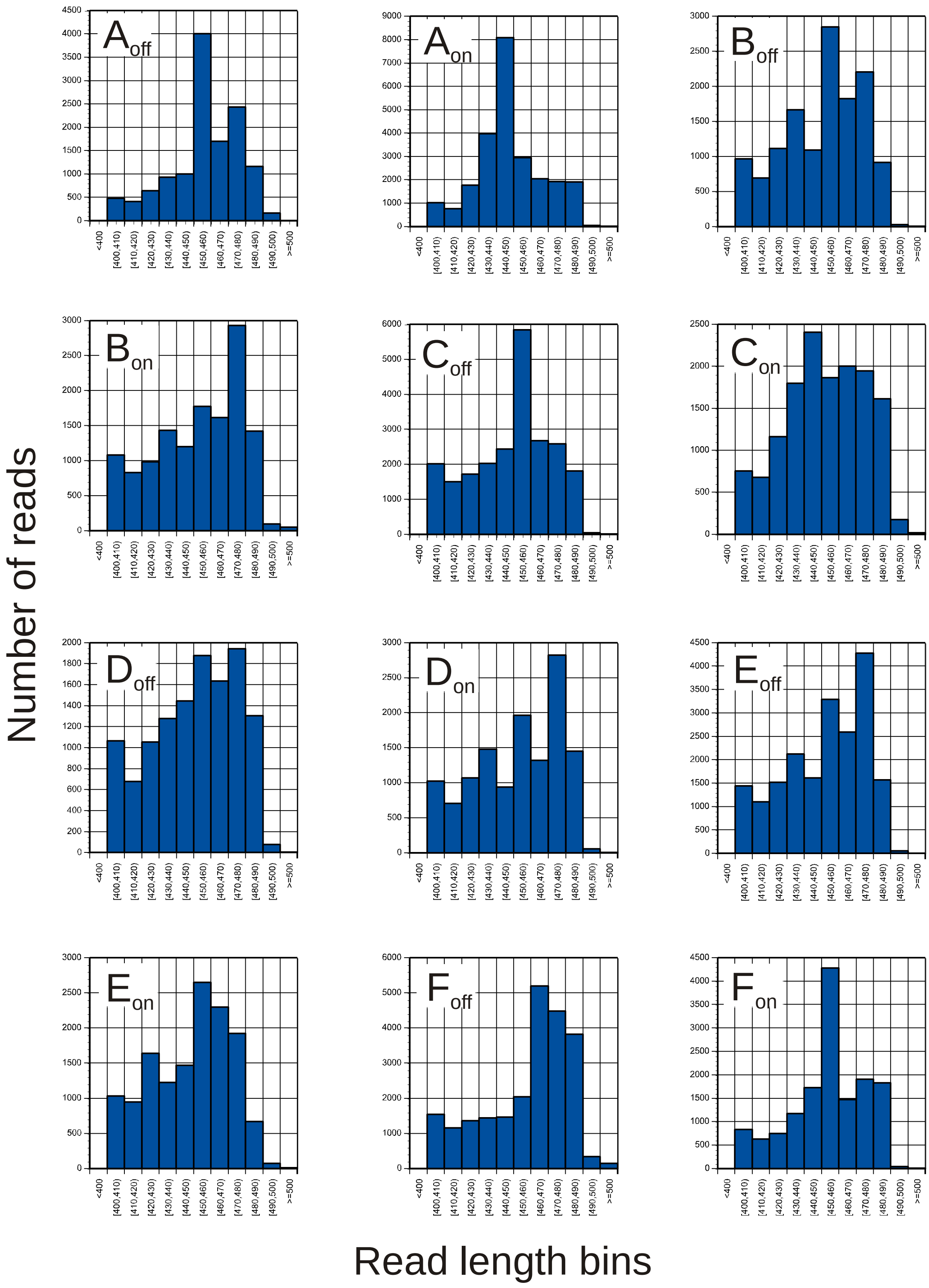
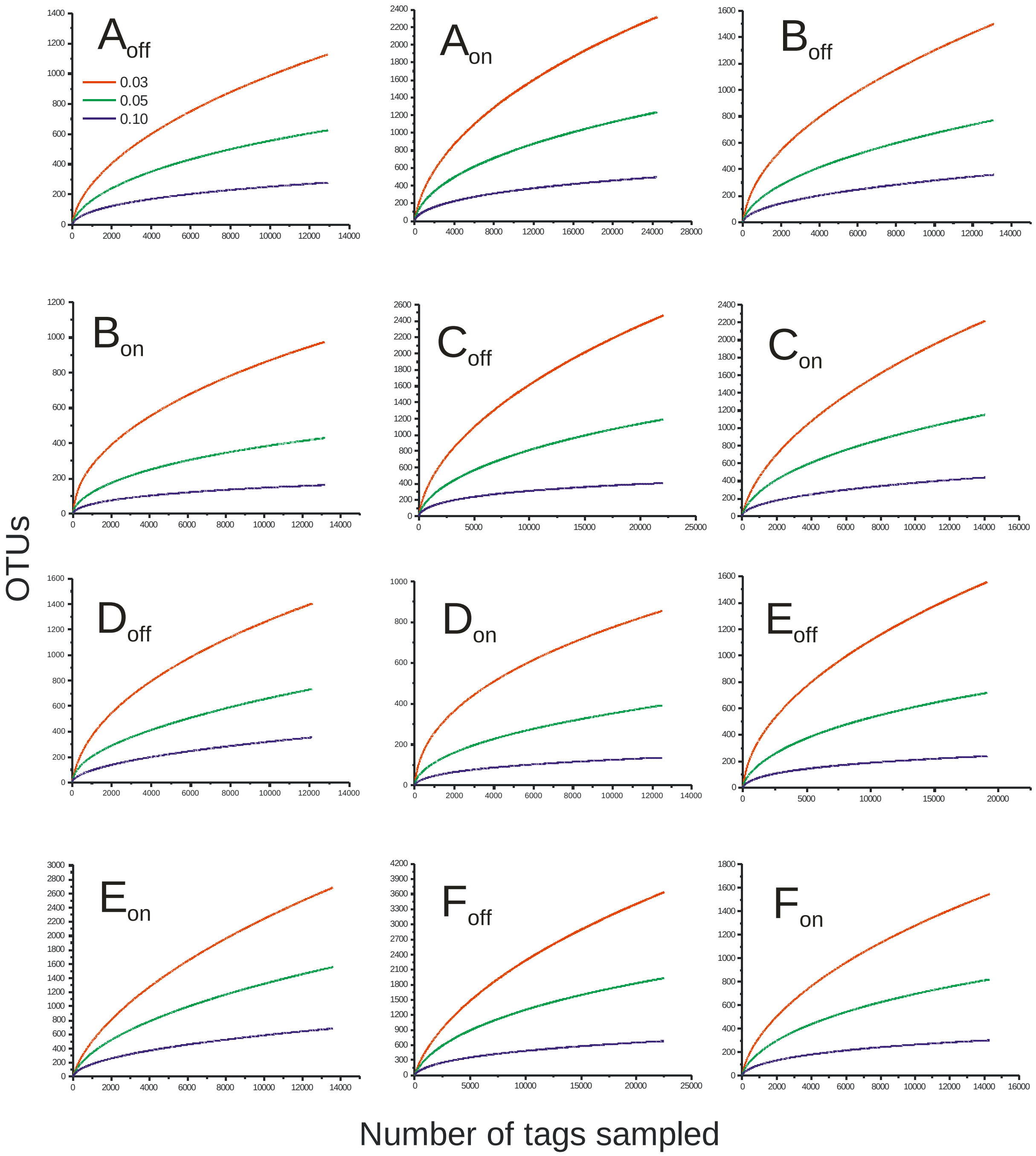
Figure S2. ***A**,* Read lengths per sample, with X_{off} and X_{on} coming from off-tumor and on-tumor samples in subject X, the data was derived from the read lengths post-processing via the RDP pyropipeline [1]. ***B**,* Rarefraction curves for each sample, the sample key is the same as use for Figure S1. These curves were generated using MOTHUR [2,3], cut off values are shown. ***C***, Venn diagram for paired samples generated using MOTHUR, each diagram shows the OTUs (at 0.03% cut-off) shared and those unique to each sample from on and off tumor. ***D***, Principle component analysis of the annotated 16S rRNA sequence data generated for on and off tumor samples of each patient (A-F), was plotted as an 0.5 x 0.5 interval density distribution. The color coding shows the natural logarithm of the densities in each segment. Where there are significant differences (P <0.05) between tumor tissue and adjacent off-tumor mucosa, a white cross is shown in that segment. The taxonomic groups contributing to the most densely populated segments are shown (and the numbers of sequences contributing are shown in parentheses).

A

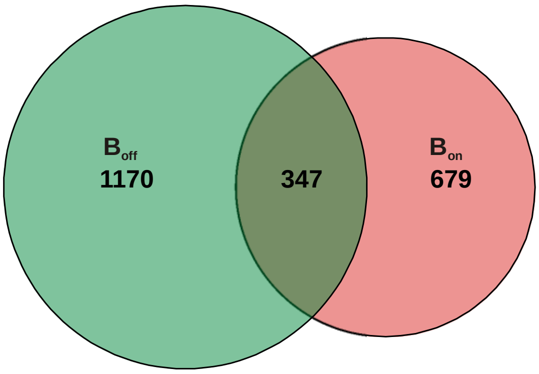


B

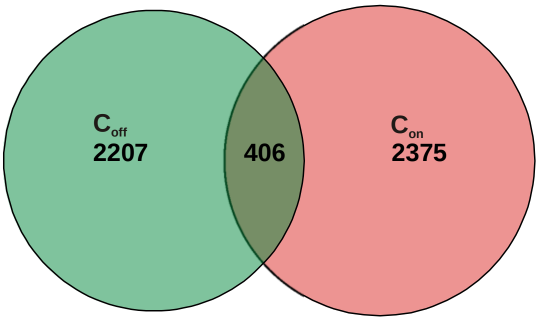

A_{off}
0.03
0.05
0.10
0 200 400 600 800 1000 1200 1400
0 2000 4000 6000 8000 10000 12000 14000
A_{on}
0 200 400 600 800 1000 1200 1400 1600 1800 2000 2200 2400
0 4000 8000 12000 16000 20000 24000 28000
B_{off}
0 200 400 600 800 1000 1200 1400 1600
0 2000 4000 6000 8000 10000 12000 14000
B_{on}
0 200 400 600 800 1000 1200
0 2000 4000 6000 8000 10000 12000 14000
C_{off}
0 200 400 600 800 1000 1200 1400 1600 1800 2000 2200 2400 2600
0 5000 10000 15000 20000 25000
C_{on}
0 200 400 600 800 1000 1200 1400 1600 1800 2000 2200 2400
0 2000 4000 6000 8000 10000 12000 14000 16000
D_{off}
0 200 400 600 800 1000 1200 1400 1600
0 2000 4000 6000 8000 10000 12000 14000
D_{on}
0 200 400 600 800 1000
0 2000 4000 6000 8000 10000 12000 14000
E_{off}
0 200 400 600 800 1000 1200 1400 1600
0 5000 10000 15000 20000
E_{on}
0 200 400 600 800 1000 1200 1400 1600 1800 2000 2200 2400 2600 2800 3000
0 2000 4000 6000 8000 10000 12000 14000
F_{off}
0 300 600 900 1200 1500 1800 2100 2400 2700 3000 3300 3600 3900 4200
0 5000 10000 15000 20000 25000
F_{on}
0 200 400 600 800 1000 1200 1400 1600 1800
0 2000 4000 6000 8000 10000 12000 14000 16000
OTUs
Number of tags sampled

C

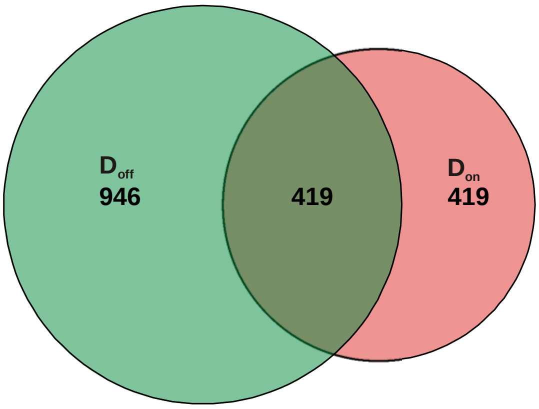
The number of species in group A_{off} is 1094
The number of species in group A_{on} is 2268
The number of species shared between groups A_{off} and A_{on} is 381
% of species that are shared in groups A_{off} and A_{on} is 12%
The total richness for all groups is 2981



The number of species in group B_{off} is 1517
The number of species in group B_{on} is 1026
The number of species shared between groups B_{off} and B_{on} is 347
% of species that are shared in groups B_{off} and B_{on} is 16%
The total richness for all groups is 2196

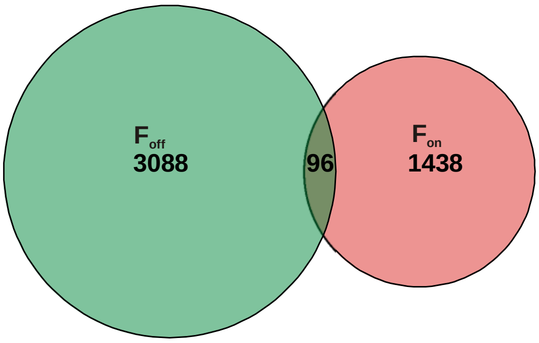


The number of species in group C_{off} is 2613
The number of species in group C_{on} is 2781
The number of species shared between groups C_{off} and C_{on} is 406
% of species that are shared in groups C_{off} and C_{on} is 8%
The total richness for all groups is 4988



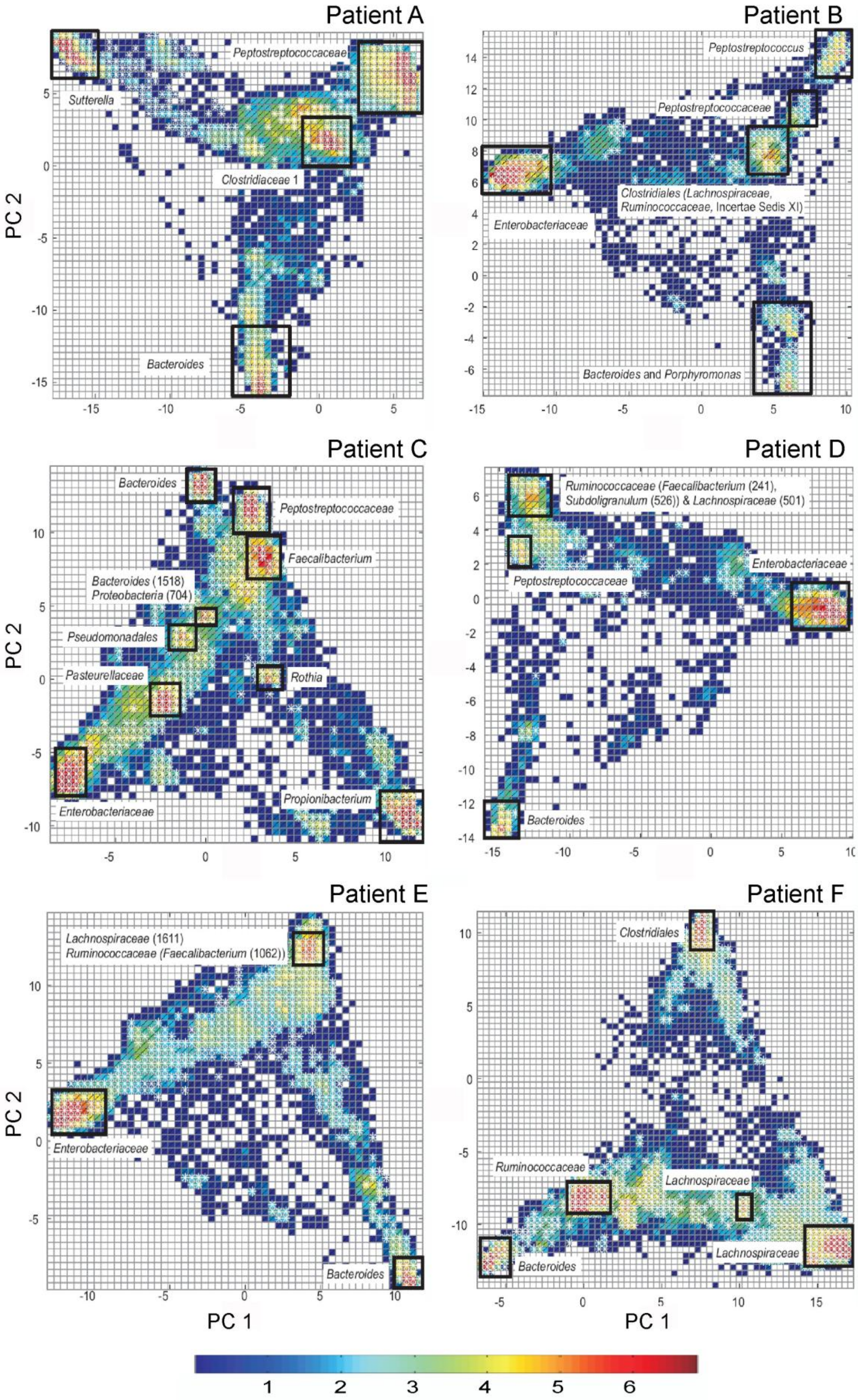
The number of species in group D_{off} is 1439
The number of species in group D_{on} is 912
The number of species shared between groups D_{off} and D_{on} is 493
% of species that are shared in groups D_{off} and D_{on} is 27%
The total richness for all groups is 1858

The number of species in group E_{off} is 706
The number of species in group E_{on} is 2038
The number of species shared between groups E_{off} and E_{on} is 164
% of species that are shared in groups E_{off} and E_{on} is 6%
The total richness for all groups is 2580



The number of species in group F_{off} is 3184
The number of species in group F_{on} is 1534
The number of species shared between groups F_{off} and F_{on} is 96
% of species that are shared in groups F_{off} and F_{on} is 2%
The total richness for all groups is 4622

D


Patient A
Peptostreptococcaceae
Sutterella
Clostridiaceae 1
Bacteroides
Patient B
Peptostreptococcus
Peptostreptococcaceae
Clostridiales (Lachnospiraceae, Ruminococcaceae, Incertae Sedis XI)
Enterobacteriaceae
Bacteroides and Porphyromonas
Patient C
Bacteroides
Peptostreptococcaceae
Faecalibacterium
Bacteroides (1518)
Proteobacteria (704)
Pseudomonadales
Pasteurellaceae
Rothia
Enterobacteriaceae
Propionibacterium
Patient D
Ruminococcaceae (Faecalibacterium (241), Subdoligranulum (526)) & Lachnospiraceae (501)
Peptostreptococcaceae
Enterobacteriaceae
Bacteroides
Patient E
Lachnospiraceae (1611)
Ruminococcaceae (Faecalibacterium (1062))
Enterobacteriaceae
Bacteroides
Patient F
Clostridiales
Ruminococcaceae
Lachnospiraceae
Lachnospiraceae
Bacteroides
PC 1
PC 2
1
2
3
4
5
6

REFERENCES

1 Cole JR et al. The Ribosomal Database Project: improved alignments and new tools for rRNA analysis. Nucl Acids Res 2009;37:D141-145.
2. Schloss PD et al. Introducing mothur: Open Source, Platform-independent, Community-supported Software for Describing and Comparing Microbial Communities. Appl Environ Microbiol 2009: AEM.01541-09.
3. Huson DH et al. Methods for comparative metagenomics. BMC Bioinformatics 2009;10 Suppl 1:S12.