Supplementary Table 4. Sequential whole genome filtering analysis for samples PCD-141 I:1 and PCD-141 I:2

Sample	PCD-141 I:1	PCD-141 I:2
All variants	9,186,019	9,186,019
Heterozygous variants	2,791,707	2,911,759
Shared heterozygous nonsynonymous, splice-site, or insertion/deletion variants with MAF<0.01 in 1000 Genomes Project	522	
Of these, any in genes in Cilia Proteome	16 (*RNF207, PPIAL4G* (two variants), *C3ORF67, TTC21A, ULK4, AGPAT9, ATXN1, PRSS1, PKHD1L1, PDLIM2, C10ORF122, ARMC4, GOLGA3, C12ORF55, MYO15A*)	
Of these, any in genes implicated in cilia motility*	1 (*ARMC4*)	

* Identified in KM Lonergan *et al* (2006). Identification of novel lung genes in bronchial epithelium by serial analysis of gene expression. Am J Respir Cell Mol Biol 35 (6):651-661; and ET O'Toole *et al* (2012). Computer-assisted image analysis of human cilia and Chlamydomonas flagella reveals both similarities and differences in axoneme structure. Cytoskeleton (Hoboken) 69 (8):577-590.