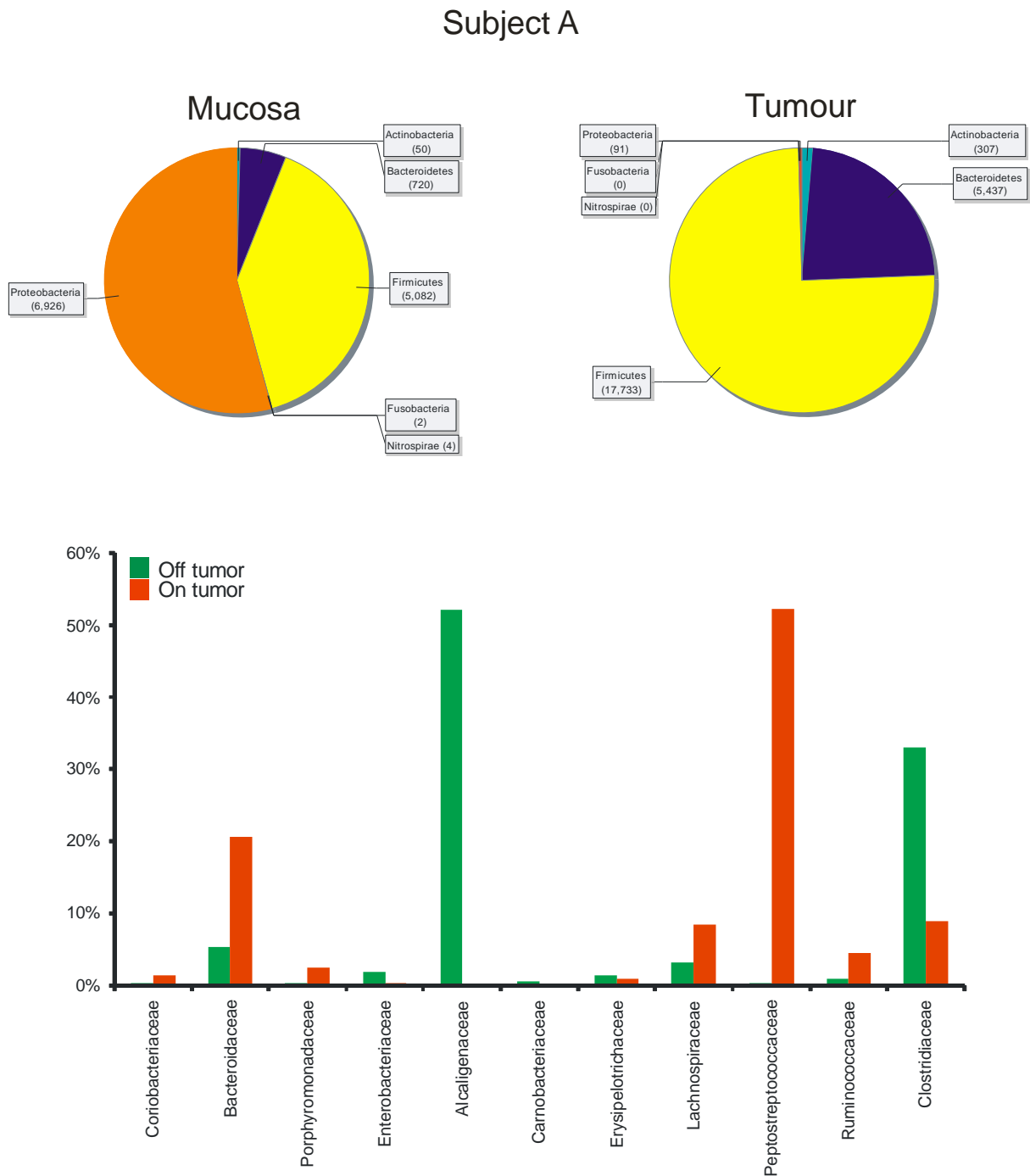
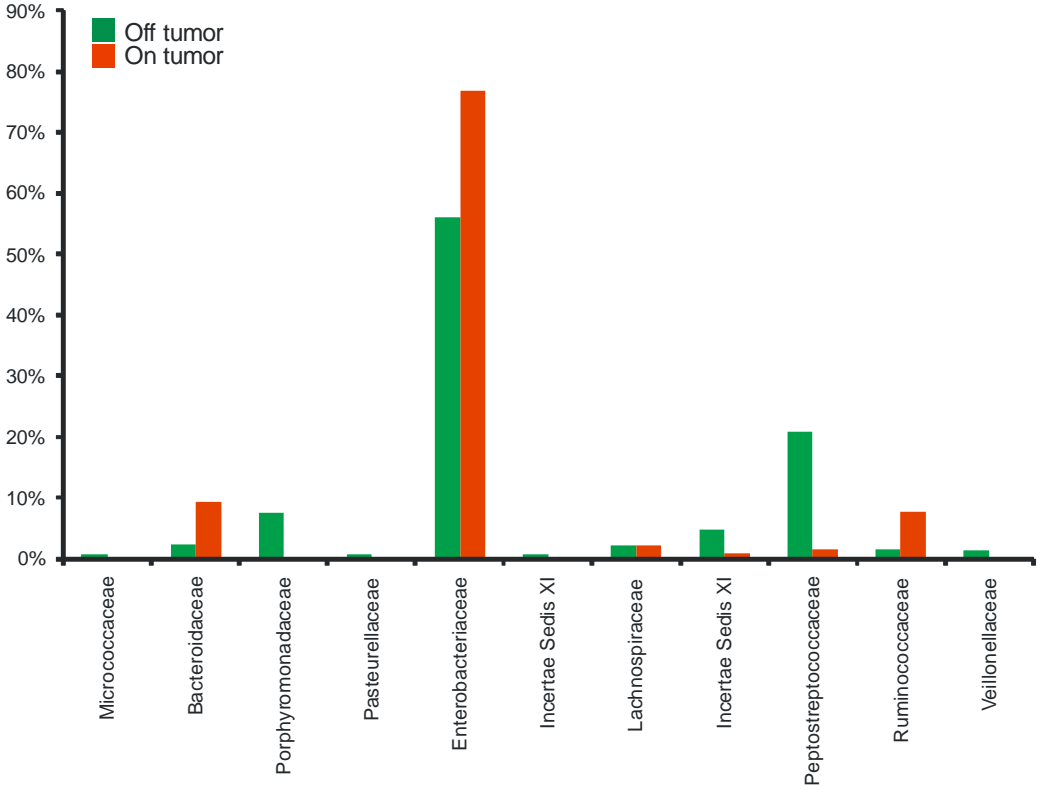
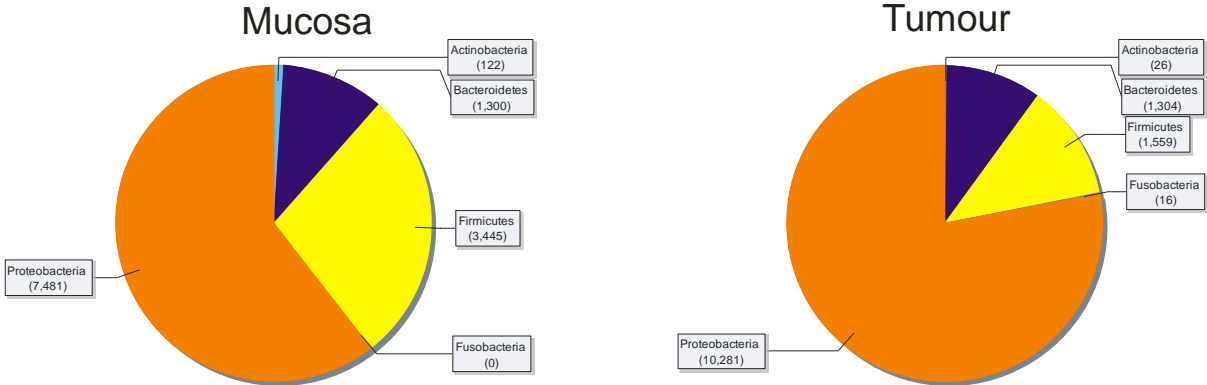


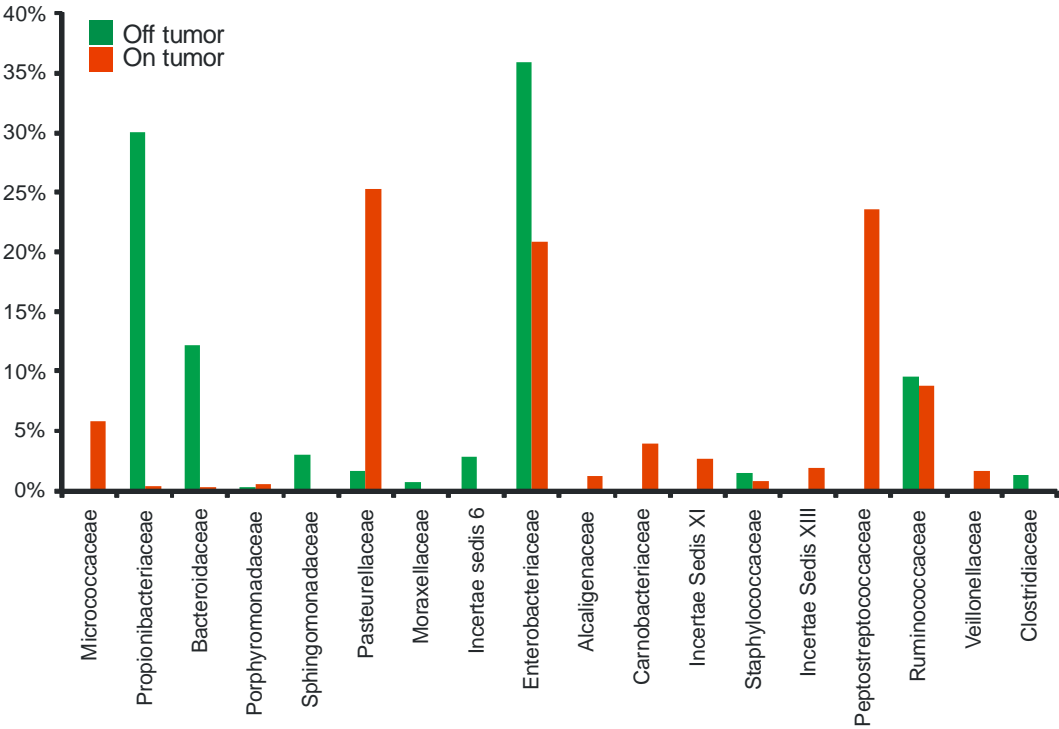
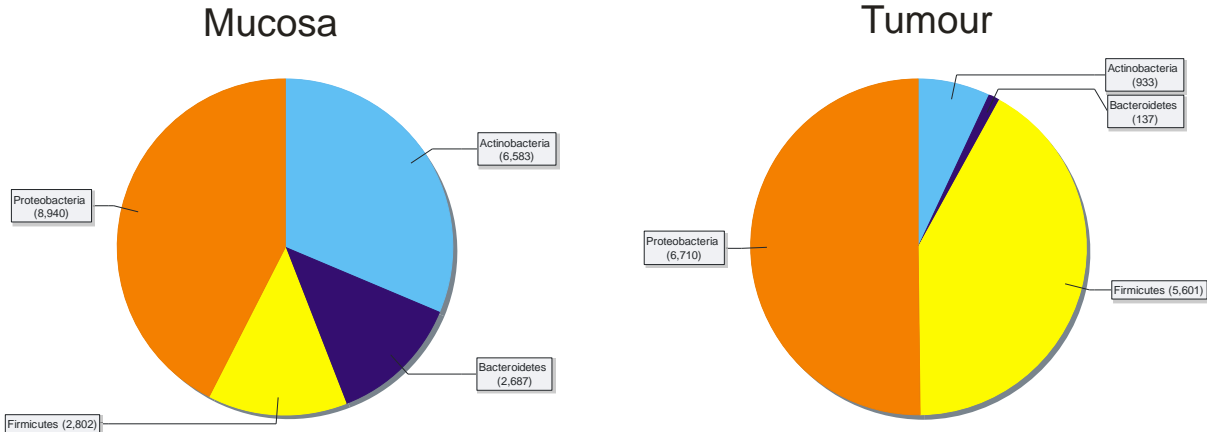
Figure S3. Taxonomic affiliation of the 16S rRNA gene reads for each paired sample set from subjects **A-F** and the combined samples (**G**). The figures were generated using MEGAN [1,2] and show in which PHYLUM (piecharts) and families (barcharts) the main alterations of levels of reads are found. In the barchart only families which were greater than 1% of the community are shown.



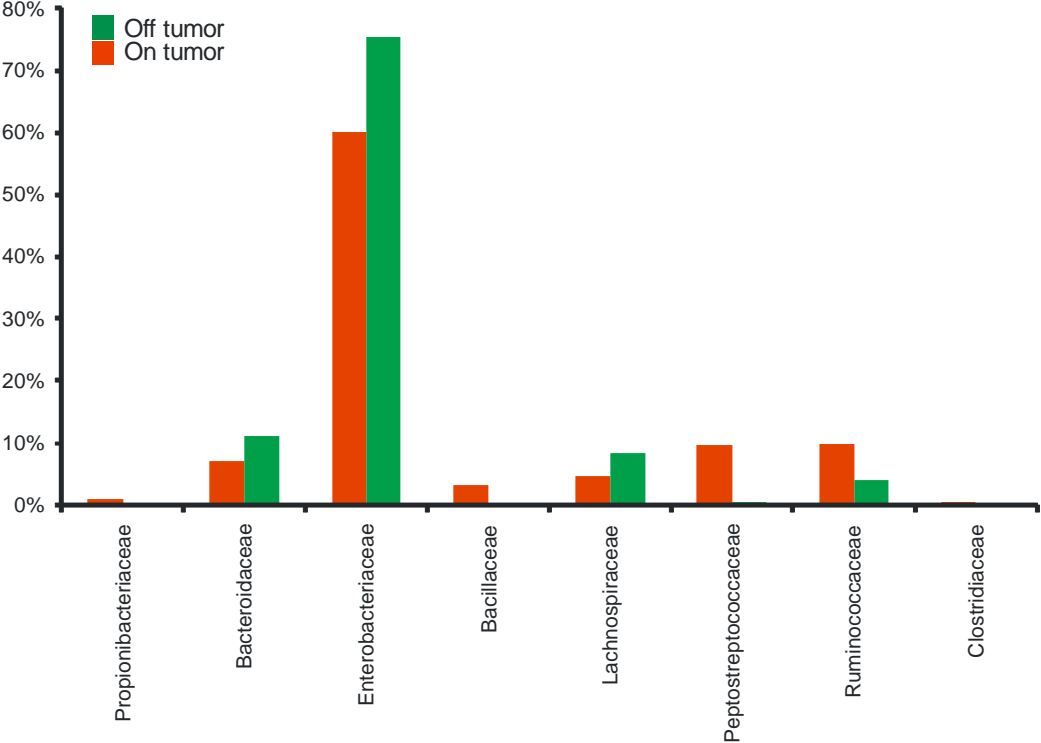
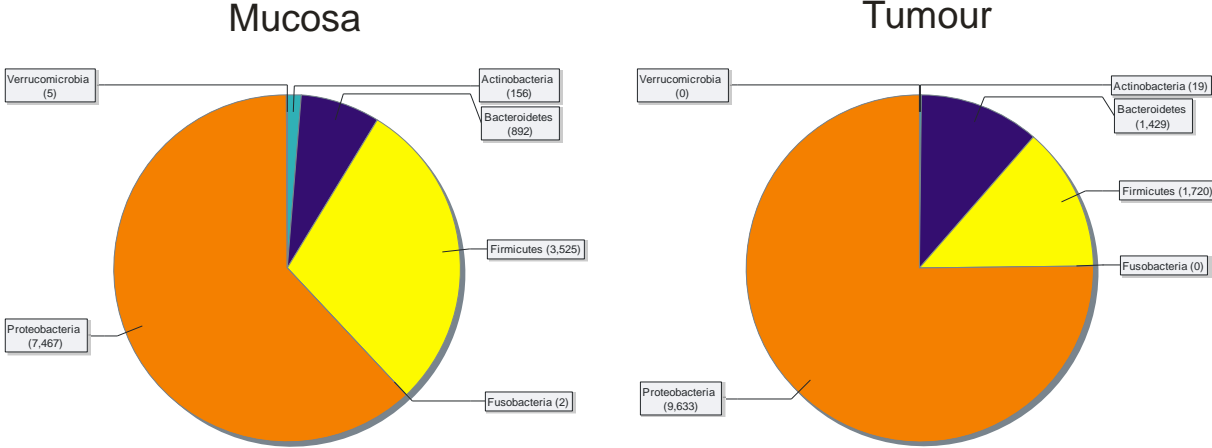
Subject B



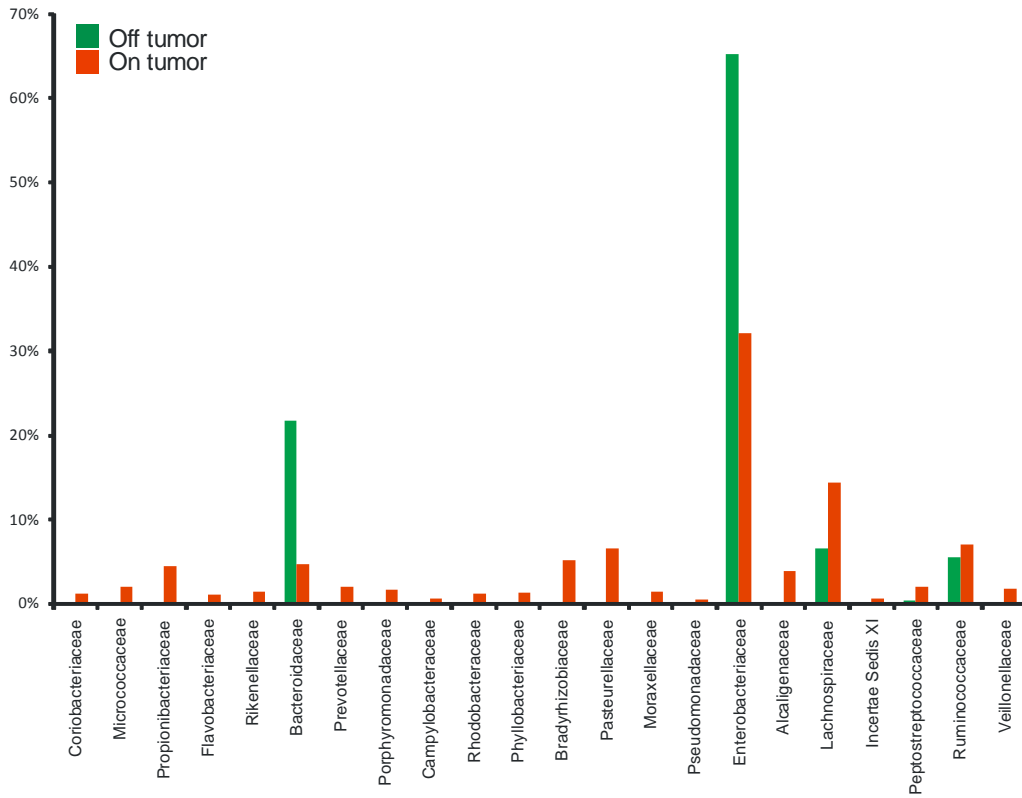
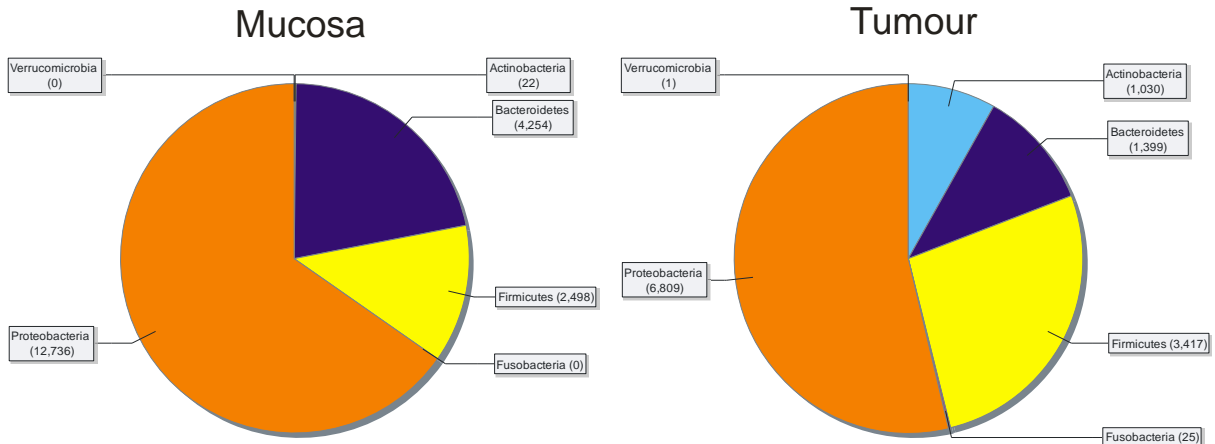
Subject C



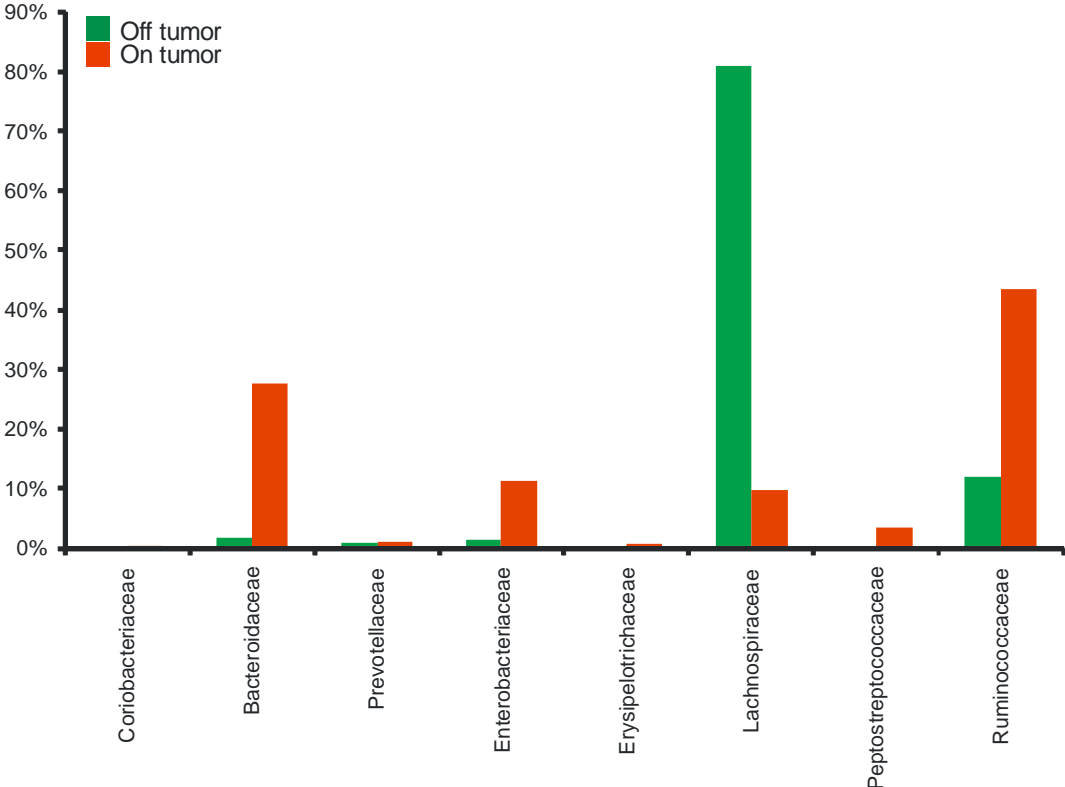
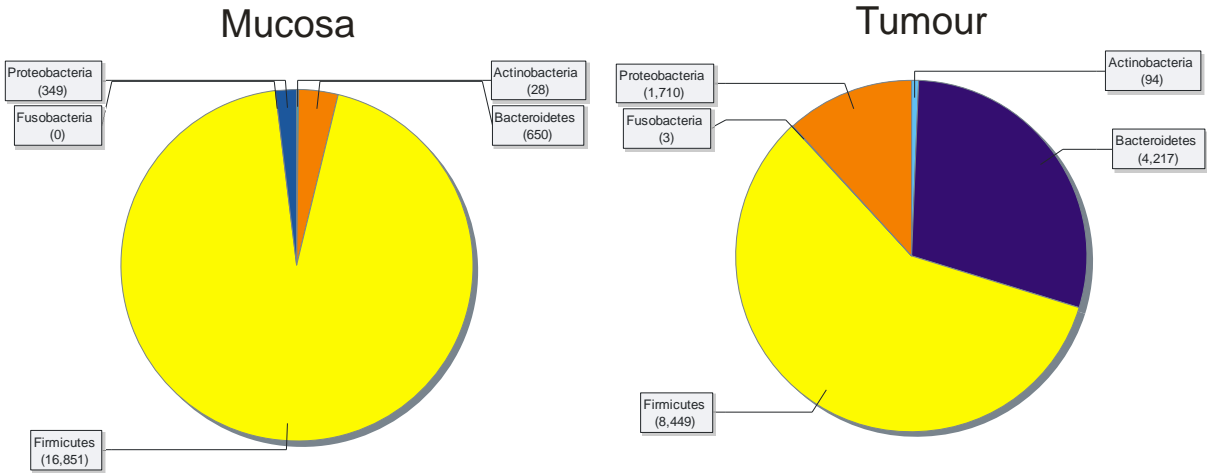
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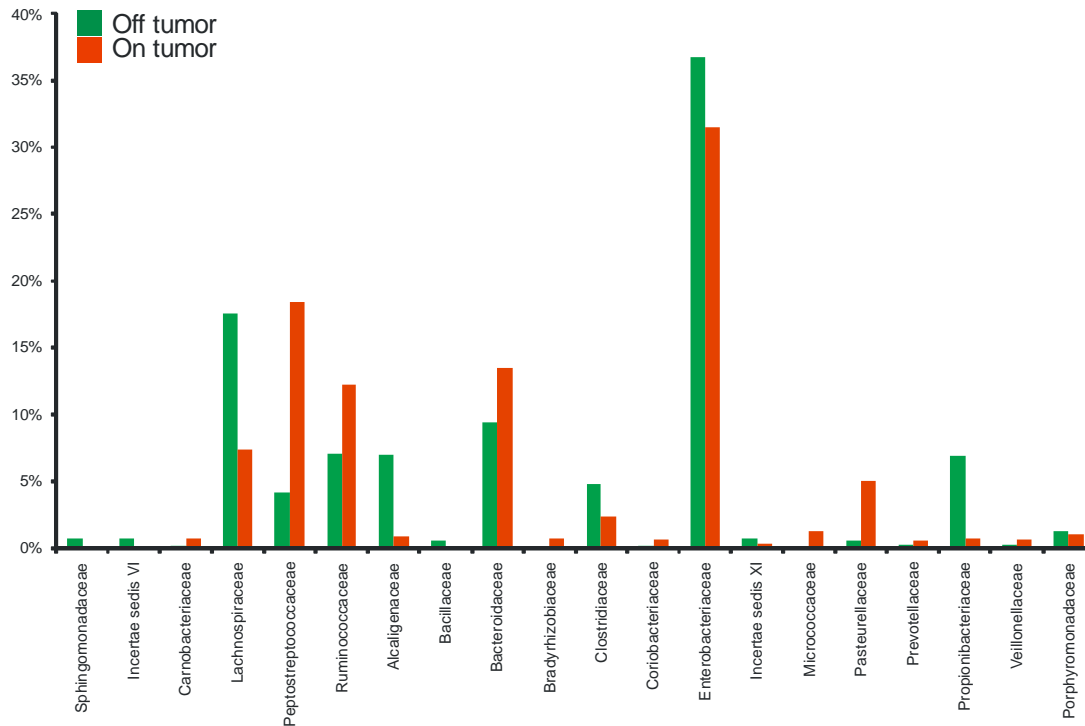
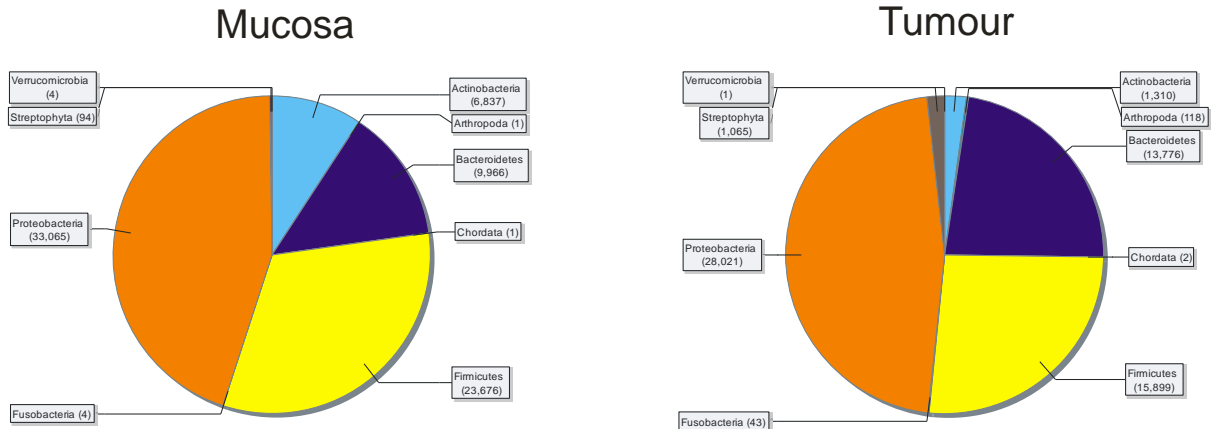
Subject E



Subject F



Combined



REFERENCES

- 1.. Huson DH et al. MEGAN analysis of metagenomic data. *Genome Research* 2007;17:377-386.
2. Letunic I et al. Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. *Bioinformatics* 2007;23:127-128.