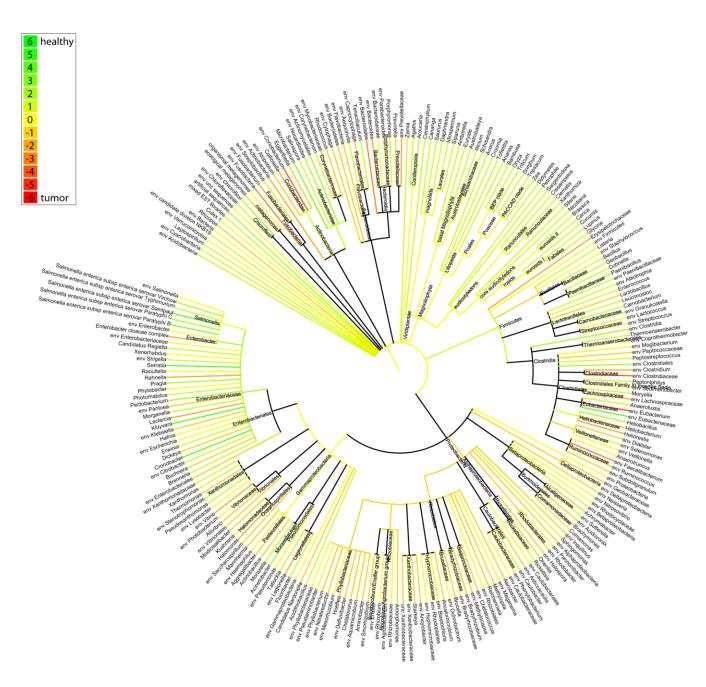
Marchesi et al., 2011 CRC Microbiome

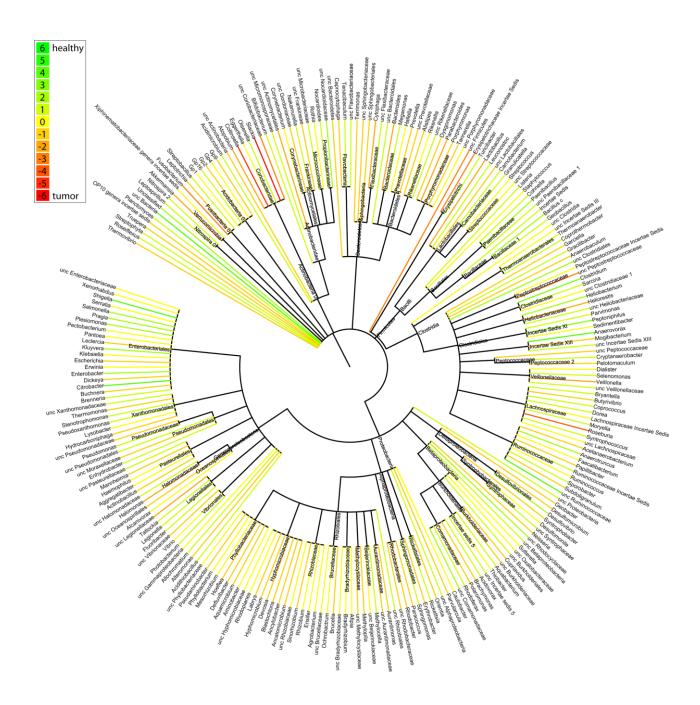
Figure S4. Consistent biases in microbiota between the on- and off-tumor samples. The overall consistency scores between +6 (green) and -6 (red) reflects how consistently clades were enriched across six patients. Trees were visualized with iTOL [5] **A**, Consistent clades derived from the EMBL annotation of SILVA sequences. **B**, Consistent clades derived from the RDP annotation of SILVA sequences. **C**, Differential annotation depth of the SSU rRNA sequences in the SILVA database [1] by EMBL and RDP. Low annotation depth means little resolution: many sequences are either well annotated by RDP (bottom right) or by EMBL (top left).





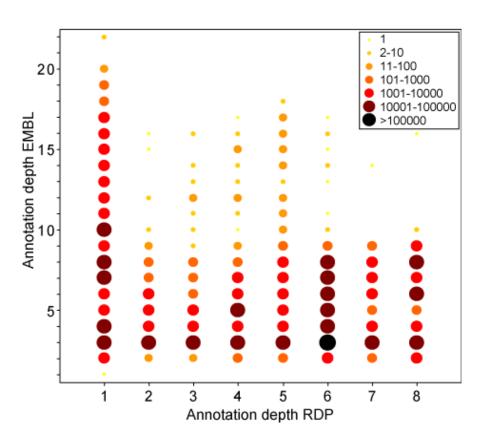
Marchesi et al., 2011 CRC Microbiome

В



Marchesi et al., 2011 CRC Microbiome

C



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1 Pruesse E, Quast C, Knittel K et al. SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucl Acids Res 2007;35:7188-7196.