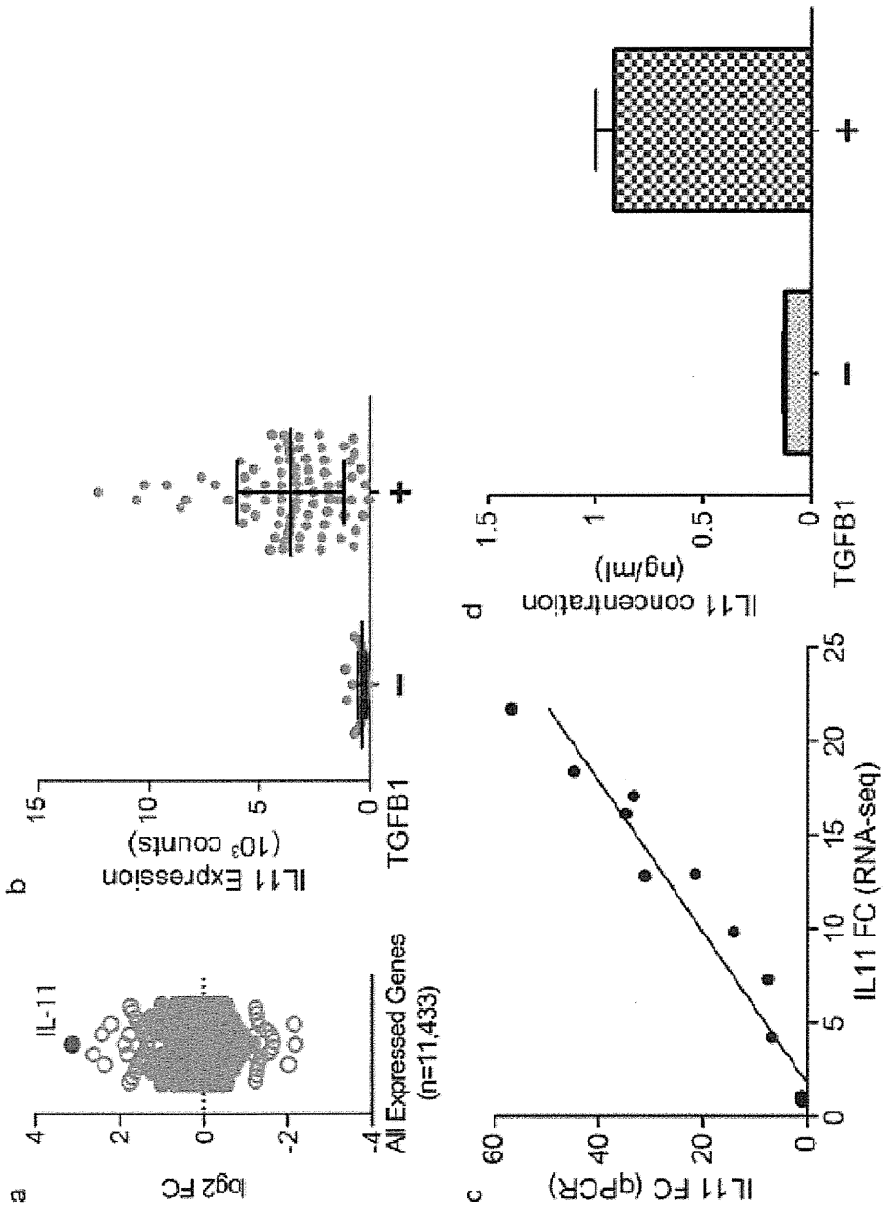

a
IL-11
log2 FC
All Expressed Genes
(n=11,433)
b
IL11 Expression
(10³ counts)
TGFB1
c
IL11 FC (qPCR)
IL11 FC (RNA-seq)
d
IL11 concentration
(ng/ml)
TGFB1

Figure 1

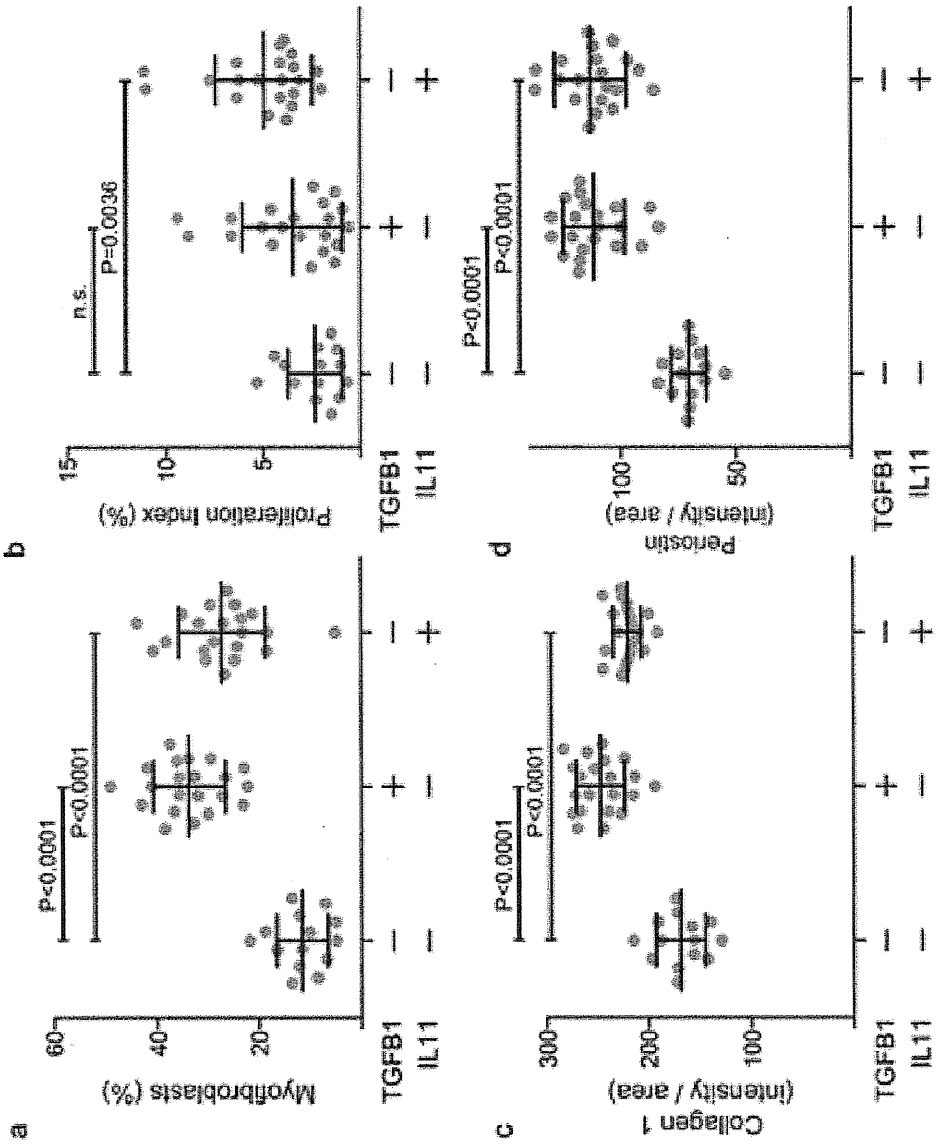

a
Myofibroblasts (%)
60
40
20
P<0.0001
P<0.0001
b
Proliferation Index (%)
15
10
5
n.s.
P=0.0036
c
Collagen 1
(intensity / area)
300
200
100
P<0.0001
P<0.0001
d
Periostin
(intensity / area)
100
50
P<0.0001
P<0.0001
TGFB1
IL11
−
+

Figure 2

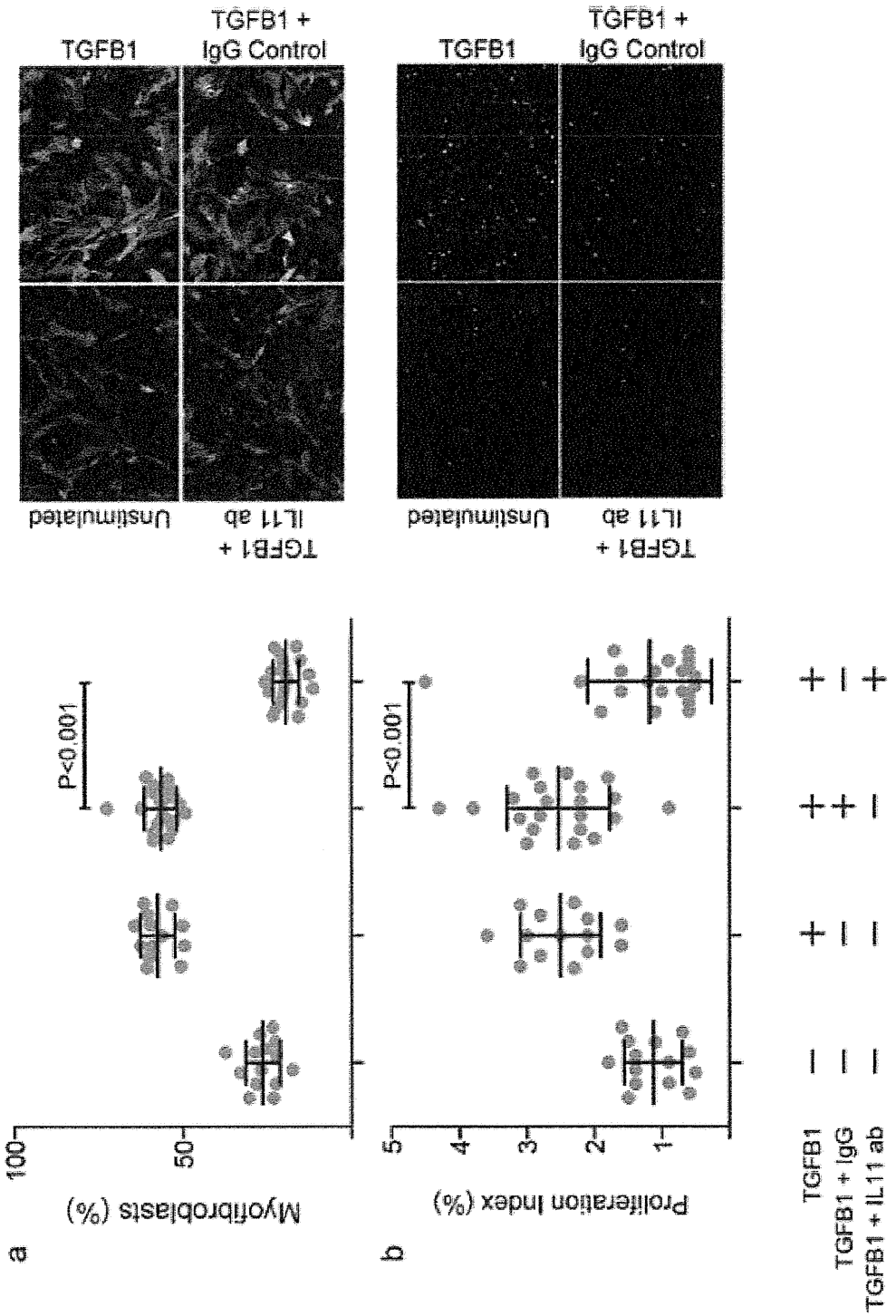


Figure 3a and 3b

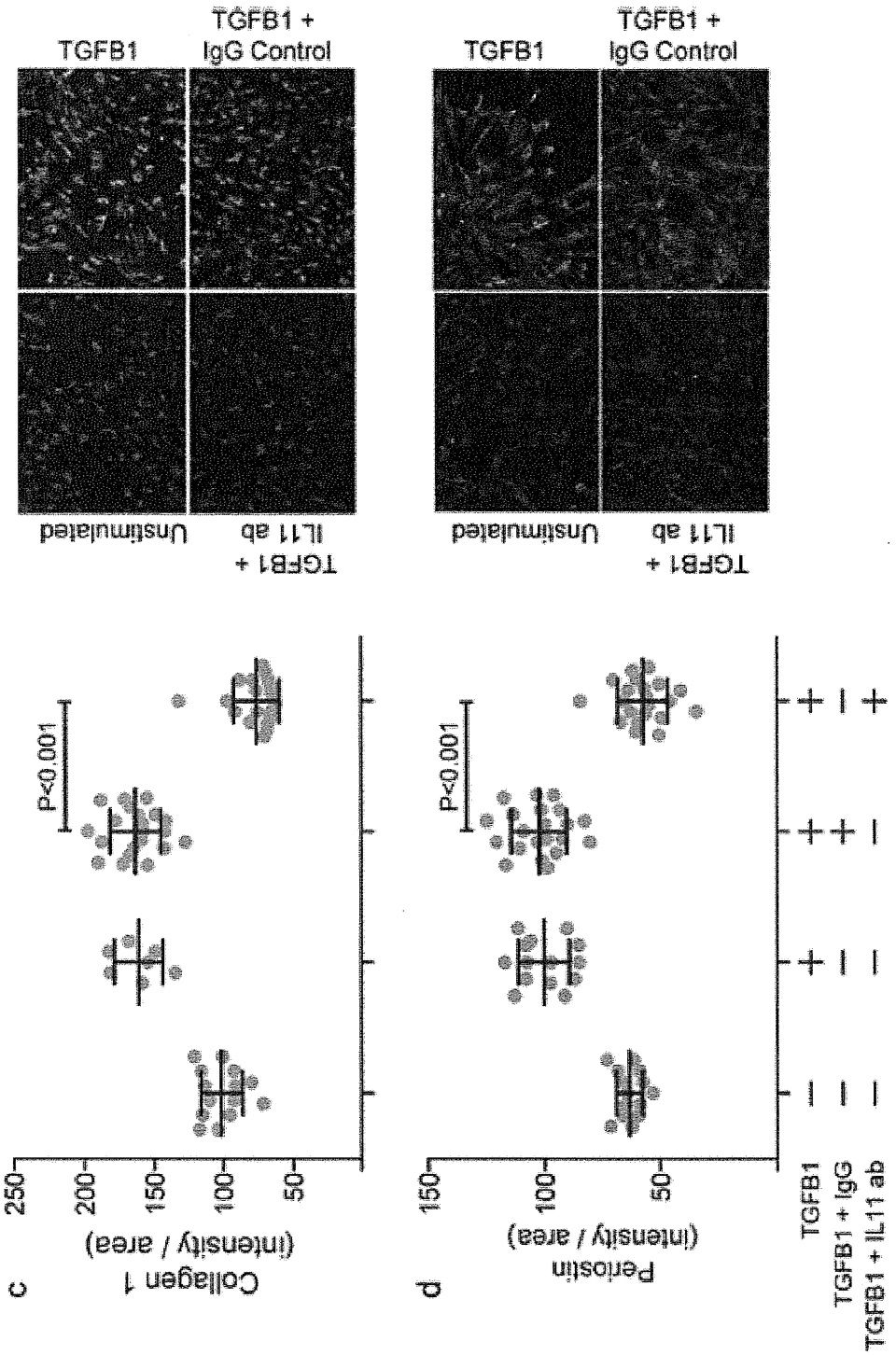


Figure 3c and 3d

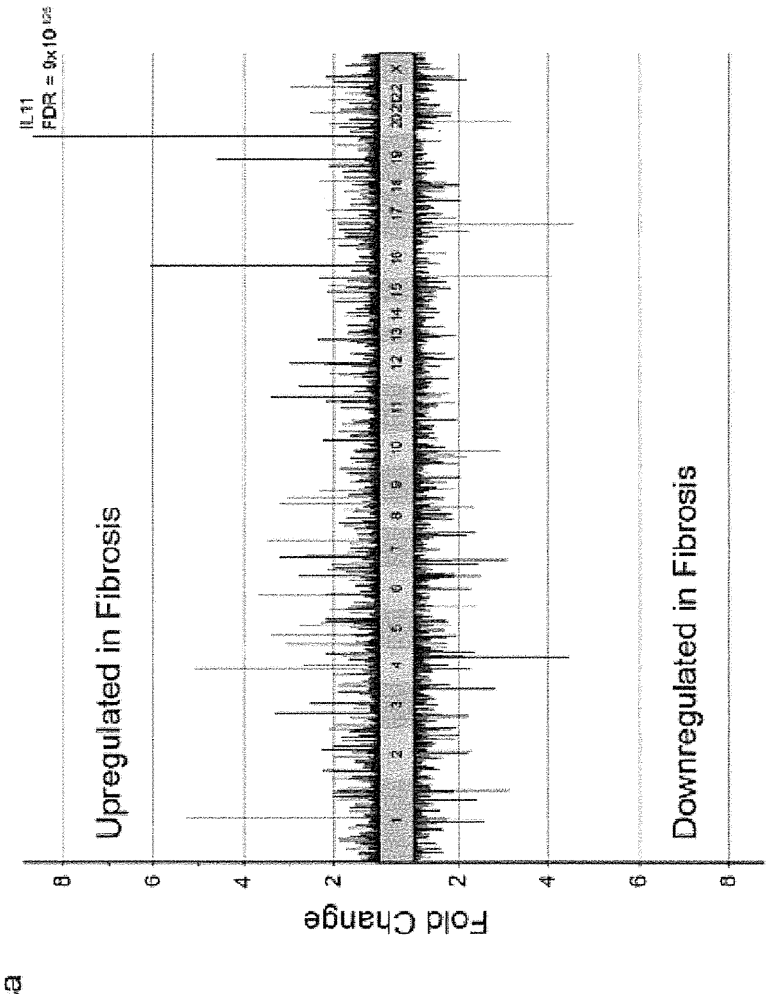

a
Fold Change
8
6
4
2
2
4
6
8
Upregulated in Fibrosis
Downregulated in Fibrosis
IL11
FDR = 9x10

Figure 4a

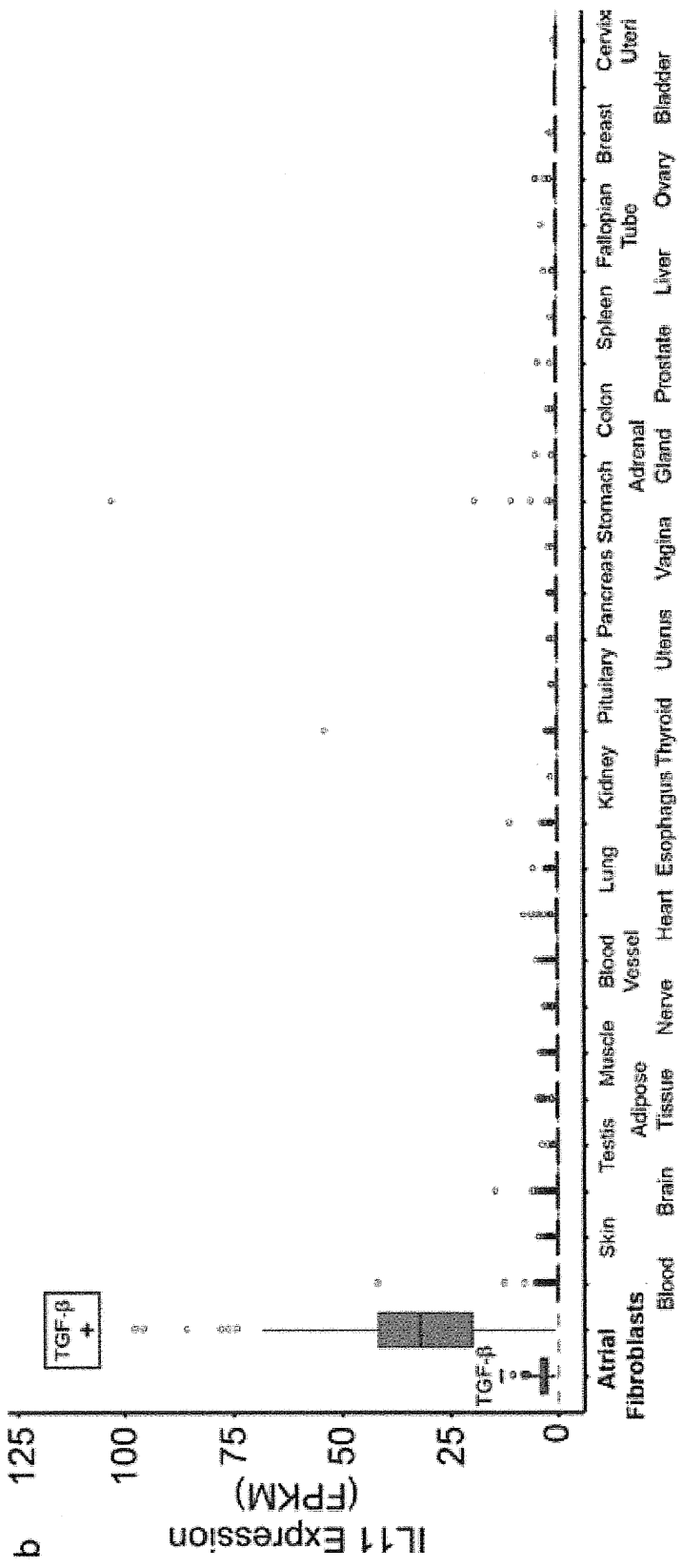

b
IL11 Expression
(FPKM)
125
100
75
50
25
0
TGF-β
+
TGF-β
−
Atrial Fibroblasts
Blood
Skin
Brain
Testis
Tissue
Muscle
Adipose
Nerve
Blood Vessel
Heart
Lung
Esophagus
Kidney
Thyroid
Pituitary
Uterus
Pancreas
Vagina
Stomach
Adrenal Gland
Colon
Prostate
Spleen
Liver
Fallopian Tube
Ovary
Breast
Cervix Uteri
Bladder

Figure 4b

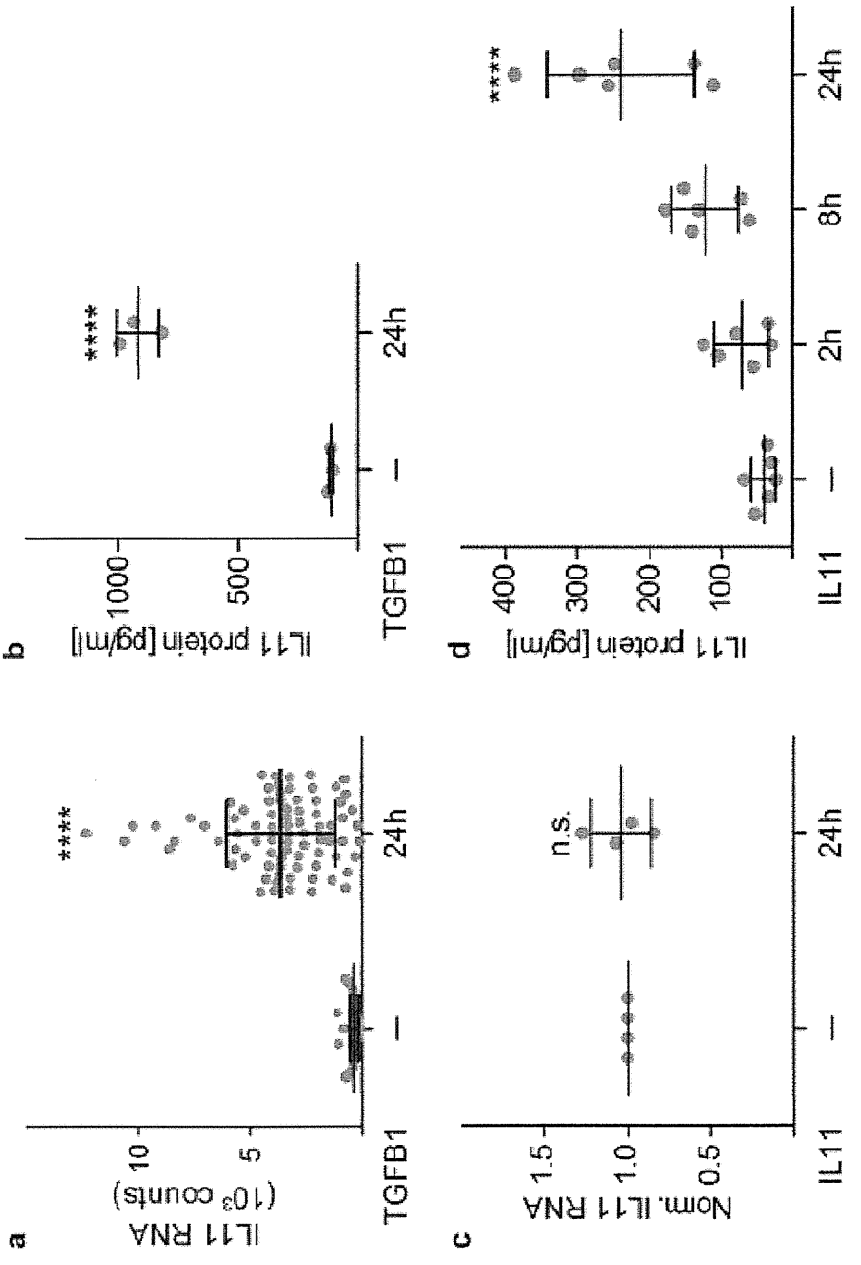

a
IL11 RNA
(10³ counts)
10
5
****
—
24h
TGFB1
b
IL11 protein [pg/ml]
1000
500
****
—
24h
TGFB1
c
Norm. IL11 RNA
1.5
1.0
0.5
n.s.
—
24h
IL11
d
IL11 protein [pg/ml]
400
300
200
100
****
—
2h
8h
24h
IL11

Figure 5

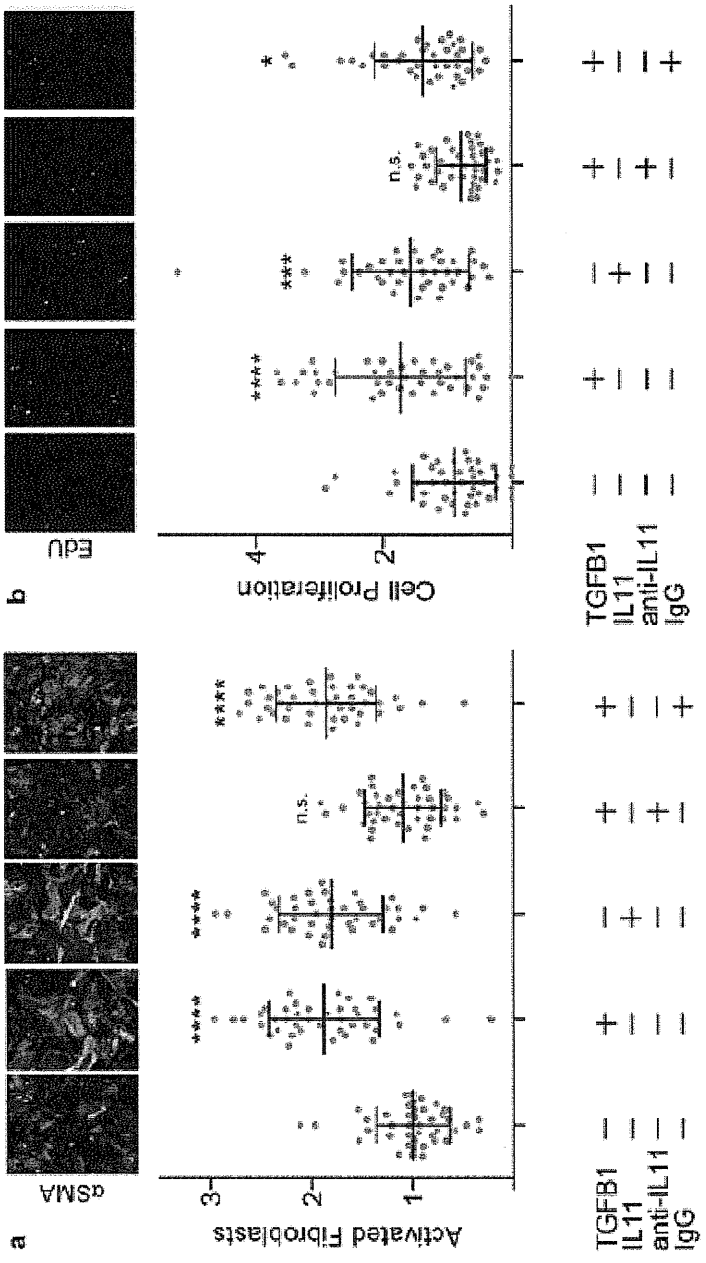


Figure 6a and 6b

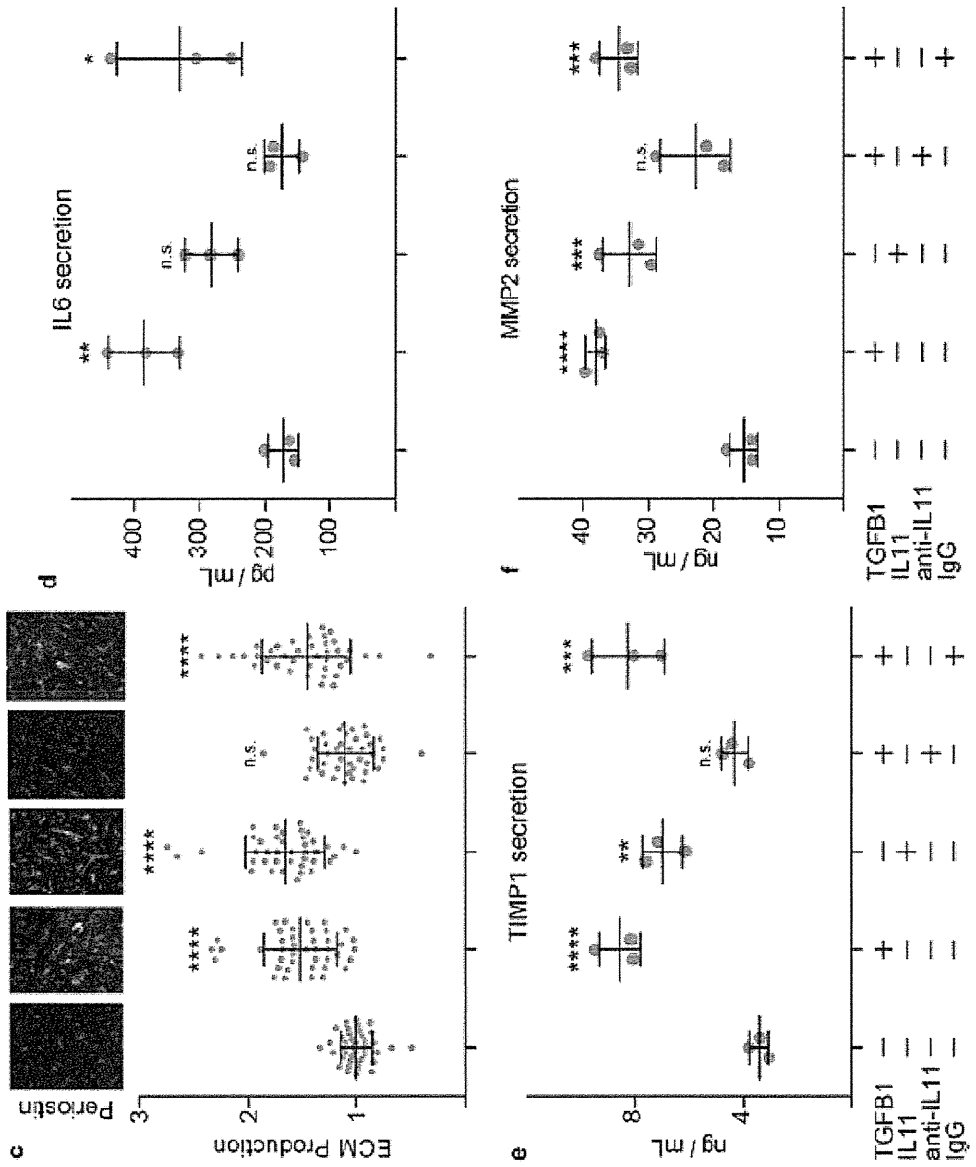


Figure 6c, 6d, 6e and 6f

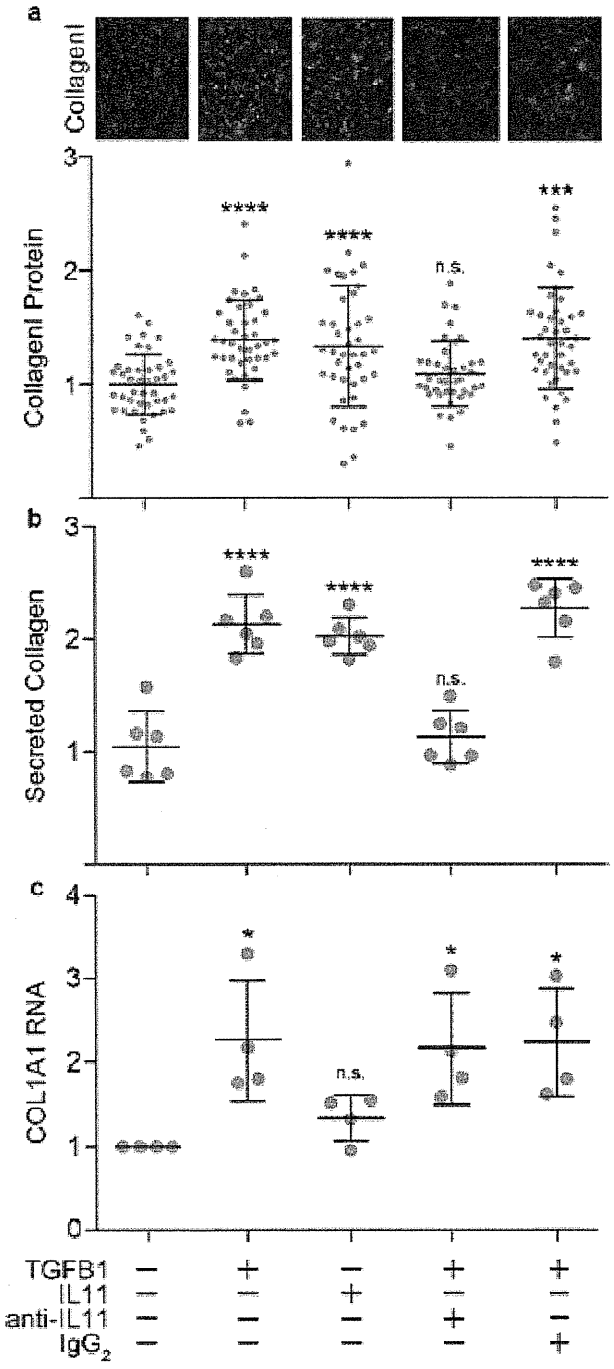

a
CollagenI
CollagenI Protein
****
****
n.s.
***
b
Secreted Collagen
****
****
n.s.
****
c
COL1A1 RNA
*
n.s.
*
*
TGFB1 − + − + +
IL11 − − + − −
anti-IL11 − − − + −
IgG2 − − − − +

Figure 7

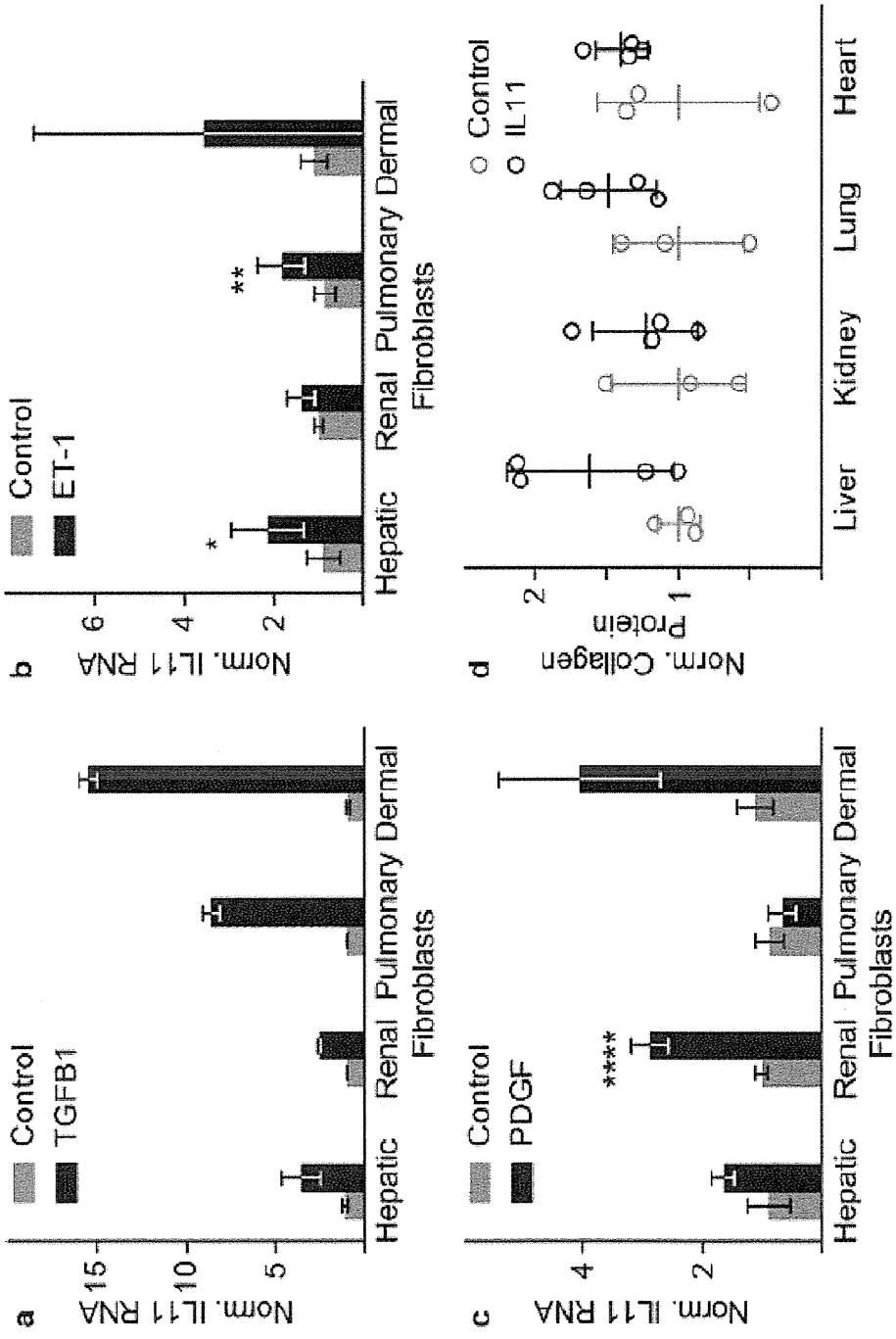


Figure 8a, 8b, 8c and 8d

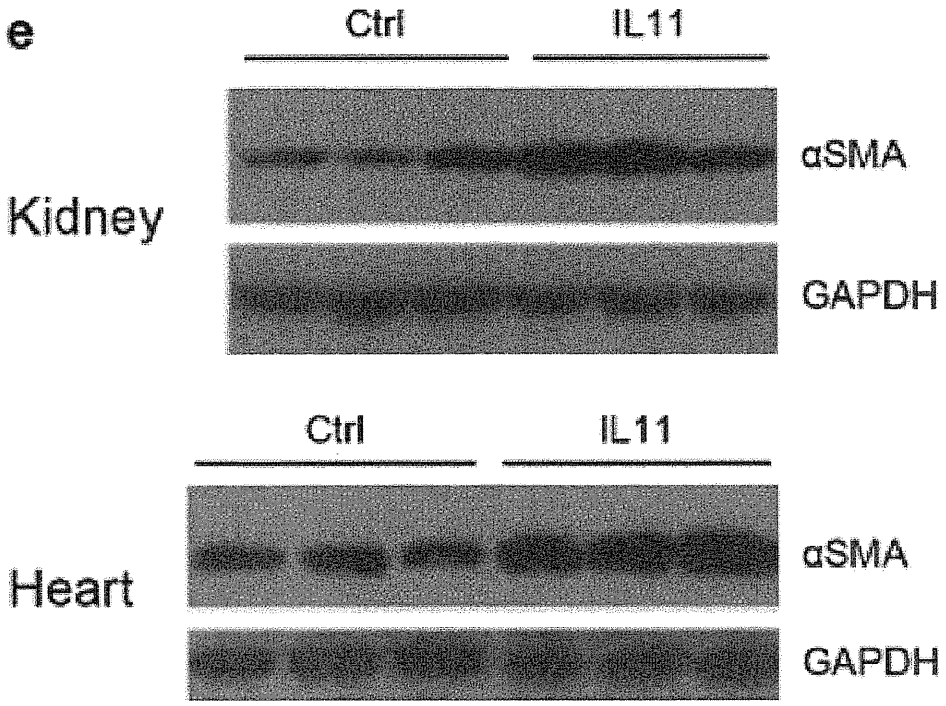


Figure 8e

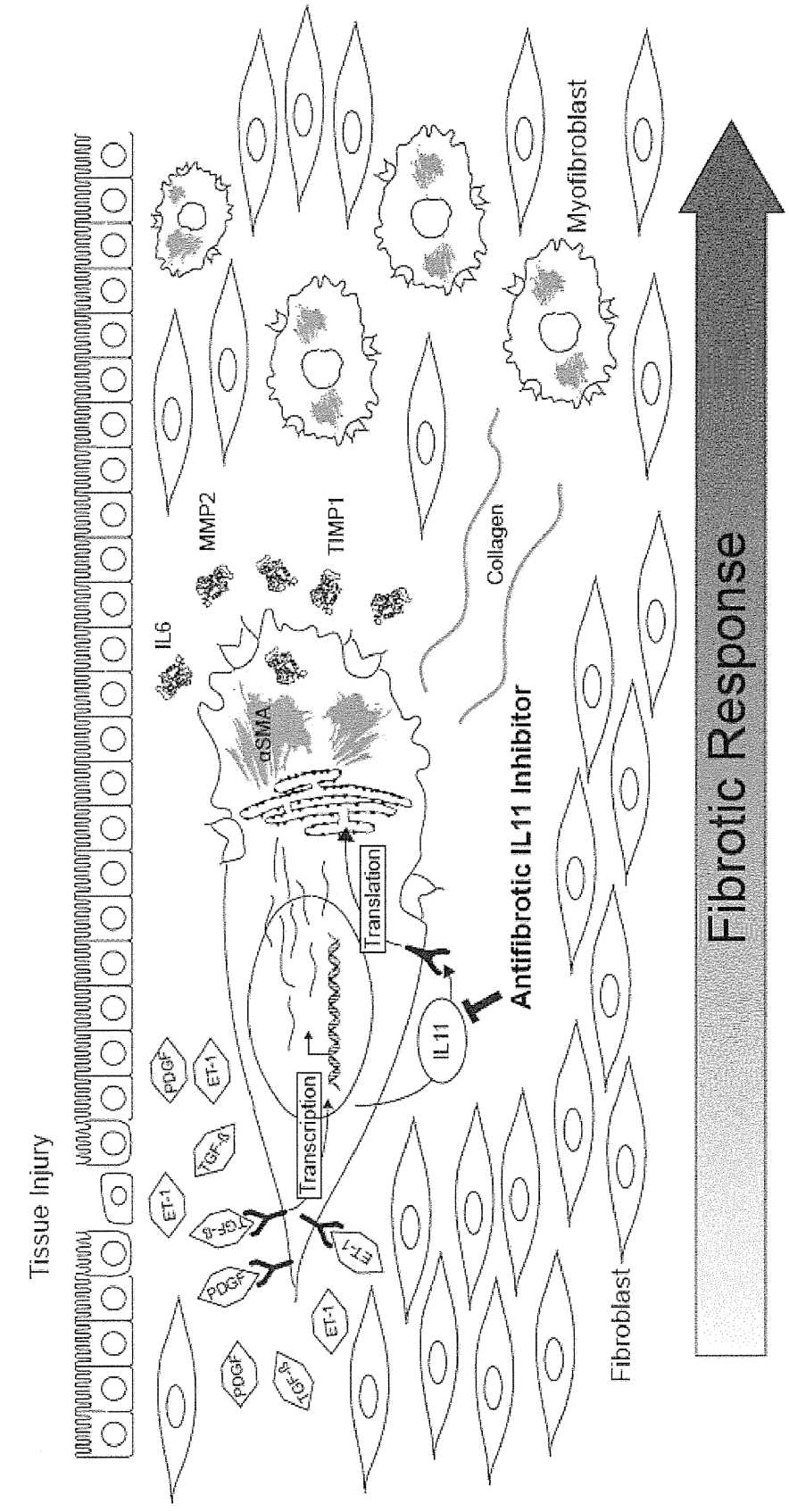

Tissue Injury
PDGF
ET-1
TGF-β
PDGF
ET-1
TGF-β
ET-1
PDGF
TGF-β
ET-1
Transcription
Translation
αSMA
IL6
MMP2
TIMP1
IL11
Antifibrotic IL11 Inhibitor
Collagen
Myofibroblast
Fibroblast
Fibrotic Response

Figure 9

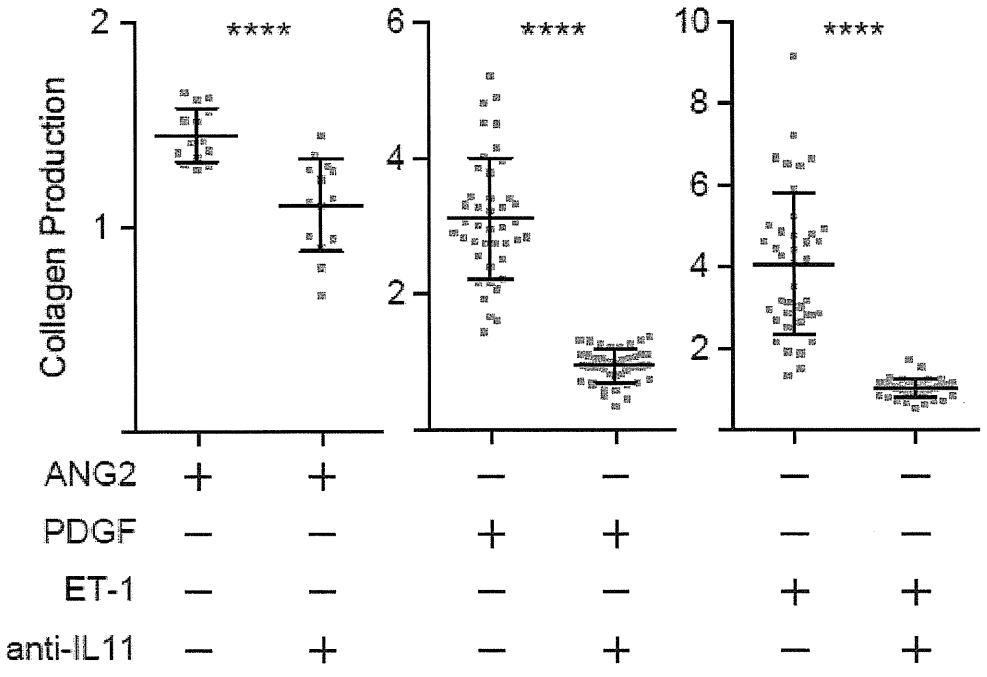


Figure 10

ACTGCCGCGGCCCTGCTGCTCAGGGCACATGCCTCCCCTCCCCAGGCCGCGGCCCAGCTGACCCTCGGGG
CTCCCCCGGCAGCGGACAGGGAAGGGTTAAAGGCCCCCGGCTCCCTGCCCCCTGCCCTGGGGAACCCCTG
GCCCTGTGGGGACATGAACTGTGTTTGCCGCCTGGTCCTGGTCGTGCTGAGCCTGTGGCCAGATACAGCT
GTCGCCCCTGGGCCACCACCTGGCCCCCCTCGAGTTTCCCCAGACCCTCGGGCCGAGCTGGACAGCACCG
TGCTCCTGACCCGCTCTCTCCTGGCGGACACGCGGCAGCTGGCTGCACAGCTGAGGGACAAATTCCCAGC
TGACGGGGACCACAACCTGGATTCCCTGCCCACCCTGGCCATGAGTGCGGGGGCACTGGGAGCTCTACAG
CTCCCAGGTGTGCTGACAAGGCTGCGAGCGGACCTACTGTCCTACCTGCGGCACGTGCAGTGGCTGCGCC
GGGCAGGTGGCTCTTCCCTGAAGACCCTGGAGCCCGAGCTGGGCACCCTGCAGGCCCGACTGGACCGGCT
GCTGCGCCGGCTGCAGCTCCTGATGTCCCGCCTGGCCCTGCCCCAGCCACCCCCGGACCCGCCGGCGCCC
CCGCTGGCGCCCCCCTCCTCAGCCTGGGGGGGCATCAGGGCCGCCCACGCCATCCTGGGGGGGCTGCACC
TGACACTTGACTGGGCCGTGAGGGGACTGCTGCTGCTGAAGACTCGGCTGTGACCCCGGGGCCCAAAGCCA
CCACCGTCCTTCCAAAGCCAGATCTTATTTATTTATTTATTTCAGTACTGGGGGCGAAACAGCCAGGTGA
TCCCCCCGCCATTATCTCCCCCTAGTTAGAGACAGTCCTTCCGTGAGGCCTGGGGGGGCATCTGTGCCTTA
TTTATACTTATTTATTTCAGGAGCAGGGGTGGGAGGCAGGTGGACTCCTGGGTCCCCGAGGAGGAGGGGA
CTGGGGTCCCGGATTCTTGGGTCTCCAAGAAGTCTGTCCACAGACTTCTGCCCTGGCTCTTCCCCATCTA
GGCCTGGGCAGGAACATATATTATTTATTTAAGCAATTACTTTTCATGTTGGGGTGGGGACGGAGGGGAA
AGGGAAGCCTGGGTTTTTGTACAAAAATGTGAGAAACCTTTGTGAGACAGAGAACAGGGAATTAAATGTG
TCATACATATCCACTTGAGGGCGATTTGTCTGAGAGCTGGGGCTGGATGCTTGGGTAACTGGGGCAGGGC
AGGTGGAGGGGAGACCTCCATTCAGGTGGAGGTCCCGAGTGGGCGGGGCAGCGACTGGGAGATGGGTCGG
TCACCCAGACAGCTCTGTGGAGGCAGGGTCTGAGCCTTGCCTGGGGCCCCGCACTGCATAGGGCCTTTTG
TTTGTTTTTTGAGATGGAGTCTCGCTCTGTTGCCTAGGCTGGAGTGCAGTGAGGCAATCTGAGGTCACTG
CAACCTCCACCTCCCGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGATTAGCTGGGATCACAGGTGTG
CACCACCATGCCCAGCTAATTATTTATTTCTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGGC
CAGGCTGGTTTCGAACTCCTGACCTCAGGTGATCCTCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAG
GTGTGAGCCACCACACCTGACCCATAGGTCTTCAATAAATATTTAATGGAAGGTTCCACAAGTCACCCTG
TGATCAACAGTACCCGTATGGGACAAAGCTGCAAGGTCAAGATGGTTCATTATGGCTGTGTTCACCATAG
CAAACTGGAAACAATCTAGATATCCAACAGTGAGGGTTAAGCAACATGGTGCATCTGTGGATAGAACGCC
ACCCAGCCGCCCGGAGCAGGGACTGTCATTCAGGGAGGCTAAGGAGAGAGGCTTGCTTGGGATATAGAAA
GATATCCTGACATTGGCCAGGCATGGTGGCTCACGCCTGTAATCCTGGCACTTTGGGAGGACGAAGCGAG
TGGATCACTGAAGTCCAAGAGTTCGAGACCGGCCTGCGAGACATGGCAAAACCCTGTCTCAAAAAAGAAA
GAATGATGTCCTGACATGAAACAGCAGGCTACAAAACCACTGCATGCTGTGATCCCAATTTTGTGTTTTT
CTTTCTATATATGGATTAAAACAAAAATCCTAAAGGGAAATACGCCAAAATGTTGACAATGACTGTCTCC
AGGTCAAAGGAGAGAGGTGGGATTGTGGGTGACTTTTAATGTGTATGATTGTCTGTATTTTACAGAATTT
CTGCCATGACTGTGTATTTTGCATGACACATTTTAAAAATAATAAACACTATTTTTAGAATAACAGAAAA
A [SEQ ID NO:1]

CCTTCCAAAGCCAGATCTT [SEQ ID NO:2]

GCCTGGGCAGGAACATATA [SEQ ID NO:3]

CCTGGGCAGGAACATATAT [SEQ ID NO:4]

GGTTCATTATGGCTGTGTT [SEQ ID NO:5]

Figure 11

GCTGTAGCTGGTGAGAGGAAGTCCTAGAGGCTATGGACACTCTGCTGCTGGGATCACCGAGATGAGCAGC
AGCTGCTCAGGGCTGAGCAGGGTCCTGGTGGCCGTGGCTACAGCCCTGGTGTCTGCCTCCTCCCCCTGCC
CCCAGGCCTGGGGCCCCCCAGGGGTCCAGTATGGGCAGCCAGGGAGGTCCGTGAAGCTGTGTTGTCCTGG
AGTGACTGCCGGGGACCCAGTGTCCTGGTTTCGGGATGGGGAGCCAAAGCTGCTCCAGGGACCTGACTCT
GGGCTAGGGCATGAACTGGTCCTGGCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCC
TGGATGGTGCACTTGGGGGCACAGTGACCCTGCAGCTGGGCTACCCTCCAGCCCGCCCTGTTGTCTCCTG
CCAAGCAGCCGACTATGAGAACTTCTCTTGCACTTGGAGTCCCAGCCAGATCAGCGGTTTACCCACCCGC
TACCTCACCTCCTACAGGAAGAAGACAGTCCTAGGAGCTGATAGCCAGAGGAGGAGTCCATCCACAGGGC
CCTGGCCATGCCCACAGGATCCCCTAGGGGCTGCCCGCTGTGTTGTCCACGGGGCTGAGTTCTGGAGCCA
GTACCGGATTAATGTGACTGAGGTGAACCCACTGGGTGCCAGCACACGCCTGCTGGATGTGAGCTTGCAG
AGCATCTTGCGCCCTGACCCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGACGCCTGC
GAGCCAGCTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCACTTCCTGCTCAAGTTCCGTTTGCAGTA
CCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGAGGAGGTGATCACAGATGCT
GTGGCTGGGCTGCCCCATGCTGTACGAGTCAGTGCCCGGGACTTTCTAGATGCTGGCACCTGGAGCACCT
GGAGCCCGGAGGCCTGGGGAACTCCGAGCACTGGGACCATACCAAAGGAGATACCAGCATGGGGCCAGCT
ACACACGCAGCCAGAGGTGGAGCCTCAGGTGGACAGCCCTGCTCCTCCAAGGCCCTCCCTCCAACCACAC
CCTCGGCTACTTGATCACAGGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTCTT
TCCTGGGACTGGTGGCTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGACGGGGTGGGAAGGATGG
ATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTCCAGGAGCTCCAAACCTGTAG
AGGACCCAGGAGGGCTTCGGCAGATTCCACCTATAATTCTGTCTTGCTGGTGTGGATAGAAACCAGGCAG
GACAGTAGATCCCTATGGTTGGATCTCAGCTGGAAGTTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTA
TTTCAAATTTGCAGCTGAAAGGTGCTTGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAA
CGTGTGTAATGTGTACATCTGTGTCCATGTGTGACCATGTGTCTGTGAAGGCCAGGGAACATGTATTCCT
CTGCATGCATGTATGTAGGTGCCTGGGAGTGTGTGTGGTCCTTGCTCTGGCCCTTTCCCTTGCAGGGTTG
TGCAGGTGTGAATAAA [SEQ ID NO:6]

GGACCATACCAAAGGAGAT [SEQ ID NO:7]

GCGTCTTTGGGAATCCTTT [SEQ ID NO:8]

GCAGGACAGTAGATCCCT [SEQ ID NO:9]

GCTCAAGGAACGTGTGTAA [SEQ ID NO:10]

Figure 12

Gene Name	*Gene ID/ Accession no.*	*siRNA name*	*siRNA sequence(5'-3')*	*SEQ ID NO:*
IL-11	NM_000641.3	siRNA 1	CCUUCCAAAGCCAGAUCUUdTdT AAGAUCUGGCUUUGGAAGGdTdT	11
IL-11	NM_000641.3	siRNA 2	GCCUGGGCAGGAACAUAUAdTdT UAUAUGUUCCUGCCCAGGCdTdT	12
IL-11	NM_000641.3	siRNA 3	CCUGGGCAGGAACAUAUAUdTdT AUAUAUGUUCCUGCCCAGGdTdT	13
IL-11	NM_000641.3	siRNA 4	GGUUCAUUAUGGCUGUGUUdTdT AACACAGCCAUAAUGAACCdTdT	14

Figure 13

Gene Name	*Gene ID/ Accession no.*	*siRNA name*	*siRNA sequence(5'-3')*	*SEQ ID NO:*
IL-11R	U32324.1	siRNA 5	GGACCAUACCAAAGGAGAUdTdT AUCUCCUUUGGUAUGGUCCdTdT	15
IL-11R	U32324.1	siRNA 6	GCGUCUUUGGGAAUCCUUUdTdT AAAGGAUUCCCAAAGACGCdTdT	16
IL-11R	U32324.1	siRNA 7	GCAGGACAGUAGAUCCCUAdTdT UAGGGAUCUACUGUCCUGCdTdT	17
IL-11R	U32324.1	siRNA 8	GCUCAAGGAACGUGUGUAAdTdT UUACACACGUUCCUUGAGCdTdT	18

Figure 14

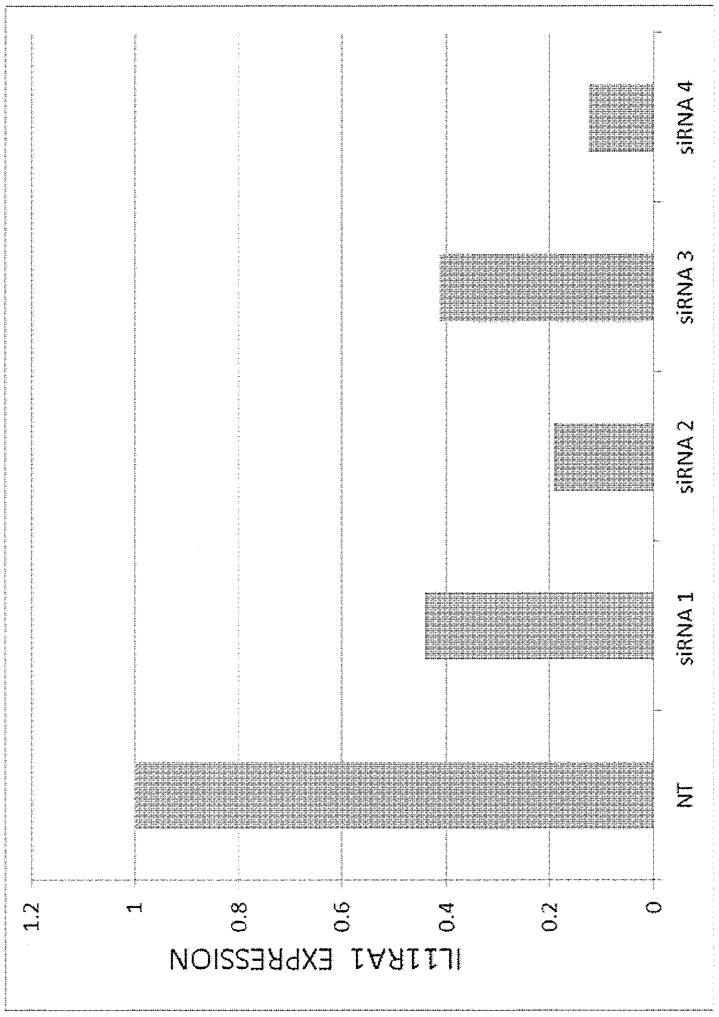

IL1RA1 EXPRESSION
1.2
1
0.8
0.6
0.4
0.2
0
NT
siRNA 1
siRNA 2
siRNA 3
siRNA 4

Figure 15

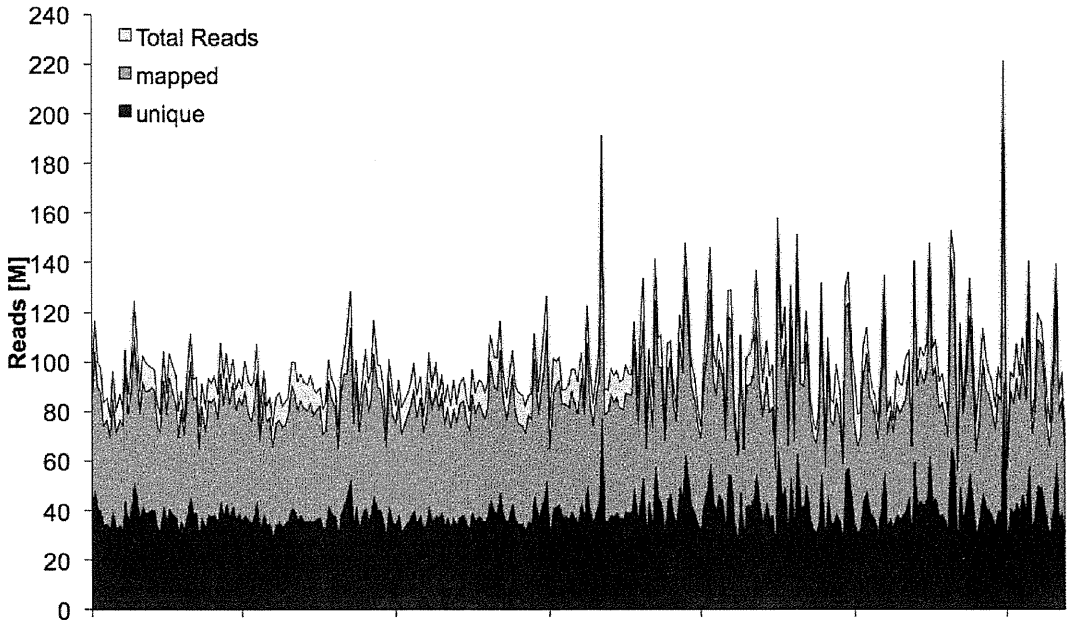


Figure 16

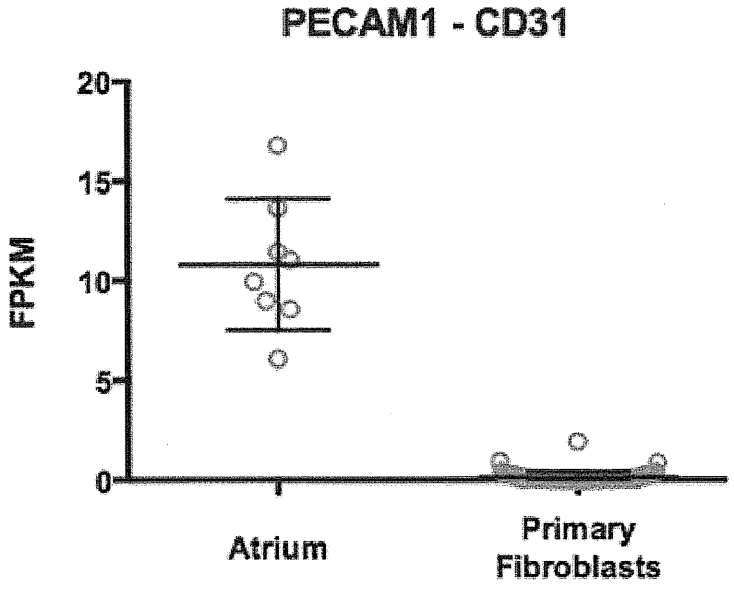


Figure 17A

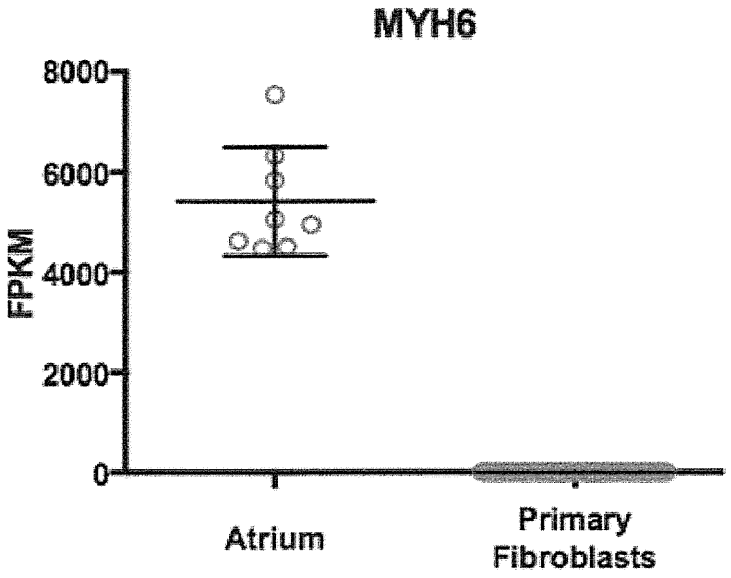


Figure 17B

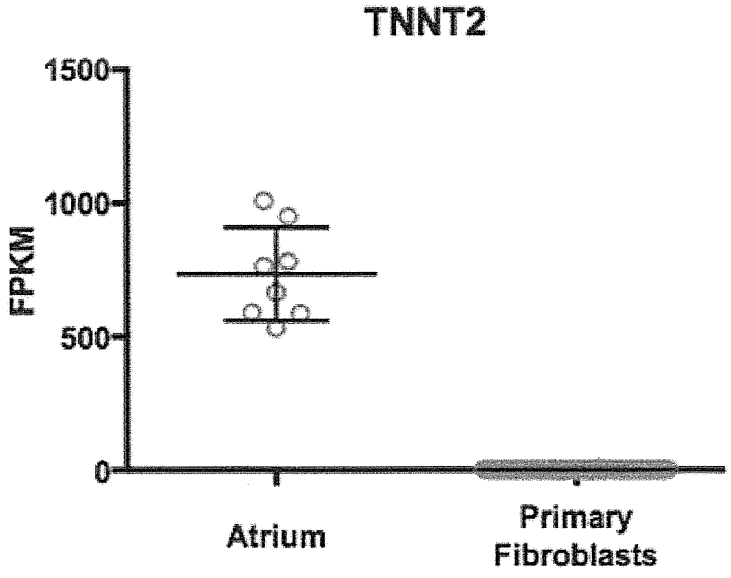


Figure 17C

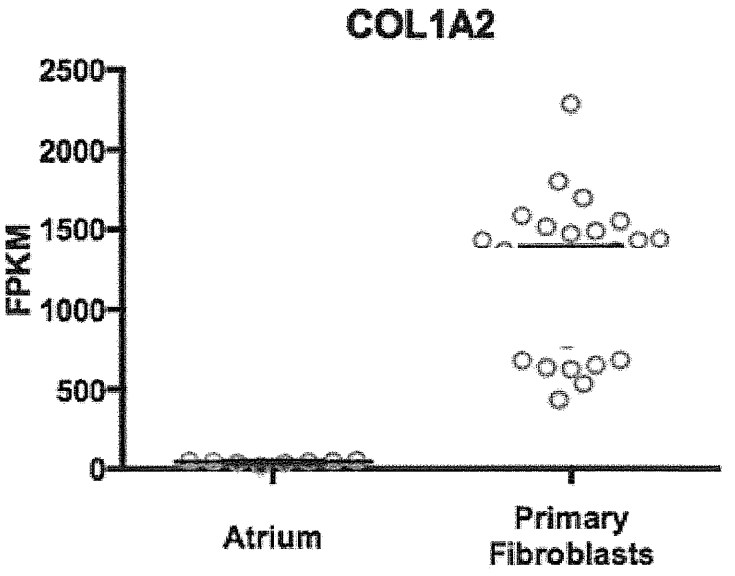


Figure 17D

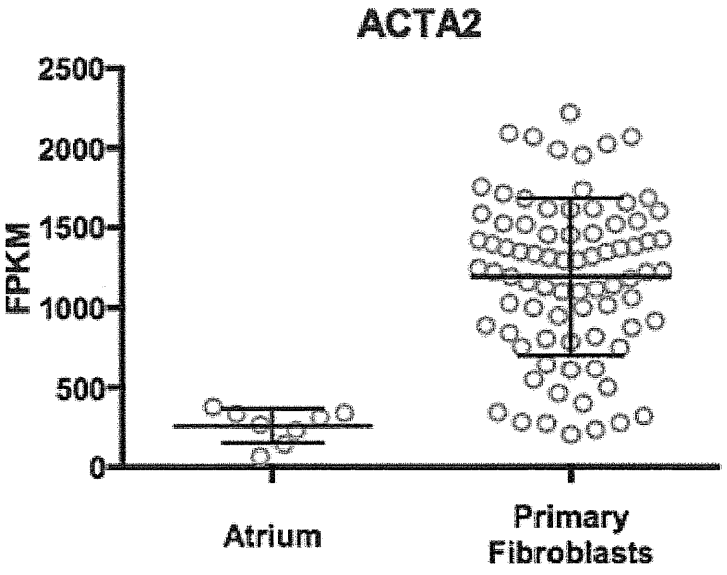


Figure 17E

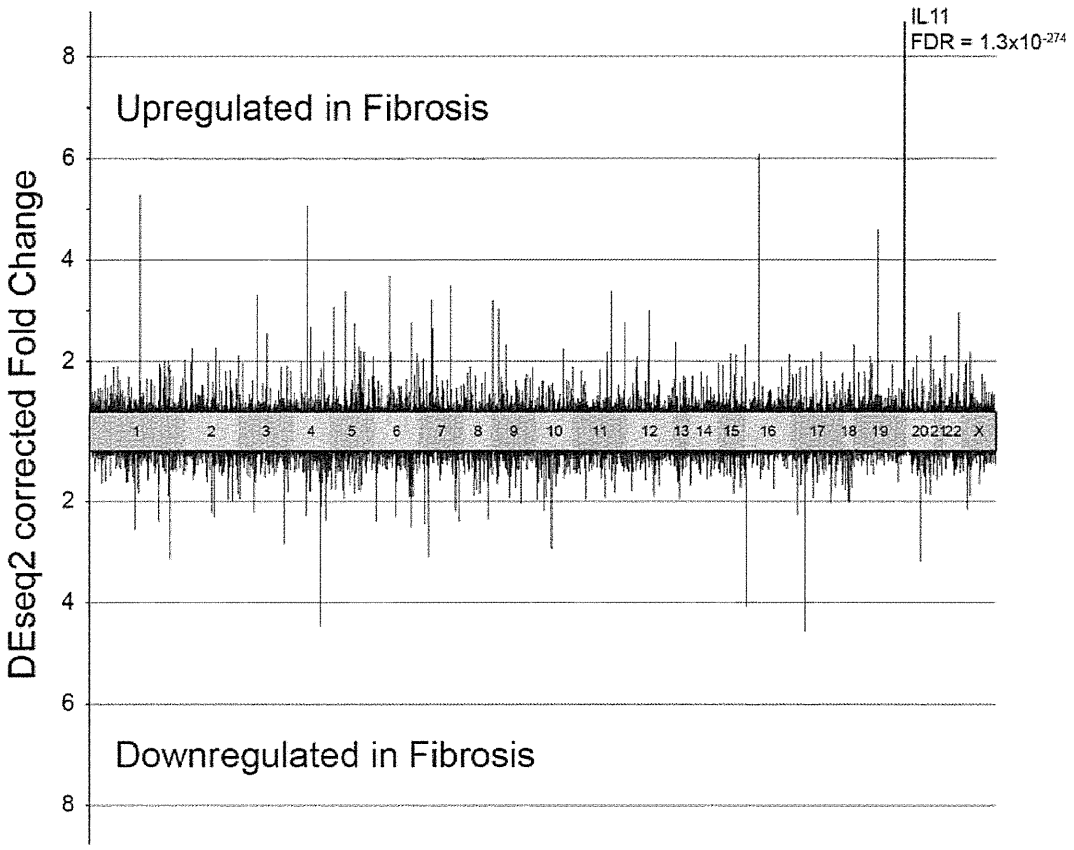


Figure 18A

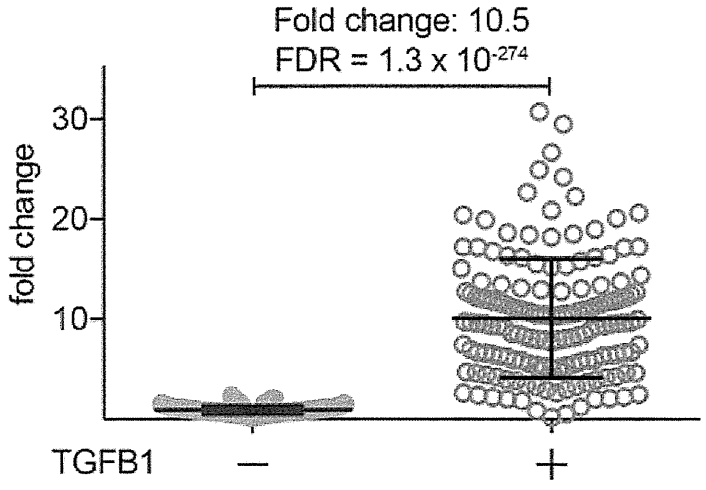


Figure 18B

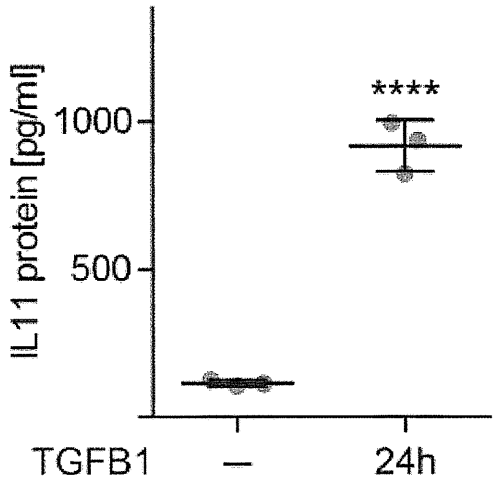


Figure 18C

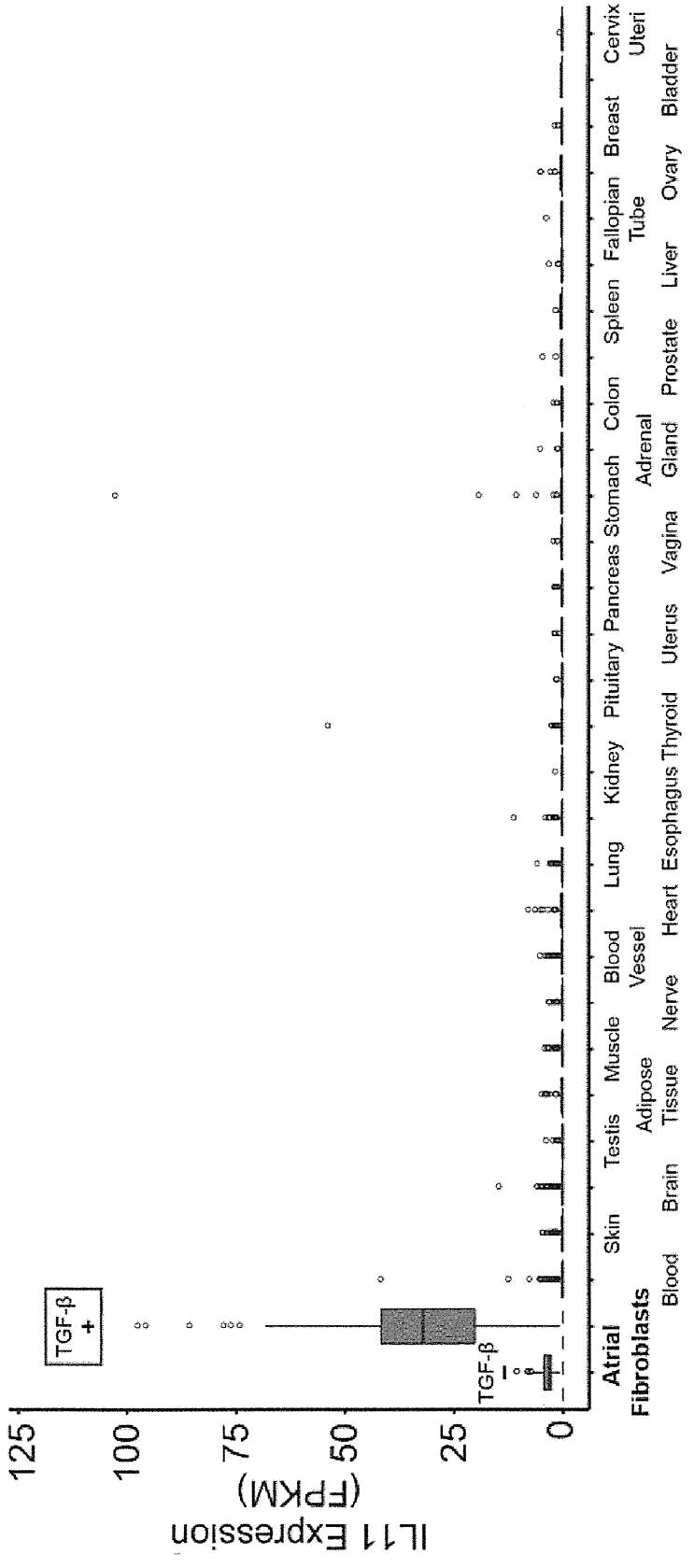

IL11 Expression
(FPKM)
125
100
75
50
25
0
TGF-β
+
TGF-β
−
Atrial
Fibroblasts
Blood
Brain
Tissue
Adipose
Nerve
Muscle
Blood
Vessel
Heart
Esophagus
Thyroid
Uterus
Vagina
Gland
Prostate
Liver
Ovary
Bladder
Skin
Testis
Lung
Kidney
Pituitary
Pancreas
Stomach
Adrenal
Colon
Spleen
Fallopian
Tube
Breast
Cervix
Uteri

Figure 18D

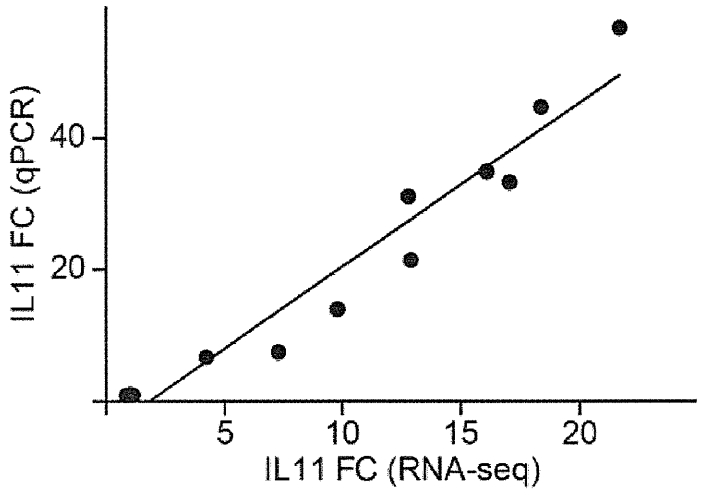


Figure 18E

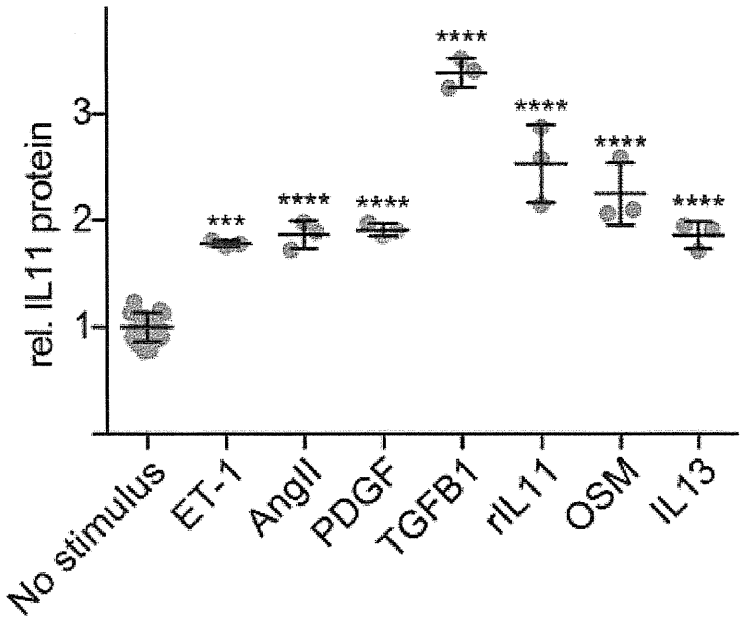


Figure 19A

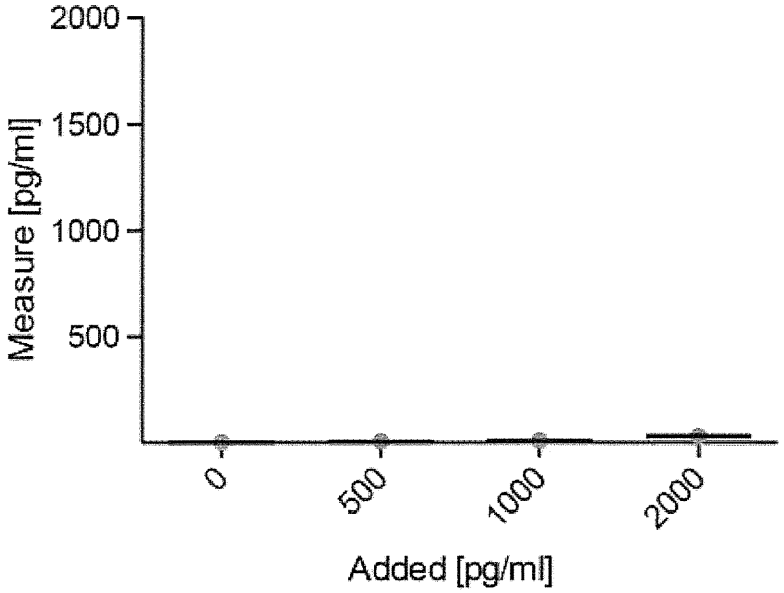


Figure 19B

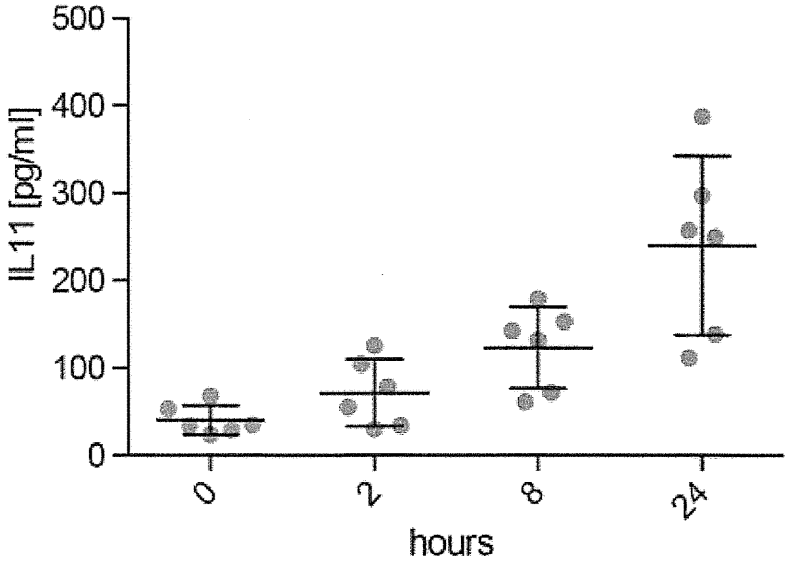


Figure 19C

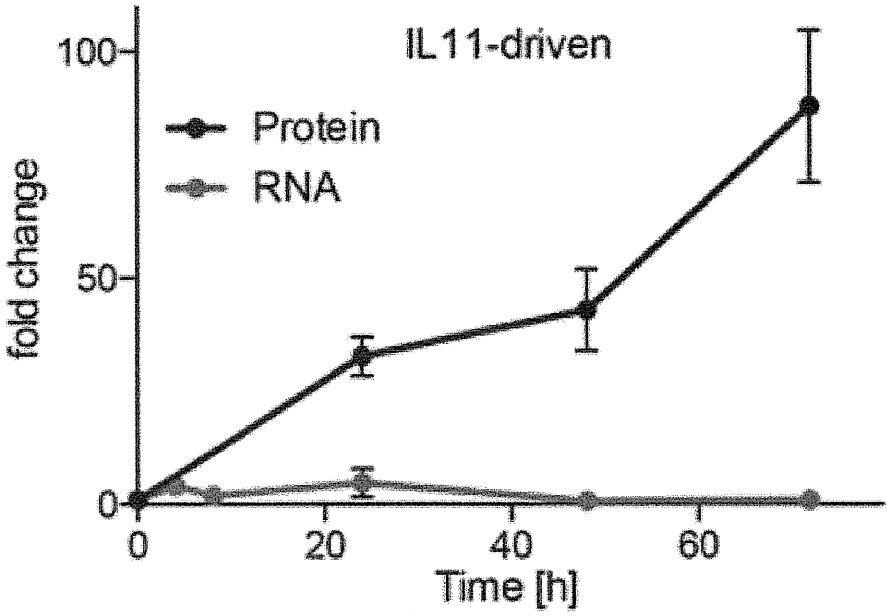


Figure 19D

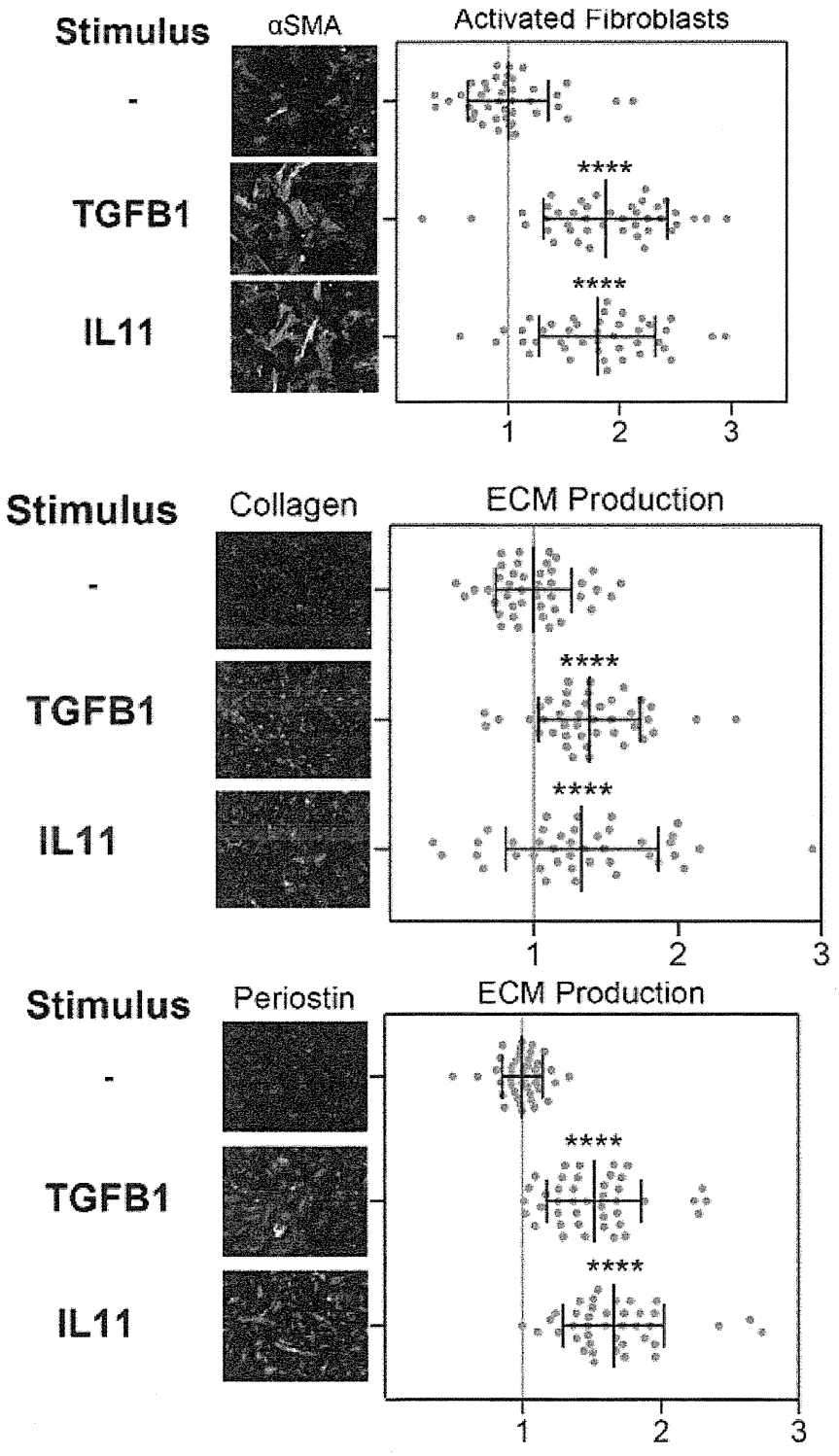

Stimulus
αSMA
Activated Fibroblasts
-
TGFB1
IL11
****
****
1
2
3
Stimulus
Collagen
ECM Production
-
TGFB1
IL11
****
****
1
2
3
Stimulus
Periostin
ECM Production
-
TGFB1
IL11
****
****
1
2
3

Figure 20A

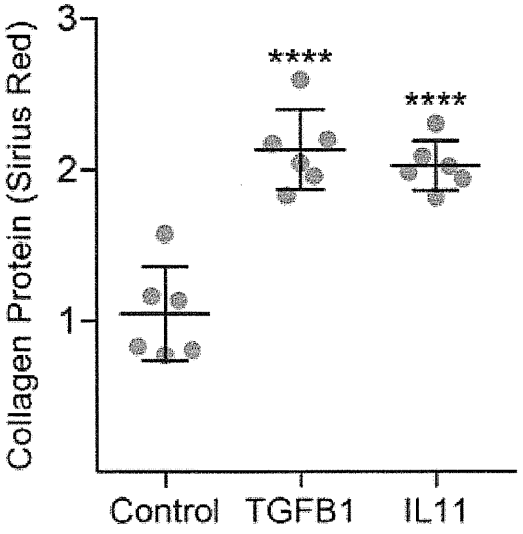


Figure 20B

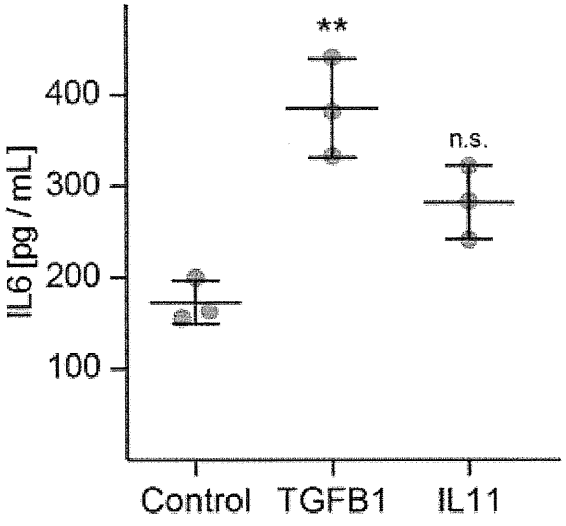


Figure 20C

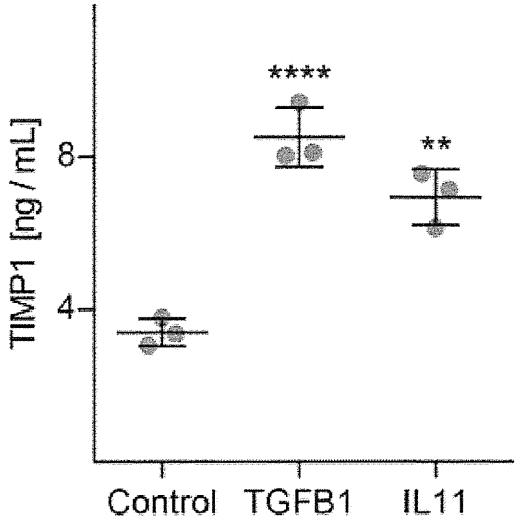


Figure 20D

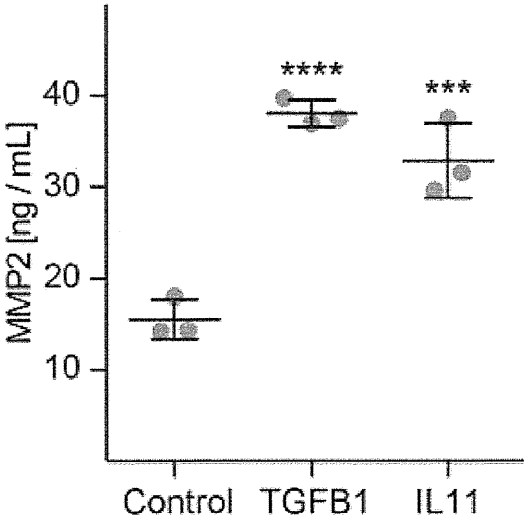


Figure 20E

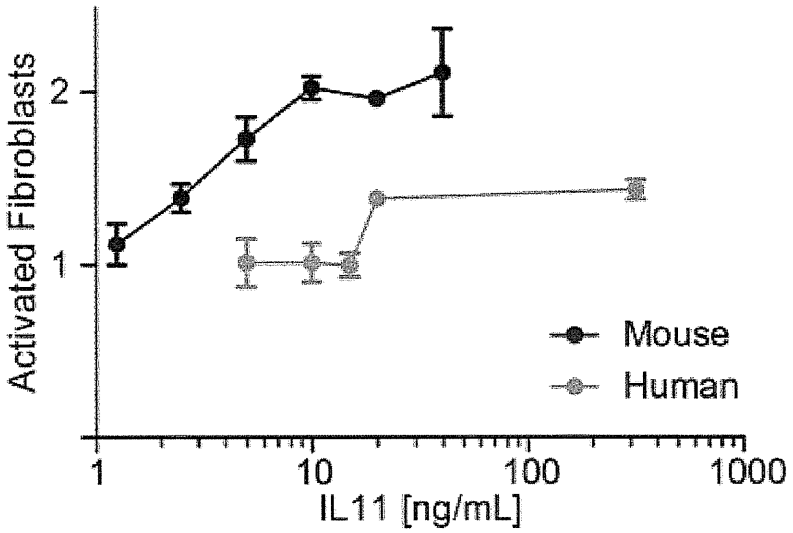

Activated Fibroblasts
2
1
Mouse
Human
1
10
100
1000
IL11 [ng/mL]

Figure 20F

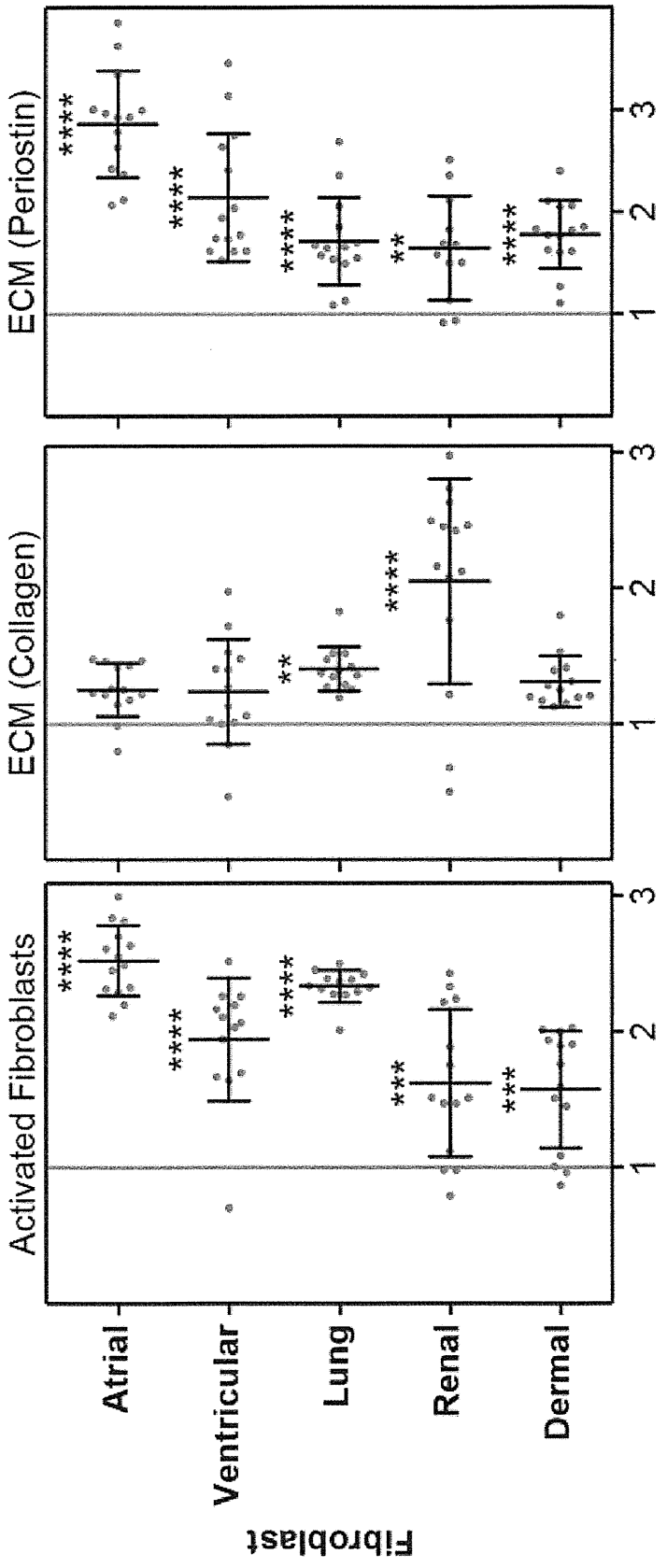

Activated Fibroblasts
ECM (Collagen)
ECM (Periostin)
Fibroblast
Atrial
Ventricular
Lung
Renal
Dermal
1
2
3
****
****
****
**
****
***
***
**
****
****

Figure 21A

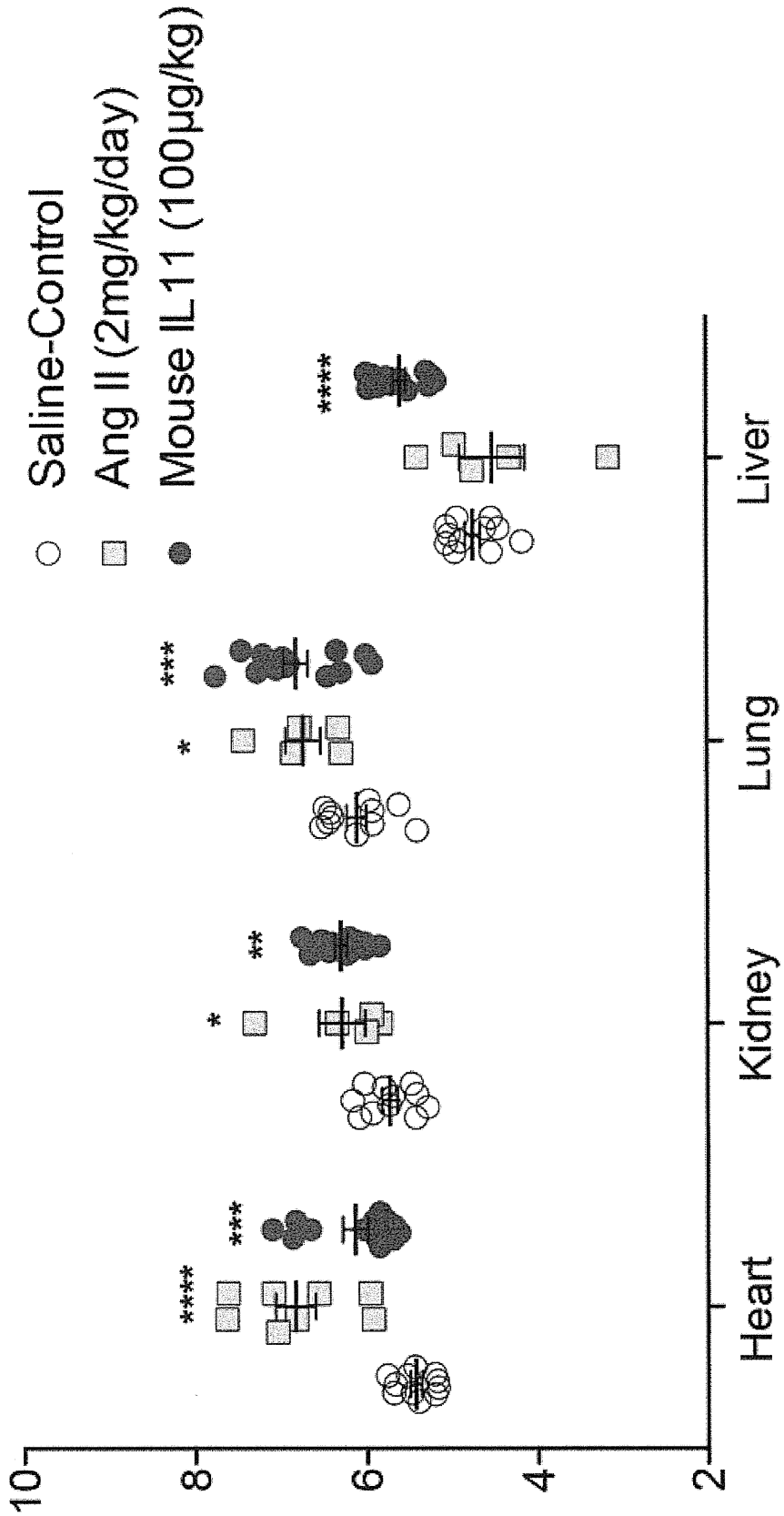

Saline-Control
Ang II (2mg/kg/day)
Mouse IL11 (100µg/kg)
10
8
6
4
2
Heart
Kidney
Lung
Liver
****
***
*
**
*
***
*
****

Figure 21B

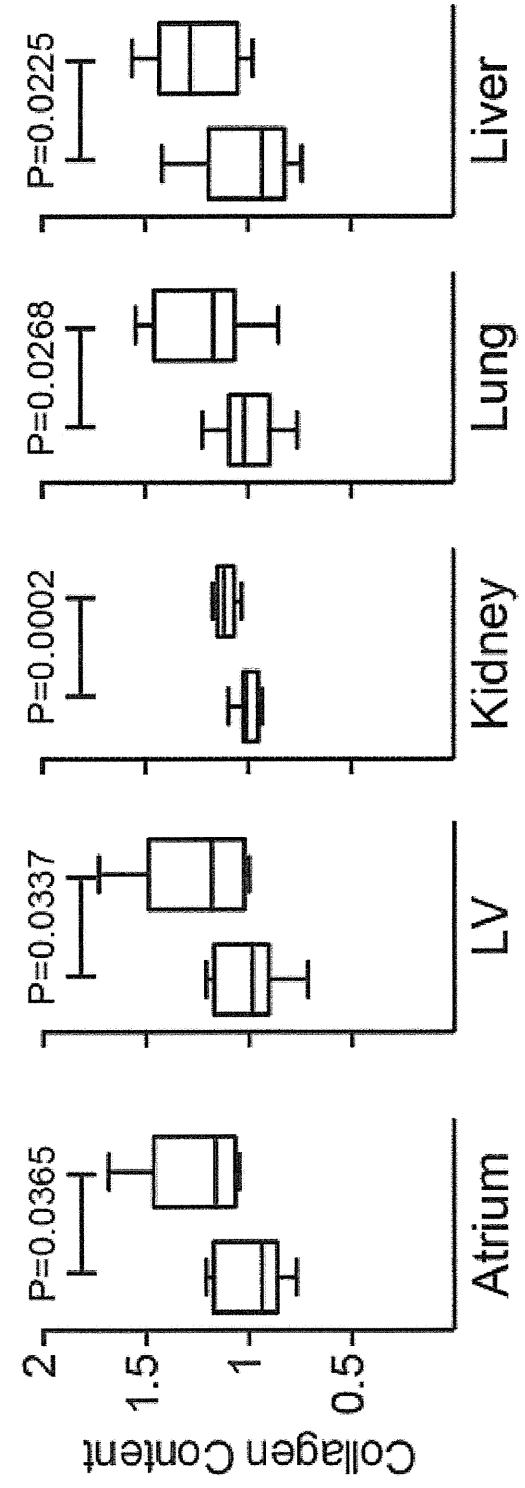

Collagen Content
2
1.5
1
0.5
P=0.0365
P=0.0337
P=0.0002
P=0.0268
P=0.0225
Atrium
LV
Kidney
Lung
Liver

Figure 21C

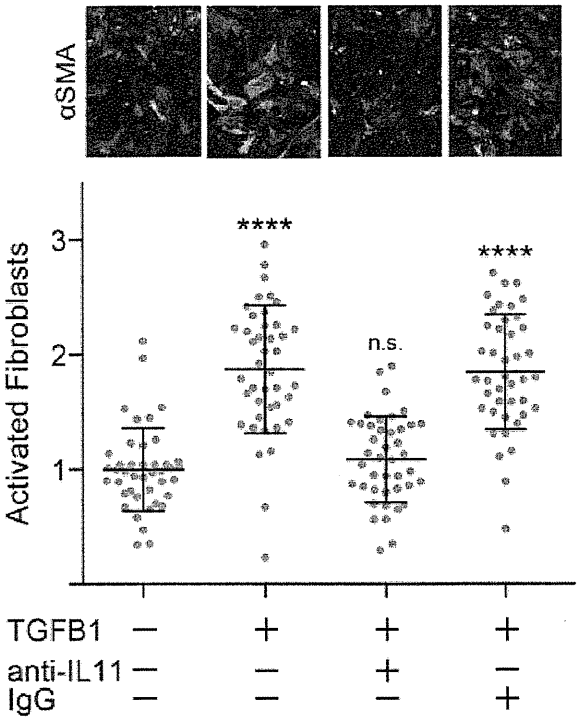


Figure 22A

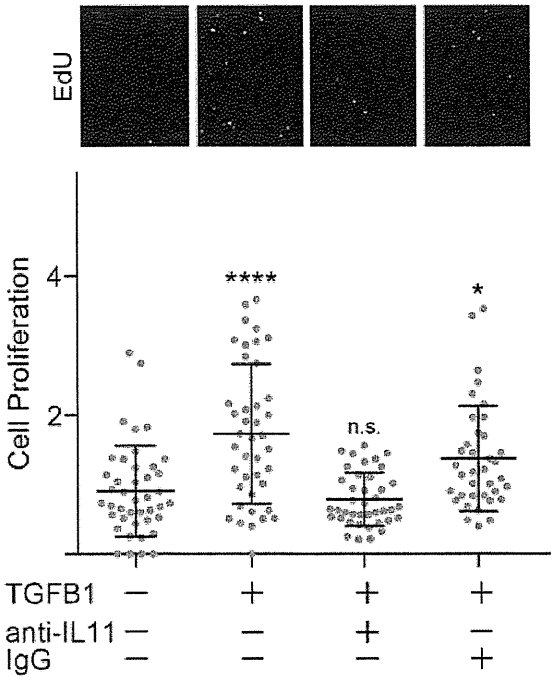


Figure 22B

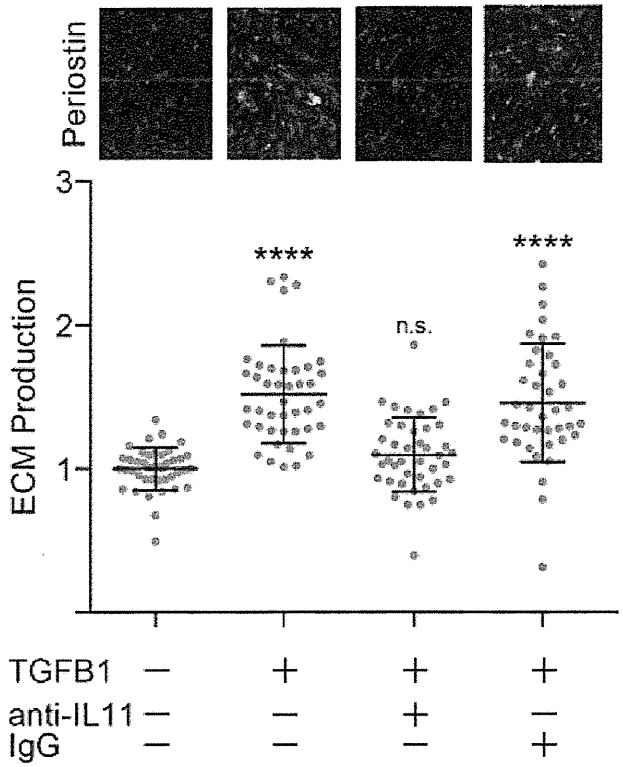


Figure 22C

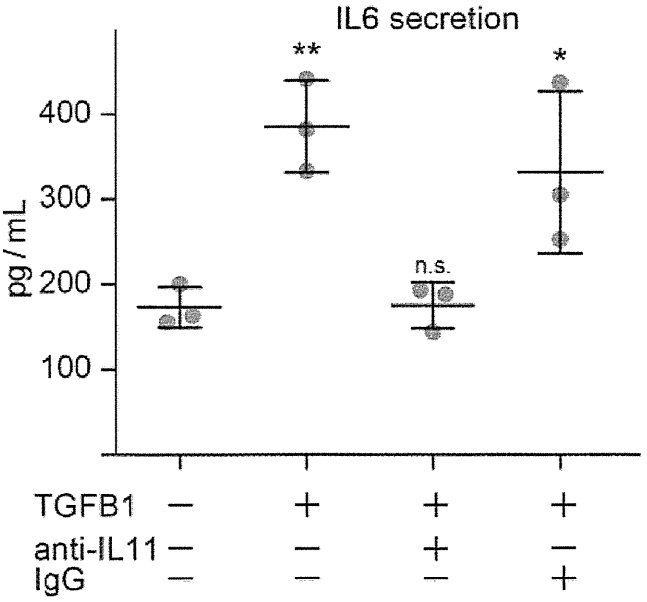


Figure 22D

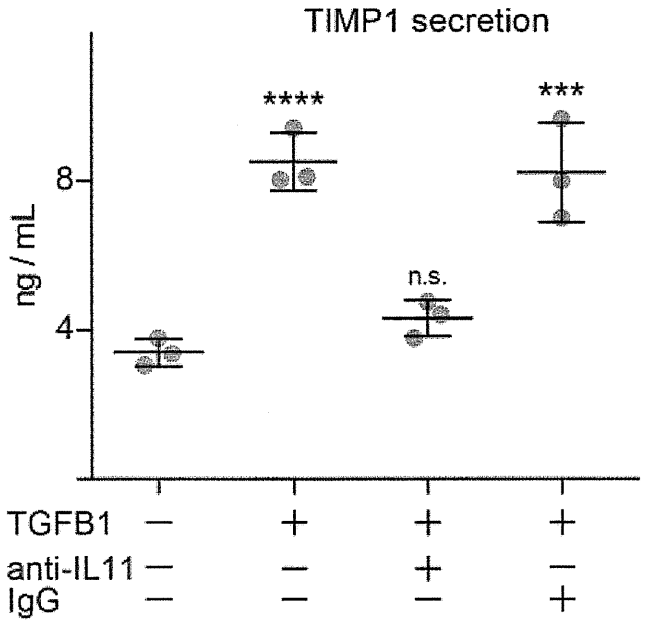


Figure 22E

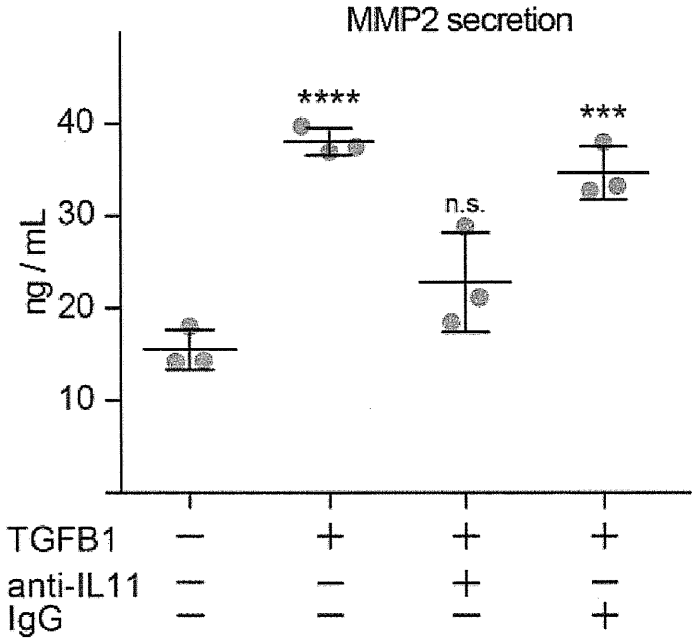


Figure 22F

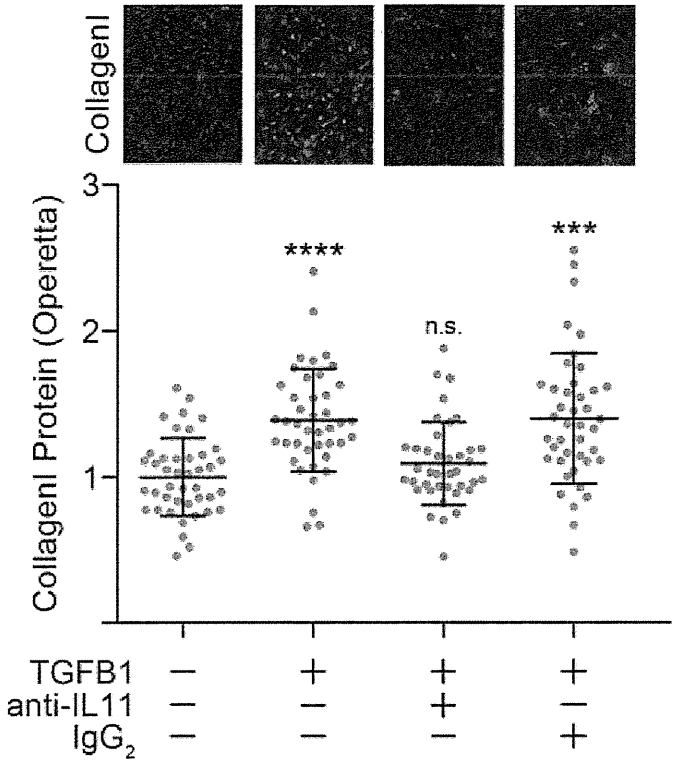


Figure 23A

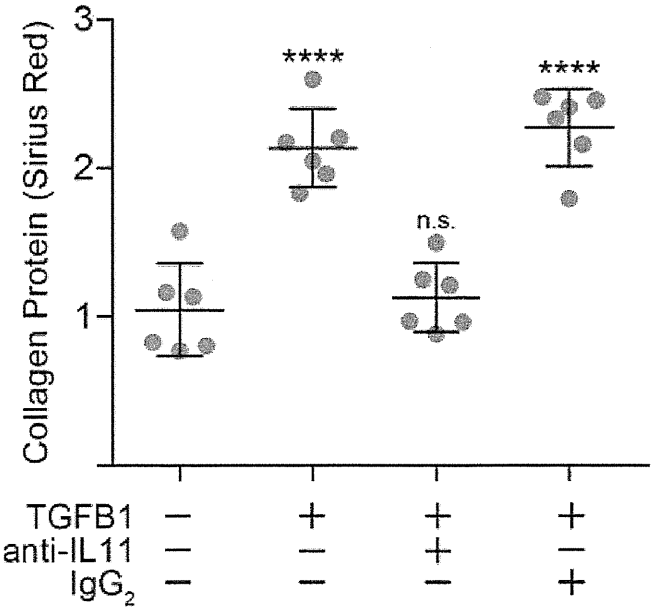


Figure 23B

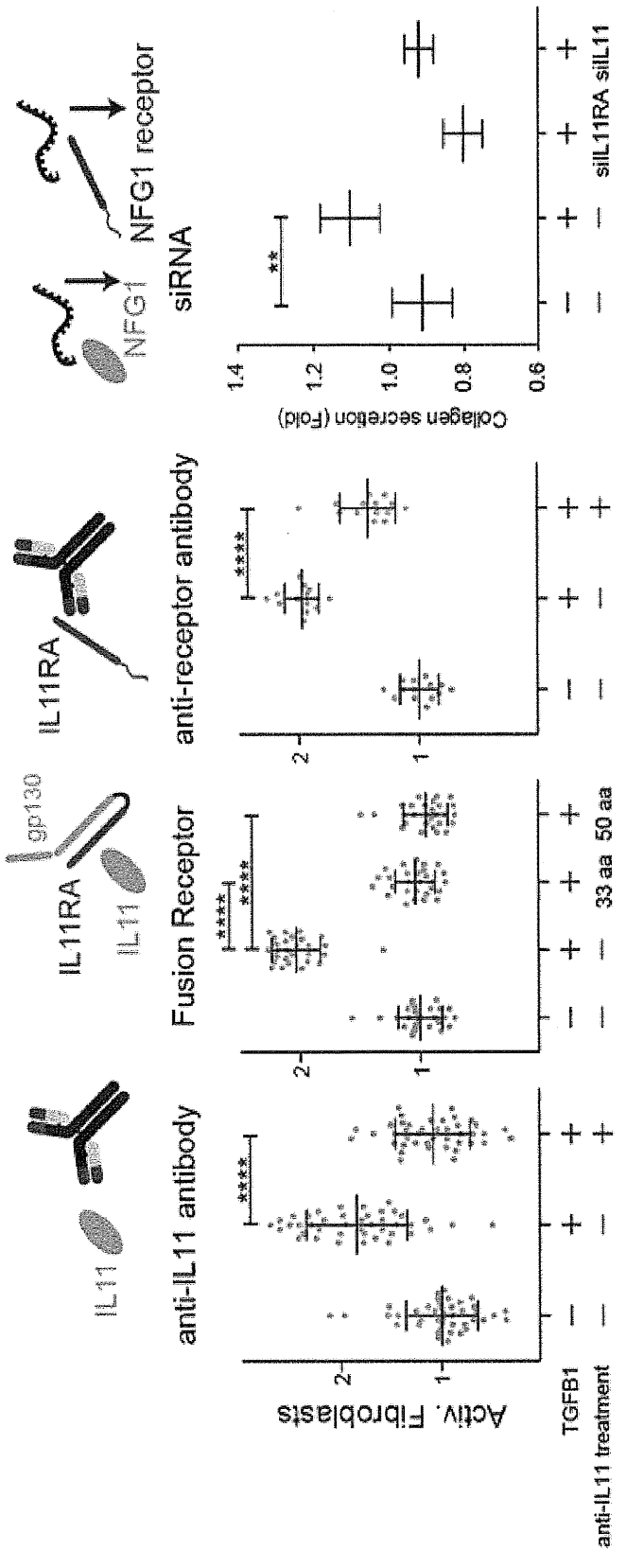

IL11
anti-IL11 antibody
gp130
IL11RA
IL11
Fusion Receptor
IL11RA
anti-receptor antibody
NFG1
NFG1 receptor
siRNA
Activ. Fibroblasts
Collagen secretion (Fold)
TGFB1
anti-IL11 treatment
33 aa
50 aa
linker between gp130 & IL11RA
siIL11RA
siIL11

Figure 24

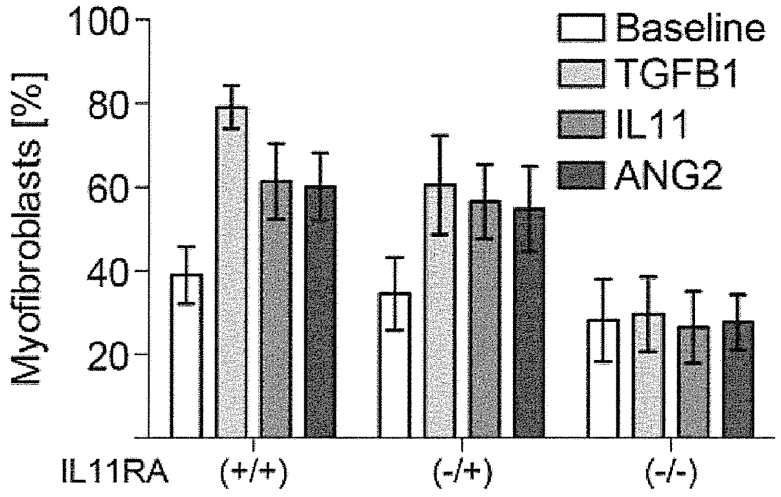


Figure 25A

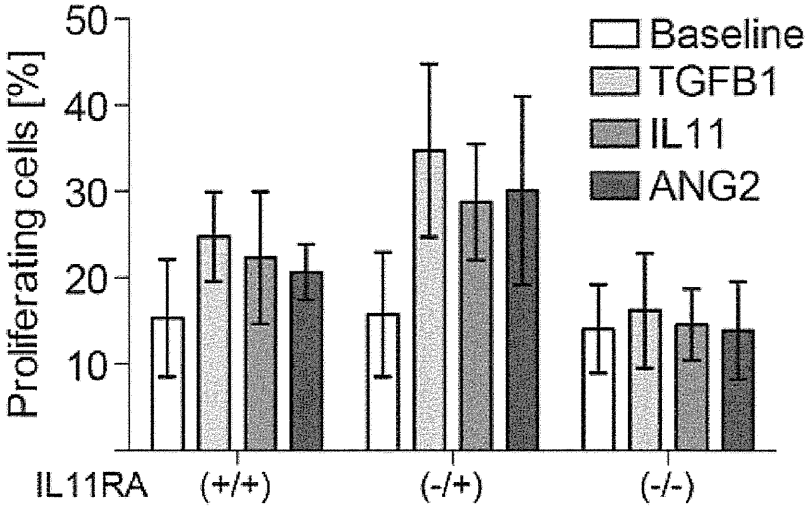


Figure 25B

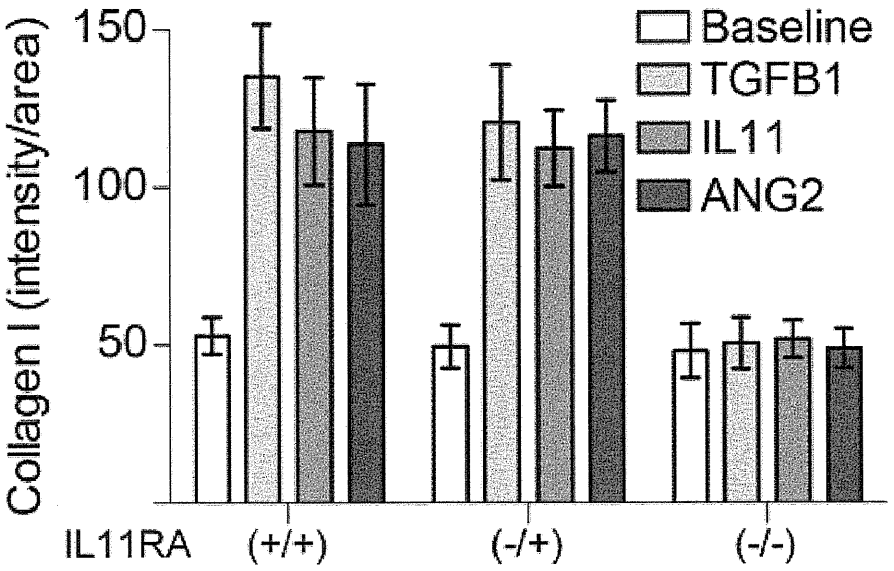


Figure 25C

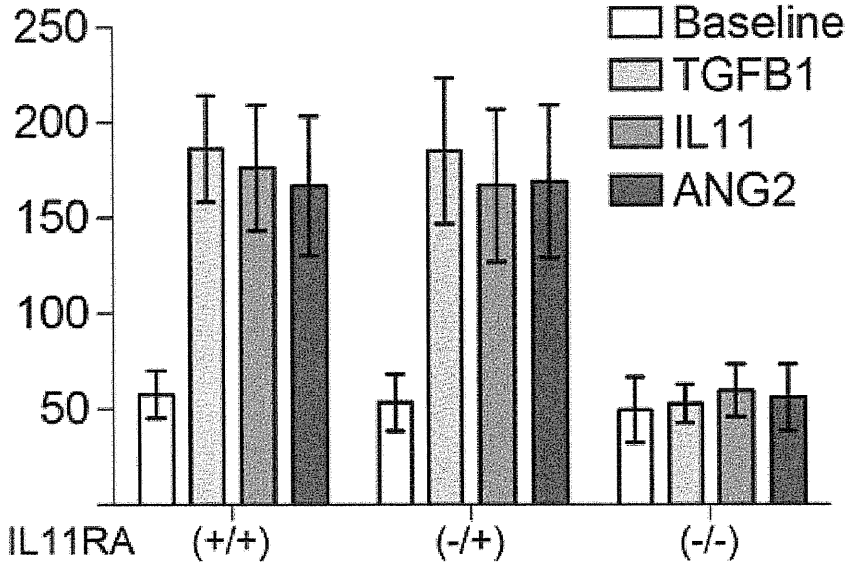


Figure 25D

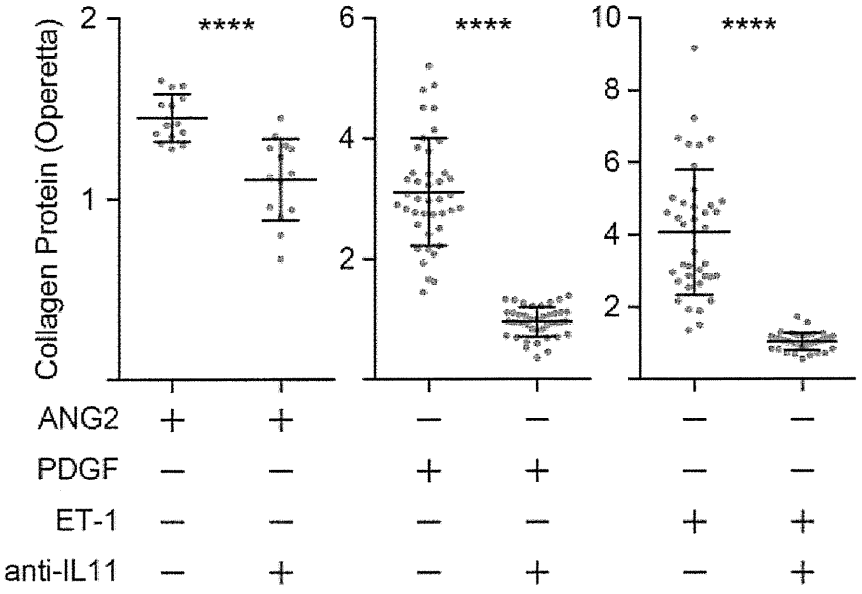


Figure 26A

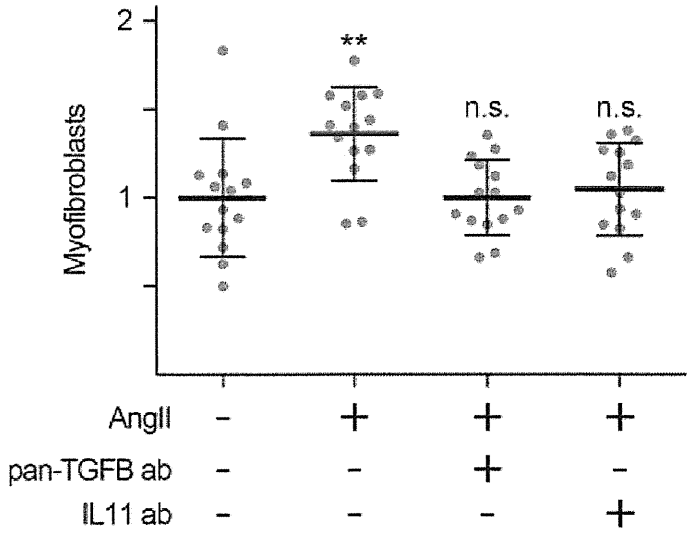


Figure 26B

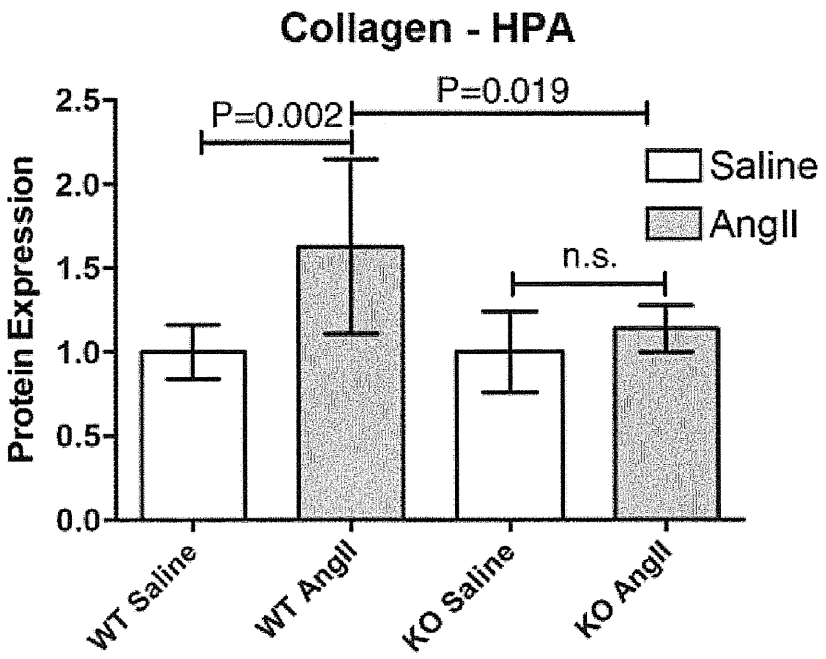


Figure 27A

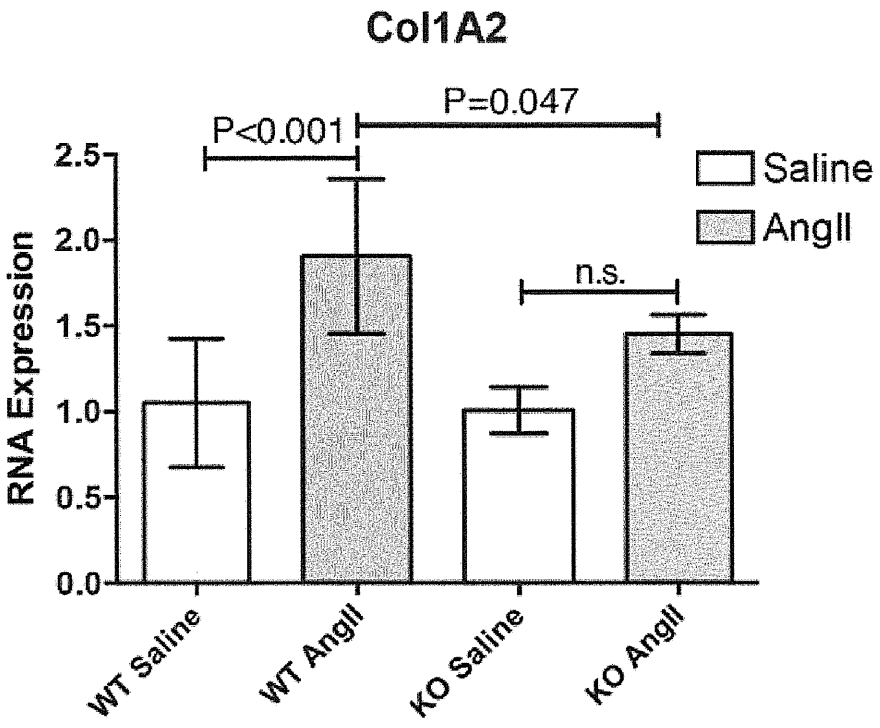


Figure 27B

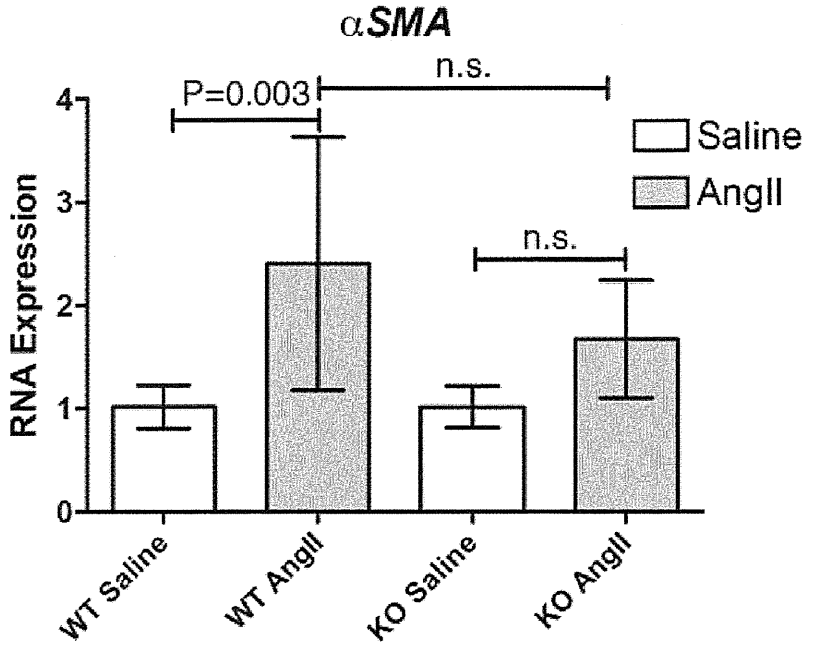


Figure 27C

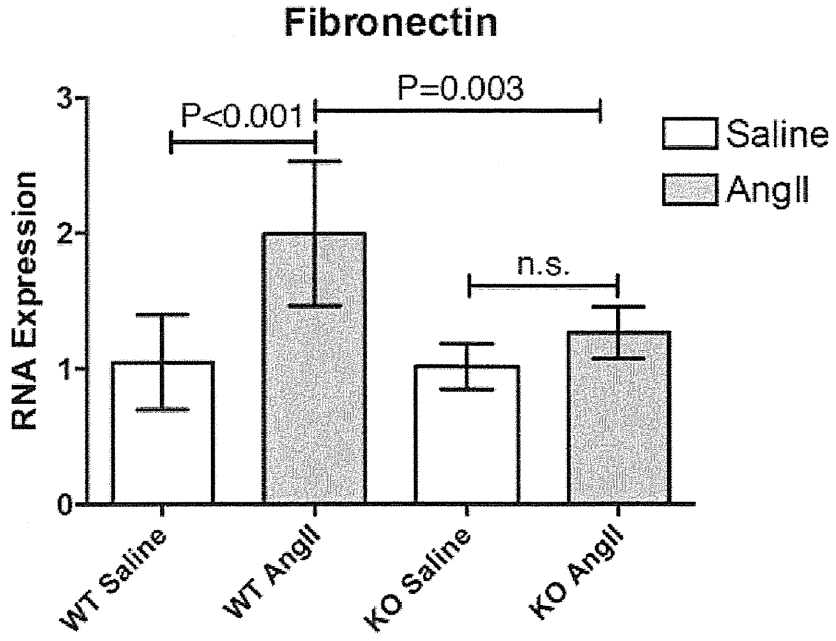


Figure 27D

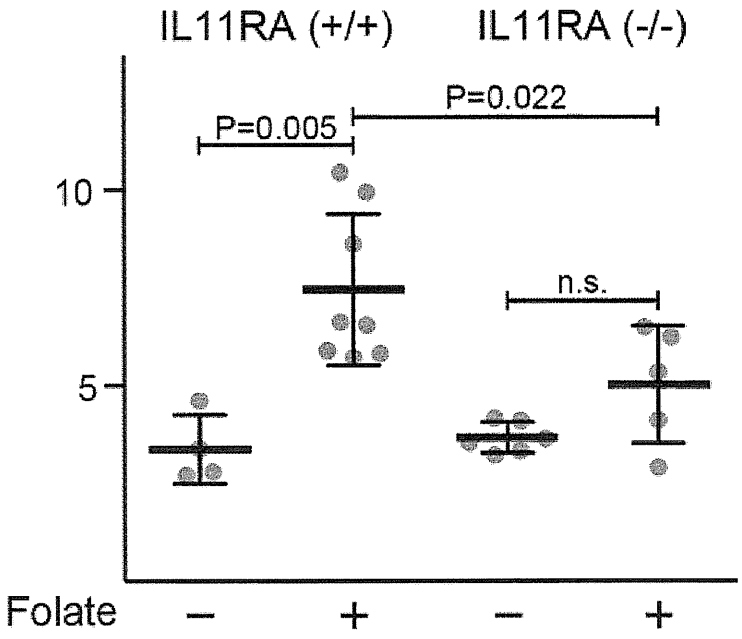


Figure 28

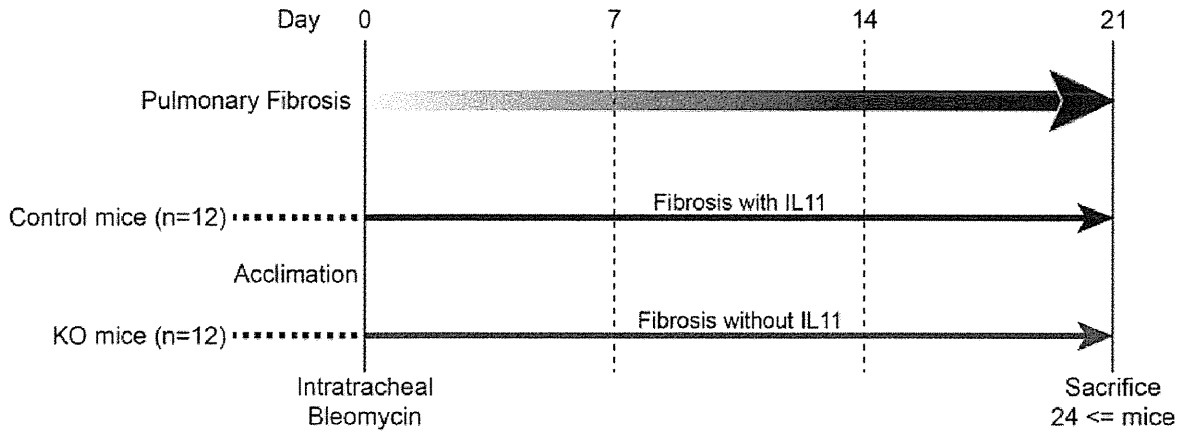


Figure 29A

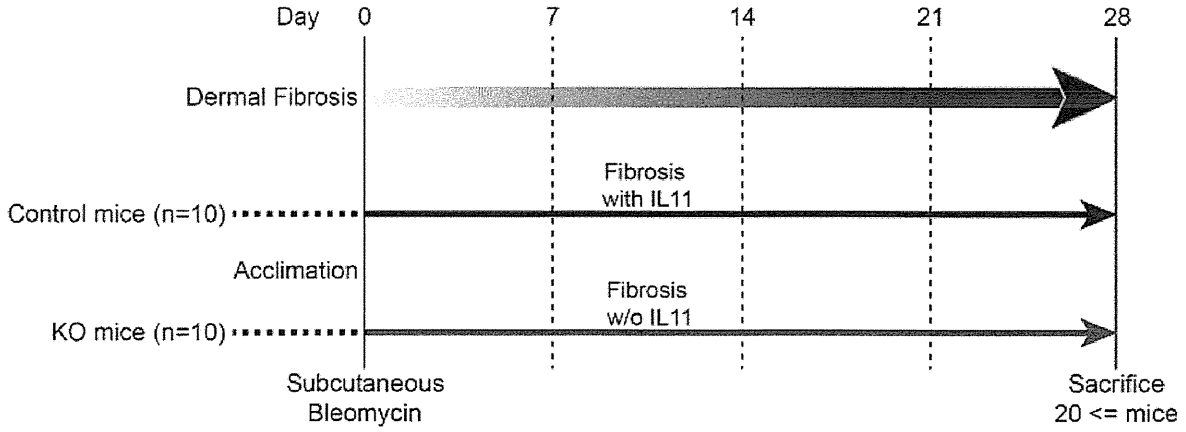


Figure 29B

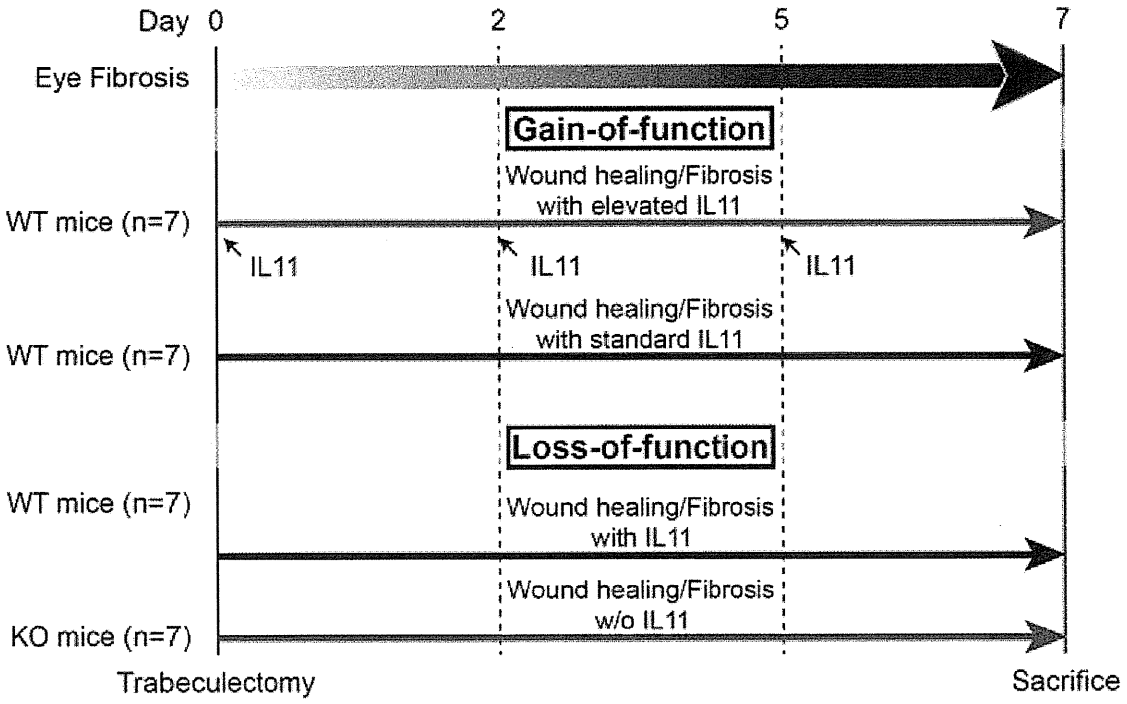

Day 0
2
5
7
Eye Fibrosis
Gain-of-function
Wound healing/Fibrosis with elevated IL11
WT mice (n=7)
IL11
IL11
IL11
Wound healing/Fibrosis with standard IL11
WT mice (n=7)
Loss-of-function
WT mice (n=7)
Wound healing/Fibrosis with IL11
Wound healing/Fibrosis w/o IL11
KO mice (n=7)
Trabeculectomy
Sacrifice

Figure 29C

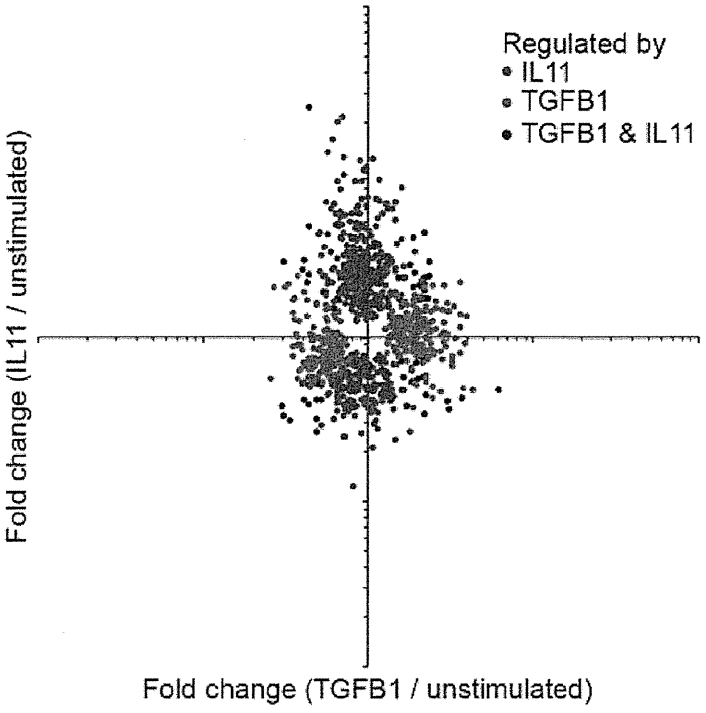


Figure 30A

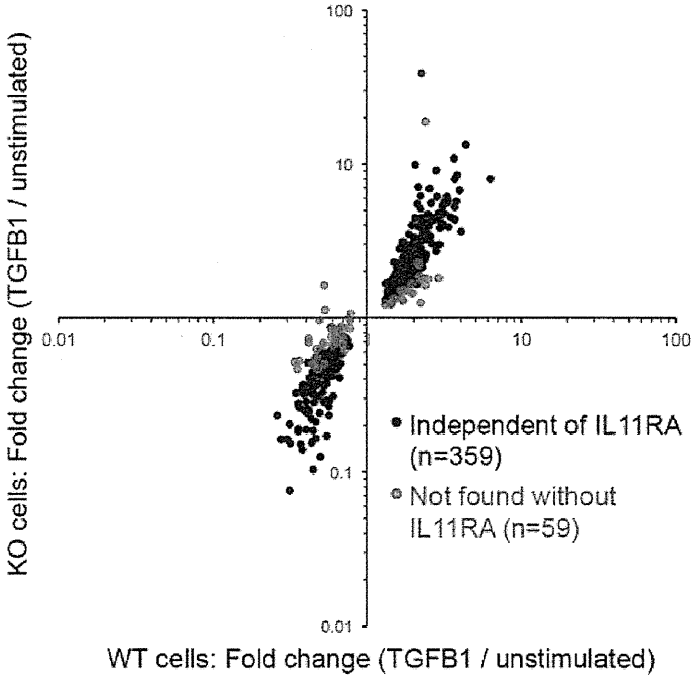


Figure 30B

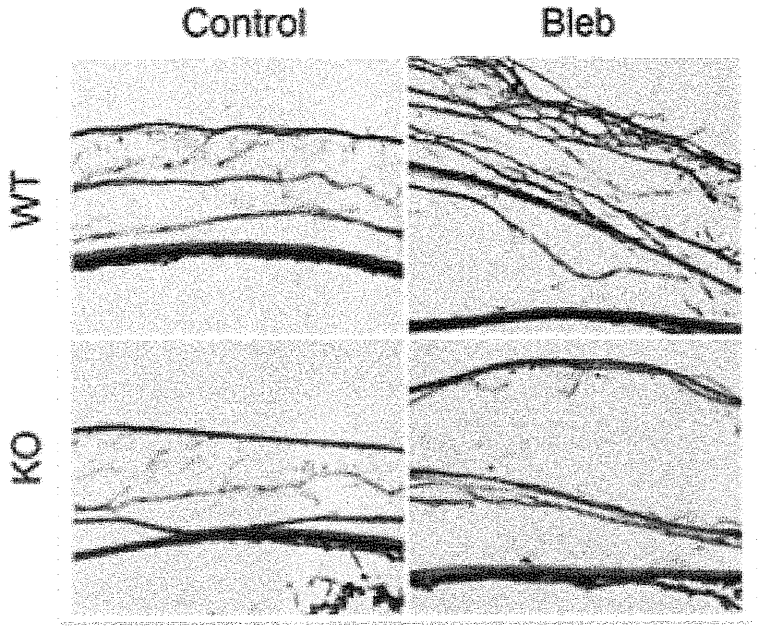


Figure 31A

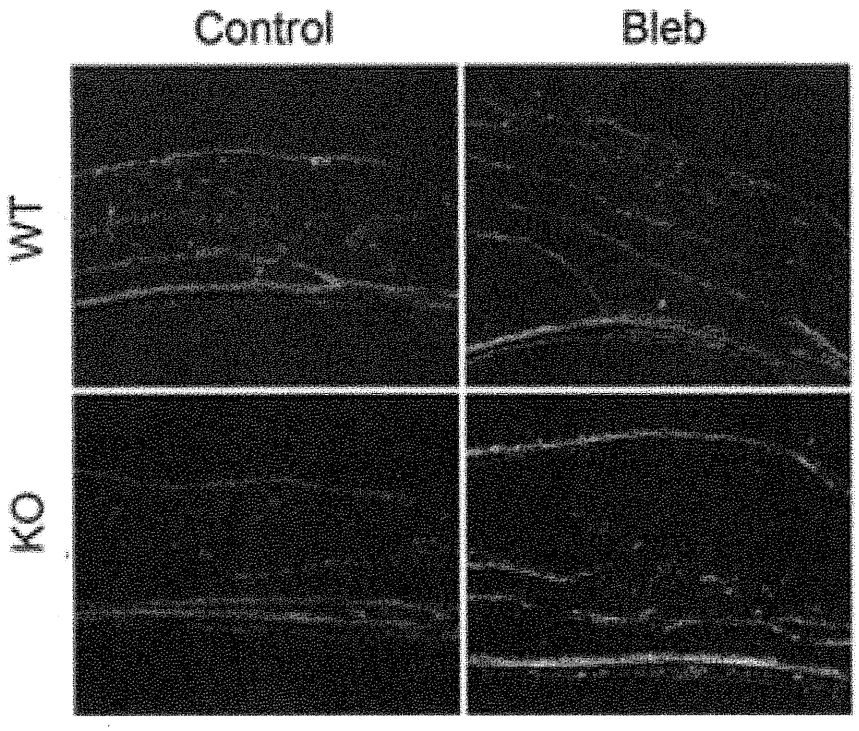


Figure 31B

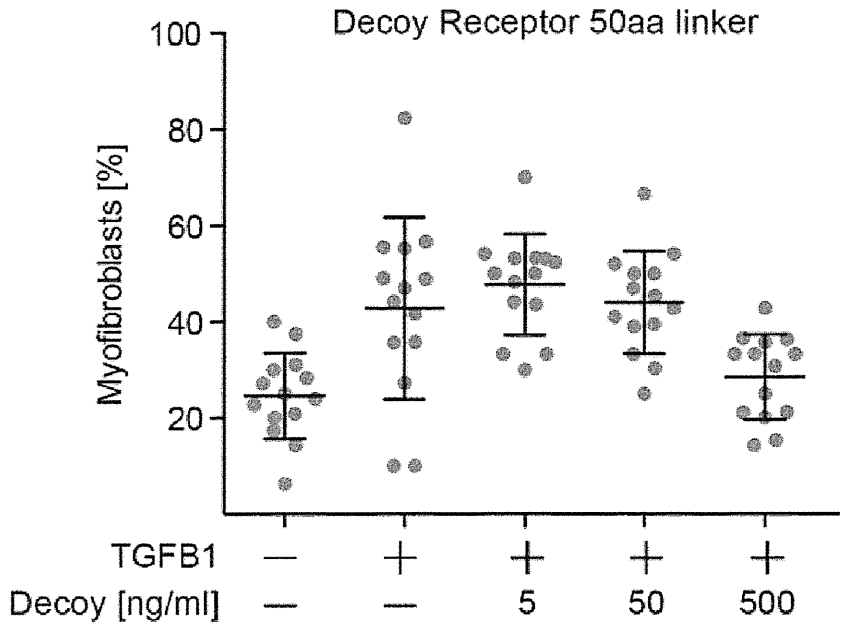


Figure 32A

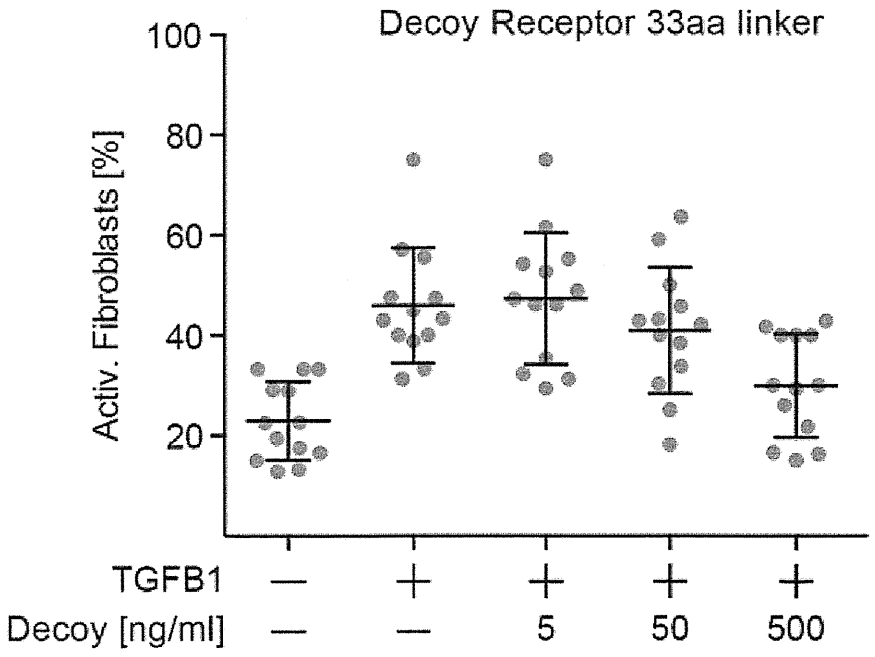


Figure 32B

SNP ID	Position (hg19)	P value	FDR	Genotype	Minor Allele	Sequence	SEQ ID NO
rs10831850	11-12566917	1.76E-07	0.0248	G/A	A	GTAAGGGATGTGAATCGGGTACTGA[A/G]GAAAGAGCCTGGATGCAGAGCCAGC	19
rs4756936	11-12599138	1.76E-07	0.0248	C/T	T	TTGATAACTTCAGCATCTGGATCAC[C/T]GTGGGATTAGCATCTGTTTGTATTT	20
rs6485827	11-12578182	1.76E-07	0.0248	C/T	C	GTGTGATTGCTTAAAAAAAACTACT[C/T]ACATTGTTTTGAATCACACCTCACA	21
rs7120273	11-12581045	1.44E-07	0.0248	T/C	T	GCTCAGCTAATCAATGACCAGTCTC[C/T]TTAATTCTTCTAATGCCTATATGGT	22
rs895468	2-223621273	2.70E-07	0.0306	G/A	G	GCAGTGCTCAGAAGAGCAGCAGCCA[A/G]TGACATTTTGGGGCTATAAGAGGTA	23

Figure 33

SNP ID	Position (hg19)	P value	FDR	Genotype	Minor Allele	Sequence	SEQ ID NO
rs1000574	19-55114775	0.0432	0.6581	C/T	T	TGTCCAGTAAATACTTAACATTTTA[C/T]GTGCA ATGTATGTCATAAATATGGG	24
rs10403345	19-56741808	0.0355	0.6372	G/A	G	GGgtgaagtttggaaacaggtatac[A/G]ttgtgatgcaatcgtca gaaccaag	25
rs10419994	19-55726220	0.0334	0.6372	C/T	T	aaaccataGTATCATCCTTCCCAAA[C/T]AGTCAAC CCAGggaatcacagagat	26
rs10426177	19-56269096	0.0103	0.6372	C/T	T	TAAGACGCTATTCTCTAATTCTGAA[C/T]GGAAG AACTCCTCTCCCAAGACATG	27
rs11084337	19-54916104	0.0370	0.6372	C/T	C	aggtggaacaacacaaagggtgggg[C/T]gaggcgtgcaattta aacattttct	28
rs11671244	19-56502995	0.0242	0.6372	C/A	A	TATTAGATTTTGTGTGGGATTTCAT[A/C]GTTAC ATTTGTTACCAGCCCAATTT	29
rs11882068	19-56227165	0.0005	0.2204	A/G	G	GATTCCAGTTCCAAGTCACATCATC[A/G]CCAG CTGGAAGACCTAGGGCAAAAG	30
rs12104147	19-54935505	0.0150	0.6372	G/A	A	ACCATGACGGTGTCCTCATTGCTTT[A/G]ACCAT TAGTAAtcattcattcattc	31
rs12608558	19-55715090	0.0275	0.6372	A/G	G	ACCTGTCACATTTTGTCAGCTCCCA[A/G]CCAC CCCCTACCACTGTCCTTATAA	32

rs12610132	19-55032293	0.0408	0.6372	A/G	G	GACACGATGTCTTCAGTCTCCAGCT[A/G]AGCT TGGACTGTGAGGATGGGTCAG	33
rs12610617	19-56443519	0.0030	0.3650	C/T	T	CTCTCAAGTTTGCCCAGGGGATACG[C/T]GGGA AGTGCCCCTGGGGGGCCGACC	34
rs160104	19-56433203	0.0012	0.2352	G/T	T	ctggtctcttccagctctggtggct[G/T]ccagtatttcttgggttgtggc ctc	35
rs16986899	19-56549510	0.0265	0.6372	T/C	C	AACAAGGTGACAGACCAGGGAGTAA[C/T]GCCT CTCAGTGATGCCTTGAGAGTC	36
rs17815373	19-56608900	0.0483	0.7007	G/A	A	CGGCAGGCAGTAGGATGGACTGCGT[A/G]GAC GGCGGCCAGCATGTAAATGAAA	37
rs1895375	19-55035001	0.0329	0.6372	T/C	C	AAGTAAGGTGTCAAGGAGGCCATGC[C/T]CACT CTGTAGGTTCTAGGAAAGAAT	38
rs2043690	19-56383651	0.0305	0.6372	T/C	T	ATGCCTGAAAGAAACAAGAGCAAAT[C/T]GTCT CAGGAGGTAGGTAATAGGATG	39
rs2194	19-56257259	0.0064	0.5195	G/A	A	AGCATATTCATTGATTTCCTTACAT[A/G]CAAAT GCTCCTTTTTAAGTGCTCAA	40
rs2288419	19-55693244	0.0140	0.6372	A/G	G	TCAGTACGTATTCCTGCATCAGTGC[A/G]TCCT GCGGTTCCTCCAACAGTCAGC	41
rs2288521	19-55708557	0.0262	0.6372	T/C	T	AGTGGAGGCCCTGGAACCCGGGACG[C/T]TGT ACAATTTCACCGTGTGGGCAGA	42
rs2288527	19-55699077	0.0454	0.6738	A/G	G	TGCCATATAATCTCAGGGTGCAACG[A/G]ATAA ACAAGGGGTGATGCCGAAGAA	43

rs2637107	19-56566741	0.0317	0.6372	G/A	A	CTCTGTCCCCTCAACTTCTTTCTAC[A/G]TGGTC ATGTCCCTTCTTTAGTTCCT	44
rs299164	19-56319796	0.0273	0.6372	A/C	C	GCAACAAAAATCTTATACATCACCA[A/C]ATGTC TGCTTAGCGGCAGAATTGCC	45
rs299169	19-56316796	0.0324	0.6372	G/A	G	GCTAGGTAAAGGACTCTGAAAATAC[A/G]GCAA CATGGAAAACATCCAGTCTCC	46
rs303997	19-56424443	0.0007	0.2204	T/C	T	TCCATTTGCCCAGTGCAGCATAGCC[C/T]GCAT TGCCAAGGTGGTCTTCCCAAC	47
rs304001	19-56423668	0.0015	0.2352	C/T	C	CGTTTAACAAAGAAGACACTGAGAT[C/T]GAGG GCCTGGAAGTGCCTTTCATTG	48
rs304002	19-56423254	0.0141	0.6372	C/T	C	TTCTACGACTTTTTCACTGCCTACA[C/T]GAGTC CCAGGAGGAAGACTTCACAA	49
rs306463	19-56497077	0.0068	0.5195	T/G	T	gccaaatgtgtttgaaaattccatt[G/T]gaagaatttatggtgaatgc atttt	50
rs310445	19-56173551	0.0396	0.6372	G/A	G	GAAGATTGTTCAAGAAAAGGCAGAG[A/G]GCAT GATGACAACACAAAATGAAGA	51
rs3745429	19-54937593	0.0233	0.6372	A/G	G	CCTGGGACTATCCCCTGGCCGGGCC[A/G]CAC ACATGTGCCCTGTGACCAGGGA	52
rs3786867	19-55684200	0.0394	0.6372	C/T	T	GCTGGCTGTGAGGAGTCCGCGAGAA[C/T]TCC CTTGCTTGTCCATGAATTTATC	53
rs4629084	19-56420157	0.0243	0.6372	G/T	G	AAGGTGAAGAGTGGGAAAAGGCAGA[G/T]GATC AGGAAAAATAACTAATGGGTA	54

rs464765	19-56430224	0.0208	0.6372	A/C	A	ggcttaataaaaggaattagagagc[A/C]ctccctcctctccaacat cttttc	55
rs4801278	19-56246520	0.0268	0.6372	G/A	A	TGGTCTGTGCTCTCCTTGCACACTC[A/G]TCTGT GGACATCACAGGAGGGAACA	56
rs4801635	19-56372705	0.0352	0.6372	C/T	C	GTGCGTATATGTGTTACAAGTGGCT[C/T]GTGTT GACCGCCTGCCTGTGGAAAG	57
rs516022	19-56609371	0.0408	0.6372	C/A	C	GCCTCGGGTGCTGACCGGGGGTGCC[A/C]TTG CTGGGCTTAGCAGGCCGGGCTT	58
rs6509882	19-55030183	0.0400	0.6372	A/G	G	TGATGTGCCACATCCTGTATAGGAA[A/G]CAGG TGATGTGGAAATGAGTCAGAC	59
rs6509883	19-55030376	0.0378	0.6372	A/G	G	CATGAAAACCCCTCAGATGGTACCA[A/G]AAAT ATAGACAATTGATCCAGAGAG	60
rs6509933	19-55683104	0.0188	0.6372	T/C	T	gtcccagctactcacacaggaggat[C/T]gcaggagtttgaaacc agcctgtgc	61
rs6509939	19-55851708	0.0337	0.6372	T/C	C	CACCCTCAGGGCCTCTCCCTGACCC[C/T]TCTC TCACCCCCGGGACCTCCCTGC	62
rs8110255	19-56568978	0.0045	0.4527	T/C	C	GCAGGTCTGTGTTCCTTGTTATGTT[C/T]CCTTG CTACAGGCACTCTCAGCCTT	63
rs8112791	19-56723492	0.0236	0.6372	C/A	C	gtcagtttgtgaacaggtaaaatca[A/C]aatgctcatgttctctaca gggaaa	64
rs873732	19-56745520	0.0194	0.6372	G/A	A	AGCCAATTCGTCAGTGAATGAGGCA[A/G]AGAA ATTGGTAAAAAGAAGGAAAGT	65

Figure 34

SNP ID	Position (hg19)	P value	FDR	Genotype	Minor Allele	Sequence	SEQ ID NO
rs2823699	21-17628689	1.62E-08	0.0033	T/C	T	TACATAGTAGGCTTAAGAGCAAATG[C/T]CTACC TTTTCCTCTGTTTTCAACTC	66
rs4973978	3-41667545	1.69E-08	0.0033	T/G	G	GTTGGTTGGTTTGTTTCCCCTTTAA[G/T]GGTGC CATTTAATGACAGATTTCAT	67
rs11744285	5-124622296	1.75E-08	0.0033	A/G	G	GCCCCGGTGACAAGAATGGCAAAAC[A/G]TTTA TTCGGCATTAACAATGTGTAA	68
rs7120273	11-12581045	3.32E-08	0.0041	T/C	T	GCTCAGCTAATCAATGACCAGTCTC[C/T]TTAAT TCTTCTAATGCCTATATGGT	69
rs10831850	11-12566917	5.12E-08	0.0041	G/A	A	GTAAGGGATGTGAATCGGGTACTGA[A/G]GAAA GAGCCTGGATGCAGAGCCAGC	70
rs4756936	11-12599138	5.12E-08	0.0041	C/T	T	TTGATAACTTCAGCATCTGGATCAC[C/T]GTGG GATTAGCATCTGTTTGTATTT	71
rs6485827	11-12578182	5.12E-08	0.0041	C/T	C	GTGTGATTGCTTAAAAAAAACTACT[C/T]ACATT GTTTTGAATCACACCTCACA	72

rs7079768	10-131271870	9.92E-08	0.0070	G/A	A	ACTTGTGCCAGGCTGGCTTTGCAAC[A/G]ATGAGCCTGAGAAGCTGTTAGAAGT	73
rs1293764	12-113425679	1.27E-07	0.0080	A/G	A	GAGACACAAGAGGTGGGCAGGTCTT[A/G]GGGATTTAGGAGTTGGGTTCAAGGC	74
rs1862945	7-50936184	6.84E-07	0.0387	G/A	A	TGAGTCTGTGAGGAGAAATGAACAA[A/G]TCTACCACAGTCATCCAGAATGAGA	75
rs10496038	2-55340963	9.41E-07	0.0484	C/T	T	ATCAGAAGGCTAAGGAACCACCTGT[C/T]TAATAGTCTGGTGCCAAACACAGGC	76
rs12669489	7-50961697	1.05E-06	0.0493	G/A	A	catcaataagaaaaacaaaaataat[A/G]taatagaaaaatgcataagagactt	77

Figure 35

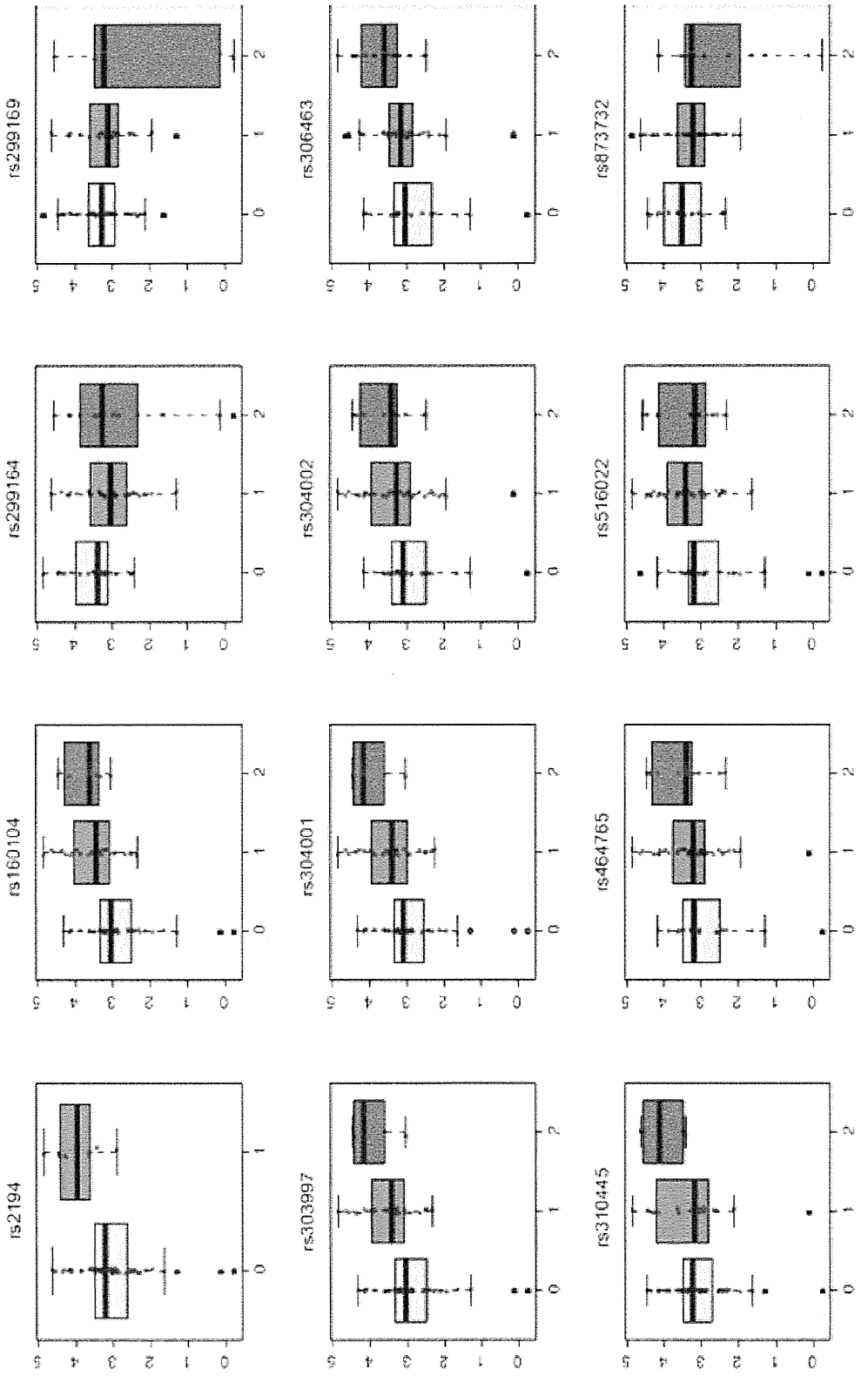

rs2194
rs160104
rs299164
rs299169
rs303997
rs304001
rs304002
rs306463
rs310445
rs464765
rs516022
rs873732

Figure 36A

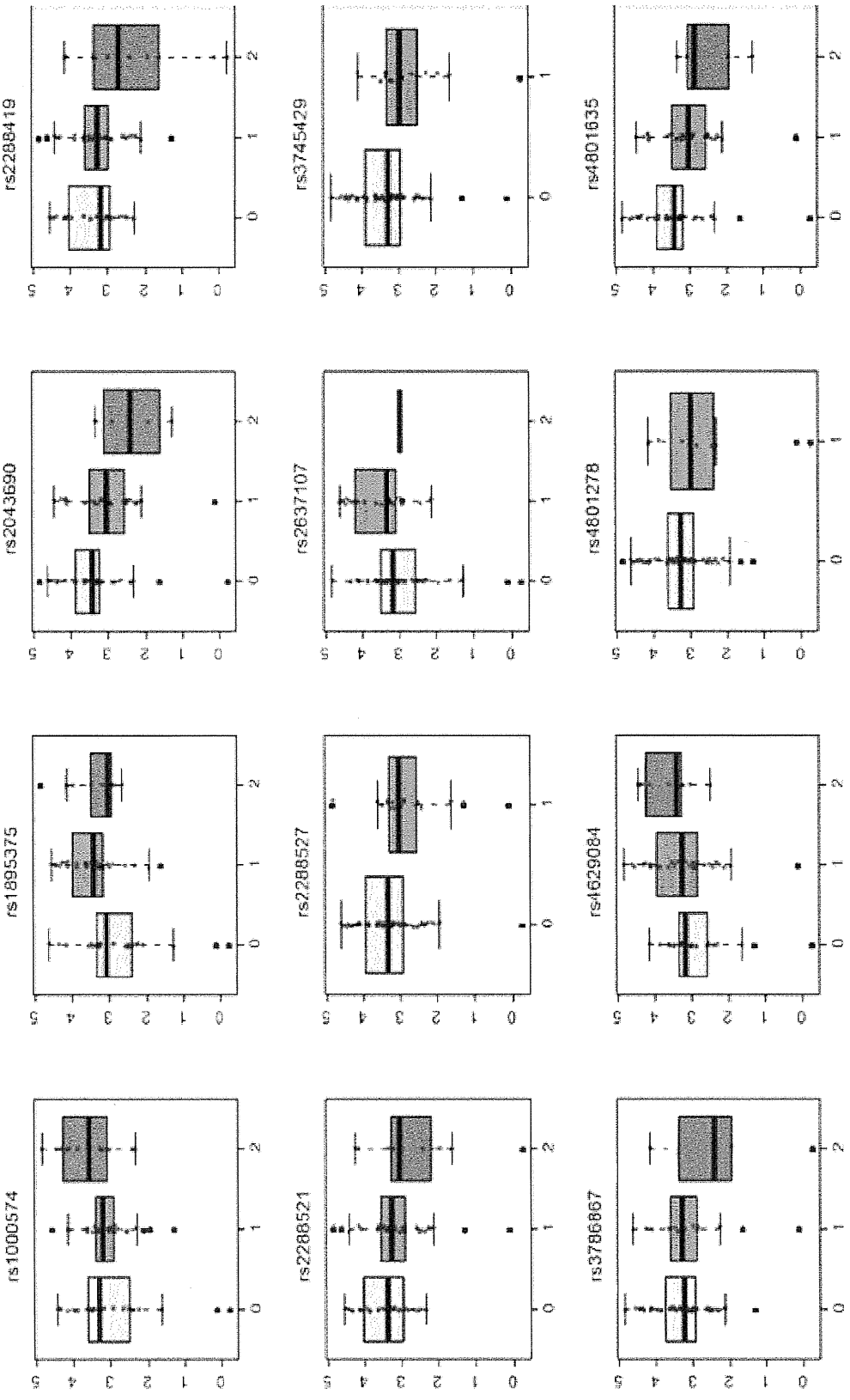

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rs2043690
rs2288419
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rs2288527
rs2637107
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rs3786867
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rs4801635

Figure 36B

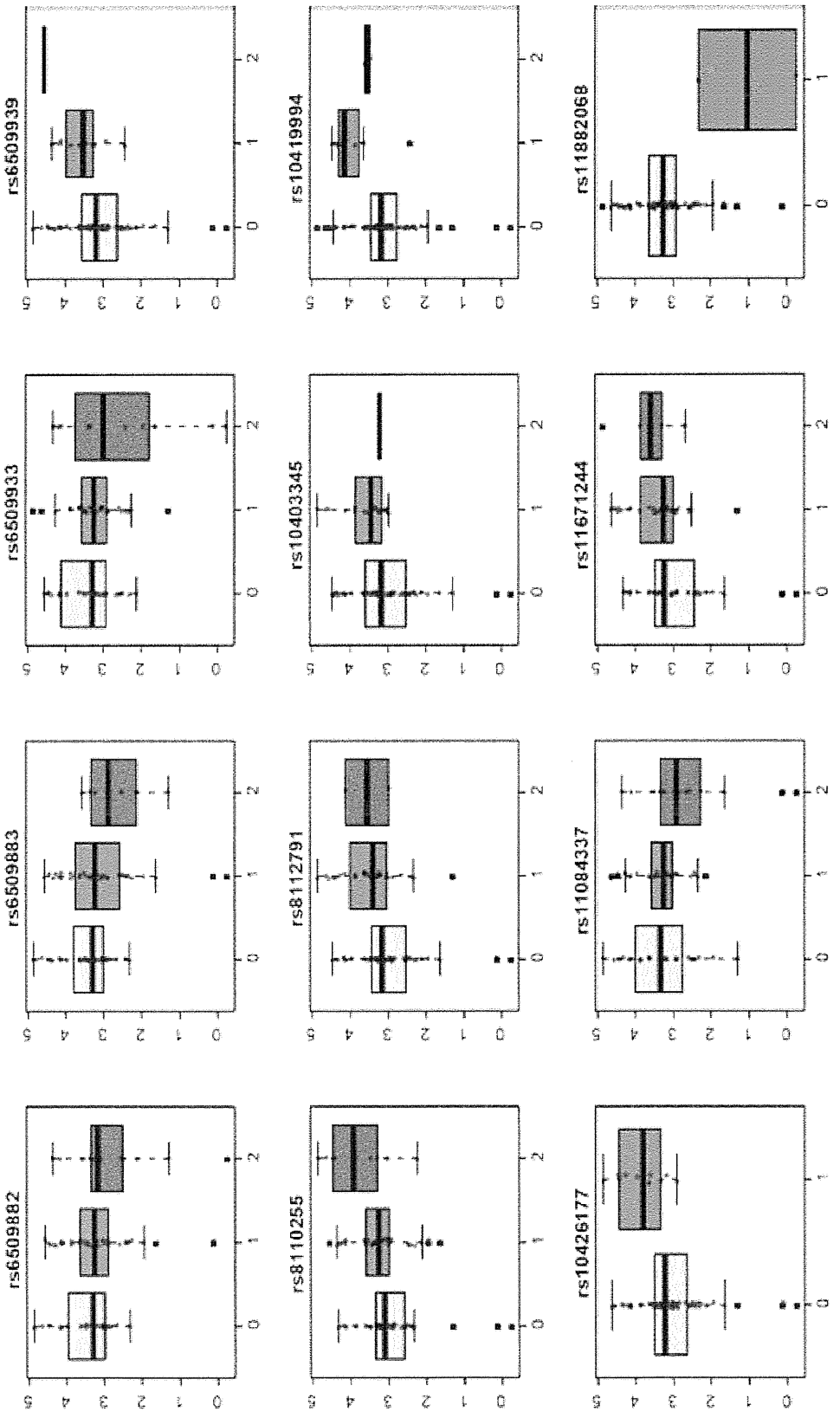

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rs6509883
rs6509933
rs6509939
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rs8112791
rs10403345
rs10419994
rs10426177
rs11084337
rs11671244
rs11882068

Figure 36C

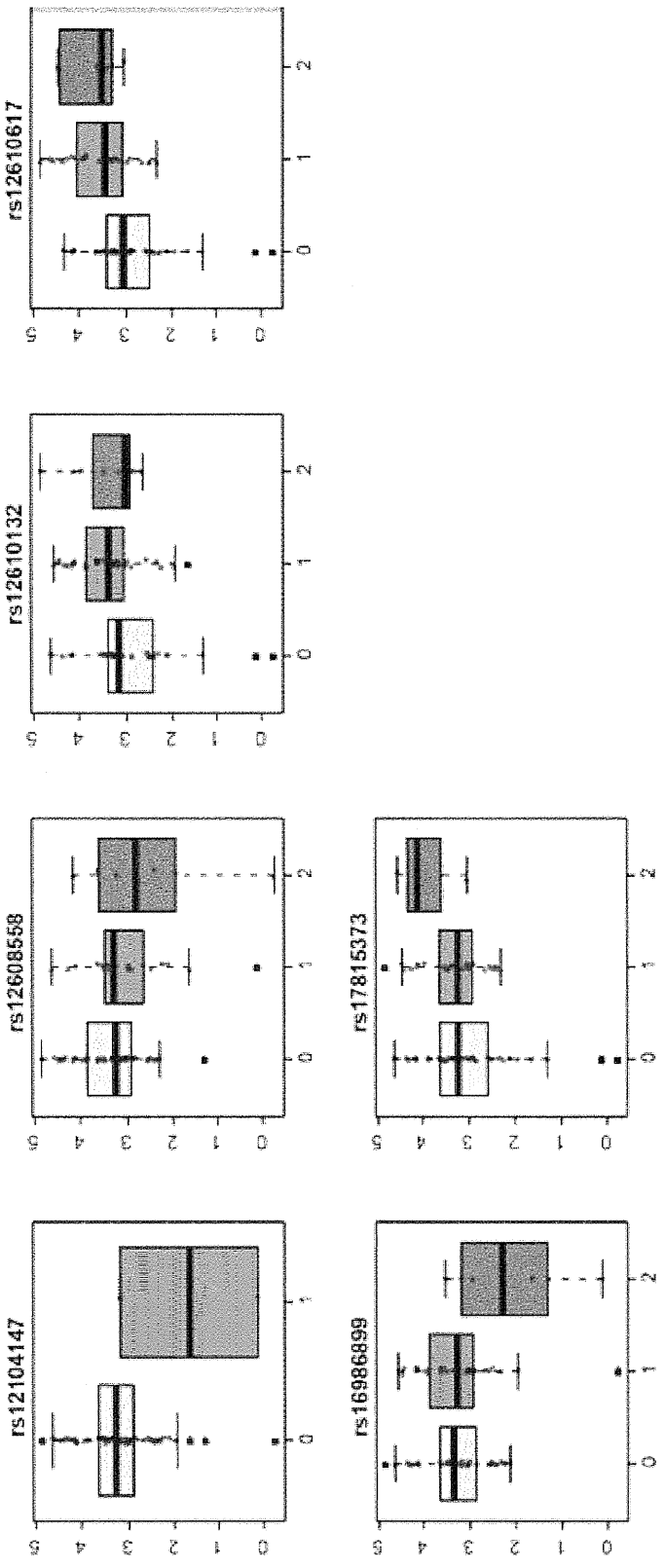

rs12610617
rs12610132
rs12608558
rs17815373
rs12104147
rs16986899

Figure 36D

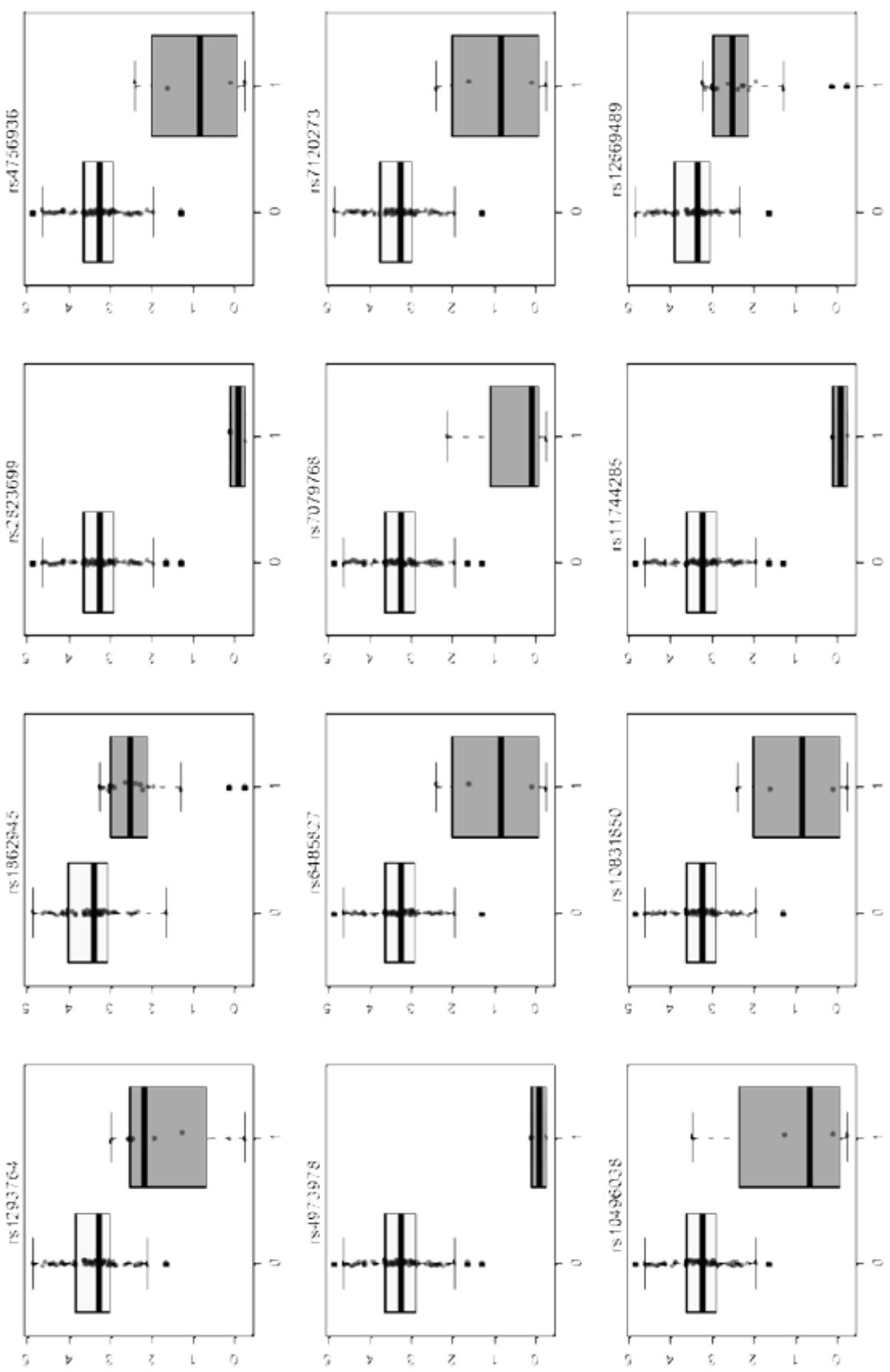

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rs2823699
rs7079768
rs11744285
rs7120273
rs12669489
rs13623945
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rs10831850
rs12937764
rs4973978
rs10486038
0
1
2
3
4
5

Figure 37

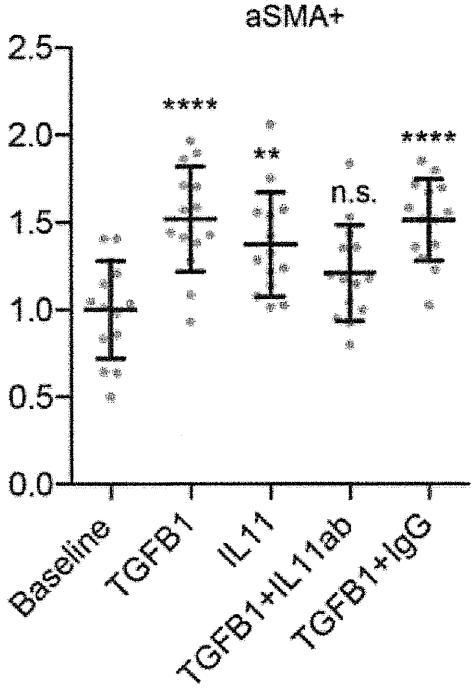


Figure 38A

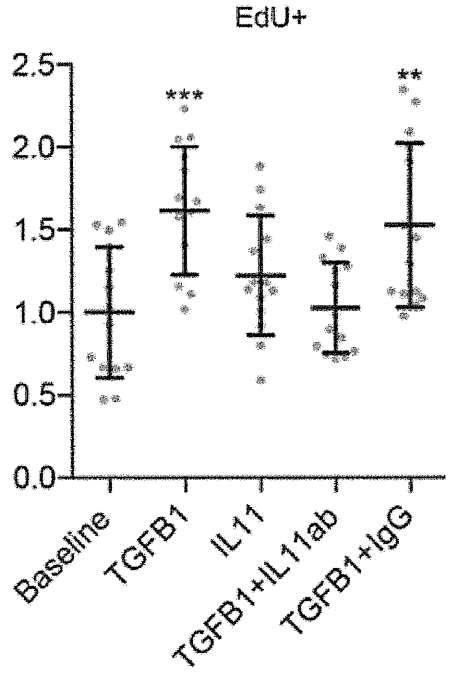


Figure 38B

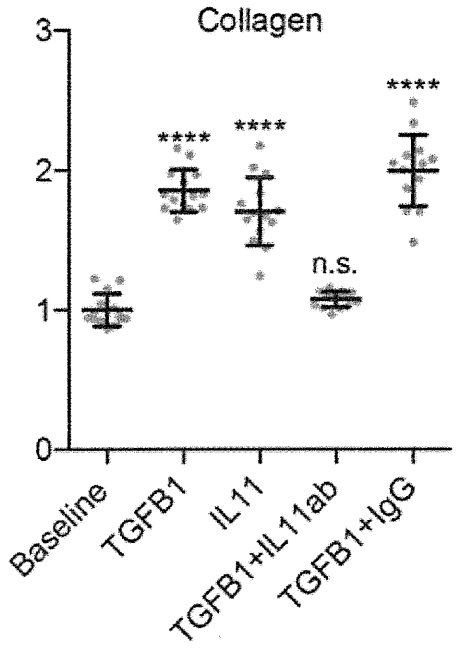


Figure 38C

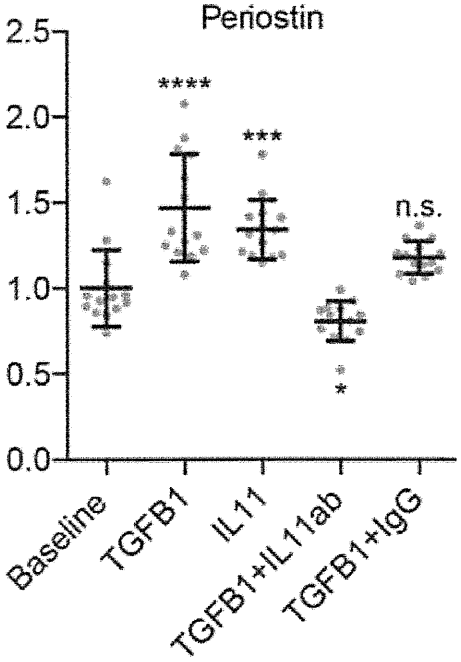


Figure 38D

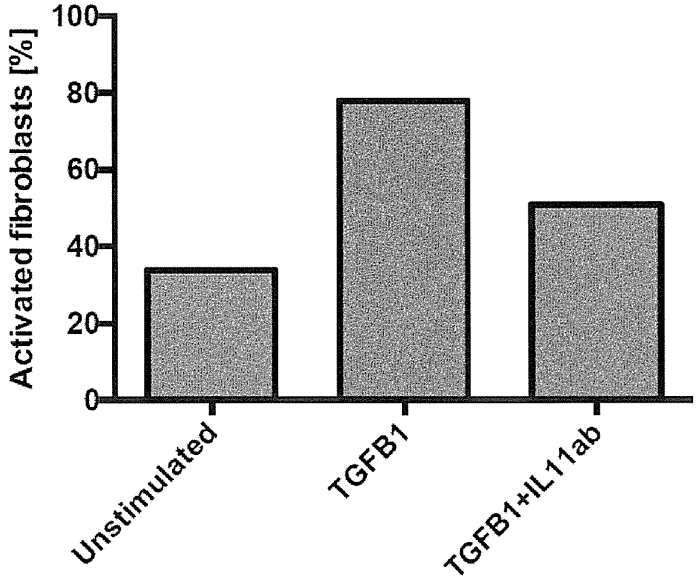


Figure 39

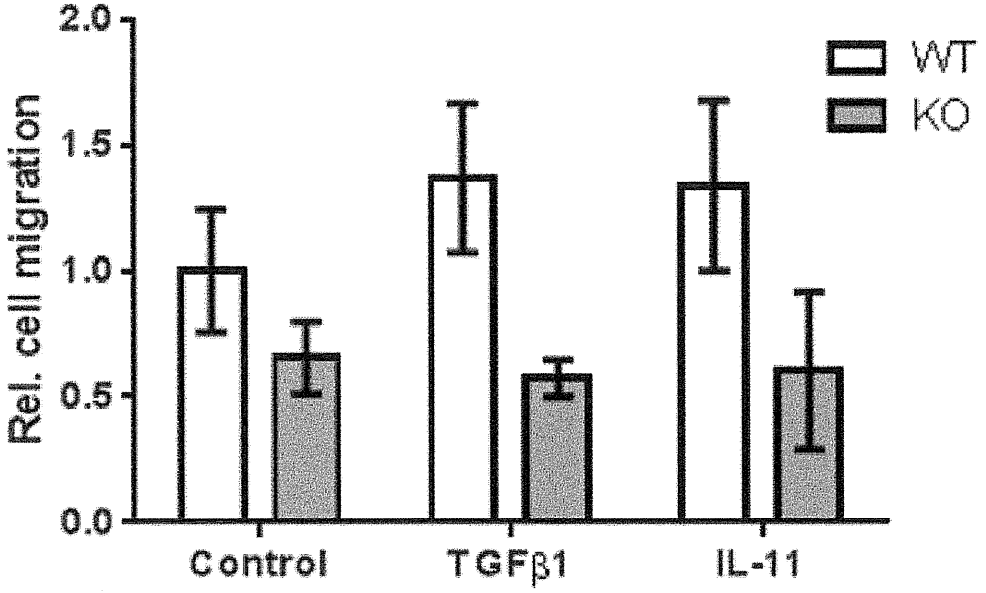


Figure 40