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Highly efficient genome editing in primary human bronchial epithelial cells differentiated at air-liquid interface. RAPITEANU ET AL. RESEARCH LETTER Efficient genome editing in primary human bronchial epithelial cells

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To the Editor:

The structure and composition of the bronchial epithelium is altered in respiratory diseases such as COPD and asthma, in which goblet cell hyperplasia and reduced numbers of ciliated cells impair mucociliary clearance. Current standard of care focuses on alleviating disease symptoms, such as airway obstruction and inflammation, using bronchodilators or steroids, respectively. Whilst these approaches are effective, they do not address the underlying pathogenic processes. An alternative way forward would be to identify and target the dysregulated cellular pathways responsible for impaired bronchial epithelial function. In this study we describe a single-step, highly efficient and easily scalable genome editing pipeline to aid the dissection of the molecular mechanisms underlying primary human bronchial epithelial cell (BEC) differentiation and function at air-liquid interface (ALI).