

Figure S1. (A) UMAP plots of expression from scRNA-seq of child airway organoids (*DNAH5*-mutated and control). (B) Dot plot showing the relative expression and the percentage of cells expressing selected marker genes across scRNA-seq clusters. (C) The KEGG enrichment of basal cells in the two groups showing the differential expression. (D) The KEGG enrichment of multiciliated cells in the two groups showing the differential expression. (E-F) GO enrichment analysis of biological processes and KEGG enrichment in club cells (*DNAH5* vs. CTRL) showing the differential expression of immune-related genes. (G-H) GO enrichment analysis of biological processes and KEGG enrichment in goblet cells (*DNAH5* vs. CTRL).

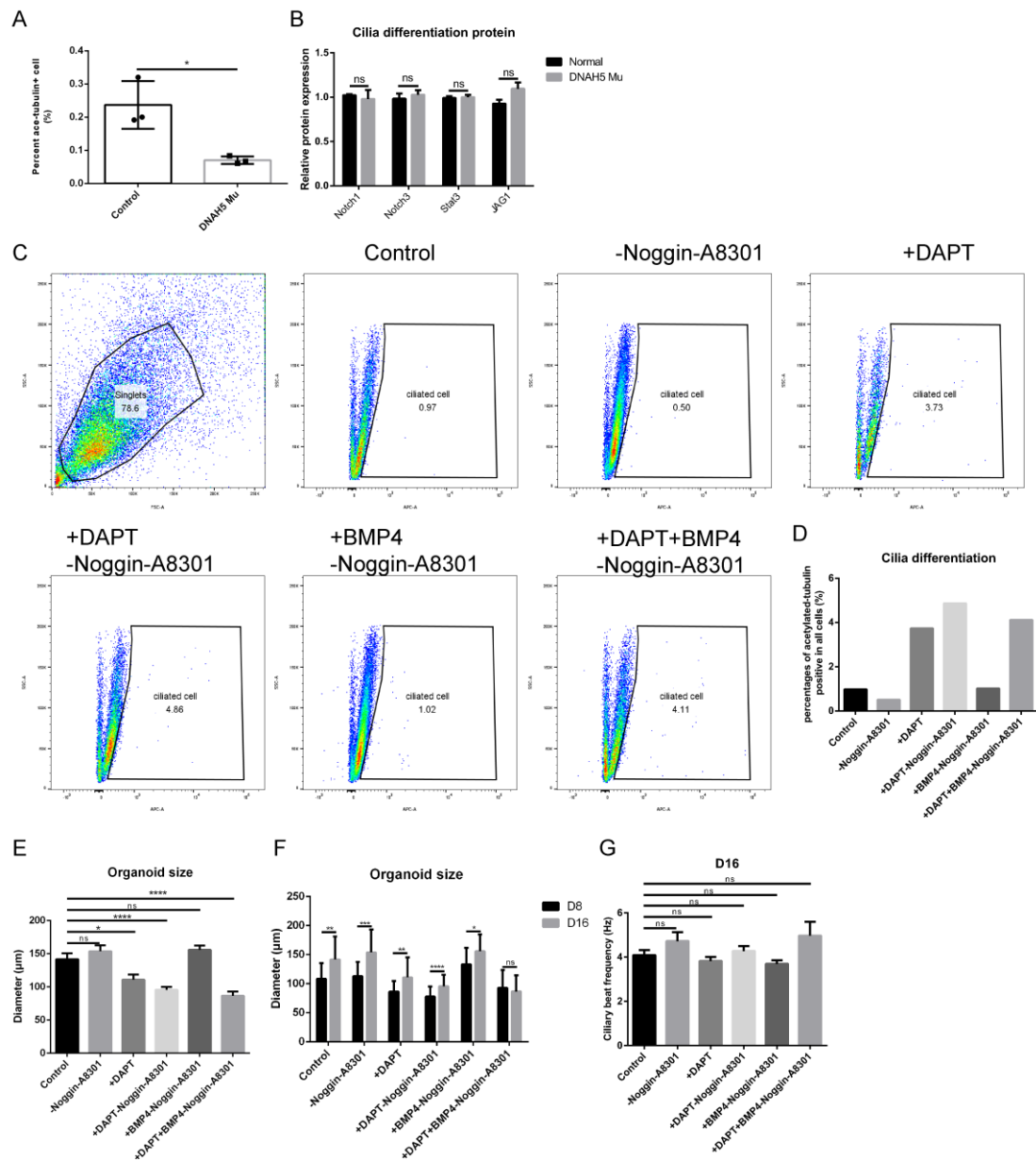


Figure S2. (A) The percentage of ace-tubulin+ cells in Hoechst33342+ cells. (B) The relative protein expression related to cilia differentiation in proteomic analysis. (C) FACS plots show that single acetylated- α -tubulin-positive cells were identified in child airway organoids induced by different treatments for 8 days. (D) Bar plots depicting the percentages of acetylated tubulin-positive cells in child airway organoids differentiated in treatments for 8 days. The highest percentage of ciliated cells was observed in the +DAPT-Noggin-A8301 group. (E) The organoid size was measured at D16. ** $p < 0.01$, *** $p < 0.001$, ns: no significance; $n = 20$ per group. (F) The organoids at D16 were larger than those at D8 in most groups. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, ns: no significance; $n = 20$ per group. (G) The ciliary beat frequency of normal child airway organoids was recorded at D16. ns: no significance; $n = 20$ per group.