The transcriptomic landscape of diffuse radiological bronchiectasis

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Bronchiectasis is a heterogeneous chronic structural lung disease in which four canonical elements of a vicious circle, *i.e.* recurrent airway infections, impaired mucociliary clearance, chronic airway inflammation and irreversible airway dilatation, have been implicated [1, 2]. Unravelling the underlying causes of bronchiectasis, which can only be ascertained in approximately 50% of patients despite exhaustive diagnostic efforts [3], is clinically relevant for optimising therapeutic interventions by targeting the core pathophysiology. There are a number of primary underlying causes, for instance, primary ciliary dyskinesia, which affects the motile cilia, cystic fibrosis, and congenital malformation. Several studies have indicated a role of genetic mutations in bronchiectasis [4–6], evidenced by the possible link with the clinical phenotypes and disease severity. These studies also suffered from a limited capacity of thoroughly identifying the genes broadly representative of pathophysiology.