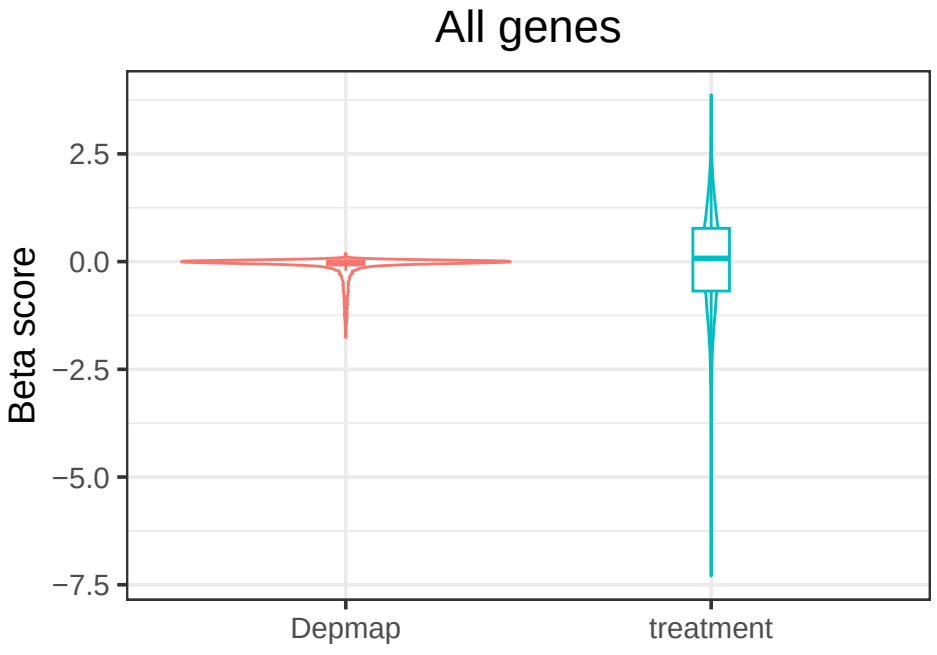
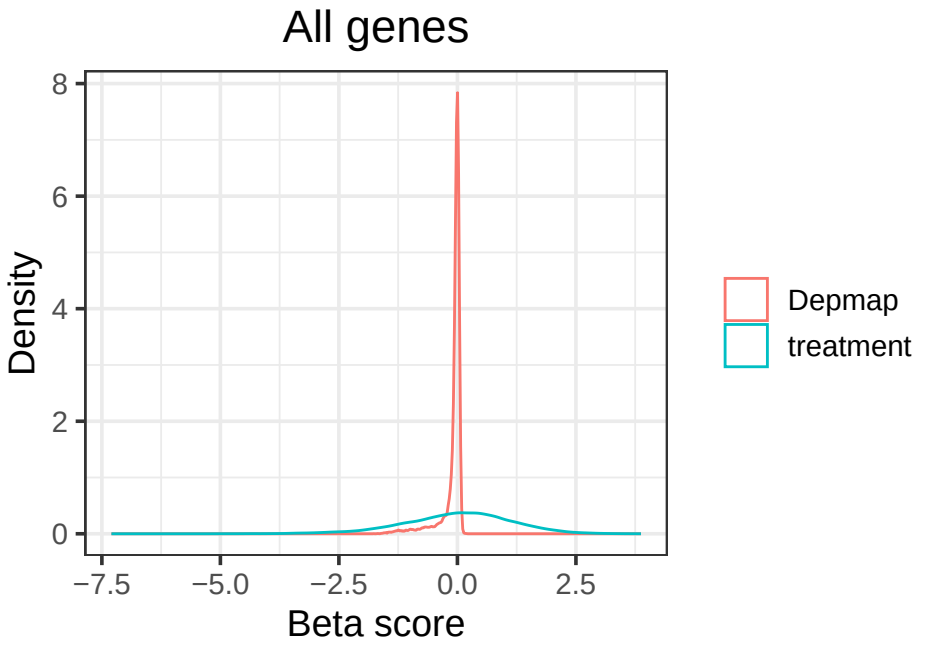
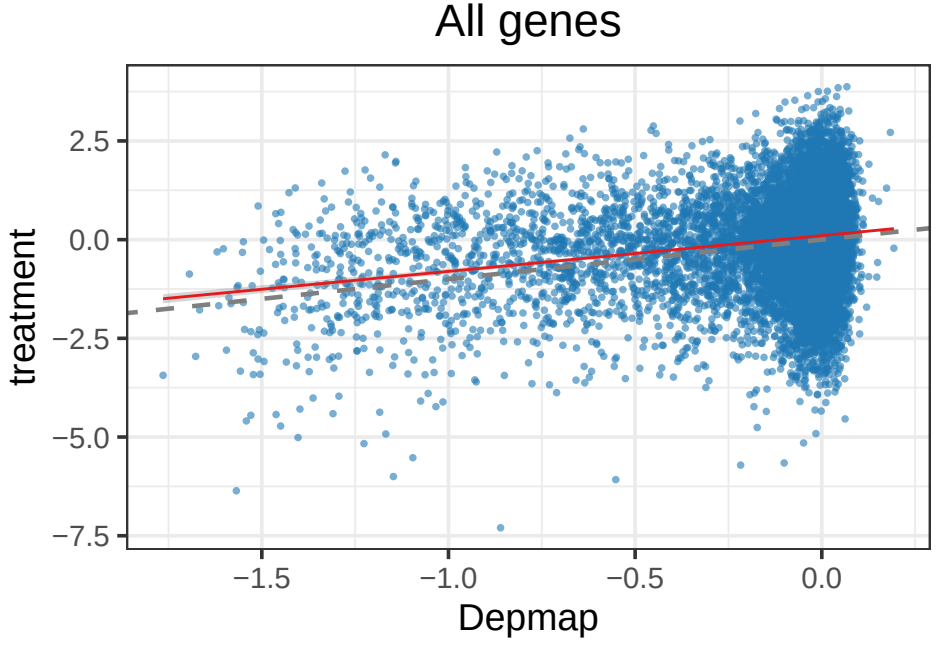
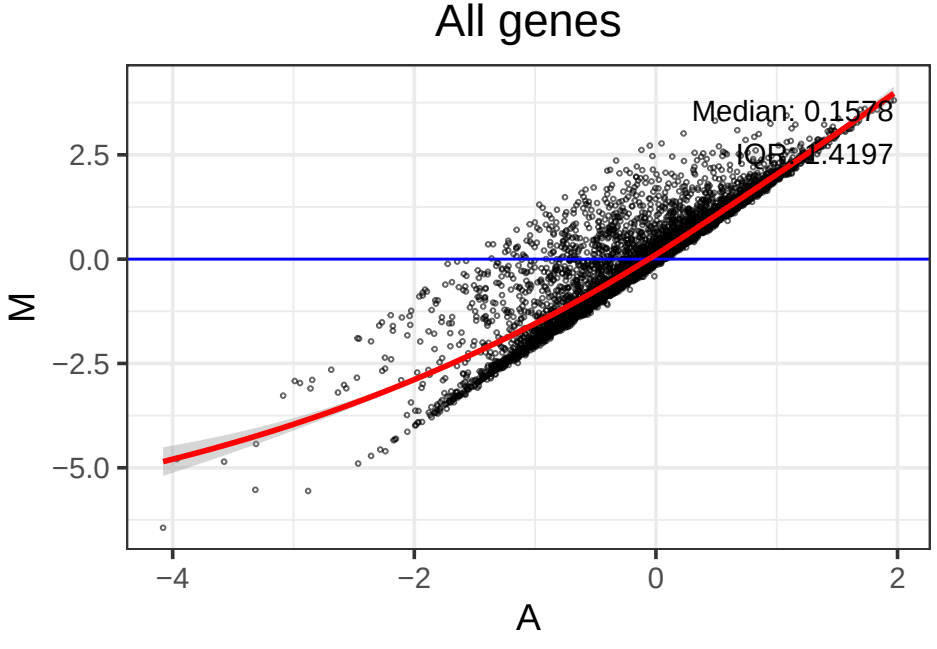
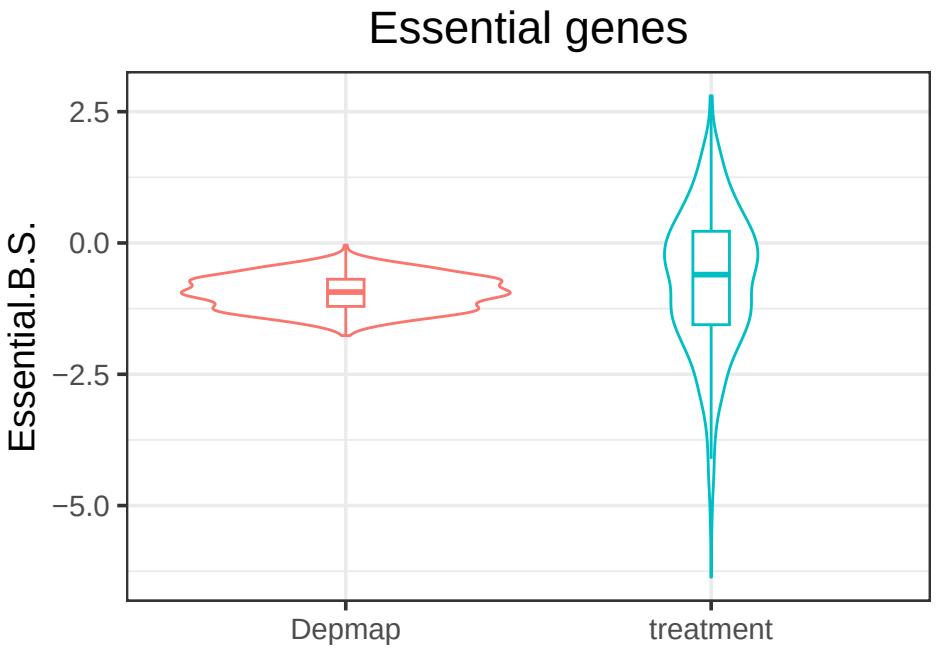
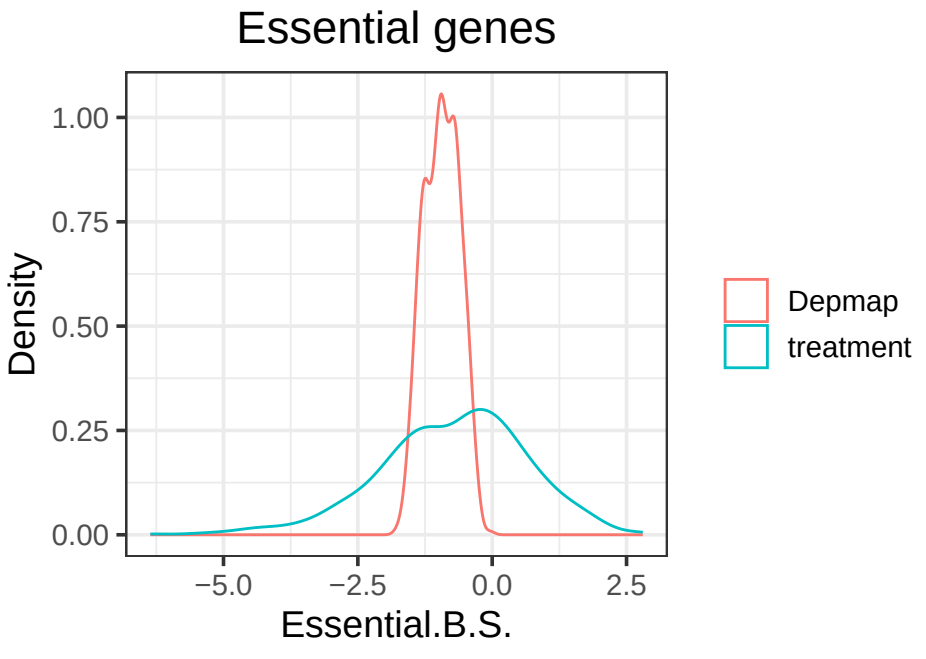

All genes
Beta score
2.5
0.0
−2.5
−5.0
−7.5
Depmap
treatment

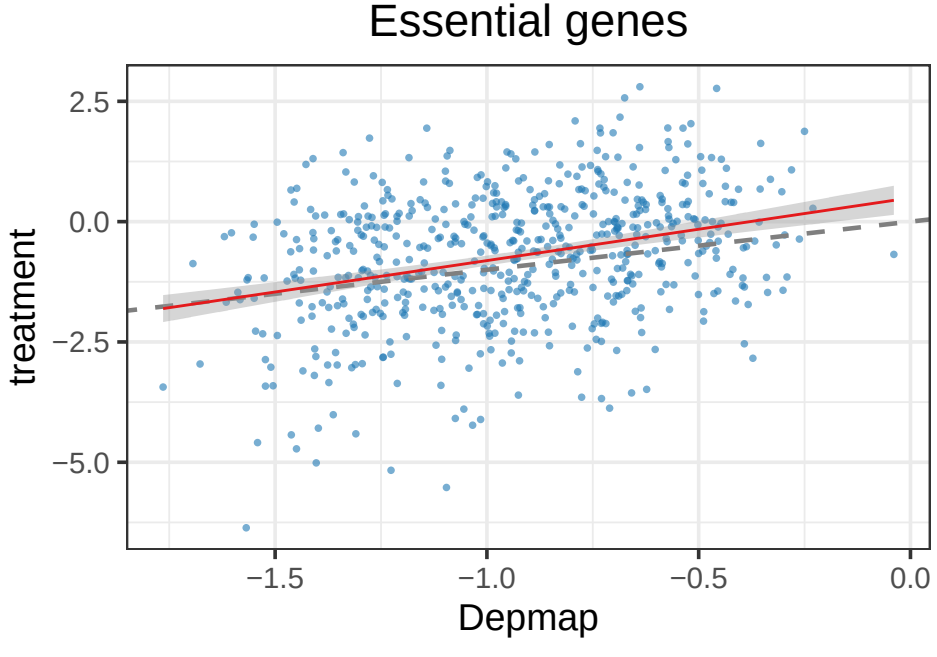

All genes
Density
8
6
4
2
0
−7.5
−5.0
−2.5
0.0
2.5
Beta score
Depmap
treatment

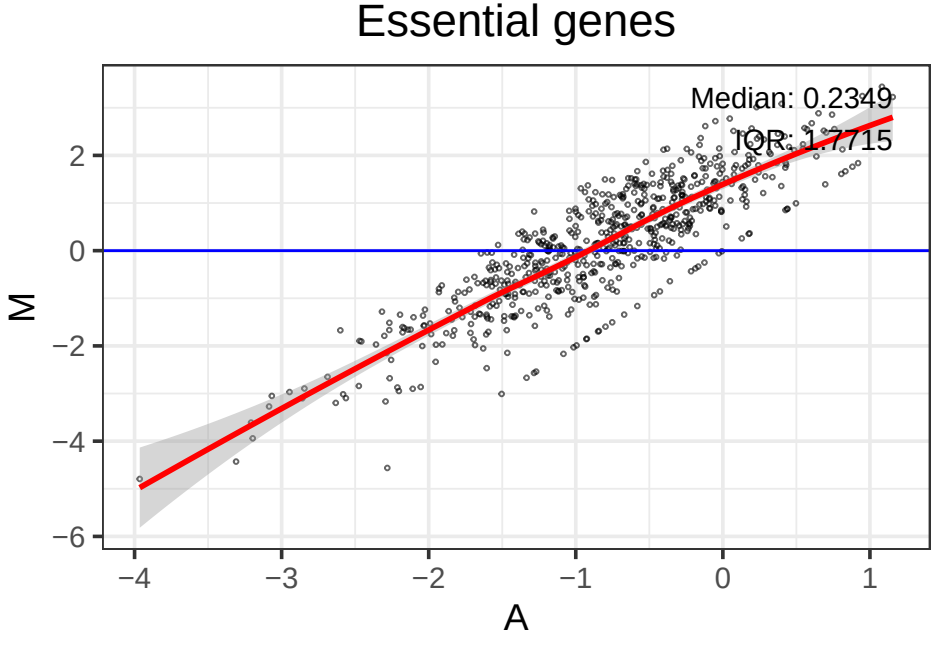

All genes
treatment
2.5
0.0
−2.5
−5.0
−7.5
−1.5
−1.0
−0.5
0.0
Depmap

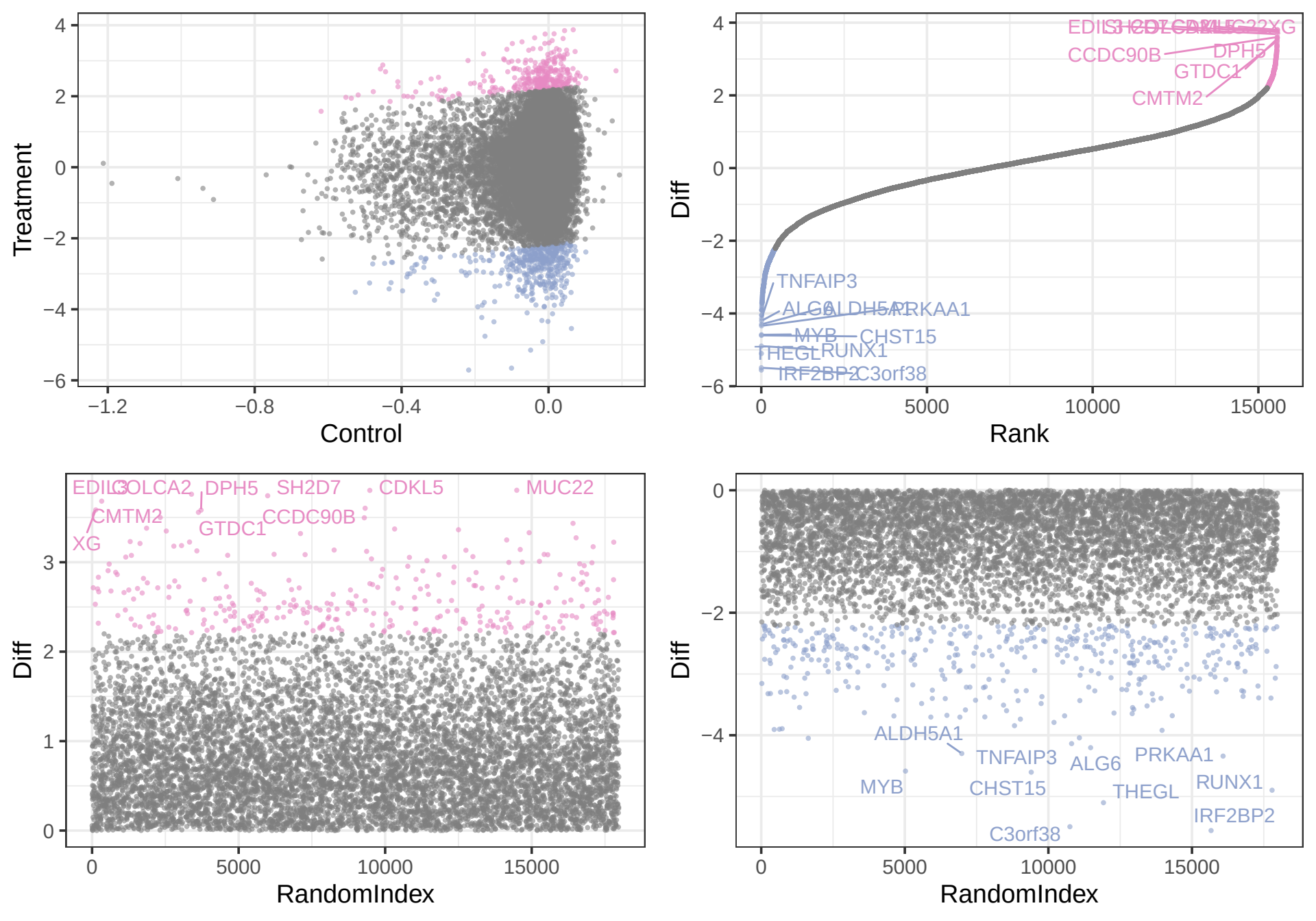

All genes
Median: 0.1578
IQR: 1.4197
M
2.5
0.0
−2.5
−5.0
−4
−2
0
2
A

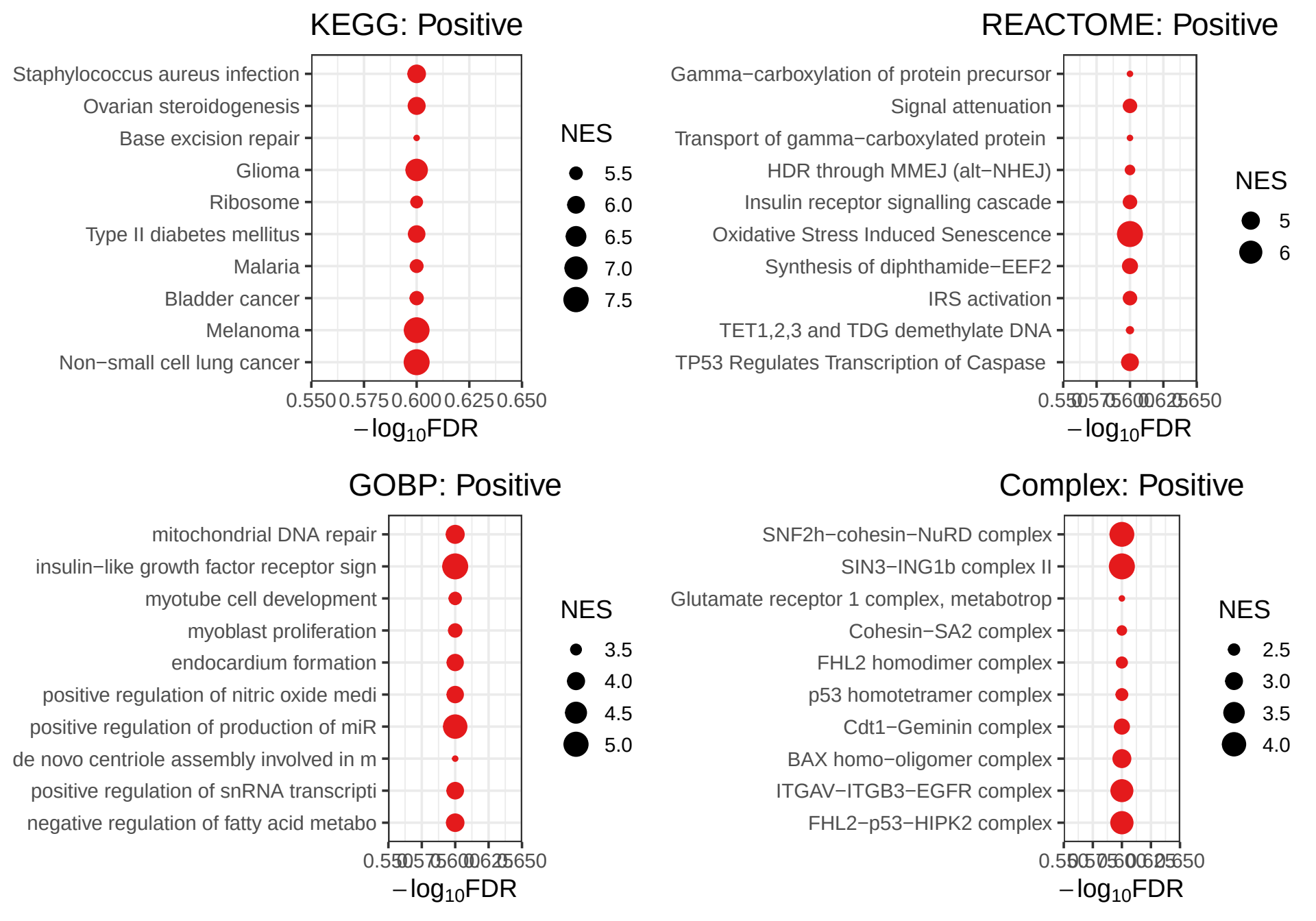

Essential genes
Essential.B.S.
2.5
0.0
−2.5
−5.0
Depmap
treatment

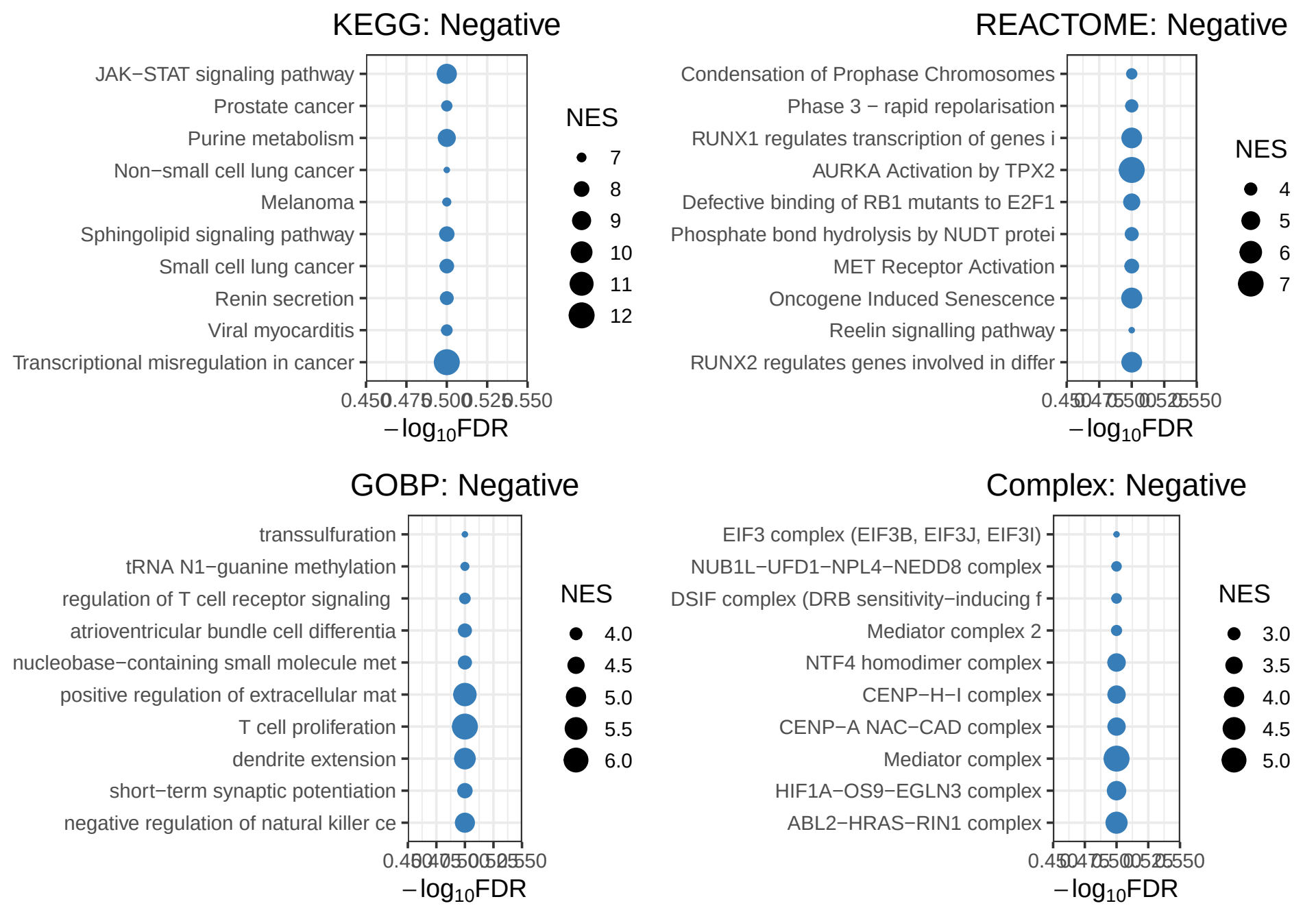

Essential genes
Density
1.00
0.75
0.50
0.25
0.00
−5.0
−2.5
0.0
2.5
Essential.B.S.
Depmap
treatment


Essential genes
treatment
2.5
0.0
−2.5
−5.0
−1.5
−1.0
−0.5
0.0
Depmap

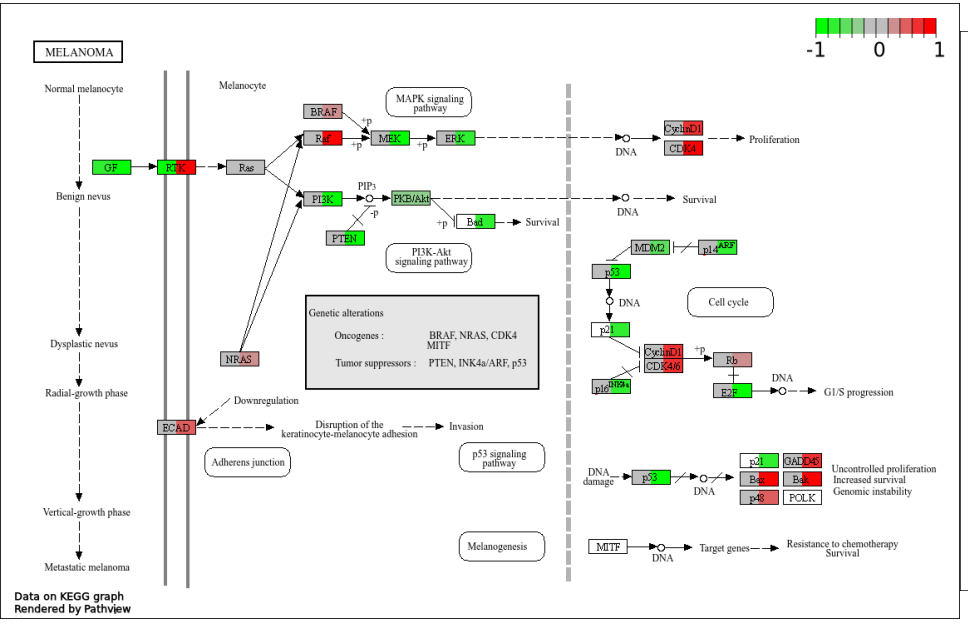

Essential genes
Median: 0.2349
IQR: 1.7715
M
2
0
−2
−4
−6
−4
−3
−2
−1
0
1
A

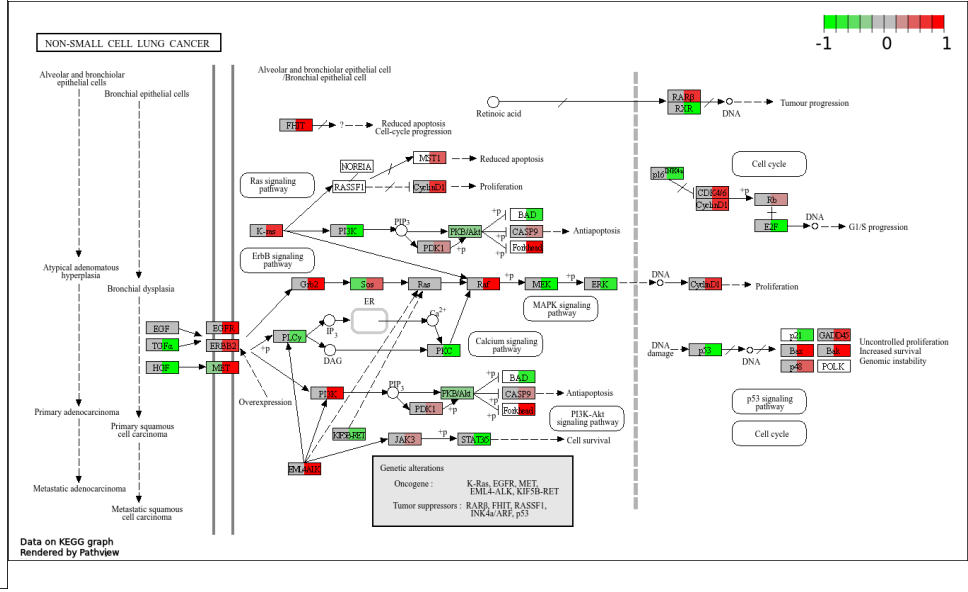

Treatment
Control
Diff
Rank
CCDC90B
DPH5
GTDC1
CMTM2
TNFAIP3
ALG6
ALDH5A1
PRKAA1
MYB
CHST15
THEGL
RUNX1
IRF2BP2
C3orf38
DPH5
SH2D7
CDKL5
MUC22
CMTM2
GTDC1
CCDC90B
XG
RandomIndex


KEGG: Positive
Staphylococcus aureus infection
Ovarian steroidogenesis
Base excision repair
Glioma
Ribosome
Type II diabetes mellitus
Malaria
Bladder cancer
Melanoma
Non−small cell lung cancer
0.550
0.575
0.600
0.625
0.650
−log10FDR
NES
5.5
6.0
6.5
7.0
7.5
REACTOME: Positive
Gamma−carboxylation of protein precursor
Signal attenuation
Transport of gamma−carboxylated protein
HDR through MMEJ (alt−NHEJ)
Insulin receptor signalling cascade
Oxidative Stress Induced Senescence
Synthesis of diphthamide−EEF2
IRS activation
TET1,2,3 and TDG demethylate DNA
TP53 Regulates Transcription of Caspase
−log10FDR
NES
5
6
GOBP: Positive
mitochondrial DNA repair
insulin−like growth factor receptor sign
myotube cell development
myoblast proliferation
endocardium formation
positive regulation of nitric oxide medi
positive regulation of production of miR
de novo centriole assembly involved in m
positive regulation of snRNA transcripti
negative regulation of fatty acid metabo
−log10FDR
NES
3.5
4.0
4.5
5.0
Complex: Positive
SNF2h−cohesin−NuRD complex
SIN3−ING1b complex II
Glutamate receptor 1 complex, metabotrop
Cohesin−SA2 complex
FHL2 homodimer complex
p53 homotetramer complex
Cdt1−Geminin complex
BAX homo−oligomer complex
ITGAV−ITGB3−EGFR complex
FHL2−p53−HIPK2 complex
−log10FDR
NES
2.5
3.0
3.5
4.0

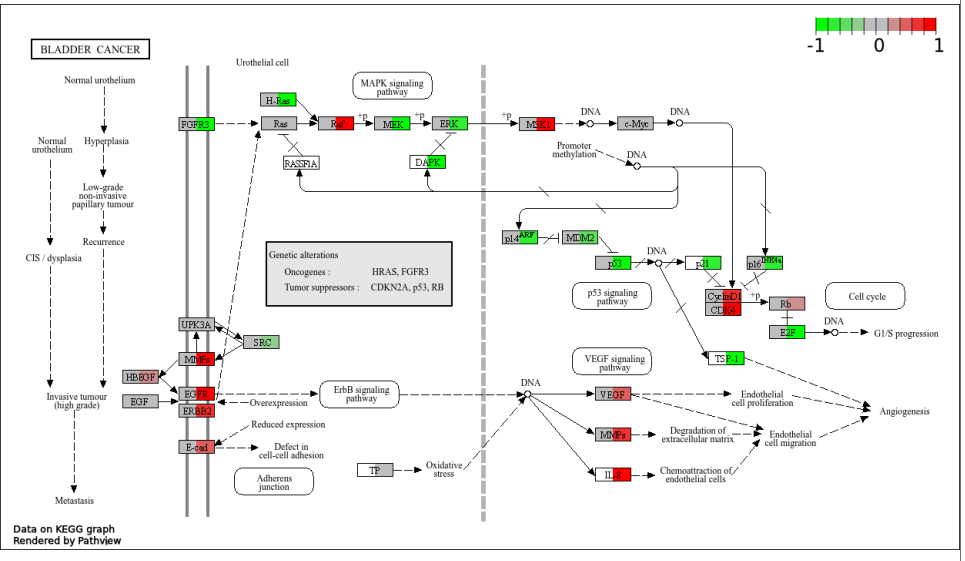

KEGG: Negative
JAK−STAT signaling pathway
Prostate cancer
Purine metabolism
Non−small cell lung cancer
Melanoma
Sphingolipid signaling pathway
Small cell lung cancer
Renin secretion
Viral myocarditis
Transcriptional misregulation in cancer
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
7
8
9
10
11
12
REACTOME: Negative
Condensation of Prophase Chromosomes
Phase 3 − rapid repolarisation
RUNX1 regulates transcription of genes i
AURKA Activation by TPX2
Defective binding of RB1 mutants to E2F1
Phosphate bond hydrolysis by NUDT protei
MET Receptor Activation
Oncogene Induced Senescence
Reelin signalling pathway
RUNX2 regulates genes involved in differ
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
4
5
6
7
GOBP: Negative
transsulfuration
tRNA N1−guanine methylation
regulation of T cell receptor signaling
atrioventricular bundle cell differentia
nucleobase−containing small molecule met
positive regulation of extracellular mat
T cell proliferation
dendrite extension
short−term synaptic potentiation
negative regulation of natural killer ce
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
4.0
4.5
5.0
5.5
6.0
Complex: Negative
EIF3 complex (EIF3B, EIF3J, EIF3I)
NUB1L−UFD1−NPL4−NEDD8 complex
DSIF complex (DRB sensitivity−inducing f
Mediator complex 2
NTF4 homodimer complex
CENP−H−I complex
CENP−A NAC−CAD complex
Mediator complex
HIF1A−OS9−EGLN3 complex
ABL2−HRAS−RIN1 complex
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
3.0
3.5
4.0
4.5
5.0

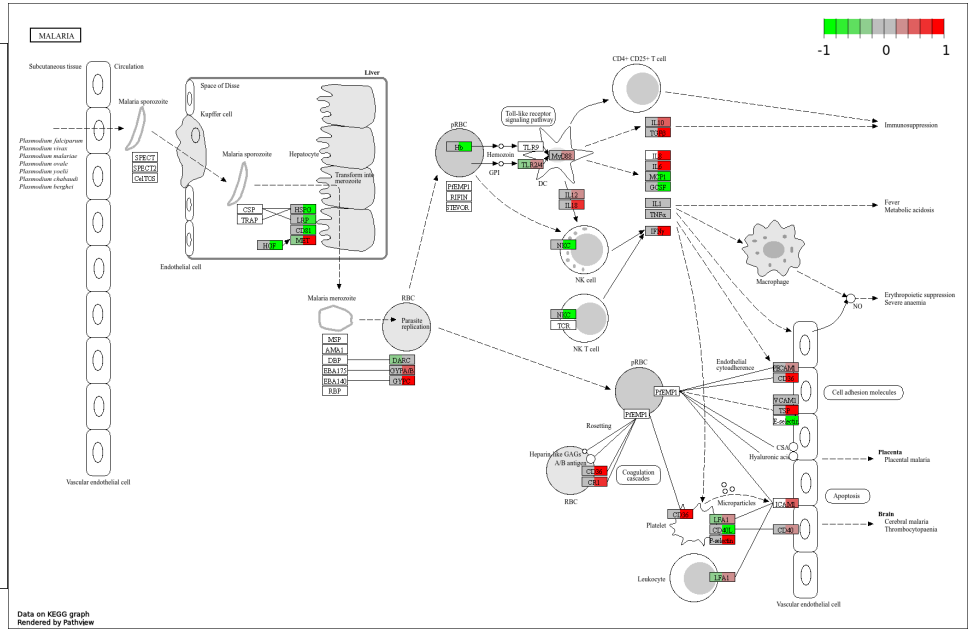
Group A


MELANOMA
-1 0 1
Normal melanocyte
Melanocyte
Benign nevus
Dysplastic nevus
Radial-growth phase
Vertical-growth phase
Metastatic melanoma
GF
RTK
Ras
BRAF
Raf
MEK
ERK
MAPK signaling pathway
PI3K
PIP3
PKB/Akt
Bad
Survival
PTEN
PI3K-Akt signaling pathway
NRAS
DNA
CyclinD1
CDK4
Proliferation
MDM2
p14ARF
p53
Cell cycle
p21
CyclinD1
CDK4/6
Rb
p16INK4a
E2F
G1/S progression
Genetic alterations
Oncogenes : BRAF, NRAS, CDK4 MITF
Tumor suppressors : PTEN, INK4a/ARF, p53
Downregulation
ECAD
Disruption of the keratinocyte-melanocyte adhesion
Invasion
Adherens junction
p53 signaling pathway
DNA damage
GADD45
Bax
Bak
p48
POLK
Uncontrolled proliferation
Increased survival
Genomic instability
Melanogenesis
MITF
Target genes
Resistance to chemotherapy
Survival
Data on KEGG graph
Rendered by Pathview

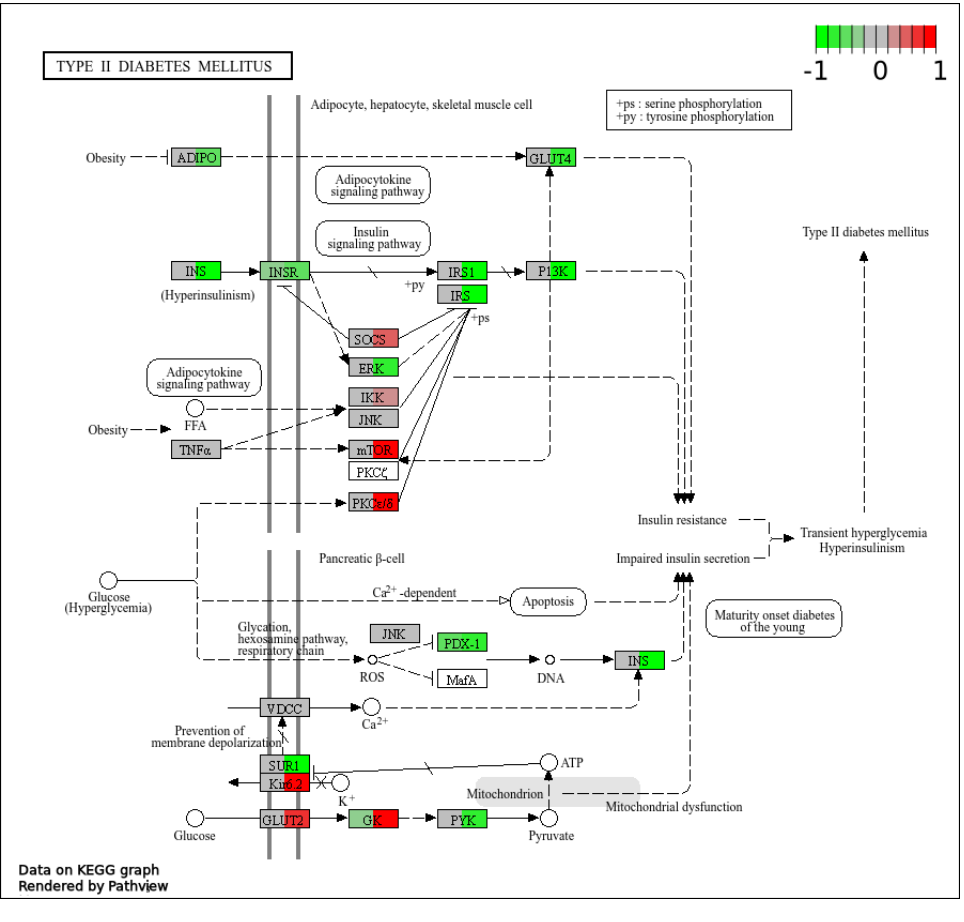

NON-SMALL CELL LUNG CANCER
-1 0 1
Alveolar and bronchiolar epithelial cells
Bronchial epithelial cells
Atypical adenomatous hyperplasia
Bronchial dysplasia
Primary adenocarcinoma
Primary squamous cell carcinoma
Metastatic adenocarcinoma
Metastatic squamous cell carcinoma
Alveolar and bronchiolar epithelial cell /Bronchial epithelial cell
Retinoic acid
FHIT
Reduced apoptosis
Cell-cycle progression
Ras signaling pathway
NORE1A
RASSF1
MST1
Reduced apoptosis
CyclinD1
Proliferation
K-ras
PI3K
PIP3
PKB/Akt
BAD
CASP9
Antiapoptosis
PDK1
Forkhead
ErbB signaling pathway
Grb2
Sos
Ras
Raf
MEK
ERK
MAPK signaling pathway
ER
EGF
TGFa
HGF
EGFR
ERBB2
MET
PLCγ
IP3
DAG
Ca2+
PKC
Calcium signaling pathway
Overexpression
KRAS-RET
JAK3
STAT3
Cell survival
EML4-ALK
PI3K-Akt signaling pathway
Genetic alterations
Oncogene : K-Ras, EGFR, MET, EML4-ALK, KIF5B-RET
Tumor suppressors : RARβ, FHIT, RASSF1, INK4a/ARF, p53
RARβ
RXR
DNA
Tumour progression
p16INK4a
Cell cycle
CDK4/6
CyclinD1
Rb
E2F
G1/S progression
Proliferation
DNA damage
p53
p21
GADD45
Bax
Bak
p48
POLK
Uncontrolled proliferation
Increased survival
Genomic instability
p53 signaling pathway
Cell cycle
Data on KEGG graph
Rendered by Pathview

Group A

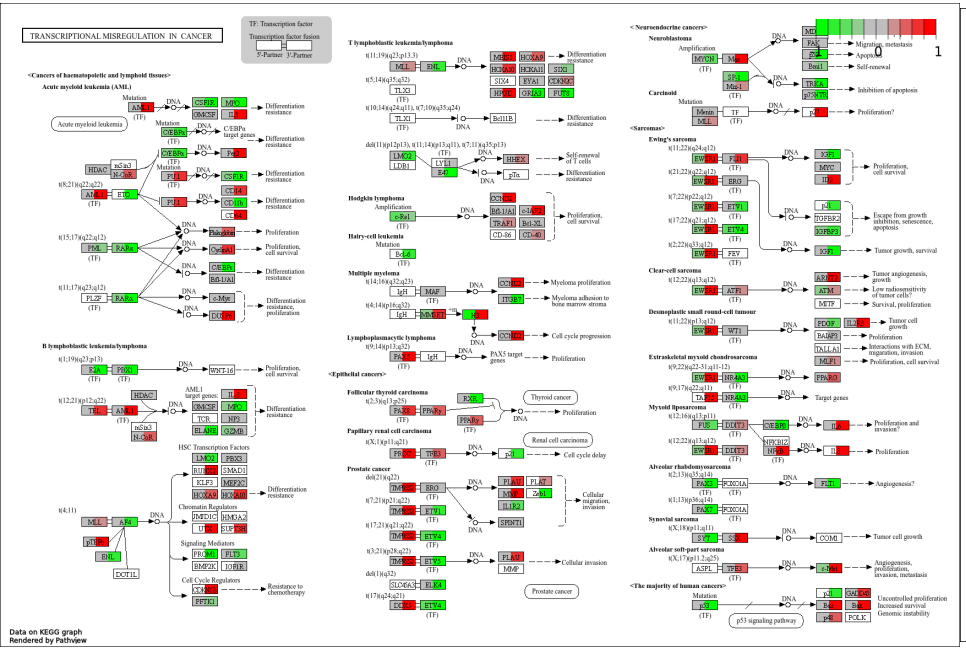

BLADDER CANCER
Urothelial cell
Normal urothelium
Hyperplasia
Low-grade non-invasive papillary tumour
Recurrence
CIS / dysplasia
Invasive tumour (high grade)
Metastasis
FGFR3
H-Ras
Ras
Raf
MEK
ERK
MAPK signaling pathway
RASSF1A
DAPK
Promoter methylation
DNA
c-Myc
p14ARF
MDM2
p53
p21
p53 signaling pathway
Cyclin D1
CDK4
Rb
E2F
Cell cycle
G1/S progression
Genetic alterations
Oncogenes : HRAS, FGFR3
Tumor suppressors : CDKN2A, p53, RB
UPK3A
SRC
MMPs
HBEGF
EGFR
ERBB2
EGF
Overexpression
ErbB signaling pathway
Reduced expression
E-cad
Defect in cell-cell adhesion
Adherens junction
TP
Oxidative stress
VEGF signaling pathway
VEGF
Endothelial cell proliferation
Angiogenesis
MMPs
Degradation of extracellular matrix
Endothelial cell migration
IL8
Chemoattraction of endothelial cells
-1
0
1
Data on KEGG graph
Rendered by Pathview

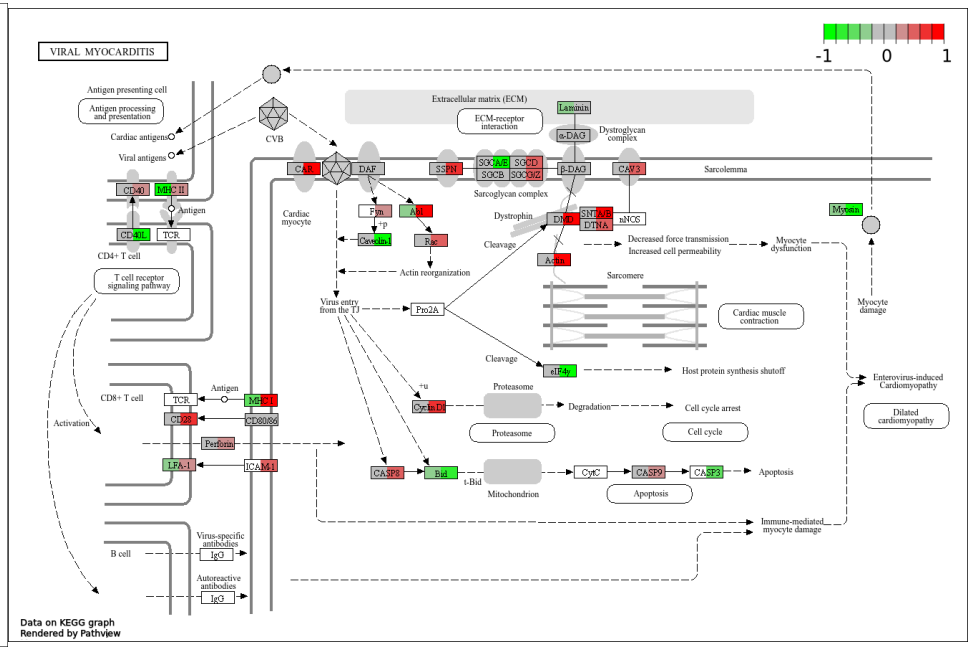

MALARIA
Subcutaneous tissue
Circulation
Malaria sporozoite
Vascular endothelial cell
Space of Disse
Liver
Kupffer cell
Malaria sporozoite
Hepatocyte
Transform into merozoite
Endothelial cell
CSP
TRAP
Malaria merozoite
RBC
Parasite replication
MSP
AMA1
EBP
RBA175
RBA140
RBP
DARC
GYPA/B
GYPC
pRBC
PfEMP1
RIFIN
STEVOR
Toll-like receptor signaling pathway
Hemozoin
GPI
TLR9
MyD88
TLR2/4
DC
CD4+ CD25+ T cell
IL10
TGFβ
Immunosuppression
IL1
IL6
MCP1
GCSF
IL2
IL4
IL3
TNFα
IFNγ
Fever
Metabolic acidosis
NK cell
IL12
Macrophage
Erythropoietic suppression
Severe anaemia
NO
NK T cell
TCR
Endothelial cytoadherence
ICAM1
VCAM1
E-selectin
Cell adhesion molecules
Rosetting
CSA
Hyaluronic acid
Placenta
Placental malaria
Heparin-like GAGs
A/B antigen
Coagulation cascades
Microparticles
Apoptosis
Brain
Cerebral malaria
Thrombocytopaenia
Platelet
Leukocyte
LFA1
Vascular endothelial cell
-1
0
1
Data on KEGG graph
Rendered by Pathview

Group A

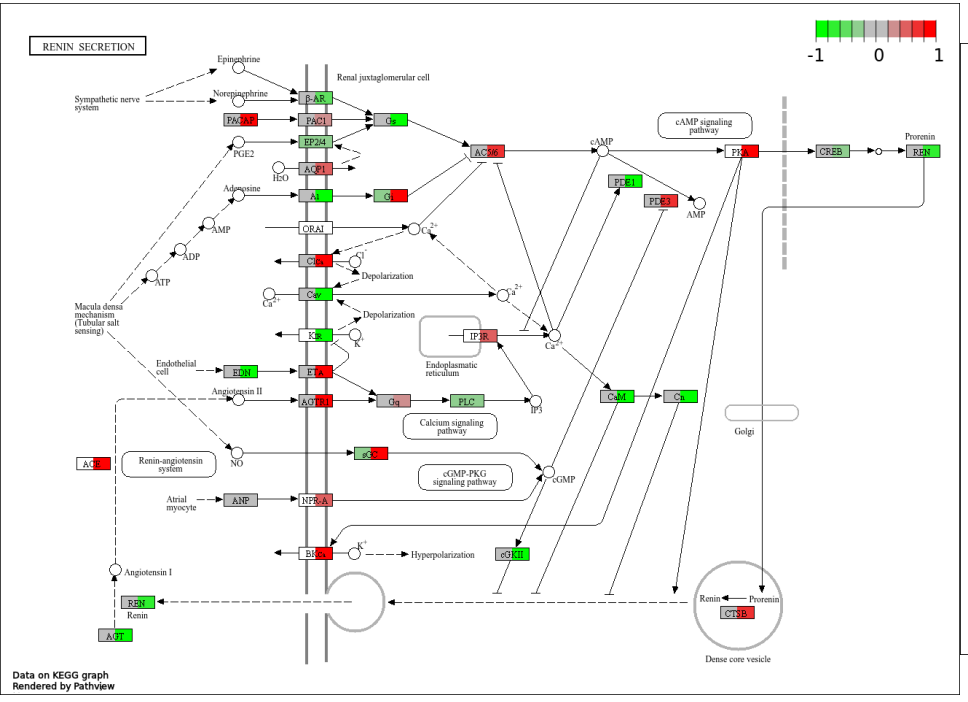

TYPE II DIABETES MELLITUS
-1
0
1
Adipocyte, hepatocyte, skeletal muscle cell
+ps : serine phosphorylation
+py : tyrosine phosphorylation
Obesity
ADIPO
GLUT4
Adipocytokine signaling pathway
Insulin signaling pathway
Type II diabetes mellitus
INS
INSR
IRS1
PI3K
(Hyperinsulinism)
+py
IRS
+ps
SOCS
ERK
Adipocytokine signaling pathway
IKK
Obesity
FFA
JNK
TNFα
mTOR
PKCζ
PKCε/θ
Insulin resistance
Transient hyperglycemia
Hyperinsulinism
Pancreatic β-cell
Impaired insulin secretion
Glucose
(Hyperglycemia)
Ca2+ -dependent
Apoptosis
Maturity onset diabetes of the young
Glycation, hexosamine pathway, respiratory chain
JNK
PDX-1
ROS
MafA
DNA
INS
VDCC
Ca2+
Prevention of membrane depolarization
SUR1
ATP
Kir6.2
K+
Mitochondrion
Mitochondrial dysfunction
Glucose
GLUT2
GK
PYK
Pyruvate
Data on KEGG graph
Rendered by Pathview

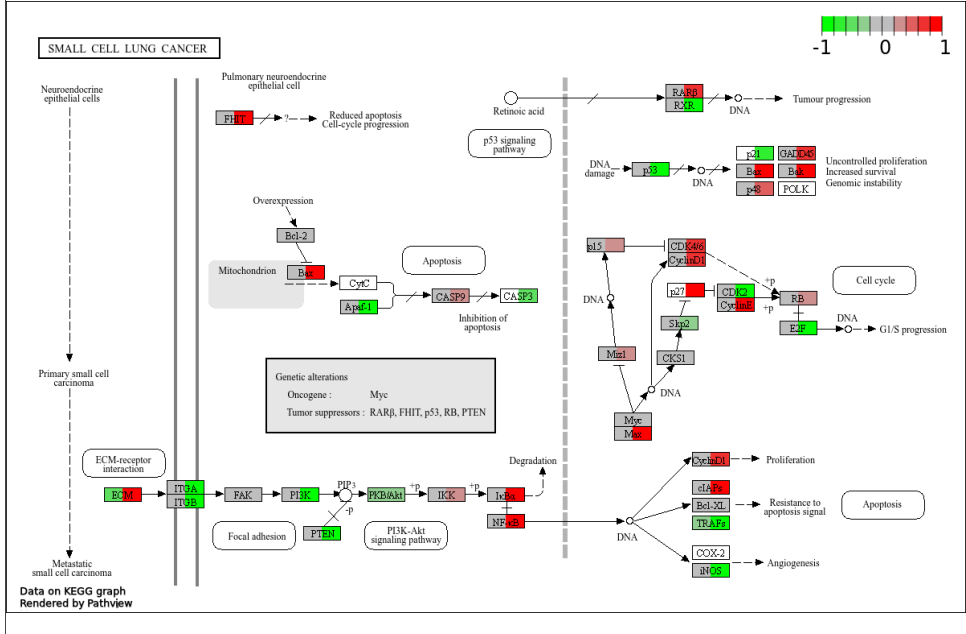
Group B


TRANSCRIPTIONAL MISREGULATION IN CANCER
TF: Transcription factor
Transcription factor fusion
5'-Partner 3'-Partner
<Cancers of haematopoietic and lymphoid tissues>
Acute myeloid leukemia (AML)
Acute myeloid leukemia
B lymphoblastic leukemia/lymphoma
HSC Transcription Factors
Chromatin Regulators
Signaling Mediators
Cell Cycle Regulators
T lymphoblastic leukemia/lymphoma
Hodgkin lymphoma
Multiple myeloma
Lymphoplasmacytic lymphoma
<Epithelial cancers>
Follicular thyroid carcinoma
Thyroid cancer
Papillary renal cell carcinoma
Renal cell carcinoma
Prostate cancer
Prostate cancer
<Neuroendocrine cancers>
Neuroblastoma
Carcinoid
<Sarcomas>
Ewing's sarcoma
Clear-cell sarcoma
Desmoplastic small round-cell tumour
Extraskeletal myxoid chondrosarcoma
Myxoid liposarcoma
Alveolar rhabdomyosarcoma
Synovial sarcoma
Alveolar soft-part sarcoma
<The majority of human cancers>
p53 signaling pathway
Data on KEGG graph
Rendered by Pathview

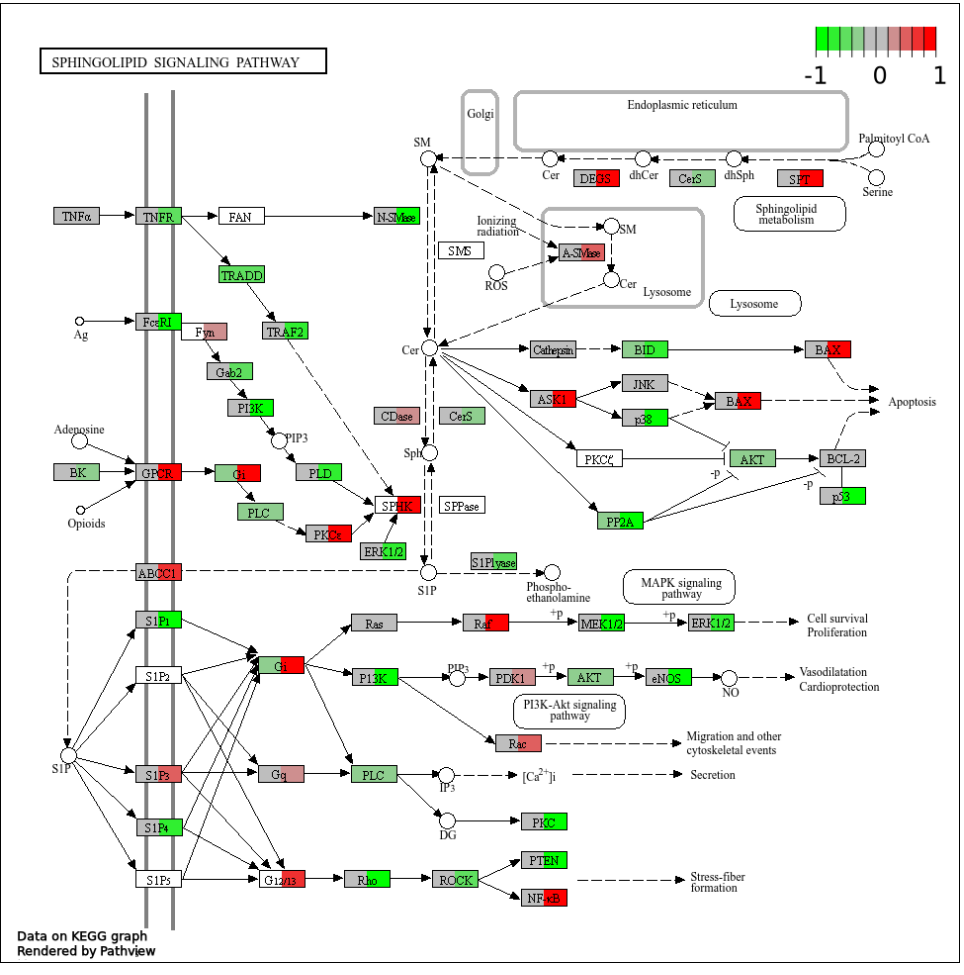

VIRAL MYOCARDITIS
Antigen presenting cell
Antigen processing and presentation
Cardiac antigens
Viral antigens
CVB
Extracellular matrix (ECM)
ECM-receptor interaction
Laminin
α-DAG
Dystroglycan complex
Sarcolemma
Sarcoglycan complex
Dystrophin
Cardiac myocyte
Cleavage
Decreased force transmission
Increased cell permeability
Myocyte dysfunction
Actin reorganization
Sarcomere
Cardiac muscle contraction
Virus entry from the TJ
Host protein synthesis shutoff
Enterovirus-induced Cardiomyopathy
Dilated cardiomyopathy
Myocyte damage
CD4+ T cell
T cell receptor signaling pathway
CD8+ T cell
Activation
Proteasome
Degradation
Cell cycle arrest
Cell cycle
Mitochondrion
Apoptosis
Immune-mediated myocyte damage
B cell
Virus-specific antibodies
Autoreactive antibodies
Data on KEGG graph
Rendered by Pathview

Group B

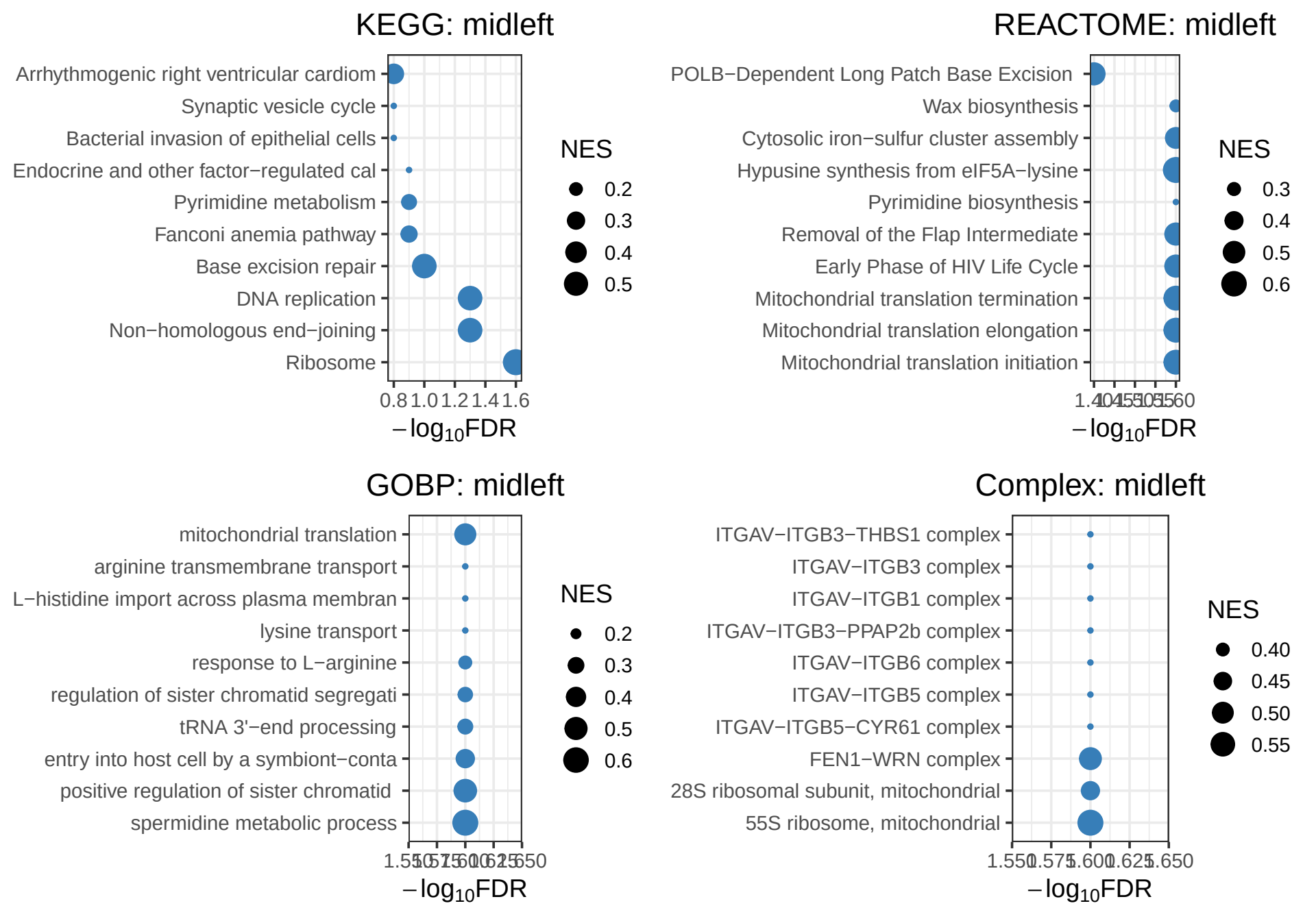

RENIN SECRETION
-1 0 1
Epinephrine
Norepinephrine
Sympathetic nerve system
Renal juxtaglomerular cell
β-AR
PAC1
Gs
PGE2
EP2/4
ACE1
HEO
AC5/6
cAMP
cAMP signaling pathway
PKA
CREB
Prorenin
REN
Adenosine
A1
Gi
PDE1
PDE3
AMP
ORAI
ATP
ADP
Depolarization
Macula densa mechanism (Tubular salt sensing)
Endothelial cell
EDN
ETA
Angiotensin II
AGTR1
Gq
PLC
IP3
CaM
Ca
Endoplasmatic reticulum
IP3R
Calcium signaling pathway
Golgi
ACE
Renin-angiotensin system
NO
sGC
cGMP-PKG signaling pathway
cGMP
Atrial myocyte
ANP
NPR-A
BKCa
Hyperpolarization
cGKII
Angiotensin I
REN
Renin
AGT
Renin
Prorenin
CTSB
Dense core vesicle
Data on KEGG graph
Rendered by Pathview

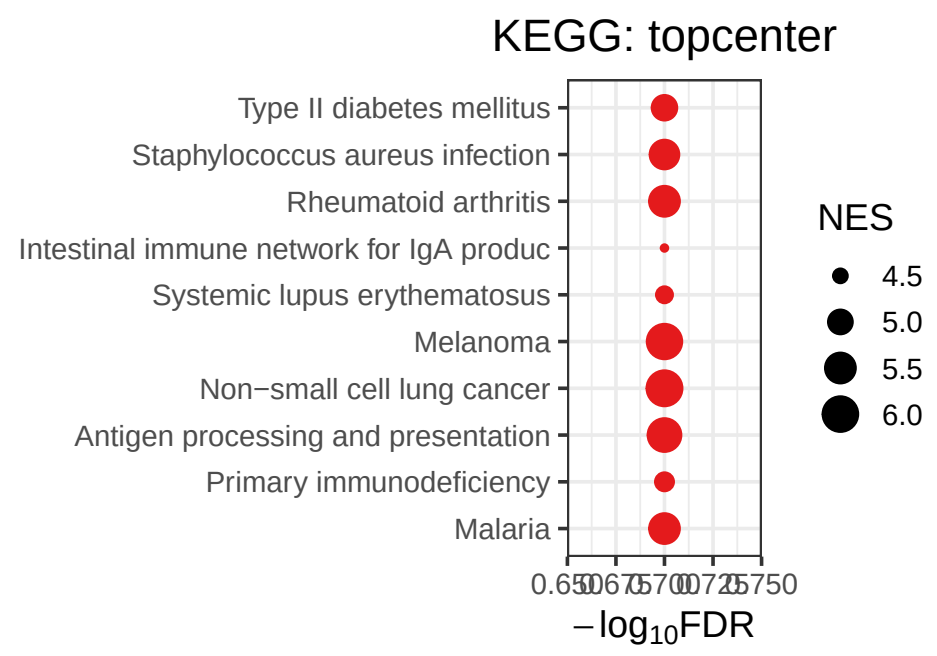

SMALL CELL LUNG CANCER
-1 0 1
Neuroendocrine epithelial cells
Pulmonary neuroendocrine epithelial cell
FHIT
Reduced apoptosis
Cell-cycle progression
p53 signaling pathway
Retinoic acid
RARβ
RXR
DNA
Tumour progression
DNA damage
p53
p21
GADD45
Bax
Bak
p48
POLK
Uncontrolled proliferation
Increased survival
Genomic instability
Overexpression
Bcl-2
Mitochondrion
Bax
Apoptosis
CytC
Apaf-1
CASP9
CASP3
Inhibition of apoptosis
Cell cycle
p15
CDK4/6
CyclinD1
p27
CDK2
CyclinE
RB
E2F
Skp2
CKS1
Myc
Max
Mad1
Primary small cell carcinoma
Genetic alterations
Oncogene : Myc
Tumor suppressors : RARβ, FHIT, p53, RB, PTEN
ECM-receptor interaction
ECM
ITGA
ITGB
FAK
PI3K
PIP3
PKB/Akt
IKK
IκBα
NFκB
Degradation
Focal adhesion
PTEN
PI3K-Akt signaling pathway
CyclinD1
Proliferation
cIAPs
Bcl-XL
TRAFs
Resistance to apoptosis signal
Apoptosis
COX-2
iNOS
Angiogenesis
Metastatic small cell carcinoma
Data on KEGG graph
Rendered by Pathview

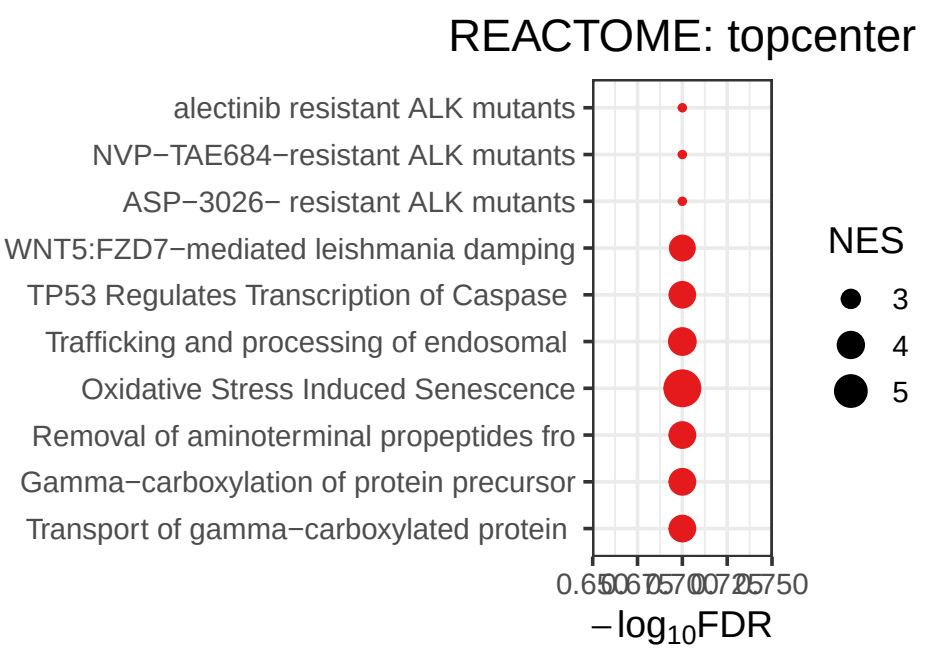
Group B

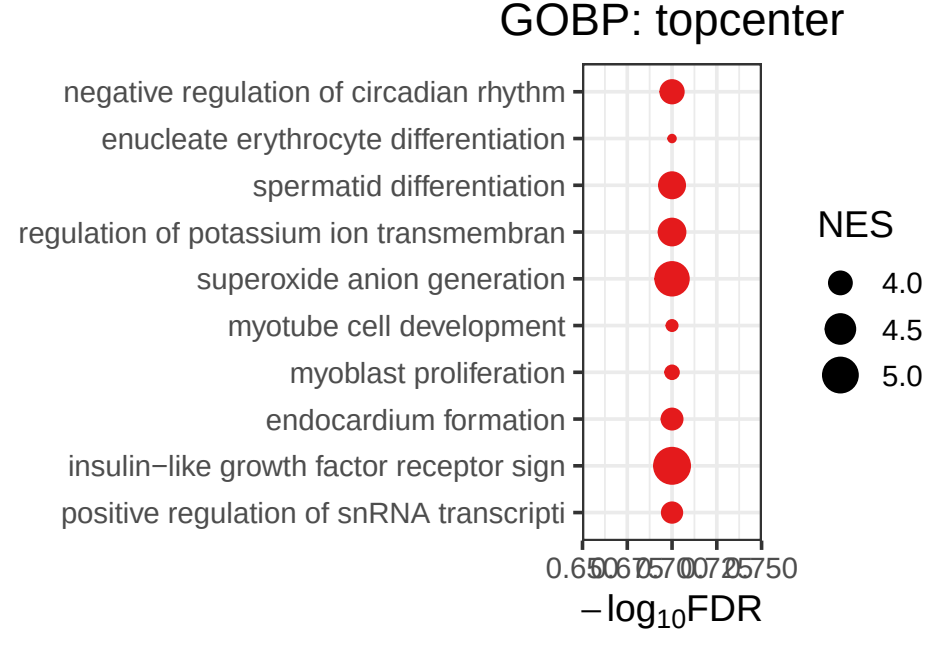

SPHINGOLIPID SIGNALING PATHWAY
-1
0
1
Golgi
Endoplasmic reticulum
SM
Cer
DEGS
dhCer
CerS
dhSph
SPT
Palmitoyl CoA
Serine
Sphingolipid metabolism
TNFα
TNFR
FAN
N-SMase
Ionizing radiation
SMS
A-SMase
ROS
Lysosome
TRADD
Ag
FcεRI
Fyn
TRAF2
Cathepsin
BID
BAX
Gab2
ASK1
JNK
Apoptosis
PI3K
p38
Adenosine
PIP3
CDase
CerS
Sph
PKCζ
AKT
BCL-2
BK
GPCR
Gi
PLD
-p
p53
PLC
SPHK
SPPase
Opioids
PKCε
ERK1/2
PP2A
ABCC1
S1Plyase
S1P
Phospho-ethanolamine
MAPK signaling pathway
S1P1
Ras
Raf
MEK1/2
ERK1/2
Cell survival
Proliferation
S1P2
Gi
PI3K
PDK1
AKT
eNOS
NO
Vasodilatation
Cardioprotection
PI3K-Akt signaling pathway
Rac
Migration and other cytoskeletal events
S1P3
Gq
PLC
[Ca2+]i
Secretion
S1P4
DG
PKC
S1P5
G12/13
Rho
ROCK
PTEN
NFκB
Stress-fiber formation
Data on KEGG graph
Rendered by Pathview

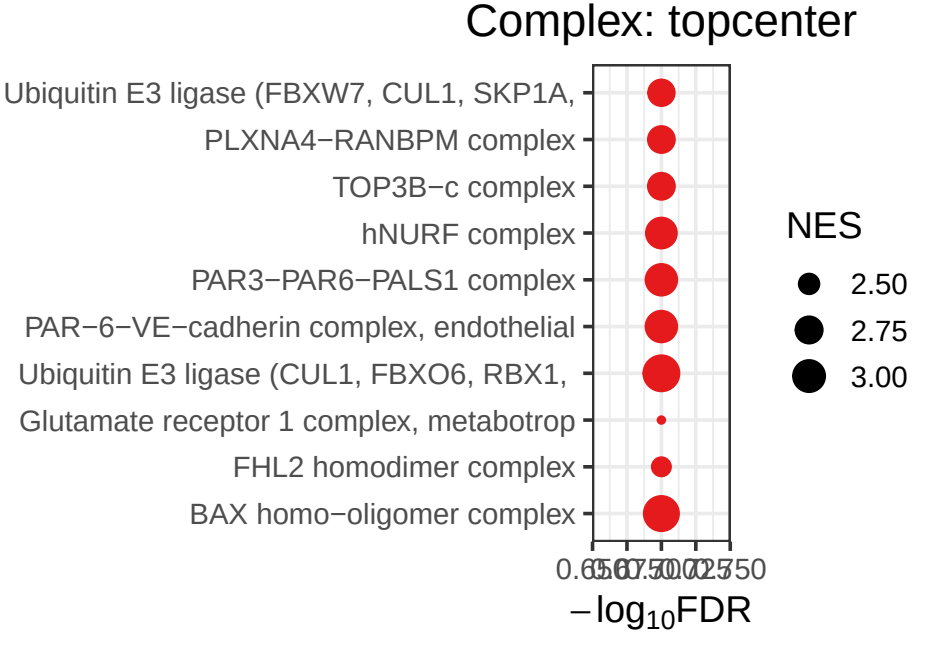

EDIL3
COLCA2
CDKL5
MUC22
SH2D7
CCDC90B
XG
CAPN15
GTDC1
CMTM2
NDOR1
PRDM10
MRPS11
FEN1
ACTR6
SKA1
VPS37A
ITGAV
ELP6
DHPS
ANKRD13D
NUP37
RAB29
TNFAIP3
ALDH5A1
PRKAA1
CHST15
RUNX1
THEGL
IRF2BP2
Treatment
Control
4
2
0
−2
−4
−6
−1.2
−0.8
−0.4
0.0

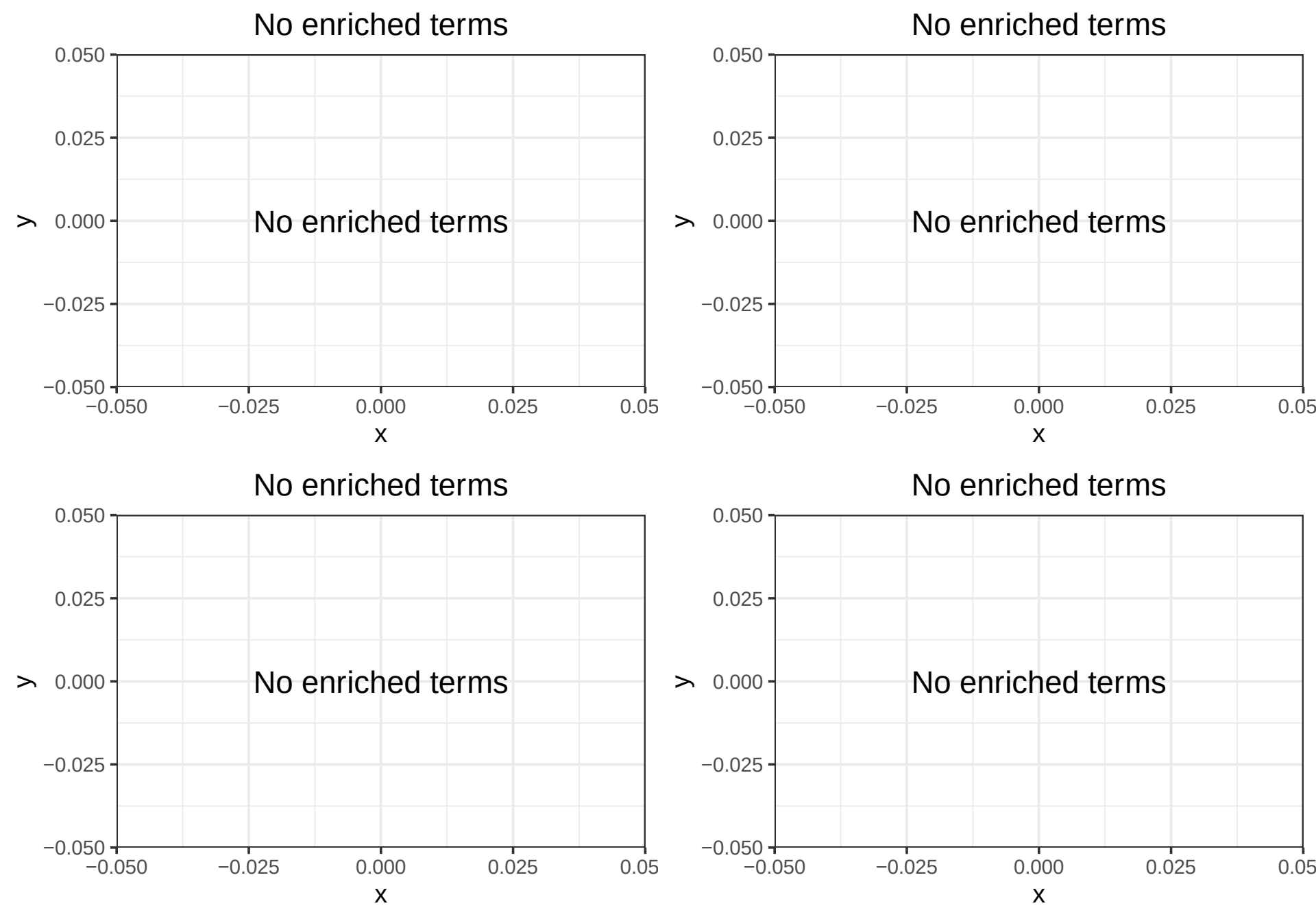

KEGG: midleft
Arrhythmogenic right ventricular cardiom
Synaptic vesicle cycle
Bacterial invasion of epithelial cells
Endocrine and other factor−regulated cal
Pyrimidine metabolism
Fanconi anemia pathway
Base excision repair
DNA replication
Non−homologous end−joining
Ribosome
0.8 1.0 1.2 1.4 1.6
−log10FDR
NES
0.2
0.3
0.4
0.5
REACTOME: midleft
POLB−Dependent Long Patch Base Excision
Wax biosynthesis
Cytosolic iron−sulfur cluster assembly
Hypusine synthesis from eIF5A−lysine
Pyrimidine biosynthesis
Removal of the Flap Intermediate
Early Phase of HIV Life Cycle
Mitochondrial translation termination
Mitochondrial translation elongation
Mitochondrial translation initiation
−log10FDR
NES
0.3
0.4
0.5
0.6
GOBP: midleft
mitochondrial translation
arginine transmembrane transport
L−histidine import across plasma membran
lysine transport
response to L−arginine
regulation of sister chromatid segregati
tRNA 3'−end processing
entry into host cell by a symbiont−conta
positive regulation of sister chromatid
spermidine metabolic process
1.550 1.575 1.600 1.625 1.650
−log10FDR
NES
0.2
0.3
0.4
0.5
0.6
Complex: midleft
ITGAV−ITGB3−THBS1 complex
ITGAV−ITGB3 complex
ITGAV−ITGB1 complex
ITGAV−ITGB3−PPAP2b complex
ITGAV−ITGB6 complex
ITGAV−ITGB5 complex
ITGAV−ITGB5−CYR61 complex
FEN1−WRN complex
28S ribosomal subunit, mitochondrial
55S ribosome, mitochondrial
1.550 1.575 1.600 1.625 1.650
−log10FDR
NES
0.40
0.45
0.50
0.55

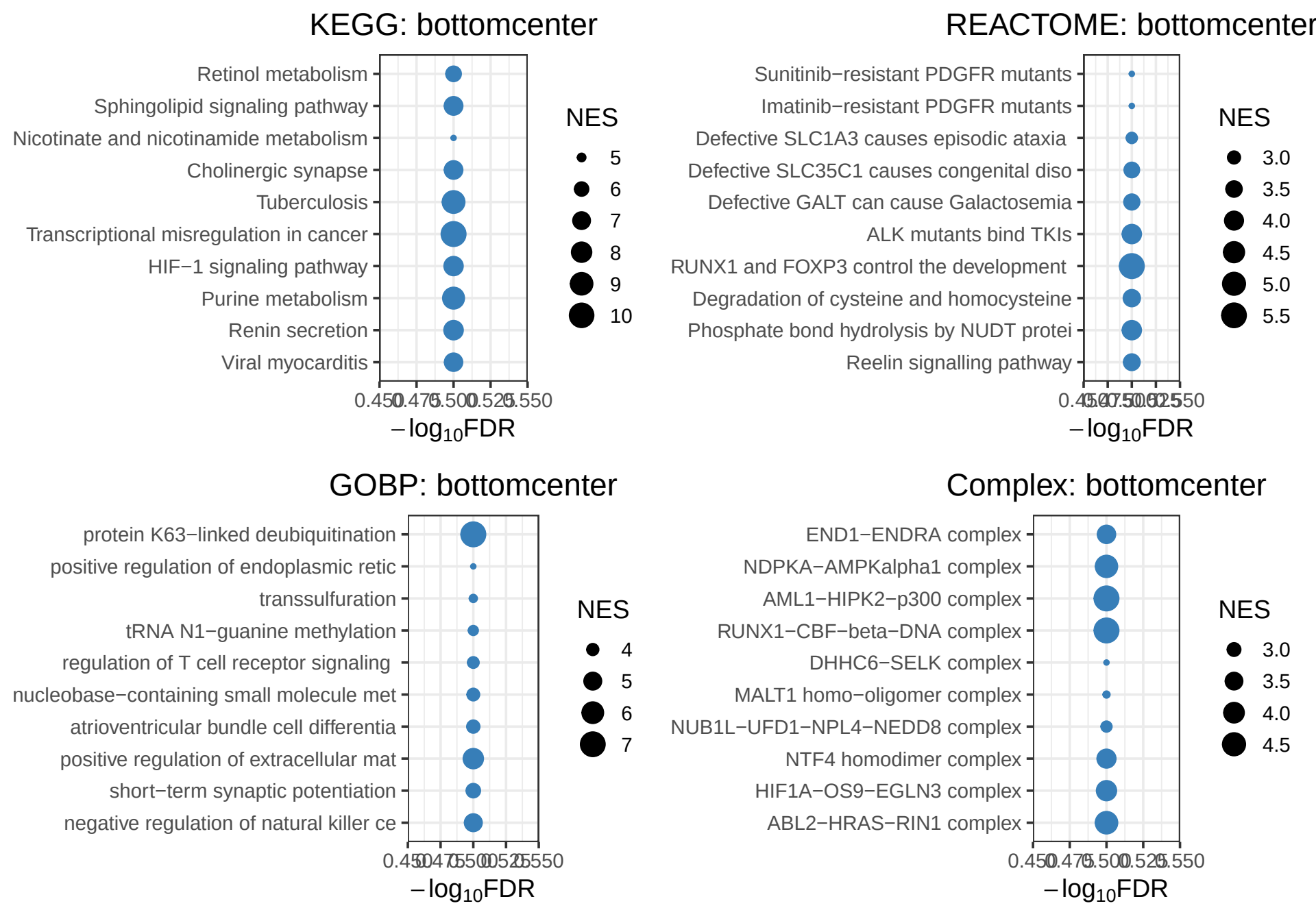

KEGG: topcenter
Type II diabetes mellitus
Staphylococcus aureus infection
Rheumatoid arthritis
Intestinal immune network for IgA produc
Systemic lupus erythematosus
Melanoma
Non−small cell lung cancer
Antigen processing and presentation
Primary immunodeficiency
Malaria
NES
4.5
5.0
5.5
6.0
0.650 0.675 0.700 0.725 0.750
−log10FDR

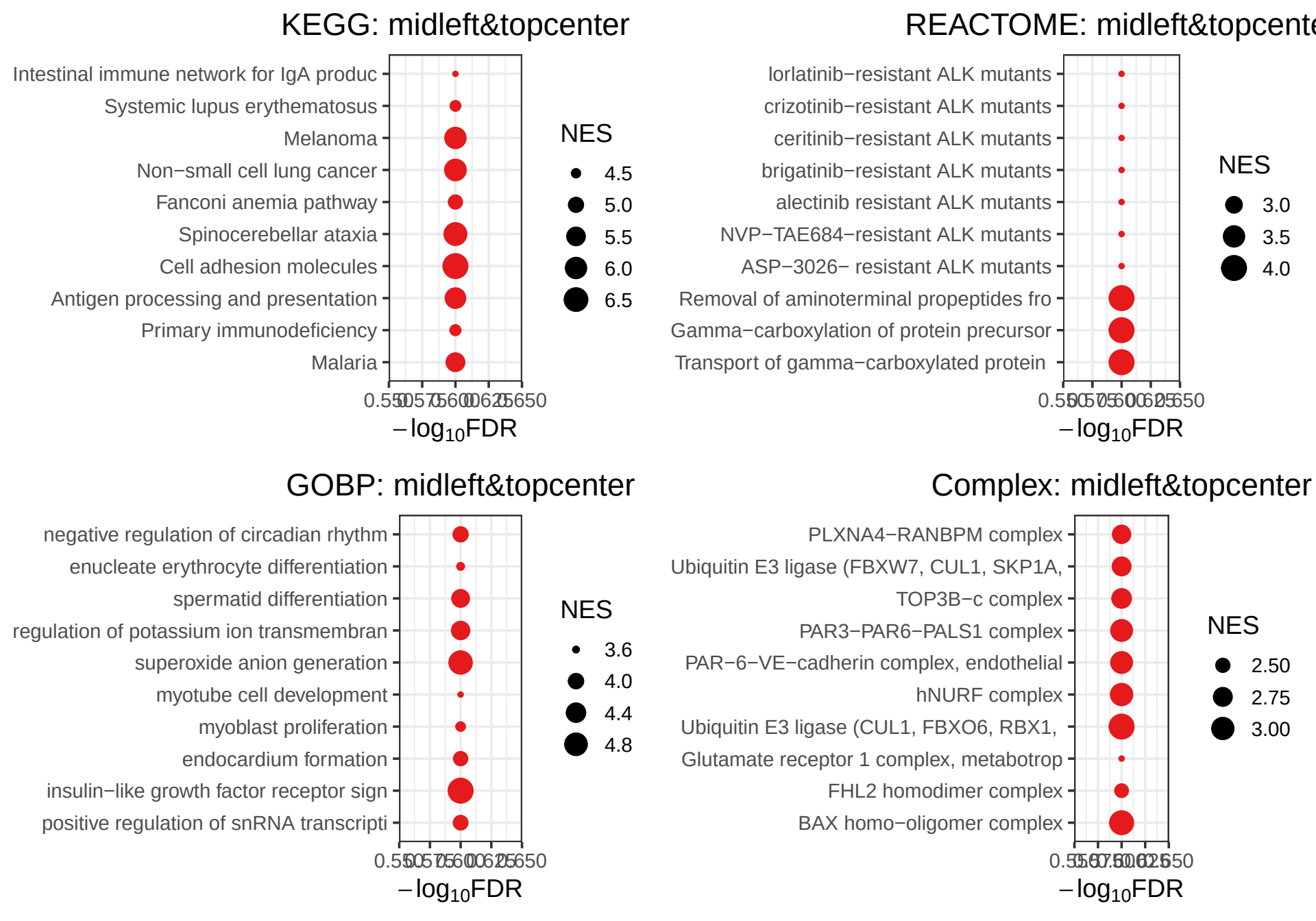

REACTOME: topcenter
alectinib resistant ALK mutants
NVP−TAE684−resistant ALK mutants
ASP−3026− resistant ALK mutants
WNT5:FZD7−mediated leishmania damping
TP53 Regulates Transcription of Caspase
Trafficking and processing of endosomal
Oxidative Stress Induced Senescence
Removal of aminoterminal propeptides fro
Gamma−carboxylation of protein precursor
Transport of gamma−carboxylated protein
NES
3
4
5
0.650 0.675 0.700 0.725 0.750
−log10FDR

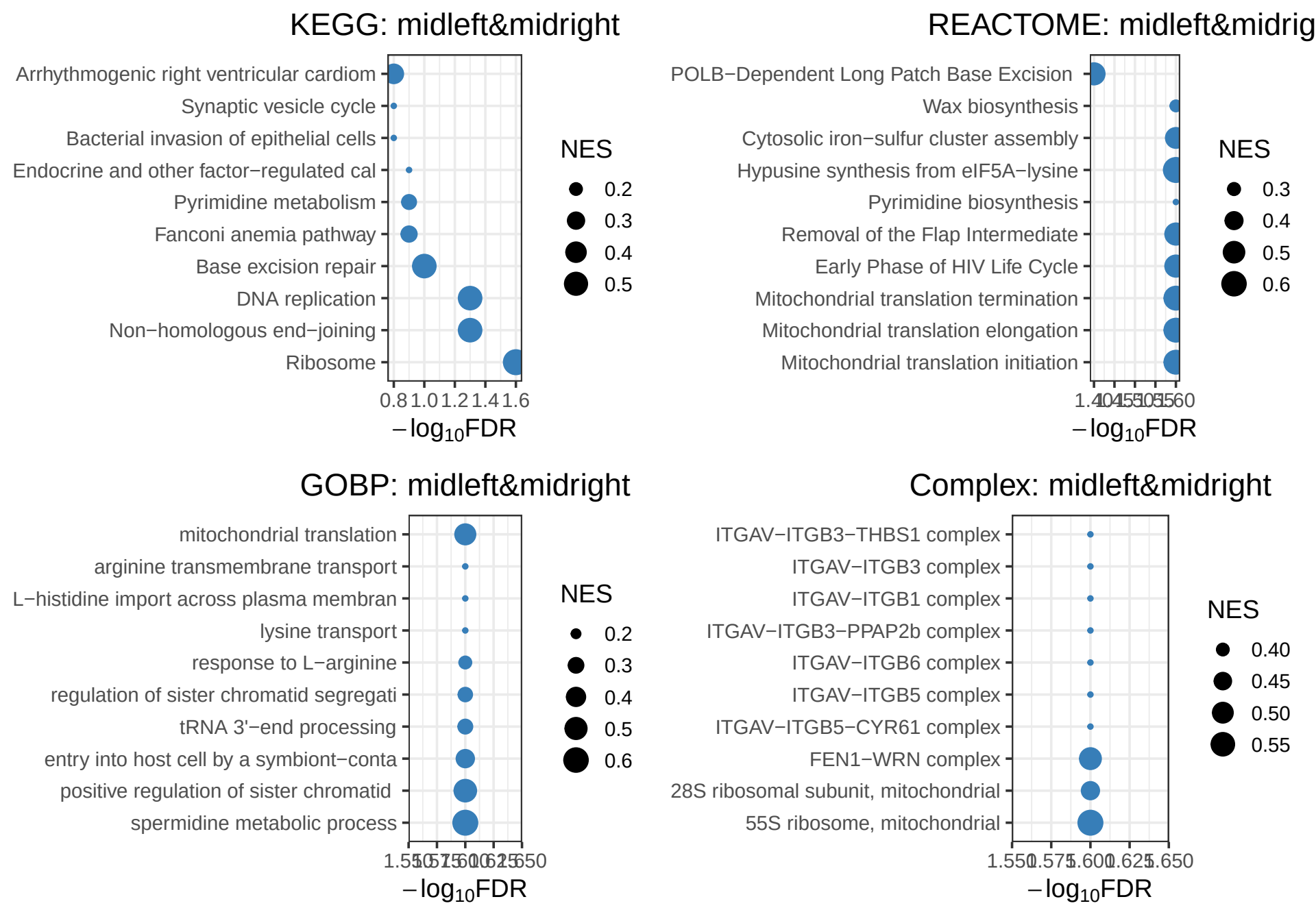

GOBP: topcenter
negative regulation of circadian rhythm
enucleate erythrocyte differentiation
spermatid differentiation
regulation of potassium ion transmembran
superoxide anion generation
myotube cell development
myoblast proliferation
endocardium formation
insulin−like growth factor receptor sign
positive regulation of snRNA transcripti
NES
4.0
4.5
5.0
0.650 0.675 0.700 0.725 0.750
−log10FDR

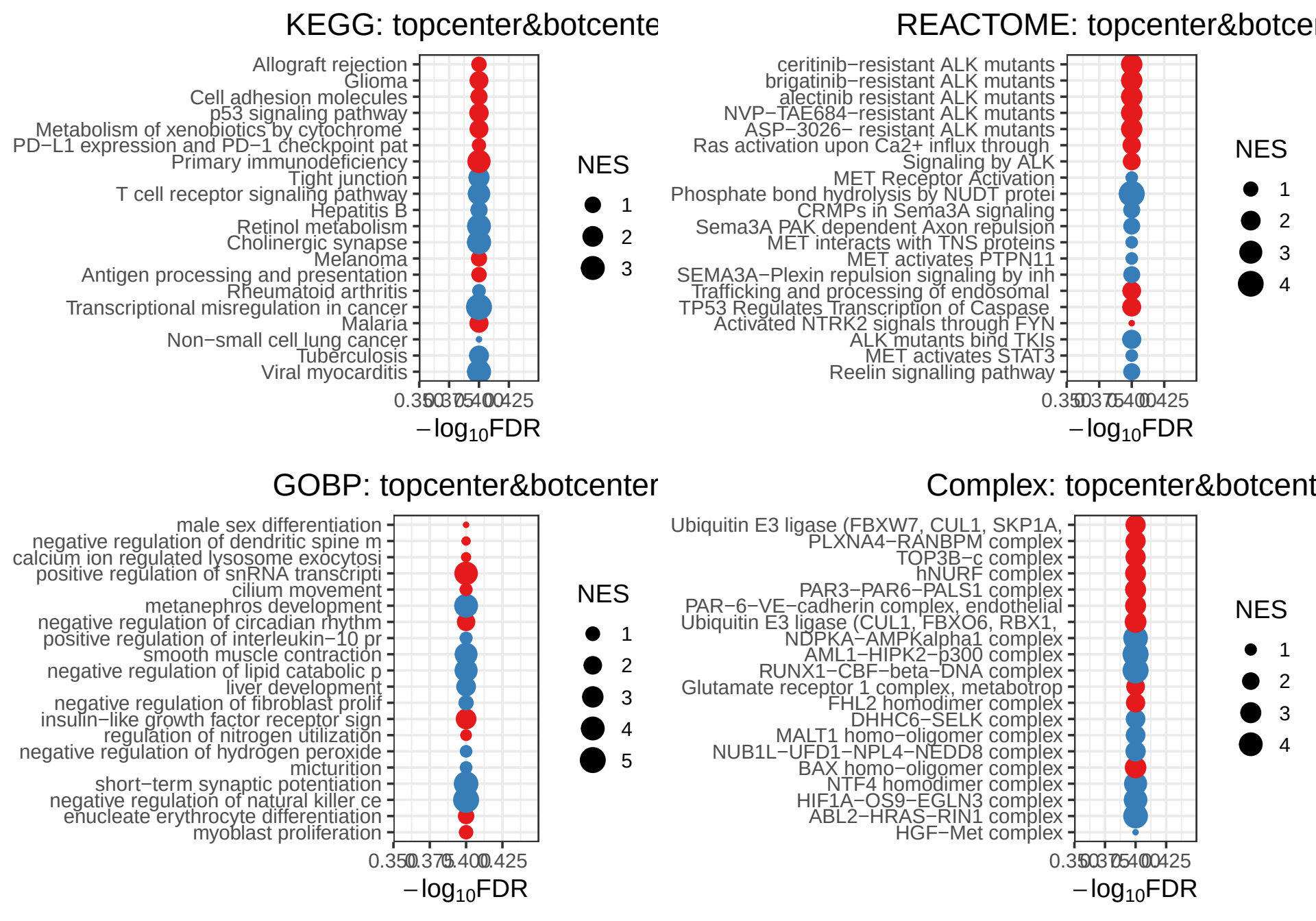

Complex: topcenter
Ubiquitin E3 ligase (FBXW7, CUL1, SKP1A,
PLXNA4−RANBPM complex
TOP3B−c complex
hNURF complex
PAR3−PAR6−PALS1 complex
PAR−6−VE−cadherin complex, endothelial
Ubiquitin E3 ligase (CUL1, FBXO6, RBX1,
Glutamate receptor 1 complex, metabotrop
FHL2 homodimer complex
BAX homo−oligomer complex
NES
2.50
2.75
3.00
0.650 0.675 0.700 0.725 0.750
−log10FDR

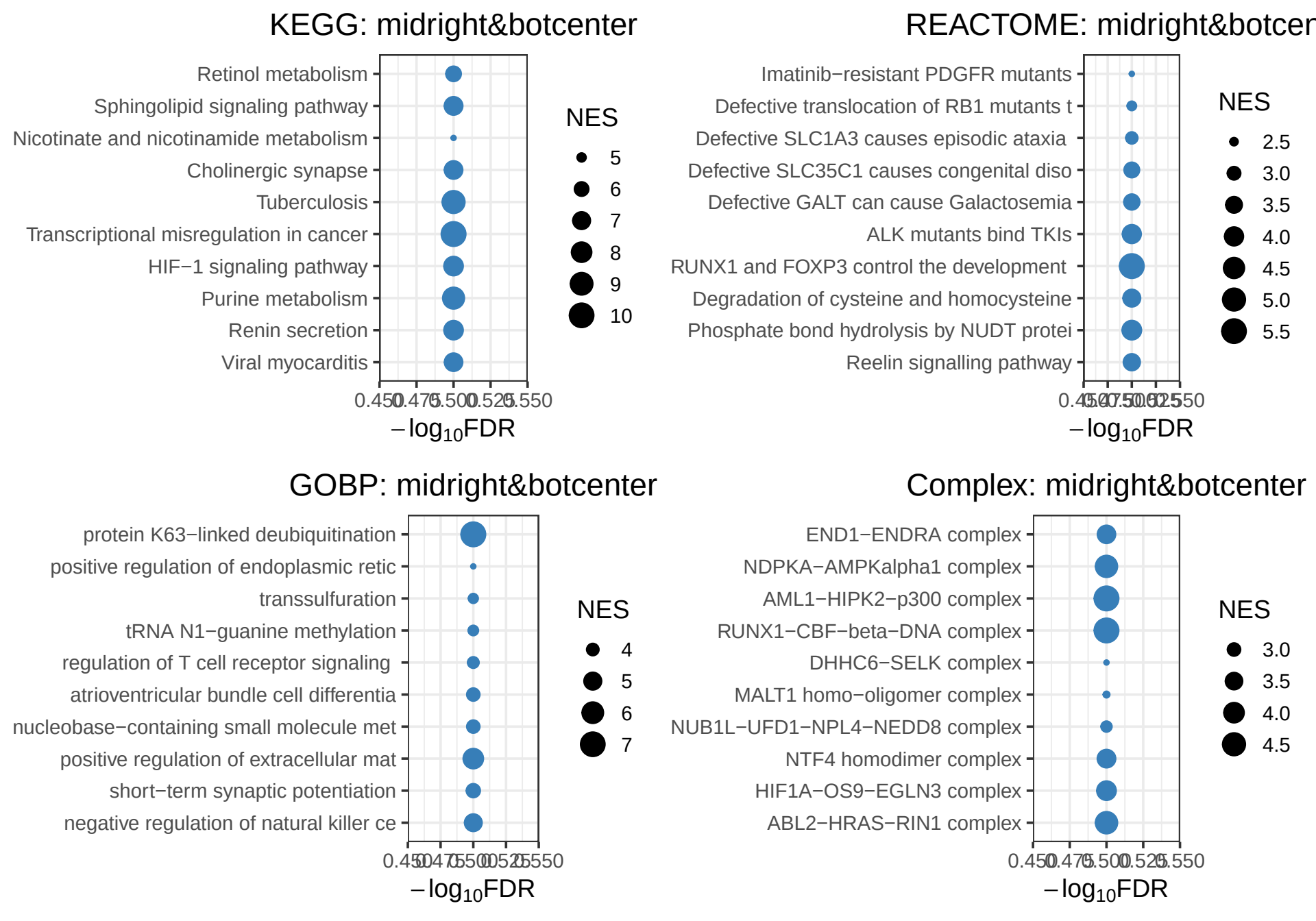

No enriched terms
No enriched terms
No enriched terms
No enriched terms
No enriched terms
No enriched terms
No enriched terms
No enriched terms
0.050
0.025
0.000
−0.025
−0.050
y
−0.050
−0.025
0.000
0.025
0.05
x


KEGG: bottomcenter
Retinol metabolism
Sphingolipid signaling pathway
Nicotinate and nicotinamide metabolism
Cholinergic synapse
Tuberculosis
Transcriptional misregulation in cancer
HIF−1 signaling pathway
Purine metabolism
Renin secretion
Viral myocarditis
NES
5
6
7
8
9
10
0.450
0.475
0.500
0.525
0.550
−log10FDR
REACTOME: bottomcenter
Sunitinib−resistant PDGFR mutants
Imatinib−resistant PDGFR mutants
Defective SLC1A3 causes episodic ataxia
Defective SLC35C1 causes congenital diso
Defective GALT can cause Galactosemia
ALK mutants bind TKIs
RUNX1 and FOXP3 control the development
Degradation of cysteine and homocysteine
Phosphate bond hydrolysis by NUDT protei
Reelin signalling pathway
NES
3.0
3.5
4.0
4.5
5.0
5.5
−log10FDR
GOBP: bottomcenter
protein K63−linked deubiquitination
positive regulation of endoplasmic retic
transsulfuration
tRNA N1−guanine methylation
regulation of T cell receptor signaling
nucleobase−containing small molecule met
atrioventricular bundle cell differentia
positive regulation of extracellular mat
short−term synaptic potentiation
negative regulation of natural killer ce
NES
4
5
6
7
0.450
0.475
0.500
0.525
0.550
−log10FDR
Complex: bottomcenter
END1−ENDRA complex
NDPKA−AMPKalpha1 complex
AML1−HIPK2−p300 complex
RUNX1−CBF−beta−DNA complex
DHHC6−SELK complex
MALT1 homo−oligomer complex
NUB1L−UFD1−NPL4−NEDD8 complex
NTF4 homodimer complex
HIF1A−OS9−EGLN3 complex
ABL2−HRAS−RIN1 complex
NES
3.0
3.5
4.0
4.5
0.450
0.475
0.500
0.525
0.550
−log10FDR

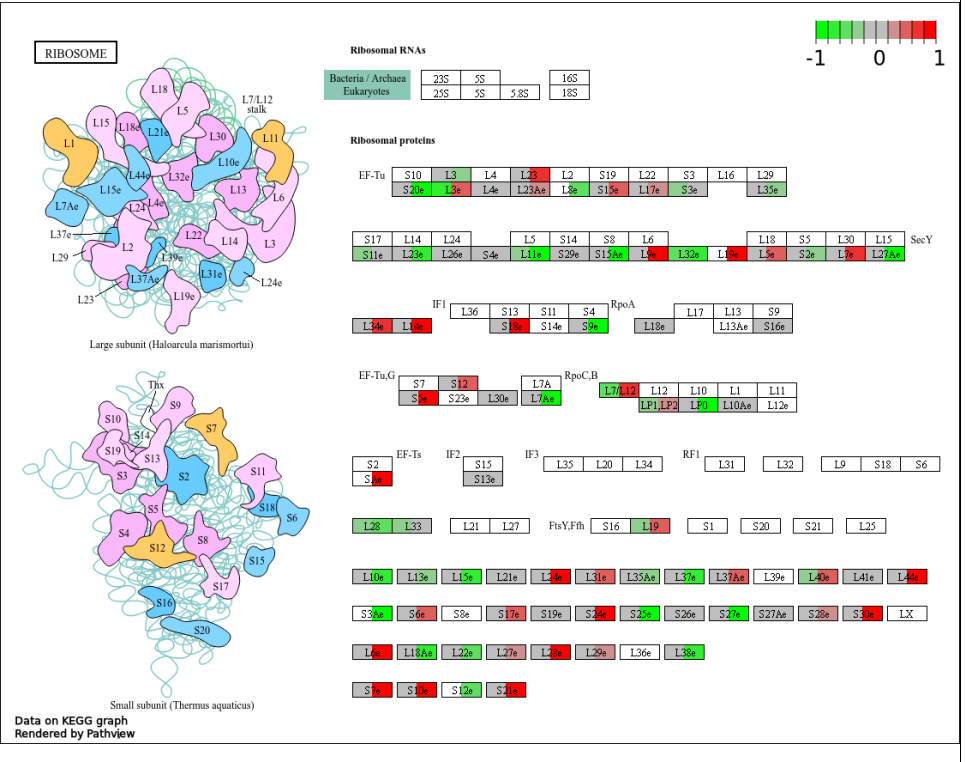

KEGG: midleft&topcenter
Intestinal immune network for IgA produc
Systemic lupus erythematosus
Melanoma
Non−small cell lung cancer
Fanconi anemia pathway
Spinocerebellar ataxia
Cell adhesion molecules
Antigen processing and presentation
Primary immunodeficiency
Malaria
NES
4.5
5.0
5.5
6.0
6.5
−log10FDR
REACTOME: midleft&topcente
lorlatinib−resistant ALK mutants
crizotinib−resistant ALK mutants
ceritinib−resistant ALK mutants
brigatinib−resistant ALK mutants
alectinib resistant ALK mutants
NVP−TAE684−resistant ALK mutants
ASP−3026− resistant ALK mutants
Removal of aminoterminal propeptides fro
Gamma−carboxylation of protein precursor
Transport of gamma−carboxylated protein
NES
3.0
3.5
4.0
−log10FDR
GOBP: midleft&topcenter
negative regulation of circadian rhythm
enucleate erythrocyte differentiation
spermatid differentiation
regulation of potassium ion transmembran
superoxide anion generation
myotube cell development
myoblast proliferation
endocardium formation
insulin−like growth factor receptor sign
positive regulation of snRNA transcripti
NES
3.6
4.0
4.4
4.8
−log10FDR
Complex: midleft&topcenter
PLXNA4−RANBPM complex
Ubiquitin E3 ligase (FBXW7, CUL1, SKP1A,
TOP3B−c complex
PAR3−PAR6−PALS1 complex
PAR−6−VE−cadherin complex, endothelial
hNURF complex
Ubiquitin E3 ligase (CUL1, FBXO6, RBX1,
Glutamate receptor 1 complex, metabotrop
FHL2 homodimer complex
BAX homo−oligomer complex
NES
2.50
2.75
3.00
−log10FDR

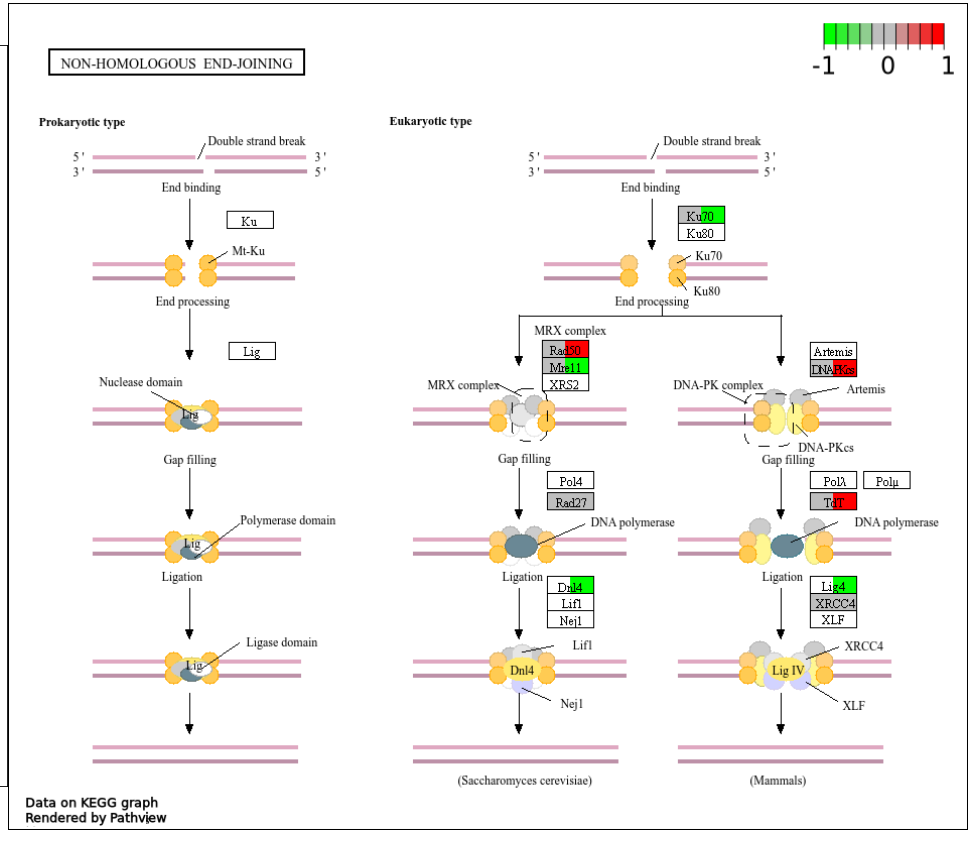

KEGG: midleft&midright
Arrhythmogenic right ventricular cardiom
Synaptic vesicle cycle
Bacterial invasion of epithelial cells
Endocrine and other factor−regulated cal
Pyrimidine metabolism
Fanconi anemia pathway
Base excision repair
DNA replication
Non−homologous end−joining
Ribosome
0.8 1.0 1.2 1.4 1.6
−log10FDR
NES
0.2
0.3
0.4
0.5
REACTOME: midleft&midrig
POLB−Dependent Long Patch Base Excision
Wax biosynthesis
Cytosolic iron−sulfur cluster assembly
Hypusine synthesis from eIF5A−lysine
Pyrimidine biosynthesis
Removal of the Flap Intermediate
Early Phase of HIV Life Cycle
Mitochondrial translation termination
Mitochondrial translation elongation
Mitochondrial translation initiation
−log10FDR
NES
0.3
0.4
0.5
0.6
GOBP: midleft&midright
mitochondrial translation
arginine transmembrane transport
L−histidine import across plasma membran
lysine transport
response to L−arginine
regulation of sister chromatid segregati
tRNA 3'−end processing
entry into host cell by a symbiont−conta
positive regulation of sister chromatid
spermidine metabolic process
−log10FDR
NES
0.2
0.3
0.4
0.5
0.6
Complex: midleft&midright
ITGAV−ITGB3−THBS1 complex
ITGAV−ITGB3 complex
ITGAV−ITGB1 complex
ITGAV−ITGB3−PPAP2b complex
ITGAV−ITGB6 complex
ITGAV−ITGB5 complex
ITGAV−ITGB5−CYR61 complex
FEN1−WRN complex
28S ribosomal subunit, mitochondrial
55S ribosome, mitochondrial
1.550 1.575 1.600 1.625 1.650
−log10FDR
NES
0.40
0.45
0.50
0.55


KEGG: topcenter&botcente
Allograft rejection
Glioma
Cell adhesion molecules
p53 signaling pathway
Metabolism of xenobiotics by cytochrome
PD−L1 expression and PD−1 checkpoint pat
Primary immunodeficiency
Tight junction
T cell receptor signaling pathway
Hepatitis B
Retinol metabolism
Cholinergic synapse
Melanoma
Antigen processing and presentation
Rheumatoid arthritis
Transcriptional misregulation in cancer
Malaria
Non−small cell lung cancer
Tuberculosis
Viral myocarditis
0.350.375.400.425
−log10FDR
NES
1
2
3
REACTOME: topcenter&botcer
ceritinib−resistant ALK mutants
brigatinib−resistant ALK mutants
alectinib resistant ALK mutants
NVP−TAE684−resistant ALK mutants
ASP−3026− resistant ALK mutants
Ras activation upon Ca2+ influx through
Signaling by ALK
MET Receptor Activation
Phosphate bond hydrolysis by NUDT protei
CRMPs in Sema3A signaling
Sema3A PAK dependent Axon repulsion
MET interacts with TNS proteins
MET activates PTPN11
SEMA3A−Plexin repulsion signaling by inh
Trafficking and processing of endosomal
TP53 Regulates Transcription of Caspase
Activated NTRK2 signals through FYN
ALK mutants bind TKIs
MET activates STAT3
Reelin signalling pathway
0.350.375.400.425
−log10FDR
NES
1
2
3
4
GOBP: topcenter&botcenter
male sex differentiation
negative regulation of dendritic spine m
calcium ion regulated lysosome exocytosi
positive regulation of snRNA transcripti
cilium movement
metanephros development
negative regulation of circadian rhythm
positive regulation of interleukin−10 pr
smooth muscle contraction
negative regulation of lipid catabolic p
liver development
negative regulation of fibroblast prolif
insulin−like growth factor receptor sign
regulation of nitrogen utilization
negative regulation of hydrogen peroxide
micturition
short−term synaptic potentiation
negative regulation of natural killer ce
enucleate erythrocyte differentiation
myoblast proliferation
0.350.375.400.425
−log10FDR
NES
1
2
3
4
5
Complex: topcenter&botcent
Ubiquitin E3 ligase (FBXW7, CUL1, SKP1A,
PLXNA4−RANBPM complex
TOP3B−c complex
hNURF complex
PAR3−PAR6−PALS1 complex
PAR−6−VE−cadherin complex, endothelial
Ubiquitin E3 ligase (CUL1, FBXO6, RBX1,
NDPKA−AMPKalpha1 complex
AML1−HIPK2−p300 complex
RUNX1−CBF−beta−DNA complex
Glutamate receptor 1 complex, metabotrop
FHL2 homodimer complex
DHHC6−SELK complex
MALT1 homo−oligomer complex
NUB1L−UFD1−NPL4−NEDD8 complex
BAX homo−oligomer complex
NTF4 homodimer complex
HIF1A−OS9−EGLN3 complex
ABL2−HRAS−RIN1 complex
HGF−Met complex
0.350.375.400.425
−log10FDR
NES
1
2
3
4

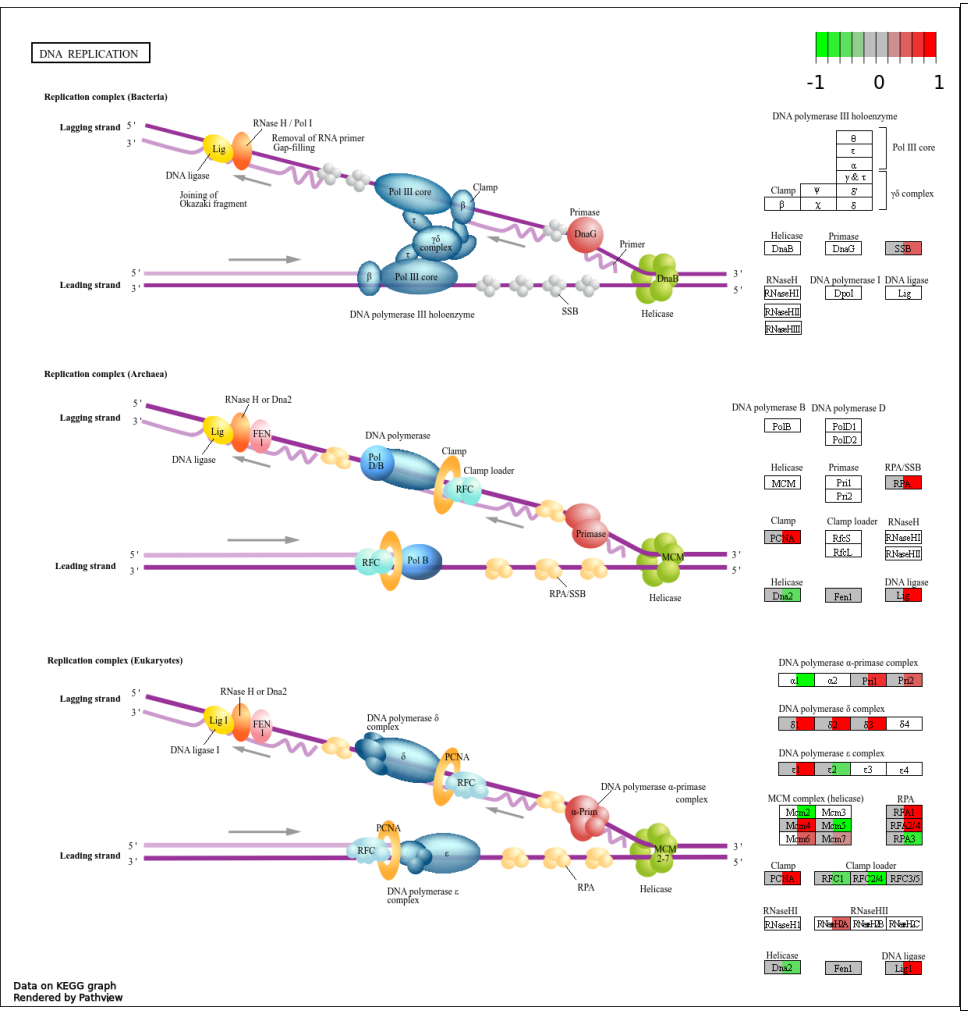

KEGG: midright&botcenter
Retinol metabolism
Sphingolipid signaling pathway
Nicotinate and nicotinamide metabolism
Cholinergic synapse
Tuberculosis
Transcriptional misregulation in cancer
HIF−1 signaling pathway
Purine metabolism
Renin secretion
Viral myocarditis
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
5
6
7
8
9
10
REACTOME: midright&botcer
Imatinib−resistant PDGFR mutants
Defective translocation of RB1 mutants t
Defective SLC1A3 causes episodic ataxia
Defective SLC35C1 causes congenital diso
Defective GALT can cause Galactosemia
ALK mutants bind TKIs
RUNX1 and FOXP3 control the development
Degradation of cysteine and homocysteine
Phosphate bond hydrolysis by NUDT protei
Reelin signalling pathway
−log10FDR
NES
2.5
3.0
3.5
4.0
4.5
5.0
5.5
GOBP: midright&botcenter
protein K63−linked deubiquitination
positive regulation of endoplasmic retic
transsulfuration
tRNA N1−guanine methylation
regulation of T cell receptor signaling
atrioventricular bundle cell differentia
nucleobase−containing small molecule met
positive regulation of extracellular mat
short−term synaptic potentiation
negative regulation of natural killer ce
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
4
5
6
7
Complex: midright&botcenter
END1−ENDRA complex
NDPKA−AMPKalpha1 complex
AML1−HIPK2−p300 complex
RUNX1−CBF−beta−DNA complex
DHHC6−SELK complex
MALT1 homo−oligomer complex
NUB1L−UFD1−NPL4−NEDD8 complex
NTF4 homodimer complex
HIF1A−OS9−EGLN3 complex
ABL2−HRAS−RIN1 complex
0.450
0.475
0.500
0.525
0.550
−log10FDR
NES
3.0
3.5
4.0
4.5

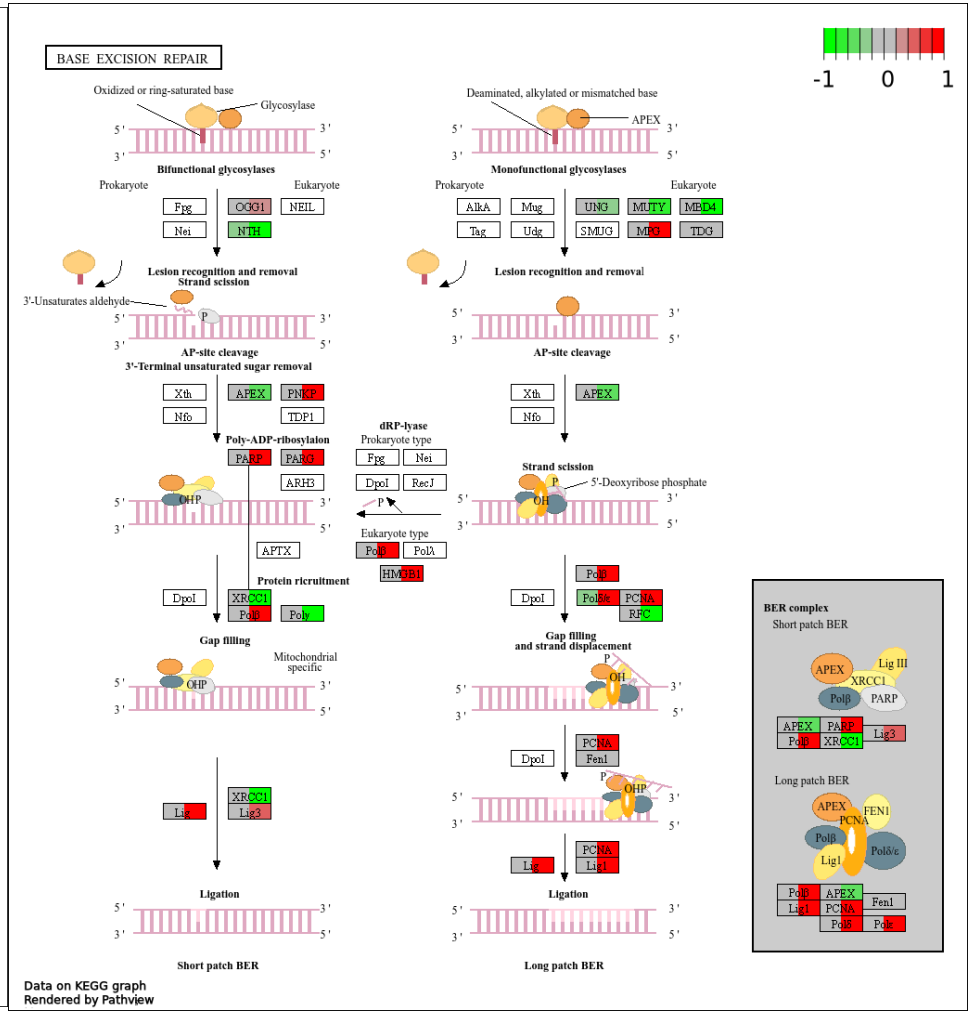
Group 1


RIBOSOME
Large subunit (Haloarcula marismortui)
Small subunit (Thermus aquaticus)
Ribosomal RNAs
Bacteria / Archaea
Eukaryotes
23S
5S
5.8S
16S
18S
Ribosomal proteins
EF-Tu
SecY
IF1
RpoA
EF-Tu,G
RpoC,B
EF-Ts
IF2
IF3
RF1
FtsY,Ffh
-1
0
1
Data on KEGG graph
Rendered by Pathview

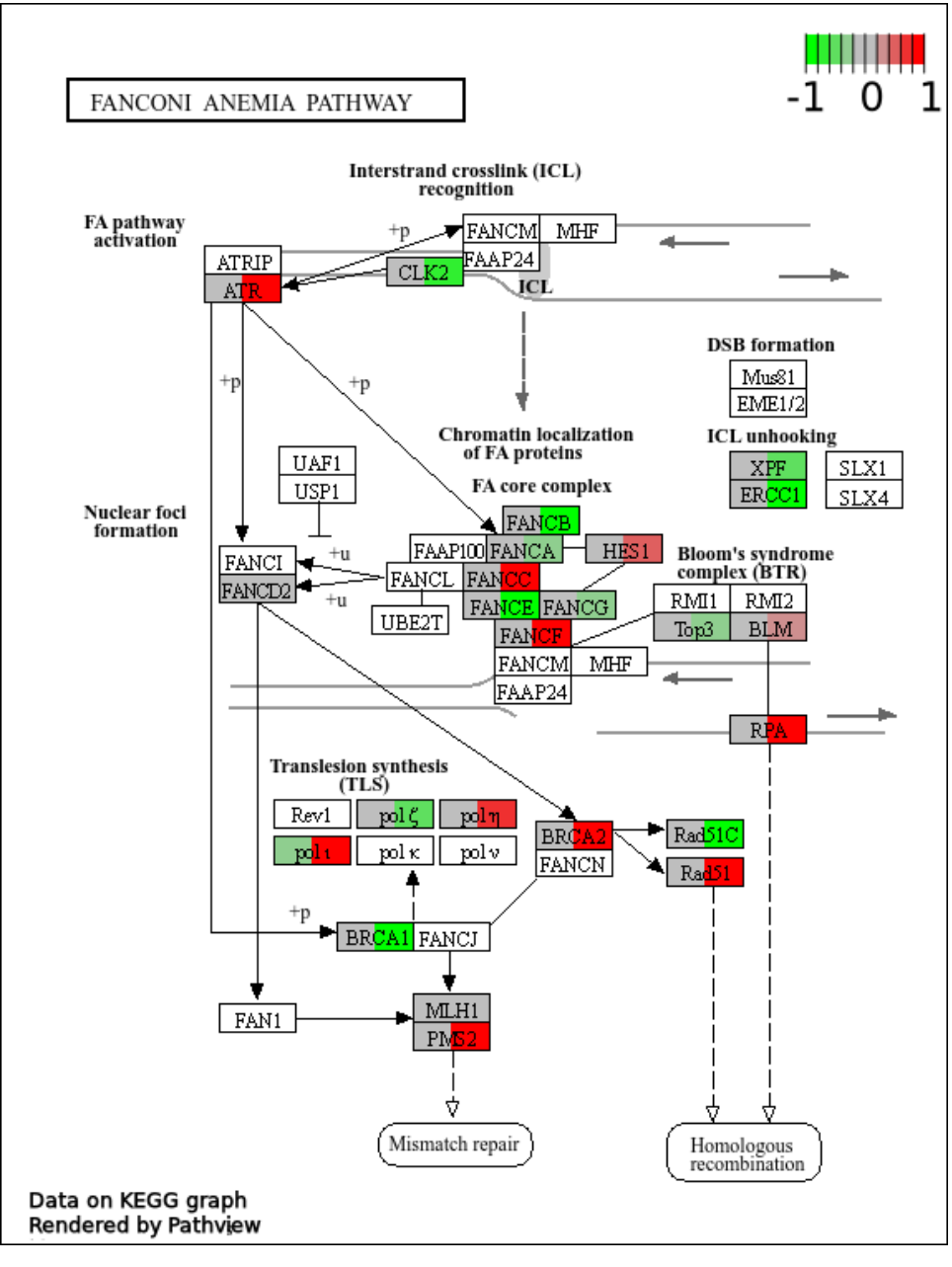

NON-HOMOLOGOUS END-JOINING
Prokaryotic type
Eukaryotic type
Double strand break
End binding
End processing
Gap filling
Ligation
Ku
Mt-Ku
Lig
Nuclease domain
Polymerase domain
Ligase domain
MRX complex
Rad50
Mre11
XRS2
Pol4
Rad27
Dnl4
Lif1
Nej1
DNA-PK complex
Artemis
DNA-PKcs
DNA polymerase
Pol λ
Pol μ
TdT
Lig4
XRCC4
XLF
Lig IV
(Saccharomyces cerevisiae)
(Mammals)
-1
0
1
Data on KEGG graph
Rendered by Pathview

Group 1

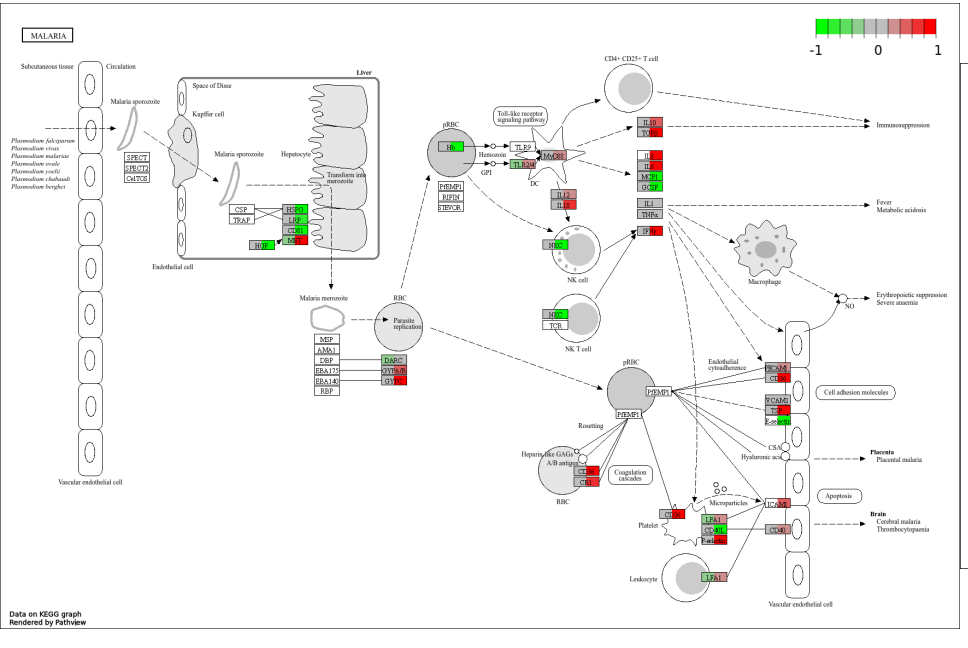

DNA REPLICATION
Replication complex (Bacteria)
Lagging strand
Leading strand
RNase H / Pol I
Removal of RNA primer
Gap-filling
Lig
DNA ligase
Joining of
Okazaki fragment
Pol III core
Clamp
γδ complex
Primase
DnaG
Primer
DnaB
SSB
Helicase
DNA polymerase III holoenzyme
Replication complex (Archaea)
RNase H or Dna2
FEN 1
DNA polymerase
Pol D/B
Clamp loader
RFC
Pol B
MCM
RPA/SSB
Replication complex (Eukaryotes)
Lig I
DNA ligase I
DNA polymerase δ complex
PCNA
DNA polymerase α-primase complex
α-Prim
DNA polymerase ε complex
-1
0
1
DNA polymerase III holoenzyme
Pol III core
Clamp
Helicase
Primase
SSB
RNaseH
DNA polymerase I
DNA ligase
DNA polymerase B
DNA polymerase D
RPA/SSB
Clamp loader
DNA polymerase α-primase complex
DNA polymerase δ complex
DNA polymerase ε complex
MCM complex (helicase)
RPA
Data on KEGG graph
Rendered by Pathview

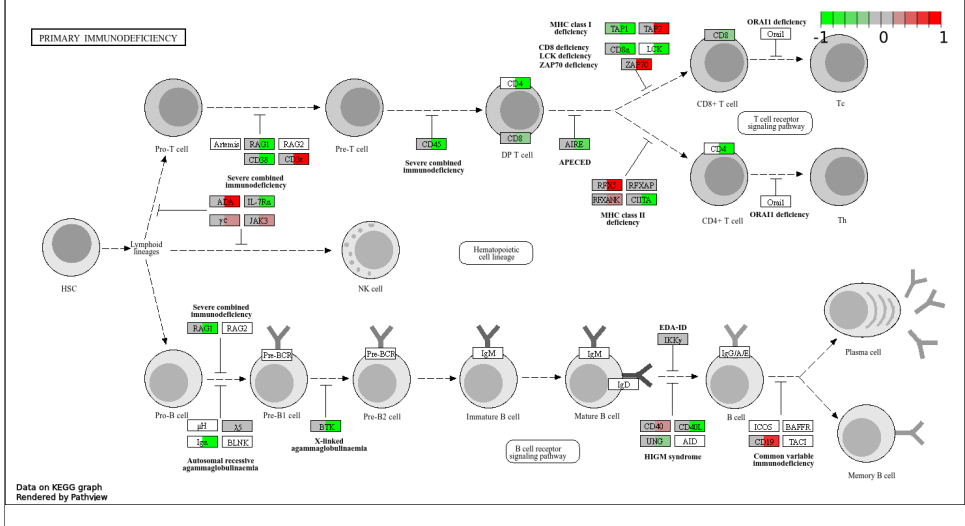

BASE EXCISION REPAIR
Oxidized or ring-saturated base
Glycosylase
Bifunctional glycosylases
Prokaryote
Eukaryote
Fpg
Nei
OGG1
NEIL
NTH
Lesion recognition and removal
Strand scission
3'-Unsaturates aldehyde
AP-site cleavage
3'-Terminal unsaturated sugar removal
Xth
Nfo
APEX
PNKP
TDP1
Poly-ADP-ribosylaion
PARP
PARG
ARH3
APTX
Protein ricruitment
XRCC1
Polβ
Polγ
DpoI
Gap filling
Mitochondrial specific
Lig
Lig3
Ligation
Short patch BER
dRP-lyase
Prokaryote type
RecJ
Eukaryote type
Polβ
Polλ
HMJB1
Deaminated, alkylated or mismatched base
Monofunctional glycosylases
AlkA
Tag
Mug
Udg
UNG
SMUG
MUTY
MBD4
MPG
TDG
Strand scission
5'-Deoxyribose phosphate
Polδ
Polδε
PCNA
RFC
Gap filling
and strand displacement
Fen1
Lig1
Long patch BER
BER complex
Short patch BER
Lig III
XRCC1
PARP
Long patch BER
FEN1
Polδ/ε
-1
0
1
Data on KEGG graph
Rendered by Pathview

Group 1

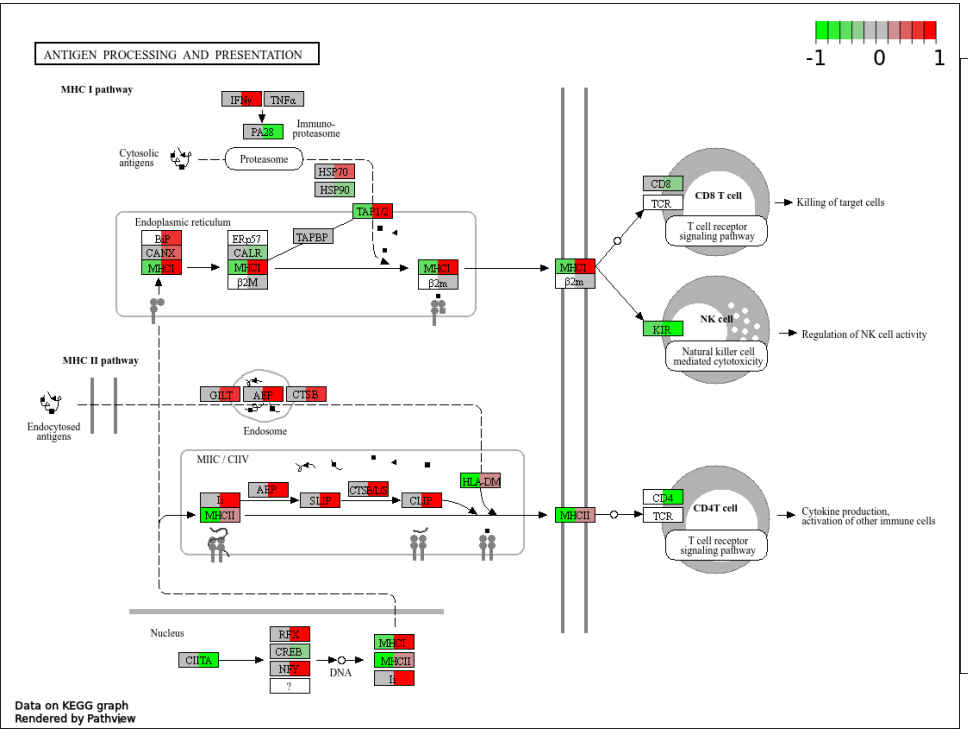

FANCONI ANEMIA PATHWAY
-1 0 1
Interstrand crosslink (ICL) recognition
FA pathway activation
ATRIP
ATR
+p
FANCM
MHF
FAAP24
CLK2
ICL
DSB formation
Mus81
EME1/2
ICL unhooking
XPF
ERCC1
SLX1
SLX4
Chromatin localization of FA proteins
FA core complex
UAF1
USP1
Nuclear foci formation
FANCB
FANCI
FANCD2
+u
FAAP100
FANCA
HES1
FANCL
FANCC
FANCE
FANCG
UBE2T
Bloom's syndrome complex (BTR)
RMI1
RMI2
Top3
BLM
FANCF
RPA
Translesion synthesis (TLS)
Rev1
pol ζ
pol η
pol ι
pol κ
pol ν
BRCA2
FANCN
Rad51C
Rad51
BRCA1
FANCJ
FAN1
MLH1
PMS2
Mismatch repair
Homologous recombination
Data on KEGG graph
Rendered by Pathview

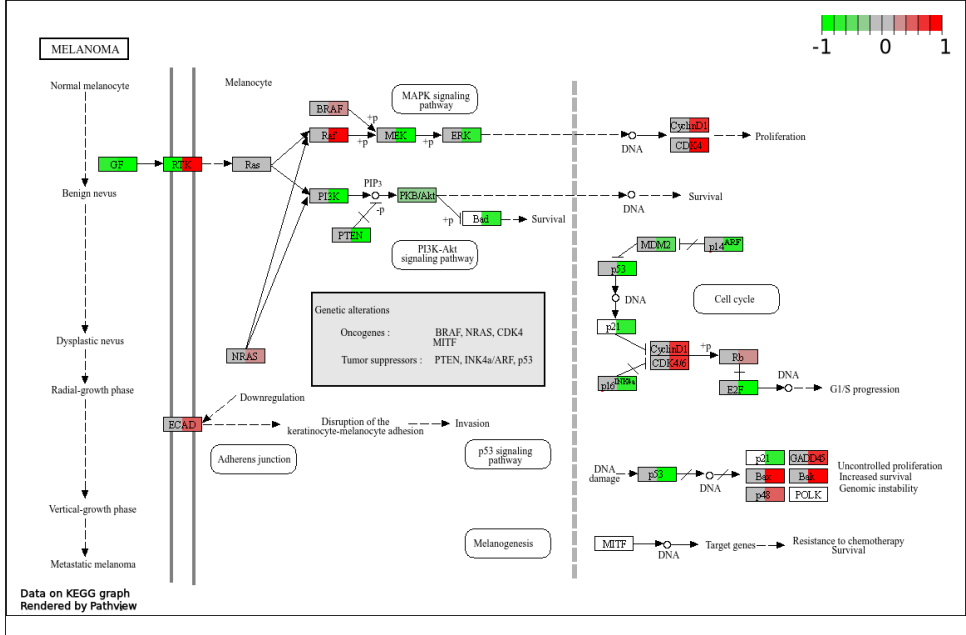
Group 2


MALARIA
-1
0
1
Subcutaneous tissue
Circulation
Liver
Space of Disse
Kupffer cell
Malaria sporozoite
Hepatocyte
Transform into merozoite
Endothelial cell
Vascular endothelial cell
Plasmodium falciparum
Plasmodium vivax
Plasmodium malariae
Plasmodium ovale
Plasmodium yoelii
Plasmodium chabaudi
Plasmodium berghei
SPECT
ORCT2
CAITOS
CSP
TRAP
HSP90
LHP
CD36
MSR
HSP
Malaria merozoite
MSP
AMA1
DBP
RBA175
RBA140
RBP
RBC
Parasite replication
DARC
GYPA/B
Q1/Q2
pRBC
PfEMP1
RIFIN
STEVOR
Toll-like receptor signaling pathway
TLR9
Hemozoin
GPI
MyD88
DC
IL12
IL18
CD4+ CD25+ T cell
IL10
TGFB
IL2
IL4
MCP1
CCR5
IL1
TNFa
IFNg
NKG2
NK cell
NKG2
TCR
NK T cell
Macrophage
Immunosuppression
Fever
Metabolic acidosis
NO
Erythropoietic suppression
Severe anaemia
Endothelial cytoadherence
ICAM1
CD36
VCAM1
E-selec
CSA
Hyaluronic acid
Placenta
Placental malaria
Cell adhesion molecules
Rosetting
Heparin-like GAGs
A/B antigen
CR1
CD55
Coagulation cascades
Microparticles
TFPI
Apoptosis
Platelet
CD36
LFA1
CD40L
Brain
Cerebral malaria
Thrombocytopaenia
Leukocyte
LFA1
Vascular endothelial cell
Data on KEGG graph
Rendered by Pathview

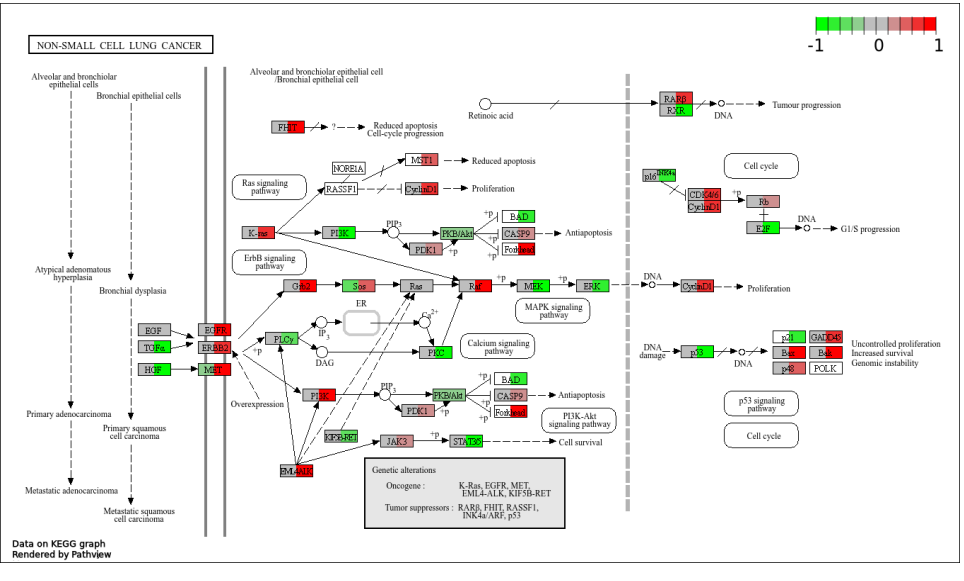

PRIMARY IMMUNODEFICIENCY
-1
0
1
HSC
Lymphoid lineages
Pro-T cell
Artemis
RAG1
RAG2
CD3E
CD3G
Severe combined immunodeficiency
Pre-T cell
CD45
Severe combined immunodeficiency
CD4
CD8
DP T cell
MHC class I deficiency
TAP1
TAP2
CD8 deficiency
LCK deficiency
ZAP70 deficiency
CD8A
LCK
ZAP70
AIRE
APECED
CD8+ T cell
ORAI1 deficiency
Orai1
Tc
T cell receptor signaling pathway
CD4+ T cell
Th
RFX5
RFXAP
RFXANC
CIITA
MHC class II deficiency
NK cell
A20
IL-7Ra
γc
JAK3
Hematopoietic cell lineage
Severe combined immunodeficiency
RAG1
RAG2
Pro-B cell
μH
λ5
Igα
BLNK
Autosomal recessive agammaglobulinaemia
Pre-B1 cell
Pre-BCR
BTK
X-linked agammaglobulinaemia
Pre-B2 cell
Pre-BCR
Immature B cell
IgM
B cell receptor signaling pathway
Mature B cell
IgM
IgD
EDA-ID
IKBG
HIGM syndrome
CD40
CD40L
UNG
AID
B cell
IgG/A/E
ICOS
BAFFR
CD19
TACI
Common variable immunodeficiency
Plasma cell
Memory B cell
Data on KEGG graph
Rendered by Pathview

Group 2

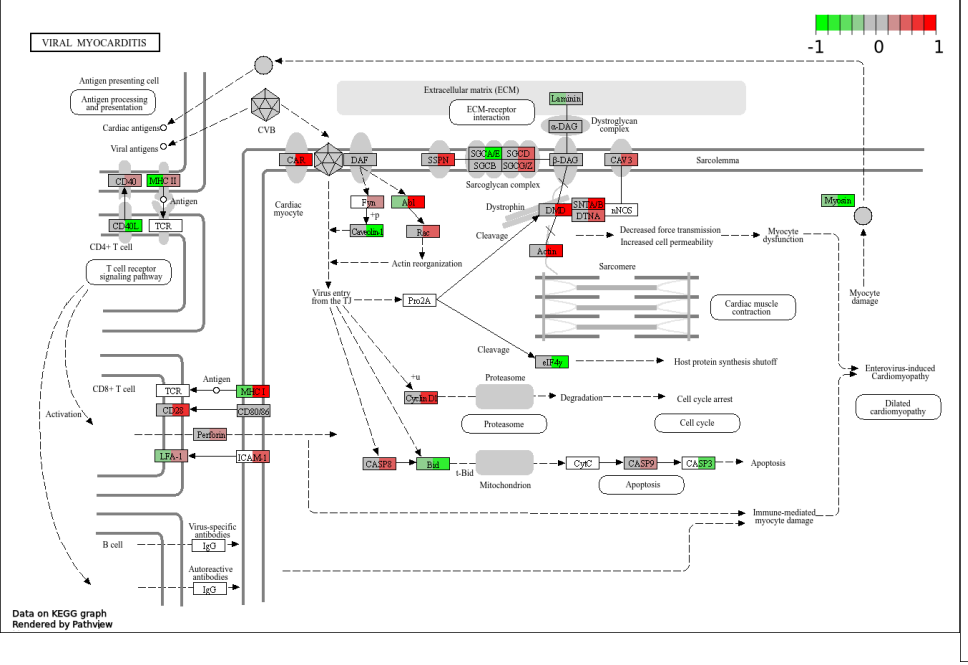

ANTIGEN PROCESSING AND PRESENTATION
-1 0 1
MHC I pathway
IFNγ
TNFα
PA28
Immuno-proteasome
Cytosolic antigens
Proteasome
HSP70
HSP90
TAP1/2
Endoplasmic reticulum
BiP
CANX
MHCI
ERp57
CALR
β2M
TAPBP
MHCI β2m
MHCI β2m
CD8
TCR
CD8 T cell
T cell receptor signaling pathway
Killing of target cells
KIR
NK cell
Natural killer cell mediated cytotoxicity
Regulation of NK cell activity
MHC II pathway
Endocytosed antigens
GILT
AEP
CTSB
Endosome
MIIC / CIIV
HLA-DM
CTSD/L/S
CLIP
MHCII
CD4
TCR
CD4T cell
T cell receptor signaling pathway
Cytokine production, activation of other immune cells
Nucleus
CIITA
RFX
CREB
NFY
?
DNA
MHCI
MHCII
Data on KEGG graph
Rendered by Pathview

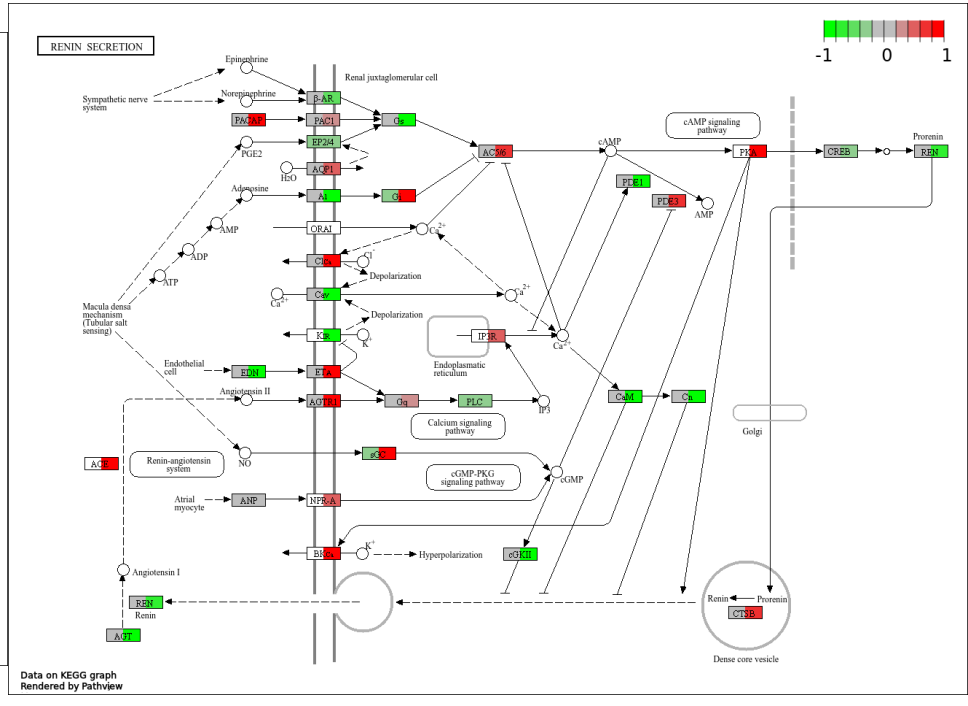

MELANOMA
-1 0 1
Normal melanocyte
Benign nevus
Dysplastic nevus
Radial-growth phase
Vertical-growth phase
Metastatic melanoma
Melanocyte
OF
FGFR
Ras
BRAF
Raf
MEK
ERK
MAPK signaling pathway
PI3K
PIP3
PKB/Akt
Bad
Survival
PTEN
PI3K-Akt signaling pathway
NRAS
Genetic alterations
Oncogenes : BRAF, NRAS, CDK4 MITF
Tumor suppressors : PTEN, INK4a/ARF, p53
DNA
CyclinD1
CDK4
Proliferation
MDM2
p14ARF
p53
Cell cycle
p21
CyclinD1
CDK4/6
p16INK4a
Rb
E2F
G1/S progression
Downregulation
ECAD
Disruption of the keratinocyte-melanocyte adhesion
Invasion
Adherens junction
p53 signaling pathway
DNA damage
p53
p21
GADD45
Bax
p48
POLK
Uncontrolled proliferation
Increased survival
Genomic instability
Melanogenesis
MITF
Target genes
Resistance to chemotherapy
Survival
Data on KEGG graph
Rendered by Pathview

Group 2

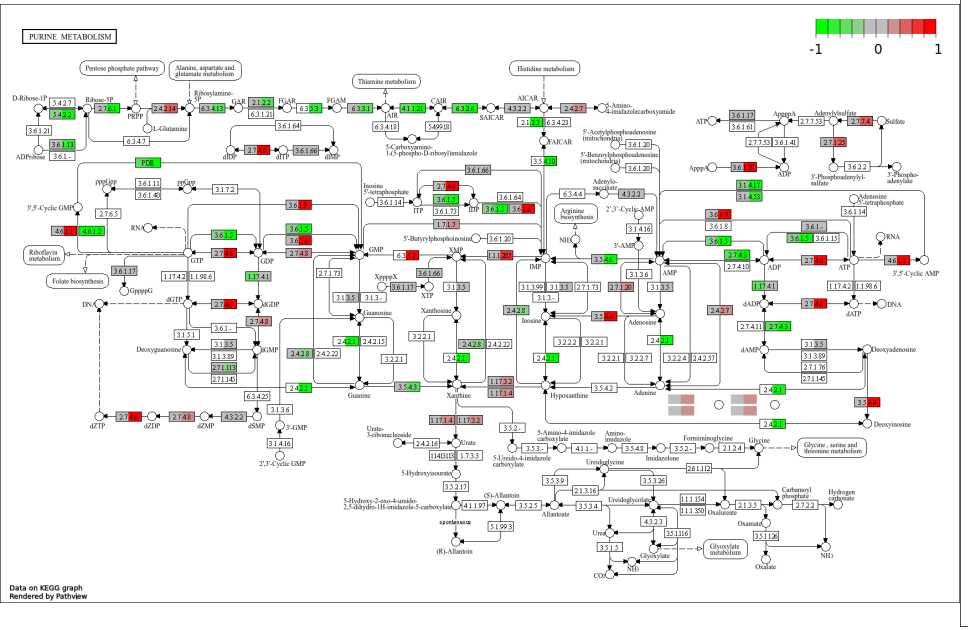

NON-SMALL CELL LUNG CANCER
-1
0
1
Alveolar and bronchiolar epithelial cells
Bronchial epithelial cells
Atypical adenomatous hyperplasia
Bronchial dysplasia
Primary adenocarcinoma
Primary squamous cell carcinoma
Metastatic adenocarcinoma
Metastatic squamous cell carcinoma
Alveolar and bronchiolar epithelial cell /Bronchial epithelial cell
Retinoic acid
RARB
RXR
DNA
Tumour progression
FHIT
Reduced apoptosis
Cell-cycle progression
Ras signaling pathway
NORE1A
RASSF1
MST1
Reduced apoptosis
CyclinD1
Proliferation
K-ras
PI3K
PIP3
PKB/Akt
BAD
CASP9
Antiapoptosis
FoxHead
PDK1
ErbB signaling pathway
Cell cycle
p16INK4a
CDK4/6
CyclinD1
Rb
E2F
DNA
G1/S progression
GRB2
Sos
Ras
Raf
MEK
ERK
MAPK signaling pathway
ER
EGF
TGFα
HGF
EGFR
ERBB2
MET
PLCγ
IP3
DAG
PKC
Calcium signaling pathway
Overexpression
PI3K
PIP3
PKB/Akt
BAD
CASP9
Antiapoptosis
FoxHead
PDK1
PI3K-Akt signaling pathway
KIF5B-RET
JAK3
STAT3
Cell survival
EML4-ALK
DNA
CyclinD1
Proliferation
DNA damage
p53
DNA
p21
GADD45
Bax
Bak
p48
POLK
Uncontrolled proliferation
Increased survival
Genomic instability
p53 signaling pathway
Cell cycle
Genetic alterations
Oncogene :
K-Ras, EGFR, MET, EML4-ALK, KIF5B-RET
Tumor suppressors :
RARB, FHIT, RASSF1, INK4a/ARF, p53
Data on KEGG graph
Rendered by Pathview

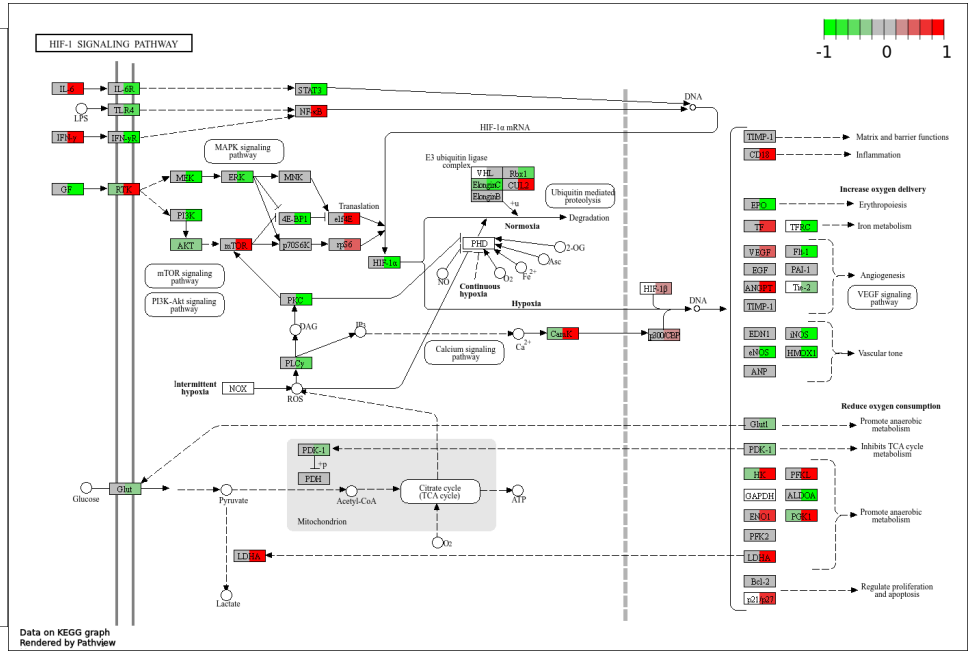
Group 4


VIRAL MYOCARDITIS
-1 0 1
Antigen presenting cell
Antigen processing and presentation
Cardiac antigens
Viral antigens
CD40
MHC II
Antigen
CD40L
TCR
CD4+ T cell
T cell receptor signaling pathway
CVB
Extracellular matrix (ECM)
ECM-receptor interaction
Laminin
α-DAG
Dystroglycan complex
CAR
DAF
SCN5A
SGCA/B
SGCD
SGCB
SGCG/Z
β-DAG
CAV3
Sarcolemma
Sarcoglycan complex
Cardiac myocyte
Fyn
Akt
Caveolin-1
Rac
Dystrophin
DMD
SNTA/B
DTNA
nNOS
Myosin
Cleavage
Decreased force transmission
Increased cell permeability
Myocyte dysfunction
Actin reorganization
Actin
Sarcomere
Virus entry from the TJ
Pro2A
Cardiac muscle contraction
Myocyte damage
Cleavage
eIF4γ
Host protein synthesis shutoff
Enterovirus-induced Cardiomyopathy
CD8+ T cell
TCR
Antigen
MHC I
CD28
CD80/86
Perforin
LFA-1
ICAM-1
Activation
Cyclin D
Proteasome
Degradation
Cell cycle arrest
Proteasome
Cell cycle
CASP8
Bid
t-Bid
Mitochondrion
CytC
CASP9
CASP3
Apoptosis
Apoptosis
Immune-mediated myocyte damage
Dilated cardiomyopathy
B cell
Virus-specific antibodies
IgG
Autoreactive antibodies
IgG
Data on KEGG graph
Rendered by Pathview

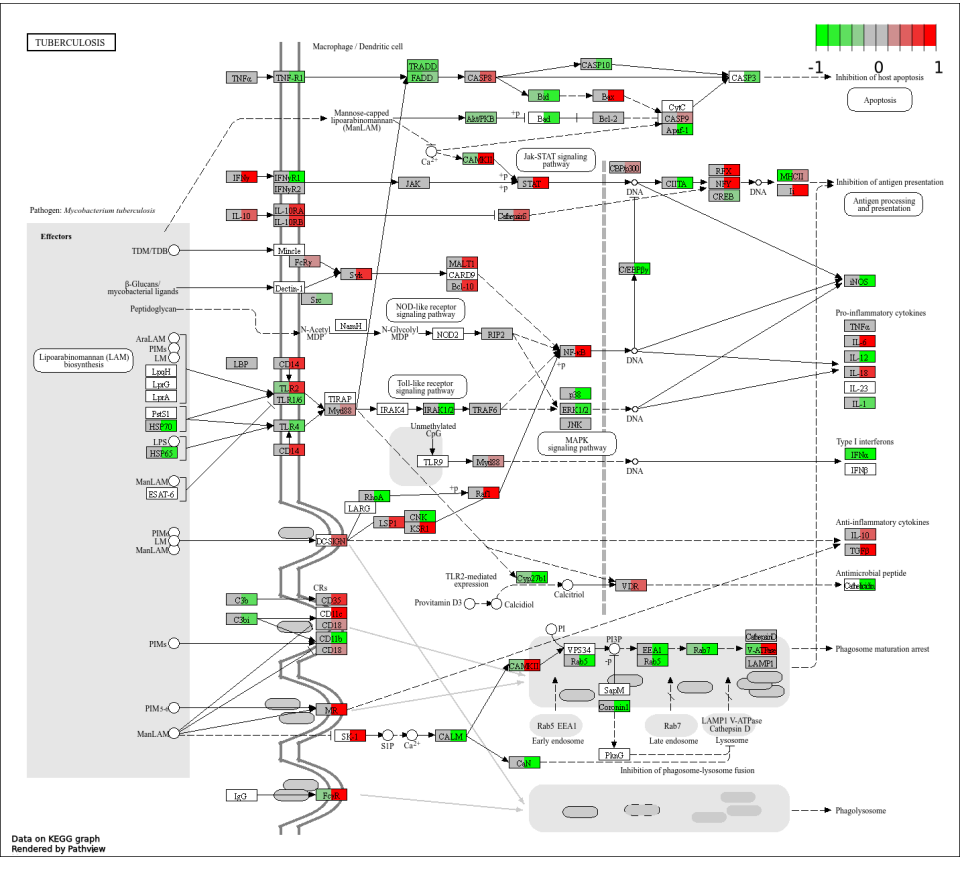

RENIN SECRETION
-1 0 1
Epinephrine
Sympathetic nerve system
Norepinephrine
Renal juxtaglomerular cell
β-AR
PAC1/AP
PAC1
Gs
EP2/4
PGE2
AC8/9
cAMP
cAMP signaling pathway
PKA
CREB
Prorenin
REN
AQP1
H2O
PDE1
PDE3
AMP
Adenosine
A1
Gi
AMP
ORAI
ADP
ATP
Macula densa mechanism (Tubular salt sensing)
Cl-
Depolarization
Cav
Ca2+
Depolarization
K+
IP3R
Endoplasmatic reticulum
Endothelial cell
EDN
ETA
Angiotensin II
AGTR1
Gq
PLC
IP3
CaM
Ca
Golgi
Calcium signaling pathway
ACE
Renin-angiotensin system
NO
sGC
cGMP-PKG signaling pathway
cGMP
Atrial myocyte
ANP
NPR-A
BKCa
K+
Hyperpolarization
cGKII
Angiotensin I
REN
Renin
AGT
Renin
Prorenin
CTSB
Dense core vesicle
Data on KEGG graph
Rendered by Pathview

Group 4

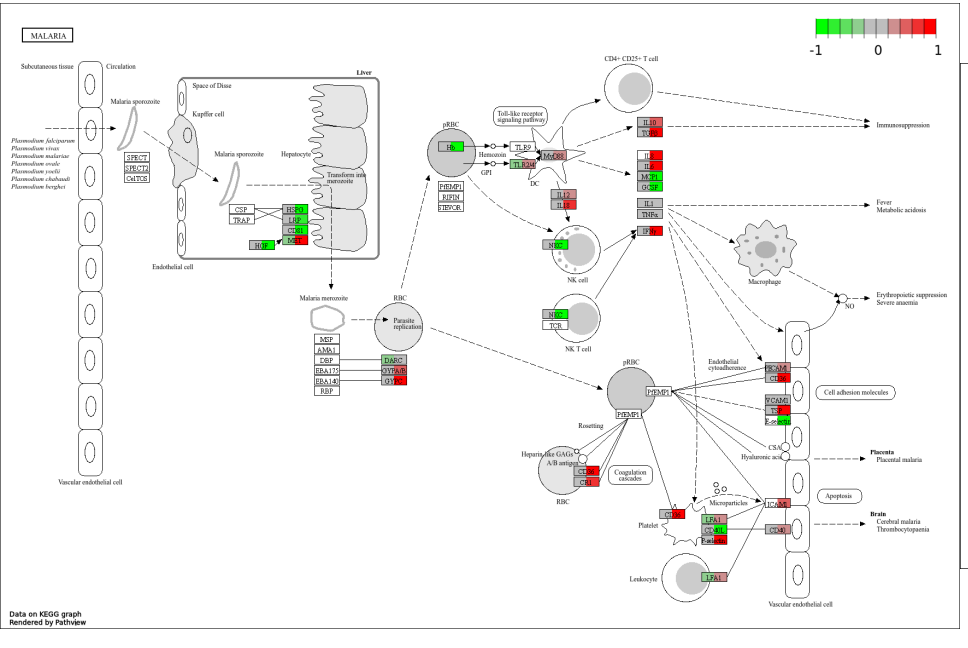

PURINE METABOLISM
-1
0
1
Data on KEGG graph
Rendered by Pathview

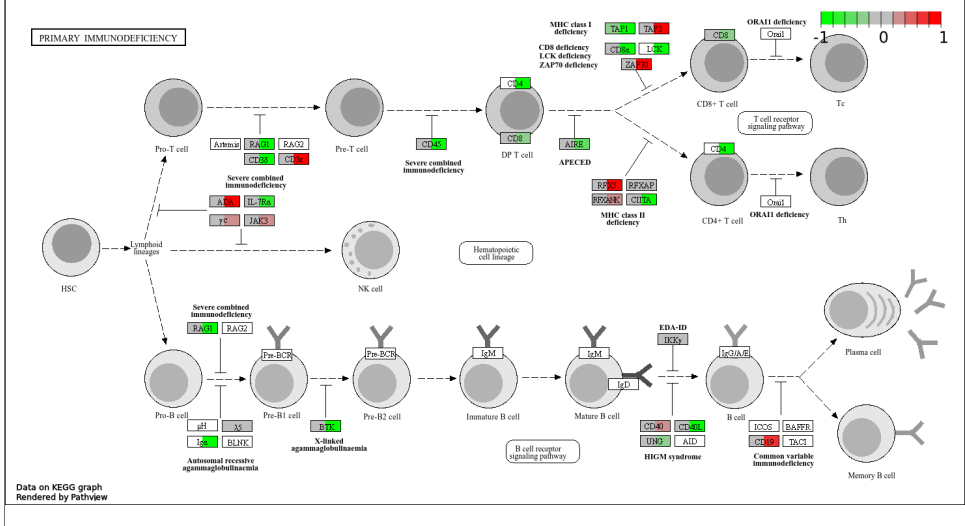

HIF-1 SIGNALING PATHWAY
-1
0
1
HIF-1α mRNA
Normoxia
Hypoxia
Continuous hypoxia
Intermittent hypoxia
Increase oxygen delivery
Reduce oxygen consumption
Data on KEGG graph
Rendered by Pathview

Group 4

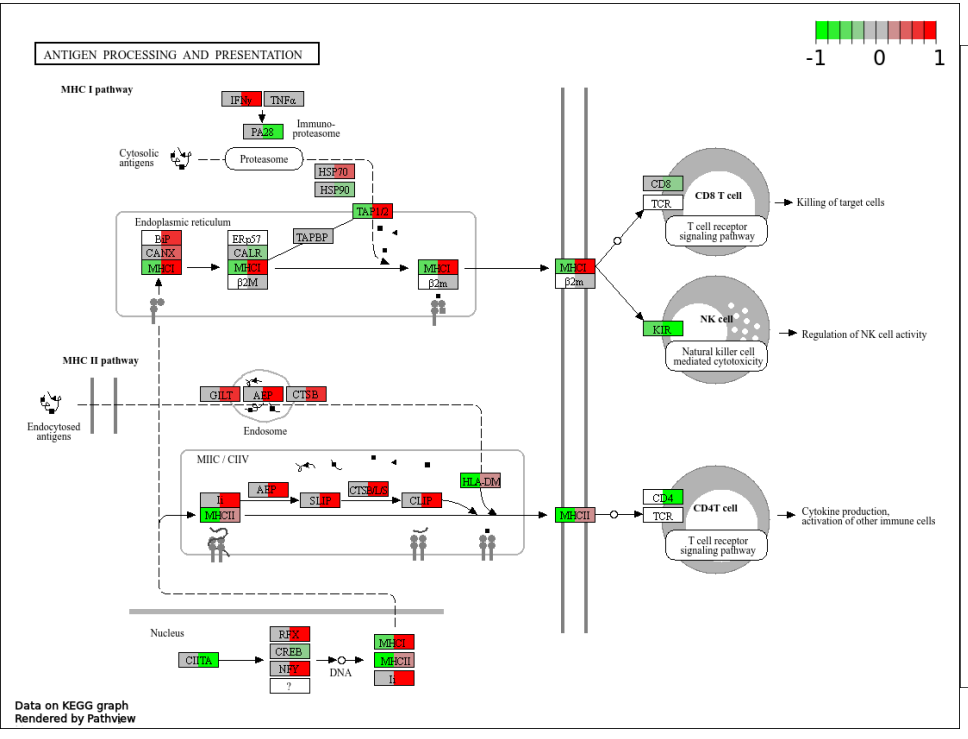

TUBERCULOSIS
Macrophage / Dendritic cell
-1
0
1
Inhibition of host apoptosis
Apoptosis
Pathogen: Mycobacterium tuberculosis
Effectors
Mannose-capped lipoarabinomannan (ManLAM)
Jak-STAT signaling pathway
Inhibition of antigen presentation
Antigen processing and presentation
NOD-like receptor signaling pathway
Toll-like receptor signaling pathway
MAPK signaling pathway
Pro-inflammatory cytokines
Type I interferons
Anti-inflammatory cytokines
Antimicrobial peptide
Phagosome maturation arrest
Inhibition of phagosome-lysosome fusion
Phagolysosome
Early endosome
Late endosome
Lysosome
Lipoarabinomannan (LAM) biosynthesis
TLR2
TLR4
TLR9
DC-SIGN
CR3
FcγR
Unmethylated CpG
TLR2-mediated expression
Provitamin D3
Calcidiol
Calcitriol
Data on KEGG graph
Rendered by Pathview

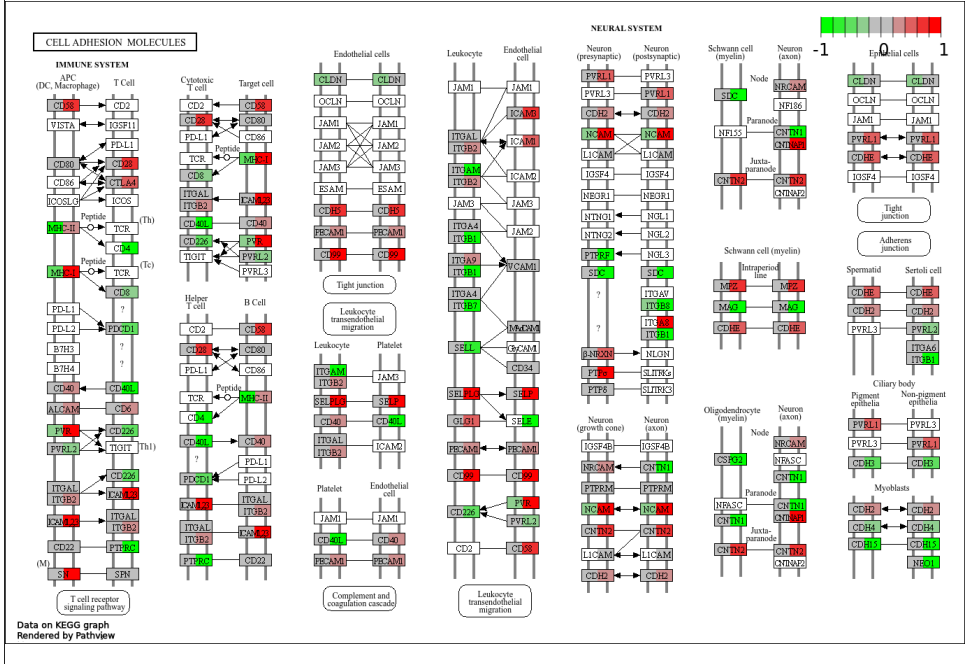
Group 1 & Group 2



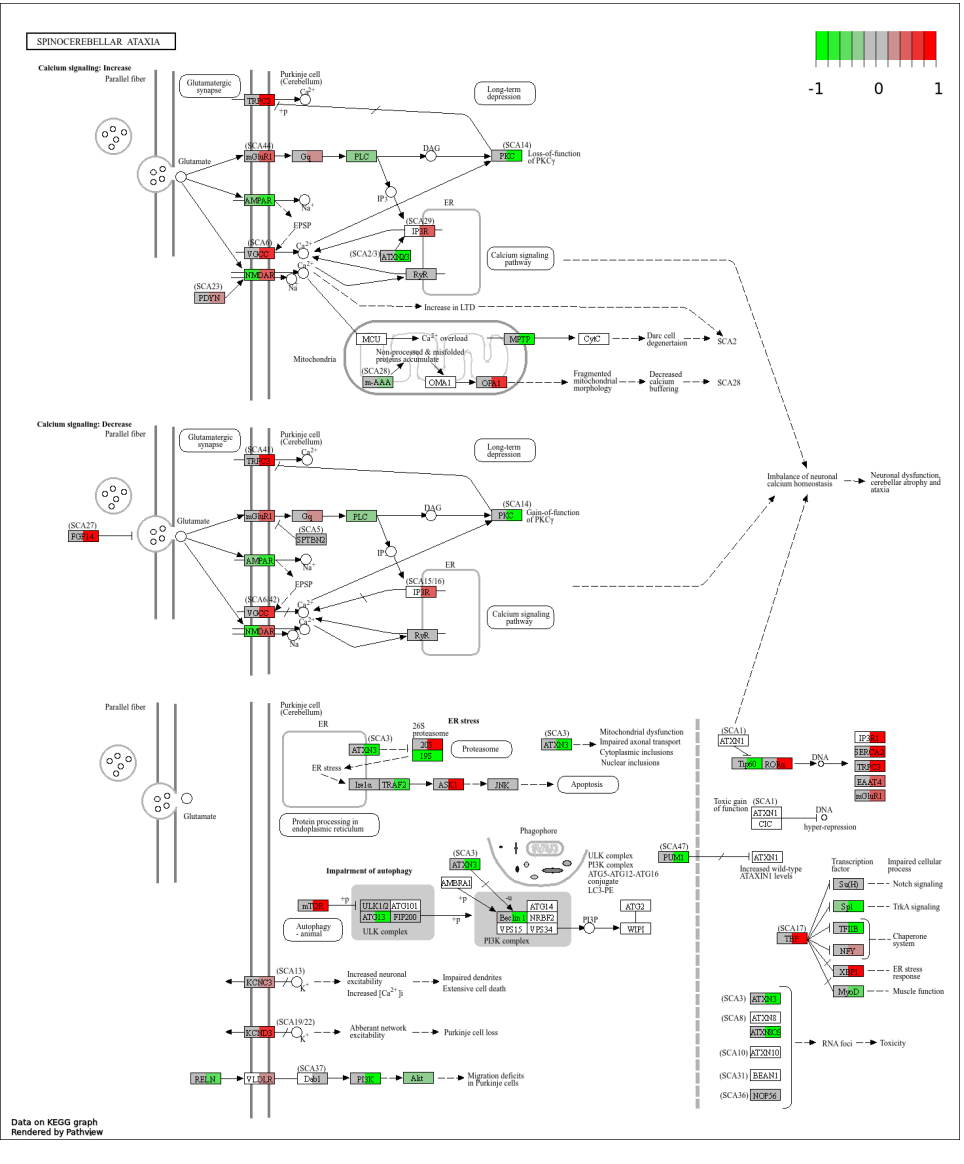


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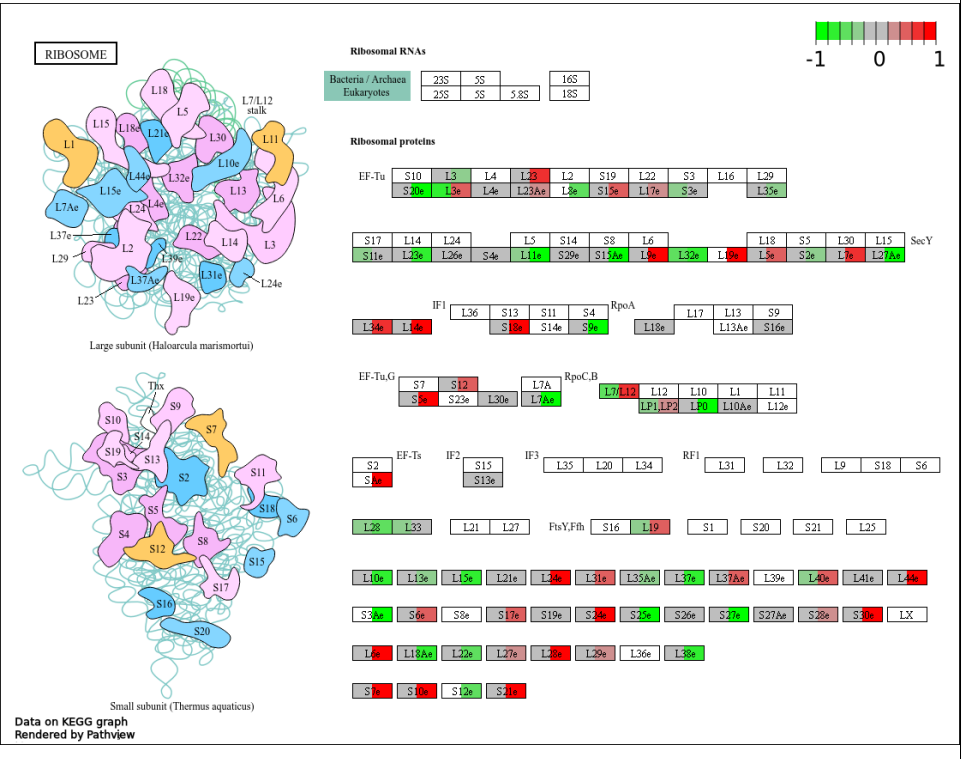


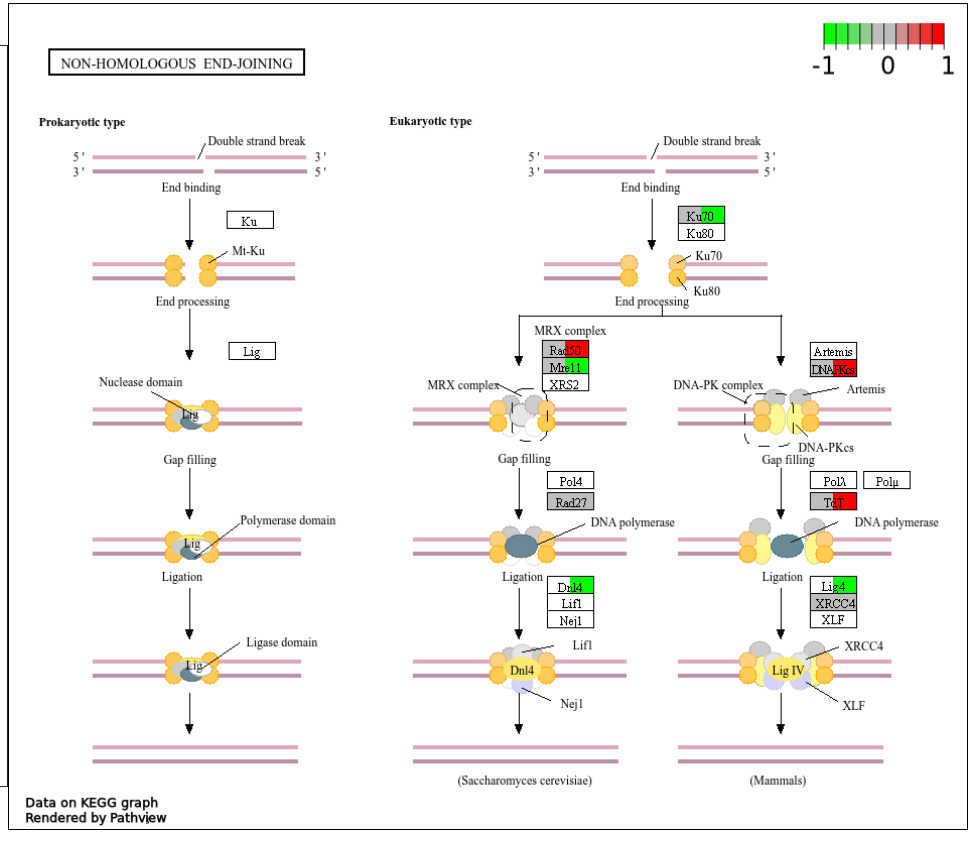


Group 1 & Group 2

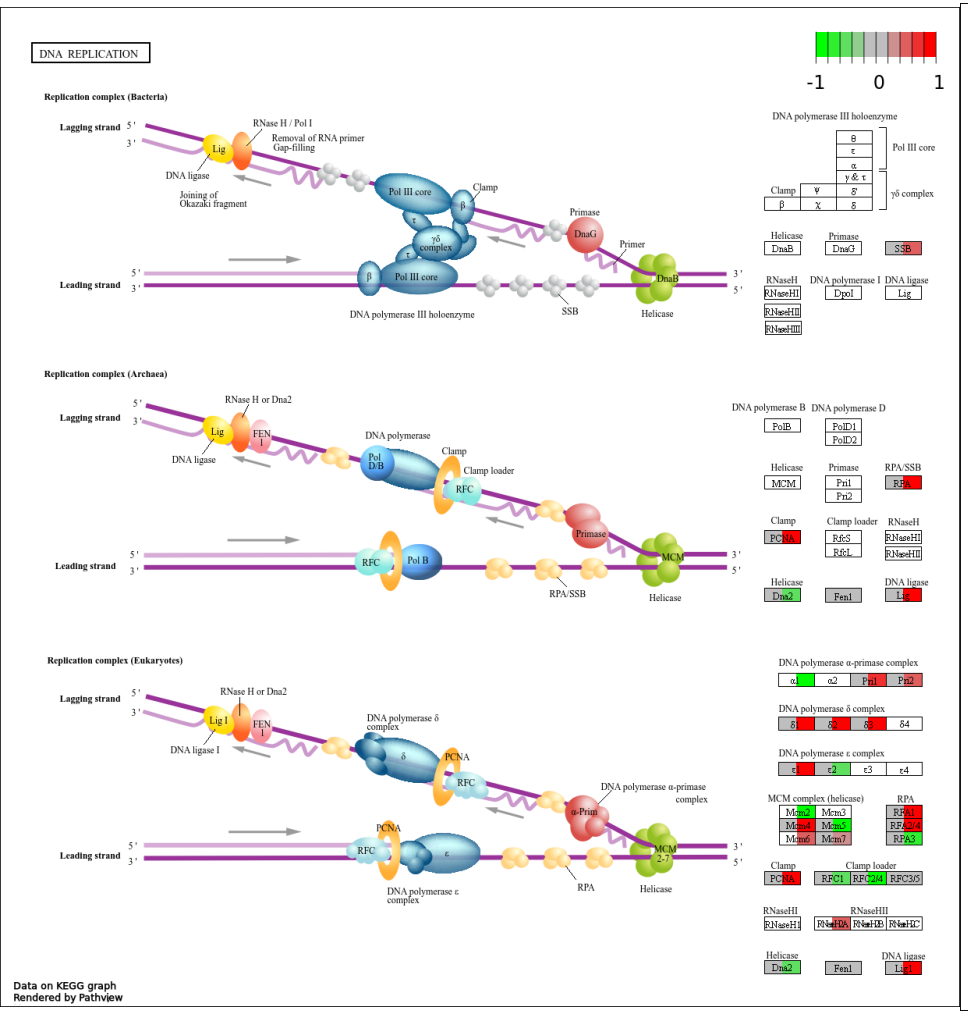


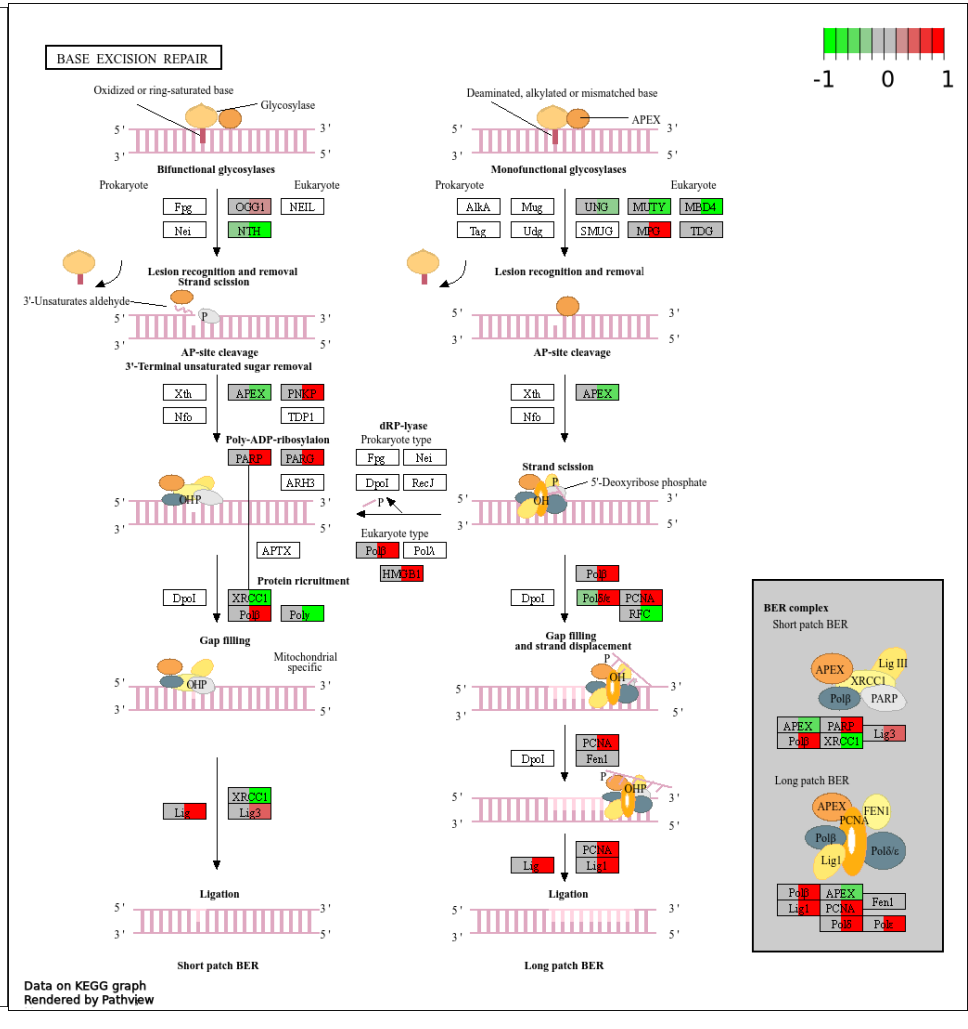
Group 1 & Group 3



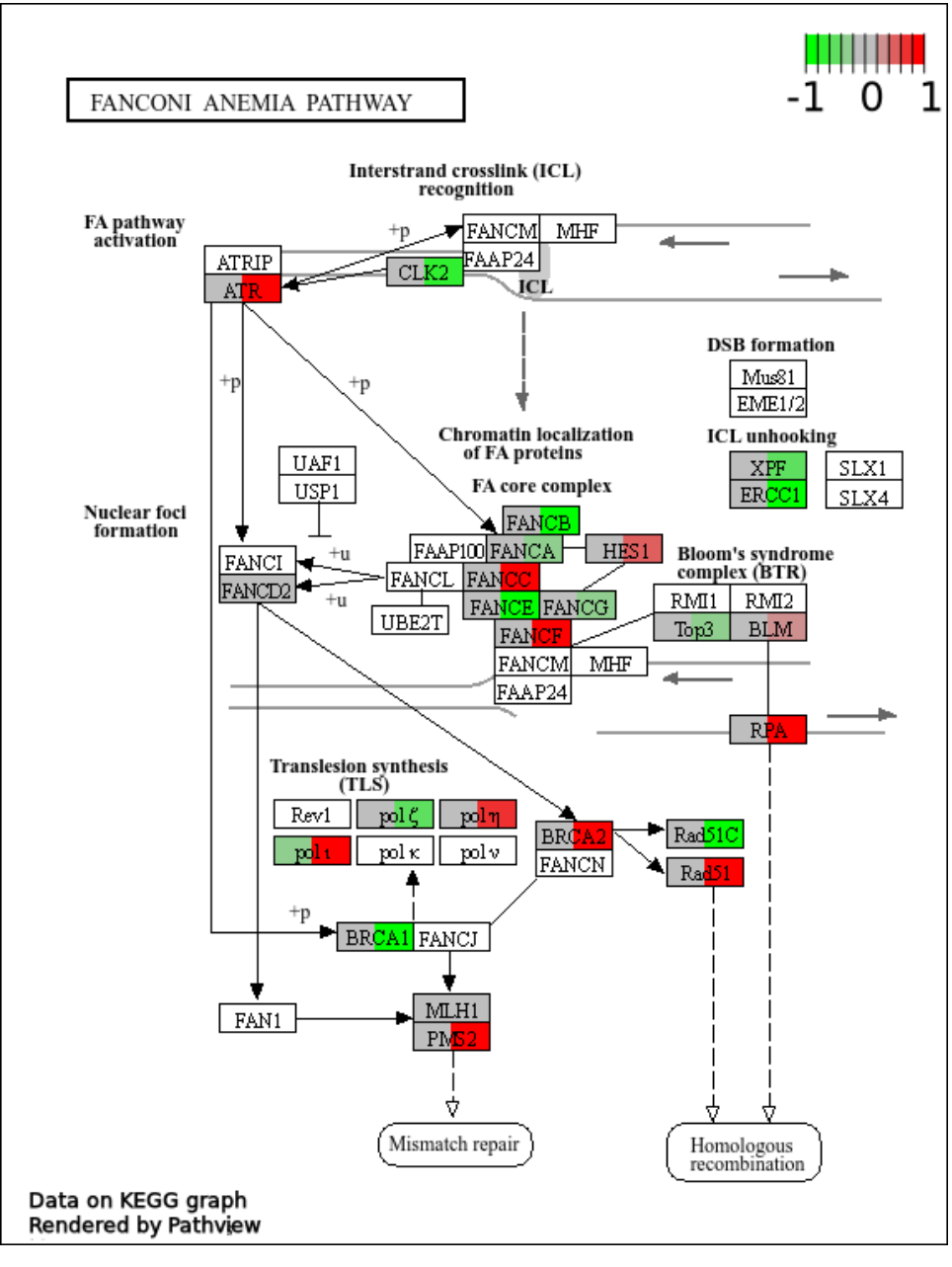


Group 1 & Group 3

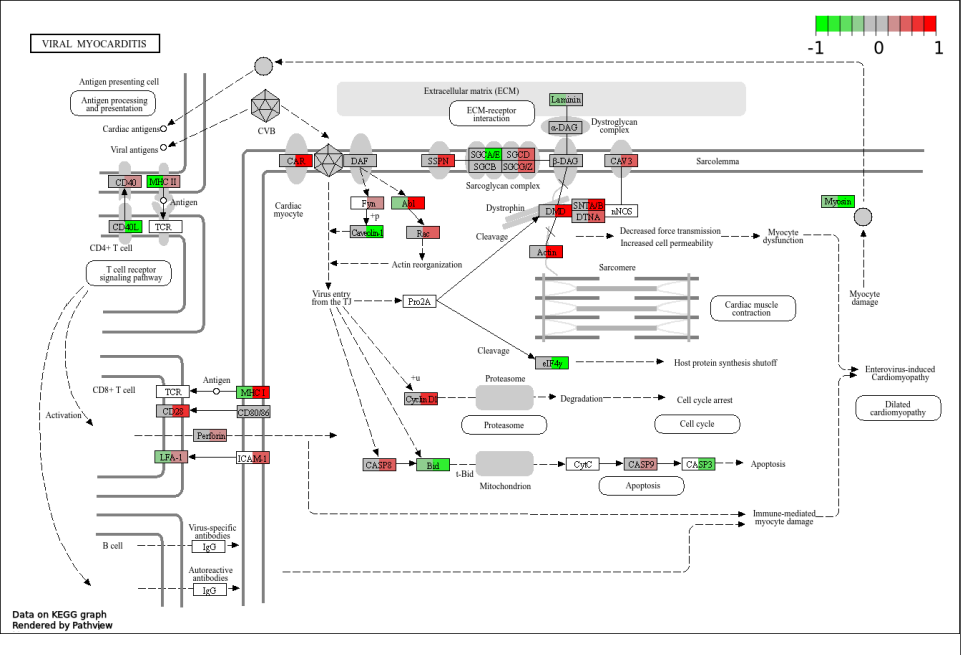


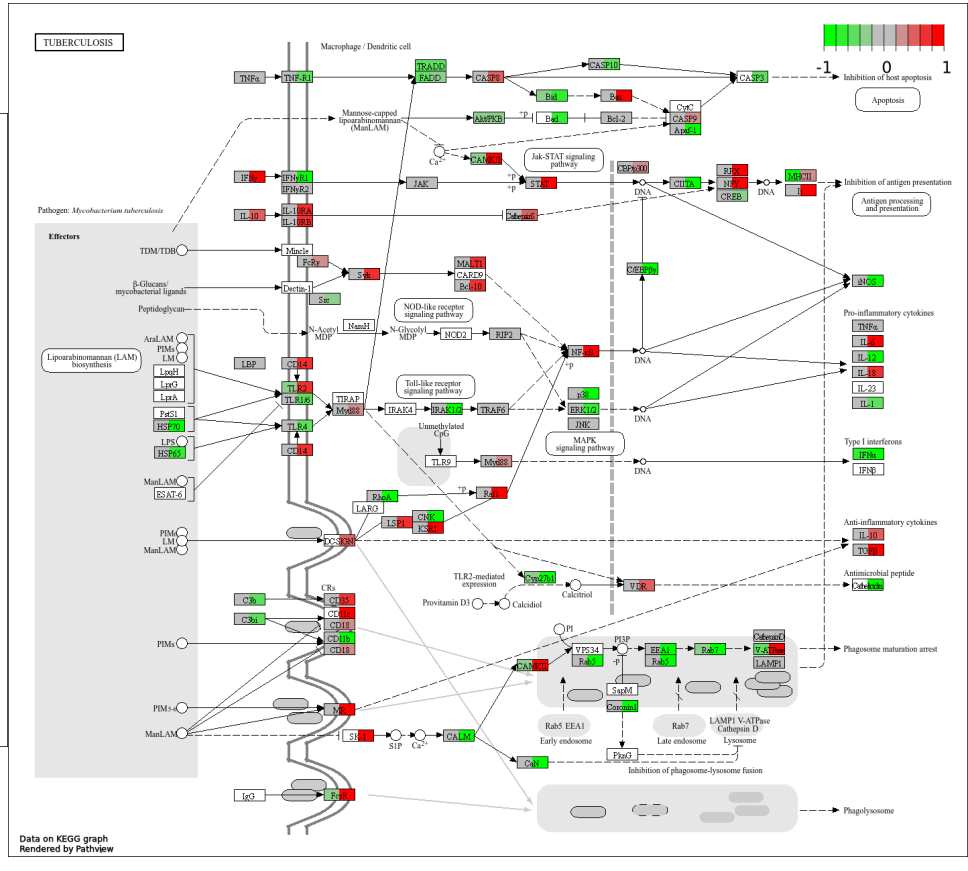


Group 1 & Group 3

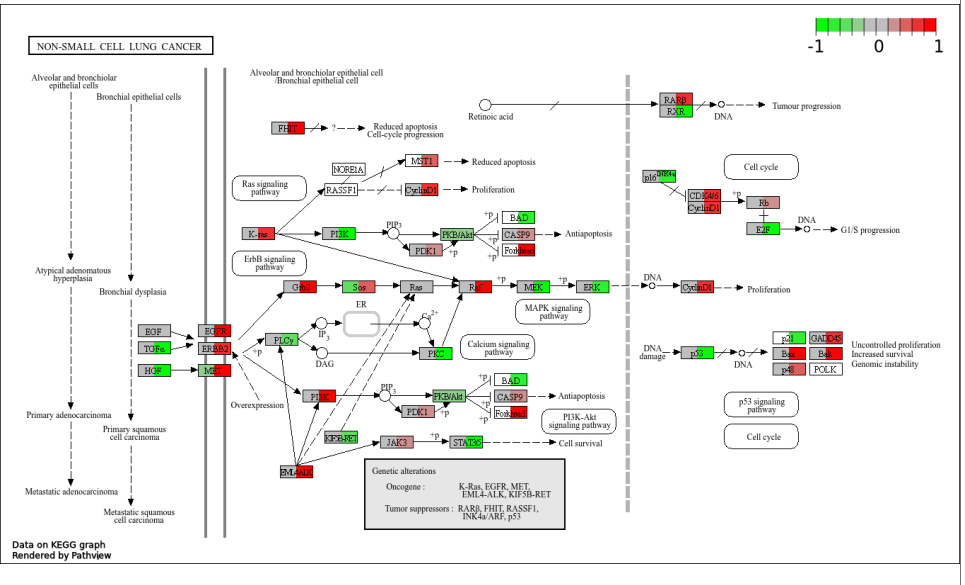


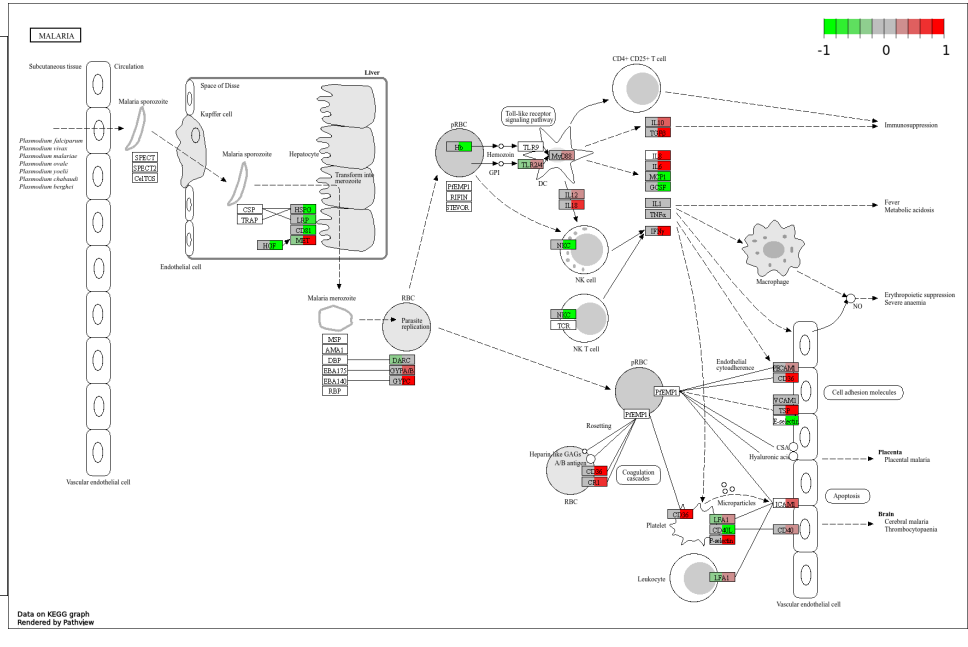
Group 2 & Group 4



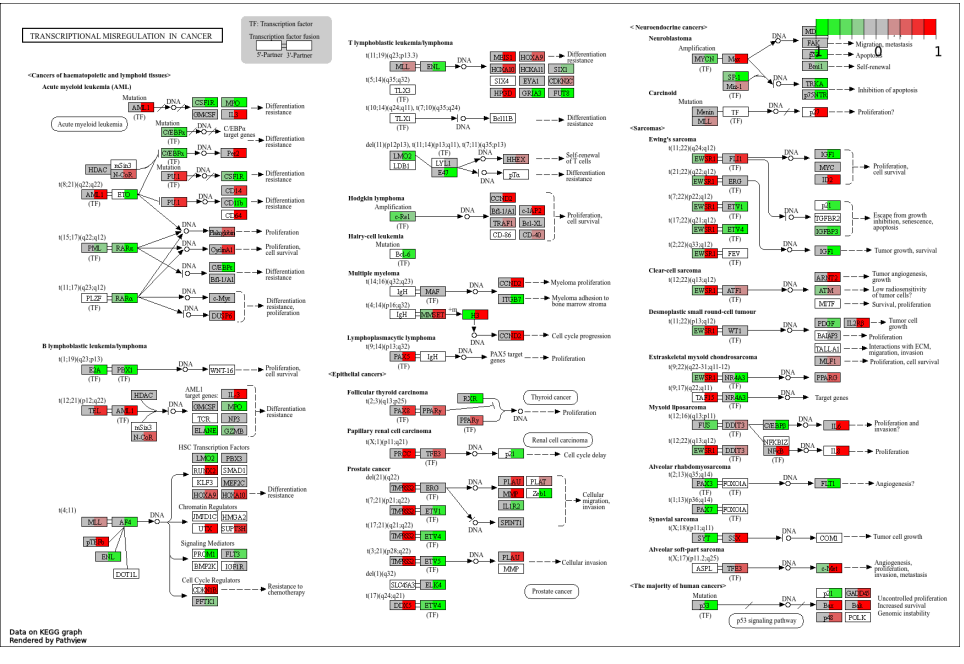


Group 2 & Group 4

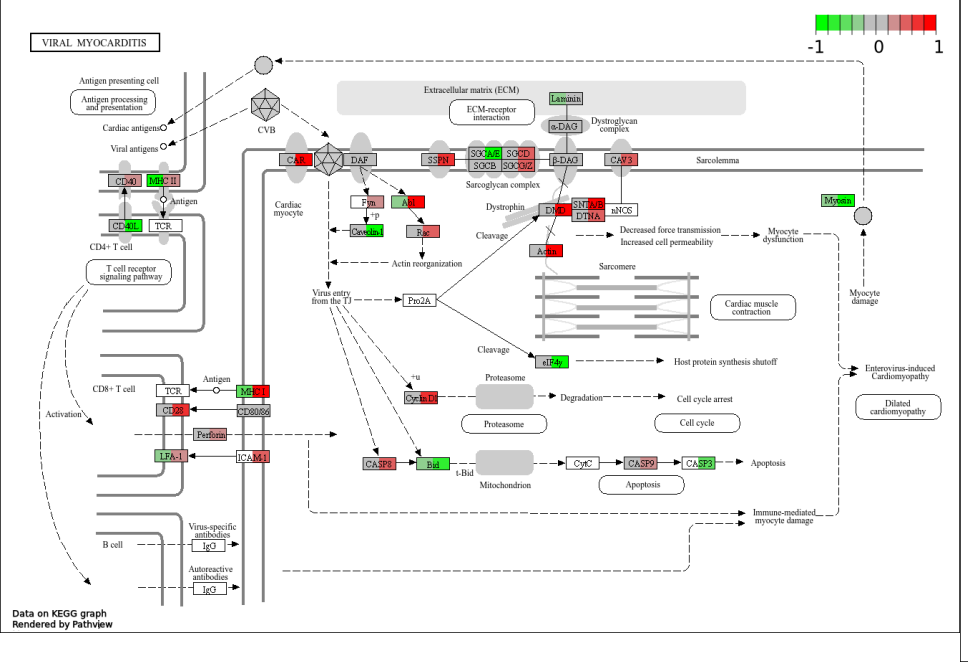


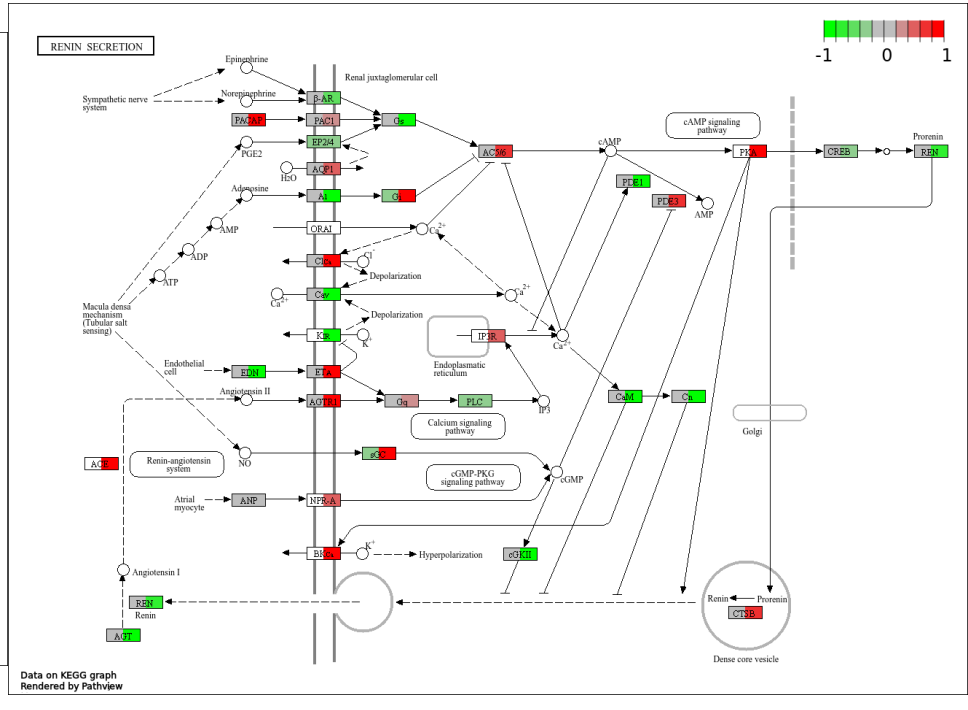


Group 2 & Group 4

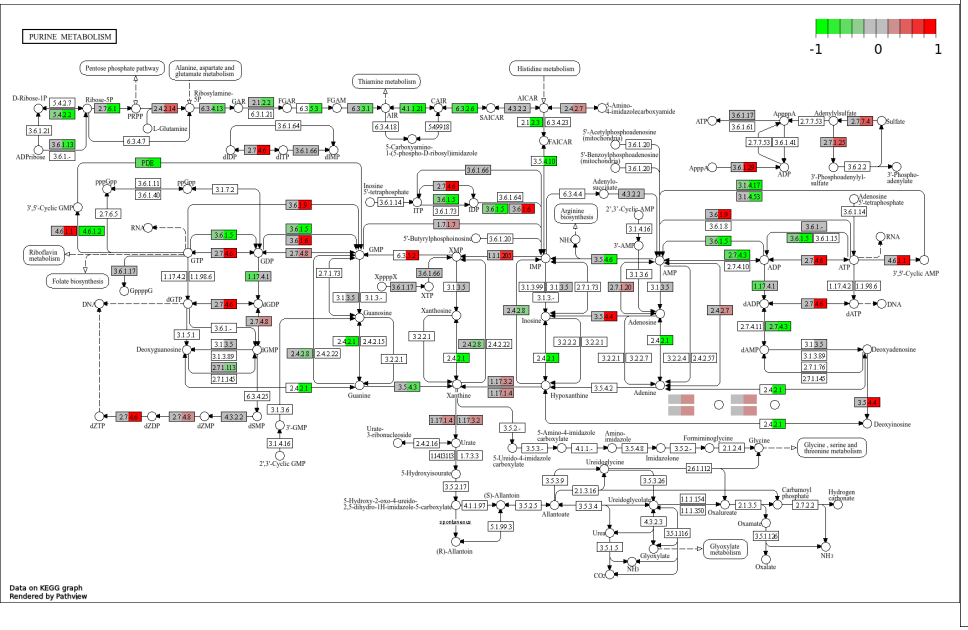


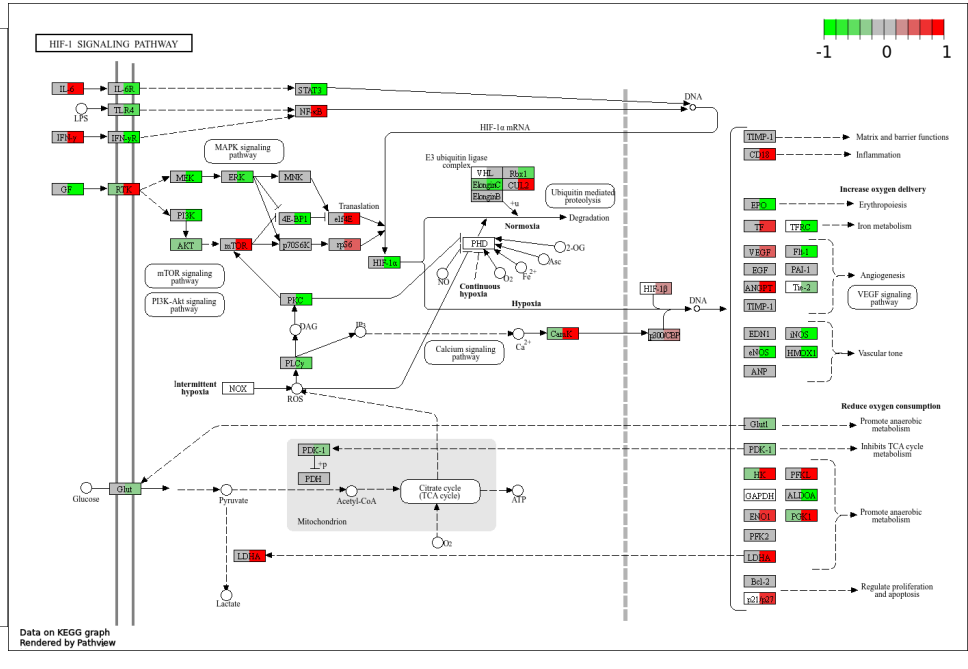
Group 3 & Group 4





Group 3 & Group 4





Group 3 & Group 4

