Introduction The lower airway microbiota is important in chronic lung disease but young children do not expectorate, making longitudinal studies difficult. Upper airway samples, of uncertain reliability, are used as a surrogate. Whilst throat swabs (TS) have shown differences in the microbiota between healthy and wheezy children [PLoS One 2012;7(10):e46803], the role of cough swabs (CS) is at present unclear. This study assessed the correlation between upper and lower airway samples as a prelude to a longitudinal study. We hypothesised that upper airway samples reflect the lower airway microbiota.

Methods TS and lower airway samples (bronchoalveolar lavage fluid, bronchial brushings or both) were collected from 35 children undergoing a clinically indicated fibre-optic bronchoscopy (FOB), including CS from 35 children. Bacterial DNA was extracted for quantitative PCR (qPCR) and 454 FLX pyrosequencing of the V3-V5 region of the 16S rRNA bacterial gene. Data analysis was performed with Quantitative Insights Into Microbial Ecology (QIIME) and Phyloseq in R.

Results FOB indications included: recurrent lower respiratory tract infections (47%); cystic fibrosis (CF) (35%), and Primary Ciliary Dyskinesia (PCD) (11%). Only seven CS amplified successfully; 375,268 high quality 16S RNA sequences were obtained from 132 upper and lower airway samples. No significant difference was seen in richness (H = 1.352, 2 d.f., p = 0.509), evenness (H = 3.942, 2 d.f., p = 0.139), Shannon’s diversity index (H = 1.38, 2 d.f., p = 0.501), and Inverse Simpson’s diversity index (F(2,91) = 0.547, p = 0.581) between TS and lower airway samples. Beta-diversity (diversity between samples) was significantly different; ≤7.2% of variation in diversity attributed to the sampling method (p = 0.002). Greater variation was observed between underlying pathologies and between patients (≤41.2% and 68.3% respectively, p = 0.001).

Conclusions CS are not useful for pyrosequencing. TS are predictive of the lower airway microbiota and can differentiate diseases. TS are therefore potentially useful in studying longitudinal changes in the microbiota in children with chronic lung diseases.