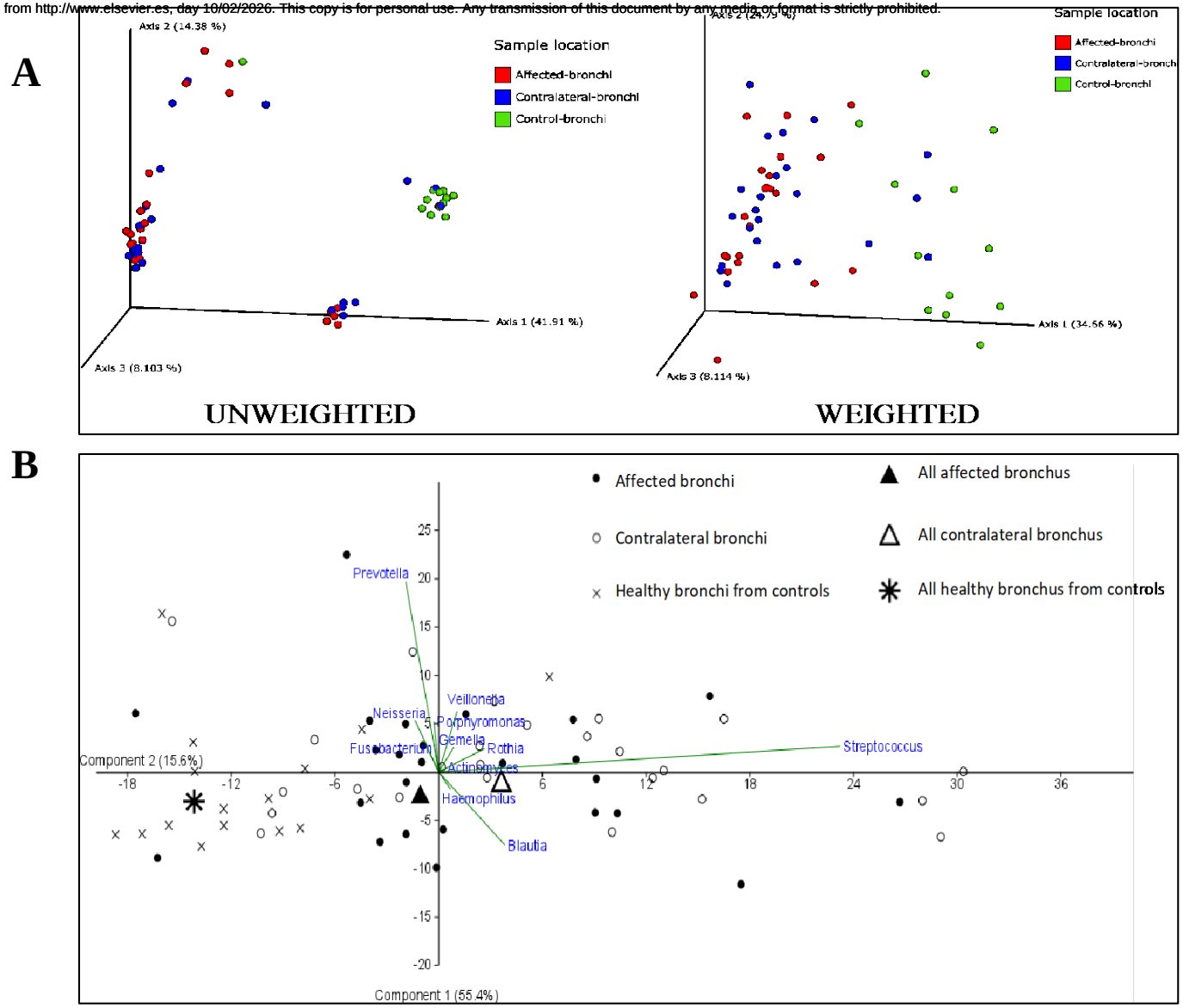
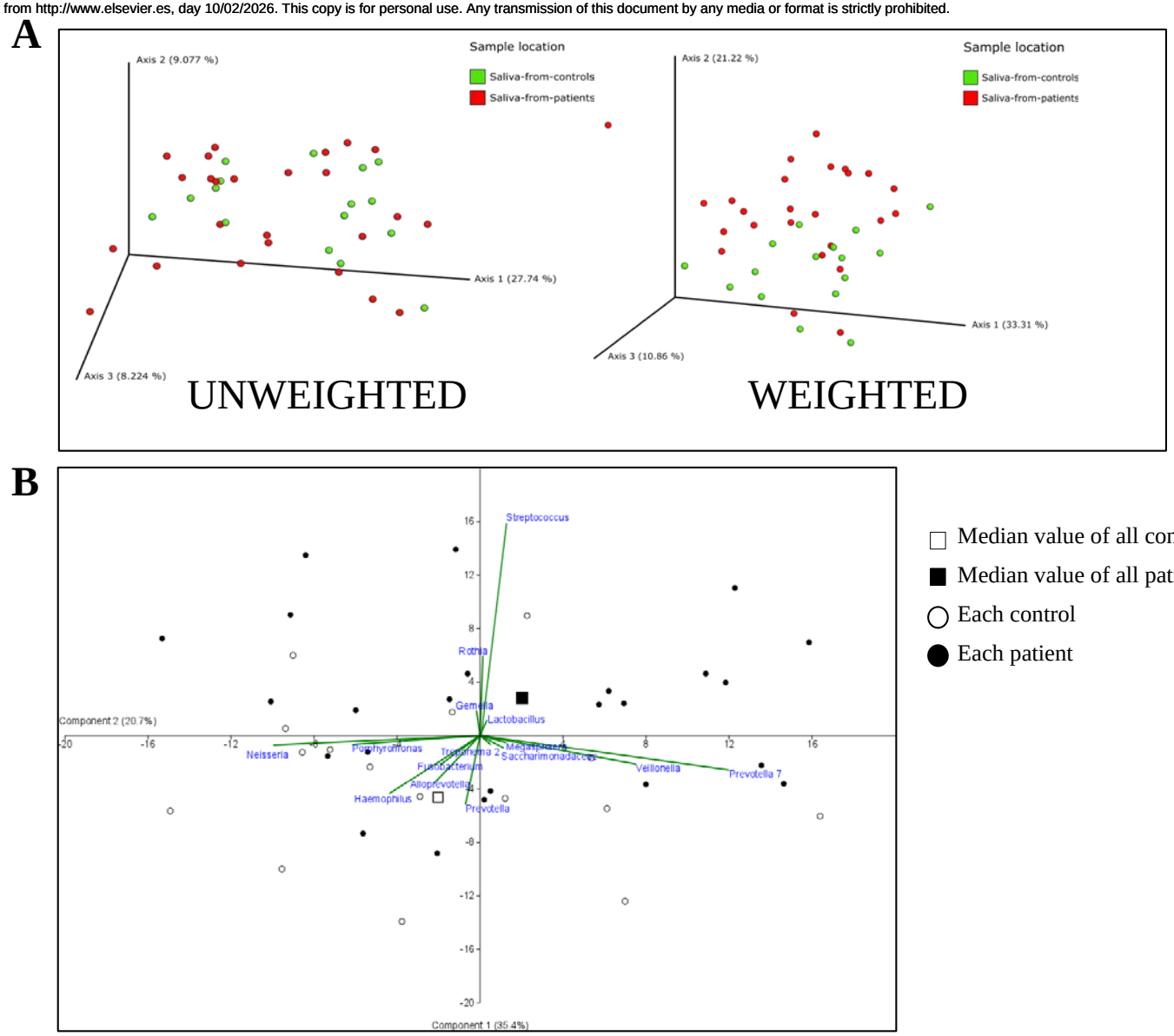
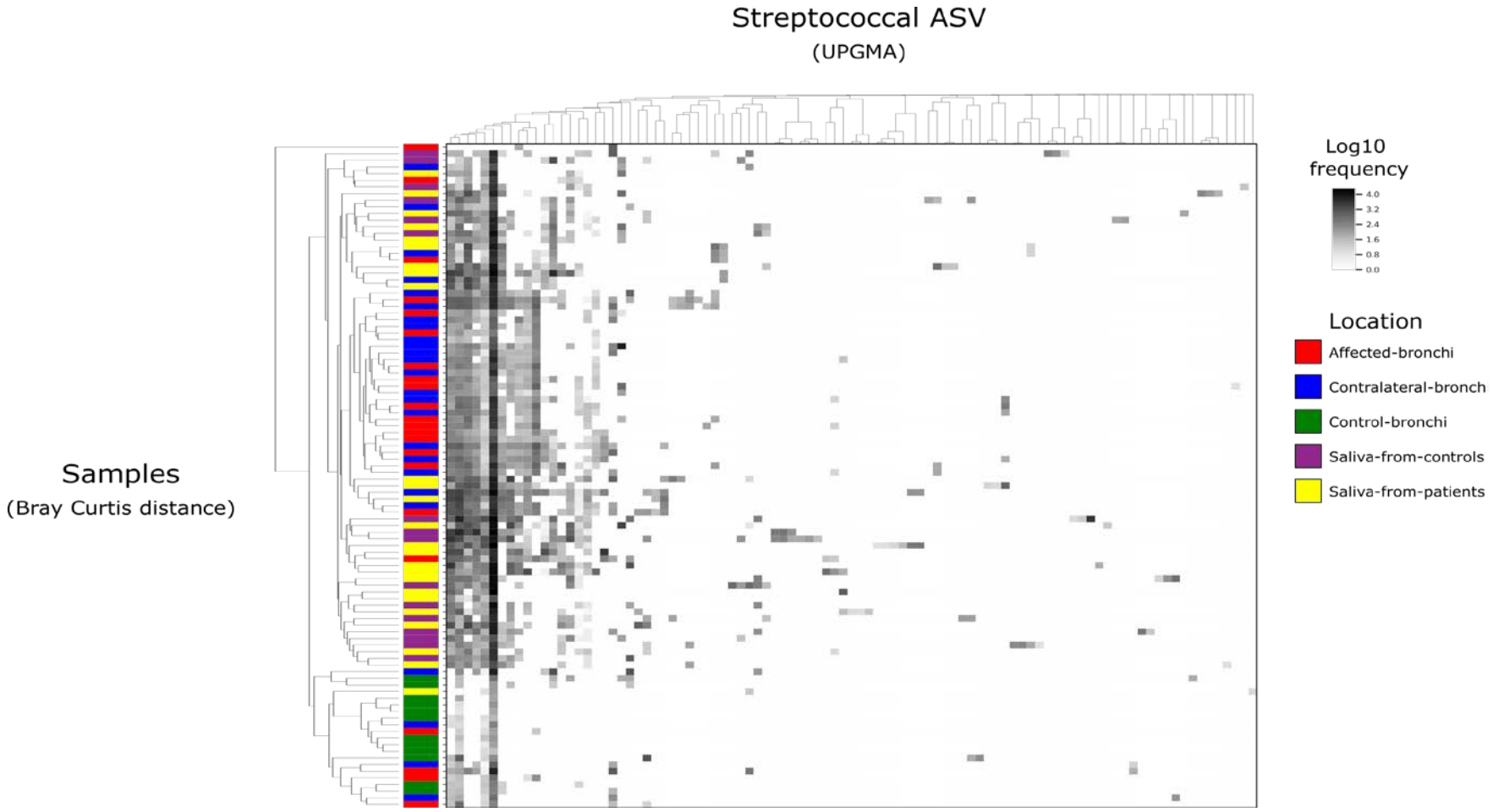


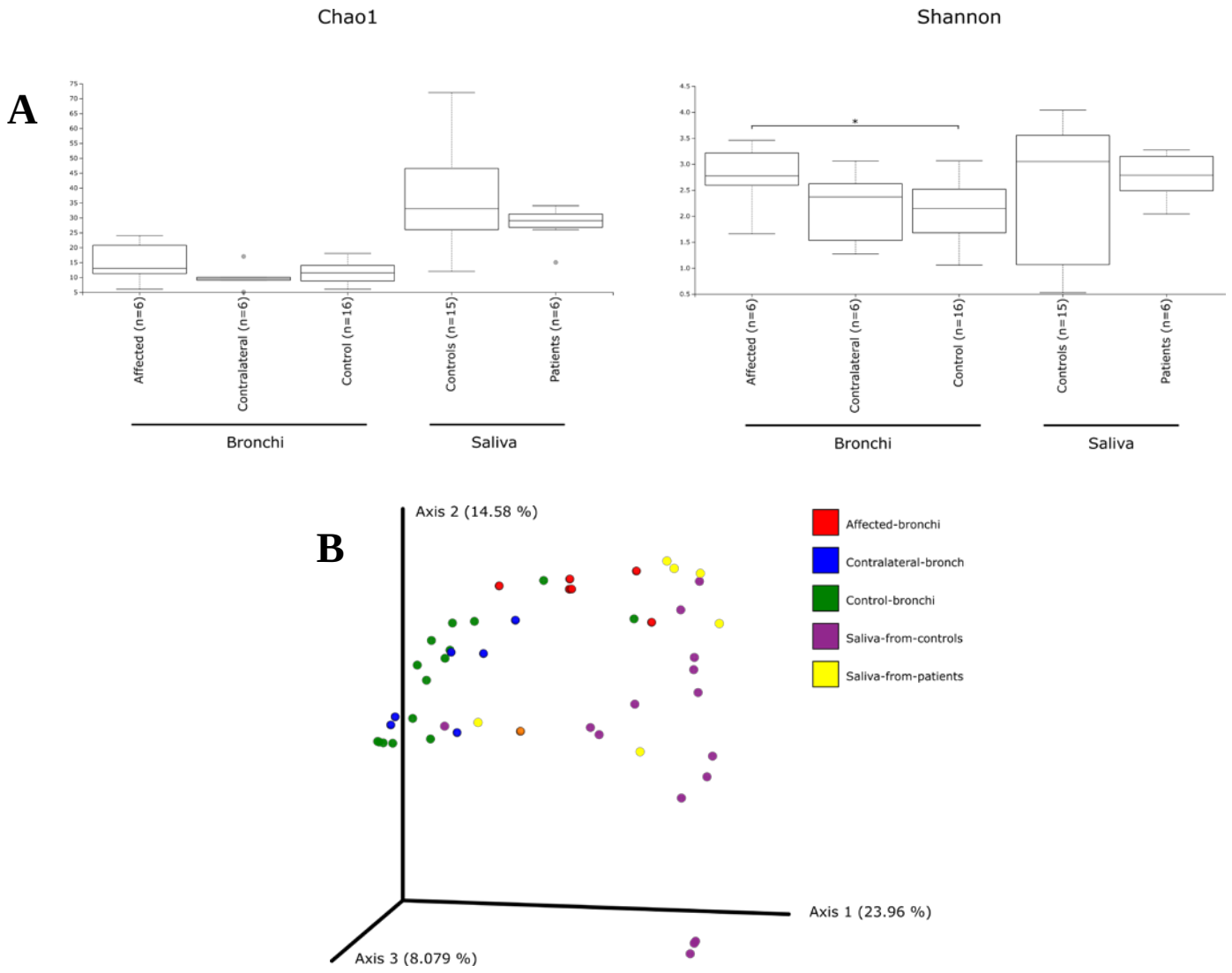
Supl. Fig. 1. Representation and comparison of the microbiota from cancer affected, contralateral and control bronchi. **A:** UniFrac beta diversity analysis of bronchi samples. Unweighted UniFrac reports differences in the presence or absences of ASVs, while weighted UniFrac also reports differences in the abundance of ASVs. **B:** PCA of most abundant genera that constituted 90% of the bronchial microbiota of both patients and controls.



Supl. Fig. 2. A: UniFrac beta diversity analysis of salivary samples. Unweighted UniFrac reports differences in the presence or absences of ASVs, while weighted UniFrac also reports differences in the abundance of ASVs. **B:** Principal Component Analysis (PCA) of the most abundant genera that constitute 90% of the total salivary microbiota.



Supl. Fig. 3. Heatmap correlating the abundance of Streptococcal ASVs (horizontal axis) with the samples (vertical axis). A total of 95 ASVs were considered.



Supl. Fig 4. A: Alpha diversity of the mycobiome detected in the different samples, significant differences ($p<0.05$) between patients and controls are highlighted by asterisks. **B:** PCoA based on Bray Curtis distances, showing the distribution of samples according to their mycobiome.