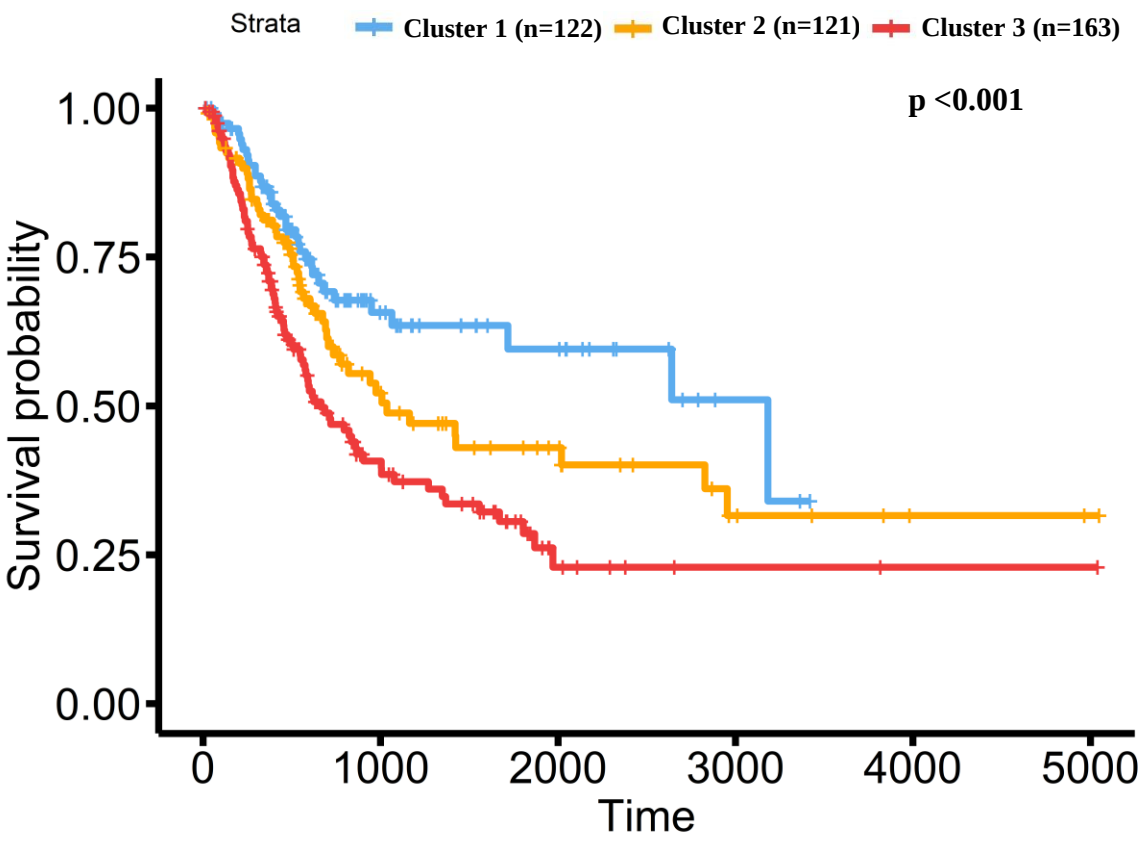
Fig. 1B

BLCA


Strata
Cluster 1 (n=122)
Cluster 2 (n=121)
Cluster 3 (n=163)
p <0.001
Survival probability
1.00
0.75
0.50
0.25
0.00
0
1000
2000
3000
4000
5000
Time

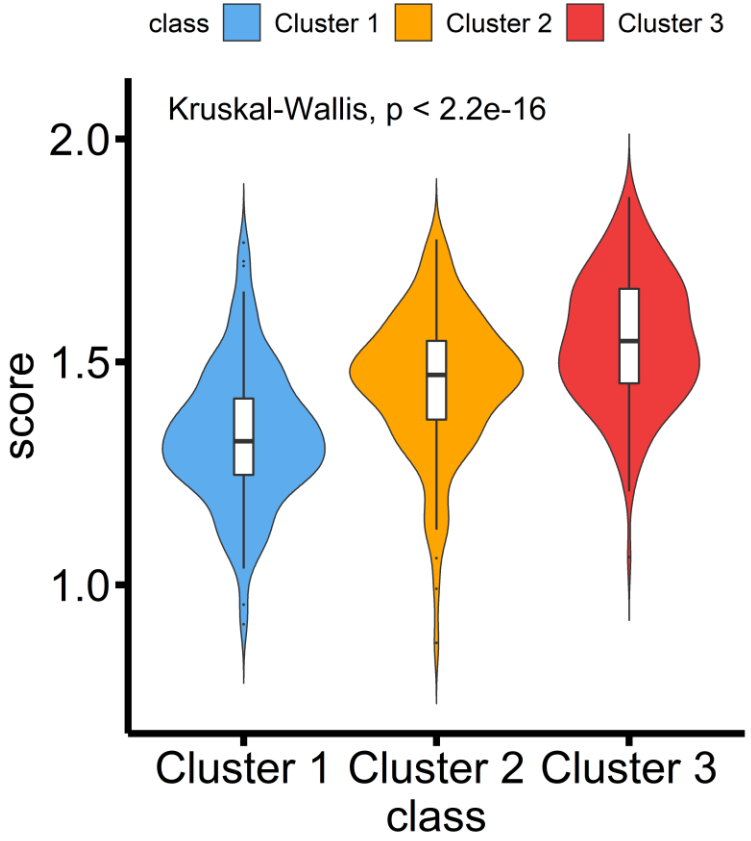
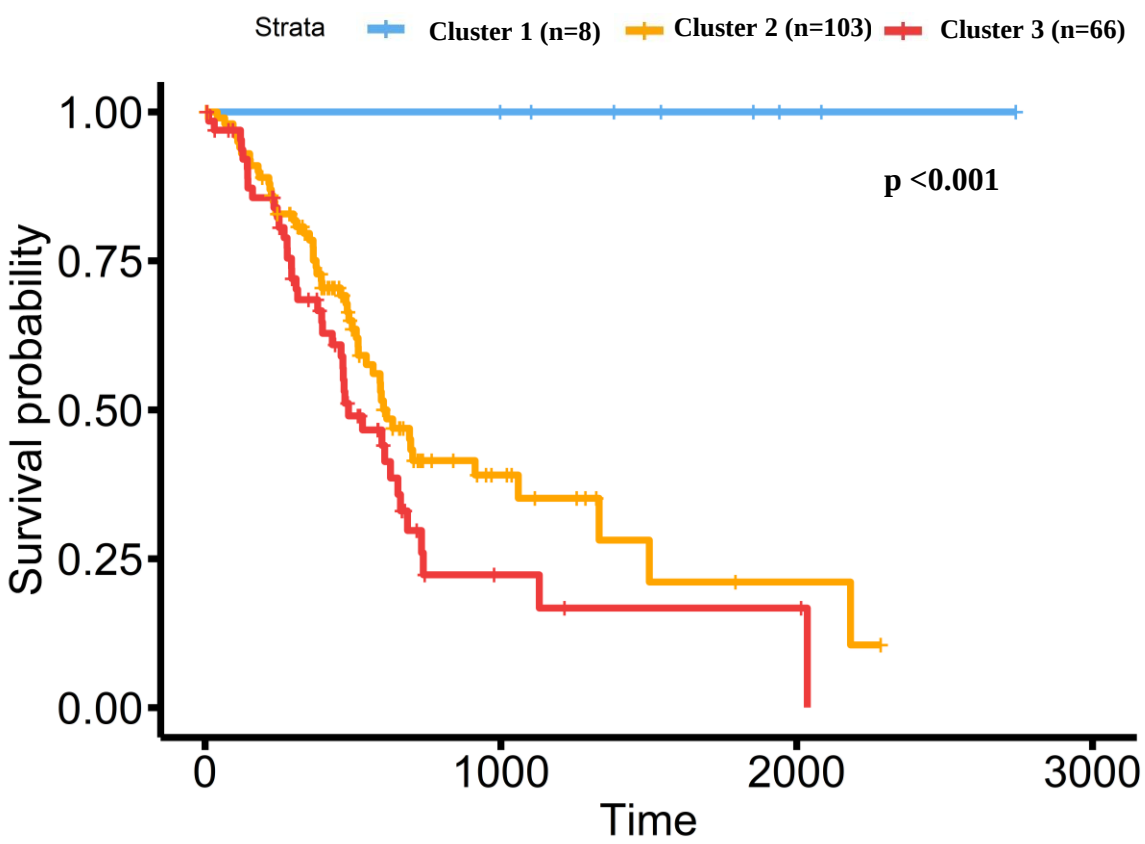

class
Cluster 1
Cluster 2
Cluster 3
Kruskal-Wallis, p < 2.2e-16
score
2.0
1.5
1.0
Cluster 1
Cluster 2
Cluster 3
class

Fig. 1B

PAAD


Strata
Cluster 1 (n=8)
Cluster 2 (n=103)
Cluster 3 (n=66)
p <0.001
Survival probability
1.00
0.75
0.50
0.25
0.00
0
1000
2000
3000
Time

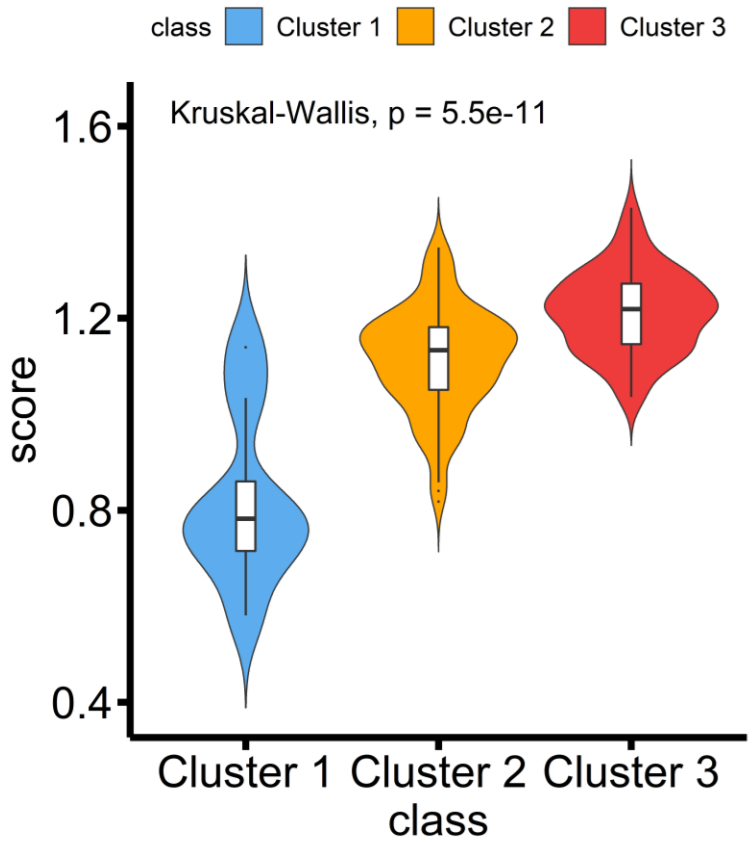
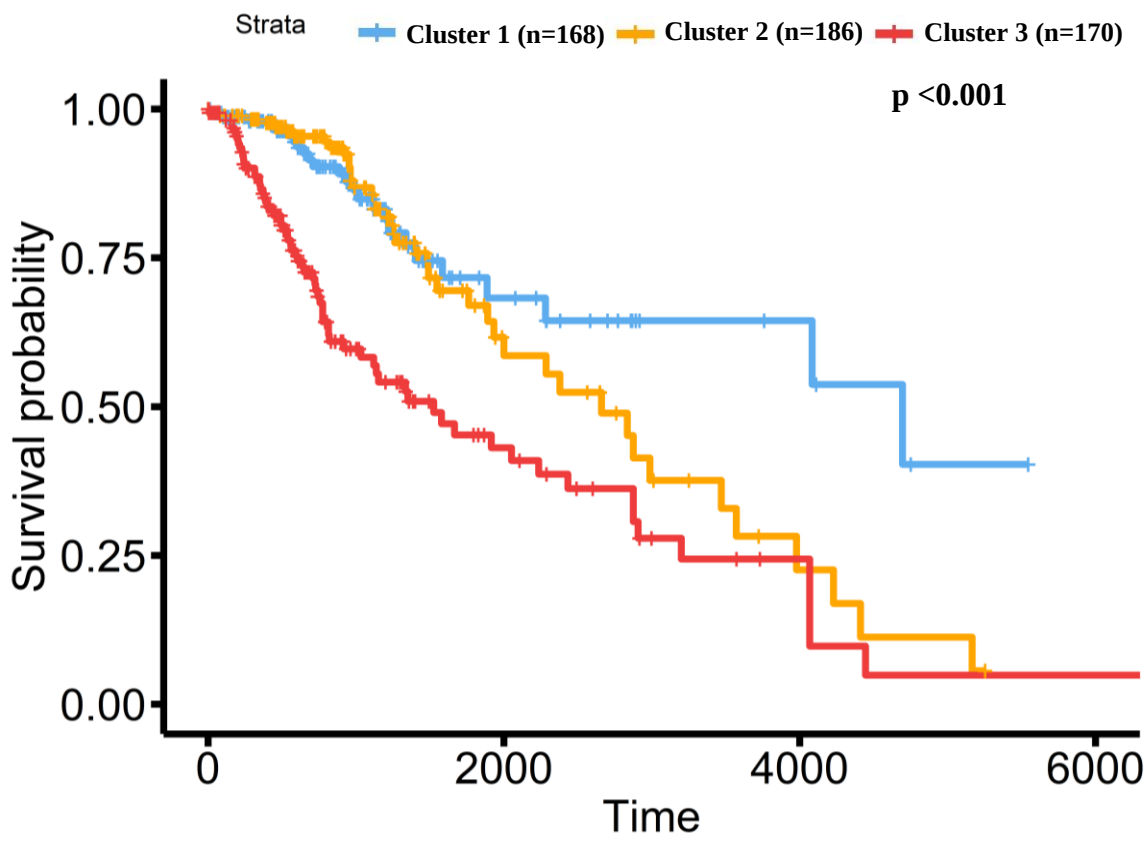

class
Cluster 1
Cluster 2
Cluster 3
Kruskal-Wallis, p = 5.5e-11
score
1.6
1.2
0.8
0.4
Cluster 1
Cluster 2
Cluster 3
class

Fig. 1B

LGG


Strata
Cluster 1 (n=168)
Cluster 2 (n=186)
Cluster 3 (n=170)
p <0.001
Survival probability
1.00
0.75
0.50
0.25
0.00
0
2000
4000
6000
Time

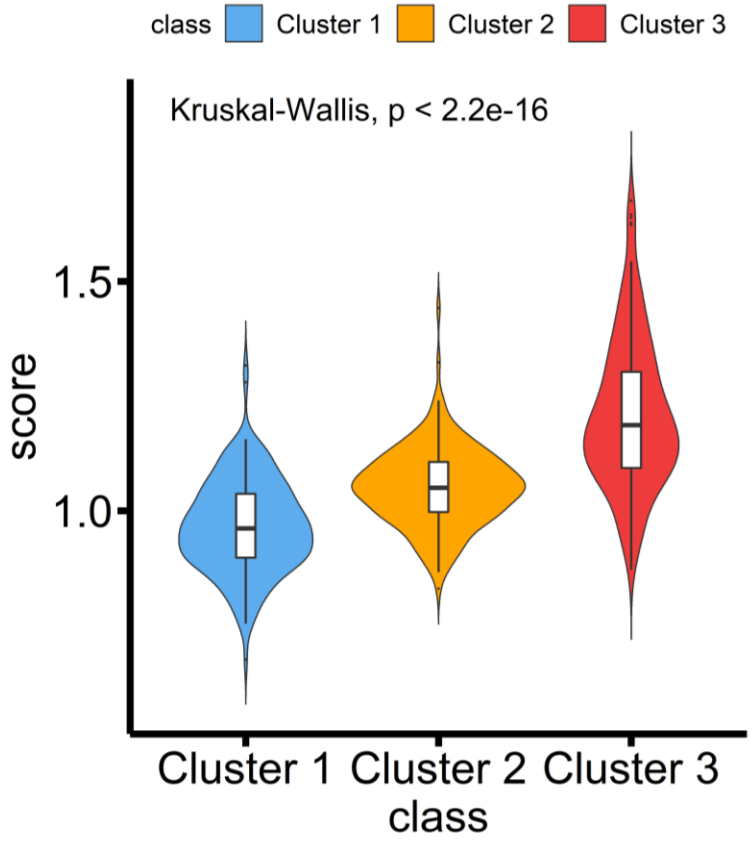
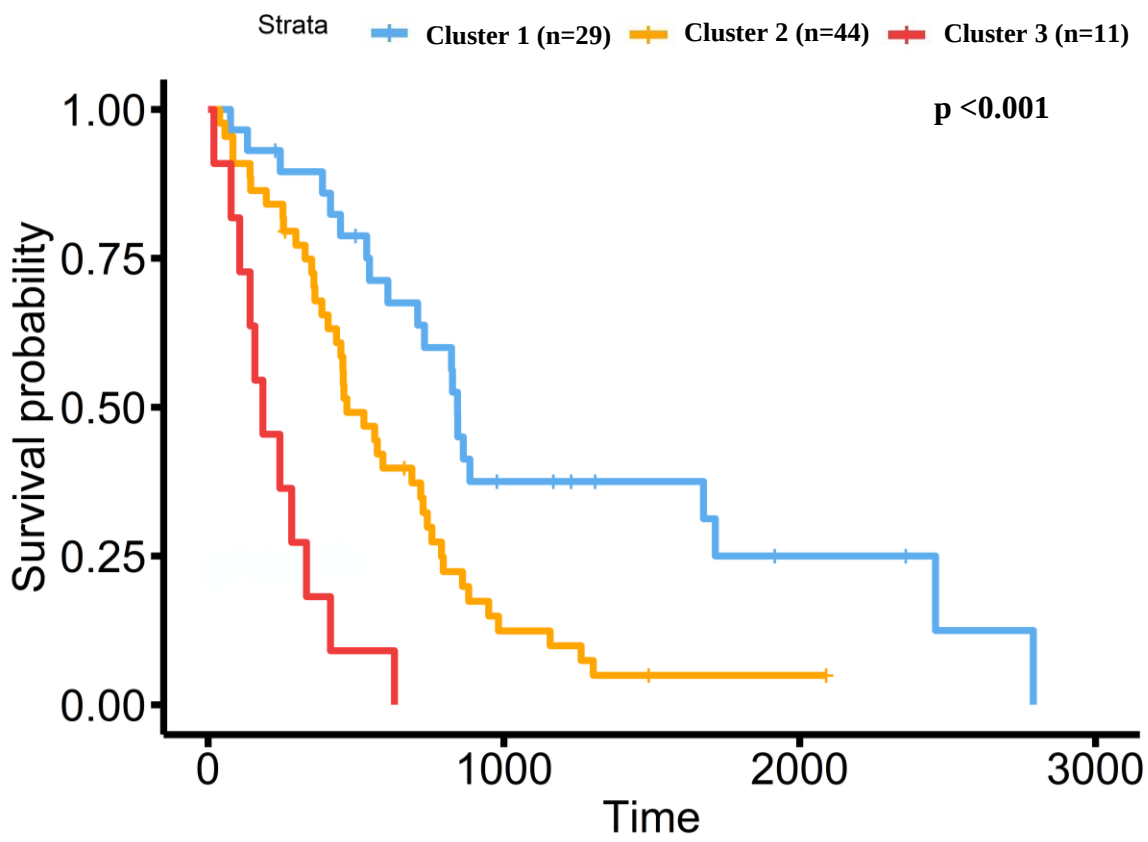

class
Cluster 1
Cluster 2
Cluster 3
Kruskal-Wallis, p < 2.2e-16
score
1.5
1.0
Cluster 1
Cluster 2
Cluster 3
class

Fig. 1B

MESO


Strata
Cluster 1 (n=29)
Cluster 2 (n=44)
Cluster 3 (n=11)
p <0.001
Survival probability
1.00
0.75
0.50
0.25
0.00
0
1000
2000
3000
Time

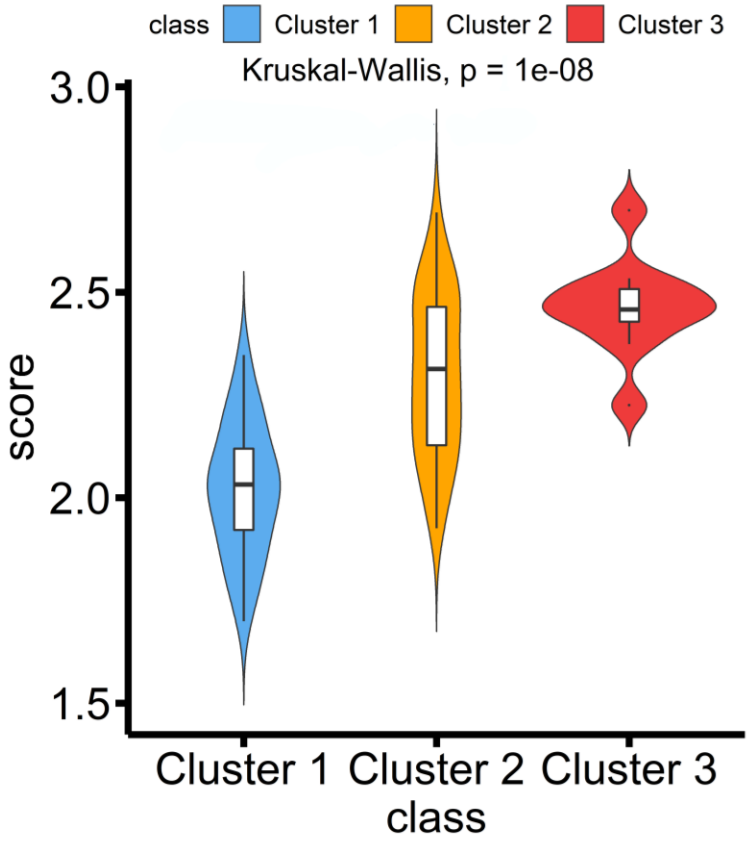
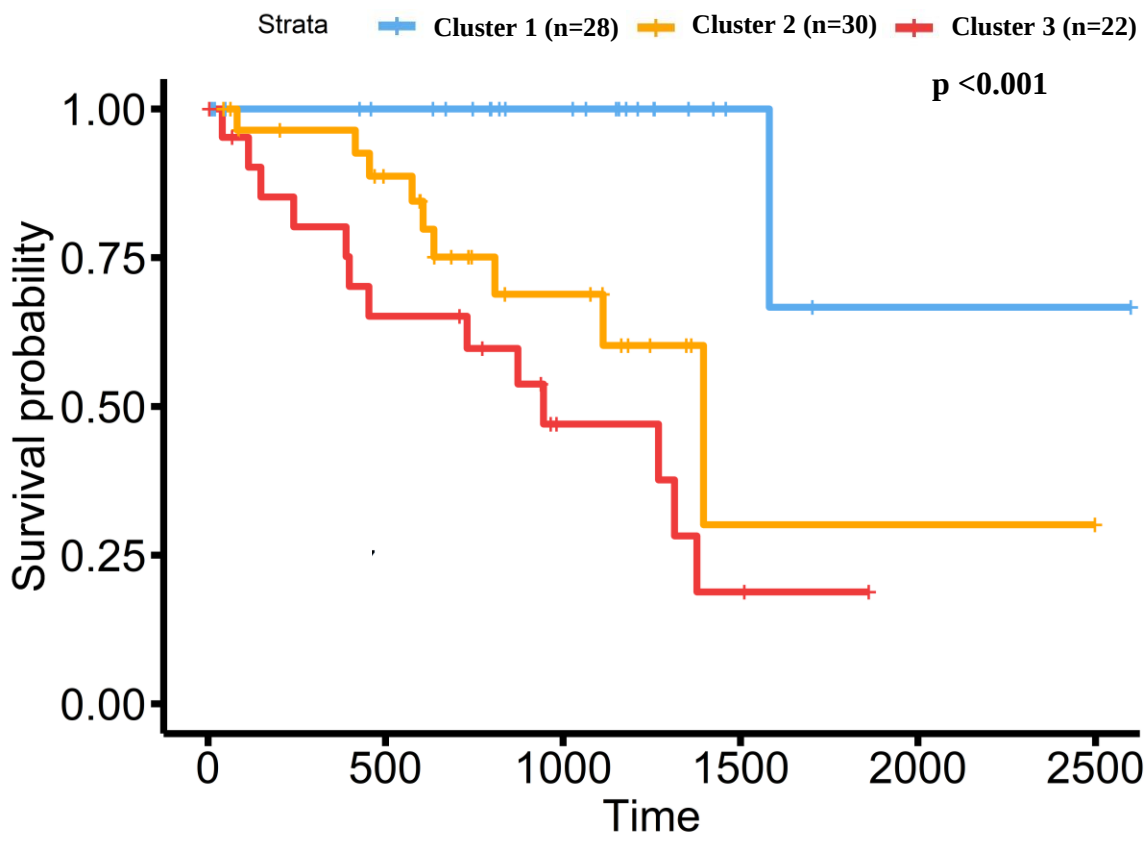

class
Cluster 1
Cluster 2
Cluster 3
Kruskal-Wallis, p = 1e-08
score
3.0
2.5
2.0
1.5
Cluster 1
Cluster 2
Cluster 3
class

Fig. 1B

UVM


Strata
Cluster 1 (n=28)
Cluster 2 (n=30)
Cluster 3 (n=22)
p <0.001
Survival probability
1.00
0.75
0.50
0.25
0.00
0
500
1000
1500
2000
2500
Time

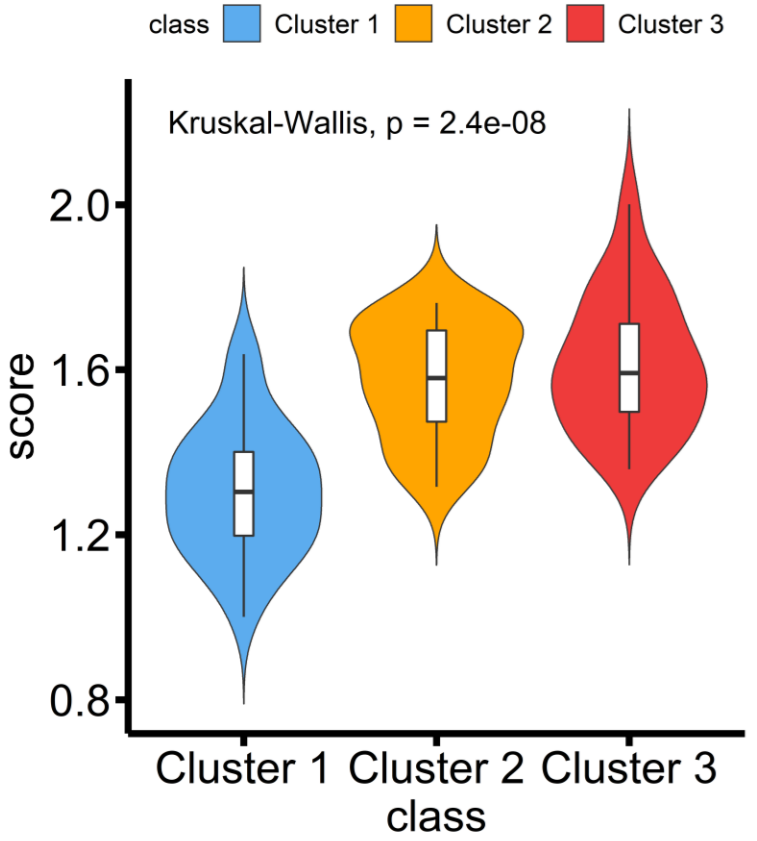

class
Cluster 1
Cluster 2
Cluster 3
Kruskal-Wallis, p = 2.4e-08
score
2.0
1.6
1.2
0.8
Cluster 1
Cluster 2
Cluster 3
class

Fig. 1C

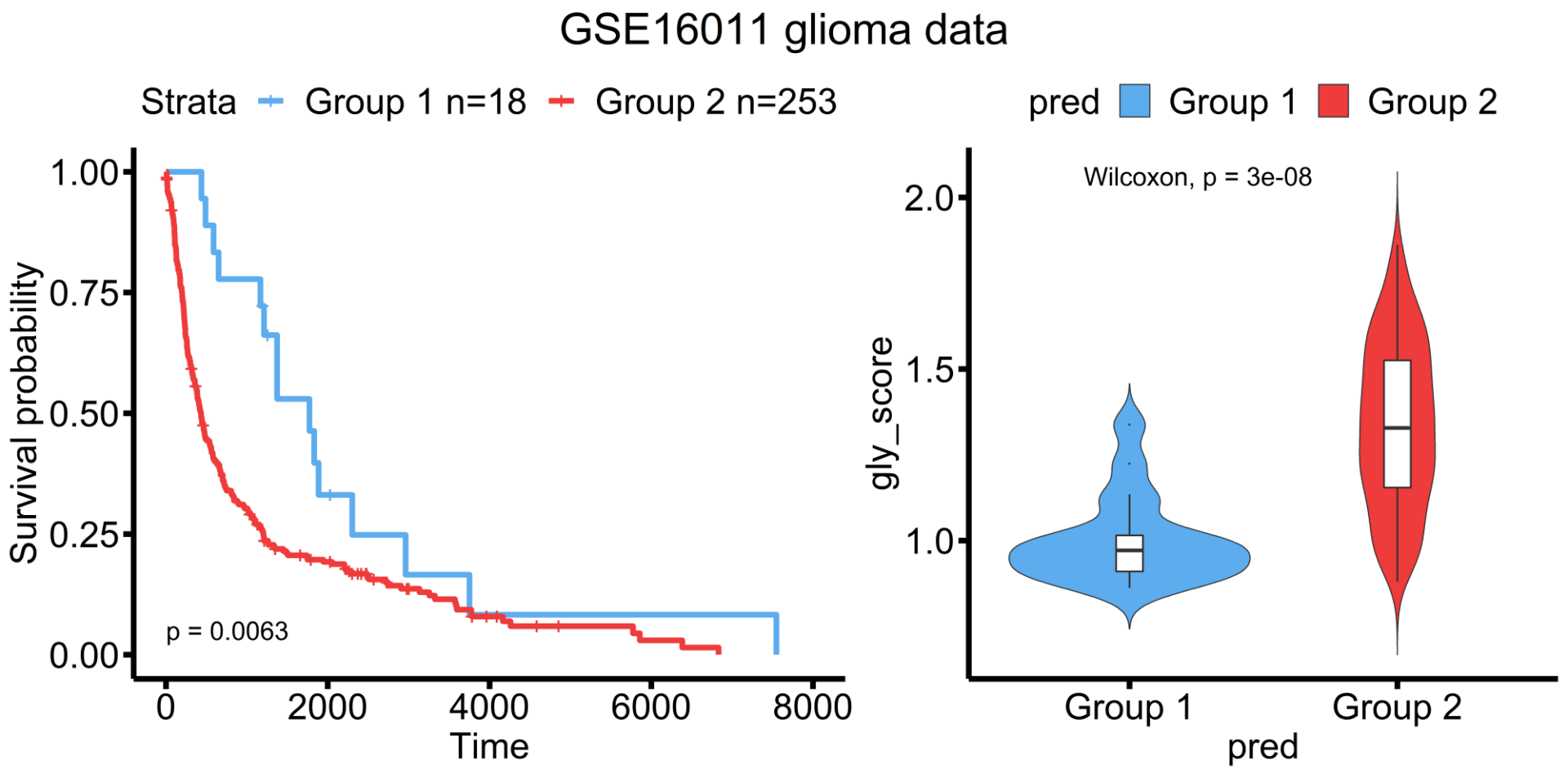

GSE16011 glioma data
Strata
Group 1 n=18
Group 2 n=253
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.0063
0
2000
4000
6000
8000
Time
pred
Group 1
Group 2
Wilcoxon, p = 3e-08
gly_score
2.0
1.5
1.0
Group 1
Group 2
pred

Fig. 1C

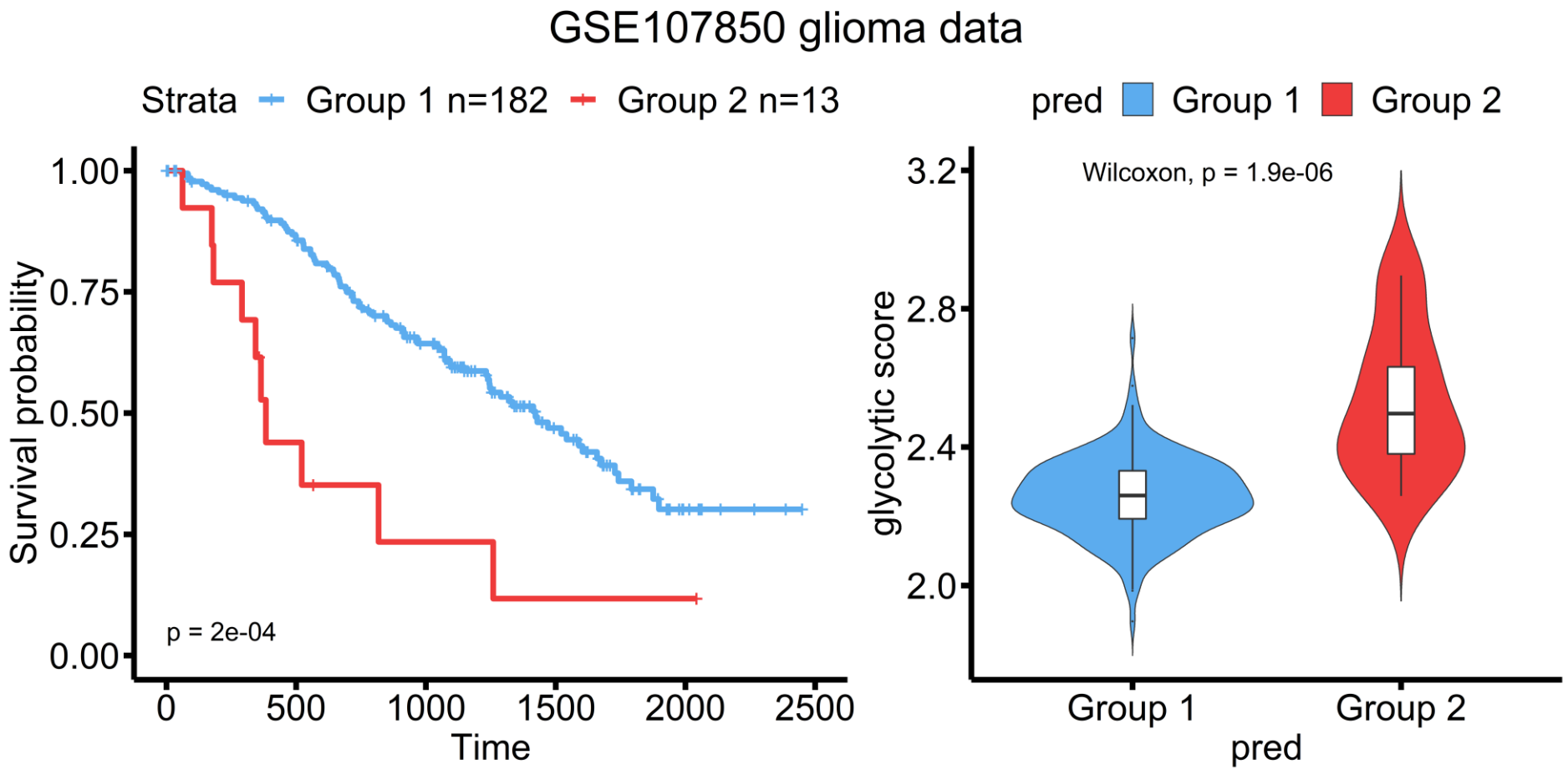

GSE107850 glioma data
Strata
Group 1 n=182
Group 2 n=13
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 2e-04
0
500
1000
1500
2000
2500
Time
pred
Group 1
Group 2
Wilcoxon, p = 1.9e-06
glycolytic score
3.2
2.8
2.4
2.0
Group 1
Group 2
pred

Fig. 1D

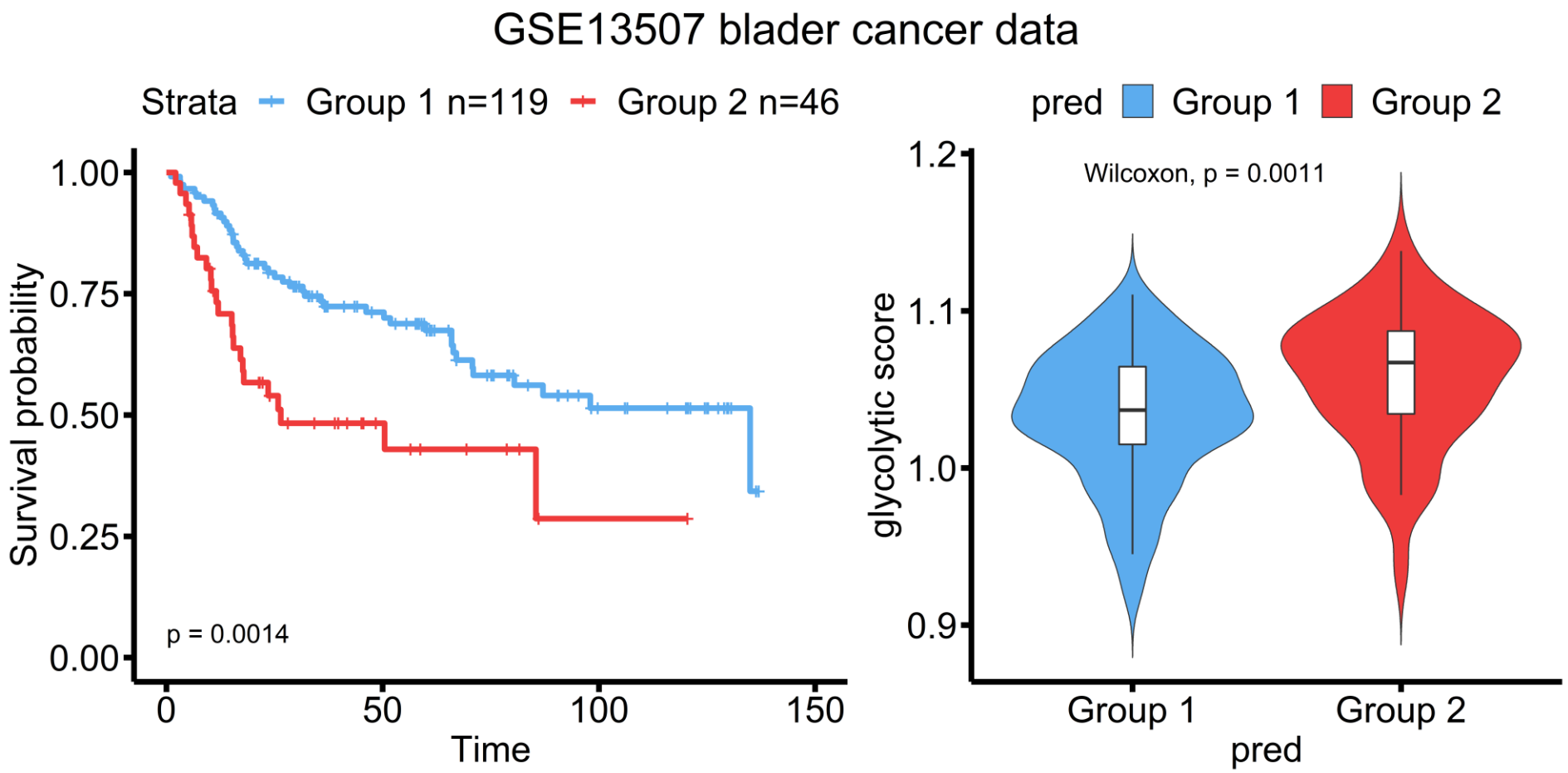

GSE13507 blader cancer data
Strata
Group 1 n=119
Group 2 n=46
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.0014
0
50
100
150
Time
pred
Group 1
Group 2
Wilcoxon, p = 0.0011
glycolytic score
1.2
1.1
1.0
0.9
Group 1
Group 2
pred

Fig. 1D

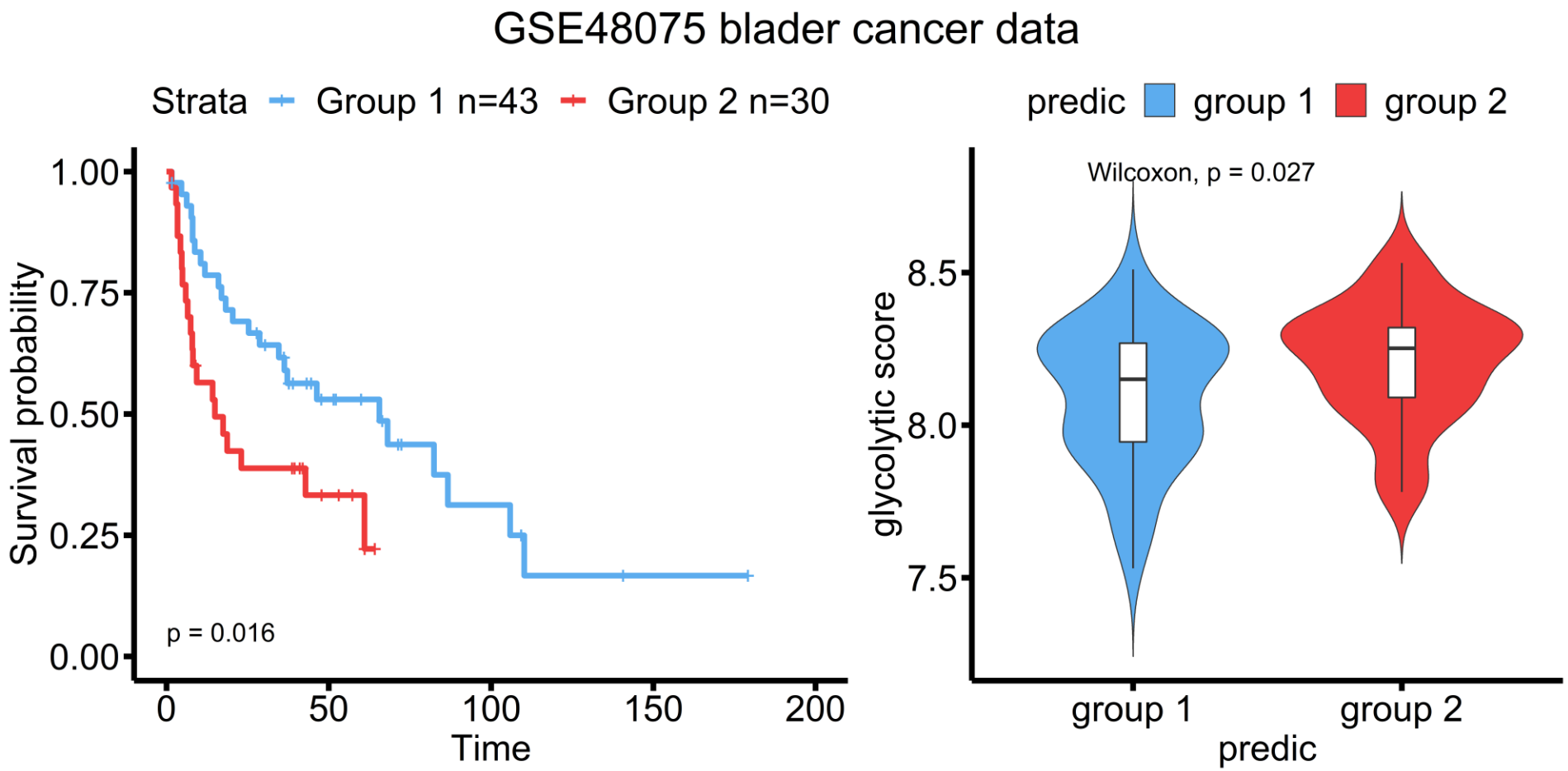

GSE48075 blader cancer data
Strata
Group 1 n=43
Group 2 n=30
Survival probability
1.00
0.75
0.50
0.25
0.00
p = 0.016
0
50
100
150
200
Time
predic
group 1
group 2
Wilcoxon, p = 0.027
glycolytic score
8.5
8.0
7.5
group 1
group 2
predic

Fig. 2A

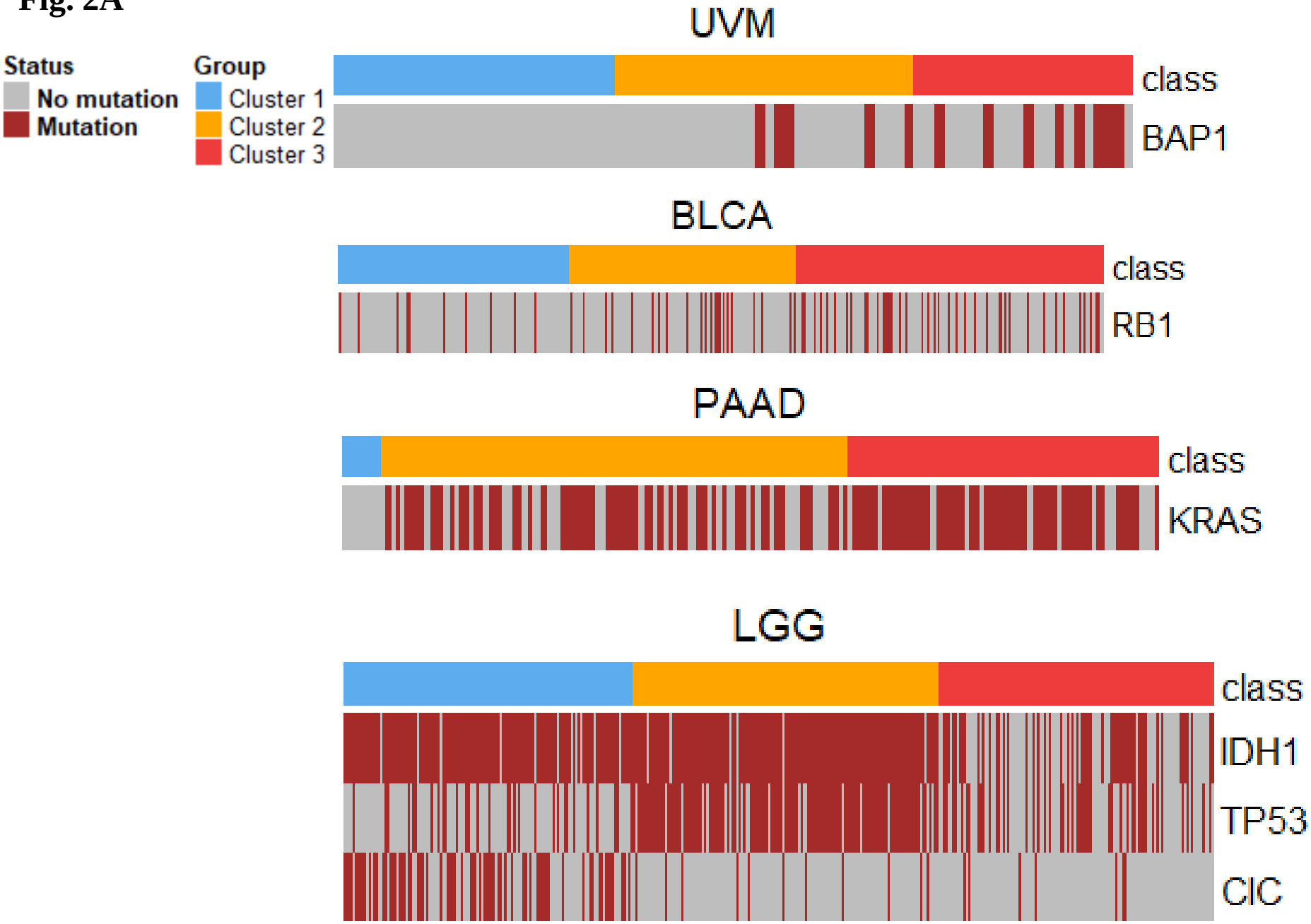

Status
No mutation
Mutation
Group
Cluster 1
Cluster 2
Cluster 3
UVM
class
BAP1
BLCA
class
RB1
PAAD
class
KRAS
LGG
class
IDH1
TP53
CIC

Fig. 2B

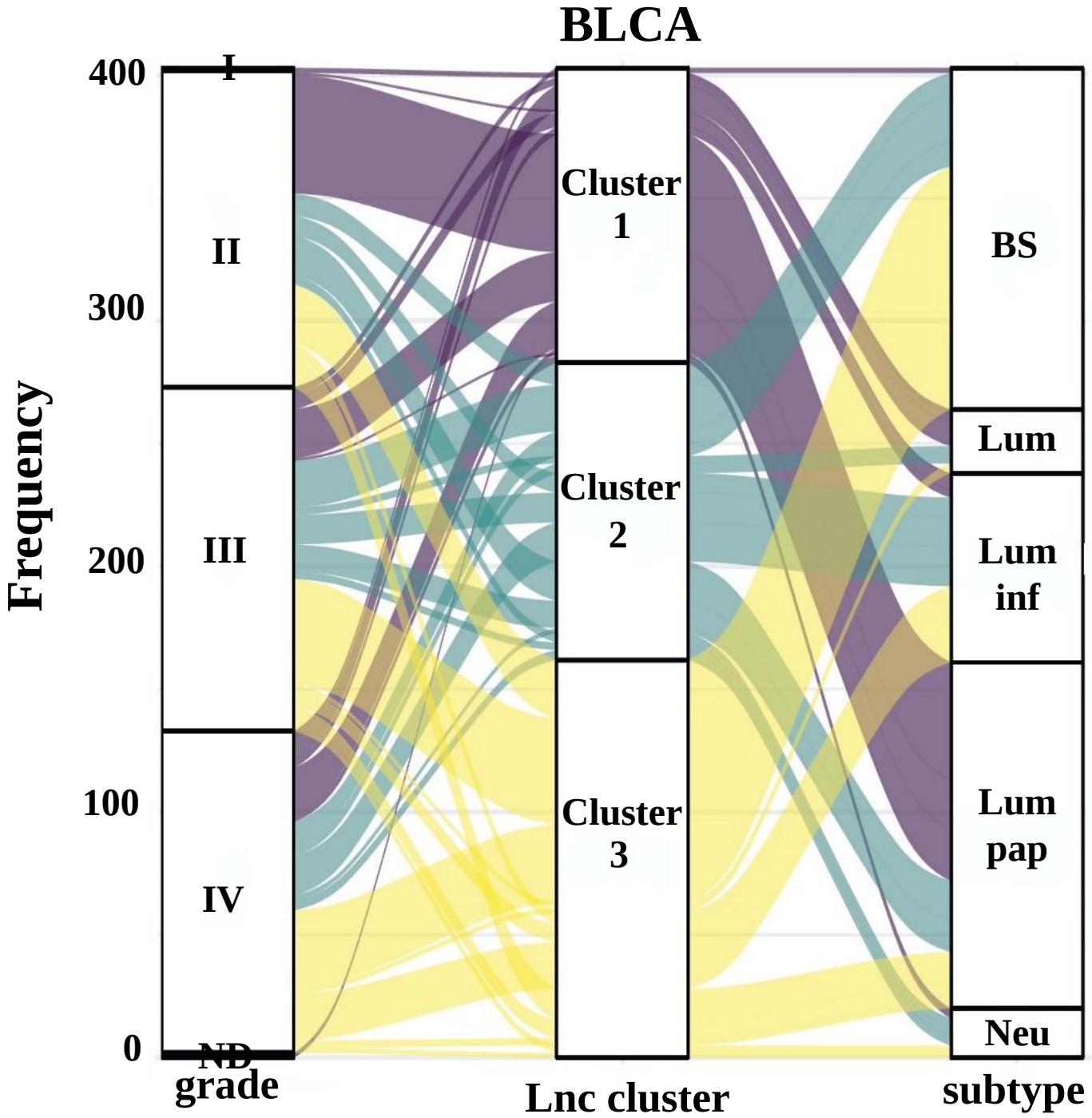

BLCA
Frequency
400
300
200
100
0
I
II
III
IV
ND
grade
Cluster 1
Cluster 2
Cluster 3
Lnc cluster
BS
Lum
Lum inf
Lum pap
Neu
subtype

Fig. 2B

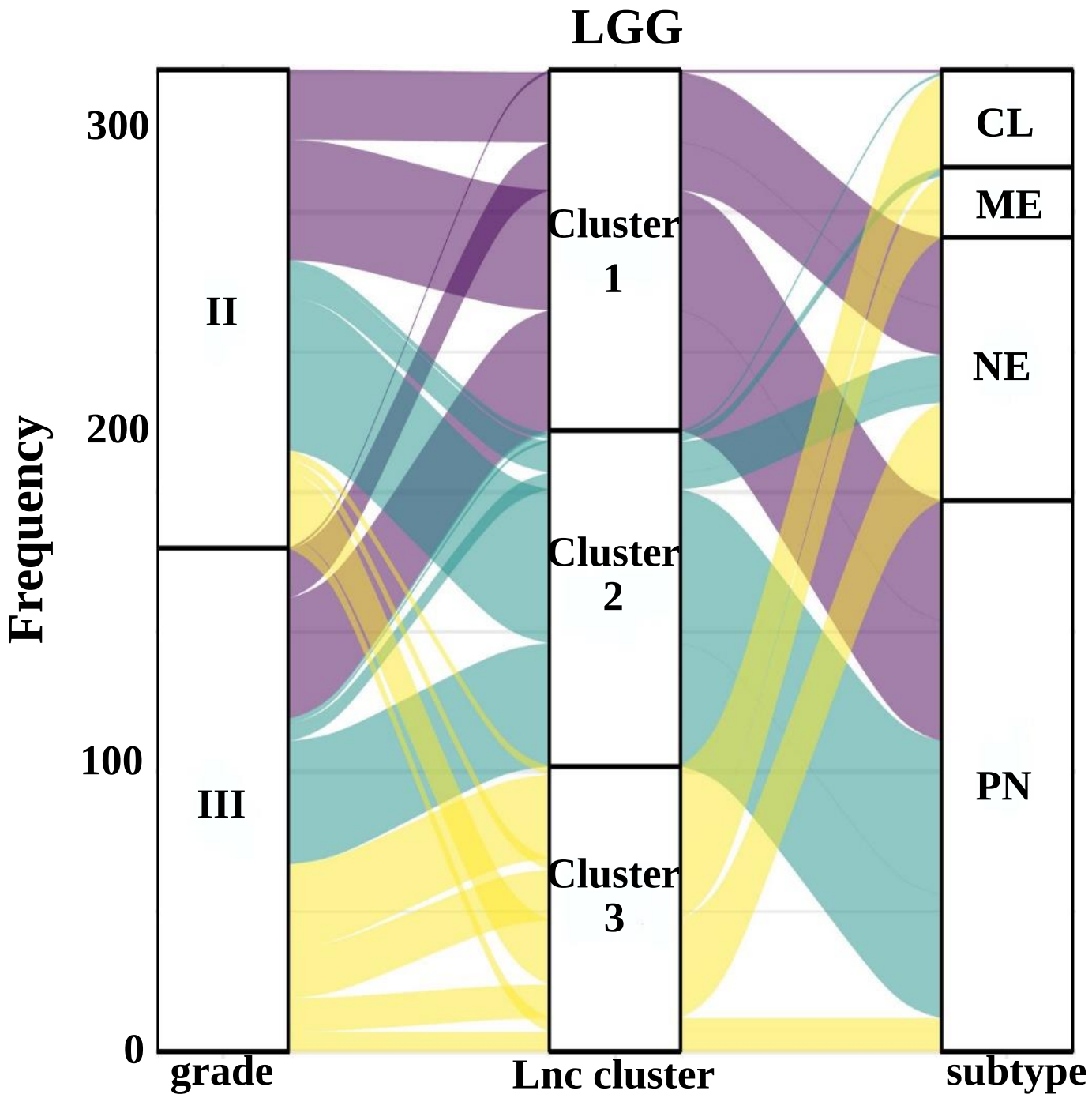

LGG
Frequency
300
200
100
0
II
III
grade
Cluster 1
Cluster 2
Cluster 3
Lnc cluster
CL
ME
NE
PN
subtype

Fig. 2B

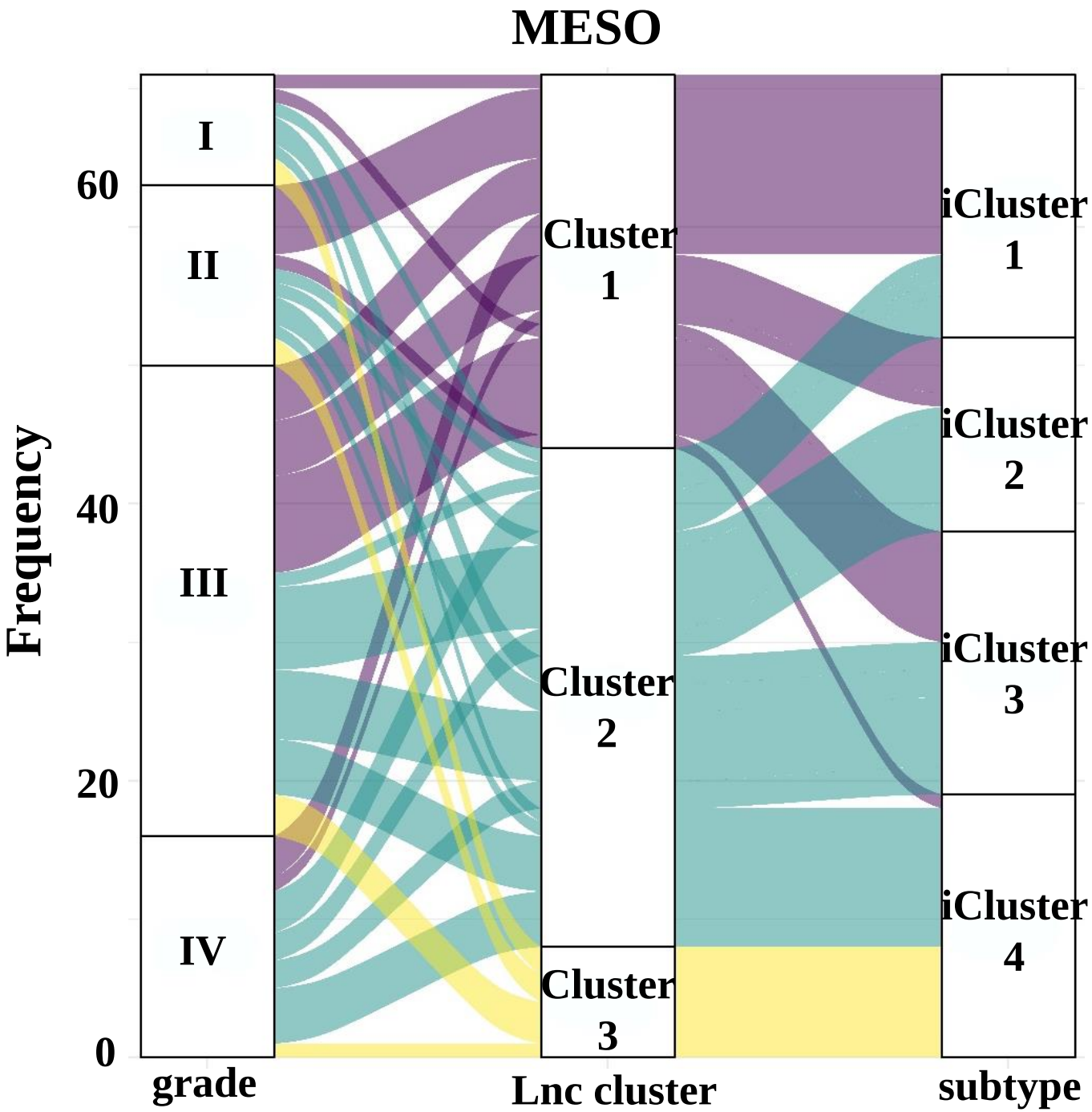

MESO
Frequency
0
20
40
60
I
II
III
IV
grade
Cluster 1
Cluster 2
Cluster 3
Lnc cluster
iCluster 1
iCluster 2
iCluster 3
iCluster 4
subtype

Fig. 2B

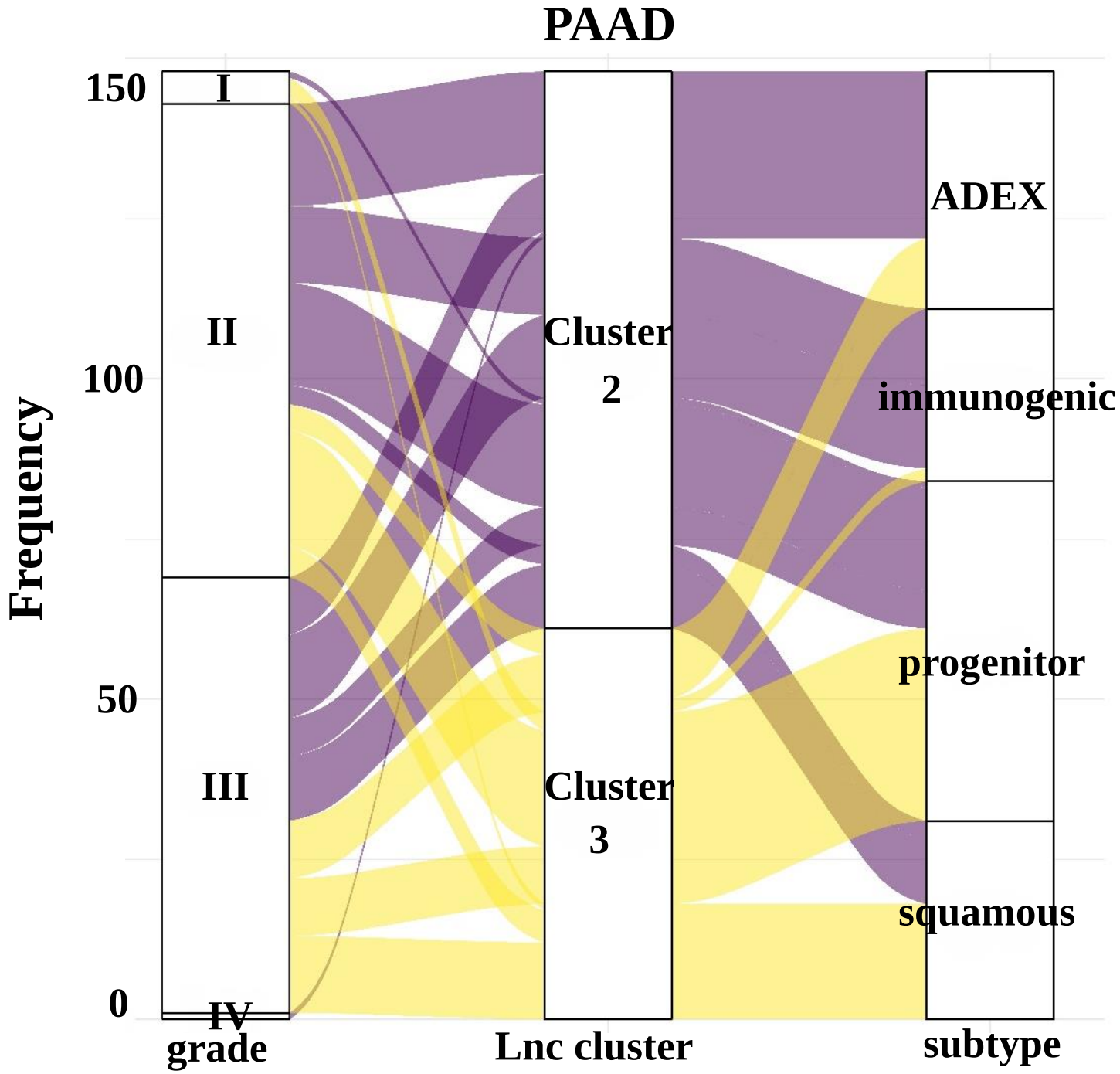

PAAD
Frequency
150
100
50
0
I
II
III
IV
grade
Cluster 2
Cluster 3
Lnc cluster
ADEX
immunogenic
progenitor
squamous
subtype

Fig. 2B

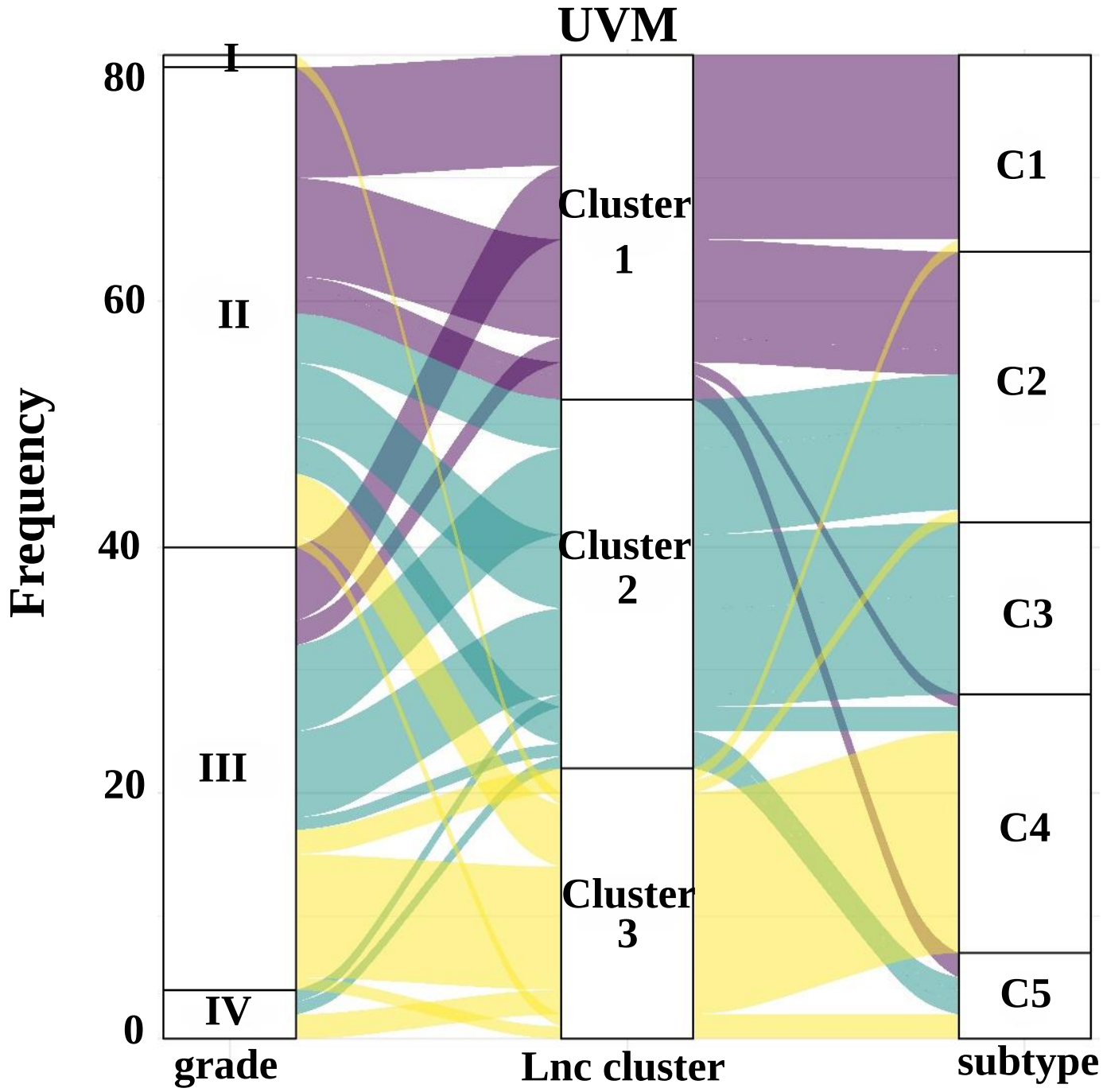

UVM
Frequency
80
60
40
20
0
I
II
III
IV
grade
Cluster 1
Cluster 2
Cluster 3
Lnc cluster
C1
C2
C3
C4
C5
subtype

Fig. 3A

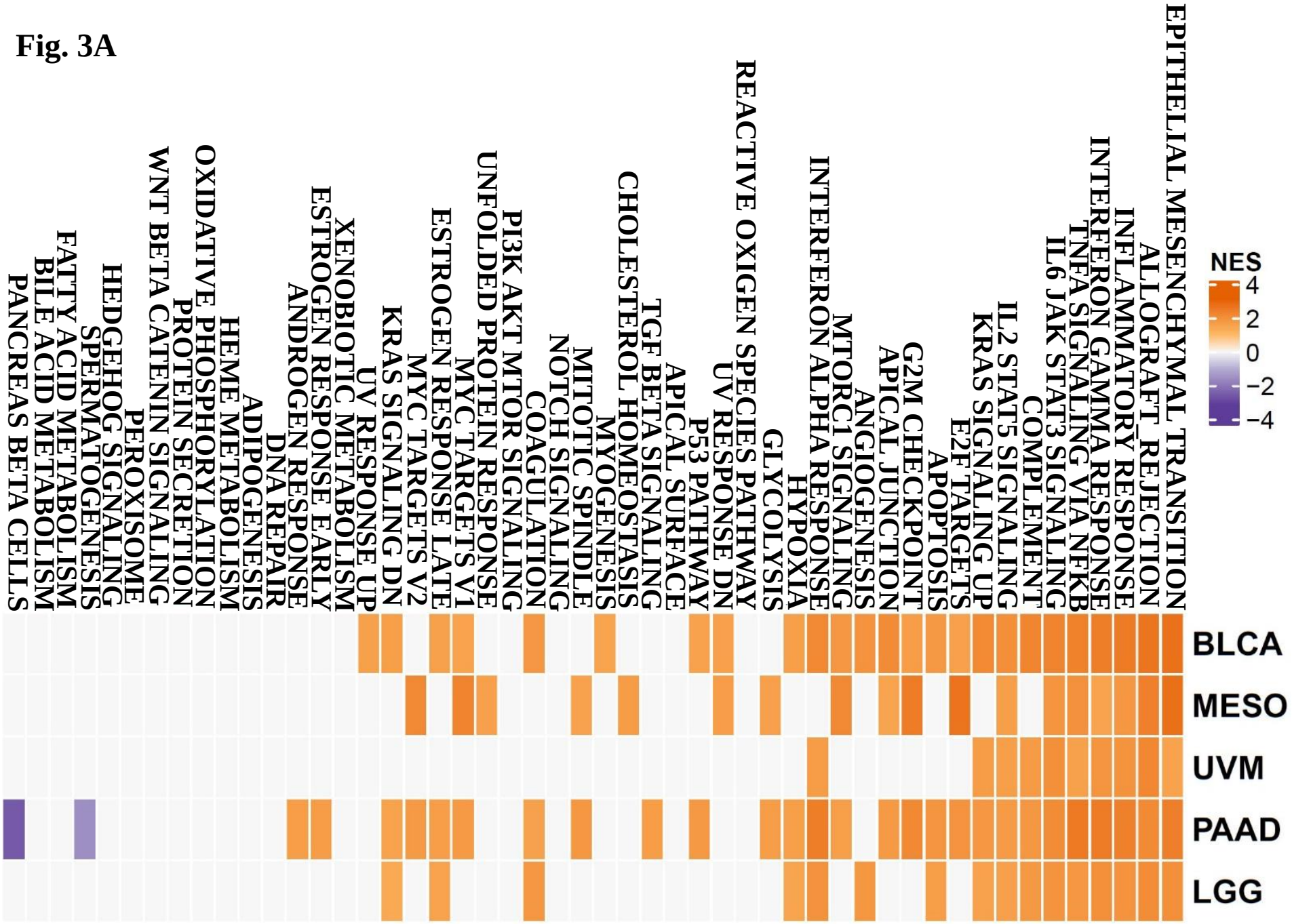

EPITHELIAL MESENCHYMAL TRANSITION
ALLOGRAFT_REJECTION
INFLAMMATORY RESPONSE
INTERFERON GAMMA RESPONSE
TNFA SIGNALING VIA NFKB
IL6 JAK STAT3 SIGNALING
COMPLEMENT
IL2 STAT5 SIGNALING
KRAS SIGNALING UP
E2F TARGETS
APOPTOSIS
G2M CHECKPOINT
APICAL JUNCTION
ANGIOGENESIS
MTORC1 SIGNALING
INTERFERON ALPHA RESPONSE
HYPOXIA
GLYCOLYSIS
REACTIVE OXIGEN SPECIES PATHWAY
UV RESPONSE DN
P53 PATHWAY
APICAL SURFACE
TGF BETA SIGNALING
CHOLESTEROL HOMEOSTASIS
MYOGENESIS
MITOTIC SPINDLE
NOTCH SIGNALING
COAGULATION
PI3K AKT MTOR SIGNALING
UNFOLDED PROTEIN RESPONSE
MYC TARGETS V1
MYC TARGETS V2
ESTROGEN RESPONSE LATE
KRAS SIGNALING DN
UV RESPONSE UP
XENOBIOTIC METABOLISM
ESTROGEN RESPONSE EARLY
ANDROGEN RESPONSE
DNA REPAIR
ADIPOGENESIS
HEME METABOLISM
OXIDATIVE PHOSPHORYLATION
PROTEIN SECRETION
WNT BETA CATENIN SIGNALING
PEROXISOME
HEDGEHOG SIGNALING
SPERMATOGENESIS
FATTY ACID METABOLISM
BILE ACID METABOLISM
PANCREAS BETA CELLS
NES
4
2
0
−2
−4
BLCA
MESO
UVM
PAAD
LGG

Fig. 3B

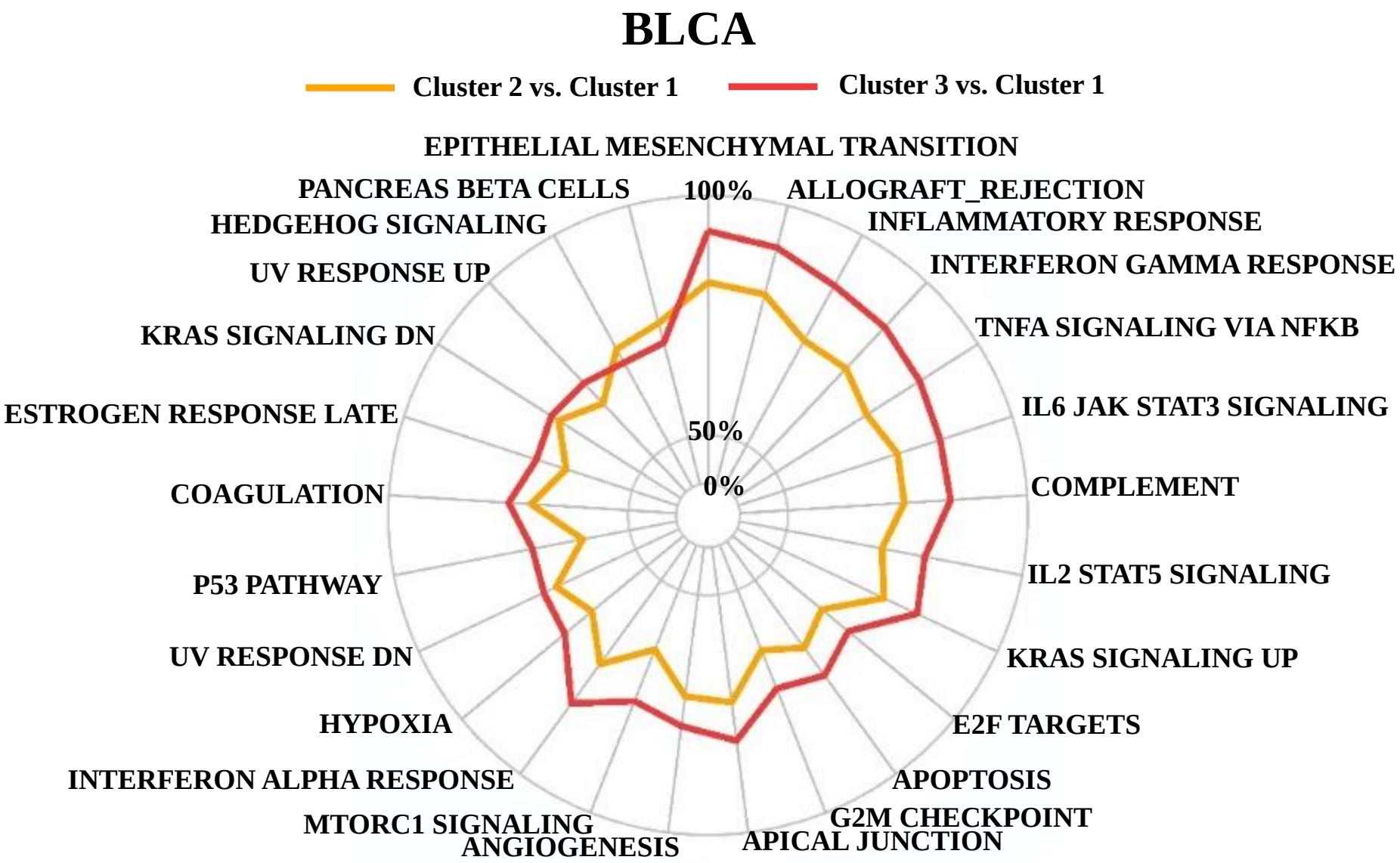

BLCA
Cluster 2 vs. Cluster 1
Cluster 3 vs. Cluster 1
EPITHELIAL MESENCHYMAL TRANSITION
ALLOGRAFT_REJECTION
INFLAMMATORY RESPONSE
INTERFERON GAMMA RESPONSE
TNFA SIGNALING VIA NFKB
IL6 JAK STAT3 SIGNALING
COMPLEMENT
IL2 STAT5 SIGNALING
KRAS SIGNALING UP
E2F TARGETS
APOPTOSIS
G2M CHECKPOINT
APICAL JUNCTION
ANGIOGENESIS
MTORC1 SIGNALING
INTERFERON ALPHA RESPONSE
HYPOXIA
UV RESPONSE DN
P53 PATHWAY
COAGULATION
ESTROGEN RESPONSE LATE
KRAS SIGNALING DN
UV RESPONSE UP
HEDGEHOG SIGNALING
PANCREAS BETA CELLS
100%
50%
0%

Fig. 3B

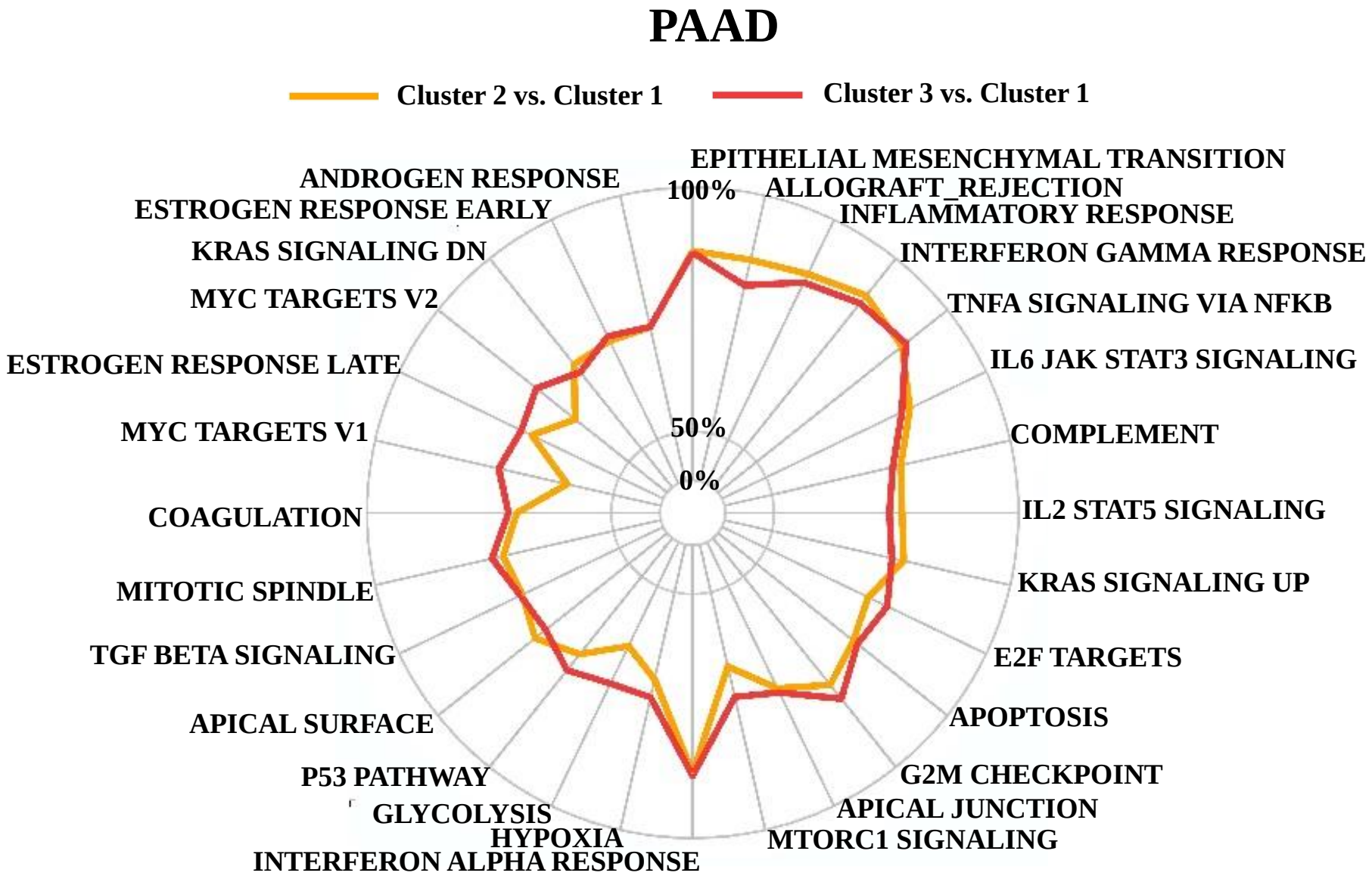

PAAD
Cluster 2 vs. Cluster 1
Cluster 3 vs. Cluster 1
100%
50%
0%
EPITHELIAL MESENCHYMAL TRANSITION
ALLOGRAFT_REJECTION
INFLAMMATORY RESPONSE
INTERFERON GAMMA RESPONSE
TNFA SIGNALING VIA NFKB
IL6 JAK STAT3 SIGNALING
COMPLEMENT
IL2 STAT5 SIGNALING
KRAS SIGNALING UP
E2F TARGETS
APOPTOSIS
G2M CHECKPOINT
APICAL JUNCTION
MTORC1 SIGNALING
HYPOXIA
INTERFERON ALPHA RESPONSE
GLYCOLYSIS
P53 PATHWAY
APICAL SURFACE
TGF BETA SIGNALING
MITOTIC SPINDLE
COAGULATION
MYC TARGETS V1
ESTROGEN RESPONSE LATE
MYC TARGETS V2
KRAS SIGNALING DN
ESTROGEN RESPONSE EARLY
ANDROGEN RESPONSE

Fig. 3B

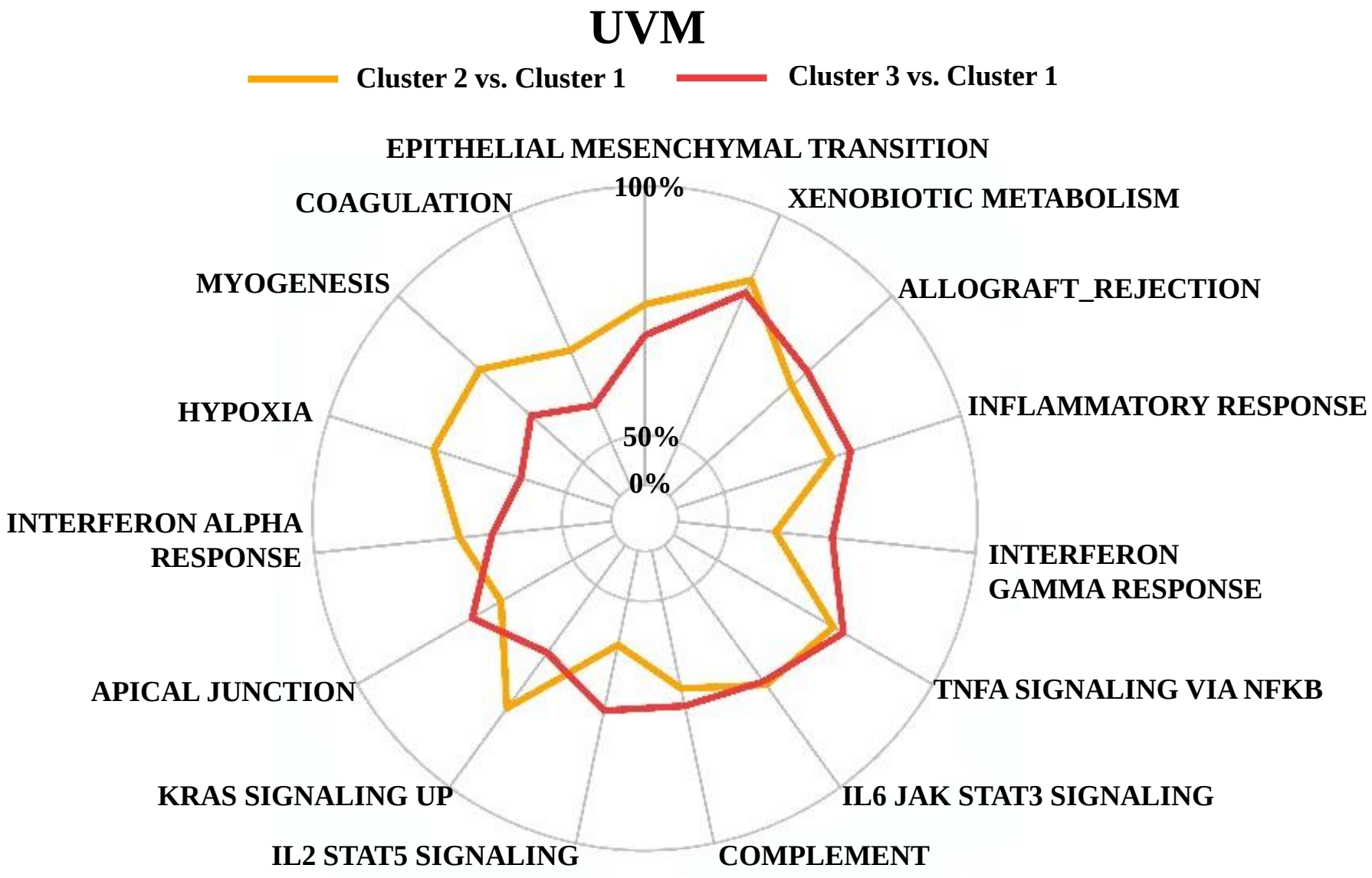

UVM
Cluster 2 vs. Cluster 1
Cluster 3 vs. Cluster 1
EPITHELIAL MESENCHYMAL TRANSITION
XENOBIOTIC METABOLISM
ALLOGRAFT_REJECTION
INFLAMMATORY RESPONSE
INTERFERON GAMMA RESPONSE
TNFA SIGNALING VIA NFKB
IL6 JAK STAT3 SIGNALING
COMPLEMENT
IL2 STAT5 SIGNALING
KRAS SIGNALING UP
APICAL JUNCTION
INTERFERON ALPHA RESPONSE
HYPOXIA
MYOGENESIS
COAGULATION
100%
50%
0%

Fig. 3B

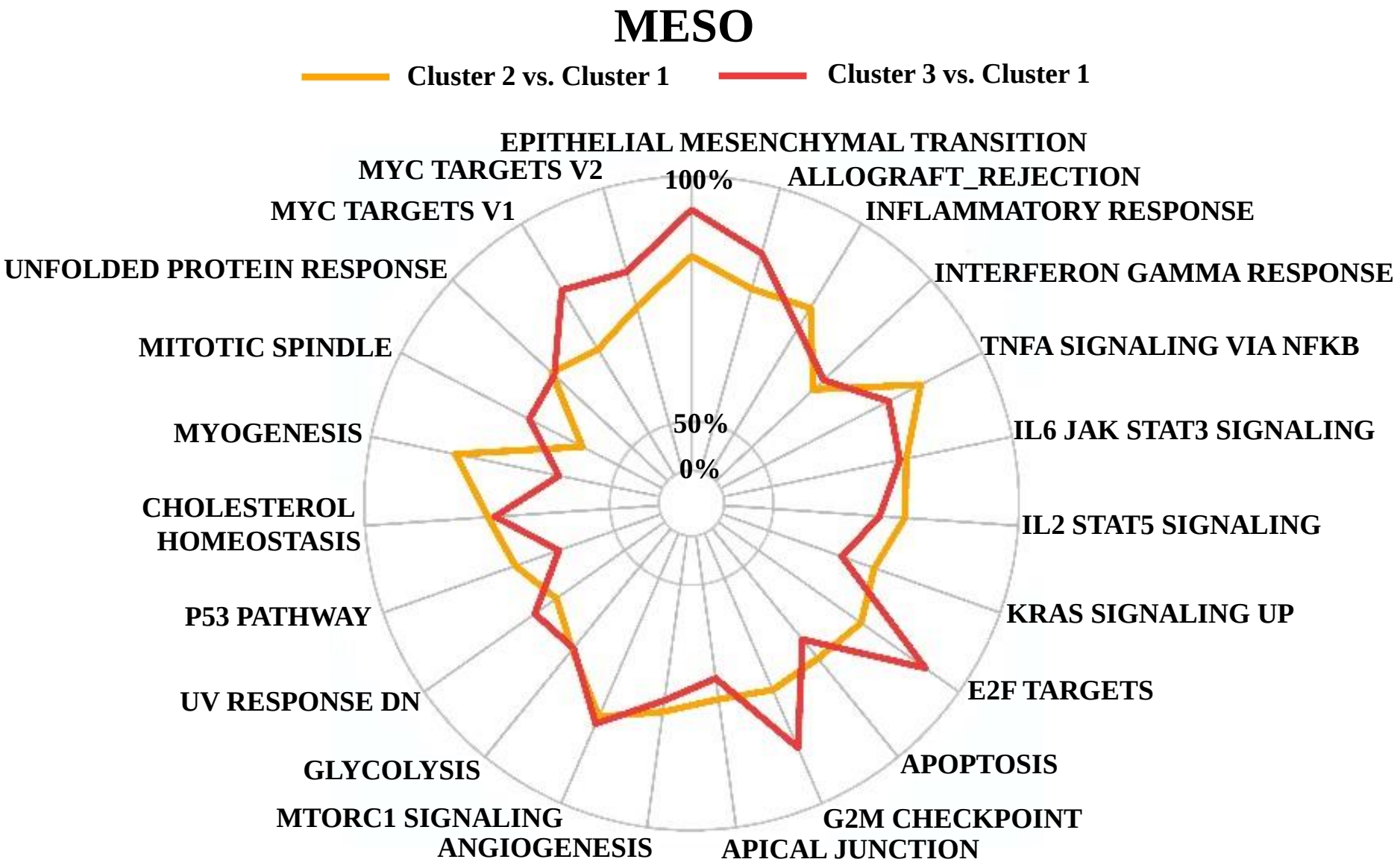

MESO
Cluster 2 vs. Cluster 1
Cluster 3 vs. Cluster 1
EPITHELIAL MESENCHYMAL TRANSITION
ALLOGRAFT_REJECTION
INFLAMMATORY RESPONSE
INTERFERON GAMMA RESPONSE
TNFA SIGNALING VIA NFKB
IL6 JAK STAT3 SIGNALING
IL2 STAT5 SIGNALING
KRAS SIGNALING UP
E2F TARGETS
APOPTOSIS
G2M CHECKPOINT
APICAL JUNCTION
ANGIOGENESIS
MTORC1 SIGNALING
GLYCOLYSIS
UV RESPONSE DN
P53 PATHWAY
CHOLESTEROL HOMEOSTASIS
MYOGENESIS
MITOTIC SPINDLE
UNFOLDED PROTEIN RESPONSE
MYC TARGETS V1
MYC TARGETS V2
100%
50%
0%

Fig. 3B

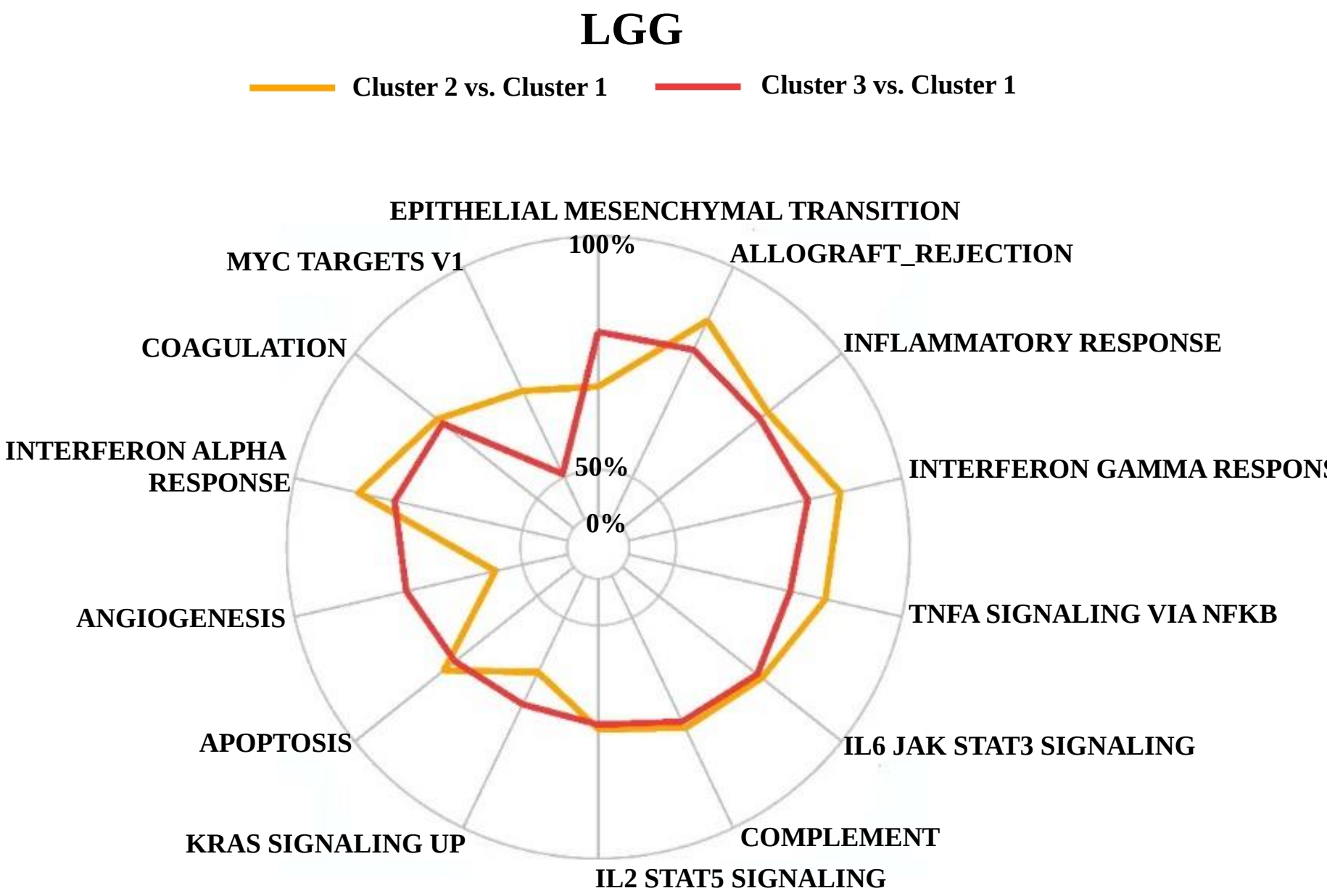

LGG
Cluster 2 vs. Cluster 1
Cluster 3 vs. Cluster 1
EPITHELIAL MESENCHYMAL TRANSITION
ALLOGRAFT_REJECTION
INFLAMMATORY RESPONSE
INTERFERON GAMMA RESPONS
TNFA SIGNALING VIA NFKB
IL6 JAK STAT3 SIGNALING
COMPLEMENT
IL2 STAT5 SIGNALING
KRAS SIGNALING UP
APOPTOSIS
ANGIOGENESIS
INTERFERON ALPHA RESPONSE
COAGULATION
MYC TARGETS V1
100%
50%
0%

Fig. 4A

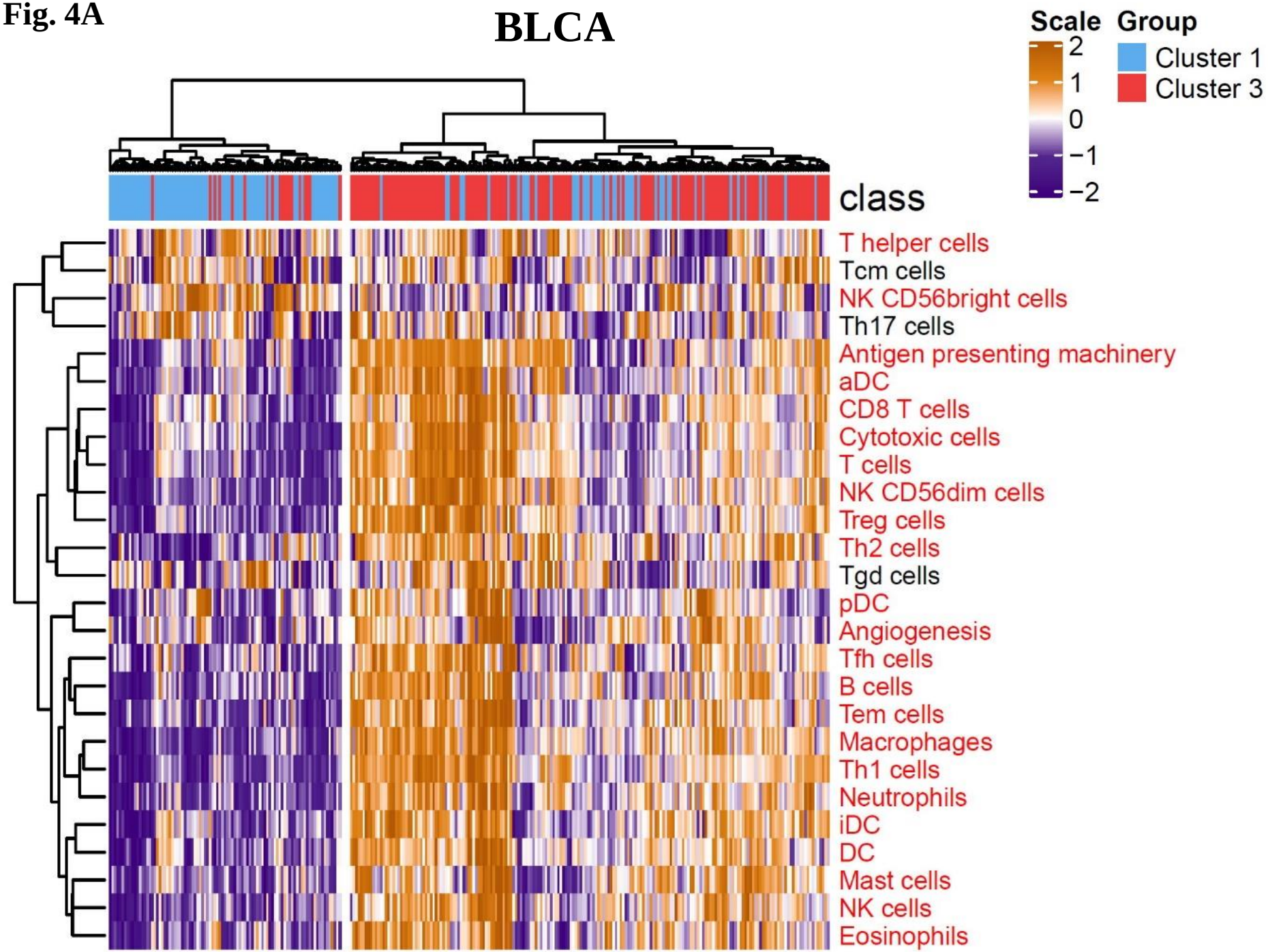

BLCA
Scale
2
1
0
−1
−2
Group
Cluster 1
Cluster 3
class
T helper cells
Tcm cells
NK CD56bright cells
Th17 cells
Antigen presenting machinery
aDC
CD8 T cells
Cytotoxic cells
T cells
NK CD56dim cells
Treg cells
Th2 cells
Tgd cells
pDC
Angiogenesis
Tfh cells
B cells
Tem cells
Macrophages
Th1 cells
Neutrophils
iDC
DC
Mast cells
NK cells
Eosinophils

Fig. 4A

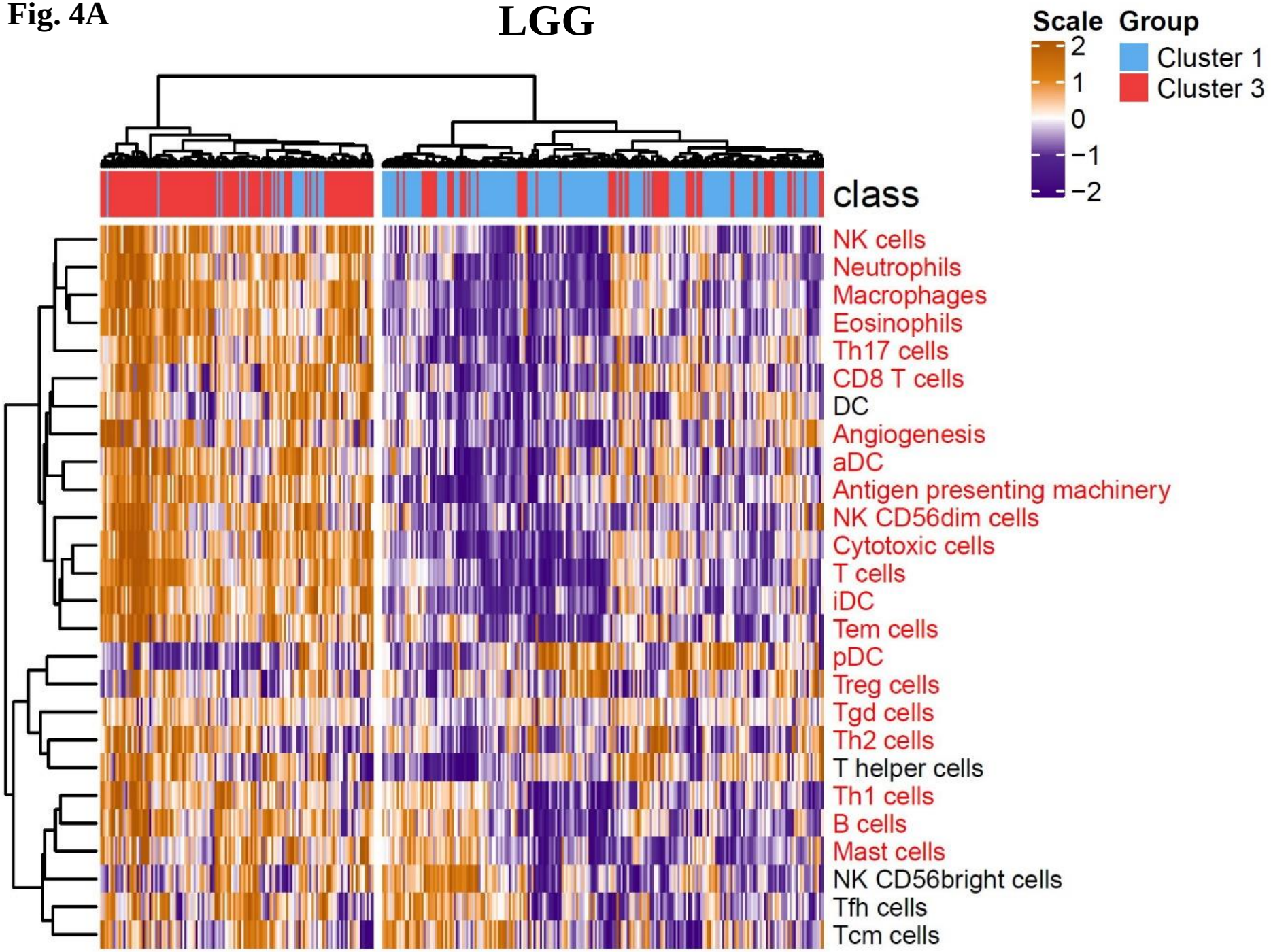

LGG
Scale
2
1
0
−1
−2
Group
Cluster 1
Cluster 3
class
NK cells
Neutrophils
Macrophages
Eosinophils
Th17 cells
CD8 T cells
DC
Angiogenesis
aDC
Antigen presenting machinery
NK CD56dim cells
Cytotoxic cells
T cells
iDC
Tem cells
pDC
Treg cells
Tgd cells
Th2 cells
T helper cells
Th1 cells
B cells
Mast cells
NK CD56bright cells
Tfh cells
Tcm cells

Fig. 4A

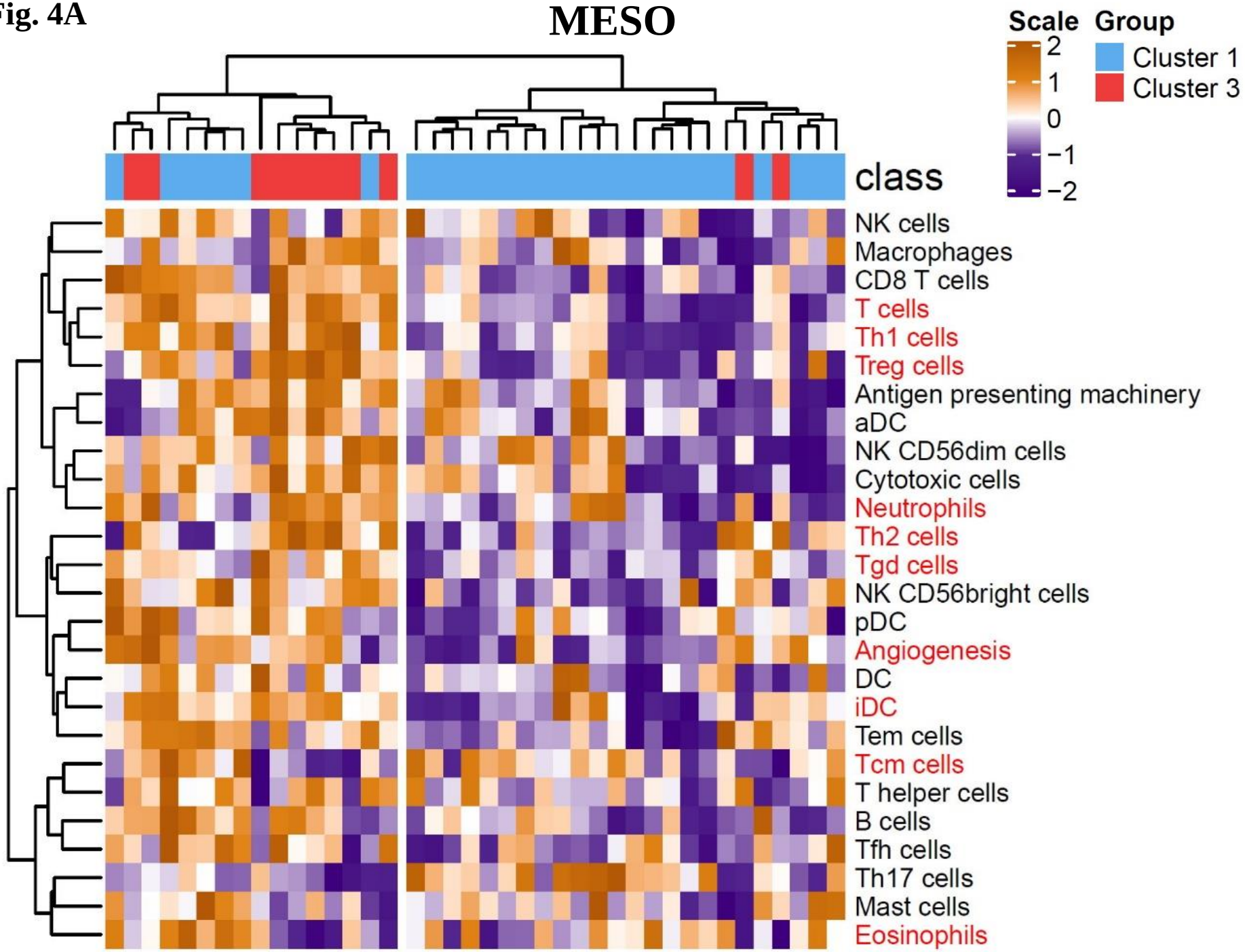

MESO
Scale
2
1
0
−1
−2
Group
Cluster 1
Cluster 3
class
NK cells
Macrophages
CD8 T cells
T cells
Th1 cells
Treg cells
Antigen presenting machinery
aDC
NK CD56dim cells
Cytotoxic cells
Neutrophils
Th2 cells
Tgd cells
NK CD56bright cells
pDC
Angiogenesis
DC
iDC
Tem cells
Tcm cells
T helper cells
B cells
Tfh cells
Th17 cells
Mast cells
Eosinophils

Fig. 4A

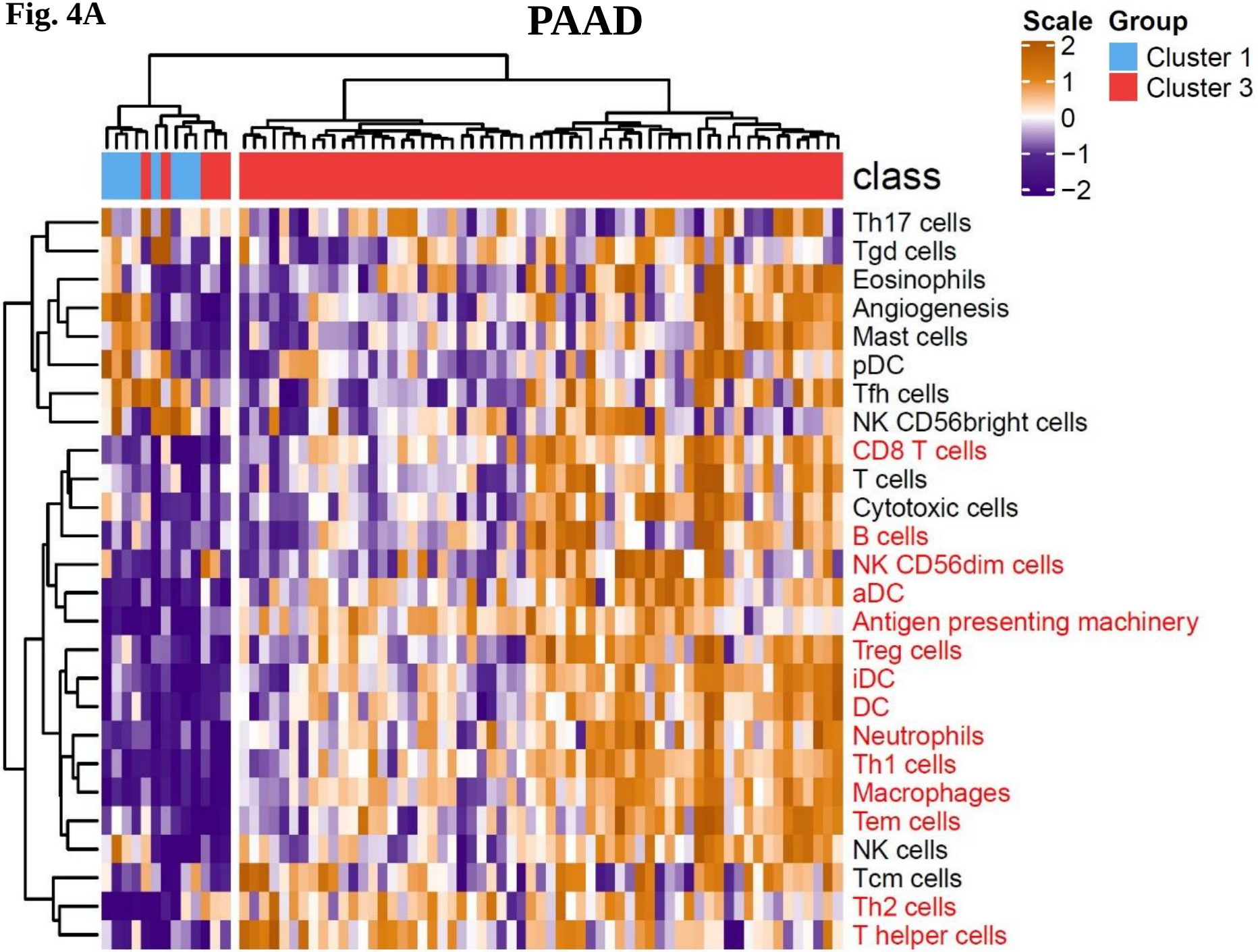

PAAD
Scale
2
1
0
−1
−2
Group
Cluster 1
Cluster 3
class
Th17 cells
Tgd cells
Eosinophils
Angiogenesis
Mast cells
pDC
Tfh cells
NK CD56bright cells
CD8 T cells
T cells
Cytotoxic cells
B cells
NK CD56dim cells
aDC
Antigen presenting machinery
Treg cells
iDC
DC
Neutrophils
Th1 cells
Macrophages
Tem cells
NK cells
Tcm cells
Th2 cells
T helper cells

Fig. 4A

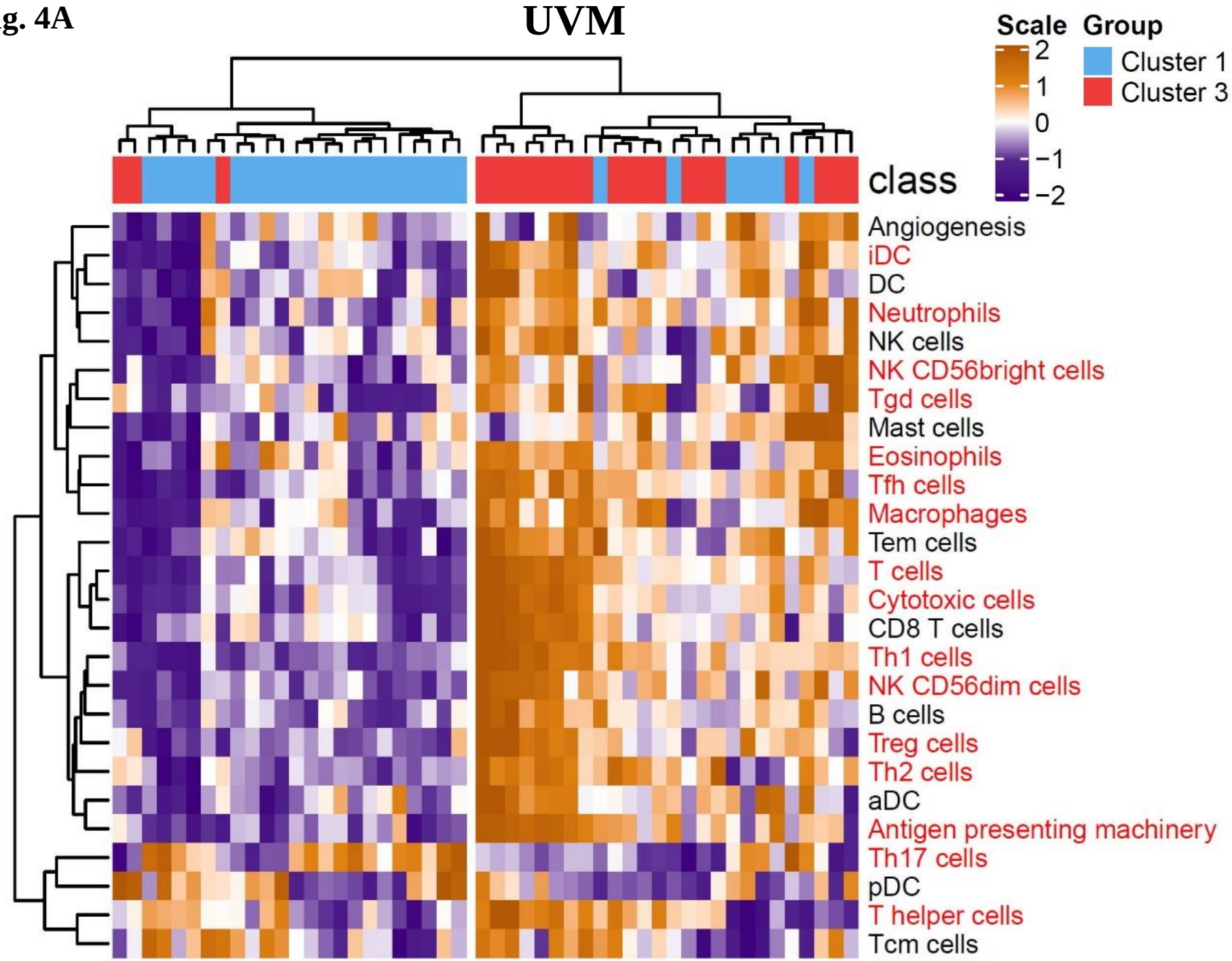

UVM
Scale
2
1
0
−1
−2
Group
Cluster 1
Cluster 3
class
Angiogenesis
iDC
DC
Neutrophils
NK cells
NK CD56bright cells
Tgd cells
Mast cells
Eosinophils
Tfh cells
Macrophages
Tem cells
T cells
Cytotoxic cells
CD8 T cells
Th1 cells
NK CD56dim cells
B cells
Treg cells
Th2 cells
aDC
Antigen presenting machinery
Th17 cells
pDC
T helper cells
Tcm cells

Fig. 4B

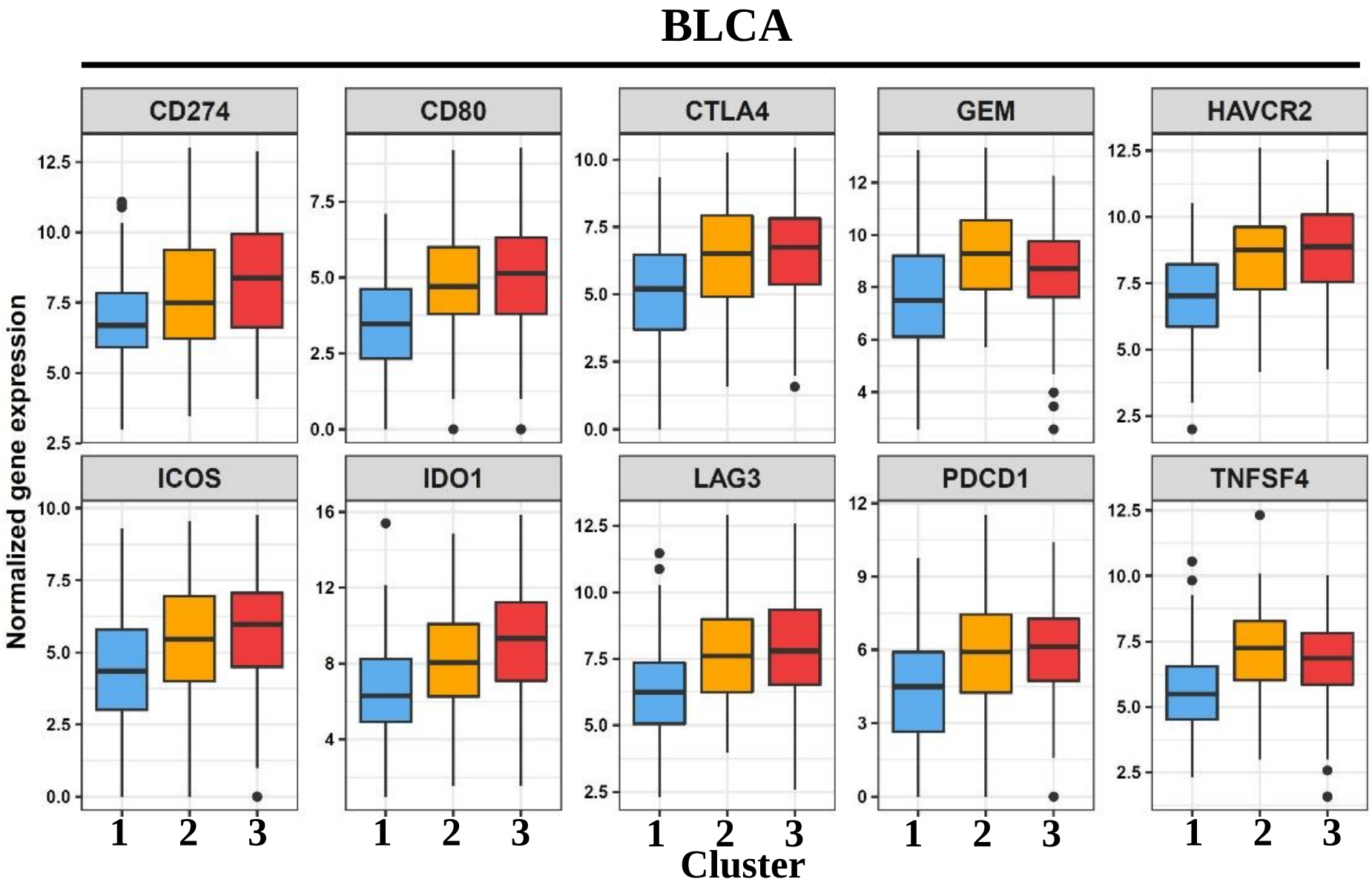

BLCA
CD274
CD80
CTLA4
GEM
HAVCR2
ICOS
IDO1
LAG3
PDCD1
TNFSF4
Normalized gene expression
Cluster
1
2
3

Fig. 4B

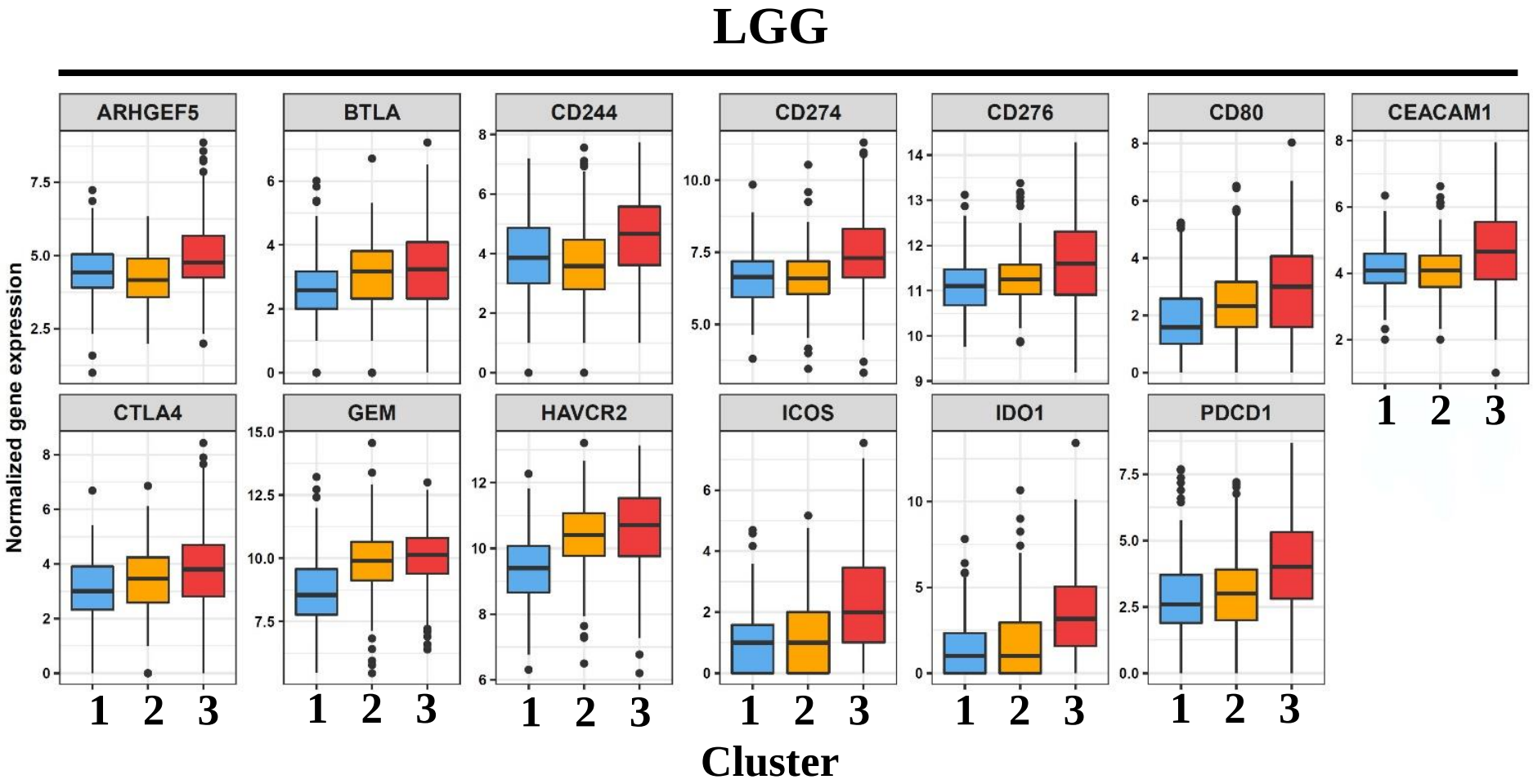

LGG
ARHGEF5
BTLA
CD244
CD274
CD276
CD80
CEACAM1
CTLA4
GEM
HAVCR2
ICOS
IDO1
PDCD1
Normalized gene expression
1 2 3
Cluster

Fig. 4B

MESO

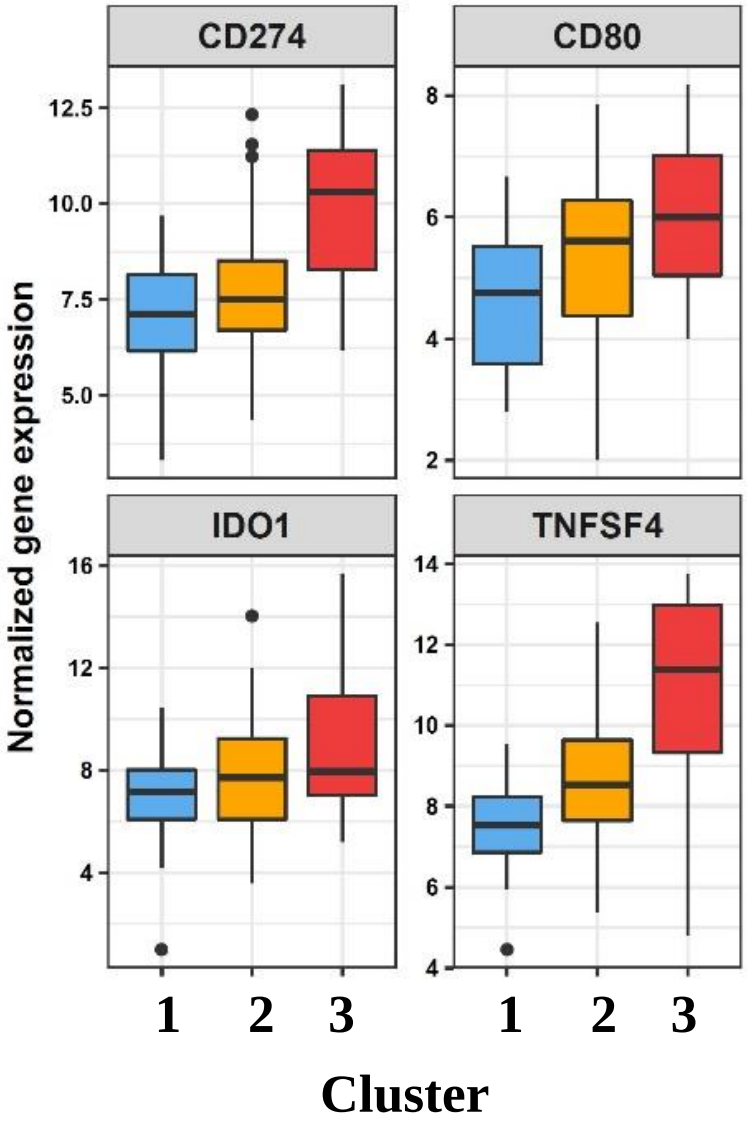

CD274
CD80
IDO1
TNFSF4
Normalized gene expression
12.5
10.0
7.5
5.0
8
6
4
2
16
12
8
4
14
12
10
8
6
4
1
2
3
1
2
3
Cluster

Fig. 4B

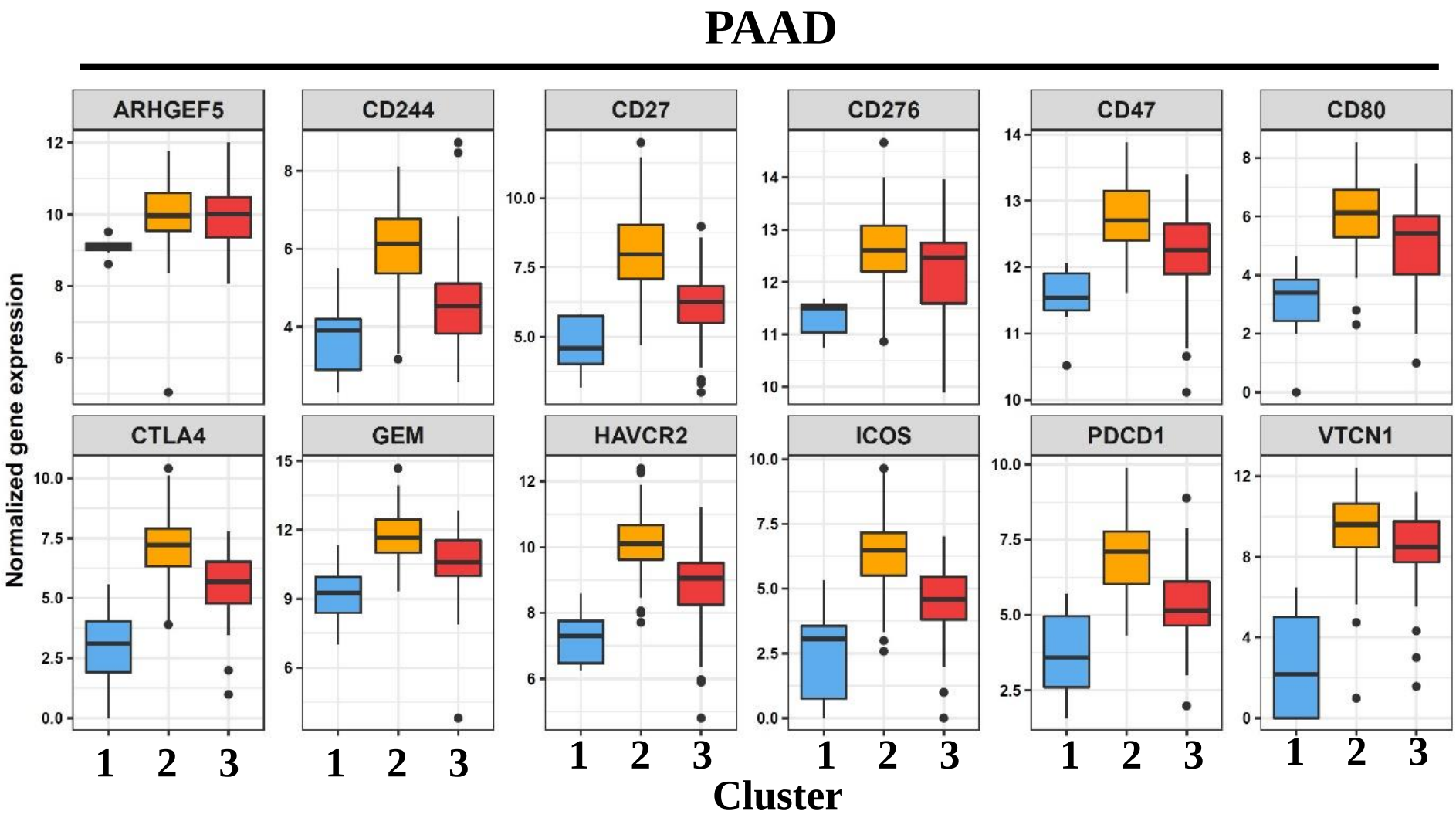

PAAD
ARHGEF5
CD244
CD27
CD276
CD47
CD80
CTLA4
GEM
HAVCR2
ICOS
PDCD1
VTCN1
Normalized gene expression
1
2
3
Cluster

Fig. 4B

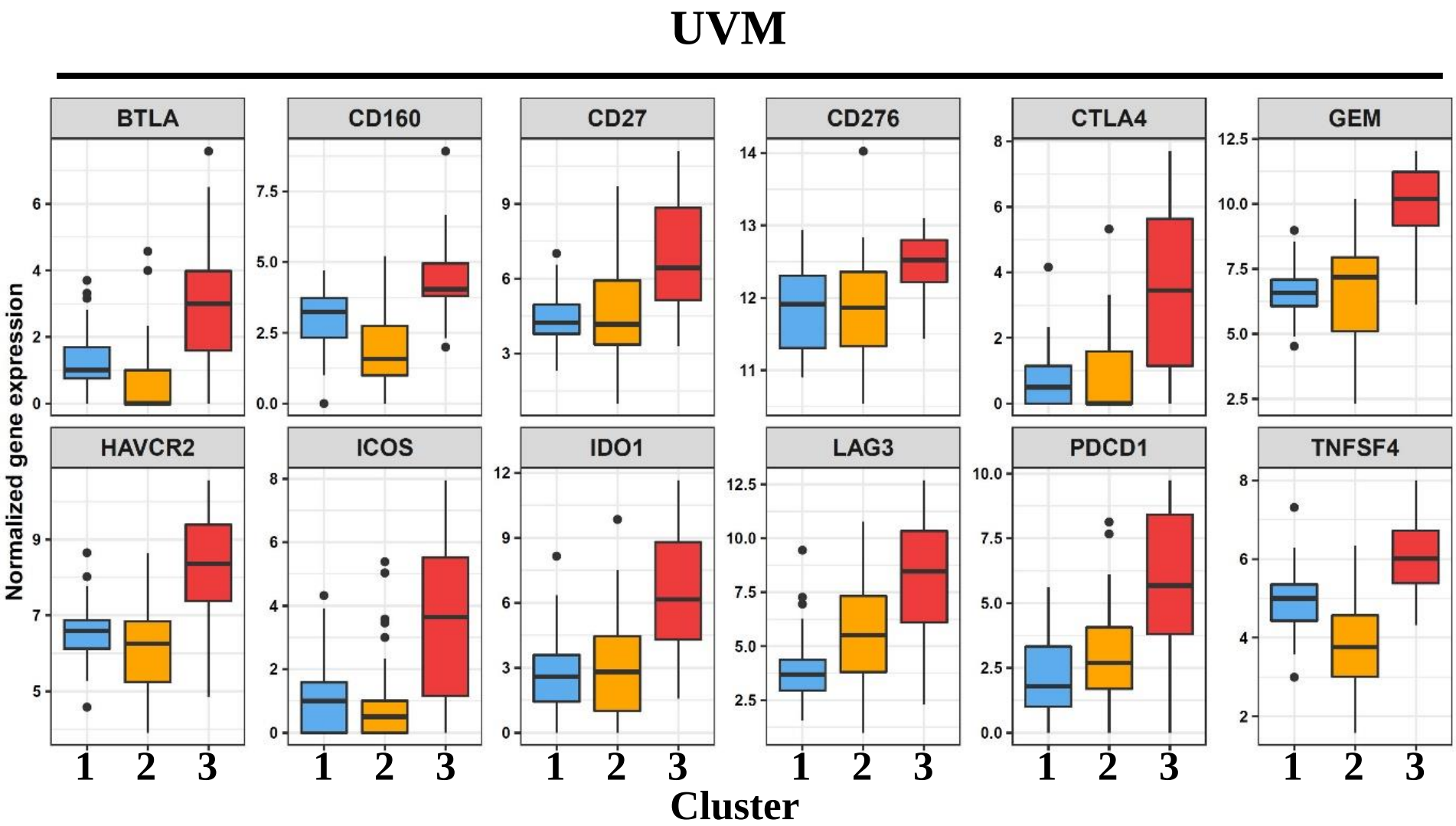

UVM
BTLA
CD160
CD27
CD276
CTLA4
GEM
HAVCR2
ICOS
IDO1
LAG3
PDCD1
TNFSF4
Normalized gene expression
1
2
3
Cluster

Fig. 4C

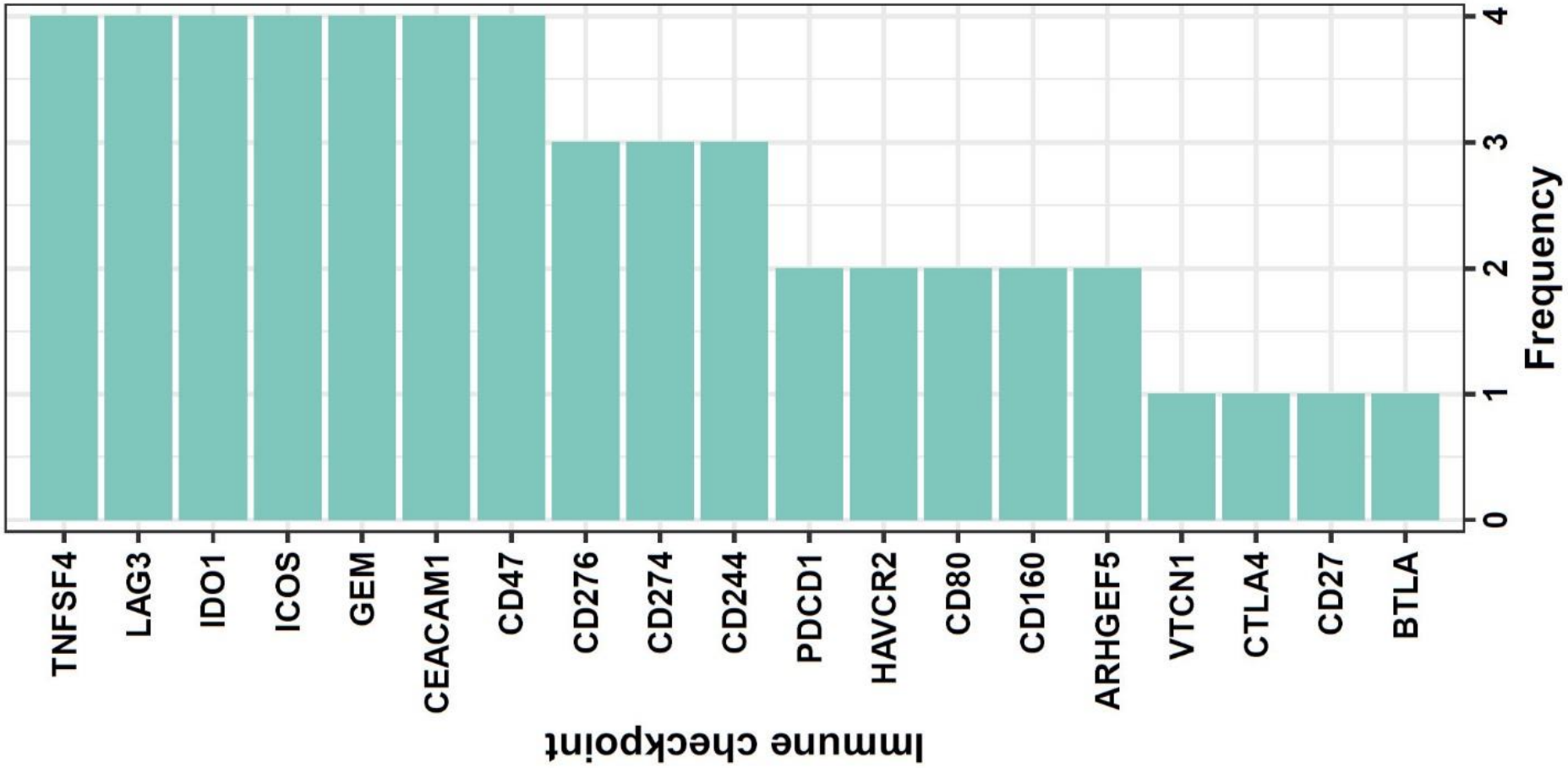

TNFSF4
LAG3
IDO1
ICOS
GEM
CEACAM1
CD47
CD276
CD274
CD244
PDCD1
HAVCR2
CD80
CD160
ARHGEF5
VTCN1
CTLA4
CD27
BTLA
Immune checkpoint
0
1
2
3
4
Frequency

Fig. 5A

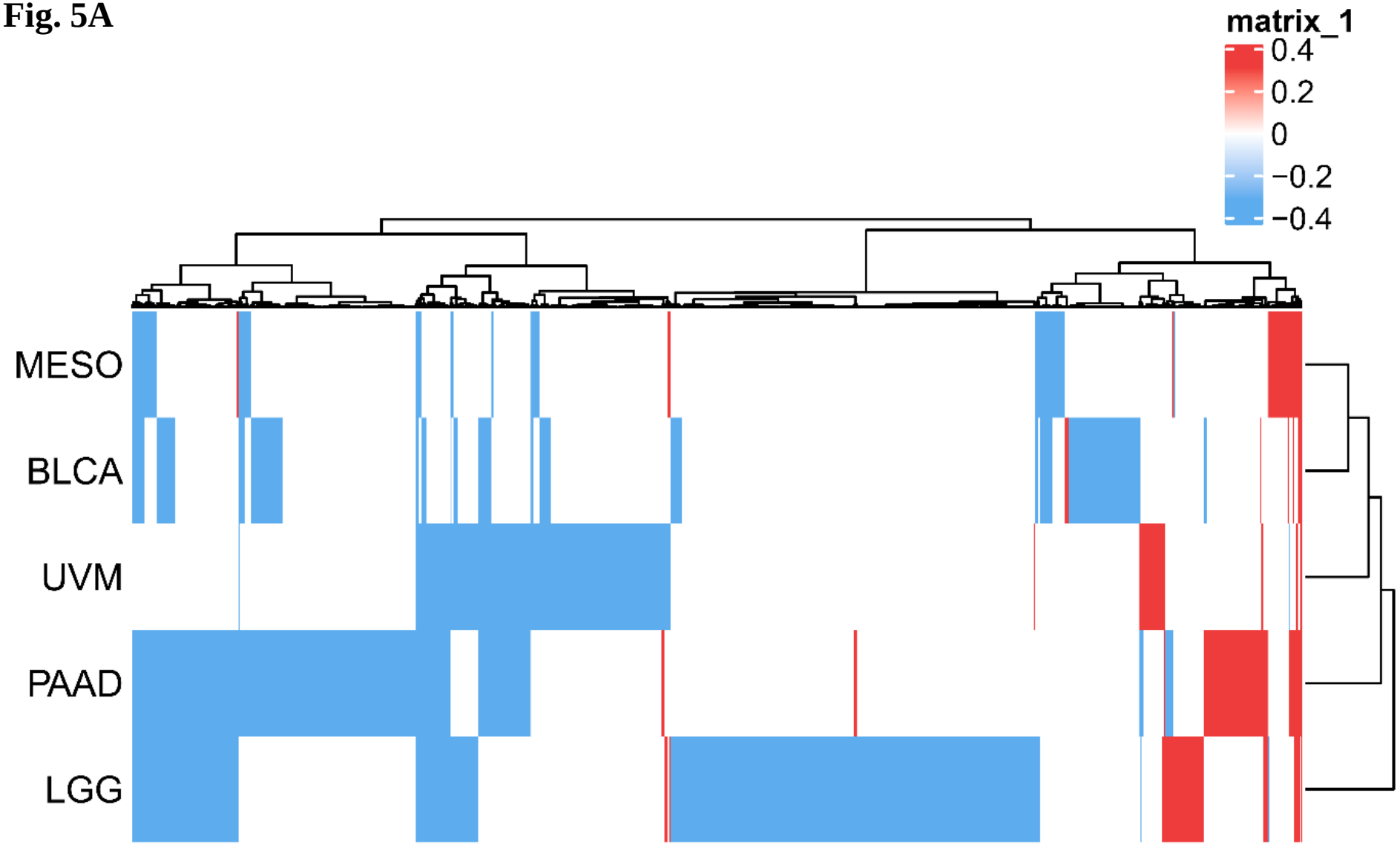


Fig. 5B

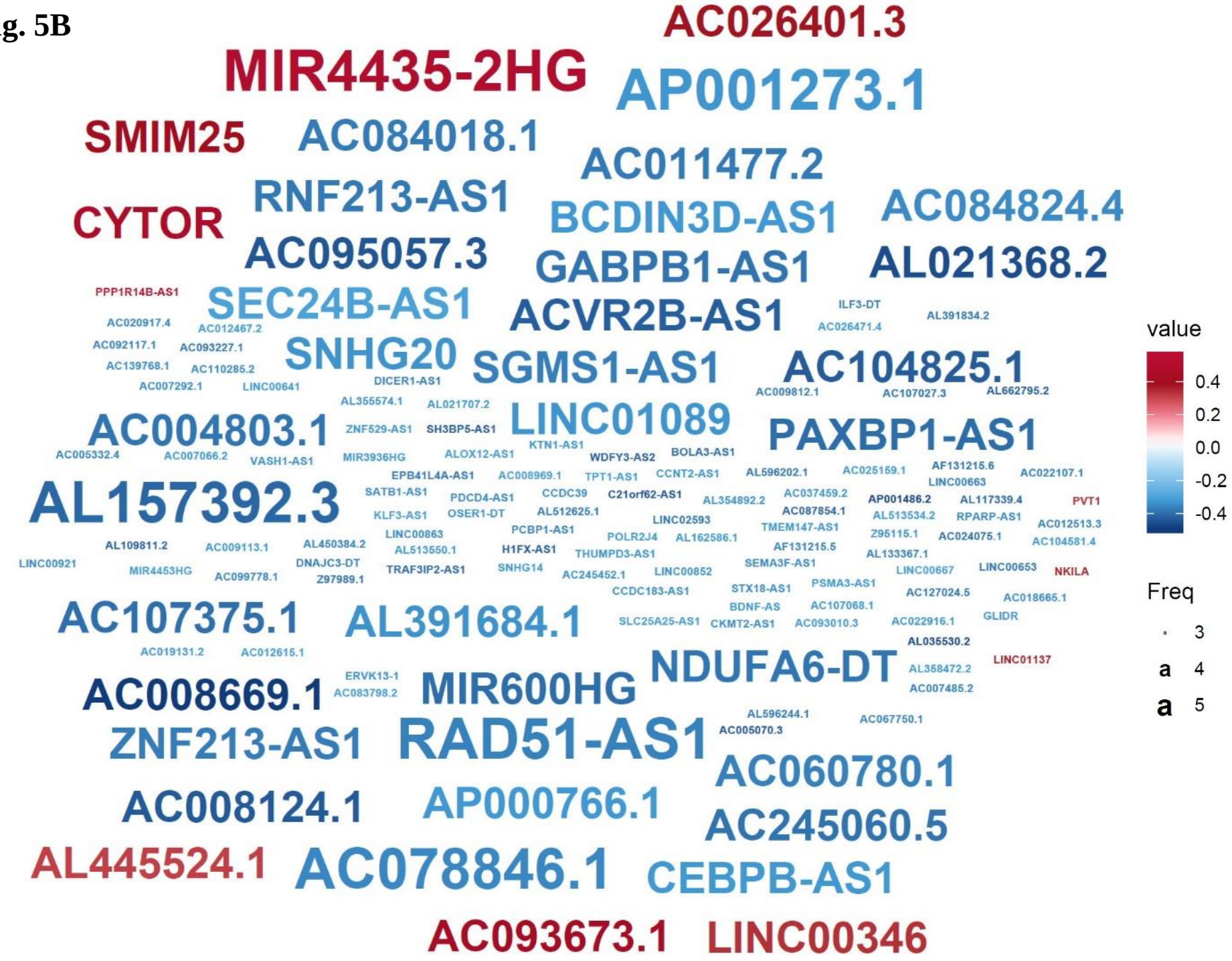

AC026401.3
MIR4435-2HG
AP001273.1
SMIM25
AC084018.1
AC011477.2
RNF213-AS1
CYTOR
BCDIN3D-AS1
AC084824.4
AC095057.3
GABPB1-AS1
AL021368.2
PPP1R14B-AS1
SEC24B-AS1
ACVR2B-AS1
ILF3-DT
AL391834.2
AC020917.4
AC012467.2
AC026471.4
AC092117.1
AC093227.1
SNHG20
SGMS1-AS1
AC104825.1
AC139768.1
AC110285.2
AC007292.1
LINC00641
DICER1-AS1
AC009812.1
AC107027.3
AL662795.2
AL355574.1
AL021707.2
LINC01089
AC004803.1
ZNF529-AS1
SH3BP5-AS1
PAXBP1-AS1
KTN1-AS1
AC005332.4
AC007066.2
VASH1-AS1
MIR3936HG
ALOX12-AS1
WDFY3-AS2
BOLA3-AS1
EPB41L4A-AS1
AC008969.1
TPT1-AS1
CCNT2-AS1
AL596202.1
AC025159.1
AF131215.6
LINC00663
AC022107.1
AL157392.3
SATB1-AS1
PDCD4-AS1
CCDC39
C21orf62-AS1
AL354892.2
AC037459.2
AP001486.2
AL117339.4
PVT1
KLF3-AS1
OSER1-DT
AL512625.1
AC087854.1
AL513534.2
RPARP-AS1
LINC02593
TMEM147-AS1
AC012513.3
LINC00863
PCBP1-AS1
POLR2J4
AL162586.1
Z95115.1
AC024075.1
AC104581.4
AL109811.2
AC009113.1
AL450384.2
AL513550.1
H1FX-AS1
THUMPD3-AS1
AF131215.5
AL133367.1
LINC00921
DNAJC3-DT
SEMA3F-AS1
MIR4453HG
TRAF3IP2-AS1
SNHG14
AC245452.1
LINC00852
LINC00667
LINC00653
NKILA
AC099778.1
Z97989.1
CCDC183-AS1
STX18-AS1
PSMA3-AS1
AC127024.5
AC018665.1
BDNF-AS
AC107068.1
AC107375.1
AL391684.1
SLC25A25-AS1
CKMT2-AS1
AC093010.3
AC022916.1
GLIDR
AL035530.2
AC019131.2
AC012615.1
NDUFA6-DT
LINC01137
AL358472.2
ERVK13-1
AC083798.2
AC008669.1
MIR600HG
AC007485.2
AL596244.1
AC067750.1
AC005070.3
ZNF213-AS1
RAD51-AS1
AC060780.1
AC008124.1
AP000766.1
AC245060.5
AL445524.1
AC078846.1
CEBPB-AS1
AC093673.1
LINC00346
value
0.4
0.2
0.0
-0.2
-0.4
Freq
3
4
5

Fig. 5C

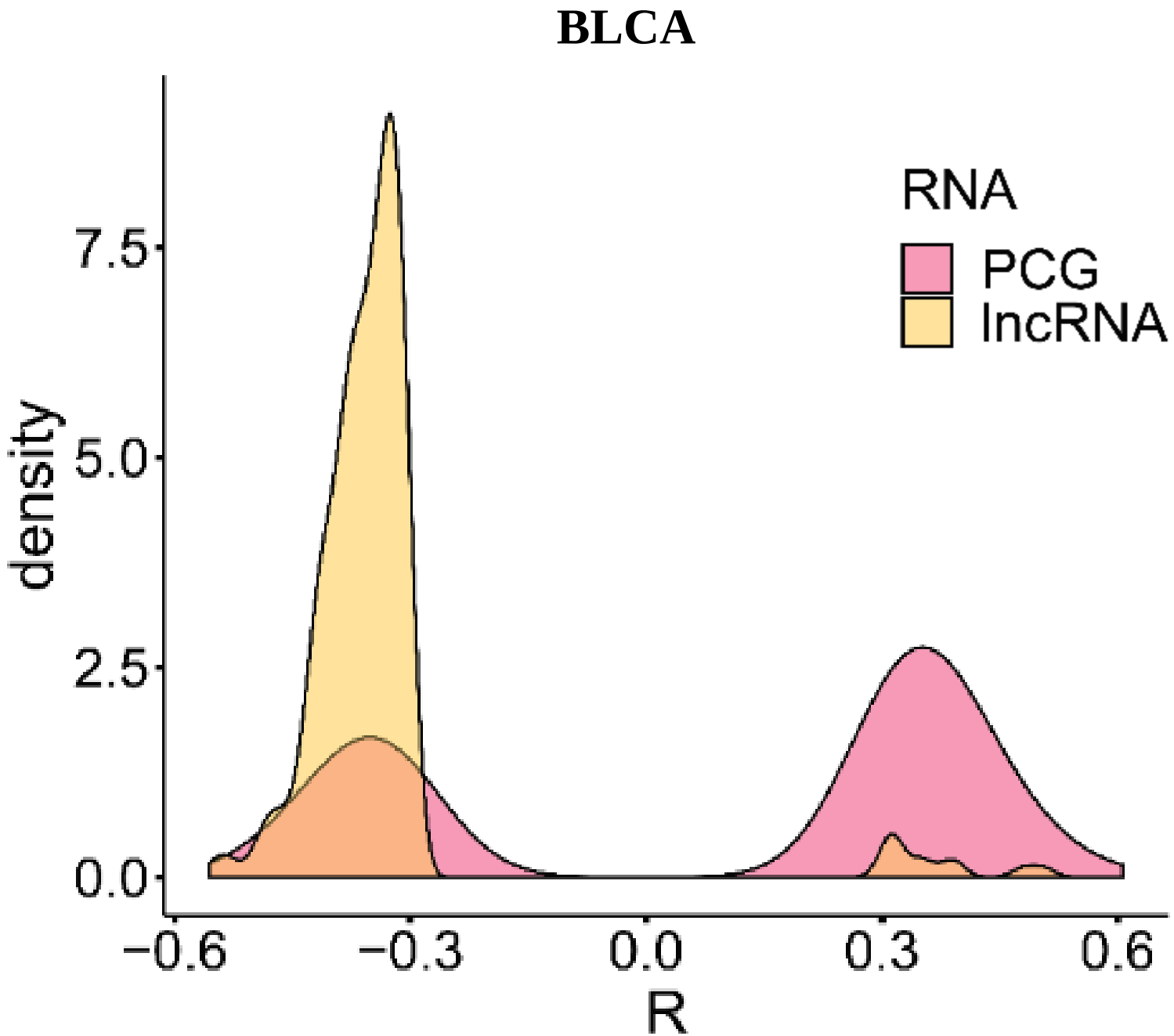


Fig. 5C

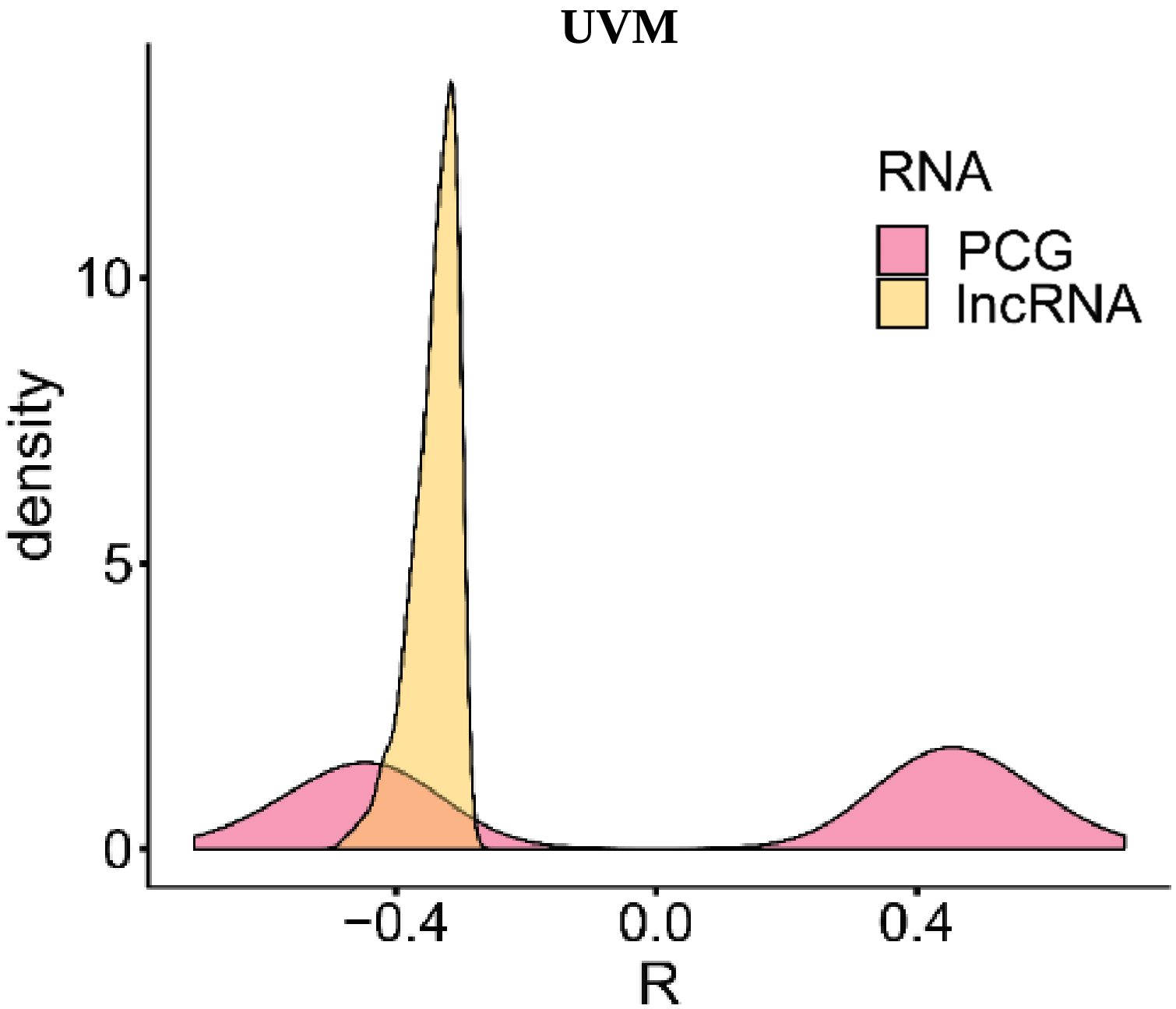


Fig. 5C

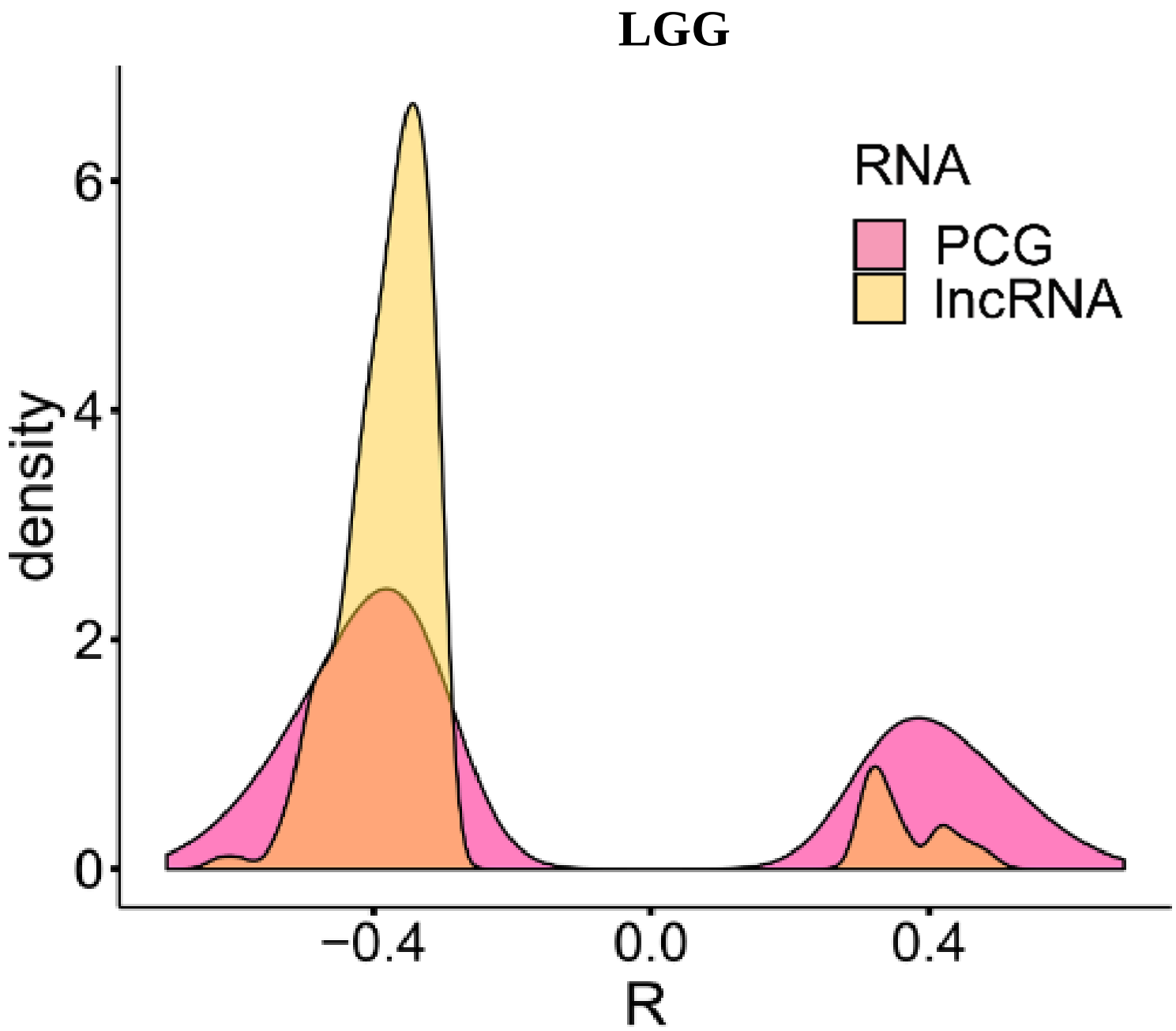


Fig. 5C

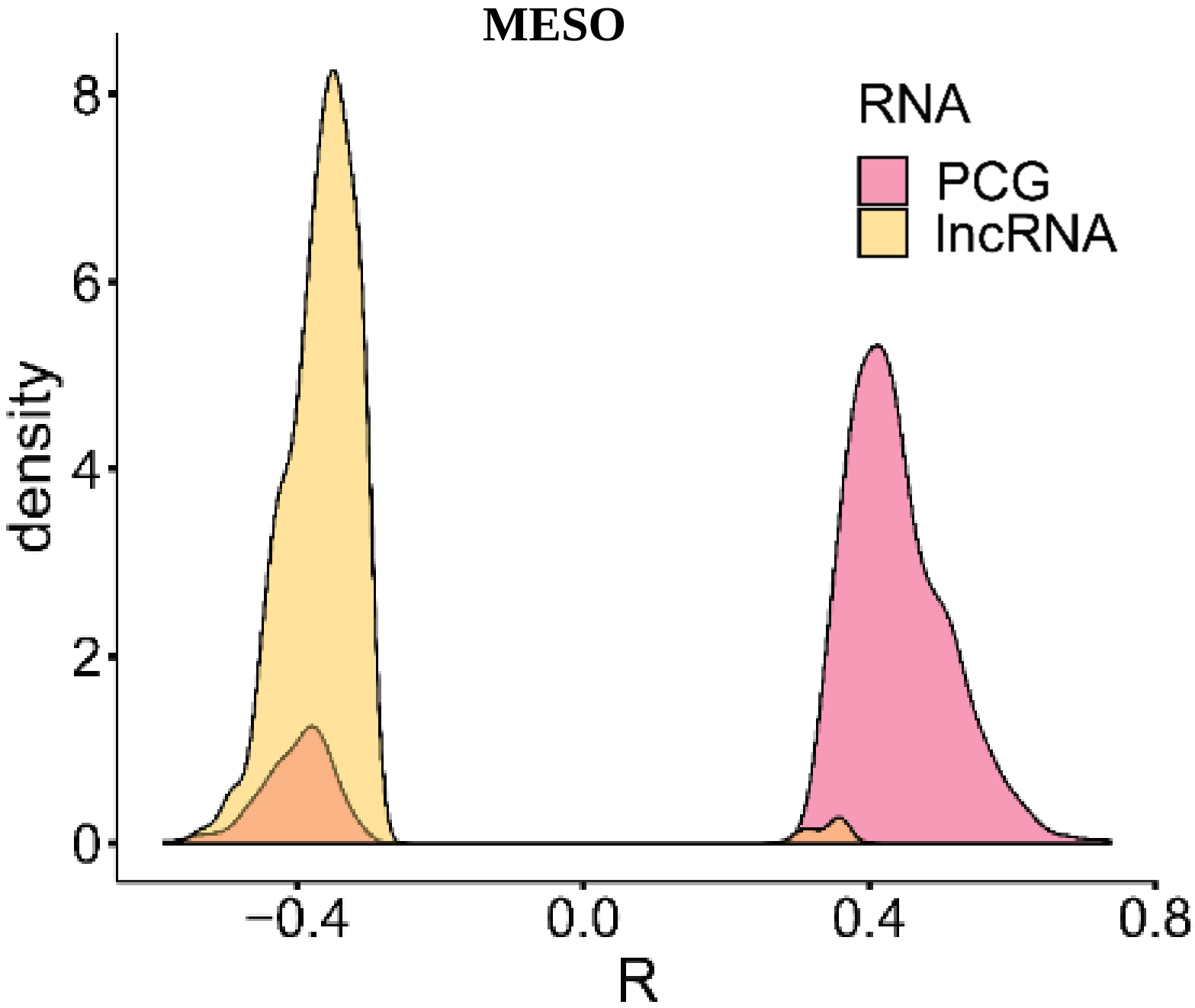


Fig. 5C

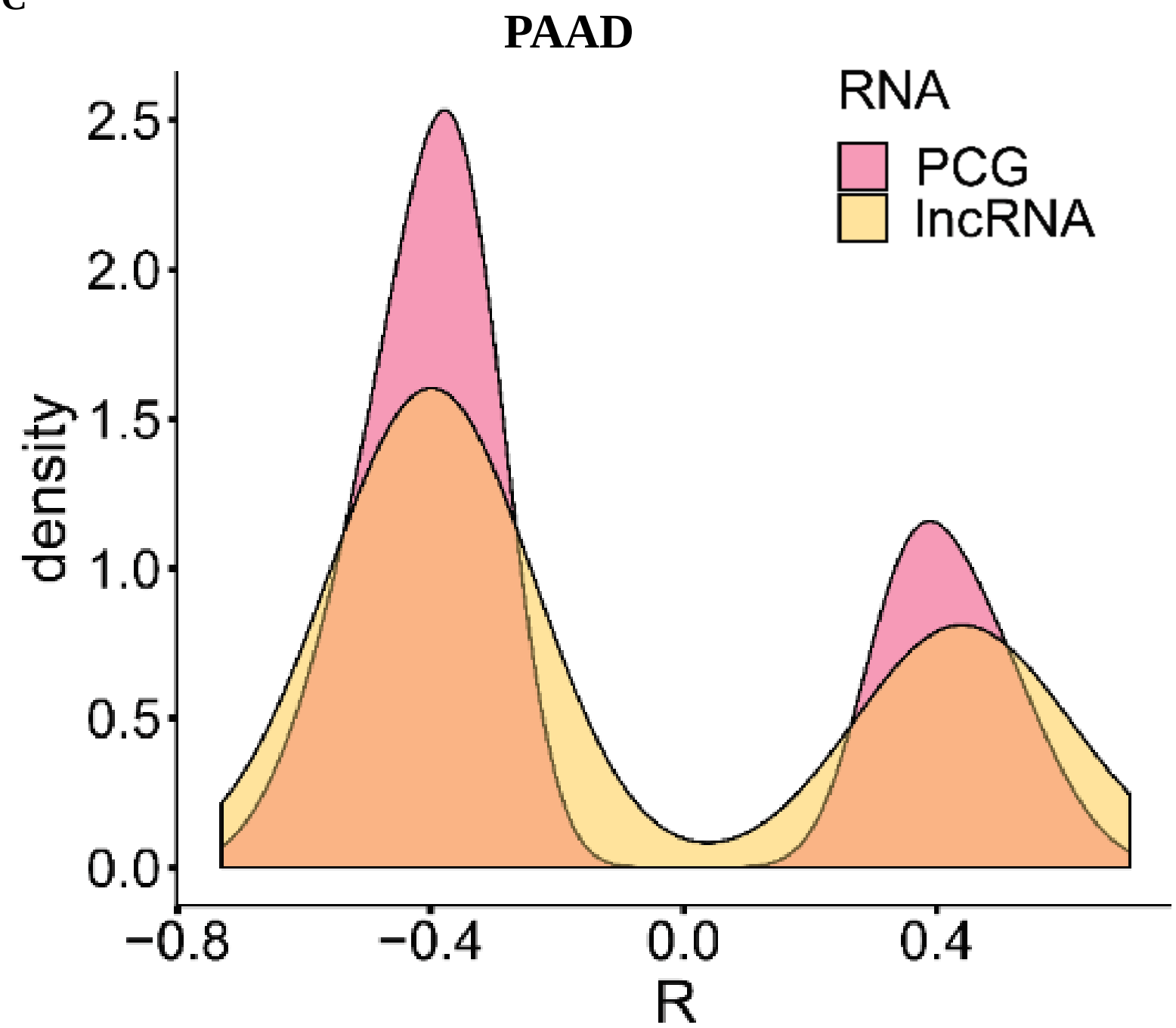


Fig. 5D

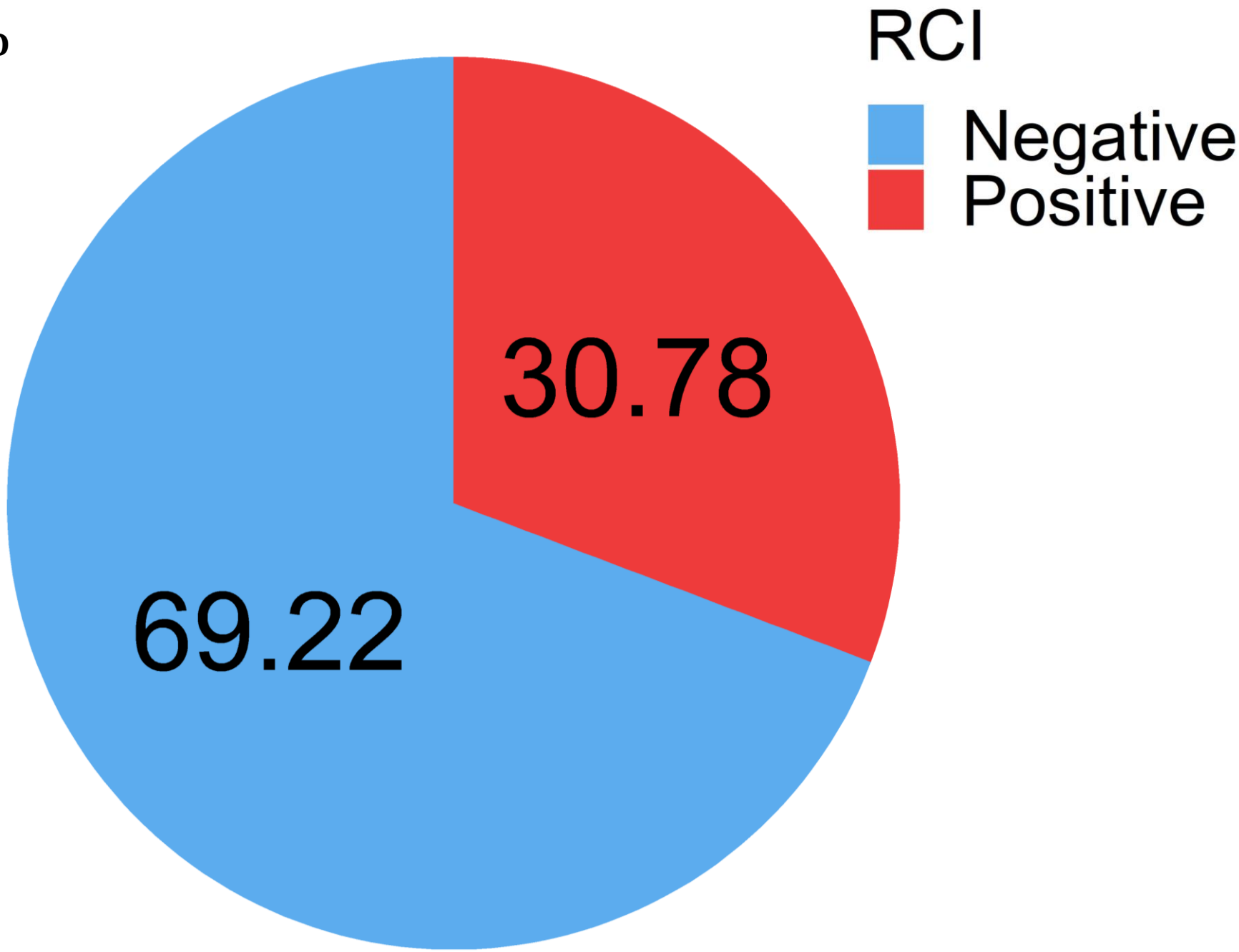


Fig. 5E

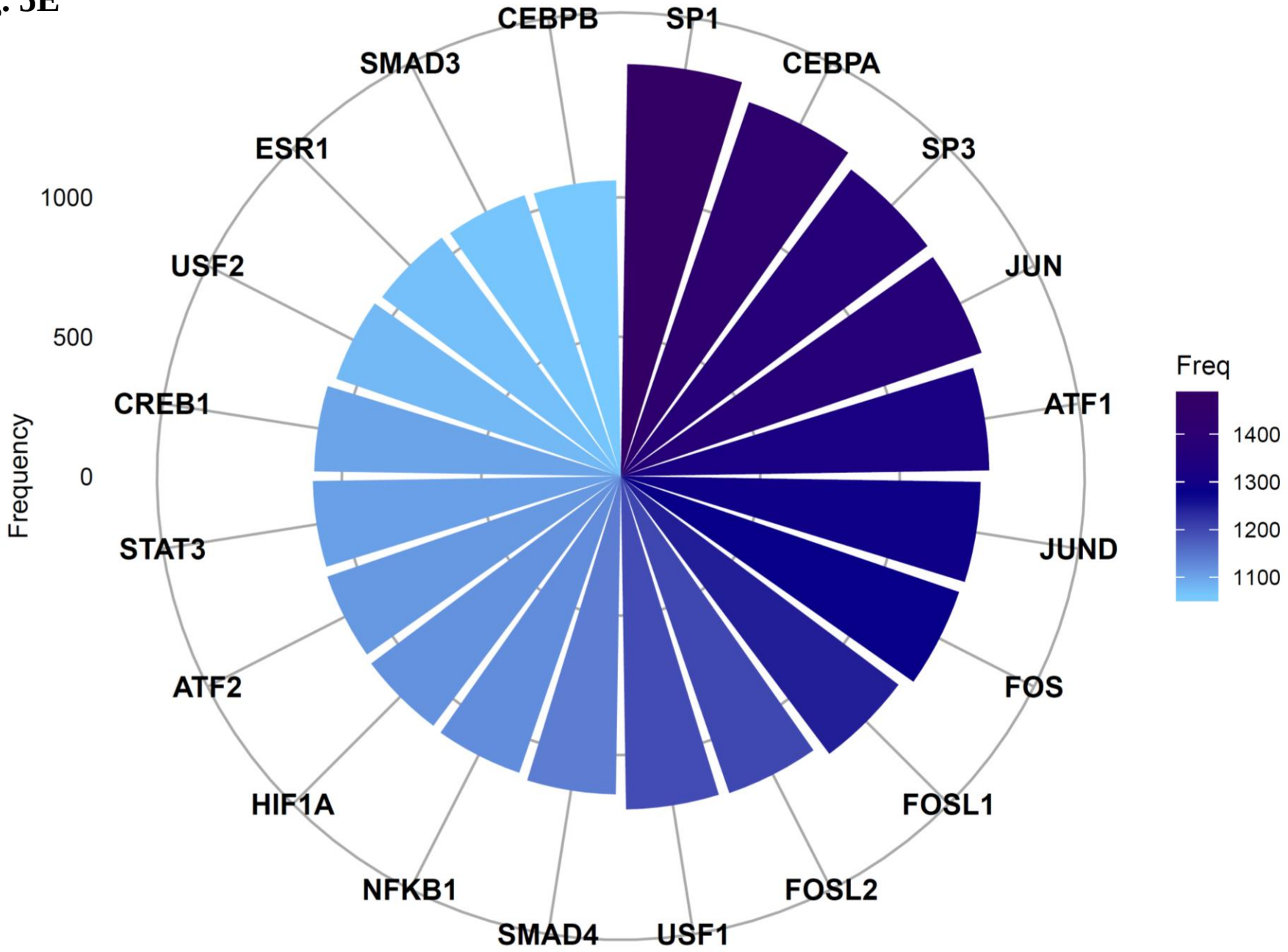

SP1
CEBPA
SP3
JUN
ATF1
JUND
FOS
FOSL1
FOSL2
USF1
SMAD4
NFKB1
HIF1A
ATF2
STAT3
CREB1
USF2
ESR1
SMAD3
CEBPB
Frequency
0
500
1000
Freq
1400
1300
1200
1100

Fig. 5F

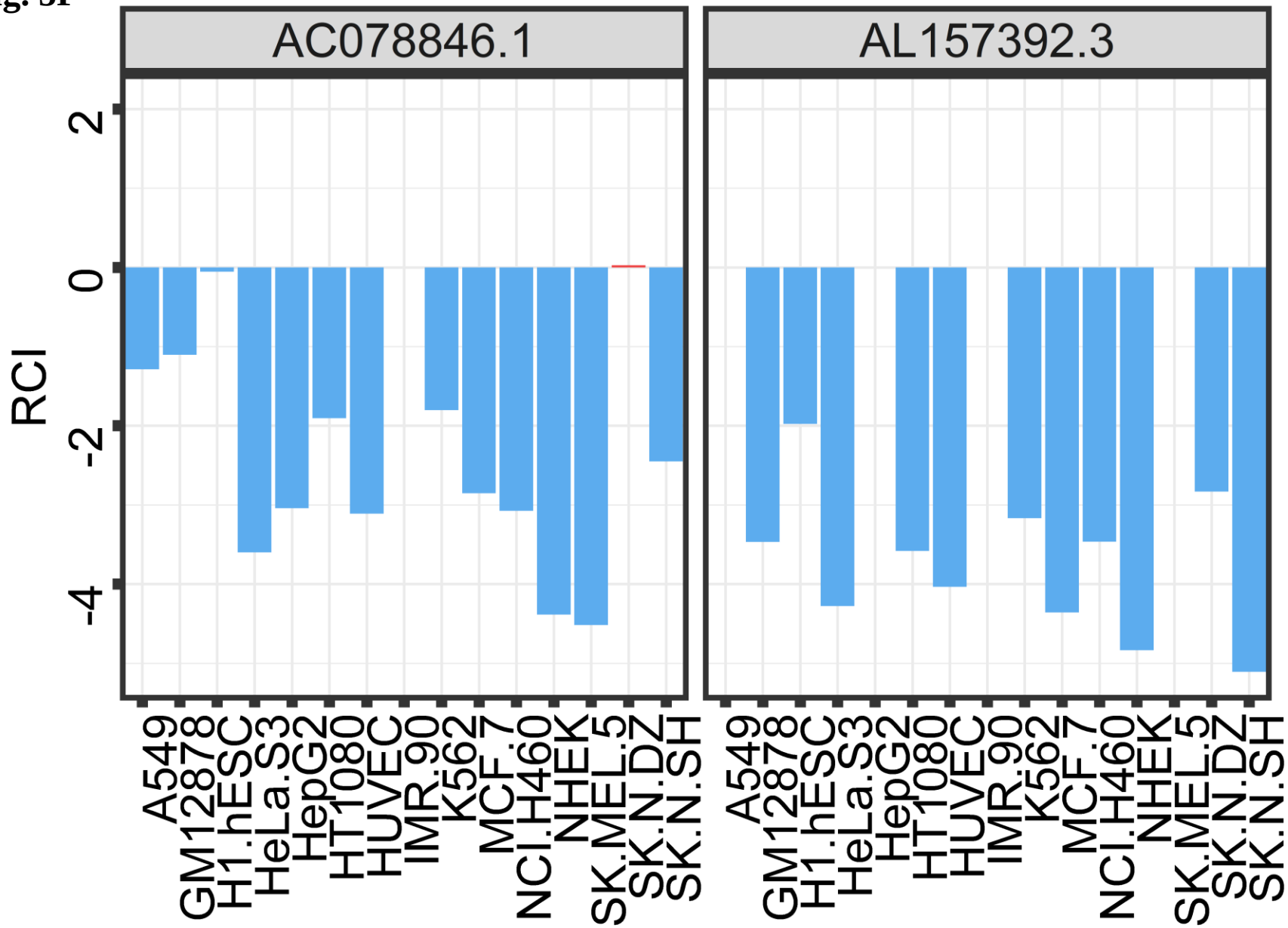

AC078846.1
AL157392.3
RCI
2
0
-2
-4
A549
GM12878
H1.hESC
HeLa.S3
HepG2
HT1080
HUVEC
IMR.90
K562
MCF.7
NCI.H460
NHEK
SK.MEL.5
SK.N.DZ
SK.N.SH

Fig. 5F

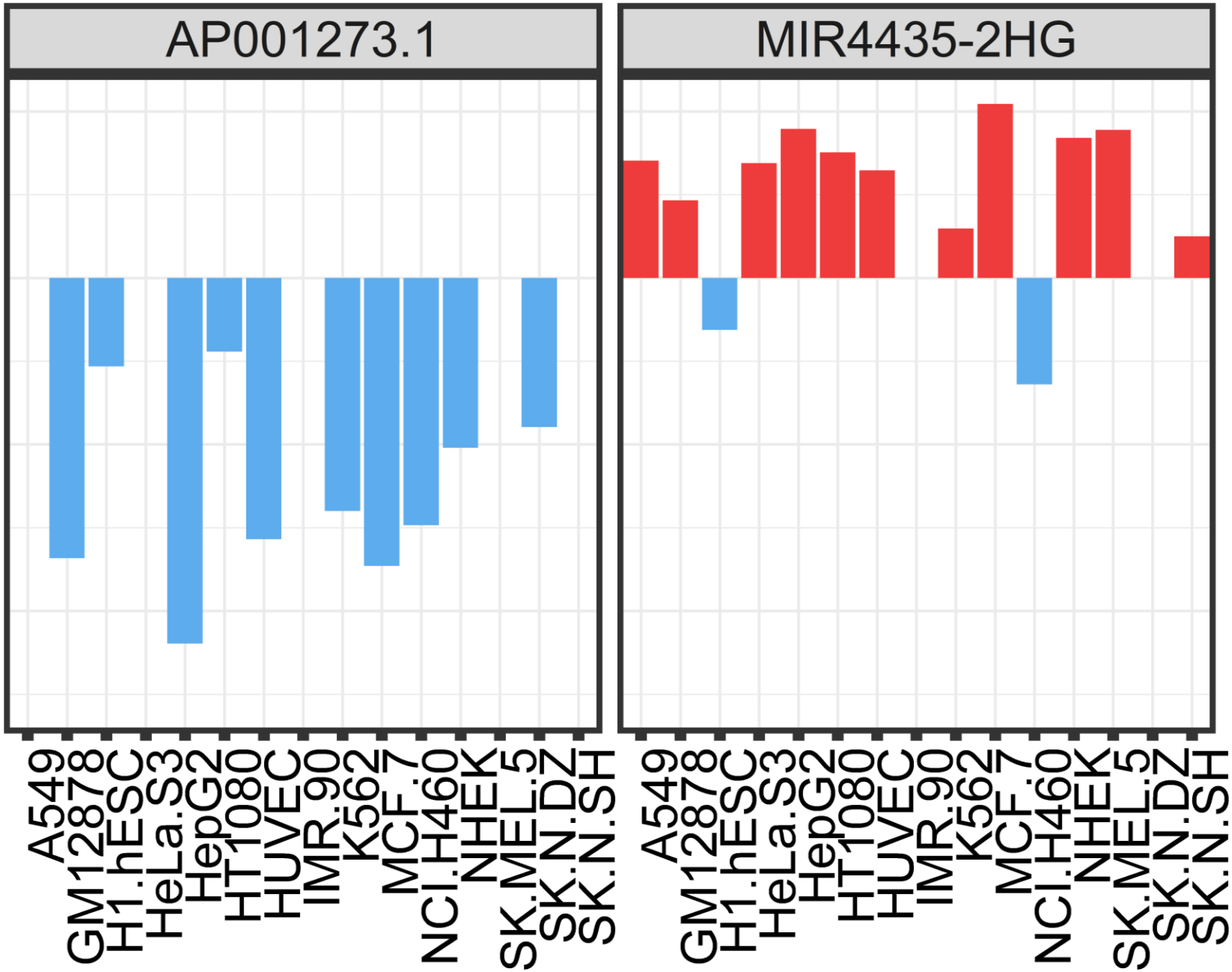

AP001273.1
MIR4435-2HG
A549
GM12878
H1.hESC
HeLa.S3
HepG2
HT1080
HUVEC
IMR.90
K562
MCF.7
NCI.H460
NHEK
SK.MEL.5
SK.N.DZ
SK.N.SH

Fig. 5F

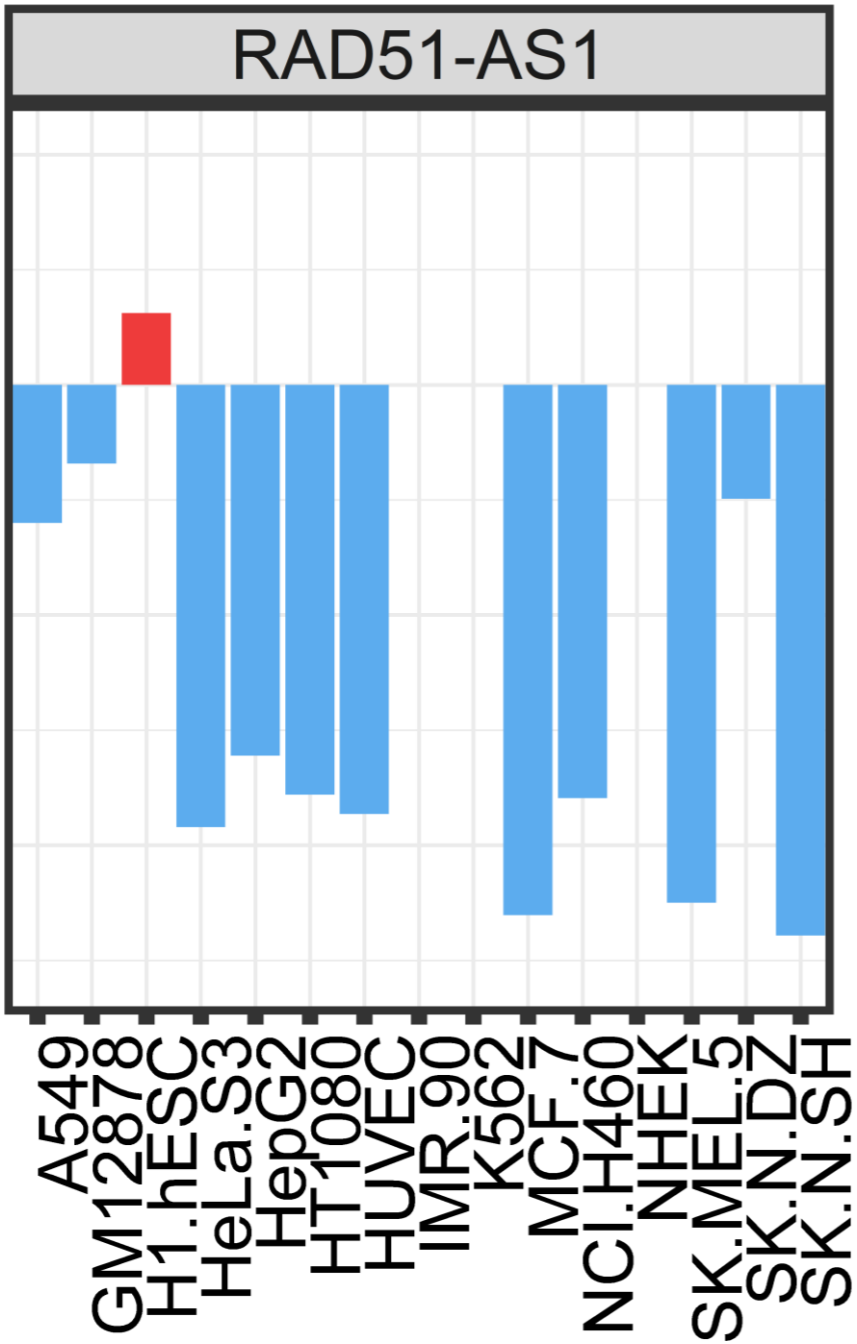

RAD51-AS1
A549
GM12878
H1.hESC
HeLa.S3
HepG2
HT1080
HUVEC
IMR.90
K562
MCF.7
NCI.H460
NHEK
SK.MEL.5
SK.N.DZ
SK.N.SH

Fig. 5G

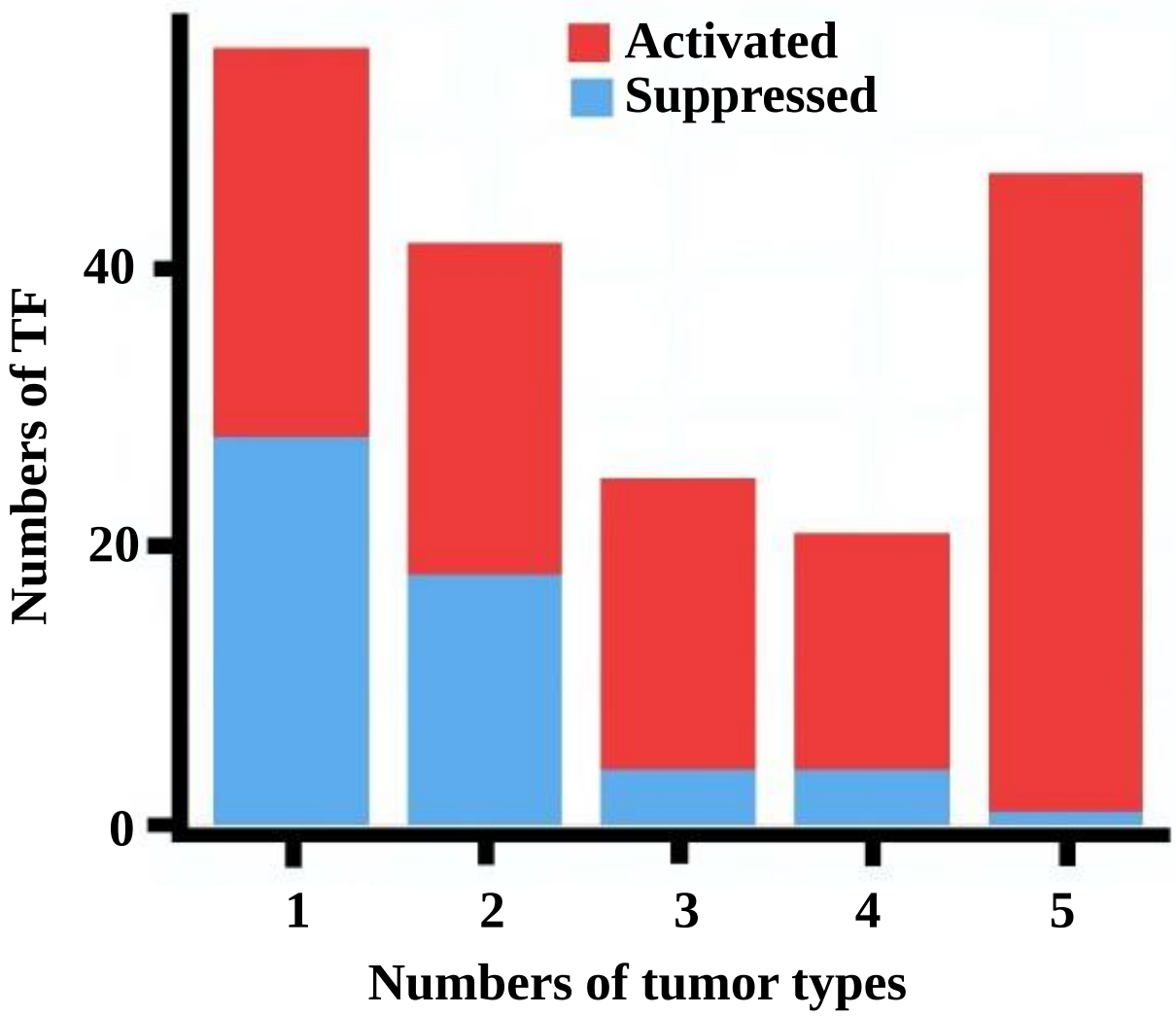

Activated
Suppressed
Numbers of TF
40
20
0
1
2
3
4
5
Numbers of tumor types

Fig. 5H

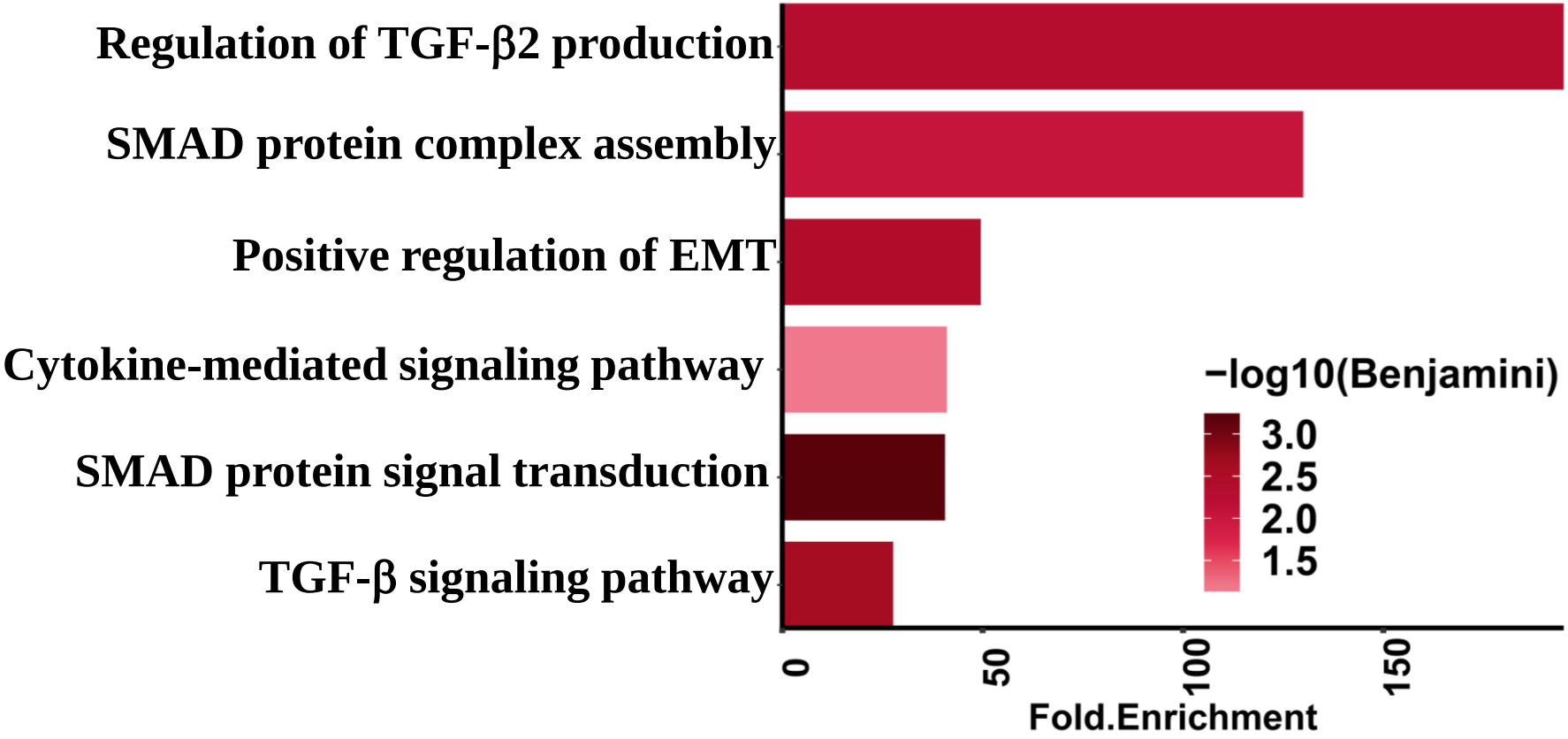

Regulation of TGF-β2 production
SMAD protein complex assembly
Positive regulation of EMT
Cytokine-mediated signaling pathway
SMAD protein signal transduction
TGF-β signaling pathway
−log10(Benjamini)
3.0
2.5
2.0
1.5
0
50
100
150
Fold.Enrichment

Fig. 5I

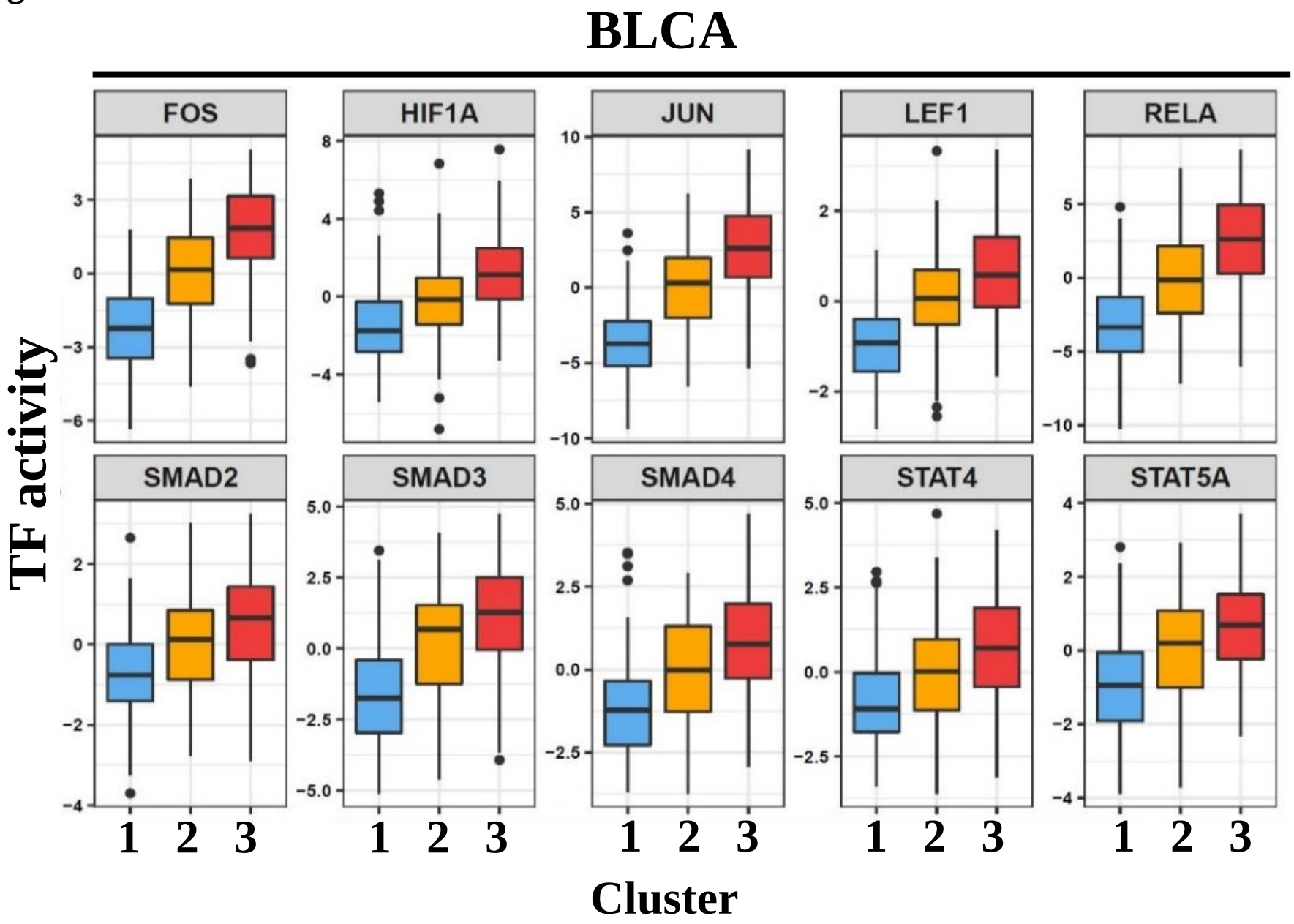

BLCA
FOS
HIF1A
JUN
LEF1
RELA
SMAD2
SMAD3
SMAD4
STAT4
STAT5A
TF activity
1 2 3
Cluster

Fig. 5I

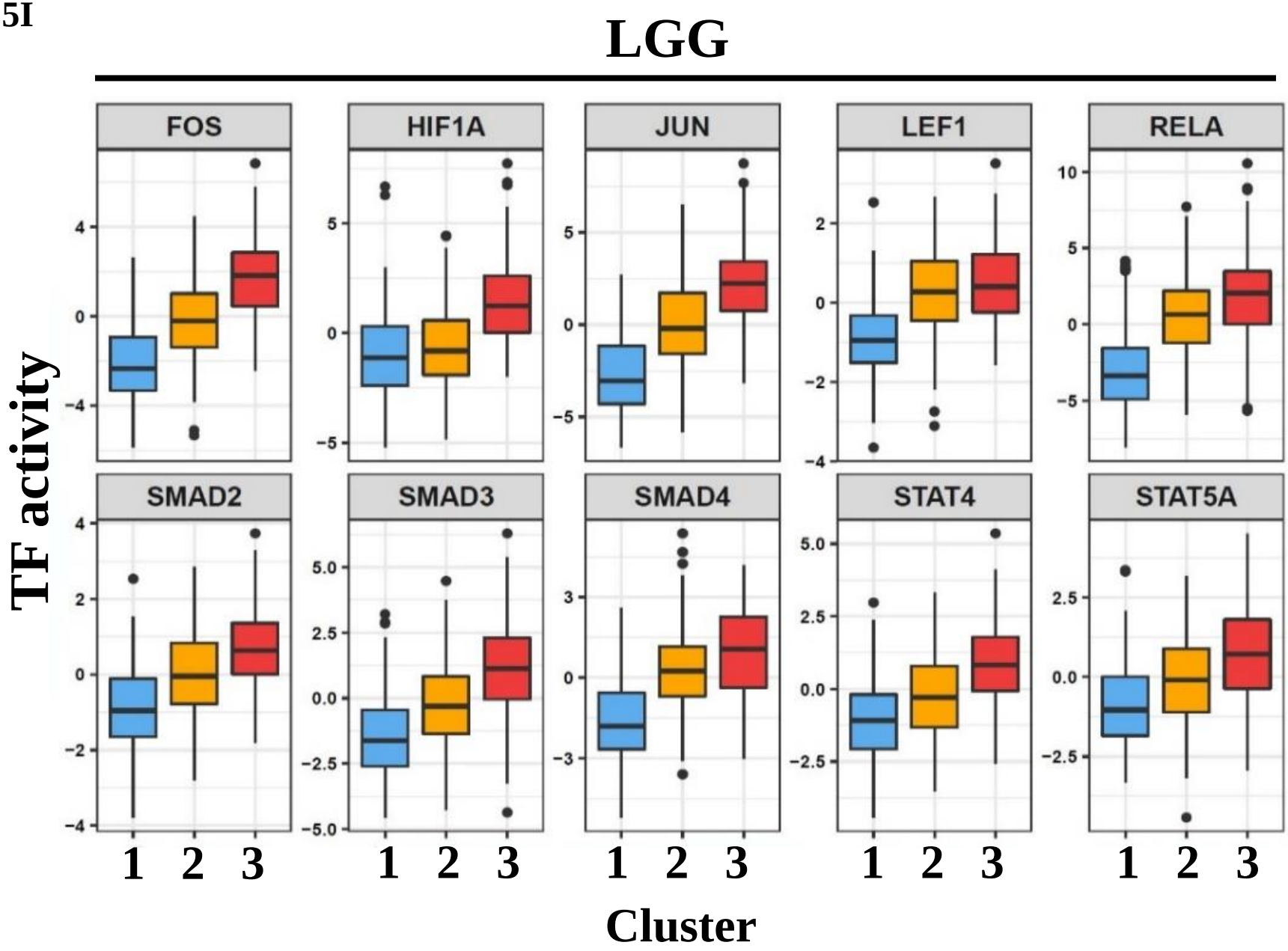

LGG
FOS
HIF1A
JUN
LEF1
RELA
SMAD2
SMAD3
SMAD4
STAT4
STAT5A
TF activity
1 2 3
Cluster

Fig. 5I

MESO

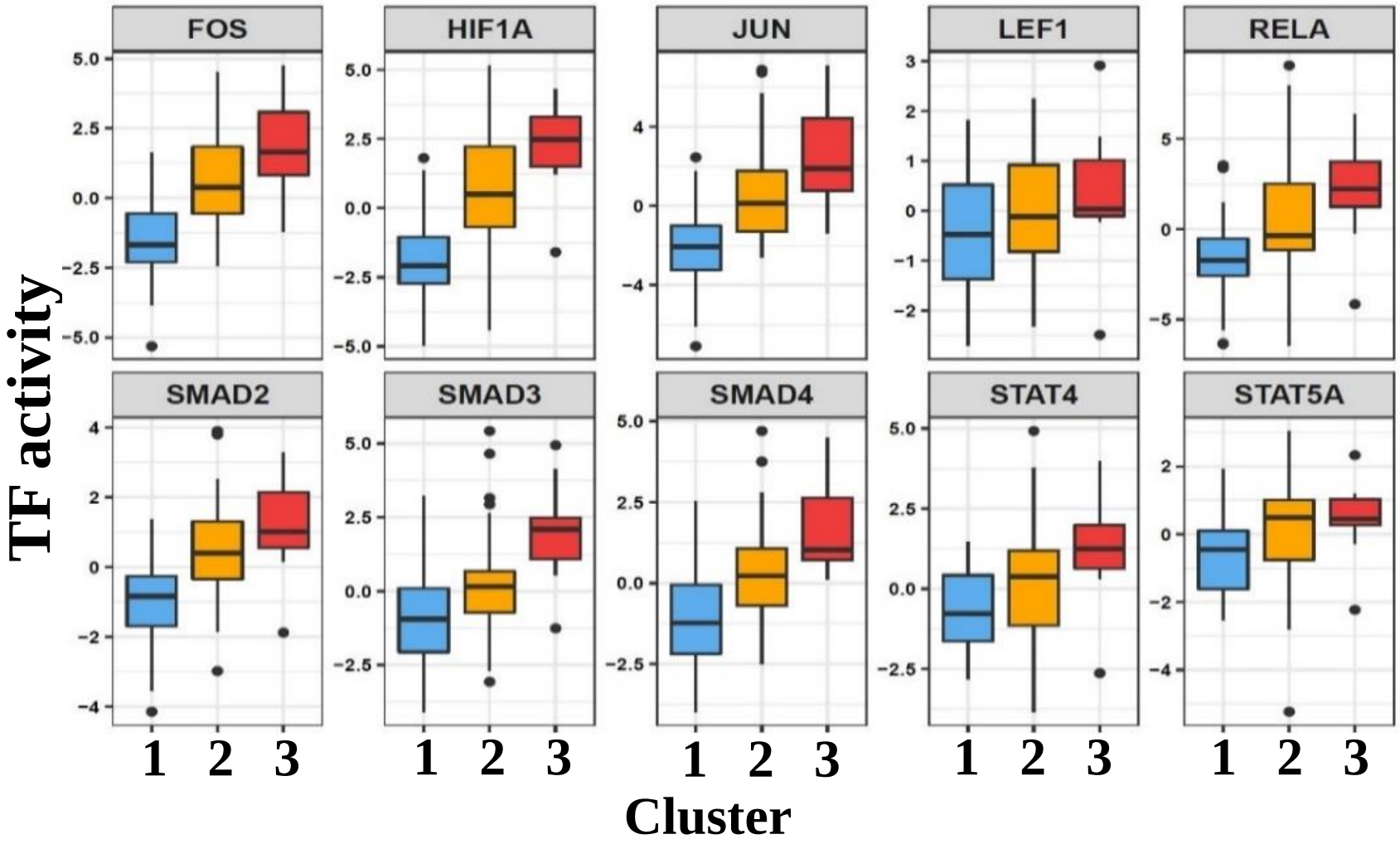

FOS
HIF1A
JUN
LEF1
RELA
SMAD2
SMAD3
SMAD4
STAT4
STAT5A
TF activity
1 2 3
Cluster

Fig. 5I

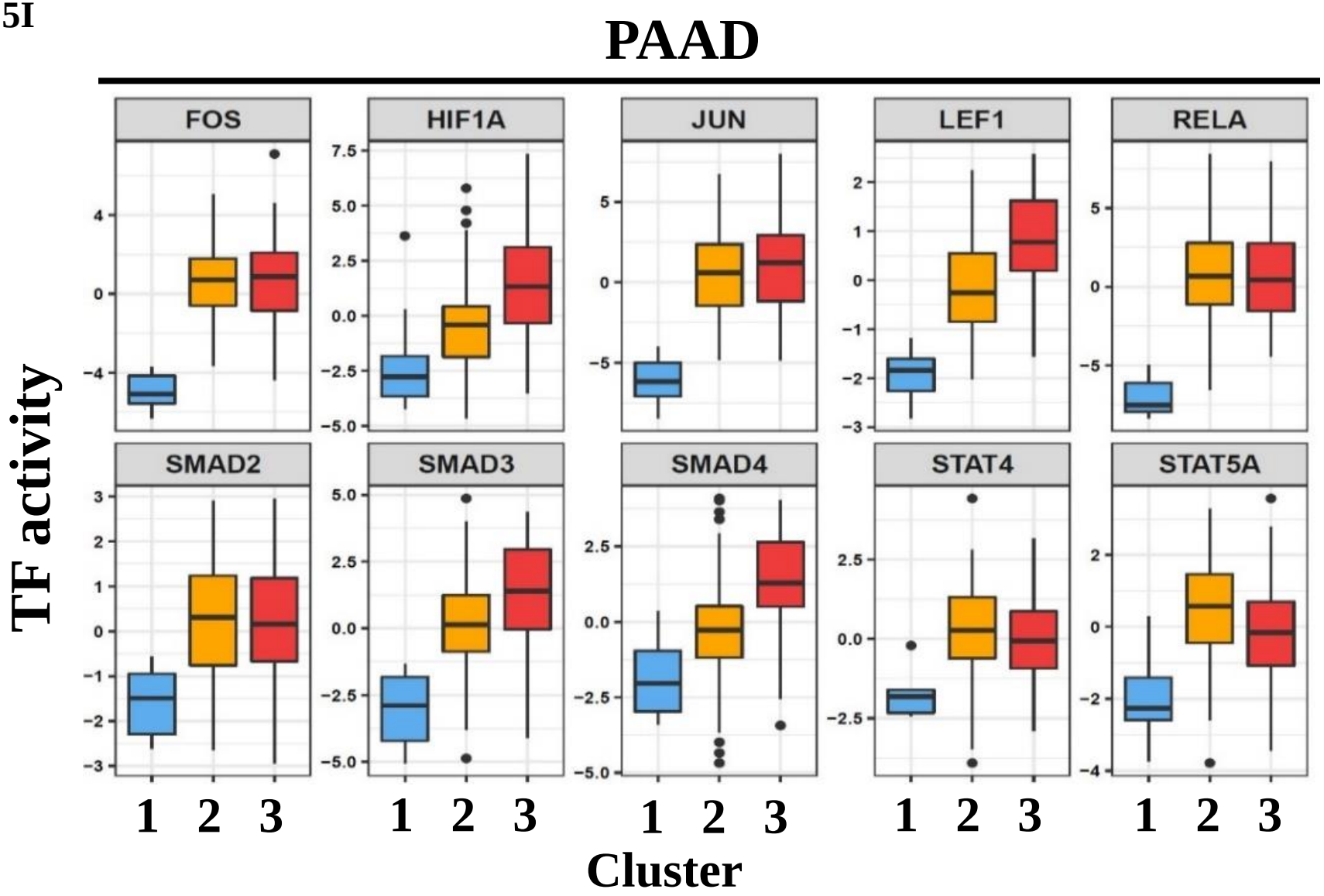

PAAD
FOS
HIF1A
JUN
LEF1
RELA
SMAD2
SMAD3
SMAD4
STAT4
STAT5A
TF activity
1 2 3
Cluster

Fig. 5I

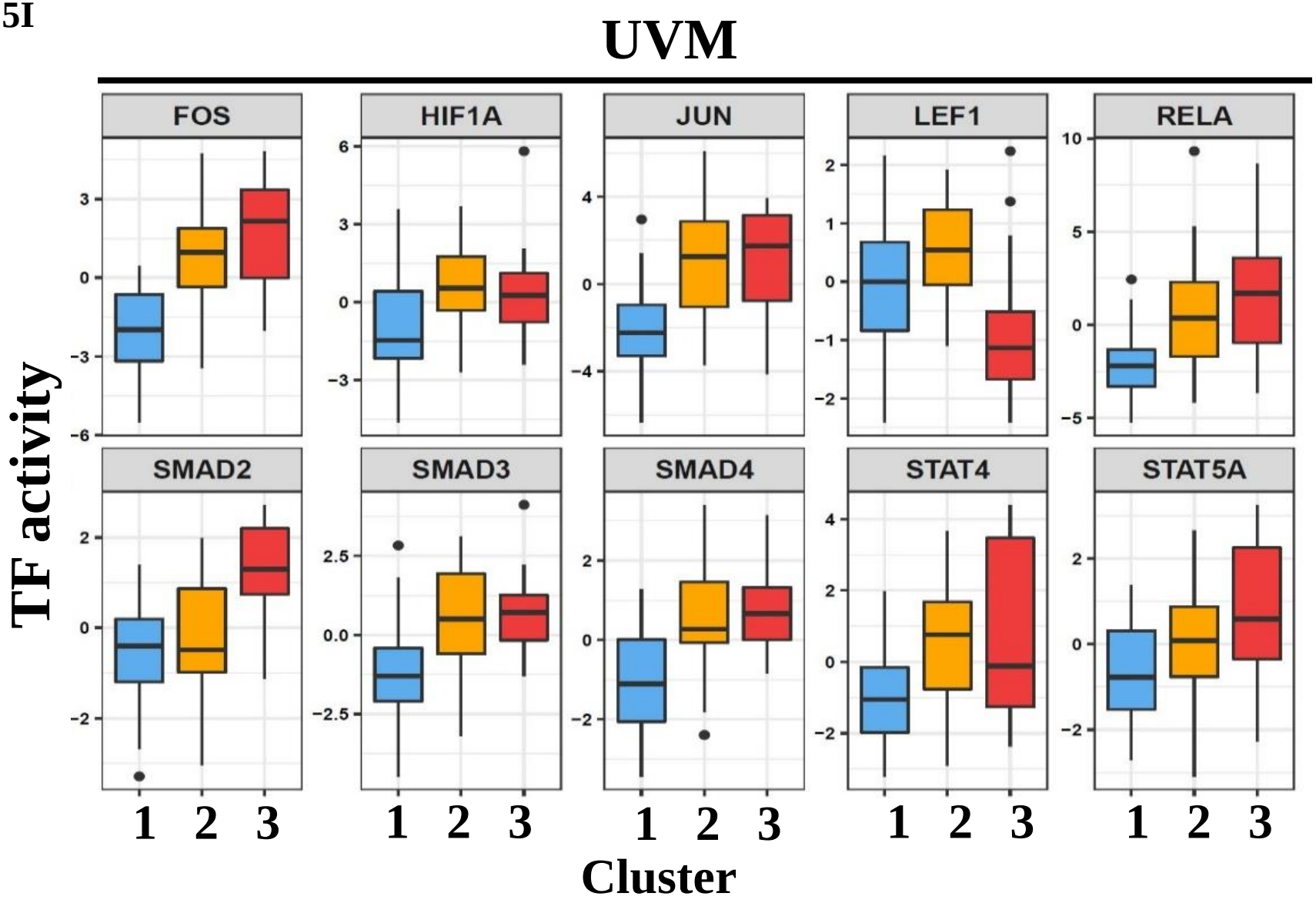

UVM
FOS
HIF1A
JUN
LEF1
RELA
SMAD2
SMAD3
SMAD4
STAT4
STAT5A
TF activity
1 2 3
Cluster

Fig. 5J

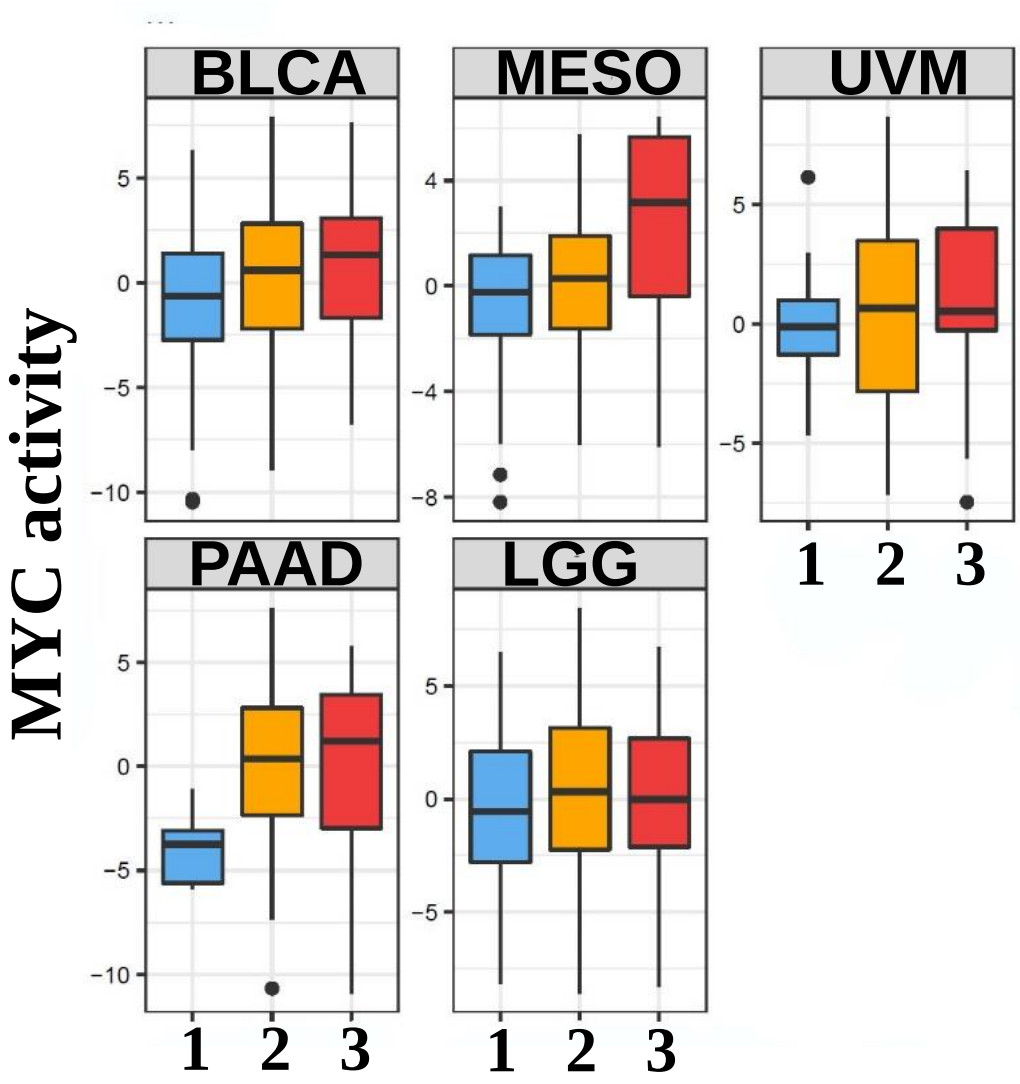


Fig. 5K

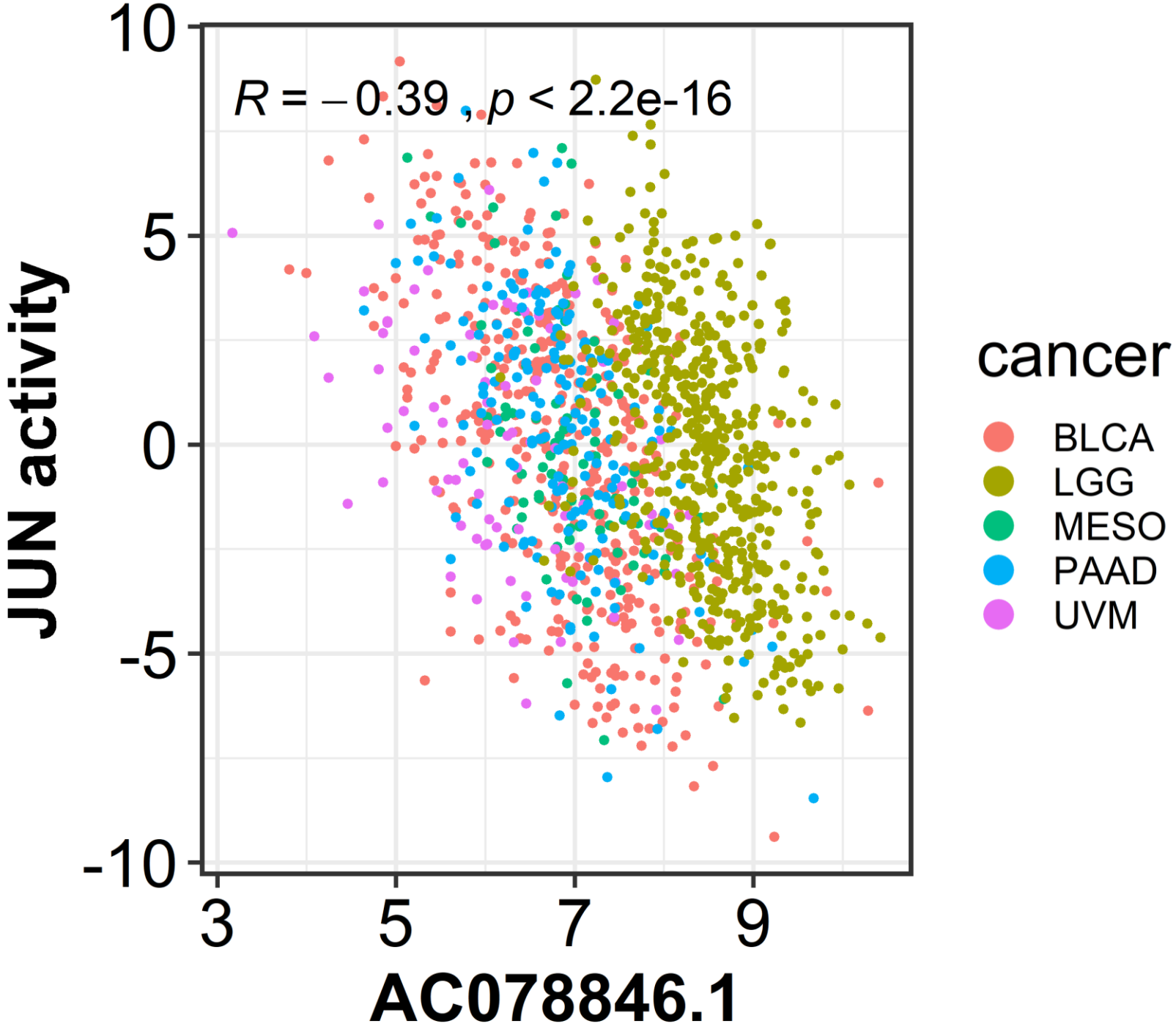

R = −0.39 , p < 2.2e-16
JUN activity
AC078846.1
10
5
0
-5
-10
3
5
7
9
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

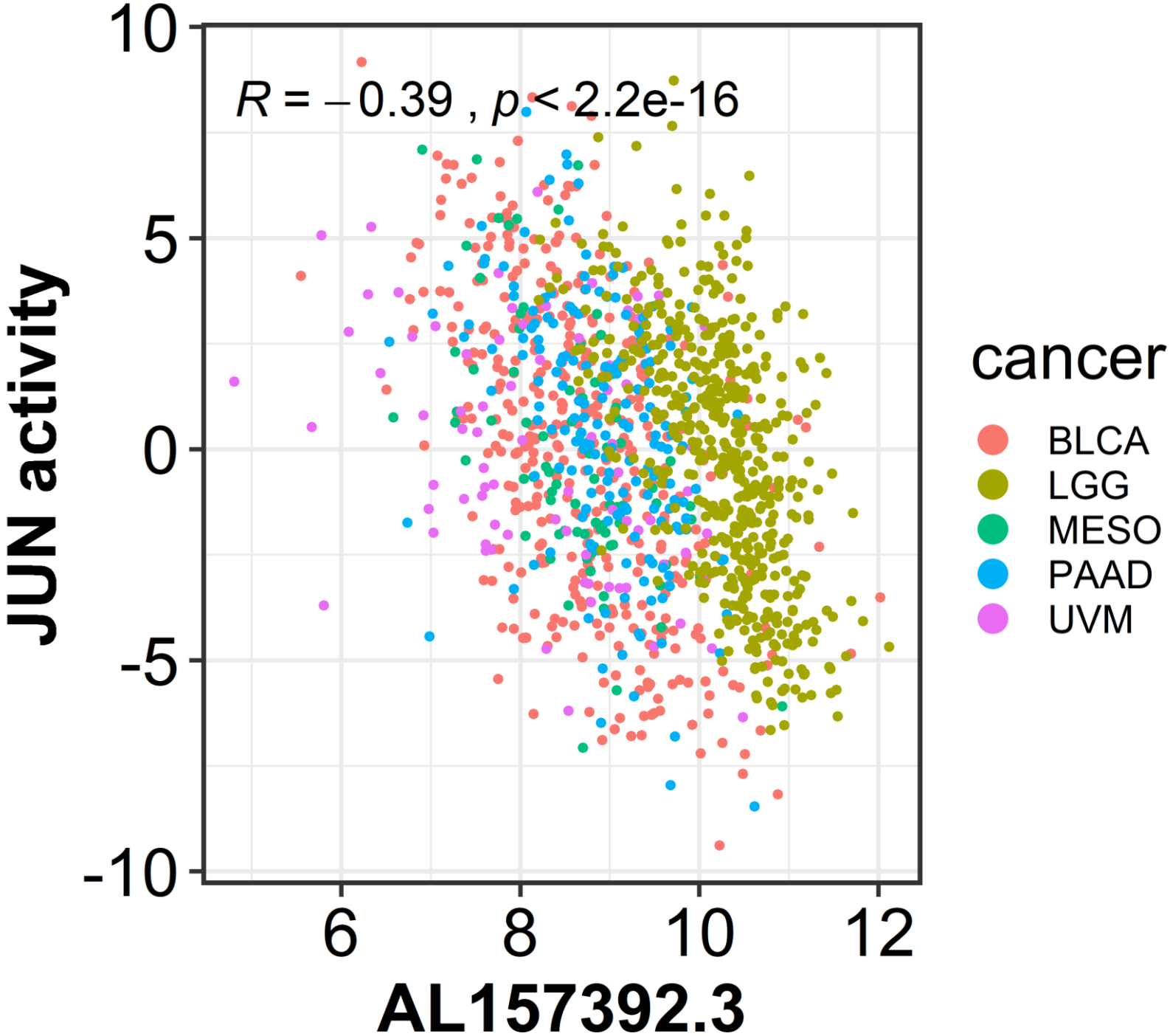

R = −0.39 , p < 2.2e-16
JUN activity
AL157392.3
10
5
0
-5
-10
6
8
10
12
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

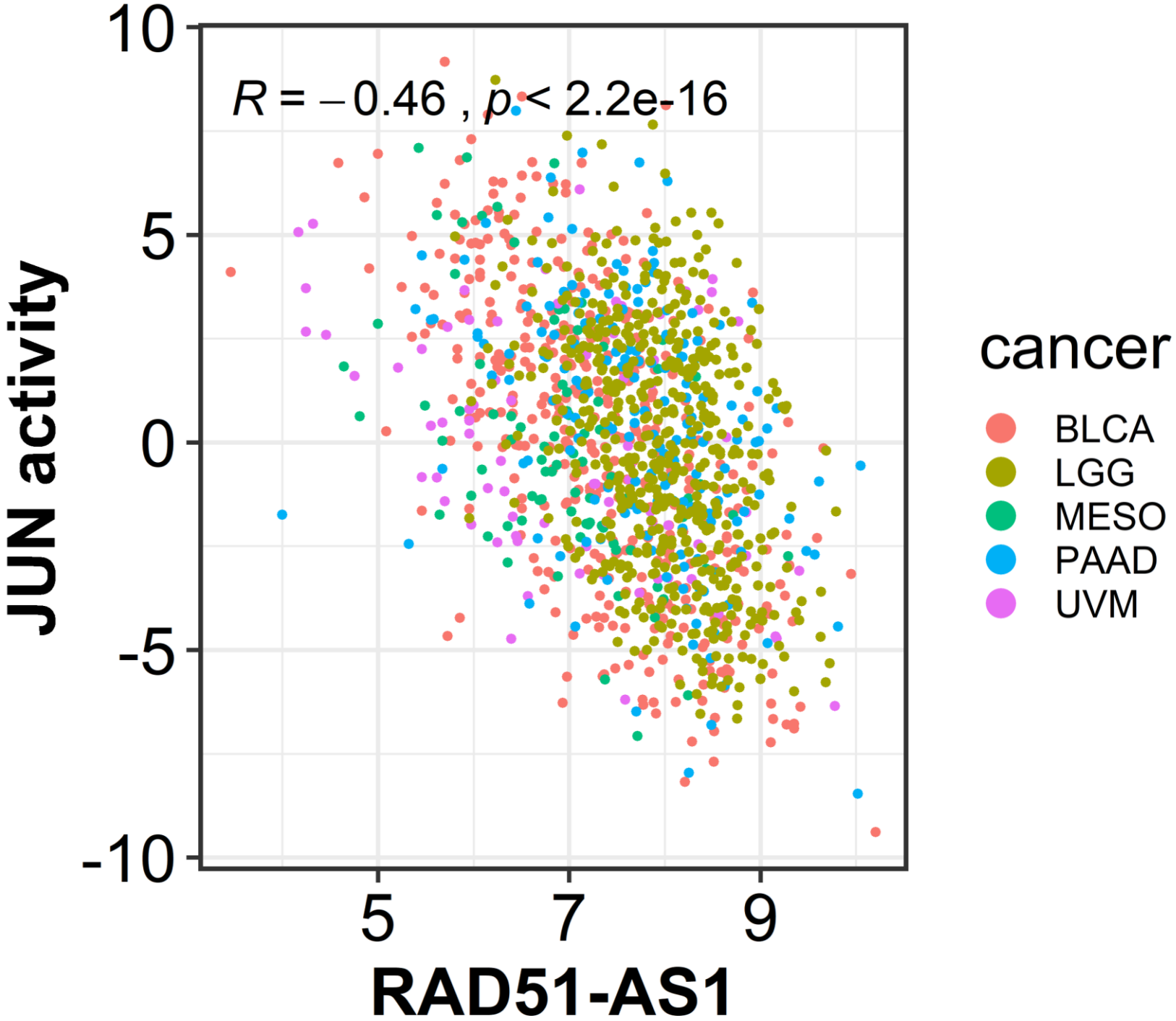

R = −0.46 , p < 2.2e-16
JUN activity
RAD51-AS1
10
5
0
-5
-10
5
7
9
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

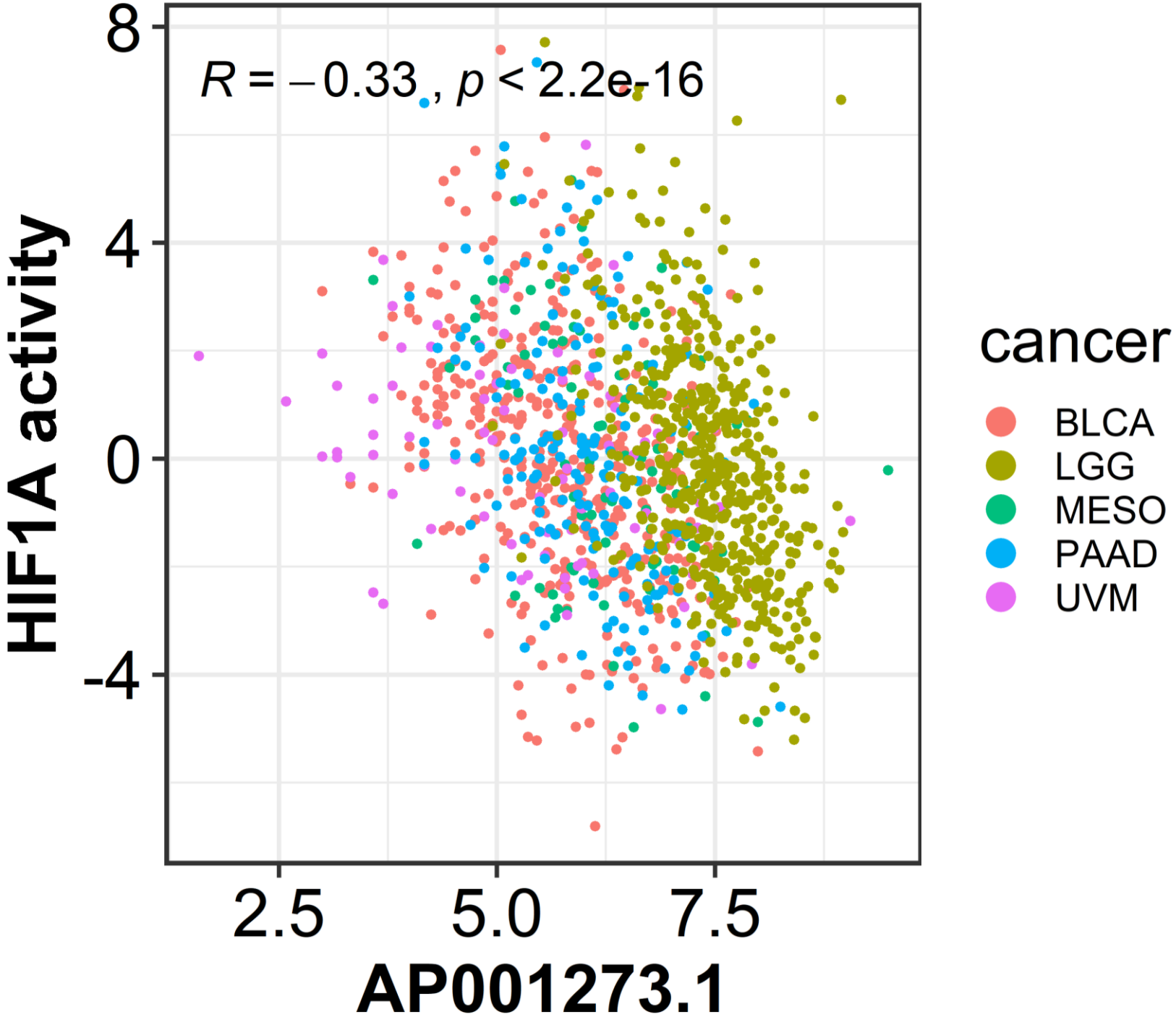

R = −0.33 , p < 2.2e-16
HIF1A activity
8
4
0
-4
2.5
5.0
7.5
AP001273.1
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

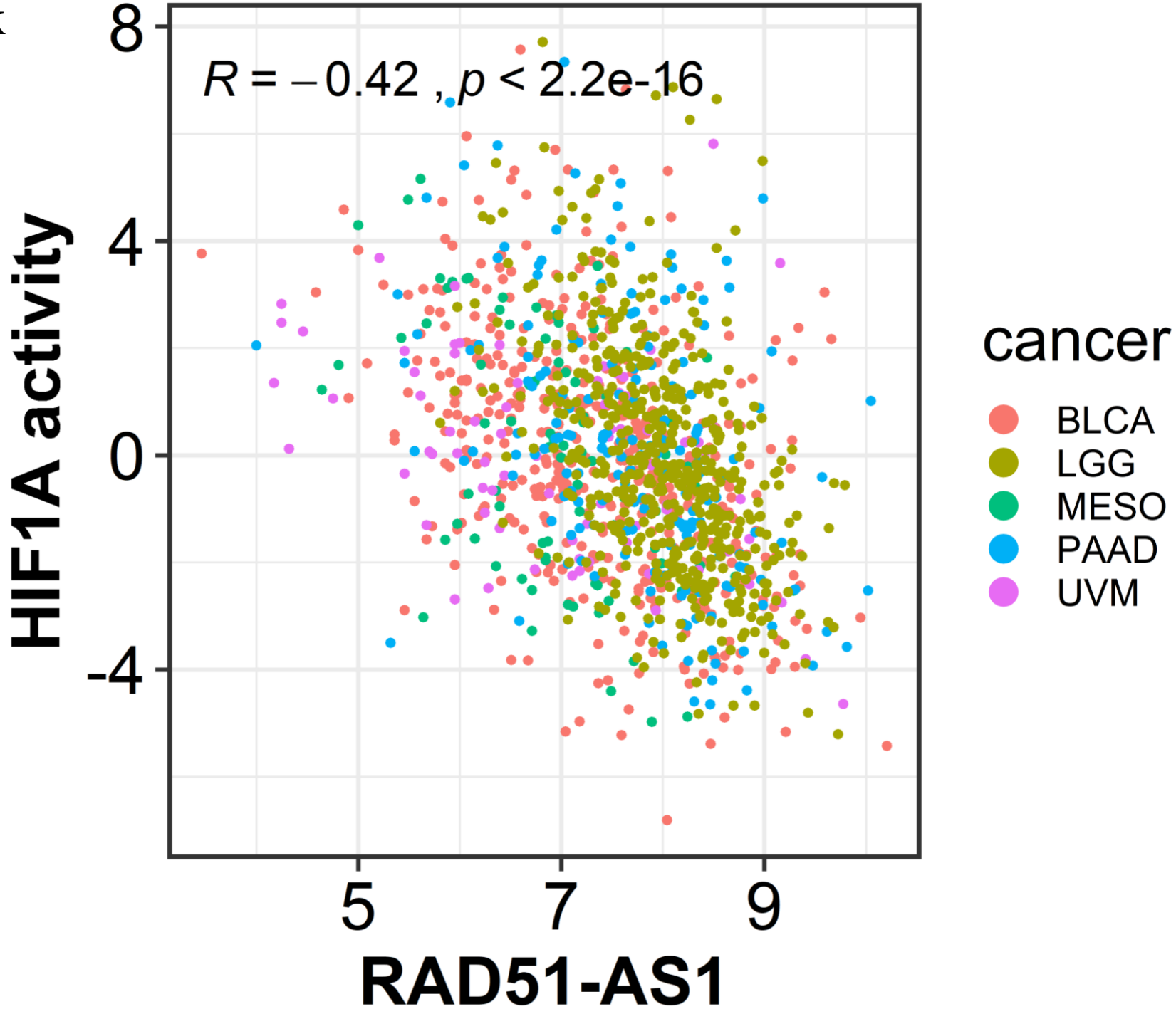

R = −0.42 , p < 2.2e-16
HIF1A activity
8
4
0
-4
5
7
9
RAD51-AS1
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

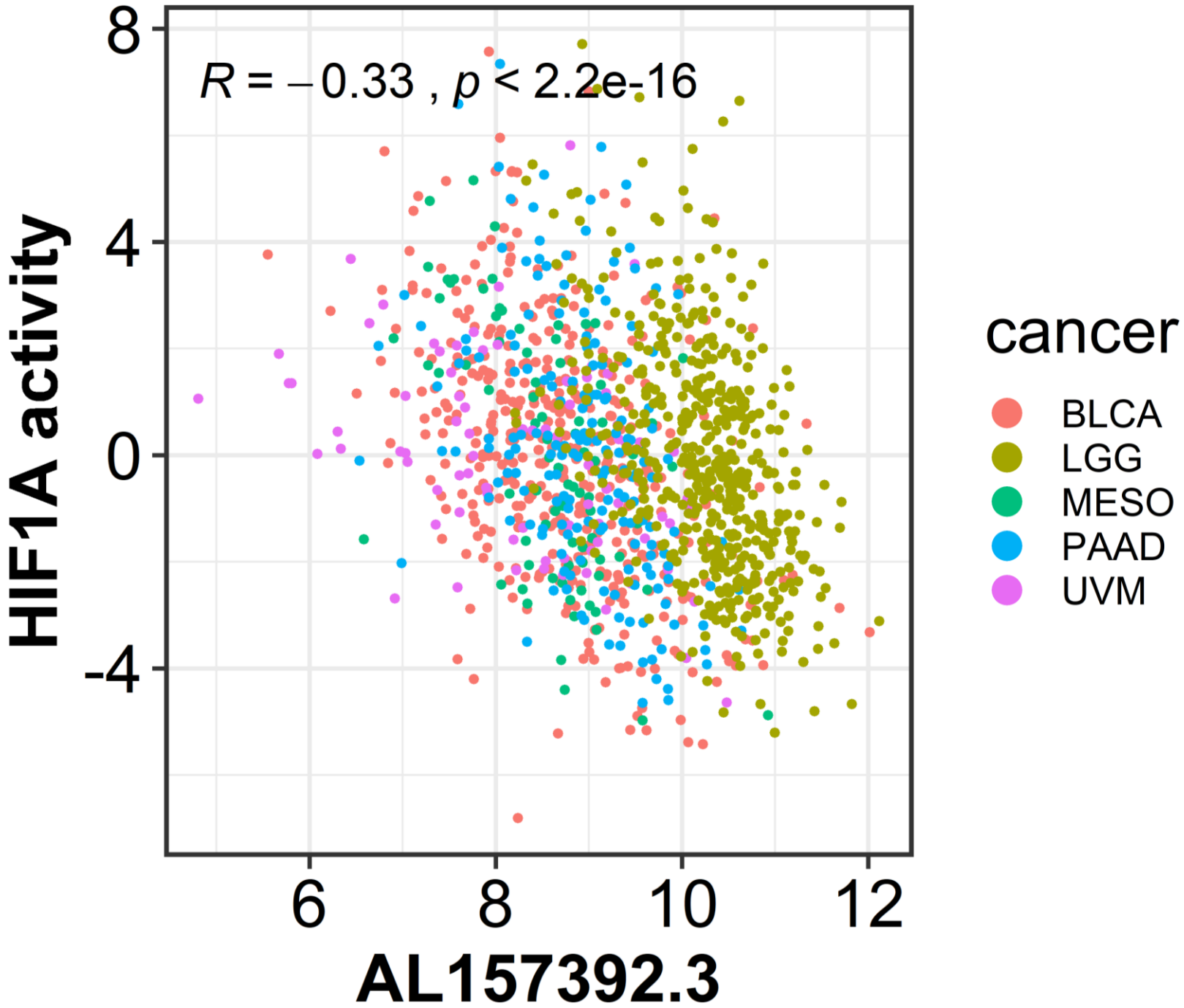

R = −0.33 , p < 2.2e-16
HIF1A activity
8
4
0
-4
6
8
10
12
AL157392.3
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

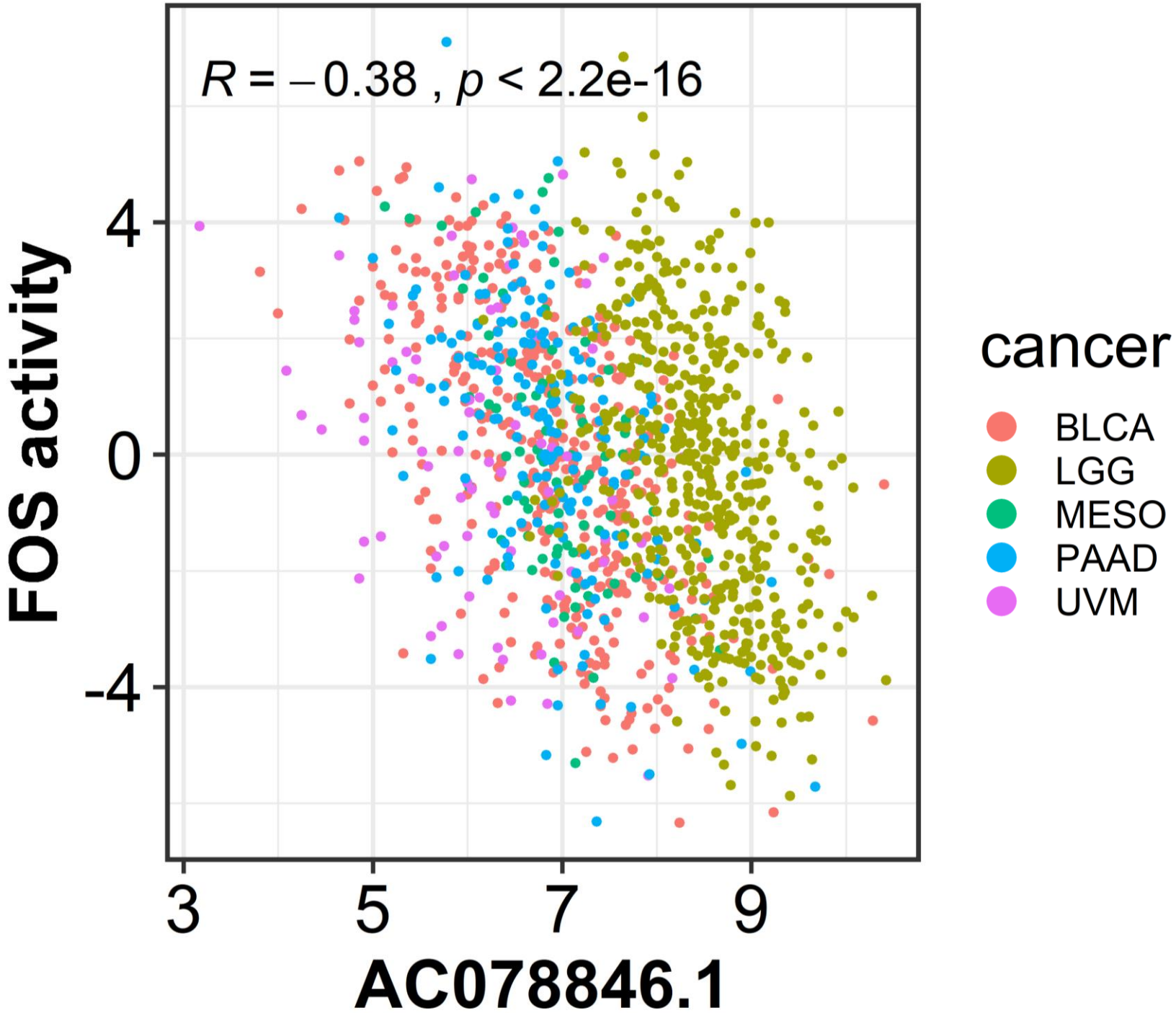

R = −0.38 , p < 2.2e-16
FOS activity
4
0
-4
3
5
7
9
AC078846.1
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 5K

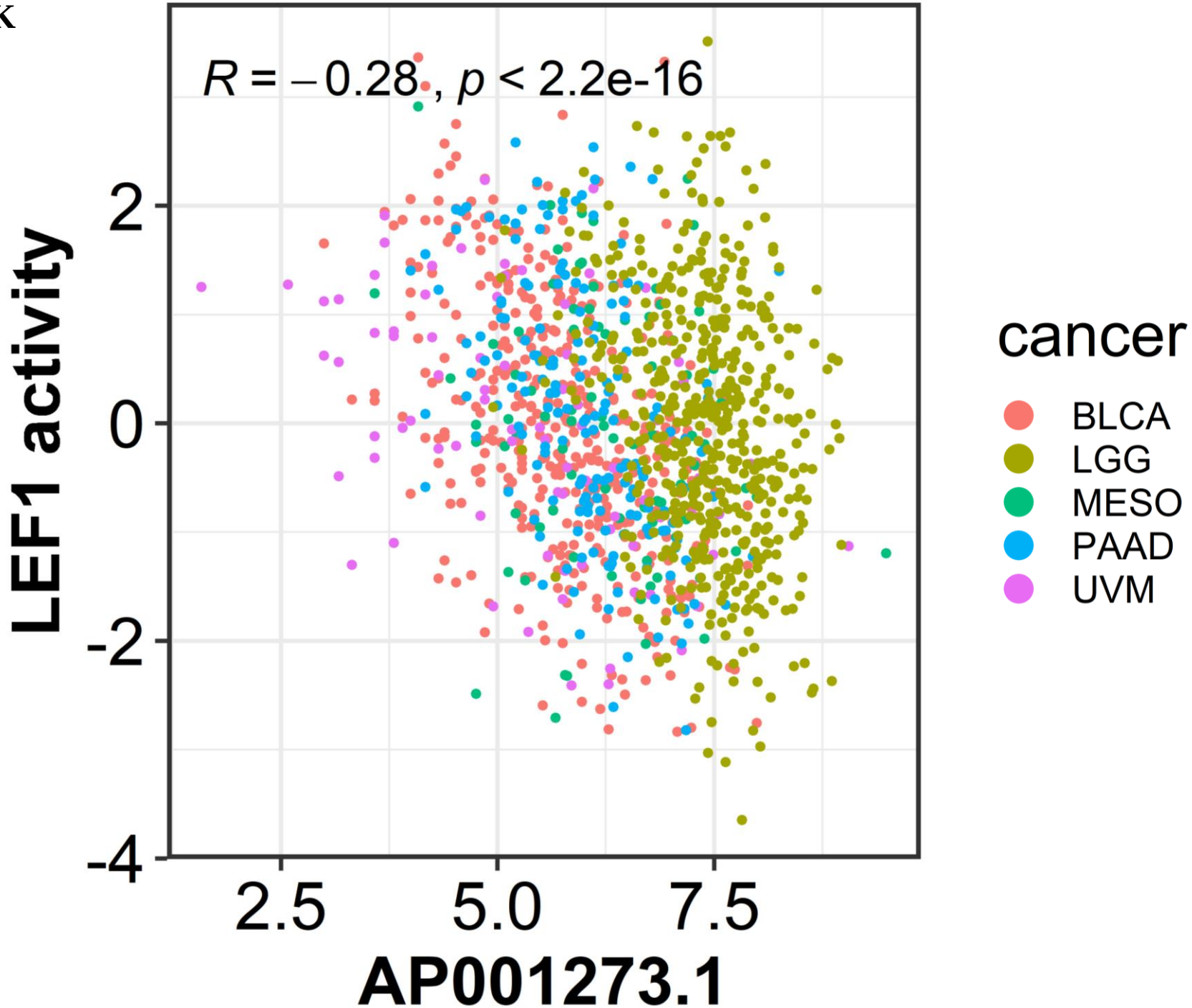

R = −0.28, p < 2.2e-16
LEF1 activity
2
0
-2
-4
2.5
5.0
7.5
AP001273.1
cancer
BLCA
LGG
MESO
PAAD
UVM

Fig. 6A

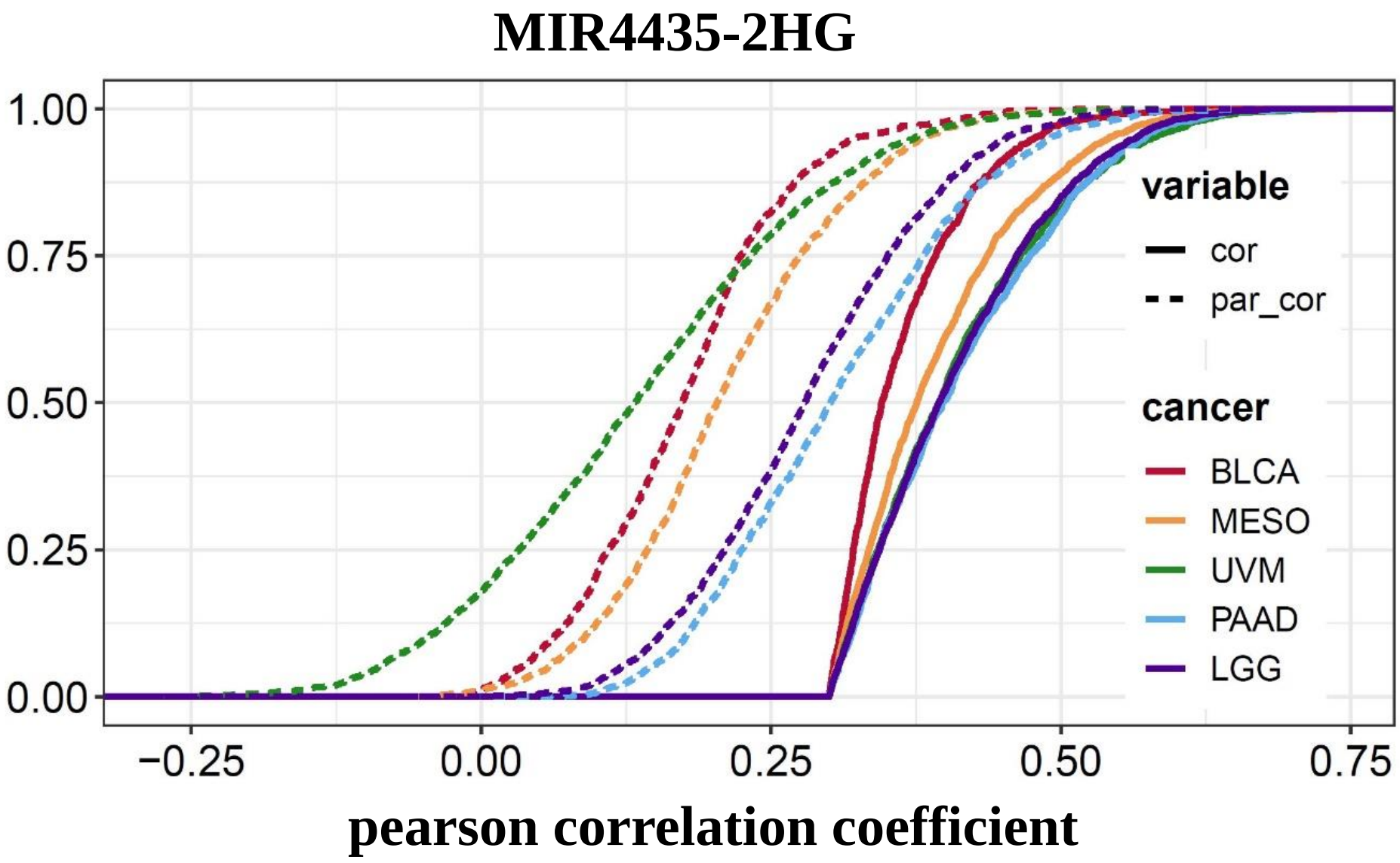

MIR4435-2HG
1.00
0.75
0.50
0.25
0.00
−0.25
0.00
0.25
0.50
0.75
pearson correlation coefficient
variable
cor
par_cor
cancer
BLCA
MESO
UVM
PAAD
LGG

Fig. 6A

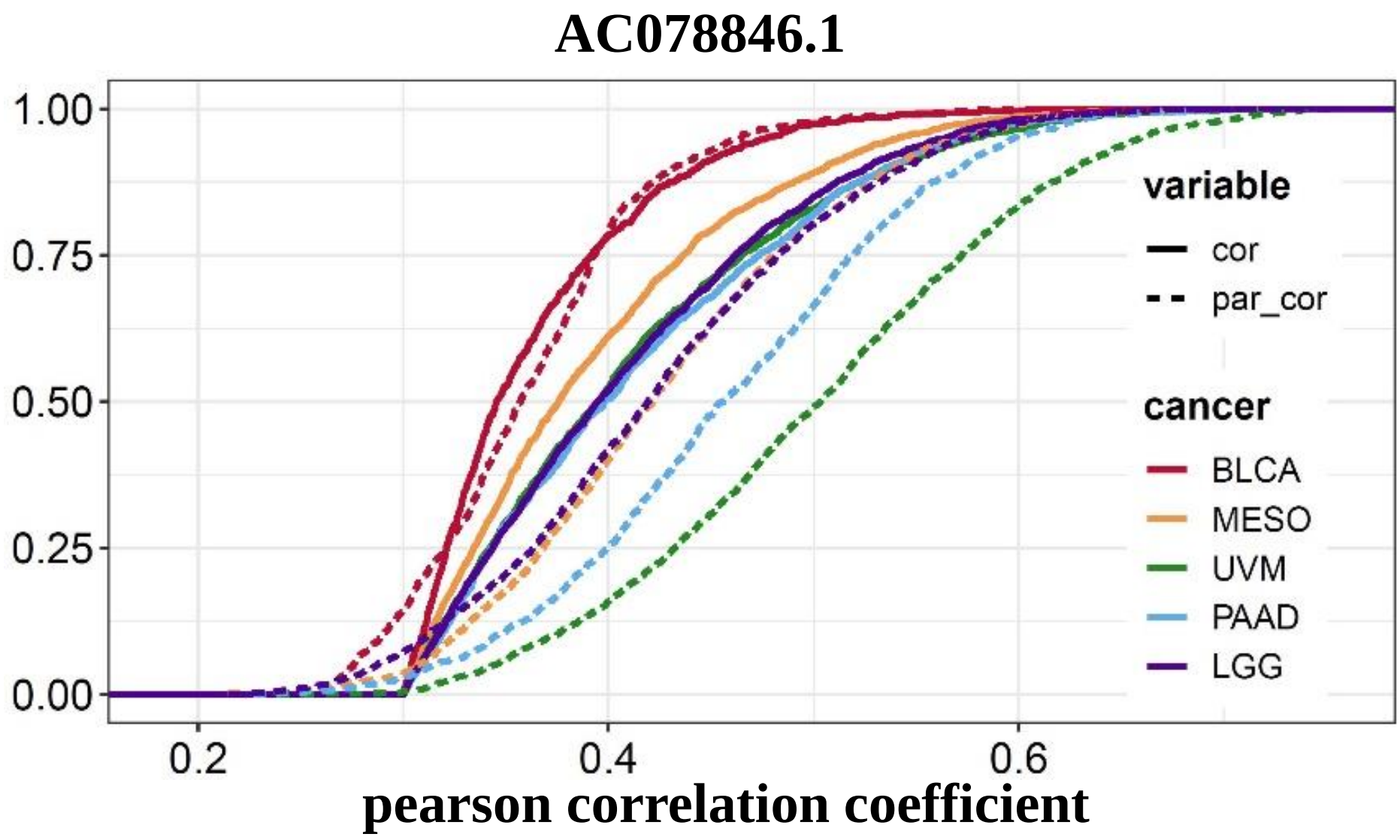

AC078846.1
1.00
0.75
0.50
0.25
0.00
0.2
0.4
0.6
pearson correlation coefficient
variable
cor
par_cor
cancer
BLCA
MESO
UVM
PAAD
LGG

Fig. 6A

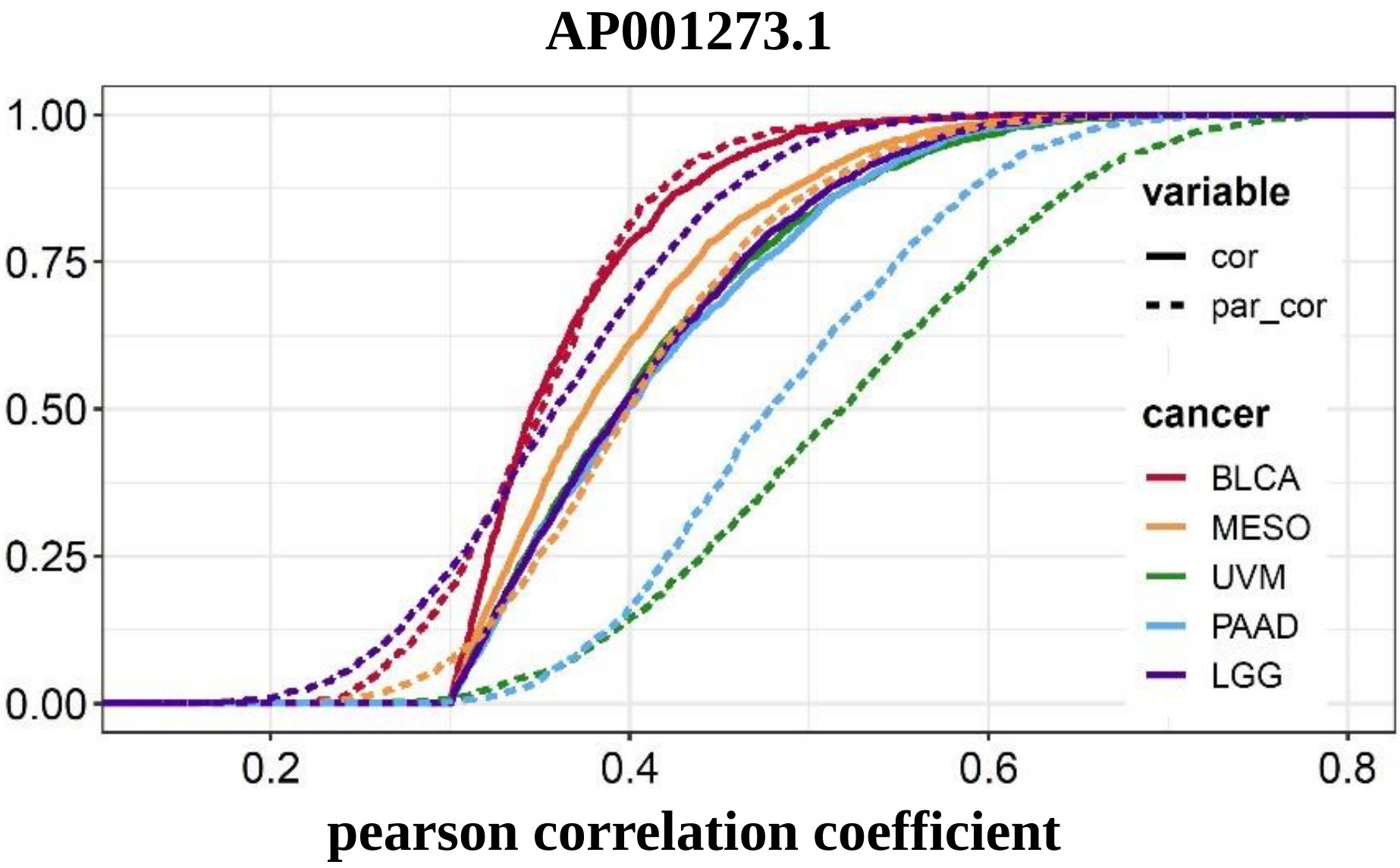

AP001273.1
1.00
0.75
0.50
0.25
0.00
0.2
0.4
0.6
0.8
variable
cor
par_cor
cancer
BLCA
MESO
UVM
PAAD
LGG
pearson correlation coefficient

Fig. 6A

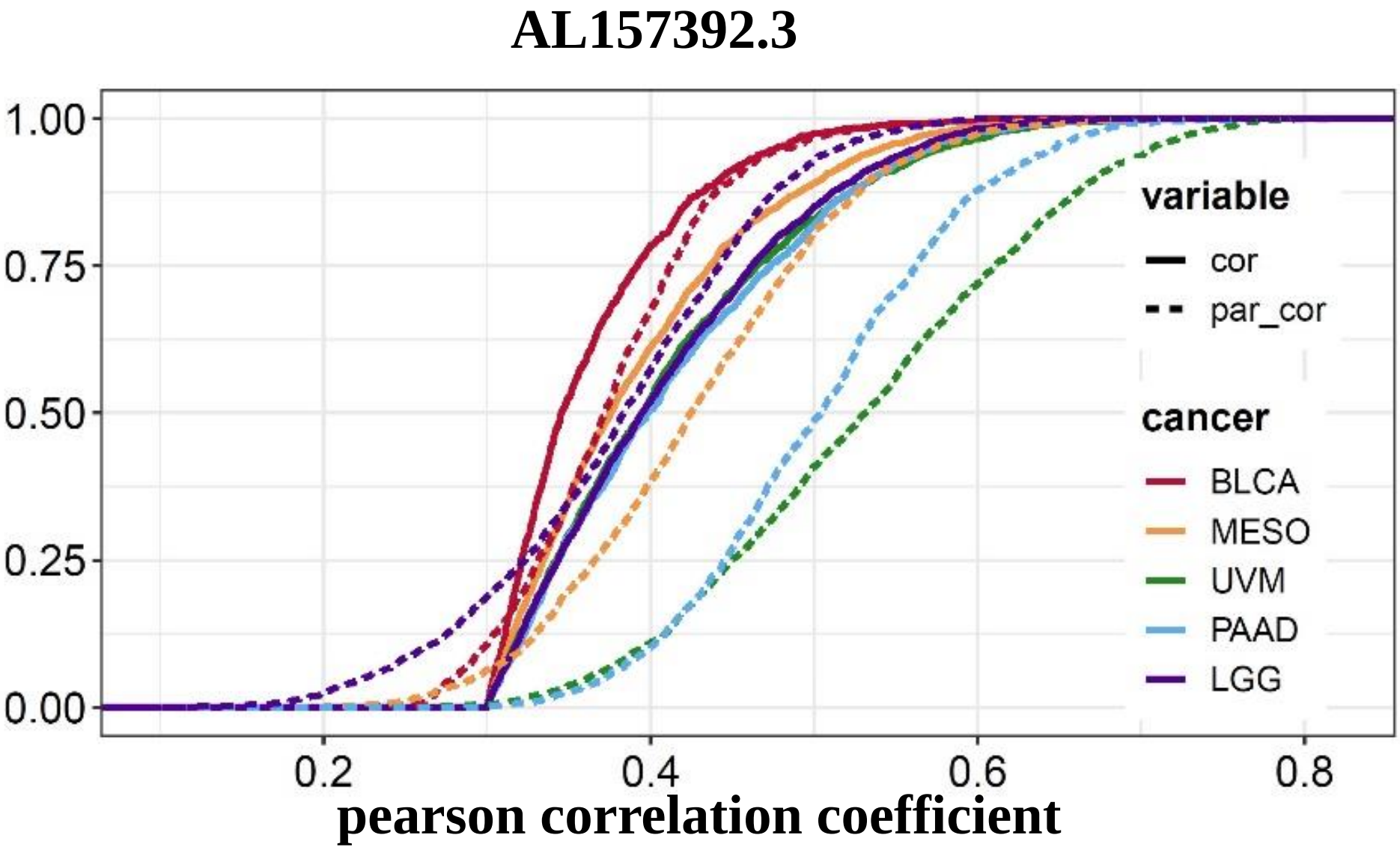

AL157392.3
1.00
0.75
0.50
0.25
0.00
0.2
0.4
0.6
0.8
pearson correlation coefficient
variable
cor
par_cor
cancer
BLCA
MESO
UVM
PAAD
LGG

Fig. 6A

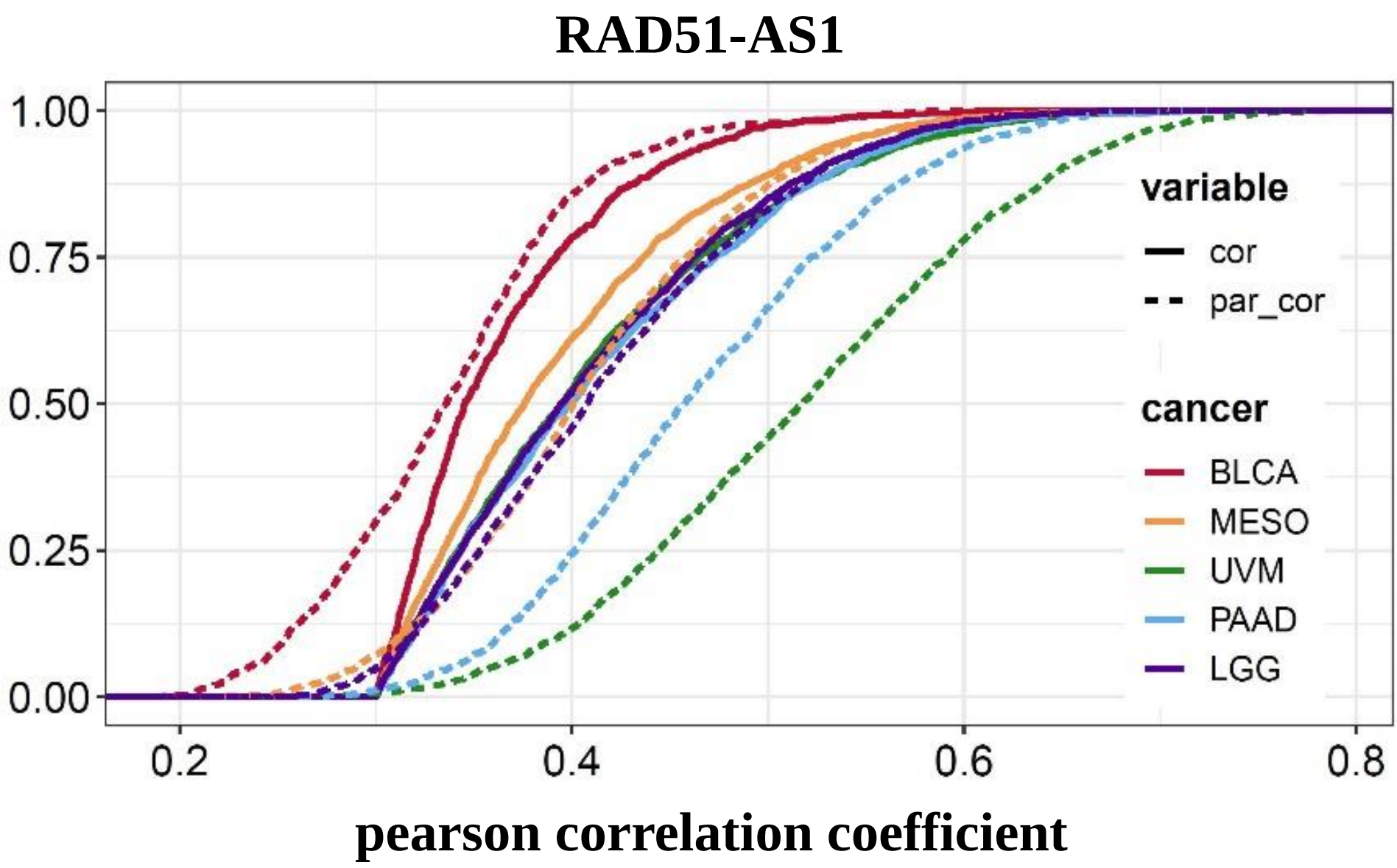

RAD51-AS1
1.00
0.75
0.50
0.25
0.00
0.2
0.4
0.6
0.8
variable
cor
par_cor
cancer
BLCA
MESO
UVM
PAAD
LGG
pearson correlation coefficient

Fig. 6B

Positive Biological pathway

- Adaptive immune response
- Immune response
- Inflammatory response
- Interferon-gamma-mediated signaling pathway
- Angiogenesis
- Cell adhesion
- Extracellular matrix disassembly
- Extracellular matrix organization
- Response to lipopolysaccharide
- Signal transduction

Fig. 6B

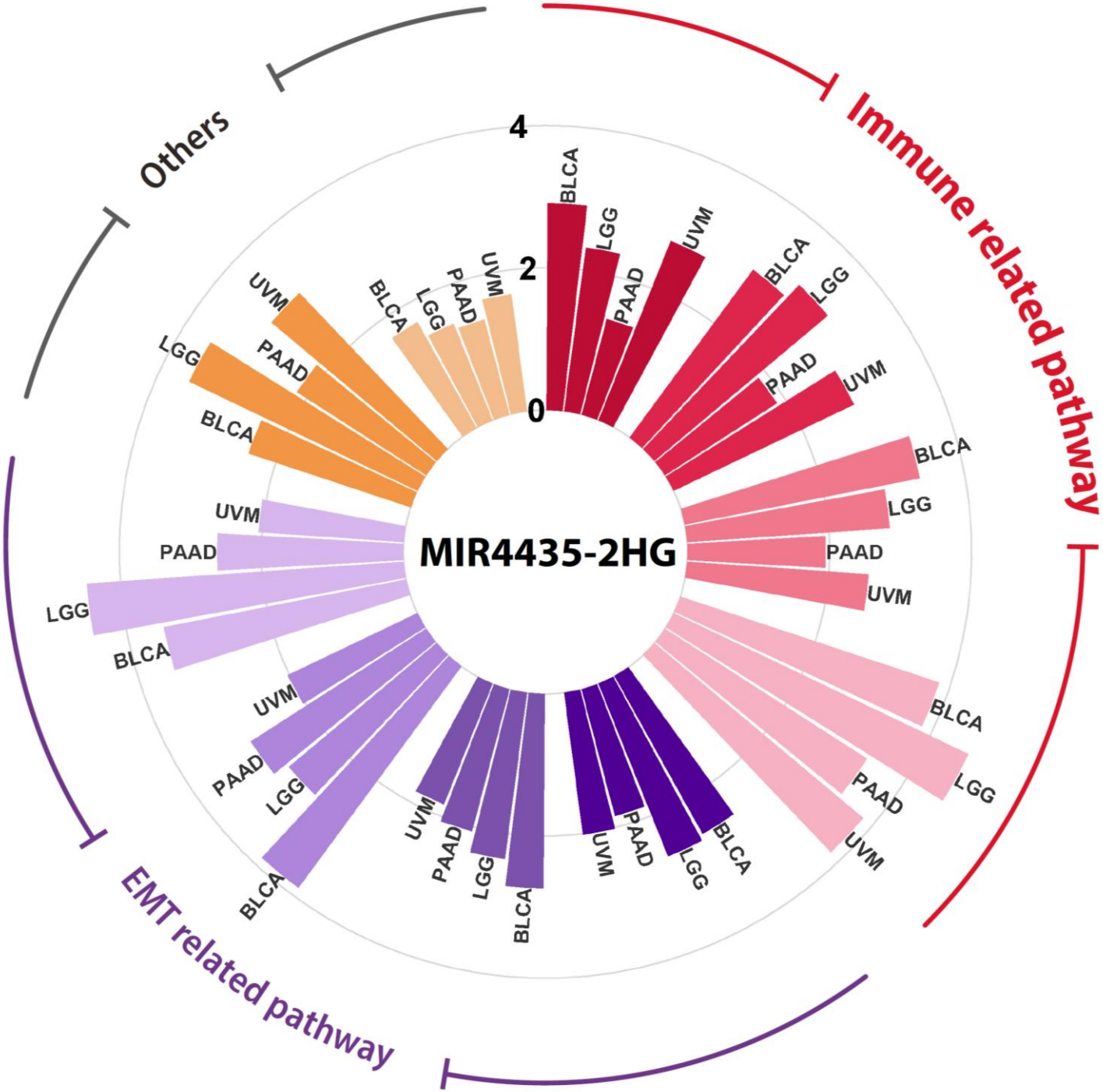

MIR4435-2HG
0
2
4
Immune related pathway
EMT related pathway
Others
BLCA
LGG
PAAD
UVM

Fig. 6C

BLCA

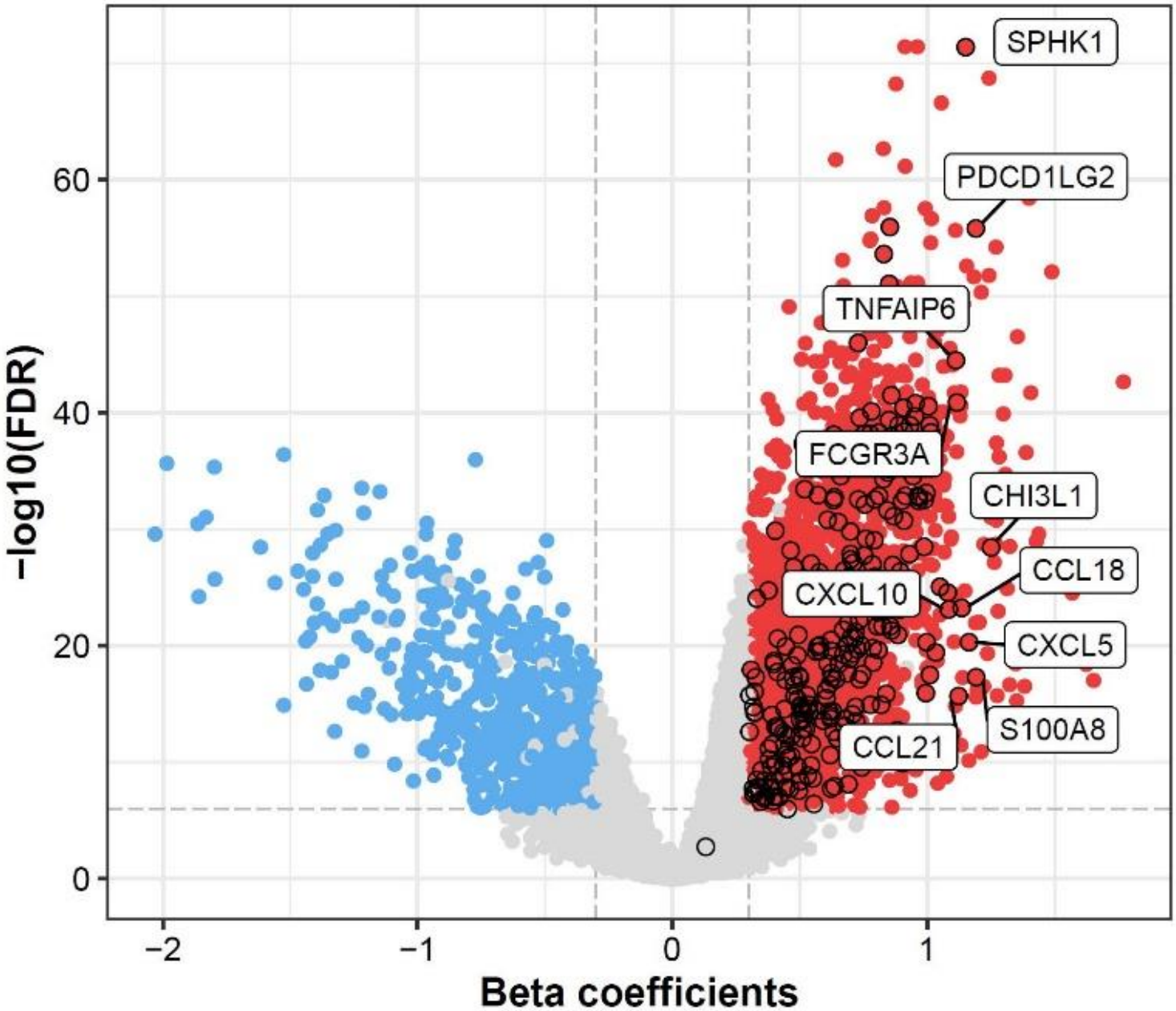

SPHK1
PDCD1LG2
TNFAIP6
FCGR3A
CHI3L1
CCL18
CXCL10
CXCL5
S100A8
CCL21
60
40
20
0
−log10(FDR)
−2
−1
0
1
Beta coefficients

Fig. 6C

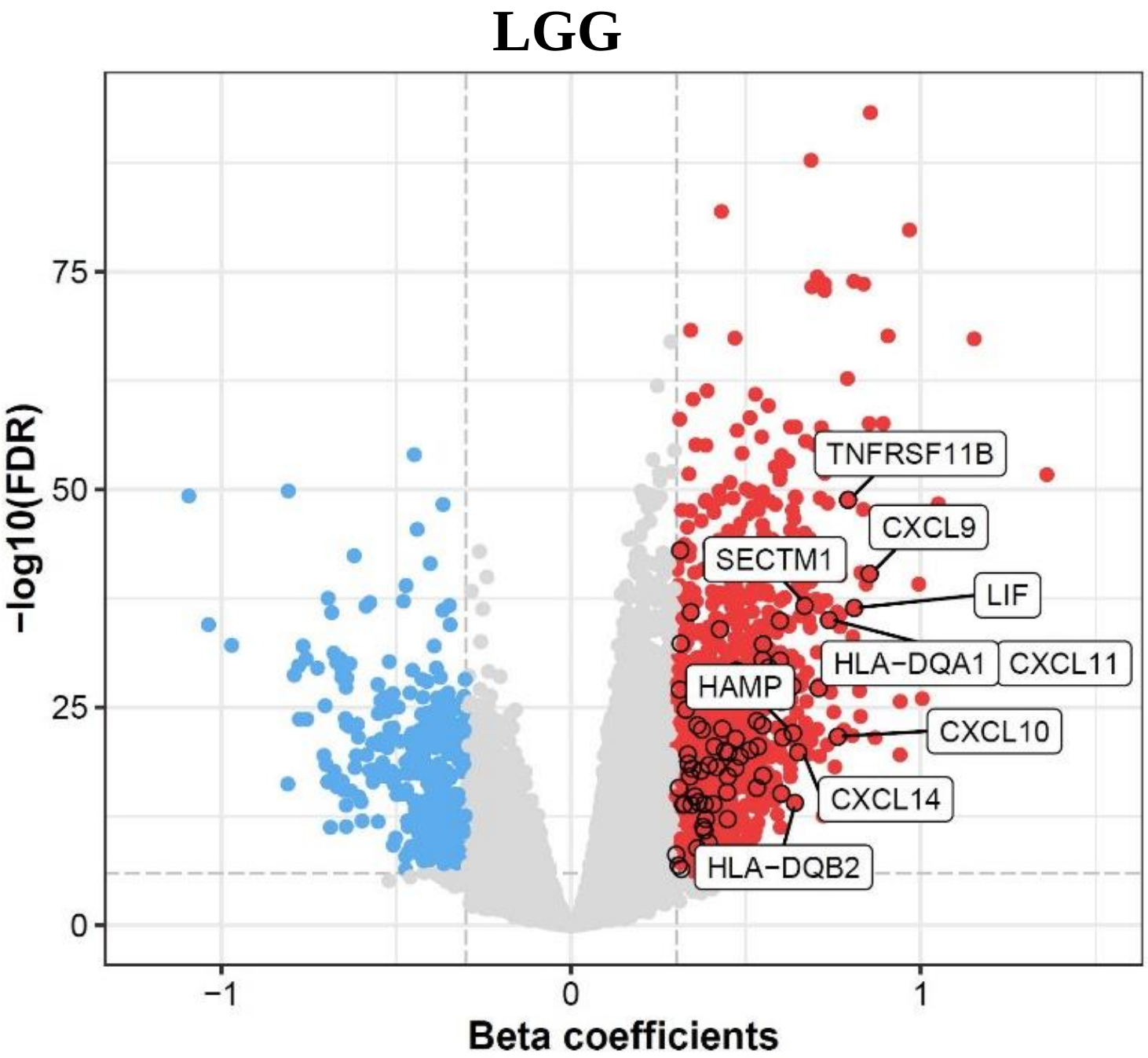

LGG
−log10(FDR)
75
50
25
0
−1
0
1
Beta coefficients
TNFRSF11B
CXCL9
SECTM1
LIF
HLA−DQA1
CXCL11
HAMP
CXCL10
CXCL14
HLA−DQB2

Fig. 6C

PAAD

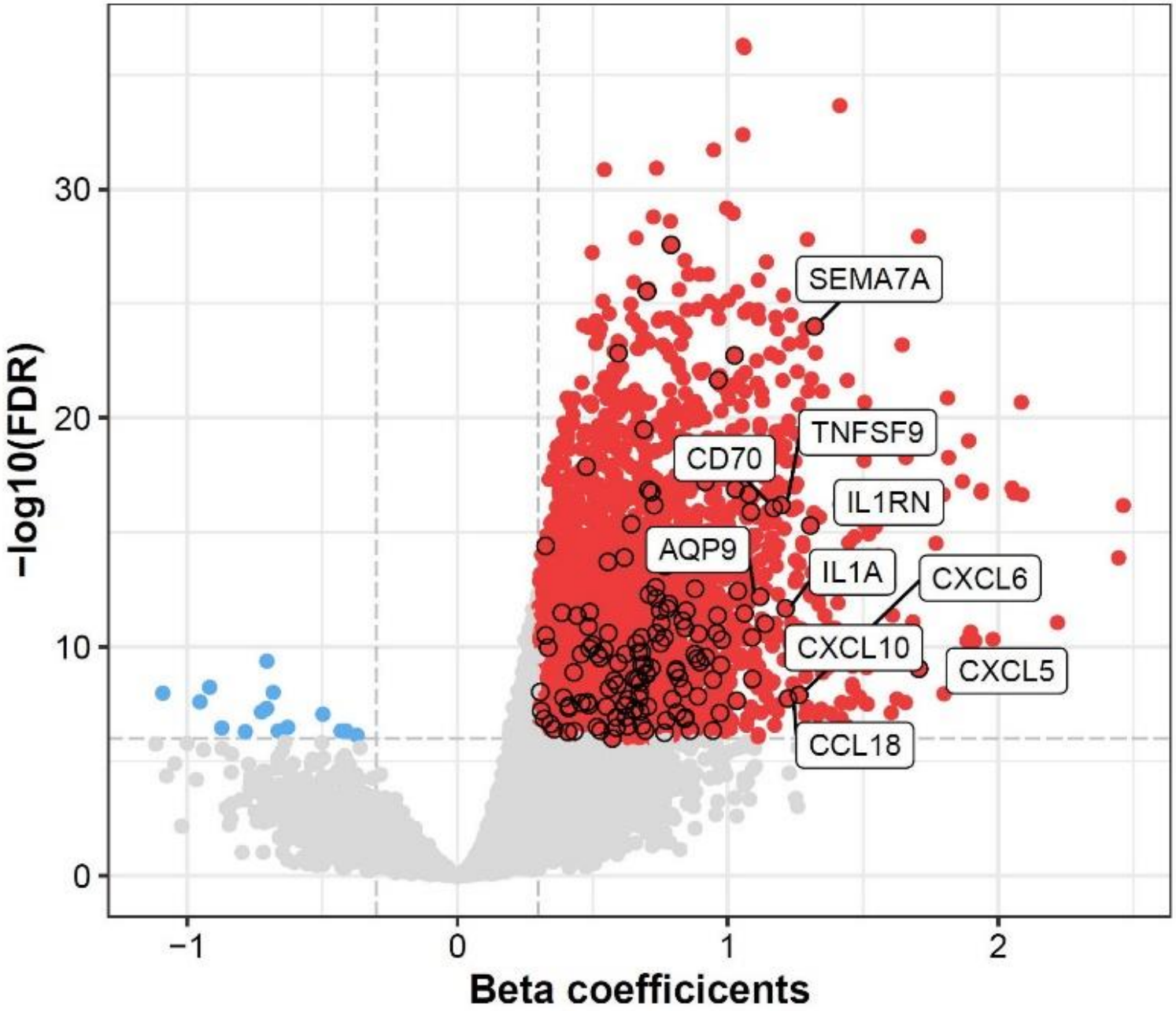
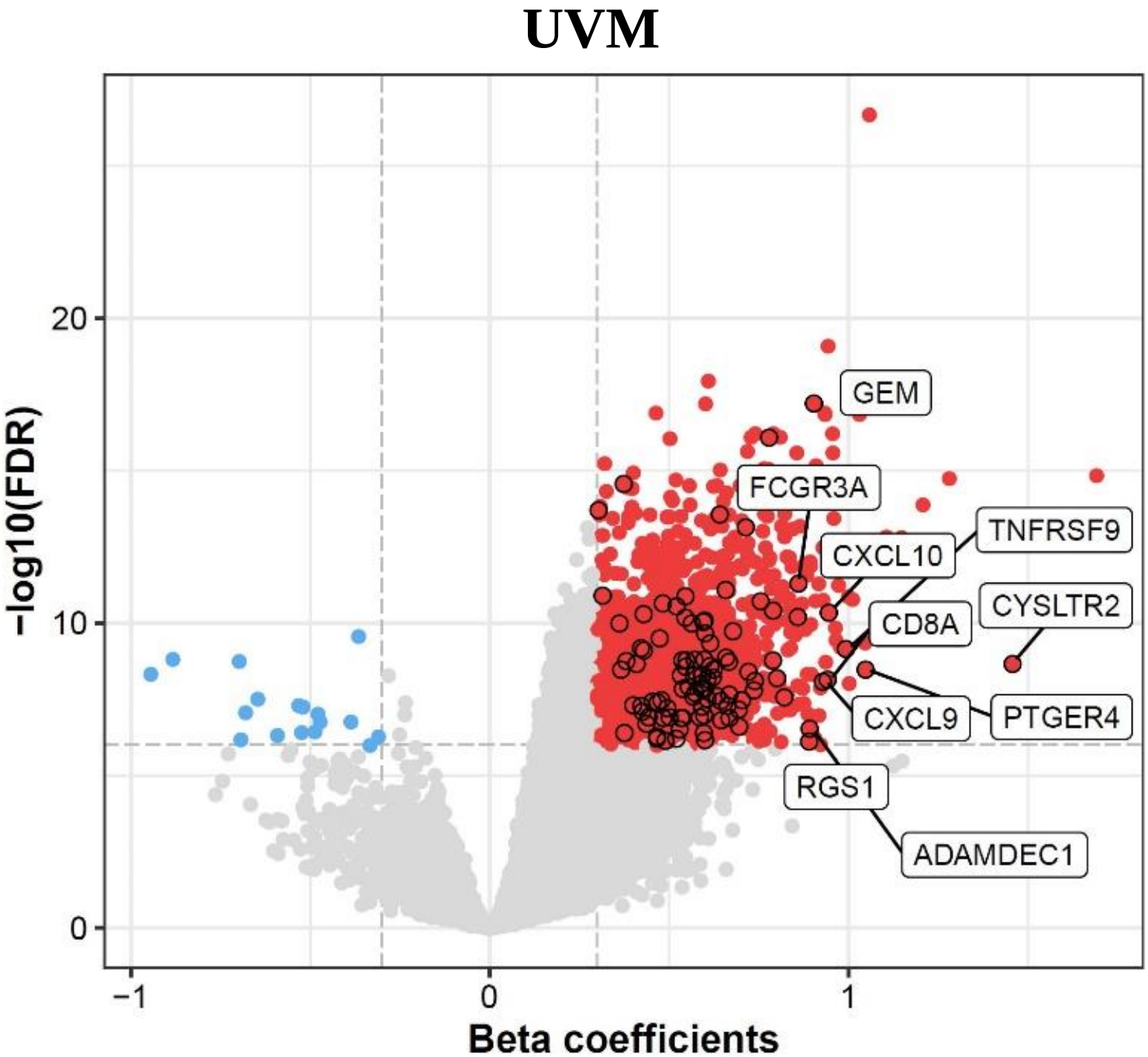

SEMA7A
TNFSF9
CD70
IL1RN
AQP9
IL1A
CXCL6
CXCL10
CXCL5
CCL18
30
20
10
0
−1
0
1
2
−log10(FDR)
Beta coefficicents

Fig. 6C


UVM
−log10(FDR)
20
10
0
−1
0
1
Beta coefficients
GEM
FCGR3A
TNFRSF9
CXCL10
CYSLTR2
CD8A
CXCL9
PTGER4
RGS1
ADAMDEC1