SUPPLEMENTARY TABLES

Systematic Review

The tissue-associated microbiota in colorectal cancer: a systematic review

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Supplementary Table S1. Microbiome methodological analysis of included studies of the mucosal microbiota of CRC patients and healthy controls.

First author, year	16S rRNA gene target region	Sequencing platform	Database for taxonomy assignment (version)	Statistical analysis for taxonomic differences
Geng, 2014 [33]	V1-V2	454 GS FLX (Roche)	NR	Univariate analysis: ANOVA and Kruskal-Wallis
Gao, 2015 [58]	V3	454 GS FLX (Roche)	RDP (11.1), SILVA (115), Greengenes (13.5)	LEfSe analysis
Mira-Pascual, 2015 [34]	V1-V3	454 GS FLX (Roche)	RDP (NR)	NR
Nakatsu, 2015 [59]	V1-V4	454 GS FLX (Roche)	Greengenes (13.8)	LEfSe analysis and Mann-Whitney U-test
Thomas, 2016 [35]	V4-V5	Ion Torrent PGM	NR	Wilcoxon rank sum test
Flemer, 2017 [57]	V3-V4	Illumina MiSeq	RDP (14)	Student t-test and Wilcoxon rank sum test
Richard, 2018 [60]	V3-V4	Illumina MiSeq	Greengenes (NR)	LEfSe analysis and One-way ANOVA
Zhang, 2019 [36]	V6	Illumina MiSeq	Greengenes (13.5)	LEfSe analysis and Mann-Whitney U-test
Wang Y, 2020 [61]	V3-V4	Illumina MiSeq	NR	Kruskal–Wallis test
Nardelli, 2021 [65]	V3-V6	Illumina MiSeq	16S-UDb (NR)	DESeq2
Osman, 2021 [68]	V3-V4	Illumina MiSeq	Greengenes (13.5) and One Codex Targeted Loci database (NR)	LEfSe analysis and Mann-Whitney U-test
Wang, 2021 [69]	NR	Illumina MiSeq	SILVA (132)	Benjamini-Hochberg false discovery rate

Abbreviations: CRC: colorectal cancer; LEfSe: Linear discriminant analysis Effect Size; NR: not reported; RDP – Ribosomal Database Project; 16S-UDb – unified 16S rRNA database.

Supplementary Table S2. Microbiome methodological analysis of included studies of CRC and non-cancerous mucosal tissues.

First author, year	16S rRNA gene target region	Sequencing platform	Database for taxonomy assignment (version)	Statistical analysis for taxonomic differences
Marchesi, 2011 [19]	V1-V3	454 GS FLX (Roche)	RDP (NR)	NR
Chen, 2012 [40]	V1-V3	454 GS FLX (Roche)	SILVA (106)	LEfSe analysis
Geng, 2013 [45]	V1-V2	454 GS FLX (Roche)	BLAST (NR)	Mann-Whitney U-test and Student t-test
Zeller, 2014 [56]	V4	Illumina MiSeq	SILVA (115)	Wilcoxon signed rank test
Allali, 2015 [37]	V1-V2	454 GS FLX (Roche)	Greengenes (NR)	Wilcoxon signed rank test
Burns, 2015 [39]	V5-V6	Illumina MiSeq	Greengenes (NR)	Wilcoxon signed rank test
Gao, 2015 [58]	V3	454 GS FLX (Roche)	RDP (11.1), SILVA (115), Greengenes (13.5)	NR
Nakatsu, 2015 [59]	V1-V4	454 GS FLX (Roche)	Greengenes (13.8)	LEfSe analysis and Mann-Whitney U-test
Brim, 2017 [38]	V1-V3	454 GS FLX (Roche)	NR	NR
Drewes, 2017 [43]	V3-V4	Illumina MiSeq	Greengenes (13.05)	Hedge's g difference statistic
Flemer, 2017 [57]	V3-V4	Illumina MiSeq	RDP (14)	Student t-test and Wilcoxon signed rank test
Gao, 2017 [44]	V4	Illumina MiSeq	NR	LEfSe analysis
Kinross, 2017 [47]	V1-V3	454 GS FLX (Roche)	NR	NR
Cremonesi, 2018 [41]	V4	Illumina MiSeq	SILVA (128)	Wilcoxon signed rank test
Hale, 2018 [46]	V3-V5	Illumina MiSeq	NR	Kruskal-Wallis test
Loke, 2018 [50]	V3-V4	Illumina MiSeq	NCBI 16S microbial database (NR)	Wilcoxon signed rank test
Richard, 2018 [60]	V3-V4	Illumina MiSeq	Greengenes (NR)	LEfSe analysis and One-way ANOVA
de Carvalho, 2019 [42]	V4	Ion Torrent PGM	Greengenes (13.8)	DESeq2

Leung, 2019 [48]	V3-V4	Illumina HiSeq	NR	Wilcoxon signed rank test, Mann-Whitney U-test, Kruskal-Wallis test and LEfSe analysis
Liu, 2019 [49]	V3-V4	Illumina MiSeq	SILVA (123)	NR
Saffarian, 2019 [52]	V3-V4	Illumina MiSeq	Greengenes (13.8) and HITdb (NR)	Kruskal-Wallis test and Zero-inflated Gaussian mixture model
Pan, 2020 [51]	V4	Illumina MiSeq	SILVA (NR)	LEfSe analysis
Sheng, 2020 [53]	V3-V4	Illumina MiSeq	NR	Mann-Whitney U-test
Wang Q, 2020 [54]	V3-V4	Ion Torrent S5TM XL	SILVA (123)	Paired zero-inflated Gaussian mixture model
Wang Y, 2020 [61]	V3-V4	Illumina MiSeq	NR	Kruskal–Wallis test
Wirth, 2020 [55]	V3-V4	Illumina MiSeq	SILVA (132)	Wilcoxon rank sum test and Friedman two-way analysis of variance
Choi, 2021 [62]	V3-V4	Illumina MiSeq	Greengenes (13.8)	LEfSe analysis and Student t-test
Liu, 2021 [63]	V4	NR	Greengenes (NR)	MaAsLin analysis
Malik, 2021 [64]	V3-V4	Illumina MiSeq	SILVA (115)	Linear mixed models and Student t-test
Nardelli, 2021 [65]	V3-V6	Illumina MiSeq	16S-UDb (NR)	DESeq2
Niccolai, 2021 [66]	V3-V4	Illumina MiSeq	NR	DESeq2
Okuda, 2021 [67]	NR	Illumina MiSeq	NR	Wilcoxon rank sum test
Zhang, 2021 [70]	V4	NR	Greengenes (NR)	Wilcoxon signed rank test with false discovery rate

Abbreviations: HITdb: human intestinal 16S rRNA gene taxonomic database; LEfSe: Linear discriminant analysis effect size; MaAsLin: Microbiome multivariable association with linear models; NR: not reported; RDP: Ribosomal Database Project; 16S-UDb – unified 16S rRNA database.

Supplementary Table S3. Quality of included CRC vs HC studies based on the Newcastle-Ottawa quality assessment scale.

First author, year	Selection	Comparability	Outcome	Total (out of 9)
Geng, 2014 [33]	★☆★★	☆☆	☆★★	5
Gao, 2015 [58]	★☆★★	★★	★★★	8
Mira-Pascual, 2015 [34]	★★★★	★★	☆★☆	7
Nakatsu, 2015 [59]	★★★★	★★	☆★★	8
Thomas, 2016 [35]	★☆★★	★★	★★★	8
Flemer, 2017 [57]	★☆☆★	★★	★★★	7
Richard, 2018 [60]	★☆★★	★☆	★★★	7
Zhang, 2019 [36]	★☆☆☆	☆★	★★☆	4
Wang Y, 2020 [61]	★☆☆☆	☆☆	☆★★	3
Nardelli, 2021 [65]	★☆☆★	★☆	★★★	6
Osman, 2021 [68]	★★★★	★★	★★☆	8
Wang, 2021 [69]	★☆☆★	☆☆	☆★☆	3

Abbreviations: CRC: colorectal cancer; HC: healthy controls.

Supplementary Table S4. Quality of included CRC vs NCT studies based on the Newcastle-Ottawa quality assessment scale.

First author, year	Selection	Comparability	Outcome	Total (out of 9)
Marchesi, 2011 [19]	★☆★★	★★	☆★☆	6
Chen, 2012 [40]	★☆★★	★★	★★★	8
Geng, 2013 [45]	★☆★★	★★	☆★☆	6
Zeller, 2014 [56]	★☆★★	★★	☆★★	7
Allali, 2015 [37]	★☆★★	★★	☆★★	7
Burns, 2015 [39]	★☆★★	★★	☆★★	7
Gao, 2015 [58]	★☆★★	★★	★★☆	7
Nakatsu, 2015 [59]	★★★★	★★	☆★★	8
Brim, 2017 [38]	★☆★★	★★	☆★☆	6
Drewes, 2017 [43]	★☆★★	★★	☆★★	7
Flemer, 2017 [57]	★☆★★	★★	★★★	8
Gao, 2017 [44]	★☆★★	★★	★★☆	7
Kinross, 2017 [47]	★☆★★	★★	★★☆	7
Cremonesi, 2018 [41]	★☆★★	★★	☆★☆	6
Hale, 2018 [46]	★★★★	★★	☆★☆	7
Loke, 2018 [50]	★★★★	★★	☆★★	8
Richard, 2018 [60]	★☆★★	★★	★★★	8
de Carvalho, 2019 [42]	★★★★	★★	☆★☆	7
Leung, 2019 [48]	★★★★	★★	☆★★	8
Liu, 2019 [49]	★☆★★	★★	☆★☆	6
Saffarian, 2019 [52]	★☆★★	★★	★★☆	7
Pan, 2020 [51]	★☆★★	★★	★★★	8
Sheng, 2020 [53]	★★★★	★★	★★☆	8
Wang Q, 2020 [54]	★☆★★	★★	★★★	8
Wang Y, 2020 [61]	★☆★★	★★	☆★★	7
Wirth, 2020 [55]	★☆★★	★★	☆★★	7
Choi, 2021 [62]	★☆★★	★★	☆★★	7
Liu, 2021 [63]	★☆★★	★★	☆★★	7
Malik, 2021 [64]	★★★★	★★	★★★	9
Nardelli, 2021 [65]	★☆★★	★★	★★★	8
Niccolai, 2021 [66]	★☆★★	★★	★★★	8
Okuda, 2021 [67]	★☆★★	★★	☆★★	7
Zhang, 2021 [70]	★★★★	★★	★★☆	8

Abbreviations: CRC: colorectal cancer; NCT: non-cancerous tissue.

Supplementary Table S5. Summary of the statistically significant microbial taxa identified in studies comparing CRC vs HC and CRC vs NCT.

		CRC vs HC		CRC vs NCT	
	Microbial taxa	**Increased in HC**	**Increased in CRC**	**Increased in NCT**	**Increased in CRC**
Phylum	Acidobacteria	-	-	1 [70]	0
	AC1	-	-	1 [70]	0
	Actinobacteria	2 [35,65]	0	4 [44,55,62,70]	0
	Armatimonadetes	-	-	1 [70]	0
	Bacteroidetes	2 [59,60]	2 [35,57]	5 [39,41,60,62,64]	0
	Chlorobi	-	-	1 [70]	0
	Chloroflexi	-	-	1 [70]	0
	Cyanobacteria	1 [35]	0	2 [64,70]	0
	Deferribacteres	-	-	1 [70]	0
	Elusimicrobia	-	-	1 [70]	0
	WPS-2 (Eremiobacterota)	-	-	1 [70]	0
	Fibrobacteres	-	-	1 [70]	0
	Firmicutes	0	1 [58]	5 [39,41,44,62]	1 [58]
	Fusobacteria	0	4 [58,60,65,68]	0	8 [37,39,41,44,48,62,66,70]
	Gemmatimonadetes	-	-	1 [70]	0
	GN02 (Gracilibacteria)	-	-	1 [70]	0
	GOUTA4	-	-	1 [70]	0
	Nitrospirae	-	-	1 [70]	0
	OD1 (Parcubacteria)	0	1 [35]	1 [70]	0
	OP3 (Omnitrophica)	-	-	1 [70]	0
	Planctomycetes	1 [35]	0	1 [70]	0
	Proteobacteria	2 [35,58]	1 [60]	1 [58]	3 [39,54,66]
	TM7 (Saccharibacteria)	-	-	1 [70]	0
	SR1	-	-	1 [70]	0
	BRC1 (Sumerlaeota)	-	-	1 [70]	0
	Synergitetes	0	1 [68]	0	1 [70]
	Verrucomicrobia	0	1 [68]	1 [70]	0
	WS4	-	-	1 [70]	0
Class	*Alphaproteobacteria*	0	2 [36,68]	0	1 [40]
	Bacilli	-	-	0	2 [40,60]
	Bacteroidia	-	-	2 [60,62]	0
	Betaproteobacteria	1 [68]	0	1 [62]	0
	Deltaproteobacteria	1 [36]	0	-	-
	Epsilonproteobacteria	0	1 [68]	0	1 [62]
	Erysipelotrichi	-	-	0	1 [60]
	Fusobacteriia	-	-	0	1 [62]
	Gammaproteobacteria	1 [35]	0	-	-
	Spirochaetes	-	-	0	1 [62]
	Synergistia	0	1 [68]	-	-
	ZB2	0	1 [35]	-	-
Order	*Acidobacteriales*	-	-	1 [70]	0
	Actinomycetales	-	-	1 [70]	0
	Bacillales	1 [59]	0	0	1 [70]
	Bacteroidales	-	-	2 [60,62]	0
	Bifidobacteriales	-	-	2 [62,70]	0
	Burkholderiales	1 [68]	0	2 [62,70]	0

	Campylobacteriales	-	-	0	2 [62,70]
	Clostridiales	0	2 [35,57]	2 [62,64]	-
	Coriobacteriia	-	-	1 [62]	0
	Desulfovibrionales	1 [36]	0	-	-
	Erysipelotrichales	-	-	1 [70]	1 [60]
	Flavobacteriales	-	-	1 [70]	0
	Fusobacteriales	0	1 [68]	0	2 [62,70]
	GCA004	-	-	0	1 [70]
	Gemellales	-	-	0	1 [70]
	Gemmatimonadales	-	-	1 [70]	0
	Lactobacillales	-	-	0	1 [60]
	Mycoplasmatales	-	-	0	1 [70]
	Myxococcales	-	-	1 [70]	0
	Phycisphaerales	1 [35]	0	-	-
	Pseudomonadales	-	-	1 [70]	0
	Rhizobiales	0	1 [36]	1 [70]	0
	Rickettsiales	-	-	1 [64]	0
	Sphingobacteriales	1 [35]	0	1 [70]	0
	Spirochaetales	-	-	0	1 [62]
	Streptophyta	-	-	1 [70]	0
	Verrucomicrobiales	0	1 [68]	-	-
	Xanthomonadales	-	-	0	1 [70]
Family	*0319-6A21*	-	-	0	1 [63]
	Alcaligenaceae	1 [68]	0	1 [62]	0
	Bifidobacteriaceae	-	-	2 [62,70]	0
	Bradyrhizobiaceae	1 [35]	0	1 [70]	0
	Campylobacteriaceae	0	1 [68]	0	2 [62,70]
	Carnobacteriaceae	-	-	0	1 [64]
	Caulobacteraceae	1 [35]	0	-	-
	Chitinophagaceae	1 [35]	0	1 [70]	0
	Christensenellaceae	0	1 [68]	-	-
	Clostridiaceae	1 [36]	0	-	-
	Comamonadaceae	-	-	1 [70]	0
	Coriobacteriaceae	-	-	2 [62,64]	1 [37]
	Desulfovibrionaceae	1 [36]	0	-	-
	Enterobacteriaceae	-	-	0	1 [42]
	Erysipelotrichaceae	-	-	2 [62,70]	1 [60]
	Flavobacteriaceae	1 [35]	0	1 [70]	0
	Fusobacteriaceae	0	1 [68]	0	3 [42,62,70]
	Gemelllaceae	-	-	0	2 [67,70]
	Halomonadaceae	-	-	0	1 [54]
	Hyphomicrobiaceae	0	1 [36]	-	-
	Intrasporangiaceae	1 [61]	0	1 [61]	1 [70]
	Koribacteraceae	-	-	1 [70]	0
	Lachnospiraceae	0	1 [35]	3 [39,62,64]	1 [37]
	Listeriaceae	-	-	1 [70]	0
	Micrococcaceae	-	-	0	1 [70]
	Mogibacteriaceae	0	1 [35]	-	-
	Moraxellaceae	-	-	1 [70]	0
	Mycoplasmataceae	-	-	0	1 [70]
	Muribaculaceae	-	-	2 [64,70]	0

	Neisseriaceae	-	-	0	1 [37]
	Nocardioidaceae	-	-	0	1 [70]
	Odoribacteraceae	0	1 [35]	1 [62]	0
	Oxalobacteraceae	-	-	1 [62]	0
	Paenibacillaceae	0	1 [36]	-	-
	Peptostreptococcaceae	-	-	0	1 [63]
	Phyllobacteriaceae	-	-	1 [70]	0
	Porphyromonadaceae	0	1 [57]	4 [37,60,62,70]	0
	Prevotellaceae	1 [36]	0	-	-
	Pseudomonadaceae	-	-	1 [70]	0
	Rikenellaceae	0	1 [35]	4 [39,46,67,70]	0
	Ruminococcaceae	0	1 [35]	7 [39,40,53,60,62,67,70]	0
	Shewanellaceae	-	-	0	1 [70]
	Sinobacteraceae	-	-	1 [61]	0
	Sphingomonadaceae	-	-	1 [70]	0
	Spirochaetaceae	-	-	0	1 [62]
	Streptococcaceae	0	1 [33]	0	2 [42,60]
	Streotomycetaceae	-	-	0	1 [70]
	Syntrophobacteraceae	-	-	0	1 [63]
	Tissierellaceae	0	1 [68]	-	-
	Verrucomicrobiaceae	0	1 [68]	-	-
	Xanthomonadaceae	1 [35]	0	0	1 [70]
Genus	*Acetanaerobacterium*	0	1 [57]	-	-
	Achromobacter	1 [35]	0	-	-
	Acidocella	-	-	1 [40]	0
	Acidovorax	1 [58]	0	-	-
	Acinetobacter	2 [35,58]	0	3 [44,52,70]	0
	Actinomyces	0	1 [57]	1 [50]	0
	Aeromonas	-	-	0	1 [42]
	Aggregatibacter	0	1 [59]	-	-
	Agrobacterium	1 [35]	0	-	-
	Akkermansia	0	1 [68]	3 [53,64,67]	0
	Alistipes	0	1 [57]	1 [50]	0
	Allisonella	0	1 [57]	-	-
	Allobaculum	-	-	1 [64]	0
	Alloprevotella	-	-	0	1 [44]
	Anaerococcus	1 [35]	0	0	1 [61]
	Anaerofustis	1 [68]	0	-	-
	Anaeroplasma	-	-	1 [64]	0
	Anaerorhabdus	1 [57]	0	-	-
	Anaerostipes	1 [57]	1 [35]	-	-
	Anaerotruncus	0	1 [35]	1 [50]	0
	Anoxybacillus	-	-	1 [45]	0
	Arthrobacter	-	-	0	1 [70]
	Bacillus	1 [35]	0	3 [40,44,61]	0
	Bacteroides	1 [59]	2 [35,57]	5 [39,42,46,50,67]	1 [58]
	Bacteroidetes_VC2_I_Bac22	1 [35]	0	-	-
	Bifidobacterium	0	1 [57]	3 [50,62,70]	0
	Bilophila	0	1 [35]	-	-
	Blautia	3 [57,59,68]	0	4 [37,46,59,60]	0
	Bosea	1 [35]	0	-	-

Bradyrhizobium	-	-	2 [61,70]	0
Brevibacterium	1 [35]	0	-	-
Brevundimonas	2 [35,58]	0	1 [48]	0
Brochothrix	-	-	1 [70]	0
Bulleidia	0	1 [68]	0	1 [37]
Burkholderia	-	-	0	1 [63]
Butyricimonas	0	1 [35]	1 [67]	1 [37]
Butyricoccus	0	1 [35]	-	-
Buttiauxella	1 [58]	0	-	-
Campylobacter	0	4 [57,59,61,68]	0	9 [37,42,44,48,61,62,64,67,70]
Candidatus	-	-	0	1 [39]
Catenibacterium	-	-	0	1 [64]
Catonella	-	-	0	1 [70]
Caulobacter	1 [58]	0	-	-
Cetobacterium	-	-	0	1 [42]
Cheryseobacterium	0	1 [36]	-	-
Chitinophaga	1 [35]	0	-	-
Citrobacter	-	-	0	1 [64]
02d06	1 [36]	0	-	-
Clostridium	0	1 [35]	2 [67,70]	1 [42]
Clostridium cluster IV	0	1 [57]	-	-
Clostridum cluster XIVa	1 [57]	0	0	0
Clostridium cluster XVIII	1 [57]	0	-	-
Christensenella	-	-	1 [50]	0
Collinsella	-	-	3 [50,62,67]	0
Coprococcus	1 [57]	0	-	-
Corynebaterium	1 [35]	0	-	-
Cryocola	1 [35]	0	-	-
Cupriavidus	1 [35]	0	-	-
Delftia	1 [35]	0	-	-
Dehalobacterium	0	2 [35,68]	-	-
Desulfovibrio	0	1 [35]	1 [50]	0
Dethiosulfatibacter	0	1 [61]	-	-
Devosia	1 [35]	1 [36]	-	-
Dialister	0	1 [68]	1 [50]	2 [44,64]
Dorea	2 [57,68]	1 [35]	1 [62]	0
Eggerthella	0	1 [35]	-	-
Eikenella	0	1 [61]	0	2 [37,67]
Enterococcus	0	1 [57]	1 [54]	2 [63,67]
Epilithonimonas	1 [58]	0	-	-
Escherichia	1 [35]	0	-	-
Escherichia-Shigella	0	2 [57,58]	-	-
Eubacterium	2 [36,68]	1 [57]	1 [62]	1 [52]
Faecalibacterium	2 [57,68]	0	5 [37,40,53,60,62]	0
Filifactor	0	1 [68]	-	-
Flavobacterium	1 [58]	0	-	-
Fretibacterium	-	-	0	1 [54]
Fusobacterium	0	6 [35,57-59,61,68]	0	19 [37,39,42,44,46-48,52-54,58,59,61-64,66,67,70]
Gemella	0	1 [59]	0	3 [37,44,59]
Gemmiger	1 [57]	0	-	-

Geobacillus	-	-	1 [44]	0
Gordonia	1 [35]	0	-	-
Granulicatella	0	3 [57,59,61]	0	3 [37,44,59]
Halomonas	-	-	0	1 [54]
Holdemania	1 [57]	1 [35]	-	-
Howardella	0	1 [57]	-	-
Hungatella	-	-	0	1 [44]
Intestinimonas	-	-	1 [50]	0
Janthinobacterium	1 [58]	0	-	-
Kaistobacter	-	-	1 [70]	0
Klebsiella	3 [35,36,57]	0	0	1 [54]
Lachnoanaerobaculum	-	-	0	2 [44,70]
Lachnobacterium	0	1 [68]	-	-
Lachnospira	0	1 [35]	1 [37]	0
Lactobacillus	1 [35]	0	1 [54]	0
Lactococcus	0	1 [58]	1 [44]	1 [58]
Leptothrix	1 [35]	0	0	1 [44]
Leptotrichia	1 [36]	2 [59,61]	1 [42]	2 [64,67]
Leuconostoc	-	-	1 [44]	0
Marvinbryantia	-	-	1 [64]	0
Megasphaera	-	-	2 [50,63]	0
Massilia	-	-	0	1 [52]
Methylobacterium	1 [35]	0	2 [40,61]	0
Mesorhizobium	1 [35]	0	-	-
Microbacterium	1 [35]	0	1 [45]	1 [70]
Micrococcus	1 [35]	0	-	-
Mitsuokella	-	-	1 [50]	1 [67]
Mogibacterium	1[36]	2 [57,61]	-	-
Morganella	-	-	1 [50]	1 [44]
Mycobacterium	1 [35]	0	-	-
Negativibacillus	-	-	1 [50]	0
Neisseria	2 [35,68]	0	1 [52]	0
Nocardioides	-	-	0	1 [70]
Ochrobactrum	1 [35]	0	1 [40]	0
Odoribacter	0	1 [35]	0	1 [42]
Oribacterium	-	-	0	1 [70]
Oscillibacter	0	1 [57]	2 [50,52]	0
Oscillospira	0	2 [35,59]	-	-
Oxalobacter	-	-	1 [62]	0
Paenibacillus	0	1 [36]	-	-
Paeniclostridium	-	-	1 [54]	0
Pantoea	-	-	1 [44]	0
Papillibacter	0	1 [35]	-	-
Parabacteroides	0	1 [35]	9 [37,40,42,44,46,53,60,62,70]	0
Paracoccus	1 [35]	0	-	-
Paraprevotella	-	-	2 [40,42]	0
Parascardovia	0	1 [33]	-	-
Parvimonas	0	4 [57,59,61,68]	0	8 [37,42,44,59,61,63,67,70]
Pedobacter	2 [35,58]	0	-	-
Peptoniphilus	-	-	0	1 [64]
Peptococcus	-	-	0	1 [70]

	Peptostreptococcus	0	5 [57-59,61,68]	0	6 [42,44,54,59,63,67]
	Phascolarctobacterium	2 [36,68]	2 [35,57]	1 [40]	0
	Phenylobacterium	1 [35]	0	-	-
	Phyllobacterium	1 [35]	0	1 [70]	0
	Porphyromonas	0	2 [33,57]	0	1 [44]
	Portiera	-	-	0	1 [39]
	Prevotella	2 [35,36]	3 [57,59,68]	5 [42,46,50,54,67]	2 [44,58]
	Propionibacterium	3 [35,58,68]	0	1 [44]	0
	Providentia	-	-	0	1 [39]
	Pseudocalvibacter	1 [35]	0	-	-
	Pseudoflavonifractor	-	-	1 [50]	0
	Pseudomonas	2 [35,58]	1 [57]	5 [42,44,50,58,70]	0
	Pseudoramibacter_Eubacterium	0	1 [35]	-	-
	Pseudoxanthomonas	1 [35]	0	-	-
	Psychrobacter	-	-	1 [70]	0
	Ralstonia	1 [35]	0	-	-
	Rahnella	1 [58]	0	-	-
	Rhodococcus	1 [35]	0	1 [50]	0
	Roseburia	0	1 [35]	1 [46]	1 [45]
	Rubrobacter	1 [35]	0	-	-
	Ruminiclostridium	-	-	0	1 [44]
	Ruminococcus	1 [35]	1 [57]	6 [37,42,53,62,66,67]	0
	Salinispora	0	1 [35]	-	-
	Schwartzia	0	2 [61,68]	0	1 [61]
	Selenomonas	0	2 [61,68]	0	4 [44,62,67,70]
	Serratia	1 [36]	0	-	-
	Shewanella	0	1 [61]	0	2 [54,70]
	Sphingobacterium	1[58]	0	-	-
	Sphingobium	1 [35]	0	1 [67]	0
	Sphingomonas	2 [35,58]	0	2 [52,70]	0
	Staphylococcus	1 [35]	2 [33,57]	-	-
	Stenotrophomonas	2 [35,58]	0	0	1 [70]
	Streptococcus	0	3 [33,57,61]	0	7 [37,48,53,58,60,61,67]
	Streptomyces	1 [61]	0	1 [61]	0
	Streptophyla	0	1 [33]	-	-
	Streptophyta	1 [35]	0	-	-
	Succinivibrio	-	-	1 [50]	0
	Sutterella	1 [68]	0	1 [62]	0
	Treponema	-	-	1 [42]	2 [62,67]
	Turicibacter	-	-	1 [64]	0
	Veillonella	0	1 [33]	2 [54,67]	0
	Victivallis	0	1 [57]	-	-
Species	*Acinetobacter junii*	-	-	0	1 [52]
	Acinetobacter johnsonii	-	-	1 [70]	0
	Aggregatibacter segmis	0	1 [59]	-	-
	Akkermansia muciniphila	0	1 [68]	-	-
	Alcaligenes faecalis	1 [35]	0	-	-
	Atopobium parvulum	1 [68]	0	-	-
	Bacillus cereus	1 [35]	0	-	-
	Bacteroides acidifaciens	-	-	1 [70]	0
	Bacteroides eggerthii	-	-	1 [54]	0

Bacteroides fragilis	0	4 [35,59,65,68]	0	3 [43,52,59]
Bacteroides caccae	-	-	1 [46]	0
Bacteroides ovatus	0	1 [59]	1 [46]	0
Bacteroides uniformis	0	1 [35]	4 [39,46,60,70]	1 [52]
Bacteroides vulgatus	1 [65]	0	-	-
Blautia producta	1 [36]	0	-	-
Blautia wexlerae	-	-	1 [52]	0
Campylobacter ureolyticus	0	1 [59]	0	1 [70]
Catenibacterium mitsuokai	-	-	0	1 [52]
Christensenella timonensis	0	1 [68]	-	-
Clostridium aldenense	-	-	0	1 [70]
Clostridium hathewayi	-	-	0	1 [70]
Clostridium hiranonis	1 [36]	0	-	-
Clostridium sensu stricto	-	-	1 [44]	0
Clostridium oroticum	1 [68]	0	-	-
Clostridium perfringens	-	-	1 [54]	0
Clostridium ramosum	-	-	1 [70]	0
Dialister invisius	-	-	0	1 [52]
Erysipelotrichaceae incertae sedis	1 [57]	0	-	-
Erwinia dispersa	-	-	1 [46]	0
Escherichia coli	1 [59]	1 [65]	-	-
Eubacterium coprostanoligenes	0	1 [68]	-	-
Eubacterium eligens	-	-	1 [56]	0
Eubacterium sulci	-	-	0	1 [52]
Eubacterium ventriosum	-	-	1 [56]	0
Faecalibacterium prausnitzii	1 [59]	0	3 [39,46,60]	0
Fusobacterium nucleatum	0	2 [65,68]	0	3 [37,43,56]
Fusobacterium periodonticum	-	-	0	1 [52]
Gemella haemolysans	0	1 [65]	-	-
Gemella morbillorum	0	1 [68]	0	2 [43,52]
Haemophilus parainfluenzae	2 [65,68]	0	-	-
Intestinimonas butyriciproducens	0	1 [68]	-	-
Kocuria palustris	-	-	1 [52]	0
Lachnoanaerobaculum orale	-	-	0	1 [70]
Lachnospiracea incertae sedis	1 [57]	0	-	-
Lachnoclostridium citroniae	-	-	0	1 [52]
Lactobacillus brevis	-	-	1 [70]	0
Lactobacillus delbruecki	1 [35]	0	-	-
Leuconostoc gelidum	-	-	0	1 [52]
Methylobacterium adhaesivum	-	-	0	1 [70]
Parabacteroides distasonis	-	-	2 [46,70]	0
Parabacteroides merdae	-	-	0	1 [52]
Parvimonas micra	0	1 [68]	0	2 [43,52]
Peptostreptococcus micros	0	1 [35]	-	-
Peptostreptococcus stomatis	0	1 [68]	0	1 [43]
Porphyromonas endodontalis	0	1 [59]	-	-
Prevotella copri	1 [36]	0	1 [46]	0
Prevotella intermedia	0	1 [59]	-	-
Prevotella stercorea	1 [36]	0	-	-

Pseudomonas veroni	1 [59]	0	2 [59,70]	0
Psychrobacter sanguinis	-	-	1 [70]	0
Ralstonia mannitolilytica	-	-	1 [52]	0
Ruminococcus bromii	0	1 [68]	1 [70]	0
Ruminococcus callidus	0	1 [68]	-	-
Ruminococcus torques	1 [65]	0	-	-
Shewanella algae	-	-	0	1 [70]
Solobacterium moorei	0	1 [68]	-	-
Streptococcus bovis	-	-	0	1 [52]
Streptococcus intermedius	0	1 [65]	-	-
Streptococcus salivarius	-	-	0	1 [56]
Vibrio cholerae	1 [59]	0	-	0

Abbreviations: CRC: colorectal cancer; HC: healthy controls; NCT: non-cancerous tissue.

Supplementary Table S6. Qualitative synthesis showing the strong and the suggestive microbial taxonomic associations with CRC.

	Microbial taxa	CRC vs HC N (%) studies	CRC vs NCT N (%) studies
Phylum	Actinobacteria	2 (20%)	4 (14%)
	Bacteroidetes		5 (17%)
	Cyanobacteria		2 (7%)
	Fusobacteria	4 (40%)	8 (28%)
Class	Alphaproteobacteria	2 (20%)	
	Bacilli		2 (7%)
	Bacteroidia		2 (7%)
Order	Bacteroidales		2 (7%)
	Bifidobacteriales		2 (7%)
	Burkholderiales		2 (7%)
	Campylobacteriales		2 (7%)
	Clostridiales	2 (20%)	2 (7%)
	Fusobacteriales		2 (7%)
Family	*Bifidobacteriaceae*		2 (7%)
	Campylobacteriaceae		2 (7%)
	Fusobacteriaceae		3 (10%)
	Gemelllaceae		2 (7%)
	Muribaculaceae		2 (7%)
	Porphyromonadaceae		4 (14%)
	Rikenellaceae		4 (14%)
	Ruminococcaceae		7 (24%)
	Streptococcaceae		2 (7%)
Genus	*Acinetobacter*	2 (20%)	3 (10%)
	Akkermansia		3 (10%)
	Bacillus		3 (10%)
	Bifidobacterium		3 (10%)
	Blautia	3 (25%)	4 (14%)
	Bradyrhizobium		2 (7%)
	Brevundimonas	2 (20%)	
	Campylobacter	4 (40%)	9 (31%)
	Collinsella		3 (10%)
	Dehalobacterium	2 (20%)	
	Eikenella		2 (7%)
	Escherichia-Shigella	2 (20%)	
	Faecalibacterium	2 (20%)	5 (17%)
	Fusobacterium	6 (60%)	19 (66%)
	Gemella		3 (10%)
	Granulicatella	3 (30%)	3 (10%)
	Klebsiella	3 (30%)	
	Lachnoanaerobaculum		2 (7%)
	Megasphaera		2 (7%)
	Methylobacterium		2 (7%)
	Neisseria	2 (20%)	
	Oscillibacter		2 (7%)
	Oscillospira	2 (20%)	
	Parabacteroides		9 (31%)
	Paraprevotella		2 (7%)
	Parvimonas	4 (40%)	8 (28%)
	Pedobacter	2 (20%)	
	Peptostreptococcus	5 (50%)	6 (21%)
	Porphyromonas	2 (20%)	

	Propionibacterium	3 (30%)	
	Pseudomonas		5 (17%)
	Ruminococcus		6 (21%)
	Schwartzia	2 (20%)	
	Selenomonas	2 (20%)	4 (14%)
	Shewanella		2 (7%)
	Sphingomonas	2 (20%)	2 (7%)
	Stenotrophomonas	2 (20%)	
	Streptococcus	3 (30%)	7 (24%)
	Veillonella		2 (7%)
Species	*Bacteroides fragilis*	4 (40%)	3 (10%)
	Faecalibacterium prausnitzii		3 (10%)
	Fusobacterium nucleatum	2 (20%)	3 (10%)
	Gemella morbillorum		2 (7%)
	Haemophilus parainfluenzae	2 (20%)	
	Parabacteroides distasonis		2 (7%)
	Parvimonas micra		2 (7%)
	Pseudomonas veroni		2 (7%)

Strong positive association (≥3 studies in same direction; none in opposite direction);
Suggestive positive association (2 studies in same direction; none in opposite direction);
Strong negative association (≥3 studies in same direction; none in opposite direction);
Suggestive negative association (2 studies in same direction; none in opposite direction).