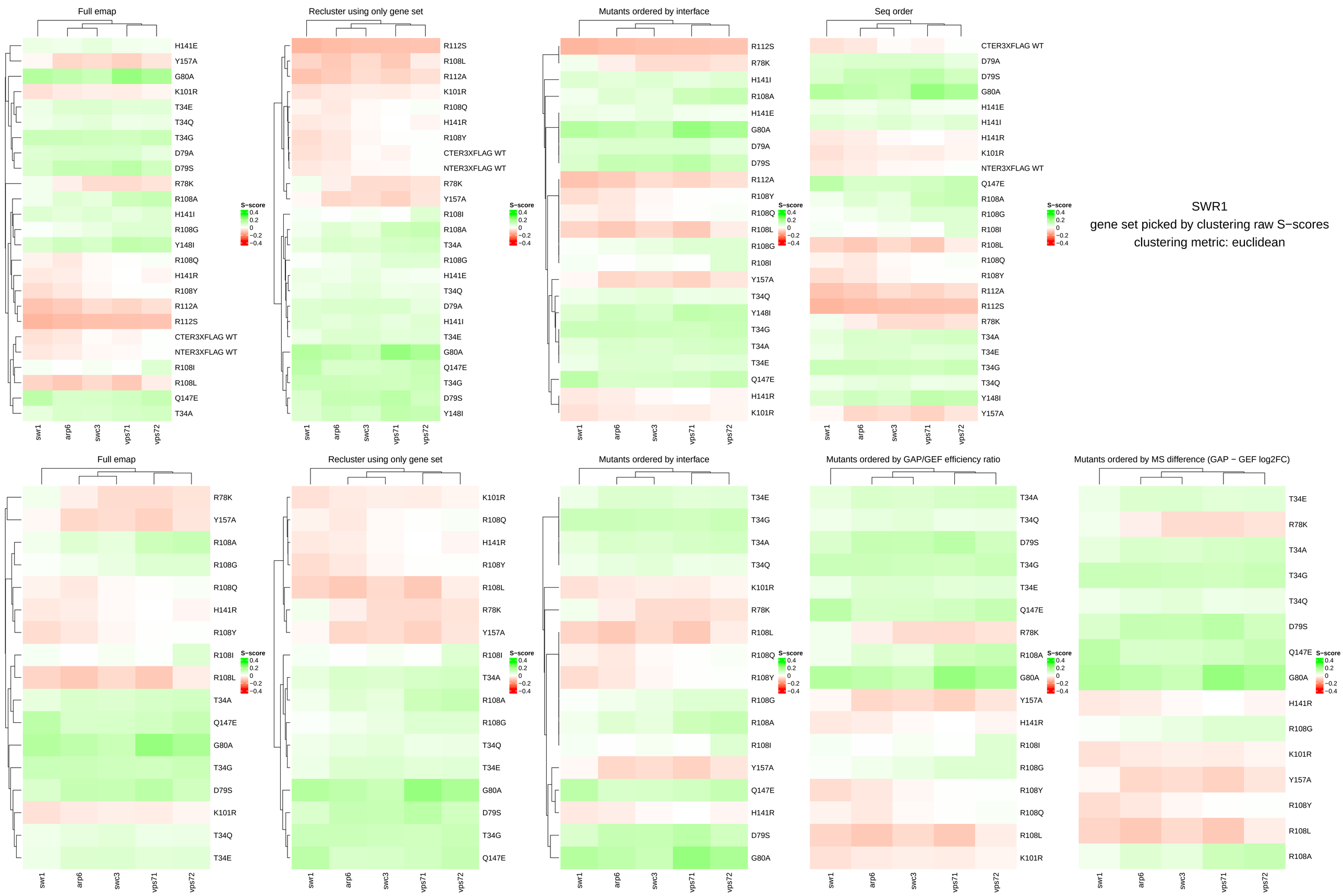
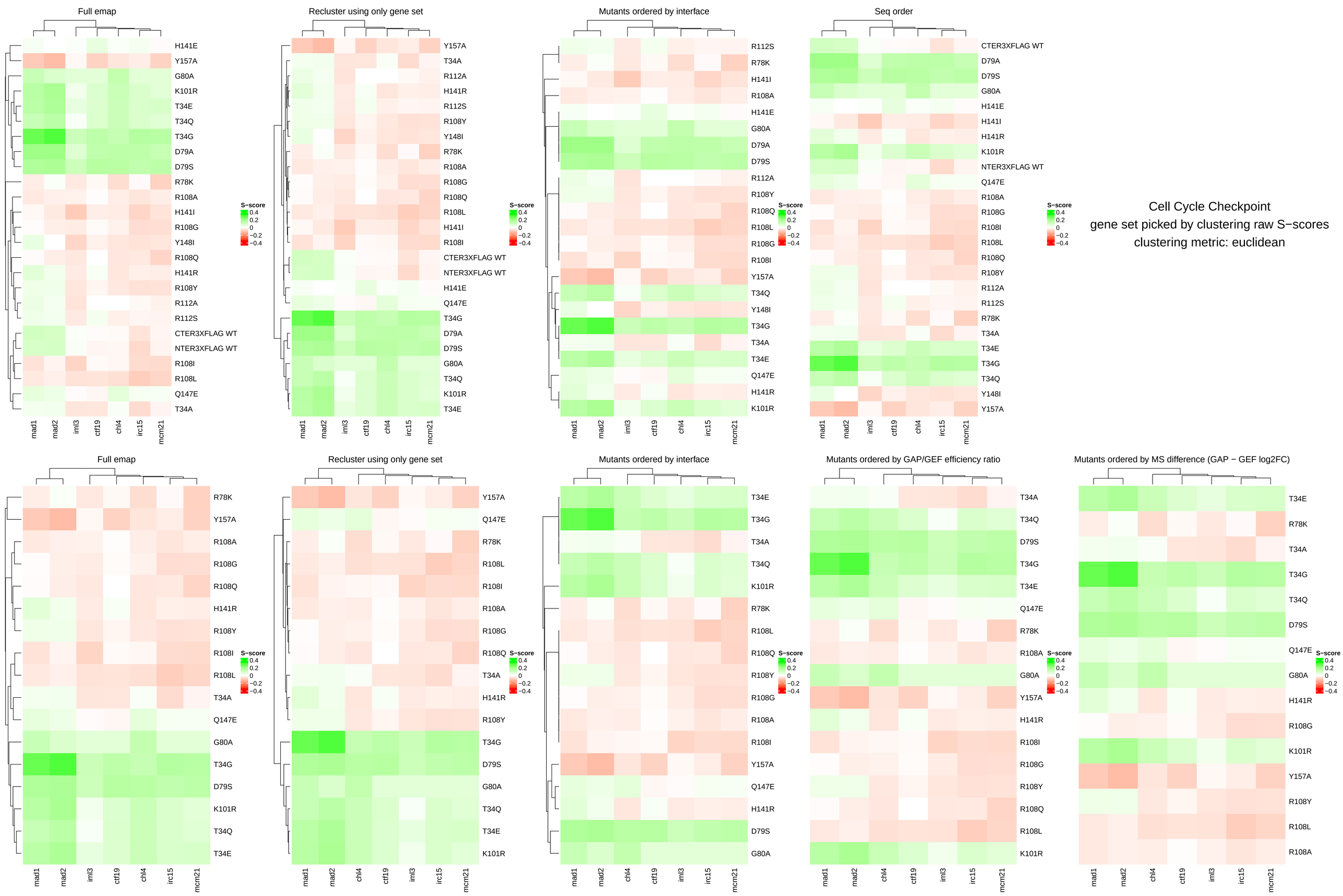
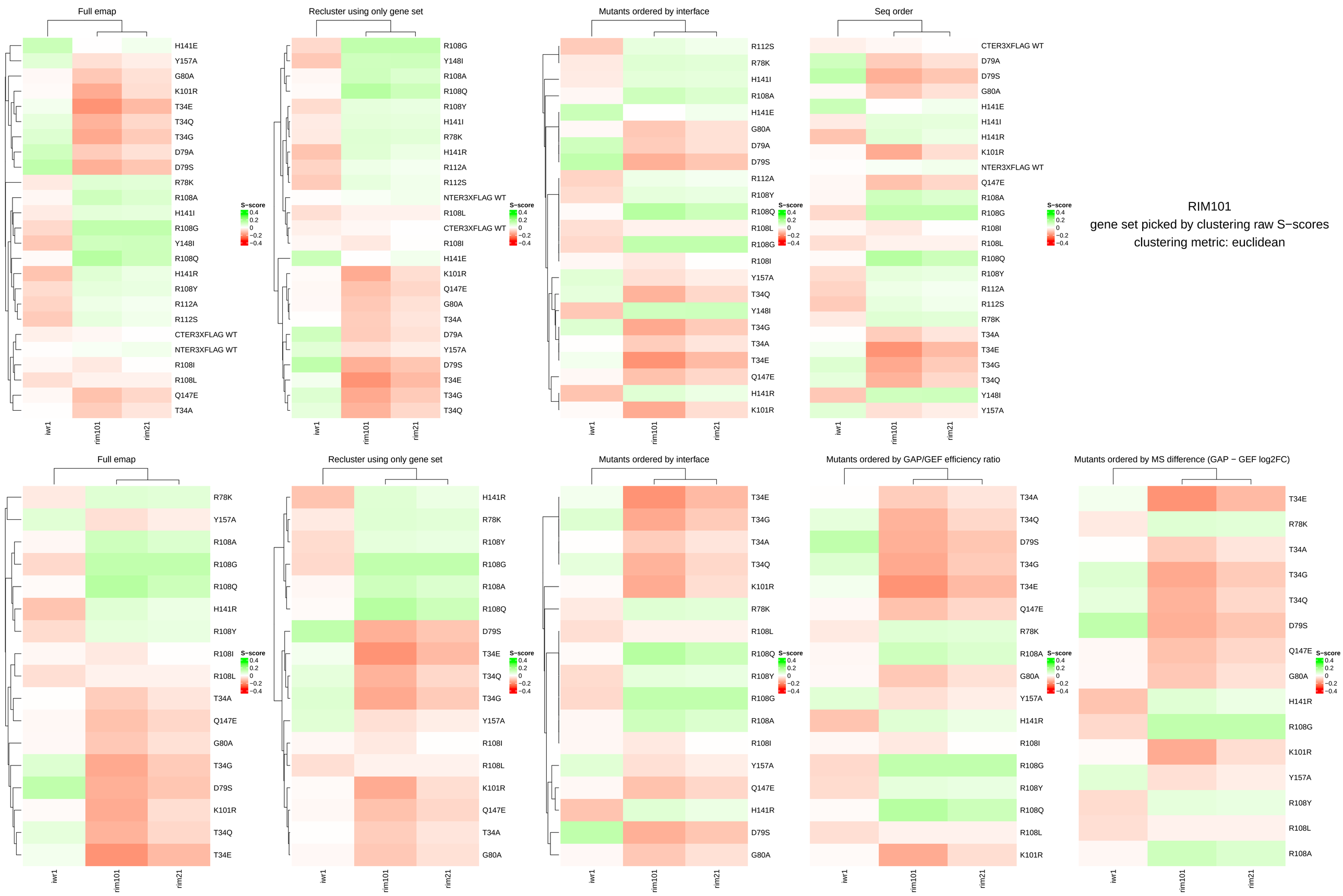
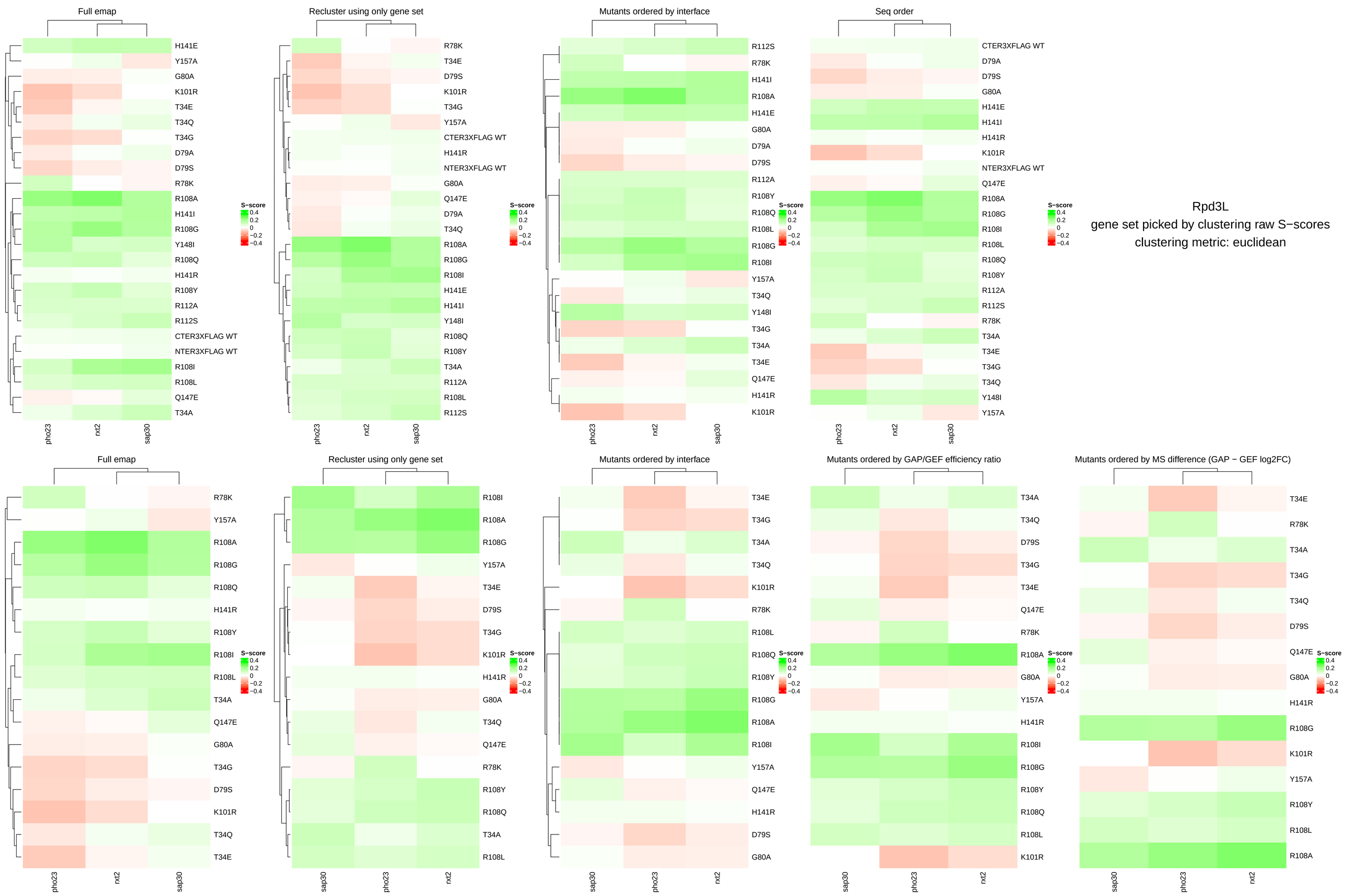
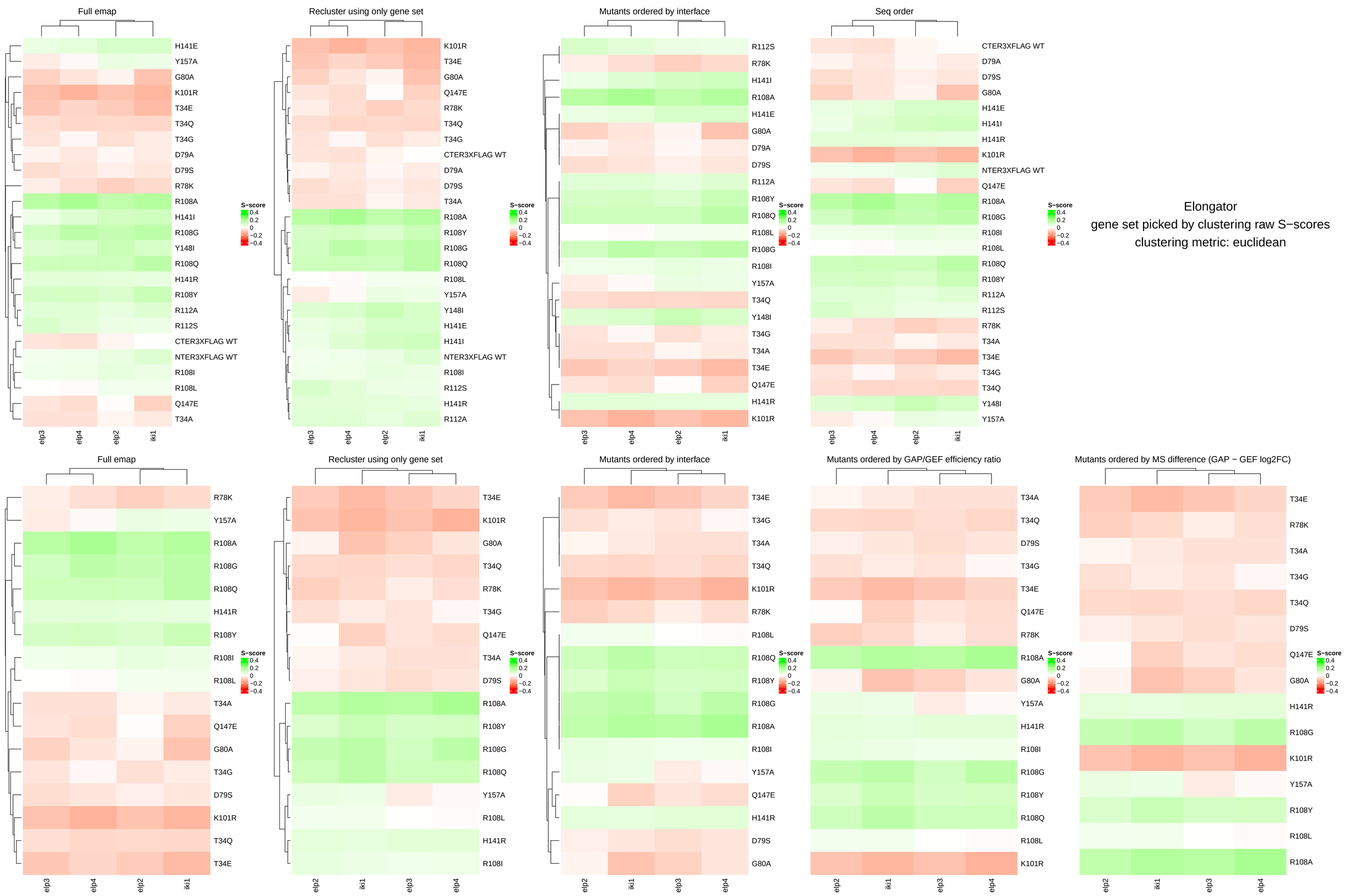

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
swr1
arp6
swc3
vps71
vps72
SWR1
gene set picked by clustering raw S−scores
clustering metric: euclidean

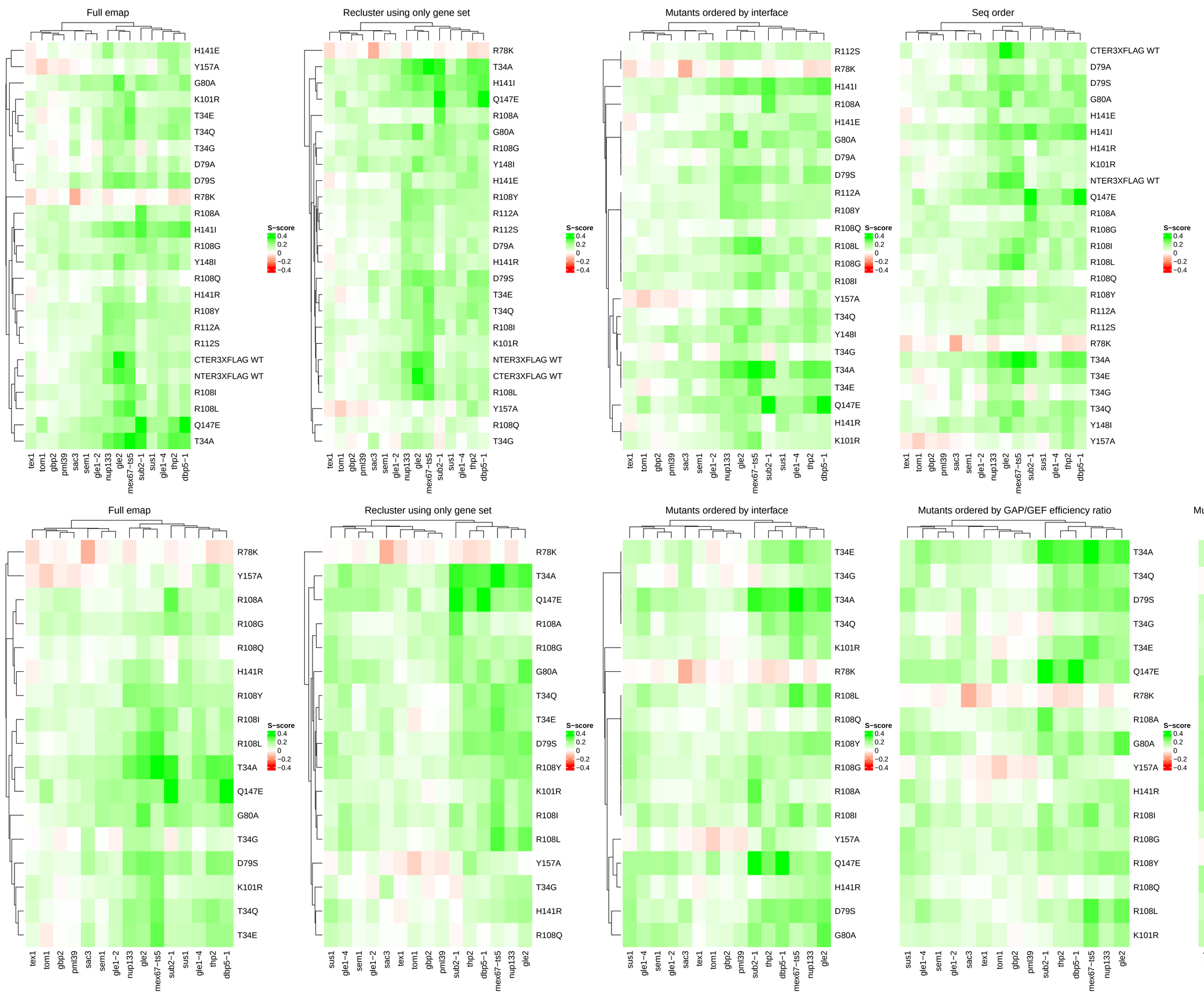

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
mad1
mad2
iml3
ctf19
chl4
irc15
mcm21
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
R112S
R78K
T34A
R112A
H141R
R108Y
Y148I
R108I
CTER3XFLAG WT
NTER3XFLAG WT
H141E
Q147E
R108L
R108Q
R108G
R108A
Cell Cycle Checkpoint
gene set picked by clustering raw S−scores
clustering metric: euclidean


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
iwr1
rim101
rim21
RIM101
gene set picked by clustering raw S−scores
clustering metric: euclidean


Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
pho23
rxt2
sap30
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R78K
T34E
D79S
K101R
T34G
Y157A
CTER3XFLAG WT
H141R
NTER3XFLAG WT
G80A
Q147E
D79A
T34Q
R108A
R108G
R108I
H141E
H141I
Y148I
R108Q
R108Y
T34A
R112A
R108L
R112S
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
R108I
R108A
R108G
Y157A
T34E
D79S
T34G
K101R
H141R
G80A
T34Q
Q147E
R78K
R108Y
R108Q
T34A
R108L
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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
sap30
pho23
rxt2


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
elp3
elp4
elp2
iki1
Elongator
gene set picked by clustering raw S−scores
clustering metric: euclidean

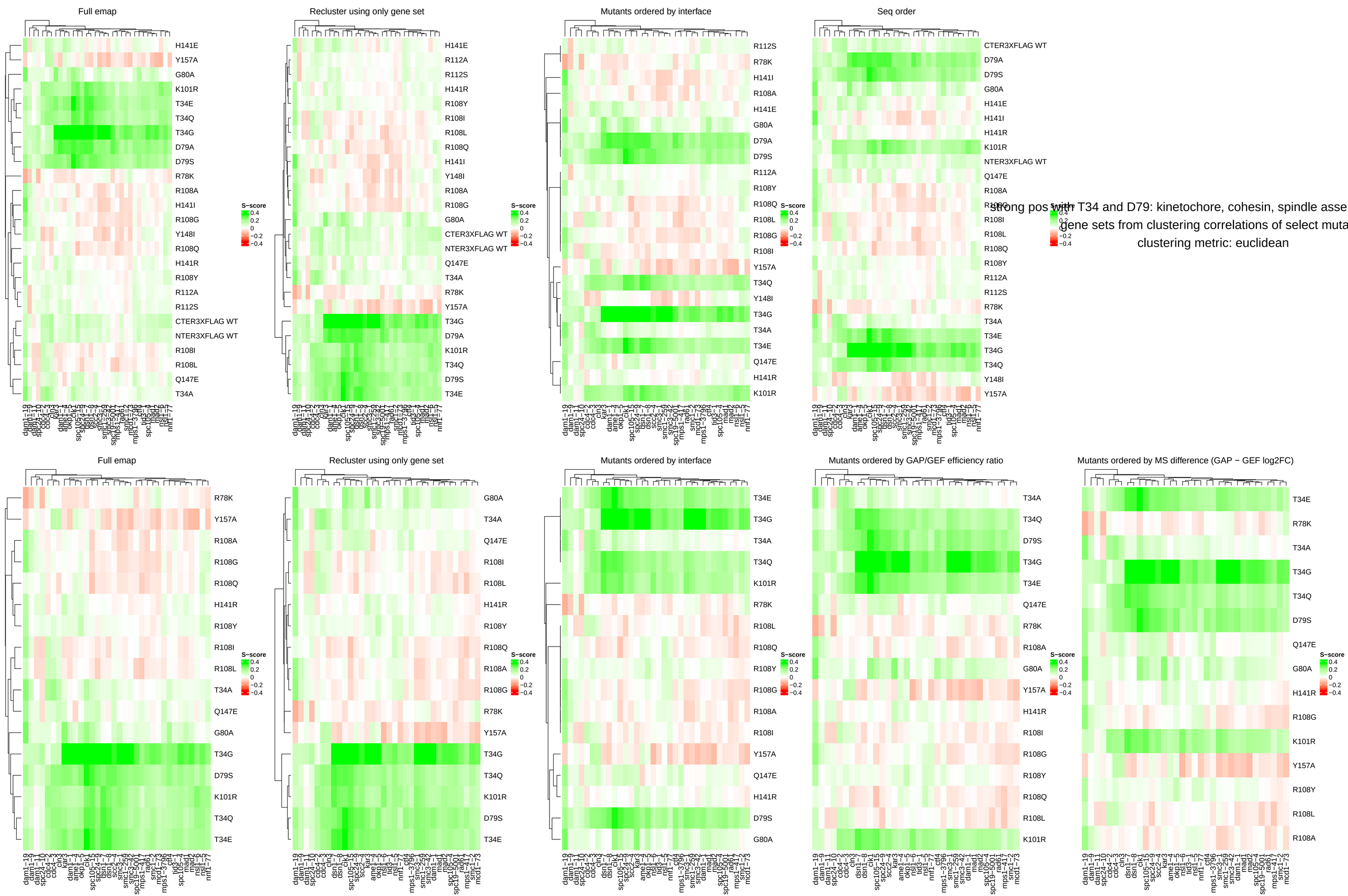
Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
src1
hog1
ssk2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108Q
R78K
T34G
Y157A
H141E
K101R
T34E
T34Q
D79A
D79S
CTER3XFLAG WT
R108A
Y148I
NTER3XFLAG WT
R108I
H141R
R108L
R108G
R108Y
R112A
R112S
T34A
H141I
G80A
Q147E
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
Y157A
R78K
R108Q
T34G
D79S
K101R
T34Q
T34E
T34A
Q147E
G80A
H141R
R108L
R108G
R108Y
R108A
R108I
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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



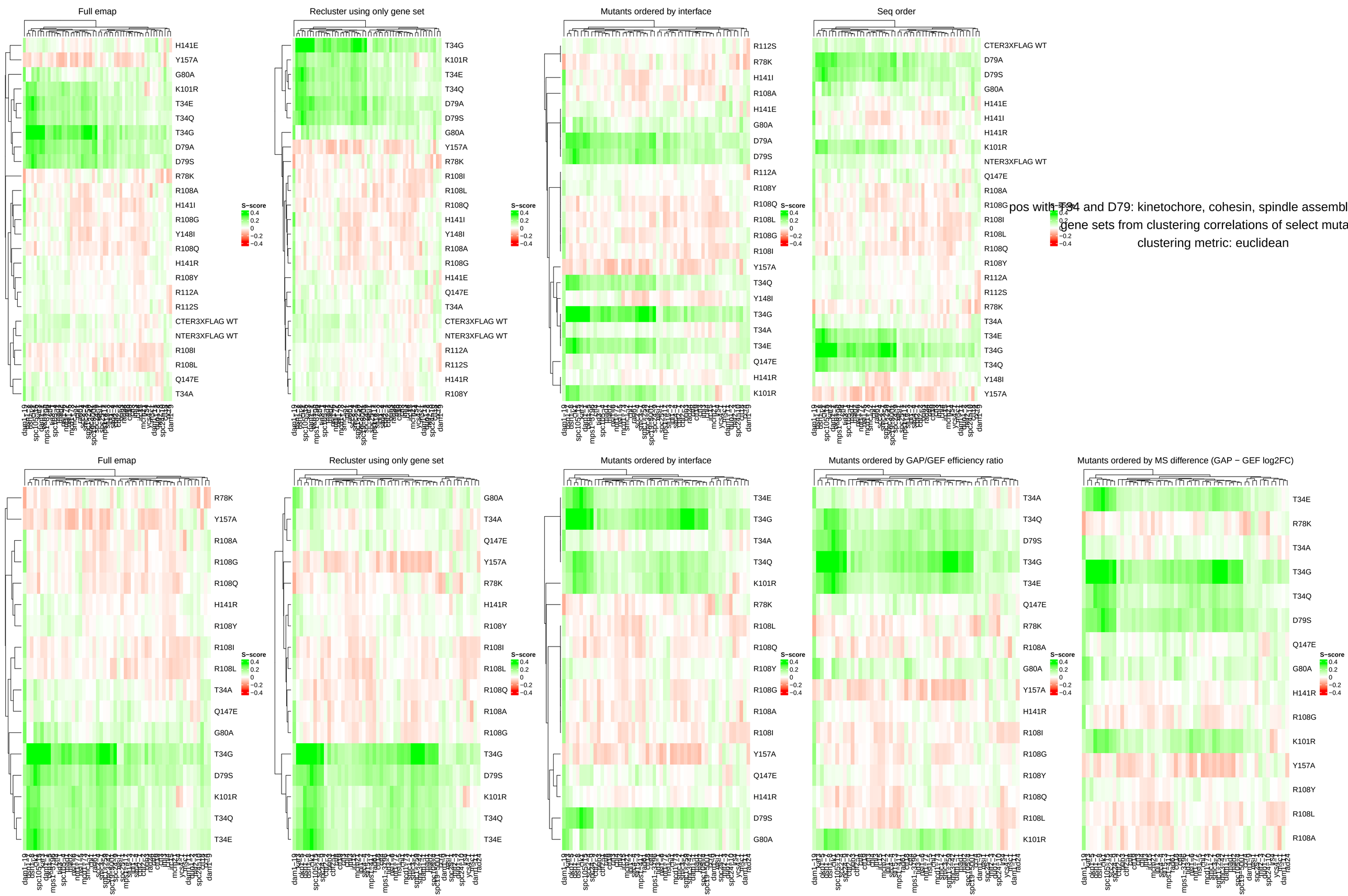
mRNA export

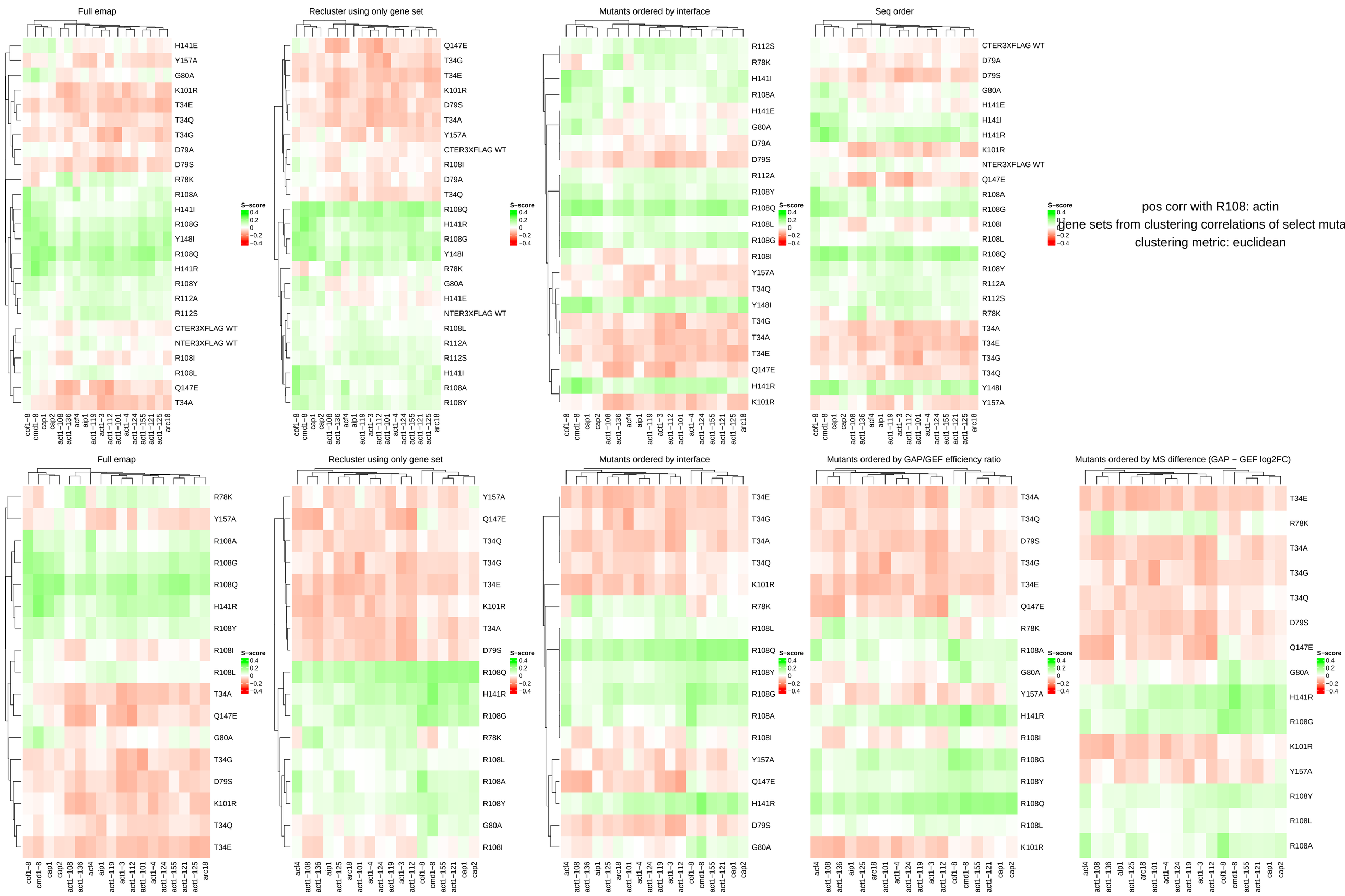
gene set picked by clustering raw S−scores

clustering metric: euclidean



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

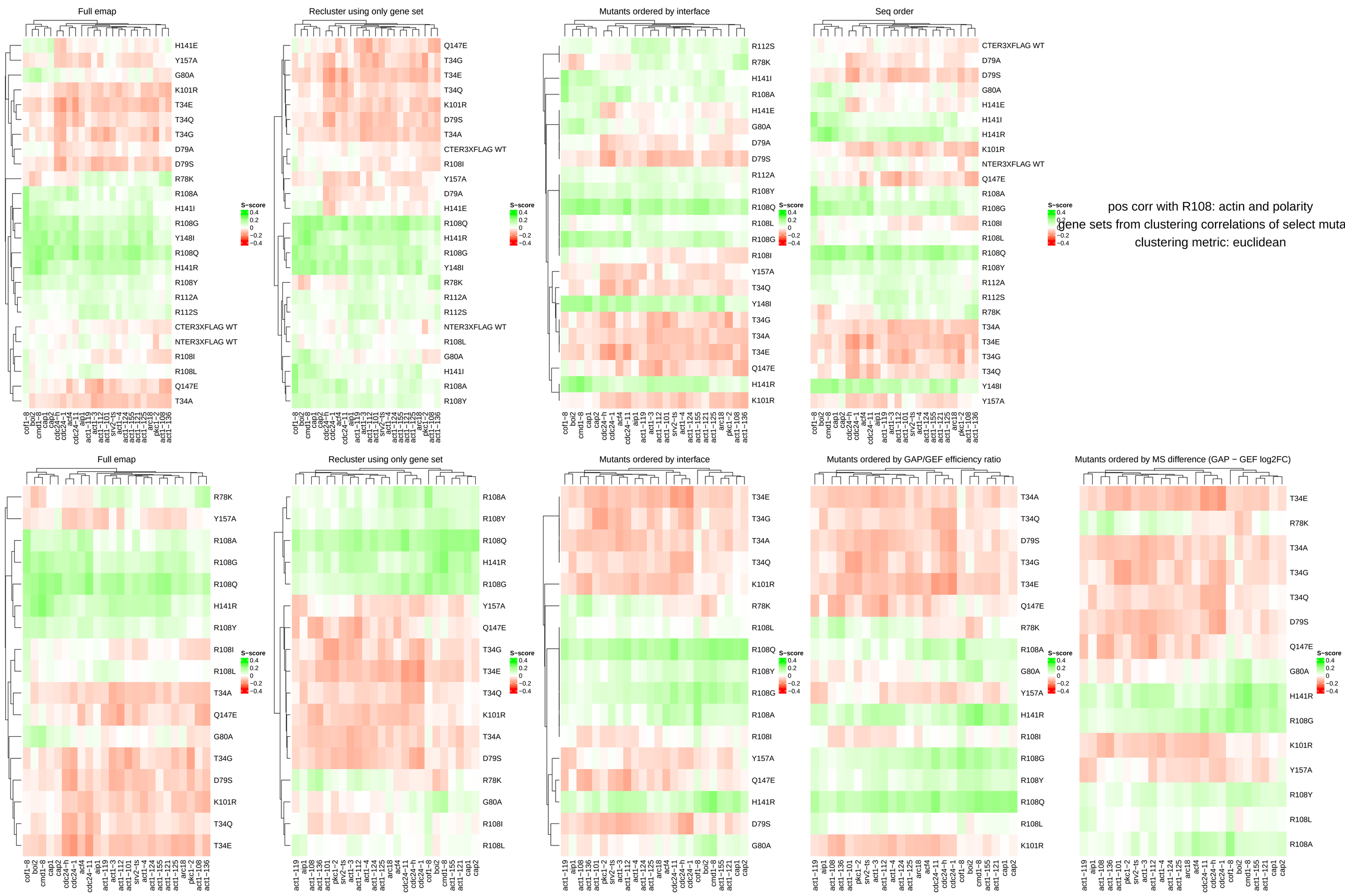

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
T34G
K101R
T34E
T34Q
D79A
D79S
G80A
Y157A
R78K
R108I
R108L
R108Q
H141I
Y148I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

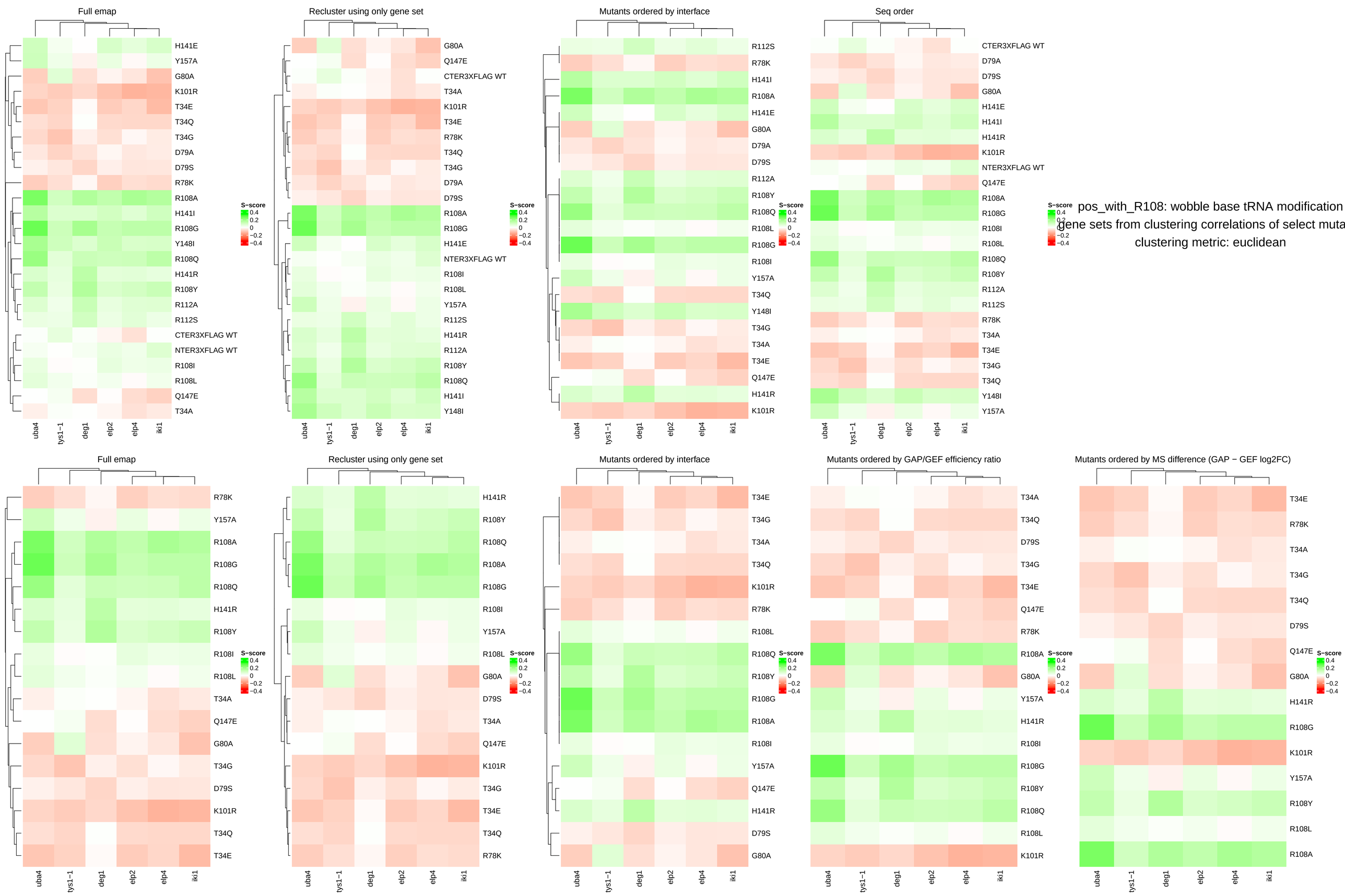


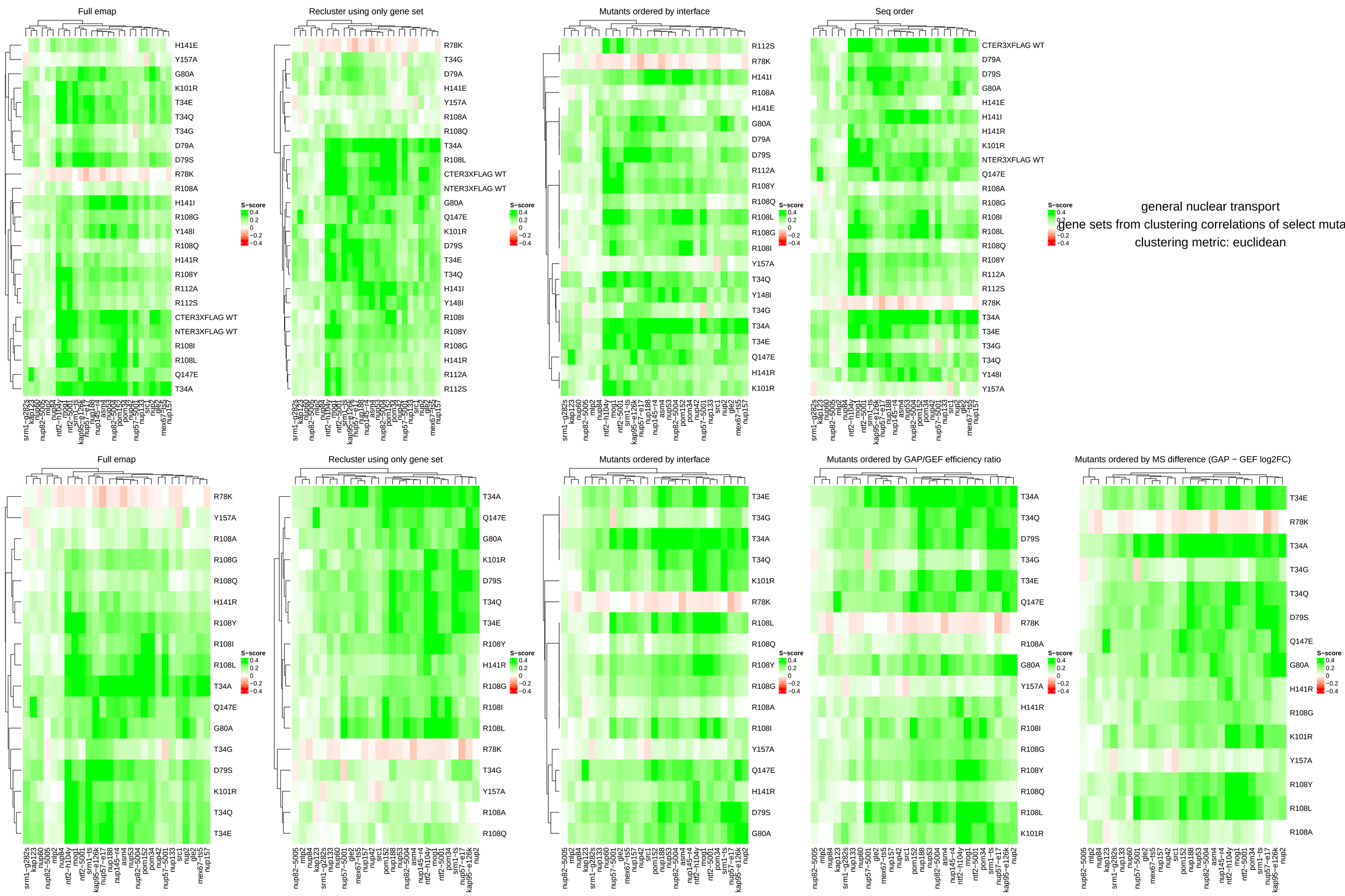
pos corr with R108: actin

gene sets from clustering correlations of select muta

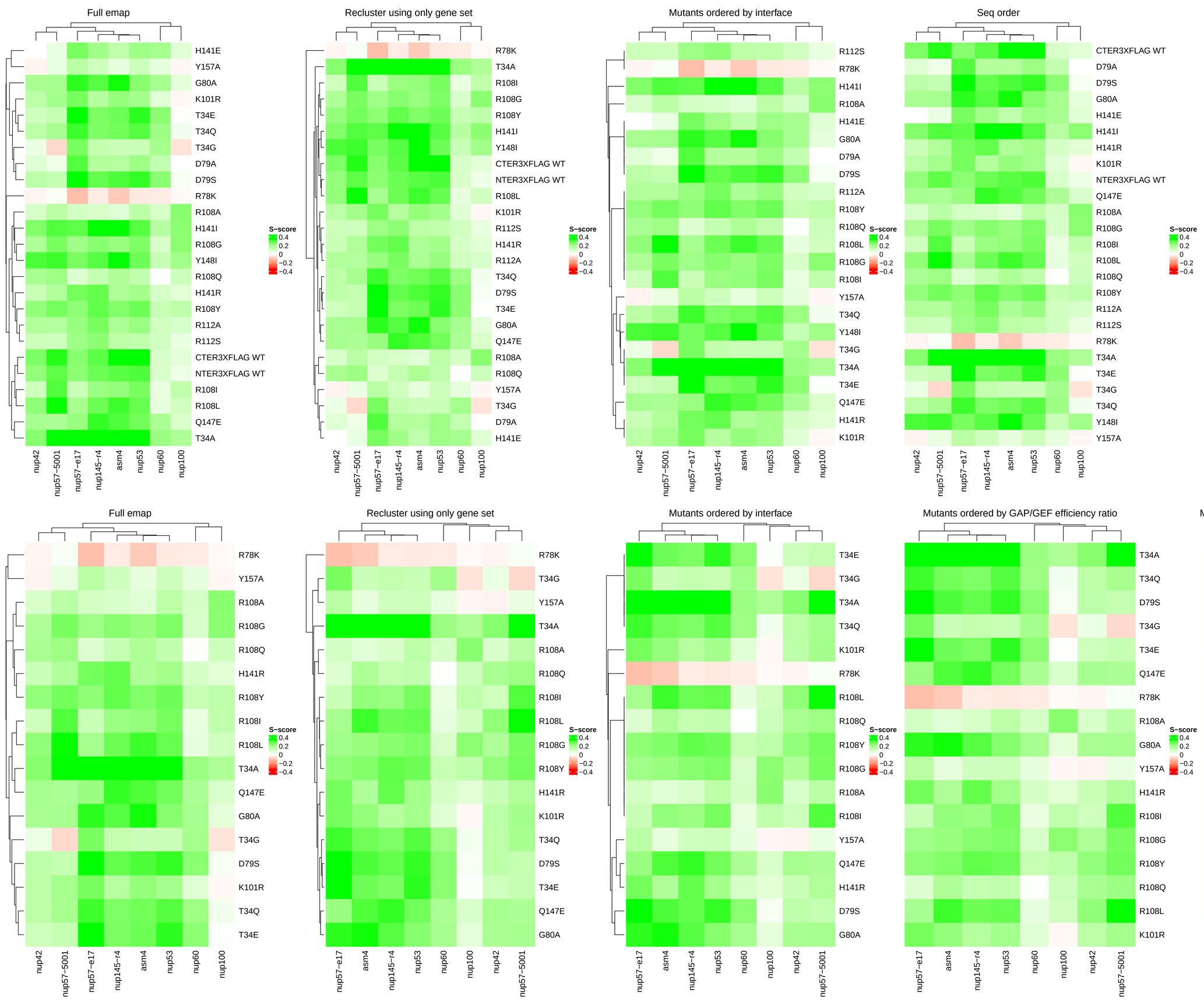
clustering metric: euclidean


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: euclidean

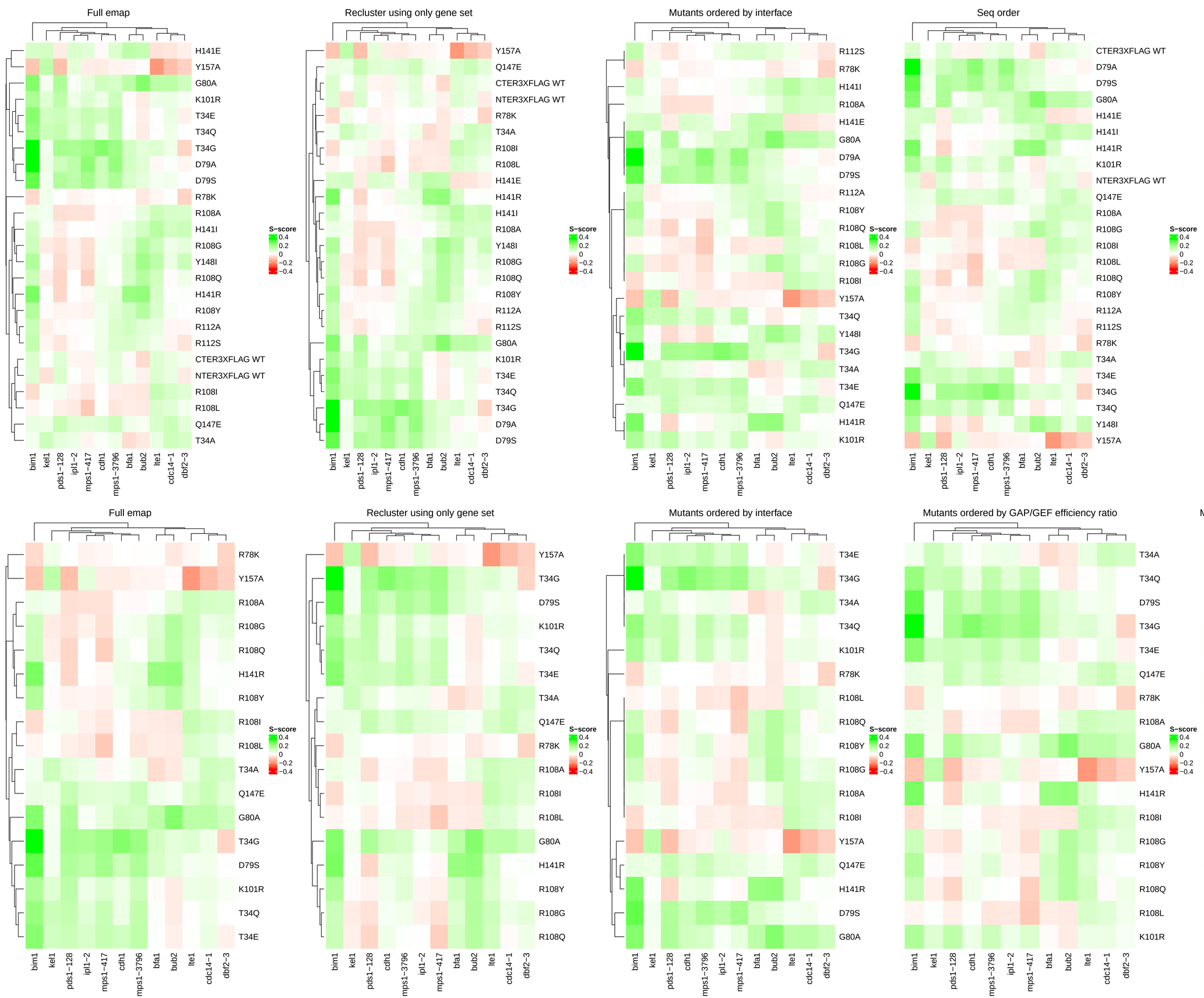

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
uba4
tys1−1
deg1
elp2
elp4
iki1
pos_with_R108: wobble base tRNA modification
gene sets from clustering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



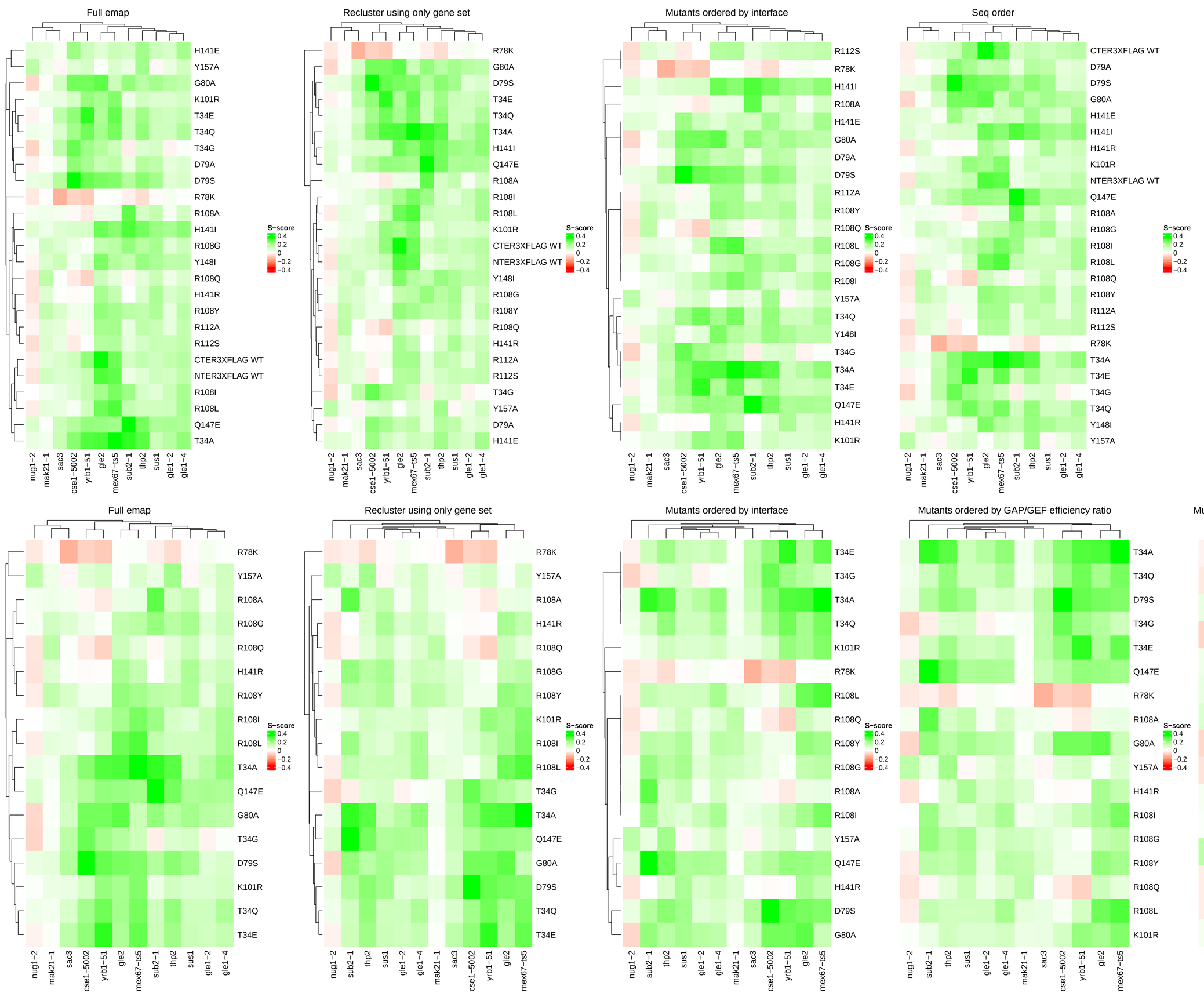
general nuclear transport
gene sets from clustering correlations of select muta
clustering metric: euclidean



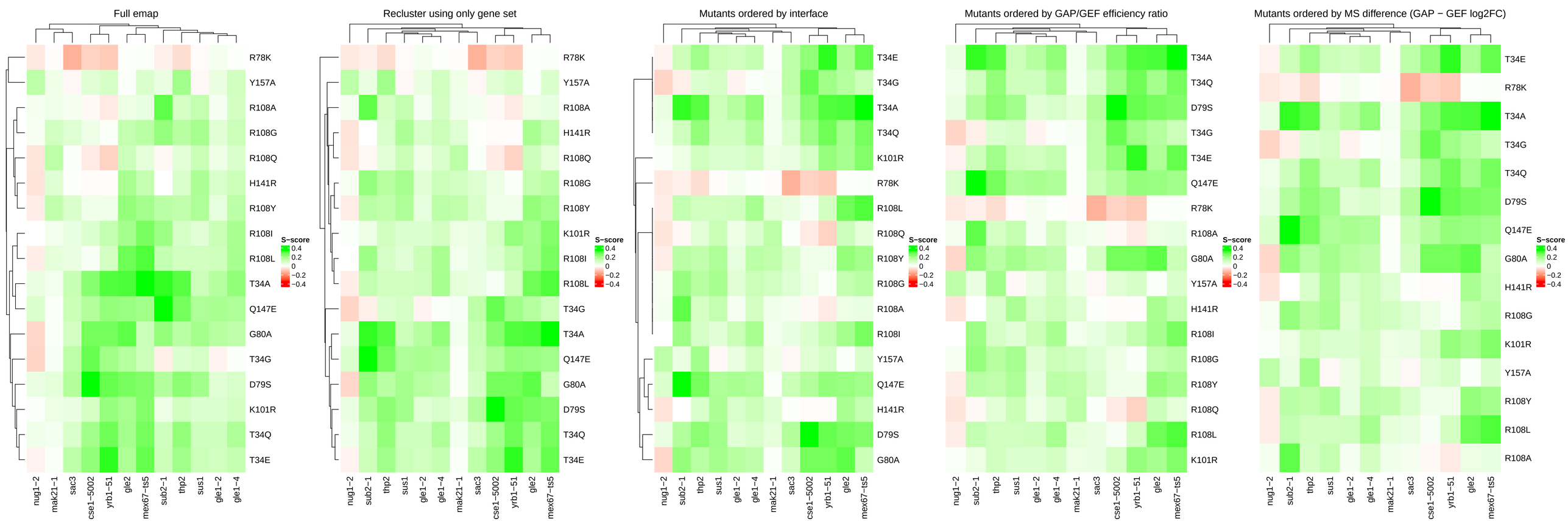
nuclear pore central transport channel
tina hand−curated processes
clustering metric: euclidean

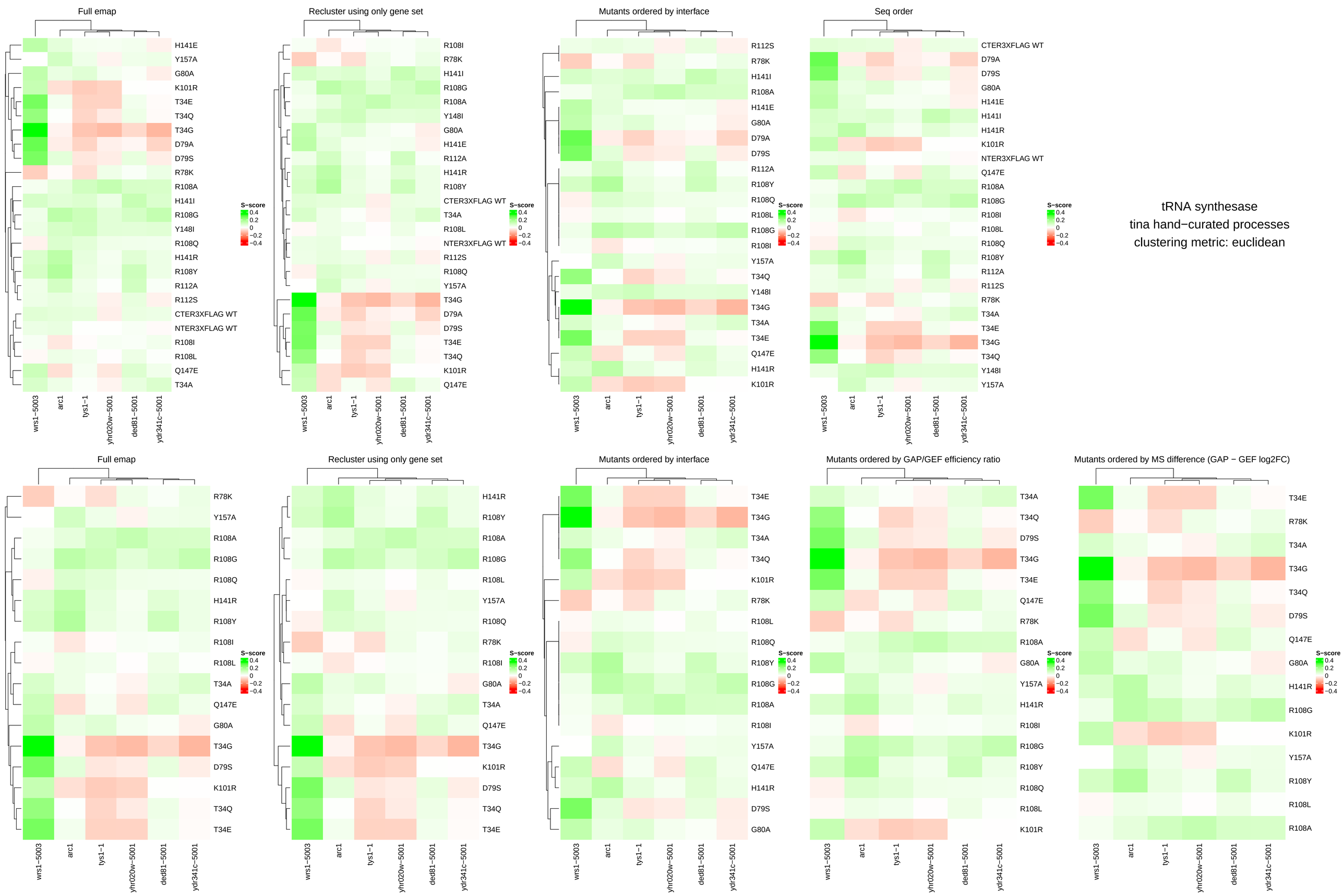


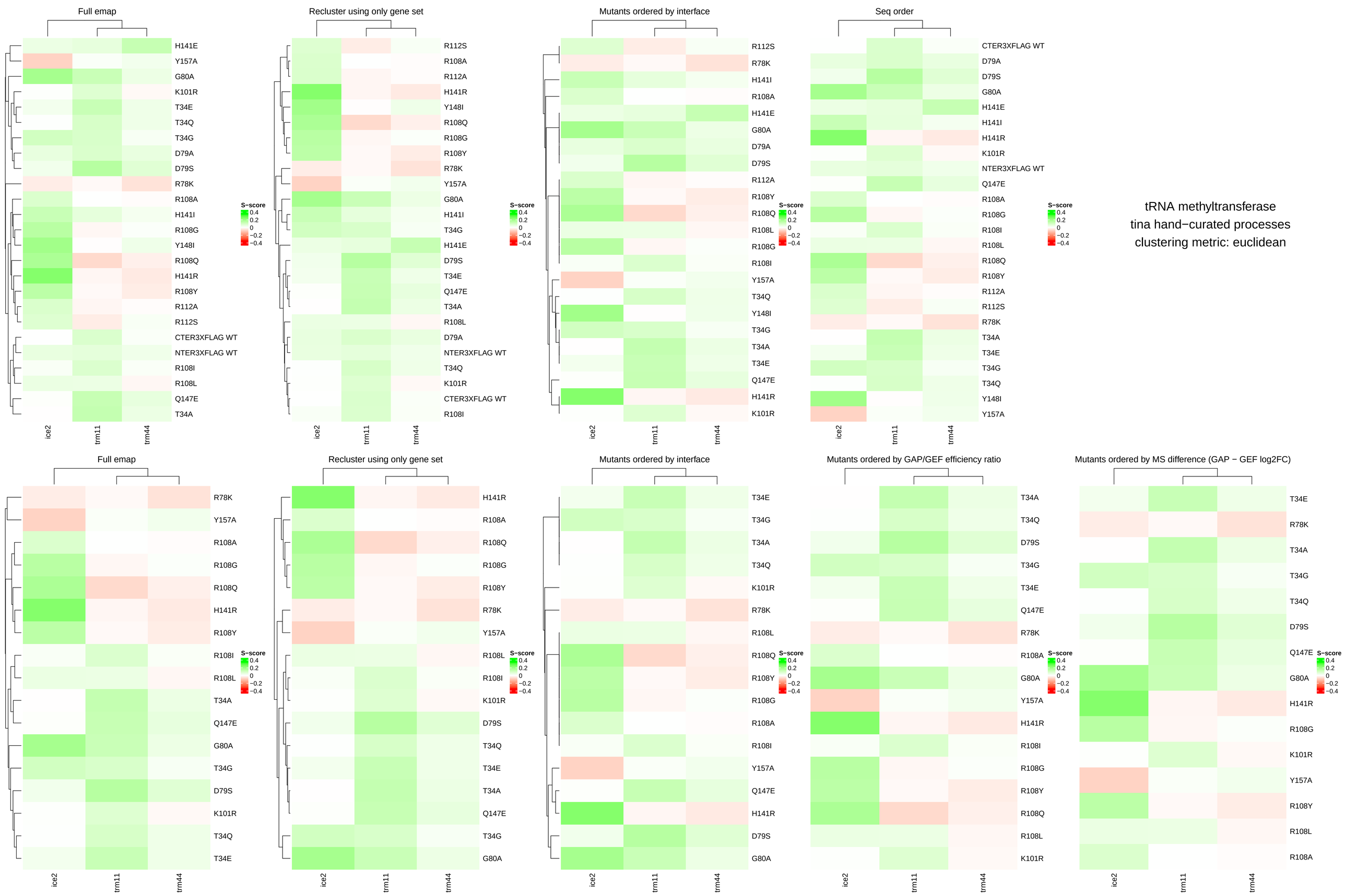
mitotic exit
tina hand−curated processes
clustering metric: euclidean



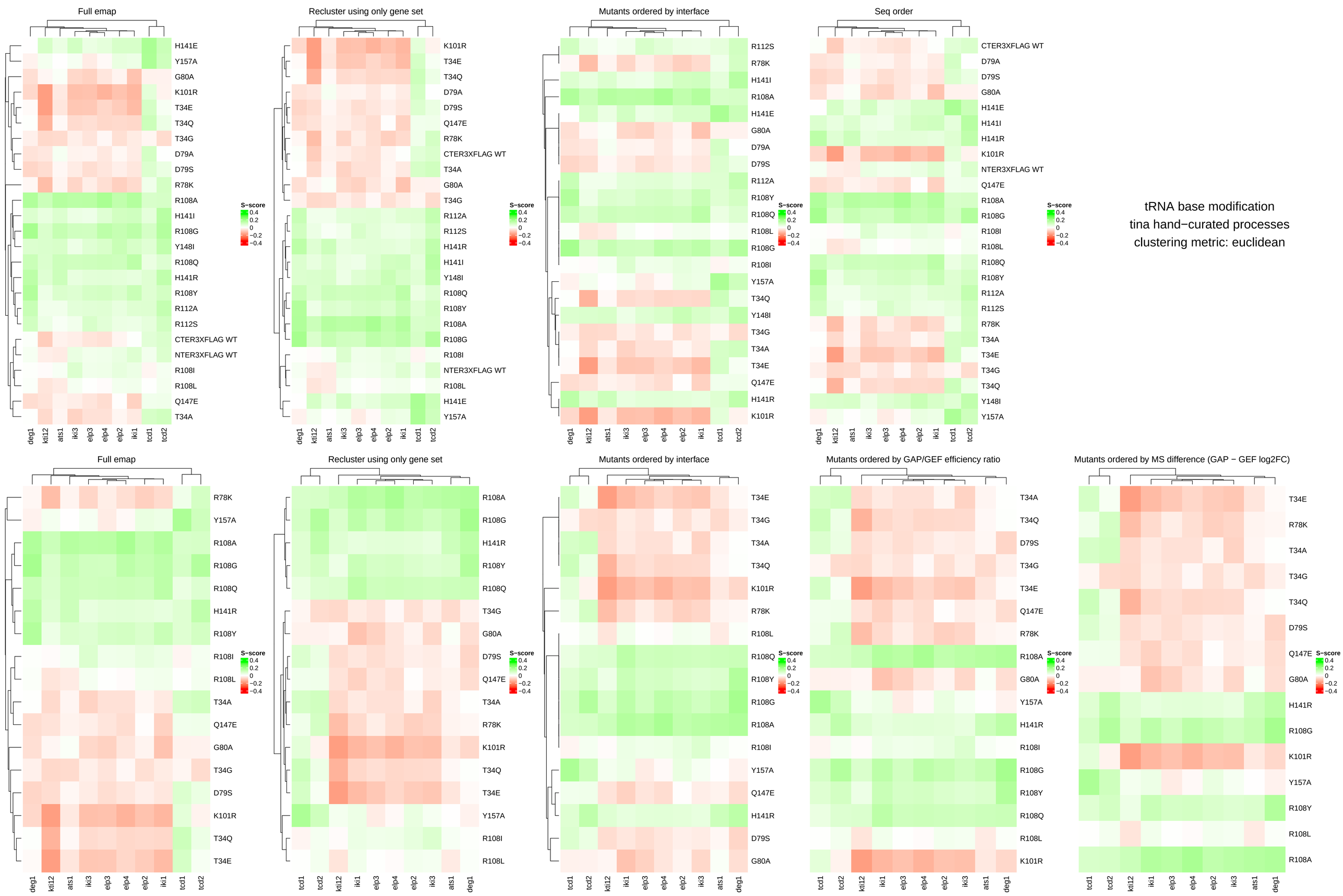
general nuclear export
tina hand−curated processes
clustering metric: euclidean

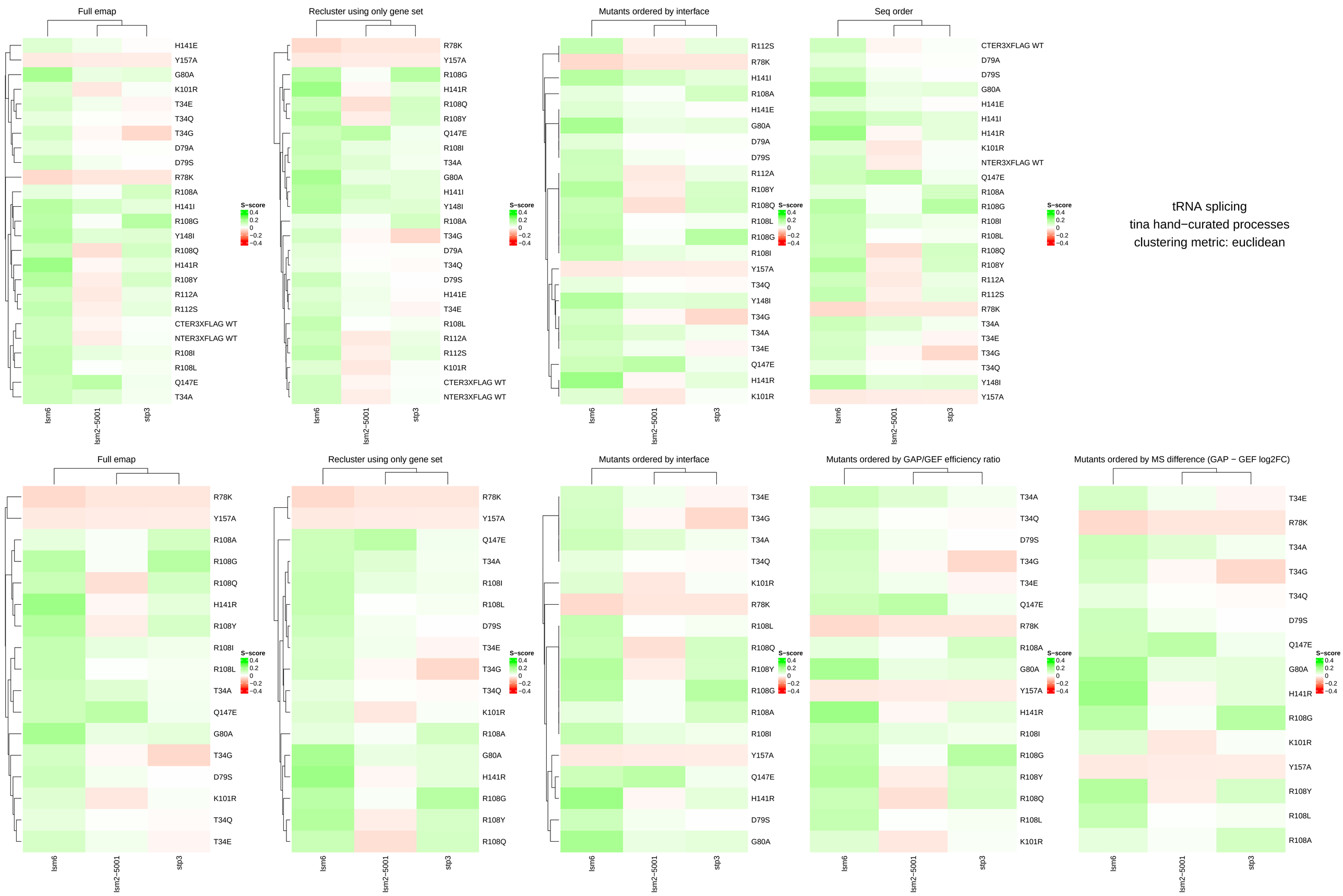


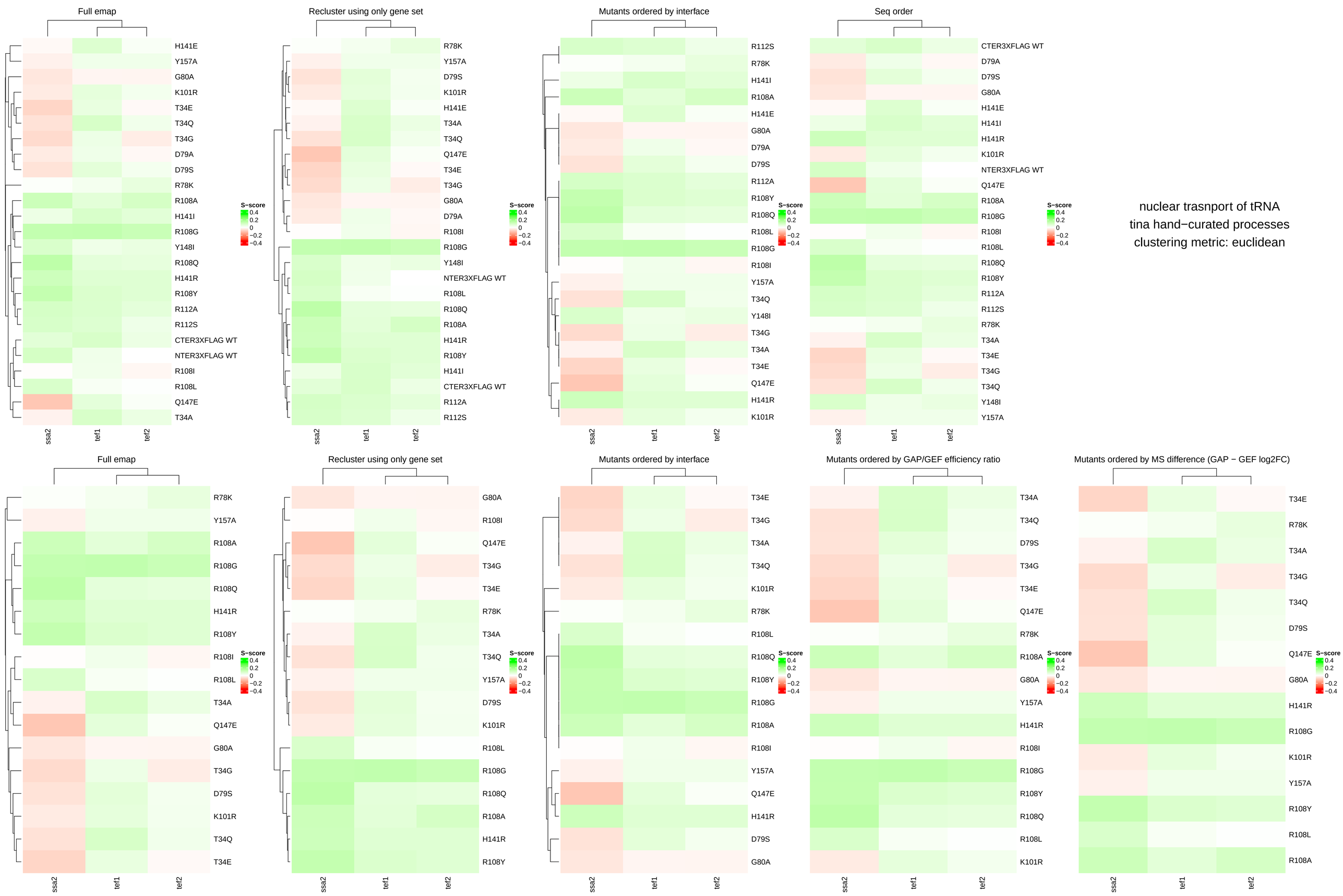

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
wrs1−5003
arc1
tys1−1
yhr020w−5001
ded81−5001
ydr341c−5001
tRNA synthesase
tina hand−curated processes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

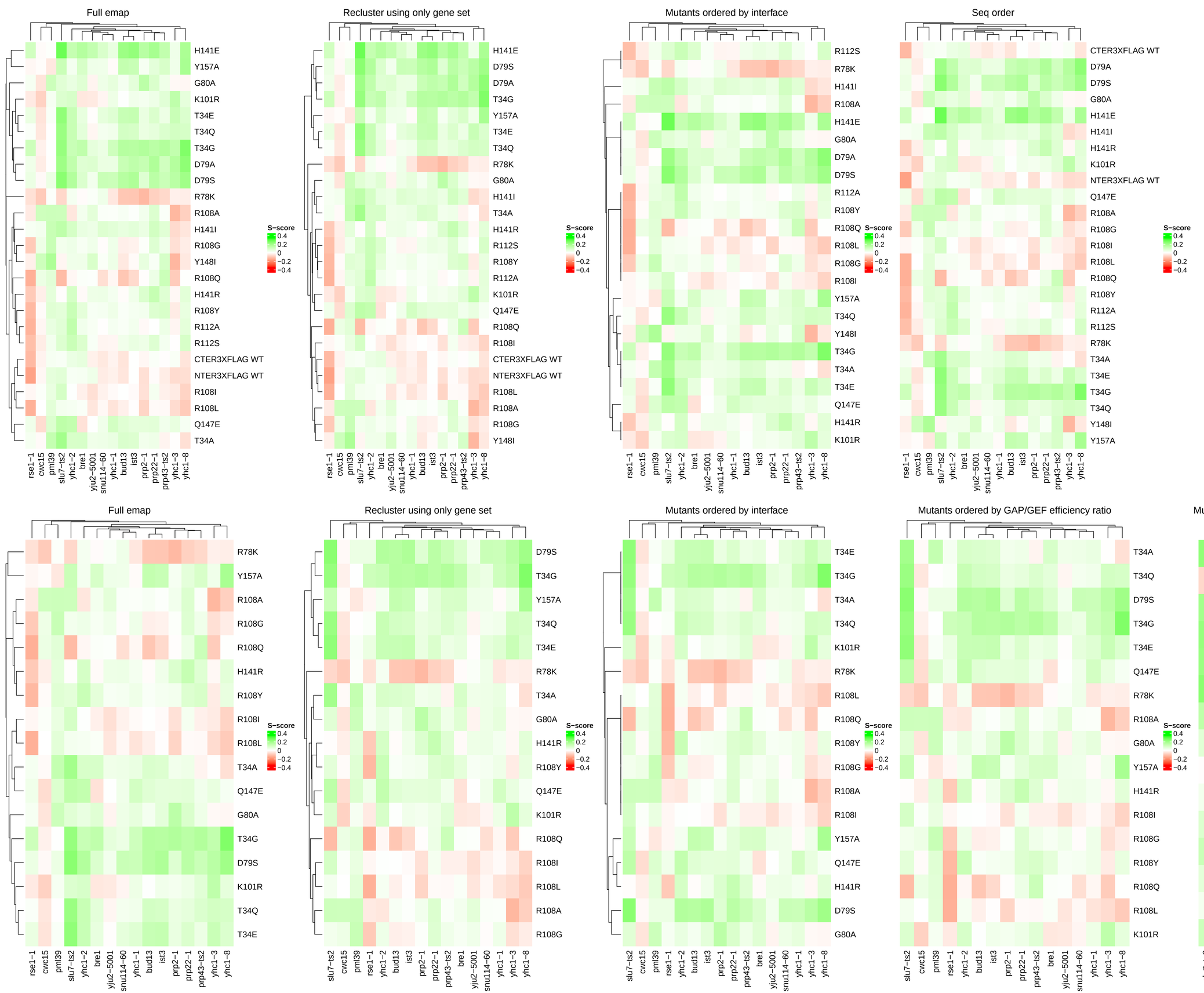


tRNA methyltransferase
tina hand−curated processes
clustering metric: euclidean

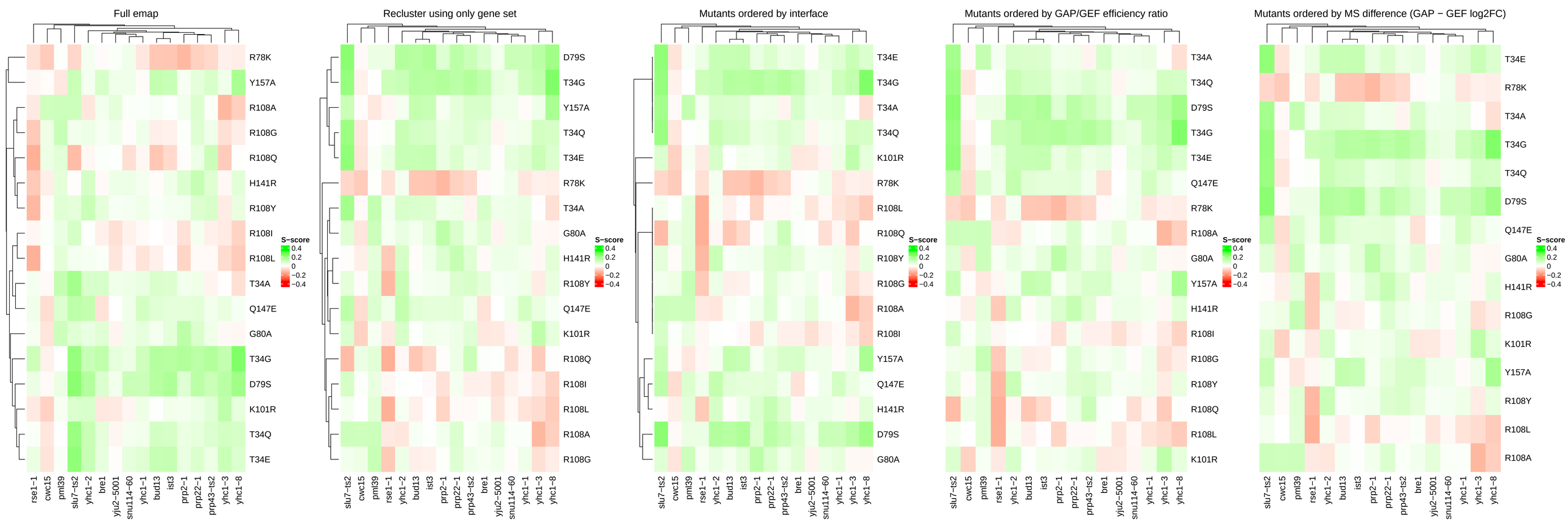

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
deg1
kti12
ats1
iki3
elp3
elp4
elp2
iki1
tcd1
tcd2
tRNA base modification
tina hand−curated processes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

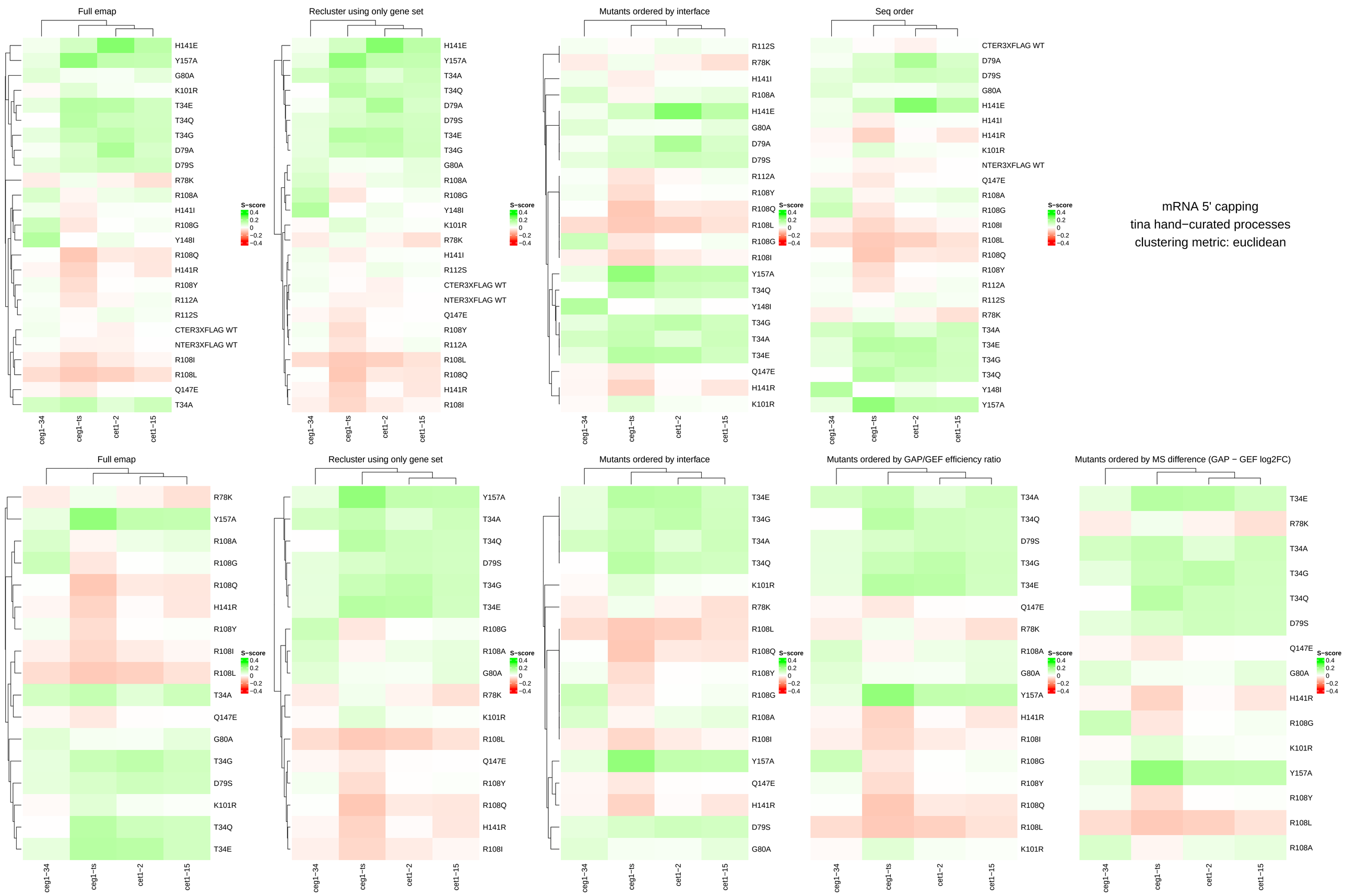

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
lsm6
lsm2−5001
stp3
tRNA splicing
tina hand−curated processes
clustering metric: euclidean

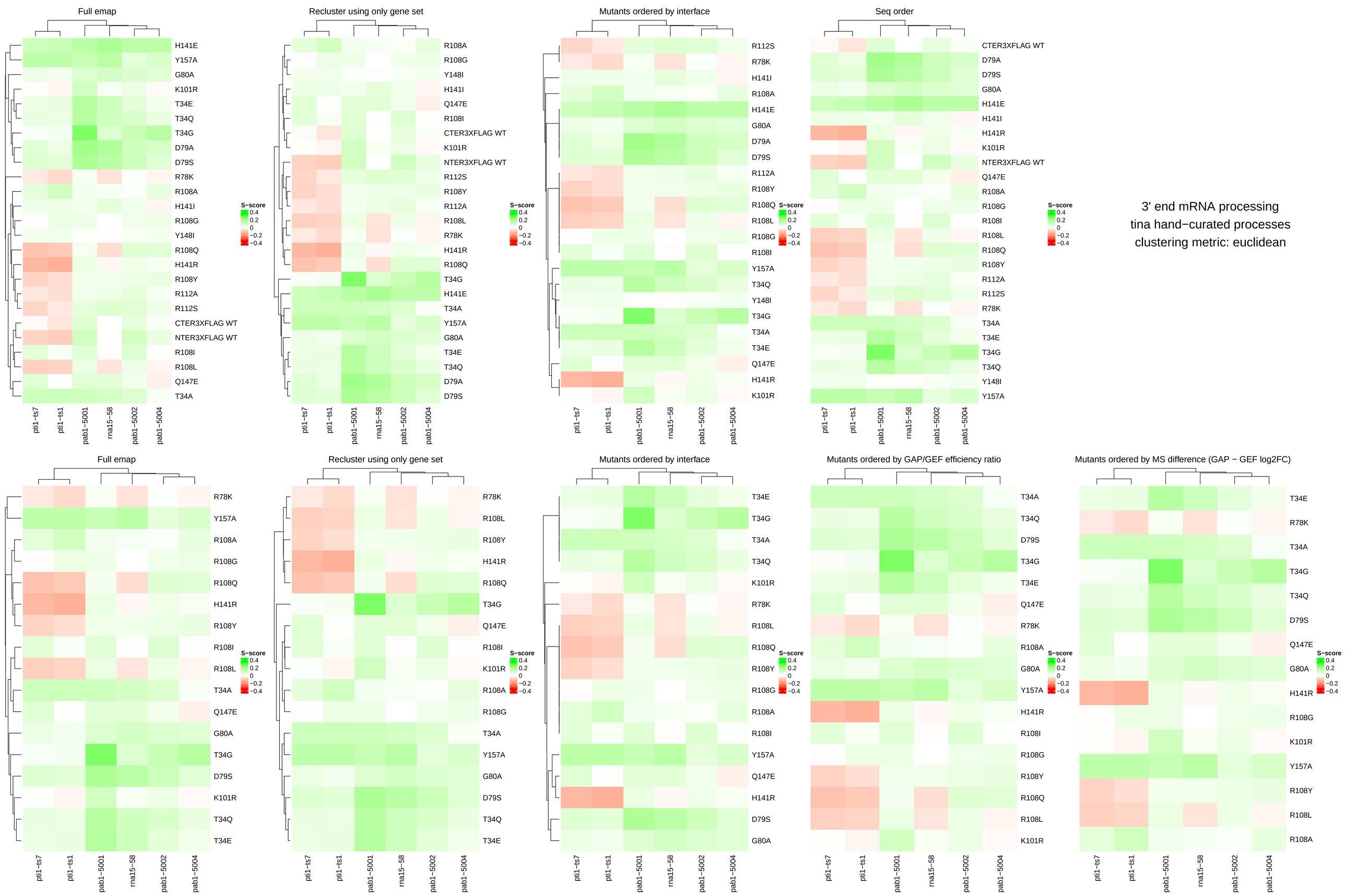

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
ssa2
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R78K
Y157A
D79S
K101R
H141E
T34A
T34Q
Q147E
T34E
T34G
G80A
D79A
R108I
R108G
Y148I
NTER3XFLAG WT
R108L
R108Q
R108A
H141R
R108Y
H141I
CTER3XFLAG WT
R112A
R112S
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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 trasnport of tRNA
tina hand−curated processes
clustering metric: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
G80A
R108I
Q147E
T34G
T34E
R78K
T34A
T34Q
Y157A
D79S
K101R
R108L
R108G
R108Q
R108A
H141R
R108Y
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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



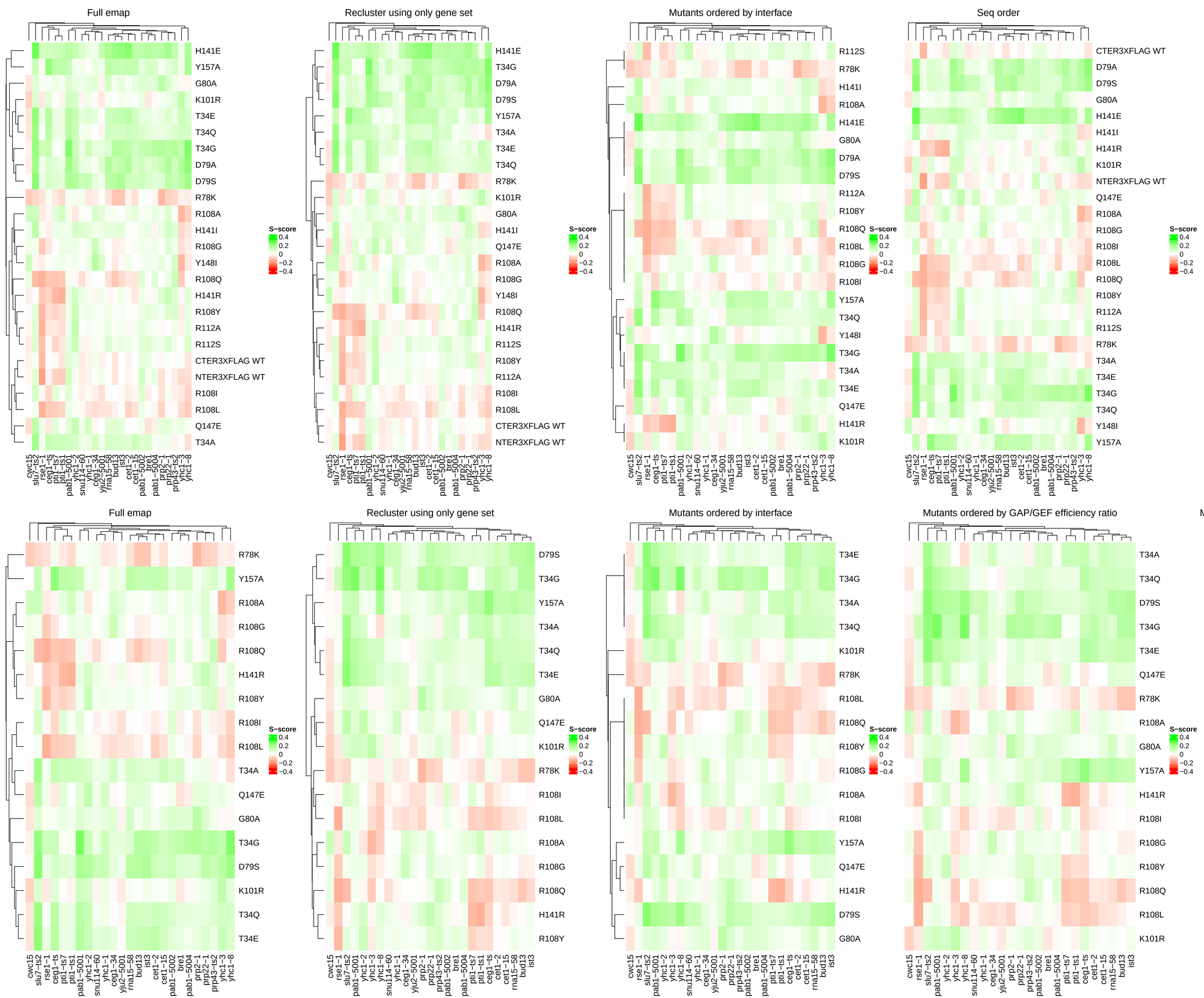
mRNA splicing
tina hand−curated processes
clustering metric: euclidean



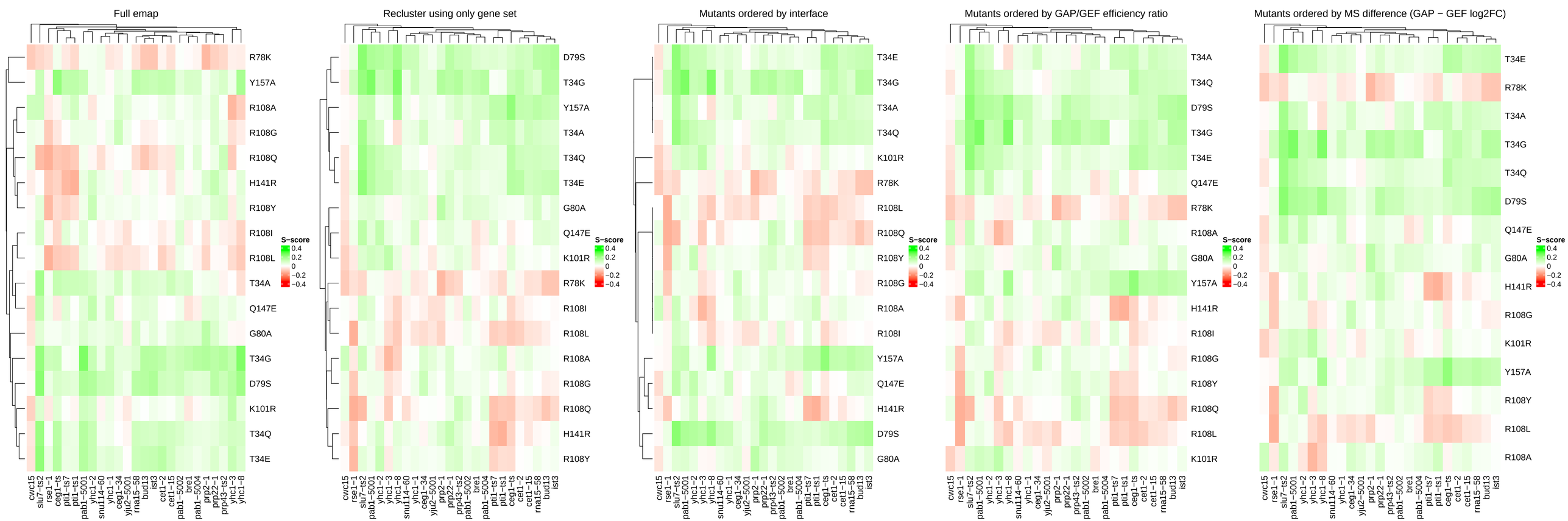

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ceg1−34
ceg1−ts
cet1−2
cet1−15
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
R108G
R108I
R108L
R108Q
H141R
R108I
R108Y
R112A
R112S
R78K
T34A
T34E
T34G
T34Q
Y148I
Y157A
mRNA 5' capping
tina hand−curated processes
clustering metric: euclidean

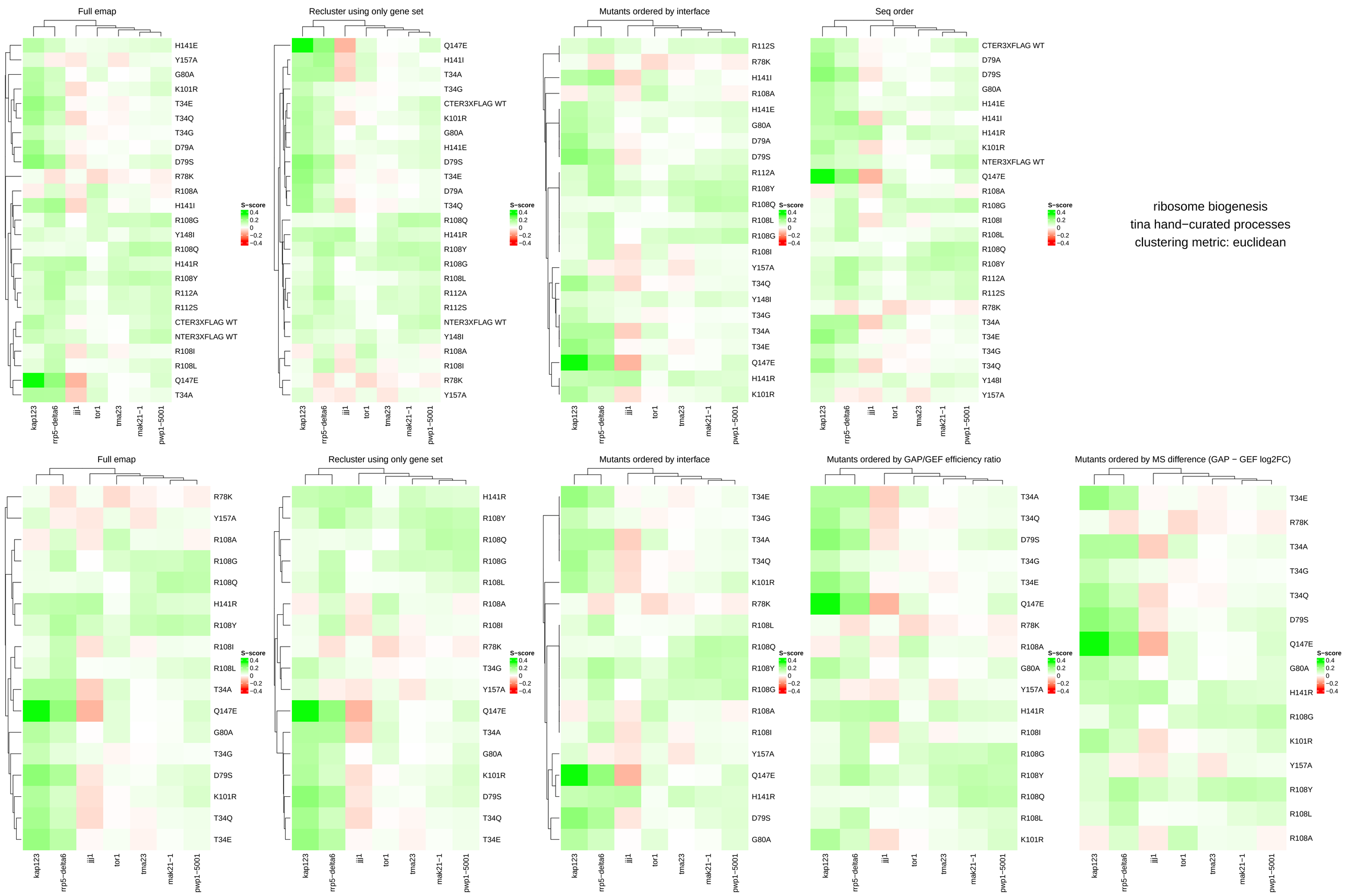


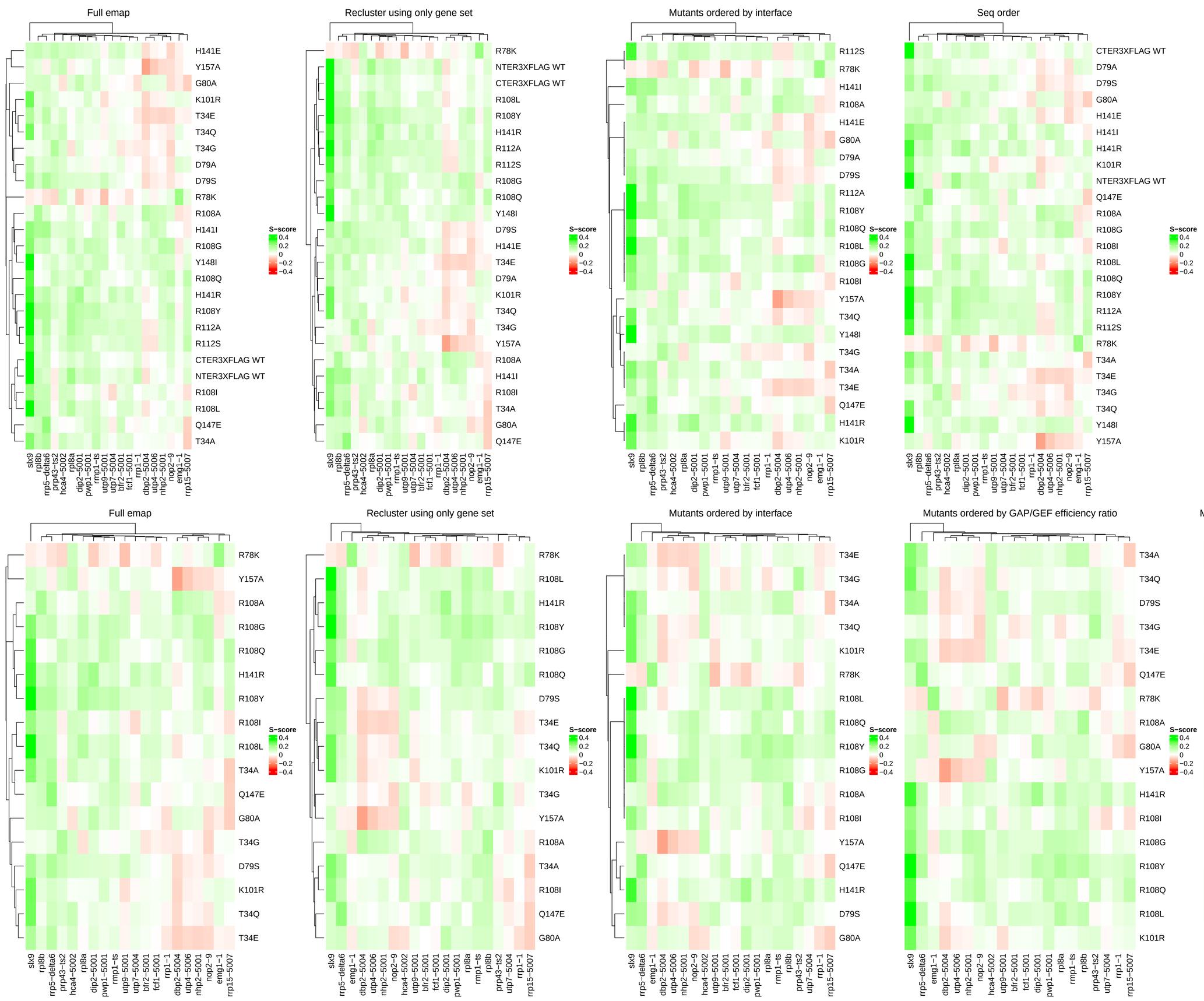
3' end mRNA processing
tina hand−curated processes
clustering metric: euclidean



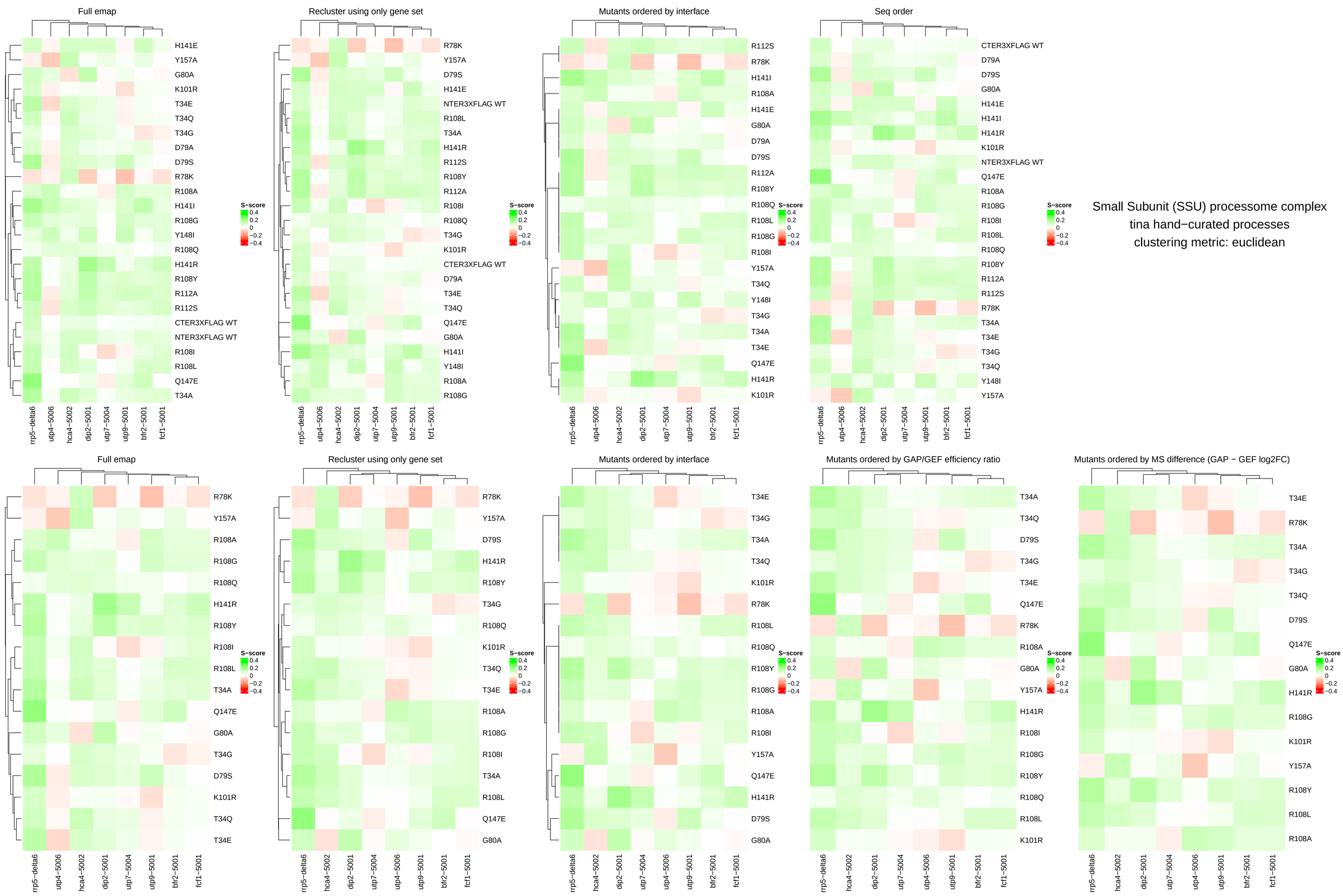
mRNA maturation
tina hand−curated processes
clustering metric: euclidean

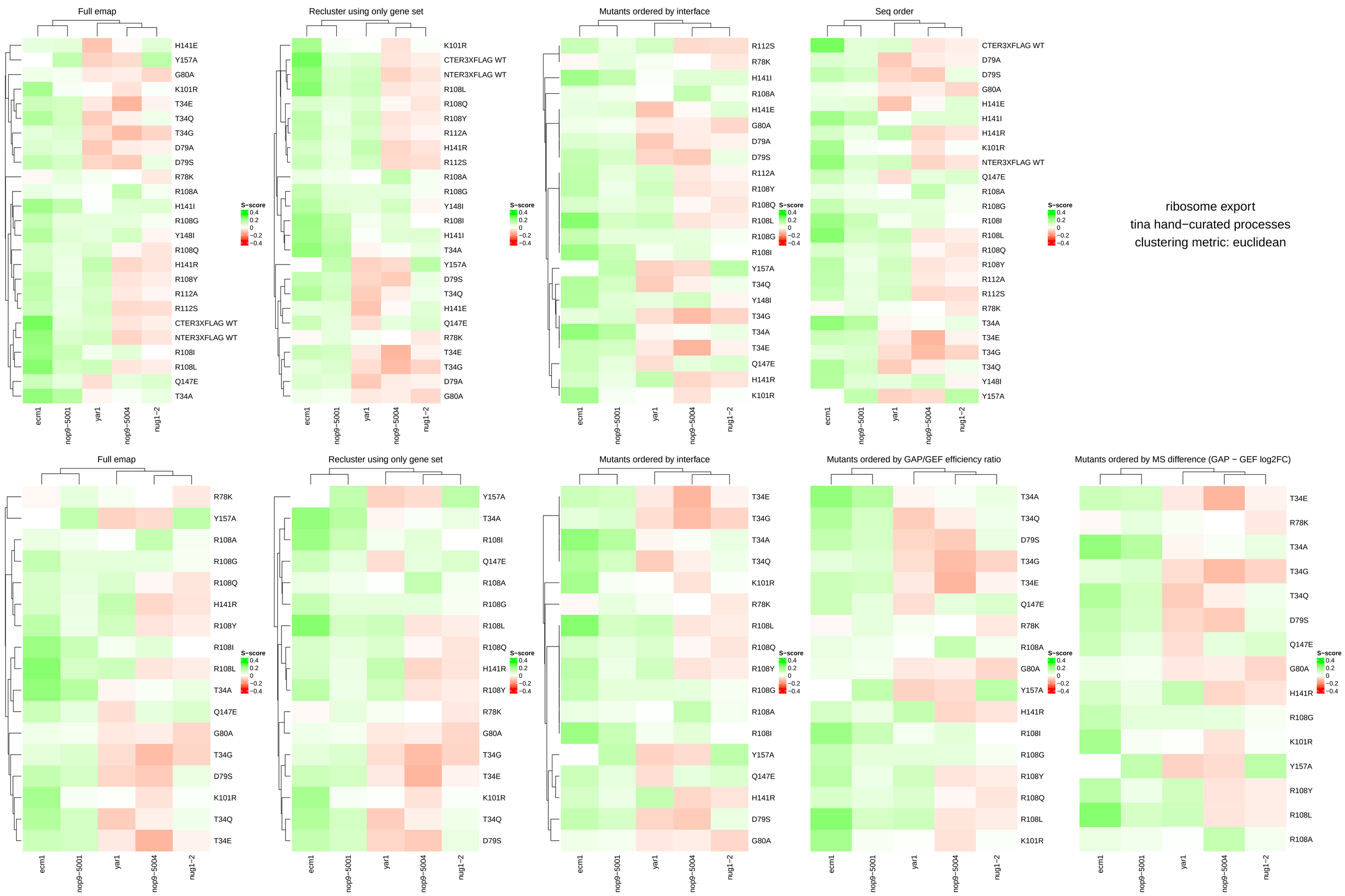


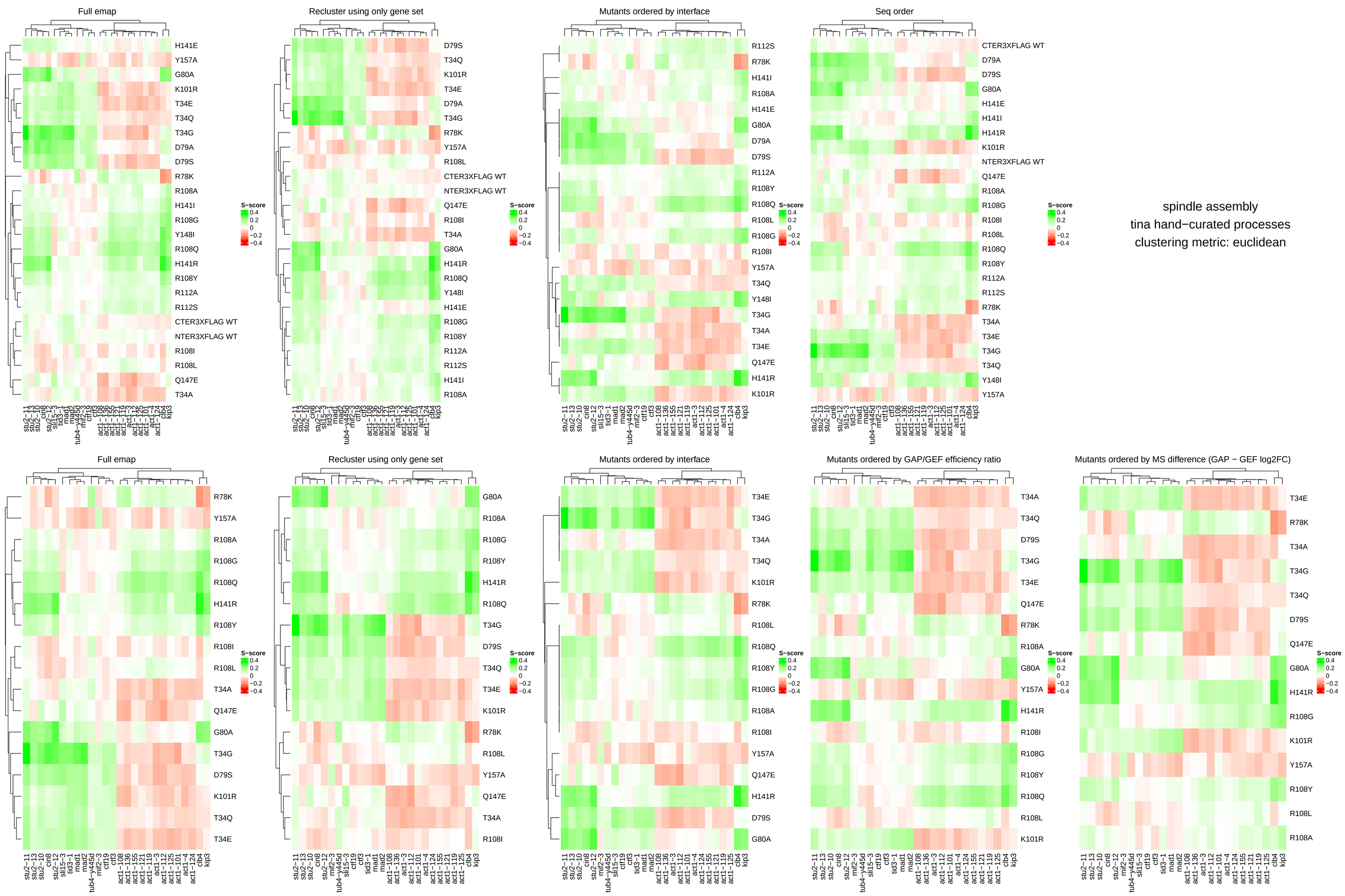

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
kap123
rrp5−delta6
jji1
tor1
tma23
mak21−1
pwp1−5001
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
ribosome biogenesis
tina hand−curated processes
clustering metric: euclidean



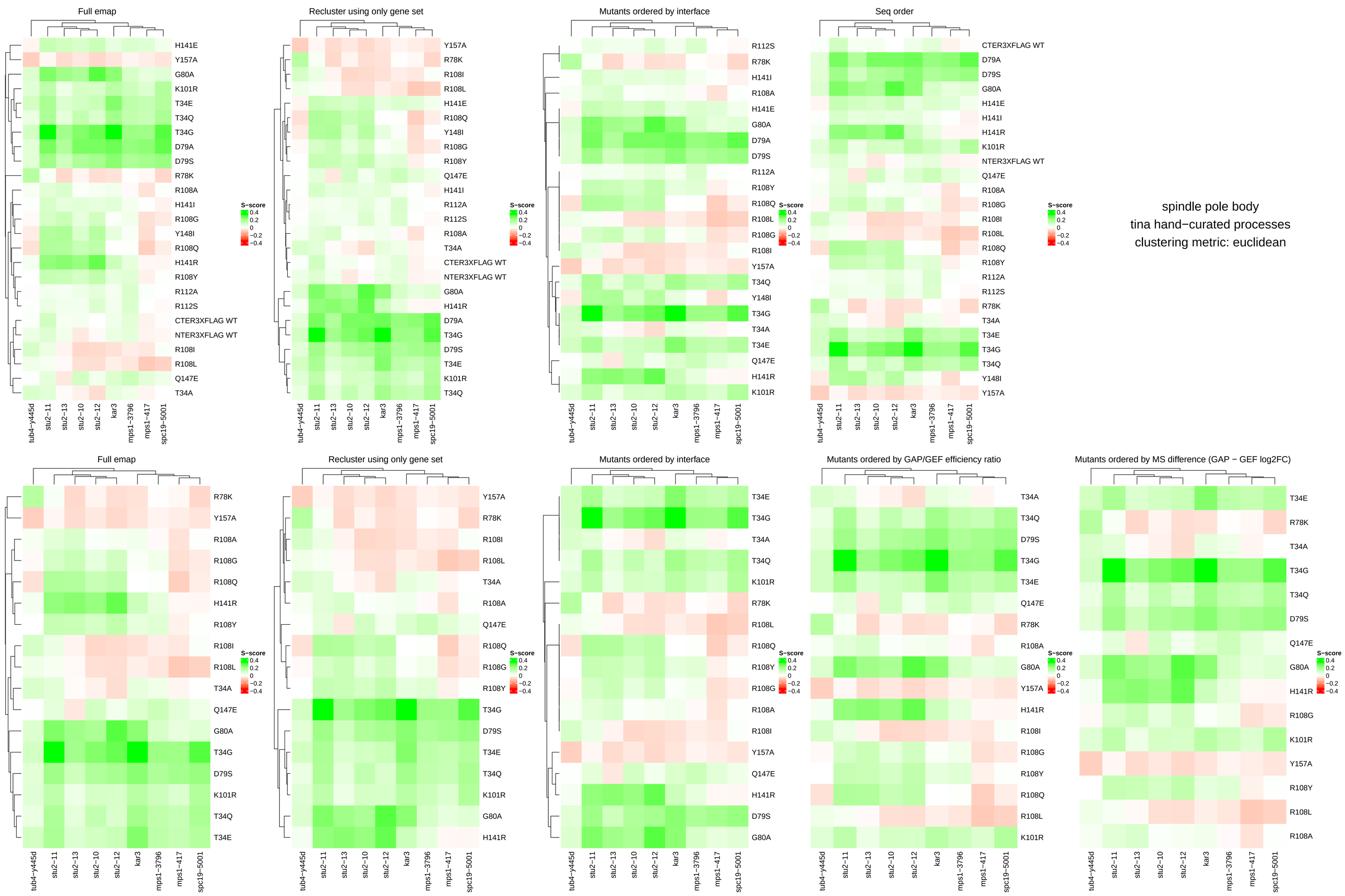
rRNA processing
tina hand−curated processes
clustering metric: euclidean


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
rrp5−delta6
utp4−5006
hca4−5002
dip2−5001
utp7−5004
utp9−5001
bfr2−5001
fcf1−5001
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
NTER3XFLAG WT
R108L
T34A
H141R
R112S
R108Y
R112A
R108I
R108Q
T34G
K101R
CTER3XFLAG WT
D79A
T34E
T34Q
Q147E
G80A
H141I
Y148I
R108A
R108G
R112S
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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
Small Subunit (SSU) processome complex
tina hand−curated processes
clustering metric: euclidean

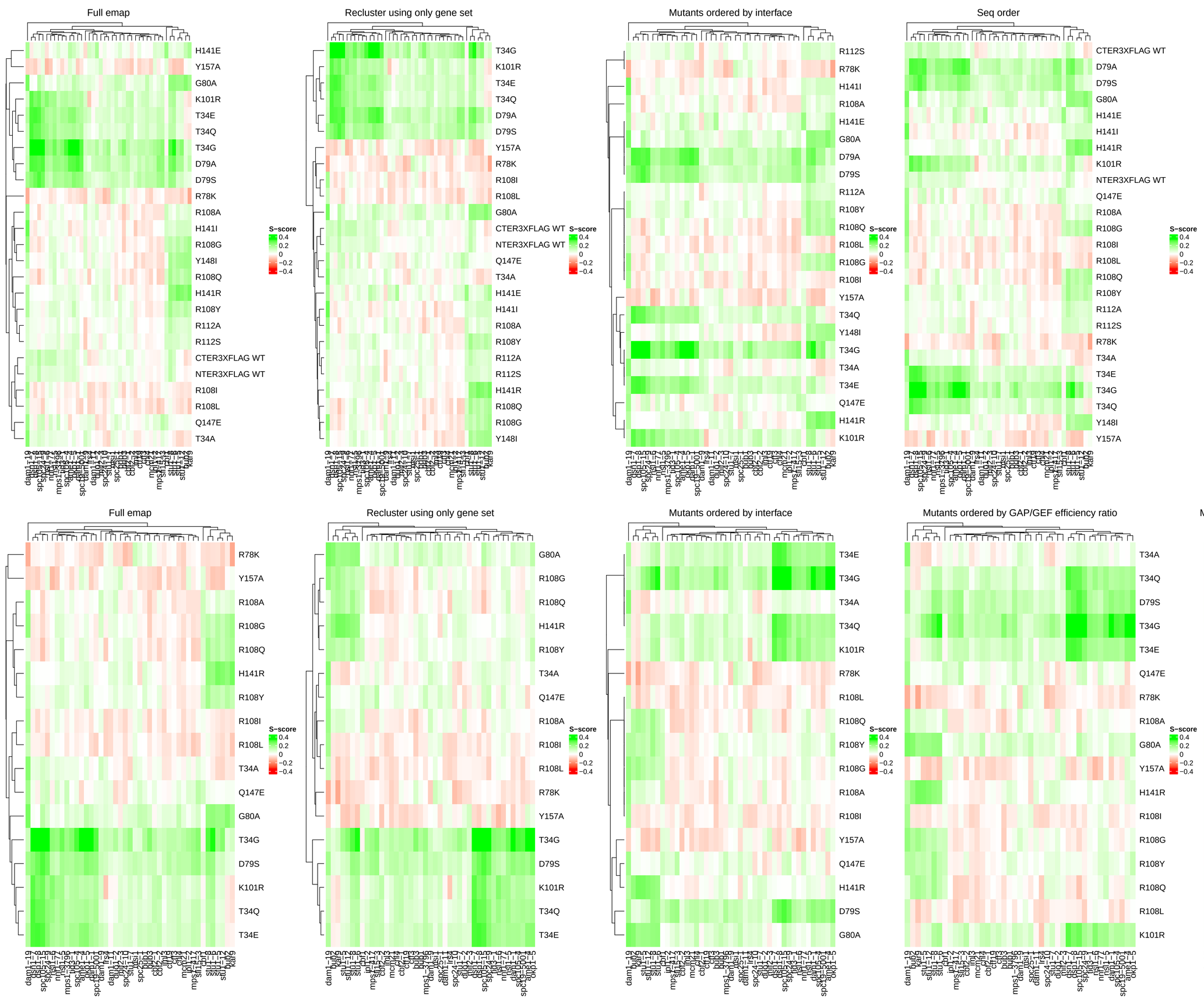

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ecm1
nop9−5001
yar1
nop9−5004
nug1−2
ribosome export
tina hand−curated processes
clustering metric: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



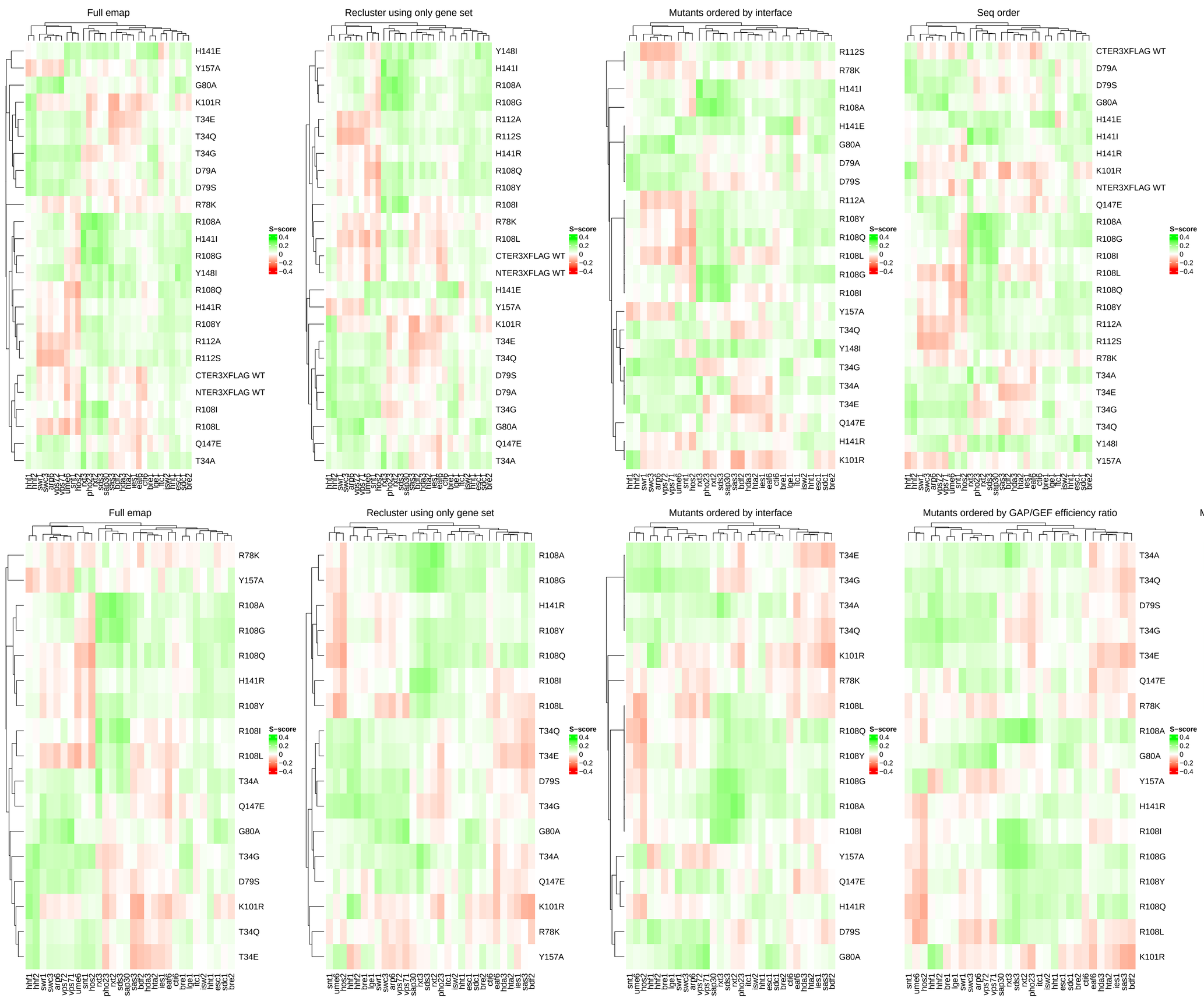
spindle assembly
tina hand−curated processes
clustering metric: euclidean



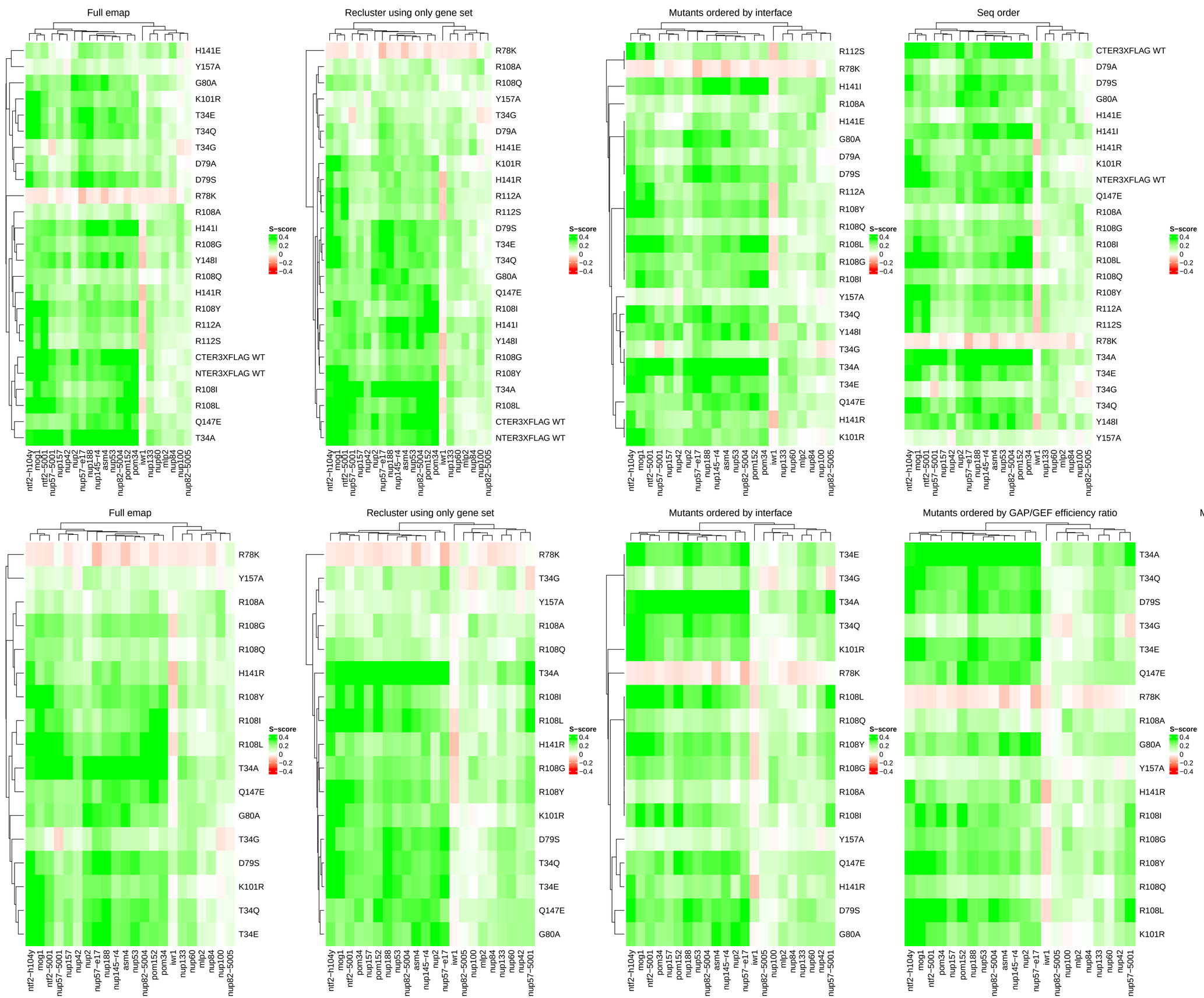
spindle pole body
tina hand−curated processes
clustering metric: euclidean



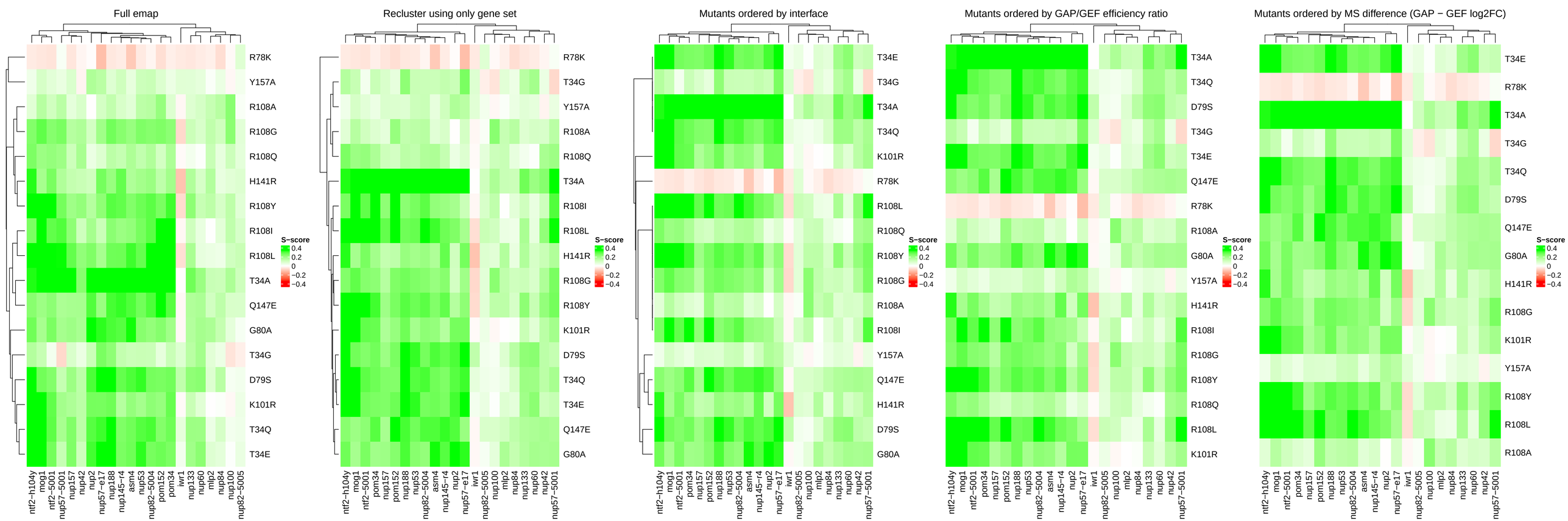
kinetochore
tina hand−curated processes
clustering metric: euclidean

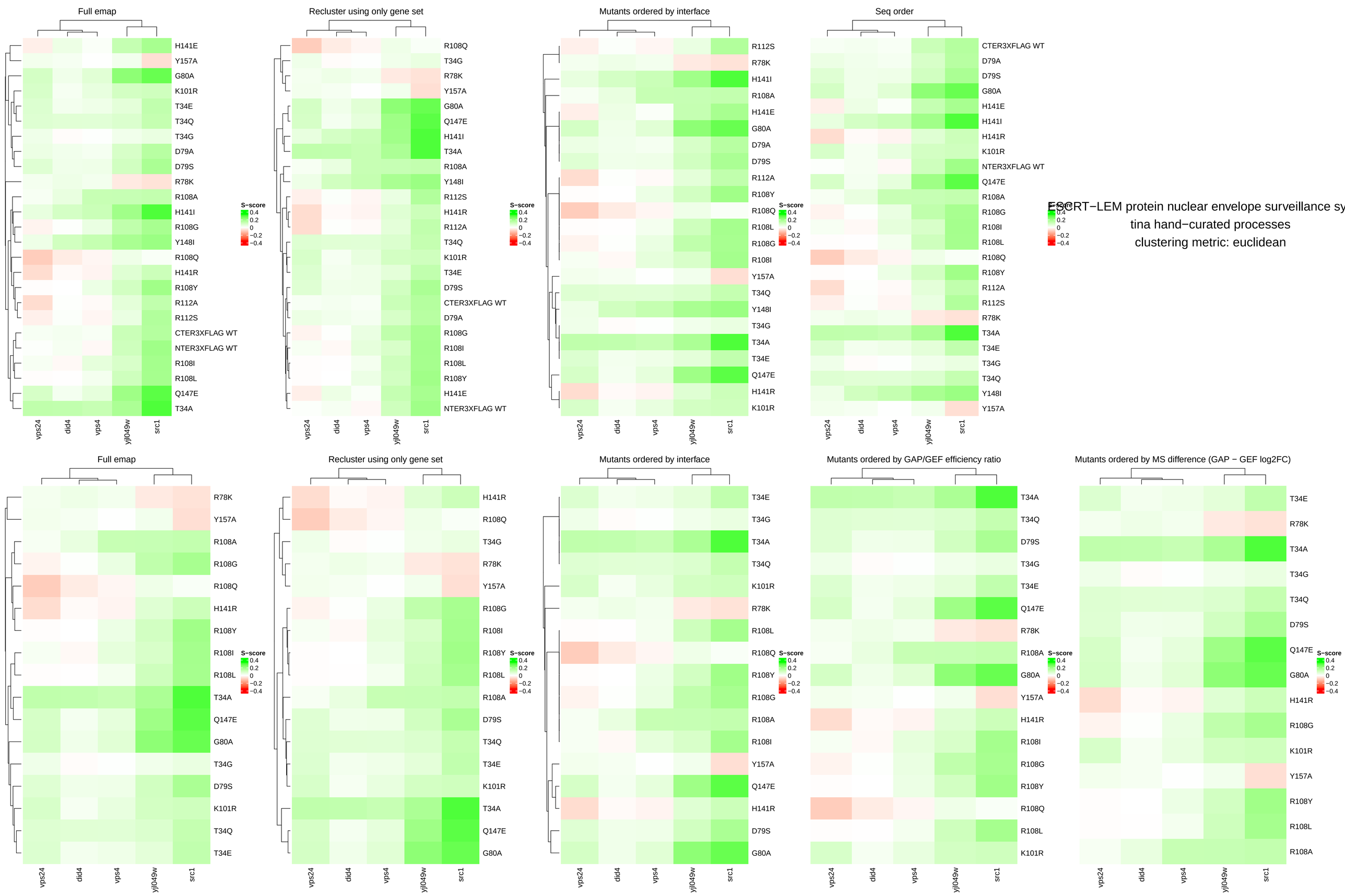


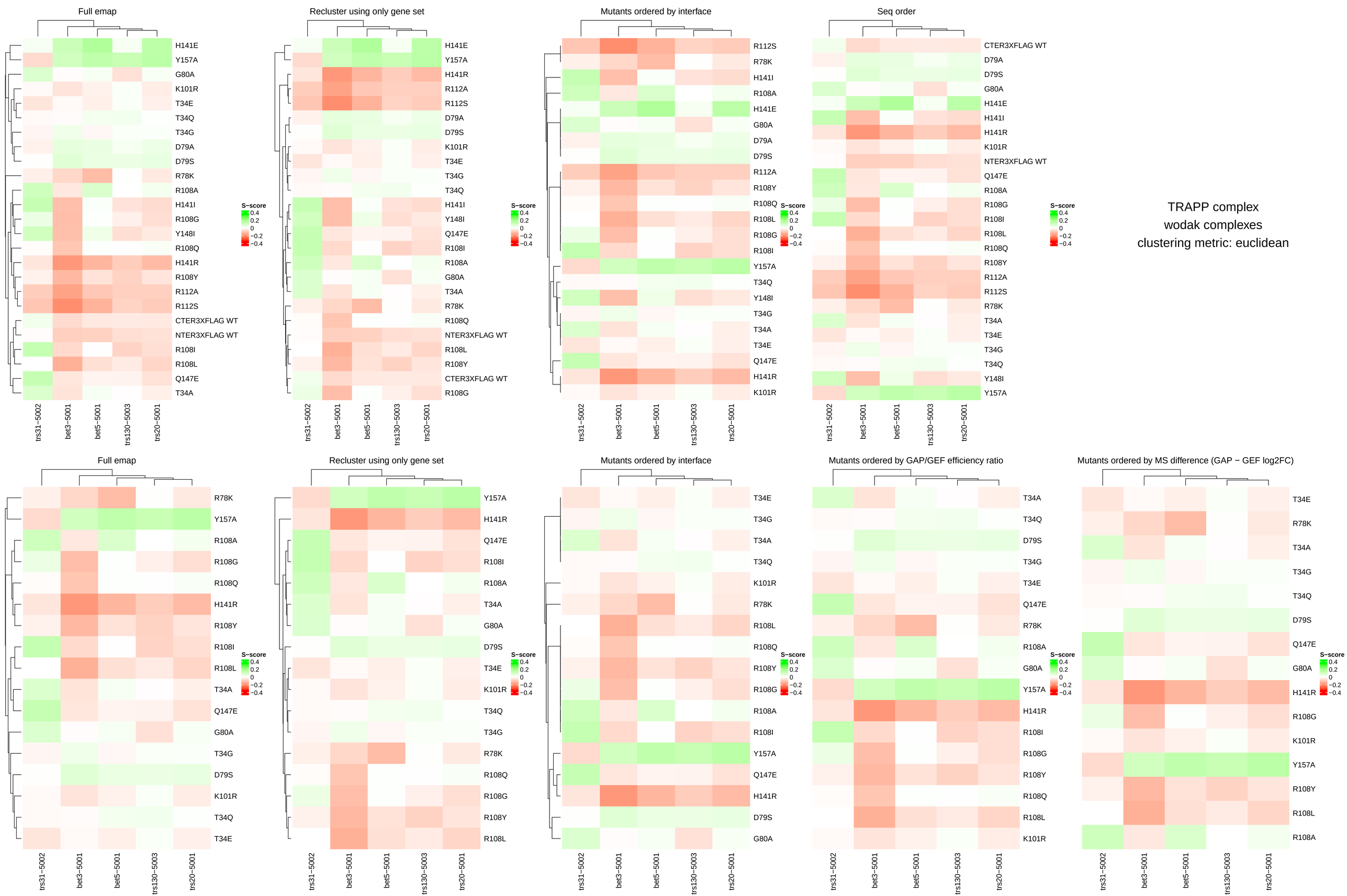
chromatin remodeling
tina hand−curated processes
clustering metric: euclidean

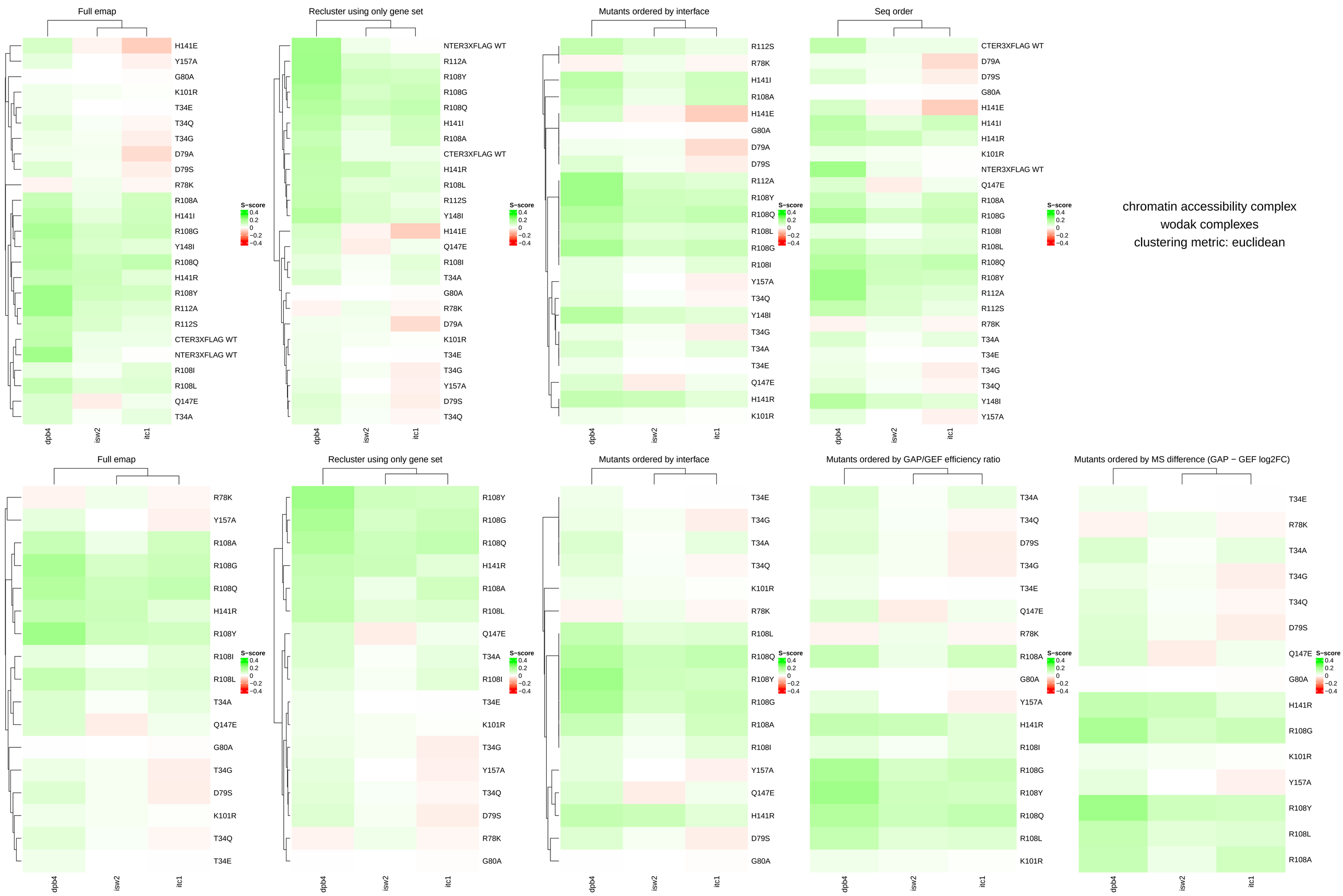


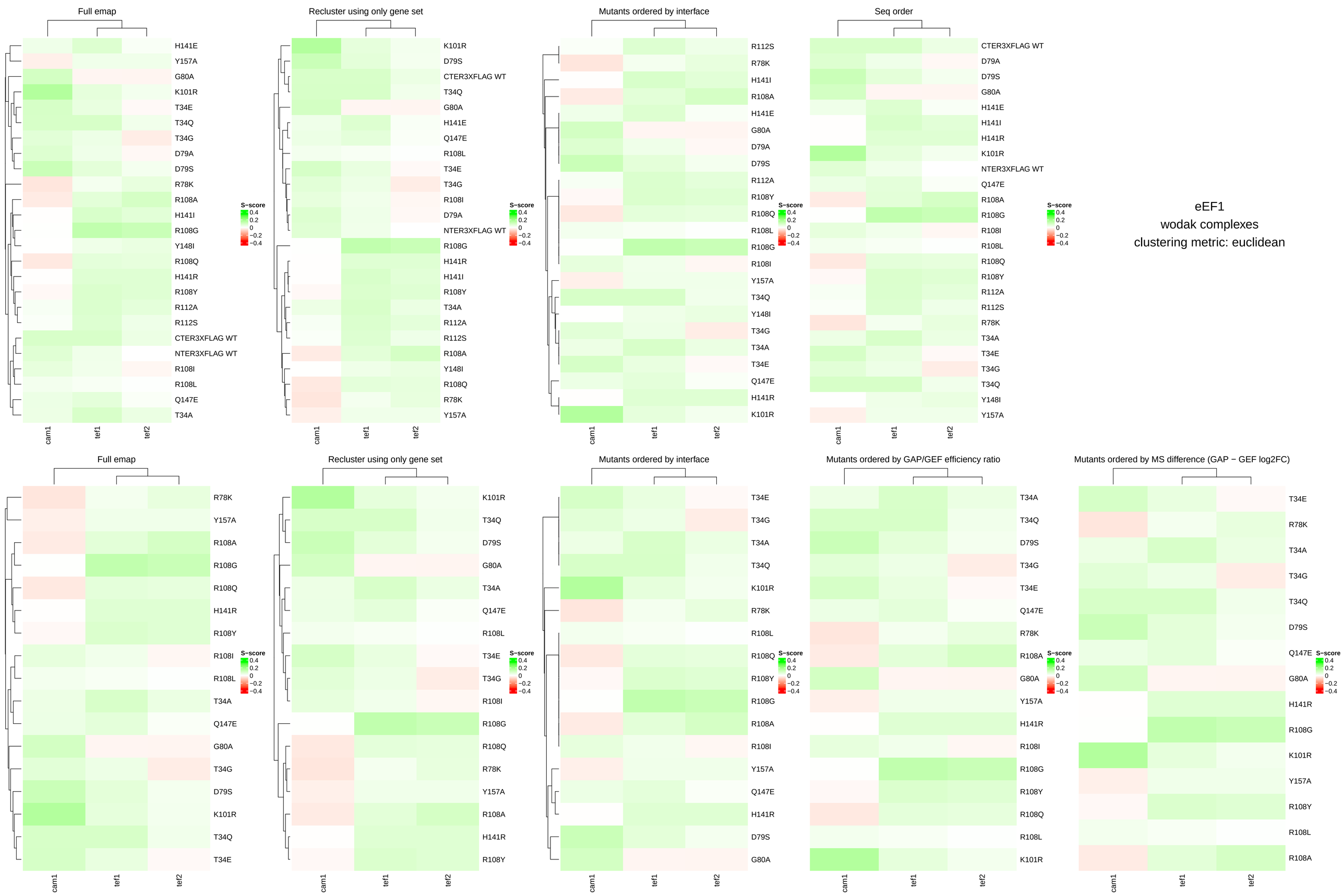
nucleocytoplasmic transport
tina hand−curated processes
clustering metric: euclidean

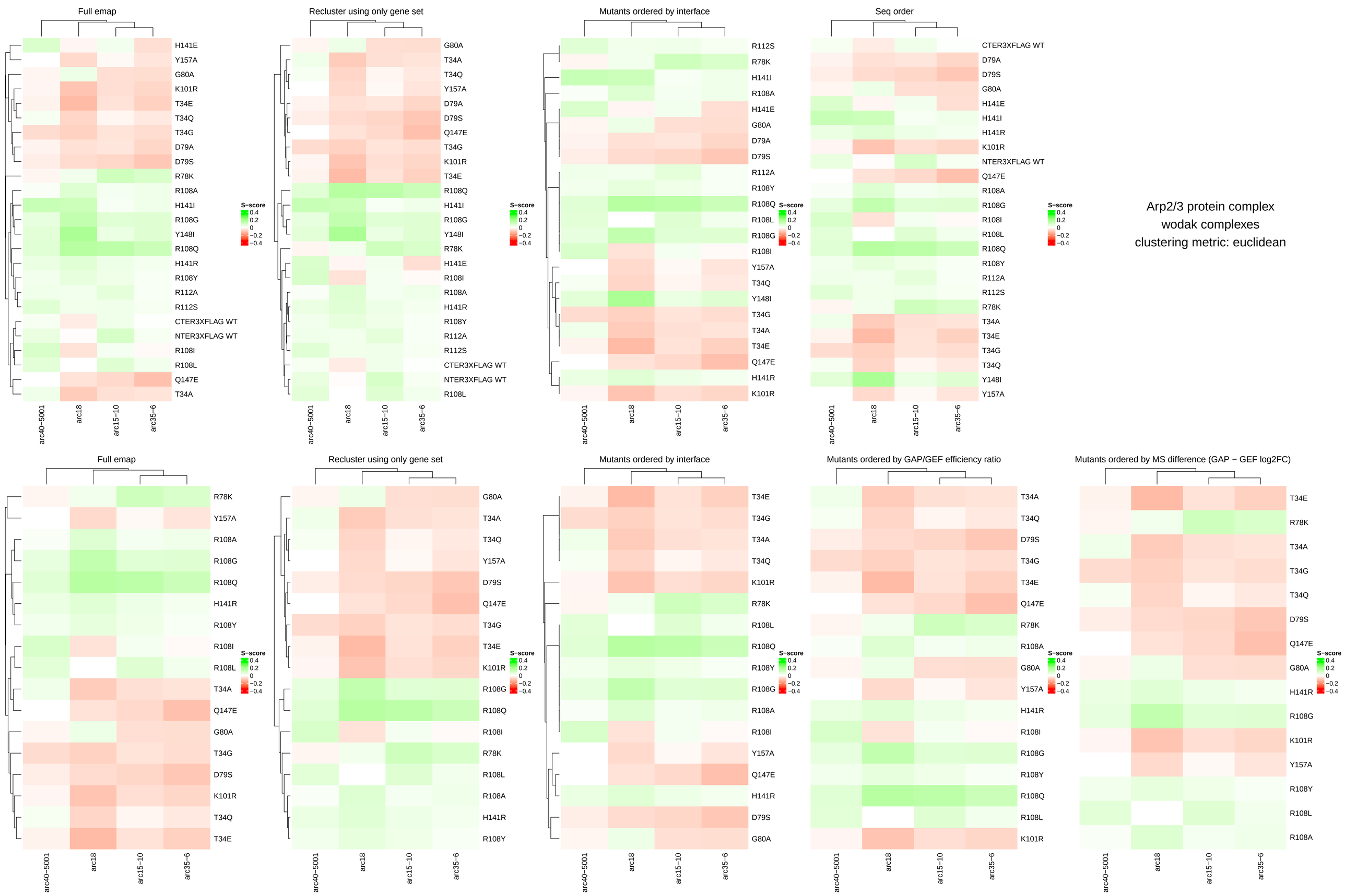


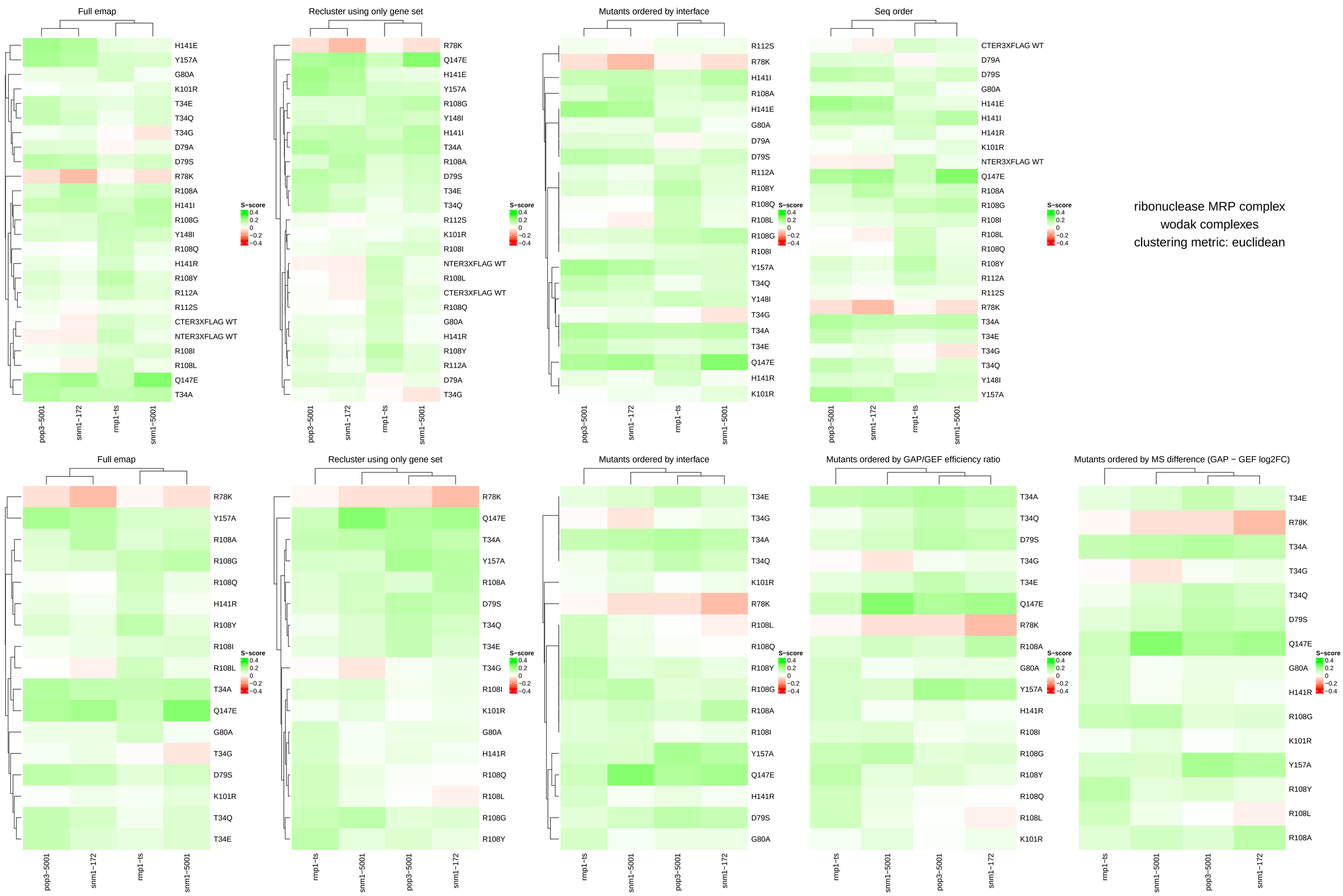

ESCRT−LEM protein nuclear envelope surveillance sy
tina hand−curated processes
clustering metric: euclidean
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
vps24
did4
vps4
yjl049w
src1


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
trs31−5002
bet3−5001
bet5−5001
trs130−5003
trs20−5001
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
R108G
TRAPP complex
wodak complexes
clustering metric: euclidean

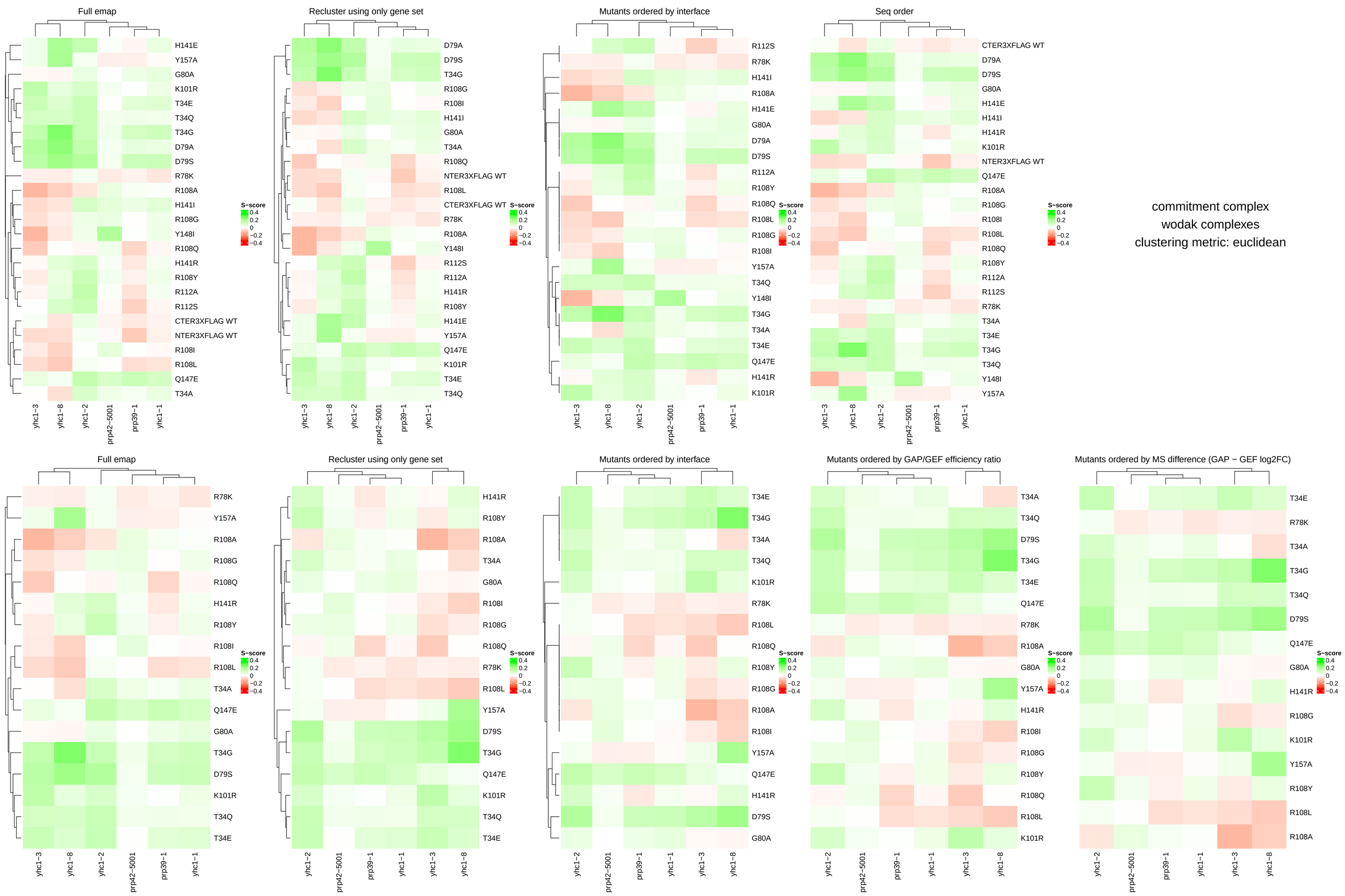

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
dpb4
isw2
itc1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
NTER3XFLAG WT
R112A
R108Y
R108G
R108Q
H141I
R108A
CTER3XFLAG WT
H141R
R108L
R112S
Y148I
H141E
Q147E
R108I
T34A
G80A
R78K
D79A
K101R
T34E
T34G
Y157A
D79S
T34Q
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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
chromatin accessibility complex
wodak complexes
clustering metric: euclidean
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
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
cam1
tef1
tef2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
K101R
D79S
CTER3XFLAG WT
T34Q
G80A
H141E
Q147E
R108L
T34E
T34G
R108I
D79A
NTER3XFLAG WT
R108G
H141R
H141I
R108Y
T34A
R112A
R112S
R108A
Y148I
R108Q
R78K
Y157A
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
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

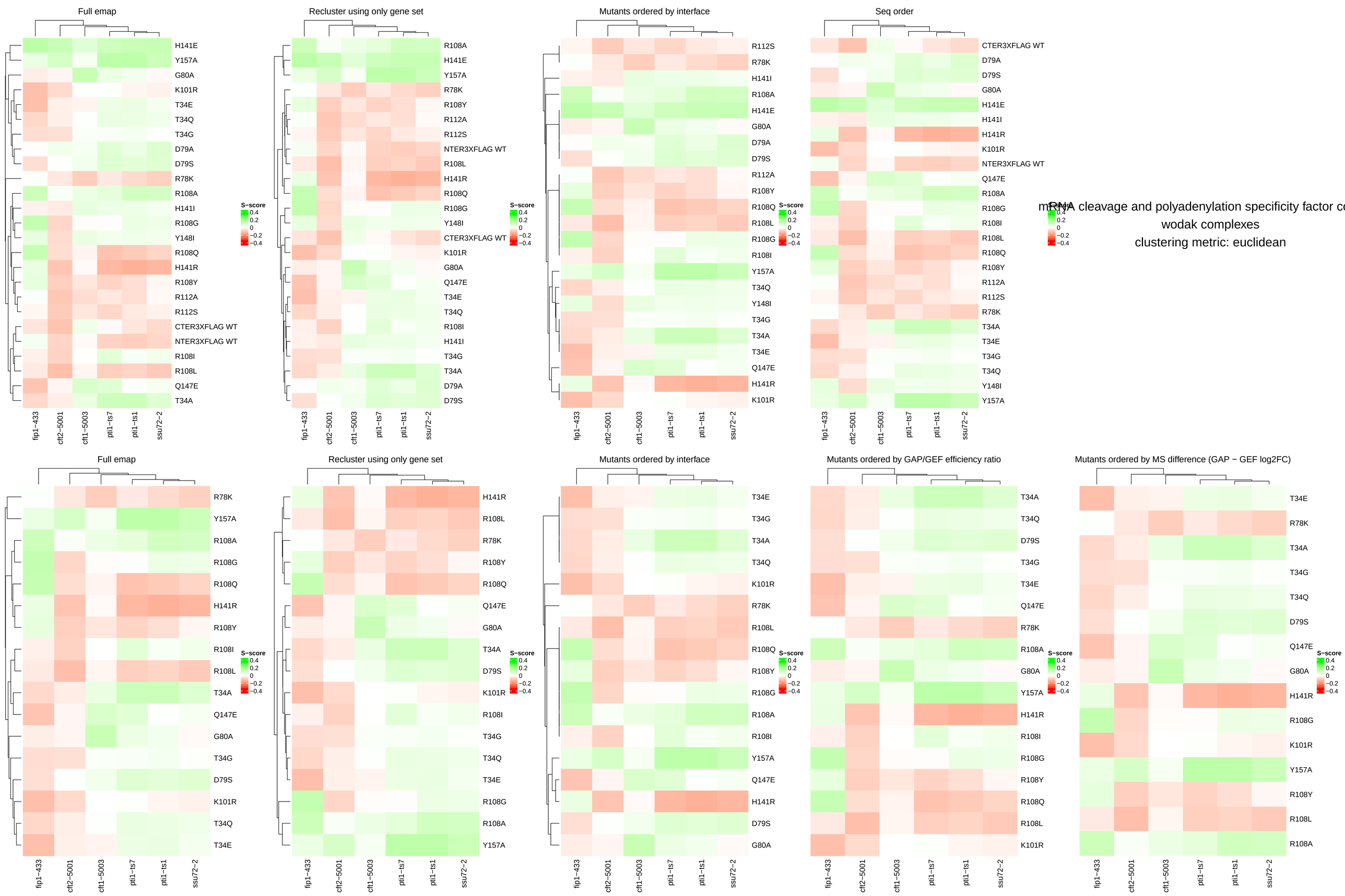

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
arc40−5001
arc18
arc15−10
arc35−6
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
Q147E
R108L
R108I
R78K
H141E
R108A
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
Arp2/3 protein complex
wodak complexes
clustering metric: euclidean

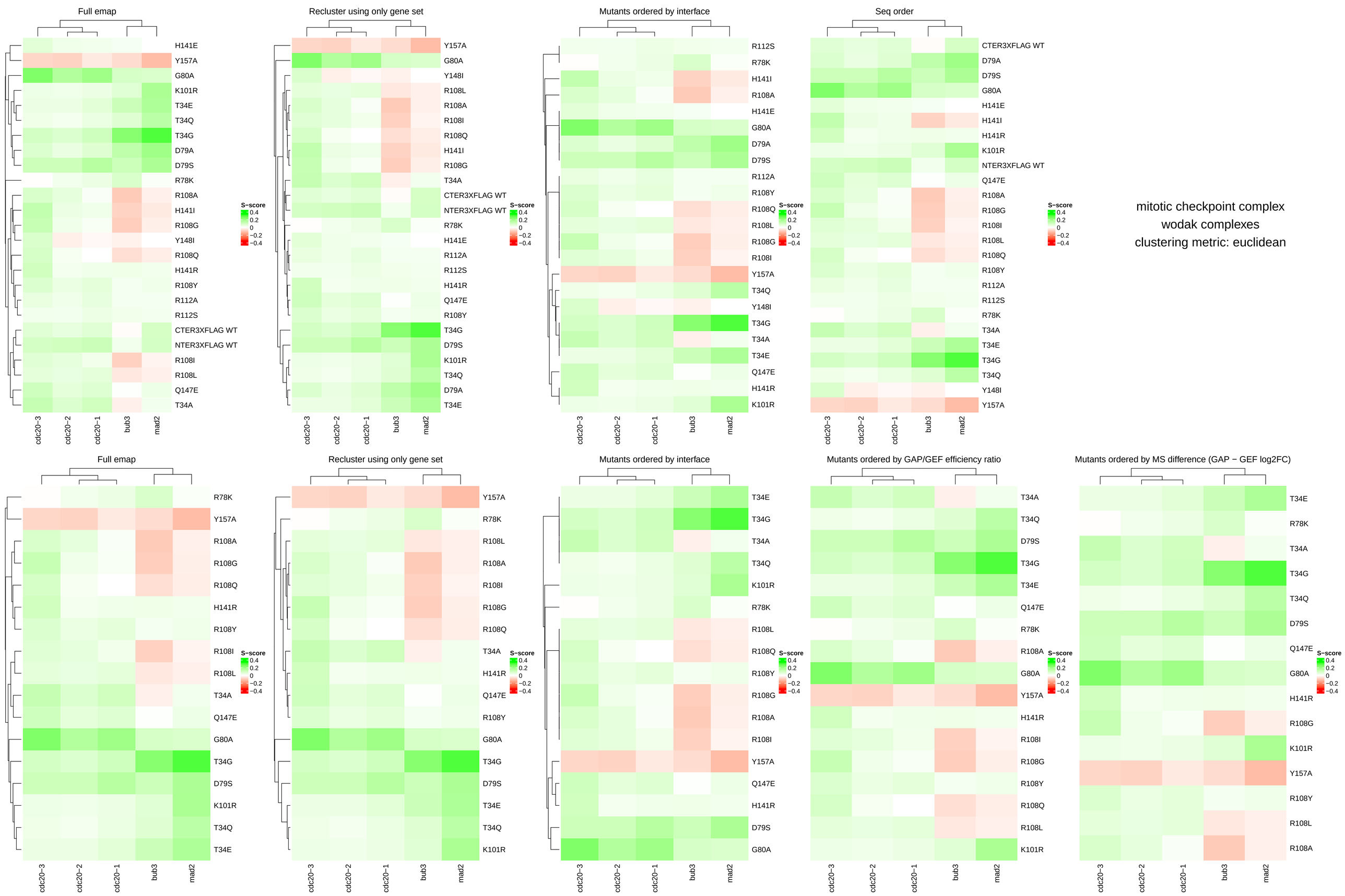


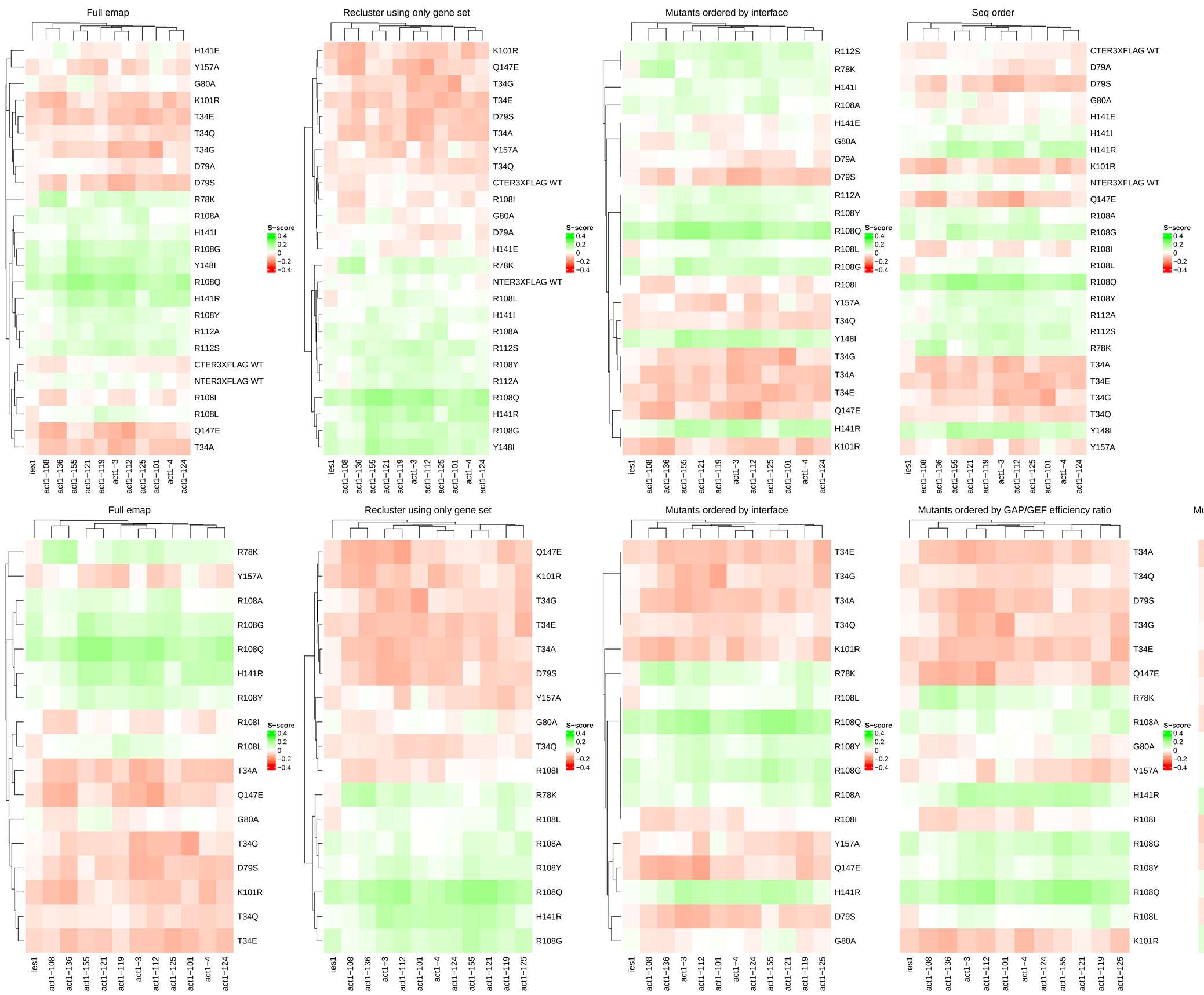
ribonuclease MRP complex
wodak complexes
clustering metric: euclidean


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
yhc1−3
yhc1−8
yhc1−2
prp42−5001
prp39−1
yhc1−1
commitment complex
wodak complexes
clustering metric: euclidean

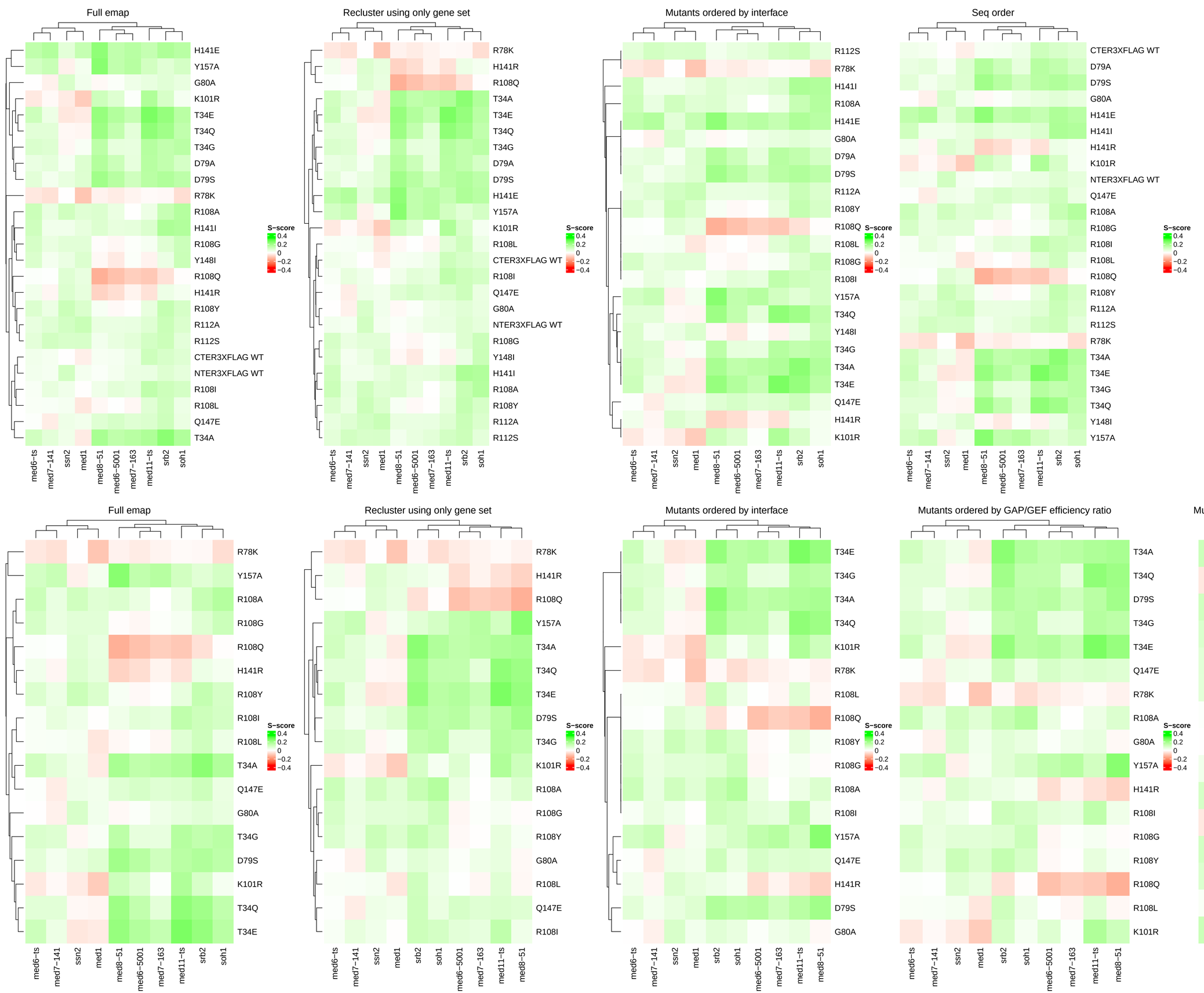
mRNA cleavage and polyadenylation specificity factor co
wodak complexes
clustering metric: euclidean



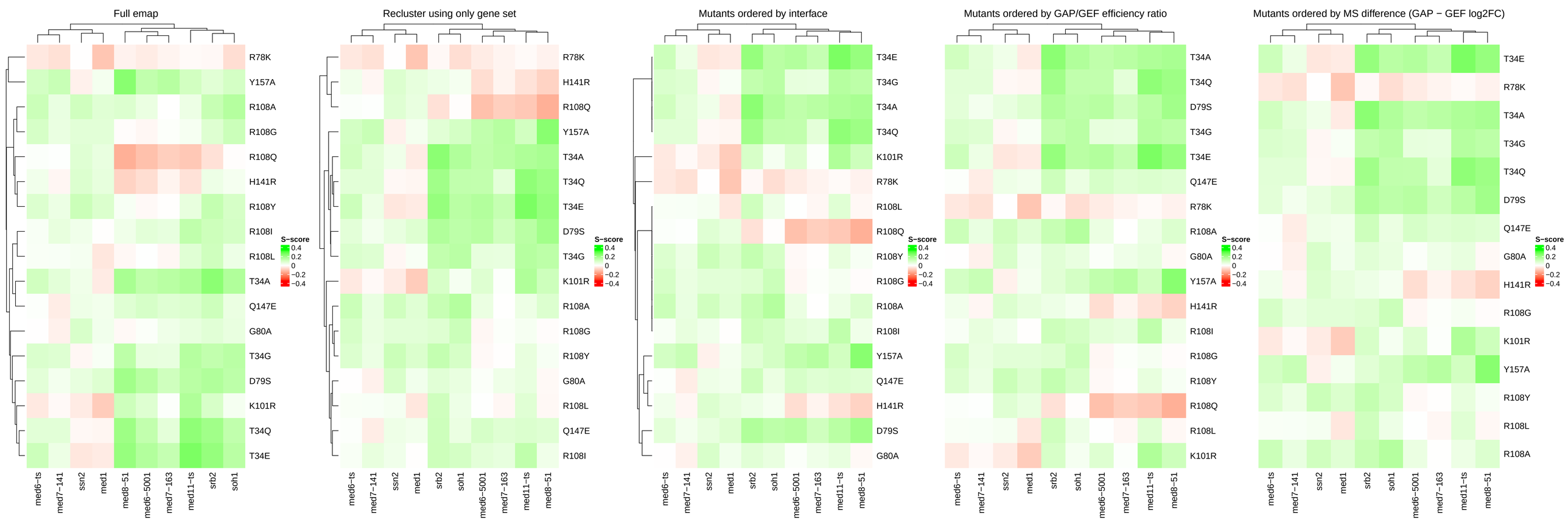

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
cdc20−3
cdc20−2
cdc20−1
bub3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



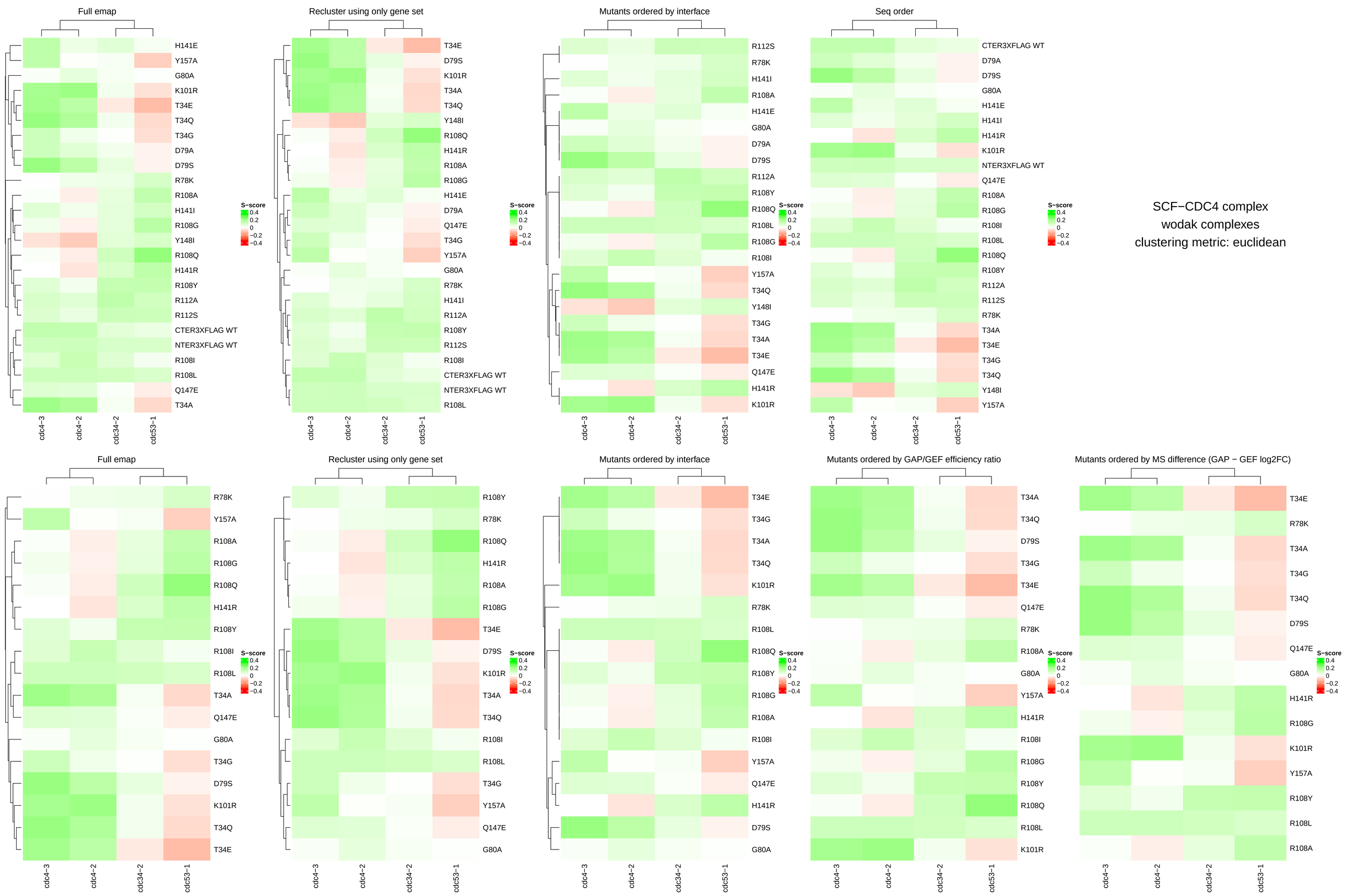
Ino80p complex
wodak complexes
clustering metric: euclidean

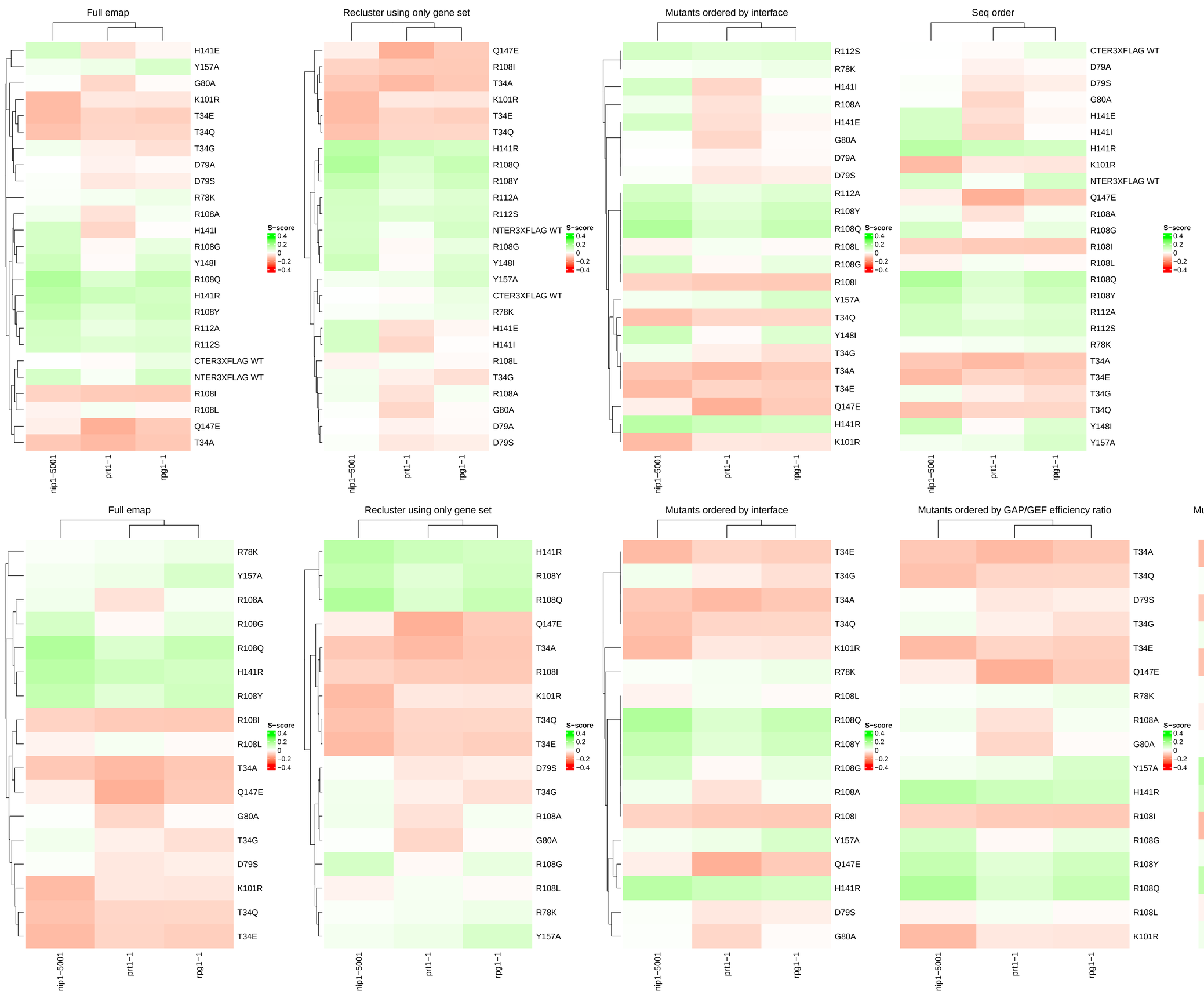


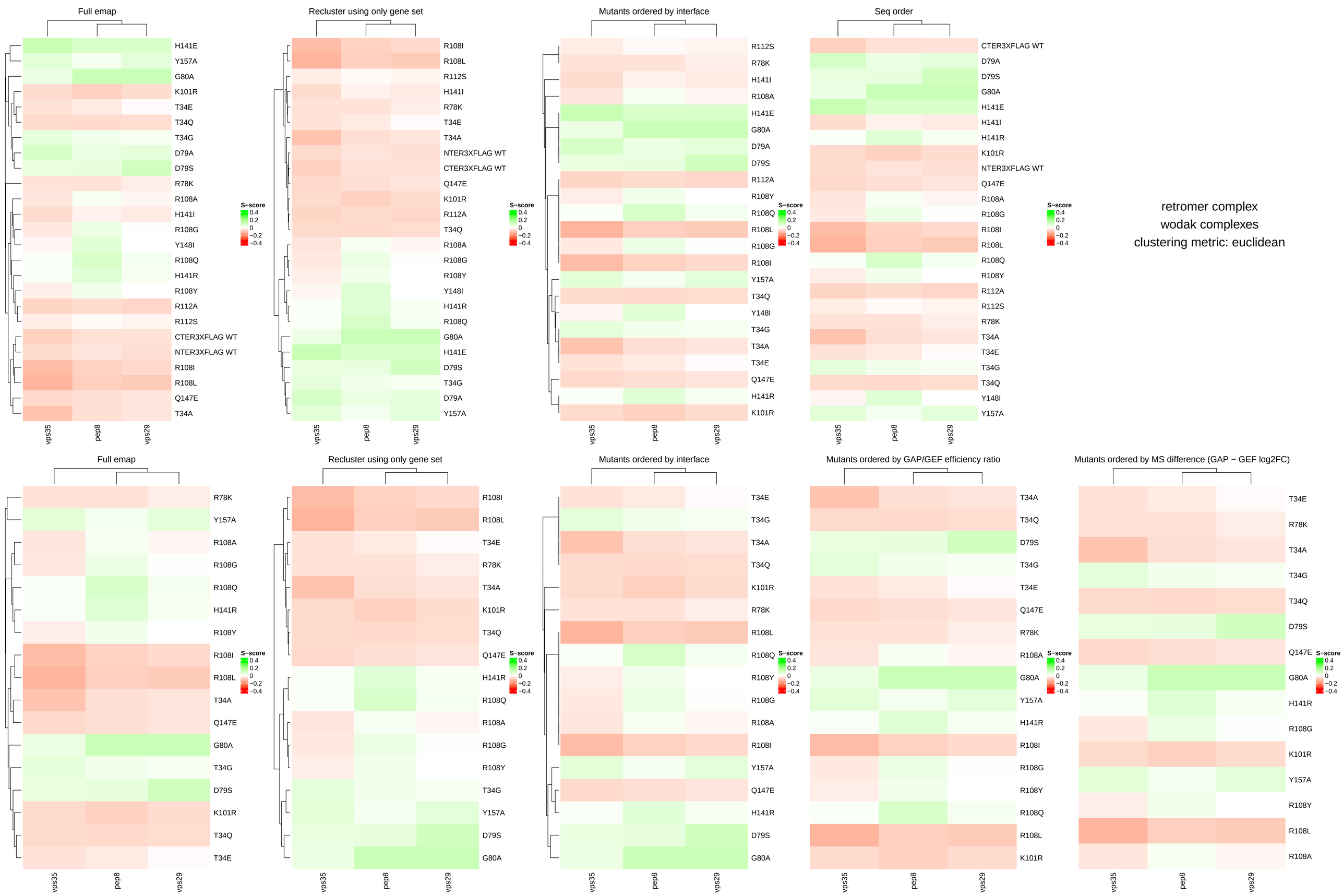
Kornberg's mediator (SRB) complex
wodak complexes
clustering metric: euclidean



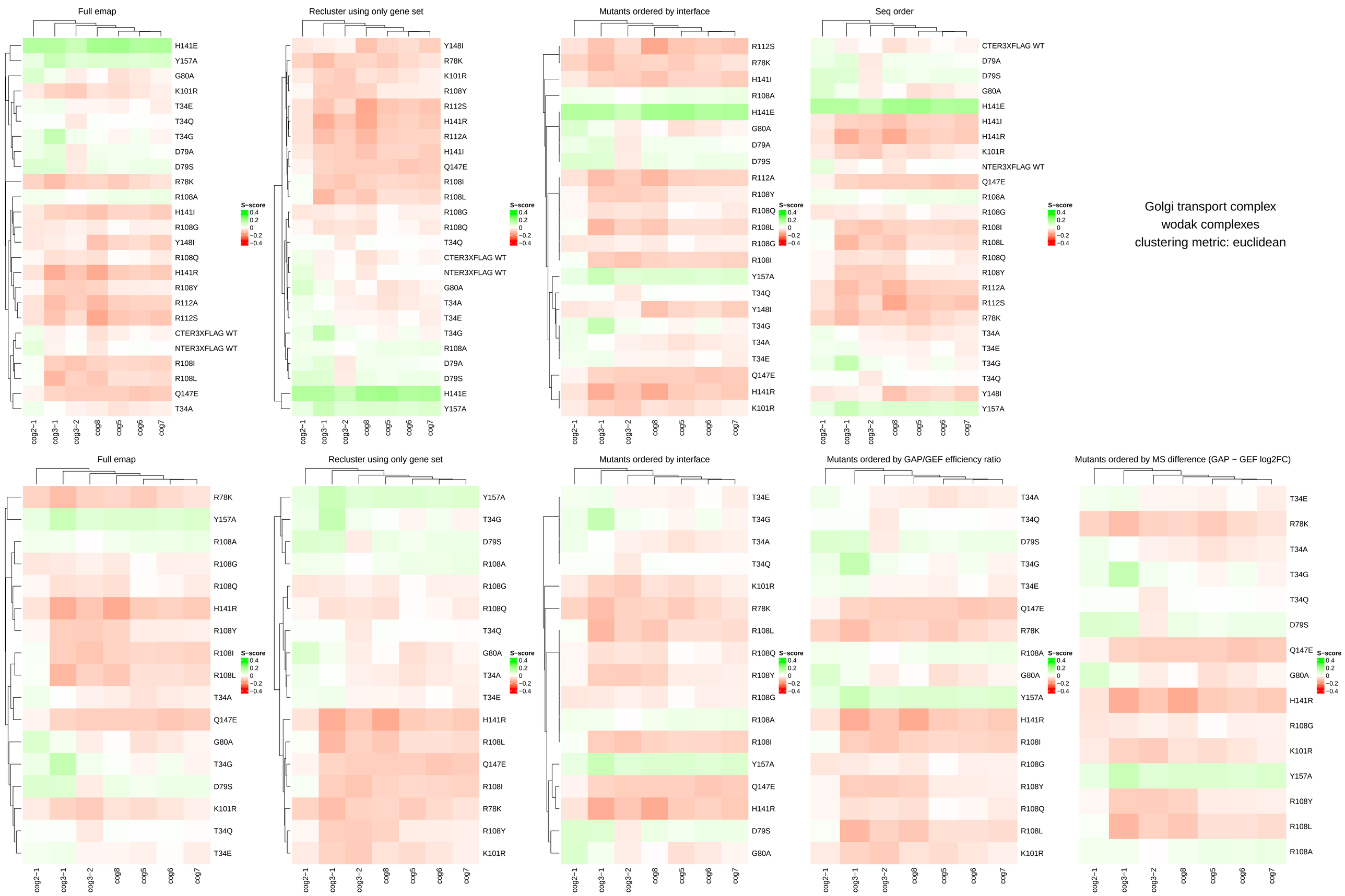
Sgv1p/Bur2p complex
wodak complexes
clustering metric: euclidean


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

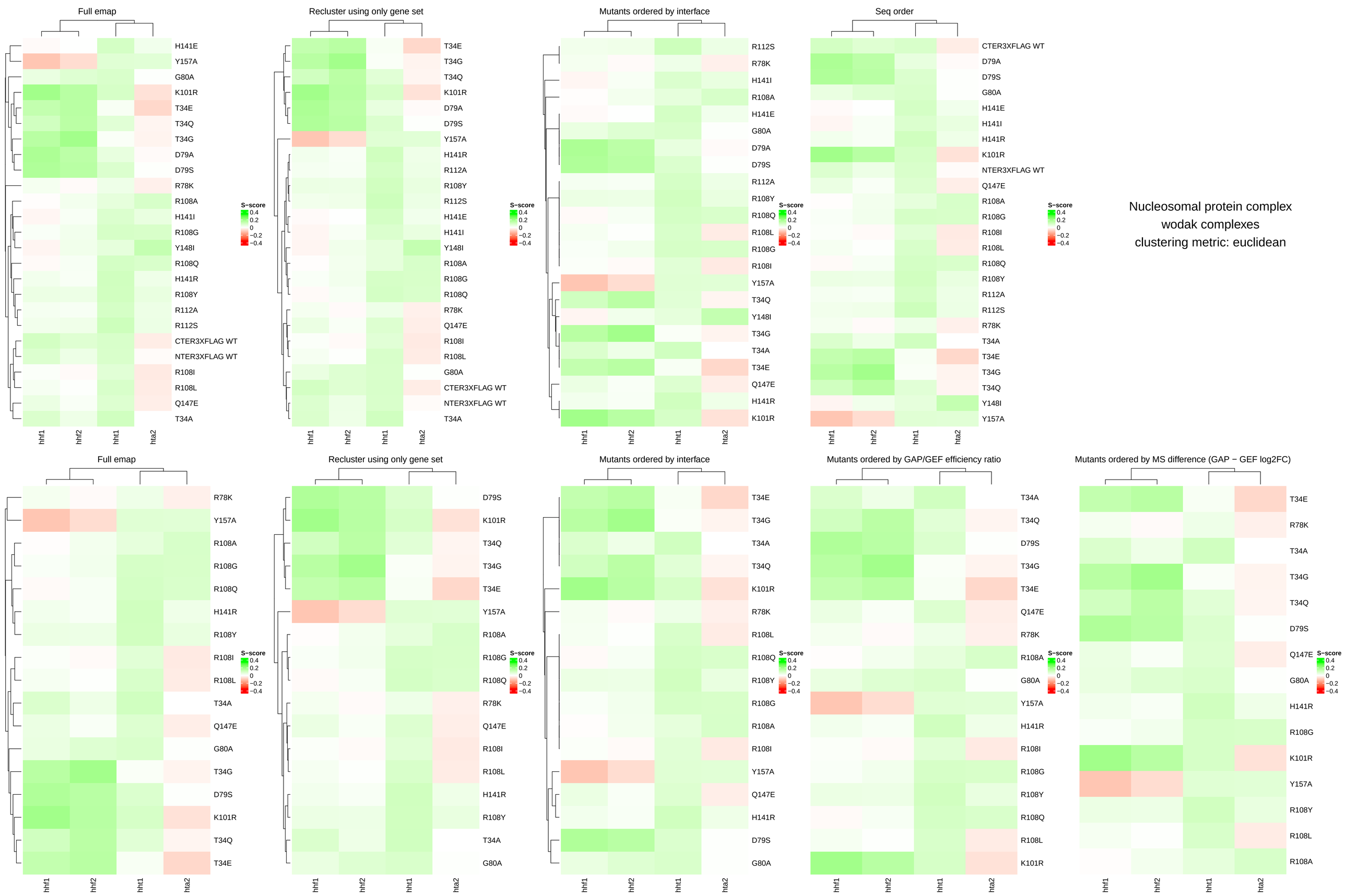

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
nip1−5001
prt1−1
rpg1−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
Q147E
R108I
T34A
K101R
T34E
T34Q
H141R
R108Q
R108Y
R112A
R112S
NTER3XFLAG WT
R108G
Y148I
Y157A
CTER3XFLAG WT
R78K
H141E
H141I
R108L
T34G
R108A
G80A
D79A
D79S
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
H141R
R108Y
R108Q
Q147E
T34A
R108I
K101R
T34Q
T34E
D79S
T34G
R108A
G80A
R108G
R108L
R78K
Y157A
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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



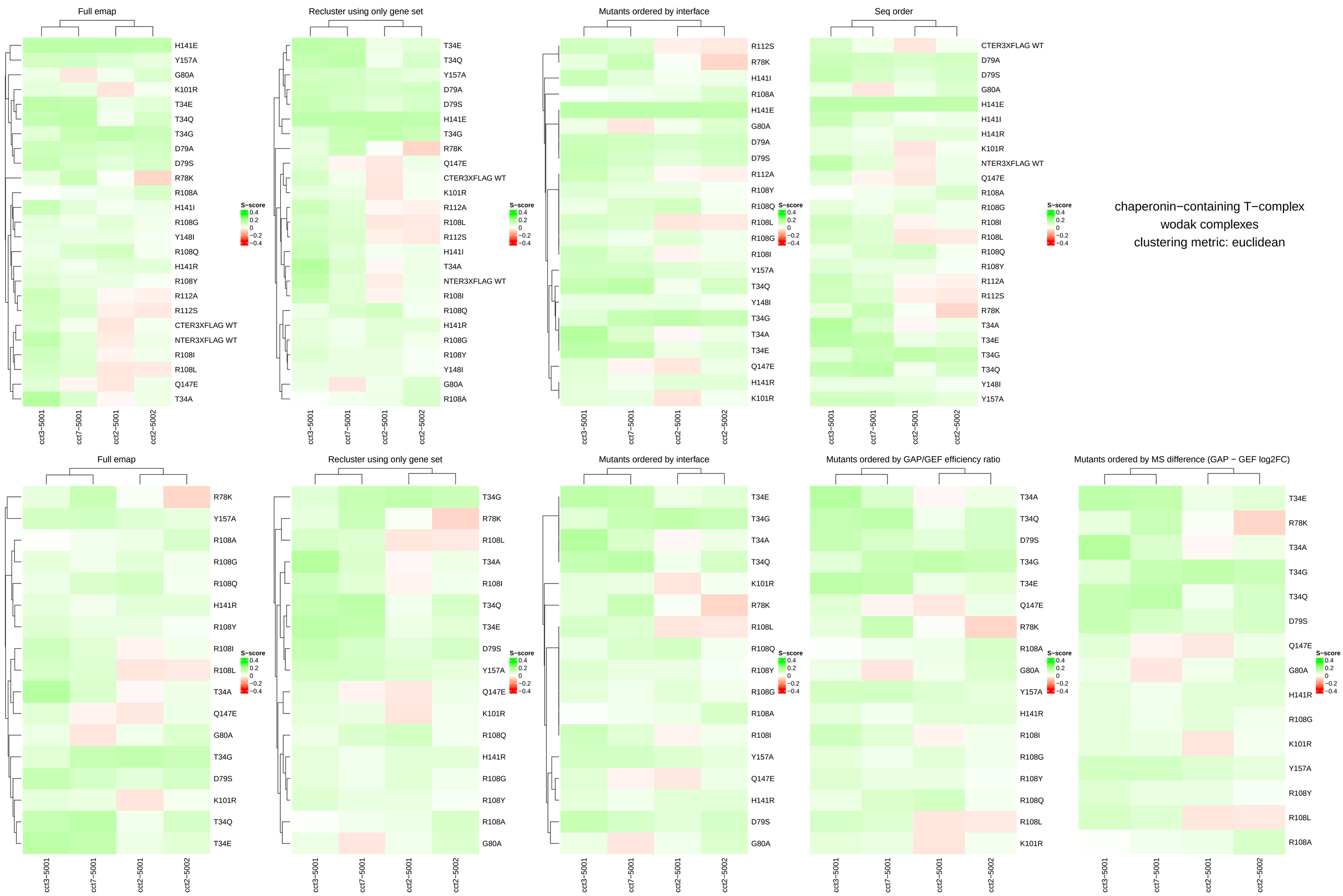
retromer complex
wodak complexes
clustering metric: euclidean

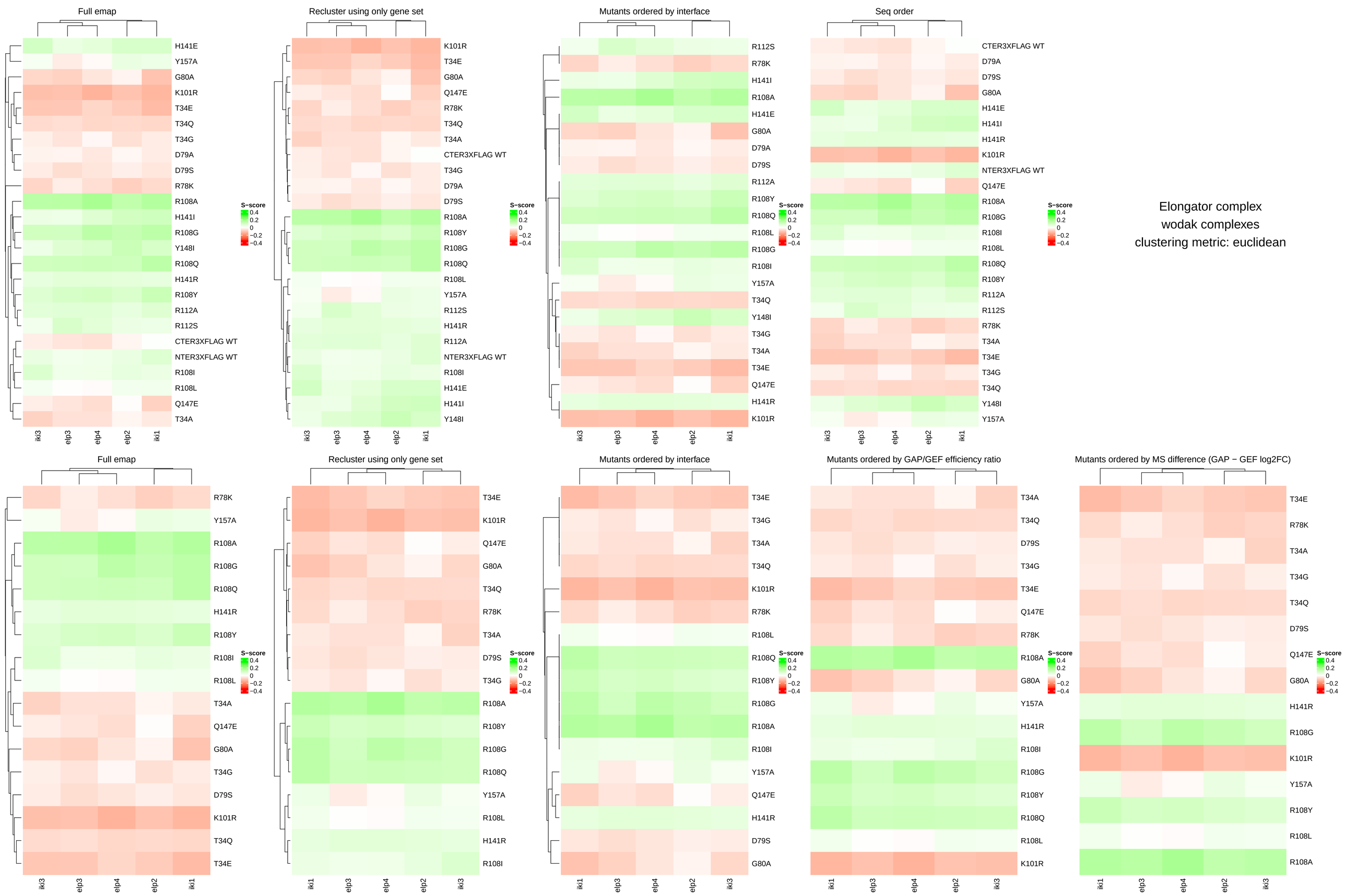


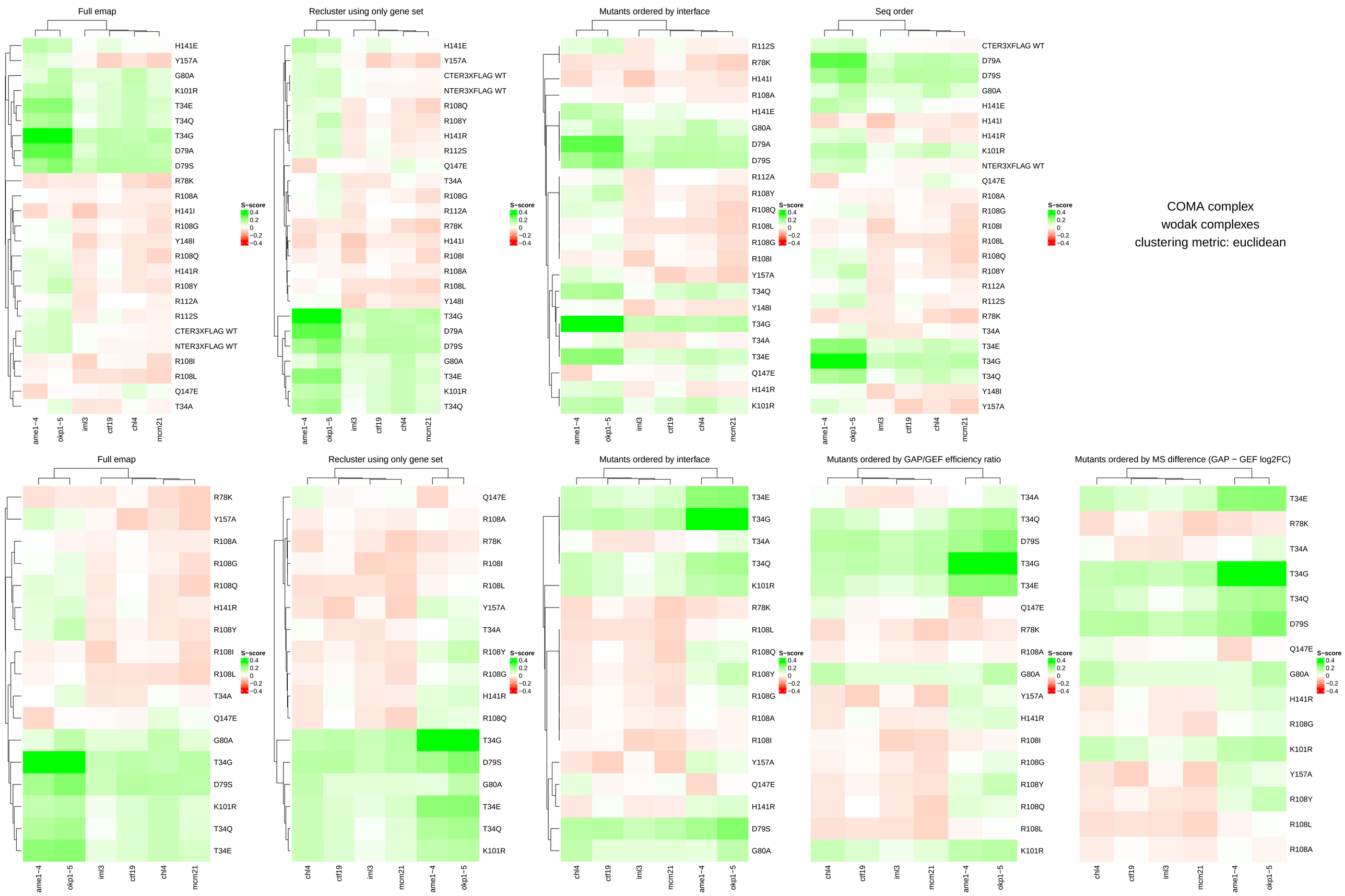
Golgi transport complex
wodak complexes
clustering metric: euclidean


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
hhf1
hhf2
hht1
hta2
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
Nucleosomal protein complex
wodak complexes
clustering metric: euclidean

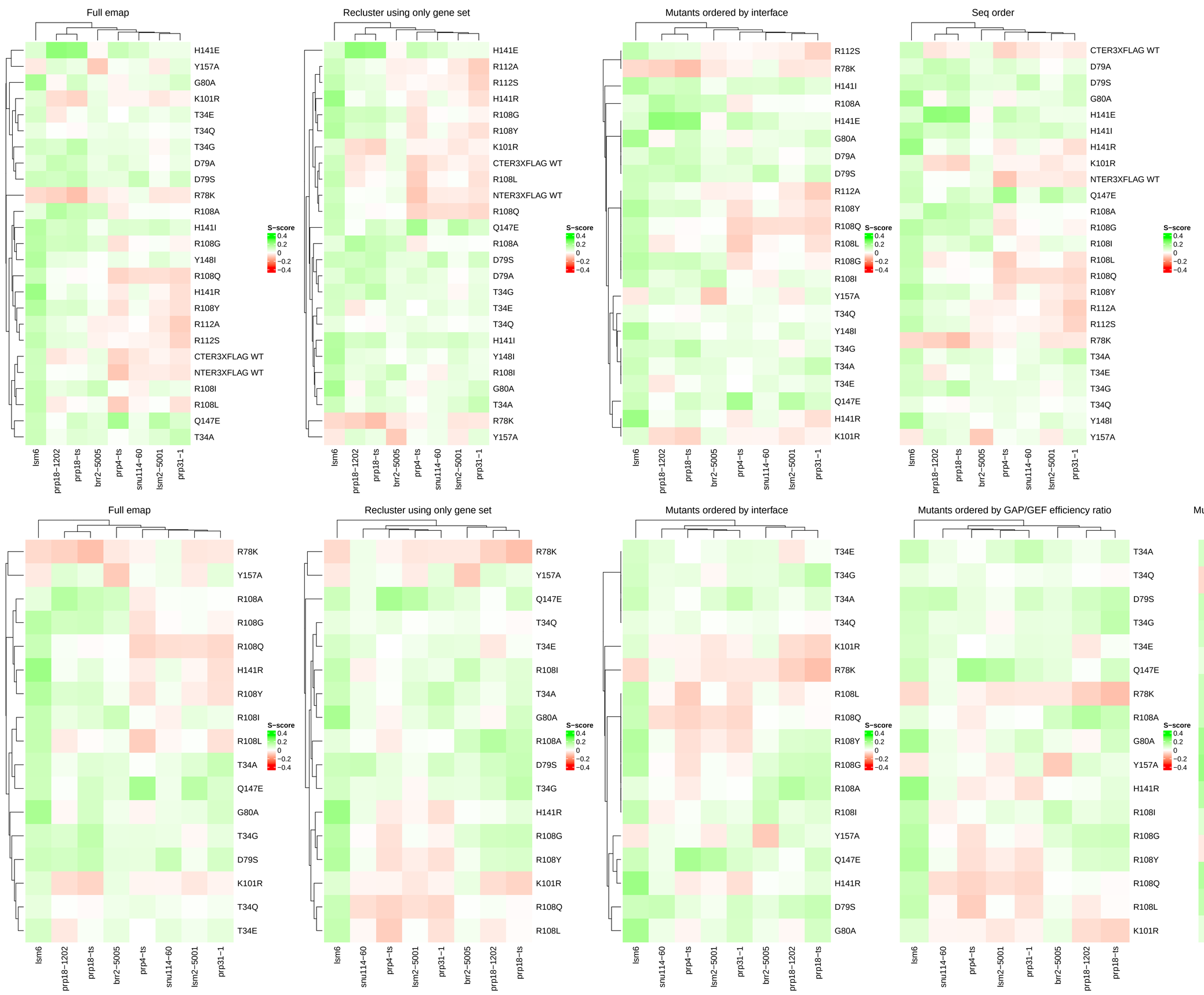
U5 snRNP complex
wodak complexes
clustering metric: euclidean


Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
cct3−5001
cct7−5001
cct2−5001
cct2−5002
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
T34E
T34Q
Y157A
D79A
D79S
H141E
T34G
R78K
Q147E
CTER3XFLAG WT
K101R
R112A
R108L
R112S
H141I
T34A
NTER3XFLAG WT
R108I
R108Q
H141R
R108G
R108Y
Y148I
G80A
R108A
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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
chaperonin−containing T−complex
wodak complexes
clustering metric: euclidean
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
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
iki3
elp3
elp4
elp2
iki1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
K101R
T34E
G80A
Q147E
R78K
T34Q
T34A
CTER3XFLAG WT
T34G
D79A
D79S
R108A
R108Y
R108G
R108Q
R108L
Y157A
R112S
H141R
R112A
NTER3XFLAG WT
R108I
H141E
H141I
Y148I
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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 complex
wodak complexes
clustering metric: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
T34E
K101R
Q147E
G80A
T34Q
R78K
T34A
D79S
T34G
R108A
R108Y
R108G
R108Q
Y157A
R108L
H141R
R108I
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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

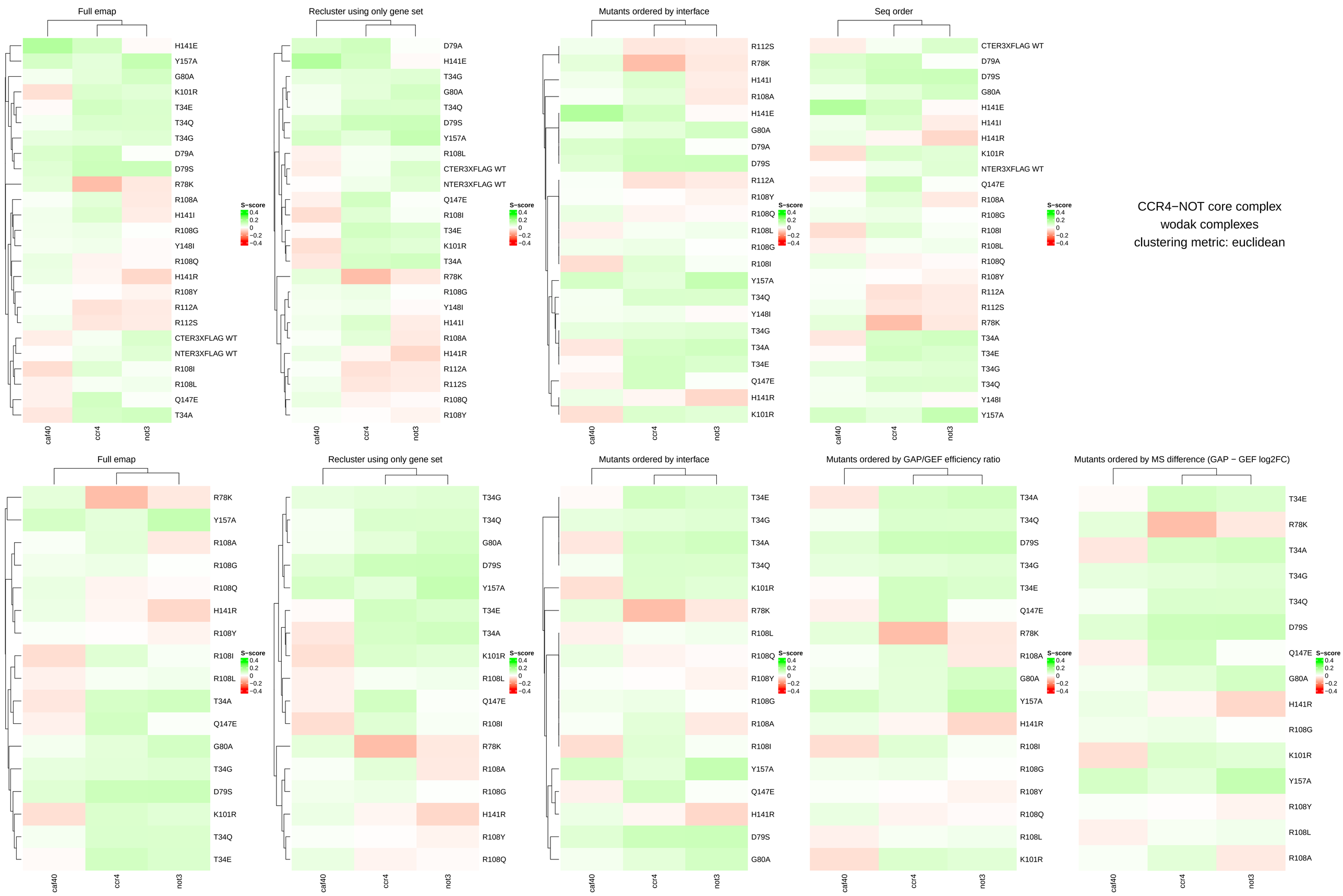


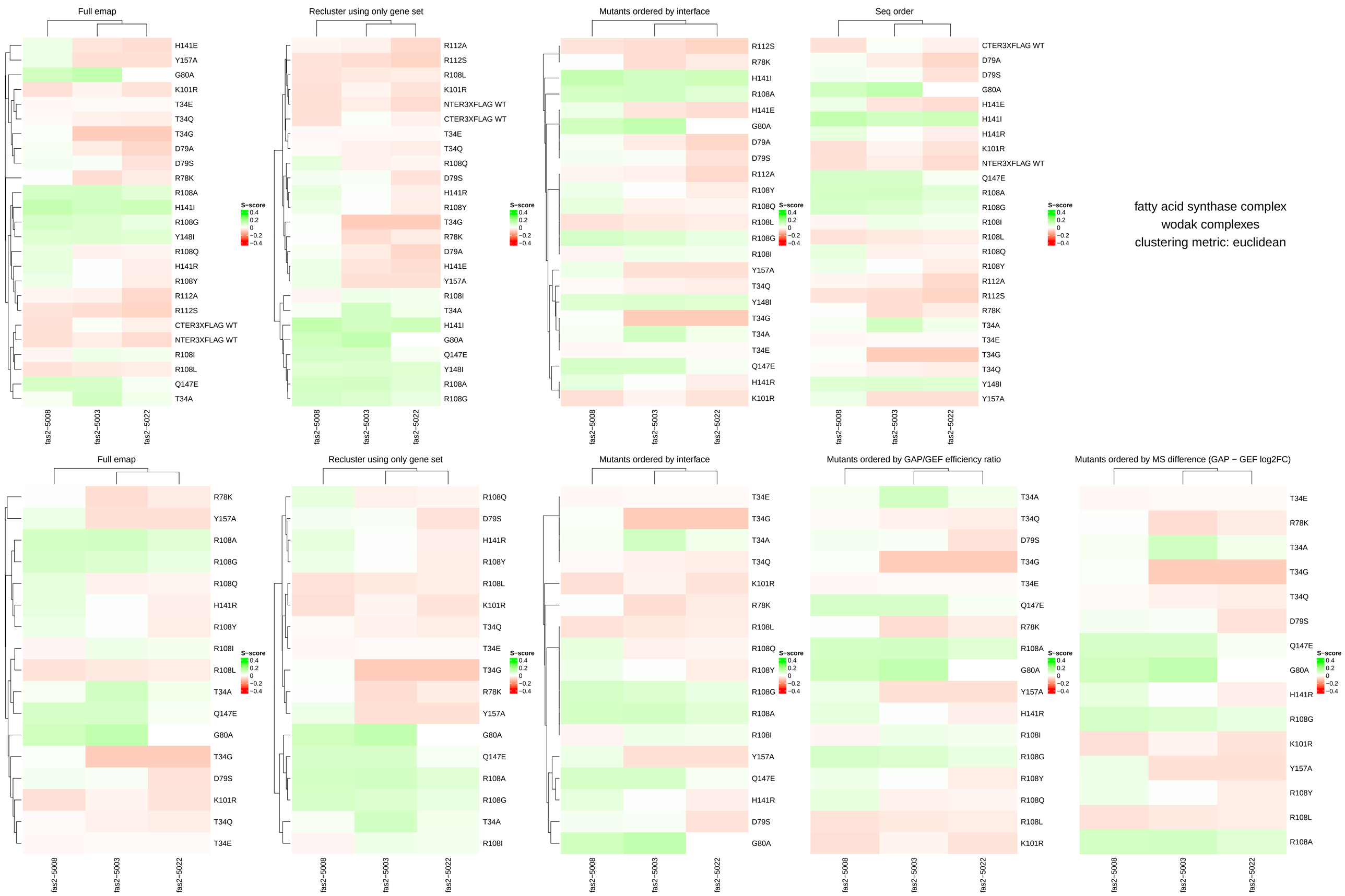
COMA complex
wodak complexes
clustering metric: euclidean

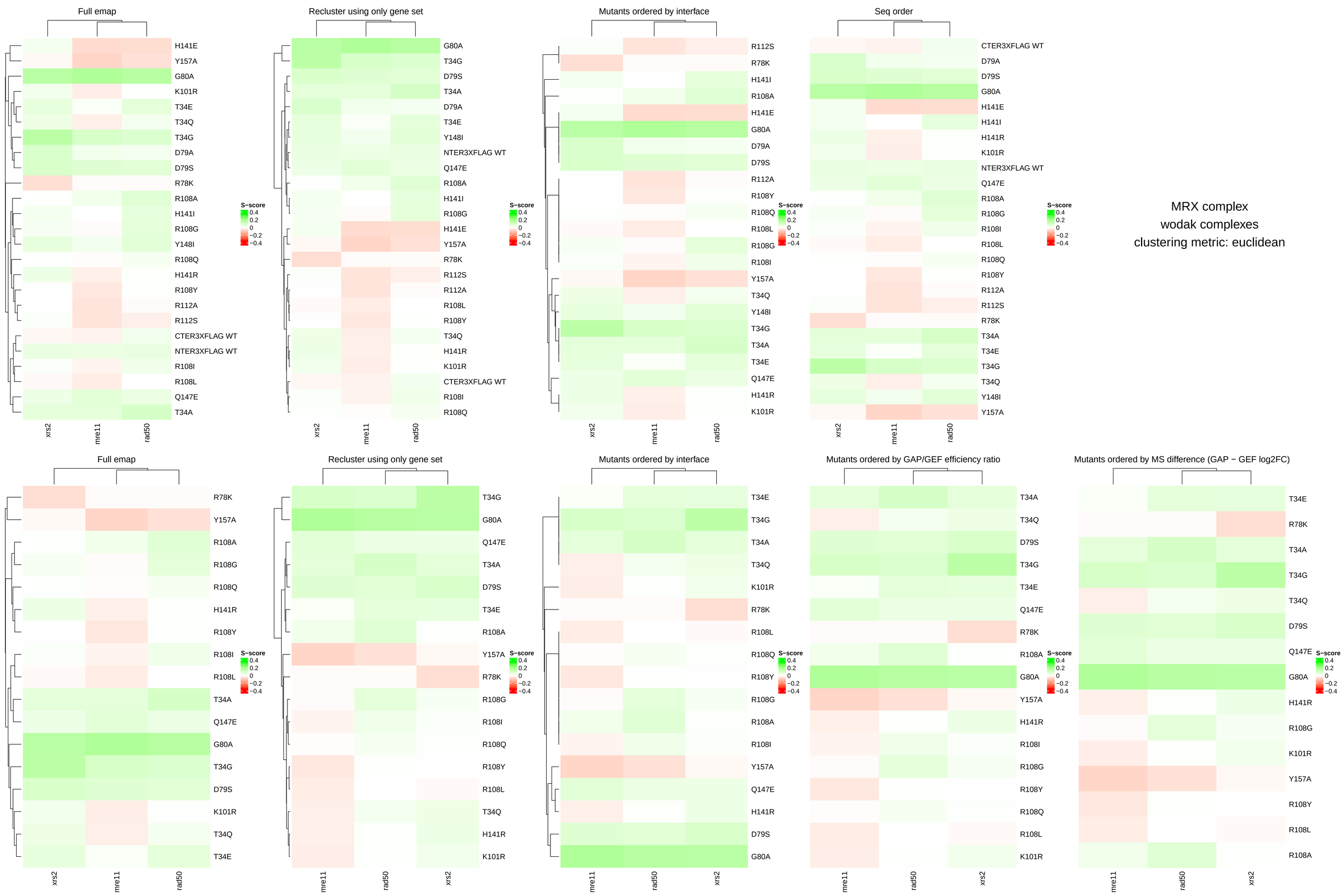


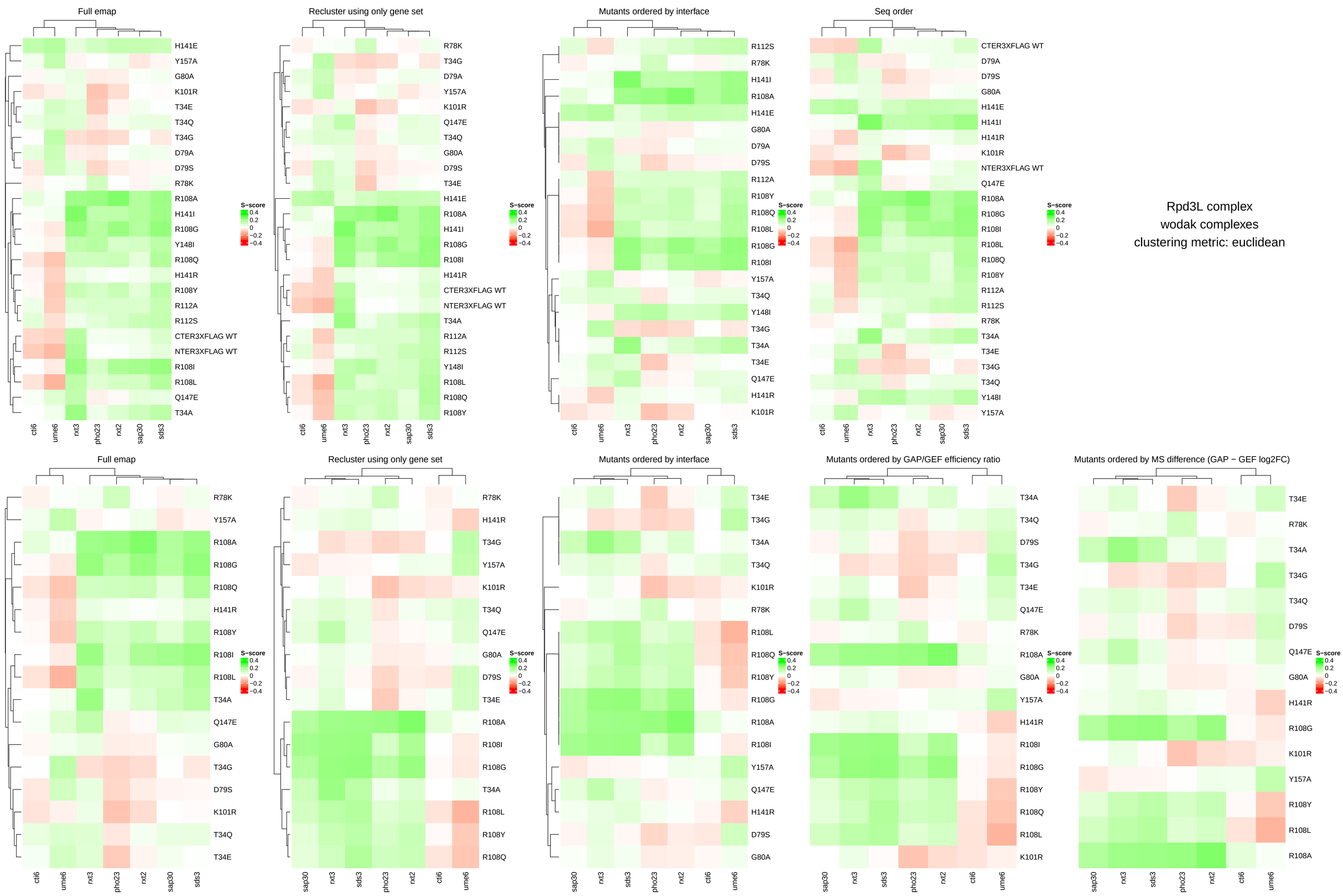
U4/U6 x U5 tri−snRNP complex
wodak complexes
clustering metric: euclidean

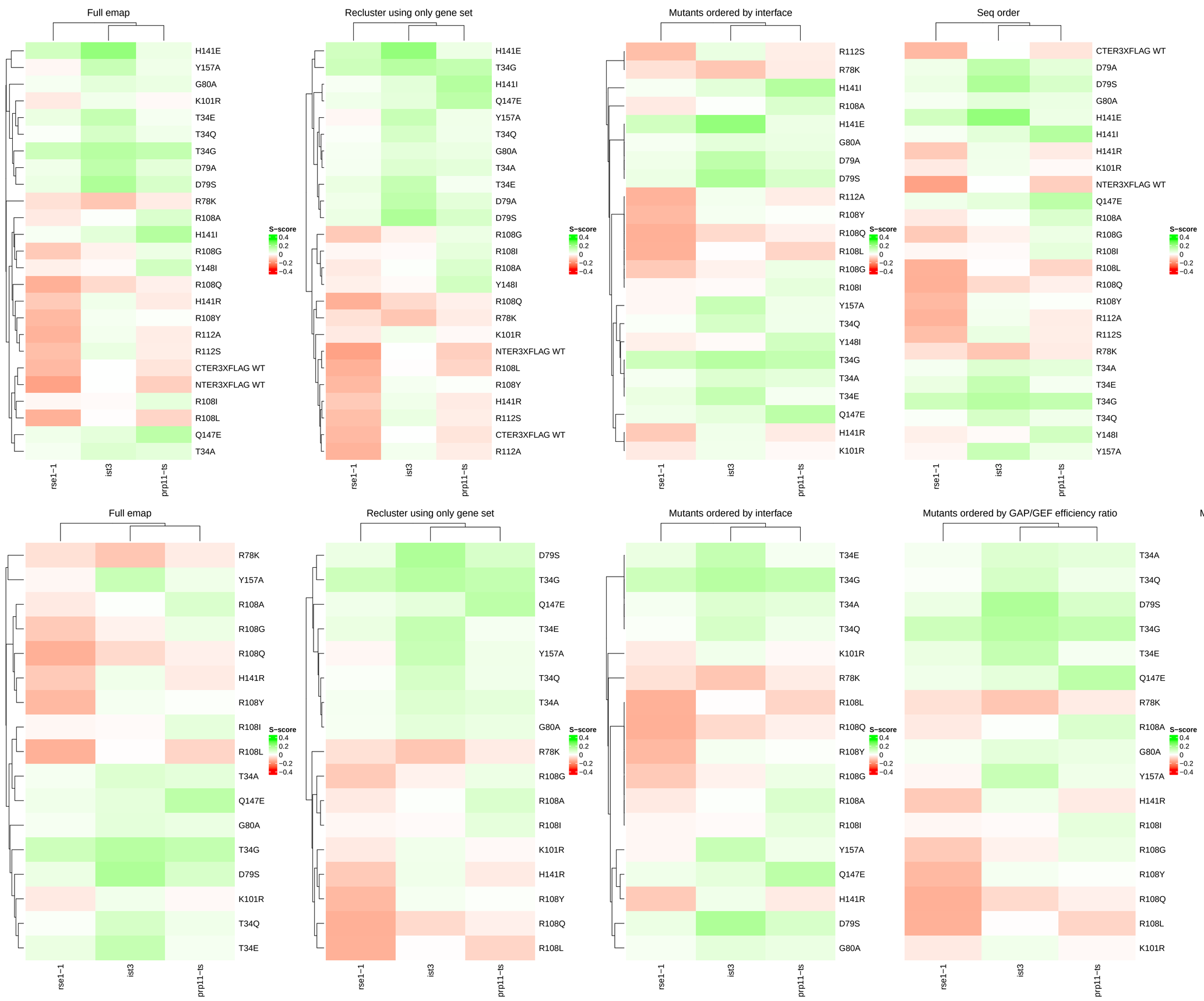
DNA replication factor C complex (Ctf18p/Ctf8p/dcc1
wodak complexes
clustering metric: euclidean
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
ctf8
ctf18
dcc1


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
caf40
ccr4
not3
CCR4−NOT core complex
wodak complexes
clustering metric: euclidean

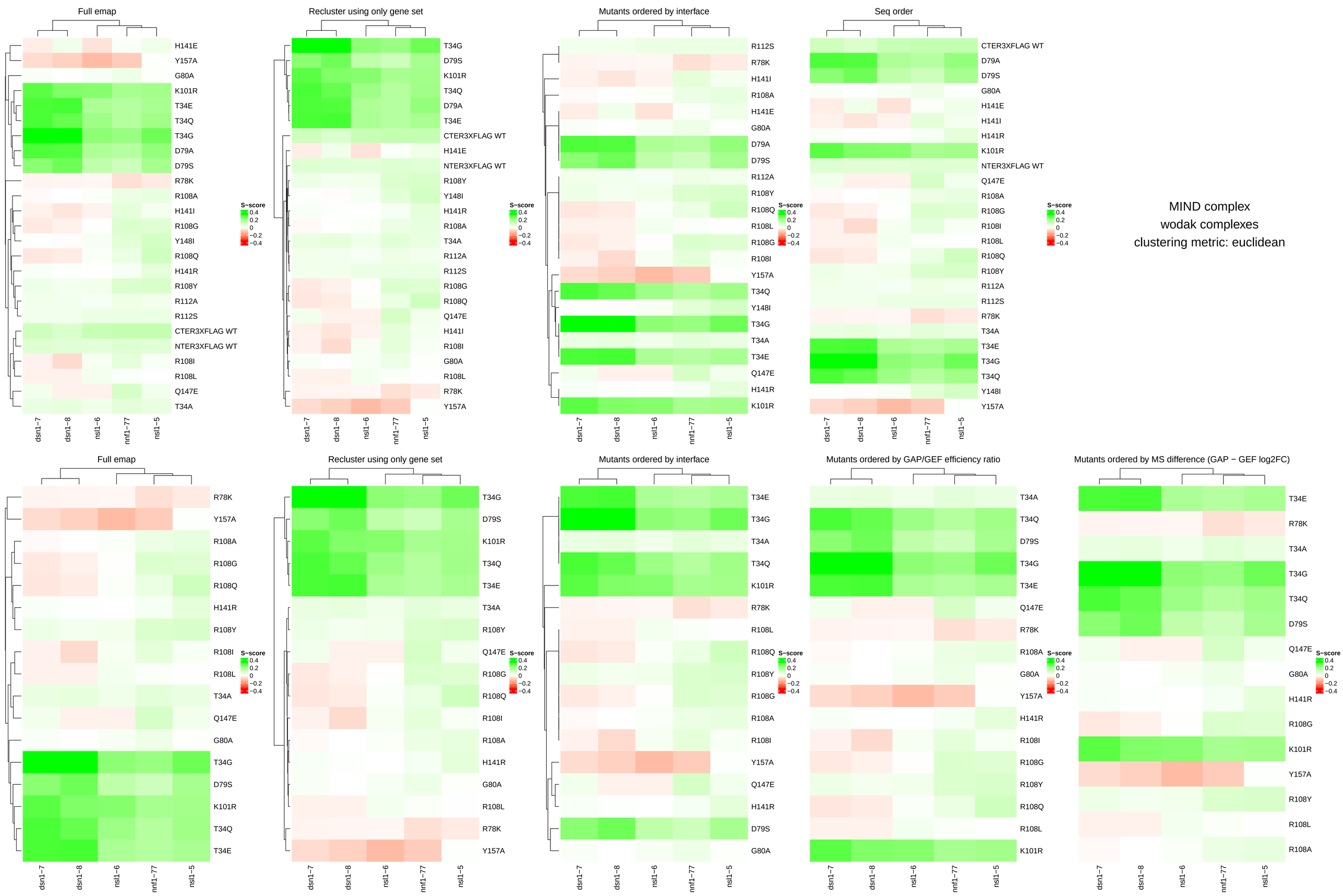

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
fas2−5008
fas2−5003
fas2−5022
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R112A
R112S
R108L
K101R
NTER3XFLAG WT
CTER3XFLAG WT
T34E
T34Q
R108Q
D79S
H141R
R108Y
T34G
R78K
D79A
H141E
Y157A
R108I
T34A
H141I
G80A
Q147E
Y148I
R108A
R108G
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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
fatty acid synthase complex
wodak complexes
clustering metric: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
R108Q
D79S
H141R
R108Y
R108L
K101R
T34Q
T34E
T34G
R78K
Y157A
G80A
Q147E
R108A
R108G
T34A
R108I
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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

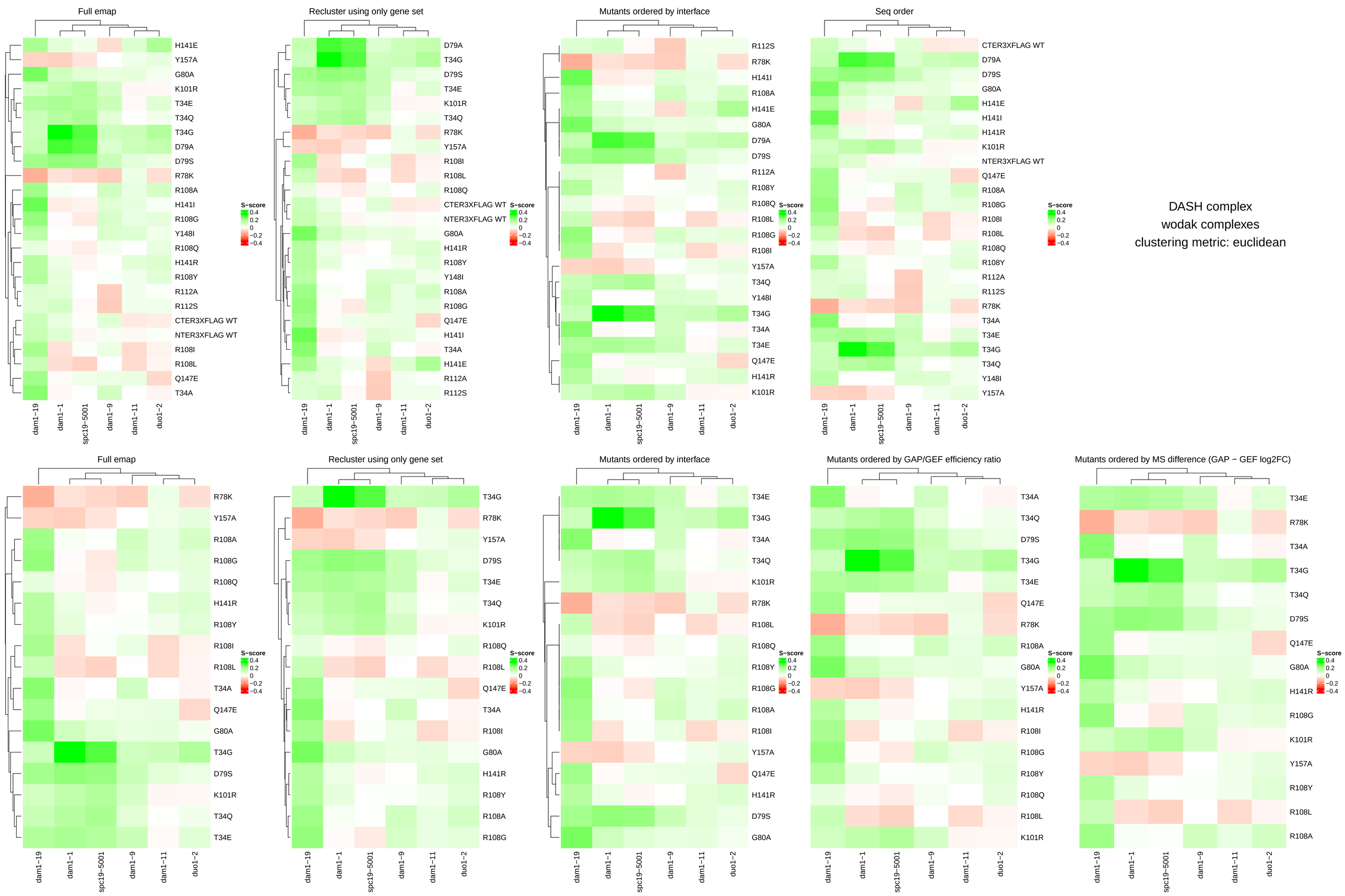

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
xrs2
mre11
rad50
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
G80A
T34G
D79S
T34A
D79A
T34E
Y148I
NTER3XFLAG WT
Q147E
R108A
H141I
R108G
H141E
Y157A
R78K
R112S
R112A
R108L
R108Y
T34Q
H141R
K101R
CTER3XFLAG WT
R108I
R108Q
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
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
cti6
ume6
rxt3
pho23
rxt2
sap30
sds3
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
Rpd3L complex
wodak complexes
clustering metric: euclidean

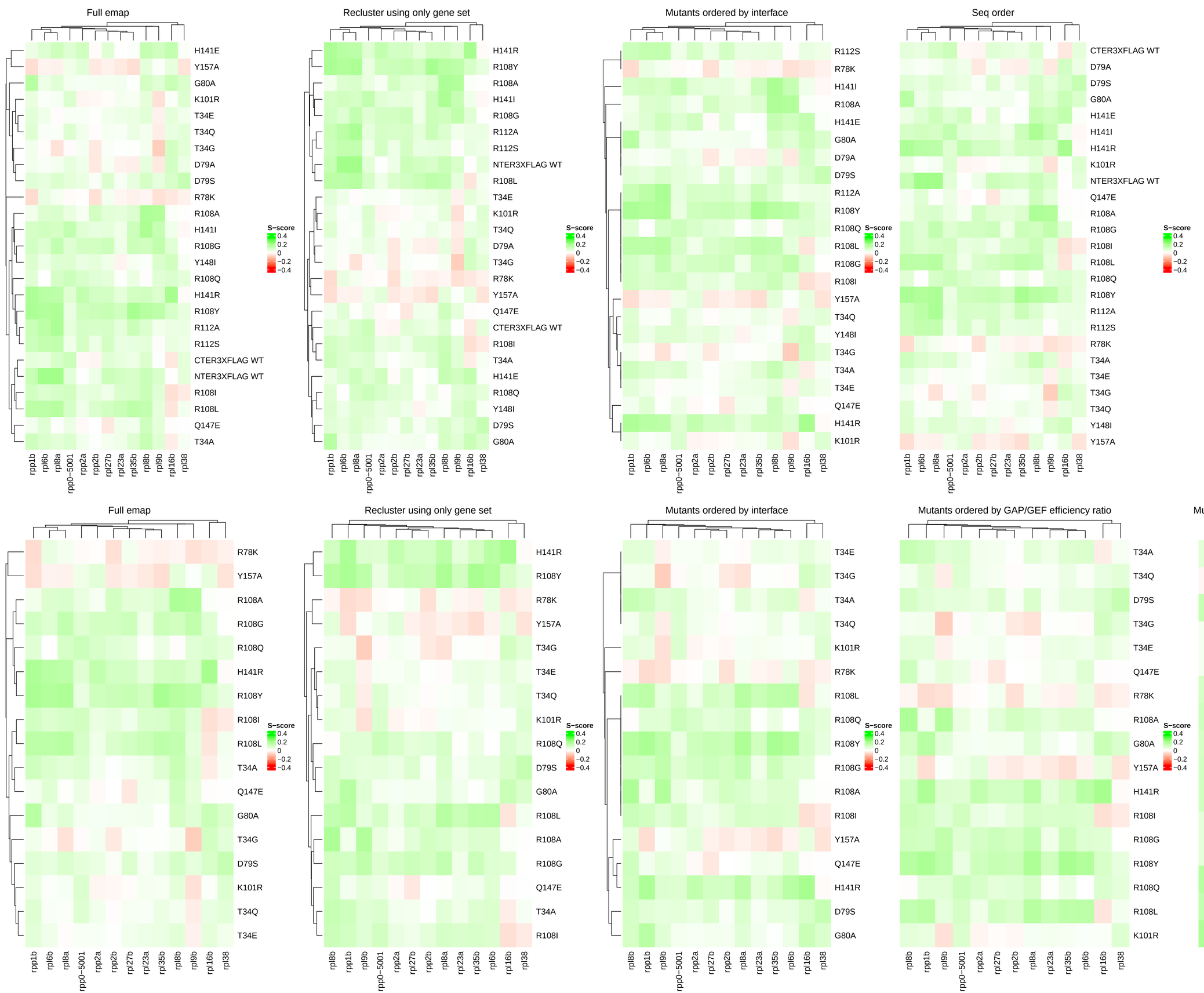


U2 snRNP complex
wodak complexes
clustering metric: euclidean

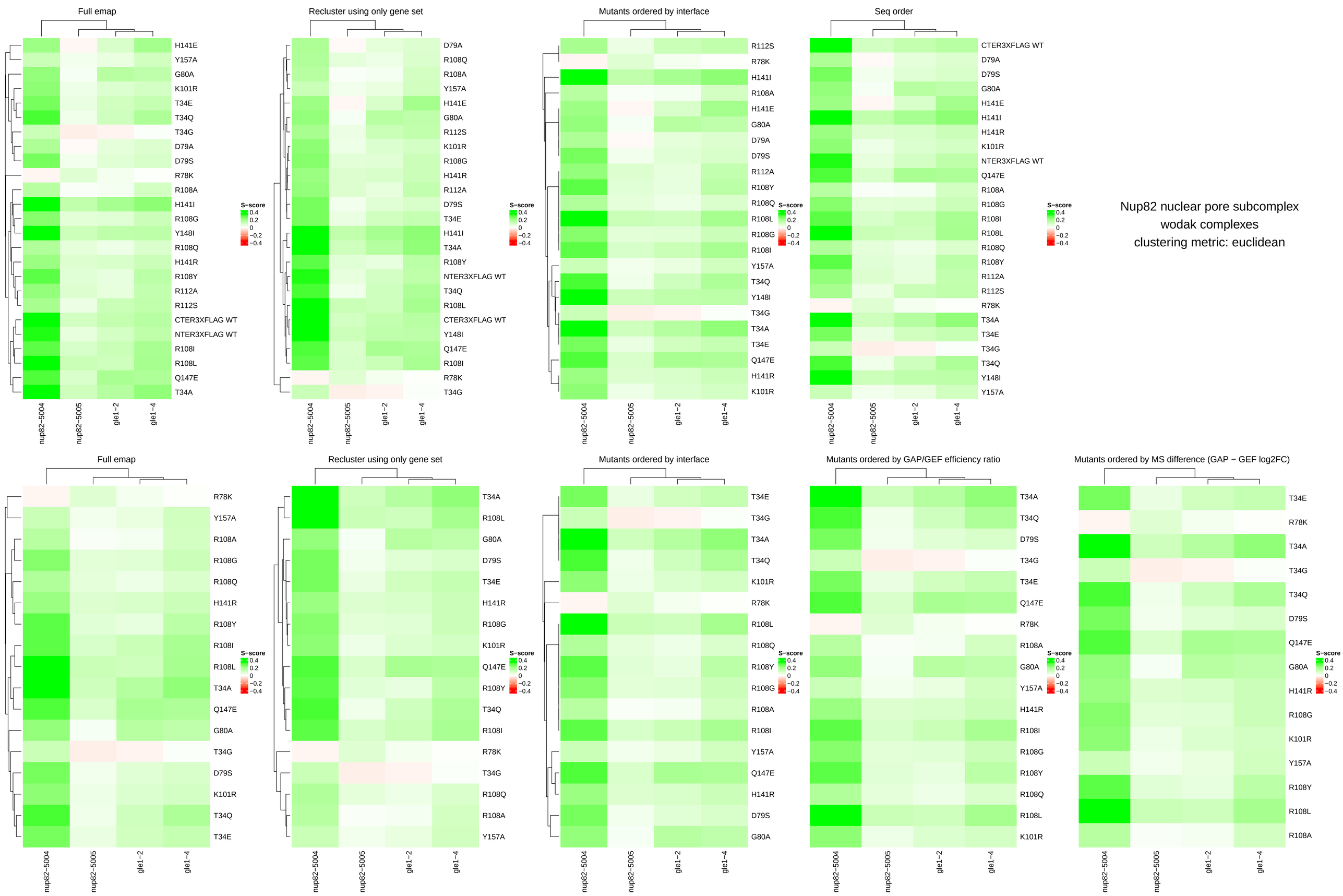

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
dsn1−7
dsn1−8
nsl1−6
nnf1−77
nsl1−5
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
MIND complex
wodak complexes
clustering metric: euclidean



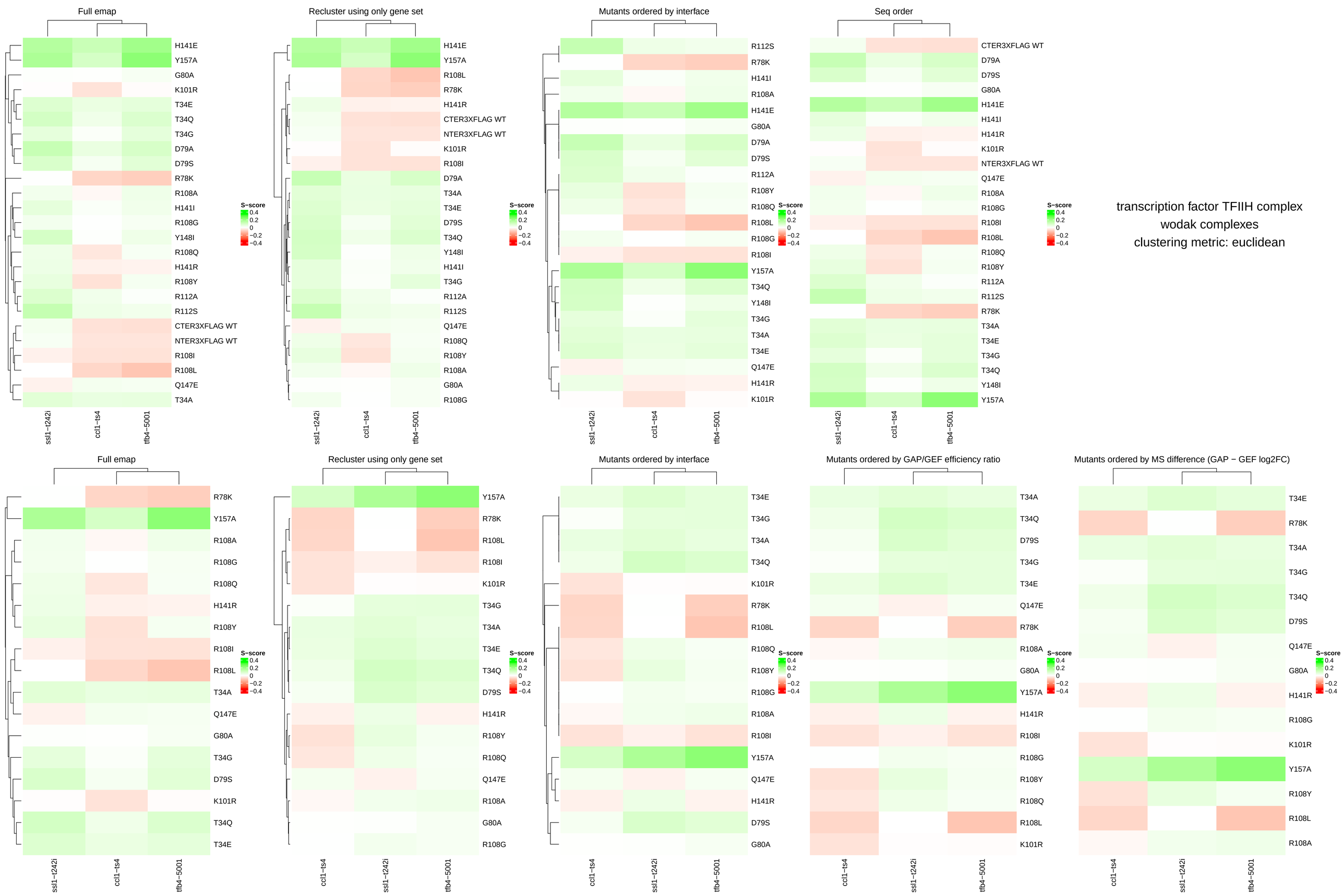
DASH complex
wodak complexes
clustering metric: euclidean

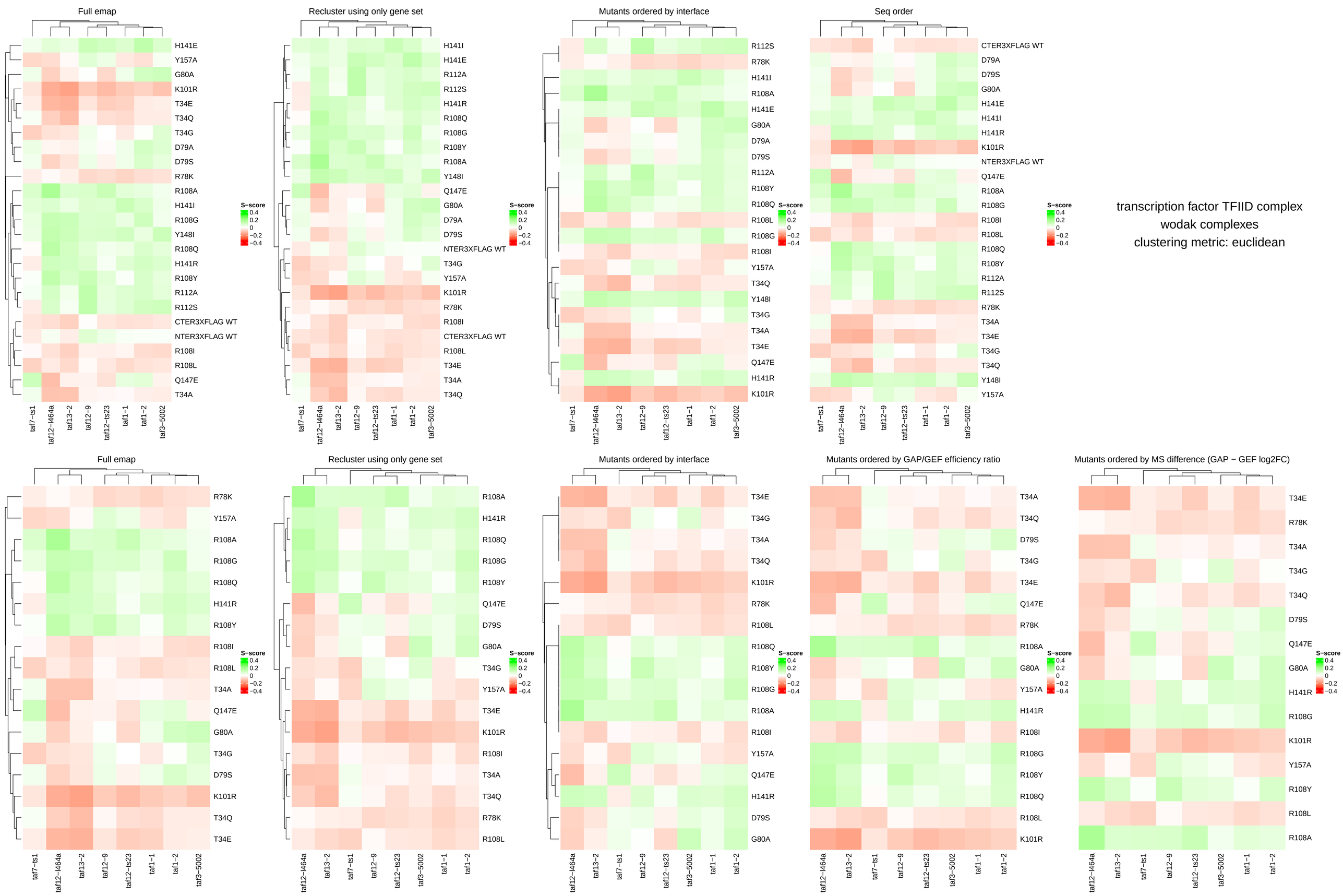


cytoplasmic ribosomal large subunit
wodak complexes
clustering metric: euclidean

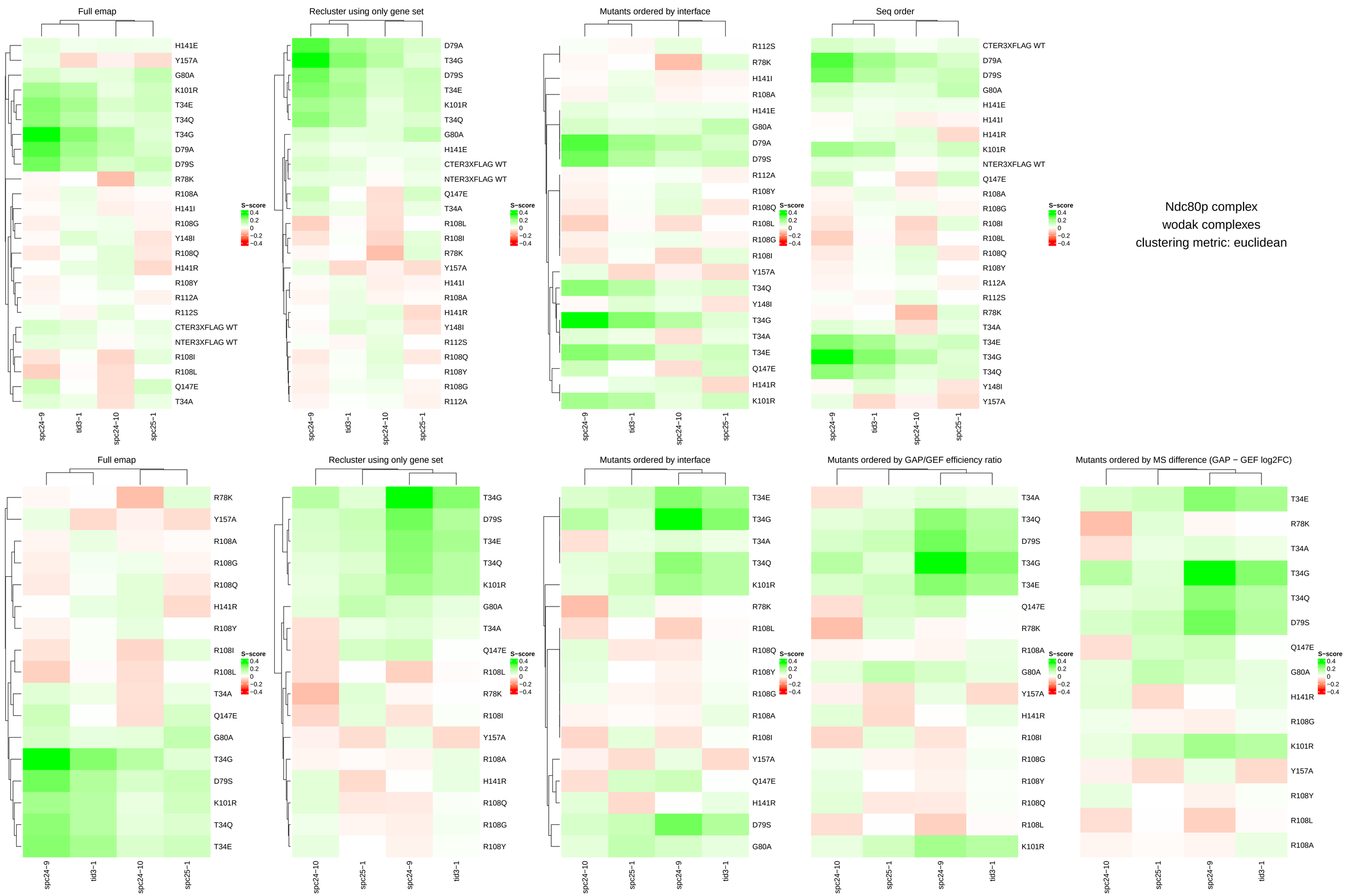


Nup82 nuclear pore subcomplex
wodak complexes
clustering metric: euclidean

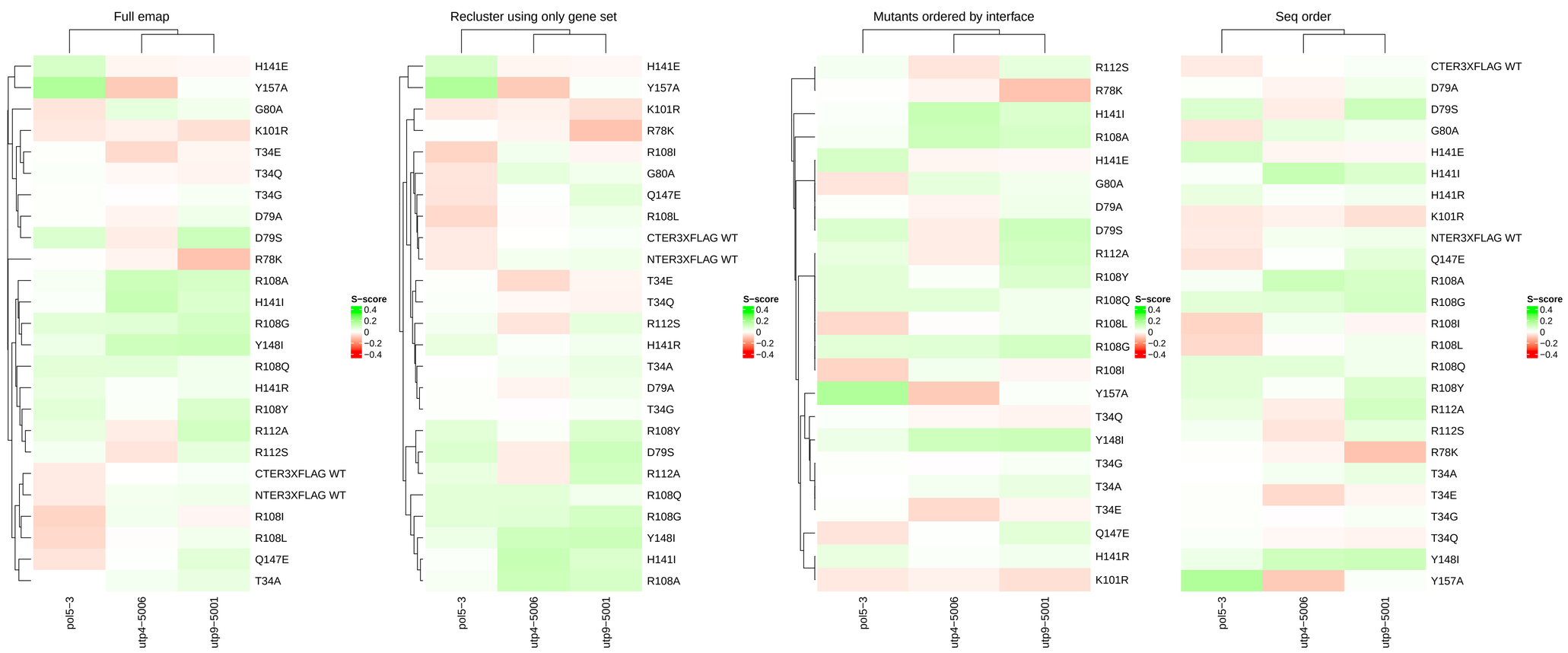

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
ssl1−t242i
ccl1−ts4
tfb4−5001
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
H141E
Y157A
R108L
R78K
H141R
CTER3XFLAG WT
NTER3XFLAG WT
K101R
R108I
D79A
T34A
T34E
D79S
T34Q
Y148I
H141I
T34G
R112A
R112S
Q147E
R108Q
R108Y
R108A
G80A
R108G
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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
transcription factor TFIIH complex
wodak complexes
clustering metric: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
Y157A
R78K
R108L
R108I
K101R
T34G
T34A
T34E
T34Q
D79S
H141R
R108Y
R108Q
Q147E
R108A
G80A
R108G
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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



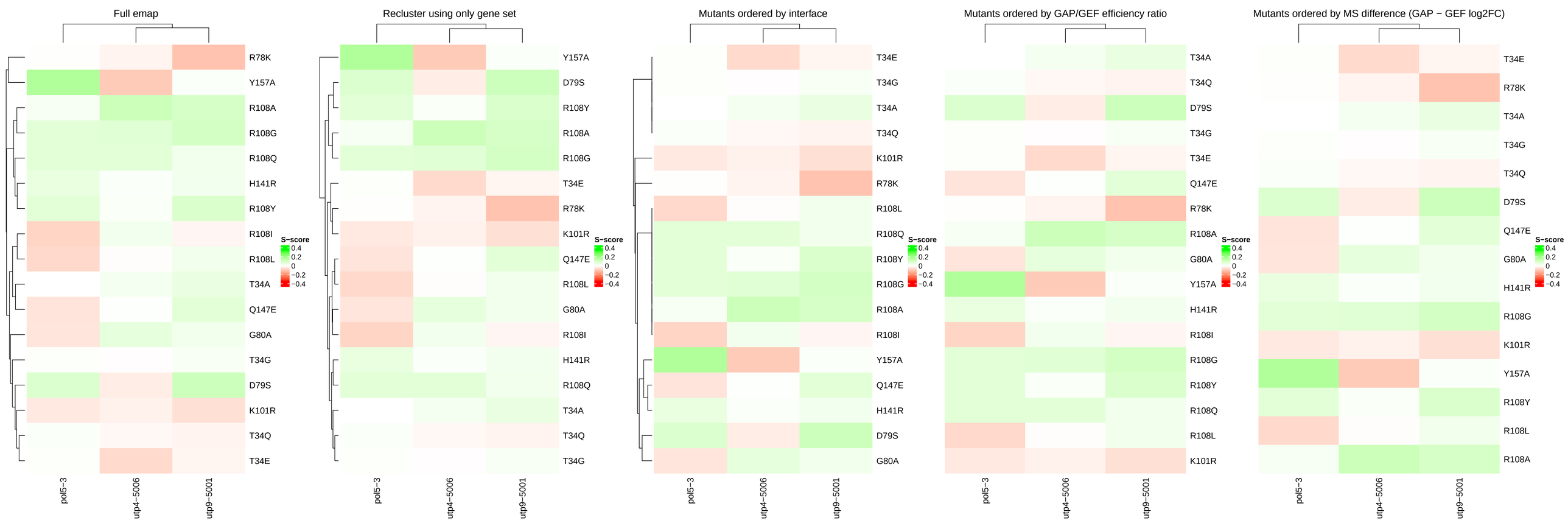
transcription factor TFIID complex
wodak complexes
clustering metric: euclidean

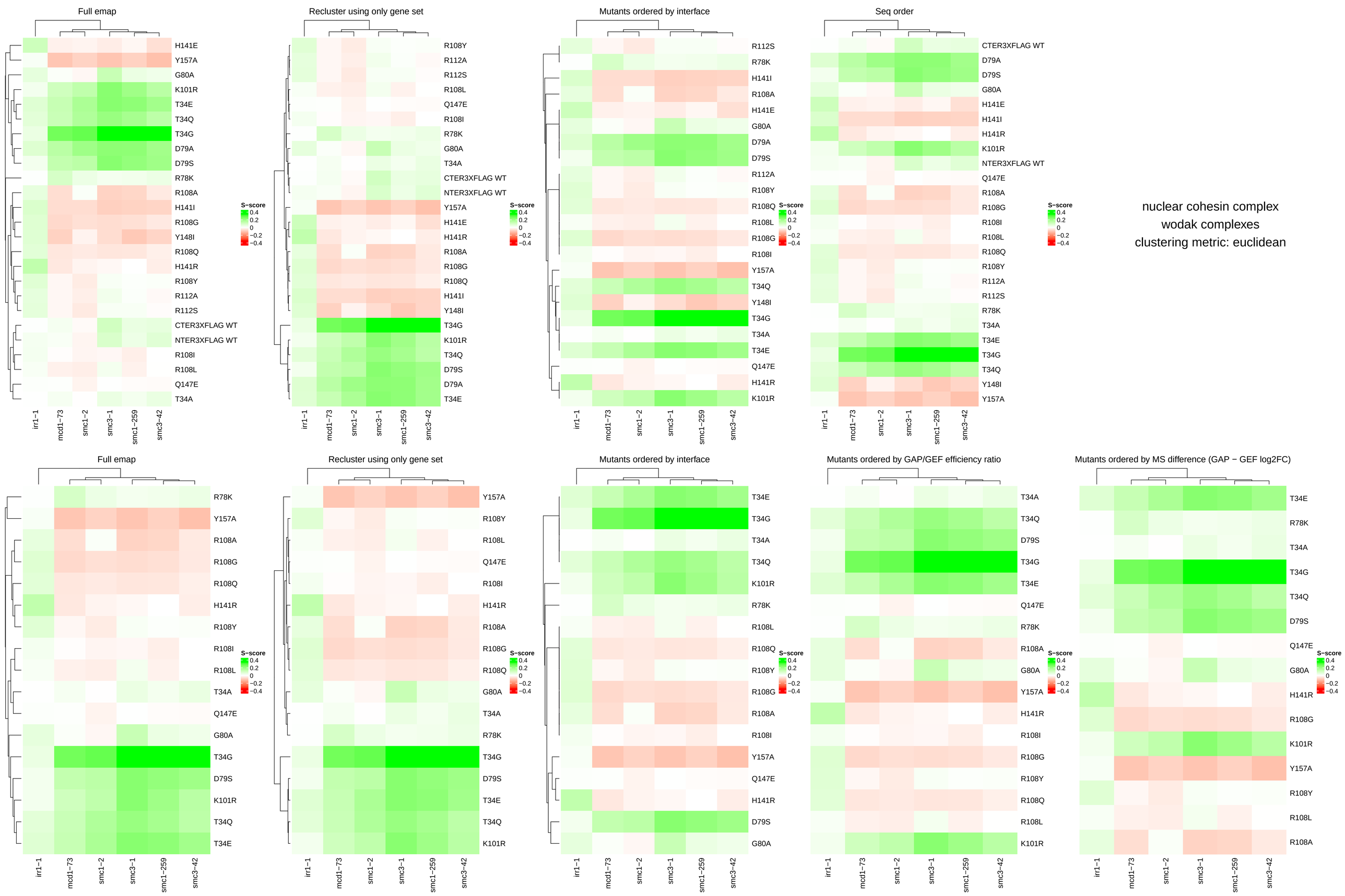


Ndc80p complex
wodak complexes
clustering metric: euclidean

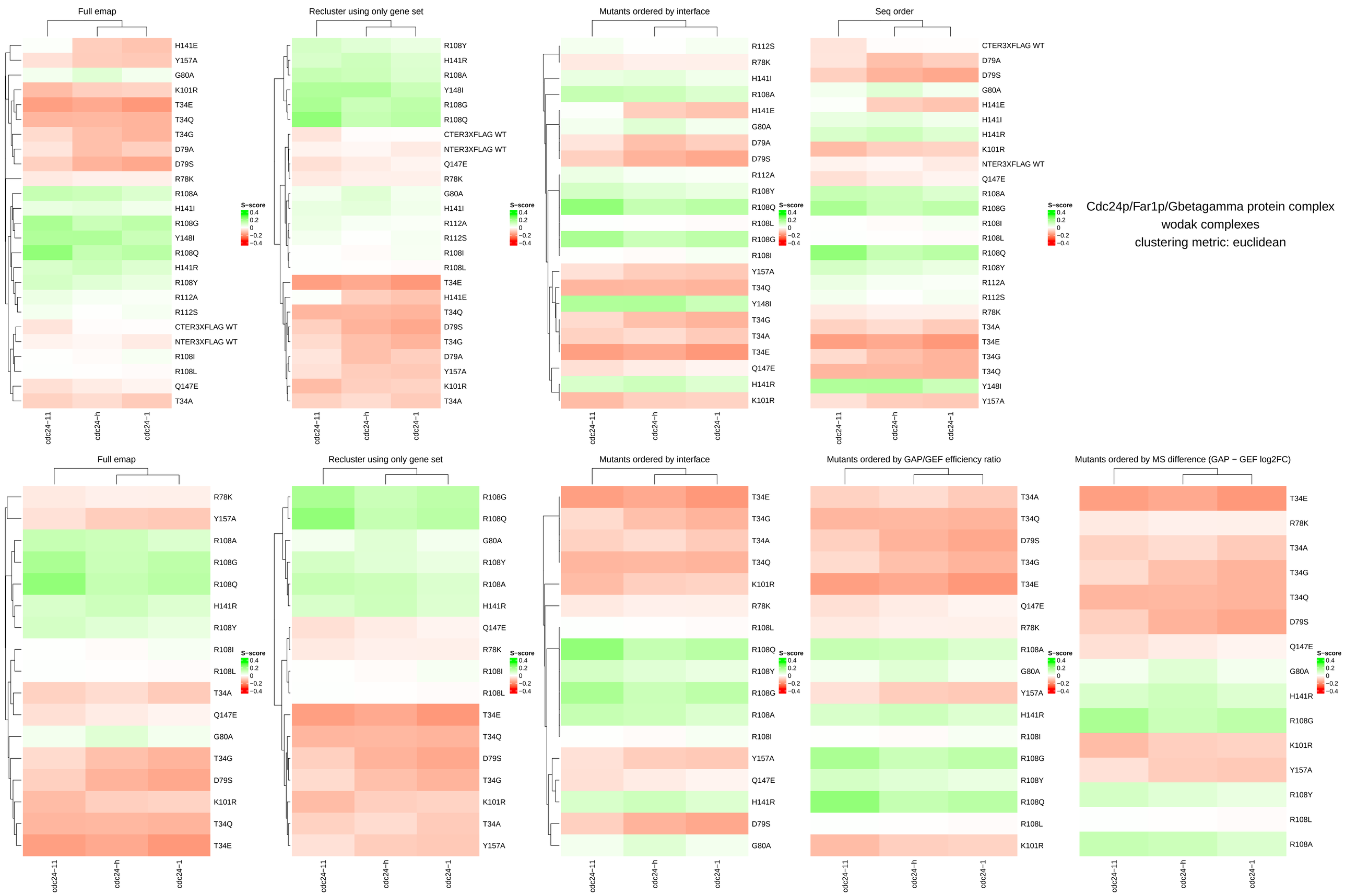


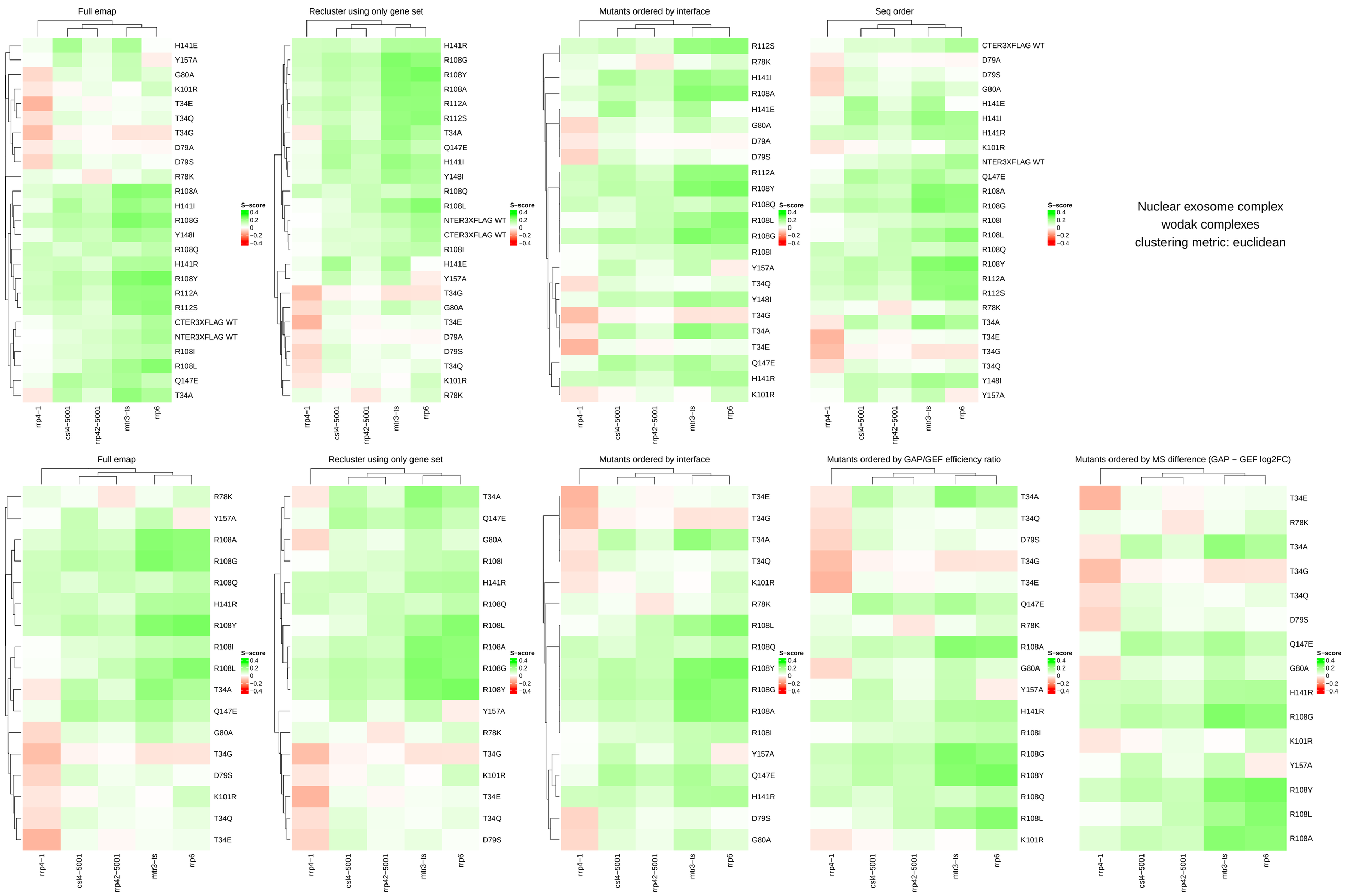
UTP A complex
wodak complexes
clustering metric: euclidean



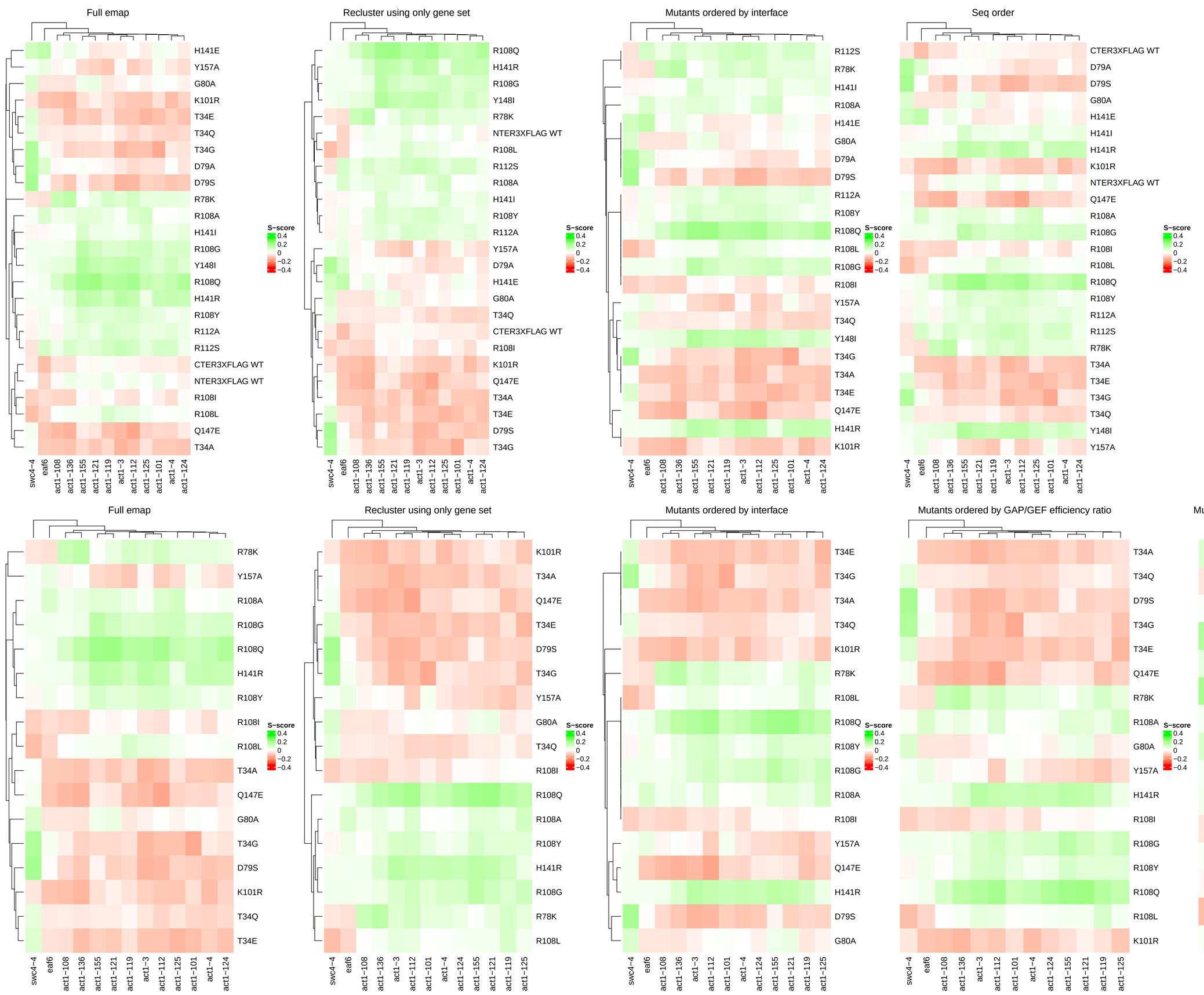


nuclear cohesin complex
wodak complexes
clustering metric: euclidean

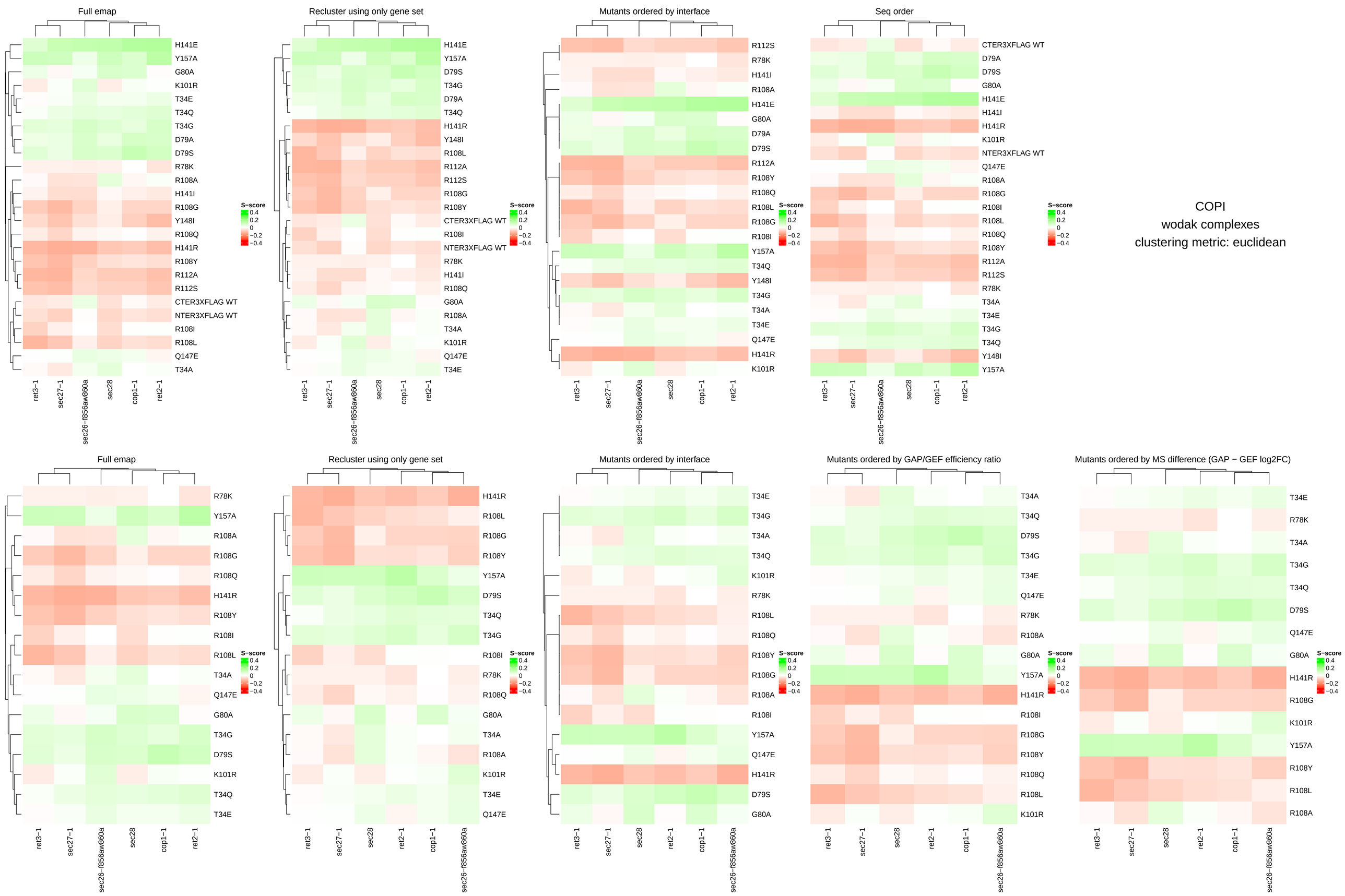

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
cdc24−11
cdc24−h
cdc24−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108Y
H141R
R108A
Y148I
R108G
R108Q
CTER3XFLAG WT
NTER3XFLAG WT
Q147E
R78K
G80A
H141I
R112A
R112S
R108I
R108L
T34E
H141E
T34Q
D79S
T34G
D79A
Y157A
K101R
T34A
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
R108G
R108Q
G80A
R108Y
R108A
H141R
Q147E
R78K
R108I
R108L
T34E
T34Q
D79S
T34G
K101R
T34A
Y157A
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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

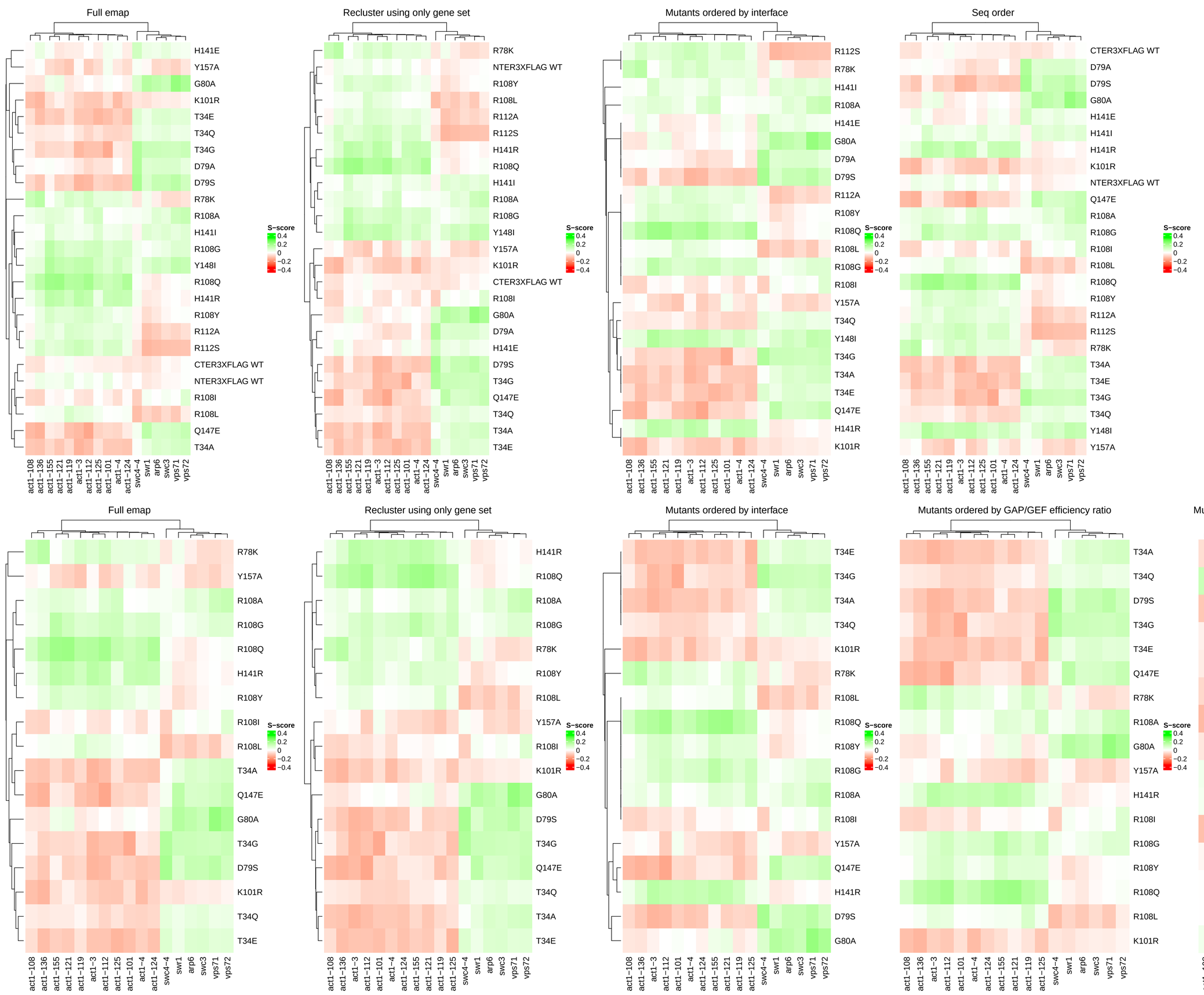


Nuclear exosome complex
wodak complexes
clustering metric: euclidean

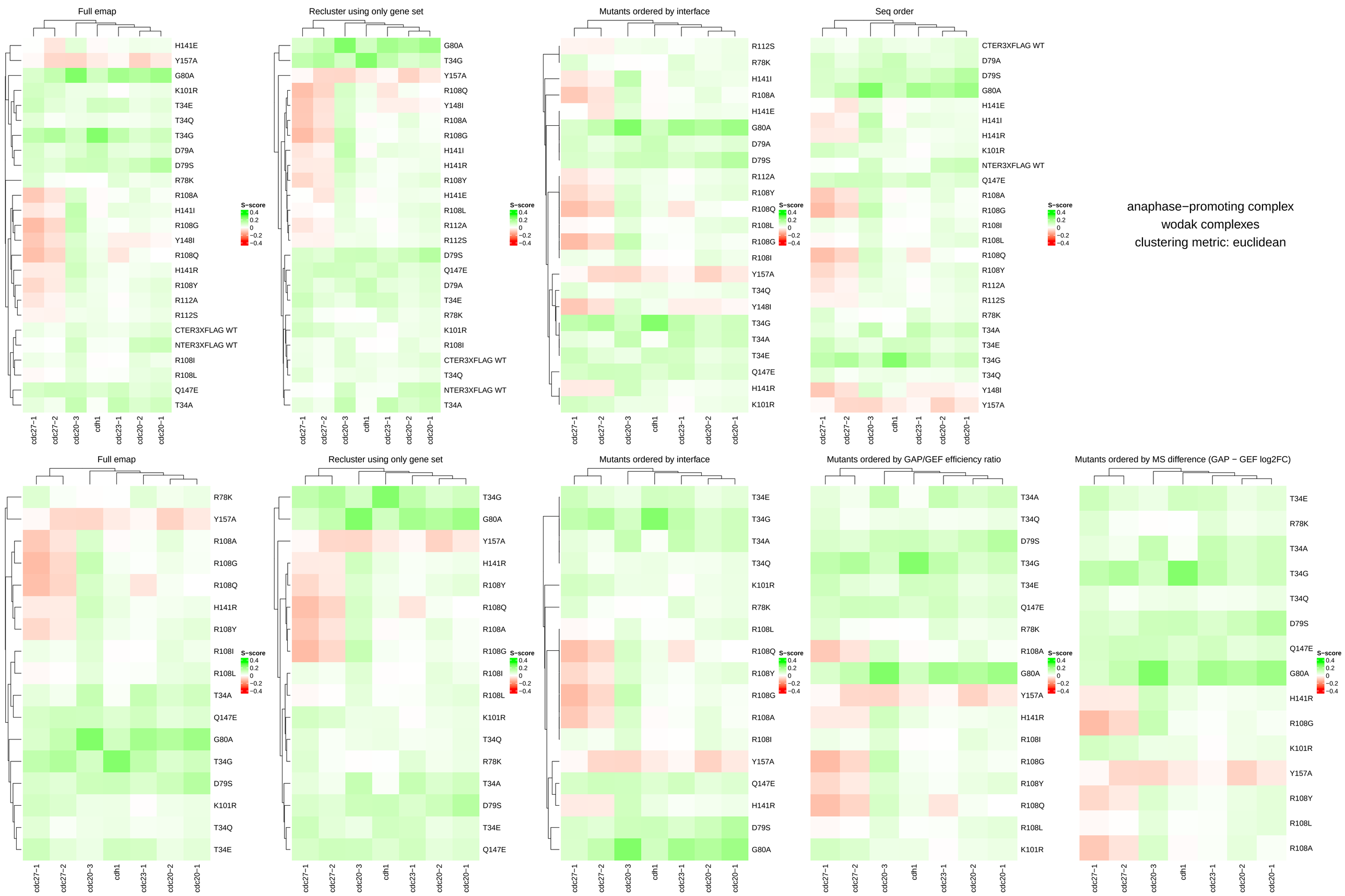


NuA4 histone acetyltransferase complex
wodak complexes
clustering metric: euclidean

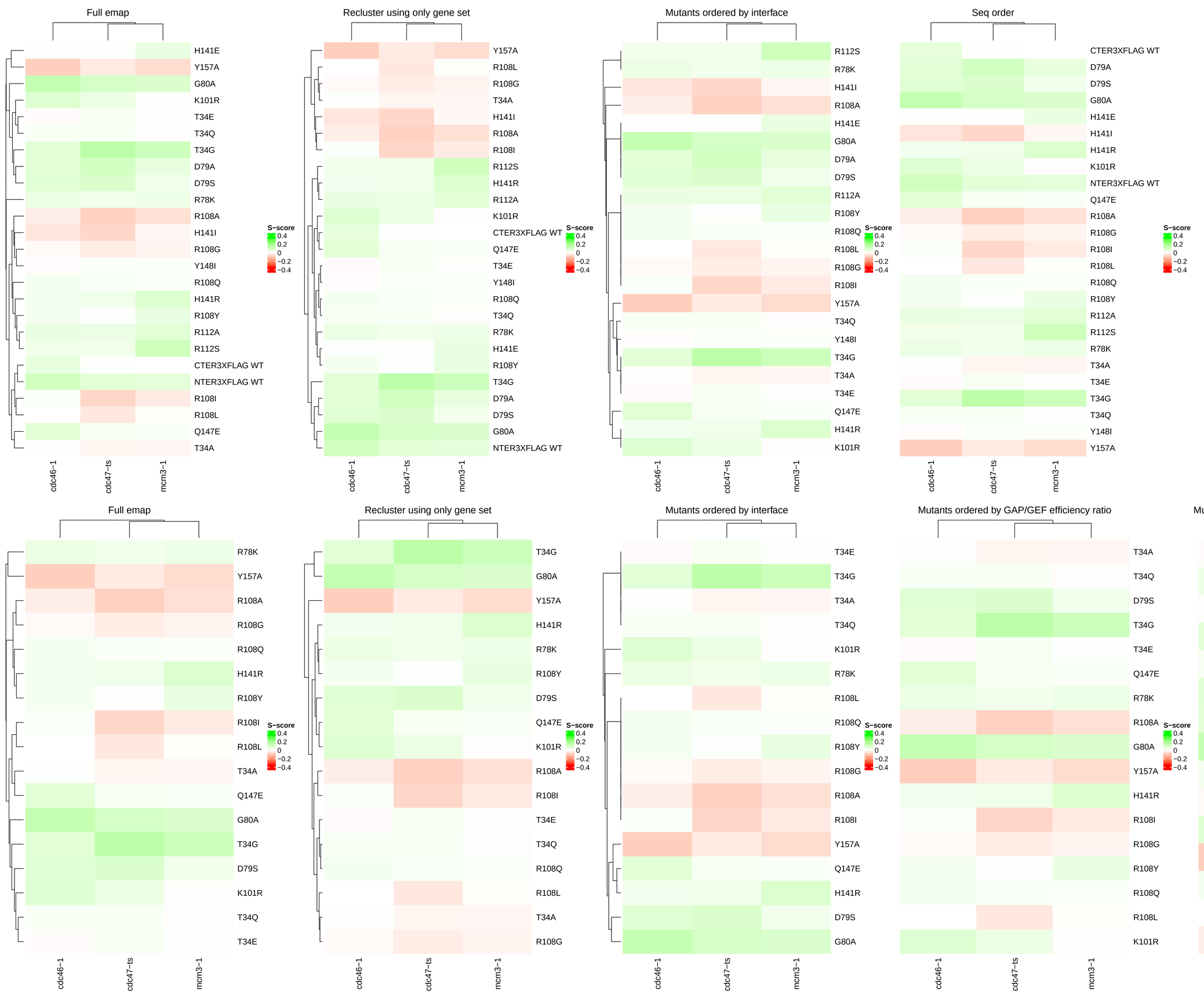

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
ret3−1
sec27−1
sec26−f856aw860a
sec28
cop1−1
ret2−1
S−score
0.4
0.2
0
−0.2
−0.4
COPI
wodak complexes
clustering metric: euclidean
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

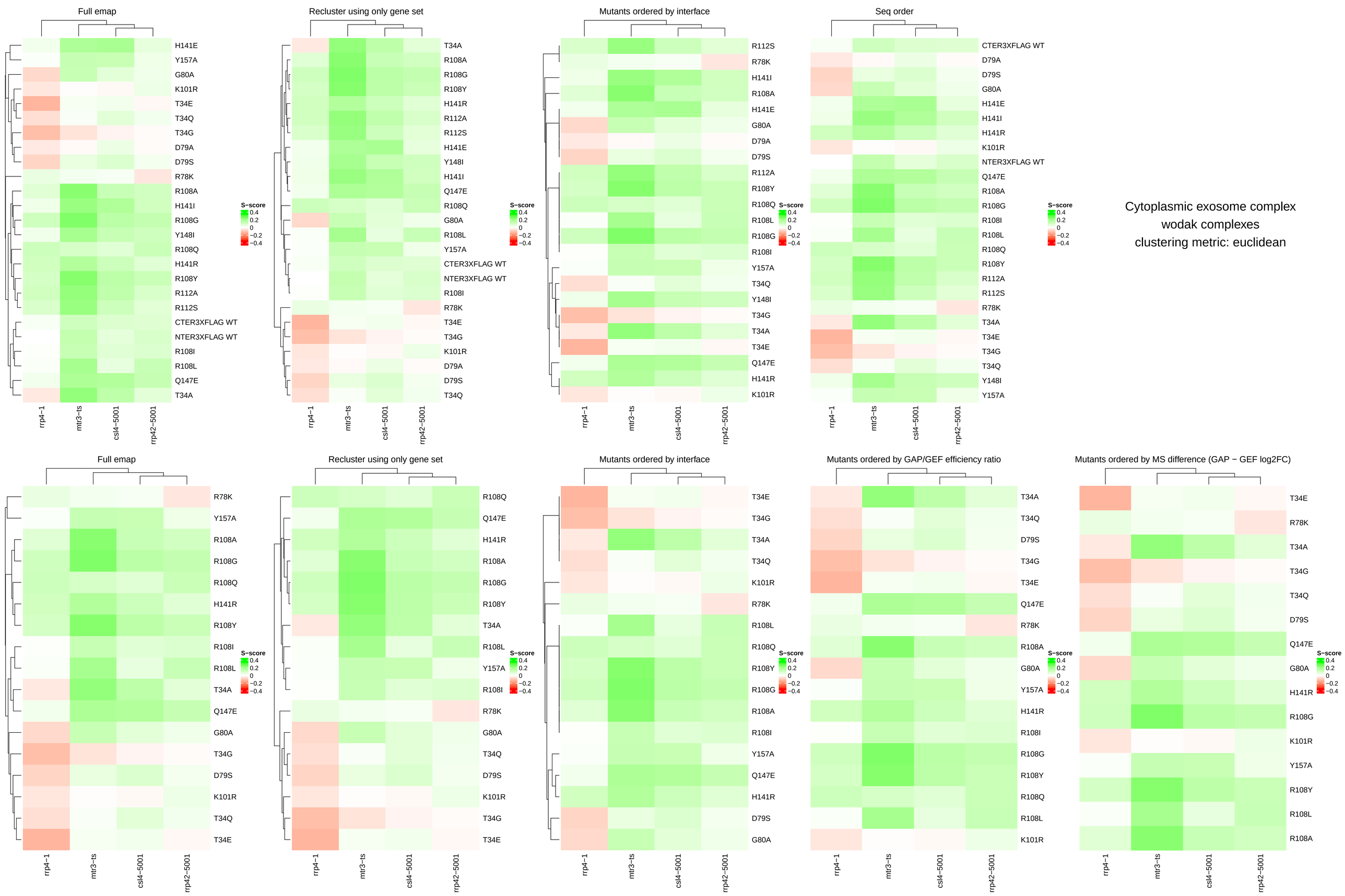


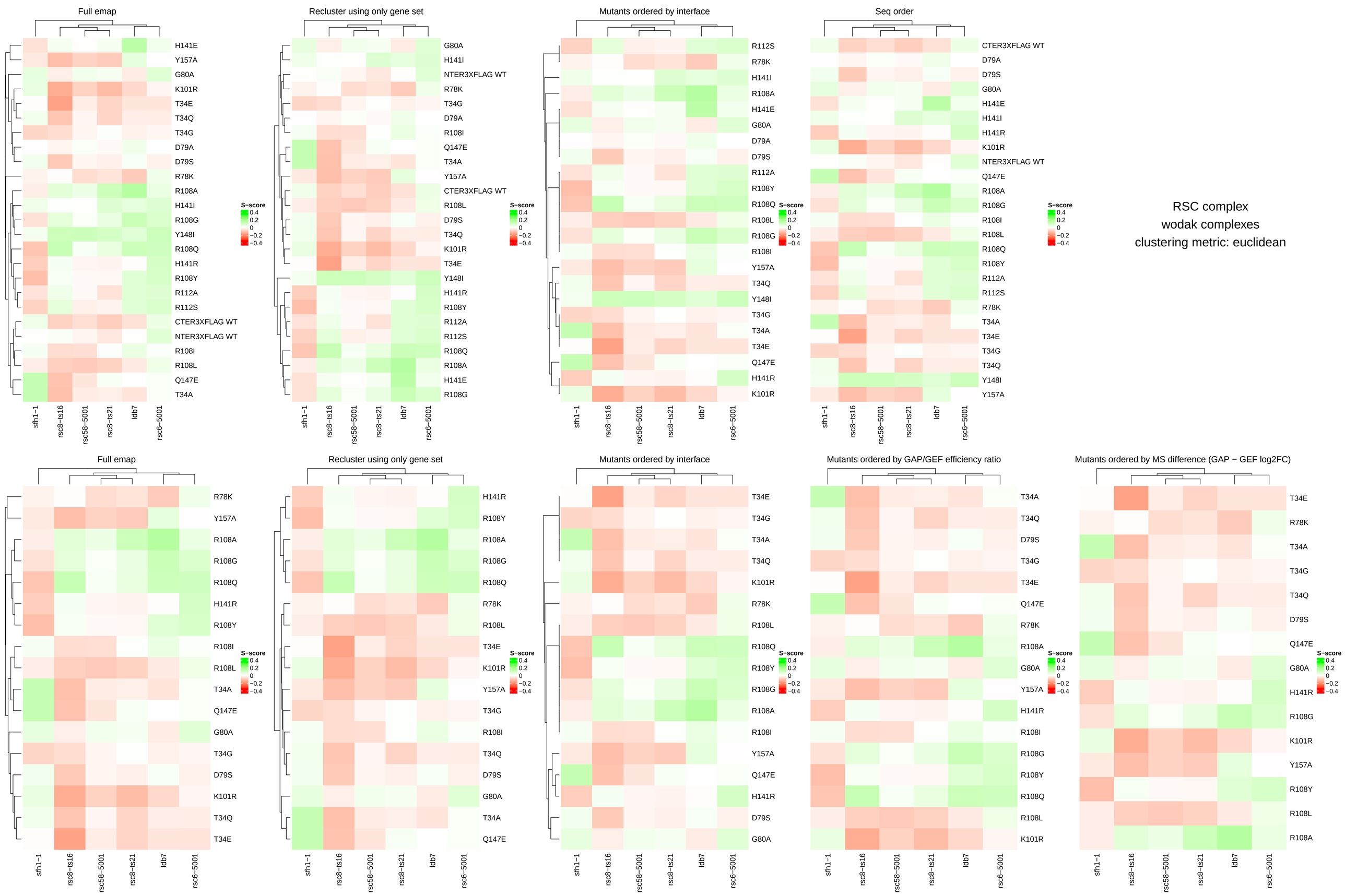
Swr1p complex
wodak complexes
clustering metric: euclidean

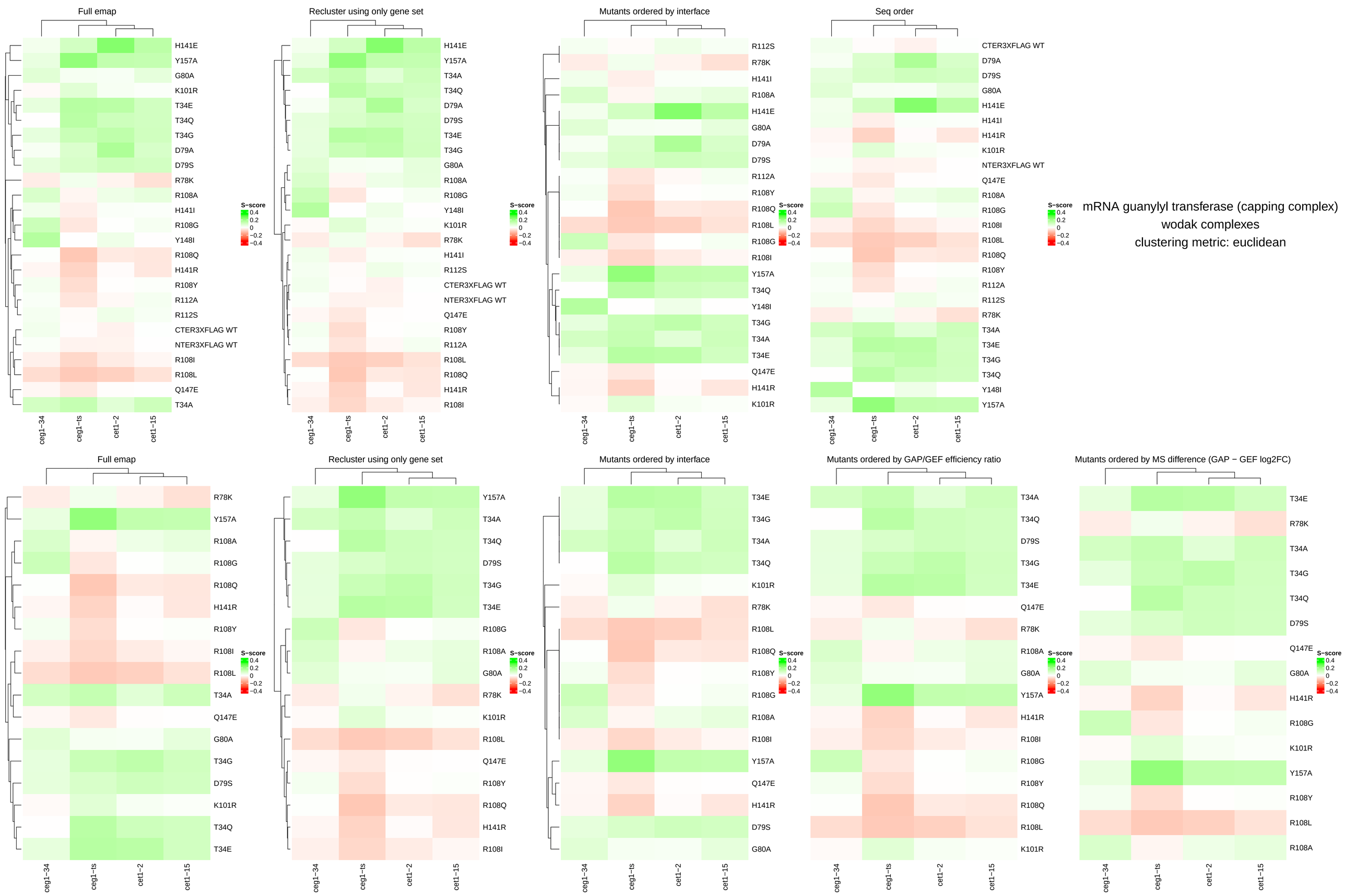


anaphase−promoting complex
wodak complexes
clustering metric: euclidean

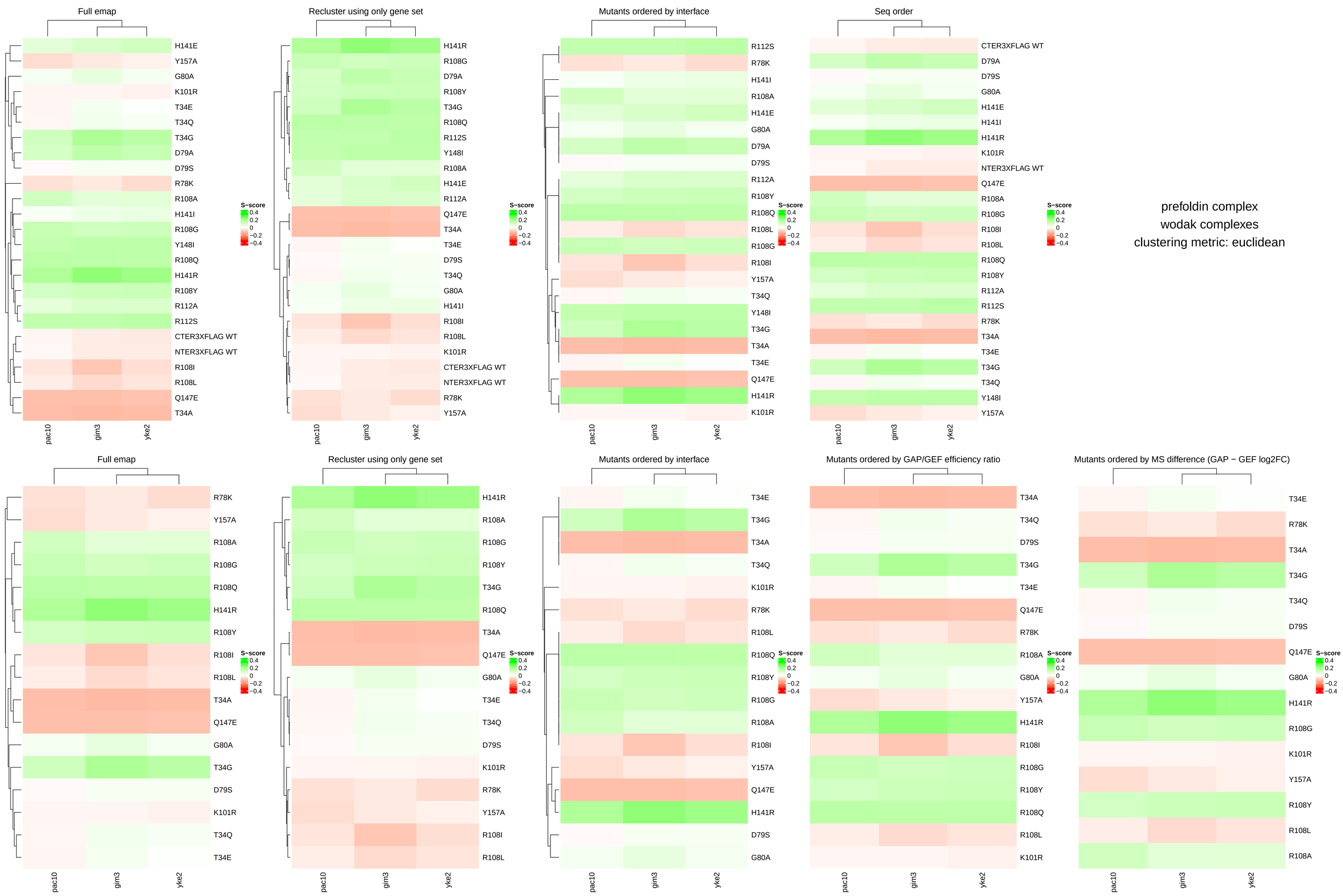

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
cdc46−1
cdc47−ts
mcm3−1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
Y157A
R108L
R108G
T34A
H141I
R108A
R108I
R112S
H141R
R112A
K101R
CTER3XFLAG WT
Q147E
T34E
Y148I
R108Q
T34Q
R78K
H141E
R108Y
T34G
D79A
D79S
G80A
NTER3XFLAG WT
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
T34G
G80A
Y157A
H141R
R78K
R108Y
D79S
Q147E
K101R
R108A
R108I
T34E
T34Q
R108Q
R108L
T34A
R108G
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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
cdc46−1
cdc47−ts
mcm3−1

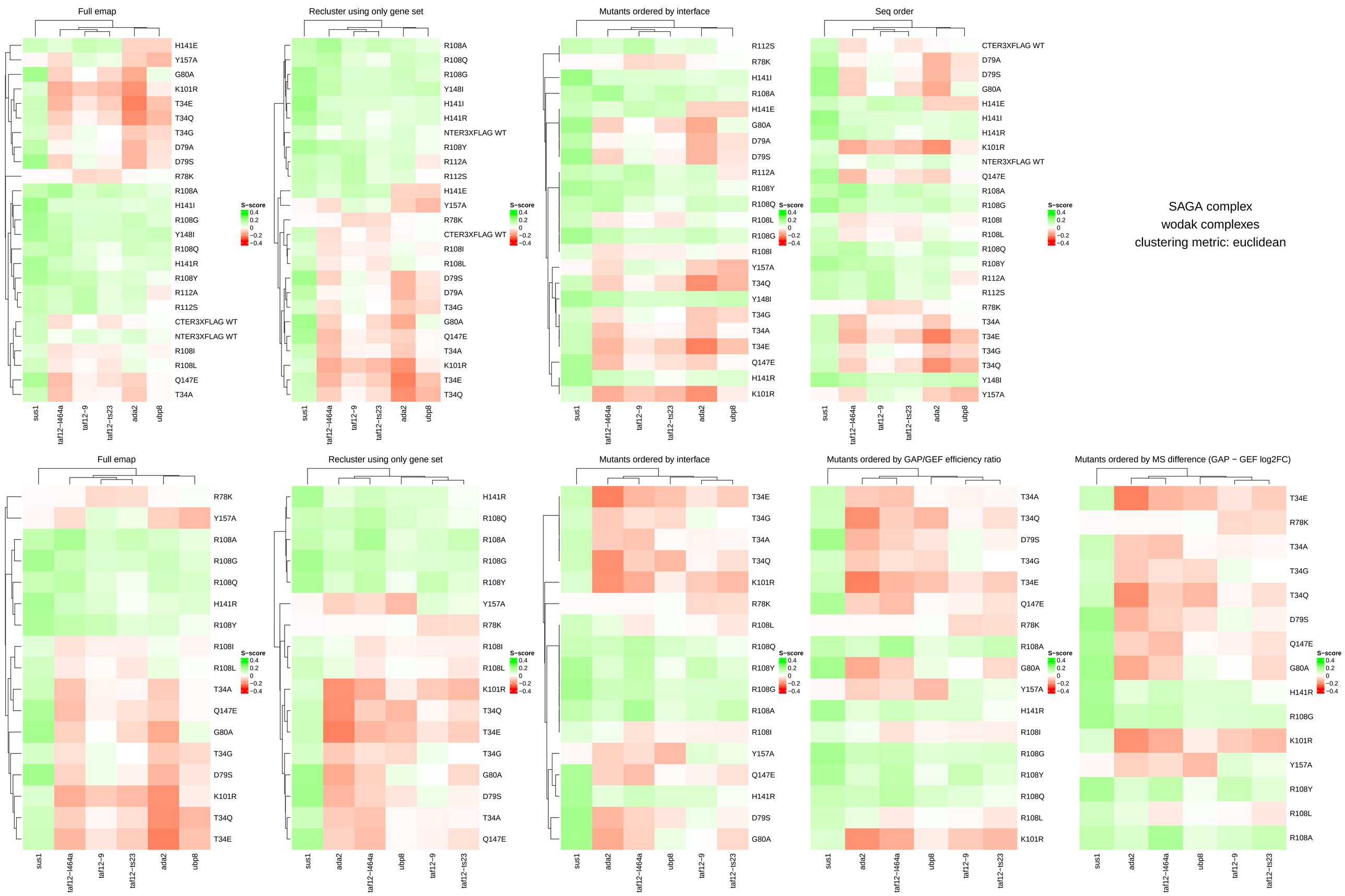

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
0.4
0.2
0
−0.2
−0.4
rrp4−1
mtr3−ts
csl4−5001
rrp42−5001
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
Cytoplasmic exosome complex
wodak complexes
clustering metric: euclidean


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
rsc8−ts16
rsc58−5001
rsc8−ts21
ldb7
rsc6−5001
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
R108G
RSC complex
wodak complexes
clustering metric: euclidean

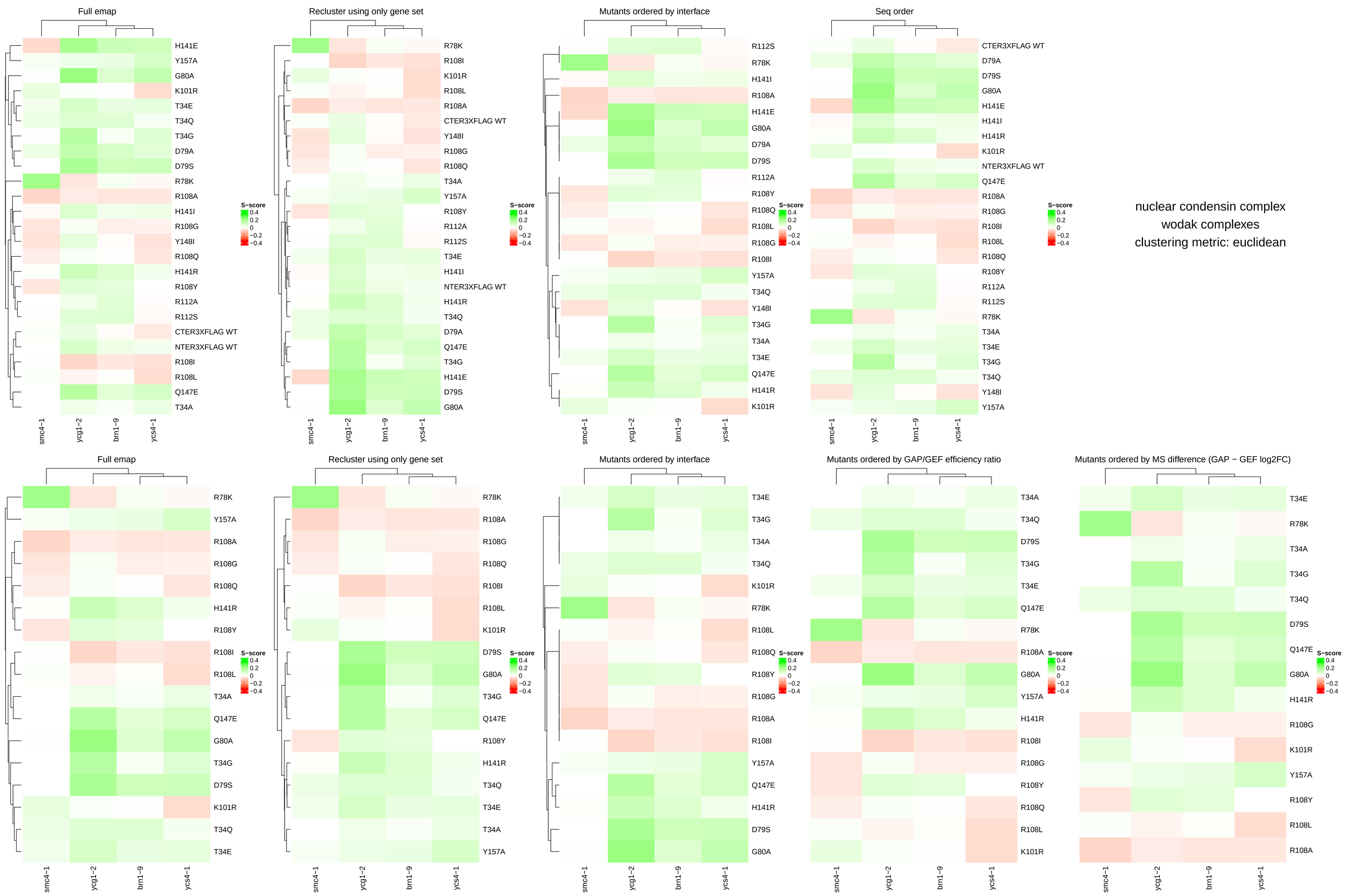


mRNA guanylyl transferase (capping complex)
wodak complexes
clustering metric: euclidean

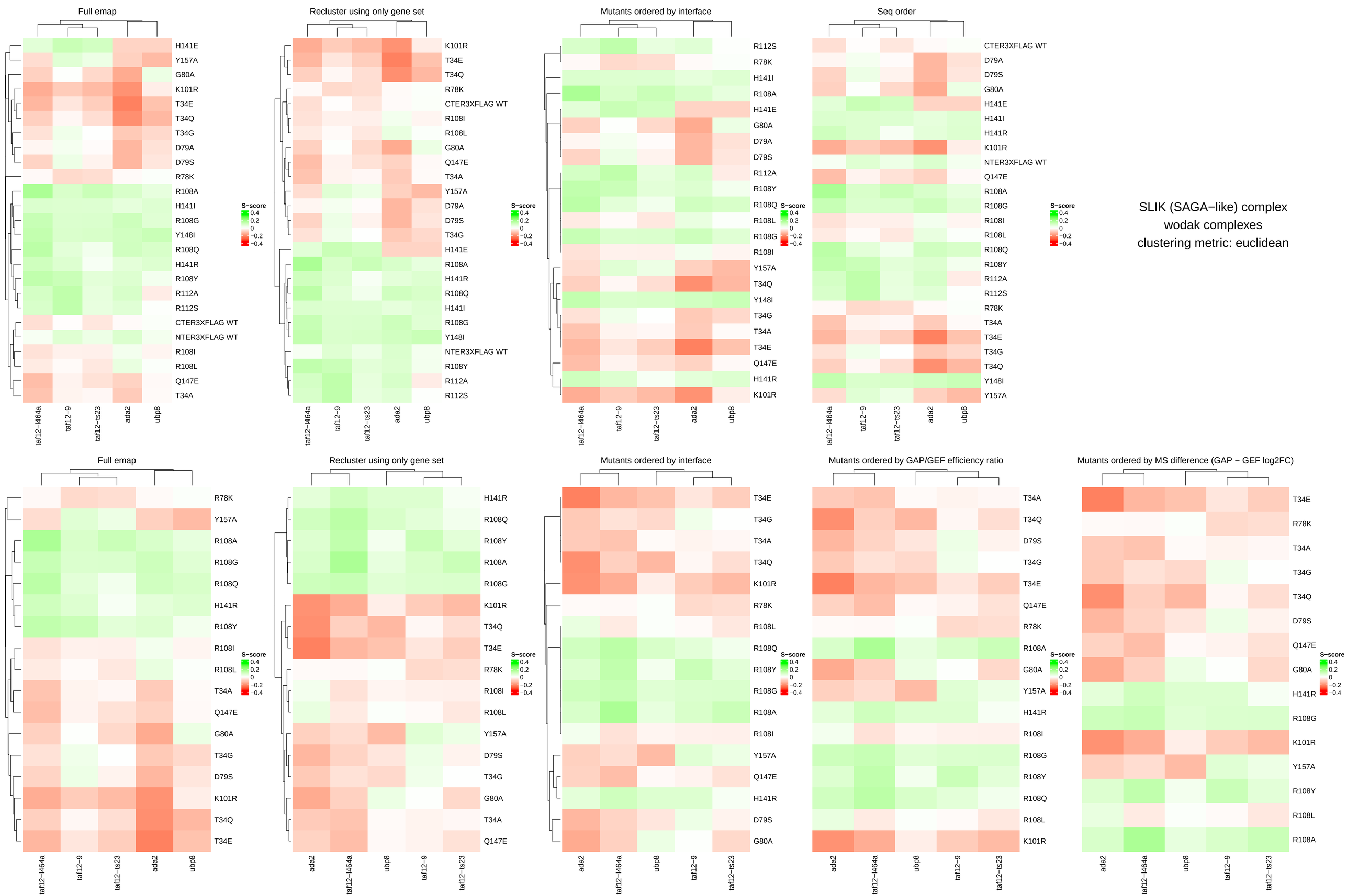

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
pac10
gim3
yke2
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
H141R
R108G
D79A
R108Y
T34G
R108Q
R112S
Y148I
R108A
H141E
R112A
Q147E
T34A
T34E
D79S
T34Q
G80A
H141I
R108I
R108L
K101R
CTER3XFLAG WT
NTER3XFLAG WT
R78K
Y157A
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
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

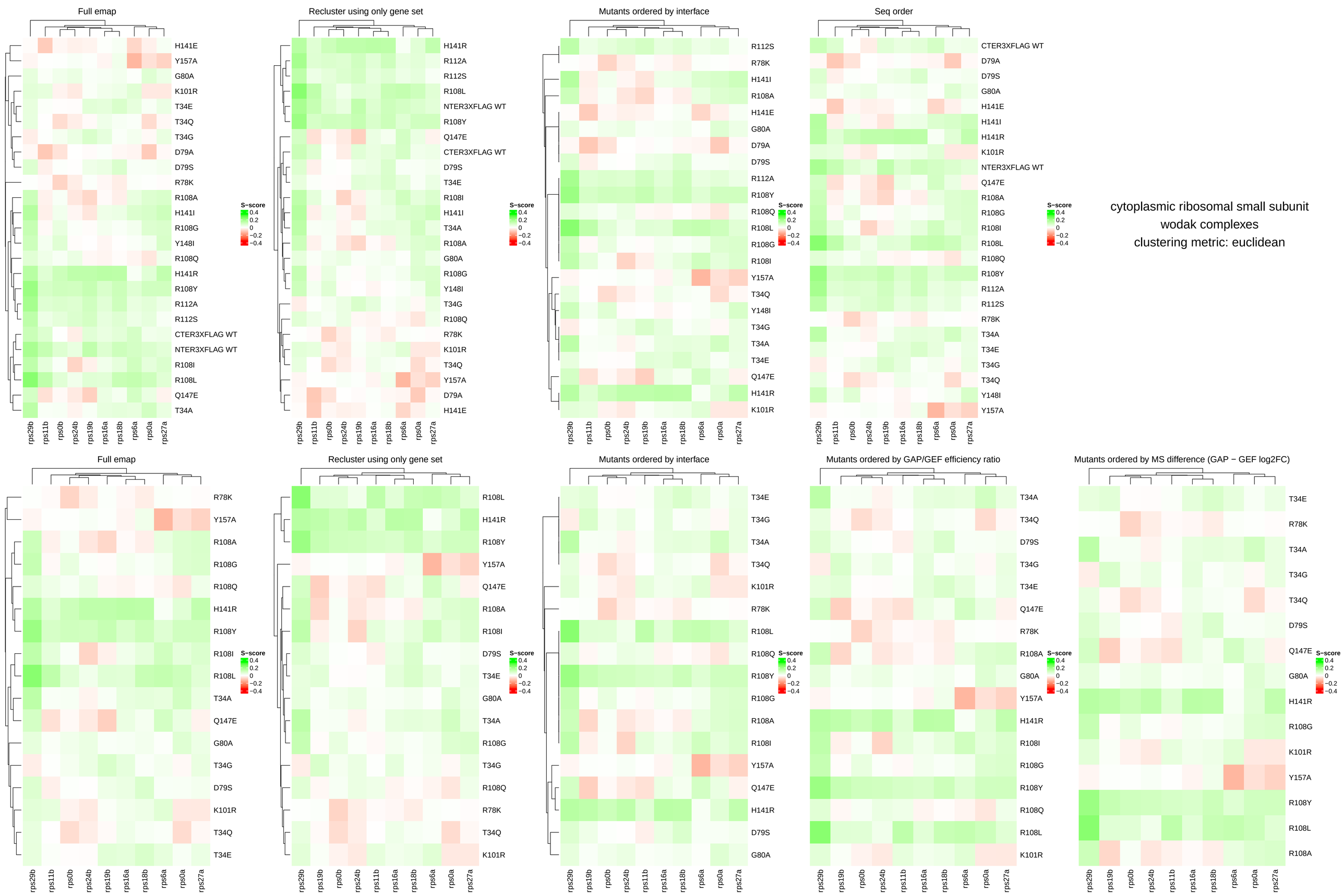


SAGA complex
wodak complexes
clustering metric: euclidean

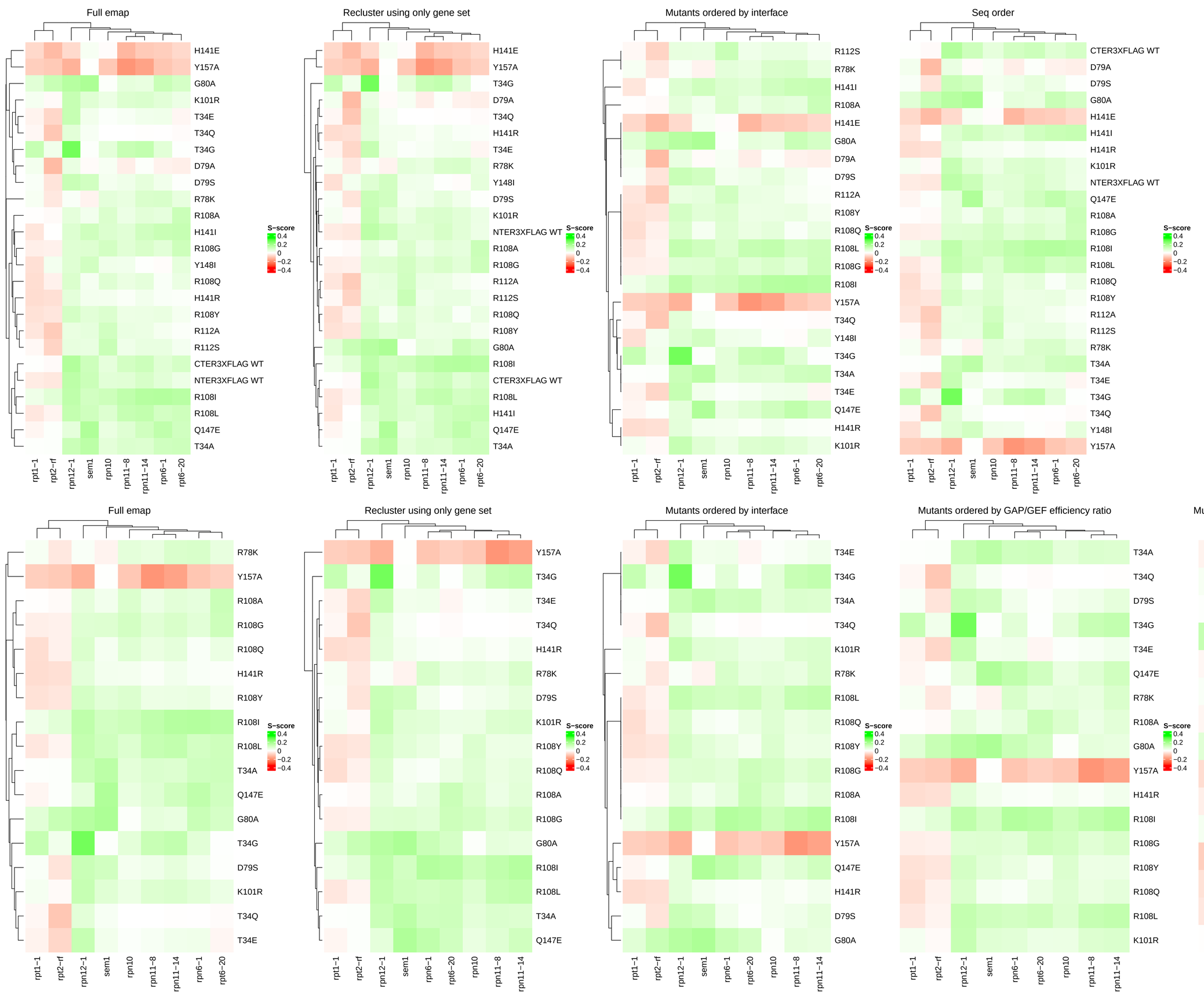


nuclear condensin complex
wodak complexes
clustering metric: euclidean


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
taf12−l464a
taf12−9
taf12−ts23
ada2
ubp8
SLIK (SAGA−like) complex
wodak complexes
clustering metric: euclidean

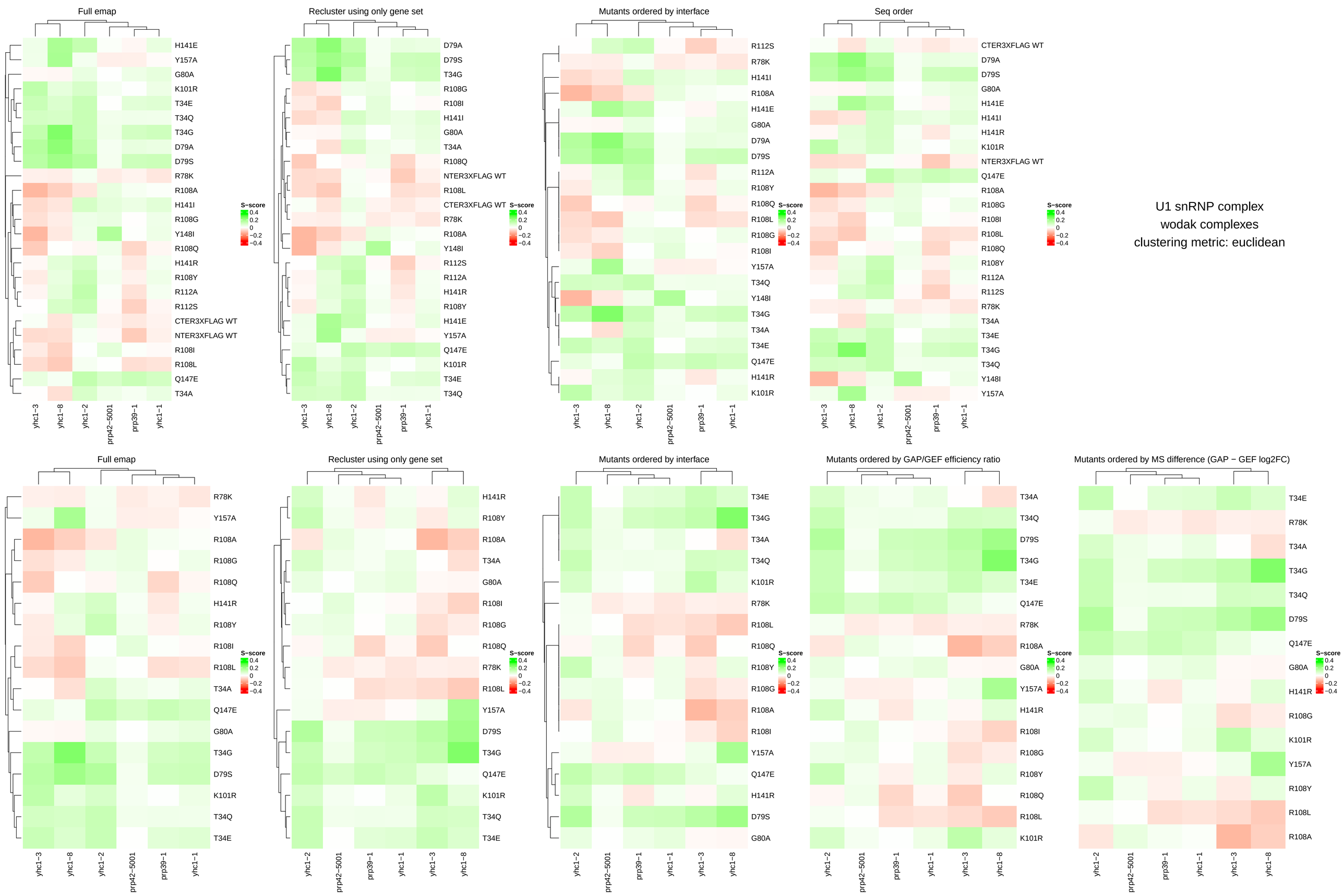


cytoplasmic ribosomal small subunit
wodak complexes
clustering metric: euclidean

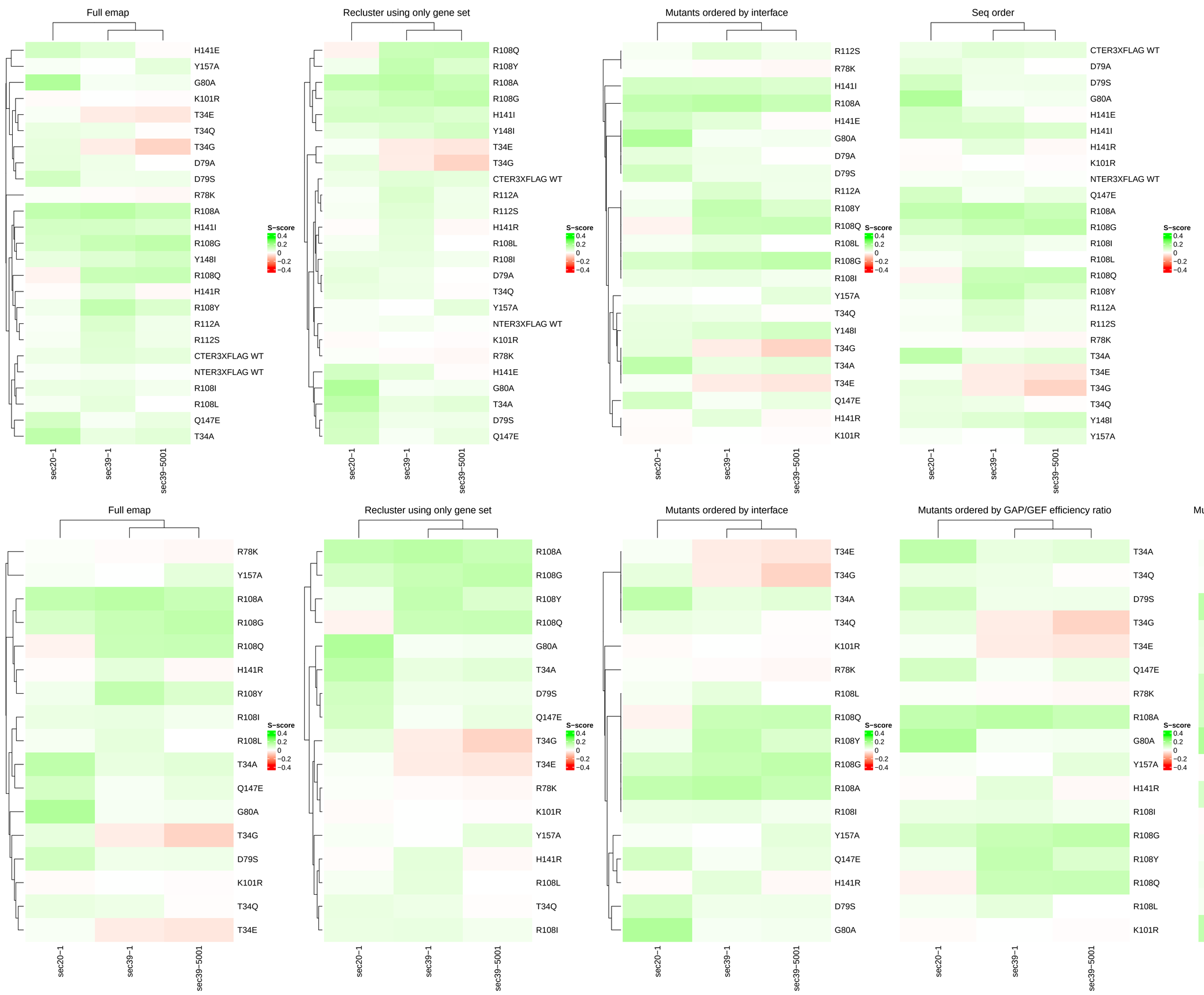


19/22S regulator
wodak complexes
clustering metric: euclidean

Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
hhf1
rrn9−5007
hht1
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
Y157A
H141E
G80A
Q147E
R108Y
R108G
R112A
H141R
R112S
R108A
R78K
Y148I
H141I
R108Q
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
K101R
T34A
T34Q
T34E
T34G
D79A
D79S
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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
RNA polymerase I upstream activating factor compl
wodak complexes
clustering metric: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
Y157A
R108I
R108L
R78K
R108A
T34A
T34Q
R108G
R108Q
Q147E
G80A
H141R
R108Y
T34G
T34E
D79S
K101R
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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
hhf1
rrn9−5007
hht1


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
yhc1−3
yhc1−8
yhc1−2
prp42−5001
prp39−1
yhc1−1
U1 snRNP complex
wodak complexes
clustering metric: euclidean

CBF3 complex
wodak complexes
clustering metric: euclidean


Full emap
H141E
Y157A
G80A
K101R
T34E
T34Q
T34G
D79A
D79S
R78K
R108A
H141I
R108G
Y148I
R108Q
H141R
R108Y
R112A
R112S
CTER3XFLAG WT
NTER3XFLAG WT
R108I
R108L
Q147E
T34A
sec20−1
sec39−1
sec39−5001
S−score
0.4
0.2
0
−0.2
−0.4
Recluster using only gene set
R108Q
R108Y
R108A
R108G
H141I
Y148I
T34E
T34G
CTER3XFLAG WT
R112A
R112S
H141R
R108L
R108I
D79A
T34Q
Y157A
NTER3XFLAG WT
K101R
R78K
H141E
G80A
T34A
D79S
Q147E
Mutants ordered by interface
R112S
R78K
H141I
R108A
H141E
G80A
D79A
D79S
R112A
R108Y
R108Q
R108L
R108G
R108I
Y157A
T34Q
Y148I
T34G
T34A
T34E
Q147E
H141R
K101R
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: euclidean
Full emap
R78K
Y157A
R108A
R108G
R108Q
H141R
R108Y
R108I
R108L
T34A
Q147E
G80A
T34G
D79S
K101R
T34Q
T34E
Recluster using only gene set
R108A
R108G
R108Y
R108Q
G80A
T34A
D79S
Q147E
T34G
T34E
R78K
K101R
Y157A
H141R
R108L
T34Q
R108I
Mutants ordered by interface
T34E
T34G
T34A
T34Q
K101R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
Y157A
Q147E
H141R
D79S
G80A
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