

Supplementary Figures and Tables

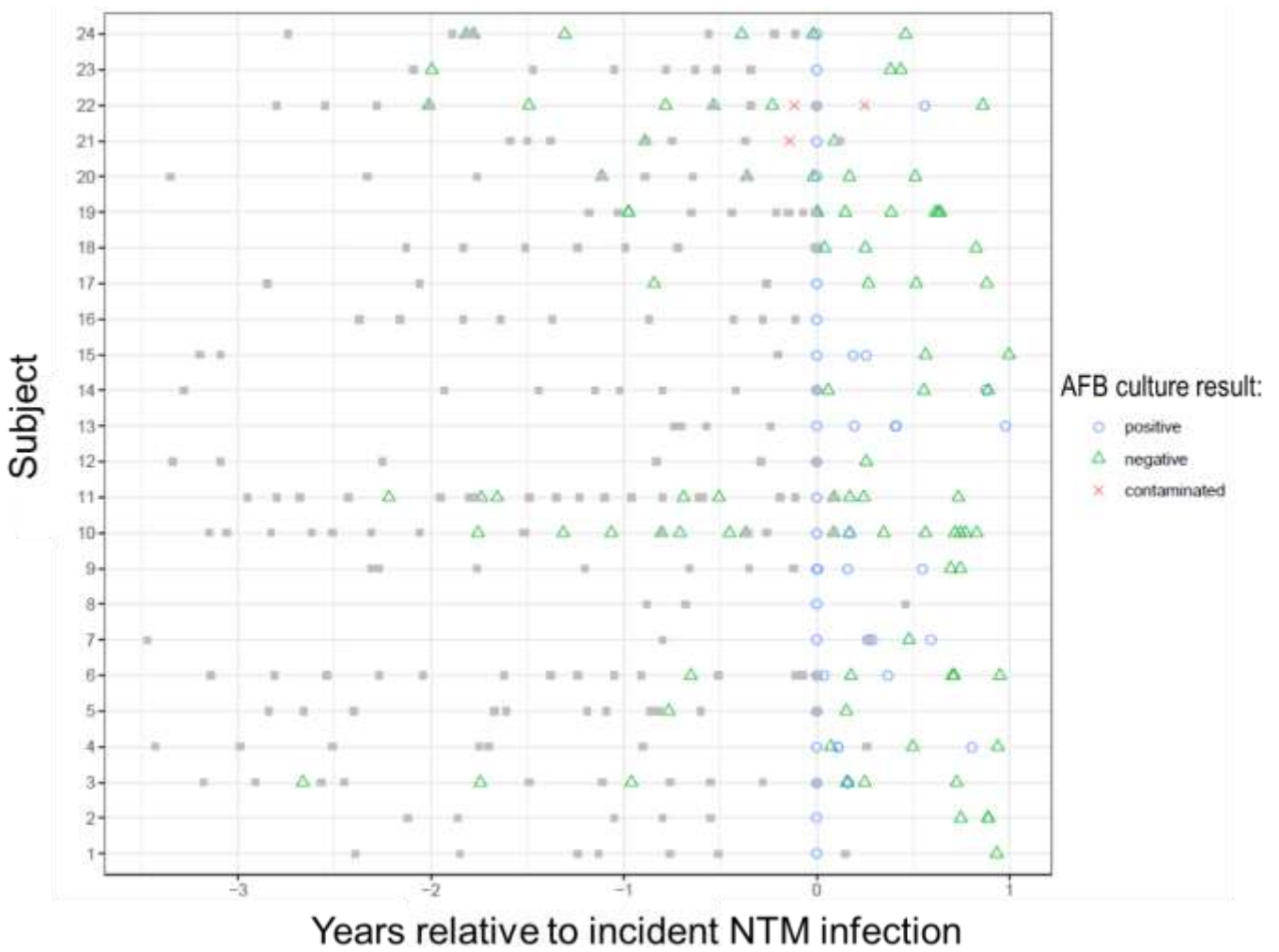


Figure S1: Subjects and timing of sputum samples relative to incident NTM infection. For each subject, sputum samples included in the study are shown (grey squares), along with the timing of each sample in years relative to incident NTM infection (Time 0). AFB culture data from electronic medical records over this time period are shown, and culture results are listed as AFB positive (blue circles), AFB negative (green triangles), or “contaminated” (i.e., AFB culture result was not able to be determined due to overgrowth of bacteria, red X).

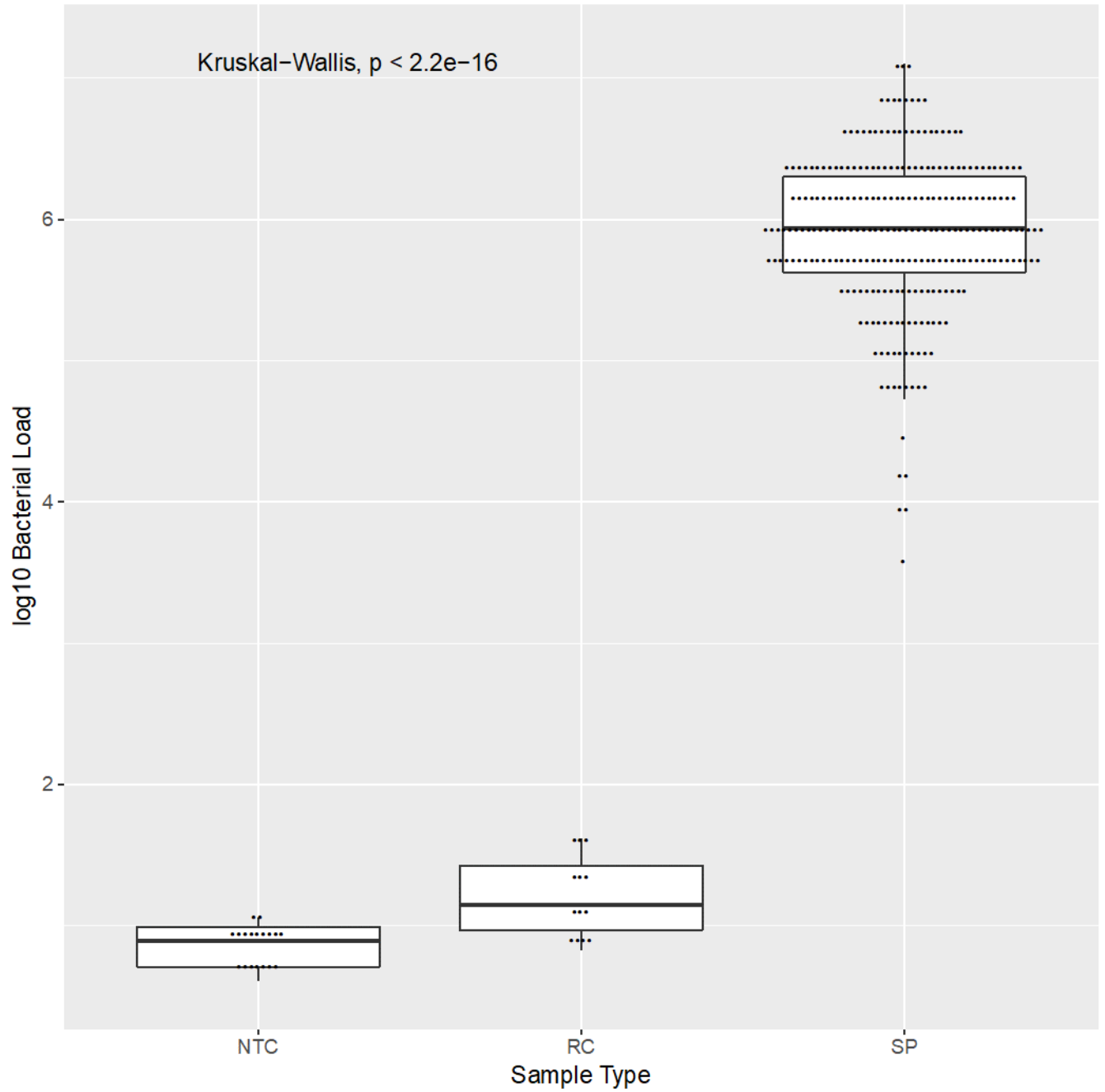


Figure S2: Total bacterial load of ddPCR controls (NTC), reagent controls (RC), and sputum samples (SP). Median and interquartile ranges shown. $p < 2.2 \times 10^{-16}$, Kruskal-Wallis.

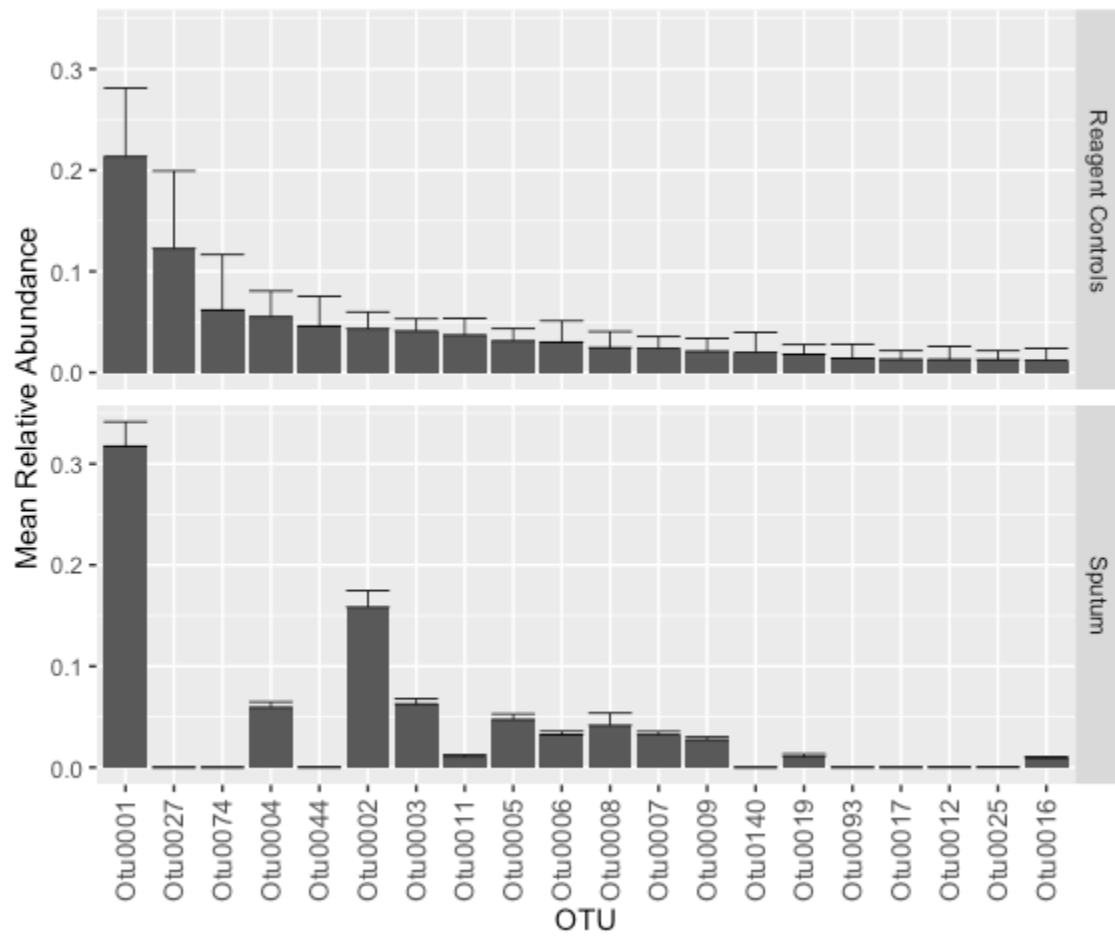


Figure S3: OTUs ranked by mean relative abundance in reagent controls, compared to mean relative abundance of these OTUs in sputum samples.

Table S1: Wilcoxon rank-sum test for NTM pulmonary disease vs no NTM pulmonary disease

Wilcoxon p value	Feature	Taxonomic label
0.027375655	OTU008_slope	<i>Rothia</i>
0.070229826	OTU003_slope	<i>Streptococcus</i>
0.070595357	OTU002	<i>Pseudomonas</i>
0.100401378	OTU024	<i>Atopobium</i>
0.11942105	OTU043	<i>Fusobacterium</i>
0.120040083	OTU001_slope	<i>Staphylococcus</i>
0.123304048	OTU016	<i>Fusobacterium</i>
0.137117698	OTU038	<i>Prevotella</i>
0.151052943	OTU034	<i>Prevotella</i>
0.151274449	OTU031	<i>Capnocytophaga</i>
0.153123645	OTU002_slope	<i>Pseudomonas</i>
0.165002276	OTU034_slope	<i>Prevotella</i>
0.181372539	OTU041	<i>Leptotrichia</i>
0.186047406	OTU038_slope	<i>Prevotella</i>
0.209247796	OTU008	<i>Rothia</i>
0.238141273	chao_slope	
0.263564437	sobs_slope	
0.263564437	OTU018_slope	<i>Pasteurellaceae_unclassified</i>
0.263564437	OTU003	<i>Streptococcus</i>
0.263564437	bacterial_load	
0.281774454	OTU006	<i>Streptococcus</i>
0.290747018	OTU035_slope	<i>Peptostreptococcus</i>
0.31962919	shannoneven_slope	
0.31962919	OTU028_slope	<i>Streptococcus</i>
0.342674393	OTU030	<i>Megasphaera</i>
0.350278937	OTU015_slope	<i>Actinomyces</i>
0.375892907	OTU025	<i>Mycoplasma</i>
0.382434657	OTU041_slope	<i>Leptotrichia</i>
0.382603801	OTU013_slope	<i>Gemella</i>
0.402618095	OTU028	<i>Streptococcus</i>
0.407384083	OTU019	<i>Rothia</i>
0.452300635	OTU005_slope	<i>Prevotella</i>
0.452300635	OTU016_slope	<i>Fusobacterium</i>
0.458975292	OTU018	<i>Pasteurellaceae_unclassified</i>
0.475869696	OTU021	<i>Prevotella</i>

0.489577427	npshannon_slope	
0.508964451	OTU027	<i>Veillonella</i>
0.512847799	OTU039	<i>Stomatobaculum</i>
0.520139176	sobs	
0.528330825	OTU001	<i>Staphylococcus</i>
0.540705495	OTU026	<i>Oribacterium</i>
0.547857087	fev1_slope	
0.568560827	shannoneven	
0.568560827	npshannon	
0.568560827	OTU036_slope	<i>Scardovia</i>
0.578041083	OTU025_slope	<i>Mycoplasma</i>
0.644518463	OTU036	<i>Scardovia</i>
0.644591052	OTU010_slope	<i>Achromobacter</i>
0.645746486	OTU039_slope	<i>Stomatobaculum</i>
0.652906777	OTU004	<i>Veillonella</i>
0.652906777	OTU007	<i>Streptococcus</i>
0.652906777	chao	
0.652906777	invsimpson	
0.652906777	bacterial_load_slope	
0.652906777	OTU027_slope	<i>Veillonella</i>
0.664396913	OTU020	<i>Porphyromonas</i>
0.674996594	OTU032	<i>Lautropia</i>
0.689315565	OTU022_slope	<i>Actinomyces</i>
0.689315565	OTU014_slope	<i>Stenotrophomonas</i>
0.690343716	OTU029	<i>Actinomyces</i>
0.696797019	OTU006_slope	<i>Streptococcus</i>
0.696797019	OTU026_slope	<i>Oribacterium</i>
0.712705603	OTU058_slope	<i>Prevotella</i>
0.715237365	OTU033	<i>Alloprevotella</i>
0.718902914	OTU035	<i>Peptostreptococcus</i>
0.734310596	OTU013	<i>Gemella</i>
0.741723331	OTU030_slope	<i>Megasphaera</i>
0.741723331	nseqs	
0.750638469	OTU032_slope	<i>Lautropia</i>
0.768387762	OTU058	<i>Prevotella</i>
0.781251456	OTU040_slope	<i>Abiotrophia</i>
0.787462728	OTU011_slope	<i>Lactobacillales_unclassified</i>
0.787462728	OTU043_slope	<i>Fusobacterium</i>
0.787462728	OTU029_slope	<i>Actinomyces</i>

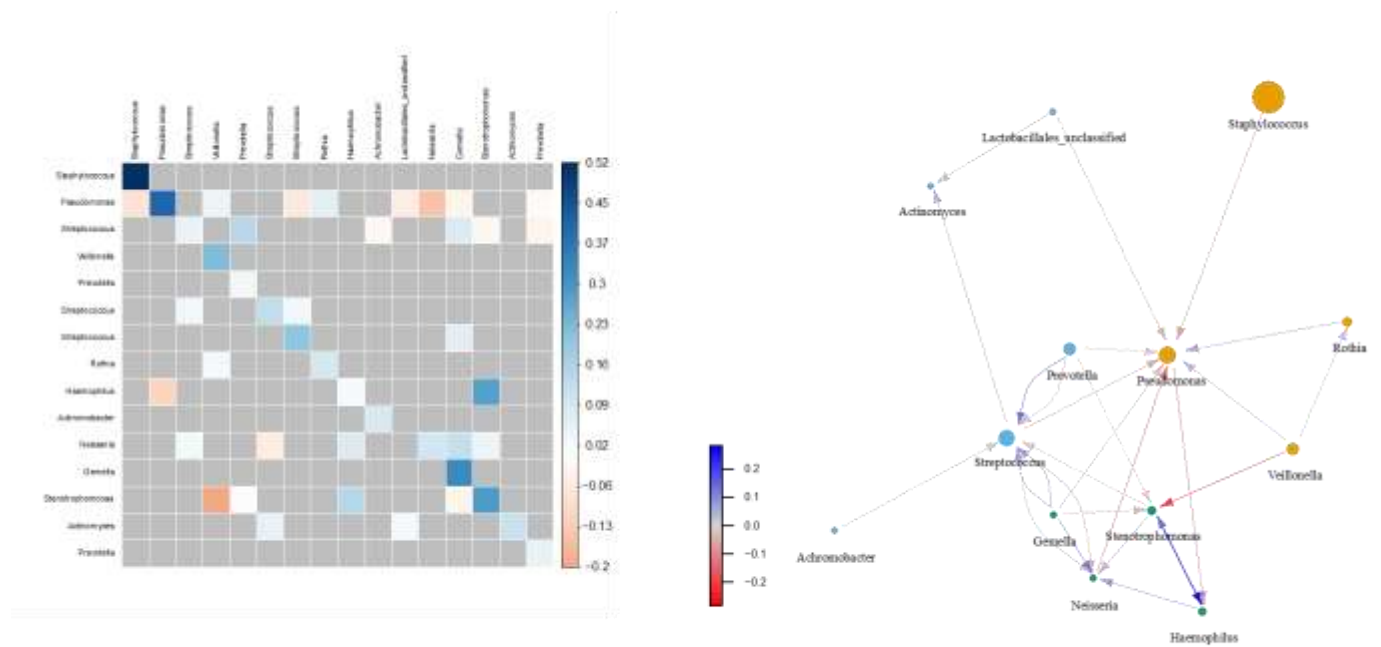
0.806082303	OTU011	<i>Lactobacillales_unclassified</i>
0.829003354	OTU015	<i>Actinomyces</i>
0.829322074	OTU040	<i>Abiotrophia</i>
0.829558108	OTU037_slope	<i>Parvimonas</i>
0.830253106	OTU020_slope	<i>Porphyromonas</i>
0.833960822	OTU024_slope	<i>Atopobium</i>
0.833960822	OTU007_slope	<i>Streptococcus</i>
0.839160839	ppFEV ₁	
0.860283668	OTU022	<i>Actinomyces</i>
0.878219734	OTU009_slope	<i>Haemophilus</i>
0.880975593	invsimpson_slope	
0.880975593	OTU017_slope	<i>Prevotella</i>
0.891232382	OTU009	<i>Haemophilus</i>
0.891232382	OTU014	<i>Stenotrophomonas</i>
0.920249553	OTU037	<i>Parvimonas</i>
0.928439055	OTU021_slope	<i>Prevotella</i>
0.928439055	OTU031_slope	<i>Capnocytophaga</i>
0.928439055	OTU005	<i>Prevotella</i>
0.928439055	OTU004_slope	<i>Veillonella</i>
0.928439055	OTU019_slope	<i>Rothia</i>
0.950254582	OTU033_slope	<i>Alloprevotella</i>
0.973897483	OTU012	<i>Neisseria</i>
0.974314802	OTU010	<i>Achromobacter</i>
0.974910629	OTU017	<i>Prevotella</i>
0.974910629	OTU023_slope	<i>Prevotella</i>
0.97555243	OTU012_slope	<i>Neisseria</i>
1	OTU023	<i>Prevotella</i>

Table S2: Wilcoxon rank-sum test for persistent vs transient NTM infection

Wilcoxon p value	Feature	Taxonomic label
0.004975637	OTU008	<i>Rothia</i>
0.020131427	OTU021	<i>Prevotella</i>
0.023474753	OTU016_slope	<i>Fusobacterium</i>
0.042370812	OTU027	<i>Veillonella</i>
0.053468302	OTU024	<i>Atopobium</i>
0.060001549	OTU030	<i>Megasphaera</i>
0.0649339	OTU004	<i>Veillonella</i>
0.075502637	chao_slope	
0.075502637	OTU008_slope	<i>Rothia</i>
0.10163525	OTU023	<i>Prevotella</i>
0.14279752	OTU033	<i>Alloprevotella</i>
0.14927577	sobs_slope	
0.165674	OTU038	<i>Prevotella</i>
0.168826507	bacterial_load	
0.172463142	OTU016	<i>Fusobacterium</i>
0.177957919	OTU043	<i>Fusobacterium</i>
0.208019261	sobs	
0.225692349	OTU032	<i>Lautropia</i>
0.265095429	OTU005	<i>Prevotella</i>
0.265095429	OTU007	<i>Streptococcus</i>
0.284451921	OTU006	<i>Streptococcus</i>
0.285650754	OTU011	<i>Lactobacillales_unclassified</i>
0.285650754	OTU038_slope	<i>Prevotella</i>
0.2863674	OTU009_slope	<i>Haemophilus</i>
0.293868827	chao	
0.293868827	OTU035_slope	<i>Peptostreptococcus</i>
0.296078891	OTU058	<i>Prevotella</i>
0.324604233	OTU011_slope	<i>Lactobacillales_unclassified</i>
0.329450939	OTU039	<i>Stomatobaculum</i>
0.355979402	OTU033_slope	<i>Alloprevotella</i>
0.357224146	invsimpson	
0.357224146	invsimpson_slope	
0.357224146	npshannon	
0.391773435	shannoneven	
0.423088859	OTU025_slope	<i>Mycoplasma</i>
0.428141966	OTU003_slope	<i>Streptococcus</i>

0.428141966	OTU018_slope	<i>Pasteurellaceae_unclassified</i>
0.441419009	OTU034	<i>Prevotella</i>
0.444059051	OTU017	<i>Prevotella</i>
0.466358293	nseqs	
0.466358293	OTU006_slope	<i>Streptococcus</i>
0.486125149	OTU009	<i>Haemophilus</i>
0.49749097	OTU029	<i>Actinomyces</i>
0.506263333	OTU003	<i>Streptococcus</i>
0.506263333	OTU036_slope	<i>Scardovia</i>
0.506263333	OTU043_slope	<i>Fusobacterium</i>
0.525171217	ppFEV ₁ _slope	
0.531412211	OTU025	<i>Mycoplasma</i>
0.544614917	OTU031	<i>Capnocytophaga</i>
0.561128496	OTU026	<i>Oribacterium</i>
0.579935439	OTU040_slope	<i>Abiotrophia</i>
0.58313706	OTU020_slope	<i>Porphyromonas</i>
0.590956	bacterial_load_slope	
0.590956	OTU030_slope	<i>Megasphaera</i>
0.613452796	OTU010	<i>Achromobacter</i>
0.681342976	OTU005_slope	<i>Prevotella</i>
0.681342976	OTU015_slope	<i>Actinomyces</i>
0.681342976	OTU019_slope	<i>Rothia</i>
0.681342976	OTU027_slope	<i>Veillonella</i>
0.681342976	OTU028_slope	<i>Streptococcus</i>
0.687438793	OTU041	<i>Leptotrichia</i>
0.6950434	OTU020	<i>Porphyromonas</i>
0.6950434	OTU037	<i>Parvimonas</i>
0.721248537	OTU022_slope	<i>Actinomyces</i>
0.721248537	OTU037_slope	<i>Parvimonas</i>
0.728361825	OTU024_slope	<i>Atopobium</i>
0.728361825	shannoneven_slope	
0.77034808	OTU014_slope	<i>Stenotrophomonas</i>
0.776331086	OTU001	<i>Staphylococcus</i>
0.776331086	OTU002_slope	<i>Pseudomonas</i>
0.776331086	OTU004_slope	<i>Veillonella</i>
0.776331086	OTU013_slope	<i>Gemella</i>
0.794508413	OTU015	<i>Actinomyces</i>
0.807381768	OTU012	<i>Neisseria</i>
0.81363666	OTU032_slope	<i>Lautropia</i>

0.818778876	OTU028	<i>Streptococcus</i>
0.820824833	OTU019	<i>Rothia</i>
0.82108662	OTU012_slope	<i>Neisseria</i>
0.825177335	OTU017_slope	<i>Prevotella</i>
0.825177335	OTU026_slope	<i>Oribacterium</i>
0.825177335	OTU031_slope	<i>Capnocytophaga</i>
0.845657832	OTU036	<i>Scardovia</i>
0.861750328	OTU035	<i>Peptostreptococcus</i>
0.86785639	OTU023_slope	<i>Prevotella</i>
0.871672832	OTU039_slope	<i>Stomatobaculum</i>
0.874635438	OTU001_slope	<i>Staphylococcus</i>
0.874635438	OTU007_slope	<i>Streptococcus</i>
0.874635438	OTU029_slope	<i>Actinomyces</i>
0.893314738	OTU040	<i>Abiotrophia</i>
0.921218802	OTU041_slope	<i>Leptotrichia</i>
0.922675042	OTU010_slope	<i>Achromobacter</i>
0.922789606	OTU002	<i>Pseudomonas</i>
0.924607496	npshannon_slope	
0.924607496	OTU021_slope	<i>Prevotella</i>
0.93986014	ppFEV ₁	
0.948405079	OTU058_slope	<i>Prevotella</i>
0.969728431	OTU022	<i>Actinomyces</i>
0.972728637	OTU018	<i>Pasteurellaceae_unclassified</i>
1	OTU013	<i>Gemella</i>
1	OTU014	<i>Stenotrophomonas</i>
1	OTU034_slope	<i>Prevotella</i>



All subjects, matrix and network graph

Figure S4: Time series bacterial community interactions for all subjects and samples. (A) ARIMA coefficient matrix and network graph for entire cohort, (B) network based on ARIMA model for all subjects and samples.