Background:
Non-Tuberculous Mycobacterium (NTM) is a well-recognised infection in patients with cystic fibrosis (CF), however tuberculous mycobacterium (Mtb) is almost never seen. CF is hypothesised to confer protection against Mtb infection through evolutionary advantage, supported by population studies demonstrating inverse correlation between tuberculosis (TB) incidence and CF gene mutation carriergship.

Case:
A 10yr old child, homozygous DF508, is admitted for two weeks of intensive physiotherapy, IV antibiotics and bronchoscopy in view of persisting cough and declining lung function that has not responded to repeated antibiotics. The initial lavage was culture negative with no AFB were seen. 6 weeks later the TB culture returned as Mtb detected.

Diagnosis of TB was unexpected and to address the possibility of exogenous contamination and identify source of infection, who genome sequencing (WGS) was performed. The isolate showed a distinct genetic mutation, representing a unique TB infection and identified to be fully sensitive. CT scan had evidence of tree in bud and there were no cavitating lesions. Two months into her standard TB treatment, her cough had resolved and there was significant improvement in lung function with FEV1 98%. She has now completed treatment and is doing well.

Discussion:
A very rarely seen case of pulmonary TB in a child with CF raises many interesting questions about mycobacterium infection, genetic protection hypotheses and host factors in disease susceptibility. Our case findings support the importance of obtaining lower airway samples for mycobacterium culture. The recommended antimicrobial treatment of TB in CF is the same as for non-CF children, however the impact of further drugs on their medication burden is significant and with additional surveillance considerations. Understanding of infections in CF continues to grow and with wider use of WGS we may be learning more about mycobacterium species and the host - disease relationship.