Supplementary Table 2. Sequential whole exome filtering process for PCD-221 II:1

Sequentially listed filtering steps	**Total variants**
Total variants	62,913
Variants in MAF<0.01 in 1000 Genomes Project	3,107
Homozygous variants	744
Homozygous nonsynonymous, splice-site, or insertion/deletion variants	76
Of these, any that appeared in less than 10/500 exomes from the UK10K_RARE cohort	8 (*EEF1D, MYO1D, CXORF69, GPR112, EXPH5, PCK1, PMS1, ARMC4*)
Of these, any in genes in Cilia Proteome	3 (*EEF1D, MYO1D, ARMC4*)
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.