# Modulation of H4K16Ac levels reduces pro-fibrotic gene expression and mitigates lung fibrosis in aged mice

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#### **Online Supplementary Materials:**

#### Methods:

#### **RNA** sequencing

Total RNA were prepared from three different primary IPF fibroblasts after transfection with either siRNA Mof or NT as described. RNA-sequencing (RNA-Seq) was performed on the Illumina NextSeq500 following the manufacturer's protocol (Illumina Inc., San Diego, CA) at the UAB Genomics Core Facility.

Briefly, RNA quality was assessed using the Agilent 2100 Bioanalyzer. RNA with a RNA Integrity Number (RIN) of ≥7.0 was used for sequencing library preparation. RNA passing quality control was converted to a sequencing ready library using the Agilent SureSelect Strand Specific mRNA library kit as per the manufacturer's instructions (Agilent, Santa Clara, CA). The cDNA libraries were quantitated using qPCR in a Roche LightCycler 480 with the Kapa Biosystems kit for Illumina library quantitation (Kapa Biosystems, Woburn, MA) prior to cluster generation. Cluster generation was performed according to the manufacturer's recommendations for onboard clustering (Illumina, San Diego, CA). We generated between 30-35 million paired end 75bp sequencing reads per sample for transcript level abundance.

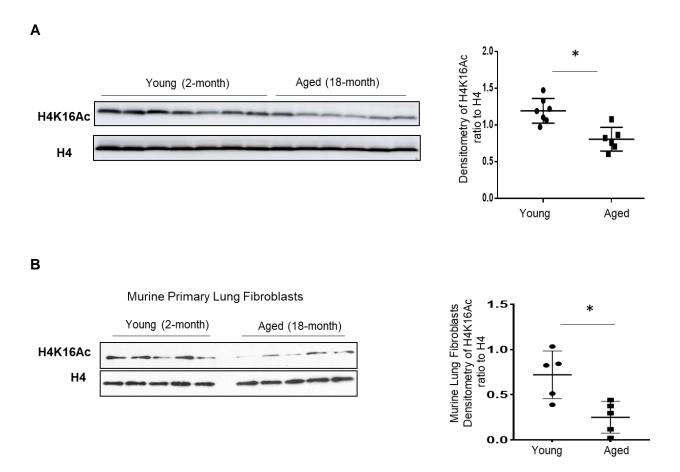
#### Data assessment:

STAR (version 2.5.3a) was used to align the raw RNA-Seq fastq reads to the reference genome from Gencode [1]. Following alignment, HTSeq-count was used to count the number of reads mapping to each gene [2]. Normalization and differential expression was then applied to the count files using DESeq2 [3].

#### **Supplementary Reference:**

- 1. Dobin, A., et al., *STAR: ultrafast universal RNA-seq aligner.* Bioinformatics, 2013. **29**(1): p. 15-21.
- 2. Anders, S., P.T. Pyl, and W. Huber, *HTSeq--a Python framework to work with high-throughput sequencing data.* Bioinformatics, 2015. **31**(2): p. 166-9.
- 3. Love, M.I., W. Huber, and S. Anders, *Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2.* Genome Biol, 2014. **15**(12): p. 550.

### **Supplementary Figures:**



## Figure S1. Histone H4K16Ac levels in young and aged mice lung tissues / primary murine lung fibroblasts.

(A) The H4K16Ac levels in young (2-month old) and aged (18-month old) mice lung tissues at baseline by western blots, H4 is the loading control. *Right*, Densitometry of H4K16Ac relative to H4, as in A. \*P < 0.05, aged (n = 6) compared to young (n = 7) mice. (B) Baseline levels H4K16Ac and H4 by WB in lung fibroblasts isolated from young (2-month) or aged (18-month) mice. *Right*, Densitometry of H4K16Ac relative to H4 as in C. \*P < 0.05, n = 5 in each group.

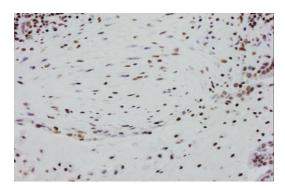
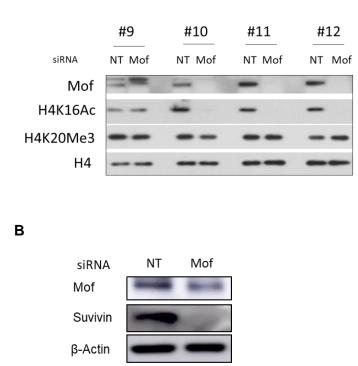


Figure S2. IPF lung fibrotic focus stain of H4K16Ac (brown), picture taken at 20 x.



**Figure S3. (A)** Four different siRNA Mof from Thermo Scientific were tested for knocking down Mof in lung fibroblasts. # 12 was used in the rest of the experiments. Western blots demonstrated the Mof, histone H4K16Ac, and H4K20me3 levels in nuclear extracts. H4 is the loading control. **(B)** IPF fibroblasts transfected with siRNA or NT, western blots demonstrated the Mof knockdown for the blot show in Figure 3B for survivin expression by western blot.

#### Analysis: MOF vs NT gene status OK SB FC2 p05 - 2018-06-11

Downregulated III No change II Upregulated Downregulated -log(p-value)

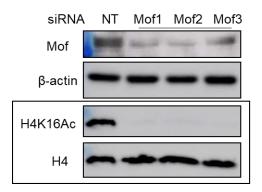


**Figure S4.** Pathways of IPF fibroblasts transfected with siRNA Mof vs NT by RNA-Seq from 3 different IPF fibroblast cell lines.

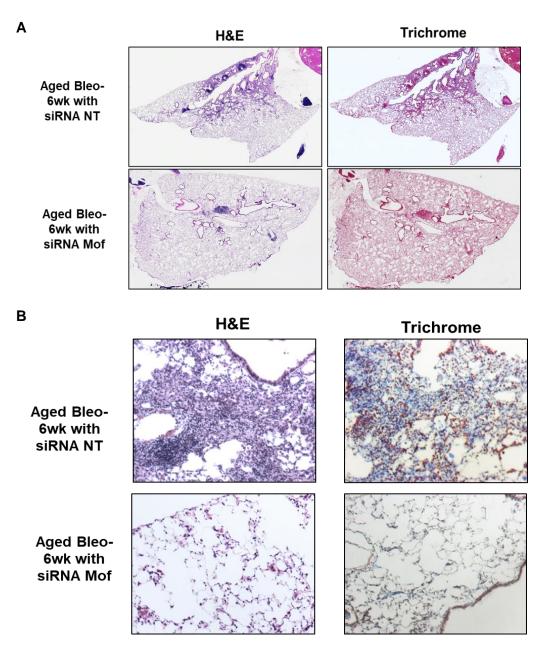
<ul> <li>In programmer 2015</li> <li>H. S. Hart, R. H. M. K. M. S. K. M. M. K. M. M. M. M. K. M. M. M. K. M. M. K. M.</li></ul>			
IDS 56 III         MARR, HURL, HURL, HURL, HURL, HOLL, HOL	MCF will get state CK 3FC plos- HASTING, 4CHETB, 4CAR2, HASTINGA,	35	Cellular Assembly and Organization, DNA Replication, Recombination, and Repair, Post-Translational Modification
IDF 5 MT gree state OK ST C2 05         +AMM-AT2, ATMURT, ATMACTR, ATTACTR, ATMACTR, ATMACTR, ATMACTR, ATMACTR, ATMACTR, ATMACTR, ATTACTR, ATMACTR, ATM	MCF shift gene states CK 58 C2 plb - HAURKI, 491081, 400C43, 4C0C43, 4C0C44, 4C0PW, 4C	32	Cell Cyrle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair
IDIS -6-11         ARXIV, ************************************	AMMCART2. ATMURTR. 4 CART3. 4 COPT2. 4 CODATL, 4 FAM2. 4 FAM2. 4 FAM2. 4 FAM2. 4 FAM3. 4 FAM3. 4 GTSE1. 4 HUUS, 4 HUUS, 4 HUUS, 4 HUUS, 4 LPM, 4 MCG7, 74 CA 4 FAC38, 4 FAC44, 4 FAC38, 4 FAC38, 4 FAC44, 4 FAC44, 4 FAC38, 4 FAC44, 4 FAC444, 4 FAC444, 4 FAC44, 4 FAC444, 4 FAC44, 4 FAC	32	Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair
IDD: 5 M Topes statis OX STC2 p05         PC(MPC2, Fab Thalm, FCOR, FCOR2, FAB Thalm, FCOR, FCOR2, FAB	15102, +0003, +00145, -001018, 04/0018, 04/0018, 04/14217, +E8/A28, +E9/A28, +E9/A28, +E9/A28, +40/142, +41/1438, +41/51/428, +41/421/41, 41/41/41, +41/41/42, +	28	Connective Tissue Disorders, Developmental Disorder, Castrointestinal Disease
IDF 5 MT gere statis CX STC2 p05         D0 protectorm, 216 Protectorm, 216 Protectorm, 2100 Group, 2003 Group, 2004 Group, 2005 Group, 2004 G	CBMF, 4CT, 4DBDCL, 4DBDCL, DN4-RC, Dnen, 4CDNUL, 4HIST.HIG, 4HISTHIB, HISTIHIB, HISTIHIB, HISTIHIB, Importinabhalbeta, Importinabhalbeta, Ink, 4KFI4, 38 4A, 4FN45, 4F04L1, FD04L21(PURIZIC), FPMILL, FFNA, 45KF02, 45C1282, FINARPBLI	26	Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair
MDF is MT gere statis OK SITC2 p05         PRC (strongel), MPC-COICU, 4-CONA,	205 protestore, 265 hotestore, adobi group acceptor physionanetase, Adobi abulint, 4400004, 480005, 400054, 400054, 400054, 40004, 47000, 470047, 47004, 47000, 470047, 47004, 47000, 470047, 4700	26	Cell Cycle, Cellular Movement, Cancer
IOD: 56 IT         MONIR, ALTINEUTCL, Cleby, FLODIA, FCDIA, 401           2018-96-11         MON, HAUNA, FORM, FADIA,	INCE SIT gene assue OC SITC pISS - APC (complex), APC COC01, 4CON42, 4CON82, 4CON82, 4CON82, 4CON54, CADC34, CADC34, CAV, 4CON1, CAV, 4CON1, CAV, 4CON1, 4CO	53	Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair
IDF 5 MT gree statis CX STC2 p05         ADR. 450CX54, 450NR, 450NR           2018-96-11         PMD PAIL, PTIMR, 440LX, 450NR, 450	EUR + COLITAL + CICIA + DLIL, esrogen reception + EXPQ, + GNCLI, Hear, +HSTH24E, Instance Masse Massee Masse M, + KNTS, + LMANL, + MUPTS, + MODI, M-cor, + MEURLIR, Moth, 29 + POLE2, Rox, Screause gamma, Strife Protesse, + SSRL, tymologe Instance, + TMPO	22	Cancer, Organismal Injury and Abnormalities, Hematological System Development and Function
IOS 56 11         4400HLAI, 440CUTG, 80CJ-840C2-640C           2016-66-11         RCX, FCML, FADERL, RCA-FSUCJ-440C           2016-66-11         RCX, FCML, FADERL, RCA-FSUCJ, SAUGLAI, FADERL, AND           1005-611         RCX, FCML, FADERL, RCA-FSUCJ, FCML, FADERL, RCA-FSUCA, FUNC           1005-611         RCX, FCML, FADERL, RCA-FSUCA, FUNC           1016-61-11         RCX, FCML, FADERL, RCA-FSUCA, FUNC           1016-61-11         RCX, FADERL, COLOR, FCG, FAGER, FADERL, FADERL, COLOR, FCG, FAGER, FADIR, COLOR, FADERL, FADERL, FADERL, COLOR, FADERL, FADERL, FADERL, FADERL, COLOR, FCG, FAGER, FADIR, FUNCA, FADERL, FADIR, COMANIL, COR- 2016-66-11           2016-66-11         MCR, AGR, AGL, AGL, AGLA, FADERL, FA	bulik, 4GLCE, Hedgebog, HSTONE, H5970, Hsp70, Immunogobulin, 4KCP12, Lk, 4MKGE1, *mir-137, 4MYOCD, *NET, PARP, 27	21	Cell Cyrle, Hematological System Development and Function, Hematopolesis
IDF 5 INT gree states OK 38 PC2 p05         +400.MT33, Apin Actimic, Apin Carein, Capa 2018-46-11           2018-46-11         IDF 5 INT gree states OK 38 PC2 p05         +501.FXX, 470.KX, 470.K	INCY SAT (2015 - HALDHLAL, HEGALF), ROL-BROZE-FANCU-F	19	Cardiovascular Disease, Developmental Disorder, Hematological Disease
IDS 56 11         MOTE VIEW, HERCH, HOURS, HOURS, HOURS, HOURS, HOURS, MOLES, HOURS, STOB4-66-11           IDDE-56 11         MODE VIEW, HERCH, HOURS, T. CHARL, PLOUCT, THEDD, HANK           IDDE-56 11         MODE VIEW, RECK, HOURS, T. CHARL, PLOUCS, THED, THED, HANK           IDDE-56 11         MODE VIEW, RECK, HOURS, T. CHARL, PLOUCS, HOUR, TOTAL, FLOUCS, HOUR, PLOUL, HOURS, HO	+JDANTS, Apile Actine, Apile careir, calear oper ( Calegerity + Collegerity + CPAS, +DCR2, +DHSI3, ECU, Em, +EX, +F, F, Krin, +ERU, +CBMIS, ID-cholearol, +LITEL, +MBP, P ghcoproteir, P38 M4PC, 24 +PRC, +PCGR4, ProCAE, Rock +SERG, +SBPS, SY(2P, +TAFIQ, ProPic, UR2, +NDDG, +ZMX13	19	Cellular Function and Maintenance, Cellular Movement, Hematological System Development and Function
IOS 56 IT         HARDOK, ALMOCK, ALCINER, FANC, PLOTARE, CHARK           2018-96 IT         HOURS, HARDOK, ALGUER, FANC, PLOTARE, FANG, PLOTA, FUB           2018-96 IT         HAR, PARIL, PERC, ALCINEL, CLONG, ALGUER, FANG, PLOTA, FUB           2018-96 IT         HAR, FANL, PELCIA, FLORARL, HARDOK, ALGUER, CLO, CLO           2018-96 IT         HAR, FANL, PELCIA, FLORARL, ALGUER, AND           2018-96 IT         HAR, FANL, PELCIA, FLORARL, ALGUER, CAN, AND           2018-96 IT         HAR, FANL, PELCIA, FLORARL, ALGUER, CAN, AND           2018-96 IT         HAR, FANL, PANL, AND, AND, AND           2018-96 IT         HAR, FANL, AND, AND           2018-96 IT         HAR, AND, AND           2018-96 IT         HARDOR, AND           2018-96 IT         HARDOR, AND           2018-96 IT         HARDOR, AND           2018-96 IT         HARDOR, AND           2018-96 IT	NOT SIT DRAFT ANTENCL, FORG, FORIS, FORIS, FORIS, FORIS, FORIS, FORIS, FORICI, FORICA, HORNOS, HEAVILIZ, FILMIC, HISTIHOM, HIS	19	Small Molecule Biochemistry, Lipid Metabolism, Cell-To-Cell Signaling and Interaction
IDE-511         HAPP, HABIGN, FARICL, FALICLS, HCDL           2018-66-11         HAPP, HARICL, FALICLS, HCDL           2018-66-11         HAPP, HCDL, FALISM, FALICL, FALISM, HARICL, HARDL, HARDL           IDE-511         HAPP, HAPLC, FALISM, FALICL, FALISM, HARDL, HARDL           IDE-511         HAPP, HAPLC, FALISM, FALICL, HADDL, H	UCF SHI (PRE-BALES OK SF72 plb - HANKONG, ARKNOK, ACLIMAR, ACKOCHA, COCCISA, COCCIA, COCCISA, COCCIA, ACKAL, ACKAL, ACKAL, ALANCIA, ANKOL, ACKAL, ANKOL, ACKAL, ANKOL, ACKAL, ANKOL, ALANCIA, ANKOL, ALANCIA, ANKOL, ALANCIA, ALANCI	17	Post-Translational Modification, Cell Cycle, Cellular Assembly and Organization
MOF is MT gere statis OK SI PC2 p05         JONAL3, 435GUMT1, 4110, 4120, 4120, 4141, 4120, 4121, 4101, 41	10, 454454, 454401, 456701, 456704, 4044512, 4601, 4501, 4501712, 45162, 4415114284, 4415114584, 44571454, 44574, 4417-41765, 18 661, 454454, 471444, 17141, 47843924, 4784464, 471623, 44584	16	Neurological Disease, Organismal Injury and Abnormalities, Cell Death and Survival
MDF is MT gere statis OK SPTC2 p05 - Mu, FLONZ, CTMA, FSCHSMI, Sind, Sind	COUD. CACS, CACSS)C 4CONL 4CENN, 4CENC, 4CUS, 4DEPOCIN, 4DONGN, 4DISTA, 45MIDSTAI, 4CAS23, 44MITH2RE, 4UXCL, 44MPR2, 44MFR2, 44MF1, 188 45MH187, RENU, 45XC2412, 45MM, 4THE1, 4THE, 4THE37, 4DE90CIN, 4DD144, ESR1, 4FMIDSTAI, 4CAS23, 44MITH2RE, 4UXCL, 44MPR2, 44MFR2, 44MF1, 188	16	Amino Acid Netabolism, Post-Translational Modification, Small Molecule Biochemistry
MOF IN Typer Earlis CK STC Caspare 3/1, CD3 group, 2018-66-11           D018-66-11         PCC STR Processor STC 2015           MOF IN Typer Earlis CK STC Caspace 3/1, CD3 group, 2010, 2016-10           MOF IN Typer Earlis CK STC 2015         PACKIA, Alp, ApJ, Actual, Alma, MTOCL, 2018-46-11           MOF IN Typer Earlis CK STC 2015         PACKIA, Alm, HADRILL, Climidulin, Climidian MUCM Receptor, No. Place 400, 2018-66-11           MOF IN Typer Earlis CK STC 2015         PHANAZ, PHANAZ, PHANAZ, PHANA,	ALL FCM2, CDK416, CDK416, CDK416, FCDK02, FCCM3, FCTM, Cpcin0, Qrinit, Cotisi, HuALL, HUALL, HUDH, H	15	Amino Acid Metabolism, Small Molecule Blochemistry, Cardiovascular System Development and Function
<ul> <li>MCH 5 MT gere status CX STC2 pdS - MCK4, Alp, ApI, 4-CUNU, cargear, FG 2018-46-11</li> <li>2018-46-11</li> <li>MCK3 MT gere status CX STC2 pdS - MCK3, And MLK6, Mmodan, Cargo 2018-46-11</li> <li>MCK3 MT gere status CX STC2 pdS - MCK3, And And AL ADDRAR, Cardonado, Cargo 2018-46-11</li> <li>MCK3 MT gere status CX STC2 pdS - MHWUZ, *MCK12, FATCU, ACBA, PC, PC, PC, PC, PC, PC, PC, PC, PC, PC</li></ul>	(g. Ceb, FCRBS, FCRB, optionogenese, Dig. 15f, Filamin, PHISZ, HISCIA, HINCIA, HINCIA, HINCIA, HINCIA, HICAB, #1U, LE-L, +UNCI, IMPZUIZ, HINCIA, MEL, MISZ, FORI, JIS SSPR1, 45748, Mer	15	Endocrine System Development and Function, Lipid Metabolism, Small Molecule Biochemistry
MCF is INT gere statis CX SFC2 pdS - H-MCRR3, Acm, H-MDRA18, Climodulo, Cut 2018-46-11. MCF is INT gere statis CX SFC2 pdS - H-MCRR3, PARCIA, ATCGA, ACRS, CP 2018-46-11. MCF is INT gere statis CX SFC2 pdS - H-H-MAXIA, AMORE - ACRO, More MCF is INT gere statis CX SFC2 pdS - H-H-J, MCCI, Mognetisin frequent yes, 1, 2018-46-11. MCF is INT gere statis CX SFC2 pdS - H-H-J, MCCI, Mognetisin frequent yes, 1, 2018-46-11. MCF is INT gere statis CX SFC2 pdS - H-H-J, MCCI, Mognetisin frequent yes, 1, 2018-46-11. MCF is INT gere statis CX SFC2 pdS - H-H-J, MCCI, MARL, PSICI, PSICJ, PSICJ, PMCCJ, FMCL, PSICJ, PSIC	MCF st MT gete states OX.58 FC2 plb2 - #ACSI4, Alp, ApJ1, 4CUM1, capsue, FCCM21, Co3, 4CUM1, calegen type N, calegen type N, cpokie, Gravit hormore, Gi43, GTFase, Hsp30, HD2, fingamma, 4/GF1, HL11, LL2 (fam/h), Insulin, Interferonablea, 12 antimin (complex), HMX16, Mmp, MTORCI, 4PB04, 4PB04, 4PB04, 4PB041, 4PB327L, 45EG284, 4FB041, GTFase, 1-10FB81	15	Cell Death and Surviral, Embryonic Development, Organ Development
MCF is NT gere static CX, STC2 pd5 - ++HMUX2, ++MC40, +C40, +C48, CP           2018-46-11           MCF is NT gere static CX, STC2 pd5 - ++HMUX2, ++MC40, +C40, HP           MCF is NT gere static CX, STC2 pd5 - 14+3-3, MCO, Angotesin Treepart Rp-1, 2018-46-11           MCF is NT gere static CX, STC2 pd5 - 14+3-3, MCO, Angotesin Treepart Rp-1, 2018-46-11           MCF is NT gere static CX, STC2 pd5 - ++HKC493, ++MBC437, +ib03, +LCC05, +LCC05, 2018-46-11           MCF is NT gere static CX, STC2 pd5 - +HKC4, HBO1, -BAOL, +MC021, BOL, +MC02, HBO1, +MC02, HBO1, +MC021, BOL, +MC121, BOL, +MC12	rin, +EDWB, HEDWB, HEMB, HEDWB, G protein, G protein alphai, G-protein beat, +GCNT4, GNR4, Gpcr, +GML1, +GR123, +GRM, Histore IS, KK (complex), +HCMG, +LGR4, 17 +184728, Ris barrolog, Rebin, 26, 51K1, +TBX428, TGV, hbulin	15	Cell Synaling, Cellular Function and Maintenance, Vitamin and Mineral Metabolism
IOC vs IVT gere status OX SFC2 pd5 - 114-3-3, IOCV, Angletesin Freesport yre, 11, 2018-46-11         2018-46-11         2018-46-11         2018-46-11         2018-46-12         2018-46-1	*MBWAX2, *MAUA2, *MAUA2, CPEM42, FUNUC227, DUNIC28, *ECT1, *FDX3, FMUA2, *MACE, *COS, HCM22, *MSTH2BF, MCA4, HEM128, LUD1, *FLCB3, *MAOA, *MAOA, *MACL, *MAOA, *MACA, *MAOA, *MACA, *MAOA, *MACA, *MAC	15	Cell-To-Cell Signaling and Interaction, Connective Tissue Development and Function, Skeletal and Muscular System Development and Function
MOT Is INT gere statis CU, SI CC pd5 - HARICH29, HABIGH29, HABIGH20, HABI	ATTER4, FLONGY, Globerin A, Calorenin proteils), FOURD, FOURD, FOURD, Collinger Mahai, HEDM1, #GAL, GMA, HQCAPS, Lith (complex), ME72, HME7A, 15 protein complex group, PRRAGL, PTras, HAB398, Ray1, 550CPP1, Tropomorin, TSV, Volage-greated calorin channel, *XBP2	14	Cardiovascular System Development and Function, Tissue Morphology, Cell-To-Cell Signaling and Interaction
	POTHS, DOARL, DANG, FELNI, FELS, FENSET, FESRA, FRAT, FORCI, FILILIS, FIETAPLS, FIETAPLS, METAPLS, HURK, FURK, 40081, FRUIT, FORICA, FRELL, IS A.M., TDOZ, FTNEN324, FTANOS, FTANOS, FURNAS, FURNAS, FURNAL, MORSI, TUPZ,	14	Cancer, Endorine System Disorders, Castrointestinal Disease
	UCF SHI GREATER SCI 2055 - 14RCAL, BICUL-BROU, BICUL-BROU-RHOUP-RHOUT-RHOU-RHOUS, HCARDS, HCARD, 2054, OCT PRULST, 4-DDIS, 4-D	13	Cellular Assembly and Organization, DNA Replication, Recombination, and Repair, Cancer
	UCF SHI GREARED KN ST PARS, AFRIND, 402113, CREA, 4CREARE, 4CREARE	13	Cellular Development, Cellular Growth and Proliferation, Connective Tissue Development and Function
25 MCF still great states OX 5872 pS6 - HABCAIL, HABCA	+86C41, +86C48, +4CPMT, +AWPCT3, +CMMT, +CMPC, C0T4, +CTMP21, +CTM821, +FPM1148, +ESC02, +GALC, +H16A, 1855C, 16, 14, +10D14, +K1F11, 18718, +M0710, +MK, +MCB41, +M2C1, +7C02, 14 +PM1022, +PM122, +PM121, 42C16, +SC104, +PM1C1, +DM121, +DM121, 45C02, +GALC, +H16A, 1855C, 16, 14, +0D14, +MC11, 18718, +MC910, +MK, +MCB41, +MC21, +7C02, 14 +PM1022, +PM122, +PM121, 42C16, +SC104, +PM1C1, +DM121, +DM121, 45C02, +GALC, +H16A, 1855C, 16, 14, +0D14, +MC31, 42C12, +MC21, +MC21, +7C02, 1400, +MC31, 42C12, +MC21,	n	Cancer, Endocrine System Disorders, Crganismal Injury and Abnormalities

**Figure S5.** RNA-Seq data for related network changes in IPF fibroblasts transfected with siRNA Mof vs NT.

Primary Murine lung fibroblasts



**Figure S6.** Testing of three different siRNA mMof for knocking down Mof in primary murine lung fibroblasts. Western blots showing Mof in whole cell lysate, or H4K16Ac in histone extracts by western blots. The loading control is  $\beta$ -actin for whole cell lysate, or H4 for histone extracts. Mof2 was used in the animal studies; sequence of siRNA mMof is in Table 2S.



**Figure S7.** 18-month old mice were subjected to bleomycin injury, then treated with siRNA NT or Mof by nasal from 3-6week after bleomycin injury. Slides are stained with H&E or with trichrome. Pictures were taken at  $4 \times (A)$ , or at  $20 \times (B)$ .

Table S1. Information of the de-identified subjects of the non-IPF or IPF samples used in this study.

Non-	Non-	Non-	Non-	IPF-a	IPF-b	IPF-c	IPF-d	IPF-e	IPF-f
IPF # 1	IPF # 2	IPF # 3	IPF # 4						
48yr,	20yr,	32yr,	61yr,	64yr,	60yr,	56yr,	48yr,	54yr,	61yr,
male	female	white,	white,	male	male	white,	black,	white,	white,
		male	female			male	male	male	female

### Table S2. siRNA sequences and Primers sequences for PCR

Name		Sequence
Mof (human) for cell culture (from Thermo Scientific, cat # J- 014800-12)	siRNA	5'-ACUUUGACGUGGAGCCGUU-3'
Non-targeting (NT) (for cells culture)	siRNA	Sense: 5'-UAAGGCUAUGAAGAGAUACUU-3', Anti-sense: 5'-GUAUCUCUUCAUAGCCUUAUU-3'.
mMof	siRNA	5'-UGAGGUGUUCCUCUACCAGCUUAGG -3'
(mouse, for <i>in vivo</i> )		
NT Negative Control (used in vivo, mouse)	siRNA	5'-AGCUACACUAUCGAGCAAUUAACUU-3'
Mof (human)	RT-PCR	F: 5'-AATGGCACAGCTGGGACTAGAACT-3'
(ENSG00000103510)		R: 5'-GCTTGGCTATAGCAACTGCCGAAT-3'
a-SMA	RT-PCR	F: 5'-ATGGCTCTGGGCTCTGTAA-3'
(human)	ChIP-PCR	R: 5'-GGAACCTAATCTGTGTCCTGTTATG-3' Set A
	Chir-r CK	F: 5'- CTTTCTTCTTTGCATGCTACCG R: 5'- GCTGGAATTTCAGGCCATTTC Set B F: 5'-GAGGTCCCTATATGGTTGTGTTAG-3' R: 5'-AGCTGAAAGCTGAAGGGTTAT-3'
Nox4 (human)	RT-PCR	F: 5'- AGATGTTGGGGGCTAGGATTG-3'
(ENSG0000086991)	ChIP-PCR	R: 5'- TCTCCTGCTTGGAACCTTCT-3' Set A F: 5'-ATCTCCTGACTCCGTGATCC-3' R: 5'-GCGTGTTAGCACTCTCTCACTTTA-3' Set B F: 5'-GAACAGCAGCAGCCACAAC-3' R: 5'-CTACCCAGAGCCGGTTTTC-3'
Col1A1 (human)	RT-PCR	F: 5'-TCGAGGGCCAAGACGAAGAC-3'
(ENSG00000108821)	ChIP-PCR	R: 5'- CGCACAACACCTTGCCGTTG-3' Set A: F: 5'-CTCTCCATTCCAACTCCCAAA-3'
		R: 5'-ATGGAGAGCAGGGAGGAA-3' Set B: F: 5'- CGTGAGTTGGTGCAAGAGAGAA-3' R: 5'-GGCCTTCCTGATTGCTTCTACA-3'
Survivin (human)	RT-PCR	F: 5'- AGCCCTTTCTCAAGGACCAC-3'
(ENSG00000089685)		R: 5'- CAGCTCCTTGAAGCAGAAGAA-3'

	ChIP-PCR	Set A:
		F: 5'- TCACTTGAGGTCAGGAGTTTG-3'
		R: 5'- CCCGAGTAGCTGAGATTAAAGG-3'
		Set B:
		F: 5'- ACCACGCCCAGCTAATTT -3'
		R: 5'- CATCACTTGAGTCCTGGAGTTC -3'
β-actin (human)	RT-PCR	F: 5'-TGCTATCCAGGCTGTGCTAT-3'
		R: 5'AGTCCATCACGATGCCAG T-3'

 $\label{eq:stable_stable_stable_stable} \textbf{Table S3.} \ \textbf{Excel file for the gene expression in siRNA Mof vs NT cells.}$