

Figure S1: Details of Figure 1c.

Figure S2: Details of Figure 2c.

Figure S3: Comparison of gene expression levels before and after pirfenidone (PFD) administration using real-time quantitative PCR. (a) *CCNE1*, (b) *SERPINE1*. We performed qRT-PCR to confirm the potential effects of PFD on the transcriptome signature of PBMCs in patients with IPF. The qRT-PCR of *CCNE1* and *SERPINE1* showed a trend similar to the transcriptome signature, though not significant because there were only three specimens.

Figure S4: Details of Figure 3c.

Figure S5: Comparison of gene expression levels before and after nintedanib (NTD) administration using real-time qPCR. (a) *ACOT7*, (b) *CCNB2*, (c) *CDK1*, (d) *SERPINE1*. We performed qRT-PCR to confirm the potential effects of NTD on the transcriptome signature of PBMCs in patients with IPF. The qRT-PCR of *ACOT7*, *CCNB2*, *CDK1*, and *SERPINE1* showed a trend similar to the transcriptome signature, though not significant because there were only three specimens.

Table S1: Details of oral medication in the patients with IPF.

Table S2: Differential gene expression in PBMCs between idiopathic pulmonary fibrosis (IPF) and healthy controls (HCs).

Table S3: Enrichment analysis of transcriptome data. Gene Ontology (biological process): IPF vs. HCs.

Table S4: Enrichment analysis of transcriptome data. Gene Ontology (molecular function): IPF vs. HCs.

Table S5: Enrichment analysis of transcriptome data. Gene Ontology (cellular component): IPF vs. HCs.

Table S6: Differential gene expression in PBMCs between before and after PFD administration.

Table S7: Differences in transcriptome levels of molecules related to PFD acting mechanisms.

Table S8: Enrichment analysis of transcriptome data. Gene Ontology (biological process): before vs. after PFD administration.

Table S9: Enrichment analysis of transcriptome data. Gene Ontology (molecular function): before vs. after PFD administration.

Table S10: Enrichment analysis of transcriptome data. Gene Ontology (cellular component): before vs. after PFD administration.

Table S11: Differential gene expression in PBMCs between before and after NTD administration.

Table S12: Differences in transcriptome levels of molecules related to NTD acting mechanisms.

Table S13: Enrichment analysis of transcriptome data. Gene Ontology (biological process): before vs. after NTD administration.

Table S14: Enrichment analysis of transcriptome data. Gene Ontology (molecular function): before vs. after NTD administration.

Table S15: Enrichment analysis of transcriptome data. Gene Ontology (cellular component): before vs. after NTD administration.

Table S16: RPM data of the representative gene expression levels.