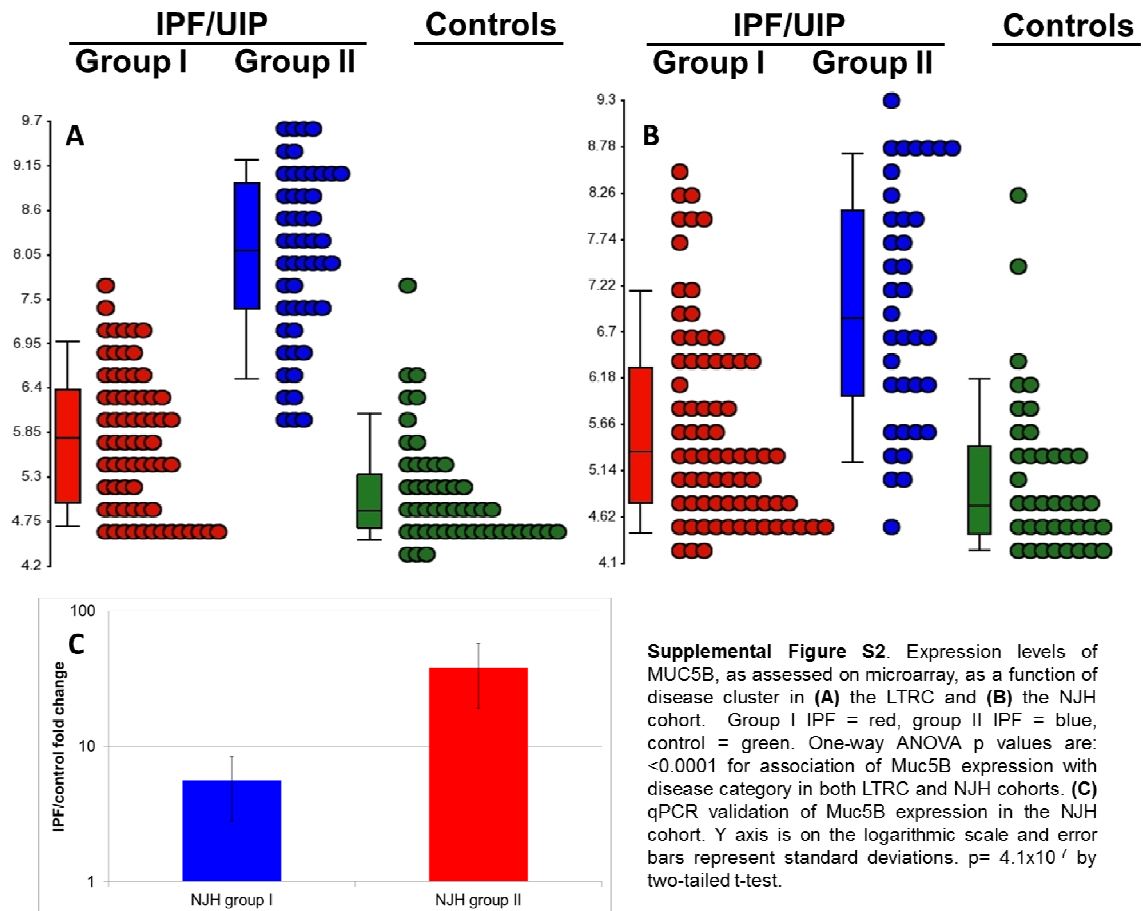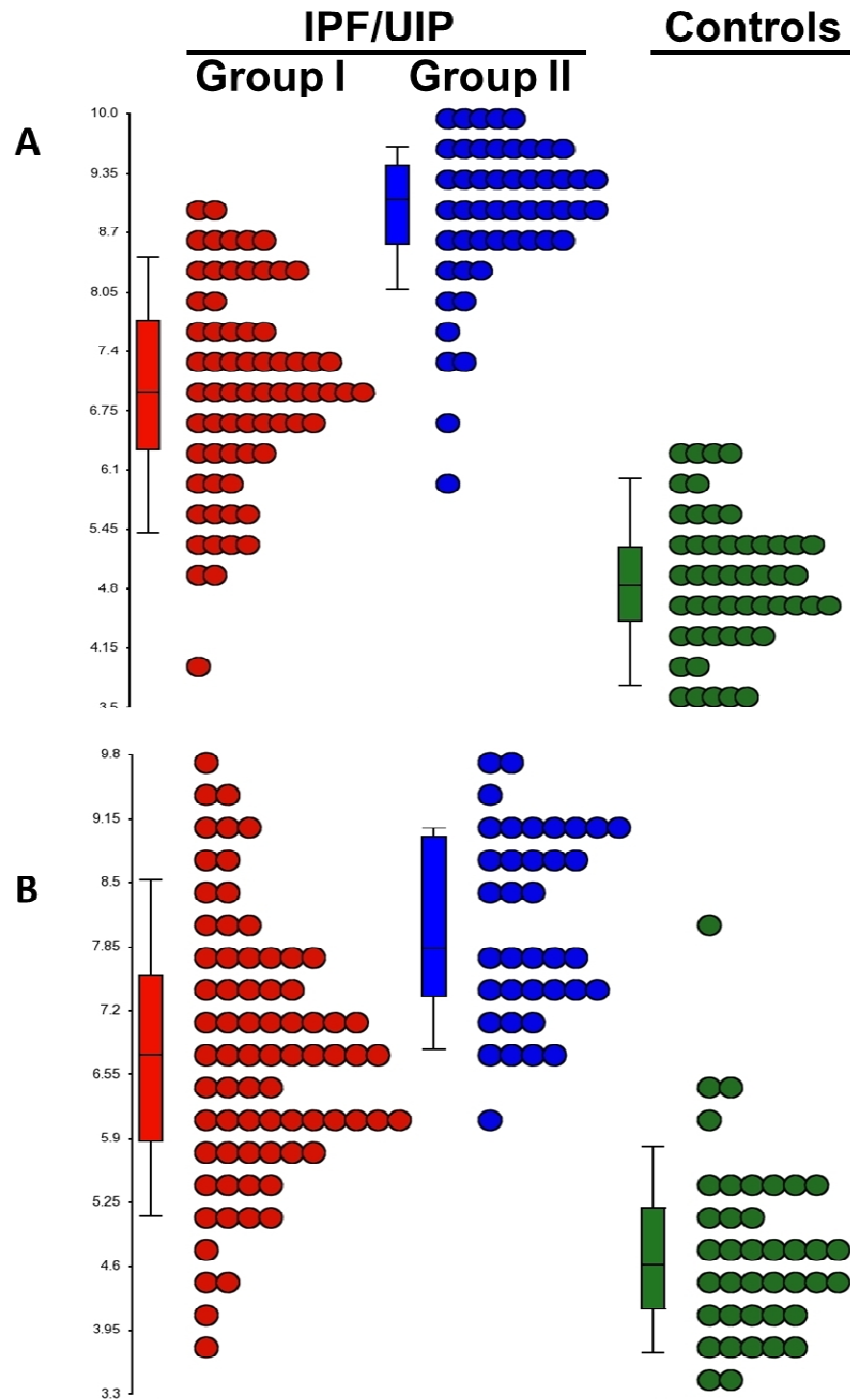**Supplemental Figure S1.** Hierarchical clustering of 119 IPF/UIP (red) and 50 control (blue) based on expression of 472 transcipts with >2 fold change between IPF and control.

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 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. **(C)** qPCR validation of Muc5B expression in the NJH cohort. Y axis is on the logarithmic scale and error bars represent standard deviations. p= 4.1×10^{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.
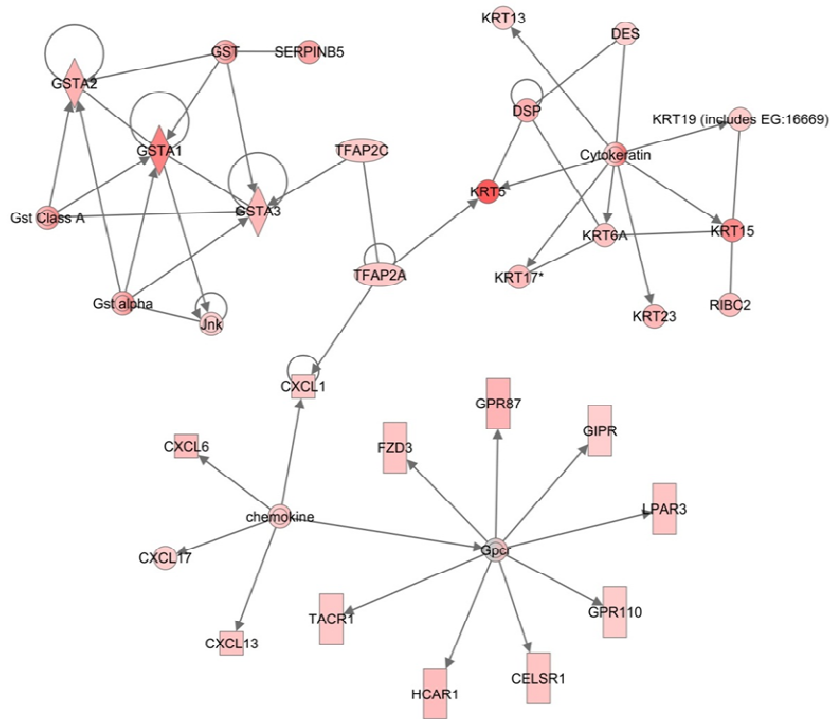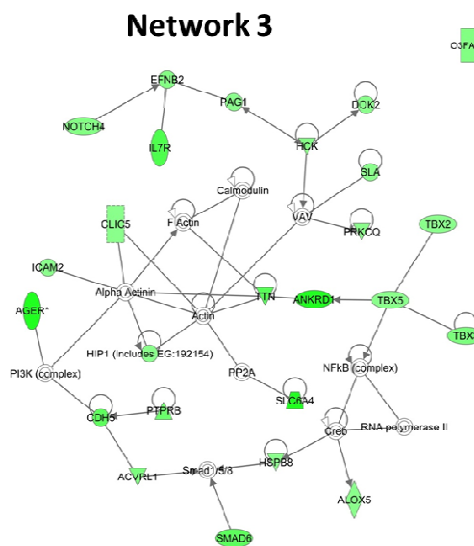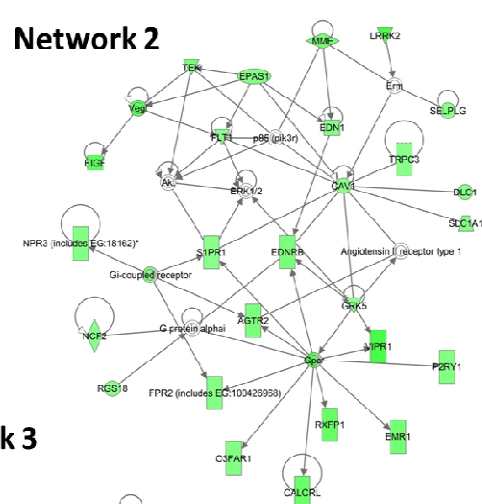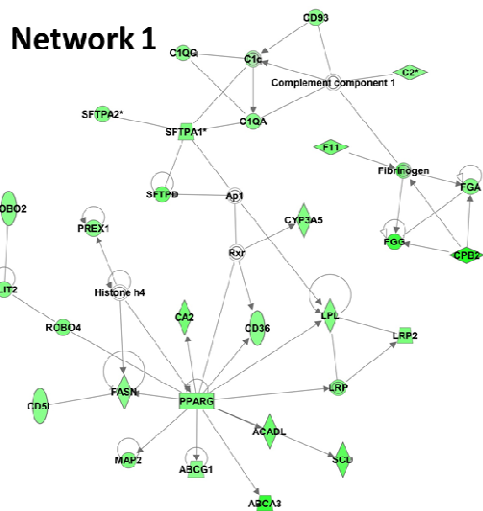
Network 2
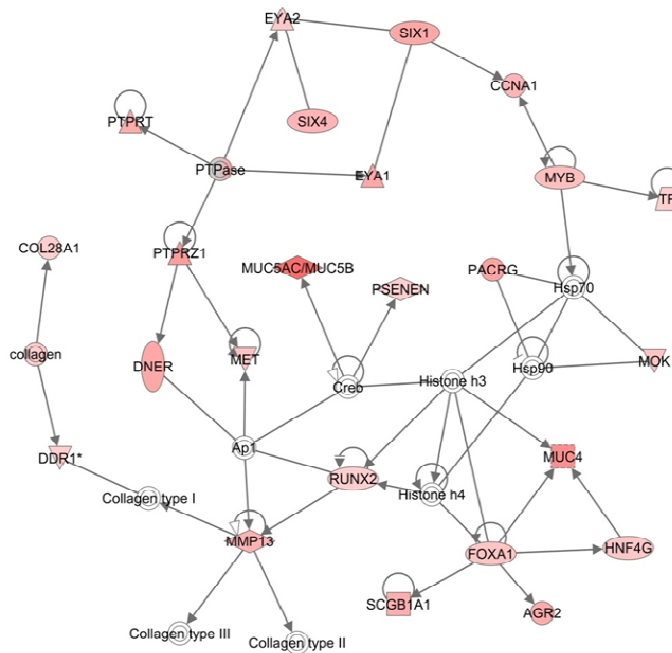
Network 3

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.

Network 1



Network 2

Network 3

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.
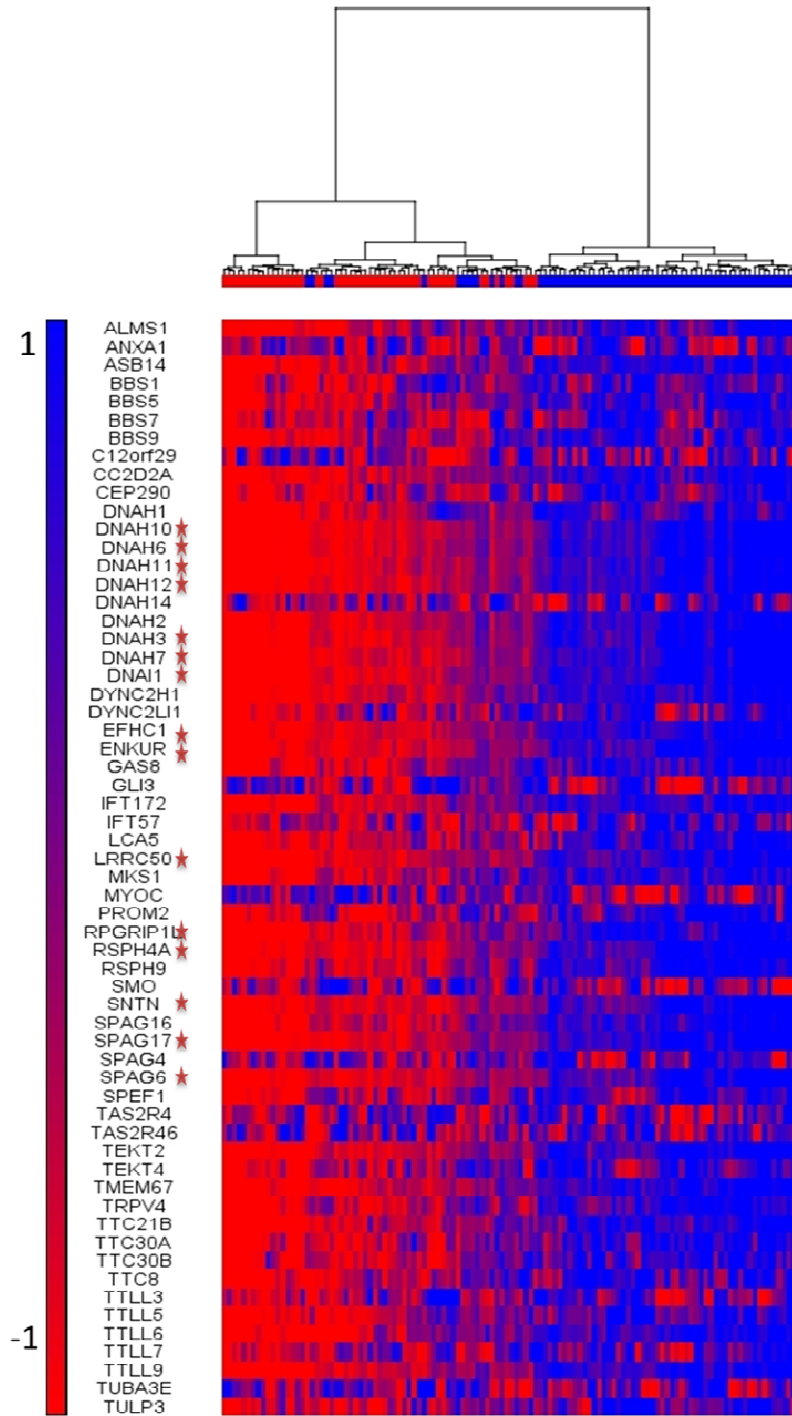
Supplemental Figure S6. Hierarchical clustering of cilium-associated genes (GO:0005929, cellular component (cilium)) across samples in groups I (blue) and II (red) in Figure 1. Asterisk next to the gene names indicates presence in cluster B in Figure 1.

A

PCA Mapping (65.2%)

B

DNAH6　　DNAH7

MUC5B　　MMP7
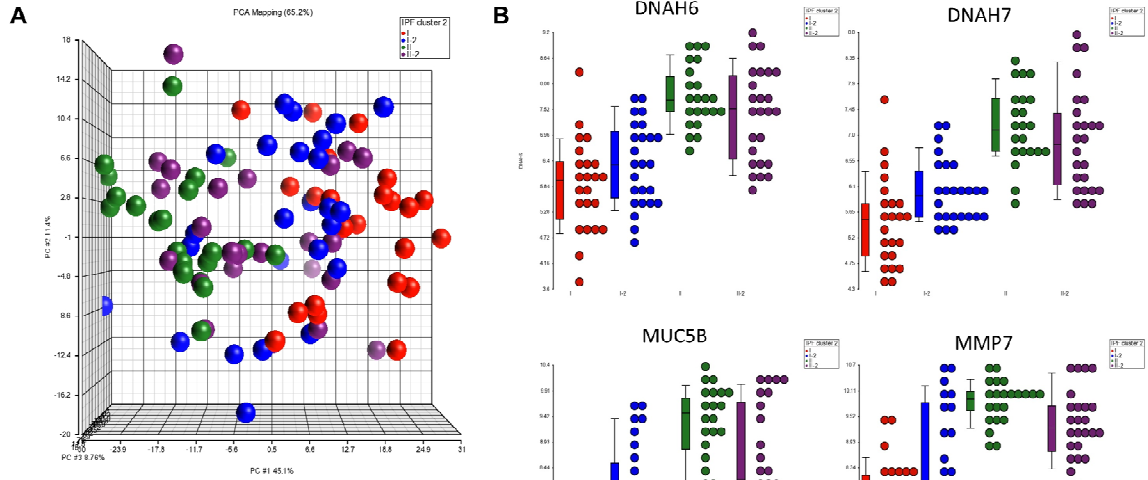
Supplemental Figure S7. (A) Principal components analysis of the initial profiles from Group I (red) and Group II (green) IPF/UIP subjects along with additional lobe profiles from the same subjects in Group I (blue) and Group II (purple). The analysis was done on 472 genes that were identified to distinguish IPF from controls at 5%FDR and >2 fold. **(B)** Expression levels of DNAH6, DNAH7, MUC5B, and MMP7, as assessed on microarray, as a function of disease cluster in the original specimens and additional lobes from the same subjects. Additional lobes from 23 Group I and 22 Group II IPF/UIP subjects were profiled. Red = original specimens from Group I, blue = additional lobes from Group I, green = original specimens from Group II, and purple = additional lobes from Group II).
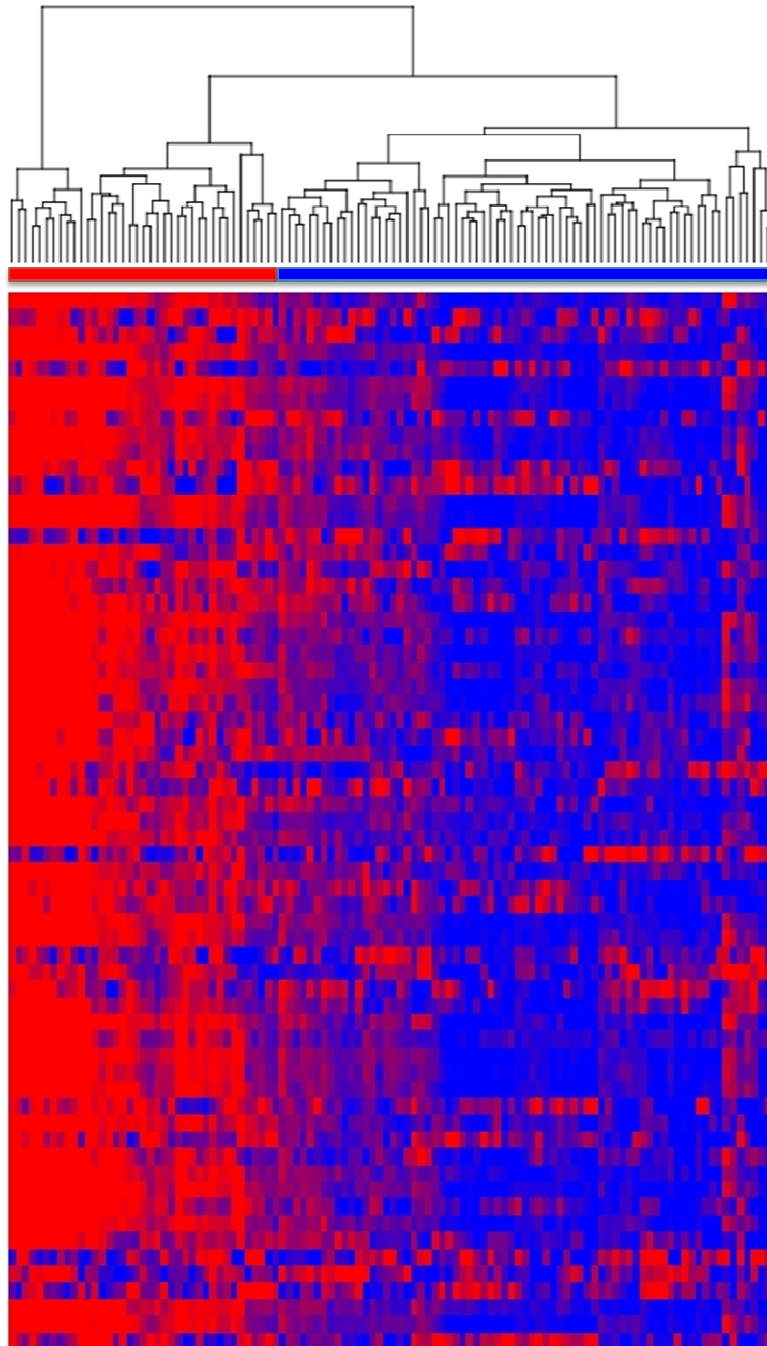
Supplemental Figure S8. Cilium-associated gene expression signature is validated in an independent cohort of IPF/UIP patients. Expression of cilium-associated genes divides the NJH cohort of 111 IPF/UIP subjects into two groups of subjects, one with high cilium gene expression (red bar; n = 39) and a group with low cilium expression (blue bar, n=72).