<table>
<thead>
<tr>
<th><strong>Title</strong></th>
<th>Tumour-associated and non-tumour-associated microbiota in colorectal cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Author(s)</strong></td>
<td>Flemer, Burkhardt; Lynch, Denise B.; Brown, Jillian R. M.; Jeffery, Ian B.; Ryan, Feargal J.; Claesson, Marcus J.; O'Riordain, Micheal G.; Shanahan, Fergus; O'Toole, Paul W.</td>
</tr>
<tr>
<td><strong>Publication date</strong></td>
<td>2017</td>
</tr>
<tr>
<td><strong>Type of publication</strong></td>
<td>Article (peer-reviewed)</td>
</tr>
</tbody>
</table>
| **Link to publisher's version** | [http://gut.bmj.com/content/66/4/633](http://gut.bmj.com/content/66/4/633)  
[http://dx.doi.org/10.1136/gutjnl-2015-309595](http://dx.doi.org/10.1136/gutjnl-2015-309595) |
| **Rights** | © 2016, the Authors. Published by the BMJ Publishing Group Limited. For permission to use (where not already granted under a licence) please go to [http://www.bmj.com/company/products-services/rights-and-licensing/](http://www.bmj.com/company/products-services/rights-and-licensing/). This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: [http://creativecommons.org/licenses/by-nc/4.0/](http://creativecommons.org/licenses/by-nc/4.0/)  
[https://creativecommons.org/licenses/by-nc/4.0/](https://creativecommons.org/licenses/by-nc/4.0/) |
| **Item downloaded from** | [http://hdl.handle.net/10468/5383](http://hdl.handle.net/10468/5383) |

Downloaded on 2019-11-18T20:09:33Z
**Supplementary Figures 1-4:** PCoA of microbiota using different distance matrices (1: Unweighted UniFrac, 2: Weighted UniFrac, 3: Spearman-rank distance, 4: binary distance).

Sample groupings according to metadata in Supplementary Table 1.
**Supplementary Figure 5:** Hierarchical Ward-linkage clustering based on the Pearson correlation coefficients of the relative abundance of OTUs in 53 tumour samples from Kostic et al.\textsuperscript{21}. Co-abundance groups were defined on the basis of the clusters in the vertical tree and named after their most notable characteristic. Column colour coding according to legend below. Row colour coding according to legend on the left. To the right, the most abundant bacterial genera as well as the most strongly connected genera in each CAG (i.e. genera with the highest numbers of significant positive correlations with other members of each respective group) are listed.
Supplementary Figure 6: Hierarchical Ward-linkage clustering based on the Pearson correlation coefficients of the relative abundance of OTUs in 48 tumour samples from Zeller et al. Zeller et al.\textsuperscript{11}. Co-abundance groups were defined on the basis of the clusters in the vertical tree and named after their most notable characteristic. Column colour coding according to legend below. Row colour coding according to legend on the left. To the right, the most abundant bacterial genera as well as the most strongly connected genera in each CAG (i.e. genera with the highest numbers of significant positive correlations with other members of each respective group) are listed.
**Supplementary Figure 7:** Hierarchical Ward-linkage clustering based on the Pearson correlation coefficients of the relative abundance of OTUs in 47 tumour samples from the here presented cohort. Co-abundance groups were defined on the basis of the clusters in the vertical tree and named after their most notable characteristic. Column colour coding according to legend below. Row colour coding according to legend on the left. To the right, the most abundant bacterial genera as well as the most strongly connected genera in each CAG (i.e. genera with the highest numbers of significant positive correlations with other members of each respective group) are listed.
**Supplementary Figure 8:** Hierarchical Ward-linkage clustering based on the Pearson correlation coefficients of the relative abundance of CAGs in 53 CRC samples from Kostic et al.\textsuperscript{21} (A) in 48 CRC samples from Zeller et al.\textsuperscript{11} (B), and in 47 tumour samples from this study (C).

**Supplementary Figure 9:** Unweighted UniFrac PCoA; A: 53 CRC samples from Kostic et al.\textsuperscript{21}; B: 48 CRC samples from Zeller et al. Zeller et al.\textsuperscript{11}; C: 47 tumours samples from this study. The location of samples on the PCoA is strongly associated with α-diversity and abundance of the bacterial co-occurrence clusters as defined in Supplementary Figures 5-7. Arrows indicate the direction of correlations for α-diversity (black) and bacterial co-occurrence networks (colours as in Supplementary Figures 5-7) with location on the PCoA. The distance from the origin and the direction correspond to the vector of x- and y-axis correlation.
**Supplementary Figure 10:** Hierarchical Ward-linkage clustering of based on the Pearson correlation of the abundance of bacterial co-occurrence clusters in each sample. (A) 53 CRC samples from Kostic *et al.*\(^{21}\); (B) 48 CRC samples from Zeller *et al.*\(^{11}\); (C) 47 tumour samples from this study.
Supplementary Figure 11: Schematic representation of relative abundance distribution for each bacterial co-occurrence cluster; (A) for 53 CRC samples from Kostic et al. \textsuperscript{21}; (B) for 48 CRC samples from Zeller et al. \textsuperscript{11}; (C) for 47 tumour samples from this study. Significant difference for each Sample Group compared to each other Sample Group in terms of α-diversity is indicated above bar. Brackets indicate p<0.1.
Supplementary Figure 12: Schematic representation of relative abundance distribution for genera with a mean abundance > 0.5%; (A) 53 CRC samples from Kostic et al.; (B) 48 CRC samples from Zeller et al.; (C) 47 tumour samples from this study.
Supplementary Figure 13: Network plots of OTUs. (A) 53 CRC samples from Kostic et al.\textsuperscript{21}; (B) 48 CRC samples from Zeller et al.\textsuperscript{11}. The size of each node (circle) is proportional to the mean abundance of each OTU. The location of each node was determined by a PCoA of the correlation distance as described in Material and Methods. Colour of each node according to the CAGs as in Supplementary Figures 5-7. The width of each edge corresponds to the p-value of the correlation between each respective node (lower p-value, higher line-width); only edges with positive correlations (p<0.1) shown. Names only shown for OTUs with a mean abundance > 0.5%.
**Supplementary Figure 14:** Network plots of genera. (A and B): 53 CRC samples from Kostic et al.\textsuperscript{21} (A); 47 tumour samples from this study (B). Colour of each node according to the bacterial co-occurrence clusters as in Supplementary Figures 5 and 7. (C and D): 48 CRC samples from Zeller et al.\textsuperscript{11} (C); 47 tumour samples from this study (D). Colour of each node according to the bacterial co-occurrence clusters as in Supplementary Figures 6 and 7. (A-D): The size of each node (circle) is proportional to the fold-change of each genus between CRC samples from each respective cohort and the healthy controls of this study. Only genera with a fold-change > 1.5 and genera which were shared between the Kostic et al. dataset and this study (A and B) and the Zeller et al. dataset and this study (C and D), respectively, are shown. The location of each node was determined by a PCoA of the correlation distance as described in Material and Methods. The width of each edge corresponds to the p-value of the correlation between each respective node (lower p-value, higher line-width); only edges with positive correlations (p<0.1) shown. Circles: increased in individuals with CRC. Triangles decreased in individuals with CRC.
Supplementary Figure 15: PCA of dietary information. The habitual diet of individuals with CRC and polyps was significantly different from the habitual diet of healthy individuals.