

Additional File

Figure S1: Unweighted Unifrac distances between tumor and normal-associated microbiota in dMMR and pMMR.

Figure S2: Venn diagram highlighting number of microbes that overlap between tumor and normal samples in relation to MMR status (dMMR = red font, pMMR = green font, red circles = tumor samples, blue circles = normal samples). Only differentially abundant microbes with a corrected p-value < 0.05 were included in this diagram.

Figure S3: Microbes significantly enriched in tumor as compared to normal samples (colon tissue and mucosa) in individuals with dMMR CRC: a) *Bacteroides fragilis* and b) *Fusobacterium nucleatum*. Figures show relative abundances of each microbe stratified by colon location (proximal or distal). Y-axis is square root transformed. For full results, please see Tables **S2-S6**.

Figure S4: Differentially abundant OTUs between patient-matched tumor and normal samples in individuals with dMMR CRC from an independent cohort. Y-axis indicates percent relative abundance of OTUs. Line color indicates directionality of change in microbial abundance: red = increased abundance relative to normal, blue = decreased abundance or no change compared to normal.

Table S1. Table S1: List of PATRIC model IDs and associated sOTUs.

Table S2. Microbes identified as differentially abundant in tumor as compared to normal samples (tissue and mucosa) from individuals with dMMR or pMMR CRC. Microbes are listed in order of significance from greatest to least. Microbes in bold font are enriched in both dMMR and pMMR samples. (Example: *Coprococcus comes* ATCC 27758 is significantly enriched in dMMR tumor samples and pMMR normal samples.) (GLMM, all microbes listed have a Benjamini-Hochberg p-value < 0.05)**Table S3:** sOTUs enriched in tumor samples (colon tissue and mucosa) as compared to normal-adjacent samples in individuals with dMMR CRC.

Table S3: sOTUs enriched in tumor samples (colon tissue and mucosa) as compared to normal adjacent samples in individuals with dMMR CRC.

Table S4: sOTUs enriched in tumor samples (colon tissue and mucosa) as compared to normal adjacent samples in individuals with pMMR CRC.

Table S5: sOTUs enriched in the proximal or distal colon (colon tissue and mucosa) of individuals with dMMR CRC.

Table S6: sOTUs enriched in the proximal or distal colon (colon tissue and mucosa) of individuals with pMMR CRC.

Table S7: Differentially abundant microbes in individuals with dMMR CRC from an independent cohort. Blue boxes highlight microbes enriched in tumor tissue samples as compared to normal-adjacent samples.

Table S8: Differentially abundant microbes in individuals with pMMR CRC from an independent cohort. Blue boxes highlight microbes enriched in tumor tissue samples as compared to normal-adjacent samples.

Figure S1

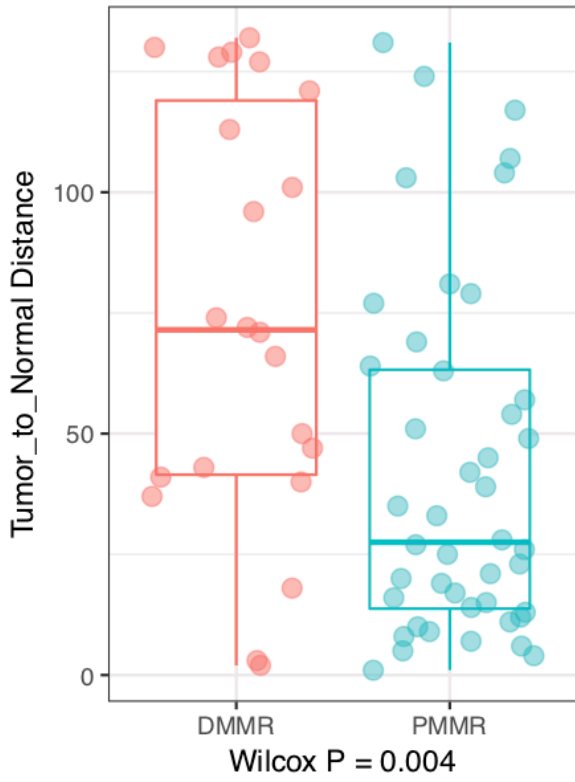


Figure S2

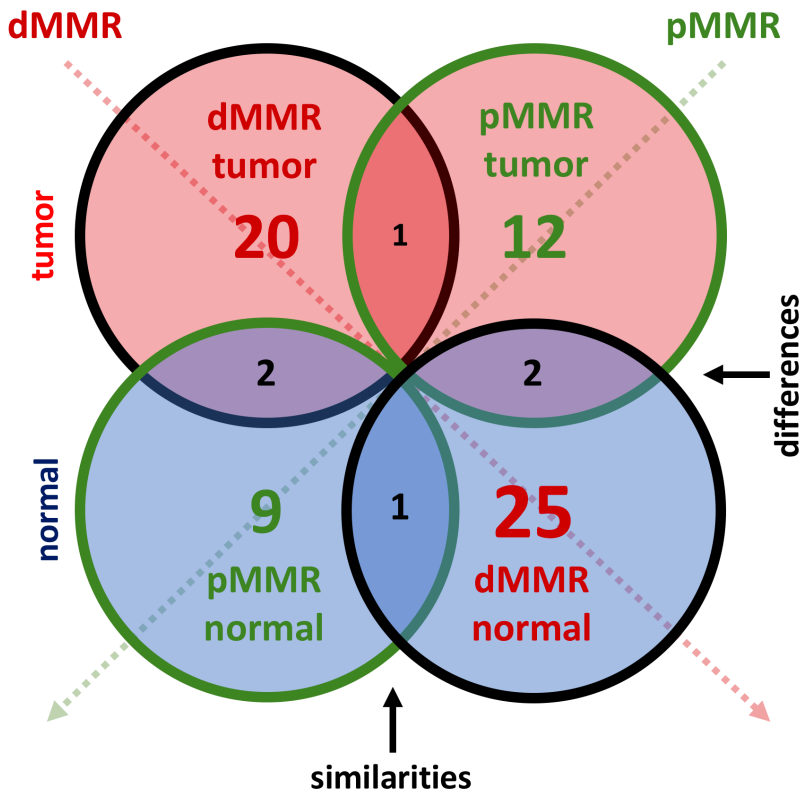
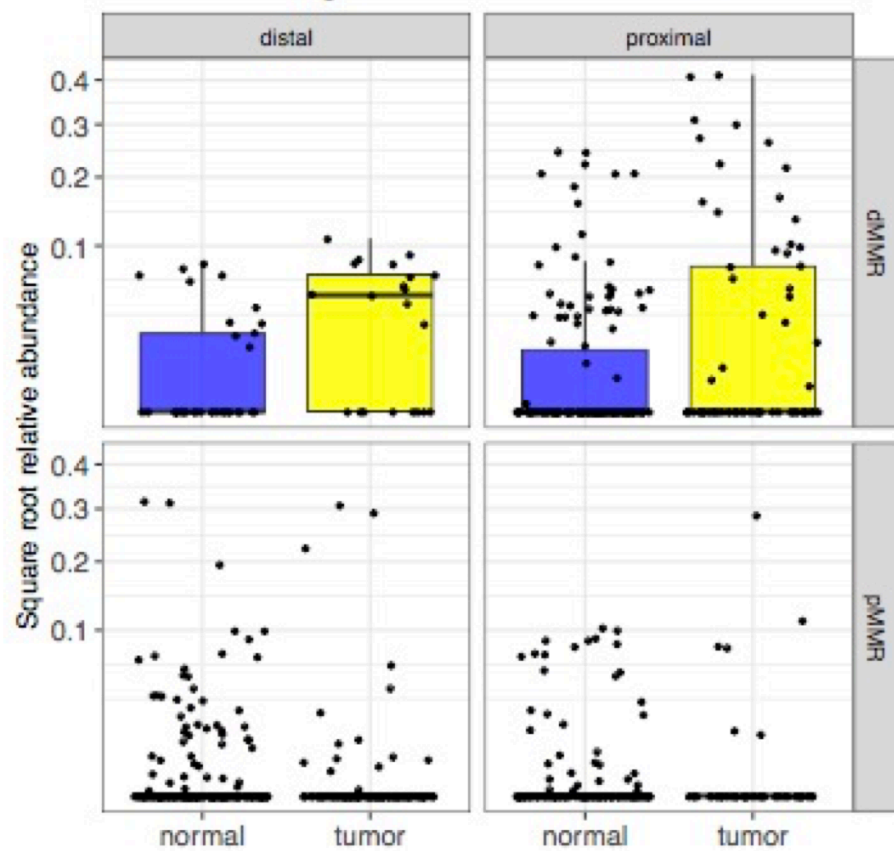


Figure S3

a) *Bacteroides fragilis*



b) *Fusobacterium nucleatum*

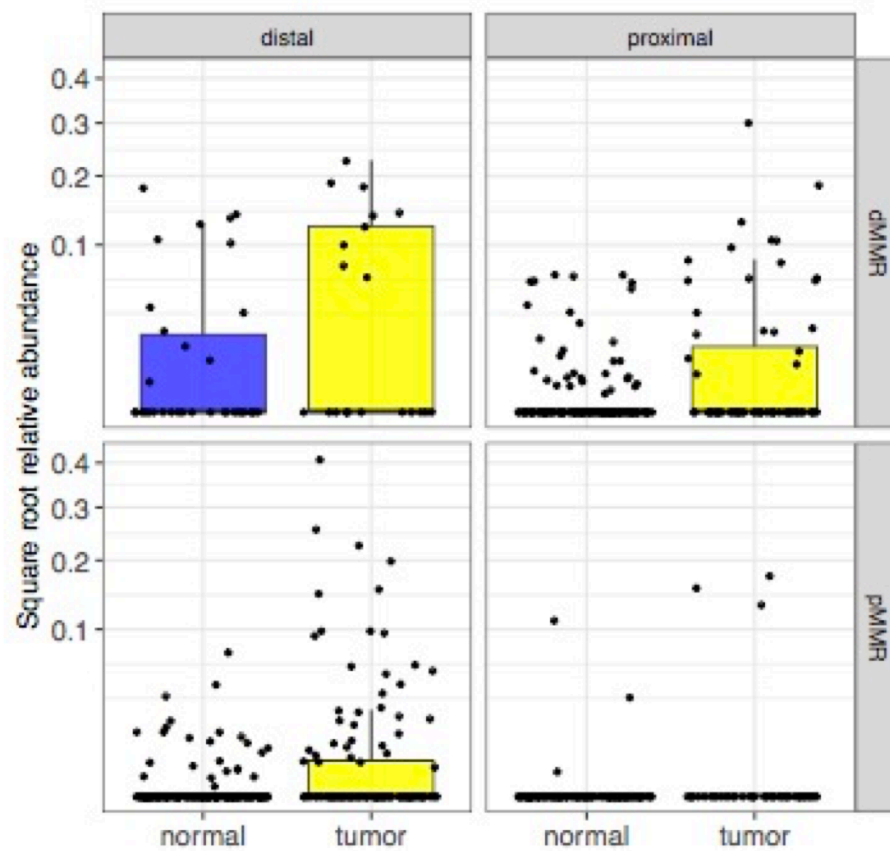


Figure S4

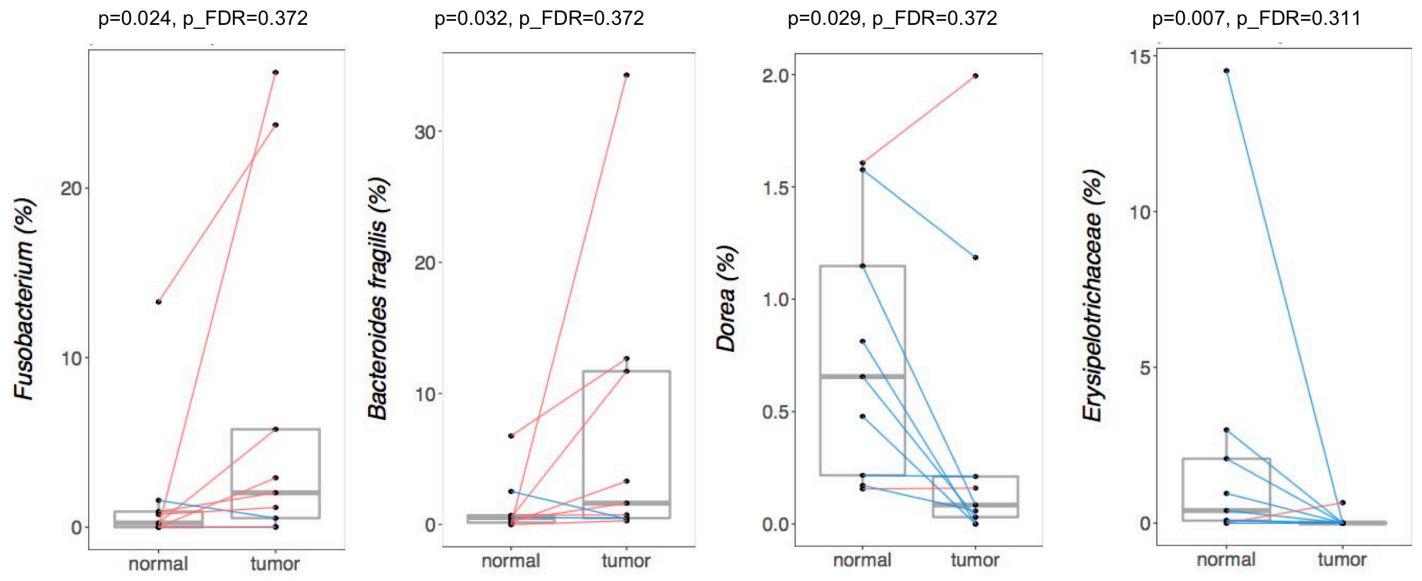


Table S1: List of PATRIC model IDs and associated sOTUs.

model	associated sOTU	direction	influence score
287.2537	9877e6b400d6b6ddd109860dd5833e9a6158a14e	Tumor	45.97450752
1304.182	139bf28e70ca27abf9e9b4fd35182e3aa13554a4	Normal	38.92835722
1512.4	325635b4eea0f4ea47d598992cdd1fe791949d5f	Tumor	30.12676086
28116.7	4a5d3ca1a784b0b59365e16d1d97f2f440751e15	Tumor	35.34356923
39488.4	3172c57e6f43b6dd00b72d6ba94b62cd4d386f07	Tumor	35.26014285
39490.3	a9d3da348fab1229c75db0a1ff5b9a8d579bf3c5	Normal	7.816469481
88431.7	b56b7e2dd2e753138a0a1d1e71f3056d12fed902	Tumor	13.35839489
214856.4	eb6dc9f905c574e9ba6937eb007f0663e85ebf0f	Normal	29.85772927
292800.4	15b516cadae4f56342986fc617b013ae81b5ce8a	Normal	36.57608786
295405.11	8b87b344acea1c9d0217ea1774d20395a65c23d3	Tumor	31.76201761
360807.5	b0e67ad37c689fd848f4ac9b923029d9c5b97b84	Tumor	5.04972306
370438.4	7a633438d89337bc55cd5c5fd04031625f5ec003	Normal	31.72251862
411460.6	0ee71c816b0045e83cc52804b39c593ef56f78ea	Normal	29.45925917
411461.4	fb4d2b05fa56f2555389e9e9f4c7ecfef185465c	Normal	9.310550435
411462.6	04f784c78098595e60b39c56bc8831a1c246d8bd	Normal	7.103736569
411462.6	071e09e58f93c64190d1facce0c7064963ca7ecb	Normal	7.103736569
411483.3	7cb3cb4d27875a6896a122af34ee4e1e25c0658d	Normal	34.23372632
411483.3	0c2b3a10e2af94b962ba7528f751204d55900582	Normal	34.23372632
435591.13	8707bac4e4749bf0b2c193cf8b359d5c0ac14986	Tumor	37.1416488
445972.6	ab05bcb443299370fc72115db48e6b4157a86442	Tumor	34.65754847
450746.3	638bf3ad37e8c44d6598b006681ad9dbac9d6f3a	Normal	5.80396739
457389.4	95a5fc04db20b1fee193023578b40f955999f970	Normal	34.48212012
457391.3	b75db79d71e49907faca3540adab49d1720f69f7	Normal	33.80304752
469599.3	c9a1c377ba9b93ac505d720a18ea2ed18f9e1fe6	Tumor	34.01896947
470146.3	c7c054e78775fd54be9ea450fca5a2cc1945d3f8	Tumor	5.518796857
479437.5	5262929392a66cf2afc6a41089cb6dfc6d3e9160	Tumor	8.53215133
511145.12	84fe91323797b143ee23d1c9a0a119f74ac695f3	Normal	2.132791605
562982.3	b3c6a6802f50753723c587db09737459a0ce4030	Tumor	38.82910147
596315.3	1f7d94002df355b116de0bddd570275227c9ef5b	Tumor	10.78621211
657313.3	5098ddd48ee0ee369bfa4ae994436891b62bb42	Normal	0.624453092
657315.3	87c90d196bf14c4b33364104d9a1ba87f9ec7674	Tumor	10.73565791
657322.3	cbe56d8d19aa6175f4664cbf2bc0532c68243477	Normal	7.089425206
663278.4	fd1b56f2f52050a8575af68b53b5a691bea5db8c	Normal	35.29485267
665956.3	c996a0be142d3ef8c7bcf5b648ca29fdccb44d47	Tumor	13.72409367
991789.3	981787c105693e6d57f925437c828c382b0b5dcc	Normal	27.6842406
997873.3	96e019fe5ef30fa9da8b0cf35c33928cac91f6e1	Normal	5.838643751
997886.3	e3dabcc0d2ce7e6a9d0bedd684e9b9c924143ce5	Normal	41.41023915
999403.4	f9f3f2e2c24d36b4d56f9b9edec4f0817714b83	Tumor	37.28440165
1078089.3	92a9e6fd06b63cc48625058e4125b1a2f2cf3048	Tumor	38.72098734
1121098.3	714bb4b42c705998173a9e4009fa21cb94b32528	Tumor	28.8562891
1262706.3	dd97ee7ed1ff7e48cf4248ea53130e398aadd0b0	Normal	33.70133074
1316586.3	df4cfc980121095e2626e4d4f42c03fdd4c8428e	Tumor	0.002482632
1414720.3	3de43bb82a62218309d99da68e342a6a97aab07f	Normal	5.829584478
1504823.3	a087ce6dca66a1ca488f78a8c14bb79845224cad	Normal	12.63862858
1637506.3	9f1cd9232177f8118fc68906e04b28bcd454311b	Tumor	7.588433686
1637509.3	bc20137757c62ad131a83a32ef6141c46b9d6897	Normal	0.00189914
1658108.3	25fc8a0281b2e510ffdcce6d197757488c61e23b	Normal	9.708804603
1737424.3	c38a8f4266e22370fdbb6dd2b031dd46c2ed486d	Normal	37.96013856
1805476.3	85d5404085808330afd5d0bac27edee00bf513c5	Normal	8.732076254
1805476.3	96ea0ee772910b0790552195b224f430d863ba5a	Normal	35.34293264

Table S2: Microbes identified as differentially abundant in tumor as compared to normal samples (tissue and mucosa) from individuals with dMMR or pMMR CRC. Microbes are listed in order of significance from greatest to least. Microbes in bold font are enriched in both dMMR and pMMR samples. (Example: *Coprococcus comes* ATCC 27758 is significantly enriched in dMMR tumor samples and pMMR normal samples.) (GLMM, all microbes listed have a Benjamini-Hochberg p-value<0.05)

dMMR Tumor	dMMR Normal
<i>Bacteroides fragilis</i> YCH46 <i>Fusobacterium periodonticum</i> 2_1_31 <i>Fusobacterium nucleatum</i> CTI-5 <i>Roseburia intestinalis</i> M50/1 <i>Bacteroides</i> sp. HPS0048 <i>Peptostreptococcus stomatis</i> DSM 17678 <i>Clostridium clostridioforme</i> 90A1 <i>[Clostridium] symbiosum</i> <i>Pseudomonas aeruginosa</i> strain NCTC10332 <i>Coprococcus comes</i> ATCC 27758 <i>Eggerthella lenta</i> DSM 2243 <i>Roseburia inulinivorans</i> <i>Bacteroides massiliensis</i> B84634 <i>Bacteroides vulgatus</i> ATCC 8482 <i>Parabacteroides distasonis</i> ATCC 8503 <i>Dorea longicatena</i> <i>Lactobacillus</i> sp. N15.MGS-260 <i>Bacteroides ovatus</i> strain ATCC 8483 <i>Subdoligranulum</i> sp. 4_3_54A2FAA <i>[Eubacterium] hallii</i>	<i>Bacteroides</i> sp. 3_1_33FAA <i>Escherichia coli</i> str. K-12 substr. MG1655 <i>Ruminococcus torques</i> ATCC 27756 <i>Bacteroides vulgatus</i> ATCC 8482 <i>Bacteroides ovatus</i> CL03T12C18 <i>Faecalibacterium prausnitzii</i> SL3/3 <i>Faecalibacterium prausnitzii</i> A2-165 <i>Bacteroides</i> sp. 3_1_13 <i>Clostridium</i> sp. JCC <i>Alistipes finegoldii</i> <i>Lachnospiraceae</i> bacterium mt14 <i>bacterium</i> LF-3 <i>Blautia</i> sp. Marseille-P2398 <i>Coprobacillus</i> sp. 8_1_38FAA <i>Ruminococcus torques</i> L2-14 <i>Eubacterium ramulus</i> <i>Dorea longicatena</i> DSM 13814 <i>Streptococcus salivarius</i> strain JF <i>Ethanoligenens harbinense</i> YUAN-3 <i>Bacteroides caccae</i> CL03T12C61 <i>Azospirillum</i> sp. CAG:260 <i>Dorea formicigenerans</i> ATCC 27755 <i>Pelotomaculum thermopropionicum</i> SI <i>Acinetobacter</i> sp. N54.MGS-139 <i>[Clostridium] propionicum</i> DSM 1682
pMMR Tumor	pMMR Normal
<i>Prevotella copri</i> DSM 18205 <i>Ruminococcus</i> sp. A254.MGS-108 <i>Odoribacter splanchnicus</i> DSM 220712 <i>Campylobacter gracilis</i> strain ATCC 33236 <i>Bacteroides cellulosilyticus</i> strain WH2 <i>Bacteroides</i> sp. 3_1_23 <i>Firmicutes</i> bacterium ASF500 <i>Clostridium boltea</i> 90A9 <i>Blautia</i> sp. Marseille-P2398 <i>Dorea longicatena</i> <i>Faecalibacterium prausnitzii</i> A2-165 <i>Ruminococcus</i> sp. A254.MGS-254	<i>Bacteroides massiliensis</i> B84634 <i>Ethanoligenens harbinense</i> YUAN-3 <i>Coprococcus comes</i> ATCC 27758 <i>Dialister invisus</i> DSM 15470 <i>Proteobacteria</i> bacterium CAG:139 <i>Clostridium</i> cf. <i>saccharolyticum</i> K10 <i>Fusicatenibacter saccharivorans</i> <i>Holdemania filiformis</i> DSM 12042 <i>Burkholderia</i> sp. K4410.MGS-135

Table S3: sOTUs enriched in tumor samples (colon tissue and mucosa) as compared to normal-adjacent samples in individuals with dMMR CRC.

OTU	effect.size	pvalue	pvalueBH	direction	dMMR/pMMR	genome ID	influence	name
8b7b344acea1c9d0217ea1774d20395a65c23d3	0.32487208	0	0	Tumor	dMMR	295405.11	927.0838	Bacteroides fragilis YCH46
b75db79d71e49907faca3540adab49d1720f69f7	-0.4871055	0	0	Normal	dMMR	457391.3	1017.9764	Bacteroides sp. 3_1_33FAA
c9a1c377ba9b93ac505d720a18ea2ed18f9e1fe6	0.91882064	0	0	Tumor	dMMR	469599.3	0	Fusobacterium periodonticum 2_1_31
df4cf980121095e2626e4d4f42c03fdd4c8428e	0.97009261	0	0	Tumor	dMMR	1316586.3	0	Fusobacterium nucleatum CTI-5
84fe91323797b143ee23d1c9a0a119f74ac695f3	-0.4259513	8.48E-179	1.27E-177	Normal	dMMR	511145.12	1452.8044	Escherichia coli str. K-12 substr. MG1655
87c90d196bf14c4b33364104d9a1ba87f9ec7674	0.58496044	7.55E-126	9.43E-125	Tumor	dMMR	657315.3	1401.3243	Roseburia intestinalis M50/1
0ee71c816b0045e83cc52804b39c593ef56f78ea	-0.6591072	2.04E-106	2.19E-105	Normal	dMMR	411460.6	1393.1467	Ruminococcus torques ATCC 27756
5270d13a0a9b613c1ac12be16cf28f1839065233	-0.4377876	1.45E-104	1.36E-103	Normal	dMMR	435590.9	1041.1283	Bacteroides vulgatus ATCC 8482
e3daabcc0d2ce7e6a9d0bedd684e9b9c924143ce5	-0.6279138	2.41E-91	2.01E-90	Normal	dMMR	997886.3	1111.0023	Bacteroides ovatus CL03T12C18
92a9e6fd06b63cc48625058e4125b1a2f2cf3048	0.59689464	4.99E-91	3.74E-90	Tumor	dMMR	1078089.3	1297.3163	Bacteroides sp. HPS0048
cbe56d8d19aa6175f4664cbf2bc0532c68243477	-0.5931651	2.24E-86	1.53E-85	Normal	dMMR	657322.3	1395.953	Faecalibacterium prausnitzii SL3/3
7cb3cb4d27875a6896a122af34ee4e1e25c0658d	-0.3841038	3.60E-85	2.25E-84	Normal	dMMR	411483.3	1615.3849	Faecalibacterium prausnitzii A2-165
1f7d94002df355b116de0bdd570275227c9ef5b	0.71386719	9.80E-82	5.65E-81	Tumor	dMMR	596315.3	156.4992	Peptostreptococcus stomatis DSM 17678
b3c6a6802f50753723c587db09737459a0ce4030	1.06029627	3.62E-79	1.94E-78	Tumor	dMMR	999403.4	1368.3447	Clostridium clostridioforme 90A1
95a5fc04db20b1fee193023578b40f95999f970	-0.4350349	2.49E-71	1.25E-70	Normal	dMMR	457389.4	1170.2812	Bacteroides sp. 3_1_13
3de43bb82a62218309d99da68e342a6a97aab07f	-0.6675574	1.57E-69	7.36E-69	Normal	dMMR	1414720.3	906.6438	Clostridium sp. JCC
325635b4eea0f4ea47d598992cdd1fe791949d5f	1.42677379	3.68E-56	1.62E-55	Tumor	dMMR	1512.4	1382.7717	[Clostridium] symbiosum
eb6dc9f905c574e9ba6937eb007f0663e85ebf0f	-0.4261092	9.27E-46	3.86E-45	Normal	dMMR	214856.4	1028.712	Alistipes finegoldii
25fc8a0281b2e510ffcdce6d197757488c61e23b	-1.7122905	6.96E-42	2.75E-41	Normal	dMMR	1658108.3	916.2228	Lachnospiraceae bacterium mt14
a087ce6dca66a1ca488f78a8c14bb79845224cad	-1.1560302	3.74E-39	1.40E-38	Normal	dMMR	1504823.3	1243.0129	bacterium LF-3
96ea0ee772910b0790552195b224f430d863ba5a	-0.4462376	1.16E-32	4.15E-32	Normal	dMMR	1805476.3	1202.5477	Blautia sp. Marseille-P2398
0c2b3a10e2af94b962ba7528f751204d55900582	-0.2694617	2.84E-28	9.67E-28	Normal	dMMR	411483.3	1615.3849	Faecalibacterium prausnitzii A2-165
f9f3f2e2c24d36b4d56f9b9edec4f0817714b83	1.06069608	1.49E-27	4.85E-27	Tumor	dMMR	999403.4	1368.3447	Clostridium clostridioforme 90A1
9877e6b400d6b6dd109860d5833e9a6158a14e	0.7120549	3.89E-26	1.22E-25	Tumor	dMMR	287.2537	1732.7964	Pseudomonas aeruginosa strain NCTC10332
638bf3ad37e8c44d6598b006681ad9dbac9d6f3a	-0.9666657	3.02E-22	9.05E-22	Normal	dMMR	450746.3	1363.6922	Coprobacillus sp. 8_1_38FAA
5098dddf48ee0ee369bfa4ae994436891b62bb42	-0.4612898	5.40E-17	1.56E-16	Normal	dMMR	657313.3	1516.1855	Ruminococcus torques L2-14
85d5404085808330afd5d0bac27edee00bf513c5	-0.4564157	2.48E-16	6.89E-16	Normal	dMMR	1805476.3	1202.5477	Blautia sp. Marseille-P2398
c7c054e78775fd54be9ea450fca5a2cc1945d3f8	0.88602974	8.61E-16	2.31E-15	Tumor	dMMR	470146.3	1182.1518	Coprococcus comes ATCC 27758
a9d3da348fab1229c75db0a1ff5b9a8d579bf3c5	-0.4264112	1.08E-14	2.79E-14	Normal	dMMR	39490.3	1407.3991	Eubacterium ramulus
071e09e58f93c6419d0dfacce0c7064963ca7ecb	-0.3480278	1.35E-14	3.38E-14	Normal	dMMR	411462.6	151.9632	Dorea longicatena DSM 13814
139bf28e70ca27abf9e9b4fd35182e3aa13554a4	-0.5072818	2.07E-12	4.85E-12	Normal	dMMR	1304.182	1395.7418	Streptococcus salivarius strain JF
fd1b56f2f52050a8575af68b53b5a691bea5db8c	-0.5595702	4.41E-12	1.00E-11	Normal	dMMR	663278.4	1208.4086	Ethanoligenens harbinense YUAN-3
5262929392a66cf2af6ca41089cb6dfcd63e9160	1.06010194	5.84E-10	1.25E-09	Tumor	dMMR	479437.5	0	Eggerthella lenta DSM 2243
b0e67ad37c689fd848f4ac9b923029d9c5b97b84	0.41181276	1.39E-09	2.89E-09	Tumor	dMMR	360807.5	1193.0967	Roseburia inulinivorans
714bb4b42c705998173a9e4009fa21cb94b32528	0.3640049	2.02E-09	4.10E-09	Tumor	dMMR	1121098.3	795.1877	Bacteroides massiliensis B84634 = Timone 84634 = DSM 17679 = JCM 13223 [PRJNA201686]
a882b133d4083ff6cc2ae50bd14dbe3d5446bb24	0.3309078	3.33E-08	6.58E-08	Tumor	dMMR	435590.9	1041.1283	Bacteroides vulgatus ATCC 8482
8707bac4e4749bf0b2c193cf8b359d5c0a14986	0.39743892	1.26E-07	2.43E-07	Tumor	dMMR	435591.13	915.4526	Parabacteroides distasonis ATCC 8503
96e019fe5ef30fa9da8b0cf35c33928cac91f6e1	-0.380227	5.51E-06	1.01E-05	Normal	dMMR	997873.3	996.4159	Bacteroides caccae CL03T12C61
b56b7e2dd2e753138a0a1d1e71f3056d12fed902	0.57075136	0.0008618	0.00143633	Tumor	dMMR	88431.7	1257.2534	Dorea longicatena
dd97ee7ed1ff7e48cf4248ea53130e398aadd0b0	-0.4085896	0.00126414	0.00197522	Normal	dMMR	1262706.3	155.0352	Azospirillum sp. CAG-260
9f1cd9232177f8118fc68906e04b28bcd454311b	0.51765698	0.00125275	0.00197522	Tumor	dMMR	1637506.3	155.1256	Lactobacillus sp. N15.MGS-260
fb4d2b05fa56f2555389e9e9f4c7ecfef185465c	-0.5372131	0.00150294	0.00230042	Normal	dMMR	411461.4	1407.3256	Dorea formicigenans ATCC 27755
7a633438d89337bc55cd5c5fd04031625f5ec003	-0.5942097	0.00173382	0.00260073	Normal	dMMR	370438.4	1376.6485	Pelotomaculum thermopropionicum SI
bc2013775f6c2ad131a83a32ef6141c46b9d6897	-0.344278	0.00290228	0.00426806	Normal	dMMR	1637509.3	136.2402	Acinetobacter sp. N54.MGS-139
4a5d3ca1a784b0b59365e16d1d97f2f440751e15	9.74443845	0.00865429	0.01248214	Tumor	dMMR	28116.7	1132.207	Bacteroides ovatus strain ATCC 8483
c996a0be142d3ef8c7bcf5b648ca29fdccb44d47	0.36683091	0.01032541	0.01461142	Tumor	dMMR	665956.3	1024.4306	Subdoligranulum sp. 4_3_54A2FAA
981787c105693e6d57f925437c828c382b0b5dccc	-0.2543321	0.0144519	0.01970714	Normal	dMMR	991789.3	1135.1437	[Clostridium] propionicum DSM 1682
3172c57e6f43b6d00b72d6ba94662cd4d386f07	0.50177131	0.02391492	0.031467	Tumor	dMMR	39488.4	1194.9277	[Eubacterium] hallii
04f784c78098595e60b39c56bc8831a1c246d8bd	-1.7723933	0.0790503	0.10048767	Normal	dMMR	411462.6	151.9632	Dorea longicatena DSM 13814
ab05bcb443299370fc72115db48e6b4157a86442	0.40121918	0.10486613	0.13108266	Tumor	dMMR	445972.6	0	Aneorotruncus colihominis DSM 17241
c38a8f4266e22370fdb6dd2b031dd46c2ed486d	-0.264655	0.1180747	0.14517382	Normal	dMMR	1737424.3	1179.3562	Blautia sp. GD8
15b516cdaae4f56342986fc617b013ae81b5ce8a	-0.2961537	0.31878833	0.35685261	Normal	dMMR	292800.4	1431.4755	Flavonifractor plautii

Table S4: sOTUs enriched in tumor samples (colon tissue and mucosa) as compared to normal-adjacent samples in individuals with pMMR CRC.

OTU	effect.size	pvalue	pvalueBH	direction	dMMR/pMMR	genome ID	Influence	name
e4bb49ce45f25c04d029c0f3c2a02ae1f780ed7e	-0.4050761	9.36E-47	4.73E-45	Normal	pMMR	1121098.3	833.960689	Bacteroides massiliensis B84634 = Timone 84634 = DSM 17679 = JCM 13223 [PRJNA201686]
d81cca4cb1da96d4aac11b5e10da796b790f6f0d	0.53859538	7.40E-37	1.49E-35	Tumor	pMMR	537011.5	827.7535	Prevotella copri DSM 18205
630f4d74a9b05aa8f65f112233ab096262308e5b	-0.3243335	1.92E-30	3.24E-29	Normal	pMMR	1121098.7	733.813729	Bacteroides massiliensis B84634 = Timone 84634 = DSM 17679 = JCM 13223
d719fd0ae85ede0c04e8ec61275300fe178d3948	0.56566892	1.50E-27	2.16E-26	Tumor	pMMR	1637497.3	616.2185	Ruminococcus sp. A254.MGS-108
8bac4e22d77ae1efc469563bab275f452e002119	0.3904693	5.68E-17	5.21E-16	Tumor	pMMR	709991.3	662.1316	Odoribacter splanchnicus DSM 220712
fa168b426edd535933f3a3828a6b828df49062a5	2.09593898	1.78E-13	1.29E-12	Tumor	pMMR	824.5	766.4971	Campylobacter gracilis strain ATCC 33236
a12bb28d688a2818753403165c417928c708839c	0.2820261	1.04E-12	6.59E-12	Tumor	pMMR	246787.4	471.1197	Bacteroides cellulosilyticus strain WH2
1c2b42abea5b6d81202bcc344ce570a43693931c	0.27970625	1.76E-12	1.04E-11	Tumor	pMMR	457390.3	450.41	Bacteroides sp. 3_1_23
0694fb7ab2fc435cd49b675a4a501d9daa2930	-0.4289683	9.38E-10	4.12E-09	Normal	pMMR	663278.4	692.2454	Ethanoligenens harbinense YUAN-3
c7c054e78775fd54be9ea450fca5a2cc1945d3f8	-0.451427	2.04E-08	8.57E-08	Normal	pMMR	470146.3	779.8438	Coprococcus comes ATCC 27758
2b0c96c19e80e9f5a838843afb06c138d7172f7	0.28328637	3.73E-08	1.51E-07	Tumor	pMMR	1378168.3	1001.5082	Firmicutes bacterium ASF500
9416469ebfb756921565fc178646cca9ca55d008	-0.33991	7.77E-08	2.91E-07	Normal	pMMR	592028.3	657.798	Dialister invisus DSM 15470
b76e229e544427d2ec5554d0665d25c8dace5ca	0.32174448	1.40E-06	4.72E-06	Tumor	pMMR	997894.4	797.9159	Clostridium bolteae 90A9
8b718f72b3c90530cc3cebdbab7e7d813658e679	0.59750509	7.94E-06	2.29E-05	Tumor	pMMR	1805476.3	675.950136	Blautia sp. Marseille-P2398
a7266616bf8e0fbf8eb7fe0988c33ef323183a1	-0.3083376	1.10E-05	3.10E-05	Normal	pMMR	1262986.3	699.4664	Proteobacteria bacterium CAG:139
d7df7ac38235e7bfd8f7509a774a0023ff193d2a	-0.2518214	2.75E-05	7.50E-05	Normal	pMMR	717608.3	679.7108	Clostridium cf. saccharolyticum K10
85f3c28e9e0bd6f89a28b03c277d3c0101634c45	-0.287788	4.65E-05	0.00011462	Normal	pMMR	1150298.4	571.5477	Fusicatenibacter saccharivorans
fd1b56f2f52050a8575af68b53b5a691bea5db8c	-0.3963119	1.04E-13	8.04E-13	Normal	pMMR	663278.4	692.2454	Ethanoligenens harbinense YUAN-3
b56b7e2dd2e753138a0a1d1e71f3056d12fed902	0.34825974	0.00121089	0.00246777	Tumor	pMMR	88431.7	821.9625	Dorea longicatena
26bf8c066146b41167a37935f3f358101696b6ee	-0.2768876	0.00122167	0.00246777	Normal	pMMR	545696.5	714.2144	Holdemania filiformis DSM 12042
aba2338cfa6a47bbec11e832e4034f127329942f	-22.191969	0.99675617	0.99999179	Normal	pMMR	717608.3	679.7108	Clostridium cf. saccharolyticum K10
354517367a6dbbdf72794656076e945a8b727e27	0.85409107	0.0069283	0.01272287	Tumor	pMMR	411483.3	621.0295	Faecalibacterium prausnitzii A2-165
d0fcb4043b758d8c8b416265dce6280d2bc137a7	-0.2757175	0.0087464	0.01577476	Normal	pMMR	1637500.3	734.2163	Burkholderia sp. K4410.MGS-135
b172803a089a26b95a72e38bd85201fa948cccdc	1.62061816	0.00979644	0.0173586	Tumor	pMMR	1637499.3	951.214904	Ruminococcus sp. A254.MGS-254
407411bafacade3dea8e72c2ec6880198037a6df	-1.645122	0.02941911	0.04952218	Normal	pMMR	445972.6	780.6051	Anaerotruncus colihominis DSM 17241
4ce870e7ea166023ba98173c91b4451f7dd0802	-0.2915874	0.03593312	0.05949581	Normal	pMMR	428126.7	669.3468	Clostridium spiroforme DSM 1552
9aabaca70ab3616bcc40b4e2e09a6d024049e7ee	-1.6820232	0.05708945	0.09152436	Normal	pMMR	1051074.3	489.8798	Streptococcus thermophilus JIM 8232
d6e7fa11f119f2b038716cba3ca721b8b39871bf	0.32736017	0.06597265	0.10251135	Tumor	pMMR	1637504.3	694.1991	Carnobacterium sp. N15.MGS-207
31feb7ea26c56019f324c5a0b5759129e162a7e1	0.37074939	0.07084033	0.1078422	Tumor	pMMR	40520.5	647.3191	Blautia obeum
3897e30a1778b4cbb87e053557cc96329d33fc01	-0.705588	0.12163092	0.17549605	Normal	pMMR	1650661.3	621.865113	Clostridium sp. GD3
e9c75d4517ae2c00d0cc63923bec93188d46d6d	-1.103821	0.14520269	0.20655594	Normal	pMMR	457391.3	482.5388	Bacteroides sp. 3_1_33FAA
2b2000704aa739ea00a45a8bed5bdd42c8cafcb8	0.62362676	0.30456543	0.40475143	Tumor	pMMR	411463.4	662.936247	Eubacterium ventriosum ATCC 27560
3172c57e6f43b6dd00b72d6ba94b62cd4d386f07	0.67857108	0.31880956	0.41281751	Tumor	pMMR	39488.4	743.1495	Eubacterium hallii
1bd214c8917453b714fe98affc8616dee4d638	0.27669832	0.81501976	0.88512899	Tumor	pMMR	515620.4	719.9872	Eubacterium eligens ATCC 27750
df4cfc980121095e2626e4d4f42c03fdd4c8428e	0.30515285	0.82946376	0.89123234	Tumor	pMMR	1316586.3	832.56	Fusobacterium nucleatum CTI-5
83d8d058f7a1bc979398d8300b2b20084da9bfec	-8.5115812	0.91955476	0.9776319	Normal	pMMR	349741.6	643.5029	Akkermansia muciniphila ATCC BAA-835
5674a6dcbc90f6ed5f456903ca7692c90d6c4d7b	-21.636361	0.99852384	0.99999179	Normal	pMMR	742725.3	629.4384	Alistipes indistinctus YIT 12060

Table S5: sOTUs enriched in the proximal or distal colon (colon tissue and mucosa) of individuals with dMMR CRC.

index	enriched in?	effect size	pvalue	pvalueBH	qvalue	taxonomy
4e5d3ca1a784b059365e16d1d97f27440751e15	distal	10.43	9.004E-03	3.554E-02	3.554E-02	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;ovatus;
638bf3ad37e8c44d6598b006681a9dbac9d6f3a	distal	2.09	1.932E-07	2.899E-06	2.899E-06	Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelotrichaceae_UCG-003;NA;
a828b133d4083f6cc2ae50bd14de3d54466b24	distal	1.91	5.581E-01	9.302E-01	9.302E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;dorei/sartorii/vulgatus;
1f7d94002df355b116de0bddd507275227c9ef5b	distal	1.73	1.849E-12	3.467E-11	3.467E-11	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococaceae;Peptostreptococcus;tomatis;
ab05bc443299370c72115db486b4157a86442	distal	1.68	6.979E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;NA;NA;
8c7e17334157e39923594420e770f6ed1e5b608	distal	1.44	6.111E-01	9.353E-01	9.353E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella;NA;
8ebcc2ad430a757d9e9c835f2c0fe604ad07d14	distal	1.25	4.990E-02	1.439E-01	1.439E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Dorea;formicigenerans;
ebc6e9f905c574e9b6937eb0070663e85ebf0f	distal	1.17	4.934E-13	1.233E-11	1.233E-11	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes;finegoldii/onderdonkii;
139f728e7c0a27abf9e9b4f4351823aa13554a4	distal	1.04	4.999E-01	8.719E-01	8.719E-01	Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococaceae;Streptococcus;NA;
9f1cd92321778118f6c8906e4b28bc454311b	distal	0.96	2.709E-03	1.355E-02	1.355E-02	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae_UCG-013;NA;
3172c57e6f43b6d00b72d6ba9462c6d4d386f07	distal	0.92	2.968E-06	3.180E-05	3.180E-05	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;NA;NA;
5098ddd48ee0e369f4a4e9943689162b2bb42	distal	0.82	4.218E-02	1.318E-01	1.318E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;NA;NA;
249bd28190c2a1fa1b8084574bb15912e4722d	distal	0.66	1.527E-03	8.812E-03	8.812E-03	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;NA;NA;
15b516cda4e4f5634298f6c17b013ae81b5ce8a	distal	0.59	1.856E-01	4.429E-01	4.429E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor;plautii;
c38a8f426e22370fd4b6dd2b031dd46c2e4d86d	distal	0.53	1.623E-01	4.222E-01	4.222E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia;massiliensis;
c7c05ae7875fd54be9ae450fca5a2cc1945d3f8	distal	0.50	2.490E-01	5.501E-01	5.501E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella_4;genus_check/comes;
88280c5ee5b050e6011169b897086055a3e4a7	distal	0.42	3.458E-01	6.825E-01	6.825E-01	Bacteria;Actinobacteria;Coriobacteria;Coriobacteriales;Eggerthellaceae;Eggerthella;lenta;
cbe56bd8d19aa6175f4664cbf2bc0532c68243d7d	distal	0.41	3.221E-03	1.510E-02	1.510E-02	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium;prausnitzii;
9e481a0c94bd9c960018e5bc929df98c43189	distal	0.29	4.867E-01	8.692E-01	8.692E-01	Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Solobacterium;moorei;
04f784c7809859e60b39c56bc8831a1246d8bd	distal	0.26	8.508E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Dorea;genus_check/longicatena/torque;
52629392a266cf2f6c641089cbdf6c43e9160	distal	0.24	5.335E-01	9.094E-01	9.094E-01	Bacteria;Actinobacteria;Coriobacteria;Coriobacteriales;Eggerthellaceae;Eggerthella;lenta;
87c90d196bf14c4b3364104d9a1ba8799ec7674	distal	0.22	2.661E-03	1.355E-02	1.355E-02	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia;intestinalis;
aa6a29c3b174f23e608d8db34b74140345d7df	distal	0.13	5.897E-01	9.353E-01	9.353E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia;faecis;
a087c6dca66a1ca488f78a8c14bb79845224cad	distal	0.11	8.869E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;UCG-003;NA;
a9d3d448fab1229c75db0a1f5b9a8d579bf3c5	distal	0.08	6.078E-01	9.353E-01	9.353E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Agathobacter;NA;
5472c79c6d7f84d65454bd8c80e450071a430607	distal	0.06	7.298E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium;cf./prausnitzii;
df4fc980121095e2626e4d442c03fdd4c8428e	proximal	-0.02	9.774E-01	9.999E-01	9.999E-01	Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Fusobacterium;nucleatum;
b0e2c85ee364dc81199bca252f3e206af4d5f6	proximal	-0.02	9.002E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae_UCG-002;NA;
96ae00772910b079055219562040863ba5a	proximal	-0.03	2.64E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia;Juti/obeum;
3de43bb82a62218309d9da68e342a6a97aab07f	proximal	-0.11	1.890E-01	4.429E-01	4.429E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_1;celatum/di sporicum/saudiense;
0c2b3a10e2af94b962ba7528f751204d55900582	proximal	-0.15	2.494E-01	5.501E-01	5.501E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium;prausnitzii;
1910ca1b089d8231b2e67f8454cddb5c020c3144	proximal	-0.20	6.014E-01	9.353E-01	9.353E-01	Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelatoclostridium;ramosum;
a7266616bf8e0fb8eb72fe0988c33ef323183a1	proximal	-0.21	4.632E-01	8.473E-01	8.473E-01	Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Parasutterella;NA;
071e09e58f93c641901facc0c7064963ca7ebc	proximal	-0.22	1.604E-01	4.222E-01	4.222E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Dorea;longicatena;
ef17e279b408157cedec4248d1ca5a6911ac4e	proximal	-0.32	4.870E-05	3.653E-04	3.653E-04	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Agathobacter;NA;
7cb3cb4d27875a6896a122af34ee4e1e25c0658d	proximal	-0.35	2.743E-05	2.286E-04	2.286E-04	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium;CM04-06;
647f0235ac545a07e5ed6c880b2318e64fd529	proximal	-0.37	1.028E-04	7.007E-04	7.007E-04	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;faecis/thetaiotaomicron;
b75db79d71e49907faca3540ada94d120f69f7	proximal	-0.40	4.621E-21	1.733E-19	1.733E-19	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;dorei/vulgatus;
e3ababc0d2ce7e6a9a0bd8e684e9b9c924143ce5	proximal	-0.42	1.145E-02	4.293E-02	4.293E-02	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;fragilis/ovatus;
c996a0be14d23ef8c7bc7b5648ca29dfcb44d47	proximal	-0.49	3.442E-01	6.825E-01	6.825E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;UBA1819;NA;
7a63348d89337bc5cd5c5fd04031625f5ced03	proximal	-0.51	7.917E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae_R-7_group;NA;
19f3f2e2c24d3664d56f9b9edec4f0817714b83	proximal	-0.58	3.659E-01	7.037E-01	7.037E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium;urinumissiliense;
25f8c0281b2e510ffcdce6d197574886c1e2eb3	proximal	-0.71	1.633E-01	4.222E-01	4.222E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eulophosium;NA;
1e2a1be1c43888849af64dfe470c7016537f01	proximal	-0.75	6.557E-03	2.732E-02	2.732E-02	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococaceae;Intestinibacter;bartlettii;
0ee71c816004d8e3c52804b39c593ef56f78ea	proximal	-0.79	3.626E-06	3.399E-05	3.399E-05	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;NA;NA;
6c63c74b65e18ec6bd353513bd0c9620820947	proximal	-0.89	7.287E-04	4.554E-03	4.554E-03	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter;NA;
5270013a0a9b613c1ac12be16cf28f1839065233	proximal	-0.93	7.78E-01	9.999E-01	9.999E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;dorei/vulgatus;
1a5db7cbf3e568848481d107f6f2da7e23425c1	proximal	-0.95	6.356E-01	9.534E-01	9.534E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinifilaceae;Odoribacter;planchnicus;
fb4d2b05fa56f255389e9e9f4c7ecfef185465c	proximal	-0.97	7.437E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Dorea;genus_check/formicigenerans/to rques;
b0e67ad37c689fd484fac9b923029d9c5b97b8a	proximal	-1.19	3.311E-01	6.825E-01	6.825E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia;inulinivorans;
8b87b44acae1c9d0217ea1774d20395a65c23d3	proximal	-1.26	3.145E-02	1.072E-01	1.072E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;dorei/fragilis;
af8924308524d319c4d3aeef5877364df563d	proximal	-1.60	4.190E-01	7.855E-01	7.855E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae_UCG-004;NA;
3897e30a1778b4cb87e053557c9c6329d33f01	proximal	-2.41	1.698E-01	4.245E-01	4.245E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminoclostridium_9;NA;
64de730cae6b29df43c1257f6ceb75eece2daea	proximal	-2.74	3.290E-02	1.073E-01	1.073E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;fragilis/xylanisolvens;
9877e6400d6b6dd10986d0d5833e9a6158a14e	proximal	-2.81	4.484E-02	1.345E-01	1.345E-01	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;aeruginosa/alcaligenes/citronellolis/delhiensis/denitrificans/fluorescens/guezennei/knackmussii/mendocina/mosselii/nitroreducens/otitidis/protegens/pseudoalcaligenes/putida/resinivorans/stutzeri/tropicalis;
2bc9c619e80e9f5a838843af0b6c138d7172f7	proximal	-3.01	2.598E-01	5.567E-01	5.567E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminoclostridium_9;NA;
95a5fc04d20b1fee193023578b40f955999f970	proximal	-3.44	1.617E-168	1.213E-166	1.213E-166	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;acidifaciens/caccaec/acacemuris/dorei/faecichinchillae/faecis/fragilis/graminisolvens/neonati/ovatus/retilotermis/sal yersiae/thetaiotaomicron/xylanisolvens;
edce63d18074b04557d5b57df0988d78e4a4ee6f	proximal	-3.45	2.476E-07	3.095E-06	3.095E-06	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae_NK4A136_group;NA;
84fe91323797b13ae23d1c9a0a1197f4ac695f3	proximal	-4.08	2.020E-02	7.215E-02	7.215E-02	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/S higella/albertii/boydii/goli/dysenteriae/fergusonii/flexneri/sonnei/vulneris;
85d5404085808330af5d0bac27ede00bf513c5	proximal	-4.88	5.627E-03	2.482E-02	2.482E-02	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia;Juti/obeum/wexlerae;
d97ae445fd4a641bd2c19b3f253967d251a8579b	proximal	-14.55	9.980E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Family_Xi;Anaerococcus;vaginalis;
dd97e7ed1ff7f4e8c4248ea53130e398aad0b0	proximal	-15.13	1.986E-01	9.999E-01	9.999E-01	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;NA;NA;NA;
8707bac4e47ab9f0b2c193c8b395dc0ca14986	proximal	-15.65	9.980E-01	9.999E-01	9.999E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Tannerellaceae;Parabacteroides;distansis;
981787c105693e6b57f925437c828382b085dcd	proximal	-16.58	9.980E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella;NA;
fd1b56f2f5205a0f5af68b35b5a691bea5db8c	proximal	-17.56	9.975E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Negativibacillus;NA;
87e27f8ad1f4b012359a25d7918bb747857b85d	proximal	-19.40	9.973E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;NA;NA;
b3c6a802f5073723c587db09737459a0ce4030	proximal	-20.60	9.966E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Bacilli;Bacillales;Family_Xi;Gemella;morbillorum;
92a9e6f0d6b6c3c48e25058e4125b1a2f2c3048	proximal	-20.86	9.915E-01	9.999E-01	9.999E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;nordii;
3256354ee0af4ea47d598992cd1fe791949df5	proximal	-20.99	9.967E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium;NA;
b56b7e2d2e753138a0a1d1e71f3056d12fe902	proximal	-21.95	9.984E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;NA;NA;
67db4f7e9b0c521ca78a13a1b0874baa173161f	proximal	-22.25	9.980E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococaceae;Intestinibacter;genus_check/bartl ettii/ilealis/timomensis;
bc2013757c62ad31a83a32ef6141c46b9d9897	proximal	-22.41	9.975E-01	9.999E-01	9.999E-01	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae_UCG-004;NA;
96e019fe5ef30fa9da8b0c35c33928ca91fe1	proximal	-23.27	9.974E-01	9.999E-01	9.999E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;caccaec;
714bb4b42c705998173a9e4009a21c6b4832528	proximal	-24.17	9.981E-01	9.999E-01	9.999E-01	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;massiliensis;
c9a1c377ba9b93ac05d720a18e2ad18f9b1fe6	proximal	-31.01	9.999E-01	9.999E-01	9.999E-01	Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Fusobacterium;nucleatum/p eriodonticum;

Table S7: Differentially abundant microbes in individuals with dMMR CRC from an independent cohort. Blue boxes highlight microbes enriched in tumor tissue samples as compared to normal adjacent samples.

OTU_Id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	Phylum	Class	Order	Family	Genus	Species
1139840	147.795	3.273	0.835	3.920	0.000	0.008	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Treponema	
1065387	36.266	2.079	0.972	2.138	0.032	0.372	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	[Prevotella]	
1096339	239.138	2.007	0.888	2.261	0.024	0.372	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium	
128205	222.417	1.800	0.837	2.150	0.032	0.372	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	fragilis
1004910	68.434	1.501	0.712	2.109	0.035	0.372	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	
144395	18.615	-1.662	0.762	-2.181	0.029	0.372	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea	
1551841	49.989	-2.234	0.936	-2.387	0.017	0.372	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	[Ruminococcus]	gnavus
1012372	32.916	-2.724	1.016	-2.682	0.007	0.311	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae		

Table S8: Differentially abundant microbes in individuals with pMMR CRC from an independent cohort. Blue boxes highlight microbes enriched in tumor tissue samples as compared to normal adjacent samples.

OTU_Id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	Phylum	Class	Order	Family	Genus	Species
106952	37.452	2.081	0.604	3.443	0.001	0.014	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Candidatus Portiera	aleyrodidarum
135755	22.419	1.879	0.551	3.412	0.001	0.014	Proteobacteria	Gammaproteobacteria	HTCC2188	HTCC2089		
1047065	10.921	1.854	0.496	3.735	0.000	0.008	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		
4357652	17.705	1.798	0.653	2.755	0.006	0.031	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Alkaliphilus	
1106195	16.367	1.769	0.546	3.236	0.001	0.018	OD1	ZB2				
609704	19.632	1.634	0.574	2.847	0.004	0.031	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Providencia	
1134730	22.018	1.535	0.548	2.799	0.005	0.031	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Candidatus Portiera	
103288	9.933	1.503	0.491	3.063	0.002	0.025	Actinobacteria	Actinobacteria	Actinomycetales			
778029	23.263	1.485	0.651	2.281	0.023	0.087	Chlorobi	BSV26	C20			
1546868	11.248	1.464	0.529	2.768	0.006	0.031	Acidobacteria	[Chloracidobacteria]	RB41			
101584	147.234	1.432	0.366	3.909	0.000	0.008	Bacteroidetes	Bacteroidia	Bacteroidales			
1135525	10.774	1.422	0.442	3.220	0.001	0.018	OD1					
1010721	19.395	1.417	0.618	2.291	0.022	0.087	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	
1108726	54.398	1.398	0.604	2.316	0.021	0.087	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	
1115384	257.797	1.322	0.434	3.045	0.002	0.025	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		
1028553	14.510	1.190	0.483	2.465	0.014	0.069	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	
1016598	208.568	-0.705	0.311	-2.265	0.024	0.087	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		
110562	54.305	-1.089	0.366	-2.973	0.003	0.028	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	
147702	56.471	-1.133	0.465	-2.434	0.015	0.071	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	prausnitzii
1138850	22.615	-1.276	0.450	-2.835	0.005	0.031	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	
195508	6.569	-1.352	0.596	-2.270	0.023	0.087	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	caccae
1067143	62.681	-1.563	0.562	-2.784	0.005	0.031	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae		
1733364	22.419	-1.596	0.549	-2.908	0.004	0.031	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis