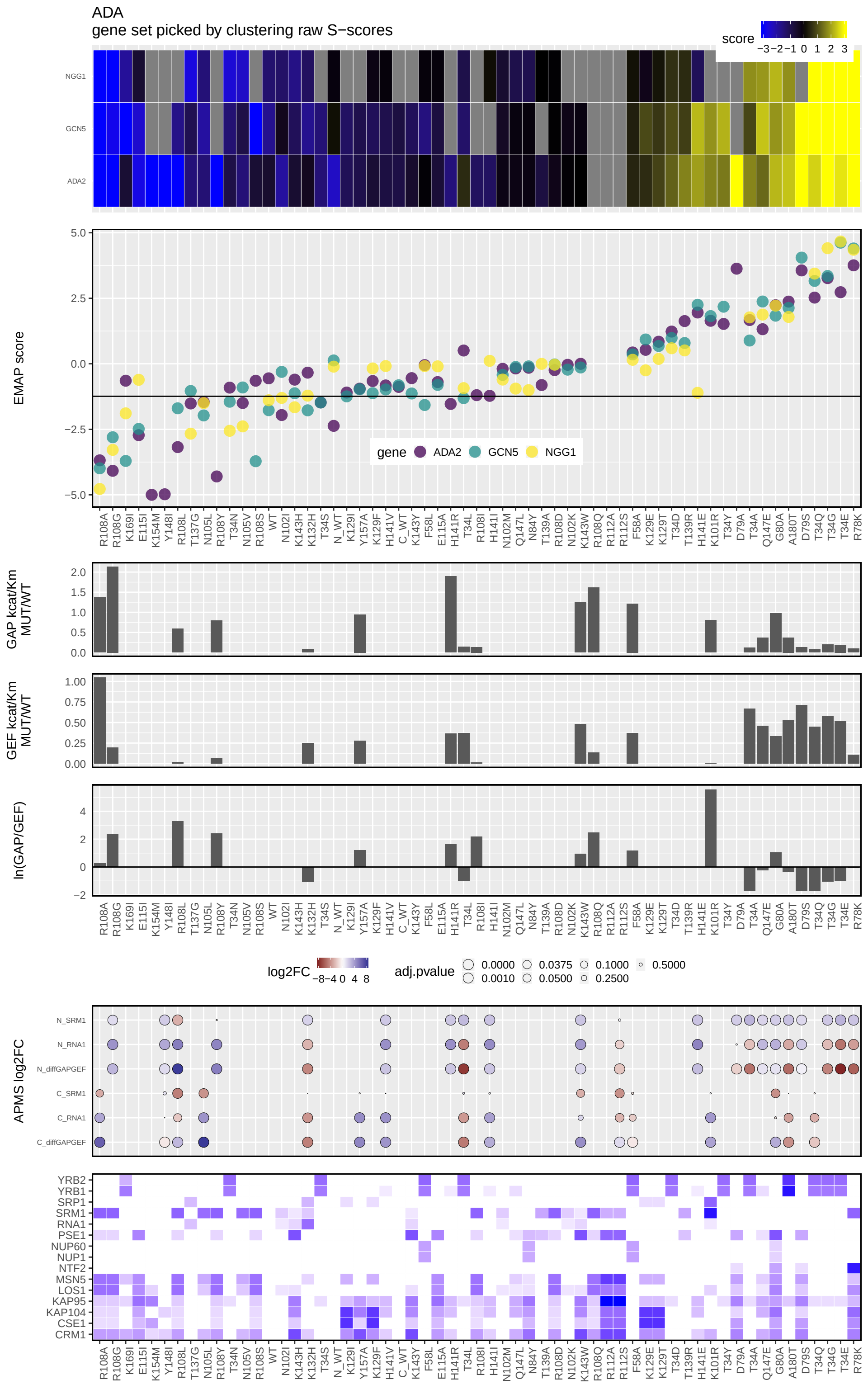
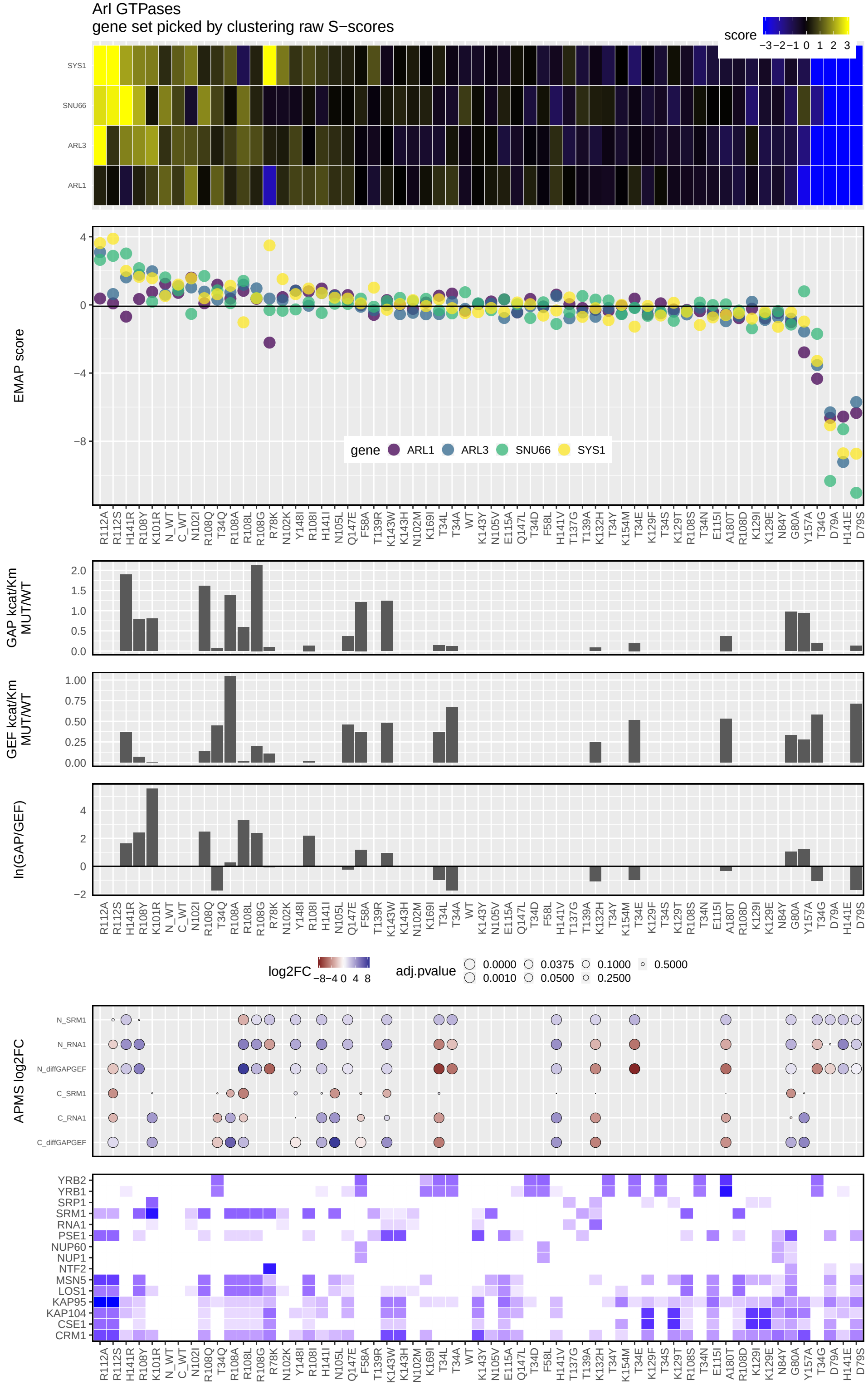
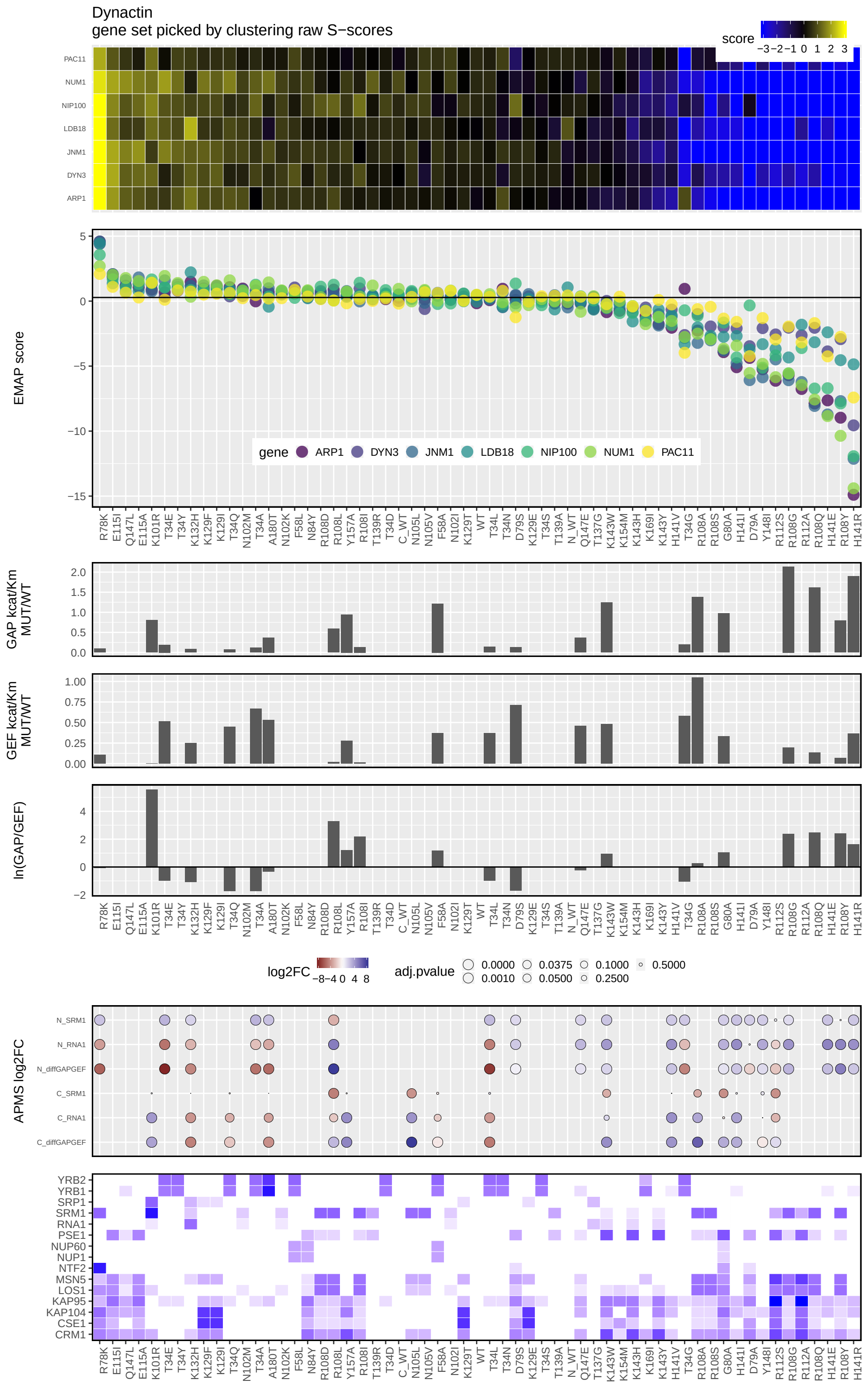
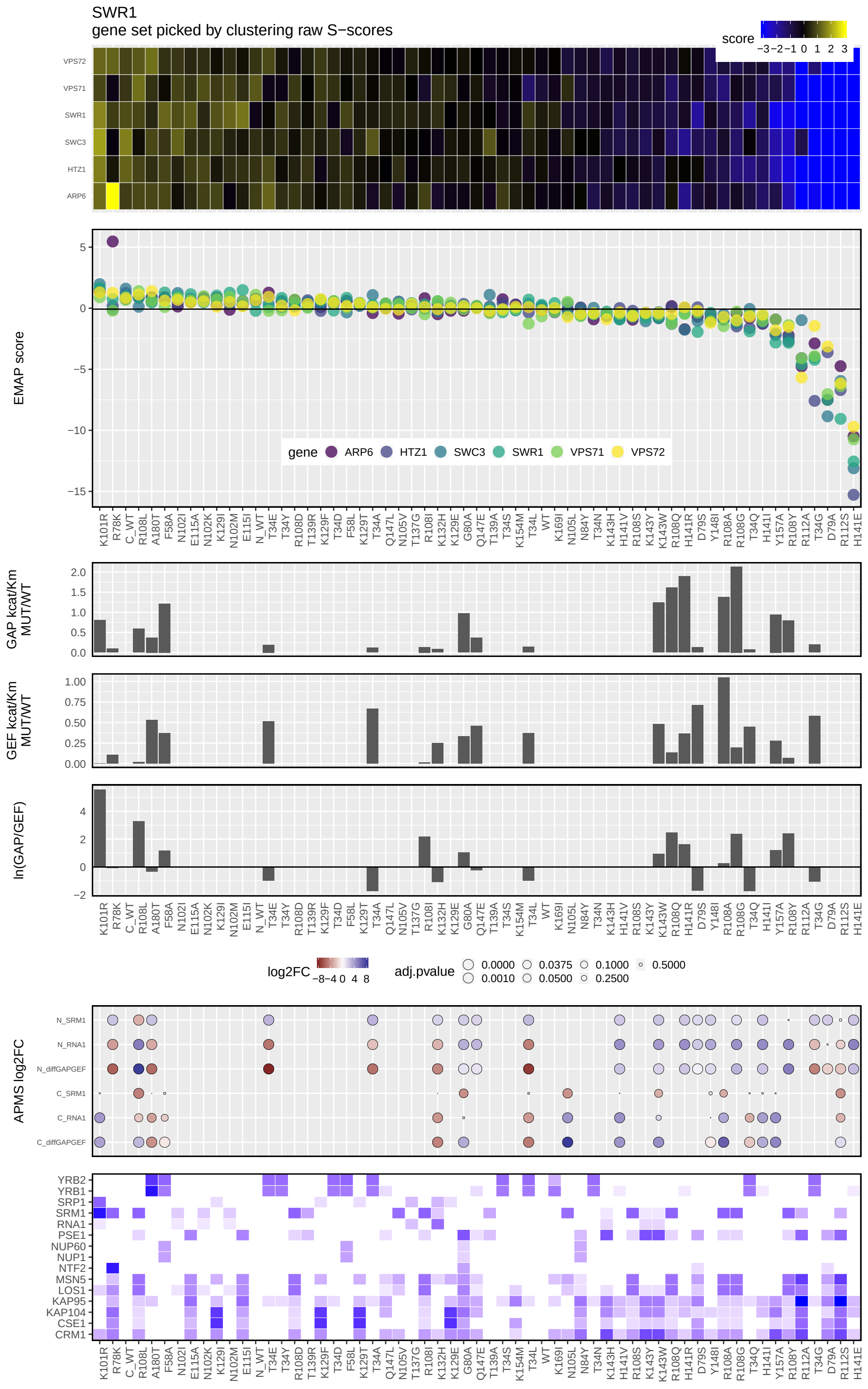

ADA
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
NGG1
GCN5
ADA2
EMAP score
gene
ADA2
GCN5
NGG1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108A R108G K169I E115I K154M Y148I R108L T137G N105L R108Y T34N N105V R108S WT N102I K143H K132H T34S N_WT K129I Y157A K129F H141V C_WT K143Y F58L E115A H141R T34L R108I H141I N102M Q147L N84Y T139A R108D N102K K143W R108Q R112A R112S F58A K129E K129T T34D T139R H141E K101R T34Y D79A T34A Q147E G80A A180T D79S T34Q T34G T34E R78K

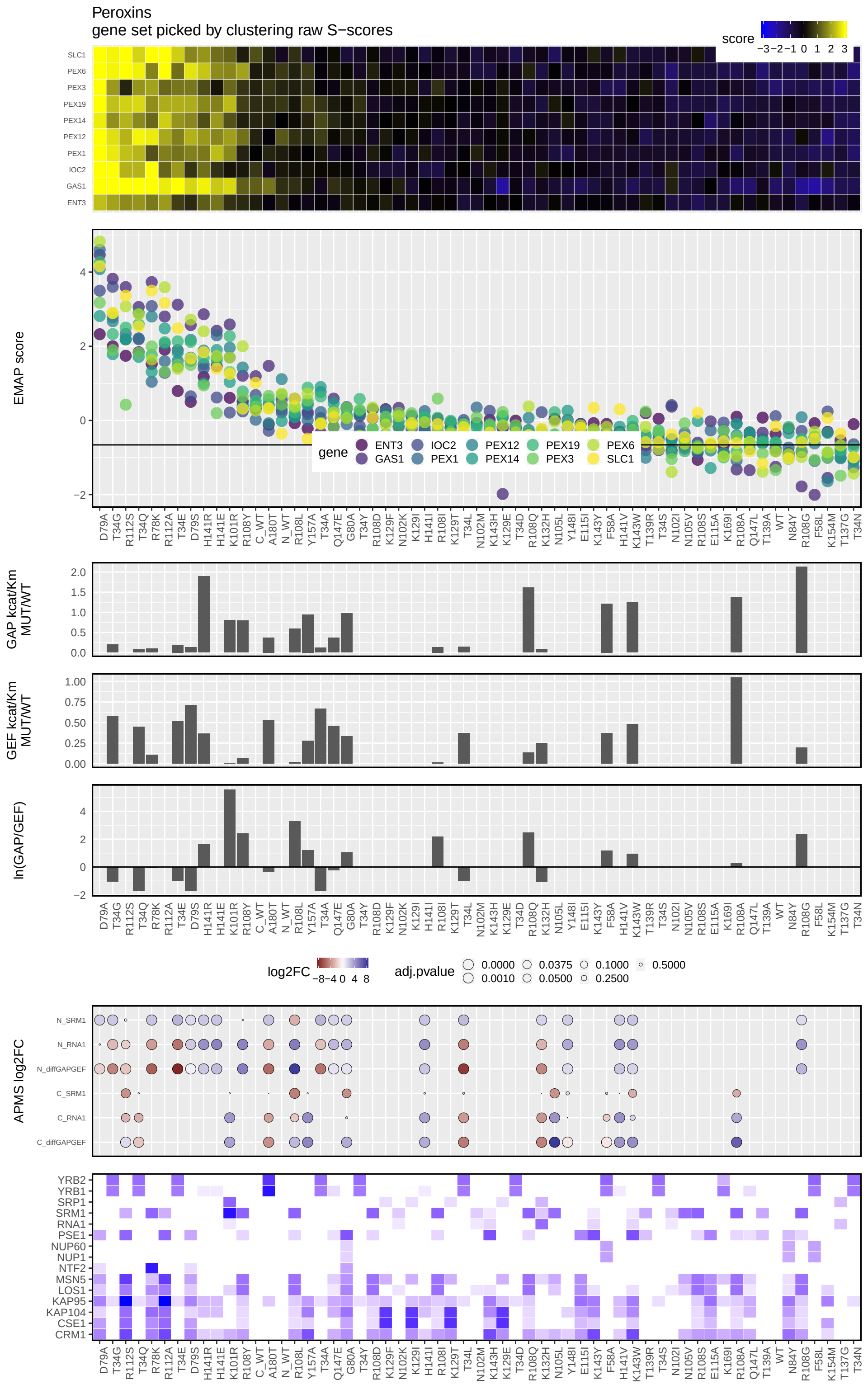
Arl GTPases
gene set picked by clustering raw S−scores

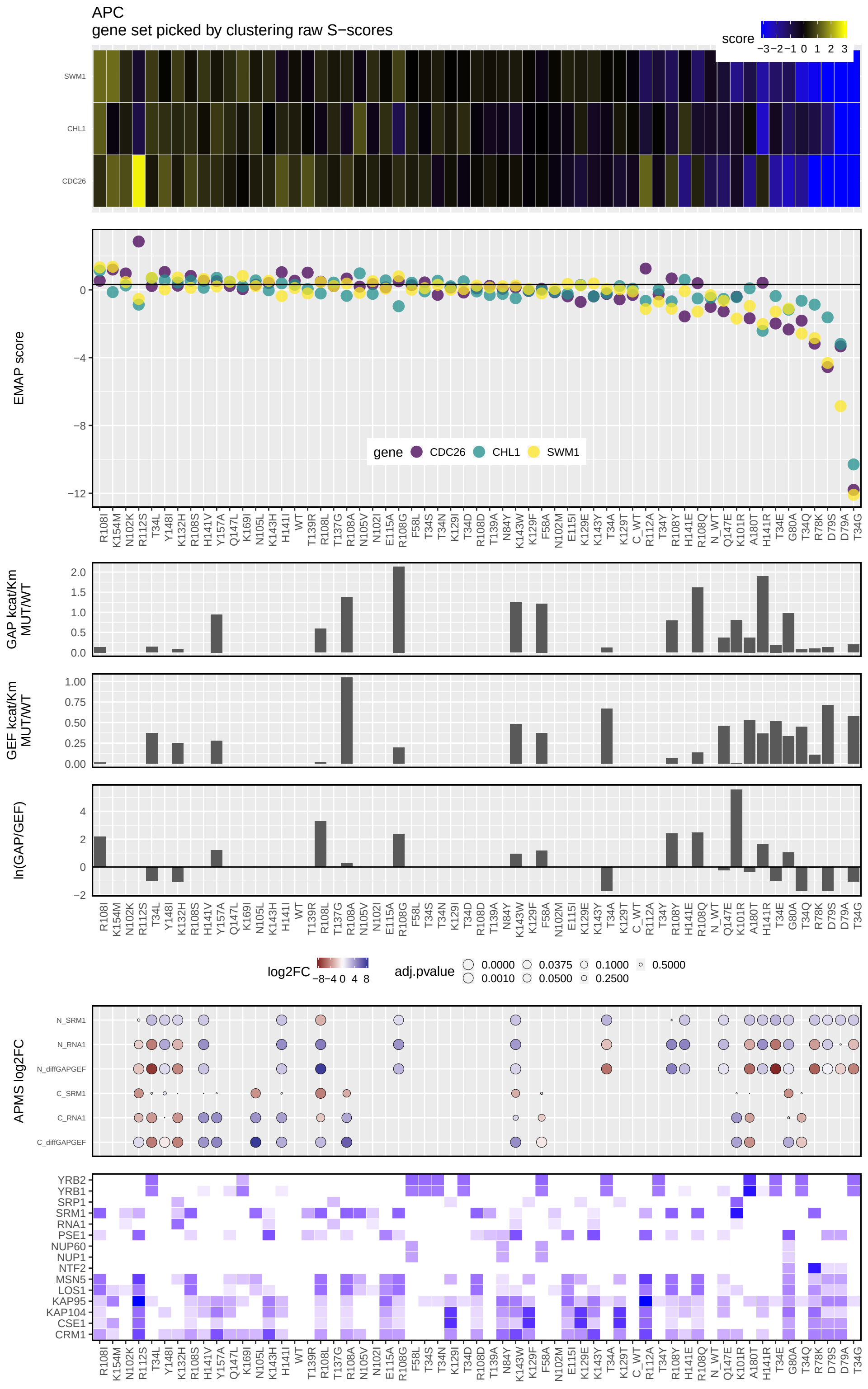


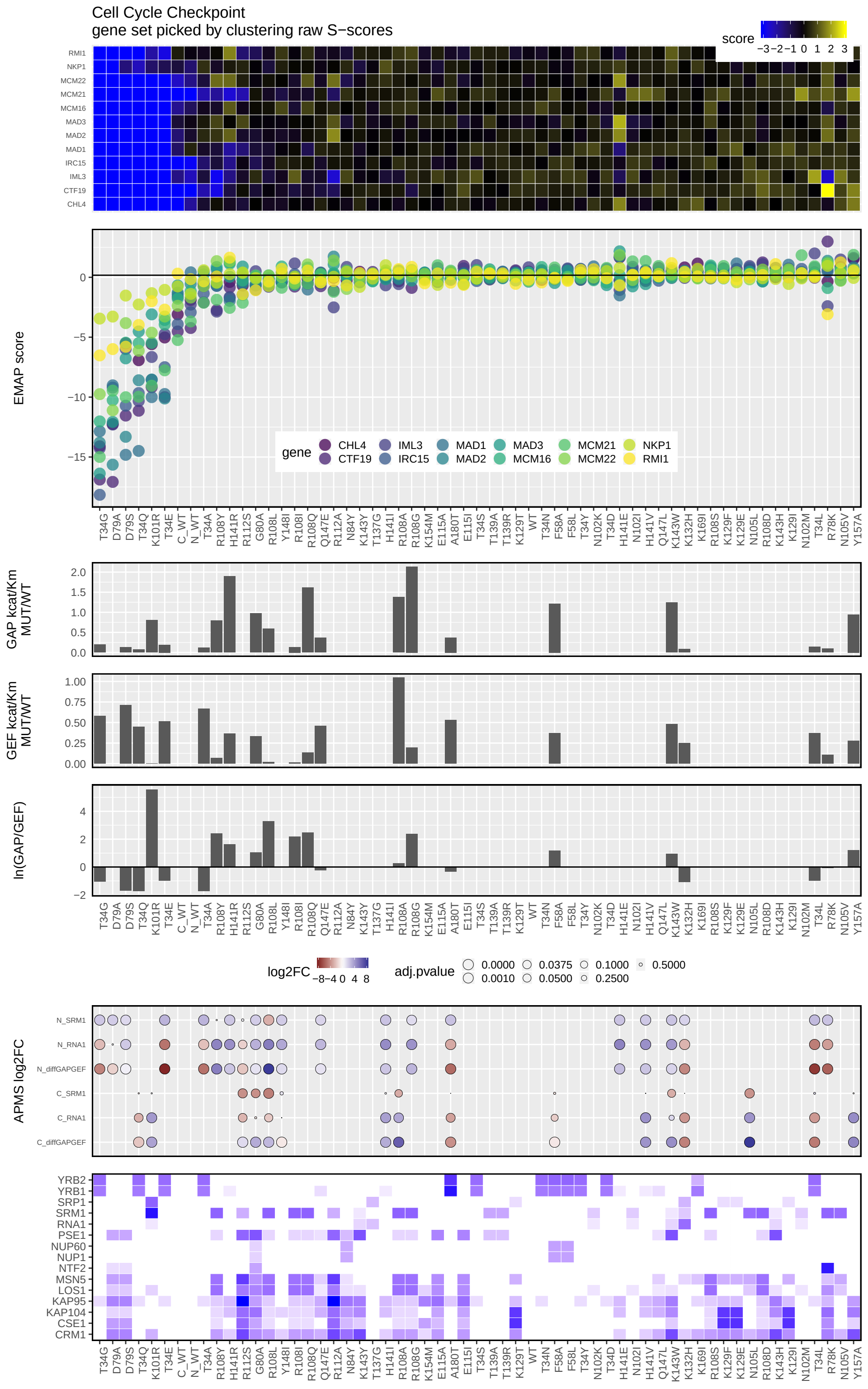
Dynactin
gene set picked by clustering raw S−scores



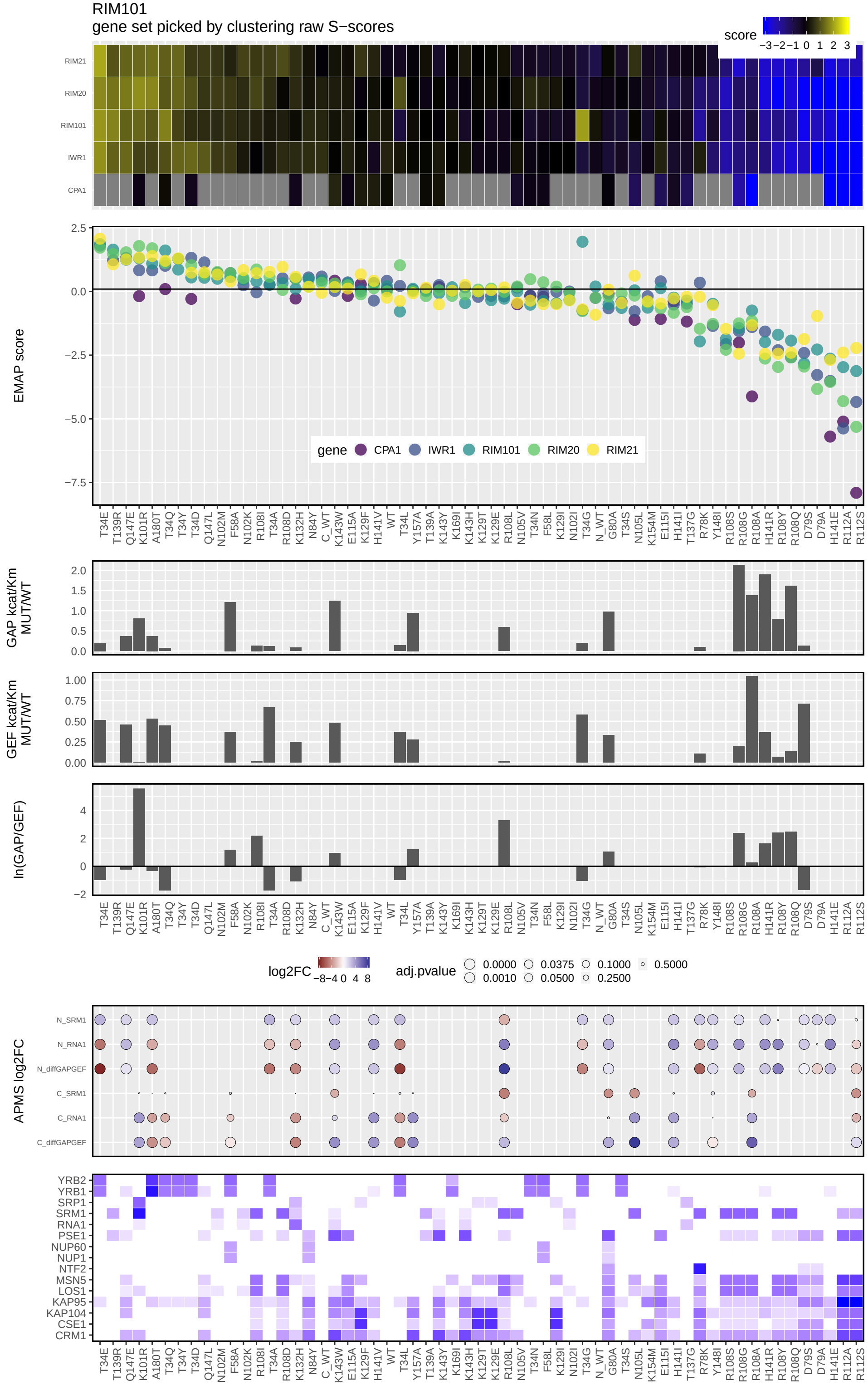

SWR1
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
VPS72
VPS71
SWR1
SWC3
HTZ1
ARP6
EMAP score
gene ARP6 HTZ1 SWC3 SWR1 VPS71 VPS72
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K101R R78K C_WT R108L A180T F58A N102I E115A N102K K129I N102M E115I N_WT T34E T34Y R108D T139R K129F T34D F58L K129T T34A Q147L N105V T137G R108I K132H K129E G80A Q147E T139A T34S K154M T34L WT K169I N105L N84Y T34N K143H H141V R108S K143Y K143W R108Q H141R D79S Y148I R108A R108G T34Q H141I Y157A R108Y R112A T34G D79A R112S H141E

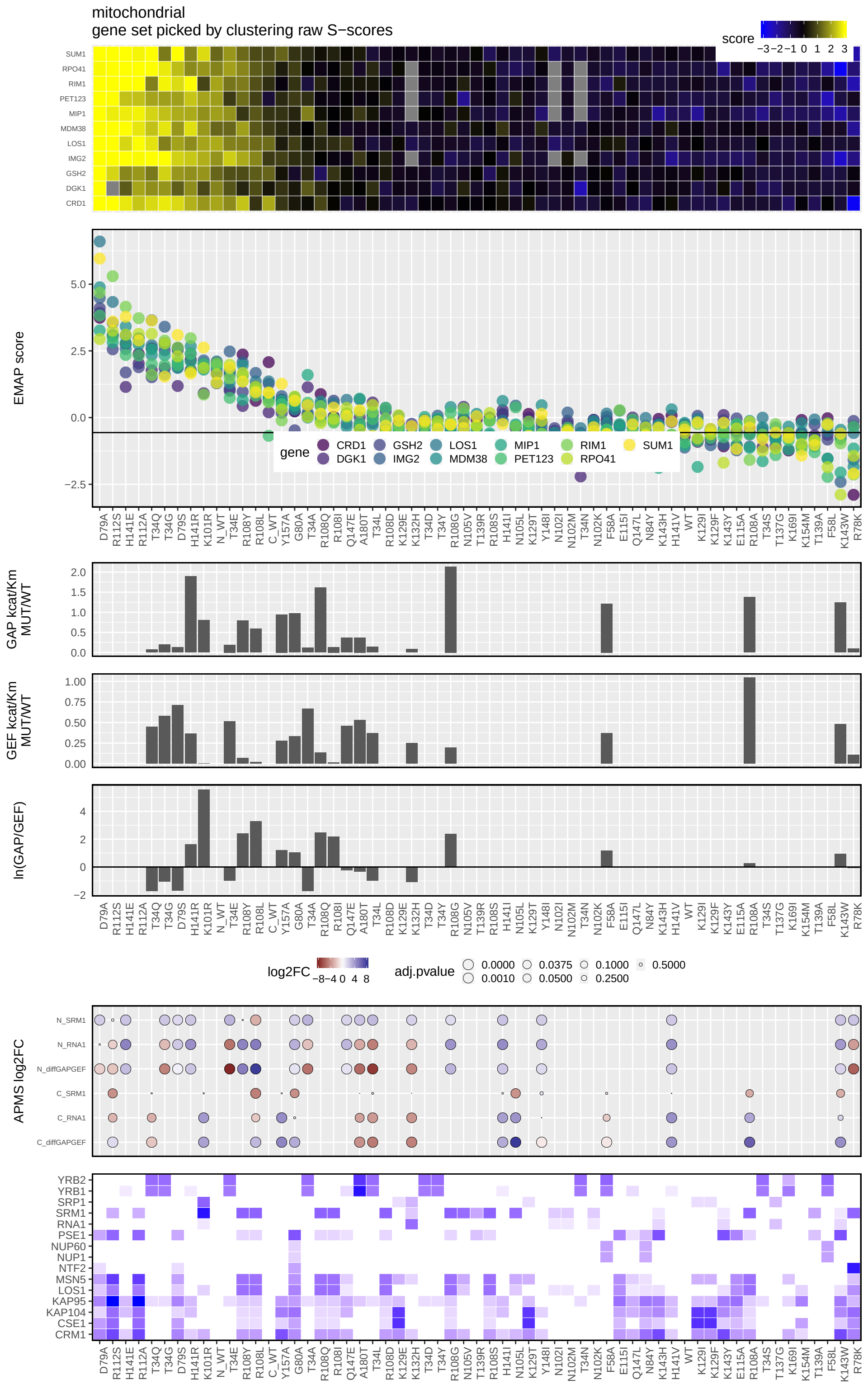

Peroxins
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SLC1
PEX6
PEX3
PEX19
PEX14
PEX12
PEX1
IOC2
GAS1
ENT3
EMAP score
gene
ENT3
GAS1
IOC2
PEX1
PEX12
PEX14
PEX19
PEX3
PEX6
SLC1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34G R112S T34Q R78K R112A T34E D79S H141R H141E K101R R108Y C_WT A180T N_WT R108L Y157A T34A Q147E G80A T34Y R108D K129F N102K K129I H141I R108I K129T T34L N102M K143H K129E T34D R108Q K132H N105L Y148I E115I K143Y F58A H141V K143W T139R T34S N102I N105V R108S E115A K169I R108A Q147L T139A WT N84Y R108G F58L K154M T137G T34N

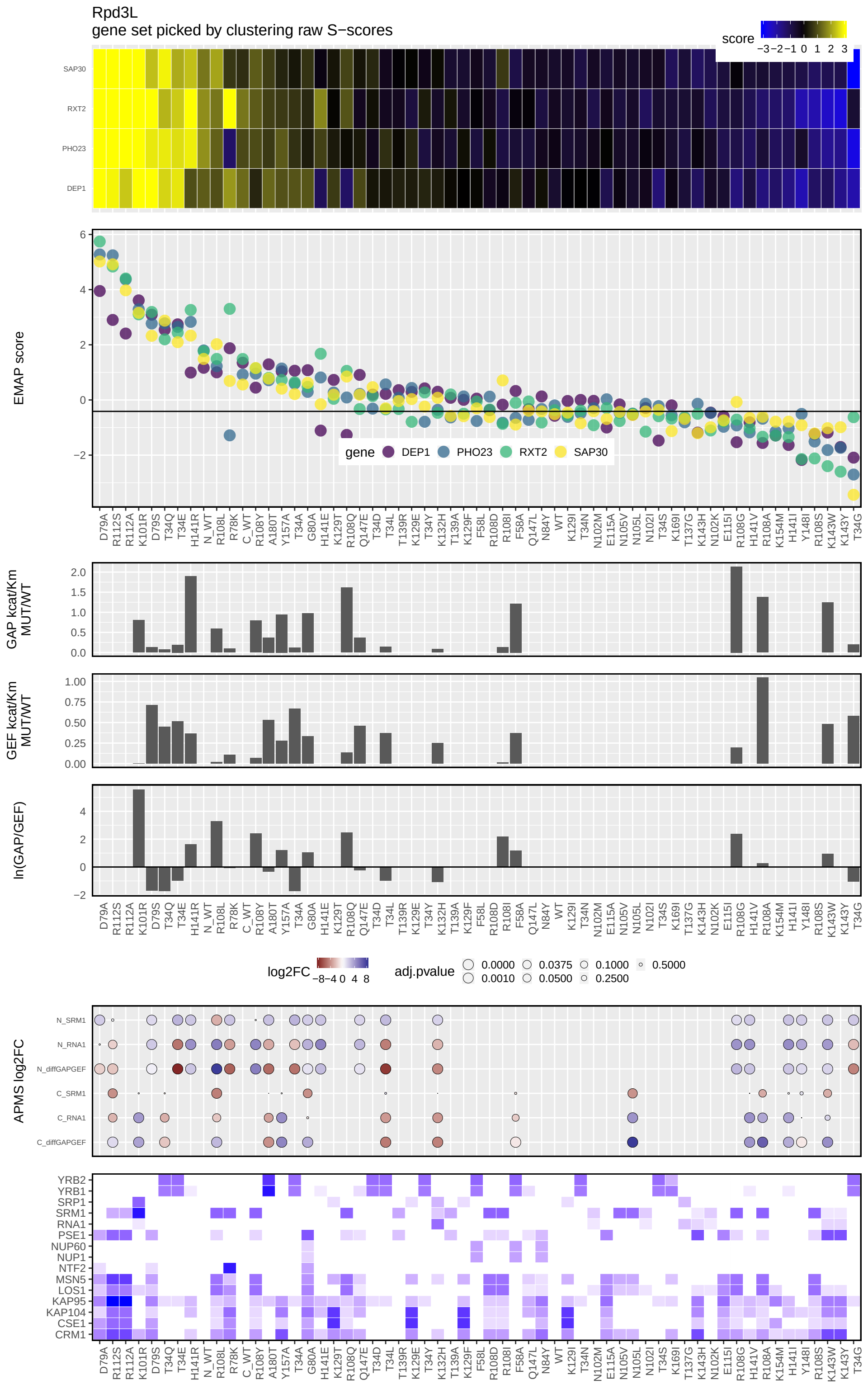

APC
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SWM1
CHL1
CDC26
EMAP score
gene CDC26 CHL1 SWM1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108I K154M N102K R112S T34L Y148I K132H R108S H141V Y157A Q147L K169I N105L K143H H141I WT T139R R108L T137G R108A N105V N102I E115A R108G F58L T34S T34N K129I T34D R108D T139A N84Y K143W K129F F58A N102M E115I K129E K143Y T34A K129T C_WT R112A T34Y R108Y H141E R108Q N_WT Q147E K101R A180T H141R T34E G80A T34Q R78K D79S D79A T34G


Cell Cycle Checkpoint
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
RMI1
NKP1
MCM22
MCM21
MCM16
MAD3
MAD2
MAD1
IRC15
IML3
CTF19
CHL4
EMAP score
gene
CHL4
CTF19
IML3
IRC15
MAD1
MAD2
MAD3
MCM16
MCM21
MCM22
NKP1
RMI1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A D79S T34Q K101R T34E C_WT N_WT T34A R108Y H141R R112S G80A R108L Y148I R108I R108Q Q147E R112A N84Y K143Y T137G H141I R108A R108G K154M E115A A180T E115I T34S T139A T139R K129T WT T34N F58A F58L T34Y N102K T34D H141E N102I H141V Q147L K143W K132H K169I R108S K129F K129E N105L R108D K143H K129I N102M T34L R78K N105V Y157A

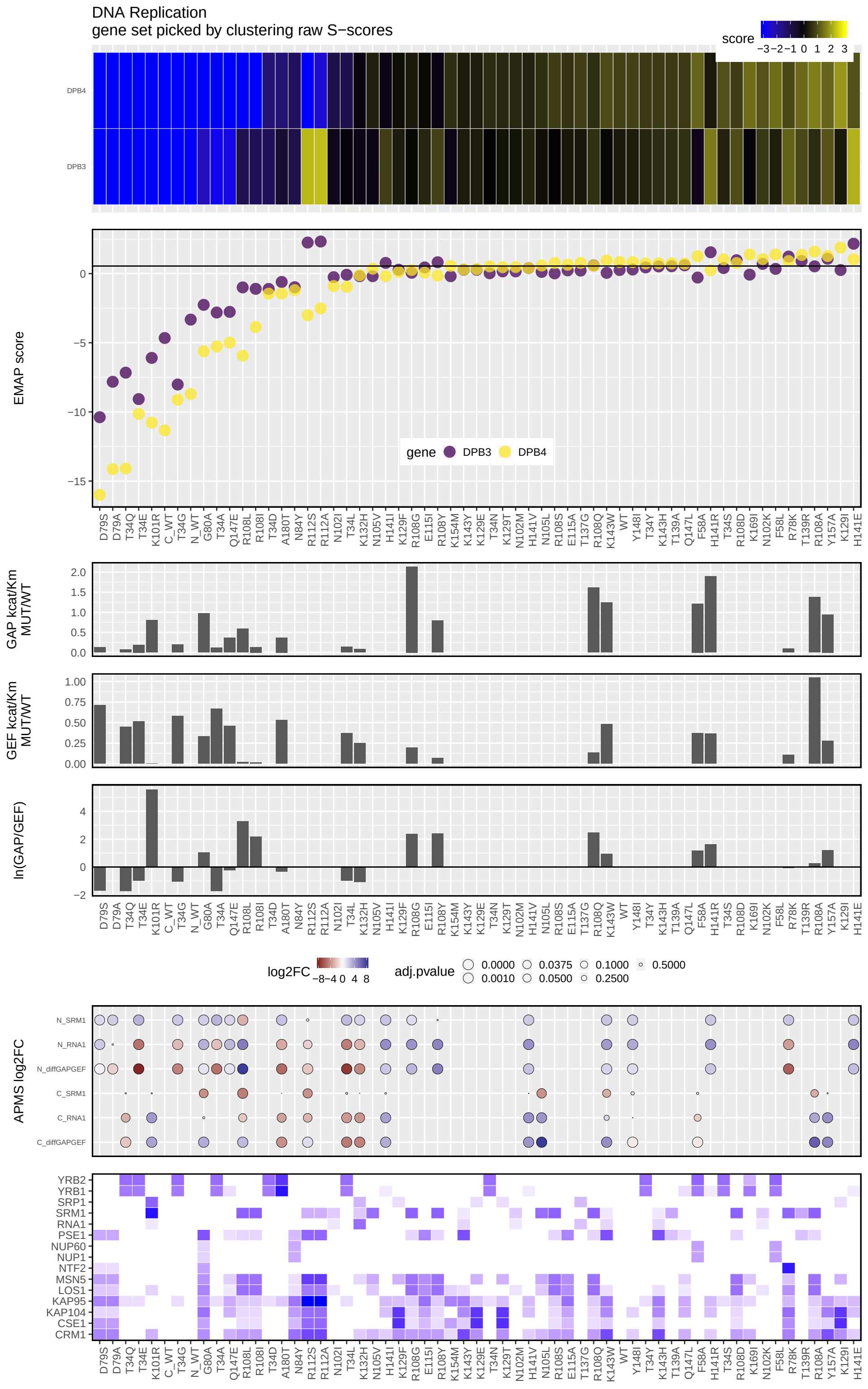
RIM101
gene set picked by clustering raw S−scores

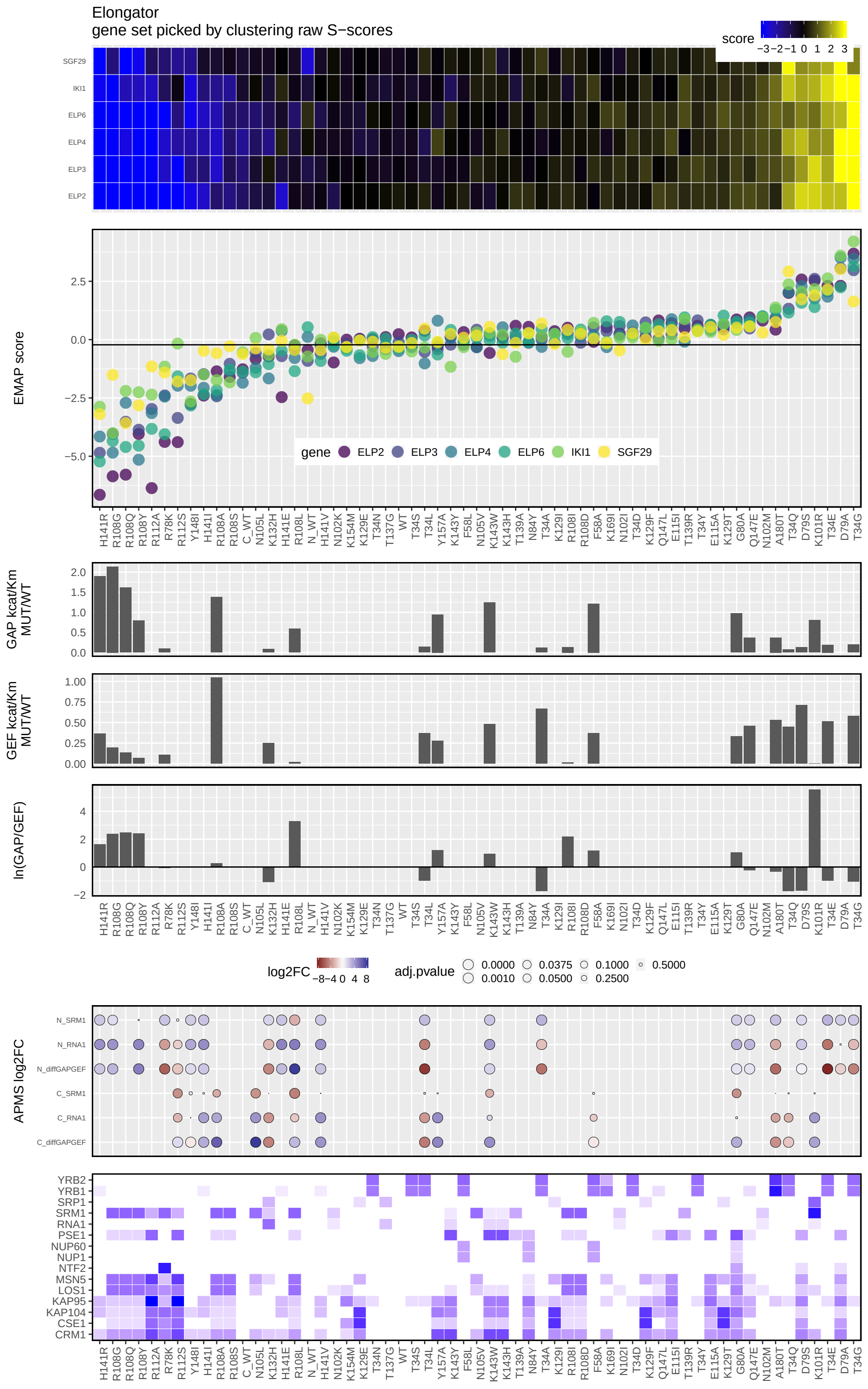


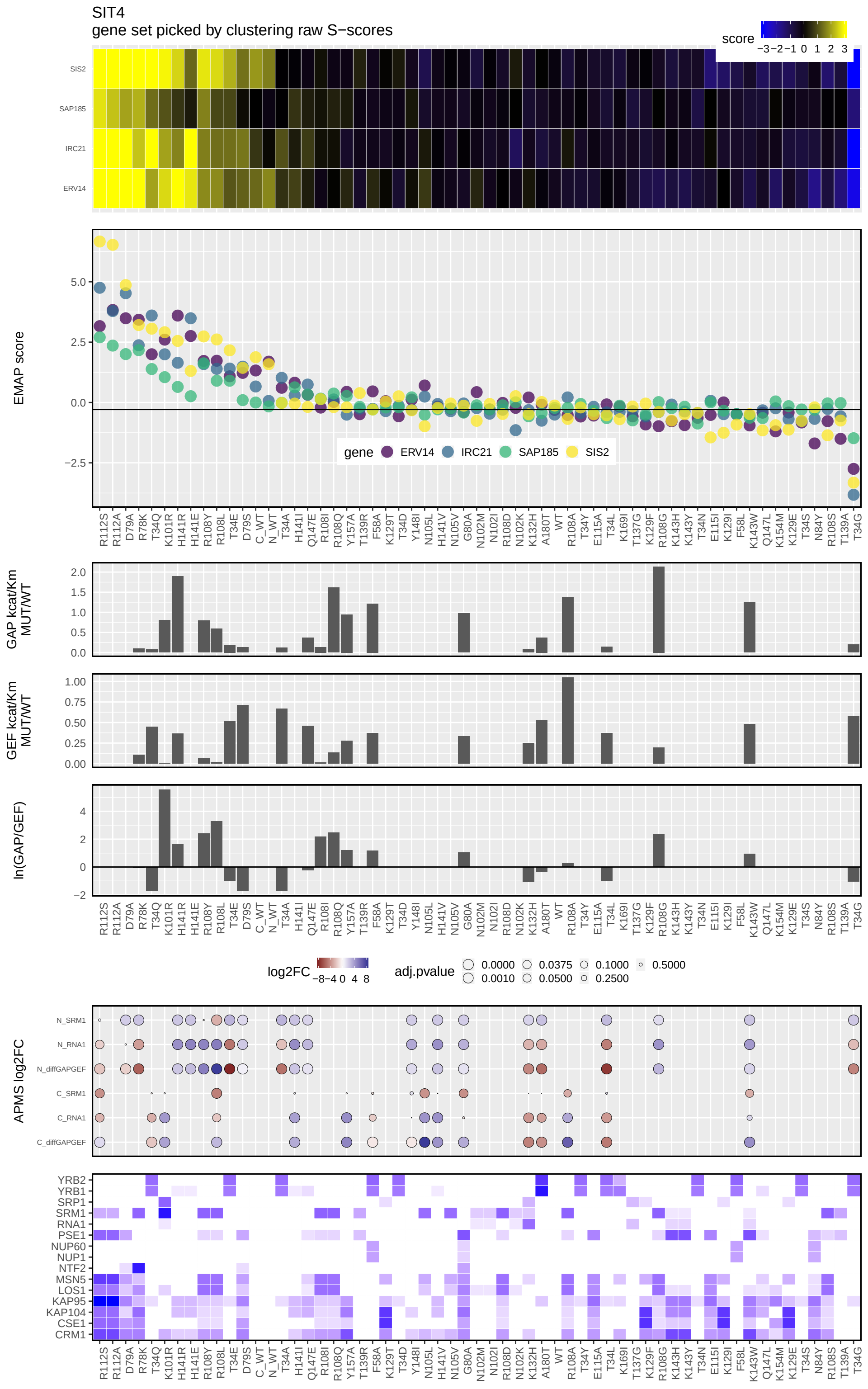

mitochondrial
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SUM1
RPO41
RIM1
PET123
MIP1
MDM38
LOS1
IMG2
GSH2
DGK1
CRD1
EMAP score
gene
CRD1 DGK1 GSH2 IMG2 LOS1 MDM38 MIP1 PET123 RIM1 RPO41 SUM1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R112S H141E R112A T34Q T34G D79S H141R K101R N_WT T34E R108Y R108L C_WT Y157A G80A T34A R108Q R108I Q147E A180T T34L R108D K129E K132H T34D T34Y R108G N105V T139R R108S H141I N105L K129T Y148I N102I N102M T34N N102K F58A E115I Q147L N84Y K143H H141V WT K129I K129F K143Y E115A R108A T34S T137G K169I K154M T139A F58L K143W R78K


Rpd3L
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SAP30
RXT2
PHO23
DEP1
EMAP score
gene DEP1 PHO23 RXT2 SAP30
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R112S R112A K101R D79S T34Q T34E H141R N_WT R108L R78K C_WT R108Y A180T Y157A T34A G80A H141E K129T R108Q Q147E T34D T34L T139R K129E T34Y K132H T139A K129F F58L R108D R108I F58A Q147L N84Y WT K129I T34N N102M E115A N105V N105L N102I T34S K169I T137G K143H N102K E115I R108G H141V R108A K154M H141I Y148I R108S K143W K143Y T34G

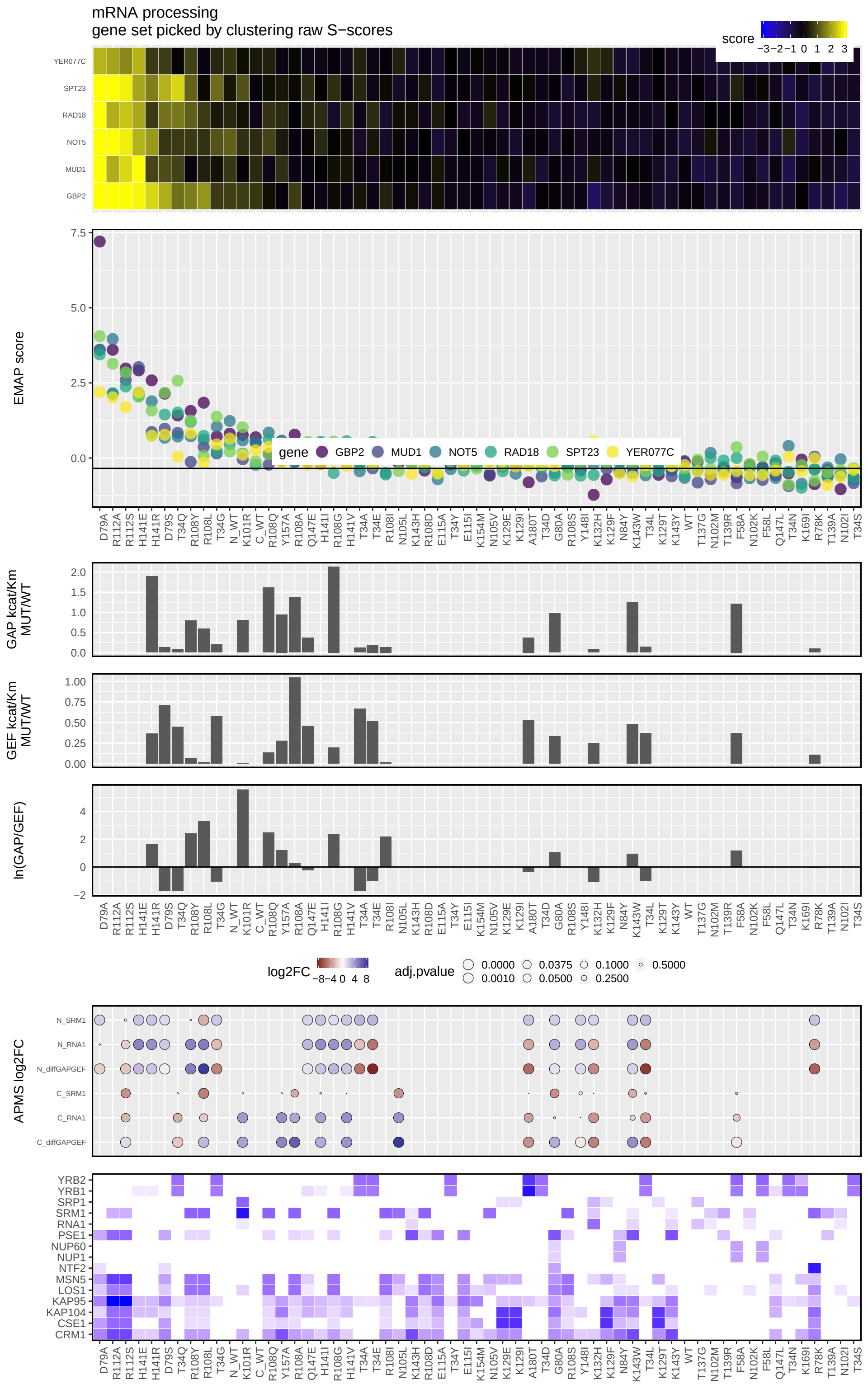
DNA Replication
gene set picked by clustering raw S−scores



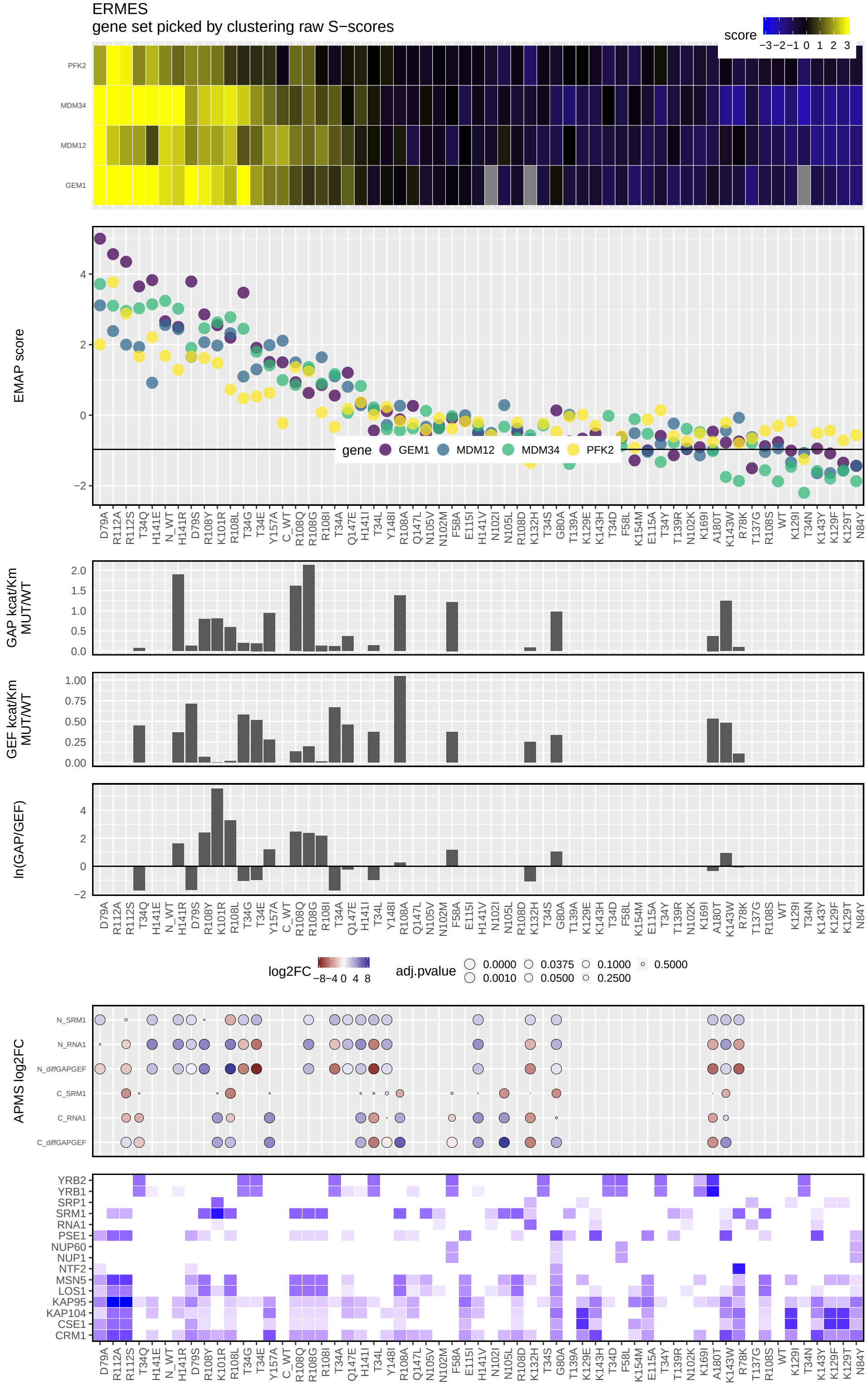

Elongator
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SGF29
IKI1
ELP6
ELP4
ELP3
ELP2
EMAP score
gene ELP2 ELP3 ELP4 ELP6 IKI1 SGF29
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141R R108G R108Q R108Y R112A R78K R112S Y148I H141I R108A R108S C_WT N105L K132H H141E R108L N_WT H141V N102K K154M K129E T34N T137G WT T34S T34L Y157A K143Y F58L N105V K143W K143H T139A N84Y T34A K129I R108I R108D F58A K169I N102I T34D K129F Q147L E115I T139R T34Y E115A K129T G80A Q147E N102M A180T T34Q D79S K101R T34E D79A T34G


SIT4
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SIS2
SAP185
IRC21
ERV14
EMAP score
5.0
2.5
0.0
−2.5
gene
ERV14
IRC21
SAP185
SIS2
R112S R112A D79A R78K T34Q K101R H141R H141E R108Y R108L T34E D79S C_WT N_WT T34A H141I Q147E R108I R108Q Y157A T139R F58A K129T T34D Y148I N105L H141V N105V G80A N102M N102I R108D N102K K132H A180T WT R108A T34Y E115A T34L K169I T137G K129F R108G K143H K143Y T34N E115I K129I F58L K143W Q147L K154M K129E T34S N84Y R108S T139A T34G
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

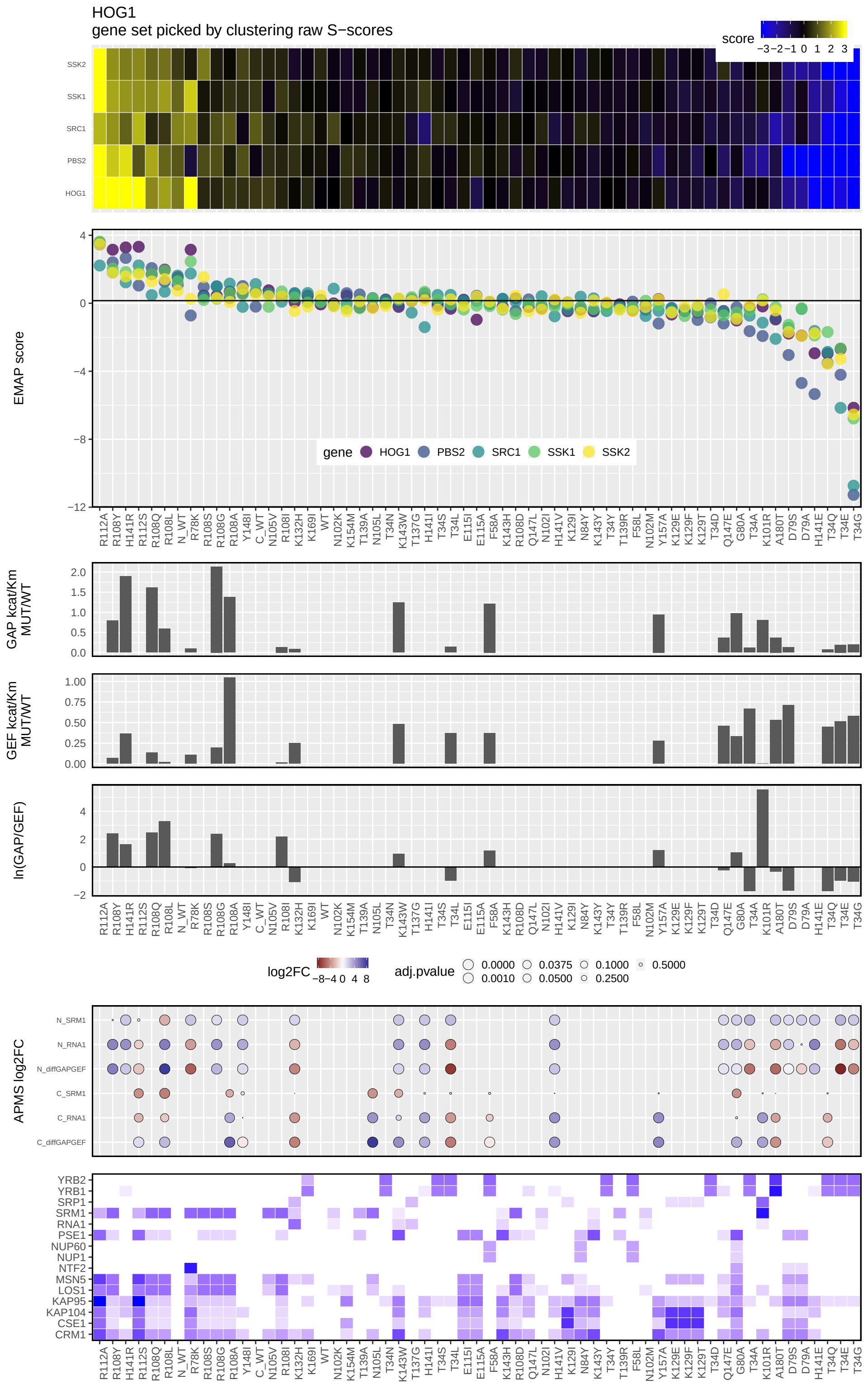
mRNA processing
gene set picked by clustering raw S−scores

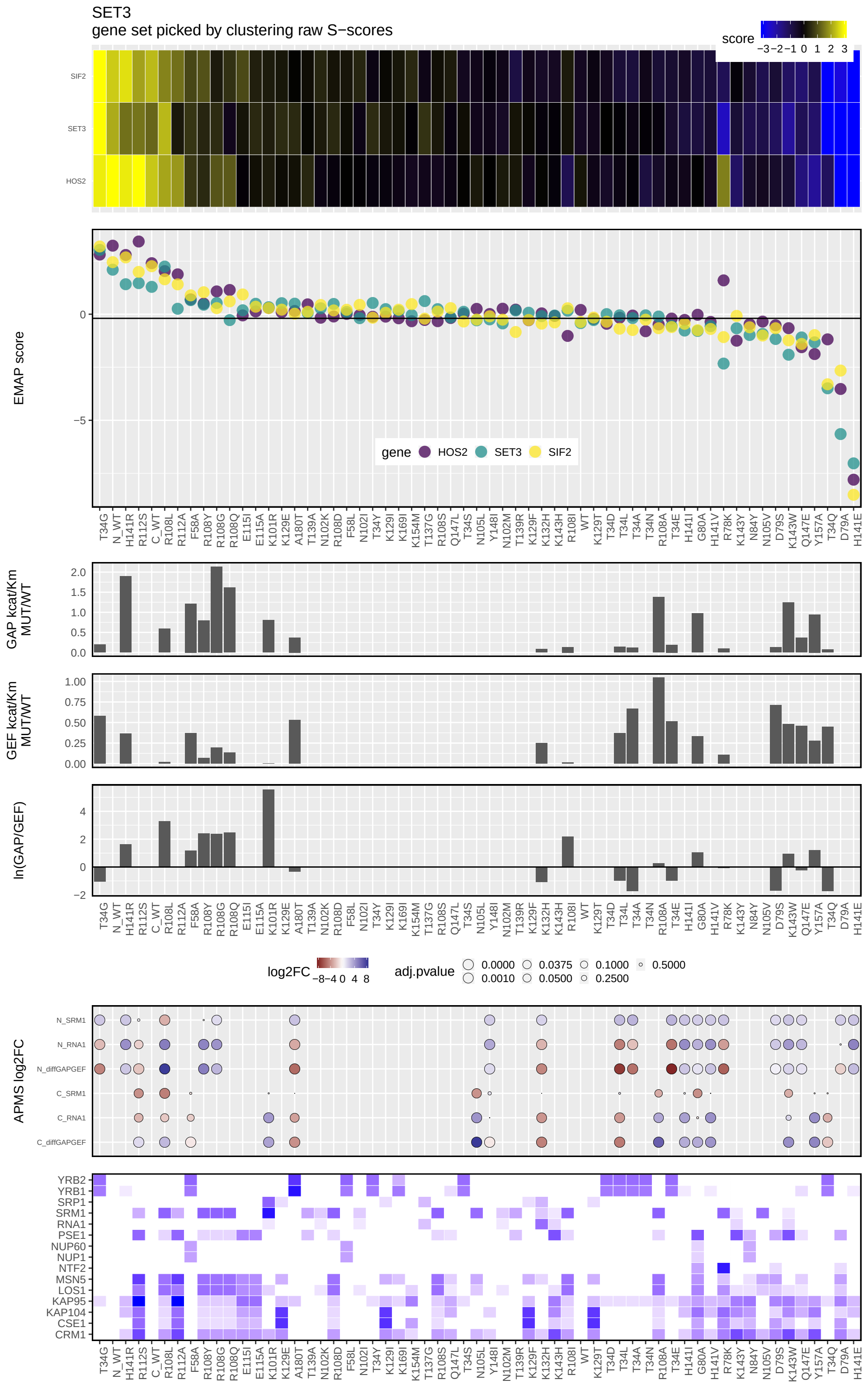


ERMES
gene set picked by clustering raw S−scores

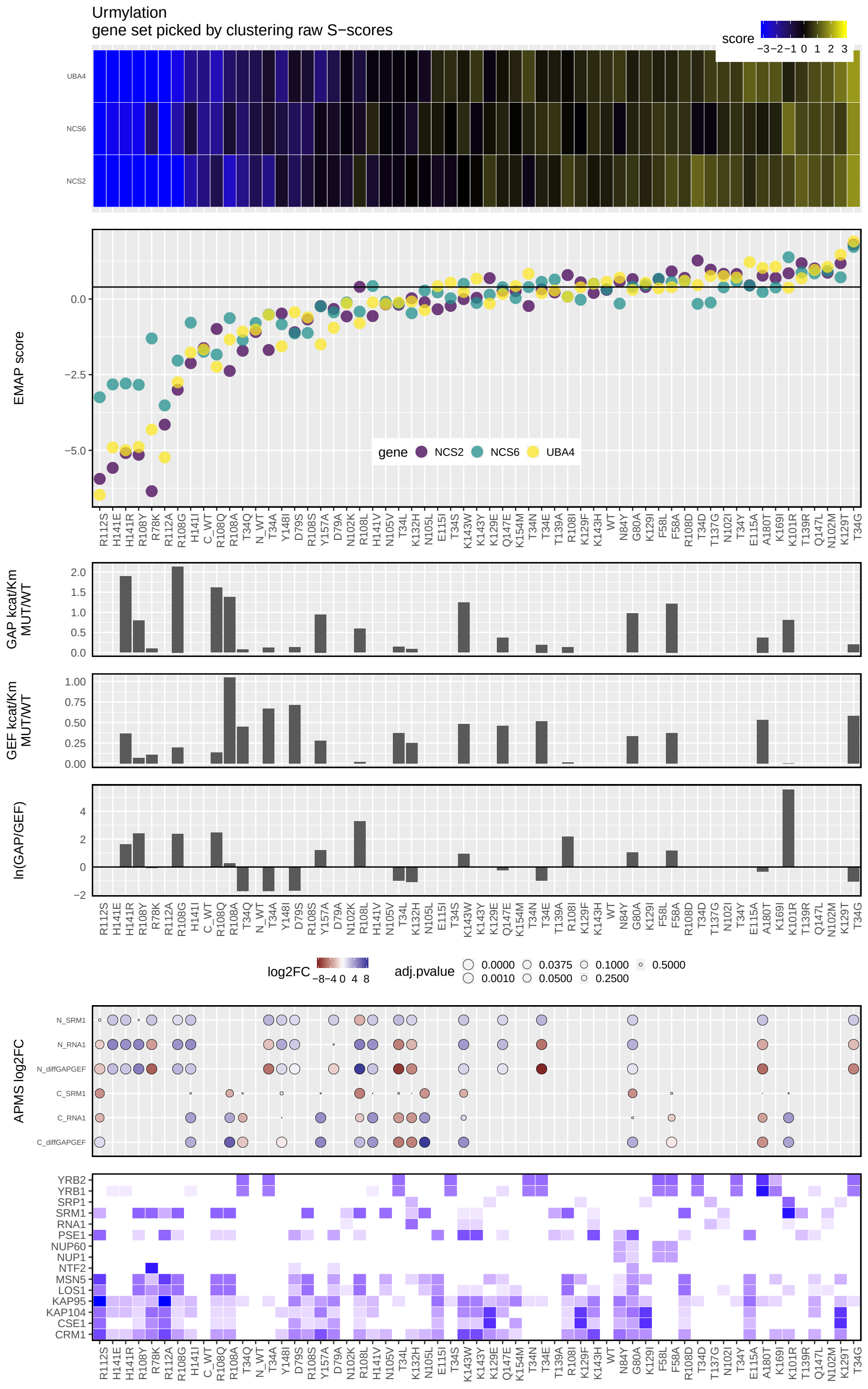


HOG1
gene set picked by clustering raw S−scores

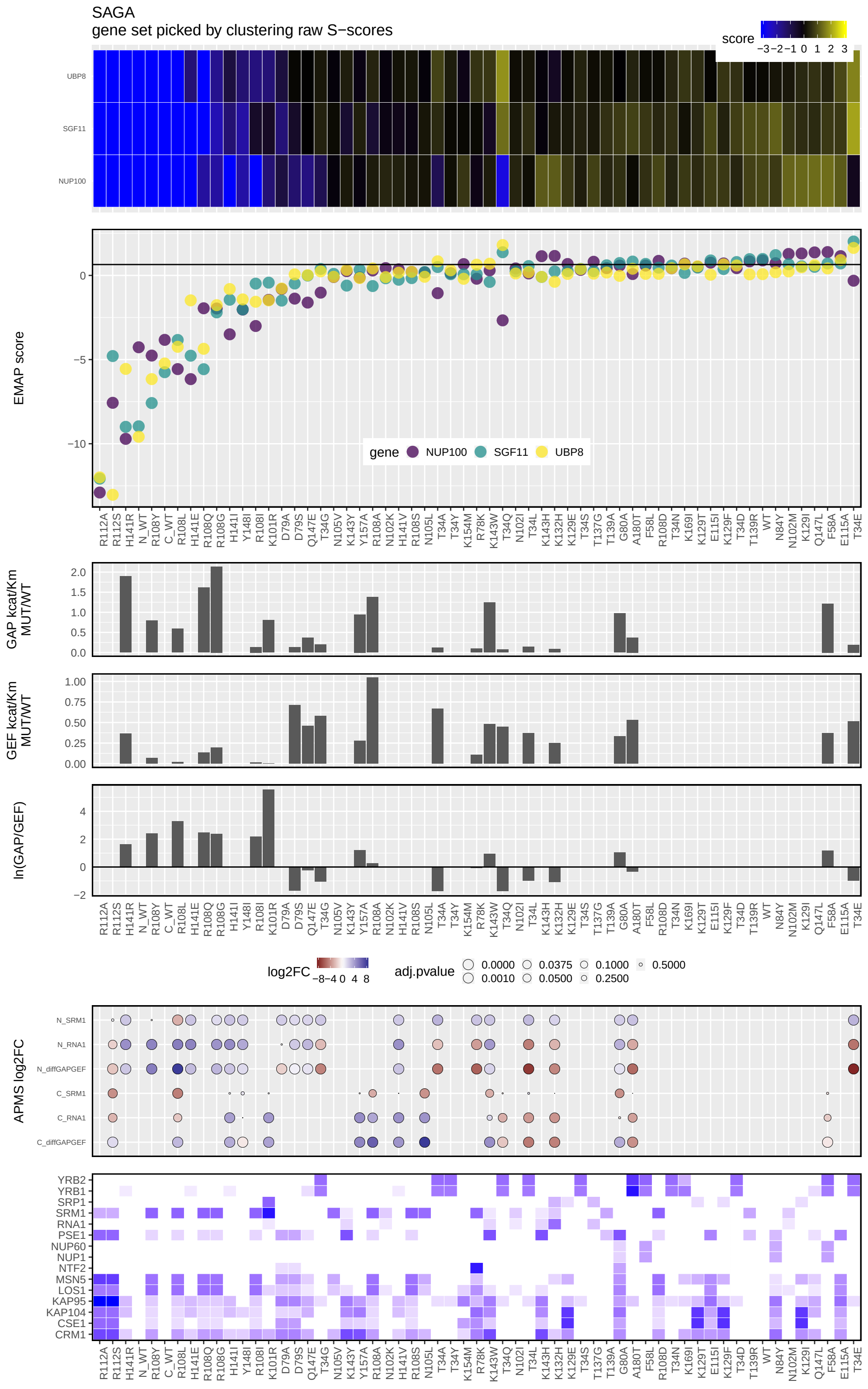



SET3
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
SIF2
SET3
HOS2
EMAP score
0
−5
gene HOS2 SET3 SIF2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G N_WT H141R R112S C_WT R108L R112A F58A R108Y R108G R108Q E115I E115A K101R K129E A180T T139A N102K R108D F58L N102I T34Y K129I K169I K154M T137G R108S Q147L T34S N105L Y148I N102M T139R K129F K132H K143H R108I WT K129T T34D T34L T34A T34N R108A T34E H141I G80A H141V R78K K143Y N84Y N105V D79S K143W Q147E Y157A T34Q D79A H141E

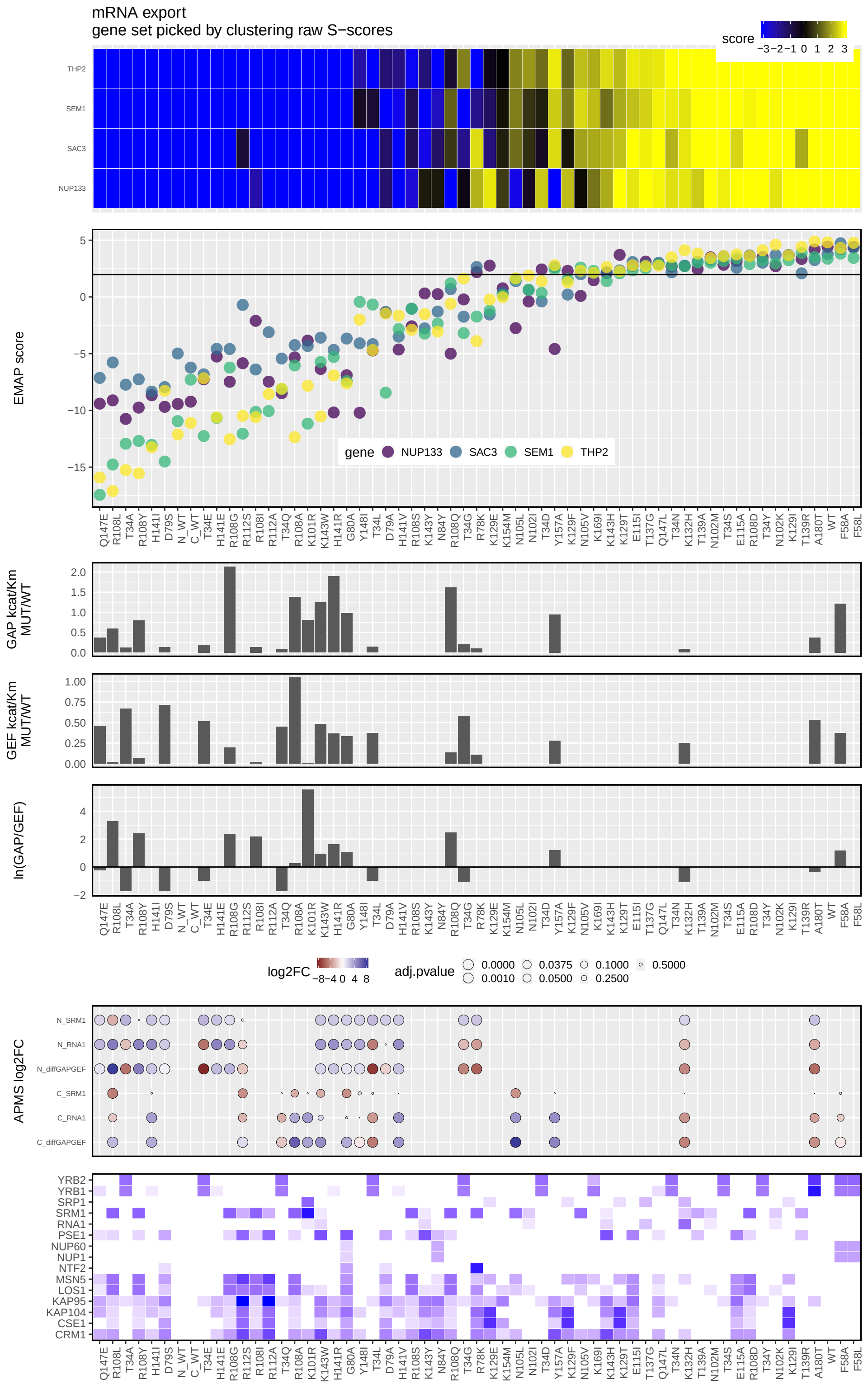
Urmylation
gene set picked by clustering raw S−scores

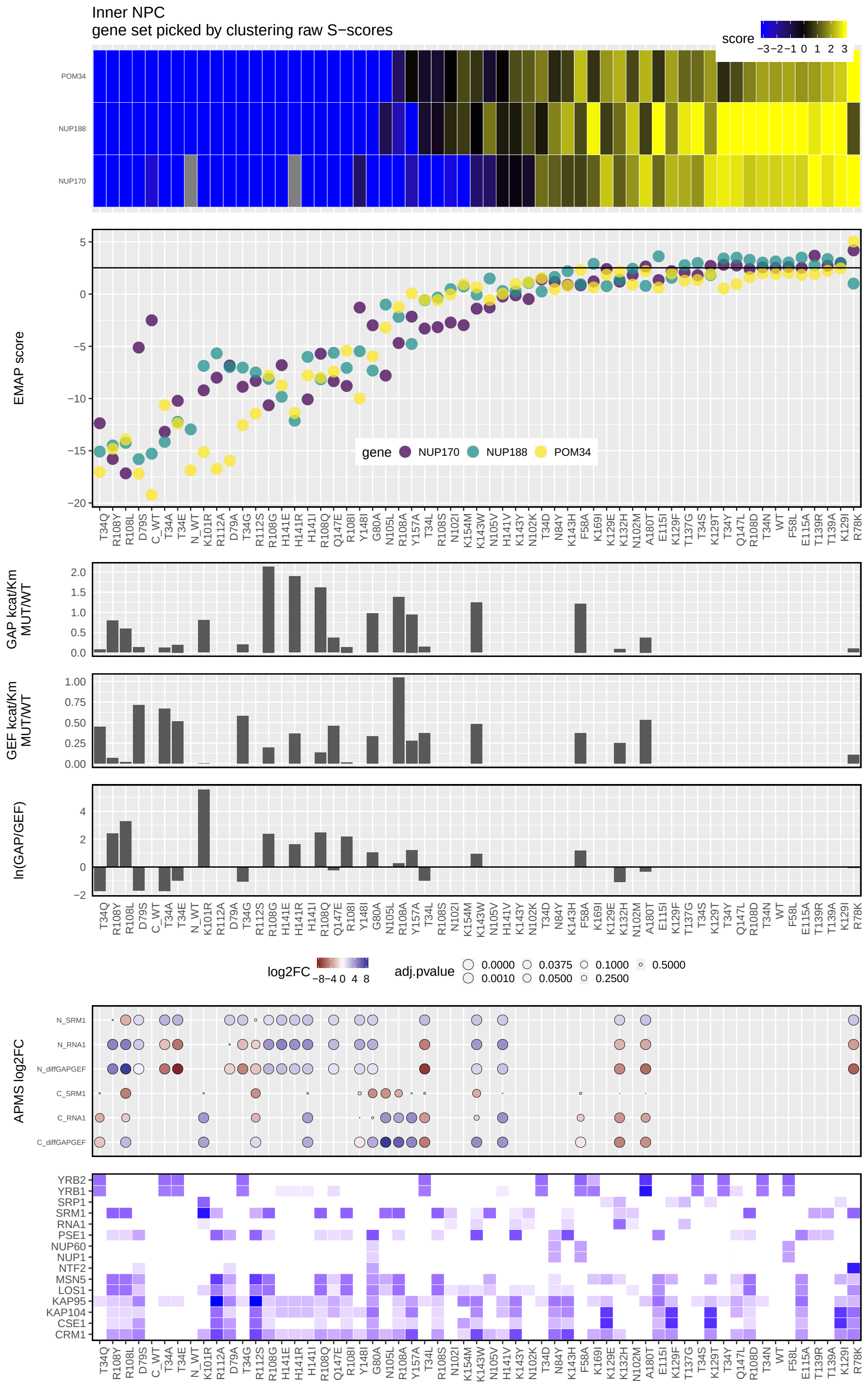


SAGA
gene set picked by clustering raw S−scores

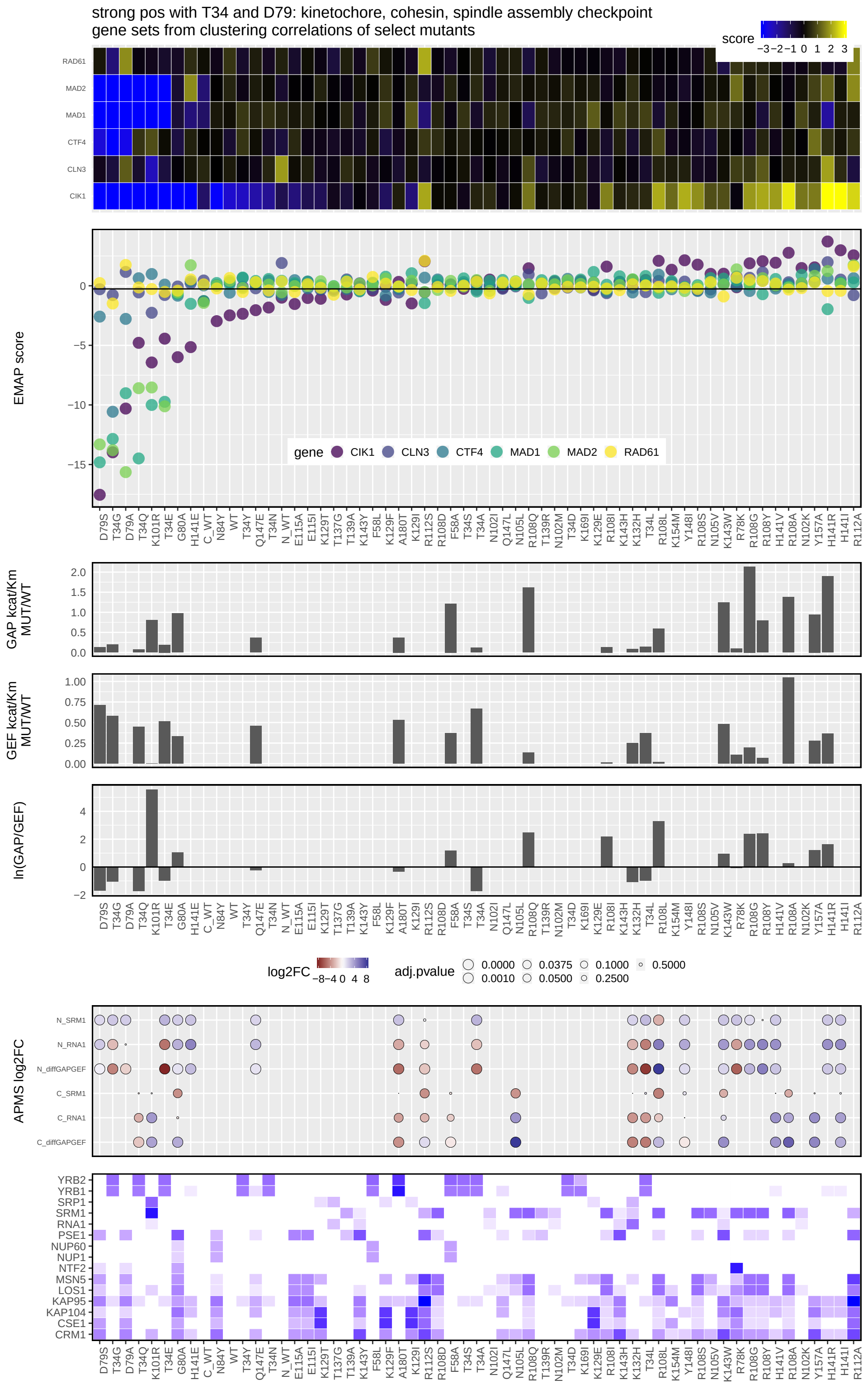


mRNA export
gene set picked by clustering raw S−scores

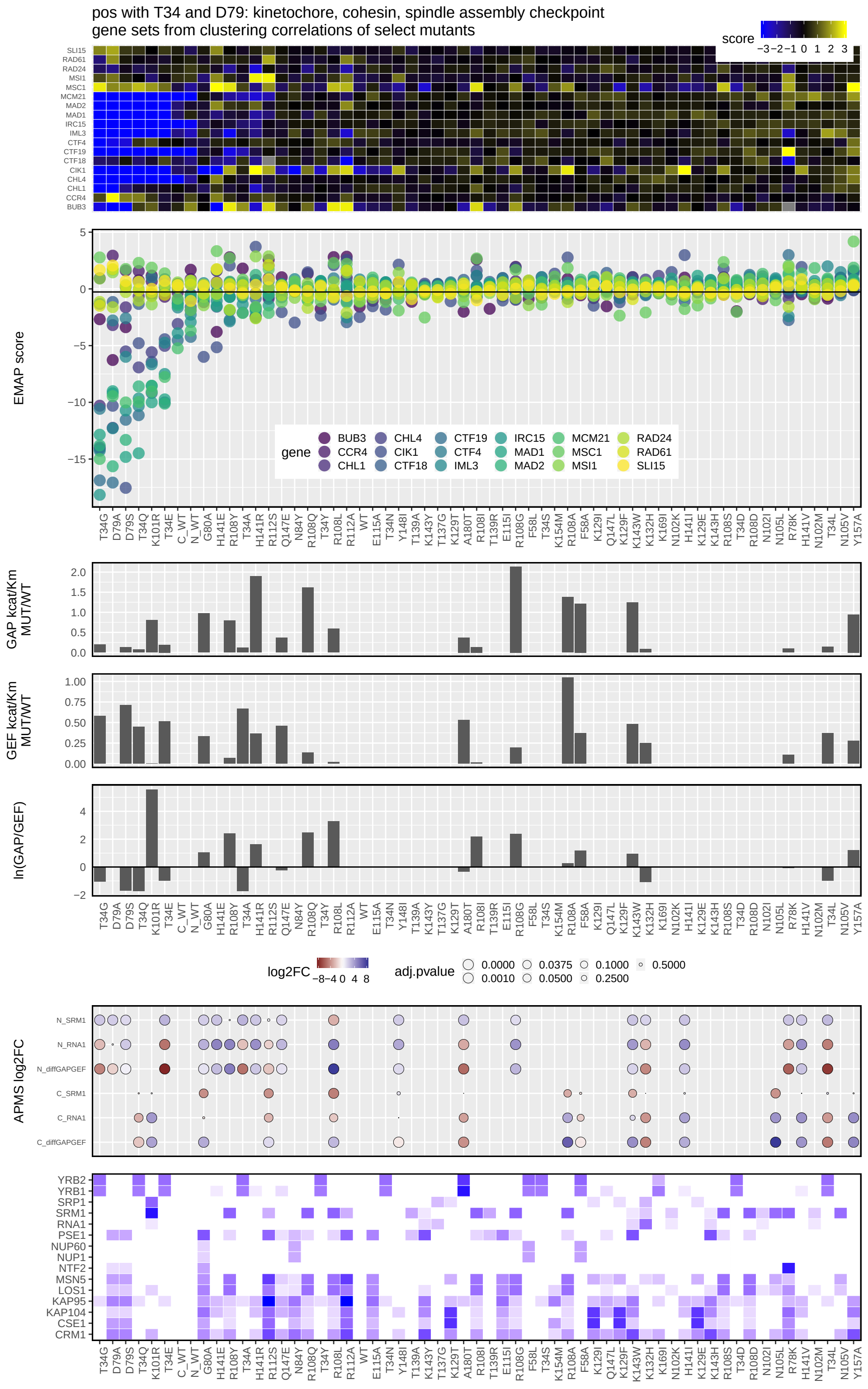



Inner NPC
gene set picked by clustering raw S−scores
score
−3 −2 −1 0 1 2 3
POM34
NUP188
NUP170
EMAP score
gene
NUP170
NUP188
POM34
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34Q R108Y R108L D79S C_WT T34A T34E N_WT K101R R112A D79A T34G R112S R108G H141E H141R H141I R108Q Q147E R108I Y148I G80A N105L R108A Y157A T34L R108S N102I K154M K143W N105V H141V K143Y N102K T34D N84Y K143H F58A K169I K129E K132H N102M A180T E115I K129F T137G T34S K129T T34Y Q147L R108D T34N WT F58L E115A T139R T139A K129I R78K

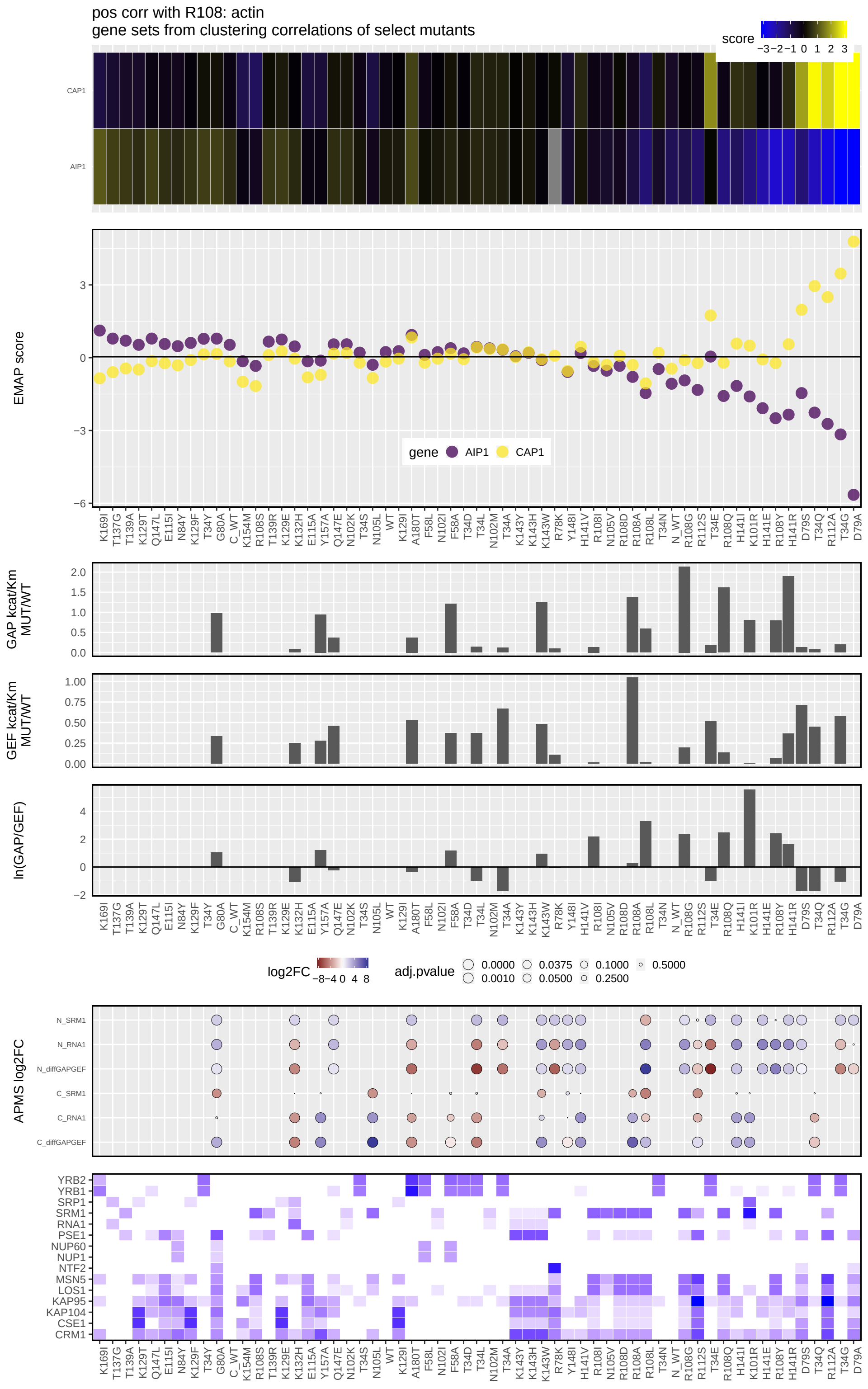
strong pos with T34 and D79: kinetochore, cohesin, spindle assembly checkpoint
gene sets from clustering correlations of select mutants



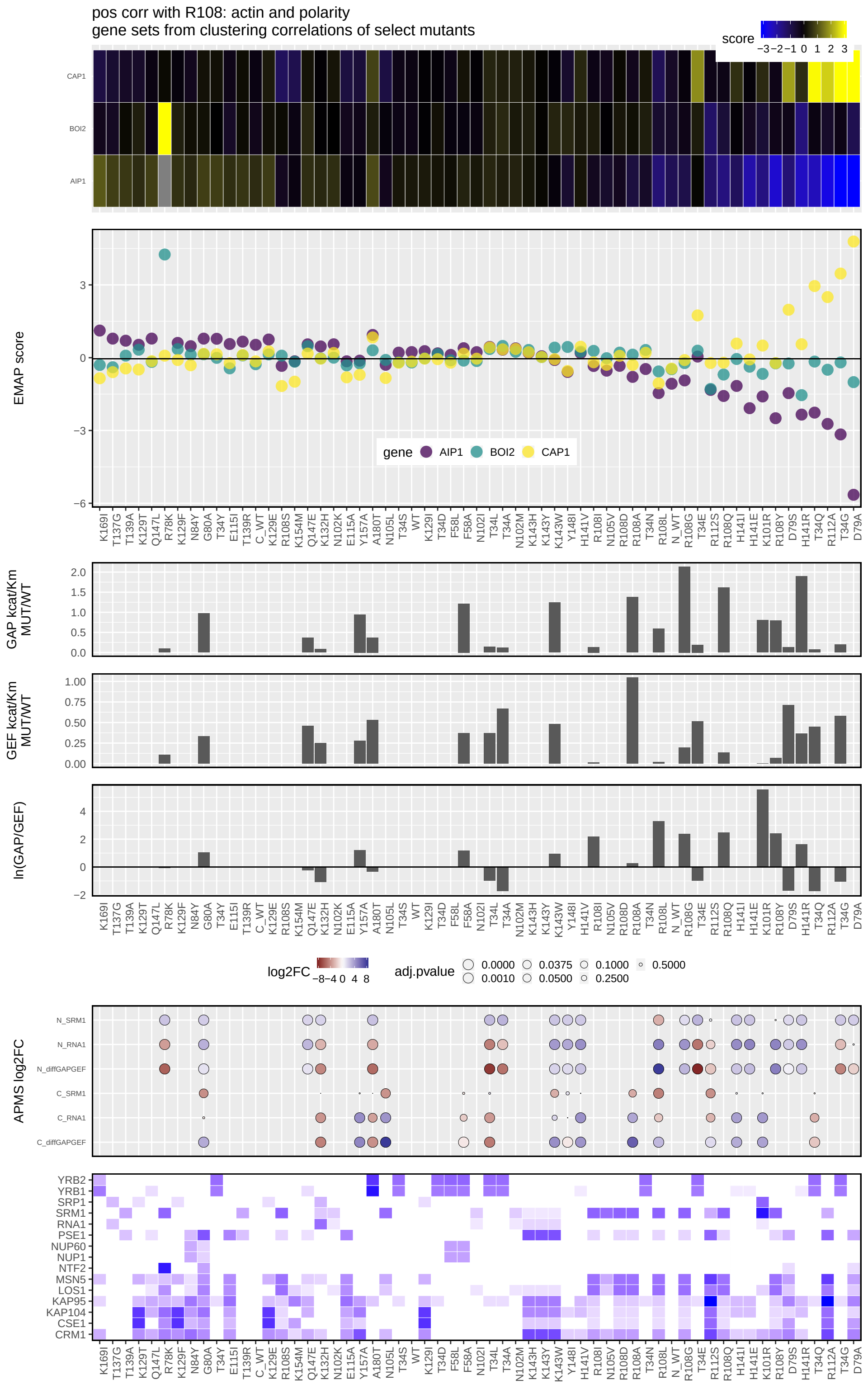
pos with T34 and D79: kinetochore, cohesin, spindle assembly checkpoint
gene sets from clustering correlations of select mutants



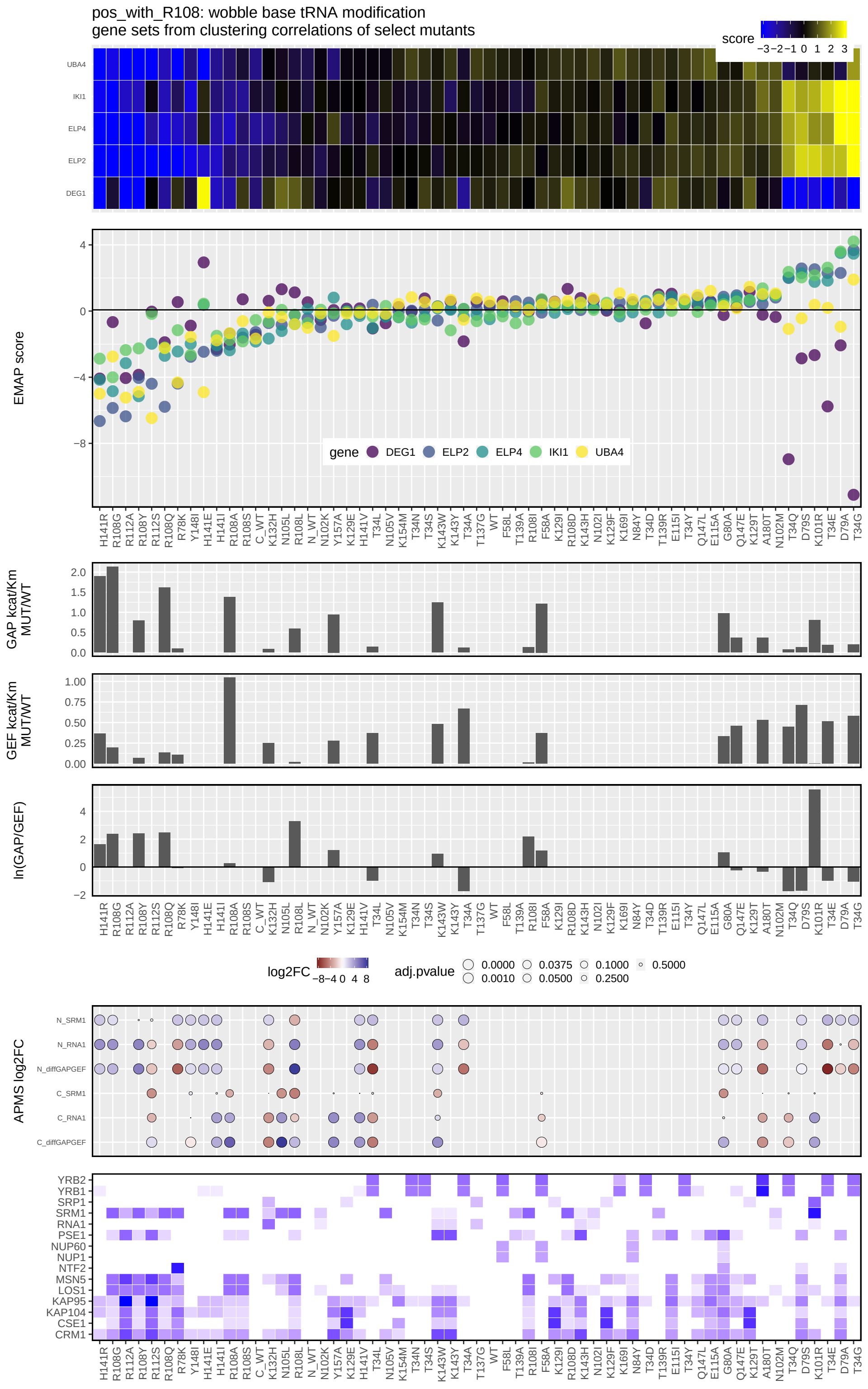
pos corr with R108: actin
gene sets from clustering correlations of select mutants

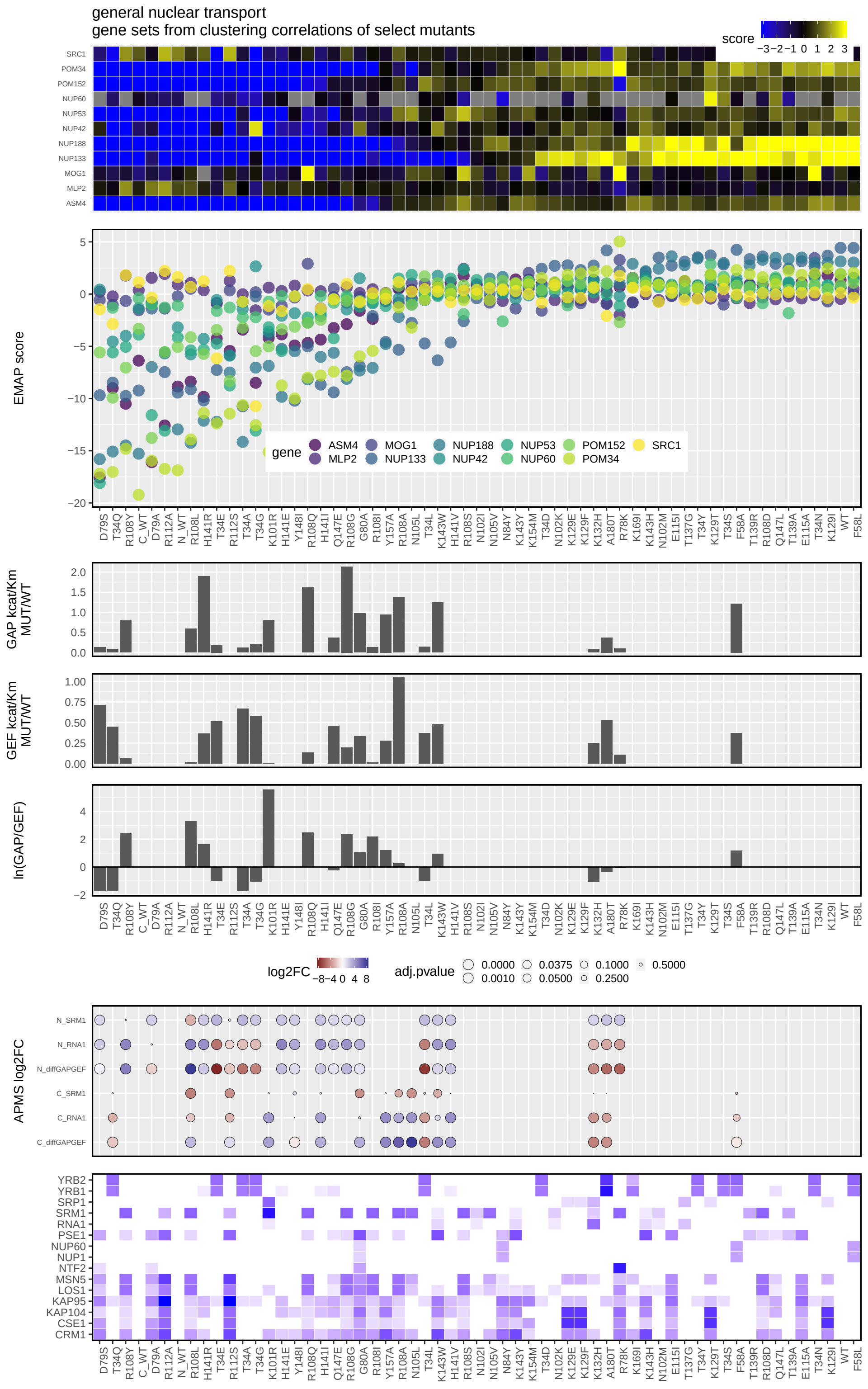


pos corr with R108: actin and polarity
gene sets from clustering correlations of select mutants

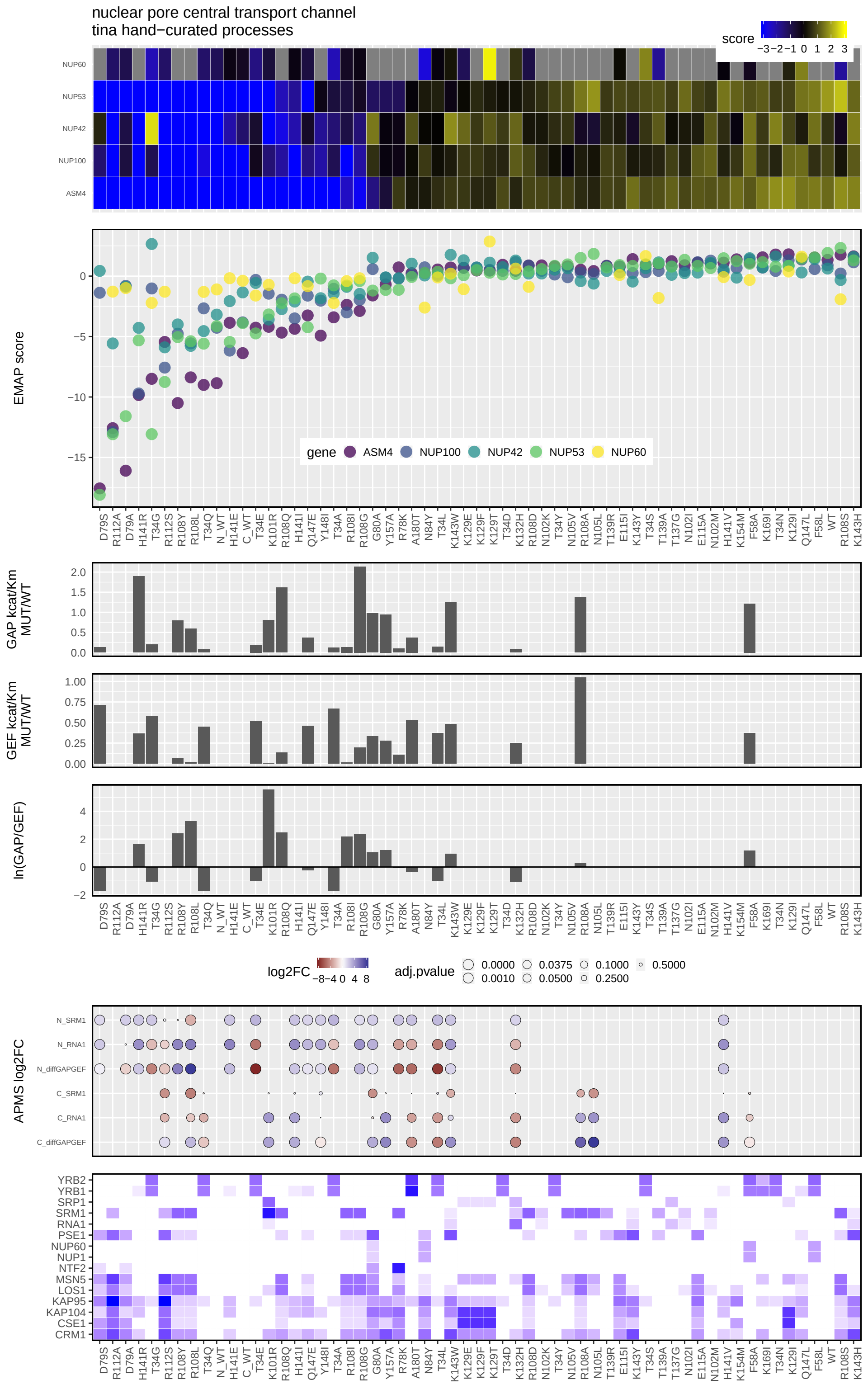


pos_with_R108: wobble base tRNA modification
gene sets from clustering correlations of select mutants

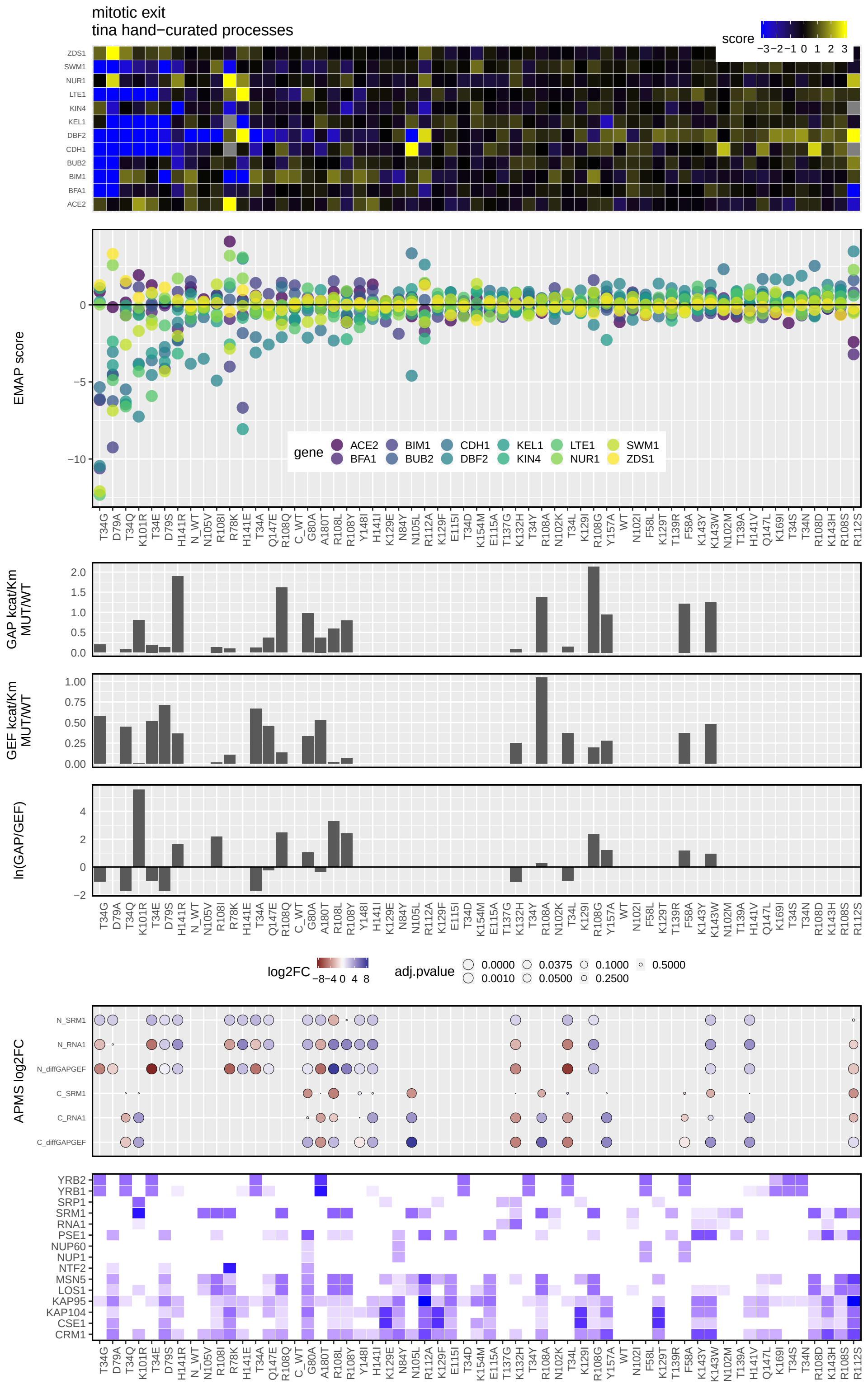


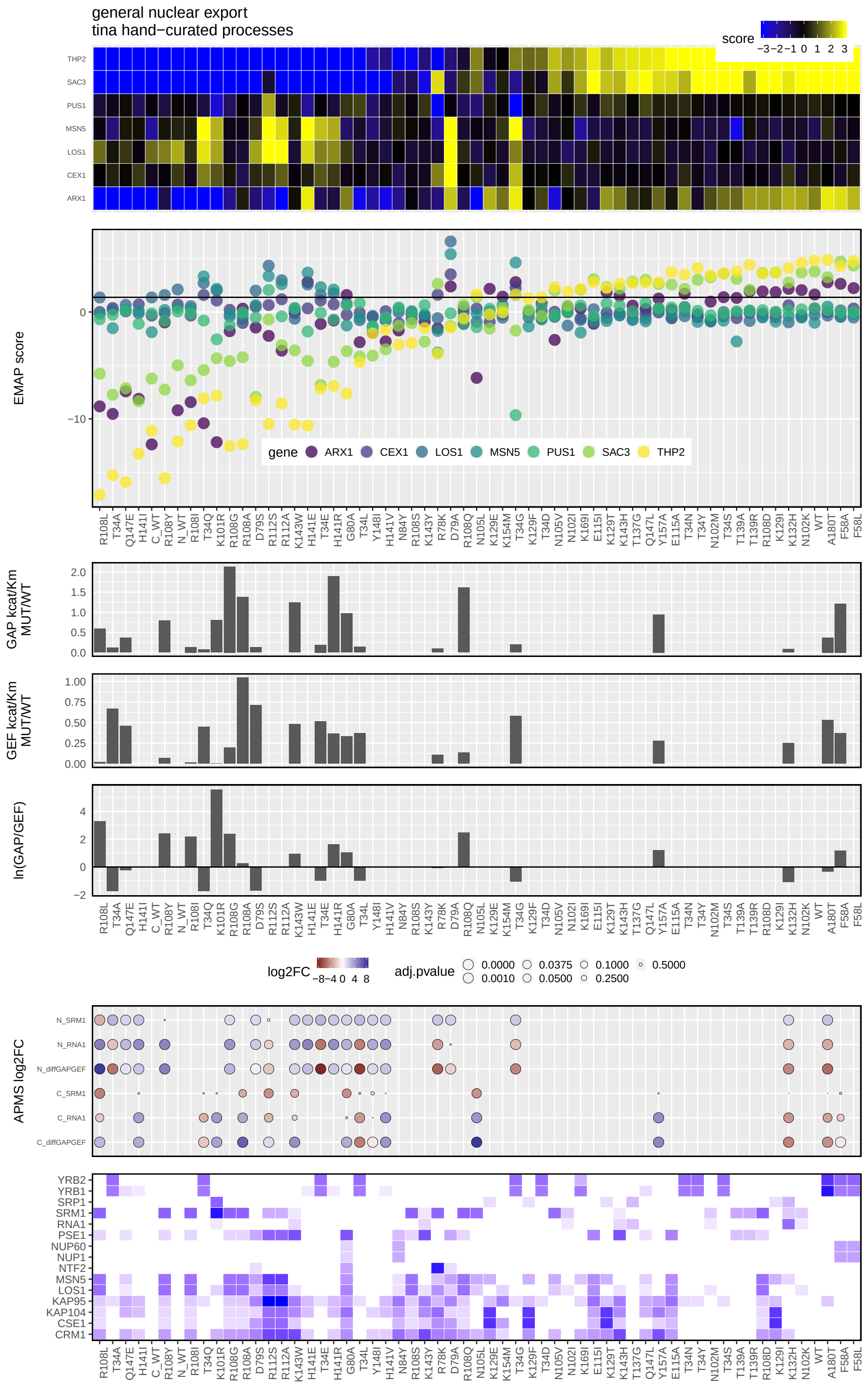

general nuclear transport
gene sets from clustering correlations of select mutants
score
−3 −2 −1 0 1 2 3
SRC1
POM34
POM152
NUP60
NUP53
NUP42
NUP188
NUP133
MOG1
MLP2
ASM4
EMAP score
gene
ASM4
MLP2
MOG1
NUP133
NUP188
NUP42
NUP53
NUP60
POM152
POM34
SRC1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79S T34Q R108Y C_WT D79A R112A N_WT R108L H141R T34E R112S T34A T34G K101R H141E Y148I R108Q H141I Q147E R108G G80A R108I Y157A R108A N105L T34L K143W H141V R108S N102I N105V N84Y K143Y K154M T34D N102K K129E K129F K132H A180T R78K K169I K143H N102M E115I T137G T34Y K129T T34S F58A T139R R108D Q147L T139A E115A T34N K129I WT F58L

nuclear pore central transport channel
tina hand−curated processes

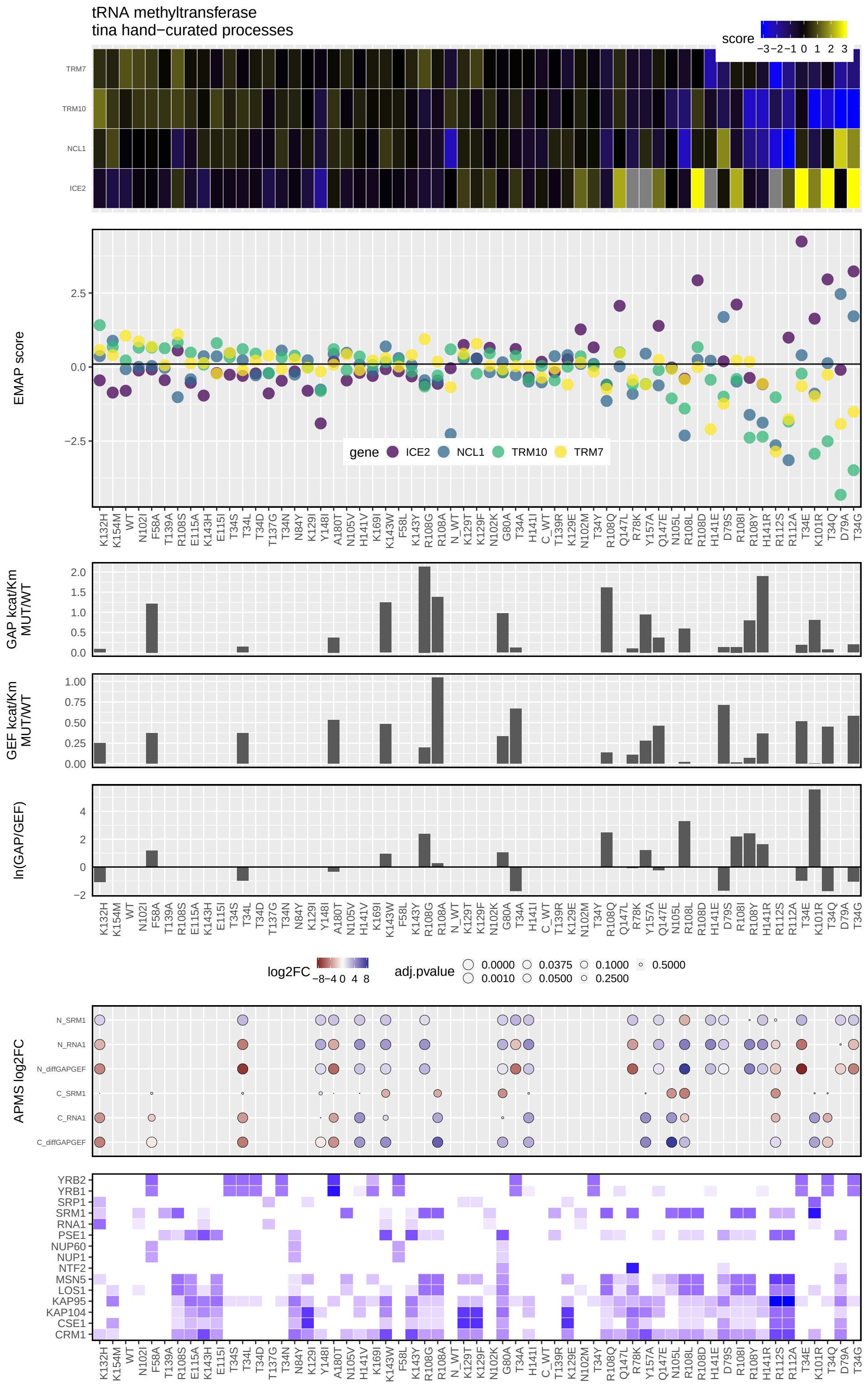


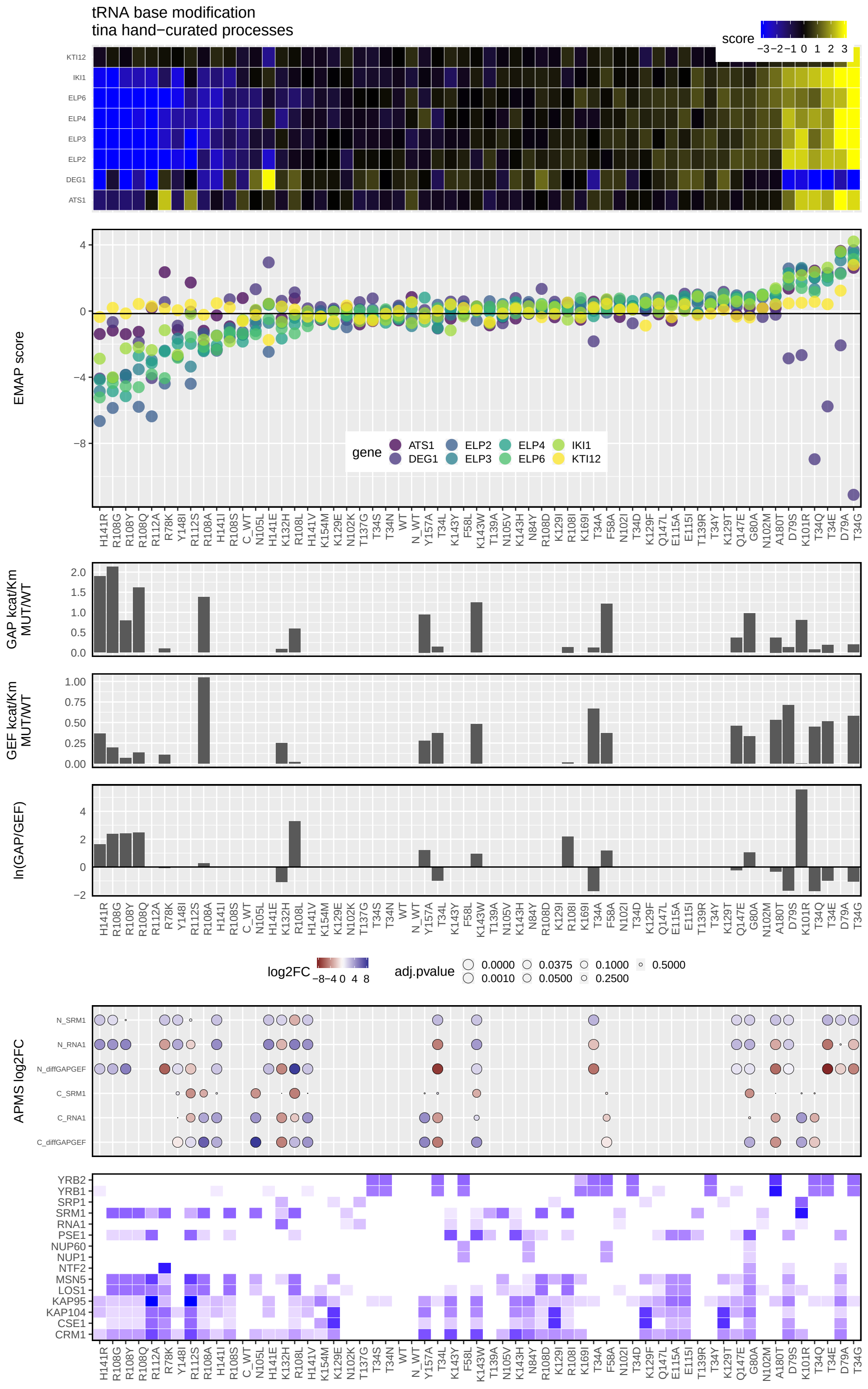
mitotic exit
tina hand−curated processes



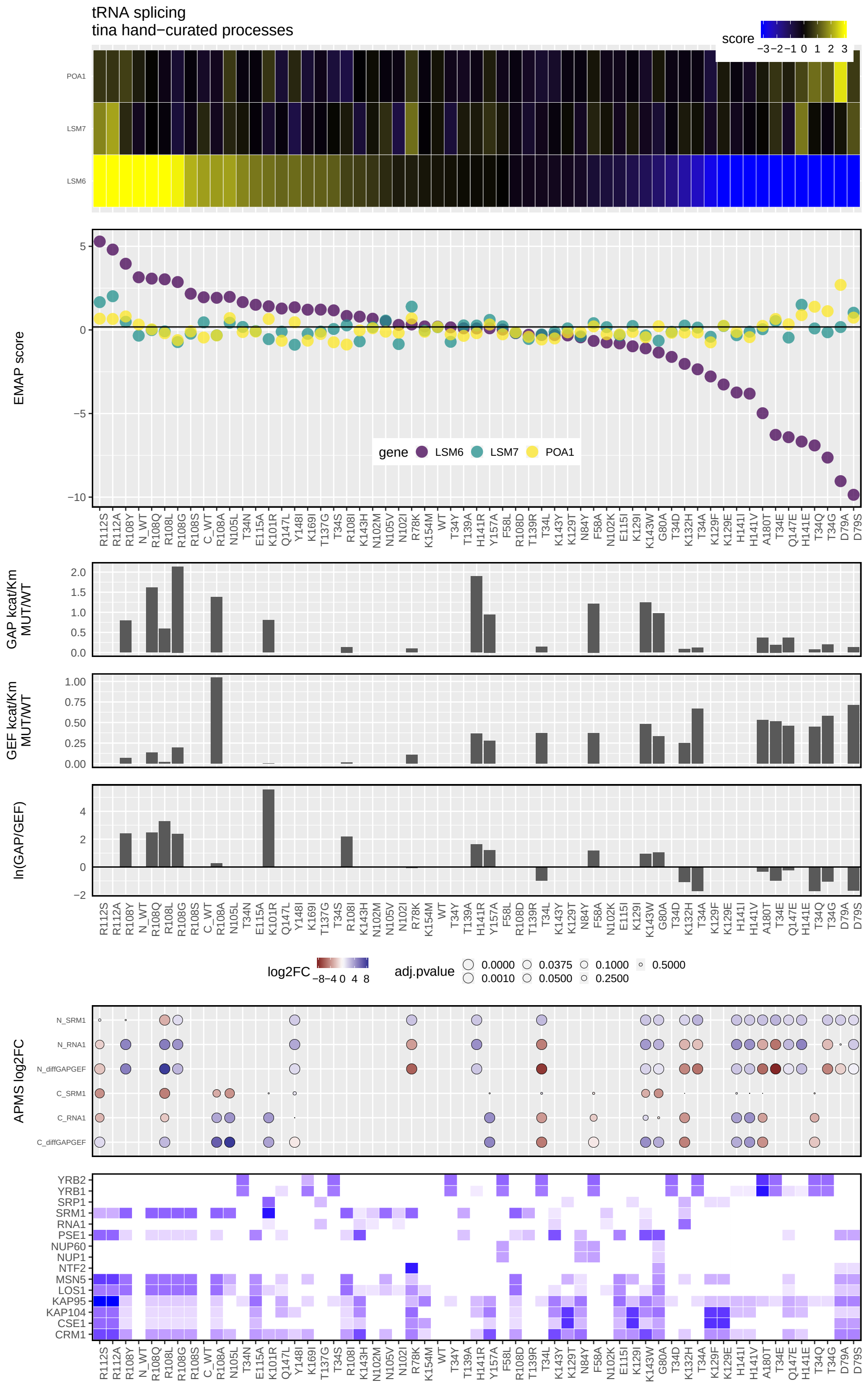

general nuclear export
tina hand−curated processes
score
−3 −2 −1 0 1 2 3
THP2
SAC3
PUS1
MSN5
LOS1
CEX1
ARX1
EMAP score
0
−10
gene ARX1 CEX1 LOS1 MSN5 PUS1 SAC3 THP2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108L T34A Q147E H141I C_WT R108Y N_WT R108I T34Q K101R R108G R108A D79S R112S R112A K143W H141E T34E H141R G80A T34L Y148I H141V N84Y R108S K143Y R78K D79A R108Q N105L K129E K154M T34G K129F T34D N105V N102I K169I E115I K129T K143H T137G Q147L Y157A E115A T34N T34Y N102M T34S T139A T139R R108D K129I K132H N102K WT A180T F58A F58L

tRNA methyltransferase
tina hand−curated processes

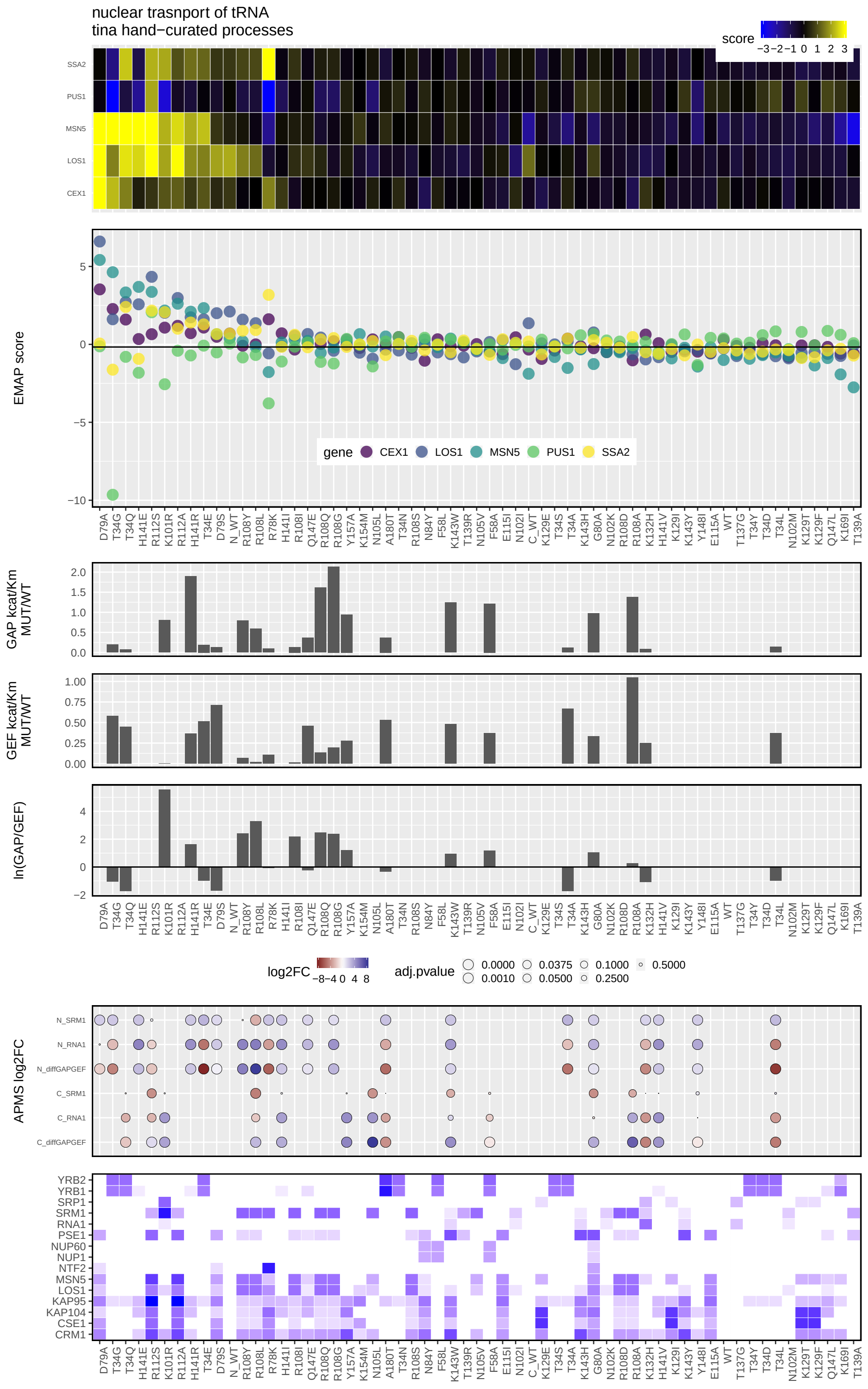


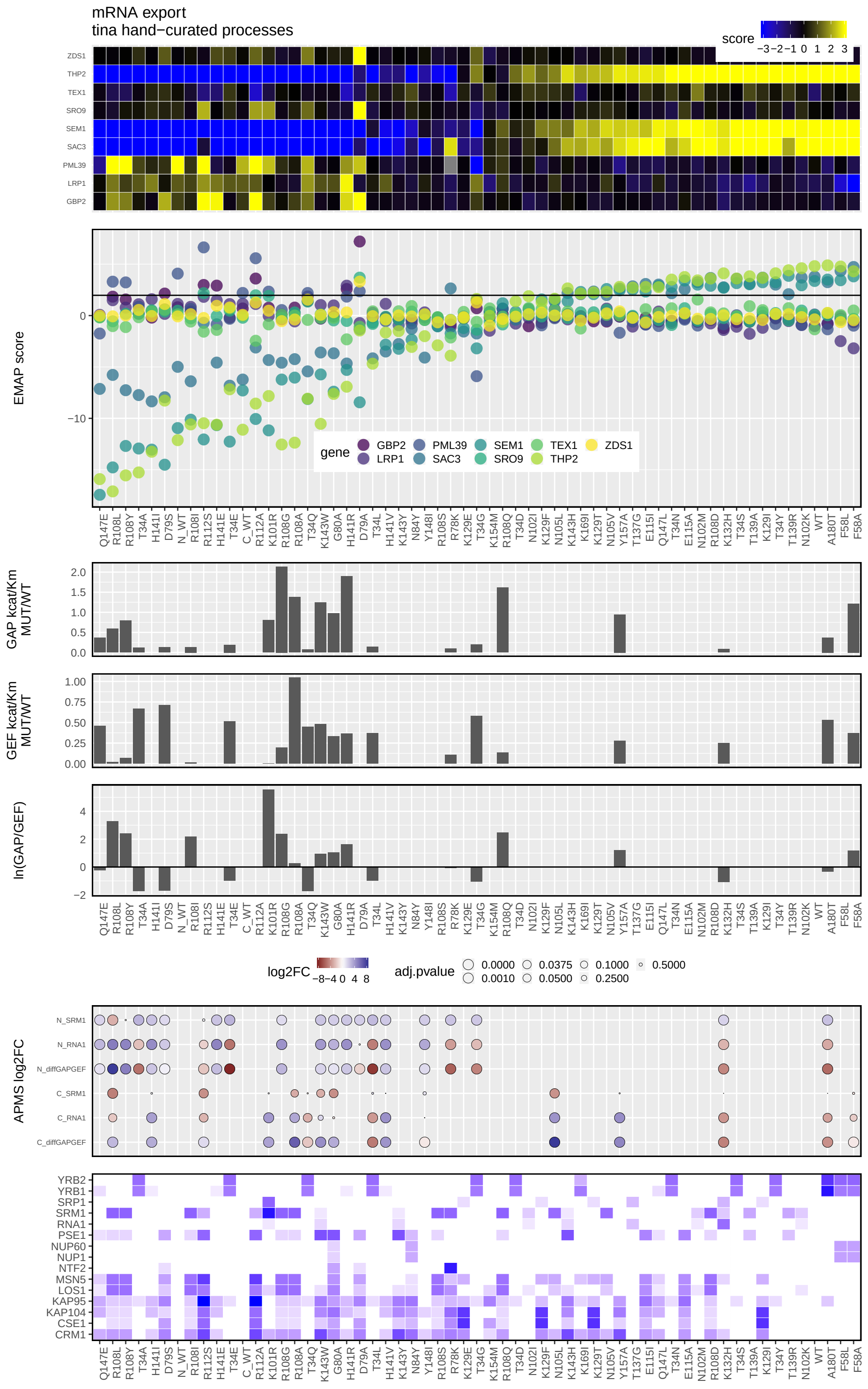

tRNA base modification
tina hand−curated processes
score
−3 −2 −1 0 1 2 3
KTI12
IKI1
ELP6
ELP4
ELP3
ELP2
DEG1
ATS1
EMAP score
gene
ATS1
DEG1
ELP2
ELP3
ELP4
ELP6
IKI1
KTI12
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141R R108G R108Y R108Q R112A R78K Y148I R112S R108A H141I R108S C_WT N105L H141E K132H R108L H141V K154M K129E N102K T137G T34S T34N WT N_WT Y157A T34L K143Y F58L K143W T139A N105V K143H N84Y R108D K129I R108I K169I T34A F58A N102I T34D K129F Q147L E115A E115I T139R T34Y K129T Q147E G80A N102M A180T D79S K101R T34Q T34E D79A T34G

tRNA splicing
tina hand−curated processes

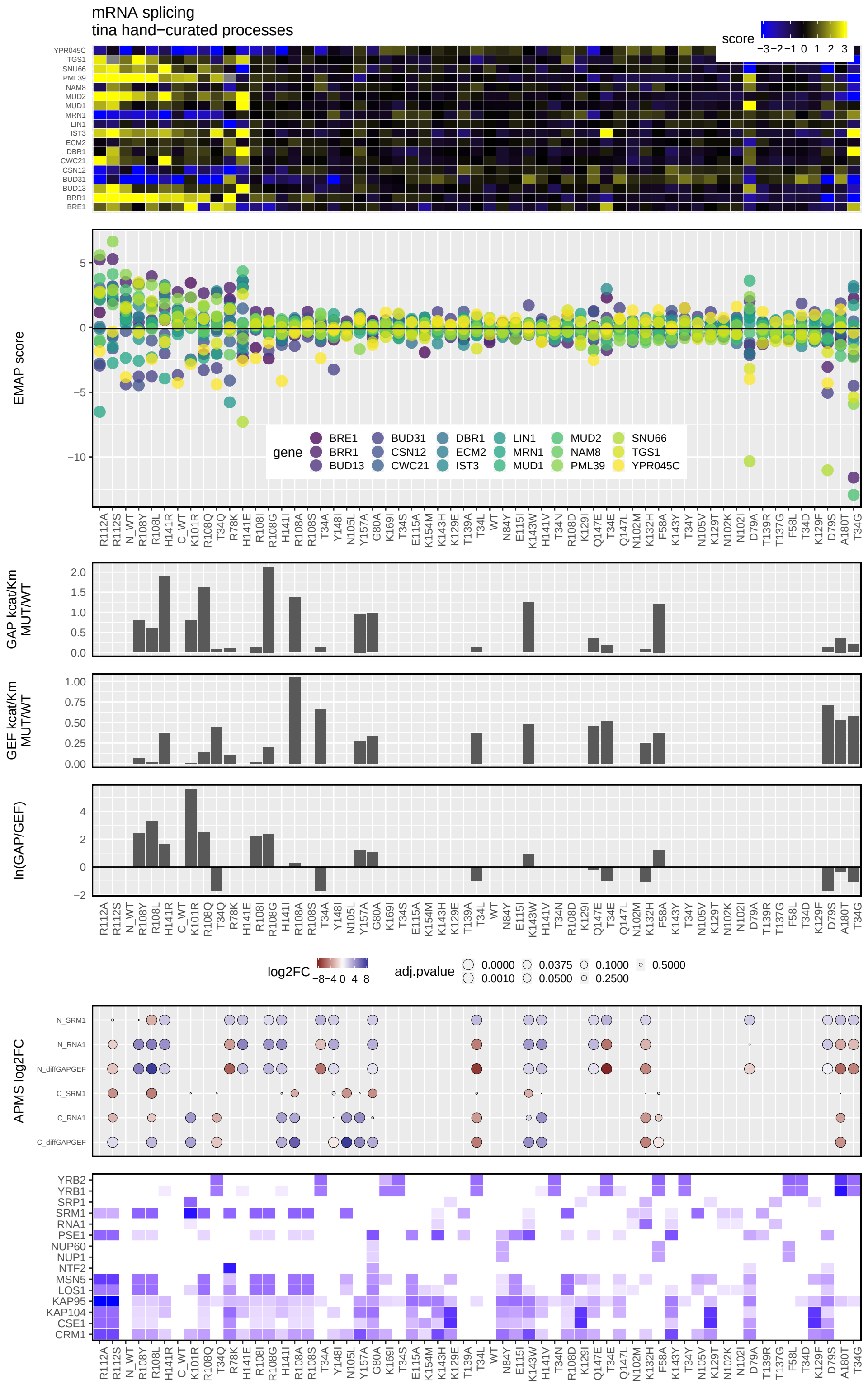


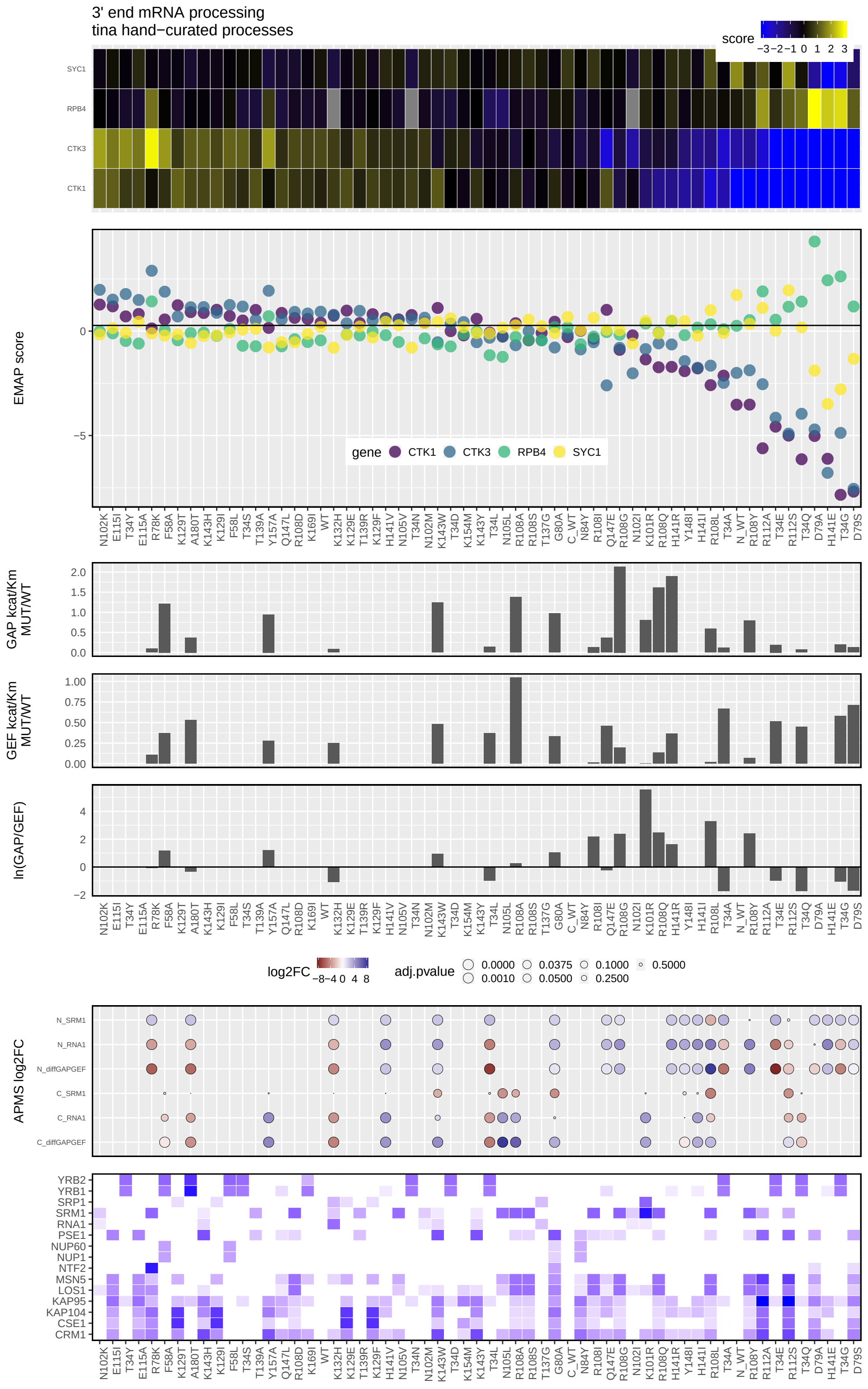
nuclear trasnport of tRNA
tina hand−curated processes



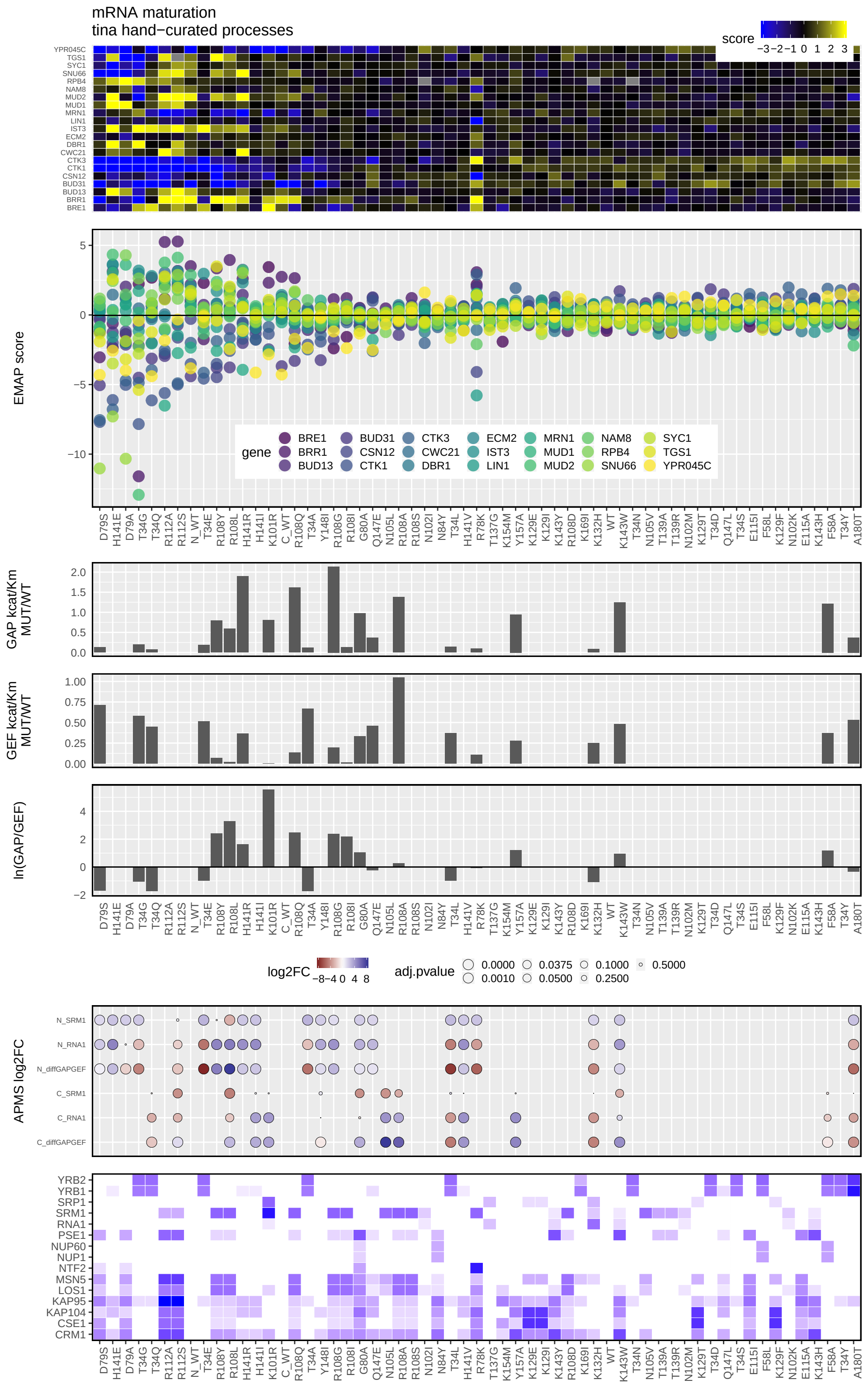

mRNA export
tina hand−curated processes
score
−3 −2 −1 0 1 2 3
ZDS1
THP2
TEX1
SRO9
SEM1
SAC3
PML39
LRP1
GBP2
EMAP score
0
−10
gene
GBP2
LRP1
PML39
SAC3
SEM1
SRO9
TEX1
THP2
ZDS1
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
Q147E R108L R108Y T34A H141I D79S N_WT R108I R112S H141E T34E C_WT R112A K101R R108G R108A T34Q K143W G80A H141R D79A T34L H141V K143Y N84Y Y148I R108S R78K K129E T34G K154M R108Q T34D N102I K129F N105L K143H K169I K129T N105V Y157A T137G E115I Q147L T34N E115A N102M R108D K132H T34S T139A K129I T34Y T139R N102K WT A180T F58L F58A
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

mRNA splicing
tina hand−curated processes

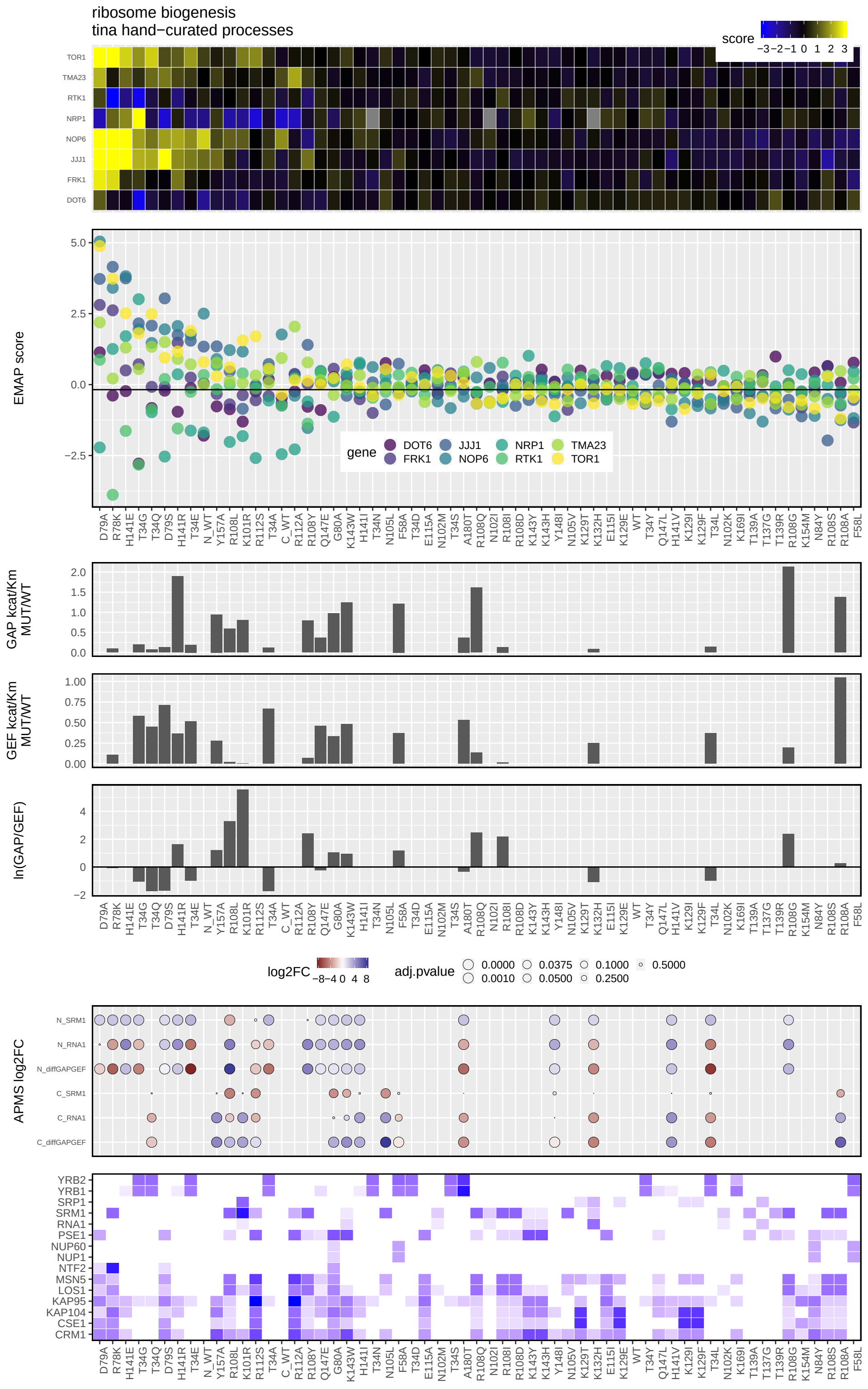



3' end mRNA processing
tina hand−curated processes
score
−3 −2 −1 0 1 2 3
SYC1
RPB4
CTK3
CTK1
EMAP score
gene CTK1 CTK3 RPB4 SYC1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N102K E115I T34Y E115A R78K F58A K129T A180T K143H K129I F58L T34S T139A Y157A Q147L R108D K169I WT K132H K129E T139R K129F H141V N105V T34N N102M K143W T34D K154M K143Y T34L N105L R108A R108S T137G G80A C_WT N84Y R108I Q147E R108G N102I K101R R108Q H141R Y148I H141I R108L T34A N_WT R108Y R112A T34E R112S T34Q D79A H141E T34G D79S

mRNA maturation
tina hand−curated processes



ribosome biogenesis
tina hand−curated processes



rRNA processing
tina hand−curated processes

score −3 −2 −1 0 1 2 3

TSR3
TSR2
SNU66
SLX9
RPS14A
RPL8B
RPL8A
RPL17B
NOP12
NGL2
DBP3
CGR1

EMAP score

gene: CGR1, DBP3, NGL2, NOP12, RPL17B, RPL8A, RPL8B, RPS14A, SLX9, SNU66, TSR2, TSR3

GAP kcat/Km MUT/WT

GEF kcat/Km MUT/WT

ln(GAP/GEF)

R108Y R112A R108Q R108G R108A R112S WT E115A T139A F58L N84Y K169I T137G T34S T34N Y148I F58A Q147L K154M H141R N102M T139R R108S T34Y R108D E115I K129F K129T N102I K143Y Y157A R108I K143H N102K A180T R108L N105V K129E T34D K129I T34L K143W K132H H141V H141I N105L C_WT R78K Q147E K101R N_WT G80A T34A T34Q T34E T34G D79A H141E D79S

log2FC −8 −4 0 4 8

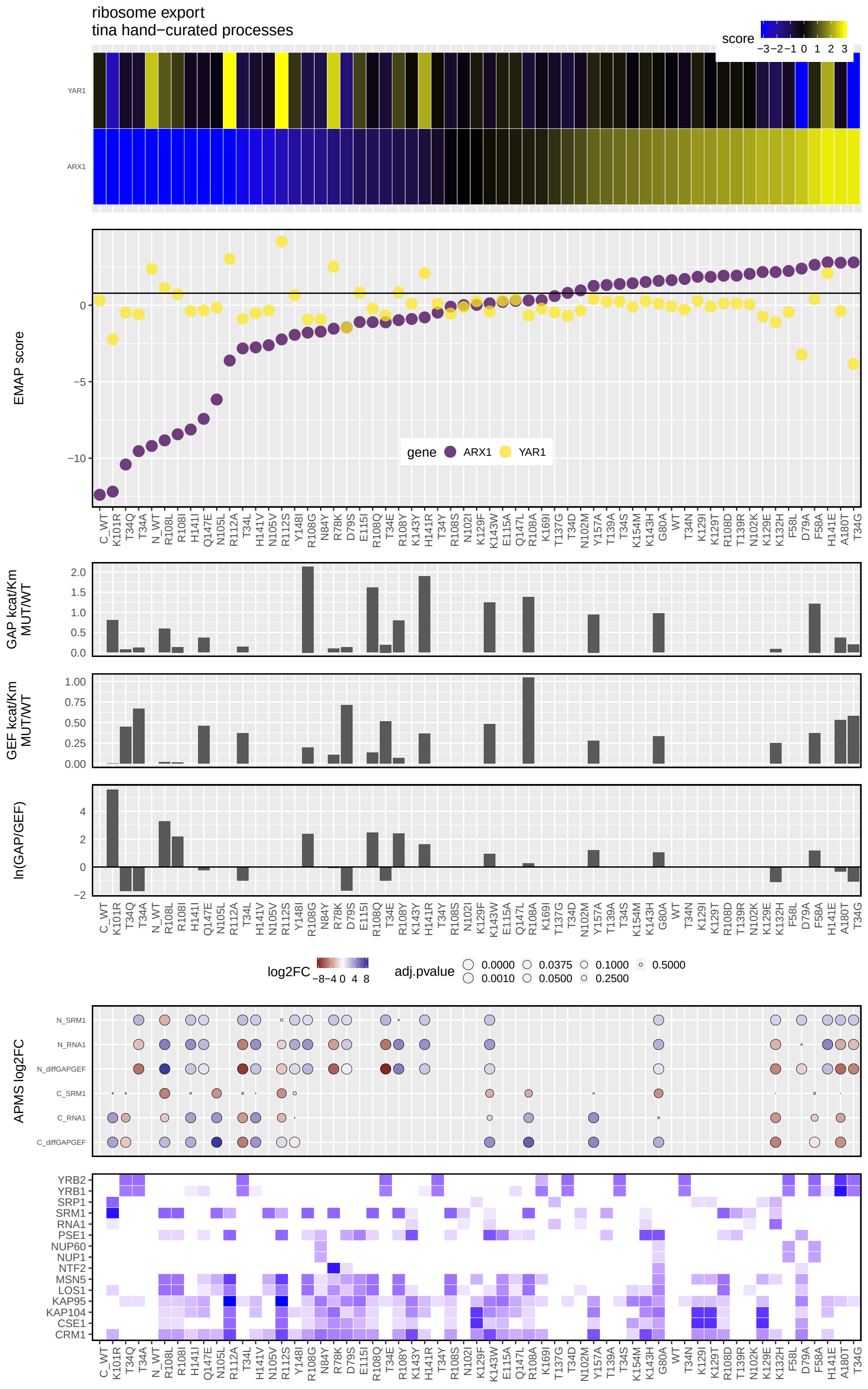
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000

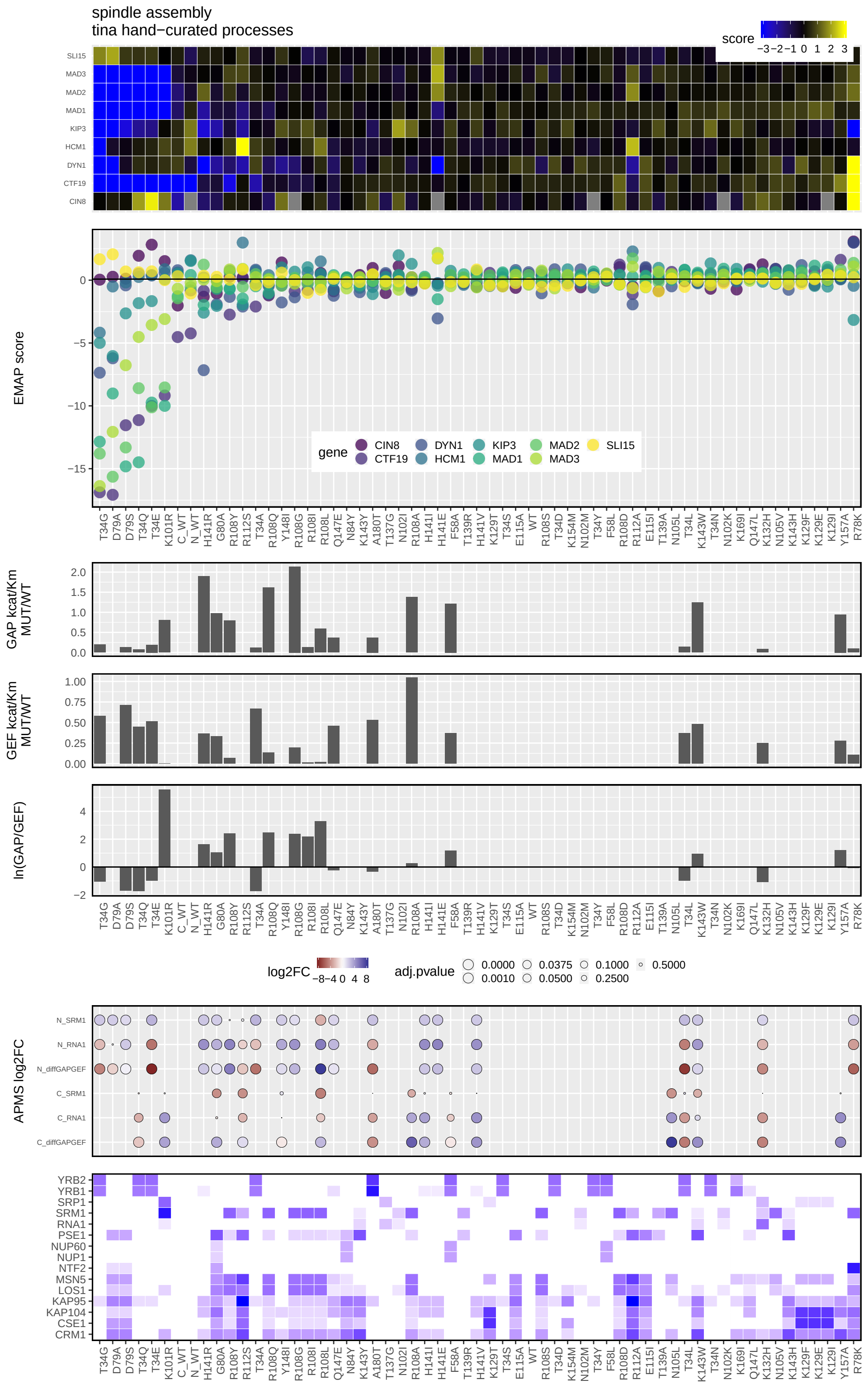
APMS log2FC

N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF

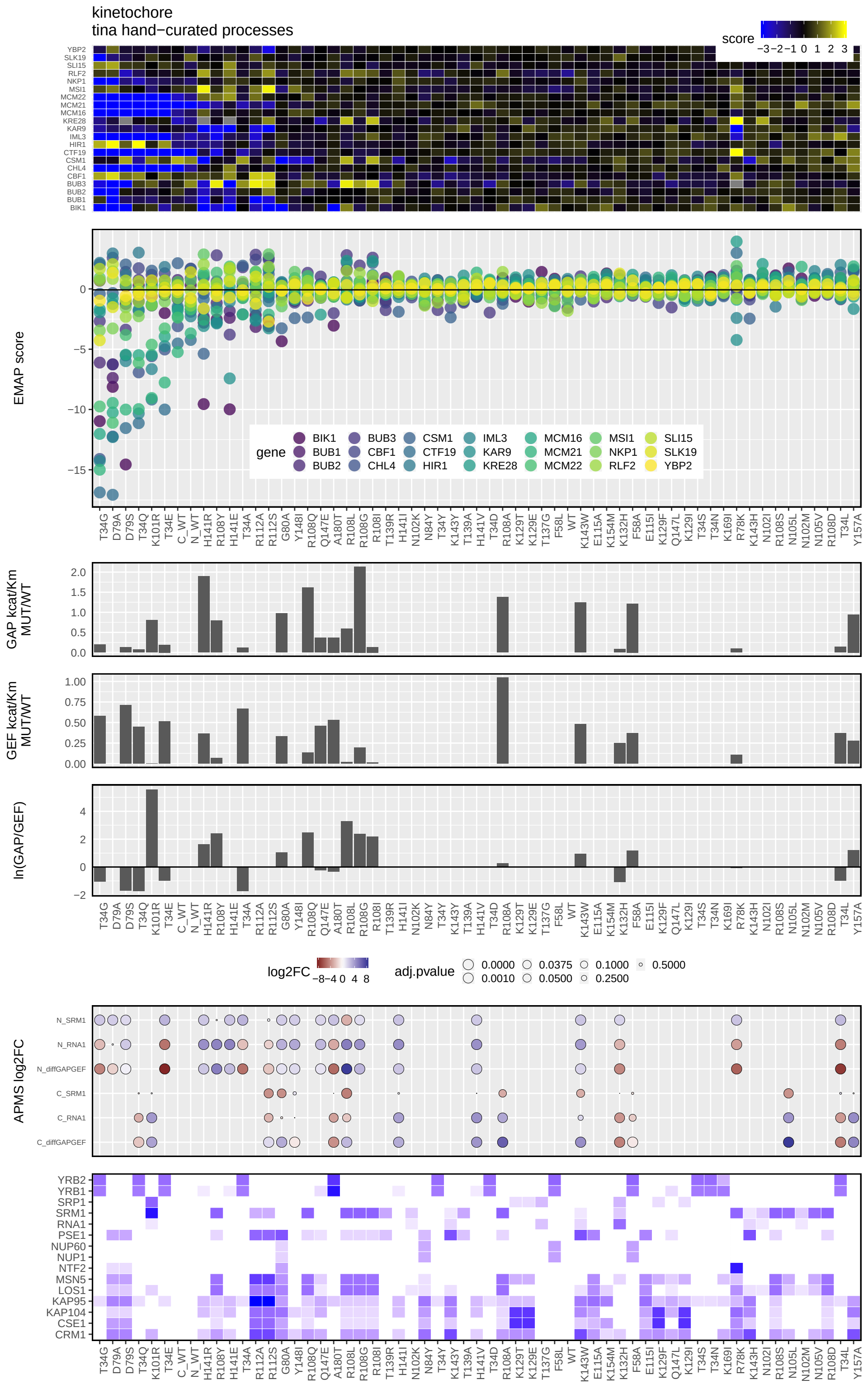
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

ribosome export
tina hand−curated processes

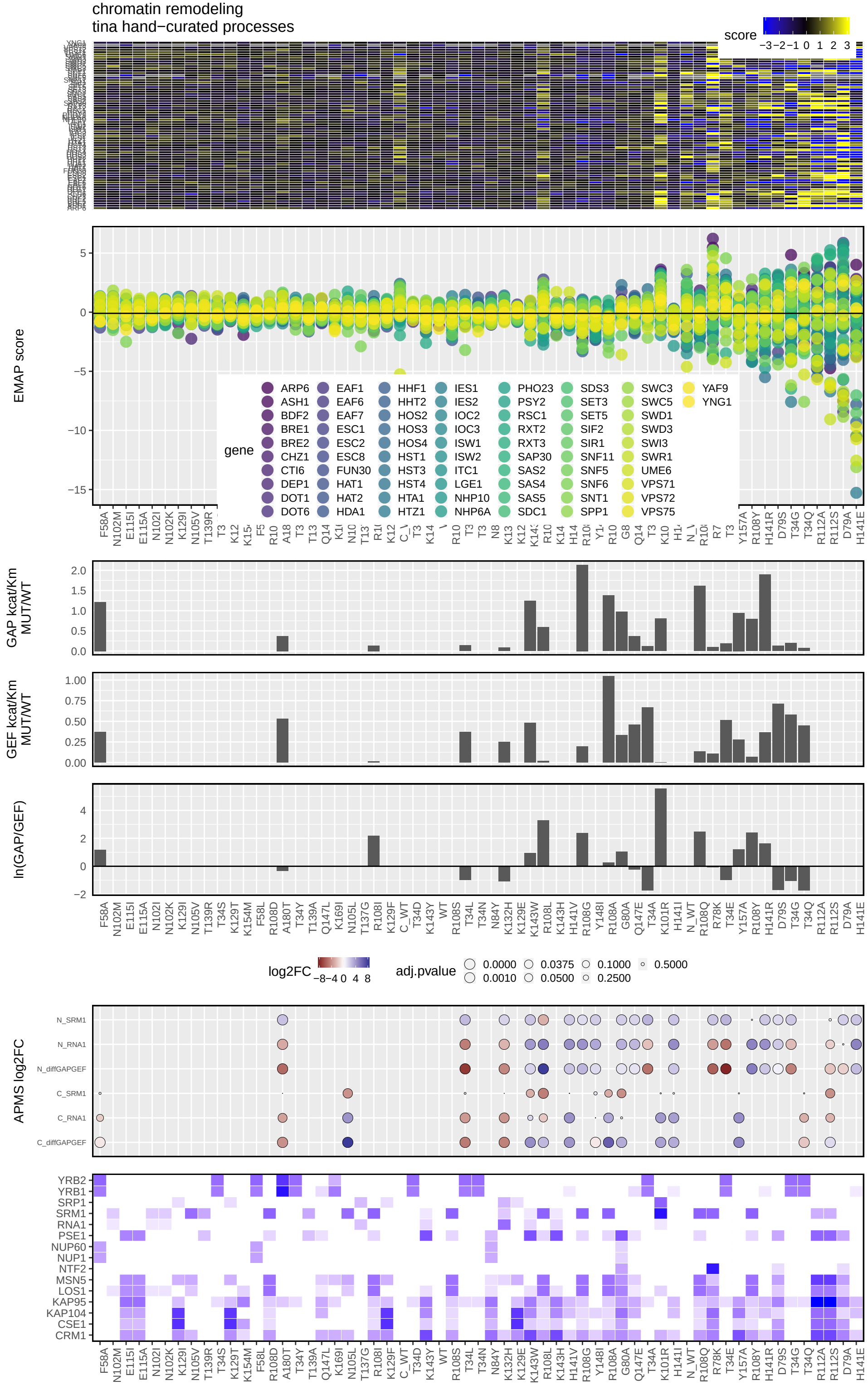


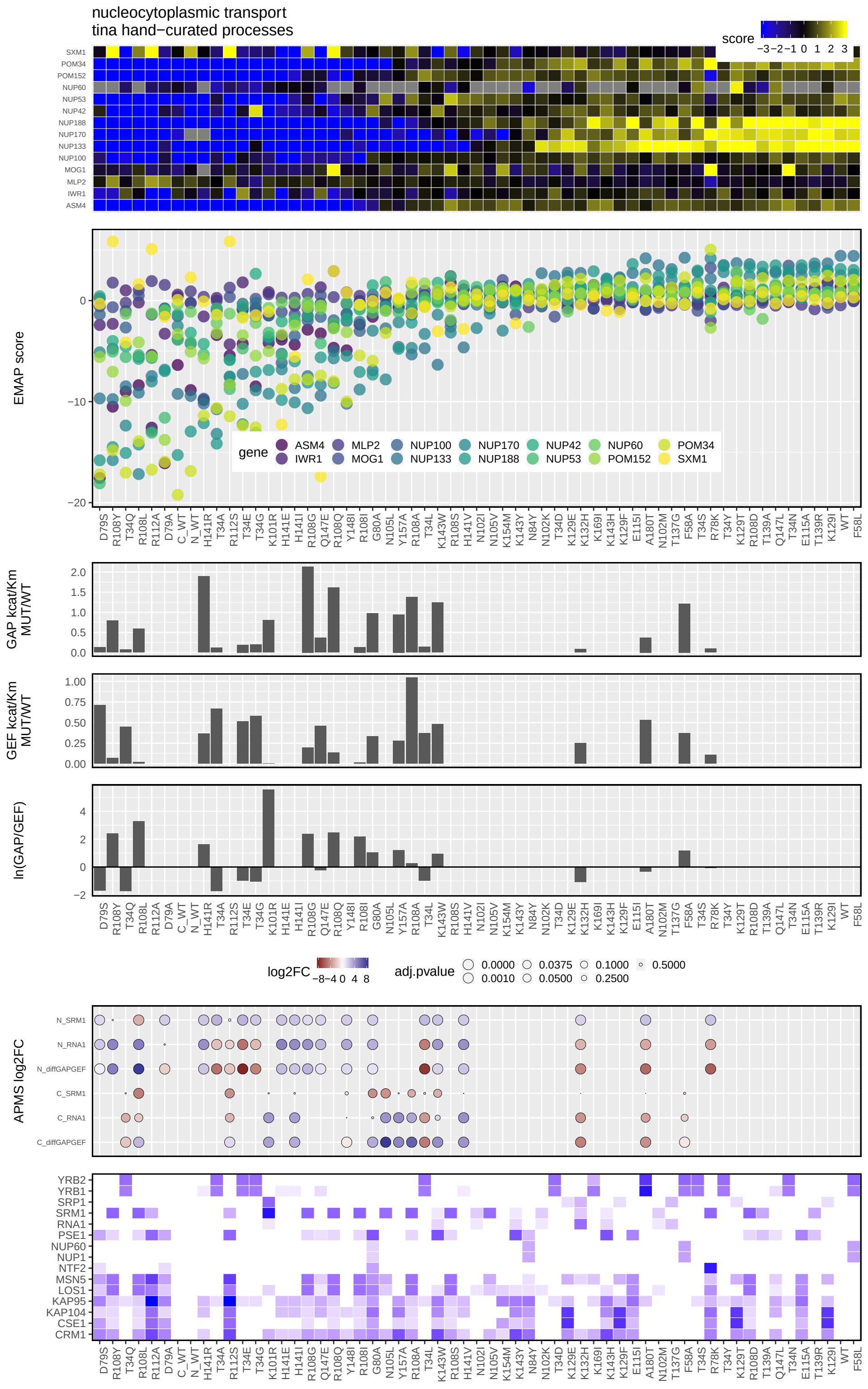

spindle assembly
tina hand−curated processes
score
−3 −2 −1 0 1 2 3
SLI15
MAD3
MAD2
MAD1
KIP3
HCM1
DYN1
CTF19
CIN8
EMAP score
gene
CIN8
CTF19
DYN1
HCM1
KIP3
MAD1
MAD2
MAD3
SLI15
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A D79S T34Q T34E K101R C_WT N_WT H141R G80A R108Y R112S T34A R108Q Y148I R108G R108I R108L Q147E N84Y K143Y A180T T137G N102I R108A H141I H141E F58A T139R H141V K129T T34S E115A WT R108S T34D K154M N102M T34Y F58L R108D R112A E115I T139A N105L T34L K143W T34N N102K K169I Q147L K132H N105V K143H K129F K129E K129I Y157A R78K

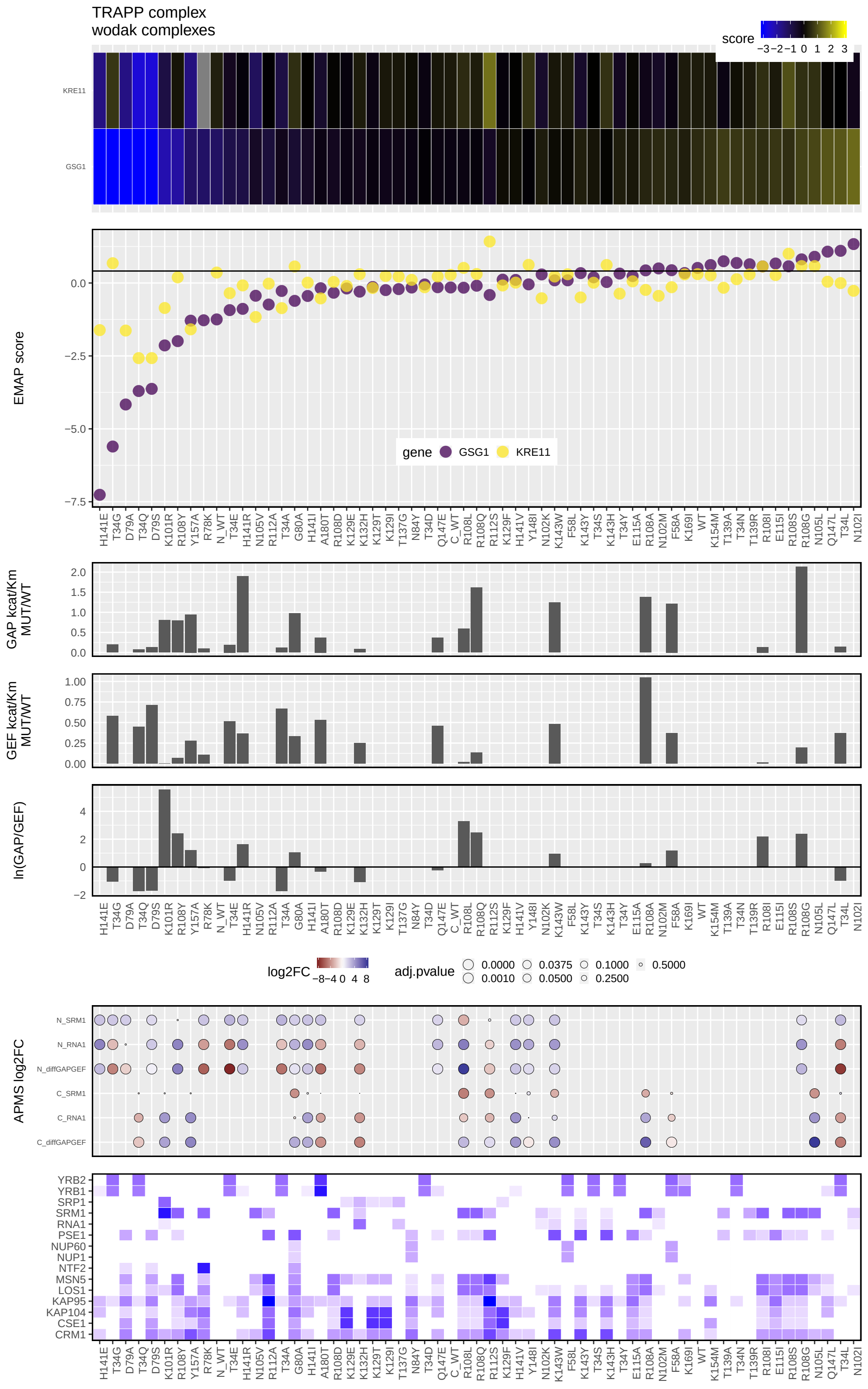
kinetochore
tina hand−curated processes

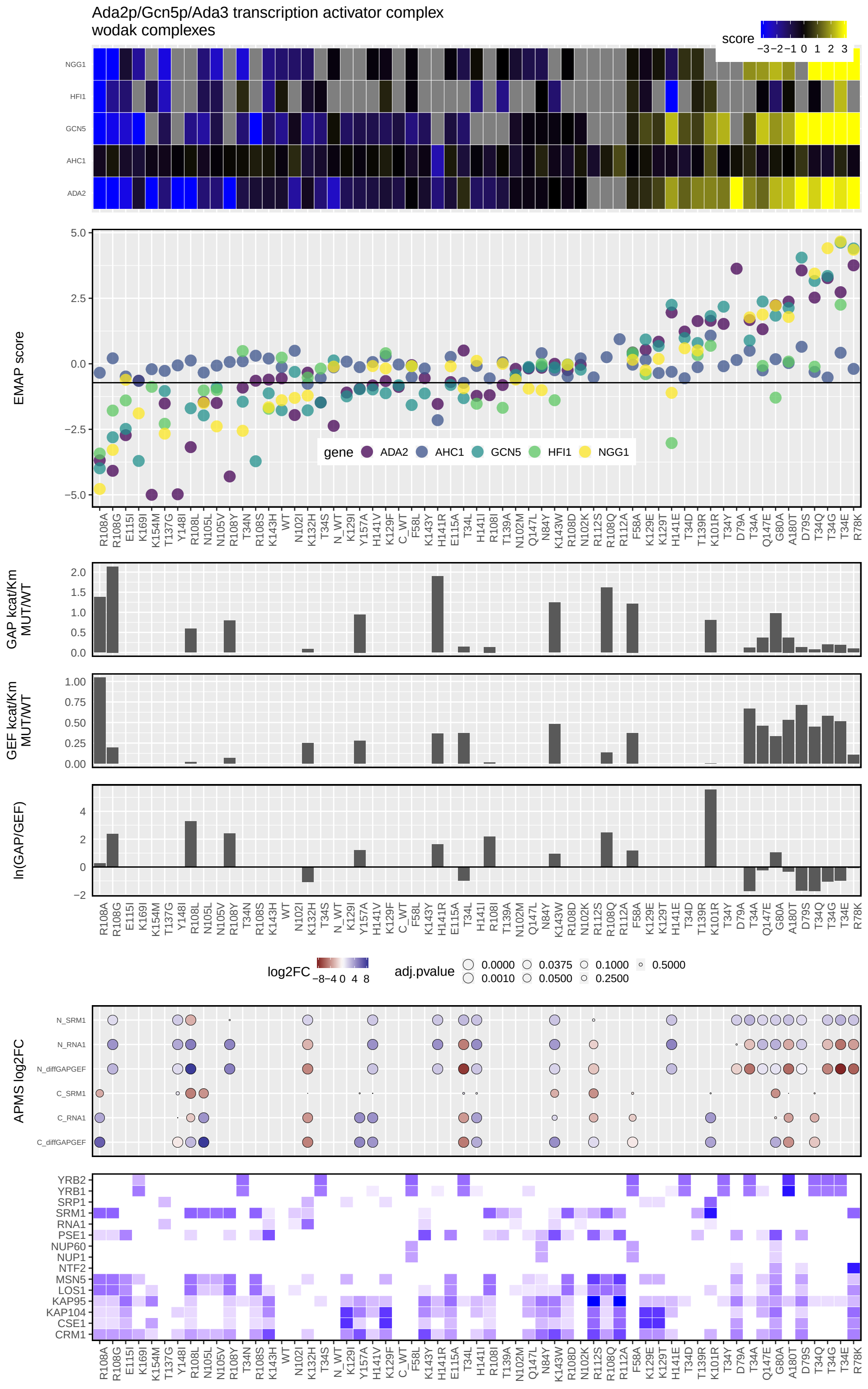


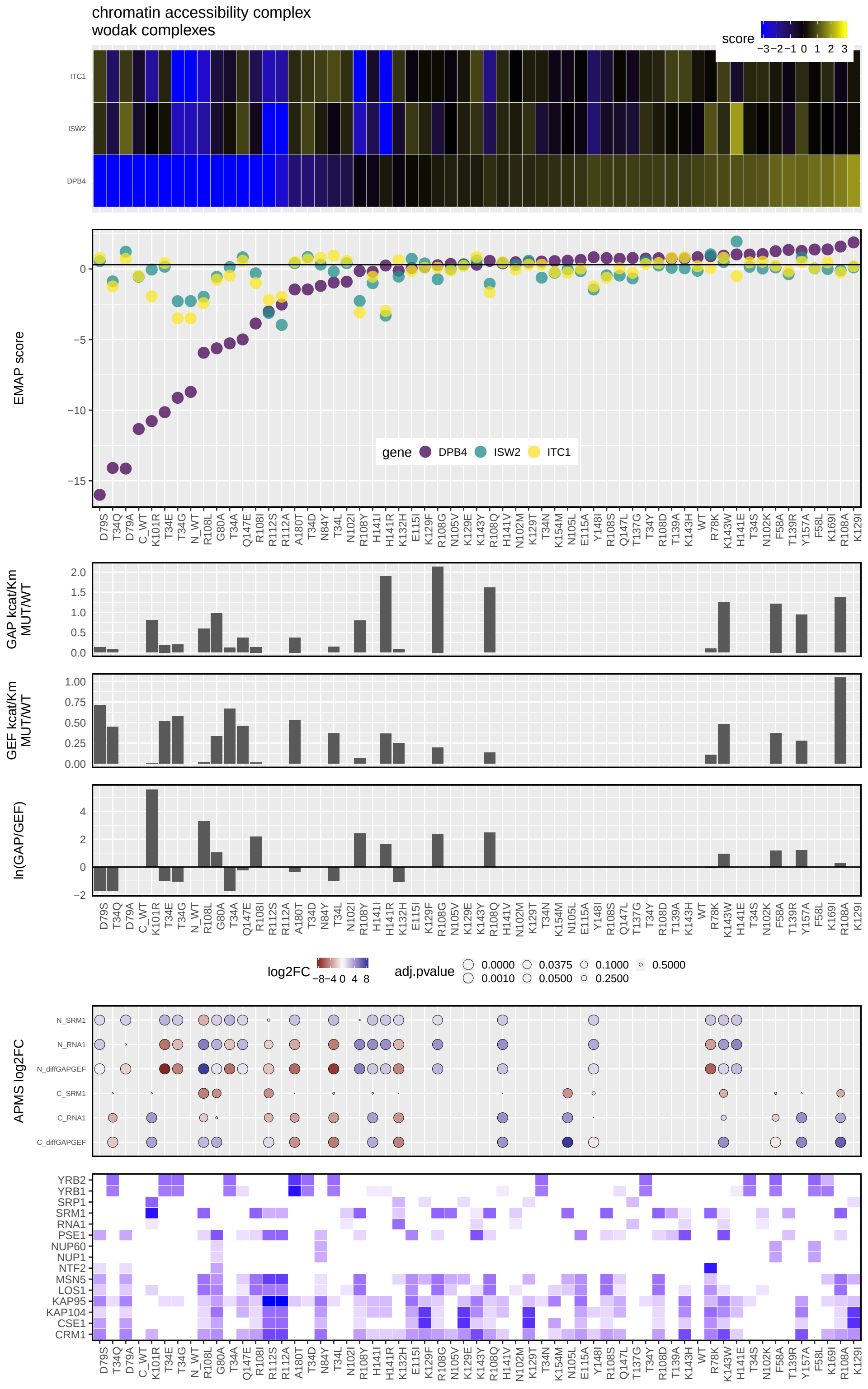
chromatin remodeling
tina hand−curated processes

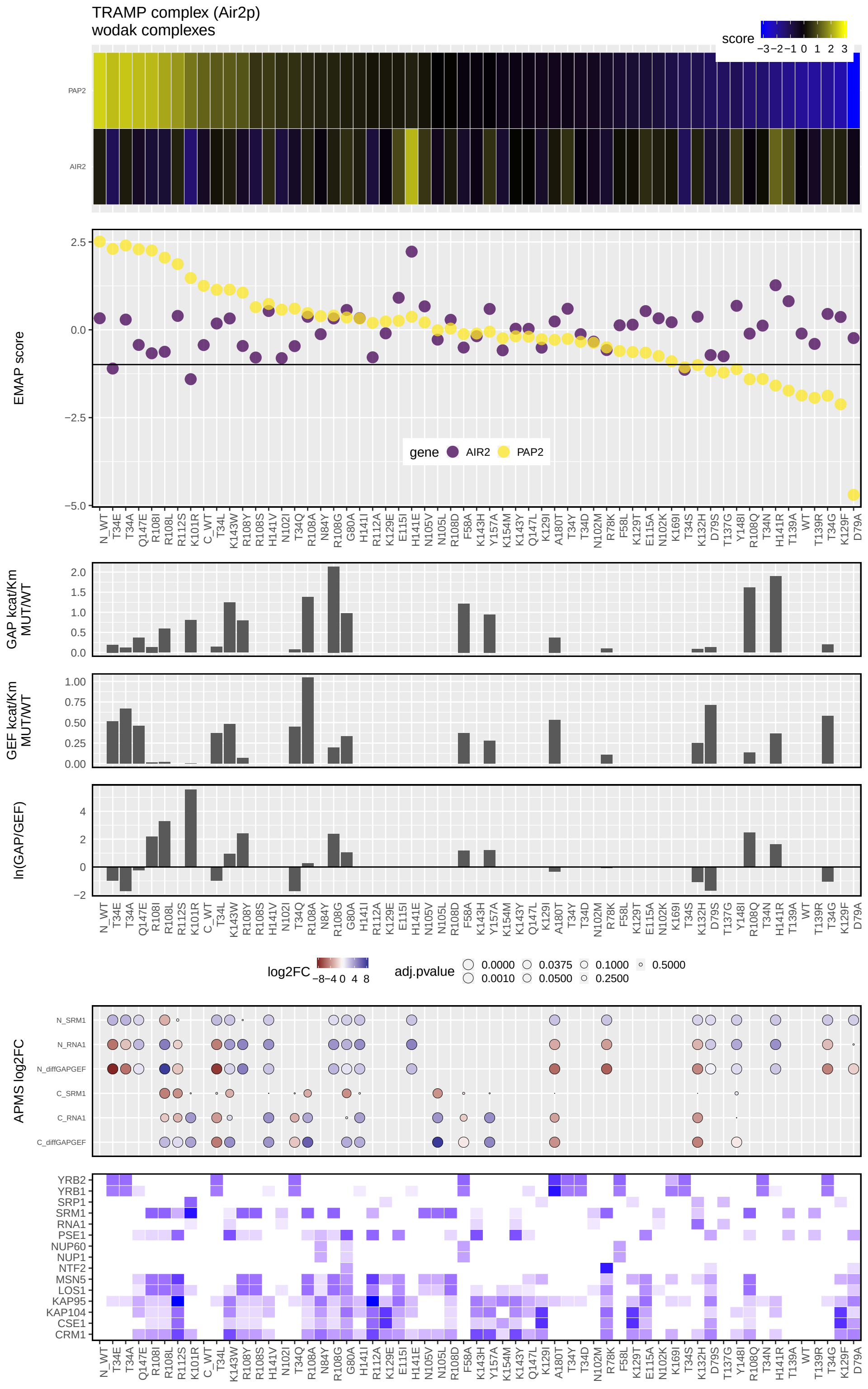


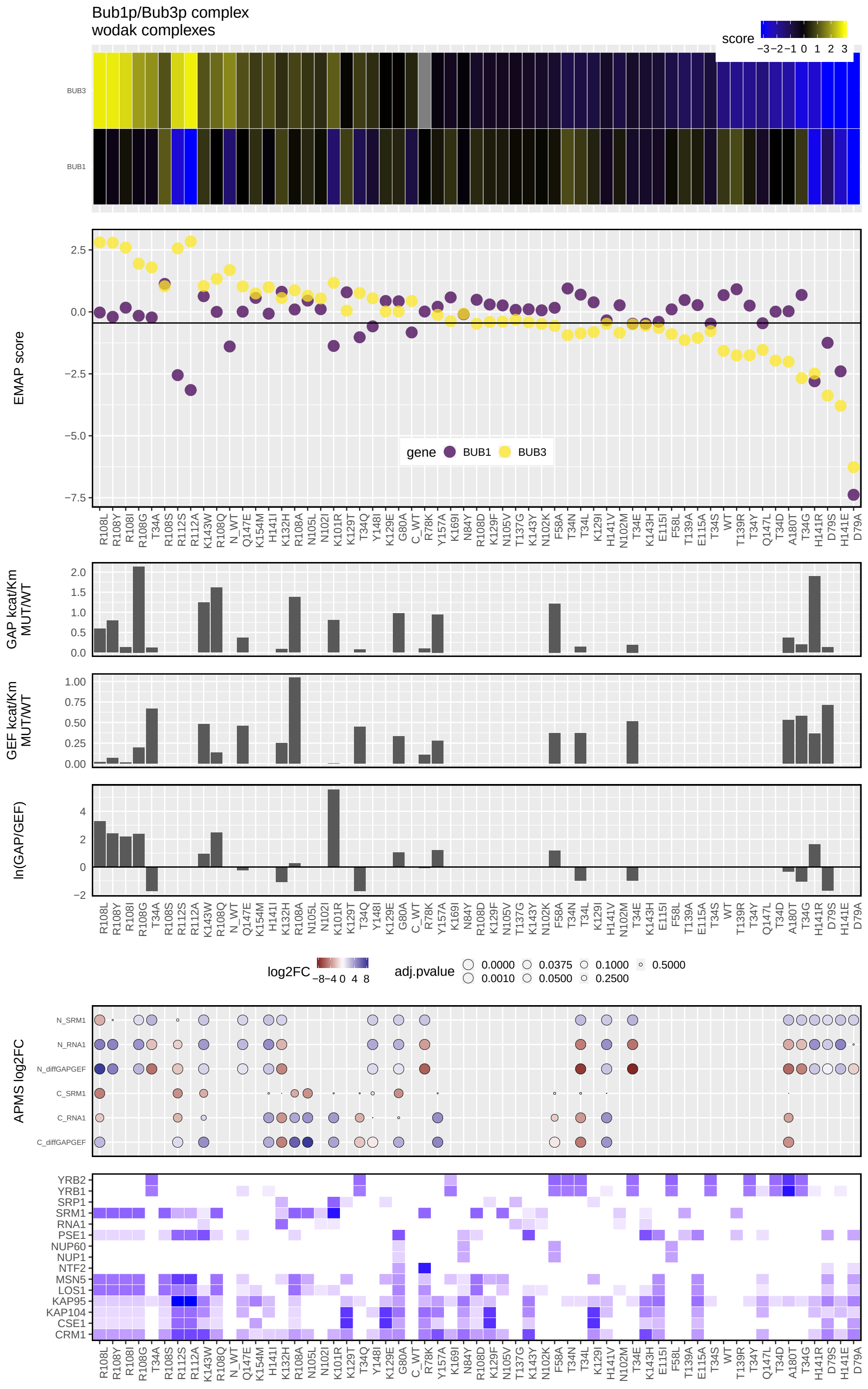

nucleocytoplasmic transport
tina hand−curated processes
score
−3 −2 −1 0 1 2 3
SXM1
POM34
POM152
NUP60
NUP53
NUP42
NUP188
NUP170
NUP133
NUP100
MOG1
MLP2
IWR1
ASM4
EMAP score
gene
ASM4 MLP2 NUP100 NUP170 NUP42 NUP60 POM34
IWR1 MOG1 NUP133 NUP188 NUP53 POM152 SXM1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

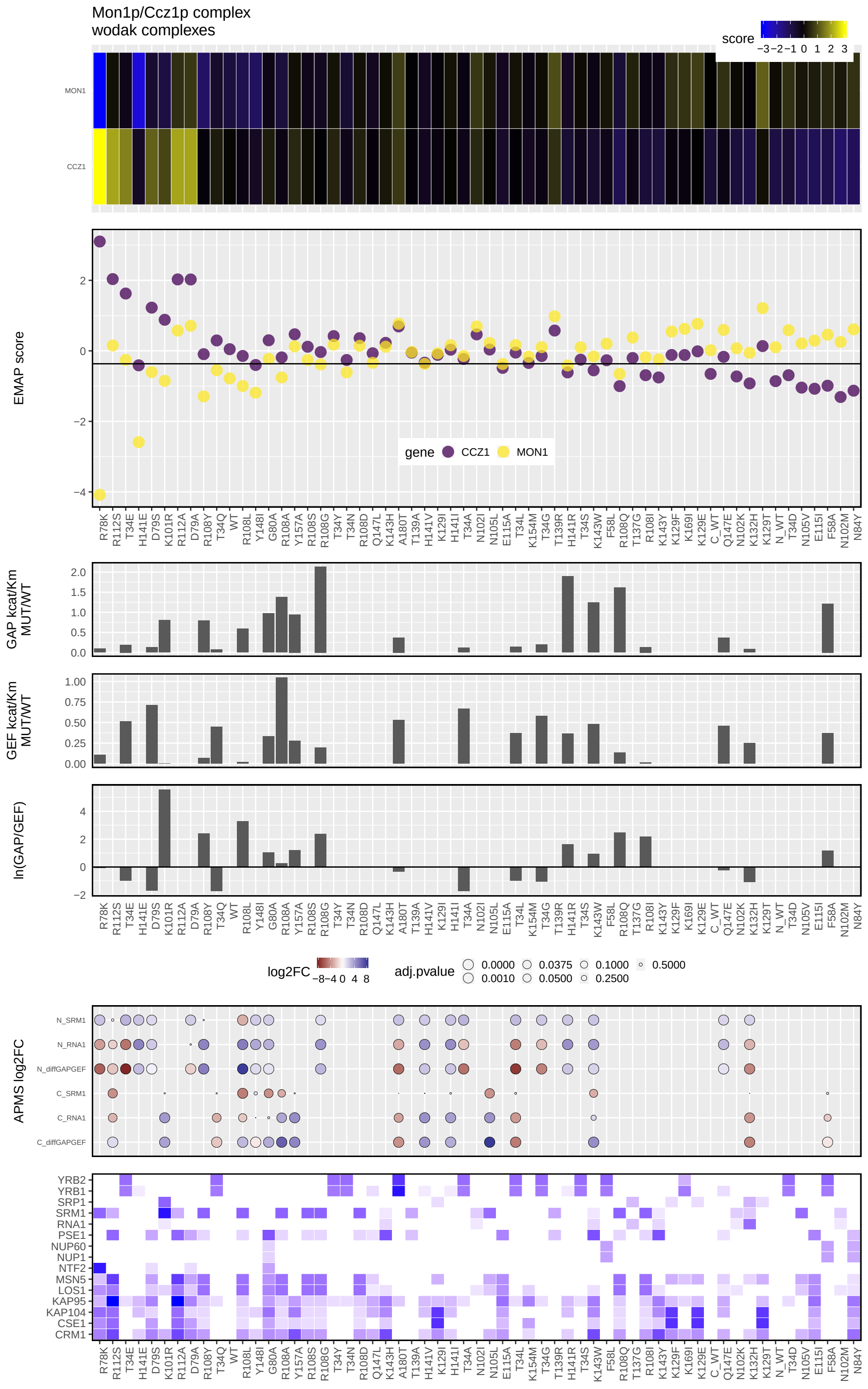

TRAPP complex
wodak complexes
score
−3 −2 −1 0 1 2 3
KRE11
GSG1
EMAP score
0.0
−2.5
−5.0
−7.5
gene
GSG1
KRE11
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E T34G D79A T34Q D79S K101R R108Y Y157A R78K N_WT T34E H141R N105V R112A T34A G80A H141I A180T R108D K129E K132H K129T K129I T137G N84Y T34D Q147E C_WT R108L R108Q R112S K129F H141V Y148I N102K K143W F58L K143Y T34S K143H T34Y E115A R108A N102M F58A K169I WT K154M T139A T34N T139R R108I E115I R108S R108G N105L Q147L T34L N102I

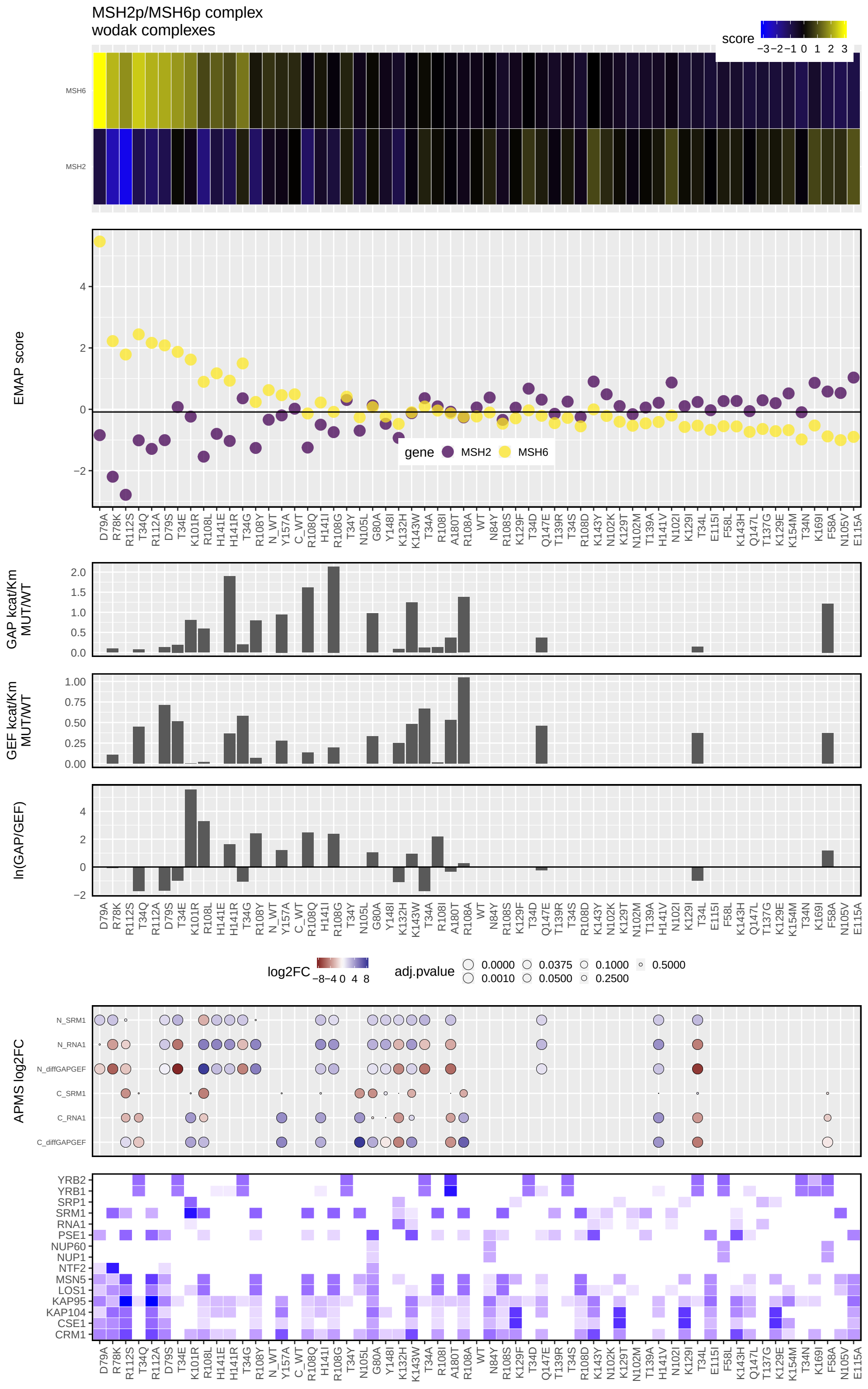

Ada2p/Gcn5p/Ada3 transcription activator complex
wodak complexes
score
−3 −2 −1 0 1 2 3
NGG1
HFI1
GCN5
AHC1
ADA2
EMAP score
5.0
2.5
0.0
−2.5
−5.0
gene
ADA2
AHC1
GCN5
HFI1
NGG1
R108A R108G E115I K169I K154M T137G Y148I R108L N105L N105V R108Y T34N R108S K143H WT N102I K132H T34S N_WT K129I Y157A H141V K129F C_WT F58L K143Y H141R E115A T34L H141I R108I T139A N102M Q147L N84Y K143W R108D N102K R112S R108Q R112A F58A K129E K129T H141E T34D T139R K101R T34Y D79A T34A Q147E G80A A180T D79S T34Q T34G T34E R78K
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

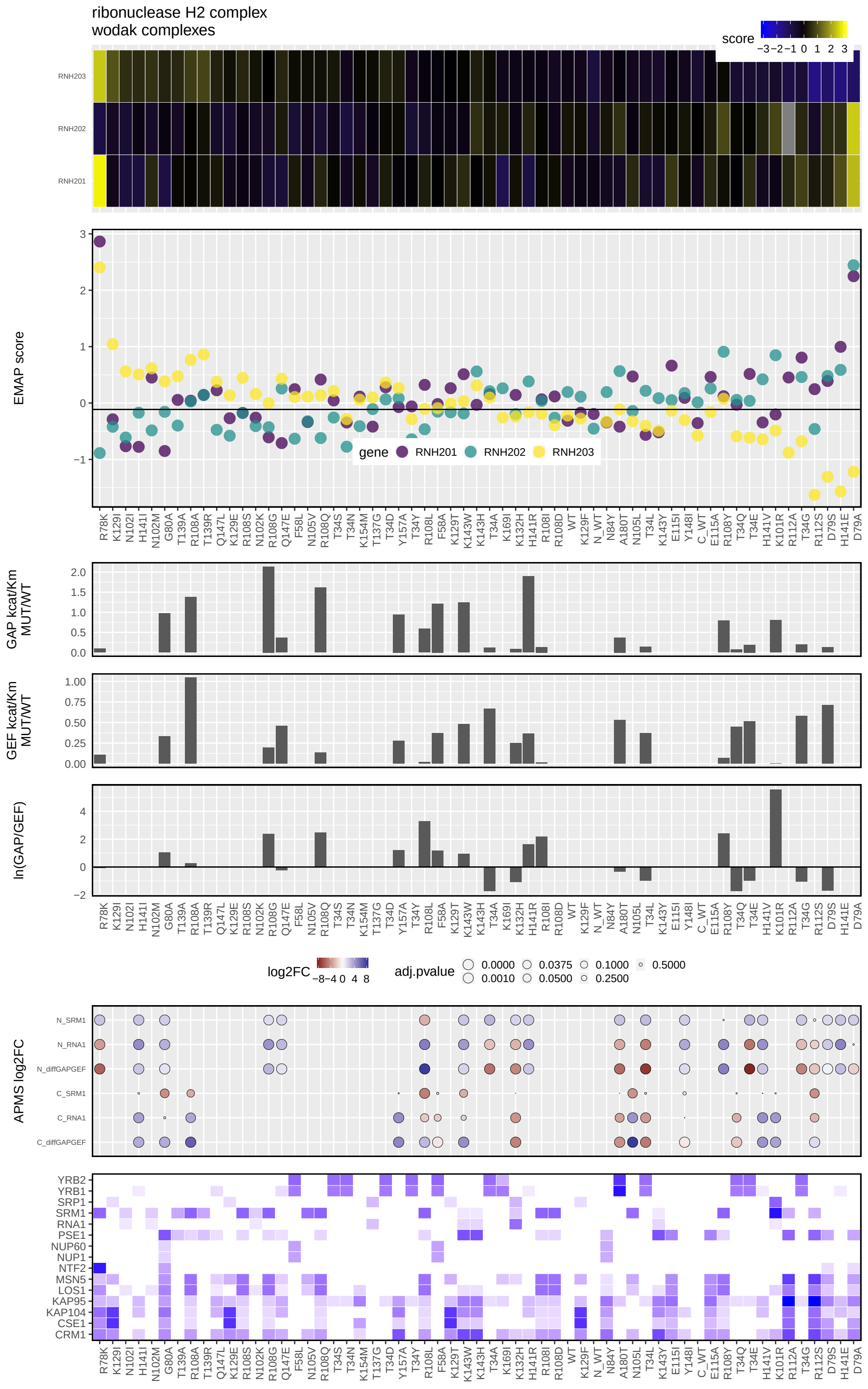

chromatin accessibility complex
wodak complexes
score
−3 −2 −1 0 1 2 3
ITC1
ISW2
DPB4
EMAP score
gene DPB4 ISW2 ITC1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79S T34Q D79A C_WT K101R T34E T34G N_WT R108L G80A T34A Q147E R108I R112S R112A A180T T34D N84Y T34L N102I R108Y H141I H141R K132H E115I K129F R108G N105V K129E K143Y R108Q H141V N102M K129T T34N K154M N105L E115A Y148I R108S Q147L T137G T34Y R108D T139A K143H WT R78K K143W H141E T34S N102K F58A T139R Y157A F58L K169I R108A K129I

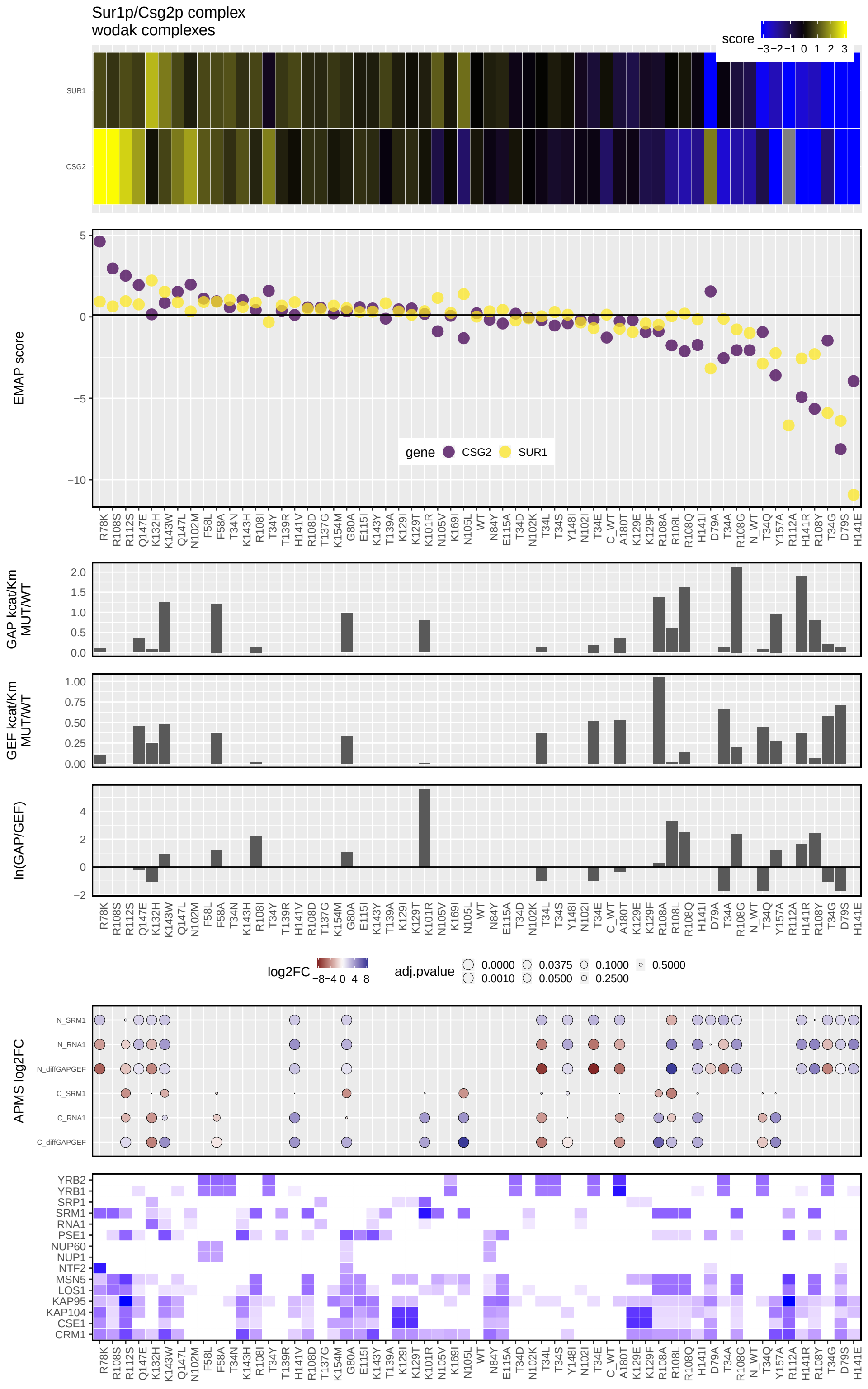

TRAMP complex (Air2p)
wodak complexes
score
−3 −2 −1 0 1 2 3
PAP2
AIR2
EMAP score
gene
AIR2
PAP2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N_WT T34E T34A Q147E R108I R108L R112S K101R C_WT T34L K143W R108Y R108S H141V N102I T34Q R108A N84Y R108G G80A H141I R112A K129E E115I H141E N105V N105L R108D F58A K143H Y157A K154M K143Y Q147L K129I A180T T34Y T34D N102M R78K F58L K129T E115A N102K K169I T34S K132H D79S T137G Y148I R108Q T34N H141R T139A WT T139R T34G K129F D79A

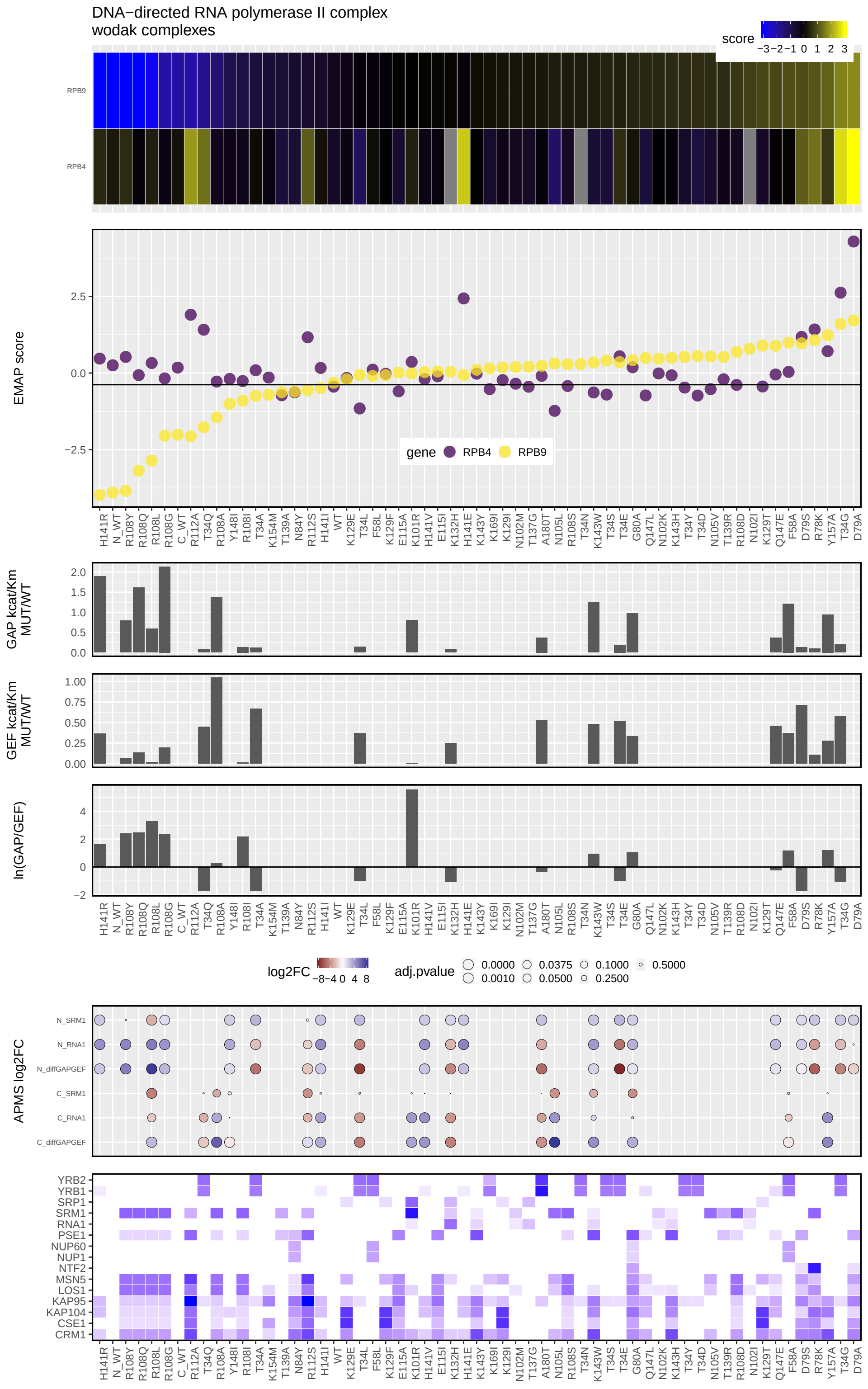

Bub1p/Bub3p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
BUB3
BUB1
EMAP score
gene
BUB1
BUB3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108L R108Y R108I R108G T34A R108S R112S R112A K143W R108Q N_WT Q147E K154M H141I K132H R108A N105L N102I K101R K129T T34Q Y148I K129E G80A C_WT R78K Y157A K169I N84Y R108D K129F N105V T137G K143Y N102K F58A T34N T34L K129I H141V N102M T34E K143H E115I F58L T139A E115A T34S WT T139R T34Y Q147L T34D A180T T34G H141R D79S H141E D79A

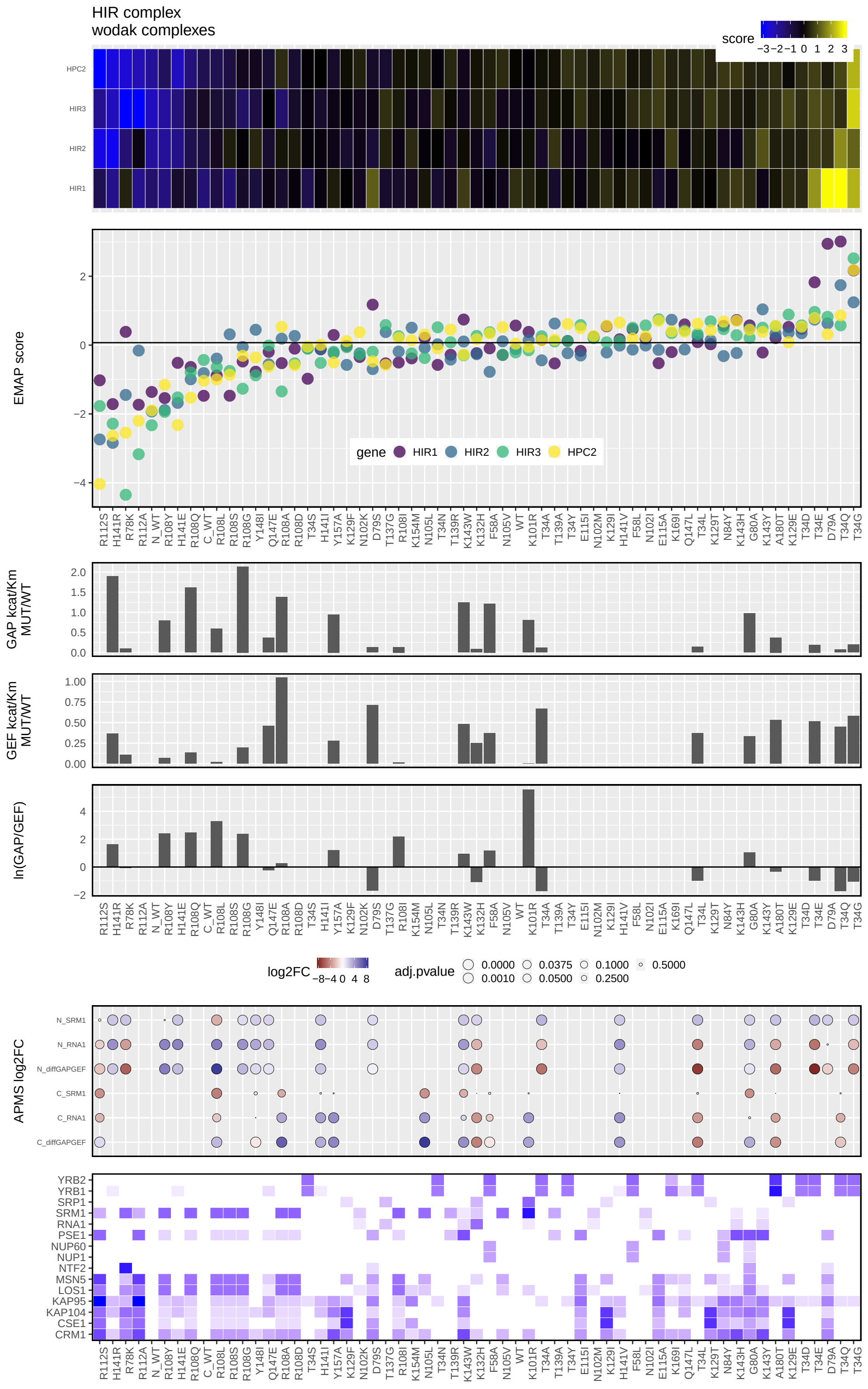

Mon1p/Ccz1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MON1
CCZ1
EMAP score
gene CCZ1 MON1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K R112S T34E H141E D79S K101R R112A D79A R108Y T34Q WT R108L Y148I G80A R108A Y157A R108S R108G T34Y T34N R108D Q147L K143H A180T T139A H141V K129I H141I T34A N102I N105L E115A T34L K154M T34G T139R H141R T34S K143W F58L R108Q T137G R108I K143Y K129F K169I K129E C_WT Q147E N102K K132H K129T N_WT T34D N105V E115I F58A N102M N84Y


MSH2p/MSH6p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MSH6
MSH2
EMAP score
gene
MSH2
MSH6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R78K R112S T34Q R112A D79S T34E K101R R108L H141E H141R T34G R108Y N_WT Y157A C_WT R108Q H141I R108G T34Y N105L G80A Y148I K132H K143W T34A R108I A180T R108A WT N84Y R108S K129F T34D Q147E T139R T34S R108D K143Y N102K K129T N102M T139A H141V N102I K129I T34L E115I F58L K143H Q147L T137G K129E K154M T34N K169I F58A N105V E115A

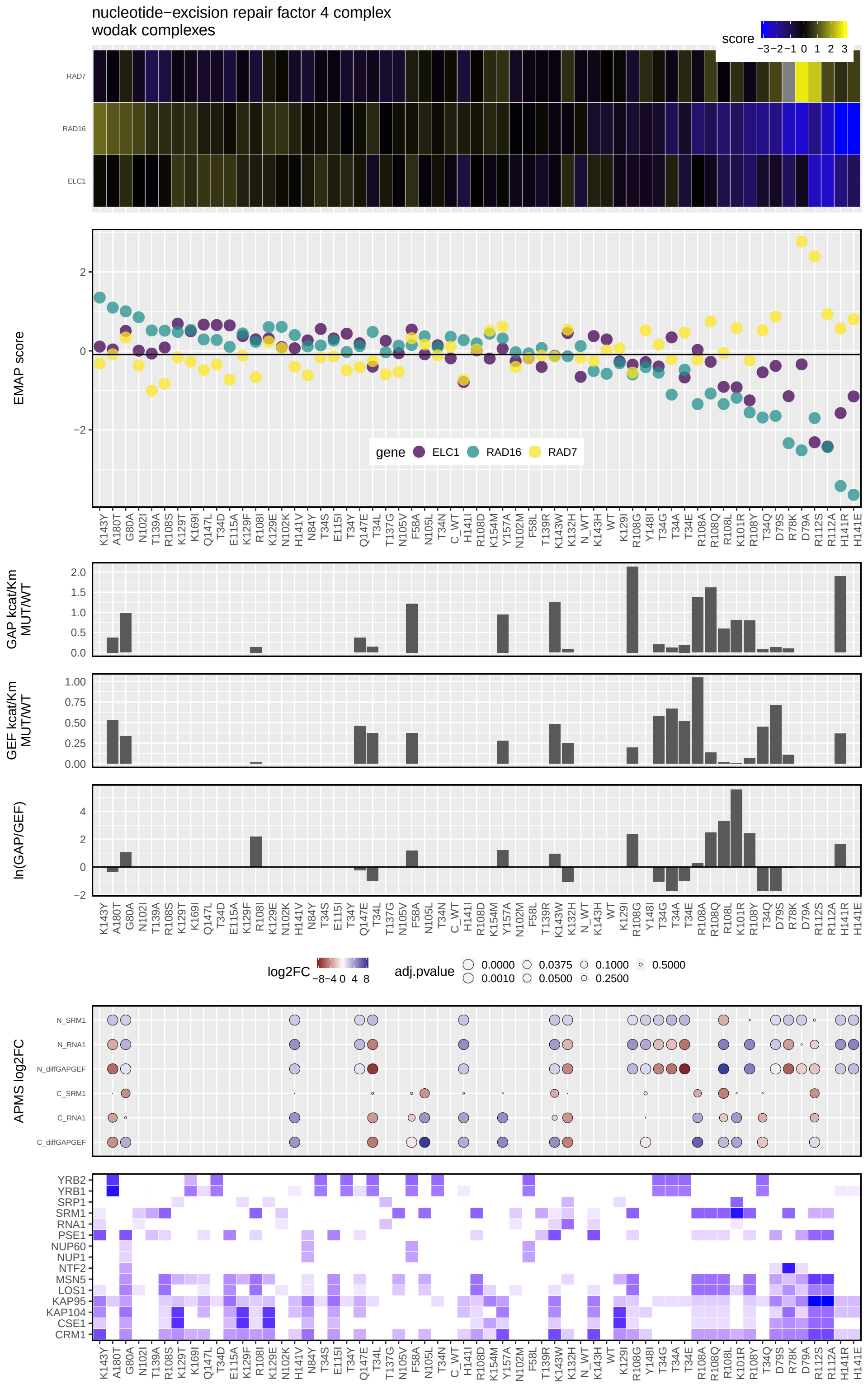

ribonuclease H2 complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RNH203
RNH202
RNH201
EMAP score
gene
RNH201
RNH202
RNH203
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K K129I N102I H141I N102M G80A T139A R108A T139R Q147L K129E R108S N102K R108G Q147E F58L N105V R108Q T34S T34N K154M T137G T34D Y157A T34Y R108L F58A K129T K143W K143H T34A K169I K132H H141R R108I R108D WT K129F N_WT N84Y A180T N105L T34L K143Y E115I Y148I C_WT E115A R108Y T34Q T34E H141V K101R R112A T34G R112S D79S H141E D79A

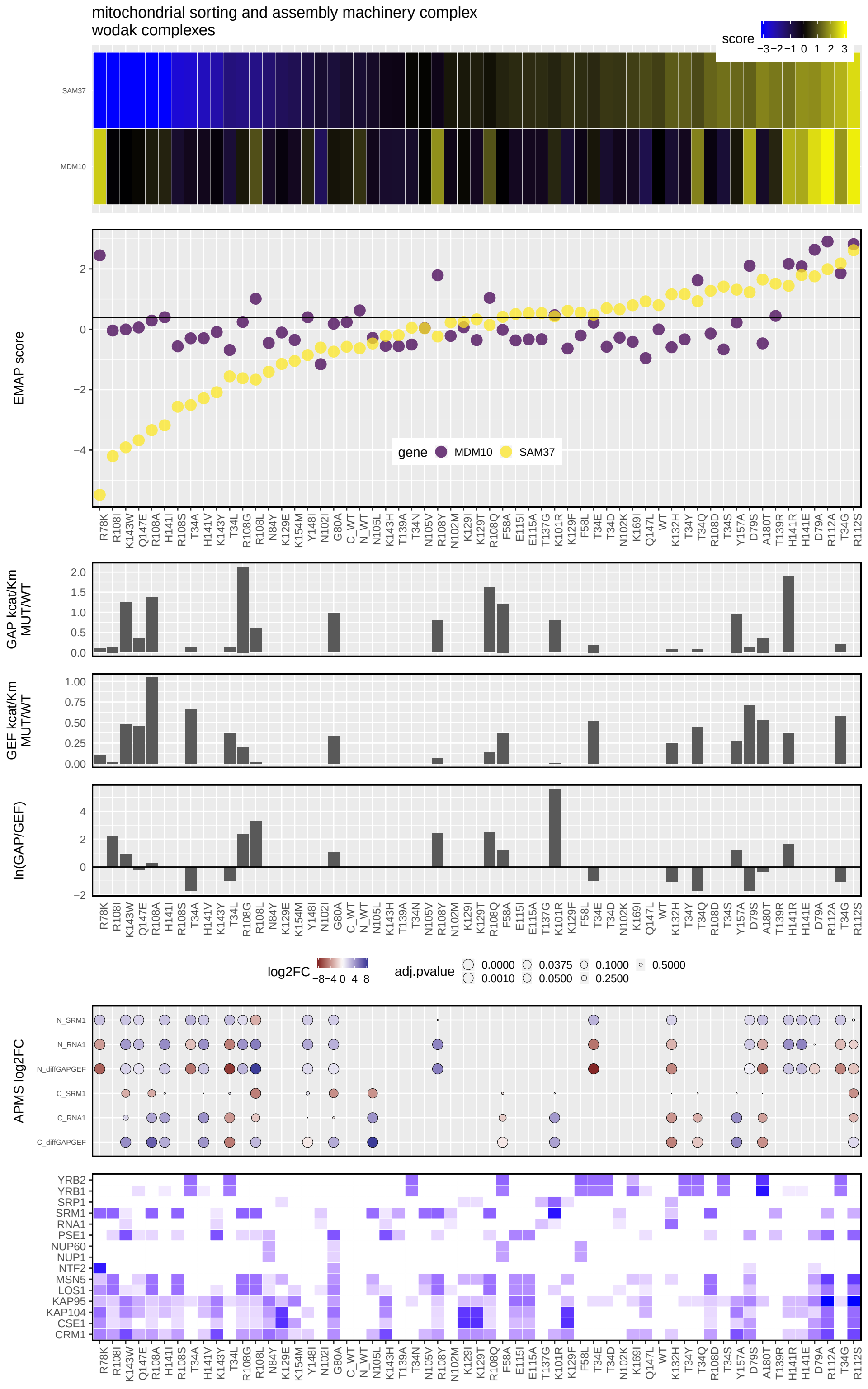

Sur1p/Csg2p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SUR1
CSG2
EMAP score
gene CSG2 SUR1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K R108S R112S Q147E K132H K143W Q147L N102M F58L F58A T34N K143H R108I T34Y T139R H141V R108D T137G K154M G80A E115I K143Y T139A K129I K129T K101R N105V K169I N105L WT N84Y E115A T34D N102K T34L T34S Y148I N102I T34E C_WT A180T K129E K129F R108A R108L R108Q H141I D79A T34A R108G N_WT T34Q Y157A R112A H141R R108Y T34G D79S H141E

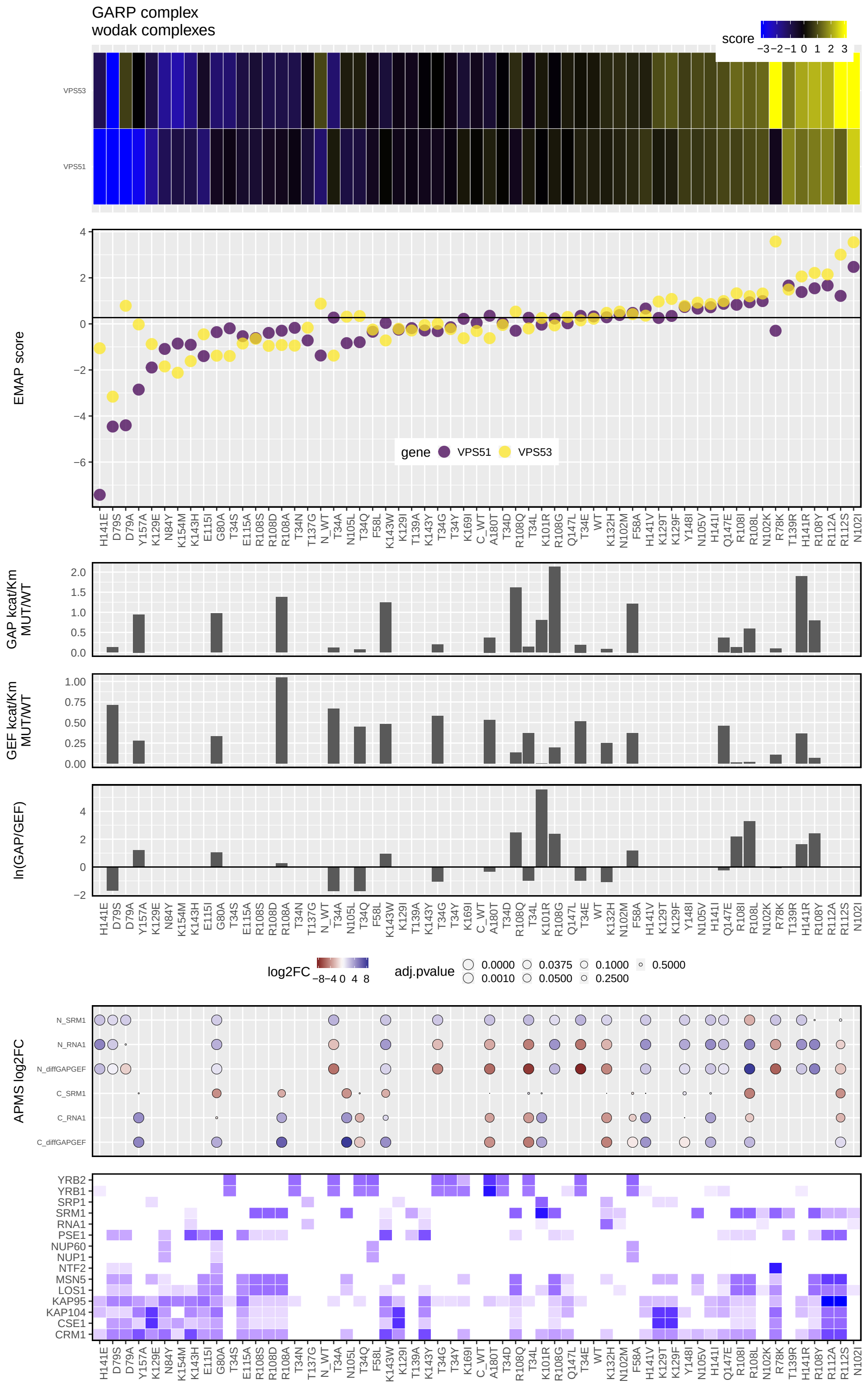

DNA−directed RNA polymerase II complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RPB9
RPB4
EMAP score
gene
RPB4
RPB9
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141R N_WT R108Y R108Q R108L R108G C_WT R112A T34Q R108A Y148I R108I T34A K154M T139A N84Y R112S H141I WT K129E T34L F58L K129F E115A K101R H141V E115I K132H H141E K143Y K169I K129I N102M T137G A180T N105L R108S T34N K143W T34S T34E G80A Q147L N102K K143H T34Y T34D N105V T139R R108D N102I K129T Q147E F58A D79S R78K Y157A T34G D79A

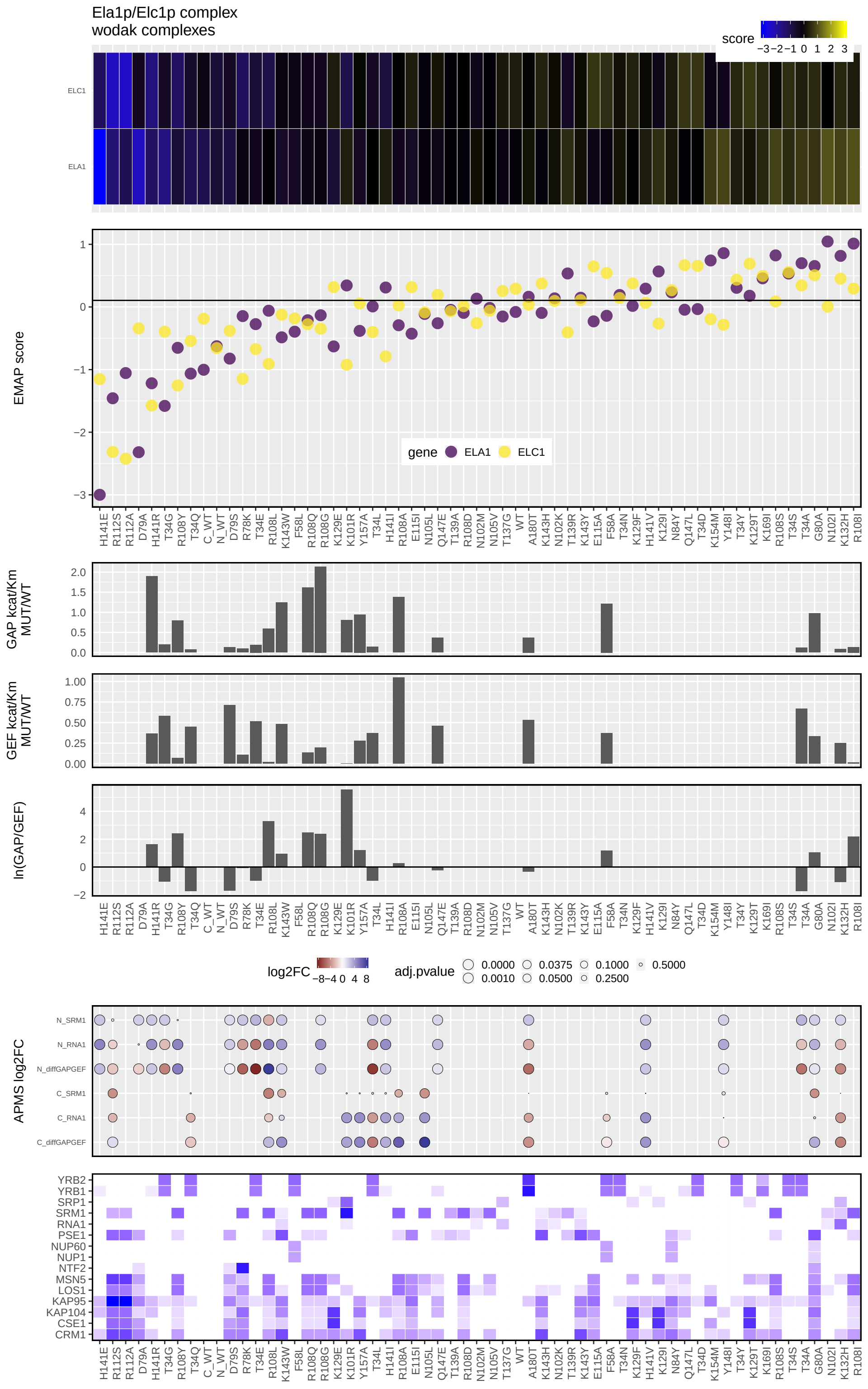

HIR complex
wodak complexes
score
−3 −2 −1 0 1 2 3
HPC2
HIR3
HIR2
HIR1
EMAP score
gene HIR1 HIR2 HIR3 HPC2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112S H141R R78K R112A N_WT R108Y H141E R108Q C_WT R108L R108S R108G Y148I Q147E R108A R108D T34S H141I Y157A K129F N102K D79S T137G R108I K154M N105L T34N T139R K143W K132H F58A N105V WT K101R T34A T139A T34Y E115I N102M K129I H141V F58L N102I E115A K169I Q147L T34L K129T N84Y K143H G80A K143Y A180T K129E T34D T34E D79A T34Q T34G

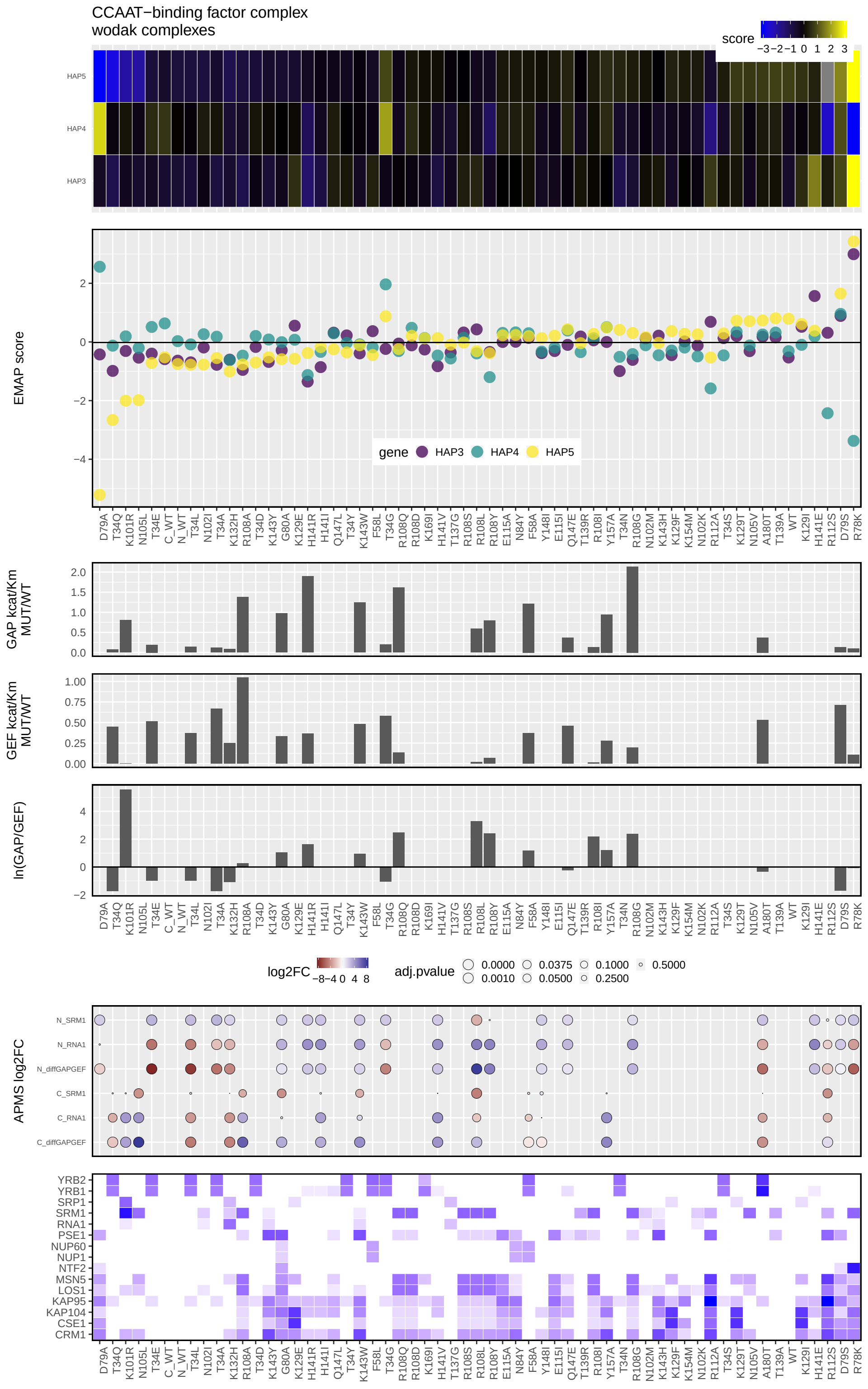
nucleotide−excision repair factor 4 complex
wodak complexes

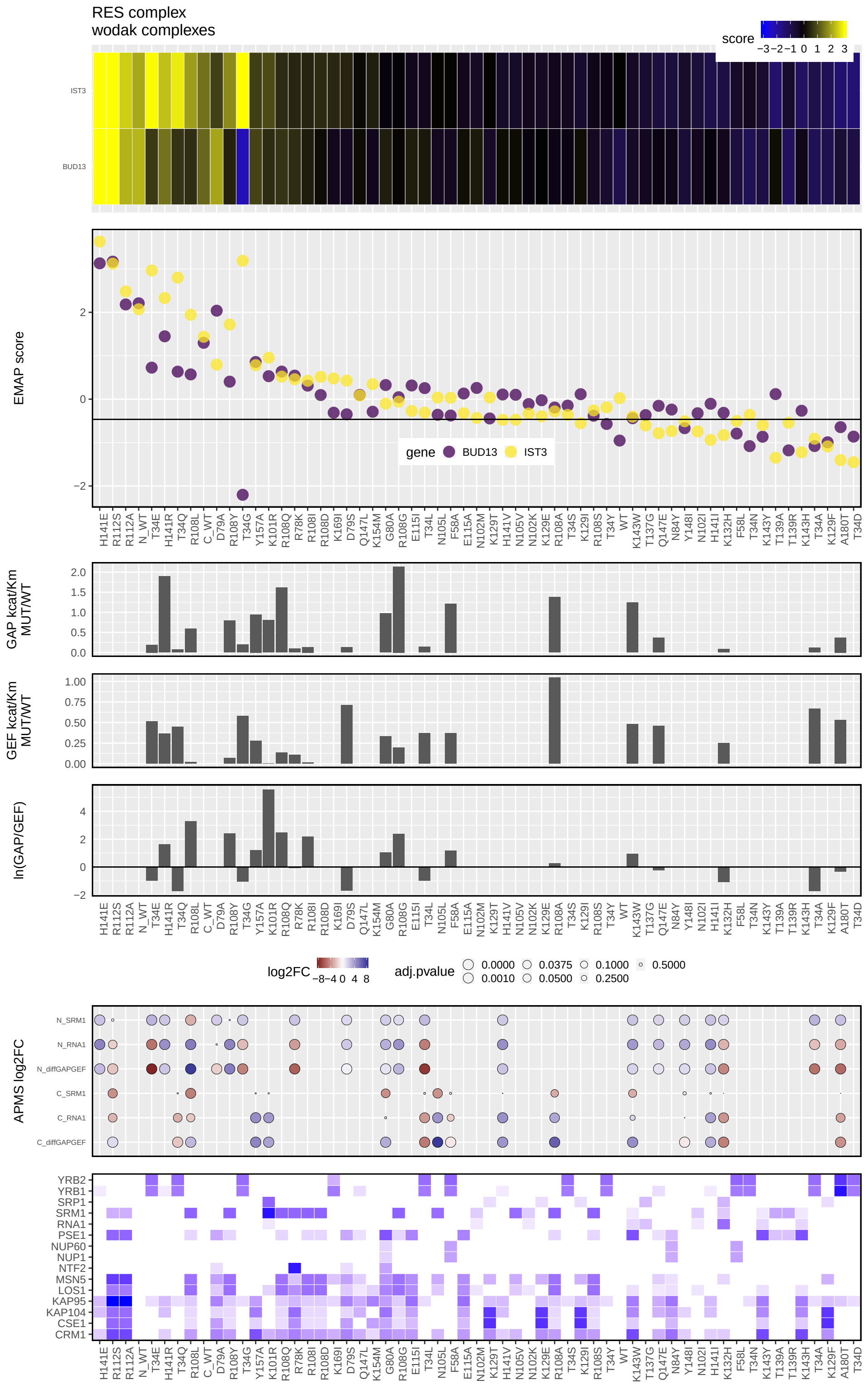


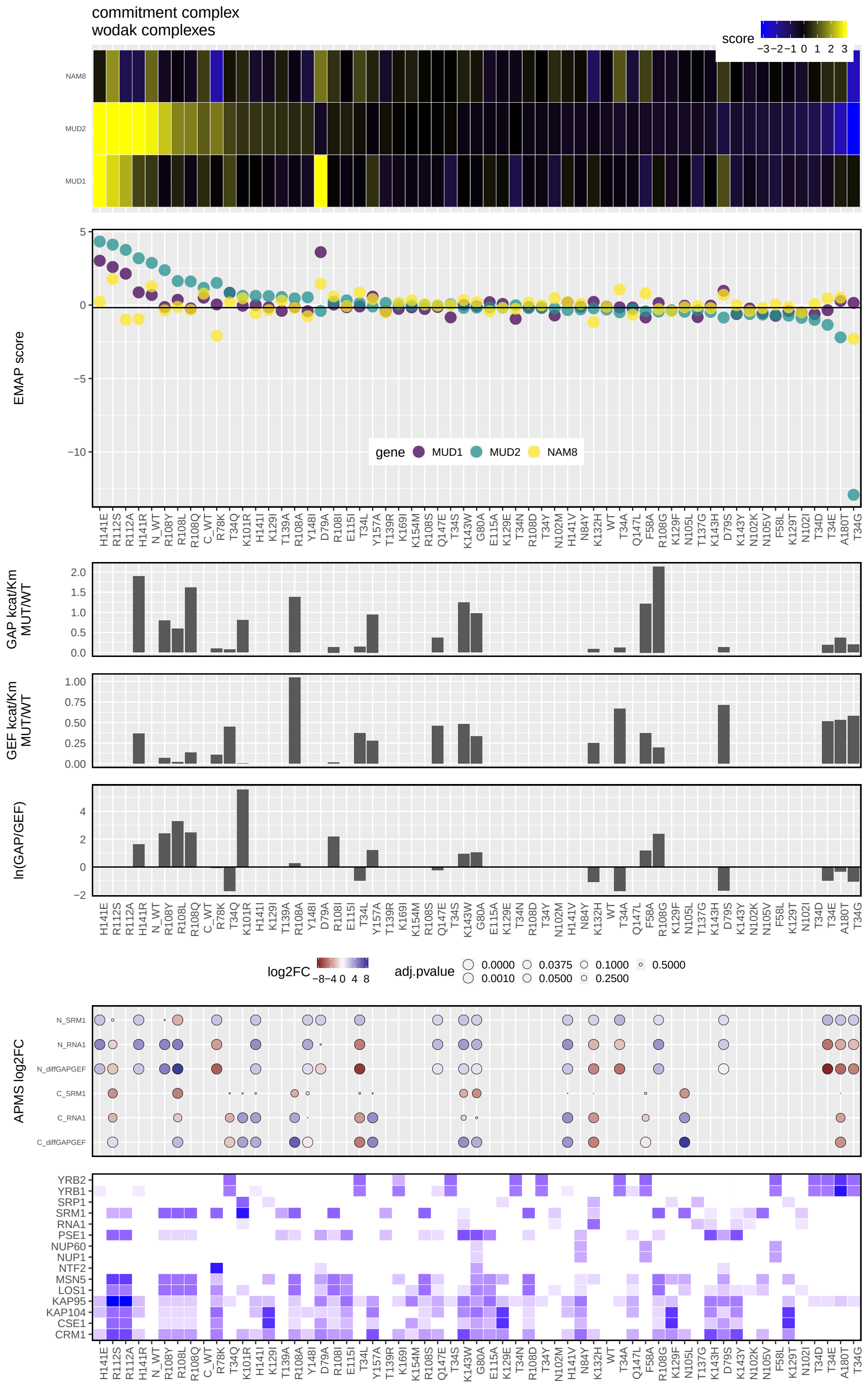

mitochondrial sorting and assembly machinery complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SAM37
MDM10
EMAP score
gene
MDM10
SAM37
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K R108I K143W Q147E R108A H141I R108S T34A H141V K143Y T34L R108G R108L N84Y K129E K154M Y148I N102I G80A C_WT N_WT N105L K143H T139A T34N N105V R108Y N102M K129I K129T R108Q F58A E115I E115A T137G K101R K129F F58L T34E T34D N102K K169I Q147L WT K132H T34Y T34Q R108D T34S Y157A D79S A180T T139R H141R H141E D79A R112A T34G R112S

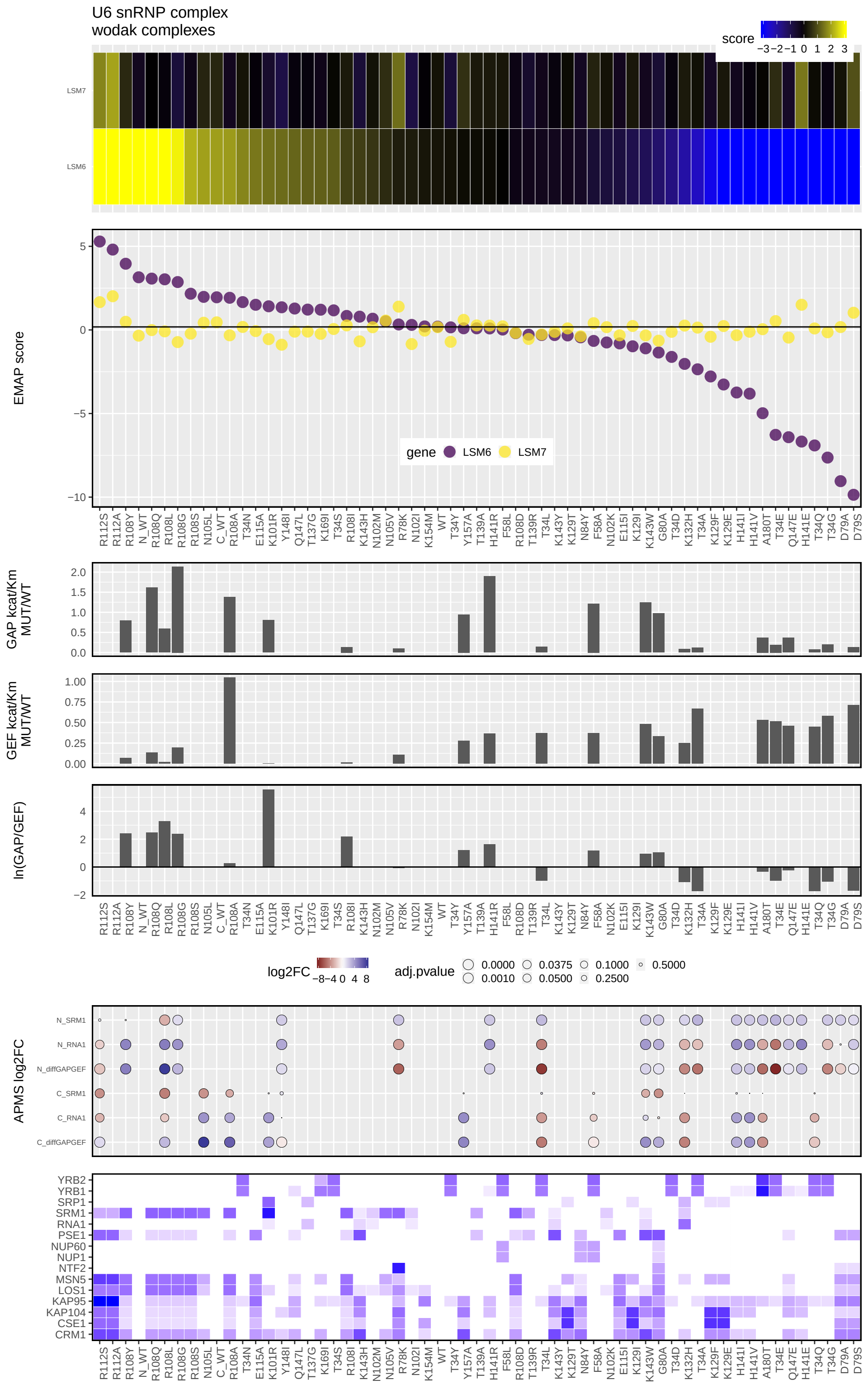

GARP complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VPS53
VPS51
EMAP score
gene
VPS51
VPS53
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E D79S D79A Y157A K129E N84Y K154M K143H E115I G80A T34S E115A R108S R108D R108A T34N T137G N_WT T34A N105L T34Q F58L K143W K129I T139A K143Y T34G T34Y K169I C_WT A180T T34D R108Q T34L K101R R108G Q147L T34E WT K132H N102M F58A H141V K129T K129F Y148I N105V H141I Q147E R108I R108L N102K R78K T139R H141R R108Y R112A R112S N102I

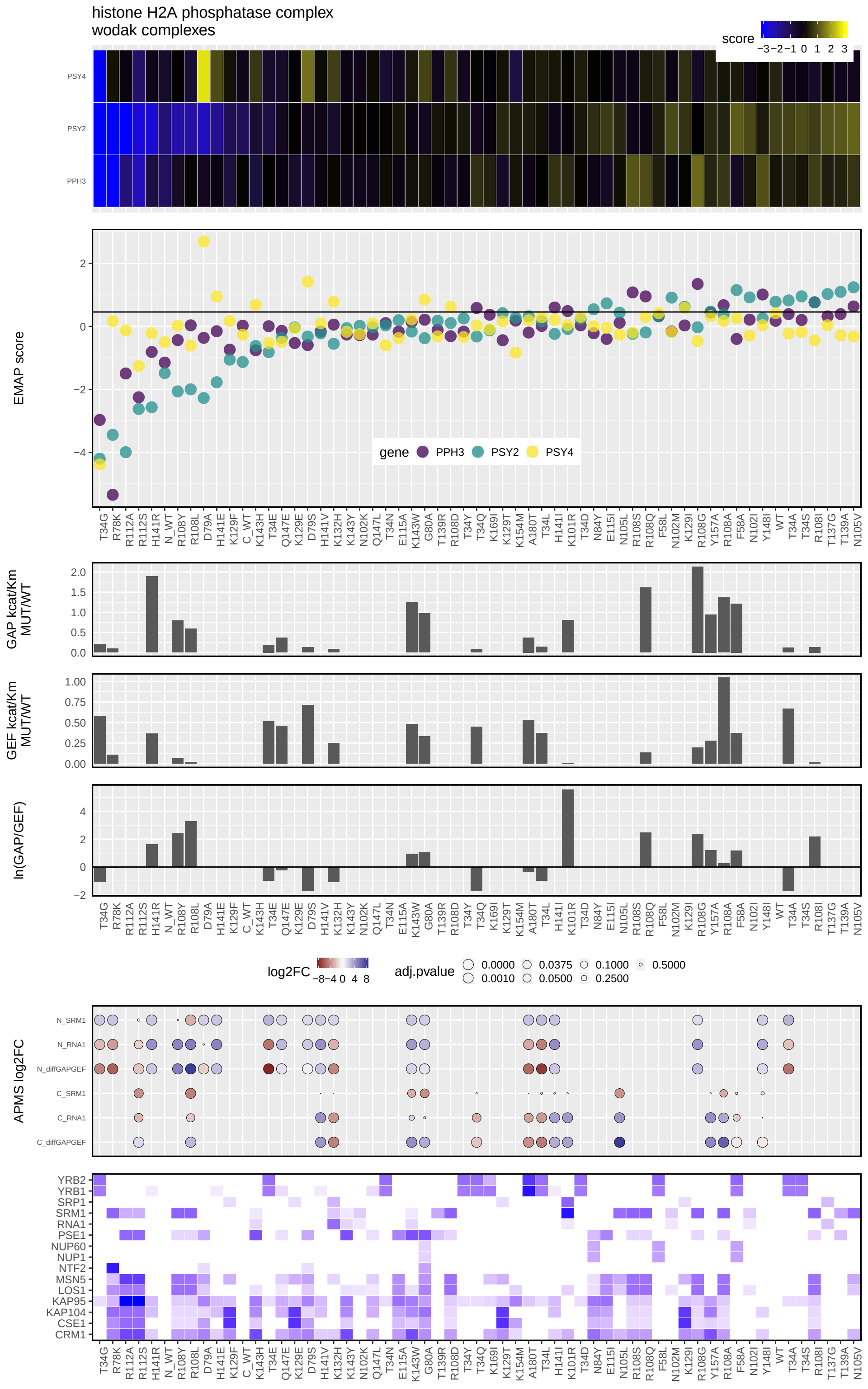

Ela1p/Elc1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
ELC1
ELA1
EMAP score
gene ELA1 ELC1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E R112S R112A D79A H141R T34G R108Y T34Q C_WT N_WT D79S R78K T34E R108L K143W F58L R108Q R108G K129E K101R Y157A T34L H141I R108A E115I N105L Q147E T139A R108D N102M N105V T137G WT A180T K143H N102K T139R K143Y E115A F58A T34N K129F H141V K129I N84Y Q147L T34D K154M Y148I T34Y K129T K169I R108S T34S T34A G80A N102I K132H R108I


CCAAT−binding factor complex
wodak complexes
score
−3 −2 −1 0 1 2 3
HAP5
HAP4
HAP3
EMAP score
gene HAP3 HAP4 HAP5
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34Q K101R N105L T34E C_WT N_WT T34L N102I T34A K132H R108A T34D K143Y G80A K129E H141R H141I Q147L T34Y K143W F58L T34G R108Q R108D K169I H141V T137G R108S R108L R108Y E115A N84Y F58A Y148I E115I Q147E T139R R108I Y157A T34N R108G N102M K143H K129F K154M N102K R112A T34S K129T N105V A180T T139A WT K129I H141E R112S D79S R78K

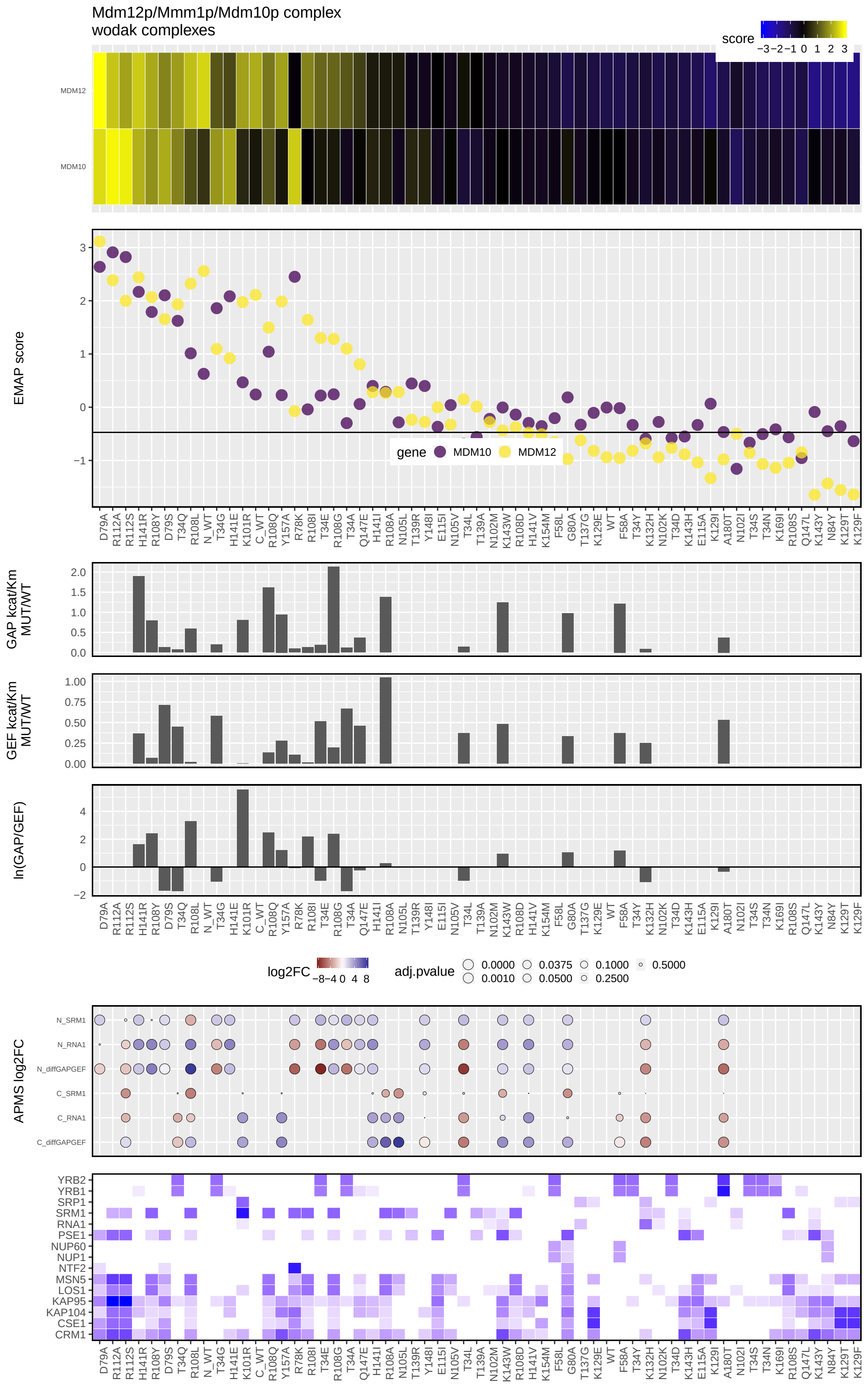

RES complex
wodak complexes
score
−3 −2 −1 0 1 2 3
IST3
BUD13
EMAP score
gene BUD13 IST3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E R112S R112A N_WT T34E H141R T34Q R108L C_WT D79A R108Y T34G Y157A K101R R108Q R78K R108I R108D K169I D79S Q147L K154M G80A R108G E115I T34L N105L F58A E115A N102M K129T H141V N105V N102K K129E R108A T34S K129I R108S T34Y WT K143W T137G Q147E N84Y Y148I N102I H141I K132H F58L T34N K143Y T139A T139R K143H T34A K129F A180T T34D

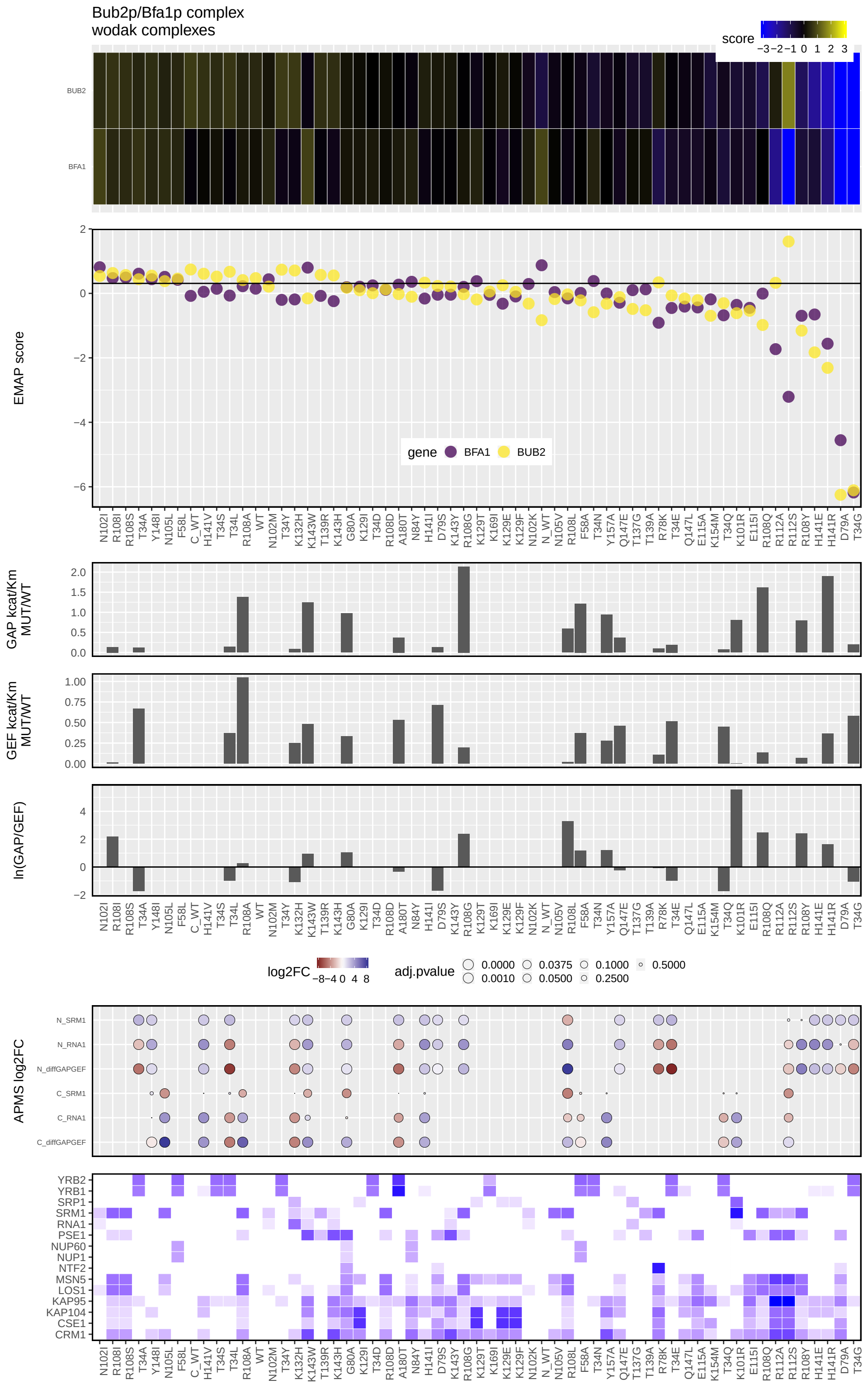

commitment complex
wodak complexes
score
−3 −2 −1 0 1 2 3
NAM8
MUD2
MUD1
EMAP score
gene MUD1 MUD2 NAM8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E R112S R112A H141R N_WT R108Y R108L R108Q C_WT R78K T34Q K101R H141I K129I T139A R108A Y148I D79A R108I E115I T34L Y157A T139R K169I K154M R108S Q147E T34S K143W G80A E115A K129E T34N R108D T34Y N102M H141V N84Y K132H WT T34A Q147L F58A R108G K129F N105L T137G K143H D79S K143Y N102K N105V F58L K129T N102I T34D T34E A180T T34G

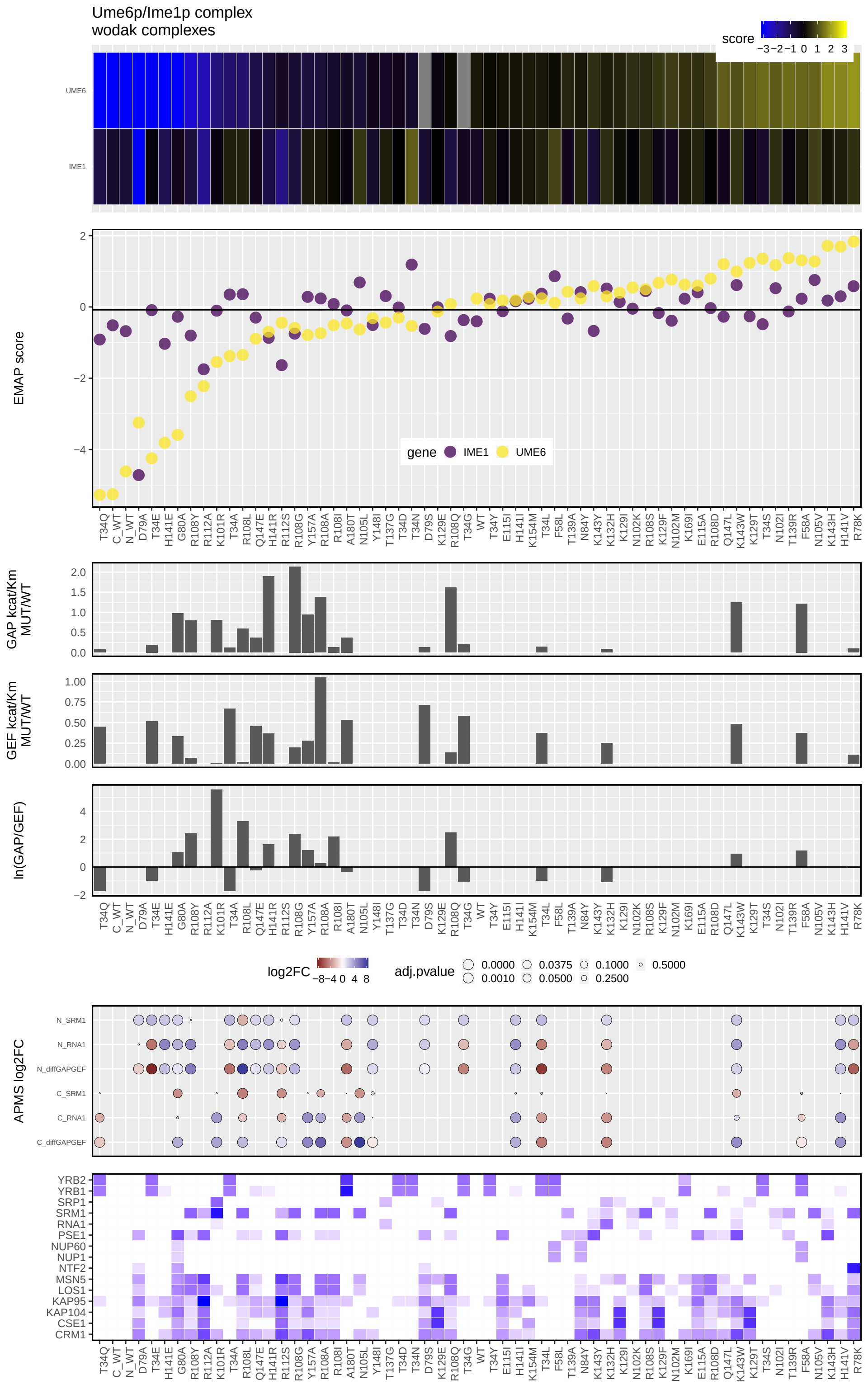

U6 snRNP complex
wodak complexes
score
−3 −2 −1 0 1 2 3
LSM7
LSM6
EMAP score
gene LSM6 LSM7
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112S R112A R108Y N_WT R108Q R108L R108G R108S N105L C_WT R108A T34N E115A K101R Y148I Q147L T137G K169I T34S R108I K143H N102M N105V R78K N102I K154M WT T34Y Y157A T139A H141R F58L R108D T139R T34L K143Y K129T N84Y F58A N102K E115I K129I K143W G80A T34D K132H T34A K129F K129E H141I H141V A180T T34E Q147E H141E T34Q T34G D79A D79S

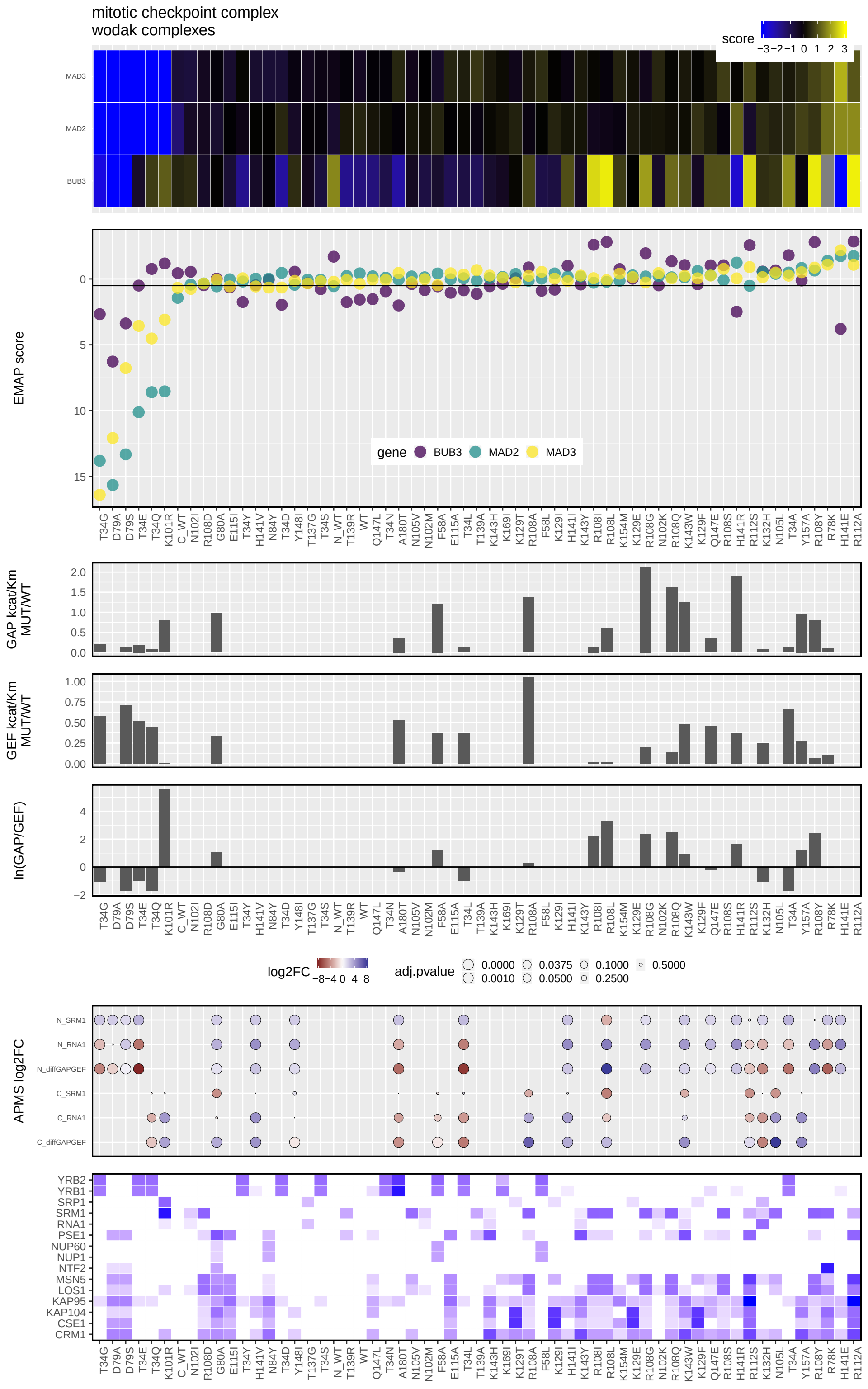

histone H2A phosphatase complex
wodak complexes
score
−3 −2 −1 0 1 2 3
PSY4
PSY2
PPH3
EMAP score
gene PPH3 PSY2 PSY4
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G R78K R112A R112S H141R N_WT R108Y R108L D79A H141E K129F C_WT K143H T34E Q147E K129E D79S H141V K132H K143Y N102K Q147L T34N E115A K143W G80A T139R R108D T34Y T34Q K169I K129T K154M A180T T34L H141I K101R T34D N84Y E115I N105L R108S R108Q F58L N102M K129I R108G Y157A R108A F58A N102I Y148I WT T34A T34S R108I T137G T139A N105V

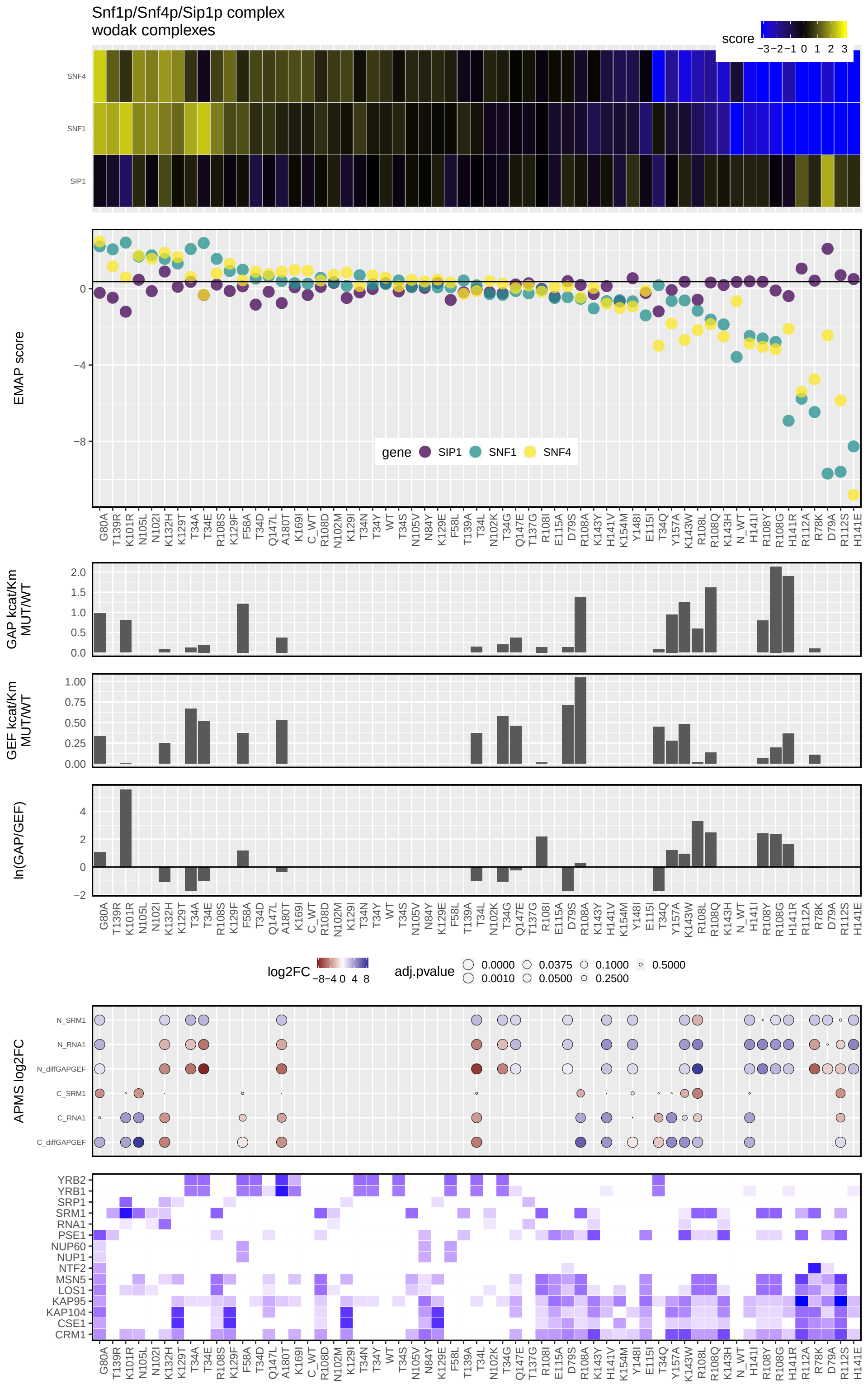
Mdm12p/Mmm1p/Mdm10p complex
wodak complexes



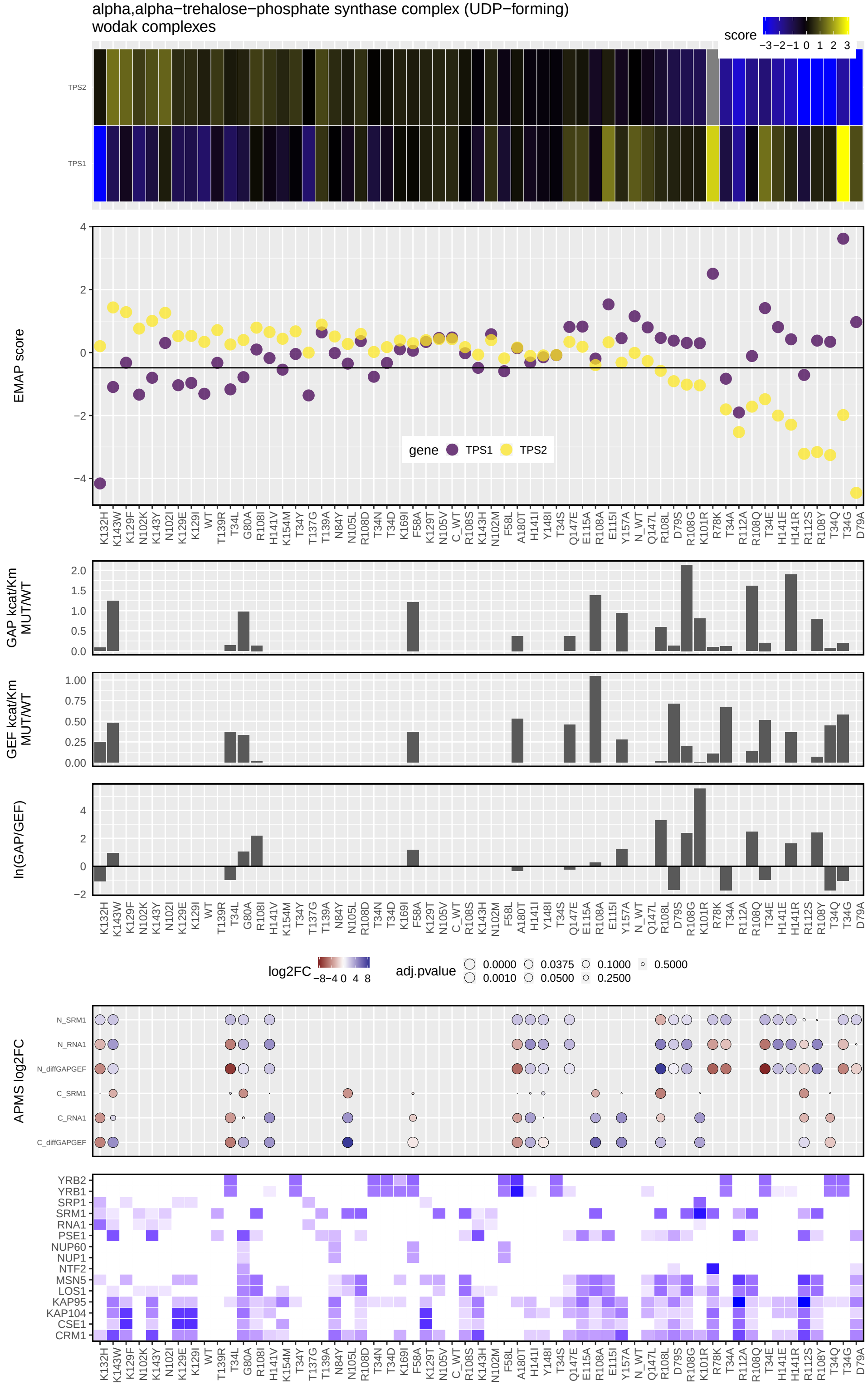

Bub2p/Bfa1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
BUB2
BFA1
EMAP score
gene
BFA1
BUB2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N102I R108I R108S T34A Y148I N105L F58L C_WT H141V T34S T34L R108A WT N102M T34Y K132H K143W T139R K143H G80A K129I T34D R108D A180T N84Y H141I D79S K143Y R108G K129T K169I K129E K129F N102K N_WT N105V R108L F58A T34N Y157A Q147E T137G T139A R78K T34E Q147L E115A K154M T34Q K101R E115I R108Q R112A R112S R108Y H141E H141R D79A T34G

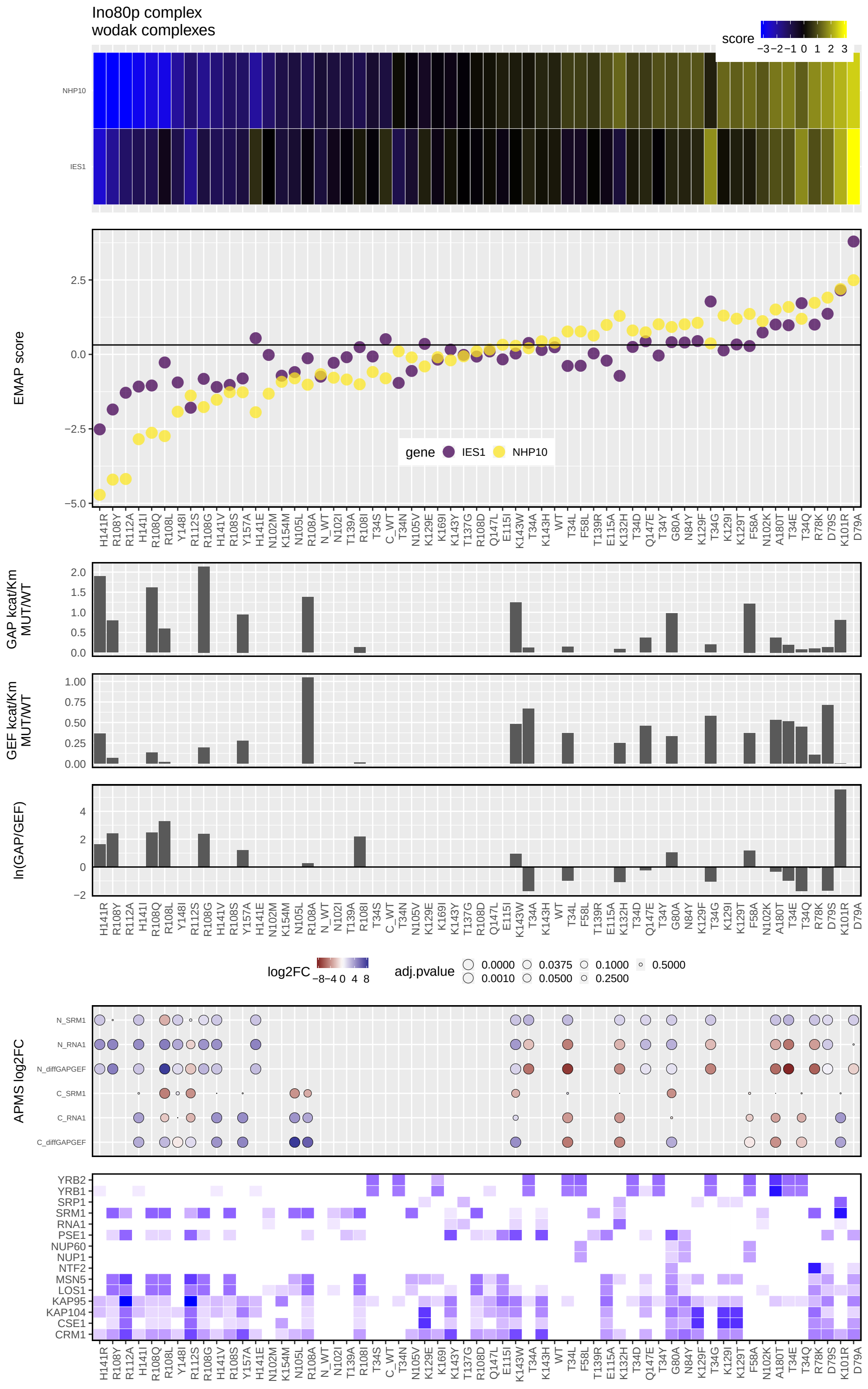

Ume6p/Ime1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UME6
IME1
EMAP score
gene
IME1
UME6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34Q C_WT N_WT D79A T34E H141E G80A R108Y R112A K101R T34A R108L Q147E H141R R112S R108G Y157A R108A R108I A180T N105L Y148I T137G T34D T34N D79S K129E R108Q T34G WT T34Y E115I H141I K154M T34L F58L T139A N84Y K143Y K132H K129I N102K R108S K129F N102M K169I E115A R108D Q147L K143W K129T T34S N102I T139R F58A N105V K143H H141V R78K

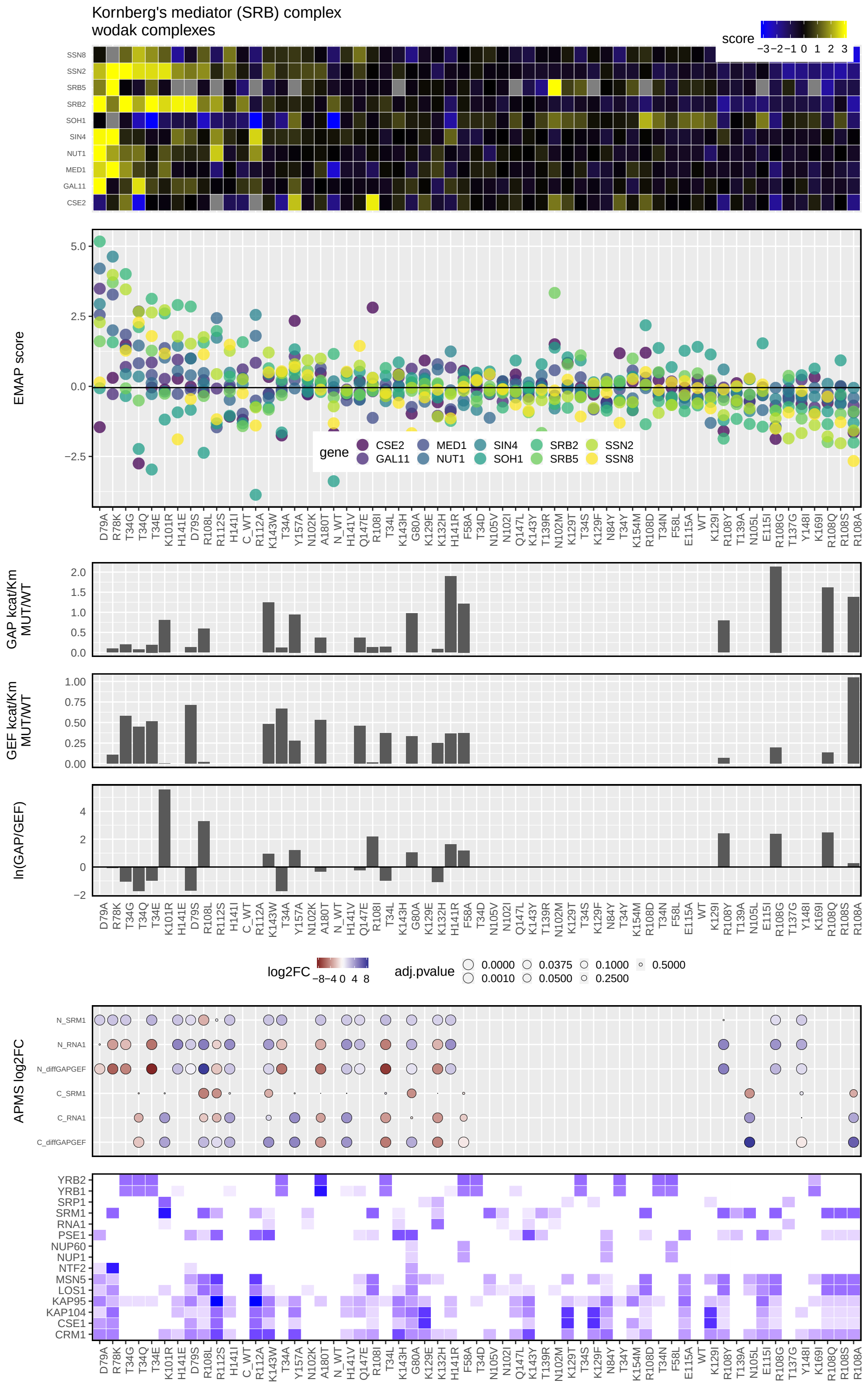

mitotic checkpoint complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MAD3
MAD2
BUB3
EMAP score
gene
BUB3
MAD2
MAD3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A D79S T34E T34Q K101R C_WT N102I R108D G80A E115I T34Y H141V N84Y T34D Y148I T137G T34S N_WT T139R WT Q147L T34N A180T N105V N102M F58A E115A T34L T139A K143H K169I K129T R108A F58L K129I H141I K143Y R108I R108L K154M K129E R108G N102K R108Q K143W K129F Q147E R108S H141R R112S K132H N105L T34A Y157A R108Y R78K H141E R112A

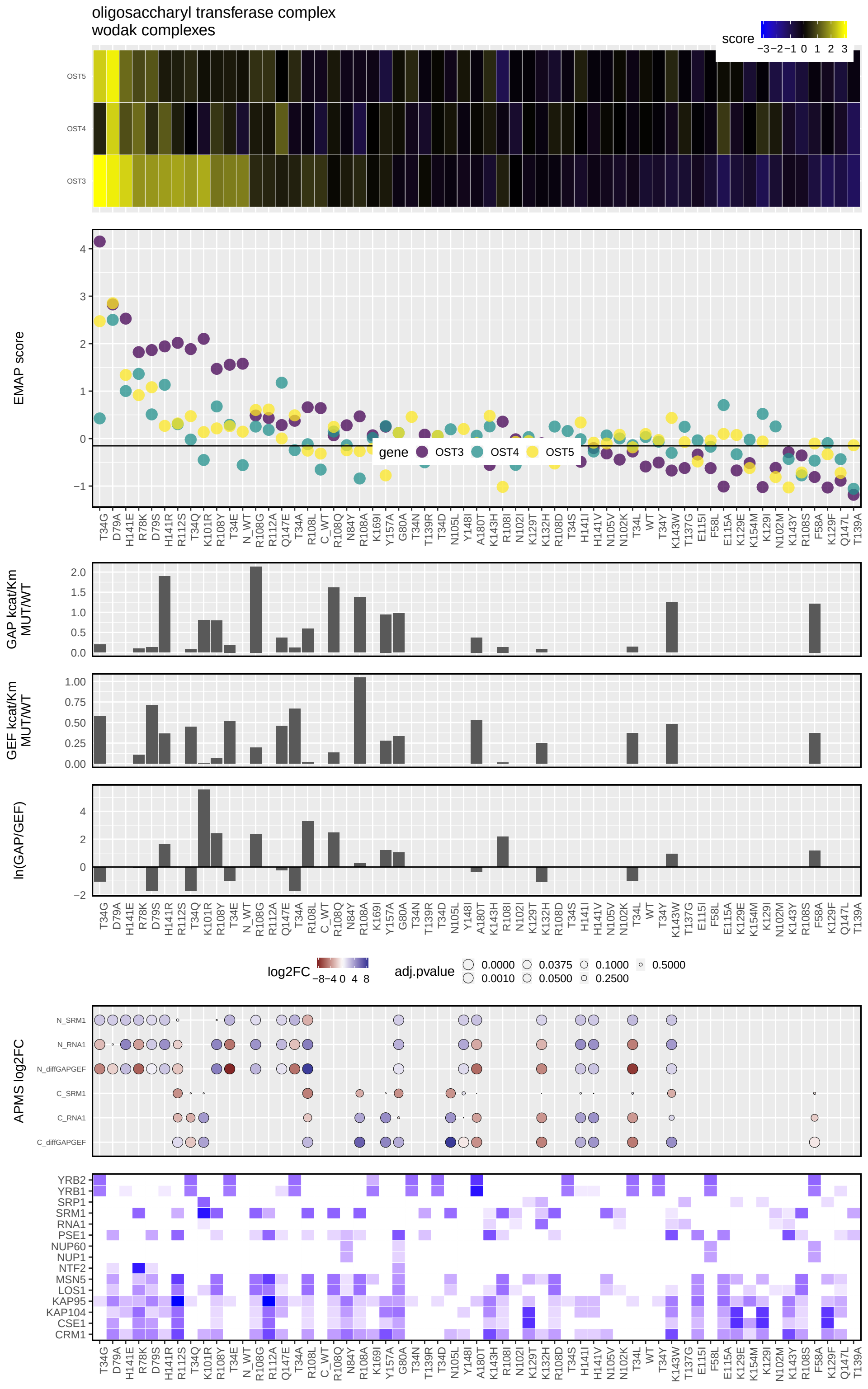

Snf1p/Snf4p/Sip1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SNF4
SNF1
SIP1
EMAP score
gene SIP1 SNF1 SNF4
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
G80A T139R K101R N105L N102I K132H K129T T34A T34E R108S K129F F58A T34D Q147L A180T K169I C_WT R108D N102M K129I T34N T34Y WT T34S N105V N84Y K129E F58L T139A T34L N102K T34G Q147E T137G R108I E115A D79S R108A K143Y H141V K154M Y148I E115I T34Q Y157A K143W R108L R108Q K143H N_WT H141I R108Y R108G H141R R112A R78K D79A R112S H141E

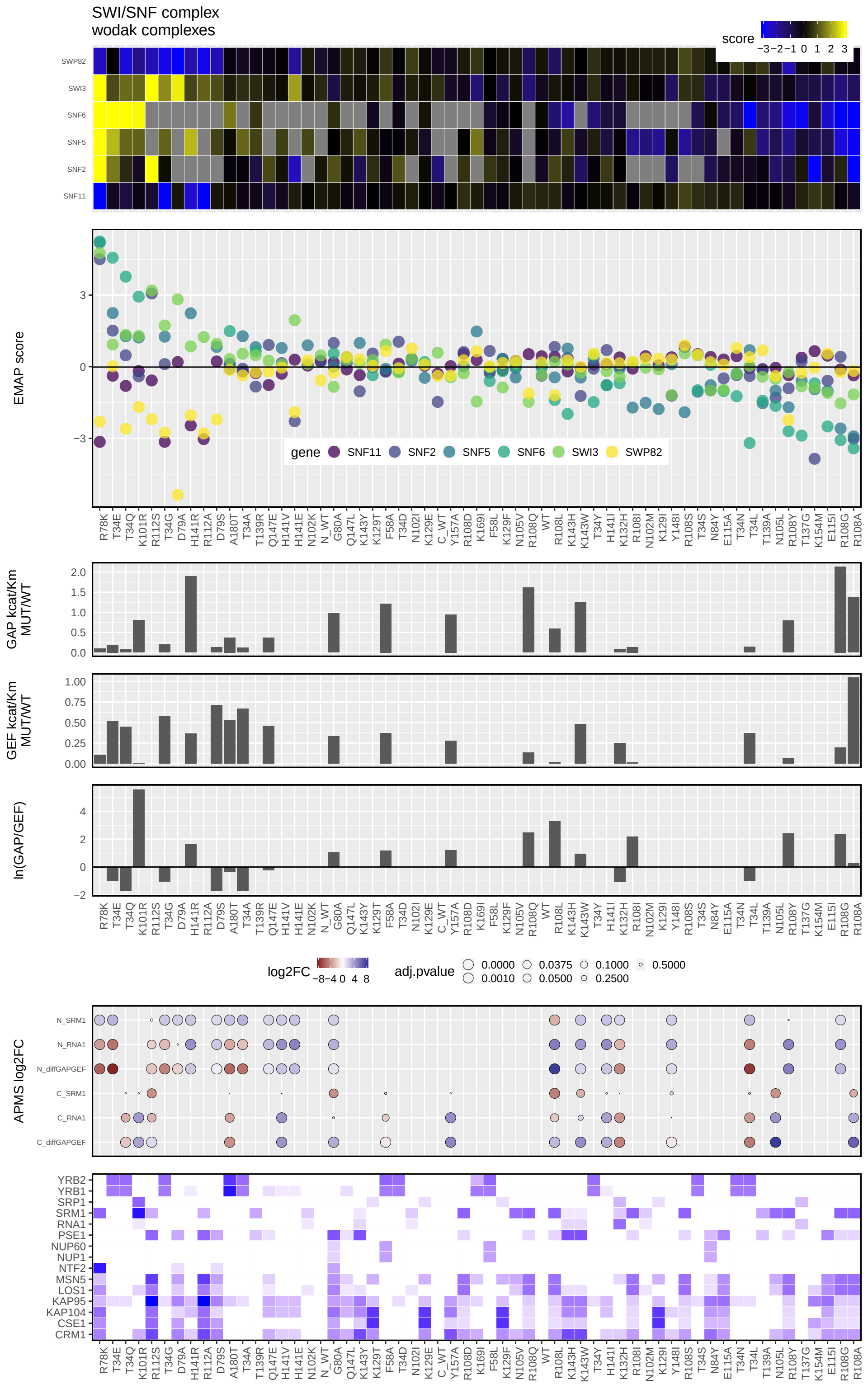
alpha,alpha−trehalose−phosphate synthase complex (UDP−forming)
wodak complexes



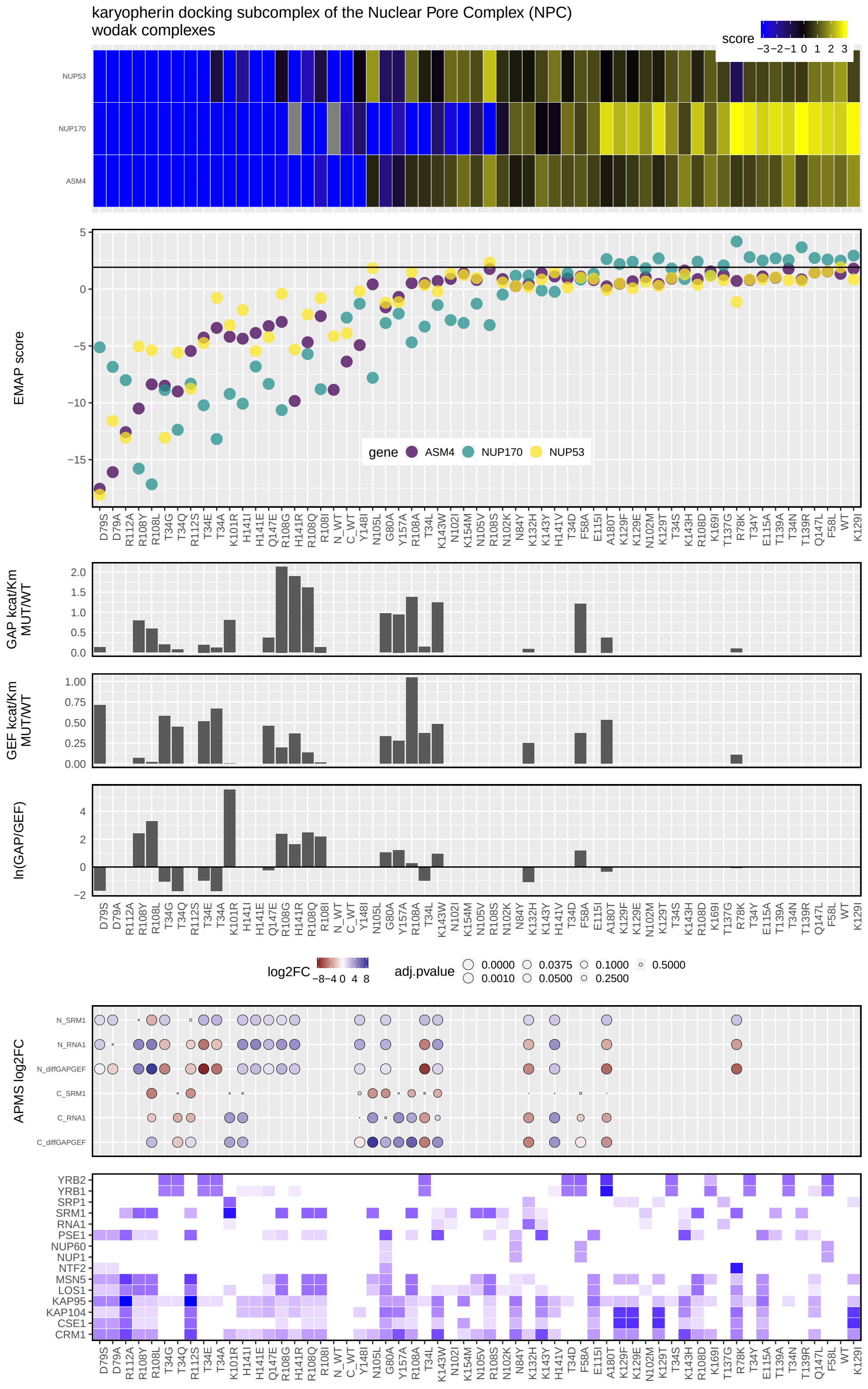

Ino80p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
NHP10
IES1
EMAP score
2.5
0.0
−2.5
−5.0
gene
IES1
NHP10
H141R R108Y R112A H141I R108Q R108L Y148I R112S R108G H141V R108S Y157A H141E N102M K154M N105L R108A N_WT N102I T139A R108I T34S C_WT T34N N105V K129E K169I K143Y T137G R108D Q147L E115I K143W T34A K143H WT T34L F58L T139R E115A K132H T34D Q147E T34Y G80A N84Y K129F T34G K129I K129T F58A N102K A180T T34E T34Q R78K D79S K101R D79A
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

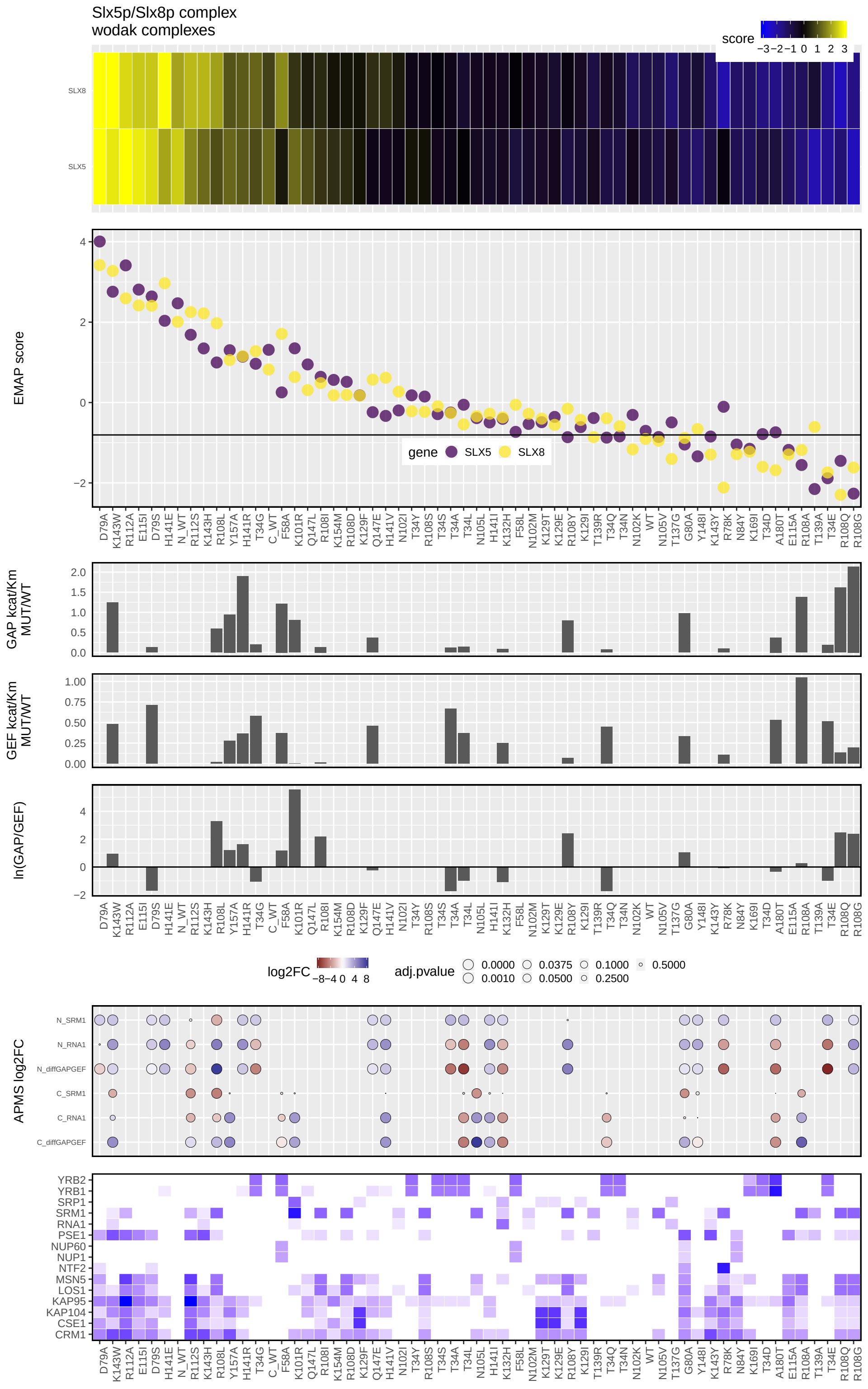

Kornberg's mediator (SRB) complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SSN8
SSN2
SRB5
SRB2
SOH1
SIN4
NUT1
MED1
GAL11
CSE2
EMAP score
5.0
2.5
0.0
−2.5
gene
CSE2
GAL11
MED1
NUT1
SIN4
SOH1
SRB2
SRB5
SSN2
SSN8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R78K T34G T34Q T34E K101R H141E D79S R108L R112S H141I C_WT R112A K143W T34A Y157A N102K A180T N_WT H141V Q147E R108I T34L K143H G80A K129E K132H H141R F58A T34D N105V N102I Q147L K143Y T139R N102M K129T T34S K129F N84Y T34Y K154M R108D T34N F58L E115A WT K129I R108Y T139A N105L E115I R108G T137G Y148I K169I R108Q R108S R108A

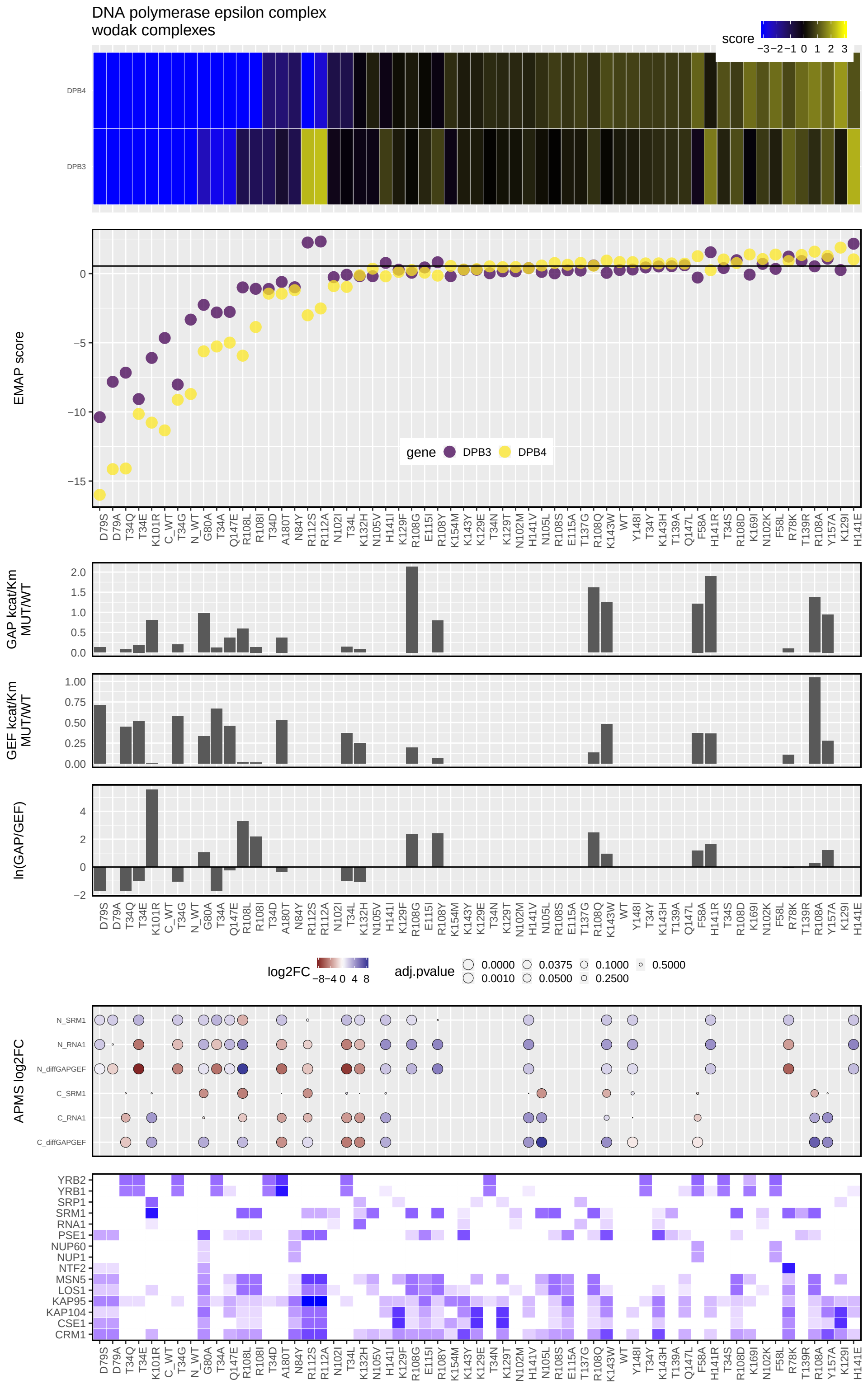

oligosaccharyl transferase complex
wodak complexes
score
−3 −2 −1 0 1 2 3
OST5
OST4
OST3
EMAP score
gene
OST3
OST4
OST5
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A H141E R78K D79S H141R R112S T34Q K101R R108Y T34E N_WT R108G R112A Q147E T34A R108L C_WT R108Q N84Y R108A K169I Y157A G80A T34N T139R T34D N105L Y148I A180T K143H R108I N102I K129T K132H R108D T34S H141I H141V N105V N102K T34L WT T34Y K143W T137G E115I F58L E115A K129E K154M K129I N102M K143Y R108S F58A K129F Q147L T139A

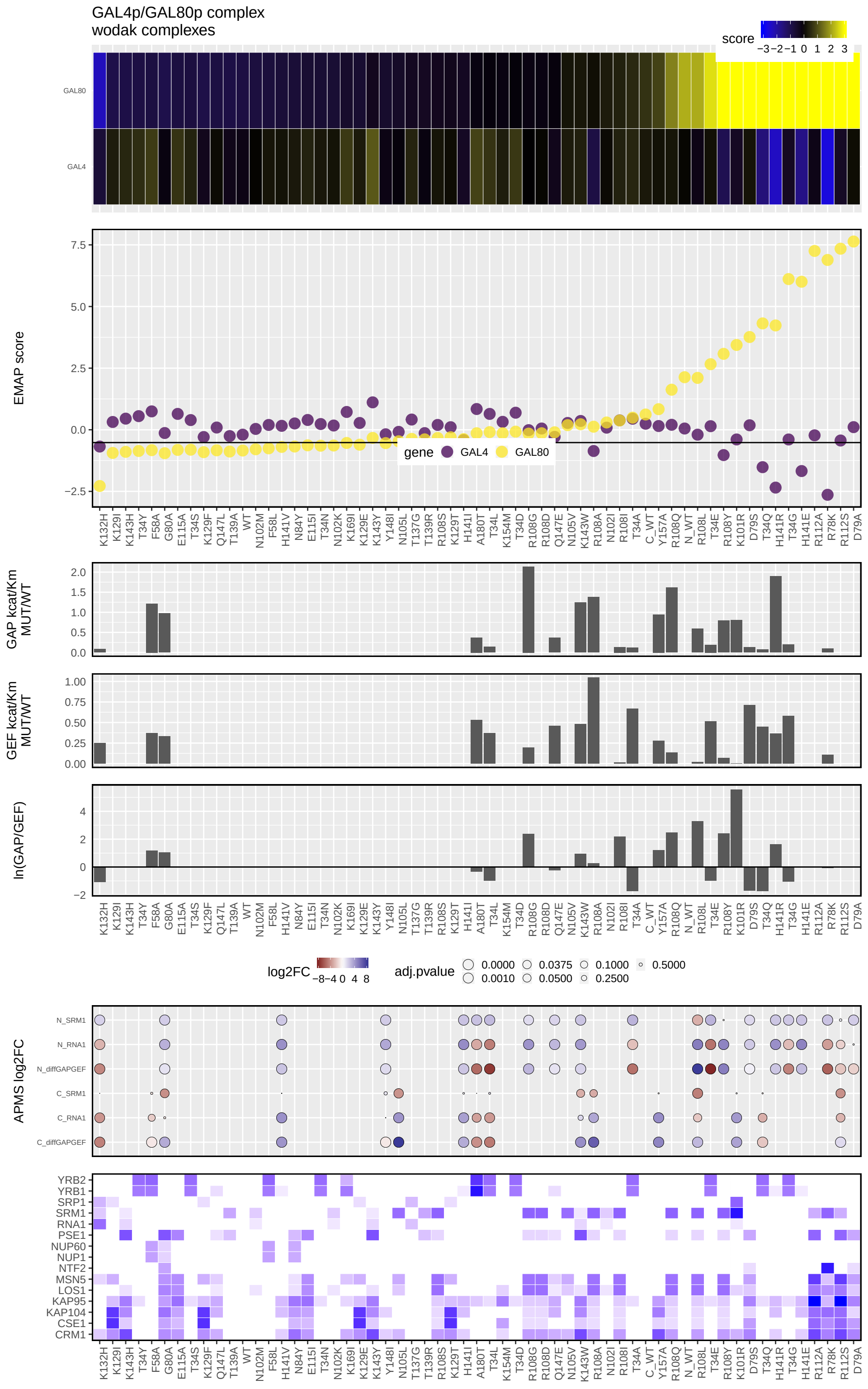

SWI/SNF complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SWP82
SWI3
SNF6
SNF5
SNF2
SNF11
EMAP score
gene SNF11 SNF2 SNF5 SNF6 SWI3 SWP82
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K T34E T34Q K101R R112S T34G D79A H141R R112A D79S A180T T34A T139R Q147E H141V H141E N102K N_WT G80A Q147L K143Y K129T F58A T34D N102I K129E C_WT Y157A R108D K169I F58L K129F N105V R108Q WT R108L K143H K143W T34Y H141I K132H R108I N102M K129I Y148I R108S T34S N84Y E115A T34N T34L T139A N105L R108Y T137G K154M E115I R108G R108A

karyopherin docking subcomplex of the Nuclear Pore Complex (NPC)
wodak complexes




Slx5p/Slx8p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SLX8
SLX5
EMAP score
gene SLX5 SLX8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A K143W R112A E115I D79S H141E N_WT R112S K143H R108L Y157A H141R T34G C_WT F58A K101R Q147L R108I K154M R108D K129F Q147E H141V N102I T34Y R108S T34S T34A T34L N105L H141I K132H F58L N102M K129T K129E R108Y K129I T139R T34Q T34N N102K WT N105V T137G G80A Y148I K143Y R78K N84Y K169I T34D A180T E115A R108A T139A T34E R108Q R108G


DNA polymerase epsilon complex
wodak complexes
score
−3 −2 −1 0 1 2 3
DPB4
DPB3
EMAP score
gene DPB3 DPB4
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79S D79A T34Q T34E K101R C_WT T34G N_WT G80A T34A Q147E R108L R108I T34D A180T N84Y R112S R112A N102I T34L K132H N105V H141I K129F R108G E115I R108Y K154M K143Y K129E T34N K129T N102M H141V N105L R108S E115A T137G R108Q K143W WT Y148I T34Y K143H T139A Q147L F58A H141R T34S R108D K169I N102K F58L R78K T139R R108A Y157A K129I H141E


GAL4p/GAL80p complex
wodak complexes
score
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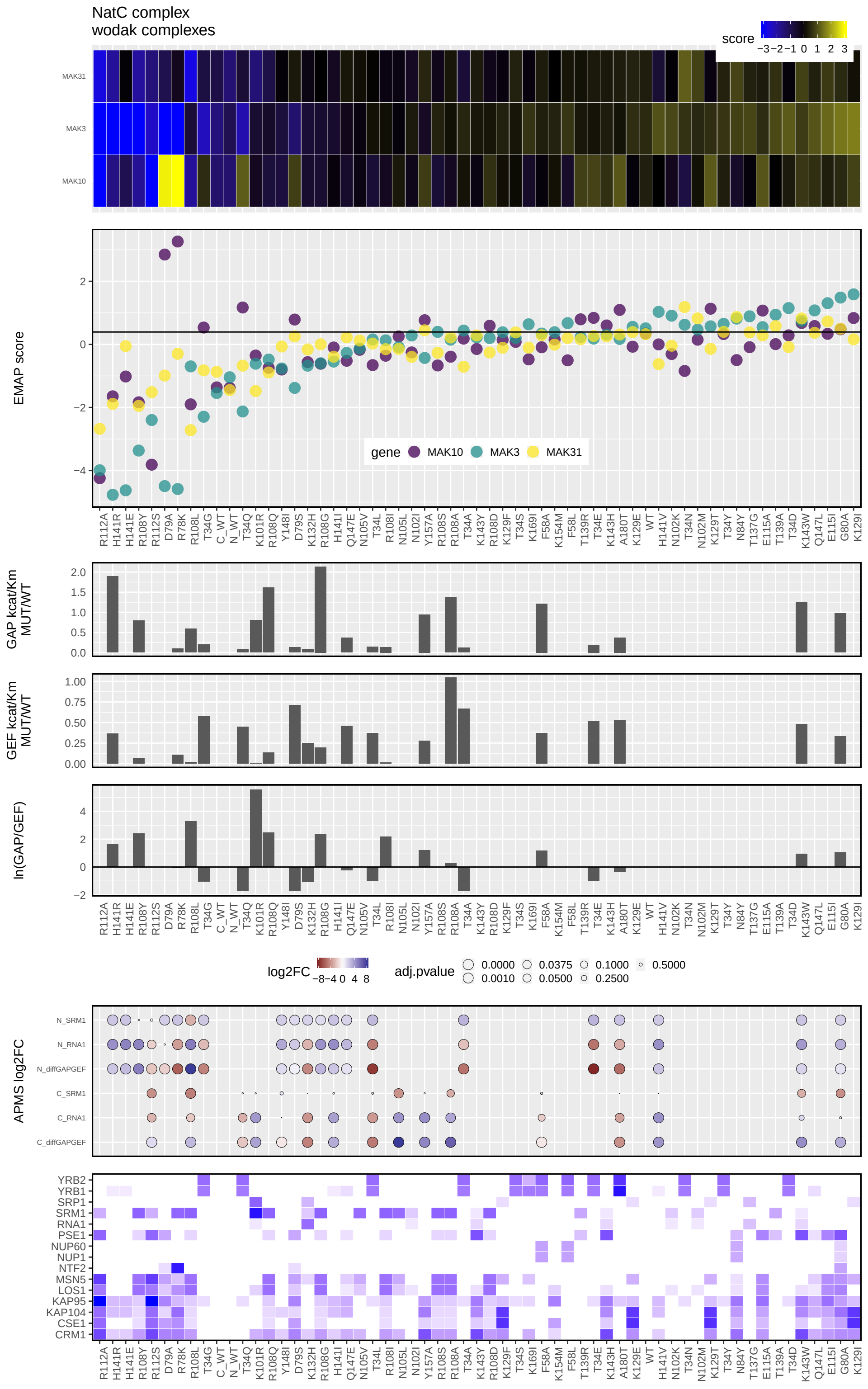
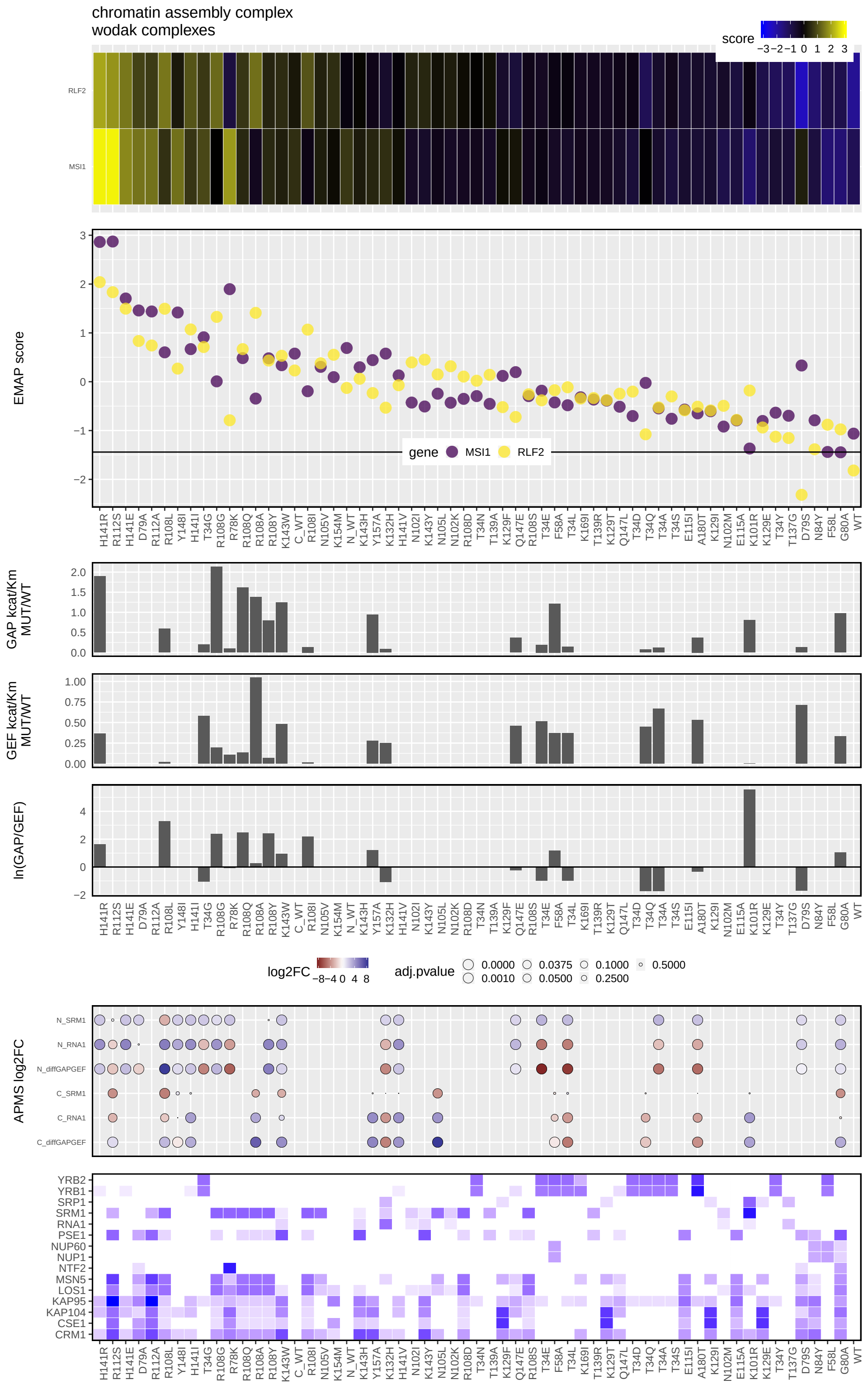
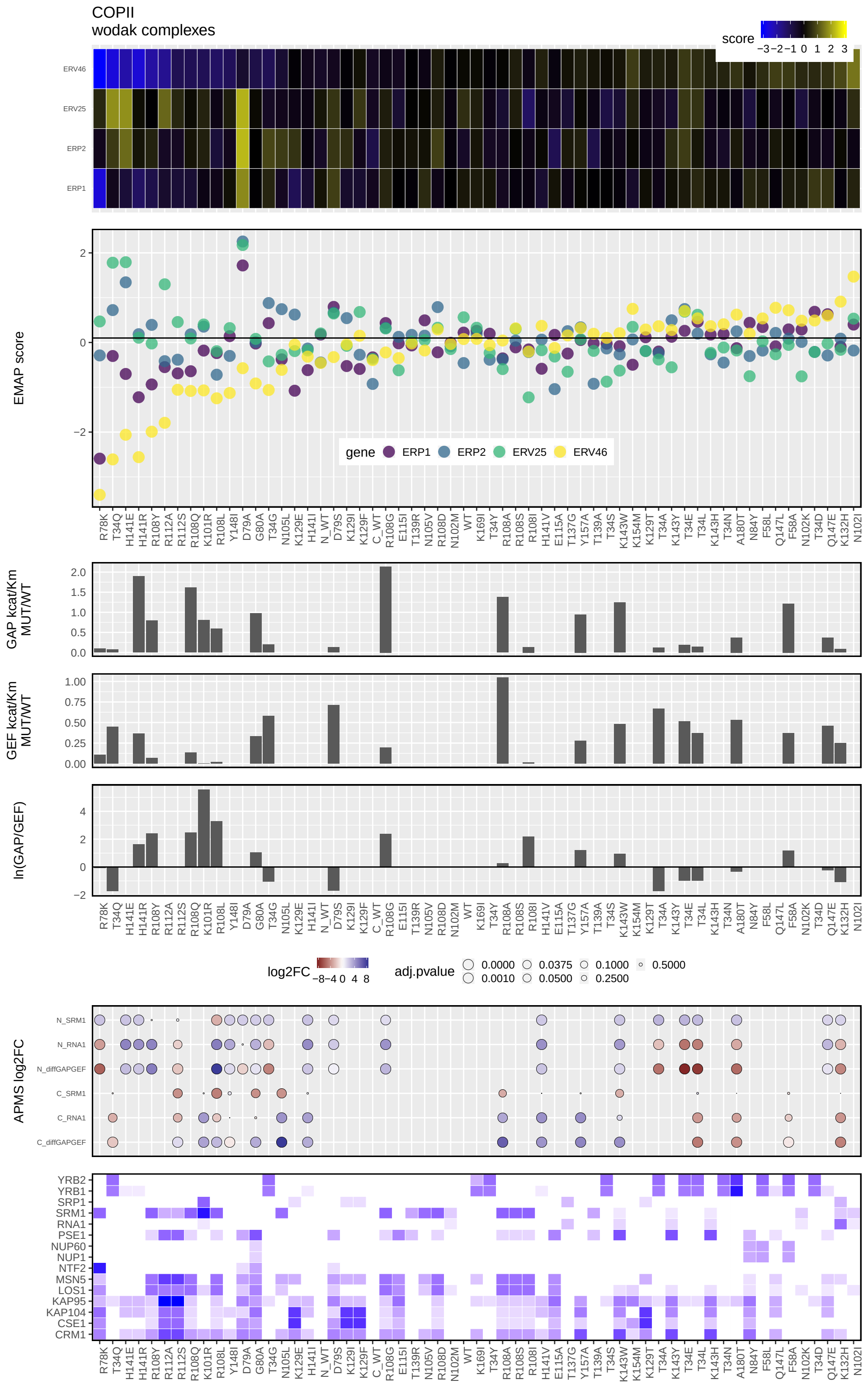
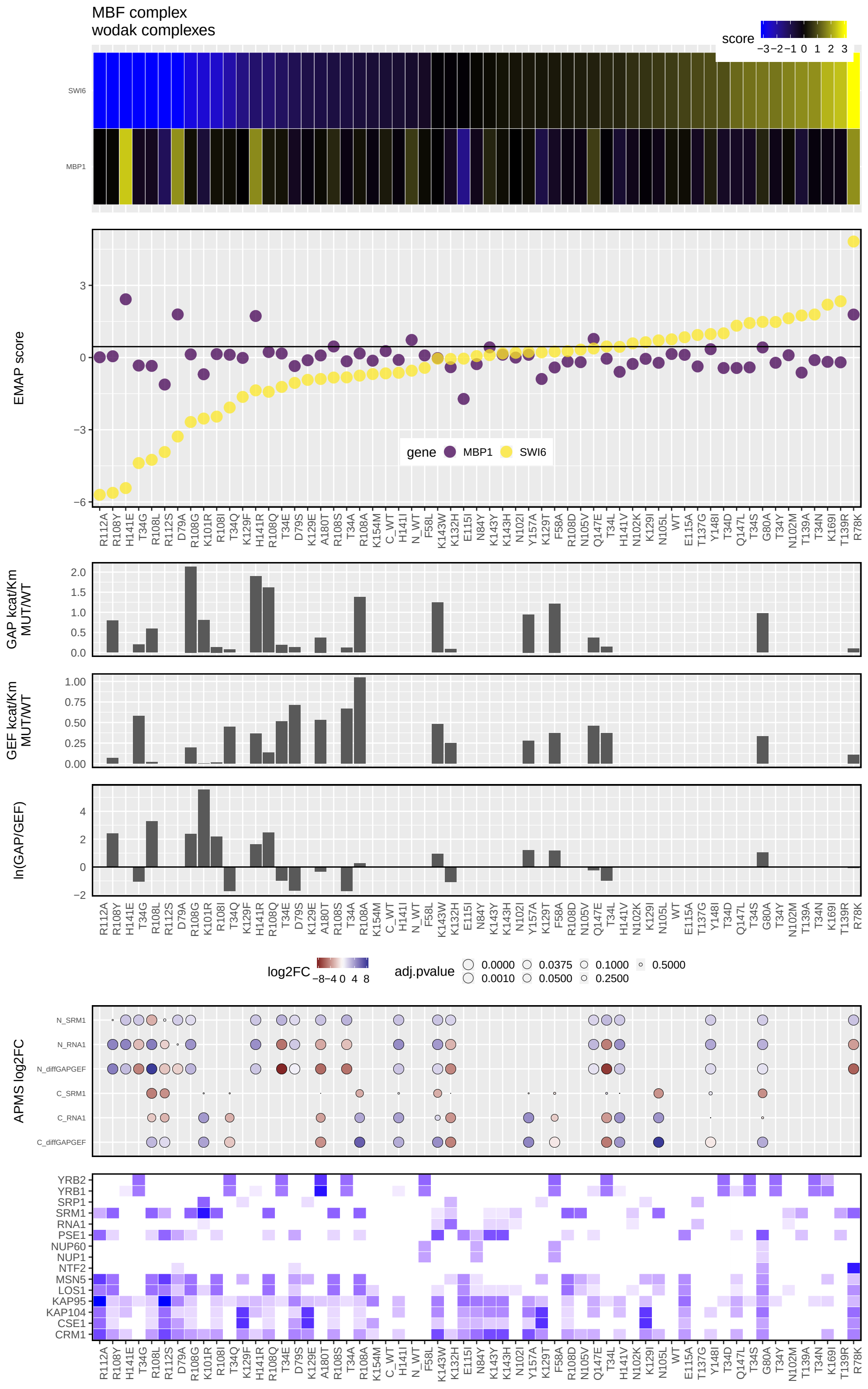
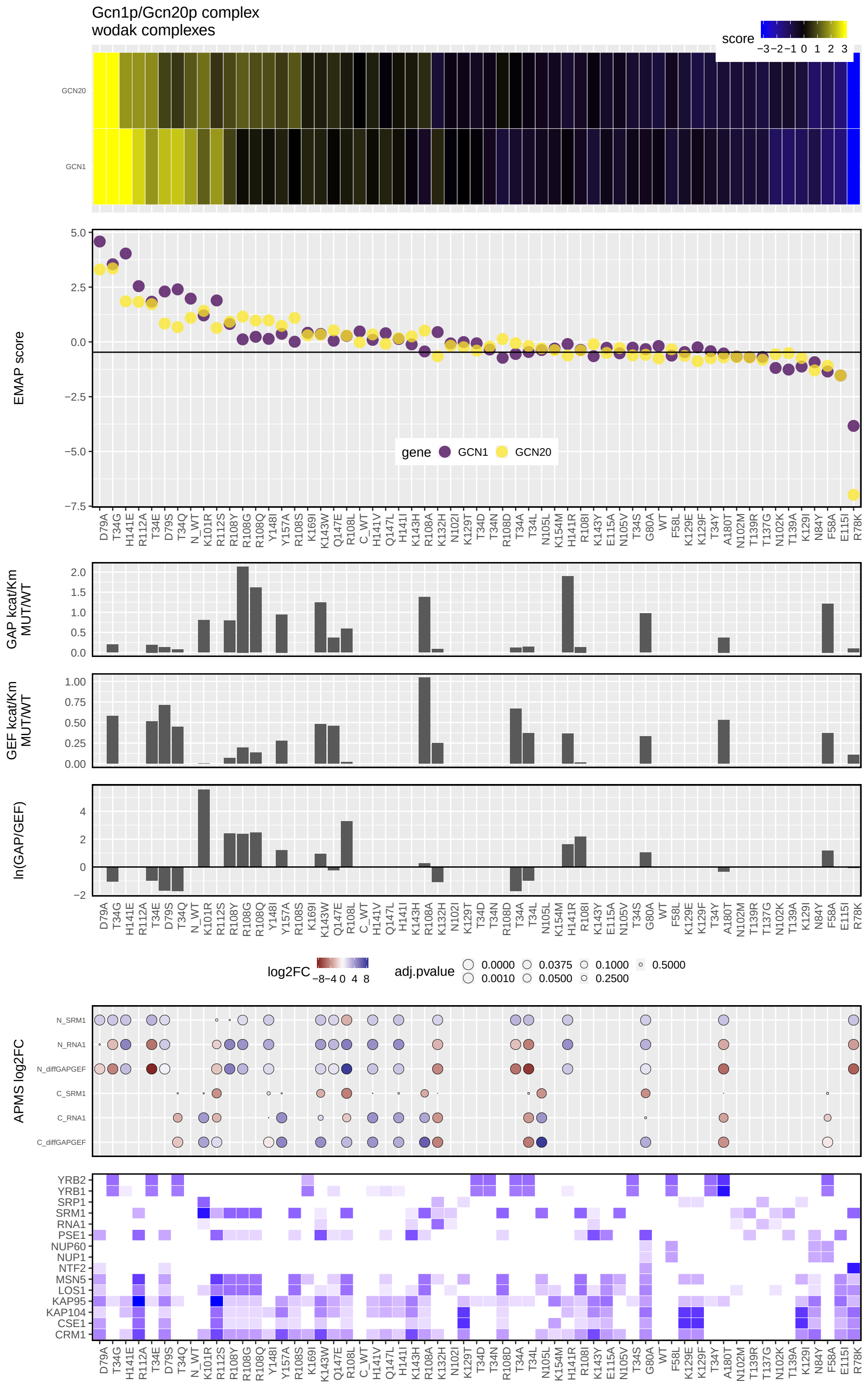
GAL80
GAL4
EMAP score
gene
GAL4
GAL80
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K132H K129I K143H T34Y F58A G80A E115A T34S K129F Q147L T139A WT N102M F58L H141V N84Y E115I T34N N102K K169I K129E K143Y Y148I N105L T137G T139R R108S K129T H141I A180T T34L K154M T34D R108G R108D Q147E N105V K143W R108A N102I R108I T34A C_WT Y157A R108Q N_WT R108L T34E R108Y K101R D79S T34Q H141R T34G H141E R112A R78K R112S D79A

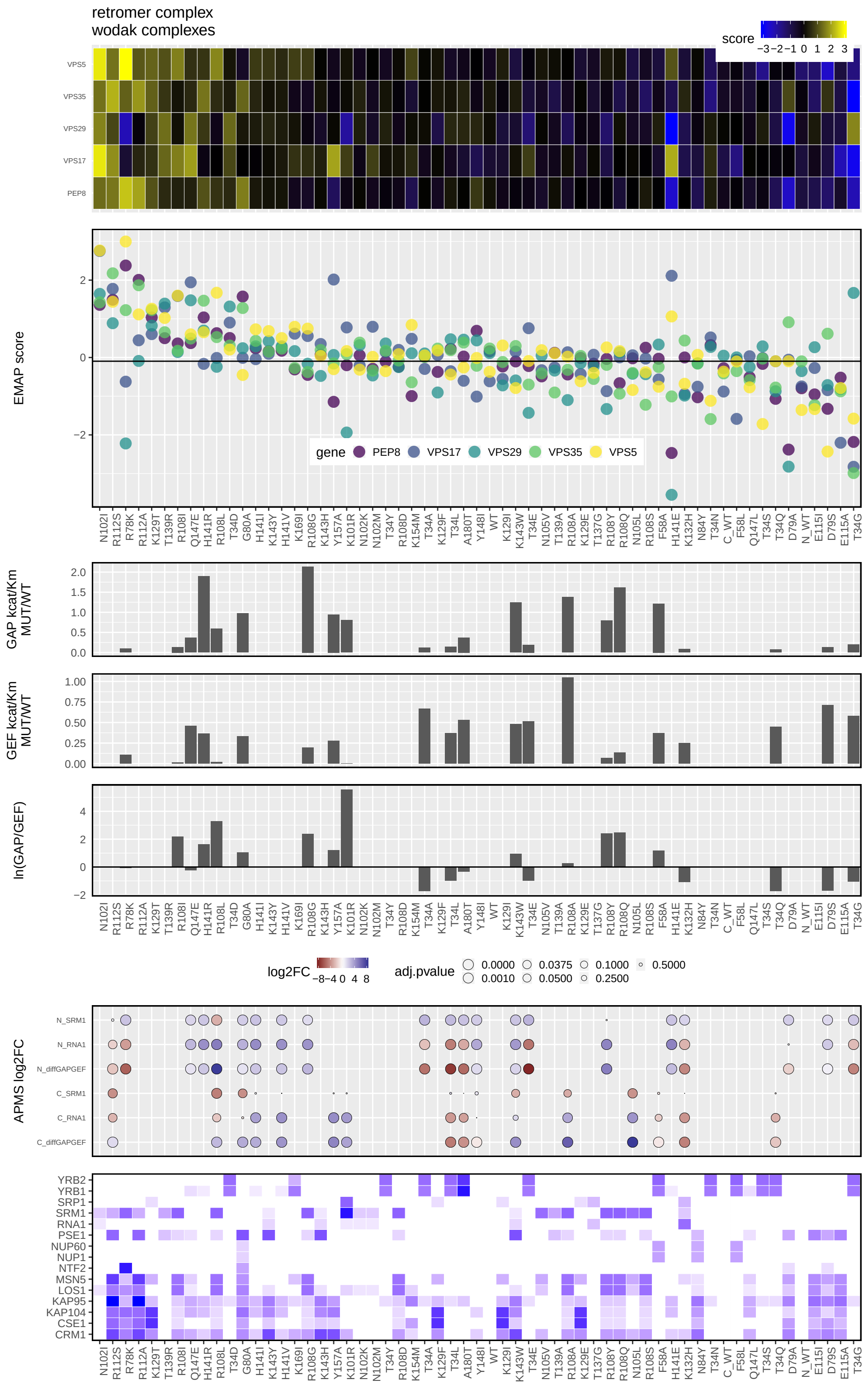

NatC complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MAK31
MAK3
MAK10
EMAP score
gene MAK10 MAK3 MAK31
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A H141R H141E R108Y R112S D79A R78K R108L T34G C_WT N_WT T34Q K101R R108Q Y148I D79S K132H R108G H141I Q147E N105V T34L R108I N105L N102I Y157A R108S R108A T34A K143Y R108D K129F T34S K169I F58A K154M F58L T139R T34E K143H A180T K129E WT H141V N102K T34N N102M K129T T34Y N84Y T137G E115A T139A T34D K143W Q147L E115I G80A K129I

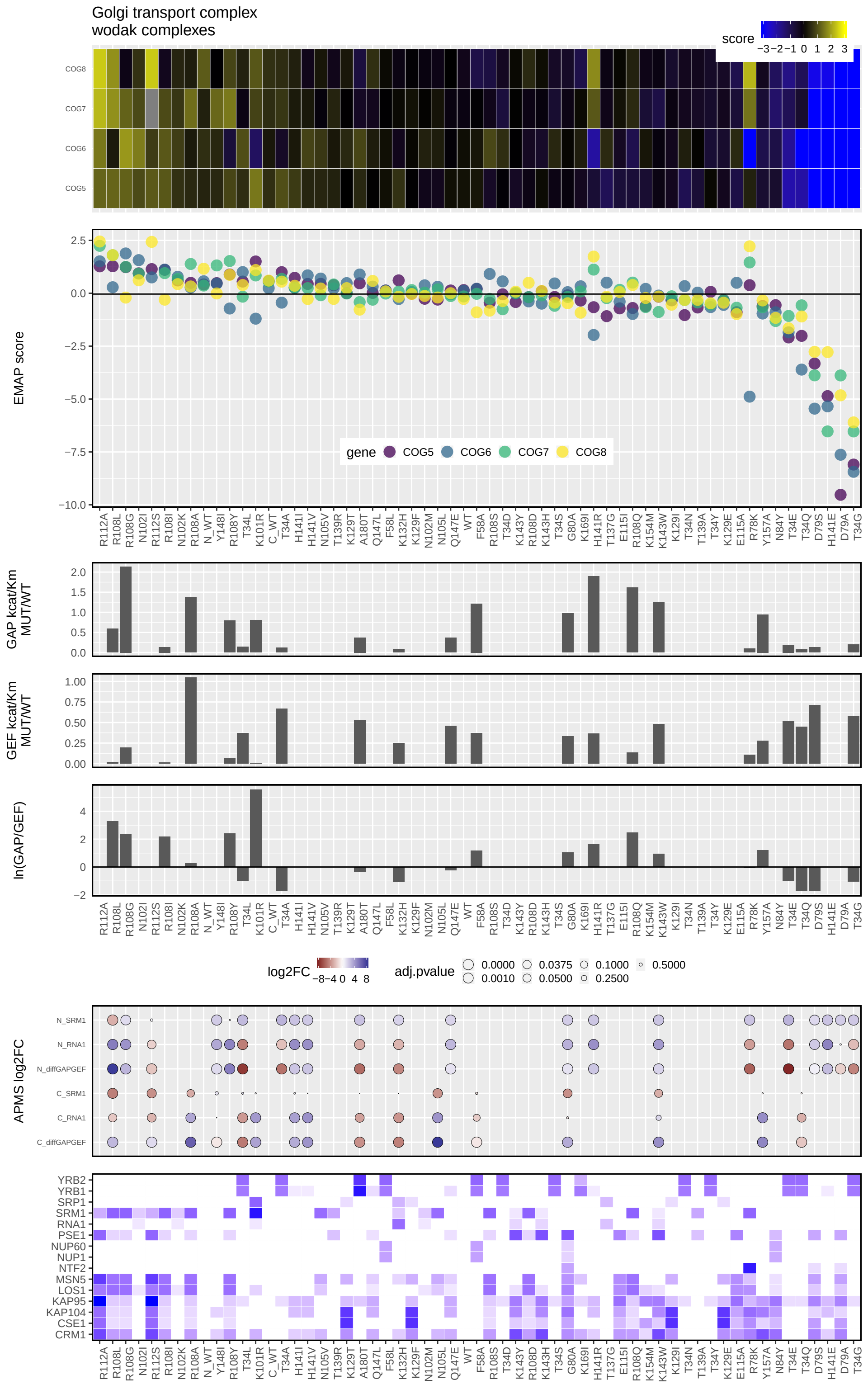

chromatin assembly complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RLF2
MSI1
EMAP score
gene
MSI1
RLF2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141R R112S H141E D79A R112A R108L Y148I H141I T34G R108G R78K R108Q R108A R108Y K143W C_WT R108I N105V K154M N_WT K143H Y157A K132H H141V N102I K143Y N105L N102K R108D T34N T139A K129F Q147E R108S T34E F58A T34L K169I T139R K129T Q147L T34D T34Q T34A T34S E115I A180T K129I N102M E115A K101R K129E T34Y T137G D79S N84Y F58L G80A WT

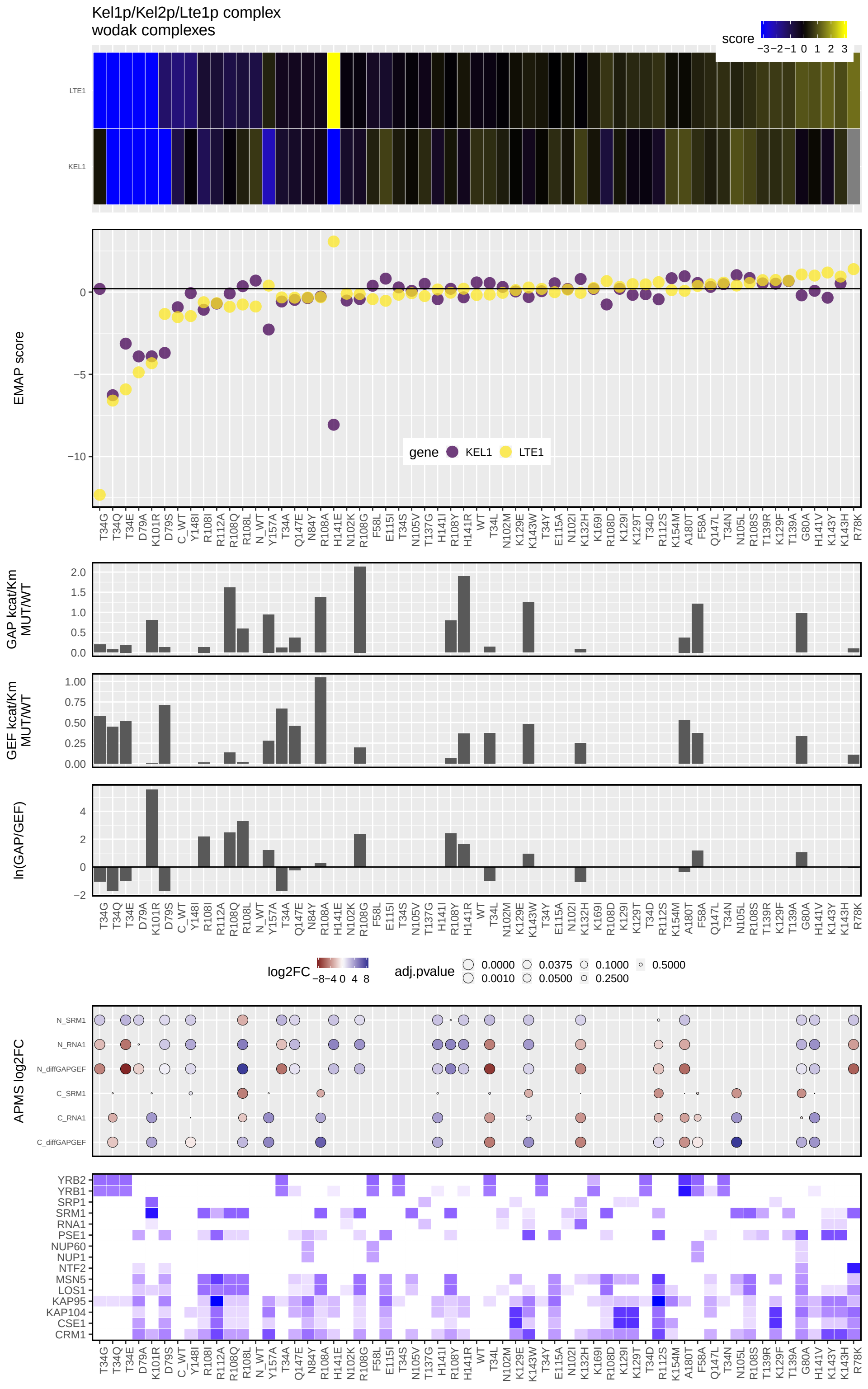

COPII
wodak complexes
score
−3 −2 −1 0 1 2 3
ERV46
ERV25
ERP2
ERP1
EMAP score
gene
ERP1
ERP2
ERV25
ERV46
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K T34Q H141E H141R R108Y R112A R112S R108Q K101R R108L Y148I D79A G80A T34G N105L K129E H141I N_WT D79S K129I K129F C_WT R108G E115I T139R N105V R108D N102M WT K169I T34Y R108A R108S R108I H141V E115A T137G Y157A T139A T34S K143W K154M K129T T34A K143Y T34E T34L K143H T34N A180T N84Y F58L Q147L F58A N102K T34D Q147E K132H N102I

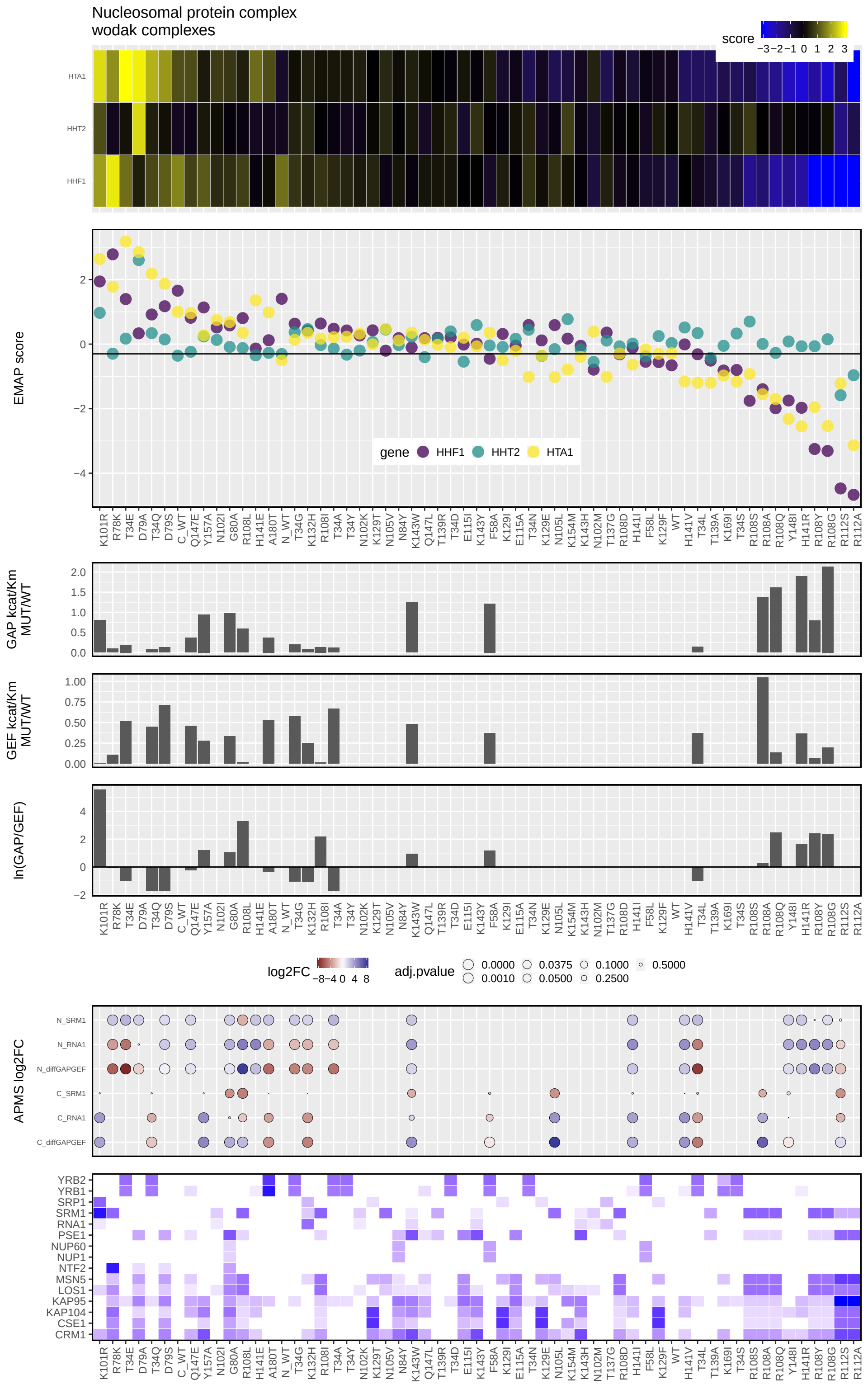

MBF complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SWI6
MBP1
EMAP score
gene
MBP1
SWI6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A R108Y H141E T34G R108L R112S D79A R108G K101R R108I T34Q K129F H141R R108Q T34E D79S K129E A180T R108S T34A R108A K154M C_WT H141I N_WT F58L K143W K132H E115I N84Y K143Y K143H N102I Y157A K129T F58A R108D N105V Q147E T34L H141V N102K K129I N105L WT E115A T137G Y148I T34D Q147L T34S G80A T34Y N102M T139A T34N K169I T139R R78K

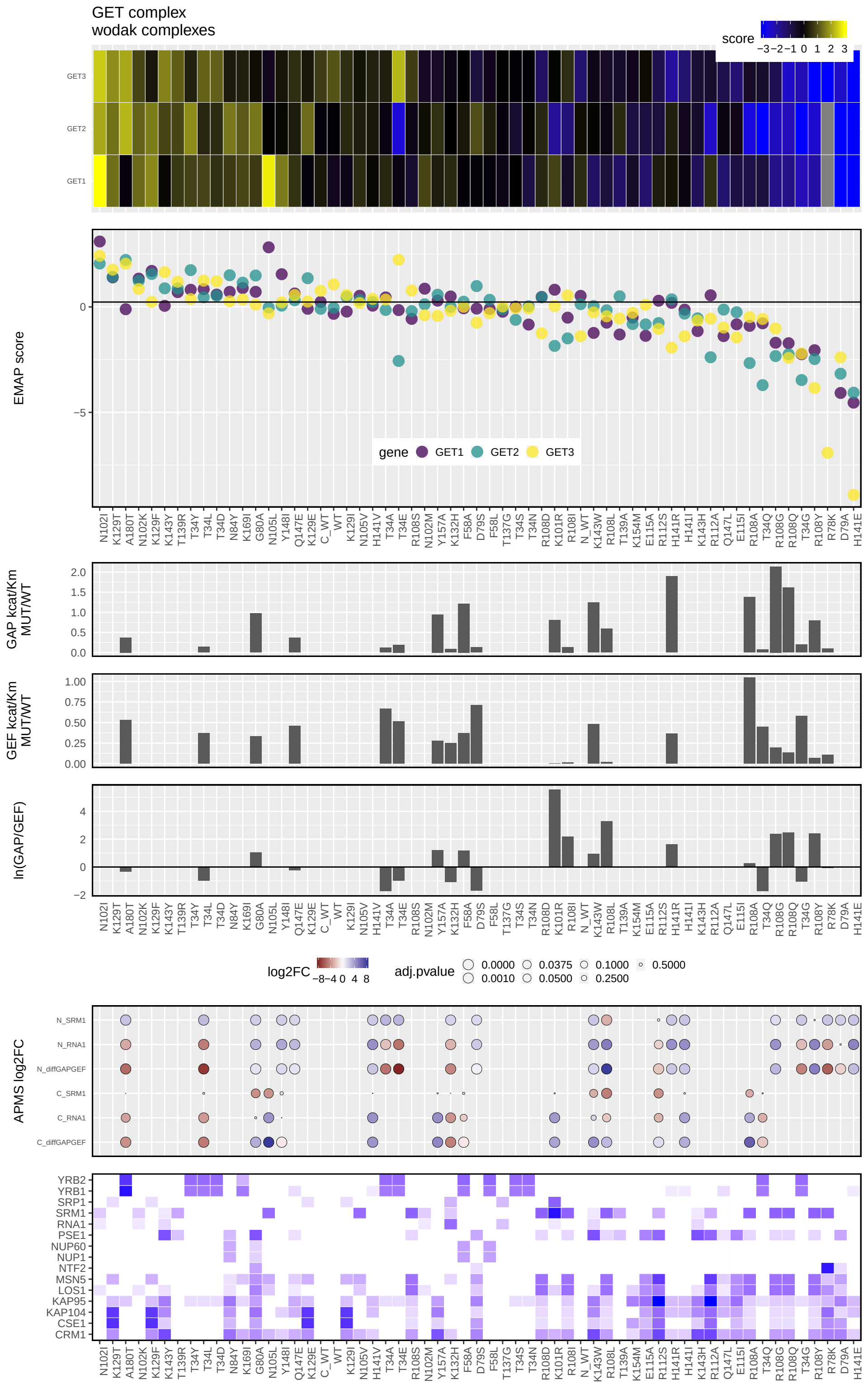

Gcn1p/Gcn20p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
GCN20
GCN1
EMAP score
gene
GCN1
GCN20
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34G H141E R112A T34E D79S T34Q N_WT K101R R112S R108Y R108G R108Q Y148I Y157A R108S K169I K143W Q147E R108L C_WT H141V Q147L H141I K143H R108A K132H N102I K129T T34D T34N R108D T34A T34L N105L K154M H141R R108I K143Y E115A N105V T34S G80A WT F58L K129E K129F T34Y A180T N102M T139R T137G N102K T139A K129I N84Y F58A E115I R78K

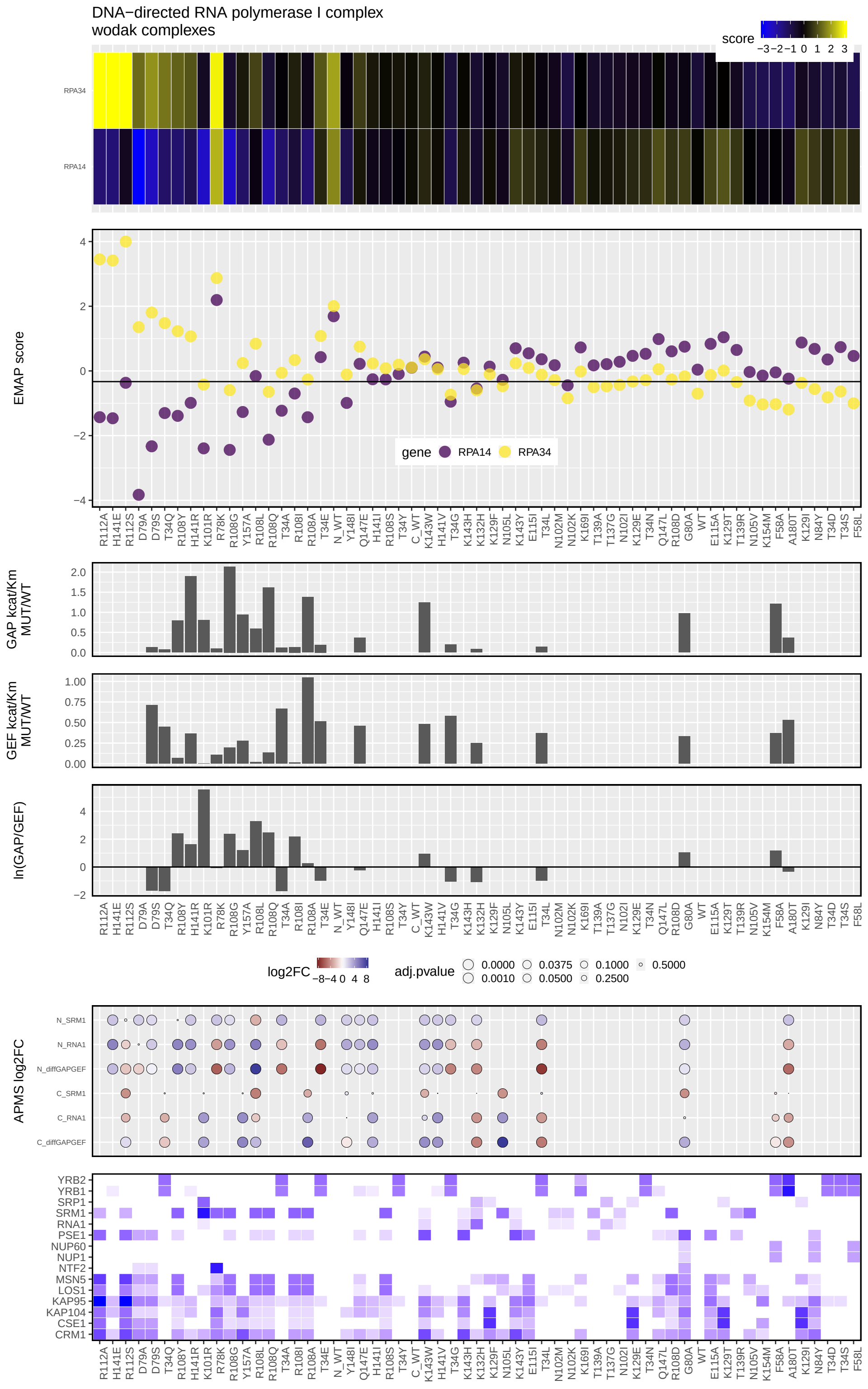

retromer complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VPS5
VPS35
VPS29
VPS17
PEP8
EMAP score
gene PEP8 VPS17 VPS29 VPS35 VPS5
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N102I R112S R78K R112A K129T T139R R108I Q147E H141R R108L T34D G80A H141I K143Y H141V K169I R108G K143H Y157A K101R N102K N102M T34Y R108D K154M T34A K129F T34L A180T Y148I WT K129I K143W T34E N105V T139A R108A K129E T137G R108Y R108Q N105L R108S F58A H141E K132H N84Y T34N C_WT F58L Q147L T34S T34Q D79A N_WT E115I D79S E115A T34G

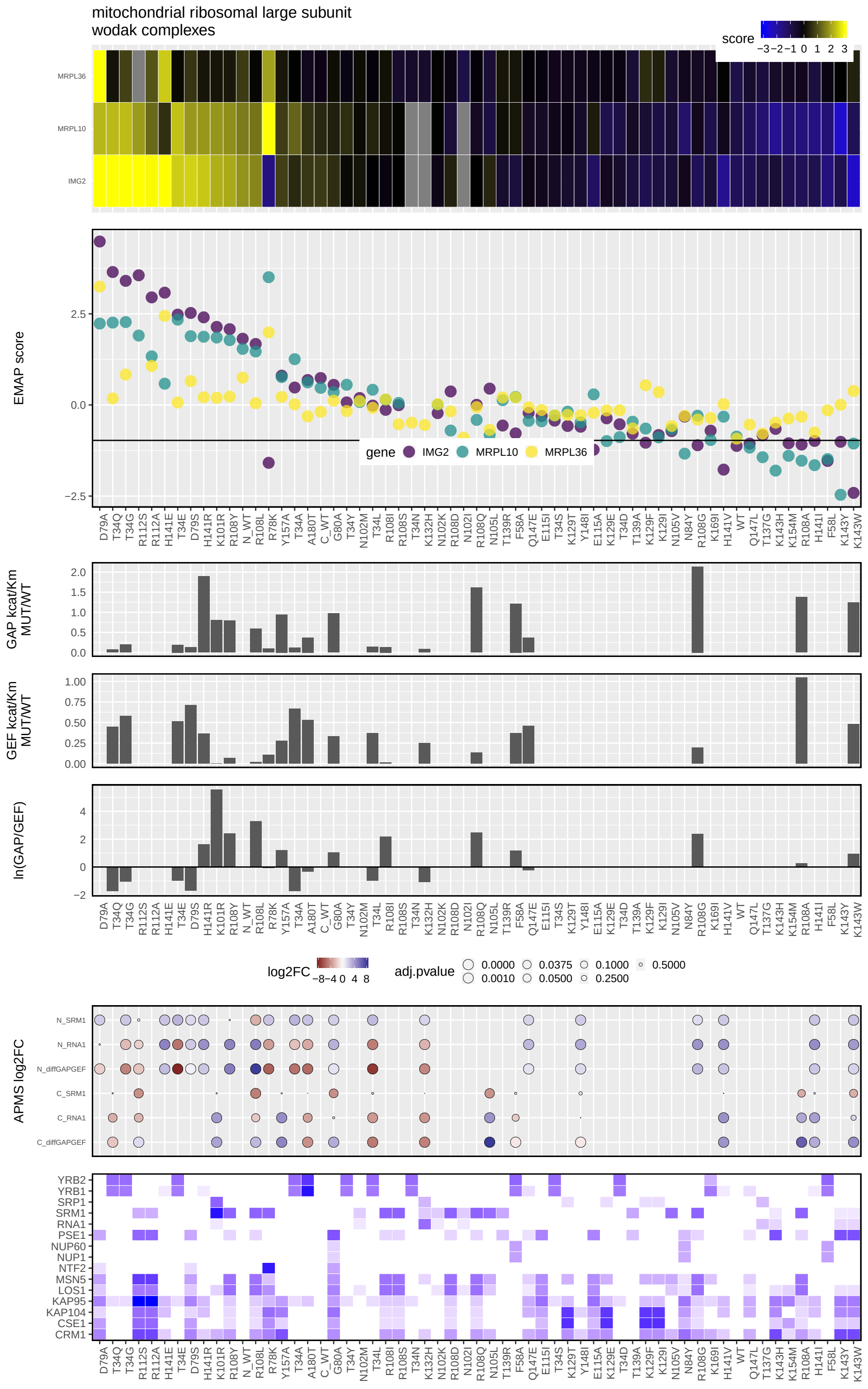

Golgi transport complex
wodak complexes
score
−3 −2 −1 0 1 2 3
COG8
COG7
COG6
COG5
EMAP score
gene COG5 COG6 COG7 COG8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A R108L R108G N102I R112S R108I N102K R108A N_WT Y148I R108Y T34L K101R C_WT T34A H141I H141V N105V T139R K129T A180T Q147L F58L K132H K129F N102M N105L Q147E WT F58A R108S T34D K143Y R108D K143H T34S G80A K169I H141R T137G E115I R108Q K154M K143W K129I T34N T139A T34Y K129E E115A R78K Y157A N84Y T34E T34Q D79S H141E D79A T34G

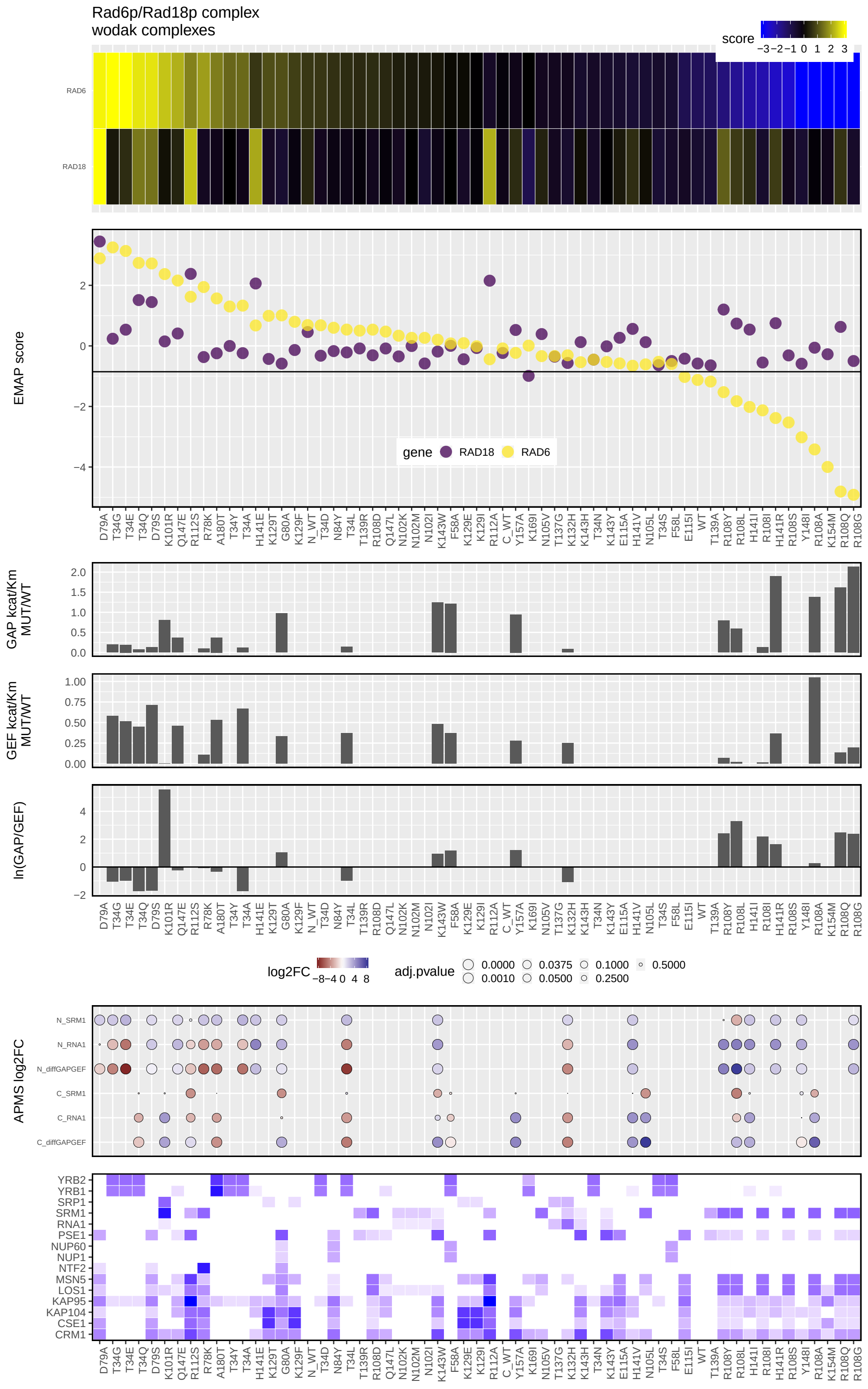

Kel1p/Kel2p/Lte1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
LTE1
KEL1
EMAP score
gene KEL1 LTE1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G T34Q T34E D79A K101R D79S C_WT Y148I R108I R112A R108Q R108L N_WT Y157A T34A Q147E N84Y R108A H141E N102K R108G F58L E115I T34S N105V T137G H141I R108Y H141R WT T34L N102M K129E K143W T34Y E115A N102I K132H K169I R108D K129I K129T T34D R112S K154M A180T F58A Q147L T34N N105L R108S T139R K129F T139A G80A H141V K143Y K143H R78K

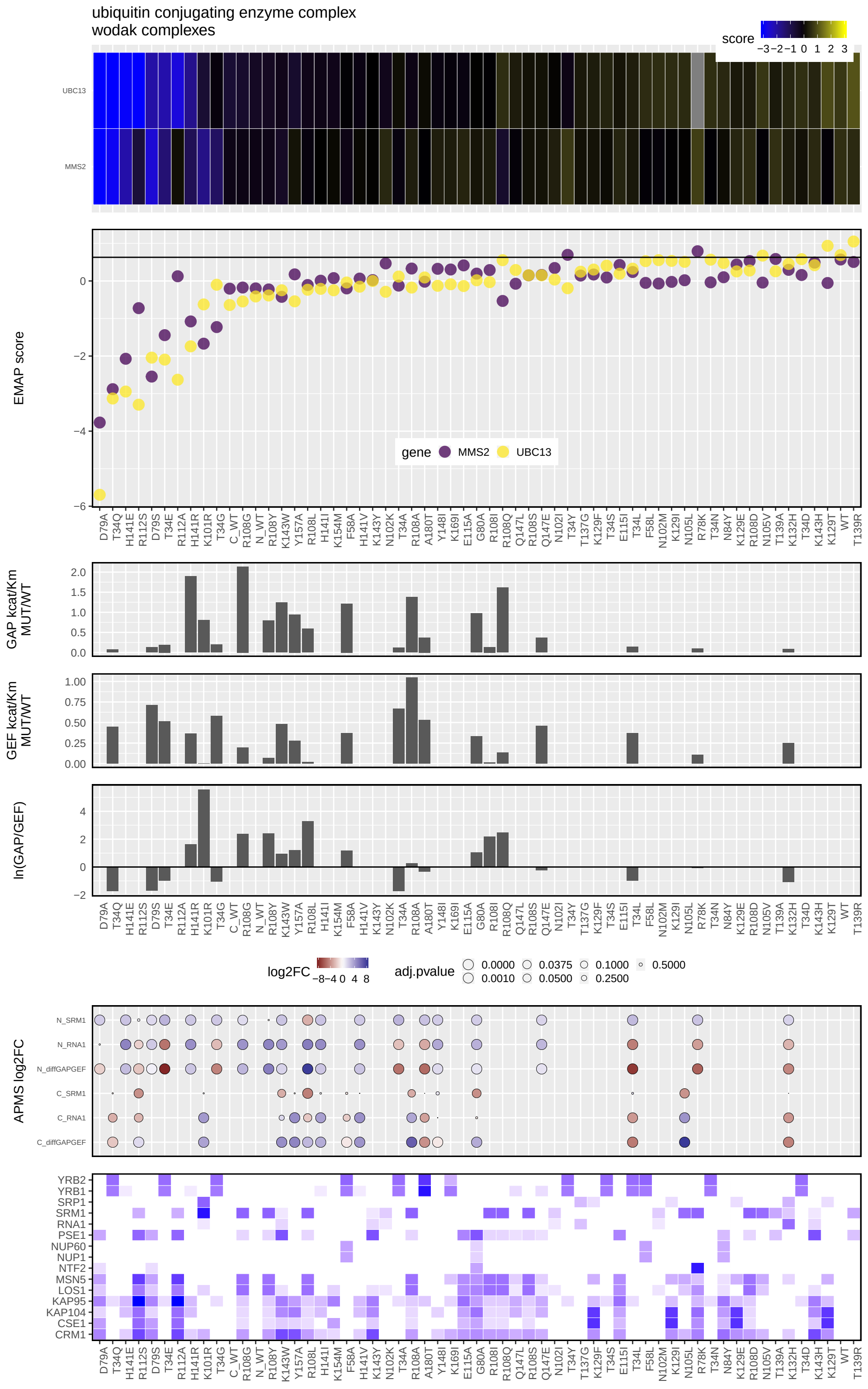

Nucleosomal protein complex
wodak complexes
score
−3 −2 −1 0 1 2 3
HTA1
HHT2
HHF1
EMAP score
gene HHF1 HHT2 HTA1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K101R R78K T34E D79A T34Q D79S C_WT Q147E Y157A N102I G80A R108L H141E A180T N_WT T34G K132H R108I T34A T34Y N102K K129T N105V N84Y K143W Q147L T139R T34D E115I K143Y F58A K129I E115A T34N K129E N105L K154M K143H N102M T137G R108D H141I F58L K129F WT H141V T34L T139A K169I T34S R108S R108A R108Q Y148I H141R R108Y R108G R112S R112A

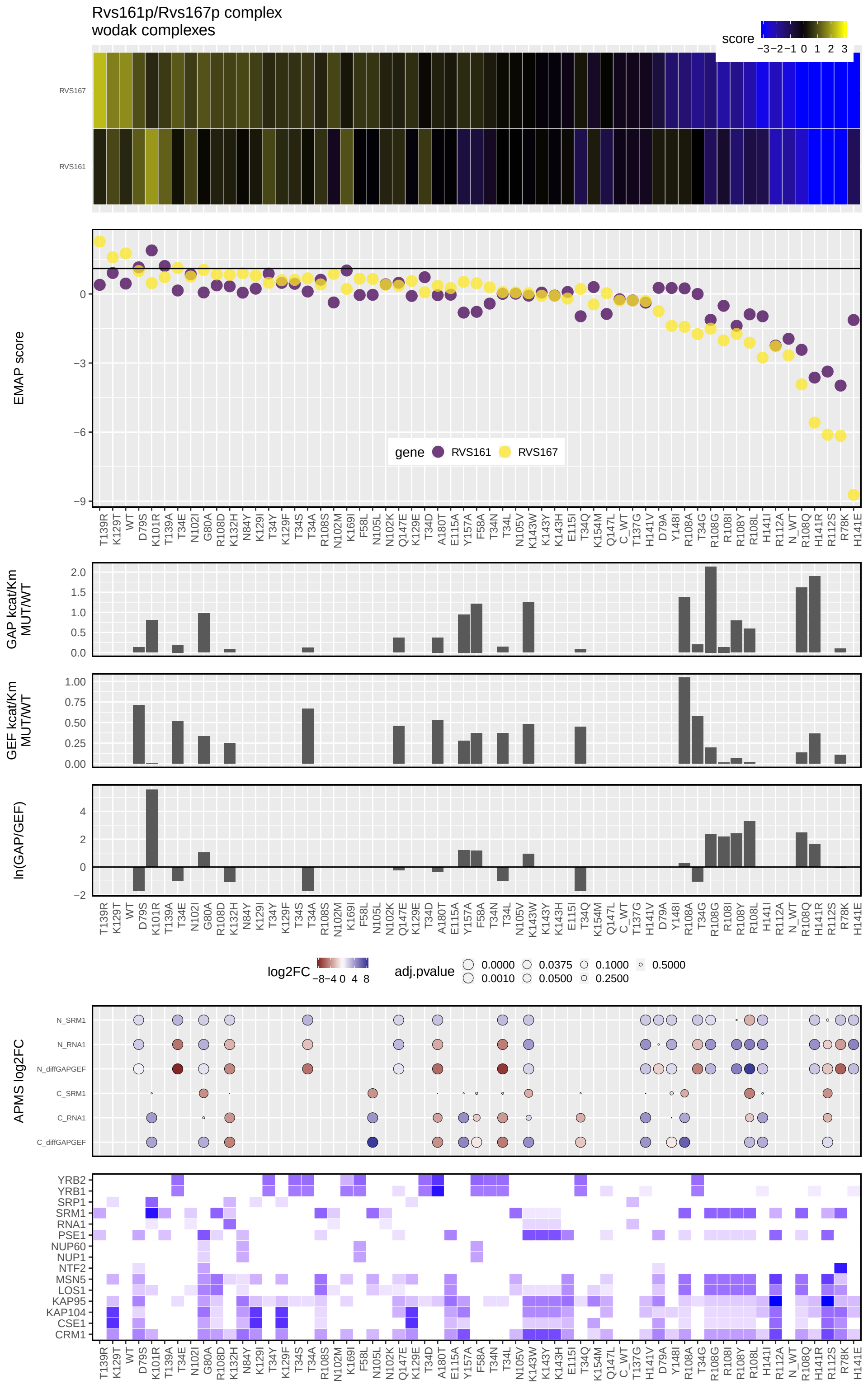

GET complex
wodak complexes
score
−3 −2 −1 0 1 2 3
GET3
GET2
GET1
EMAP score
gene GET1 GET2 GET3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N102I K129T A180T N102K K129F K143Y T139R T34Y T34L T34D N84Y K169I G80A N105L Y148I Q147E K129E C_WT WT K129I N105V H141V T34A T34E R108S N102M Y157A K132H F58A D79S F58L T137G T34S T34N R108D K101R R108I N_WT K143W R108L T139A K154M E115A R112S H141R H141I K143H R112A Q147L E115I R108A T34Q R108G R108Q T34G R108Y R78K D79A H141E

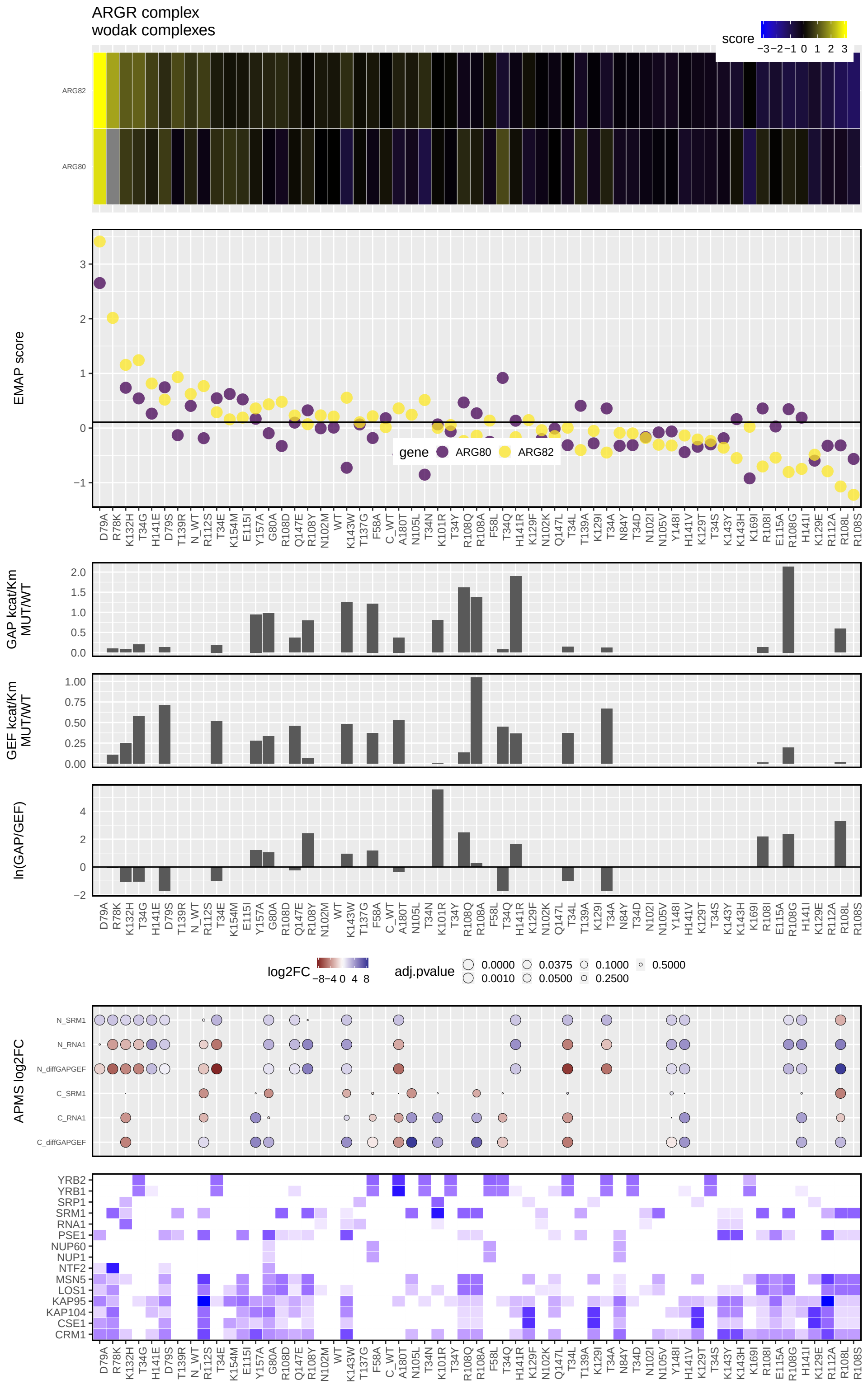

DNA−directed RNA polymerase I complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RPA34
RPA14
EMAP score
gene
RPA14
RPA34
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A H141E R112S D79A D79S T34Q R108Y H141R K101R R78K R108G Y157A R108L R108Q T34A R108I R108A T34E N_WT Y148I Q147E H141I R108S T34Y C_WT K143W H141V T34G K143H K132H K129F N105L K143Y E115I T34L N102M N102K K169I T139A T137G N102I K129E T34N Q147L R108D G80A WT E115A K129T T139R N105V K154M F58A A180T K129I N84Y T34D T34S F58L

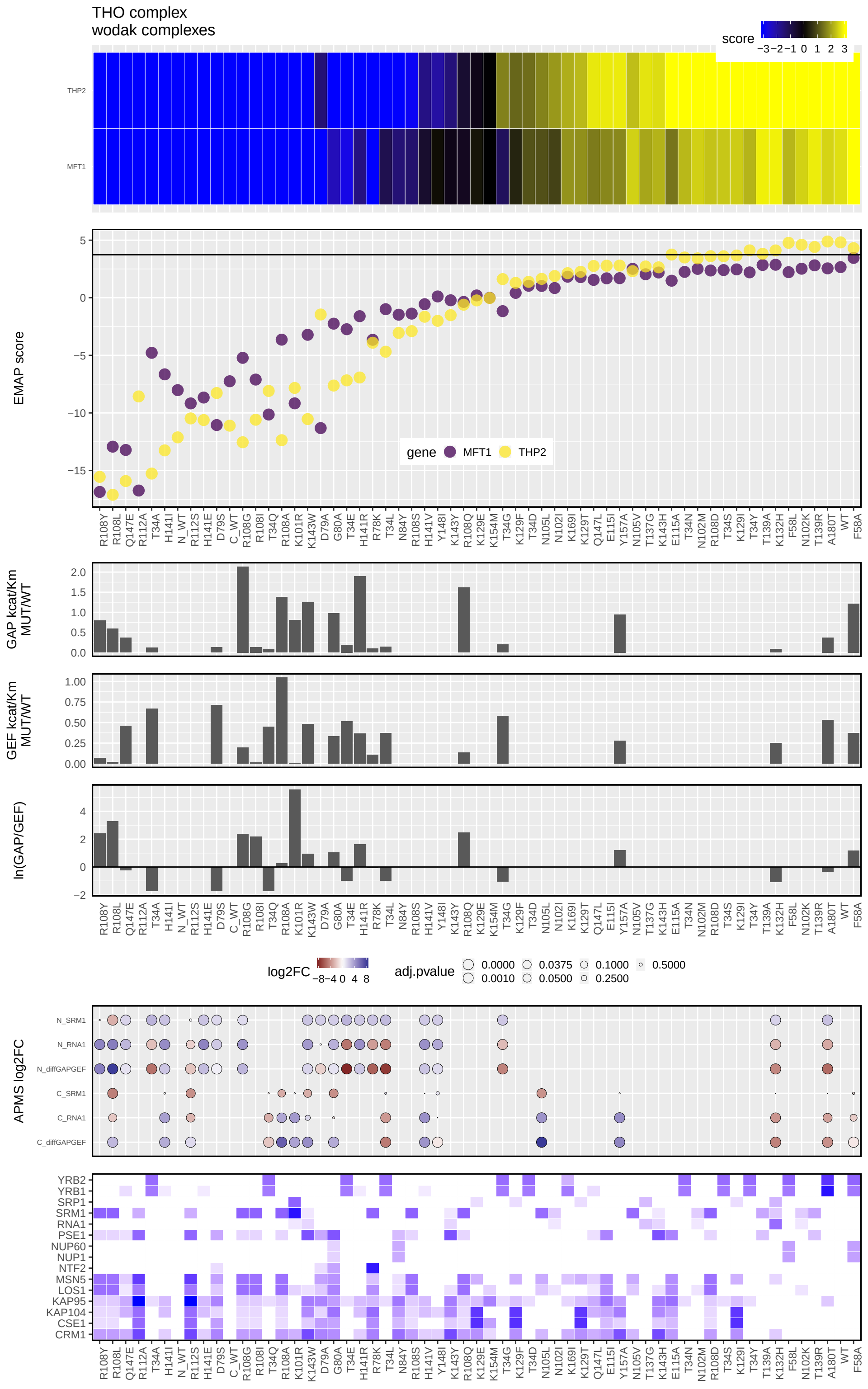

mitochondrial ribosomal large subunit
wodak complexes
score
−3 −2 −1 0 1 2 3
MRPL36
MRPL10
IMG2
EMAP score
gene
IMG2
MRPL10
MRPL36
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34Q T34G R112S R112A H141E T34E D79S H141R K101R R108Y N_WT R108L R78K Y157A T34A A180T C_WT G80A T34Y N102M T34L R108I R108S T34N K132H N102K R108D N102I R108Q N105L T139R F58A Q147E E115I T34S K129T Y148I E115A K129E T34D T139A K129F K129I N105V N84Y R108G K169I H141V WT Q147L T137G K143H K154M R108A H141I F58L K143Y K143W

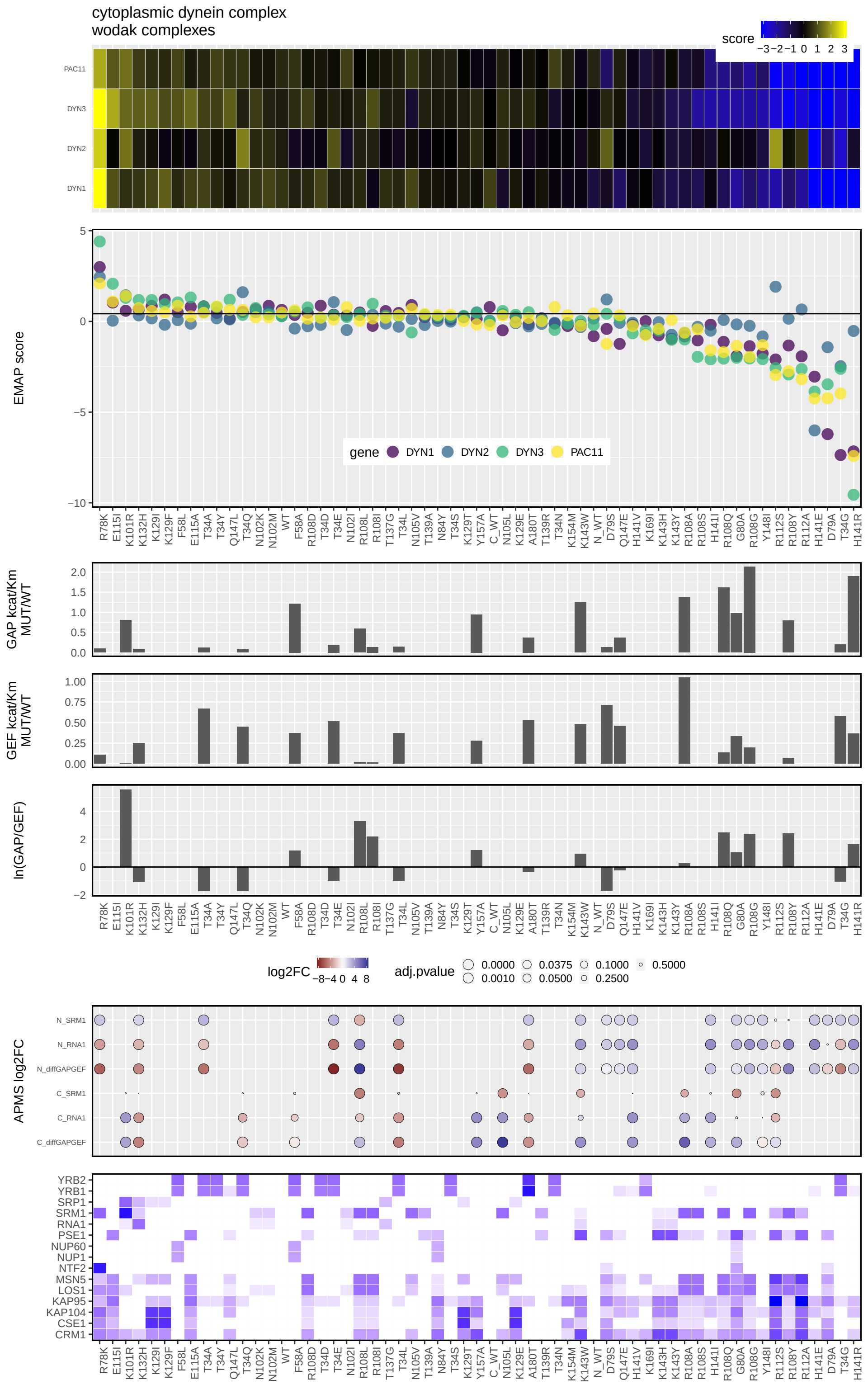

Rad6p/Rad18p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RAD6
RAD18
EMAP score
gene
RAD18
RAD6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34G T34E T34Q D79S K101R Q147E R112S R78K A180T T34Y T34A H141E K129T G80A K129F N_WT T34D N84Y T34L T139R R108D Q147L N102K N102M N102I K143W F58A K129E K129I R112A C_WT Y157A K169I N105V T137G K132H K143H T34N K143Y E115A H141V N105L T34S F58L E115I WT T139A R108Y R108L H141I R108I H141R R108S Y148I R108A K154M R108Q R108G

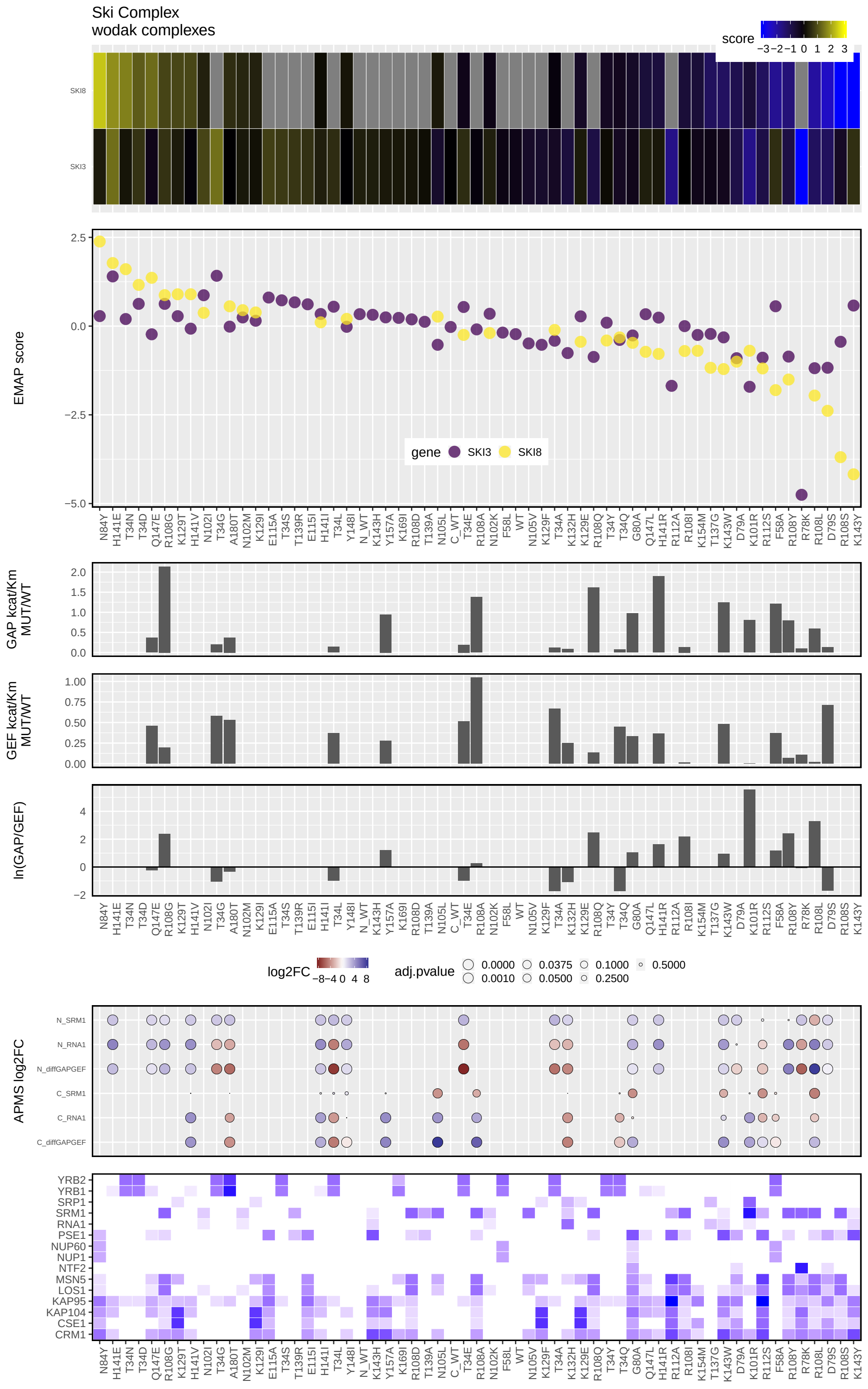

ubiquitin conjugating enzyme complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UBC13
MMS2
EMAP score
gene
MMS2
UBC13
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34Q H141E R112S D79S T34E R112A H141R K101R T34G C_WT R108G N_WT R108Y K143W Y157A R108L H141I K154M F58A H141V K143Y N102K T34A R108A A180T Y148I K169I E115A G80A R108I R108Q Q147L R108S Q147E N102I T34Y T137G K129F T34S E115I T34L F58L N102M K129I N105L R78K T34N N84Y K129E R108D N105V T139A K132H T34D K143H K129T WT T139R

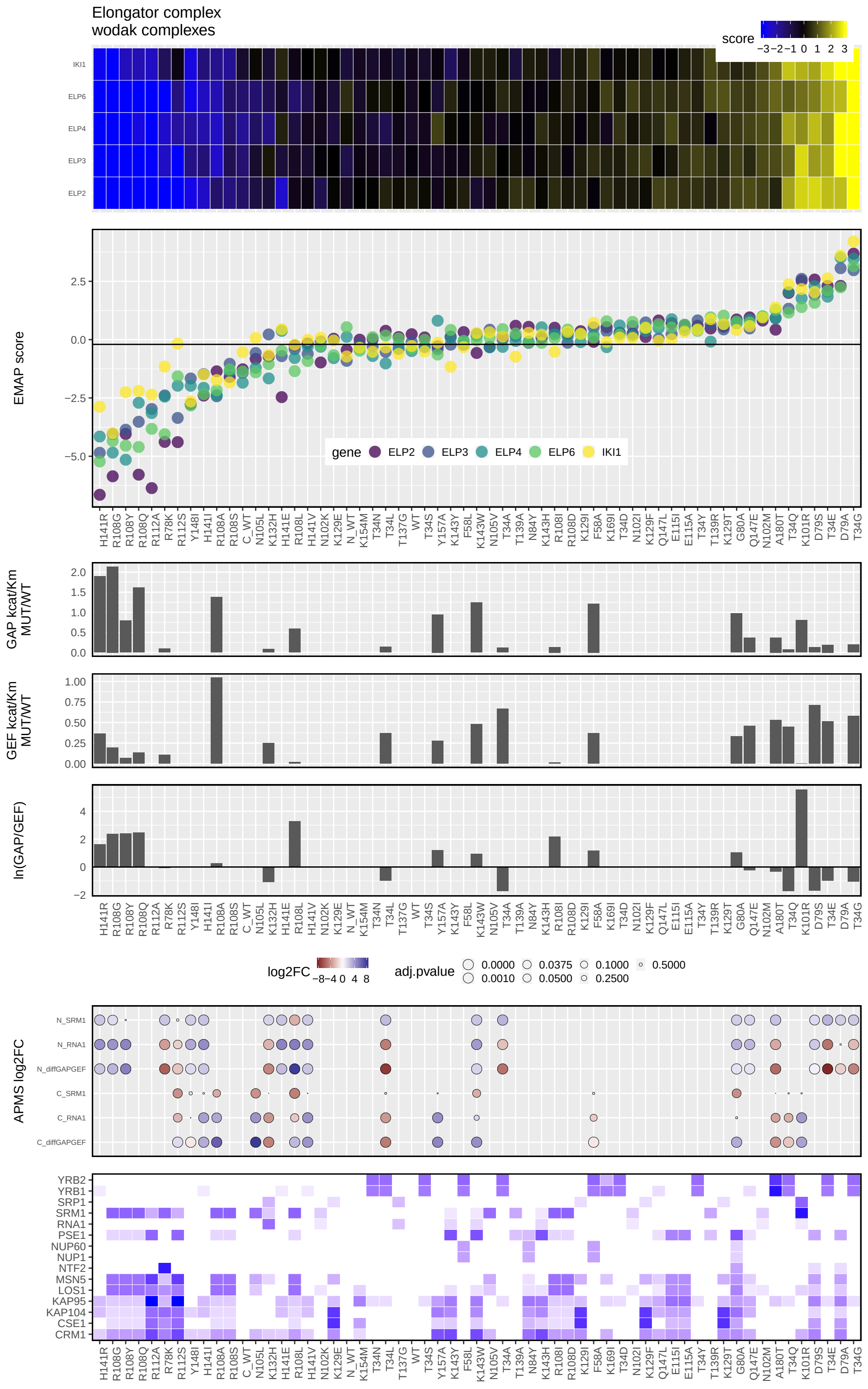

Rvs161p/Rvs167p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RVS167
RVS161
EMAP score
gene
RVS161
RVS167
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T139R K129T WT D79S K101R T139A T34E N102I G80A R108D K132H N84Y K129I T34Y K129F T34S T34A R108S N102M K169I F58L N105L N102K Q147E K129E T34D A180T E115A Y157A F58A T34N T34L N105V K143W K143Y K143H E115I T34Q K154M Q147L C_WT T137G H141V D79A Y148I R108A T34G R108G R108I R108Y R108L H141I R112A N_WT R108Q H141R R112S R78K H141E

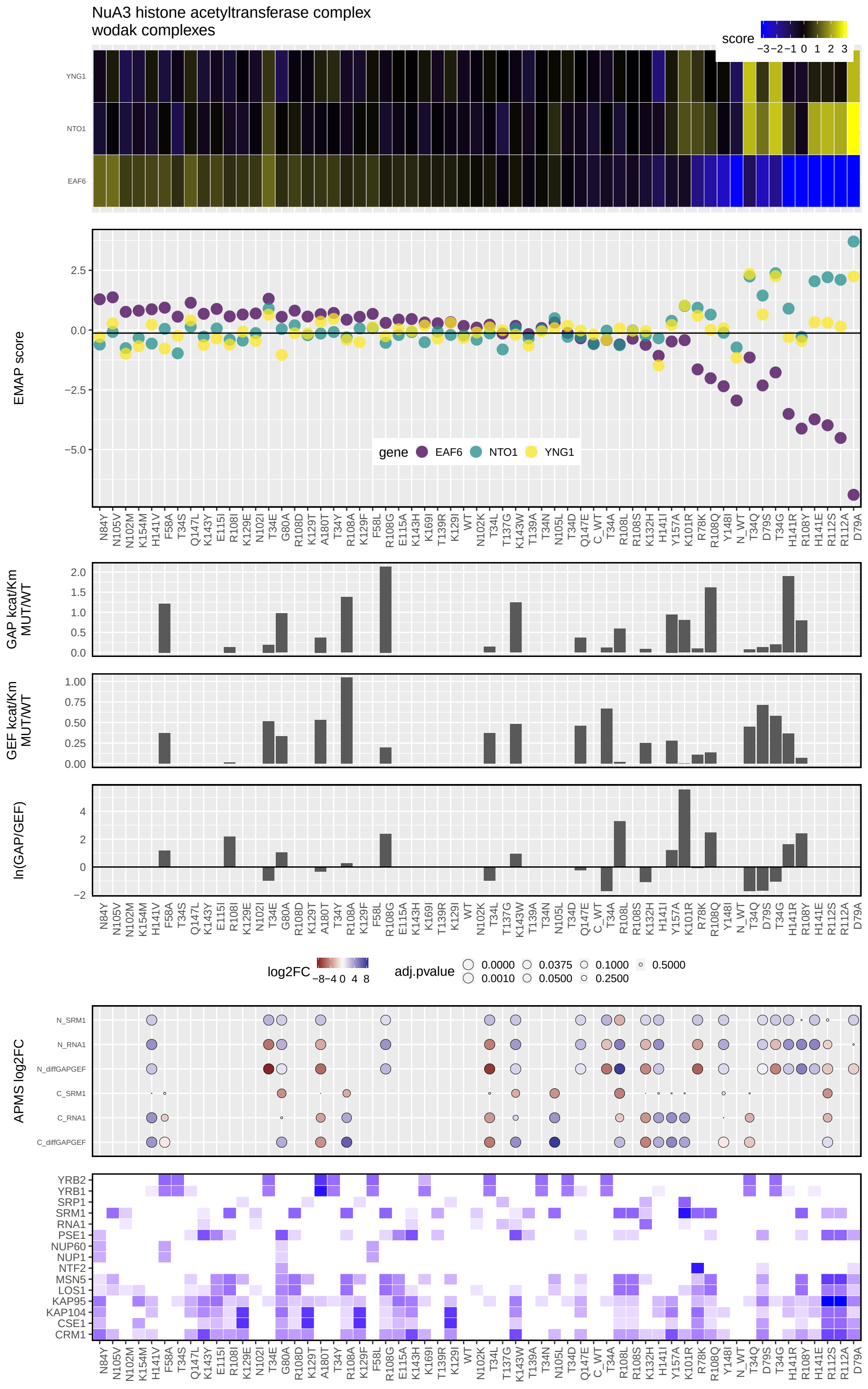

ARGR complex
wodak complexes
score
−3 −2 −1 0 1 2 3
ARG82
ARG80
EMAP score
gene
ARG80
ARG82
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R78K K132H T34G H141E D79S T139R N_WT R112S T34E K154M E115I Y157A G80A R108D Q147E R108Y N102M WT K143W T137G F58A C_WT A180T N105L T34N K101R T34Y R108Q R108A F58L T34Q H141R K129F N102K Q147L T34L T139A K129I T34A N84Y T34D N102I N105V Y148I H141V K129T T34S K143Y K143H K169I R108I E115A R108G H141I K129E R112A R108L R108S

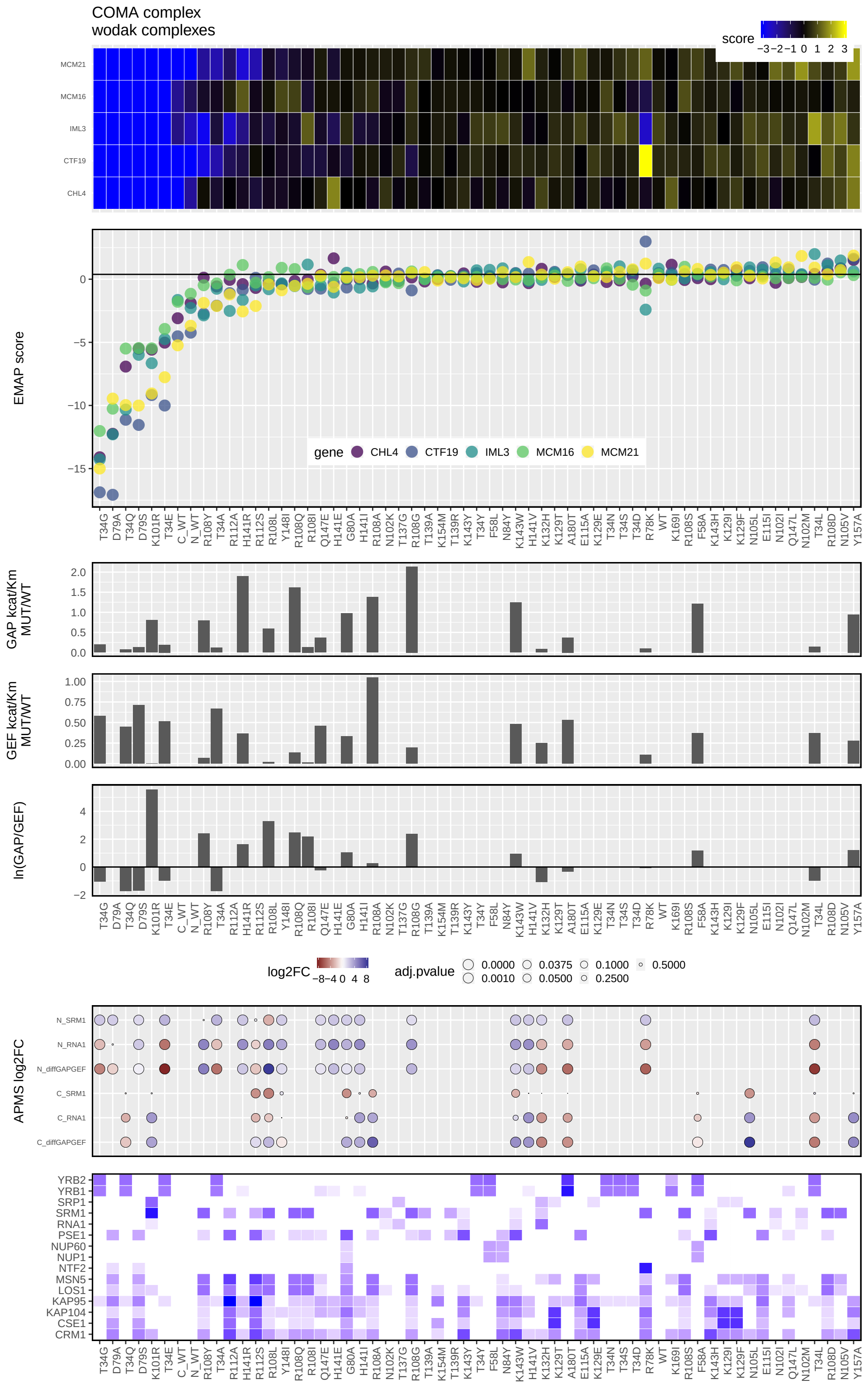

THO complex
wodak complexes
score
−3 −2 −1 0 1 2 3
THP2
MFT1
EMAP score
gene MFT1 THP2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108Y R108L Q147E R112A T34A H141I N_WT R112S H141E D79S C_WT R108G R108I T34Q R108A K101R K143W D79A G80A T34E H141R R78K T34L N84Y R108S H141V Y148I K143Y R108Q K129E K154M T34G K129F T34D N105L N102I K169I K129T Q147L E115I Y157A N105V T137G K143H E115A T34N N102M R108D T34S K129I T34Y T139A K132H F58L N102K T139R A180T WT F58A

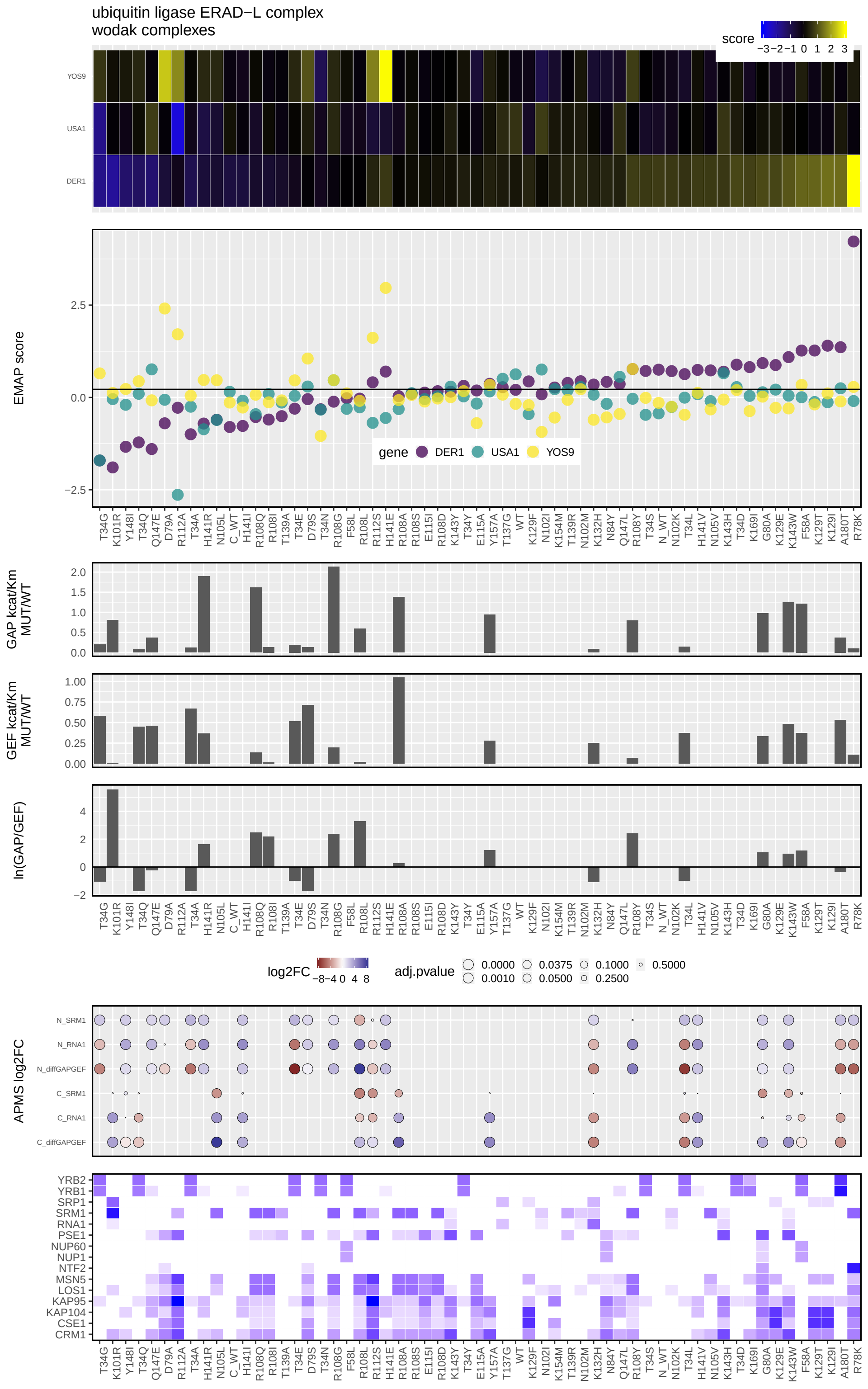

cytoplasmic dynein complex
wodak complexes
score
−3 −2 −1 0 1 2 3
PAC11
DYN3
DYN2
DYN1
EMAP score
gene
DYN1
DYN2
DYN3
PAC11
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K E115I K101R K132H K129I K129F F58L E115A T34A T34Y Q147L T34Q N102K N102M WT F58A R108D T34D T34E N102I R108L R108I T137G T34L N105V T139A N84Y T34S K129T Y157A C_WT N105L K129E A180T T139R T34N K154M K143W N_WT D79S Q147E H141V K169I K143H K143Y R108A R108S H141I R108Q G80A R108G Y148I R112S R108Y R112A H141E D79A T34G H141R

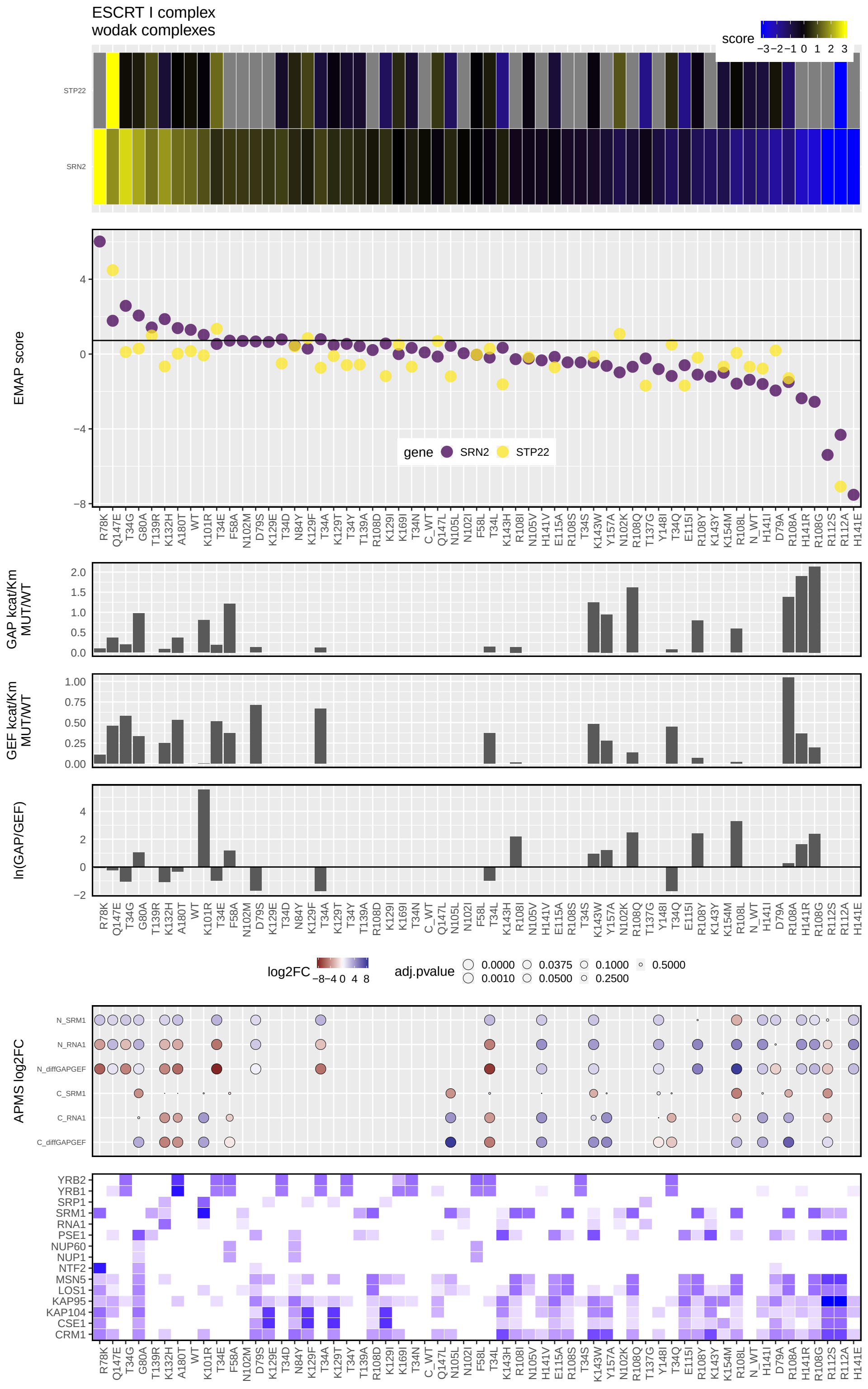

Ski Complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SKI8
SKI3
EMAP score
2.5
0.0
−2.5
−5.0
gene
SKI3
SKI8
N84Y H141E T34N T34D Q147E R108G K129T H141V N102I T34G A180T N102M K129I E115A T34S T139R E115I H141I T34L Y148I N_WT K143H Y157A K169I R108D T139A N105L C_WT T34E R108A N102K F58L WT N105V K129F T34A K132H K129E R108Q T34Y T34Q G80A Q147L H141R R112A R108I K154M T137G K143W D79A K101R R112S F58A R108Y R78K R108L D79S R108S K143Y
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

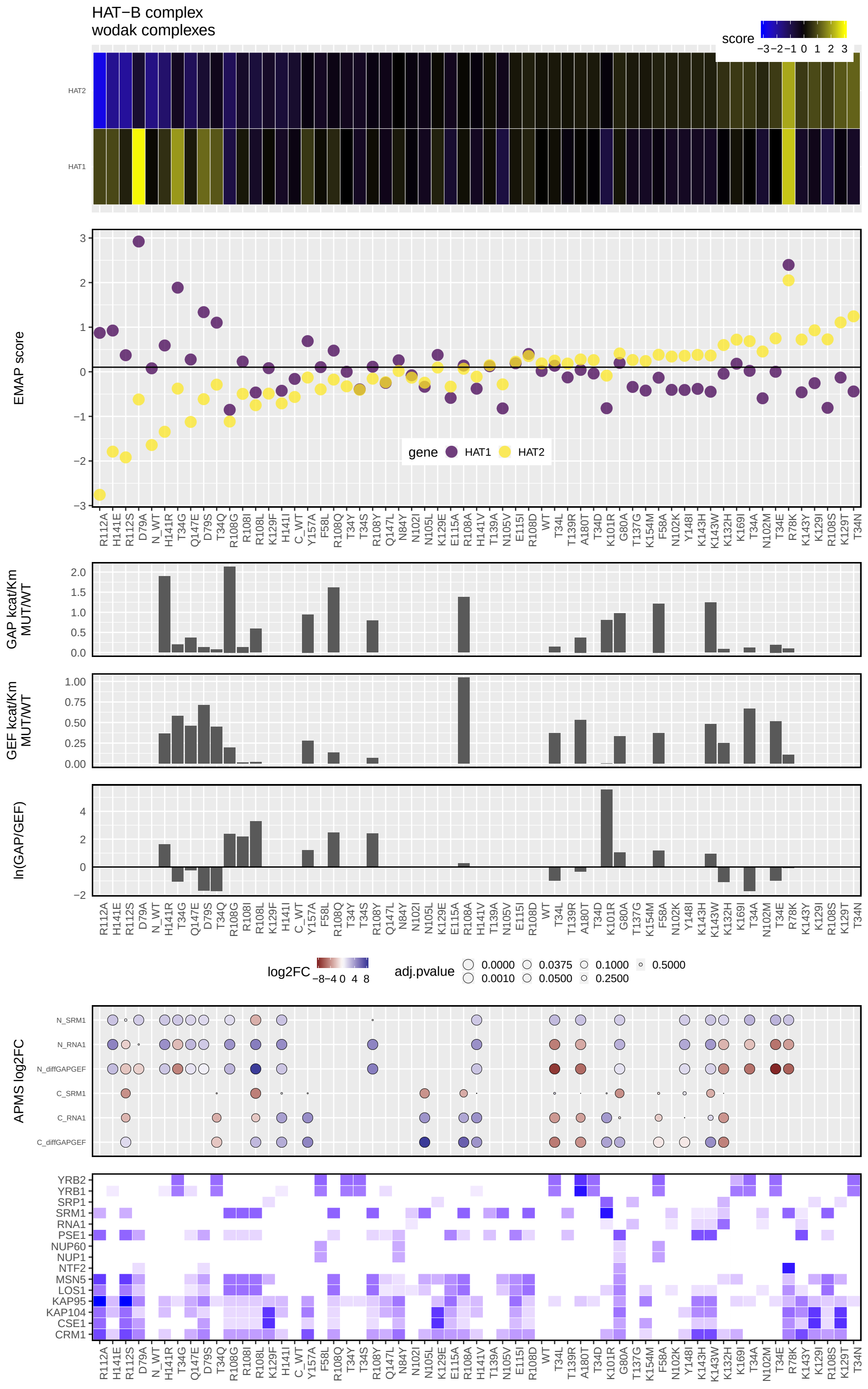

Elongator complex
wodak complexes
score
−3 −2 −1 0 1 2 3
IKI1
ELP6
ELP4
ELP3
ELP2
EMAP score
2.5
0.0
−2.5
−5.0
gene
ELP2
ELP3
ELP4
ELP6
IKI1
H141R R108G R108Y R108Q R112A R78K R112S Y148I H141I R108A R108S C_WT N105L K132H H141E R108L H141V N102K K129E N_WT K154M T34N T34L T137G WT T34S Y157A K143Y F58L K143W N105V T34A T139A N84Y K143H R108I R108D K129I F58A K169I T34D N102I K129F Q147L E115I E115A T34Y T139R K129T G80A Q147E N102M A180T T34Q K101R D79S T34E D79A T34G
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1


NuA3 histone acetyltransferase complex
wodak complexes
score
−3 −2 −1 0 1 2 3
YNG1
NTO1
EAF6
EMAP score
2.5
0.0
−2.5
−5.0
gene EAF6 NTO1 YNG1
N84Y N105V N102M K154M H141V F58A T34S Q147L K143Y E115I R108I K129E N102I T34E G80A R108D K129T A180T T34Y R108A K129F F58L R108G E115A K143H K169I T139R K129I WT N102K T34L T137G K143W T139A T34N N105L T34D Q147E C_WT T34A R108L R108S K132H H141I Y157A K101R R78K R108Q Y148I N_WT T34Q D79S T34G H141R R108Y H141E R112S R112A D79A
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1


COMA complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MCM21
MCM16
IML3
CTF19
CHL4
EMAP score
gene
CHL4
CTF19
IML3
MCM16
MCM21
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A T34Q D79S K101R T34E C_WT N_WT R108Y T34A R112A H141R R112S R108L Y148I R108Q R108I Q147E H141E G80A H141I R108A N102K T137G R108G T139A K154M T139R K143Y T34Y F58L N84Y K143W H141V K132H K129T A180T E115A K129E T34N T34S T34D R78K WT K169I R108S F58A K143H K129I K129F N105L E115I N102I Q147L N102M T34L R108D N105V Y157A


ubiquitin ligase ERAD−L complex
wodak complexes
score
−3 −2 −1 0 1 2 3
YOS9
USA1
DER1
EMAP score
2.5
0.0
−2.5
gene DER1 USA1 YOS9
T34G K101R Y148I T34Q Q147E D79A R112A T34A H141R N105L C_WT H141I R108Q R108I T139A T34E D79S T34N R108G F58L R108L R112S H141E R108A R108S E115I R108D K143Y T34Y E115A Y157A T137G WT K129F N102I K154M T139R N102M K132H N84Y Q147L R108Y T34S N_WT N102K T34L H141V N105V K143H T34D K169I G80A K129E K143W F58A K129T K129I A180T R78K
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1


ESCRT I complex
wodak complexes
score
−3 −2 −1 0 1 2 3
STP22
SRN2
EMAP score
gene
SRN2
STP22
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K Q147E T34G G80A T139R K132H A180T WT K101R T34E F58A N102M D79S K129E T34D N84Y K129F T34A K129T T34Y T139A R108D K129I K169I T34N C_WT Q147L N105L N102I F58L T34L K143H R108I N105V H141V E115A R108S T34S K143W Y157A N102K R108Q T137G Y148I T34Q E115I R108Y K143Y K154M R108L N_WT H141I D79A R108A H141R R108G R112S R112A H141E


HAT−B complex
wodak complexes
score
−3 −2 −1 0 1 2 3
HAT2
HAT1
EMAP score
gene
HAT1
HAT2
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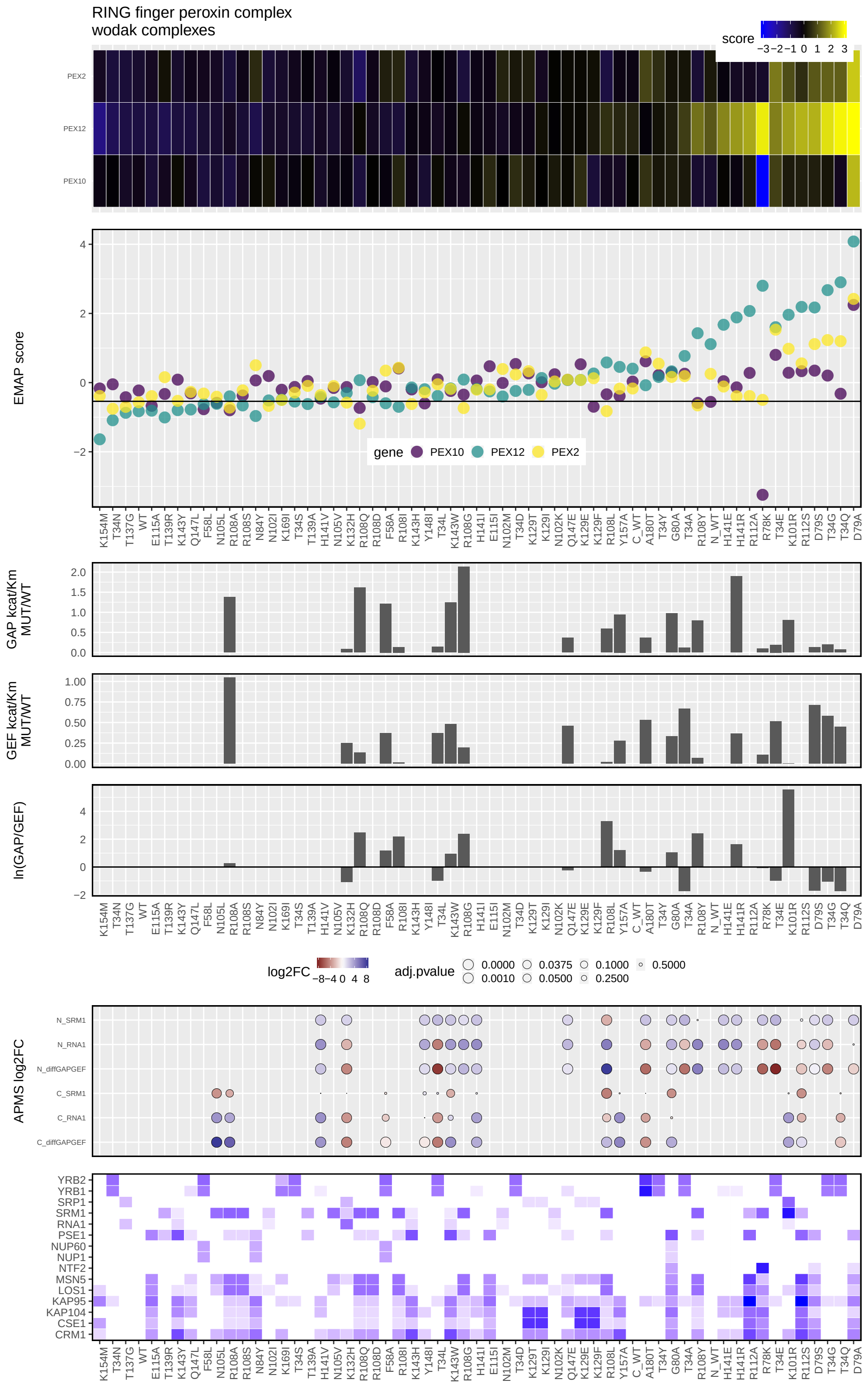
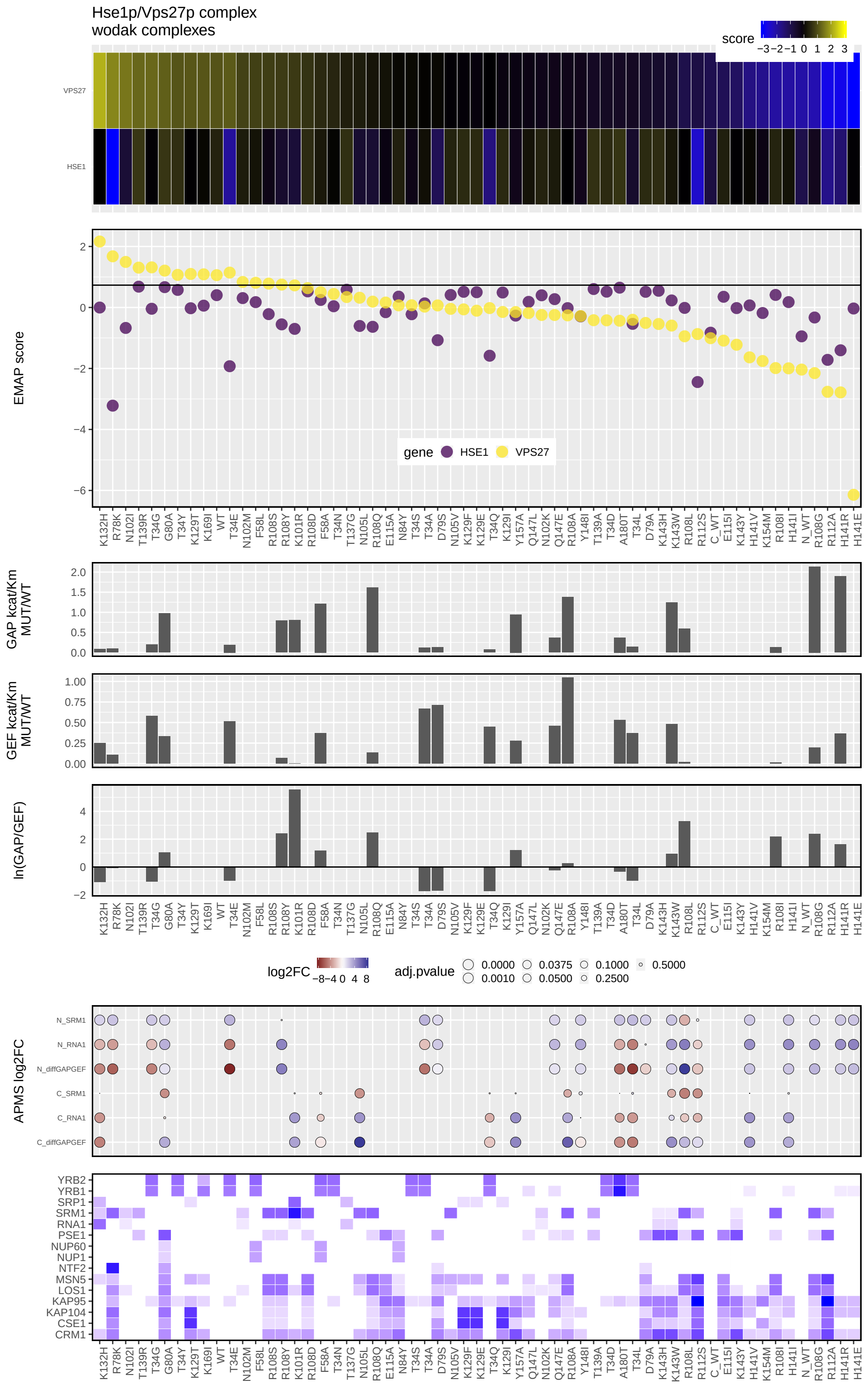
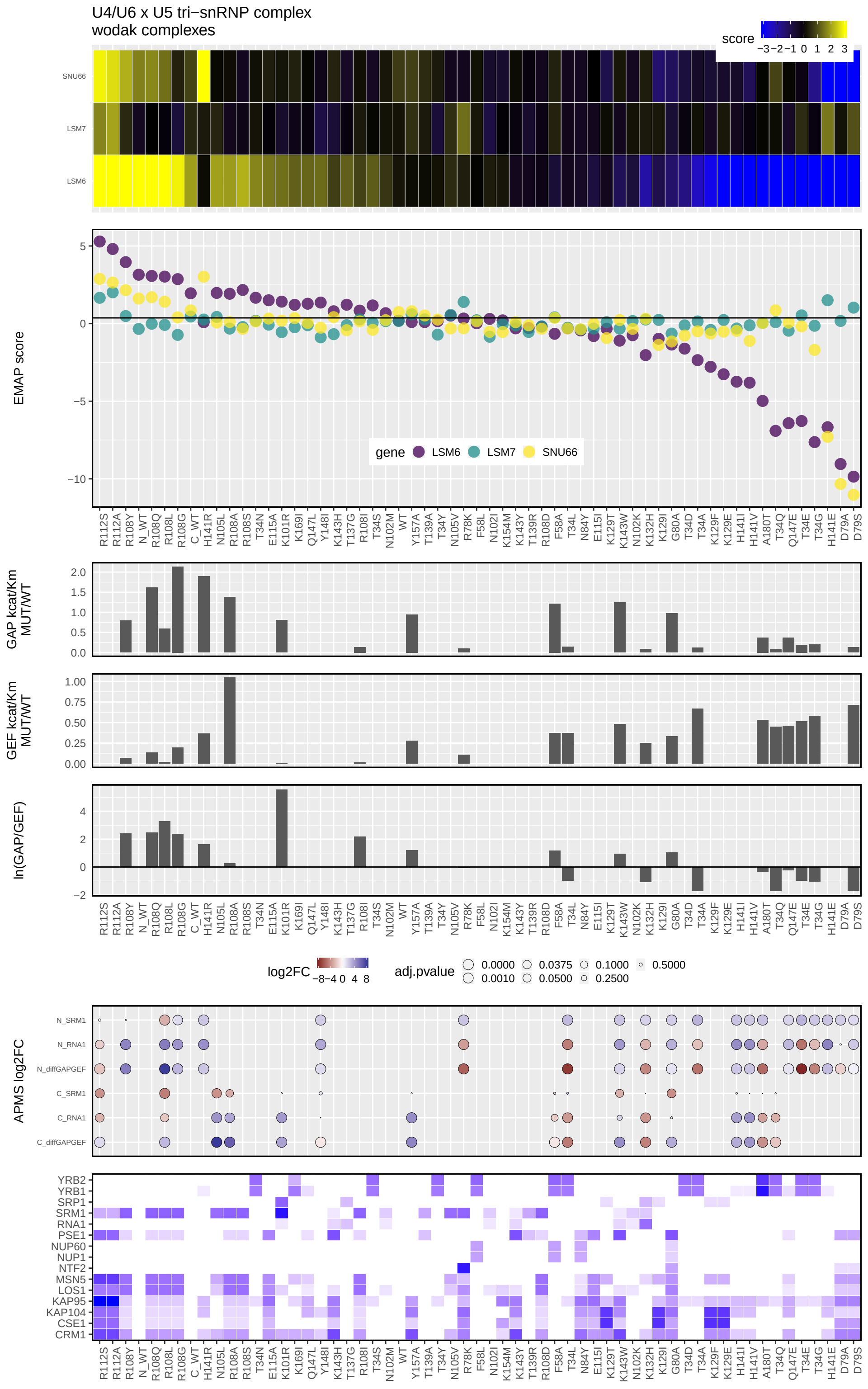
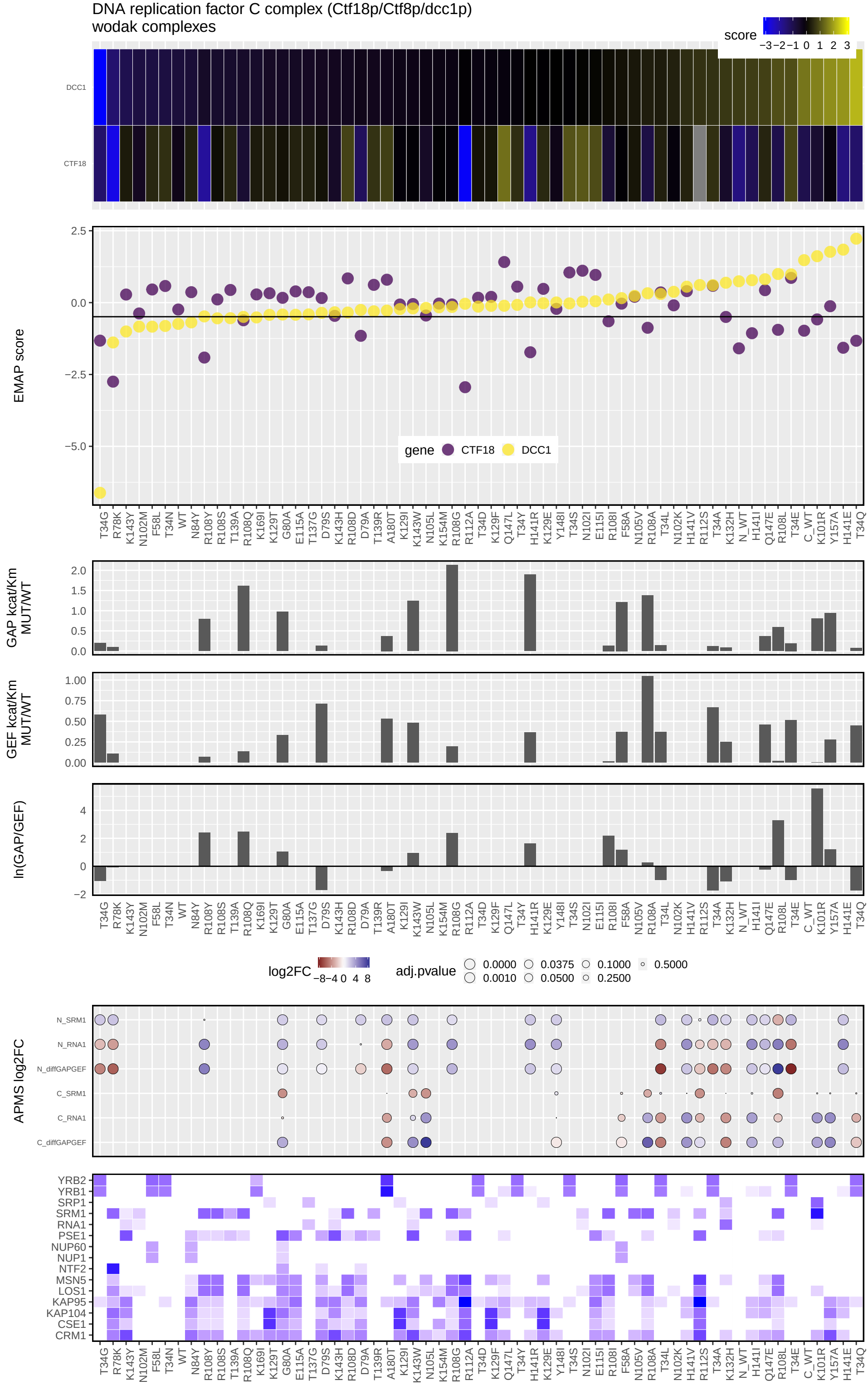
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A H141E R112S D79A N_WT H141R T34G Q147E D79S T34Q R108G R108I R108L K129F H141I C_WT Y157A F58L R108Q T34Y T34S R108Y Q147L N84Y N102I N105L K129E E115A R108A H141V T139A N105V E115I R108D WT T34L T139R A180T T34D K101R G80A T137G K154M F58A N102K Y148I K143H K143W K132H K169I T34A N102M T34E R78K K143Y K129I R108S K129T T34N

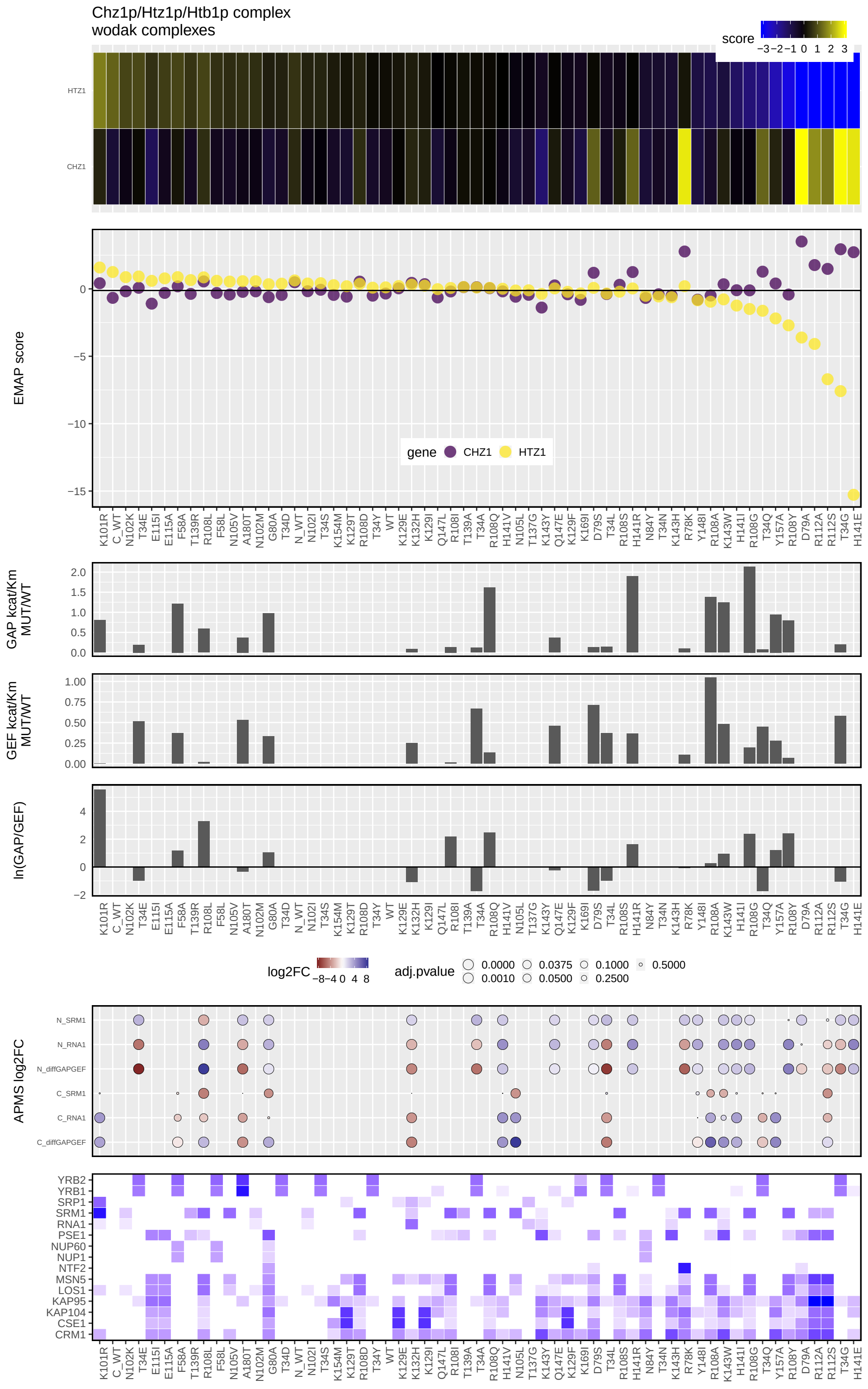

RING finger peroxin complex
wodak complexes
score
−3 −2 −1 0 1 2 3
PEX2
PEX12
PEX10
EMAP score
gene PEX10 PEX12 PEX2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K154M T34N T137G WT E115A T139R K143Y Q147L F58L N105L R108A R108S N84Y N102I K169I T34S T139A H141V N105V K132H R108Q R108D F58A R108I K143H Y148I T34L K143W R108G H141I E115I N102M T34D K129T K129I N102K Q147E K129E K129F R108L Y157A C_WT A180T T34Y G80A T34A R108Y N_WT H141E H141R R112A R78K T34E K101R R112S D79S T34G T34Q D79A


Hse1p/Vps27p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VPS27
HSE1
EMAP score
gene
HSE1
VPS27
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K132H R78K N102I T139R T34G G80A T34Y K129T K169I WT T34E N102M F58L R108S R108Y K101R R108D F58A T34N T137G N105L R108Q E115A N84Y T34S T34A D79S N105V K129F K129E T34Q K129I Y157A Q147L N102K Q147E R108A Y148I T139A T34D A180T T34L D79A K143H K143W R108L R112S C_WT E115I K143Y H141V K154M R108I H141I N_WT R108G R112A H141R H141E

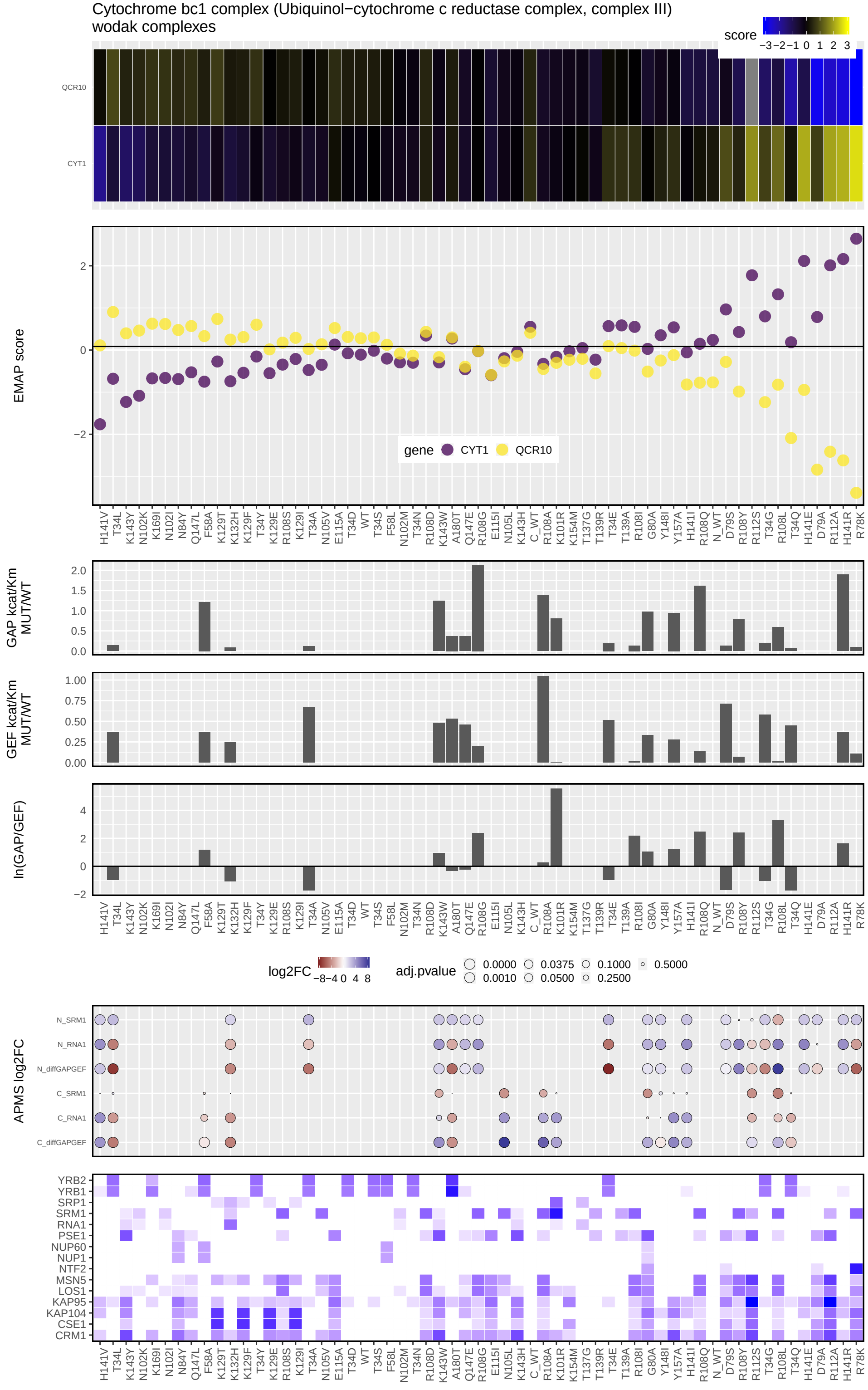

U4/U6 x U5 tri−snRNP complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SNU66
LSM7
LSM6
EMAP score
gene LSM6 LSM7 SNU66
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112S R112A R108Y N_WT R108Q R108L R108G C_WT H141R N105L R108A R108S T34N E115A K101R K169I Q147L Y148I K143H T137G R108I T34S N102M WT Y157A T139A T34Y N105V R78K F58L N102I K154M K143Y T139R R108D F58A T34L N84Y E115I K129T K143W N102K K132H K129I G80A T34D T34A K129F K129E H141I H141V A180T T34Q Q147E T34E T34G H141E D79A D79S

DNA replication factor C complex (Ctf18p/Ctf8p/dcc1p)
wodak complexes

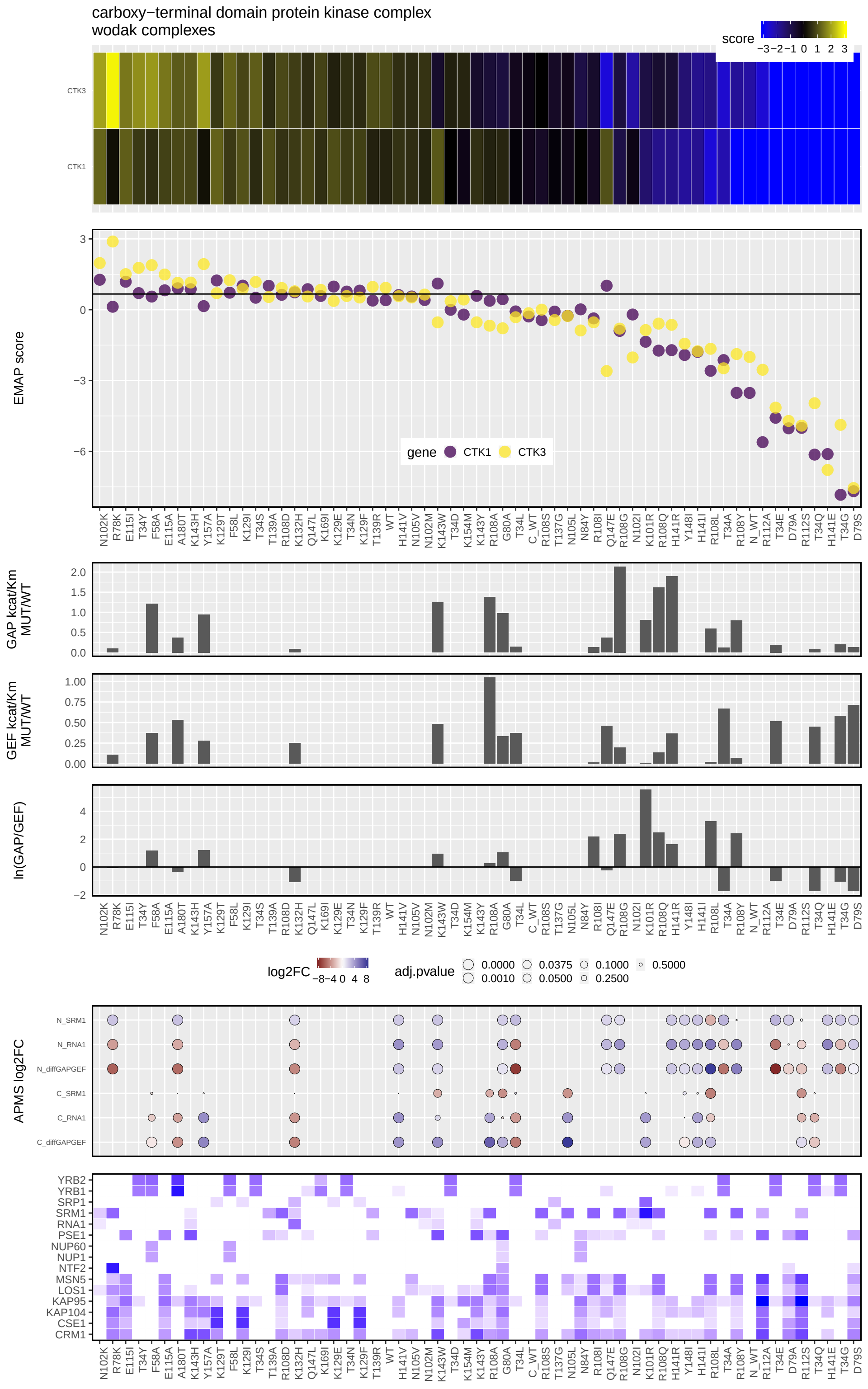


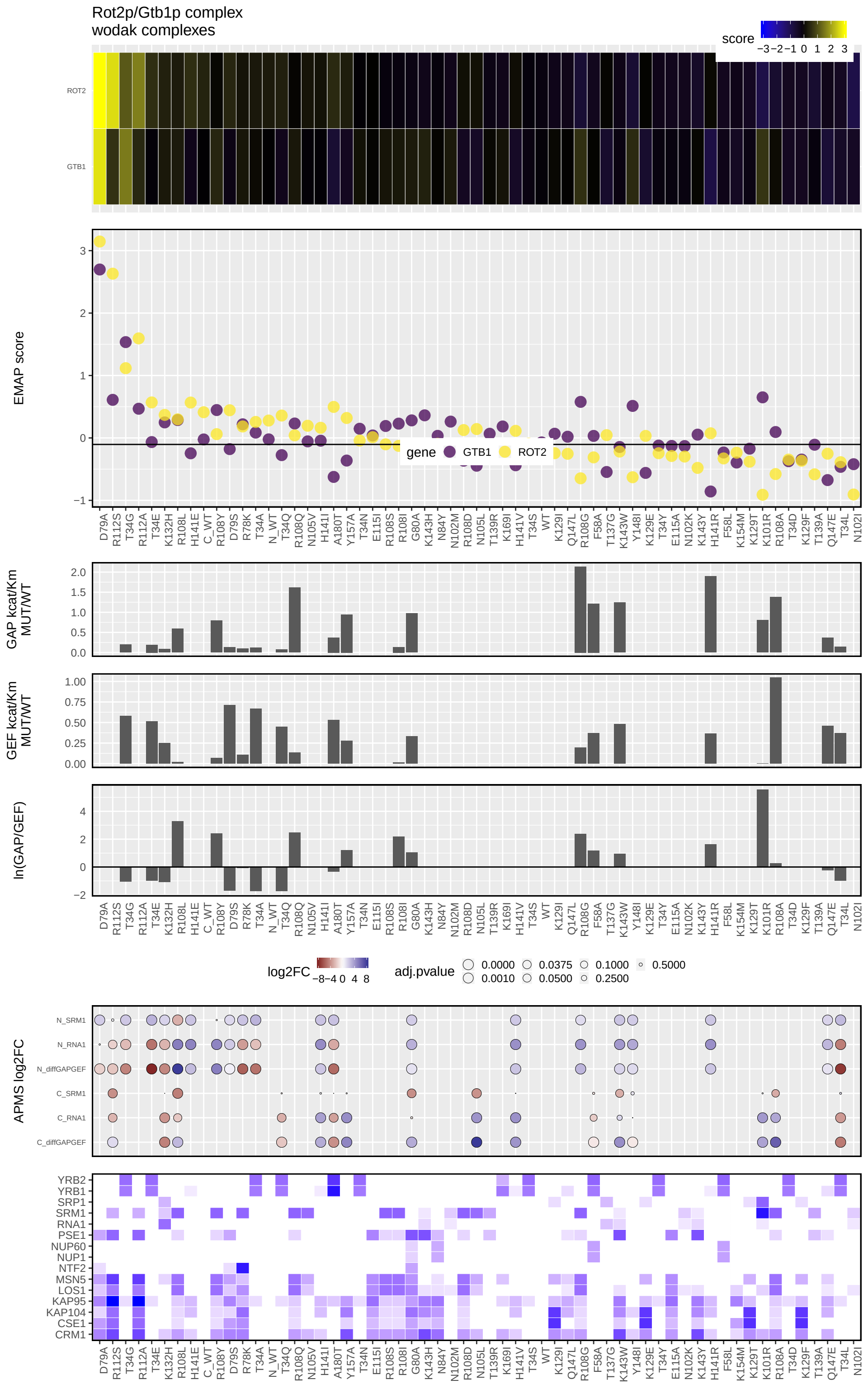

Chz1p/Htz1p/Htb1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
HTZ1
CHZ1
EMAP score
gene
CHZ1
HTZ1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K101R C_WT N102K T34E E115I E115A F58A T139R R108L F58L N105V A180T N102M G80A T34D N_WT N102I T34S K154M K129T R108D T34Y WT K129E K132H K129I Q147L R108I T139A T34A R108Q H141V N105L T137G K143Y Q147E K129F K169I D79S T34L R108S H141R N84Y T34N K143H R78K Y148I R108A K143W H141I R108G T34Q Y157A R108Y D79A R112A R112S T34G H141E

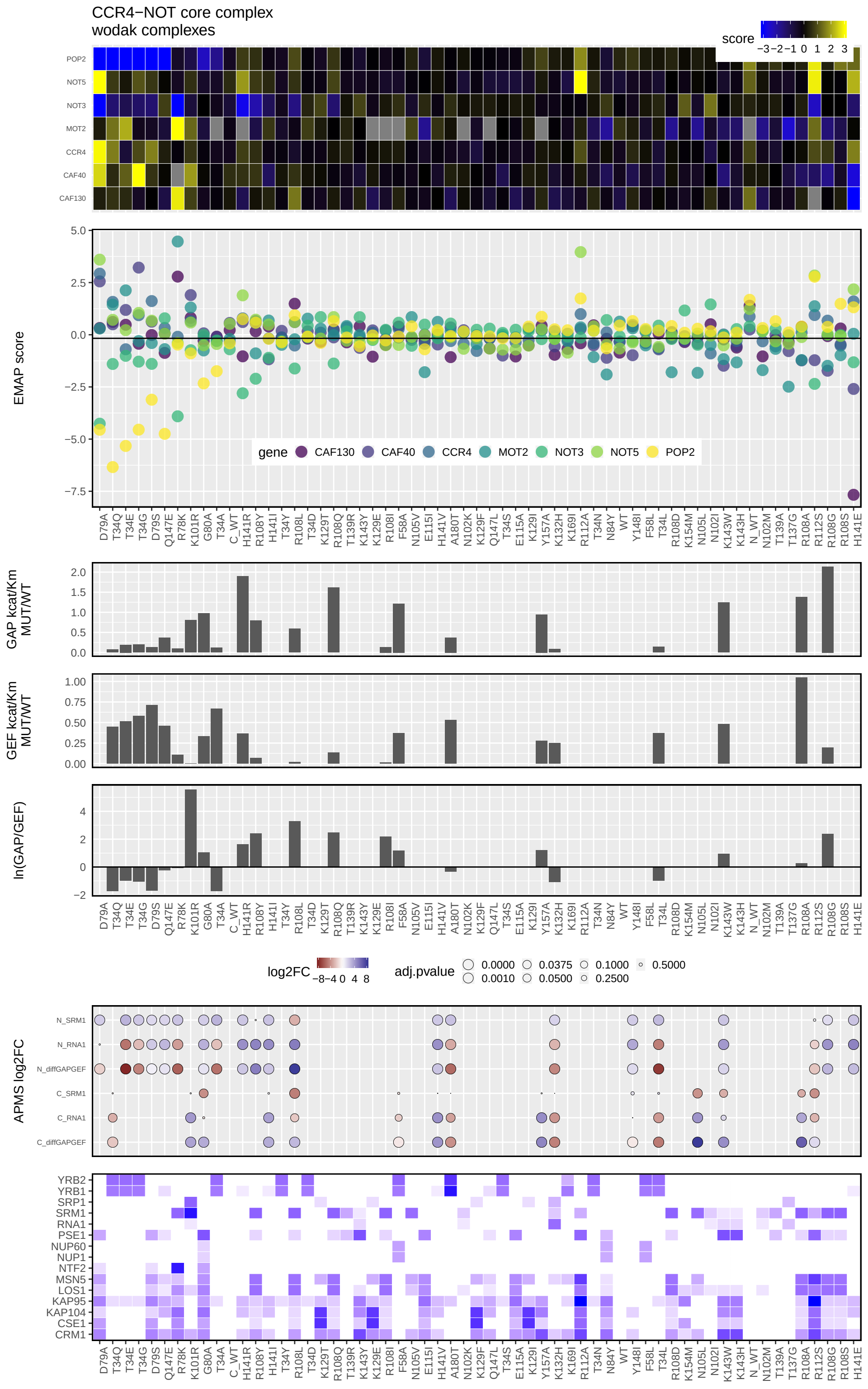
Cytochrome bc1 complex (Ubiquinol−cytochrome c reductase complex, complex III)
wodak complexes

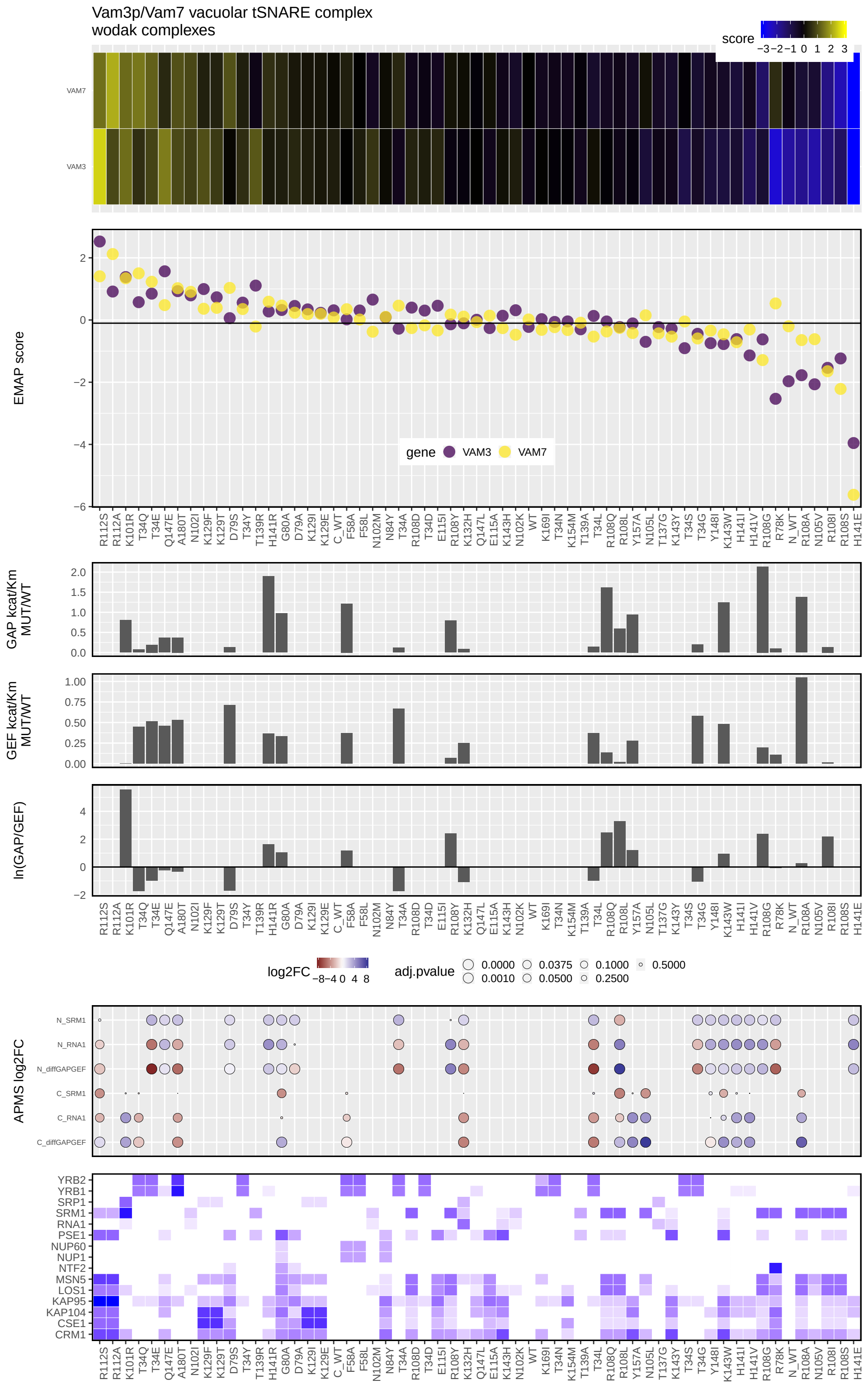


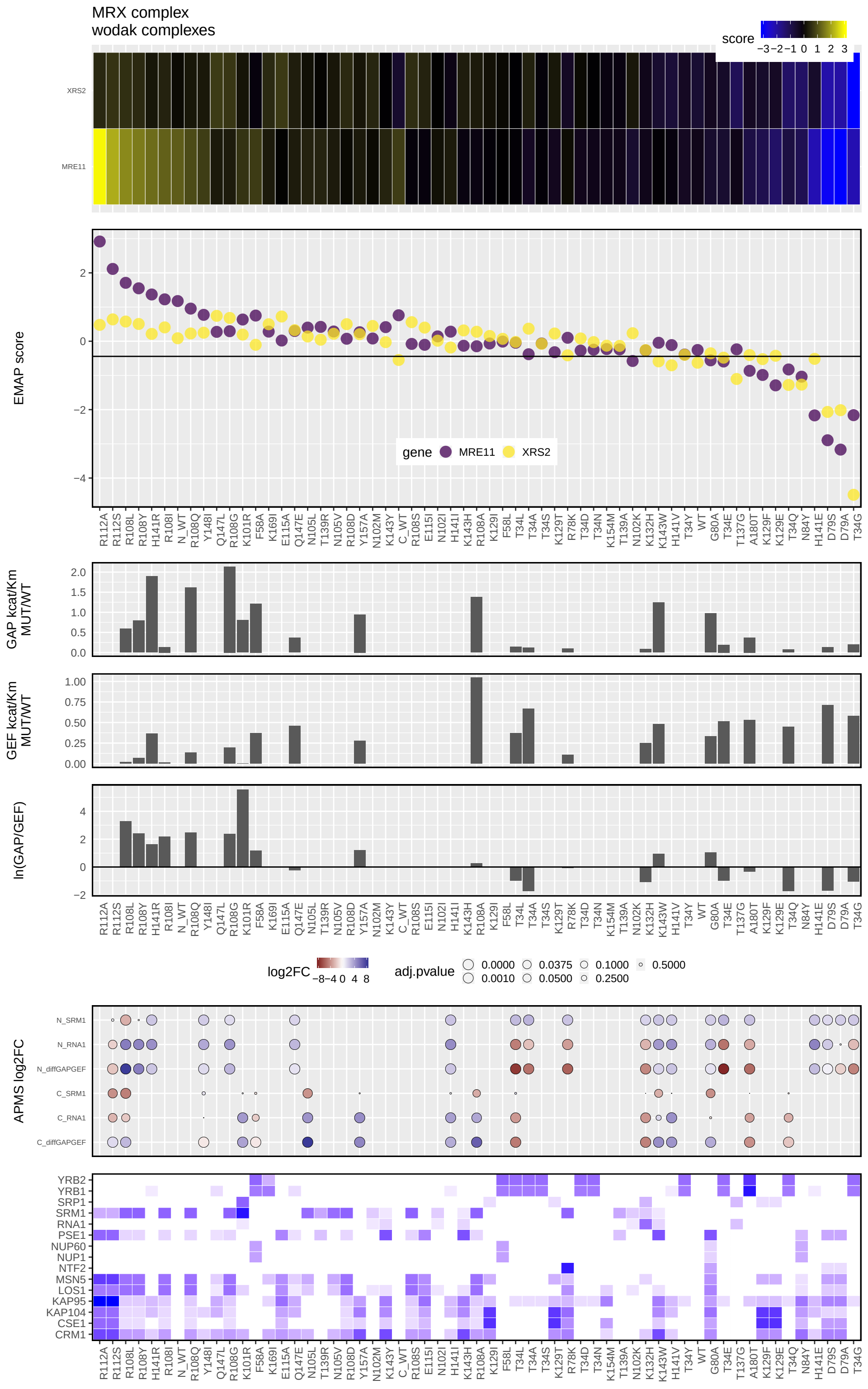
carboxy−terminal domain protein kinase complex
wodak complexes

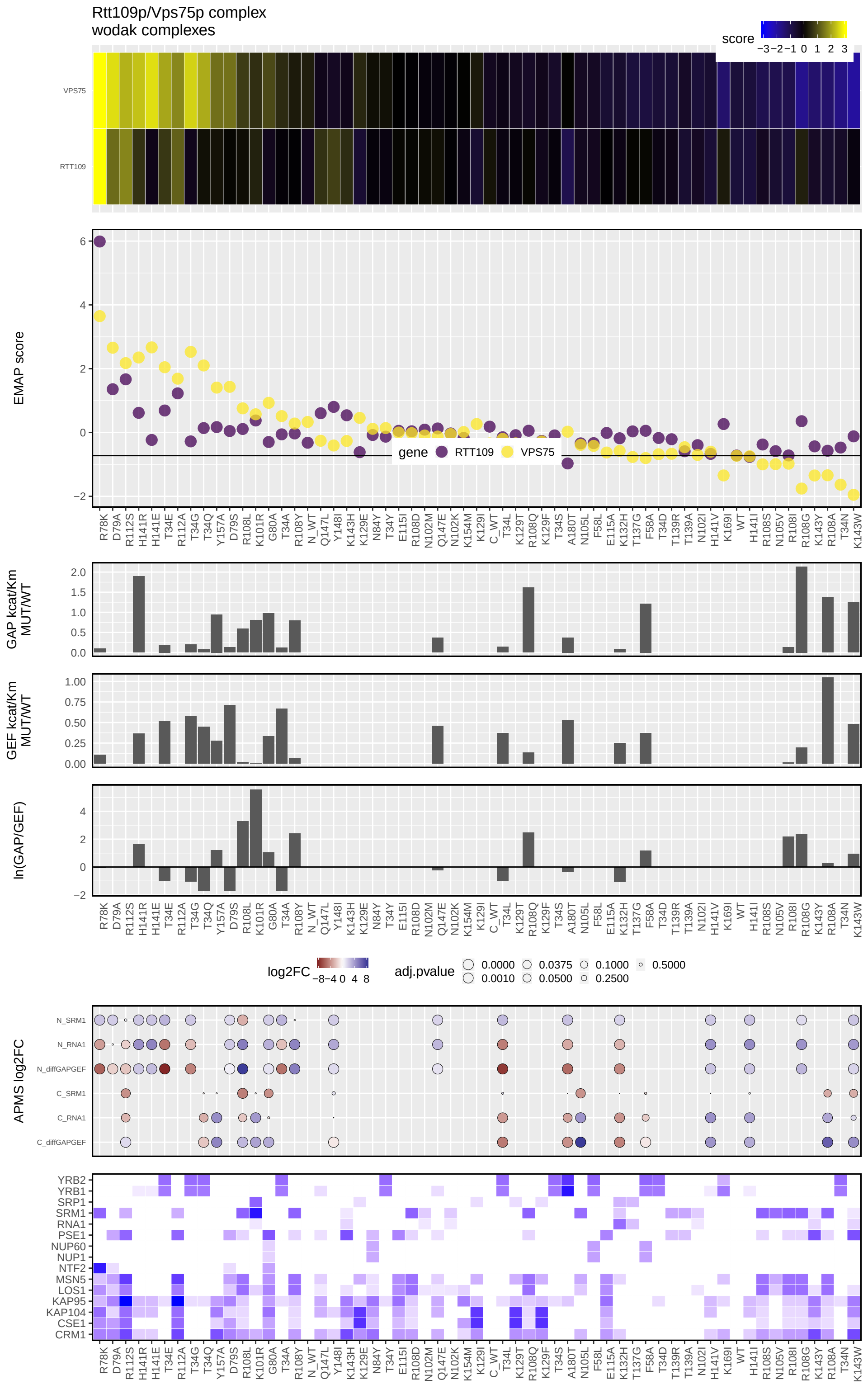


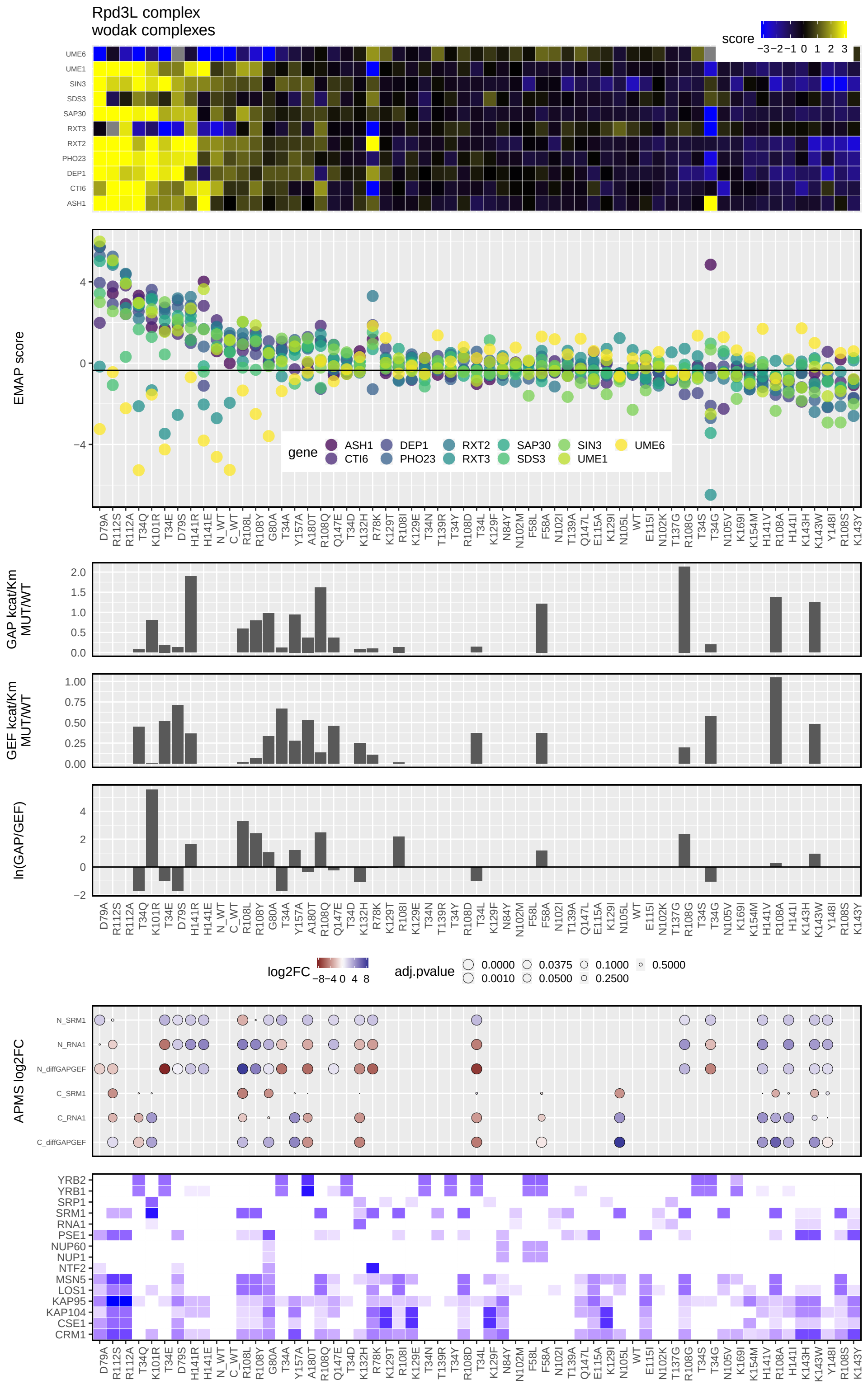

Rot2p/Gtb1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
ROT2
GTB1
EMAP score
gene
GTB1
ROT2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R112S T34G R112A T34E K132H R108L H141E C_WT R108Y D79S R78K T34A N_WT T34Q R108Q N105V H141I A180T Y157A T34N E115I R108S R108I G80A K143H N84Y N102M R108D N105L T139R K169I H141V T34S WT K129I Q147L R108G F58A T137G K143W Y148I K129E T34Y E115A N102K K143Y H141R F58L K154M K129T K101R R108A T34D K129F T139A Q147E T34L N102I

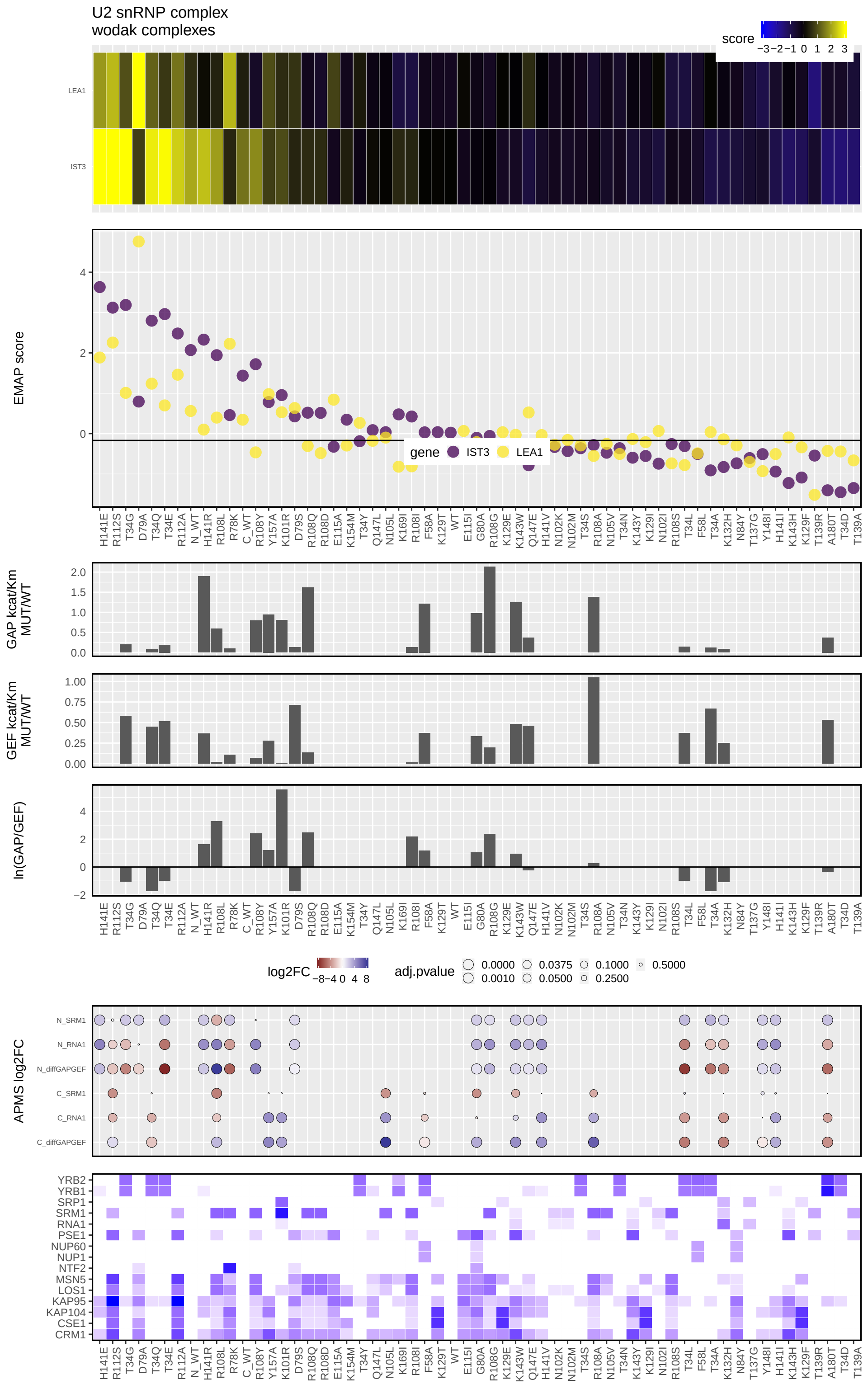

CCR4−NOT core complex
wodak complexes
score
−3 −2 −1 0 1 2 3
POP2
NOT5
NOT3
MOT2
CCR4
CAF40
CAF130
EMAP score
gene
CAF130
CAF40
CCR4
MOT2
NOT3
NOT5
POP2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34Q T34E T34G D79S Q147E R78K K101R G80A T34A C_WT H141R R108Y H141I T34Y R108L T34D K129T R108Q T139R K143Y K129E R108I F58A N105V E115I H141V A180T N102K K129F Q147L T34S E115A K129I Y157A K132H K169I R112A T34N N84Y WT Y148I F58L T34L R108D K154M N105L N102I K143W K143H N_WT N102M T139A T137G R108A R112S R108G R108S H141E

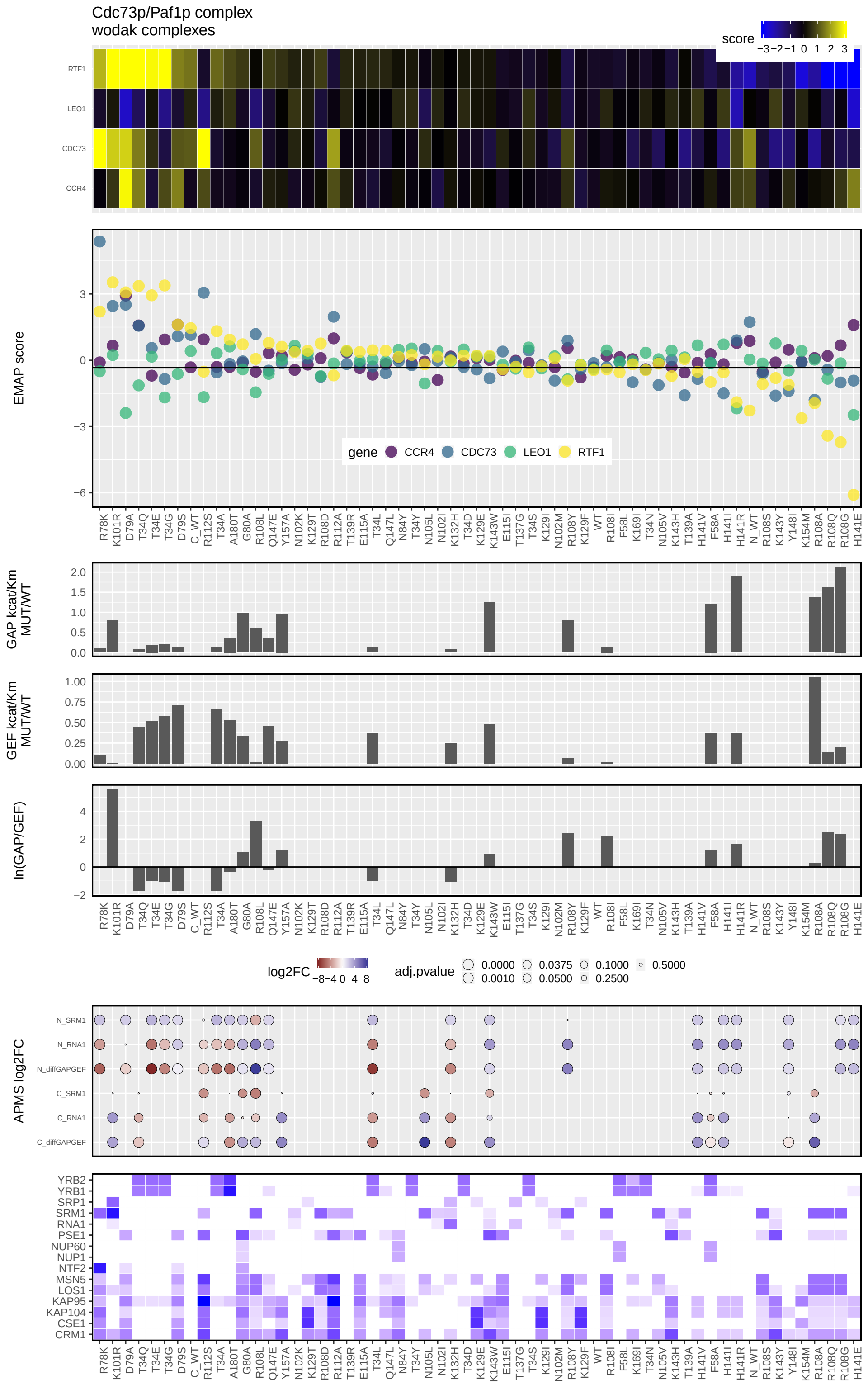

Vam3p/Vam7 vacuolar tSNARE complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VAM7
VAM3
EMAP score
gene VAM3 VAM7
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112S R112A K101R T34Q T34E Q147E A180T N102I K129F K129T D79S T34Y T139R H141R G80A D79A K129I K129E C_WT F58A F58L N102M N84Y T34A R108D T34D E115I R108Y K132H Q147L E115A K143H N102K WT K169I T34N K154M T139A T34L R108Q R108L Y157A N105L T137G K143Y T34S T34G Y148I K143W H141I H141V R108G R78K N_WT R108A N105V R108I R108S H141E

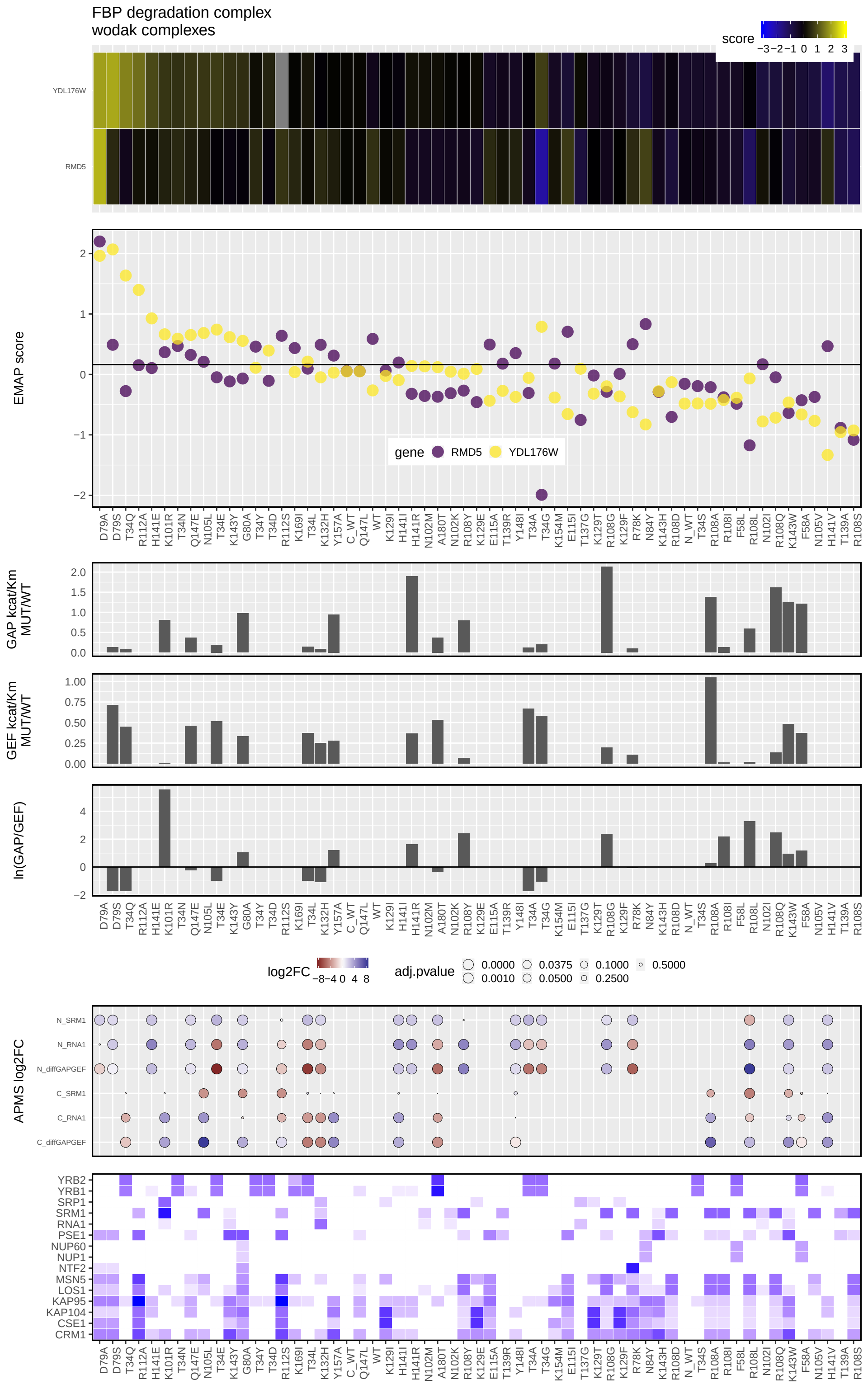

MRX complex
wodak complexes
score
−3 −2 −1 0 1 2 3
XRS2
MRE11
EMAP score
gene
MRE11
XRS2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A R112S R108L R108Y H141R R108I N_WT R108Q Y148I Q147L R108G K101R F58A K169I E115A Q147E N105L T139R N105V R108D Y157A N102M K143Y C_WT R108S E115I N102I H141I K143H R108A K129I F58L T34L T34A T34S K129T R78K T34D T34N K154M T139A N102K K132H K143W H141V T34Y WT G80A T34E T137G A180T K129F K129E T34Q N84Y H141E D79S D79A T34G

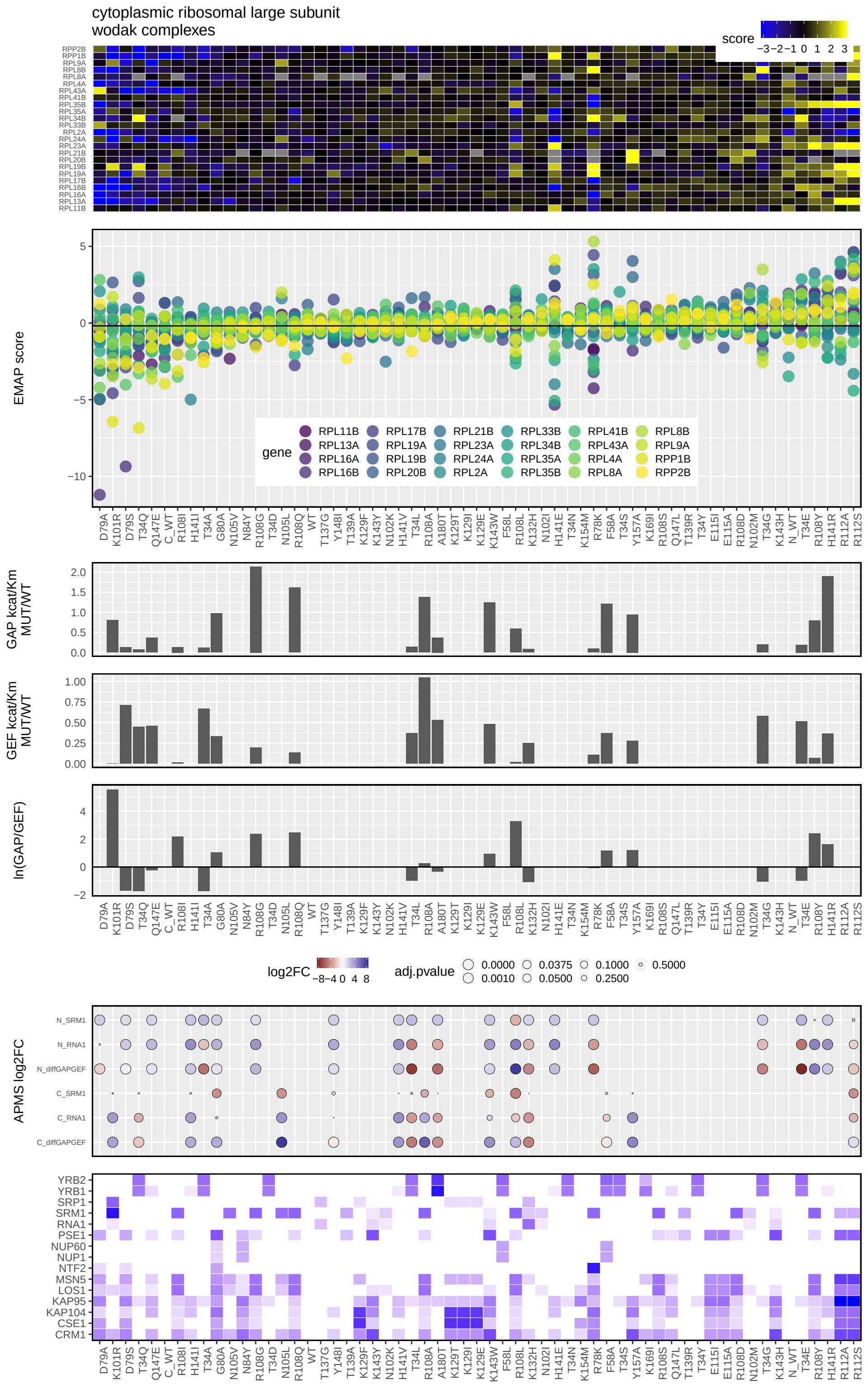

Rtt109p/Vps75p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VPS75
RTT109
EMAP score
gene
RTT109
VPS75
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K D79A R112S H141R H141E T34E R112A T34G T34Q Y157A D79S R108L K101R G80A T34A R108Y N_WT Q147L Y148I K143H K129E N84Y T34Y E115I R108D N102M Q147E N102K K154M K129I C_WT T34L K129T R108Q K129F T34S A180T N105L F58L E115A K132H T137G F58A T34D T139R T139A N102I H141V K169I WT H141I R108S N105V R108I R108G K143Y R108A T34N K143W

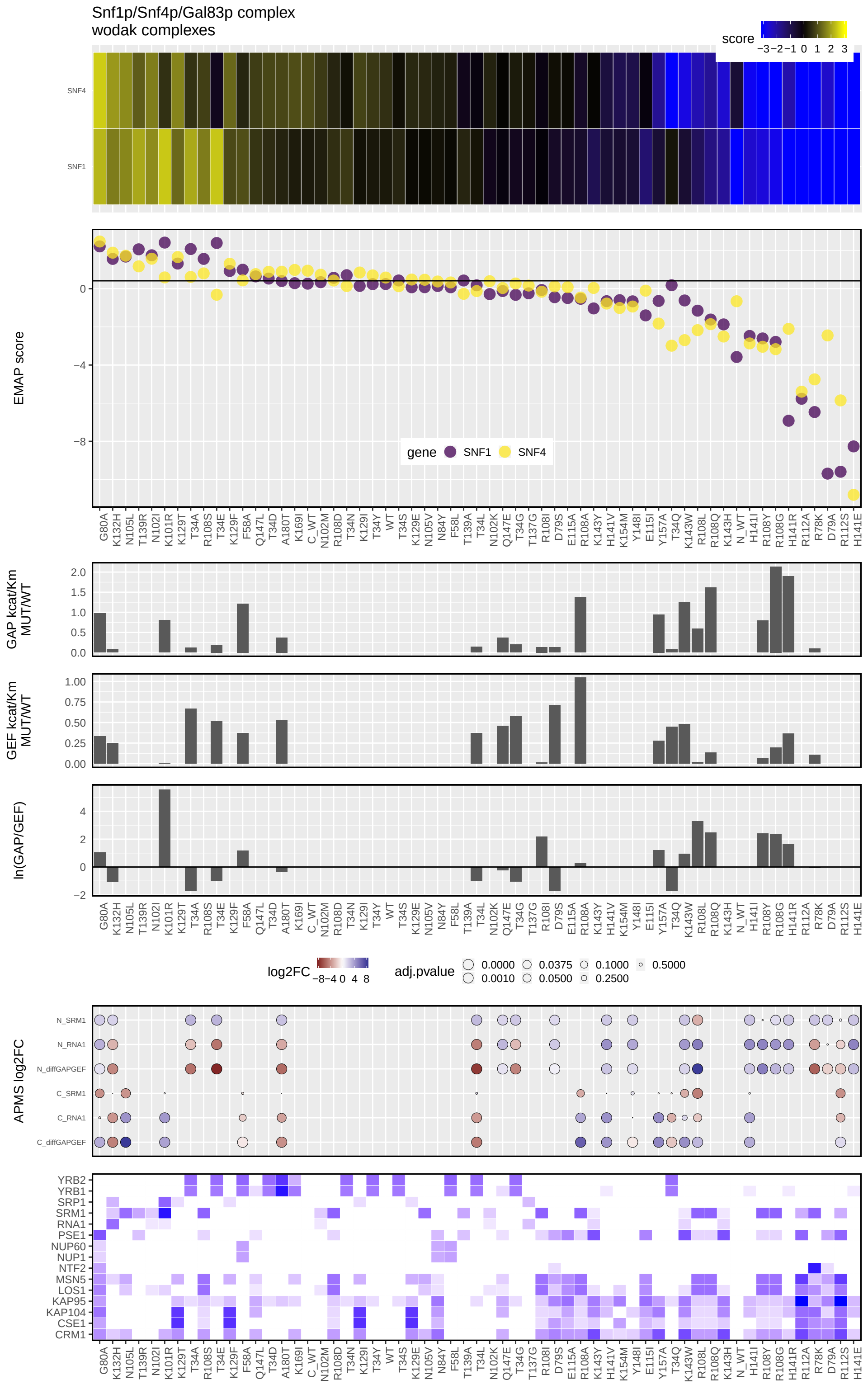

Rpd3L complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UME6
UME1
SIN3
SDS3
SAP30
RXT3
RXT2
PHO23
DEP1
CTI6
ASH1
EMAP score
gene
ASH1
CTI6
DEP1
PHO23
RXT2
RXT3
SAP30
SDS3
SIN3
UME1
UME6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R112S R112A T34Q K101R T34E D79S H141R H141E N_WT C_WT R108L R108Y G80A T34A Y157A A180T R108Q Q147E T34D K132H R78K K129T R108I K129E T34N T139R T34Y R108D T34L K129F N84Y N102M F58L F58A N102I T139A Q147L E115A K129I N105L WT E115I N102K T137G R108G T34S T34G N105V K169I K154M H141V R108A H141I K143H K143W Y148I R108S K143Y


U2 snRNP complex
wodak complexes
score
−3 −2 −1 0 1 2 3
LEA1
IST3
EMAP score
gene
IST3
LEA1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E R112S T34G D79A T34Q T34E R112A N_WT H141R R108L R78K C_WT R108Y Y157A K101R D79S R108Q R108D E115A K154M T34Y Q147L N105L K169I R108I F58A K129T WT E115I G80A R108G K129E K143W Q147E H141V N102K N102M T34S R108A N105V T34N K143Y K129I N102I R108S T34L F58L T34A K132H N84Y T137G Y148I H141I K143H K129F T139R A180T T34D T139A

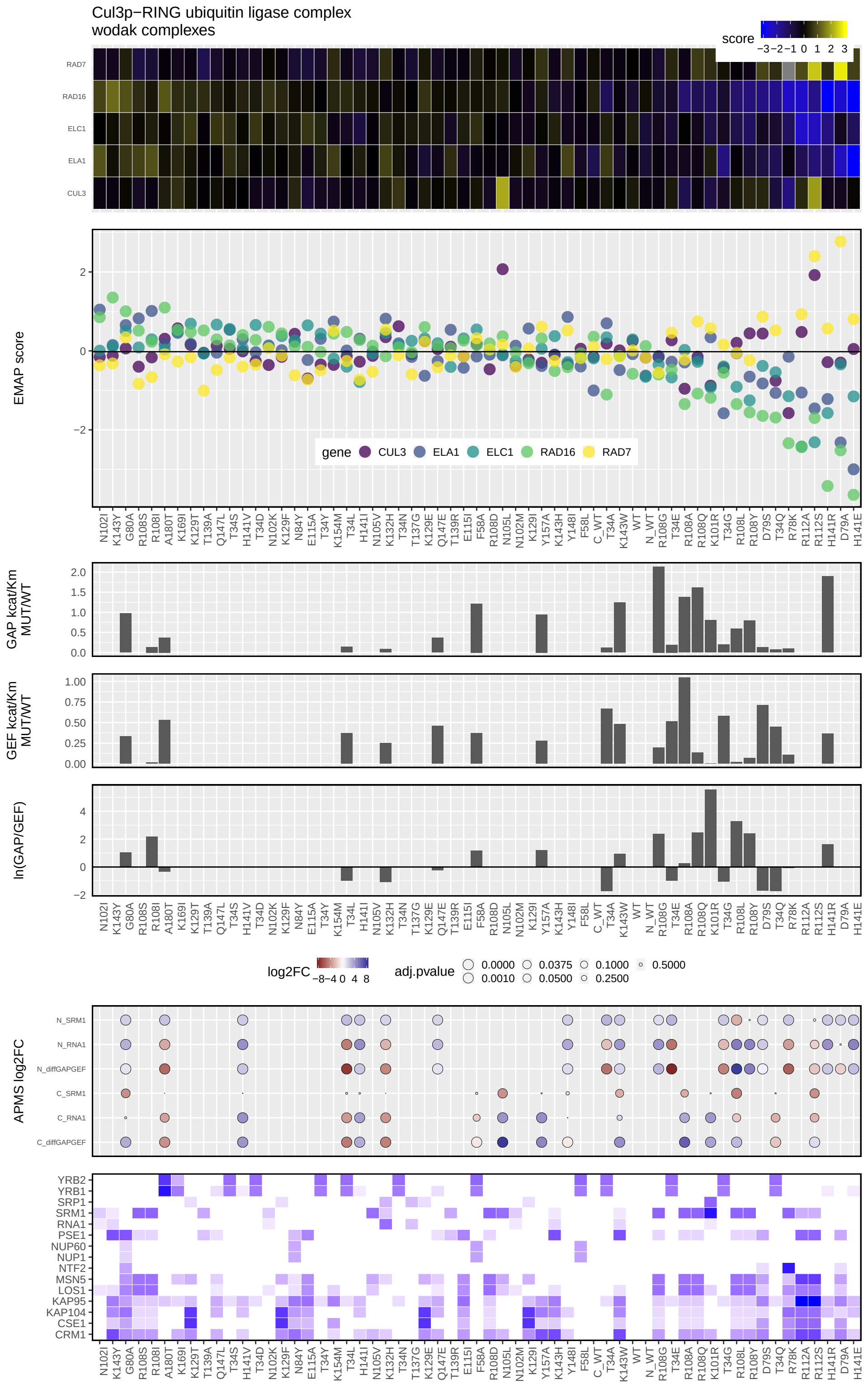

Cdc73p/Paf1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RTF1
LEO1
CDC73
CCR4
EMAP score
gene CCR4 CDC73 LEO1 RTF1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K K101R D79A T34Q T34E T34G D79S C_WT R112S T34A A180T G80A R108L Q147E Y157A N102K K129T R108D R112A T139R E115A T34L Q147L N84Y T34Y N105L N102I K132H T34D K129E K143W E115I T137G T34S K129I N102M R108Y K129F WT R108I F58L K169I T34N N105V K143H T139A H141V F58A H141I H141R N_WT R108S K143Y Y148I K154M R108A R108Q R108G H141E

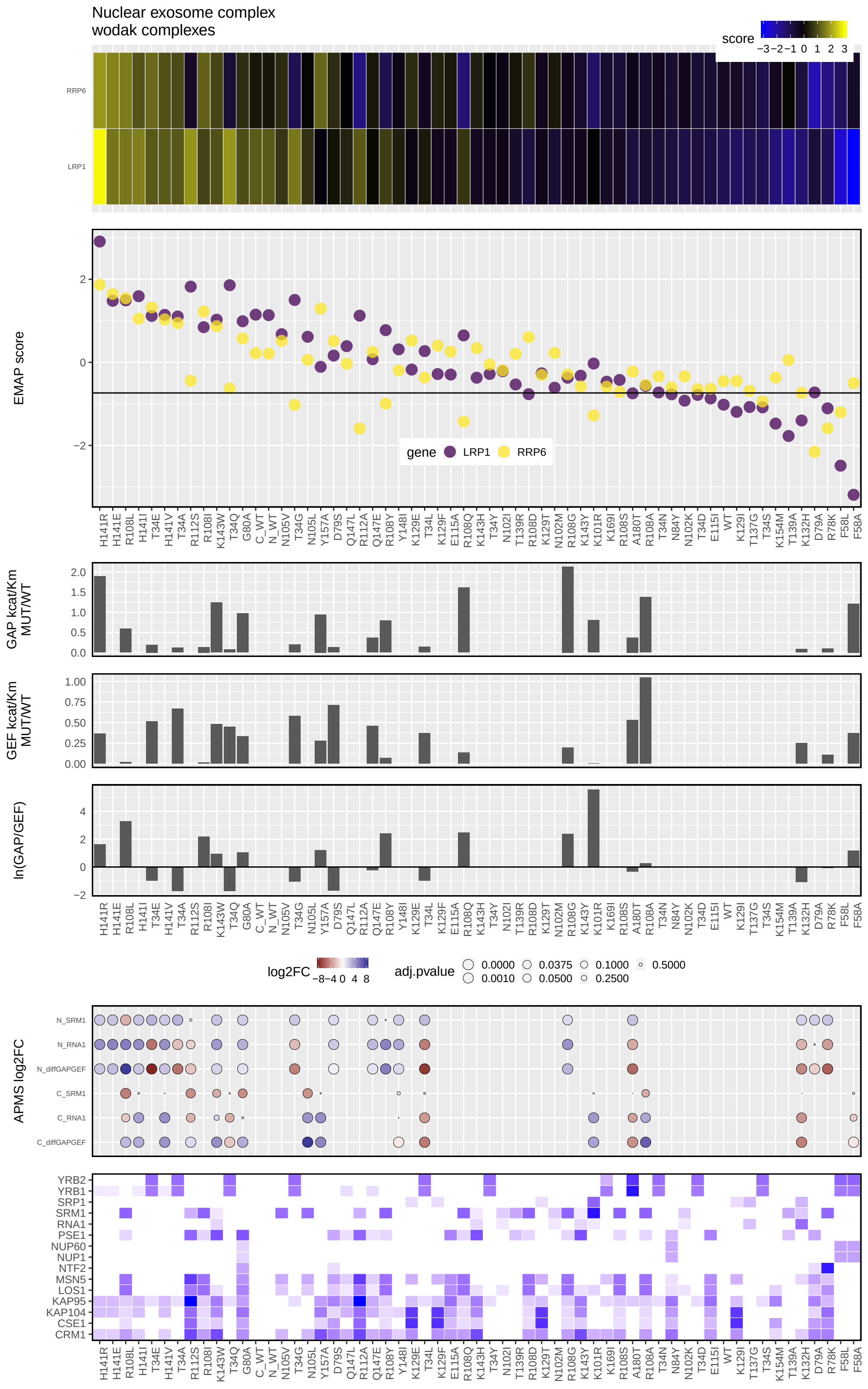

FBP degradation complex
wodak complexes
score
−3 −2 −1 0 1 2 3
YDL176W
RMD5
EMAP score
gene
RMD5
YDL176W
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A D79S T34Q R112A H141E K101R T34N Q147E N105L T34E K143Y G80A T34Y T34D R112S K169I T34L K132H Y157A C_WT Q147L WT K129I H141I H141R N102M A180T N102K R108Y K129E E115A T139R Y148I T34A T34G K154M E115I T137G K129T R108G K129F R78K N84Y K143H R108D N_WT T34S R108A R108I F58L R108L N102I R108Q K143W F58A N105V H141V T139A R108S

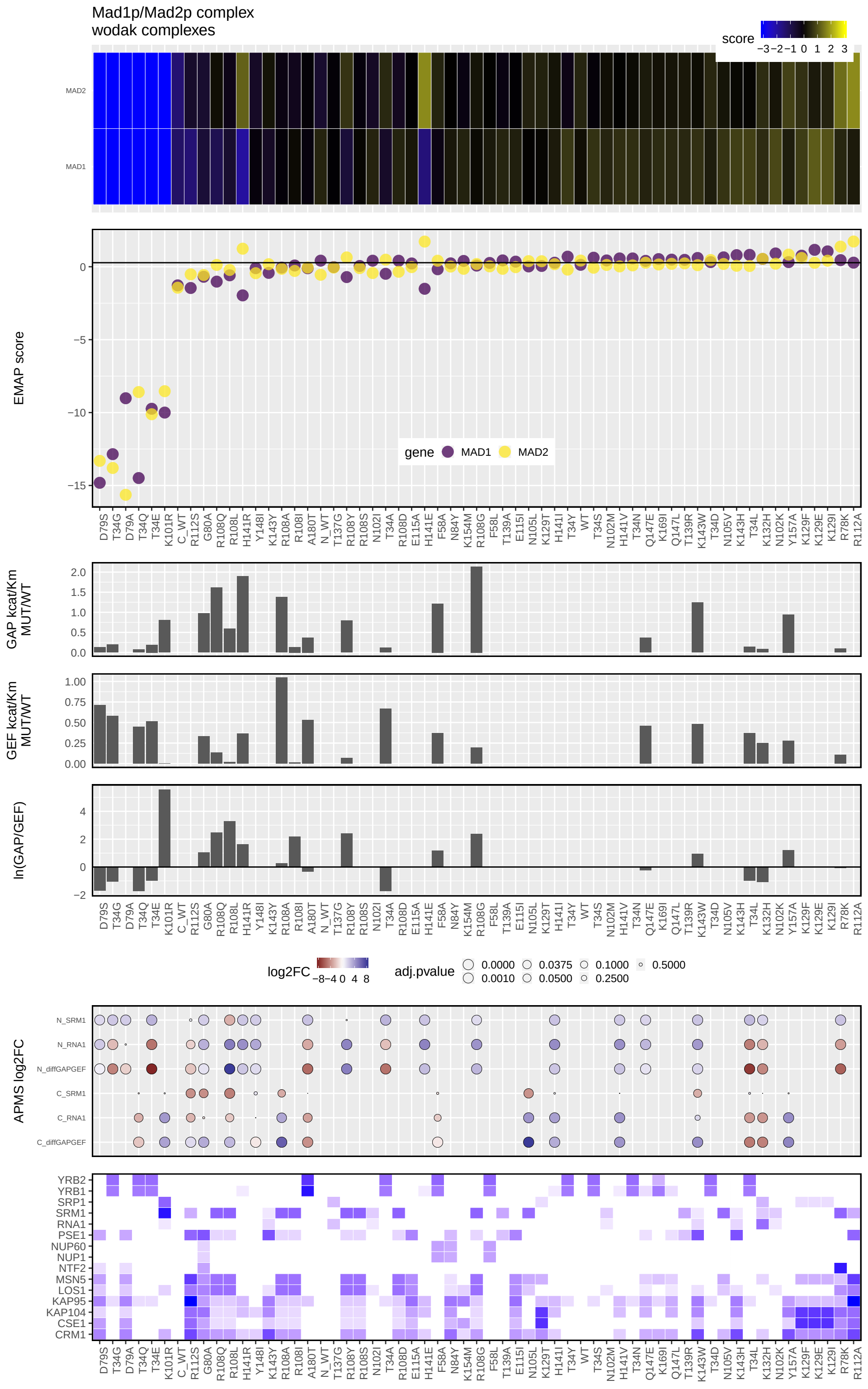

cytoplasmic ribosomal large subunit
wodak complexes
score
−3 −2 −1 0 1 2 3
RPP2B
RPP1B
RPL9A
RPL8B
RPL8A
RPL4A
RPL43A
RPL41B
RPL35B
RPL35A
RPL34B
RPL33B
RPL2A
RPL24A
RPL23A
RPL21B
RPL20B
RPL19B
RPL19A
RPL17B
RPL16B
RPL16A
RPL13A
RPL11B
EMAP score
gene
RPL11B RPL17B RPL21B RPL33B RPL41B RPL8B
RPL13A RPL19A RPL23A RPL34B RPL43A RPL9A
RPL16A RPL19B RPL24A RPL35A RPL4A RPP1B
RPL16B RPL20B RPL2A RPL35B RPL8A RPP2B
D79A K101R D79S T34Q Q147E C_WT R108I H141I T34A G80A N105V N84Y R108G T34D N105L R108Q WT T137G Y148I T139A K129F K143Y N102K H141V T34L R108A A180T K129T K129I K129E K143W F58L R108L K132H N102I H141E T34N K154M R78K F58A T34S Y157A K169I R108S Q147L T139R T34Y E115I E115A R108D N102M T34G K143H N_WT T34E R108Y H141R R112A R112S
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

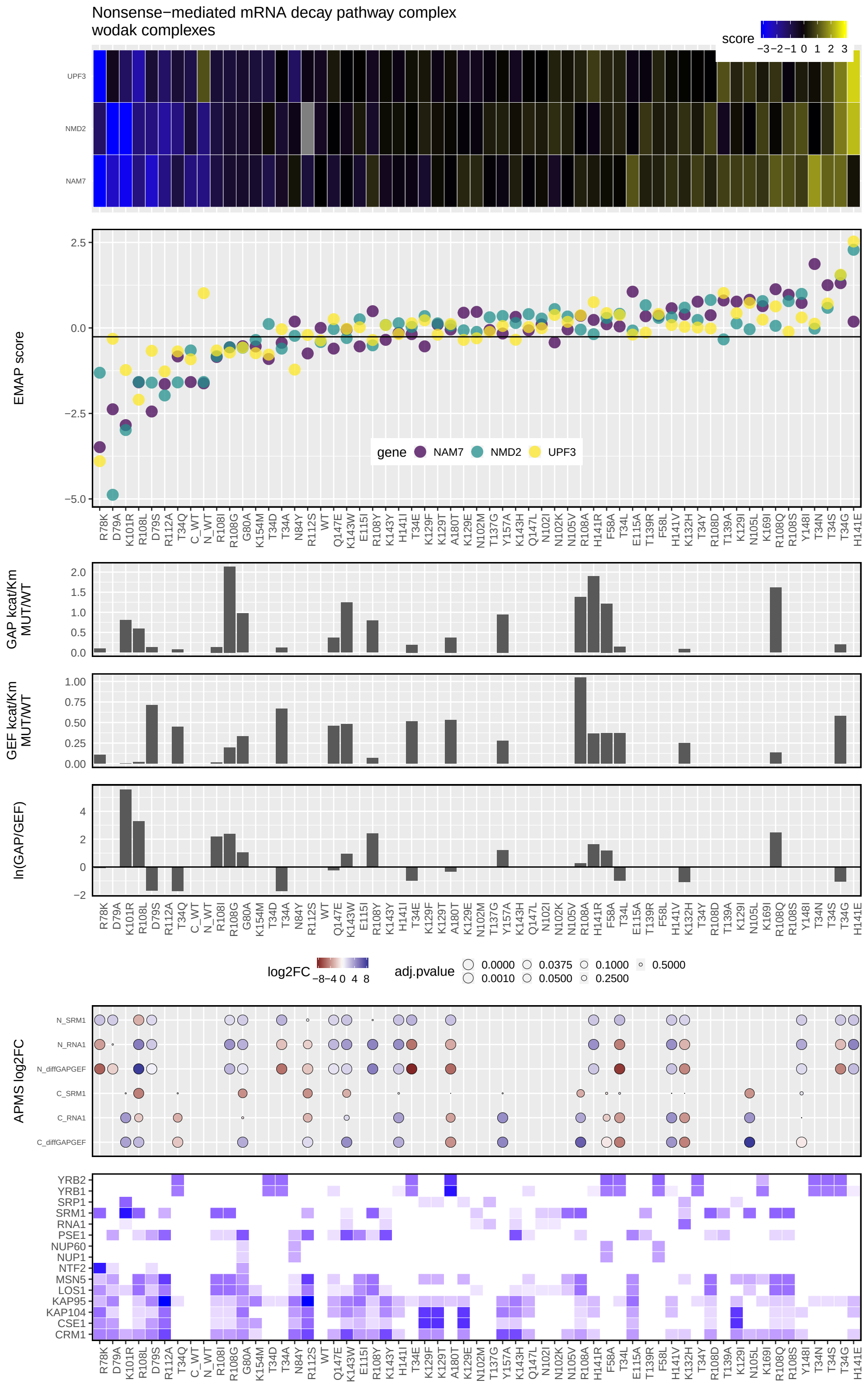

Snf1p/Snf4p/Gal83p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SNF4
SNF1
EMAP score
gene
SNF1
SNF4
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
G80A K132H N105L T139R N102I K101R K129T T34A R108S T34E K129F F58A Q147L T34D A180T K169I C_WT N102M R108D T34N K129I T34Y WT T34S K129E N105V N84Y F58L T139A T34L N102K Q147E T34G T137G R108I D79S E115A R108A K143Y H141V K154M Y148I E115I Y157A T34Q K143W R108L R108Q K143H N_WT H141I R108Y R108G H141R R112A R78K D79A R112S H141E

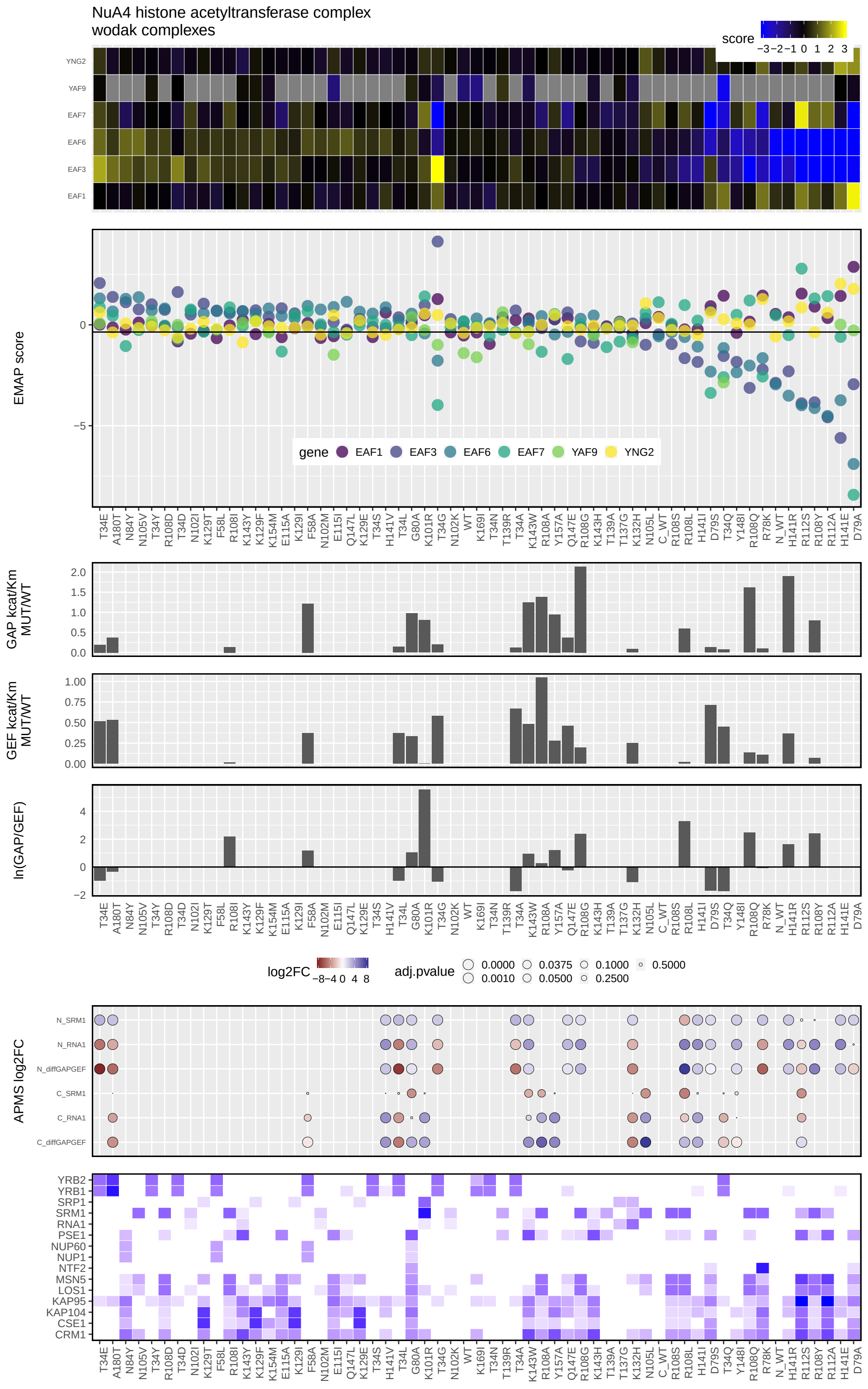
Cul3p−RING ubiquitin ligase complex
wodak complexes

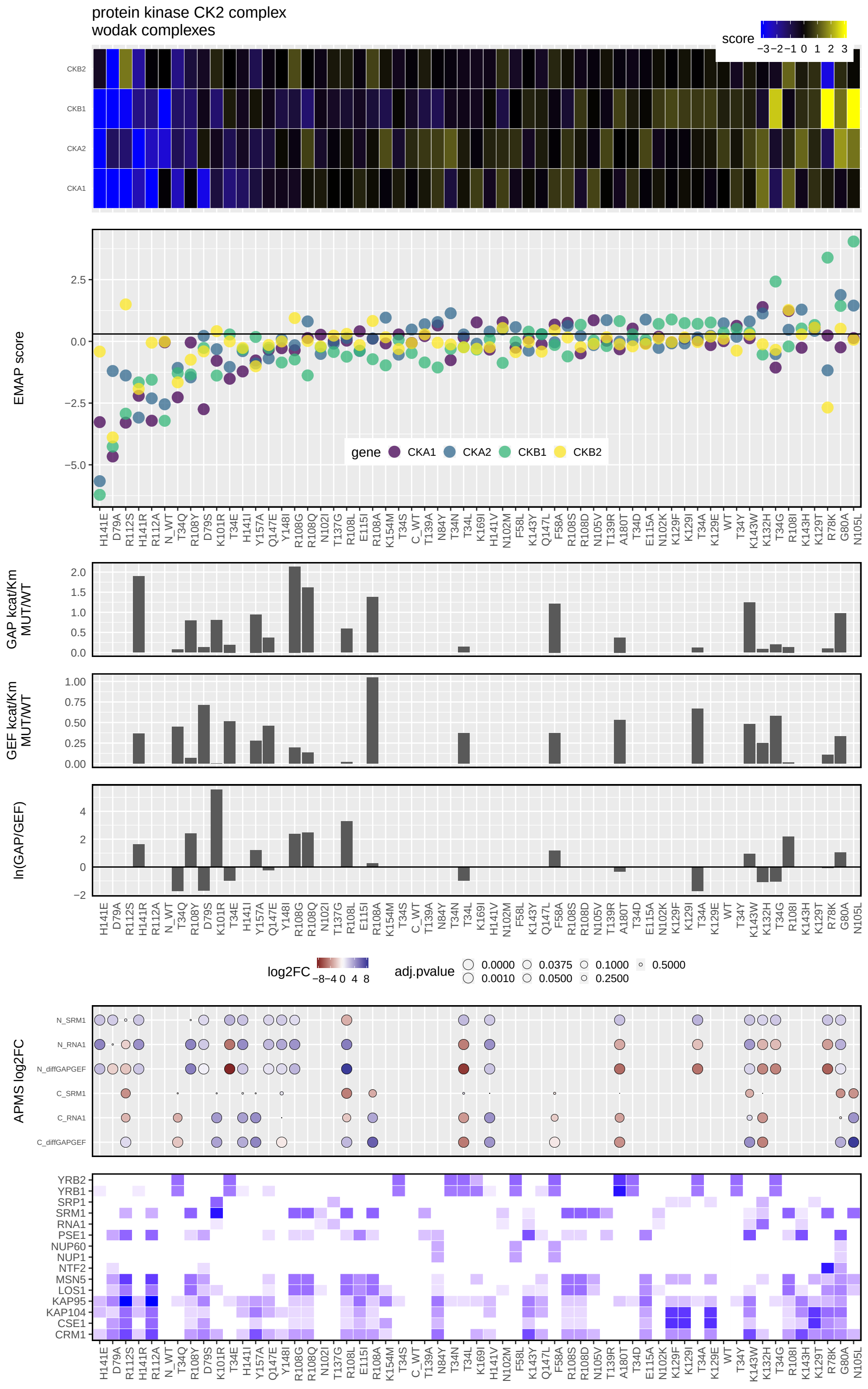


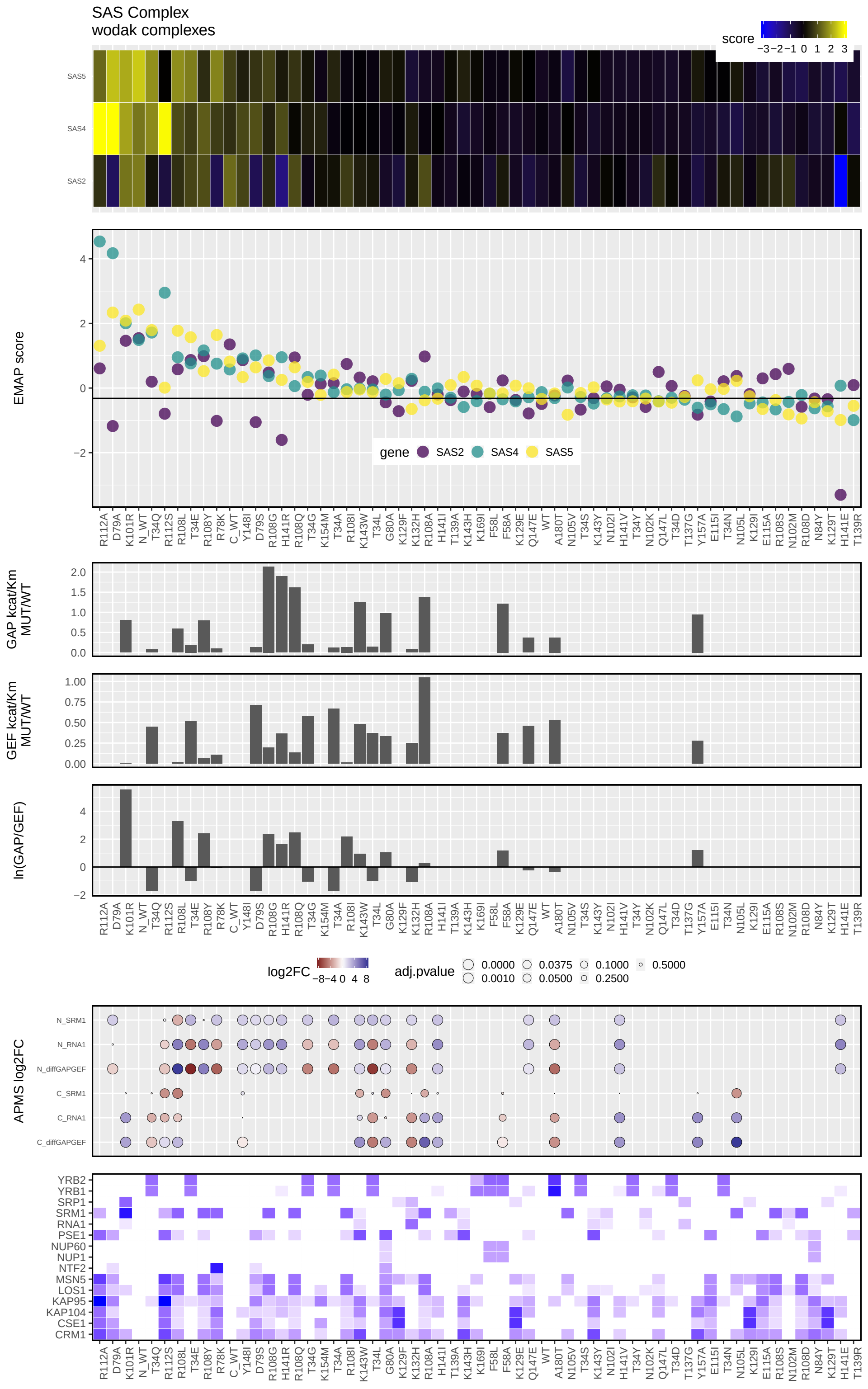

Nuclear exosome complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RRP6
LRP1
EMAP score
gene
LRP1
RRP6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141R H141E R108L H141I T34E H141V T34A R112S R108I K143W T34Q G80A C_WT N_WT N105V T34G N105L Y157A D79S Q147L R112A Q147E R108Y Y148I K129E T34L K129F E115A R108Q K143H T34Y N102I T139R R108D K129T N102M R108G K143Y K101R K169I R108S A180T R108A T34N N84Y N102K T34D E115I WT K129I T137G T34S K154M T139A K132H D79A R78K F58L F58A

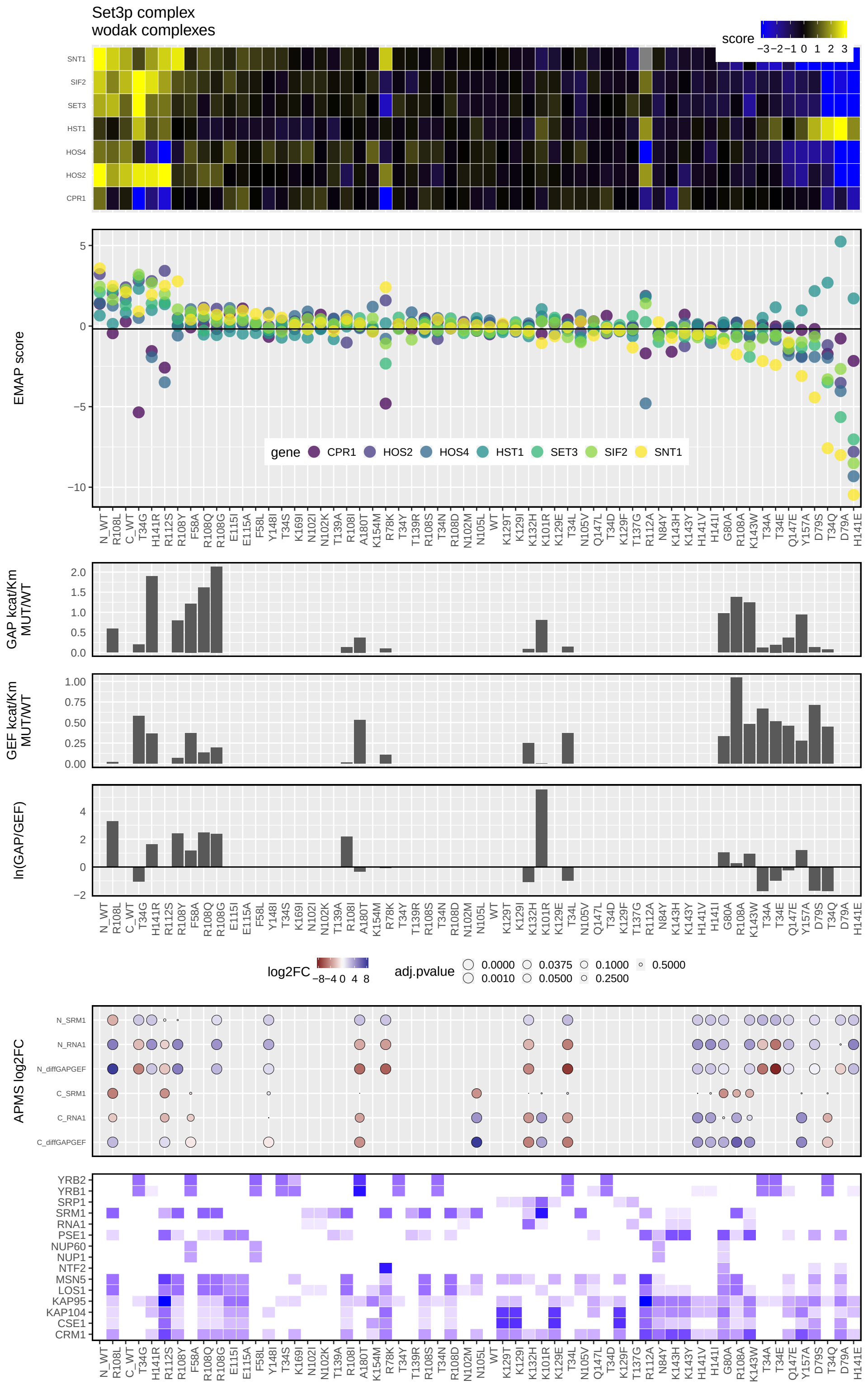

Mad1p/Mad2p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MAD2
MAD1
EMAP score
gene MAD1 MAD2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79S T34G D79A T34Q T34E K101R C_WT R112S G80A R108Q R108L H141R Y148I K143Y R108A R108I A180T N_WT T137G R108Y R108S N102I T34A R108D E115A H141E F58A N84Y K154M R108G F58L T139A E115I N105L K129T H141I T34Y WT T34S N102M H141V T34N Q147E K169I Q147L T139R K143W T34D N105V K143H T34L K132H N102K Y157A K129F K129E K129I R78K R112A

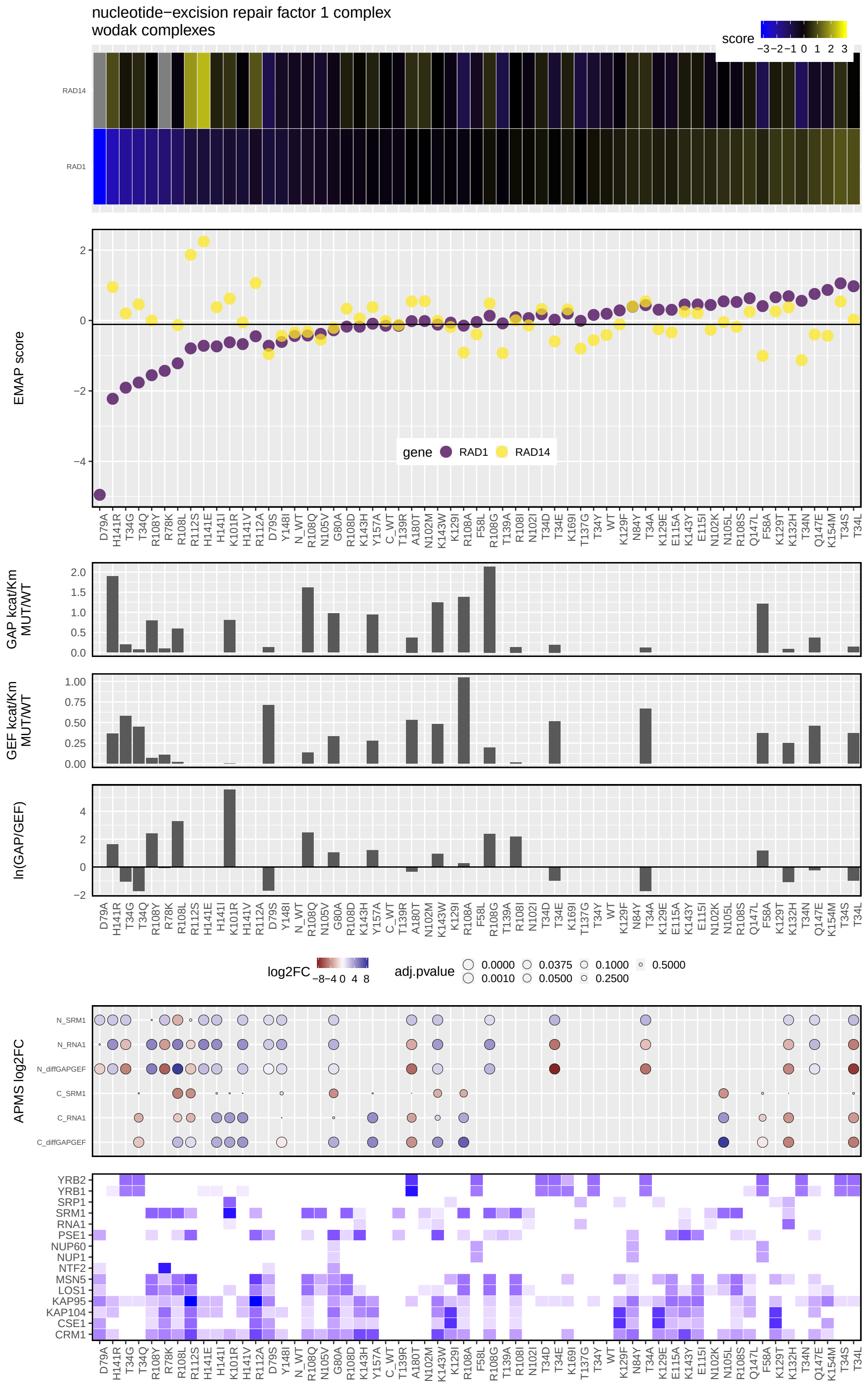

Nonsense−mediated mRNA decay pathway complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UPF3
NMD2
NAM7
EMAP score
gene NAM7 NMD2 UPF3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K D79A K101R R108L D79S R112A T34Q C_WT N_WT R108I R108G G80A K154M T34D T34A N84Y R112S WT Q147E K143W E115I R108Y K143Y H141I T34E K129F K129T A180T K129E N102M T137G Y157A K143H Q147L N102I N102K N105V R108A H141R F58A T34L E115A T139R F58L H141V K132H T34Y R108D T139A K129I N105L K169I R108Q R108S Y148I T34N T34S T34G H141E


NuA4 histone acetyltransferase complex
wodak complexes
score
−3 −2 −1 0 1 2 3
YNG2
YAF9
EAF7
EAF6
EAF3
EAF1
EMAP score
gene EAF1 EAF3 EAF6 EAF7 YAF9 YNG2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34E A180T N84Y N105V T34Y R108D T34D N102I K129T F58L R108I K143Y K129F K154M E115A K129I F58A N102M E115I Q147L K129E T34S H141V T34L G80A K101R T34G N102K WT K169I T34N T139R T34A K143W R108A Y157A Q147E R108G K143H T139A T137G K132H N105L C_WT R108S R108L H141I D79S T34Q Y148I R108Q R78K N_WT H141R R112S R108Y R112A H141E D79A

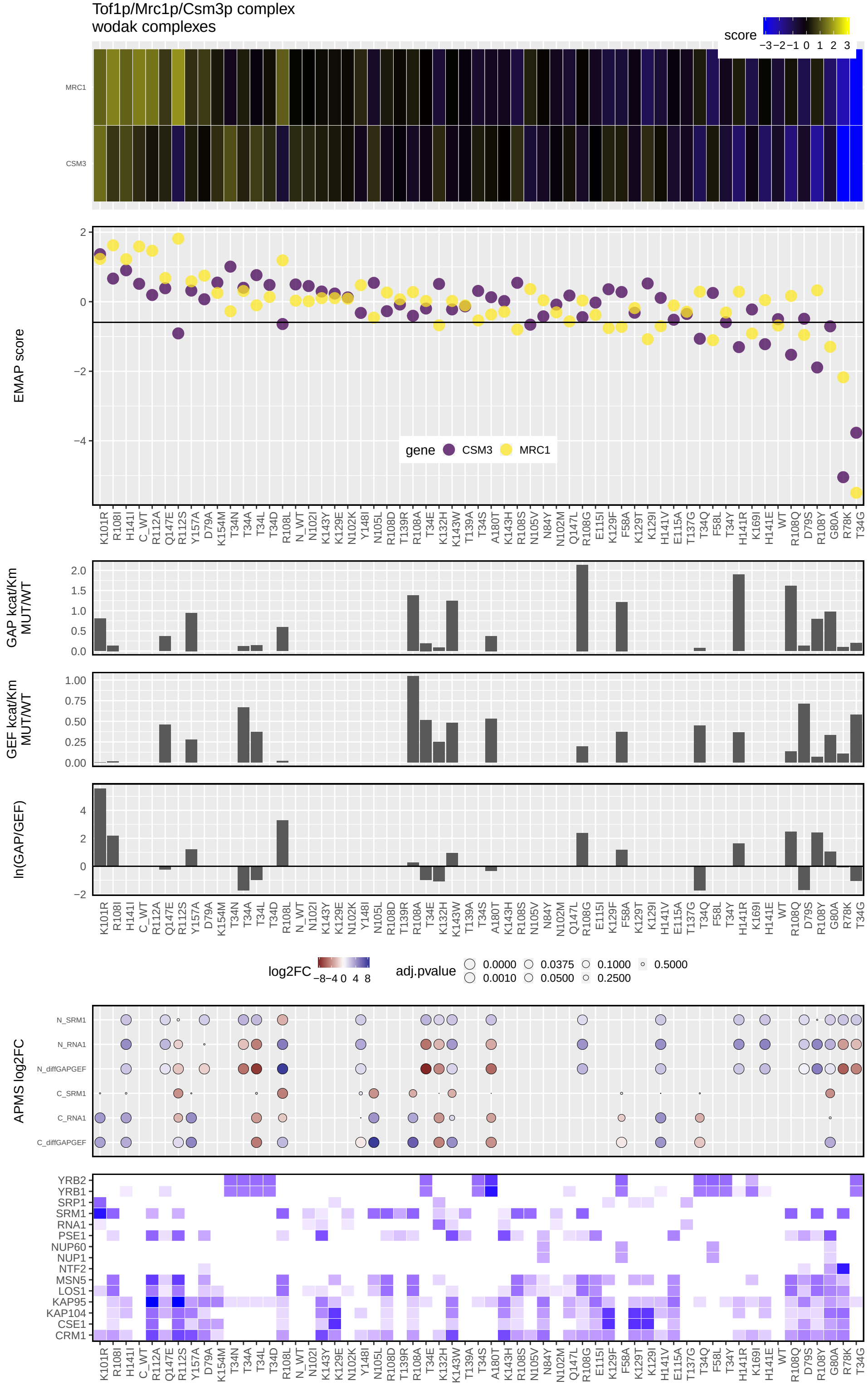

protein kinase CK2 complex
wodak complexes
score
−3 −2 −1 0 1 2 3
CKB2
CKB1
CKA2
CKA1
EMAP score
gene CKA1 CKA2 CKB1 CKB2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E D79A R112S H141R R112A N_WT T34Q R108Y D79S K101R T34E H141I Y157A Q147E Y148I R108G R108Q N102I T137G R108L E115I R108A K154M T34S C_WT T139A N84Y T34N T34L K169I H141V N102M F58L K143Y Q147L F58A R108S R108D N105V T139R A180T T34D E115A N102K K129F K129I T34A K129E WT T34Y K143W K132H T34G R108I K143H K129T R78K G80A N105L

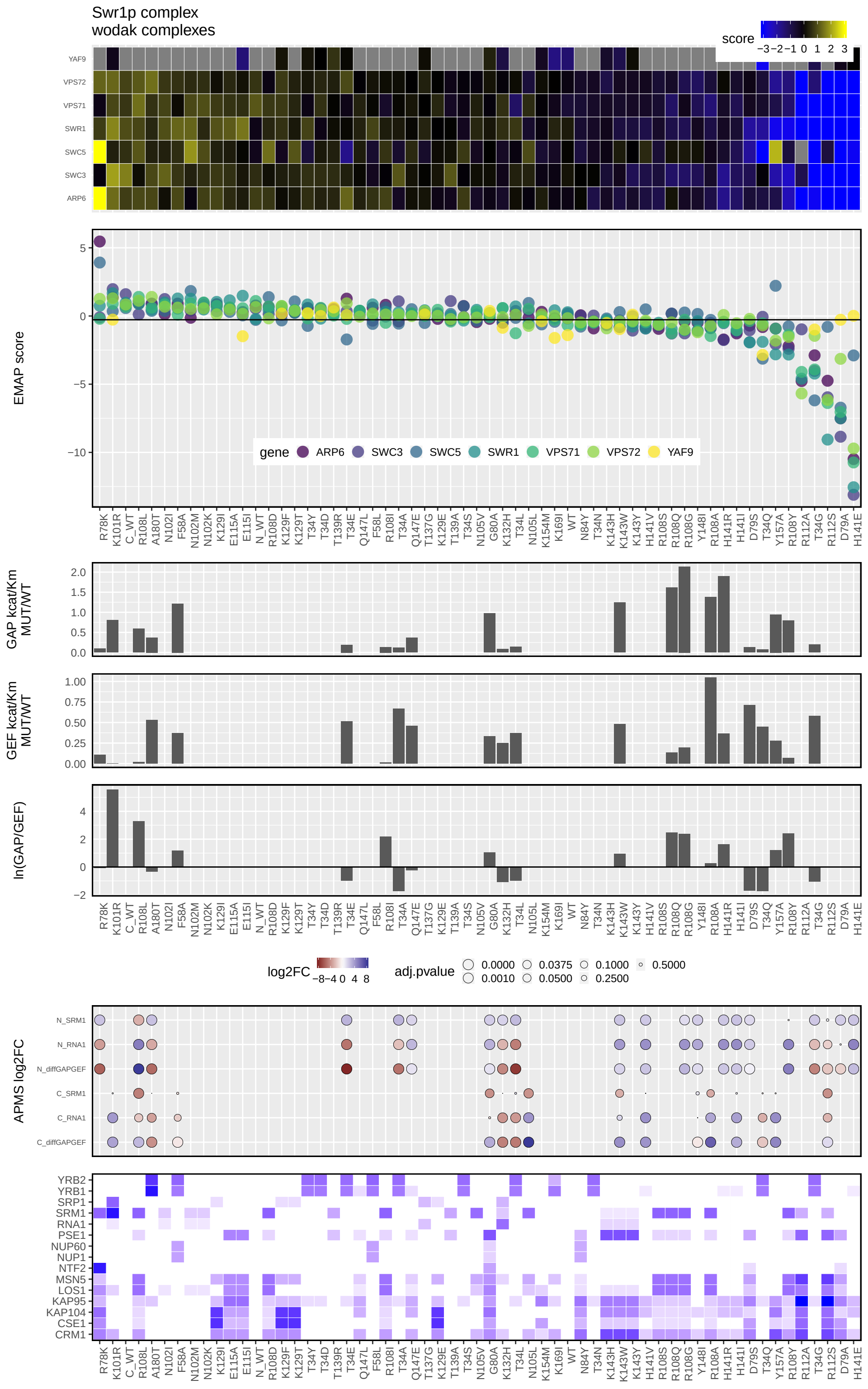

SAS Complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SAS5
SAS4
SAS2
EMAP score
gene SAS2 SAS4 SAS5
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A D79A K101R N_WT T34Q R112S R108L T34E R108Y R78K C_WT Y148I D79S R108G H141R R108Q T34G K154M T34A R108I K143W T34L G80A K129F K132H R108A H141I T139A K143H K169I F58L F58A K129E Q147E WT A180T N105V T34S K143Y N102I H141V T34Y N102K Q147L T34D T137G Y157A E115I T34N N105L K129I E115A R108S N102M R108D N84Y K129T H141E T139R

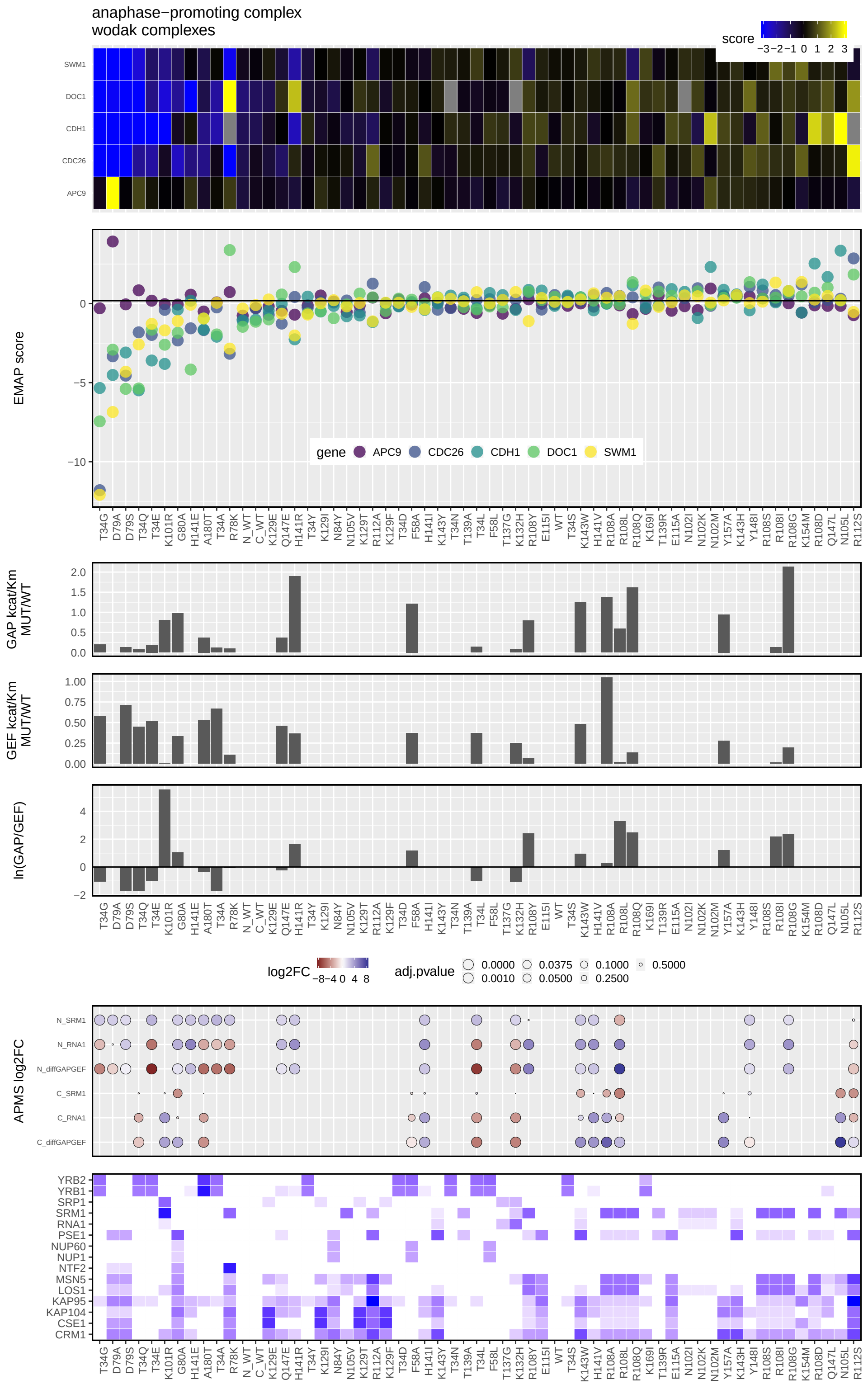

Set3p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SNT1
SIF2
SET3
HST1
HOS4
HOS2
CPR1
EMAP score
gene CPR1 HOS2 HOS4 HST1 SET3 SIF2 SNT1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N_WT R108L C_WT T34G H141R R112S R108Y F58A R108Q R108G E115I E115A F58L Y148I T34S K169I N102I N102K T139A R108I A180T K154M R78K T34Y T139R R108S T34N R108D N102M N105L WT K129T K129I K132H K101R K129E T34L N105V Q147L T34D K129F T137G R112A N84Y K143H K143Y H141V H141I G80A R108A K143W T34A T34E Q147E Y157A D79S T34Q D79A H141E


nucleotide−excision repair factor 1 complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RAD14
RAD1
EMAP score
gene
RAD1
RAD14
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A H141R T34G T34Q R108Y R78K R108L R112S H141E H141I K101R H141V R112A D79S Y148I N_WT R108Q N105V G80A R108D K143H Y157A C_WT T139R A180T N102M K143W K129I R108A F58L R108G T139A R108I N102I T34D T34E K169I T137G T34Y WT K129F N84Y T34A K129E E115A K143Y E115I N102K N105L R108S Q147L F58A K129T K132H T34N Q147E K154M T34S T34L

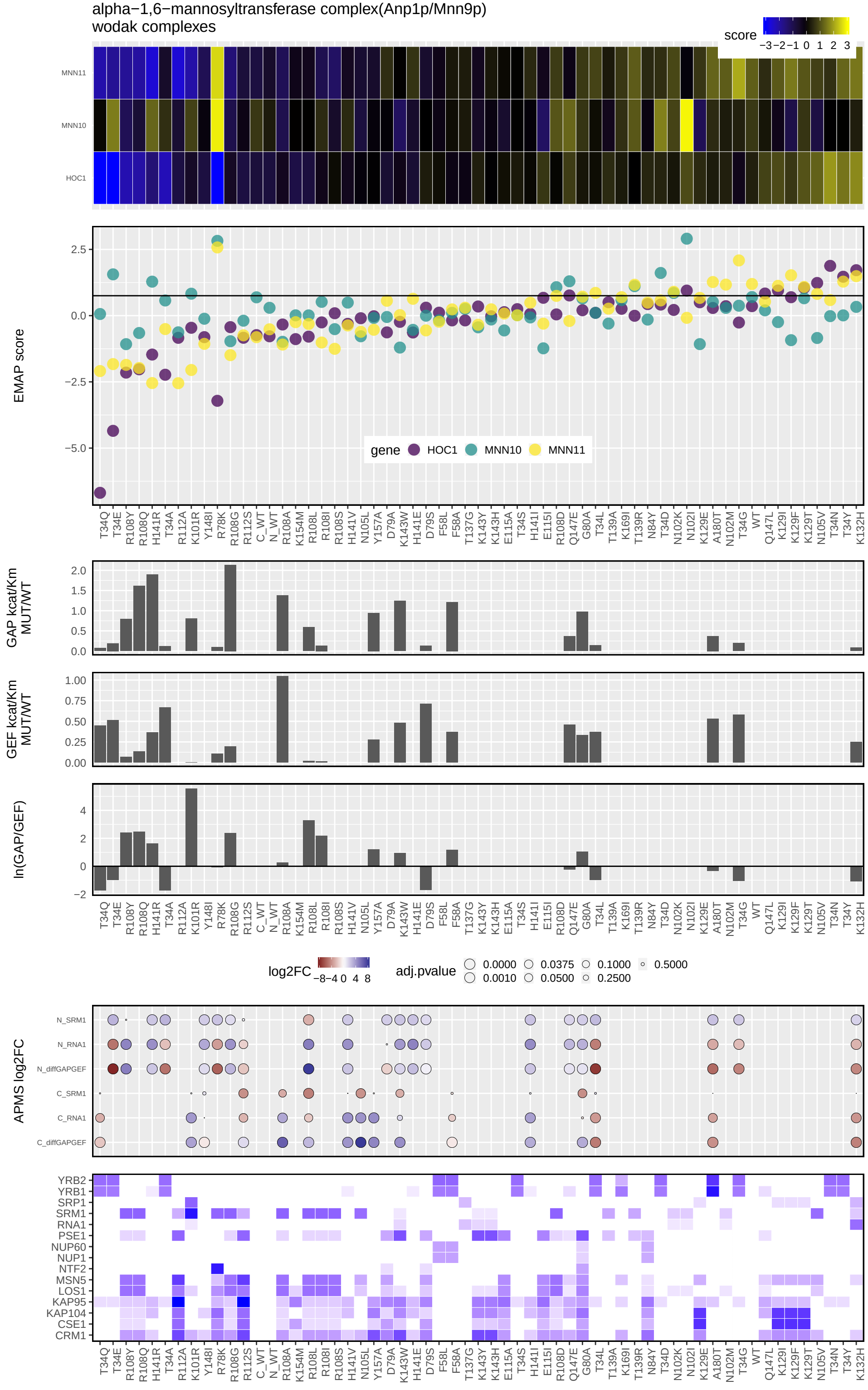
Tof1p/Mrc1p/Csm3p complex
wodak complexes

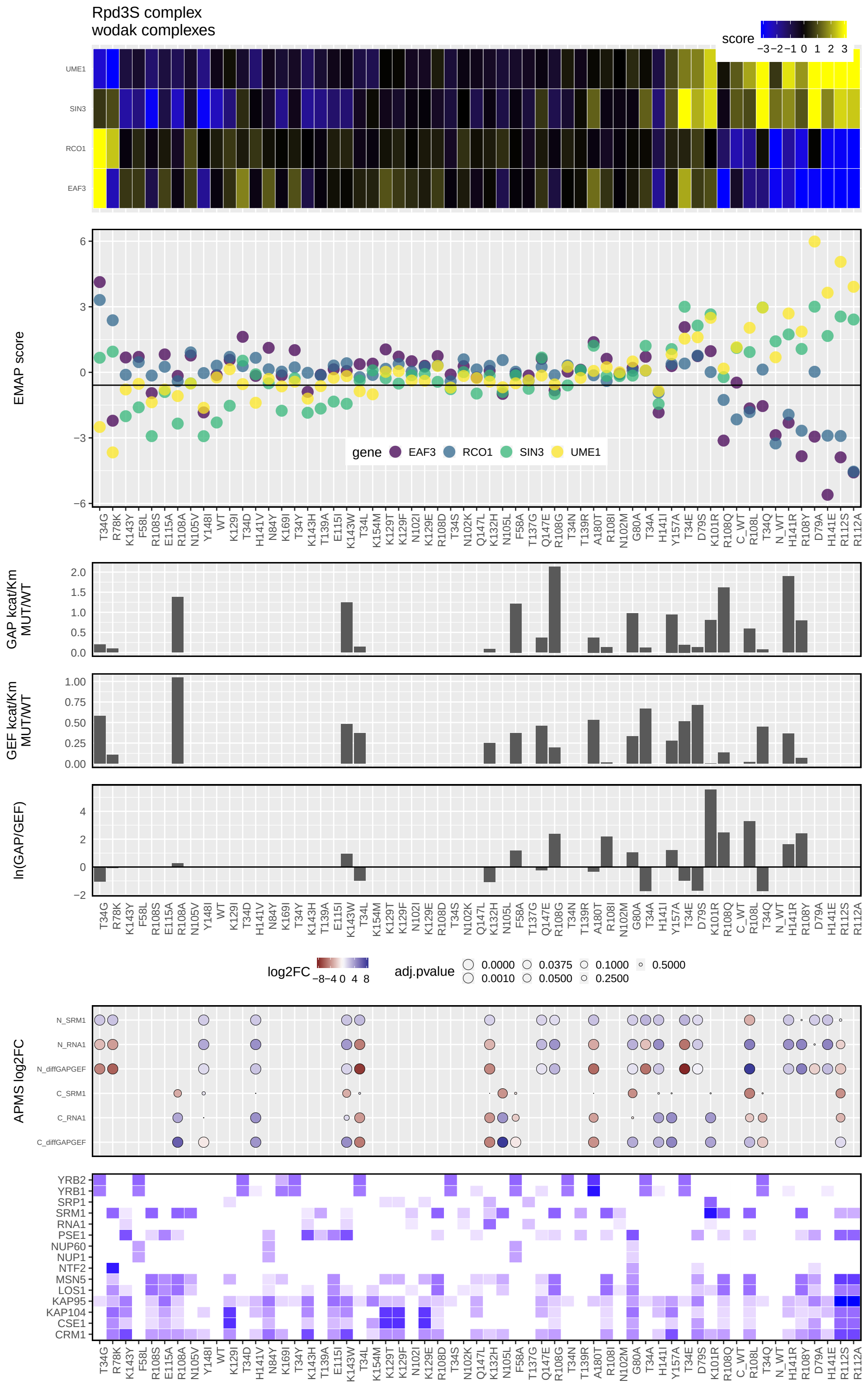


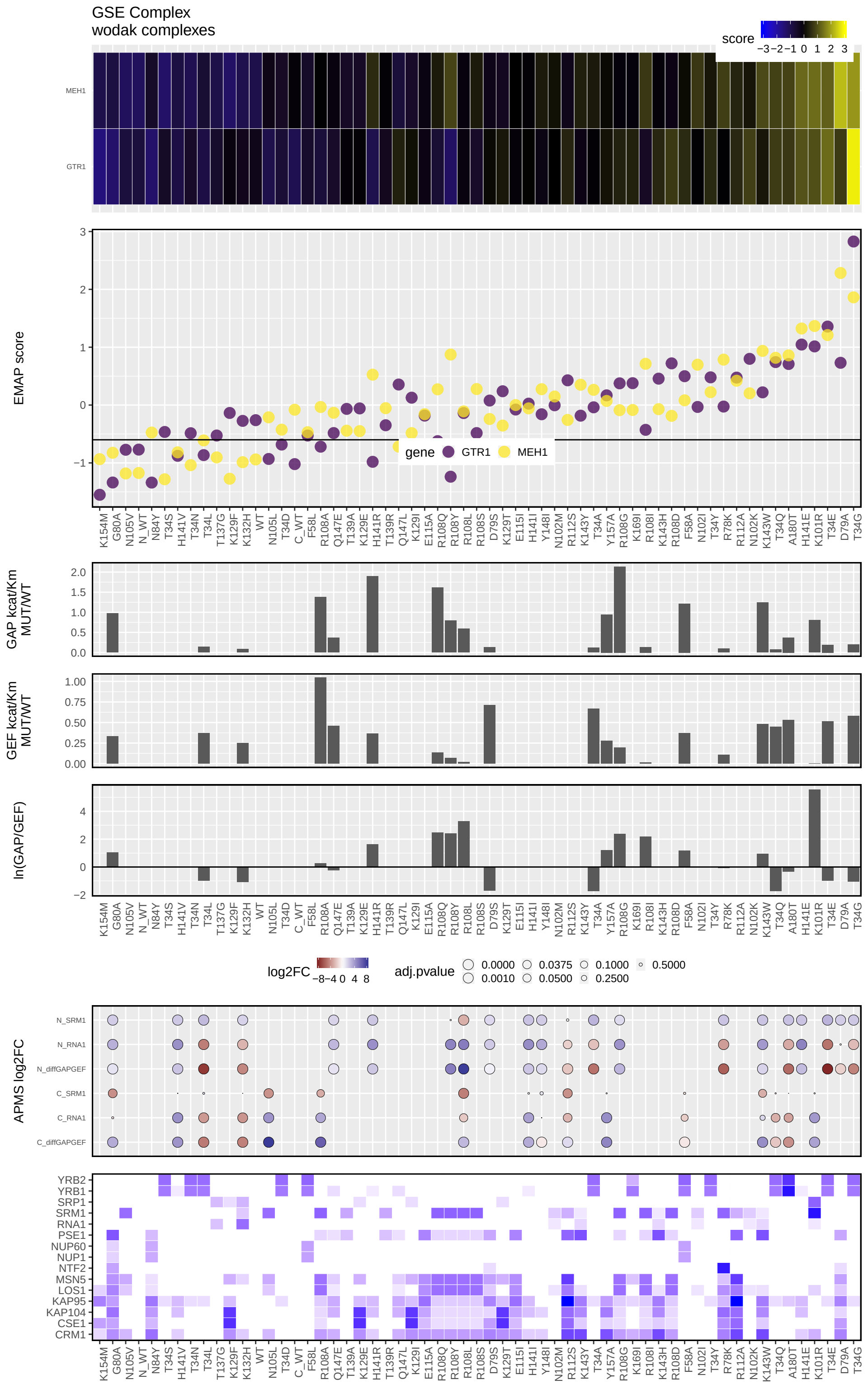

Swr1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
YAF9
VPS72
VPS71
SWR1
SWC5
SWC3
ARP6
EMAP score
gene ARP6 SWC3 SWC5 SWR1 VPS71 VPS72 YAF9
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000 0.0375 0.1000 0.5000
0.0010 0.0500 0.2500
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K K101R C_WT R108L A180T N102I F58A N102M N102K K129I E115A E115I N_WT R108D K129F K129T T34Y T34D T139R T34E Q147L F58L R108I T34A Q147E T137G K129E T139A T34S N105V G80A K132H T34L N105L K154M K169I WT N84Y T34N K143H K143W K143Y H141V R108S R108Q R108G Y148I R108A H141R H141I D79S T34Q Y157A R108Y R112A T34G R112S D79A H141E

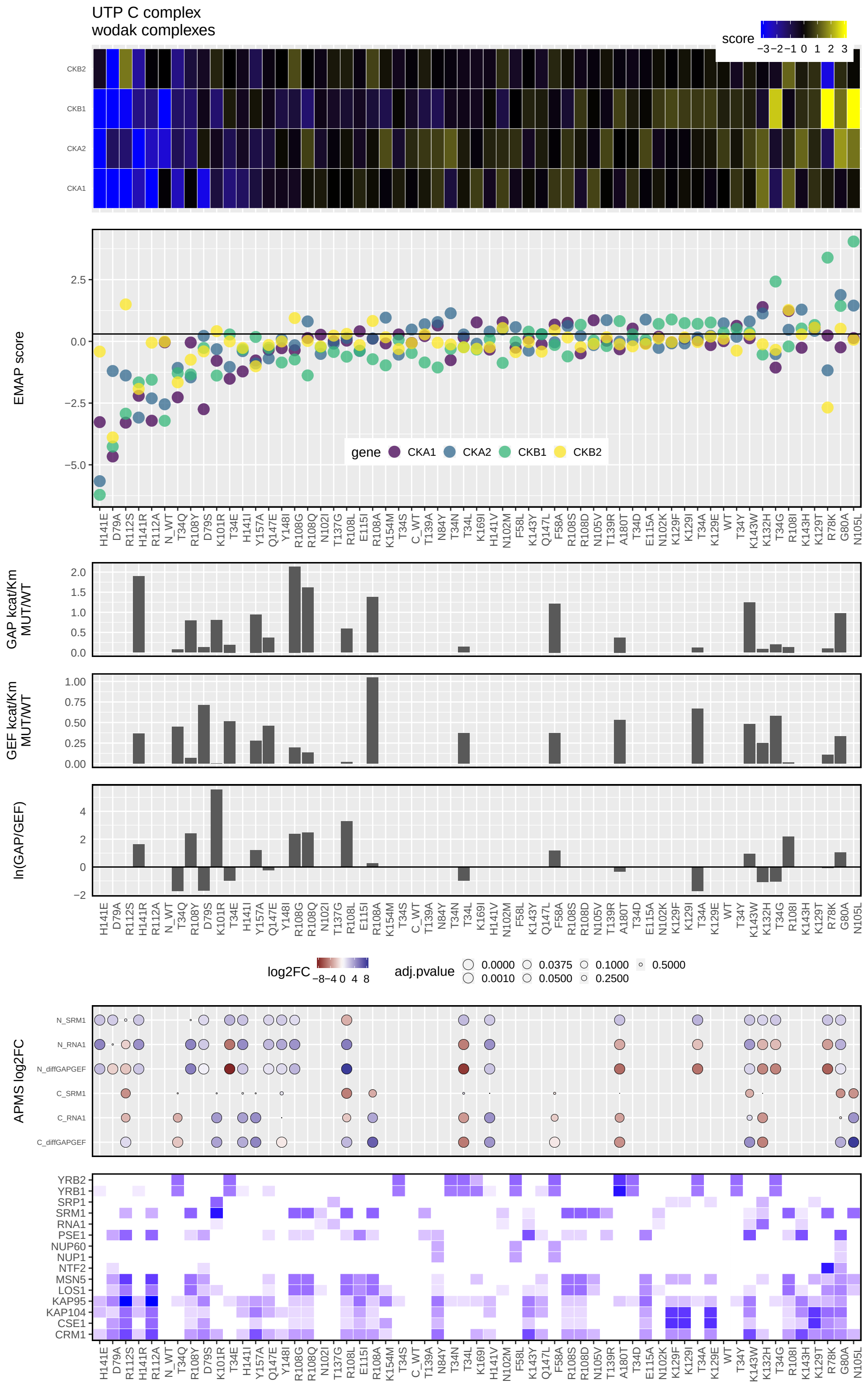

anaphase−promoting complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SWM1
DOC1
CDH1
CDC26
APC9
EMAP score
gene APC9 CDC26 CDH1 DOC1 SWM1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A D79S T34Q T34E K101R G80A H141E A180T T34A R78K N_WT C_WT K129E Q147E H141R T34Y K129I N84Y N105V K129T R112A K129F T34D F58A H141I K143Y T34N T139A T34L F58L T137G K132H R108Y E115I WT T34S K143W H141V R108A R108L R108Q K169I T139R E115A N102I N102K N102M Y157A K143H Y148I R108S R108I R108G K154M R108D Q147L N105L R112S

alpha−1,6−mannosyltransferase complex(Anp1p/Mnn9p)
wodak complexes

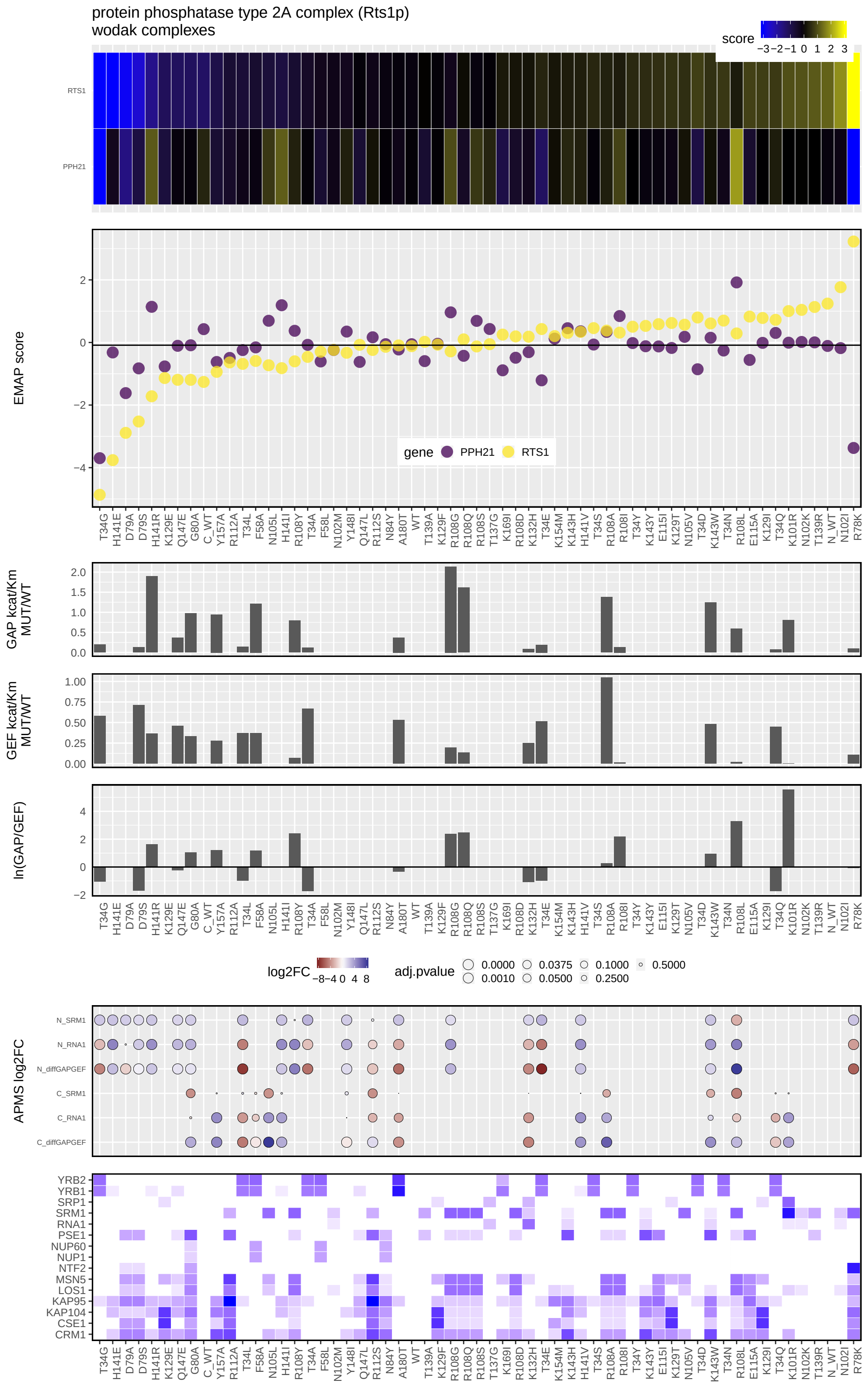



Rpd3S complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UME1
SIN3
RCO1
EAF3
EMAP score
gene EAF3 RCO1 SIN3 UME1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G R78K K143Y F58L R108S E115A R108A N105V Y148I WT K129I T34D H141V N84Y K169I T34Y K143H T139A E115I K143W T34L K154M K129T K129F N102I K129E R108D T34S N102K Q147L K132H N105L F58A T137G Q147E R108G T34N T139R A180T R108I N102M G80A T34A H141I Y157A T34E D79S K101R R108Q C_WT R108L T34Q N_WT H141R R108Y D79A H141E R112S R112A

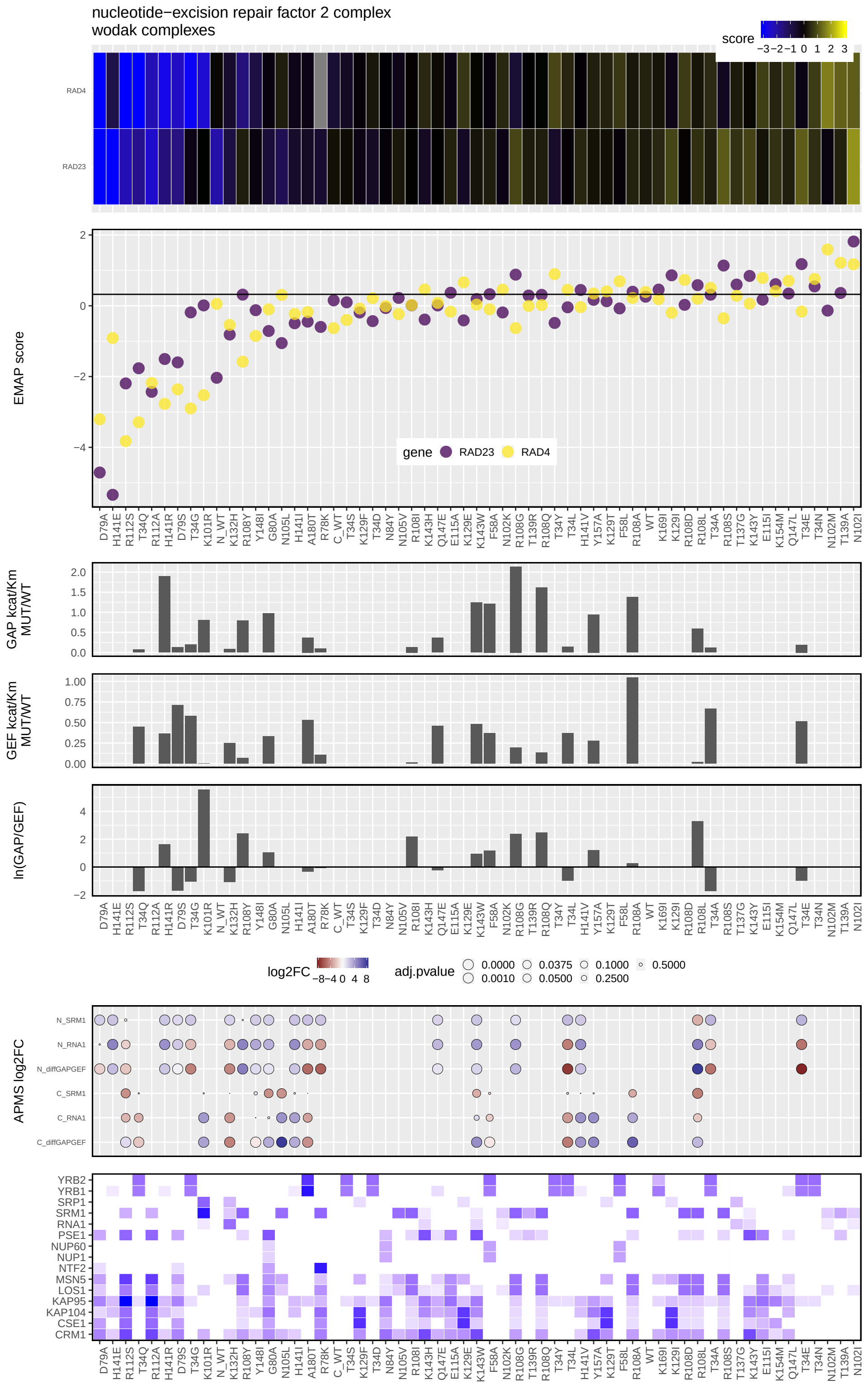

GSE Complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MEH1
GTR1
EMAP score
gene GTR1 MEH1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K154M G80A N105V N_WT N84Y T34S H141V T34N T34L T137G K129F K132H WT N105L T34D C_WT F58L R108A Q147E T139A K129E H141R T139R Q147L K129I E115A R108Q R108Y R108L R108S D79S K129T E115I H141I Y148I N102M R112S K143Y T34A Y157A R108G K169I R108I K143H R108D F58A N102I T34Y R78K R112A N102K K143W T34Q A180T H141E K101R T34E D79A T34G

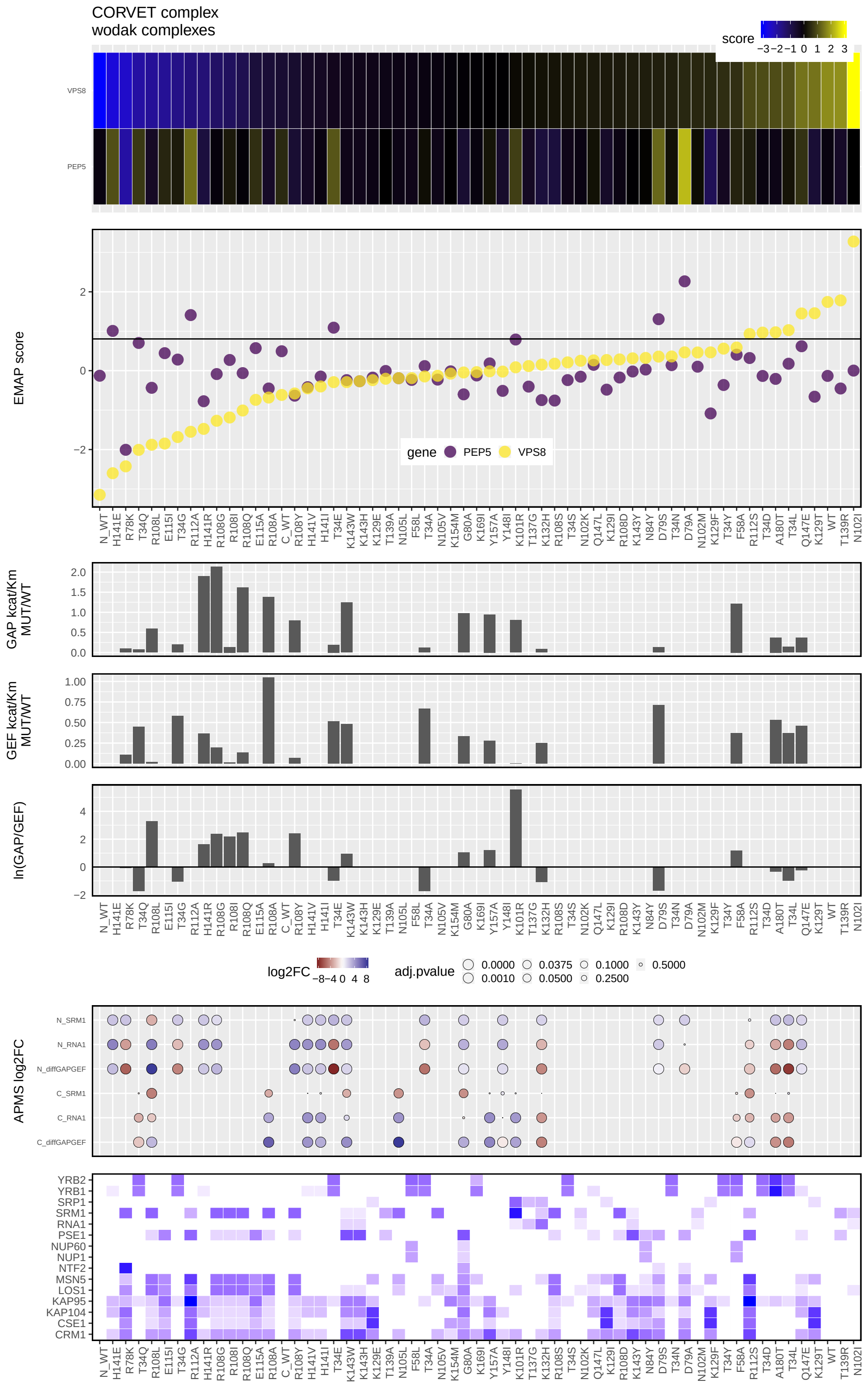

UTP C complex
wodak complexes
score
−3 −2 −1 0 1 2 3
CKB2
CKB1
CKA2
CKA1
EMAP score
2.5
0.0
−2.5
−5.0
gene
CKA1
CKA2
CKB1
CKB2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E D79A R112S H141R R112A N_WT T34Q R108Y D79S K101R T34E H141I Y157A Q147E Y148I R108G R108Q N102I T137G R108L E115I R108A K154M T34S C_WT T139A N84Y T34N T34L K169I H141V N102M F58L K143Y Q147L F58A R108S R108D N105V T139R A180T T34D E115A N102K K129F K129I T34A K129E WT T34Y K143W K132H T34G R108I K143H K129T R78K G80A N105L

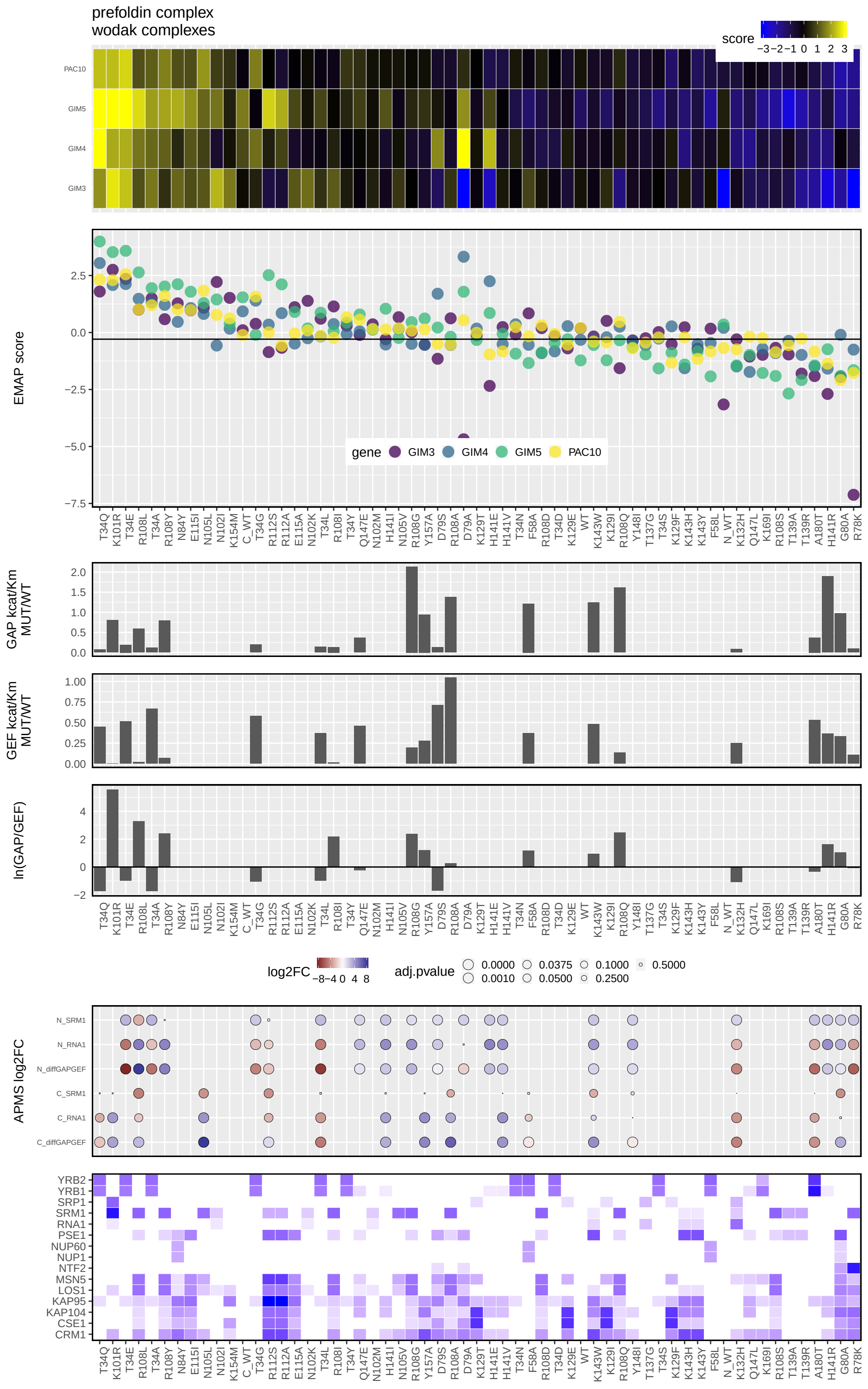
protein phosphatase type 2A complex (Rts1p)
wodak complexes

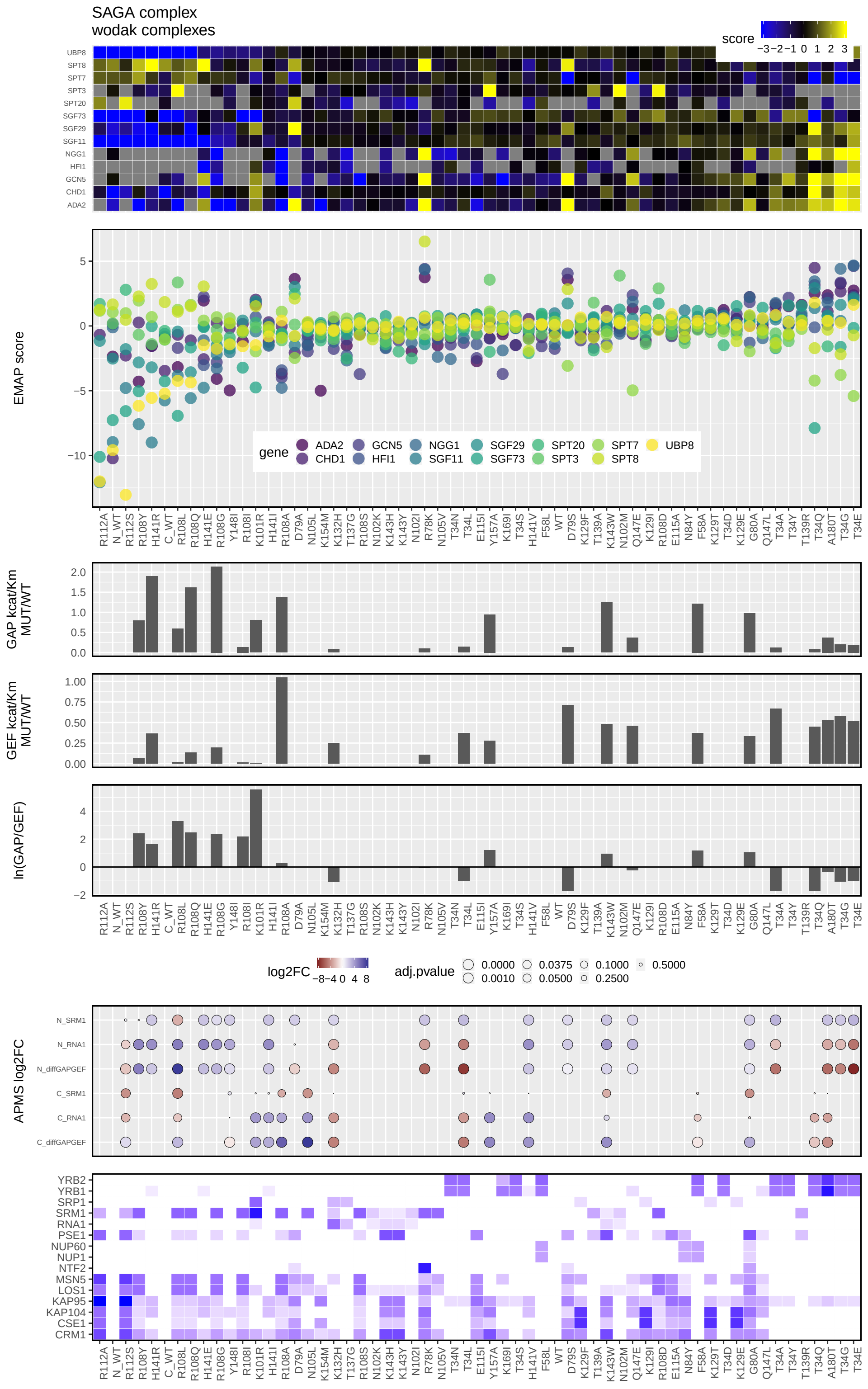


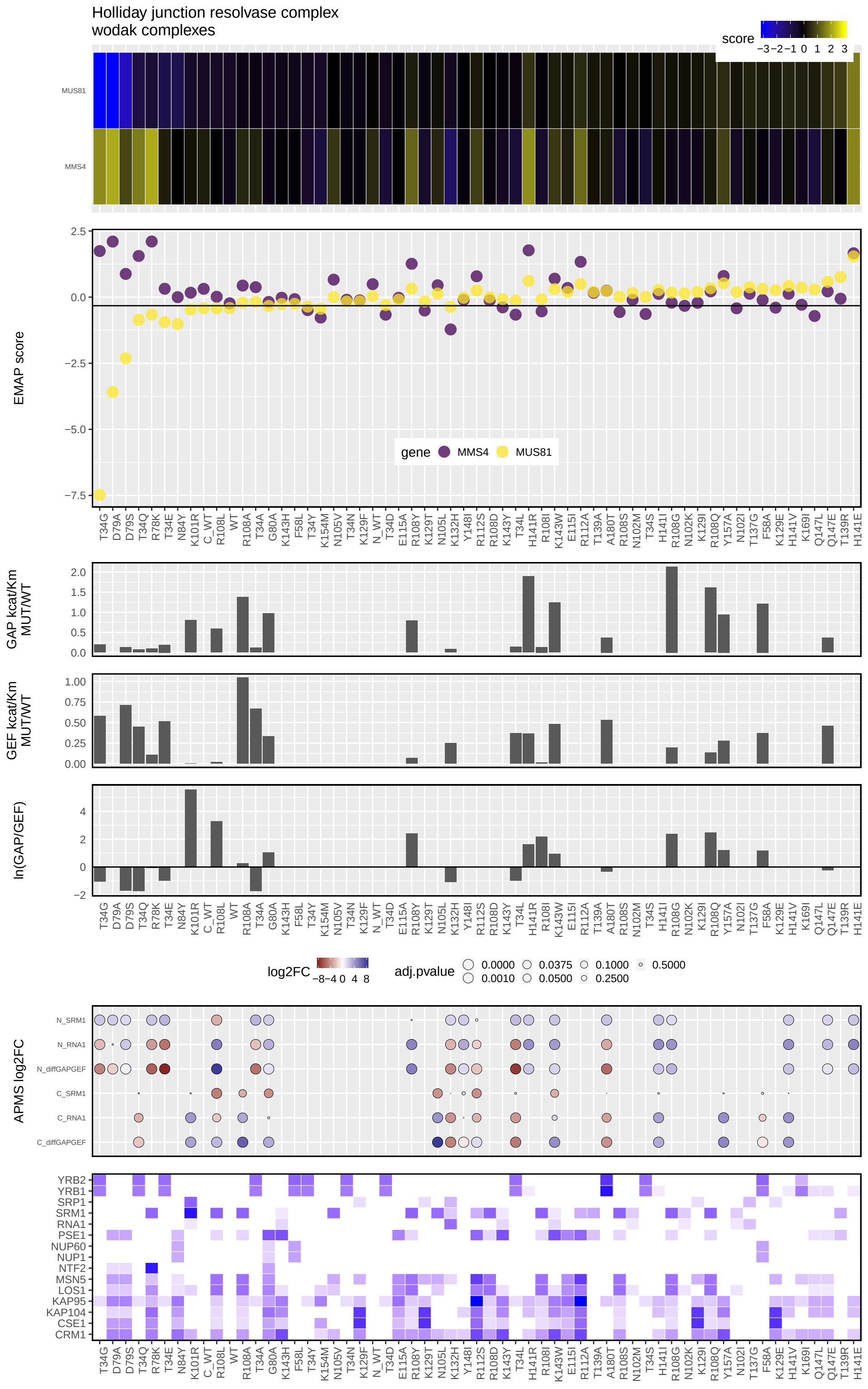
nucleotide−excision repair factor 2 complex
wodak complexes

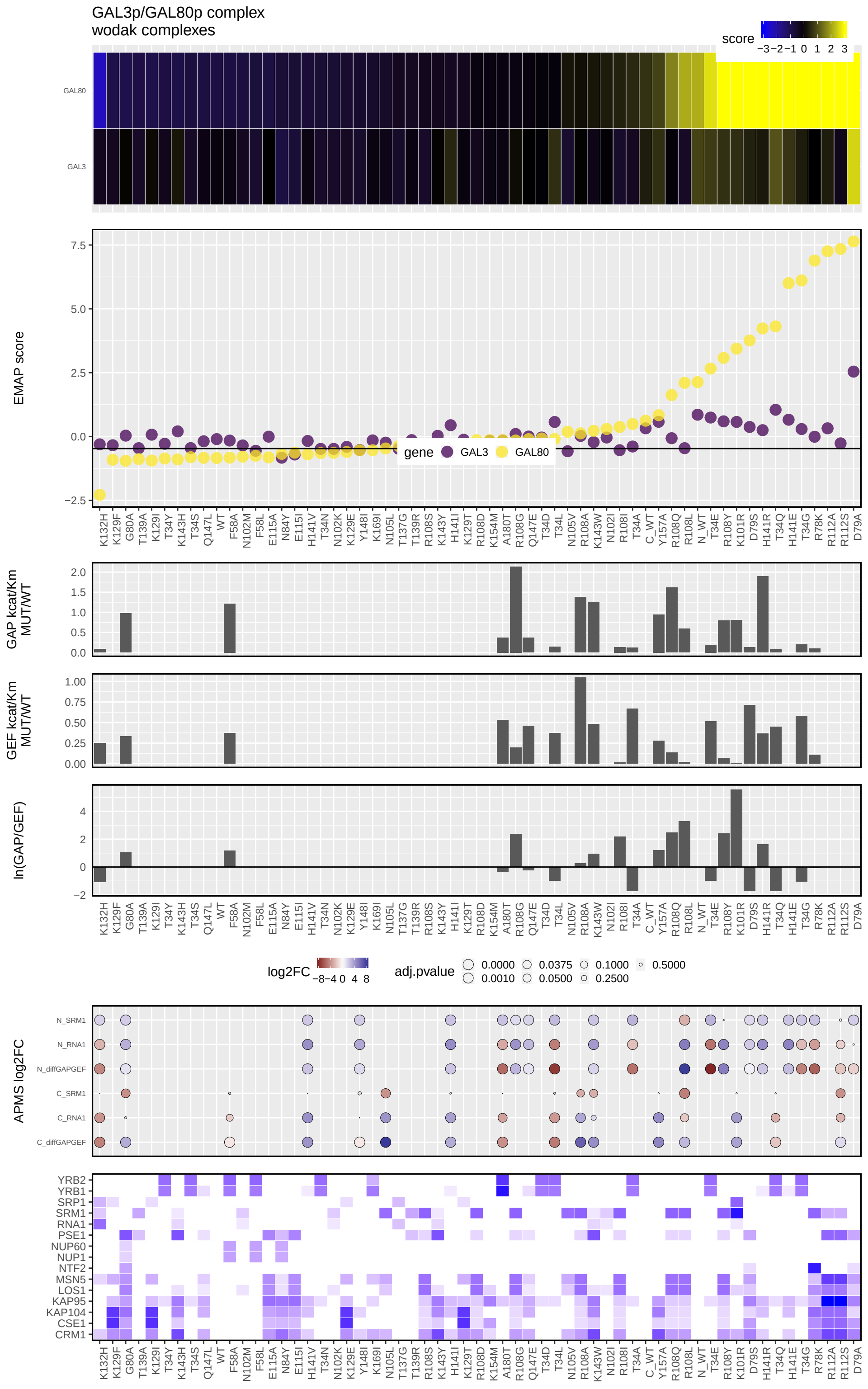


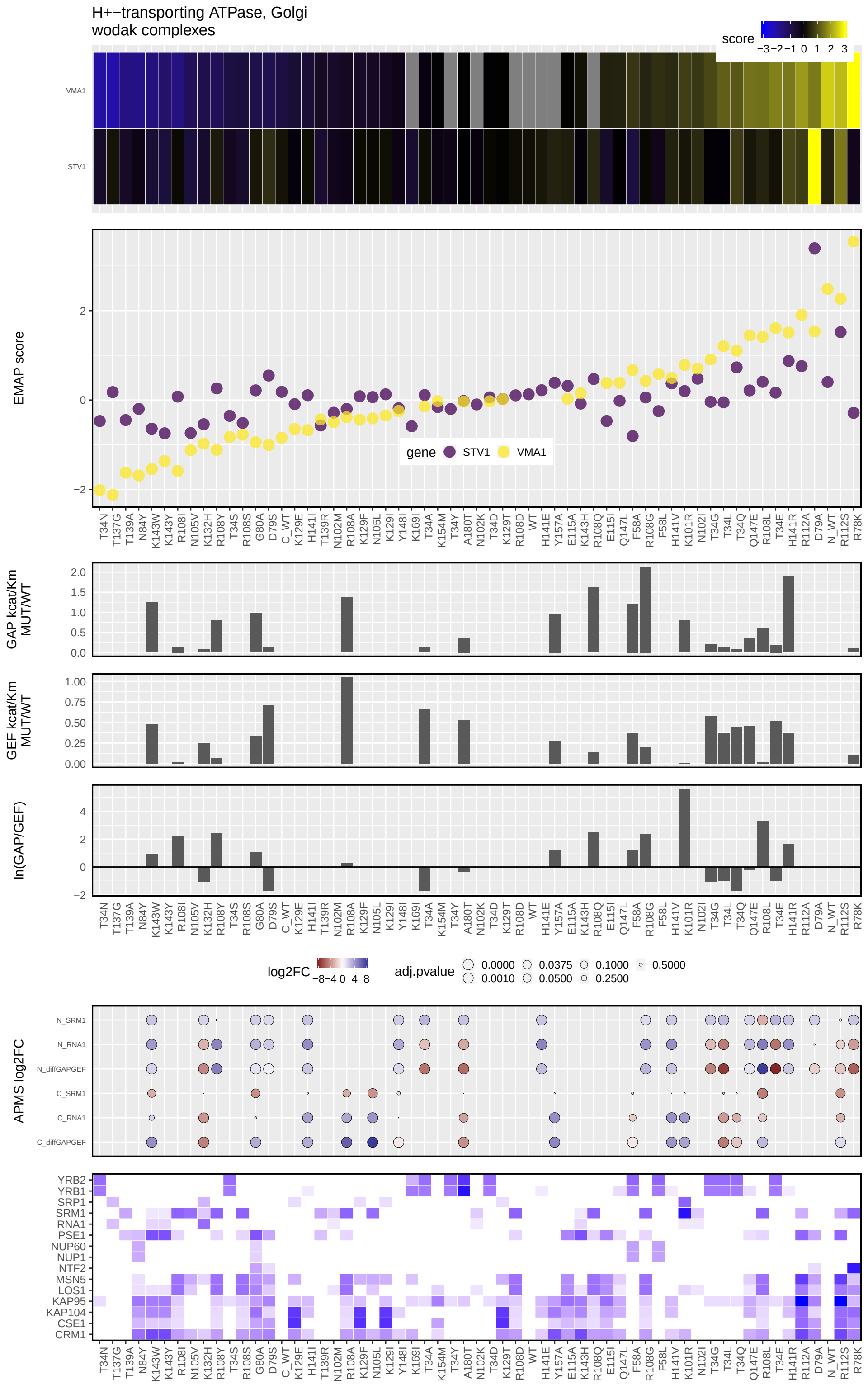

CORVET complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VPS8
PEP5
EMAP score
gene
PEP5
VPS8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
N_WT H141E R78K T34Q R108L E115I T34G R112A H141R R108G R108I R108Q E115A R108A C_WT R108Y H141V H141I T34E K143W K143H K129E T139A N105L F58L T34A N105V K154M G80A K169I Y157A Y148I K101R T137G K132H R108S T34S N102K Q147L K129I R108D K143Y N84Y D79S T34N D79A N102M K129F T34Y F58A R112S T34D A180T T34L Q147E K129T WT T139R N102I

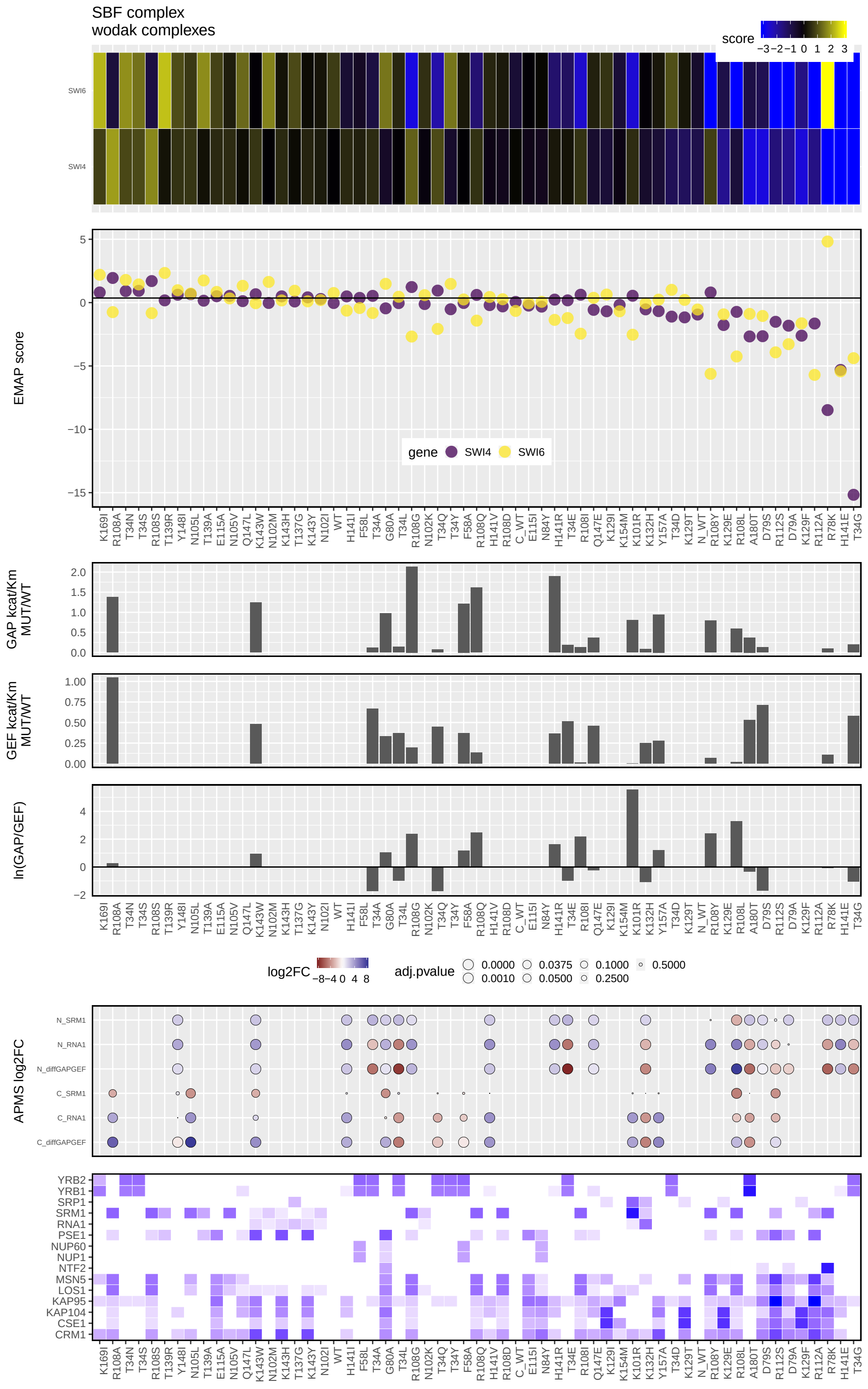

prefoldin complex
wodak complexes
score
−3 −2 −1 0 1 2 3
PAC10
GIM5
GIM4
GIM3
EMAP score
gene GIM3 GIM4 GIM5 PAC10
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34Q K101R T34E R108L T34A R108Y N84Y E115I N105L N102I K154M C_WT T34G R112S R112A E115A N102K T34L R108I T34Y Q147E N102M H141I N105V R108G Y157A D79S R108A D79A K129T H141E H141V T34N F58A R108D T34D K129E WT K143W K129I R108Q Y148I T137G T34S K129F K143H K143Y F58L N_WT K132H Q147L K169I R108S T139A T139R A180T H141R G80A R78K

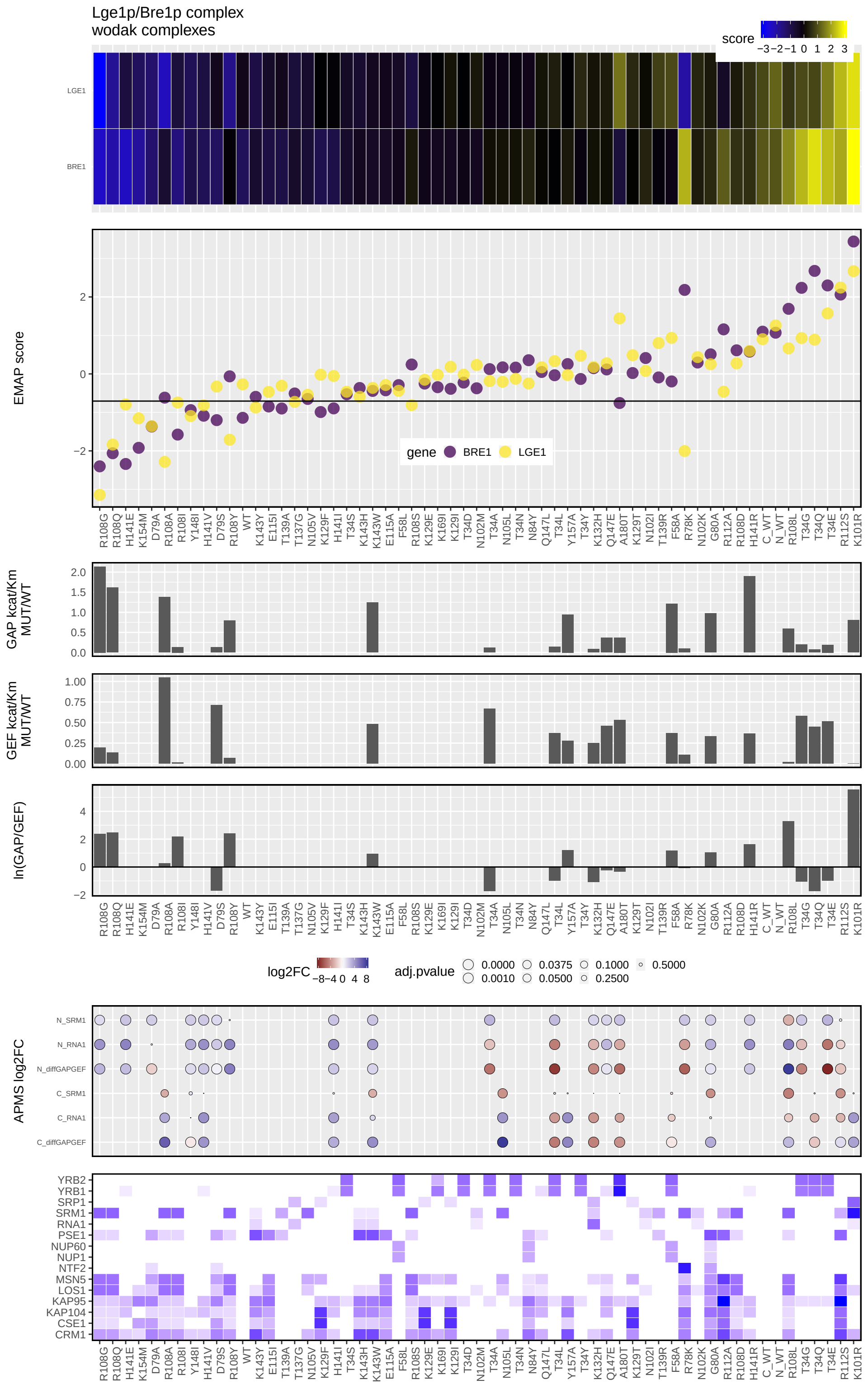

SAGA complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UBP8
SPT8
SPT7
SPT3
SPT20
SGF73
SGF29
SGF11
NGG1
HFI1
GCN5
CHD1
ADA2
EMAP score
gene
ADA2
CHD1
GCN5
HFI1
NGG1
SGF11
SGF29
SGF73
SPT20
SPT3
SPT7
SPT8
UBP8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A N_WT R112S R108Y H141R C_WT R108L R108Q H141E R108G Y148I R108I K101R H141I R108A D79A N105L K154M K132H T137G R108S N102K K143H K143Y N102I R78K N105V T34N T34L E115I Y157A K169I T34S H141V F58L WT D79S K129F T139A K143W N102M Q147E K129I R108D E115A N84Y F58A K129T T34D K129E G80A Q147L T34A T34Y T139R T34Q A180T T34G T34E

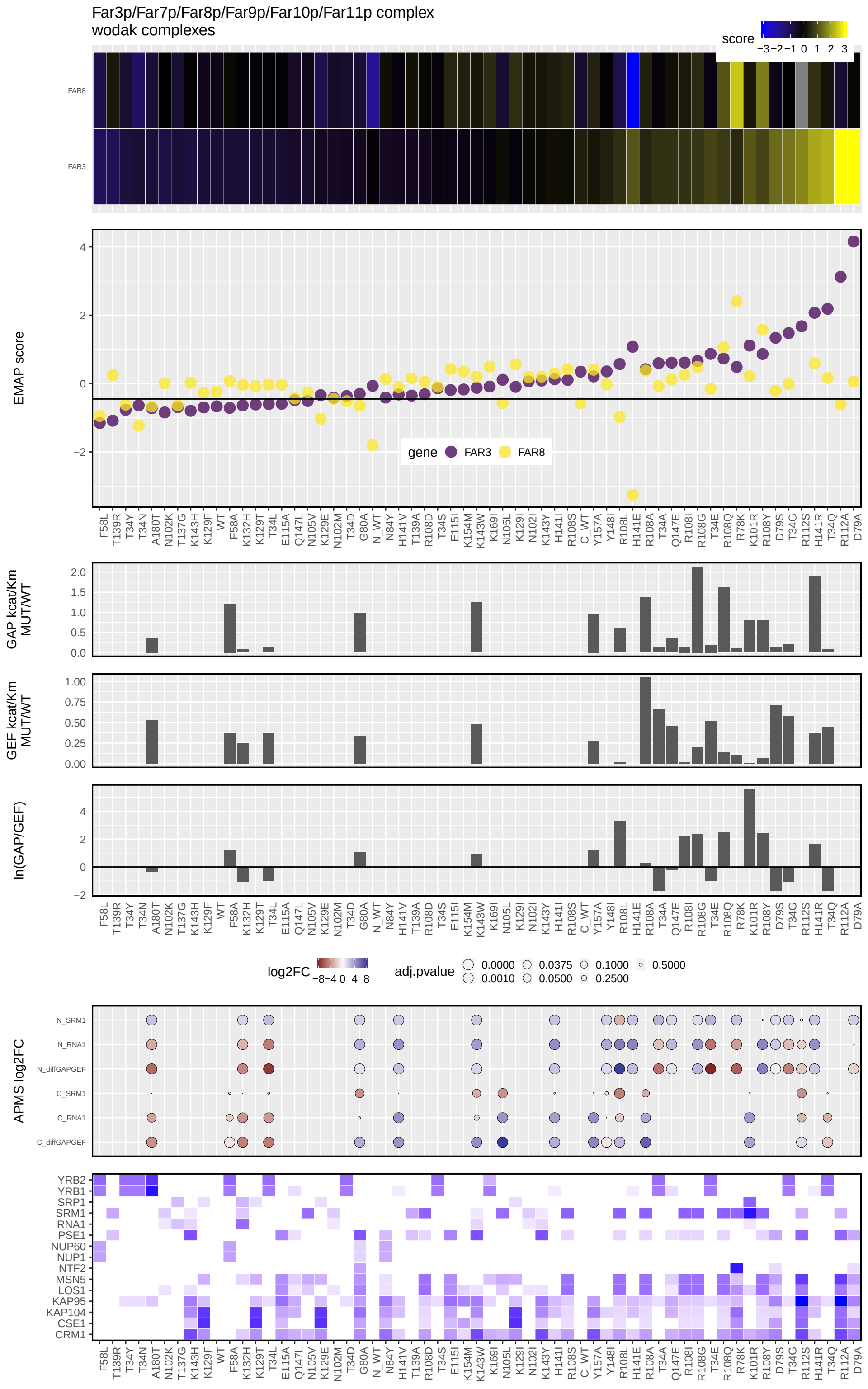

Holliday junction resolvase complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MUS81
MMS4
EMAP score
gene
MMS4
MUS81
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A D79S T34Q R78K T34E N84Y K101R C_WT R108L WT R108A T34A G80A K143H F58L T34Y K154M N105V T34N K129F N_WT T34D E115A R108Y K129T N105L K132H Y148I R112S R108D K143Y T34L H141R R108I K143W E115I R112A T139A A180T R108S N102M T34S H141I R108G N102K K129I R108Q Y157A N102I T137G F58A K129E H141V K169I Q147L Q147E T139R H141E

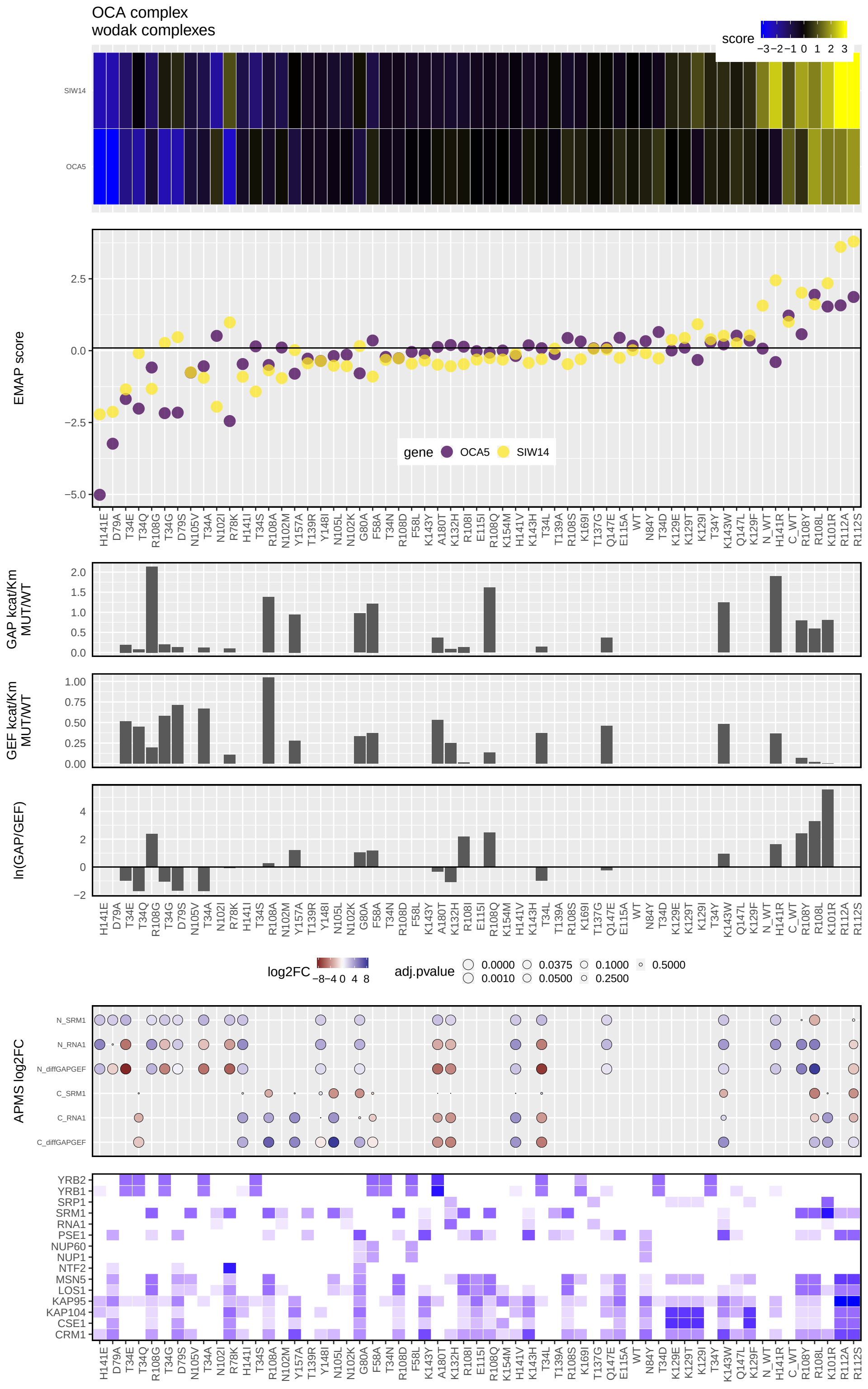

GAL3p/GAL80p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
GAL80
GAL3
EMAP score
gene
GAL3
GAL80
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K132H K129F G80A T139A K129I T34Y K143H T34S Q147L WT F58A N102M F58L E115A N84Y E115I H141V T34N N102K K129E Y148I K169I N105L T137G T139R R108S K143Y H141I K129T R108D K154M A180T R108G Q147E T34D T34L N105V R108A K143W N102I R108I T34A C_WT Y157A R108Q R108L N_WT T34E R108Y K101R D79S H141R T34Q H141E T34G R78K R112A R112S D79A

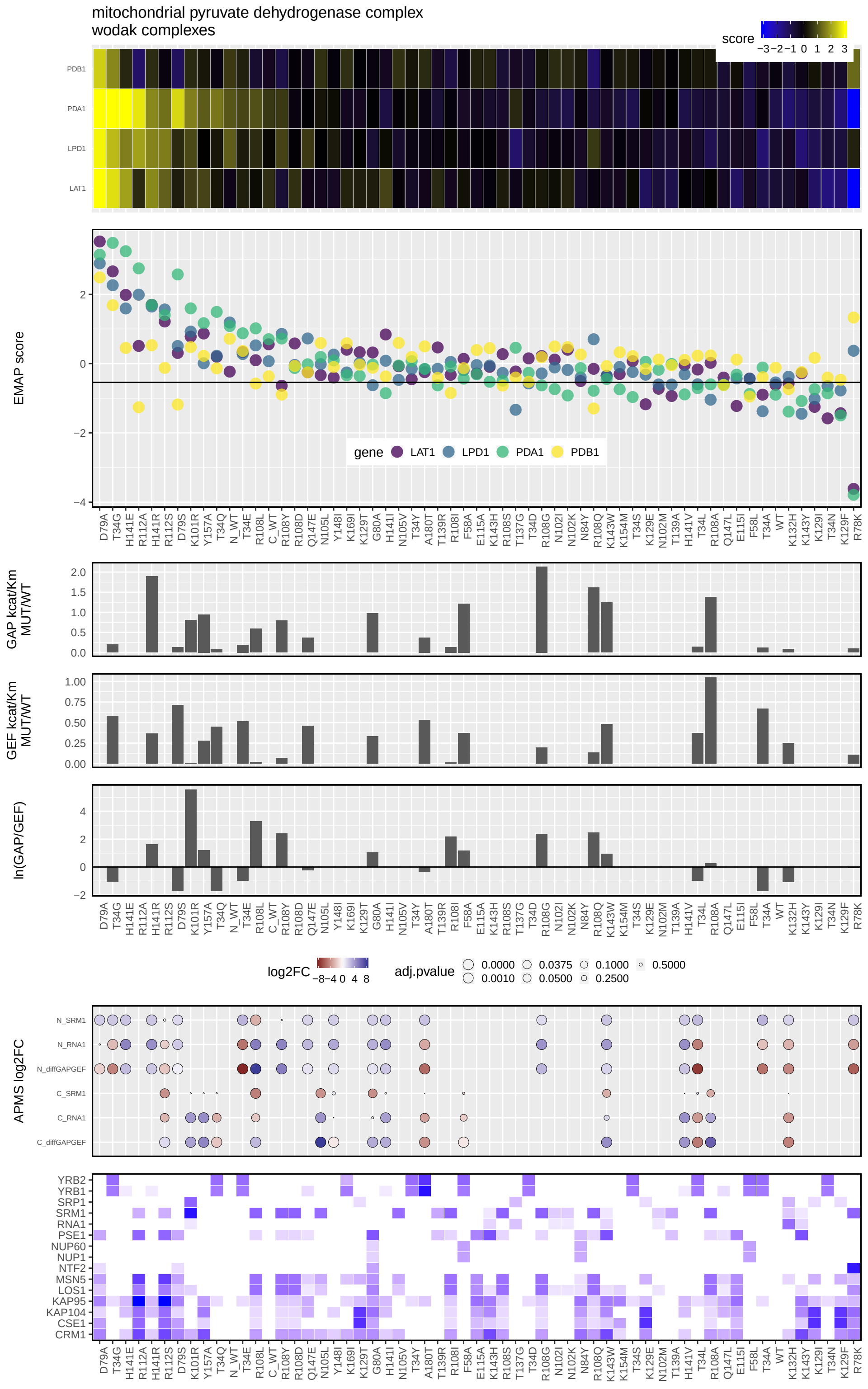

H+−transporting ATPase, Golgi
wodak complexes
score
−3 −2 −1 0 1 2 3
VMA1
STV1
EMAP score
gene
STV1
VMA1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34N T137G T139A N84Y K143W K143Y R108I N105V K132H R108Y T34S R108S G80A D79S C_WT K129E H141I T139R N102M R108A K129F N105L K129I Y148I K169I T34A K154M T34Y A180T N102K T34D K129T R108D WT H141E Y157A E115A K143H R108Q E115I Q147L F58A R108G F58L H141V K101R N102I T34G T34L T34Q Q147E R108L T34E H141R R112A D79A N_WT R112S R78K

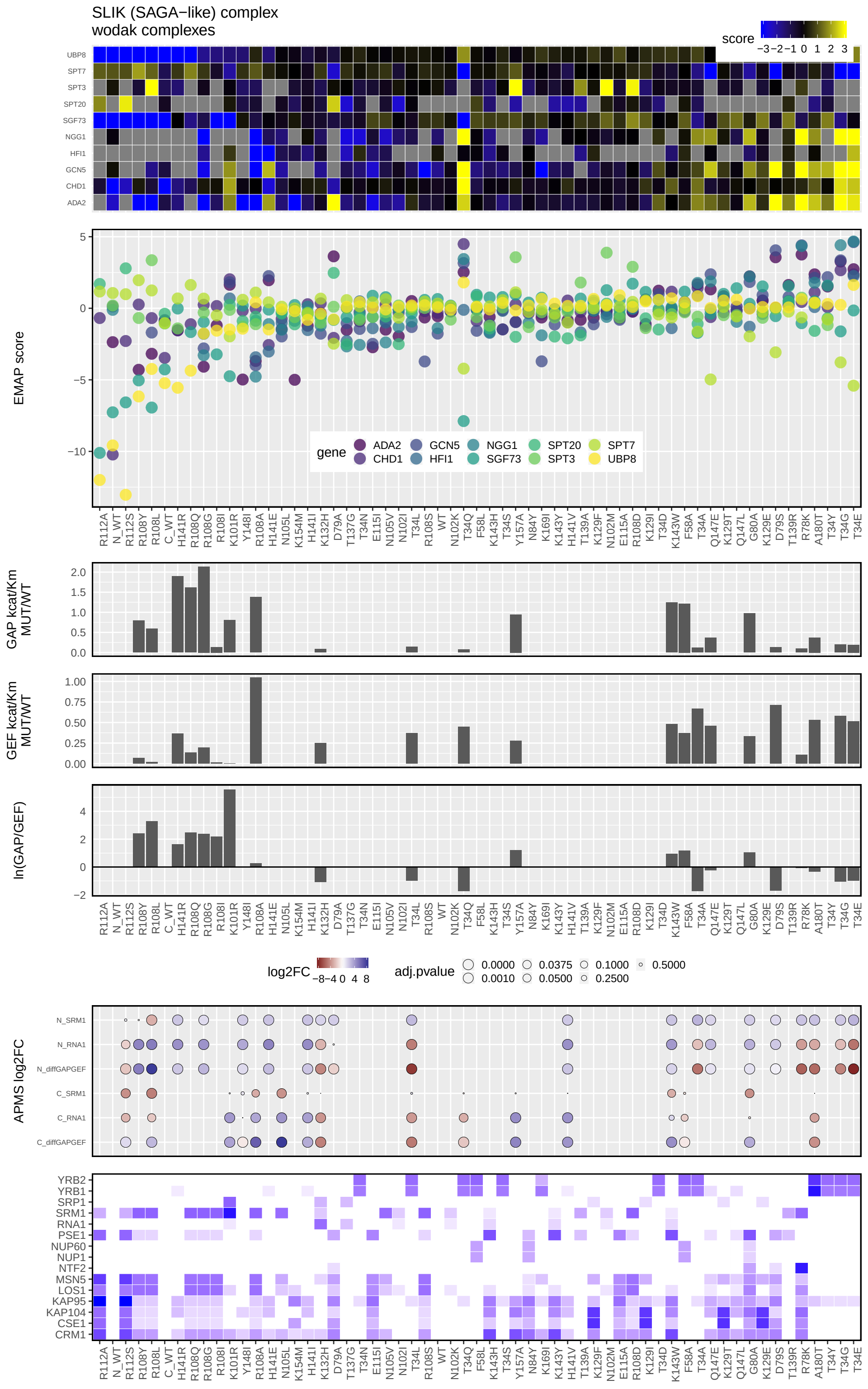

SBF complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SWI6
SWI4
EMAP score
gene SWI4 SWI6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
K169I R108A T34N T34S R108S T139R Y148I N105L T139A E115A N105V Q147L K143W N102M K143H T137G K143Y N102I WT H141I F58L T34A G80A T34L R108G N102K T34Q T34Y F58A R108Q H141V R108D C_WT E115I N84Y H141R T34E R108I Q147E K129I K154M K101R K132H Y157A T34D K129T N_WT R108Y K129E R108L A180T D79S R112S D79A K129F R112A R78K H141E T34G

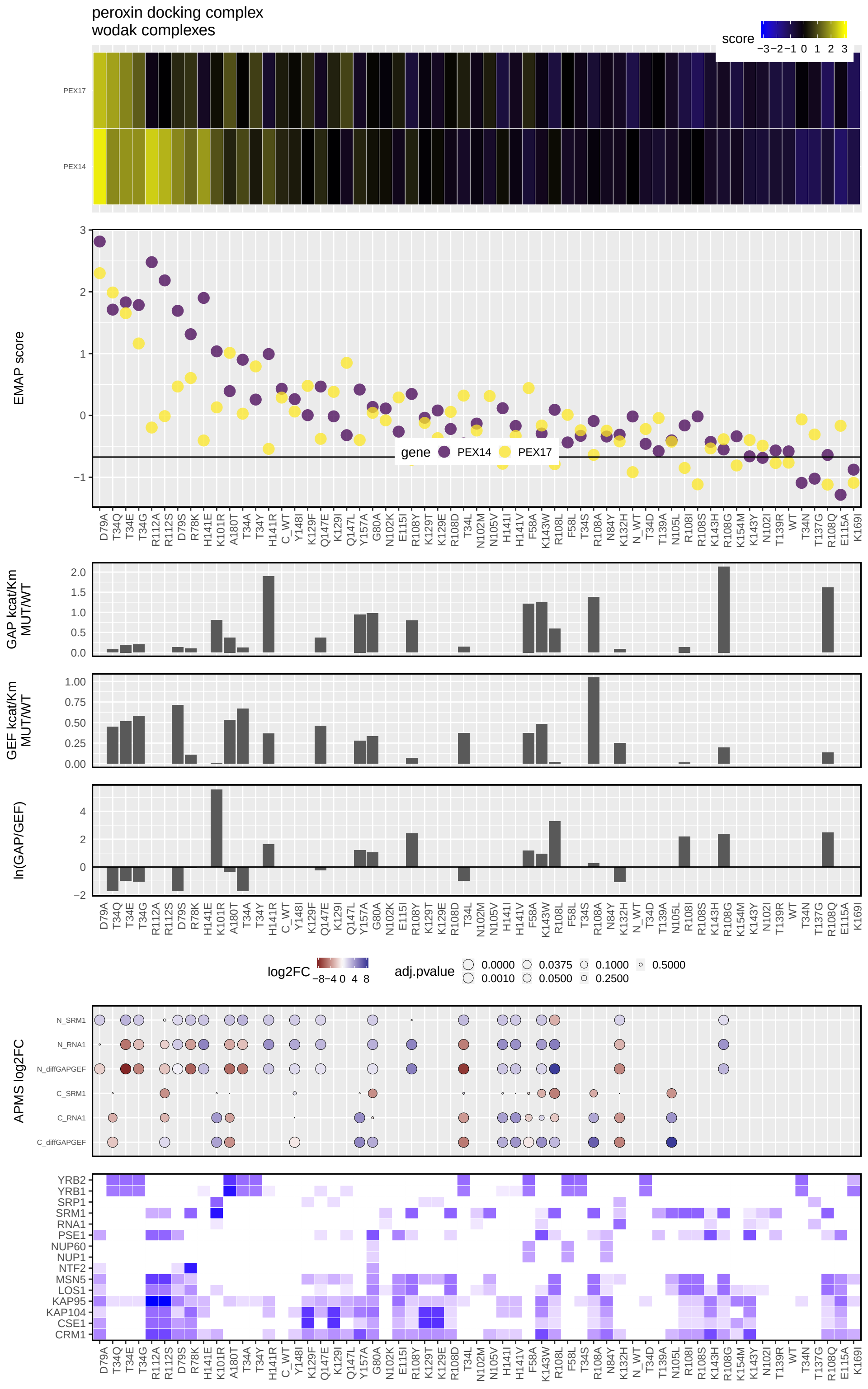

Lge1p/Bre1p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
LGE1
BRE1
EMAP score
gene
BRE1
LGE1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108G R108Q H141E K154M D79A R108A R108I Y148I H141V D79S R108Y WT K143Y E115I T139A T137G N105V K129F H141I T34S K143H K143W E115A F58L R108S K129E K169I K129I T34D N102M T34A N105L T34N N84Y Q147L T34L Y157A T34Y K132H Q147E A180T K129T N102I T139R F58A R78K N102K G80A R112A R108D H141R C_WT N_WT R108L T34G T34Q T34E R112S K101R


Far3p/Far7p/Far8p/Far9p/Far10p/Far11p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
FAR8
FAR3
EMAP score
gene FAR3 FAR8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
F58L T139R T34Y T34N A180T N102K T137G K143H K129F WT F58A K132H K129T T34L E115A Q147L N105V K129E N102M T34D G80A N_WT N84Y H141V T139A R108D T34S E115I K154M K143W K169I N105L K129I N102I K143Y H141I R108S C_WT Y157A Y148I R108L H141E R108A T34A Q147E R108I R108G T34E R108Q R78K K101R R108Y D79S T34G R112S H141R T34Q R112A D79A

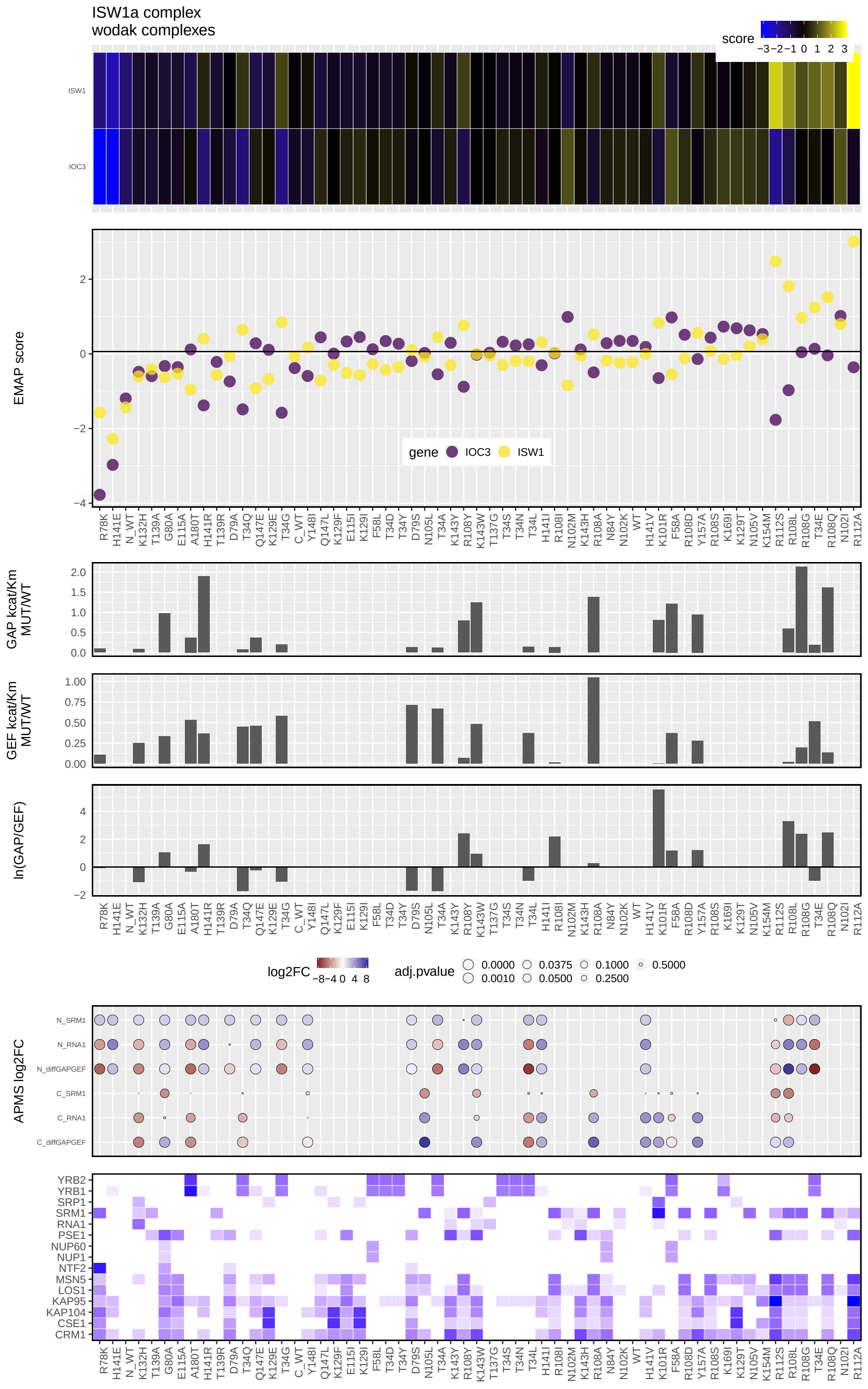

OCA complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SIW14
OCA5
EMAP score
2.5
0.0
−2.5
−5.0
gene
OCA5
SIW14
H141E D79A T34E T34Q R108G T34G D79S N105V T34A N102I R78K H141I T34S R108A N102M Y157A T139R Y148I N105L N102K G80A F58A T34N R108D F58L K143Y A180T K132H R108I E115I R108Q K154M H141V K143H T34L T139A R108S K169I T137G Q147E E115A WT N84Y T34D K129E K129T K129I T34Y K143W Q147L K129F N_WT H141R C_WT R108Y R108L K101R R112A R112S
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

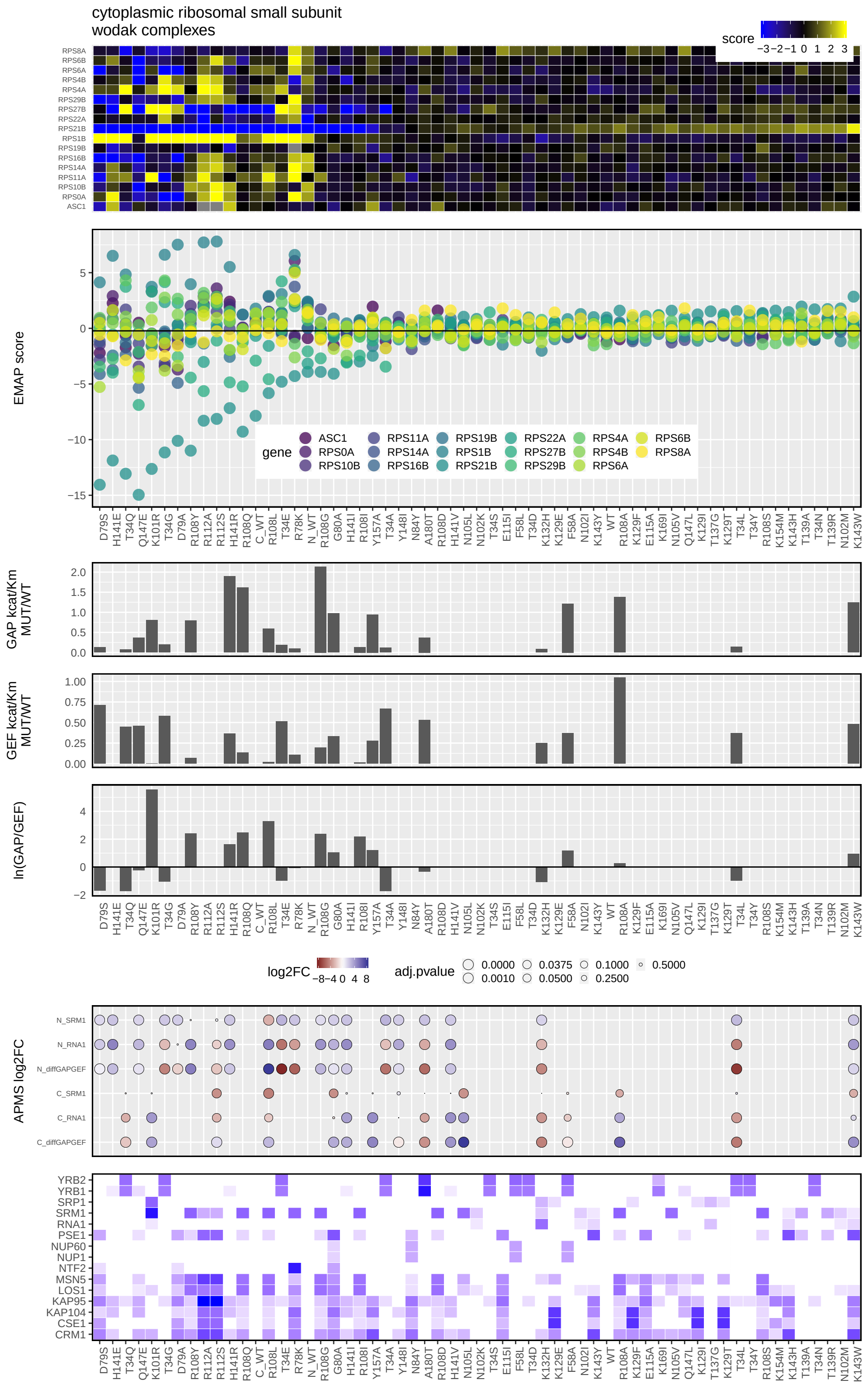

mitochondrial pyruvate dehydrogenase complex
wodak complexes
score
−3 −2 −1 0 1 2 3
PDB1
PDA1
LPD1
LAT1
EMAP score
gene LAT1 LPD1 PDA1 PDB1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34G H141E R112A H141R R112S D79S K101R Y157A T34Q N_WT T34E R108L C_WT R108Y R108D Q147E N105L Y148I K169I K129T G80A H141I N105V T34Y A180T T139R R108I F58A E115A K143H R108S T137G T34D R108G N102I N102K N84Y R108Q K143W K154M T34S K129E N102M T139A H141V T34L R108A Q147L E115I F58L T34A WT K132H K143Y K129I T34N K129F R78K

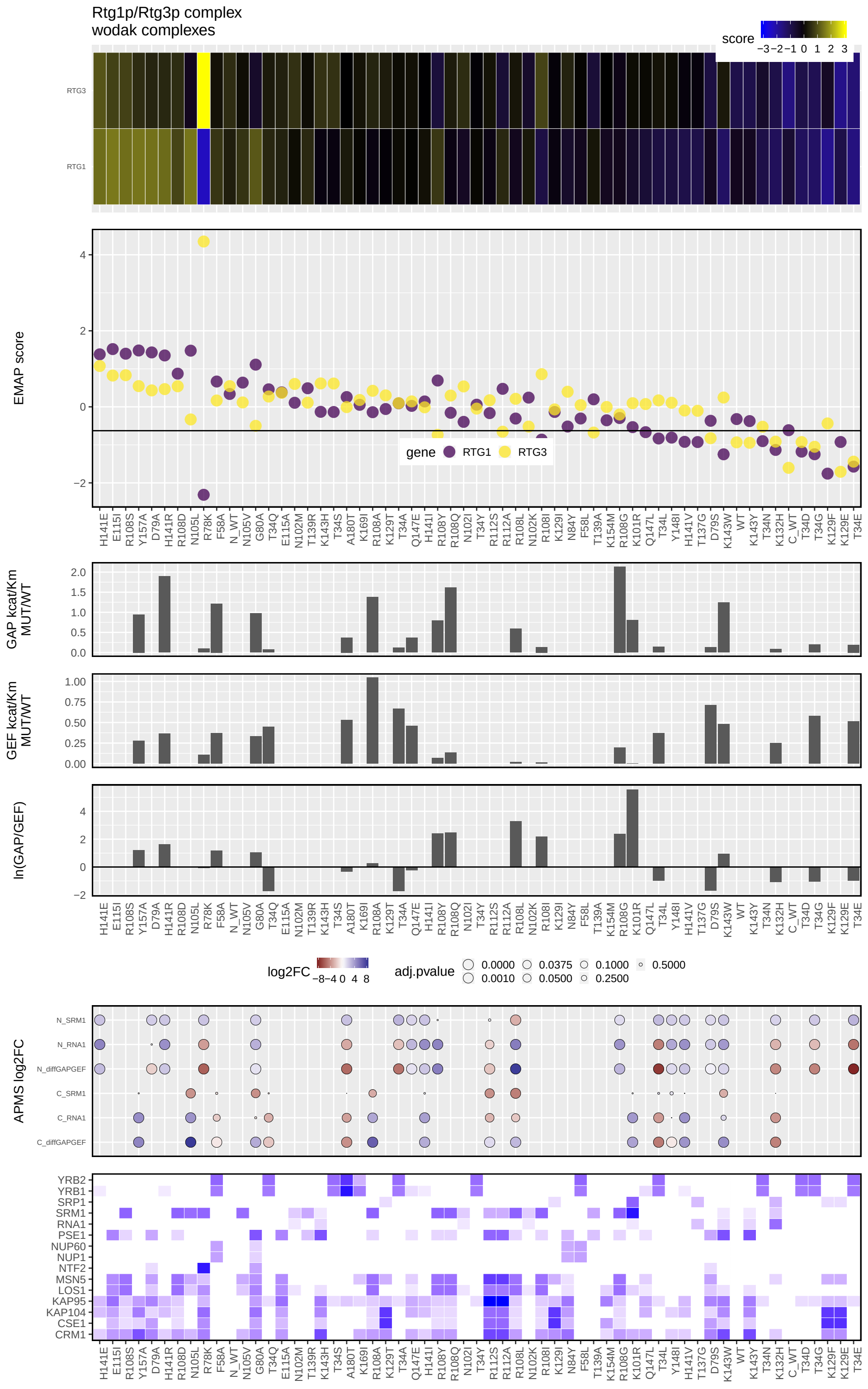

SLIK (SAGA−like) complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UBP8
SPT7
SPT3
SPT20
SGF73
NGG1
HFI1
GCN5
CHD1
ADA2
EMAP score
gene
ADA2
CHD1
GCN5
HFI1
NGG1
SGF73
SPT20
SPT3
SPT7
UBP8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R112A N_WT R112S R108Y R108L C_WT H141R R108Q R108G R108I K101R Y148I R108A H141E N105L K154M H141I K132H D79A T137G T34N E115I N105V N102I T34L R108S WT N102K T34Q F58L K143H T34S Y157A N84Y K169I K143Y H141V T139A K129F N102M E115A R108D K129I T34D K143W F58A T34A Q147E K129T Q147L G80A K129E D79S T139R R78K A180T T34Y T34G T34E

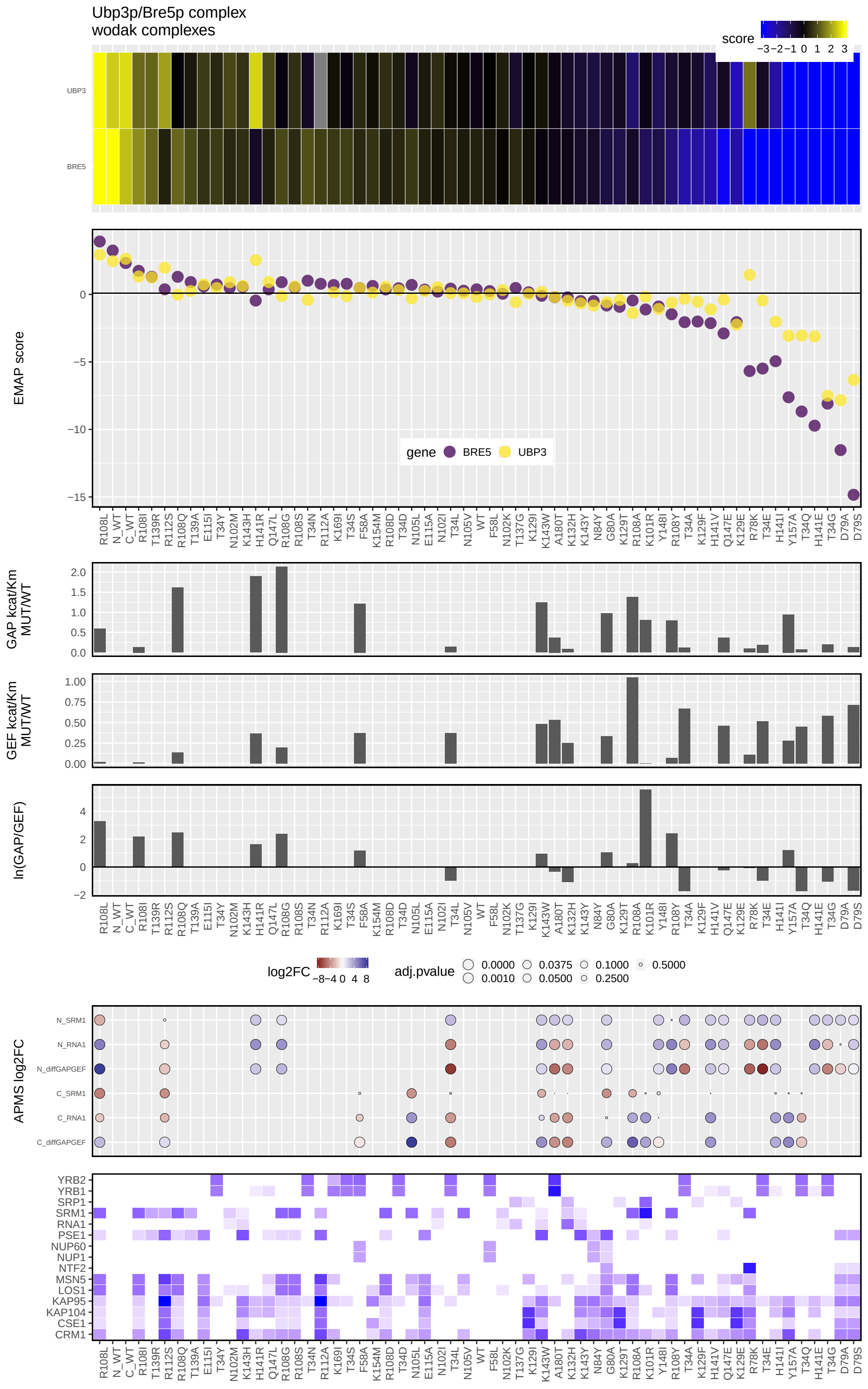

peroxin docking complex
wodak complexes
score
−3 −2 −1 0 1 2 3
PEX17
PEX14
EMAP score
gene
PEX14
PEX17
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34Q T34E T34G R112A R112S D79S R78K H141E K101R A180T T34A T34Y H141R C_WT Y148I K129F Q147E K129I Q147L Y157A G80A N102K E115I R108Y K129T K129E R108D T34L N102M N105V H141I H141V F58A K143W R108L F58L T34S R108A N84Y K132H N_WT T34D T139A N105L R108I R108S K143H R108G K154M K143Y N102I T139R WT T34N T137G R108Q E115A K169I

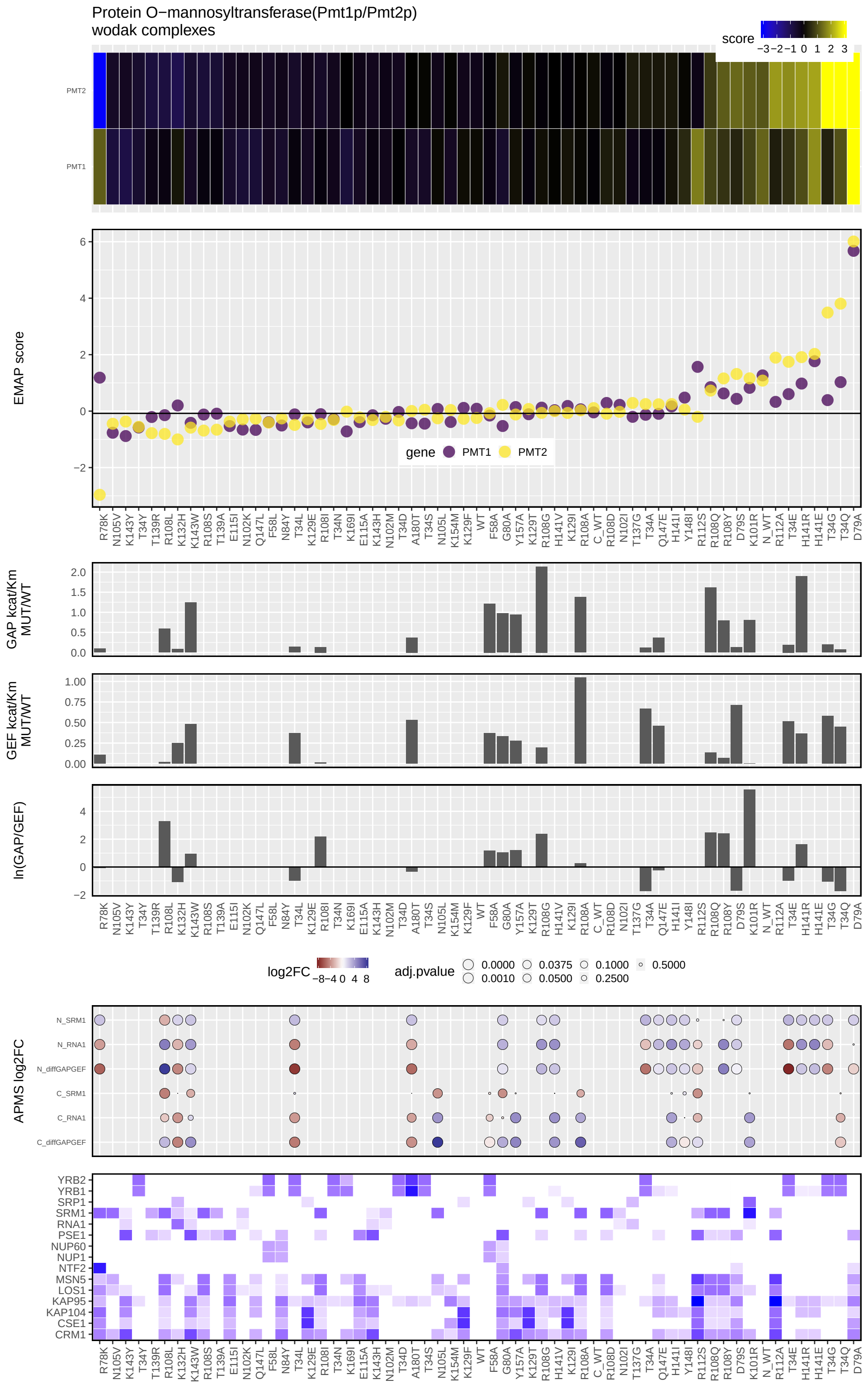
ISW1a complex
wodak complexes

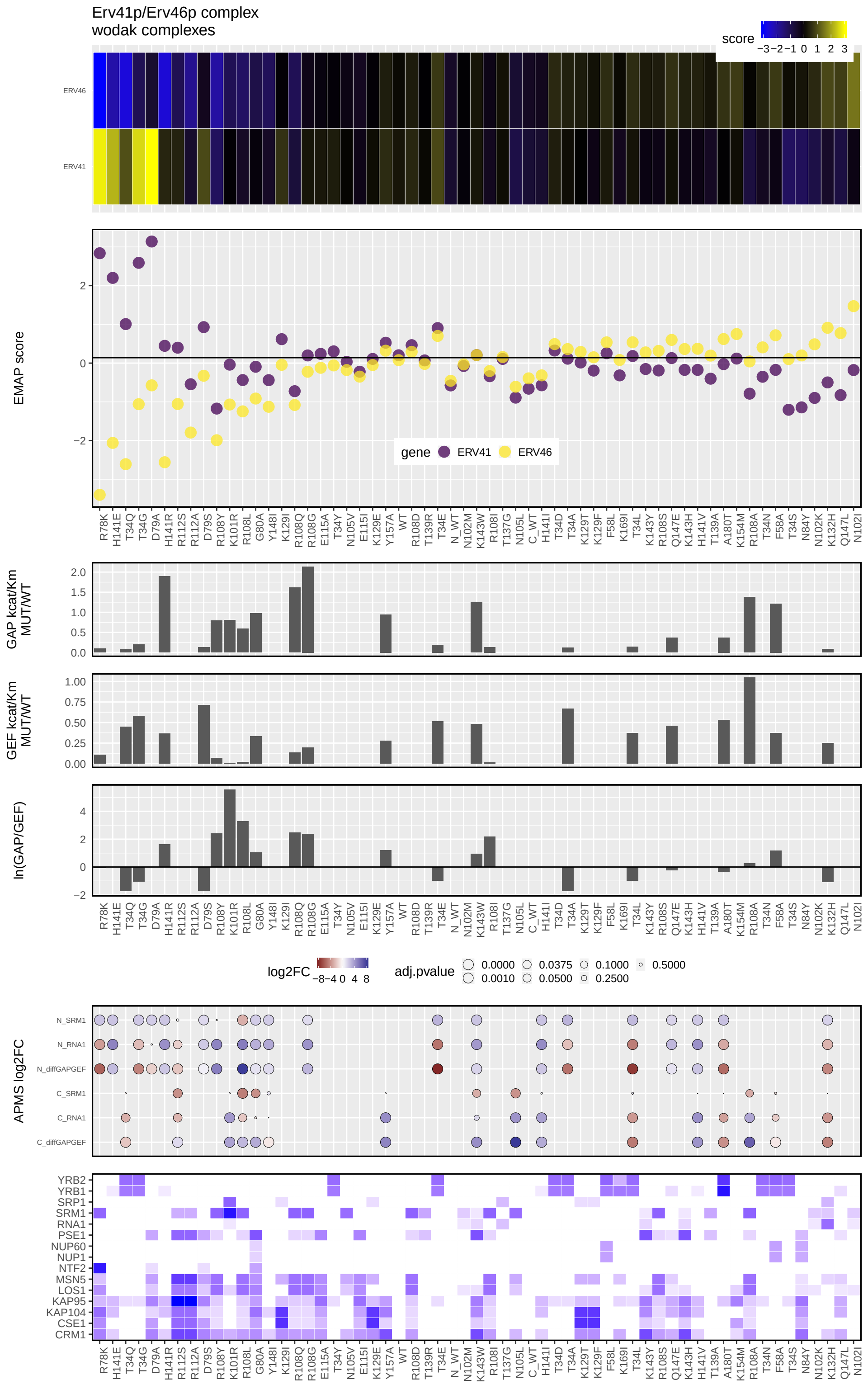


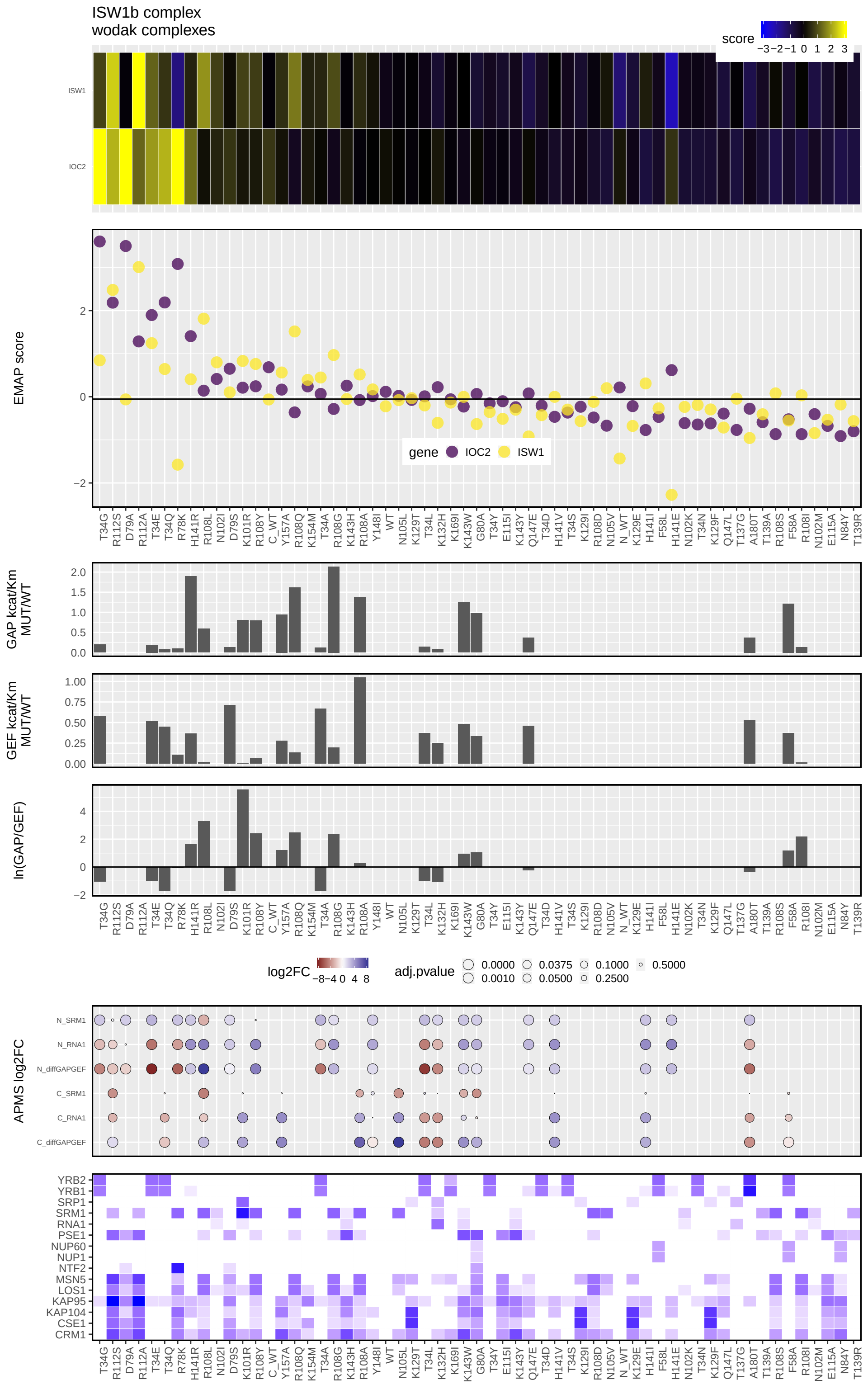

cytoplasmic ribosomal small subunit
wodak complexes
score
−3 −2 −1 0 1 2 3
RPS8A
RPS6B
RPS6A
RPS4B
RPS4A
RPS29B
RPS27B
RPS22A
RPS21B
RPS1B
RPS19B
RPS16B
RPS14A
RPS11A
RPS10B
RPS0A
ASC1
EMAP score
gene
ASC1
RPS0A
RPS10B
RPS11A
RPS14A
RPS16B
RPS19B
RPS1B
RPS21B
RPS22A
RPS27B
RPS29B
RPS4A
RPS4B
RPS6A
RPS6B
RPS8A
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79S H141E T34Q Q147E K101R T34G D79A R108Y R112A R112S H141R R108Q C_WT R108L T34E R78K N_WT R108G G80A H141I R108I Y157A T34A Y148I N84Y A180T R108D H141V N105L N102K T34S E115I F58L T34D K132H K129E F58A N102I K143Y WT R108A K129F E115A K169I N105V Q147L K129I T137G K129T T34L T34Y R108S K154M K143H T139A T34N T139R N102M K143W

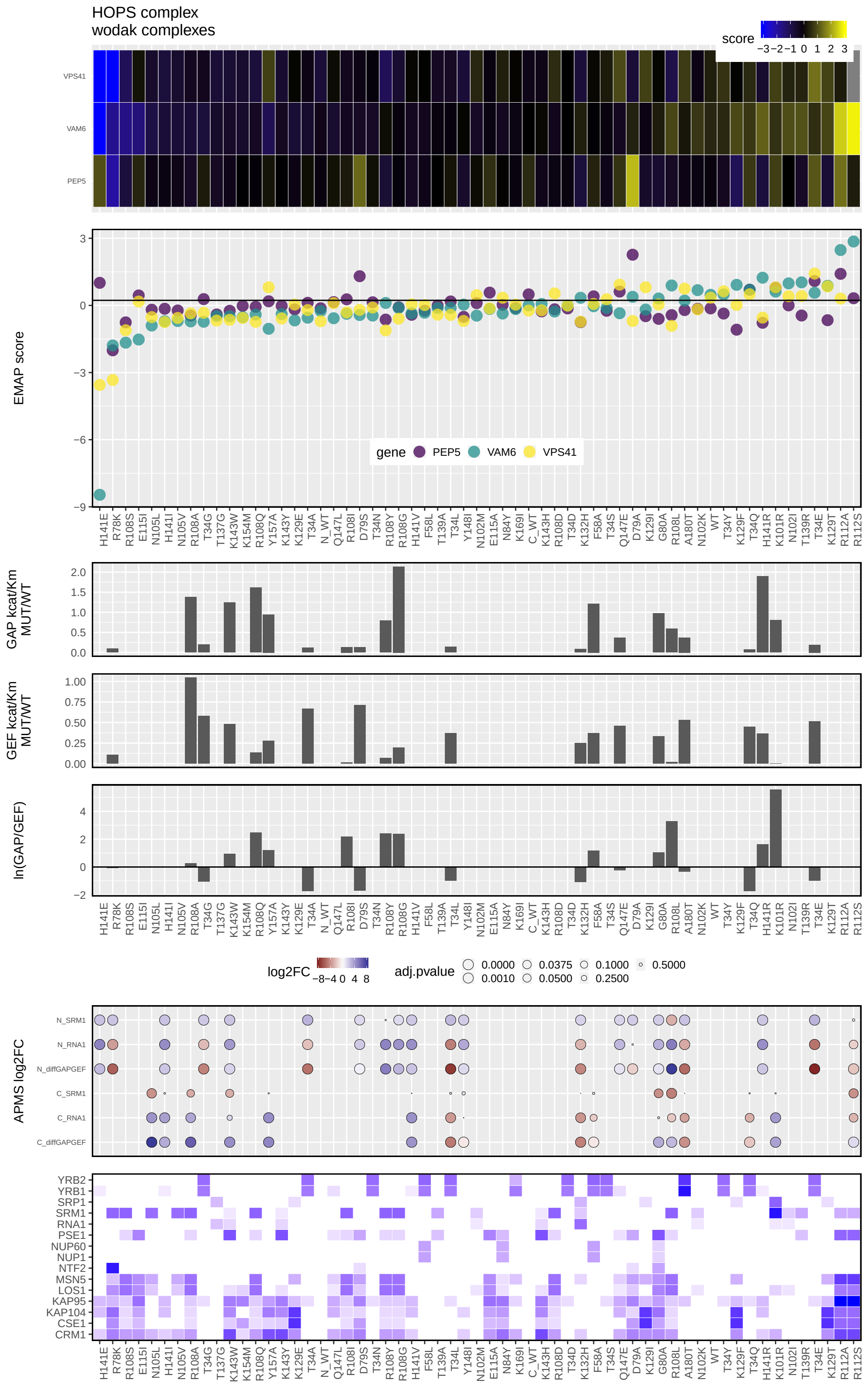

Rtg1p/Rtg3p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RTG3
RTG1
EMAP score
gene RTG1 RTG3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E E115I R108S Y157A D79A H141R R108D N105L R78K F58A N_WT N105V G80A T34Q E115A N102M T139R K143H T34S A180T K169I R108A K129T T34A Q147E H141I R108Y R108Q N102I T34Y R112S R112A R108L N102K R108I K129I N84Y F58L T139A K154M R108G K101R Q147L T34L Y148I H141V T137G D79S K143W WT K143Y T34N K132H C_WT T34D T34G K129F K129E T34E

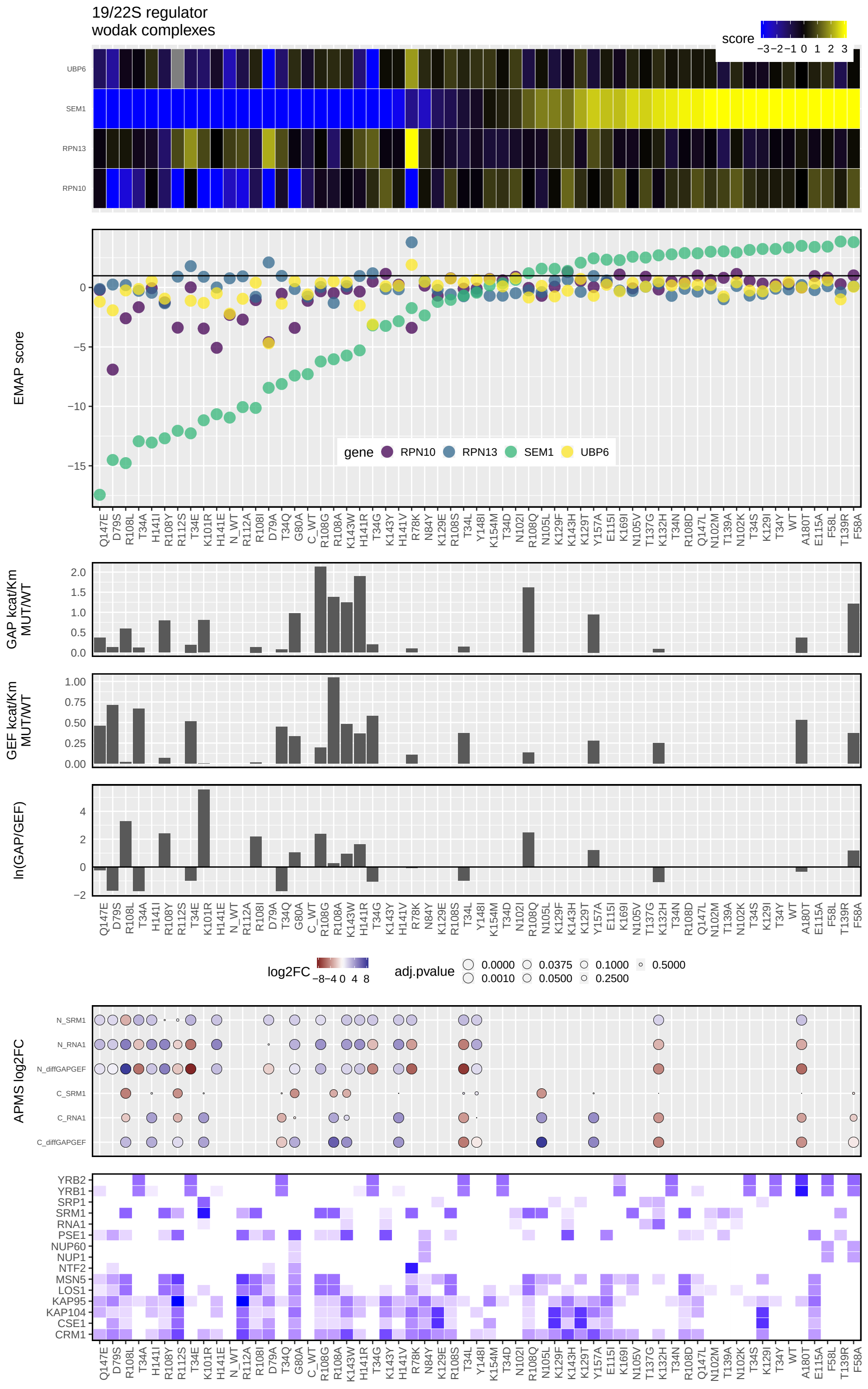

Ubp3p/Bre5p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
UBP3
BRE5
EMAP score
gene
BRE5
UBP3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108L N_WT C_WT R108I T139R R112S R108Q T139A E115I T34Y N102M K143H H141R Q147L R108G R108S T34N R112A K169I T34S F58A K154M R108D T34D N105L E115A N102I T34L N105V WT F58L N102K T137G K129I K143W A180T K132H K143Y N84Y G80A K129T R108A K101R Y148I R108Y T34A K129F H141V Q147E K129E R78K T34E H141I Y157A T34Q H141E T34G D79A D79S

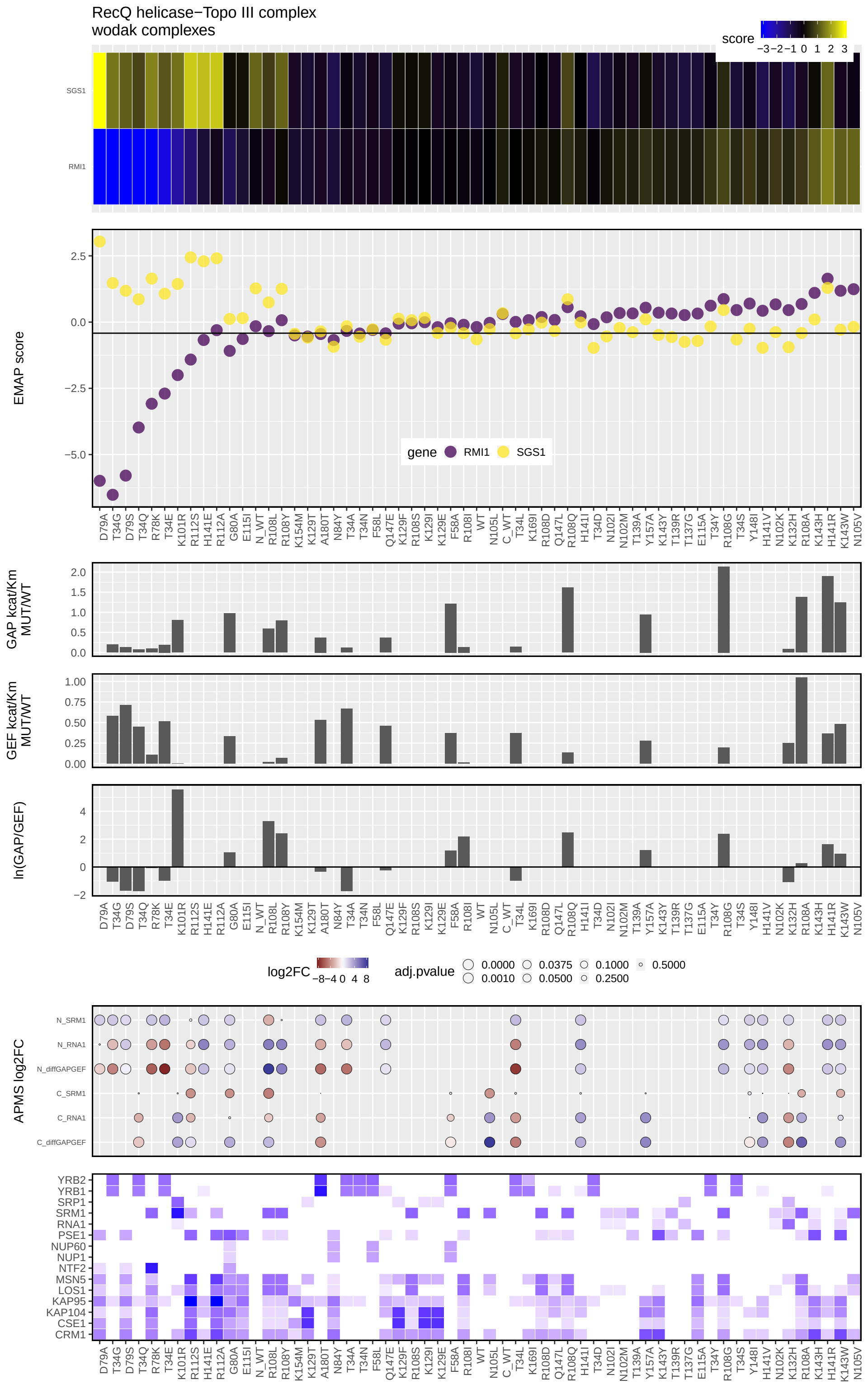

Protein O−mannosyltransferase(Pmt1p/Pmt2p)
wodak complexes
score
−3 −2 −1 0 1 2 3
PMT2
PMT1
EMAP score
gene
PMT1
PMT2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K N105V K143Y T34Y T139R R108L K132H K143W R108S T139A E115I N102K Q147L F58L N84Y T34L K129E R108I T34N K169I E115A K143H N102M T34D A180T T34S N105L K154M K129F WT F58A G80A Y157A K129T R108G H141V K129I R108A C_WT R108D N102I T137G T34A Q147E H141I Y148I R112S R108Q R108Y D79S K101R N_WT R112A T34E H141R H141E T34G T34Q D79A

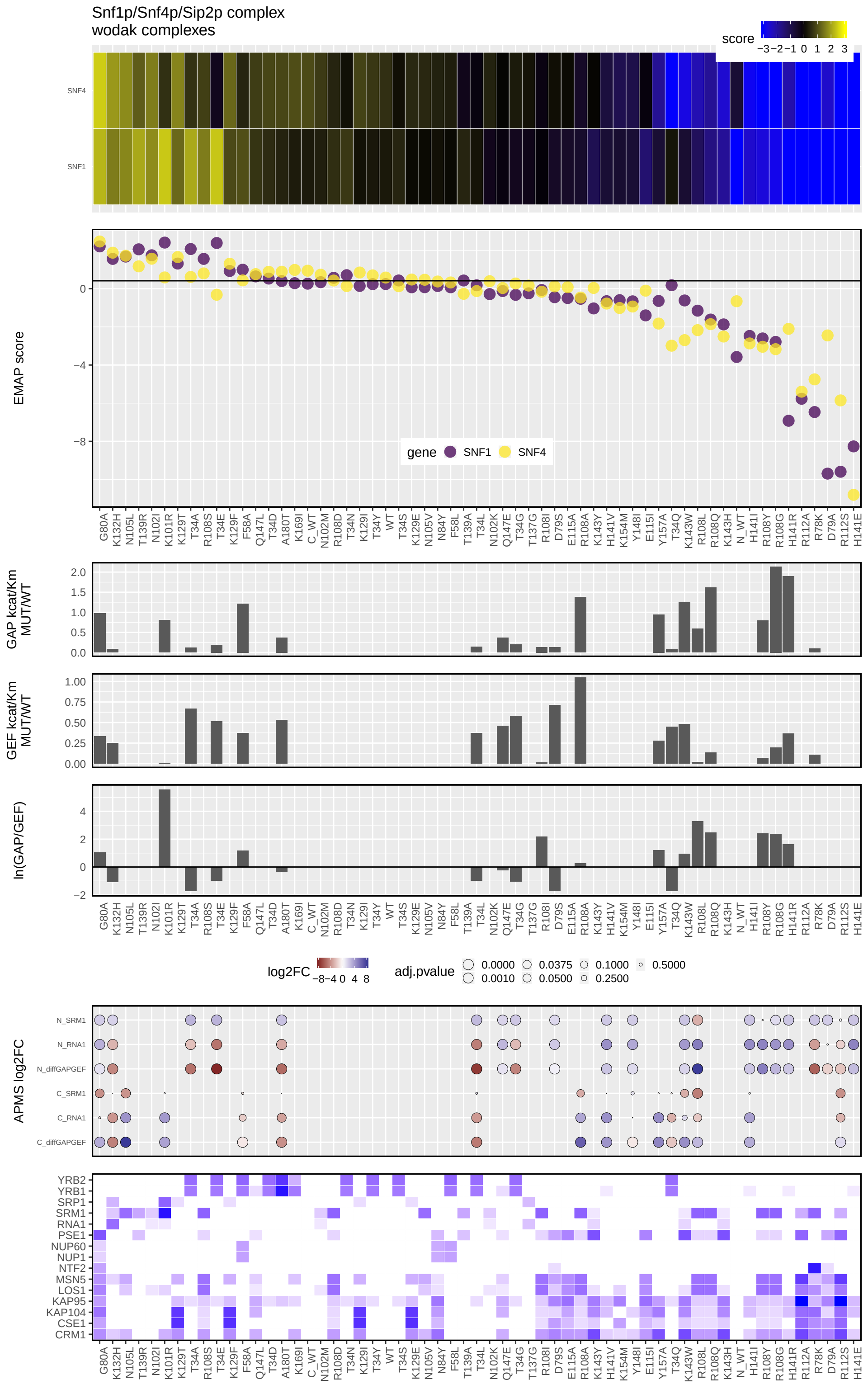

Erv41p/Erv46p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
ERV46
ERV41
EMAP score
gene
ERV41
ERV46
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K H141E T34Q T34G D79A H141R R112S R112A D79S R108Y K101R R108L G80A Y148I K129I R108Q R108G E115A T34Y N105V E115I K129E Y157A WT R108D T139R T34E N_WT N102M K143W R108I T137G N105L C_WT H141I T34D T34A K129T K129F F58L K169I T34L K143Y R108S Q147E K143H H141V T139A A180T K154M R108A T34N F58A T34S N84Y N102K K132H Q147L N102I

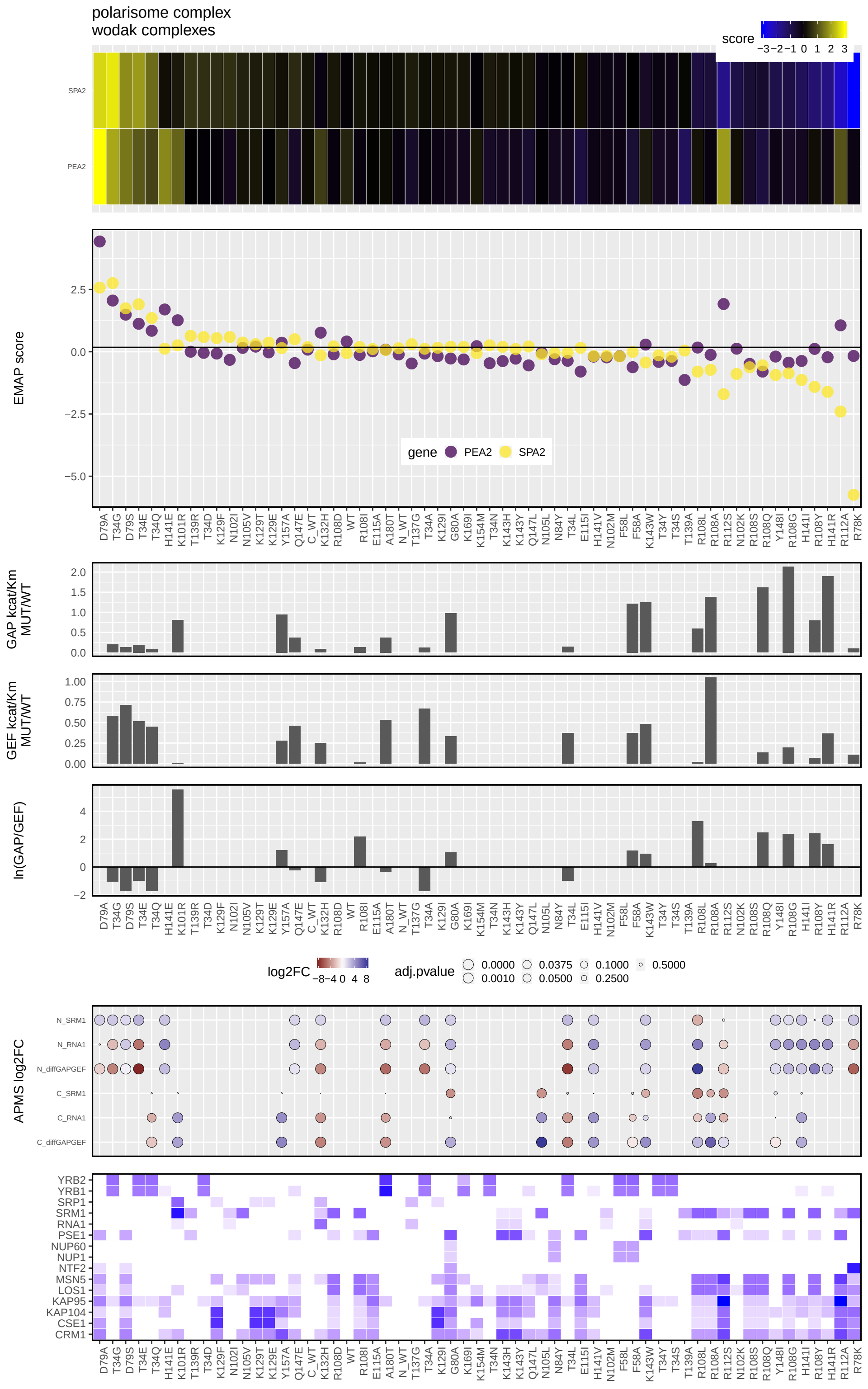

ISW1b complex
wodak complexes
score
−3 −2 −1 0 1 2 3
ISW1
IOC2
EMAP score
gene
IOC2
ISW1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G R112S D79A R112A T34E T34Q R78K H141R R108L N102I D79S K101R R108Y C_WT Y157A R108Q K154M T34A R108G K143H R108A Y148I WT N105L K129T T34L K132H K169I K143W G80A T34Y E115I K143Y Q147E T34D H141V T34S K129I R108D N105V N_WT K129E H141I F58L H141E N102K T34N K129F Q147L T137G A180T T139A R108S F58A R108I N102M E115A N84Y T139R

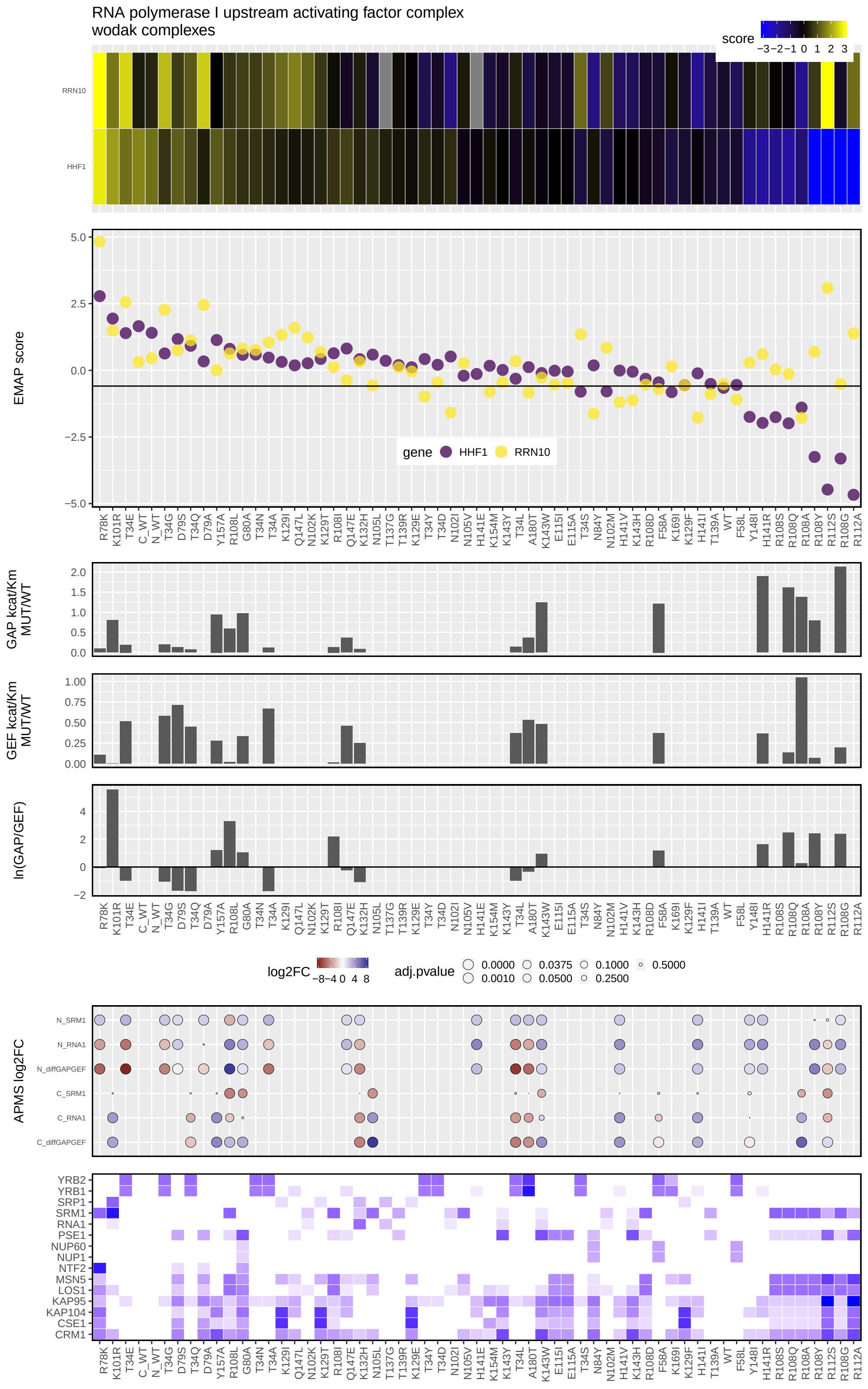

HOPS complex
wodak complexes
score
−3 −2 −1 0 1 2 3
VPS41
VAM6
PEP5
EMAP score
gene PEP5 VAM6 VPS41
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141E R78K R108S E115I N105L H141I N105V R108A T34G T137G K143W K154M R108Q Y157A K143Y K129E T34A N_WT Q147L R108I D79S T34N R108Y R108G H141V F58L T139A T34L Y148I N102M E115A N84Y K169I C_WT K143H R108D T34D K132H F58A T34S Q147E D79A K129I G80A R108L A180T N102K WT T34Y K129F T34Q H141R K101R N102I T139R T34E K129T R112A R112S

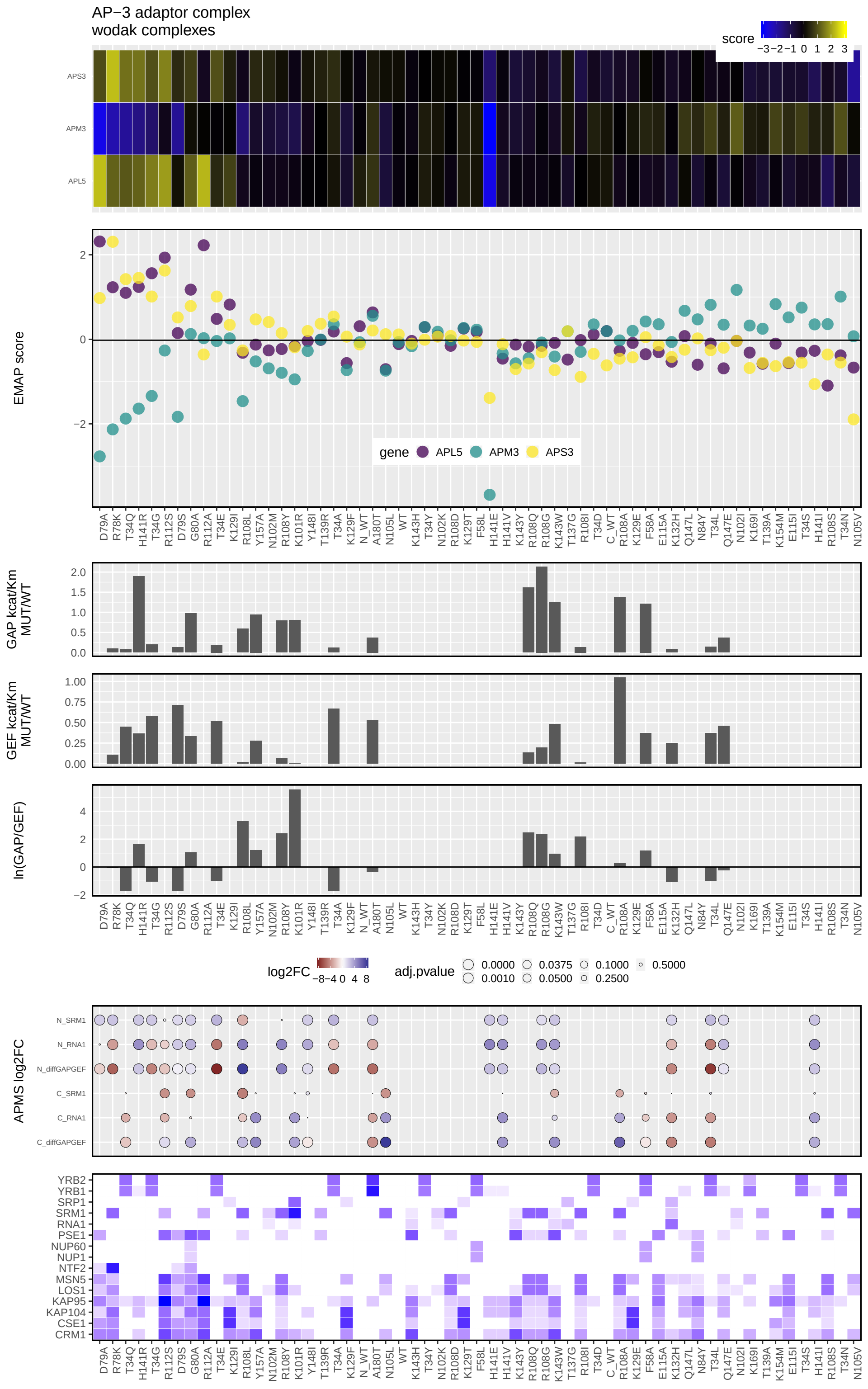

19/22S regulator
wodak complexes
score
−3 −2 −1 0 1 2 3
UBP6
SEM1
RPN13
RPN10
EMAP score
gene RPN10 RPN13 SEM1 UBP6
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
Q147E D79S R108L T34A H141I R108Y R112S T34E K101R H141E N_WT R112A R108I D79A T34Q G80A C_WT R108G R108A K143W H141R T34G K143Y H141V R78K N84Y K129E R108S T34L Y148I K154M T34D N102I R108Q N105L K129F K143H K129T Y157A E115I K169I N105V T137G K132H T34N R108D Q147L N102M T139A N102K T34S K129I T34Y WT A180T E115A F58L T139R F58A

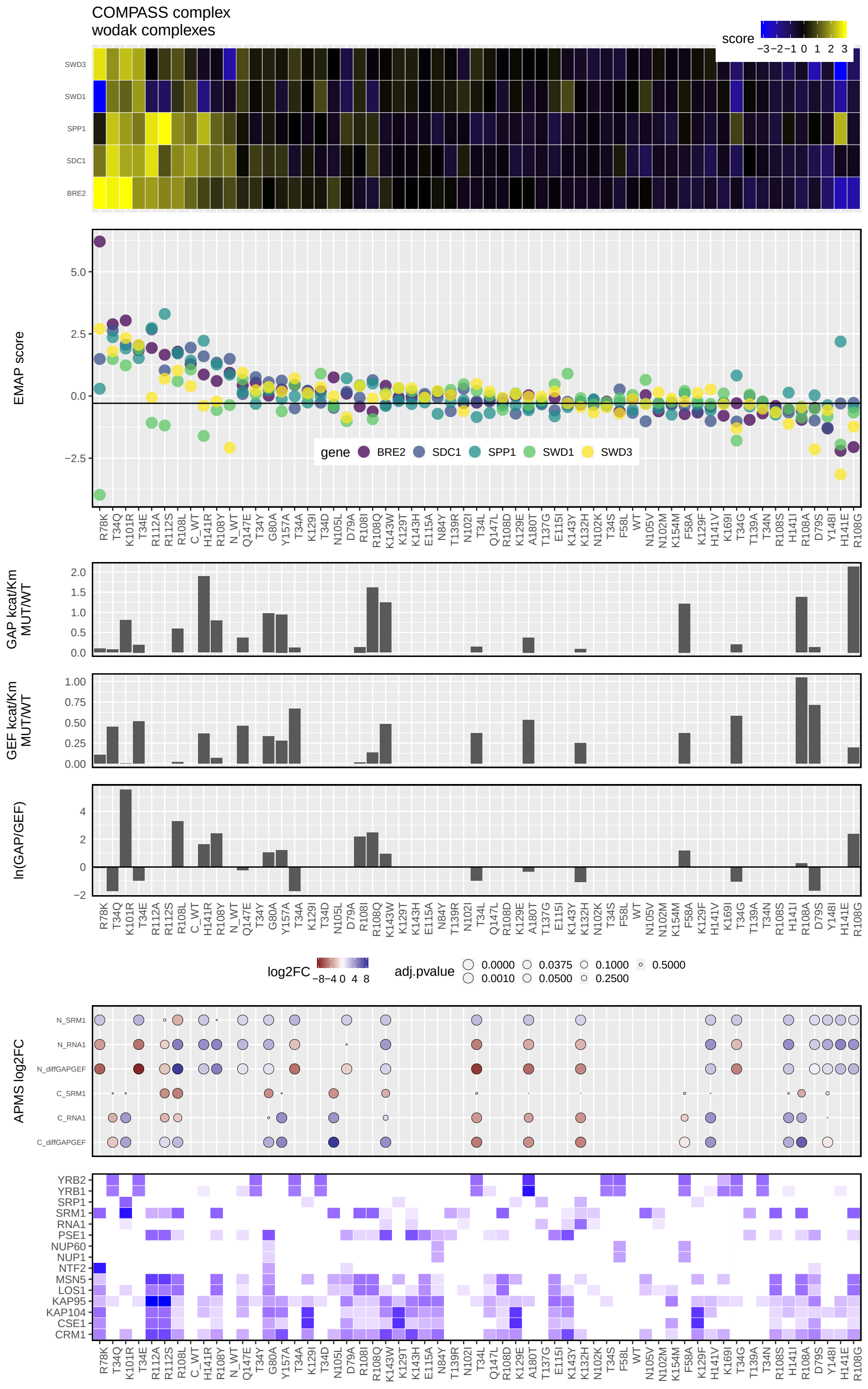

RecQ helicase−Topo III complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SGS1
RMI1
EMAP score
gene
RMI1
SGS1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A T34G D79S T34Q R78K T34E K101R R112S H141E R112A G80A E115I N_WT R108L R108Y K154M K129T A180T N84Y T34A T34N F58L Q147E K129F R108S K129I K129E F58A R108I WT N105L C_WT T34L K169I R108D Q147L R108Q H141I T34D N102I N102M T139A Y157A K143Y T139R T137G E115A T34Y R108G T34S Y148I H141V N102K K132H R108A K143H H141R K143W N105V

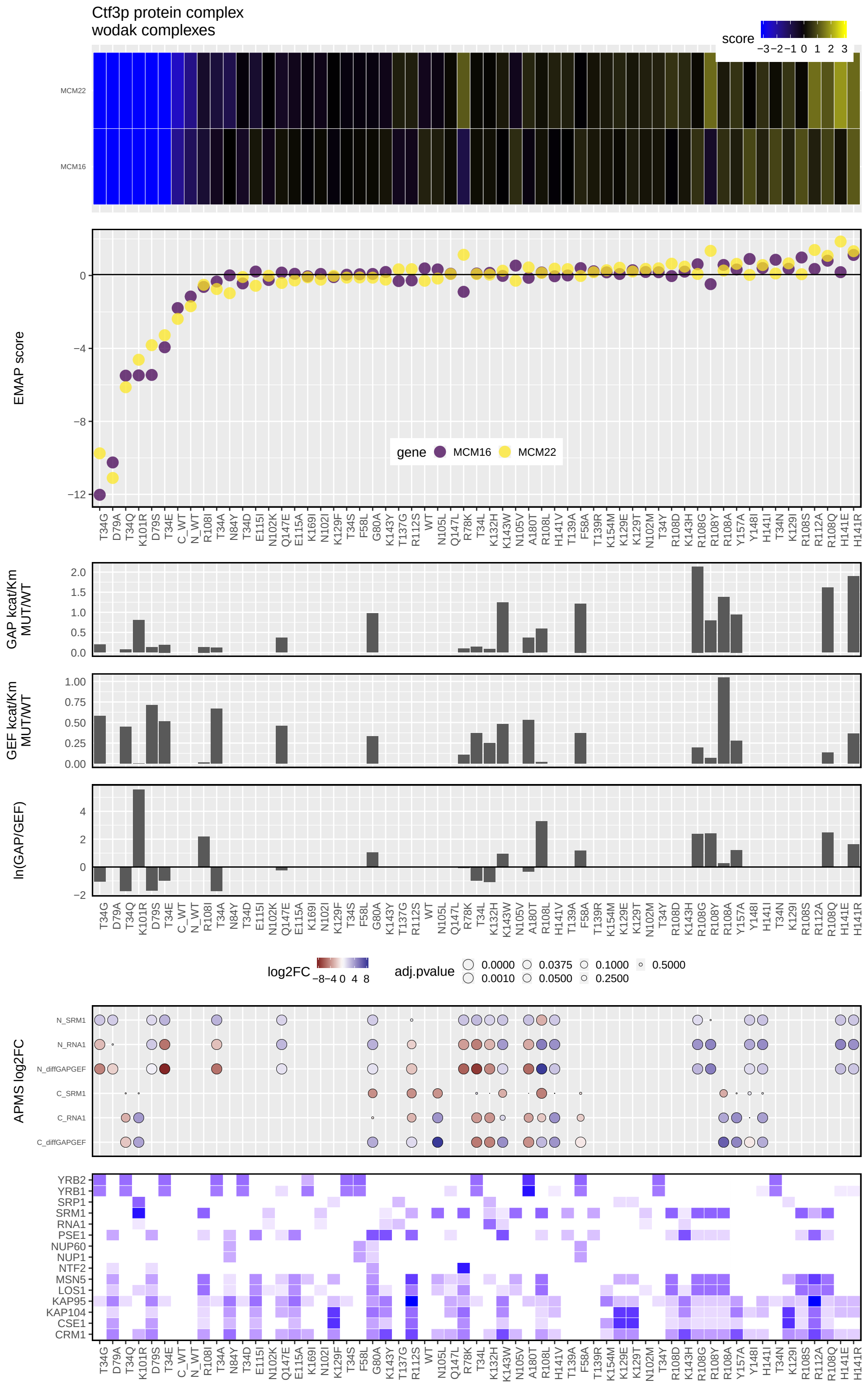

Snf1p/Snf4p/Sip2p complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SNF4
SNF1
EMAP score
gene
SNF1
SNF4
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
G80A K132H N105L T139R N102I K101R K129T T34A R108S T34E K129F F58A Q147L T34D A180T K169I C_WT N102M R108D T34N K129I T34Y WT T34S K129E N105V N84Y F58L T139A T34L N102K Q147E T34G T137G R108I D79S E115A R108A K143Y H141V K154M Y148I E115I Y157A T34Q K143W R108L R108Q K143H N_WT H141I R108Y R108G H141R R112A R78K D79A R112S H141E


polarisome complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SPA2
PEA2
EMAP score
2.5
0.0
−2.5
−5.0
gene
PEA2
SPA2
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
D79A T34G D79S T34E T34Q H141E K101R T139R T34D K129F N102I N105V K129T K129E Y157A Q147E C_WT K132H R108D WT R108I E115A A180T N_WT T137G T34A K129I G80A K169I K154M T34N K143H K143Y Q147L N105L N84Y T34L E115I H141V N102M F58L F58A K143W T34Y T34S T139A R108L R108A R112S N102K R108S R108Q Y148I R108G H141I R108Y H141R R112A R78K
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

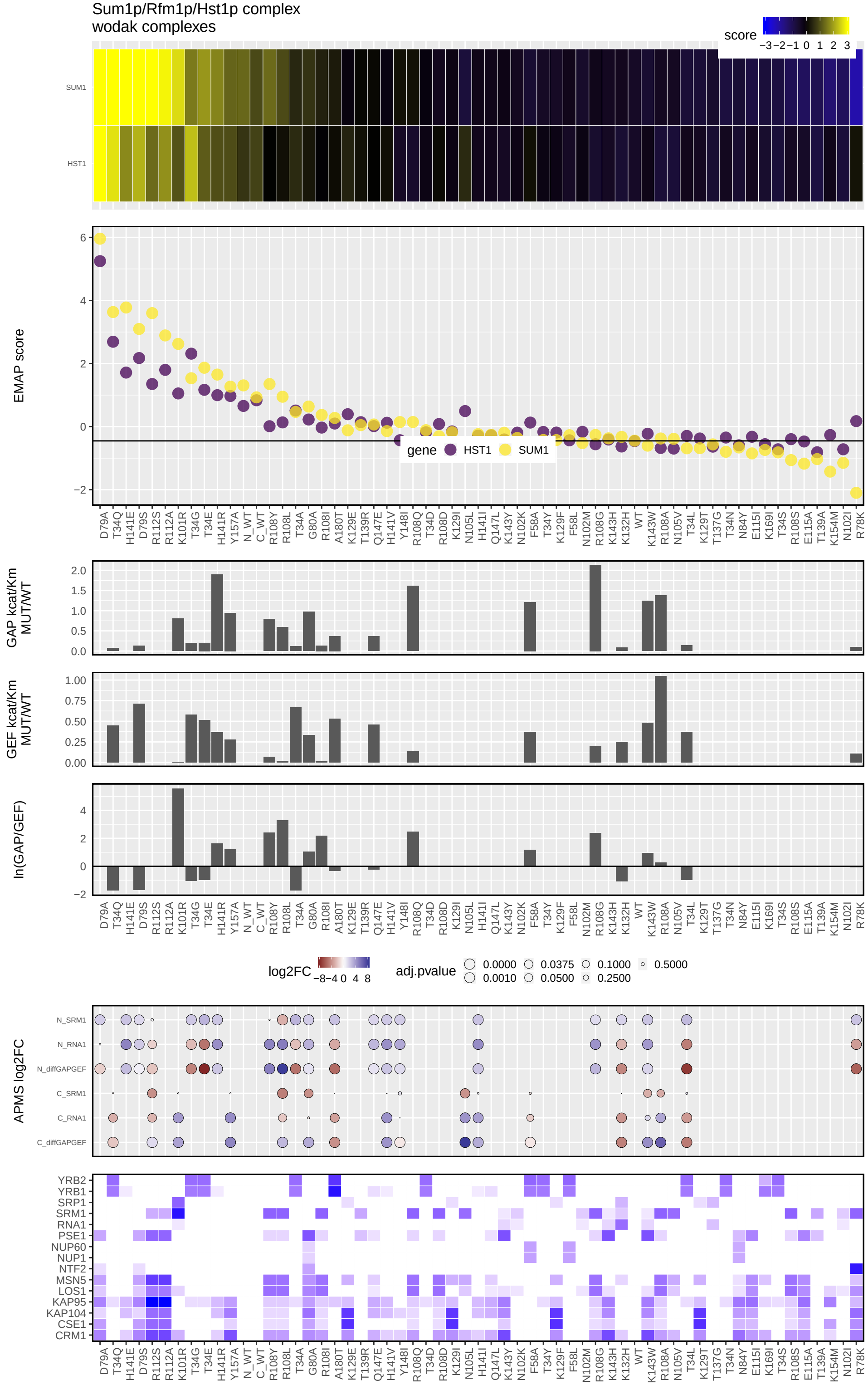

RNA polymerase I upstream activating factor complex
wodak complexes
score
−3 −2 −1 0 1 2 3
RRN10
HHF1
EMAP score
gene HHF1 RRN10
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R78K K101R T34E C_WT N_WT T34G D79S T34Q D79A Y157A R108L G80A T34N T34A K129I Q147L N102K K129T R108I Q147E K132H N105L T137G T139R K129E T34Y T34D N102I N105V H141E K154M K143Y T34L A180T K143W E115I E115A T34S N84Y N102M H141V K143H R108D F58A K169I K129F H141I T139A WT F58L Y148I H141R R108S R108Q R108A R108Y R112S R108G R112A

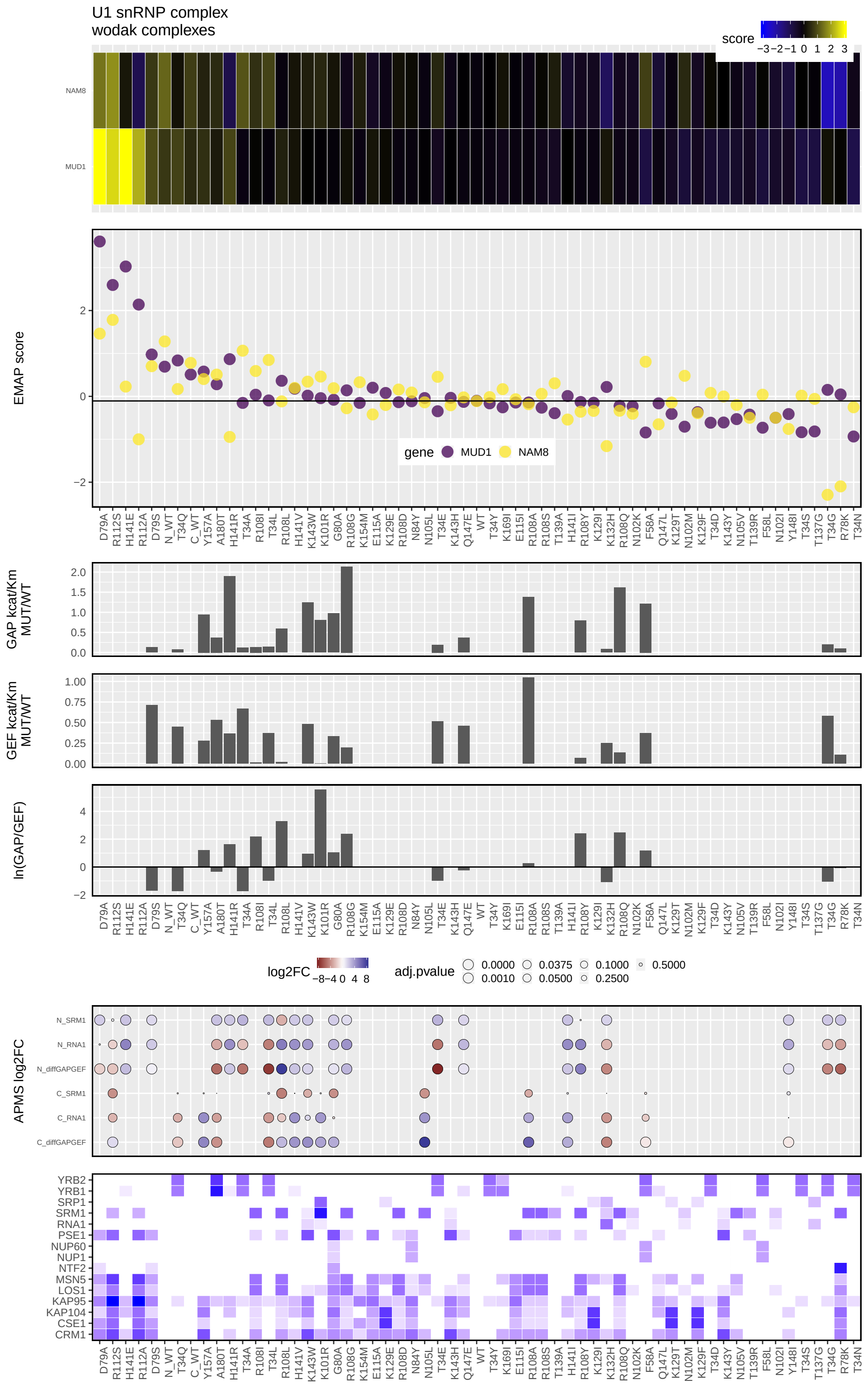

AP−3 adaptor complex
wodak complexes
score
−3 −2 −1 0 1 2 3
APS3
APM3
APL5
EMAP score
gene APL5 APM3 APS3
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R78K T34Q H141R T34G R112S D79S G80A R112A T34E K129I R108L Y157A N102M R108Y K101R Y148I T139R T34A K129F N_WT A180T N105L WT K143H T34Y N102K R108D K129T F58L H141E H141V K143Y R108Q R108G K143W T137G R108I T34D C_WT R108A K129E F58A E115A K132H Q147L N84Y T34L Q147E N102I K169I T139A K154M E115I T34S H141I R108S T34N N105V

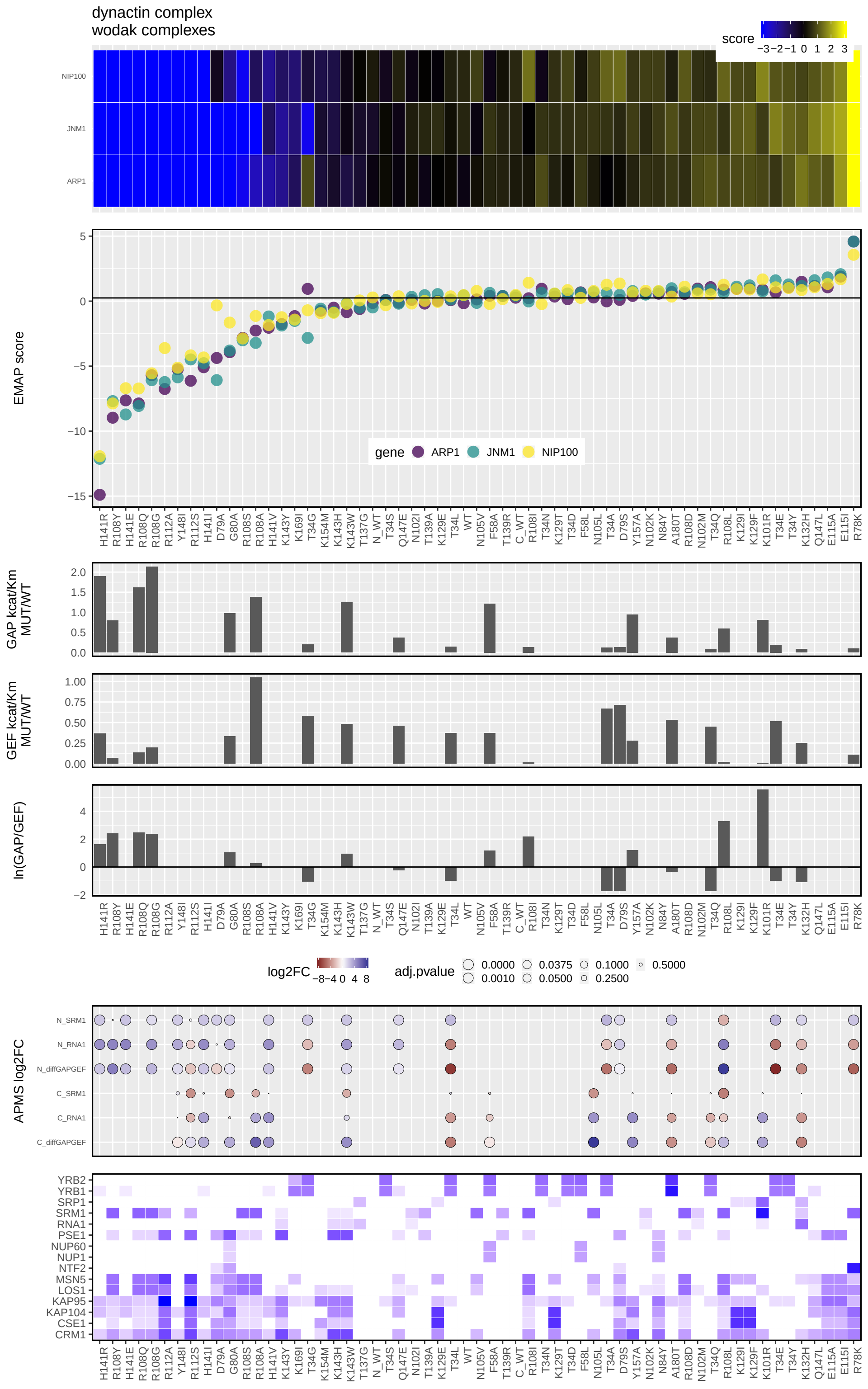

COMPASS complex
wodak complexes
score
−3 −2 −1 0 1 2 3
SWD3
SWD1
SPP1
SDC1
BRE2
EMAP score
5.0
2.5
0.0
−2.5
gene
BRE2
SDC1
SPP1
SWD1
SWD3
R78K T34Q K101R T34E R112A R112S R108L C_WT H141R R108Y N_WT Q147E T34Y G80A Y157A T34A K129I T34D N105L D79A R108I R108Q K143W K129T K143H E115A N84Y T139R N102I T34L Q147L R108D K129E A180T T137G E115I K143Y K132H N102K T34S F58L WT N105V N102M K154M F58A K129F H141V K169I T34G T139A T34N R108S H141I R108A D79S Y148I H141E R108G
GAP kcat/Km MUT/WT
2.0
1.5
1.0
0.5
0.0
GEF kcat/Km MUT/WT
1.00
0.75
0.50
0.25
0.00
ln(GAP/GEF)
4
2
0
−2
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1

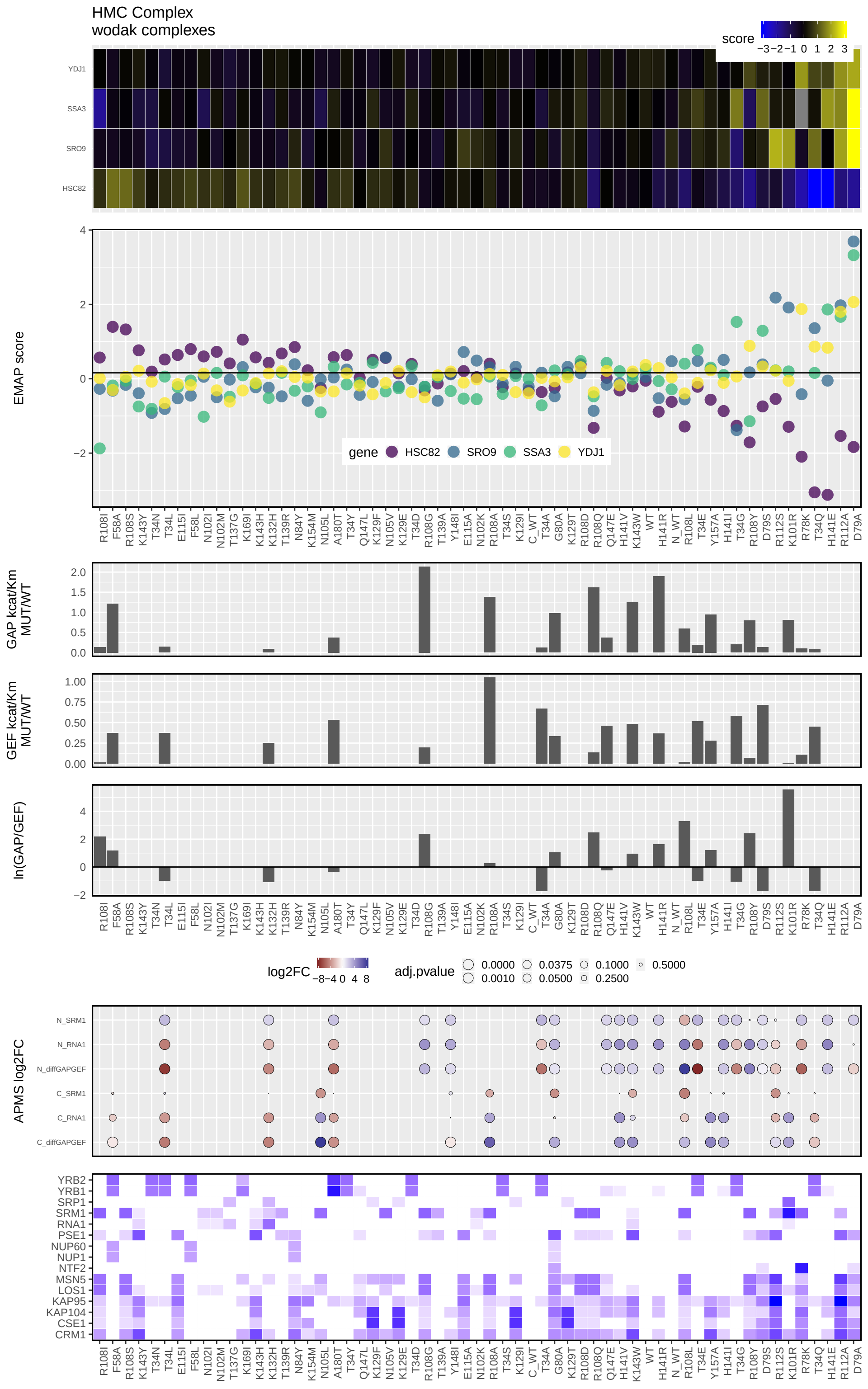

Ctf3p protein complex
wodak complexes
score
−3 −2 −1 0 1 2 3
MCM22
MCM16
EMAP score
gene
MCM16
MCM22
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
T34G D79A T34Q K101R D79S T34E C_WT N_WT R108I T34A N84Y T34D E115I N102K Q147E E115A K169I N102I K129F T34S F58L G80A K143Y T137G R112S WT N105L Q147L R78K T34L K132H K143W N105V A180T R108L H141V T139A F58A T139R K154M K129E K129T N102M T34Y R108D K143H R108G R108Y R108A Y157A Y148I H141I T34N K129I R108S R112A R108Q H141E H141R

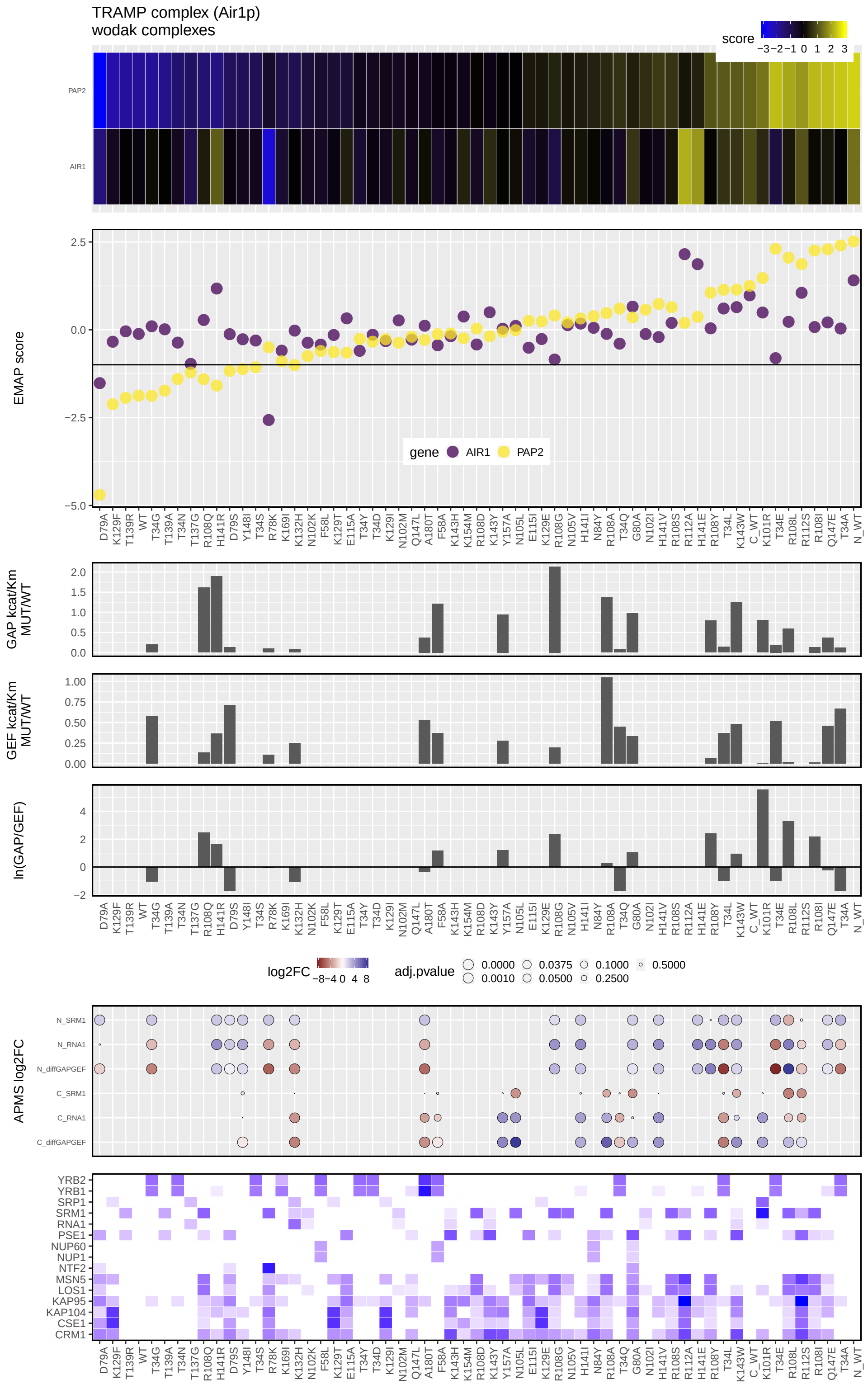
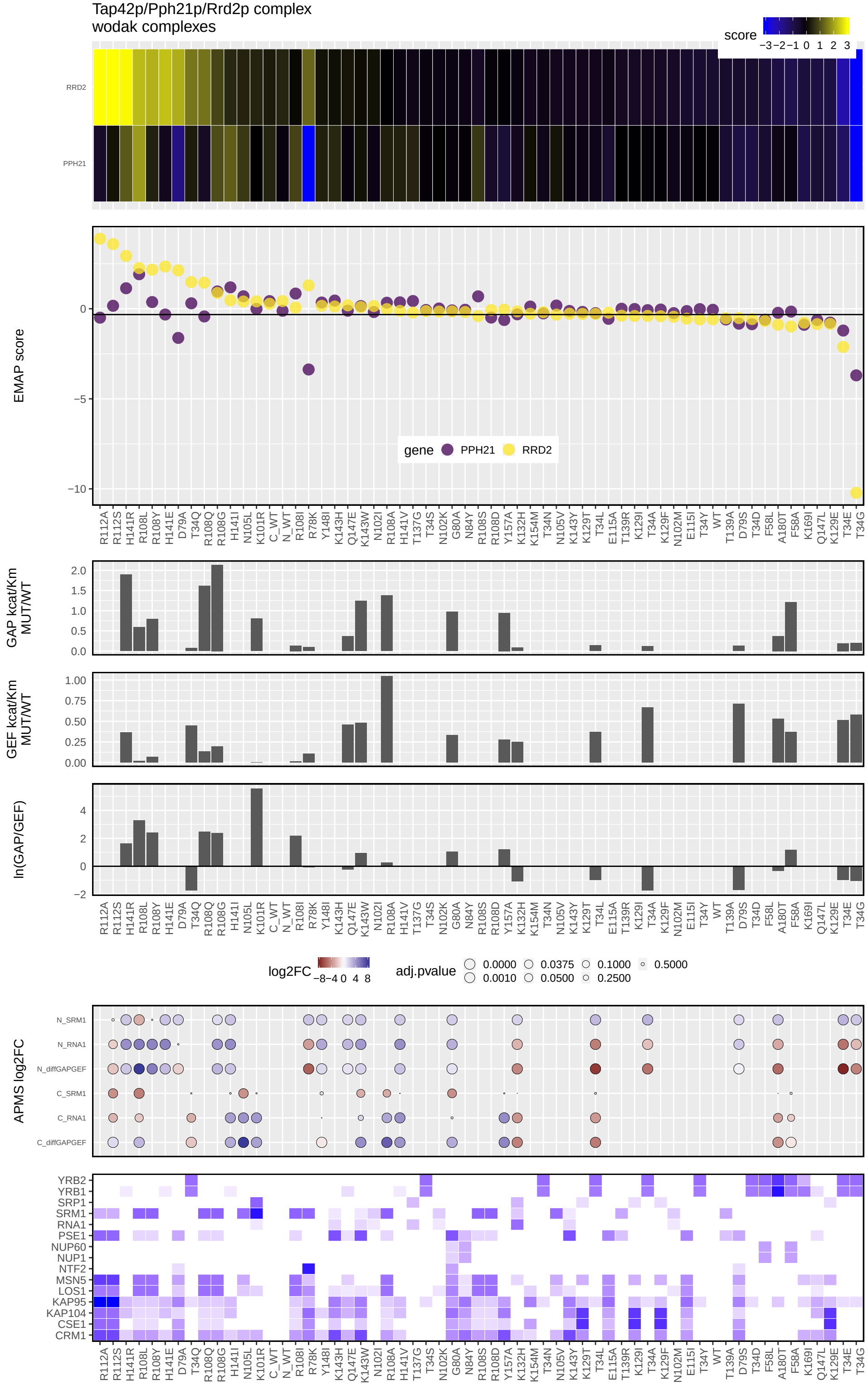
Sum1p/Rfm1p/Hst1p complex
wodak complexes




U1 snRNP complex
wodak complexes
score
−3 −2 −1 0 1 2 3
NAM8
MUD1
EMAP score
gene
MUD1
NAM8
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A R112S H141E R112A D79S N_WT T34Q C_WT Y157A A180T H141R T34A R108I T34L R108L H141V K143W K101R G80A R108G K154M E115A K129E R108D N84Y N105L T34E K143H Q147E WT T34Y K169I E115I R108A R108S T139A H141I R108Y K129I K132H R108Q N102K F58A Q147L K129T N102M K129F T34D K143Y N105V T139R F58L N102I Y148I T34S T137G T34G R78K T34N


dynactin complex
wodak complexes
score
−3 −2 −1 0 1 2 3
NIP100
JNM1
ARP1
EMAP score
gene ARP1 JNM1 NIP100
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
H141R R108Y H141E R108Q R108G R112A Y148I R112S H141I D79A G80A R108S R108A H141V K143Y K169I T34G K154M K143H K143W T137G N_WT T34S Q147E N102I T139A K129E T34L WT N105V F58A T139R C_WT R108I T34N K129T T34D F58L N105L T34A D79S Y157A N102K N84Y A180T R108D N102M T34Q R108L K129I K129F K101R T34E T34Y K132H Q147L E115A E115I R78K


HMC Complex
wodak complexes
score
−3 −2 −1 0 1 2 3
YDJ1
SSA3
SRO9
HSC82
EMAP score
gene HSC82 SRO9 SSA3 YDJ1
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC −8 −4 0 4 8
adj.pvalue 0.0000 0.0010 0.0375 0.0500 0.1000 0.2500 0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
R108I F58A R108S K143Y T34N T34L E115I F58L N102I N102M T137G K169I K143H K132H T139R N84Y K154M N105L A180T T34Y Q147L K129F N105V K129E T34D R108G T139A Y148I E115A N102K R108A T34S K129I C_WT T34A G80A K129T R108D R108Q Q147E H141V K143W WT H141R N_WT R108L T34E Y157A H141I T34G R108Y D79S R112S K101R R78K T34Q H141E R112A D79A


TRAMP complex (Air1p)
wodak complexes
score
−3 −2 −1 0 1 2 3
PAP2
AIR1
EMAP score
2.5
0.0
−2.5
−5.0
gene
AIR1
PAP2
GAP kcat/Km MUT/WT
GEF kcat/Km MUT/WT
ln(GAP/GEF)
log2FC
−8 −4 0 4 8
adj.pvalue
0.0000
0.0010
0.0375
0.0500
0.1000
0.2500
0.5000
APMS log2FC
N_SRM1
N_RNA1
N_diffGAPGEF
C_SRM1
C_RNA1
C_diffGAPGEF
YRB2
YRB1
SRP1
SRM1
RNA1
PSE1
NUP60
NUP1
NTF2
MSN5
LOS1
KAP95
KAP104
CSE1
CRM1
D79A K129F T139R WT T34G T139A T34N T137G R108Q H141R D79S Y148I T34S R78K K169I K132H N102K F58L K129T E115A T34Y T34D K129I N102M Q147L A180T F58A K143H K154M R108D K143Y Y157A N105L E115I K129E R108G N105V H141I N84Y R108A T34Q G80A N102I H141V R108S R112A H141E R108Y T34L K143W C_WT K101R T34E R108L R112S R108I Q147E T34A N_WT

Tap42p/Pph21p/Rrd2p complex
wodak complexes