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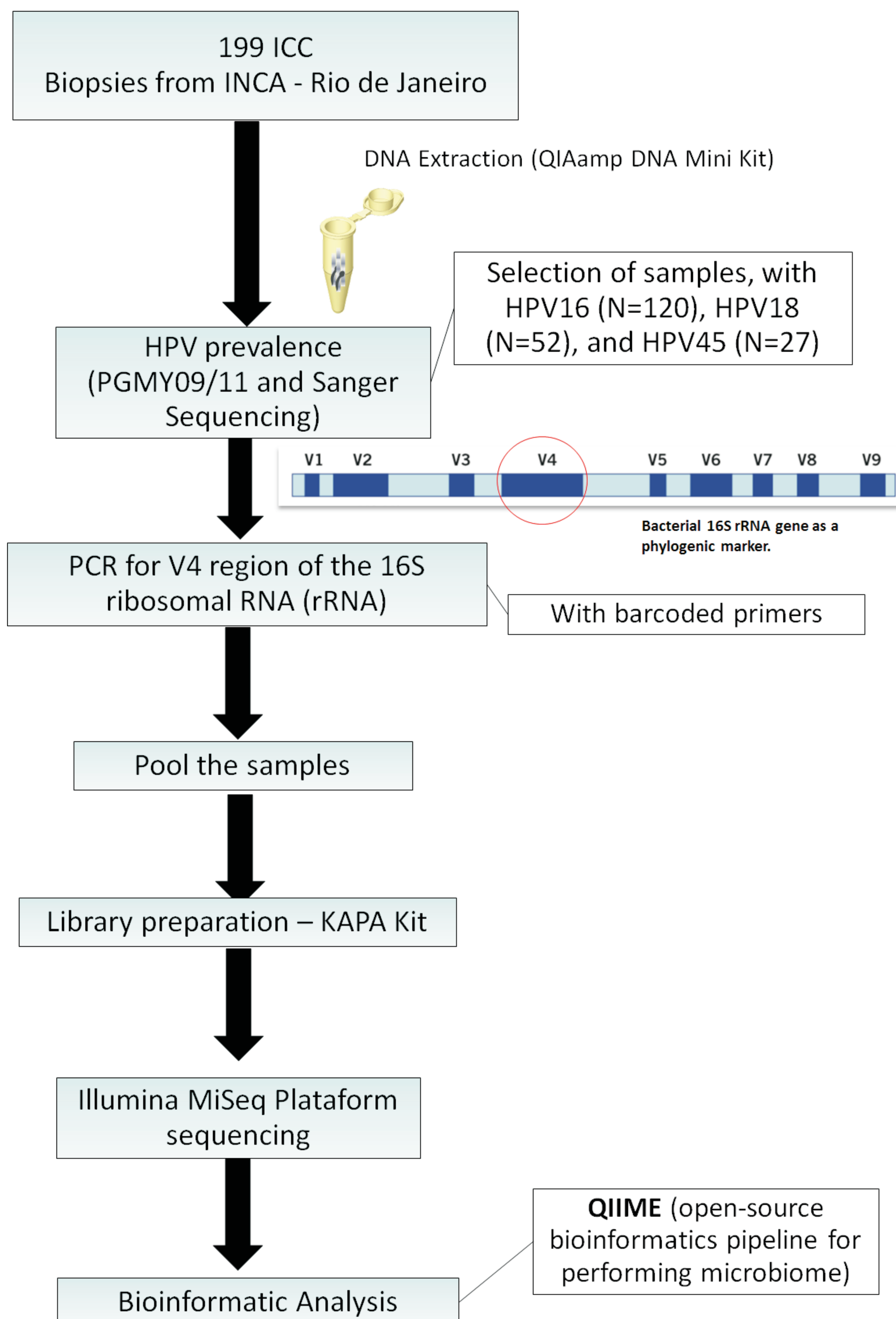
INTRODUCTION

Despite all progress regarding HPV-induced cervical carcinogenesis, risk factors for HPV-infection persistence and clearance are still unclear. Recent data suggests cervico-vaginal microbiota as an important element influencing HPV acquisition, persistence and cervical lesion progressions. Characterization of the microbiota diversity in cervical specimens is one of the initial steps to understand the mechanisms involved in cervical cancer pathogenesis.

GOALS

Describe the microbiome present in invasive cervical cancer (ICC) biopsies of patients from Rio de Janeiro, Brazil and their association with clinical and biological characteristics.

METHODS



RESULTS

Table 1. HPV prevalence in ICC in a Brazilian cohort from Rio de Janeiro. Samples were randomly selected from the three most prevalent HPV infections

HPV type	N	%
16	370	62.3
18	77	13.0
45	33	5.6
35	12	2.0
58	11	1.9
52	8	1.3
73	8	1.3
31	7	1.2
33	7	1.2
39	6	1.0
59	6	1.0
26	2	0.3
51	2	0.3
56	2	0.3
68	2	0.3
83	1	0.2
Co-infection	20	3.4
Undetermined	20	3.4
Total	594	100.0

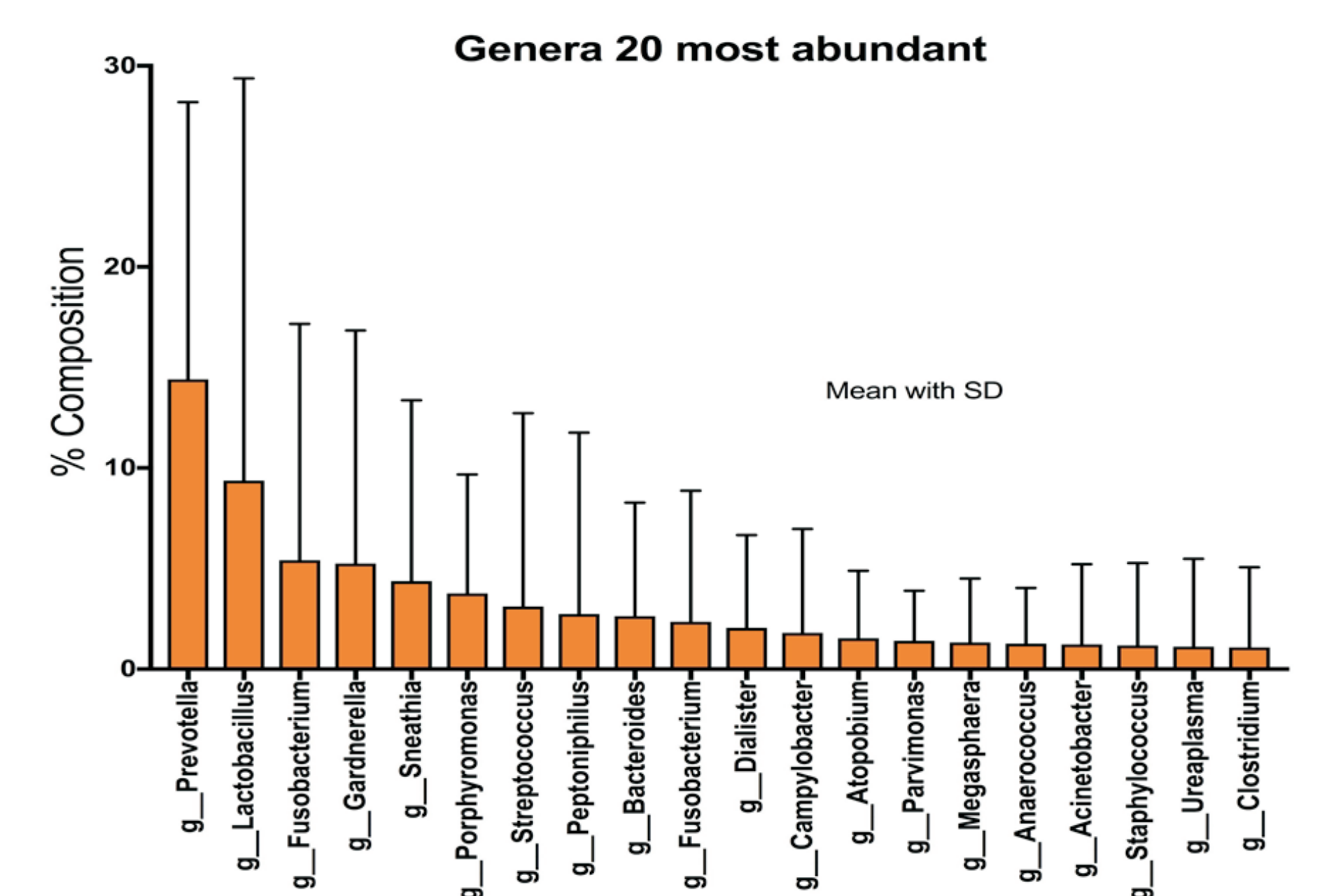


Figure 1. Composition of the most abundant genera of bacteria present in the DNA extracted from cervical cancer biopsies.

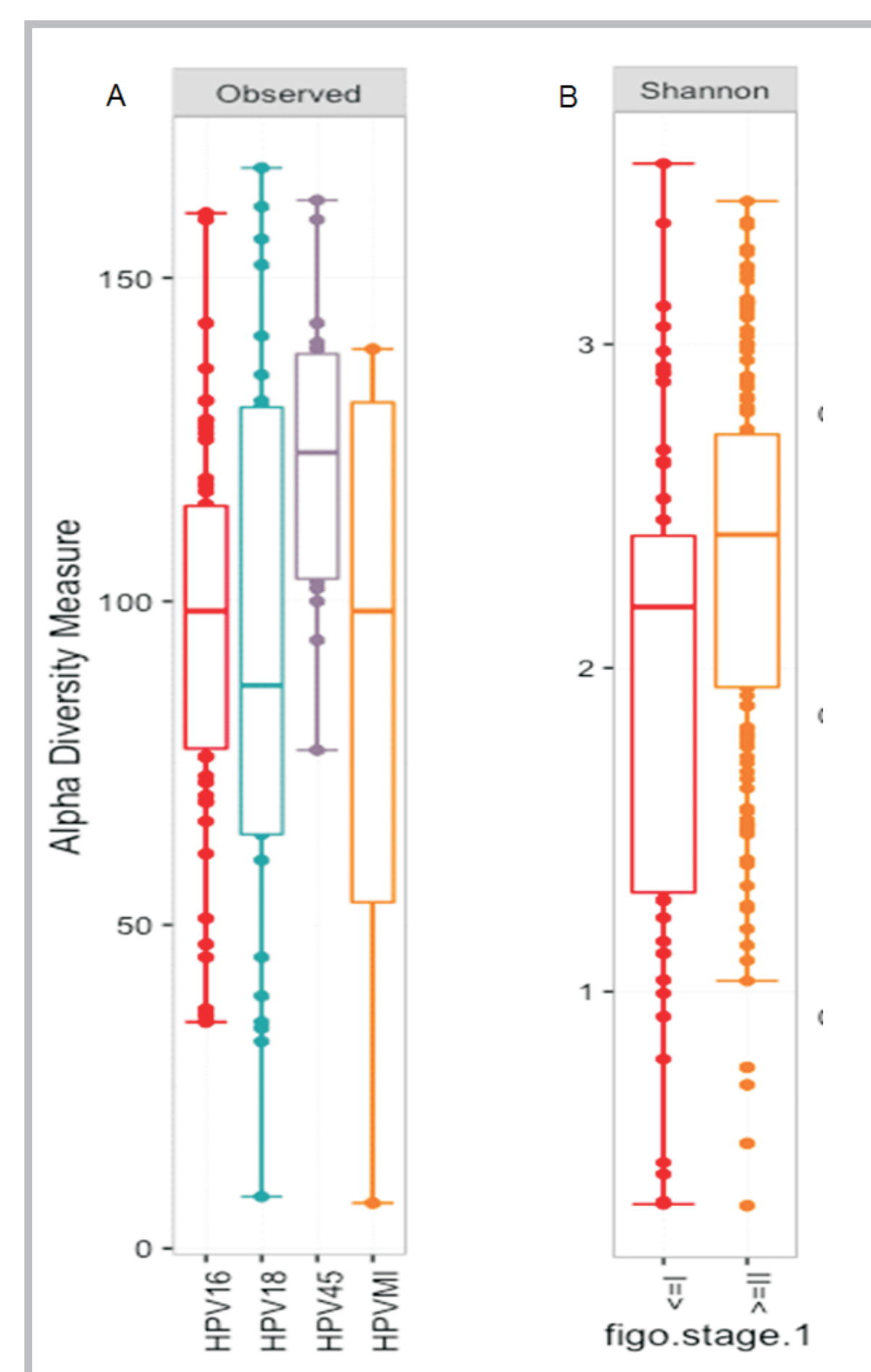


Figure 3. Alpha diversity by HPV type and FIGO staging. HPV45 positive samples had statistically higher level of diversity (Observed) than HPV16 and HPV18 positive cancers ($p=0.0059$ and 0.0001). Advanced FIGO stages (\geq II) displayed higher Observed and Shannon diversity ($p=0.0403$ and 0.0009 , respectively). Statistical significance was assessed by ANOVA test.

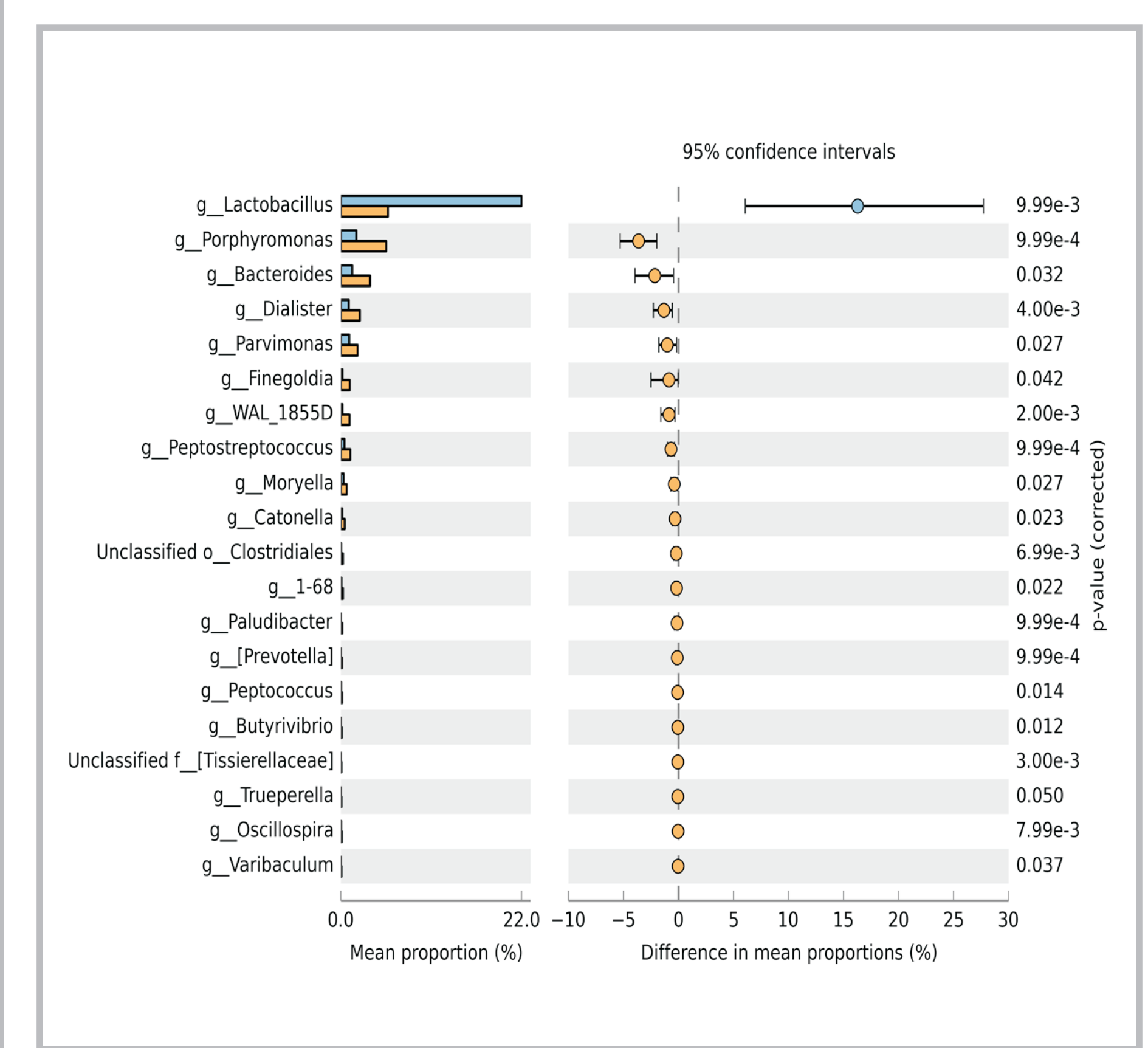


Figure 2. Distribution of the bacteria genus by tumor staging. *Lactobacillus* were more abundant in early cancer stages (\leq I) than in advanced ones (\geq II), $p<0.05$. Differently, the other genus, i.e. *Porphyromonas*, *Bacteroides*, *Dialister*, *Parvimonas*, *Finegoldia*, were more abundant, with statistical significance ($p<0.05$) in advanced stages (\geq II). Statistical significance was assessed by ANOVA test using the STAMP software.

CONCLUSION

Preliminary results shows:

- (1) We are able to identify microbiome in DNA from tissues,
- (2) Higher abundance of anaerobic and gram negative bacteria,
- (3) Point out differences of diversity by HPV types,
- (4) and by HPV staging.