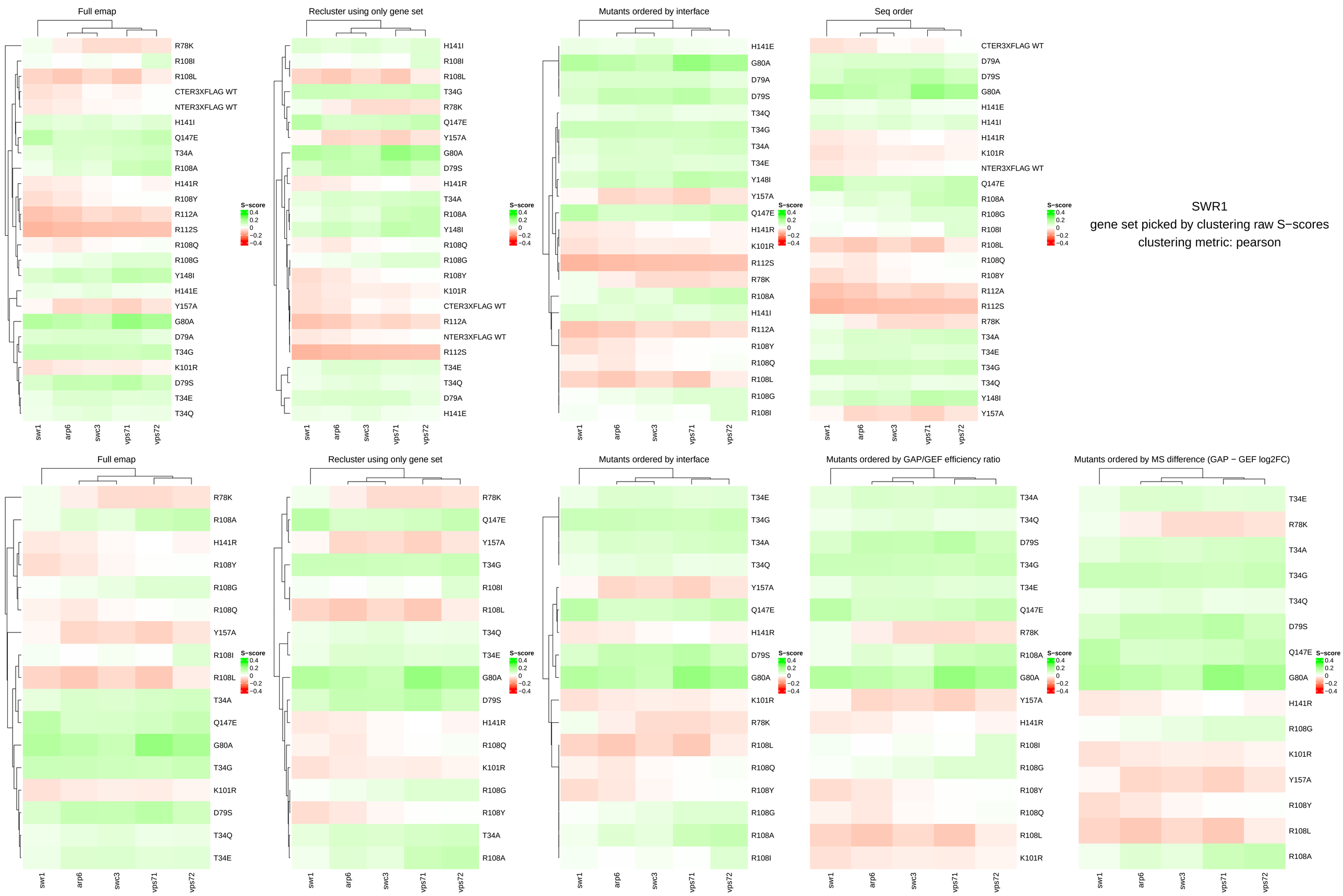
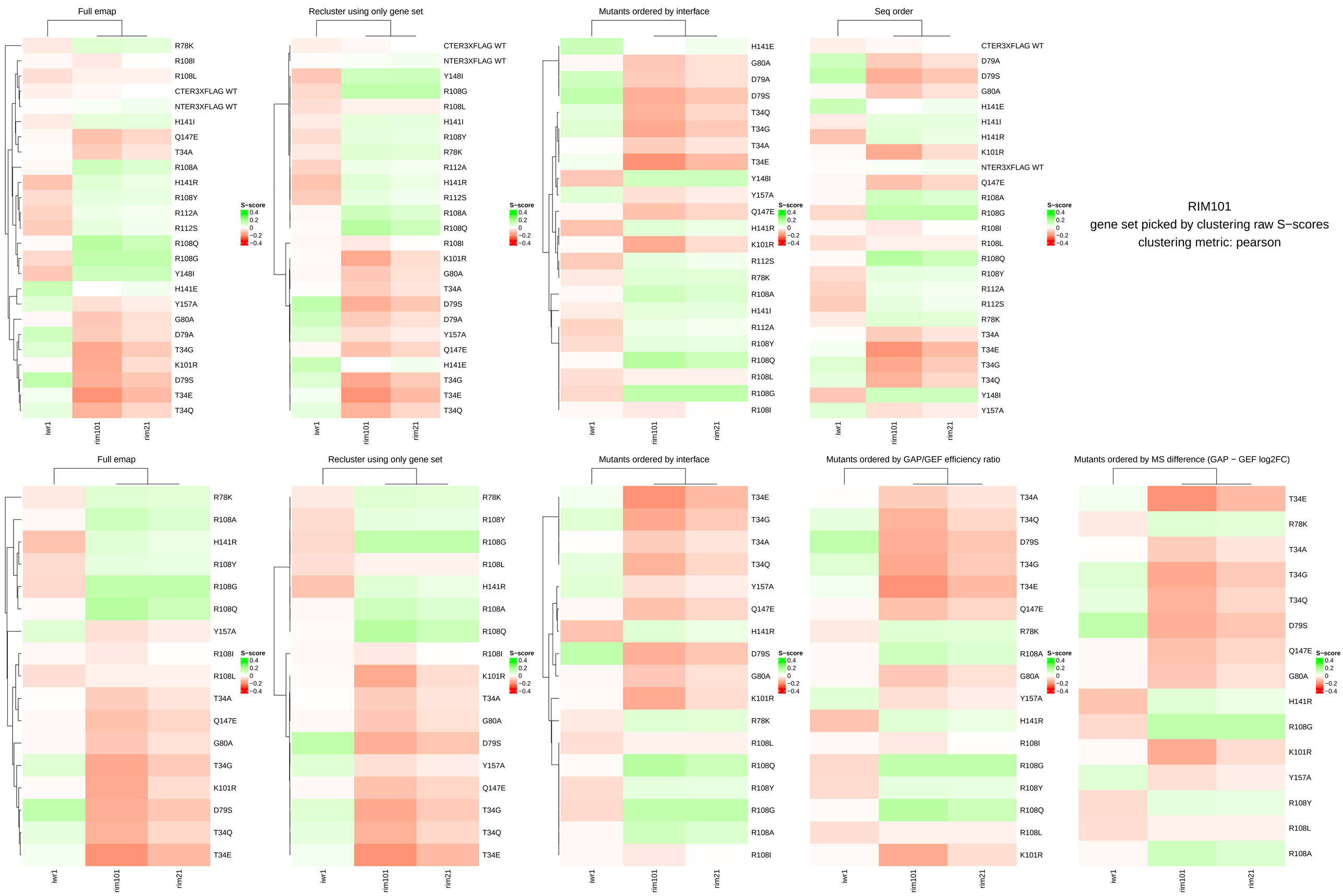
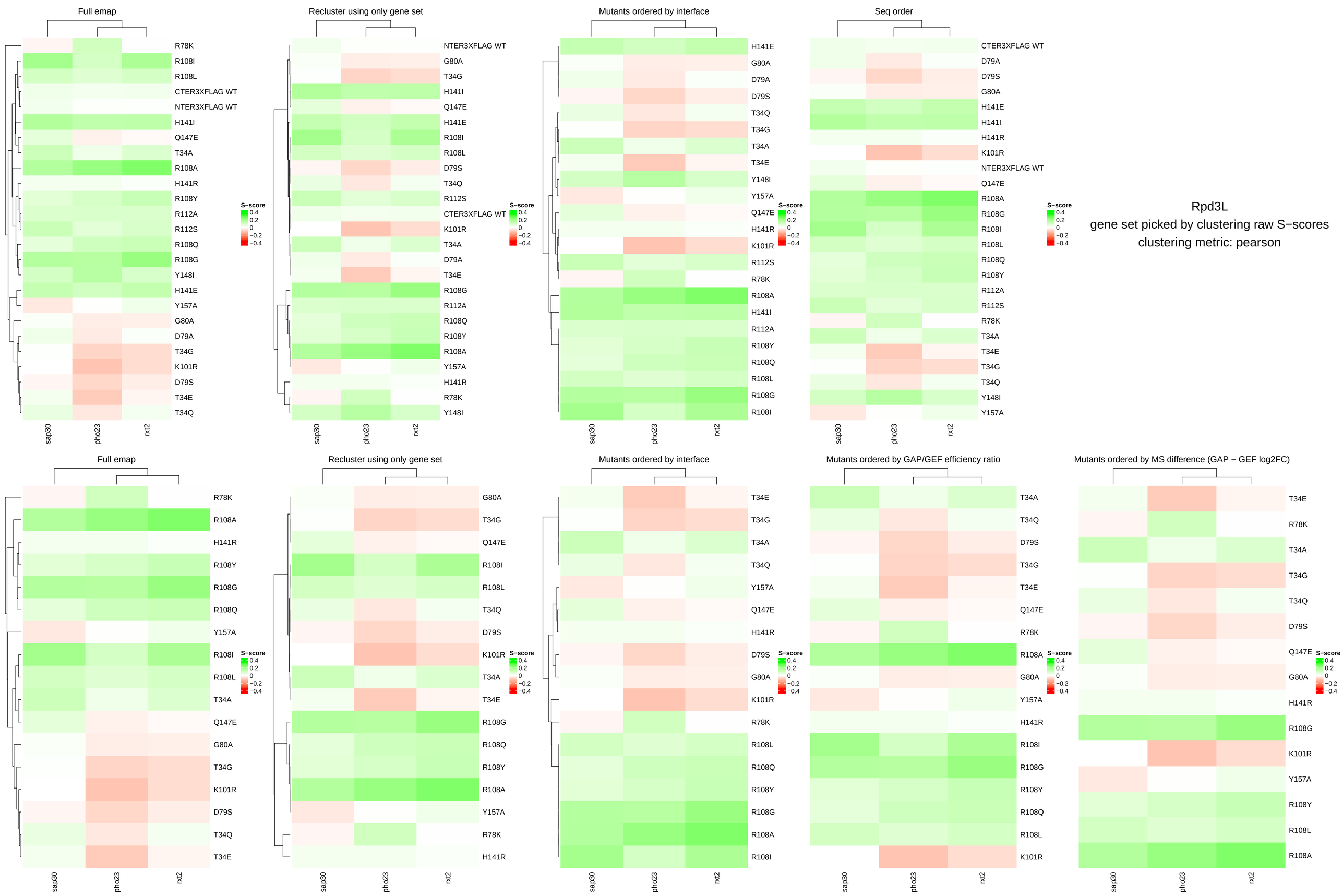
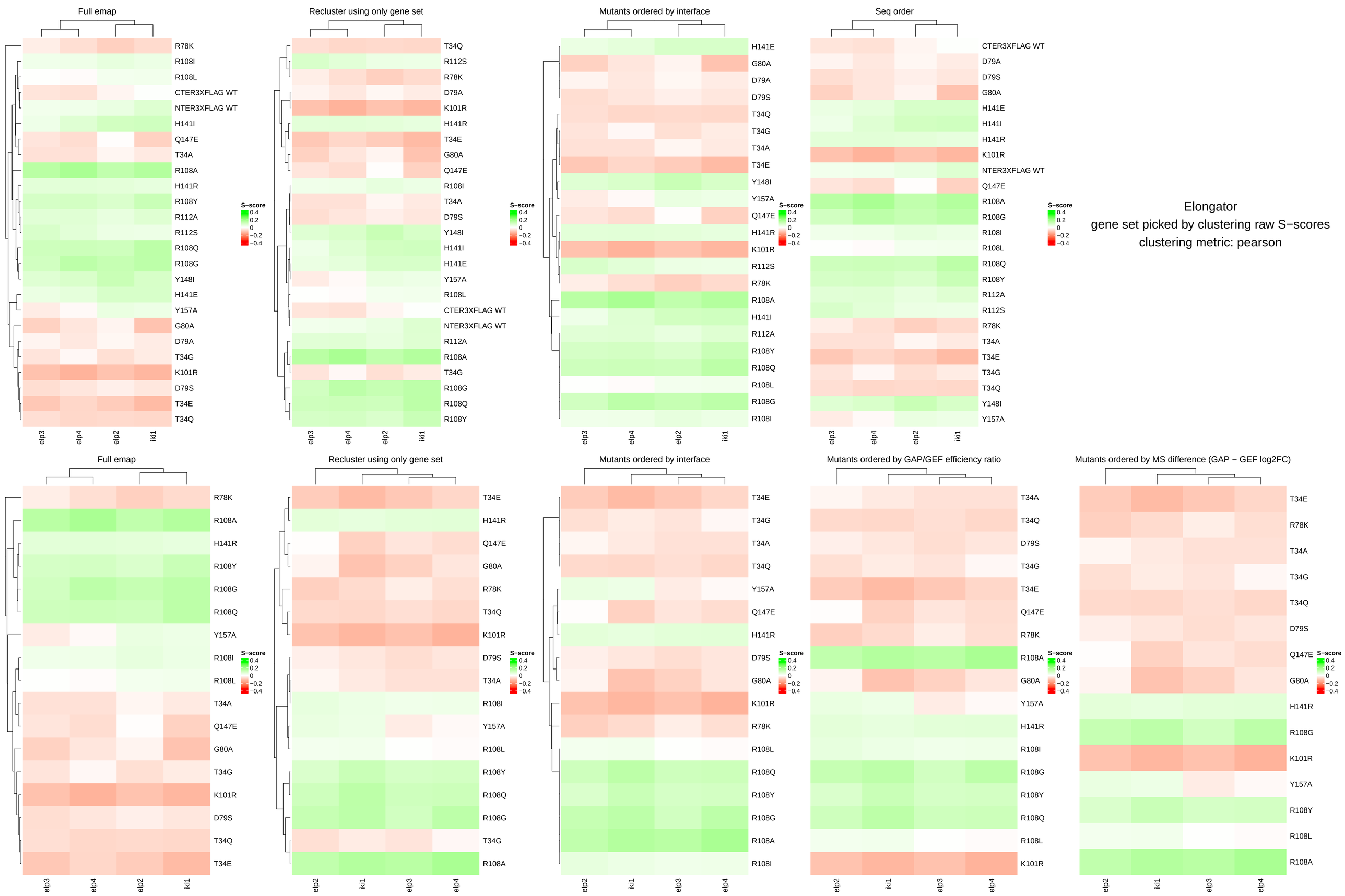
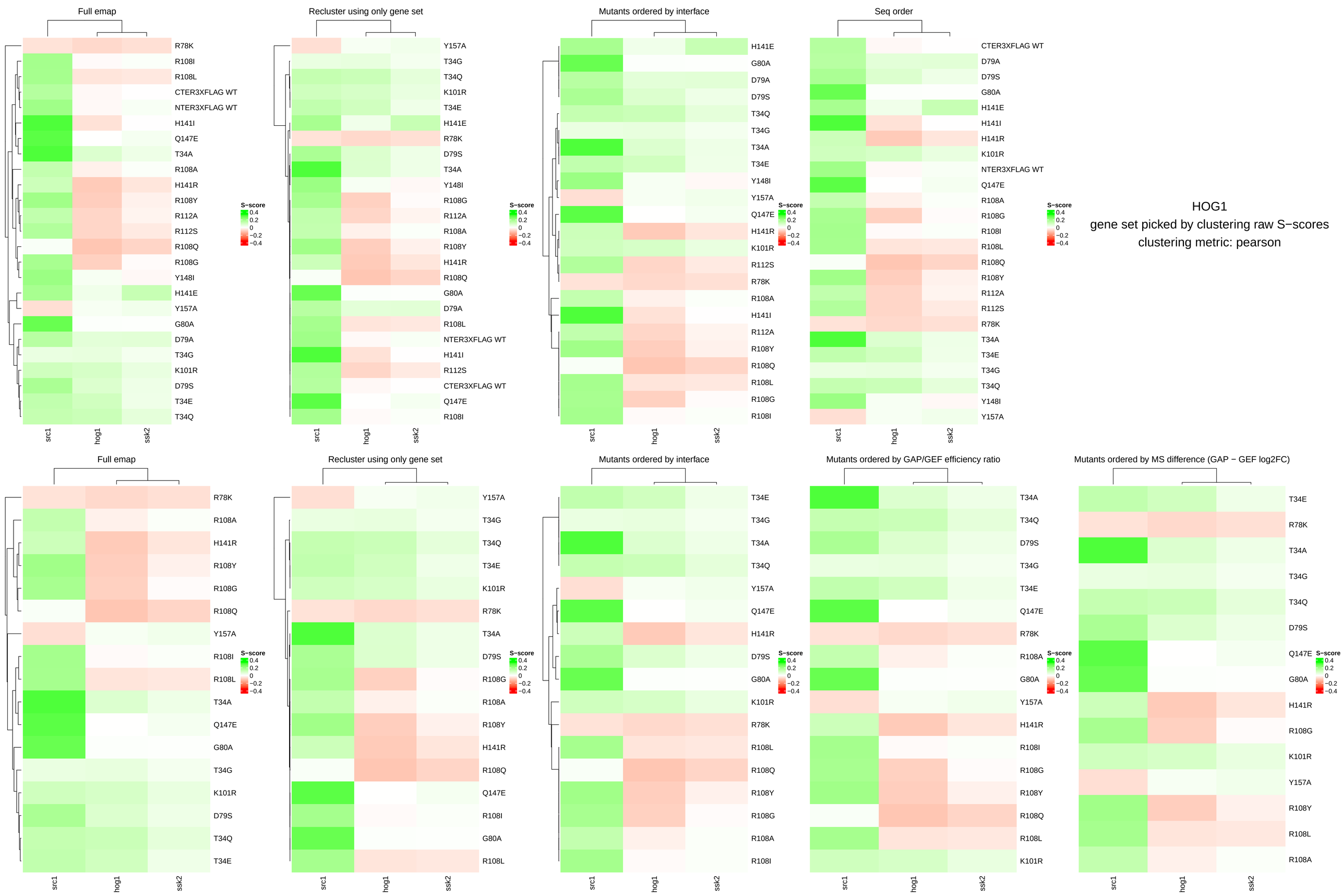

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
swr1
arp6
swc3
vps71
vps72
SWR1
gene set picked by clustering raw S−scores
clustering metric: pearson

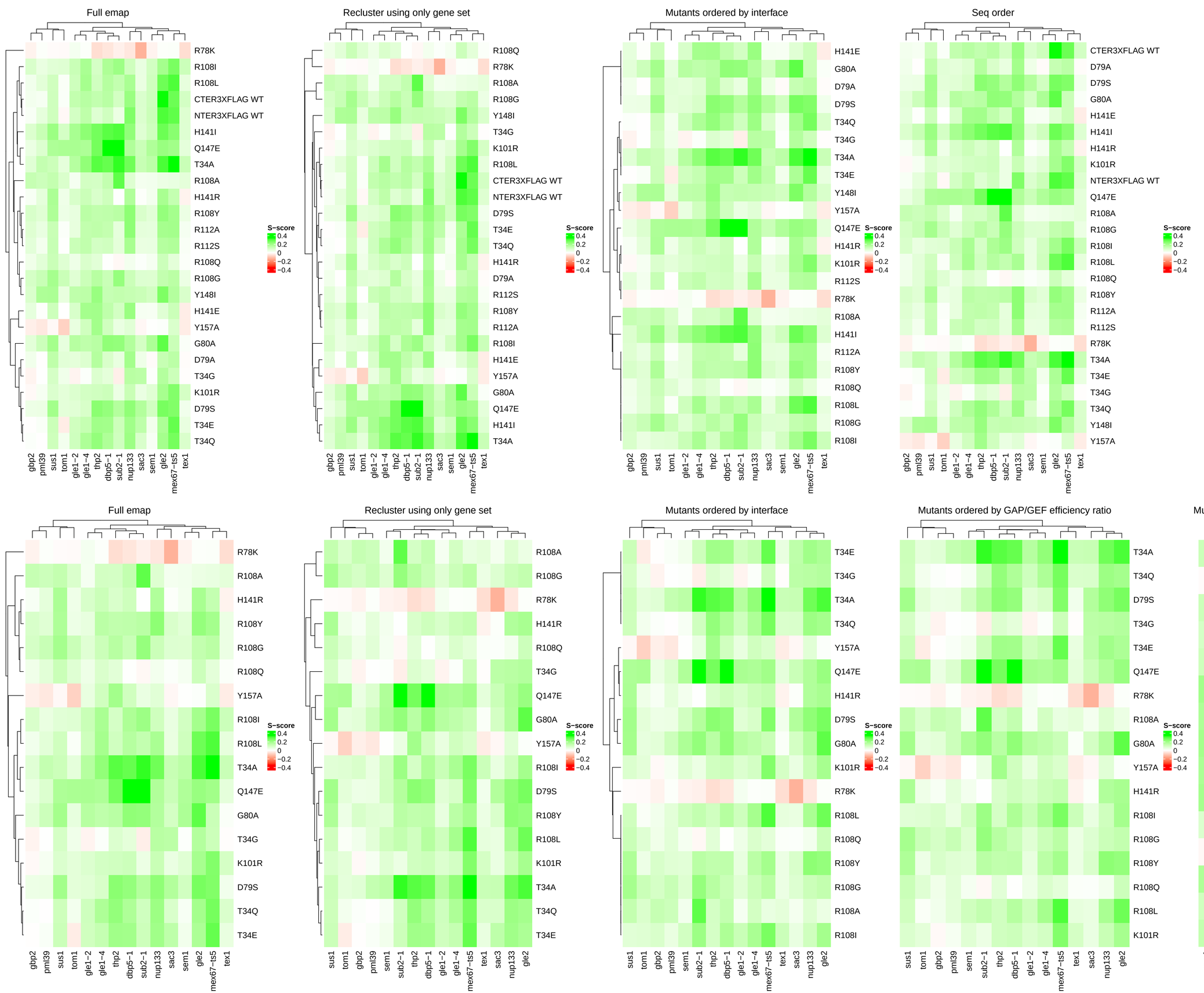
Cell Cycle Checkpoint
gene set picked by clustering raw S−scores
clustering metric: pearson


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
iwr1
rim101
rim21
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
CTER3XFLAG WT
NTER3XFLAG WT
Y148I
R108G
R108L
H141I
R108Y
R78K
R112A
H141R
R112S
R108A
R108Q
R108I
K101R
G80A
T34A
D79S
D79A
Y157A
Q147E
H141E
T34G
T34E
T34Q
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
RIM101
gene set picked by clustering raw S−scores
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
R78K
R108Y
R108G
R108L
H141R
R108A
R108Q
R108I
K101R
T34A
G80A
D79S
Y157A
Q147E
T34G
T34Q
T34E
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

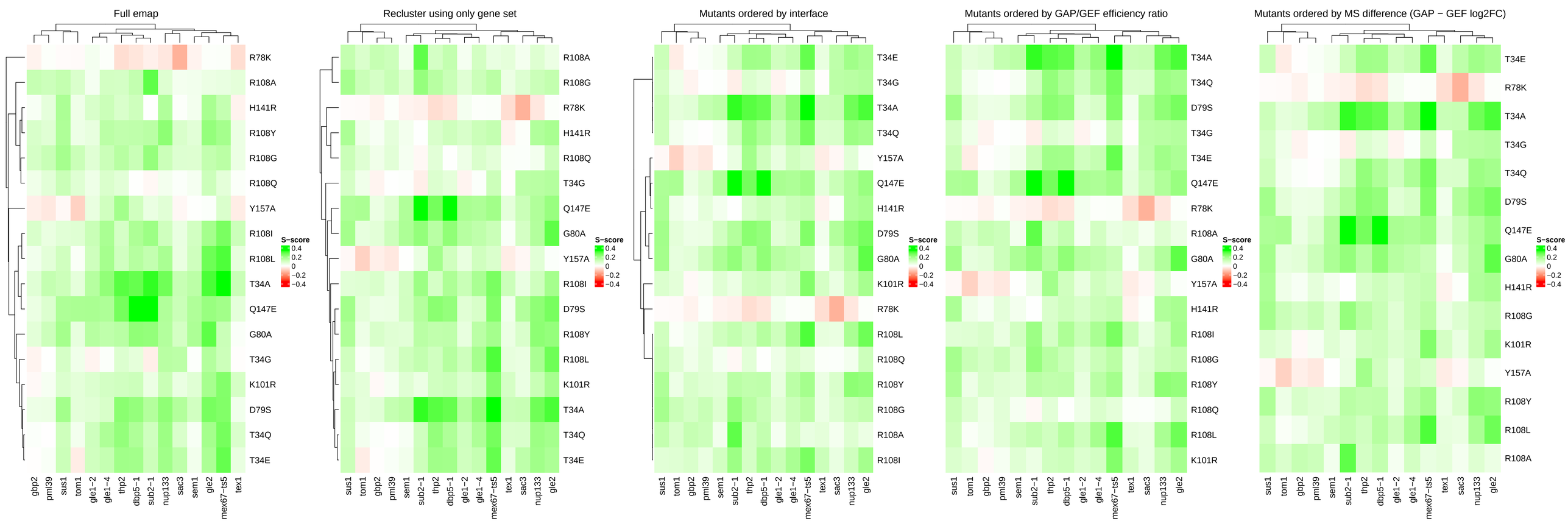

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
sap30
pho23
rxt2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
NTER3XFLAG WT
G80A
T34G
H141I
Q147E
H141E
R108I
R108L
D79S
T34Q
R112S
CTER3XFLAG WT
K101R
T34A
D79A
T34E
R108G
R112A
R108Q
R108Y
R108A
Y157A
H141R
R78K
Y148I
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Rpd3L
gene set picked by clustering raw S−scores
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
G80A
T34G
Q147E
R108I
R108L
T34Q
D79S
K101R
T34A
T34E
R108G
R108Q
R108Y
R108A
Y157A
R78K
H141R
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

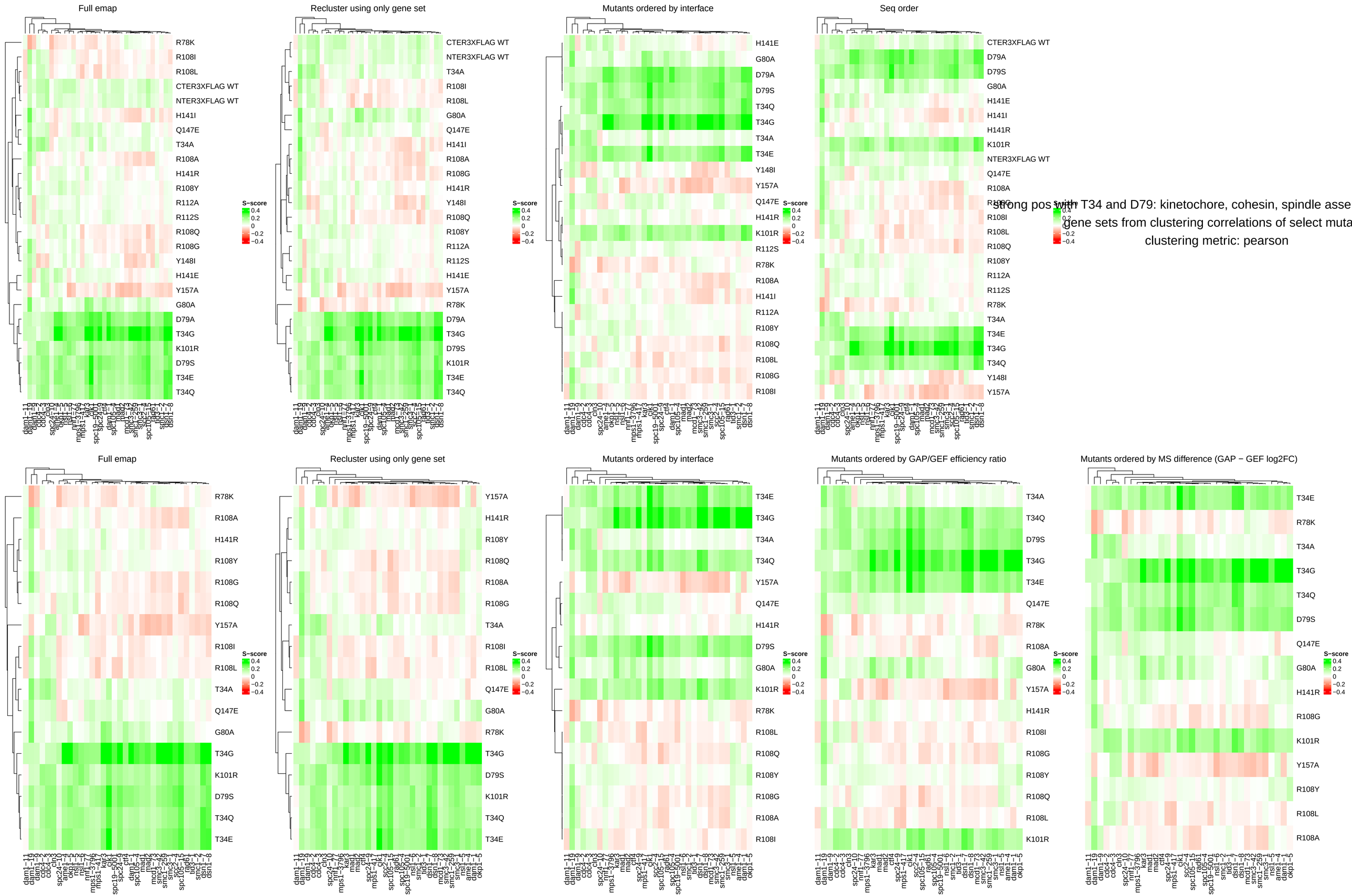

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
elp3
elp4
elp2
iki1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
T34Q
R112S
R78K
D79A
K101R
H141R
T34E
G80A
Q147E
R108I
T34A
D79S
Y148I
H141I
H141E
Y157A
R108L
CTER3XFLAG WT
NTER3XFLAG WT
R112A
R108A
T34G
R108G
R108Q
R108Y
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Elongator
gene set picked by clustering raw S−scores
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34E
H141R
Q147E
G80A
R78K
T34Q
K101R
D79S
T34A
R108I
Y157A
R108L
R108Y
R108Q
R108G
T34G
R108A
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
src1
hog1
ssk2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
Y157A
T34G
T34Q
K101R
T34E
H141E
R78K
D79S
T34A
Y148I
R108G
R112A
R108A
R108Y
H141R
R108Q
G80A
D79A
R108L
NTER3XFLAG WT
H141I
R112S
CTER3XFLAG WT
Q147E
R108I
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
HOG1
gene set picked by clustering raw S−scores
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

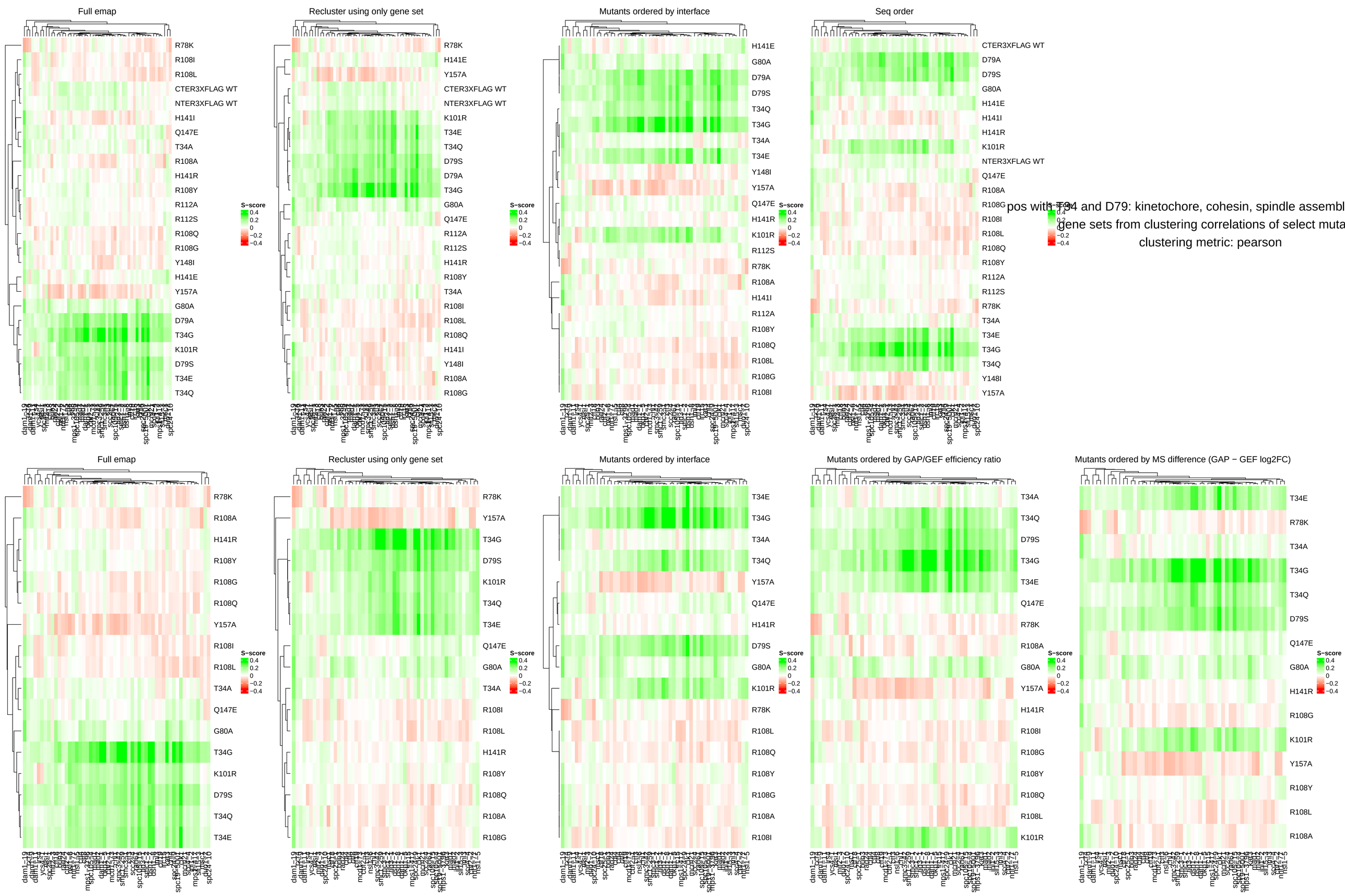


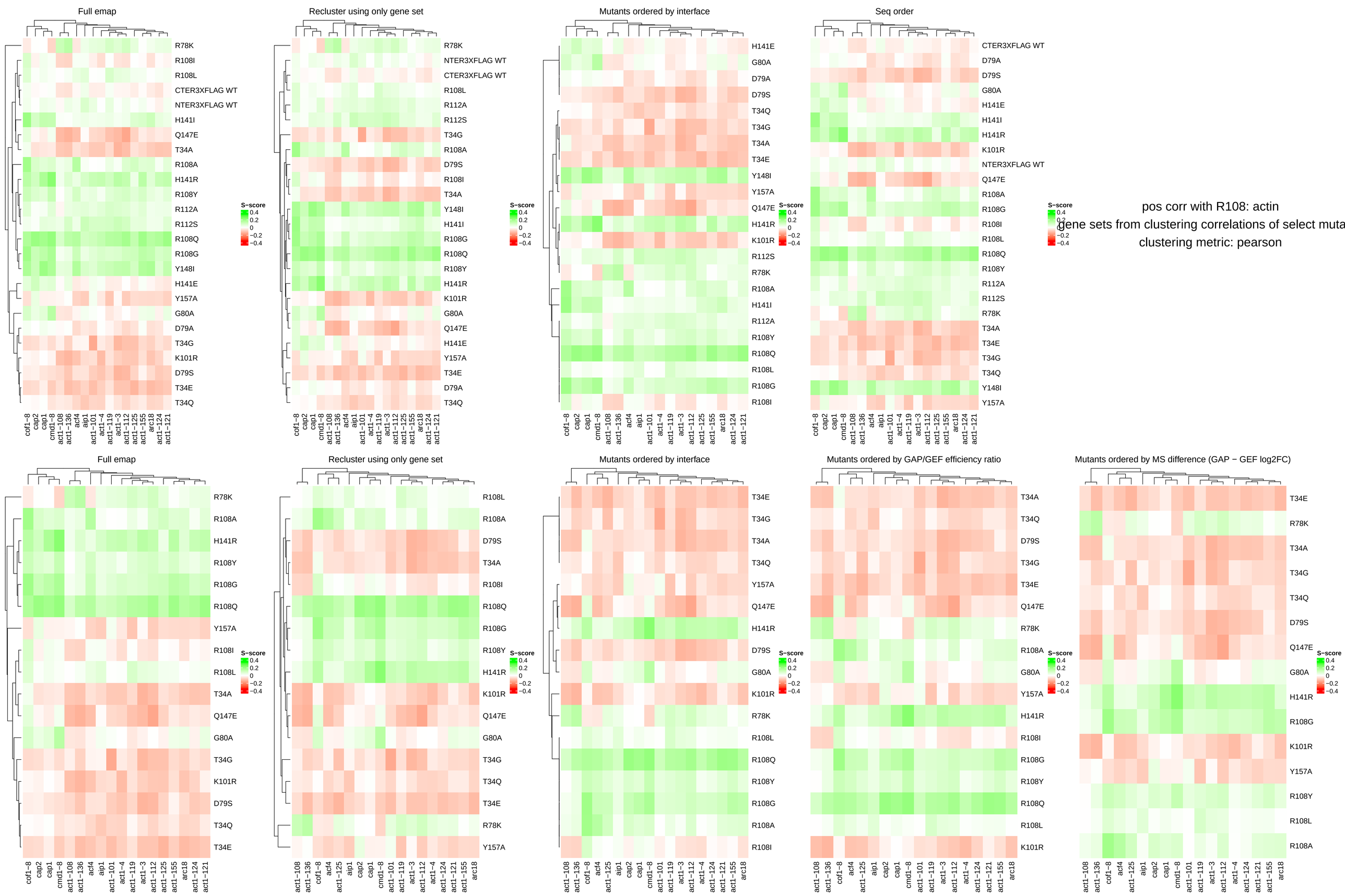
mRNA export
gene set picked by clustering raw S−scores
clustering metric: pearson



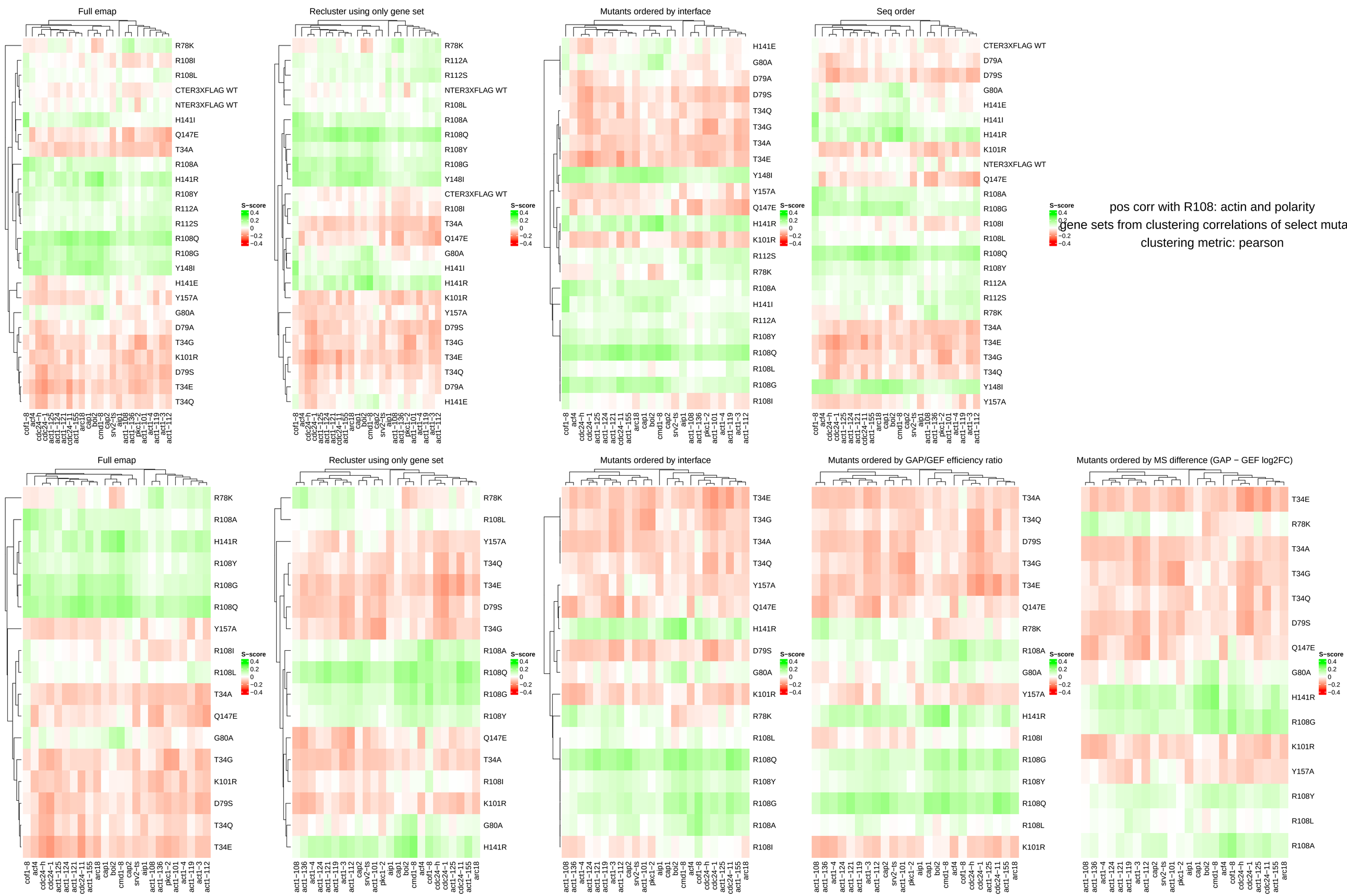


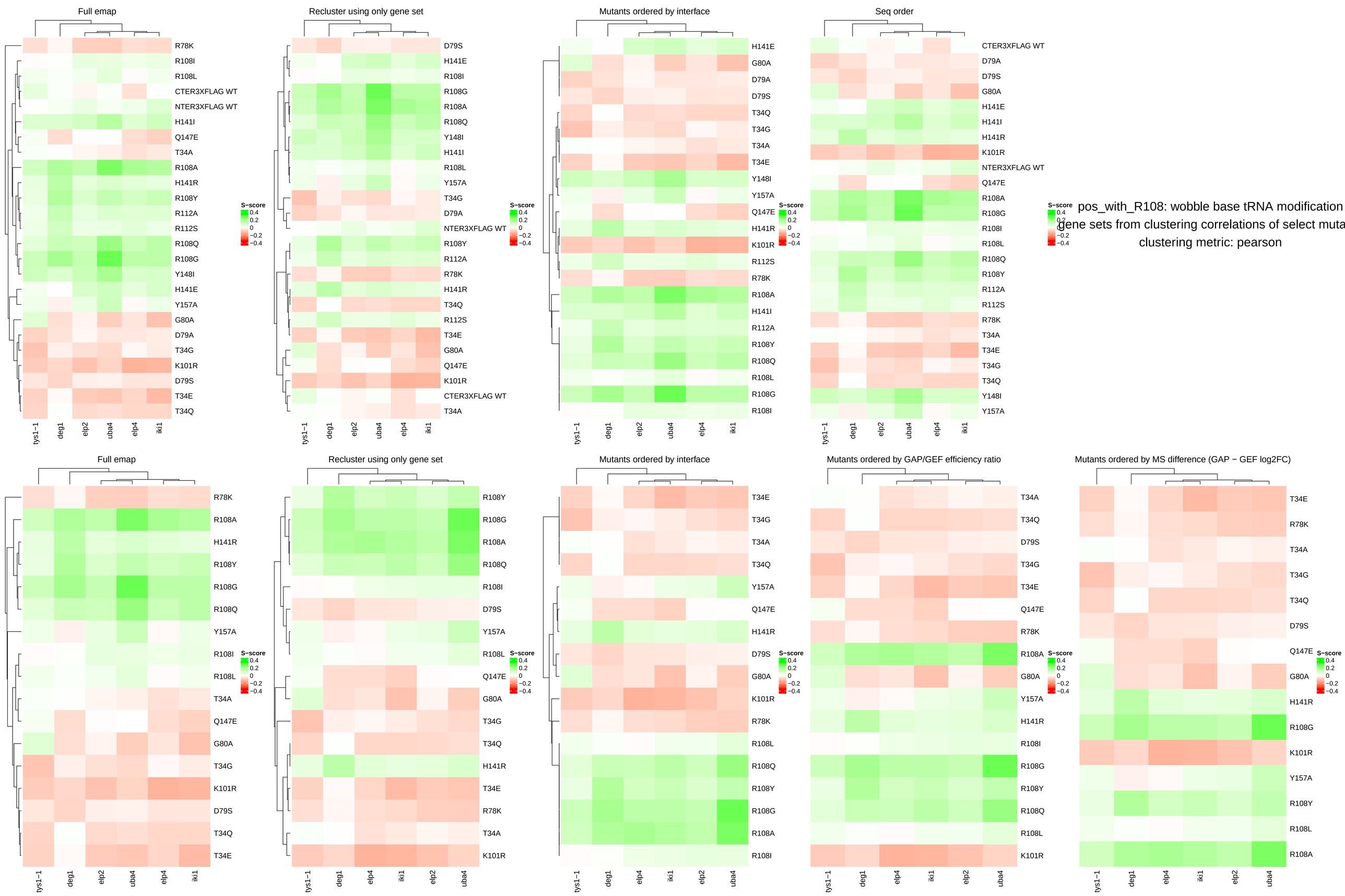
Strong pos with T34 and D79: kinetochore, cohesin, spindle asse
gene sets from clustering correlations of select muta
clustering metric: pearson

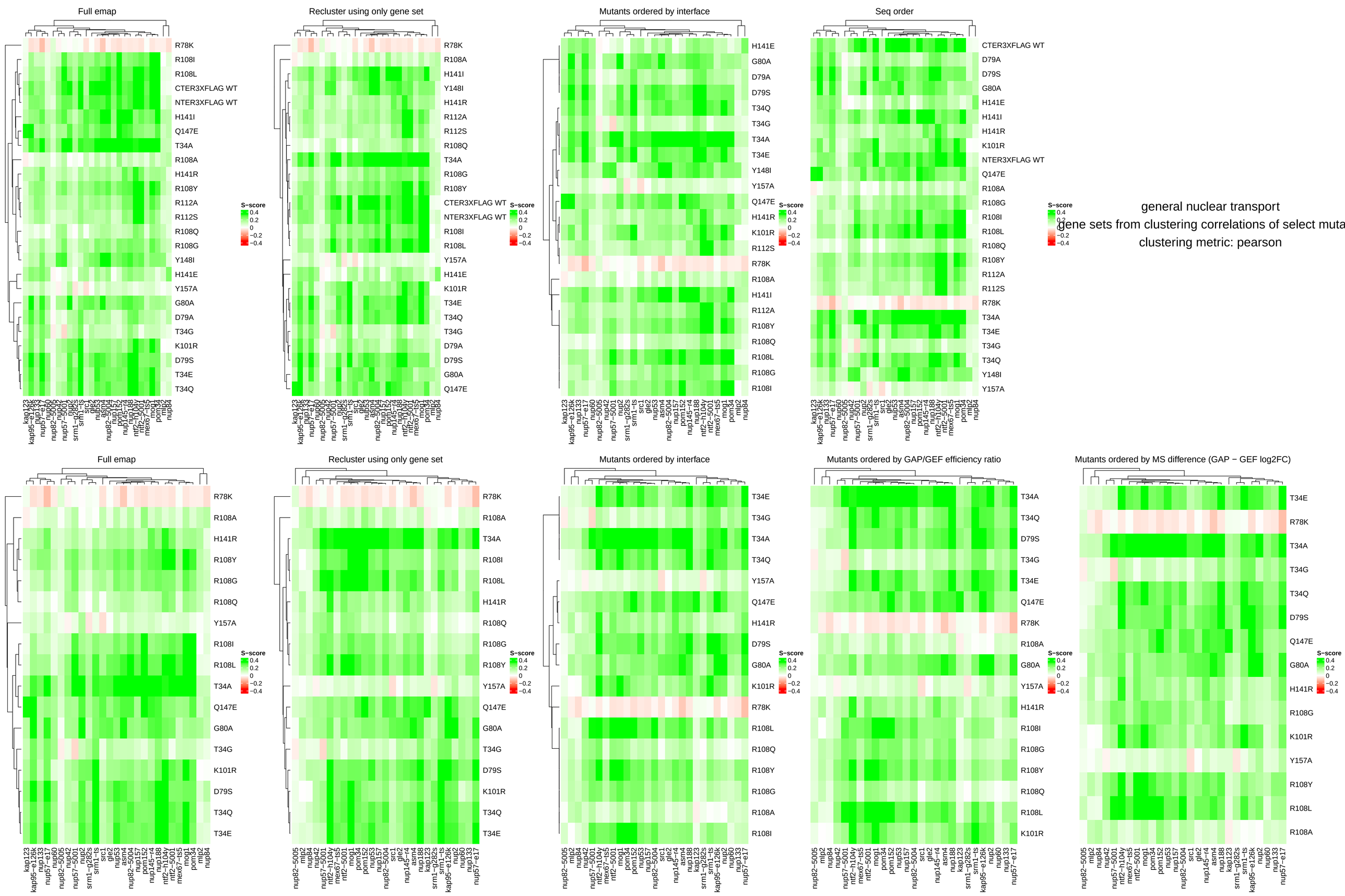

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
pos with T34 and D79: kinetochore, cohesin, spindle assembl
gene sets from clustering correlations of select muta
clustering metric: pearson

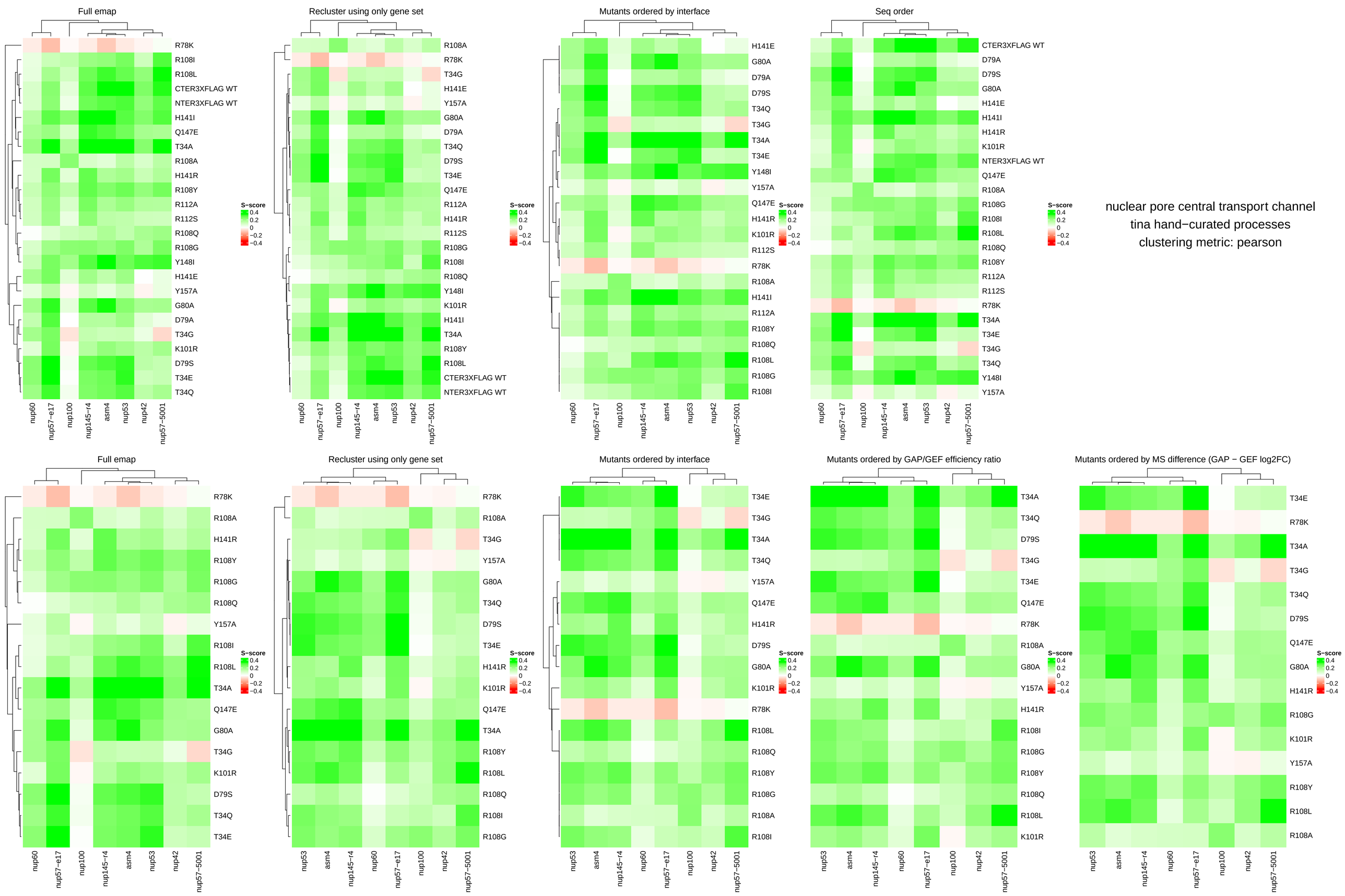


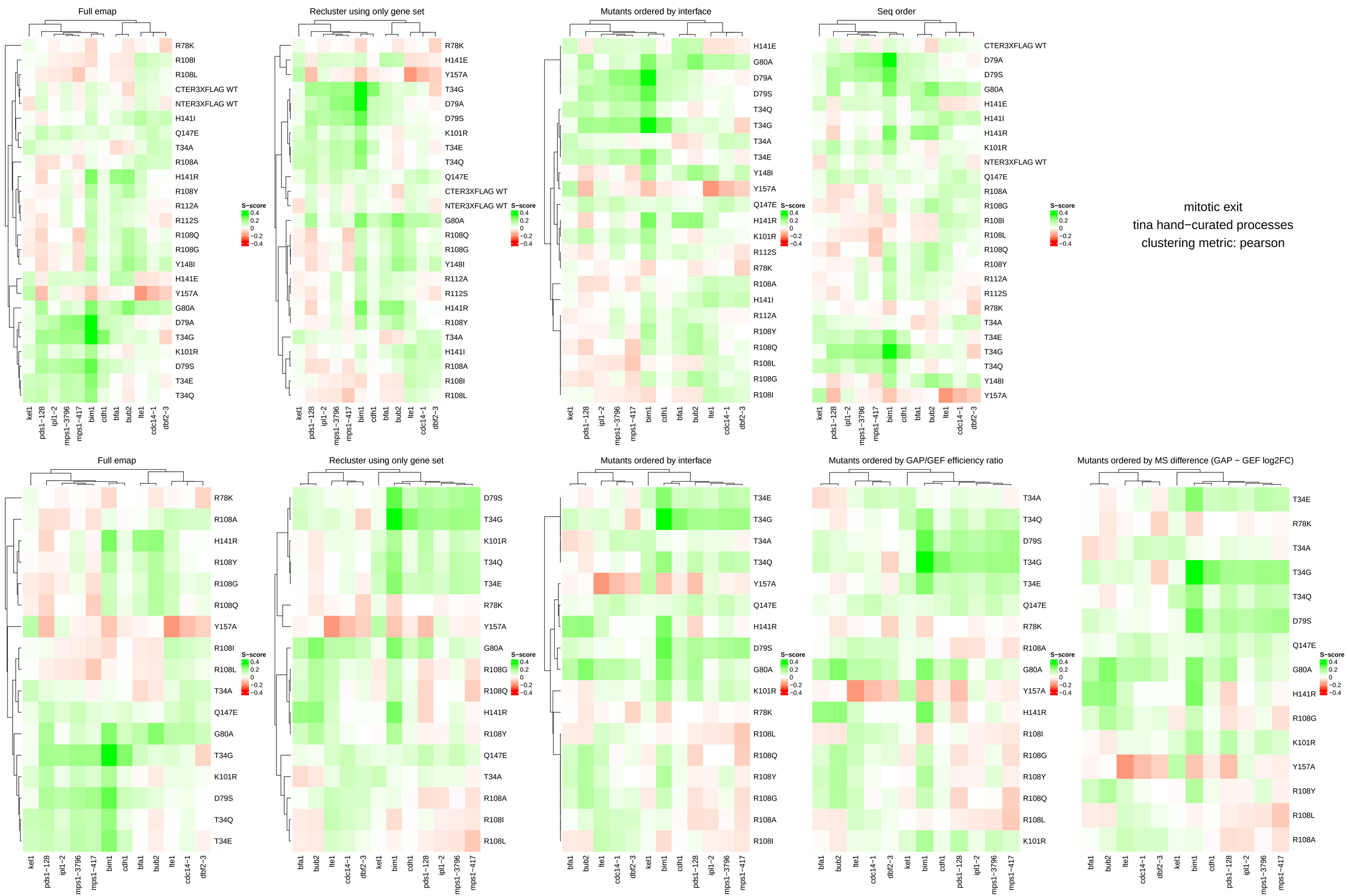
pos corr with R108: actin
gene sets from clustering correlations of select muta
clustering metric: pearson

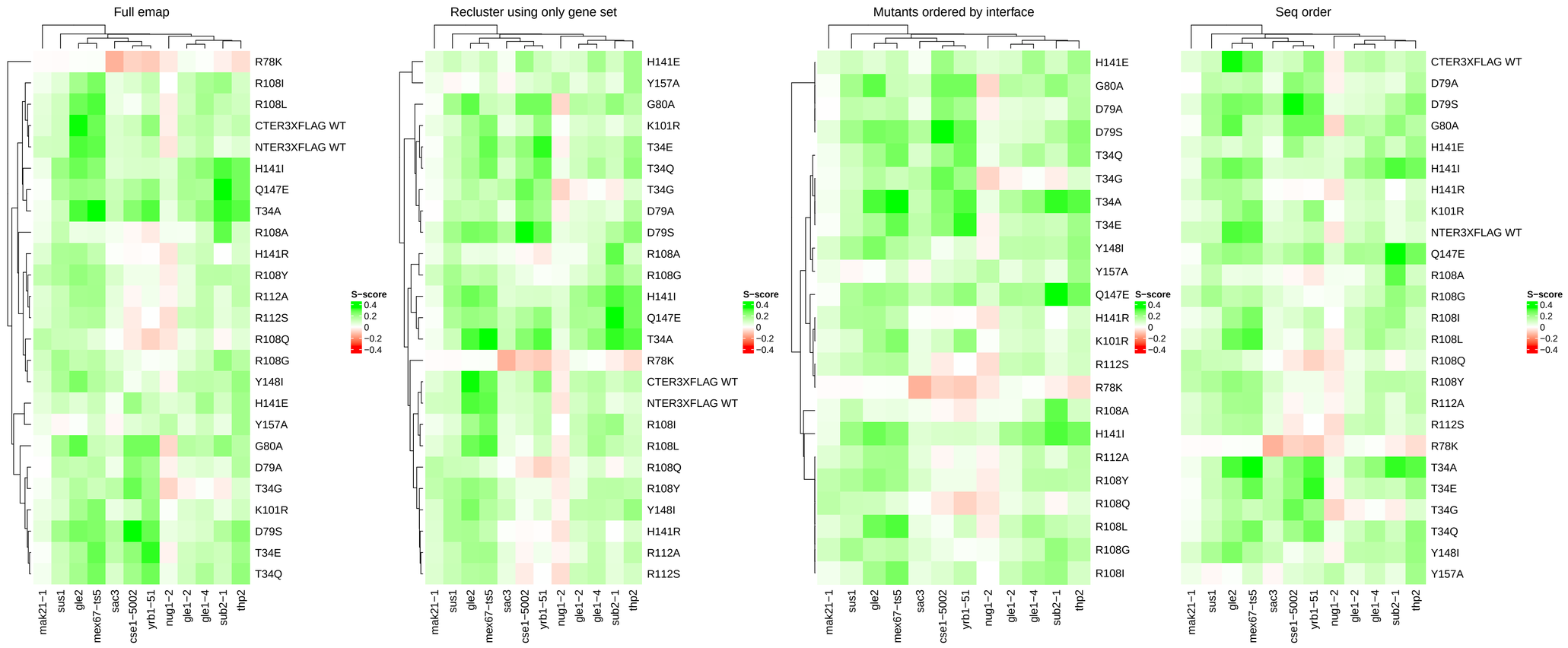

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
pos corr with R108: actin and polarity
gene sets from clustering correlations of select muta
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
tys1−1
deg1
elp2
uba4
elp4
iki1
pos_with_R108: wobble base tRNA modification
gene sets from clustering correlations of select muta
clustering metric: pearson

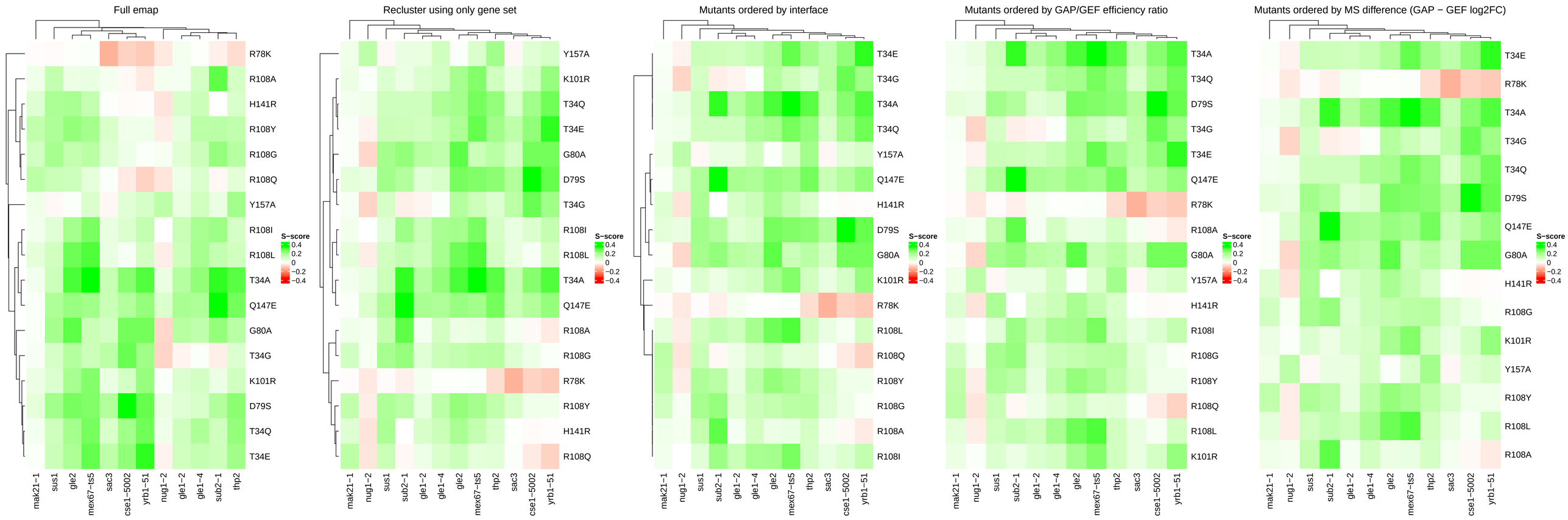

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
general nuclear transport
gene sets from clustering correlations of select muta
clustering metric: pearson

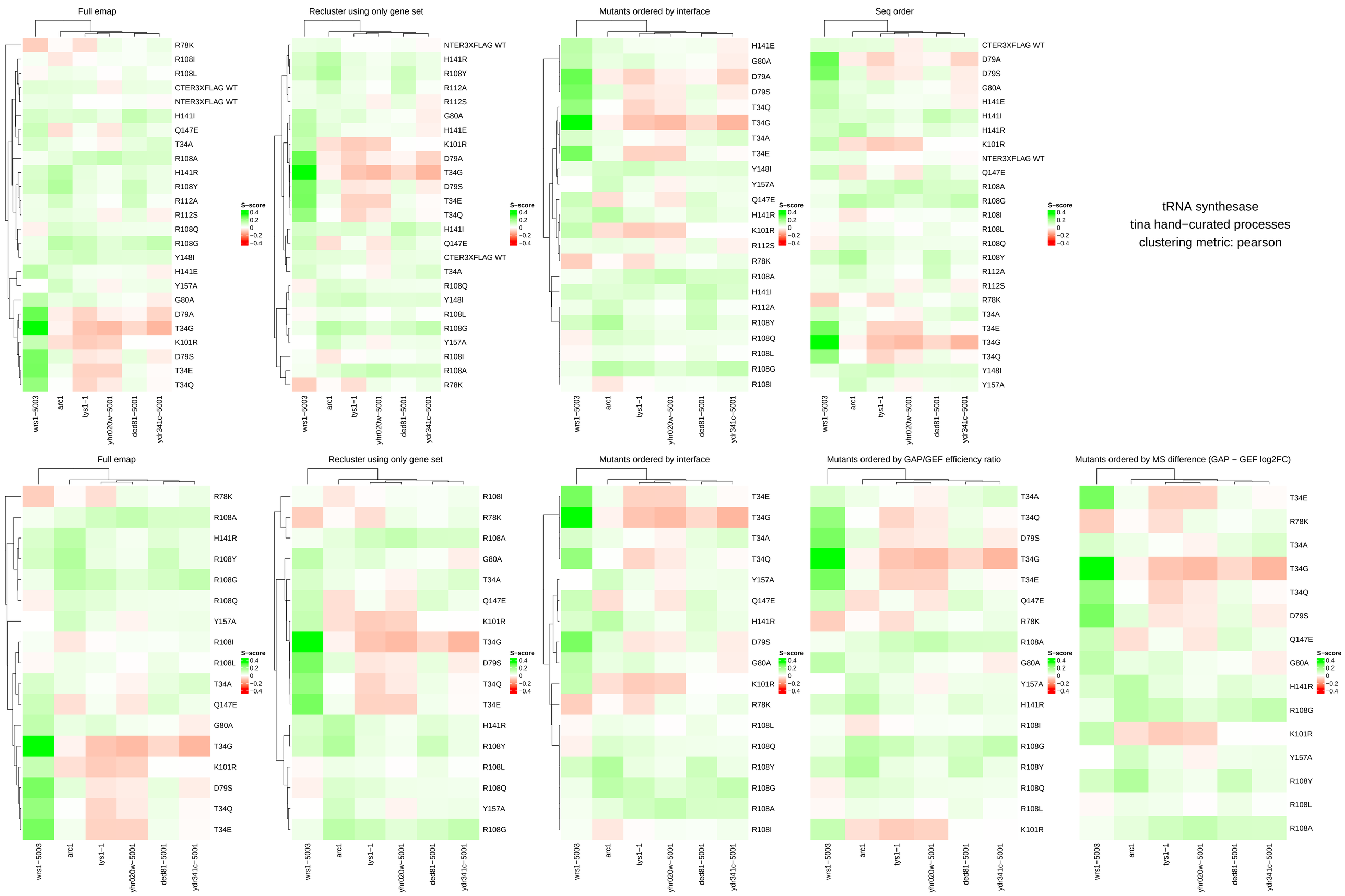

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
nup60
nup57−e17
nup100
nup145−r4
asm4
nup53
nup42
nup57−5001
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
nuclear pore central transport channel
tina hand−curated processes
clustering metric: pearson

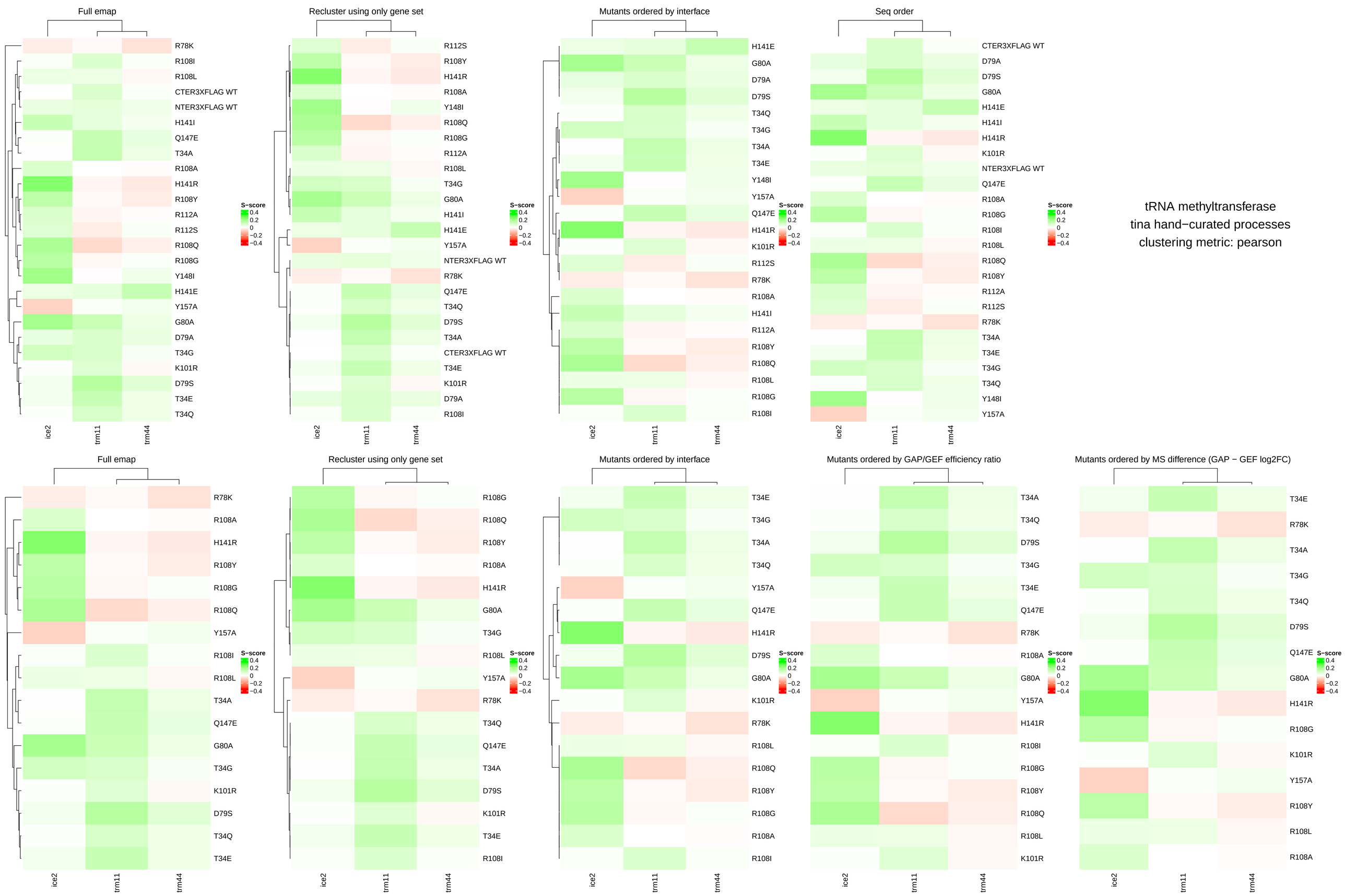

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
kel1
pds1−128
ipl1−2
mps1−3796
mps1−417
bim1
cdh1
bfa1
bub2
lte1
cdc14−1
dbf2−3
mitotic exit
tina hand−curated processes
clustering metric: pearson



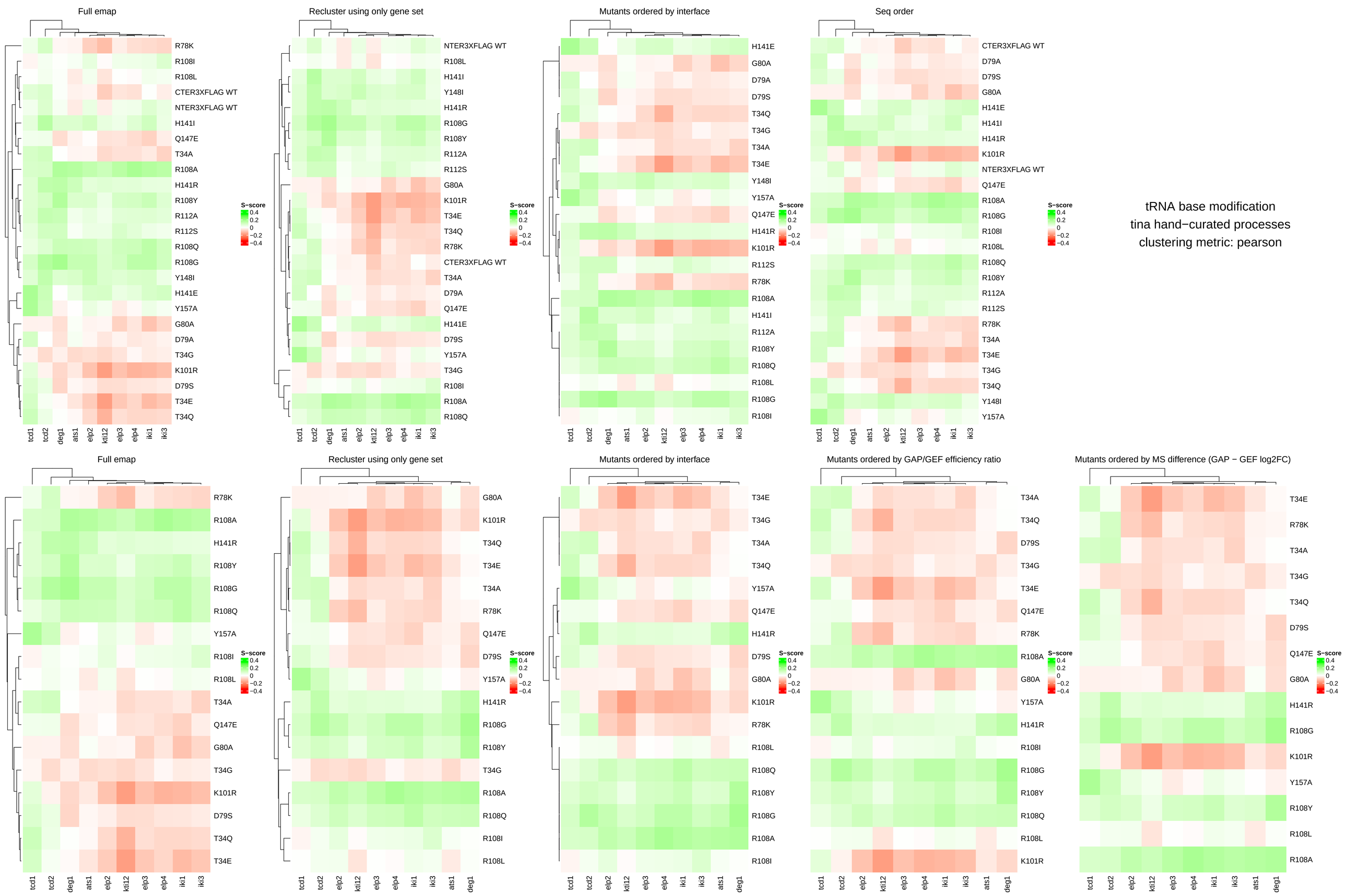
general nuclear export
tina hand−curated processes
clustering metric: pearson

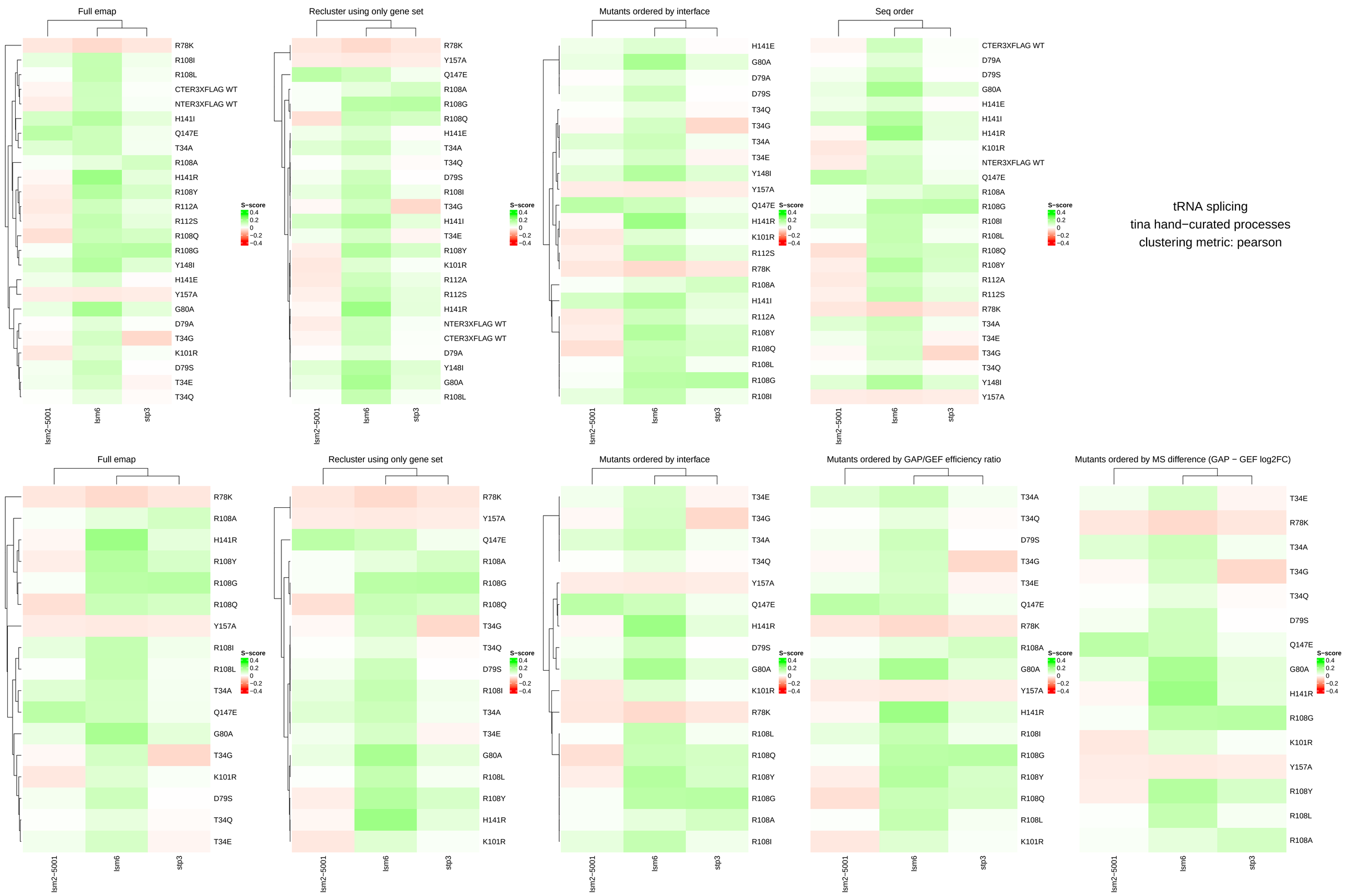


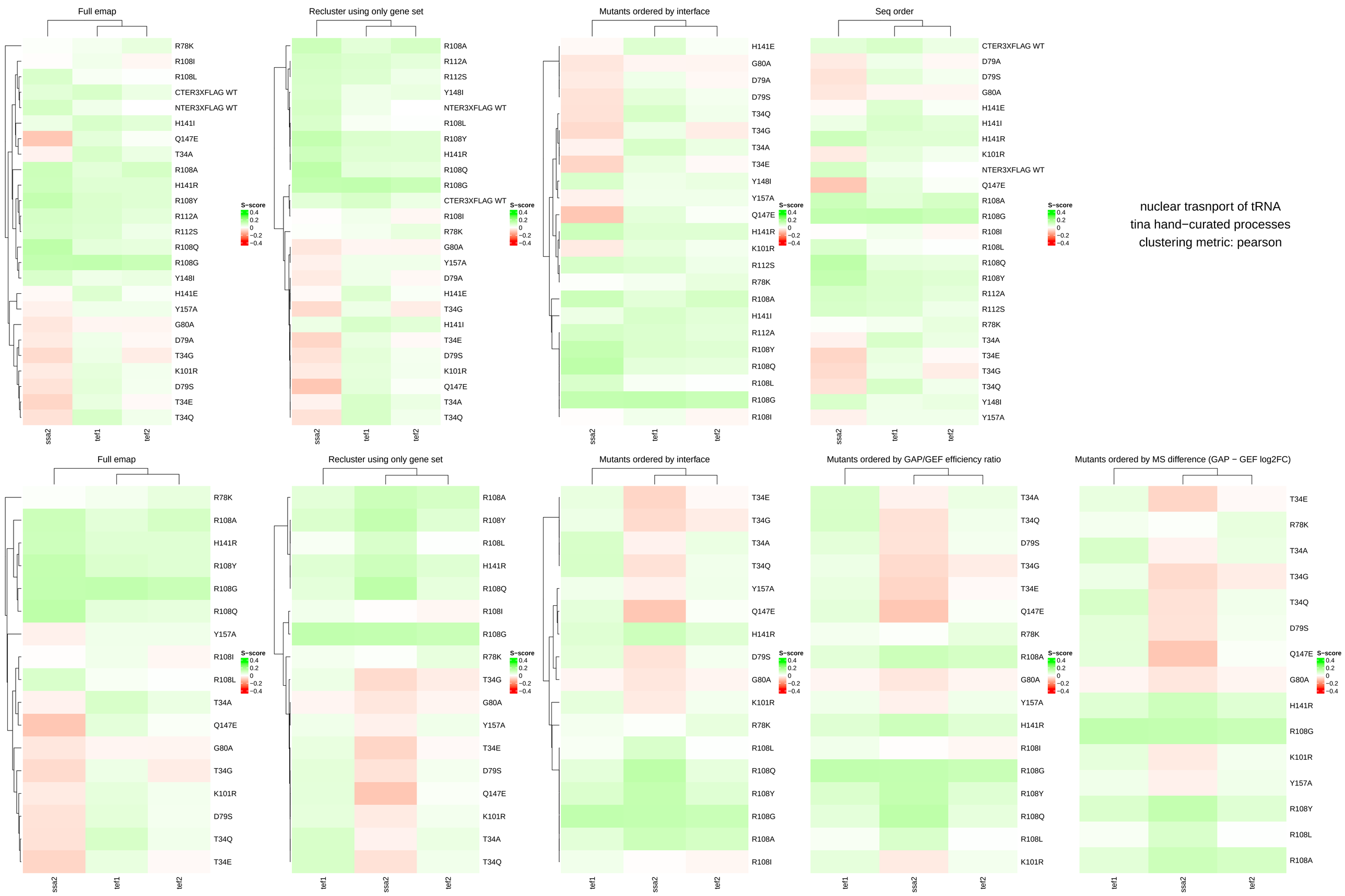

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
wrs1−5003
arc1
tys1−1
yhr020w−5001
ded81−5001
ydr341c−5001
tRNA synthesase
tina hand−curated processes
clustering metric: pearson

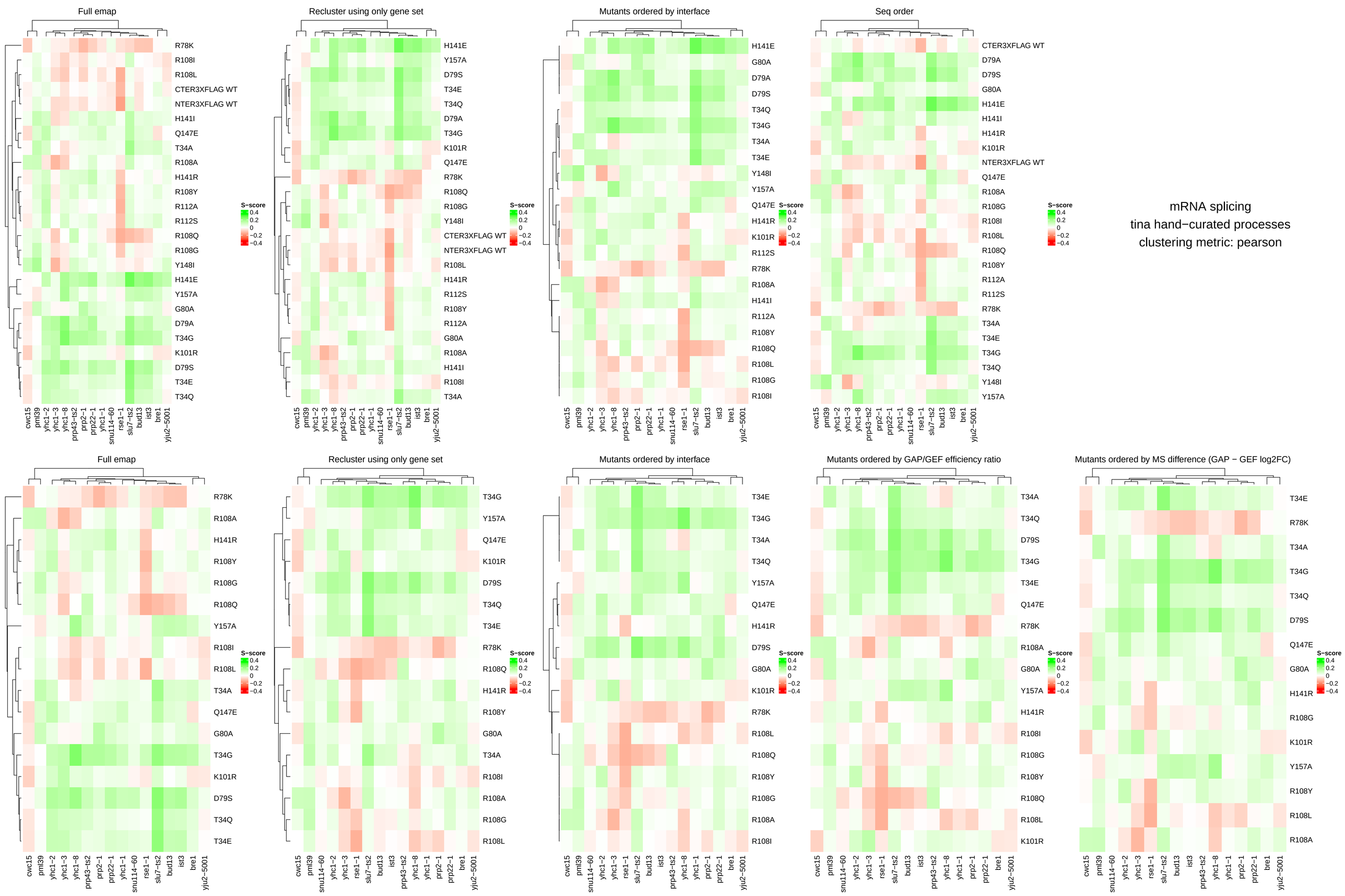


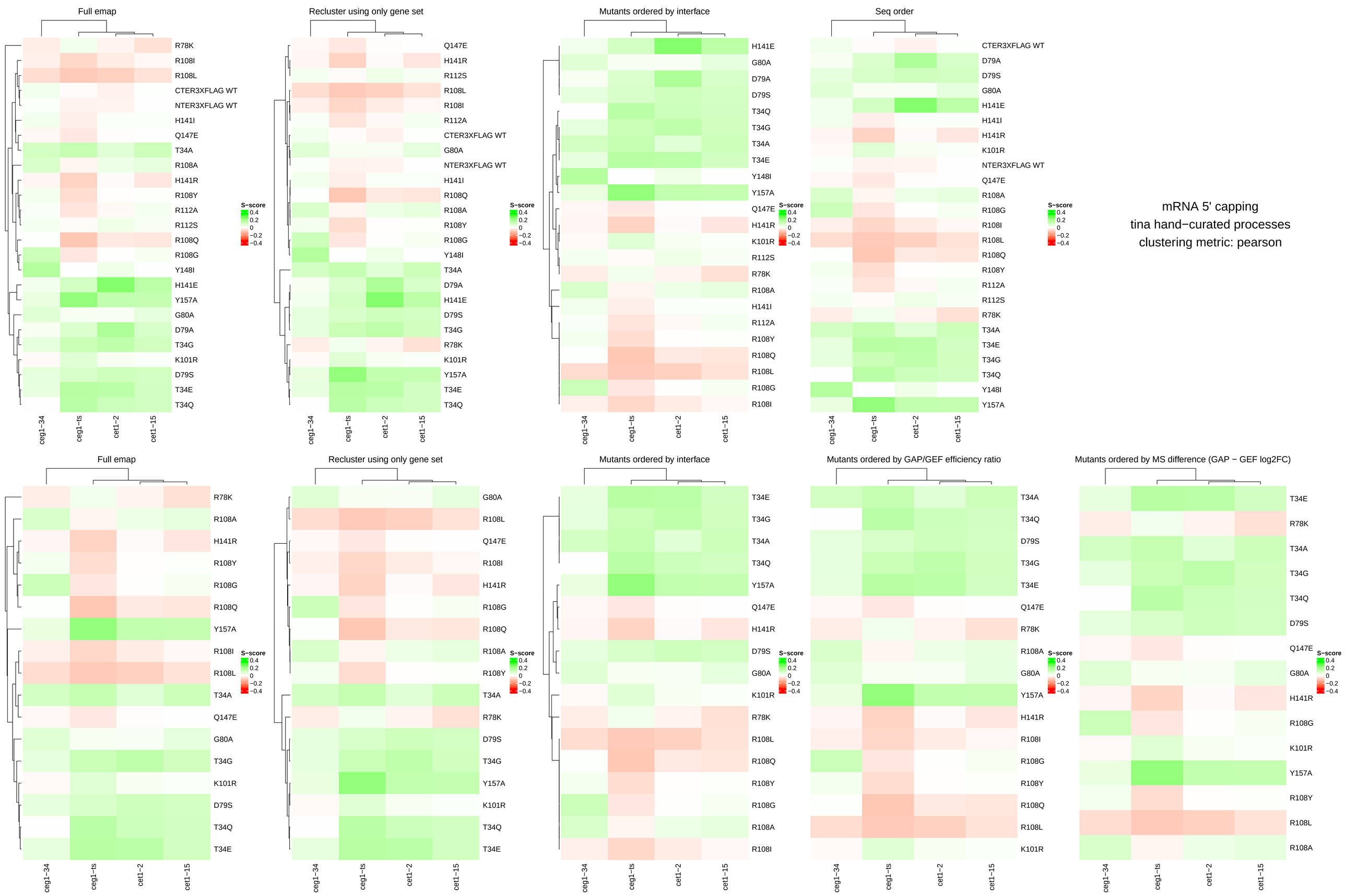
tRNA methyltransferase
tina hand−curated processes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
tcd1
tcd2
deg1
ats1
elp2
kti12
elp3
elp4
iki1
iki3
tRNA base modification
tina hand−curated processes
clustering metric: pearson

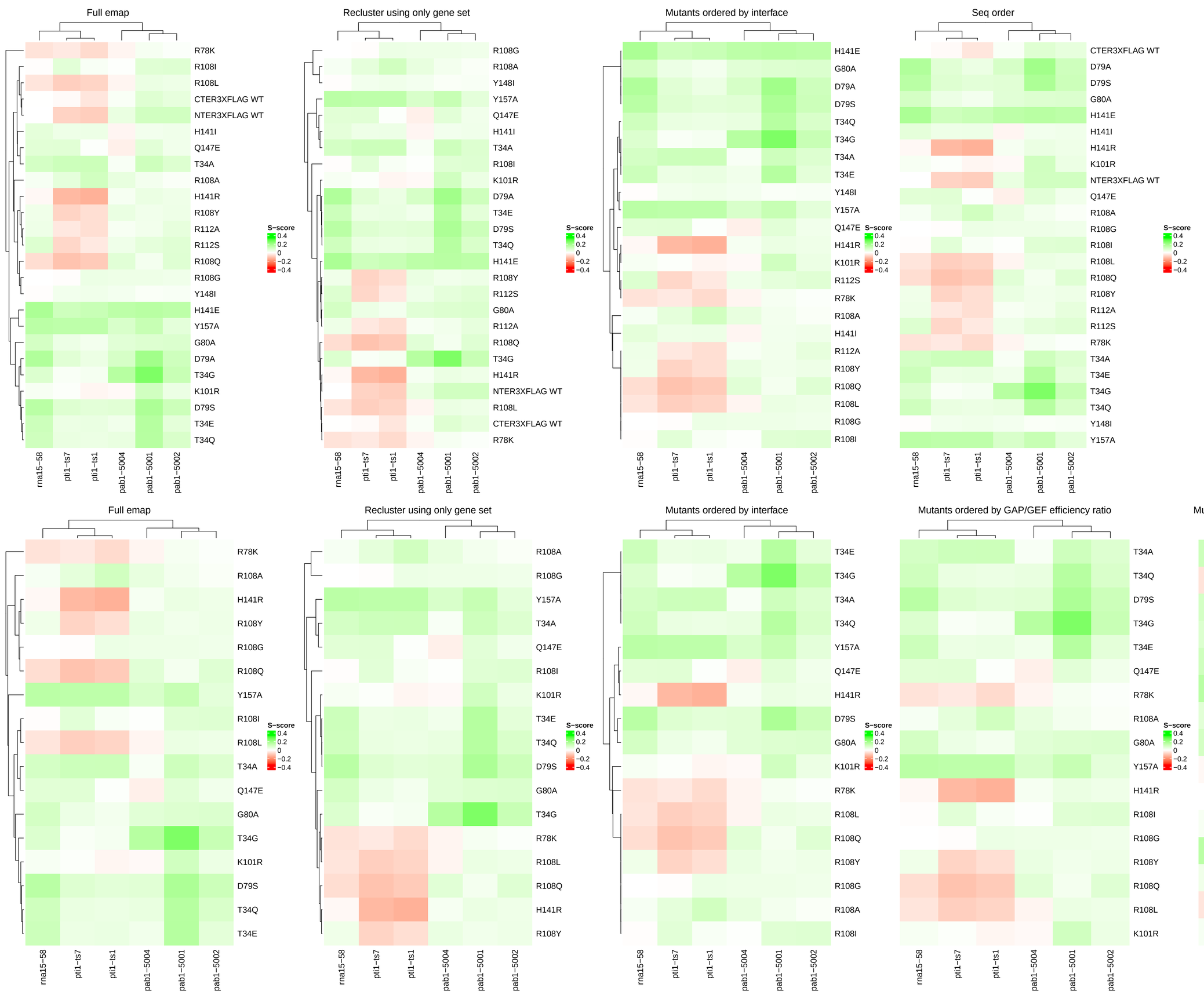

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R78K
Y157A
Q147E
R108A
R108G
R108Q
H141E
T34A
T34Q
D79S
R108I
T34G
H141I
T34E
R108Y
K101R
R112A
R112S
H141R
NTER3XFLAG WT
CTER3XFLAG WT
D79A
Y148I
G80A
R108L
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
tRNA splicing
tina hand−curated processes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R78K
Y157A
Q147E
R108A
R108G
R108Q
T34G
T34Q
D79S
R108I
T34A
T34E
G80A
R108L
R108Y
H141R
K101R
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A
lsm2−5001
lsm6
stp3
S−score
0.4
0.2
0
−0.2
−0.4


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
ssa2
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108A
R112A
R112S
Y148I
NTER3XFLAG WT
R108L
R108Y
H141R
R108Q
R108G
CTER3XFLAG WT
R108I
R78K
G80A
Y157A
D79A
H141E
T34G
H141I
T34E
D79S
K101R
Q147E
T34A
T34Q
ssa2
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
ssa2
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
ssa2
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
nuclear trasnport of tRNA
tina hand−curated processes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
ssa2
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108A
R108Y
R108L
H141R
R108Q
R108I
R108G
R78K
T34G
G80A
Y157A
T34E
D79S
Q147E
K101R
T34A
T34Q
tef1
ssa2
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
tef1
ssa2
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
tef1
ssa2
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A
tef1
ssa2
tef2
S−score
0.4
0.2
0
−0.2
−0.4

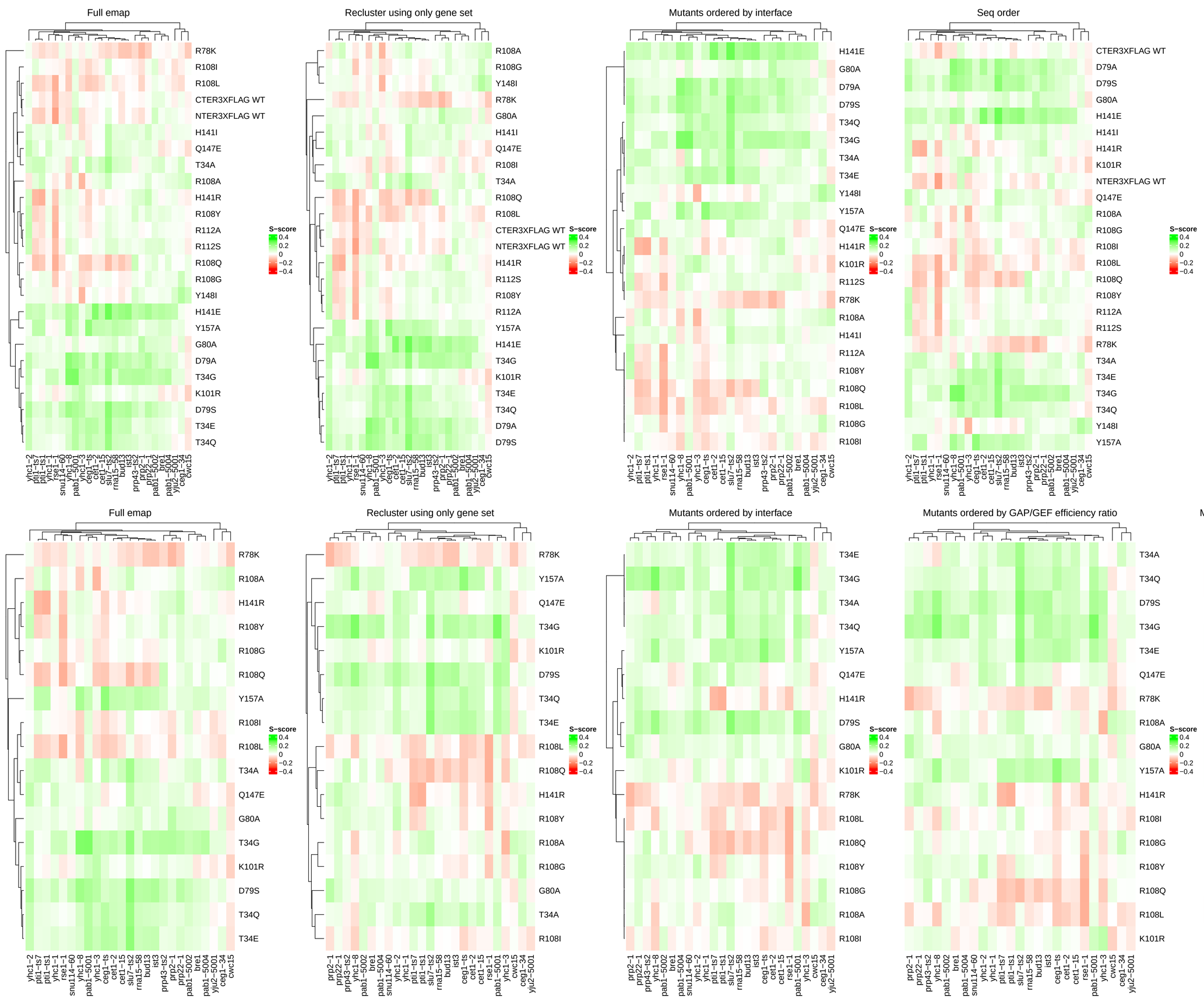

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
cwc15
pml39
yhc1−2
yhc1−3
yhc1−8
prp43−ts2
prp2−1
prp22−1
yhc1−1
snu114−60
rse1−1
slu7−ts2
bud13
ist3
bre1
yju2−5001
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
mRNA splicing
tina hand−curated processes
clustering metric: pearson



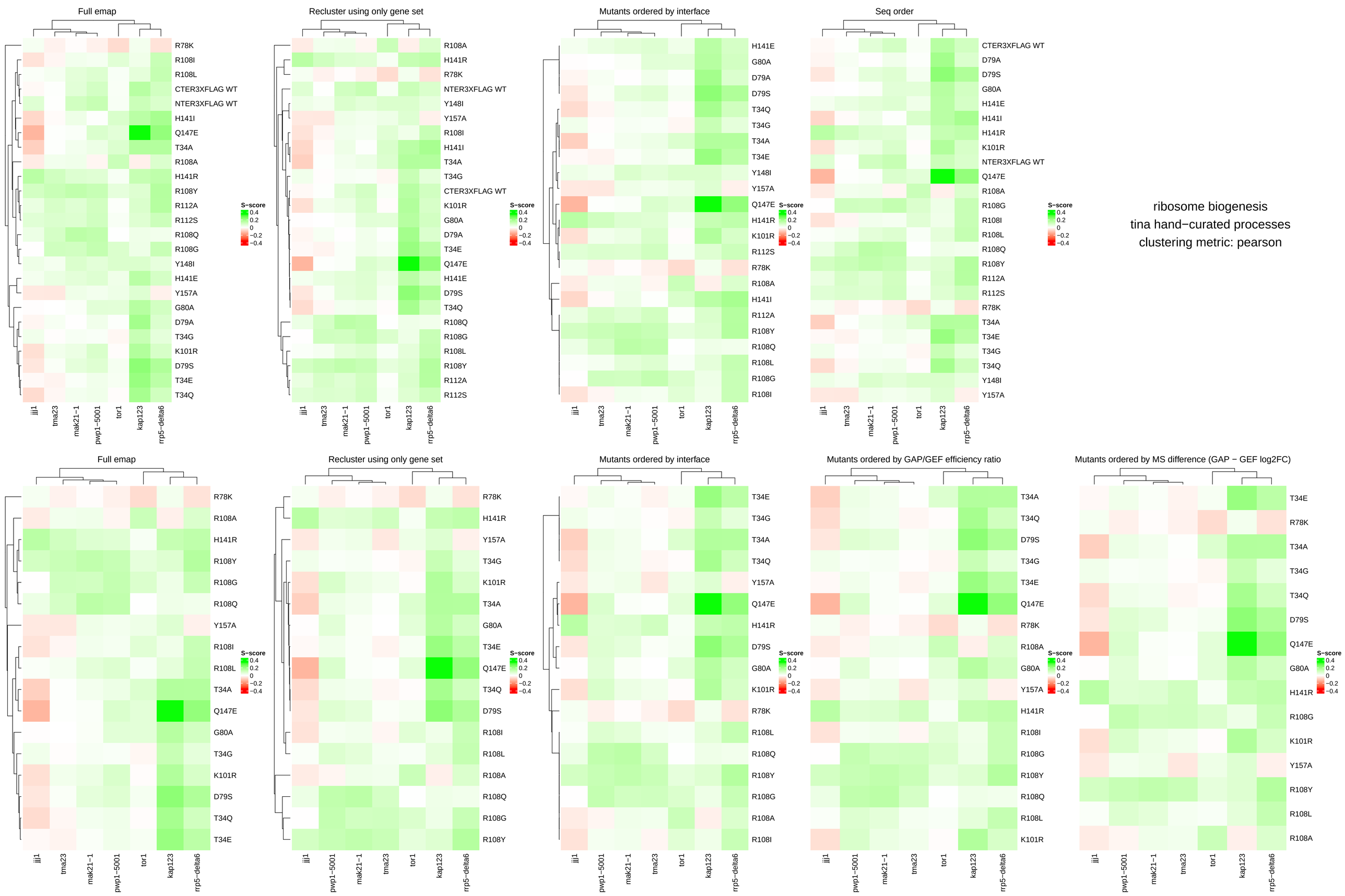
mRNA 5' capping
tina hand−curated processes
clustering metric: pearson

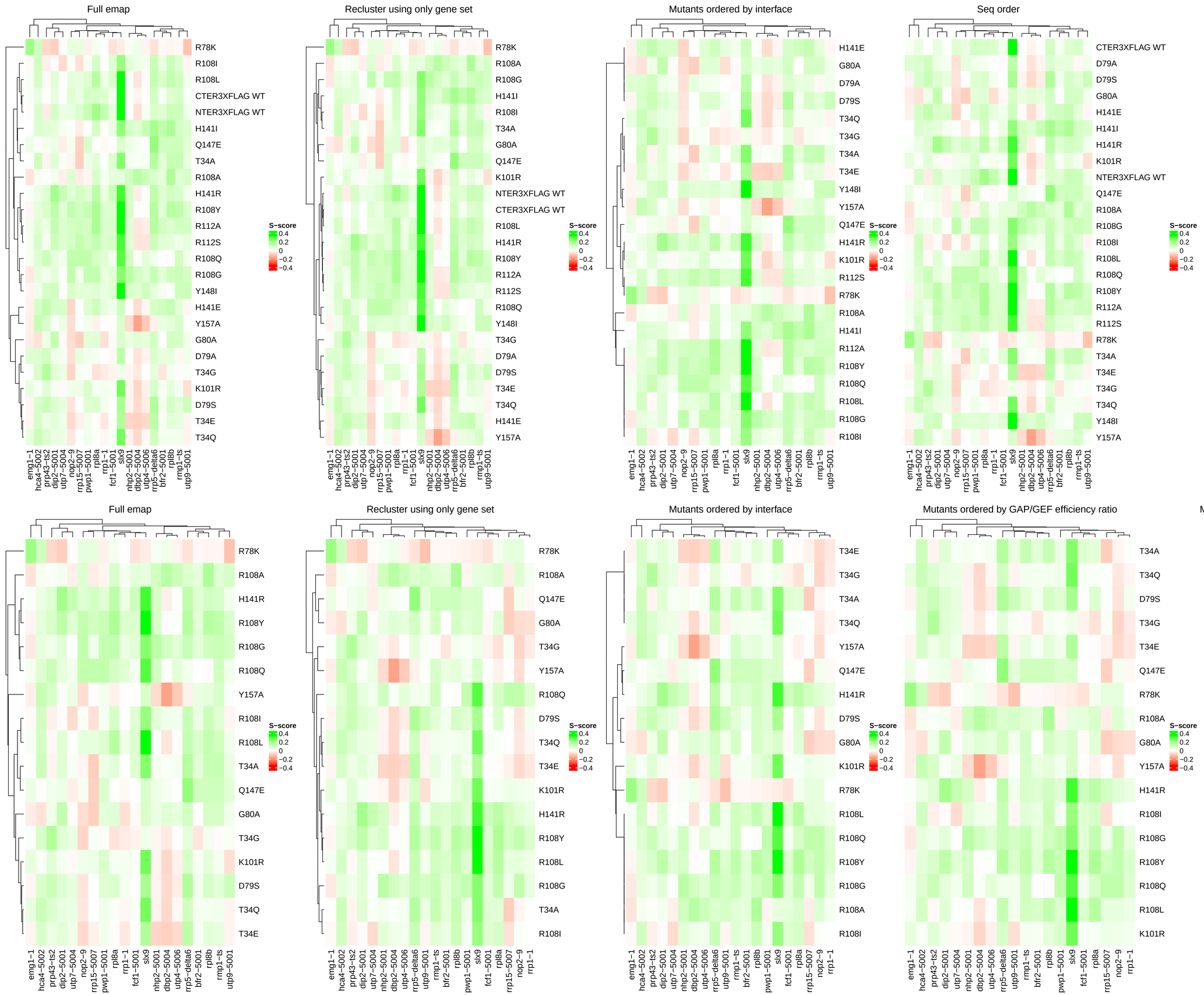


3' end mRNA processing
tina hand−curated processes
clustering metric: pearson

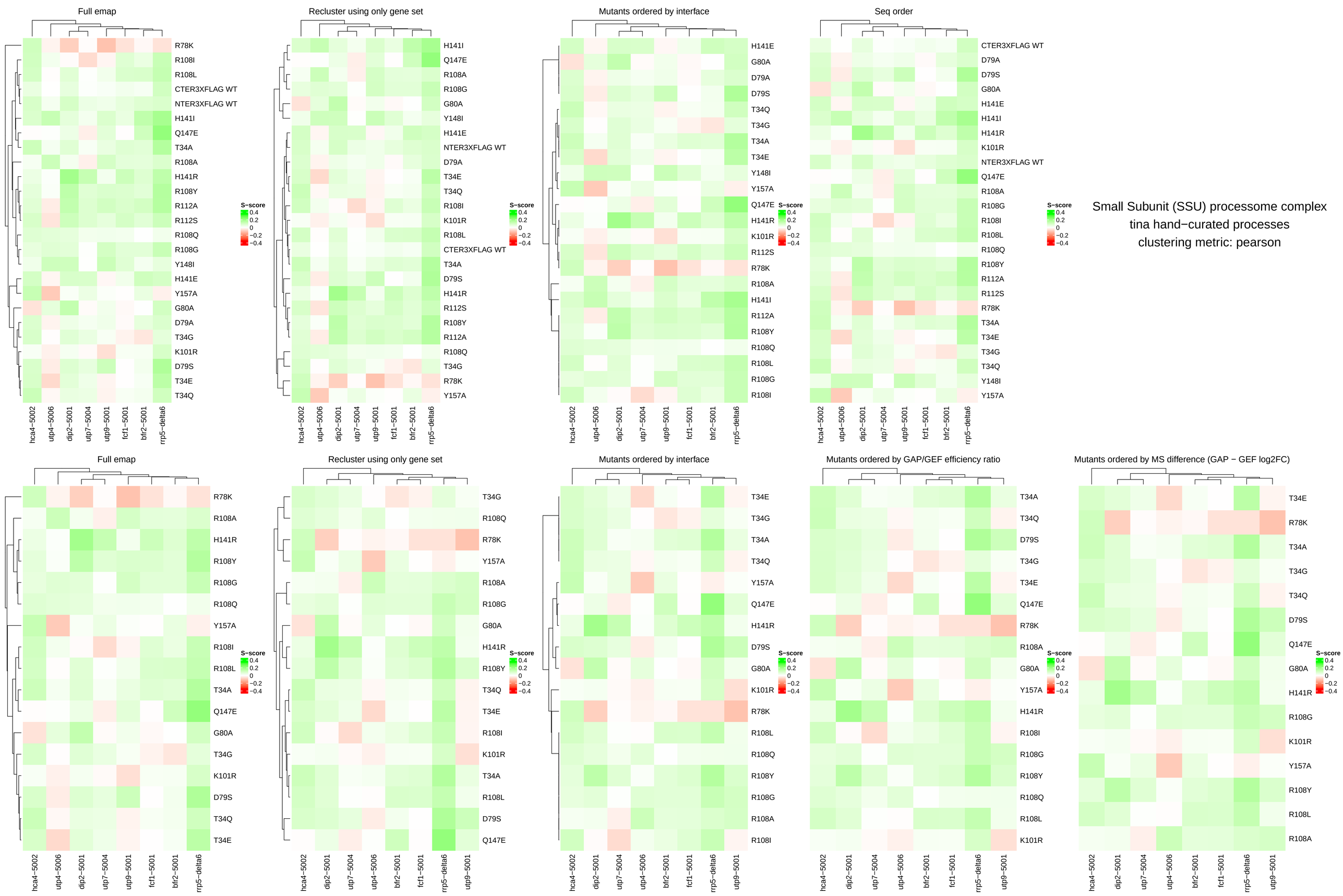


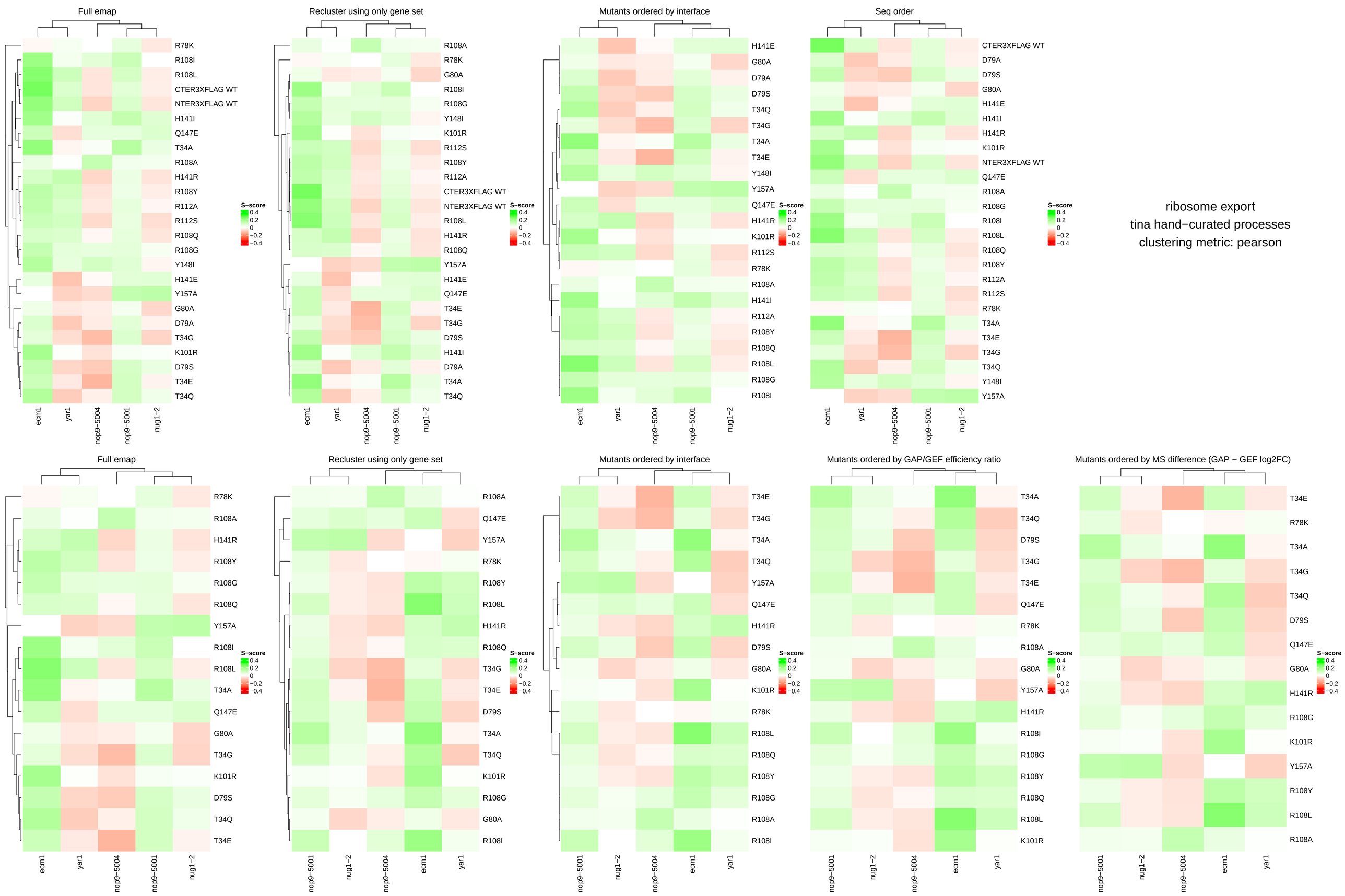
mRNA maturation
tina hand−curated processes
clustering metric: pearson

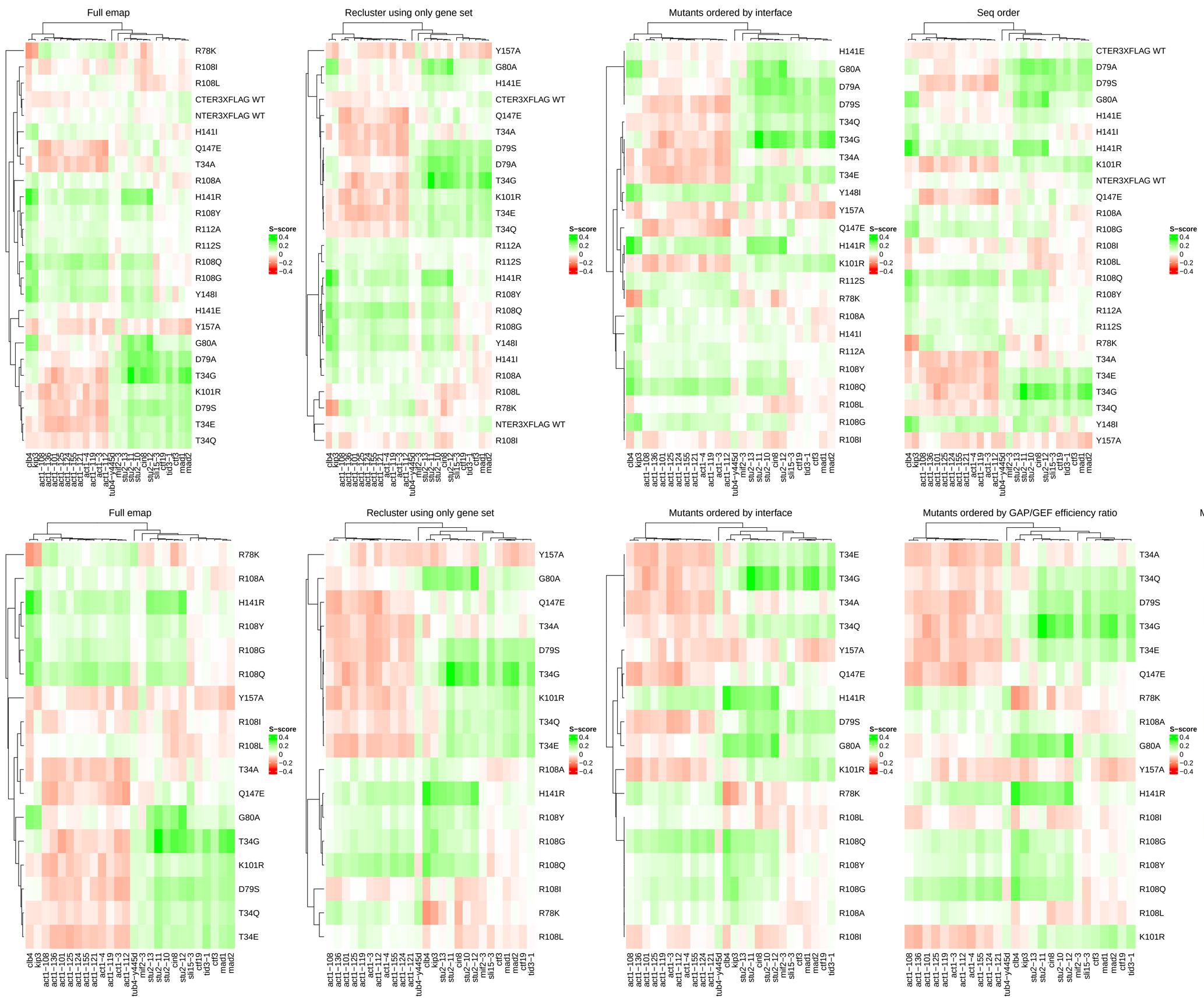

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
jji1
tma23
mak21−1
pwp1−5001
tor1
kap123
rrp5−delta6
ribosome biogenesis
tina hand−curated processes
clustering metric: pearson



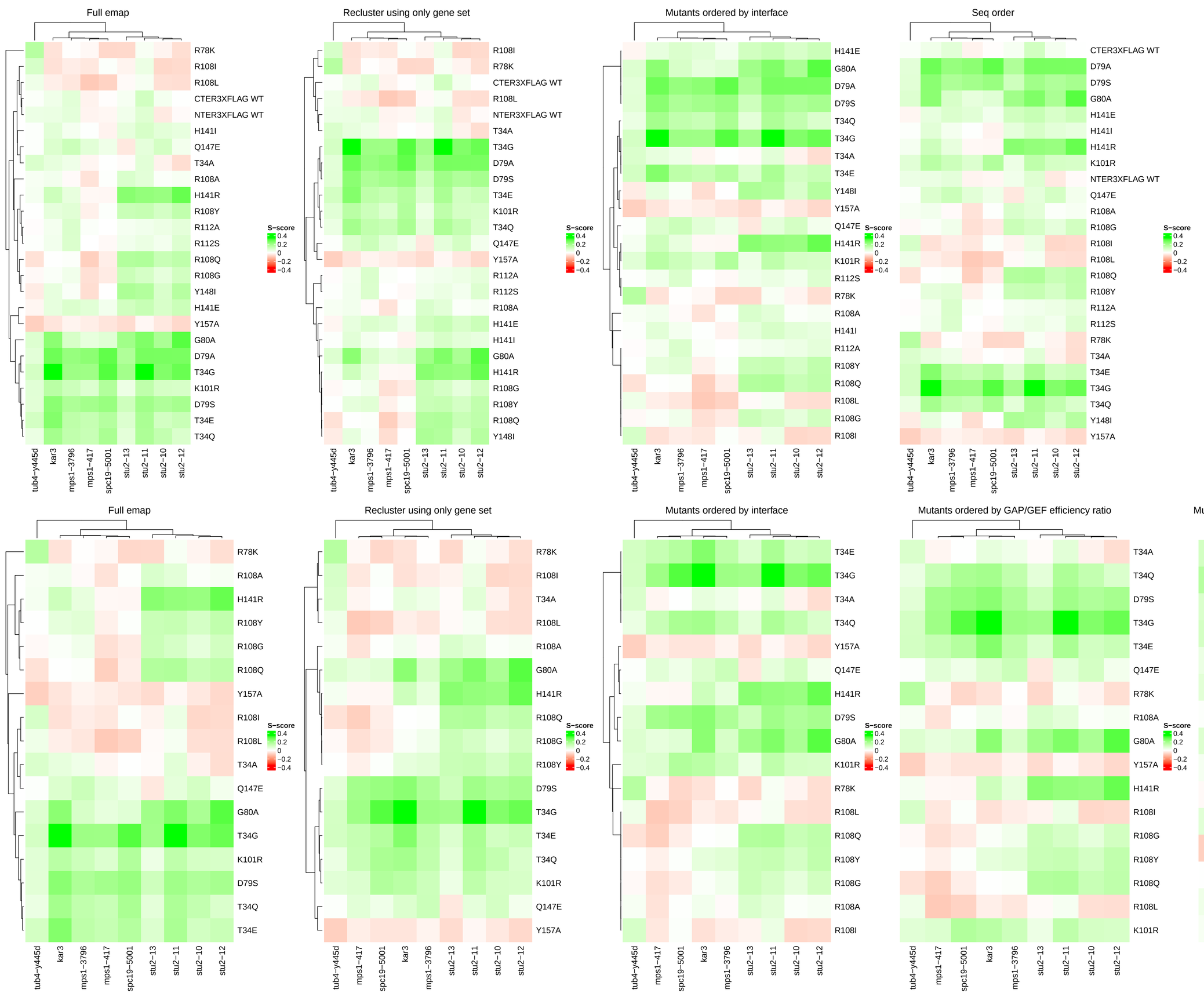
rRNA processing
tina hand−curated processes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
hca4−5002
utp4−5006
dip2−5001
utp7−5004
utp9−5001
fcf1−5001
bfr2−5001
rrp5−delta6
Small Subunit (SSU) processome complex
tina hand−curated processes
clustering metric: pearson

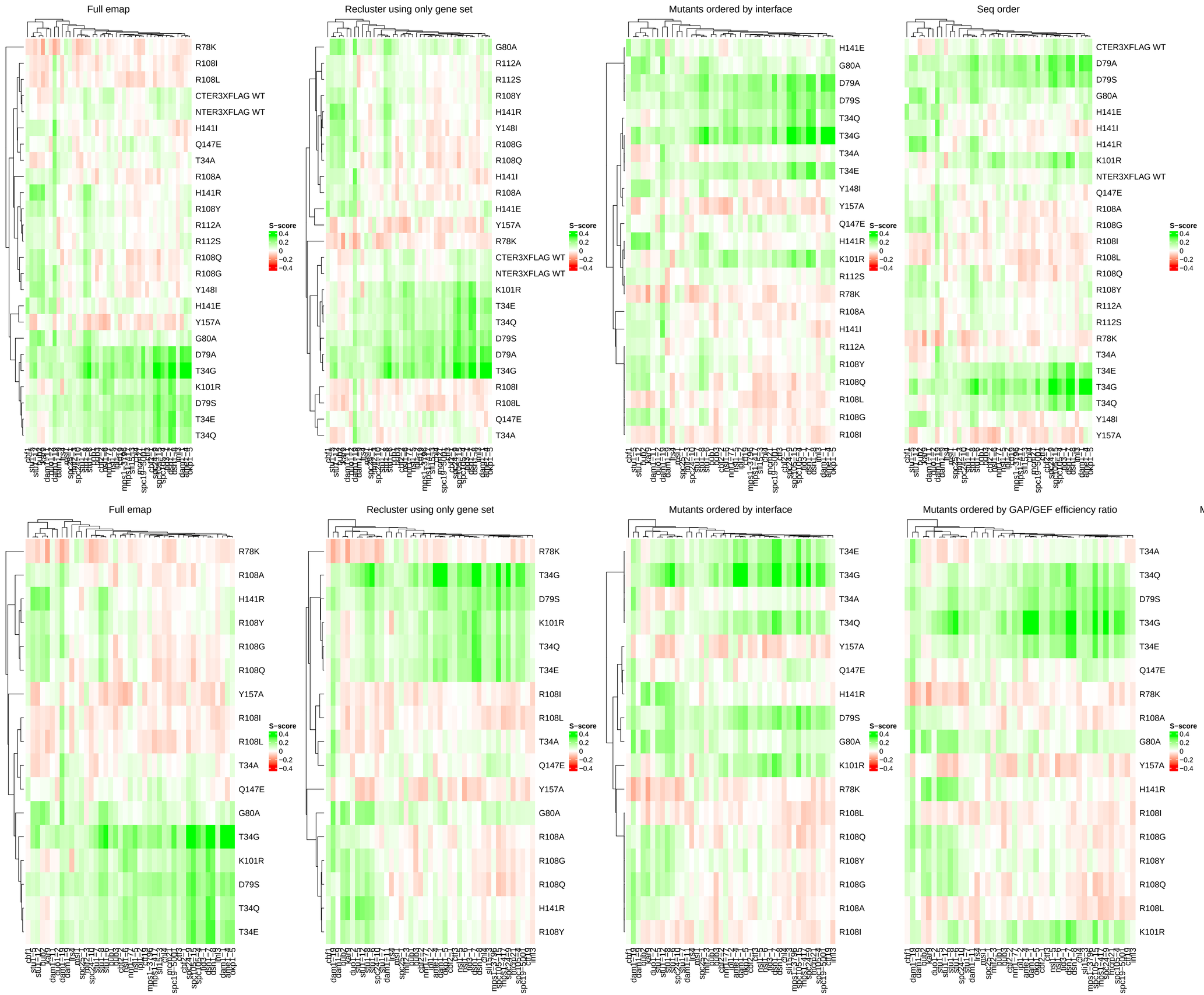

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ecm1
yar1
nop9−5004
nop9−5001
nug1−2
ribosome export
tina hand−curated processes
clustering metric: pearson



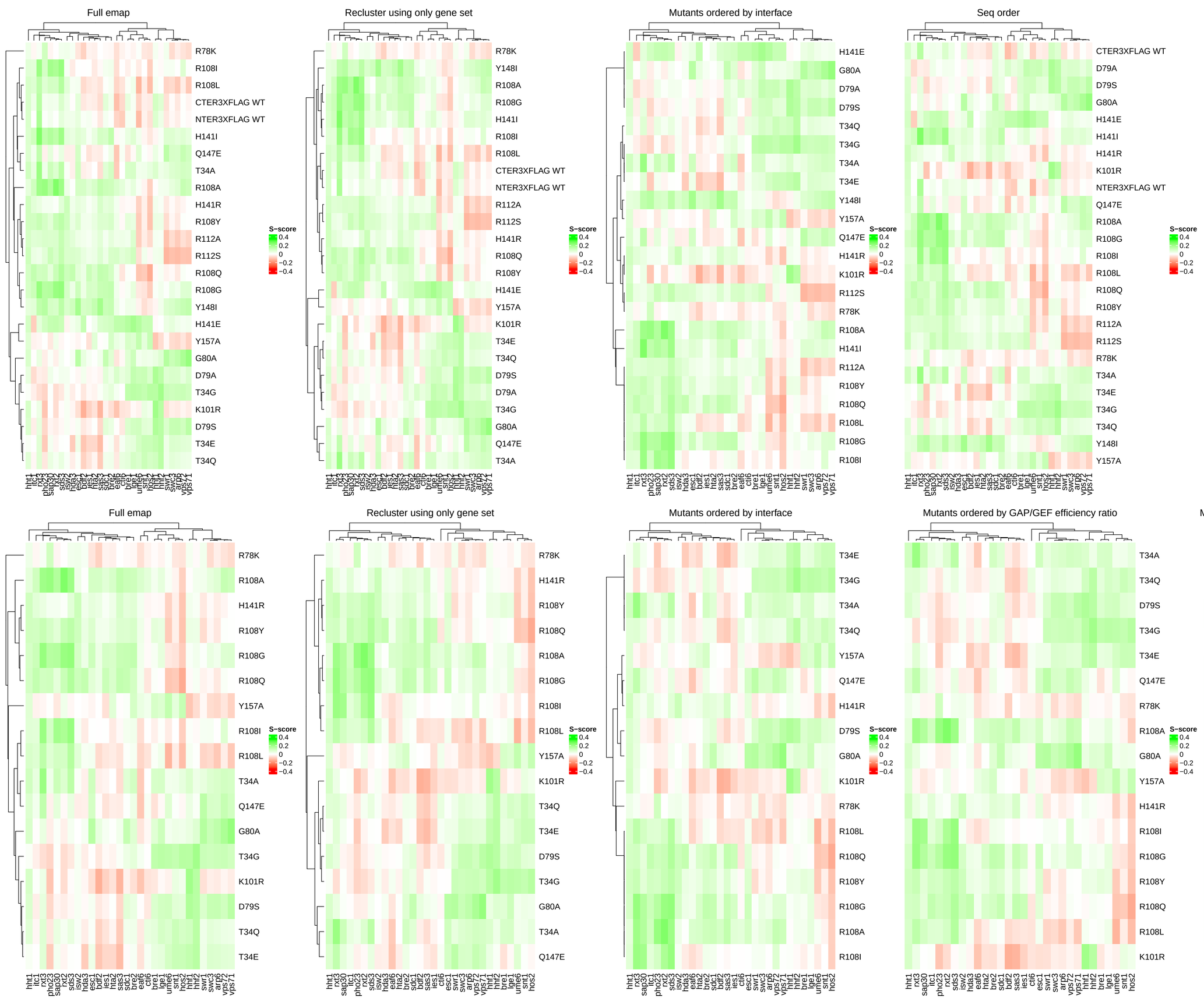
spindle assembly
tina hand−curated processes
clustering metric: pearson



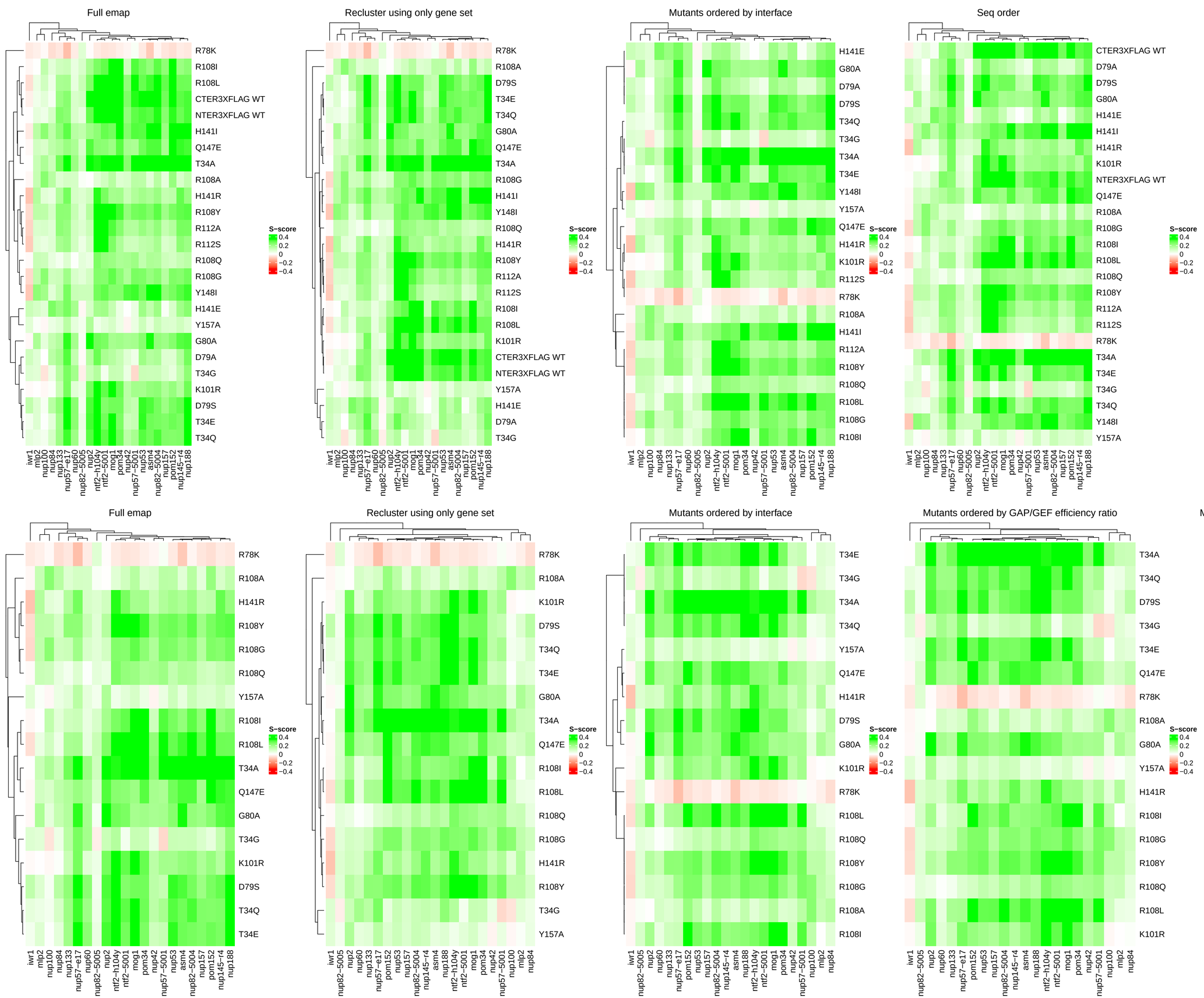
spindle pole body
tina hand−curated processes
clustering metric: pearson



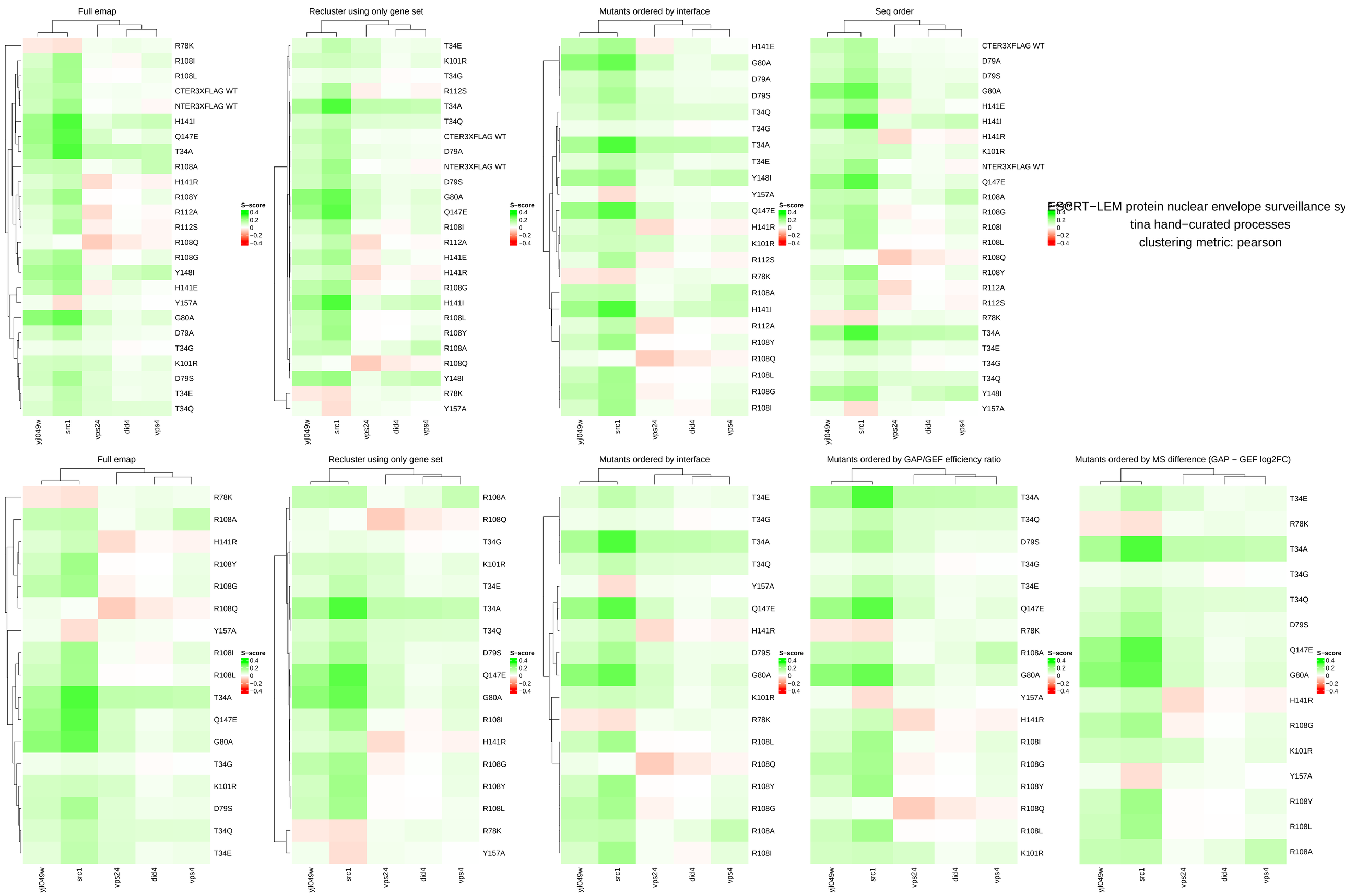
kinetochore
tina hand−curated processes
clustering metric: pearson

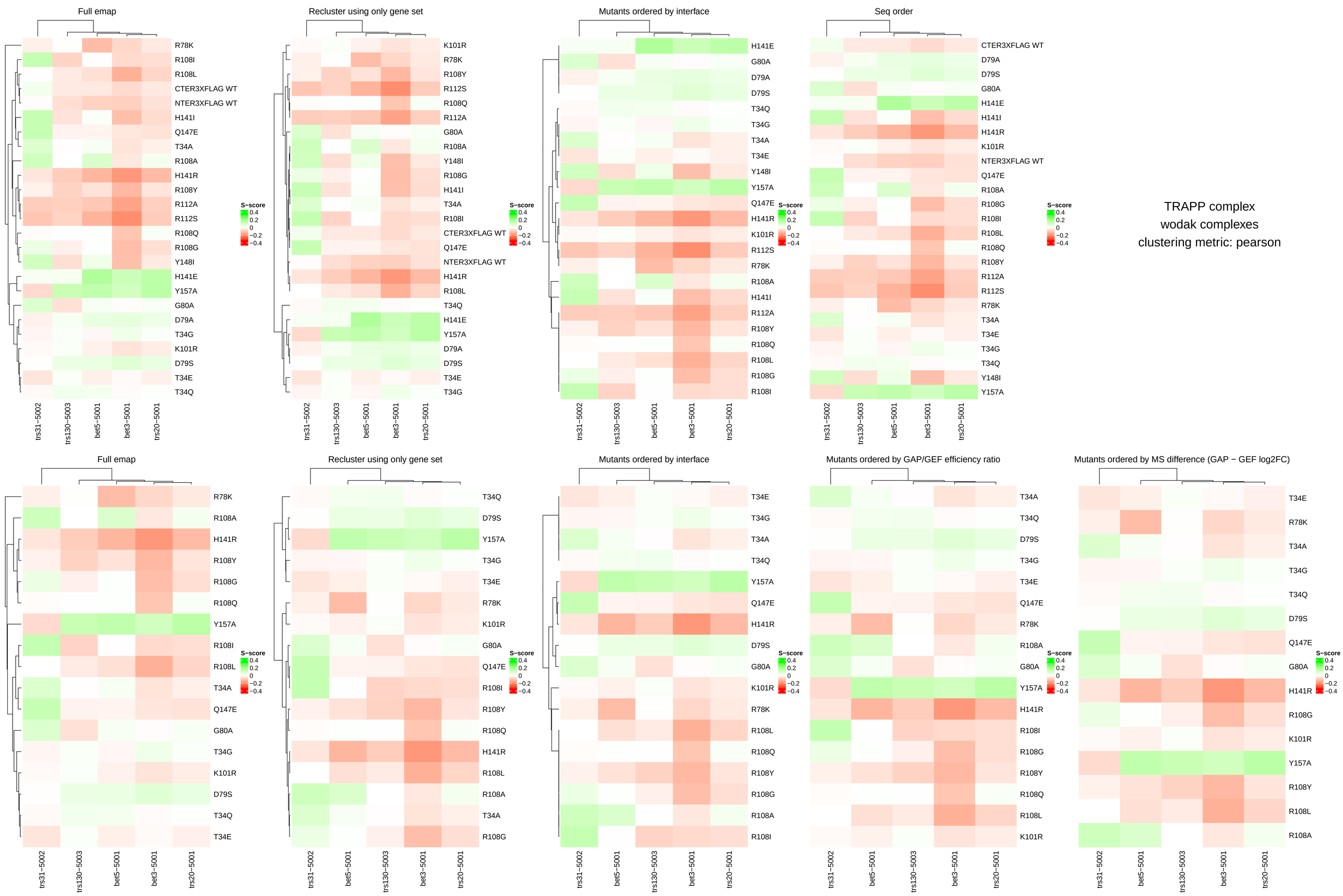


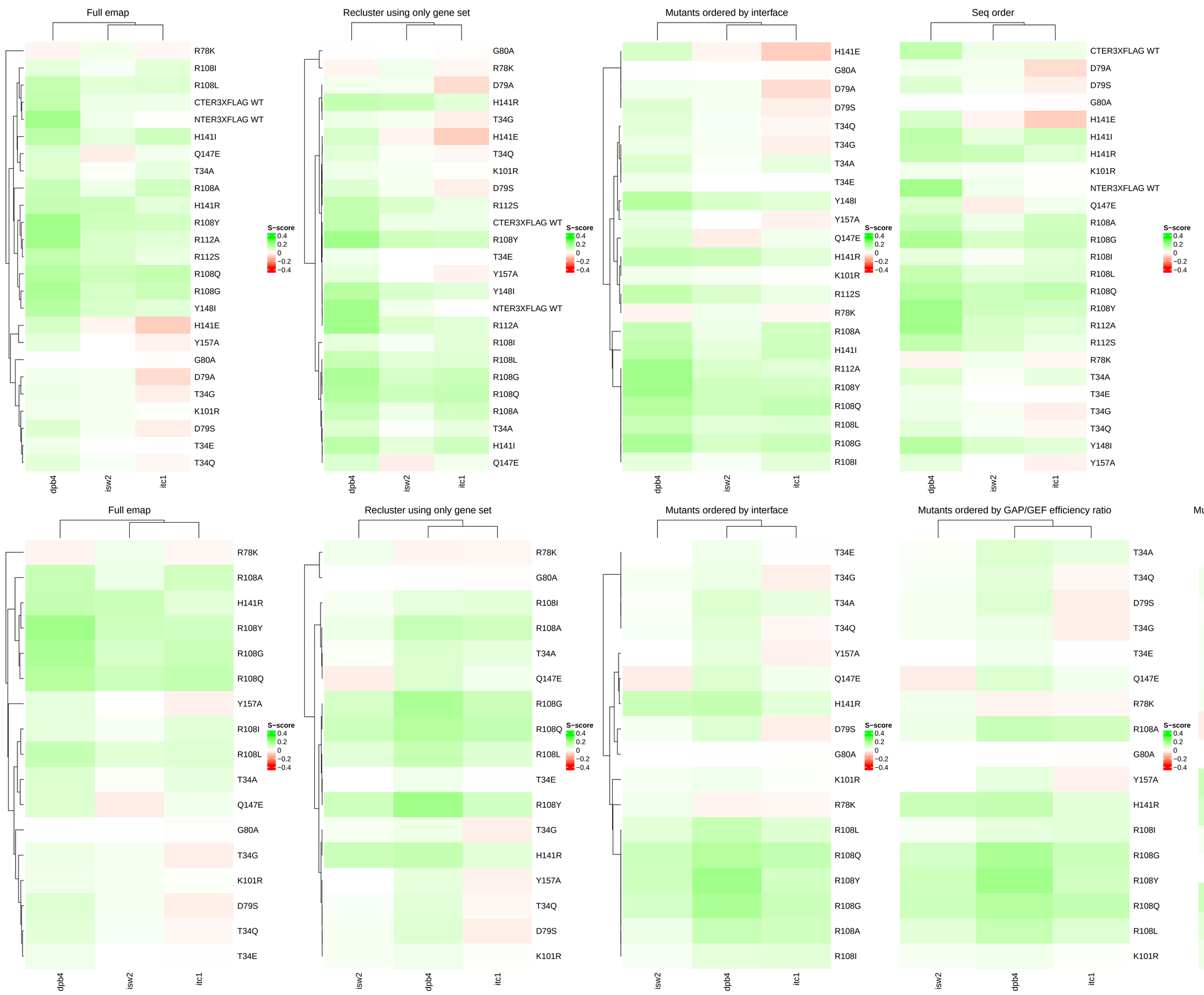
chromatin remodeling
tina hand−curated processes
clustering metric: pearson



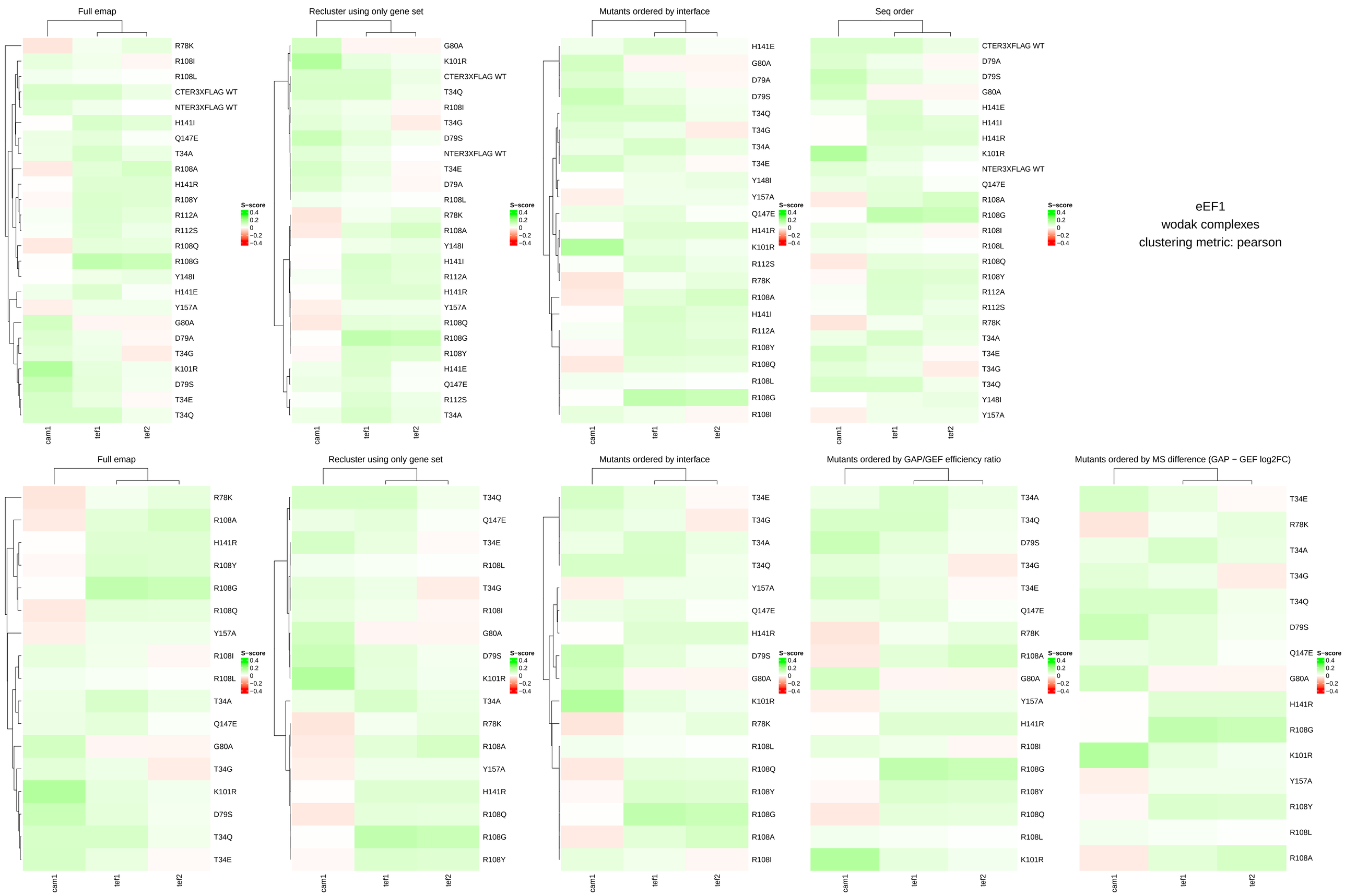
nucleocytoplasmic transport
tina hand−curated processes
clustering metric: pearson

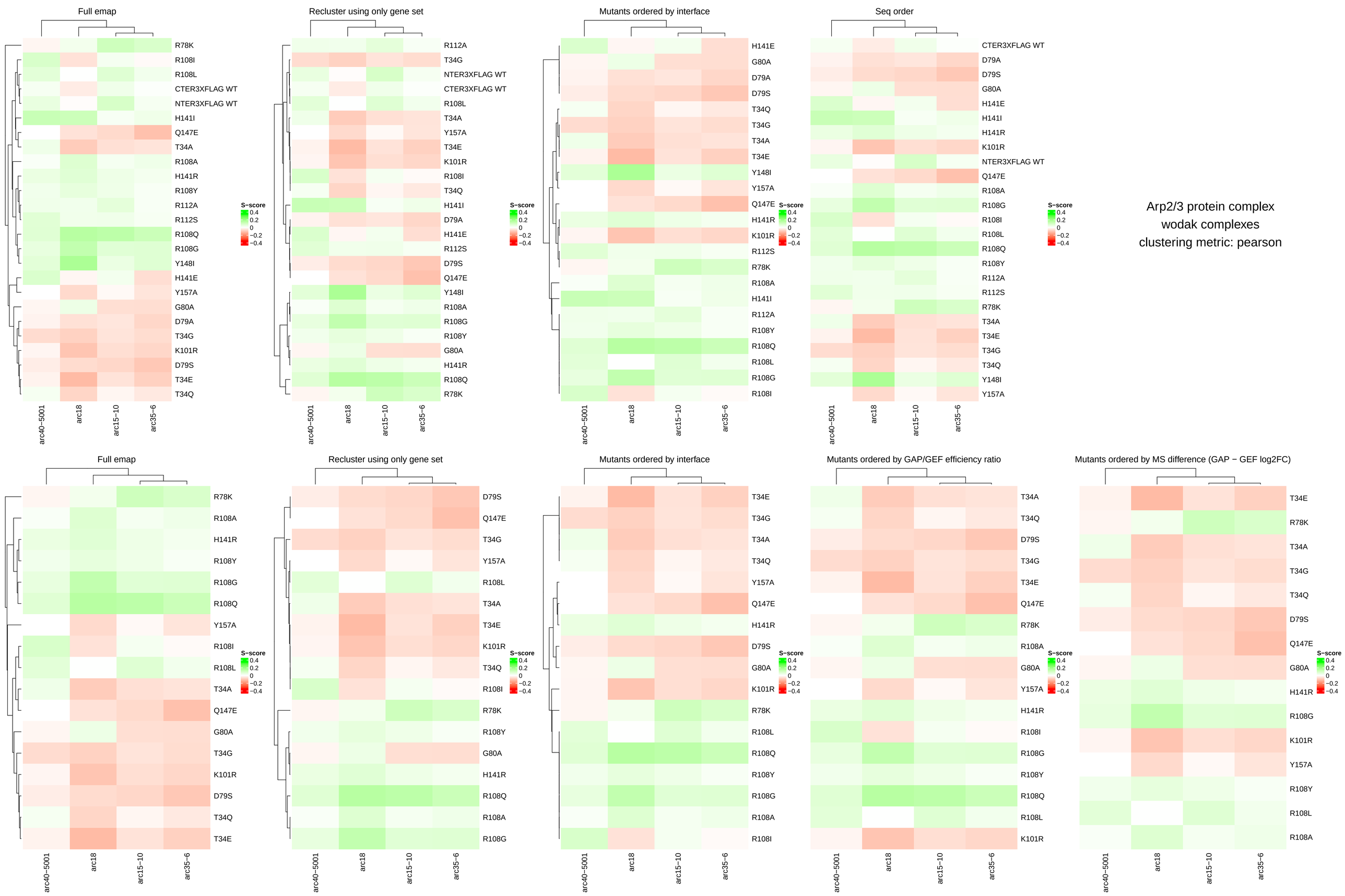

ESCRT−LEM protein nuclear envelope surveillance sy
tina hand−curated processes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
yjl049w
src1
vps24
did4
vps4


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
trs31−5002
trs130−5003
bet5−5001
bet3−5001
trs20−5001
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
K101R
R78K
R108Y
R112S
R108Q
R112A
G80A
R108A
Y148I
R108G
H141I
T34A
R108I
CTER3XFLAG WT
Q147E
NTER3XFLAG WT
H141R
R108L
T34Q
H141E
Y157A
D79A
D79S
T34E
T34G
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
TRAPP complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34Q
D79S
Y157A
T34G
T34E
R78K
K101R
G80A
Q147E
R108I
R108Y
R108Q
H141R
R108L
R108A
T34A
R108G
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

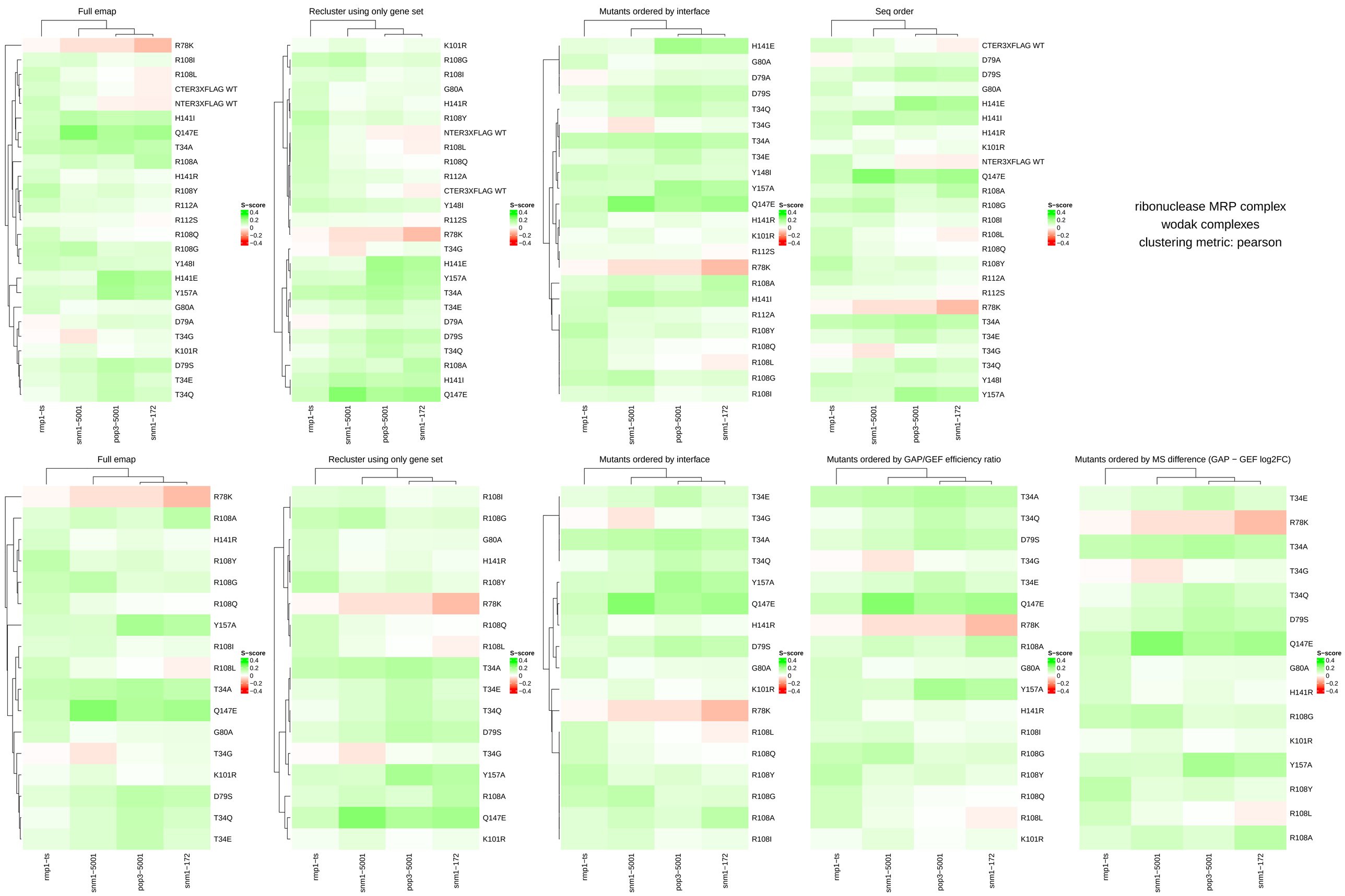


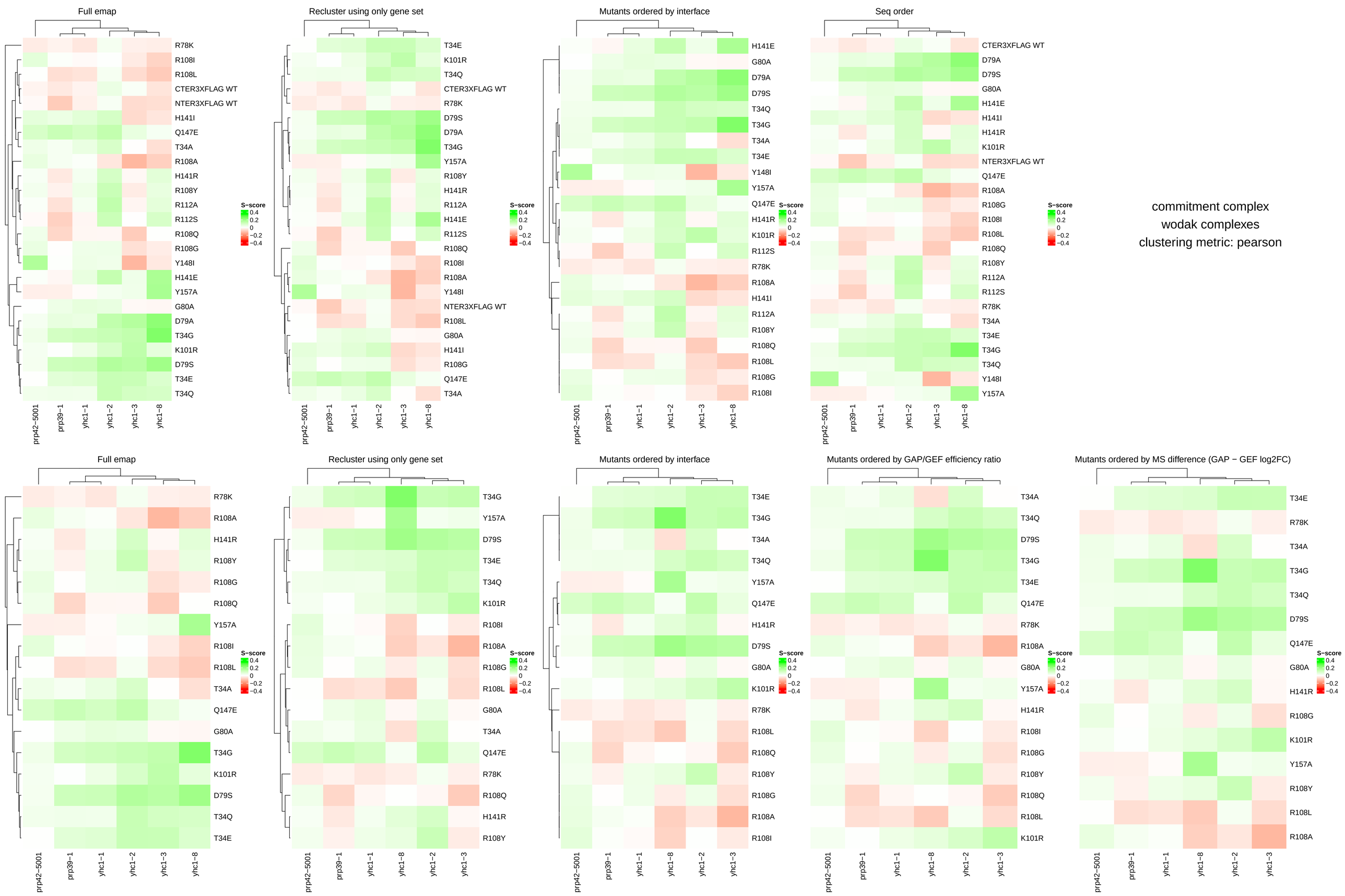
chromatin accessibility complex
wodak complexes
clustering metric: pearson


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
cam1
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
G80A
K101R
CTER3XFLAG WT
T34Q
R108I
T34G
D79S
NTER3XFLAG WT
T34E
D79A
R108L
R78K
R108A
Y148I
H141I
R112A
H141R
Y157A
R108Q
R108G
R108Y
H141E
Q147E
R112S
T34A
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
eEF1
wodak complexes
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

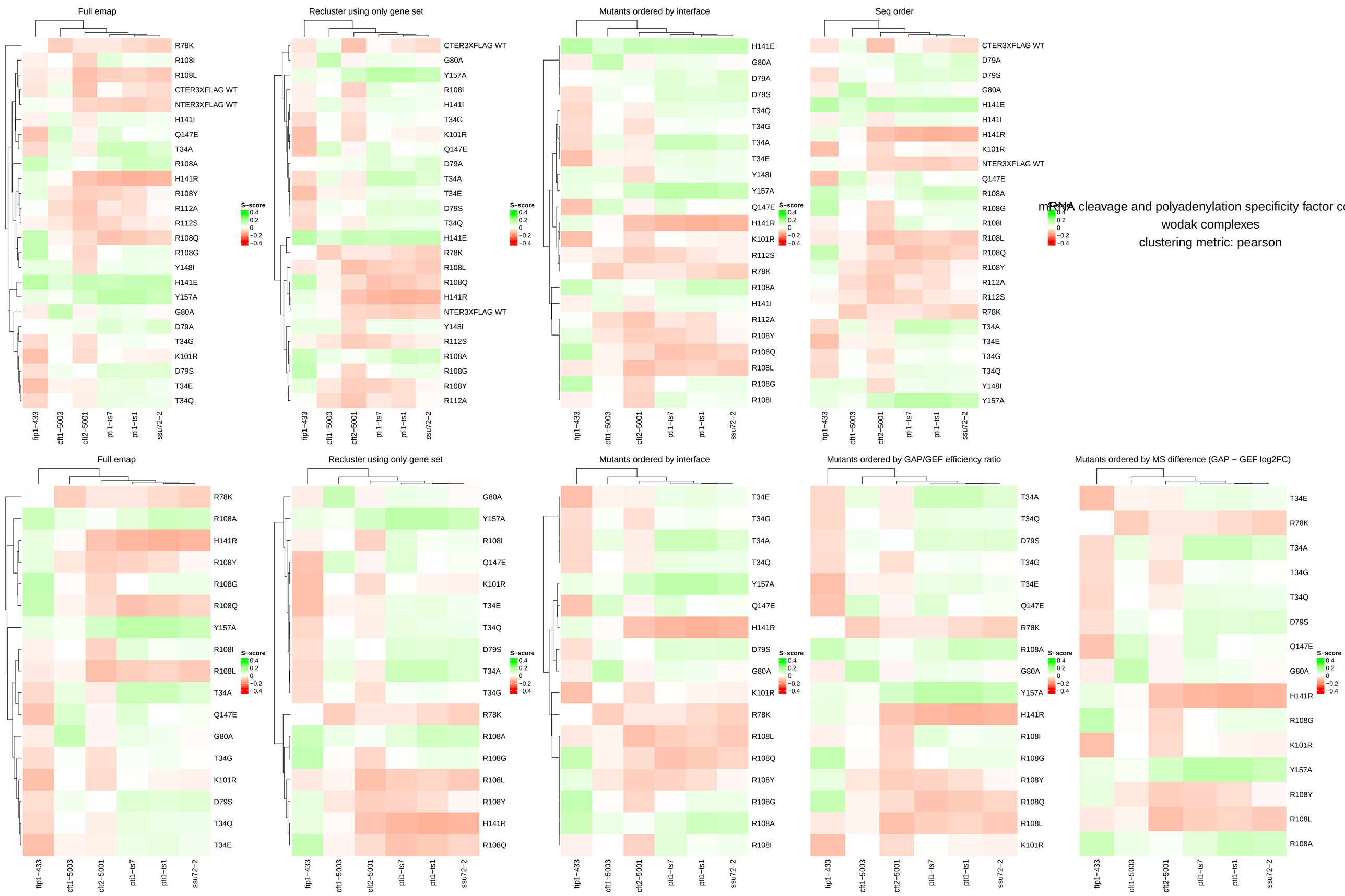


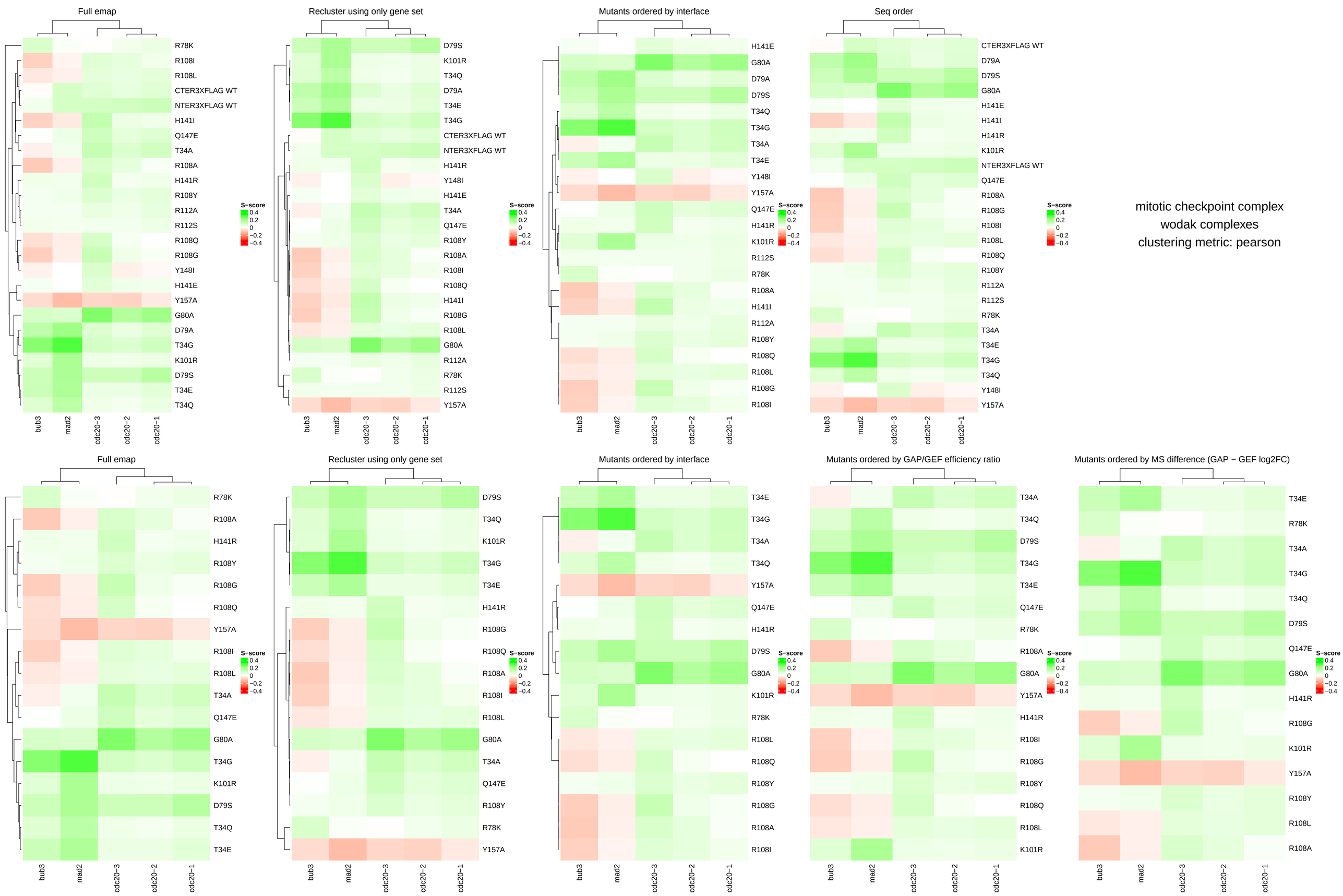
Arp2/3 protein complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
rmp1−ts
snm1−5001
pop3−5001
snm1−172
ribonuclease MRP complex
wodak complexes
clustering metric: pearson

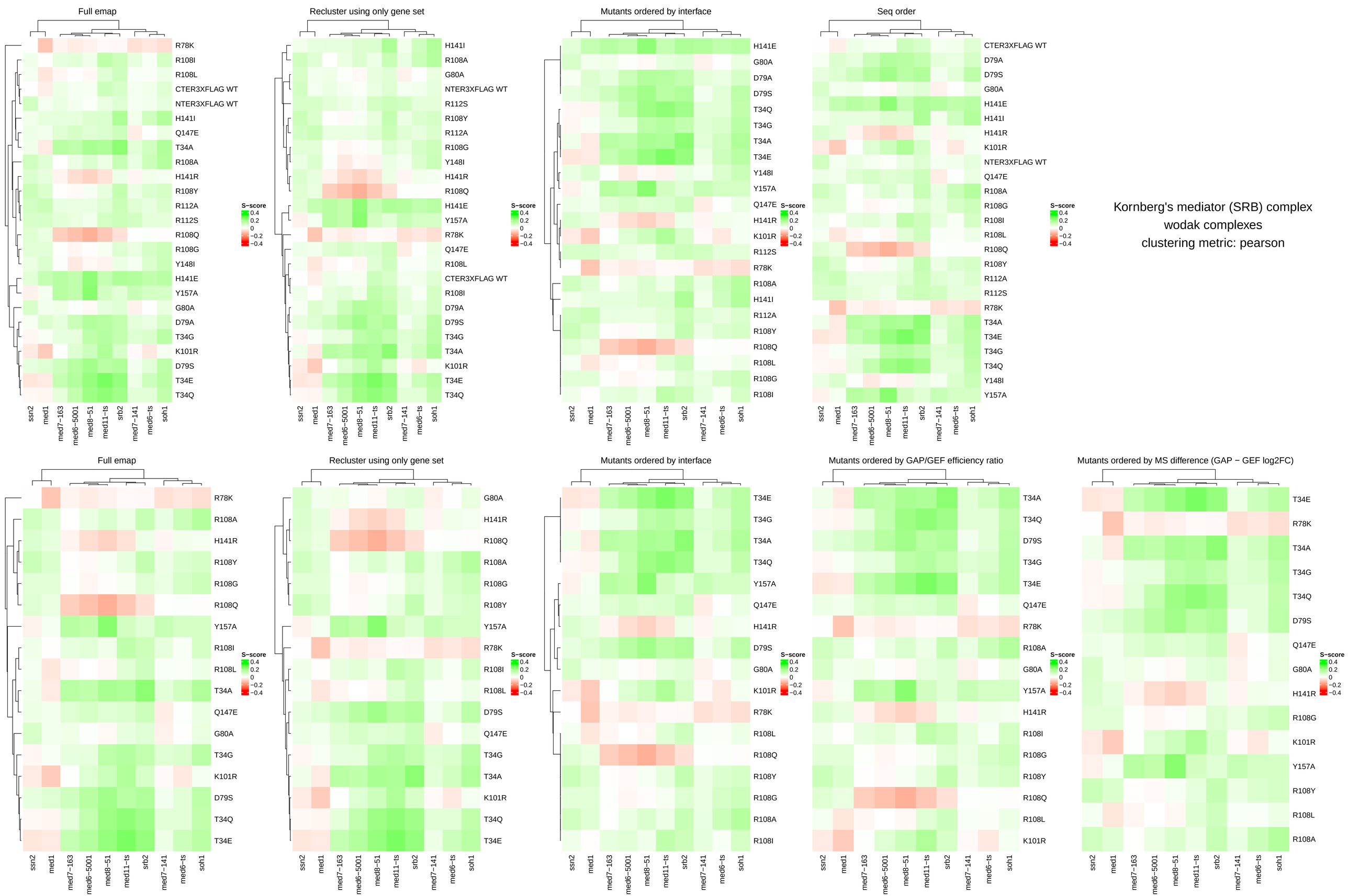

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
prp42−5001
prp39−1
yhc1−1
yhc1−2
yhc1−3
yhc1−8
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
commitment complex
wodak complexes
clustering metric: pearson

mRNA cleavage and polyadenylation specificity factor co
wodak complexes
clustering metric: pearson

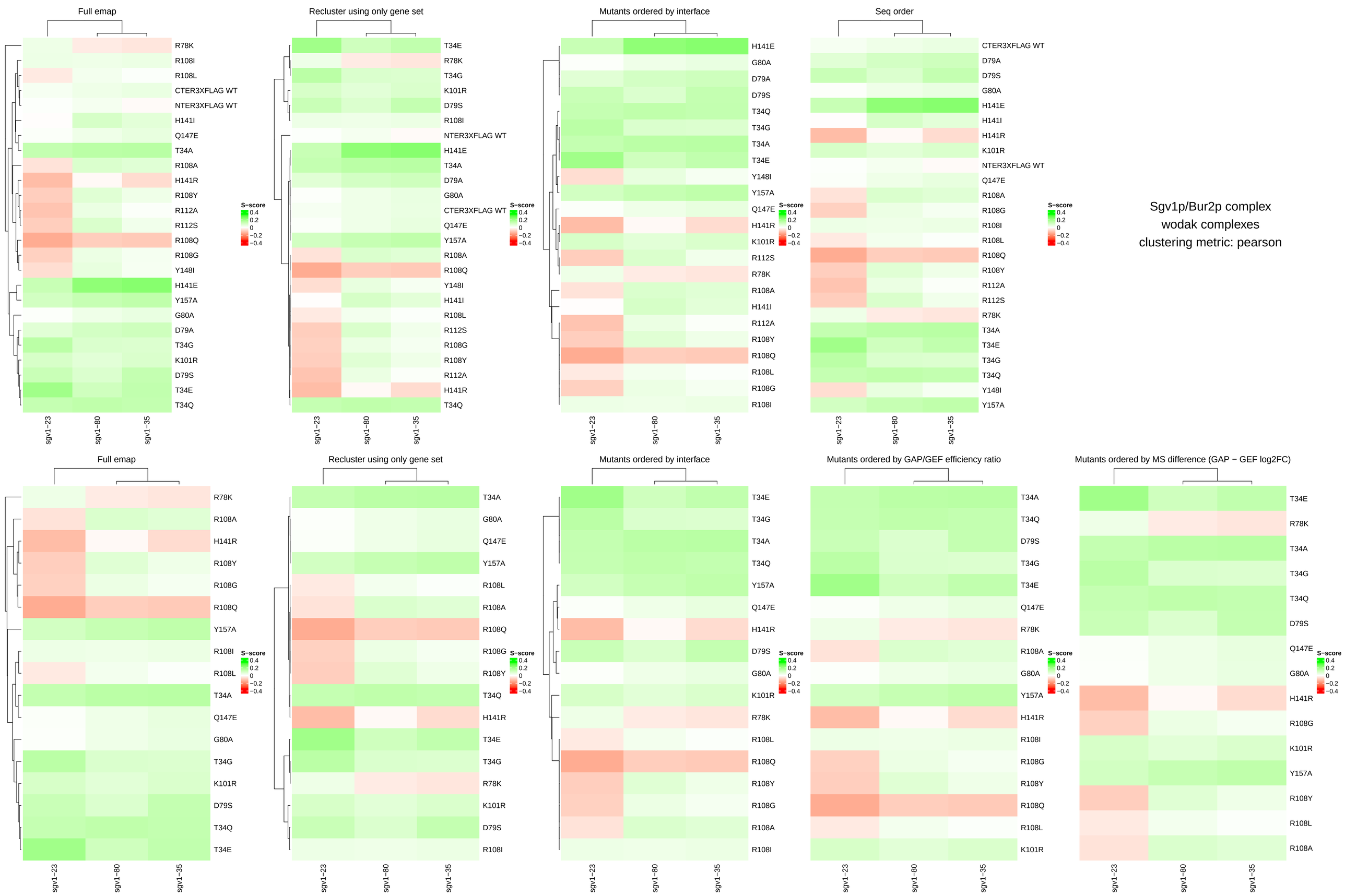


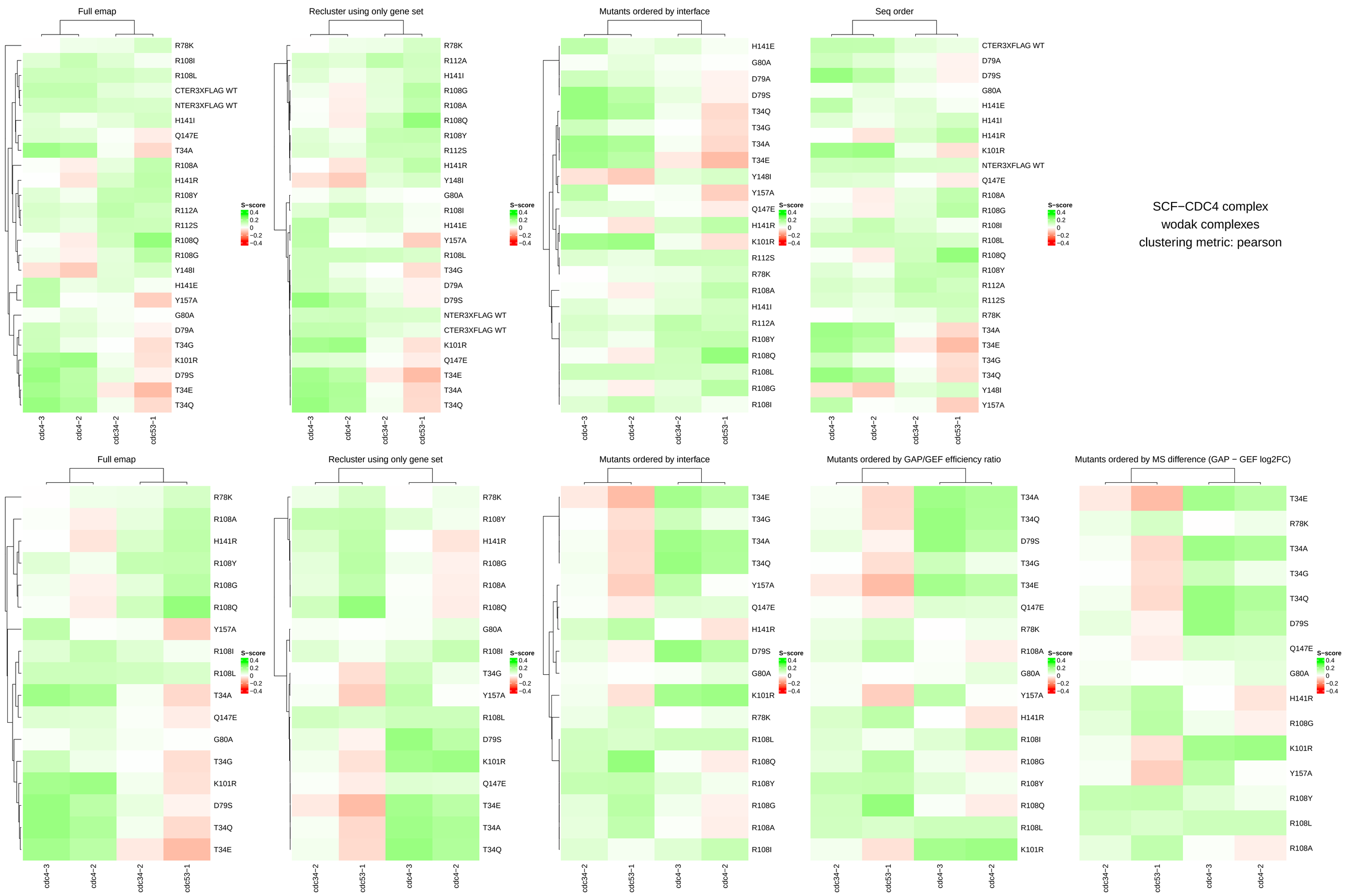

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
bub3
mad2
cdc20−3
cdc20−2
cdc20−1
mitotic checkpoint complex
wodak complexes
clustering metric: pearson

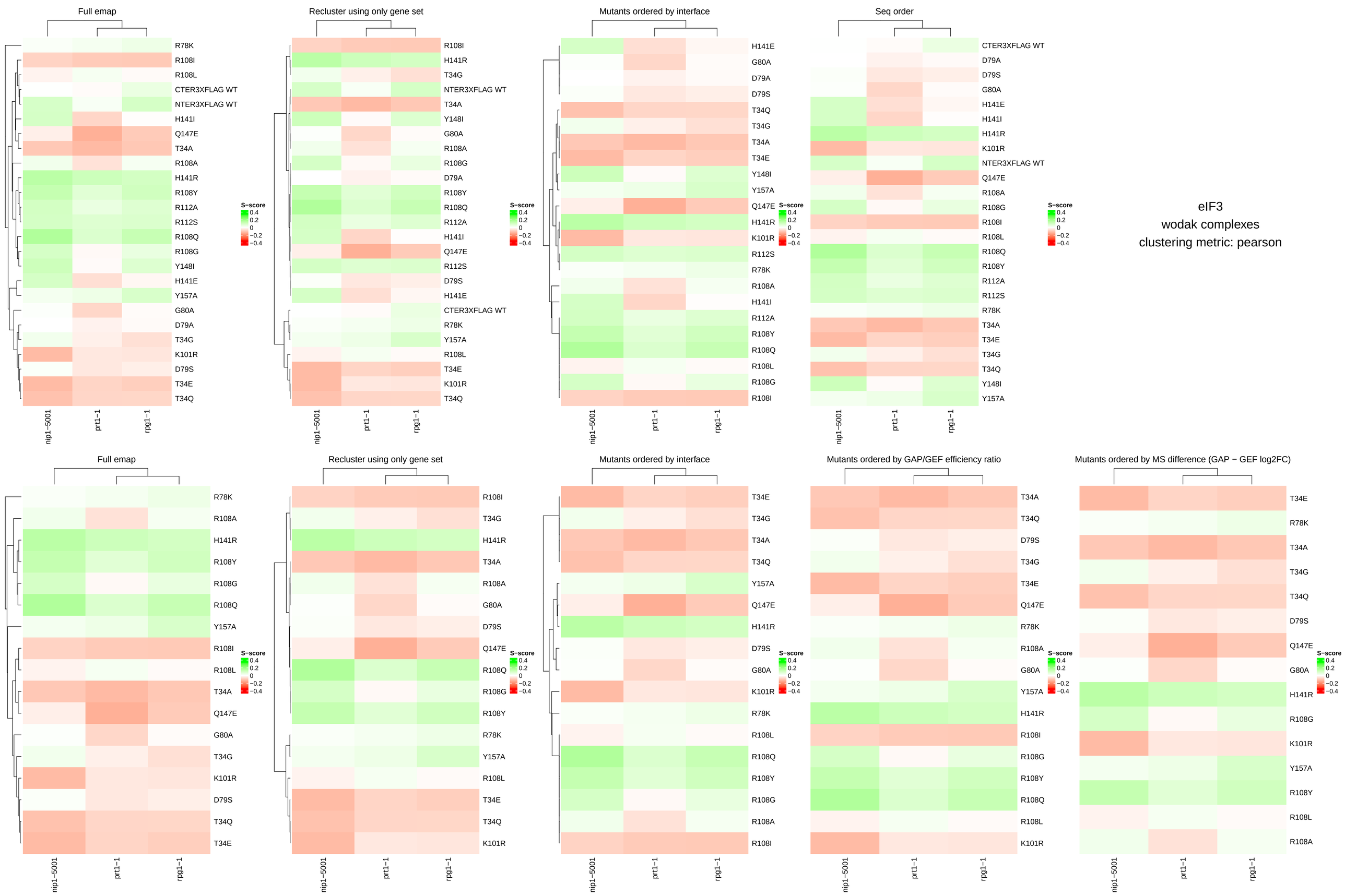
Ino80p complex
wodak complexes
clustering metric: pearson

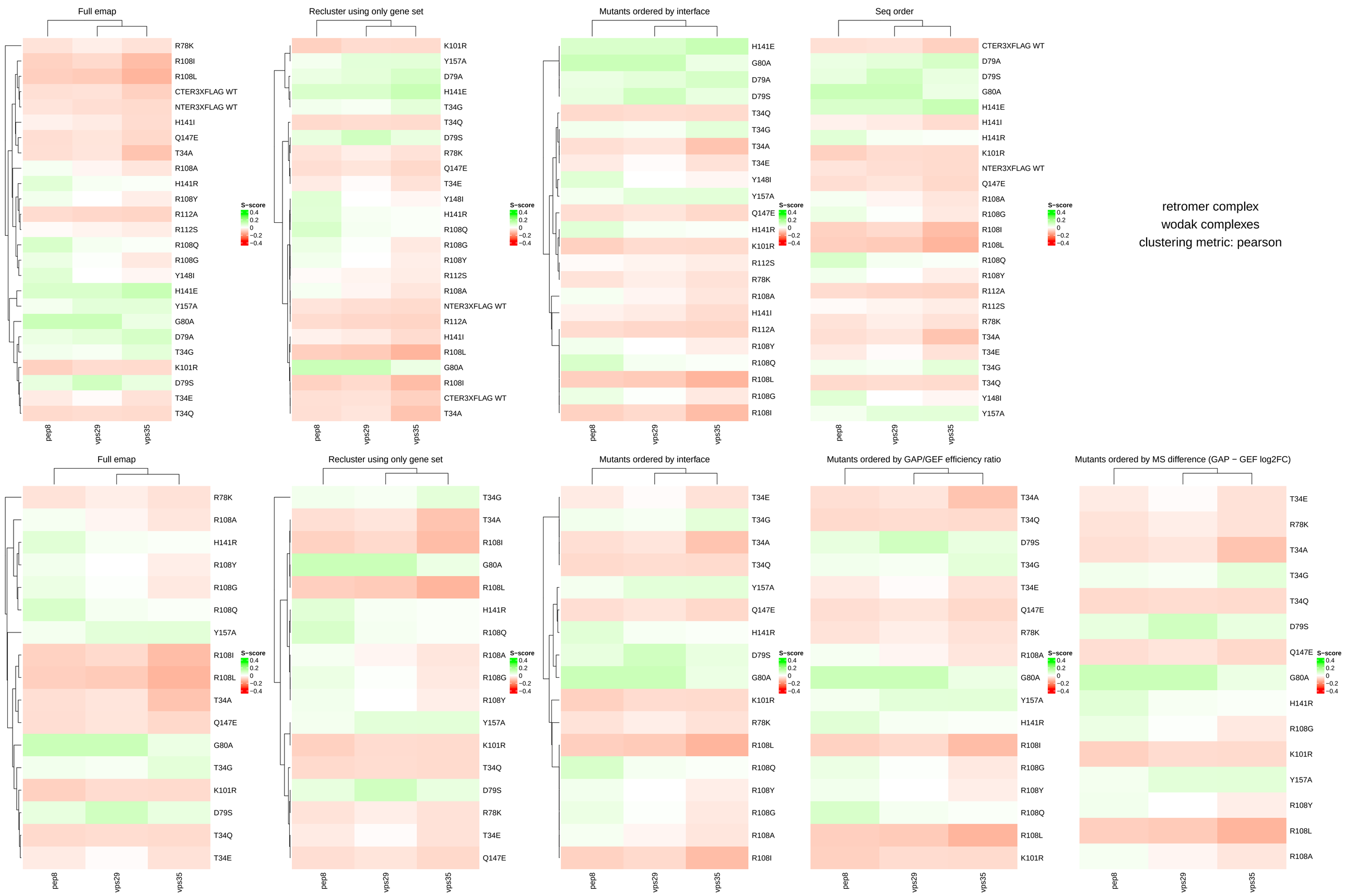


Kornberg's mediator (SRB) complex
wodak complexes
clustering metric: pearson

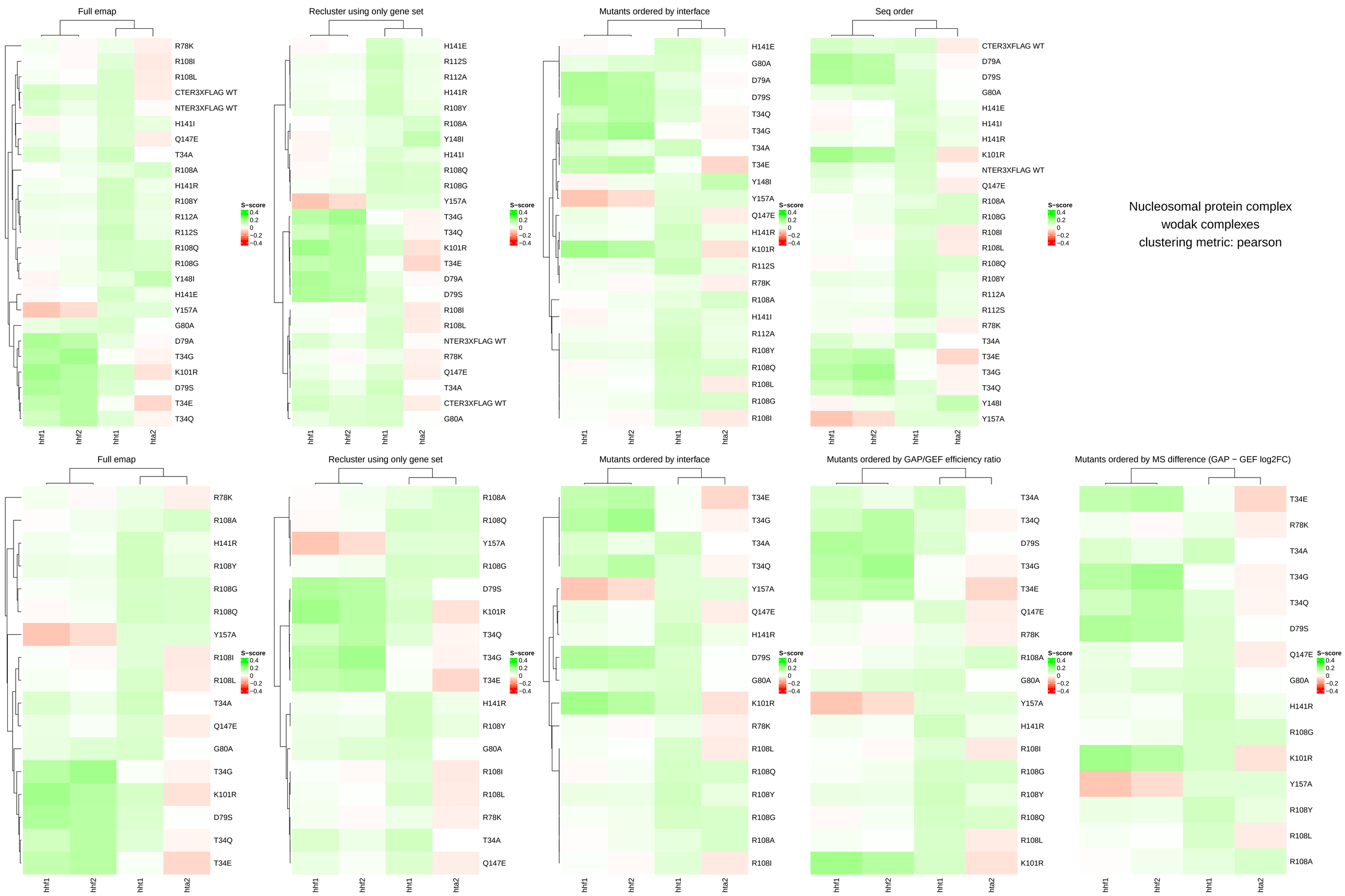

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
sgv1−23
sgv1−80
sgv1−35
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
T34E
R78K
T34G
K101R
D79S
R108I
NTER3XFLAG WT
H141E
T34A
D79A
G80A
CTER3XFLAG WT
Q147E
Y157A
R108A
R108Q
Y148I
H141I
R108L
R112S
R108G
R108Y
R112A
H141R
T34Q
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Sgv1p/Bur2p complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34A
G80A
Q147E
Y157A
R108L
R108A
R108Q
R108G
R108Y
T34Q
H141R
T34E
T34G
R78K
K101R
D79S
R108I
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

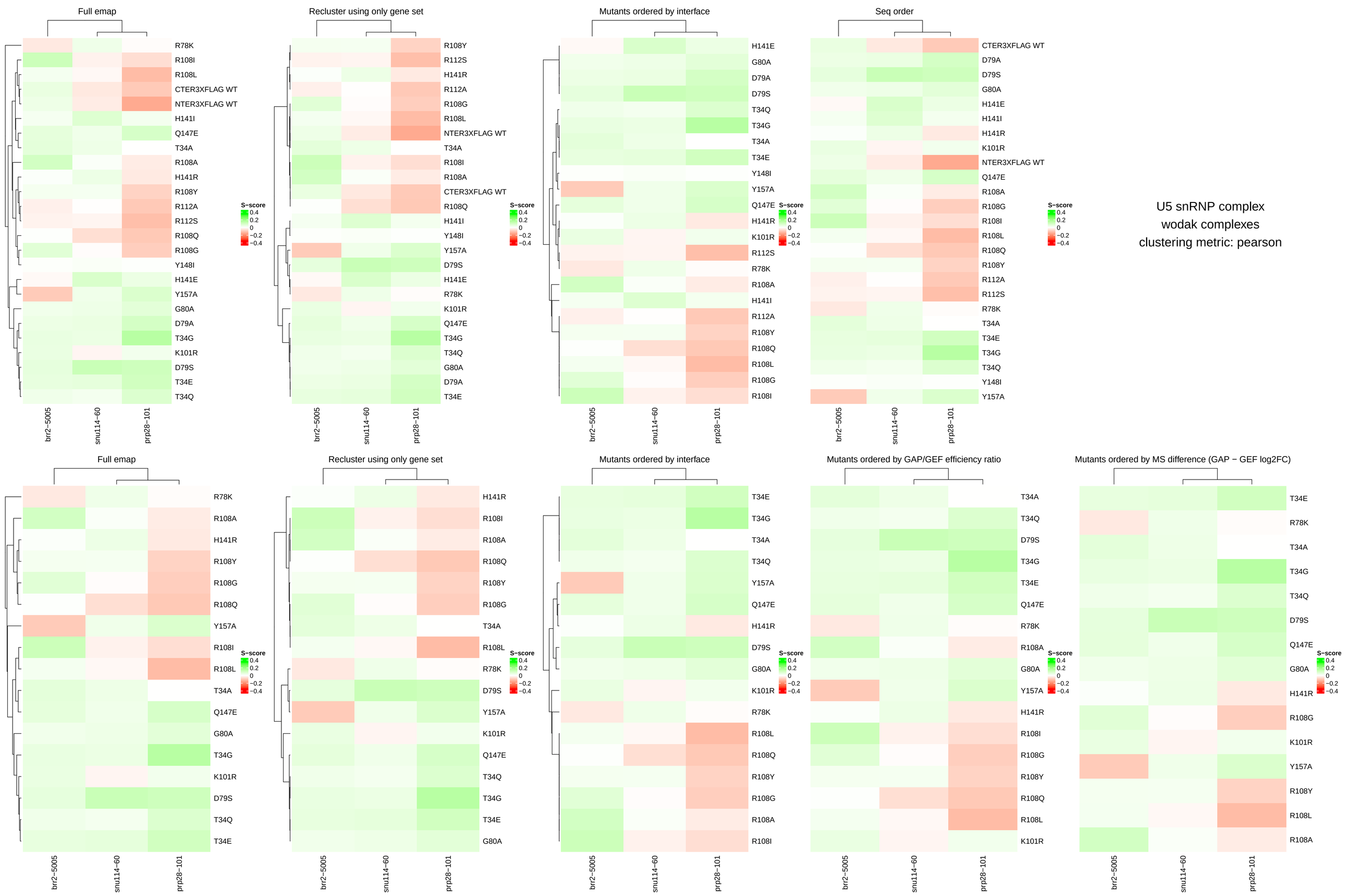

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
cdc4−3
cdc4−2
cdc34−2
cdc53−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R78K
R112A
H141I
R108G
R108A
R108Q
R108Y
R112S
H141R
Y148I
G80A
R108I
H141E
Y157A
R108L
T34G
D79A
D79S
NTER3XFLAG WT
CTER3XFLAG WT
K101R
Q147E
T34E
T34A
T34Q
cdc4−3
cdc4−2
cdc34−2
cdc53−1
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
cdc4−3
cdc4−2
cdc34−2
cdc53−1
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
cdc4−3
cdc4−2
cdc34−2
cdc53−1
SCF−CDC4 complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
cdc4−3
cdc4−2
cdc34−2
cdc53−1
Recluster using only gene set
R78K
R108Y
H141R
R108G
R108A
R108Q
G80A
R108I
T34G
Y157A
R108L
D79S
K101R
Q147E
T34E
T34A
T34Q
cdc34−2
cdc53−1
cdc4−3
cdc4−2
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
cdc34−2
cdc53−1
cdc4−3
cdc4−2
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
cdc34−2
cdc53−1
cdc4−3
cdc4−2
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A
cdc34−2
cdc53−1
cdc4−3
cdc4−2

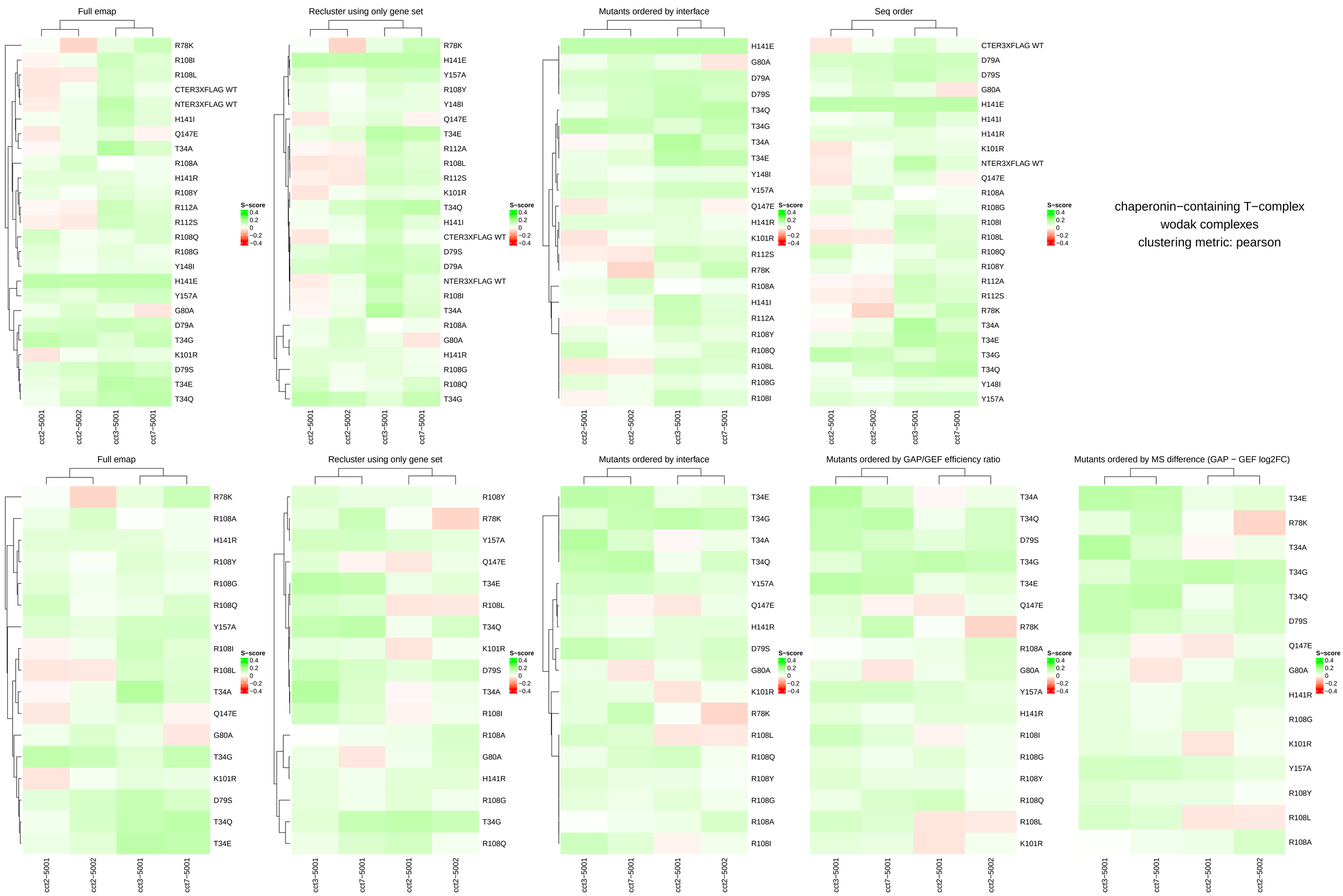

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
nip1−5001
prt1−1
rpg1−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108I
H141R
T34G
NTER3XFLAG WT
T34A
Y148I
G80A
R108A
R108G
D79A
R108Y
R108Q
R112A
H141I
Q147E
R112S
D79S
H141E
CTER3XFLAG WT
R78K
Y157A
R108L
T34E
K101R
T34Q
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
eIF3
wodak complexes
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

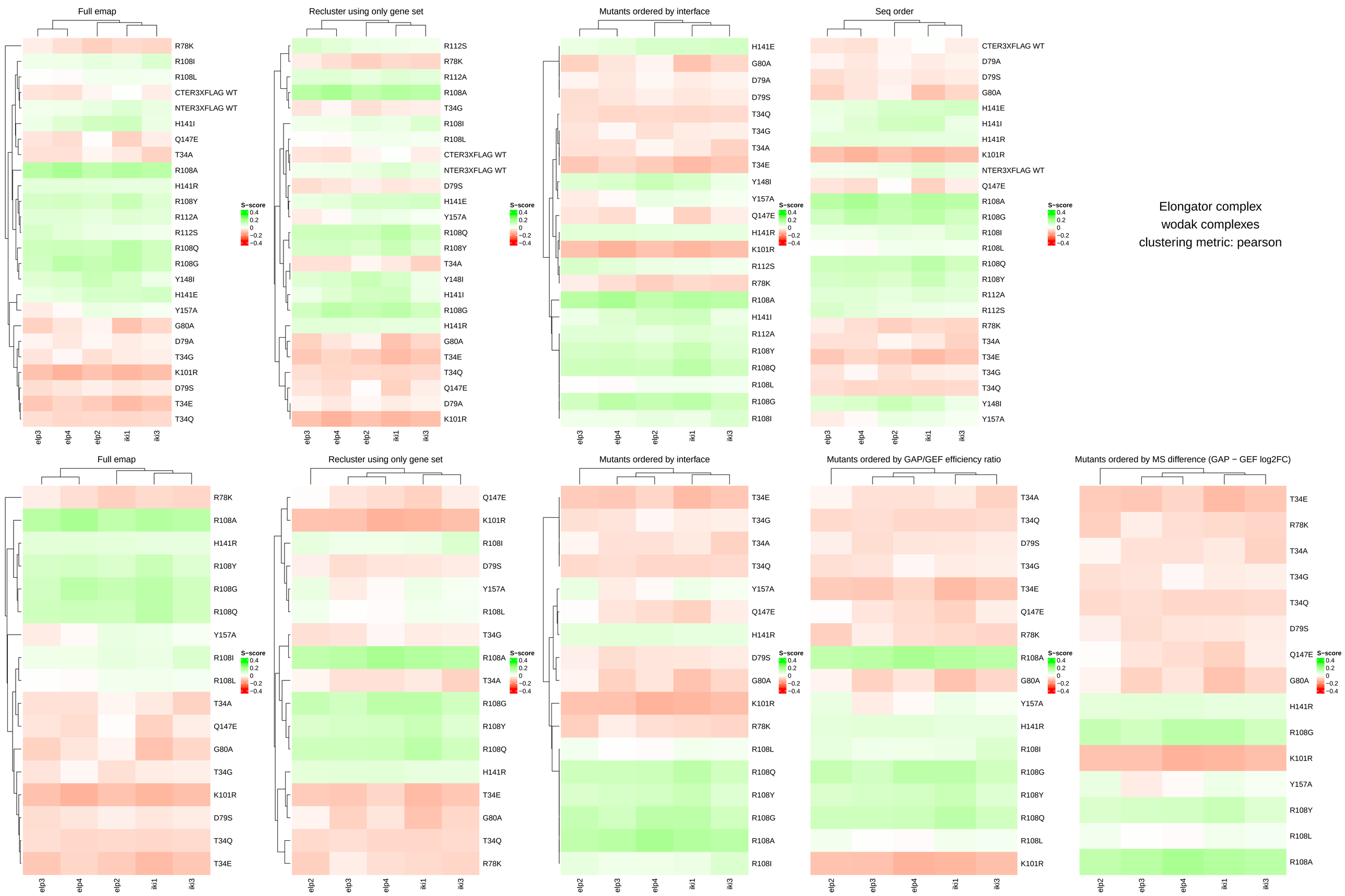

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
pep8
vps29
vps35
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
K101R
Y157A
D79A
H141E
T34G
T34Q
D79S
R78K
Q147E
T34E
Y148I
H141R
R108Q
R108G
R108Y
R112S
R108A
NTER3XFLAG WT
R112A
H141I
R108L
G80A
R108I
CTER3XFLAG WT
T34A
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
retromer complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34G
T34A
R108I
G80A
R108L
H141R
R108Q
R108A
R108G
R108Y
Y157A
K101R
T34Q
D79S
R78K
T34E
Q147E
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

Golgi transport complex
wodak complexes
clustering metric: pearson

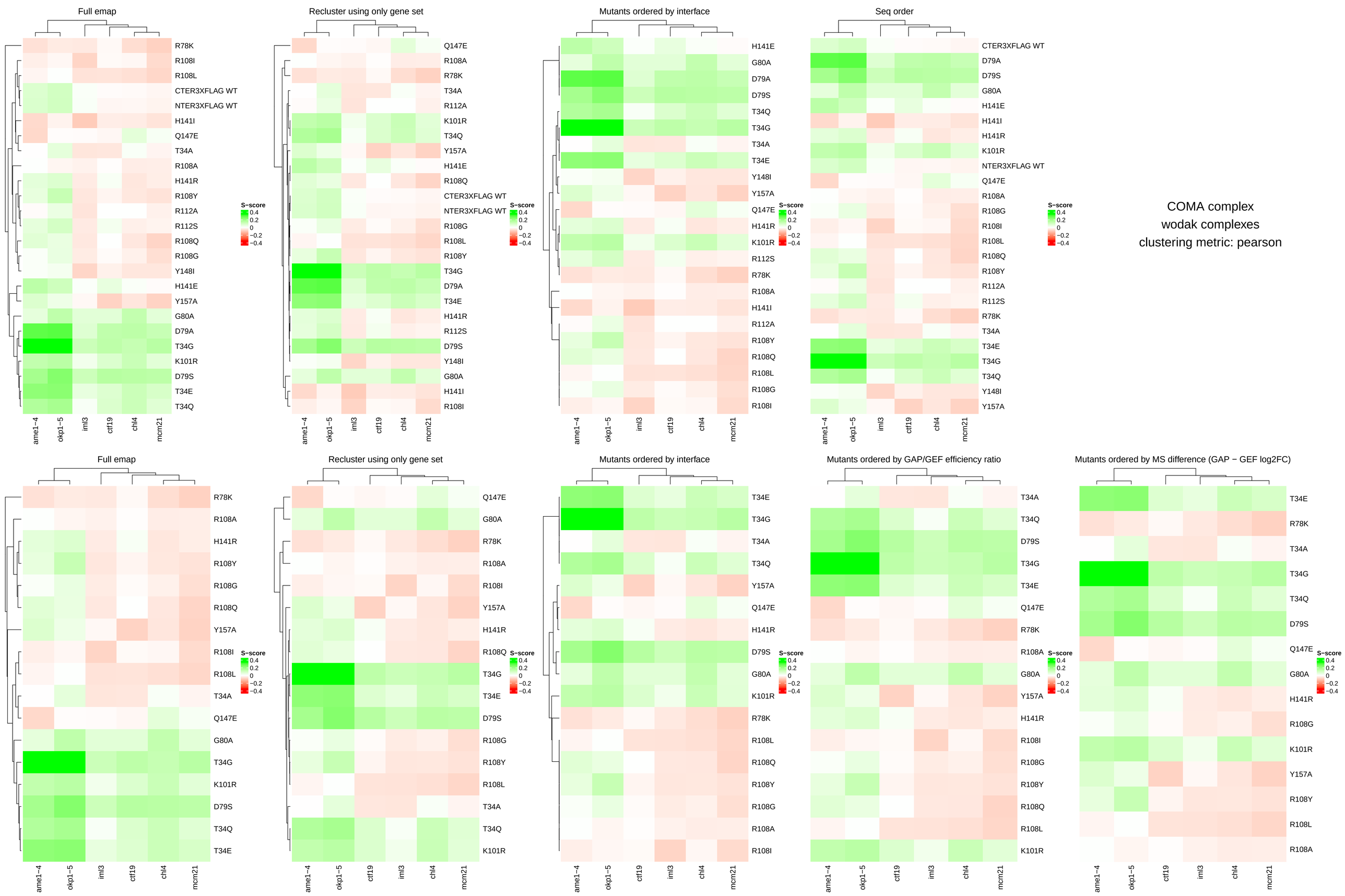

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
hhf1
hhf2
hht1
hta2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
H141E
R112S
R112A
H141R
R108Y
R108A
Y148I
H141I
R108Q
R108G
Y157A
T34G
T34Q
K101R
T34E
D79A
D79S
R108I
R108L
NTER3XFLAG WT
R78K
Q147E
T34A
CTER3XFLAG WT
G80A
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
Nucleosomal protein complex
wodak complexes
clustering metric: pearson


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
brr2−5005
snu114−60
prp28−101
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108Y
R112S
H141R
R112A
R108G
R108L
NTER3XFLAG WT
T34A
R108I
R108A
CTER3XFLAG WT
R108Q
H141I
Y148I
Y157A
D79S
H141E
R78K
K101R
Q147E
T34G
T34Q
G80A
D79A
T34E
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
U5 snRNP complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
H141R
R108I
R108A
R108Q
R108Y
R108G
T34A
R108L
R78K
D79S
Y157A
K101R
Q147E
T34Q
T34G
T34E
G80A
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

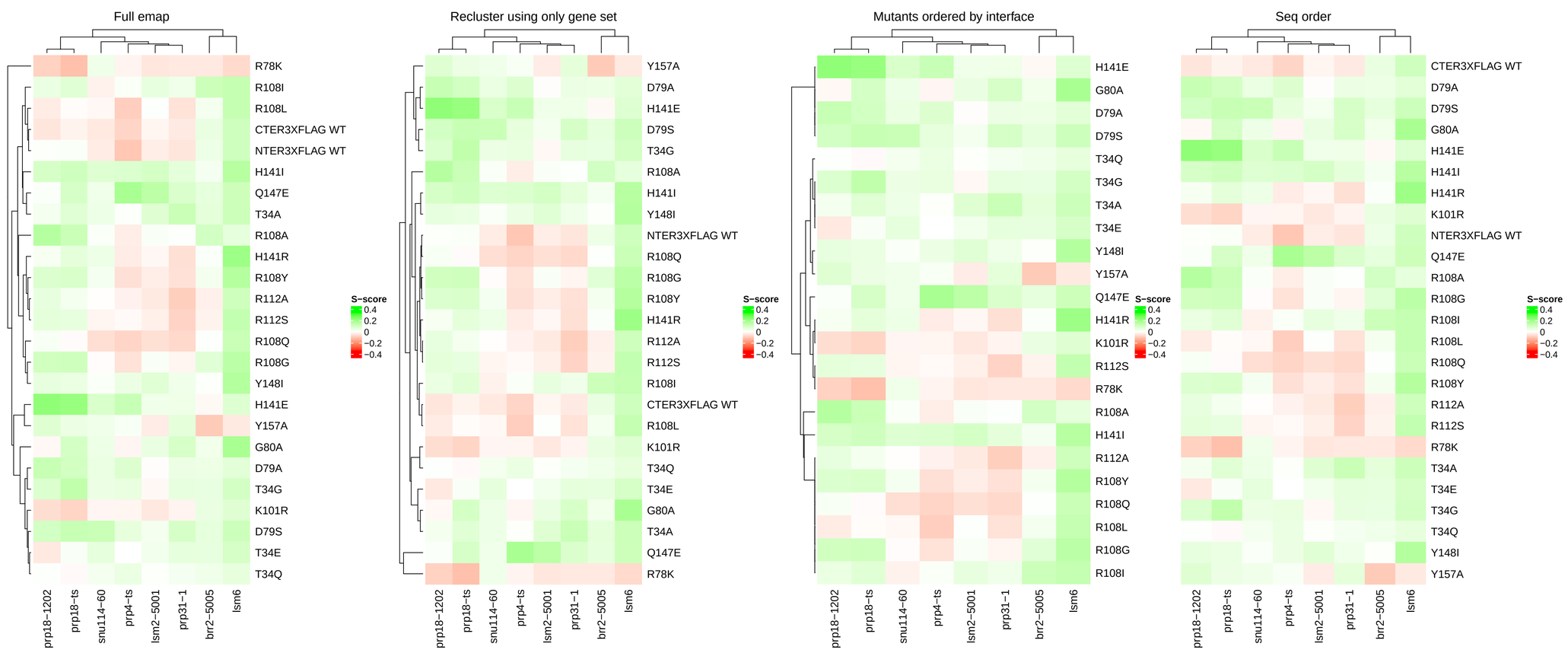

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
cct2−5001
cct2−5002
cct3−5001
cct7−5001
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R78K
H141E
Y157A
R108Y
Y148I
Q147E
T34E
R112A
R108L
R112S
K101R
T34Q
H141I
CTER3XFLAG WT
D79S
D79A
NTER3XFLAG WT
R108I
T34A
R108A
G80A
H141R
R108G
R108Q
T34G
cct2−5001
cct2−5002
cct3−5001
cct7−5001
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
cct2−5001
cct2−5002
cct3−5001
cct7−5001
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
cct2−5001
cct2−5002
cct3−5001
cct7−5001
chaperonin−containing T−complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
cct2−5001
cct2−5002
cct3−5001
cct7−5001
Recluster using only gene set
R108Y
R78K
Y157A
Q147E
T34E
R108L
T34Q
K101R
D79S
T34A
R108I
R108A
G80A
H141R
R108G
T34G
R108Q
cct3−5001
cct7−5001
cct2−5001
cct2−5002
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
cct3−5001
cct7−5001
cct2−5001
cct2−5002
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
cct3−5001
cct7−5001
cct2−5001
cct2−5002
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A
cct3−5001
cct7−5001
cct2−5001
cct2−5002



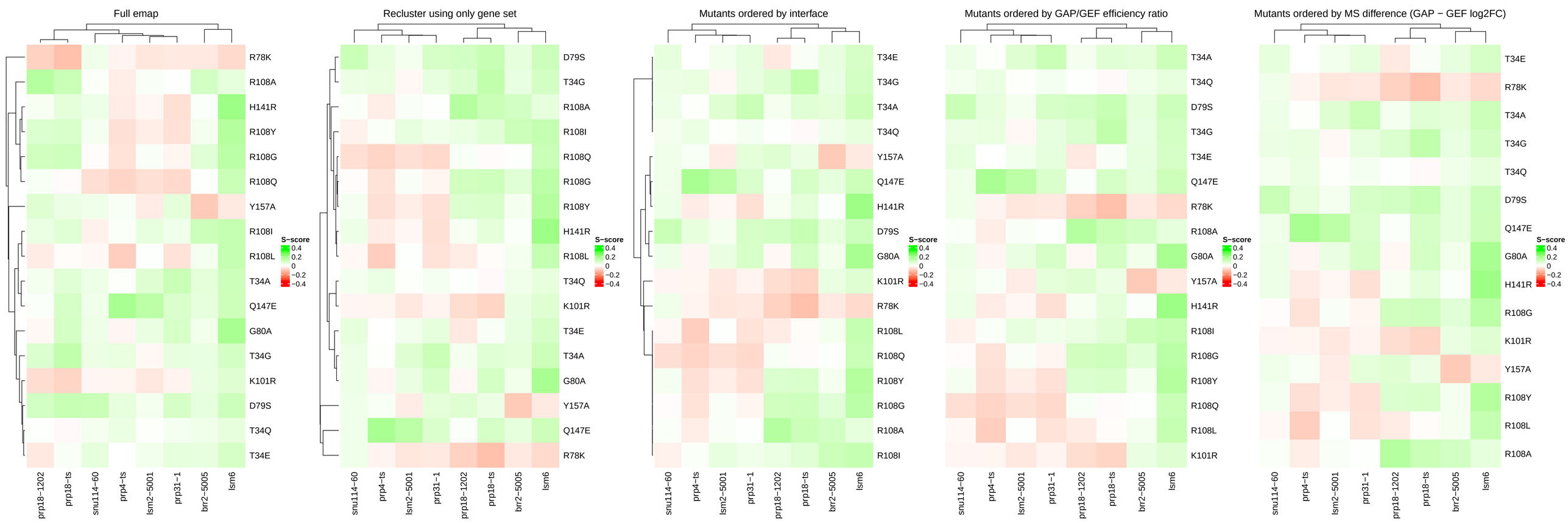
Elongator complex
wodak complexes
clustering metric: pearson

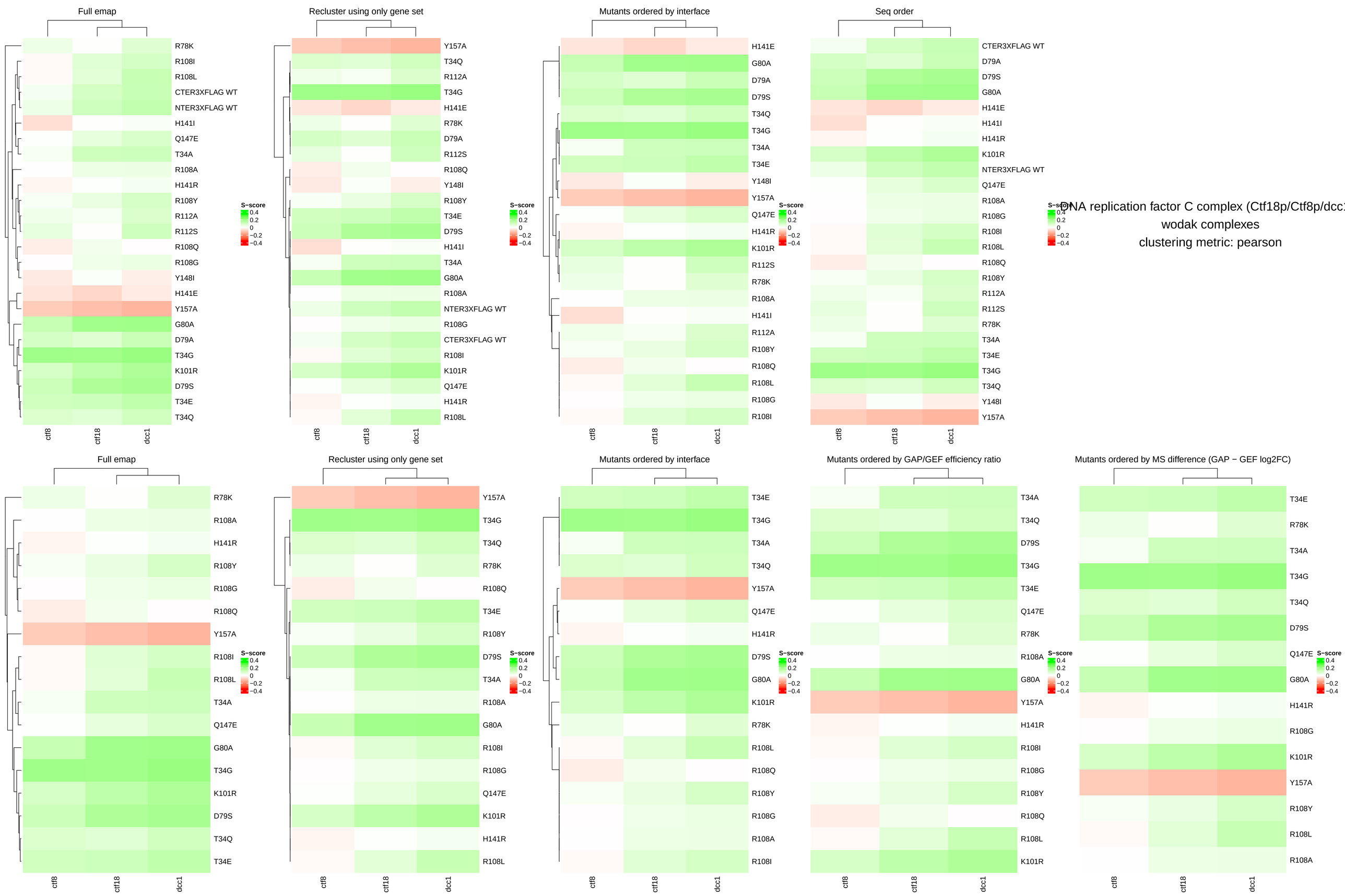


COMA complex
wodak complexes
clustering metric: pearson

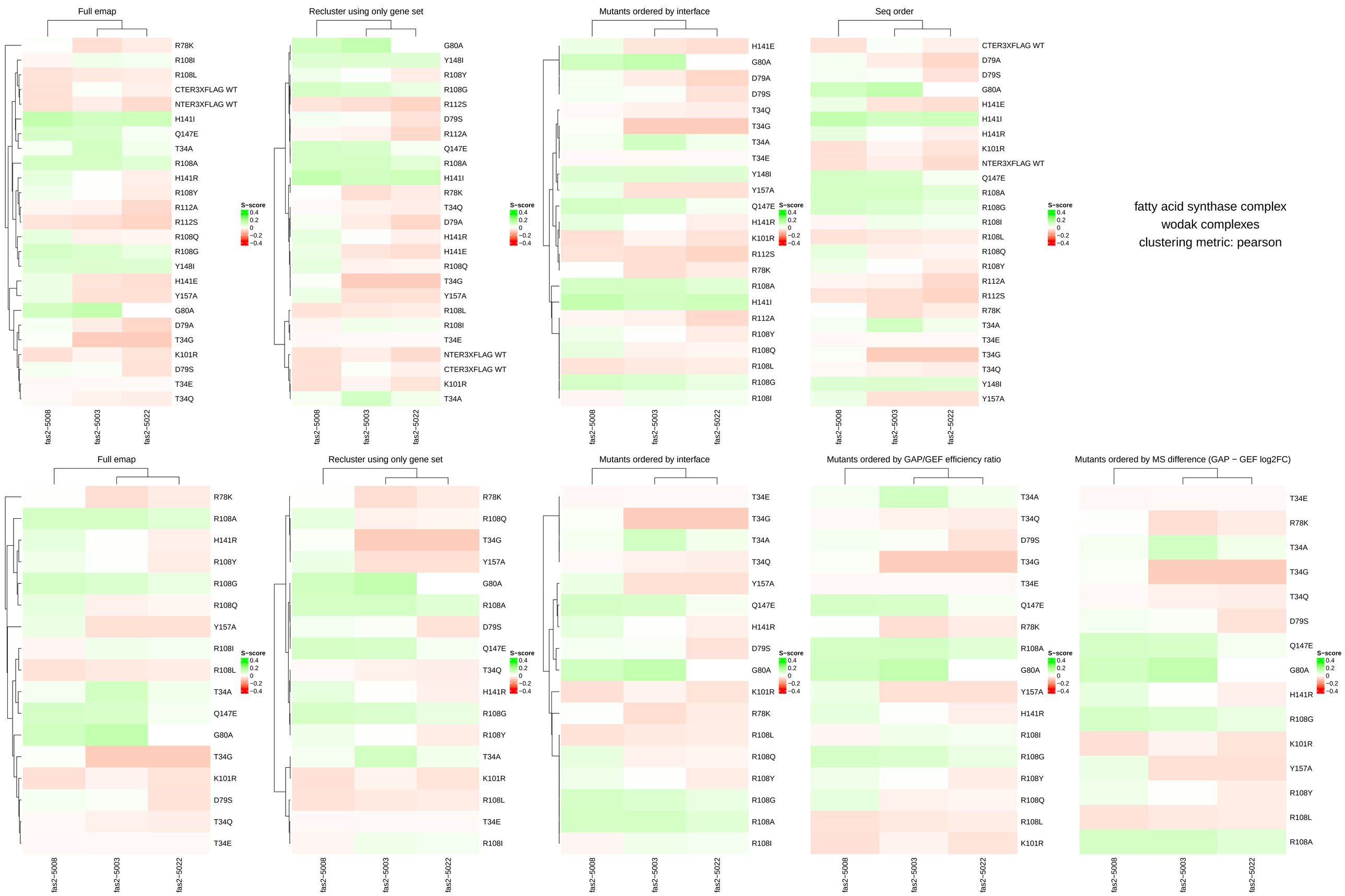


U4/U6 x U5 tri−snRNP complex
wodak complexes
clustering metric: pearson



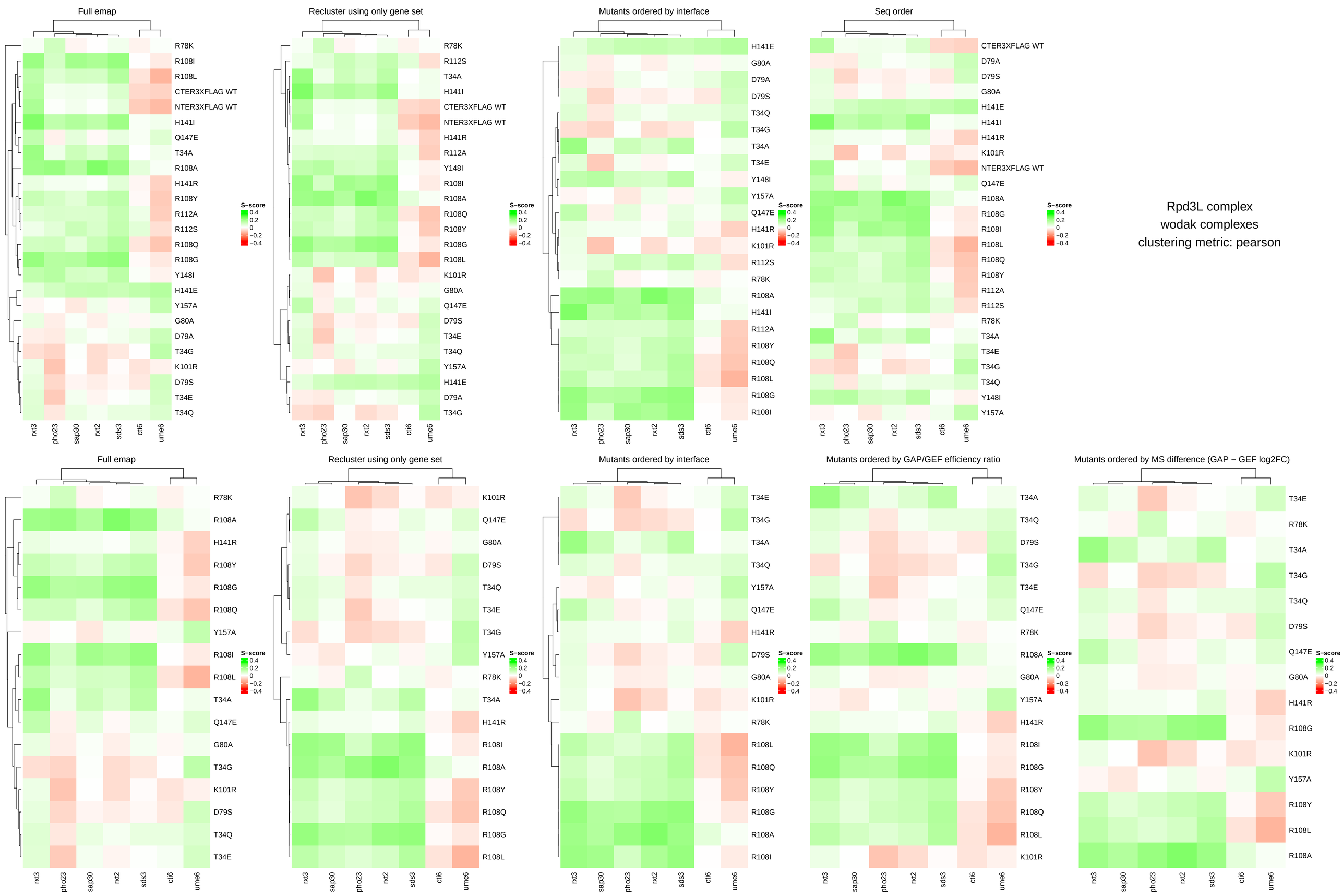

DNA replication factor C complex (Ctf18p/Ctf8p/dcc1
wodak complexes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ctf8
ctf18
dcc1
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
Y157A
T34Q
R112A
T34G
H141E
R78K
D79A
R112S
R108Q
Y148I
R108Y
T34E
D79S
H141I
T34A
G80A
R108A
NTER3XFLAG WT
R108G
CTER3XFLAG WT
R108I
K101R
Q147E
H141R
R108L
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Y157A
T34G
T34Q
R78K
R108Q
T34E
R108Y
D79S
T34A
R108A
G80A
R108I
R108G
Q147E
K101R
H141R
R108L
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
caf40
ccr4
not3
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108G
D79A
Y148I
H141I
R108A
H141E
H141R
R108Y
R78K
R112A
R108Q
R112S
Y157A
Q147E
R108I
T34G
CTER3XFLAG WT
G80A
NTER3XFLAG WT
R108L
K101R
T34E
T34Q
D79S
T34A
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A
CCR4−NOT core complex
wodak complexes
clustering metric: pearson



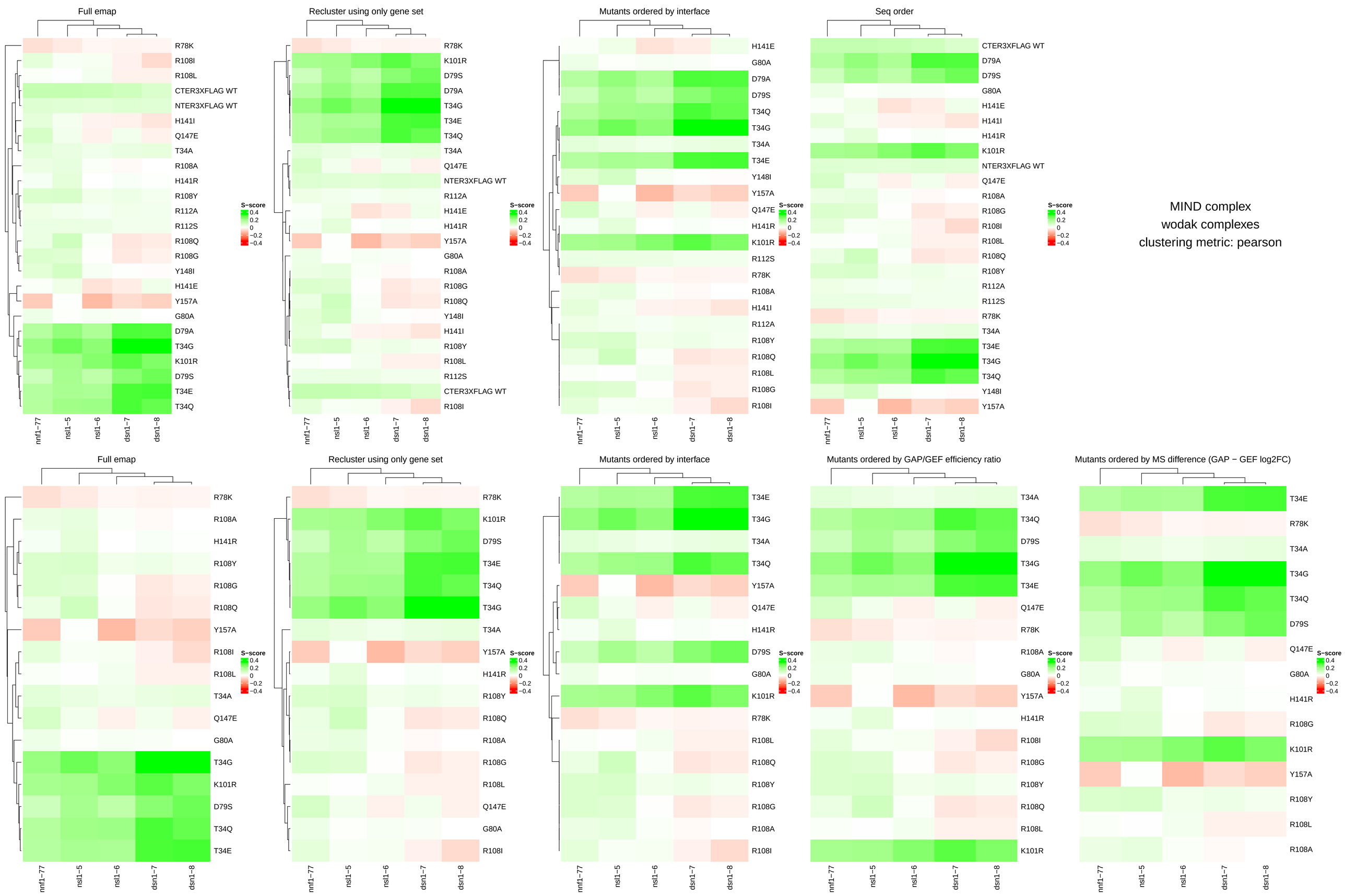
fatty acid synthase complex
wodak complexes
clustering metric: pearson

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
xrs2
mre11
rad50
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
G80A
Q147E
R108A
R78K
H141E
D79S
D79A
T34G
R112S
Y157A
H141R
K101R
R112A
NTER3XFLAG WT
T34Q
R108Y
T34E
R108L
Y148I
CTER3XFLAG WT
T34A
R108I
R108G
H141I
R108Q
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
MRX complex
wodak complexes
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

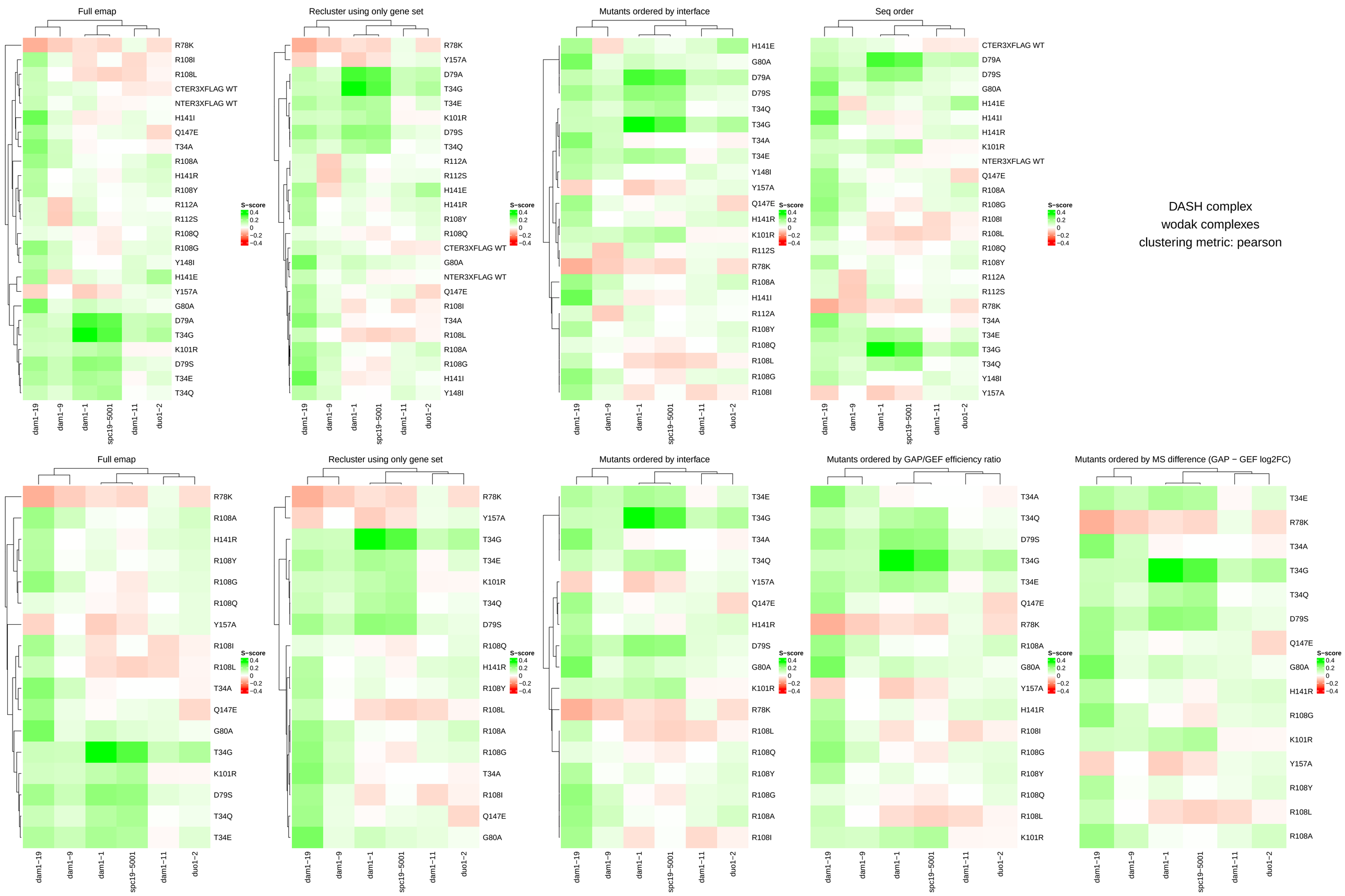


Rpd3L complex
wodak complexes
clustering metric: pearson

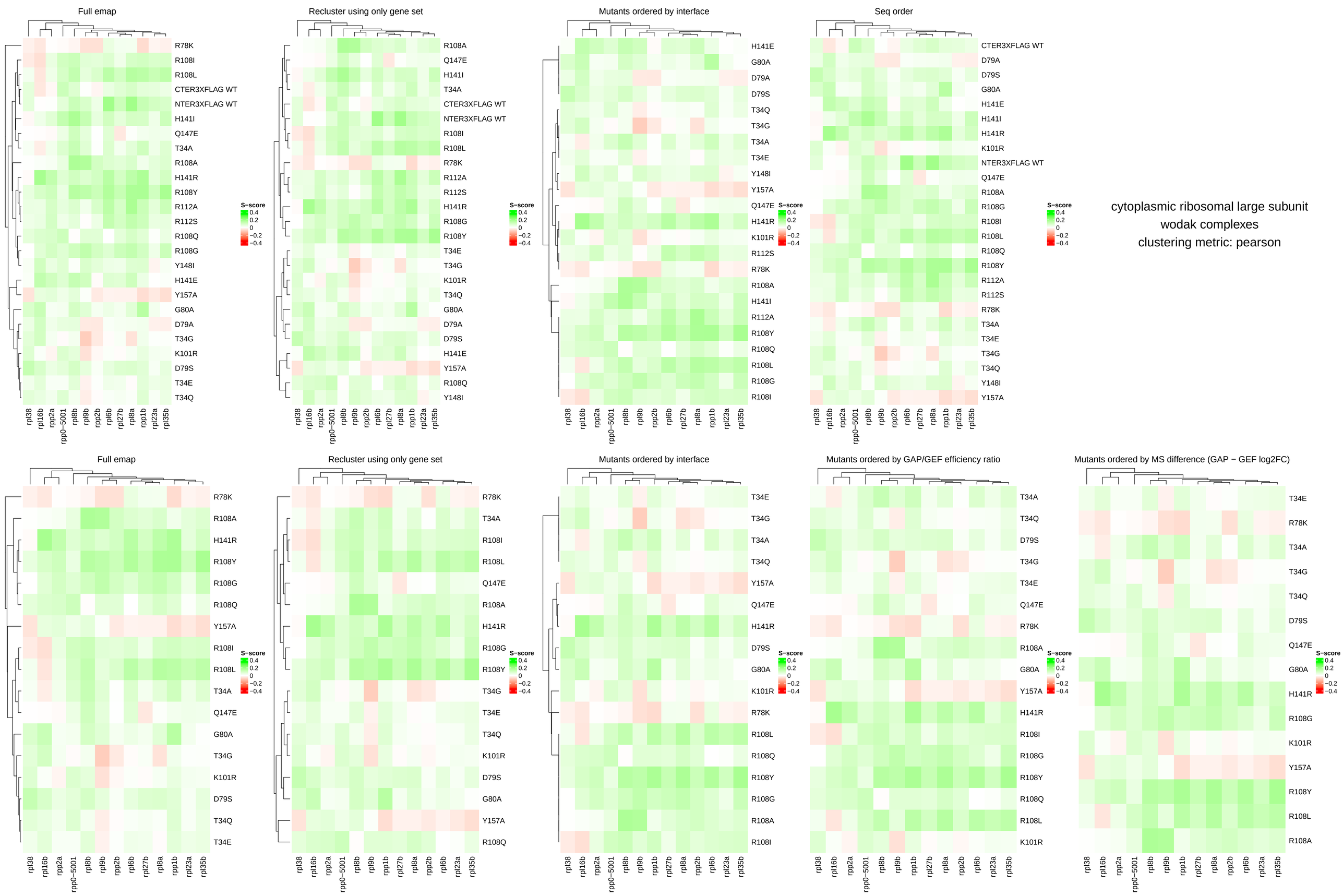
Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
ist3
rse1−1
prp11−ts
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
H141E
T34E
R112S
H141R
T34G
NTER3XFLAG WT
R108L
Y157A
D79S
K101R
D79A
T34Q
R108Y
T34A
G80A
CTER3XFLAG WT
R112A
R78K
R108G
R108Q
R108I
Y148I
Q147E
H141I
R108A
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
U2 snRNP complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34E
H141R
T34G
R108L
T34Q
Y157A
D79S
K101R
R108Y
T34A
G80A
R78K
R108G
R108Q
R108I
Q147E
R108A
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

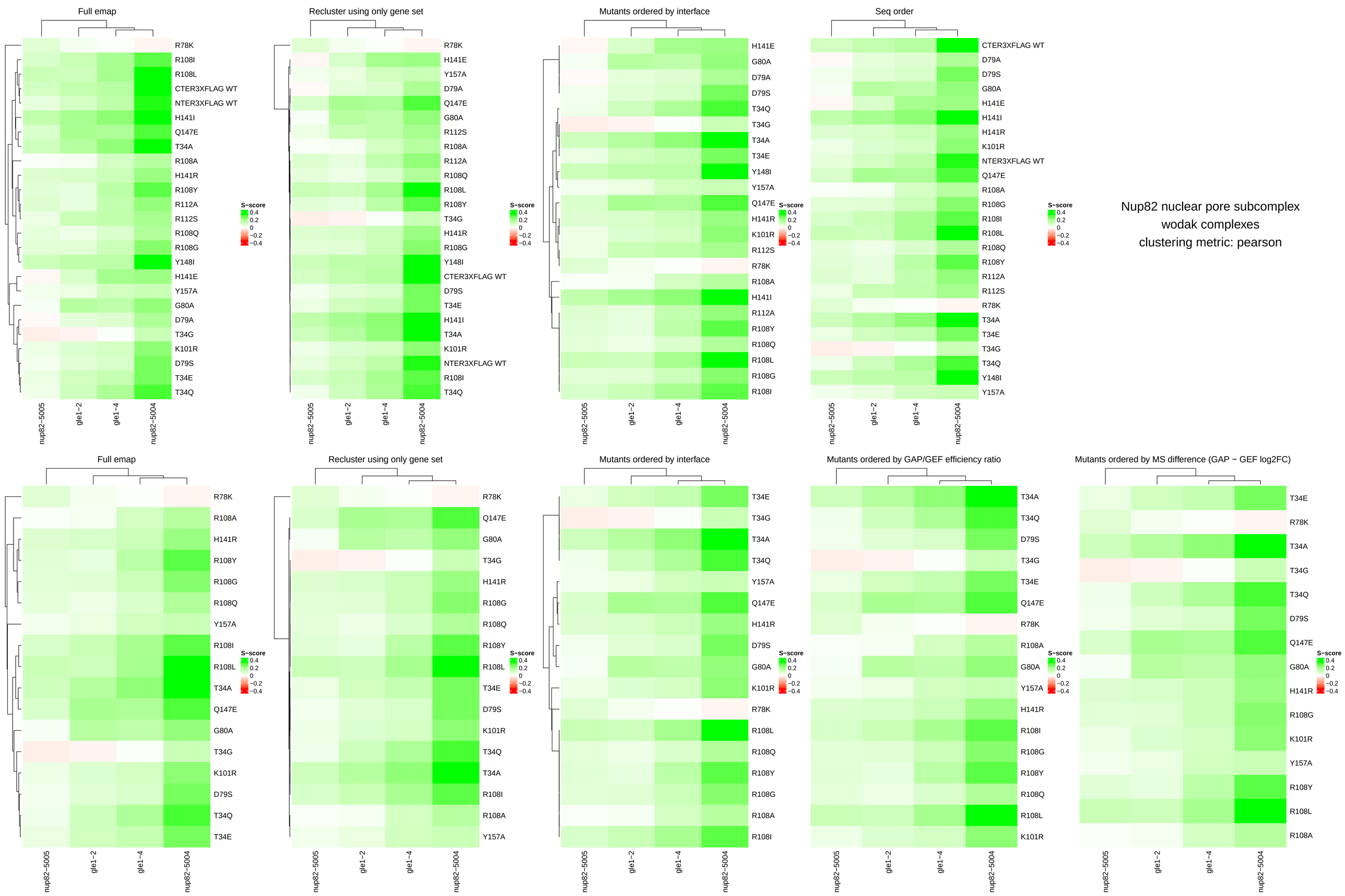


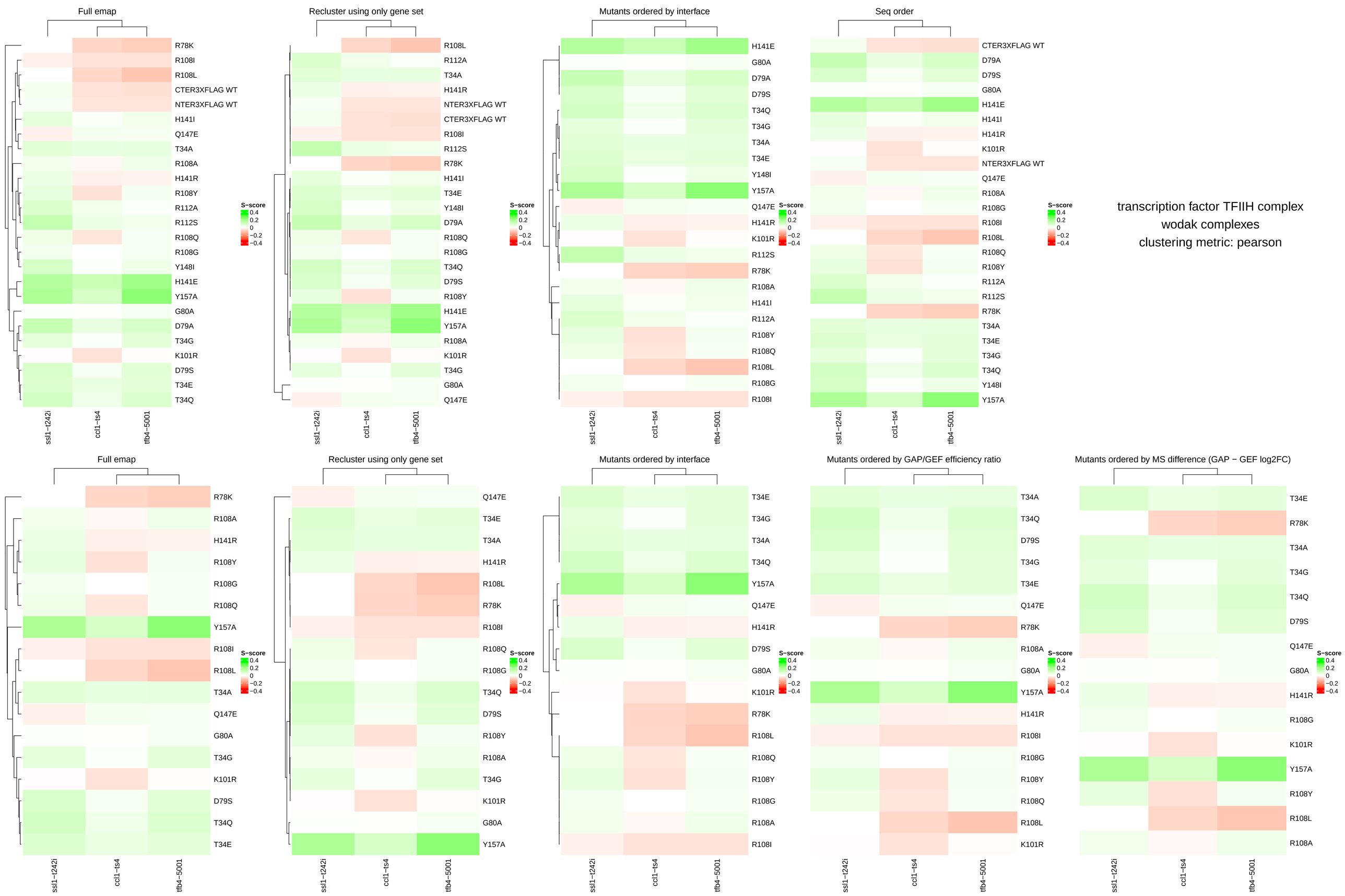
MIND complex
wodak complexes
clustering metric: pearson

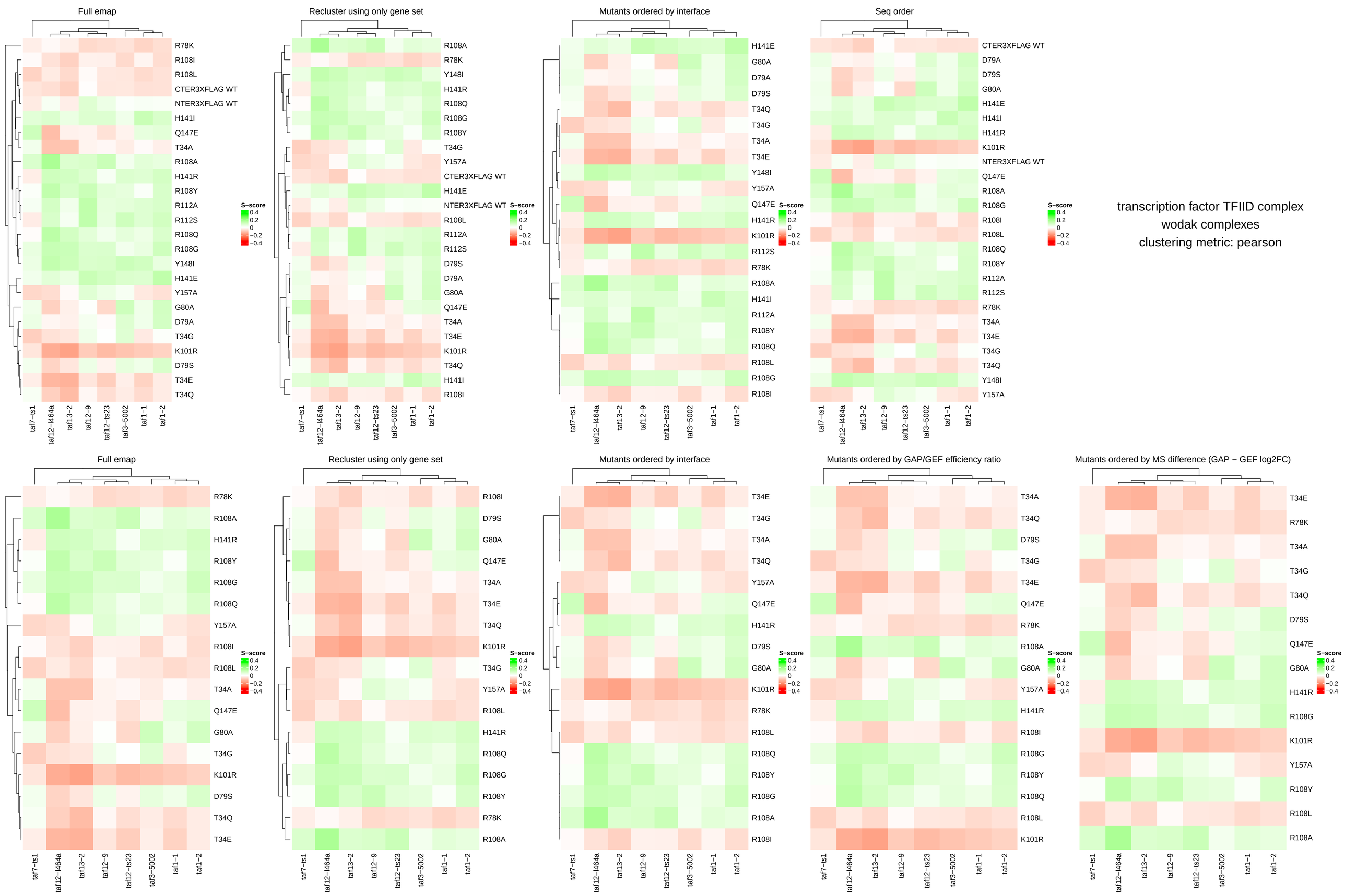


DASH complex
wodak complexes
clustering metric: pearson

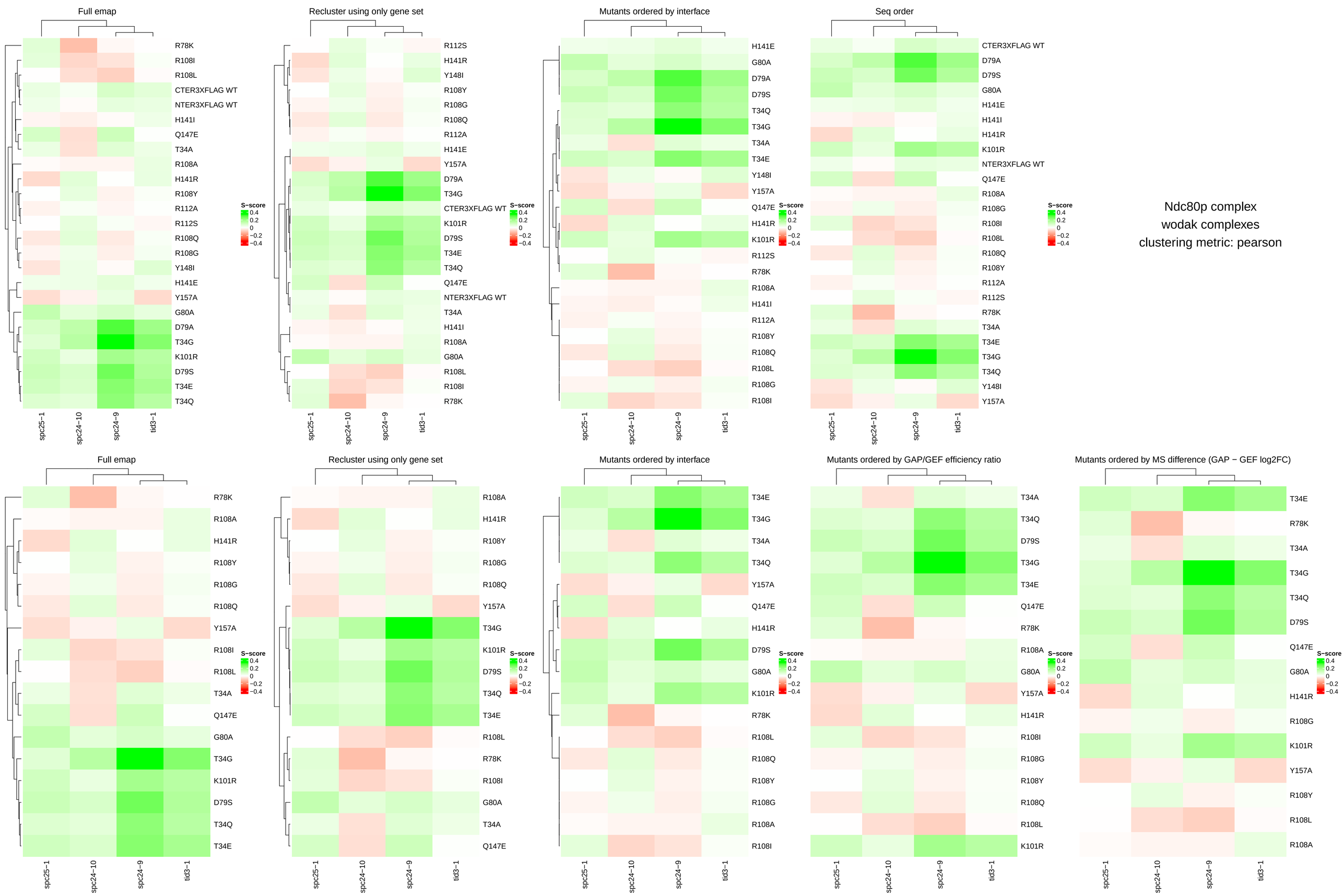

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
rpl38
rpl16b
rpp2a
rpp0−5001
rpl8b
rpl9b
rpp2b
rpl6b
rpl27b
rpl8a
rpp1b
rpl23a
rpl35b
cytoplasmic ribosomal large subunit
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
nup82−5005
gle1−2
gle1−4
nup82−5004
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
Nup82 nuclear pore subcomplex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ssl1−t242i
ccl1−ts4
tfb4−5001
transcription factor TFIIH complex
wodak complexes
clustering metric: pearson

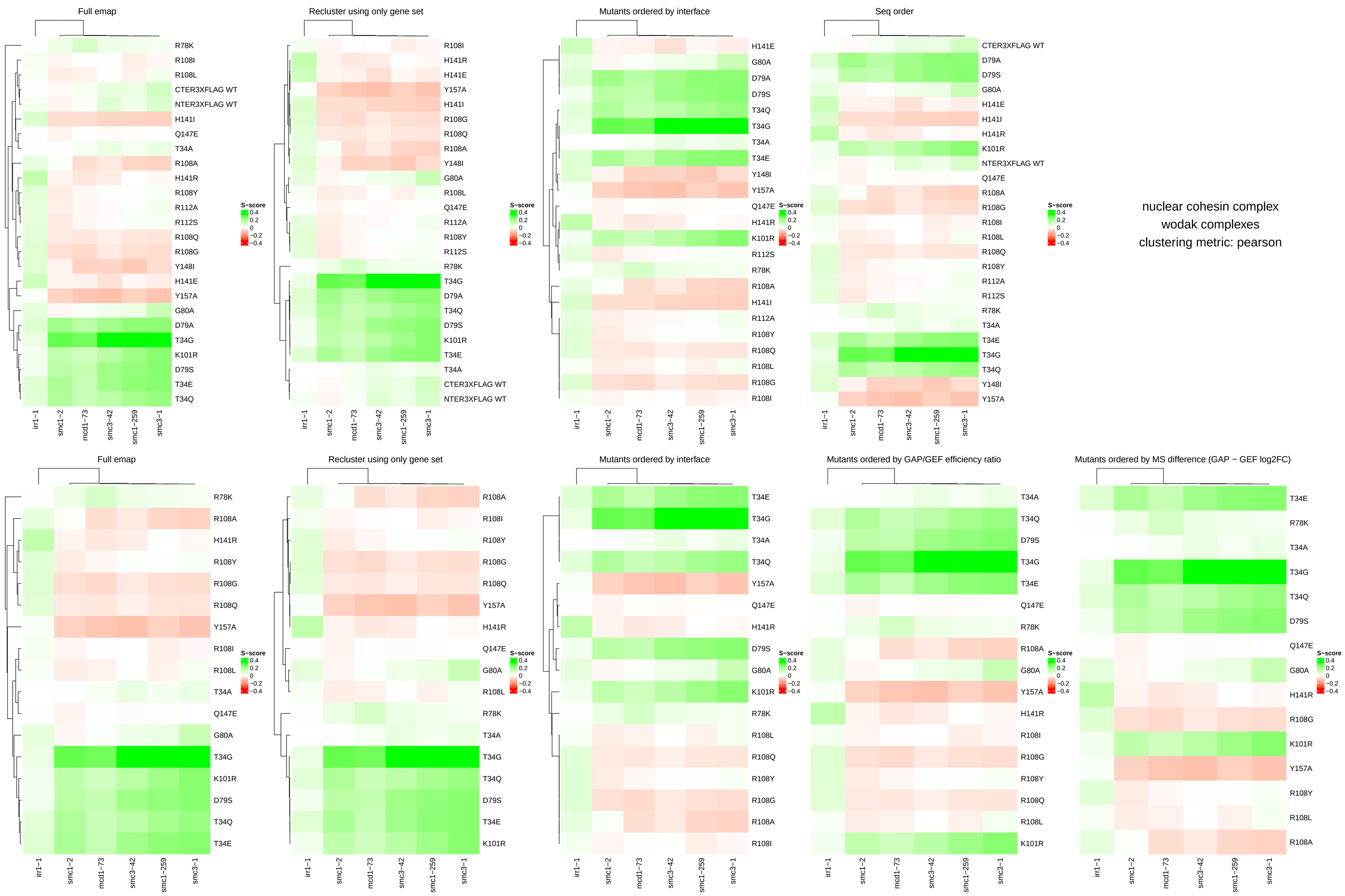


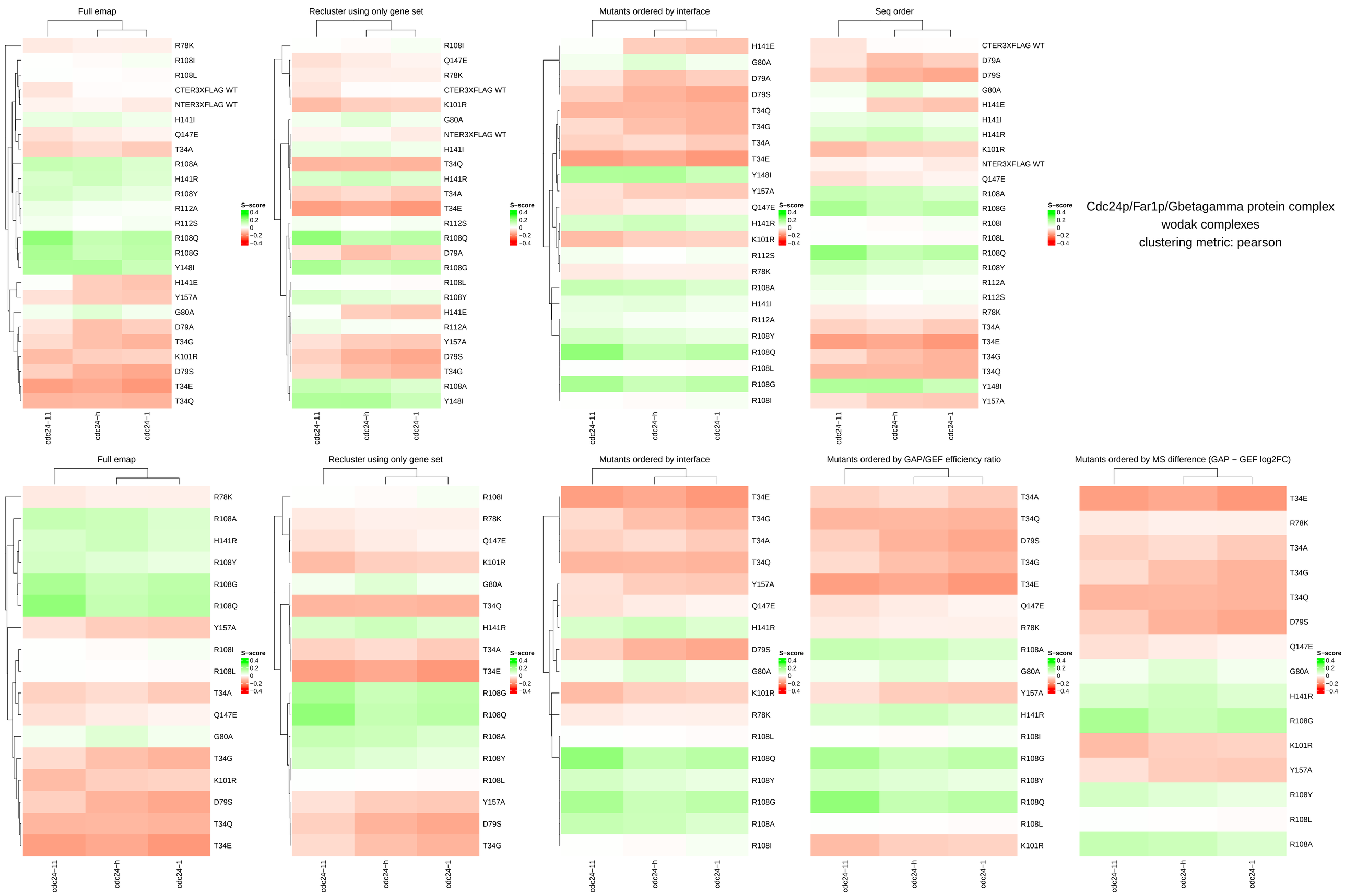
transcription factor TFIID complex
wodak complexes
clustering metric: pearson

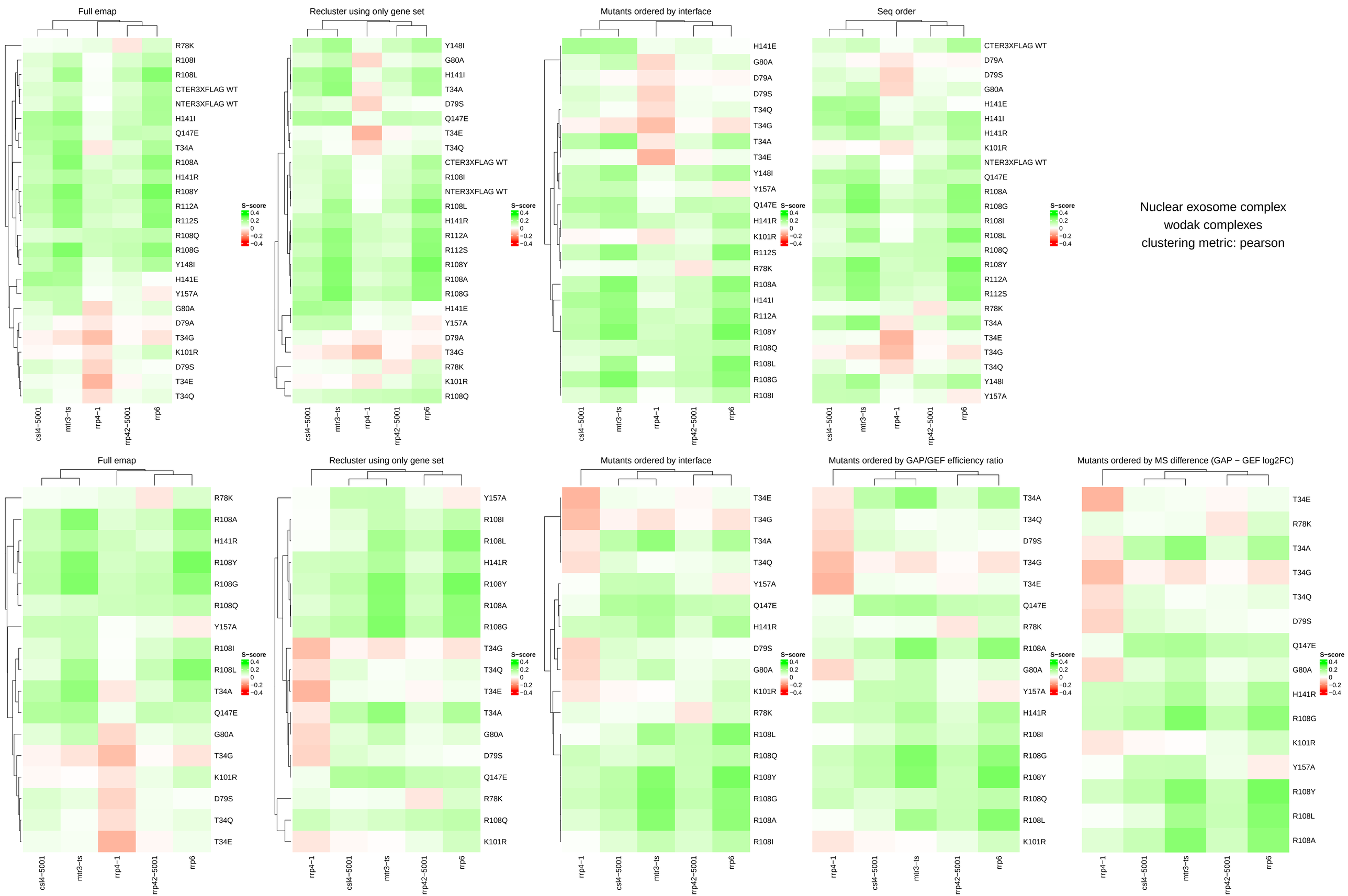


Ndc80p complex
wodak complexes
clustering metric: pearson

UTP A complex
wodak complexes
clustering metric: pearson

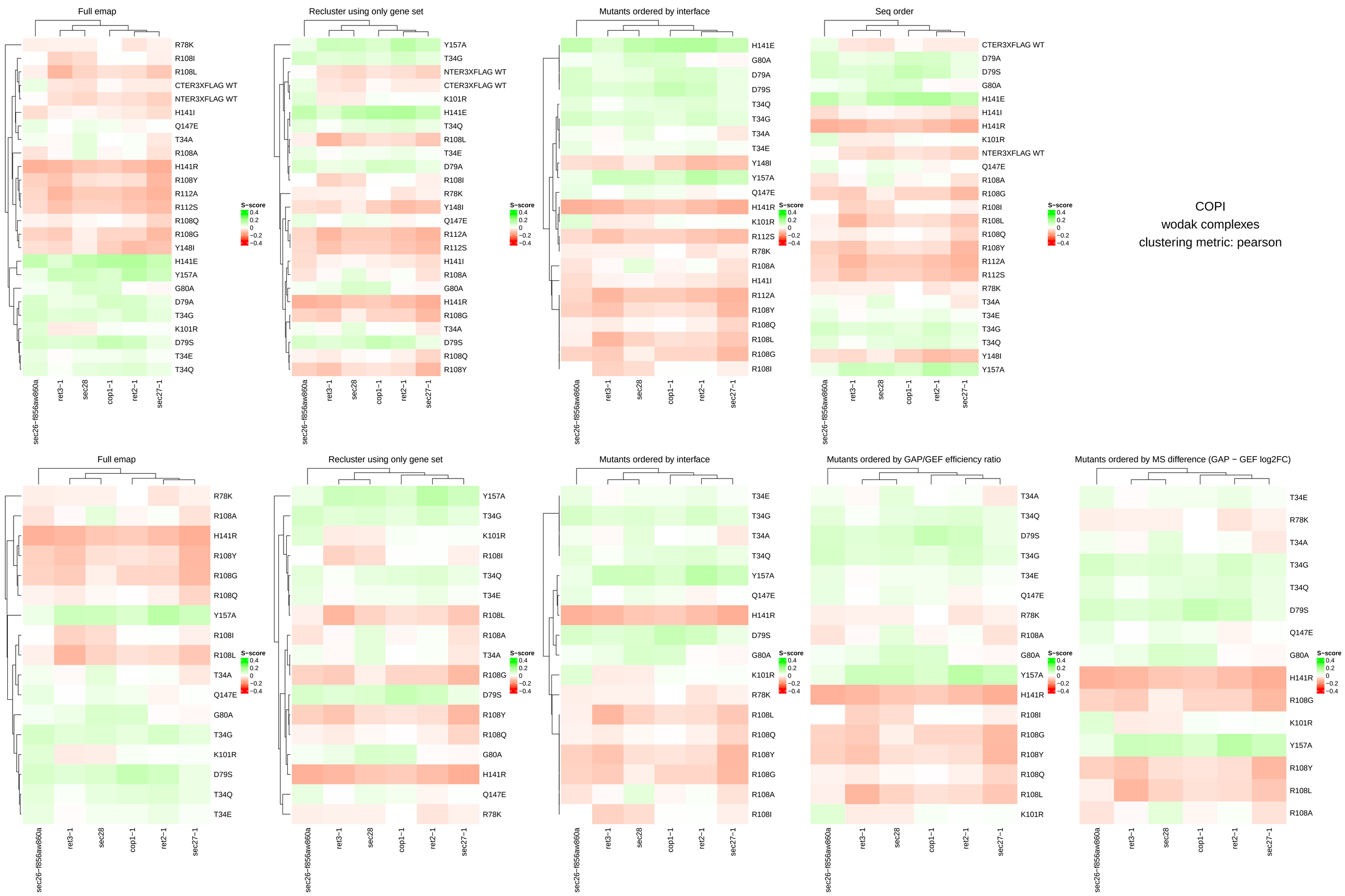

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
irr1−1
smc1−2
mcd1−73
smc3−42
smc1−259
smc3−1
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
nuclear cohesin complex
wodak complexes
clustering metric: pearson

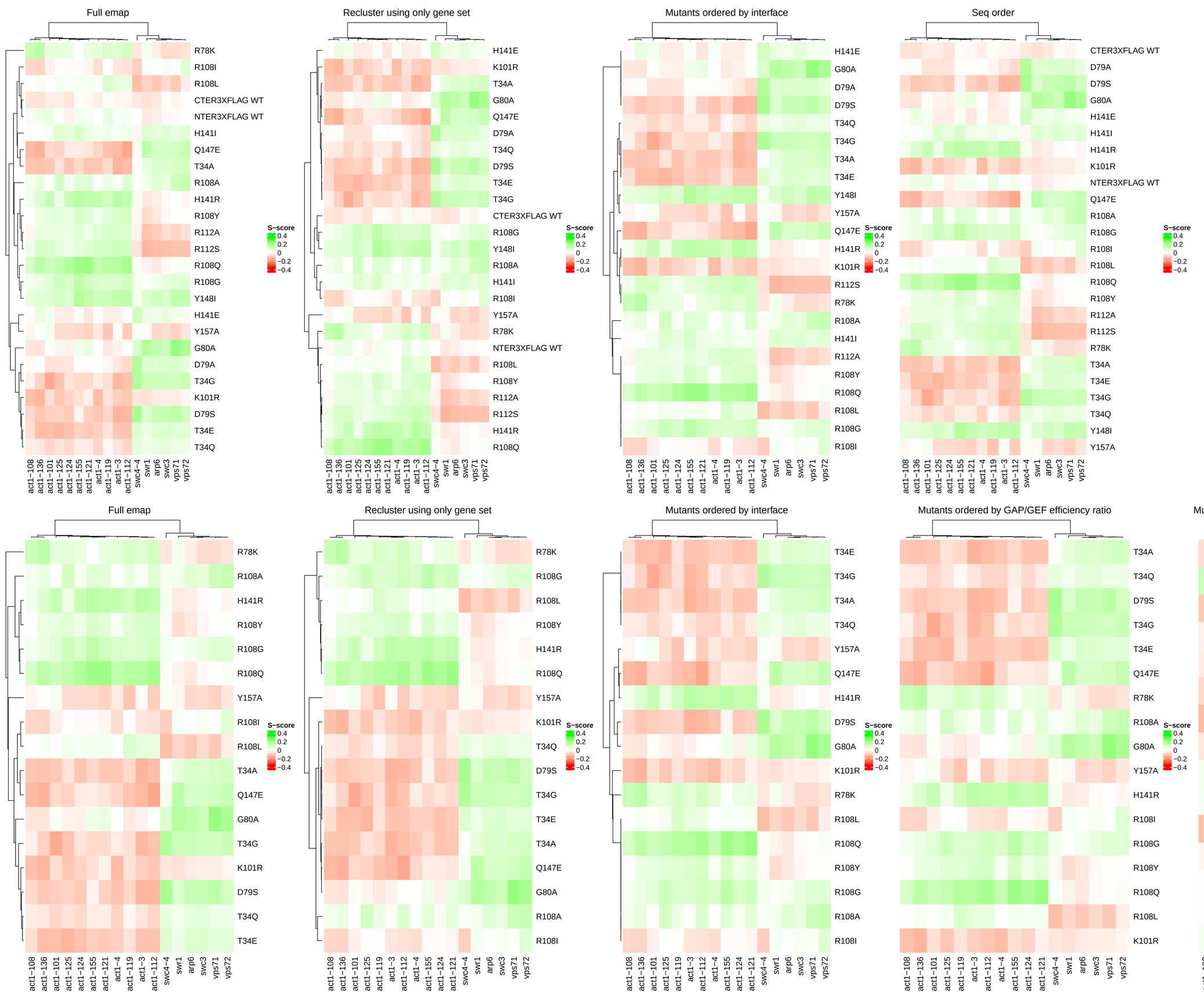

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
cdc24−11
cdc24−h
cdc24−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108I
Q147E
R78K
CTER3XFLAG WT
K101R
G80A
NTER3XFLAG WT
H141I
T34Q
H141R
T34A
T34E
R112S
R108Q
D79A
R108G
R108L
R108Y
H141E
R112A
Y157A
D79S
T34G
R108A
Y148I
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Cdc24p/Far1p/Gbetagamma protein complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
R108I
R78K
Q147E
K101R
G80A
T34Q
H141R
T34A
T34E
R108G
R108Q
R108A
R108Y
R108L
Y157A
D79S
T34G
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A



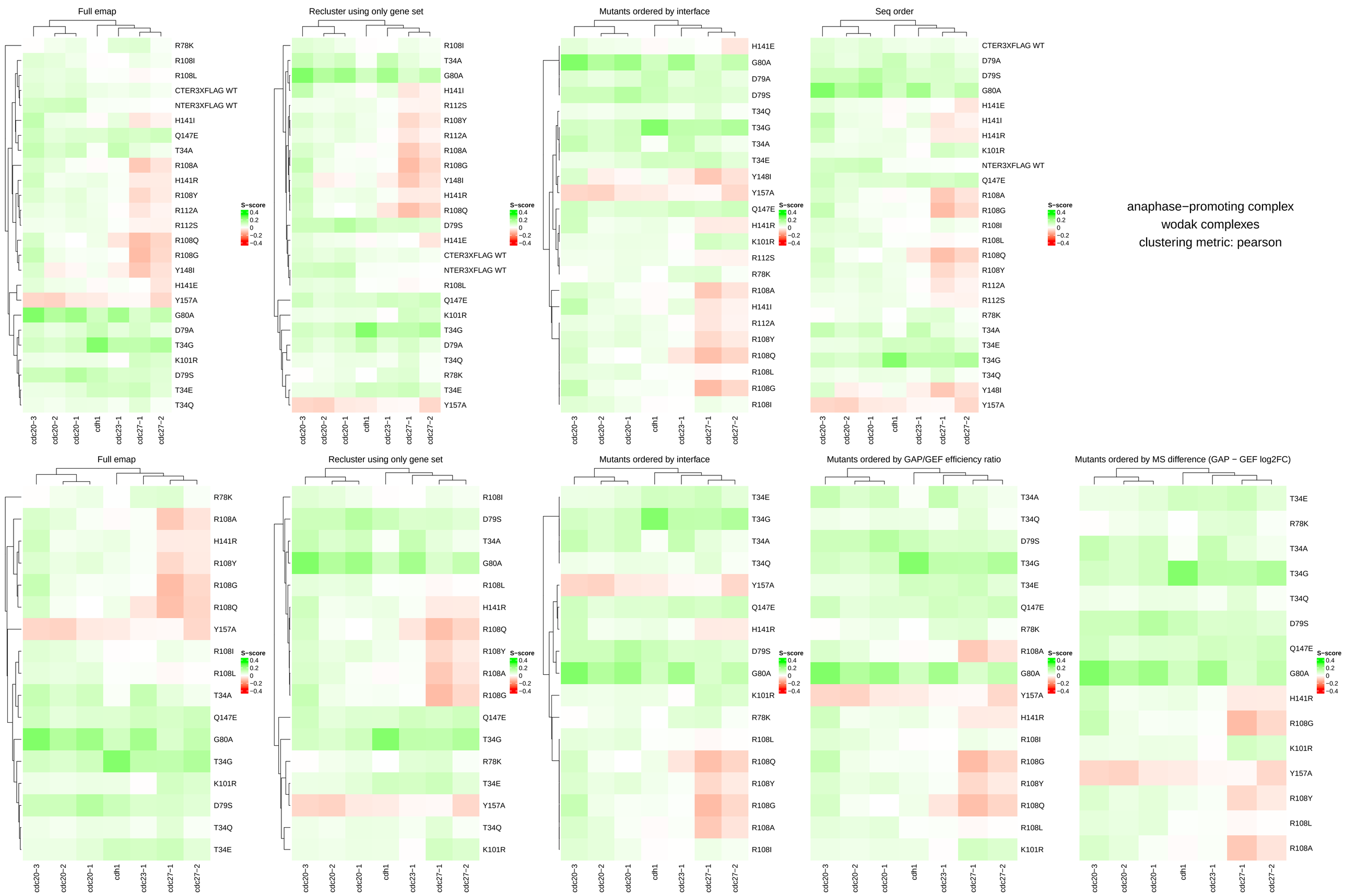
Nuclear exosome complex
wodak complexes
clustering metric: pearson

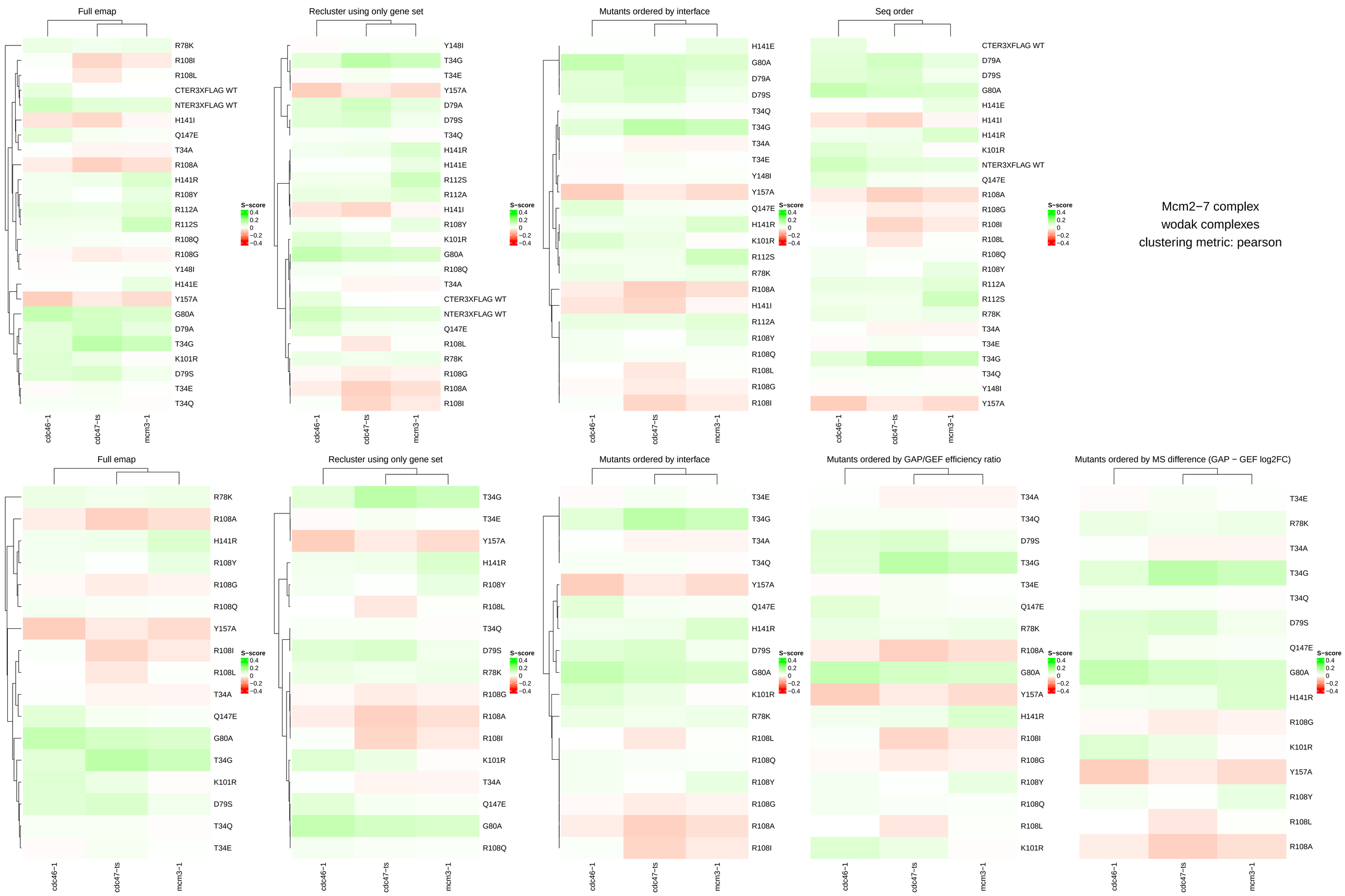
NuA4 histone acetyltransferase complex
wodak complexes
clustering metric: pearson

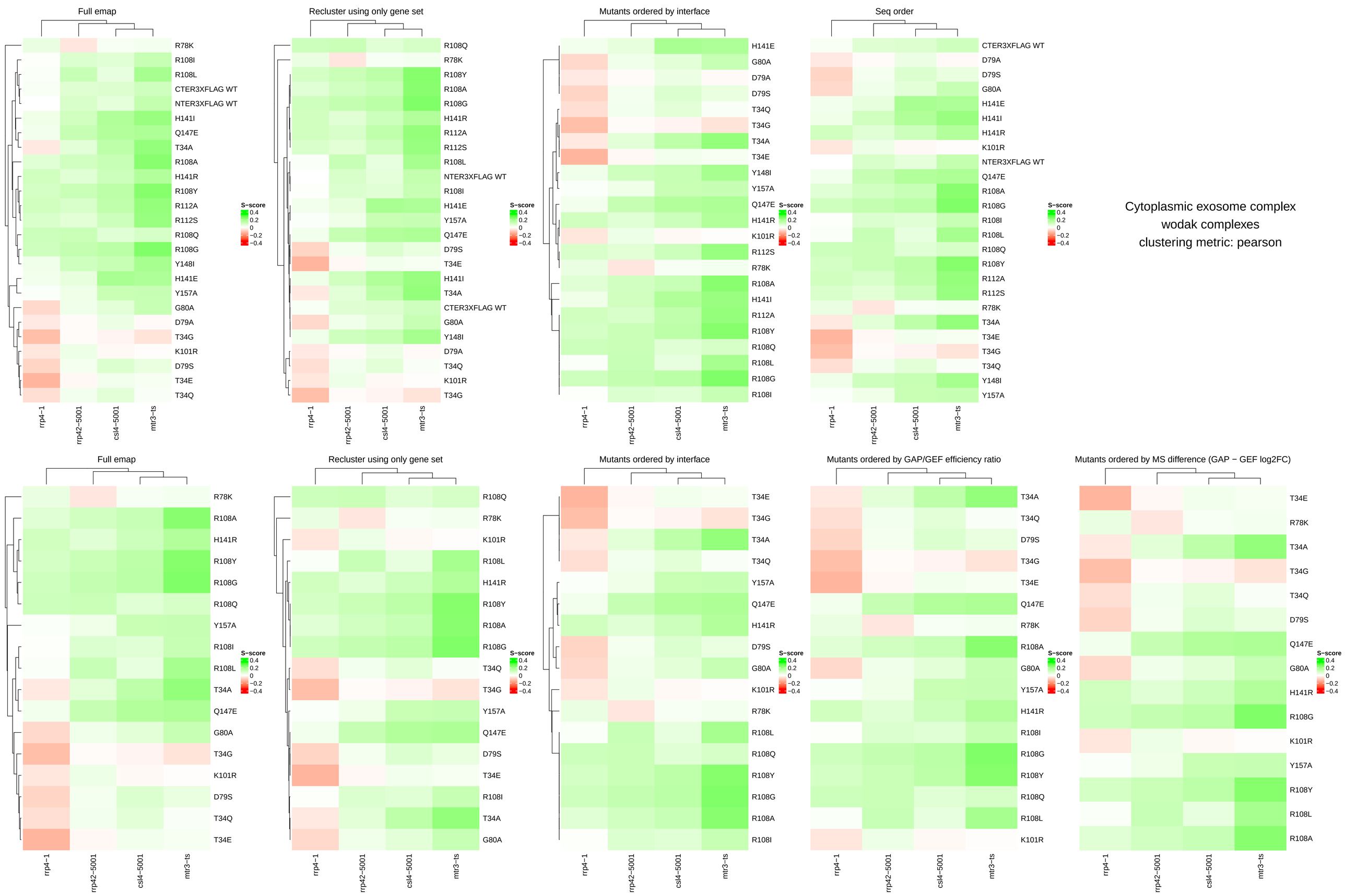

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
sec26−f856aw860a
ret3−1
sec28
cop1−1
ret2−1
sec27−1
COPI
wodak complexes
clustering metric: pearson

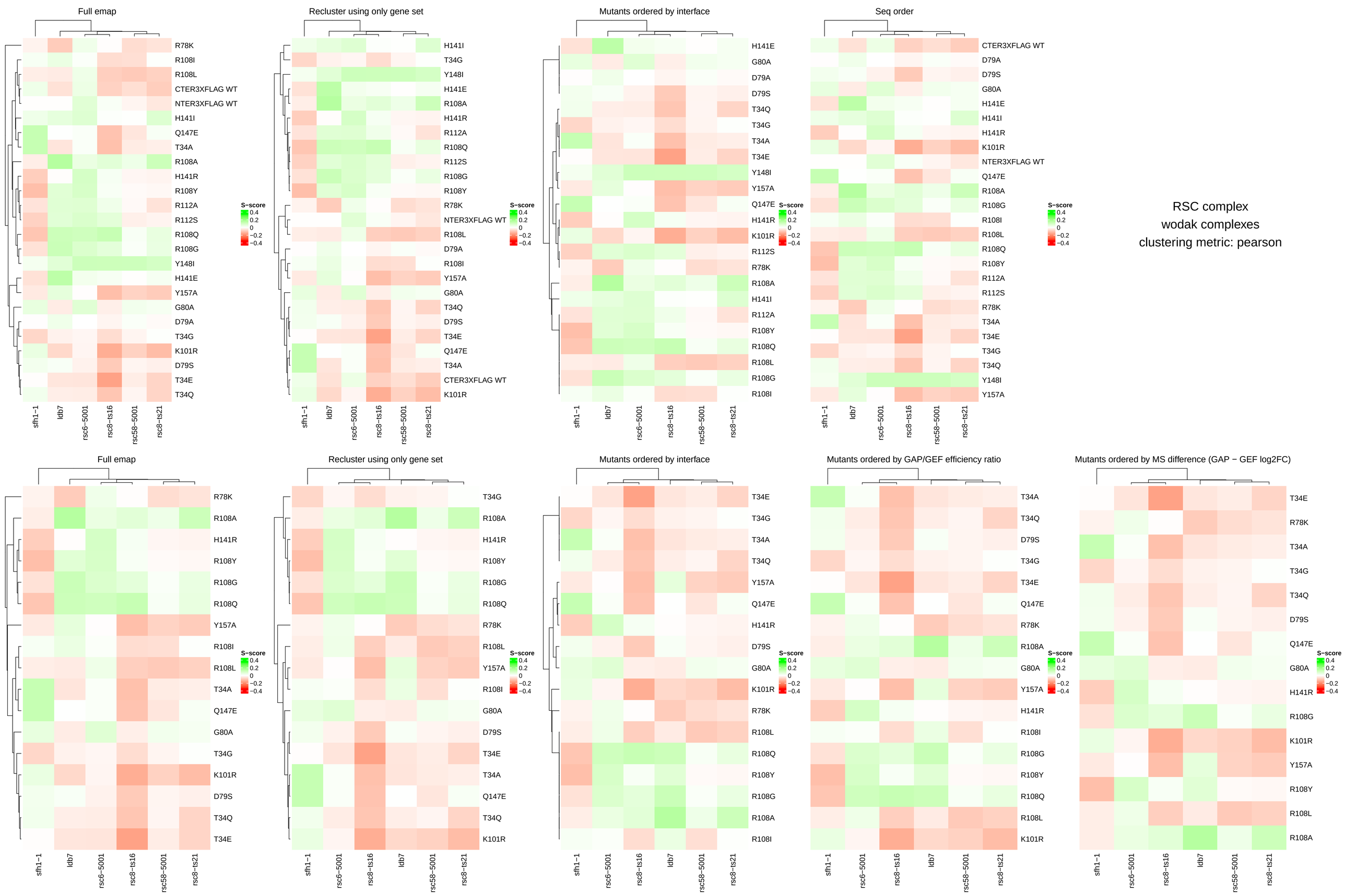


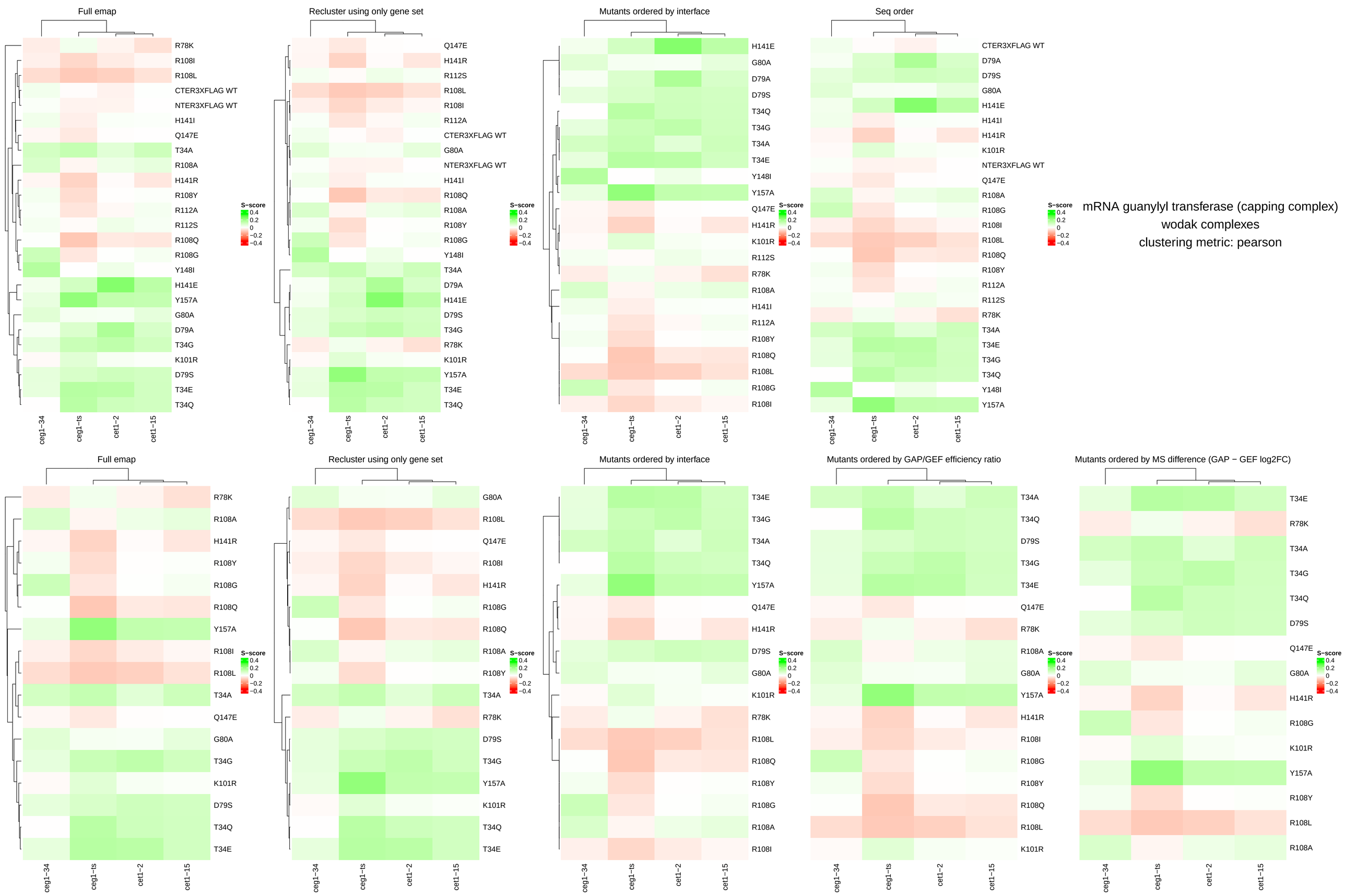
Swr1p complex
wodak complexes
clustering metric: pearson

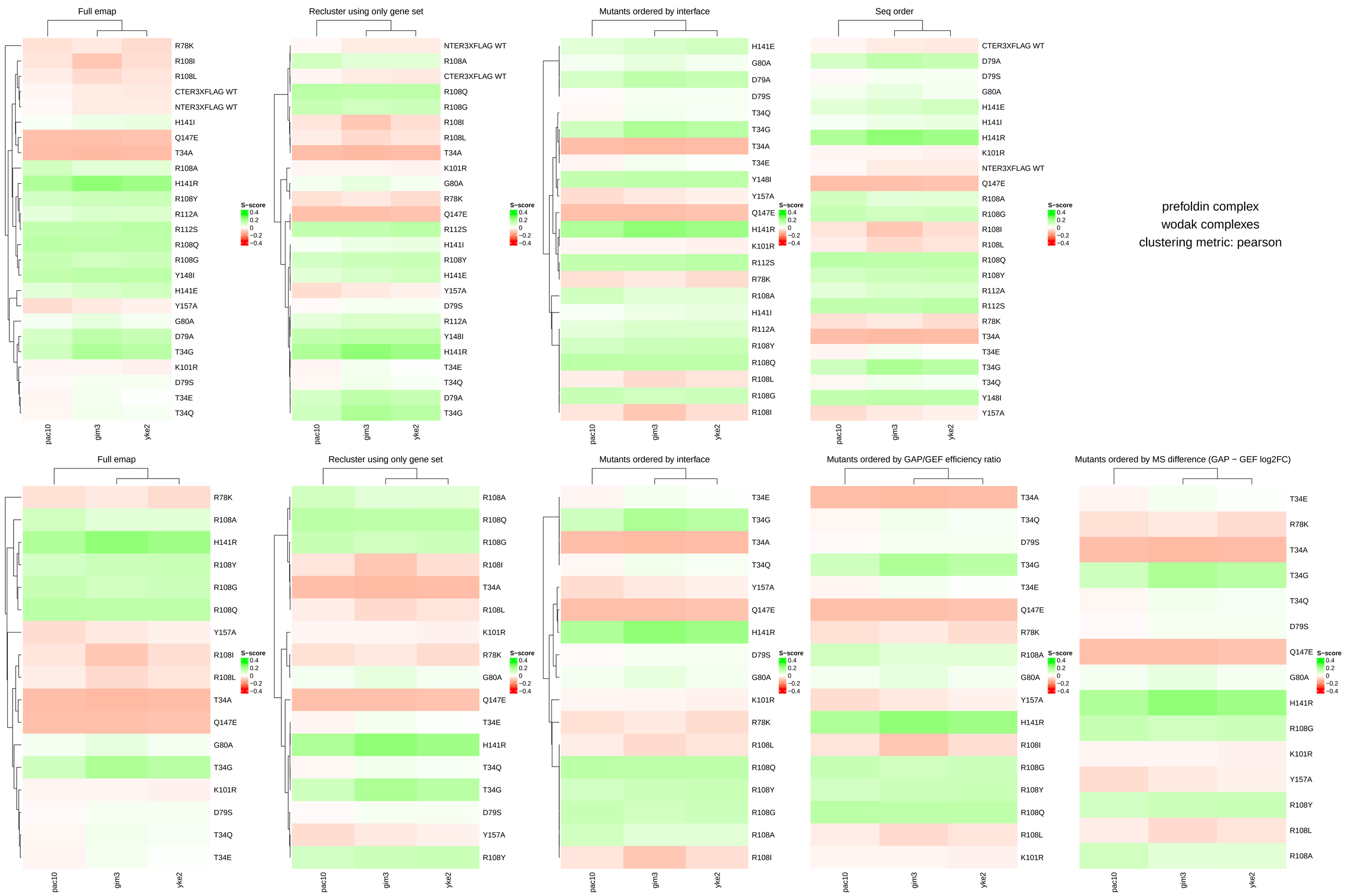

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
cdc20−3
cdc20−2
cdc20−1
cdh1
cdc23−1
cdc27−1
cdc27−2
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
anaphase−promoting complex
wodak complexes
clustering metric: pearson

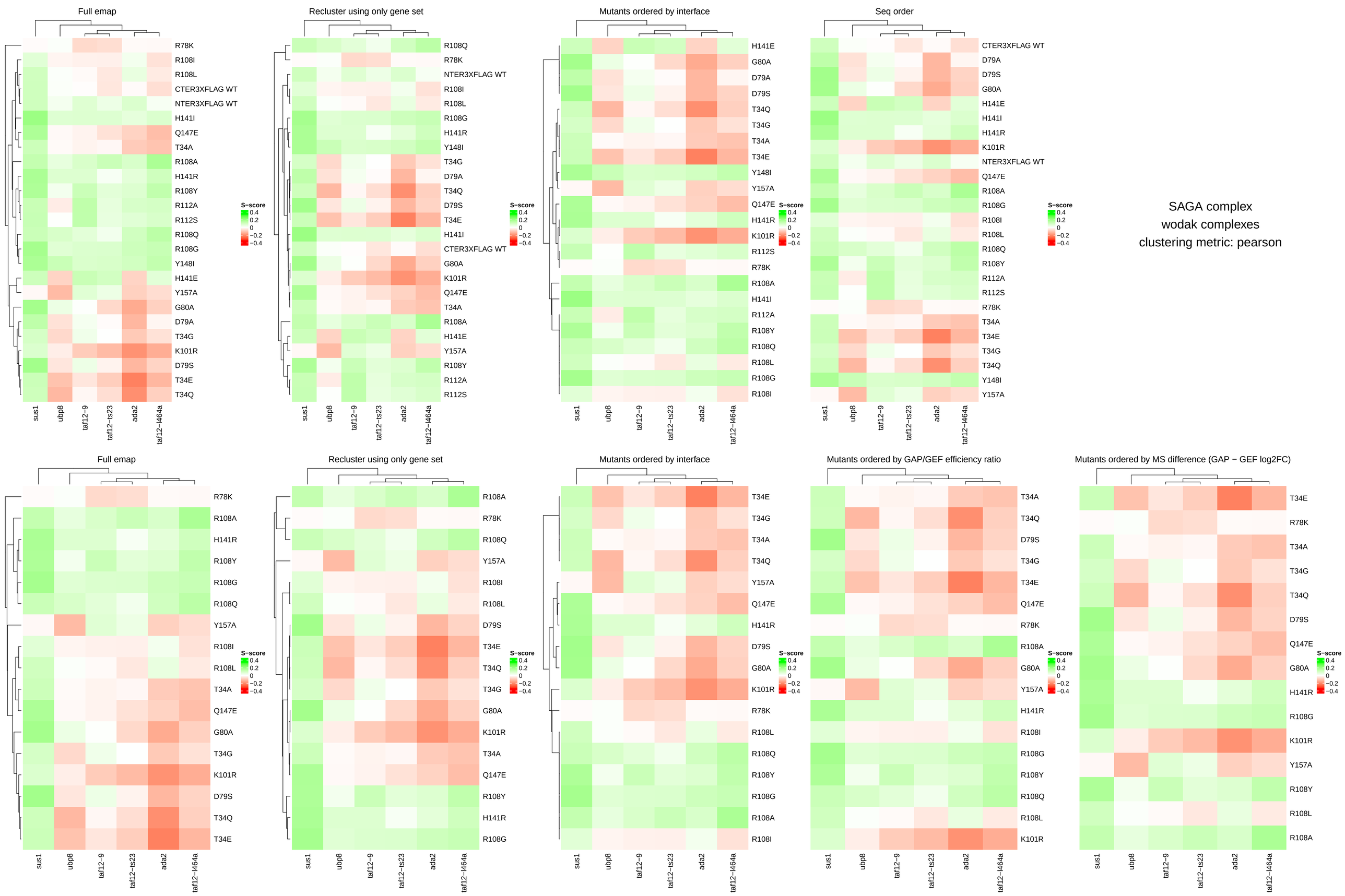

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
cdc46−1
cdc47−ts
mcm3−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
Y148I
T34G
T34E
Y157A
D79A
D79S
T34Q
H141R
H141E
R112S
R112A
H141I
R108Y
K101R
G80A
R108Q
T34A
CTER3XFLAG WT
NTER3XFLAG WT
Q147E
R108L
R78K
R108G
R108A
R108I
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Mcm2−7 complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34G
T34E
Y157A
H141R
R108Y
R108L
T34Q
D79S
R78K
R108G
R108A
R108I
K101R
T34A
Q147E
G80A
R108Q
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
rrp4−1
rrp42−5001
csl4−5001
mtr3−ts
Cytoplasmic exosome complex
wodak complexes
clustering metric: pearson

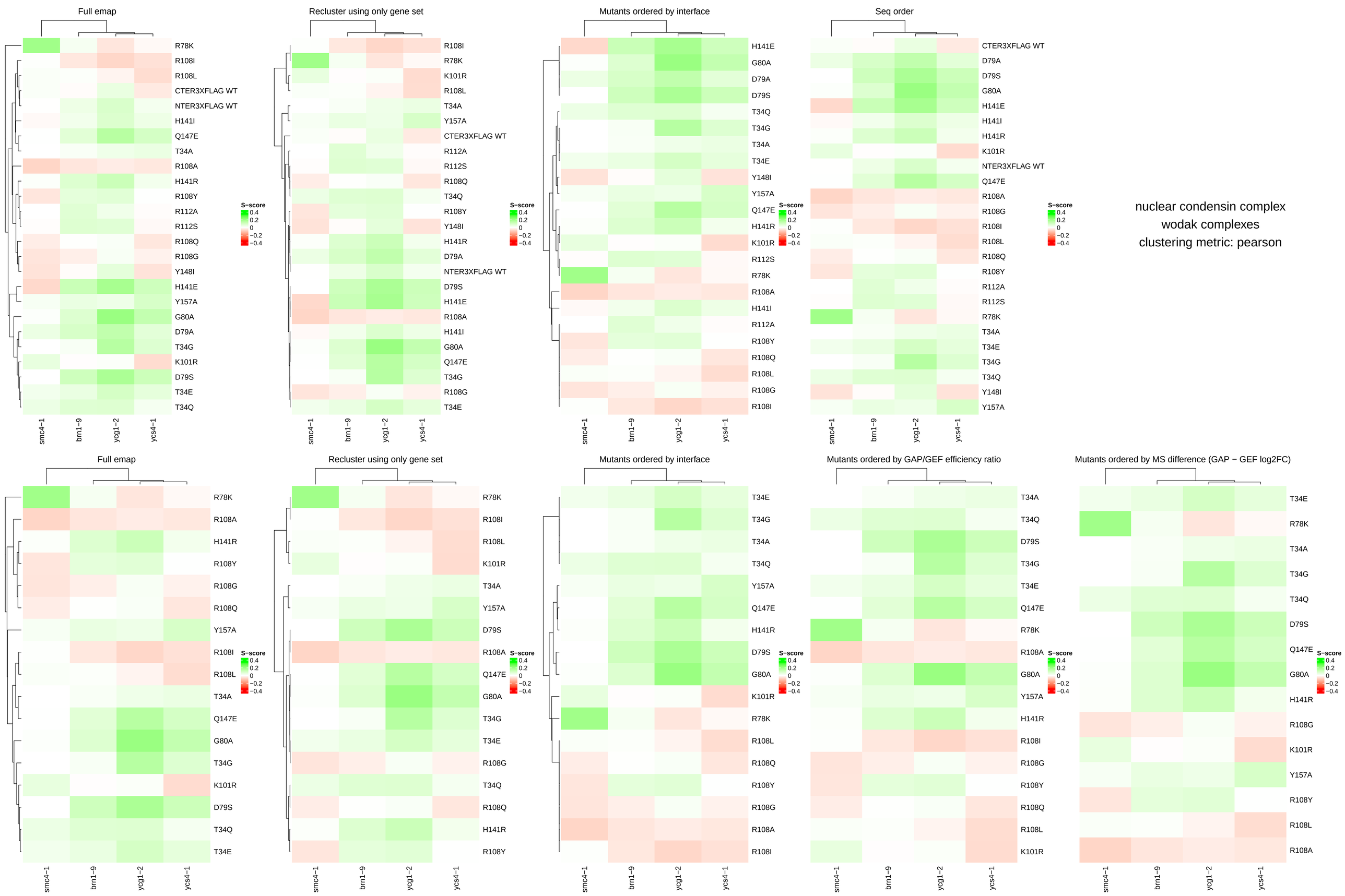

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
sfh1−1
ldb7
rsc6−5001
rsc8−ts16
rsc58−5001
rsc8−ts21
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
RSC complex
wodak complexes
clustering metric: pearson

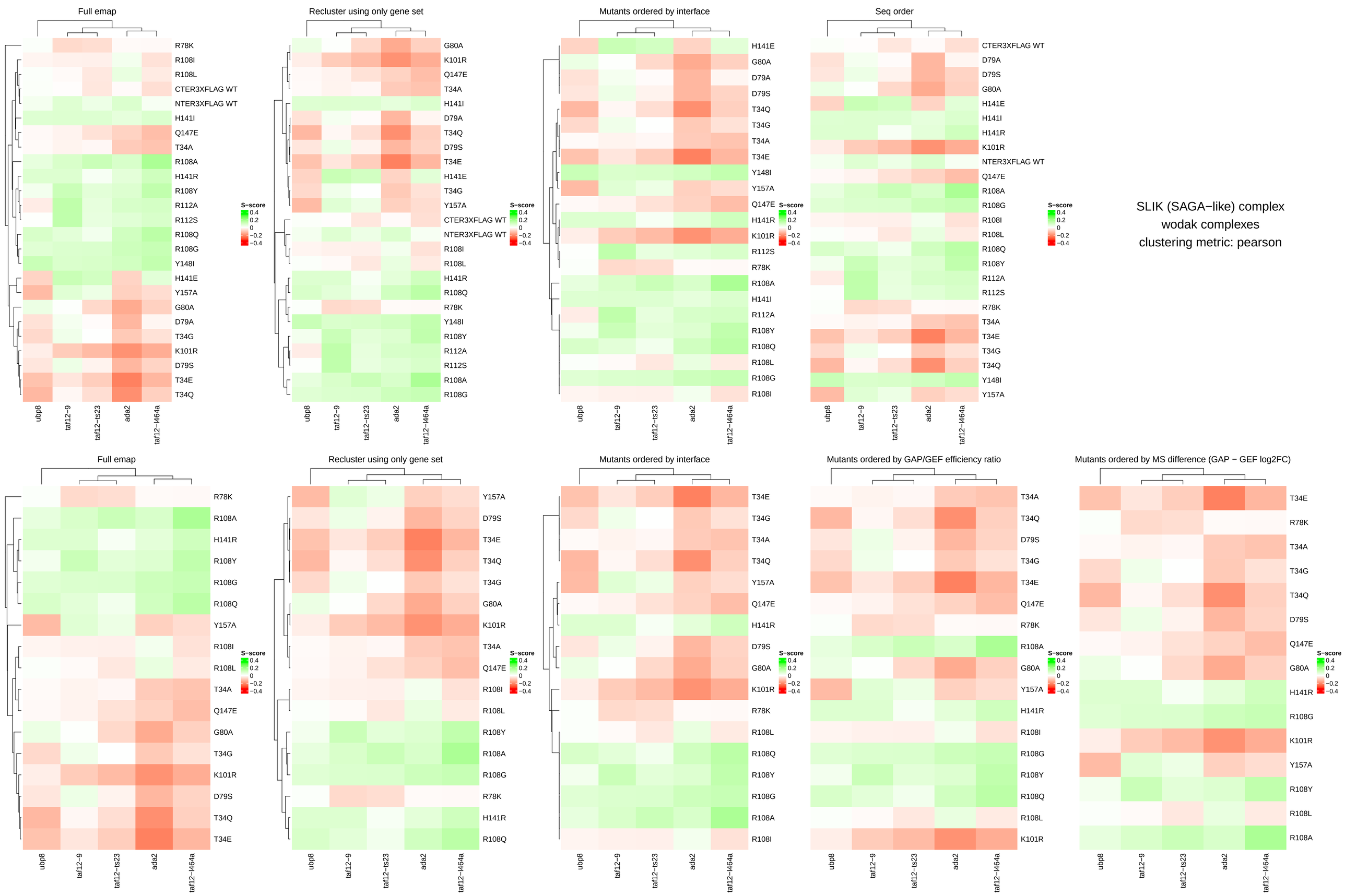

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
ceg1−34
ceg1−ts
cet1−2
cet1−15
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
Q147E
H141R
R112S
R108L
R108I
R112A
CTER3XFLAG WT
G80A
NTER3XFLAG WT
H141I
R108Q
R108A
R108Y
R108G
Y148I
T34A
D79A
H141E
D79S
T34G
R78K
K101R
Y157A
T34E
T34Q
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
mRNA guanylyl transferase (capping complex)
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
G80A
R108L
Q147E
R108I
H141R
R108G
R108Q
R108A
R108Y
T34A
R78K
D79S
T34G
Y157A
K101R
T34Q
T34E
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

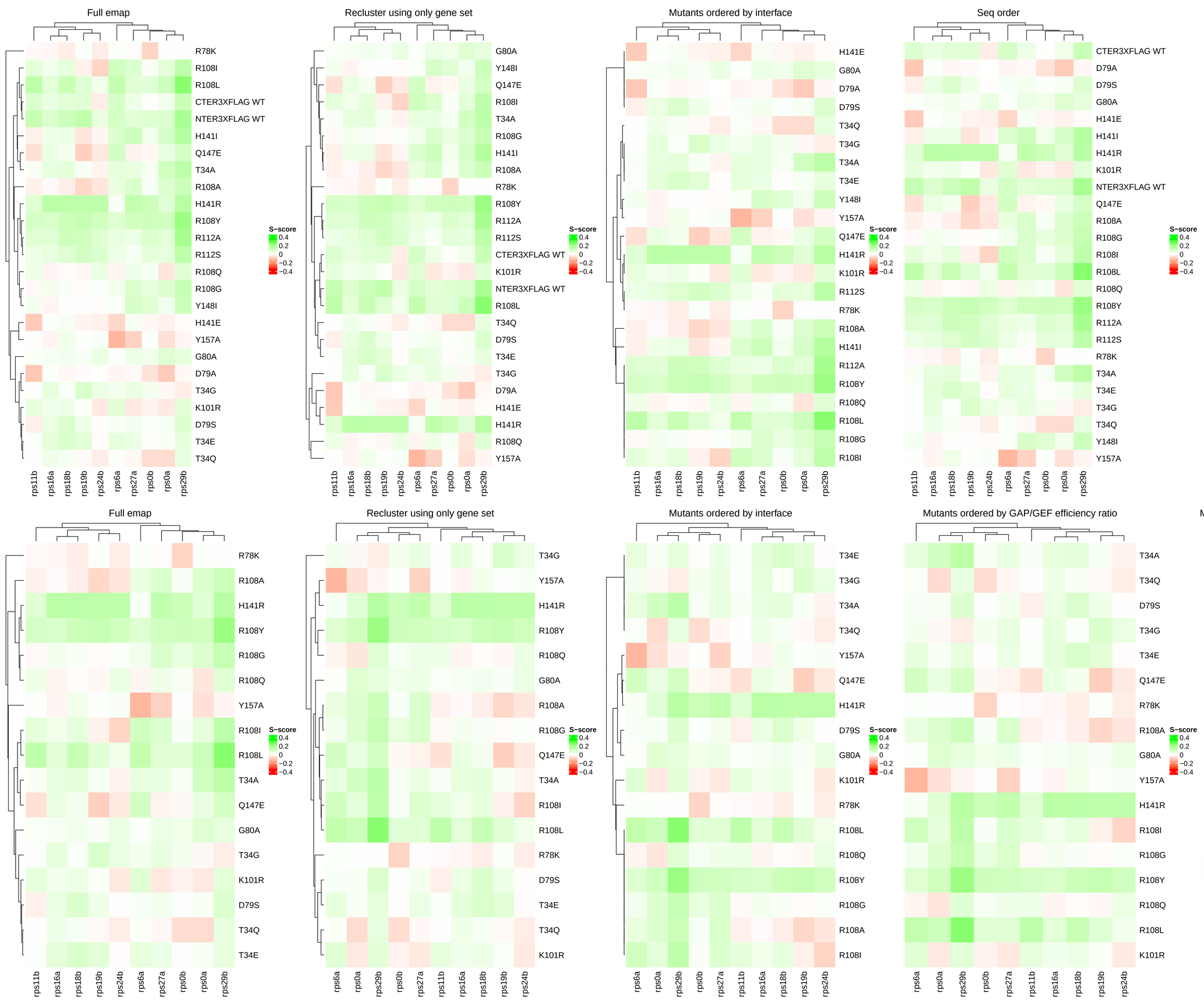

Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
pac10
gim3
yke2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
NTER3XFLAG WT
R108A
CTER3XFLAG WT
R108Q
R108G
R108I
R108L
T34A
K101R
G80A
R78K
Q147E
R112S
H141I
R108Y
H141E
Y157A
D79S
R112A
Y148I
H141R
T34E
T34Q
D79A
T34G
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
prefoldin complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
R108A
R108Q
R108G
R108I
T34A
R108L
K101R
R78K
G80A
Q147E
T34E
H141R
T34Q
T34G
D79S
Y157A
R108Y
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A



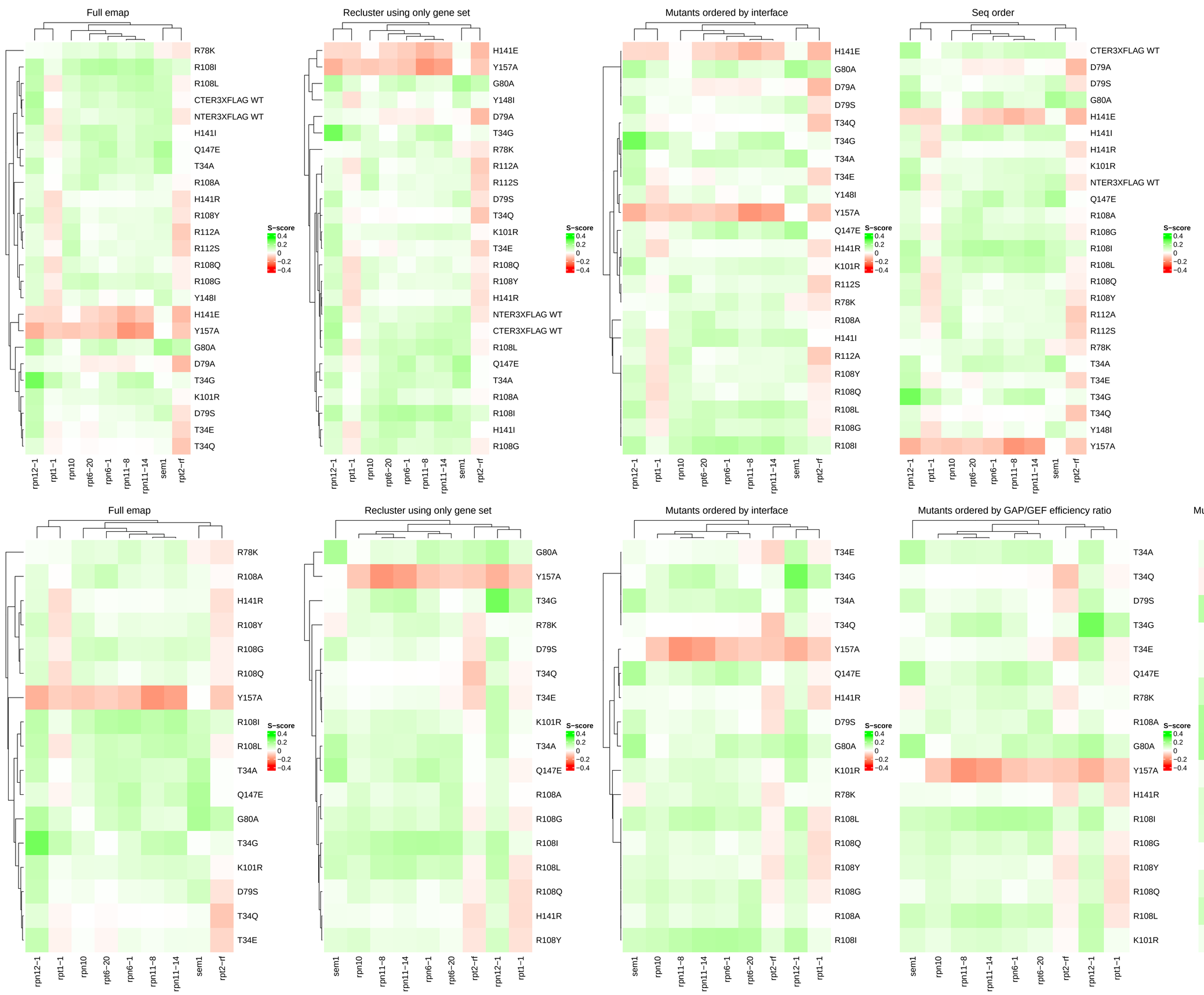
SAGA complex
wodak complexes
clustering metric: pearson


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
smc4−1
brn1−9
ycg1−2
ycs4−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108I
R78K
K101R
R108L
T34A
Y157A
CTER3XFLAG WT
R112A
R112S
R108Q
T34Q
R108Y
Y148I
H141R
D79A
NTER3XFLAG WT
D79S
H141E
R108A
H141I
G80A
Q147E
T34G
R108G
T34E
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
nuclear condensin complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
R78K
R108I
R108L
K101R
T34A
Y157A
D79S
R108A
Q147E
G80A
T34G
T34E
R108G
T34Q
R108Q
H141R
R108Y
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A

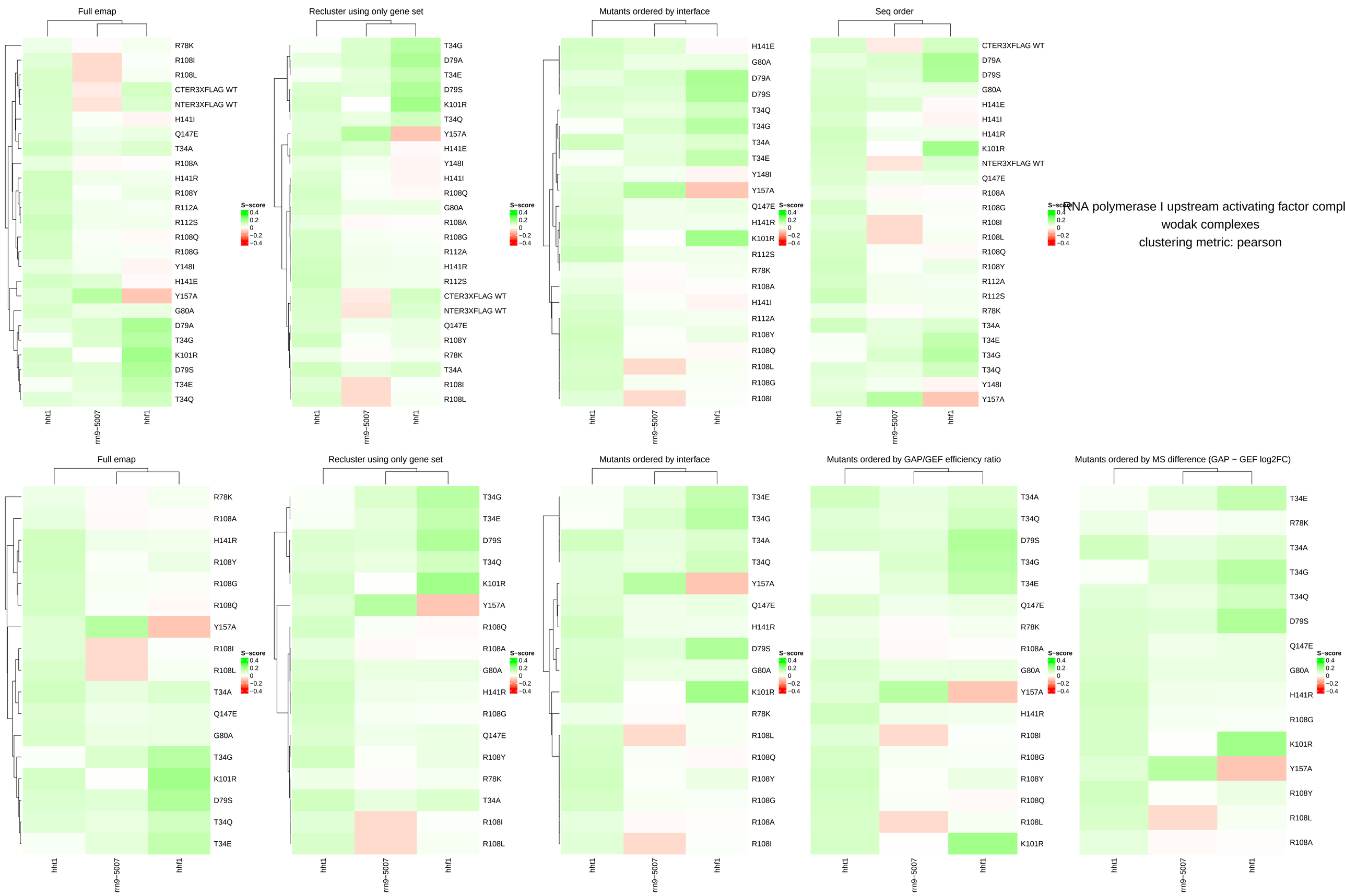

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ubp8
taf12−9
taf12−ts23
ada2
taf12−l464a
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
SLIK (SAGA−like) complex
wodak complexes
clustering metric: pearson

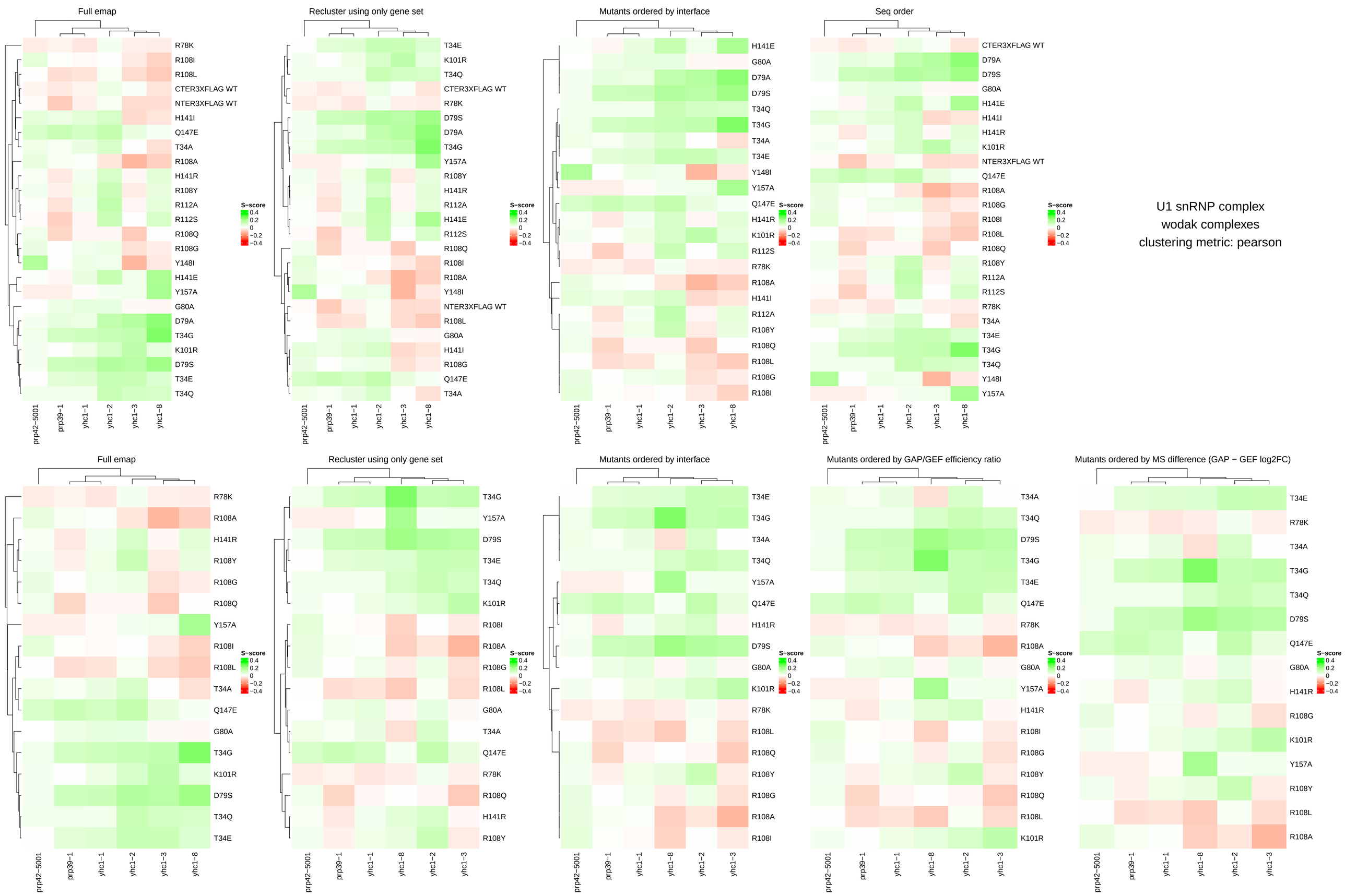


cytoplasmic ribosomal small subunit
wodak complexes
clustering metric: pearson

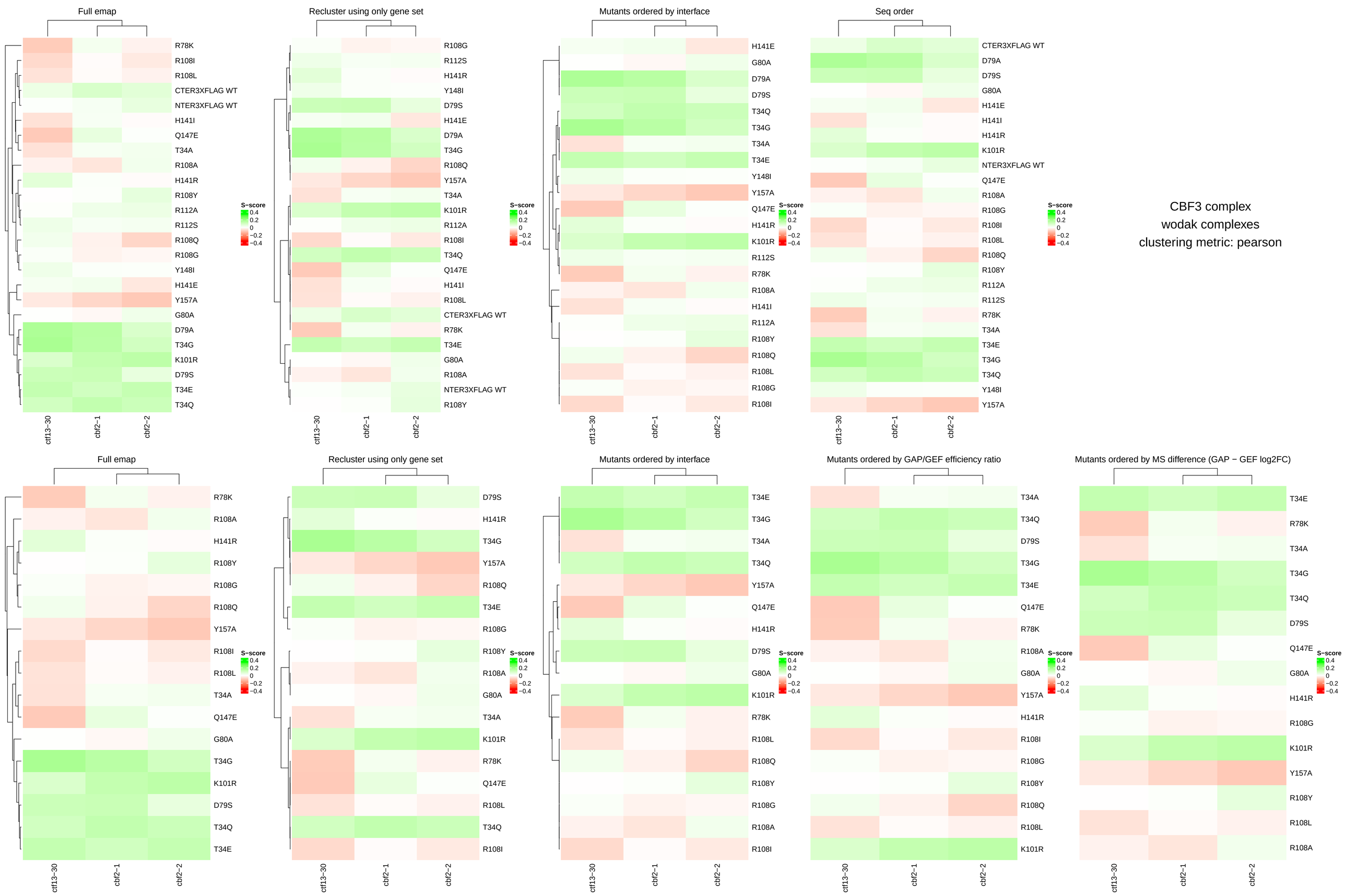


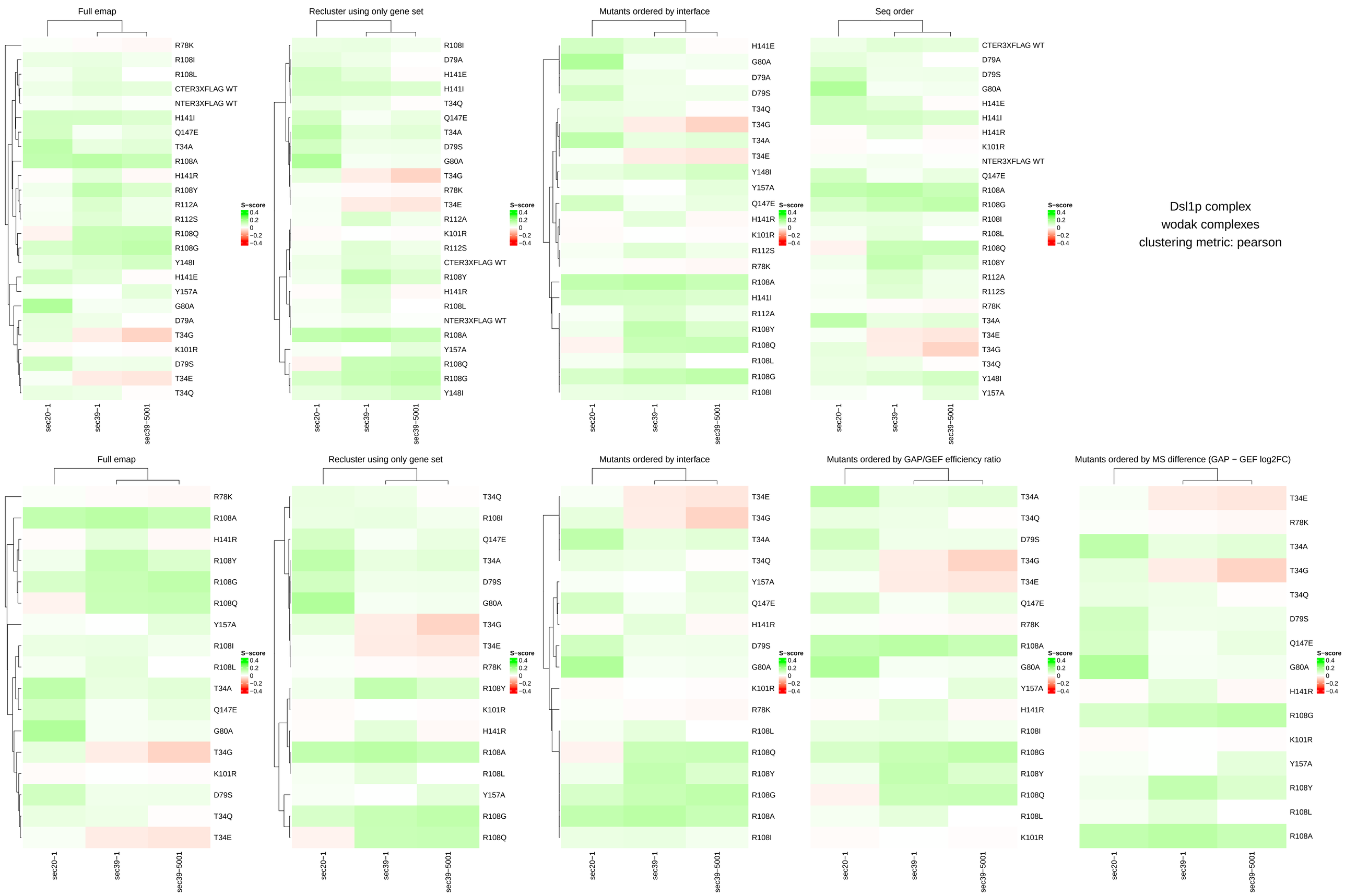
19/22S regulator
wodak complexes
clustering metric: pearson


RNA polymerase I upstream activating factor compl
wodak complexes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
hht1
rrn9−5007
hhf1



U1 snRNP complex
wodak complexes
clustering metric: pearson


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
ctf13−30
cbf2−1
cbf2−2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108G
R112S
H141R
Y148I
D79S
H141E
D79A
T34G
R108Q
Y157A
T34A
K101R
R112A
R108I
T34Q
Q147E
H141I
R108L
CTER3XFLAG WT
R78K
T34E
G80A
R108A
NTER3XFLAG WT
R108Y
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
CBF3 complex
wodak complexes
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A


Full emap
R78K
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
H141I
Q147E
T34A
R108A
H141R
R108Y
R112A
R112S
R108Q
R108G
Y148I
H141E
Y157A
G80A
D79A
T34G
K101R
D79S
T34E
T34Q
sec20−1
sec39−1
sec39−5001
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108I
D79A
H141E
H141I
T34Q
Q147E
T34A
D79S
G80A
T34G
R78K
T34E
R112A
K101R
R112S
CTER3XFLAG WT
R108Y
H141R
R108L
NTER3XFLAG WT
R108A
Y157A
R108Q
R108G
Y148I
Mutants ordered by interface
H141E
G80A
D79A
D79S
T34Q
T34G
T34A
T34E
Y148I
Y157A
Q147E
H141R
K101R
R112S
R78K
R108A
H141I
R112A
R108Y
R108Q
R108L
R108G
R108I
Seq order
CTER3XFLAG WT
D79A
D79S
G80A
H141E
H141I
H141R
K101R
NTER3XFLAG WT
Q147E
R108A
R108G
R108I
R108L
R108Q
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
Dsl1p complex
wodak complexes
clustering metric: pearson
Full emap
R78K
R108A
H141R
R108Y
R108G
R108Q
Y157A
R108I
R108L
T34A
Q147E
G80A
T34G
K101R
D79S
T34Q
T34E
Recluster using only gene set
T34Q
R108I
Q147E
T34A
D79S
G80A
T34G
T34E
R78K
R108Y
K101R
H141R
R108A
R108L
Y157A
R108G
R108Q
Mutants ordered by interface
T34E
T34G
T34A
T34Q
Y157A
Q147E
H141R
D79S
G80A
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Mutants ordered by GAP/GEF efficiency ratio
T34A
T34Q
D79S
T34G
T34E
Q147E
R78K
R108A
G80A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
Mutants ordered by MS difference (GAP − GEF log2FC)
T34E
R78K
T34A
T34G
T34Q
D79S
Q147E
G80A
H141R
R108G
K101R
Y157A
R108Y
R108L
R108A
sec20−1
sec39−1
sec39−5001