Figure S1. Alpha diversity was measured in HR/MET, LR GISTs and microGISTs and stratified according to patients' gender, by Shannon (A) and Simpson (B) indexes. The same was done for GIST vs microGISTs comparison (C and D). The obtained values are shown as boxplot and the non-parametric tests Kruskal-Wallis and Wilcoxon were used to compare data distribution among groups.

Figure S2. Principal coordinate analysis (PCoA) plots based on weighted and unweighted UniFrac and Bray–Curtis dissimilarities are shown. Results revealed significant differences between microGIST, low-risk and high-risk/metastatic GISTs (A). Composition of the gut microbiota significantly change between the three cohorts (B) unweighted and (C) weighted UniFrac measures of beta-diversity visualized using PCoA.

Figure S3. Bar charts representing the phyla relative abundances in micro and GIST groups. In particular, relative abundances represent the mean of the observed abundances per phylum in each group. Outer and inner donut chart represents tumor and healthy counterpart tissues, respectively.

Figure S4. Bar charts representing the phyla relative abundances in LR and HR/MET and GIST groups. In particular, relative abundances represent the mean of the observed abundances per phylum in each group. Outer and inner donut chart represents tumor and healthy counterpart tissues, respectively.

Figure S1

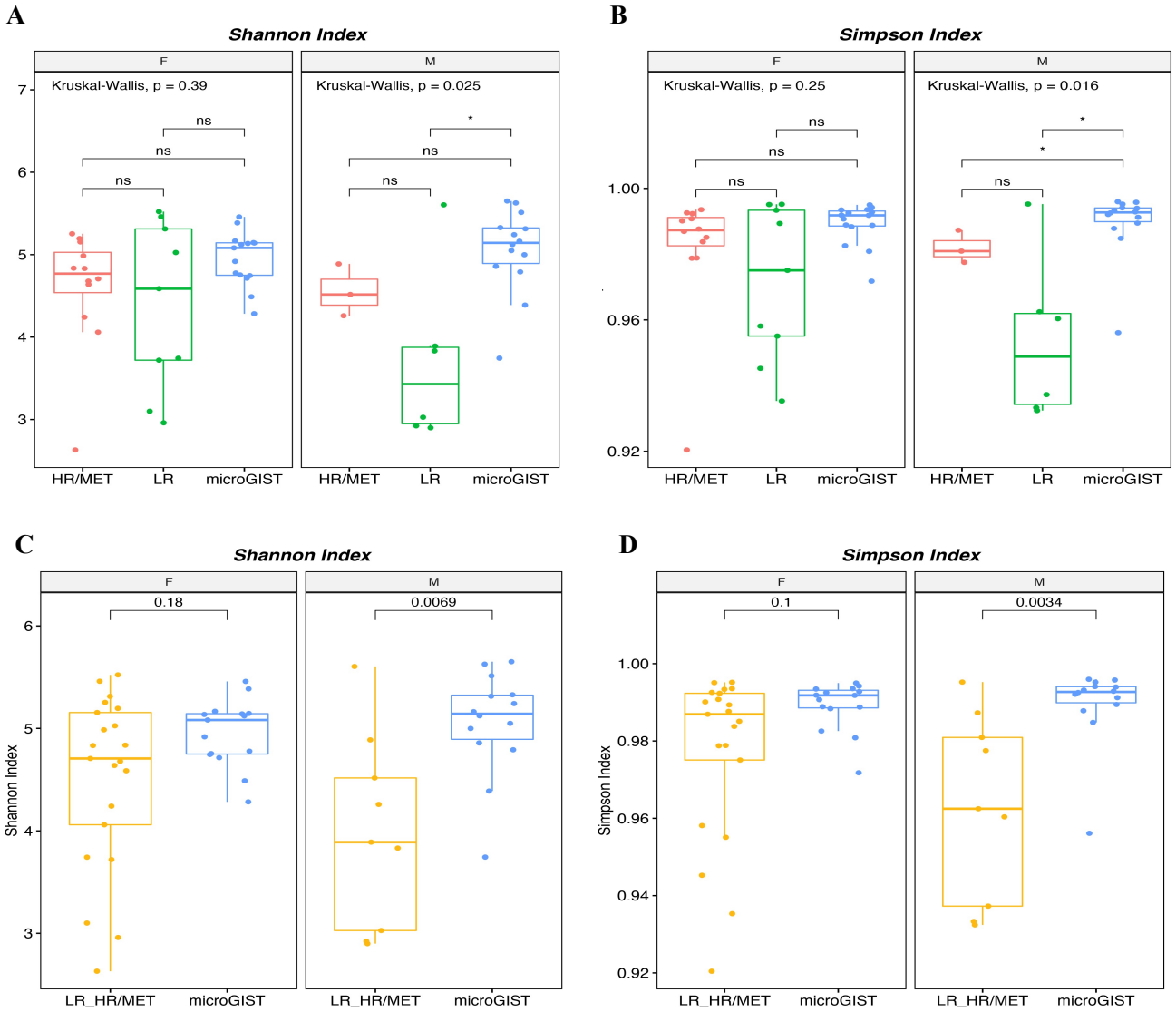

A
Shannon Index
F
M
Kruskal-Wallis, p = 0.39
Kruskal-Wallis, p = 0.025
ns
ns
ns
*
ns
ns
7
6
5
4
3
HR/MET
LR
microGIST
B
Simpson Index
Kruskal-Wallis, p = 0.25
Kruskal-Wallis, p = 0.016
1.00
0.96
0.92
C
Shannon Index
0.18
0.0069
LR_HR/MET
microGIST
D
Simpson Index
0.1
0.0034
1.00
0.98
0.96
0.94
0.92

Figure S2

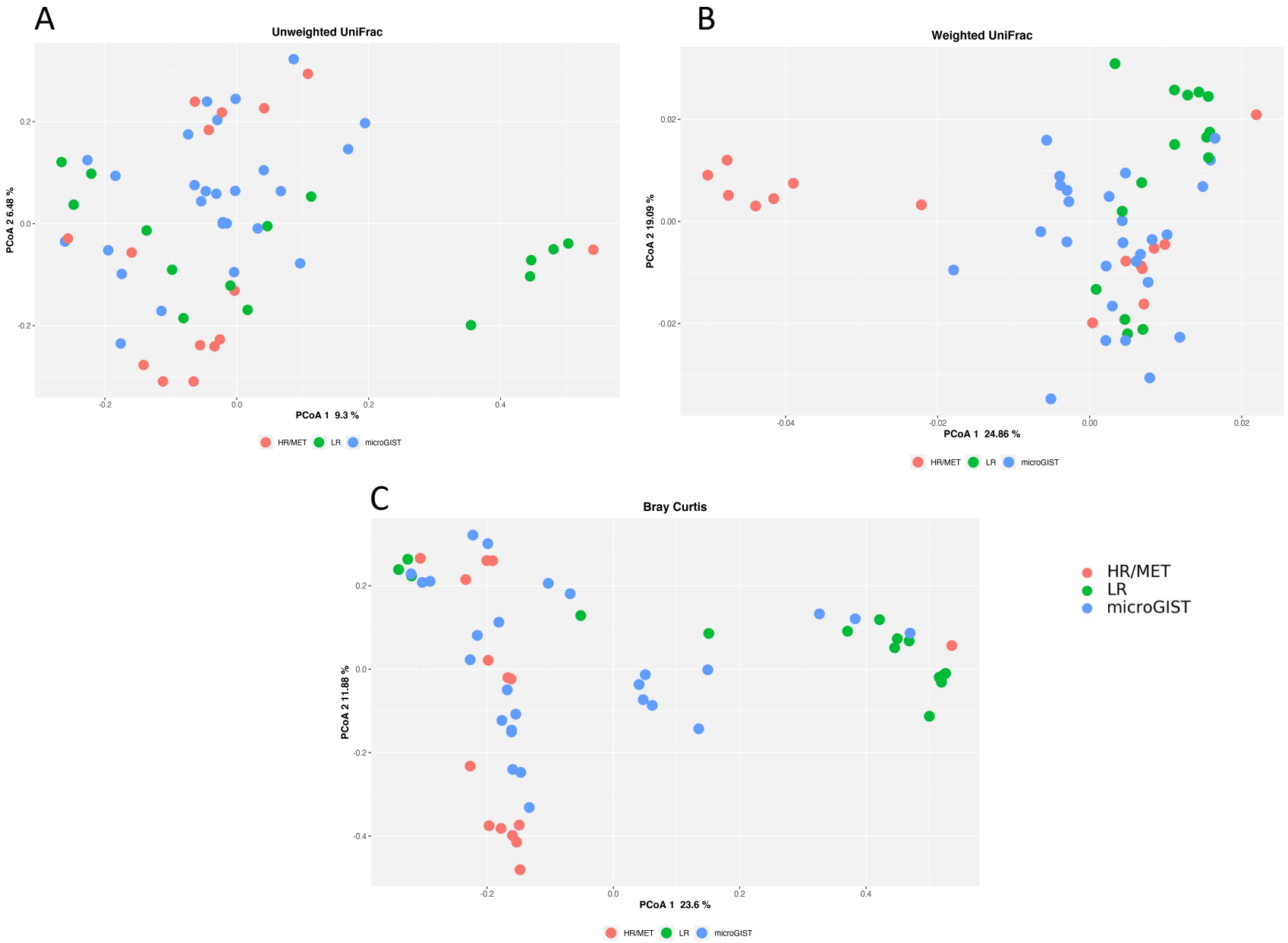

A
Unweighted UniFrac
PCoA 2 6.48 %
PCoA 1 9.3 %
HR/MET
LR
microGIST
B
Weighted UniFrac
PCoA 2 19.09 %
PCoA 1 24.86 %
HR/MET
LR
microGIST
C
Bray Curtis
PCoA 2 11.88 %
PCoA 1 23.6 %
HR/MET
LR
microGIST
HR/MET
LR
microGIST

Figure S3

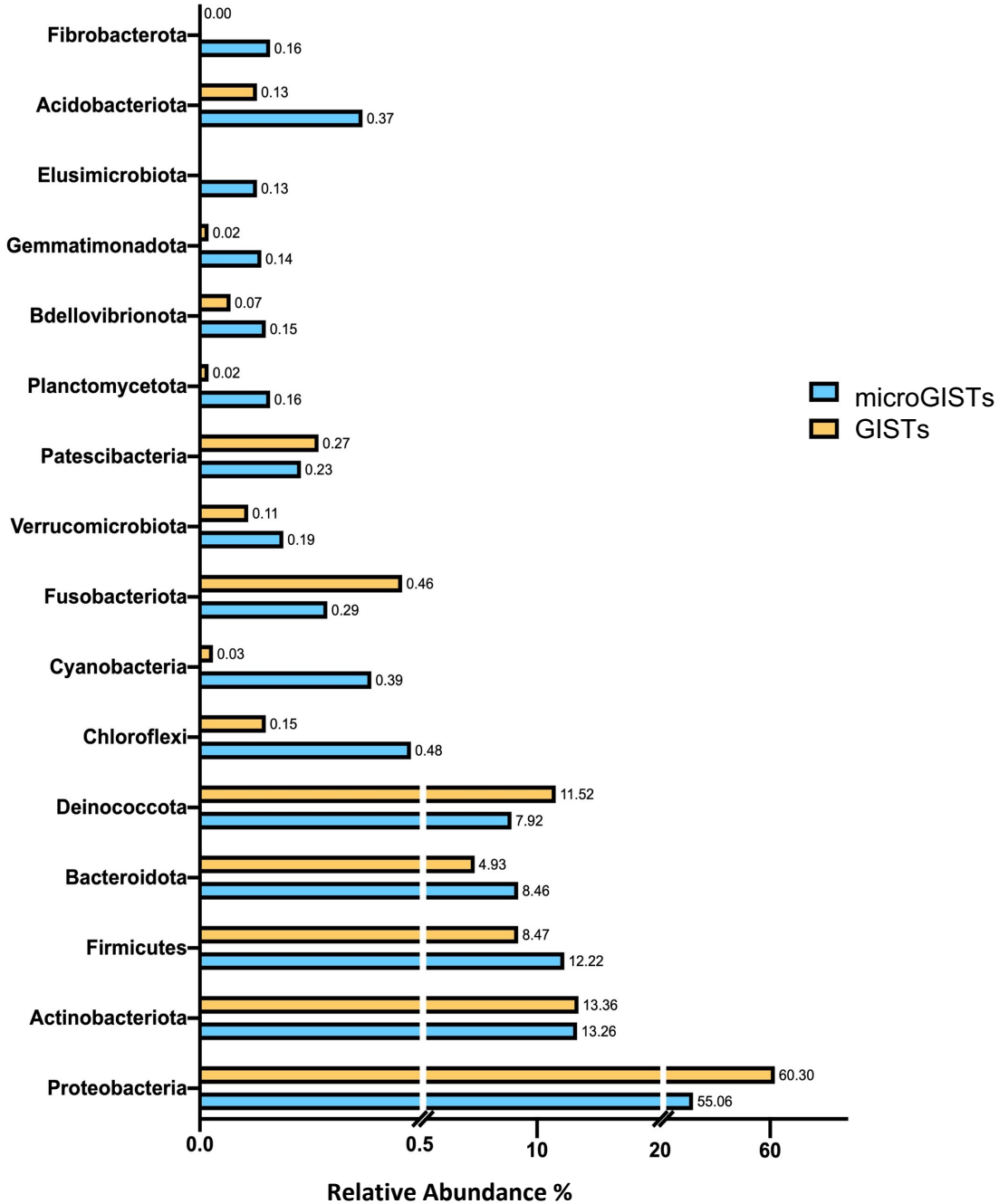
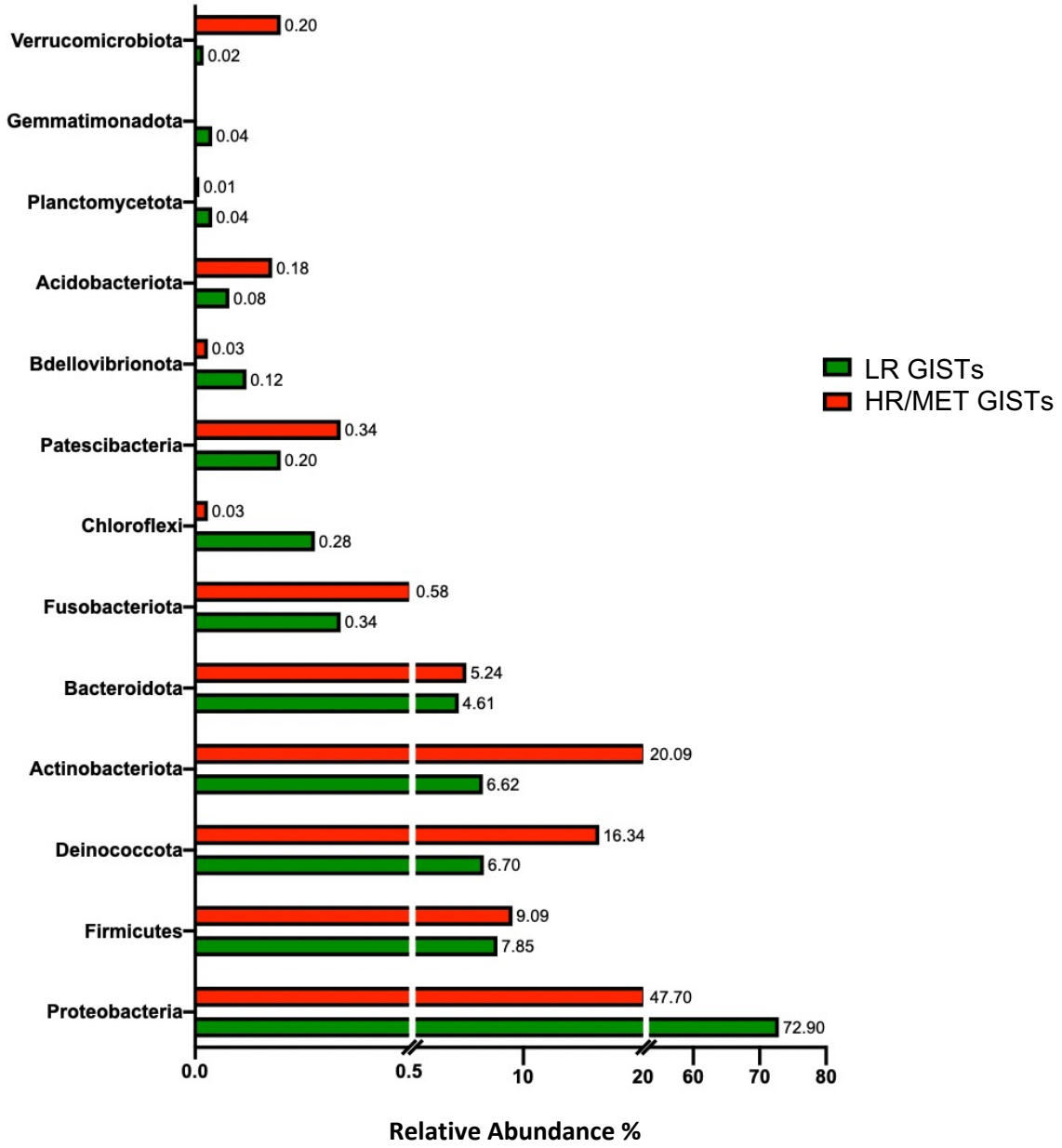

Fibrobacterota
0.00
0.16
Acidobacteriota
0.13
0.37
Elusimicrobiota
0.13
Gemmatimonadota
0.02
0.14
Bdellovibrionota
0.07
0.15
Planctomycetota
0.02
0.16
Patescibacteria
0.27
0.23
Verrucomicrobiota
0.11
0.19
Fusobacteriota
0.46
0.29
Cyanobacteria
0.03
0.39
Chloroflexi
0.15
0.48
Deinococcota
11.52
7.92
Bacteroidota
4.93
8.46
Firmicutes
8.47
12.22
Actinobacteriota
13.36
13.26
Proteobacteria
60.30
55.06
0.0
0.5
10
20
60
Relative Abundance %
microGISTs
GISTs

Figure S4


Verrucomicrobiota
0.20
0.02
Gemmatimonadota
0.04
Planctomycetota
0.01
0.04
Acidobacteriota
0.18
0.08
Bdellovibrionota
0.03
0.12
Patescibacteria
0.34
0.20
Chloroflexi
0.03
0.28
Fusobacteriota
0.58
0.34
Bacteroidota
5.24
4.61
Actinobacteriota
20.09
6.62
Deinococcota
16.34
6.70
Firmicutes
9.09
7.85
Proteobacteria
47.70
72.90
LR GISTs
HR/MET GISTs
0.0
0.5
10
20
60
70
80
Relative Abundance %