

Figure S1. Comparison of univariable cross-sectional associations with adjusted cross-sectional

associations between airway infections. As in Figure 2 in the main text, forest plots show the odds ratio (circles) and 99% confidence intervals (bars) of having positive cultures for each of the eight studied organisms within each study year comparing presence versus absence of a positive culture for each of the other seven organisms in the same year. This supplemental figure adds an additional cluster of forest plots for each cross-sectional relationship to show the results of univariable relationships. The outcomes parallel those shown in Figure 2: (A) MSSA: methicillin sensitive *Staphylococcus aureus*, (B) PA: *Pseudomonas aeruginosa*, (C) MRSA: methicillin resistant *S aureus*, (D) BCC: *Burkholderia cepacia* complex, (E) SM: *Stenotrophomonas maltophilia*, (F) AX: *Achromobacter xylosoxidans*, (G) CS: *Candida* species, (H) AS: *Aspergillus* species. Utah Red results show univariable relationships unadjusted by the presence of other organisms or clinical characteristics. Purple results are from models adjusted by the presence of the remaining six other organisms. Turquoise results are from models additionally adjusted for clinical characteristics: age, sex, late diagnosis of CF, best FEV₁% in each year, annual number of APE, pancreatic sufficiency and diabetes status and weight-for-age z-score.

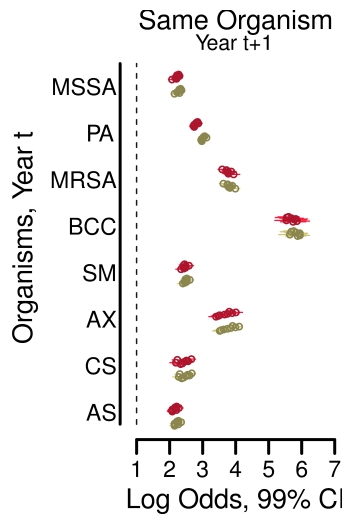


Figure S2. Adjusted associations between each airway infection in years 2003-2010 with itself in years 2004-2011. Forest plots show the log odds (circles) and 99% confidence intervals (bars) by logistic regression of having positive cultures in years $t+1$ for each of the eight studied organisms when the same organism was present in respective years t where $t=2003-2010$. The outcomes for years $t+1$ were (A) MSSA: methicillin-sensitive *Staphylococcus aureus*, (B) PA: *Pseudomonas aeruginosa*, (C) MRSA: methicillin-resistant *S aureus*, (D) BCC: *Burkholderia cepacia* complex, (E) SM: *Stenotrophomonas maltophilia*, (F) AX: *Achromobacter xylosoxidans*, (G) CS: *Candida* species, (H) AS: *Aspergillus* species. Utah Red results are from models adjusted by the presence of the other seven organisms. Green results are from models additionally adjusted for clinical characteristics in years t : age, sex, late diagnosis of CF, best FEV₁% in each year, annual number of APE, pancreatic sufficiency and diabetes status and weight-for-age z -score.

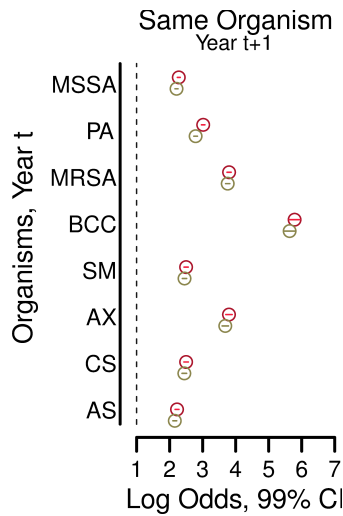


Figure S3. Adjusted associations between each airway infection in year t with itself in year $t+1$. Each forest plot show the log odds (circles) and 99% confidence intervals (bars) by GEEGLM utilizing the entire 2003-2011 CFFPR data set for each of the eight studied organisms in year $t+1$ when the same organism was present in respective years t where $t=2003-2010$. The outcomes from years $t+1$ were: (A) MSSA: methicillin-sensitive *Staphylococcus aureus*, (B) PA: *Pseudomonas aeruginosa*, (C) MRSA: methicillin-resistant *S aureus*, (D) BCC: *Burkholderia cepacia* complex, (E) SM: *Stenotrophomonas maltophilia*, (F) AX: *Achromobacter xylosoxidans*, (G) CS: *Candida* species, (H) AS: *Aspergillus* species when the same organism was present in culture for year t . Utah Red results are from models adjusted by the presence of the other seven organisms. Green results are from models additionally adjusted for clinical characteristics in years t : age, sex, late diagnosis of CF, best FEV₁% in each year, annual number of APE, pancreatic sufficiency and diabetes status and weight-for-age z-score.