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鼻腔及口腔微生物菌叢在氣喘的角色
The role of nasal and oral microbiome in asthma

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中文摘要

背景：氣喘是呼吸道對許多過敏原反應過度而發生慢性反覆性的呼吸道發炎疾病。微生物菌叢與呼吸道黏膜上皮細胞緊密接觸，微生物菌叢失調可能是導致呼吸道慢性發炎的重要原因之一。上下呼吸道不論結構上或功能上皆緊密相關，因此，鼻腔及口腔微生物菌叢失調，亦可能對於下呼吸道慢性發炎，如氣喘的疾病控制，造成顯著的影響。微生物菌叢在氣喘病患急性發作易感性上所扮演的角色。

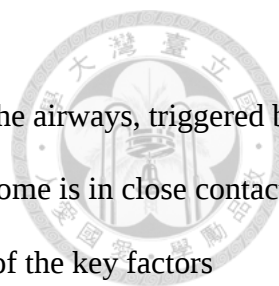
方法：本研究在國立臺灣大學醫學院附設醫院及其新竹分院進行。收案診斷為氣喘的成人病患，並追蹤三個月。所有病患在收案後均接受鼻腔和口腔微生物菌叢的檢查。

結果：本研究一共收案 61 名氣喘病患。病患年齡中位數為 44 歲（範圍：21 – 72 歲）。男性佔所有病患比例的 18%。回歸分析發現：鼻腔細菌叢的 alpha 多樣性與 ACT 分數呈負相關和 eosinophil 數量呈正相關，但與 IgE 濃度跟 FEV1/FVC 數值的相關性不顯著。收案後三個月內，34% 的病患曾經有氣喘急性惡化。曾經發生氣喘急性惡化病患的鼻腔細菌叢的 alpha 多樣性 (alpha diversity) 有低於無急性惡化病患的傾向。兩組間鼻腔細菌叢組成不同。相較於未發生氣喘急性惡化病患，曾經發生急性惡化的患者鼻腔在種的層級有較低比例的 *Cutibacterium acnes* ($1.44 \pm 2.14\%$ vs. $4.11 \pm 6.34\%$, $P = 0.019$)、*Anaerococcus Octavius* ($0.06 \pm 0.26\%$ vs. $0.54 \pm 1.31\%$, $P = 0.029$)、*Pseudomonas yamanorum* ($0.02 \pm 0.08\%$ vs. $0.40 \pm 0.97\%$, $P = 0.019$)、*Acinetobacter johnsonii* ($0.02 \pm 0.08\%$ vs. $0.07 \pm 0.19\%$, $P = 0.015$)、*Pseudobdellovibrio exovor* ($0.01 \pm 0.03\%$ vs. $0.13 \pm 0.27\%$, $P = 0.037$) 和 *Brevibacillus marinus* ($0.002 \pm 0.01\%$ vs. $0.05 \pm 0.14\%$, $P = 0.032$)；在屬的層級有較低比例的 *Cutibacterium* ($1.55 \pm 2.19\%$ vs. $4.36 \pm 6.42\%$, $P = 0.015$)、*Anaerococcus* ($0.09 \pm 0.36\%$ vs. $1.02 \pm 2.36\%$, $P = 0.018$)、*Lactobacillus* ($0.00 \pm 0.00\%$ vs. $0.34 \pm 0.95\%$, $P = 0.031$)、*Blautia* ($0.001 \pm 0.004\%$ vs. $0.11 \pm 0.34\%$, $P = 0.039$)、*Pseudobdellovibrio* ($0.01 \pm 0.03\%$ vs. $0.07 \pm 0.19\%$, $P = 0.036$)、*Brevibacillus* ($0.003 \pm 0.01\%$ vs. $0.06 \pm 0.13\%$, $P = 0.016$)；在門的層級有較低比例的 *Cyanobacteria* ($0.00 \pm 0.00\%$ vs. $0.02 \pm 0.07\%$, $P = 0.046$)。在口腔細菌叢方面，我們發現口腔細菌叢的 alpha 多樣性與 ACT 分數、eosinophil 數量、IgE 濃度和 FEV1/FVC 數值的相關性不顯著。兩組間，口腔細菌叢的 alpha 多樣性和 beta 多樣性皆無顯著差異。然而，相較於未發生氣喘急性惡化病患，曾經發生急性惡化的患者口腔在種的層級有較低比例的 *Streptococcus sanguis* ($0.29 \pm 0.32\%$ vs. $0.69 \pm 1.08\%$, $P = 0.036$)、*Streptococcus gwanjuense* ($0.02 \pm 0.05\%$ vs. $0.16 \pm 0.43\%$, $P = 0.041$)、*Actinomyces graevenitzi* ($0.04 \pm 0.06\%$ vs. $0.17 \pm 0.38\%$, $P = 0.033$)、*Butyrivibrio hungatei* ($0.01 \pm 0.02\%$ vs. $0.04 \pm 0.06\%$, $P = 0.047$) 和 *Leptotrichia buccalis* ($0.004 \pm 0.01\%$ vs. $0.02 \pm 0.05\%$, $P = 0.035$)；在屬的層級有較低比例的 *Butyrivibrio* ($0.02 \pm 0.02\%$ vs.

0.04±0.06%, P = 0.048)。

結論：曾急性惡化的氣喘病患，其鼻腔細菌叢的 alpha 多樣性似乎低於未曾氣喘急性惡化病患。曾氣喘急性惡化患者的鼻腔中，在屬的層級有較低比例的 *Cutibacterium*、*Anaerococcus*、*Lactobacillus*、*Blautia*、*Pseudobdellovibrio* 和 *Brevibacillus*。口腔細菌叢的 alpha 多樣性和 beta 多樣性在曾急性發作與未曾急性發作病患中皆無顯著差異。本研究未收案健康人做比較，且收案人數較少。鼻腔微生物和氣喘急性發作易感性的機轉，需要進一步以動物介入實驗探討。

關鍵字：鼻腔衛生物菌叢、口腔微生物菌叢、氣喘、急性發作、alpha 多樣性

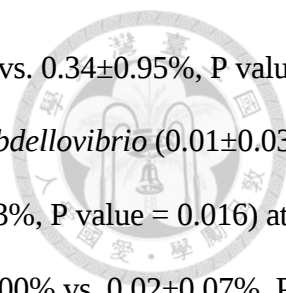


Abstract

Background: Asthma is a chronic and recurrent inflammatory disease of the airways, triggered by an overreaction of the respiratory system to various allergens. The microbiome is in close contact with the respiratory mucosal epithelial cells, and its dysbiosis may be one of the key factors contributing to chronic airway inflammation. The upper and lower respiratory tracts are closely related both structurally and functionally. Therefore, dysbiosis of the nasal and oral microbiota may also significantly impact the control of chronic lower airway inflammation, such as in asthma. The role of the microbiome in the susceptibility to acute exacerbations in asthma patients is also noteworthy.

Methods: The study conducted at National Taiwan University Hospital in Taipei and its Hsinchu Branch in Taiwan. Adult patients diagnosed with asthma were recruited at 3-month follow-up. All patients underwent nasal and oral microbiome examinations after enrollment.

Results: A total of 61 patients with asthma were enrolled. The mean patient age was 44 years (range: 21–72 years). Men comprised 18% (11/61) of all patients. Within the 3-month period, 34% of the patients experienced exacerbations. Patients with exacerbated asthma tended to have lower nasal alpha diversity than those without exacerbations. Nasal alpha diversity may correlate negatively with ACT scores and positively with eosinophil counts, but not with IgE levels or value of FEV1/FVC. The nasal bacterial composition differed between the two groups. Compared to patient with non-exacerbated asthma, those with exacerbated asthma had a lower proportion of nasal *Cutibacterium acnes* ($1.44 \pm 2.14\%$ vs. $4.11 \pm 6.34\%$, P value = 0.019), *Anaerococcus octavius* ($0.06 \pm 0.26\%$ vs. $0.54 \pm 1.31\%$, P value = 0.029), *Pseudomonas yamanorum* ($0.02 \pm 0.08\%$ vs. $0.40 \pm 0.97\%$, P value = 0.019), *Acinetobacter johnsonii* ($0.02 \pm 0.08\%$ vs. $0.07 \pm 0.19\%$, P value = 0.015), *Pseudobdellovibrio exovorus* ($0.01 \pm 0.03\%$ vs. $0.13 \pm 0.27\%$, P value = 0.037), and *Brevibacillus marinus* ($0.002 \pm 0.01\%$ vs. $0.05 \pm 0.14\%$, P value = 0.032) at species level, had a lower proportion of nasal *Cutibacterium* ($1.55 \pm 2.19\%$ vs. $4.36 \pm 6.42\%$, P value = 0.015), *Anaerococcus*



(0.09±0.36% vs. 1.02±2.36%, P value = 0.018), *Lactobacillus* (0.00±0.00% vs. 0.34±0.95%, P value = 0.031), *Blautia* (0.001±0.004% vs. 0.11±0.34%, P value = 0.039), *Pseudobdellovibrio* (0.01±0.03% vs. 0.07±0.19%, P value = 0.036), *Brevibacillus* (0.003±0.01% vs. 0.06±0.13%, P value = 0.016) at the genus level, and had a lower proportion of nasal *Cyanobacteria* (0.00±0.00% vs. 0.02±0.07%, P value = 0.046) at the phylum level. There were no differences in oral alpha diversity and beta diversity between the two groups. Oral alpha diversity index was not associated with ACT score, eosinophil count, IgE level or value of FEV1/FVC. However, compared with patients with non-exacerbated asthma, those with exacerbated asthma had a lower proportion of oral *Streptococcus sanguis* (0.29±0.32% vs. 0.69±1.08%, P value = 0.036), *Streptococcus gwanjuense* (0.02±0.05% vs. 0.16±0.43%, P value = 0.041), *Actinomyces graevenitzi* (0.04±0.06% vs. 0.17±0.38%, P value = 0.033), *Butyrivibrio hungatei* (0.01±0.02% vs. 0.04±0.06%, P value = 0.047), and *Leptotrichia buccalis* (0.004±0.01% vs. 0.02±0.05%, P value = 0.035) at the species level, and had a lower proportion of oral *Butyrivibrio* (0.02±0.02% vs. 0.04±0.06%, P value = 0.048) at the genus level.

Discussion: The nasal microbiome may be an important factor influencing susceptibility to asthma exacerbations. Patients with exacerbated asthma seemed to have lower alpha diversity in their nasal microbiome compared to those with non-exacerbated asthma. Patients with exacerbated asthma had a lower proportion of nasal *Cutibacterium*, *Anaerococcus*, *Lactobacillus*, *Blautia*, *Pseudobdellovibrio*, and *Brevibacillus* at the genus level. There were no significant differences in the alpha diversity and beta diversity of the oral microbiome between patients who had experienced exacerbations and those who had not. This study did not include healthy individuals for comparison, and the sample size was relatively small. Further animal interventional studies are needed to explore the mechanisms by which nasal microbiome may influence susceptibility to asthma exacerbations.

Key word: nasal microbiome, oral microbiome, asthma, exacerbation, alpha diversity

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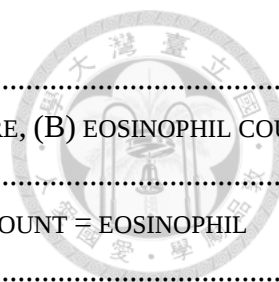


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Introduction

Asthma is a common complex respiratory disease characterized by chronic airway inflammation with history of respiratory symptoms that vary over time and in intensity, together with variable expiratory airflow limitation. It affects more than 300 million people worldwide and is responsible for over 20 million disability-adjusted life years¹. Asthma is a complex disease resulting from genetic, epigenetic, and environmental determinants. Genetic studies have identified numerous genetic polymorphisms associated with asthma susceptibility, but these genetic variants alone are unable to explain the most variability in asthma risk². Environmental exposures are also thought to contribute to the increased prevalence of asthma.

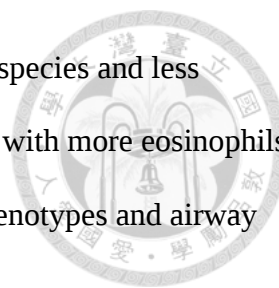
Microbiomes consist of all microorganisms present in an environment. In microbiome studies, alpha diversity measures the variety of species (species richness) and the evenness of their abundances within a particular area or ecosystem. It provides insight into the complexity and health of a microbial community in a single sample or environment³. Beta diversity assesses the change in species composition between different environments or samples. It reflects the ecological distance or dissimilarity between microbial communities across various conditions^{4,5}. Gamma diversity represents the total diversity of species within a large region or landscape, encompassing multiple environments or ecosystems. It combines alpha and beta diversity to provide a comprehensive view of biodiversity on a larger scale⁶. Dysbiosis is defined as imbalance of the microbial community and loss of microbial diversity.

The human microbiome is defined as all microorganisms present in or on the human body, which influence immunity through microbial structural ligands and microbial metabolites⁷. Different microbiomes in the airway were associated with immune responses in adult asthma⁸. *Haemophilus*, *Moraxella*, *Neisseria*, *Fusobacterium*, *Streptococcus*, and *Veillonella* were higher in the airways of patients with asthma, while nasal *Corynebacterium* and *Dolosigranulum* were lower in these patients⁹⁻¹³. Nasal beta diversity showed a clear separation between patients with controlled

and uncontrolled asthma¹⁴. Compared to patients with poorly controlled asthma, the top three most common bacterial genera in the nasal cavities of patients with controlled asthma were *Flavonifractor*, *Pseudoflavonifractor*, and *Anaerobium*, all belonging to the same phylum¹⁴. Due to limitations in experimental techniques in the early days¹⁵, most studies only explored up to the genus level. There are no relevant studies that explore down to the species level.

16S ribosomal RNA (16S rRNA) is an essential component of the small subunit of the prokaryotic ribosome. It contains nine highly variable regions, known as V1-V9, with specific sequences that can be used for bacterial phylogeny and classification. Partial sequencing of regions such as V3-V4 is often chosen for its ability to provide detailed taxonomic resolution at the genus level and sometimes down to the species level. Full-length sequencing of the V1-V9 region spans the entire length of the 16S rRNA gene, approximately 1500 base pairs, covering all nine hypervariable regions. Sequencing the entire 16S rRNA gene provides the most comprehensive taxonomic resolution and is useful for identifying a broader range of bacterial taxa^{15,16}. Early microbiome studies, due to technical limitations, mostly used partial region sequencing, with literature largely exploring down to the genus level. Exploring down to the species level could potentially be more beneficial for precision medicine.

The airway microbiome has an important role in asthma pathophysiology. Some studies found the composition of the bronchial microbiome was different between those with allergic respiratory disease and healthy subjects¹⁷⁻¹⁹. Increasing evidence showed that the bacterial microbiome of different mucosal surfaces might play a critical role in asthma^{20,21}. Patients with asthma have higher microbiome diversity and an altered composition, with more *Proteobacteria* and less *Bacteroidetes* compared with healthy subjects²². Asthma phenotype based on characteristics of airway inflammation are increasingly recognized as an important prognostic indicator²³. The eosinophilic and neutrophilic airway inflammation correlates with variations in the microbiome across patients with asthma^{12,19}. Patients with asthma who had the lowest levels of eosinophils had an altered



bacterial abundance profile, with more *Neisseria*, *Bacteroides*, and *Rothia* species and less *Sphingomonas*, *Halomonas*, and *Aeribacillus* species compared with those with more eosinophils and healthy subjects¹². The relationships between asthma inflammatory phenotypes and airway microbiology are likely to be complex and bidirectional.

The relative abundance of certain microbes, including members of *Comamonadaceae*, *Sphingomonadaceae*, and *Oxalobacteraceae* families, correlate with airway hyperreactivity in asthma²⁴. Administered treatments, particularly corticosteroids, may also greatly affect the composition of lung microbiota in asthmatic individuals^{9,24}. The enrichment of bacterial families *Microbacteriaceae* and *Pasteurellaceae* at baseline in inhaled corticosteroid (ICS) non-responders, and *Streptococcaceae*, *Fusobacteriaceae* and *Sphingomonadaceae* in ICS responders⁹. The microbiota's dynamic patterns and compositions are related to exacerbations in asthmatic children, treated with daily ICS¹¹. The cohort indicated that airway microbiome dominated by *Corynebacterium* and *Dolosigranulum* genera were associated with favorable clinical outcomes compared to microbiome dominated by more pathogenic bacteria: *Staphylococcus*, *Streptococcus*, and *Moraxella*¹¹. Severe asthma patients have a higher prevalence of *Actinobacteria*, which correlates with disease outcomes, including total severity scores in Asthma Control Questionnaires, and sputum leucocyte and bronchial eosinophil levels¹⁷. There are fewer studies on the oral and nasal microbiomes in adult asthma, and there is a lack of discussion regarding exacerbations. However, this is clinically significant.

Our hypothesis was nasal and oral bacterial microbiome diversity and composition may influence asthma outcomes. We wanted to investigate the relationship between nasal and oral microbiome diversity and composition with asthma outcomes down to the species level.



Material and Method

Study design and participants

A prospective observational study was conducted at the National Taiwan University Hospital in Taipei and its Hsinchu Branch between January 2023 and May 2024. The study enrolled adult patients diagnosed with asthma according to the Global Initiative for Asthma (GINA) guidelines²⁵, overseen by a chest physician. Exclusion criteria included age under 20 years, recent use of intranasal steroids or systemic antibiotics within three months, nasal surgery within six months prior to screening, and comorbidities such as chronic obstructive pulmonary disease. Ethical approval for the study was obtained from the Institutional Review Board of National Taiwan University Hospital (Approval No. 202206145RINA).

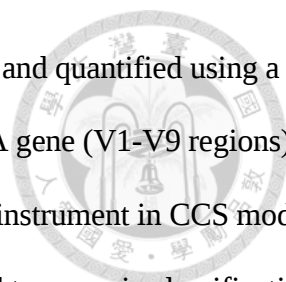
Assessment

Participants underwent comprehensive assessments including demographic data collection, laboratory testing, pulmonary function tests, asthma severity evaluation, and exacerbation monitoring. The Asthma Control Test (ACT) was employed to assess asthma control, with scores ranging from 5 to 25; scores below 20 indicated poorly controlled asthma²⁵. Asthma exacerbations were categorized as moderate or severe based on clinical criteria, with severe exacerbations requiring systemic corticosteroids or hospitalization²⁶.

Sample collection

Nasal and oral microbiome samples were collected by trained rhinologists from the middle meatus and oropharynx, ensuring strict protocols to prevent contamination. Swab samples were immediately stored at -80°C until processing.

Sample processing and sequencing



Genomic DNA was extracted using the QIAamp PowerFecal DNA Kit and quantified using a Qubit 4.0 Fluorometer. PCR amplification targeted the full-length 16S rRNA gene (V1-V9 regions) using barcoded primers. Sequencing was performed on a PacBio Sequel IIe instrument in CCS mode, with bioinformatic analysis conducted using DADA2 for ASV inference and taxonomic classification against the NCBI database. Diversity analyses included alpha and beta diversity metrics, with statistical comparisons performed using appropriate tests.

Sequence Analysis and Bioinformatic Processing

Circular consensus sequence (CCS) reads were generated with a minimum predicted accuracy of 0.9 and at least 3 passes using PacBio's official workflow through SMRT Link software. Following demultiplexing, CCS reads underwent further processing using DADA2 (version 1.20) to obtain amplicon sequence variants (ASVs) with single nucleotide resolution^{27,28}. The DADA2 workflow included quality filtering, dereplication, learning dataset-specific error models, ASV inference, and chimera removal, with trimming and filtering set to tolerate a maximum of two expected errors per read (maxEE = 2).

The DADA2 algorithm accurately resolves ASVs from the full-length 16S rRNA gene sequences with minimal error. Taxonomic classification was performed using the feature-classifier²⁹ and classify-consensus-vsearch³⁰ algorithms in QIIME2³¹, leveraging NCBI database information. Sequence similarity among ASVs was analyzed via multiple sequence alignment using MAFFT in QIIME2³²⁻³⁴.

Diversity Analysis

Alpha diversity metrics (Simpson index, Shannon index, Pielou evenness index, Observed features index, Menhinick's richness index, Margalef's richness index, and Faith index) were used to assess species complexity within individual samples. Community richness was evaluated using

Menhinick's and Margalef's richness indices, while Shannon and Simpson indices assessed diversity based on abundance and evenness.

Beta diversity analysis, utilizing weighted and unweighted UniFrac metrics^{4,5}, assessed differences in species complexity among samples. Principal Coordinate Analysis (PCoA)³⁵ and Non-metric multidimensional scaling (NMDS) were employed to visualize multidimensional data based on distance matrices³⁶. Anosim, MRPP, and supervised methods such as partial-least-squares discriminant analysis (PLS-DA) and t-distributed stochastic neighbor embedding (t-SNE) were used to evaluate community structure differences and identify significant biomarkers. Hierarchical clustering via Unweighted Pair-group Method with Arithmetic Means (UPGMA) was performed to interpret arithmetic distances.

Statistical analyses included Welch's t-test for continuous variables to determine significant biomarkers, conducted using R software with phyloseq, vegan, mixOmics, and stat packages. Linear discriminant analysis of effect size (LEfSe) combined with linear discriminant analysis (LDA) was adopted to explore the differences in taxonomic composition³⁷. In this study, taxa with LDA score $(\log_{10}) > 4$ was considered significant.

Statistical Analysis

Continuous variables were presented as median $\pm$ standard deviation and compared using the Mann-Whitney U test. Categorical variables were expressed as percentages and compared using the chi-square test. Using Pearson correlation, we statistically analyzed the relationship between alpha diversity and ACT score, eosinophil count, IgE level, and value of FEV1/FVC. Statistical significance was defined as $p < 0.05$.



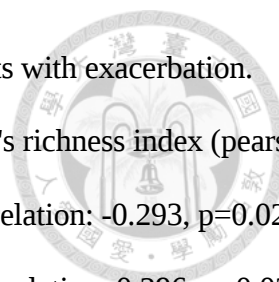
Result

Patient cohort

In total, 61 patients with asthma were enrolled in the study. The mean patient age was 44 years (range: 21–72 years). Men comprised 18% (11/61) of all patients. Twenty-eight patients had poorly controlled asthma initially. Twenty-eight percent (17/61) had an eosinophil count >300 cells/ μL , and 60.7% had allergies. The median IgE level was 64.7 IU/mL (range: <4.45 –1710 IU/mL). Nine patients had an obstructive lung pattern. There were no significant differences in these characteristics between the exacerbation and non-exacerbation groups. Within the 3-month period, 34% of the patients experienced exacerbations. The clinical characteristics of the patients are summarized in Table 1.

Nasal microbiome in patients with asthma

The quality of nasal samples is shown in Figure 1. A plateau suggests sufficient sampling in nasal microbiome. The quality of 13 samples was relatively poor. Among all samples, the Rank Abundance Curve of the nasal microbiome is shown in Figure 2. The length of the curve represents species richness; a longer curve indicates a greater number of species within the community. The curve indicated that nasal species richness was lower in patients with exacerbated asthma than in those with non-exacerbated asthma. Alpha diversity of the nasal microbiome is shown in Figure 3. The index of nasal alpha diversity tended to be lower in patients with exacerbation compared to those without exacerbation, including Shannon index (3.35 ± 1.75 vs. 4.06 ± 1.38 , Wilcoxon P value = 0.11), Simpson index (0.76 ± 0.22 vs. 0.85 ± 0.20 , Wilcoxon P value = 0.18), Pielou evenness index (0.56 ± 0.19 vs. 0.67 ± 0.19 , Wilcoxon P value = 0.12), Observed features index (63.00 ± 66.64 vs. 60.00 ± 42.65 , Wilcoxon P value = 0.088), Menhinick's richness index (0.60 ± 0.54 vs. 0.66 ± 0.41 , Wilcoxon P value = 0.11), Margalef's richness index (4.88 ± 7.23 vs. 7.05 ± 3.98 , Wilcoxon P value = 0.077), and Faith index (9.83 ± 6.73 vs. 12.33 ± 8.80 , Wilcoxon P value = 0.100). The richness and



evenness of bacterial species in the nasal cavity tended to be lower in patients with exacerbation. Observed features index (pearson ccorrelation: -0.295, $p=0.021$), Menhinick's richness index (pearson ccorrelation: -0.260, $p=0.043$), and Margalef's richness index (pearson ccorrelation: -0.293, $p=0.022$) correlated negatively with ACT score (Figure 4A). Faith index (pearson ccorrelation: 0.296, $p=0.020$) correlated positively with eosinophil count (Figure 4B). Nasal alpha diversity index was not associated with IgE level and value of FEV1/FVC (Figure 4C and 4D).

Microbiome compositions between the two groups were measured by NMDS, PCA, PCoA, PLS-DA, tSNE and UPGMA (Figure 5). The community structures between two groups statistically differed by MRPP ($P = 0.037$) but not by Anosim ($P = 0.257$) and PERANOVA. ($P = 0.096$). The results exhibited the specific structure in nasal bacterial community composition among subjects with and without exacerbation.

There was a total of 3269 nasal ASVs, of which 5.9% were common to both the exacerbation and non-exacerbation groups (Figure 6A). The most common nasal bacterial communities at the phylum level were *Proteobacteria*, followed by *Firmicutes* and *Actinobacteria* (Figure 6B1, 6B2 and 6B3). The most common nasal bacterial communities at the species level were *Bradyrhizobium embrapense*, followed by *Corynebacterium accolens* (Figure 6C1, 6C2, 6C3 and 6C4). Then, we used Welch's t-test to find significant differences in the nasal community between the two groups. Patients with exacerbation had a lower proportion of nasal *Cutibacterium acnes* ($1.44\pm2.14\%$ vs. $4.11\pm6.34\%$, P value = 0.019), *Anaerococcus octavius* ($0.06\pm0.26\%$ vs. $0.54\pm1.31\%$, P value = 0.029), *Pseudomonas yamanorum* ($0.02\pm0.08\%$ vs. $0.40\pm0.97\%$, P value = 0.019), *Acinetobacter johnsonii* ($0.02\pm0.08\%$ vs. $0.07\pm0.19\%$, P value = 0.015), *Pseudobdellovibrio exovor* ($0.01\pm0.03\%$ vs. $0.13\pm0.27\%$, P value = 0.037), and *Brevibacillus marinus* ($0.002\pm0.01\%$ vs. $0.05\pm0.14\%$, P value = 0.032) at the species level (Figure 7A1 and 7A2, Supplementary table 1), had a lower proportion of nasal *Cutibacterium* ($1.55\pm2.19\%$ vs. $4.36\pm6.42\%$, P value = 0.015), *Anaerococcus* ($0.09\pm0.36\%$ vs. $1.02\pm2.36\%$, P value = 0.018), *Lactobacillus* ($0.00\pm0.00\%$ vs. $0.34\pm0.95\%$, P value = 0.031), *Blautia*

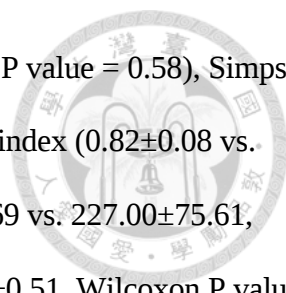
($0.001 \pm 0.004\%$ vs. $0.11 \pm 0.34\%$, P value = 0.039), *Pseudobdellovibrio* ($0.01 \pm 0.03\%$ vs. $0.07 \pm 0.19\%$, P value = 0.036), *Brevibacillus* ($0.003 \pm 0.01\%$ vs. $0.06 \pm 0.13\%$, P value = 0.016) at the genus level (Figure 7B), and had a lower proportion of nasal *Cyanobacteria* ($0.00 \pm 0.00\%$ vs. $0.02 \pm 0.07\%$, P value = 0.046) at the phylum level (Figure 6C). We used LEfSe analysis. The samples from patients with exacerbated asthma were less enriched with *Cutibacterium acnes* (species) (LAD > 4.0, P = 0.008) and *Burkholderiales* (order) (LDA > 4.0, P = 0.45) (Figure 7D).

Among 48 samples with good quality, Alpha diversity of the nasal microbiome is shown in Figure 2. The index of nasal alpha diversity tended to be lower in patients with exacerbation compared to those without exacerbation, including Shannon index (3.54 ± 1.69 vs. 3.92 ± 1.68 , Wilcoxon P value = 0.156), Simpson index (0.76 ± 0.22 vs. 0.85 ± 0.23 , Wilcoxon P value = 0.073), and Observed features index (63.00 ± 33.69 vs. 64.00 ± 63.67 , Wilcoxon P value = 0.154). The richness and evenness of bacterial species in the nasal cavity tended to be lower in patients with exacerbation. Shannon index (pearson ccorrelation: -0.295, $p=0.021$), and Observed features index (pearson ccorrelation: -0.260, $p=0.043$) correlated negatively with ACT score (Figure 9A). Nasal alpha diversity index was not associated with eosinophil count, IgE level and value of FEV1/FVC (Figure 9B, 9C and 9D).

Microbiome compositions between the two groups were measured by NMDS, PCA, and PCoA (Figure 10). The community structures between two groups did not differ by Anosim (P = 0.523) and PERANOVA. (P = 0.517). The results demonstrated a similar structure in nasal bacterial community composition among subjects with and without exacerbation.

Oral microbiome in patients with asthma

The Rank Abundance Curve of the oral microbiome is shown in Figure 11. The curve indicated that nasal species richness was mildly lower in patients with exacerbated asthma than in those with non-exacerbated asthma. Alpha diversity of the oral microbiome is shown in Figure 12. The index of oral alpha diversity tended to be lower in patients with exacerbation compared to those without

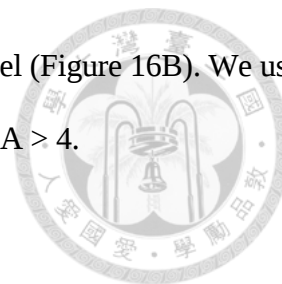


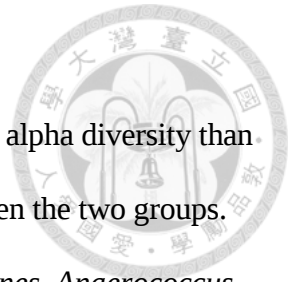
exacerbation, including Shannon index (6.40 ± 0.89 vs. 6.33 ± 0.81 , Wilcoxon P value = 0.58), Simpson index (0.97 ± 0.05 vs. 0.97 ± 0.05 , Wilcoxon P value = 0.44), Pielou evenness index (0.82 ± 0.08 vs. 0.80 ± 0.07 , Wilcoxon P value = 0.27), Observed features index (238.00 ± 66.69 vs. 227.00 ± 75.61 , Wilcoxon P value = 1.000), Menhinick's richness index (1.67 ± 0.45 vs. 1.66 ± 0.51 , Wilcoxon P value = 0.22), Margalef's richness index (23.84 ± 6.1 vs. 22.78 ± 7.43 , Wilcoxon P value = 0.83), and Faith index (13.12 ± 1.93 vs. 12.58 ± 3.54 , Wilcoxon P value = 0.33). The richness and evenness of bacterial species in the oral cavity showed no differences between the two groups. Oral alpha diversity index was not associated with ACT score, eosinophil count, IgE level or value of FEV1/FVC (Figure 13A, 13B, 13C and 13D).

Microbiome compositions between the two groups were measured by NMDS, PCA, PCoA, PLS-DA, tSNE and UPGMA (Figure 14). The community structures between two groups statistically not differed by MRPP (P = 0.912), Anosim (P = 0.260) and PERANOVA. (P = 0.887). In other words, the results demonstrated a similar structure in oral bacterial community composition among subjects with and without exacerbation.

There was a total of 9775 oral ASVs, of which 11.9% were common to both the exacerbation and non-exacerbation groups (Figure 15A). The most common oral bacterial communities at the phylum level were *Firmicutes*, followed by *Proteobacteria* and *Bacteroidota* (Figure 11B1, 11B2 and 11B3). At the species level, the most common bacteria were *Neisseria perflava*, followed by *Streptococcus salivarius* (Figure 15C1, 15C2, 15C3 and 15C4). Welch's t-test identified significant differences in the oral community between the two groups. Patients with exacerbation had a lower proportion of oral *Streptococcus sanguis* ($0.29 \pm 0.32\%$ vs. $0.69 \pm 1.08\%$, P value = 0.036), *Streptococcus gwanjuense* ($0.02 \pm 0.05\%$ vs. $0.16 \pm 0.43\%$, P value = 0.041), *Actinomyces graevenitzi* ($0.04 \pm 0.06\%$ vs. $0.17 \pm 0.38\%$, P value = 0.033), *Butyrivibrio hungatei* ($0.01 \pm 0.02\%$ vs. $0.04 \pm 0.06\%$, P value = 0.047), and *Leptotrichia buccalis* ($0.004 \pm 0.01\%$ vs. $0.02 \pm 0.05\%$, P value = 0.035) at the species level (Figure 16A1 and 16A2, supplementary table 2), and had a lower proportion of oral

Butyrivibrio ($0.02 \pm 0.02\%$ vs. $0.04 \pm 0.06\%$, P value = 0.048) at the genus level (Figure 16B). We used LEfSe analysis. The two groups showed no differences in bacteria when $LDA > 4$.

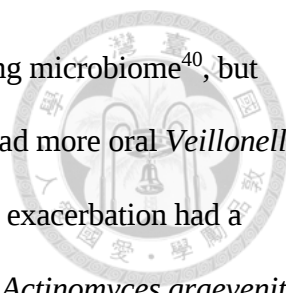




Discussion

In our study, we found that patients with exacerbated asthma had lower alpha diversity than those without exacerbations. The nasal bacterial composition differed between the two groups. Patients with exacerbation had a lower proportion of nasal *Cutibacterium acnes*, *Anaerococcus octavius*, *Pseudomonas amonius*, *Acinetobacter johnsonii*, *Pseudobdellovibrio exovor*, and *Brevibacillus marinus*. *Cutibacterium acnes*, *Anaerococcus octavius* and *Acinetobacter johnsonii* at species level, had a lower proportion of nasal *Cutibacterium*, *Anaerococcus*, *Lactobacillus*, *Blautia*, *Pseudobdellovibrio*, and *Brevibacillus* at the genus level, and had a lower proportion of nasal *Cyanobacteria* at the phylum level. There were no differences in oral bacterial richness, evenness, and composition between the two groups. However, patients with exacerbations had a lower proportion of oral *Streptococcus sanguis*, *Streptococcus gwanjuense*, *Actinomyces graevenitzii*, *Butyrivibrio hungatei*, and *Leptotrichia buccalis* at species level and had a lower proportion of oral *Butyrivibrio* at the genus level.

The nasal microbiome acts as a primary defense against inhaled pathogens and allergens. *Haemophilus*, *Moraxella*, and *Streptococcus* in the upper airway were associated with increased exacerbations in childhood asthma⁸. Our study focused on adult asthma and indicated that the nasal bacterial composition differed between the two groups. Patients without exacerbation had a higher proportion of nasal *Cutibacterium*, *Anaerococcus*, *Lactobacillus*, *Blautia*, *Pseudobdellovibrio*, and *Brevibacillus* at the genus level. *Lactobacillus* in gut was associated with decreased risk of atopy³⁸. *Lactobacillus* strains have been shown to influence the immune system by modulating cytokine production, enhancing the activity of regulatory T cells, and improving the gut barrier function³⁹. This can lead to a more balanced immune response and reduced inflammation, which is crucial in managing allergic reactions and asthma³⁹. More clinical trials and longitudinal studies are required to confirm the efficacy and safety of specific *Lactobacillus* strains in preventing and managing asthma.

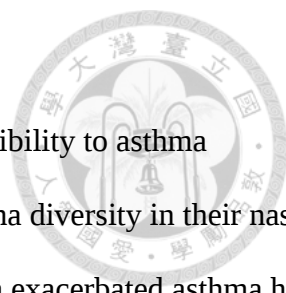


The oral microbiome significantly influences the composition of the lung microbiome⁴⁰, but studies on the oral microbiome in asthma are limited. Patients with asthma had more oral *Veillonella* and less *Streptococcus* than healthy subjects⁴¹. In our study, patients without exacerbation had a higher proportion of oral *Streptococcus sanguis*, *Streptococcus gwanjuense*, *Actinomyces graevenitzi*, *Butyrivibrio hungatei*, and *Leptotrichia buccalis* at the species level, and had a higher proportion of oral *Butyrivibrio* at the genus level. These bacteria have not been proven to be associated with asthma. However, there is limited research on the oral microbiome in asthma, and the oral microbiome can affect the lung microbiome. Further studies are needed to verify the relationships and mechanisms involved.

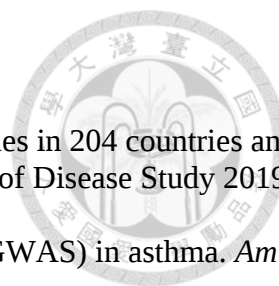
Previous microbiome studies commonly used partial sequencing of 16S rRNA regions. The advantages of this method include shorter read length, which reduces sequencing costs and data processing requirements, and its suitability for large-scale studies due to efficient amplification and sequencing. However, it may not distinguish between closely related species, and the specific primers used for partial region amplification might not universally amplify all bacterial taxa, potentially leading to biased results. The newer technique is full-length sequencing. The benefits of this method include coverage of all hypervariable regions, offering the highest taxonomic resolution, and a greater likelihood of identifying rare and less abundant bacteria due to full-length sequencing. However, full-length sequencing is more expensive and data-intensive, and longer reads may reduce the number of samples that can be processed simultaneously^{15,16}.

Some limitations were found in our study. First, although all participants had no history of antibiotic use or systemic steroid therapy within the past 3 months, we cannot entirely exclude the possibility that medication may influence the nasal and oral bacterial composition. Second, the sample size was small. Third, our study did not include healthy individuals, so it was not possible to compare the differences between healthy individuals and asthma patients.

Conclusion

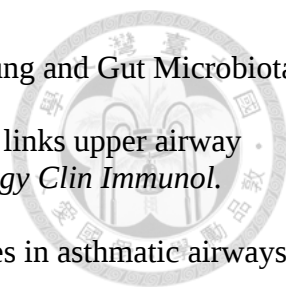


The nasal microbiome may be an important factor influencing susceptibility to asthma exacerbations. Patients with exacerbated asthma seemed to have lower alpha diversity in their nasal microbiome compared to those with non-exacerbated asthma. Patients with exacerbated asthma had a lower proportion of nasal *Cutibacterium*, *Anaerococcus*, *Lactobacillus*, *Blautia*, *Pseudobdellovibrio*, and *Brevibacillus* at the genus level. There were no significant differences in the alpha diversity and beta diversity of the oral microbiome between patients who had experienced exacerbations and those who had not. This study did not include healthy individuals for comparison, and the sample size was relatively small. Further animal studies are needed to explore the mechanisms by which nasal microbiome may influence susceptibility to asthma exacerbations.

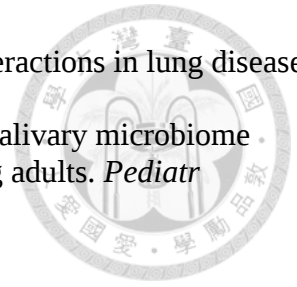


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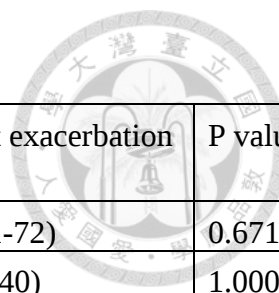
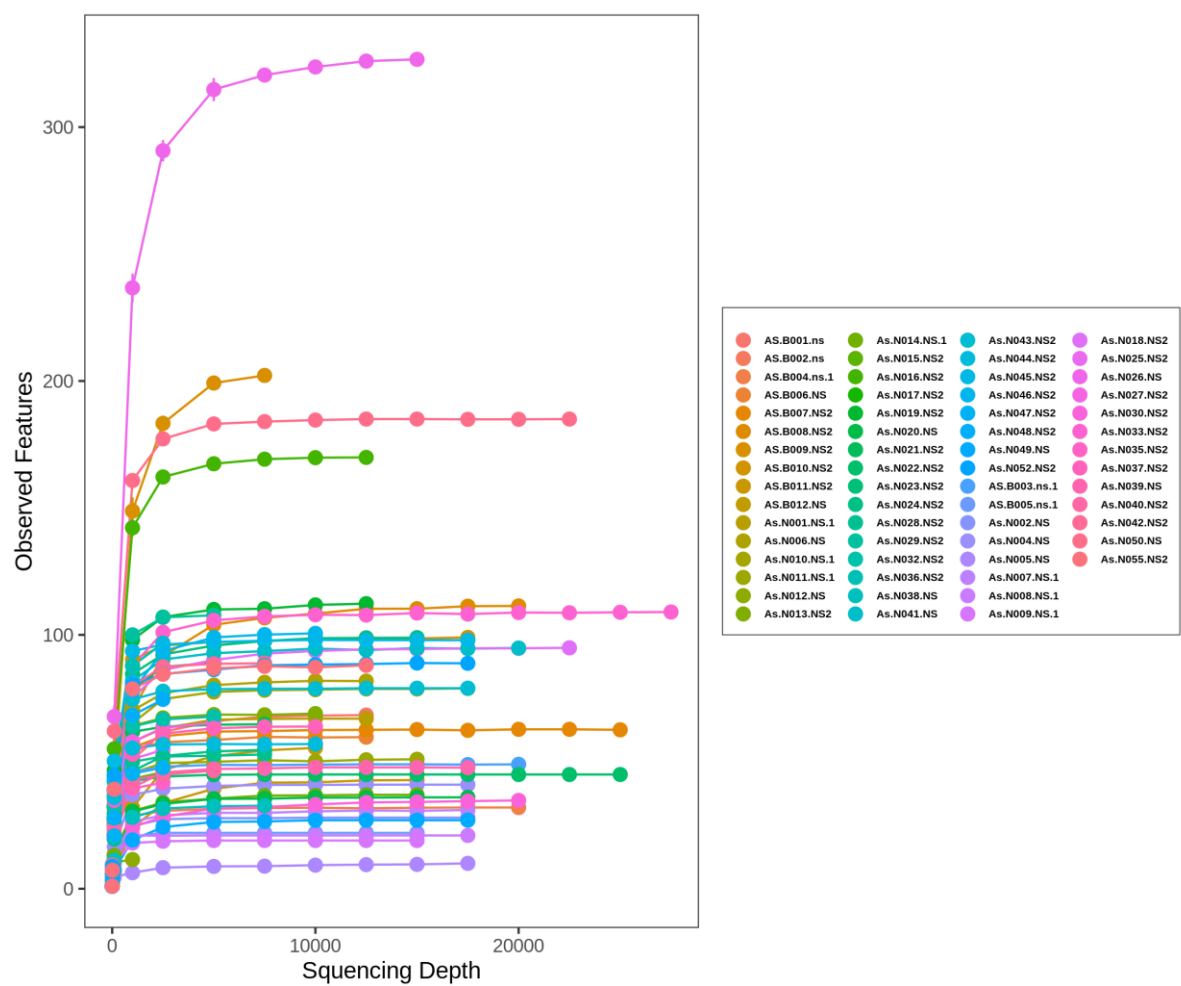


Table 1. Characteristics of patients with asthma

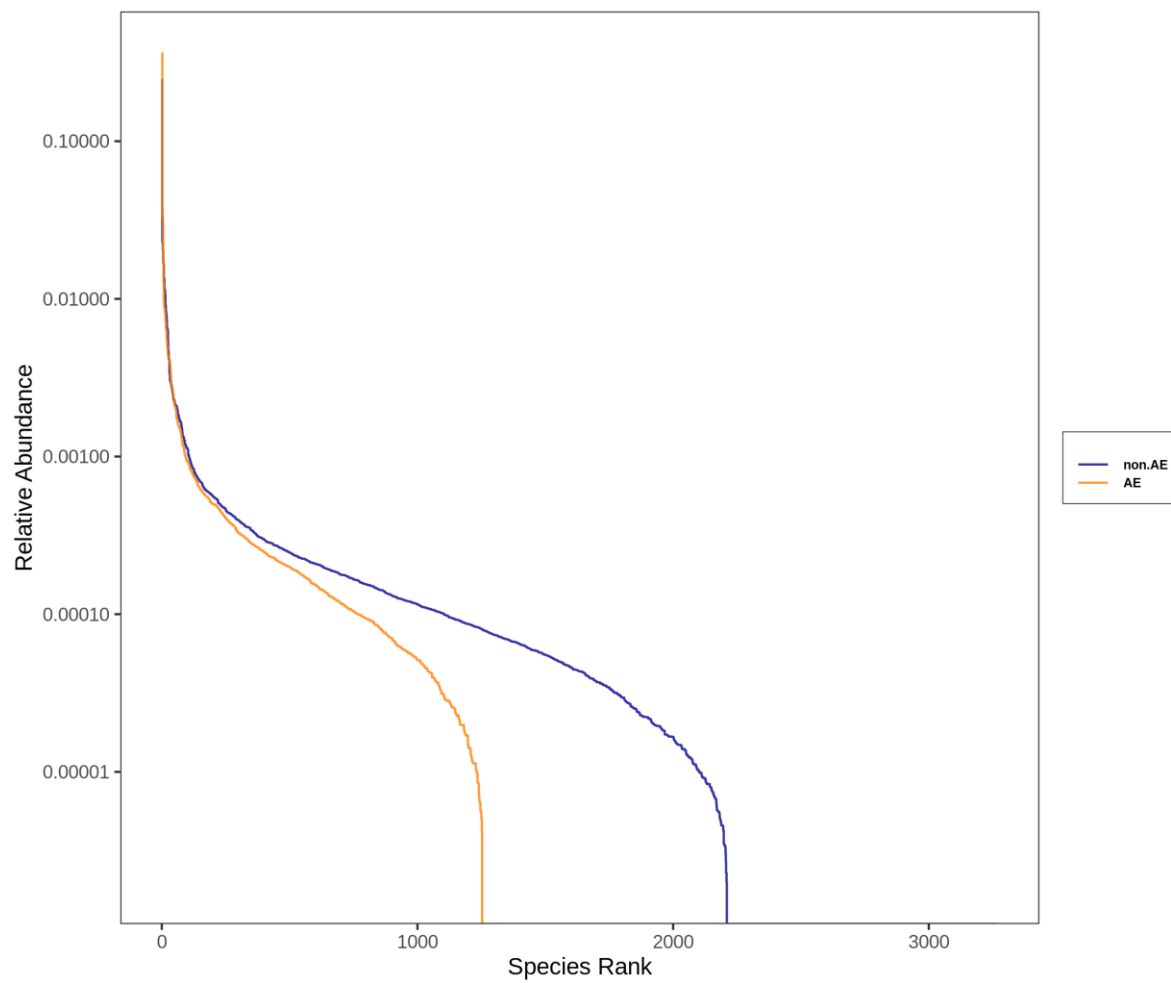
	All (n=61)	With exacerbation (n=21)	Without exacerbation (n=40)	P value
Age	44 (21-72)	44 (22-71)	43.5 (21-72)	0.671
Man	19.7% (12/61)	19% (4/21)	20% (8/40)	1.000
ACT	22 (12-25)	22 (12-25)	22 (16-25)	0.630
ACT<20	27.9% (17/61)	38.1% (8/21)	22.5% (9/40)	0.237
Eosinophil	158 (0-1527)	142 (0-420)	16.3 (17-1527)	0.093
Eosinophil ≥30	27.9% (17/61)	14.3% (3/21)	35.0% (14/40)	0.113
IgE	64.7 (<4.45-1710)	64.7 (5.1-1541)	78.3 (<4.45-1710)	0.927
Allergy	60.7% (37/61)	47.6% (10/21)	67.5% (27/40)	0.171
Obstructive lung pattern (FEV1/FVC<0.7)	14.8% (9/61)	9.5% (2/21)	17.5% (7/40)	0.479



Figure 1. Rarefaction Curve of the nasal microbiome.



**Figure 2. Rank Abundance Curve of the nasal microbiome. AE= with exacerbation;
non.AE=without exacerbation**



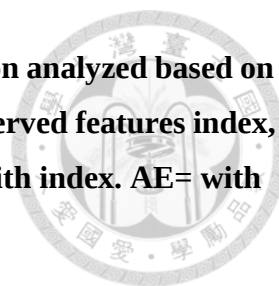
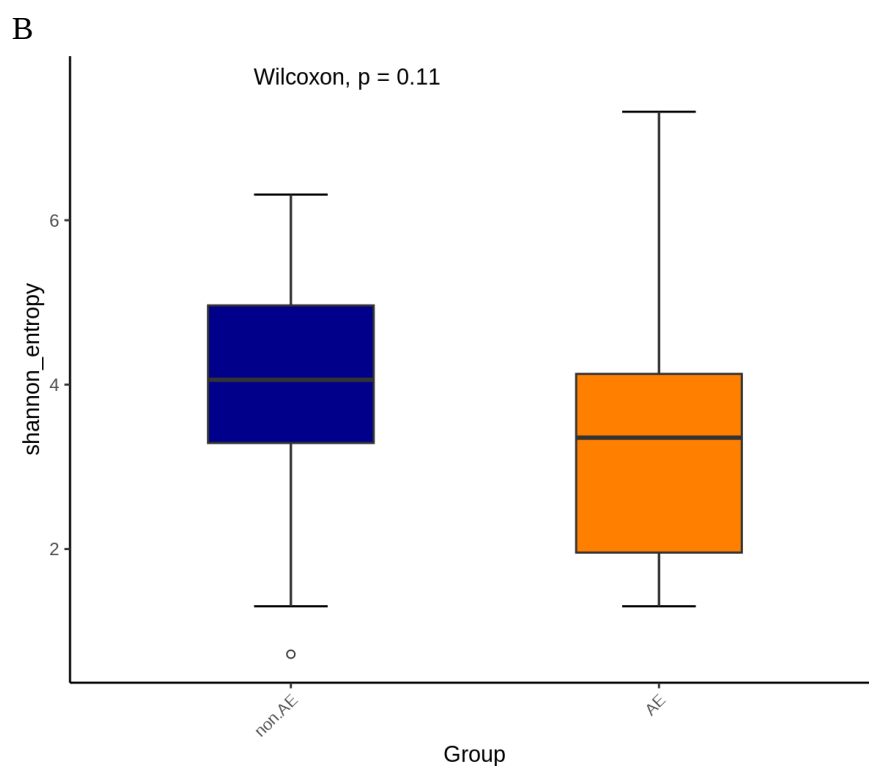
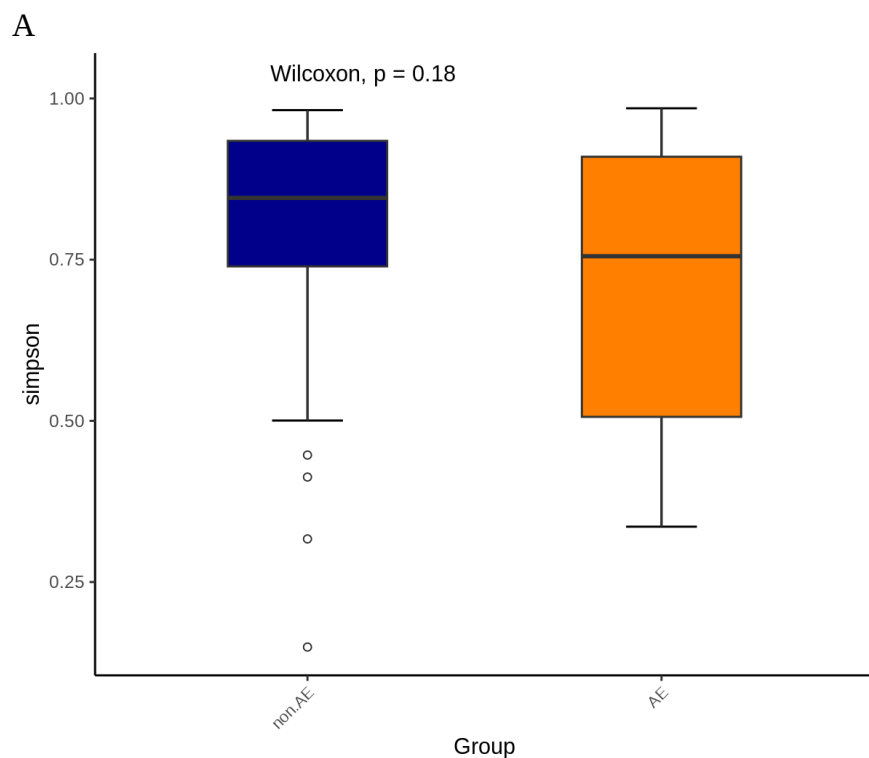
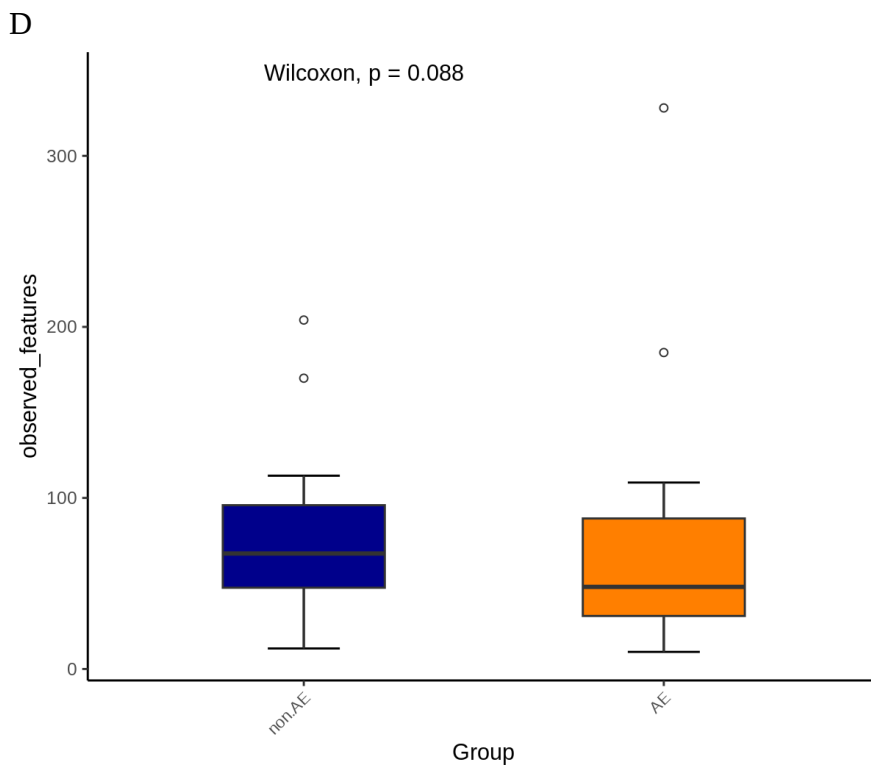
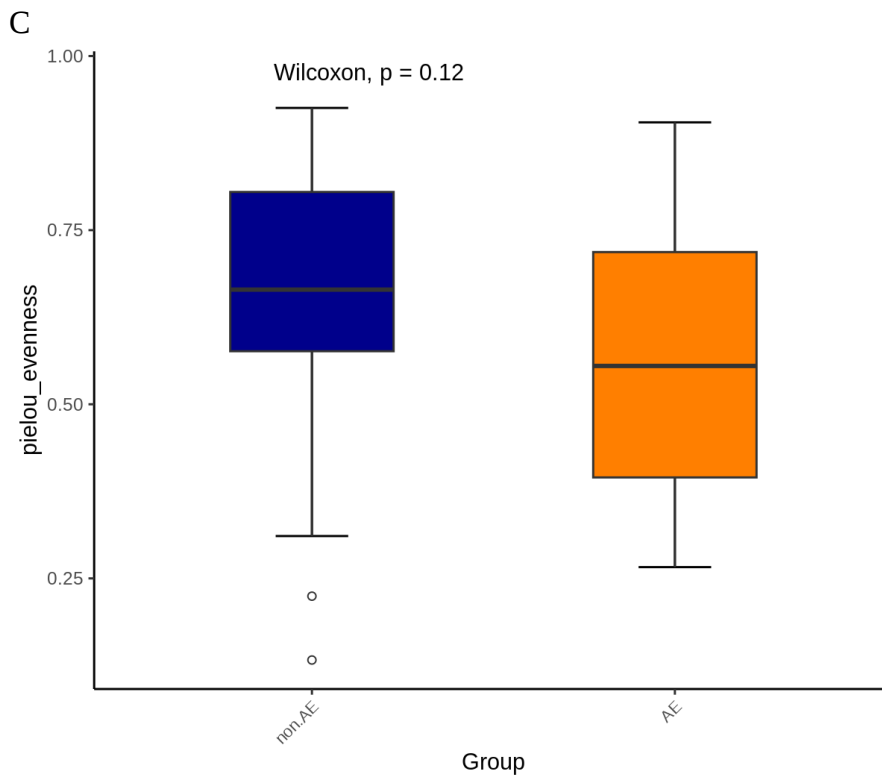
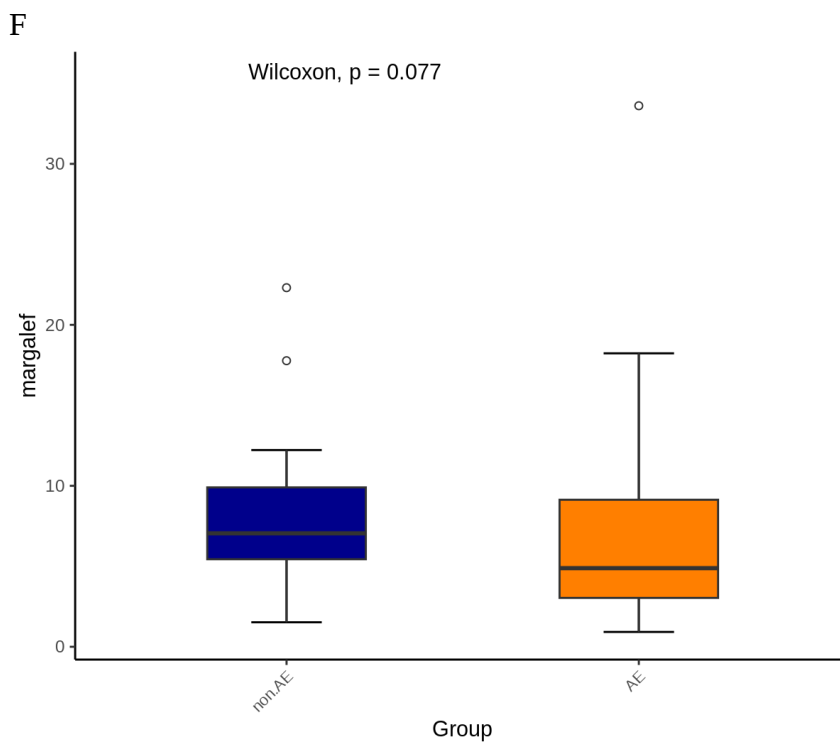
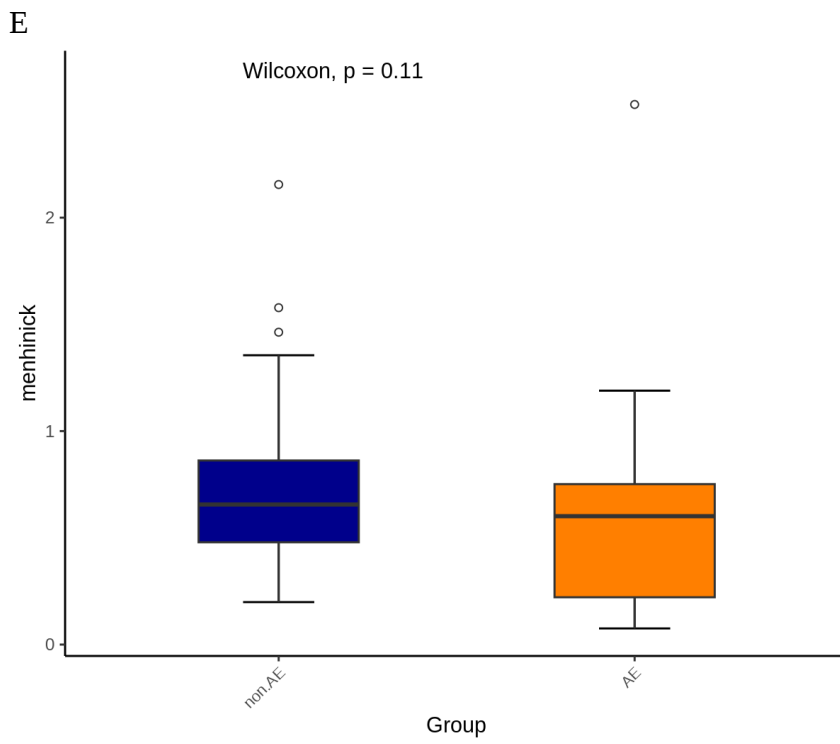


Figure 3. Nasal alpha diversity in asthma with and without exacerbation analyzed based on (A) Simpson index, (B) Shannon index, (C) Pielou evenness index, (D) Observed features index, (E) Menhinick's richness index, (F) Margalef's richness index, and (G) Faith index. AE= with exacerbation; non.AE=without exacerbation







G

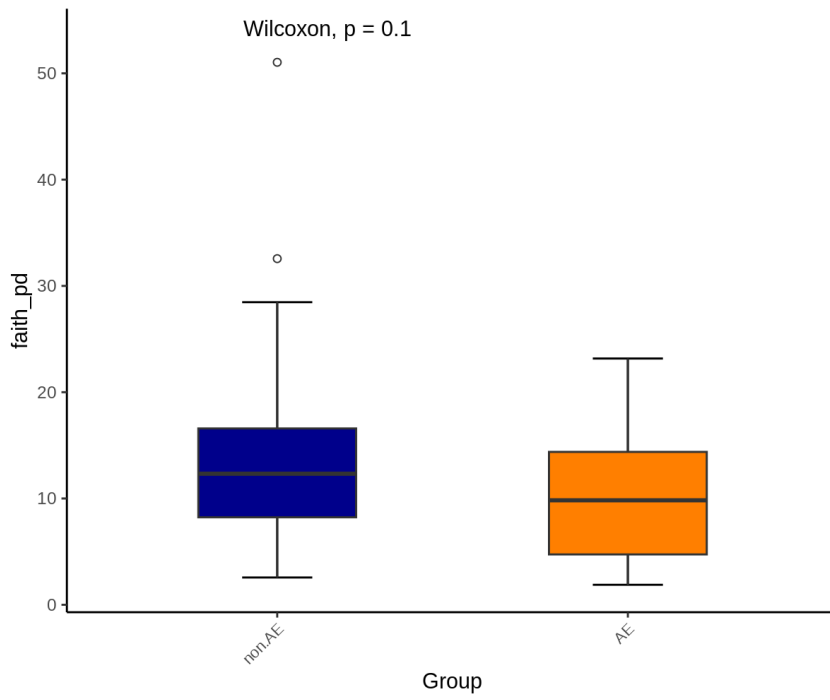
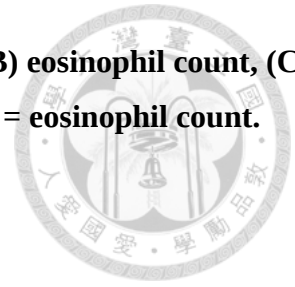
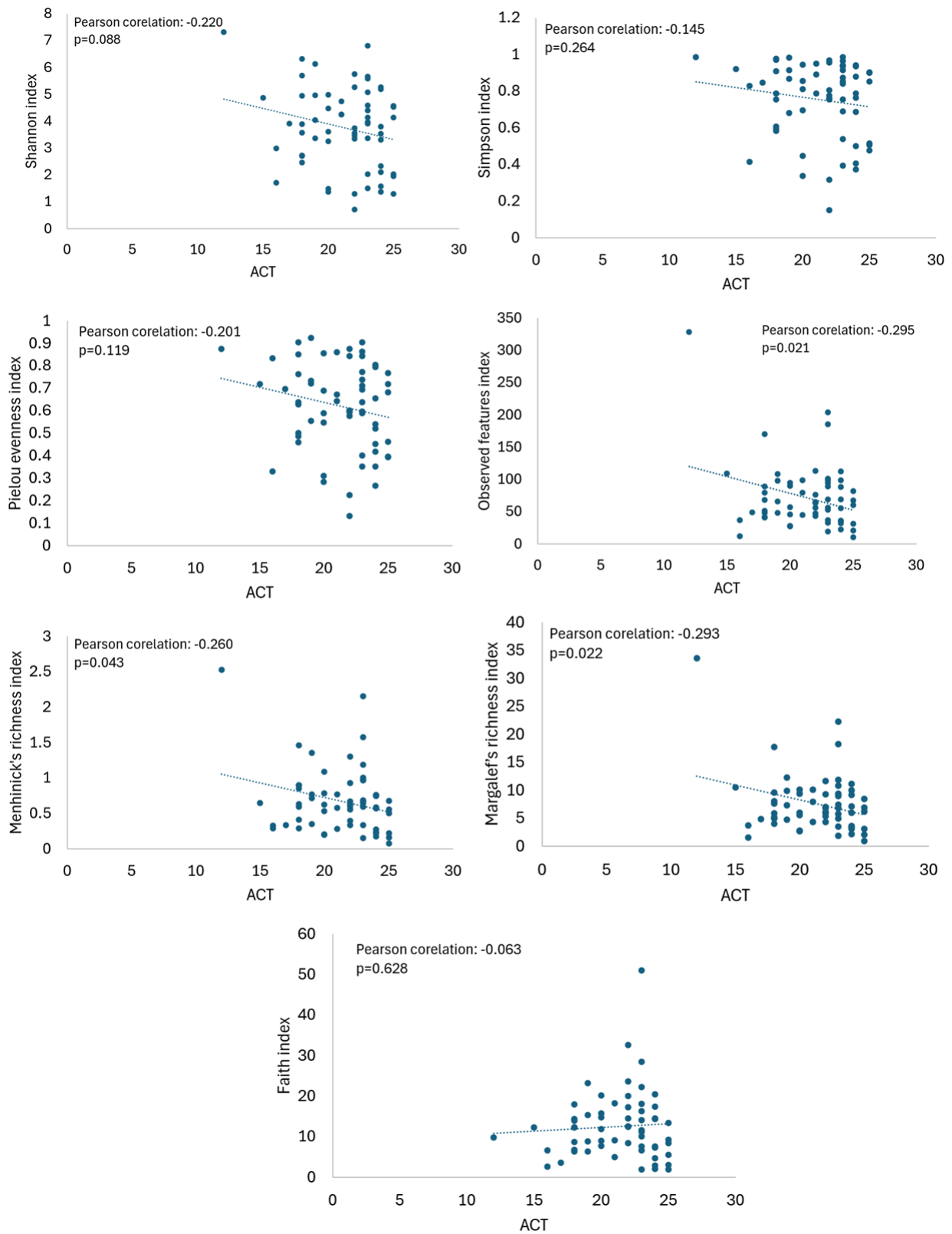


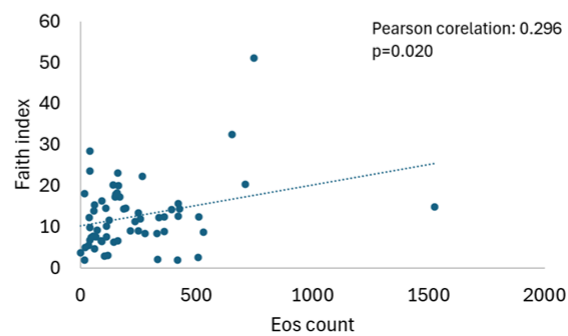
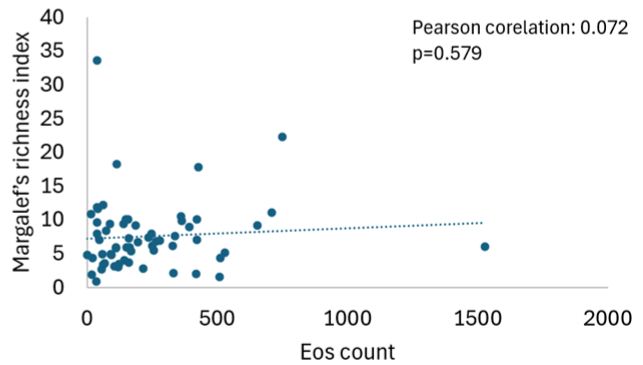
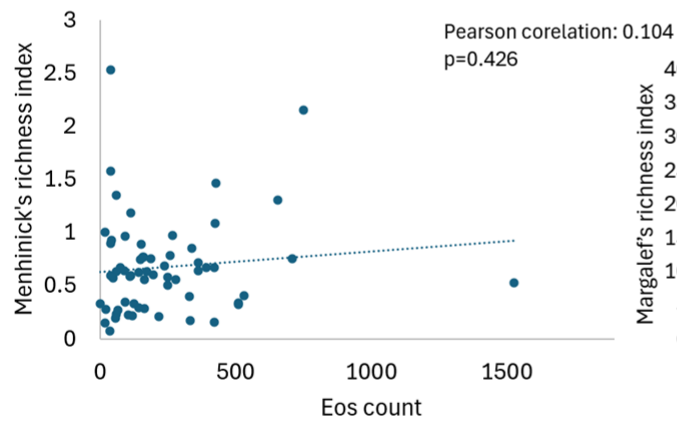
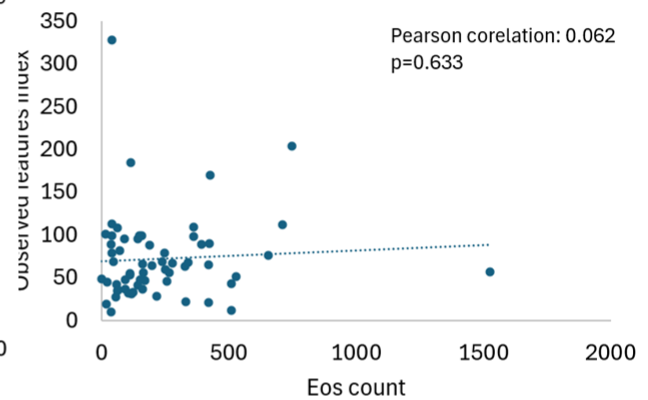
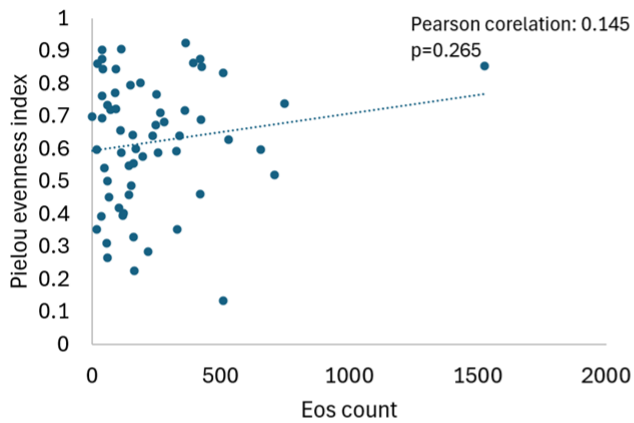
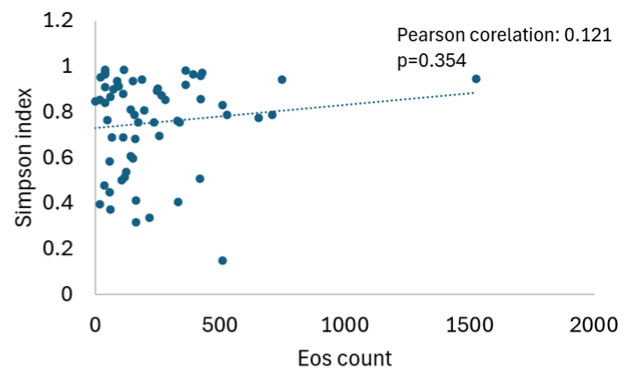
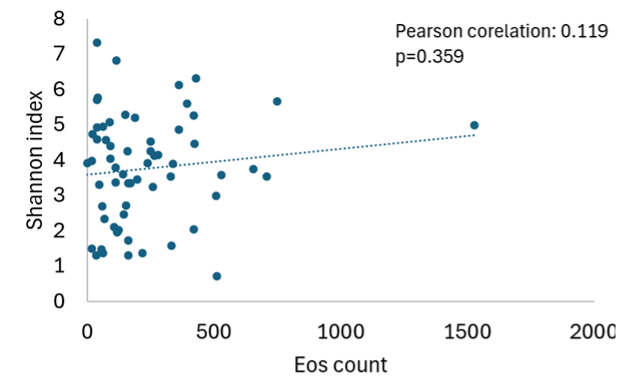
Figure 4. Relationships of nasal alpha diversity with (A) ACT score, (B) eosinophil count, (C) IgE level, and (D) lung function. ACT = asthma control test; ess count = eosinophil count.

A



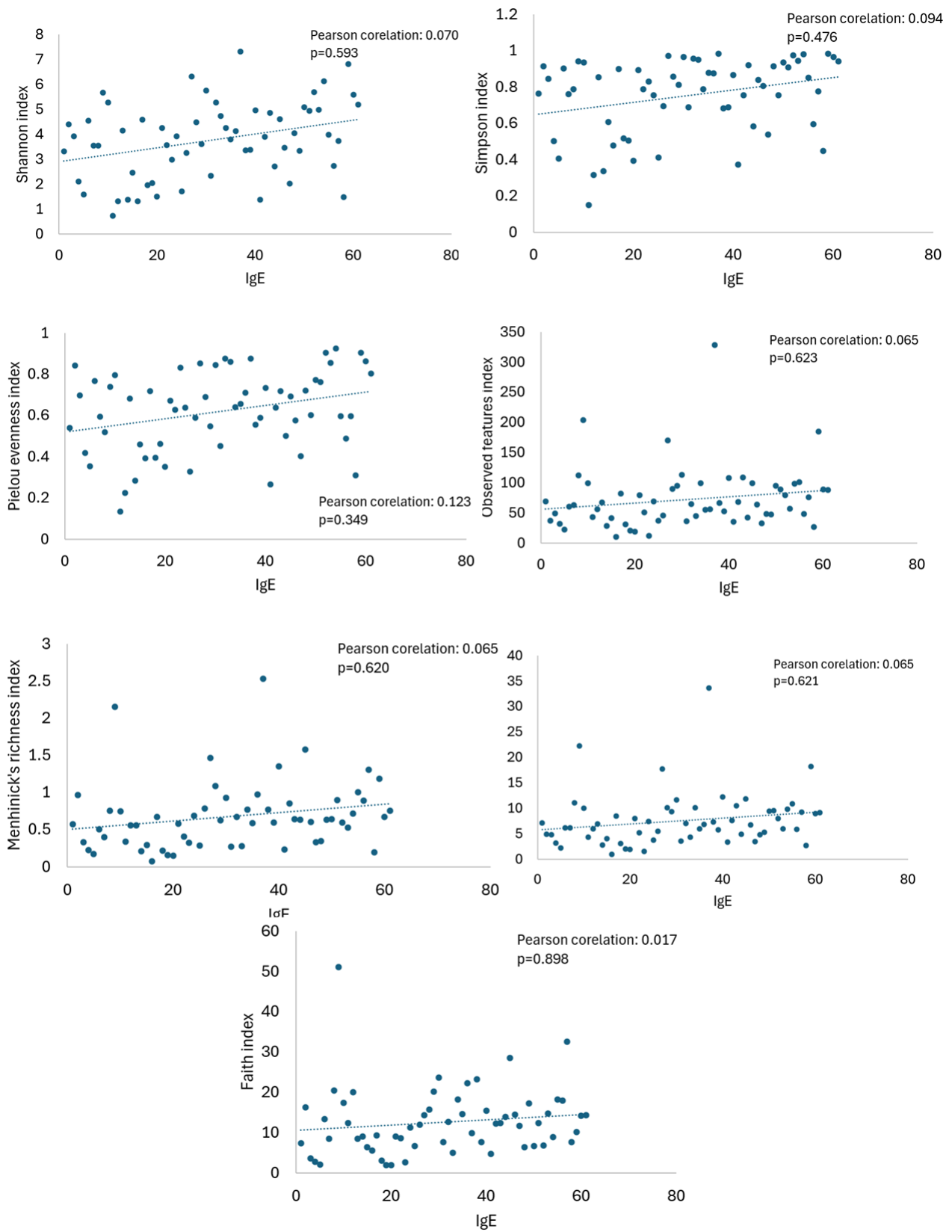


B



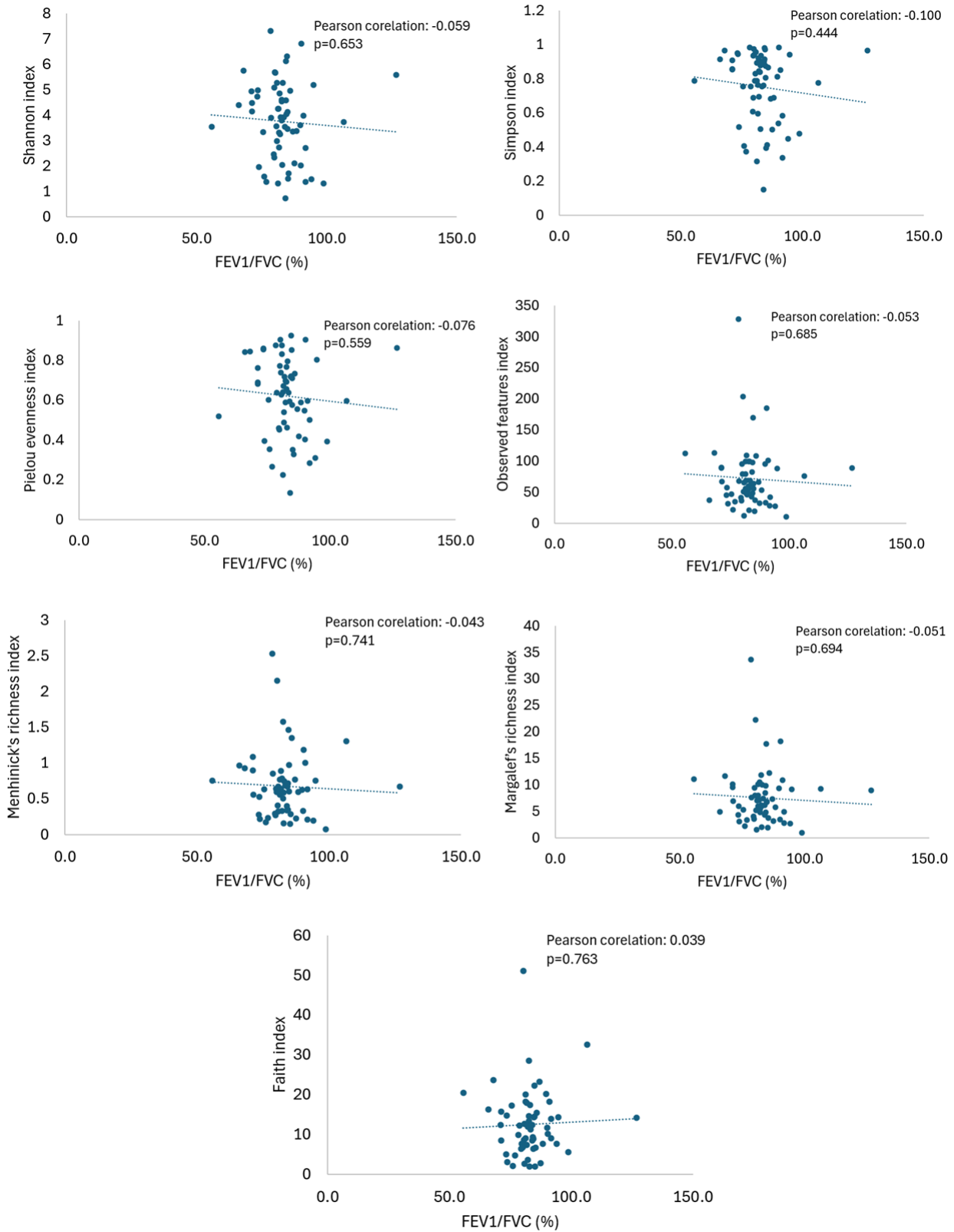


C





D



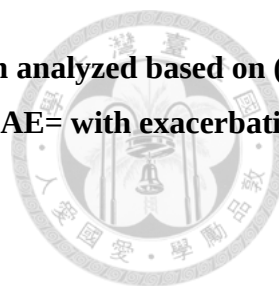
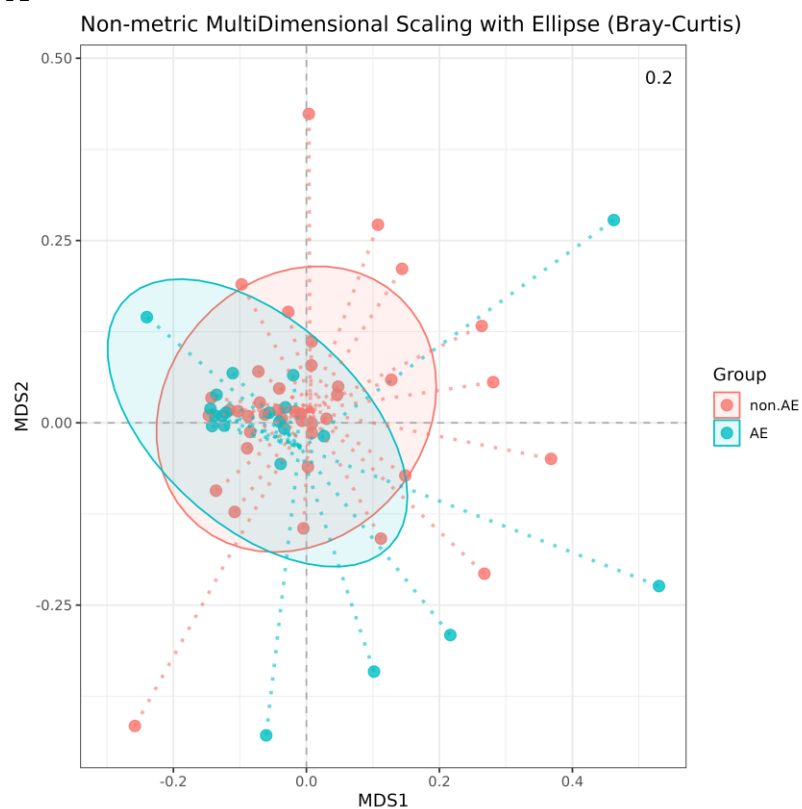


Figure 5. Nasal beta diversity in asthma with and without exacerbation analyzed based on (A) NMDS, (B) PCA, (C) PCoA, (D) PLS-DA, (E) tSNE, and (F) UPGMA. AE= with exacerbation; non.AE=without exacerbation

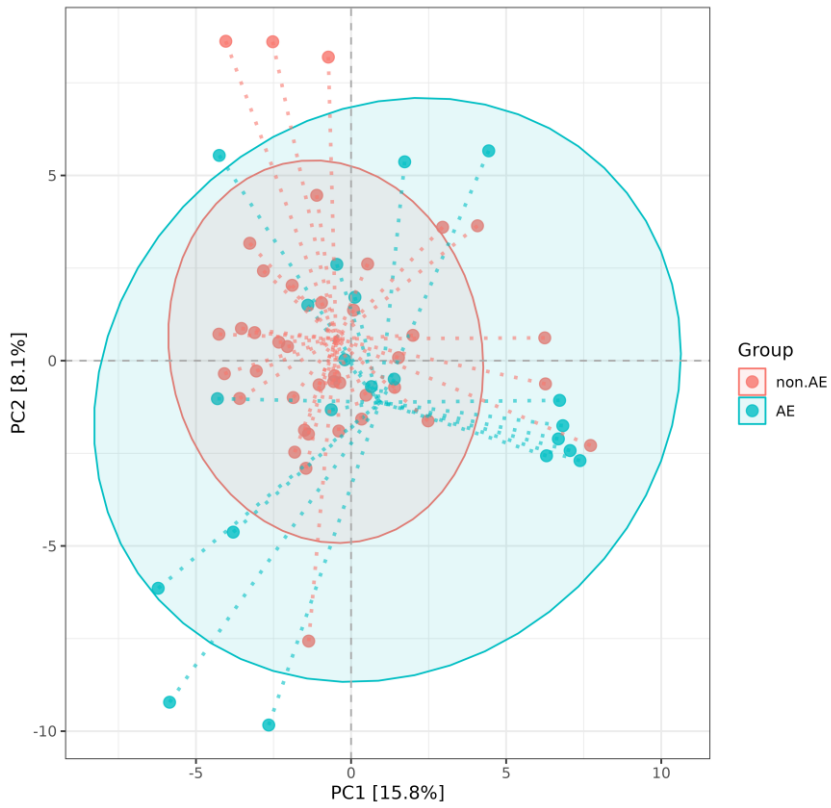
A





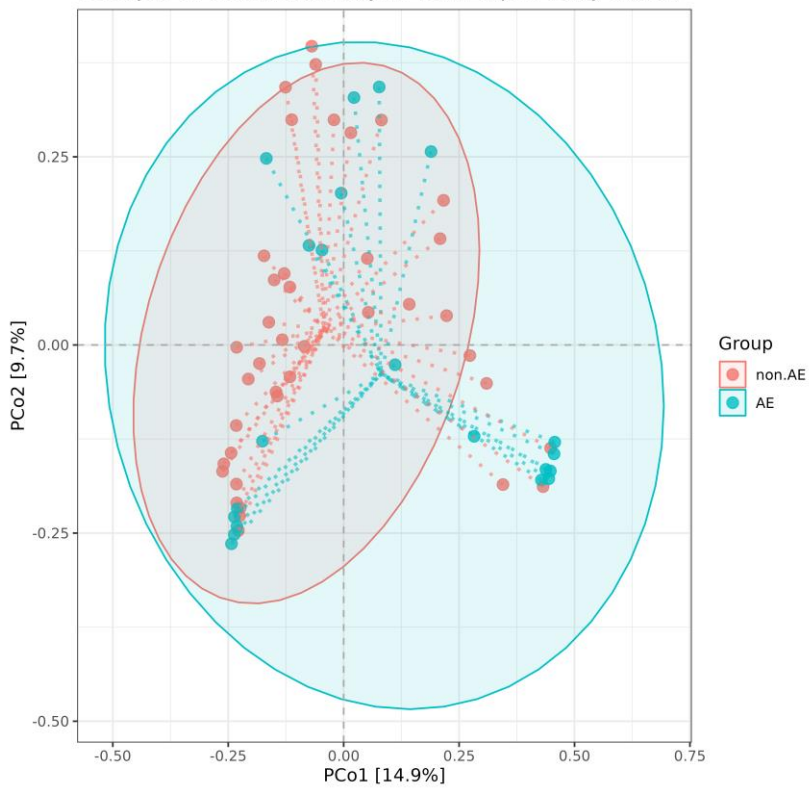
B

Principal Components Analysis with Ellipse

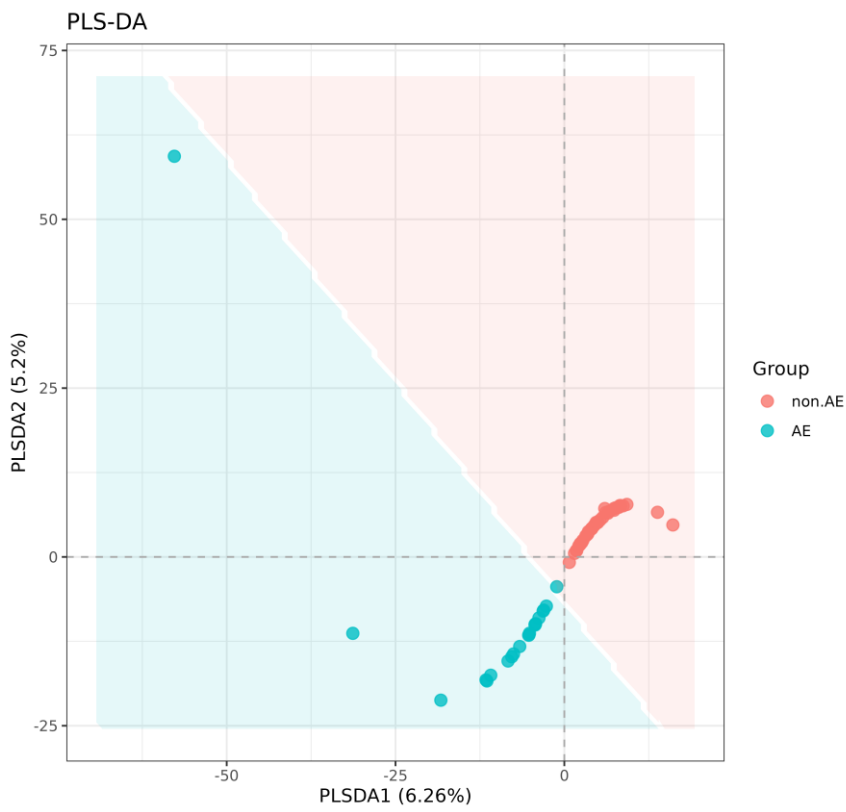


C

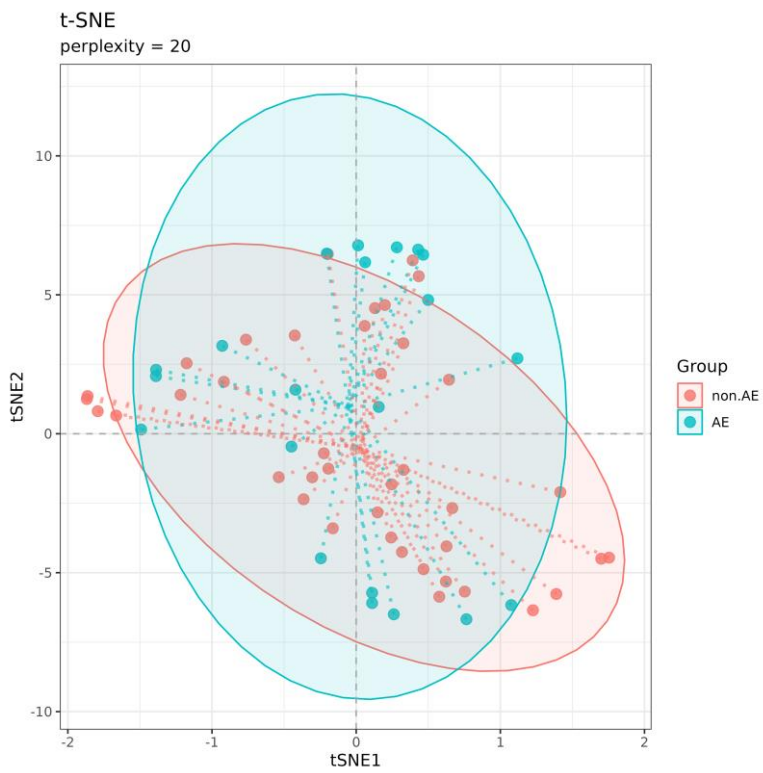
Principal Co-ordinates Analysis with Ellipse (Bray-Curtis)



D



E



F

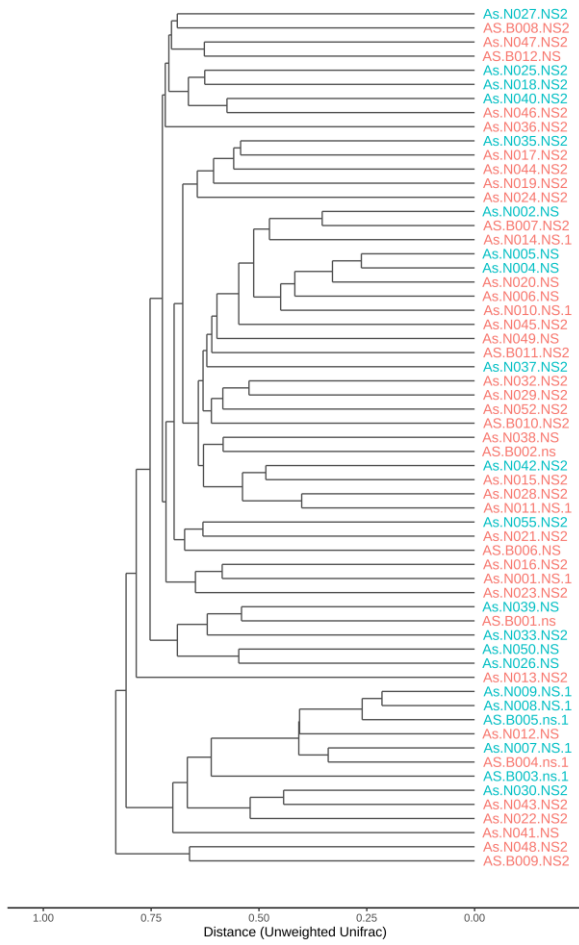
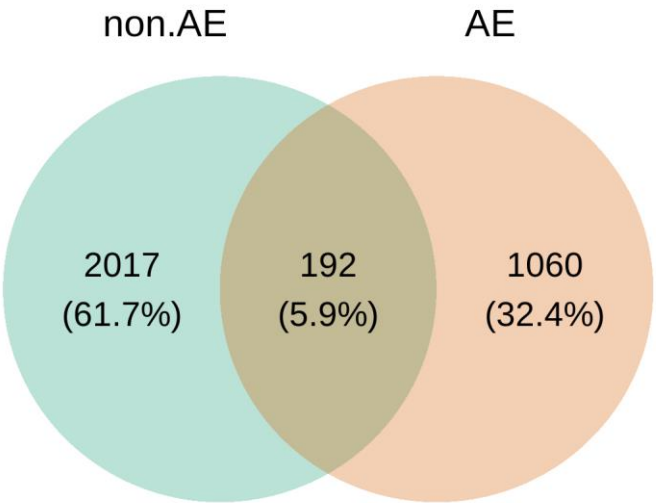


Figure 6. Nasal taxa composition in asthma with and without exacerbation classified according to different (A) Distribution, (B1, B2 & B3) Phylum, (C1, C2, C3 & C4) Species. AE= with exacerbation; non.AE=without exacerbation

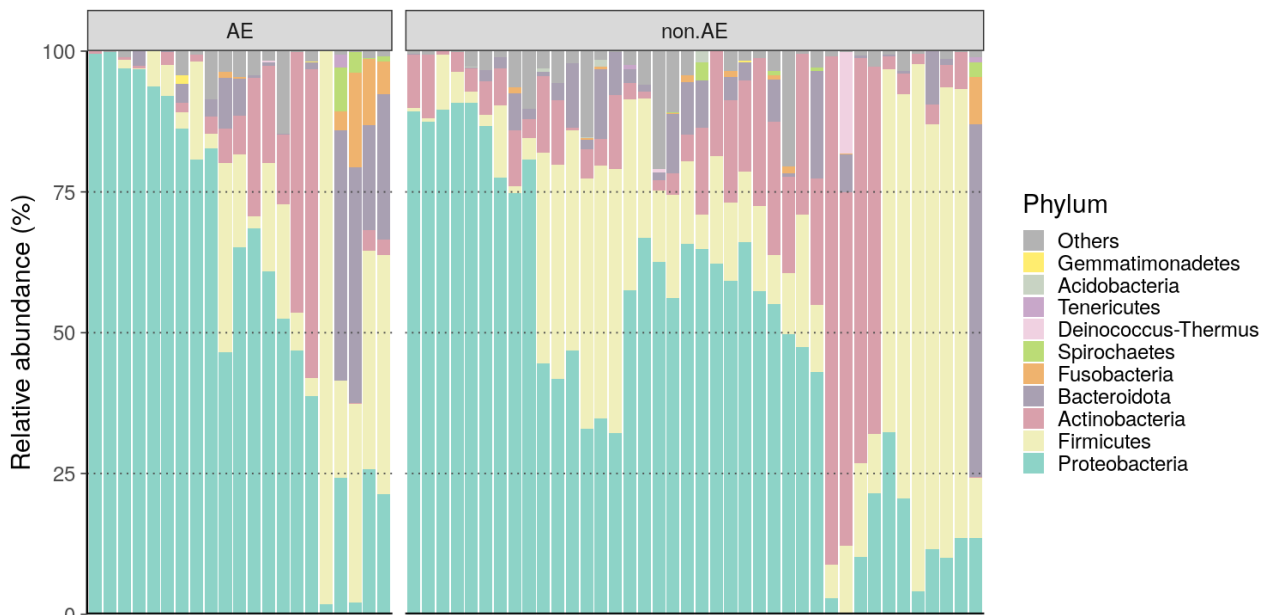


A

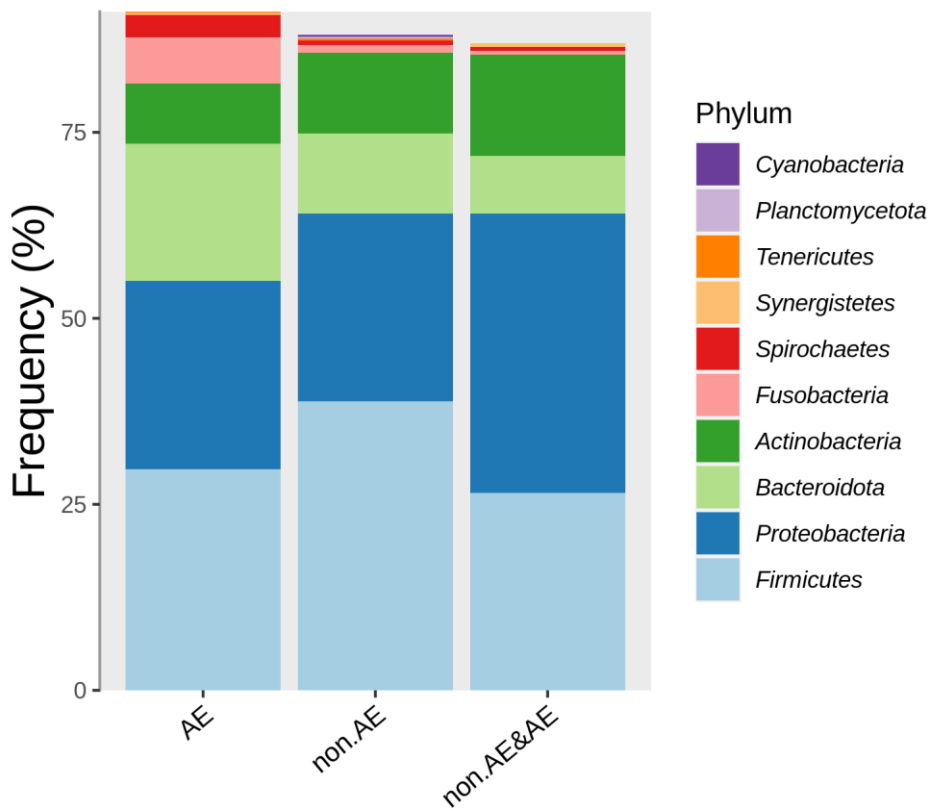




B1



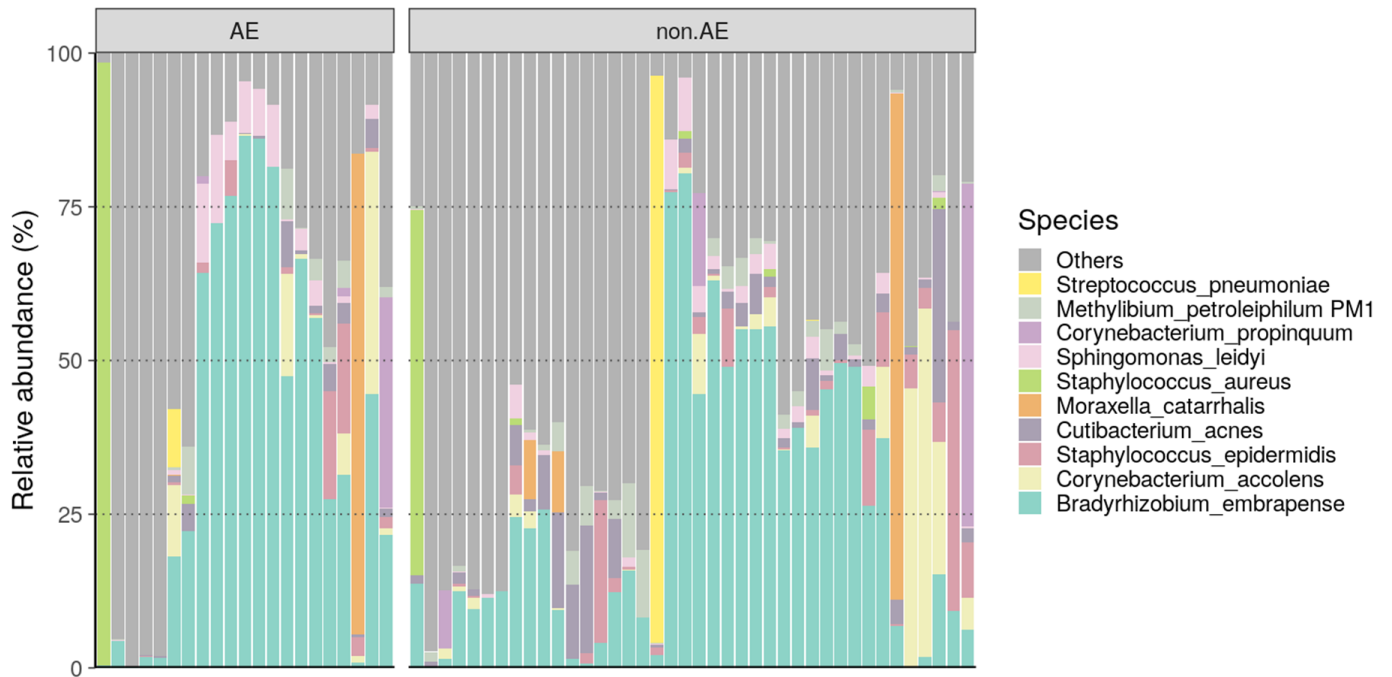
B2



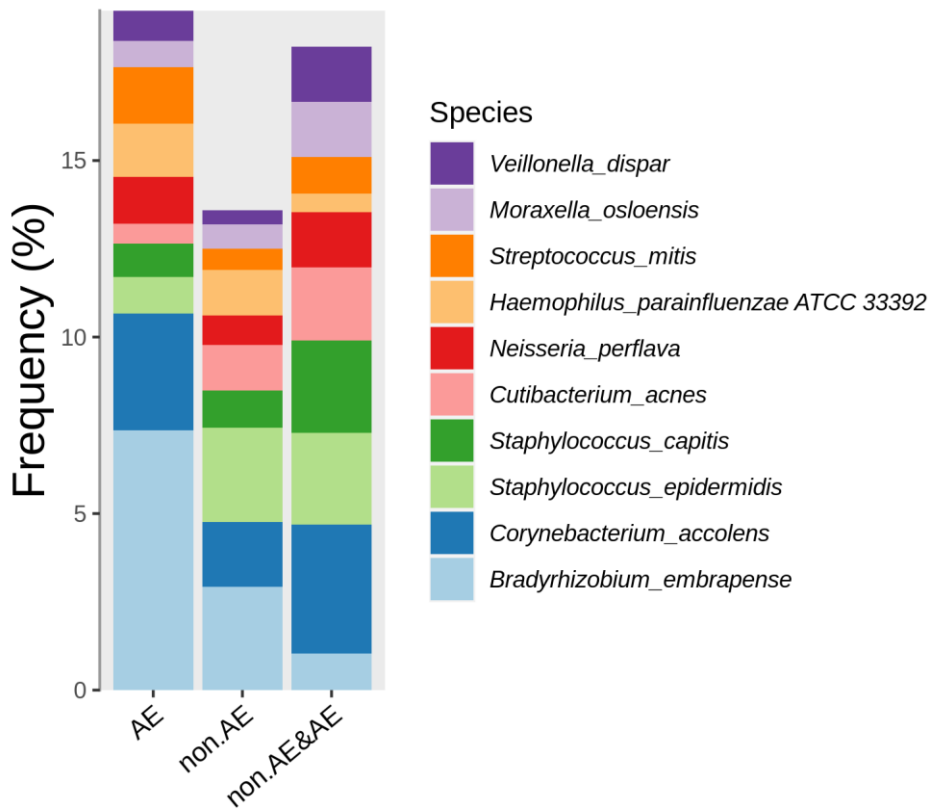




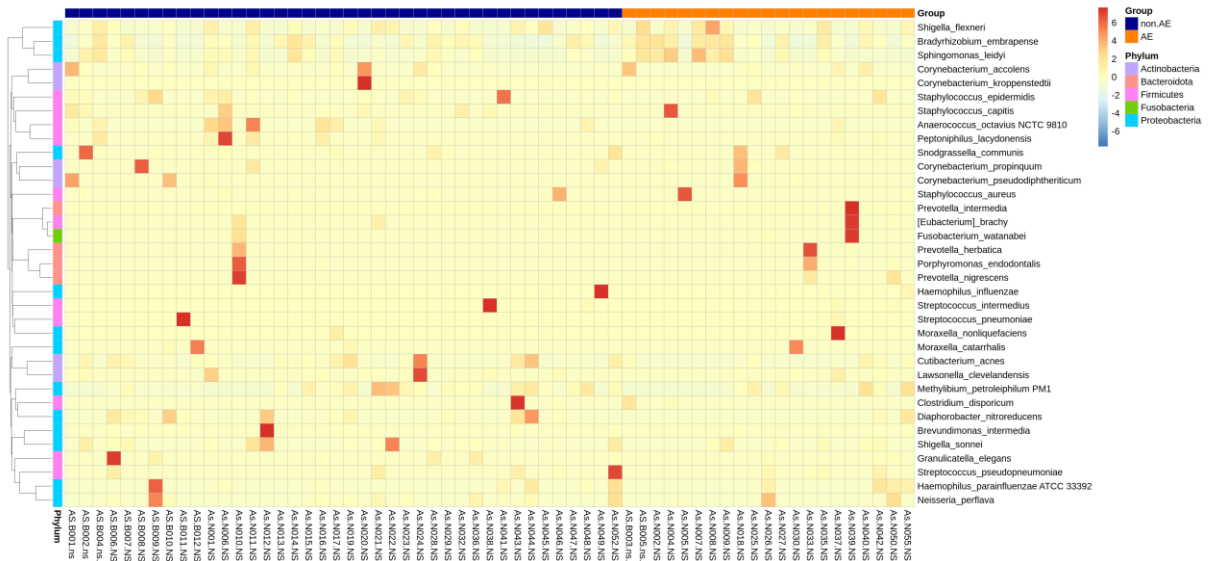
C1



C2



C3



C4

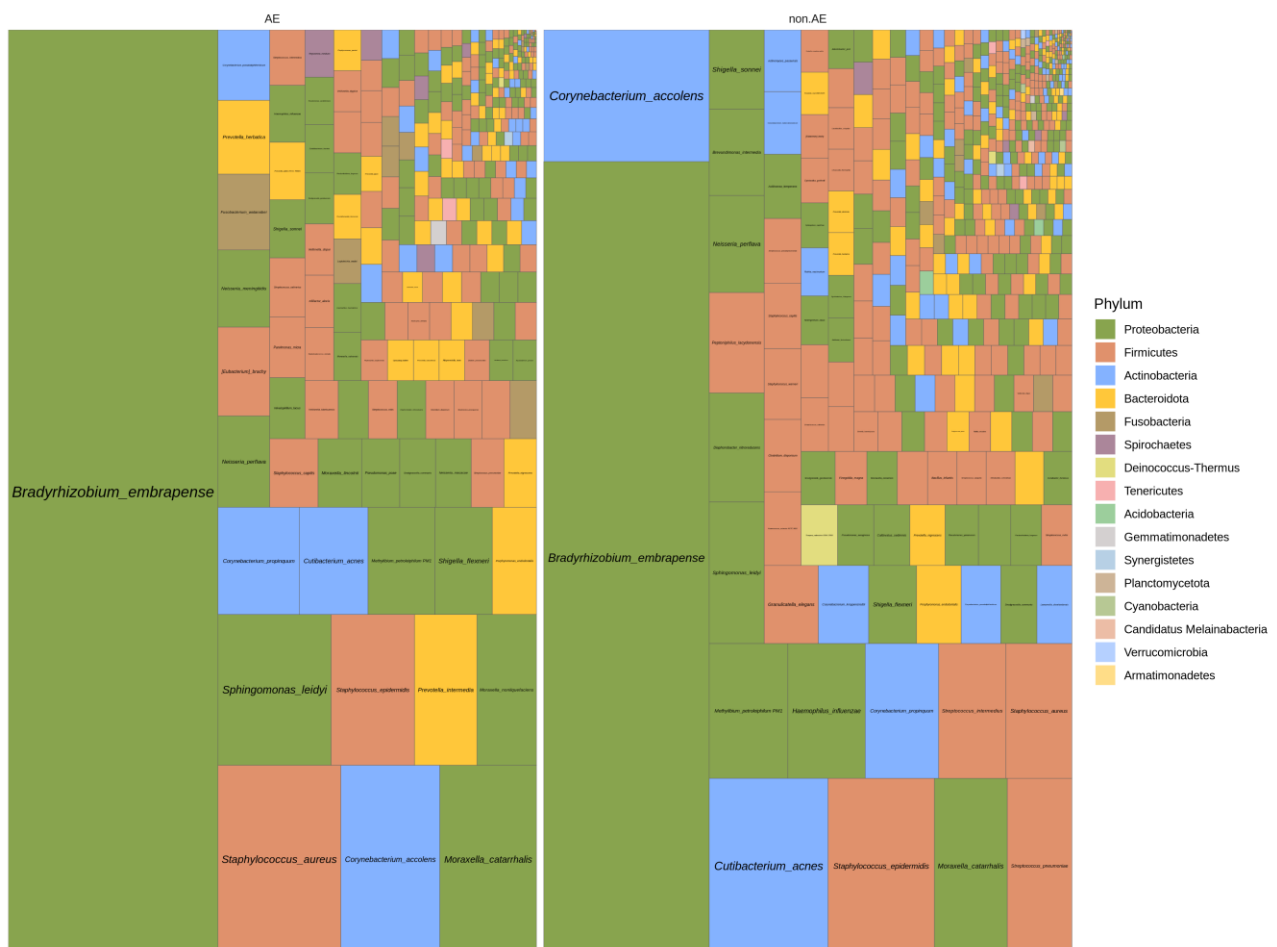
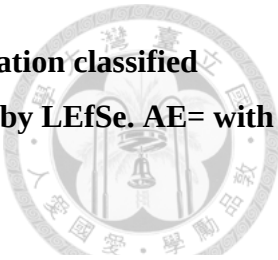
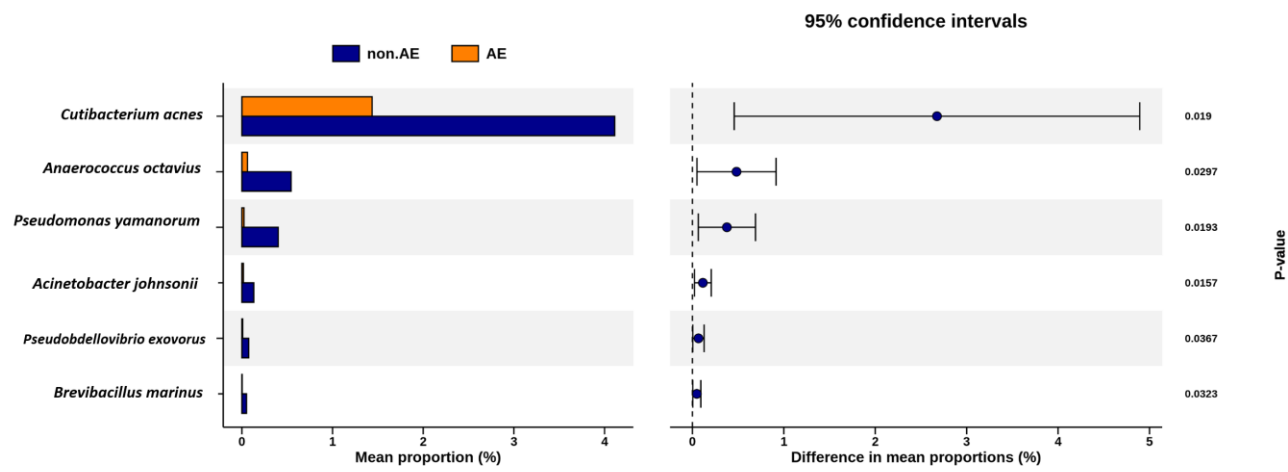


Figure 7. Differences in nasal taxa in asthma with and without exacerbation classified according to different (A) species, (B) genus, (C) phylum. (D) analyzed by LEfSe. AE= with exacerbation; non.AE=without exacerbation

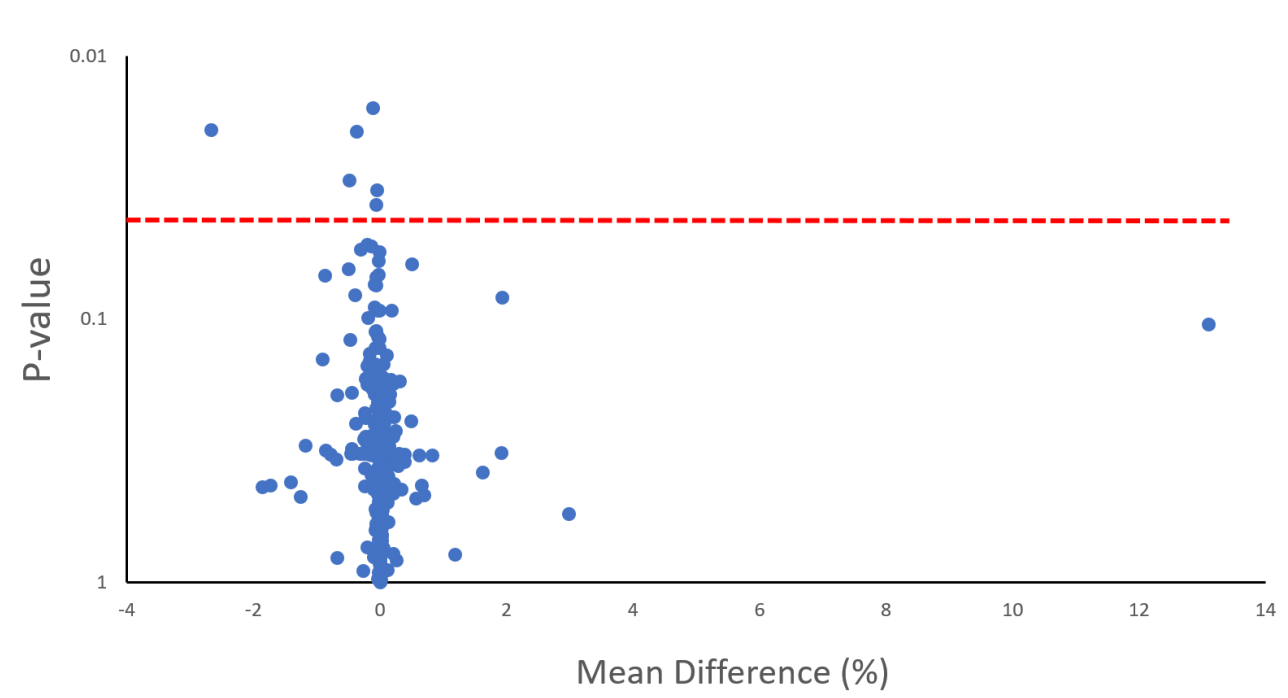


A1



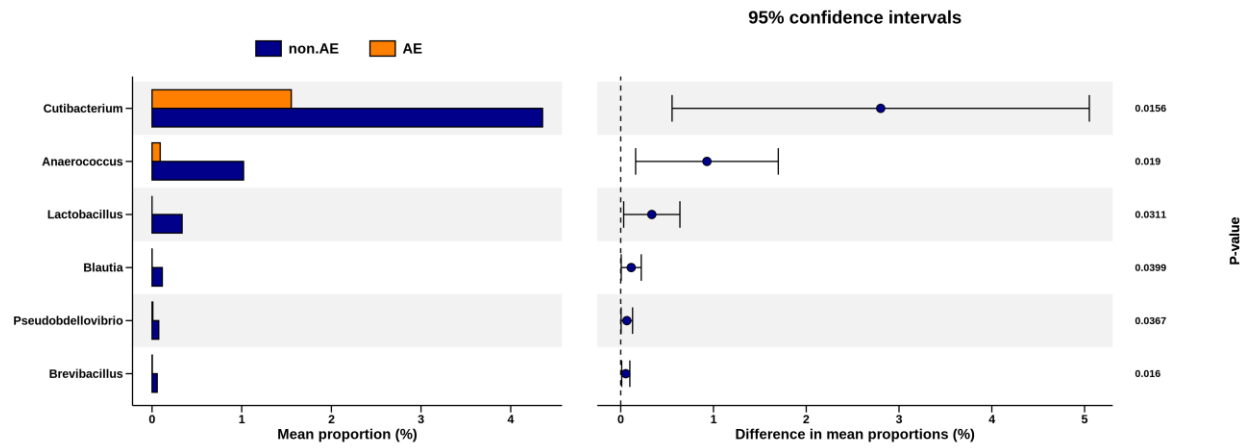
A2

Bacteria abundance between asthma patients with/without AE

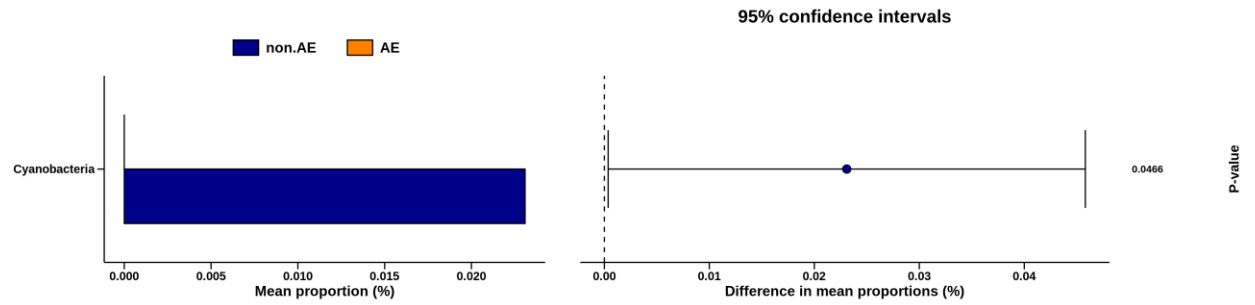




B

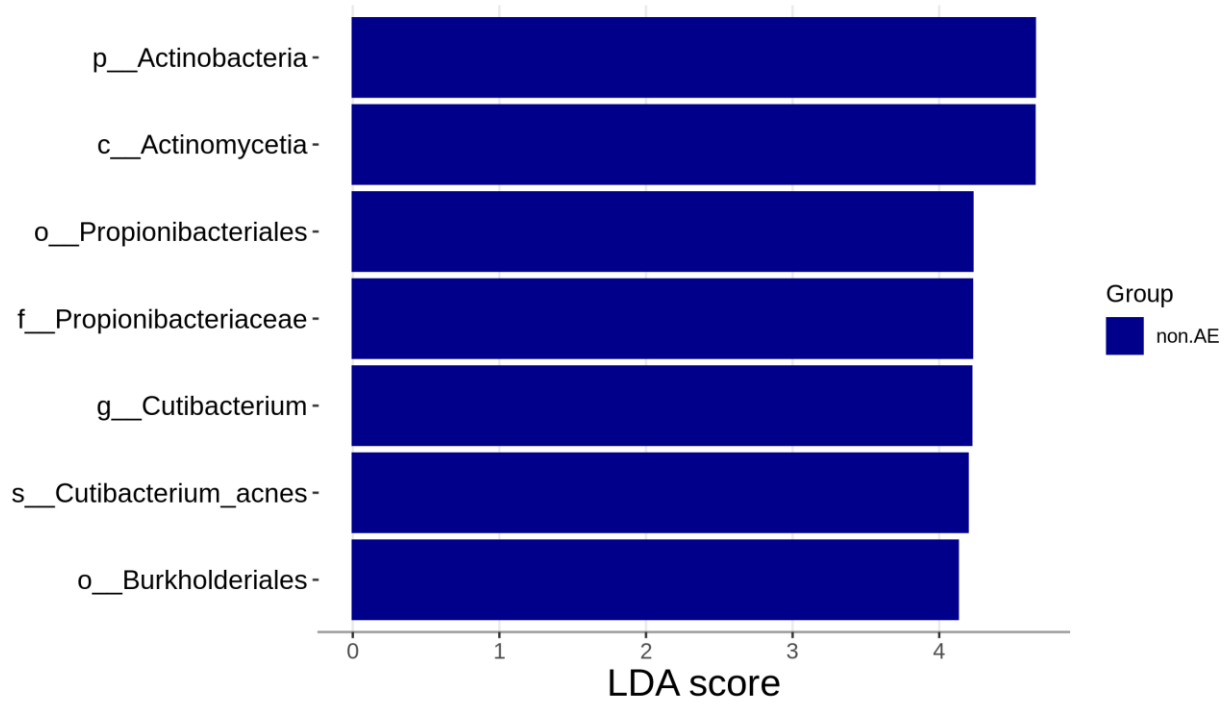


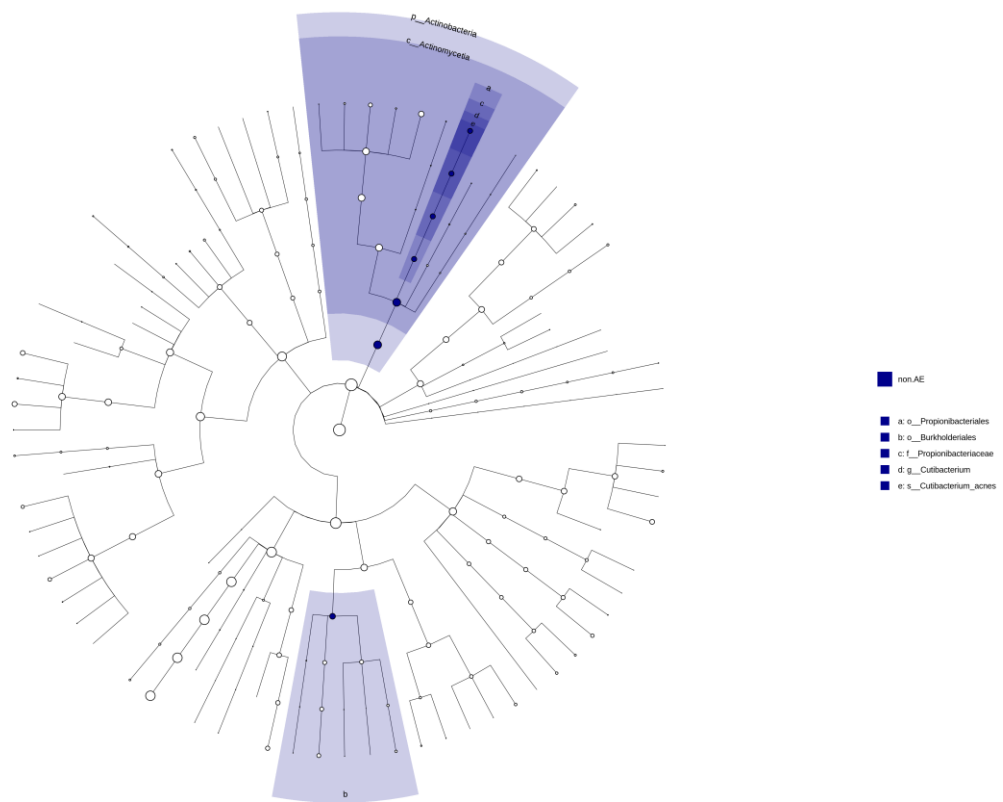
C





D

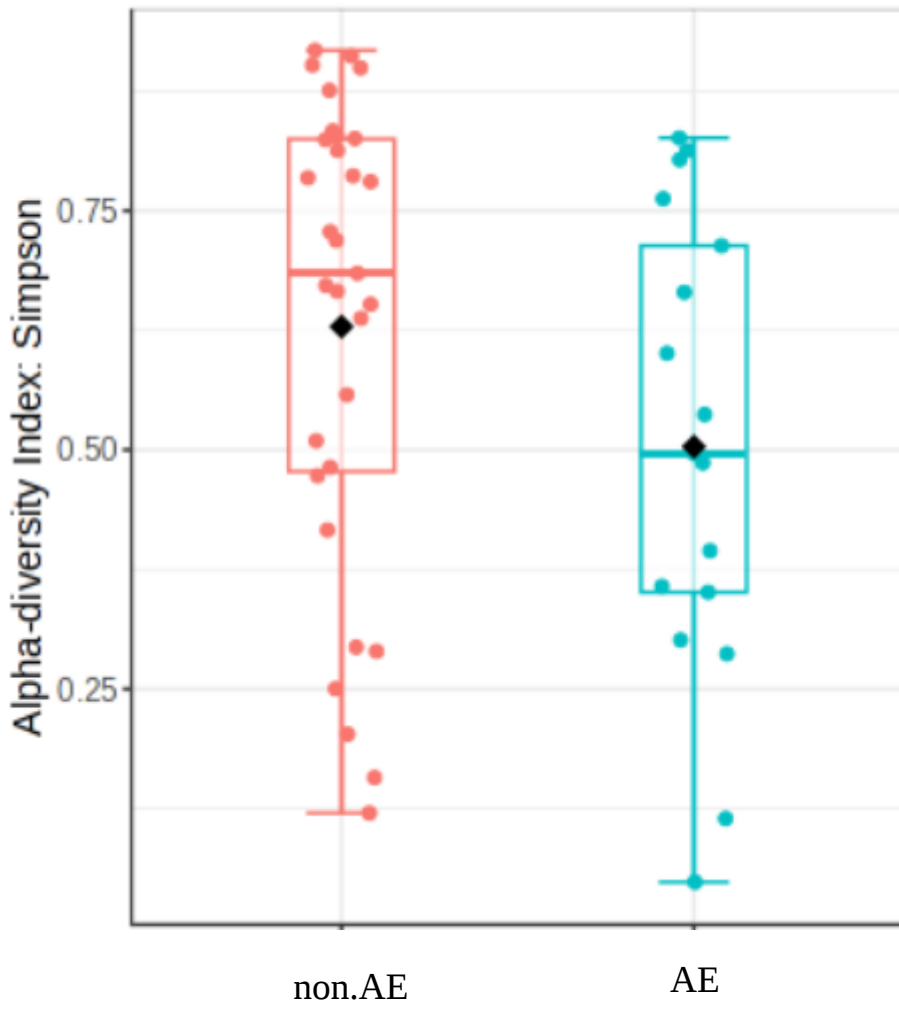




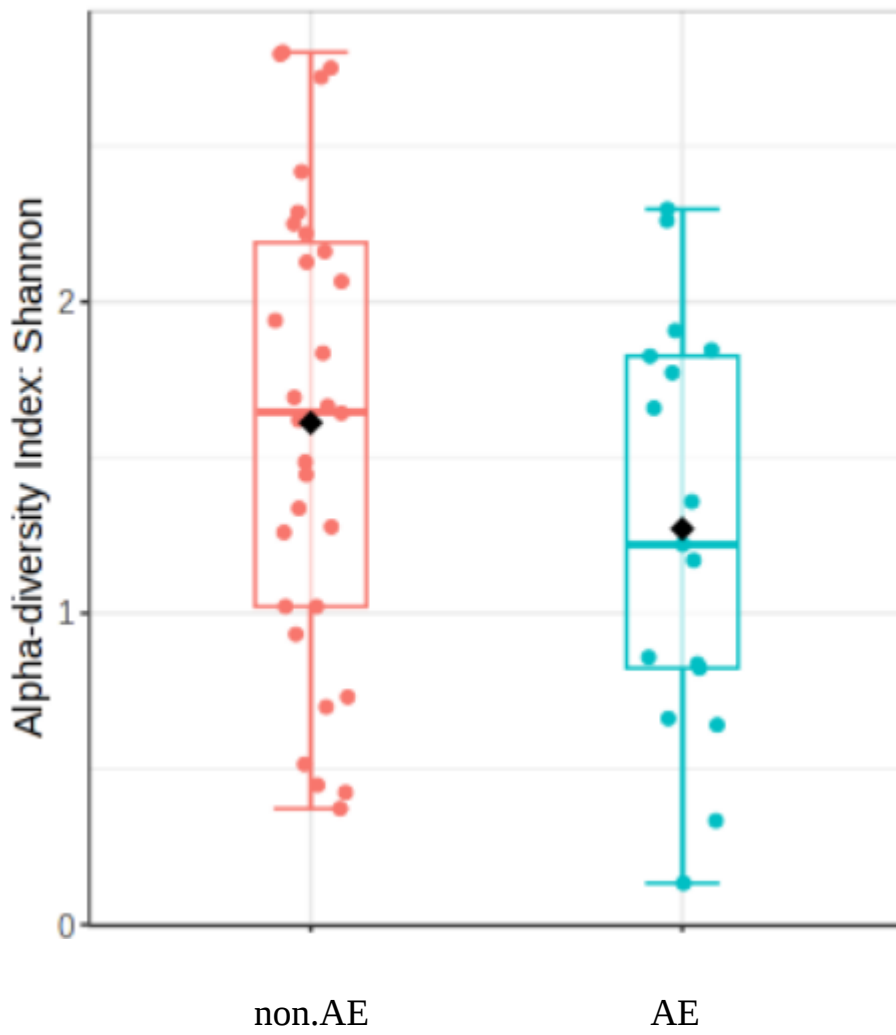
Select 200 most abundant taxa as the background cladogram.

Figure 8. Nasal alpha diversity (good quality samples) in asthma with and without exacerbation analyzed based on (A) Simpson index, (B) Shannon index, and (C) Observed features index. AE= with exacerbation; non.AE=without exacerbation

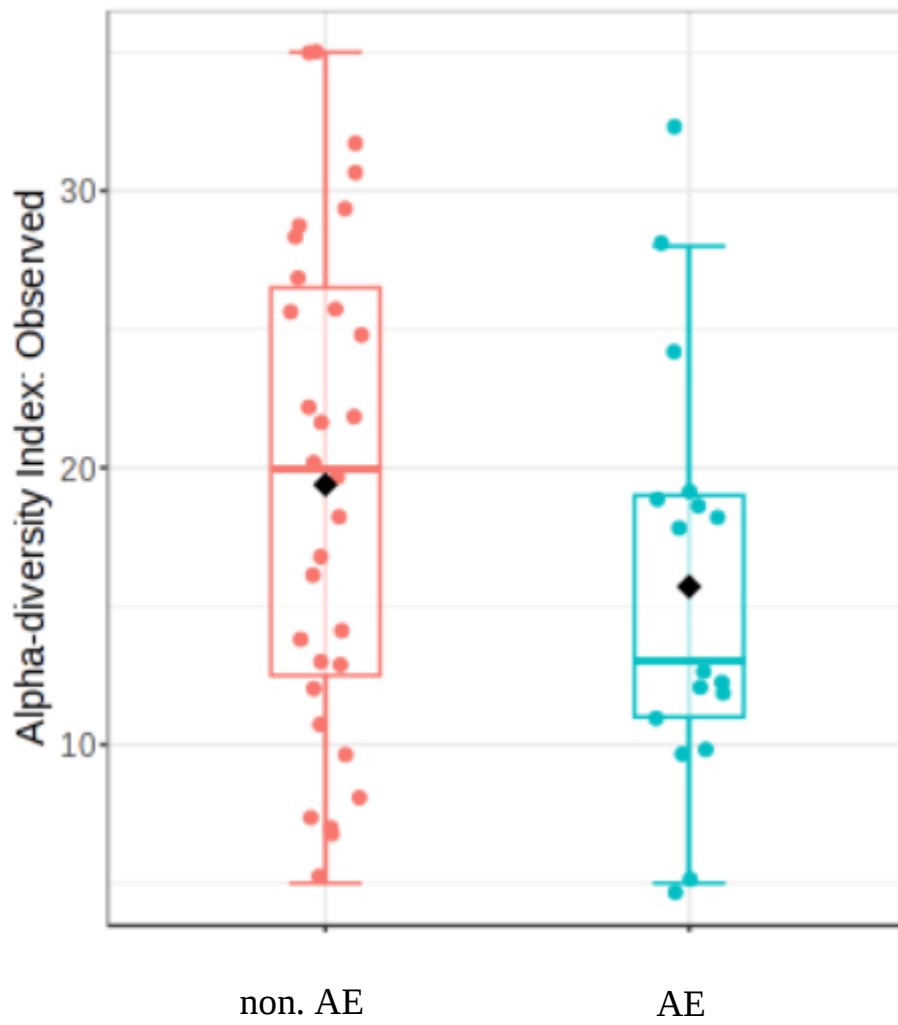
A



B



C



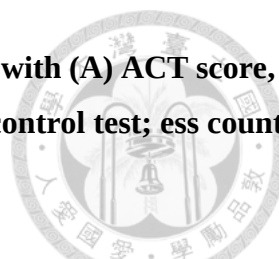
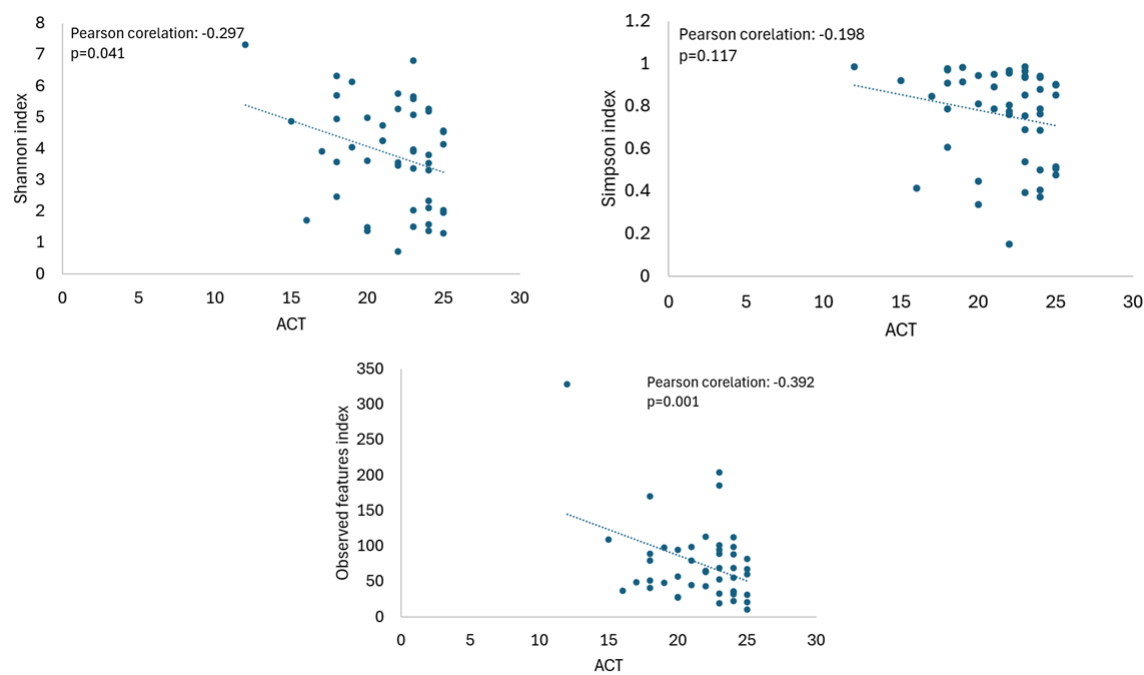
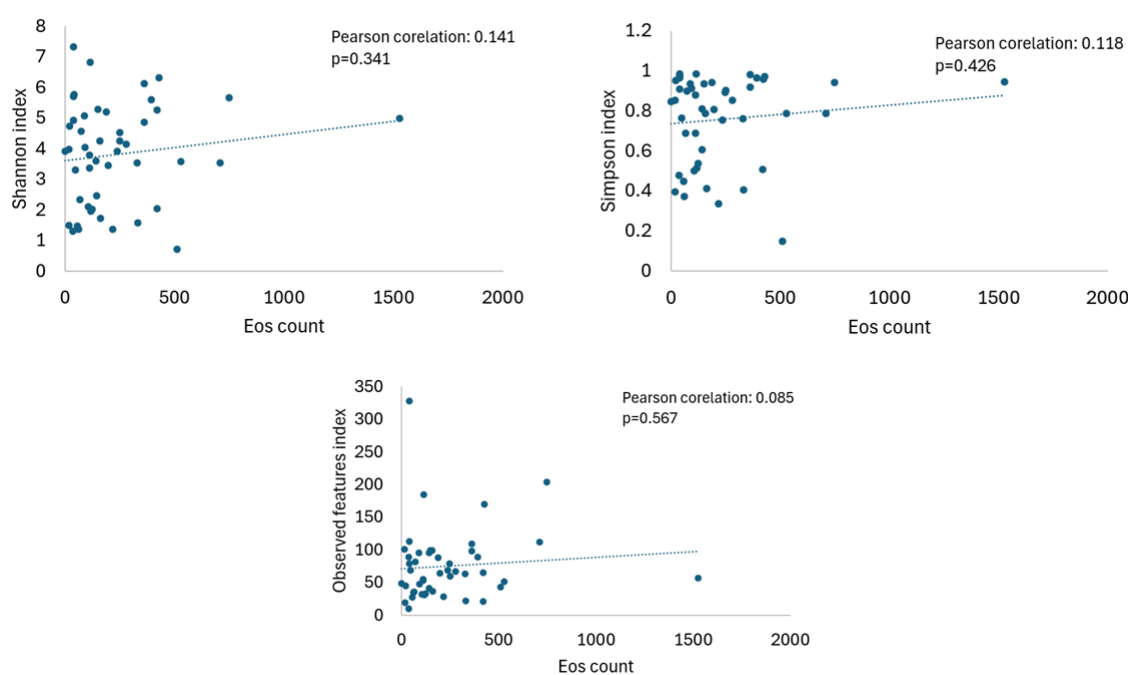


Figure 9. Relationships of nasal alpha diversity (good quality samples) with (A) ACT score, (B) eosinophil count, (C) IgE level, and (D) lung function. ACT = asthma control test; ess count = eosinophil count.

A

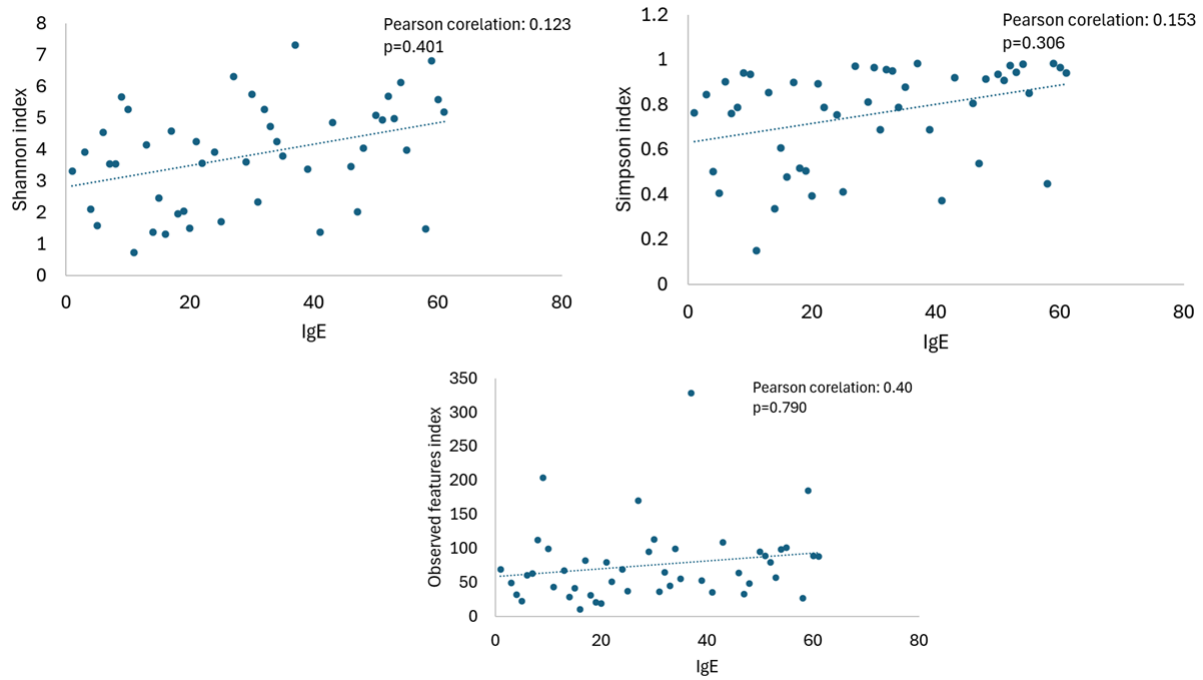


B

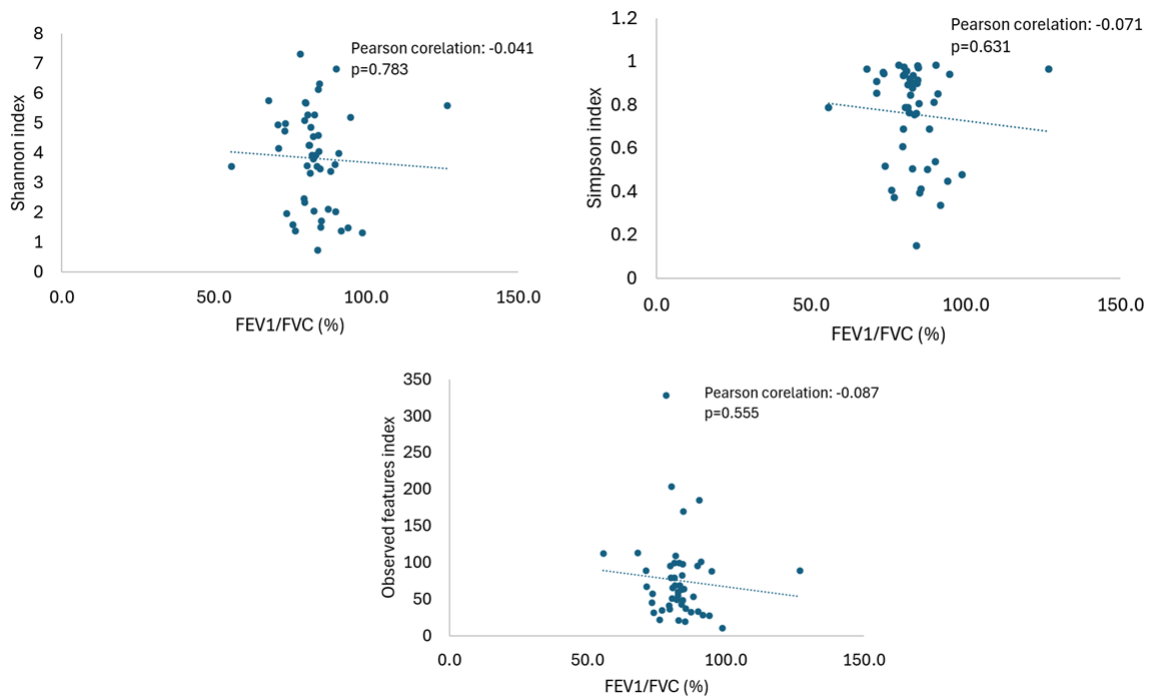




C



D



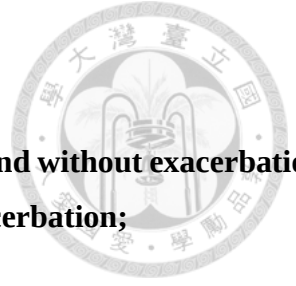
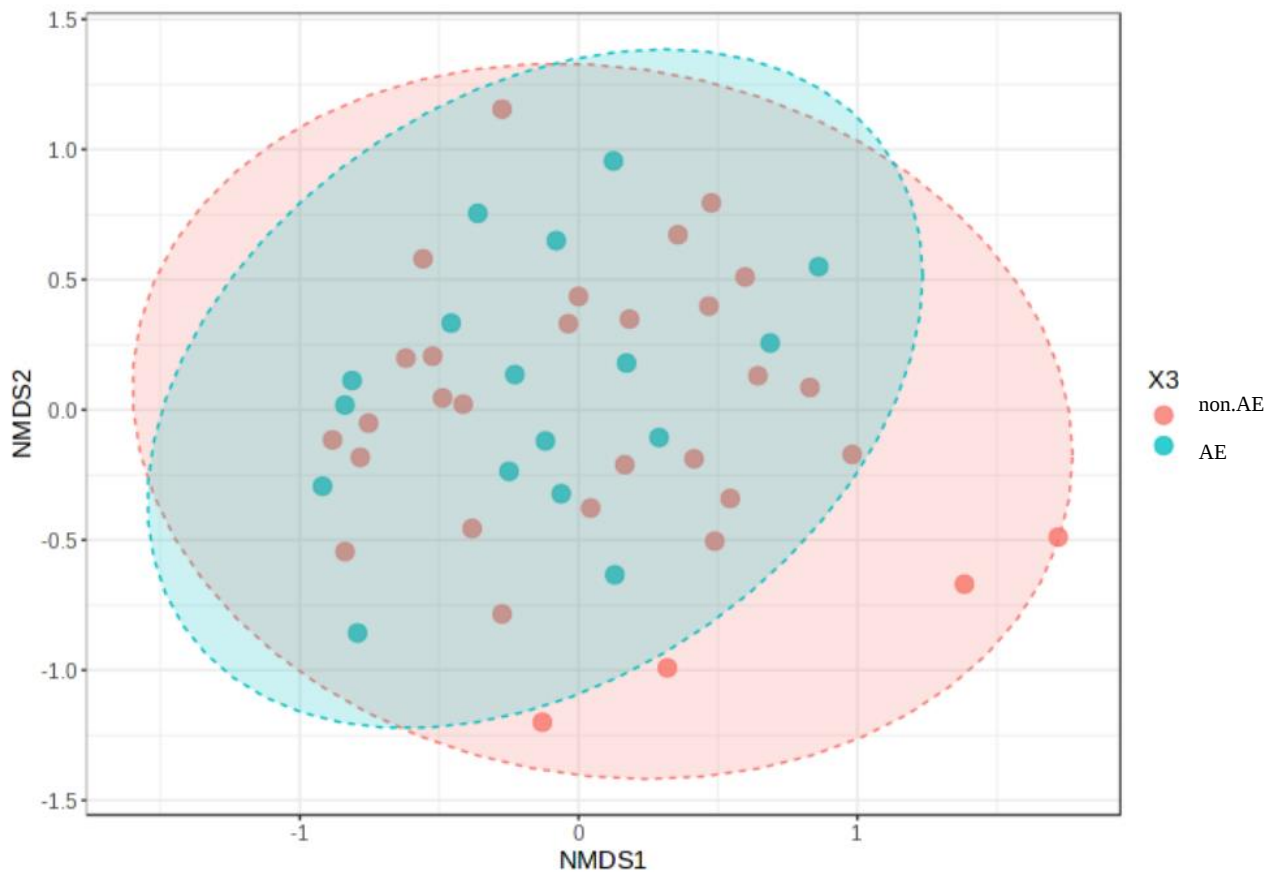
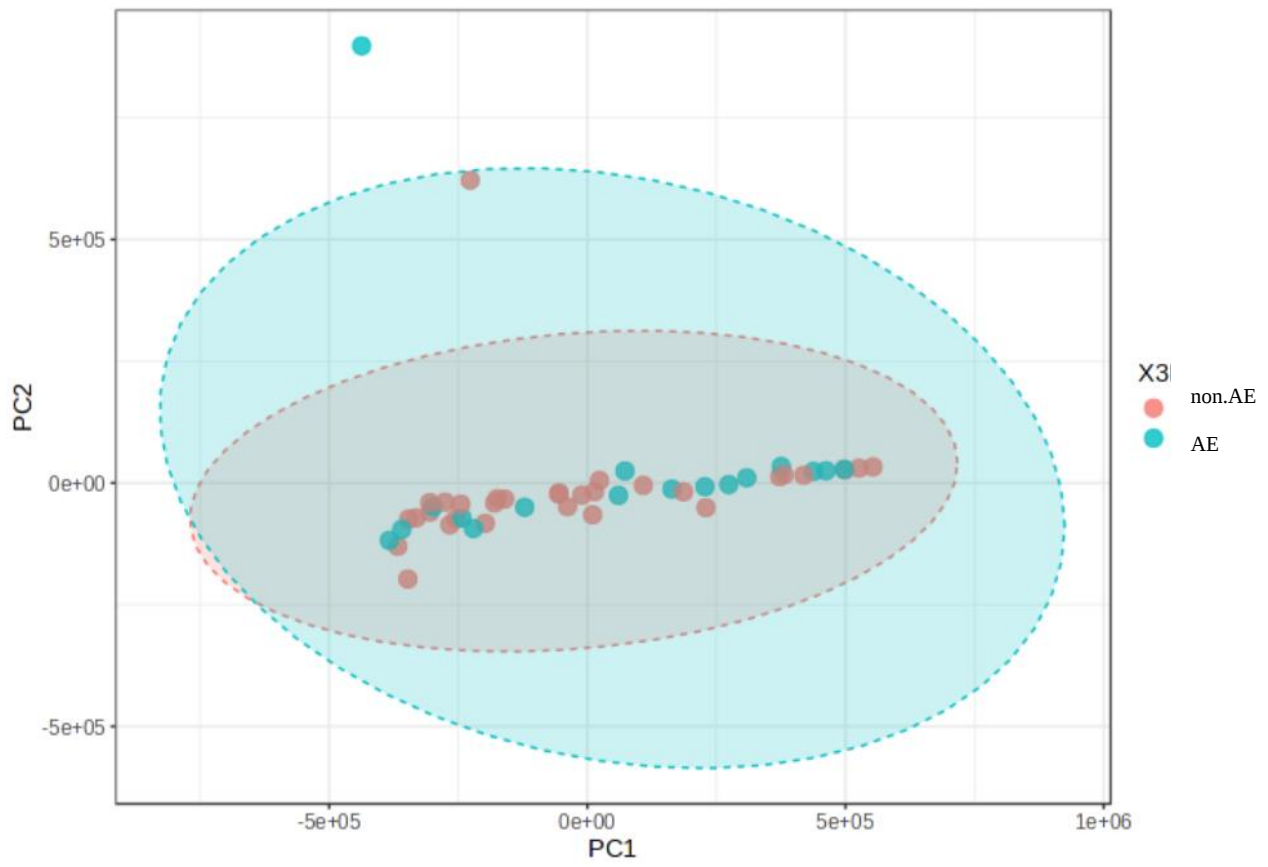


Figure 10. Nasal beta diversity (good quality samples) in asthma with and without exacerbation analyzed based on (A) NMDS, (B) PCA, and (C) PCoA. AE= with exacerbation; non.AE=without exacerbation

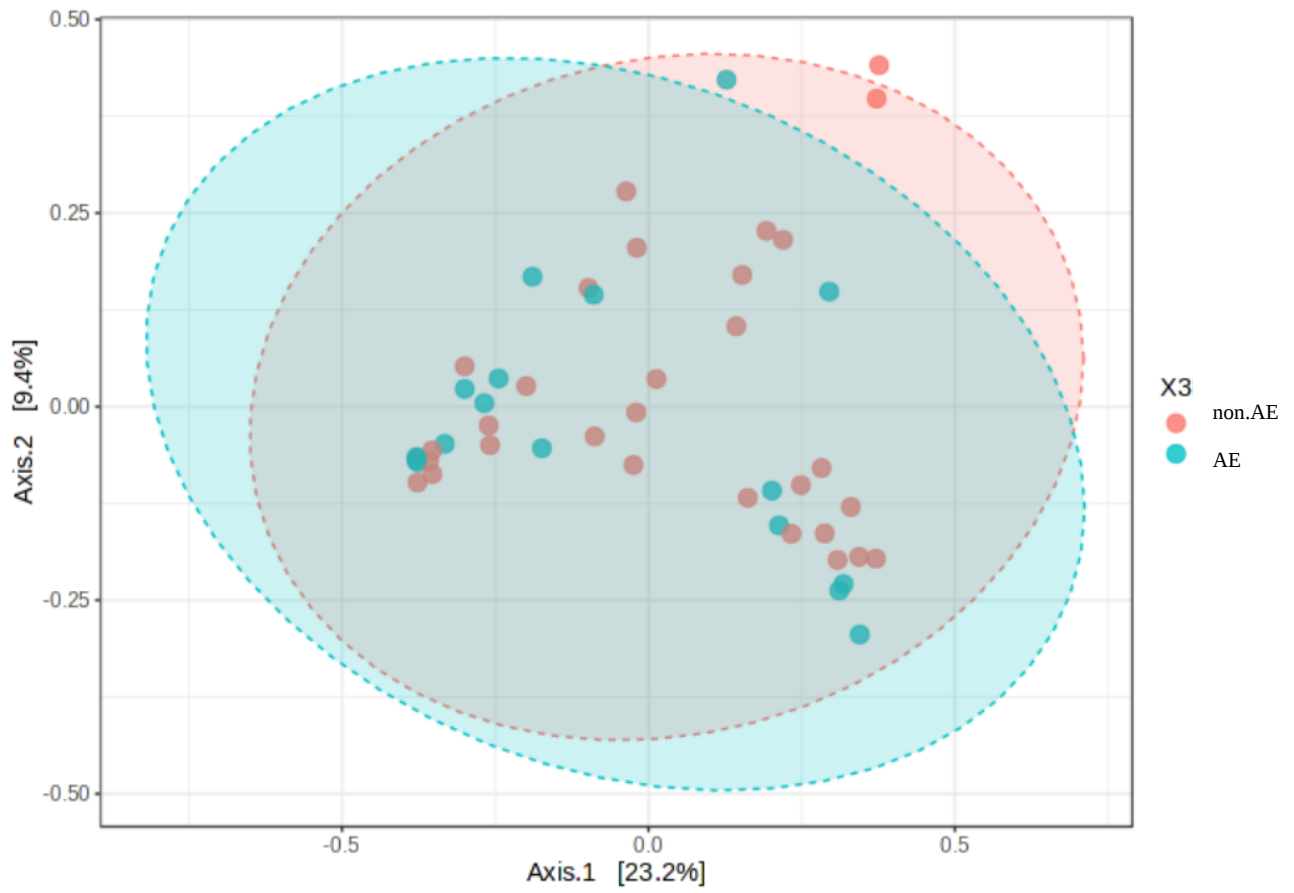
A



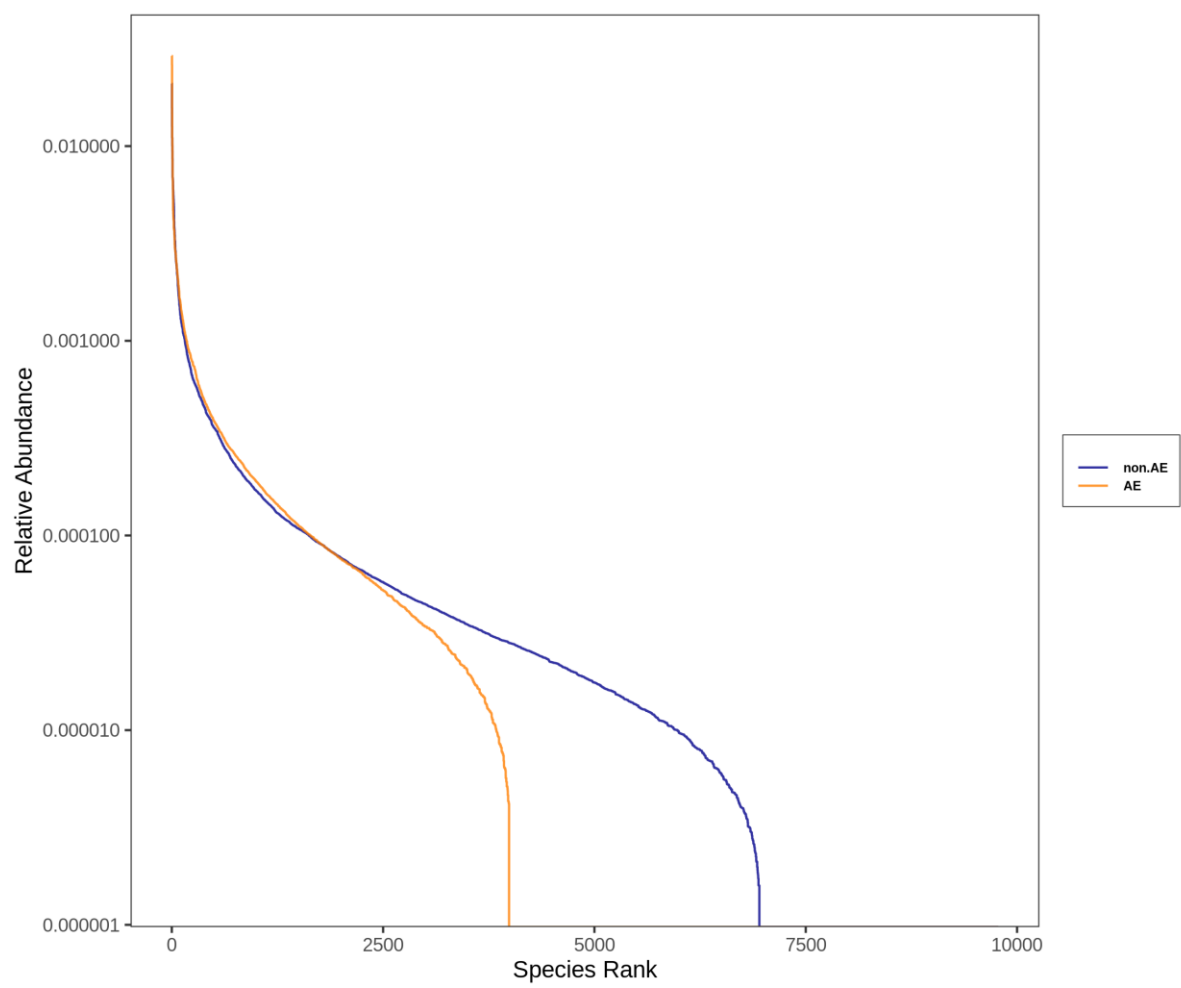
B



C



**Figure 11. Rank Abundance Curve of oral microbiome. AE= with exacerbation;
non.AE=without exacerbation**



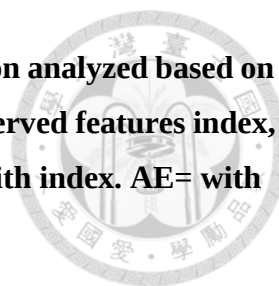
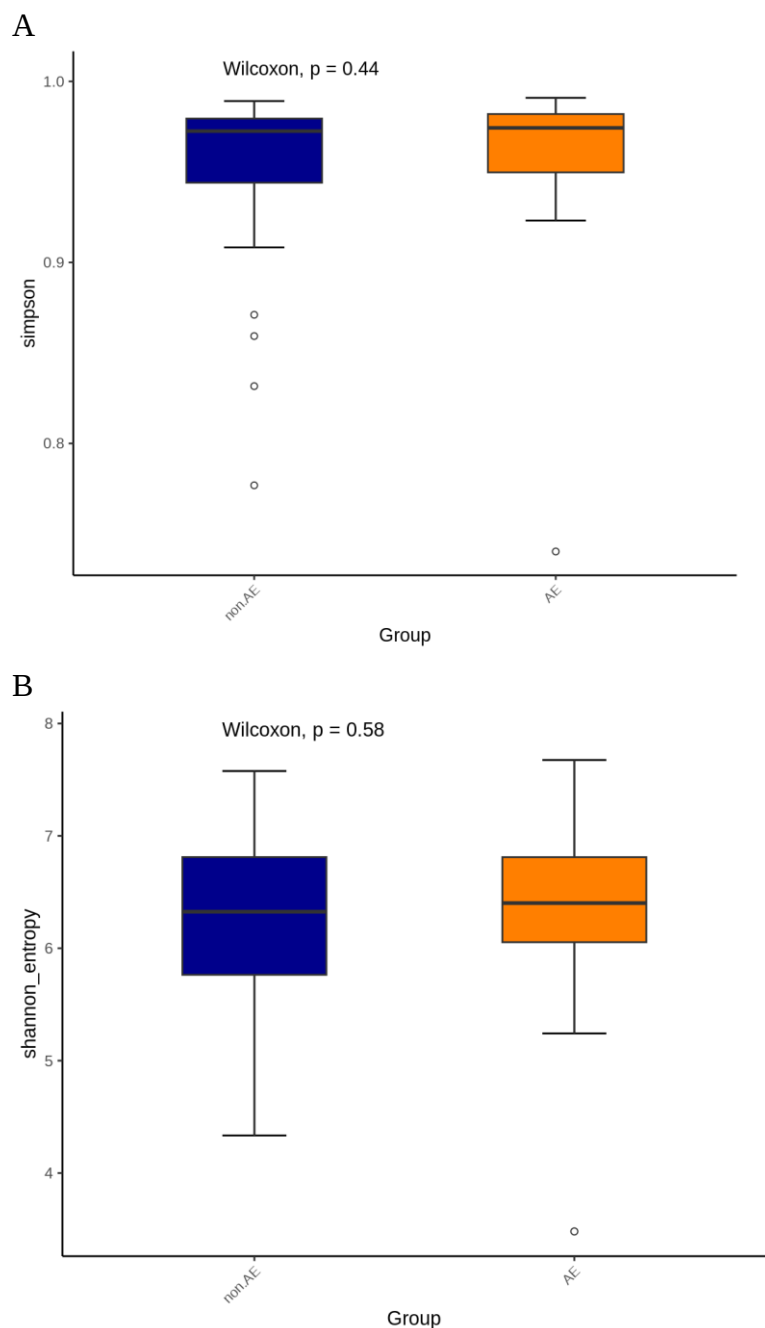
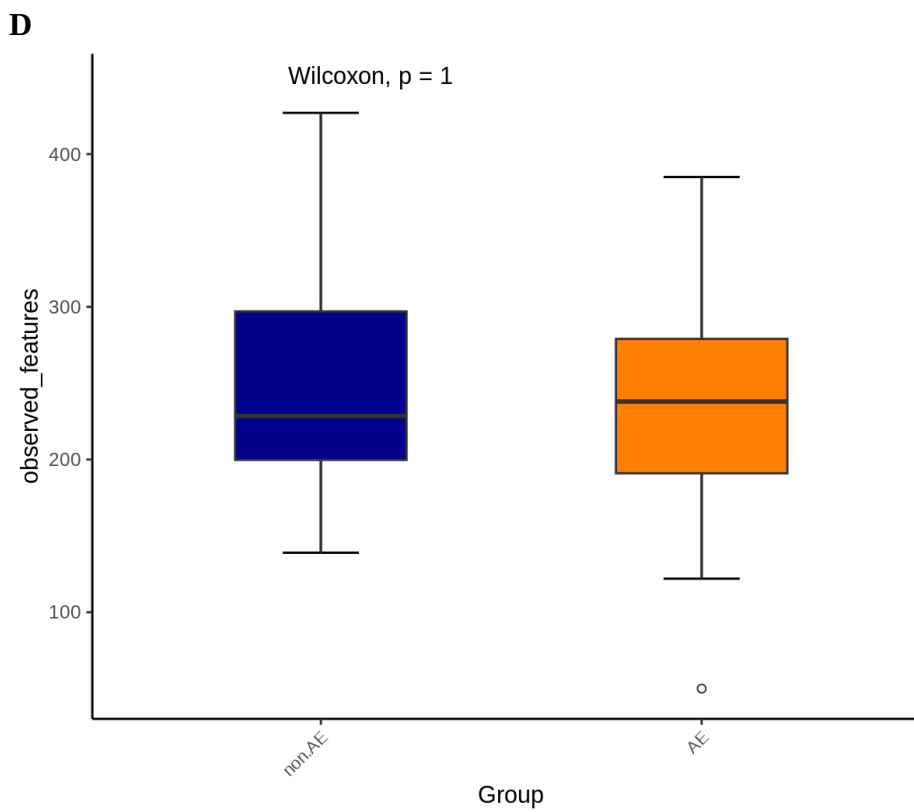
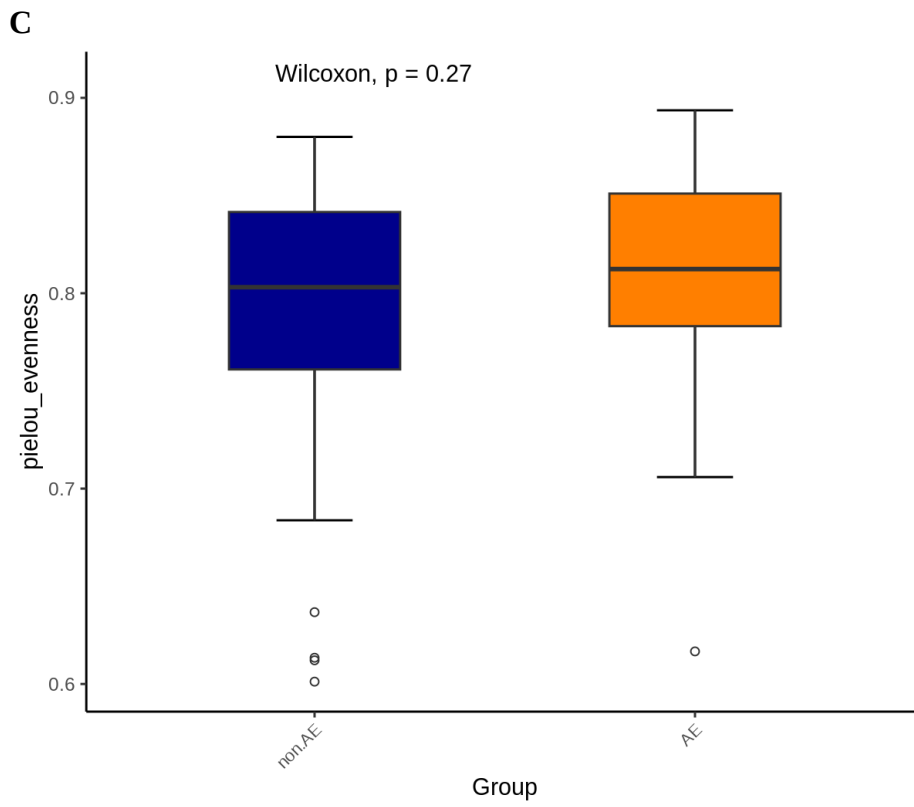
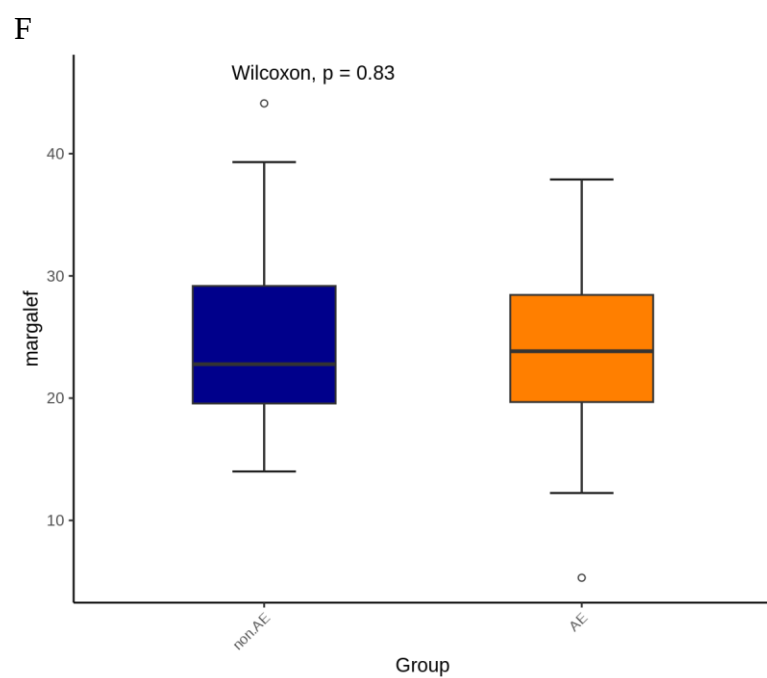
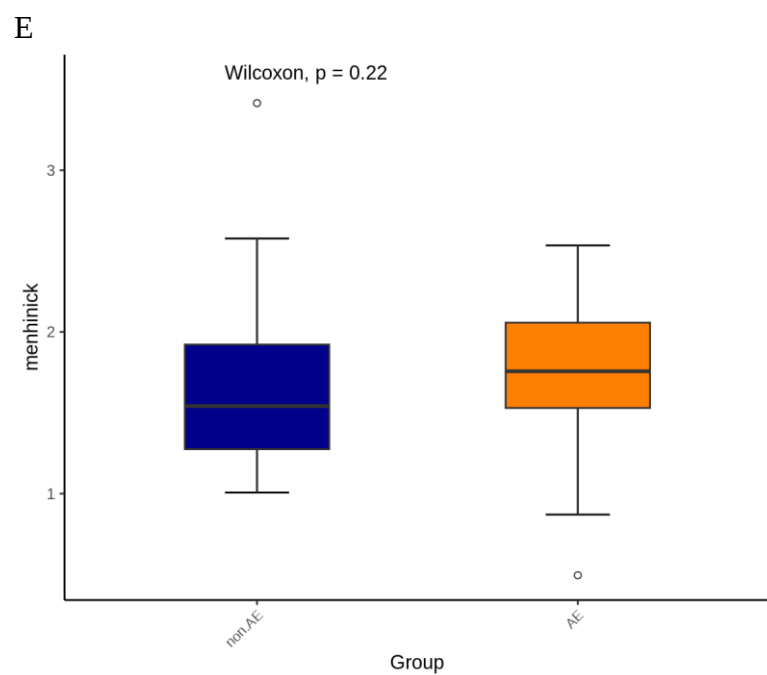


Figure 12. Oral alpha diversity in asthma with and without exacerbation analyzed based on (A) Simpson index, (B) Shannon index, (C) Pielou evenness index, (D) Observed features index, (E) Menhinick's richness index, (F) Margalef's richness index, and (G) Faith index. AE= with exacerbation; non.AE=without exacerbation







G

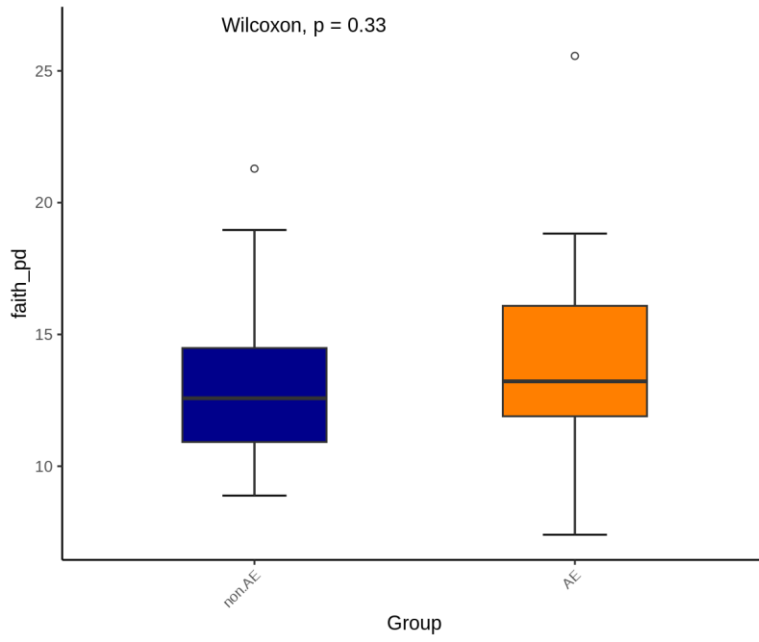
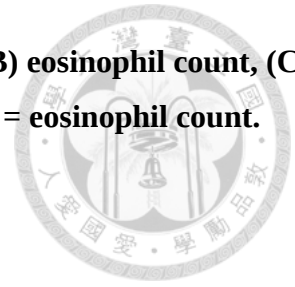
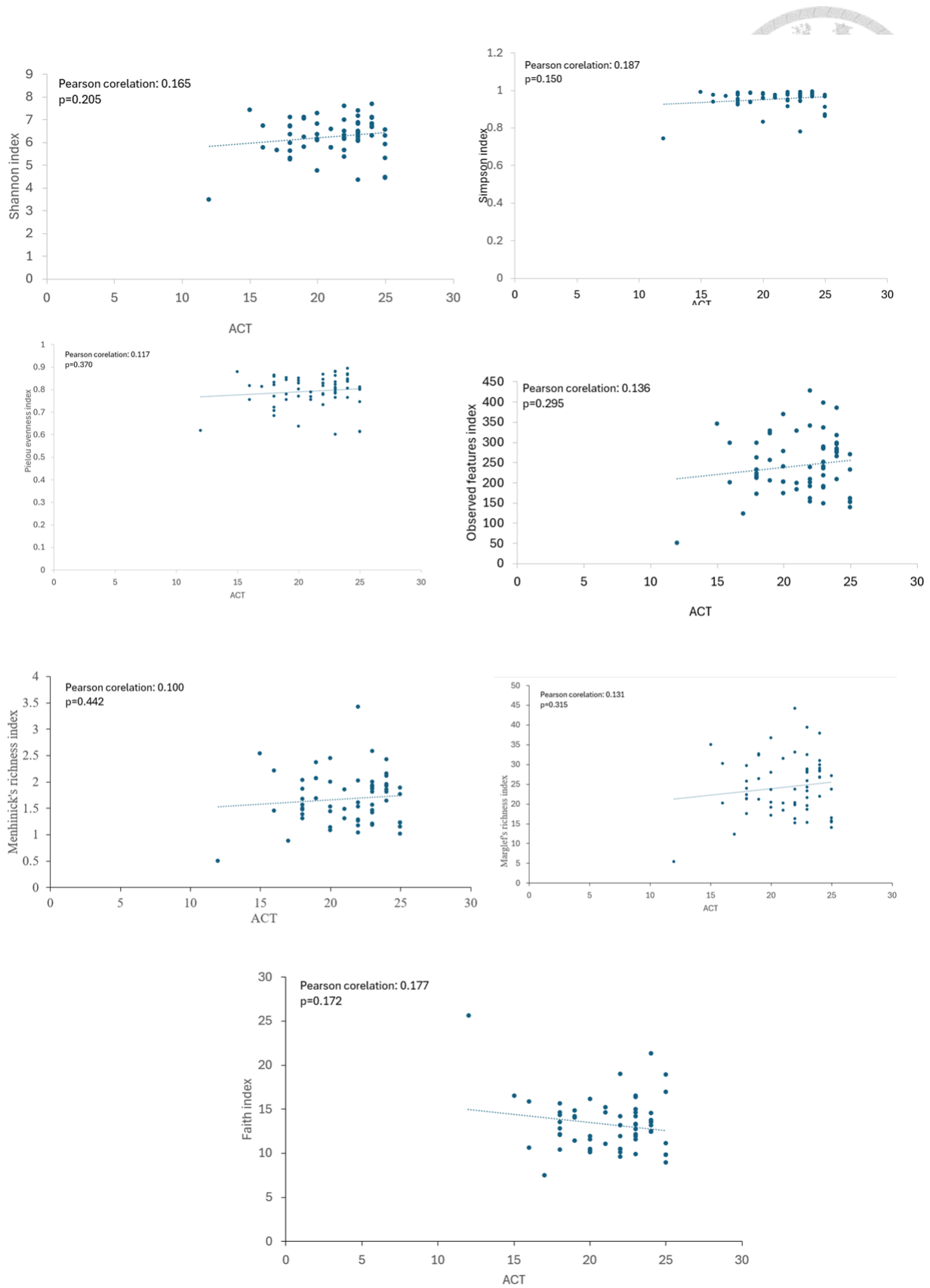


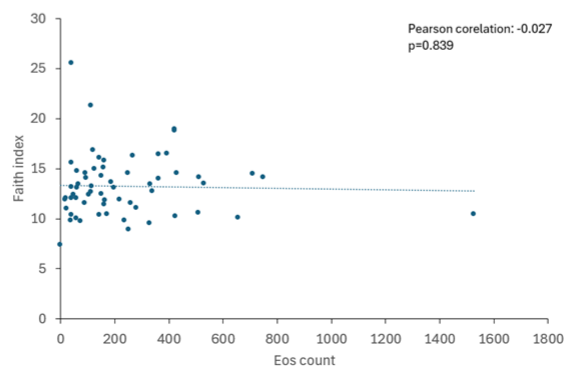
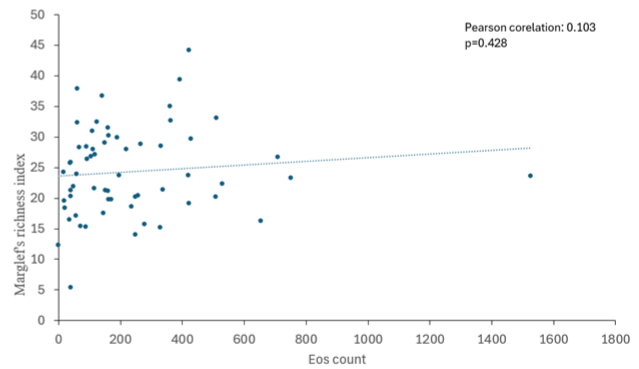
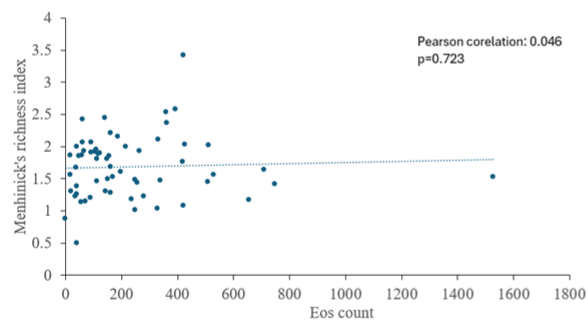
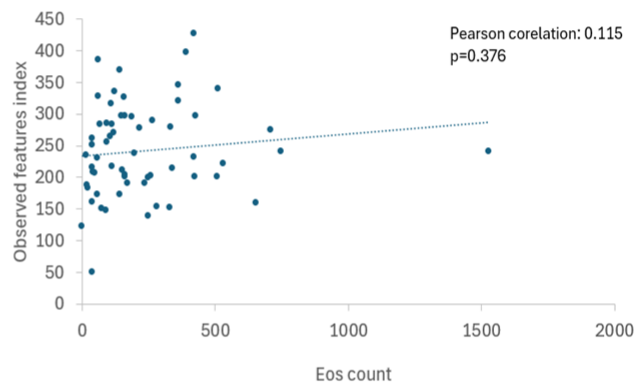
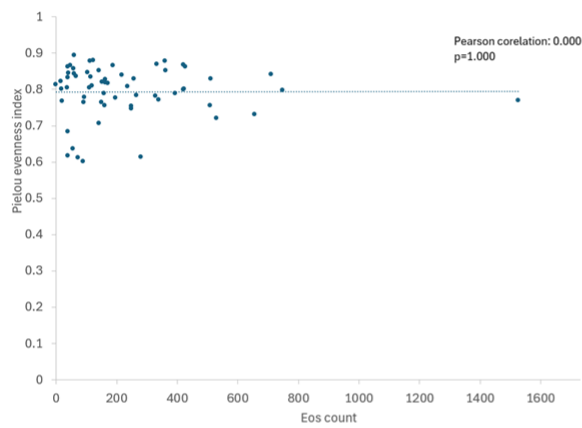
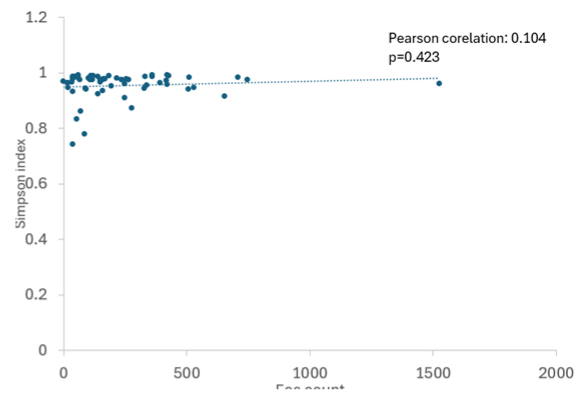
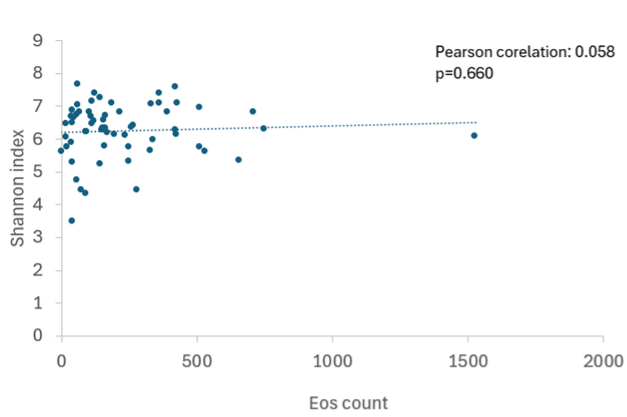
Figure 13. Relationships of oral alpha diversity with (A) ACT score, (B) eosinophil count, (C) IgE level, and (D) lung function. ACT = asthma control test; ess count = eosinophil count.

A

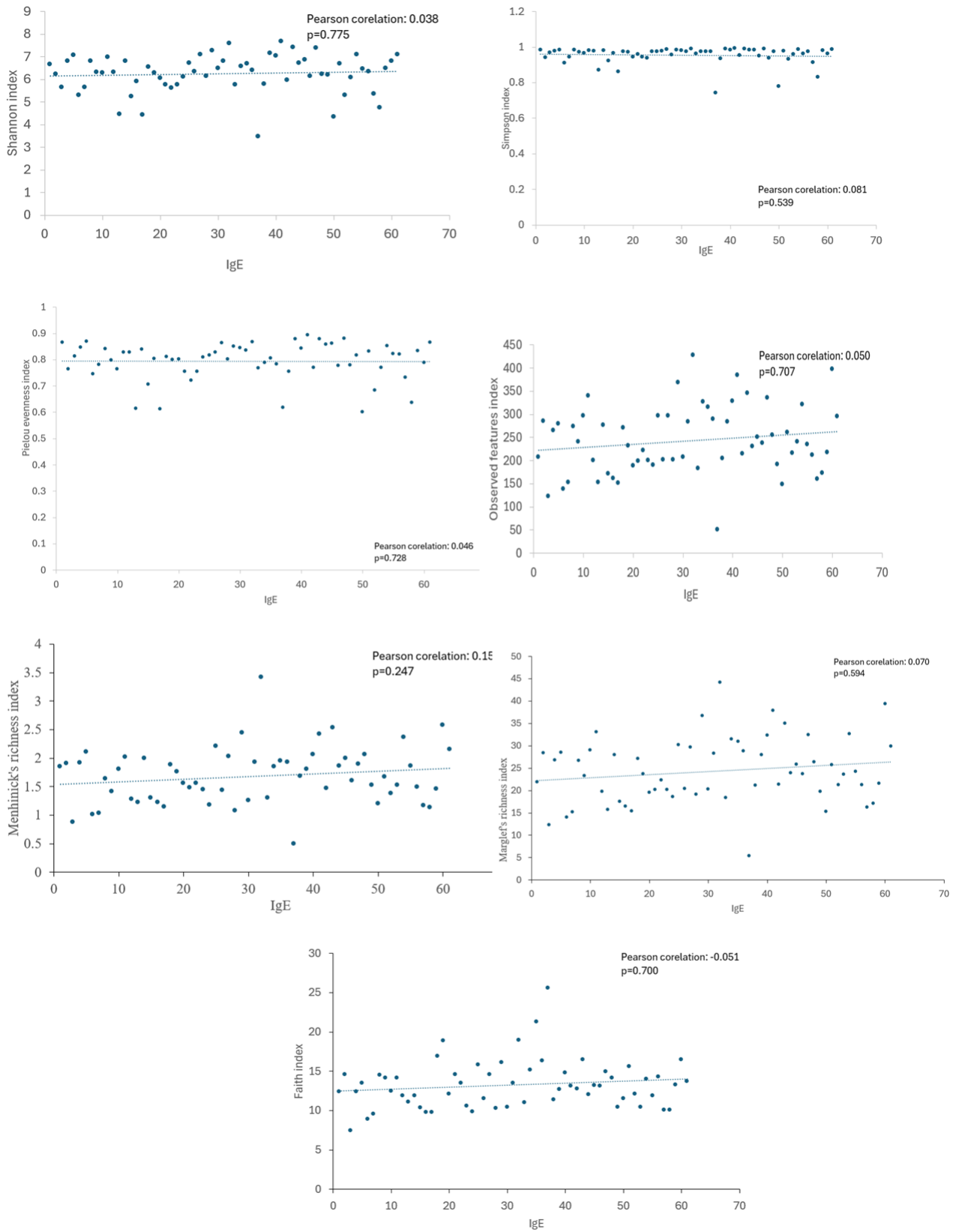




B

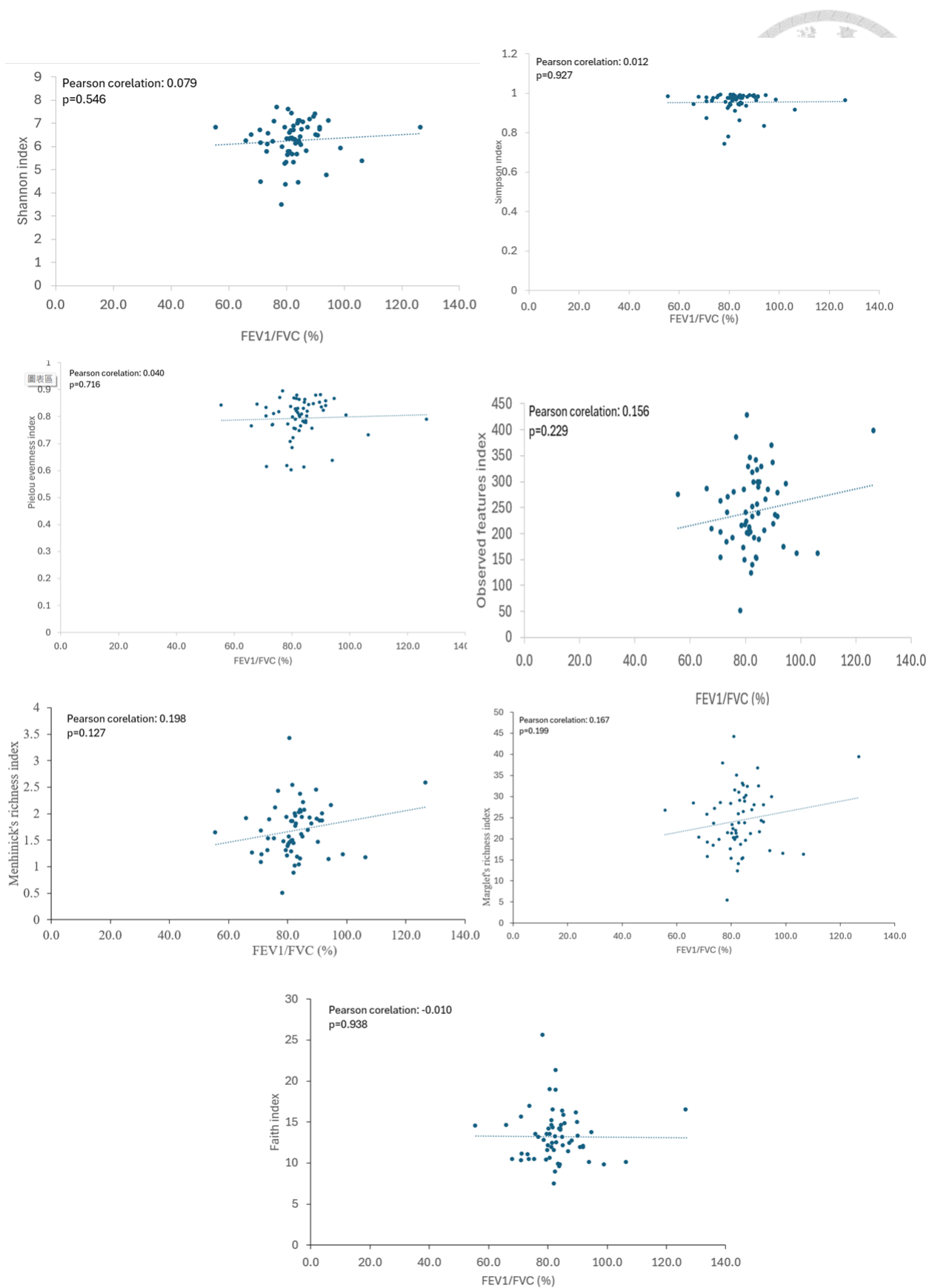


C



D





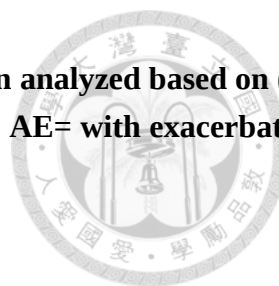
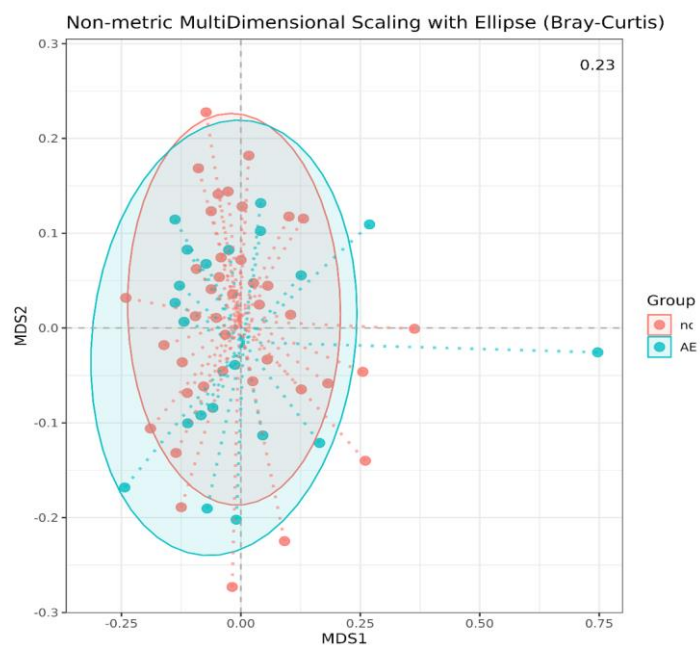
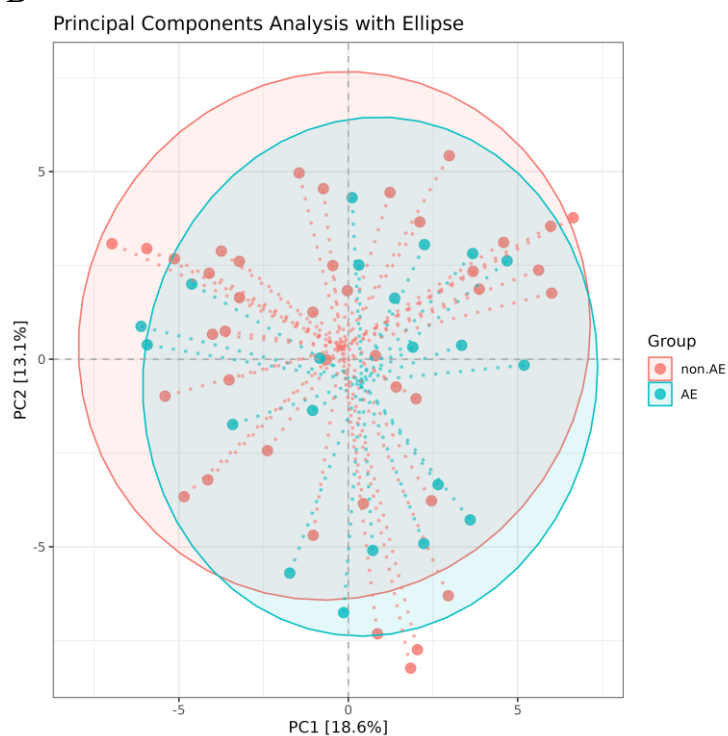


Figure 14. Oral beta diversity in asthma with and without exacerbation analyzed based on (A) NMDS, (B) PCA, (C) PCoA, (D) PLS-DA, (E) tSNE, and (F) UPGMA. AE= with exacerbation; non.AE=without exacerbation

A

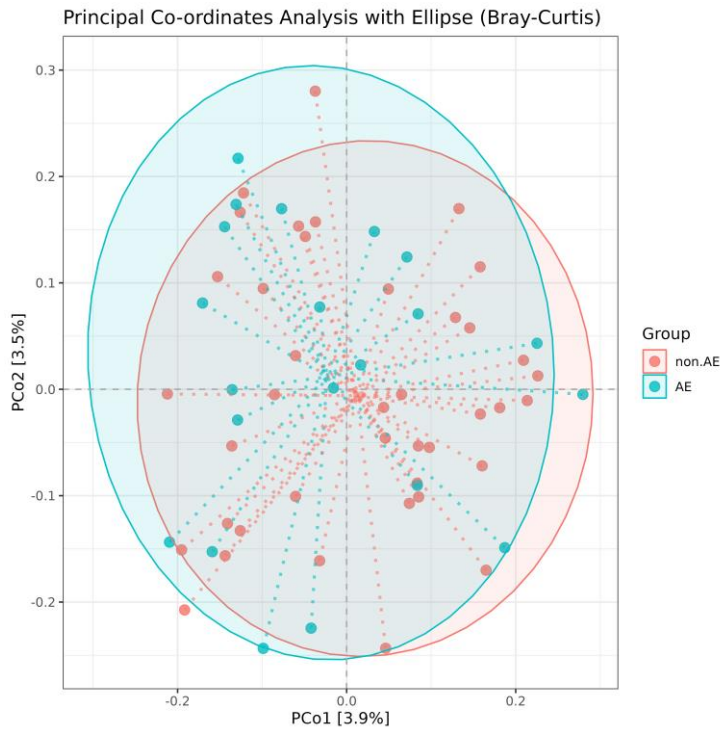


B

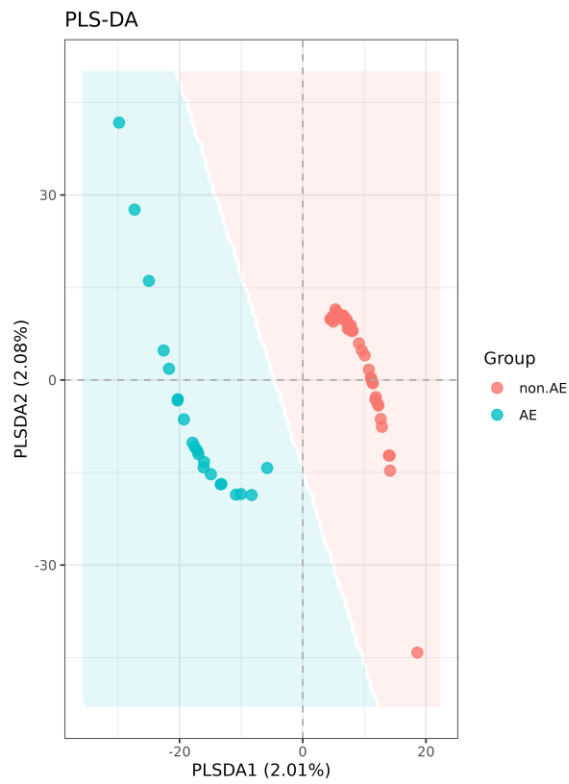




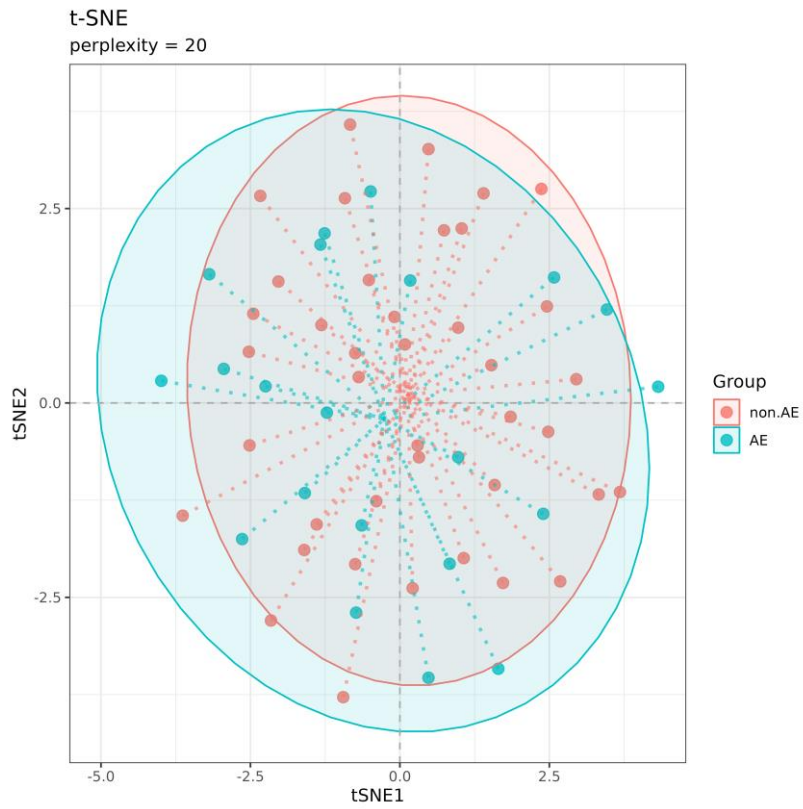
C



D

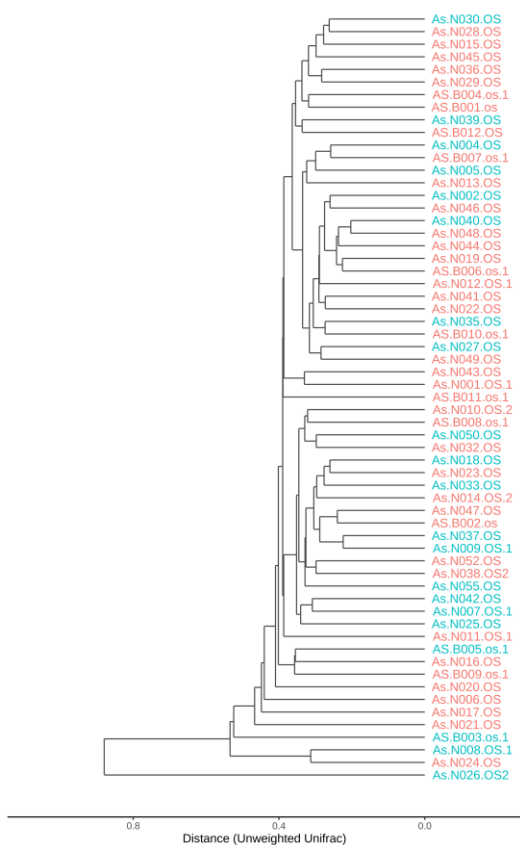


E



F





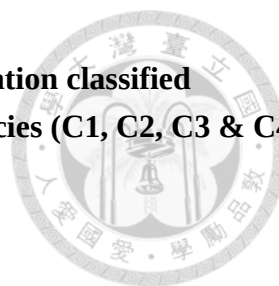
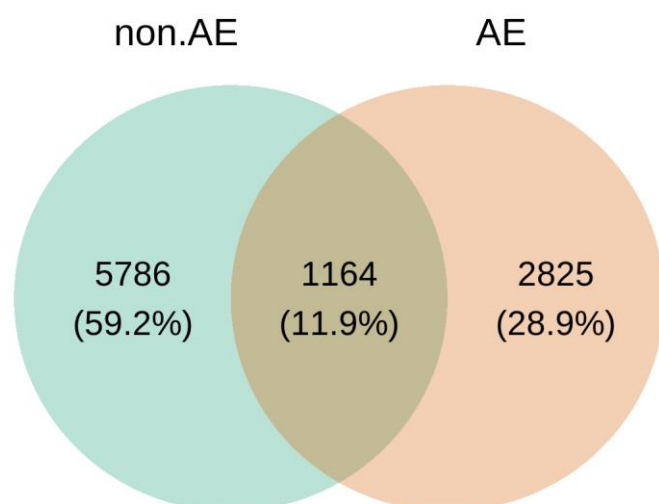


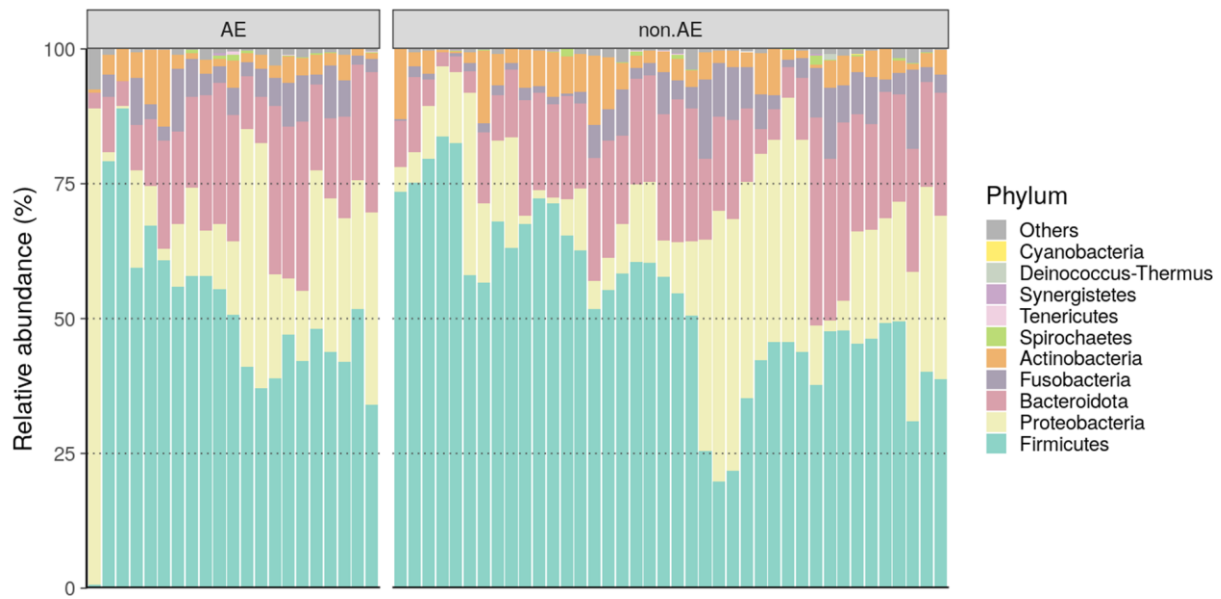
Figure 15. Oral taxa composition in asthma with and without exacerbation classified according to different distribution (A), phylum (B1, B2 & B3) and species (C1, C2, C3 & C4). AE= with exacerbation; non.AE=without exacerbation

A

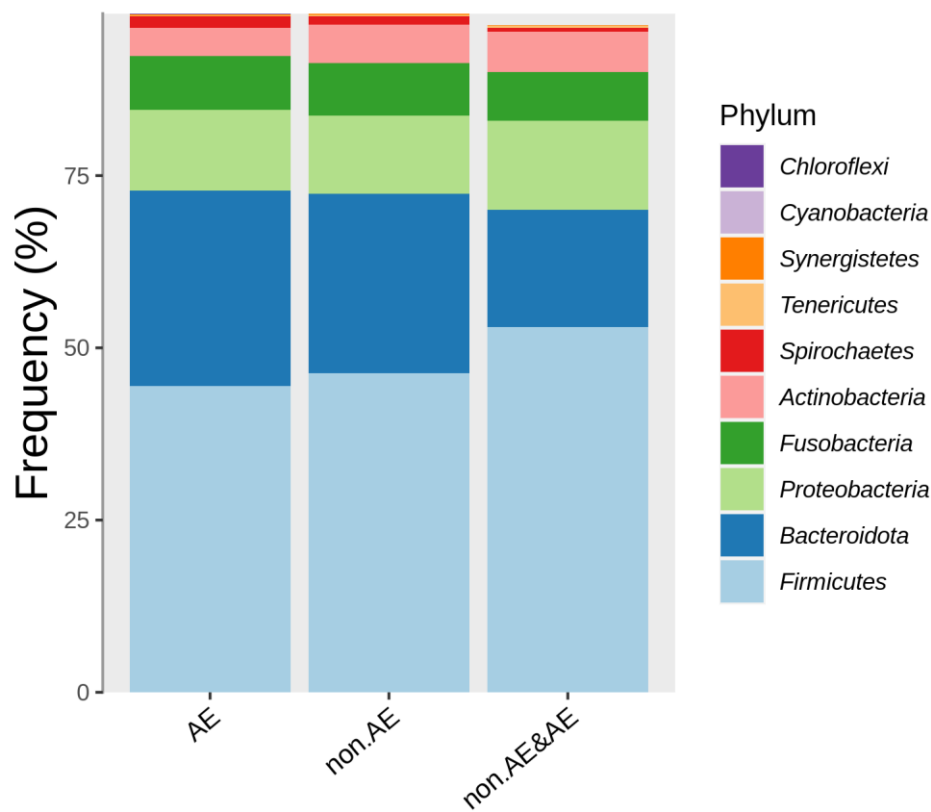




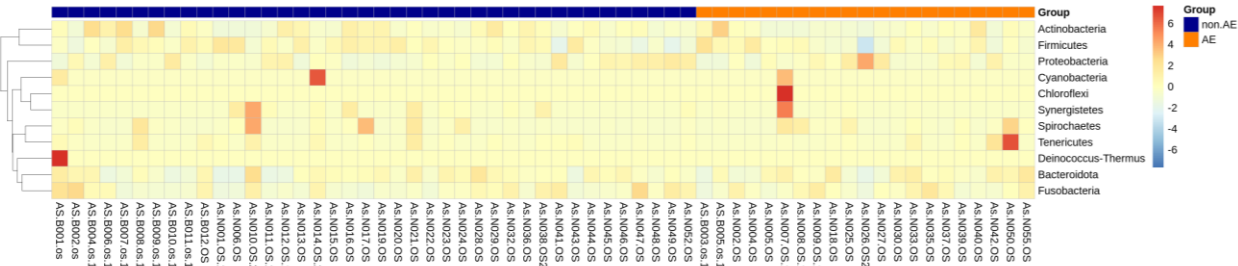
B1



B2

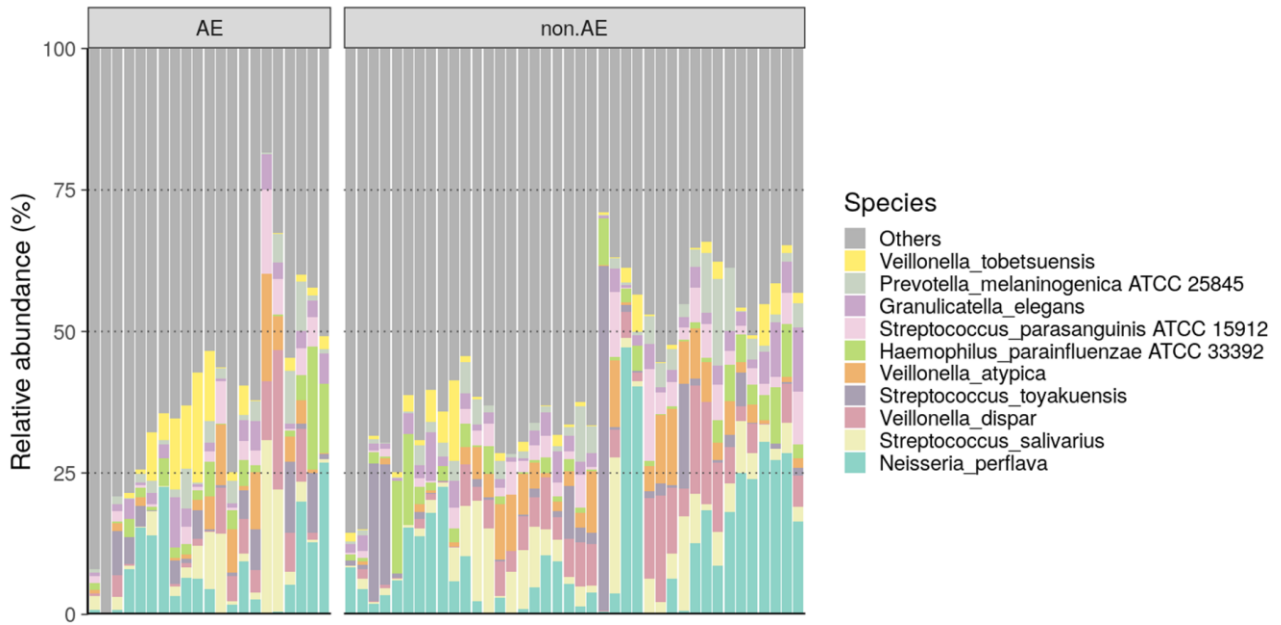


B3

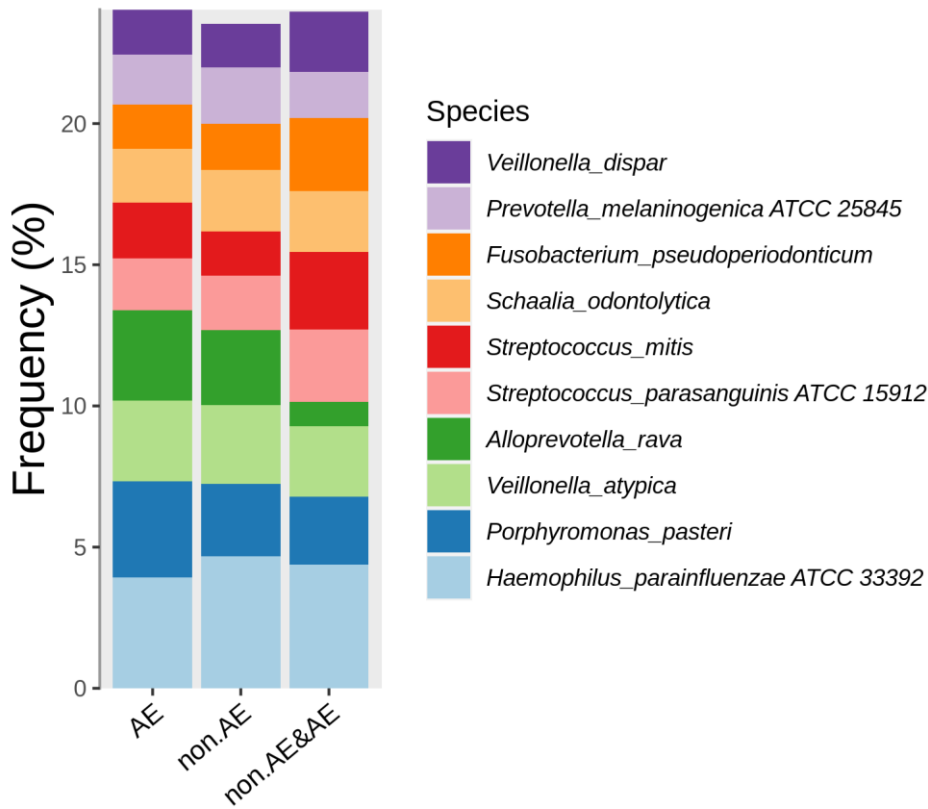




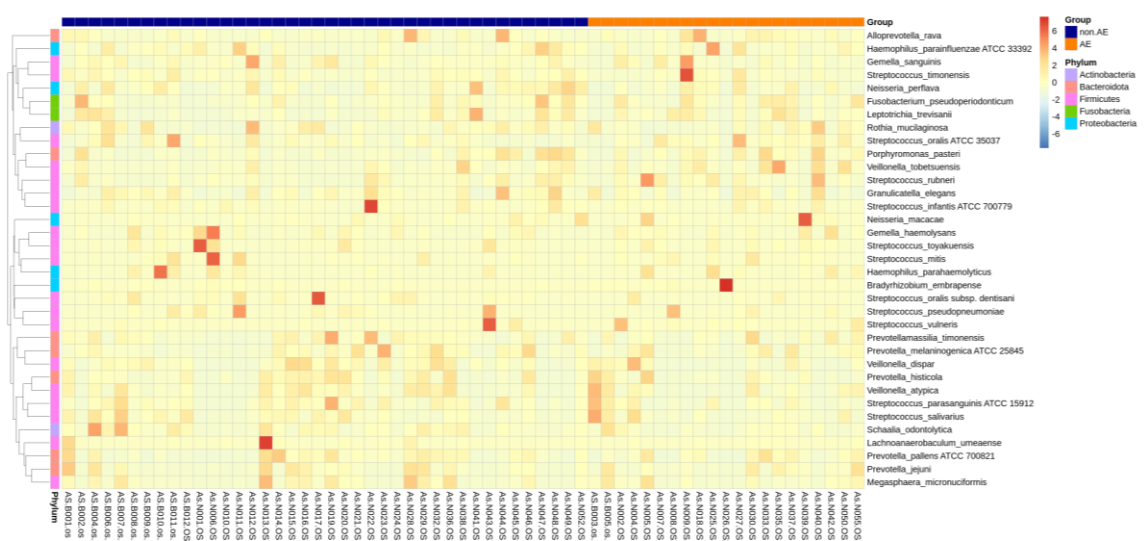
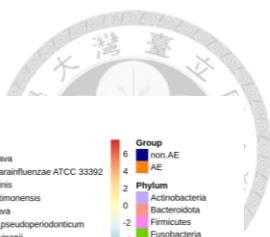
C1



C2



C3



D3

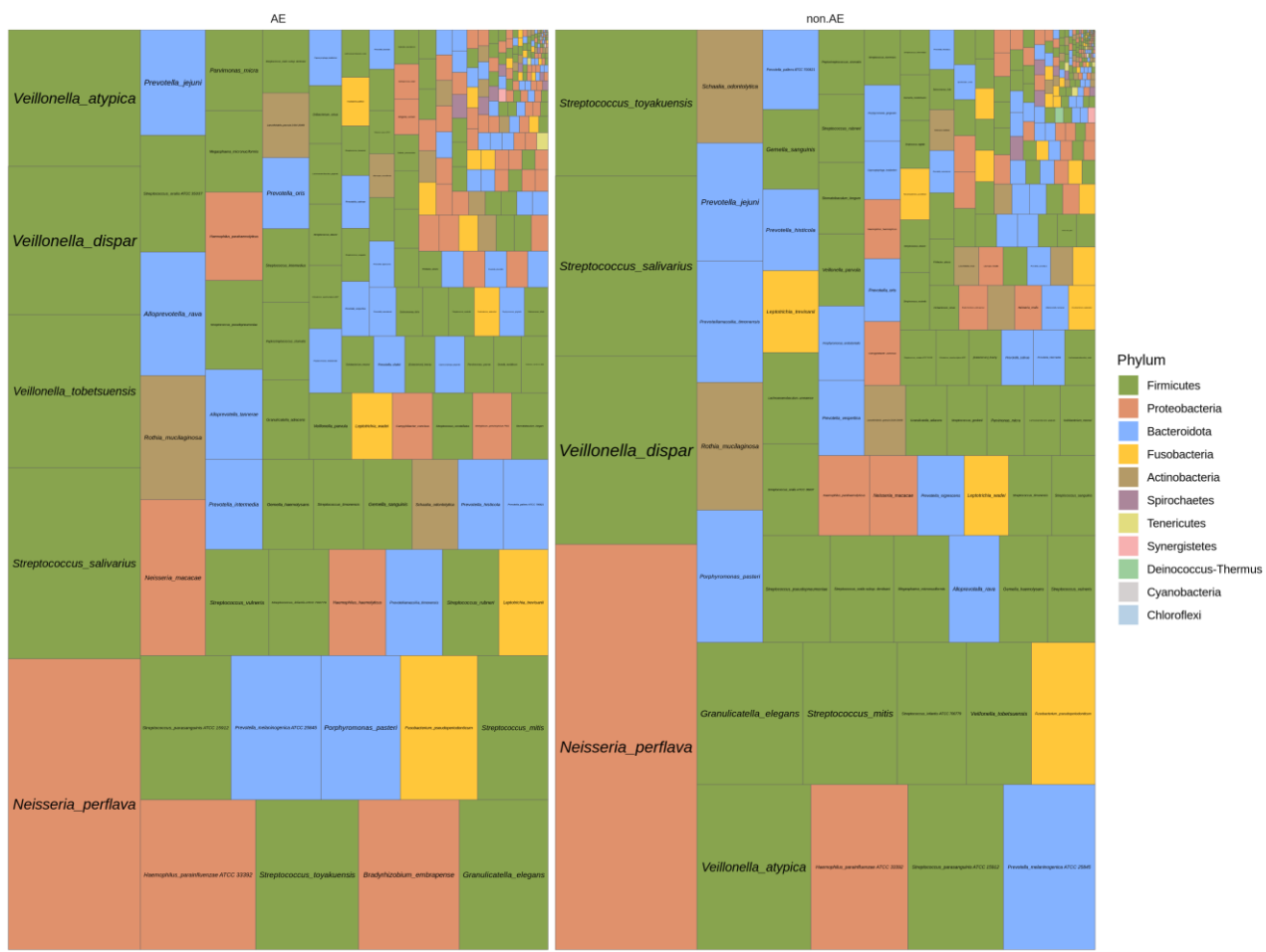
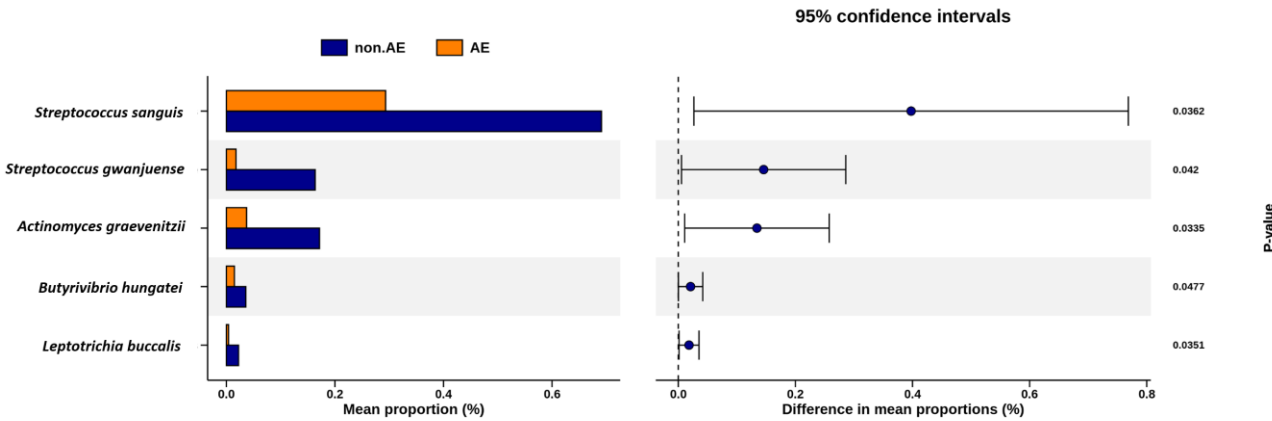




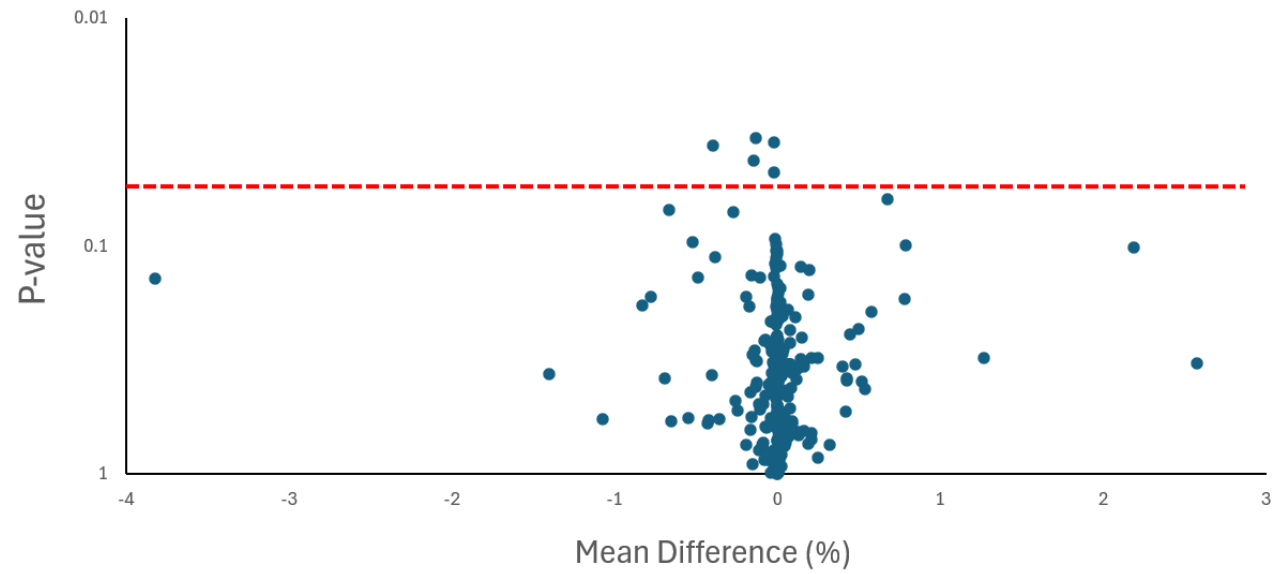
Figure 16. Differences in oral taxa in asthma with and without exacerbation classified according to different species (A1 & A2) and genus (B). AE= with exacerbation; non.AE=without exacerbation

A1

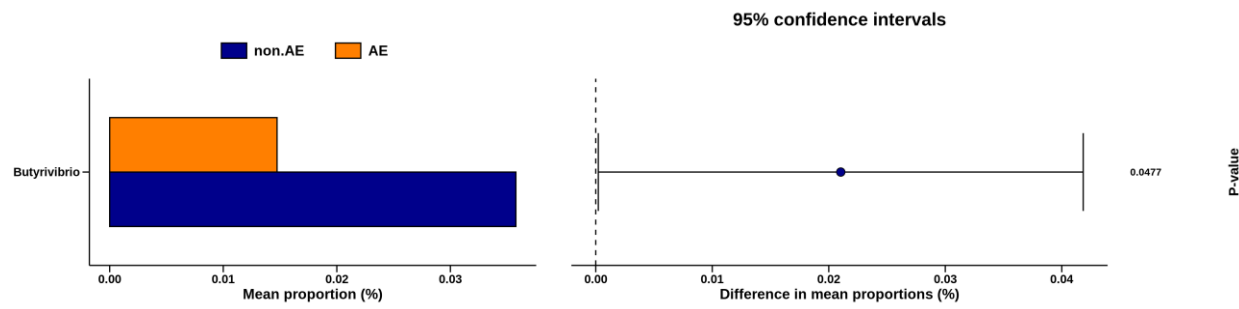


A2

Bacteria abundance between asthma patients with/without AE



B



Supplementary table 1. Differences in nasal taxa in asthma with and without exacerbation.

AE= with exacerbation; non.AE=without exacerbation

Taxonomy	mean (non.AE)	Sd (non.AE)	mean(AE)	sd(AE)	p-value	q-value	Mean Difference	95% lower CI	95% upper CI
<i>Acinetobacter_johnsonii</i>	0.13079	0.269645	0.016455	0.075408	0.015718	1	-0.11433	0.022514	0.206156
<i>Cutibacterium_acnes</i>	4.111714	6.341921	1.436342	2.137006	0.019027	1	-2.67537	0.457136	4.893608
<i>Pseudomonas_yamanorum</i>	0.400974	0.973357	0.023699	0.075266	0.01934	1	-0.37728	0.064435	0.690117
<i>Anaerococcus_octavius</i> NCTC 9810	0.543644	1.311089	0.061141	0.258059	0.029707	1	-0.4825	0.049711	0.915296
<i>Brevibacillus_marinus</i>	0.050907	0.135556	0.002944	0.013489	0.032306	1	-0.04796	0.004254	0.091673
<i>Pseudobdellovibrio_exovorus</i> JSS	0.074915	0.189871	0.008701	0.02911	0.036655	1	-0.06621	0.004304	0.128123
<i>Lactobacillus_crispatus</i>	0.211342	0.666513	0	0	0.051891	1	-0.21134	-0.00182	0.424503
<i>Pseudomonas_reidholzensis</i>	0.155347	0.462399	0.008616	0.035085	0.052796	1	-0.14673	-0.00186	0.295321
<i>Metabacillus_schmidteae</i>	0.308964	0.984215	0	0	0.054164	1	-0.30896	-0.0058	0.623731
<i>Sinocapsa_zengkensis</i>	0.014015	0.044908	0	0	0.055515	1	-0.01402	-0.00035	0.028378
<i>Coxiella_burnetii</i>	0.023839	0.077815	0	0	0.059947	1	-0.02384	-0.00105	0.048725
<i>Pseudomonas_poae</i>	0.036102	0.128749	0.53327	1.147814	0.06164	1	0.497168	-1.02093	0.026595
<i>Staphylococcus_warneri</i>	0.523755	1.662168	0.02209	0.101228	0.064455	1	-0.50167	-0.03156	1.03489
<i>Corynebacterium_haemomassiliense</i>	0.02939	0.098984	0	0	0.067892	1	-0.02939	-0.00227	0.061047
<i>Diaphorobacter_nitroreducens</i>	1.202399	2.568276	0.325736	1.101551	0.068337	1	-0.87666	-0.06815	1.821476
<i>Merdimonas_faecis</i>	0.064489	0.218061	0	0	0.068944	1	-0.06449	-0.00525	0.134229
<i>Anaerococcus_nagya</i>	0.118949	0.296478	0.024502	0.10033	0.073568	1	-0.09445	-0.00933	0.198222
<i>Brevundimonas_vesicularis</i>	0.073522	0.209731	0.010144	0.046488	0.074125	1	-0.06338	-0.00643	0.133187
<i>Corynebacterium_tuberculo</i> stearicum	0.463187	1.386444	0.065815	0.164465	0.081013	1	-0.39737	-0.05122	0.845962
<i>Sphingomonas_leidy</i>	1.525706	2.174113	3.451306	4.618941	0.082747	1	1.9256	-4.12001	0.268808
<i>Lachnoclostridium_pacaense</i>	0.095615	0.347834	0	0	0.090007	1	-0.09561	-0.01563	0.206857
<i>Alloprevotella_rava</i>	0.028995	0.150117	0.209343	0.457221	0.092387	1	0.180348	-0.39288	0.032184
<i>Paraburkholderia_bryophila</i>	0.037223	0.136594	0	0	0.092717	1	-0.03722	-0.00646	0.080908
<i>Brevundimonas_diminuta</i>	0.01266	0.046473	0	0	0.092817	1	-0.01266	-0.0022	0.027523
<i>Acinetobacter_junii</i>	0.19891	0.743945	0	0	0.098813	1	-0.19891	-0.03902	0.436835
<i>Bradyrhizobium_embra</i> pense	25.64023	22.76012	38.73754	31.83565	0.10418	1	13.09731	-29.0536	2.858987
<i>Pelomonas_saccharophila</i>	0.072586	0.273604	0.001946	0.008918	0.110854	1	-0.07064	-0.01694	0.15822
<i>Lacisediminimonas_profundi</i>	0.094626	0.284565	0.016769	0.076847	0.111375	1	-0.07786	-0.01865	0.174363
<i>Veillonella_parvula</i>	0.05336	0.165481	0.009068	0.041555	0.116336	1	-0.04429	-0.0114	0.099982
[<i>Eubacterium</i>] <i>_rectale</i> ATCC 33656	0.019729	0.078082	0	0	0.118116	1	-0.01973	-0.00524	0.0447
<i>Pleomorphomonas_oryzae</i>	0.010513	0.041678	0	0	0.11872	1	-0.01051	-0.00282	0.023842
<i>Acidovorax_temperans</i>	0.472768	1.879862	0	0	0.119781	1	-0.47277	-0.12844	1.073977

<i>Comamonas_suwonensis</i>	0.079333	0.322991	0	0	0.128396	1	-0.07933	-0.02396	0.182631
<i>Gehongia_tenuis</i>	0.015367	0.062593	0	0	0.128577	1	-0.01537	-0.00465	0.035385
<i>Ruminococcus_gauvreauii</i>	0.161332	0.667644	0	0	0.134511	1	-0.16133	-0.05219	0.374855
<i>Pseudoleptotrichia_goodfellowii</i>	0	0	0.106851	0.315954	0.136879	1	0.106851	-0.25067	0.036969
<i>Peptoniphilus_lacydonensis</i>	1.124294	3.767733	0.215242	0.550082	0.142145	1	-0.90905	-0.31726	2.135366
<i>Agrobacterium_rhizogenes</i>	0.217491	0.645412	0.056465	0.168067	0.144073	1	-0.16103	-0.05699	0.379039
<i>Capnocytophaga_granulosa</i>	0.003907	0.024708	0.061087	0.173293	0.147863	1	0.057181	-0.13638	0.022015
<i>Acetivibrio_alkalicellulosi</i>	0.074395	0.319099	0	0	0.148374	1	-0.07439	-0.02766	0.176448
<i>Prevotella_denticola</i>	0.208801	0.872261	0.006102	0.027964	0.150016	1	-0.2027	-0.0765	0.4819
<i>Camelliibacillus_cellulosilyticus</i>	0.150414	0.651128	0	0	0.152025	1	-0.15041	-0.05783	0.358655
<i>Streptococcus_australis</i>	0.092016	0.398399	0	0	0.152097	1	-0.09202	-0.0354	0.21943
<i>Gemella_sanguinis</i>	0.065187	0.201603	0.014452	0.066229	0.153136	1	-0.05073	-0.01949	0.120955
<i>Staphylococcus_saprophyticus</i> subsp. <i>saprophyticus</i> ATCC 15305 = NCTC 7292	0.098442	0.434576	0	0	0.15992	1	-0.09844	-0.04054	0.237427
<i>Pseudoflavonifractor_capillosus</i> ATCC 29799	0.022298	0.098441	0	0	0.159937	1	-0.0223	-0.00918	0.053781
<i>Dysgonomonas_gadei</i> ATCC BAA-286	0.026996	0.119181	0	0	0.15994	1	-0.027	-0.01112	0.065112
<i>Hominisplanchenecus_faecis</i>	0.038615	0.170502	0	0	0.160006	1	-0.03861	-0.01591	0.093144
<i>Leptospira_johnsonii</i>	0.122631	0.541686	0	0	0.160168	1	-0.12263	-0.05061	0.29587
<i>Anaerococcus_provencensis</i>	0.12654	0.55929	0	0	0.160414	1	-0.12654	-0.05233	0.305409
<i>Ruminococcoides_bili</i>	0.015164	0.067217	0	0	0.161603	1	-0.01516	-0.00633	0.03666
<i>Kingella_bonacorsii</i>	0.007974	0.035352	0	0	0.161649	1	-0.00797	-0.00333	0.01928
<i>Corynebacterium_durum</i>	0.011053	0.049004	0	0	0.161686	1	-0.01105	-0.00462	0.026725
<i>Staphylococcus_borealis</i>	0.016581	0.073665	0	0	0.162532	1	-0.01658	-0.00698	0.04014
<i>Brevibacillus_thermorum</i>	0.006724	0.029893	0	0	0.162828	1	-0.00672	-0.00284	0.016284
<i>Aerococcus_viridans</i>	0.021766	0.096955	0	0	0.163607	1	-0.02177	-0.00924	0.052773
<i>Schlegelella_aquatica</i>	0.05377	0.239781	0	0	0.164059	1	-0.05377	-0.02292	0.130456
<i>Fusicatenibacter_saccharivorans</i>	0.013826	0.061779	0	0	0.164878	1	-0.01383	-0.00593	0.033584
<i>Sphingomonas_arenae</i>	0.032543	0.145523	0	0	0.165196	1	-0.03254	-0.014	0.079083
<i>Eikenella_corrodens</i>	0	0	0.035711	0.113788	0.165851	1	0.035711	-0.08751	0.016085
<i>Acinetobacter_lwoffii</i>	0.008684	0.038898	0	0	0.16591	1	-0.00868	-0.00376	0.021124
<i>Gemmiger_gallinarum</i>	0.009533	0.042746	0	0	0.166338	1	-0.00953	-0.00414	0.023204
<i>Streptococcus_sanguinis</i>	0.310064	0.860219	0.094919	0.32858	0.167312	1	-0.21514	-0.09294	0.523232
<i>Anaerococcus_urinomassiliensis</i>	0.231604	1.044082	0	0	0.168543	1	-0.2316	-0.10231	0.565518
<i>Corynebacterium_oculi</i>	0.00476	0.021483	0	0	0.16904	1	-0.00476	-0.00211	0.01163
<i>Parabacteroides_merdae</i>	0.018722	0.084592	0	0	0.169492	1	-0.01872	-0.00833	0.045776

<i>Janthinobacterium_lividum</i>	0.086974	0.384056	0.001998	0.009156	0.169816	1	-0.08498	-0.03791	0.207861
<i>Capnocytophaga_leadbetteri</i>	0.037596	0.229735	0.210545	0.53474	0.169897	1	0.172949	-0.42521	0.079314
<i>Peptostreptococcus_stomatis</i>	0.001116	0.007059	0.312177	1.005337	0.17162	1	0.31106	-0.76869	0.146568
<i>Prevotella_nanceiensis</i>	0.000573	0.003626	0.20435	0.664676	0.175388	1	0.203776	-0.50633	0.098782
<i>Treponema_amylovorum</i>	0	0	0.099306	0.324354	0.175942	1	0.099306	-0.24695	0.048338
<i>Corynebacterium_matruchotii</i>	0.058968	0.270888	0	0	0.176441	1	-0.05897	-0.02767	0.145602
<i>Curvibacter_fontanus</i>	0.300778	0.906195	0.094184	0.212257	0.176645	1	-0.20659	-0.09641	0.509599
<i>Aggregatibacter_aprophilus</i> ATCC 33389	0.026197	0.120752	0	0	0.177877	1	-0.0262	-0.01242	0.064815
<i>Vampirovibrio_chlorellavorus</i>	0.013603	0.062972	0	0	0.179691	1	-0.0136	-0.00654	0.033743
<i>Conexibacter_arvalis</i>	0.014869	0.068986	0	0	0.180645	1	-0.01487	-0.00719	0.036932
<i>Streptococcus_rubneri</i>	0.142302	0.602193	0.01243	0.050724	0.183056	1	-0.12987	-0.06385	0.323598
<i>Afipia_carboxidovorans</i>	0.028376	0.134373	0	0	0.189428	1	-0.02838	-0.0146	0.071351
<i>Shigella_sonnei</i>	0.863985	1.908431	0.409041	0.742075	0.189439	1	-0.45494	-0.23116	1.141047
<i>Lachnoanaerobaculum_umeaense</i>	0	0	0.111008	0.374619	0.189613	1	0.111008	-0.28153	0.059517
<i>Bradyrhizobium_liaoningense</i>	0.011991	0.056869	0	0	0.190091	1	-0.01199	-0.0062	0.030178
<i>Caedimonas_varicaedens</i>	0	0	0.064178	0.217039	0.190506	1	0.064178	-0.16297	0.034617
<i>Granulicella_tundricola</i> MP5ACTX9	0.06492	0.308559	0	0	0.191029	1	-0.06492	-0.03376	0.163602
<i>Rubellimicrobium_mesophilum</i>	0.015491	0.073783	0	0	0.19194	1	-0.01549	-0.00811	0.039088
<i>Staphylococcus_haemolyticus</i>	0.090908	0.424611	0.001737	0.00796	0.191971	1	-0.08917	-0.04667	0.225007
<i>Catonella_massiliensis</i>	0	0	0.153089	0.521001	0.193196	1	0.153089	-0.39025	0.084068
<i>Pseudomonas_psychrotolerans</i>	0.052223	0.249905	0	0	0.193986	1	-0.05222	-0.0277	0.132146
<i>Granulicatella_elegans</i>	0.819902	3.255034	0.133012	0.36548	0.194552	1	-0.68689	-0.36502	1.738803
<i>Streptococcus_anginosus</i>	0.002038	0.012887	0.055443	0.184134	0.199251	1	0.053406	-0.1373	0.030491
<i>Wansuia_hejianensis</i>	0.004547	0.022165	0	0	0.2021	1	-0.00455	-0.00254	0.011636
<i>Dolosigranulum_pigrum</i>	0	0	0.137419	0.481688	0.205925	1	0.137419	-0.35668	0.081842
<i>Dorea_longicatena</i>	0.016341	0.080364	0	0	0.20601	1	-0.01634	-0.00936	0.042043
<i>Stutzerimonas_stutzeri</i>	0.039799	0.19595	0	0	0.206517	1	-0.0398	-0.02287	0.102467
<i>Blautia_wexlerae</i> DSM 19850	0.028918	0.143586	0	0	0.21029	1	-0.02892	-0.017	0.074839
<i>Brevundimonas_staleyii</i>	0.021813	0.108328	0	0	0.210381	1	-0.02181	-0.01283	0.056458
<i>Prevotella_shahii</i>	0	0	0.063875	0.227864	0.213619	1	0.063875	-0.1676	0.039848
<i>Actinomyces_oris</i>	0.012684	0.05745	0.001134	0.005194	0.214309	1	-0.01155	-0.00695	0.030048
<i>Lautropia_mirabilis</i>	0.004643	0.025932	0.061223	0.202537	0.216779	1	0.05658	-0.14907	0.035909
<i>Anaerostipes_butyricus</i>	0.063505	0.320049	0	0	0.216972	1	-0.0635	-0.03885	0.165861
<i>Roseburia_faecis</i>	0.023579	0.119653	0	0	0.220077	1	-0.02358	-0.01469	0.061846
<i>Dysgonomonas_oryzarvi</i>	0.008905	0.045361	0	0	0.221816	1	-0.0089	-0.0056	0.023412
<i>Bacillus_tropicus</i>	0.037298	0.135745	0.008695	0.039847	0.222533	1	-0.0286	-0.01791	0.075111

<i>Sphingobium_naphthae</i>	0.248716	1.250346	0.006253	0.028656	0.227603	1	-0.24246	-0.15759	0.642517
<i>Faecalibacterium_longum</i>	0.014795	0.076432	0	0	0.228194	1	-0.0148	-0.00965	0.039239
<i>Leptotrichia_trevisanii</i>	0.00513	0.023314	0.103134	0.362085	0.229628	1	0.098004	-0.26296	0.066948
<i>Streptococcus_vulneris</i>	0.014739	0.09322	0.128464	0.418568	0.23257	1	0.113725	-0.30611	0.078656
<i>Fumia_xinanensis</i>	0.007785	0.040702	0	0	0.233704	1	-0.00778	-0.00523	0.020802
<i>Leptotrichia_wadei</i>	0.028587	0.174061	0.247544	0.811109	0.235128	1	0.218957	-0.5915	0.153584
<i>Prevotella_copri</i> DSM 18205	0.225722	1.188693	0	0	0.237003	1	-0.22572	-0.15444	0.605885
<i>Mediterraneibacter_[Ruminococcus] faecis</i> JCM 15917	0.082035	0.436422	0	0	0.241693	1	-0.08203	-0.05754	0.221609
<i>Breznakia_pachnodae</i>	0.013385	0.071317	0	0	0.242404	1	-0.01338	-0.00942	0.036193
<i>Shigella_flexneri</i>	0.742572	0.962926	1.236655	1.765306	0.243553	1	0.494082	-1.34488	0.356717
<i>[Eubacterium]_saphenum</i>	0.00892	0.047728	0	0	0.244382	1	-0.00892	-0.00634	0.024184
<i>Elizabethkingia_bruuniana</i>	0.00173	0.010941	0.067885	0.254251	0.247267	1	0.066155	-0.18193	0.04962
<i>Lawsonella_clevelandensis</i>	0.542221	1.967831	0.159031	0.485653	0.24954	1	-0.38319	-0.27794	1.044316
<i>Adhaeribacter_rhizoryzae</i>	0.054478	0.27036	0.004298	0.019695	0.249762	1	-0.05018	-0.03667	0.137027
<i>Paracoccus_salipaludis</i>	0.020466	0.110808	0	0	0.249849	1	-0.02047	-0.01497	0.055904
<i>Laceyella_putida</i>	0.08511	0.4616	0	0	0.250649	1	-0.08511	-0.06252	0.232737
<i>Barnesiella_intestinihominis</i>	0.015786	0.085637	0	0	0.25076	1	-0.01579	-0.0116	0.043174
<i>Actinomyces_massiliensis</i> 4401292	0.020802	0.113324	0	0	0.252727	1	-0.0208	-0.01544	0.057044
<i>Eubacterium_nodatum</i> ATCC 33099	0	0	0.033811	0.131583	0.252816	1	0.033811	-0.09371	0.026085
<i>Negativicoccus_massiliensis</i>	0.014027	0.076445	0	0	0.252914	1	-0.01403	-0.01042	0.038475
<i>Romboutsia_timonensis</i>	0.066589	0.363142	0	0	0.253211	1	-0.06659	-0.04955	0.182727
<i>Nevskia_terrae</i>	0.020733	0.113811	0	0	0.256288	1	-0.02073	-0.01567	0.057131
<i>Aquabacterium_terrae</i>	0.009787	0.055215	0.063456	0.208207	0.25877	1	0.053669	-0.14975	0.042413
<i>Schlegelella_brevitalea</i>	0.007405	0.04091	0	0	0.259283	1	-0.0074	-0.00568	0.020489
<i>Luoshenia_tenuis</i>	0.011214	0.062639	0	0	0.264427	1	-0.01121	-0.00882	0.031247
<i>Treponema_medium</i>	0.028669	0.181317	0.277515	0.986877	0.265101	1	0.248846	-0.70103	0.203342
<i>Capnocytophaga_ochracea</i>	0.02352	0.13341	0	0	0.271672	1	-0.02352	-0.01915	0.066186
<i>Cutibacterium_avidum</i> ATCC 25577	0.078044	0.443257	0	0	0.272281	1	-0.07804	-0.06372	0.219805
<i>Veillonella_massiliensis</i>	0	0	0.038129	0.1555	0.274459	1	0.038129	-0.10891	0.032653
<i>Paraburkholderia_functorum</i>	0.358997	0.606502	0.214368	0.412063	0.276055	1	-0.14463	-0.11883	0.408087
<i>Streptococcus_gordonii</i>	0.039559	0.177225	0.007651	0.035062	0.277898	1	-0.03191	-0.02661	0.090429
<i>Geobacillus_stearothermophilus</i>	0.235125	1.351676	0	0	0.278007	1	-0.23512	-0.19716	0.667412
<i>Duncaniella_dubosii</i>	0.071714	0.412297	0	0	0.278043	1	-0.07171	-0.06015	0.203573
<i>Dialister_pneumosintes</i>	0	0	0.206485	0.849166	0.278359	1	0.206485	-0.59302	0.180051
<i>Granulicatella_adiacens</i>	0.145302	0.600916	0.035039	0.160567	0.2816	1	-0.11026	-0.09329	0.313814
<i>Solibaculum_mannosilyticum</i>	0.049901	0.289434	0	0	0.28222	1	-0.0499	-0.04266	0.142467

<i>Ligilactobacillus_murinus</i>	0.022483	0.130762	0	0	0.283526	1	-0.02248	-0.01934	0.064302
<i>Finegoldia_magna</i>	0.343548	1.417766	0.091482	0.290402	0.285007	1	-0.25207	-0.21715	0.721281
<i>Sphingobium_yanoikuyae</i>	0.021808	0.101331	0.080278	0.234003	0.285439	1	0.05847	-0.16892	0.051983
<i>Aminipila_terrae</i>	0.000541	0.003421	0.081125	0.337995	0.287582	1	0.080584	-0.23444	0.073273
<i>Treponema_maltophilum</i>	0.013523	0.085527	0.128984	0.482206	0.288985	1	0.115461	-0.33631	0.105387
<i>Ketobacter_alkanivorans</i>	0.016424	0.083404	0.002103	0.009635	0.289797	1	-0.01432	-0.01265	0.041291
<i>Stenotrophomonas_[Pseudomonas] hibiscicola</i>	0.023525	0.139534	0	0	0.292839	1	-0.02353	-0.0211	0.06815
<i>Lihuaxuella_thermophila</i>	0.217098	1.287973	0	0	0.292955	1	-0.2171	-0.19482	0.629012
<i>Catonella_morbi ATCC 51271</i>	0.075809	0.452219	0	0	0.295557	1	-0.07581	-0.06882	0.220436
<i>Kocuria_palustris</i>	0.046028	0.274963	0	0	0.296242	1	-0.04603	-0.04191	0.133966
<i>Prevotella_loescheii</i>	0.031915	0.135818	0.008275	0.029795	0.297604	1	-0.02364	-0.02153	0.068811
<i>Brachy bacterium_massiliense</i>	0.030031	0.180307	0	0	0.298645	1	-0.03003	-0.02763	0.087696
<i>Paracoccus_sphaerophysae</i>	0.023577	0.142039	0	0	0.300271	1	-0.02358	-0.02185	0.069003
<i>Prevotella_baroniae</i>	0	0	0.119277	0.514869	0.301061	1	0.119277	-0.35364	0.115089
<i>Unknown</i>	3.47504	5.129098	2.294774	3.608885	0.301112	1	-1.18027	-1.08626	3.446795
<i>Capnocytophaga_gingivalis</i>	0.003544	0.022413	0.149592	0.634357	0.304122	1	0.146048	-0.43487	0.142778
<i>Eubacterium_sulci ATCC 35585</i>	0	0	0.122594	0.535155	0.306338	1	0.122594	-0.36619	0.121006
<i>Pseudomonas_aeruginosa</i>	0.445904	2.743752	0	0	0.310356	1	-0.4459	-0.43159	1.323399
<i>Thermicanus_aegyptius</i>	0.04054	0.24962	0	0	0.310681	1	-0.04054	-0.03929	0.120372
<i>Acetivibrio_cellulolyticus</i>	0.011254	0.069708	0	0	0.313529	1	-0.01125	-0.01104	0.033548
<i>Brevundimonas_intermedia</i>	0.96935	5.333945	0.107651	0.313184	0.314686	1	-0.8617	-0.84906	2.572463
<i>Neisseria_shayegani 871</i>	0	0	0.050783	0.225993	0.315418	1	0.050783	-0.15365	0.052088
<i>Haemophilus_para haemolyticus</i>	0	0	0.079528	0.354162	0.315752	1	0.079528	-0.24074	0.081685
<i>Staphylococcus_hominis</i>	0.008543	0.034075	0.002523	0.011562	0.316207	1	-0.00602	-0.00591	0.017952
<i>Duncanella_freteri</i>	0.061633	0.386476	0	0	0.319378	1	-0.06163	-0.06197	0.185234
<i>Porphyromonas_gingivalis</i>	0	0	0.071311	0.321376	0.321373	1	0.071311	-0.2176	0.074977
<i>Truepera_radiovictrix DSM 17093</i>	0.453762	2.860358	0	0	0.321893	1	-0.45376	-0.46103	1.368549
<i>Prevotella_intermedia</i>	0.022019	0.113079	1.929968	8.608532	0.321942	1	1.907948	-5.82664	2.01074
<i>Actinomyces_pacaensis</i>	0.46604	2.947499	0	0	0.323475	1	-0.46604	-0.47662	1.408696
<i>Bifidobacterium_longum subsp. suillum</i>	0.026296	0.166313	0	0	0.323475	1	-0.0263	-0.02689	0.079486
<i>Blautia_producta ATCC 27340 = DSM 2950</i>	0.011273	0.071297	0	0	0.323475	1	-0.01127	-0.01153	0.034075
<i>Brevundimonas_bullata</i>	0.028302	0.178997	0	0	0.323475	1	-0.0283	-0.02894	0.085548
<i>Caldovatus_sediminis</i>	0.434211	2.746188	0	0	0.323475	1	-0.43421	-0.44406	1.312484
<i>Chryseosolibacter_indicus</i>	0.048655	0.307721	0	0	0.323475	1	-0.04865	-0.04976	0.147069
<i>Dehalobacterium_formicoaceticum</i>	0.031895	0.20172	0	0	0.323475	1	-0.03189	-0.03262	0.096408

<i>Domibacillus_enclensis</i>	0.012603	0.07971	0	0	0.323475	1	-0.0126	-0.01289	0.038096
<i>Domibacillus_robiginosus</i>	0.0891	0.563517	0	0	0.323475	1	-0.0891	-0.09112	0.269322
<i>Dysgonomonas_alginatilytica</i>	0.008613	0.054476	0	0	0.323475	1	-0.00861	-0.00881	0.026036
<i>Intestinimonas_timonensis</i>	0.0063	0.039846	0	0	0.323475	1	-0.0063	-0.00644	0.019044
<i>Novosphingobium_arvoryzae</i>	0.001412	0.00893	0	0	0.323475	1	-0.00141	-0.00144	0.004268
<i>Phocaeicola_coprocola</i> DSM 17136	0.062977	0.398304	0	0	0.323475	1	-0.06298	-0.06441	0.190361
<i>Prevotella_disiens</i>	0.098548	0.62327	0	0	0.323475	1	-0.09855	-0.10078	0.297879
<i>Protaetiobacter_larvae</i>	0.002269	0.014352	0	0	0.323475	1	-0.00227	-0.00232	0.006859
<i>Pseudomonas_helleri</i>	0.011349	0.071775	0	0	0.323475	1	-0.01135	-0.01161	0.034303
<i>Pseudonocardia_carboxydivorans</i>	0.003325	0.021032	0	0	0.323475	1	-0.00333	-0.0034	0.010052
<i>Roseateles_depolymerans</i>	0.000709	0.004483	0	0	0.323475	1	-0.00071	-0.00072	0.002143
<i>Salinisphaera_aquimarina</i>	0.049304	0.311824	0	0	0.323475	1	-0.0493	-0.05042	0.14903
<i>Sphingomonas_olei</i>	0.000756	0.00478	0	0	0.323475	1	-0.00076	-0.00077	0.002284
<i>Streptococcus_alactolyticus</i>	0.006694	0.042336	0	0	0.323475	1	-0.00669	-0.00685	0.020234
<i>Streptococcus_cristatus</i> AS 1.3089	0.027798	0.175812	0	0	0.323475	1	-0.0278	-0.02843	0.084026
<i>Syntrophotalea_carbinolica</i> DSM 2380	0.00315	0.019923	0	0	0.323475	1	-0.00315	-0.00322	0.009522
<i>Telmatospirillum_siberiense</i>	0.013454	0.085093	0	0	0.323475	1	-0.01345	-0.01376	0.040668
<i>Acidocella_aluminiidurans</i>	0.007919	0.050083	0	0	0.323475	1	-0.00792	-0.0081	0.023936
<i>Acidovorax_antarcticus</i>	0.00402	0.025424	0	0	0.323475	1	-0.00402	-0.00411	0.012151
<i>Acidovorax_radici</i> N35	0.022444	0.141951	0	0	0.323475	1	-0.02244	-0.02295	0.067843
<i>Acidovorax_wautersii</i>	0.000989	0.006252	0	0	0.323475	1	-0.00099	-0.00101	0.002988
<i>Acinetobacter_albensis</i>	0.00422	0.026693	0	0	0.323475	1	-0.00422	-0.00432	0.012757
<i>Acinetobacter_indicus</i> CIP 110367	0.000457	0.002889	0	0	0.323475	1	-0.00046	-0.00047	0.001381
<i>Aeromonas_caviae</i>	0.001116	0.007059	0	0	0.323475	1	-0.00112	-0.00114	0.003374
<i>Aeromonas_salmonicida</i> subsp. <i>masoucida</i>	0.012949	0.081899	0	0	0.323475	1	-0.01295	-0.01324	0.039142
<i>Agrococcus_sediminis</i>	0.011947	0.075562	0	0	0.323475	1	-0.01195	-0.01222	0.036113
<i>Alistipes_dispar</i>	0.078063	0.493713	0	0	0.323475	1	-0.07806	-0.07983	0.23596
<i>Alistipes_megaquti</i>	0.00945	0.059769	0	0	0.323475	1	-0.00945	-0.00966	0.028565
<i>Alistipes_senegalensis</i> JC50	0.001484	0.009388	0	0	0.323475	1	-0.00148	-0.00152	0.004487
<i>Alistipes_shahii</i>	0.00402	0.025424	0	0	0.323475	1	-0.00402	-0.00411	0.012151
<i>Alkalihalobacillus_nanhaisediminis</i>	0.082797	0.523655	0	0	0.323475	1	-0.0828	-0.08468	0.25027
<i>Allobacillus_salarius</i>	0.00601	0.038011	0	0	0.323475	1	-0.00601	-0.00615	0.018166
<i>Allobacillus_saliphilus</i>	0.016828	0.10643	0	0	0.323475	1	-0.01683	-0.01721	0.050866
<i>Amaricoccus_kaplicensis</i>	0.082787	0.523588	0	0	0.323475	1	-0.08279	-0.08467	0.250238
<i>Ammonifex_thiophilus</i>	0.082564	0.522182	0	0	0.323475	1	-0.08256	-0.08444	0.249566
<i>Amnibacterium_kyonggiense</i>	0.004759	0.030099	0	0	0.323475	1	-0.00476	-0.00487	0.014385

<i>Anaerobacillus_alkaliphilus</i>	0.001717	0.01086	0	0	0.323475	1	-0.00172	-0.00176	0.00519
<i>Anaerotignum_faecicola</i>	0.014572	0.092161	0	0	0.323475	1	-0.01457	-0.0149	0.044046
<i>Anaerotignum_lactatifermentans</i>	0.023413	0.148078	0	0	0.323475	1	-0.02341	-0.02394	0.070771
<i>Arcticibacter_tournemirensis</i>	0.033046	0.209001	0	0	0.323475	1	-0.03305	-0.0338	0.099888
<i>Atopostipes_suicloacalis</i>	0.001029	0.006506	0	0	0.323475	1	-0.00103	-0.00105	0.003109
<i>Aurantisolimonas_haloimpatiens</i>	0.001116	0.007059	0	0	0.323475	1	-0.00112	-0.00114	0.003374
<i>Bacillus_carboniphilus</i>	0.059355	0.375397	0	0	0.323475	1	-0.05936	-0.0607	0.179413
<i>Bacillus_mesophilus</i>	0.010202	0.064526	0	0	0.323475	1	-0.0102	-0.01043	0.030839
<i>Bacillus_yapensis</i>	0.012557	0.079417	0	0	0.323475	1	-0.01256	-0.01284	0.037956
<i>Bacteroides_fragilis</i>	0.022612	0.143008	0	0	0.323475	1	-0.02261	-0.02312	0.068348
<i>Bacteroides_neonati</i>	0.008054	0.050937	0	0	0.323475	1	-0.00805	-0.00824	0.024344
<i>Bacteroides_zoogloformans</i>	0.003555	0.022482	0	0	0.323475	1	-0.00355	-0.00364	0.010745
<i>Barnesiella_viscericola</i>	0.017719	0.112067	0	0	0.323475	1	-0.01772	-0.01812	0.05356
<i>Bdellovibrio_bacteriovorus</i>	0.021233	0.134289	0	0	0.323475	1	-0.02123	-0.02171	0.064181
<i>Bifidobacterium_adolescentis</i> ATCC 15703	0.003546	0.022425	0	0	0.323475	1	-0.00355	-0.00363	0.010718
<i>Bifidobacterium_adolescentis</i> JCM 15918	0.020908	0.132234	0	0	0.323475	1	-0.02091	-0.02138	0.063198
<i>Bifidobacterium_animalis</i> subsp. <i>lactis</i>	0.00628	0.03972	0	0	0.323475	1	-0.00628	-0.00642	0.018983
<i>Bifidobacterium_faecale</i>	0.019005	0.120198	0	0	0.323475	1	-0.019	-0.01944	0.057446
<i>Bifidobacterium_porcinum</i>	0.071894	0.454694	0	0	0.323475	1	-0.07189	-0.07352	0.217312
<i>Bilophila_wadsworthia</i>	0.002284	0.014444	0	0	0.323475	1	-0.00228	-0.00234	0.006903
<i>Blautia_coccoides</i>	0.005857	0.037045	0	0	0.323475	1	-0.00586	-0.00599	0.017705
<i>Blautia_hydrogenotrophica</i>	0.001028	0.0065	0	0	0.323475	1	-0.00103	-0.00105	0.003106
<i>Blautia_obeum</i> ATCC 29174	0.007401	0.046807	0	0	0.323475	1	-0.0074	-0.00757	0.02237
<i>Blautia_provencensis</i>	0.036513	0.230931	0	0	0.323475	1	-0.03651	-0.03734	0.110369
<i>Bosea_vestrisii</i> 34635	0.012164	0.076935	0	0	0.323475	1	-0.01216	-0.01244	0.03677
<i>Bradyrhizobium_centroseomatis</i>	0.003606	0.022806	0	0	0.323475	1	-0.00361	-0.00369	0.0109
<i>Bradyrhizobium_elkanii</i>	0.000992	0.006277	0	0	0.323475	1	-0.00099	-0.00101	0.003
<i>Bradyrhizobium_murdochi</i>	0.009074	0.057388	0	0	0.323475	1	-0.00907	-0.00928	0.027427
<i>Brevundimonas_subvibrioides</i>	0.004687	0.029644	0	0	0.323475	1	-0.00469	-0.00479	0.014168
<i>Bryobacter_aggregatus</i>	0.03112	0.196822	0	0	0.323475	1	-0.03112	-0.03183	0.094067
<i>Burkholderia_multivorans</i>	0.073523	0.465001	0	0	0.323475	1	-0.07352	-0.07519	0.222237
<i>Caecibacter_massiliensis</i>	0.043999	0.278275	0	0	0.323475	1	-0.044	-0.045	0.132996
<i>Caldibacillus_debilis</i>	0.025832	0.163374	0	0	0.323475	1	-0.02583	-0.02642	0.078081
<i>Campylobacter_hominis</i>	0.003875	0.024509	0	0	0.323475	1	-0.00388	-0.00396	0.011713
<i>Campylobacter_rectus</i>	0.020825	0.131712	0	0	0.323475	1	-0.02083	-0.0213	0.062949

<i>Campylobacter_ureolyticus</i>	0.047792	0.302263	0	0	0.323475	1	-0.04779	-0.04888	0.14446
<i>Cardiobacterium_valvarum</i>	0.022444	0.141951	0	0	0.323475	1	-0.02244	-0.02295	0.067843
<i>Caulobacter_vibrioides</i>	0.044114	0.279	0	0	0.323475	1	-0.04411	-0.04511	0.133342
<i>Cavicella_subterranea</i>	0.013414	0.084839	0	0	0.323475	1	-0.01341	-0.01372	0.040547
<i>Changpingibacter_yushuensis</i>	0.024631	0.155777	0	0	0.323475	1	-0.02463	-0.02519	0.074451
<i>Chryseobacterium_indologenes</i> NBRC 14944	0.019327	0.122233	0	0	0.323475	1	-0.01933	-0.01977	0.058419
<i>Chryseobacterium_koreense</i>	0.004027	0.025469	0	0	0.323475	1	-0.00403	-0.00412	0.012172
<i>Citrobacter_koseri</i>	0.002363	0.014942	0	0	0.323475	1	-0.00236	-0.00242	0.007141
<i>Cloacibacterium_caeni</i>	0.006245	0.039497	0	0	0.323475	1	-0.00625	-0.00639	0.018877
<i>Clostridium_tunisiense</i>	0.001098	0.006946	0	0	0.323475	1	-0.0011	-0.00112	0.00332
<i>Cohnella_candidum</i>	0.141786	0.896735	0	0	0.323475	1	-0.14179	-0.145	0.428576
<i>Cohnella_nanjingensis</i>	0.099637	0.630161	0	0	0.323475	1	-0.09964	-0.1019	0.301172
<i>Collinsella_aerofaciens</i>	0.040031	0.253177	0	0	0.323475	1	-0.04003	-0.04094	0.121001
<i>Coprococcus_eutactus</i>	0.001675	0.010593	0	0	0.323475	1	-0.00167	-0.00171	0.005063
<i>Corynebacterium_aurimucosum</i>	0.006095	0.038548	0	0	0.323475	1	-0.00609	-0.00623	0.018423
<i>Corynebacterium_hansenii</i>	0.001676	0.010601	0	0	0.323475	1	-0.00168	-0.00171	0.005066
<i>Corynebacterium_jeddahense</i>	0.005125	0.032415	0	0	0.323475	1	-0.00513	-0.00524	0.015492
<i>Corynebacterium_jeikeium</i>	0.005943	0.037584	0	0	0.323475	1	-0.00594	-0.00608	0.017963
<i>Corynebacterium_lipophiloflavum</i>	0.000678	0.004289	0	0	0.323475	1	-0.00068	-0.00069	0.00205
<i>Corynebacterium_macginleyi</i>	0.083369	0.527271	0	0	0.323475	1	-0.08337	-0.08526	0.251998
<i>Corynebacterium_resistens</i> DSM 45100	0.002714	0.017163	0	0	0.323475	1	-0.00271	-0.00278	0.008202
<i>Corynebacterium_simulans</i>	0.00444	0.028084	0	0	0.323475	1	-0.00444	-0.00454	0.013422
<i>Corynebacterium_suicordis</i>	0.148471	0.939011	0	0	0.323475	1	-0.14847	-0.15184	0.448781
<i>Corynebacterium_urealyticum</i> DSM 7109	0.004266	0.026984	0	0	0.323475	1	-0.00427	-0.00436	0.012896
<i>Criibacterium_bergeronii</i>	0.09651	0.610383	0	0	0.323475	1	-0.09651	-0.0987	0.29172
<i>Cuneatibacter_caecimuris</i>	0.002966	0.018756	0	0	0.323475	1	-0.00297	-0.00303	0.008964
<i>Cutibacterium_namnetense</i>	0.007372	0.046625	0	0	0.323475	1	-0.00737	-0.00754	0.022284
<i>Cytobacillus_gottheilii</i>	0.249827	1.580042	0	0	0.323475	1	-0.24983	-0.2555	0.755149
<i>Defluviicoccus_vanus</i>	0.004744	0.030003	0	0	0.323475	1	-0.00474	-0.00485	0.014339
<i>Deinococcus_soli</i> (ex Cha et al. 2016)	0.014745	0.093255	0	0	0.323475	1	-0.01474	-0.01508	0.044569
<i>Dellagloba_algida</i>	0.085266	0.53927	0	0	0.323475	1	-0.08527	-0.0872	0.257733
<i>Denitratisoma_oestradiolicum</i>	0.06375	0.403188	0	0	0.323475	1	-0.06375	-0.0652	0.192695
<i>Dermacoccus_barathri</i>	0.075034	0.474557	0	0	0.323475	1	-0.07503	-0.07674	0.226805
<i>Dialister_micraerophilus</i>	0.025748	0.162847	0	0	0.323475	1	-0.02575	-0.02633	0.077829

<i>Dialister_propionificiens</i>	0.139115	0.879842	0	0	0.323475	1	-0.13912	-0.14227	0.420503
<i>Drancourtella_massiliensis</i>	0.005938	0.037553	0	0	0.323475	1	-0.00594	-0.00607	0.017948
<i>Dubosiella_newyorkensis</i>	0.076713	0.485177	0	0	0.323475	1	-0.07671	-0.07845	0.23188
<i>Duncaniella_muris</i>	0.002747	0.017376	0	0	0.323475	1	-0.00275	-0.00281	0.008305
<i>Empedobacter_falsenii genomovar 1</i>	0.005855	0.03703	0	0	0.323475	1	-0.00586	-0.00599	0.017698
<i>Enterobacter_quasihormaechei</i>	0.023282	0.147245	0	0	0.323475	1	-0.02328	-0.02381	0.070373
<i>Enteroclosterbolteae</i>	0.013782	0.087163	0	0	0.323475	1	-0.01378	-0.01409	0.041658
<i>Epilithonimonas_pallida</i>	0.054928	0.347395	0	0	0.323475	1	-0.05493	-0.05617	0.16603
<i>Epilithonimonas_vandammei</i>	0.042741	0.270319	0	0	0.323475	1	-0.04274	-0.04371	0.129194
<i>Erysipelatoclostridium_[Clostridium] cocleatum</i>	0.040134	0.253829	0	0	0.323475	1	-0.04013	-0.04104	0.121312
<i>Erysipelatoclostridium_[Clostridium] saccharogumia</i>	0.005513	0.034865	0	0	0.323475	1	-0.00551	-0.00564	0.016663
<i>Erysipelothrix_inopinata</i>	0.008633	0.054599	0	0	0.323475	1	-0.00863	-0.00883	0.026094
<i>Eubacterium_coprostanoligenes</i>	0.029653	0.187542	0	0	0.323475	1	-0.02965	-0.03033	0.089632
<i>Eubacterium_ramulus</i> ATCC 29099	0.013007	0.082265	0	0	0.323475	1	-0.01301	-0.0133	0.039317
<i>Ewingella_americana</i>	0.013922	0.088048	0	0	0.323475	1	-0.01392	-0.01424	0.042081
<i>Exiguobacterium_aurantiacum</i>	0.203957	1.289938	0	0	0.323475	1	-0.20396	-0.20859	0.616499
<i>Ezakiella_coagulans</i>	0.007809	0.049391	0	0	0.323475	1	-0.00781	-0.00799	0.023605
<i>Faecalibacterium_gallinarum</i>	0.073634	0.4657	0	0	0.323475	1	-0.07363	-0.0753	0.222572
<i>Faecalibacterium_prausnitzii</i>	0.018089	0.114406	0	0	0.323475	1	-0.01809	-0.0185	0.054678
<i>Faecalicatena_faecalis</i>	0.006965	0.044053	0	0	0.323475	1	-0.00697	-0.00712	0.021054
<i>Faecalimonas_umbilicata</i>	0.015251	0.096455	0	0	0.323475	1	-0.01525	-0.0156	0.046099
<i>Ferruginibacter_alkalilentus</i>	0.00307	0.019413	0	0	0.323475	1	-0.00307	-0.00314	0.009278
<i>Fimbriimonas_ginsengisoli</i>	0.006003	0.037969	0	0	0.323475	1	-0.006	-0.00614	0.018147
<i>Flavobacterium_plurextorum</i>	0.019364	0.122472	0	0	0.323475	1	-0.01936	-0.0198	0.058533
<i>Flavobacterium_proteolyticum</i>	0.017572	0.111136	0	0	0.323475	1	-0.01757	-0.01797	0.053115
<i>Gaiella_occulta</i>	0.002541	0.016073	0	0	0.323475	1	-0.00254	-0.0026	0.007682
<i>Galactobacillus_timonensis</i>	0.005004	0.031645	0	0	0.323475	1	-0.005	-0.00512	0.015124
<i>Gardnerella_vaginalis</i> ATCC 14018 = JCM 11026	0.000741	0.004689	0	0	0.323475	1	-0.00074	-0.00076	0.002241
<i>Gemmobacter_tilapiae</i>	0.003454	0.021843	0	0	0.323475	1	-0.00345	-0.00353	0.01044
<i>Gleimiaeuropaea</i>	0.003149	0.019917	0	0	0.323475	1	-0.00315	-0.00322	0.009519
<i>Gloeocapsopsis_dulcis</i>	0.009074	0.057388	0	0	0.323475	1	-0.00907	-0.00928	0.027428
<i>Glutamicibacter_protophormiae</i>	0.004194	0.026524	0	0	0.323475	1	-0.00419	-0.00429	0.012677
<i>Gorbachella_massiliensis</i>	0.00217	0.013721	0	0	0.323475	1	-0.00217	-0.00222	0.006558
<i>Gordonia_oryzae</i>	0.002001	0.012656	0	0	0.323475	1	-0.002	-0.00205	0.006049

<i>Gordonia_sputi</i>	0.001144	0.007232	0	0	0.323475	1	-0.00114	-0.00117	0.003456
<i>Gulosibacter_hominis</i>	0.000914	0.005782	0	0	0.323475	1	-0.00091	-0.00093	0.002763
<i>Halomonas_muralis</i>	0.001524	0.009637	0	0	0.323475	1	-0.00152	-0.00156	0.004606
<i>Helicobacter_canadensis</i>	0.129942	0.821824	0	0	0.323475	1	-0.12994	-0.13289	0.392774
<i>Heminiphilus_faecis</i>	0.021902	0.138518	0	0	0.323475	1	-0.0219	-0.0224	0.066202
<i>Herbaspirillum_aquaticum</i>	0.0024	0.01518	0	0	0.323475	1	-0.0024	-0.00245	0.007255
<i>Hyphomicrobium_zavarzinii</i>	0.059009	0.373203	0	0	0.323475	1	-0.05901	-0.06035	0.178364
<i>Ideonella_sakaiensis</i>	0.002232	0.014119	0	0	0.323475	1	-0.00223	-0.00228	0.006748
<i>Klebsiella_pneumoniae</i>	0.002268	0.014347	0	0	0.323475	1	-0.00227	-0.00232	0.006857
<i>Lacrimispora_amygdalina</i>	0.001256	0.007944	0	0	0.323475	1	-0.00126	-0.00128	0.003797
<i>Lacrimispora_saccharolytica</i>	0.009844	0.062259	0	0	0.323475	1	-0.00984	-0.01007	0.029756
<i>Lactocaseibacillus_paracasei</i>	0.002284	0.014444	0	0	0.323475	1	-0.00228	-0.00234	0.006903
<i>Lactocaseibacillus_rhamnosus</i>	0.011715	0.074091	0	0	0.323475	1	-0.01171	-0.01198	0.03541
<i>Lactiplantibacillus_plantarum</i>	0.001484	0.009388	0	0	0.323475	1	-0.00148	-0.00152	0.004487
<i>Lactobacillus_gallinarum</i>	0.001233	0.007801	0	0	0.323475	1	-0.00123	-0.00126	0.003728
<i>Lactobacillus_iners</i>	0.001202	0.007602	0	0	0.323475	1	-0.0012	-0.00123	0.003633
<i>Lactobacillus_paragasseri</i>	0.112176	0.709464	0	0	0.323475	1	-0.11218	-0.11472	0.339074
<i>Lactobacillus_rogosae</i>	0.009212	0.058263	0	0	0.323475	1	-0.00921	-0.00942	0.027845
<i>Legionella_pneumophila</i>	0.000558	0.00353	0	0	0.323475	1	-0.00056	-0.00057	0.001687
<i>Lichenihabitsans_psoromatis</i>	0.018901	0.119538	0	0	0.323475	1	-0.0189	-0.01933	0.057131
<i>Ligilactobacillus_salivarius</i>	0.020476	0.129499	0	0	0.323475	1	-0.02048	-0.02094	0.061892
<i>Lysinibacillus_telephonicus</i>	0.040418	0.255623	0	0	0.323475	1	-0.04042	-0.04133	0.12217
<i>Massilia_neuiana</i>	0.047088	0.297809	0	0	0.323475	1	-0.04709	-0.04816	0.142332
<i>Massilia_timonae</i>	0.001727	0.010922	0	0	0.323475	1	-0.00173	-0.00177	0.00522
<i>Massilibacillus_massiliensis</i>	0.060022	0.379615	0	0	0.323475	1	-0.06002	-0.06138	0.181429
<i>Massilimicrobiota_timonensis</i>	0.00296	0.018723	0	0	0.323475	1	-0.00296	-0.00303	0.008948
<i>Mediterraneibacter_massiliensis</i>	0.005513	0.034865	0	0	0.323475	1	-0.00551	-0.00564	0.016663
<i>Megamonas_funiformis</i> YIT 11815	0.154703	0.978429	0	0	0.323475	1	-0.1547	-0.15821	0.46762
<i>Merdibacter_massiliensis</i>	0.000913	0.005777	0	0	0.323475	1	-0.00091	-0.00093	0.002761
<i>Mesorhizobium_plurifarum</i>	0.004393	0.027784	0	0	0.323475	1	-0.00439	-0.00449	0.013279
<i>Metamycoplasma_faucium</i>	0.020285	0.128291	0	0	0.323475	1	-0.02028	-0.02074	0.061314
<i>Methylarcula_marina</i>	0.011794	0.074591	0	0	0.323475	1	-0.01179	-0.01206	0.035649
<i>Methylobacterium_brachiatum</i>	0.001962	0.012409	0	0	0.323475	1	-0.00196	-0.00201	0.005931
<i>Methylobacterium_iners</i>	0.001701	0.01076	0	0	0.323475	1	-0.0017	-0.00174	0.005143
<i>Methylobacterium_oryzae</i> CBMB20	0.001985	0.012553	0	0	0.323475	1	-0.00198	-0.00203	0.005999
<i>Methylobacterium_persicinum</i>	0.086515	0.547169	0	0	0.323475	1	-0.08652	-0.08848	0.261508

<i>Methylobacterium_radiotolerans</i> JCM 2831	0.008368	0.052923	0	0	0.323475	1	-0.00837	-0.00856	0.025293
<i>Methylobacterium_album</i> BG8	0.030657	0.193895	0	0	0.323475	1	-0.03066	-0.03135	0.092668
<i>Microbacterium_marinilacus</i>	0.005921	0.037446	0	0	0.323475	1	-0.00592	-0.00606	0.017896
<i>Micrococcus_antarcticus</i>	0.026805	0.169533	0	0	0.323475	1	-0.02681	-0.02741	0.081025
<i>Micrococcus_endophyticus</i>	0.000858	0.005424	0	0	0.323475	1	-0.00086	-0.00088	0.002592
<i>Micromonospora_globbae</i>	0.037347	0.236205	0	0	0.323475	1	-0.03735	-0.03819	0.112889
<i>Microvirga_pudoricolor</i>	0.004327	0.027369	0	0	0.323475	1	-0.00433	-0.00443	0.01308
<i>Mogibacterium_neglectum</i>	0.001953	0.012354	0	0	0.323475	1	-0.00195	-0.002	0.005904
<i>Moraxella_atlantiae</i>	0.007196	0.045515	0	0	0.323475	1	-0.0072	-0.00736	0.021753
<i>Mycobacterium_barrassiae</i>	0.015609	0.098718	0	0	0.323475	1	-0.01561	-0.01596	0.04718
<i>Mycolicibacterium_vaccae</i>	0.018691	0.118212	0	0	0.323475	1	-0.01869	-0.01912	0.056497
<i>Mycolicibacterium_wolinskyi</i>	0.000335	0.002119	0	0	0.323475	1	-0.00033	-0.00034	0.001013
<i>Negativibacillus_massiliensis</i>	0.010632	0.06724	0	0	0.323475	1	-0.01063	-0.01087	0.032136
<i>Neoactinobaculum_massiliense</i>	0.000674	0.004262	0	0	0.323475	1	-0.00067	-0.00069	0.002037
<i>Nocardioideae_cavernae</i>	0.004075	0.025774	0	0	0.323475	1	-0.00408	-0.00417	0.012318
<i>Nocardioideae_plantarum</i>	0.015773	0.099756	0	0	0.323475	1	-0.01577	-0.01613	0.047677
<i>Novosphingobium_aromaticivorans</i>	0.003705	0.023431	0	0	0.323475	1	-0.0037	-0.00379	0.011198
<i>Novosphingobium_endophyticum</i>	0.032053	0.202722	0	0	0.323475	1	-0.03205	-0.03278	0.096887
<i>Novosphingobium_fontis</i>	0.008226	0.052026	0	0	0.323475	1	-0.00823	-0.00841	0.024865
<i>Odoribacter_splanchnicus</i>	0.001484	0.009388	0	0	0.323475	1	-0.00148	-0.00152	0.004487
<i>Oliverpabstia_intestinalis</i>	0.007202	0.045551	0	0	0.323475	1	-0.0072	-0.00737	0.02177
<i>Olsenella_phocaensis</i>	0.001852	0.011716	0	0	0.323475	1	-0.00185	-0.00189	0.005599
<i>Ottowia_flava</i>	0.013545	0.085667	0	0	0.323475	1	-0.01355	-0.01385	0.040943
<i>Ottowia_shaoquanensis</i>	0.001483	0.009378	0	0	0.323475	1	-0.00148	-0.00152	0.004482
<i>Paenibacillus_antri</i>	0.009374	0.059289	0	0	0.323475	1	-0.00937	-0.00959	0.028336
<i>Paenibacillus_nanensis</i>	0.028645	0.18117	0	0	0.323475	1	-0.02865	-0.0293	0.086586
<i>Paenibacillus_provencensis</i>	0.049835	0.315185	0	0	0.323475	1	-0.04984	-0.05097	0.150636
<i>Paludibaculum_fermentans</i>	0.001953	0.012354	0	0	0.323475	1	-0.00195	-0.002	0.005904
<i>Paludisphaera_soli</i>	0.007534	0.047651	0	0	0.323475	1	-0.00753	-0.00771	0.022774
<i>Parabacteroides_distasonis</i> ATCC 8503	0.009547	0.060381	0	0	0.323475	1	-0.00955	-0.00976	0.028858
<i>Paracoccus_acridae</i>	0.016736	0.105846	0	0	0.323475	1	-0.01674	-0.01712	0.050587
<i>Paracoccus_contaminans</i>	0.06919	0.437597	0	0	0.323475	1	-0.06919	-0.07076	0.209141
<i>Paracoccus_fontiphilus</i>	0.149753	0.947124	0	0	0.323475	1	-0.14975	-0.15315	0.452658
<i>Paracoccus_kocurii</i>	0.007091	0.04485	0	0	0.323475	1	-0.00709	-0.00725	0.021435
<i>Parageobacillus_thermantarcticus</i>	0.001842	0.011653	0	0	0.323475	1	-0.00184	-0.00188	0.005569

<i>Paramuribaculum_intestinale</i>	0.001717	0.01086	0	0	0.323475	1	-0.00172	-0.00176	0.00519
<i>Pararcticibacter_amylolyticus</i>	0.027373	0.173121	0	0	0.323475	1	-0.02737	-0.02799	0.082739
<i>Pedobacter_hiemivivus</i>	0.001663	0.010519	0	0	0.323475	1	-0.00166	-0.0017	0.005027
<i>Pedobacter_rhizosphaerae</i>	0.003686	0.023314	0	0	0.323475	1	-0.00369	-0.00377	0.011142
<i>Peptoniphilus_duerdenii</i> ATCC BAA-1640	0.002593	0.016402	0	0	0.323475	1	-0.00259	-0.00265	0.007839
<i>Peptoniphilus_grossensis</i> ph5	0.018709	0.118328	0	0	0.323475	1	-0.01871	-0.01913	0.056552
<i>Peptoniphilus_urinimassiliensis</i>	0.024822	0.156989	0	0	0.323475	1	-0.02482	-0.02539	0.07503
<i>Perlucidibaca_piscinae</i>	0.00148	0.009361	0	0	0.323475	1	-0.00148	-0.00151	0.004474
<i>Petroclostridium_xylanilyticum</i>	0.024807	0.156894	0	0	0.323475	1	-0.02481	-0.02537	0.074984
<i>Phascolarctobacterium_faecium</i>	0.017719	0.112067	0	0	0.323475	1	-0.01772	-0.01812	0.05356
<i>Phocaeicola_dorei</i>	0.027459	0.173664	0	0	0.323475	1	-0.02746	-0.02808	0.082999
<i>Phocaeicola_plebeius</i> DSM 17135	0.023449	0.148305	0	0	0.323475	1	-0.02345	-0.02398	0.070879
<i>Phocaeicola_vulgatus</i> ATCC 8482	0.011725	0.074152	0	0	0.323475	1	-0.01172	-0.01199	0.03544
<i>Planococcus_citrus</i>	0.005906	0.037356	0	0	0.323475	1	-0.00591	-0.00604	0.017853
<i>Porphyromonas_bennonis</i>	0.00778	0.049206	0	0	0.323475	1	-0.00778	-0.00796	0.023517
<i>Porphyromonas_catoniae</i> ATCC 51270	0.007088	0.044827	0	0	0.323475	1	-0.00709	-0.00725	0.021424
<i>Prevotella_bergensis</i>	0.006113	0.038662	0	0	0.323475	1	-0.00611	-0.00625	0.018477
<i>Prevotella_buccae</i> ATCC 33574	0.000926	0.005858	0	0	0.323475	1	-0.00093	-0.00095	0.0028
<i>Prevotella_buccalis</i>	0.073911	0.467453	0	0	0.323475	1	-0.07391	-0.07559	0.223409
<i>Prevotella_multisaccharivorax</i>	0.012096	0.076504	0	0	0.323475	1	-0.0121	-0.01237	0.036563
<i>Prevotella_ruminicola</i>	0.003434	0.02172	0	0	0.323475	1	-0.00343	-0.00351	0.010381
<i>Priestia_megaterium</i> NBRC 15308 = ATCC 14581	0.005718	0.036163	0	0	0.323475	1	-0.00572	-0.00585	0.017283
<i>Propionibacterium_westphaliense</i>	0.03628	0.229456	0	0	0.323475	1	-0.03628	-0.0371	0.109664
<i>Pseudomonas_alcaliphila</i>	0.003947	0.024964	0	0	0.323475	1	-0.00395	-0.00404	0.011931
<i>Pseudomonas_arcuscaelestis</i>	0.006671	0.04219	0	0	0.323475	1	-0.00667	-0.00682	0.020164
<i>Pseudomonas_fragi</i>	0.011172	0.070657	0	0	0.323475	1	-0.01117	-0.01143	0.033769
<i>Pseudomonas_spelaei</i>	0.010191	0.064451	0	0	0.323475	1	-0.01019	-0.01042	0.030803
<i>Pseudomonas_weihenstephanensis</i>	0.046673	0.295188	0	0	0.323475	1	-0.04667	-0.04773	0.141079
<i>Pseudoneobacillus_rhizosphaerae</i>	0.00148	0.009361	0	0	0.323475	1	-0.00148	-0.00151	0.004474
<i>Pseudoxanthomonas_japonensis</i>	0.00444	0.028084	0	0	0.323475	1	-0.00444	-0.00454	0.013422
<i>Raoultella_planticola</i>	0.010887	0.068853	0	0	0.323475	1	-0.01089	-0.01113	0.032907
<i>Rhizobium_rosettiformans</i> W3	0.021932	0.138707	0	0	0.323475	1	-0.02193	-0.02243	0.066292
<i>Rhodopseudomonas_palustris</i>	0.027843	0.176096	0	0	0.323475	1	-0.02784	-0.02848	0.084161
<i>Robertmurraya_kyonggiensis</i>	0.030607	0.193578	0	0	0.323475	1	-0.03061	-0.0313	0.092517
<i>Robinsoniella_peoriensis</i>	0.000344	0.002176	0	0	0.323475	1	-0.00034	-0.00035	0.00104

<i>Romboutsia_ilealis</i>	0.002747	0.017376	0	0	0.323475	1	-0.00275	-0.00281	0.008305
<i>Roseomonas_mucosa</i>	0.014555	0.092054	0	0	0.323475	1	-0.01455	-0.01489	0.043995
<i>Roseomonas_nepalensis</i>	0.025819	0.163295	0	0	0.323475	1	-0.02582	-0.02641	0.078044
<i>Roseomonas_rosea</i>	0.001233	0.007801	0	0	0.323475	1	-0.00123	-0.00126	0.003728
<i>Rothia_kristinae</i>	0.002287	0.014464	0	0	0.323475	1	-0.00229	-0.00234	0.006913
<i>Rubneribacter_badeniensis</i>	0.001256	0.007944	0	0	0.323475	1	-0.00126	-0.00128	0.003797
<i>Rubribacterium_polymorphum</i>	0.036978	0.233868	0	0	0.323475	1	-0.03698	-0.03782	0.111772
<i>Rubrobacter_bracarensis</i>	0.001233	0.007801	0	0	0.323475	1	-0.00123	-0.00126	0.003728
<i>Ructibacterium_gallinarum</i>	0.043459	0.274861	0	0	0.323475	1	-0.04346	-0.04445	0.131364
<i>Ruminococcus_albus</i>	0.009212	0.058263	0	0	0.323475	1	-0.00921	-0.00942	0.027845
<i>Ruminococcus_callidus</i>	0.035547	0.22482	0	0	0.323475	1	-0.03555	-0.03635	0.107448
<i>Sabulicella_rubraurantiaca</i>	0.000837	0.005295	0	0	0.323475	1	-0.00084	-0.00086	0.00253
<i>Scardovia_wiggisiae</i>	0.01956	0.123705	0	0	0.323475	1	-0.01956	-0.02	0.059122
<i>Serpentinimonas_maccroryi</i>	0.025899	0.163797	0	0	0.323475	1	-0.0259	-0.02649	0.078283
<i>Skermanella_aerolata</i>	0.001236	0.007815	0	0	0.323475	1	-0.00124	-0.00126	0.003735
<i>Sphingobacterium_multivorum</i>	0.021416	0.135447	0	0	0.323475	1	-0.02142	-0.0219	0.064734
<i>Sphingobium_jiangsuense</i>	0.007804	0.049359	0	0	0.323475	1	-0.0078	-0.00798	0.02359
<i>Sphingobium_limneticum</i>	0.024142	0.152689	0	0	0.323475	1	-0.02414	-0.02469	0.072975
<i>Sphingomonas_astaxanthinifaciens</i> DSM 22298	0.014127	0.089344	0	0	0.323475	1	-0.01413	-0.01445	0.0427
<i>Sphingomonas_dokdonensis</i>	0.018735	0.118491	0	0	0.323475	1	-0.01874	-0.01916	0.05663
<i>Sphingomonas_ginsenosidimutans</i>	0.021733	0.13745	0	0	0.323475	1	-0.02173	-0.02223	0.065692
<i>Sphingomonas_hankookensis</i>	0.018304	0.115766	0	0	0.323475	1	-0.0183	-0.01872	0.055328
<i>Sphingomonas_humi</i>	0.037775	0.23891	0	0	0.323475	1	-0.03777	-0.03863	0.114182
<i>Sphingomonas_kaistensis</i>	0.013654	0.086358	0	0	0.323475	1	-0.01365	-0.01396	0.041273
<i>Sphingomonas_panni</i>	0.007107	0.044946	0	0	0.323475	1	-0.00711	-0.00727	0.021481
<i>Sphingorhabdus_pulchriflava</i>	0.00638	0.040351	0	0	0.323475	1	-0.00638	-0.00652	0.019285
<i>Spirosoma_validum</i>	0.074702	0.472456	0	0	0.323475	1	-0.0747	-0.0764	0.225801
<i>Stagnimonas_aquatica</i>	0.002512	0.015888	0	0	0.323475	1	-0.00251	-0.00257	0.007593
<i>Staphylococcus_caprae</i>	0.004381	0.027706	0	0	0.323475	1	-0.00438	-0.00448	0.013241
<i>Staphylococcus_equorum</i>	0.015944	0.100841	0	0	0.323475	1	-0.01594	-0.01631	0.048195
<i>Staphylococcus_ureilyticus</i>	0.008107	0.051275	0	0	0.323475	1	-0.00811	-0.00829	0.024506
<i>Streptococcus_agalactiae</i> ATCC 13813	0.293732	1.857727	0	0	0.323475	1	-0.29373	-0.3004	0.887862
<i>Streptococcus_mutans</i>	0.000837	0.005295	0	0	0.323475	1	-0.00084	-0.00086	0.00253
<i>Streptococcus_thermophilus</i>	0.007433	0.047009	0	0	0.323475	1	-0.00743	-0.0076	0.022467
<i>Sulfurovum_lithotrophicum</i>	0.024454	0.154661	0	0	0.323475	1	-0.02445	-0.02501	0.073917
<i>Sutterella_massiliensis</i>	0.005025	0.03178	0	0	0.323475	1	-0.00502	-0.00514	0.015188

<i>Tautonia_sociabilis</i>	0.002232	0.014119	0	0	0.323475	1	-0.00223	-0.00228	0.006748
<i>Tepidimonas_ignava</i>	0.000457	0.002889	0	0	0.323475	1	-0.00046	-0.00047	0.001381
<i>Tepidisphaera_mucosa</i>	0.001674	0.010589	0	0	0.323475	1	-0.00167	-0.00171	0.005061
<i>Thauera_aminoaromatica</i>	0.007691	0.048643	0	0	0.323475	1	-0.00769	-0.00787	0.023248
<i>Thermobacillus_composti</i> KWC4	0.004934	0.031205	0	0	0.323475	1	-0.00493	-0.00505	0.014914
<i>Thermomonas_aquatica</i>	0.003628	0.022943	0	0	0.323475	1	-0.00363	-0.00371	0.010965
<i>Thermomonas_brevis</i>	0.040694	0.257371	0	0	0.323475	1	-0.04069	-0.04162	0.123005
<i>Tsuneonella_rigui</i>	0.001082	0.006842	0	0	0.323475	1	-0.00108	-0.00111	0.00327
<i>Turicibacter_sanquinis</i>	0.000947	0.005987	0	0	0.323475	1	-0.00095	-0.00097	0.002861
<i>Tyzzereella_[Clostridium]_colinum</i>	0.003882	0.024554	0	0	0.323475	1	-0.00388	-0.00397	0.011735
<i>Ureibacillus_chungkukjangi</i>	0.029653	0.187542	0	0	0.323475	1	-0.02965	-0.03033	0.089632
<i>Vescimonas_fastidiosa</i>	0.022051	0.139461	0	0	0.323475	1	-0.02205	-0.02255	0.066653
<i>Vulcaniibacterium_thermophilum</i>	0.015577	0.098517	0	0	0.323475	1	-0.01558	-0.01593	0.047084
<i>[Clostridium]_leptum</i>	0.010406	0.065812	0	0	0.323475	1	-0.01041	-0.01064	0.031454
<i>[Eubacterium]_siraeum</i>	0.007683	0.04859	0	0	0.323475	1	-0.00768	-0.00786	0.023223
<i>Actinomyces_dentalis</i>	0.030426	0.192431	0	0	0.323475	1	-0.03043	-0.03112	0.091968
<i>Bacillus_infantis</i>	0.320786	2.028832	0	0	0.323475	1	-0.32079	-0.32807	0.969638
<i>Bacteroides_uniformis</i>	0.023784	0.150423	0	0	0.323475	1	-0.02378	-0.02432	0.071892
<i>Blautia_glucerasea</i>	0.014569	0.092144	0	0	0.323475	1	-0.01457	-0.0149	0.044038
<i>Christensenella_massiliensis</i>	0.00344	0.021757	0	0	0.323475	1	-0.00344	-0.00352	0.010398
<i>Clostridium_phoceensis</i>	0.041281	0.261082	0	0	0.323475	1	-0.04128	-0.04222	0.124779
<i>Corynebacterium_pilbarens</i>	0.005695	0.036017	0	0	0.323475	1	-0.00569	-0.00582	0.017214
<i>Eisenbergiella_massiliensis</i>	0.020082	0.127009	0	0	0.323475	1	-0.02008	-0.02054	0.060701
<i>Eubacterium_xylanophilum</i>	0.029584	0.187108	0	0	0.323475	1	-0.02958	-0.03026	0.089425
<i>Flavonifractor_plautii</i>	0.006167	0.039006	0	0	0.323475	1	-0.00617	-0.00631	0.018642
<i>Frisingicoccus_caecimuris</i>	0.004587	0.029009	0	0	0.323475	1	-0.00459	-0.00469	0.013864
<i>Glucibacter_canis</i>	0.018759	0.118644	0	0	0.323475	1	-0.01876	-0.01918	0.056703
<i>Haliangium_tepidum</i>	0.014569	0.092144	0	0	0.323475	1	-0.01457	-0.0149	0.044038
<i>Imtechella_halotolerans</i>	0.147675	0.933979	0	0	0.323475	1	-0.14767	-0.15103	0.446376
<i>Leptotrichia_hofstadii</i>	0.029333	0.185521	0	0	0.323475	1	-0.02933	-0.03	0.088666
<i>Metabacillus_niabensis</i>	0.012271	0.07761	0	0	0.323475	1	-0.01227	-0.01255	0.037092
<i>Metamycoplasma_salivarium</i>	0.003922	0.024803	0	0	0.323475	1	-0.00392	-0.00401	0.011854
<i>Microbacterium_flavescens</i>	0.017343	0.109687	0	0	0.323475	1	-0.01734	-0.01774	0.052423
<i>Microbacterium_oxydans</i>	0.002511	0.015884	0	0	0.323475	1	-0.00251	-0.00257	0.007591
<i>Mucisphaera_calidilacus</i>	0.007352	0.0465	0	0	0.323475	1	-0.00735	-0.00752	0.022224
<i>Oleiharenicola_lentus</i>	0.008663	0.054788	0	0	0.323475	1	-0.00866	-0.00886	0.026185

<i>Paenibacillus_vini</i>	0.000851	0.005382	0	0	0.323475	1	-0.00085	-0.00087	0.002572
<i>Phenylobacterium_aquaticum</i>	0.014041	0.088803	0	0	0.323475	1	-0.01404	-0.01436	0.042441
<i>Phenylobacterium_falsum</i>	0.004336	0.027422	0	0	0.323475	1	-0.00434	-0.00443	0.013106
<i>Planctopirus_ephydatiae</i>	0.008672	0.054844	0	0	0.323475	1	-0.00867	-0.00887	0.026211
<i>Planifilum_fimeticola</i>	0.025209	0.159438	0	0	0.323475	1	-0.02521	-0.02578	0.0762
<i>Singulisphaera_rosea</i>	0.004331	0.027394	0	0	0.323475	1	-0.00433	-0.00443	0.013092
<i>Staphylococcus_pasteuri</i>	0.022974	0.145297	0	0	0.323475	1	-0.02297	-0.02349	0.069442
<i>Ureaplasma_urealyticum</i> serovar 8 str. ATCC 27618	0.017326	0.109576	0	0	0.323475	1	-0.01733	-0.01772	0.05237
<i>Streptococcus_qwangjuense</i>	0.033173	0.146465	0.322755	1.309114	0.32423	1	0.289582	-0.88694	0.307777
<i>Donqia_mobilis</i>	0.036783	0.14216	0.011616	0.053229	0.324246	1	-0.02517	-0.02554	0.075873
<i>Prevotella_pallens</i> ATCC 700821	0.028744	0.12837	0.412415	1.740771	0.325159	1	0.383671	-1.1769	0.40956
<i>Ruminiclostridium_cellobioparum</i> DSM 1351 = ATCC 15832	0.171836	1.020483	0.010768	0.049347	0.325326	1	-0.16107	-0.16593	0.488068
<i>Cardiobacterium_hominis</i>	0	0	0.271224	1.233393	0.32563	1	0.271224	-0.83266	0.29021
<i>Blautia_pseudococcoides</i>	0.008903	0.050064	0.000968	0.004436	0.325693	1	-0.00793	-0.00818	0.024051
<i>Corynebacterium_kroppenstedtii</i>	0.799495	5.021546	0.011027	0.050534	0.326845	1	-0.78847	-0.81764	2.394571
<i>Bacillus_capparis</i>	0.127781	0.808158	0.001262	0.005781	0.328238	1	-0.12652	-0.13195	0.384992
<i>Chryseobacterium_hagamense</i>	0	0	0.003529	0.016171	0.329257	1	0.003529	-0.01089	0.003832
<i>Deinococcus_antarcticus</i>	0	0	0.010092	0.046249	0.329257	1	0.010092	-0.03114	0.01096
<i>Parachloleplasma_brassicae</i> 0502	0	0	0.0641	0.293745	0.329257	1	0.0641	-0.19781	0.069611
<i>Prevotella_micans</i>	0	0	0.015748	0.072165	0.329257	1	0.015748	-0.0486	0.017101
<i>Sphingomonas_zeibaulis</i>	0	0	0.045843	0.210077	0.329257	1	0.045843	-0.14147	0.049783
<i>Streptococcus_peroris</i> ATCC 700780	0	0	0.009413	0.043134	0.329257	1	0.009413	-0.02905	0.010222
<i>Acetivibrio_saccincola</i>	0	0	0.01927	0.088305	0.329257	1	0.01927	-0.05947	0.020926
<i>Acinetobacter_baumannii</i>	0	0	0.005808	0.026615	0.329257	1	0.005808	-0.01792	0.006307
<i>Acinetobacter_oryzae</i>	0	0	0.003312	0.01518	0.329257	1	0.003312	-0.01022	0.003597
<i>Acinetobacter_proteolyticus</i>	0	0	0.013036	0.059738	0.329257	1	0.013036	-0.04023	0.014157
<i>Acinetobacter_pullicarnis</i>	0	0	0.028652	0.131298	0.329257	1	0.028652	-0.08842	0.031115
<i>Acinetobacter_septicus</i>	0	0	0.0733	0.335903	0.329257	1	0.0733	-0.2262	0.079601
<i>Actinomyces_marseillensis</i>	0	0	0.007084	0.032465	0.329257	1	0.007084	-0.02186	0.007693
<i>Anaerococcus_vaginalis</i> ATCC 51170	0	0	0.00535	0.024519	0.329257	1	0.00535	-0.01651	0.00581
<i>Anaeromyxobacter_dehalogenans</i>	0	0	0.003892	0.017836	0.329257	1	0.003892	-0.01201	0.004227
<i>Azospira_oryzae</i> PS	0	0	0.012422	0.056924	0.329257	1	0.012422	-0.03833	0.01349
<i>Bacillulicoccus_massiliensis</i>	0	0	0.011655	0.053408	0.329257	1	0.011655	-0.03597	0.012656
<i>Bacillus_velezensis</i>	0	0	0.019802	0.090745	0.329257	1	0.019802	-0.06111	0.021504
<i>Brucella_lupini</i>	0	0	0.009937	0.045539	0.329257	1	0.009937	-0.03067	0.010792

<i>Bulleidia_extracta</i>	0	0	0.041928	0.192139	0.329257	1	0.041928	-0.12939	0.045533
<i>Butyrivibrio_hungatei</i>	0	0	0.002834	0.012986	0.329257	1	0.002834	-0.00874	0.003077
<i>Campylobacter_massiliensis</i>	0	0	0.022954	0.105187	0.329257	1	0.022954	-0.07083	0.024927
<i>Campylobacter_showae</i>	0	0	0.024937	0.114277	0.329257	1	0.024937	-0.07696	0.027081
<i>Caulobacter_henricii</i>	0	0	0.027098	0.124177	0.329257	1	0.027098	-0.08362	0.029427
<i>Cellulosimicrobium_funkei</i>	0	0	0.009316	0.042693	0.329257	1	0.009316	-0.02875	0.010117
<i>Comamonas_testosteroni</i>	0	0	0.004828	0.022126	0.329257	1	0.004828	-0.0149	0.005243
<i>Coprobacter_fastidiosus</i> NSB1	0	0	0.000828	0.003795	0.329257	1	0.000828	-0.00256	0.000899
<i>Corynebacterium_vitaeruminis</i>	0	0	0.01946	0.089178	0.329257	1	0.01946	-0.06005	0.021133
<i>Dermacoccus_nishinomiyaensis</i>	0	0	0.052564	0.24088	0.329257	1	0.052564	-0.16221	0.057083
<i>Diplocloster_agilis</i>	0	0	0.023809	0.109105	0.329257	1	0.023809	-0.07347	0.025855
<i>Eikenella_halliae</i>	0	0	0.001984	0.00909	0.329257	1	0.001984	-0.00612	0.002154
<i>Flaviflagellibacter_deserti</i>	0	0	0.004626	0.021197	0.329257	1	0.004626	-0.01427	0.005023
<i>Fusobacterium_hwasookii</i> ChDC F128	0	0	0.005384	0.024674	0.329257	1	0.005384	-0.01662	0.005847
<i>Gordonia_hongkongensis</i>	0	0	0.034046	0.156018	0.329257	1	0.034046	-0.10506	0.036973
<i>Hydrogenophaga_flava</i>	0	0	0.050027	0.229251	0.329257	1	0.050027	-0.15438	0.054327
<i>Janibacter_melonis</i>	0	0	0.009316	0.042693	0.329257	1	0.009316	-0.02875	0.010117
<i>Lachnoanaerobaculum_saburreum</i> DSM 3986	0	0	0.031738	0.145444	0.329257	1	0.031738	-0.09794	0.034467
<i>Lautropia_dentalis</i>	0	0	0.009068	0.041555	0.329257	1	0.009068	-0.02798	0.009848
<i>Leptotrichia_buccalis</i>	0	0	0.002834	0.012986	0.329257	1	0.002834	-0.00874	0.003077
<i>Leptotrichia_hongkongensis</i>	0	0	0.001134	0.005194	0.329257	1	0.001134	-0.0035	0.001231
<i>Leptotrichia_massiliensis</i>	0	0	0.0017	0.007792	0.329257	1	0.0017	-0.00525	0.001846
<i>Microbacter_margulisiae</i>	0	0	0.010989	0.050356	0.329257	1	0.010989	-0.03391	0.011933
<i>Microbacterium_paraoxydans</i>	0	0	0.021887	0.100297	0.329257	1	0.021887	-0.06754	0.023768
<i>Microbacterium_testaceum</i>	0	0	0.002691	0.012334	0.329257	1	0.002691	-0.00831	0.002923
<i>Mobiluncus_mulieris</i>	0	0	0.001984	0.00909	0.329257	1	0.001984	-0.00612	0.002154
<i>Mogibacterium_timidum</i>	0	0	0.002521	0.011551	0.329257	1	0.002521	-0.00778	0.002737
<i>Moraxella_lincolnii</i>	0	0	0.613794	2.812759	0.329257	1	0.613794	-1.89415	0.666558
<i>Mycobacterium_kyogaense</i>	0	0	0.020082	0.092027	0.329257	1	0.020082	-0.06197	0.021808
<i>Mycoplasma_feliminum</i>	0	0	0.043622	0.199899	0.329257	1	0.043622	-0.13461	0.047371
<i>Neisseria_meningitidis</i>	0	0	0.816322	3.740856	0.329257	1	0.816322	-2.51914	0.886496
<i>Neisseria_oralis</i>	0	0	0.053559	0.245437	0.329257	1	0.053559	-0.16528	0.058163
<i>Niabella_hibiscisoli</i>	0	0	0.013622	0.062424	0.329257	1	0.013622	-0.04204	0.014793
<i>Nitrosomonas_oligotropha</i>	0	0	0.002331	0.010682	0.329257	1	0.002331	-0.00719	0.002531
<i>Orrella_dioscoreae</i>	0	0	0.08303	0.380492	0.329257	1	0.08303	-0.25623	0.090168
<i>Paludibacter_jiangxiensis</i>	0	0	0.054277	0.248729	0.329257	1	0.054277	-0.1675	0.058943

<i>Paludibacter_propionici</i> WB4	0	0	0.009918	0.045451	0.329257	1	0.009918	-0.03061	0.010771
<i>Paracoccus_sanguinis</i>	0	0	0.009523	0.043642	0.329257	1	0.009523	-0.02939	0.010342
<i>Parvimonas_parva</i>	0	0	0.006518	0.029868	0.329257	1	0.006518	-0.02011	0.007078
<i>Patulibacter_minatonensis</i> DSM 18081	0	0	0.013664	0.062616	0.329257	1	0.013664	-0.04217	0.014839
<i>Pedobacter_nyackensis</i>	0	0	0.004298	0.019695	0.329257	1	0.004298	-0.01326	0.004667
<i>Peptoanaerobacter_[Eubacterium] yurii</i> subsp. <i>margaretiae</i> ATCC 43715	0	0	0.026071	0.119472	0.329257	1	0.026071	-0.08045	0.028312
<i>Peptoanaerobacter_stomatis</i>	0	0	0.027805	0.127416	0.329257	1	0.027805	-0.0858	0.030195
<i>Petrocella_atlantisensis</i>	0	0	0.0017	0.007792	0.329257	1	0.0017	-0.00525	0.001846
<i>Prevotella_maculosa</i>	0	0	0.000567	0.002597	0.329257	1	0.000567	-0.00175	0.000615
<i>Prevotella_oralis</i> ATCC 33269	0	0	0.002756	0.012629	0.329257	1	0.002756	-0.0085	0.002993
<i>Prevotella_oulorum</i>	0	0	0.04364	0.199985	0.329257	1	0.04364	-0.13467	0.047392
<i>Prevotella_pleuritidis</i>	0	0	0.021259	0.097423	0.329257	1	0.021259	-0.06561	0.023087
<i>Pseudomonas_extremaustralis</i> 14-3	0	0	0.024354	0.111604	0.329257	1	0.024354	-0.07516	0.026447
<i>Pseudomonas_huaxiensis</i>	0	0	0.012159	0.055721	0.329257	1	0.012159	-0.03752	0.013204
<i>Pseudomonas_putida</i>	0	0	0.061792	0.283167	0.329257	1	0.061792	-0.19069	0.067104
<i>Pseudomonas_toyotomiensis</i>	0	0	0.004169	0.019104	0.329257	1	0.004169	-0.01287	0.004527
<i>Pseudoxanthomonas_helianthi</i>	0	0	0.00799	0.036614	0.329257	1	0.00799	-0.02466	0.008677
<i>Qipengyuania_sediminis</i>	0	0	0.005827	0.026704	0.329257	1	0.005827	-0.01798	0.006328
<i>Ralstonia_pickettii</i>	0	0	0.005797	0.026567	0.329257	1	0.005797	-0.01789	0.006296
<i>Reyranella_soli</i>	0	0	0.013877	0.063592	0.329257	1	0.013877	-0.04282	0.01507
<i>Rhodobacter_flagellatus</i>	0	0	0.002277	0.010436	0.329257	1	0.002277	-0.00703	0.002473
<i>Rhodococcus_corynebacterioides</i>	0	0	0.018012	0.08254	0.329257	1	0.018012	-0.05558	0.01956
<i>Selenomonas_felix</i>	0	0	0.008218	0.03766	0.329257	1	0.008218	-0.02536	0.008924
<i>Selenomonas_infelix</i>	0	0	0.016732	0.076675	0.329257	1	0.016732	-0.05163	0.01817
<i>Selenomonas_timonae</i>	0	0	0.00255	0.011687	0.329257	1	0.00255	-0.00787	0.00277
<i>Serratia_grimesii</i>	0	0	0.01074	0.049215	0.329257	1	0.01074	-0.03314	0.011663
<i>Sinanaerobacter_chloroacetimidivorans</i>	0	0	0.000567	0.002597	0.329257	1	0.000567	-0.00175	0.000615
<i>Sporolactobacillus_putidus</i>	0	0	0.003222	0.014764	0.329257	1	0.003222	-0.00994	0.003499
<i>Staphylococcus_auricularis</i>	0	0	0.02138	0.097973	0.329257	1	0.02138	-0.06598	0.023217
<i>Staphylococcus_pseudoxylosus</i>	0	0	0.015035	0.068901	0.329257	1	0.015035	-0.0464	0.016328
<i>Stenotrophomonas_acidaminiphila</i>	0	0	0.006832	0.031308	0.329257	1	0.006832	-0.02108	0.007419
<i>Streptococcus_anginosus</i> SK52 = DSM 20563	0	0	0.001984	0.00909	0.329257	1	0.001984	-0.00612	0.002154
<i>Treponema_socranskii</i> subsp. <i>paredis</i>	0	0	0.002267	0.010389	0.329257	1	0.002267	-0.007	0.002462
<i>Velocimicrobium_porci</i>	0	0	0.012154	0.055697	0.329257	1	0.012154	-0.03751	0.013199

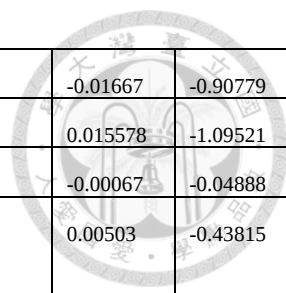
<i>Wolinella_succinogenes</i>	0	0	0.006327	0.028993	0.329257	1	0.006327	-0.01952	0.006871
<i>Xanthobacter_flavus</i>	0	0	0.001863	0.008539	0.329257	1	0.001863	-0.00575	0.002023
<i>Aquabacterium_olei</i>	0	0	0.001276	0.005848	0.329257	1	0.001276	-0.00394	0.001386
<i>Bifidobacterium_pseudocatenulatum</i>	0	0	0.000638	0.002924	0.329257	1	0.000638	-0.00197	0.000693
<i>Propionivibrio_militaris</i>	0	0	0.000638	0.002924	0.329257	1	0.000638	-0.00197	0.000693
<i>Thermoactinomyces_vulgaris</i>	0	0	0.032516	0.149008	0.329257	1	0.032516	-0.10034	0.035311
<i>Tepidiphilus_succinatimandens</i>	0.051729	0.307008	0.003821	0.017512	0.331163	1	-0.04791	-0.05054	0.146359
<i>Campylobacter_conciscus</i>	0.011436	0.072327	0.055125	0.195913	0.333845	1	0.04369	-0.13526	0.04788
<i>Fusobacterium_pseudoperiodonticum</i>	0.026529	0.132516	0.310378	1.315739	0.335793	1	0.283849	-0.88395	0.316255
<i>Methylibium_petroleiphilum PM1</i>	2.06894	2.892335	1.376697	2.538989	0.340334	1	-0.69224	-0.75413	2.138616
<i>Alloprevotella_tanneriae</i>	0.014677	0.067363	0.066953	0.241391	0.341431	1	0.052276	-0.16383	0.059282
<i>Flavobacterium_piscis</i>	0.000756	0.004781	0.027587	0.12642	0.342531	1	0.026831	-0.08439	0.030731
<i>Oribacterium_sinus</i>	0.001116	0.007059	0.037123	0.170117	0.343857	1	0.036006	-0.11347	0.041456
<i>Fusobacterium_nucleatum</i> subsp. <i>nucleatum</i> ATCC 25586	0.005372	0.033975	0.163997	0.751528	0.345203	1	0.158625	-0.50085	0.183603
<i>Megasphaera_micronuciformis</i>	0.033659	0.122196	0.16172	0.603023	0.346646	1	0.128061	-0.40476	0.148638
<i>Acidaminobacter_hydrogenoformans</i>	0.03871	0.181277	0.09059	0.212157	0.347127	1	0.05188	-0.16236	0.058596
<i>Neisseria_macacae</i>	0.116715	0.394791	0.49665	1.792616	0.348401	1	0.379935	-1.20367	0.443804
<i>Schwartzia_succinivorans</i>	0.020014	0.12658	0.000999	0.004578	0.348483	1	-0.01902	-0.02151	0.059541
<i>Tannerella_serpentiformis</i>	0.001116	0.007059	0.028338	0.129861	0.348549	1	0.027222	-0.08637	0.031924
<i>Vitreimonas_flagellata</i>	0.000762	0.004818	0.014919	0.06837	0.354536	1	0.014158	-0.04531	0.016994
<i>Treponema_denticola</i>	0.009196	0.058158	0.06702	0.277077	0.3552	1	0.057824	-0.18504	0.069387
<i>Acinetobacter_piscicola</i>	0.000926	0.005858	0.017191	0.078779	0.355995	1	0.016265	-0.05216	0.019634
<i>Veillonella_tobetsuensis</i>	0.108076	0.522668	0.388994	1.328987	0.361112	1	0.280918	-0.90428	0.342447
<i>Erysipelatoclostridium_[Clostridium]</i> <i>spiroforme</i>	0.000343	0.002167	0.00537	0.024607	0.361201	1	0.005027	-0.01625	0.006191
<i>Pseudomonas_azotoformans</i>	0.154716	0.484556	0.265387	0.428658	0.36487	1	0.110672	-0.35415	0.132804
<i>Aquisediminimonas_profunda</i>	0.026947	0.120382	0.008074	0.037001	0.36563	1	-0.01887	-0.02263	0.06038
<i>Rothia_nasimurium</i>	0.268353	1.697212	0.023549	0.107914	0.368978	1	-0.2448	-0.29981	0.789422
<i>Cloacibacterium_normanense</i>	0.064877	0.314654	0.017183	0.078743	0.369442	1	-0.04769	-0.05816	0.15355
<i>Gemmatimonas_phototrophica</i>	0.007322	0.046307	0.074271	0.334424	0.371999	1	0.066949	-0.21975	0.085849
<i>Labilithrix_luteola</i>	0.085627	0.451193	0.019359	0.088715	0.374824	1	-0.06627	-0.08266	0.215198
<i>Sphingomonas_koreensis</i>	0.002756	0.017433	0.010908	0.039652	0.378257	1	0.008151	-0.02689	0.010586
<i>Acinetobacter_quillouiae</i>	0.008388	0.053048	0.088064	0.40356	0.378288	1	0.079676	-0.264	0.104642
<i>Fusobacterium_nucleatum</i> subsp. <i>animalis</i>	0.025829	0.163357	0.002834	0.012986	0.381467	1	-0.023	-0.02952	0.075513
<i>Moraxella_nonliquefaciens</i>	0.182677	1.15535	1.805268	8.272778	0.381616	1	1.622591	-5.40267	2.157488

<i>Stomatobaculum_longum</i>	0.019373	0.088943	0.005951	0.027271	0.383552	1	-0.01342	-0.01723	0.044078
<i>Aggregatibacter_actinomycetemcomitans</i>	0.001395	0.008824	0.013036	0.059738	0.384915	1	0.011641	-0.03895	0.015668
<i>Sediminibacterium_salmonum NBRC 103935</i>	0.169239	0.620315	0.067089	0.290954	0.385537	1	-0.10215	-0.13168	0.335981
<i>Prevotella_oris</i>	0.091954	0.550038	0.014713	0.063454	0.385548	1	-0.07724	-0.10061	0.255096
<i>Tannerella_forsythia</i>	0.104803	0.662835	0.012321	0.05646	0.386033	1	-0.09248	-0.12078	0.305745
<i>Staphylococcus_lugdunensis</i>	0.032344	0.109642	0.088163	0.278448	0.386045	1	0.055819	-0.18644	0.074797
<i>Prevotella_melaninogenica ATCC 25845</i>	0.299013	0.804042	0.163868	0.410073	0.388213	1	-0.13514	-0.17594	0.446233
<i>Aquabacterium_parvum</i>	0.090552	0.212137	0.18578	0.474509	0.390199	1	0.095228	-0.31973	0.129277
<i>Neisseria_cinerea</i>	0.006739	0.042624	0.00085	0.003896	0.391091	1	-0.00589	-0.00784	0.019616
<i>Aggregatibacter_kilianii</i>	0.024949	0.119855	0.156661	0.688507	0.394434	1	0.131712	-0.44697	0.18355
<i>Comamonas_fluminis</i>	0.005718	0.036163	0.046056	0.211054	0.394757	1	0.040338	-0.13696	0.056284
<i>Bifidobacterium_bifidum</i>	0.013903	0.087928	0.100545	0.460754	0.403062	1	0.086642	-0.29787	0.124585
<i>Aliarcobacter_cryaerophilus</i>	0.064713	0.287095	0.174735	0.560834	0.407092	1	0.110022	-0.37852	0.158476
<i>Lancefieldella_rimae</i>	0.001674	0.010589	0.01122	0.051418	0.409616	1	0.009546	-0.03315	0.014053
<i>Bacteroides_caccae</i>	0.019262	0.121822	0.12452	0.570621	0.412926	1	0.105258	-0.36732	0.156803
<i>Streptococcus_intermedius</i>	1.810626	10.74207	0.394978	1.292685	0.415693	1	-1.41565	-2.06116	4.892457
<i>Streptococcus_timonensis</i>	0.038782	0.212751	0.127682	0.470002	0.418135	1	0.088901	-0.31149	0.133685
<i>Sphingopyxis_soli</i>	0.047248	0.290747	0.009251	0.042395	0.422334	1	-0.038	-0.05663	0.132624
<i>Filifactor_alocis</i>	0.091271	0.416979	0.307597	1.174981	0.422362	1	0.216326	-0.76441	0.331762
<i>Haemophilus_influenzae</i>	2.125951	13.40799	0.392917	1.800572	0.426088	1	-1.73303	-2.61929	6.085355
<i>Kocuria_rhizophila</i>	0.048992	0.232349	0.017772	0.058684	0.426272	1	-0.03122	-0.04702	0.109458
<i>Fusobacterium_watanabei</i>	0.143417	0.904823	0.803722	3.676304	0.426738	1	0.660305	-2.3536	1.032993
<i>Capnocytophaga_sputigena</i>	0.003349	0.021178	0.018875	0.086498	0.42694	1	0.015527	-0.05536	0.024309
<i>Actinomyces_graevenitzii</i>	0.012494	0.062659	0.003967	0.01818	0.428102	1	-0.00853	-0.01291	0.029962
<i>Streptococcus_pseudopneumoniae</i>	0.469738	1.80646	0.224482	0.522004	0.428895	1	-0.24526	-0.3724	0.862916
<i>Niallia_circulans</i>	0.175666	1.111007	0.033332	0.152746	0.430506	1	-0.14233	-0.21856	0.50323
<i>Streptococcus_pneumoniae</i>	2.310971	14.57792	0.452473	2.073494	0.433279	1	-1.8585	-2.88209	6.599089
<i>Ligilactobacillus_aviarius</i>	0.142755	0.828563	0.03544	0.162408	0.433302	1	-0.10731	-0.16613	0.380754
<i>Niveispirillum_lacus</i>	0.254019	0.501672	0.414159	0.849474	0.433855	1	0.16014	-0.57348	0.253201
<i>Streptococcus_oralis ATCC 35037</i>	0.214194	0.649138	0.109354	0.404522	0.44187	1	-0.10484	-0.16624	0.375916
<i>Parvimonas_micra</i>	0.104059	0.46367	0.440034	1.935685	0.441893	1	0.335974	-1.22699	0.555044
<i>Veillonella_dispar</i>	0.140443	0.47623	0.295727	0.849687	0.444588	1	0.155283	-0.56607	0.255503
<i>Prevotellamassilia_timonensis</i>	0.097283	0.342778	0.246852	0.847404	0.445385	1	0.149569	-0.54773	0.248593
<i>Thaurea_phenylacetica</i>	0.024748	0.156518	0.115278	0.52827	0.450804	1	0.09053	-0.33514	0.154078

<i>Lachnoanaerobaculum gingivalis</i>	0.003907	0.024708	0.017853	0.081812	0.453524	1	0.013946	-0.05185	0.023961
<i>Haemophilus seminalis</i>	0.01014	0.044813	0.043074	0.197392	0.458925	1	0.032934	-0.12369	0.057825
<i>Haemophilus haemolyticus</i>	0.063395	0.273546	0.26836	1.229781	0.45918	1	0.204965	-0.77018	0.360248
<i>Streptococcus downii</i>	0.03077	0.135834	0.012401	0.05683	0.461931	1	-0.01837	-0.03129	0.068032
<i>Cutibacterium granulosum</i> DSM 20700	0.087711	0.288052	0.046217	0.150382	0.462734	1	-0.04149	-0.07083	0.153822
<i>Veillonella atypica</i>	0.101771	0.389843	0.227027	0.717206	0.46307	1	0.125256	-0.47078	0.22027
[<i>Eubacterium</i>] <i>brachy</i>	0.241418	1.095674	0.940538	4.245594	0.466296	1	0.69912	-2.65692	1.258682
<i>Staphylococcus epidermidis</i>	3.652045	8.21359	2.392734	5.268377	0.4708	1	-1.25931	-2.21456	4.733185
<i>Acinetobacter modestus</i>	0.006222	0.02982	0.016818	0.063653	0.476851	1	0.010596	-0.04083	0.019633
<i>Prevotella herbatia</i>	0.222454	1.40692	0.782096	3.419194	0.479319	1	0.559643	-2.16794	1.048654
<i>Kingella denitrificans</i> ATCC 33394	0.022725	0.143728	0.006234	0.028569	0.48768	1	-0.01649	-0.03098	0.063965
<i>Solitalea canadensis</i> DSM 3403	0.011055	0.069915	0.040647	0.186266	0.489407	1	0.029592	-0.11673	0.057545
<i>Sphingomonas yunnanensis</i>	0.030536	0.193128	0.008557	0.039213	0.491834	1	-0.02198	-0.0419	0.085858
<i>Anaerobacterium chartisolvans</i>	0.025092	0.08765	0.073767	0.313973	0.493625	1	0.048676	-0.19378	0.096428
<i>Abiotrophia defectiva</i>	0.04647	0.266543	0.160411	0.729434	0.495925	1	0.113941	-0.45469	0.226813
<i>Desulfovibrio intestinalis</i>	0.004777	0.021398	0.002103	0.009635	0.504705	1	-0.00267	-0.0053	0.010648
<i>Kaistella carnis</i>	0.002541	0.016073	0.008592	0.039372	0.506065	1	0.00605	-0.02456	0.01246
<i>Nitrospirillum amazonense</i>	0.011063	0.069966	0.035815	0.164123	0.515359	1	0.024752	-0.10213	0.052631
<i>Prevotella veroralis</i>	0.003628	0.022943	0.011614	0.053222	0.517835	1	0.007986	-0.0331	0.017127
<i>Sediminibacterium soli</i>	0.109962	0.695458	0.035677	0.163492	0.523646	1	-0.07428	-0.15833	0.306899
<i>Lachnoanaerobaculum orale</i>	0.011436	0.072327	0.035432	0.162371	0.525295	1	0.023996	-0.1008	0.052805
<i>Curvibacter gracilis</i>	0.029253	0.131413	0.073764	0.303718	0.527702	1	0.044511	-0.18786	0.098841
<i>Stigmatella erecta</i>	0.037051	0.194687	0.015568	0.071342	0.536033	1	-0.02148	-0.04766	0.090626
<i>Delftia acidovorans</i>	0.090382	0.571626	0.032466	0.117958	0.540814	1	-0.05792	-0.13136	0.247192
<i>Streptococcus cristatus</i> ATCC 51100	0.042595	0.177494	0.022014	0.087061	0.546001	1	-0.02058	-0.04724	0.088398
<i>Staphylococcus aureus</i>	1.763765	9.402349	4.741443	21.39936	0.549123	1	2.977678	-13.0892	7.13384
<i>Campylobacter gracilis</i>	0.015348	0.097069	0.04066	0.178316	0.550264	1	0.025312	-0.11123	0.060609
<i>Prevotella koreensis</i>	0.002593	0.016402	0.007084	0.032465	0.556889	1	0.004491	-0.02001	0.011032
<i>Klebsiella aerogenes</i> KCTC 2190	0.003629	0.022951	0.00968	0.044358	0.563426	1	0.006051	-0.02731	0.015208
<i>Comamonas sediminis</i>	0.03921	0.148292	0.071182	0.227129	0.56429	1	0.031972	-0.14408	0.080134
<i>Sediminibacterium goheungense</i>	0.050112	0.258668	0.023128	0.105987	0.568041	1	-0.02698	-0.06712	0.121084
<i>Corynebacterium amycolatium</i>	0.007447	0.040042	0.018923	0.086717	0.570452	1	0.011476	-0.05261	0.029657
<i>Hyphomicrobium vulgare</i>	0.002177	0.013771	0.000851	0.003898	0.572923	1	-0.00133	-0.00337	0.006023
<i>Streptococcus salivarius</i>	0.279554	0.804109	0.411795	0.938547	0.586714	1	0.132241	-0.6213	0.356814
<i>Paenibacillus barengoltzii</i>	0.106973	0.676558	0.045407	0.208081	0.598561	1	-0.06157	-0.17173	0.294861
<i>Gemella haemolysans</i>	0.185558	0.746158	0.116541	0.305381	0.612484	1	-0.06902	-0.20235	0.340386

<i>Chryseobacterium_ oncorhynchi</i>	0.048125	0.214488	0.075386	0.194369	0.618158	1	0.027261	-0.13668	0.082156
<i>Caulobacter_ segnis</i>	0.037718	0.169484	0.021298	0.091917	0.625569	1	-0.01642	-0.05056	0.083402
<i>Moraxella_ osloensis</i>	0.32445	0.695186	0.249614	0.498922	0.630574	1	-0.07484	-0.23545	0.385119
<i>Peptidiphaga_ gingivicola</i>	0.015213	0.096215	0.032656	0.14965	0.6319	1	0.017443	-0.09113	0.056246
<i>Micrococcus_ luteus</i>	0.018972	0.080111	0.03086	0.100382	0.641514	1	0.011888	-0.06333	0.039553
<i>Schaalia_ odontolytica</i>	0.068192	0.220679	0.098453	0.268799	0.66026	1	0.030261	-0.1689	0.108374
<i>Rhizomicrobium_ electricum</i>	0.059409	0.217031	0.086926	0.242238	0.664923	1	0.027517	-0.15521	0.100174
<i>Treponema_ socranskii</i>	0.015011	0.094935	0.024505	0.077397	0.676204	1	0.009494	-0.05491	0.035924
<i>Hypericibacter_ adhaerens</i>	0.009312	0.058894	0.015003	0.047445	0.68457	1	0.005691	-0.03367	0.022293
<i>Comamonas_ terrigena</i>	0.074666	0.272284	0.050922	0.180761	0.685838	1	-0.02374	-0.09325	0.140732
<i>Diaphorobacter_ caeni</i>	0.004759	0.030099	0.002595	0.01189	0.691188	1	-0.00216	-0.00869	0.013023
<i>Fusobacterium_ nucleatum</i> subsp. <i>polymorphum</i> ATCC 10953	0.055934	0.246996	0.085129	0.282576	0.691511	1	0.029195	-0.17719	0.118797
<i>Methylobacterium_ goesingense</i>	0.017084	0.10805	0.030805	0.141165	0.699432	1	0.01372	-0.08542	0.057978
<i>Streptococcus_ constellatus</i>	0.022819	0.100895	0.014567	0.066753	0.703909	1	-0.00825	-0.03503	0.051534
<i>Reyranella_ massiliensis</i> 521	0.139708	0.383862	0.109992	0.229963	0.707304	1	-0.02972	-0.12793	0.187366
<i>Streptococcus_ oralis</i> subsp. <i>tigurinus</i> <i>AZ_3a</i>	0.015069	0.095302	0.026574	0.121778	0.708851	1	0.011506	-0.07365	0.050635
<i>Gemella_ morbillorum</i>	0.013615	0.086112	0.021061	0.070342	0.718294	1	0.007445	-0.04869	0.033799
<i>Clostridium_ disporicum</i>	0.546555	3.431206	0.335895	1.338509	0.733714	1	-0.21066	-1.02376	1.445083
<i>Coprococcus_ comes</i> ATCC 27758	0.027971	0.176906	0.046205	0.211738	0.737694	1	0.018234	-0.12789	0.091423
<i>Prevotella_ jejuni</i>	0.097939	0.294665	0.148258	0.652166	0.739723	1	0.05032	-0.35913	0.258492
<i>Actinomyces_ naeslundii</i>	0.009764	0.051984	0.015565	0.071328	0.743933	1	0.005801	-0.04168	0.030078
<i>Kineothrix_ alysoides</i>	0.006995	0.044239	0.01126	0.051601	0.749496	1	0.004266	-0.03116	0.022627
<i>Rothia_ dentocariosa</i> ATCC 17931	0.070644	0.235704	0.098402	0.356581	0.749936	1	0.027757	-0.2041	0.148586
<i>Mediterraneibacter_ glycyrrhizinilyticu</i> <i>s</i>	0.044017	0.164933	0.06705	0.307259	0.751391	1	0.023033	-0.17086	0.124792
<i>Prevotella_ bivia</i>	0.007245	0.045821	0.004555	0.020872	0.754367	1	-0.00269	-0.01444	0.019819
<i>Acidibacter_ ferrireducens</i>	0.215696	0.492272	0.183186	0.326933	0.759305	1	-0.03251	-0.17904	0.244057
<i>Porphyromonas_ pasteri</i>	0.16943	0.427874	0.224944	0.769158	0.761403	1	0.055514	-0.42704	0.316014
<i>Rothia_ mucilaginosa</i>	0.104846	0.297691	0.082908	0.26185	0.768313	1	-0.02194	-0.12711	0.170991
<i>Staphylococcus_ capitis</i>	0.476199	1.310614	0.675538	3.0171	0.775209	1	0.199339	-1.62378	1.225101
<i>Alysiella_ crassa</i>	0.001116	0.007059	0.0017	0.007792	0.775568	1	0.000584	-0.0047	0.003536
<i>Moraxella_ catarrhalis</i>	2.547228	13.11058	3.731794	17.05878	0.782751	1	1.184566	-9.85611	7.486979
<i>Solobacterium_ moorei</i>	0.072478	0.376878	0.052296	0.211587	0.789854	1	-0.02018	-0.13068	0.171044
<i>Prevotella_ vespertina</i>	0.116892	0.517023	0.089672	0.286565	0.792351	1	-0.02722	-0.17875	0.233186
<i>Snodgrassella_ gandavensis</i>	0.366493	2.136145	0.258	1.134356	0.796471	1	-0.10849	-0.72943	0.94642

<i>Oribacterium_asaccharolyticum</i> ACB7	0.009981	0.041635	0.01277	0.040362	0.800972	1	0.00279	-0.02498	0.019403
<i>Corynebacterium_accolens</i>	4.401401	11.67437	3.71417	9.25297	0.802693	1	-0.68723	-4.8087	6.183167
<i>Prevotella_illustrans</i>	0.004465	0.028237	0.003117	0.014285	0.805416	1	-0.00135	-0.00955	0.012243
<i>Fusobacterium_nucleatum</i> subsp. <i>animalis</i> ATCC 51191	0.044194	0.264327	0.031299	0.143428	0.805785	1	-0.0129	-0.09159	0.11738
<i>Porphyromonas_endodontalis</i>	0.711302	4.458485	0.967933	4.005712	0.820273	1	0.256632	-2.51871	2.005449
<i>Aquabacterium_commune</i>	0.006737	0.042609	0.009251	0.042395	0.827198	1	0.002514	-0.02563	0.020599
<i>Selenomonas_sputigena</i> ATCC 35185	0.011359	0.071843	0.014244	0.041638	0.843485	1	0.002885	-0.032	0.026229
<i>Prevotella_histicola</i>	0.040133	0.147298	0.033092	0.123929	0.84444	1	-0.00704	-0.06474	0.078828
<i>Lancefieldella_parvula</i> DSM 20469	0.004744	0.030003	0.006234	0.028569	0.850008	1	0.001491	-0.01729	0.014313
<i>Spodiobacter_cordis</i>	0.015904	0.085513	0.020403	0.0935	0.855148	1	0.004499	-0.05406	0.045065
<i>Neisseria_elongata</i> subsp. <i>nitroreducens</i>	0.013568	0.069171	0.016481	0.052922	0.855408	1	0.002913	-0.03485	0.029019
<i>Stenotrophomonas_maltophilia</i>	0.014244	0.052553	0.011813	0.054136	0.867217	1	-0.00243	-0.02677	0.031628
<i>Oribacterium_parvum</i> ACB1	0.002232	0.014119	0.002834	0.012986	0.868365	1	0.000601	-0.00787	0.00667
<i>Haemophilus_sputorum</i> CCUG 13788	0.015297	0.067545	0.017762	0.059376	0.883952	1	0.002465	-0.03627	0.031342
<i>Streptococcus_toyakuensis</i>	0.138959	0.525441	0.162867	0.654579	0.885822	1	0.023908	-0.35979	0.31197
<i>Micrococcus_yunnanensis</i>	0.041446	0.257337	0.05014	0.229772	0.893488	1	0.008695	-0.13875	0.121361
<i>Corynebacterium_pseudodiphtheriticu</i> <i>m</i>	0.621477	2.608282	0.732176	3.260342	0.893717	1	0.1107	-1.78238	1.560985
<i>Streptococcus_infantis</i> ATCC 700779	0.070874	0.169518	0.064703	0.188756	0.900761	1	-0.00617	-0.09339	0.105733
<i>Muribaculum_gordoncarteri</i>	0.03411	0.201745	0.029191	0.107879	0.90168	1	-0.00492	-0.07441	0.084249
<i>Corynebacterium_propinquum</i>	2.012054	9.152071	1.746245	7.449816	0.903299	1	-0.26581	-4.1088	4.640418
<i>Paracoccus_marinus</i>	0.10093	0.221389	0.112248	0.409507	0.907025	1	0.011317	-0.20849	0.185852
<i>Fretibacterium_fastidiosum</i>	0.019473	0.123159	0.022976	0.10529	0.907905	1	0.003503	-0.0641	0.057097
<i>Peptococcus_niger</i>	0.048849	0.308946	0.056123	0.219712	0.915763	1	0.007274	-0.14453	0.129982
<i>Terrimonas_sugianensis</i>	0.003755	0.023747	0.004356	0.019961	0.917187	1	0.000601	-0.01217	0.010966
<i>Streptococcus_mitis</i>	0.361405	1.039805	0.335454	0.856038	0.917377	1	-0.02595	-0.47435	0.526248
<i>Sphingomonas_desiccabilis</i>	0.000837	0.005295	0.00073	0.003343	0.923193	1	-0.00011	-0.00212	0.002331
<i>Brevundimonas_huaxiensis</i>	0.015144	0.095779	0.017065	0.070406	0.92937	1	0.001921	-0.0452	0.04136
<i>Prevotella_salivae</i>	0.037181	0.141146	0.040525	0.152954	0.934072	1	0.003343	-0.08463	0.077939
<i>Pedobacter_steynii</i>	0.014076	0.068889	0.015527	0.071155	0.939399	1	0.001451	-0.0398	0.036894
<i>Pedobacter_chitinilyticus</i>	0.009152	0.057883	0.010092	0.046249	0.945261	1	0.00094	-0.02831	0.026434
<i>Haemophilus_parainfluenzae</i> ATCC 33392	0.362488	1.270961	0.348922	0.763261	0.958729	1	-0.01357	-0.50894	0.536067
<i>Streptococcus_oralis</i> subsp. <i>dentisani</i>	0.182919	0.682686	0.175747	0.49399	0.962682	1	-0.00717	-0.29882	0.31316
<i>Neisseria_perflava</i>	0.990962	2.960143	0.958485	3.015885	0.968121	1	-0.03248	-1.59959	1.664542



<i>Snodgrassella_communis</i>	0.49842	1.886354	0.481754	1.601941	0.971222	1	-0.01667	-0.90779	0.941125
<i>Prevotella_nigrescens</i>	0.438146	2.771077	0.453724	1.442878	0.977063	1	0.015578	-1.09521	1.06405
<i>Pseudomonas_allii</i>	0.026868	0.097295	0.026193	0.087961	0.978238	1	-0.00067	-0.04888	0.050233
<i>Streptococcus_parasanguinis</i> ATCC 15912	0.317996	0.666863	0.323026	0.847888	0.981297	1	0.00503	-0.43815	0.428091
<i>Streptococcus_koreensis</i>	0.024323	0.108331	0.024818	0.10458	0.986242	1	0.000495	-0.05808	0.057088
<i>Cutibacterium_modestum</i>	0.070413	0.23271	0.070307	0.251055	0.998725	1	-0.00011	-0.13348	0.133689

Supplementary table 2. Differences in oral taxa in asthma with and without exacerbation. AE= with exacerbation; non.AE=without exacerbation

Taxonomy	mean(non. AE)	sd(non.AE)	mean(AE)	sd(AE)	p-value	q-value	Mean Difference	95% lower CI	95% upper CI
<i>Actinomyces_graevenitzii</i>	0.171582	0.378676	0.037196	0.057005	0.03351	1	-0.13439	0.010999	0.257771
<i>Leptotrichia_buccalis</i>	0.022405	0.051857	0.004033	0.009313	0.035101	1	-0.01837	0.001344	0.035401
<i>Streptococcus_sanguinis</i>	0.691041	1.083625	0.293407	0.315853	0.036151	1	-0.39763	0.026709	0.768559
<i>Streptococcus_gwangjuense</i>	0.163556	0.434633	0.017734	0.045362	0.041963	1	-0.14582	0.005562	0.286082
<i>Butyrivibrio_hungatei</i>	0.035767	0.057052	0.014738	0.023637	0.047712	1	-0.02103	0.000219	0.041839
<i>Prevotella_intermedia</i>	0.34853	0.83149	1.02585	1.478317	0.062415	1	0.67732	-1.39232	0.037678
<i>Schaalia_odontolytica</i>	1.492091	1.773205	0.82575	1.039459	0.069734	1	-0.66634	-0.0555	1.388187
<i>Streptococcus_vaginalis</i>	0.280539	0.92478	0.008627	0.033588	0.070798	1	-0.27191	-0.02417	0.567995
<i>Bifidobacterium_longum</i> subsp. <i>suillum</i>	0.012476	0.045893	0	0	0.093491	1	-0.01248	-0.0022	0.027153
<i>Prevotella_nigrescens</i>	0.749533	1.803804	0.230361	0.507376	0.095992	1	-0.51917	-0.0955	1.133847
<i>Selenomonas_flueggei</i>	0.008072	0.0301	0	0	0.097859	1	-0.00807	-0.00155	0.017698
<i>Alloprevotella_tanneriae</i>	0.237936	0.307302	1.023119	2.07277	0.099419	1	0.785182	-1.73275	0.162386
<i>Veillonella_tobetsuensis</i>	1.846674	2.801898	4.036692	5.536626	0.100947	1	2.190018	-4.83769	0.457656
<i>Pseudomonas_reidholzensis</i>	0.001415	0.00538	0	0	0.104247	1	-0.00142	-0.00031	0.003136
<i>Olsenella_phocaeensis</i>	0.007022	0.026741	0	0	0.104804	1	-0.00702	-0.00153	0.015574
<i>Metamycoplasma_orale</i>	0.001277	0.004917	0	0	0.108384	1	-0.00128	-0.0003	0.00285
<i>Prevotella_vespertina</i>	0.687019	1.320407	0.301204	0.530149	0.111596	1	-0.38582	-0.09228	0.863906
<i>Christensenella_massiliensis</i>	0.00544	0.021207	0	0	0.112803	1	-0.00544	-0.00134	0.012222
<i>Porphyromonas_catoniae</i> ATCC 51270	0.021584	0.045649	0.008278	0.019927	0.119788	1	-0.01331	-0.00356	0.030176
<i>Petrocella_atlantisensis</i>	0.004963	0.018447	0.025991	0.058326	0.121491	1	0.021028	-0.0481	0.006043
<i>Selenomonas_sputigena</i> ATCC 35185	0.050353	0.089659	0.190237	0.393975	0.123273	1	0.139884	-0.32104	0.04127
<i>Eubacterium_nodatum</i> ATCC 33099	0.011014	0.030124	0.002941	0.009302	0.125084	1	-0.00807	-0.00232	0.018467
<i>Capnocytophaga_gingivalis</i>	0.137121	0.276447	0.335832	0.541975	0.127312	1	0.198712	-0.45809	0.060666
<i>Neisseria_oralis</i>	0.237863	0.628795	0.078468	0.147086	0.133849	1	-0.1594	-0.05083	0.369621
<i>Schaalia_cardiffensis</i>	0.022431	0.092982	0	0	0.135151	1	-0.02243	-0.00731	0.052168
<i>Streptococcus_gordonii</i>	0.560166	2.023798	0.073075	0.10391	0.1369	1	-0.48709	-0.16157	1.135751
<i>Rothia_dentocariosa</i> ATCC 17931	0.239845	0.414612	0.130737	0.140602	0.137641	1	-0.10911	-0.03607	0.254285

<i>Neisseria_perflava</i>	11.4918	11.65649	7.672699	8.027878	0.138883	1	-3.81911	-1.27775	8.915959
<i>Schaalia_meyeri</i>	0.003487	0.014915	0	0	0.147325	1	-0.00349	-0.00128	0.008257
<i>Schwartzia_succinivorans</i>	0.001291	0.004119	0.005645	0.013145	0.152947	1	0.004354	-0.01045	0.001745
<i>Ornithinibacillus_contaminans</i>	0.002775	0.011985	0.021205	0.056369	0.153522	1	0.018431	-0.04432	0.007455
<i>Neisseria_meningitidis</i>	0	0	0.006108	0.019293	0.162321	1	0.006108	-0.01489	0.002674
<i>Selenomonas_infelix</i>	0.04267	0.086444	0.230649	0.593078	0.163765	1	0.18798	-0.45907	0.083107
<i>Streptococcus_oralis</i> subsp. <i>dentisani</i>	1.368303	3.10336	0.587932	1.202495	0.166343	1	-0.78037	-0.33448	1.895225
<i>Streptococcus_cristatus</i> ATCC 51100	0.396545	0.663431	0.207322	0.392216	0.167529	1	-0.18922	-0.08177	0.46022
<i>Breznakia_pachnodae</i>	0.000749	0.003372	0	0	0.168036	1	-0.00075	-0.00033	0.001827
<i>Haemophilus_haemolyticus</i>	0.427461	0.700398	1.206005	2.462528	0.170097	1	0.778544	-1.91726	0.360174
<i>Alterileibacterium_massiliense</i>	0.001295	0.005882	0	0	0.171533	1	-0.0013	-0.00059	0.003176
<i>Streptococcus_agalactiae</i> ATCC 13813	0.001756	0.008053	0	0	0.175808	1	-0.00176	-0.00082	0.004331
<i>Christensenella_minuta</i>	0.00217	0.009583	0.017324	0.049215	0.177065	1	0.015155	-0.03772	0.007414
<i>Lachnoanaerobaculum_umeae</i> <i>nse</i>	1.017398	3.841912	0.186296	0.284462	0.181146	1	-0.8311	-0.4032	2.065401
<i>Corynebacterium_durum</i>	0.006104	0.028569	0	0	0.18441	1	-0.0061	-0.00303	0.01524
<i>Prevotella_aurantiaca</i>	0.177645	0.822388	0.002086	0.00956	0.184809	1	-0.17556	-0.08748	0.438601
<i>Curvibacter_gracilis</i>	0	0	0.001632	0.005454	0.185578	1	0.001632	-0.00411	0.000851
<i>Peptoanaerobacter_stomatis</i>	0.003103	0.010898	0.000638	0.002924	0.185911	1	-0.00247	-0.00123	0.006159
<i>Galactobacillus_timonensis</i>	0.001033	0.005232	0.024956	0.080253	0.1875	1	0.023923	-0.06048	0.012638
<i>Selenomonas_timonae</i>	0.007651	0.024276	0.071169	0.213872	0.189887	1	0.063518	-0.16112	0.03408
<i>Mycoplasma_feliminum</i>	0.002971	0.014176	0	0	0.192644	1	-0.00297	-0.00156	0.007505
<i>Streptococcus_rubneri</i>	0.622984	0.868487	1.200208	1.876666	0.193661	1	0.577224	-1.46756	0.313107
<i>Blautia_hominis</i>	0.001847	0.009008	0	0	0.202253	1	-0.00185	-0.00103	0.004728
<i>Prevotella_buccae</i> ATCC 33574	0.007561	0.017749	0.041246	0.116644	0.202905	1	0.033685	-0.08702	0.019651
<i>Campylobacter_showae</i>	0.034702	0.073068	0.144773	0.381953	0.205132	1	0.110071	-0.28518	0.065037
<i>Actinomyces_dentalis</i>	0.001253	0.006189	0	0	0.207984	1	-0.00125	-0.00073	0.003232
<i>Prolixibacter_denitrificans</i>	0.000764	0.00483	0.011138	0.036416	0.208293	1	0.010374	-0.02701	0.006259
<i>Prevotella_dentalis</i> DSM 3688	0.015906	0.034836	0.006844	0.020692	0.208335	1	-0.00906	-0.0052	0.023319
<i>Johnsonella_ignava</i> ATCC 51276	0.000179	0.001135	0.003177	0.010578	0.21001	1	0.002998	-0.00782	0.001828
<i>Actinomyces_oris</i>	0.007409	0.019321	0.003024	0.007626	0.212771	1	-0.00438	-0.00258	0.011354
<i>Fusobacterium_nucleatum</i>	0.097196	0.1657	0.054796	0.097116	0.213322	1	-0.0424	-0.02505	0.10985

<i>subsp. polymorphum</i> ATCC 10953									
<i>[Eubacterium]_saphenum</i>	0.019163	0.059628	0.006583	0.014992	0.21359	1	-0.01258	-0.00749	0.03265
<i>Diplocloster_agilis</i>	0.003366	0.016845	0	0	0.213749	1	-0.00337	-0.00202	0.008754
<i>Neisseria_cinerea</i>	0.043994	0.151407	0.011755	0.04149	0.213778	1	-0.03224	-0.01919	0.083673
<i>Selenomonas_noxia</i>	0.008078	0.026173	0.002419	0.008959	0.221756	1	-0.00566	-0.00352	0.014838
<i>Streptococcus_oralis</i> ATCC 35037	1.01904	1.428761	1.514704	1.551294	0.230779	1	0.495664	-1.3196	0.328272
<i>Prevotella_illustrans</i>	0.007527	0.036966	0.081859	0.276647	0.234344	1	0.074332	-0.2007	0.052036
Unknown	0.696904	0.789382	1.144681	1.625343	0.244849	1	0.447778	-1.22206	0.326508
<i>Arachnia_propionica</i>	0.000969	0.005194	0	0	0.245254	1	-0.00097	-0.00069	0.00263
<i>Prevotella_baroniae</i>	0.046307	0.089835	0.19653	0.578828	0.250783	1	0.150223	-0.41494	0.114497
<i>Campylobacter_rectus</i>	0.011557	0.029335	0.004254	0.019495	0.250889	1	-0.0073	-0.00531	0.019913
<i>Peptococcus_simiae</i>	0	0	0.00739	0.029106	0.258311	1	0.00739	-0.02064	0.005859
<i>Spodiobacter_cordis</i>	0.147159	0.384506	0.073931	0.092084	0.258574	1	-0.07323	-0.05559	0.202049
<i>Lautropia_mirabilis</i>	0.186857	0.395896	0.10754	0.139594	0.259602	1	-0.07932	-0.06027	0.2189
<i>Tannerella_serpentiformis</i>	0.06797	0.108561	0.146153	0.304745	0.266846	1	0.078182	-0.22036	0.063997
<i>Howardella_ureilytica</i>	0.001242	0.004664	0.004097	0.011018	0.267647	1	0.002854	-0.00805	0.002338
<i>Shuttleworthia_satelles</i> DSM 14600	0.053474	0.250514	0.008644	0.021882	0.267833	1	-0.04483	-0.0358	0.125456
<i>Prevotella_maculosa</i>	0.002353	0.008909	0.000628	0.002877	0.268481	1	-0.00173	-0.00137	0.00482
<i>Klebsiella_pneumoniae</i>	0.032908	0.187479	0	0	0.27374	1	-0.03291	-0.02705	0.092866
<i>Pelomonas_saccharophila</i>	0.003448	0.019659	0	0	0.27417	1	-0.00345	-0.00284	0.009735
<i>Perlabentimonas_gracilis</i>	0.001599	0.009133	0	0	0.274972	1	-0.0016	-0.00132	0.00452
<i>Bacilliculturomica_massiliensis</i>	0.007922	0.021569	0.003376	0.010672	0.275478	1	-0.00455	-0.00372	0.012809
<i>Fusobacterium_nucleatum</i> subsp. <i>vincentii</i> ATCC 51190	0.065231	0.174403	0.031974	0.059172	0.279676	1	-0.03326	-0.02782	0.09433
<i>Metamycoplasma_salivarium</i>	0.007325	0.02	0.039117	0.131167	0.282402	1	0.031791	-0.09177	0.028187
<i>Shigella_flexneri</i>	0.005587	0.025474	0.044681	0.161875	0.28424	1	0.039094	-0.11313	0.034947
<i>Streptococcus_shenyangsis</i>	0.137535	0.806887	0	0	0.287643	1	-0.13754	-0.12052	0.39559
<i>Alysiella_crassa</i>	0.001595	0.008568	0.007418	0.023756	0.288538	1	0.005823	-0.01691	0.005268
<i>Olsenella_profusa</i> DSM 13989	0.002238	0.013162	0	0	0.28877	1	-0.00224	-0.00197	0.006448
<i>Kingella_bonacorsii</i>	0.043368	0.187533	0.010917	0.030077	0.291271	1	-0.03245	-0.02881	0.093709
<i>Leptotrichia_hongkongensis</i>	0.017916	0.047443	0.007693	0.027697	0.292958	1	-0.01022	-0.00906	0.029505
<i>Prevotella_oralis</i> ATCC 33269	0.004422	0.014193	0.019589	0.063661	0.293311	1	0.015167	-0.04443	0.014093
<i>Olsenella_uli</i> DSM 7084	0.001274	0.005402	0.033811	0.139261	0.297233	1	0.032537	-0.09595	0.030872

<i>Neisseria_shayeganii</i> 871	0.152869	0.913715	0.000863	0.003955	0.299212	1	-0.15201	-0.14022	0.444231
<i>Parvimonas_parva</i>	0.12351	0.310993	0.330877	0.882323	0.307722	1	0.207366	-0.6188	0.204072
<i>Prevotella_shahii</i>	0.104331	0.220992	0.349492	1.064755	0.308673	1	0.245161	-0.73392	0.243597
<i>Neisseria_macacae</i>	0.763967	1.723145	2.028248	5.446472	0.311004	1	1.264281	-3.79222	1.263654
<i>Capnocytophaga_ochracea</i>	0.001511	0.00798	0.005733	0.017895	0.31381	1	0.004221	-0.01269	0.004244
<i>Sphingomonas_leidy</i>	0.018381	0.05986	0.161423	0.633355	0.314027	1	0.143042	-0.43184	0.14576
<i>Prevotella_herbat</i>	0.195149	0.825805	0.05922	0.128022	0.314443	1	-0.13593	-0.13345	0.405307
<i>Fusobacterium_nucleatum</i> <i>subsp. animalis</i> ATCC 51191	0.17072	0.726256	0.046934	0.202277	0.319234	1	-0.12379	-0.1234	0.370973
<i>Campylobacter_gracilis</i>	0.036081	0.073689	0.02149	0.04035	0.321843	1	-0.01459	-0.01463	0.043815
<i>Moraxella_catarrhalis</i>	0.005036	0.031849	0	0	0.323475	1	-0.00504	-0.00515	0.015222
<i>Acidaminococcus_fermentans</i> DSM 20731	0.000467	0.002951	0	0	0.323475	1	-0.00047	-0.00048	0.00141
<i>Acinetobacter_lwoffii</i>	0.001625	0.010275	0	0	0.323475	1	-0.00162	-0.00166	0.004911
<i>Actinomyces_johnsonii</i>	0.005511	0.034854	0	0	0.323475	1	-0.00551	-0.00564	0.016658
<i>Alistipes_senegalensis</i> JC50	0.0007	0.004427	0	0	0.323475	1	-0.0007	-0.00072	0.002116
<i>Aquabacterium_parvum</i>	0.000399	0.002524	0	0	0.323475	1	-0.0004	-0.00041	0.001206
<i>Bacillus_proteolyticus</i>	0.001625	0.010275	0	0	0.323475	1	-0.00162	-0.00166	0.004911
<i>Bacillus_tropicus</i>	0.000251	0.001588	0	0	0.323475	1	-0.00025	-0.00026	0.000759
<i>Blautia_phocaensis</i>	0.000525	0.00332	0	0	0.323475	1	-0.00052	-0.00054	0.001587
<i>Blautia_provencensis</i>	0.00105	0.006641	0	0	0.323475	1	-0.00105	-0.00107	0.003174
<i>Brevundimonas_albigilva</i>	0.000812	0.005138	0	0	0.323475	1	-0.00081	-0.00083	0.002455
<i>Brochothrix_thermosphacta</i>	0.000159	0.001006	0	0	0.323475	1	-0.00016	-0.00016	0.000481
<i>Campylobacter_curvus</i>	0.000604	0.003822	0	0	0.323475	1	-0.0006	-0.00062	0.001827
<i>Capnocytophaga_endodontalis</i>	0.000897	0.005676	0	0	0.323475	1	-0.0009	-0.00092	0.002712
<i>Corynebacterium_accolens</i>	0.000812	0.005138	0	0	0.323475	1	-0.00081	-0.00083	0.002455
<i>Duncaniella_dubosii</i>	0.011286	0.071382	0	0	0.323475	1	-0.01129	-0.01154	0.034116
<i>Duncaniella_freteri</i>	0.005425	0.034308	0	0	0.323475	1	-0.00542	-0.00555	0.016397
<i>Enterocloster_bolteae</i>	0.0007	0.004427	0	0	0.323475	1	-0.0007	-0.00072	0.002116
<i>Eubacterium_coprostanoligene</i> s	0.000525	0.00332	0	0	0.323475	1	-0.00052	-0.00054	0.001587
<i>Fumia_xinanensis</i>	0.00105	0.00664	0	0	0.323475	1	-0.00105	-0.00107	0.003174
<i>Fusimonas_intestini</i>	0.000787	0.00498	0	0	0.323475	1	-0.00079	-0.00081	0.00238
<i>Fusobacterium_massiliense</i>	0.00105	0.00664	0	0	0.323475	1	-0.00105	-0.00107	0.003174
<i>Haemophilus_pittmaniae</i>	0.000463	0.002929	0	0	0.323475	1	-0.00046	-0.00047	0.0014
<i>Imtechella_halotolerans</i>	0.004808	0.030411	0	0	0.323475	1	-0.00481	-0.00492	0.014534
<i>Kineothrix_alysoides</i>	0.000875	0.005533	0	0	0.323475	1	-0.00087	-0.00089	0.002645

<i>Kingella_negevensis</i>	0.000634	0.004012	0	0	0.323475	1	-0.00063	-0.00065	0.001917
<i>Klebsiella_africana</i>	0.010589	0.066971	0	0	0.323475	1	-0.01059	-0.01083	0.032007
<i>Kocuria_rhizophila</i>	0.000233	0.001475	0	0	0.323475	1	-0.00023	-0.00024	0.000705
<i>Lactacaseibacillus_rhamnosus</i>	0.00032	0.002023	0	0	0.323475	1	-0.00032	-0.00033	0.000967
<i>Lactobacillus_paragasseri</i>	0.003838	0.024275	0	0	0.323475	1	-0.00384	-0.00393	0.011602
<i>Lactobacillus_rogosae</i>	0.000612	0.003873	0	0	0.323475	1	-0.00061	-0.00063	0.001851
<i>Lawsonella_clevelandensis</i>	0.00058	0.00367	0	0	0.323475	1	-0.00058	-0.00059	0.001754
<i>Ligilactobacillus_murinus</i>	0.001312	0.0083	0	0	0.323475	1	-0.00131	-0.00134	0.003967
<i>Limosilactobacillus_fermentum</i>	0.001439	0.009103	0	0	0.323475	1	-0.00144	-0.00147	0.004351
<i>Limosilactobacillus_urinaemul eris</i>	0.004178	0.026422	0	0	0.323475	1	-0.00418	-0.00427	0.012628
<i>Marseilla_massiliensis</i>	0.0018	0.011386	0	0	0.323475	1	-0.0018	-0.00184	0.005442
<i>Mogibacterium_pumilum</i>	0.000694	0.00439	0	0	0.323475	1	-0.00069	-0.00071	0.002098
<i>Mogibacterium_vescum</i>	0.002799	0.017703	0	0	0.323475	1	-0.0028	-0.00286	0.008461
<i>Negativibacillus_massiliensis</i>	0.002362	0.01494	0	0	0.323475	1	-0.00236	-0.00242	0.00714
<i>Neglectibacter_timonensis</i>	0.000875	0.005533	0	0	0.323475	1	-0.00087	-0.00089	0.002645
<i>Parabacteroides_goldsteinii</i> DSM 19448 = WAL 12034	0.000437	0.002767	0	0	0.323475	1	-0.00044	-0.00045	0.001322
<i>Paracoccus_marinus</i>	0.000248	0.001567	0	0	0.323475	1	-0.00025	-0.00025	0.000749
<i>Polyangium_fumosum</i>	0.000628	0.003971	0	0	0.323475	1	-0.00063	-0.00064	0.001898
<i>Prevotella_bivia</i>	0.001482	0.009371	0	0	0.323475	1	-0.00148	-0.00152	0.004479
<i>Prevotella_enoeca</i>	0.000422	0.002667	0	0	0.323475	1	-0.00042	-0.00043	0.001274
<i>Pseudoramibacter_alactolyticu s ATCC 23263</i>	0.000159	0.001006	0	0	0.323475	1	-0.00016	-0.00016	0.000481
<i>Qiania_dongpingensis</i>	0.00105	0.00664	0	0	0.323475	1	-0.00105	-0.00107	0.003174
<i>Romboutsia_ilealis</i>	0.002362	0.01494	0	0	0.323475	1	-0.00236	-0.00242	0.00714
<i>Ruminiclostridium_cellobiopar um subsp. termitidis</i>	0.00386	0.024416	0	0	0.323475	1	-0.00386	-0.00395	0.011669
<i>Ruminococcoides_bili</i>	0.000612	0.003873	0	0	0.323475	1	-0.00061	-0.00063	0.001851
<i>Ruminococcus_callidus</i>	0.00245	0.015494	0	0	0.323475	1	-0.00245	-0.00251	0.007405
<i>Ruminococcus_gauvreauii</i>	0.00175	0.011067	0	0	0.323475	1	-0.00175	-0.00179	0.005289
<i>Scardovia_wiggisiae</i>	0.00064	0.004046	0	0	0.323475	1	-0.00064	-0.00065	0.001934
<i>Sneathia_sanguinegens</i>	0.003199	0.02023	0	0	0.323475	1	-0.0032	-0.00327	0.009668
<i>Staphylococcus_epidermidis</i>	0.001611	0.010187	0	0	0.323475	1	-0.00161	-0.00165	0.004869
<i>Streptococcus_downei</i> MFe28	0.001393	0.008807	0	0	0.323475	1	-0.00139	-0.00142	0.004209
<i>Streptococcus_pneumoniae</i>	0.011286	0.071382	0	0	0.323475	1	-0.01129	-0.01154	0.034116
<i>Streptococcus_thermophilus</i>	0.001004	0.006349	0	0	0.323475	1	-0.001	-0.00103	0.003035

<i>Treponema bryantii</i>	0.001202	0.007603	0	0	0.323475	1	-0.0012	-0.00123	0.003634
<i>Treponema parvum</i>	0.000251	0.001588	0	0	0.323475	1	-0.00025	-0.00026	0.000759
<i>Truepera radiovictrix</i> DSM 17093	0.026046	0.164728	0	0	0.323475	1	-0.02605	-0.02664	0.078729
<i>Weissella confusa</i>	0.000785	0.004966	0	0	0.323475	1	-0.00079	-0.0008	0.002373
<i>[Eubacterium] siraeum</i>	0.006124	0.038734	0	0	0.323475	1	-0.00612	-0.00626	0.018512
<i>Colibacter massiliensis</i>	0.007231	0.045734	0	0	0.323475	1	-0.00723	-0.0074	0.021858
<i>Roseburia faecis</i>	0.002717	0.017181	0	0	0.323475	1	-0.00272	-0.00278	0.008211
<i>Bradyrhizobium embraense</i>	0.255976	0.595012	2.834458	11.75325	0.327025	1	2.578482	-7.93117	2.774209
<i>Kingella kingae</i> ATCC 23330	0.002386	0.013404	0.012414	0.044969	0.328769	1	0.010028	-0.03085	0.010798
<i>Breznakia blatticola</i>	0	0	0.000419	0.001918	0.329257	1	0.000419	-0.00129	0.000455
<i>Cutibacterium modestum</i>	0	0	0.000779	0.003571	0.329257	1	0.000779	-0.0024	0.000846
<i>Actinomyces gerencseriae</i>	0	0	0.000646	0.00296	0.329257	1	0.000646	-0.00199	0.000701
<i>Aquabacterium terrae</i>	0	0	0.015409	0.070614	0.329257	1	0.015409	-0.04755	0.016734
<i>Aquidimimonas profunda</i>	0	0	0.003269	0.014979	0.329257	1	0.003269	-0.01009	0.00355
<i>Arachnia rubra</i>	0	0	0.000695	0.003187	0.329257	1	0.000695	-0.00215	0.000755
<i>Bdellovibrio bacteriovorus</i>	0	0	0.035488	0.162626	0.329257	1	0.035488	-0.10951	0.038538
<i>Bosea eneeae</i> 34614	0	0	0.039223	0.179744	0.329257	1	0.039223	-0.12104	0.042595
<i>Bradyrhizobium liaoningense</i>	0	0	0.001401	0.006419	0.329257	1	0.001401	-0.00432	0.001521
<i>Brevundimonas vesicularis</i>	0	0	0.010273	0.047076	0.329257	1	0.010273	-0.0317	0.011156
<i>Caecibacter massiliensis</i>	0	0	0.00186	0.008522	0.329257	1	0.00186	-0.00574	0.002019
<i>Chryseobacterium gambrini</i>	0	0	0.034554	0.158346	0.329257	1	0.034554	-0.10663	0.037524
<i>Citroniella saccharovorans</i>	0	0	0.00093	0.004261	0.329257	1	0.00093	-0.00287	0.00101
<i>Cloacibacterium normanense</i>	0	0	0.027083	0.124109	0.329257	1	0.027083	-0.08358	0.029411
<i>Comamonas suwonensis</i>	0	0	0.036889	0.169045	0.329257	1	0.036889	-0.11384	0.04006
<i>Curvibacter fontanus</i>	0	0	0.029884	0.136948	0.329257	1	0.029884	-0.09222	0.032453
<i>Dermabacter vaginalis</i>	0	0	0.001092	0.005004	0.329257	1	0.001092	-0.00337	0.001186
<i>Flavobacterium microcysteis</i>	0	0	0.074711	0.34237	0.329257	1	0.074711	-0.23056	0.081134
<i>Flexilinea flocculi</i>	0	0	0.001159	0.005311	0.329257	1	0.001159	-0.00358	0.001259
<i>Gardnerella swidsinskii</i>	0	0	0.001085	0.004971	0.329257	1	0.001085	-0.00335	0.001178
<i>Herbaspirillum aquaticum</i>	0	0	0.014197	0.065058	0.329257	1	0.014197	-0.04381	0.015417
<i>Janthinobacterium lividum</i>	0	0	0.031752	0.145507	0.329257	1	0.031752	-0.09799	0.034482
<i>Ligilactobacillus salivarius</i>	0	0	0.001697	0.007775	0.329257	1	0.001697	-0.00524	0.001842
<i>Lysobacter gummosus</i>	0	0	0.054633	0.250358	0.329257	1	0.054633	-0.16859	0.059329
<i>Niveispirillum lacus</i>	0	0	0.049029	0.22468	0.329257	1	0.049029	-0.1513	0.053244
<i>Odoribacter denticanis</i>	0	0	0.001064	0.004874	0.329257	1	0.001064	-0.00328	0.001155
<i>Paenibacillus barengoltzii</i>	0	0	0.001092	0.005004	0.329257	1	0.001092	-0.00337	0.001186

<i>Parabacteroides_johnsonii</i>	0	0	0.000987	0.004522	0.329257	1	0.000987	-0.00305	0.001072
<i>Parascardovia_denticolens</i>	0	0	0.002983	0.01367	0.329257	1	0.002983	-0.00921	0.003239
<i>Pedobacter_antarcticus</i>	0	0	0.000431	0.001973	0.329257	1	0.000431	-0.00133	0.000468
<i>Porphyromonas_asaccharolyti</i> <i>ca</i> DSM 20707	0	0	0.000771	0.003535	0.329257	1	0.000771	-0.00238	0.000838
<i>Prevotella_micans</i>	0	0	0.00565	0.025894	0.329257	1	0.00565	-0.01744	0.006136
<i>Pseudomonas_yamanorum</i>	0	0	0.075645	0.346649	0.329257	1	0.075645	-0.23344	0.082148
<i>Ralstonia_mannitolilytica</i>	0	0	0.031752	0.145507	0.329257	1	0.031752	-0.09799	0.034482
<i>Reyranella_massiliensis</i> 521	0	0	0.020546	0.094152	0.329257	1	0.020546	-0.0634	0.022312
<i>Sandaracinobacter_sibiricus</i>	0	0	0.006279	0.028775	0.329257	1	0.006279	-0.01938	0.006819
<i>Sphingomonas_koreensis</i>	0	0	0.052298	0.239659	0.329257	1	0.052298	-0.16139	0.056794
<i>Staphylococcus_auricularis</i>	0	0	0.001638	0.007507	0.329257	1	0.001638	-0.00506	0.001779
<i>Streptococcus_constellatus</i> <i>subsp. pharyngis</i>	0	0	0.007743	0.035484	0.329257	1	0.007743	-0.0239	0.008409
<i>Streptococcus_vestibularis</i> ATCC 49124	0	0	0.006802	0.031169	0.329257	1	0.006802	-0.02099	0.007386
<i>Wielierella_bovis</i>	0	0	0.00293	0.013426	0.329257	1	0.00293	-0.00904	0.003182
<i>Methylibium_petroleiphilum</i> PM1	0.000479	0.003029	0.480486	2.201865	0.329728	1	0.480008	-1.48228	0.52227
<i>Streptococcus_sinensis</i>	0.013457	0.074847	0.001674	0.007672	0.330073	1	-0.01178	-0.01236	0.035929
<i>Bifidobacterium_dentium</i>	0.000411	0.0026	0.078913	0.361625	0.331728	1	0.078502	-0.24311	0.08611
<i>Pseudobdellovibrio_exovorus</i> JSS	0.000239	0.001514	0.043893	0.201142	0.331845	1	0.043653	-0.13521	0.047906
<i>Pseudomonas_azotoformans</i>	0.000867	0.005485	0.142418	0.652642	0.332148	1	0.141551	-0.43863	0.155532
<i>Acidibacter_ferrireducens</i>	0.000409	0.002584	0.049963	0.22896	0.333148	1	0.049554	-0.15378	0.054669
<i>Eikenella_halliae</i>	0.036235	0.154215	0.011744	0.02738	0.334686	1	-0.02449	-0.02612	0.075102
<i>Shigella_sonnei</i>	0.003418	0.018338	0.162722	0.740128	0.335816	1	0.159304	-0.49625	0.177639
<i>Neisseria_mucosa</i>	0.001785	0.011288	0.121218	0.555491	0.336305	1	0.119433	-0.37231	0.133444
<i>Prevotella_multiformis</i> DSM 16608	0.02594	0.124567	0.157888	0.608711	0.33705	1	0.131948	-0.4113	0.147405
<i>Pseudostreptobacillus_hongko</i> <i>ngensis</i>	0.004529	0.020063	0.001234	0.005653	0.337657	1	-0.0033	-0.00354	0.010133
<i>Moraxella_osloensis</i>	0.000696	0.004404	0.036422	0.166905	0.338446	1	0.035725	-0.11171	0.040259
<i>Parvimonas_micra</i>	0.524528	1.016668	0.923053	1.72626	0.33902	1	0.398525	-1.2382	0.441148
<i>Prevotella_pleuritidis</i>	0.031112	0.065772	0.156435	0.590984	0.344155	1	0.125323	-0.39499	0.144341
<i>Diaphorobacter_nitroreducens</i>	0.002482	0.015697	0.053699	0.246078	0.352036	1	0.051217	-0.16332	0.060886
<i>Paludibacter_jiangxiensis</i>	0.036065	0.212116	0.004628	0.021208	0.358627	1	-0.03144	-0.03696	0.099839

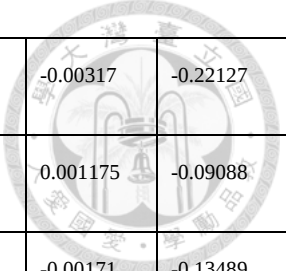
<i>Neisseria_elongata</i> subsp. <i>nitroreducens</i>	0.051742	0.126209	0.13961	0.419589	0.358644	1	0.087868	-0.28225	0.106518
<i>Neisseria_bacilliformis</i> ATCC BAA-1200	0.001957	0.00738	0.006983	0.024024	0.359489	1	-0.005026	-0.01616	0.006112
<i>Corynebacterium_tuberculoste</i> <i>aricum</i>	0.001983	0.01254	0.031752	0.145507	0.360487	1	0.02977	-0.0961	0.036561
<i>Veillonella_dispar</i>	5.324933	5.273994	3.921652	5.857086	0.363747	1	-1.40328	-1.68834	4.494899
<i>Prevotellamassilia_timonensis</i>	1.602371	1.854091	1.196482	1.547841	0.368695	1	-0.40589	-0.49354	1.305318
<i>Pseudomonas_poeae</i>	0.005783	0.027663	0.027374	0.10623	0.370257	1	0.02159	-0.07059	0.027408
<i>Streptococcus_constellatus</i>	0.109259	0.345754	0.533334	2.142012	0.377968	1	0.424075	-1.40407	0.555925
<i>Leptotrichia_buccalis</i> C-1013-b	0.000764	0.00483	0.007953	0.036443	0.378725	1	0.007189	-0.02383	0.009457
<i>Phocaeicola_abscessus</i> CCUG 55929	0.004563	0.028861	0.015898	0.054205	0.379474	1	0.011335	-0.03739	0.014721
<i>Fusobacterium_periodonticum</i>	0.00137	0.008667	0.013778	0.06314	0.380642	1	0.012408	-0.04125	0.016439
<i>Streptococcus_infantis</i> ATCC 700779	1.96447	4.412204	1.275459	1.602885	0.381184	1	-0.68901	-0.87536	2.253385
<i>Oribacterium_sinus</i>	0.260174	0.323994	0.378301	0.563667	0.383115	1	0.118127	-0.39146	0.155209
<i>Treponema_socranskii</i> subsp. <i>buccale</i>	0.000928	0.005872	0.008113	0.037179	0.389137	1	0.007185	-0.02419	0.009821
<i>Streptococcus_intermedius</i>	0.263492	0.791135	0.690701	2.15608	0.389334	1	0.427209	-1.43463	0.580217
<i>Alloprevotella_rava</i>	1.07294	2.06777	1.592012	2.295112	0.391031	1	0.519072	-1.73071	0.692566
<i>Streptococcus_koreensis</i>	0.397876	0.688886	0.274214	0.434557	0.395437	1	-0.12366	-0.16555	0.412871
<i>Leptotrichia_shahii</i>	0.046873	0.289408	0.007624	0.020501	0.39841	1	-0.03925	-0.05369	0.132192
<i>Selenomonas_artemidis</i>	0.00175	0.00735	0.005213	0.017753	0.400465	1	0.003463	-0.01182	0.004891
<i>Cardiobacterium_hominis</i>	0.067301	0.38449	0.015605	0.039991	0.404868	1	-0.0517	-0.07237	0.175767
<i>Metamycoplasma_faucium</i>	0.010761	0.027251	0.005637	0.020138	0.408872	1	-0.00512	-0.00722	0.017473
<i>Solobacterium_moorei</i>	0.49209	0.919297	0.360654	0.297558	0.412789	1	-0.13144	-0.18801	0.450878
<i>Prevotella_denticola</i>	0.074086	0.162615	0.042826	0.129674	0.417508	1	-0.03126	-0.04556	0.108078
<i>Veillonella_massiliensis</i>	0.044445	0.135981	0.130261	0.467958	0.419791	1	0.085816	-0.30236	0.130725
<i>Sinanaerobacter_chloroacetimi</i> <i>divorans</i>	0.007245	0.02066	0.01272	0.026898	0.420946	1	0.005475	-0.01915	0.008196
<i>Lautropia_dentalis</i>	0.030977	0.103679	0.016728	0.029146	0.421636	1	-0.01425	-0.02108	0.049576
<i>Porphyromonas_pasteri</i>	1.742874	2.391375	2.281461	2.501885	0.422268	1	0.538587	-1.88168	0.804509
<i>Oribacterium_parvum</i> ACB1	0.151954	0.256032	0.215999	0.317062	0.429866	1	0.064045	-0.22695	0.098864
<i>Catonella_massiliensis</i>	0.121115	0.161819	0.167085	0.23635	0.430853	1	0.04597	-0.16353	0.071591
<i>Ottowia_shaoquanensis</i>	0.045468	0.209489	0.017265	0.06009	0.432294	1	-0.0282	-0.04336	0.099764

<i>Mobiluncus_mulieris</i>	0.002497	0.00721	0.008008	0.031295	0.434917	1	0.005511	-0.0199	0.008883
<i>Paraburkholderia_bryophila</i>	0.003246	0.020527	0.000638	0.002924	0.434954	1	-0.00261	-0.00407	0.009283
<i>Stomatobaculum_longum</i>	0.651176	0.923702	0.484069	0.71072	0.436445	1	-0.16711	-0.26063	0.594848
<i>Fusobacterium_nucleatum</i> <i>subsp. nucleatum ATCC 25586</i>	0.022239	0.104794	0.055522	0.178694	0.438875	1	0.033282	-0.12015	0.053589
<i>Lachnoclostridium_edouardi</i>	0.000787	0.00498	0.003719	0.017044	0.448869	1	0.002932	-0.01082	0.004956
<i>Treponema_maltophilum</i>	0.010143	0.04677	0.018028	0.033129	0.449127	1	0.007885	-0.02862	0.012852
<i>Kingella_denitrificans ATCC</i> <i>33394</i>	0.011373	0.038355	0.006101	0.015523	0.45111	1	-0.00527	-0.00864	0.019184
<i>Capnocytophaga_sputigena</i>	0.136484	0.618525	0.060981	0.092756	0.453832	1	-0.0755	-0.12601	0.277012
<i>Fusobacterium_simiae</i>	0.001055	0.004668	0.004641	0.021269	0.453939	1	0.003586	-0.01336	0.006187
<i>Dialister_pneumosintes</i>	0.116789	0.220313	0.178091	0.334905	0.454974	1	0.061302	-0.2268	0.104195
<i>Leptotrichia_hofstadii</i>	0.012984	0.050248	0.00664	0.015633	0.466476	1	-0.00634	-0.01101	0.0237
<i>Porphyromonas_endodontalis</i>	0.679359	2.016106	0.418422	0.791706	0.474729	1	-0.26094	-0.46543	0.98731
<i>Streptococcus_australis</i>	0.335566	0.5035	0.249823	0.431645	0.490363	1	-0.08574	-0.16242	0.333906
<i>Lachnoanaerobaculum_gingiva</i> <i>lis</i>	0.502301	0.814194	0.391113	0.449601	0.494822	1	-0.11119	-0.21272	0.435093
<i>Moryella_indoligenes</i>	0.00472	0.023674	0.001854	0.008498	0.495624	1	-0.00287	-0.00551	0.01124
<i>Corynebacterium_matruchotii</i>	0.002202	0.008794	0.001028	0.004713	0.500075	1	-0.00117	-0.00229	0.004634
<i>Peptidiphaga_gingivicola</i>	0.007989	0.035388	0.003555	0.01629	0.506147	1	-0.00443	-0.00883	0.017702
<i>Eubacterium_sulci ATCC</i> <i>35585</i>	0.227674	0.262603	0.302745	0.48281	0.513141	1	0.075071	-0.30769	0.157548
<i>Lancefieldella_rimae</i>	0.189633	1.006541	0.081878	0.214299	0.519218	1	-0.10776	-0.22626	0.441773
<i>Megasphaera_micronuciformis</i>	1.177312	1.717886	0.929465	1.25648	0.523551	1	-0.24785	-0.52642	1.022114
<i>Streptococcus_mutans</i>	0.008278	0.033681	0.004178	0.016721	0.52778	1	-0.0041	-0.00882	0.017018
<i>Fusobacterium_pseudoperiodo</i> <i>nticum</i>	1.80386	2.509909	2.220411	2.416989	0.531395	1	0.41655	-1.74847	0.915373
<i>Staphylococcus_aureus</i>	0.011576	0.047906	0.026909	0.105356	0.532327	1	0.015333	-0.06525	0.034579
<i>Peptococcus_niger</i>	0.084597	0.249942	0.123125	0.220146	0.538766	1	0.038528	-0.16378	0.086721
<i>Treponema_socranskii subsp.</i> <i>paredis</i>	0.001824	0.005594	0.003003	0.007695	0.538835	1	0.001179	-0.00505	0.002689
<i>Haemophilus_seminalis</i>	0.04023	0.099467	0.065866	0.179374	0.548528	1	0.025636	-0.11225	0.060976
<i>Prevotella_koreensis</i>	0.03873	0.163775	0.074216	0.242666	0.551725	1	0.035486	-0.1559	0.084927
<i>Porphyromonas_gingivalis</i>	0.40243	1.557064	0.241919	0.542707	0.559318	1	-0.16051	-0.38732	0.708344
<i>Chryseobacterium_reticuliterm</i> <i>itis</i>	0.016682	0.044253	0.011314	0.027764	0.564232	1	-0.00537	-0.01317	0.023902
<i>Streptococcus_parasanguinis</i>	3.157421	3.3659	2.612447	3.587914	0.568194	1	-0.54497	-1.37065	2.460595

ATCC 15912									
<i>Capnocytophaga granulosa</i>	0.102489	0.395076	0.062062	0.151436	0.569598	1	-0.04043	-0.10117	0.182028
<i>Granulicatella elegans</i>	3.01636	2.451344	2.657824	2.274517	0.572057	1	-0.35854	-0.91102	1.628095
<i>Streptococcus toyakuensis</i>	4.158451	10.82544	3.084954	3.796457	0.574751	1	-1.0735	-2.73952	4.886519
<i>Prevotella nanceiensis</i>	0.207913	0.258266	0.261061	0.38666	0.574997	1	0.053148	-0.24469	0.138391
<i>Aminipila terrae</i>	0.040967	0.086262	0.031034	0.051606	0.576582	1	-0.00993	-0.02547	0.04534
<i>Capnocytophaga bilanii</i>	0.010596	0.043073	0.006287	0.016397	0.577684	1	-0.00431	-0.01111	0.019724
<i>Streptococcus pseudopneumoniae</i>	1.440768	3.223675	1.016266	2.595086	0.579951	1	-0.4245	-1.10657	1.955573
<i>Streptococcus mitis</i>	2.675752	6.42799	2.02631	2.722703	0.583339	1	-0.64944	-1.70785	3.006732
<i>Anaerobacterium chartisolvans</i>	0.125502	0.312846	0.218619	0.739924	0.586488	1	0.093117	-0.44179	0.255554
<i>Tannerella forsythia</i>	0.056213	0.249123	0.033371	0.075485	0.594968	1	-0.02284	-0.06288	0.108565
<i>Parachloleplasma brassicae</i> 0502	0.000269	0.001703	0.000638	0.002924	0.598579	1	0.000369	-0.00179	0.001051
<i>Streptococcus downii</i>	0.307933	0.444423	0.39789	0.704268	0.598609	1	0.089957	-0.43579	0.255872
<i>Prevotella melaninogenica</i> ATCC 25845	3.019184	3.379912	2.588047	2.823619	0.599545	1	-0.43114	-1.20916	2.071432
<i>Eikenella corrodens</i>	0.0944	0.496517	0.050603	0.121746	0.599664	1	-0.0438	-0.12291	0.210508
<i>Dialister invisus</i> DSM 15470	0.082082	0.219579	0.058092	0.136931	0.602499	1	-0.02399	-0.06773	0.115712
<i>Desulfohalobium propionicus</i> DSM 2032	0.001589	0.005112	0.003403	0.015596	0.609188	1	0.001814	-0.00906	0.005435
<i>Selenomonas felix</i>	0.198466	0.446971	0.257534	0.419748	0.61226	1	0.059068	-0.29237	0.174234
<i>Lachnoanaerobaculum orale</i>	0.337391	0.469152	0.263157	0.583162	0.617546	1	-0.07423	-0.22515	0.373614
<i>Prevotella multisaccharivorax</i>	0.004262	0.022626	0.002169	0.009942	0.618891	1	-0.00209	-0.00628	0.010468
<i>Prevotella salivae</i>	0.35091	0.471155	0.291829	0.422461	0.620593	1	-0.05908	-0.17967	0.297828
<i>Treponema lecithinolyticum</i>	0.012235	0.048517	0.007104	0.032557	0.625573	1	-0.00513	-0.01582	0.026082
<i>Filifactor alocis</i>	0.228963	0.582945	0.16453	0.428441	0.625638	1	-0.06443	-0.19897	0.327835
<i>Leptotrichia wadei</i>	0.708564	2.007997	0.540152	0.760547	0.640141	1	-0.16841	-0.54949	0.886313
<i>Aggregatibacter aphrophilus</i> ATCC 33389	0.076161	0.15754	0.099051	0.191213	0.640581	1	0.02289	-0.12159	0.075811
<i>Granulicatella adiacens</i>	0.581189	0.818254	0.74127	1.457487	0.644823	1	0.160082	-0.86485	0.544687
<i>Treponema socranskii</i>	0.007342	0.032135	0.010486	0.020902	0.646998	1	0.003144	-0.01682	0.010534
<i>Streptococcus oralis</i> subsp. <i>tigurinus</i> AZ_3a	0.184699	0.492221	0.251927	0.567027	0.64834	1	0.067228	-0.36367	0.229214
<i>Peptostreptococcus stomatis</i>	0.591396	1.104908	0.720812	1.02886	0.651433	1	0.129415	-0.70297	0.444139
<i>Prevotella oris</i>	0.452385	1.806611	0.663437	1.733434	0.65841	1	0.211052	-1.16746	0.745352
<i>Leptotrichia trevisanii</i>	0.911043	1.264589	1.041641	1.065247	0.672092	1	0.130598	-0.74734	0.486146

<i>Campylobacter_conciscus</i>	0.458528	0.571882	0.532235	0.709065	0.683452	1	0.073707	-0.43793	0.290516
<i>Cryptobacterium_curtum</i>	0.002943	0.0124	0.005152	0.023611	0.691826	1	0.00221	-0.01354	0.009123
<i>Streptococcus_timonensis</i>	0.69296	0.738511	0.902198	2.419627	0.702529	1	0.209238	-1.33078	0.912304
<i>Lachnoanaerobaculum_saburreum</i> DSM 3986	0.146094	0.463242	0.190317	0.418363	0.707347	1	0.044224	-0.28003	0.19158
<i>Fusobacterium_hwasookii</i> ChDC F128	0.009818	0.031092	0.007199	0.023067	0.711199	1	-0.00262	-0.0115	0.016738
<i>Cardiobacterium_valvarum</i>	0.001623	0.007166	0.002712	0.012427	0.713937	1	0.001089	-0.00712	0.00494
<i>Eggerthia_catenaformis</i>	0.003652	0.013282	0.005597	0.022767	0.721115	1	0.001945	-0.01301	0.009115
<i>Prevotella_pallens</i> ATCC 700821	0.8856	0.96954	0.800455	0.857706	0.726514	1	-0.08515	-0.40202	0.572315
<i>Oribacterium_asaccharolyticum</i> ACB7	0.362305	0.482436	0.411809	0.547911	0.729055	1	0.049504	-0.337	0.237994
<i>Haemophilus_paraahaemolyticus</i>	0.819544	2.243419	1.006418	1.895229	0.733138	1	0.186874	-1.28288	0.909133
<i>Acetivibrio_alkalicellulosi</i>	0.006277	0.033001	0.010155	0.046538	0.736379	1	0.003879	-0.02717	0.019412
<i>Streptococcus_vulneris</i>	1.02368	4.083299	1.342047	3.224319	0.740238	1	0.318368	-2.23663	1.59989
<i>Veillonella_parvula</i>	0.659721	1.37782	0.565285	0.851911	0.742795	1	-0.09444	-0.47899	0.667865
<i>Prevotella_jejuni</i>	1.55579	2.407995	1.364769	2.01602	0.74411	1	-0.19102	-0.97909	1.361136
<i>Gemella_morbillorum</i>	0.268518	0.410752	0.31091	0.525984	0.749892	1	0.042392	-0.31067	0.225883
<i>Prevotella_histicola</i>	0.905411	0.978608	0.820963	1.143143	0.775255	1	-0.08445	-0.5111	0.679993
<i>Haemophilus_influenzae</i>	0.004184	0.015684	0.006061	0.027775	0.776571	1	0.001877	-0.01532	0.011563
<i>Cutibacterium_acnes</i>	0.004078	0.015189	0.003003	0.013762	0.781155	1	-0.00107	-0.00667	0.008822
<i>Peptoanaerobacter_[Eubacterium]_yurii</i>	0.00133	0.007024	0.000927	0.004249	0.78165	1	-0.0004	-0.00249	0.003299
<i>Gemella_haemolysans</i>	1.031121	1.874016	0.919115	1.246662	0.781702	1	-0.11201	-0.69395	0.917965
<i>Streptococcus_anginosus</i>	0.121464	0.33987	0.102543	0.198572	0.784985	1	-0.01892	-0.11925	0.157093
<i>Abiotrophia_defectiva</i>	0.062324	0.134344	0.073249	0.17019	0.800015	1	0.010925	-0.09793	0.076081
<i>Pseudoleptotrichia_goodfellowii</i>	0.298848	0.491622	0.26914	0.401839	0.800938	1	-0.02971	-0.20585	0.265262
<i>Prevotella_mizrahi</i>	0.0087	0.029524	0.007092	0.021053	0.807082	1	-0.00161	-0.01153	0.014742
<i>Campylobacter_massiliensis</i>	0.098926	0.337941	0.082426	0.207174	0.814482	1	-0.0165	-0.12364	0.156634
<i>Leptotrichia_massiliensis</i>	0.115118	0.422529	0.137295	0.313061	0.817381	1	0.022176	-0.21391	0.169554
<i>Treponema_denticola</i>	0.033184	0.083698	0.037942	0.076143	0.82379	1	0.004758	-0.04756	0.038044
<i>Prevotella_marshii</i> DSM 16973 = JCM 13450	0.005353	0.033855	0.003958	0.015318	0.825839	1	-0.00139	-0.01124	0.014027
<i>Mogibacterium_timidum</i>	0.013417	0.045773	0.0166	0.057965	0.828426	1	0.003183	-0.03282	0.026452

<i>Treponema_medium</i>	0.061915	0.153362	0.06997	0.132732	0.8321	1	0.008054	-0.08408	0.067973
<i>Actinomyces_marseillensis</i>	0.201214	0.211527	0.217969	0.329143	0.834002	1	0.016755	-0.17882	0.145309
<i>Haemophilus_parainfluenzae</i> ATCC 33392	3.206543	3.906919	3.452049	5.04389	0.846971	1	0.245506	-2.81367	2.322663
<i>Prevotella_veroralis</i>	0.03427	0.112454	0.040614	0.134383	0.854294	1	0.006345	-0.07597	0.063277
<i>Rothia_mucilaginosa</i>	1.689654	1.693904	1.611579	1.670475	0.863809	1	-0.07807	-0.83528	0.991425
<i>Capnocytophaga_leadbetteri</i>	0.420792	1.978328	0.36051	0.799018	0.866924	1	-0.06028	-0.657	0.777563
<i>Aggregatibacter_kilianii</i>	0.074124	0.217779	0.082575	0.167468	0.86701	1	0.008451	-0.10927	0.092364
<i>Anaeroglobus_geminatus</i>	0.086025	0.318015	0.074765	0.243349	0.878244	1	-0.01126	-0.13556	0.158082
<i>Bulleidia_extracta</i>	0.017518	0.06228	0.015382	0.045712	0.87949	1	-0.00214	-0.02599	0.030257
<i>Fretibacterium_fastidiosum</i>	0.022449	0.055162	0.019711	0.079301	0.888583	1	-0.00274	-0.03681	0.04229
<i>Sinocapsa_zengkensis</i>	0.001923	0.009892	0.001623	0.007436	0.894547	1	-0.0003	-0.00422	0.004823
<i>Paludibacter_propionigenes</i> WB4	0.005662	0.024082	0.004977	0.016178	0.89561	1	-0.00068	-0.00972	0.011089
<i>Treponema_pectinovorum</i>	0.001633	0.010327	0.001356	0.006213	0.896634	1	-0.00028	-0.00397	0.004526
<i>Veillonella_atypica</i>	3.765604	4.039161	3.613806	4.876795	0.903362	1	-0.1518	-2.36863	2.672223
<i>Streptococcus_anginosus SK52</i> = DSM 20563	0.031184	0.086764	0.028017	0.100902	0.903514	1	-0.00317	-0.04946	0.055793
<i>Slackia_exigua ATCC 700122</i>	0.008342	0.029993	0.009246	0.029202	0.909894	1	0.000904	-0.01694	0.015129
<i>Prevotella_loescheii</i>	0.043284	0.093926	0.040697	0.079615	0.910352	1	-0.00259	-0.04339	0.048566
<i>Catonella_morbi ATCC 51271</i>	0.068151	0.144693	0.075137	0.26149	0.91038	1	0.006986	-0.13322	0.119245
<i>Treponema_amylovorum</i>	0.031928	0.140983	0.028799	0.083622	0.913898	1	-0.00313	-0.05454	0.060794
<i>Lancefieldella_parvula DSM</i> 20469	0.580153	0.741116	0.604046	0.985626	0.922897	1	0.023892	-0.52269	0.474906
<i>Mogibacterium_neglectum</i>	0.109104	0.150514	0.105233	0.153378	0.92537	1	-0.00387	-0.07913	0.086868
<i>[Eubacterium]_infirmum</i>	0.040019	0.214808	0.043079	0.074316	0.935503	1	0.00306	-0.07854	0.072417
<i>[Eubacterium]_brachy</i>	0.360688	1.196453	0.34142	0.686907	0.936643	1	-0.01927	-0.4638	0.502333
<i>Fusobacterium_watanabei</i>	0.237232	0.542662	0.247588	0.475448	0.939021	1	0.010356	-0.2814	0.26069
<i>Alloscardovia_omnicolens</i>	0.001542	0.0073	0.001697	0.007775	0.940301	1	0.000155	-0.00431	0.003997
<i>Prevotella_oulorum</i>	0.061611	0.103816	0.063557	0.125434	0.951735	1	0.001946	-0.06676	0.06287
<i>Muribaculum_gordoncarteri</i>	0.02334	0.081741	0.024747	0.099905	0.956056	1	0.001407	-0.05289	0.050079
<i>Peptoanaerobacter_[Eubacteri</i> <i>um] yurii subsp. margaretae</i> ATCC 43715	0.02575	0.06844	0.026733	0.079595	0.961949	1	0.000983	-0.0425	0.040529
<i>Gemella_sanguinis</i>	0.88958	1.065294	0.872738	1.456695	0.962953	1	-0.01684	-0.71636	0.750047
<i>Haemophilus_sputorum CCUG</i> 13788	0.15321	0.354014	0.156345	0.367369	0.974579	1	0.003135	-0.20083	0.19456



<i>Fusobacterium_nucleatum</i> <i>subsp. animalis</i>	0.117292	0.52466	0.114126	0.345036	0.977549	1	-0.00317	-0.22127	0.227605
<i>Ruminiclostridium_cellobiopar</i> <i>um DSM 1351 = ATCC 15832</i>	0.098504	0.202257	0.099679	0.143358	0.97914	1	-0.001175	-0.09088	0.08853
<i>Selenomonas_bovis</i>	0.053736	0.300438	0.052024	0.223434	0.980031	1	-0.00171	-0.13489	0.138311
<i>Actinomyces_bouchesdurhonen</i> <i>sis</i>	0.107144	0.36284	0.109663	0.38071	0.98022	1	0.002519	-0.20672	0.201683
<i>Streptococcus_salivarius</i>	5.102076	5.491916	5.062031	7.979089	0.983715	1	-0.04004	-3.93235	4.012437
<i>Peptoanaerobacter_[Eubacteri</i> <i>um] yurii subsp. schtitka</i>	0.00838	0.052999	0.00829	0.027476	0.99308	1	-9E-05	-0.02053	0.020708
<i>Millionella_massiliensis</i>	0.001484	0.007341	0.001489	0.006823	0.997829	1	5.17E-06	-0.00381	0.003801