

Title	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer
Authors	Mangifesta, Marta; Mancabelli, Leonardo; Milani, Christian; Gaiani, Federica; de'Angelis, Nicola; de'Angelis, Gian Luigi; van Sinderen, Douwe; Ventura, Marco; Turroni, Francesca
Publication date	2018-09-18
Original Citation	Mangifesta, M., Mancabelli, L., Milani, C., Gaiani, F., de'Angelis, N., de'Angelis, G.L., van Sinderen, D., Ventura, M. and Turroni, F., 2018. Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. Scientific reports, 8(1),(13974). DOI:10.1038/s41598-018-32413-2
Type of publication	Article (peer-reviewed)
Link to publisher's version	https://www.nature.com/articles/s41598-018-32413-2 - 10.1038/s41598-018-32413-2
Rights	© The Author(s) 2018 - https://creativecommons.org/licenses/by/4.0/
Download date	2026-08-10 21:03:00
Item downloaded from	https://hdl.handle.net/10468/8668

Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer

Marta Mangifesta¹, Leonardo Mancabelli¹, Christian Milani¹, Federica Gaiani², Nicola de' Angelis³,
Gian Luigi de' Angelis², Douwe van Sinderen⁴, Marco Ventura^{1,5} and Francesca Turrone^{1,5}

Laboratory of Probiogenomics, Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Parma, Italy¹; Gastroenterology and Endoscopy Unit, University Hospital of Parma, Parma, Italy²; Department of HPB Surgery and Liver Transplantation, Henri-Mondor Hospital, Université Paris Est-UPEC, Créteil, France³; School of Microbiology & APC Microbiome Institute, University College Cork, Cork, Ireland⁴; Microbiome Research Hub, University of Parma, Parma, Italy⁵;

Supplementary information

Additional files

Table S1: Clinicopathologic data of 12 patients with polyps after colonoscopy

Table S2: 16S rRNA microbial profiling data

Table S3: List of the public CRC datasets

Figure S1: Evaluation of alpha-diversity in CMP and HMT samples

Table S1. Clinicopathologic data of 12 patients with polyps after colonoscopy.

Samples	Sex	height (cm)	weight (kg)	BMI	symptoms	bowel motion	n° polyps	CMP sites	HMT sites	histology
1	M	180	96	29.6	pain/abdominal swelling	infrequent	2	rectum	sigmoid	hyperplastic
2	F	165	60	22.2	pain/abdominal swelling	infrequent	1	sigmoid	rectum	hyperplastic
3	F	180	75	23.1	pain/abdominal swelling	regular	2	sigmoid	rectum	hyperplastic
4	M	175	60	19.6	no symptoms	regular	5	transverse colon	sigmoid	hyperplastic
5	M	160	68	26.5	no symptoms	regular	2	sigmoid	sigmoid	tubular adenomas
6	M	175	83	25.6	pain/abdominal swelling	regular	2	transverse colon	sigmoid	tubular adenomas
7	M	162	71	26.1	no symptoms	regular	2	ascending colon	sigmoid	tubular adenomas
8	F	145	37	17.6	hematochezia	constipation	1	rectum	sigmoid	hyperplastic
9	F	165	72	26.5	pain/abdominal swelling	infrequent	1	sigmoid	rectum	hyperplastic
11	F	153	72	30.7	no symptoms	regular	2	sigmoid	rectum	hyperplastic
12	M	176	84	27.2	no symptoms	regular	1	sigmoid	sigmoid	hyperplastic
13	M	162	80	30.5	no symptoms	regular	1	ascending colon	sigmoid	tubular adenomas

Table S2: 16S rRNA microbial profiling data.

Samples	Number of sequenced pe reads	Number of pe reads with mean quality > 20	Number of merged pe reads	Human sequences	Length outside bounds of 100 and 400	Ambiguous bases	Homopolymers > 7	Mismatch in primers >1	Reverse primer not found	Final Read Number
1_HMP	76352	75090	66727	556	0	0	3	31987	68	34113
1_CMP	99597	96947	89782	7454	0	0	4	28562	103	53659
2_HMP	262569	249759	242886	34817	0	0	17	5835	199	202018
2_CMP	120637	117531	114142	3698	0	0	2	2869	72	107501
3_HMP	70571	68276	60599	12564	0	772	29	3025	81	44127
3_CMP	62914	59825	53078	16100	0	578	31	2535	51	33783
4_HMP	65358	64641	60572	3578	0	1051	24	4918	115	63516
4_CMP	41247	39954	35490	15046	0	738	7	4171	102	59414
5_HMP	91031	89145	82349	12725	0	1239	1	3872	109	59684
5_CMP	78916	77830	71003	6571	0	808	3	3050	82	39719
6_HMP	77288	76378	70066	5161	0	1684	8	4183	135	70286
6_CMP	59515	58448	51852	8190	0	1411	1	4043	101	60432
7_HMP	95790	94194	84655	8359	0	884	9	3838	144	51676
7_CMP	74620	73970	66399	410	0	710	16	3179	68	42553
8_HMP	78125	76939	70644	14093	0	825	1	4052	180	52284
8_CMP	101175	98829	91152	44626	0	558	14	3538	99	49062
9_HMP	64850	64070	57440	98	0	825	1	4052	180	52284
9_CMP	76965	75690	68954	15683	0	558	14	3538	99	49062
11_HMP	84825	83923	76741	3315	0	1538	2	4067	114	67705
11_CMP	66890	65438	57745	1064	0	1228	1	3651	98	51703
12_HMP	87497	85409	78754	9015	0	1307	6	4065	86	64275
12_CMP	77867	75333	68322	1779	0	950	4	4755	81	60753
13_HMP	80426	79034	73216	5866	0	835	9	4447	107	61952
13_CMP	64472	63420	56664	4241	0	0	2	4511	337	47573

Supplementary Figure legend

Figure S1. Evaluation of alpha-diversity in CMP and HMT samples. Panel A shows the average rarefaction curve representing variation of the Chao1 diversity index at increasing sequencing depth of CMP and HMT samples. Panel B displays the average rarefaction curve representing all 24 samples: dashed lines represents all 12 CMP samples and straight lines represents all 12 HMT samples. X-axis show the number of reads.

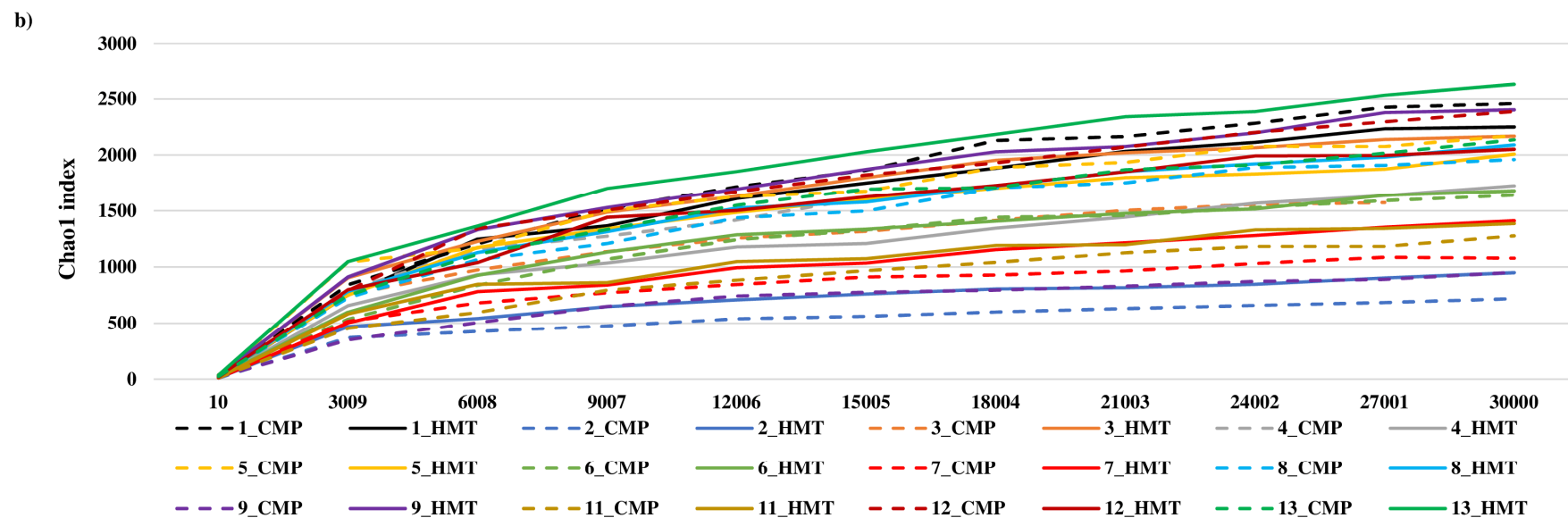
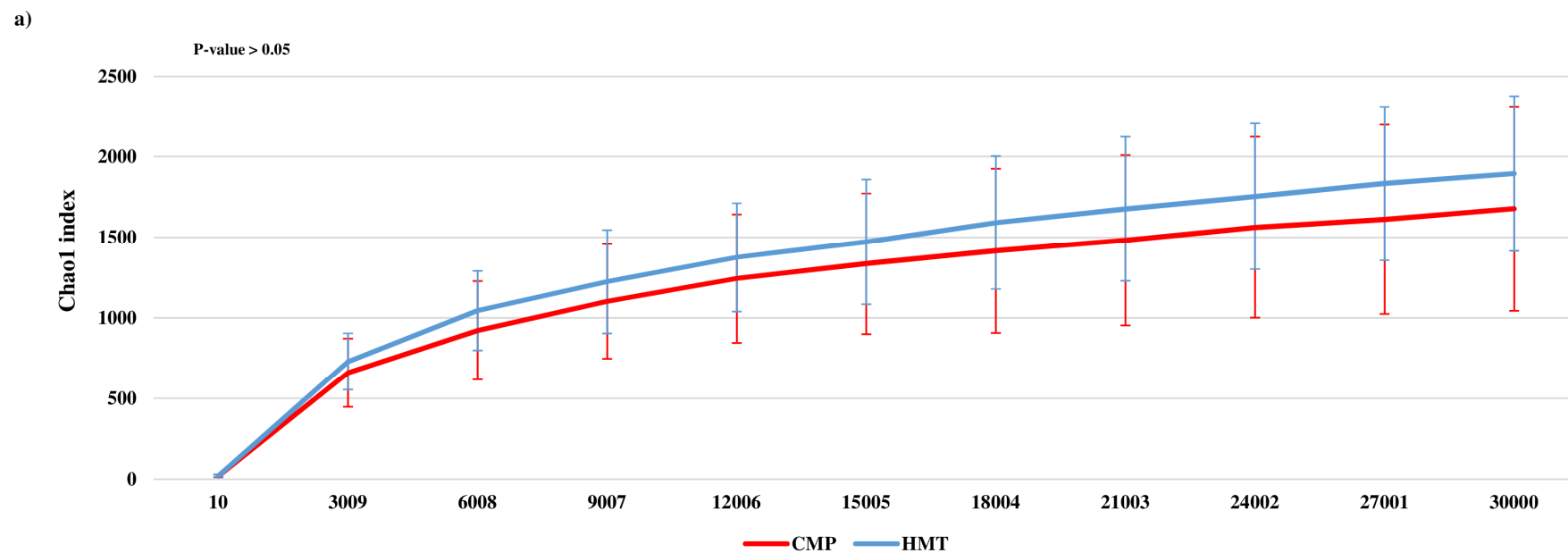


Figure S1