Annex

Table S1. Overlapping differentially expressed genes identified across the three studies

GEO	No	Gene	
GSE180415 & GSE17978 & GSE1724, 10921, 44723, and 40839	2	*SECTM1, RBP1*	
GSE180415 & GSE1724, 10921, 44723, and 40839	11	*NUAK1, XYLT1, ABAT, TRPA1, TIMP3, RTP4, TNFRSF21, CDH2, DACT1, NREP, NAP1L3*	
GSE180415 & GSE17978	55	*ADAM12, MGP, PDLIM4, NETO2, MFAP4, DENND3, SPARC, COL1A1, GCH1, CD163L1, KAZALD1, STXBP2, CCDC80, COL5A1, ADAMTS2, TPPP3, PTGFRN, SERPINB2, PTGDS, DGAT2, LAMA4, THY1, FMOD, LCP1, FABP3, BST2, THBS2, PTGS1, SPP1, AREG, HAPLN3, CD9, INHBA, KCNC4, KIF21B, SLC29A3, CPZ, CLDN1, ADA, LGMN, VCAM1, CHN1, CD200, POSTN, COL1A2, BATF, RARRES2, GAS7, SEMA3C, USP18, AFAP1, ID3, COL3A1, ADORA1, PPP1R14C*	
GSE17978 & GSE1724, 10921, 44723, and 40839	24	*OAS1, TNFRSF14, STOM, TTC3, NFKBIA, SIPA1L1, CALB2, NINJ1, GBP2, BCL6, PROCR, TRIAP1, ASB1, TRIM22, HHAT, ITGBL1, NR1H3, NFIB, CBR3, GLRX2, ANKFY1, STAT5B, BTN3A2, PMEPA1*	

A table demonstrates the overlapping genes between three studies: GSE180415 (Hanmandlu et al. 2022) and GSE17978 (Emblom-Callahan et al. 2010) and GSE1724, 10921, 44723, and 40839 (Plantier et al. 2016). *Abbreviations:* GEO: gene expression omnibus; GSE: Gene expression omnibus series

Table S2. Overlapping GO terms identified across three independent transcriptomic studies

GEO	No	GO ID	Category	GO term
GSE180415 & GSE17978	16	GO:0007155	BP	cell adhesion
		GO:0030198	BP	extracellular matrix organization
		GO:0030199	BP	collagen fibril organization
		GO:0005886	CC	plasma membrane
		GO:0062023	CC	collagen-containing extracellular matrix
		GO:0005615	CC	extracellular space
		GO:0005576	CC	extracellular region
		GO:0009986	CC	cell surface
		GO:0031012	CC	extracellular matrix
		GO:0005604	CC	basement membrane
		GO:0005581	CC	collagen trimer
		GO:0005788	CC	endoplasmic reticulum lumen
		GO:0001725	CC	microfibril
		GO:0005201	MF	extracellular matrix structural constituent
		GO:0005178	MF	integrin binding
		GO:0048407	MF	platelet-derived growth factor binding
GSE17978 & GSE1724, 10921, 44723, and 40839	3	GO:0009615	BP	response to virus
		GO:0005829	CC	cytosol
		GO:0005515	MF	protein binding

A table demonstrates the overlapping GO terms between three studies: GSE180415 (Hanmandlu et al. 2022) and GSE17978 (Emblom-Callahan et al. 2010) and GSE1724, 10921, 44723, and 40839 (Plantier et al. 2016). *Abbreviations:* GO: gene ontology; GEO: gene expression omnibus; GSE: gene expression omnibus series; BP: biological process; CC: cellular component; and MF: molecular function

Table S3. A list of 475 DEGs identified from primary lung fibroblasts of 33 IPF patients and 10 controls, ranked in descending order of $\log_2$FC

Gene	Control	IPF	$\log_2$FC	adj p (Bonferroni)
SCUBE1	0±0	1.42±1.81	13.03	1.005.E-04
BMP5	0.02±0.04	2.7±2.58	11.18	2.700.E-04
TMEM176B	0±0	1.07±1.44	10.91	3.721.E-04
C7	0±0.01	1.18±1.18	9.15	6.985.E-08
HSD17B2	0.02±0.06	1.83±1.83	8.88	1.335.E-04
CFTR	0±0.01	0.81±1.08	8.68	1.124.E-03
NKD2	0.01±0.02	1.21±1.27	8.54	2.562.E-05
HMGCLL1	0.04±0.07	1.49±1.37	6.79	4.835.E-04
ADH1B	0.46±0.67	3.84±2.48	6.63	2.044.E-03
RASL12	0.14±0.2	2.36±1.78	6.47	6.650.E-05
GDF10	0.09±0.12	1.7±1.62	6.41	9.334.E-03
HBG1	0.02±0.03	0.65±0.78	6.13	4.057.E-03
ADAMTS8	0.91±0.7	4.35±2.67	6.08	7.672.E-05

Gene	**Control**	**IPF**	**log$_2$FC**	**adj *p* (Bonferroni)**
ADAMTS19	0.13±0.18	2.02±1.59	5.96	1.092.E-03
ADH1A	0.04±0.07	0.97±1.13	5.93	7.946.E-03
EDNRB	0.53±0.94	4.43±2.03	5.92	3.477.E-04
FGFR4	0.24±0.21	2.6±1.77	5.91	1.144.E-05
LOC105375566	0.04±0.06	1.03±0.96	5.81	4.515.E-03
TNFSF15	0.37±0.3	2.64±1.71	5.81	9.899.E-05
RIPOR3-AS1	0.05±0.06	0.97±1.02	5.77	1.800.E-03
C3	0.31±0.26	2.77±1.65	5.65	1.374.E-03
HBG2	0.07±0.07	1.19±1.22	5.58	1.937.E-02
PTGDS	0.15±0.26	1.9±1.39	5.45	1.161.E-03
GRIK4	0.05±0.06	0.94±0.98	5.31	8.694.E-03
LAMA3	0.71±0.31	4.02±1.44	5.23	4.088.E-13
MYOC	0.07±0.13	1.2±0.93	5.08	1.983.E-03
PURPL	0.07±0.07	1.03±0.95	5.05	2.044.E-03
LOC101927057	0.16±0.11	1.94±1.02	5.01	3.538.E-11
TUBBP2	0.2±0.06	1.75±1.62	4.96	6.009.E-03
SMIM41	0.14±0.07	1.33±1.34	4.92	9.395.E-03
ADGRD1	0.11±0.16	1.21±1.03	4.86	1.861.E-02
CCND2	0.46±0.57	2.52±1.9	4.85	3.660.E-02
PDK4	2.72±0.99	5.33±2.35	4.79	1.457.E-02
RGS18	0.2±0.15	1.65±1.41	4.79	2.989.E-03
ARHGAP28	0.59±0.48	2.95±1.85	4.77	6.391.E-04
ABCC6	0.04±0.06	0.57±0.58	4.51	3.203.E-03
F11R	0.14±0.16	1.27±1.14	4.50	2.227.E-02
PAPPA	3.84±0.69	7.23±1.73	4.42	5.399.E-06
CPZ	0.08±0.13	0.88±0.78	4.37	7.763.E-03
PPL	0.09±0.17	0.99±0.88	4.32	1.150.E-02
PITX1	0.24±0.29	1.63±1.33	4.26	1.293.E-02
LOC107986606	0.1±0.13	1.04±0.85	4.25	1.322.E-02
OAS2	0.39±0.28	1.95±1.45	4.19	1.130.E-03
BDKRB2	2.78±0.92	6.18±1.67	4.16	1.647.E-07
RIPOR2	0.47±0.54	2.71±1.29	4.16	1.662.E-04
NSG1	0.27±0.33	1.75±1.24	4.16	1.968.E-03
SCN2A	1±0.38	3.73±1.24	4.11	3.920.E-10
FAM198B-AS1	0.2±0.29	1.67±0.89	4.03	3.950.E-05
LOC105377329	0.06±0.13	0.72±0.59	4.01	3.828.E-03
ABCA6	0.95±0.59	3.59±1.38	4.01	1.461.E-06
CXCL5	1.71±0.81	4.17±1.91	4.01	3.737.E-03
CFD	0.42±0.43	2.17±1.41	3.98	1.586.E-03
RSPO3	0.52±0.25	2.14±1.39	3.93	2.715.E-02

Table S3 (*Continued*)

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
LRRN4CL	0.55±0.62	2.86±1.2	3.91	4.271.E-05
RARRES2	0.97±0.82	3.55±1.62	3.88	5.430.E-04
STON2	0.12±0.13	0.96±0.84	3.86	8.297.E-03
PTGES	1.15±0.53	3.77±1.37	3.85	1.016.E-07
MUSK	0.65±0.52	2.44±1.51	3.80	3.584.E-03
FIBIN	1.45±0.67	4.23±1.39	3.76	7.794.E-08
DLL1	0.23±0.14	1.26±1.1	3.74	4.667.E-03
TSPAN12	1.41±0.44	3.73±1.56	3.73	4.820.E-05
GREB1	0.12±0.2	0.94±0.77	3.65	2.547.E-02
RIPOR3	0.86±0.38	3±1.2	3.65	9.166.E-07
CCN5	0.25±0.15	1.3±1.04	3.64	6.025.E-03
DPP4-DT	0.19±0.18	1.26±0.79	3.63	1.170.E-04
GASK1B	2.3±1.17	5.92±1.02	3.61	1.261.E-10
TARID	0.29±0.17	1.58±0.86	3.57	2.715.E-07
TCF21	2.78±0.66	5.75±1.47	3.56	5.887.E-09
LOC105375153	0.13±0.08	0.77±0.79	3.55	4.774.E-02
ABCA8	2.25±0.67	5.17±1.2	3.50	1.632.E-08
SELENOP	2.98±0.75	5.98±1.18	3.47	1.062.E-07
FBN2	4.54±1.85	8.39±1.4	3.45	7.718.E-05
LOC107986020	0.81±0.49	2.41±1.48	3.42	1.937.E-02
KCNJ2	2.23±0.79	5.19±1.07	3.41	1.693.E-10
TG	0.17±0.13	0.94±0.86	3.41	3.966.E-02
ANKRD29	0.68±0.57	2.73±1.01	3.37	4.179.E-06
LOC101928674	0.15±0.09	0.83±0.72	3.36	1.383.E-02
LINC01936	0.24±0.32	1.41±0.84	3.35	2.425.E-02
DHRS3	1.59±0.89	4.29±1.25	3.33	3.416.E-06
GDF15	2.18±0.52	4.43±1.36	3.32	1.830.E-04
BTG2	1.25±0.38	3.2±1.31	3.29	1.423.E-04
HLA-DMB	0.59±0.22	2.22±1.02	3.27	3.889.E-06
GPRC5B	0.98±0.83	3.27±1.31	3.26	4.728.E-04
CPM	0.87±0.44	3.03±0.87	3.26	1.142.E-10
CYP1B1	4.23±1.21	7.28±1.41	3.25	1.016.E-04
SERPINF1	1.73±1.42	4.81±1.5	3.19	2.074.E-03
VWA5A	2.79±1.08	5.63±1.35	3.18	3.966.E-06
MAN1C1	0.7±0.3	2.19±1.27	3.18	1.293.E-02
CLIC2	0.73±0.45	2.43±1.23	3.17	6.985.E-04
CLCA2	0.25±0.18	1.13±0.89	3.16	2.944.E-02
LINC02015	0.21±0.26	1.17±0.73	3.15	1.290.E-02
SEZ6L2	0.18±0.21	1.05±0.63	3.14	6.391.E-03
GGT1	0.23±0.08	1.07±0.82	3.14	1.571.E-03
C2	0.29±0.23	1.4±0.75	3.13	3.782.E-05

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
SNCA	0.8±0.67	2.69±1.31	3.12	1.357.E-02
FBLN1	2.2±1.28	5.11±1.48	3.08	6.208.E-04
FAM83B	0.14±0.14	0.83±0.54	3.08	1.678.E-03
LOC107985134	0.62±0.35	2.09±1.11	3.08	7.001.E-03
IL16	0.99±0.57	2.98±1.17	3.06	4.133.E-04
VAMP8	0.5±0.63	2.12±1.16	3.06	2.761.E-02
CYGB	1.95±0.78	4.2±1.39	3.04	1.983.E-04
IQGAP2	1.13±0.4	2.9±1.24	3.03	2.562.E-04
SVEP1	4.95±0.86	7.74±1.22	3.03	5.155.E-09
PSG8-AS1	0.11±0.11	0.65±0.44	3.00	1.678.E-04
IFI44L	1.32±0.41	2.94±1.48	3.00	1.315.E-02
SLC40A1	2.57±0.64	4.91±1.28	2.99	7.962.E-06
FAM83H	0.31±0.14	1.29±0.87	2.99	3.874.E-03
IGSF10	0.76±0.3	2.44±0.97	2.96	4.179.E-06
TNFRSF21	1.49±0.67	3.58±1.32	2.96	3.310.E-04
CAND1.11	0.09±0.08	0.55±0.36	2.90	3.218.E-03
BMP4	1.55±0.54	3.42±1.41	2.90	1.309.E-03
CXCL2	0.88±0.3	2.23±1.24	2.88	1.815.E-02
C15orf48	0.45±0.28	1.74±0.8	2.86	2.013.E-05
ATP8B4	1.21±0.34	2.97±1.15	2.85	5.262.E-05
PRKG2	3.41±1	6.13±0.84	2.83	4.484.E-09
DPP4	4.11±0.91	6.65±1.18	2.82	4.377.E-06
SCN7A	1.49±0.54	3.19±1.55	2.80	3.401.E-02
BMP2	1.58±0.35	3.33±1.16	2.80	3.005.E-03
IP6K3	0.34±0.19	1.37±0.69	2.78	4.286.E-05
PRCD	0.28±0.13	1.15±0.67	2.75	1.216.E-03
TXNIP	3.37±0.86	5.8±1.21	2.75	5.125.E-06
CEMIP	4.84±1.87	7.97±1.2	2.73	2.608.E-03
LOC105376236	0.45±0.34	1.66±0.72	2.71	4.896.E-04
MCC	2.9±0.73	5.31±0.88	2.71	2.486.E-08
P2RY1	1.74±0.61	3.69±1.31	2.71	4.682.E-04
SERPING1	1.01±0.43	2.69±0.92	2.70	2.532.E-05
KCND1	0.19±0.07	0.81±0.58	2.69	1.223.E-02
QPRT	2.16±0.71	4.18±1.16	2.67	1.333.E-04
TFPI2	6.27±1.01	8.61±1.26	2.66	2.410.E-03
CSRNP3	0.94±0.75	2.76±1.06	2.66	4.682.E-03
MME	5.96±0.71	8.33±1.12	2.66	4.515.E-07
TNFSF10	0.42±0.37	1.48±0.86	2.65	4.637.E-02
NR4A2	1.7±0.27	3.3±1.16	2.64	4.759.E-03
IFITM1	1.85±0.9	4.13±0.98	2.62	4.118.E-06

Table S3 (*Continued*)

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
MEDAG	2.42±0.57	4.28±1.4	2.61	4.240.E-03
DNAI3	0.95±0.22	2.46±0.92	2.60	4.774.E-06
TEK	2.71±0.67	4.79±1.22	2.59	2.898.E-04
LOC105379082	0.49±0.28	1.52±0.88	2.58	1.008.E-02
ZFP2	0.16±0.1	0.73±0.37	2.58	1.010.E-05
C16orf89	0.36±0.2	1.21±0.77	2.56	4.362.E-02
EPAS1	5.85±0.91	8.31±0.96	2.54	1.135.E-07
TXLNB	0.24±0.12	0.93±0.54	2.53	5.796.E-04
ICAM1	1.81±0.74	3.88±0.9	2.53	2.669.E-06
RAB27B	1.31±0.59	3.11±1	2.52	4.987.E-05
CABLES1	2.69±0.56	4.83±0.97	2.52	6.818.E-09
C5orf66	0.26±0.18	0.96±0.6	2.50	1.469.E-02
MOXD1	3.39±0.74	5.77±0.73	2.49	6.147.E-13
FBXO32	2±0.54	3.63±1.37	2.48	2.898.E-02
ADAMTS14	0.74±0.2	1.98±0.88	2.48	2.090.E-04
TMEM140	1.26±0.46	2.97±0.85	2.48	9.243.E-07
HLA-DMA	1.02±0.35	2.61±0.75	2.48	1.158.E-07
OVCH1	0.82±0.5	2.37±0.74	2.47	7.931.E-06
ACOT12	0.32±0.23	1.16±0.59	2.46	4.713.E-03
ICAM4	0.43±0.22	1.45±0.6	2.45	1.601.E-05
LOC107986064	0.4±0.19	1.3±0.66	2.44	5.826.E-04
INSYN2A	0.72±0.25	1.95±0.82	2.43	5.231.E-04
SPRY1	1.2±0.38	2.75±0.91	2.42	2.303.E-05
DDIT4	1.82±0.66	3.65±1.01	2.41	2.654.E-04
KCNJ2-AS1	0.21±0.15	0.84±0.4	2.41	1.119.E-03
ARHGEF3	1.26±0.47	2.95±0.78	2.40	1.020.E-05
THRB	1.48±0.61	3.11±1.23	2.40	8.190.E-03
ASPA	0.36±0.23	1.25±0.58	2.39	4.743.E-04
FAXDC2	1.05±0.45	2.45±1	2.38	2.501.E-03
TAS2R4	0.2±0.09	0.75±0.49	2.37	4.698.E-03
FOSB	2.39±0.46	4.02±1.3	2.36	5.338.E-03
FAM43A	1.64±0.7	3.23±1.17	2.36	2.898.E-02
SLC16A14	1.87±0.6	3.53±1.16	2.33	2.242.E-03
CELSR3	0.88±0.27	2.15±0.82	2.32	2.532.E-04
IFI30	1.38±0.42	2.93±0.88	2.31	6.238.E-05
ADAMTSL4	1.42±0.36	2.97±0.91	2.30	2.120.E-05
GJD3	0.47±0.37	1.46±0.69	2.29	4.606.E-03
TP53I11	3.2±0.78	5.05±1.21	2.27	4.987.E-03
IL13RA2	2.63±0.63	4.56±0.94	2.27	3.279.E-05
PTGS1	5.25±0.69	7.07±1.3	2.27	4.591.E-03
CFB	1.87±0.48	3.53±0.97	2.26	5.887.E-05

Gene	Control	IPF	$\log_2$FC	adj p (Bonferroni)
TLR3	0.96±0.6	2.37±0.95	2.25	1.907.E-02
CCL2	4.61±0.87	6.61±1.19	2.24	1.103.E-03
RFTN2	0.78±0.31	1.97±0.78	2.23	2.898.E-03
APOL1	1.81±0.64	3.39±1.09	2.22	8.389.E-03
SNAP25	1.98±0.55	3.68±0.95	2.21	7.672.E-05
LINC01914	0.25±0.16	0.85±0.45	2.20	1.482.E-02
PARP15	0.42±0.18	1.2±0.66	2.19	1.800.E-02
CFAP54	0.75±0.17	1.85±0.71	2.19	1.784.E-04
INMT	2.8±1.29	5.1±1.14	2.19	1.425.E-02
FRK	1.56±0.64	3.05±1.04	2.18	1.432.E-02
GPNMB	5.05±1.91	7.66±1.07	2.17	4.408.E-02
LOC105369344	0.19±0.11	0.68±0.37	2.17	3.782.E-03
SLC4A11	0.4±0.11	1.19±0.52	2.16	2.944.E-05
MPZ	0.23±0.16	0.79±0.42	2.13	1.356.E-02
LINC00685	0.19±0.1	0.66±0.38	2.13	2.806.E-03
SLC16A4	3.74±0.41	5.35±1.05	2.13	1.490.E-03
TLCD2	2.1±0.38	3.72±0.84	2.13	8.145.E-06
LINC00545	0.19±0.14	0.67±0.35	2.12	7.290.E-03
ABCA1	5.56±0.6	7.41±1	2.12	1.678.E-05
NR4A3	1.31±0.29	2.5±0.99	2.11	2.822.E-02
LOC107985349	0.51±0.22	1.36±0.66	2.10	7.992.E-03
SLC25A27	0.51±0.28	1.37±0.66	2.09	1.327.E-02
TNFAIP6	3.52±0.63	5.14±1.25	2.09	7.595.E-03
ADAMTS13	0.32±0.13	0.93±0.56	2.07	3.401.E-02
SLC44A3-AS1	0.24±0.14	0.78±0.39	2.06	5.018.E-03
CCDC69	0.64±0.22	1.54±0.74	2.05	1.556.E-02
TMEM51	1.7±0.46	3.24±0.79	2.05	7.901.E-06
GPRC5A	3.93±0.41	5.56±1.01	2.05	2.761.E-04
KIAA1217	1.87±0.63	3.33±1.04	2.04	1.800.E-02
SLC2A9	0.58±0.29	1.52±0.6	2.03	2.120.E-03
NEK10	3.17±0.42	4.81±0.95	2.02	3.737.E-05
MMP15	0.65±0.29	1.58±0.7	2.02	1.556.E-02
PODN	2.4±0.72	3.95±1.11	2.01	2.288.E-02
CKMT2	0.48±0.2	1.31±0.51	2.01	6.025.E-04
GALNT15	3.83±0.68	5.69±0.8	2.00	2.166.E-07
PLD1	3.11±0.29	4.65±0.96	1.99	7.885.E-04
LOC105369844	0.54±0.3	1.45±0.5	1.99	2.547.E-04
PLA2R1	2.61±0.87	4.44±0.81	1.99	3.584.E-04
IL6R	2.42±0.42	4.1±0.65	1.97	7.687.E-10
LOC107985915	0.34±0.22	1±0.45	1.96	6.360.E-03

Table S3 (*Continued*)

Gene	**Control**	**IPF**	**log$_2$FC**	**adj *p* (Bonferroni)**
MYCBPAP	0.21±0.08	0.63±0.37	1.96	2.623.E-02
SGIP1	4.39±0.61	6.14±0.85	1.95	2.471.E-05
LNCTAM34A	0.46±0.18	1.24±0.42	1.94	3.645.E-05
FAM227A	0.59±0.15	1.41±0.63	1.94	4.332.E-03
RAB3IL1	1.06±0.53	2.33±0.69	1.93	2.212.E-03
BATF2	0.31±0.14	0.88±0.43	1.93	7.855.E-03
C4B	0.77±0.21	1.63±0.71	1.92	3.340.E-02
LINC01943	0.4±0.15	1.09±0.35	1.89	6.726.E-06
ZNF578	1.61±0.57	2.97±0.83	1.89	6.009.E-03
SOD2	6.69±0.22	8.25±0.94	1.88	2.303.E-04
SLC43A2	1.6±0.31	2.88±0.86	1.88	1.470.E-03
TPP1	3.22±0.23	4.65±0.95	1.87	9.594.E-04
PPP1R3C	4.86±0.29	6.48±0.85	1.87	1.845.E-06
SEMA4G	0.41±0.18	1.05±0.5	1.86	4.545.E-02
SLC44A3	0.66±0.29	1.54±0.59	1.85	7.626.E-03
PLS3-AS1	0.18±0.08	0.56±0.21	1.85	8.556.E-05
TGFB3	1.05±0.28	2.18±0.55	1.83	4.591.E-05
LOC105371267	0.45±0.15	1.12±0.51	1.83	1.490.E-02
PSMB9	1.67±0.66	3.04±0.94	1.83	2.486.E-02
MAOA	4.44±0.61	6.08±0.87	1.83	9.105.E-05
MIR381HG	0.18±0.12	0.54±0.26	1.82	1.421.E-02
LINC00663	0.49±0.13	1.16±0.58	1.79	4.621.E-02
CCDC113	1.41±0.33	2.7±0.5	1.79	2.044.E-08
AMPD3	2.5±0.41	4.02±0.56	1.78	1.399.E-09
CATSPERE	0.5±0.15	1.21±0.46	1.78	9.716.E-04
SOCAR	0.19±0.08	0.54±0.29	1.78	2.334.E-02
ZNF610	1.21±0.33	2.33±0.68	1.78	9.517.E-04
RDH10	4.61±0.88	6.28±0.93	1.78	1.540.E-02
LINC01535	0.25±0.09	0.69±0.34	1.77	2.547.E-02
F10	1.92±0.37	3.23±0.8	1.77	3.630.E-04
HNMT	3.12±0.89	4.74±0.94	1.77	5.369.E-03
PRKCH	0.75±0.26	1.64±0.56	1.75	5.582.E-03
PGM5P3-AS1	0.33±0.11	0.83±0.4	1.73	1.968.E-02
LOC105376278	0.45±0.25	1.13±0.39	1.72	1.845.E-03
LOC105376208	0.24±0.1	0.66±0.25	1.72	8.084.E-04
TMEM217	0.9±0.19	1.84±0.58	1.72	5.613.E-04
ZNF425	1.09±0.14	2.11±0.58	1.71	5.186.E-05
BEST1	2.06±0.39	3.41±0.6	1.70	1.571.E-06
DTX4	2.85±0.53	4.17±1.01	1.69	3.142.E-02
CASP10	1.9±0.49	3.26±0.61	1.69	9.822.E-05
NR4A1	2.42±0.33	3.59±0.9	1.69	4.133.E-02

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
ZBED3	0.45±0.2	1.07±0.44	1.67	2.501.E-02
TNFRSF1B	2.73±0.44	4.12±0.74	1.67	3.996.E-05
SPATA18	3.19±0.5	4.57±0.87	1.67	3.523.E-03
MIR34AHG	1.72±0.48	2.91±0.77	1.66	1.019.E-02
IGFBP4	7.97±0.39	9.29±0.98	1.66	2.166.E-02
LAMA4	7.88±0.55	9.54±0.49	1.66	9.929.E-13
TMEM198B	1.22±0.32	2.21±0.74	1.66	4.057.E-02
CMBL	2.71±0.23	4.02±0.75	1.65	1.057.E-04
FRY	3.91±0.78	5.47±0.92	1.65	8.770.E-03
NYNRIN	3.03±0.29	4.25±0.97	1.65	3.767.E-02
FGF7	6.79±0.74	8.37±0.81	1.64	2.196.E-04
SPIRE2	0.76±0.18	1.62±0.4	1.64	2.456.E-06
FBXO27	0.61±0.35	1.39±0.46	1.64	2.974.E-02
ZNF233	1.23±0.39	2.31±0.61	1.63	1.148.E-03
ANGPTL2	4.95±0.38	6.31±0.85	1.63	3.386.E-03
CLSTN3	1.51±0.26	2.6±0.65	1.62	9.639.E-04
MUC1	0.75±0.21	1.6±0.4	1.62	1.524.E-05
NHLRC4	0.34±0.12	0.83±0.36	1.61	4.591.E-02
GABARAPL1	4.88±0.56	6.31±0.84	1.60	4.499.E-03
IL1R1	5.99±0.29	7.33±0.84	1.60	5.597.E-04
C1QTNF1	2.68±0.65	4.1±0.63	1.59	1.481.E-04
ACSF2	2.88±0.29	4.21±0.64	1.59	2.761.E-06
ZHX2	1.52±0.26	2.57±0.68	1.59	4.164.E-03
SDHAP3	0.59±0.24	1.31±0.4	1.58	5.811.E-03
ADM	5.99±0.44	7.44±0.72	1.58	1.601.E-06
APOL3	1.7±0.67	2.97±0.69	1.56	1.069.E-02
CSF1	3.46±0.45	4.89±0.53	1.56	1.647.E-09
TRANK1	3.61±0.48	4.97±0.71	1.56	1.522.E-04
EXPH5	3.72±0.39	5±0.83	1.55	1.922.E-03
LOC100287290	1.67±0.28	2.74±0.69	1.55	3.096.E-03
CREG1	3.86±0.84	5.37±0.77	1.55	4.088.E-03
LINC02709	0.6±0.19	1.29±0.38	1.55	4.347.E-04
CSDC2	1.67±0.6	2.9±0.63	1.55	4.438.E-03
ORAI3	2.54±0.44	3.79±0.74	1.54	2.257.E-03
C1R	6.07±0.67	7.48±0.88	1.53	4.591.E-03
CTSK	6.95±0.73	8.34±0.91	1.53	1.556.E-02
HSPD1P11	2.01±0.43	3.15±0.75	1.53	1.769.E-02
TMTC1	6.99±0.88	8.62±0.66	1.53	3.096.E-05
PLTP	2.66±0.3	3.89±0.69	1.53	1.693.E-04
DHX58	1.78±0.52	2.99±0.58	1.53	2.684.E-04

Table S3 (*Continued*)

Gene	**Control**	**IPF**	**log$_2$FC**	**adj *p* (Bonferroni)**
ZNF815P	0.72±0.22	1.45±0.45	1.51	3.005.E-03
TNFRSF14	2.81±0.4	4.01±0.74	1.51	3.096.E-03
LOC102724397	0.54±0.17	1.14±0.4	1.50	1.556.E-02
EFEMP1	6.87±0.54	8.26±0.77	1.50	1.475.E-04
ARRDC4	4.15±0.49	5.47±0.78	1.50	4.926.E-03
QSOX1	8.27±0.3	9.54±0.78	1.50	1.586.E-03
DLGAP1-AS1	1.13±0.23	2.11±0.33	1.49	5.796.E-08
PLEKHO2	4.95±0.33	6.3±0.61	1.49	9.090.E-08
PLAT	4.85±0.36	6.05±0.92	1.49	3.081.E-02
NPL	0.52±0.2	1.12±0.34	1.48	1.678.E-02
KCTD12	5.59±0.35	6.87±0.67	1.47	2.044.E-04
NAV1	5.95±0.34	7.24±0.72	1.46	7.245.E-05
AZIN2	0.95±0.29	1.79±0.45	1.45	1.693.E-03
MANBA	4.73±0.35	5.96±0.75	1.44	8.968.E-04
LOC728743	0.8±0.2	1.55±0.4	1.44	6.513.E-04
BMS1P14	2.07±0.5	3.29±0.46	1.44	5.552.E-06
SEMA3B	2.35±0.45	3.51±0.66	1.43	5.384.E-03
CDHR3	0.88±0.34	1.67±0.49	1.43	4.835.E-02
GLRX	5.27±0.73	6.66±0.69	1.41	6.009.E-04
ANTXR1	6.45±0.26	7.63±0.75	1.40	8.267.E-03
TMEM150A	1.52±0.22	2.43±0.6	1.38	1.049.E-02
TSGA10	0.84±0.1	1.52±0.47	1.38	1.815.E-02
MILR1	2.14±0.55	3.29±0.59	1.38	2.486.E-03
PNRC1	3.74±0.22	4.84±0.74	1.37	2.867.E-02
C1S	6.87±0.59	8.15±0.71	1.37	1.830.E-03
STAT2	6.07±0.42	7.36±0.57	1.37	2.486.E-06
LITAF	5.39±0.38	6.67±0.55	1.37	9.975.E-08
LOC102724149	0.55±0.15	1.09±0.37	1.36	3.538.E-02
SRPX	4.16±0.34	5.41±0.49	1.36	5.475.E-08
TPCN1	2.63±0.19	3.65±0.71	1.36	2.105.E-02
AQP11	1.14±0.27	1.97±0.48	1.35	3.599.E-03
HEBP1	3.87±0.41	5.1±0.56	1.35	8.556.E-06
HELZ2	2.91±0.21	3.97±0.67	1.34	1.394.E-03
GNG11	7.18±0.16	8.29±0.75	1.32	1.556.E-03
TMCC1-AS1	0.74±0.21	1.39±0.37	1.31	4.515.E-02
GTF2IP20	0.64±0.14	1.22±0.36	1.31	1.800.E-02
PLXNB1	3.48±0.33	4.53±0.77	1.31	2.730.E-02
C1RL-AS1	1.76±0.31	2.73±0.49	1.31	6.391.E-04
FBLN5	5.49±0.45	6.69±0.64	1.31	2.959.E-04
USP53	5.51±0.29	6.59±0.73	1.30	1.632.E-02
PMP22	5.9±0.39	7.01±0.84	1.30	2.303.E-02

Gene	Control	IPF	$\log_2$FC	adj p (Bonferroni)
IGF2R	7.28±0.2	8.35±0.8	1.30	2.501.E-02
SH3D19	5.07±0.33	6.24±0.6	1.30	1.647.E-05
CYB561	2.92±0.54	4.07±0.56	1.29	1.617.E-03
RHOBTB3	7.78±0.45	8.97±0.67	1.28	8.602.E-04
UBE2L6	3.98±0.44	5.18±0.51	1.28	3.615.E-07
OAF	3.03±0.64	4.2±0.62	1.28	6.360.E-03
ZFP14	2.24±0.5	3.31±0.53	1.28	1.188.E-03
TGM2	5.27±0.45	6.41±0.69	1.28	9.868.E-03
INPP4B	4.85±0.35	6.05±0.49	1.28	3.752.E-08
NPC1	5.87±0.35	6.99±0.73	1.28	3.477.E-03
ZNF154	2.2±0.44	3.19±0.63	1.26	3.569.E-02
MXI1	3.05±0.28	4.06±0.67	1.25	8.206.E-03
VSIR	3.11±0.73	4.33±0.56	1.25	7.397.E-03
PLEKHH2	3.31±0.64	4.47±0.6	1.25	8.846.E-03
SLC2A11	1.64±0.27	2.53±0.49	1.25	3.889.E-03
SSH2	4.73±0.17	5.73±0.75	1.24	2.837.E-02
TOB1	3.21±0.27	4.29±0.48	1.24	5.994.E-06
SLC18B1	2.52±0.31	3.48±0.62	1.23	1.281.E-02
JUNB	4.63±0.43	5.69±0.7	1.22	1.556.E-02
ASTN2	1.91±0.17	2.82±0.44	1.22	1.830.E-04
FLRT2	6.03±0.33	7.06±0.71	1.21	2.684.E-02
SESN1	3.96±0.22	4.96±0.62	1.21	3.615.E-03
NID2	6.73±0.39	7.78±0.72	1.21	1.033.E-02
CARMIL1	4.55±0.48	5.7±0.5	1.20	5.186.E-06
SQOR	4.79±0.47	5.92±0.5	1.19	1.234.E-05
SIK2	5.22±0.16	6.24±0.59	1.19	4.881.E-04
NABP1	7.36±0.48	8.48±0.58	1.18	2.608.E-04
GRN	6.07±0.25	7.04±0.74	1.17	3.386.E-02
CYP27A1	2.76±0.48	3.79±0.5	1.17	1.472.E-03
BTN3A3	2.91±0.59	3.96±0.55	1.17	1.283.E-02
IFITM3	4.25±0.41	5.31±0.56	1.16	1.693.E-04
TFPI	7.18±0.26	8.22±0.59	1.15	1.723.E-04
CCDC169	1.37±0.29	2.15±0.36	1.15	2.593.E-03
RAB29	4.36±0.39	5.44±0.44	1.14	3.233.E-07
MTHFR	3.36±0.31	4.37±0.46	1.14	1.208.E-05
SQSTM1	8.22±0.52	9.31±0.6	1.13	9.441.E-04
THEMIS2	1.99±0.21	2.81±0.55	1.13	4.347.E-02
MANSC1	1.84±0.3	2.66±0.49	1.12	3.279.E-02
CREBRF	4.72±0.48	5.75±0.58	1.11	1.203.E-02
SHFL	2.66±0.56	3.68±0.38	1.10	4.881.E-04

Table S3 (*Continued*)

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
FAM210B	4.86±0.26	5.84±0.56	1.10	8.190.E-04
ATXN7L1	2.77±0.26	3.67±0.5	1.10	5.658.E-03
FBXO6	1.72±0.35	2.54±0.42	1.10	1.540.E-02
VAT1	6.54±0.24	7.5±0.63	1.09	7.092.E-03
SLC26A6	2.8±0.3	3.7±0.49	1.09	7.290.E-03
BTN3A1	3.37±0.52	4.39±0.43	1.09	2.959.E-04
TNFAIP2	4.06±0.43	5.02±0.62	1.07	9.243.E-03
PGPEP1	4.39±0.34	5.32±0.58	1.07	8.038.E-03
NR1H3	2.68±0.32	3.56±0.54	1.07	1.464.E-02
TOB2	4±0.24	4.97±0.41	1.06	1.891.E-06
GID4	2.74±0.24	3.61±0.49	1.06	1.046.E-02
DTX3L	4.74±0.42	5.75±0.46	1.06	1.502.E-04
SIDT2	3.73±0.21	4.6±0.6	1.05	2.273.E-02
SELENBP1	3.65±0.21	4.51±0.58	1.04	2.669.E-02
BTN3A2	3.72±0.52	4.72±0.45	1.04	2.730.E-04
CTSA	5.51±0.19	6.41±0.59	1.04	3.523.E-03
TNS2	3.61±0.39	4.52±0.53	1.04	1.127.E-02
TBC1D2B	5.4±0.17	6.31±0.54	1.04	1.411.E-03
GNPDA1	5.01±0.39	5.94±0.59	1.03	4.743.E-03
ZNF555	2.58±0.43	3.49±0.37	1.03	5.628.E-04
WIPI1	5.29±0.25	6.21±0.54	1.03	1.152.E-03
PROS1	4.9±0.4	5.86±0.5	1.03	6.772.E-04
DOCK4	5.51±0.3	6.43±0.54	1.03	2.608.E-03
ZNF589	1.87±0.17	2.64±0.27	1.02	6.802.E-05
RNF213	7.39±0.17	8.31±0.52	1.02	5.597.E-04
UBE2E3	7.29±0.66	6.35±0.45	-1.01	2.303.E-05
RAD18	6.45±0.2	5.3±0.74	-1.01	1.693.E-02
KCNJ8	5.17±0.31	4.07±0.65	-1.01	1.861.E-02
LOC107984035	3.48±0.36	2.55±0.45	-1.02	3.218.E-03
MIS18BP1	7.01±0.22	5.82±0.79	-1.02	3.966.E-02
NES	7.48±0.43	6.33±0.8	-1.03	3.401.E-02
TNFRSF12A	8.2±0.15	7.04±0.7	-1.03	1.876.E-04
DOCK10	7.02±0.19	5.88±0.64	-1.03	2.059.E-04
DCK	6.46±0.26	5.3±0.71	-1.04	2.517.E-03
BIRC2	8.91±0.39	7.78±0.64	-1.04	2.959.E-04
PLEKHF2	5.77±0.35	4.7±0.49	-1.05	8.297.E-08
UBASH3B	7.64±0.47	6.51±0.64	-1.06	3.233.E-04
LOC105374010	3.3±0.39	2.32±0.52	-1.06	2.700.E-02
FZD7	6.81±0.41	5.64±0.65	-1.11	6.482.E-05
CBR3-AS1	1.4±0.32	0.8±0.26	-1.12	1.739.E-02
ATP1B1	6.58±0.23	5.36±0.63	-1.13	1.754.E-06

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
NCEH1	8.38±0.48	7.16±0.73	-1.13	2.273.E-03
UAP1	8.73±0.31	7.46±0.76	-1.13	6.314.E-04
RGS20	5.27±0.68	4.15±0.68	-1.14	8.175.E-04
BCAT1	9.68±0.28	8.46±0.51	-1.15	1.280.E-06
SPDL1	7.35±0.28	6.01±0.85	-1.16	1.861.E-02
ARID3B	2.12±0.36	1.31±0.35	-1.16	6.985.E-04
LMO4	7.17±0.44	5.99±0.47	-1.17	8.206.E-10
CAVIN4	2.59±0.55	1.68±0.46	-1.17	7.687.E-03
UBL3	6.76±0.39	5.54±0.53	-1.18	3.279.E-08
CDKN2D	3.55±0.36	2.46±0.49	-1.18	3.493.E-05
FSTL3	6.56±0.36	5.3±0.57	-1.19	5.201.E-07
MACIR	5.61±0.38	4.35±0.6	-1.21	2.120.E-06
SMAD7	5.5±0.62	4.23±0.72	-1.23	6.970.E-04
KCNS3	4.18±0.37	2.88±0.8	-1.23	3.325.E-02
MB21D2	5.12±0.24	3.72±0.89	-1.24	7.626.E-03
KIRREL3	5.17±0.36	3.83±0.71	-1.25	1.463.E-04
GPR137C	3.39±0.32	2.19±0.63	-1.27	3.203.E-03
PRDM8	4.67±0.7	3.43±0.7	-1.28	1.693.E-03
PPP2R3A	7.29±0.4	5.97±0.47	-1.30	9.761.E-13
LOC105378031	2.26±0.61	1.36±0.4	-1.30	9.426.E-04
TRNP1	6.44±0.71	4.87±1.07	-1.37	4.957.E-02
ADTRP	2.19±0.7	1.27±0.46	-1.38	5.430.E-03
CBR3	4.83±0.44	3.4±0.73	-1.40	2.700.E-05
SCARA3	7.64±0.47	6.01±0.93	-1.41	3.066.E-04
ADAMTS6	6.64±0.41	5.05±0.83	-1.43	1.179.E-05
LOC101928352	1.21±0.28	0.54±0.3	-1.45	4.774.E-02
CARD10	2.7±0.23	1.45±0.66	-1.45	1.161.E-02
BRIP1	7.13±0.26	5.28±1.23	-1.47	1.330.E-02
RFLNB	6.66±0.46	5.09±0.71	-1.48	4.637.E-08
SLC26A4	1.35±0.59	0.64±0.27	-1.54	6.452.E-04
LZTS1	3.3±0.41	1.88±0.69	-1.56	2.227.E-04
LINC01415	2.11±0.36	1.01±0.49	-1.58	1.097.E-03
CD274	4.95±0.49	3.27±0.88	-1.61	5.338.E-05
PSD4	4.21±0.67	2.61±0.91	-1.62	2.989.E-03
LOC105377123	3.35±0.49	1.81±0.76	-1.63	1.209.E-03
GPR39	2.59±0.32	1.32±0.48	-1.64	7.351.E-07
FOXD1	5.64±0.6	3.8±1	-1.66	1.504.E-04
PLEK2	3.54±0.69	1.95±0.91	-1.67	1.515.E-02
OXTR	6.89±0.67	4.88±1.26	-1.72	2.105.E-03
ATP10A	6.63±0.37	4.67±1.02	-1.77	3.538.E-08

Table S3 (*Continued*)

Gene	**Control**	**IPF**	**$\log_2$FC**	**adj *p* (Bonferroni)**
PRSS3	3.4±0.78	1.74±0.91	-1.82	2.288.E-02
S1PR1	4.25±1.77	2.92±1.04	-1.90	8.694.E-03
LIN7A	5.91±0.57	4.03±0.61	-1.93	1.487.E-18
HHIP-AS1	1.76±0.45	0.66±0.35	-1.99	1.968.E-07
EYA2	2.3±0.76	0.93±0.59	-2.06	4.987.E-03
IL21R	4.3±1.02	2.27±1.02	-2.08	2.730.E-04
BTBD11	2.53±0.63	0.94±0.67	-2.16	4.255.E-04
LOC105371393	1.5±0.3	0.45±0.35	-2.19	4.972.E-04
TRIM55	3.95±1.29	1.81±1.21	-2.23	3.477.E-02
SEMA7A	6.86±0.62	4.08±1.41	-2.29	1.100.E-05
GRPR	3.89±0.86	1.64±0.99	-2.44	5.170.E-05
DRD1	1.35±0.58	0.32±0.36	-2.53	7.123.E-03
AMIGO2	7.04±0.44	4.19±0.92	-2.65	4.606.E-19
HAPLN1	2.09±1.84	1.14±0.8	-2.72	7.916.E-03
EML5	4.74±1.12	1.95±0.9	-3.10	1.261.E-15
HHIP	4.17±0.81	1.24±1.03	-3.16	6.177.E-06
MYH11	1.89±1.27	0.34±0.54	-3.42	1.094.E-02

Values are presented as mean ± standard error of the mean. *p*-values shown are Bonferroni-adjusted values from the Exact test. *Abbreviations:* IPF: idiopathic pulmonary fibrosis; log2FC: $\log_2$ fold change of IPF/Control; DEG: differentially expressed gene

Table S4. Comprehensive list of GO terms and pathways enriched in our study

A total of 475 differentially expressed genes						
Term ID	**Category**	**Term name**	**Count**	**Gene**	**Fold enrichment**	**FDR**
GO:0030335	BP	positive regulation of cell migration	20	*CD274, CARMIL1, SEMA7A, GRN, CEMIP, MYOC, F10, TNFAIP6, CSF1, SEMA3B, SEMA4G, SOD2, SSH2, VSIR, FAM83H, BMP2, GPNMB, S1PR1, CCL2, DRD1*	3.50	1.143.E-02
GO:0006956	BP	complement activation	7	*C4B, CFD, C3, C7, C1S, CFB, C2*	12.18	1.799.E-02
GO:0006958	BP	complement activation, classical pathway	8	*C4B, C3, C7, C1S, C1R, SERPING1, CFB, C2*	8.59	1.799.E-02
GO:0006508	BP	proteolysis	29	*CFD, CPM, C1S, C1R, PLAT, CPZ, C2, DPP4, ADAMTS14, ADAMTS13, ADAMTS19, CASP10, CTSK, CLCA2, FBXO6, PGPEP1, PRSS3, ADAMTS8, GGT1, ADAMTS6, TGM2, CTSA, MME, OVCH1, F10, MMP15, PAPPA, TPP1, CFB*	2.38	1.799.E-02
GO:0006954	BP	inflammatory response	23	*SEMA7A, MACIR, TNFAIP6, CSF1, IL1R1, RARRES2, ADM, F11R, TNFRSF1B, CXCL2, CXCL5, C3, C4B, FAM210B, NR4A1, BMP2, SCUBE1, THEMIS2, BDKRB2, TXNIP, CCL2, APOL3, TLR3*	2.69	1.799.E-02
GO:0008285	BP	negative regulation of cell population proliferation	23	*CDKN2D, IFITM1, BTG2, TGFB3, ADM, PODN, TOB2, SOD2, DLL1, TOB1, BMP5, BMP4, BMP2, BRIP1, GPNMB, PMP22, CYP1B1, QSOX1, SPRY1, ADAMTS8, TP53I11, TNS2, PTGES*	2.68	1.799.E-02
GO:0001666	BP	response to hypoxia	14	*KCNJ8, TGFB3, EPAS1, MTHFR, ADM, PLAT, SOD2, CYGB, NR4A2, DPP4, BMP2, DDIT4, TEK, BIRC2*	3.97	1.799.E-02
GO:0007155	BP	cell adhesion	26	*SRPX, RIPOR2, TNFAIP6, CLSTN3, LAMA4, LAMA3, AMIGO2, ICAM4, F11R, NID2, FBLN5, HAPLN1, ICAM1, DPP4, FLRT2, GPNMB, CCN5, CLCA2, S1PR1, CYP1B1, CCL2, SVEP1, TNFRSF12A, ATP1B1, THEMIS2, TLR3*	2.35	3.758.E-02

Table S4 (*Continued*)

A total of 475 differentially expressed genes						
GO:0005576	CC	extracellular region	98	*CSF1, HHIP, PROS1, ICAM4, PLAT, IFI30, C4B, FGF7, EFEMP1, TNFSF10, SVEP1, IL13RA2, PRSS3, PTGDS, IL6R, TGM2, KIRREL3, IGFBP4, IL1R1, SERPINF1, PAPPA, SELENOP, SERPING1, PLA2R1, CFB, CFD, FBN2, CEMIP, FBLN1, NID2, FBLN5, C2, DPP4, C3, ADAMTS14, ADAMTS13, FLRT2, C7, ADAMTS19, CLCA2, PLTP, CTSA, VAT1, TGFB3, RARRES2, TFPI2, BMP5, BMP4, IGSF10, BMP2, TG, PLXNB1, FGFR4, CPM, TNFAIP6, ADM, CXCL2, HAPLN1, CXCL5, HEBP1, C1QTNF1, ADAMTSL4, CTSK, RSPO3, QSOX1, ADAMTS8, ADAMTS6, MYOC, OVCH1, ABCC6, IL16, AMPD3, TNFRSF1B, NPC1, FIBIN, PLEKHO2, CFAP54, GRN, C1S, C1R, LAMA4, PRCD, LAMA3, SEMA3B, TFPI, DLL1, FSTL3, CREG1, CCL2, APOL1, APOL3, SNCA, F10, GDF15, PODN, NEK10, TEK, FRK*	2.21	1.413.E-11
GO:0005615	CC	extracellular space	77	*MOXD1, CPM, CSF1, TNFAIP6, PROS1, TNFAIP2, ADM, PLAT, CPZ, CXCL2, CXCL5, HAPLN1, ICAM1, C4B, FGF7, EFEMP1, C1QTNF1, CTSK, CCN5, TNFSF10, RSPO3, QSOX1, SVEP1, IL13RA2, PRSS3, PTGDS, GGT1, IL6R, MYOC, IGFBP4, SERPINF1, IL16, GPRC5B, MMP15, PAPPA, ANGPTL2, SERPING1, TLR3, CFB, CFD, FBN2, GRN, C1S, C1R, FBLN1, TFPI, NID2, FBLN5, FSTL3, C2, SELENBP1, C3, MUC1, SCUBE1, ADAMTS13, FLRT2, C7, CREG1, CCL2, APOL1, PLTP, SNCA, ZBED3, CBR3, GDF10, F10, TGFB3, GDF15, TNFSF15, RARRES2, TFPI2, PODN, SSH2, BMP5, BMP4, BMP2, TG*	2.15	3.258.E-08
GO:0005886	CC	plasma membrane	159	*IFITM3, IFITM1, OXTR, CSF1, CLSTN3, HHIP, PROS1, ICAM4, GRPR, F11R, ANTXR1, CELSR3, BEST1, ICAM1, MILR1, C4B, EDNRB, MPZ, TNFSF10, IL13RA2, GGT1, LZTS1, IL6R, TNS2, SLC16A4, TGM2, ARRDC4, KIRREL3, GABARAPL1, PRKCH, MUSK, IL1R1, TBC1D2B, ATP1B1, ORAI3, PLA2R1, CFTR, CFB, SIDT2, RASL12, CD274, SEMA7A, CEMIP, UAP1, LIN7A, IQGAP2, SEZ6L2, PLD1, NID2, PPL, DPP4, C3, SCUBE1, FLRT2, C7, CLCA2, TNFRSF14, PLEK2, DRD1, ABCA1, CARMIL1, ATP8B4, TGFB3, ABCA6, TNFSF15, FZD7, SLC4A11, RAB27B, ABCA8, MCC, GNG11, IGF2R, SLC16A14, SMAD7, SLC2A9, BMP2, NCEH1, SPIRE2, MYCBPAP, PLXNB1, SLC26A4, SCN2A, FGFR4, SLC26A6, CPM, SNAP25, DOCK4, SLC44A3, SLC40A1, GRIK4, TSPAN12, LITAF, VSIR, UBL3, C1QTNF1, CTSK, BDKRB2, CLIC2, TAS2R4, SH3D19, GPR39, MANBA, TMEM150A, KCND1, BTN3A1, TNFRSF12A, MME, SLC2A11, SGIP1, ABCC6, IL16, BTN3A3, BTN3A2, TNFRSF1B, VAMP8, GPRC5B, GPRC5A, GJD3, NPC1, MMP15, CDHR3, TLCD2, TNFRSF21, TLR3, RGS18, GRN, PLEKHH2, SLC43A2, ADH1B, ADH1A, SEMA3B, AMIGO2, ATP10A, TFPI, DLL1, NKD2, MUC1, GPNMB, P2RY1, S1PR1, IL21R, RAB29, RGS20, SCN7A, KCNJ2, SNCA, RFTN2, F10, KCNJ8, STAT2, CAVIN4, SEMA4G, ADGRD1, KCNS3, PMP22, AQP11, SPRY1, TEK, FRK*	1.48	1.708.E-06

A total of 475 differentially expressed genes						
GO:0062023	CC	collagen-containing extracellular matrix	24	*GDF10, FBN2, SRPX, SEMA7A, MYOC, TGFB3, GDF15, LAMA4, SERPINF1, RARRES2, LAMA3, SEMA3B, FBLN1, PODN, NID2, FBLN5, HAPLN1, ICAM1, EFEMP1, ADAMTSL4, SERPING1, ANGPTL2, ADAMTS8, TGM2*	3.23	1.516.E-04
GO:0070062	CC	extracellular exosome	74	*CPM, BTG2, PROS1, QPRT, PLAT, F11R, HNMT, ICAM1, HEBP1, DOCK10, C4B, EFEMP1, UBL3, TNFSF10, QSOX1, PTGDS, GGT1, TGM2, PRKCH, MYOC, MME, SERPINF1, CMBL, ATP1B1, VAMP8, EML5, GPRC5B, GPRC5A, NPC1, SELENOP, ANGPTL2, SERPING1, SQSTM1, CFB, CFD, CD274, GRN, C1R, LAMA4, LAMA3, RHOBTB3, FBLN1, GLRX, LIN7A, IQGAP2, NID2, PPL, FBLN5, C2, PTGS1, DPP4, SELENBP1, C3, MUC1, FLRT2, C7, CREG1, MAN1C1, RAB29, MYH11, CTSA, VAT1, CARMIL1, GDF15, GREB1, RAB27B, SOD2, IGF2R, PSMB9, GNPDA1, C16ORF89, TPP1, SLC26A4, FRK*	1.72	2.560.E-04
GO:0031012	CC	extracellular matrix	17	*FBN2, RARRES2, TFPI2, FBLN1, FBLN5, HAPLN1, ADAMTS14, ADAMTS13, EFEMP1, FLRT2, MMP15, ADAMTS19, CCN5, ADAMTS8, ADAMTS6, TLR3, TGM2*	3.97	3.748.E-04
GO:0009986	CC	cell surface	27	*SRPX, CPM, CLSTN3, HHIP, PLAT, IQGAP2, TFPI, ANTXR1, ICAM1, DPP4, C3, HLA-DMA, SCUBE1, ADAMTS13, P2RY1, MME, TGFB3, IL1R1, IGF2R, BMP2, GPRC5B, GJD3, AQP11, ADTRP, TEK, PLA2R1, CFTR*	2.13	2.172.E-02
GO:0016020	CC	membrane	133	*IFITM3, IFITM1, OXTR, CSF1, CLSTN3, ICAM4, TMEM140, ANTXR1, CELSR3, BEST1, ICAM1, DOCK10, NYNRIN, CYP1B1, SVEP1, GGT1, IL6R, SLC16A4, KIRREL3, GABARAPL1, PRKCH, IL1R1, ATP1B1, INPP4B, PAPPA, SELENOP, ORAI3, ADTRP, ASTN2, CFTR, PTGES, SIDT2, FBN2, SEMA7A, FAXDC2, TMTC1, IQGAP2, SEZ6L2, PLD1, PPL, DPP4, HELZ2, RNF213, RDH10, TNFRSF14, HMGCLL1, FAM83B, ZBED3, ABCA1, CTSA, VAT1, ANKRD29, ATP8B4, ABCA6, TNFSF15, FZD7, GREB1, SLC4A11, ARHGAP28, ABCA8, NSG1, IGF2R, SLC2A9, NCEH1, MANSC1, SLC26A4, SCN2A, FGFR4, SLC26A6, CPM, GASK1B, SRPX, SNAP25, DOCK4, SLC44A3, SLC40A1, TMEM51, GRIK4, TSPAN12, VSIR, PSD4, CLIC2, TAS2R4, GPR39, BTN3A1, MME, SLC2A11, ABCC6, BTN3A3, BTN3A2, TNFRSF1B, FAM210B, C15ORF48, VAMP8, GPRC5B, NPC1, OAS2, MMP15, TMEM217, CDHR3, CFAP54, TNFRSF21, TLR3, GRN, AMIGO2, ATP10A, DLL1, SLC25A27, SELENBP1, HLA-DMA, ZFP14, MUC1, HLA-DMB, GPNMB, HSD17B2, MAN1C1, IL21R, RAB29, APOL1, TP53I11, KCNJ2, APOL3, SNCA, TMEM176B, DHRS3, ADGRD1, LRRN4CL, KCNS3, PMP22, C16ORF89, SPRY1, SMIM41, CYB561*	1.28	3.487.E-02

Table S4 (*Continued*)

A total of 475 differentially expressed genes						
GO:0005515	MF	protein binding	314	*IFITM3, IFITM1, HHIP, UBE2L6, ICAM4, F11R, IFI30, ANTXR1, ICAM1, C4B, MILR1, EDNRB, UBASH3B, DHX58, TNFSF10, PDK4, CCN5, CYP1B1, FBXO6, ATXN7L1, PRSS3, PTGDS, JUNB, TNS2, ARRDC4, GABARAPL1, PRKCH, MUSK, NHLRC4, IL1R1, SERPINF1, ZFP2, KIAA1217, INPP4B, PPP1R3C, PAPPA, DDIT4, ORAI3, SERPING1, TXNIP, KCTD12, SIK2, SPATA18, CFTR, CFB, PTGES, MAOA, EPAS1, FAXDC2, TMTC1, PPL, C2, C3, HELZ2, BRIP1, RNF213, ADAMTS13, RDH10, FAM43A, ABCA1, VAT1, CARMIL1, TNFSF15, FZD7, MTHFR, RAB27B, GNG11, PARP15, TG, CREBRF, SCN2A, RAD18, SRPX, BTG2, SLC44A3, QPRT, TCF21, TMEM51, STON2, LITAF, VSIR, MEDAG, C1QTNF1, UBL3, MIS18BP1, ADAMTSL4, CASP10, CTSK, CLIC2, GPR39, BATF2, ZHX2, TMEM150A, MYOC, TNFRSF12A, MME, BTN3A1, VWA5A, IL16, BTN3A3, RAB3IL1, AMPD3, BTN3A2, FAM210B, VAMP8, GJD3, GPRC5A, MMP15, ARHGEF3, ANGPTL2, PLEKHO2, TLR3, GRN, MACIR, SLC43A2, ADH1B, ADH1A, AMIGO2, NPL, FSTL3, PTGS1, NKD2, HLA-DMA, ZFP14, HLA-DMB, GPNMB, HSD17B2, APOL1, APOL3, CBR3, CDKN2D, RFTN2, F10, GDF15, STAT2, TMEM176B, SQOR, CAVIN4, NR1H3, PODN, PSMB9, THEMIS2, CSDC2, FOSB, ZNF578, CYB561, FRK, RIPOR3, PRDM8, RIPOR2, CSF1, GALNT15, CLSTN3, FBXO27, PROS1, PLAT, TMEM140, CELSR3, BEST1, DOCK10, FGF7, EFEMP1, CCND2, SESN1, SVEP1, IL13RA2, GGT1, MB21D2, PITX1, LZTS1, IL6R, SLC16A4, TGM2, KIRREL3, CARD10, SCARA3, LMO4, IGFBP4, UBE2E3, ACOT12, TBC1D2B, ATP1B1, TXLNB, ADTRP, ZNF555, SQSTM1, FBN2, RASL12, CD274, SEMA7A, CEMIP, USP53, RHOBTB3, LIN7A, FBLN1, PLD1, NID2, FBLN5, DPP4, FAM83H, SCUBE1, MYH11, TNFRSF14, ZNF425, DRD1, PLTP, IP6K3, FAM83B, ANKRD29, ATP8B4, HBG2, TGFB3, RARRES2, AZIN2, NSG1, MCC, FBXO32, SSH2, ACSF2, IGF2R, BMP5, SMAD7, BMP4, SLC2A9, NR4A2, NR4A1, TSGA10, BMP2, NR4A3, SPIRE2, NABP1, MYCBPAP, TPP1, PLXNB1, MANSC1, SLC26A4, FGFR4, NES, SLC26A6, PLEKHF2, MOXD1, SNAP25, DOCK4, THRB, TNFAIP6, SLC40A1, TNFAIP2, TSPAN12, CXCL2, CXCL5, INSYN2A, PSD4, BDKRB2, SPDL1, PGPEP1, SH3D19, DNAI3, DTX3L, SGIP1, NAV1, WIPI1, TNFRSF1B, DCK, INMT, C15ORF48, NPC1, OAS2, CDHR3, BCAT1, ASPA, TNFRSF21, TRIM55, BIRC2, RGS18, PLEKHH2, C1S, C1R, LAMA4, SEMA3B, GLRX, ATP10A, TOB2, DLL1, TOB1, CYGB, CKMT2, SELENBP1, MUC1, P2RY1, MXI1, RAB29, MAN1C1, S1PR1, IL21R, SCN7A, CCL2, RGS20, KCNJ2, SNCA, KCNJ8, EYA2, CABLES1, SEMA4G, ARID3B, PPP2R3A, SOD2, PNRC1, TPCN1, ADGRD1, GNPDA1, PMP22, SPRY1, TEK, SHFL*	1.13	9.424.E-03

A total of 475 differentially expressed genes						
hsa04610	KEGG	Complement and coagulation cascades	14	*CFD, C1S, F10, C1R, PROS1, PLAT, TFPI, C2, C3, C4B, C7, BDKRB2, SERPING1, CFB*	6.79	2.761.E-05
hsa04060	KEGG	Cytokine-cytokine receptor interaction	21	*GDF10, TNFRSF12A, CSF1, IL1R1, TGFB3, GDF15, TNFSF15, IL16, TNFRSF1B, CXCL2, CXCL5, BMP5, BMP4, BMP2, TNFSF10, IL21R, CCL2, TNFRSF14, IL13RA2, IL6R, TNFRSF21*	3.01	2.534.E-03
hsa05323	KEGG	Rheumatoid arthritis	10	*HLA-DMA, HLA-DMB, CSF1, TGFB3, CTSK, CCL2, TEK, CXCL2, CXCL5, ICAM1*	4.49	3.089.E-02
hsa05150	KEGG	Staphylococcus aureus infection	10	*C4B, CFD, C3, HLA-DMA, HLA-DMB, C1S, C1R, CFB, ICAM1, C2*	4.18	3.926.E-02
402 up-regulated genes						
Term ID	Category	Term name	Count	Gene	Fold enrichment	FDR
GO:0006956	BP	complement activation	7	*C4B, CFD, C3, C7, C1S, CFB, C2*	14.42	9.947.E-03
GO:0006958	BP	complement activation, classical pathway	8	*C4B, C3, C7, C1S, C1R, SERPING1, CFB, C2*	10.17	9.947.E-03
GO:0006508	BP	proteolysis	27	*CFD, CPM, C1S, C1R, PLAT, CPZ, C2, DPP4, ADAMTS14, ADAMTS13, ADAMTS19, CASP10, CTSK, CLCA2, FBXO6, PGPEP1, ADAMTS8, GGT1, TGM2, CTSA, MME, OVCH1, F10, MMP15, PAPPA, TPP1, CFB*	2.62	9.947.E-03
GO:0006954	BP	inflammatory response	21	*TNFAIP6, CSF1, IL1R1, RARRES2, ADM, F11R, TNFRSF1B, CXCL2, CXCL5, C3, C4B, FAM210B, NR4A1, BMP2, SCUBE1, THEMIS2, BDKRB2, TXNIP, CCL2, APOL3, TLR3*	2.90	1.730.E-02
GO:0008285	BP	negative regulation of cell population proliferation	21	*IFITM1, BTG2, TGFB3, ADM, PODN, TOB2, SOD2, DLL1, TOB1, BMP5, BMP4, BMP2, GPNMB, PMP22, CYP1B1, QSOX1, SPRY1, ADAMTS8, TP53I11, TNS2, PTGES*	2.90	1.730.E-02
GO:0030335	BP	positive regulation of cell migration	16	*CARMIL1, GRN, CEMIP, MYOC, F10, TNFAIP6, CSF1, SEMA3B, SEMA4G, SOD2, SSH2, VSIR, FAM83H, BMP2, GPNMB, CCL2*	3.32	3.547.E-02
GO:0009617	BP	response to bacterium	10	*C15ORF48, CFD, C3, BMP2, DHX58, RAB29, CCL2, SCN7A, CFB, C2*	5.15	4.046.E-02

Table S4 (*Continued*)

A total of 475 differentially expressed genes						
GO:0005576	CC	extracellular region	92	*CPM, CSF1, TNFAIP6, PROS1, ADM, ICAM4, PLAT, IFI30, CXCL2, CXCL5, HEBP1, C4B, FGF7, EFEMP1, C1QTNF1, ADAMTSL4, CTSK, TNFSF10, RSPO3, QSOX1, SVEP1, IL13RA2, ADAMTS8, PTGDS, IL6R, TGM2, MYOC, OVCH1, IGFBP4, IL1R1, SERPINF1, ABCC6, IL16, AMPD3, TNFRSF1B, NPC1, PAPPA, SELENOP, FIBIN, SERPING1, PLEKHO2, PLA2R1, CFAP54, CFB, CFD, FBN2, GRN, CEMIP, C1S, C1R, PRCD, LAMA4, SEMA3B, LAMA3, FBLN1, TFPI, NID2, DLL1, FBLN5, C2, DPP4, C3, ADAMTS14, ADAMTS13, FLRT2, C7, ADAMTS19, CREG1, CLCA2, CCL2, APOL1, PLTP, APOL3, SNCA, CTSA, VAT1, F10, TGFB3, GDF15, RARRES2, TFPI2, PODN, BMP5, BMP4, IGSF10, BMP2, TG, NEK10, PLXNB1, TEK, FGFR4, FRK*	2.45	8.954.E-14
GO:0005615	CC	extracellular space	73	*MOXD1, CPM, CSF1, TNFAIP6, PROS1, TNFAIP2, ADM, PLAT, CPZ, CXCL2, CXCL5, ICAM1, C4B, FGF7, EFEMP1, C1QTNF1, CTSK, CCN5, TNFSF10, RSPO3, QSOX1, SVEP1, IL13RA2, PTGDS, GGT1, IL6R, MYOC, IGFBP4, SERPINF1, IL16, GPRC5B, MMP15, PAPPA, ANGPTL2, SERPING1, TLR3, CFB, CFD, FBN2, GRN, C1S, C1R, FBLN1, TFPI, NID2, FBLN5, C2, SELENBP1, C3, MUC1, SCUBE1, ADAMTS13, FLRT2, C7, CREG1, CCL2, APOL1, PLTP, SNCA, ZBED3, GDF10, F10, TGFB3, GDF15, TNFSF15, RARRES2, TFPI2, PODN, SSH2, BMP5, BMP4, BMP2, TG*	2.41	3.337.E-10
GO:0005886	CC	plasma membrane	132	*IFITM3, IFITM1, CSF1, CLSTN3, PROS1, ICAM4, F11R, ANTXR1, CELSR3, BEST1, ICAM1, MILR1, C4B, EDNRB, MPZ, TNFSF10, IL13RA2, GGT1, IL6R, TNS2, SLC16A4, TGM2, ARRDC4, GABARAPL1, PRKCH, MUSK, IL1R1, TBC1D2B, ORAI3, PLA2R1, CFTR, CFB, SIDT2, RASL12, CEMIP, IQGAP2, SEZ6L2, PLD1, NID2, PPL, DPP4, C3, SCUBE1, FLRT2, C7, CLCA2, TNFRSF14, ABCA1, CARMIL1, ATP8B4, TGFB3, ABCA6, TNFSF15, SLC4A11, RAB27B, ABCA8, MCC, GNG11, IGF2R, SLC16A14, SLC2A9, BMP2, SPIRE2, MYCBPAP, PLXNB1, SCN2A, FGFR4, SLC26A6, CPM, SNAP25, DOCK4, SLC44A3, SLC40A1, GRIK4, TSPAN12, LITAF, VSIR, C1QTNF1, CTSK, BDKRB2, CLIC2, TAS2R4, SH3D19, MANBA, TMEM150A, KCND1, BTN3A1, MME, SLC2A11, SGIP1, ABCC6, IL16, BTN3A3, BTN3A2, TNFRSF1B, VAMP8, GPRC5B, GPRC5A, GJD3, NPC1, MMP15, CDHR3, TLCD2, TNFRSF21, TLR3, RGS18, GRN, PLEKHH2, SLC43A2, ADH1B, ADH1A, SEMA3B, TFPI, DLL1, NKD2, MUC1, GPNMB, P2RY1, RAB29, SCN7A, KCNJ2, SNCA, RFTN2, F10, STAT2, SEMA4G, ADGRD1, PMP22, AQP11, SPRY1, TEK, FRK*	1.46	8.095.E-05

A total of 475 differentially expressed genes						
GO:0062023	CC	collagen-containing extracellular matrix	22	*GDF10, FBN2, SRPX, MYOC, TGFB3, GDF15, LAMA4, SERPINF1, RARRES2, LAMA3, SEMA3B, FBLN1, PODN, NID2, FBLN5, ICAM1, EFEMP1, ADAMTSL4, SERPING1, ANGPTL2, ADAMTS8, TGM2*	3.51	1.118.E-04
GO:0070062	CC	extracellular exosome	66	*CPM, BTG2, PROS1, QPRT, PLAT, F11R, HNMT, ICAM1, HEBP1, C4B, EFEMP1, TNFSF10, QSOX1, PTGDS, GGT1, TGM2, PRKCH, MYOC, MME, SERPINF1, CMBL, VAMP8, GPRC5B, GPRC5A, NPC1, SELENOP, ANGPTL2, SERPING1, SQSTM1, CFB, CFD, GRN, C1R, LAMA4, LAMA3, RHOBTB3, FBLN1, GLRX, IQGAP2, NID2, PPL, FBLN5, C2, PTGS1, DPP4, SELENBP1, C3, MUC1, FLRT2, C7, CREG1, MAN1C1, RAB29, CTSA, VAT1, CARMIL1, GDF15, GREB1, RAB27B, SOD2, IGF2R, PSMB9, GNPDA1, C16ORF89, TPP1, FRK*	1.82	1.230.E-04
GO:0031012	CC	extracellular matrix	15	*FBN2, RARRES2, TFPI2, FBLN1, FBLN5, ADAMTS14, ADAMTS13, EFEMP1, FLRT2, MMP15, ADAMTS19, CCN5, ADAMTS8, TLR3, TGM2*	4.15	8.569.E-04
GO:0016020	CC	membrane	118	*IFITM3, IFITM1, CSF1, CLSTN3, ICAM4, TMEM140, ANTXR1, CELSR3, BEST1, ICAM1, NYNRIN, CYP1B1, SVEP1, GGT1, IL6R, SLC16A4, GABARAPL1, PRKCH, IL1R1, INPP4B, PAPPA, SELENOP, ORAI3, ASTN2, CFTR, PTGES, SIDT2, FBN2, FAXDC2, TMTC1, IQGAP2, SEZ6L2, PLD1, PPL, DPP4, HELZ2, RNF213, RDH10, TNFRSF14, HMGCLL1, FAM83B, ZBED3, ABCA1, CTSA, VAT1, ANKRD29, ATP8B4, ABCA6, TNFSF15, GREB1, SLC4A11, ARHGAP28, ABCA8, NSG1, IGF2R, SLC2A9, MANSC1, SCN2A, FGFR4, SLC26A6, CPM, GASK1B, SRPX, SNAP25, DOCK4, SLC44A3, SLC40A1, TMEM51, GRIK4, TSPAN12, VSIR, CLIC2, TAS2R4, BTN3A1, MME, SLC2A11, ABCC6, BTN3A3, BTN3A2, TNFRSF1B, FAM210B, C15ORF48, VAMP8, GPRC5B, NPC1, OAS2, MMP15, TMEM217, CDHR3, CFAP54, TNFRSF21, TLR3, GRN, DLL1, SLC25A27, SELENBP1, HLA-DMA, ZFP14, MUC1, HLA-DMB, GPNMB, HSD17B2, MAN1C1, RAB29, APOL1, TP53I11, KCNJ2, APOL3, SNCA, TMEM176B, DHRS3, ADGRD1, LRRN4CL, PMP22, C16ORF89, SPRY1, SMIM41, CYB561*	1.34	7.766.E-03
GO:0009986	CC	cell surface	25	*SRPX, CPM, CLSTN3, PLAT, IQGAP2, TFPI, ANTXR1, ICAM1, DPP4, C3, HLA-DMA, SCUBE1, ADAMTS13, P2RY1, MME, TGFB3, IL1R1, IGF2R, BMP2, GPRC5B, GJD3, AQP11, TEK, PLA2R1, CFTR*	2.33	7.766.E-03
GO:0005102	MF	signaling receptor binding	20	*ABCA1, BTN3A1, TNFSF15, IGFBP4, LAMA4, RARRES2, LAMA3, ADM, PLAT, BTN3A3, WIPI1, BTN3A2, DPP4, C3, BMP2, TNFSF10, RSPO3, CCL2, ANGPTL2, FRK*	3.06	2.101.E-02

Table S4 (*Continued*)

A total of 475 differentially expressed genes						
GO:0005515	MF	protein binding	264	*IFITM3, IFITM1, UBE2L6, ICAM4, F11R, IFI30, ANTXR1, ICAM1, C4B, MILR1, EDNRB, DHX58, TNFSF10, PDK4, CCN5, CYP1B1, FBXO6, ATXN7L1, PTGDS, JUNB, TNS2, ARRDC4, GABARAPL1, PRKCH, MUSK, NHLRC4, IL1R1, SERPINF1, ZFP2, KIAA1217, INPP4B, PPP1R3C, PAPPA, DDIT4, ORAI3, SERPING1, TXNIP, KCTD12, SIK2, SPATA18, CFTR, CFB, PTGES, MAOA, EPAS1, FAXDC2, TMTC1, PPL, C2, C3, HELZ2, RNF213, ADAMTS13, RDH10, FAM43A, ABCA1, VAT1, CARMIL1, TNFSF15, MTHFR, RAB27B, GNG11, PARP15, TG, CREBRF, SCN2A, SRPX, BTG2, SLC44A3, QPRT, TCF21, TMEM51, STON2, LITAF, VSIR, MEDAG, C1QTNF1, ADAMTSL4, CASP10, CTSK, CLIC2, BATF2, ZHX2, TMEM150A, MYOC, MME, BTN3A1, VWA5A, IL16, BTN3A3, RAB3IL1, AMPD3, BTN3A2, FAM210B, VAMP8, GJD3, GPRC5A, MMP15, ARHGEF3, ANGPTL2, PLEKHO2, TLR3, GRN, SLC43A2, ADH1B, ADH1A, NPL, PTGS1, NKD2, HLA-DMA, ZFP14, HLA-DMB, GPNMB, HSD17B2, APOL1, APOL3, RFTN2, F10, GDF15, STAT2, TMEM176B, SQOR, NR1H3, PODN, PSMB9, THEMIS2, CSDC2, FOSB, ZNF578, CYB561, FRK, RIPOR3, RIPOR2, CSF1, GALNT15, CLSTN3, FBXO27, PROS1, PLAT, TMEM140, CELSR3, BEST1, FGF7, EFEMP1, CCND2, SESN1, SVEP1, IL13RA2, GGT1, PITX1, IL6R, SLC16A4, TGM2, IGFBP4, ACOT12, TBC1D2B, TXLNB, ZNF555, SQSTM1, FBN2, RASL12, CEMIP, USP53, RHOBTB3, FBLN1, PLD1, NID2, FBLN5, DPP4, FAM83H, SCUBE1, TNFRSF14, ZNF425, PLTP, IP6K3, FAM83B, ANKRD29, ATP8B4, HBG2, TGFB3, RARRES2, AZIN2, NSG1, MCC, FBXO32, SSH2, ACSF2, IGF2R, BMP5, BMP4, SLC2A9, NR4A2, NR4A1, TSGA10, BMP2, NR4A3, SPIRE2, NABP1, MYCBPAP, TPP1, PLXNB1, MANSC1, FGFR4, SLC26A6, MOXD1, SNAP25, DOCK4, THRB, TNFAIP6, SLC40A1, TNFAIP2, TSPAN12, CXCL2, CXCL5, INSYN2A, BDKRB2, PGPEP1, SH3D19, DNAI3, DTX3L, SGIP1, NAV1, WIPI1, TNFRSF1B, INMT, C15ORF48, NPC1, OAS2, CDHR3, ASPA, TNFRSF21, RGS18, PLEKHH2, C1S, C1R, LAMA4, SEMA3B, GLRX, TOB2, DLL1, TOB1, CYGB, CKMT2, SELENBP1, MUC1, P2RY1, MXI1, RAB29, MAN1C1, SCN7A, CCL2, KCNJ2, SNCA, CABLES1, SEMA4G, SOD2, PNRC1, TPCN1, ADGRD1, GNPDA1, PMP22, SPRY1, TEK, SHFL*	1.13	2.101.E-02
hsa04610	KEGG	Complement and coagulation cascades	14	*CFD, C1S, F10, C1R, PROS1, PLAT, TFPI, C2, C3, C4B, C7, BDKRB2, SERPING1, CFB*	7.94	3.886.E-06

A total of 475 differentially expressed genes						
hsa04060	KEGG	Cytokine-cytokine receptor interaction	19	*GDF10, CSF1, IL1R1, TGFB3, GDF15, TNFSF15, IL16, TNFRSF1B, CXCL2, CXCL5, BMP5, BMP4, BMP2, TNFSF10, CCL2, TNFRSF14, IL13RA2, IL6R, TNFRSF21*	3.18	3.045.E-03
hsa05323	KEGG	Rheumatoid arthritis	10	*HLA-DMA, HLA-DMB, CSF1, TGFB3, CTSK, CCL2, TEK, CXCL2, CXCL5, ICAM1*	5.25	8.688.E-03
hsa05150	KEGG	Staphylococcus aureus infection	10	*C4B, CFD, C3, HLA-DMA, HLA-DMB, C1S, C1R, CFB, ICAM1, C2*	4.89	1.128.E-02
R-HSA-168256	REACTOME	Immune System	69	*IFITM3, SNAP25, IFITM1, CSF1, TNFAIP6, FBXO27, PROS1, UBE2L6, ICAM4, IFI30, CXCL2, IFI44L, ICAM1, C4B, CASP10, CTSK, DHX58, QSOX1, FBXO6, IL13RA2, JUNB, IL6R, MANBA, DTX3L, MME, BTN3A1, IL1R1, BTN3A3, IL16, AMPD3, BTN3A2, TNFRSF1B, VAMP8, OAS2, TXNIP, SERPING1, PLEKHO2, SQSTM1, TLR3, CFB, CFD, GRN, C1S, MAOA, C1R, IQGAP2, DTX4, PLD1, PPL, C2, C3, HLA-DMA, MUC1, HLA-DMB, RNF213, C7, CREG1, CCL2, TNFRSF14, SNCA, CTSA, VAT1, ATP8B4, TNFSF15, STAT2, FBXO32, SOD2, IGF2R, FRK*	1.60	1.799.E-02
R-HSA-1474244	REACTOME	Extracellular matrix organization	19	*FBN2, MUSK, TGFB3, LAMA4, LAMA3, FBLN1, ICAM4, F11R, NID2, FBLN5, ICAM1, BMP4, BMP2, ADAMTS14, SCUBE1, EFEMP1, MMP15, CTSK, ADAMTS8*	2.98	1.799.E-02
R-HSA-2129379	REACTOME	Molecules associated with elastic fibers	7	*FBN2, BMP4, BMP2, EFEMP1, TGFB3, FBLN1, FBLN5*	9.58	1.799.E-02
R-HSA-1566948	REACTOME	Elastic fiber formation	7	*FBN2, BMP4, BMP2, EFEMP1, TGFB3, FBLN1, FBLN5*	8.06	3.653.E-02

This table provides the full list of significantly enriched GO terms and pathways associated with the whole and up-regulated differentially expressed genes of our study. Enrichment significance values correspond to FDR-adjusted p-values (FDR < 0.05). *Abbreviations:* GO: gene ontology; FDR: false discovery rate; BP: biological process; CC: cellular component; MF: molecular function; KEGG: Kyoto encyclopedia of genes and genomes

Table S5. A list of GO terms and pathways of 85 shared genes among four studies

Term ID	Category	Term name	Count	Gene	Fold Enrichment	FDR
GO:0005576	CC	extracellular region	29	*CFD, CEMIP, C1S, LAMA4, ADM, FBLN1, CXCL2, FSTL3, DPP4, ADAMTS14, EFEMP1, ADAMTS19, CTSK, RSPO3, IL13RA2, PRSS3, PTGDS, TGFB3, IL1R1, GDF15, RARRES2, TFPI2, AMPD3, TNFRSF1B, IGSF10, BMP2, PAPPA, SELENOP, SERPING1*	3.30	5.696.E-07
GO:0005615	CC	extracellular space	26	*CFD, MOXD1, C1S, TNFAIP2, ADM, FBLN1, CPZ, CXCL2, FSTL3, ICAM1, EFEMP1, CTSK, RSPO3, IL13RA2, PRSS3, PTGDS, CBR3, TGFB3, GDF15, RARRES2, TFPI2, SSH2, BMP2, GPRC5B, PAPPA, SERPING1*	3.67	5.696.E-07
GO:0062023	CC	collagen-containing extracellular matrix	8	*EFEMP1, TGFB3, GDF15, LAMA4, RARRES2, SERPING1, FBLN1, ICAM1*	5.44	2.633.E-02
GO:0009897	CC	external side of plasma membrane	8	*IL1R1, CTSK, BTN3A3, TNFRSF14, BTN3A2, IL13RA2, ANTXR1, ICAM1*	5.10	2.891.E-02
GO:0031012	CC	extracellular matrix	6	*ADAMTS14, EFEMP1, ADAMTS19, RARRES2, TFPI2, FBLN1*	7.08	3.852.E-02
hsa04060	KEGG	Cytokine-cytokine receptor interaction	9	*BMP2, IL1R1, TGFB3, GDF15, TNFRSF14, TNFRSF1B, IL13RA2, CXCL2, TNFRSF21*	5.73	1.608.E-02
R-HSA-1474244	REACTOME	Extracellular matrix organization	9	*BMP2, ADAMTS14, EFEMP1, TGFB3, LAMA4, CTSK, FBLN1, F11R, ICAM1*	5.52	4.135.E-02

Enrichment significance values correspond to FDR-adjusted p-values (FDR < 0.05). *Abbreviations:* GO: gene ontology; FDR: false discovery rate; CC: cellular component; KEGG: Kyoto encyclopedia of genes and genomes

Table S6. Comparison of enriched GO terms identified across four studies

Study	GO ID	Category	Term name
GSE180415 & our study	GO:0030335	BP	positive regulation of cell migration
	GO:0016020	CC	membrane
GSE17978 & our study	GO:0008285	BP	negative regulation of cell population proliferation
	GO:0006954	BP	inflammatory response
	GO:0006508	BP	proteolysis
	GO:0070062	CC	extracellular exosome
GSE180415 & GSE17978 & our study	GO:0007155	BP	cell adhesion
	GO:0005886	CC	plasma membrane
	GO:0062023	CC	collagen-containing extracellular matrix
	GO:0005615	CC	extracellular space
	GO:0005576	CC	extracellular region
	GO:0009986	CC	cell surface
	GO:0031012	CC	extracellular matrix
GSE17978 & GSE1724, 10921, 44723, and 40839 & our study	GO:0005515	MF	protein binding

A table showing shared GO terms among our study and three other studies: GSE180415 (Hanmandlu et al. 2022) and GSE17978 (Emblom-Callahan et al. 2010) and GSE1724, 10921, 44723, and 40839 (Plantier et al. 2016). *Abbreviations:* GO: gene ontology; DEG: differentially expressed gene; GSE: gene expression omnibus series; BP: biological process; CC: cellular component; MF: molecular function

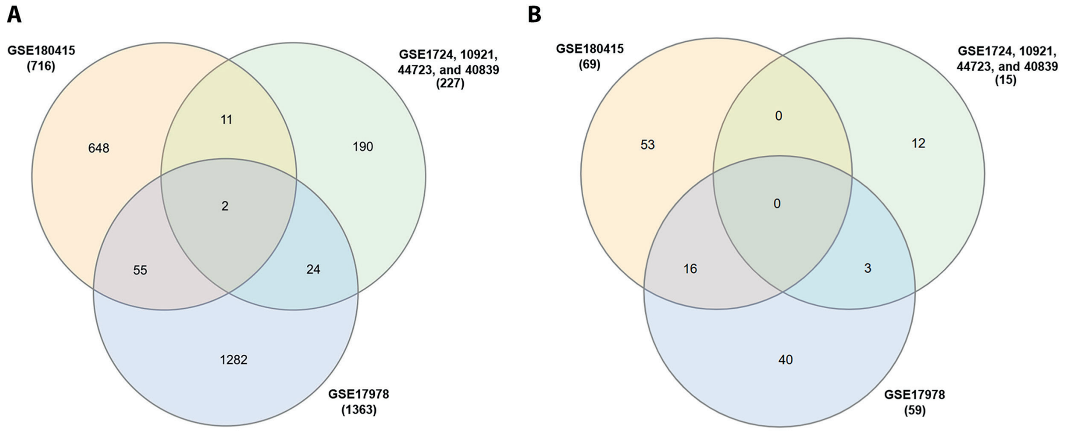

Figure S1. Venn diagrams comparing DEGs and GO terms across three studies.

(a) Overlap of DEGs and (b) overlap of enriched GO terms among three datasets: GSE180415 (Hanmandlu et al. 2022), GSE17978 (Emblom-Callahan et al. 2010), and GSE1724, 10921, 44723, and 40839 (Plantier et al. 2016). The number of DEGs and GO terms identified in each dataset is indicated in parentheses. *Abbreviations:* GSE: Gene expression omnibus series; GO: gene ontology; DEGs: differentially expressed genes

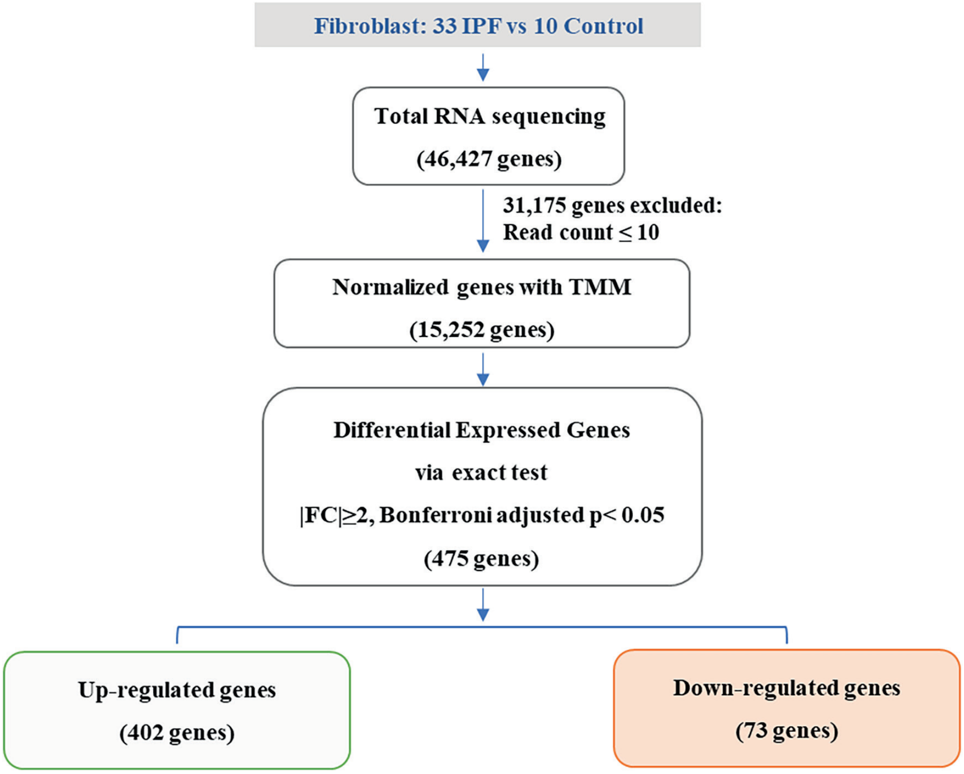

Figure S2. Workflow for differentially expressed gene selection.

Flowchart illustrating the selection process of differentially expressed genes following total RNA sequencing analysis of lung fibroblasts from 33 IPF patients and 10 controls. *Abbreviations:* IPF: idiopathic pulmonary fibrosis; TMM: trimmed mean of M-values; FC: fold change of IPF/control

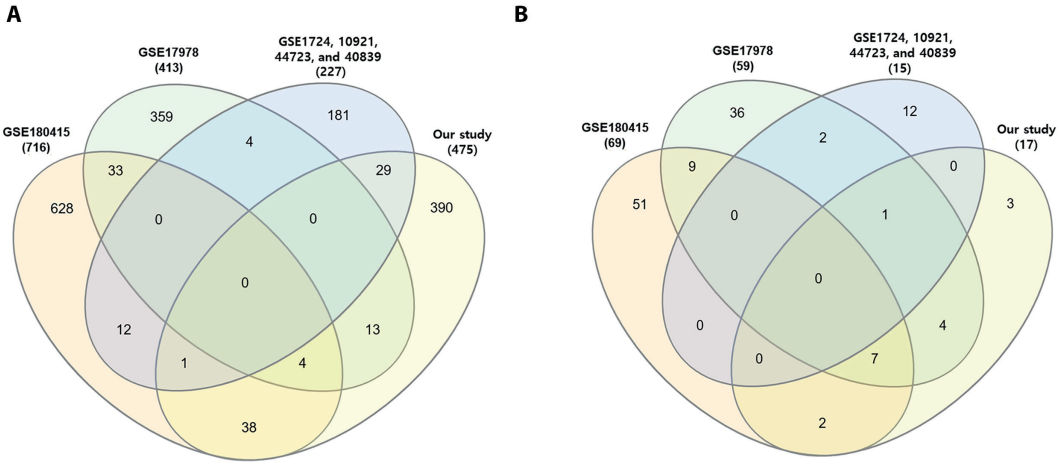

Figure S3. Combined study Venn diagrams.

Venn diagrams comparing (a) differentially expressed genes and (b) GO terms across datasets from GSE180415 (Hanmandlu et al. 2022), GSE17978 (Emblom-Callahan et al. 2010), and GSE1724, 10921, 44723, and 40839 (Plantier et al. 2016), and the present study. The number of DEGs and GO terms identified in each dataset is indicated in parentheses. *Abbreviations:* GSE: Gene expression omnibus series; GO: gene ontology