

**E Appendix for use with Longitudinal
Investigation of the Airway Microbiota in Children
with Chronic Suppurative Lung Diseases**

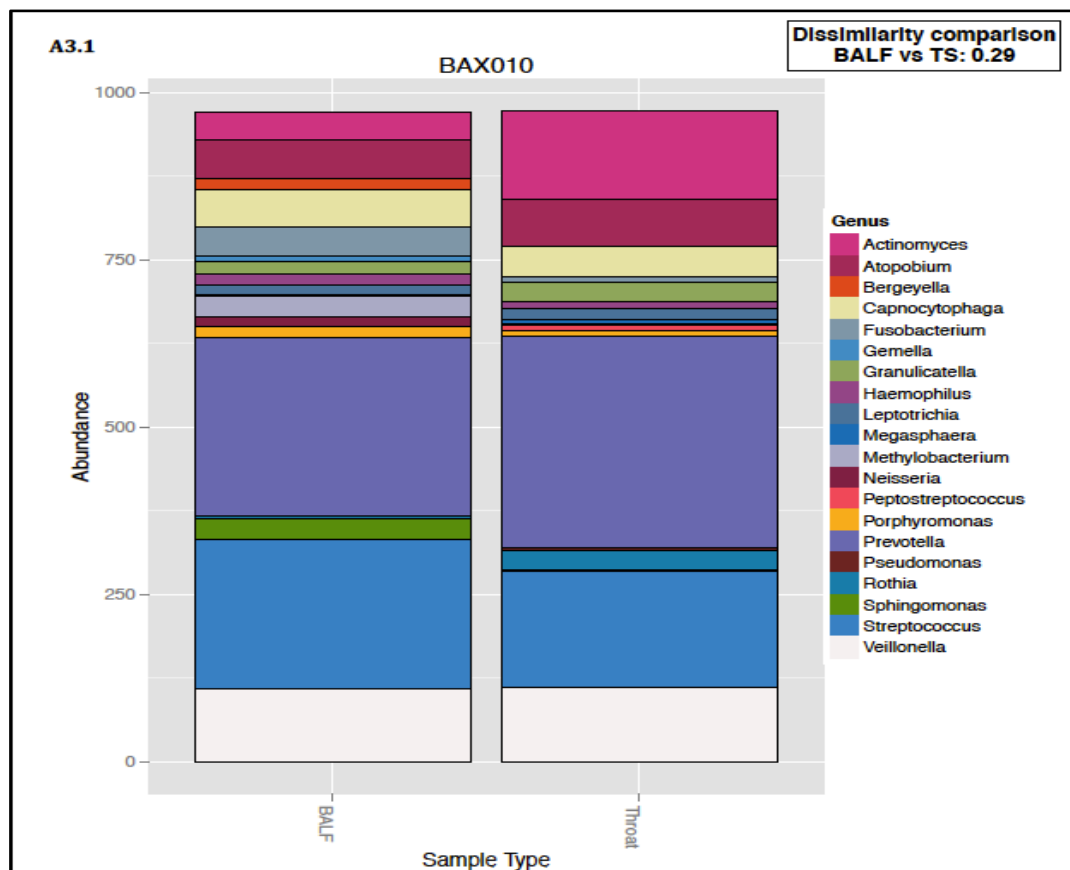
**Bushra Ahmed
September 2017**

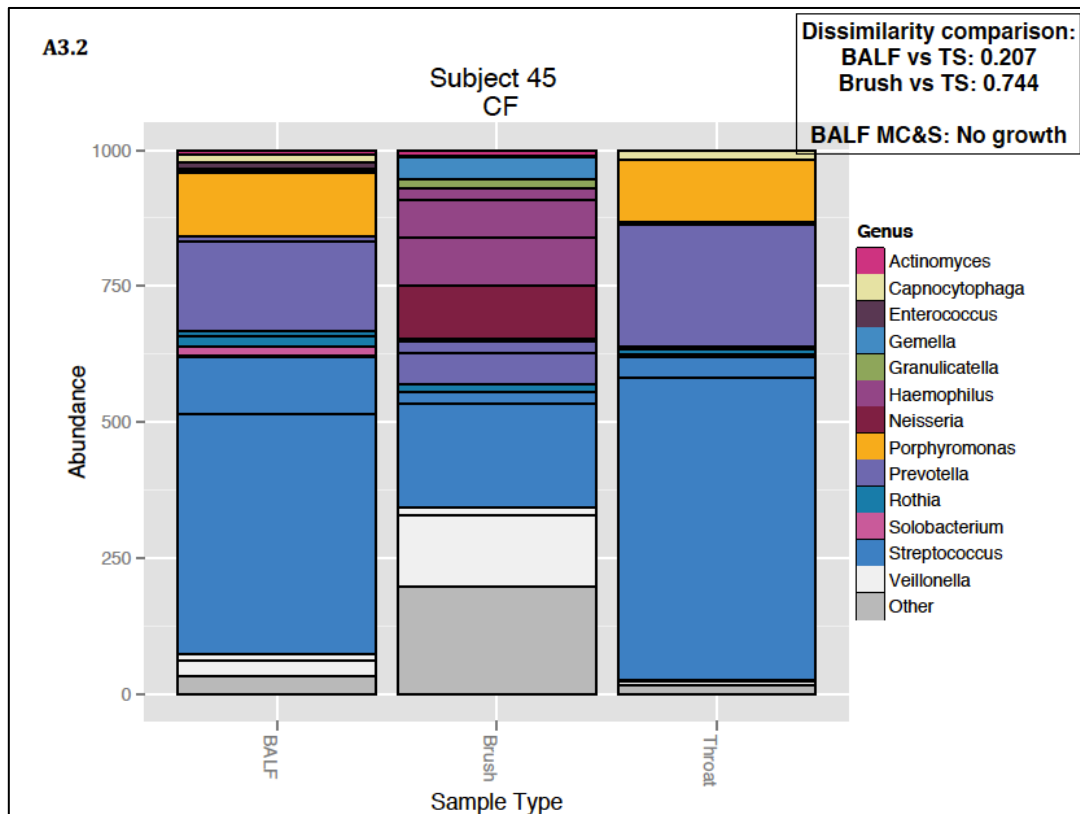
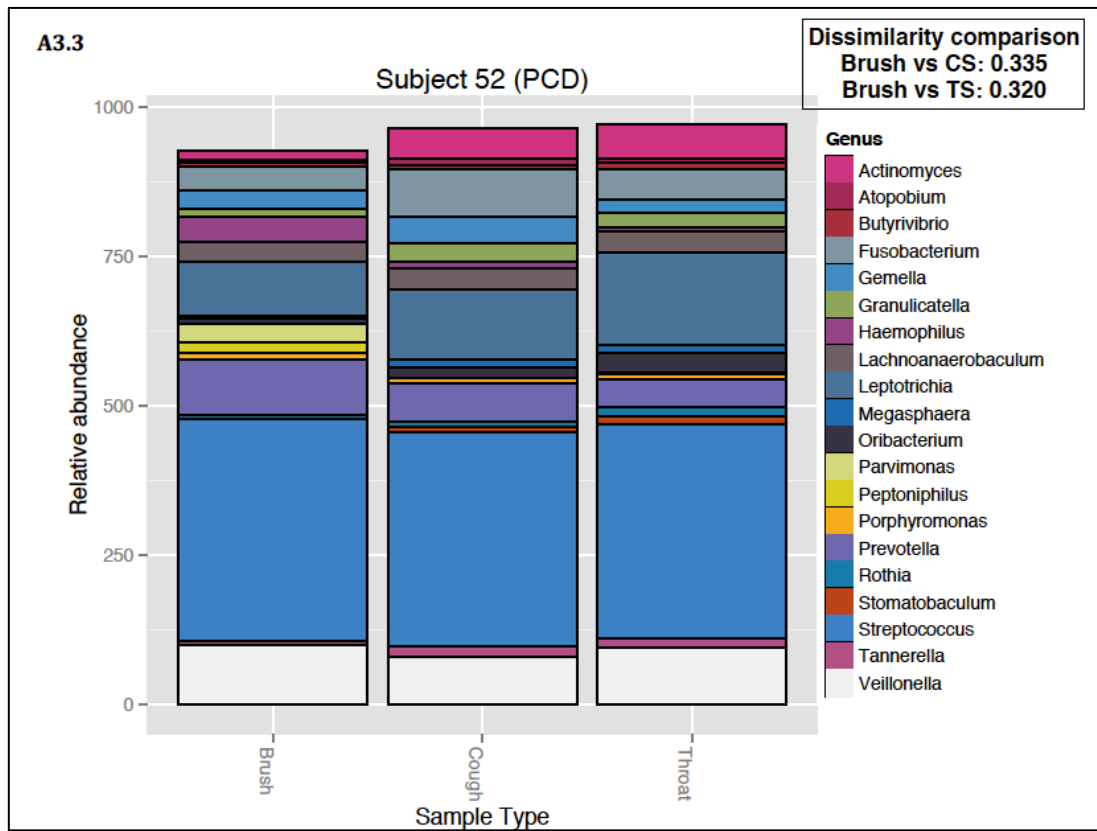
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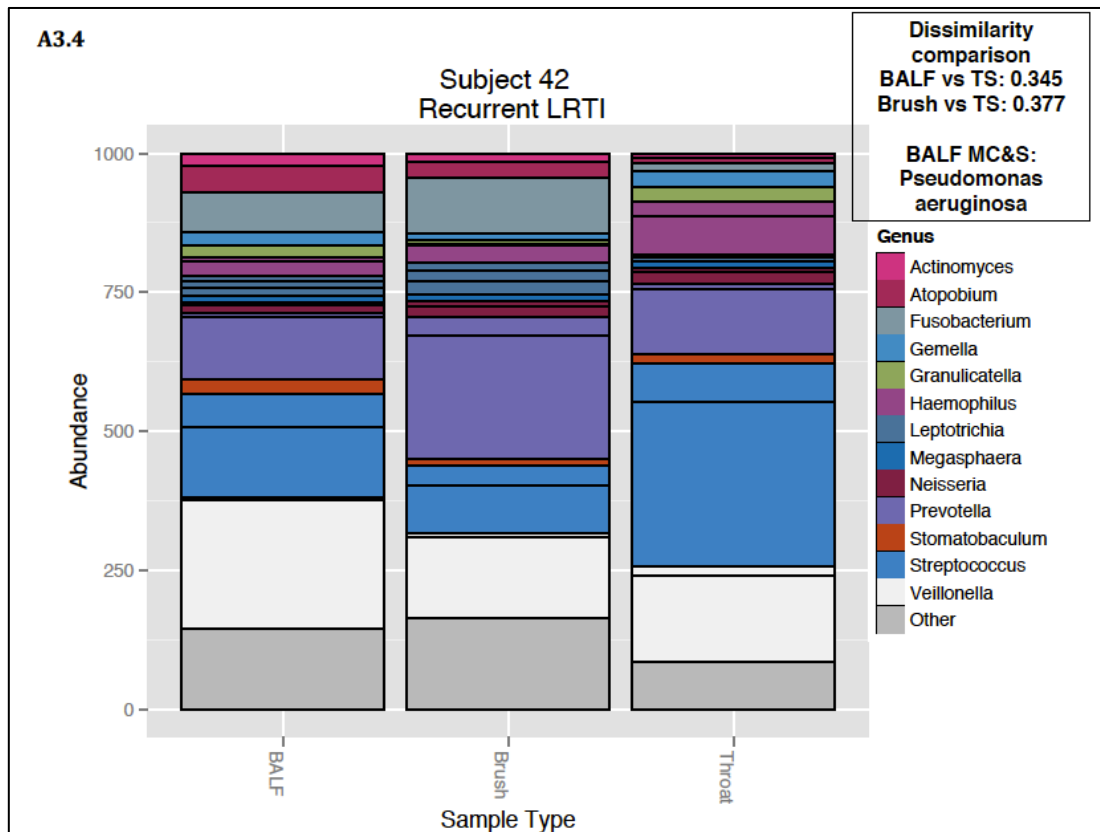
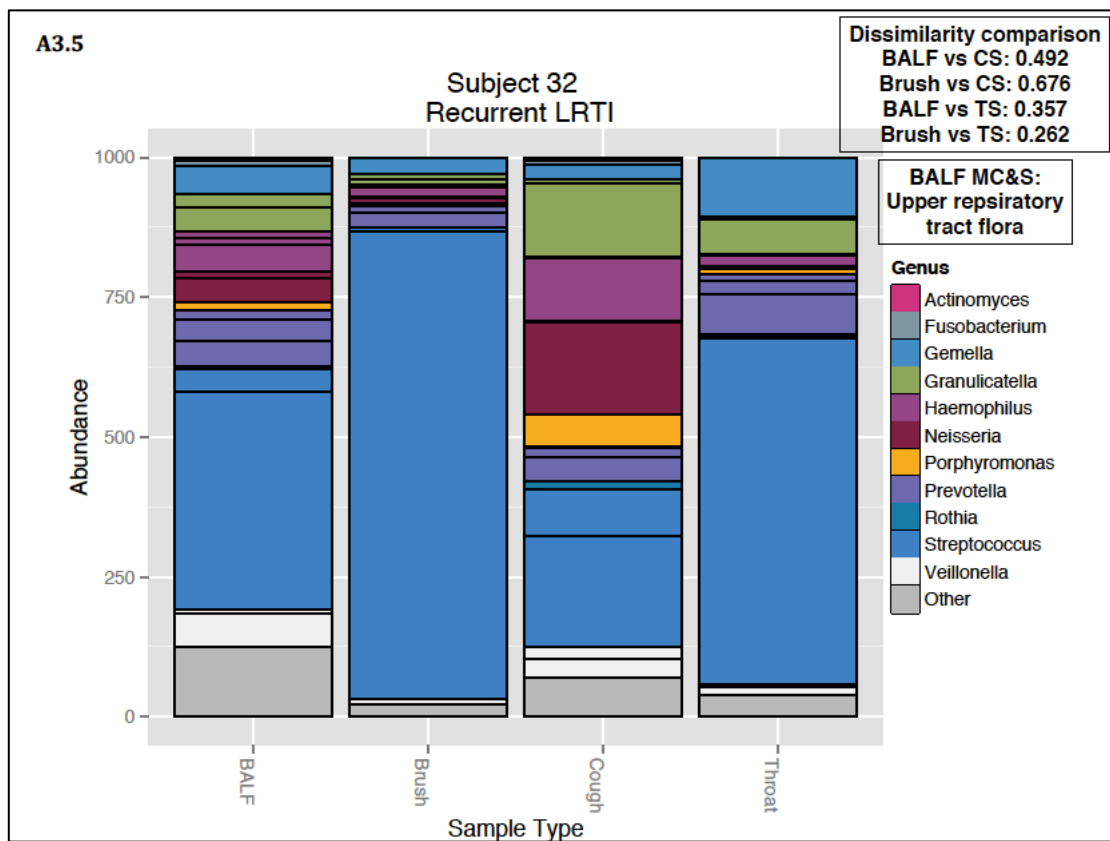
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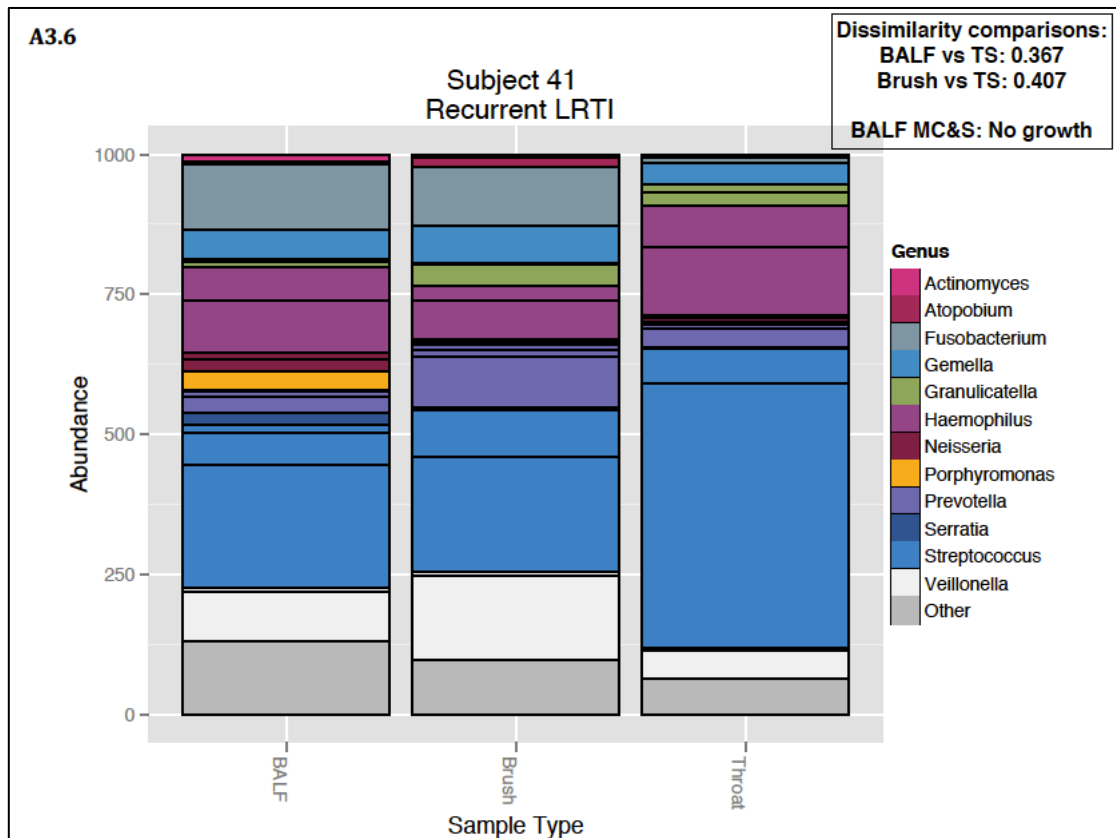
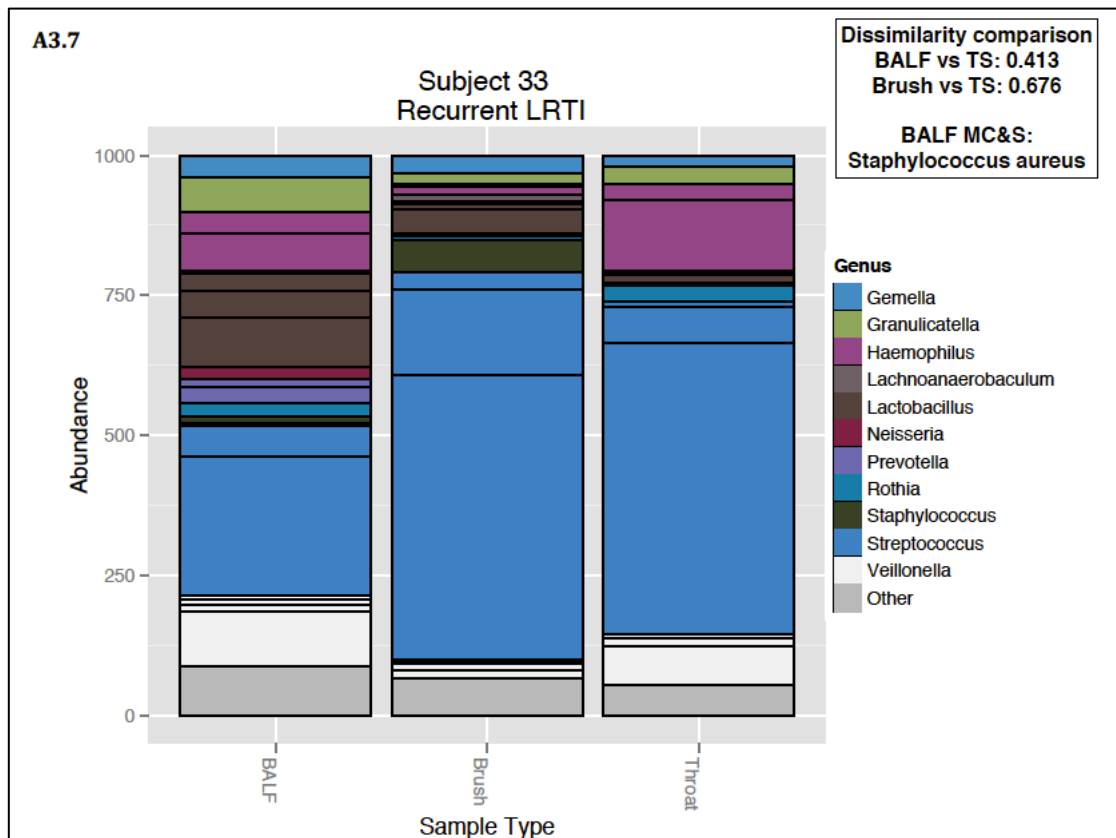
A3: E Appendix for use in conjunction with Chapter 3: Individual patient barplots comparing the upper and lower airway microbiota

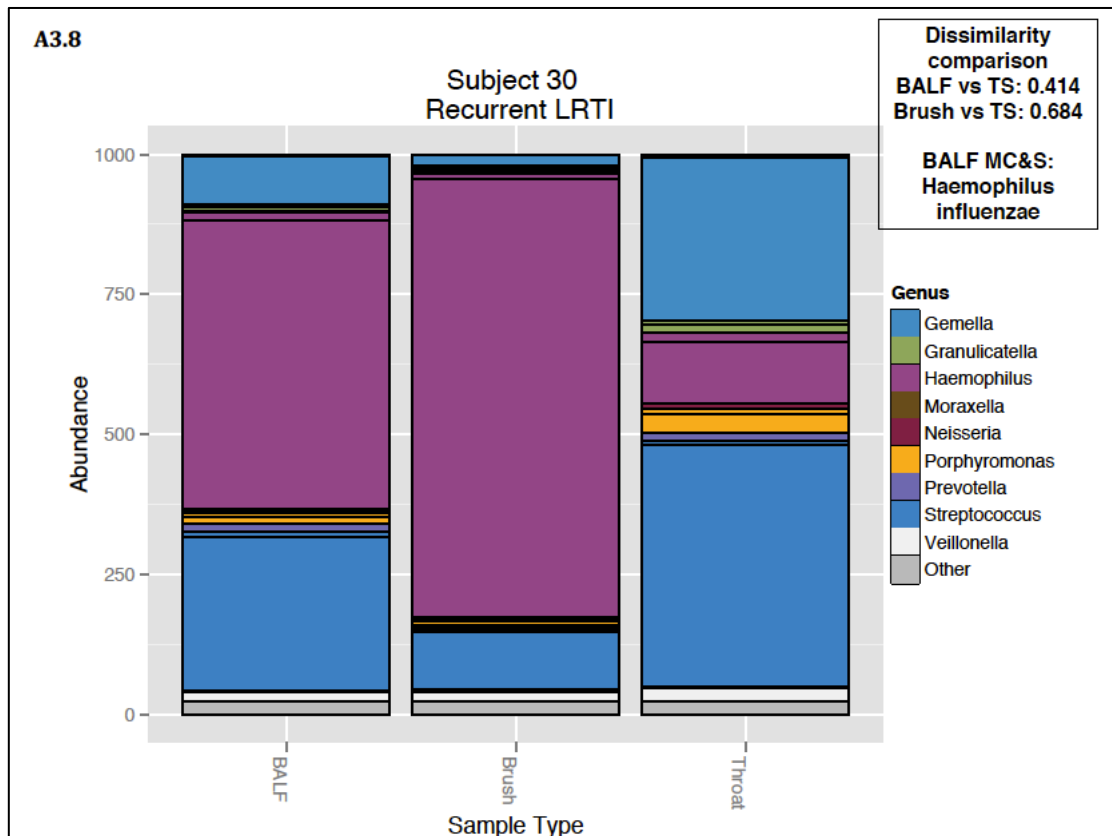
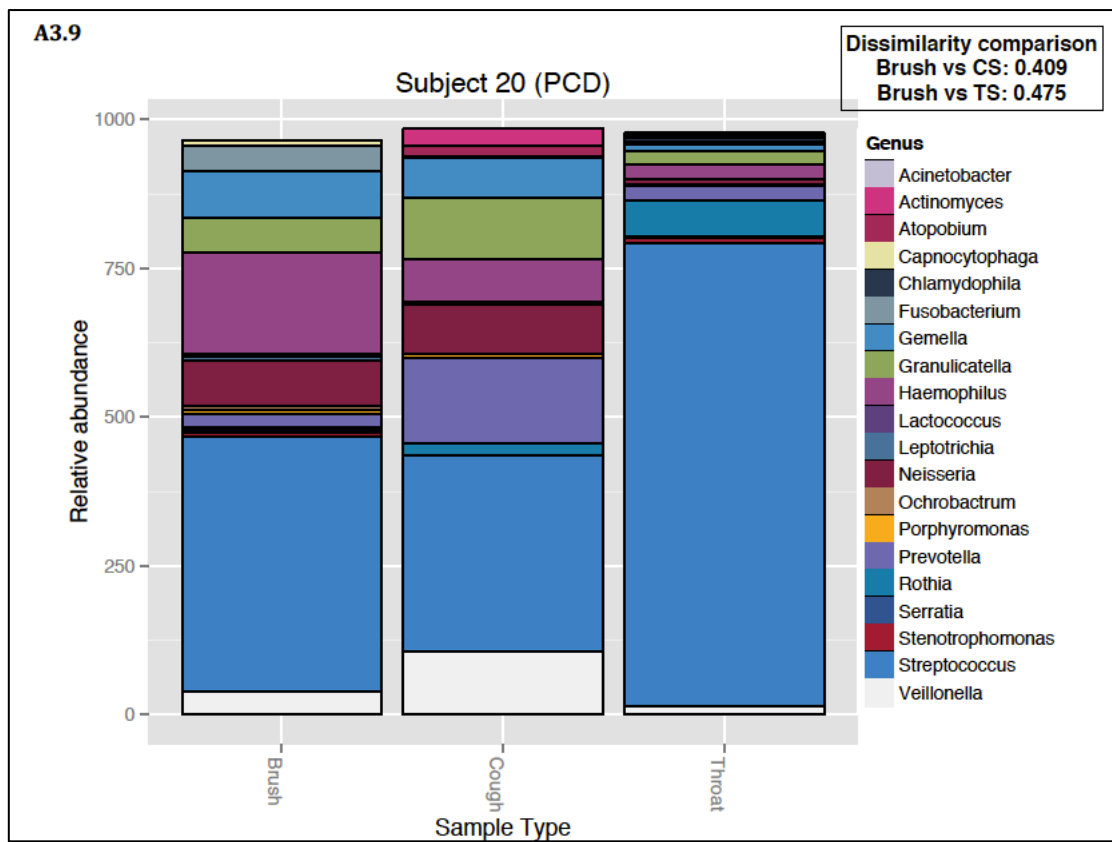
Figures A3.1 – A3.40 shown. Each figure represents an individual patient and each barplot an individual sample type (either cough swab (Cough), throat swab (throat), bronchoalveolar lavage fluid (BALF) or bronchial brushing (Brush)). The relative abundance of the most common genera for each sample type is shown by the height of the corresponding bar. Constructed using rarefied data. Barplots have been organised from the most similar on Bray Curtis dissimilarity to the least similar.

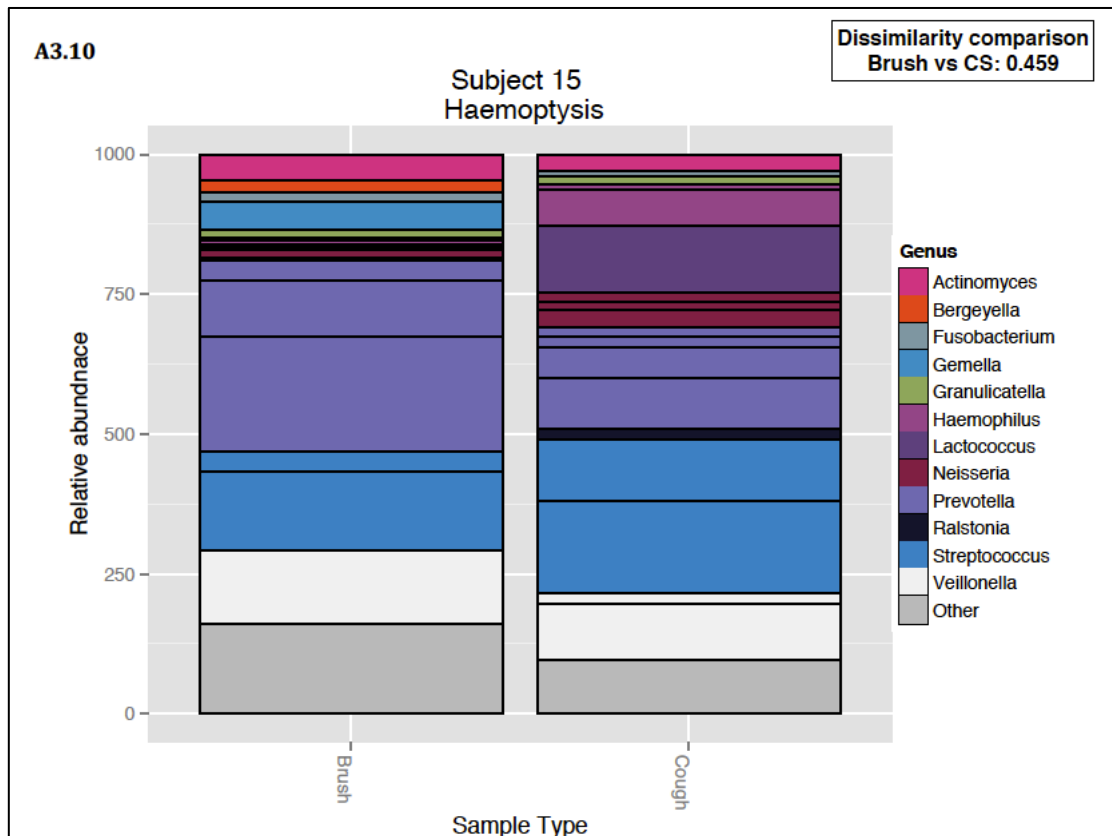
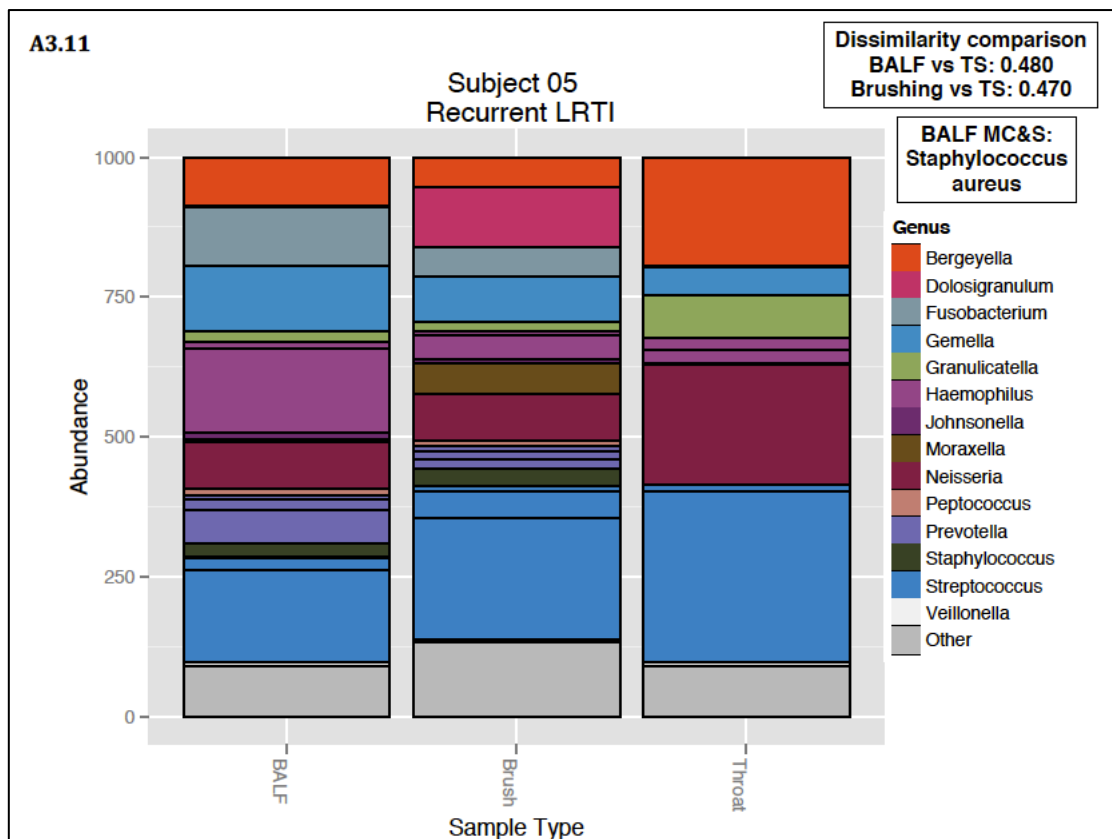


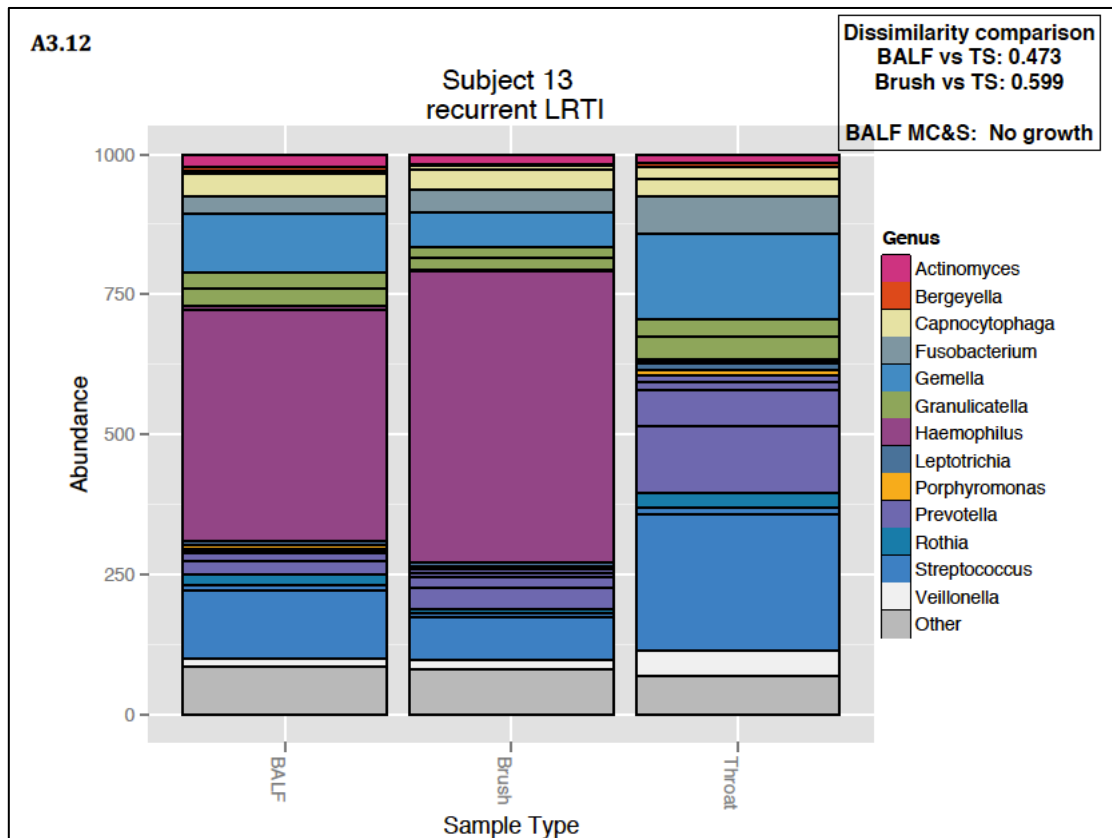
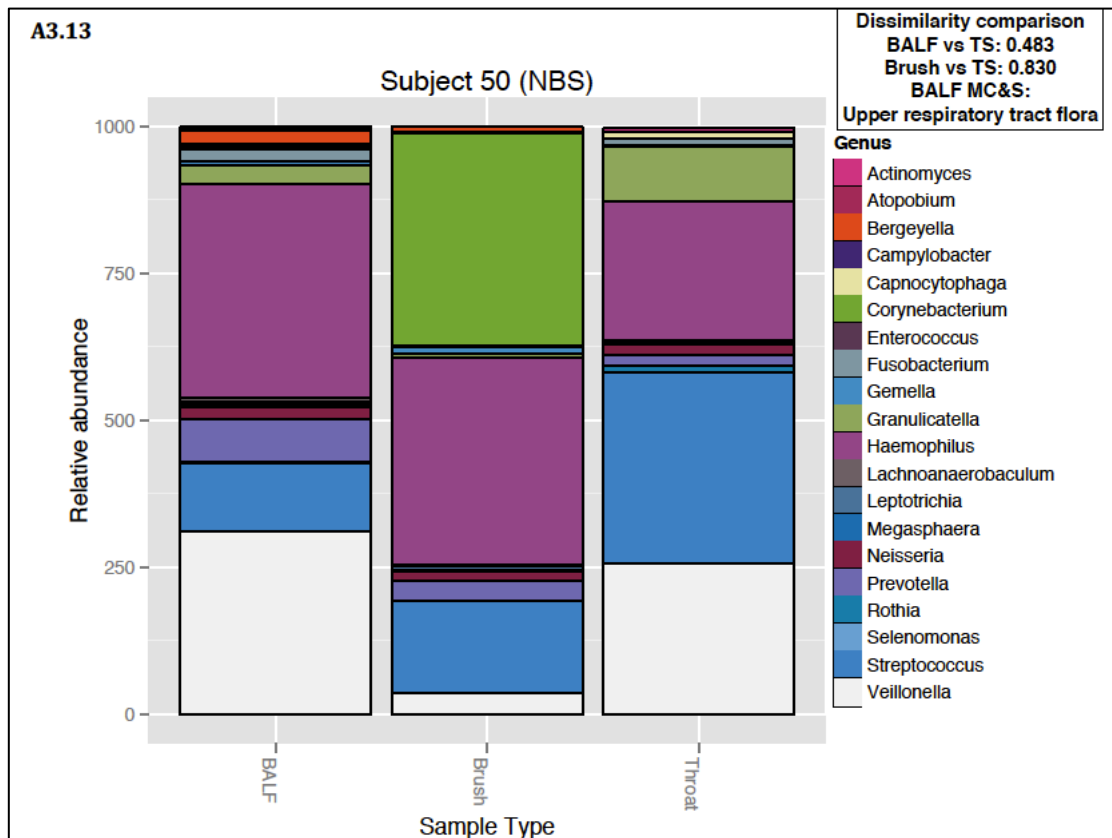


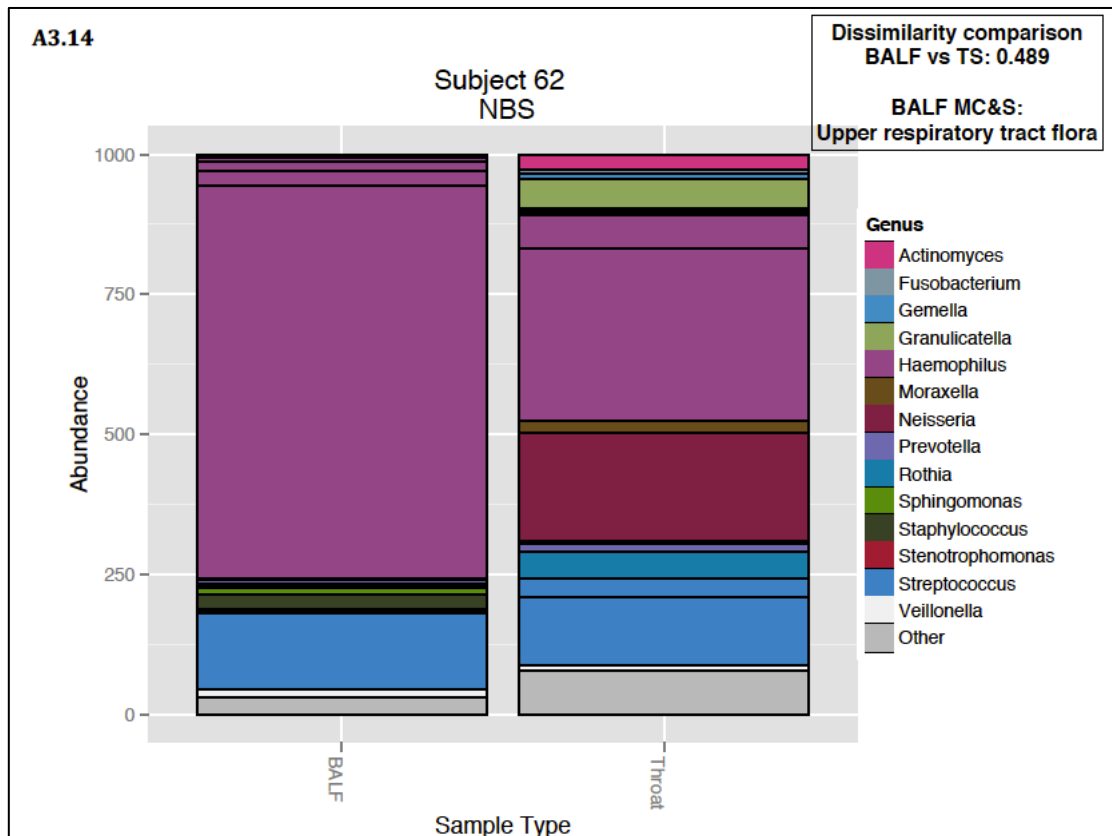
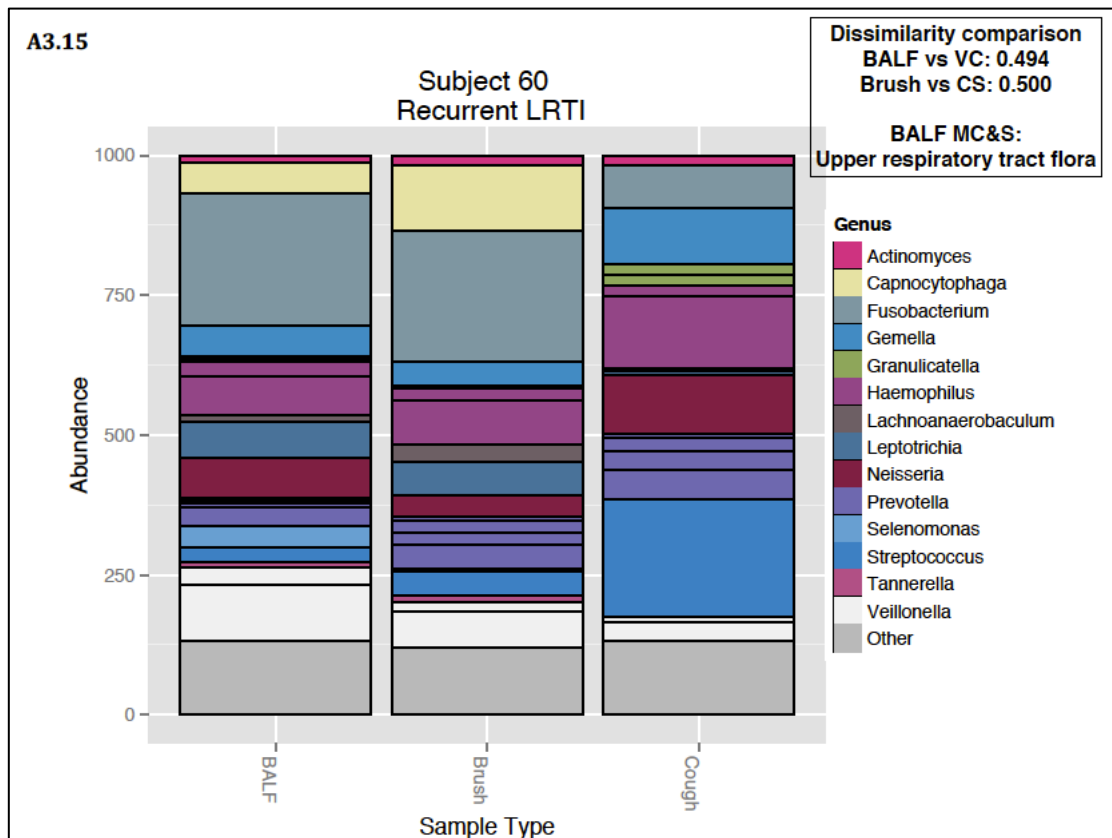


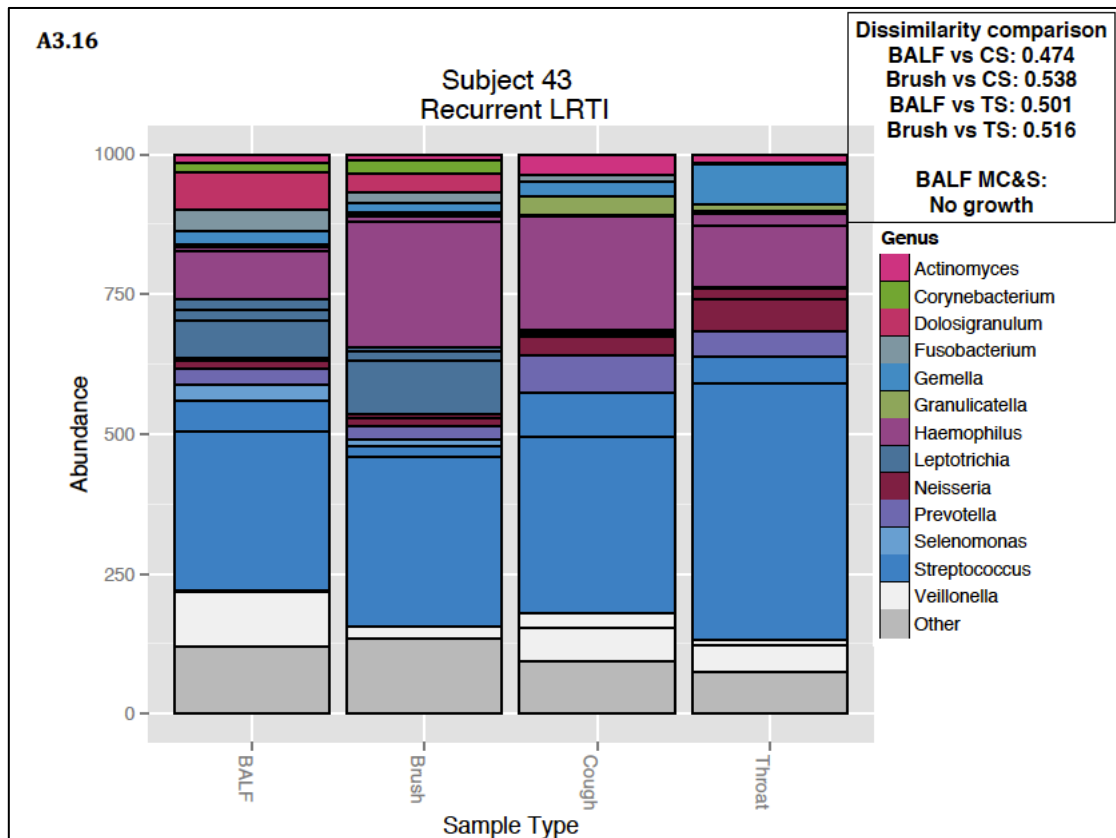
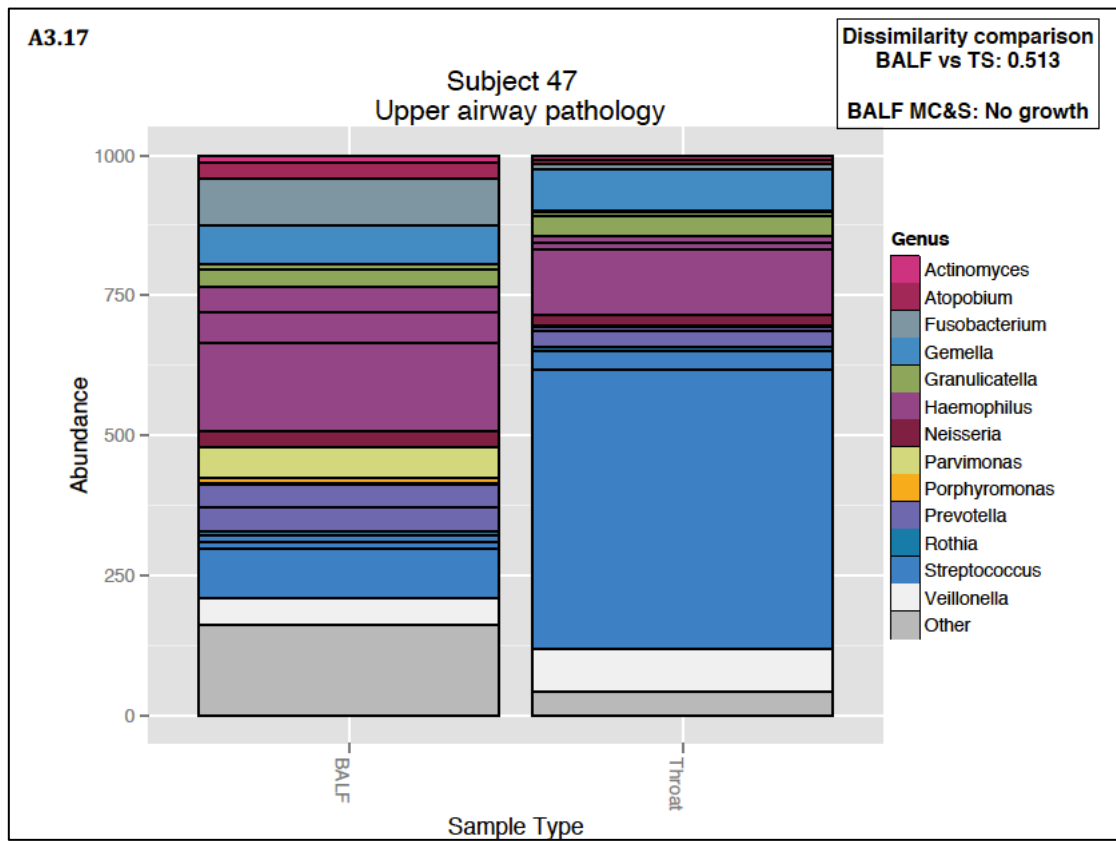


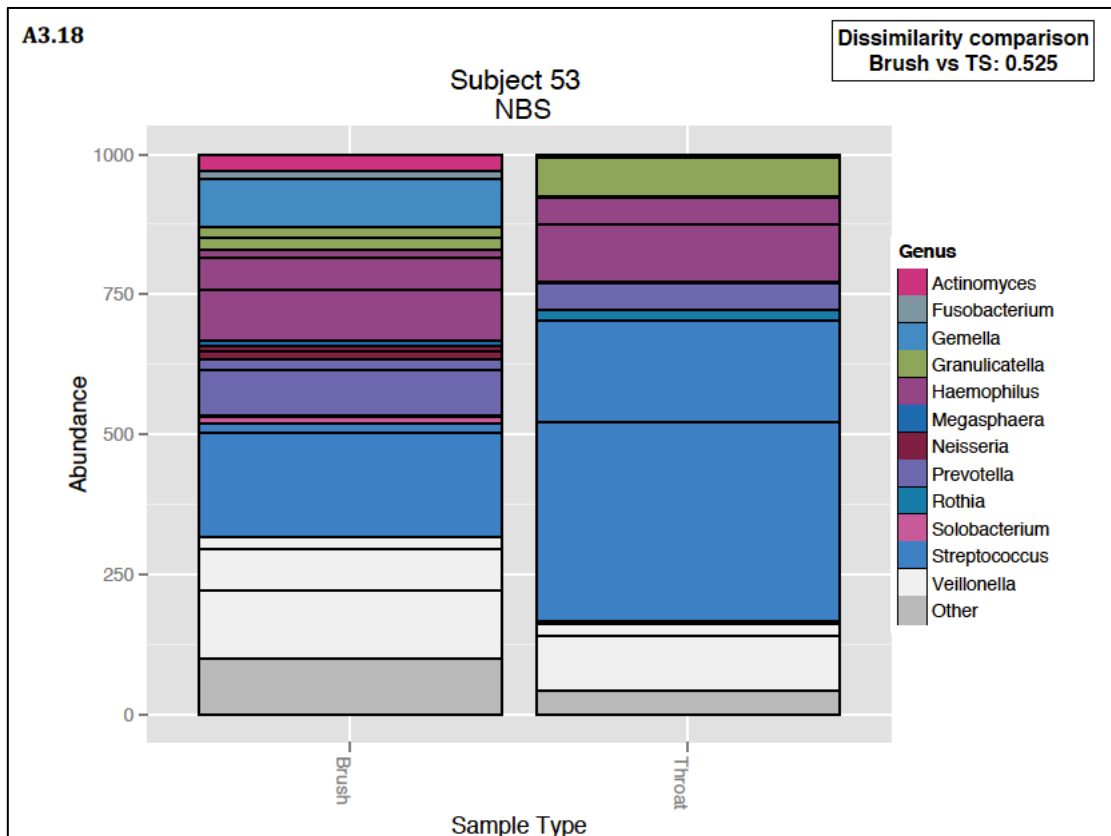
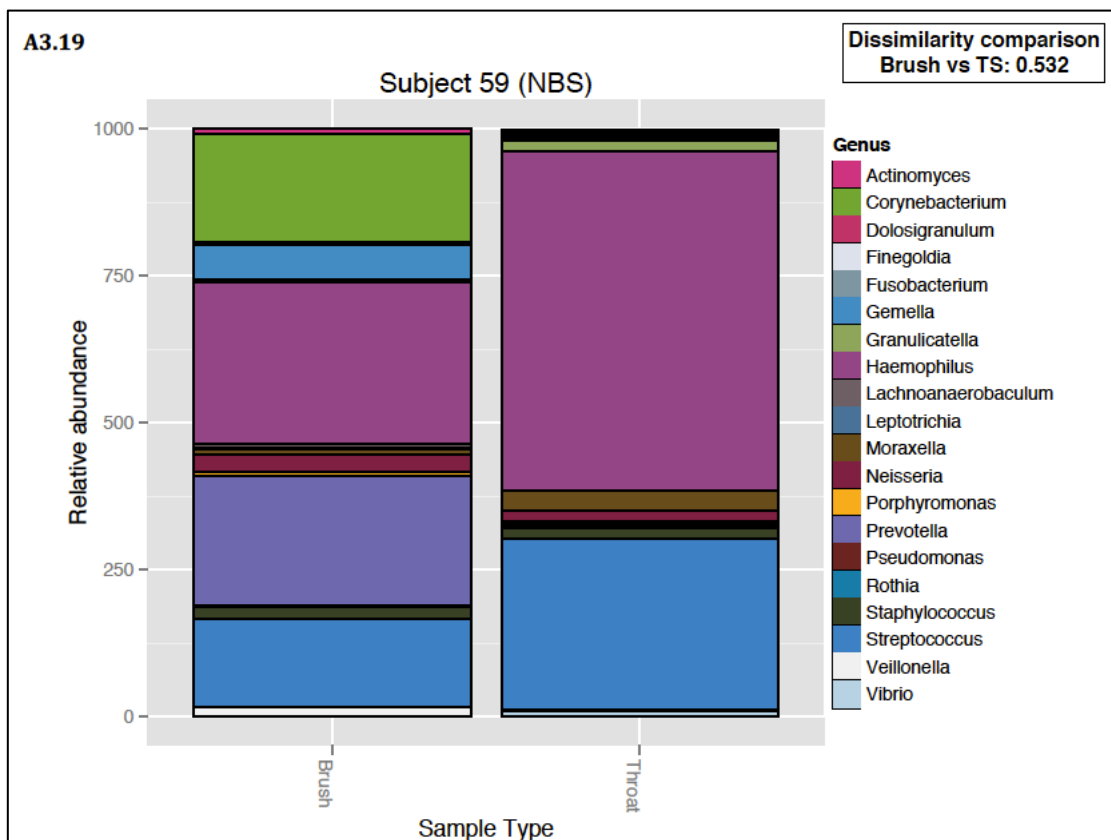


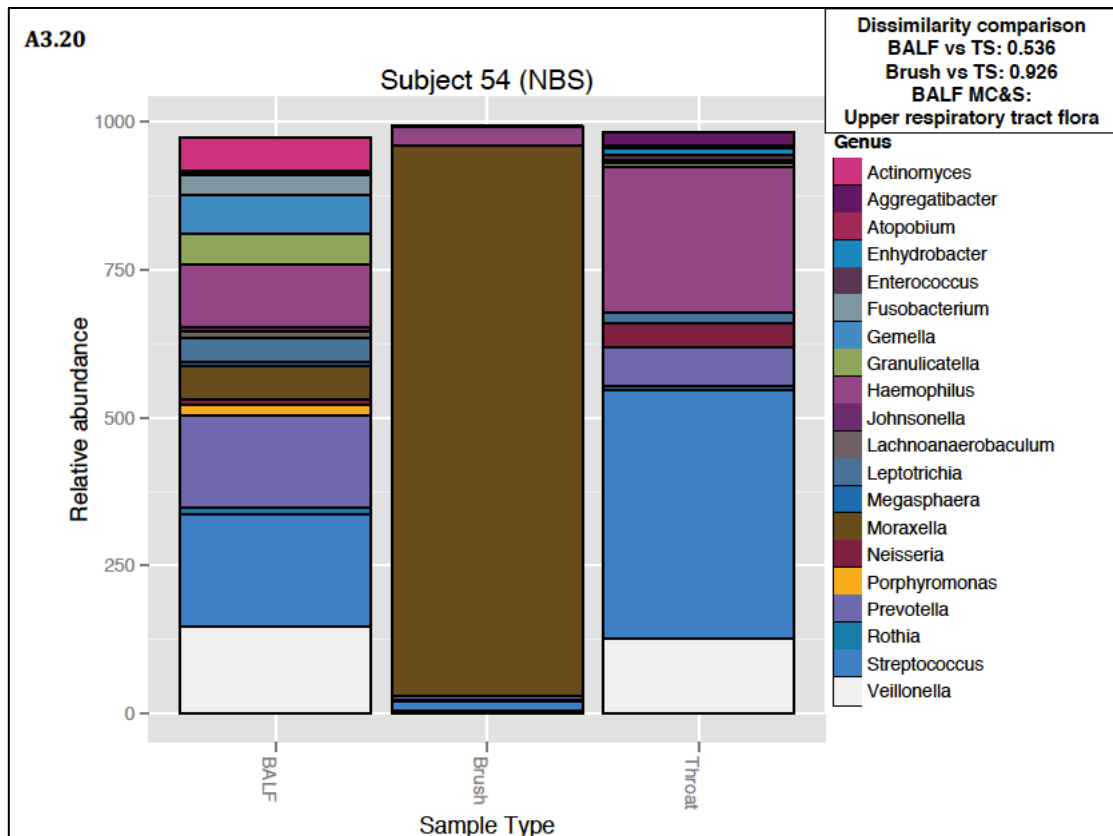
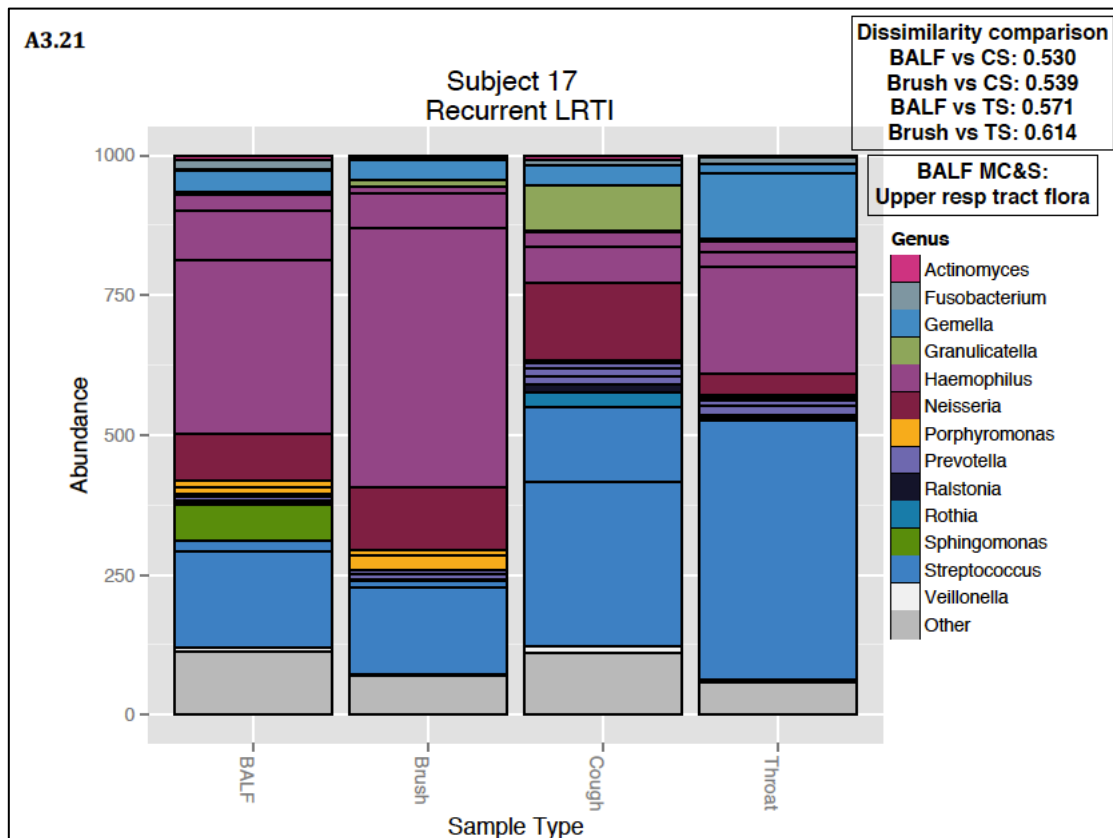


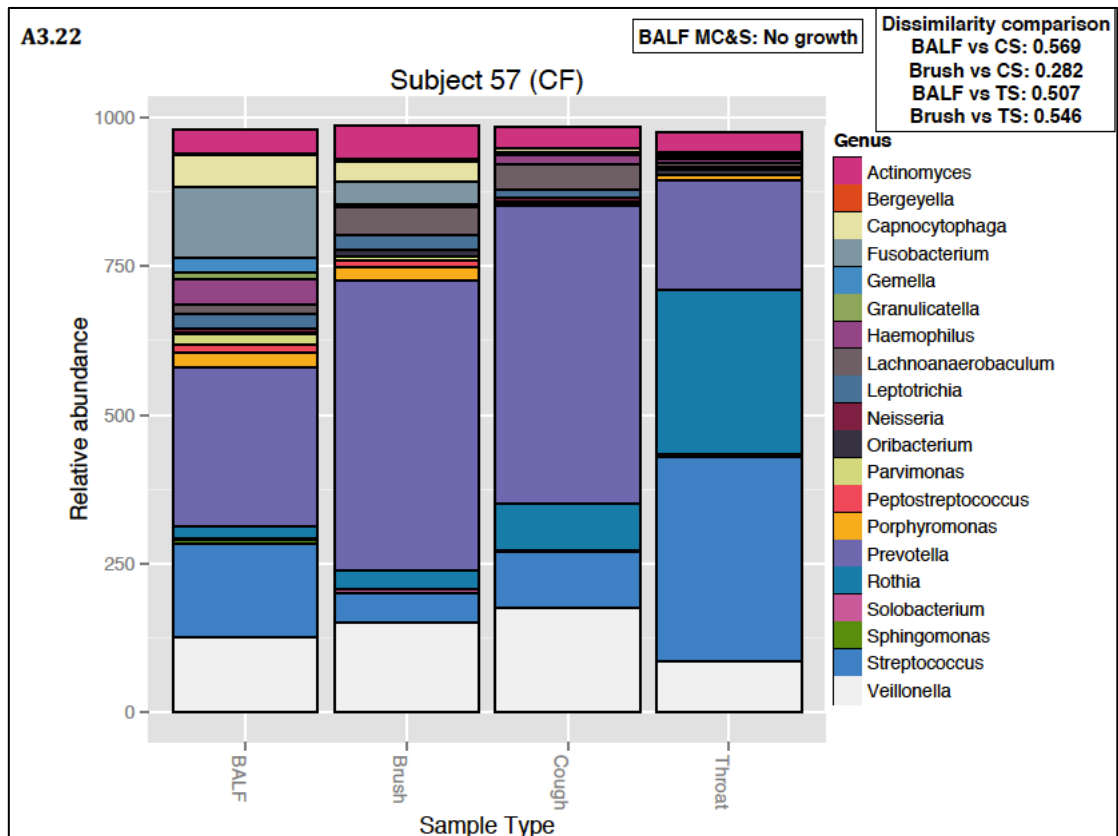
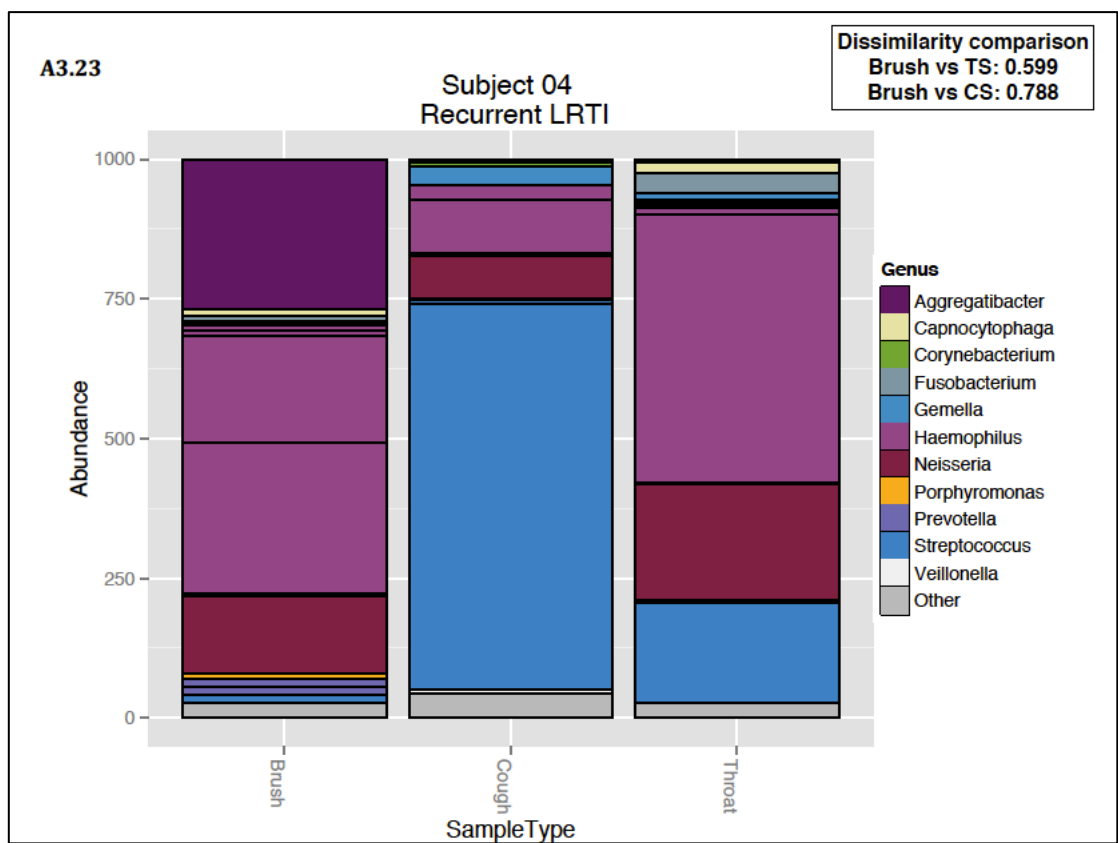


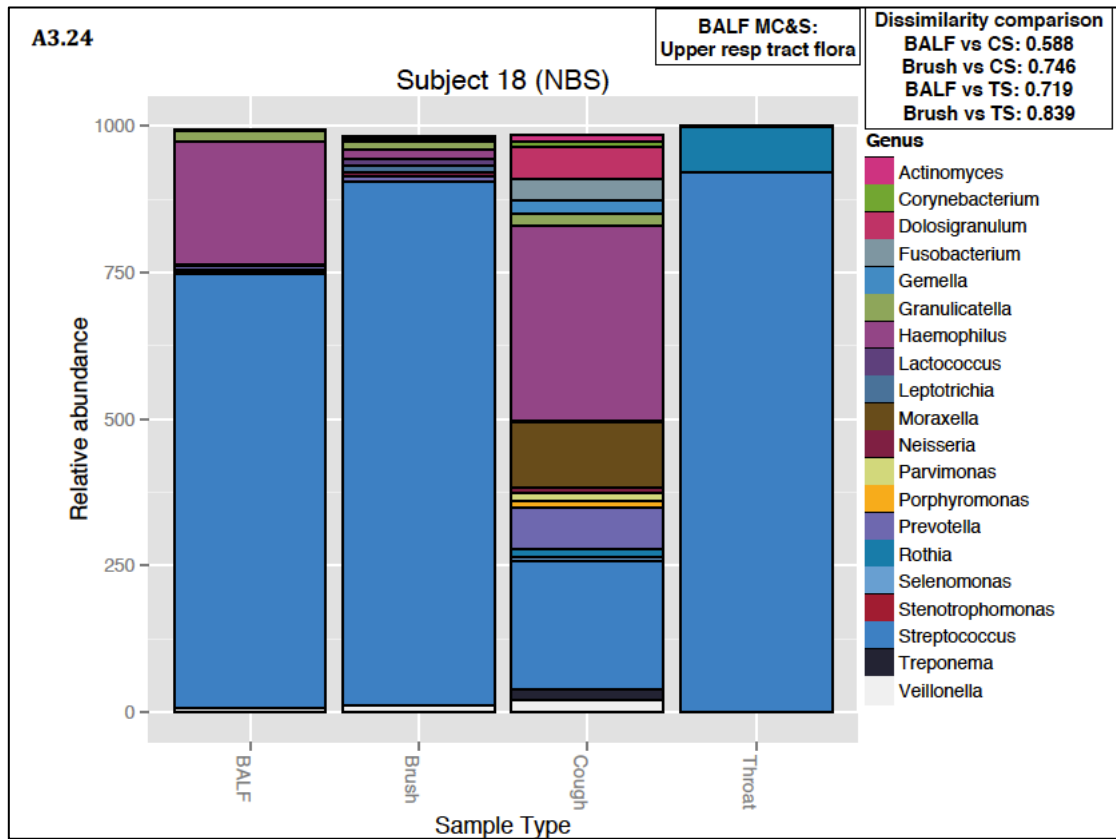
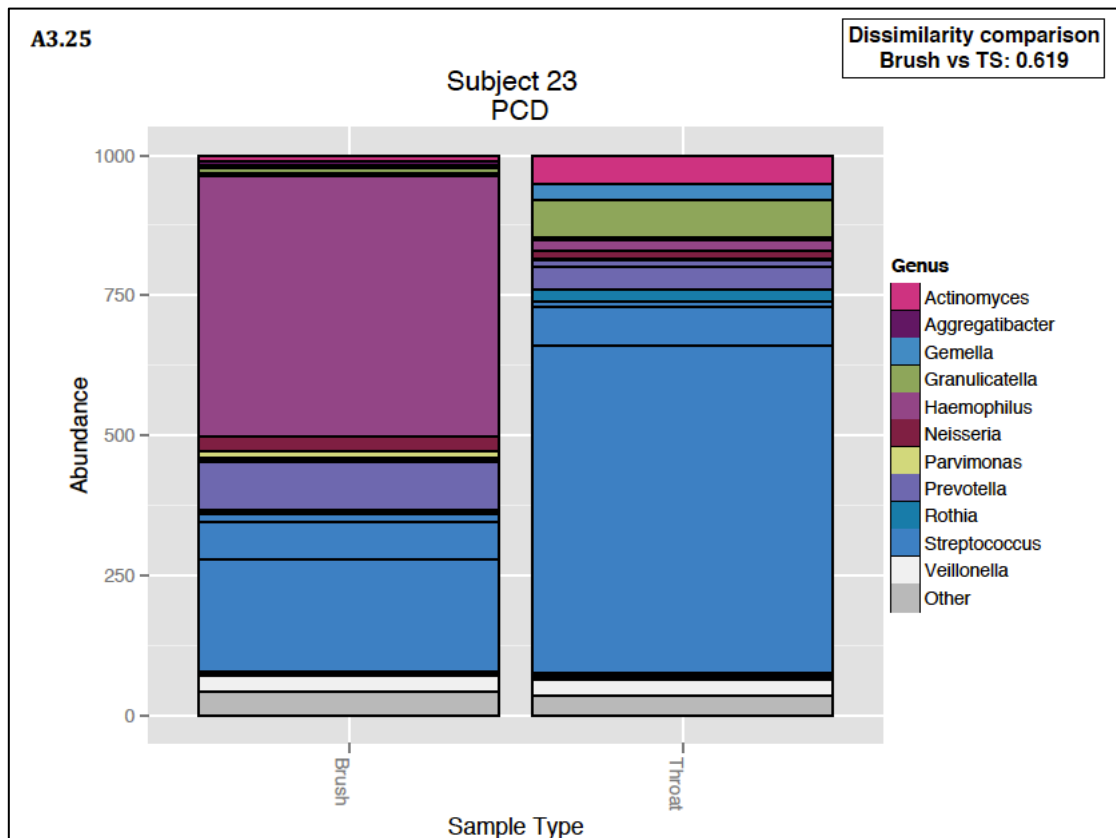


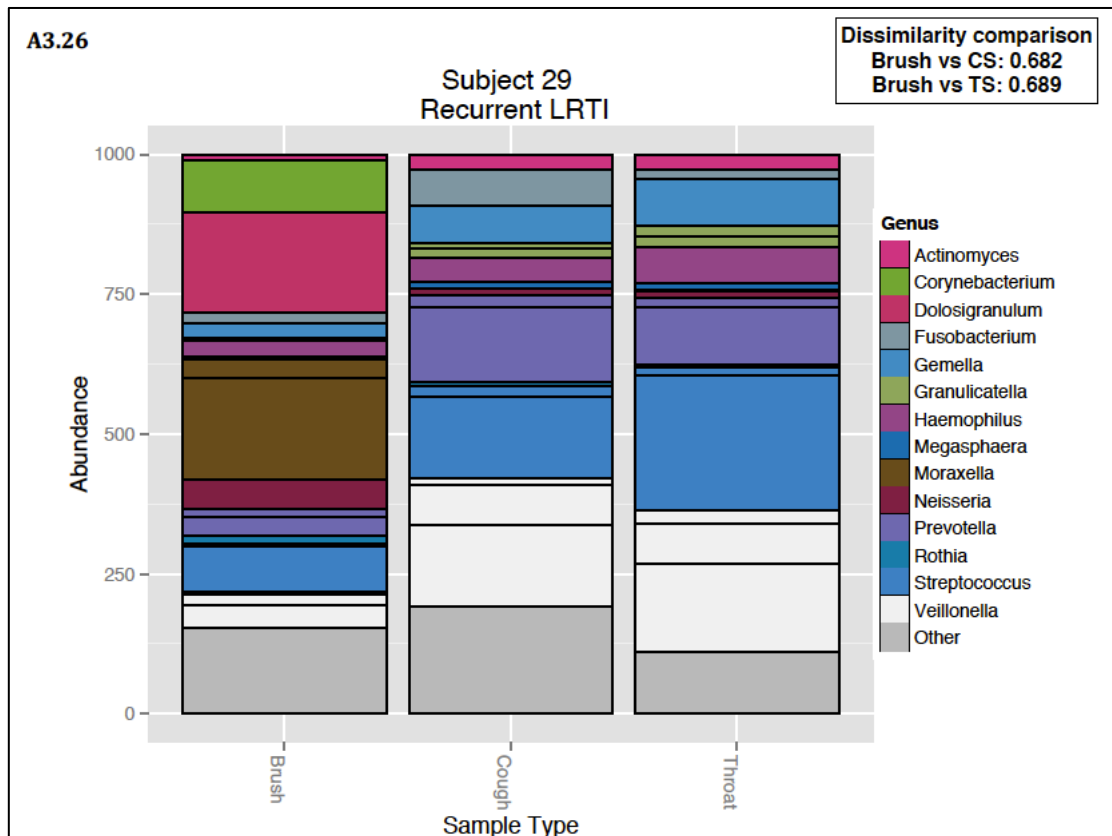
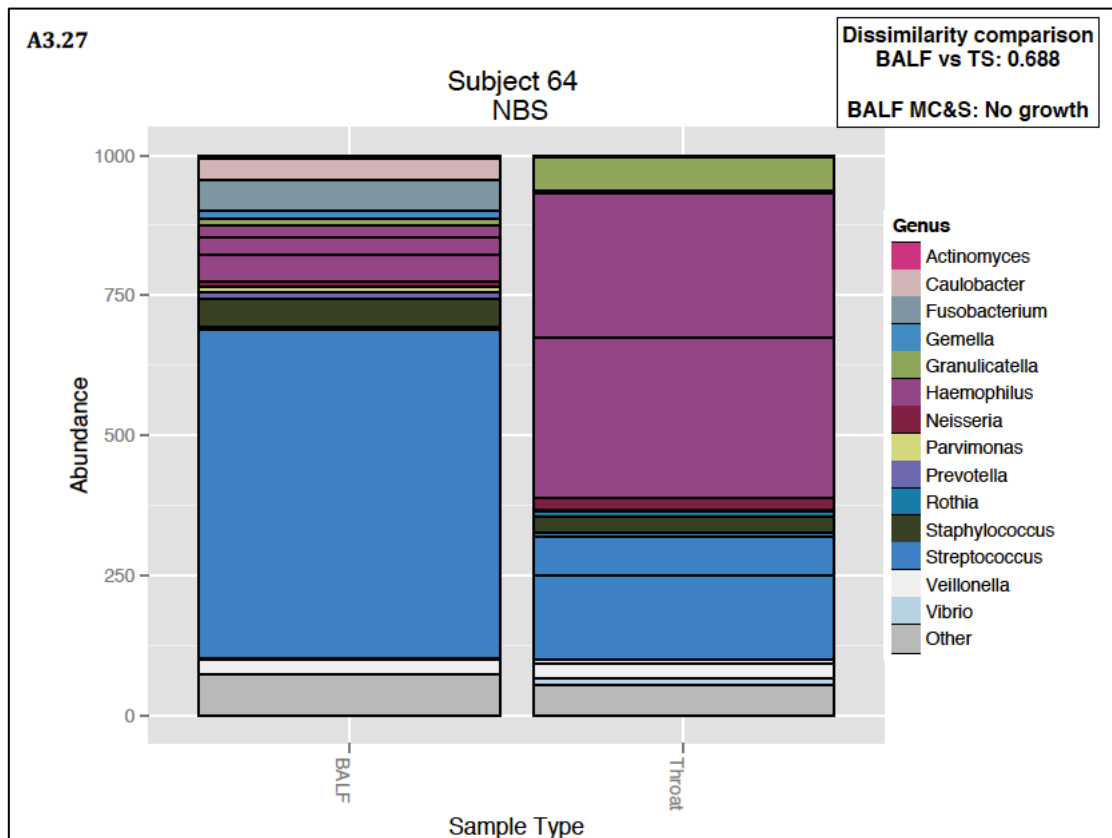


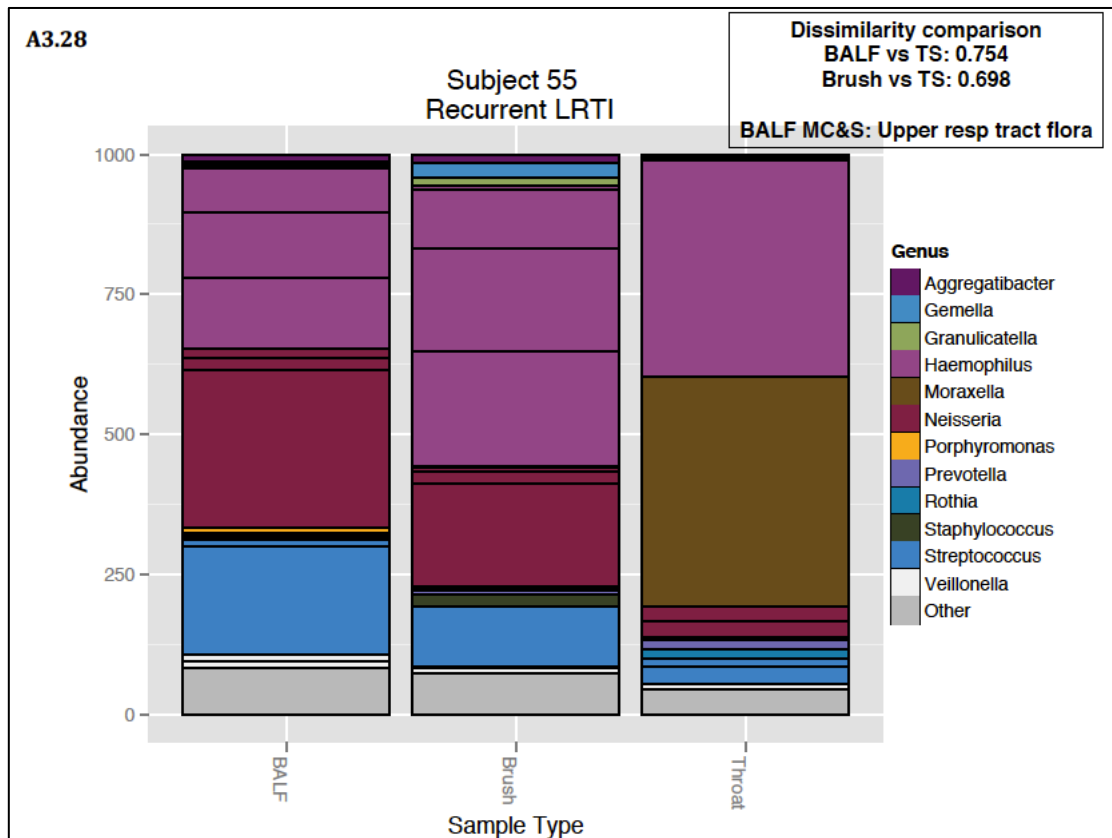
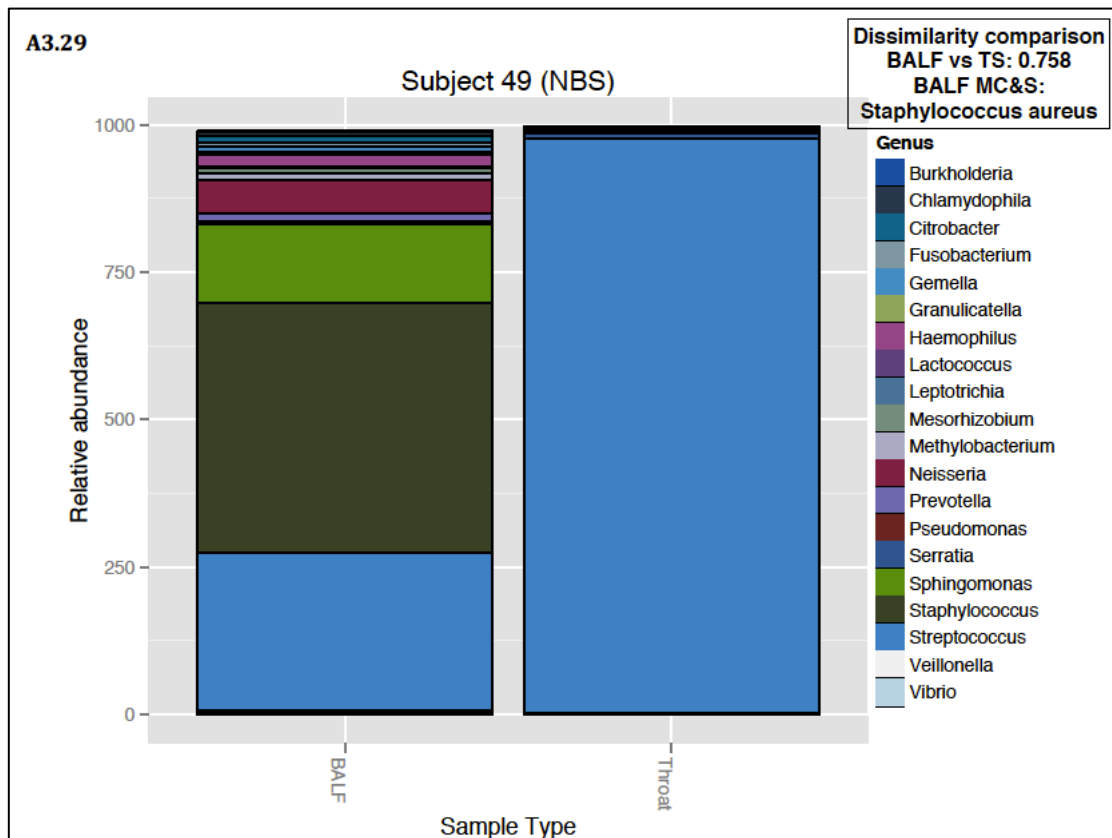


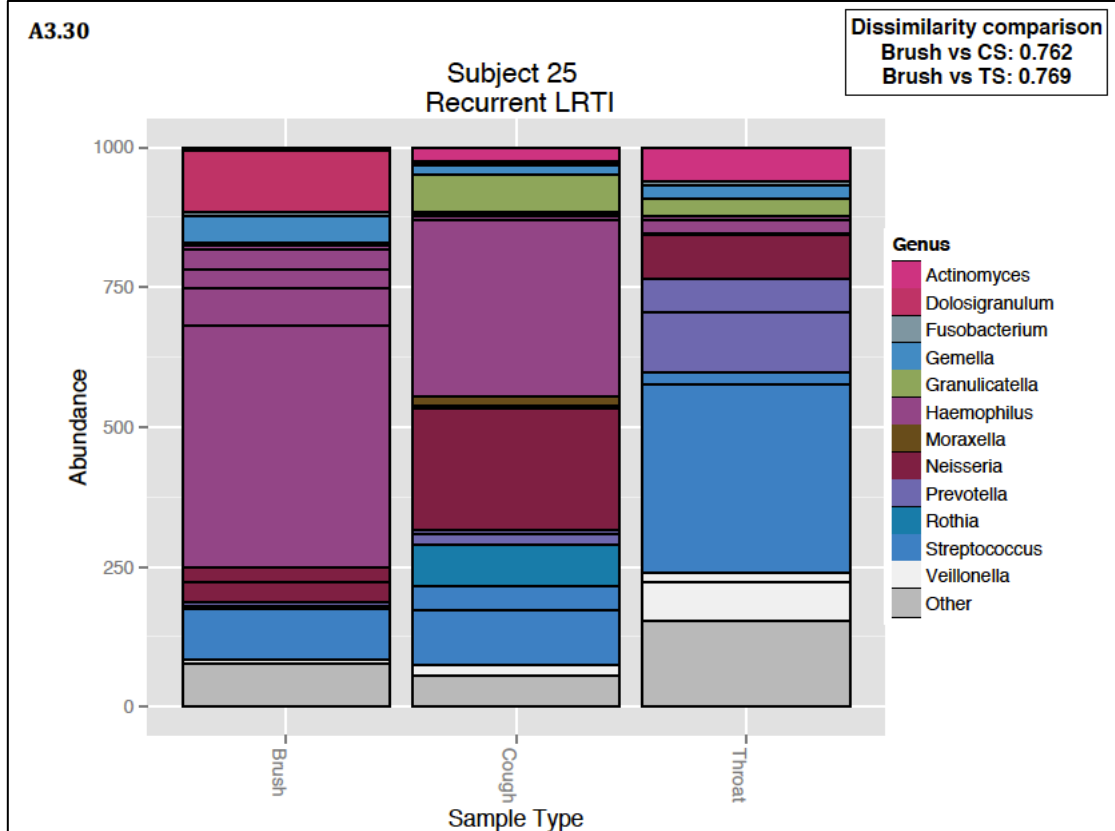
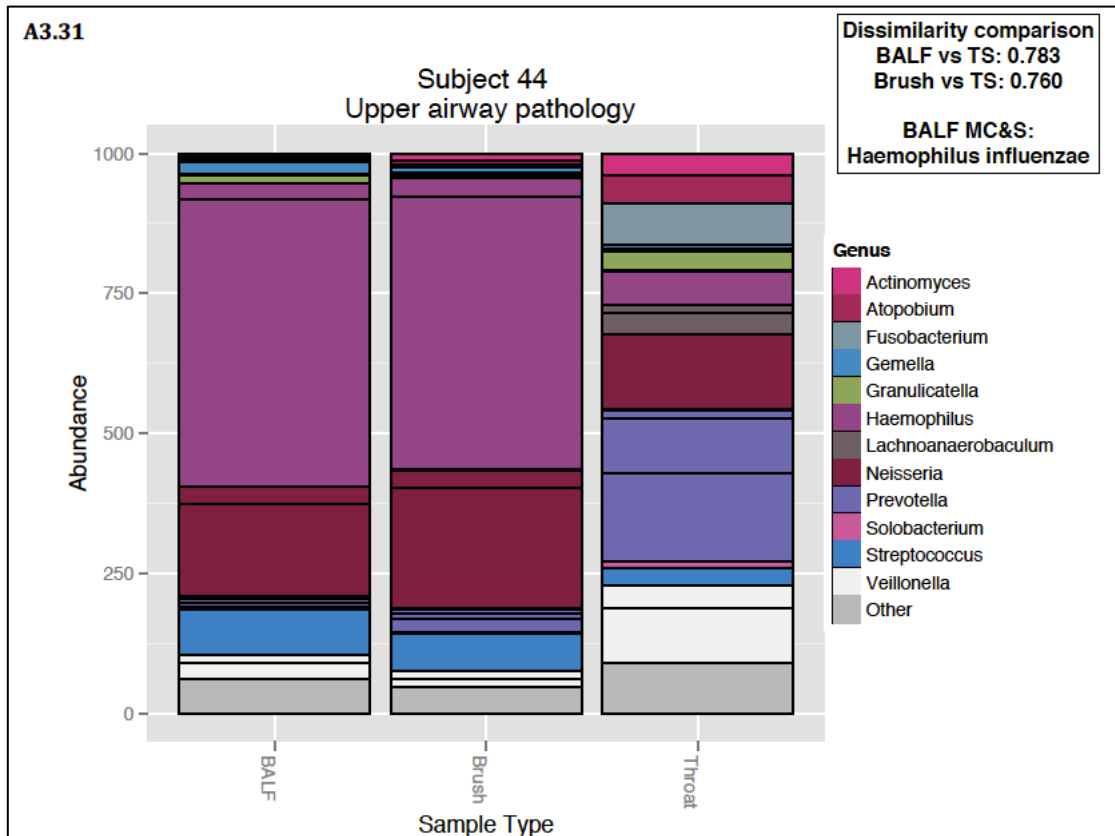


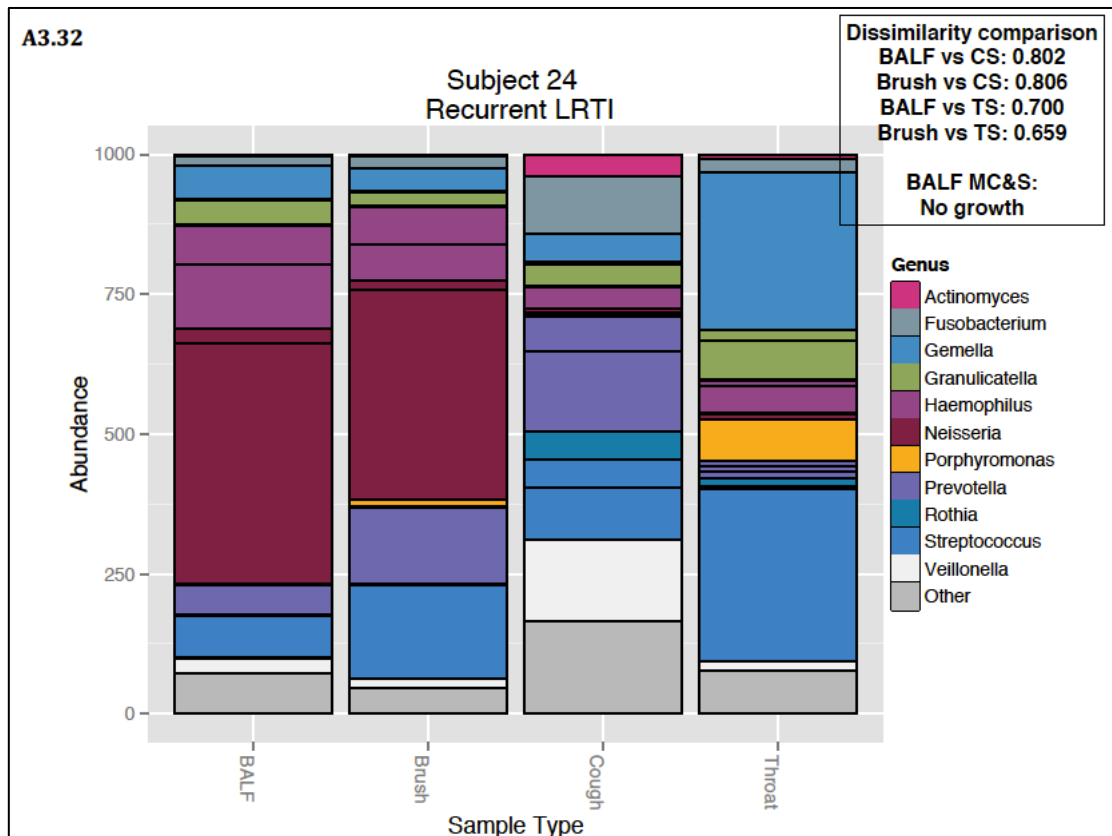
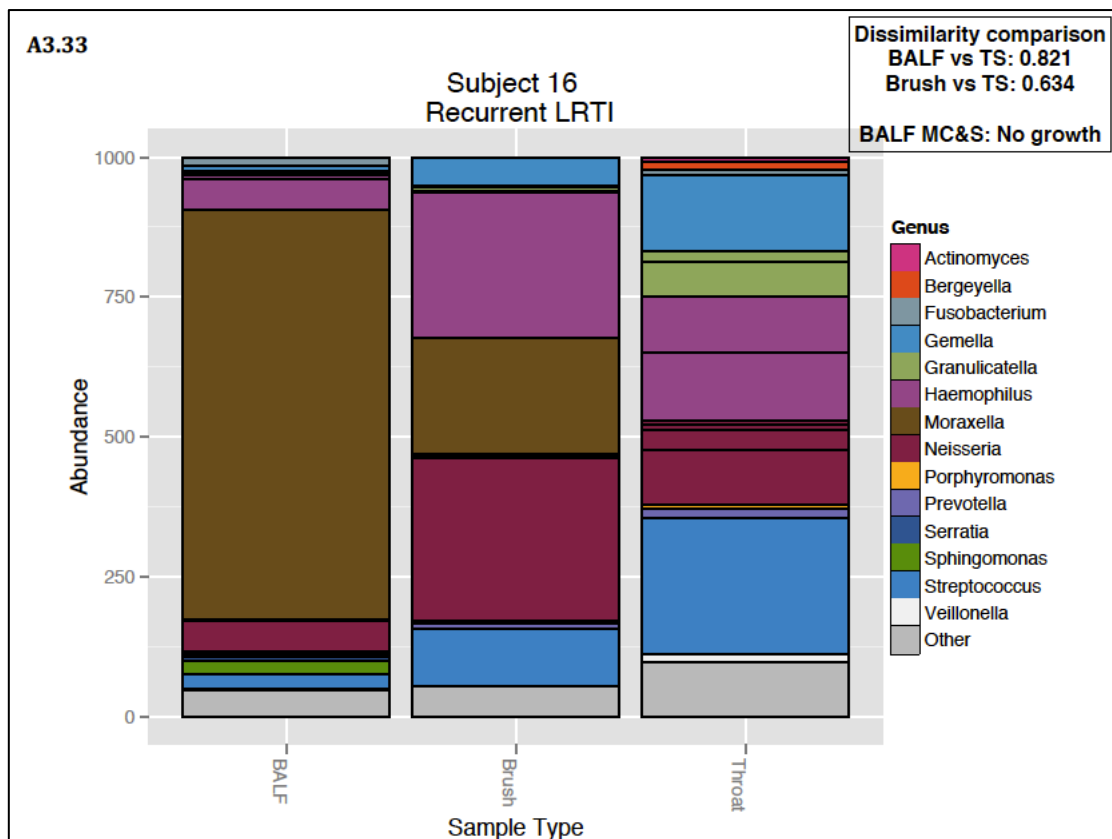


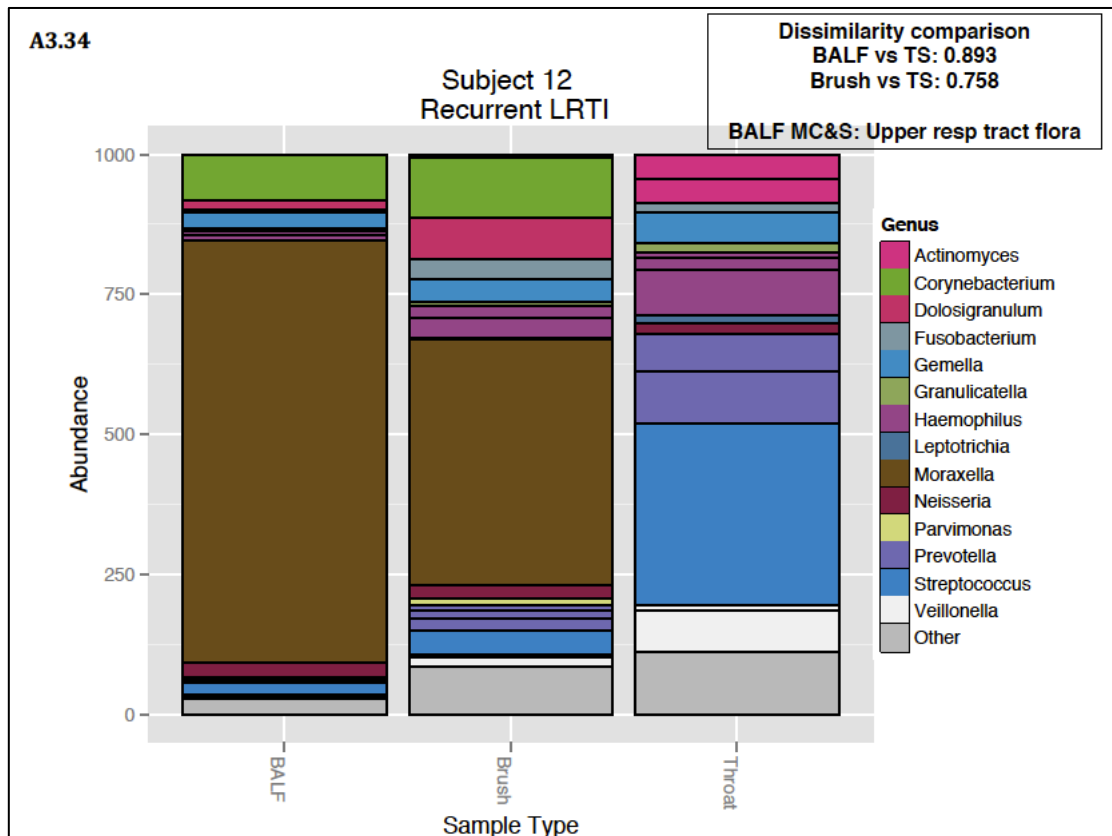
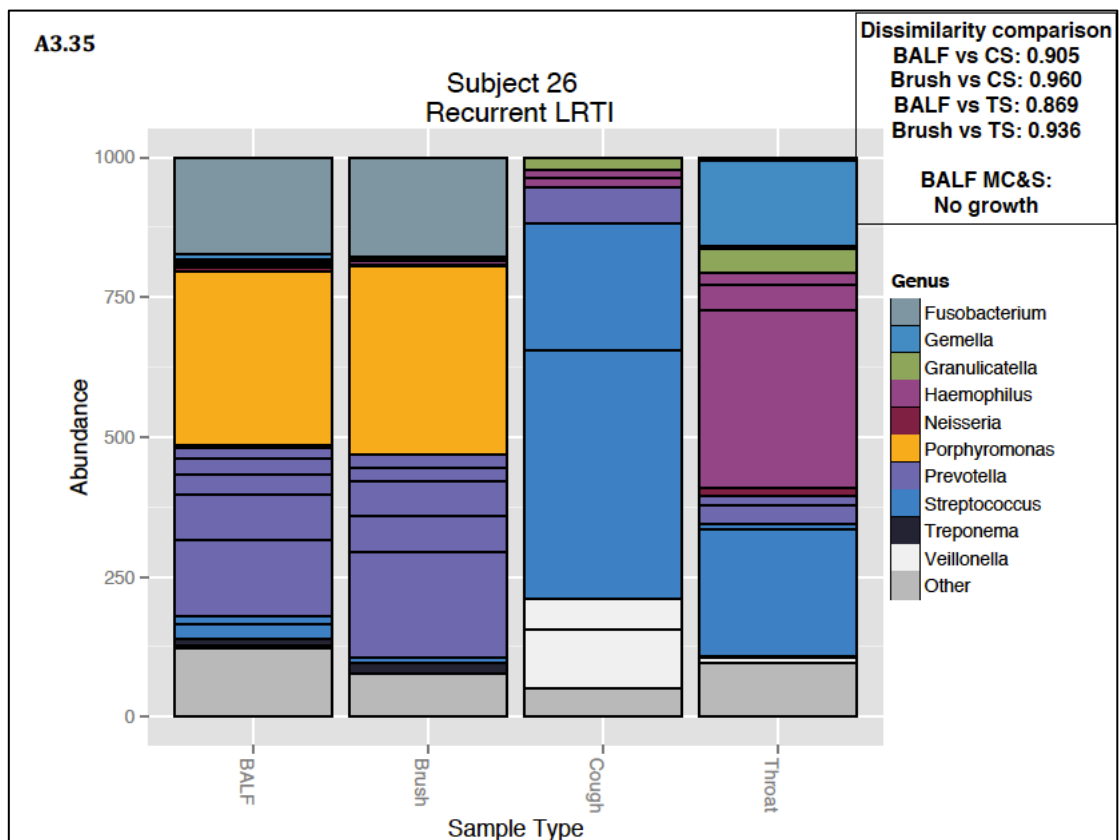


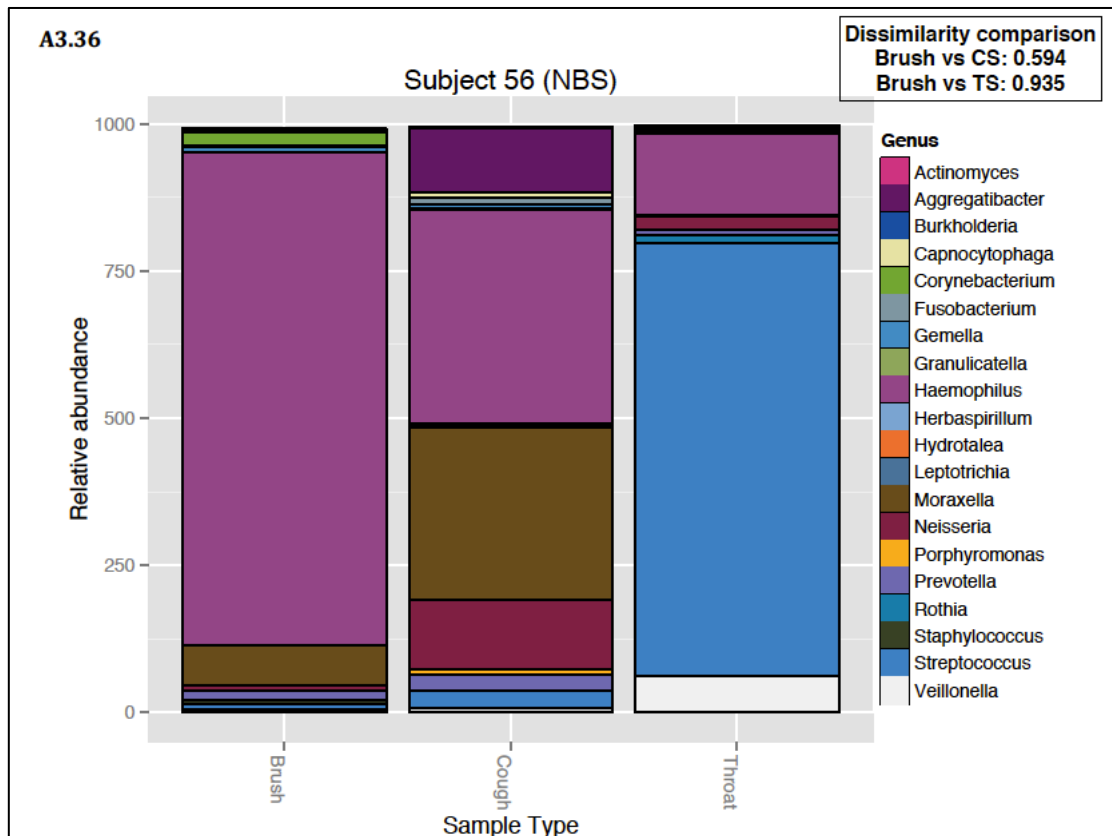
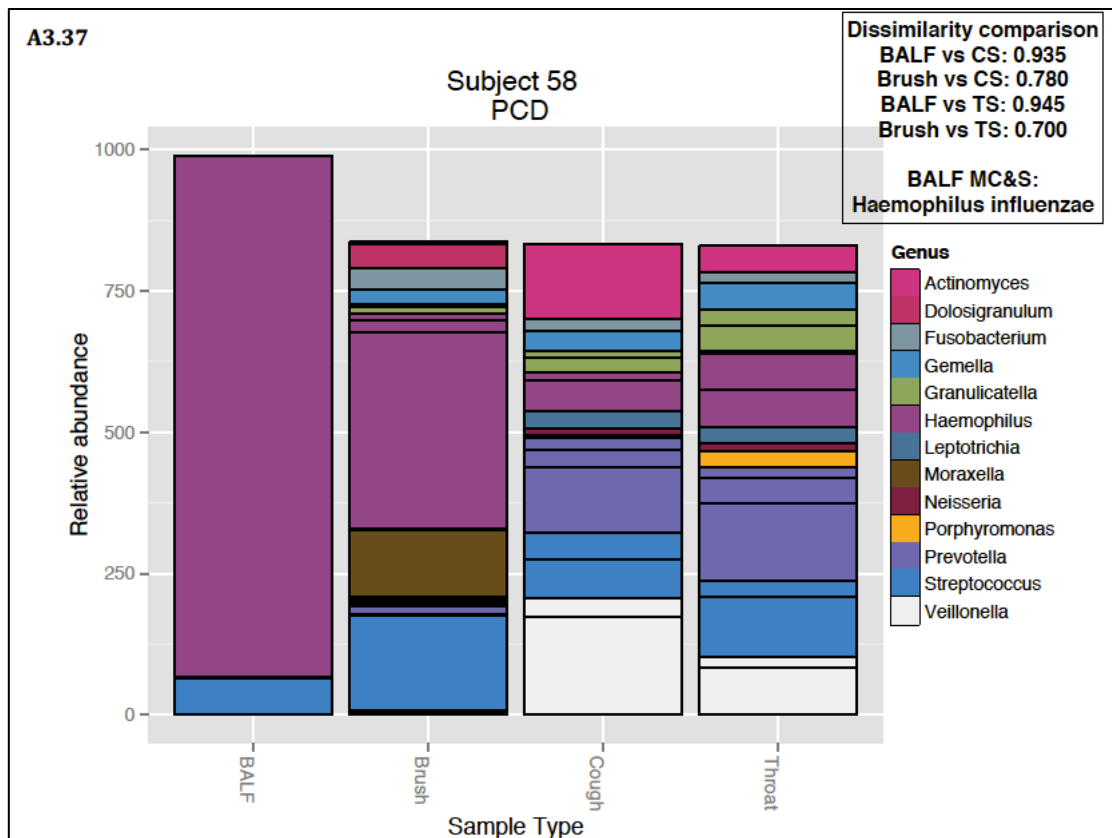


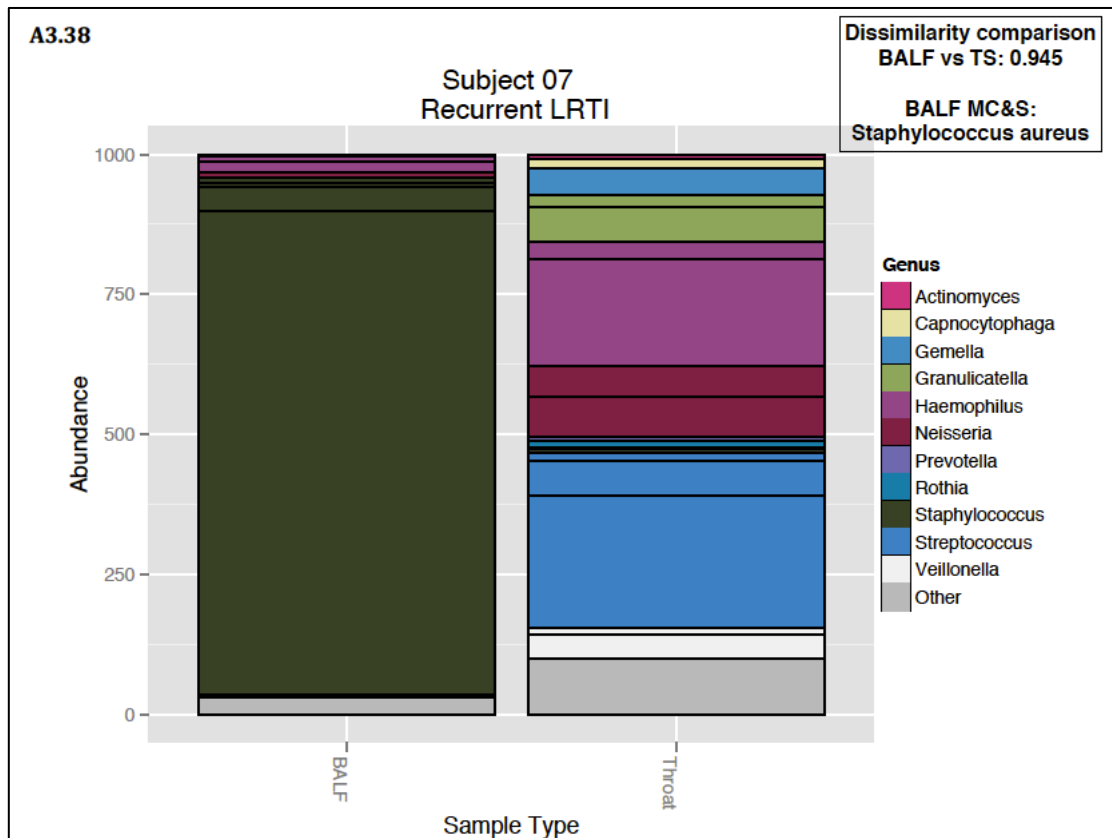
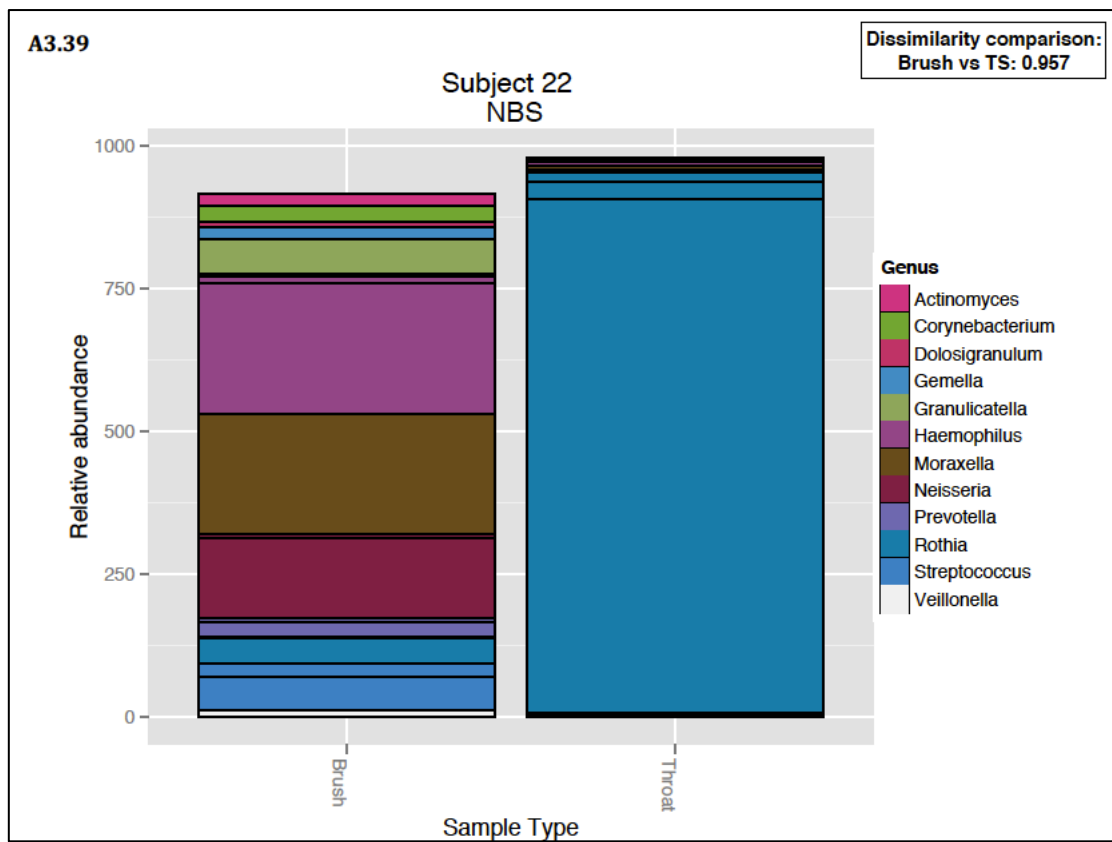


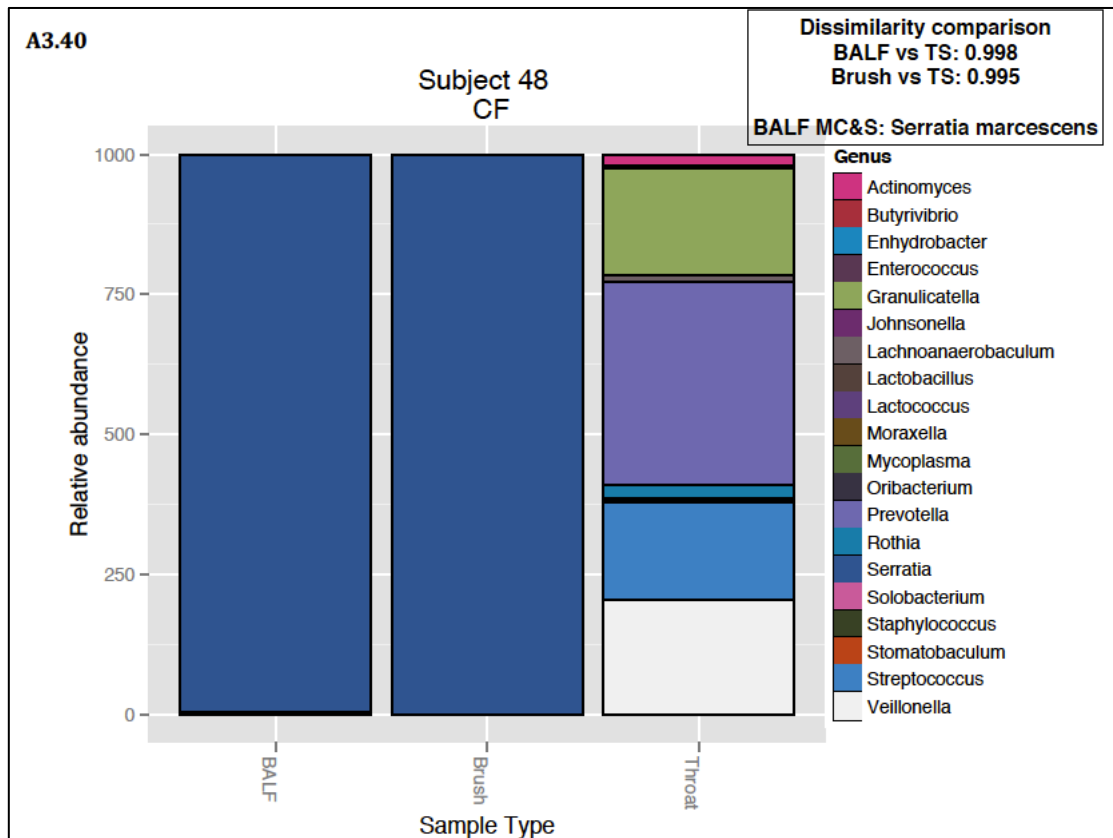










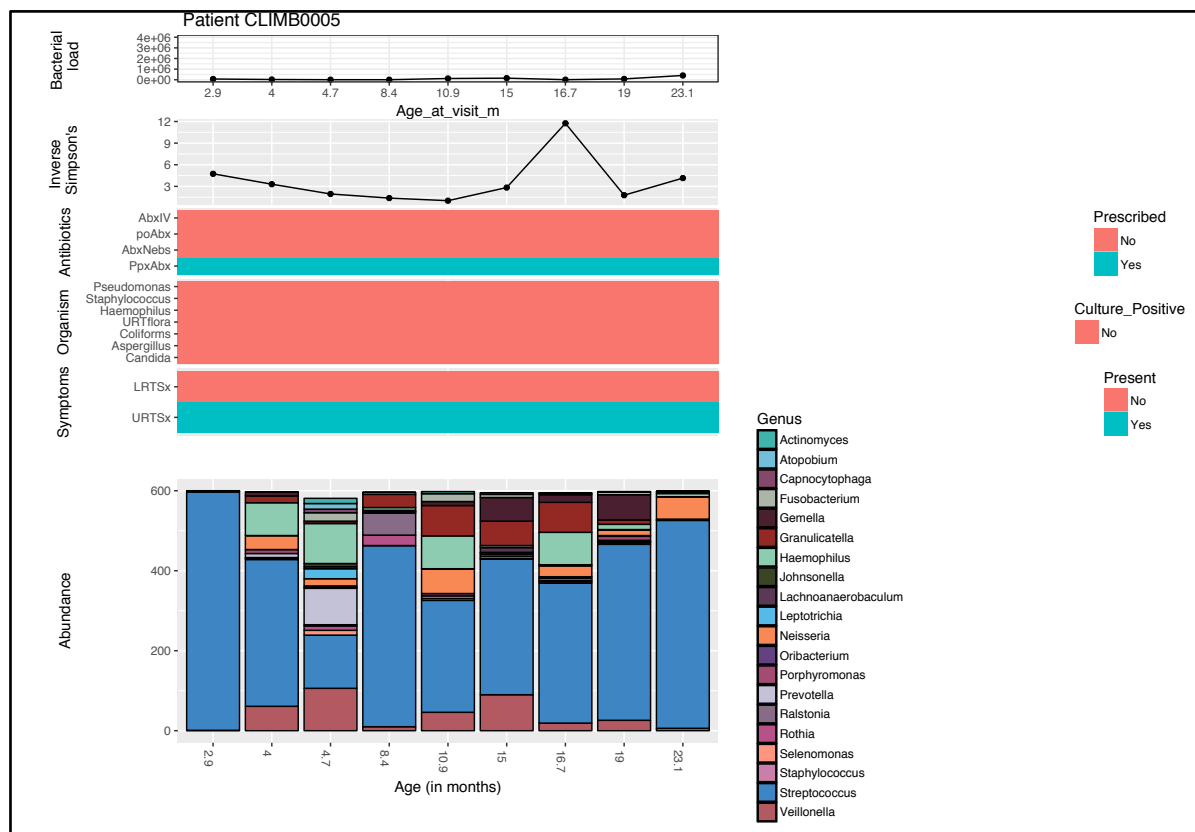


A4: E Appendix for use in conjunction with Chapter 4: Individual patient barplots for infants with cystic fibrosis (CF) diagnosed on newborn screening (NBS)

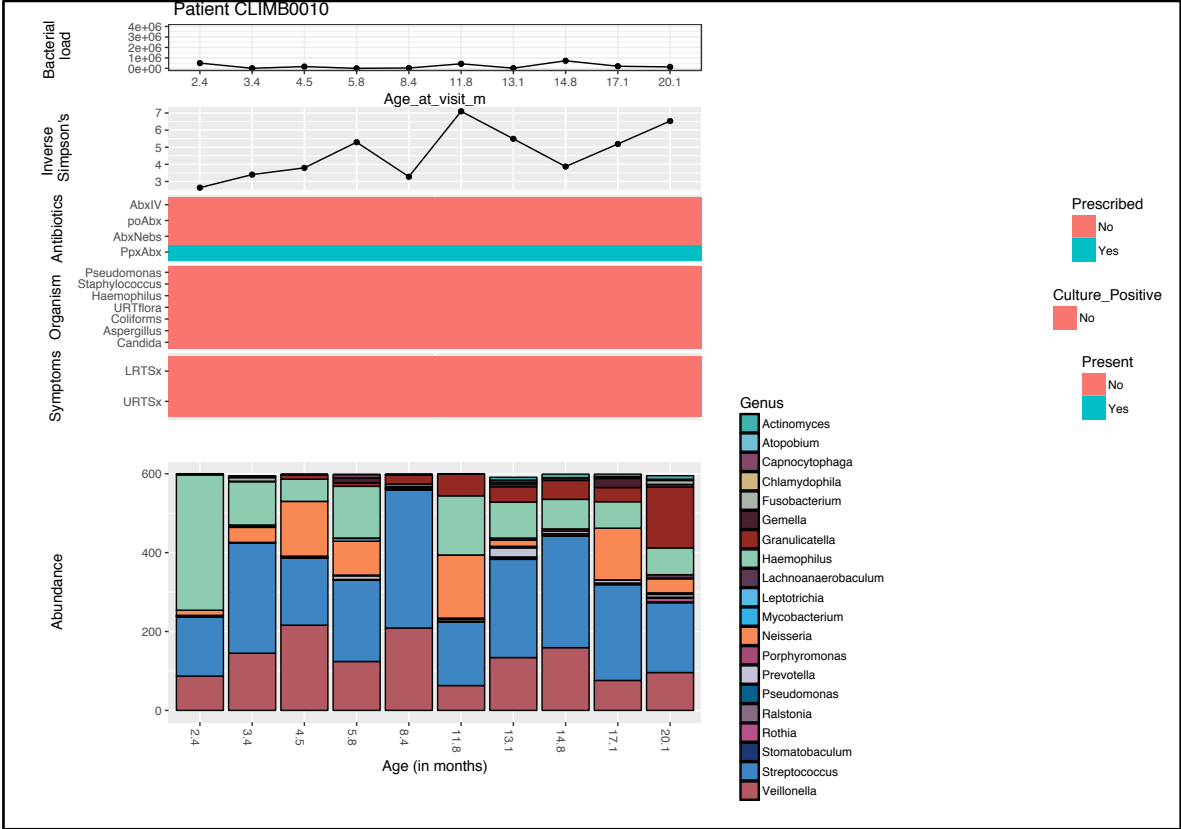
A4.1 = A4.25 illustrate the changes in relative abundance of OTUs against bacterial load (16S rRNA copies per swab), diversity changes and clinical variables with age in each patient in NBS in whom data was available after rarefaction. Patients have been arranged by age at recruitment.

(a) Patients recruited at age 1 – 2 months.

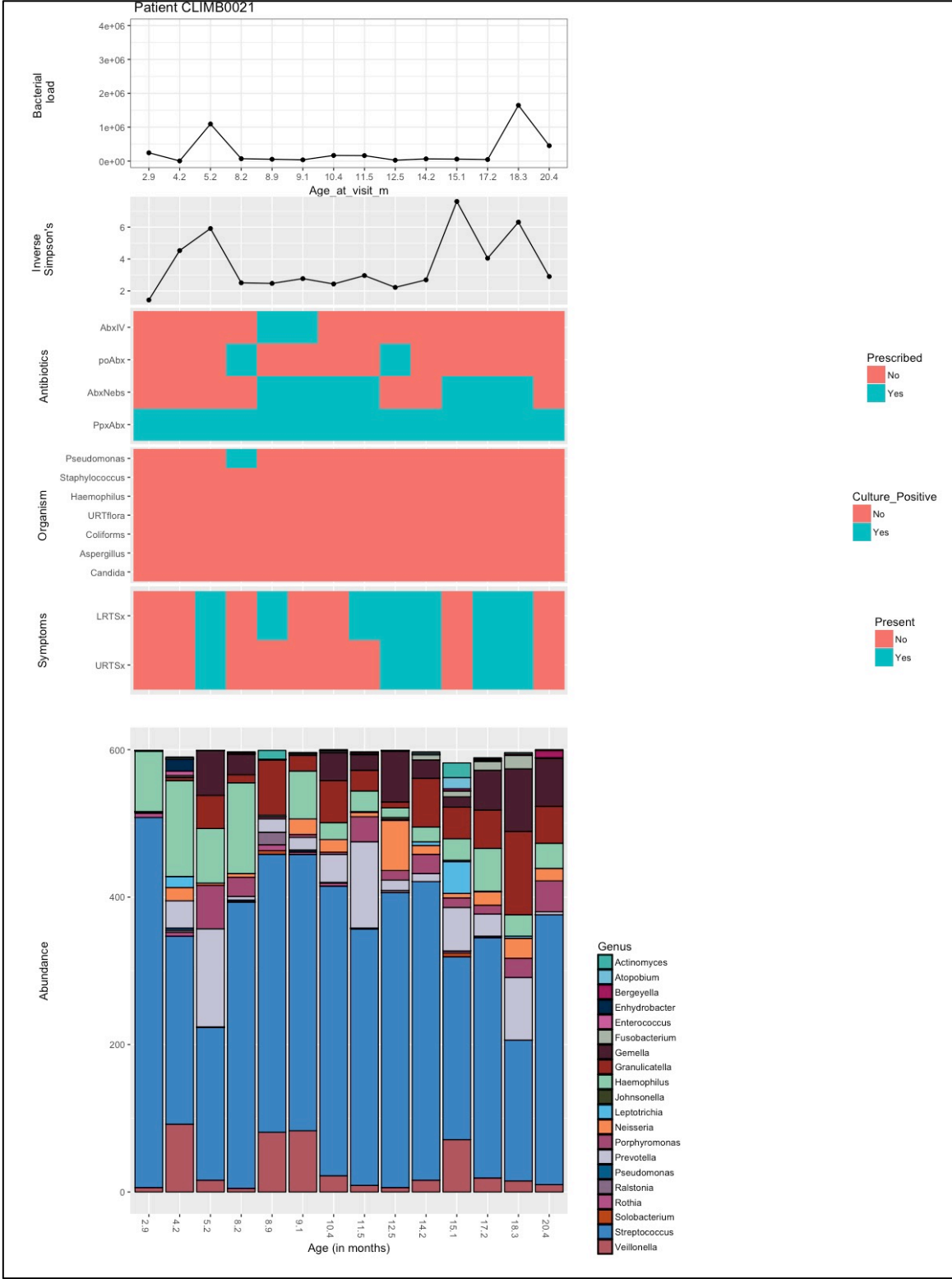
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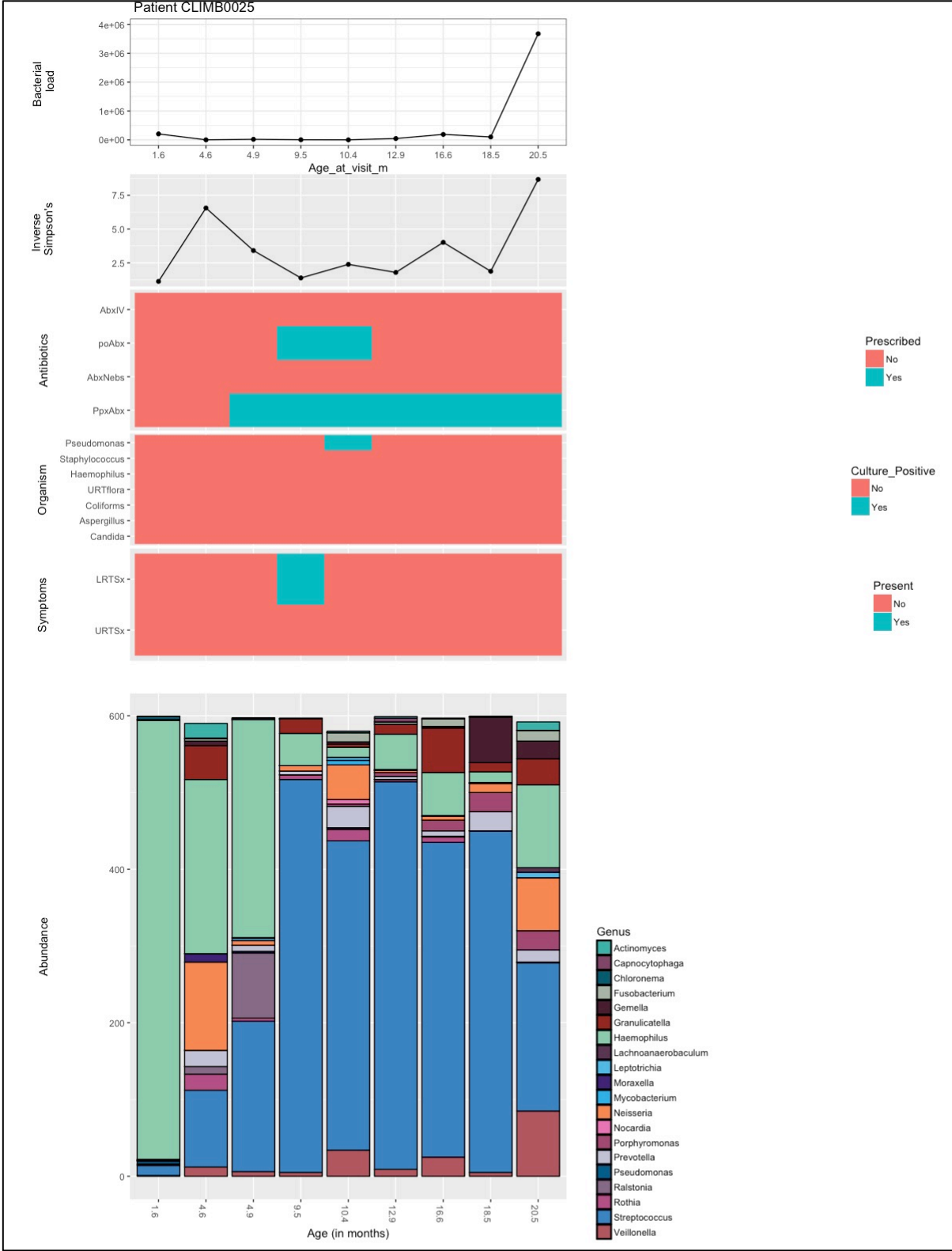
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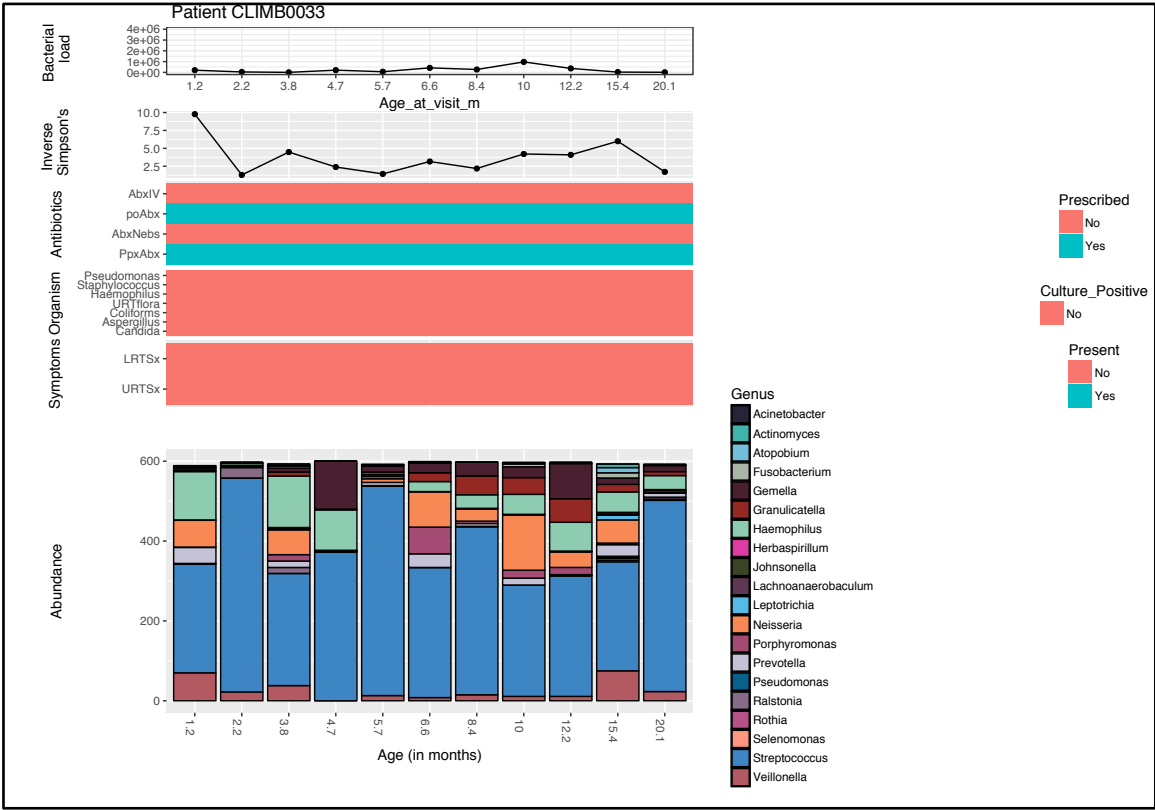
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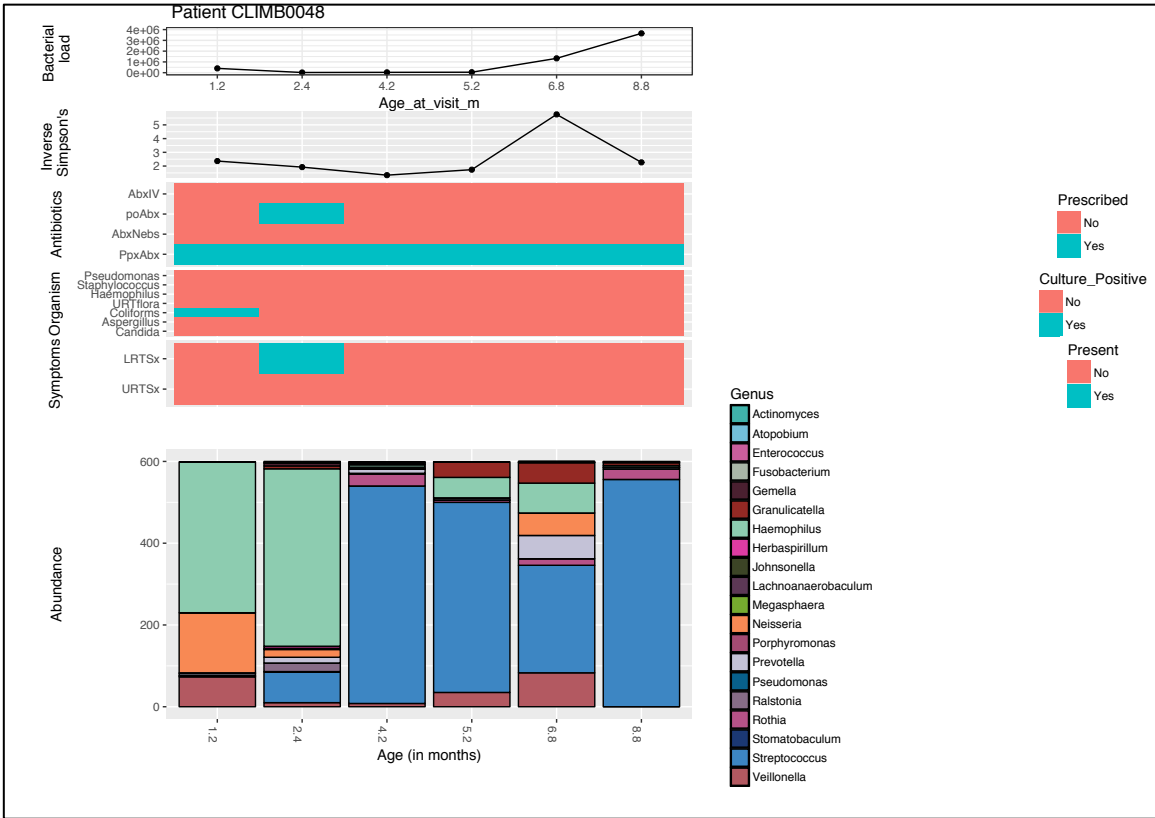
A4.4: CLIMB0025



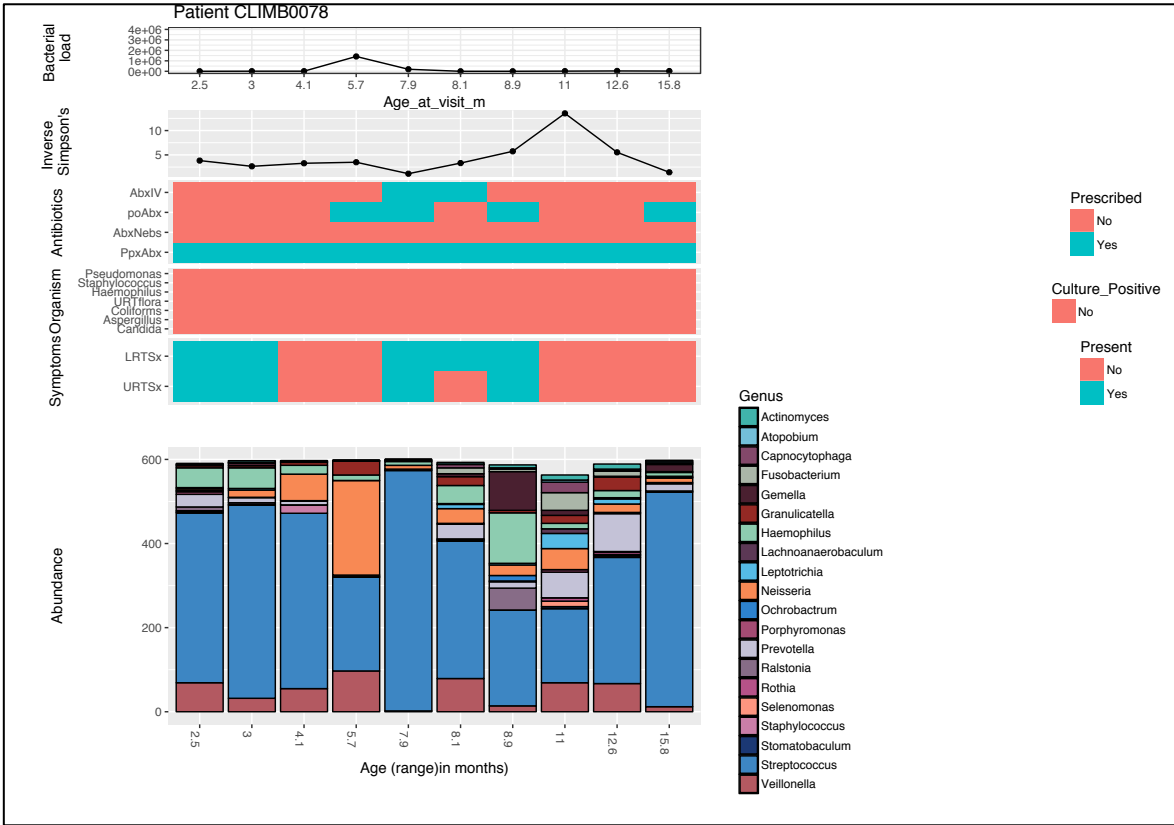
A4.5: CLIMB0033



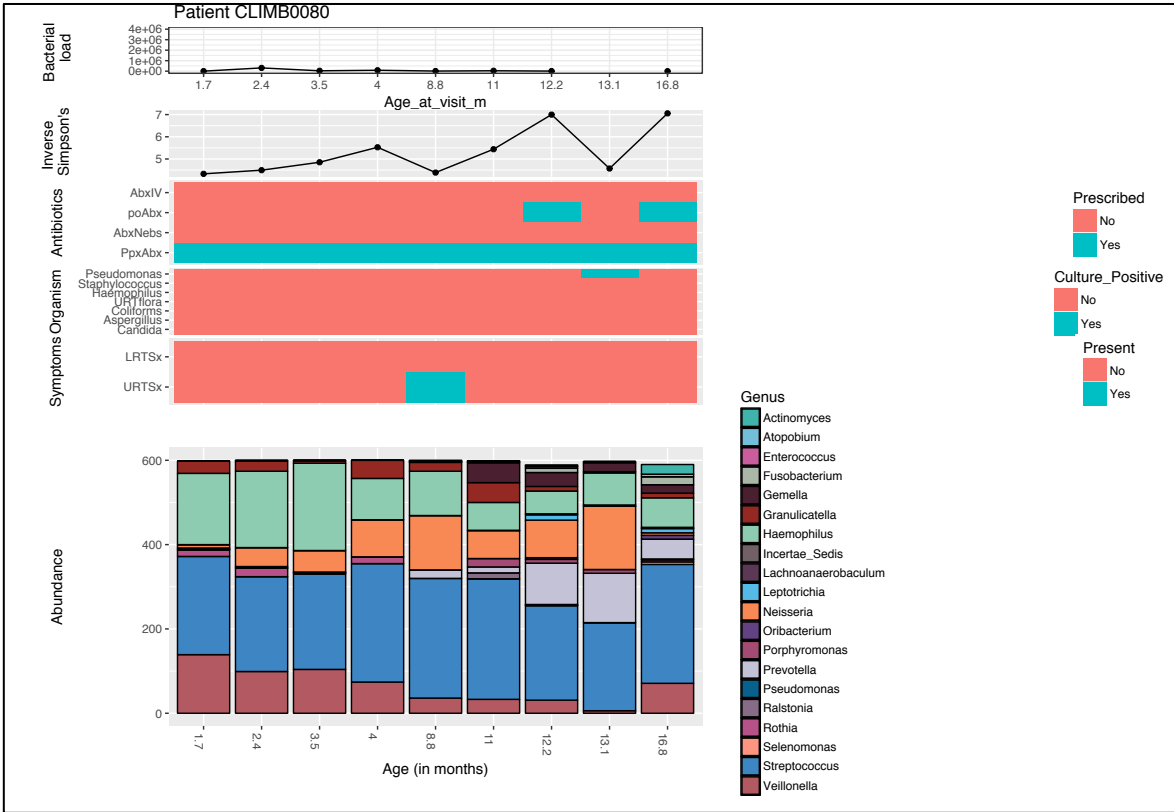
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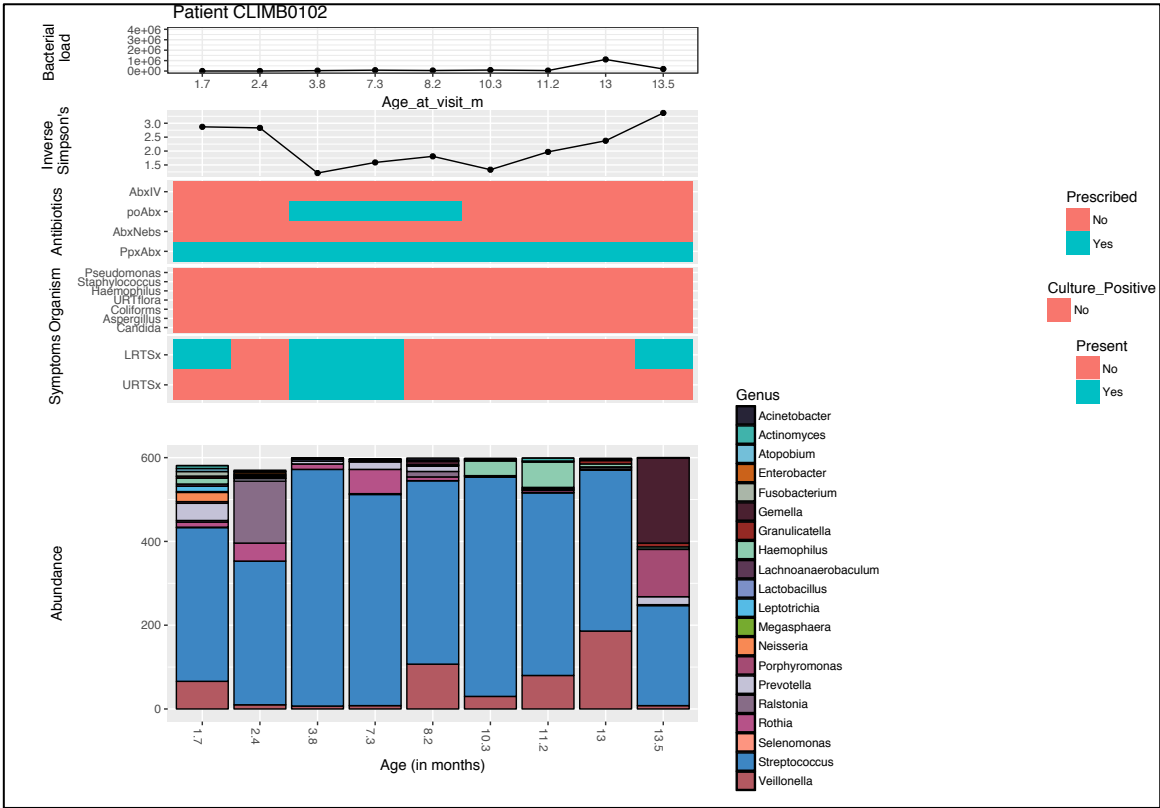
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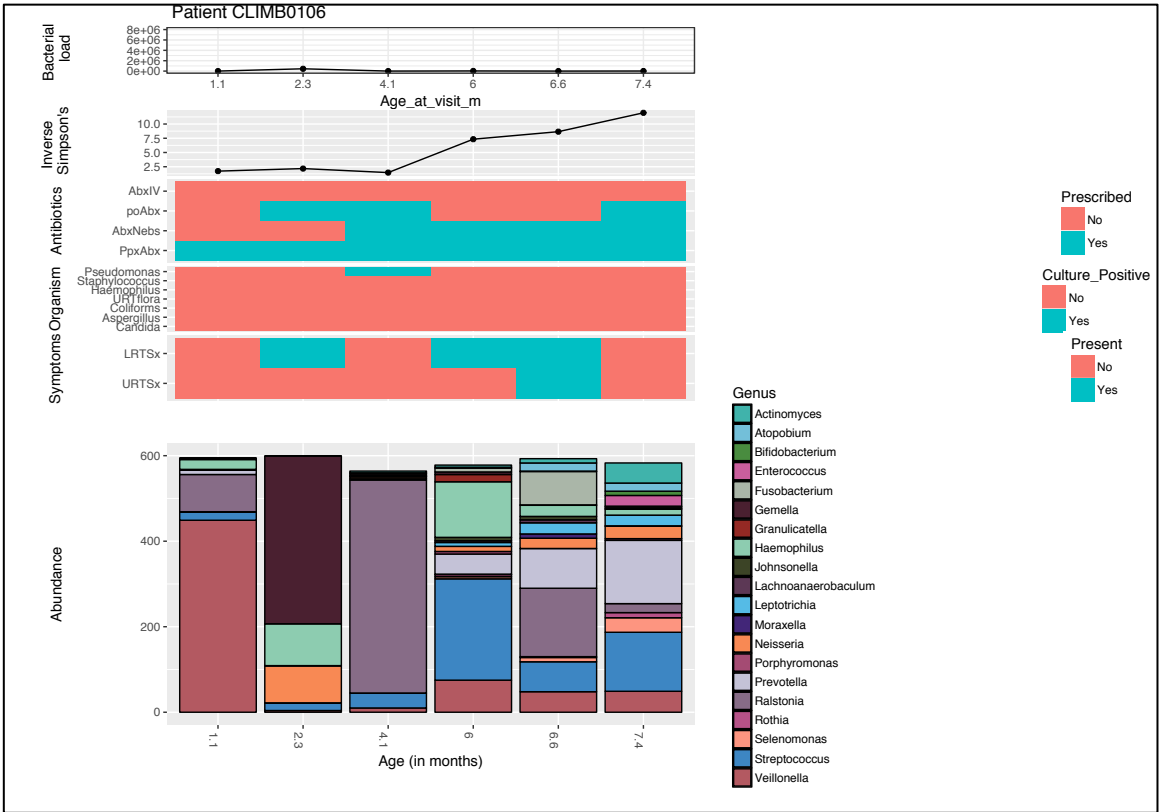
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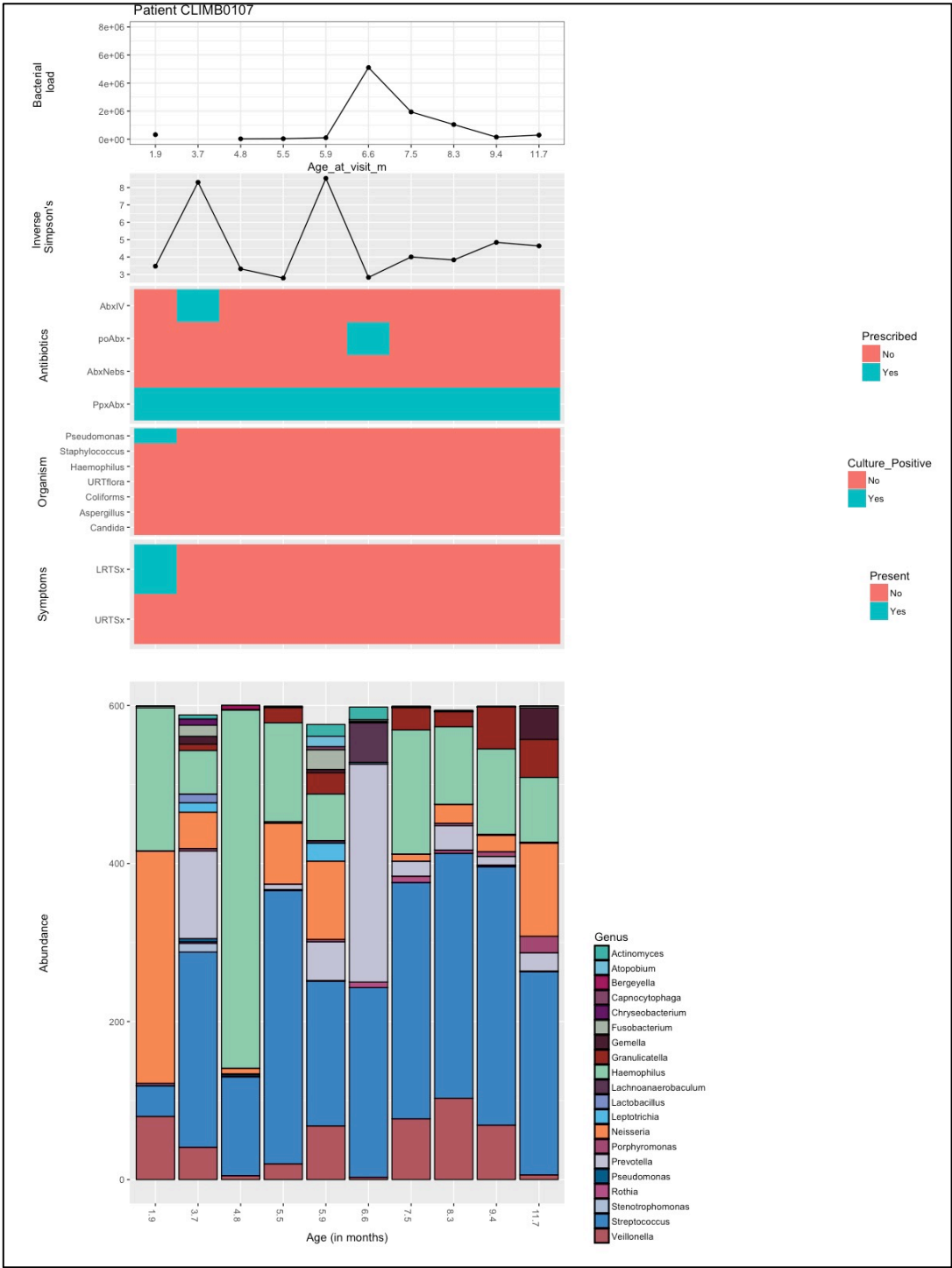
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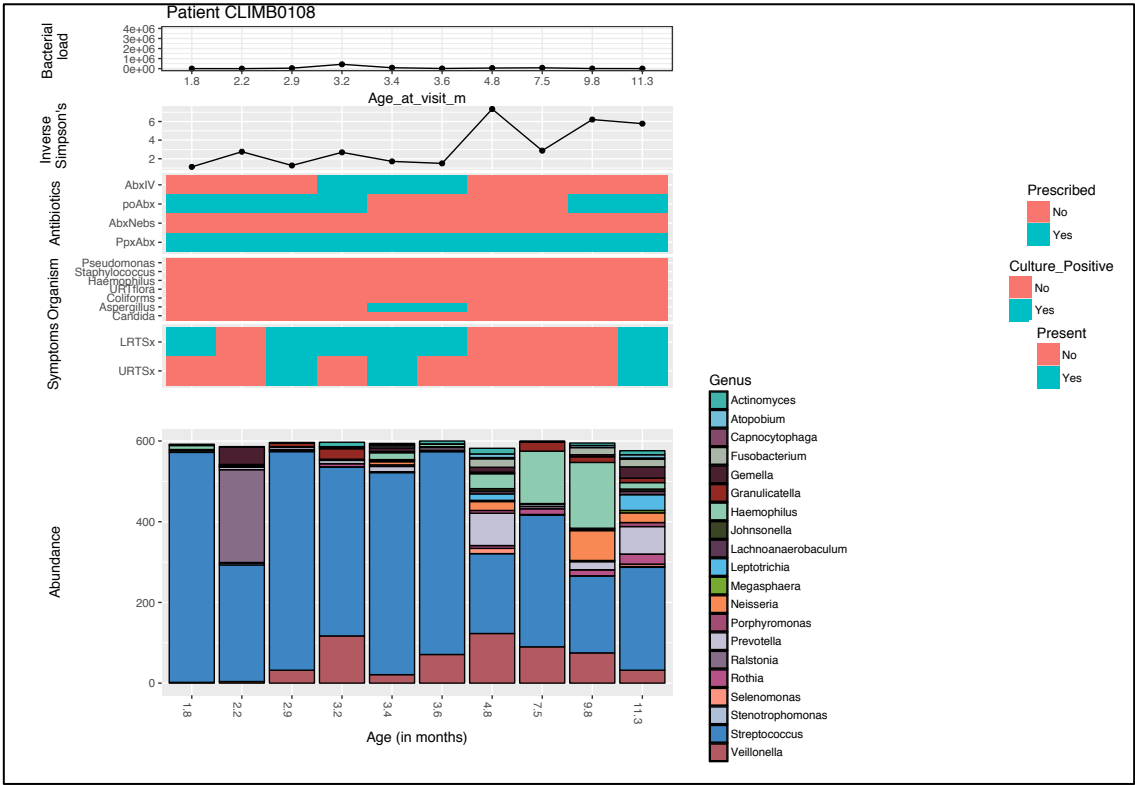
A4.10: CLIMB0106



A4.11: CLIMB0107

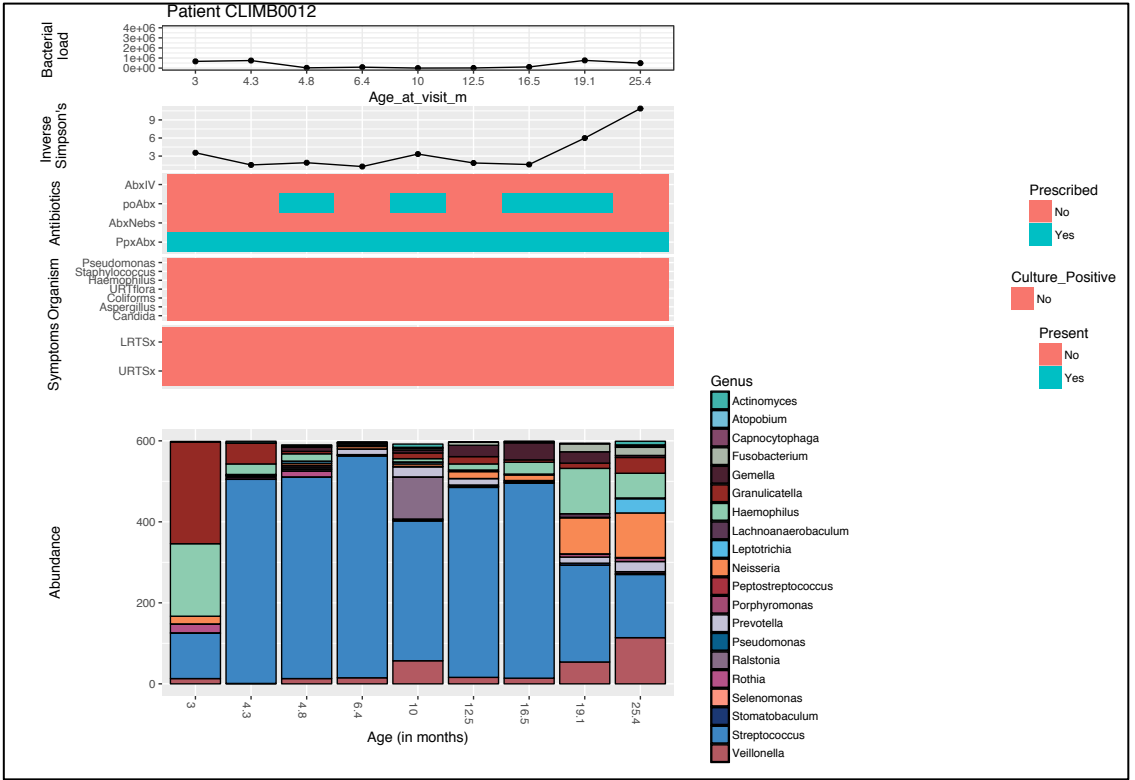


A4.12: CLIMB0108

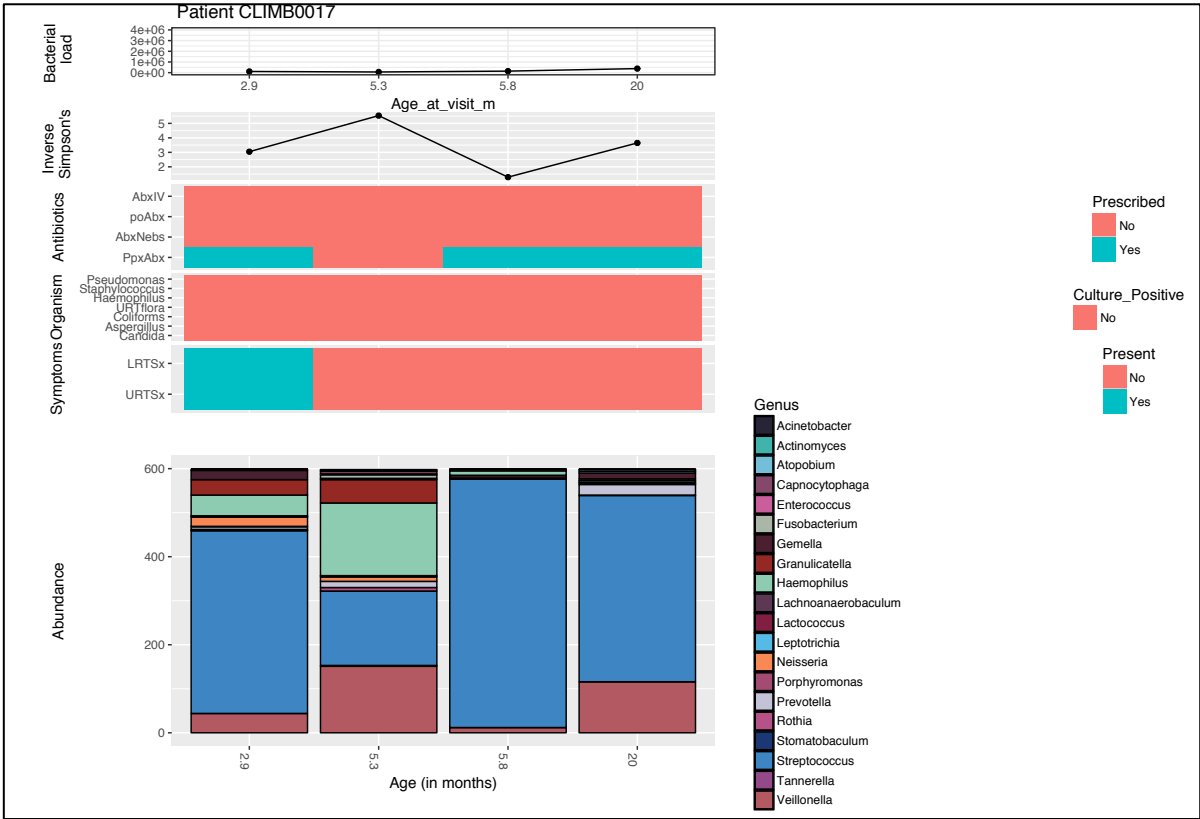


(b) Patients recruited at age 2 – 3 months.

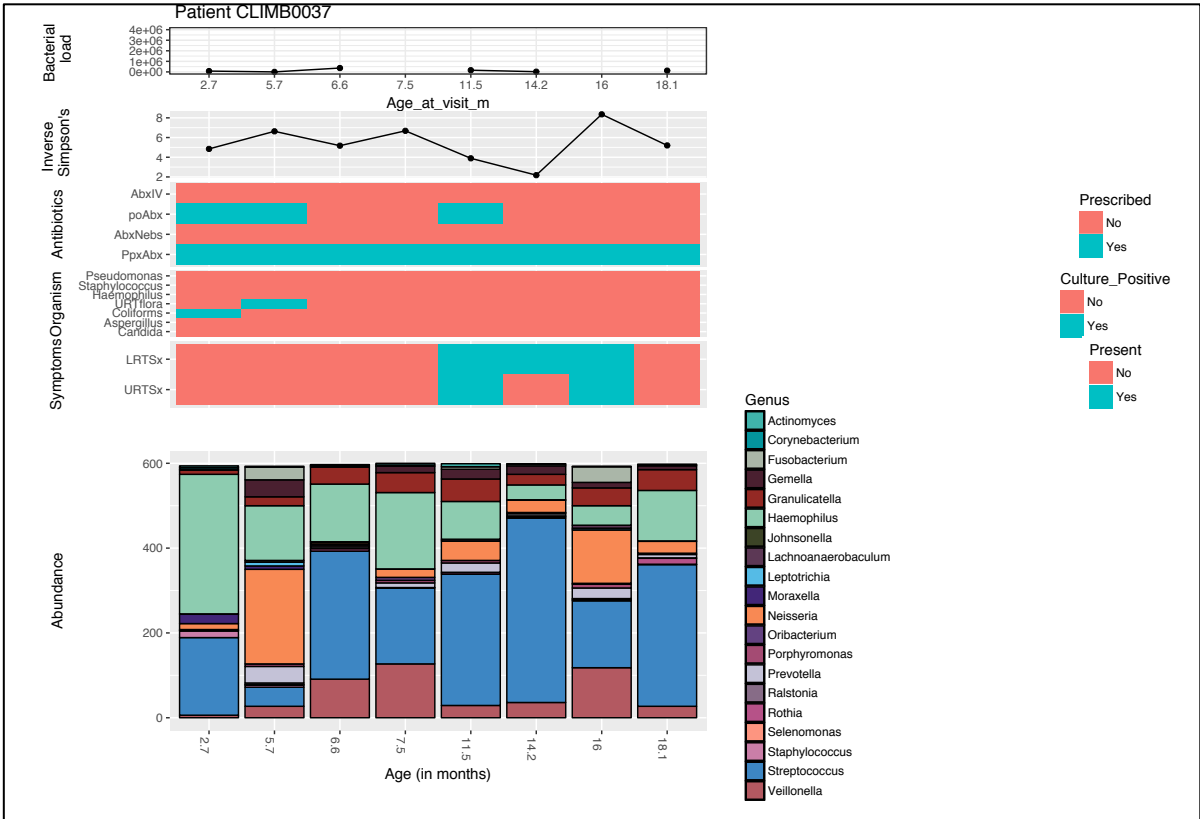
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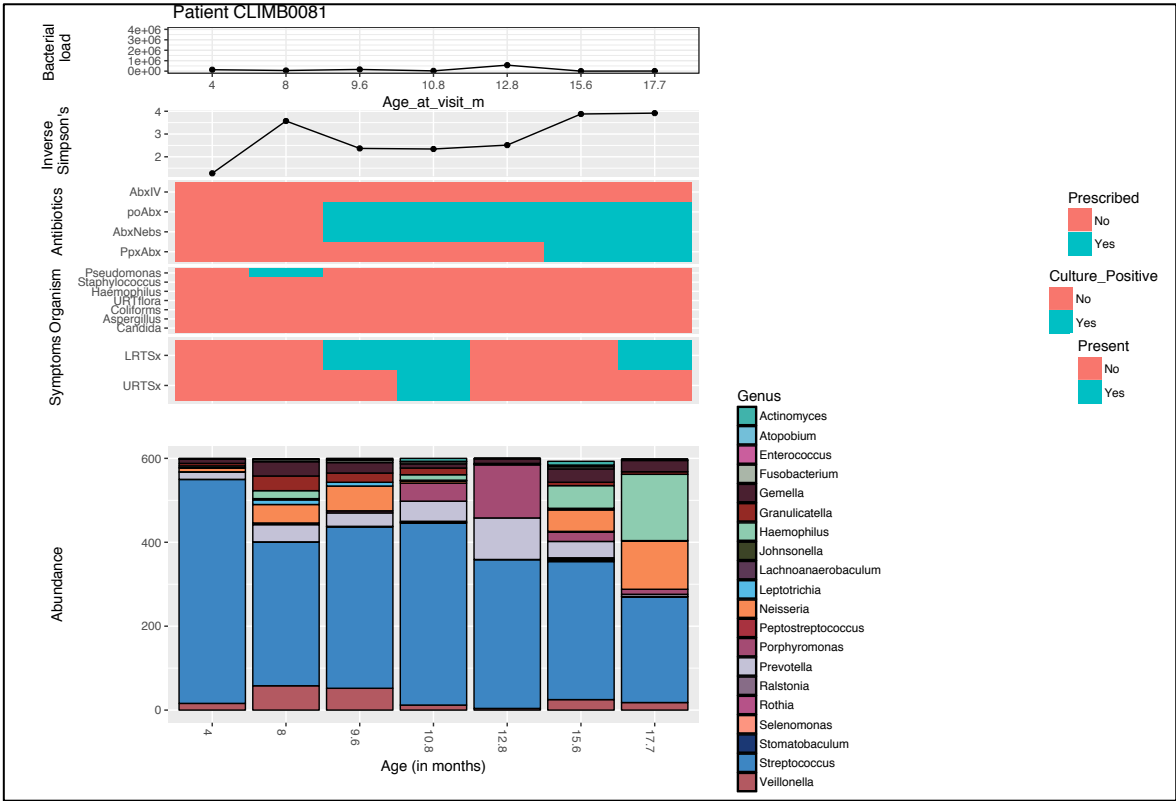
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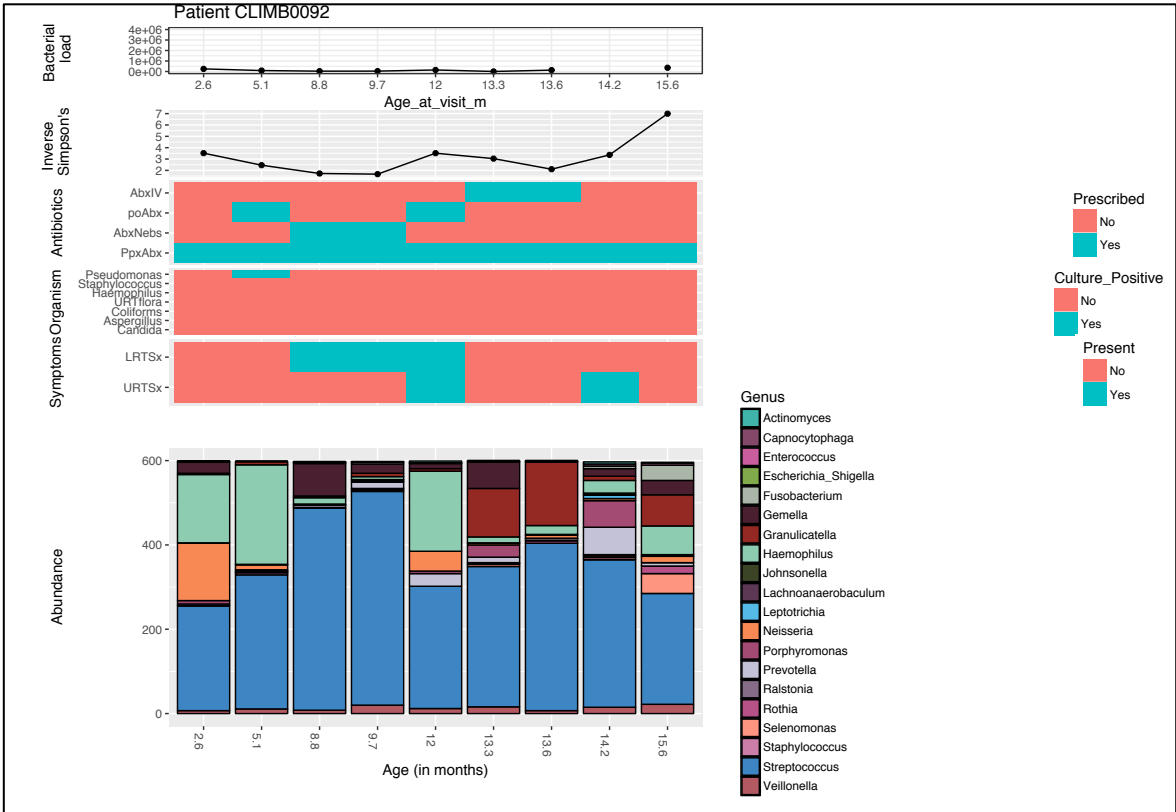
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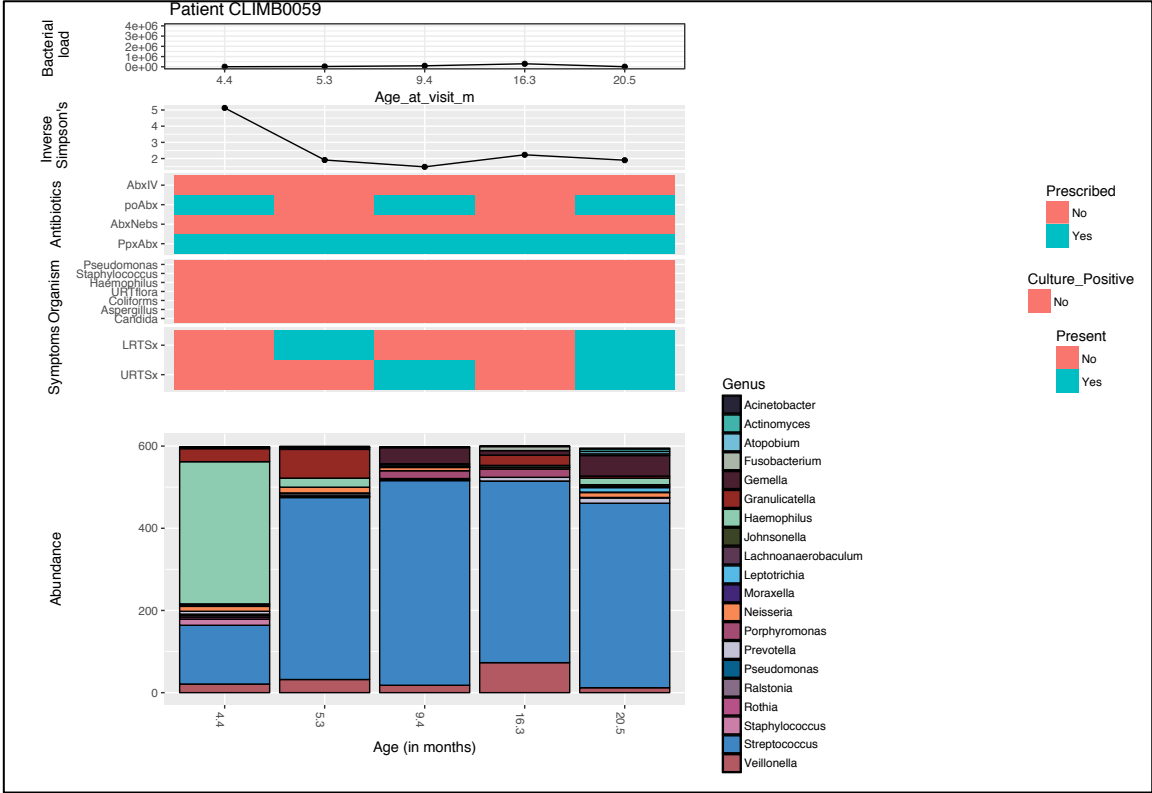
A4.16: CLIMB0081



A4.17: CLIMB0092

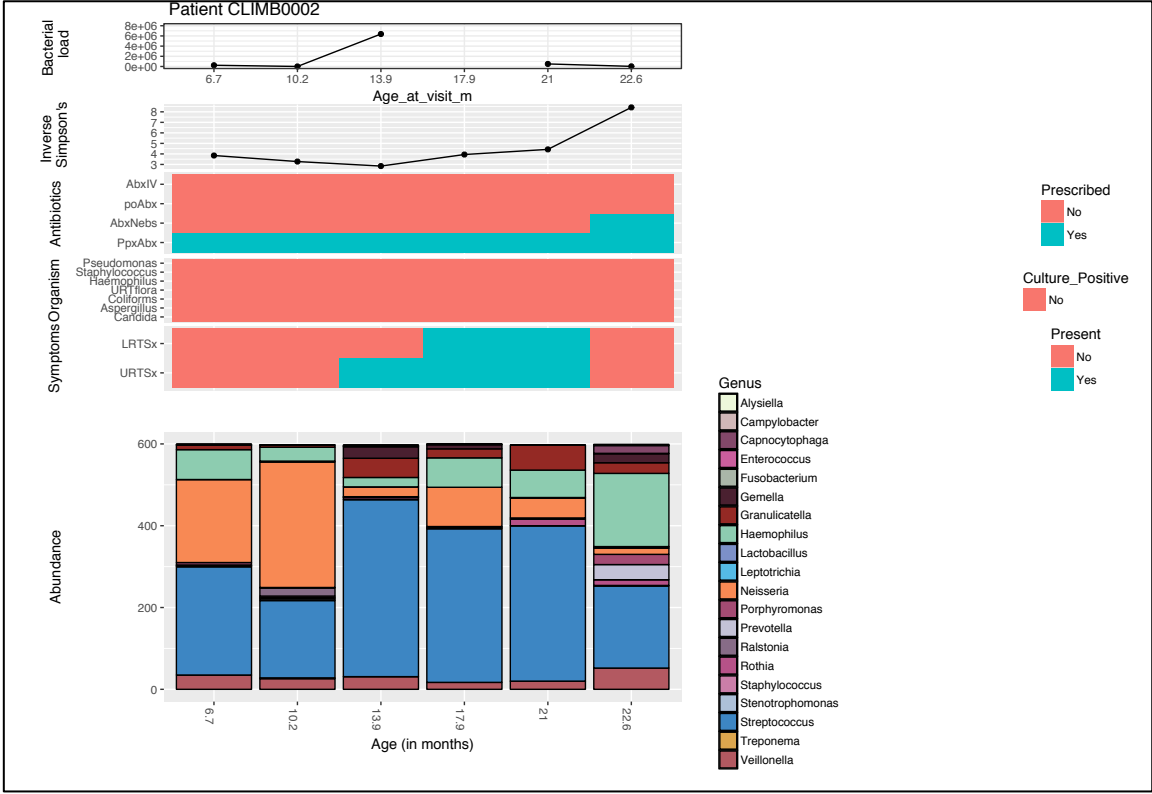


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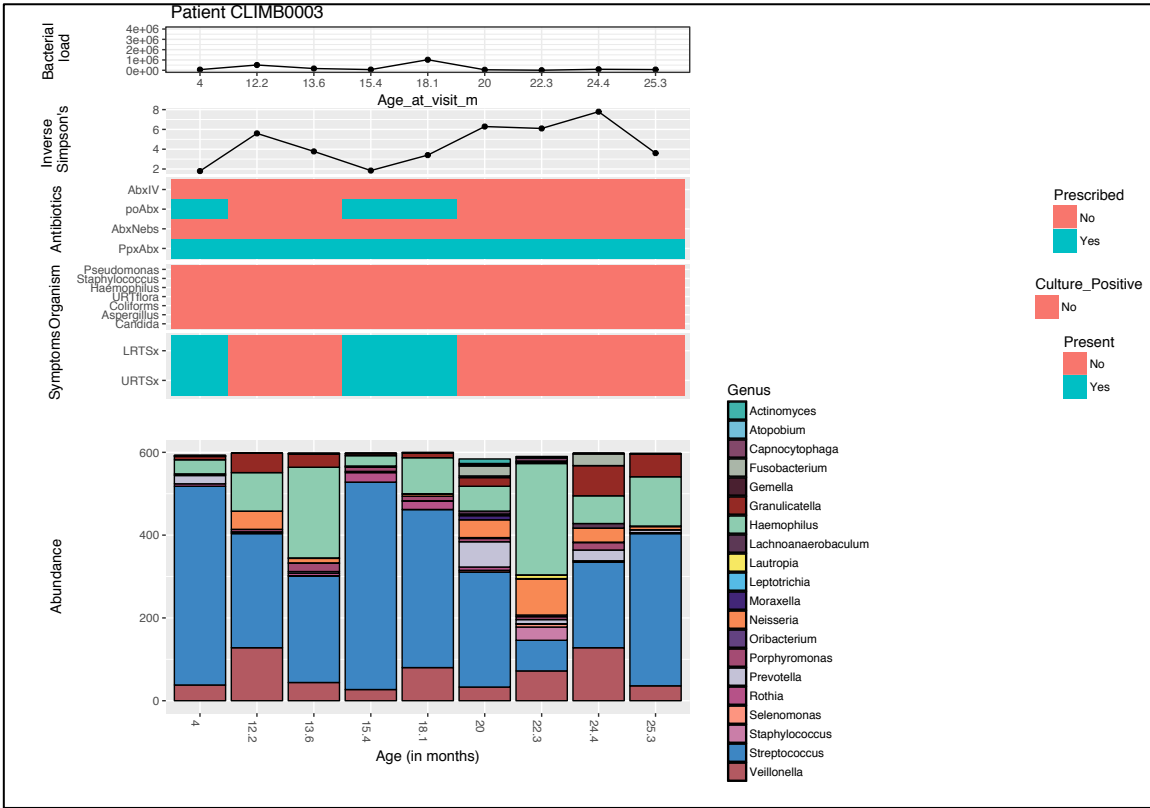


(c) Patient recruited at age 3 – 5 months.

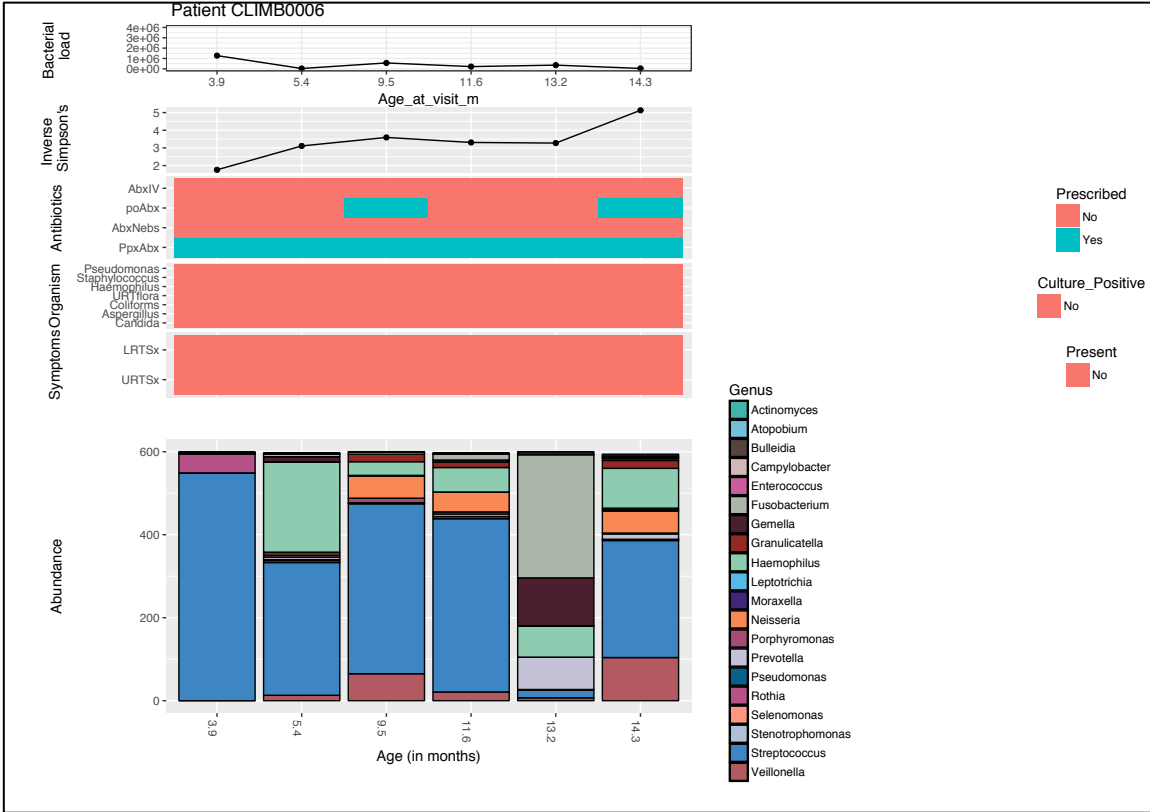
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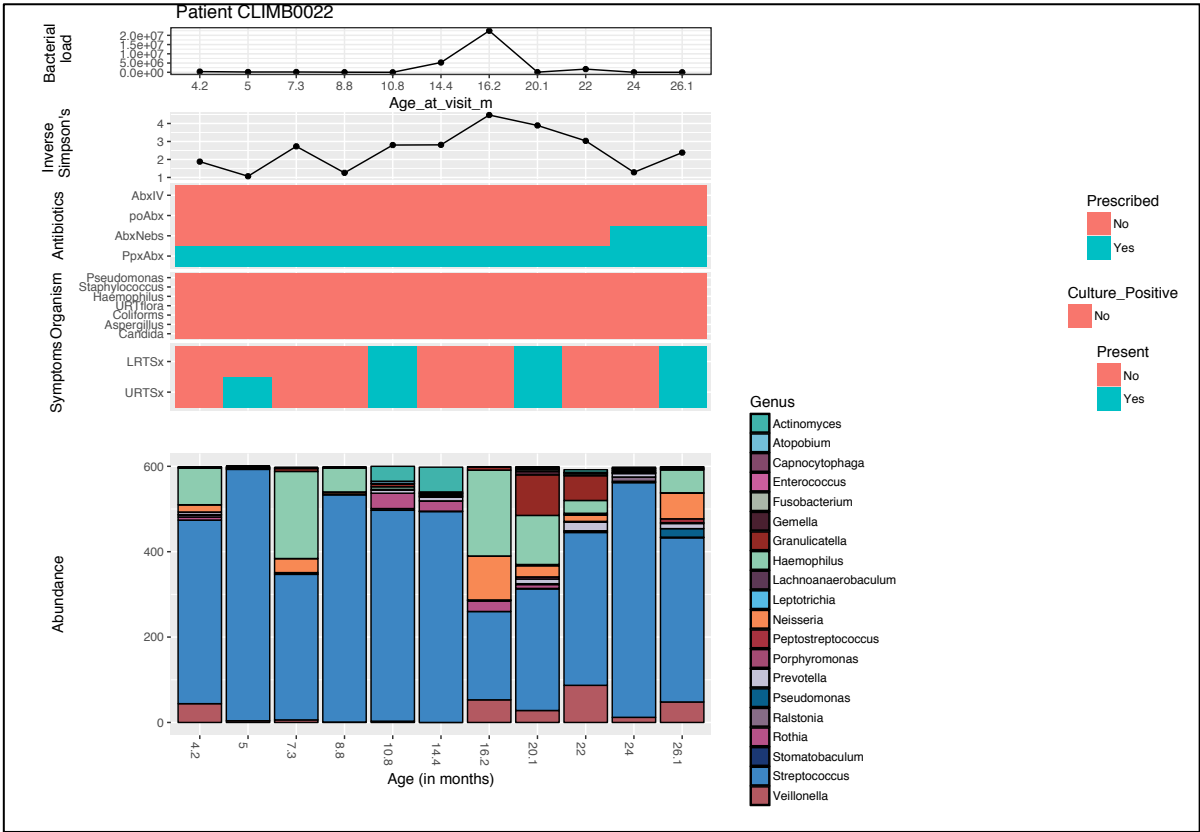
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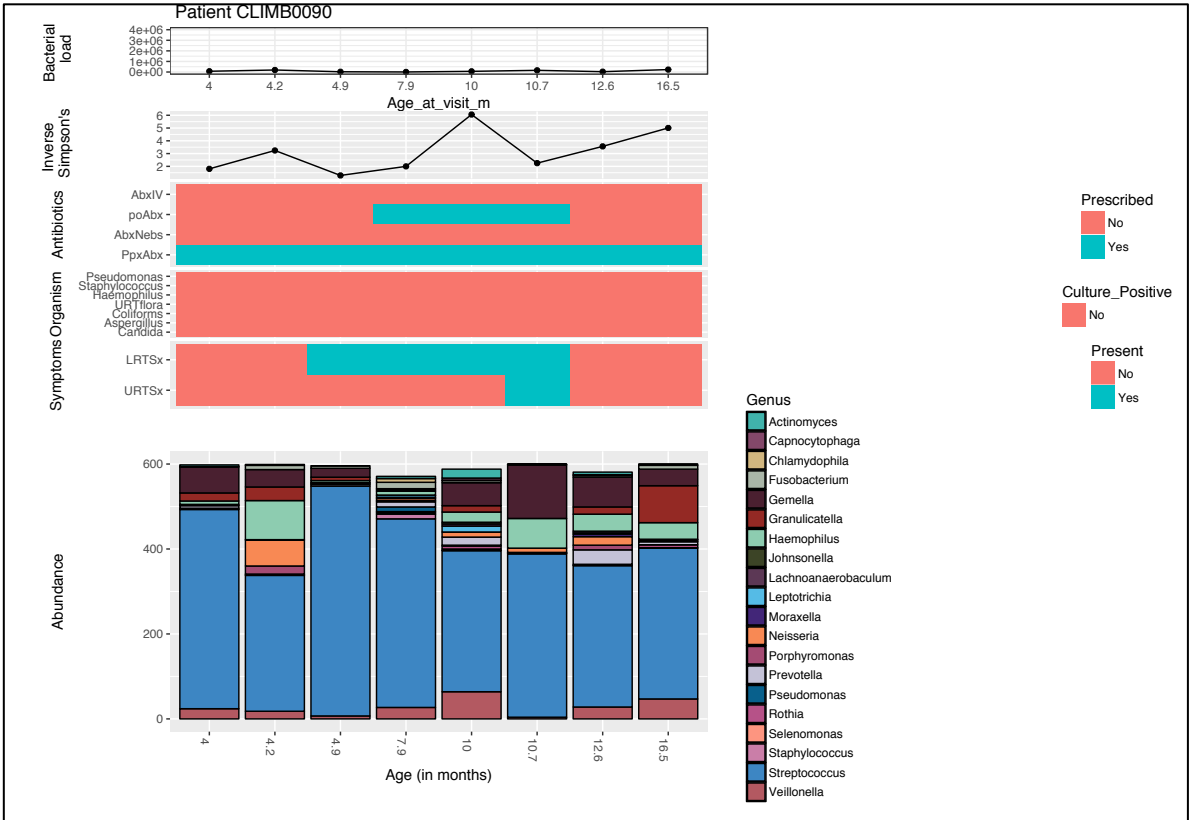
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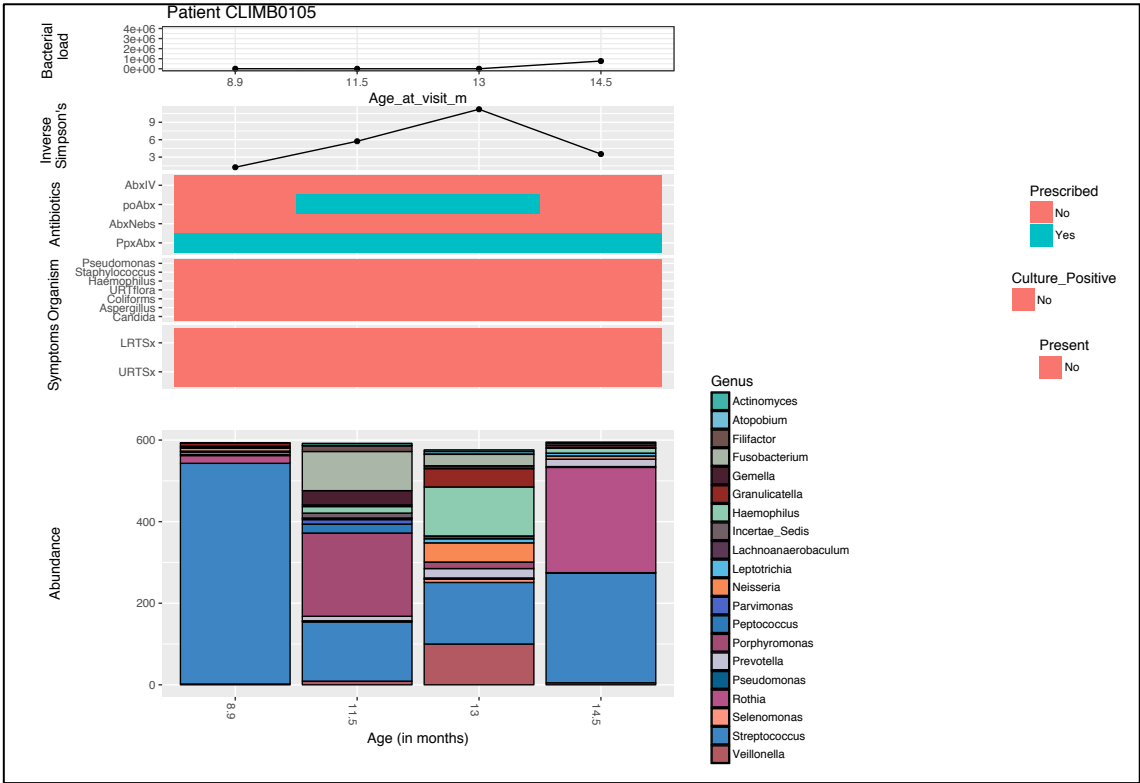
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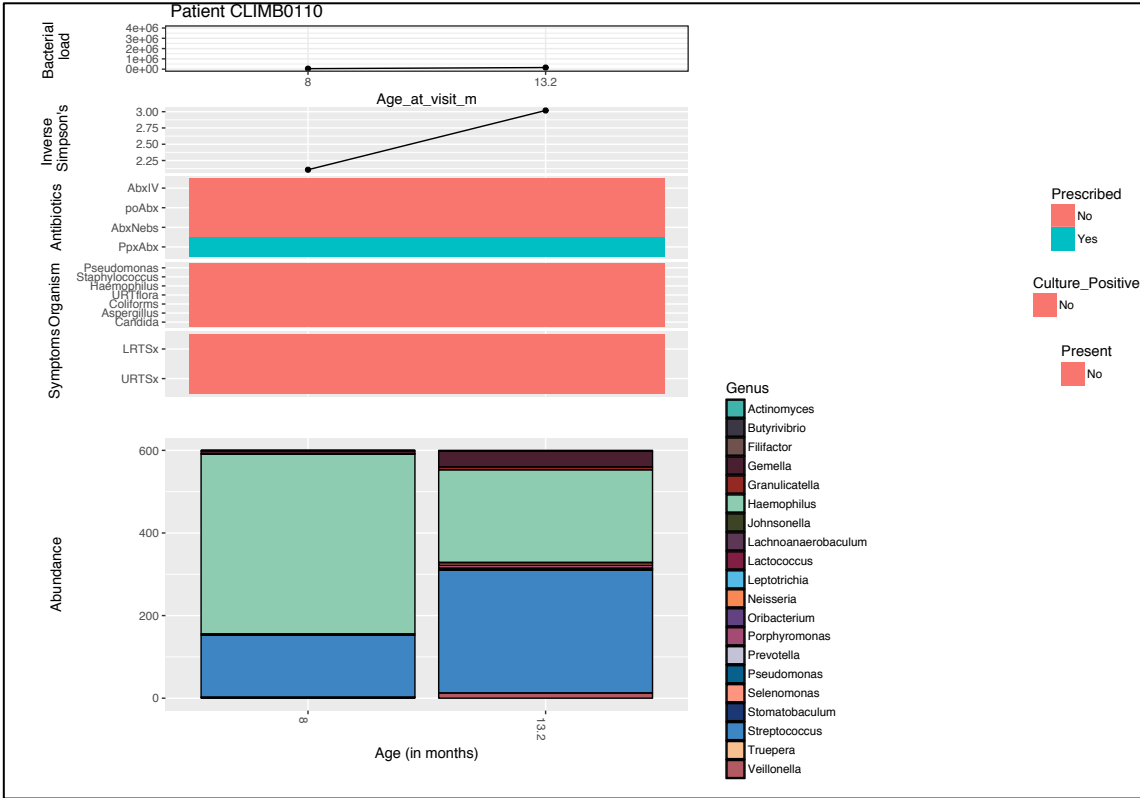
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A4.24: CLIMB0105

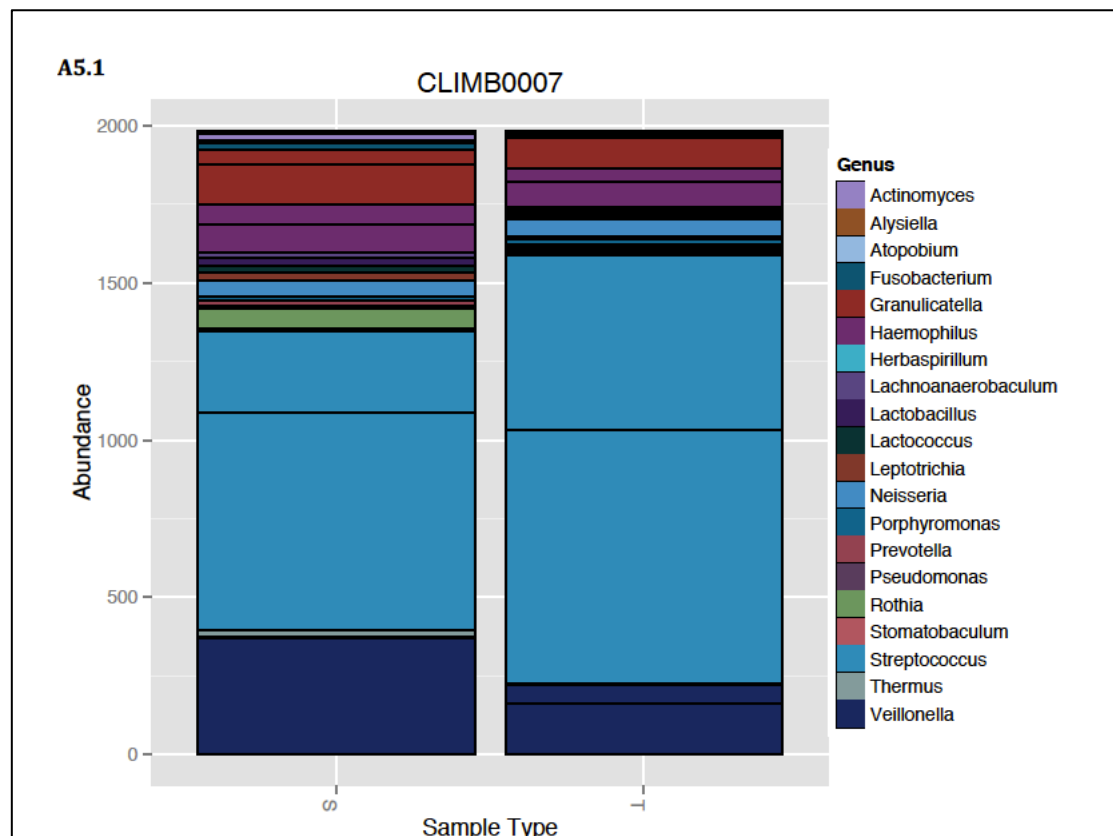


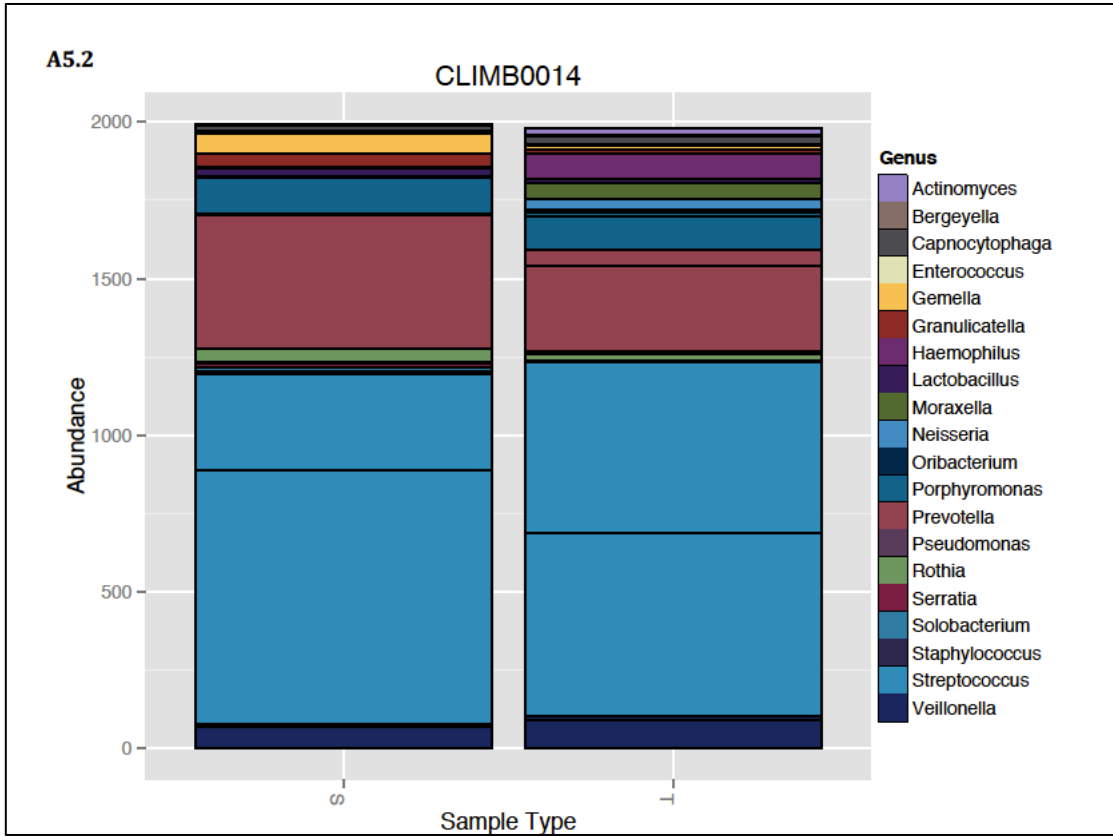
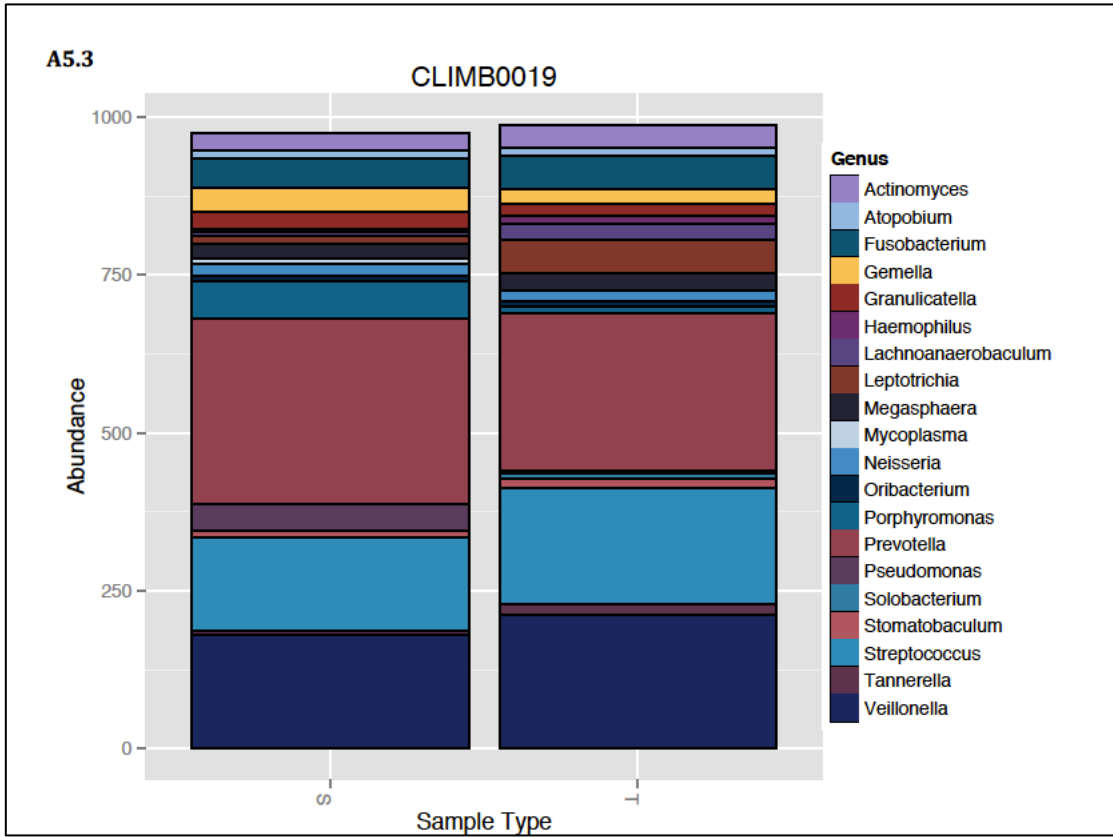
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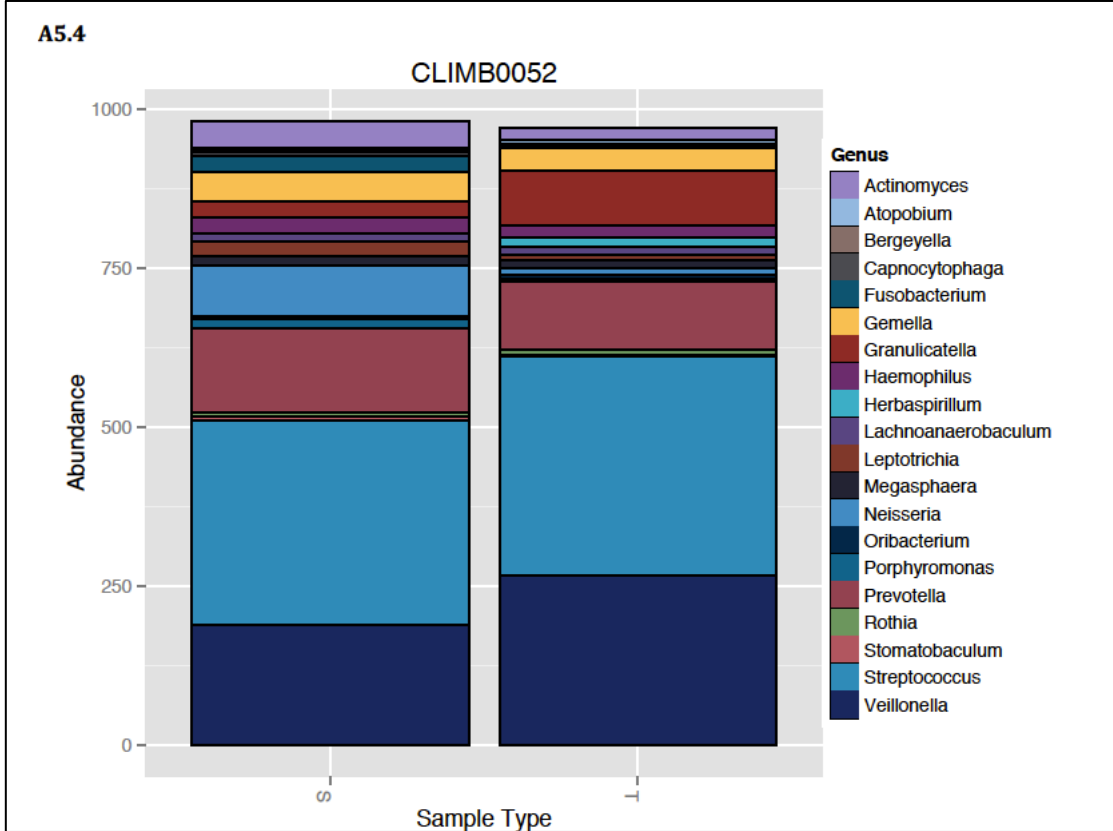
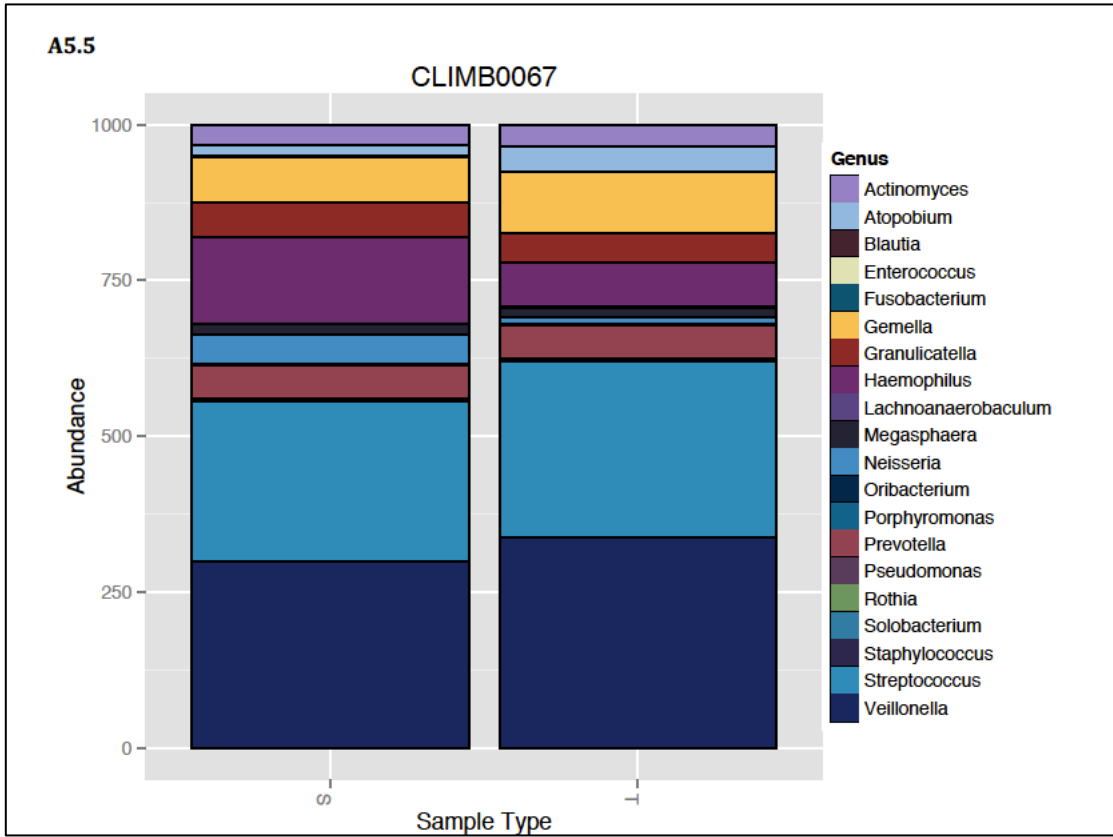


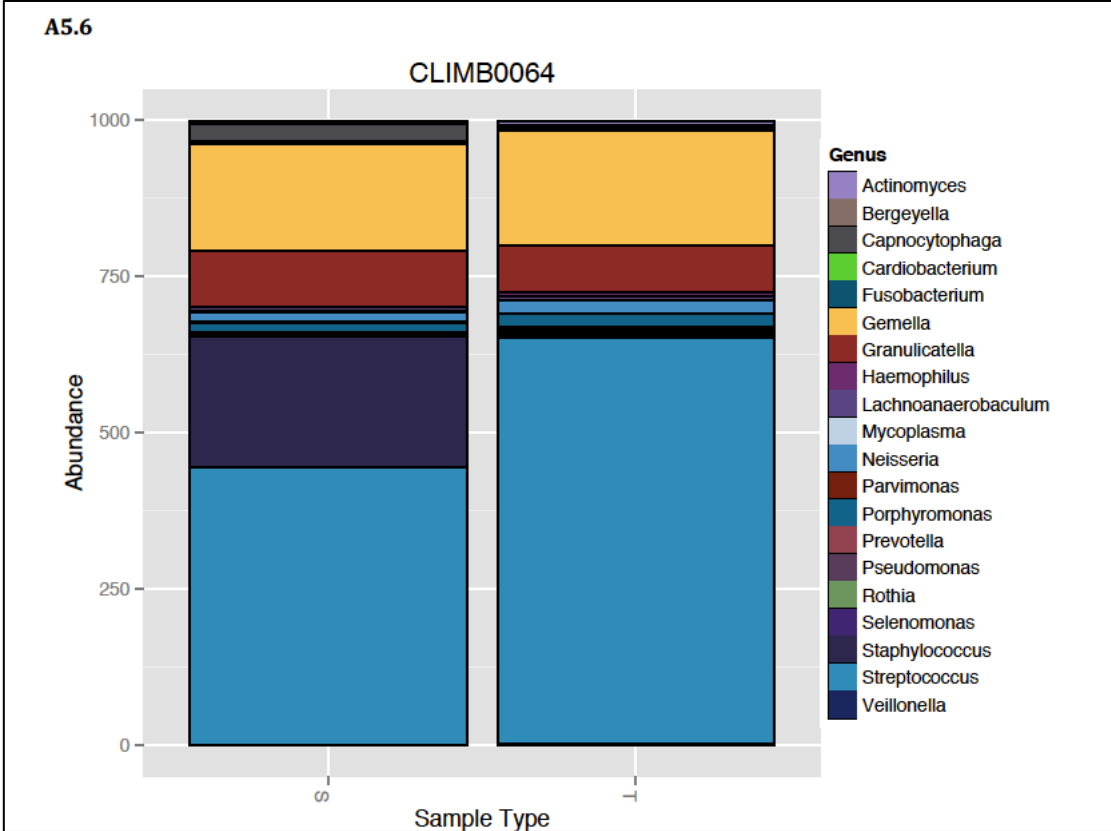
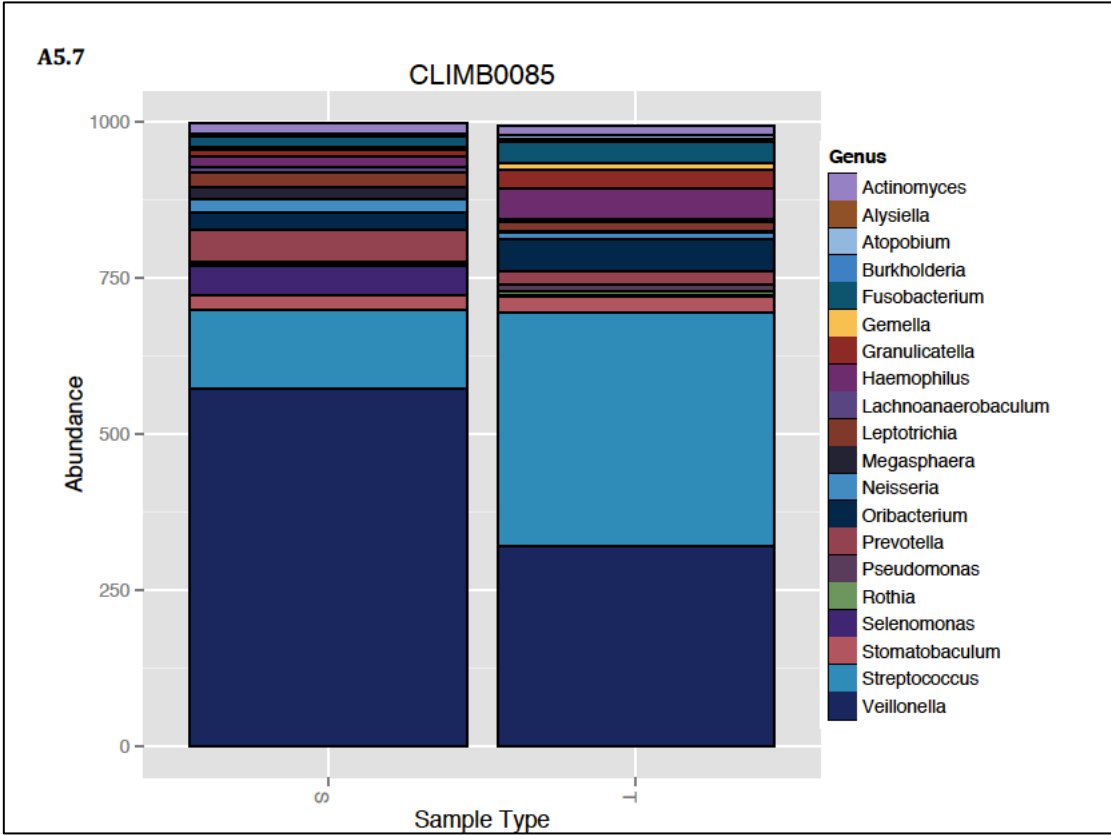
A5: E Appendix for use in conjunction with Chapter 5: Individual patient barplots comparing the airway microbiota on throat swabs and sputum samples in children with cystic fibrosis (CF) or primary ciliary dyskinesia (PCD)

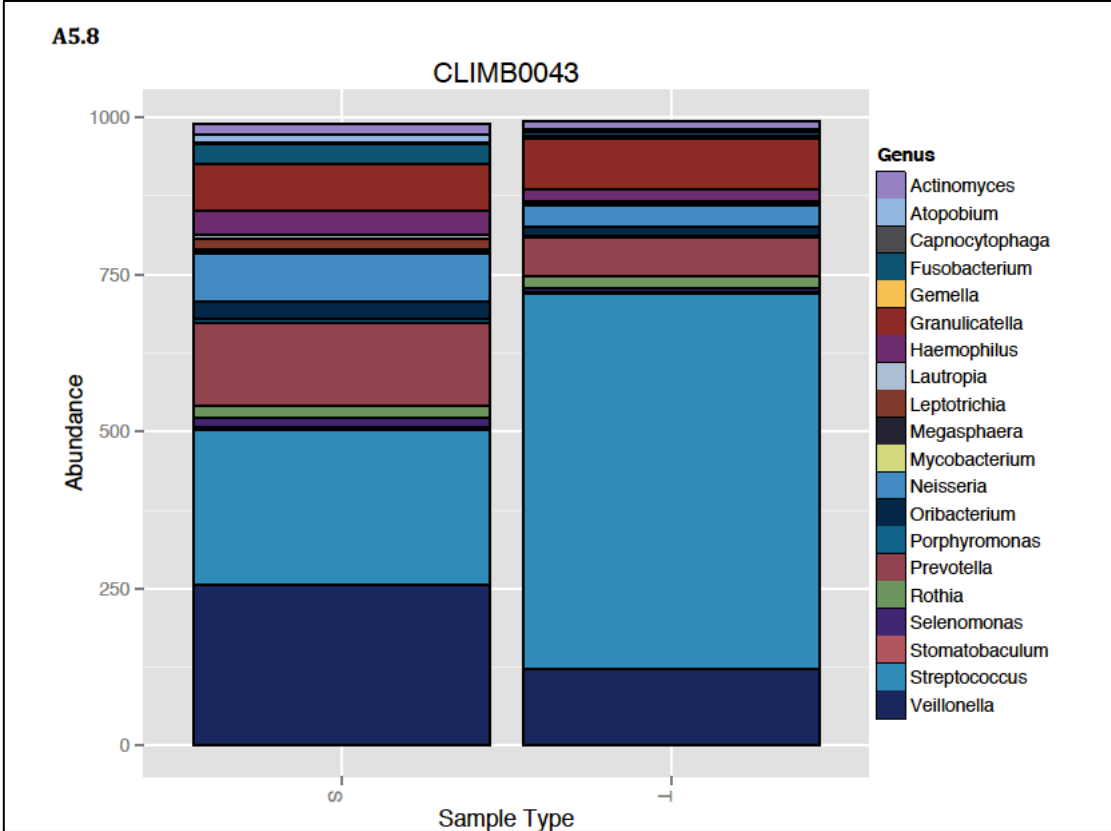
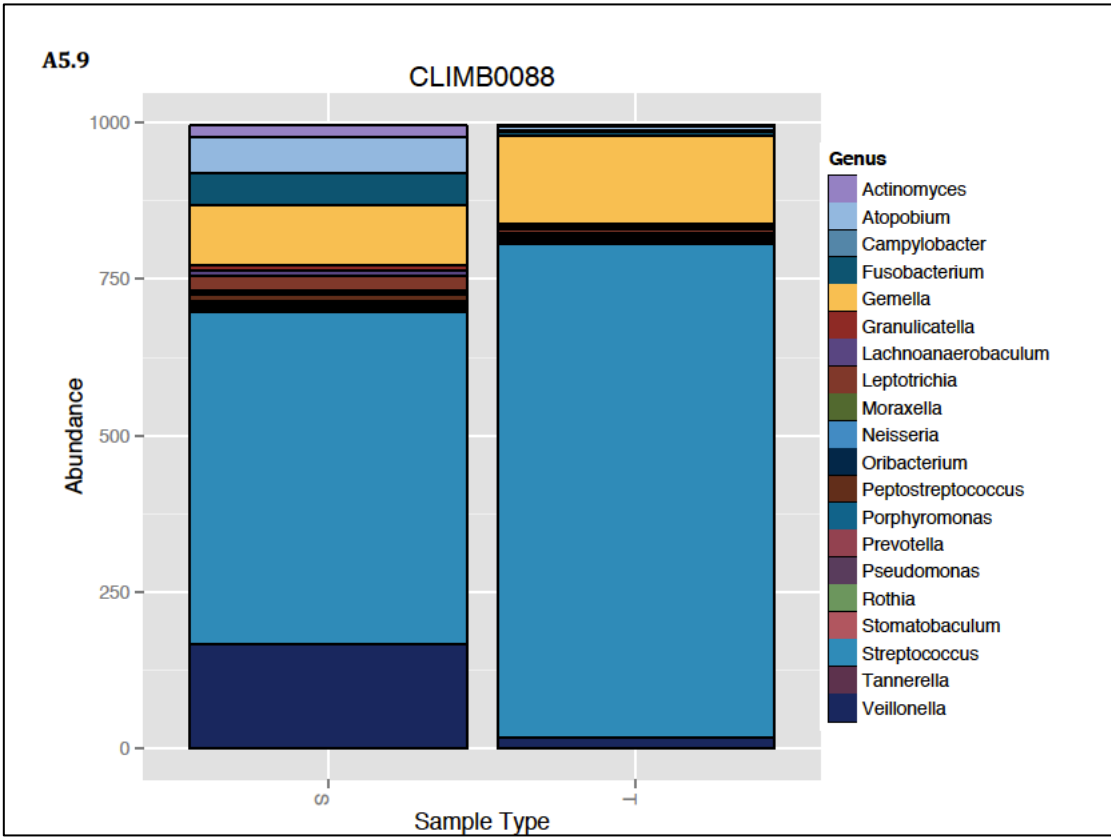
A5.1 – A5.16 shown. Each figure represents an individual patient and each barplot an individual sample type (spontaneously expectorated sputum (S) or throat swab (T)). The relative abundance of the most common genera for each sample type is shown by the height of the corresponding bar. Constructed using rarefied data. Barplots have been organised from the most similar to the least similar.

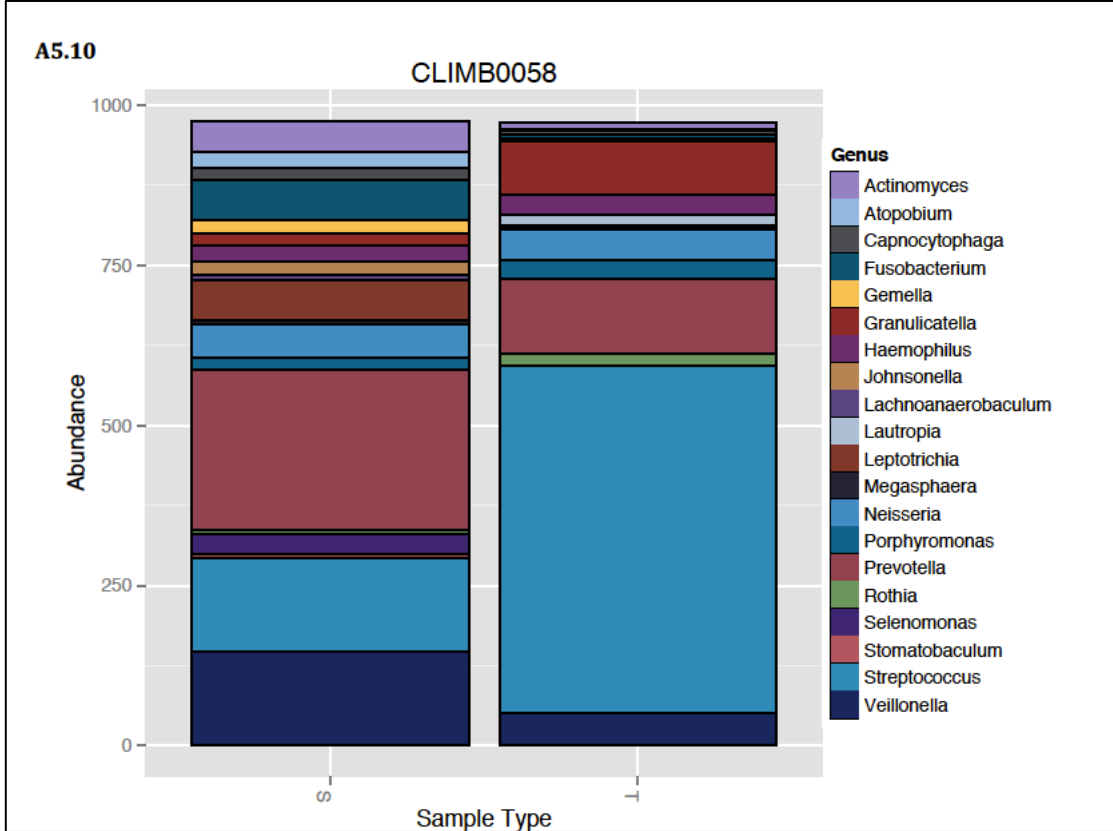
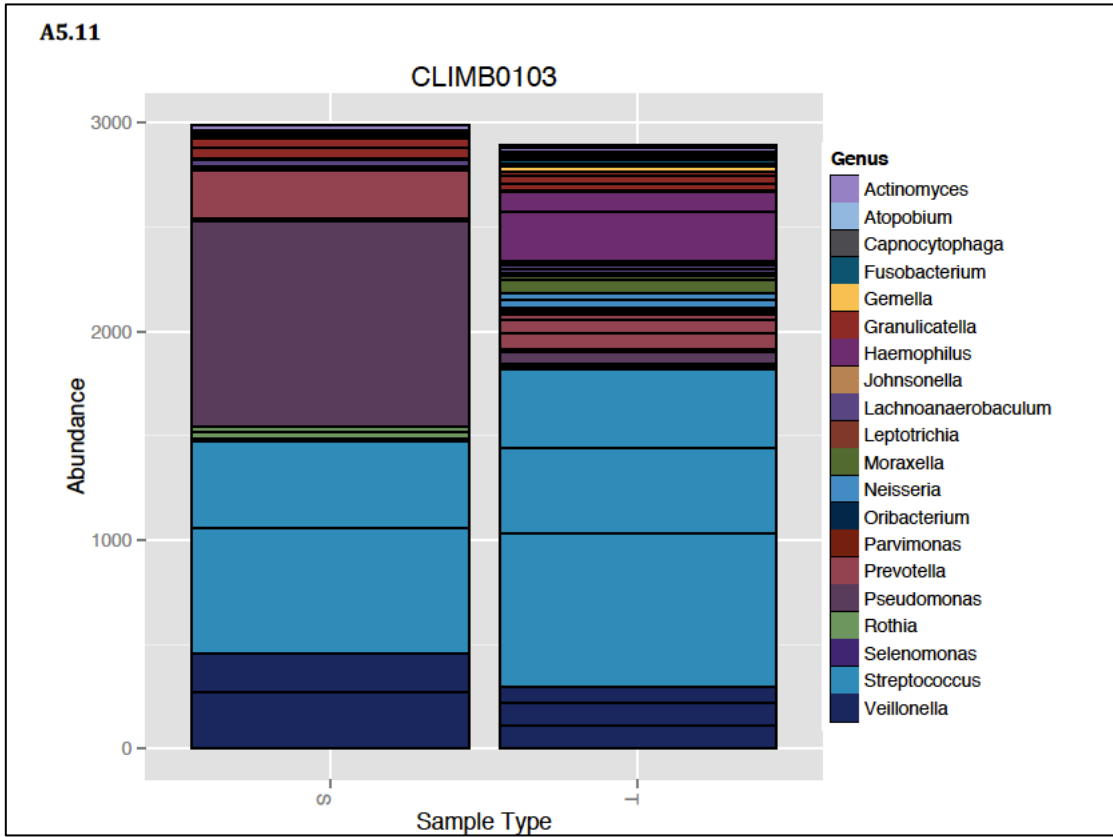


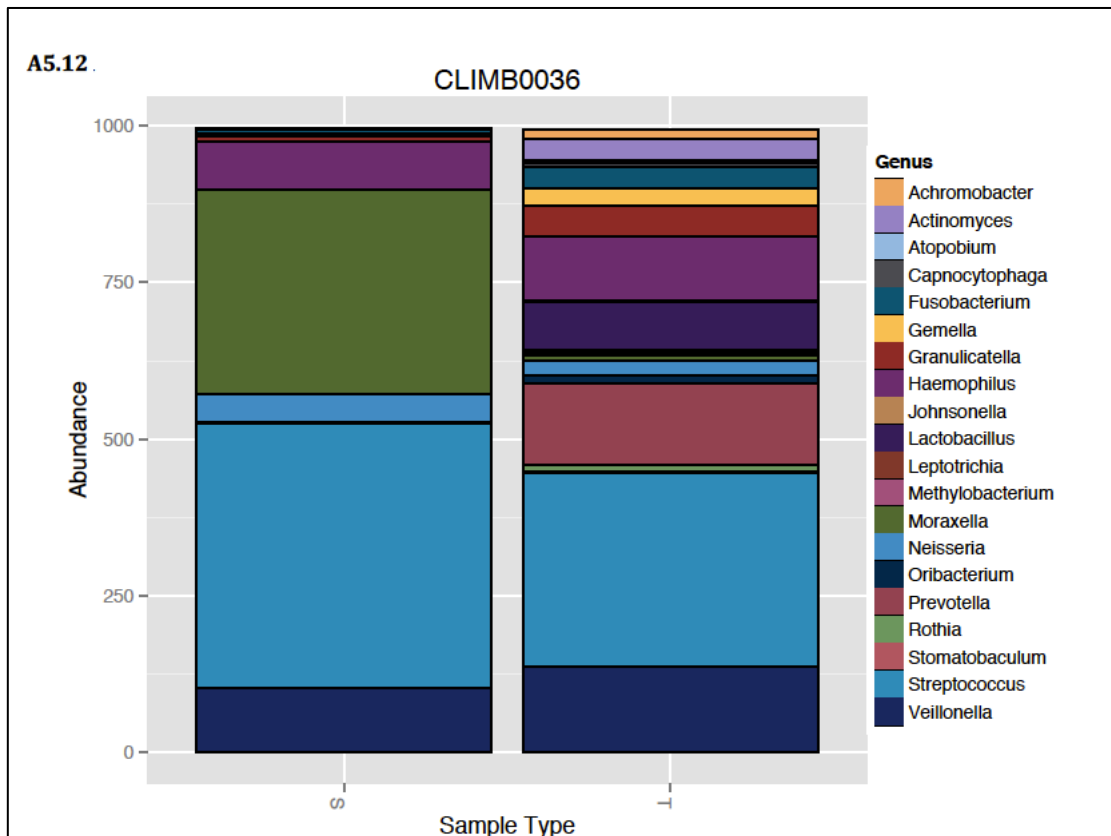
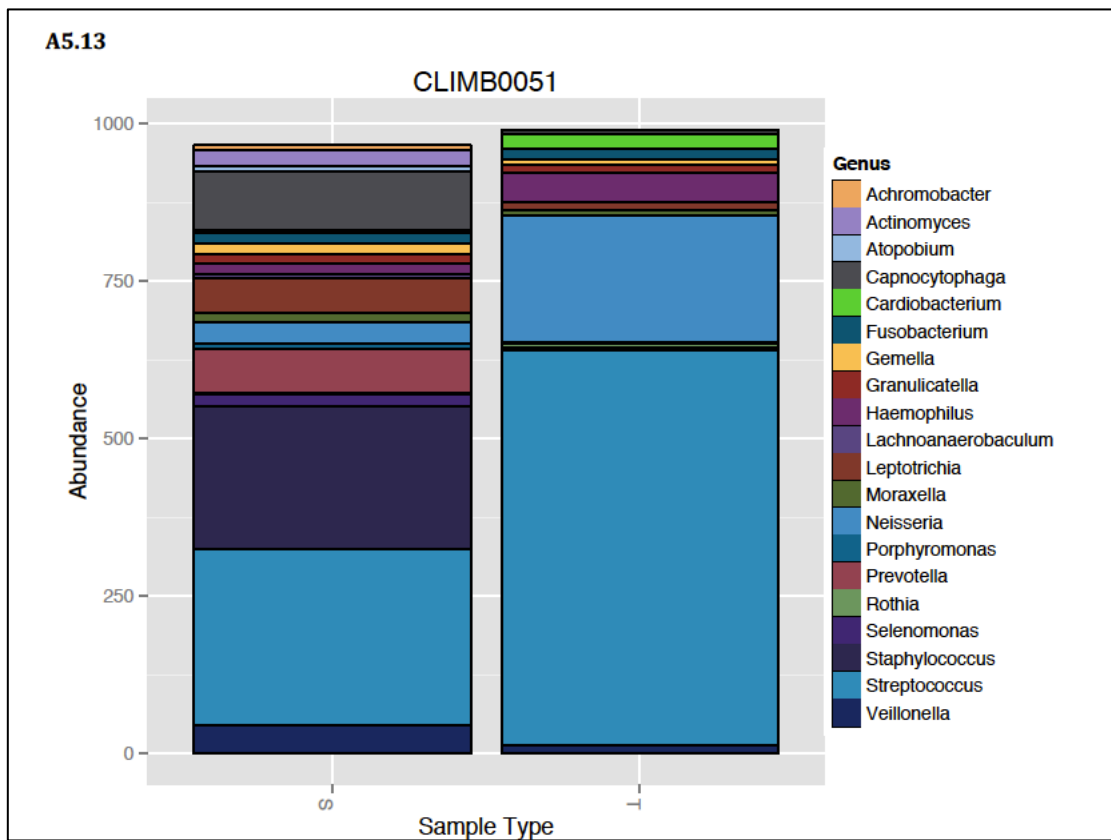


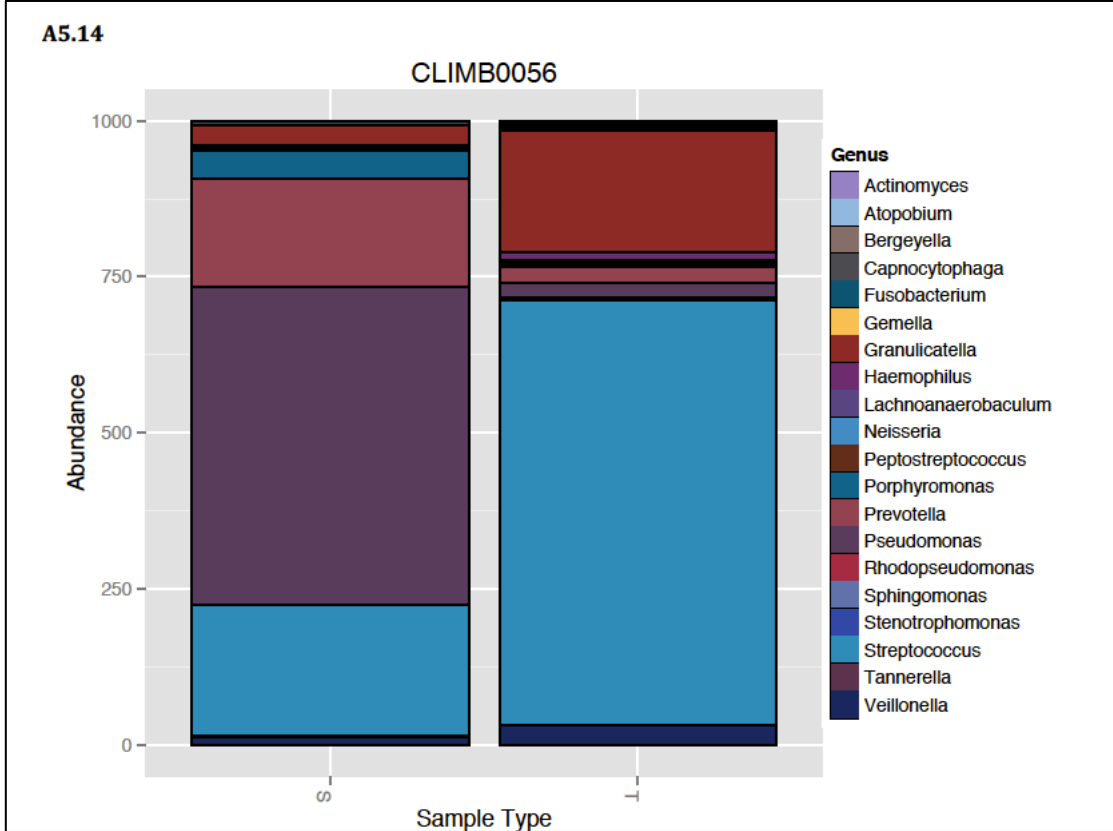
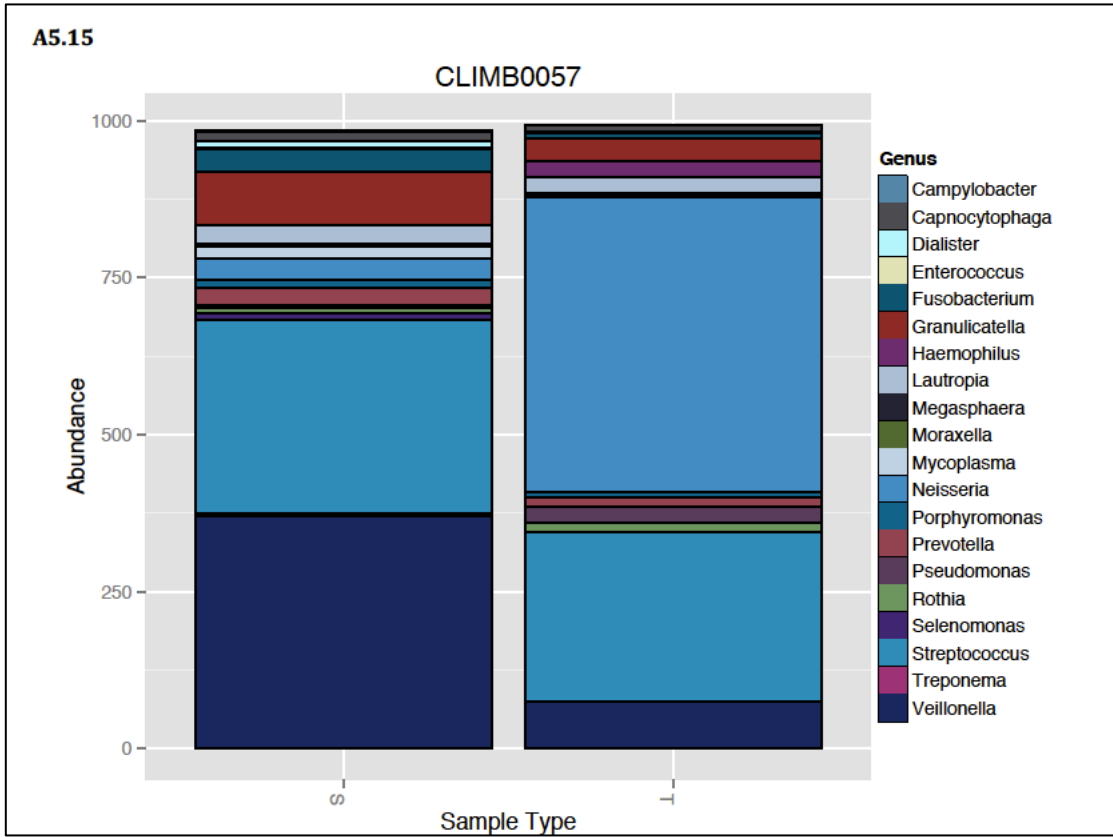




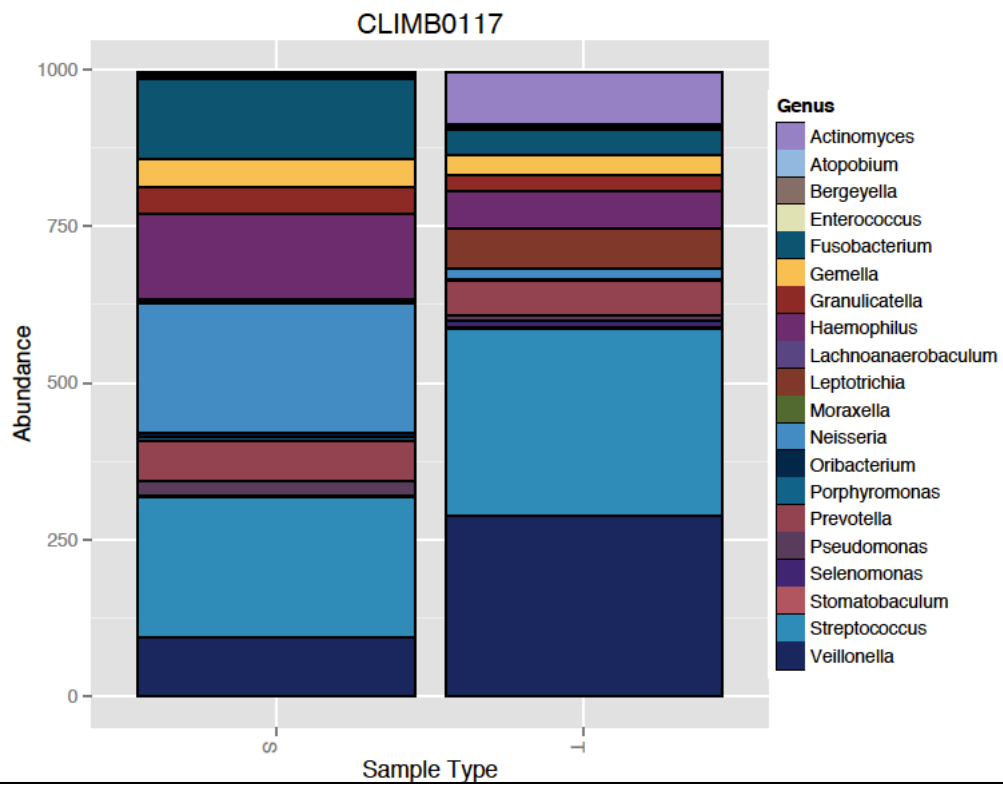








A5.16



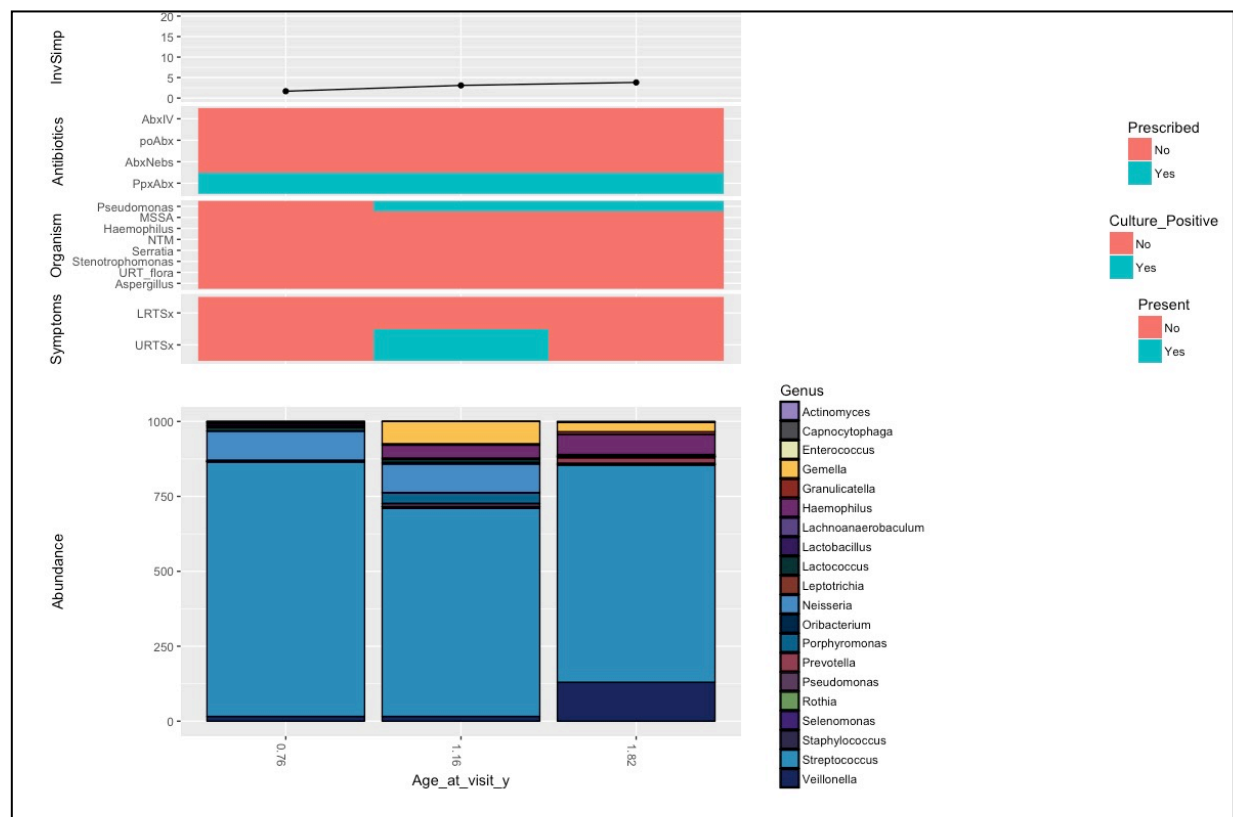
A6: E Appendix for use in conjunction with Chapter 5: Individual patient barplots for older children with cystic fibrosis (CF)

A6.1 – A6.31 illustrate changes in relative abundance of OTUs against spirometry measurements (FEV₁ % predicted), diversity changes (Inverse Simpson's) and clinical variables (antibiotic use, organisms grown on clinical microbiology and presence of upper and lower airway symptoms) for each CF patient (excluding NBS) in the CLIMB study. Overall, no consistent changes in the microbiota were seen with clinical variables. Organised by: (a) bacterial growths on clinical microbiology and (b) increasing age.

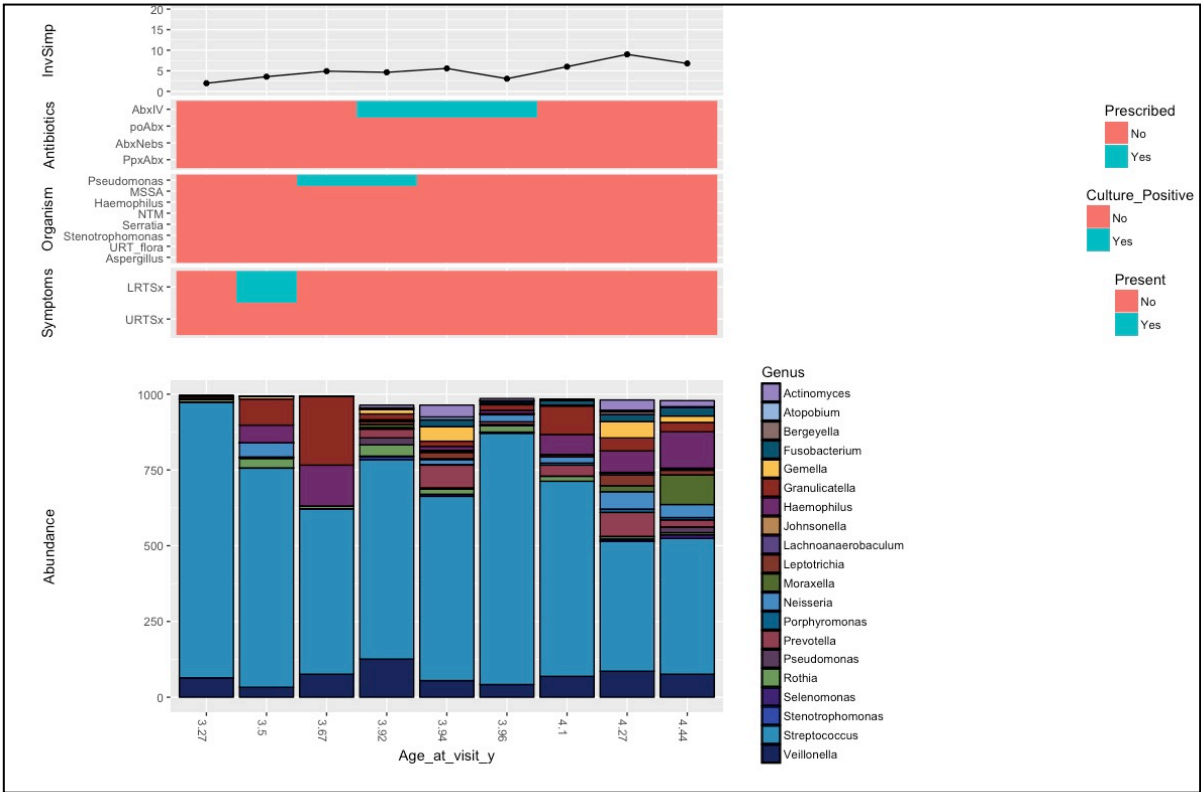
P.aeruginosa

Shown below are any patients who grew *P.aeruginosa*. If another organism grown during study period in addition to *P.aeruginosa*, this has also been shown under *P.aeruginosa*.

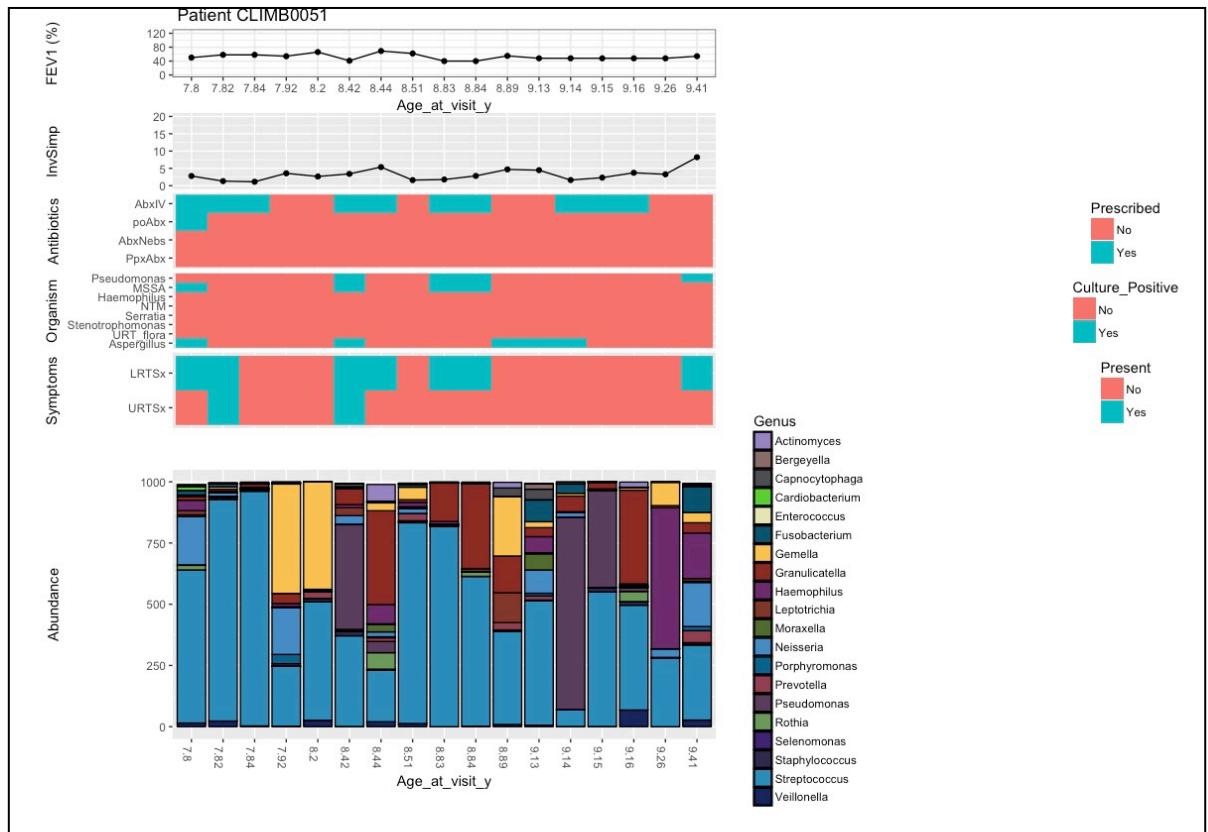
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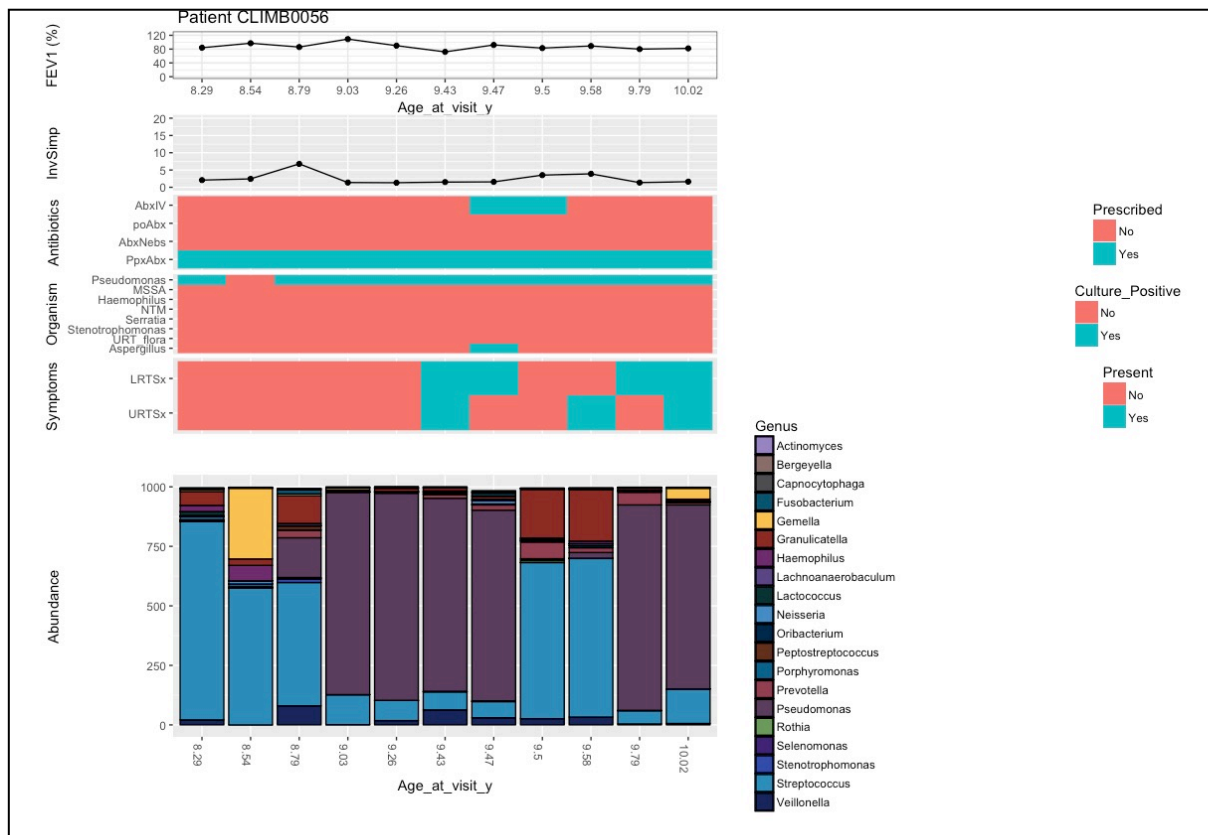
A6.2: CLIMB0038



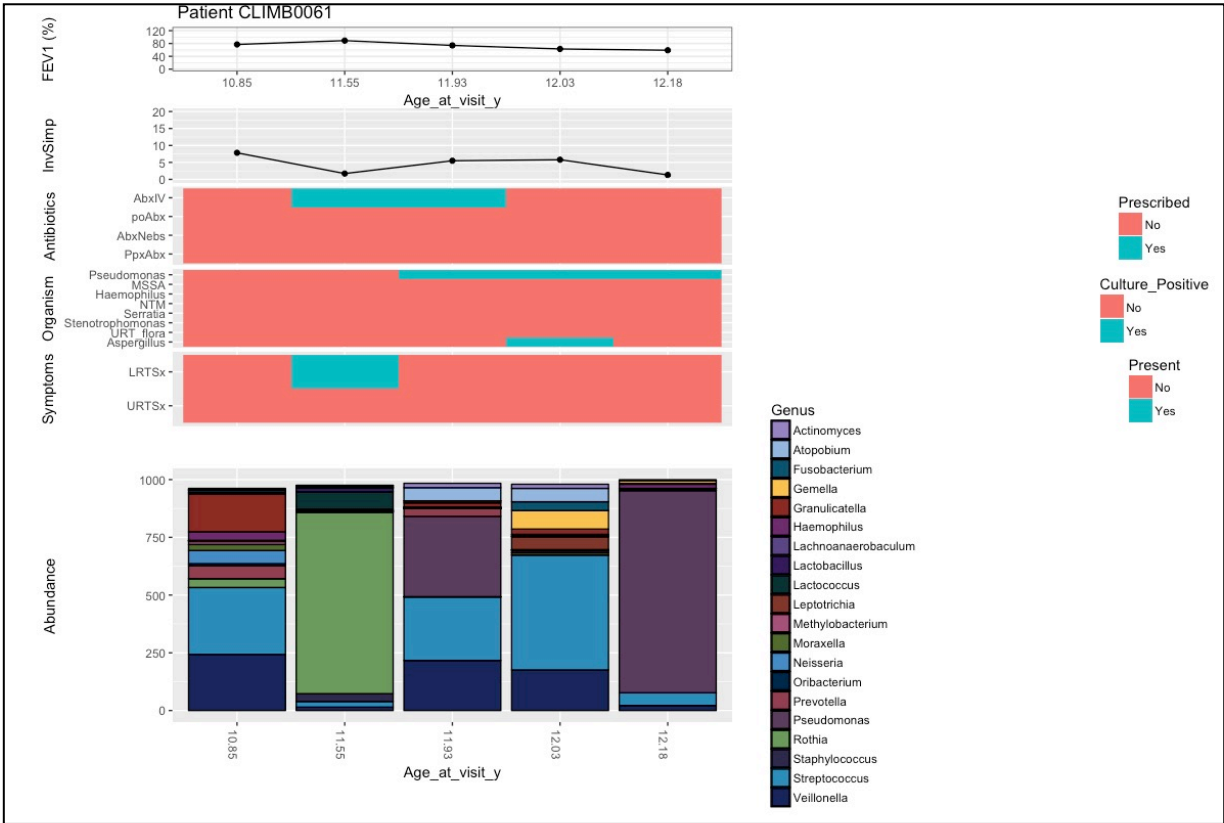
A6.3: CLIMB0051



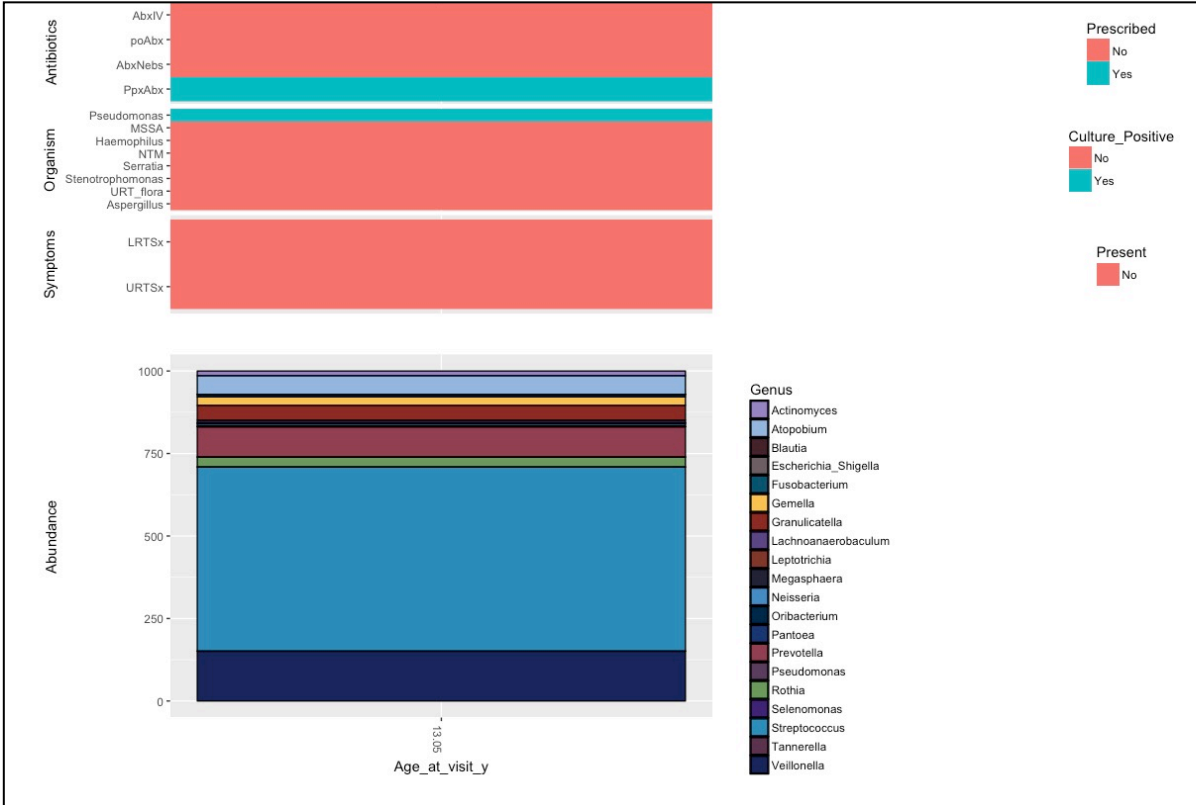
A6.4: CLIMB0056



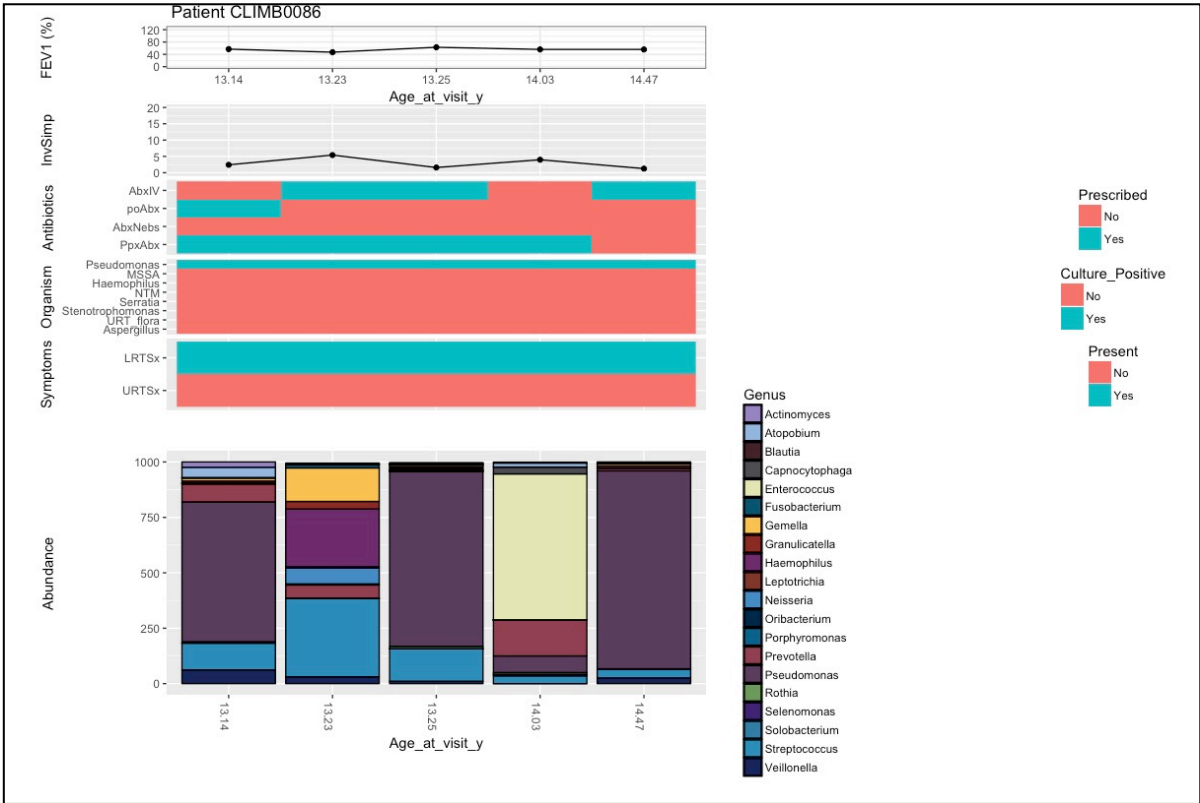
A6.5: CLIMB0061



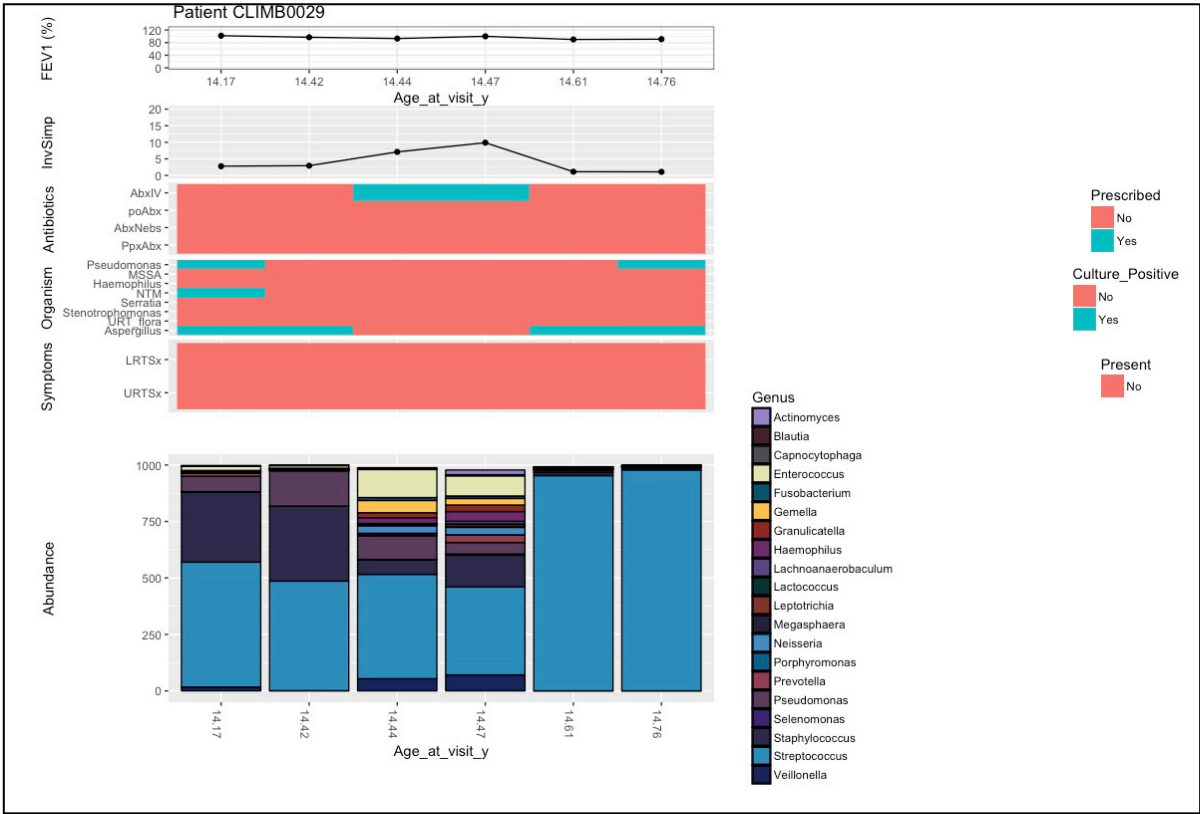
A6.6: CLIMB0042



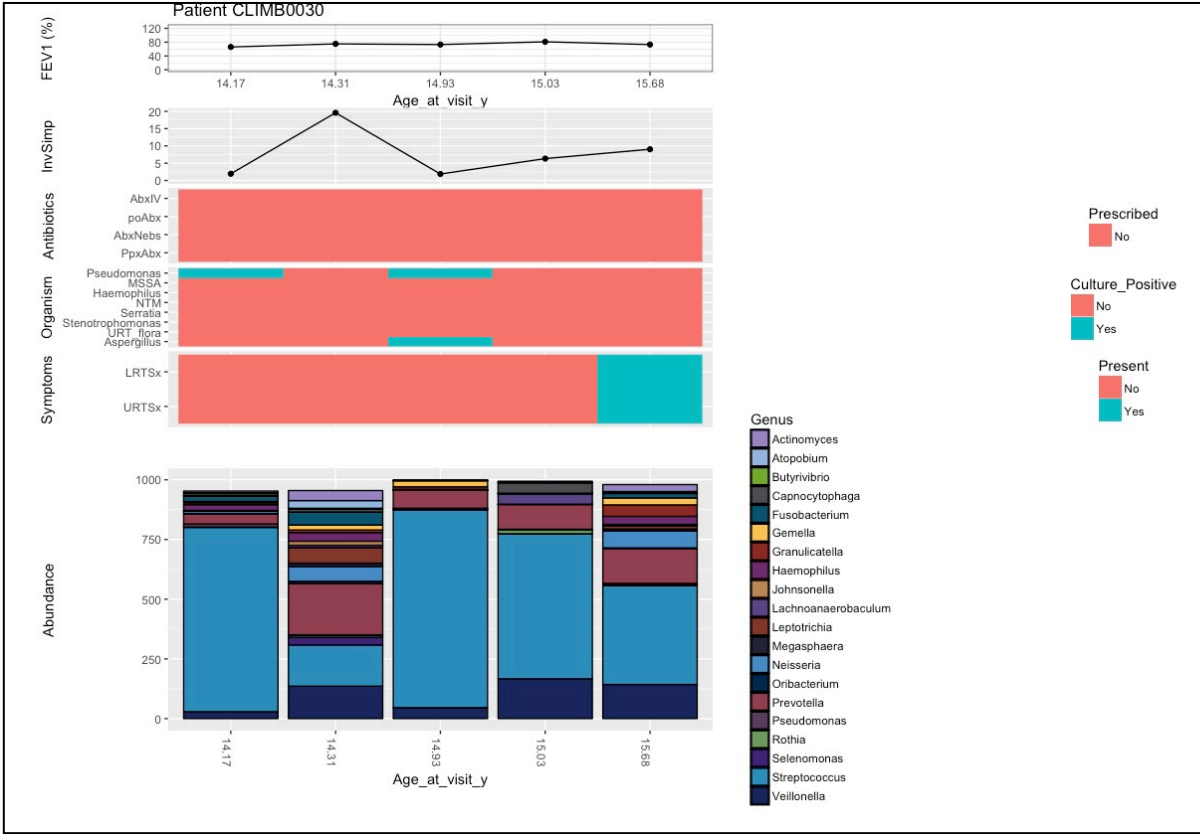
A6.7: CLIMB0086



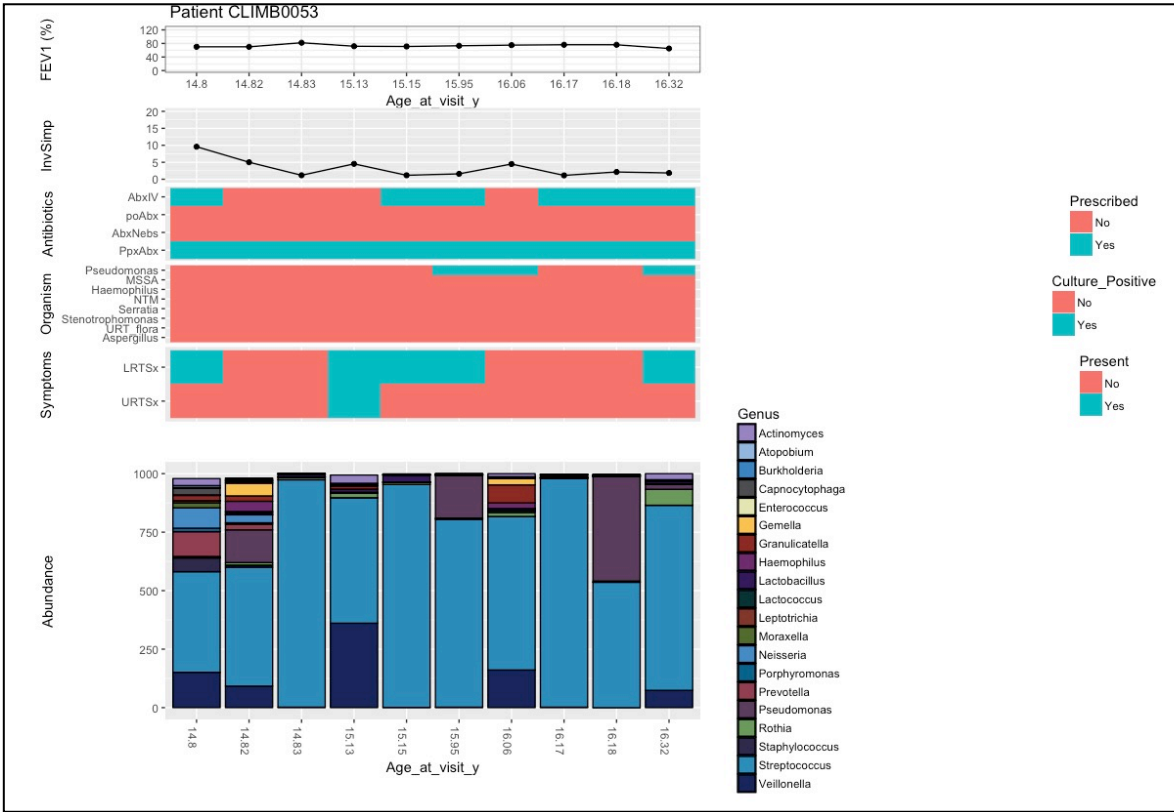
A6.8: CLIMB0029



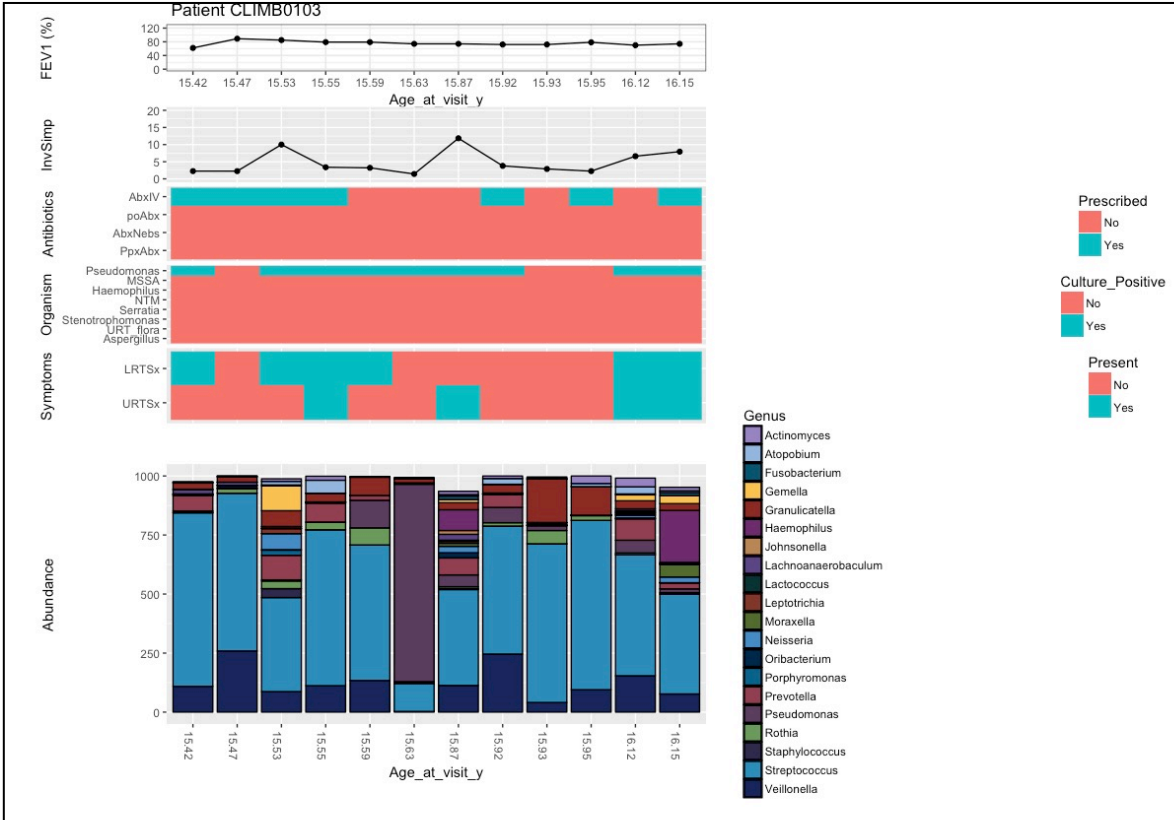
A6.9: CLIMB0030



A6.10: CLIMB0053

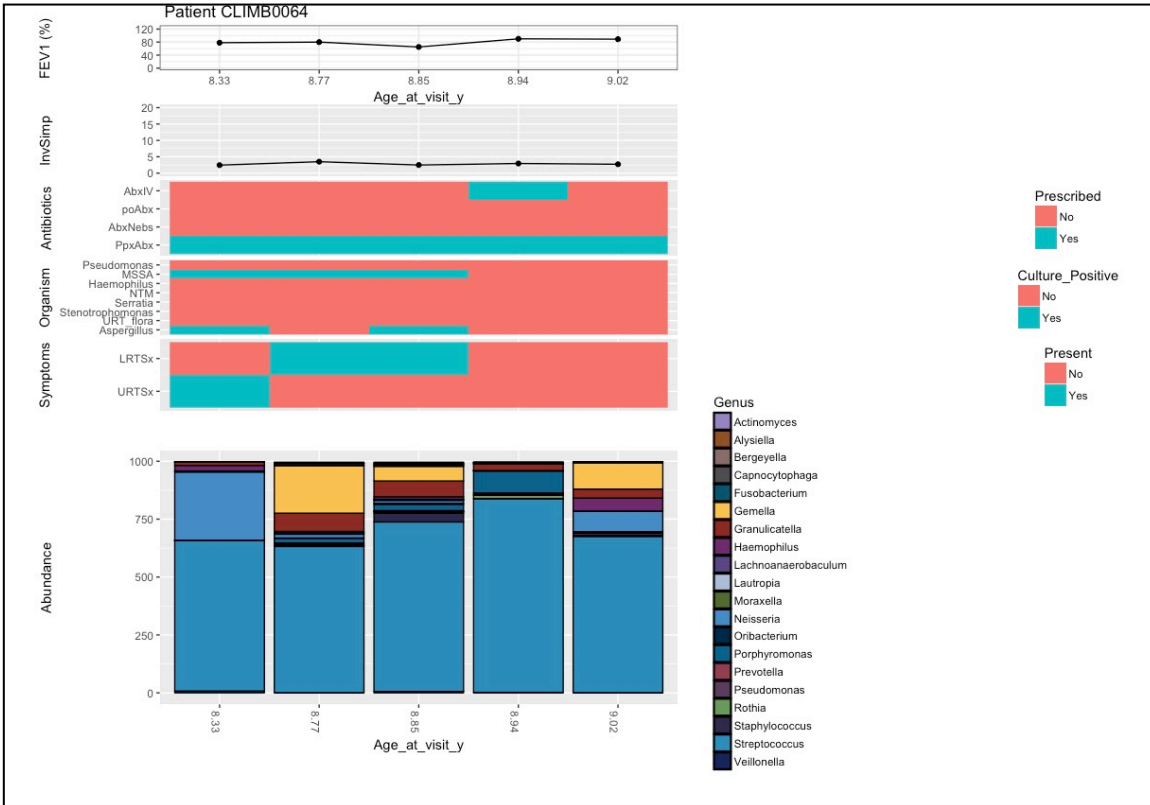


A6.11: CLIMB0103

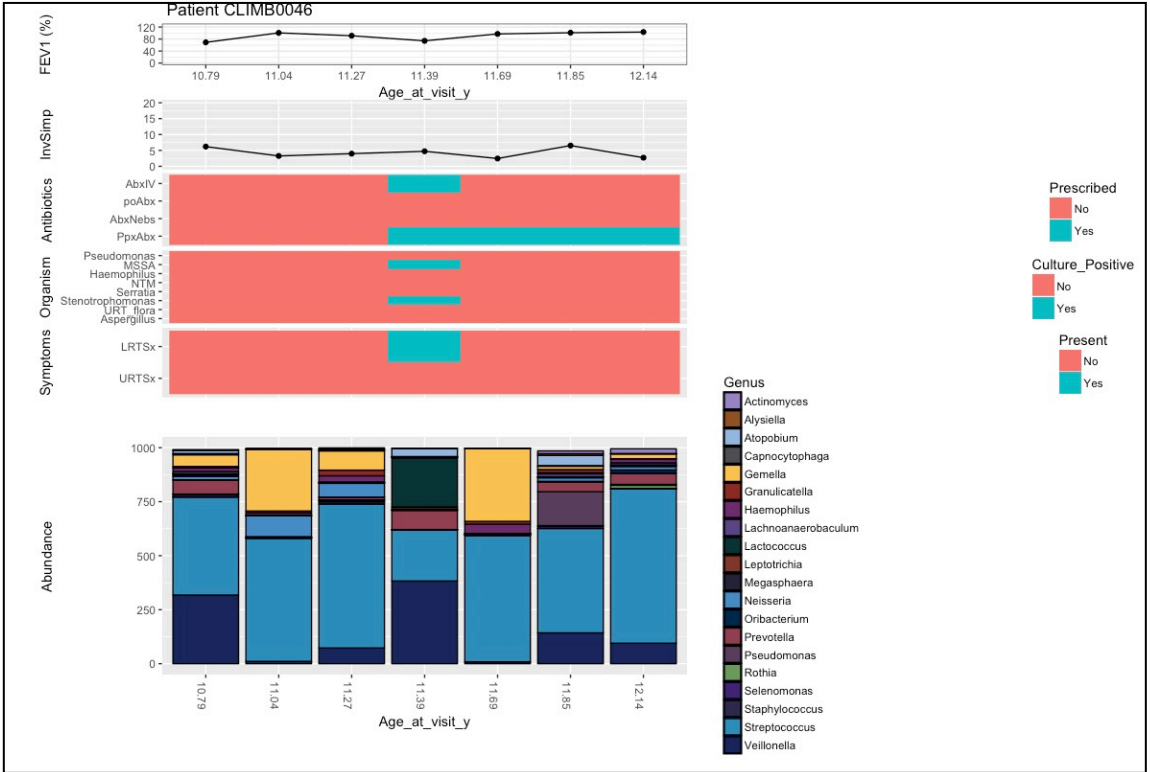


Methicillin sensitive *Staphylococcus aureus* (MMSA)

A6.12: CLIMB0064

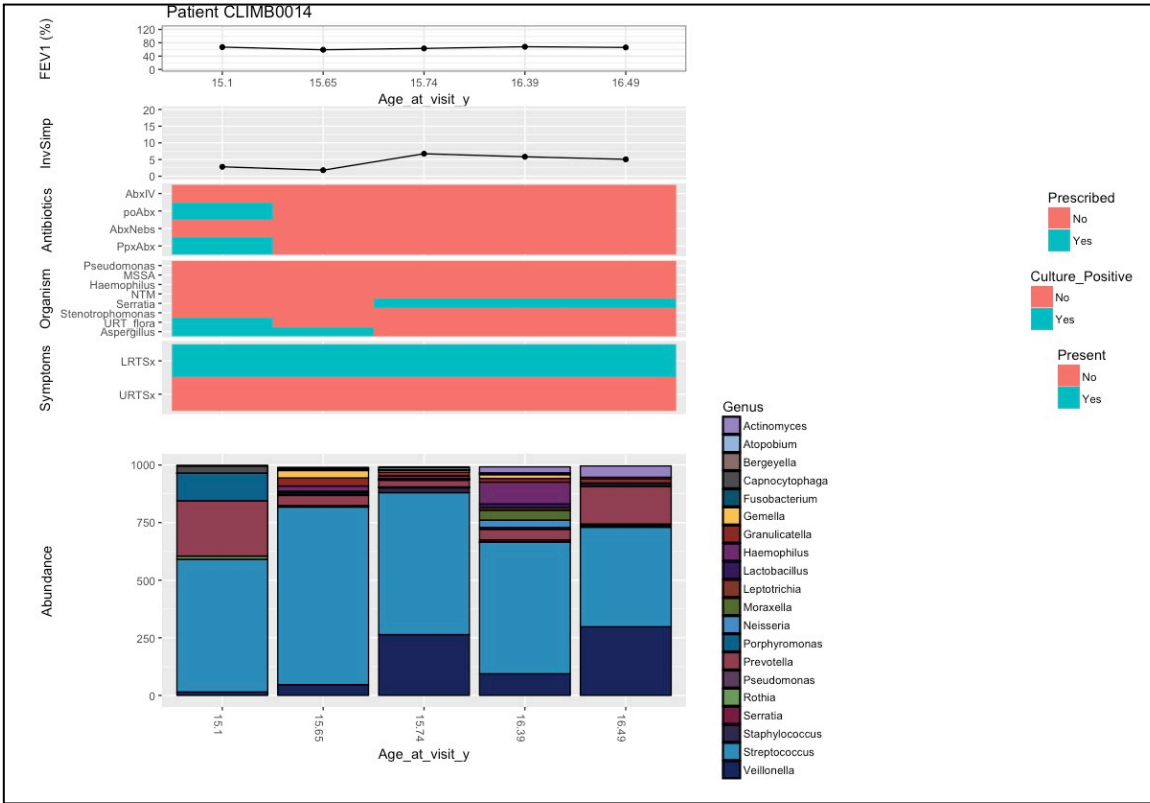


A6.13: CLIMB0046

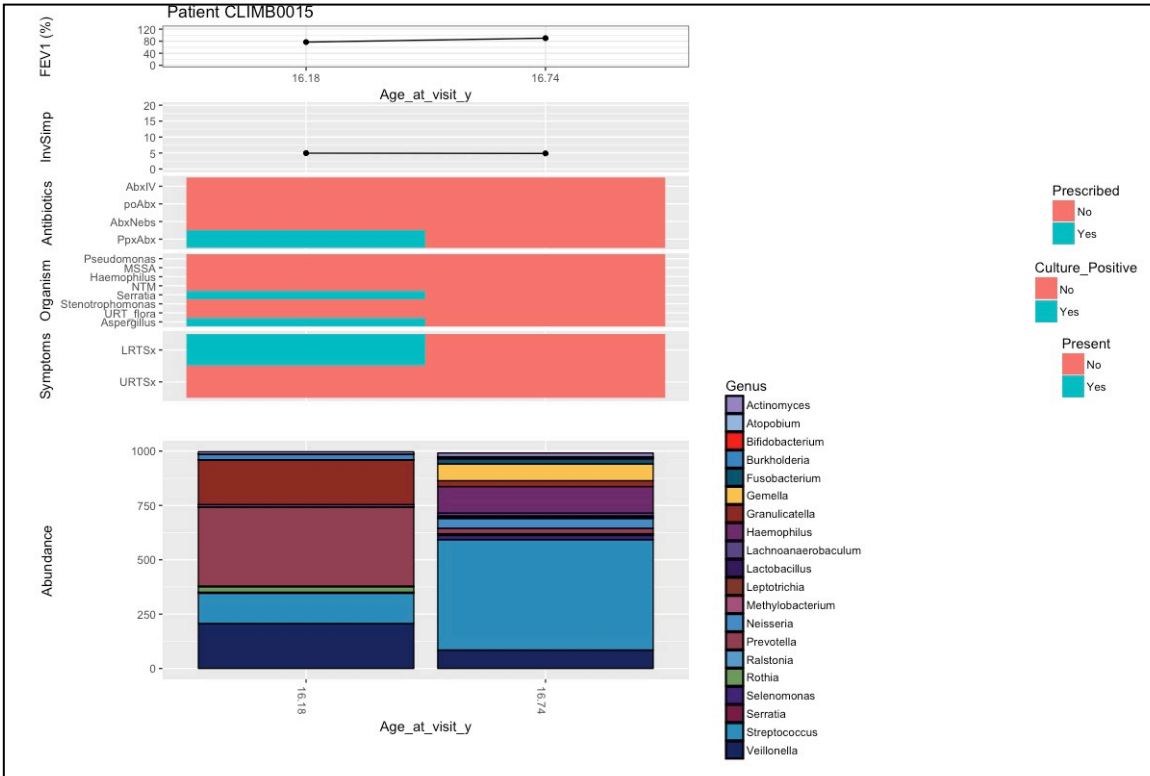


Serratia marcescens

A6.14: CLIMB0014

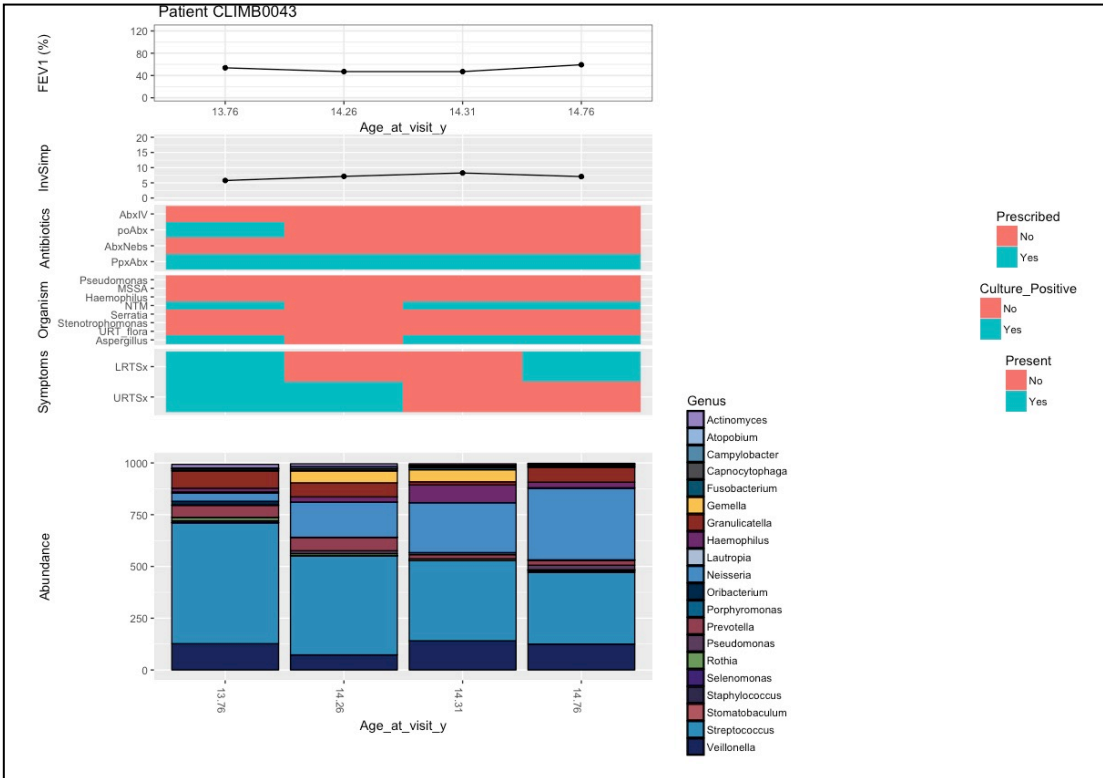


A6.15: CLIMB0015



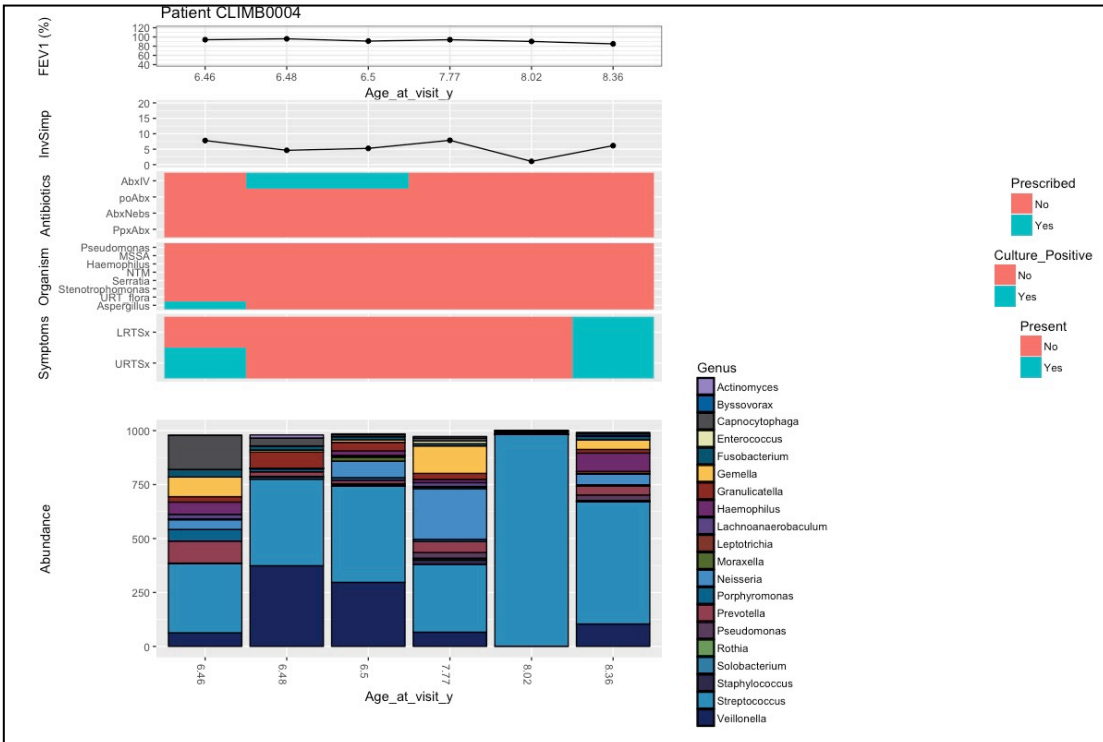
Non-tuberculous mycobacterium (NTM)

A6.16: CLIMB0043

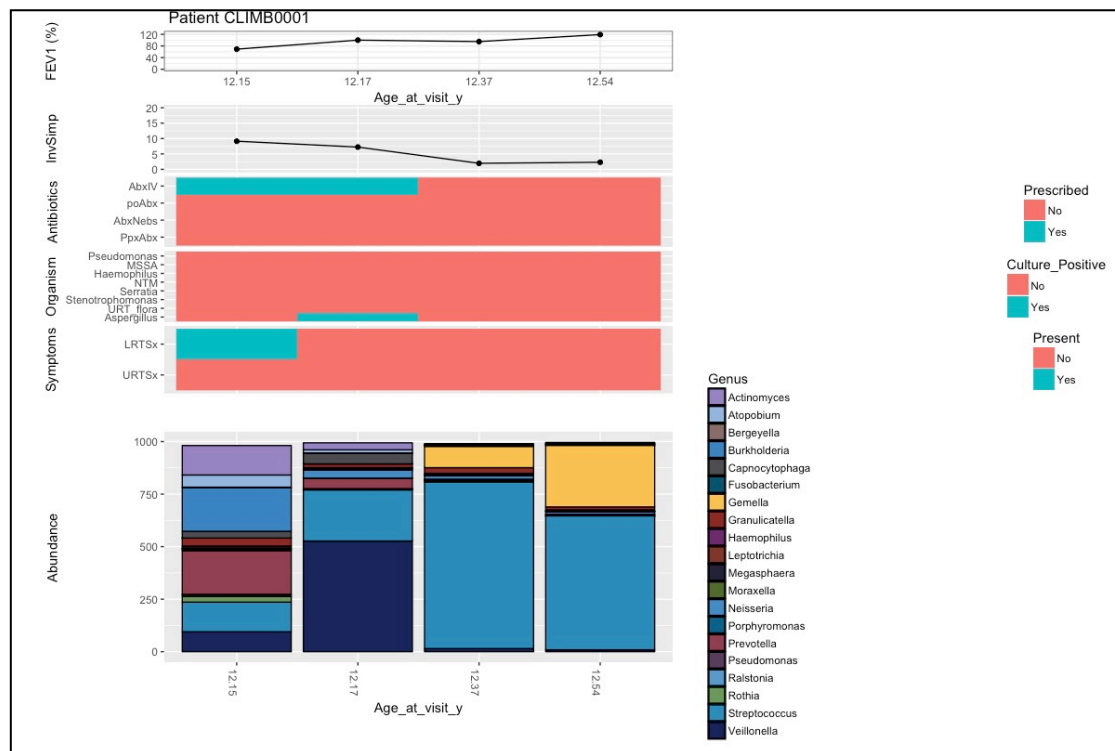


Aspergillus fumigatus

A6.17: CLIMB0004

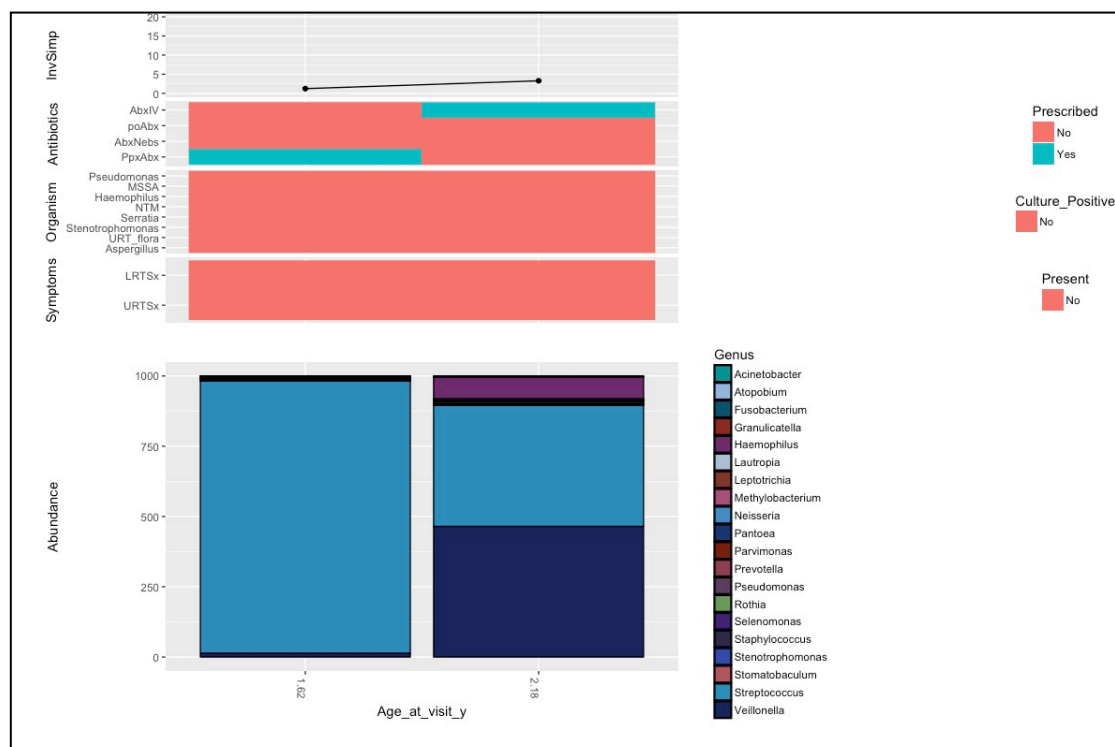


A6.18: CLIMB0001

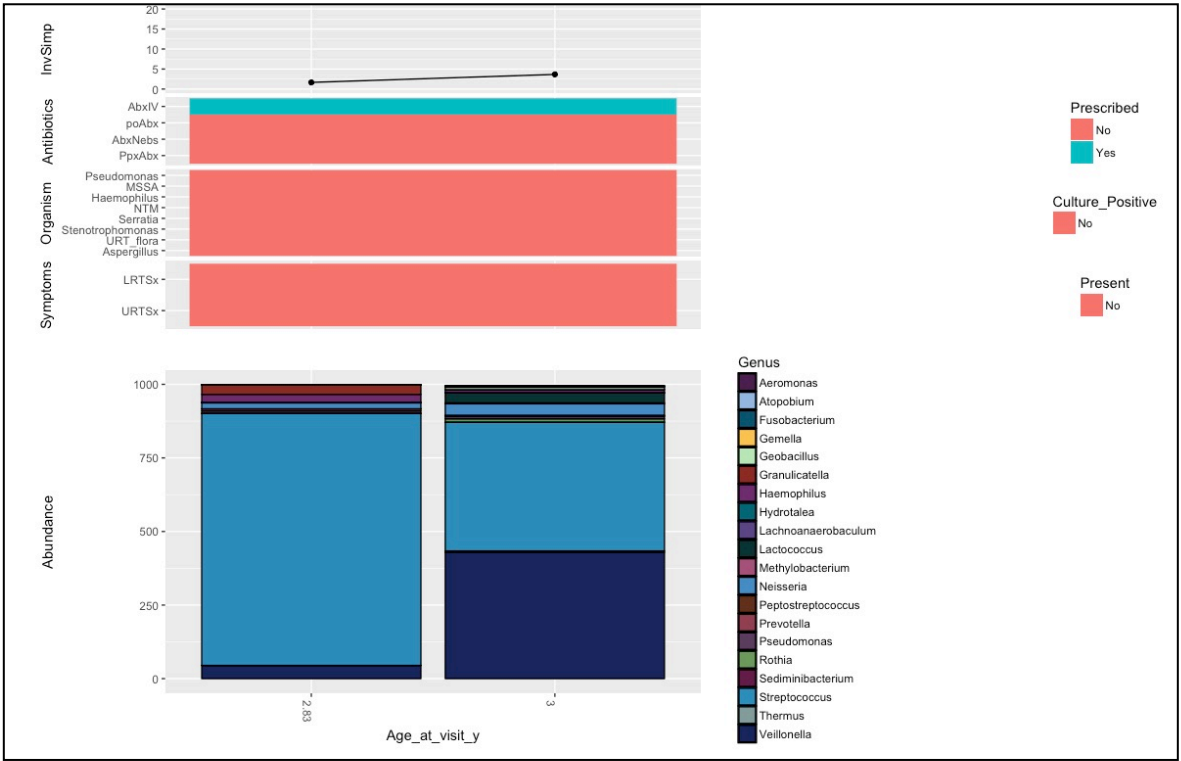


No growth

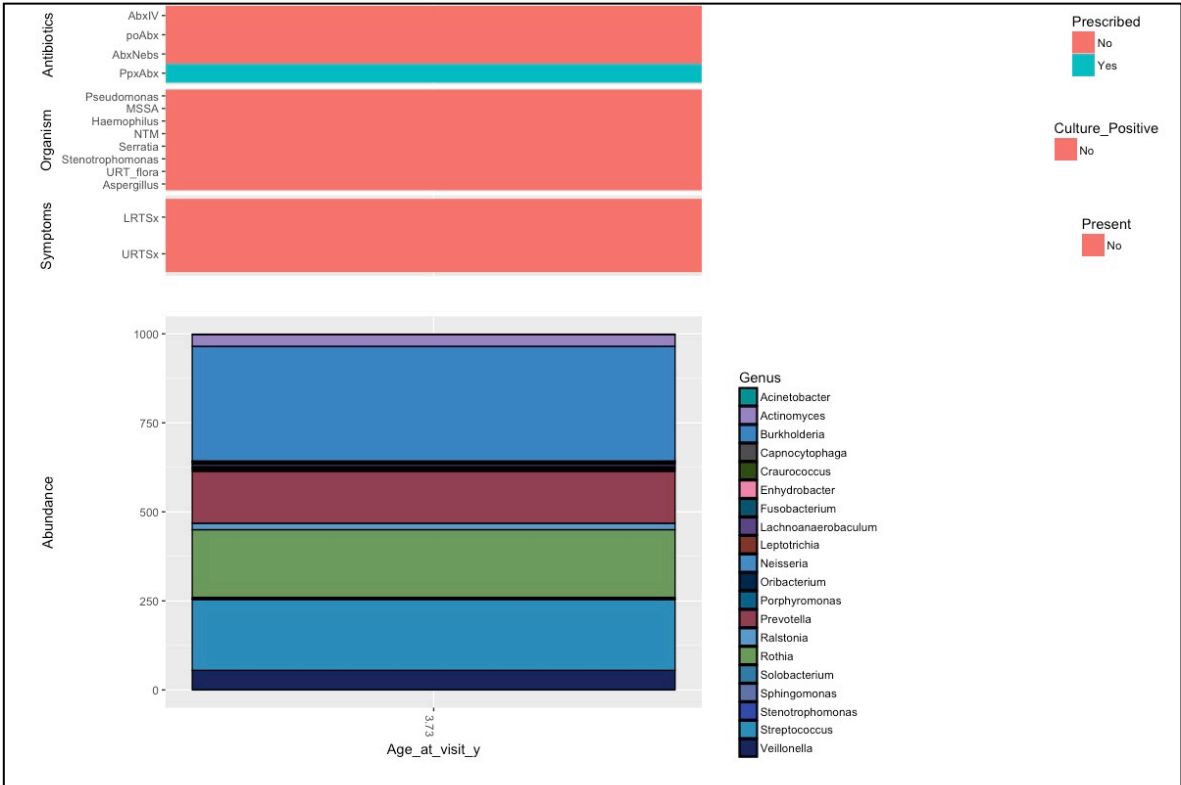
A6.19: CLIMB0076



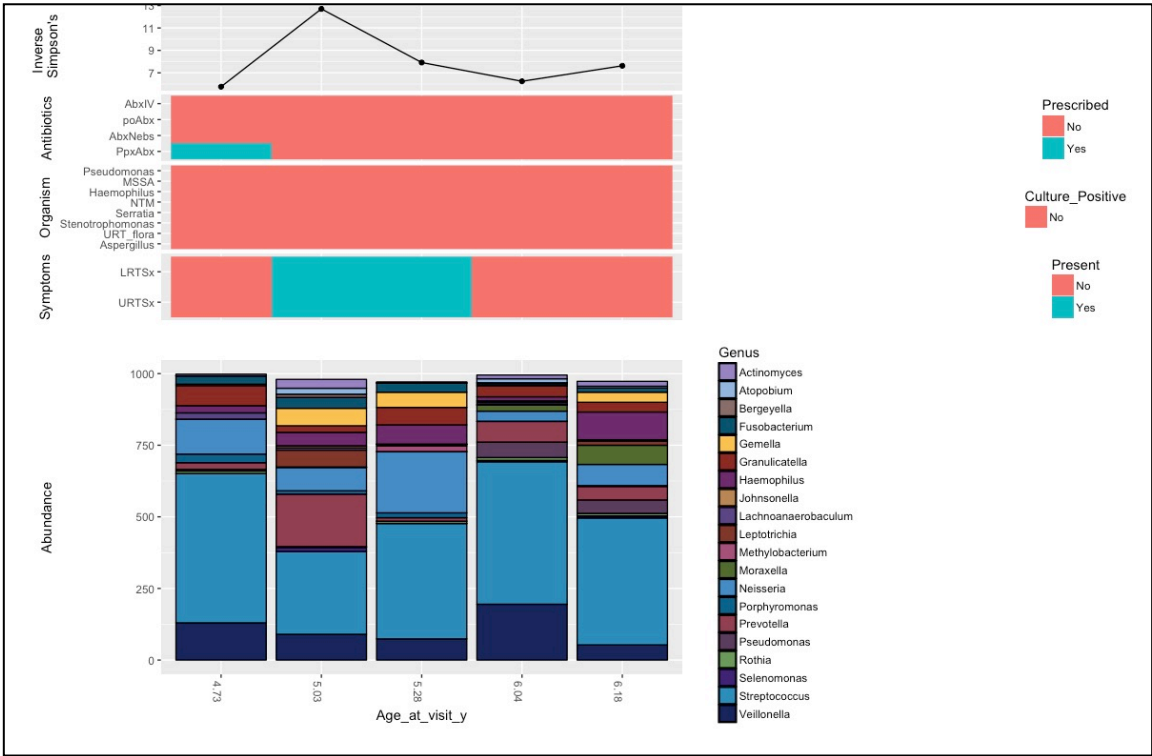
A6.20: CLIMB0077



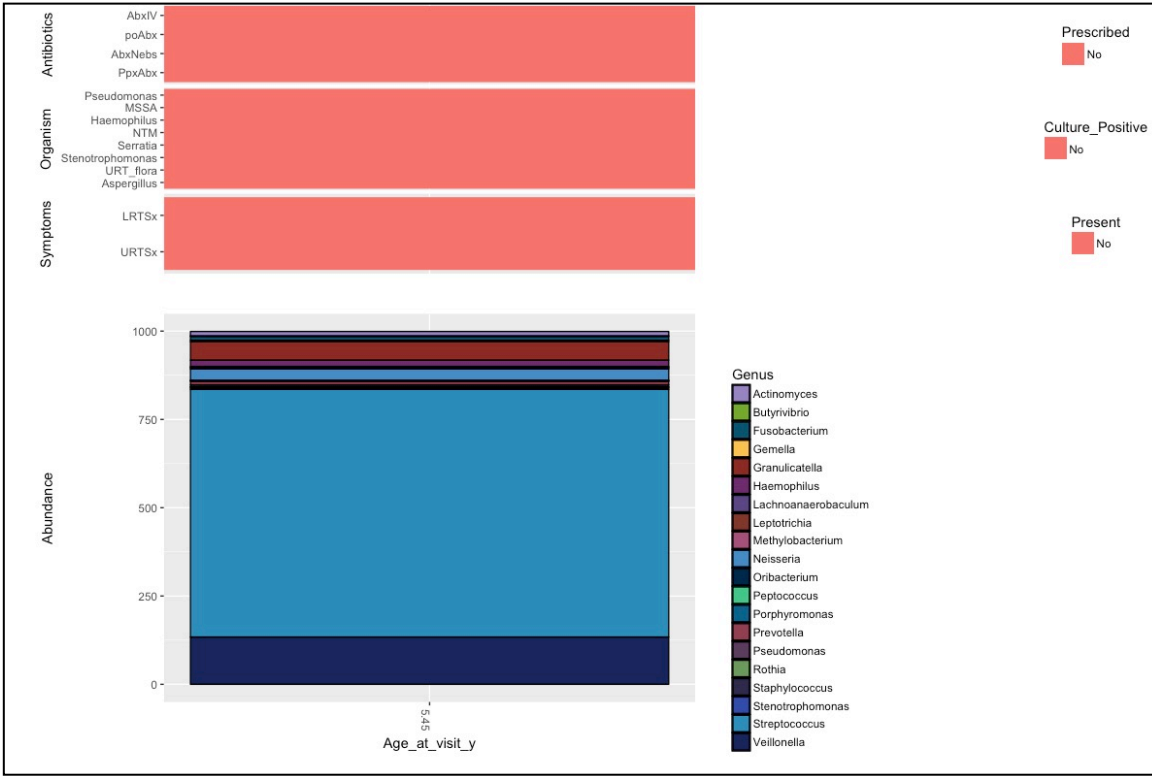
A6.21: CLIMB0060



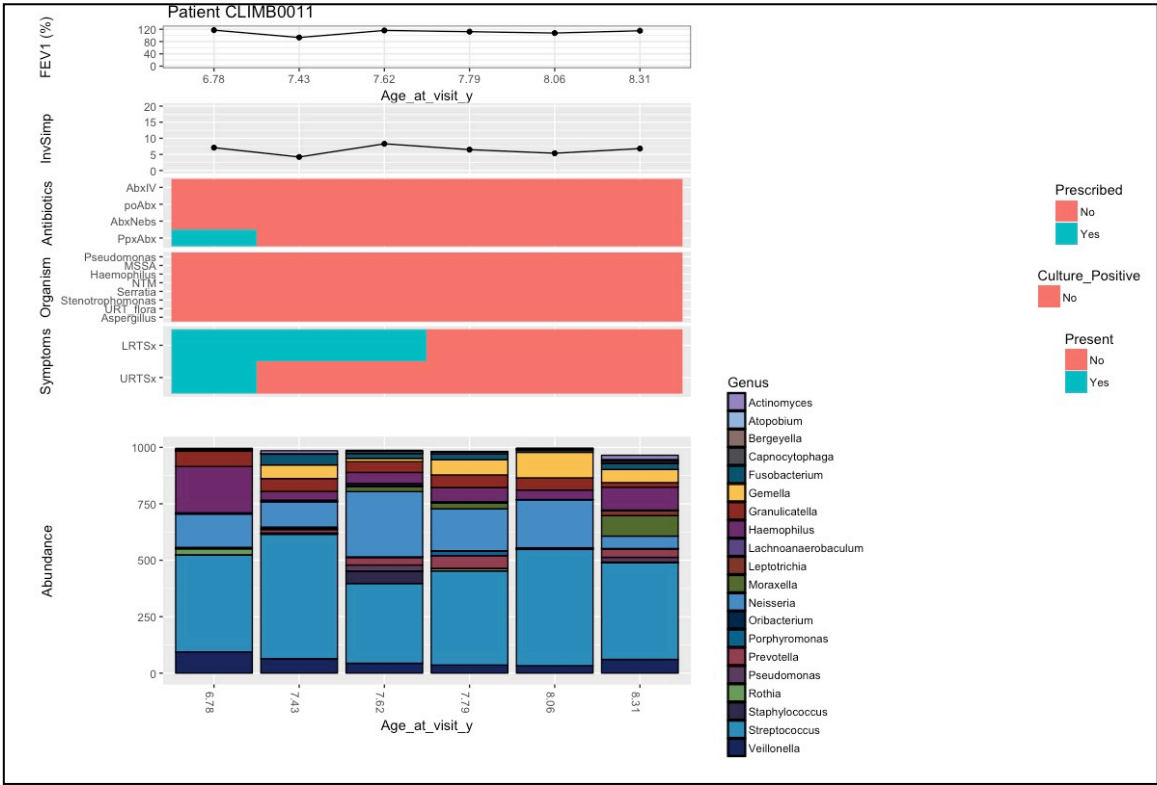
A6.22: CLIMB0034



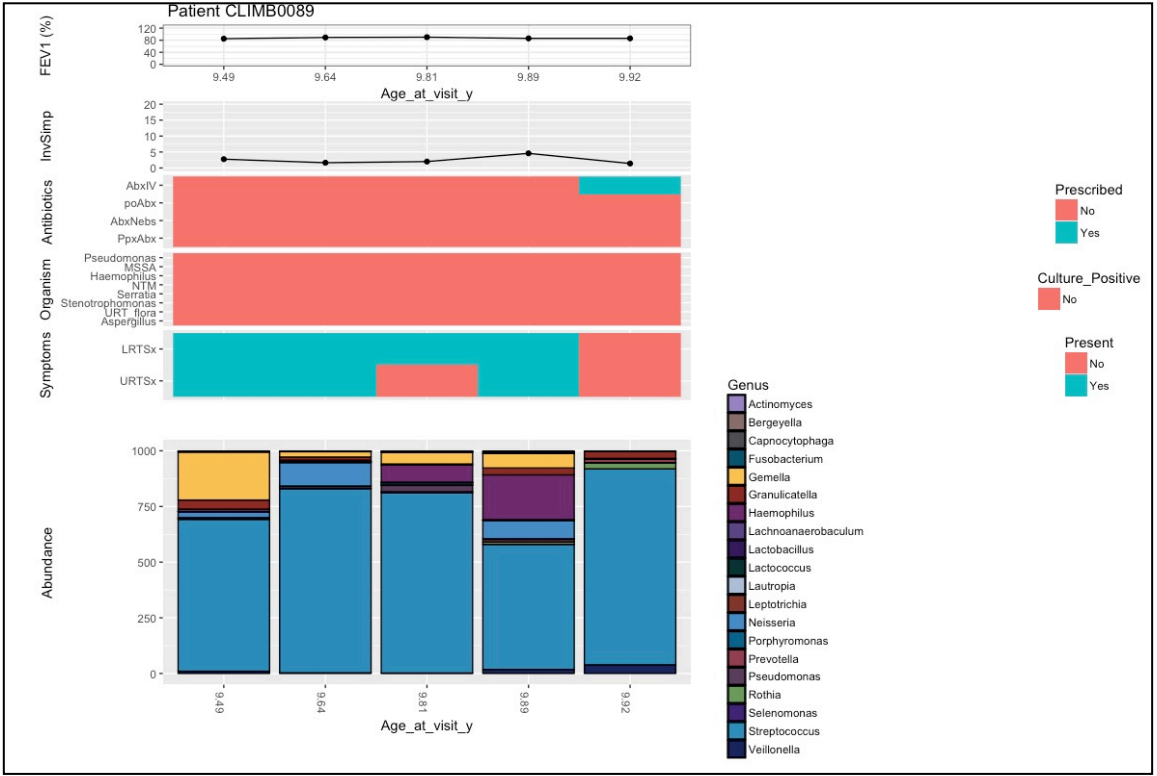
A6.23: CLIMB0093



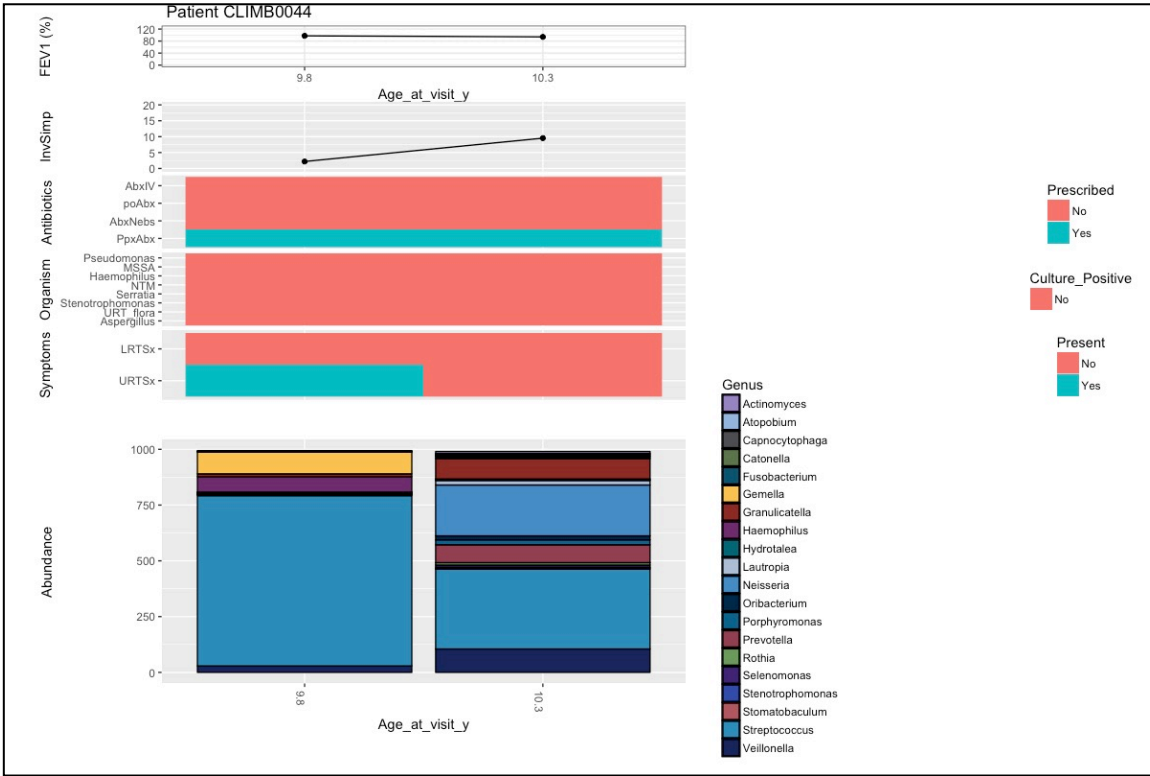
A6.24: CLIMB0011



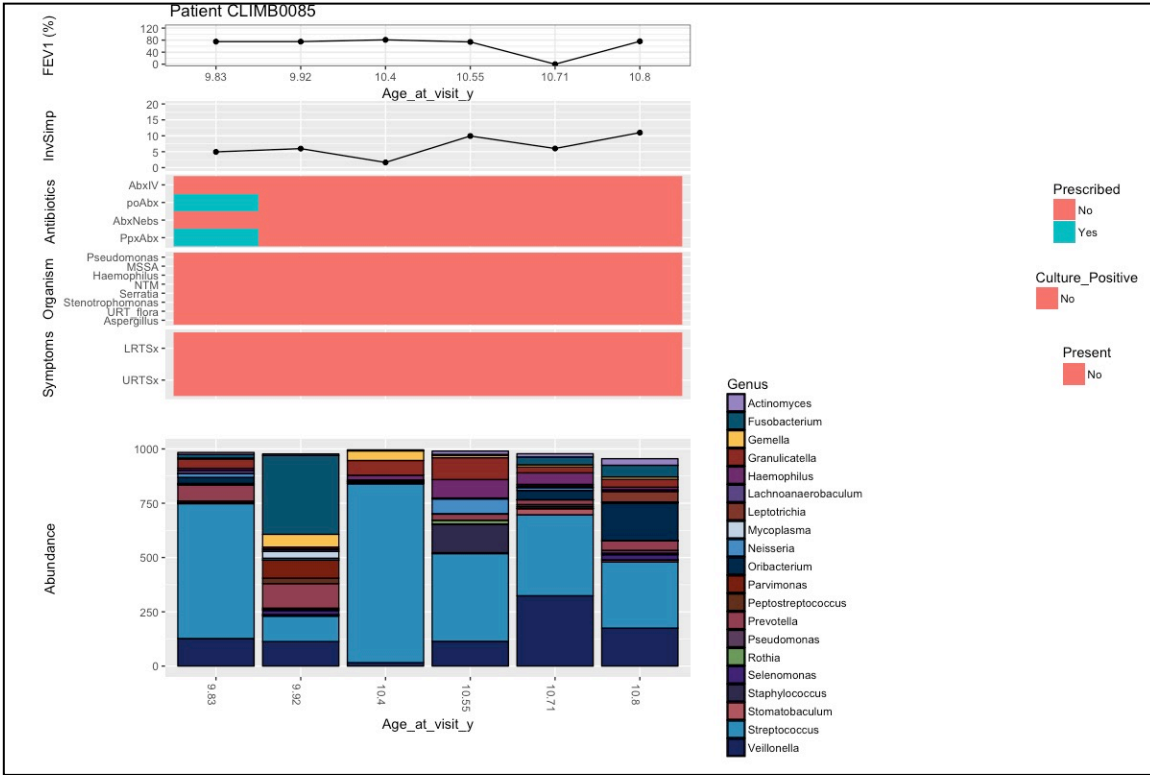
A6.25: CLIMB0089



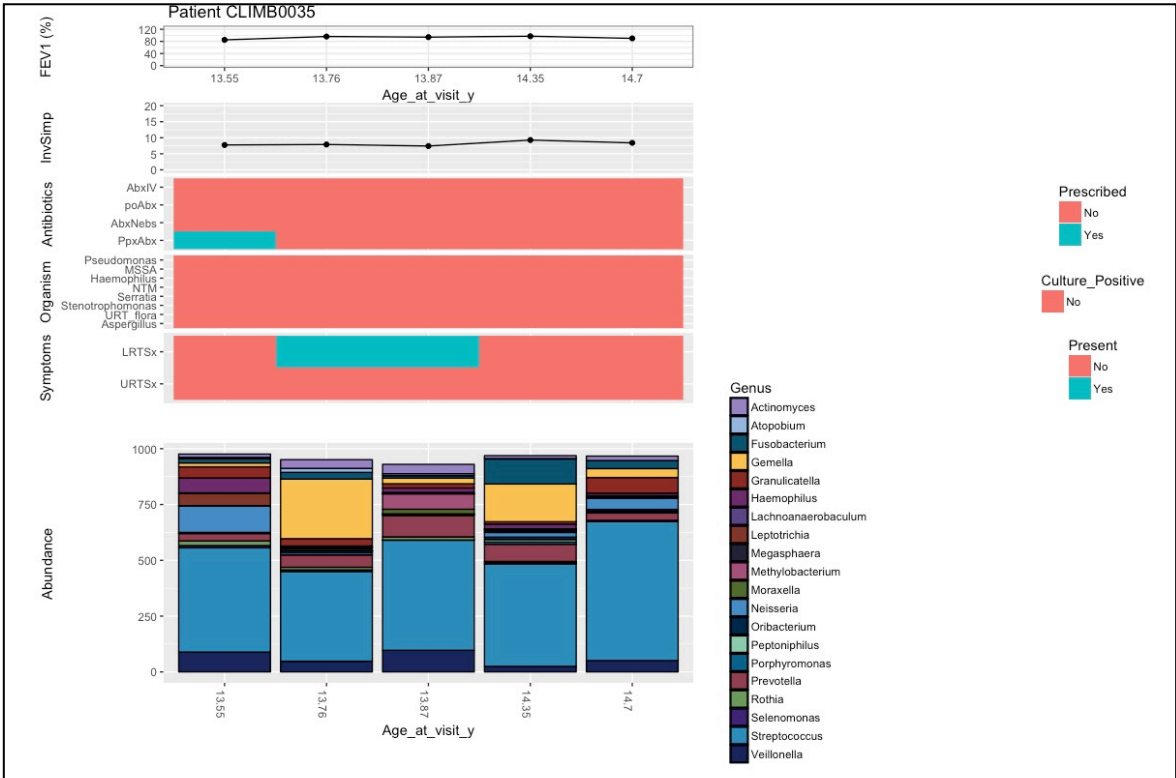
A6.26: CLIMB0044



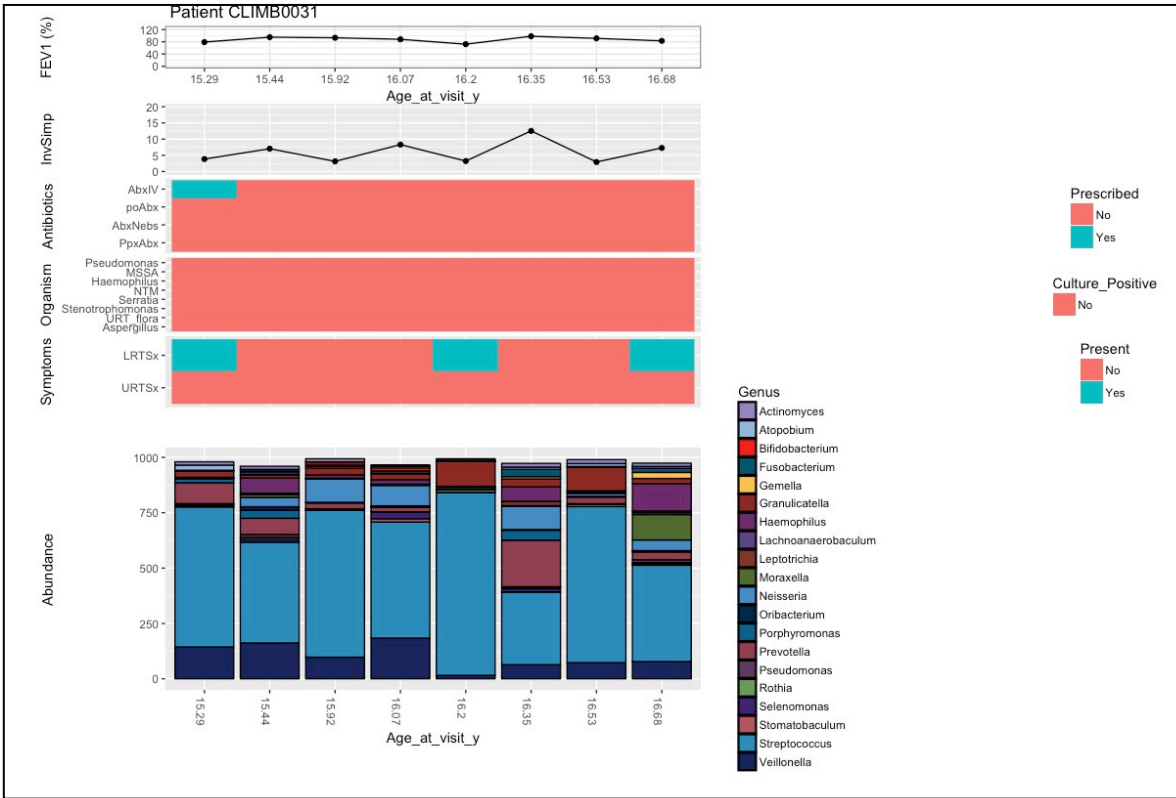
A6.27: CLIMB0085



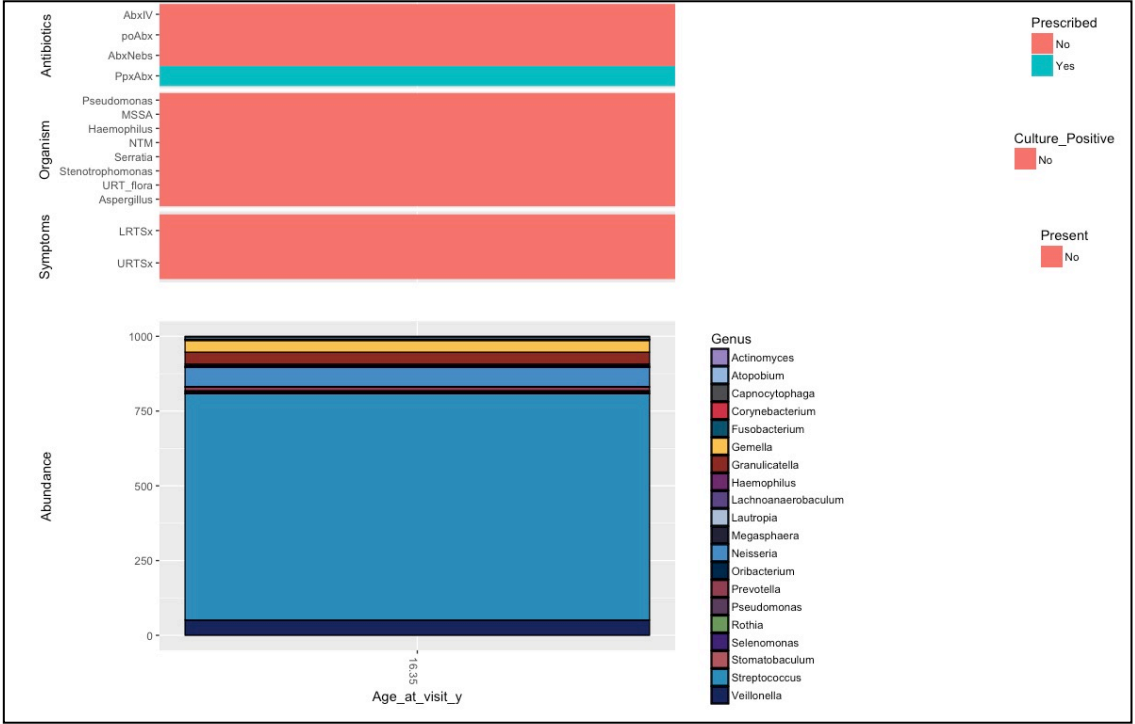
A6.28: CLIMB0035



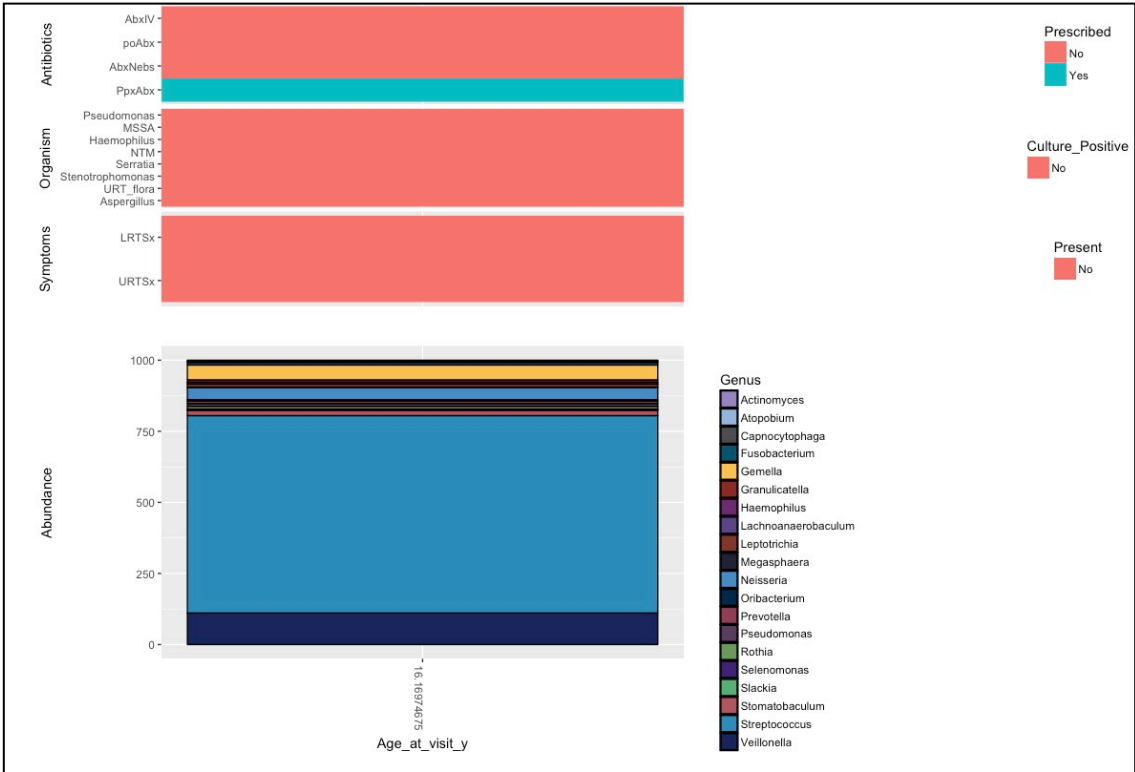
A6.29: CLIMB0031



A6.30: CLIMB0055



A6.31: CLIMB0054

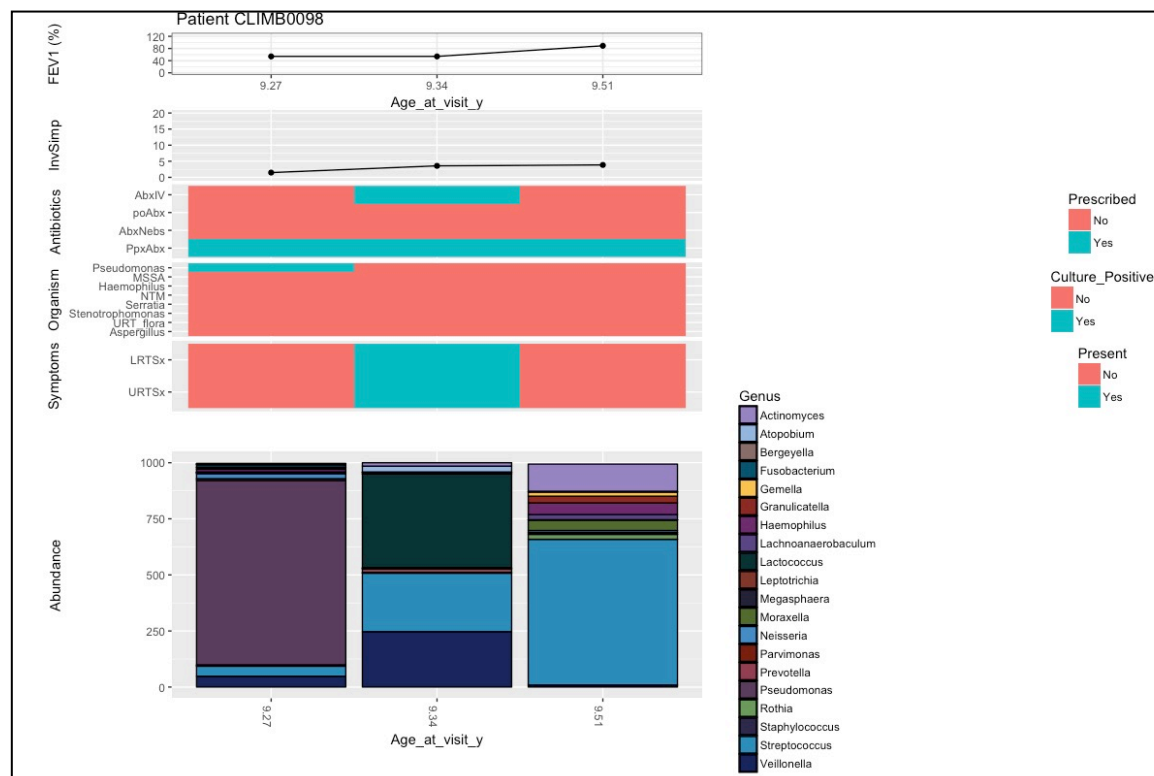


A7: E Appendix for use in conjunction with Chapter 5: Individual patient barplots for children with Primary Ciliary Dyskinesia (PCD)

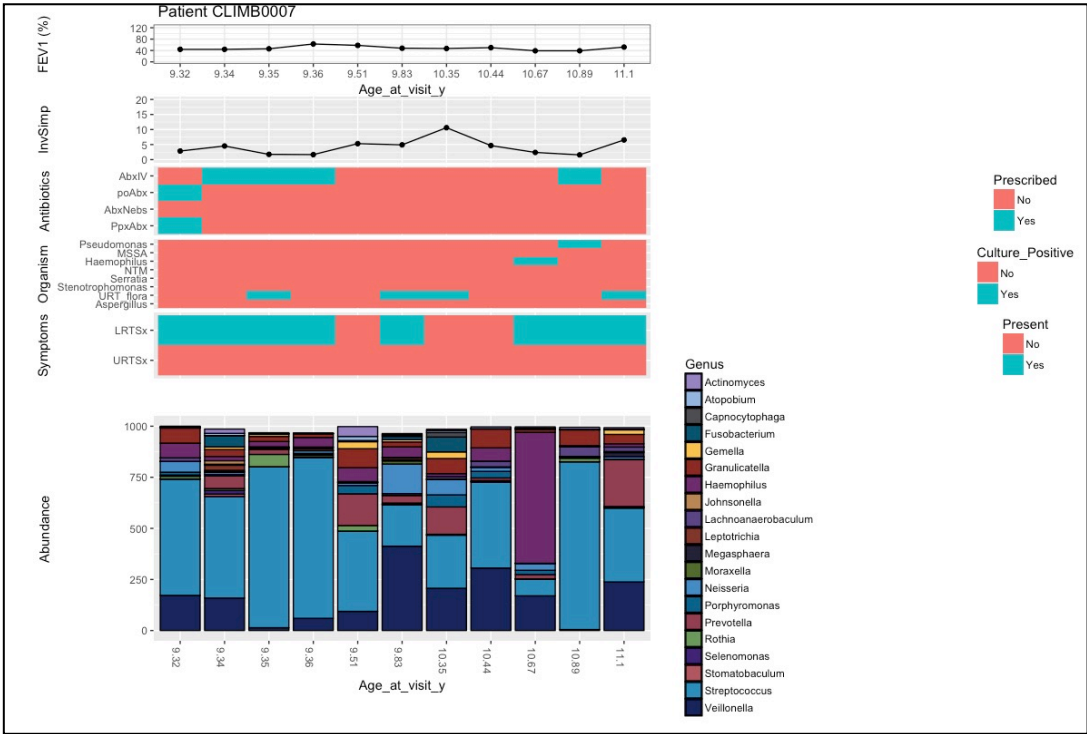
A7.1 – A7.30 illustrate changes in relative abundance of OTUs against spirometry measurements (FEV₁ % predicted), diversity changes (Inverse Simpson's) and clinical variables (antibiotic use, organisms grown on clinical microbiology and presence of upper and lower airway symptoms) for each PCD patient in the CLIMB study. Overall, no consistent changes in the microbiota were seen with clinical variables. Organised by: (a) bacterial growths on clinical microbiology and (b) increasing age.

P.aeruginosa

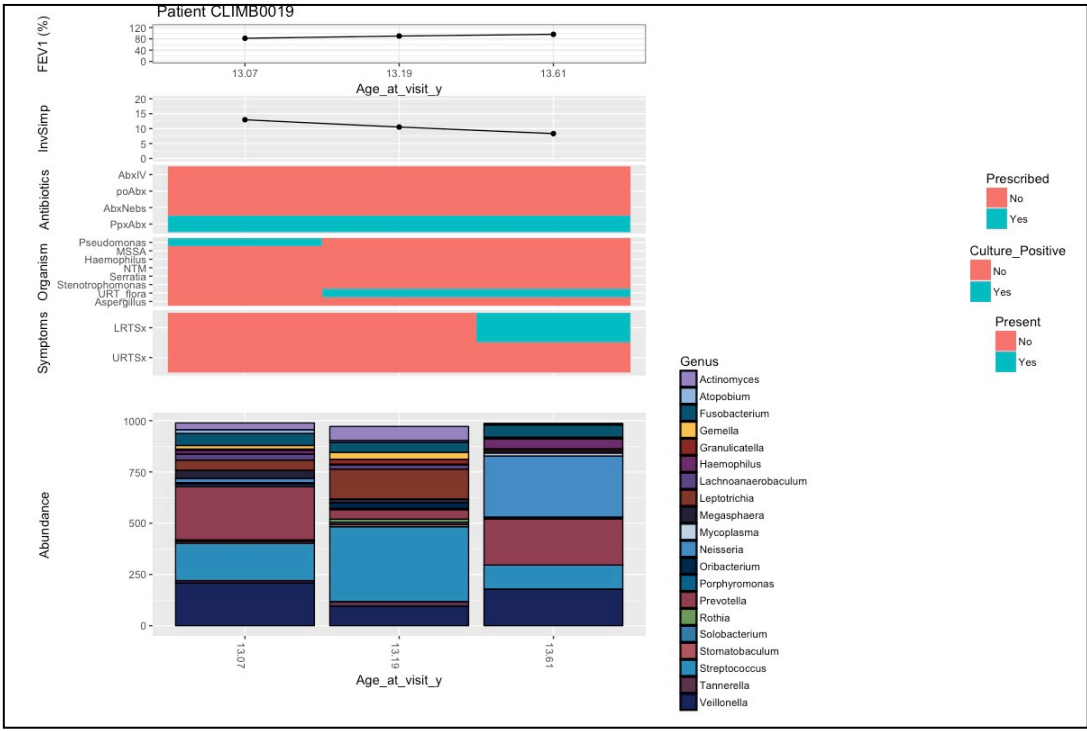
A7.1: CLIMB0098



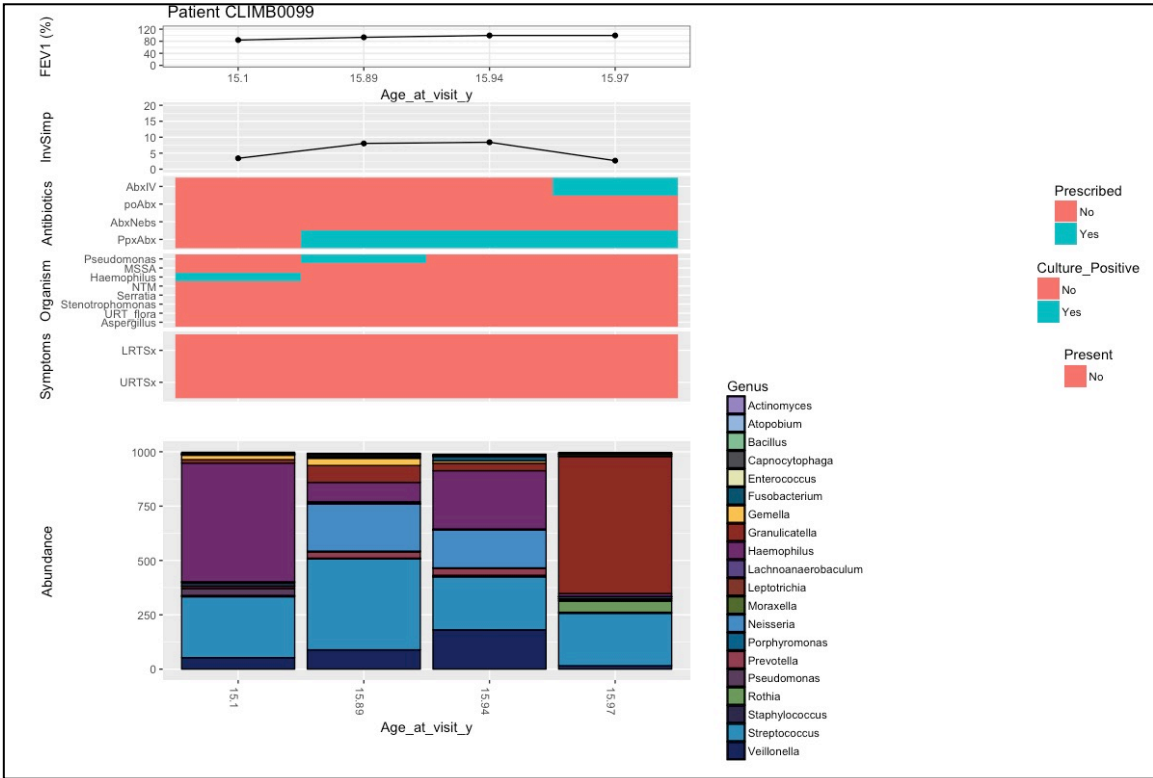
A7.2: CLIMB0007



A7.3: CLIMB0019

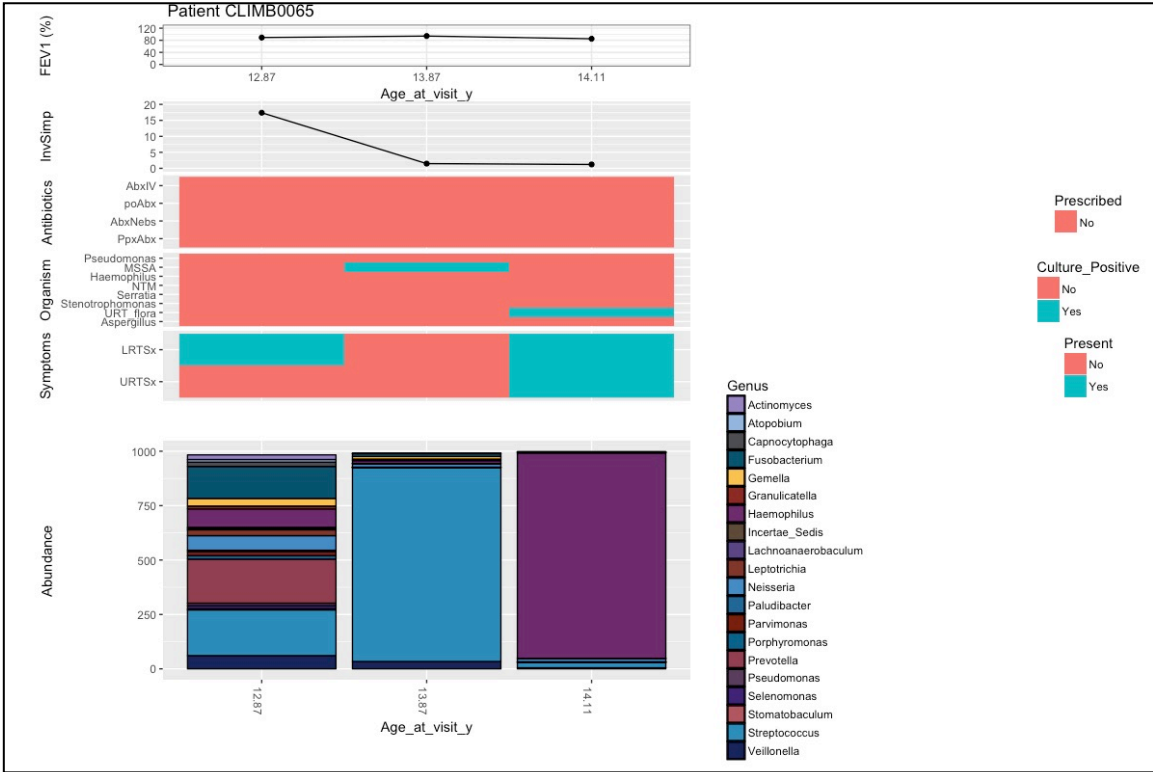


A7.4: CLIMB0099

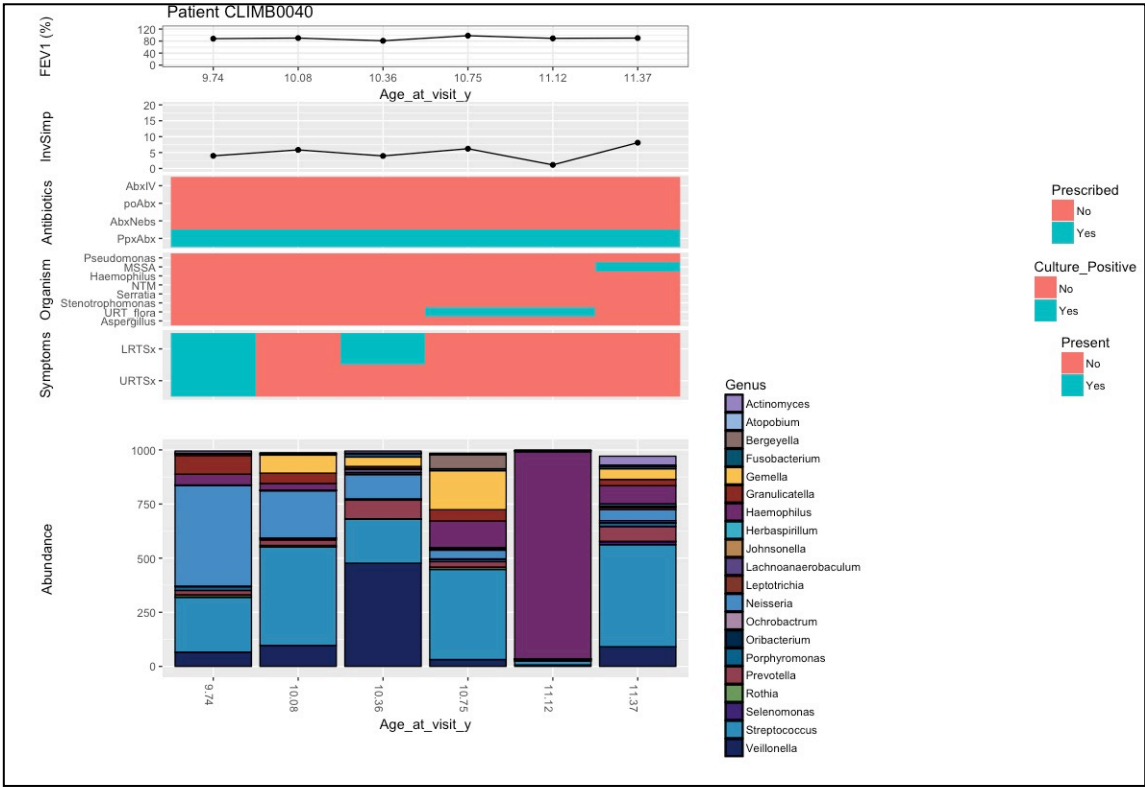


MSSA

A7.5: CLIMB0065

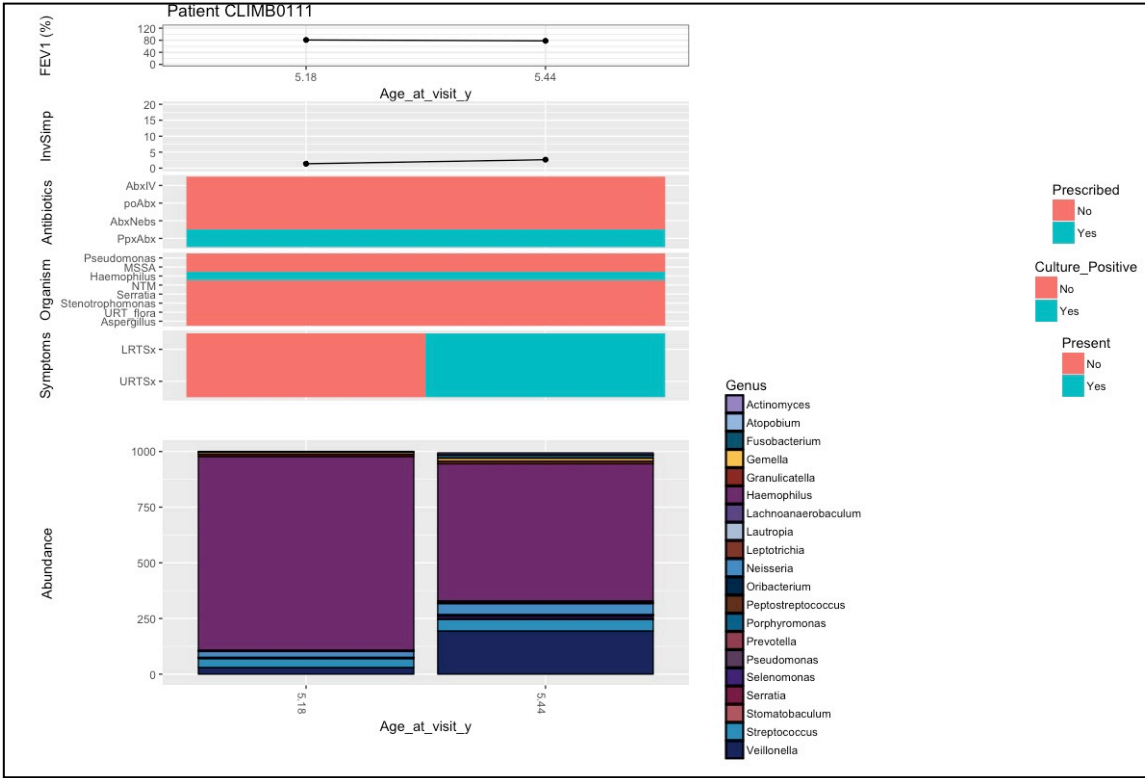


A7.6: CLIMB0040

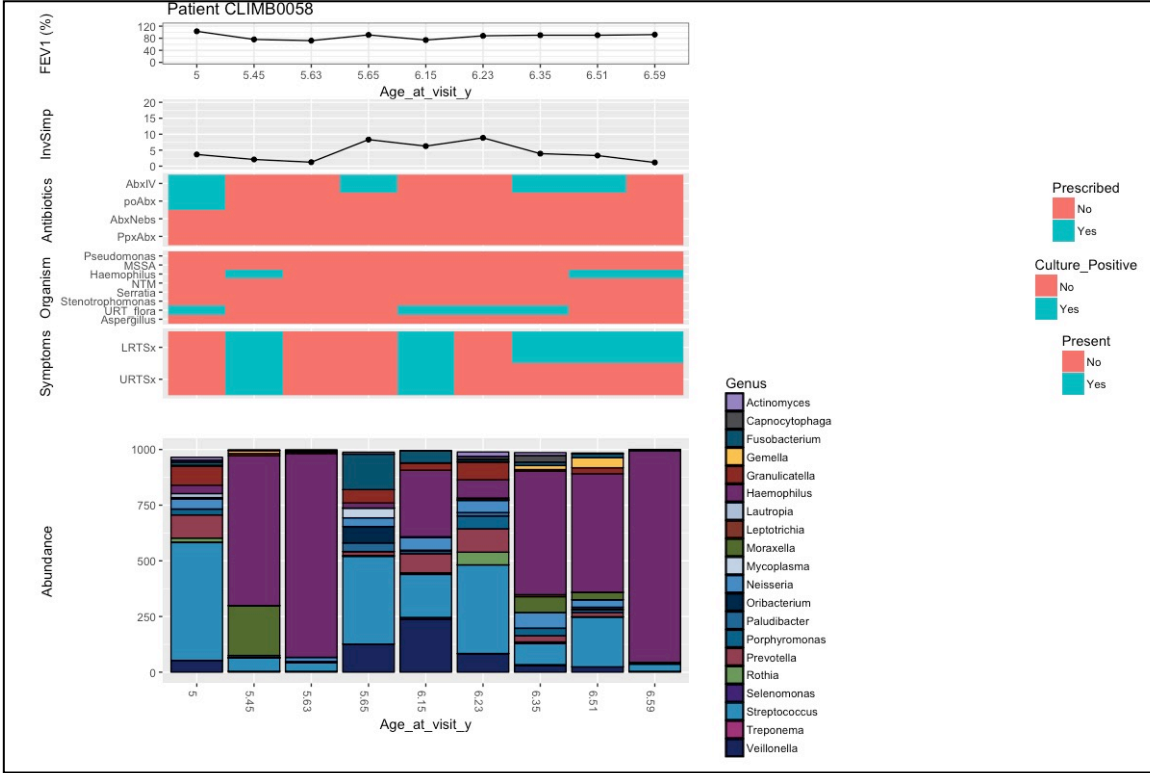


Haemophilus influenzae

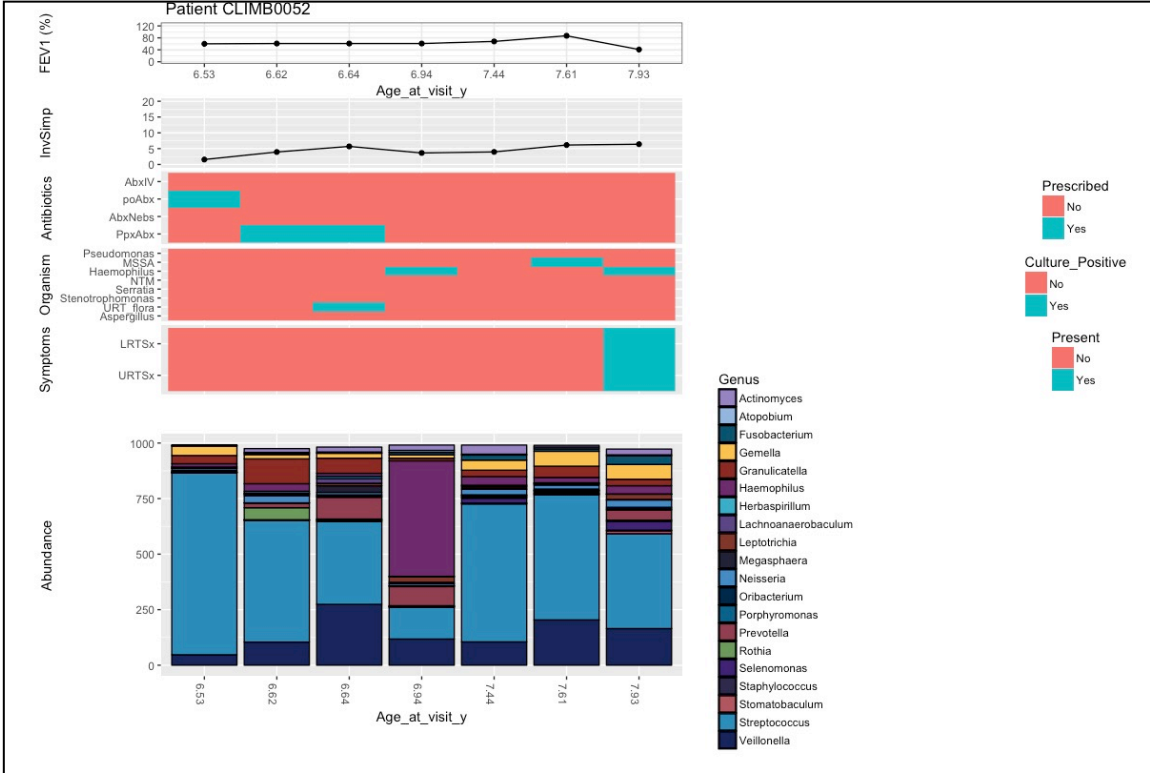
A7.7: CLIMB0111



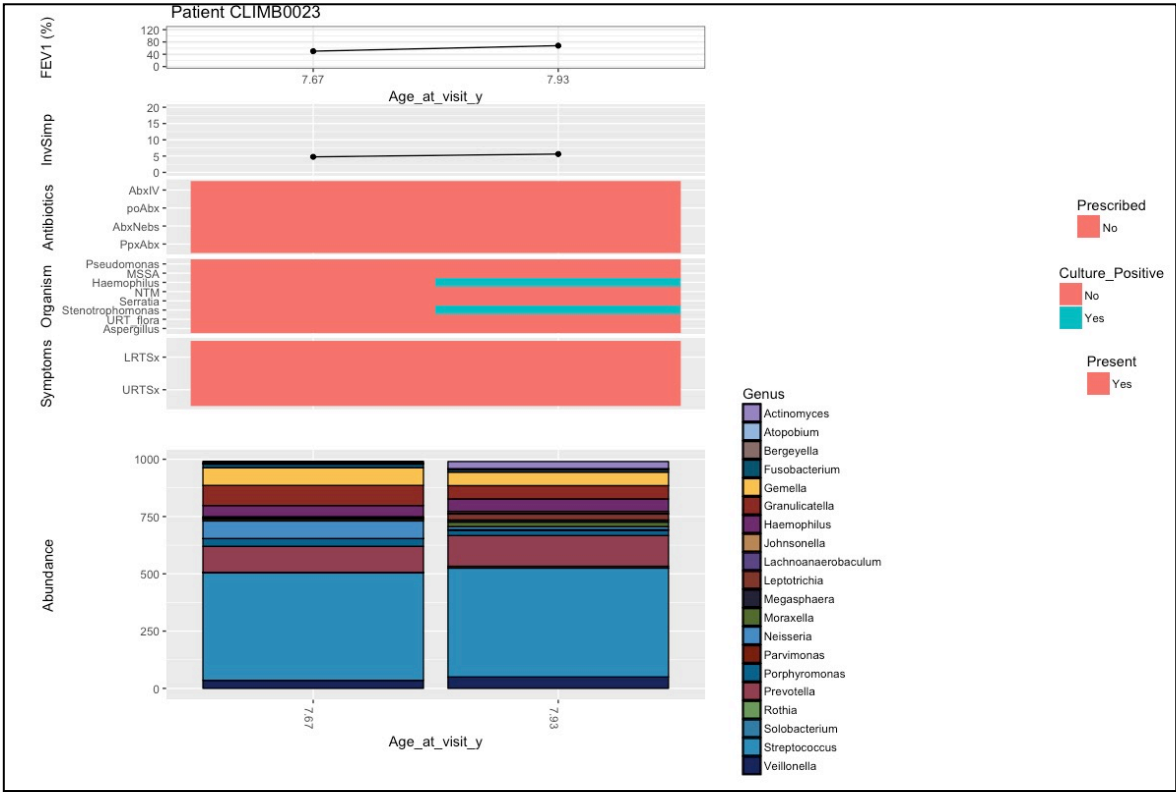
A7.8: CLIMB0058



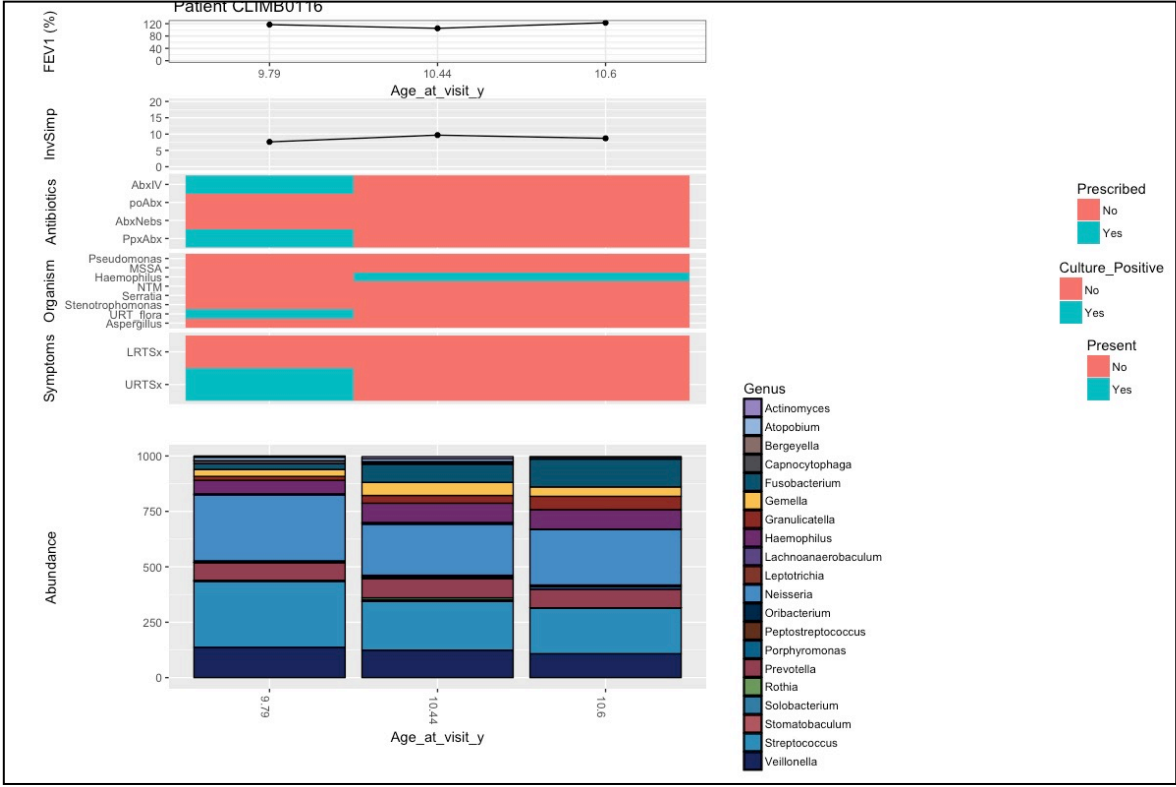
A7.9: CLIMB0052



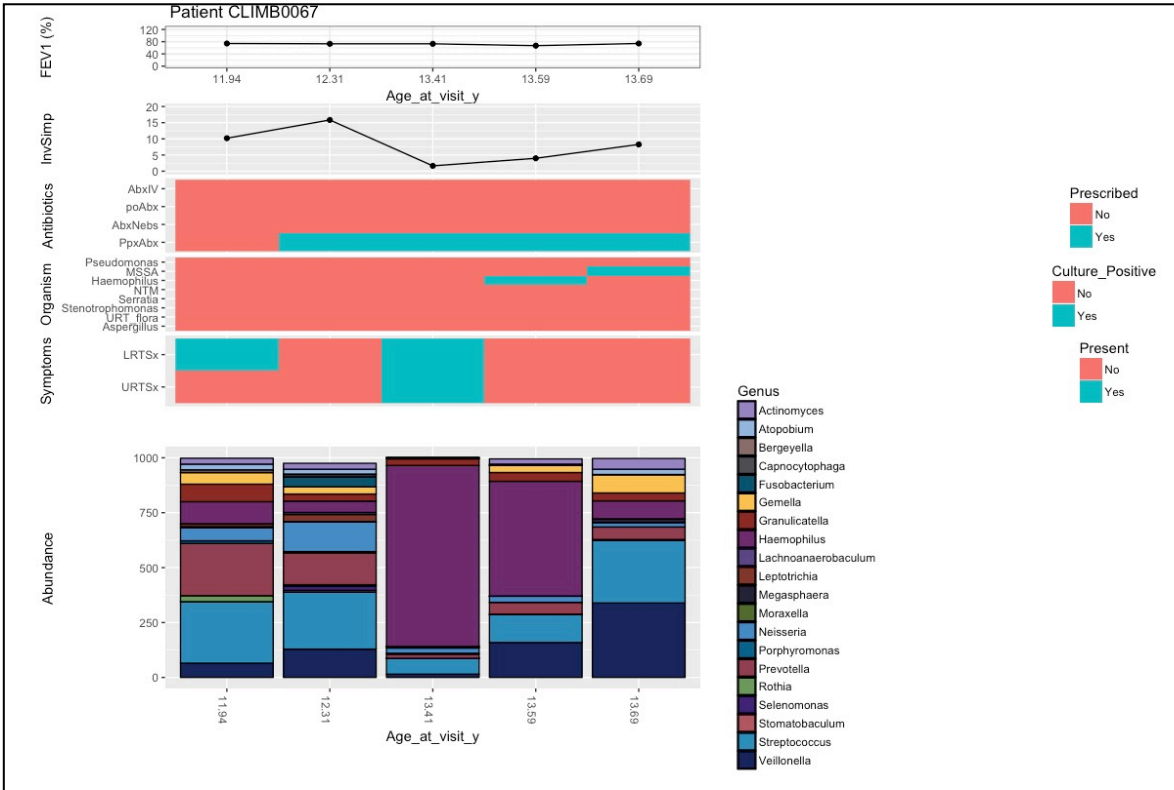
A7.10: CLIMB0023



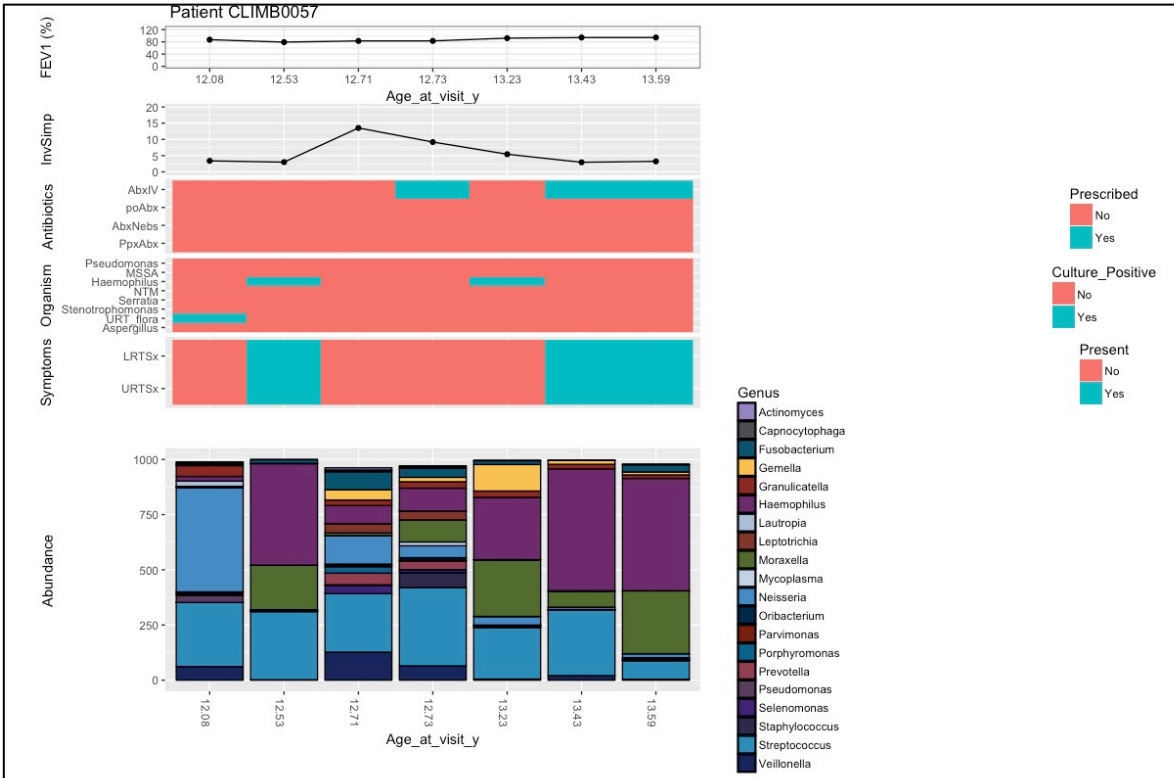
A7.11: CLIMB0116



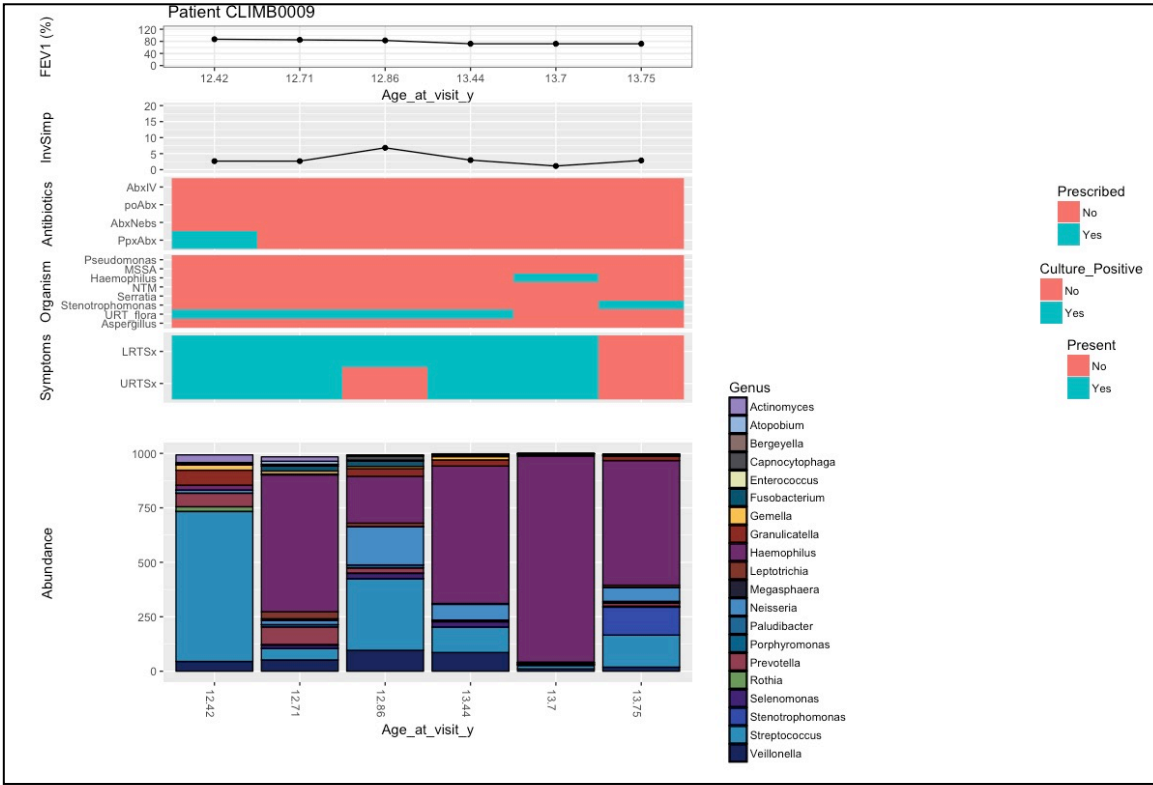
A7.12: CLIMB0067



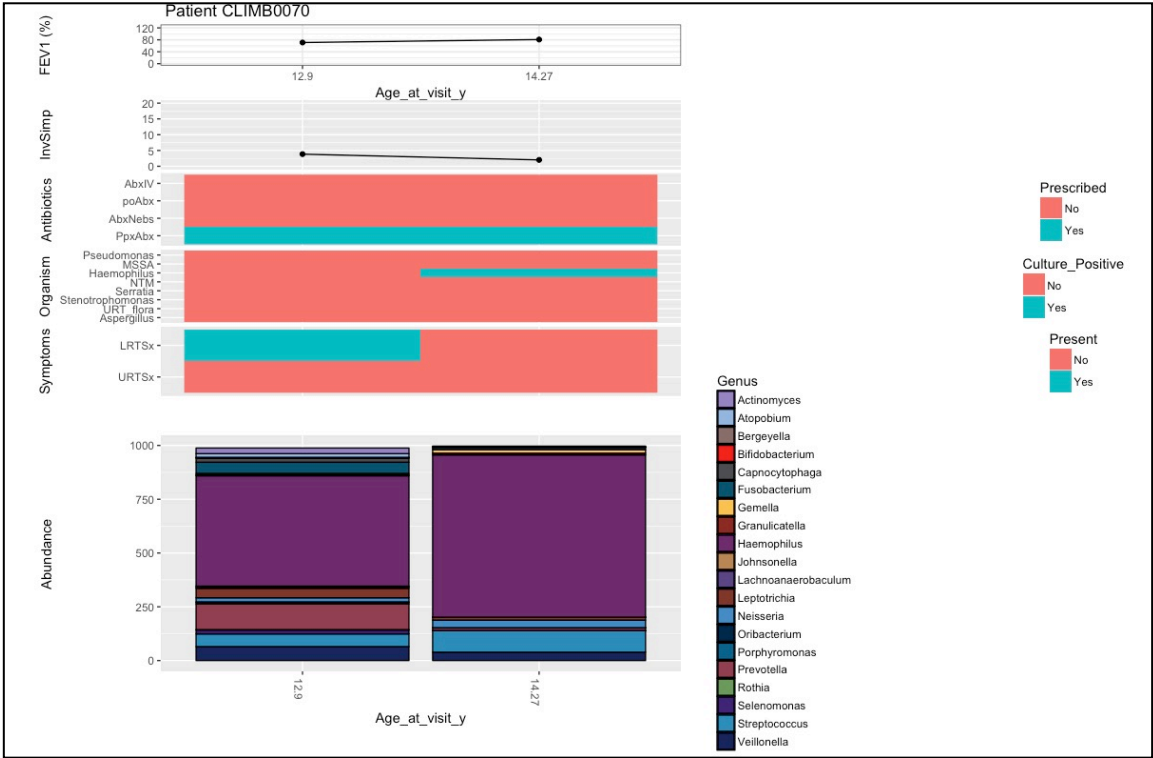
A7.13: CLIMB0057



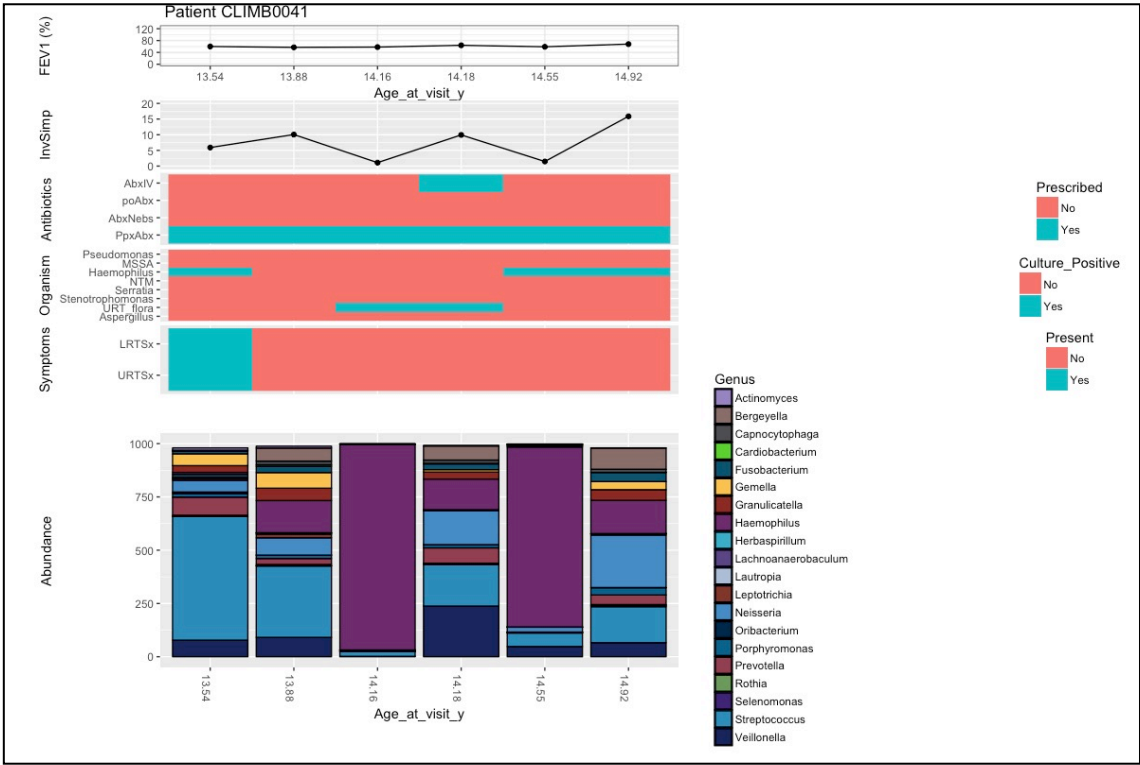
A7.14: CLIMB0009



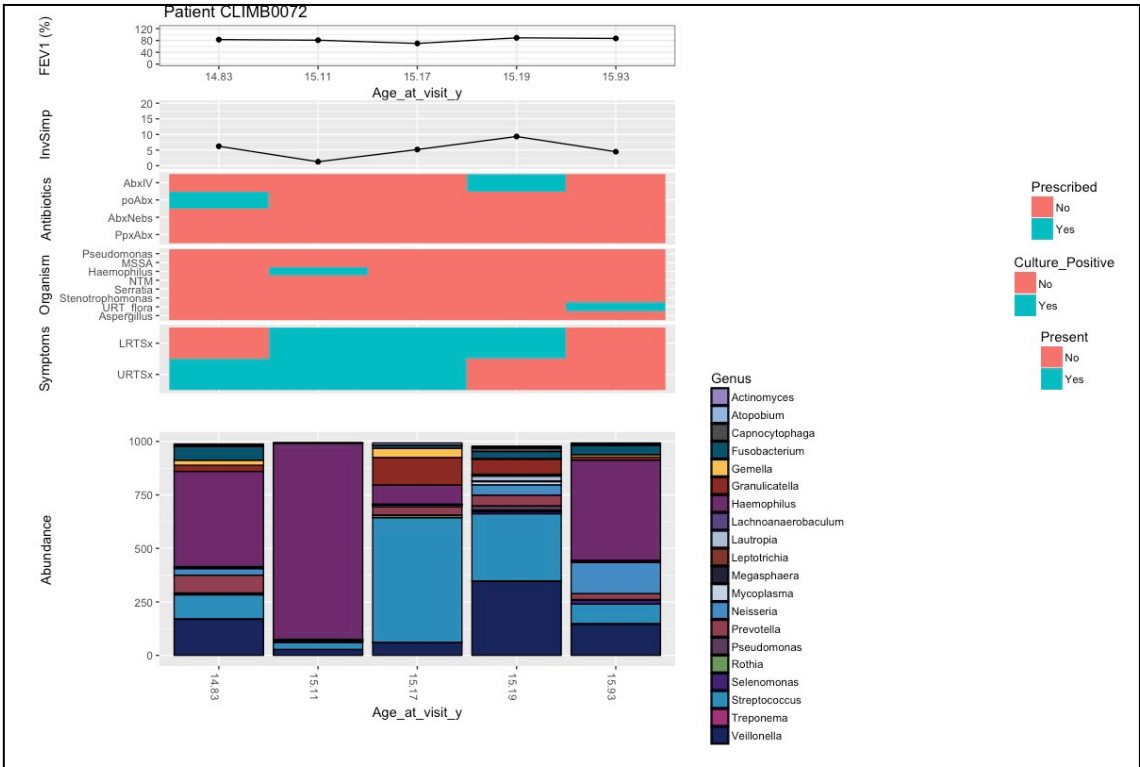
A7.15: CLIMB0070



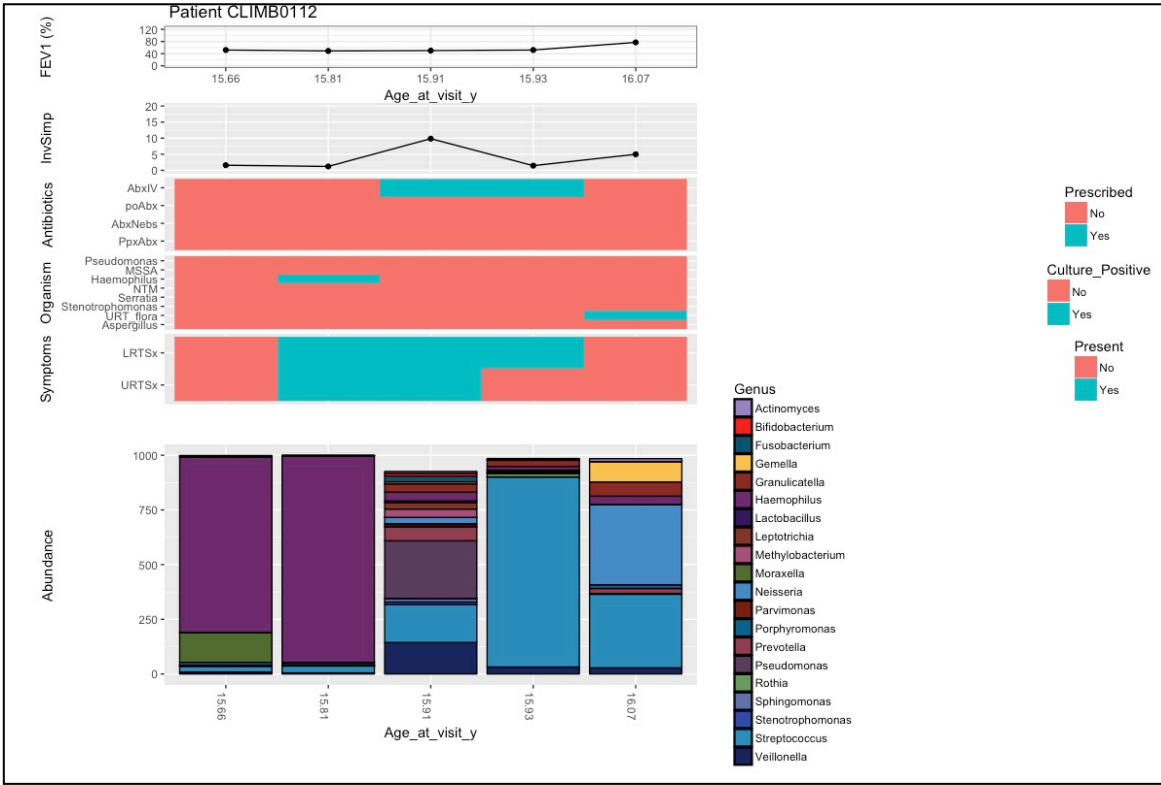
A7.16: CLIMB0041



A7.17: CLIMB0072

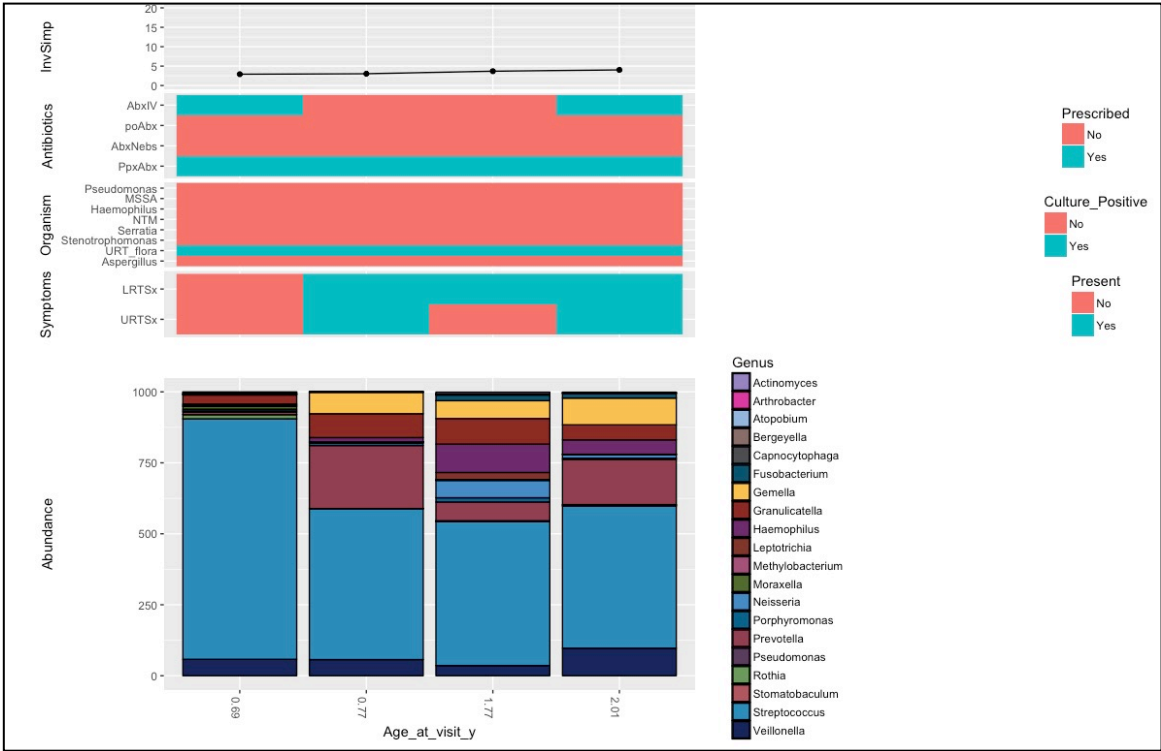


A7.18: CLIMB0112

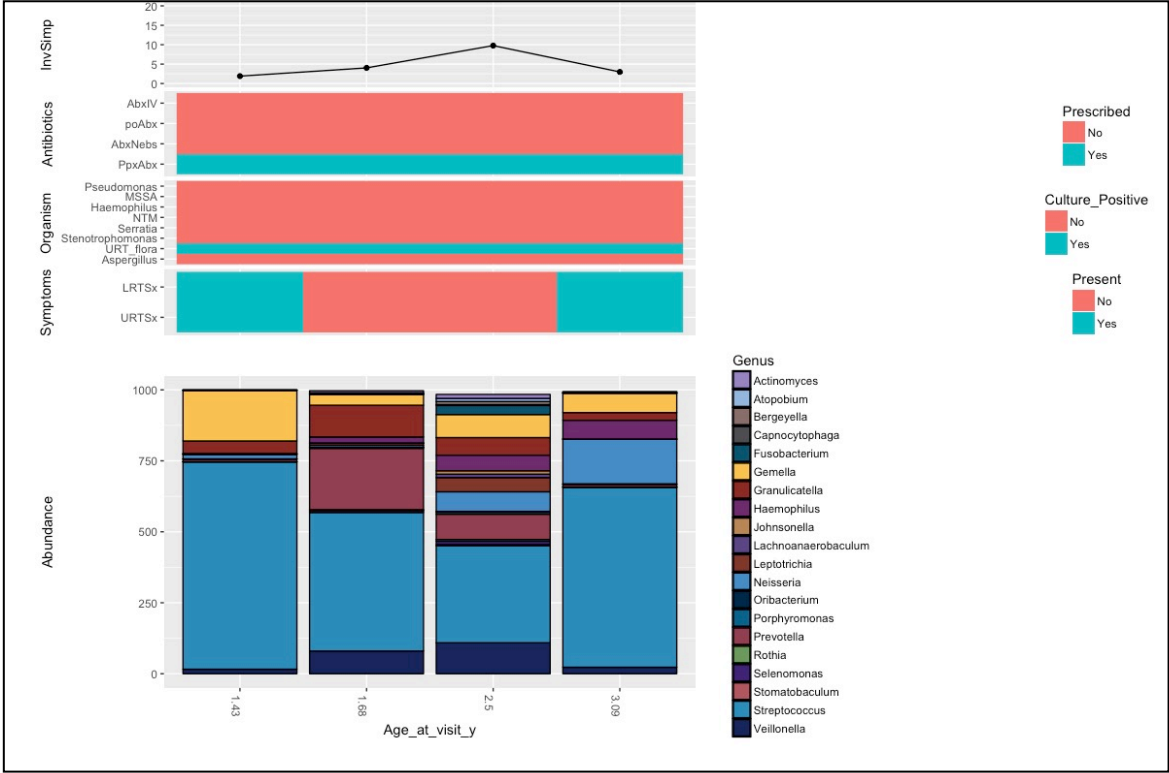


“Upper respiratory tract flora”

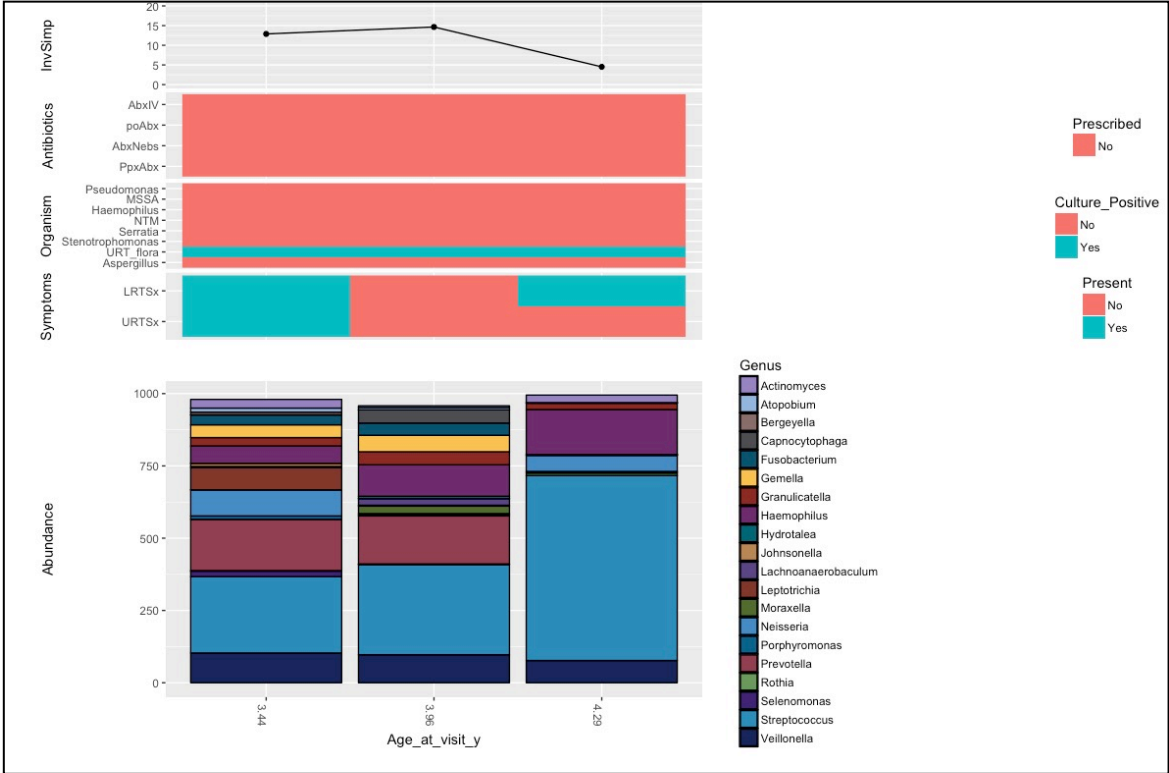
A7.19: CLIMB0062



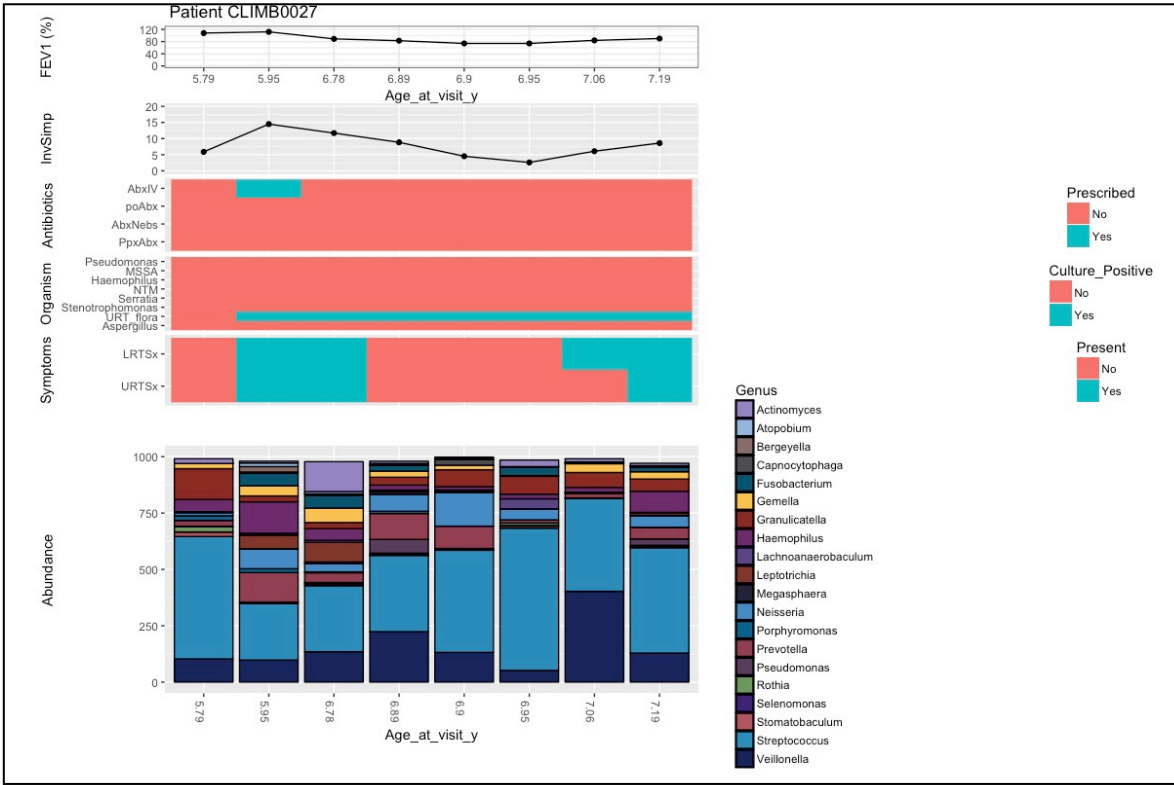
A7.20: CLIMB0039



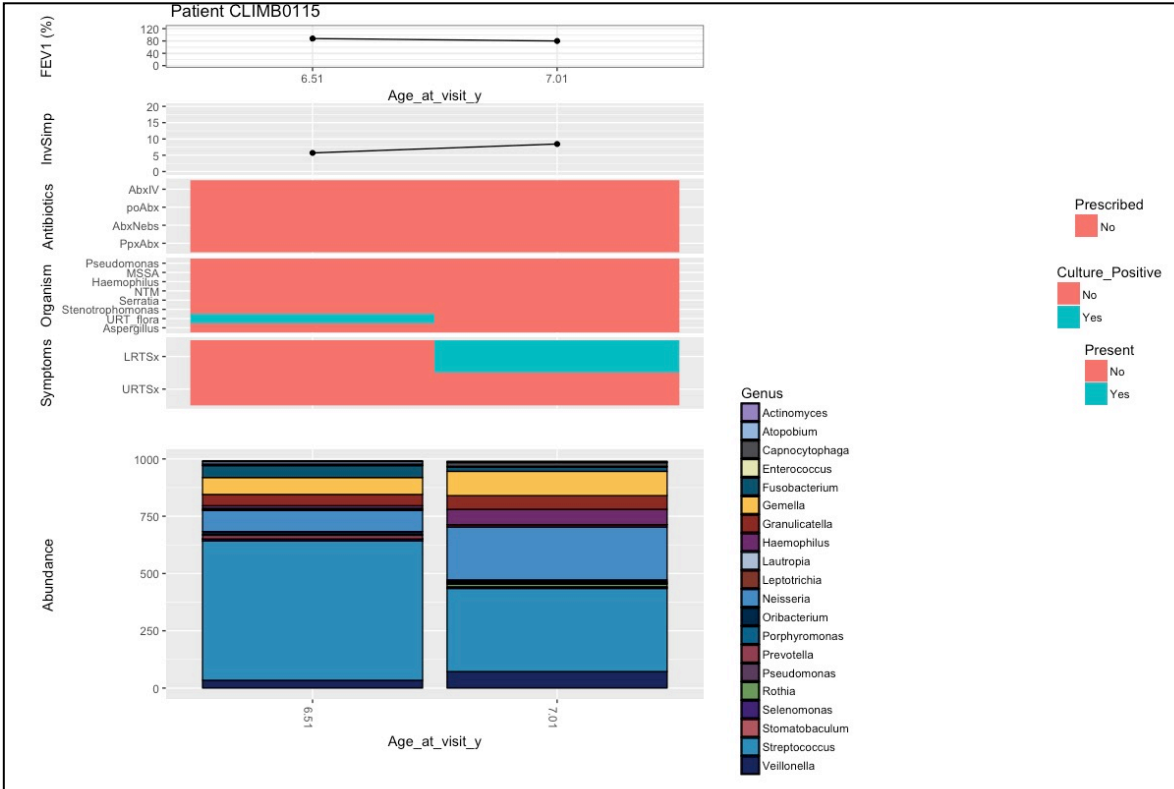
A7.21: CLIMB0026



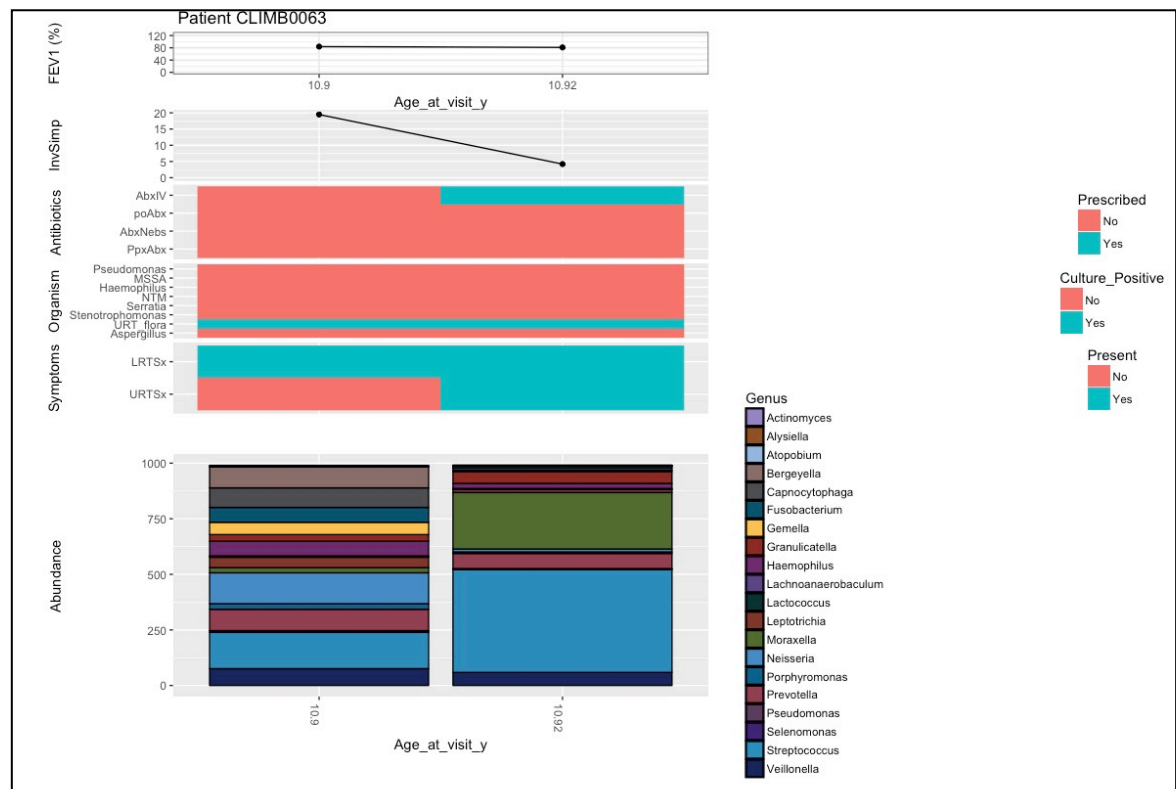
A7.22: CLIMB0027



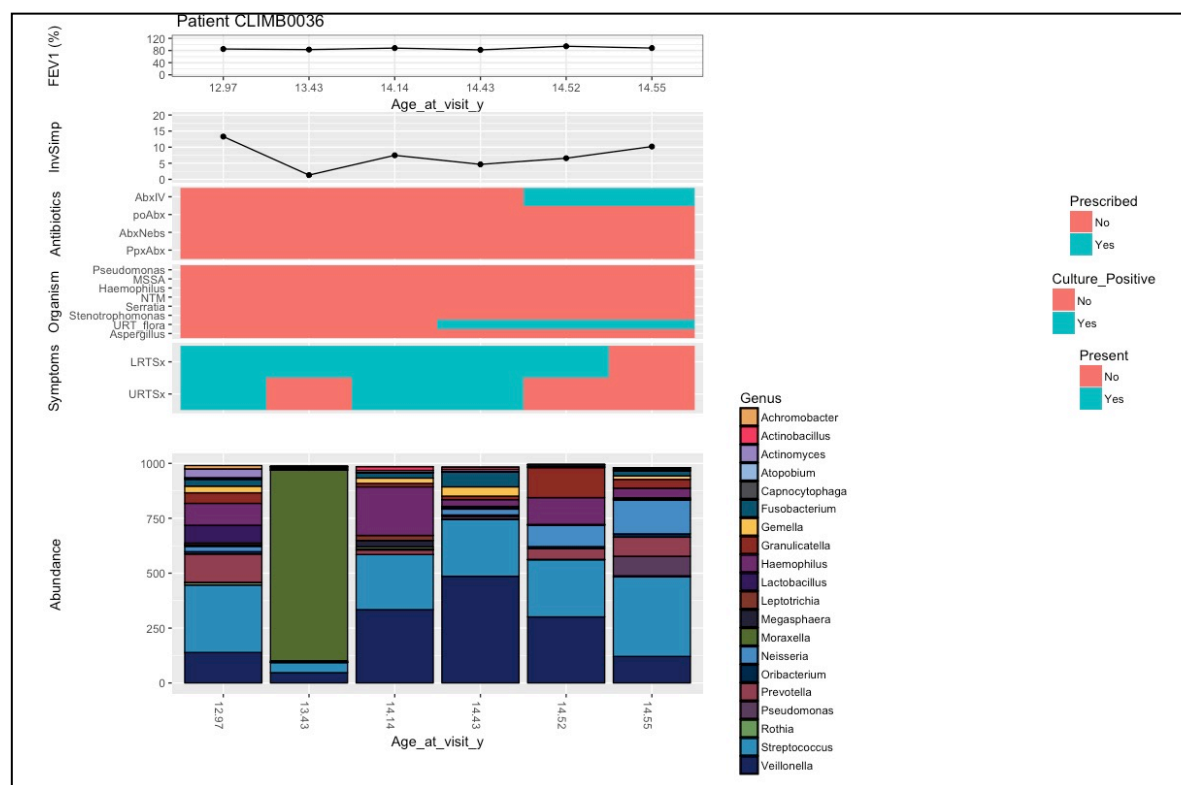
A7.23: CLIMB0115



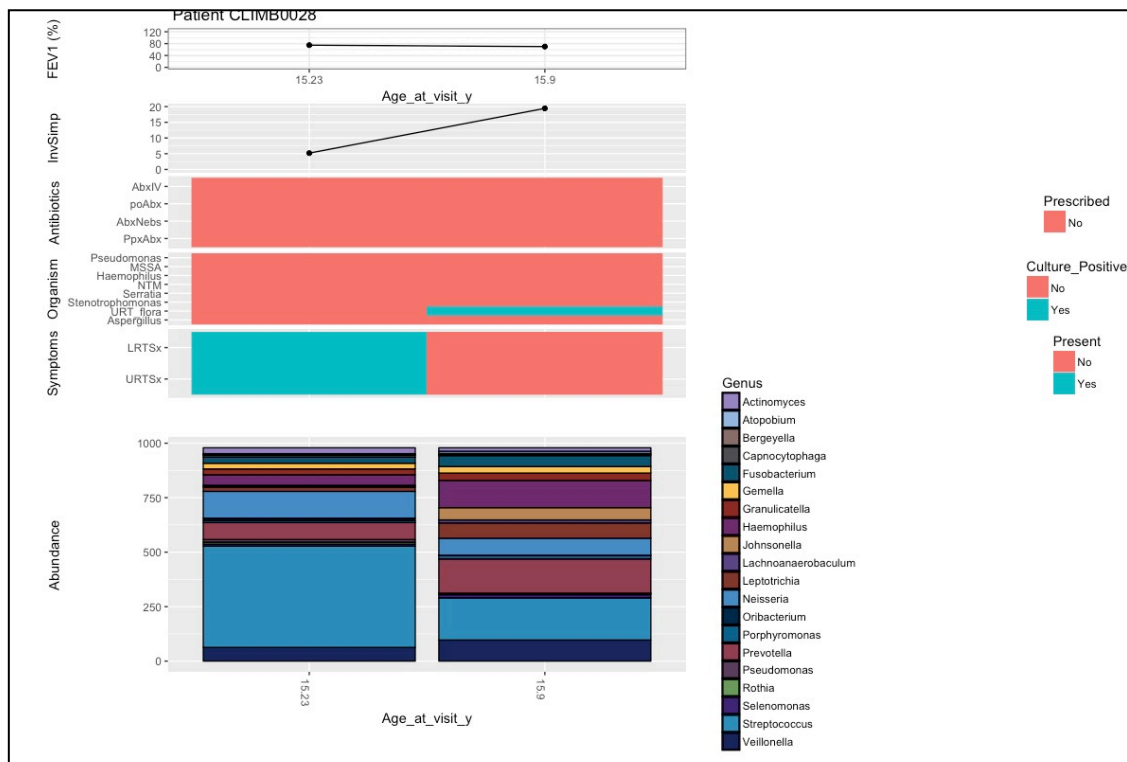
A7.24: CLIMB0063



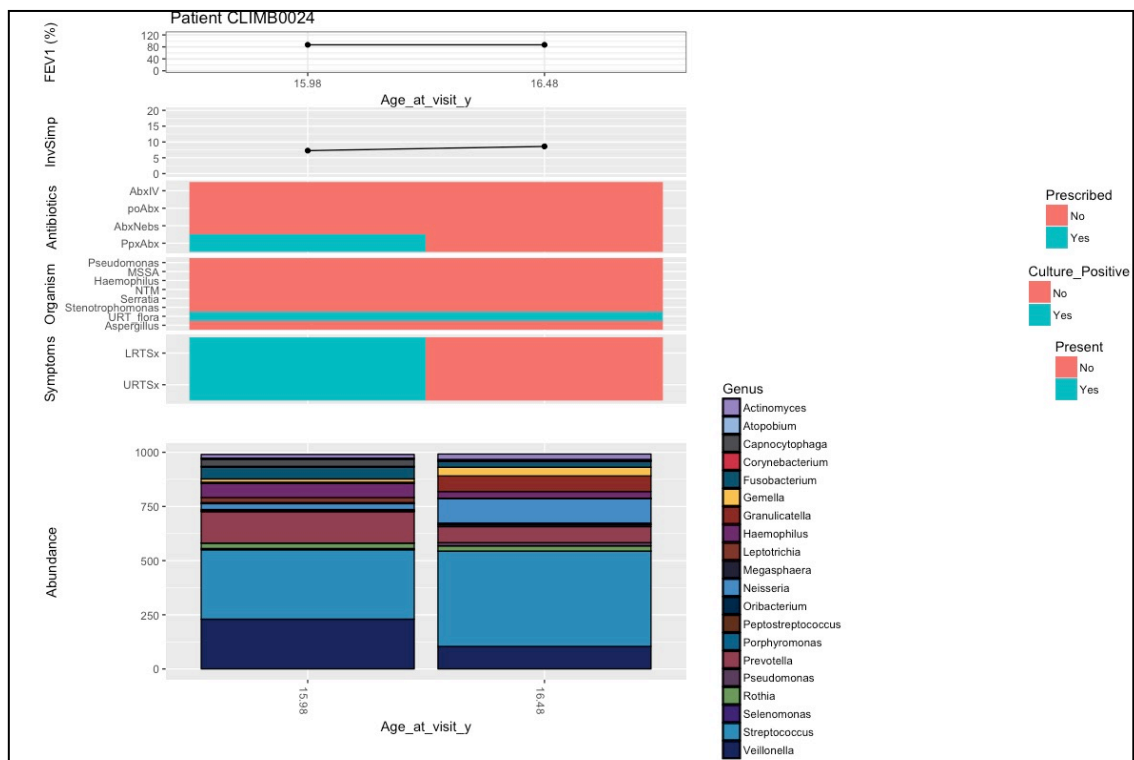
A7.25: CLIMB0036



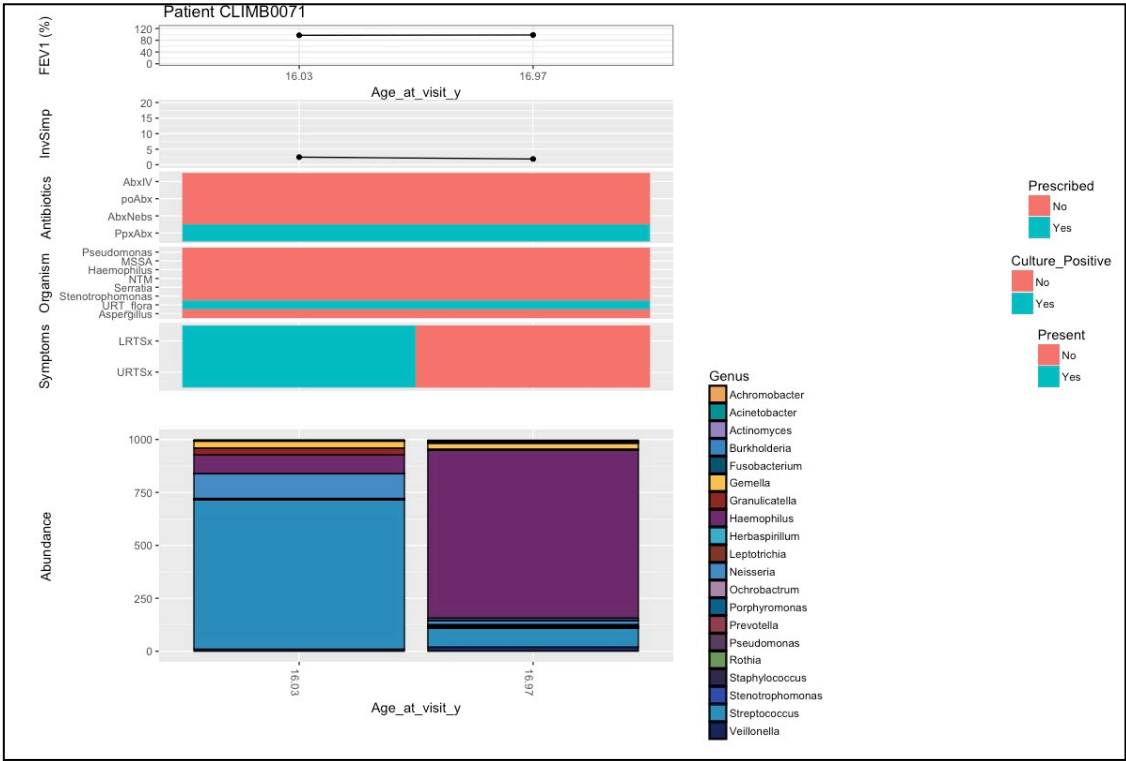
A7.26: CLIMB0028



A7.27: CLIMB0024

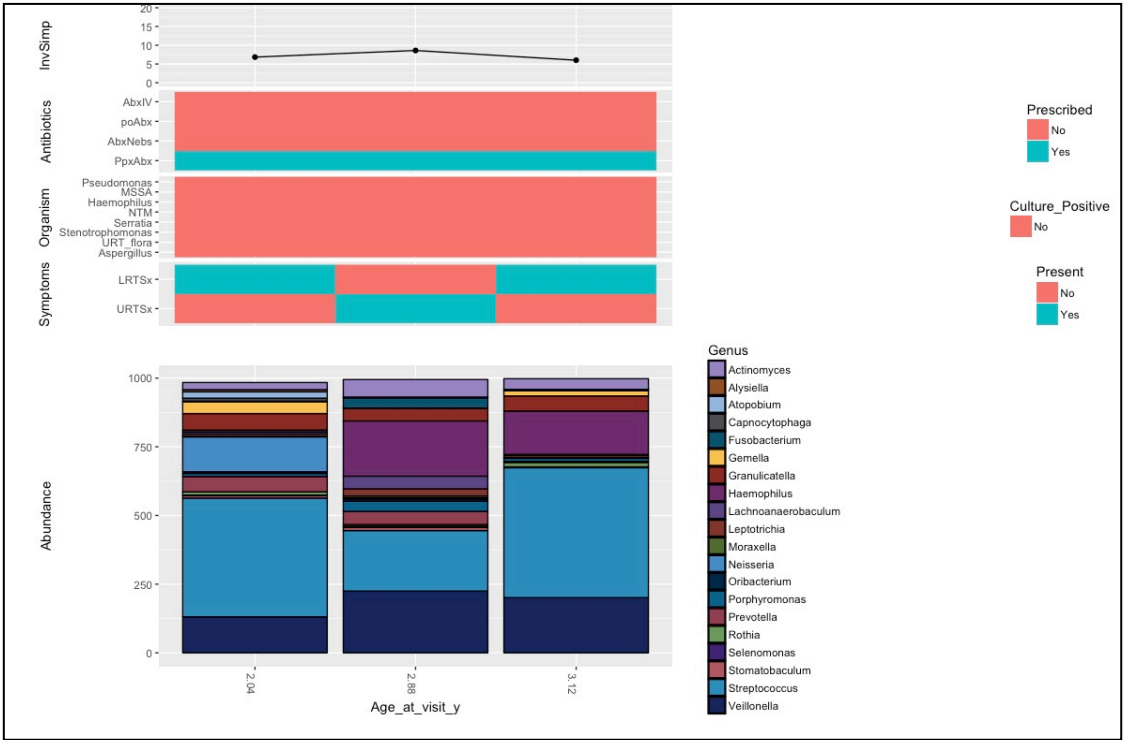


A7.28: CLIMB0071



Normal

A7.29: CLIMB0047



A7.30: CLIMB0117

