**Supplemental Figure S1.** Hierarchical clustering of 119 IPF/UIP (red) and 50 control (blue) based on expression of 472 transcripts with >2 fold change between IPF and control.
Supplemental Figure S2. Expression levels of MUC5B, as assessed on microarray, as a function of disease cluster in (A) the LTRC and (B) the NJH cohort. Group I IFN = red, group II IFN = blue, control = green. One-way ANOVA p values are <0.0001 for association of Muc5b expression with disease category in both LTRC and NJH cohorts. (C) qRT-PCR validation of Muc5b expression in the NJH cohort. Y axis is on the log2 scale and error bars represent standard deviations. p=4.1x10^-7 by two-tailed t-test.
Supplemental Figure S3. Expression levels of MMP7, as assessed on microarray, as a function of disease cluster in (A) the LTRC and (B) the NJH cohort. Group I IPF = red, group II IPF = blue, control = green. One-way ANOVA p values are: <0.0001 for association of Muc5B expression with disease category in both LTRC and NJH cohorts.
Supplemental Figure S4. Most significant networks (score >40) of genes that are upregulated at >1.5 fold change in Group II compared to Group I IPF. Shown are networks 2 and 3 (network 1 is shown in the main figure in the manuscript). Genes are colored by fold change.
Supplemental Figure S5. Most significant networks (score >40) of genes that are downregulated at >1.5 fold change in Group II compared to Group I IPF. Shown are networks 1, 2, and 3. Genes are colored by fold change.
Supplemental Figure S6. Hierarchical clustering of cillum-associated genes (GO:0005929, cellular component (cilium)) across samples in groups I (blue) and II (red) in Figure 1. Asterisk next to the gene names indicates presence in cluster B in Figure 1.
Supplemental Figure S7. (A) Principal components analysis of the initial profiles from Group I (blue) and Group II (green) IPPUHP subjects along with additional profiles from the same subjects in Group I (blue) and Group II (green). The analysis was done in 2D space and the same dataset to distinguish IPP from control at SNP/DPK and 1-log fold. (B) Biexpressions of DNAH5, DNAH7, MUC5B, and MMP7, as measured by intensity, as a function of adjacent statuses in the original specimens and additional samples from the same subjects. Additional tissue from 23 Group I and 22 Group II IPP-UHP subjects were collected. Red is original specimens from Group I, blue is additional tissue from Group I, green is original specimens from Group II, and purple is additional tissue from Group II.
Supplemental Figure S8. Cilium-associated gene expression signature is validated in an independent cohort of IPF/UIP patients. Expression of cilium-associated genes divides the NIH cohort of 111 IPF/UIP subjects into two groups of subjects, one with high cilium gene expression (red bar; n = 30) and a group with low cilium expression (blue bar, n=72).