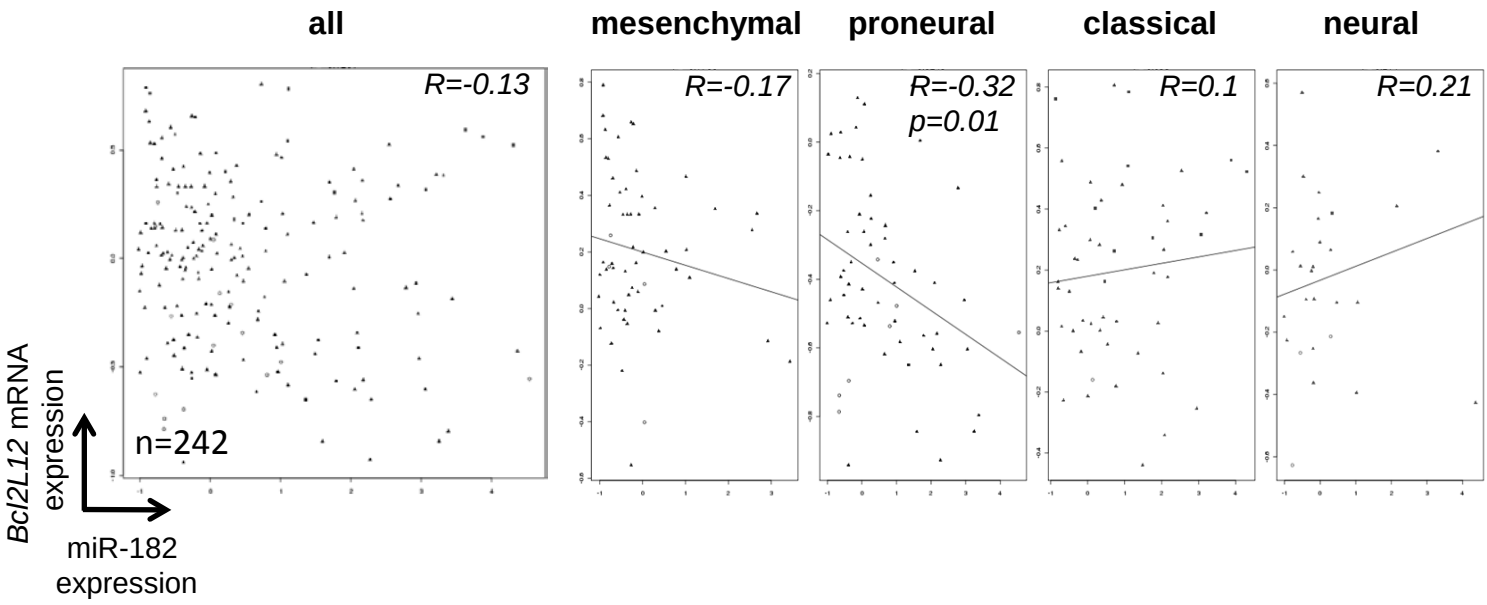
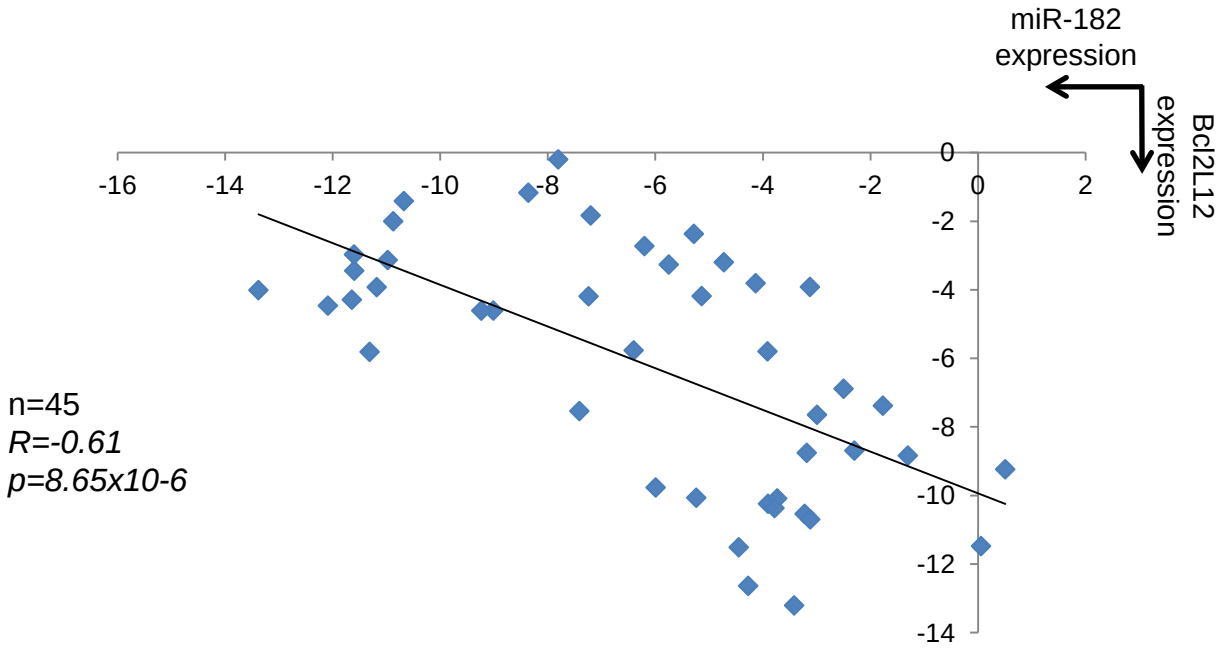
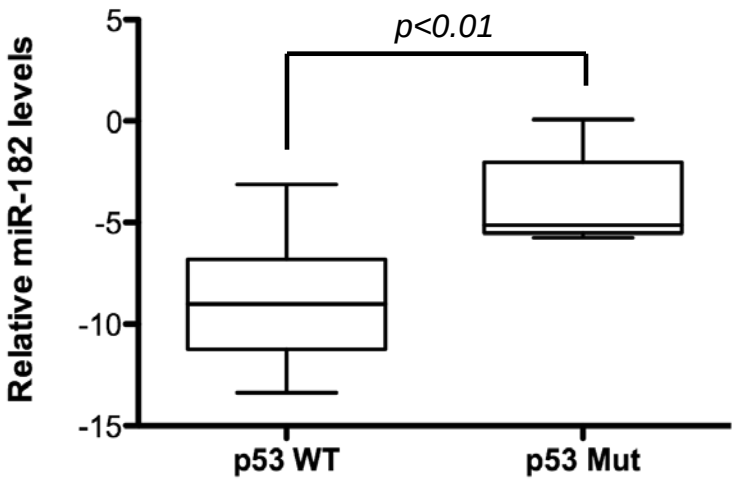
A


all
mesenchymal
proneural
classical
neural
R=-0.13
R=-0.17
R=-0.32
p=0.01
R=0.1
R=0.21
n=242
Bcl2L12 mRNA expression
miR-182 expression

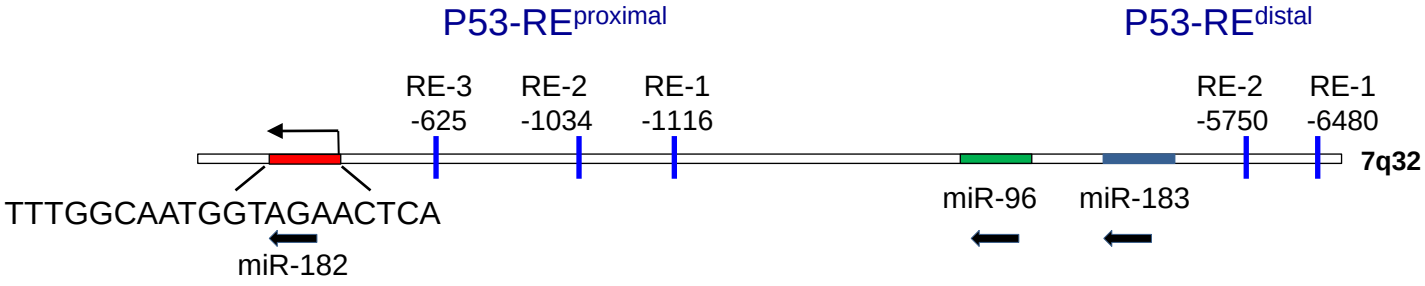
B


miR-182 expression
Bcl2L12 expression
-16
-14
-12
-10
-8
-6
-4
-2
0
2
0
-2
-4
-6
-8
-10
-12
-14
n=45
R=-0.61
p=8.65x10-6

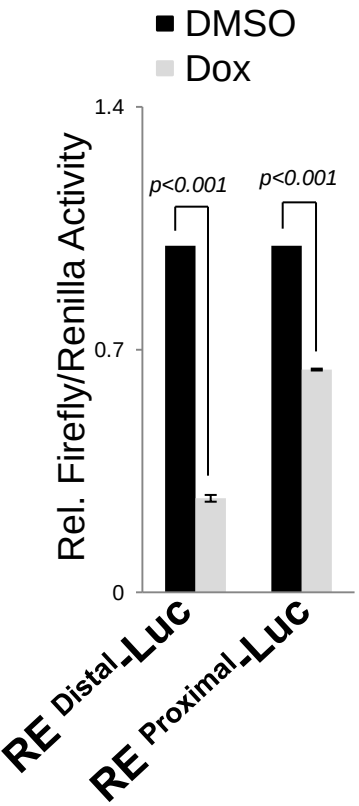
A


p<0.01
Relative miR-182 levels
5
0
-5
-10
-15
p53 WT
p53 Mut

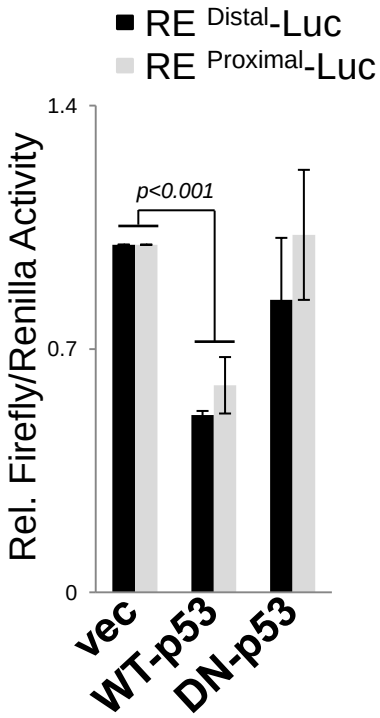
B


P53-RE proximal
P53-RE distal
RE-3
-625
RE-2
-1034
RE-1
-1116
RE-2
-5750
RE-1
-6480
7q32
TTTGGCAATGGTAGAACTCA
miR-182
miR-96
miR-183

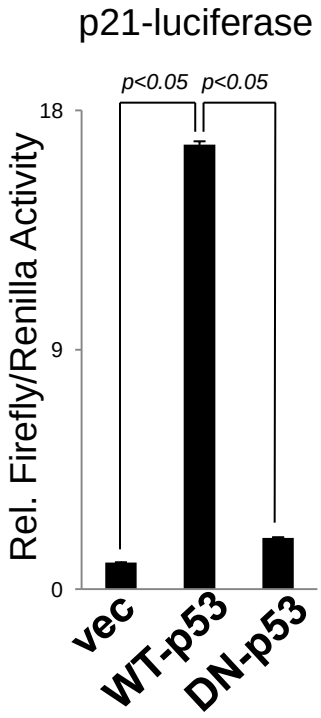
C


DMSO
Dox
Rel. Firefly/Renilla Activity
1.4
0.7
0
p<0.001
p<0.001
RE Distal-Luc
RE Proximal-Luc

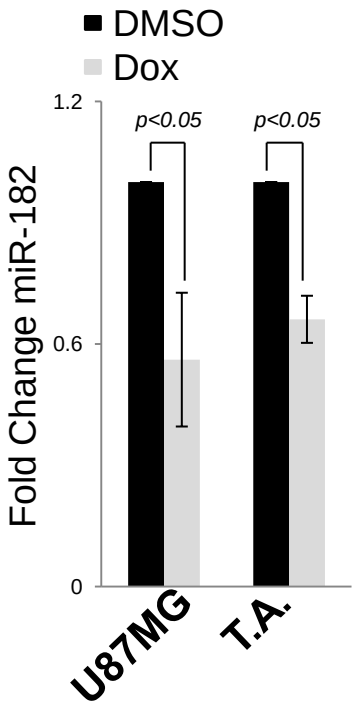
D

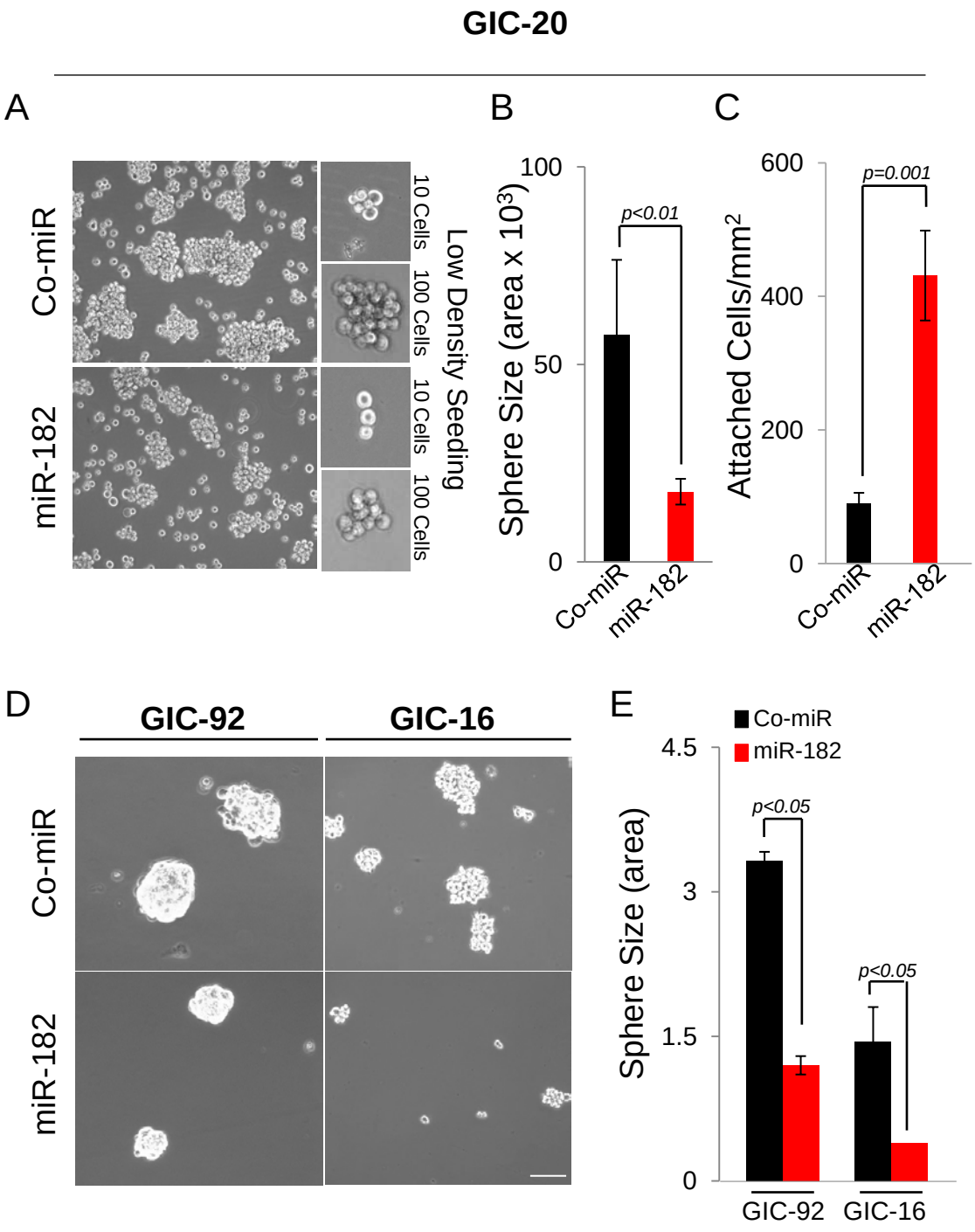

RE Distal-Luc
RE Proximal-Luc
Rel. Firefly/Renilla Activity
1.4
0.7
0
p<0.001
vec
WT-p53
DN-p53

E

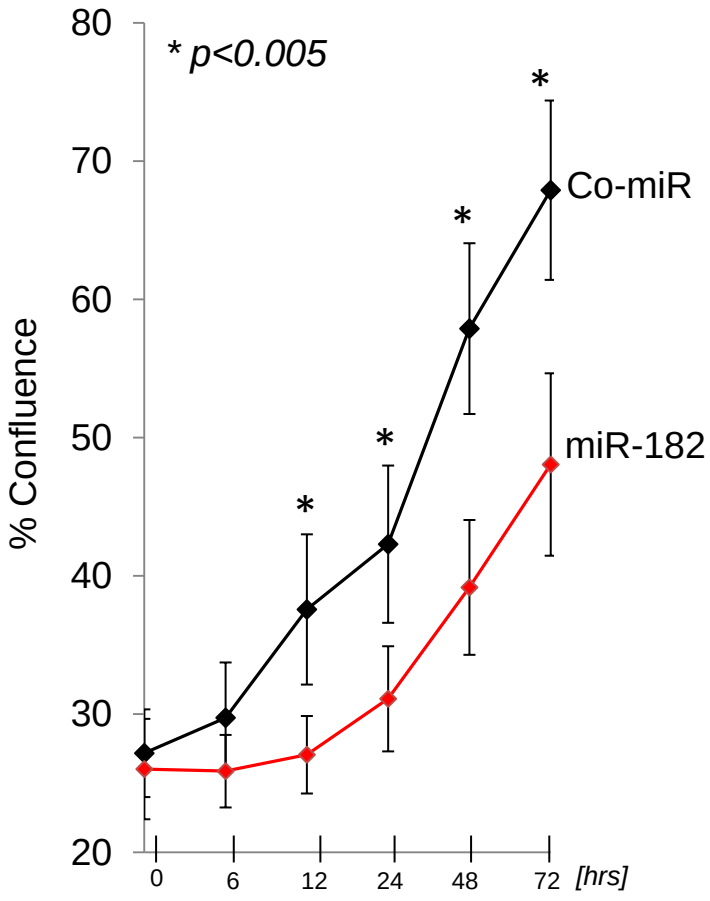

p21-luciferase
Rel. Firefly/Renilla Activity
18
9
0
p<0.05
p<0.05
vec
WT-p53
DN-p53

F

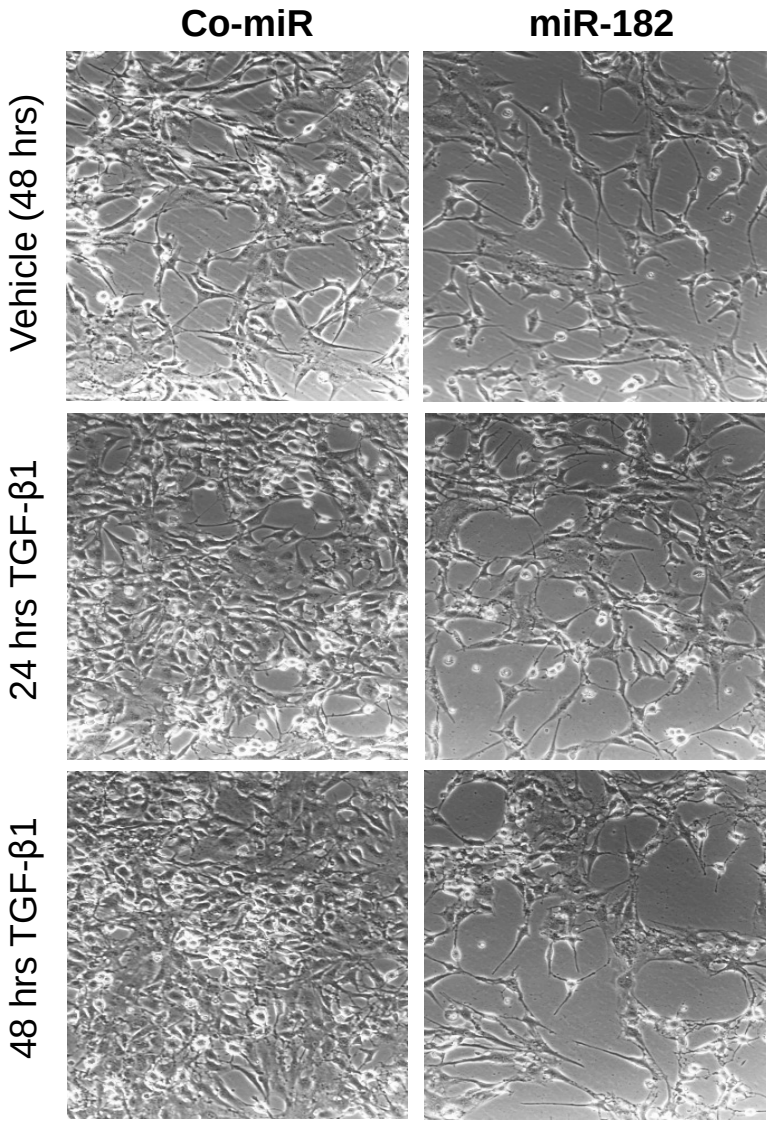

DMSO
Dox
Fold Change miR-182
1.2
0.6
0
p<0.05
p<0.05
U87MG
T.A.


GIC-20
A
Co-miR
miR-182
10 Cells
100 Cells
10 Cells
100 Cells
Low Density Seeding
B
Sphere Size (area x 10³)
100
50
0
p<0.01
Co-miR
miR-182
C
Attached Cells/mm²
600
400
200
0
p=0.001
Co-miR
miR-182
D
GIC-92
GIC-16
Co-miR
miR-182
E
Co-miR
miR-182
Sphere Size (area)
4.5
3
1.5
0
p<0.05
p<0.05
GIC-92
GIC-16

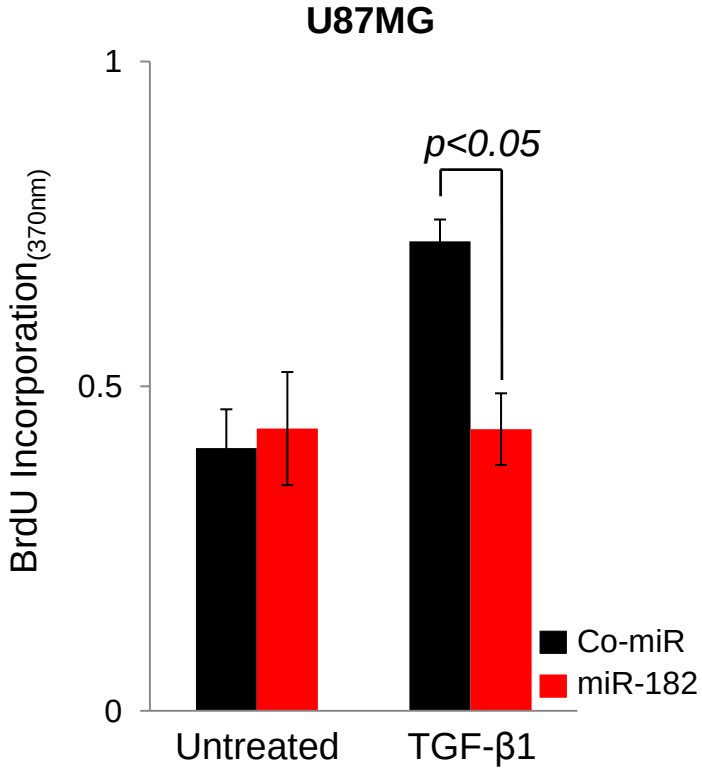
A

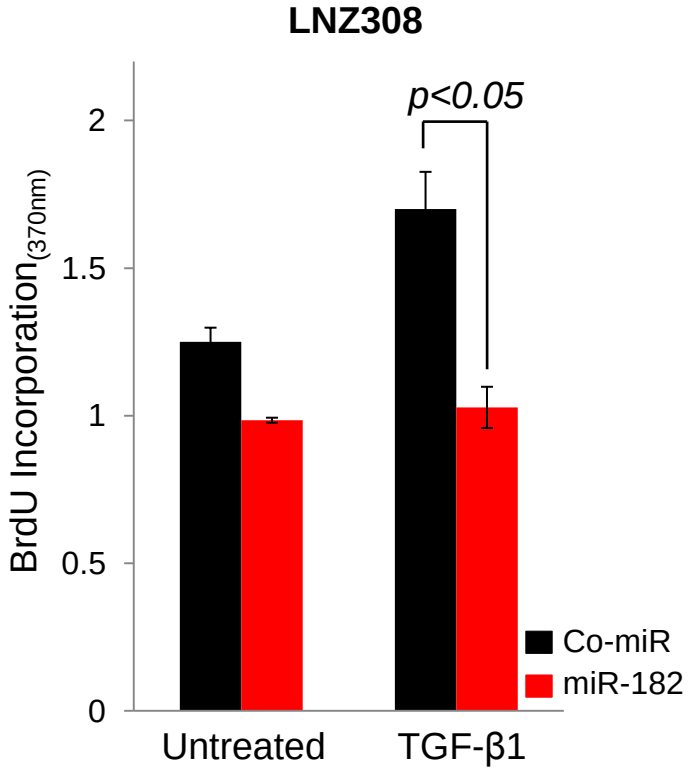

* p<0.005
% Confluence
80
70
60
50
40
30
20
0
6
12
24
48
72
[hrs]
Co-miR
miR-182
*
*
*
*

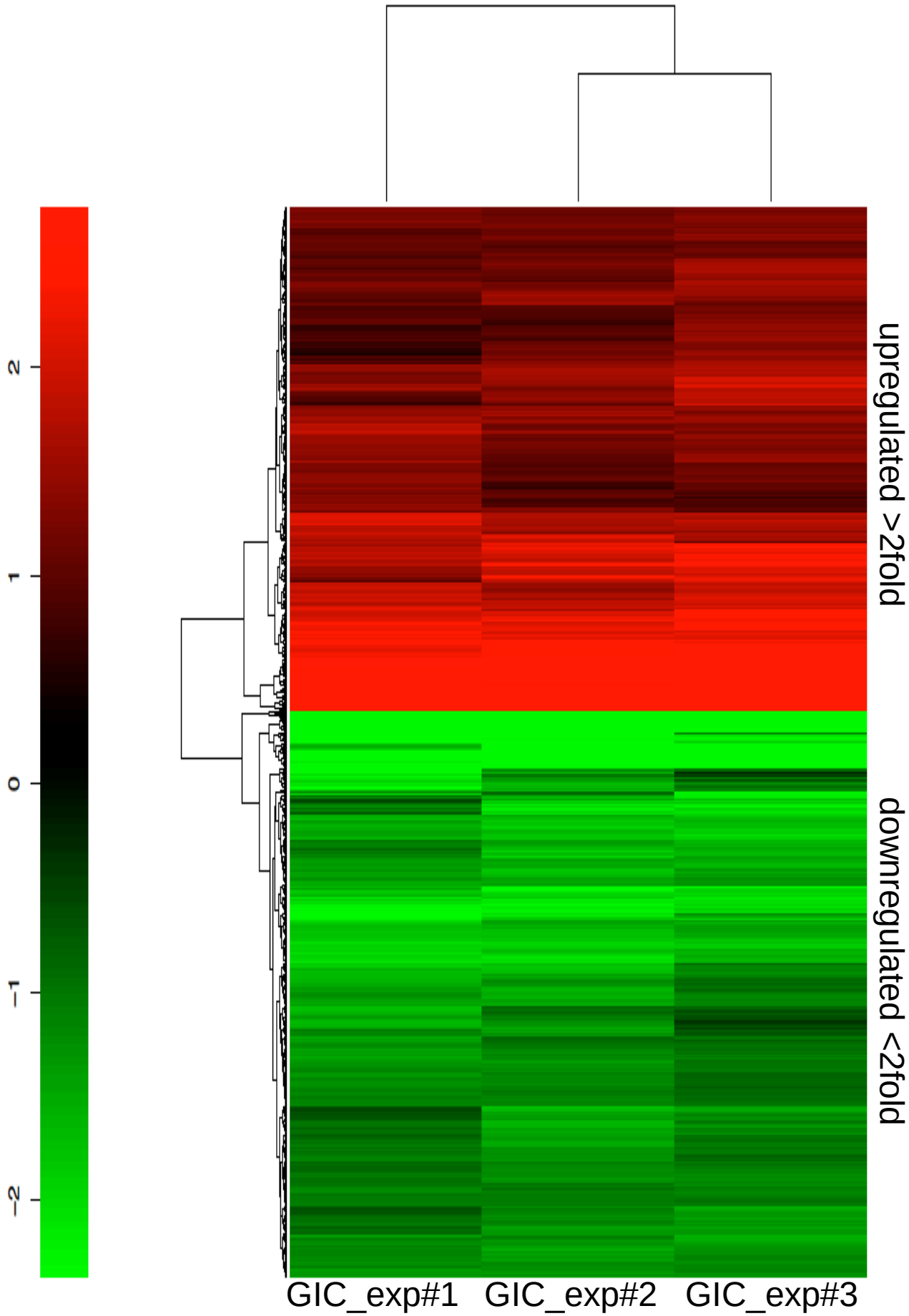
B


Co-miR
miR-182
Vehicle (48 hrs)
24 hrs TGF-β1
48 hrs TGF-β1

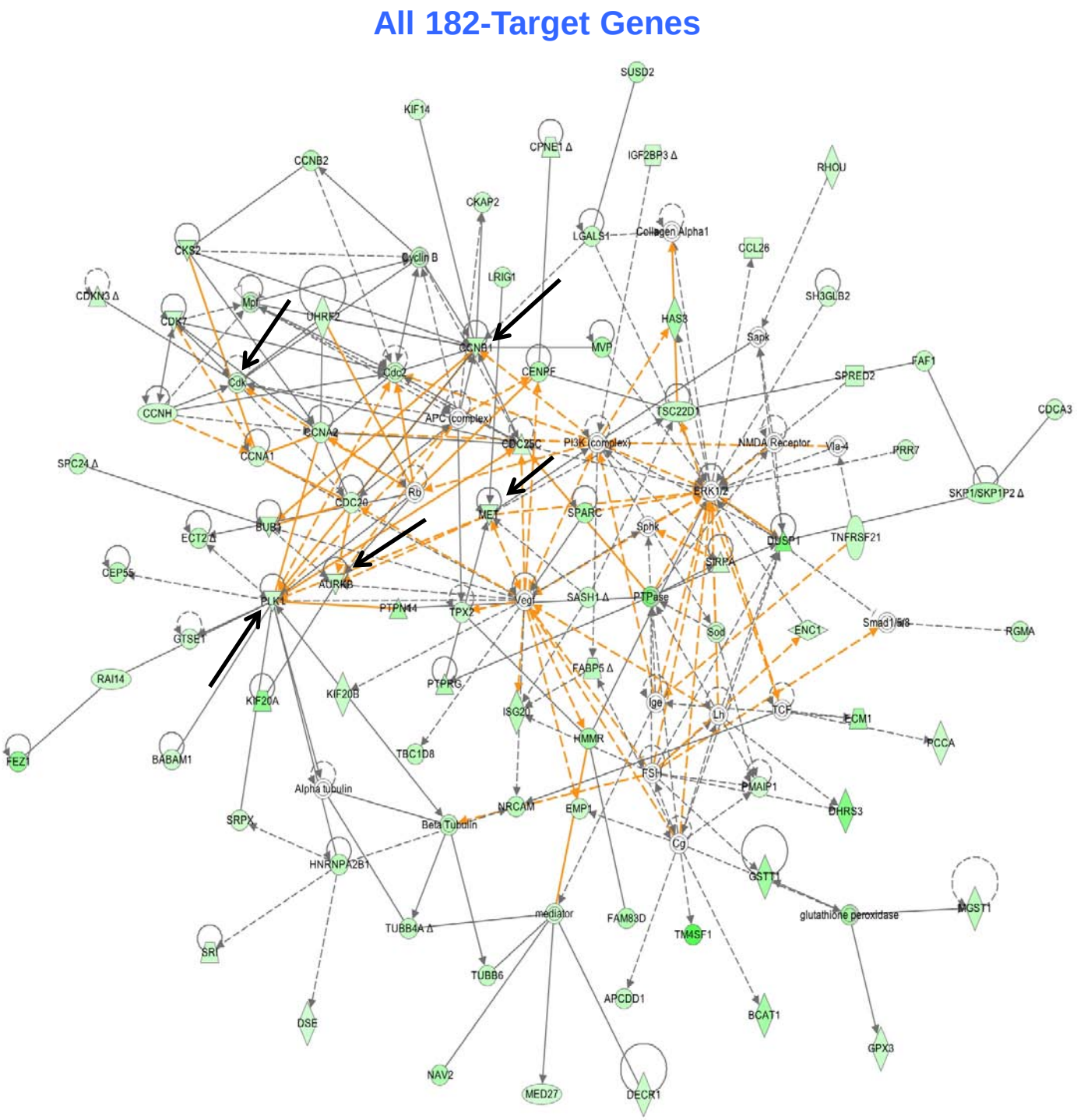
C


U87MG
BrdU Incorporation(370nm)
1
0.5
0
p<0.05
Co-miR
miR-182
Untreated
TGF-β1


LNZ308
BrdU Incorporation(370nm)
2
1.5
1
0.5
0
p<0.05
Co-miR
miR-182
Untreated
TGF-β1

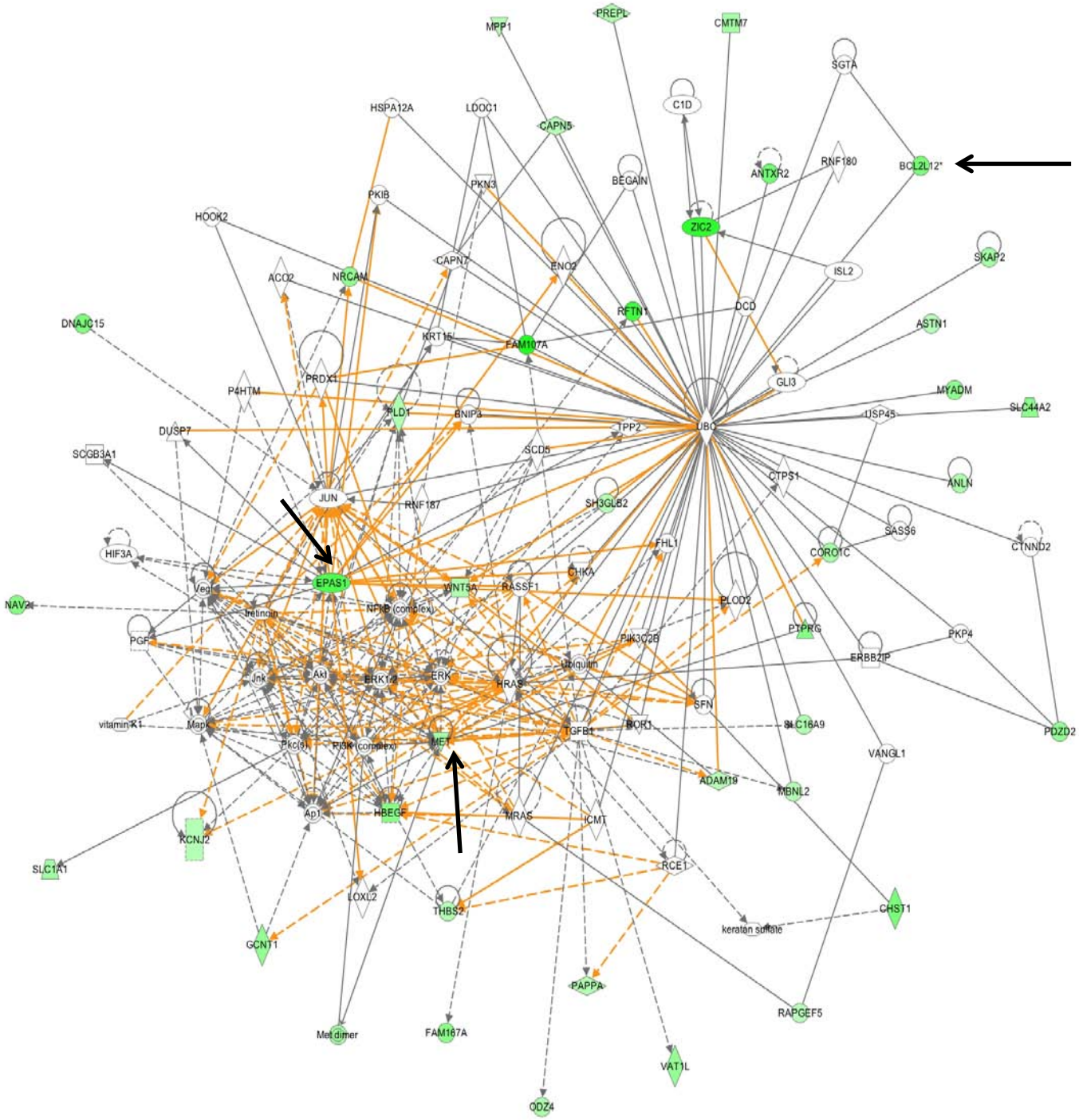

2
1
0
−1
−2
upregulated >2fold
downregulated <2fold
GIC_exp#1
GIC_exp#2
GIC_exp#3

A


All 182-Target Genes
SUSD2
KIF14
CPNE1 Δ
IGF2BP3 Δ
RHOJ
CCNB2
CKAP2
LGALS1
Collagen Alpha1
CCL26
CKS2
Cyclin B
LRIG1
SH3GLB2
CDKN3 Δ
Mpl
UHRF2
HAS3
CDK7
CCNB1
MVP
Sapk
Cdk
Cdc2
CENPF
FAF1
SPRED2
CCNH
APC (complex)
TSC22D1
CDCA3
CCNA2
CDC25C
PI3K (complex)
NMDA Receptor
Vla-4
PRR7
CCNA1
SPC24 Δ
Rb
ERK1/2
SKP1/SKP1P2 Δ
CDC20
MET
SPARC
Sphk
ECT2 Δ
BUB1
DUSP1
TNFRSF21
CEP55
SIRPA
AURKB
PLK1
Vegf
SASH1 Δ
PTPase
PTPN14
TPX2
Sod
ENC1
Smad1/5/8
RGMA
GTSE1
FABP5 Δ
RAI14
PTPRG
KIF20A
KIF20B
Ige
Lh
TCF
ECM1
ISG20
HMMR
PCCA
FEZ1
BABAM1
TBC1D8
FSH
PMAIP1
Alpha tubulin
DHRS3
SRPX
NRCAM
EMP1
Beta Tubulin
Cg
HNRNPA2B1
GSTT1
mediator
FAM83D
glutathione peroxidase
MGST1
TUBB4A Δ
TM4SF1
SRI
TUBB6
APCDD1
BCAT1
DSE
GPX3
NAV2
MED27
DECR1

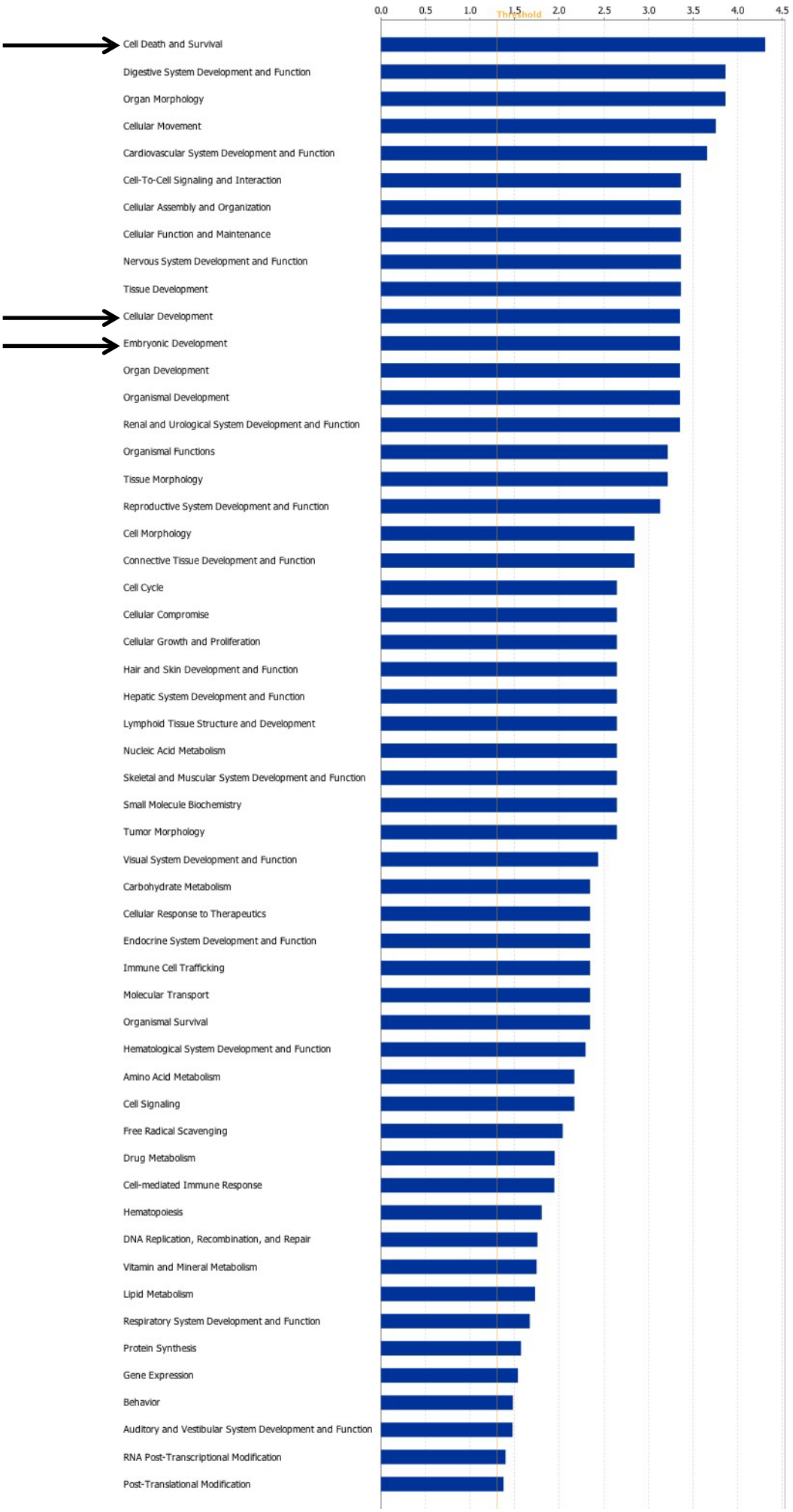
B

Direct 182-Target Genes

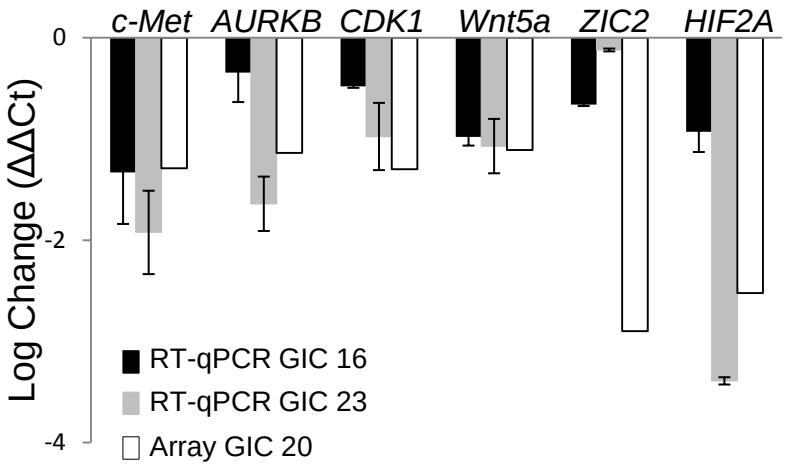


C

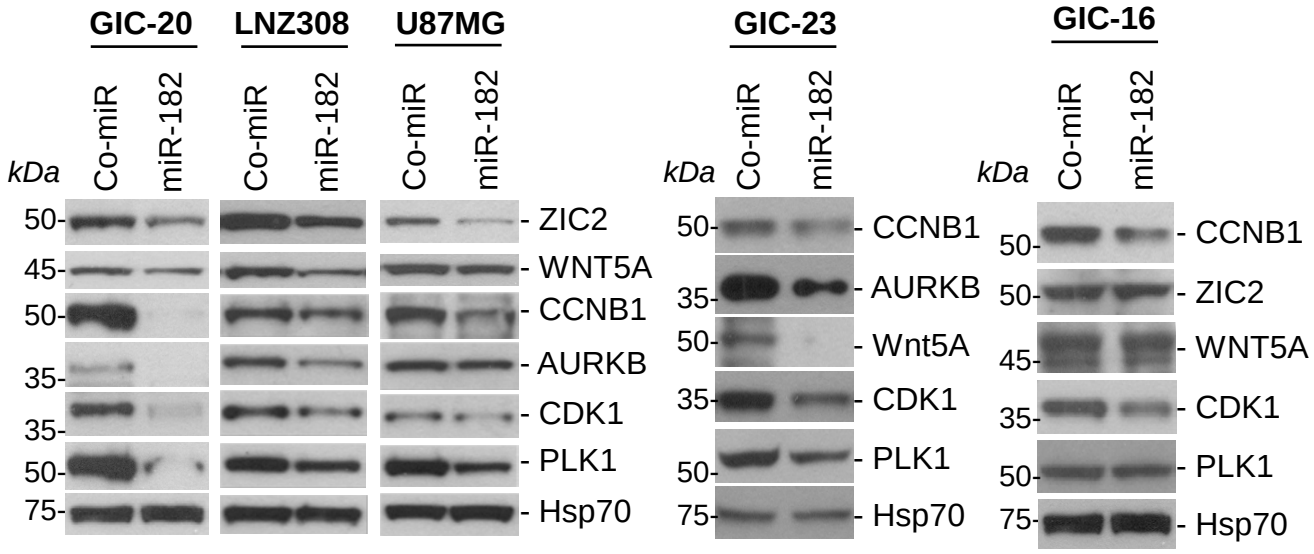
Upstream Regulator	Molecule Type	Predicted Activation State	Activation *z*-score	*p*-value of overlap	
1. CDKN1A	kinase	Activated	2.127	1.91E-17	All 182 Target Gene dataset
2. TP53	transcription regulator		-0.448	2.93E-15	
3. ERBB2	kinase	Inhibited	-3.196	9.08E-13	
4. TGFB1	growth factor	Inhibited	-4.628	2.45E-12	
5. HGF	growth factor	Inhibited	-4.786	3.05E-10	
1. TGFB1	growth factor	Inhibited	-2.533	0.0000274	Direct 182 Target Gene dataset


0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
Threshold
Cell Death and Survival
Digestive System Development and Function
Organ Morphology
Cellular Movement
Cardiovascular System Development and Function
Cell-To-Cell Signaling and Interaction
Cellular Assembly and Organization
Cellular Function and Maintenance
Nervous System Development and Function
Tissue Development
Cellular Development
Embryonic Development
Organ Development
Organismal Development
Renal and Urological System Development and Function
Organismal Functions
Tissue Morphology
Reproductive System Development and Function
Cell Morphology
Connective Tissue Development and Function
Cell Cycle
Cellular Compromise
Cellular Growth and Proliferation
Hair and Skin Development and Function
Hepatic System Development and Function
Lymphoid Tissue Structure and Development
Nucleic Acid Metabolism
Skeletal and Muscular System Development and Function
Small Molecule Biochemistry
Tumor Morphology
Visual System Development and Function
Carbohydrate Metabolism
Cellular Response to Therapeutics
Endocrine System Development and Function
Immune Cell Trafficking
Molecular Transport
Organismal Survival
Hematological System Development and Function
Amino Acid Metabolism
Cell Signaling
Free Radical Scavenging
Drug Metabolism
Cell-mediated Immune Response
Hematopoiesis
DNA Replication, Recombination, and Repair
Vitamin and Mineral Metabolism
Lipid Metabolism
Respiratory System Development and Function
Protein Synthesis
Gene Expression
Behavior
Auditory and Vestibular System Development and Function
RNA Post-Transcriptional Modification
Post-Translational Modification

A

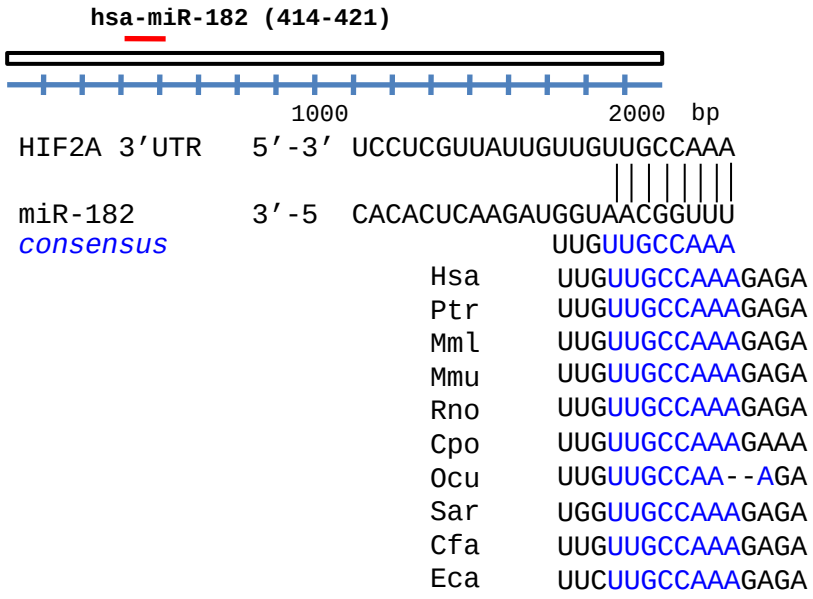

c-Met
AURKB
CDK1
Wnt5a
ZIC2
HIF2A
0
-2
-4
Log Change (ΔΔCt)
RT-qPCR GIC 16
RT-qPCR GIC 23
Array GIC 20

B


GIC-20
LNZ308
U87MG
GIC-23
GIC-16
Co-miR
miR-182
kDa
50-
45-
35-
75-
ZIC2
WNT5A
CCNB1
AURKB
CDK1
PLK1
Hsp70
Wnt5A

A

HIF2A 3'-UTR (2043 bp)



Conserved

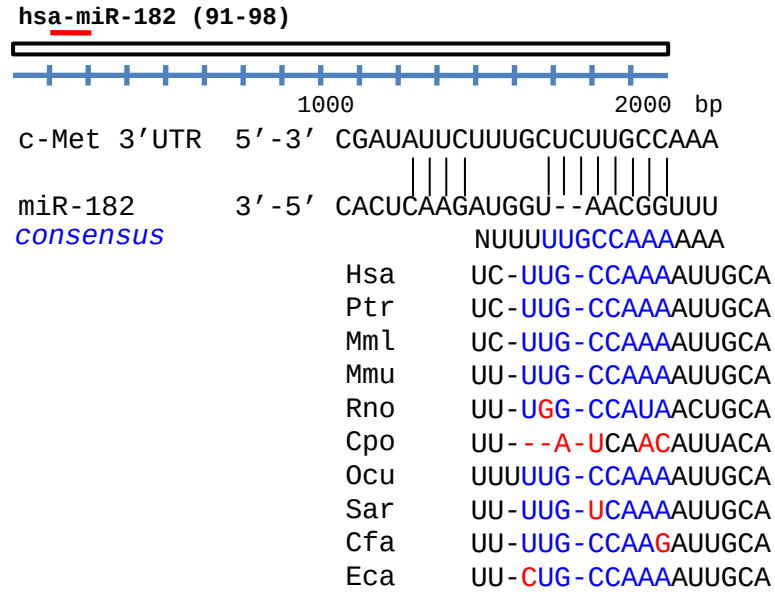
microRNA	HIF2A 3'UTR position	Seed Match	Context + score
hsa-miR-182	414-421	8mer	-0.24

Poorly Conserved

microRNA	HIF2A 3'UTR position	Seed Match	Context + score
hsa-miR-182	1653-1660	8mer	-0.32

B

c-Met 3'-UTR (2262 bp)

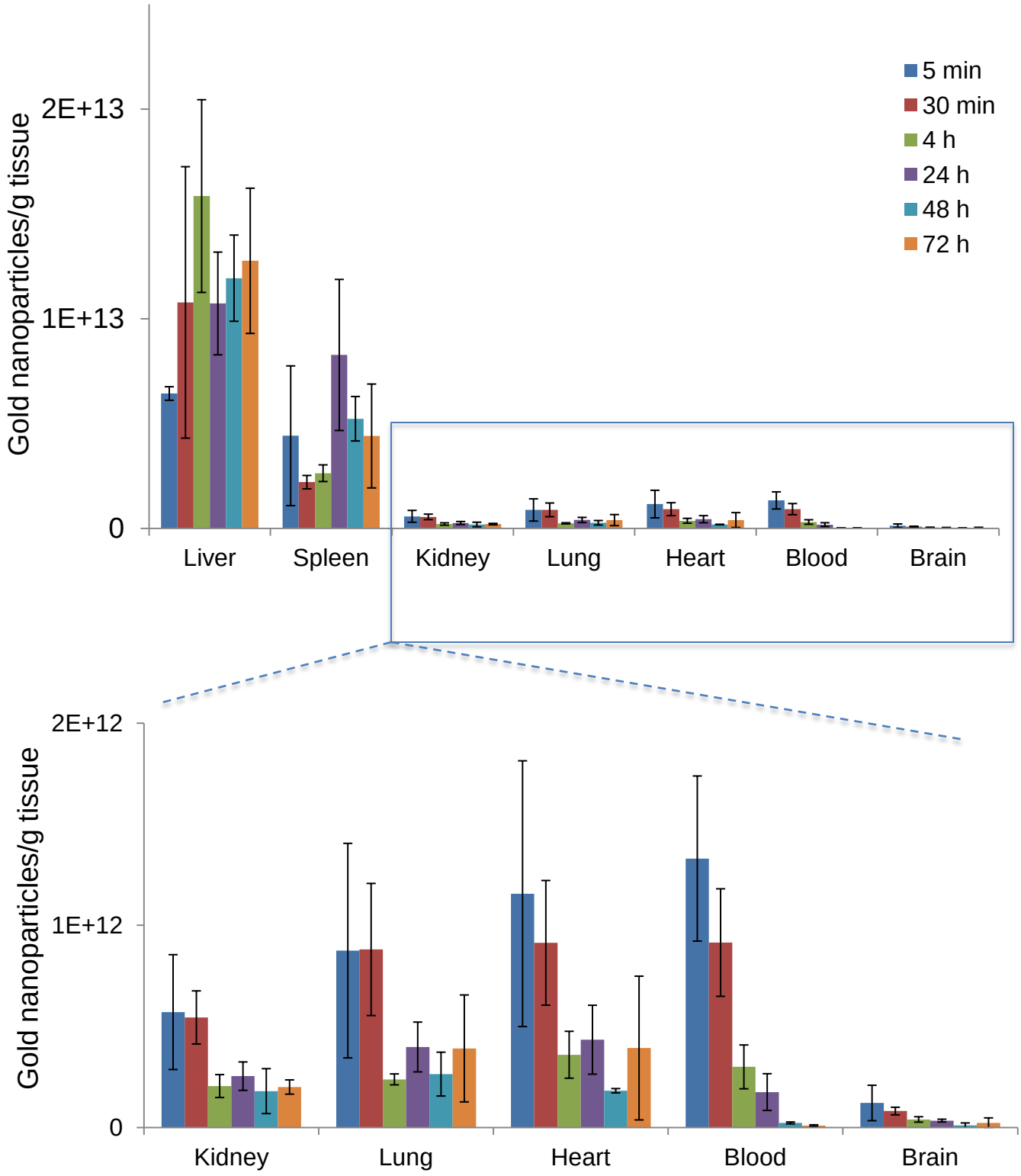


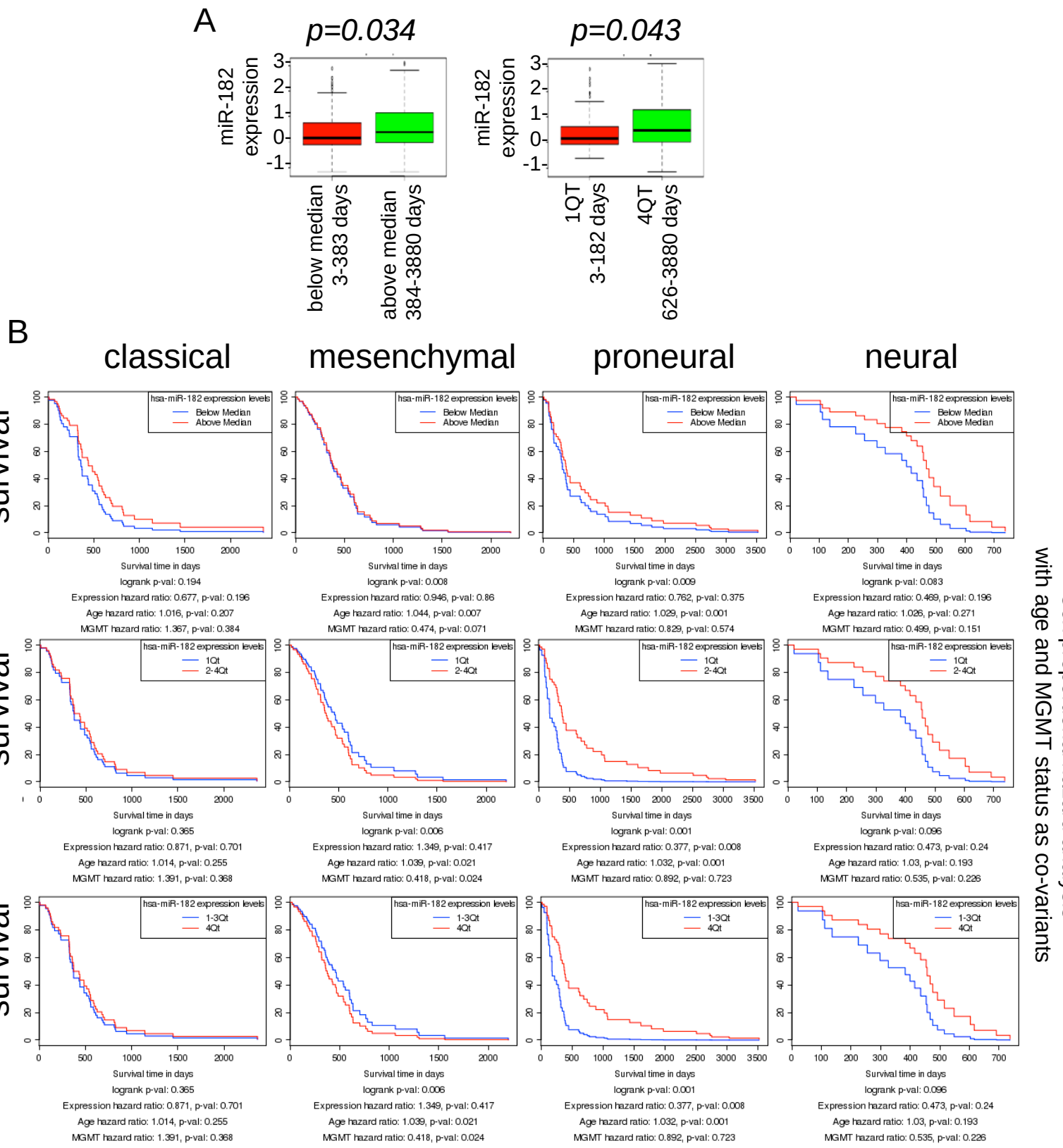
Conserved

microRNA	c-Met 3'UTR position	Seed Match	Context + score
hsa-miR-182	91-98	8mer	-0.35

Poorly Conserved

microRNA	c-Met 3'UTR position	Seed Match	Context + score
hsa-miR-182	698-704	7mer-m8	-0.02
hsa-miR-182	1655-1661	7mer-m8	-0.11


Gold nanoparticles/g tissue
2E+13
1E+13
0
5 min
30 min
4 h
24 h
48 h
72 h
Liver
Spleen
Kidney
Lung
Heart
Blood
Brain
Gold nanoparticles/g tissue
2E+12
1E+12
0
Kidney
Lung
Heart
Blood
Brain


A
p=0.034
miR-182 expression
below median 3-383 days
above median 384-3880 days
p=0.043
miR-182 expression
1QT 3-182 days
4QT 626-3880 days
B
classical
mesenchymal
proneural
neural
survival
hsa-miR-182 expression levels
Below Median
Above Median
1Qt
2-4Qt
1-3Qt
4Qt
Survival time in days
logrank p-val: 0.194
Expression hazard ratio: 0.677, p-val: 0.196
Age hazard ratio: 1.016, p-val: 0.207
MGMT hazard ratio: 1.367, p-val: 0.384
logrank p-val: 0.008
Expression hazard ratio: 0.946, p-val: 0.86
Age hazard ratio: 1.044, p-val: 0.007
MGMT hazard ratio: 0.474, p-val: 0.071
logrank p-val: 0.009
Expression hazard ratio: 0.762, p-val: 0.375
Age hazard ratio: 1.029, p-val: 0.001
MGMT hazard ratio: 0.829, p-val: 0.574
logrank p-val: 0.083
Expression hazard ratio: 0.469, p-val: 0.196
Age hazard ratio: 1.026, p-val: 0.271
MGMT hazard ratio: 0.499, p-val: 0.151
logrank p-val: 0.365
Expression hazard ratio: 0.871, p-val: 0.701
Age hazard ratio: 1.014, p-val: 0.255
MGMT hazard ratio: 1.391, p-val: 0.368
logrank p-val: 0.006
Expression hazard ratio: 1.349, p-val: 0.417
Age hazard ratio: 1.039, p-val: 0.021
MGMT hazard ratio: 0.418, p-val: 0.024
logrank p-val: 0.001
Expression hazard ratio: 0.377, p-val: 0.008
Age hazard ratio: 1.032, p-val: 0.001
MGMT hazard ratio: 0.892, p-val: 0.723
logrank p-val: 0.096
Expression hazard ratio: 0.473, p-val: 0.24
Age hazard ratio: 1.03, p-val: 0.193
MGMT hazard ratio: 0.535, p-val: 0.226
Cox proportional hazard analysis
with age and MGMT status as co-variants