

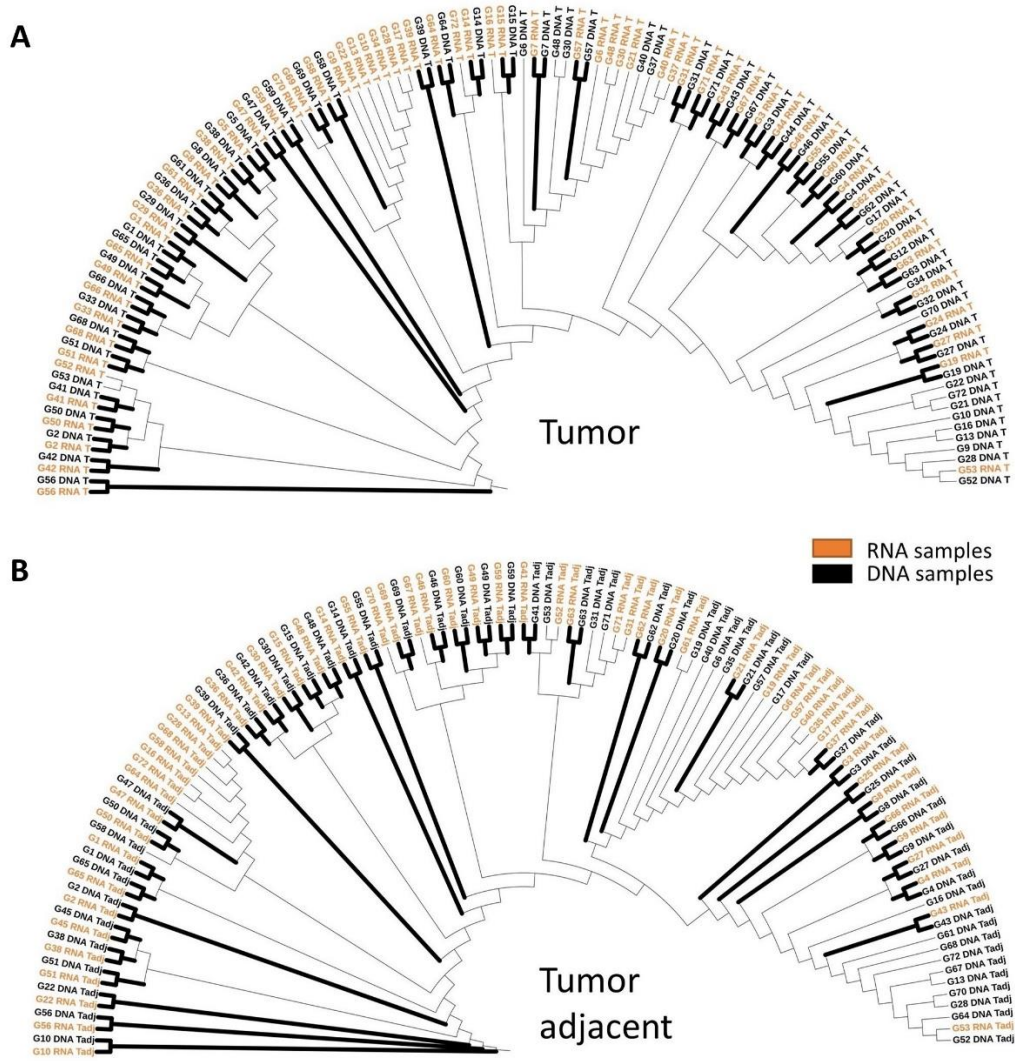
SUPPLEMENTAL MATERIALS

Comparison of Genomic and Transcriptional Microbiome Analysis in Gastric Cancer Patients and Healthy Individuals

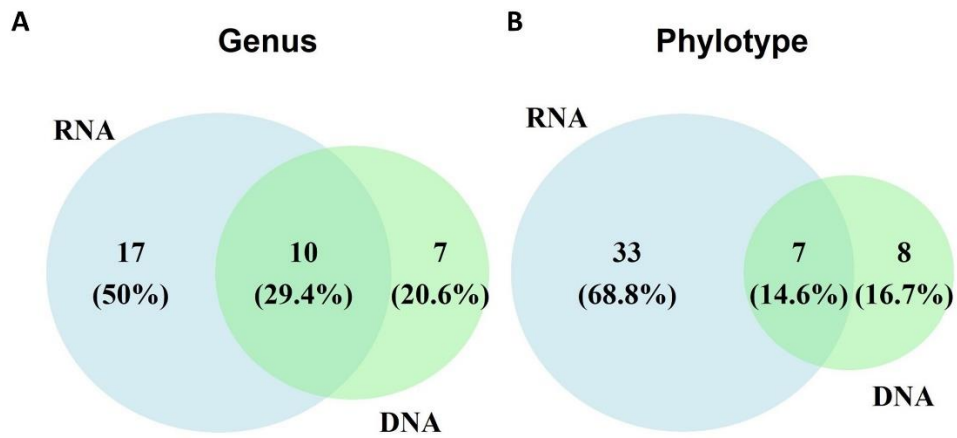
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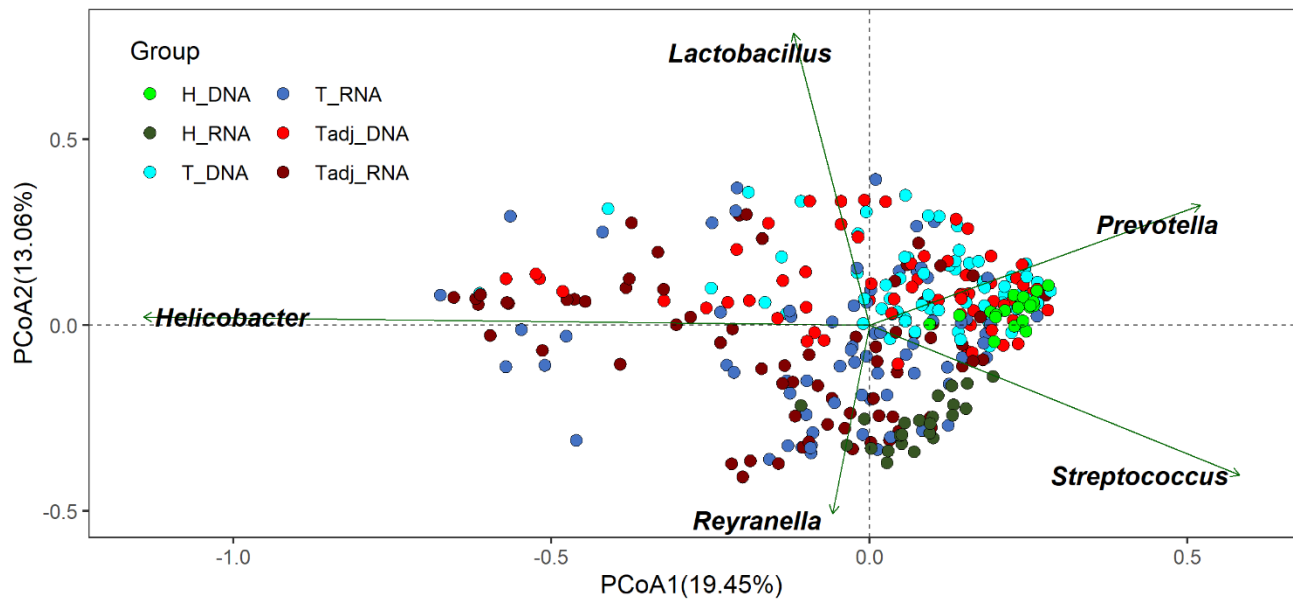
SUPPLEMENTARY FIGURES



Supplementary Fig.1 Group-average agglomerative hierarchical clustering at the phylotype level, based on global bacterial profiles. Clustering of 64 paired GC tumor (A), 58 paired GC tumor adjacent (B) DNA and RNA samples according to individual and general bacterial profiles.



Supplementary Fig.2 Venn diagrams show the number of common and group specific detected differences between GC and control group at genus (A) and at phylotype (B) levels.



Supplementary Fig.3 Principal coordinate analysis (PCoA) of bacterial beta diversity of all study groups at genus level.

SUPPLEMENTARY TABLES

Supplementary materials available by the following link:

<https://figshare.com/s/63b6ceaf15a127fe98c8>

Supplementary Table S1: Clinical data of study cohort

Supplementary Table S2: Phylotype table with relative abundance (%) for each study sample with bacterial taxonomy for each phylotype.

Supplementary Table S3: PERMANOVA and ANOSIM analysis results.

Supplementary Table S4: Summary table of the Mann-Whitney and FDR tests results based on study groups comparisons.

Supplementary Table S5: Summary table of the Mann-Whitney and FDR tests results based on high (>15%) and low (<15%) relative abundance of *H. pylori*. Comparisons performed on tumor tissue DNA samples (7·1); on tumor tissue RNA samples (7·2); on tumor adjacent tissue DNA samples (7·3); on tumor adjacent tissue RNA samples (7·4).

Supplementary Table S6: Summary table of the Mann-Whitney, FDR, and PERMANOVA tests results based on study groups comparisons by gender.

Supplementary Table S7: Summary table of the Mann-Whitney, FDR, and PERMANOVA tests results based on study groups comparisons by age.