Table 1. Protein Signature of Diacetyl Injury to Multiciliated Cells^a

primary protein	protein description [†]	mean	in phosho-
name		fold- change	protein signature?
DNAI1_HUMAN	dynein intermediate chain 1, axonemal	-29.3	
DTHD1_HUMAN	death domain-containing protein 1	-27.6	
DJB13_HUMAN	DnaJ homologue subfamily B member 13	-26.6	
KAD7_HUMAN	adenylate kinase 7	-26.2	
DYH9_HUMAN	dynein heavy chain 9, axonemal	-19.2	
DYH5_HUMAN	dynein heavy chain 5, axonemal	–17.5	
CA087_HUMAN	uncharacterized protein C1orf87	-16.1	Y
TP53B_HUMAN	tumor suppressor p53-binding protein 1 ^b	-15.6	Y
CU059_HUMAN	uncharacterized protein C21orf59	-14.8	
WDR35_HUMAN	WD repeat-containing protein 35	-14.6	
EFHC1_HUMAN	EF-hand domain-containing protein 1	-13.0	
RSH4A_HUMAN	radial spoke head protein 4 homologue A	-11.8	Y
CA173_HUMAN	uncharacterized protein C1orf173	-11.8	Y
WDR54_HUMAN	WD repeat-containing protein 54	-11.5	
ODF3B_HUMAN	outer dense fiber protein 3B	-11.4	Υ
NDK5_HUMAN	nucleoside diphosphate kinase homologue 5	-11.1	
MAP1A_HUMAN	microtubule-associated protein 1A	-10.5	Y
CROCC_HUMAN	rootletin	-10.4	Υ
RSPH9_HUMAN	radial spoke head protein 9 homologue	-10.3	
IDLC_HUMAN	axonemal dynein light intermediate polypeptide 1	-10.2	Y
PITM1_HUMAN	membrane-associated phosphatidylinositol transfer protein 1	-9.3	
PCM1_HUMAN	pericentriolar material 1 protein	n –8.8	
HEAT2_HUMAN	HEAT repeat-containing protein 2	-7.9	
RSPH1_HUMAN	radial spoke head 1 homologue	-7.8	

primary protein name	protein description [†]	mean fold- change	in phosho- protein signature?
FBXW9_HUMAN	F-box/WD repeat-containing protein 9	-7.0	Y
MIEAP_HUMAN	mitochondria-eating protein	-6.8	Υ
LZTL1_HUMAN	leucine zipper transcription factor-like protein 1	-6.3	
CROL3_HUMAN	putative ciliary rootlet coiled- coil protein-like 3 protein	-6.3	Υ
KAD8_HUMAN	adenylate kinase 8	-5.9	
AL3B1_HUMAN	aldehyde dehydrogenase family 3 member B1	- 5.5	
SAMH1_HUMAN	SAM domain and HD domain- containing protein 1 ^b	-5.2	Υ
IFT46_HUMAN	intraflagellar transport protein 46 homologue	-4.9	

aProteins ranked by average fold change of \sim -5-fold or greater in DA- versus PBS-treated HBECs (quantified by two or more peptides, CV < 30% for replicate injections of QC pool; p < 0.1, paired t test w/FDR correction) and localization to cytoplasm/membranes of ciliated cells of human bronchi by the Human Protein Atlas (http://www.proteinatlas.org).

bProteins with nuclear localization.