SUPPLEMENTARY MATERIALS

TITLE

Characterization of the consensus mucosal microbiome of colorectal cancer

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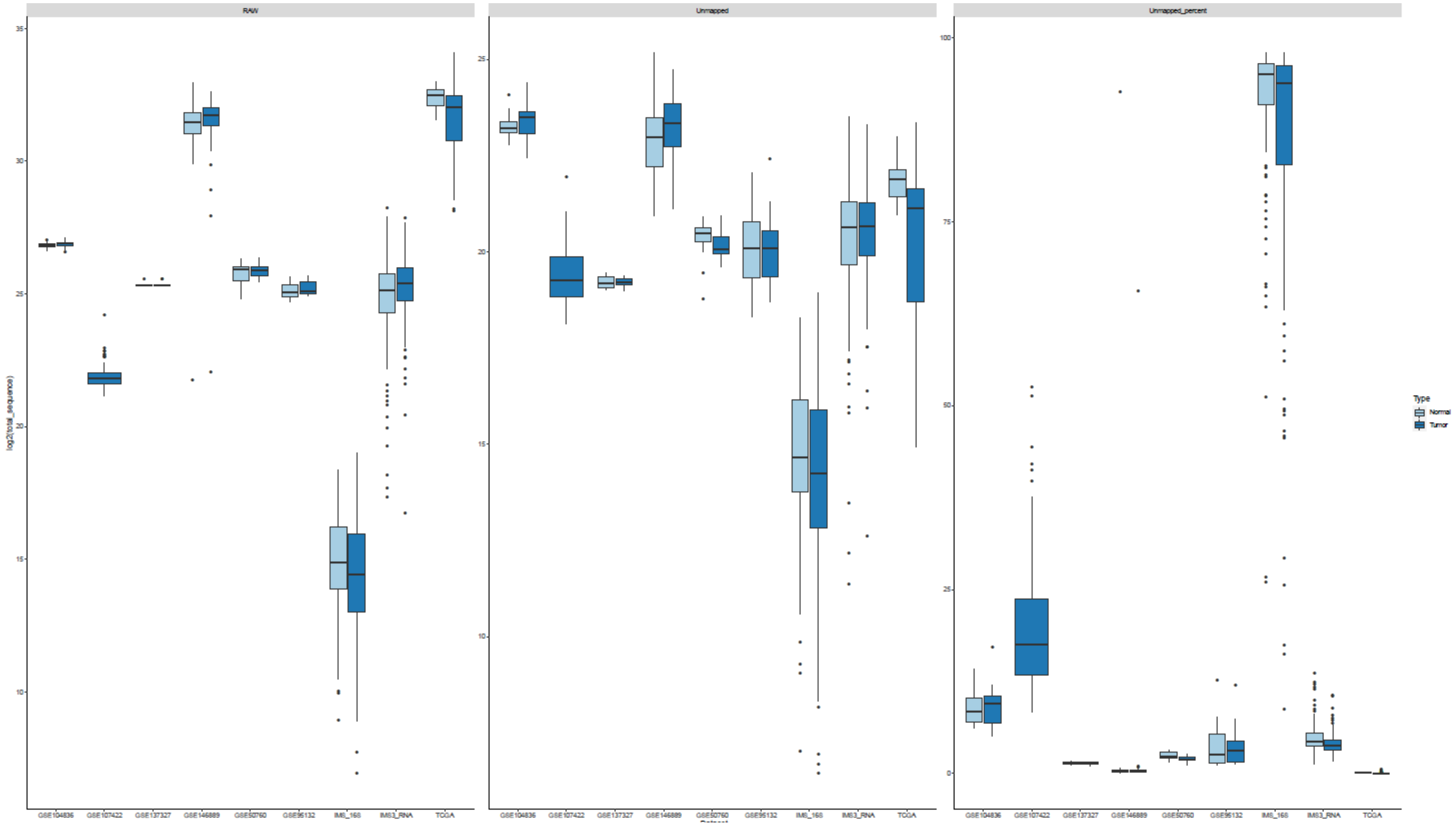
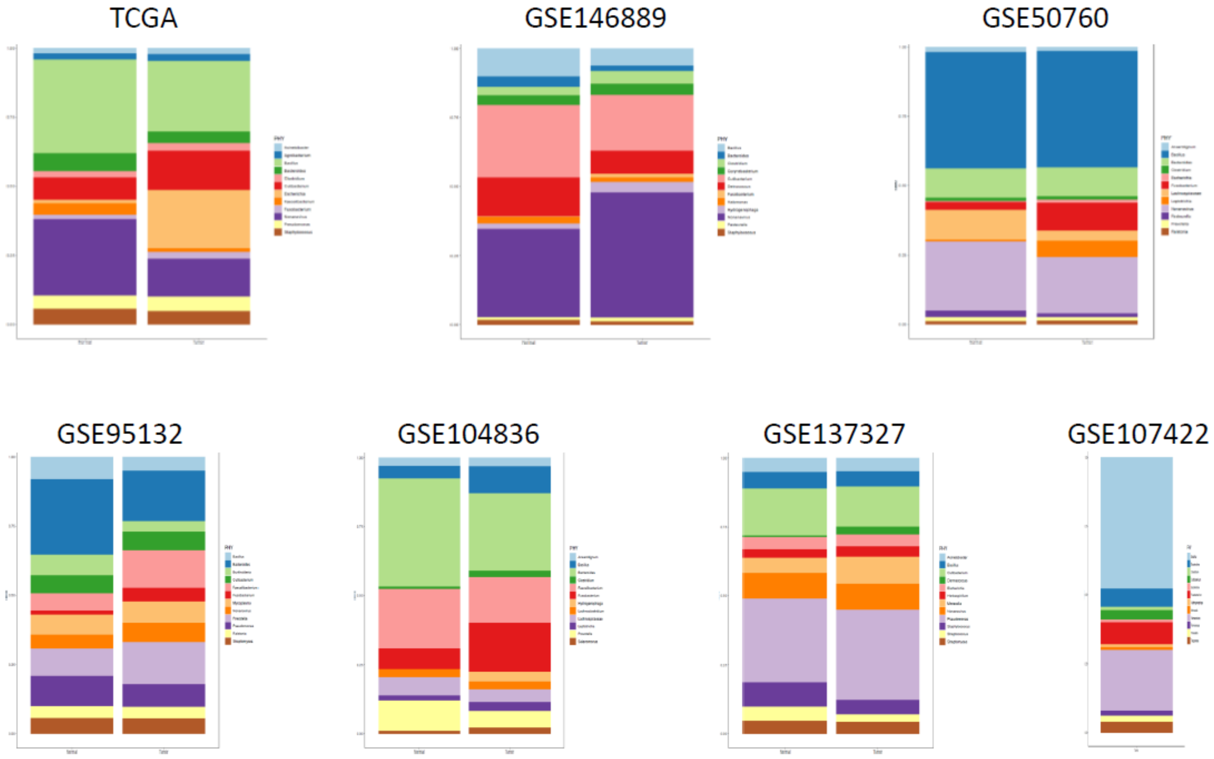
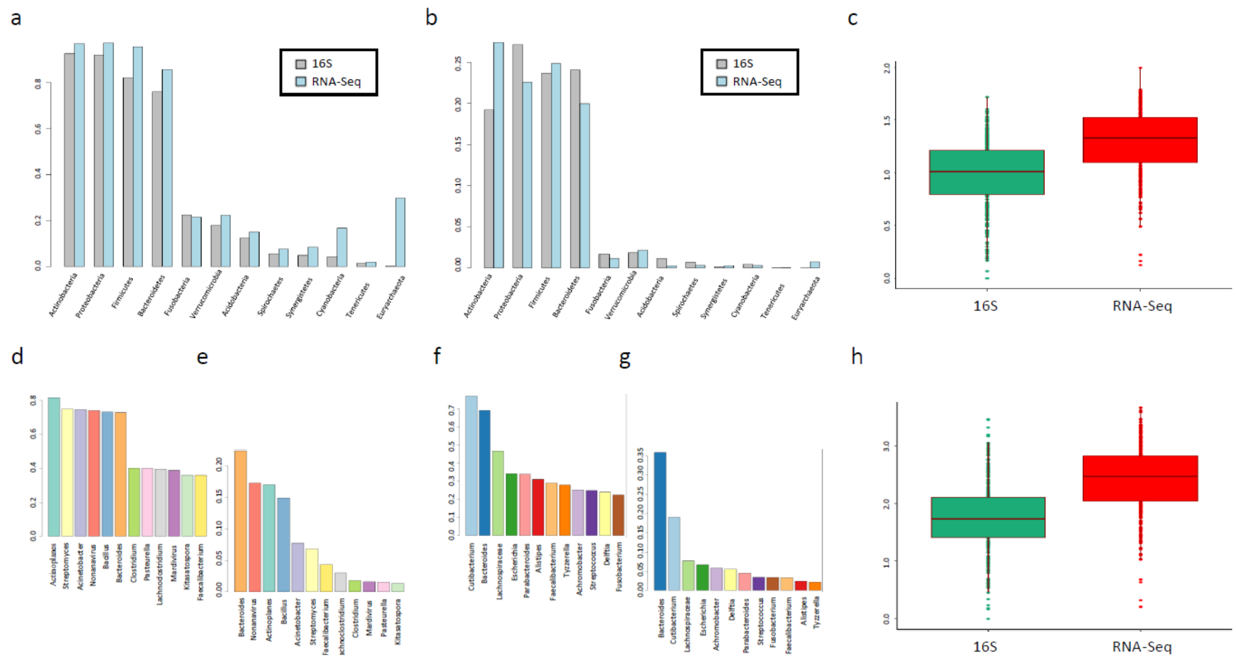


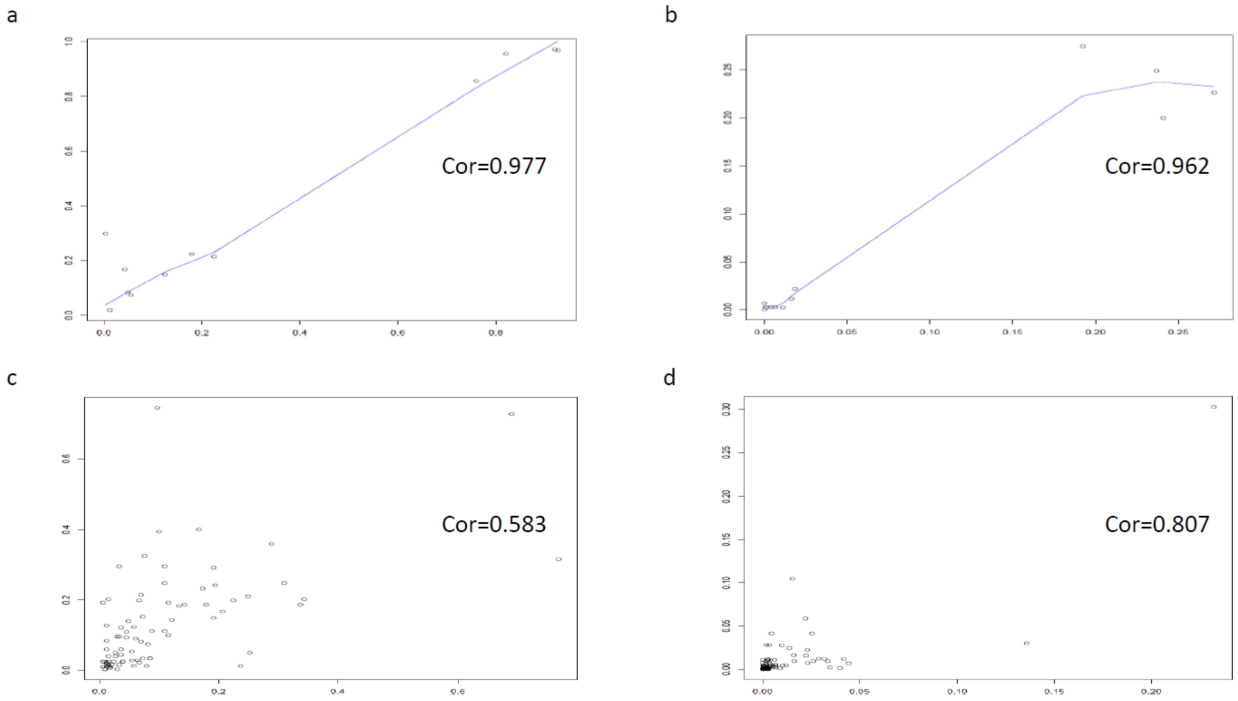
Supplemental Figure 1. Sequence reads tracking for each dataset involved in the study. X-axis are the names of the eight datasets. The Y-axis is for the RAW and Unmapped panels are the log2 scaled total sequences; Y-axis for the `Unmapped_percent` panel indicates the percentages of the unmapped reads. The values in the Y-axis were plotted with standard error bars for each sample set included in a dataset.



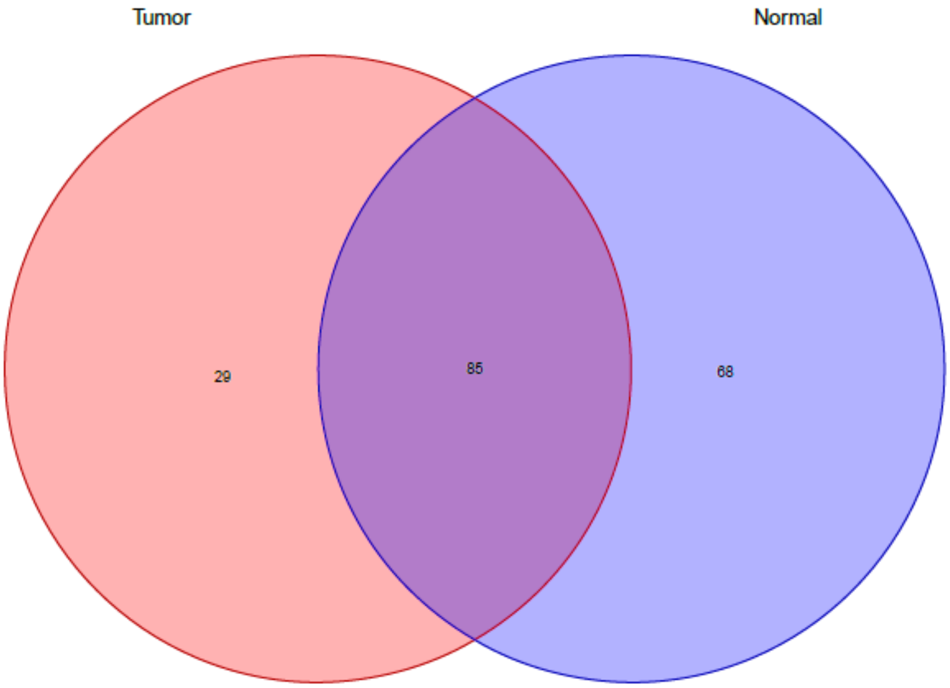
Supplemental Figure 2. Genus-level microbial compositional changes for each dataset. The top 12 most enriched genera identified from each cohort: TCGA, GSE146889, GSE50760, GSE95132, GSE104836, GSE137327, and GSE107422.



Supplemental Figure 3. Microbial compositional and abundance comparisons between 16S and RNA-Seq at the Phylum- and Genus-level. Prevalent (a) and abundant (b) phyla values identified from 16S and RNA-Seq platforms. Most prevalent (d-e) and abundant (f-g) phyla identified from 16S and RNA-Seq platforms. The boxplots of microbial diversity through the Shannon index comparisons at the phylum (c) and genus (h) levels.



Supplemental Figure 4. Pearson correlation coefficients between 16S and RNA-Seq at the Phylum- and Genus-level. Phylum-level prevalence (a) and abundances (b) between 16S and RNA-Seq data; Genus-level prevalence (c) and abundances (d) between 16S and RNA-Seq data.



Supplemental Figure 5. Venn diagram of the consensus microbial species between tumor and normal samples. Venn diagram showing the number of overlapped and unique species between tumor and normal groups.