intake (mg/day) category in each diagnosis group.

	Control		Polyps	
	O.P.<32.15 (n=17)	O.P.≥32.15 (n=8)	O.P.<32.15 (n=27)	O.P.≥32.15 (n=8)
Microbial families (% Abundance)				
Bifidobacteriaceae	16.28 ± 14.39	6.17 ± 7.00 *	12.34 ± 12.31	7.04 ± 9.64
Peptostreptococcaceae	6.54 ± 9.35	4.98 ± 4.62	4.72 ± 5.36	6.49 ± 5.22
Prevotellaceae	1.07 ± 0.89	8.41 ± 9.60	2.50 ± 4.83	8.45 ± 14.5
Lachnospiraceae	18.87 ± 7.36	21.85 ± 7.16	21.45 ± 8.83	23.76 ± 9.91
Coriobacteriaceae	6.36 ± 4.18	5.66 ± 4.27	10.63 ± 8.77	9.23 ± 10.49
Enterobacteriaceae	3.12 ± 5.76	2.70 ± 3.59	1.26 ± 3.15	0.46 ± 0.49
Bacteroidaceae	5.46 ± 7.60	3.87 ± 5.09	4.34 ± 4.78	4.27 ± 3.37
Ruminococcaceae	11.26 ± 3.27	14.92 ± 5.25	11.12 ± 4.98	14.72 ± 6.21
Veillonellaceae	1.43 ± 1.94	1.03 ± 0.65	2.86 ± 5.41	0.79 ± 0.85
Akkermansiaceae	0.81 ± 1.21	0.14 ± 0.11	1.66 ± 3.94	0.54 ± 0.70
Streptococcaceae	1.14 ± 1.83	2.69 ± 5.30	0.92 ± 1.46	0.73 ± 0.57
Methanobacteriaceae	2.11 ± 3.05	0.99 ± 1.51	1.77 ± 2.95	0.89 ± 1.75
Eggerthellaceae	3.41 ± 2.25	2.92 ± 1.14	4.05 ± 2.21	3.99 ± 2.00
Erysipelatoclostridiaceae	1.10 ± 1.29	1.30 ± 0.78	1.43 ± 1.87	1.3 ± 0.69
Erysipelotrichaceae	1.53 ± 1.78	1.86 ± 2.43	1.28 ± 2.09	2.25 ± 2.47
Clostridiaceae	0.85 ± 0.55	0.64 ± 0.26	0.91 ± 0.65	1.36 ± 1.35
Oscillospiraceae	2.75 ± 1.50	2.40 ± 1.62	2.20 ± 1.76	2.29 ± 0.96
Christensenellaceae	1.70 ± 1.23	1.42 ± 0.64	1.10 ± 1.16	1.68 ± 1.35
Eubacterium_coprostanoligenes_group	1.25 ± 0.66	1.12 ± 0.36	1.19 ± 0.74	1.29 ± 0.57
Others	12.96 ± 10.20	14.93 ± 13.66	12.27 ± 10.54	8.47 ± 4.33
SCFAs (mM)				
Acetic acid	37.13 ± 14.42	64.75 ± 18.37 ⁺	51.62 ± 30.02	44.51 ± 21.89
Butyric acid	9.23 ± 5.36	21.40 ± 8.95 ⁺	12.13 ± 8.39	10.46 ± 4.41
Propionic acid	10.95 ± 5.27	18.08 ± 7.99 ⁺	17.20 ± 9.66	12.49 ± 4.64
Isobutyric acid	0.83 ± 0.75	1.10 ± 1.55	0.98 ± 1.18	0.75 ± 0.53
Isovaleric acid	1.90 ± 1.11	2.24 ± 2.66	2.07 ± 1.68	1.74 ± 0.84
Valeric acid	1.84 ± 1.19	2.74 ± 2.13	1.60 ± 1.18	1.35 ± 0.66
Caproic acid	0.72 ± 1.04	1.12 ± 1.00	0.31 ± 0.59	0.15 ± 0.39
Amino acids (mM)				
Total amino acids	49.29 ± 23.68	46.96 ± 28.64	52.49 ± 24.19	37.80 ± 9.13
Protein amino acids	48.27 ± 22.83	45.73 ± 27.36	50.93 ± 23.13	37.47 ± 9.22
Biogenic amines	0.86 ± 1.19	1.12 ± 1.86	1.39 ± 2.25	0.19 ± 0.26
Ammonium	27.53 ± 17.01	30.59 ± 18.65	31.74 ± 18.75	21.33 ± 7.85

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (†) U Mann-Whitney statistically significant difference ($p < 0.05$) in metabolite between the two levels of consumption in the diagnosis groups. O.T., other polyphenols; SCFAs, short chain fatty acids.

Table S10. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to calcium intake (mg/day) category in each diagnosis group.

	Control		Polyps	
	Ca<900	Ca≥900	Ca<900	Ca≥900
	(n=13)	(n=12)	(n=19)	(n=16)
Microbial families (% Abundance)				
Bifidobacteriaceae	13.69 ± 15.62	12.35 ± 10.75	13.00 ± 12.41	8.90 ± 11.08
Peptostreptococcaceae	3.67 ± 3.40	8.61 ± 10.74	3.57 ± 3.13	6.97 ± 6.74
Prevotellaceae	4.49 ± 7.70	2.26 ± 4.35	4.03 ± 6.19	3.65 ± 10.35
Lachnospiraceae	19.23 ± 6.53	20.46 ± 8.27	20.46 ± 8.07	23.78 ± 9.92
Coriobacteriaceae	4.84 ± 2.76	7.54 ± 4.97	11.00 ± 8.71	9.50 ± 9.65
Enterobacteriaceae	4.36 ± 6.53	1.50 ± 2.32	0.72 ± 1.01	1.50 ± 3.99
Bacteroidaceae	6.39 ± 9.06	3.39 ± 2.68	2.88 ± 2.61	6.03 ± 5.56
Ruminococcaceae	11.92 ± 4.56	12.99 ± 4.04	12.11 ± 4.09	11.75 ± 6.78
Veillonellaceae	2.04 ± 1.99	0.50 ± 0.38 *	3.53 ± 6.29	1.03 ± 1.36
Akkermansiaceae	0.54 ± 1.04	0.66 ± 1.08	0.53 ± 0.92	2.44 ± 4.96
Streptococcaceae	1.60 ± 4.23	1.67 ± 2.10	0.81 ± 0.99	0.94 ± 1.64
Methanobacteriaceae	1.34 ± 2.13	2.21 ± 3.19	2.66 ± 3.35	0.27 ± 0.33 *
Eggerthellaceae	3.00 ± 1.55	3.52 ± 2.35	4.21 ± 2.24	3.84 ± 2.06
Erysipelatoclostridiaceae	1.22 ± 1.19	1.11 ± 1.13	1.14 ± 1.89	1.70 ± 1.34 *
Erysipelotrichaceae	1.95 ± 2.36	1.28 ± 1.45	1.59 ± 2.14	1.40 ± 2.30
Clostridiaceae	0.76 ± 0.47	0.81 ± 0.52	0.86 ± 0.61	1.19 ± 1.07
Oscillospiraceae	2.58 ± 1.48	2.70 ± 1.61	2.64 ± 1.49	1.73 ± 1.63
Christensenellaceae	1.61 ± 1.16	1.61 ± 1.03	1.49 ± 1.34	0.92 ± 0.98 *
Eubacterium_coprostanoligenes_group	1.11 ± 0.47	1.32 ± 0.68	1.44 ± 0.64	0.96 ± 0.69
Others	13.66 ± 11.50	13.50 ± 11.29	11.33 ± 8.05	11.49 ± 11.37
SCFAs (mM)				
Acetic acid	51.94 ± 21.55	39.49 ± 17.31	38.88 ± 18.19	63.2 ± 32.66 ⁺
Butyric acid	13.70 ± 9.82	12.51 ± 7.75	9.73 ± 5.61	14.15 ± 9.13
Propionic acid	13.70 ± 7.99	12.71 ± 6.00	13.27 ± 7.56	19.51 ± 9.48 ⁺
Isobutyric acid	0.53 ± 0.59	1.33 ± 1.28 ⁺	0.92 ± 0.87	0.93 ± 1.29
Isovaleric acid	1.38 ± 1.09	2.69 ± 2.02 ⁺	2.15 ± 1.35	1.81 ± 1.74
Valeric acid	1.78 ± 0.86	2.50 ± 2.06	1.69 ± 1.14	1.37 ± 1.01
Caproic acid	0.98 ± 0.88	0.70 ± 1.19	0.36 ± 0.69	0.16 ± 0.30
Amino acids (mM)				
Total amino acids	41.54 ± 26.83	56.14 ± 20.83	53.19 ± 24.02	44.31 ± 20.10
Protein amino acids	40.48 ± 25.87	55.01 ± 19.7	52.17 ± 23.24	42.73 ± 18.48
Biogenic amines	0.90 ± 1.32	0.99 ± 1.55	0.83 ± 1.35	1.46 ± 2.64
Ammonium	25.16 ± 18.68	32.14 ± 15.44	31.66 ± 19.29	26.63 ± 14.89

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (⁺) U Mann-Whitney statistically significant difference (p < 0.05) in metabolite between the two levels of consumption in the diagnosis groups. Ca, Calcium; SCFAs, short chain fatty acids.

Table S11. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to ethanol intake (g/day) category in each diagnosis group.

	Control		Polyps	
	Ethanol<12	Ethanol≥12	Ethanol<12	Ethanol≥12
	(n=19)	(n=6)	(n=23)	(n=12)
Microbial families (% Abundance)				
Bifidobacteriaceae	12.56 ± 11.74	14.60 ± 18.49	13.86 ± 13.51	5.88 ± 4.69
Peptostreptococcaceae	7.36 ± 8.88	1.87 ± 0.79	3.52 ± 2.96	8.21 ± 7.33 *
Prevotellaceae	3.16 ± 6.50	4.22 ± 6.07	3.34 ± 5.81	4.84 ± 11.83
Lachnospiraceae	18.89 ± 6.57	22.79 ± 9.25	20.23 ± 8.92	25.34 ± 8.47
Coriobacteriaceae	5.94 ± 4.39	6.77 ± 3.42	11.62 ± 9.98	7.82 ± 6.59
Enterobacteriaceae	3.08 ± 5.47	2.69 ± 4.04	0.67 ± 0.91	1.87 ± 4.60
Bacteroidaceae	5.73 ± 7.67	2.47 ± 1.63	4.11 ± 4.83	4.73 ± 3.76
Ruminococcaceae	12.42 ± 4.25	12.47 ± 4.71	11.05 ± 5.33	13.66 ± 5.34
Veillonellaceae	1.32 ± 1.73	1.24 ± 1.43	3.44 ± 5.72	0.38 ± 0.33 *
Akkermansiaceae	0.75 ± 1.16	0.11 ± 0.10	1.95 ± 4.22	0.36 ± 0.60
Streptococcaceae	1.23 ± 1.78	2.92 ± 6.22	0.95 ± 1.53	0.73 ± 0.73
Methanobacteriaceae	2.10 ± 2.94	0.65 ± 1.08	1.35 ± 2.61	1.99 ± 3.00
Eggerthellaceae	3.32 ± 1.99	3.04 ± 2.01	3.85 ± 2.22	4.41 ± 2.00
Erysipelatoclostridiaceae	1.12 ± 1.24	1.31 ± 0.81	1.19 ± 1.34	1.80 ± 2.16
Erysipelotrichaceae	1.55 ± 1.83	1.89 ± 2.53	1.20 ± 1.92	2.09 ± 2.61
Clostridiaceae	0.89 ± 0.51	0.46 ± 0.15	0.80 ± 0.62	1.41 ± 1.11
Oscillospiraceae	2.88 ± 1.62	1.88 ± 0.80	2.34 ± 1.73	2.00 ± 1.35
Christensenellaceae	1.79 ± 1.15	1.04 ± 0.52	1.13 ± 1.27	1.42 ± 1.11
Eubacterium_coprostanoligenes_group	1.29 ± 0.64	0.96 ± 0.23	1.16 ± 0.73	1.32 ± 0.63
Others	12.62 ± 10.11	16.63 ± 14.68	12.26 ± 10.63	9.75 ± 7.22
SCFAs (mM)				
Acetic acid	43.06 ± 21.08	55.17 ± 15.31	48.59 ± 30.67	52.69 ± 23.88
Butyric acid	11.64 ± 7.99	17.83 ± 10.03	11.78 ± 8.36	11.68 ± 6.39
Propionic acid	12.38 ± 7.46	15.91 ± 4.70	16.44 ± 9.58	15.51 ± 7.93
Isobutyric acid	0.97 ± 1.18	0.74 ± 0.43	0.93 ± 0.94	0.92 ± 1.32
Isovaleric acid	2.13 ± 1.91	1.63 ± 0.77	2.13 ± 1.56	1.75 ± 1.49
Valeric acid	2.02 ± 1.69	2.46 ± 1.12	1.50 ± 0.99	1.64 ± 1.29
Caproic acid	0.83 ± 1.07	0.91 ± 0.97	0.13 ± 0.29	0.53 ± 0.81
Amino acids (mM)				
Total amino acids	45.64 ± 26.59	57.77 ± 16.41	54.89 ± 23.22	38.09 ± 16.62 ⁺
Protein amino acids	44.55 ± 25.41	56.67 ± 16.3	53.39 ± 22.31	37.25 ± 15.41 ⁺
Biogenic amines	0.95 ± 1.46	0.91 ± 1.33	1.33 ± 2.32	0.72 ± 1.33
Ammonium	26.37 ± 18.49	35.28 ± 10.98 ⁺	33.18 ± 18.67	22.04 ± 12.04

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (†) U Mann-Whitney statistically significant difference (p < 0.05) in metabolite between the two levels of consumption in the diagnosis groups. SCFAs, short chain fatty acids.

Table S12. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to dibenzo (a) anthracene intake ($\mu\text{g}/\text{day}$) category in each diagnosis group.

	Control		Polyps	
	DiB(a)A<0.07 (n=19)	DiB(a)A \geq 0.07 (n=6)	DiB(a)A<0.07 (n=24)	DiB(a)A \geq 0.07 (n=11)
Microbial families (% Abundance)				
Bifidobacteriaceae	12.45 \pm 11.76	14.94 \pm 18.41	11.92 \pm 13.44	9.39 \pm 7.46
Peptostreptococcaceae	7.17 \pm 8.95	2.49 \pm 1.91	4.50 \pm 4.09	6.49 \pm 7.36
Prevotellaceae	3.38 \pm 6.53	3.54 \pm 6.03	3.25 \pm 5.69	5.17 \pm 12.35
Lachnospiraceae	18.64 \pm 6.36	23.56 \pm 9.33	21.47 \pm 9.42	23.09 \pm 8.28
Coriobacteriaceae	5.88 \pm 4.40	6.95 \pm 3.33	10.81 \pm 9.80	9.24 \pm 7.45
Enterobacteriaceae	3.59 \pm 5.62	1.07 \pm 2.15	0.69 \pm 0.90	1.92 \pm 4.82
Bacteroidaceae	5.68 \pm 7.69	2.63 \pm 1.67	3.24 \pm 3.45	6.69 \pm 5.55
Ruminococcaceae	12.01 \pm 3.97	13.79 \pm 5.26	11.64 \pm 5.69	12.61 \pm 4.91
Veillonellaceae	1.31 \pm 1.73	1.27 \pm 1.44	2.94 \pm 5.71	1.19 \pm 1.42
Akkermansiaceae	0.74 \pm 1.16	0.13 \pm 0.13	1.06 \pm 2.28	2.16 \pm 5.36
Streptococcaceae	2.02 \pm 3.74	0.41 \pm 0.16	1.00 \pm 1.520	0.59 \pm 0.57
Methanobacteriaceae	2.07 \pm 2.96	0.74 \pm 1.06	1.74 \pm 3.07	1.18 \pm 1.81
Eggerthellaceae	3.34 \pm 1.99	2.99 \pm 2.01	4.11 \pm 2.09	3.89 \pm 2.33
Erysipelatoclostridiaceae	1.12 \pm 1.24	1.33 \pm 0.78	1.27 \pm 1.33	1.69 \pm 2.28
Erysipelotrichaceae	1.23 \pm 1.44	2.89 \pm 2.92	1.37 \pm 1.96	1.80 \pm 2.69
Clostridiaceae	0.87 \pm 0.52	0.53 \pm 0.22	1.03 \pm 0.92	0.97 \pm 0.73
Oscillospiraceae	2.79 \pm 1.63	2.16 \pm 1.02	2.40 \pm 1.82	1.83 \pm 0.89
Christensenellaceae	1.74 \pm 1.14	1.18 \pm 0.76	1.23 \pm 1.24	1.24 \pm 1.20
Eubacterium_coprostanoligenes_group	1.26 \pm 0.64	1.05 \pm 0.31	1.21 \pm 0.71	1.22 \pm 0.68
Others	12.71 \pm 10.04	16.36 \pm 14.95	13.13 \pm 10.52	7.64 \pm 5.79
SCFAs (mM)				
Acetic acid	42.85 \pm 20.64	55.85 \pm 16.73	51.3 \pm 30.77	47.15 \pm 22.78
Butyric acid	12.02 \pm 8.85	16.63 \pm 8.00	12.37 \pm 8.19	10.38 \pm 6.42
Propionic acid	12.71 \pm 7.68	14.87 \pm 4.10	15.83 \pm 9.27	16.76 \pm 8.54
Isobutyric acid	0.97 \pm 1.18	0.73 \pm 0.43	0.82 \pm 0.95	1.15 \pm 1.30
Isovaleric acid	2.13 \pm 1.91	1.64 \pm 0.75	1.95 \pm 1.60	2.11 \pm 1.41
Valeric acid	2.02 \pm 1.69	2.45 \pm 1.13	1.43 \pm 0.99	1.80 \pm 1.28
Caproic acid	0.81 \pm 1.05	0.95 \pm 1.03	0.21 \pm 0.53	0.40 \pm 0.60
Amino acids (mM)				
Total amino acids	46.87 \pm 26.54	53.85 \pm 19.16	52.59 \pm 24.44	41.57 \pm 15.72
Protein amino acids	45.60 \pm 25.33	53.33 \pm 18.94	51.14 \pm 23.51	40.68 \pm 14.45
Biogenic amines	1.12 \pm 1.55	0.38 \pm 0.50	1.29 \pm 2.28	0.75 \pm 1.38
Ammonium	27.29 \pm 18.68	32.36 \pm 11.95	32.21 \pm 18.92	23.14 \pm 11.77

Values are presented as mean \pm standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. DiB(a)A, dibenzo (a) anthracene; SCFAs, short chain fatty acids.

Table S13. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to total polycyclic aromatic hydrocarbons intake ($\mu\text{g}/\text{day}$) category in each diagnosis group.

	Control		Polyps	
	PAHs<0.75 (n=9)	PAHs \geq 0.75 (n=16)	PAHs<0.75 (n=10)	PAHs \geq 0.75 (n=25)
Microbial families (% Abundance)				
Bifidobacteriaceae	9.95 \pm 13.19	14.79 \pm 13.38	11.83 \pm 10.43	10.85 \pm 12.54
Peptostreptococcaceae	2.61 \pm 2.36	7.97 \pm 9.49 *	5.01 \pm 4.01	5.17 \pm 5.82
Prevotellaceae	4.75 \pm 6.37	2.67 \pm 6.33	2.76 \pm 5.51	4.30 \pm 9.15
Lachnospiraceae	21.03 \pm 5.60	19.14 \pm 8.18	19.31 \pm 7.24	23.05 \pm 9.52
Coriobacteriaceae	3.02 \pm 1.99	7.89 \pm 4.01 *	9.62 \pm 9.95	10.59 \pm 8.86
Enterobacteriaceae	4.25 \pm 5.78	2.27 \pm 4.71	0.47 \pm 0.45	1.32 \pm 3.26
Bacteroidaceae	9.01 \pm 9.99	2.67 \pm 2.45 *	5.97 \pm 6.01	3.66 \pm 3.59
Ruminococcaceae	13.25 \pm 4.65	11.98 \pm 4.12	12.91 \pm 2.56	11.56 \pm 6.20
Veillonellaceae	1.09 \pm 1.18	1.42 \pm 1.87	3.16 \pm 5.42	2.08 \pm 4.66
Akkermansiaceae	0.73 \pm 1.22	0.52 \pm 0.96	1.77 \pm 3.28	1.26 \pm 3.63
Streptococcaceae	2.12 \pm 5.08	1.36 \pm 1.89	1.21 \pm 1.23	0.74 \pm 1.33
Methanobacteriaceae	0.29 \pm 0.39	2.57 \pm 3.06 *	2.65 \pm 3.96	1.13 \pm 1.99
Eggerthellaceae	2.27 \pm 0.83	3.80 \pm 2.20 *	3.70 \pm 1.72	4.18 \pm 2.30
Erysipelatoclostridiaceae	0.77 \pm 0.55	1.39 \pm 1.33	0.68 \pm 0.34	1.69 \pm 1.89
Erysipelotrichaceae	0.93 \pm 2.03	2.02 \pm 1.88 *	1.11 \pm 1.53	1.66 \pm 2.40
Clostridiaceae	0.61 \pm 0.32	0.88 \pm 0.53	0.84 \pm 0.69	1.08 \pm 0.92
Oscillospiraceae	2.30 \pm 1.20	2.83 \pm 1.67	3.05 \pm 1.78	1.89 \pm 1.43
Christensenellaceae	1.43 \pm 1.06	1.71 \pm 1.10	1.88 \pm 1.43	0.97 \pm 1.02 *
Eubacterium_coprostanoligenes_group	1.03 \pm 0.42	1.32 \pm 0.64	1.43 \pm 0.64	1.13 \pm 0.71
Others	18.56 \pm 13.26	10.79 \pm 9.08	10.64 \pm 6.39	11.71 \pm 10.67
SCFAs (mM)				
Acetic acid	56.72 \pm 23.11	39.92 \pm 16.21	33.27 \pm 15.84	56.69 \pm 29.52 ⁺
Butyric acid	16.39 \pm 10.45	11.29 \pm 7.32	8.29 \pm 4.21	13.13 \pm 8.31
Propionic acid	14.92 \pm 9.36	12.27 \pm 5.34	11.19 \pm 7.04	18.10 \pm 8.96 ⁺
Isobutyric acid	0.39 \pm 0.42	1.21 \pm 1.18 ⁺	0.85 \pm 0.41	0.95 \pm 1.24
Isovaleric acid	1.10 \pm 0.79	2.52 \pm 1.88 ⁺	2.08 \pm 0.53	1.96 \pm 1.78
Valeric acid	1.69 \pm 0.76	2.37 \pm 1.85	1.36 \pm 0.67	1.62 \pm 1.21
Caproic acid	0.94 \pm 0.97	0.79 \pm 1.08	0.18 \pm 0.36	0.30 \pm 0.61
Amino acids (mM)				
Total amino acids	35.93 \pm 21.01	55.64 \pm 24.45 ⁺	42.78 \pm 10.79	51.67 \pm 25.42
Protein amino acids	35.07 \pm 20.76	54.43 \pm 23.11 ⁺	42.15 \pm 10.86	50.14 \pm 24.24
Biogenic amines	0.75 \pm 1.23	1.05 \pm 1.52	0.48 \pm 1.26	1.37 \pm 2.24 ⁺
Ammonium	23.58 \pm 15.02	31.28 \pm 18.20	25.78 \pm 11.89	30.79 \pm 19.14

Values are presented as mean \pm standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (⁺) U Mann-Whitney statistically significant difference ($p < 0.05$) in metabolite between the two levels of consumption in the diagnosis groups. PAHs, polycyclic aromatic hydrocarbons; SCFAs, short chain fatty acids.

Table S14. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to 2-amino-1-methyl-6-phenylimidazo intake (ng/day) category in each diagnosis group.

	Control		Polyps	
	PhIP<40 (n=8)	PhIP≥40 (n=17)	PhIP<40 (n=12)	PhIP≥40 (n=23)
Microbial families (% Abundance)				
Bifidobacteriaceae	14.27 ± 14.15	12.48 ± 13.21	9.80 ± 9.33	11.82 ± 13.1
Peptostreptococcaceae	6.52 ± 11.28	5.82 ± 6.46	6.60 ± 7.23	4.36 ± 3.94
Prevotellaceae	1.45 ± 1.96	4.34 ± 7.41	4.00 ± 11.73	3.78 ± 5.97
Lachnospiraceae	17.29 ± 5.57	21.02 ± 7.83	21.71 ± 10.40	22.12 ± 8.41
Coriobacteriaceae	4.38 ± 3.02	6.96 ± 4.40	8.38 ± 6.93	11.32 ± 9.97
Enterobacteriaceae	4.28 ± 6.10	2.38 ± 4.62	1.82 ± 4.59	0.69 ± 0.97
Bacteroidaceae	4.81 ± 4.98	5.02 ± 7.69	5.22 ± 4.66	3.85 ± 4.36
Ruminococcaceae	11.32 ± 3.82	12.96 ± 4.47	11.20 ± 3.56	12.34 ± 6.19
Veillonellaceae	1.40 ± 1.53	1.25 ± 1.72	4.40 ± 7.53	1.34 ± 2.08
Akkermansiaceae	1.33 ± 1.37	0.25 ± 0.64 *	1.53 ± 3.07	1.34 ± 3.77
Streptococcaceae	2.83 ± 5.51	1.07 ± 1.45	1.05 ± 1.17	0.78 ± 1.39
Methanobacteriaceae	1.52 ± 2.68	1.87 ± 2.75	1.72 ± 3.66	1.49 ± 2.18
Eggerthellaceae	2.88 ± 1.97	3.43 ± 1.98	4.57 ± 2.26	3.76 ± 2.06
Erysipelatoclostridiaceae	1.04 ± 1.18	1.23 ± 1.15	0.83 ± 0.68	1.70 ± 1.94
Erysipelotrichaceae	1.10 ± 1.80	1.88 ± 2.04	2.03 ± 2.41	1.23 ± 2.06
Clostridiaceae	0.81 ± 0.60	0.77 ± 0.43	1.04 ± 0.71	1.00 ± 0.94
Oscillospiraceae	3.15 ± 1.80	2.40 ± 1.35	2.75 ± 1.82	1.95 ± 1.44
Christensenellaceae	1.61 ± 0.93	1.61 ± 1.16	1.35 ± 1.07	1.17 ± 1.29
Eubacterium_coprostanoligenes_group	1.22 ± 0.83	1.21 ± 0.45	1.43 ± 0.60	1.10 ± 0.73
Others	16.79 ± 11.36	12.08 ± 11.09	8.58 ± 6.23	12.88 ± 10.74
SCFAs (mM)				
Acetic acid	42.1 ± 20.44	47.79 ± 20.52	38.67 ± 25.22	55.90 ± 28.41 ⁺
Butyric acid	11.37 ± 10.36	13.96 ± 8.06	9.76 ± 6.32	12.79 ± 8.18
Propionic acid	10.63 ± 6.20	14.45 ± 7.16	14.11 ± 9.35	17.18 ± 8.73
Isobutyric acid	0.75 ± 0.73	0.99 ± 1.18	1.30 ± 1.35	0.73 ± 0.86
Isovaleric acid	1.73 ± 1.11	2.14 ± 1.94	2.59 ± 1.65	1.69 ± 1.39
Valeric acid	1.40 ± 0.51	2.47 ± 1.78	1.38 ± 0.75	1.63 ± 1.23
Caproic acid	0.43 ± 0.69	1.04 ± 1.11	0.13 ± 0.30	0.34 ± 0.64
Amino acids (mM)				
Total amino acids	43.87 ± 19.56	50.75 ± 27.16	49.51 ± 24.55	48.93 ± 21.84
Protein amino acids	42.95 ± 18.68	49.58 ± 26.14	48.42 ± 24.09	47.56 ± 20.49
Biogenic amines	0.77 ± 1.21	1.03 ± 1.52	0.95 ± 1.34	1.21 ± 2.34
Ammonium	26.72 ± 8.19	29.35 ± 20.32	32.1 ± 22.09	27.93 ± 14.67

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (†) U Mann-Whitney statistically significant difference (p < 0.05) in metabolite between the two levels of consumption in the diagnosis groups. PhIP, 2-amino-1-methyl-6-phenylimidazo (4,5,b) pyridine; SCFAs, short chain fatty acids.

Table S15. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to 2-amino-3,8 dimethylimidazo intake (ng/day) category in each diagnosis group.

	Control		Polyps	
	MelQx<50 (n=17)	MelQx≥50 (n=8)	MelQx<50 (n=28)	MelQx≥50 (n=7)
Microbial families (% Abundance)				
Bifidobacteriaceae	12.96 ± 11.64	13.24 ± 17.08	12.23 ± 12.86	6.73 ± 4.59
Peptostreptococcaceae	6.31 ± 9.45	5.49 ± 4.28	5.11 ± 5.67	5.18 ± 3.84
Prevotellaceae	2.28 ± 3.77	5.84 ± 9.66	4.37 ± 9.05	1.81 ± 2.96
Lachnospiraceae	19.20 ± 6.94	21.14 ± 8.30	20.75 ± 8.55	26.91 ± 9.66
Coriobacteriaceae	4.80 ± 3.00	8.98 ± 4.93	9.35 ± 9.41	14.18 ± 6.59
Enterobacteriaceae	3.59 ± 5.86	1.71 ± 2.74	1.14 ± 3.09	0.85 ± 0.82
Bacteroidaceae	6.33 ± 7.76	2.02 ± 2.85 *	4.96 ± 4.74	1.78 ± 1.31
Ruminococcaceae	11.97 ± 3.71	13.41 ± 5.41	11.20 ± 5.35	14.92 ± 4.86
Veillonellaceae	1.10 ± 1.34	1.74 ± 2.17	2.88 ± 5.30	0.41 ± 0.29
Akkermansiaceae	0.84 ± 1.20	0.07 ± 0.05 *	1.62 ± 3.86	0.53 ± 1.12
Streptococcaceae	2.05 ± 3.94	0.74 ± 0.95	0.88 ± 1.30	0.86 ± 1.44
Methanobacteriaceae	1.73 ± 2.80	1.80 ± 2.56	1.49 ± 2.90	1.88 ± 2.03
Eggerthellaceae	3.26 ± 2.19	3.23 ± 1.46	4.04 ± 2.21	4.05 ± 1.98
Erysipelatoclostridiaceae	0.84 ± 0.86	1.86 ± 1.40 *	1.13 ± 1.16	2.47 ± 2.83
Erysipelotrichaceae	1.38 ± 1.85	2.18 ± 2.23	1.17 ± 1.80	2.84 ± 3.13
Clostridiaceae	0.83 ± 0.52	0.69 ± 0.41	0.95 ± 0.90	1.27 ± 0.64
Oscillospiraceae	2.77 ± 1.49	2.37 ± 1.64	2.32 ± 1.74	1.83 ± 0.76
Christensenellaceae	1.65 ± 1.08	1.52 ± 1.12	1.28 ± 1.34	1.02 ± 0.40
Eubacterium_coprostanoligenes_group	1.15 ± 0.64	1.34 ± 0.43	1.16 ± 0.65	1.45 ± 0.87
Others	14.98 ± 11.93	10.63 ± 9.35	11.99 ± 9.97	9.05 ± 7.91
SCFAs (mM)				
Acetic acid	42.43 ± 21.09	53.49 ± 17.15	48.16 ± 28.19	57.33 ± 29.36
Butyric acid	11.46 ± 8.86	16.67 ± 7.78	10.97 ± 7.35	14.84 ± 8.60
Propionic acid	11.78 ± 5.65	16.30 ± 8.84	15.63 ± 9.40	18.11 ± 7.00
Isobutyric acid	0.75 ± 0.68	1.27 ± 1.58	0.97 ± 1.13	0.75 ± 0.83
Isovaleric acid	1.74 ± 1.09	2.59 ± 2.59	2.08 ± 1.59	1.68 ± 1.25
Valeric acid	1.68 ± 1.02	3.08 ± 2.12 ⁺	1.40 ± 0.93	2.12 ± 1.50
Caproic acid	0.48 ± 0.75	1.63 ± 1.13 ⁺	0.17 ± 0.32	0.66 ± 1.01
Amino acids (mM)				
Total amino acids	47.92 ± 24.28	49.88 ± 27.48	48.85 ± 21.97	50.25 ± 26.08
Protein amino acids	47.09 ± 23.41	48.24 ± 26.29	47.71 ± 21.04	48.44 ± 24.70
Biogenic amines	0.68 ± 1.17	1.50 ± 1.77	1.00 ± 2.08	1.59 ± 1.92
Ammonium	28.41 ± 17.48	28.72 ± 17.83	30.44 ± 18.18	25.03 ± 13.87

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. (⁺) U Mann-Whitney statistically significant difference (p < 0.05) in metabolite between the two levels of consumption in the diagnosis groups. MelQx, 2-amino-3,8 dimethylimidazo (4,5,f) quinoxaline; SCFAs, short chain fatty acids.

Table S16. Microbial abundance and faecal SCFAs, amino acids, biogenic amines and ammonium concentrations according to nitrites intake (mg/day) category in each diagnosis group.

	Control		Polyps	
	Nitrites<1.69 (n=6)	Nitrites≥1.69 (n=19)	Nitrites<1.69 (n=12)	Nitrites≥1.69 (n=23)
Microbial families (% Abundance)				
Bifidobacteriaceae	23.98 ± 11.58	9.60 ± 12.01 *	17.28 ± 13.77	7.92 ± 9.50 *
Peptostreptococcaceae	12.94 ± 13.91	3.87 ± 3.48	3.32 ± 2.66	6.06 ± 6.10
Prevotellaceae	2.32 ± 2.14	3.77 ± 7.14 *	3.59 ± 5.51	3.99 ± 9.45
Lachnospiraceae	16.26 ± 6.26	20.95 ± 7.37	20.60 ± 9.06	22.70 ± 9.07
Coriobacteriaceae	5.44 ± 2.39	6.36 ± 4.58	11.32 ± 6.79	9.79 ± 10.13
Enterobacteriaceae	1.91 ± 3.84	3.32 ± 5.47	0.34 ± 0.41	1.46 ± 3.38
Bacteroidaceae	2.33 ± 1.20	5.78 ± 7.67	4.00 ± 3.80	4.49 ± 4.82
Ruminococcaceae	10.74 ± 4.32	12.97 ± 4.22	10.25 ± 5.21	12.83 ± 5.40
Veillonellaceae	1.36 ± 1.14	1.28 ± 1.79	2.95 ± 6.21	2.09 ± 4.06
Akkermansiaceae	0.70 ± 0.93	0.56 ± 1.10	2.08 ± 5.14	1.05 ± 2.30
Streptococcaceae	4.40 ± 5.96	0.76 ± 1.18	0.76 ± 0.73	0.93 ± 1.53
Methanobacteriaceae	0.39 ± 0.42	2.18 ± 2.94	1.51 ± 2.43	1.60 ± 2.92
Eggerthellaceae	2.49 ± 0.75	3.49 ± 2.16	3.99 ± 2.55	4.07 ± 1.95
Erysipelatoclostridiaceae	0.45 ± 0.20	1.40 ± 1.22 *	1.21 ± 1.57	1.50 ± 1.74
Erysipelotrichaceae	0.91 ± 0.76	1.86 ± 2.18	1.71 ± 2.54	1.40 ± 2.02
Clostridiaceae	0.96 ± 0.64	0.73 ± 0.43	0.81 ± 0.67	1.11 ± 0.93
Oscillospiraceae	2.58 ± 1.40	2.66 ± 1.58	2.26 ± 1.55	2.20 ± 1.66
Christensenellaceae	1.36 ± 0.37	1.69 ± 1.21	1.60 ± 1.71	1.04 ± 0.82
Eubacterium_coprostanoligenes_group	1.23 ± 0.74	1.21 ± 0.54	0.97 ± 0.77	1.34 ± 0.63 *
Others	7.27 ± 4.41	15.58 ± 11.97	9.44 ± 6.99	12.42 ± 10.66
SCFAs (mM)				
Acetic acid	39.41 ± 23.77	48.04 ± 19.25	44.50 ± 21.73	52.86 ± 31.15
Butyric acid	12.44 ± 11.28	13.34 ± 8.12	9.69 ± 5.20	12.82 ± 8.56
Propionic acid	11.14 ± 7.74	13.89 ± 6.81	15.85 ± 9.80	16.27 ± 8.68
Isobutyric acid	0.75 ± 0.80	0.97 ± 1.12	1.01 ± 0.89	0.88 ± 1.16
Isovaleric acid	1.70 ± 0.98	2.11 ± 1.89	2.27 ± 1.47	1.85 ± 1.56
Valeric acid	1.60 ± 0.62	2.29 ± 1.74	1.48 ± 0.84	1.58 ± 1.20
Caproic acid	0.63 ± 0.79	0.92 ± 1.10	0.08 ± 0.14	0.37 ± 0.66
Amino acids (mM)				
Total amino acids	50.00 ± 19.31	48.09 ± 26.73	58.82 ± 28.18	44.07 ± 17.42
Protein amino acids	48.86 ± 18.42	47.01 ± 25.72	57.34 ± 26.80	42.91 ± 16.62
Biogenic amines	0.93 ± 1.38	0.95 ± 1.45	1.29 ± 2.48	1.03 ± 1.81
Ammonium	25.66 ± 8.86	29.41 ± 19.23	35.82 ± 22.69	25.99 ± 13.17

Values are presented as mean ± standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. SCFAs, short chain fatty acids.

Table S17. Differences in microbial abundance and faecal SCFAs and amino acids concentrations according to N-nitrosodimethylamine intake ($\mu\text{g}/\text{day}$) category in each diagnosis group.

	Control		Polyps	
	NDMA<0.126 (n=7)	NDMA \geq 0.126 (n=18)	NDMA<0.126 (n=11)	NDMA \geq 0.126 (n=24)
Microbial families (% Abundance)				
Bifidobacteriaceae	21.36 \pm 12.65	9.82 \pm 12.32 *	14.39 \pm 12.74	9.63 \pm 11.36
Peptostreptococcaceae	11.88 \pm 13.01	3.77 \pm 3.55	3.16 \pm 2.85	6.02 \pm 5.95
Prevotellaceae	2.25 \pm 1.96	3.87 \pm 7.33 *	5.92 \pm 7.37	2.91 \pm 8.57
Lachnospiraceae	17.90 \pm 7.18	20.57 \pm 7.39	17.85 \pm 6.8	23.87 \pm 9.34
Coriobacteriaceae	6.05 \pm 2.72	6.17 \pm 4.63	11.89 \pm 9.91	9.59 \pm 8.75
Enterobacteriaceae	1.67 \pm 3.56	3.50 \pm 5.58	0.40 \pm 0.48	1.39 \pm 3.32
Bacteroidaceae	2.08 \pm 1.28	6.07 \pm 7.79	3.83 \pm 3.42	4.55 \pm 4.90
Ruminococcaceae	10.71 \pm 3.95	13.10 \pm 4.30	10.61 \pm 5.02	12.56 \pm 5.57
Veillonellaceae	2.16 \pm 2.35	0.97 \pm 1.18	3.29 \pm 6.43	1.97 \pm 3.99
Akkermansiaceae	0.60 \pm 0.88	0.59 \pm 1.12	2.26 \pm 5.36	1.01 \pm 2.26
Streptococcaceae	3.81 \pm 5.66	0.79 \pm 1.21	0.54 \pm 0.54	1.02 \pm 1.52
Methanobacteriaceae	1.33 \pm 2.51	1.92 \pm 2.78	1.20 \pm 2.28	1.73 \pm 2.94
Eggerthellaceae	2.58 \pm 0.72	3.51 \pm 2.22	3.92 \pm 2.57	4.10 \pm 1.96
Erysipelatoclostridiaceae	1.00 \pm 1.49	1.23 \pm 1.01	0.57 \pm 0.46	1.78 \pm 1.88 *
Erysipelotrichaceae	1.40 \pm 1.49	1.72 \pm 2.15	1.19 \pm 1.64	1.65 \pm 2.41
Clostridiaceae	1.03 \pm 0.61	0.69 \pm 0.41	0.66 \pm 0.56	1.17 \pm 0.93
Oscillospiraceae	2.44 \pm 1.33	2.72 \pm 1.61	2.86 \pm 1.67	1.93 \pm 1.51
Christensenellaceae	1.73 \pm 1.03	1.56 \pm 1.11	1.76 \pm 1.71	0.99 \pm 0.83
Eubacterium_coprostanoligenes_group	1.24 \pm 0.67	1.2 \pm 0.56	1.03 \pm 0.55	1.30 \pm 0.75
Others	6.78 \pm 4.23	16.23 \pm 11.97	12.66 \pm 8.99	10.82 \pm 9.94
SCFAs (mM)				
Acetic acid	43.09 \pm 23.78	47.09 \pm 19.35	38.22 \pm 16.13	55.39 \pm 31.11
Butyric acid	12.48 \pm 10.30	13.38 \pm 8.36	9.30 \pm 5.50	12.87 \pm 8.31
Propionic acid	12.12 \pm 7.53	13.66 \pm 6.93	13.05 \pm 7.19	17.53 \pm 9.43
Isobutyric acid	0.70 \pm 0.74	1.00 \pm 1.15	1.07 \pm 0.93	0.86 \pm 1.13
Isovaleric acid	1.61 \pm 0.92	2.17 \pm 1.93	2.38 \pm 1.49	1.82 \pm 1.54
Valeric acid	1.69 \pm 0.61	2.30 \pm 1.79	1.65 \pm 0.82	1.50 \pm 1.19
Caproic acid	0.65 \pm 0.72	0.92 \pm 1.13	0.22 \pm 0.38	0.29 \pm 0.62
Amino acids (mM)				
Total amino acids	49.60 \pm 17.66	48.14 \pm 27.50	53.37 \pm 25.19	47.18 \pm 21.36
Protein amino acids	48.55 \pm 16.83	47.03 \pm 26.46	52.83 \pm 24.60	45.57 \pm 19.97
Biogenic amines	0.83 \pm 1.28	0.99 \pm 1.48	0.38 \pm 0.64	1.45 \pm 2.36
Ammonium	24.99 \pm 8.27	29.88 \pm 19.68	34.77 \pm 22.45	26.88 \pm 14.34

Values are presented as mean \pm standard deviation. (*) Differential microbial family abundance according to linear effect size discriminant analysis (LEfSe) at a threshold of 2.0 for the comparison of samples from each category of consumption in diagnosis groups. No significant differences were found by U Mann-Whitney analysis ($p < 0.05$) of metabolites between the two consumption levels. NDMA, N-nitrosodimethylamine; SCFAs, short chain fatty acids.

Table S18. Spearman correlation between the relative abundance of Bifidobacteriaceae and faecal SCFAs concentration according to clinical diagnosis group.

SCFAs (mM)	Bifidobacteriaceae	
	ρ	p-value
Control		
Acetic acid	-0.208	0.319
Butyric acid	-0.087	0.679
Propionic acid	-0.219	0.293
Isobutyric acid	-0.001	0.997
Isovaleric acid	0.037	0.861
Valeric acid	0.124	0.556
Caproic acid	0.247	0.233
Polyps		
Acetic acid	-0.053	0.764
Butyric acid	-0.104	0.554
Propionic acid	0.018	0.916
Isobutyric acid	0.234	0.176
Isovaleric acid	0.247	0.152
Valeric acid	0.079	0.651
Caproic acid	-0.293	0.088

Correlation values are presented as Spearman's rank correlation coefficient (ρ) and its associated p-value.