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Thomasclavelia ramosa is a Specific Signature of Hepatocellular Carcinoma among Patients with Alcohol-Related Liver Disease: a Culturomics and Metagenomics Case-Control Study

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INTRODUCTION

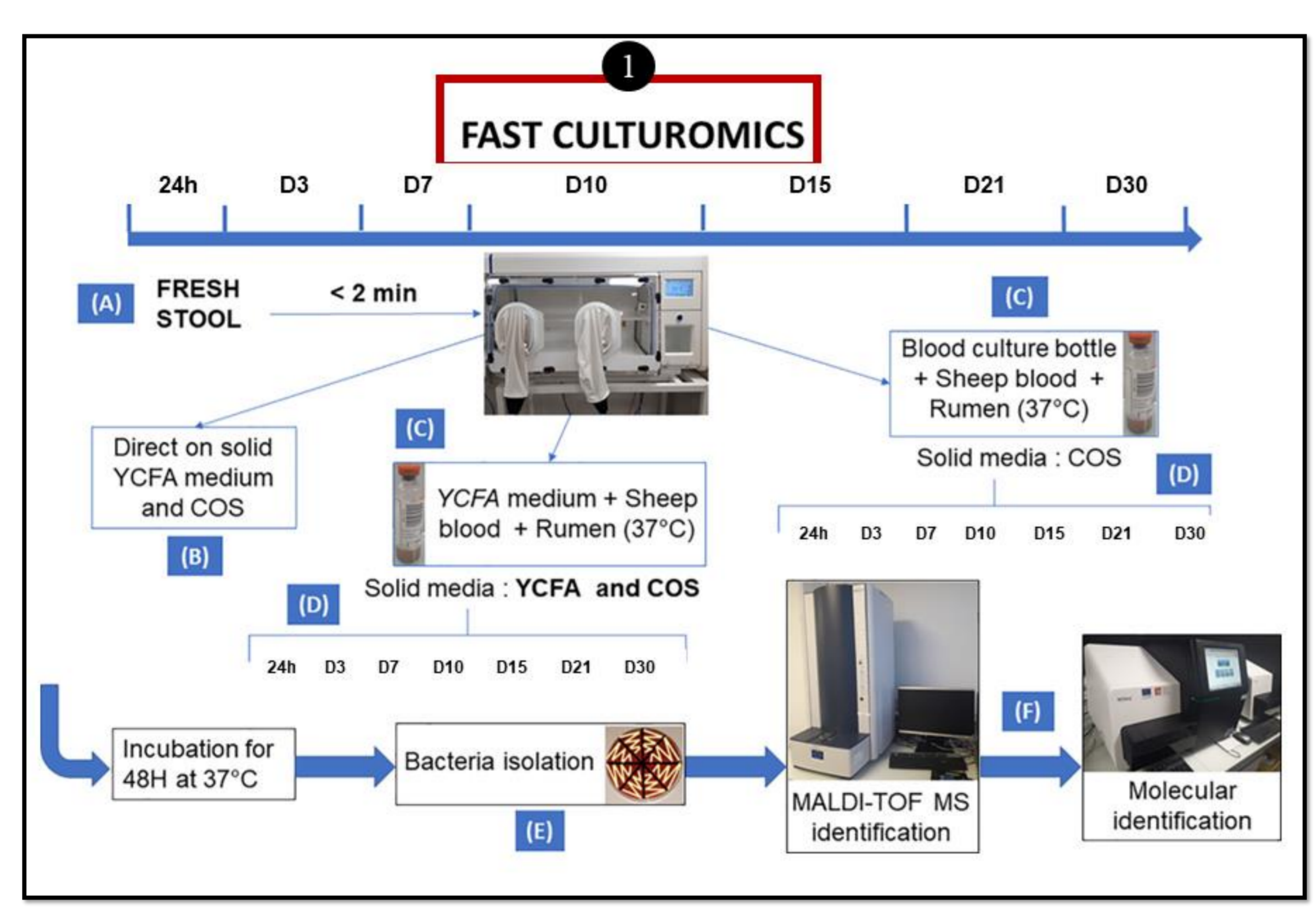
Hepatocellular carcinoma (HCC) is associated with chronic liver disease, and its major risk factors include viral hepatitis infection, and alcohol liver diseases (ALD) [1]. HCC is the most common form of liver cancer, forming almost 90% of cases [2]. Recent studies suggest that the gut microbiota can enhance liver carcinogenesis, moreover, treatment with broad-spectrum antibiotics prevented spontaneous HCC development in mice [3]. Several metagenomic studies have investigated gut dysbiosis in patients with ALD [4]. However, no study described gut dysbiosis in patients with ALD or HCC based on the culturomics approach. Culturomics is a high-throughput culture method based on diversified culture conditions, which was found to be complementary to metagenomics [5].

OBJECTIVES

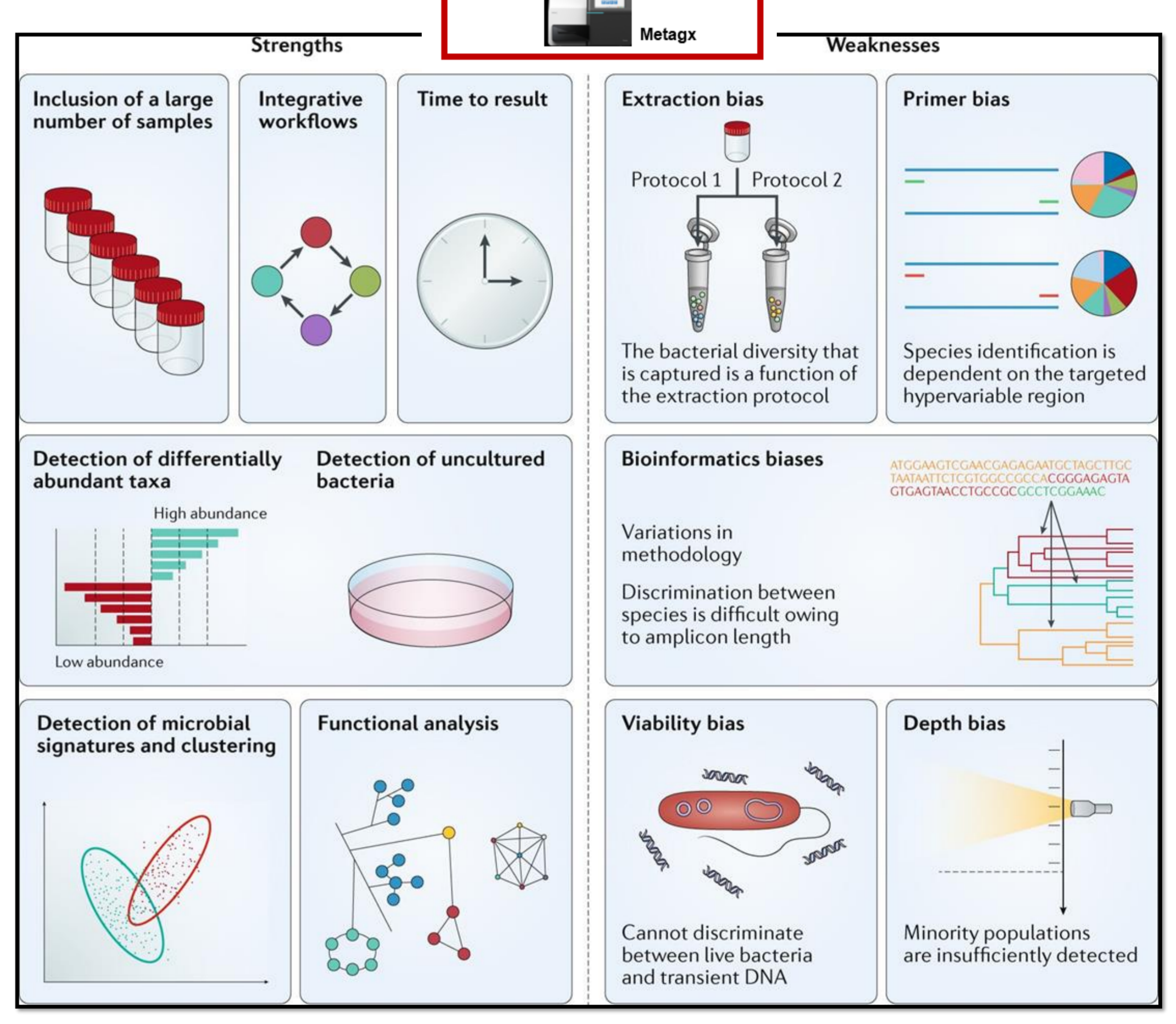
This study aims to characterize the microbial signature in patients with ALD and ALD-associated HCC using both culturomics and large-scale sequencing (v3v4 region 16S rRNA amplicon sequencing).

METHODOLOGY

- 24 Control
- 16 ALD-NoHCC
- 19 ALD-HCC

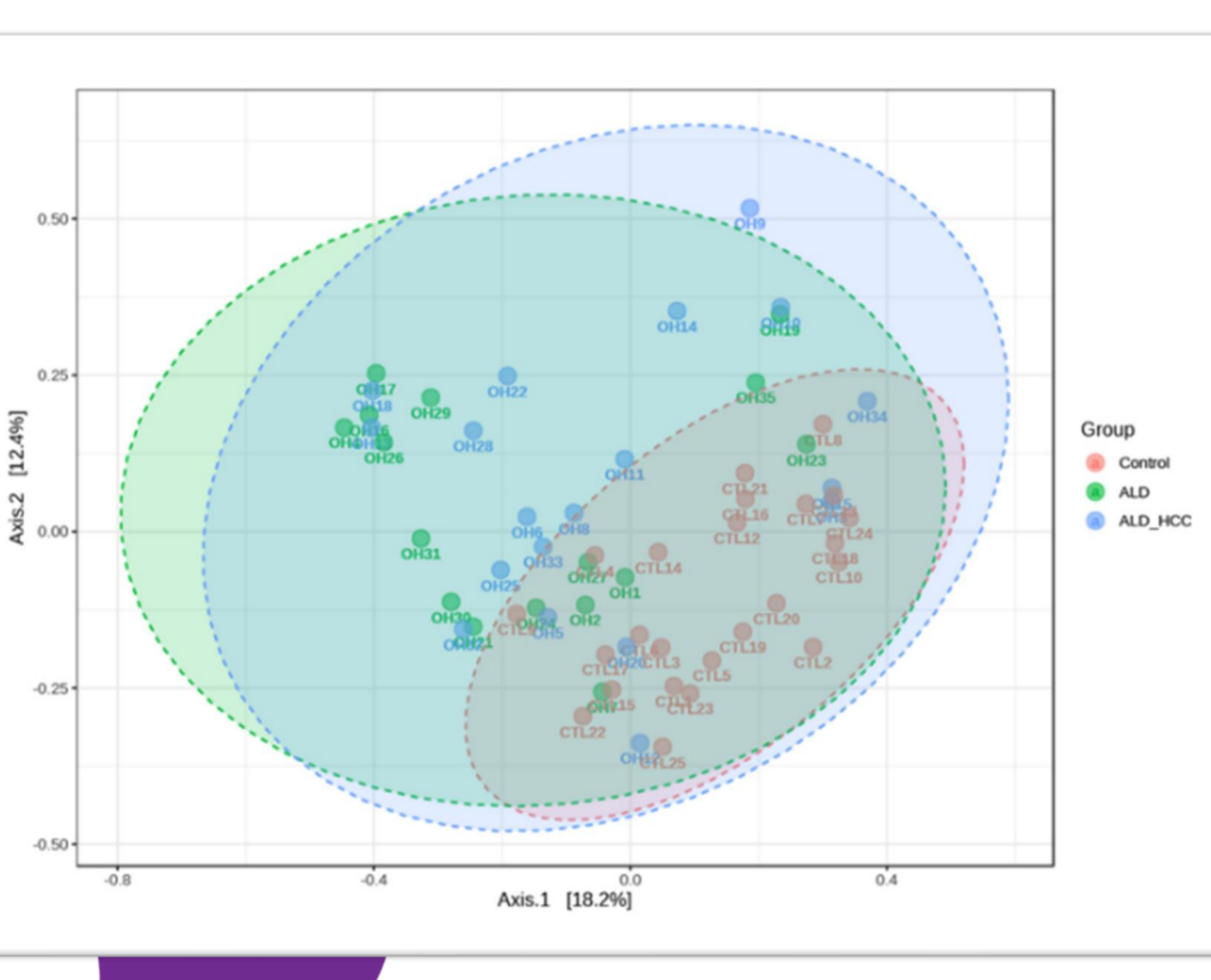


16S rRNA sequencing



RESULTS

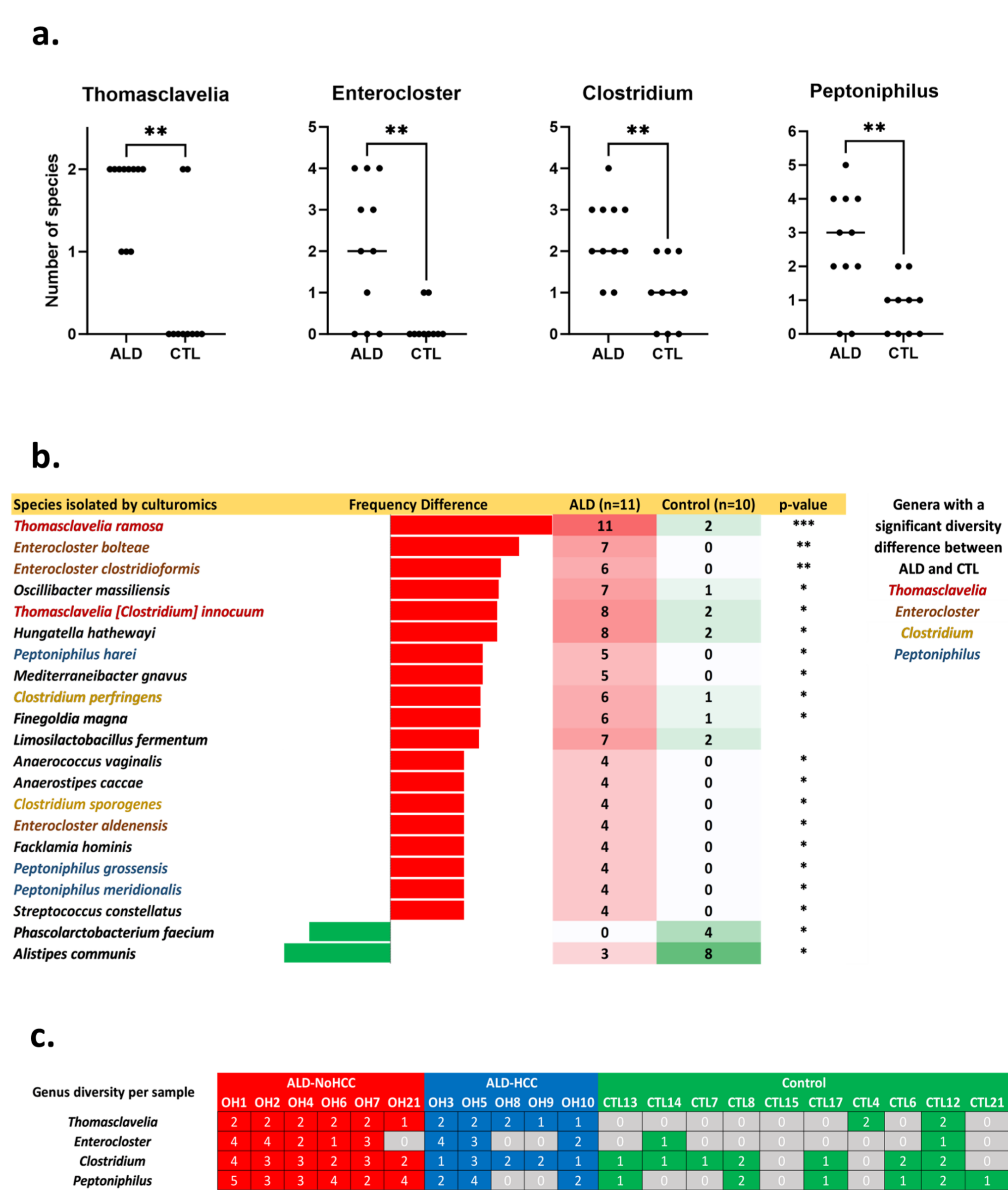
Result. 1 PCoA plot of beta diversity



Result. 2 Differentially abundant species (16S rRNA)



Result. 3 Diversity assessment by culturomics



CONCLUSIONS

- Characteristics of the ALD and ALD-HCC associated dysbiosis in our study showed an enrichment in potentially pathogenic *T. ramosa*, *M. gnavus* and *G. formicilis*.
- Unlike earlier research, our study reported the abundance of *T. ramosa* for the first time in patients with ALD-HCC by two complementary techniques.
- Our findings should be further verified through large-scale studies and animal experiments especially to investigate the mechanisms by which *T. ramosa* and *G. formicilis* contribute to carcinogenesis.

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