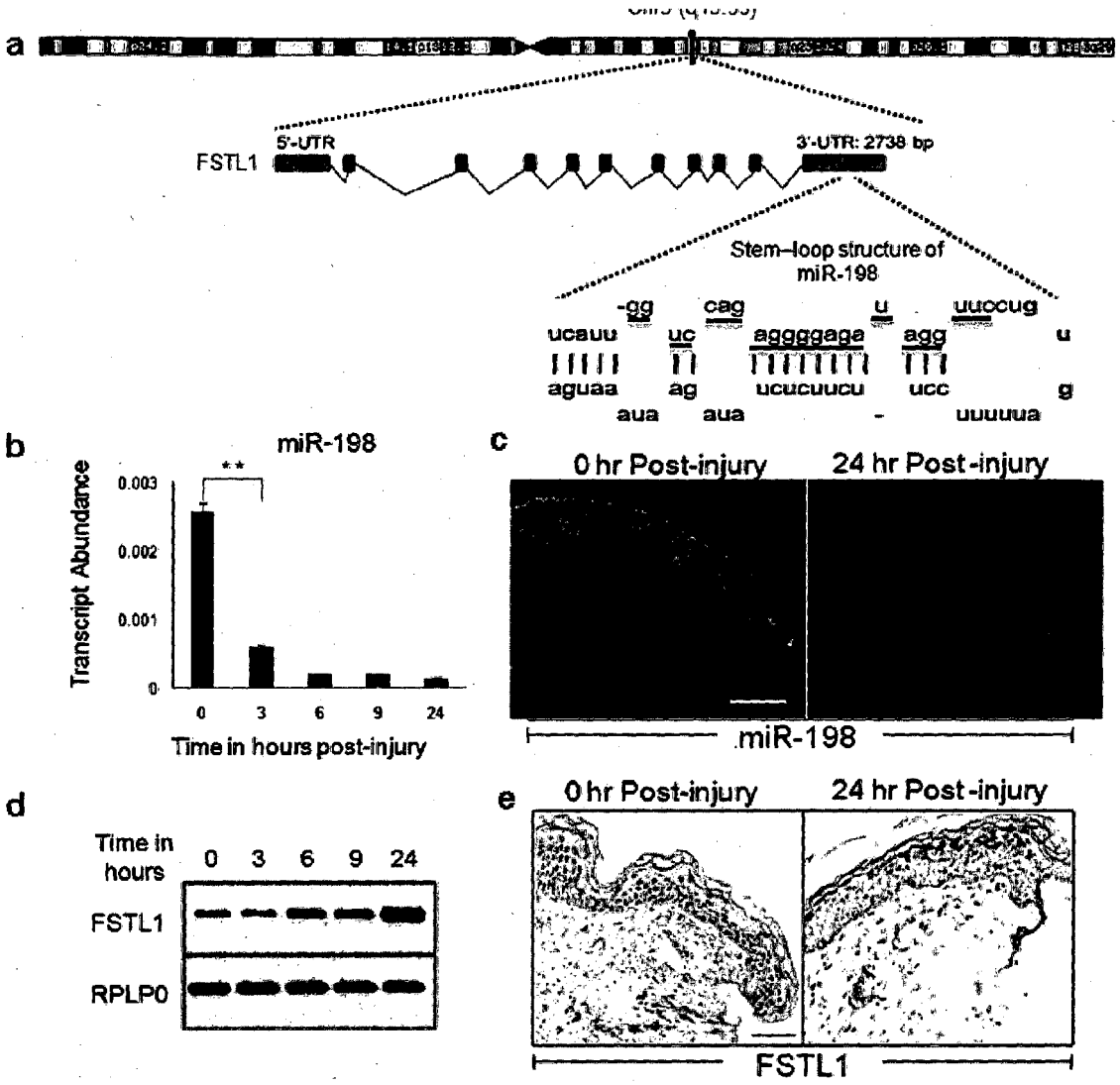

a
5'-UTR
FSTL1
3'-UTR: 2738 bp
Stem–loop structure of miR-198
-gg cag u uuccug
ucauu uc aggggaga agg u
aguaa ag ucucuucu ucc g
aua aua - uuuuua
b
miR-198
Transcript Abundance
0.003
0.002
0.001
0
**
0 3 6 9 24
Time in hours post-injury
c
0 hr Post-injury
24 hr Post-injury
miR-198
d
Time in hours
0 3 6 9 24
FSTL1
RPLP0
e
0 hr Post-injury
24 hr Post-injury
FSTL1

FIG. 1

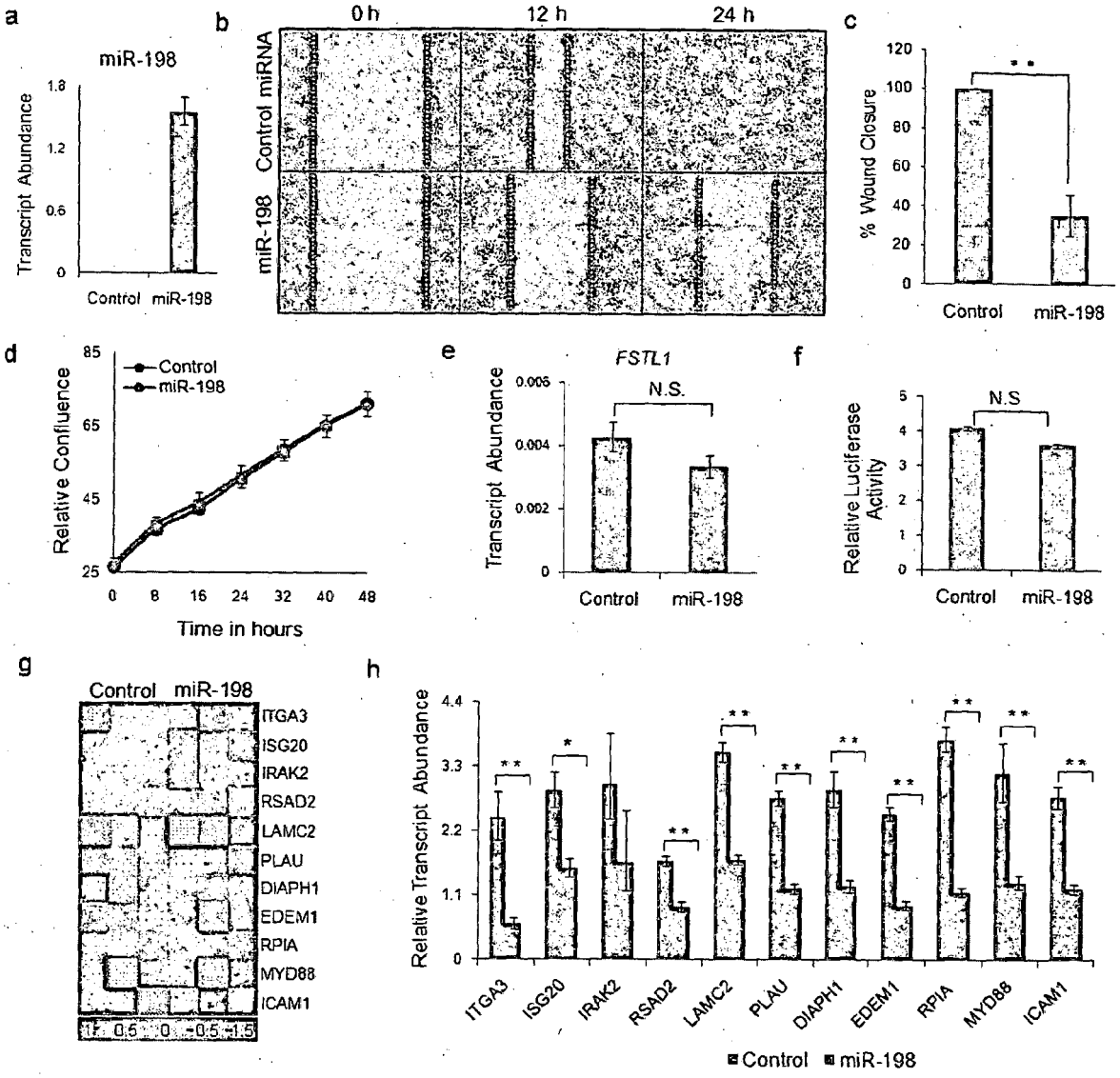

a
miR-198
Transcript Abundance
1.8
1.2
0.6
0
Control miR-198
b
0 h
12 h
24 h
Control miRNA
miR-198
c
% Wound Closure
120
100
80
60
40
20
0
**
Control
miR-198
d
Relative Confluence
85
65
45
25
Control
miR-198
0 8 16 24 32 40 48
Time in hours
e
FSTL1
Transcript Abundance
0.006
0.004
0.002
0
N.S.
Control
miR-198
f
Relative Luciferase Activity
5
4
3
2
1
0
N.S
Control
miR-198
g
Control miR-198
ITGA3
ISG20
IRAK2
RSAD2
LAMC2
PLAU
DIAPH1
EDEM1
RPIA
MYD88
ICAM1
1 0.5 0 -0.5 -1
h
Relative Transcript Abundance
4.4
3.3
2.2
1.1
0
ITGA3 ISG20 IRAK2 RSAD2 LAMC2 PLAU DIAPH1 EDEM1 RPIA MYD88 ICAM1
Control miR-198

FIG. 2

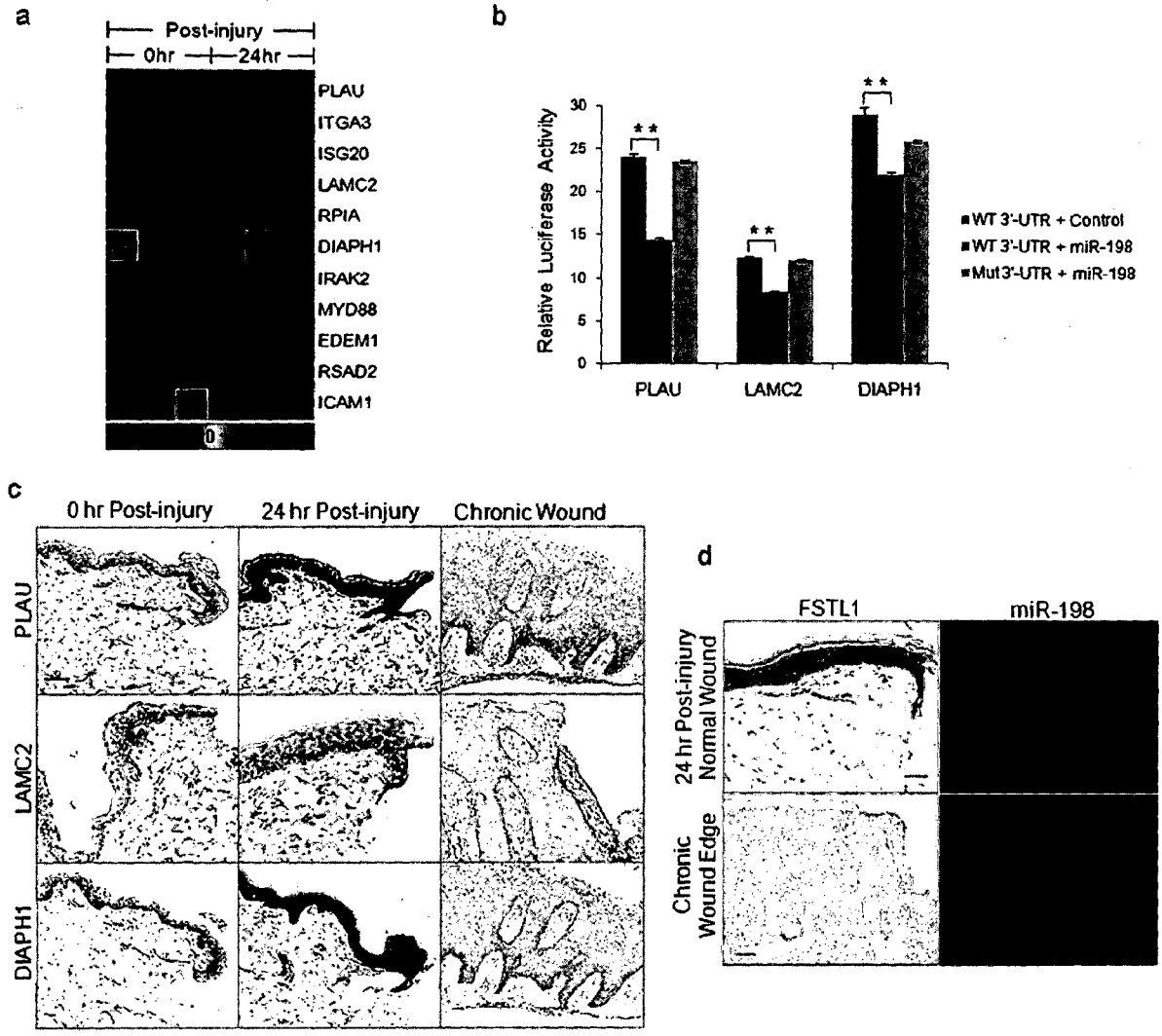

a
Post-injury
0hr
24hr
PLAU
ITGA3
ISG20
LAMC2
RPIA
DIAPH1
IRAK2
MYD88
EDEM1
RSAD2
ICAM1
b
Relative Luciferase Activity
30
25
20
15
10
5
0
**
**
**
PLAU
LAMC2
DIAPH1
WT 3'-UTR + Control
WT 3'-UTR + miR-198
Mut3'-UTR + miR-198
c
0 hr Post-injury
24 hr Post-injury
Chronic Wound
PLAU
LAMC2
DIAPH1
d
FSTL1
miR-198
24 hr Post-injury Normal Wound
Chronic Wound Edge

FIG. 3

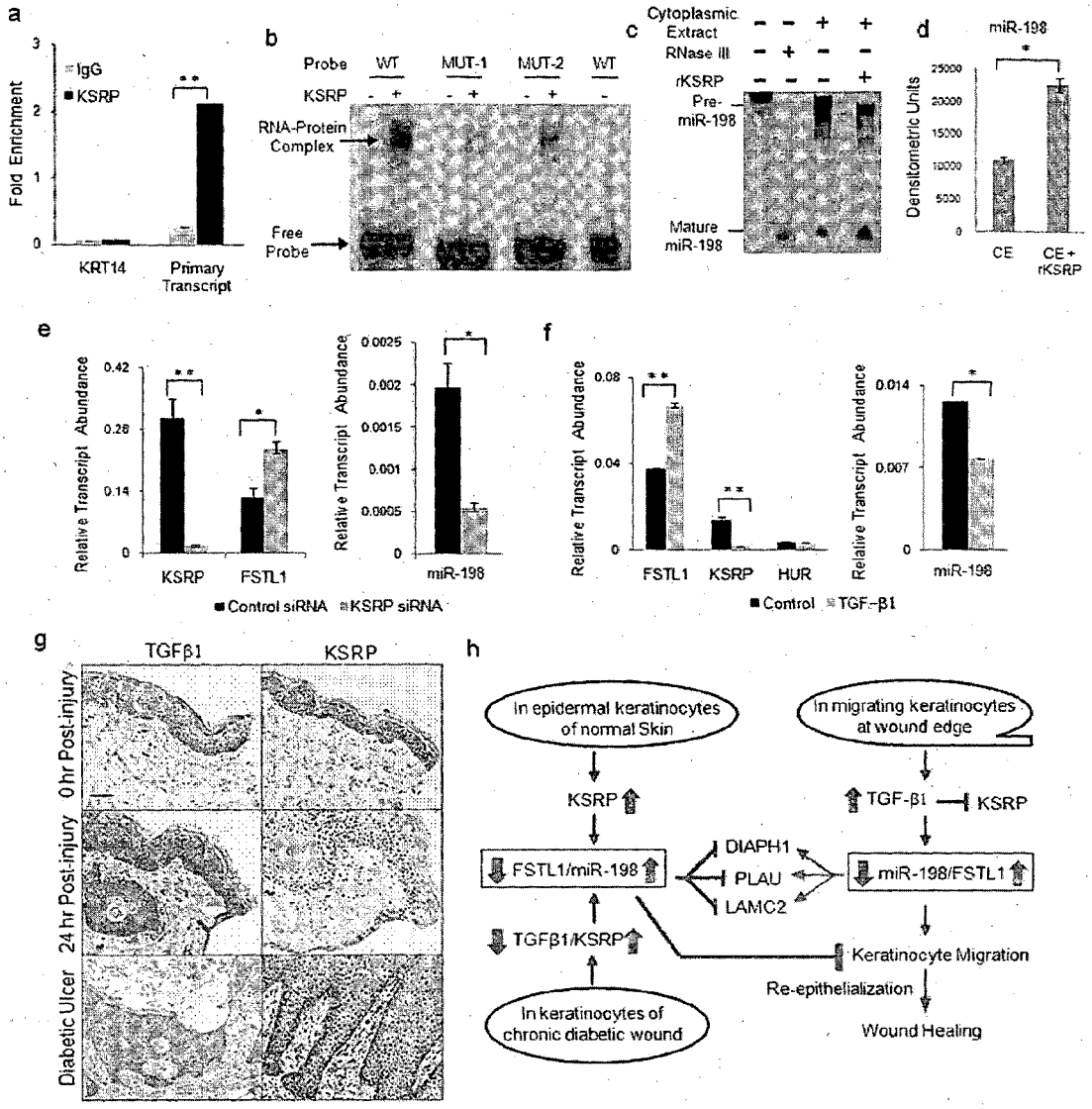

a
Fold Enrichment
IgG
KSRP
KRT14
Primary Transcript
b
Probe
WT
MUT-1
MUT-2
WT
KSRP
RNA-Protein Complex
Free Probe
c
Cytoplasmic Extract
RNase III
rKSRP
Pre-miR-198
Mature miR-198
d
miR-198
Densitometric Units
CE
CE + rKSRP
e
Relative Transcript Abundance
KSRP
FSTL1
miR-198
Control siRNA
KSRP siRNA
f
Relative Transcript Abundance
FSTL1
KSRP
HUR
miR-198
Control
TGF-β1
g
TGFβ1
KSRP
0 hr Post-injury
24 hr Post-injury
Diabetic Ulcer
h
In epidermal keratinocytes of normal Skin
In migrating keratinocytes at wound edge
KSRP
TGF-β1
KSRP
FSTL1/miR-198
DIAPH1
PLAU
LAMC2
miR-198/FSTL1
TGFβ1/KSRP
Keratinocyte Migration
Re-epithelialization
Wound Healing
In keratinocytes of chronic diabetic wound

FIG. 4

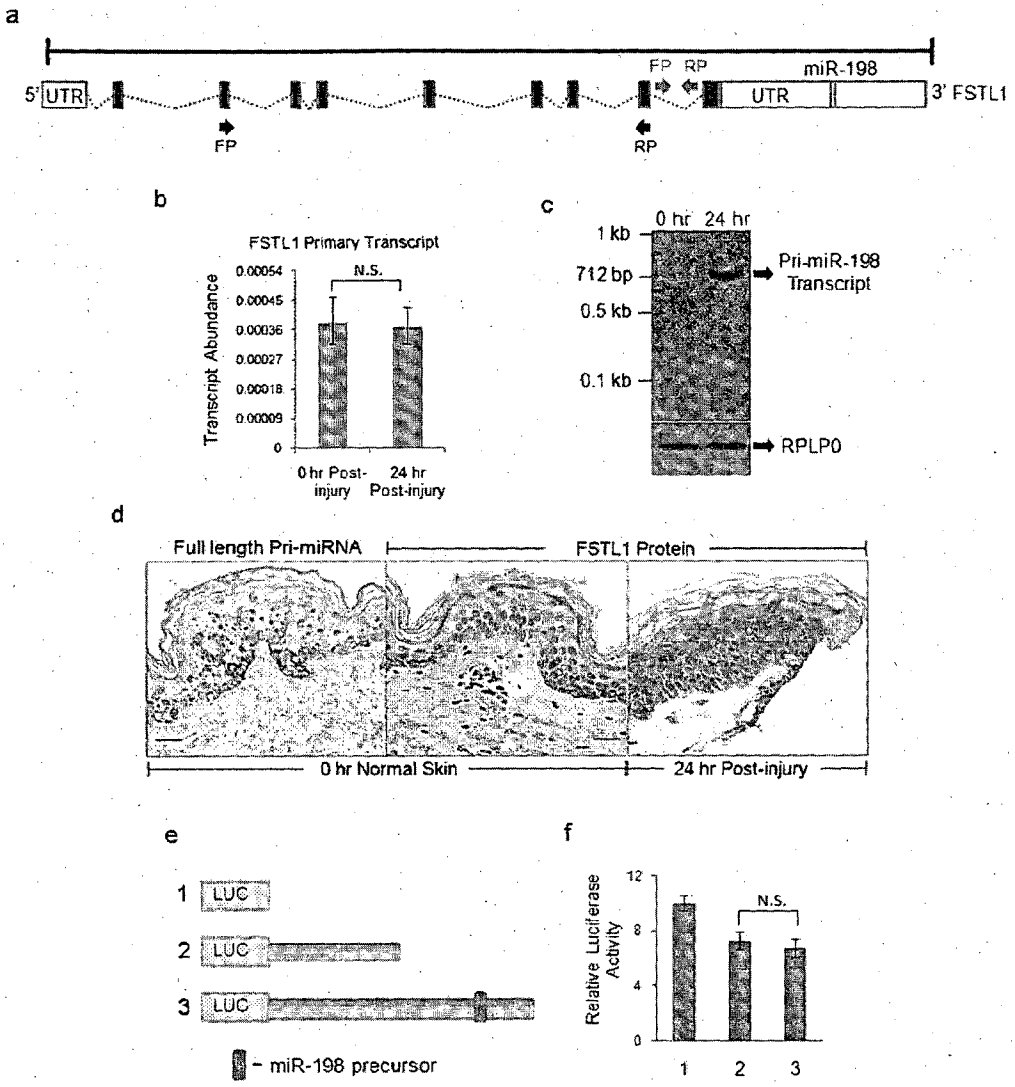

a
5' UTR
FP
RP
FP RP
miR-198
UTR
3' FSTL1
b
FSTL1 Primary Transcript
Transcript Abundance
0.00054
0.00045
0.00036
0.00027
0.00018
0.00009
0
N.S.
0 hr Post-injury
24 hr Post-injury
c
0 hr 24 hr
1 kb
712 bp
0.5 kb
0.1 kb
Pri-miR-198 Transcript
RPLP0
d
Full length Pri-miRNA
FSTL1 Protein
0 hr Normal Skin
24 hr Post-injury
e
1 LUC
2 LUC
3 LUC
- miR-198 precursor
f
Relative Luciferase Activity
12
8
4
0
N.S.
1
2
3

FIG. 5

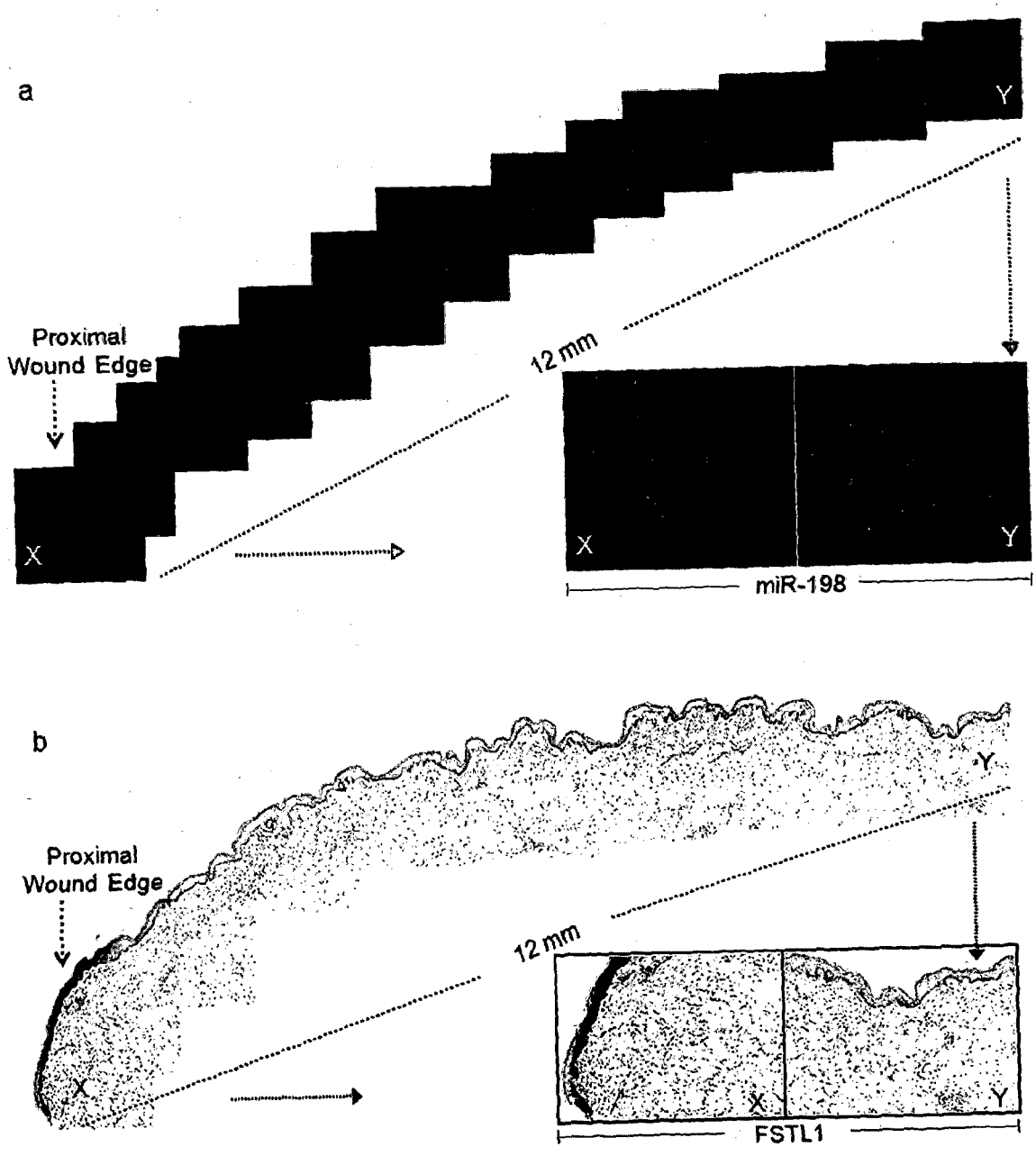

a
Y
Proximal
Wound Edge
12 mm
X
X
Y
miR-198
b
Y
Proximal
Wound Edge
12 mm
X
X
Y
FSTL1

FIG. 6

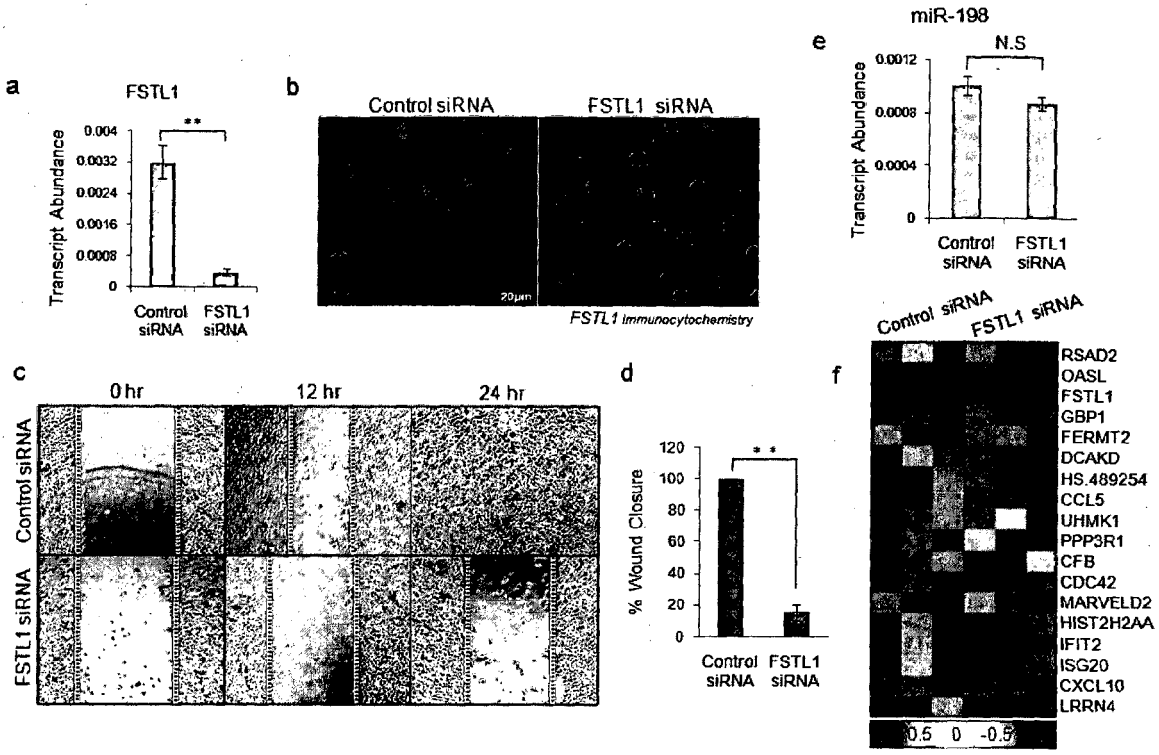


FIG. 7

PLAU 3'UTR : 5' AGCAACUUGUCUUUUUCUGGACU 3'
DIAPH1 3' UTR : 5' UUAUGCCCUUGCCUCUCUGGACG 3'
LAMC2 3' UTR : 5' CUGCCACCUUCAAGUUCUGGACC 3'

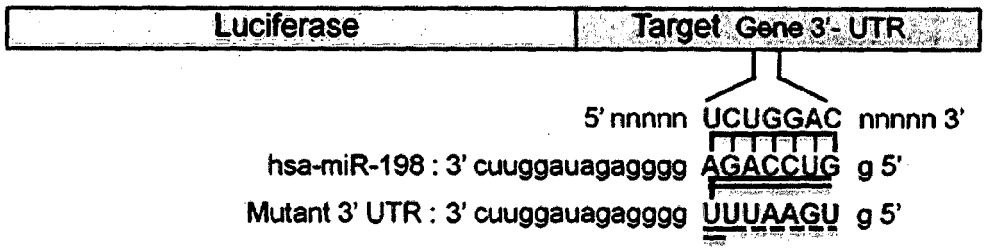


FIG. 8

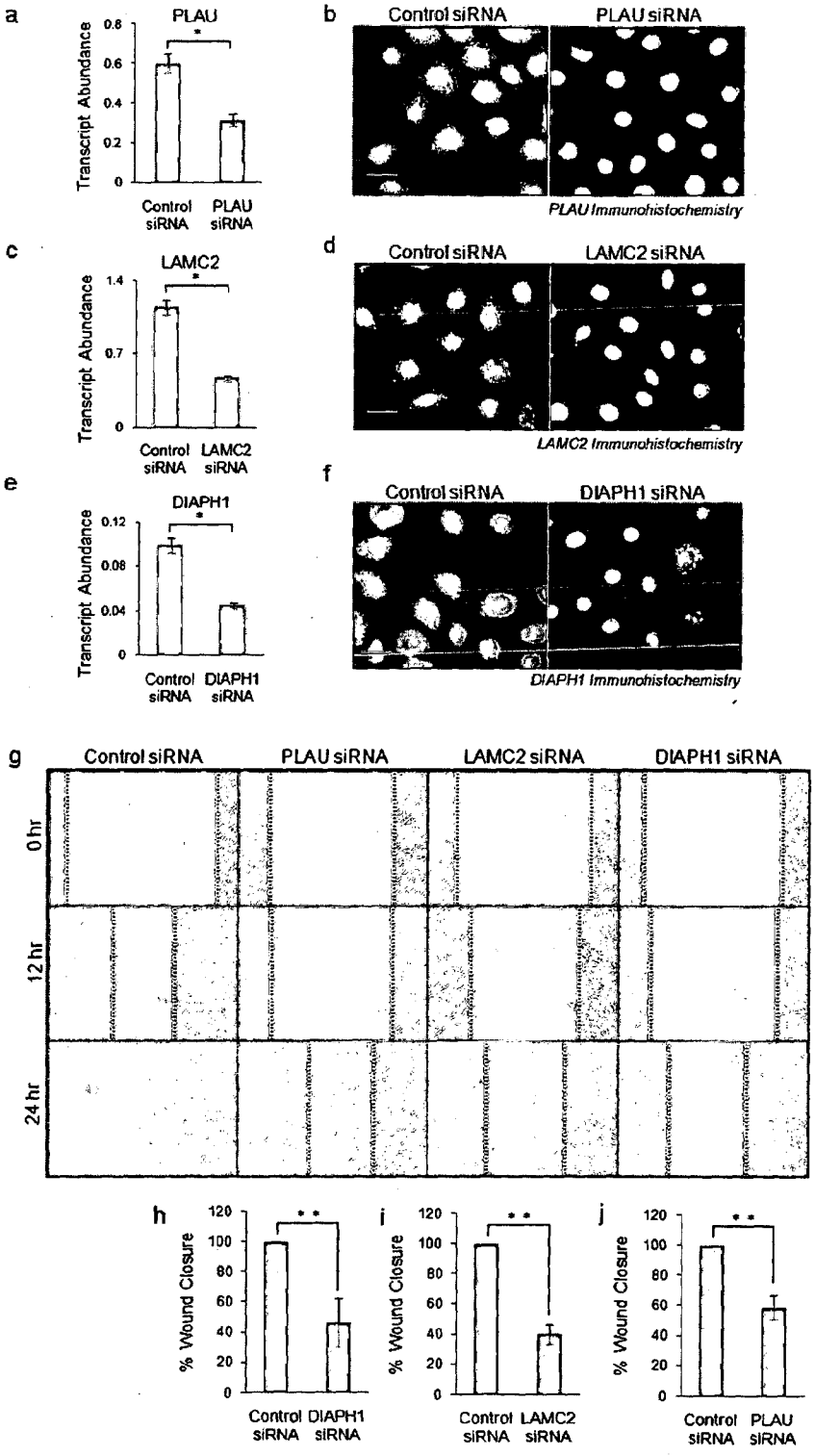

a
PLAU
Transcript Abundance
0.8
0.6
0.4
0.2
0
*
Control siRNA
PLAU siRNA
b
Control siRNA
PLAU siRNA
PLAU Immunohistochemistry
c
LAMC2
Transcript Abundance
1.4
0.7
0
*
Control siRNA
LAMC2 siRNA
d
Control siRNA
LAMC2 siRNA
LAMC2 Immunohistochemistry
e
DIAPH1
Transcript Abundance
0.12
0.08
0.04
0
*
Control siRNA
DIAPH1 siRNA
f
Control siRNA
DIAPH1 siRNA
DIAPH1 Immunohistochemistry
g
Control siRNA
PLAU siRNA
LAMC2 siRNA
DIAPH1 siRNA
0 hr
12 hr
24 hr
h
% Wound Closure
120
100
80
60
40
20
0
**
Control siRNA
DIAPH1 siRNA
i
% Wound Closure
120
100
80
60
40
20
0
**
Control siRNA
LAMC2 siRNA
j
% Wound Closure
120
100
80
60
40
20
0
**
Control siRNA
PLAU siRNA

FIG. 9

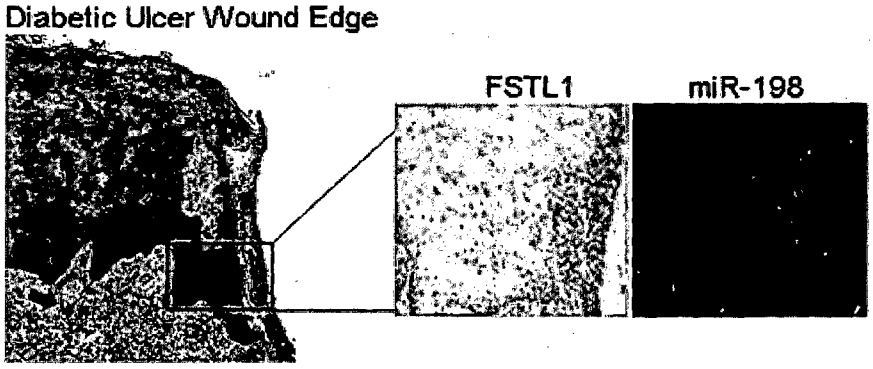
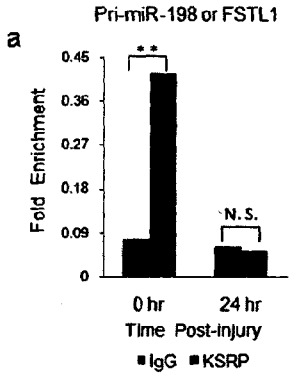


FIG. 10



b

Pre miR-198 WT- 5' TCATTGGTCC AGAGGGGAGA TAGGTTCCTG TGATTTTTCC TTCTTCTCTA TAGAATAAAT GA 3'
Pre miR-198 M1- 5' TCATTGGTCC AGAGGGGAGA TAGGTTCCTC TCATTTTTCC TTCTTCTCTA TAGAATAAAT GA 3'
Pre miR-198 M2- 5'TCATTGGTCC AGAGGGGAGA TACCTTCCTG TGATTTTTCC TTCTTCTCTA TAGAATAAAT GA 3'

FIG. 11

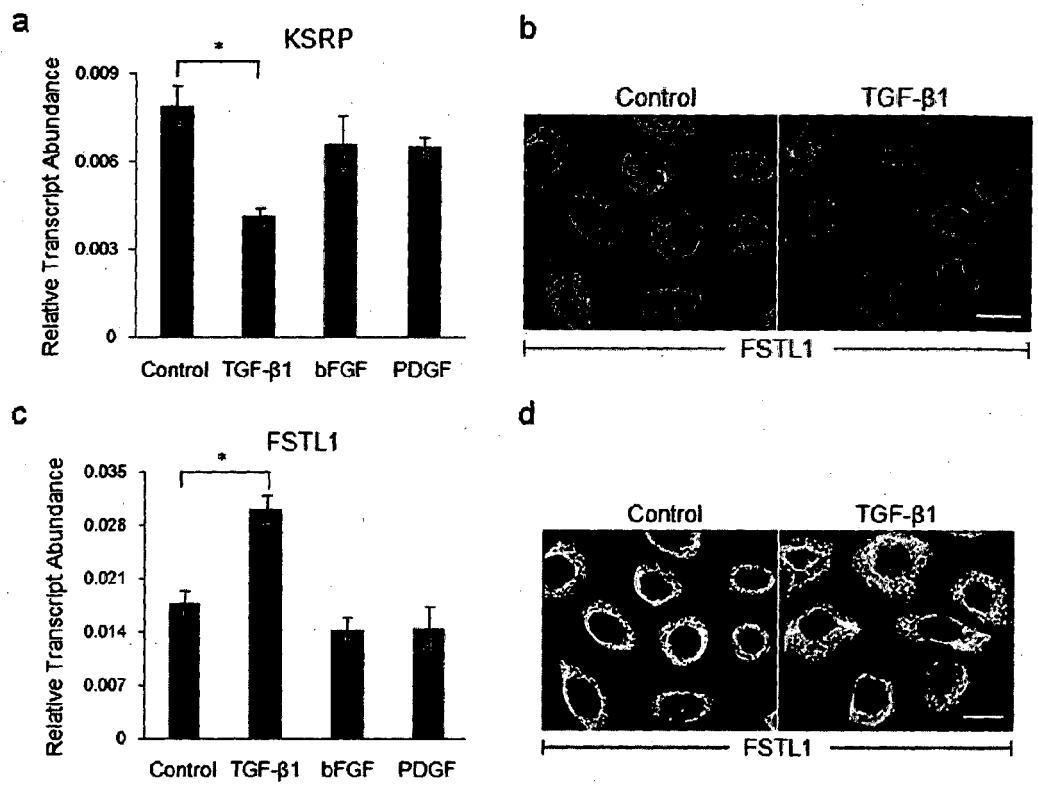

a
KSRP
*
Relative Transcript Abundance
0.009
0.006
0.003
0
Control
TGF-β1
bFGF
PDGF
b
Control
TGF-β1
FSTL1
c
FSTL1
*
Relative Transcript Abundance
0.035
0.028
0.021
0.014
0.007
0
Control
TGF-β1
bFGF
PDGF
d
Control
TGF-β1
FSTL1

FIG. 12

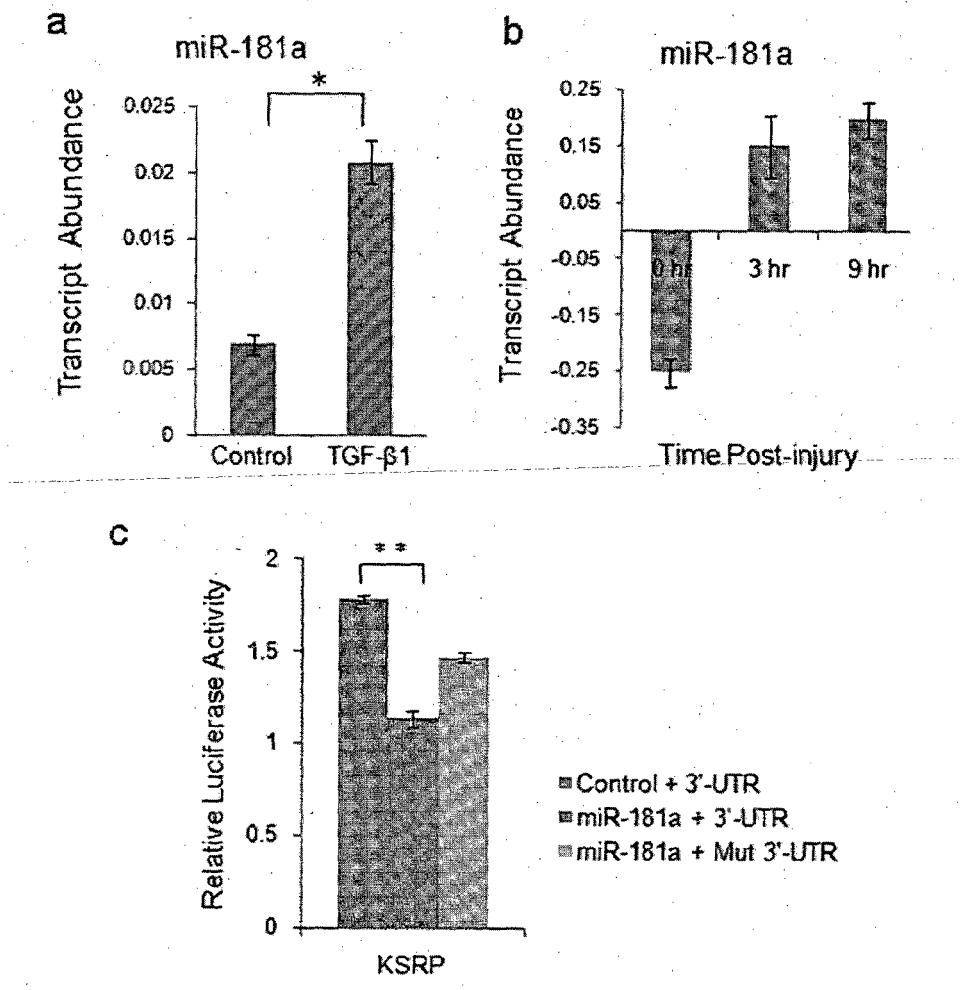

a
miR-181a
Transcript Abundance
0.025
0.02
0.015
0.01
0.005
0
*
Control
TGF-β1
b
miR-181a
Transcript Abundance
0.25
0.15
0.05
-0.05
-0.15
-0.25
-0.35
0 hr
3 hr
9 hr
Time Post-injury
c
Relative Luciferase Activity
2
1.5
1
0.5
0
* *
KSRP
Control + 3'-UTR
miR-181a + 3'-UTR
miR-181a + Mut 3'-UTR

FIG. 13

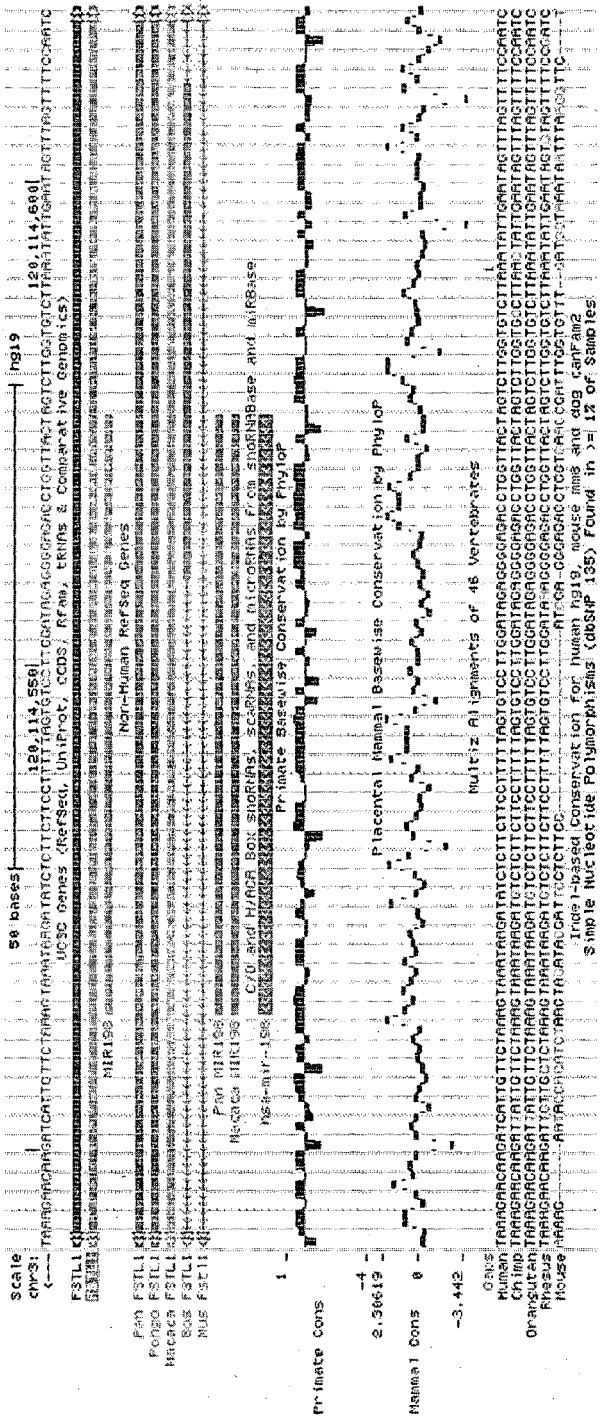

Scale
chr3:
50 bases
120,114,550
hg19
120,114,600
UCSC Genes (RefSeq, UniProt, CCDS, Rfam, tRNAs & Comparative Genomics)
FSTL1
Pan FSTL1
Pongo FSTL1
Macaca FSTL1
Bos FSTL1
Mus FSTL1
MIR199
Non-Human RefSeq Genes
Pan MIR199
Macaca MIR199
C/D and H/ACA Box snoRNAs, scaRNAs, and microRNAs from snoRNABase and miRBase
hsa-mir-199a
Primate Basewise Conservation by PhyloP
Primate Cons
1 -
0
-4
2.36619 -
Placental Mammal Basewise Conservation by PhyloP
Mammal Cons
0 -
-3.442 -
Multiz Alignments of 46 Vertebrates
Genes
Human
Chimp
Orangutan
Rhesus
Mouse
Indel-based conservation for human hg19, mouse mm9 and dog canFam2
Simple Nucleotide Polymorphisms (dbSNP 135) Found in >= 1% of Samples

FIG. 14

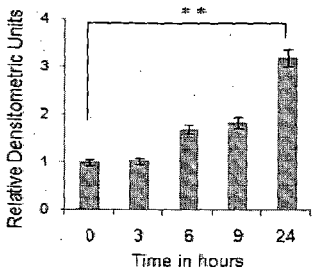

Relative Densitometric Units
Time in hours
0
3
6
9
24
**

Fig. 15

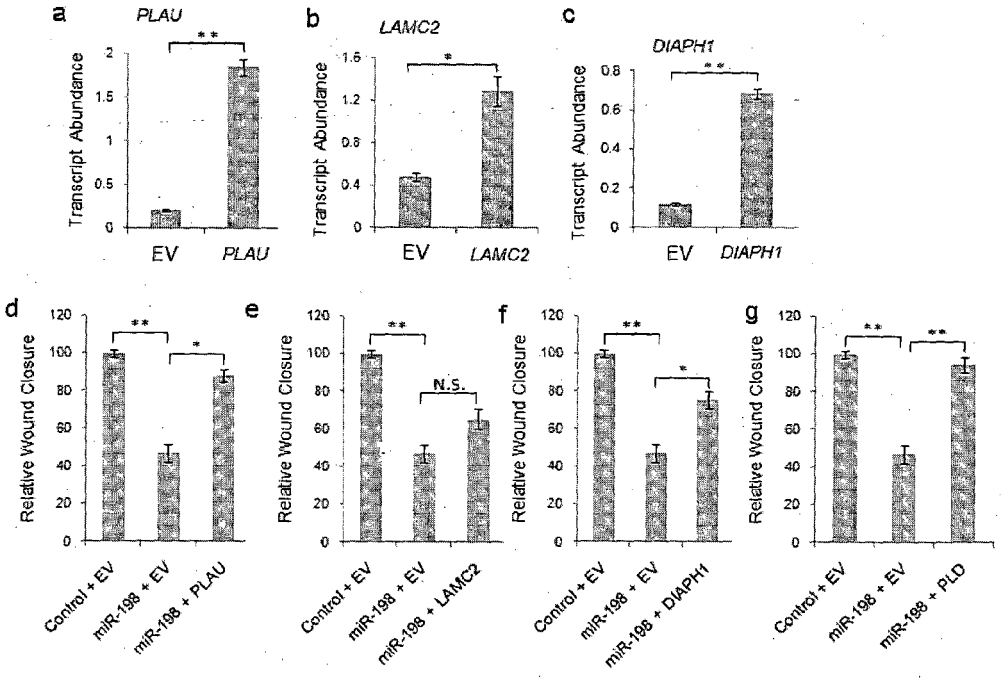

a
PLAU
Transcript Abundance
EV
PLAU
b
LAMC2
EV
LAMC2
c
DIAPH1
EV
DIAPH1
d
Relative Wound Closure
Control + EV
miR-198 + EV
miR-198 + PLAU
e
N.S.
miR-198 + LAMC2
f
miR-198 + DIAPH1
g
miR-198 + PLD

Fig.16

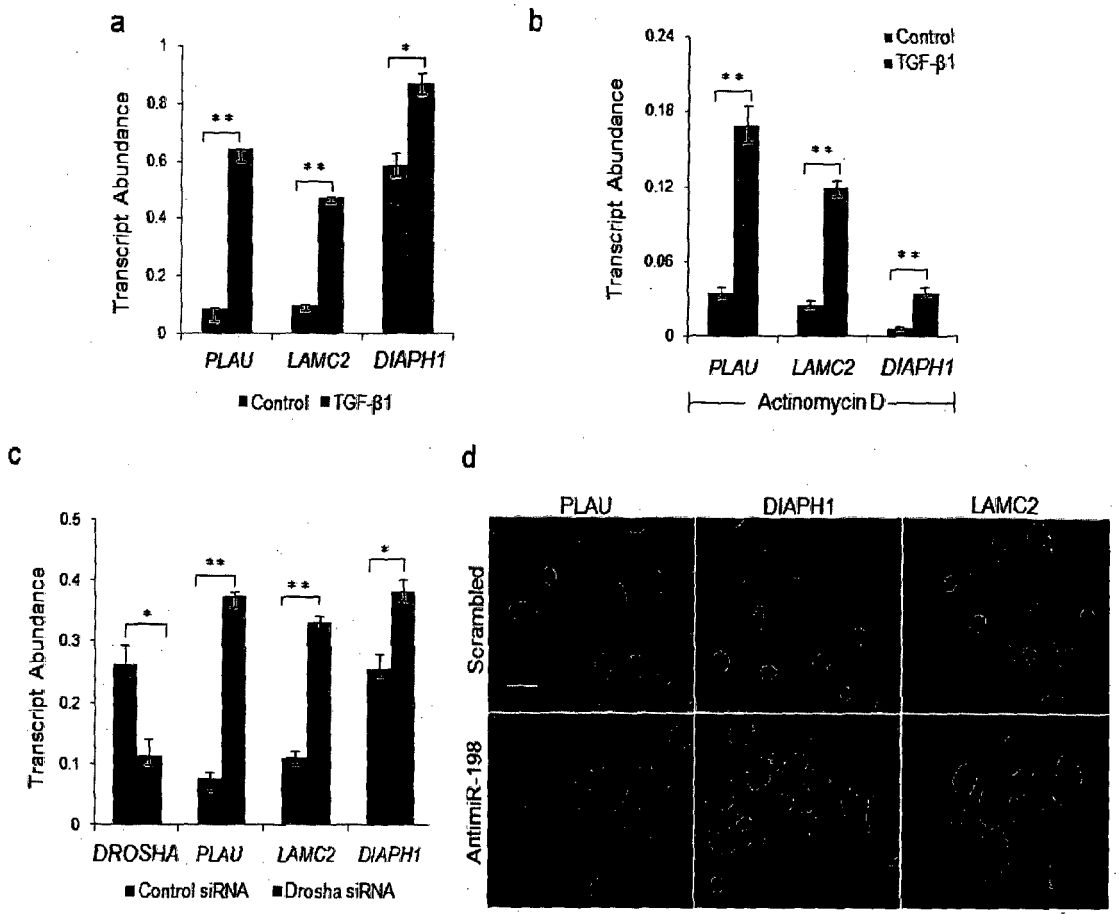

a
Transcript Abundance
PLAU
LAMC2
DIAPH1
Control
TGF-β1
b
Control
TGF-β1
Actinomycin D
c
DROSHA
Control siRNA
Drosha siRNA
d
PLAU
DIAPH1
LAMC2
Scrambled
AntimiR-198

Fig. 17

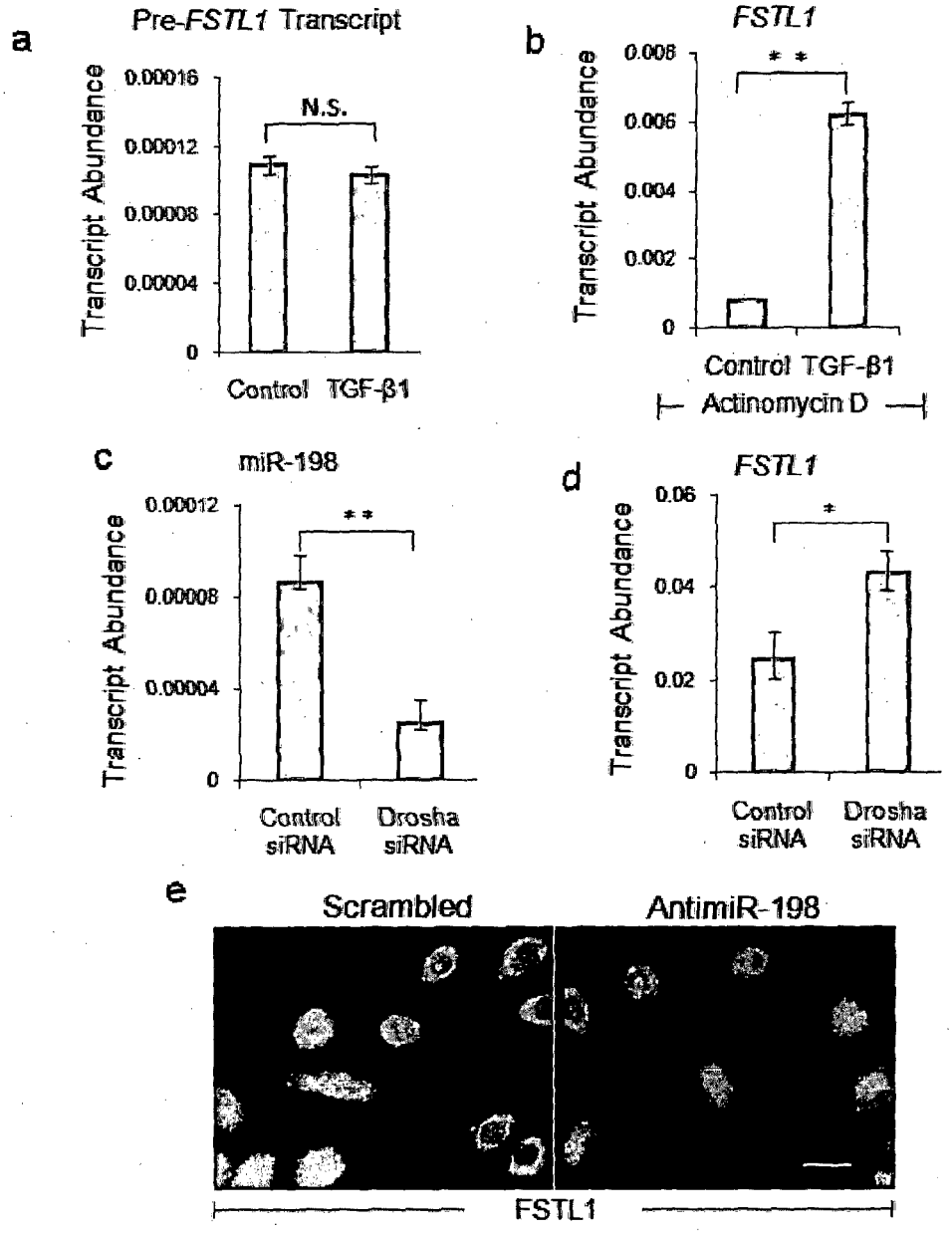

a
Pre-FSTL1 Transcript
Transcript Abundance
0.00016
0.00012
0.00008
0.00004
0
N.S.
Control
TGF-β1
b
FSTL1
Transcript Abundance
0.008
0.006
0.004
0.002
0
* *
Control
TGF-β1
Actinomycin D
c
miR-198
Transcript Abundance
0.00012
0.00008
0.00004
0
* *
Control siRNA
Drosha siRNA
d
FSTL1
Transcript Abundance
0.06
0.04
0.02
0
*
Control siRNA
Drosha siRNA
e
Scrambled
AntimiR-198
FSTL1

Fig. 18