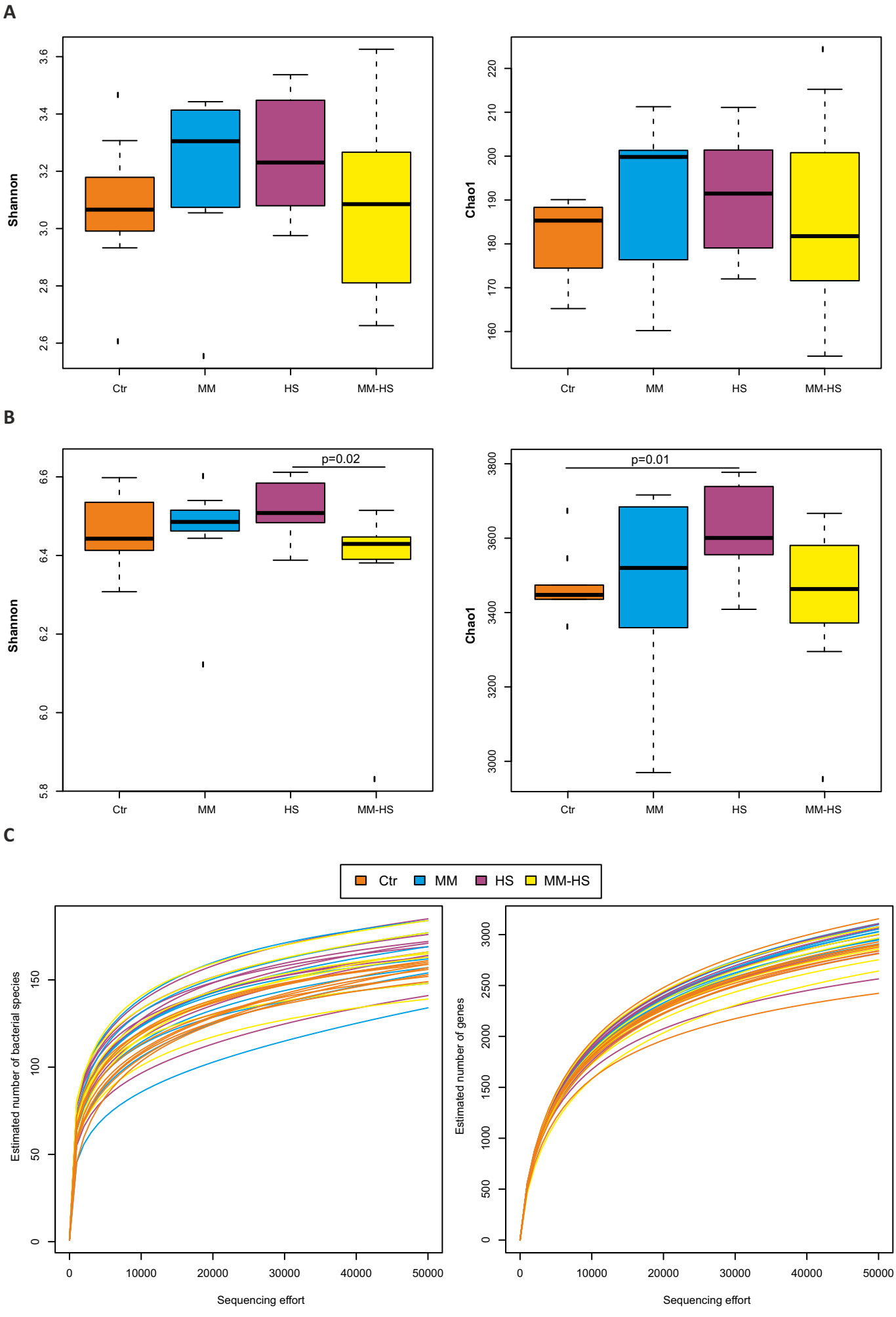
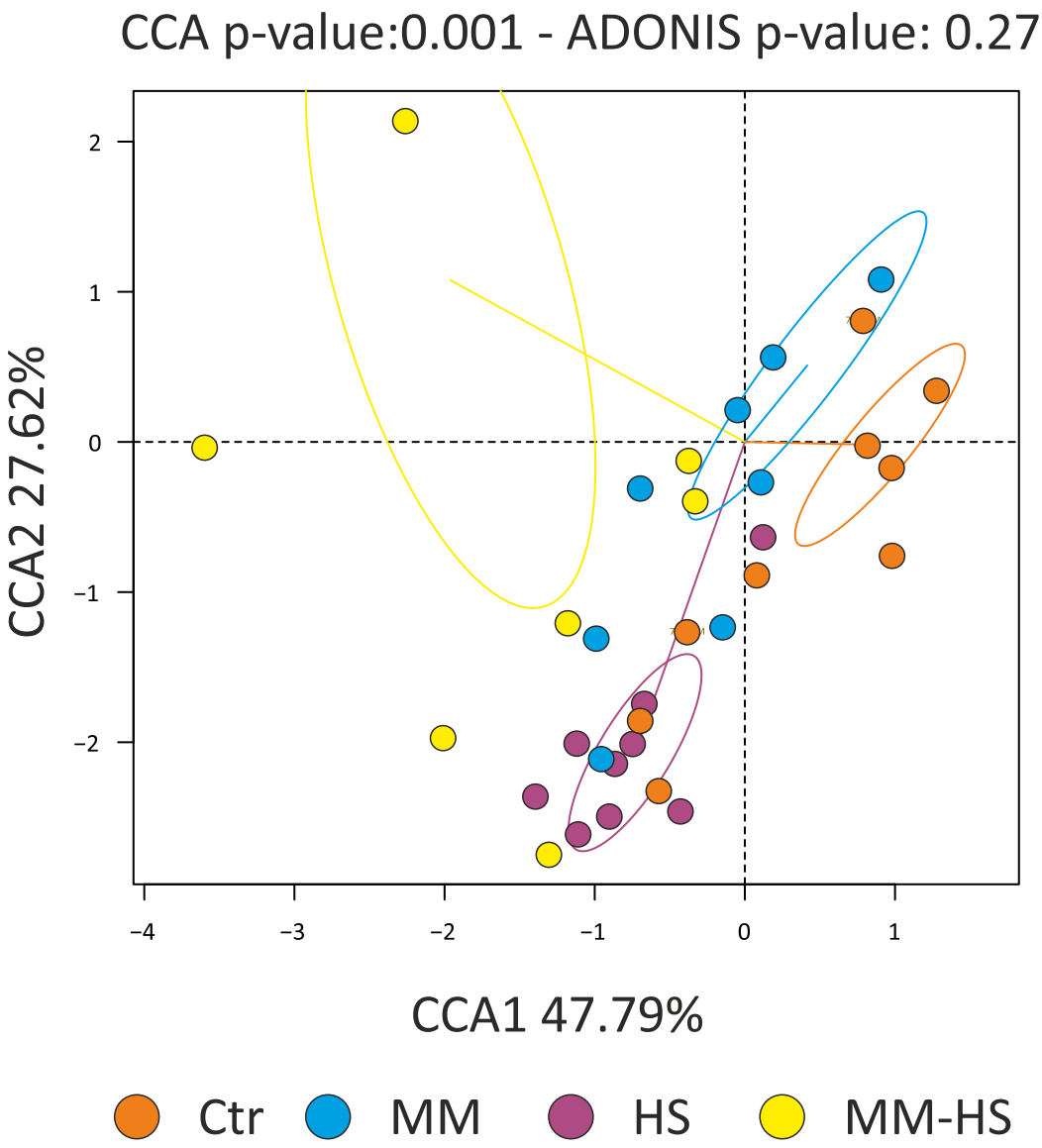
Supplementary Figure 1. Bacterial and functional diversity in tongue biofilms from halitosis and halitosis-free individuals. Diversity (Shannon) and richness (Chao1) indexes were calculated using both the number of bacterial species (A) and genes (B) detected in the metatranscriptomes, obtained by Nextseq Illumina RNAseq. Rarefaction curves (C) were calculated for the same number of reads in each sample ($5x10^4$), annotated to a bacterial species (left) or a gene (right). Differences were calculated using Wilcoxon test.

Supplementary Figure 2. Functional differences between halitosis groups. The graph shows the results of a Canonical Correspondence Analysis (CCA) based on microbial gene expression in the different groups studied (*Ctr, MM, HS* and *MM-HS*). An ADONIS test was used.


A
Shannon
2.6
2.8
3.0
3.2
3.4
3.6
Ctr
MM
HS
MM-HS
Chao1
160
170
180
190
200
210
220
Ctr
MM
HS
MM-HS
B
Shannon
5.8
6.0
6.2
6.4
6.6
p=0.02
Ctr
MM
HS
MM-HS
Chao1
3000
3200
3400
3600
3800
p=0.01
Ctr
MM
HS
MM-HS
C
Ctr
MM
HS
MM-HS
Estimated number of bacterial species
0
50
100
150
0
10000
20000
30000
40000
50000
Sequencing effort
Estimated number of genes
0
500
1000
1500
2000
2500
3000
0
10000
20000
30000
40000
50000
Sequencing effort


CCA p-value:0.001 - ADONIS p-value: 0.27
CCA2 27.62%
CCA1 47.79%
2
1
0
−1
−2
−4
−3
−2
−1
0
1
Ctr
MM
HS
MM-HS