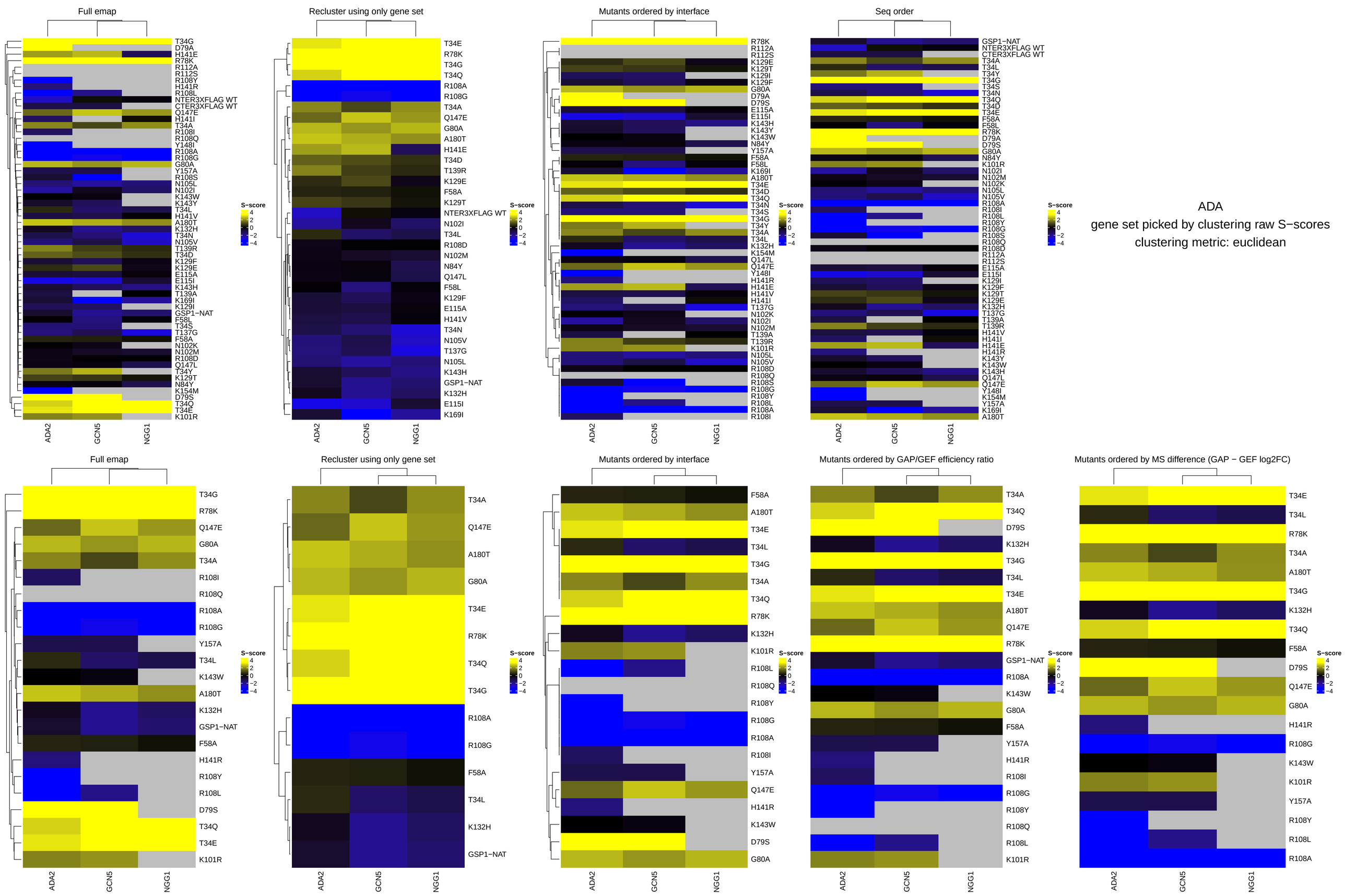
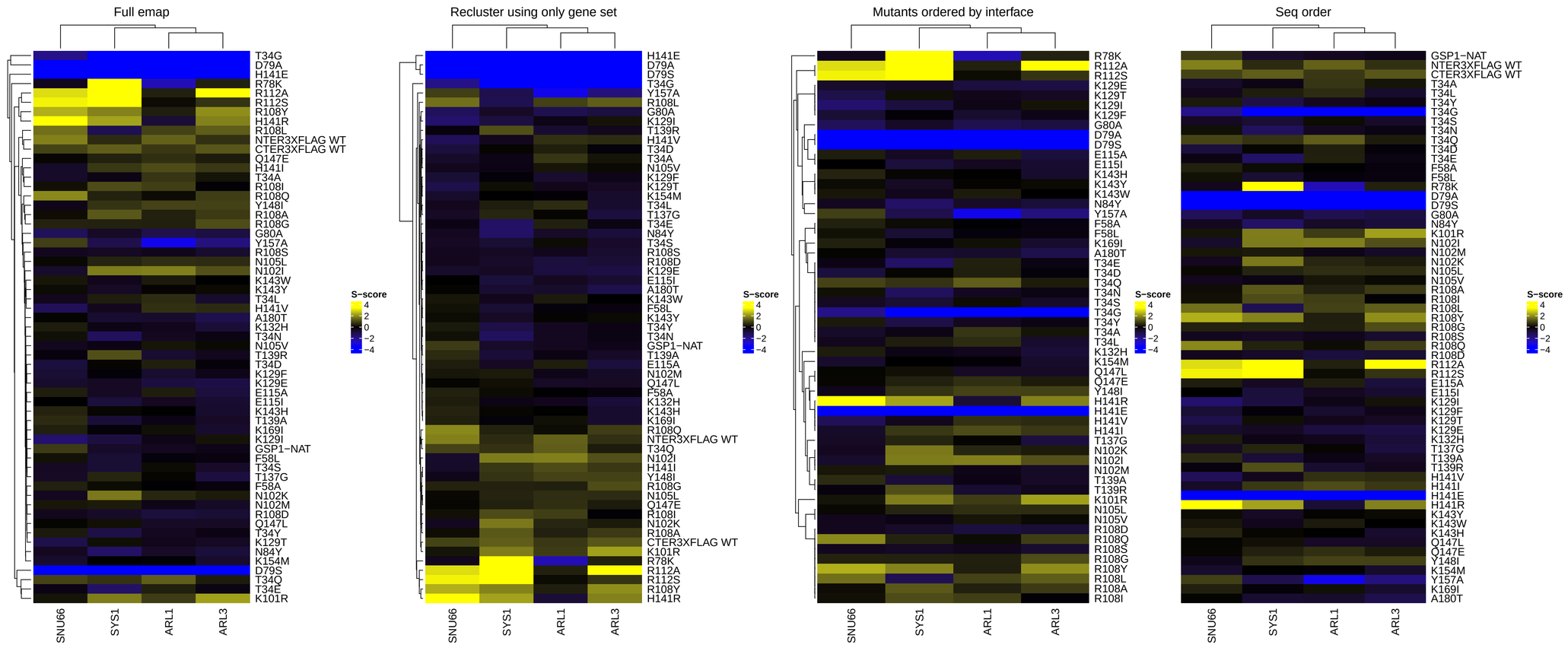


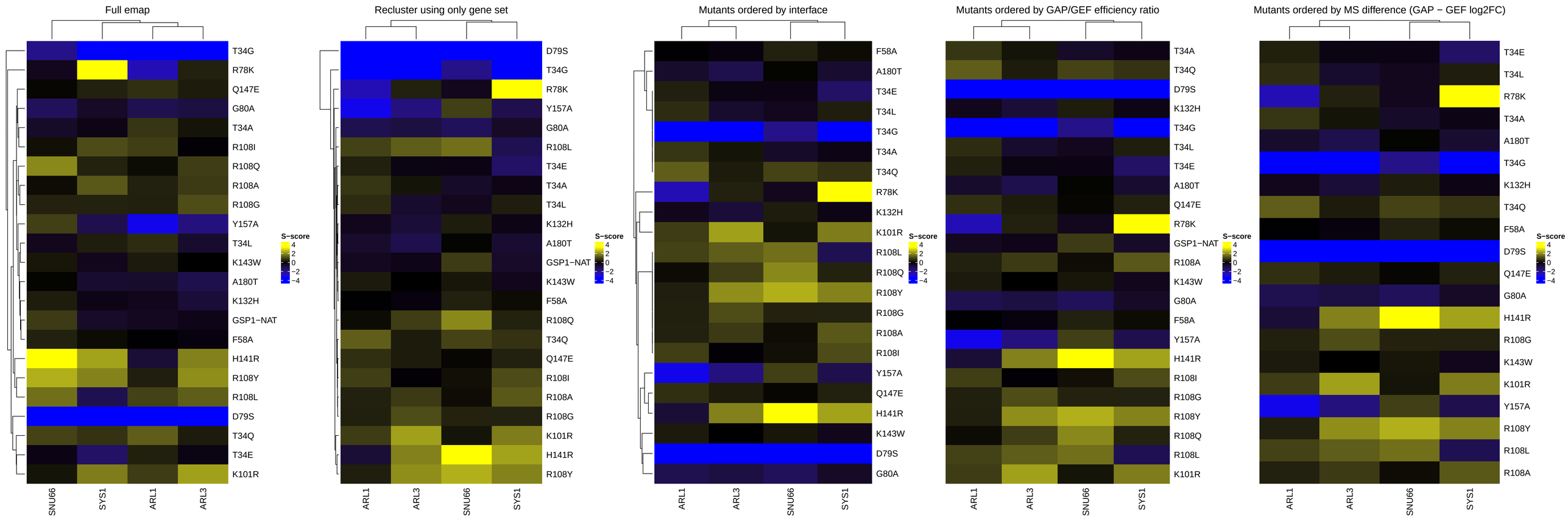
ADA

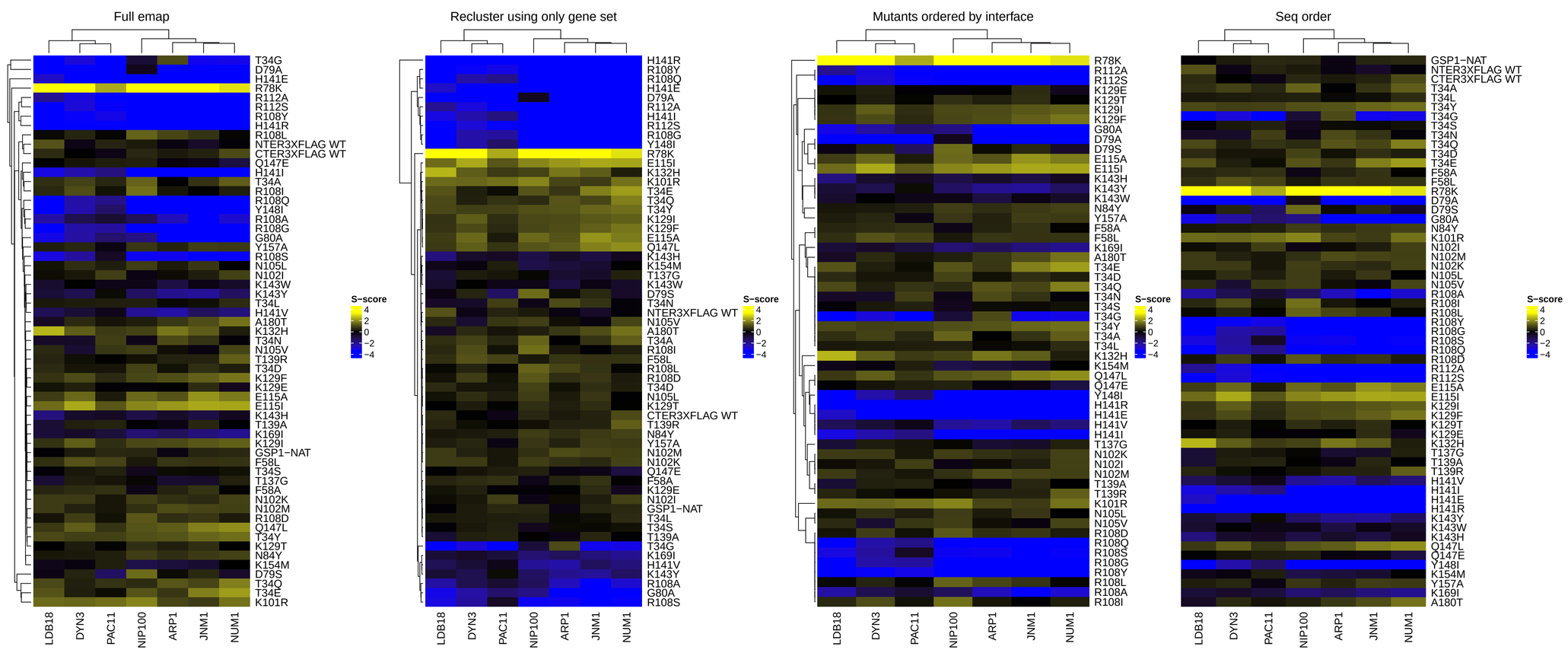
gene set picked by clustering raw S−scores

clustering metric: euclidean



Arl GTPases
gene set picked by clustering raw S−scores
clustering metric: euclidean

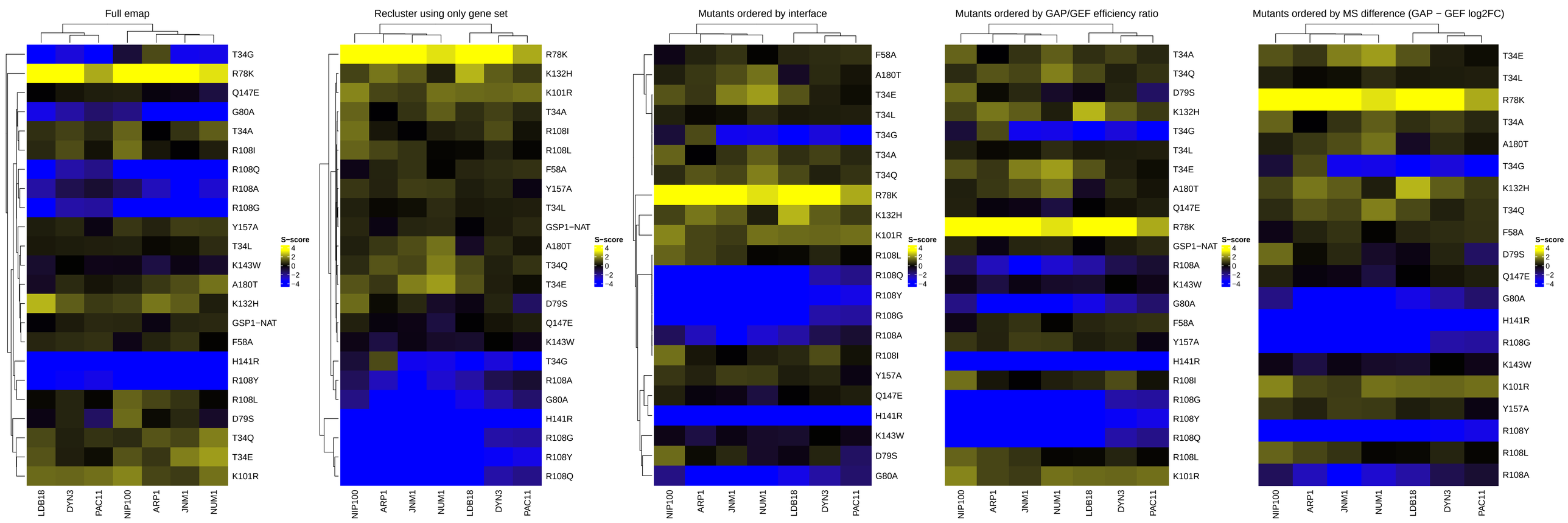


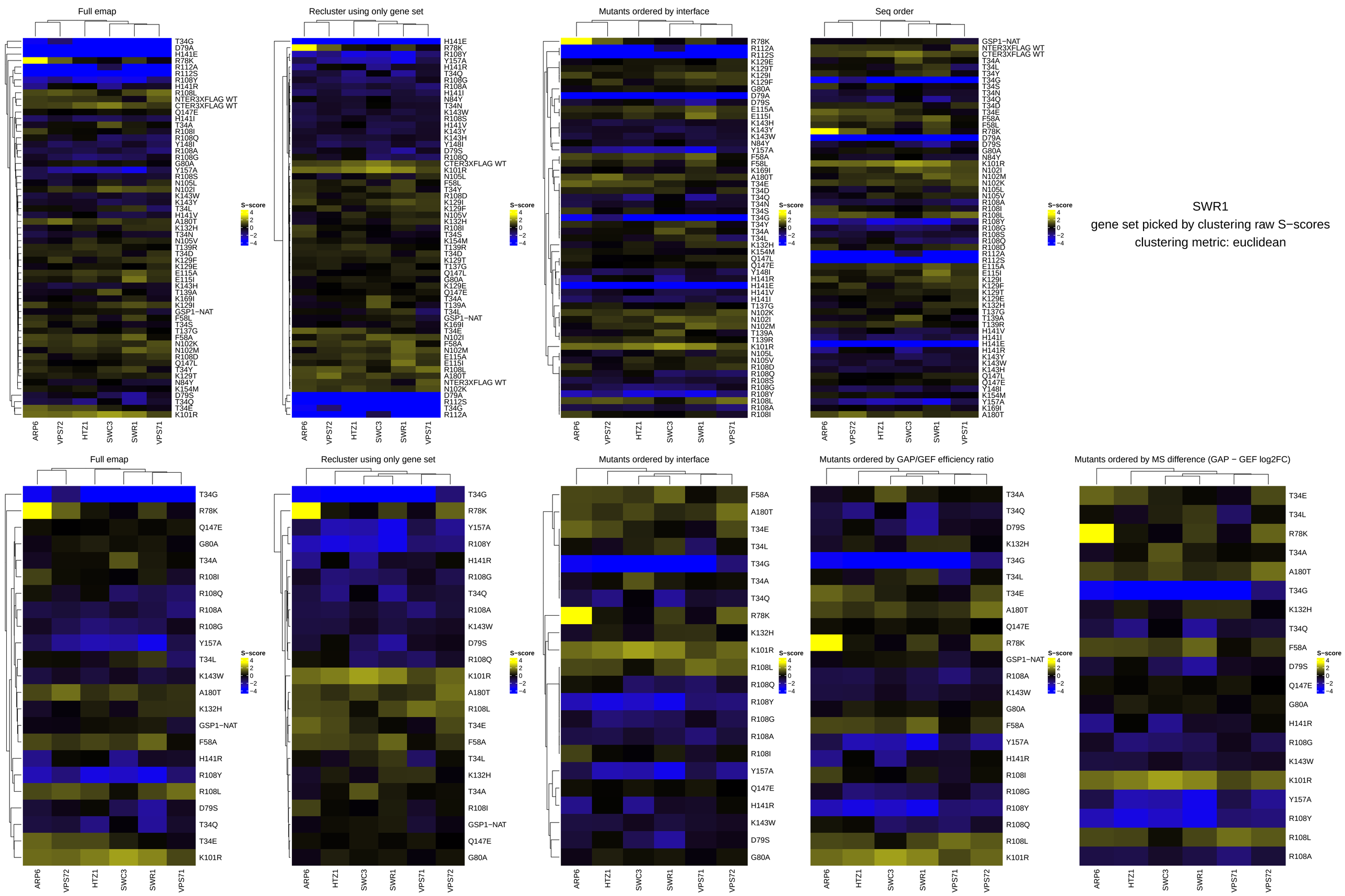


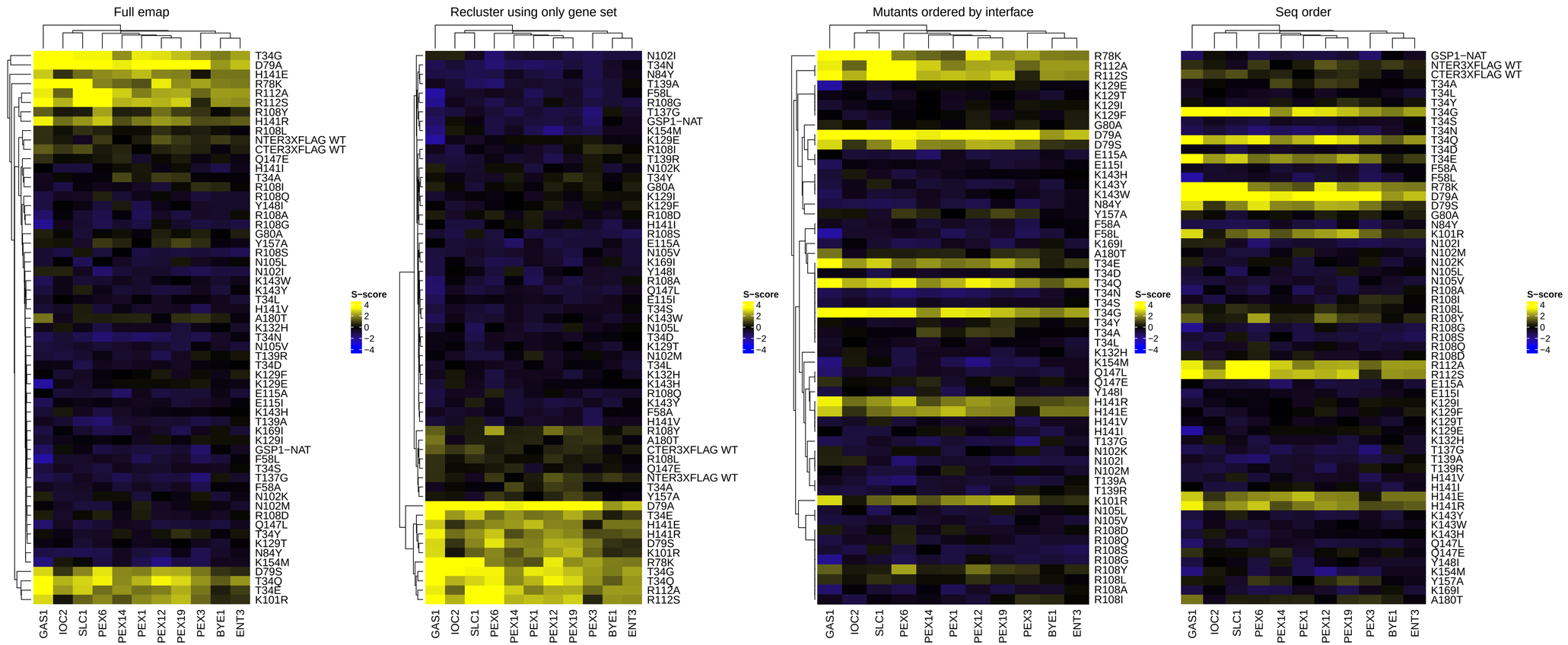
Dynactin

gene set picked by clustering raw S−scores

clustering metric: euclidean



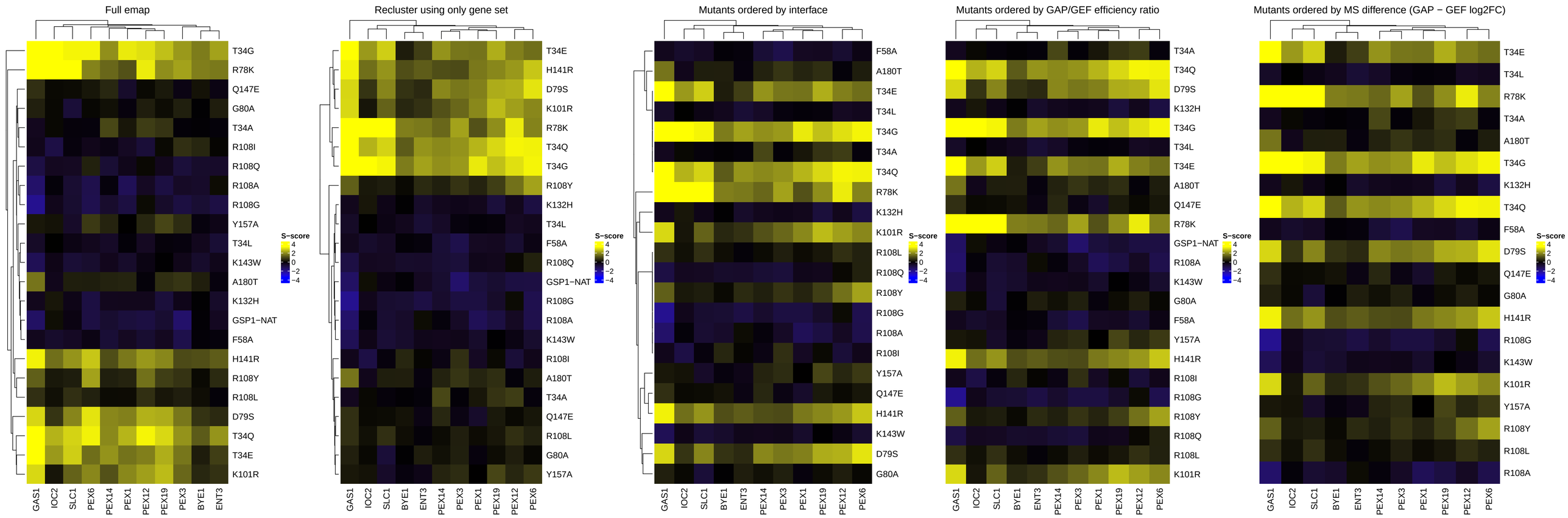

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
ARP6
VPS72
HTZ1
SWC3
SWR1
VPS71
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
SWR1
gene set picked by clustering raw S−scores
clustering metric: euclidean

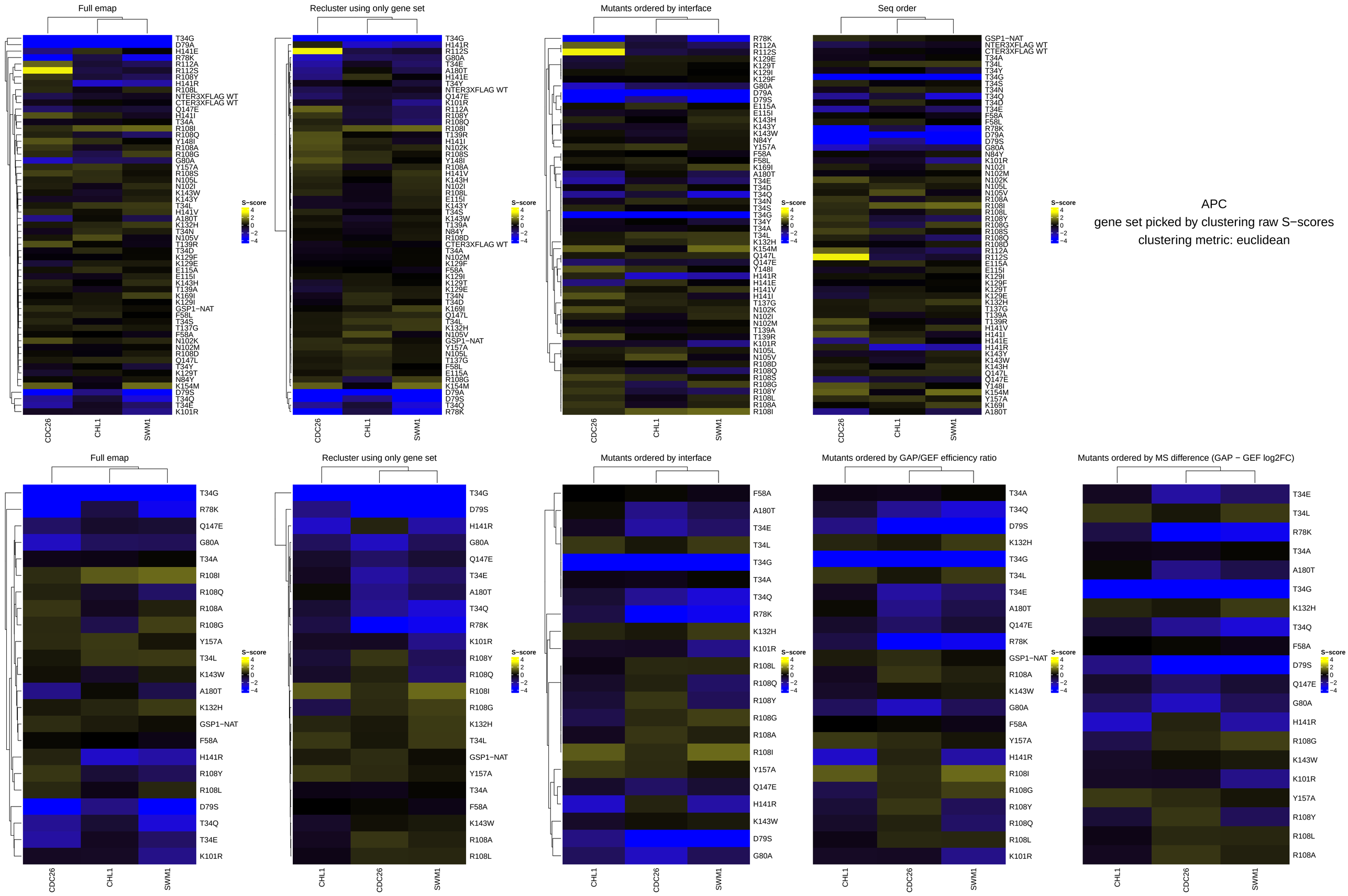


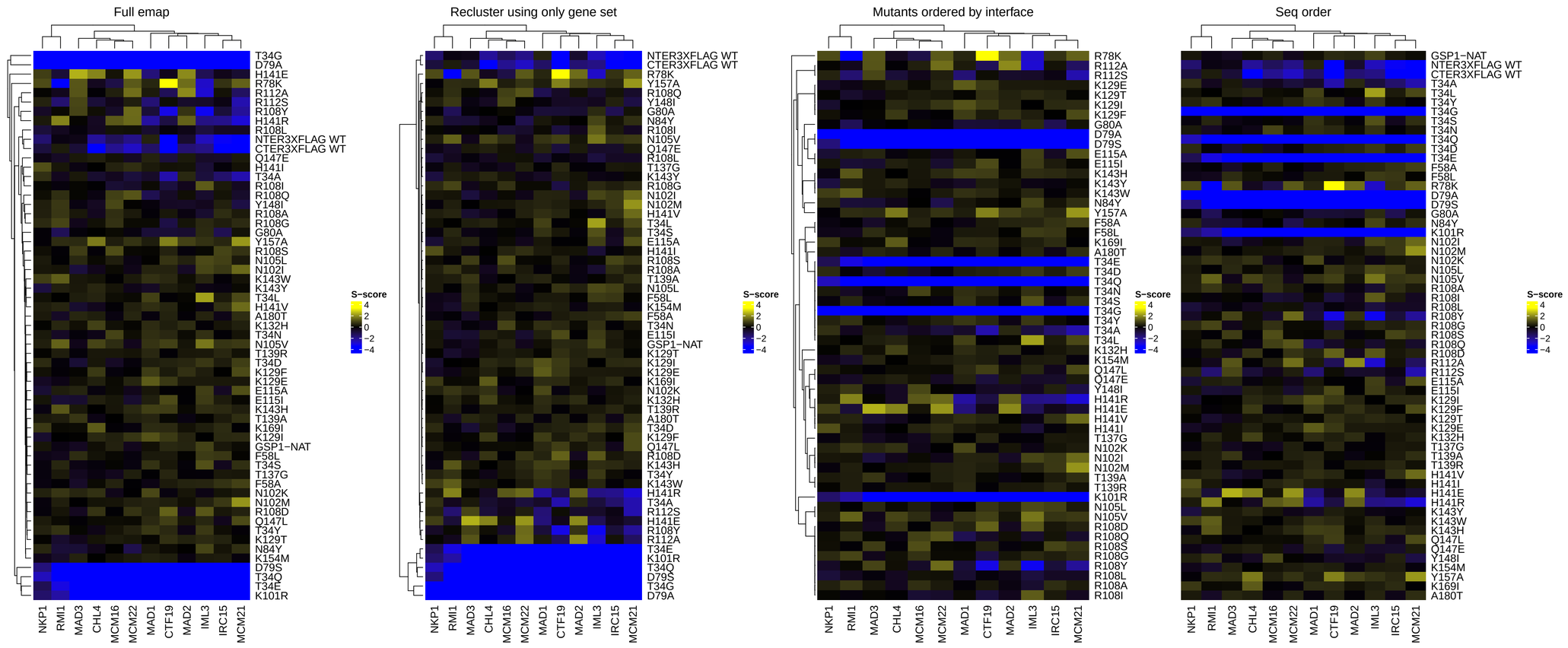
Peroxins

gene set picked by clustering raw S−scores

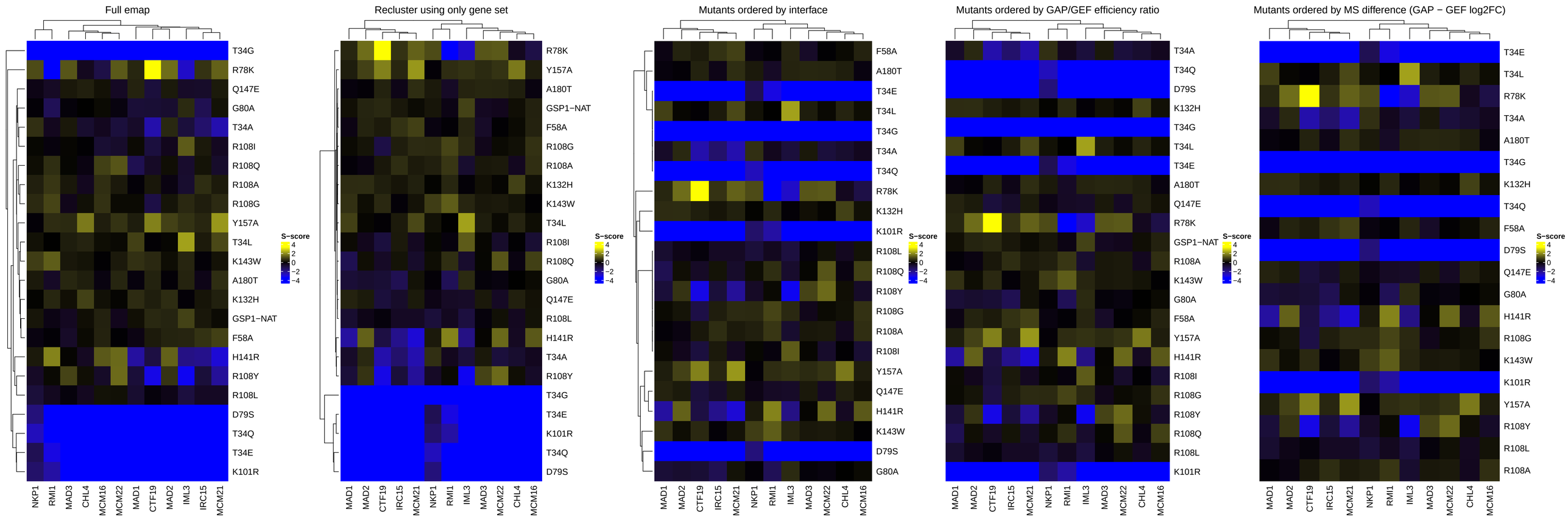
clustering metric: euclidean

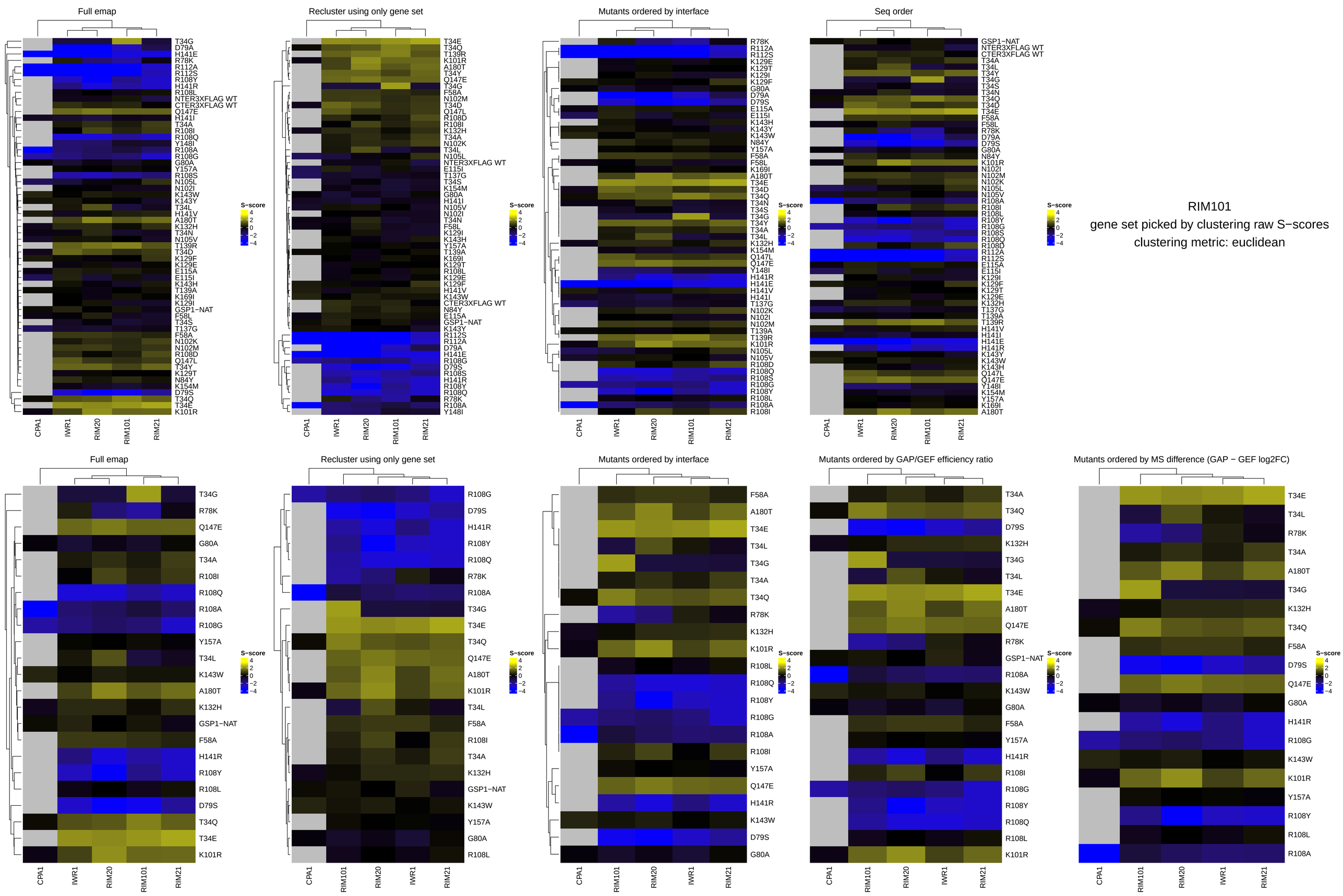


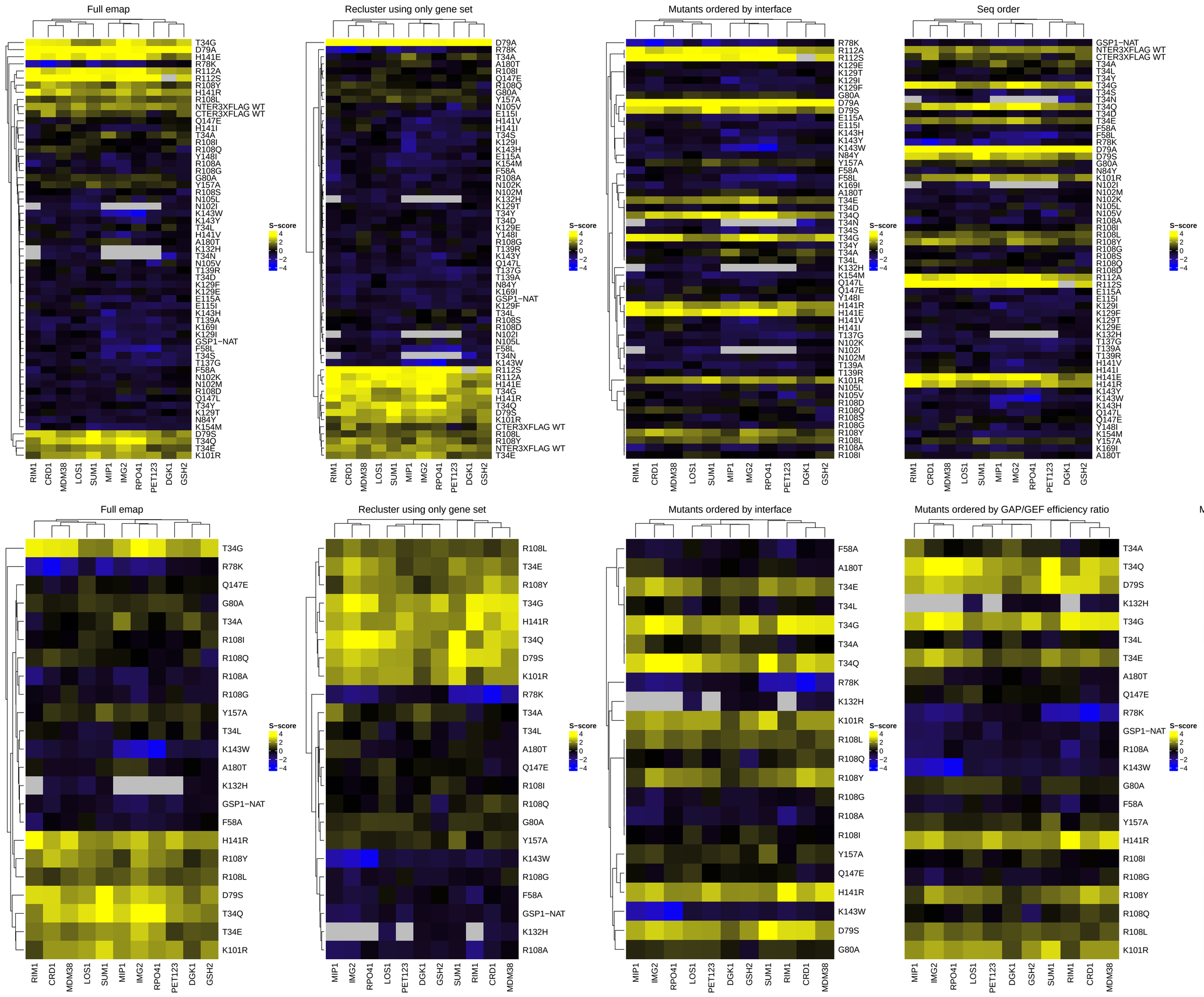

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
CDC26
CHL1
SWM1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
APC
gene set picked by clustering raw S−scores
clustering metric: euclidean



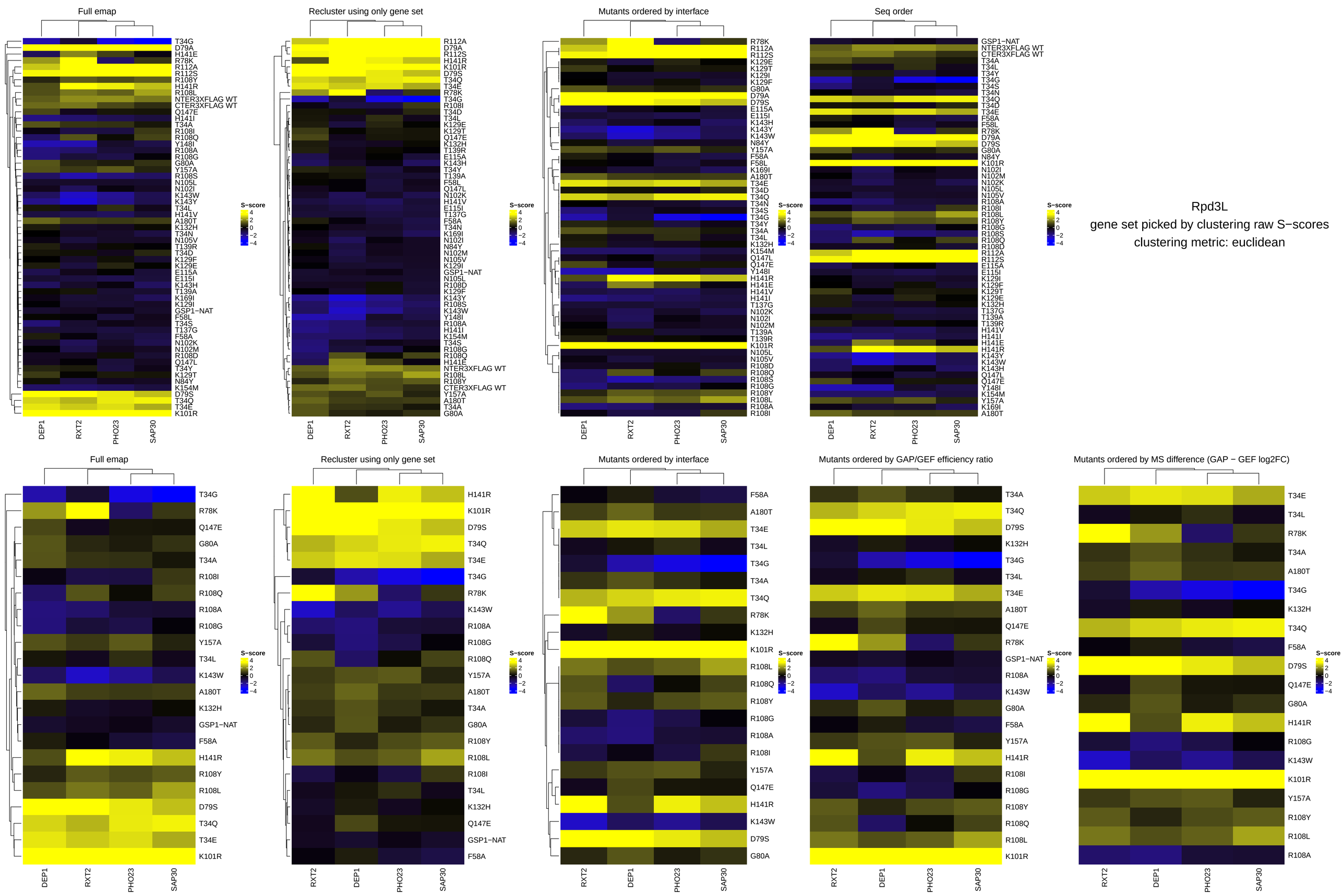
Cell Cycle Checkpoint
gene set picked by clustering raw S−scores
clustering metric: euclidean

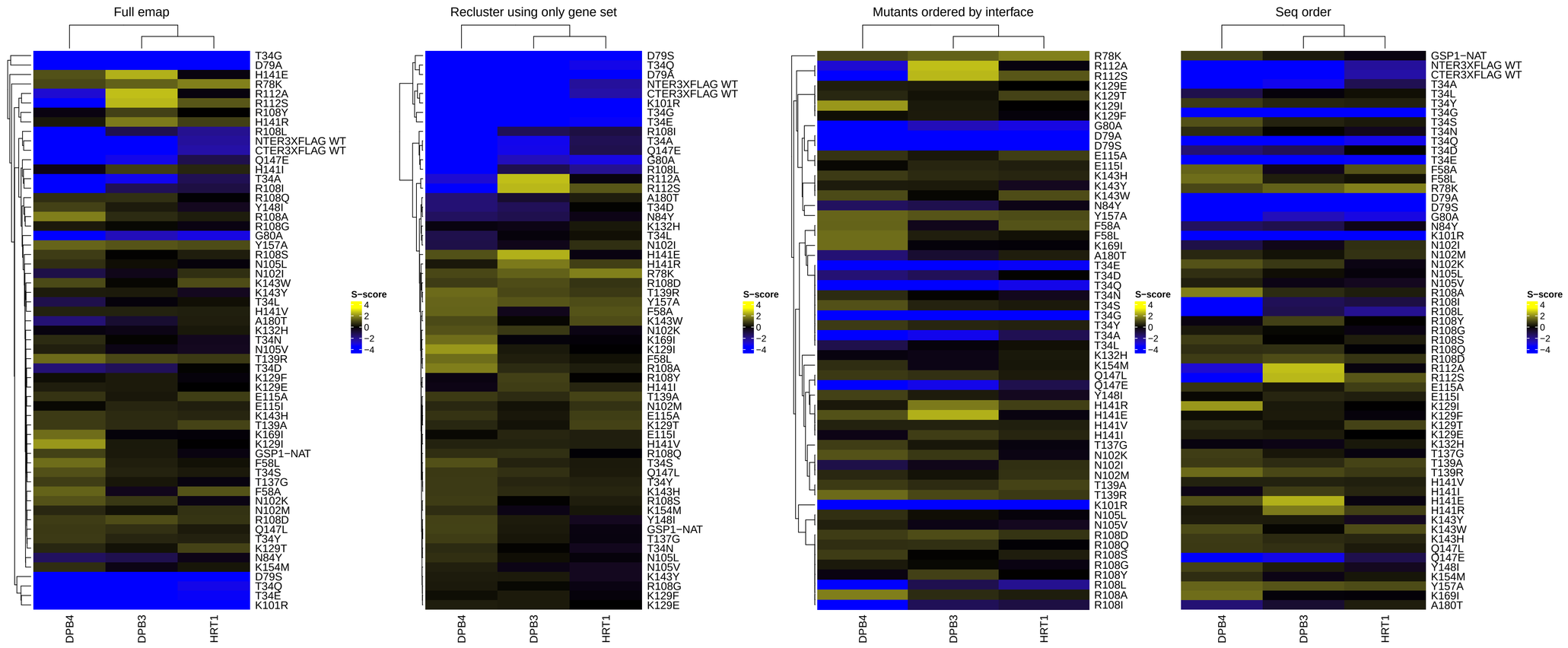



Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CPA1
IWR1
RIM20
RIM101
RIM21
RIM101
gene set picked by clustering raw S−scores
clustering metric: euclidean

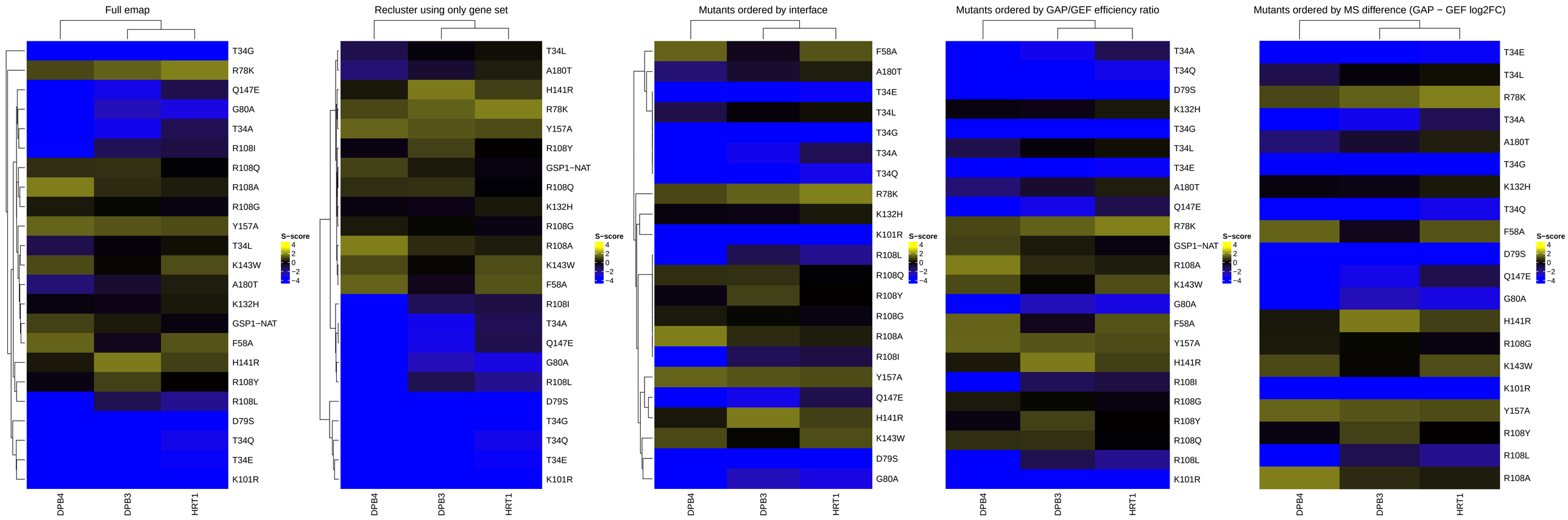


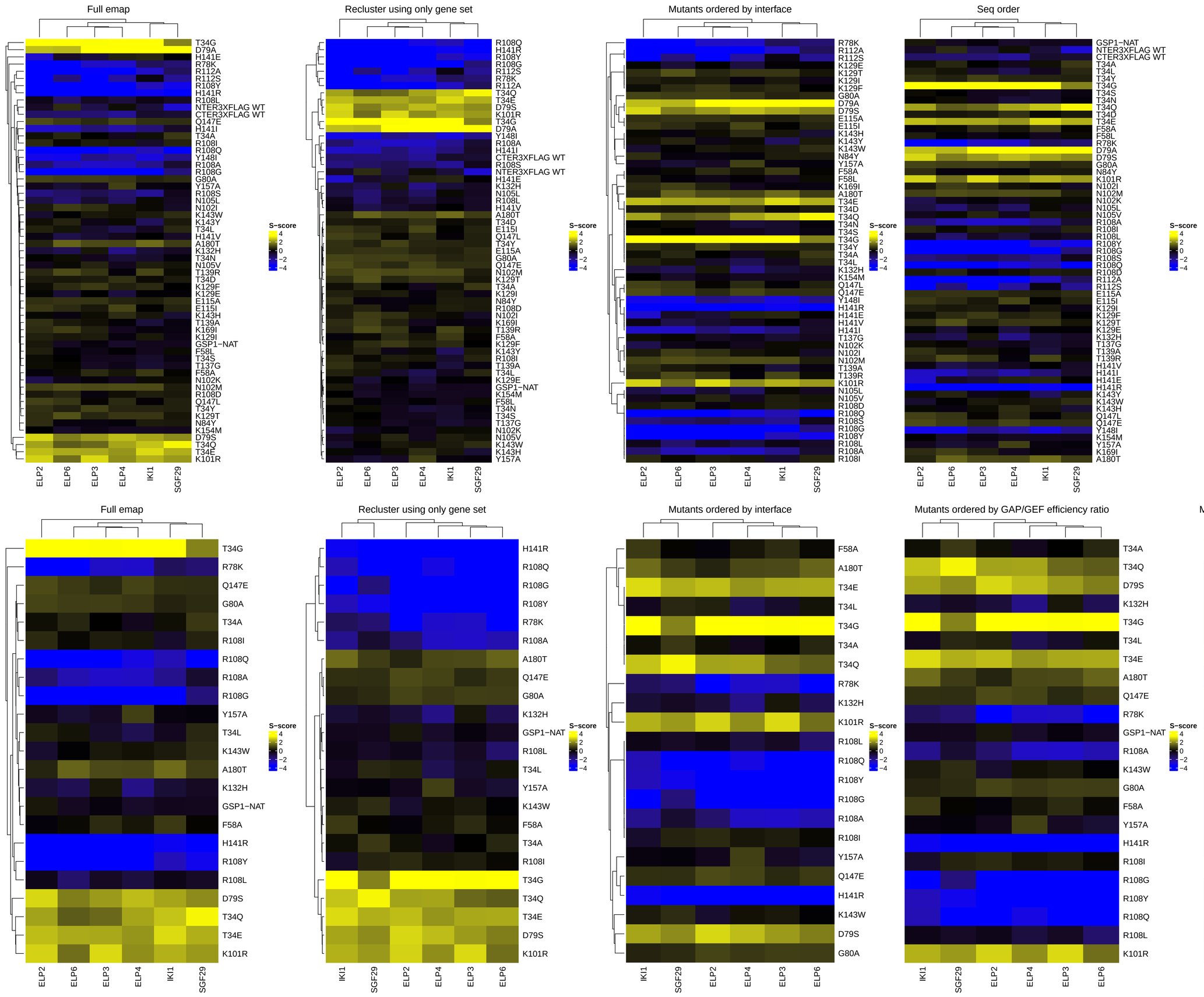
mitochondrial
gene set picked by clustering raw S−scores
clustering metric: euclidean


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
4
2
0
−2
−4
DEP1
RXT2
PHO23
SAP30
Rpd3L
gene set picked by clustering raw S−scores
clustering metric: euclidean



DNA Replication
gene set picked by clustering raw S−scores
clustering metric: euclidean

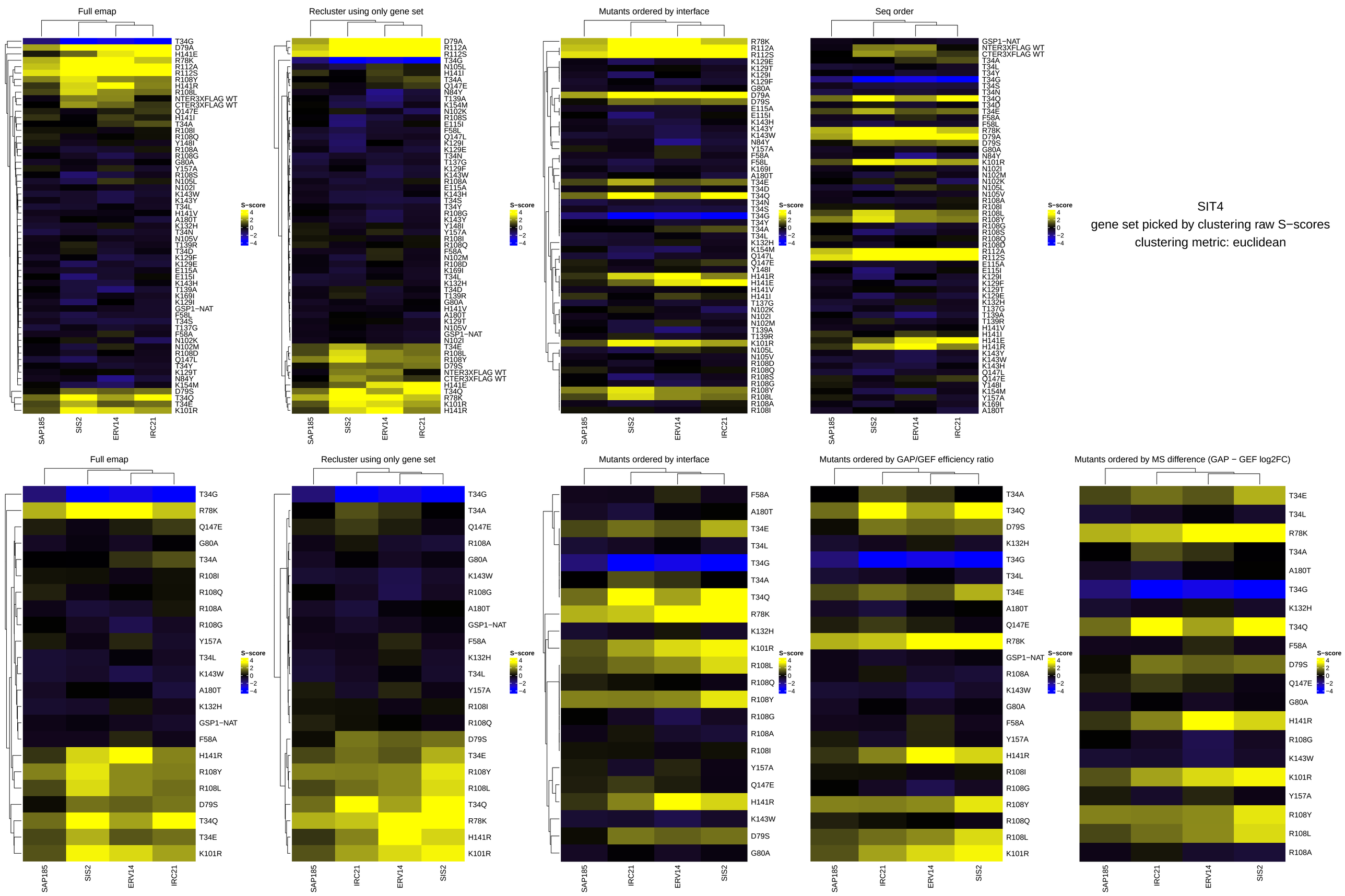


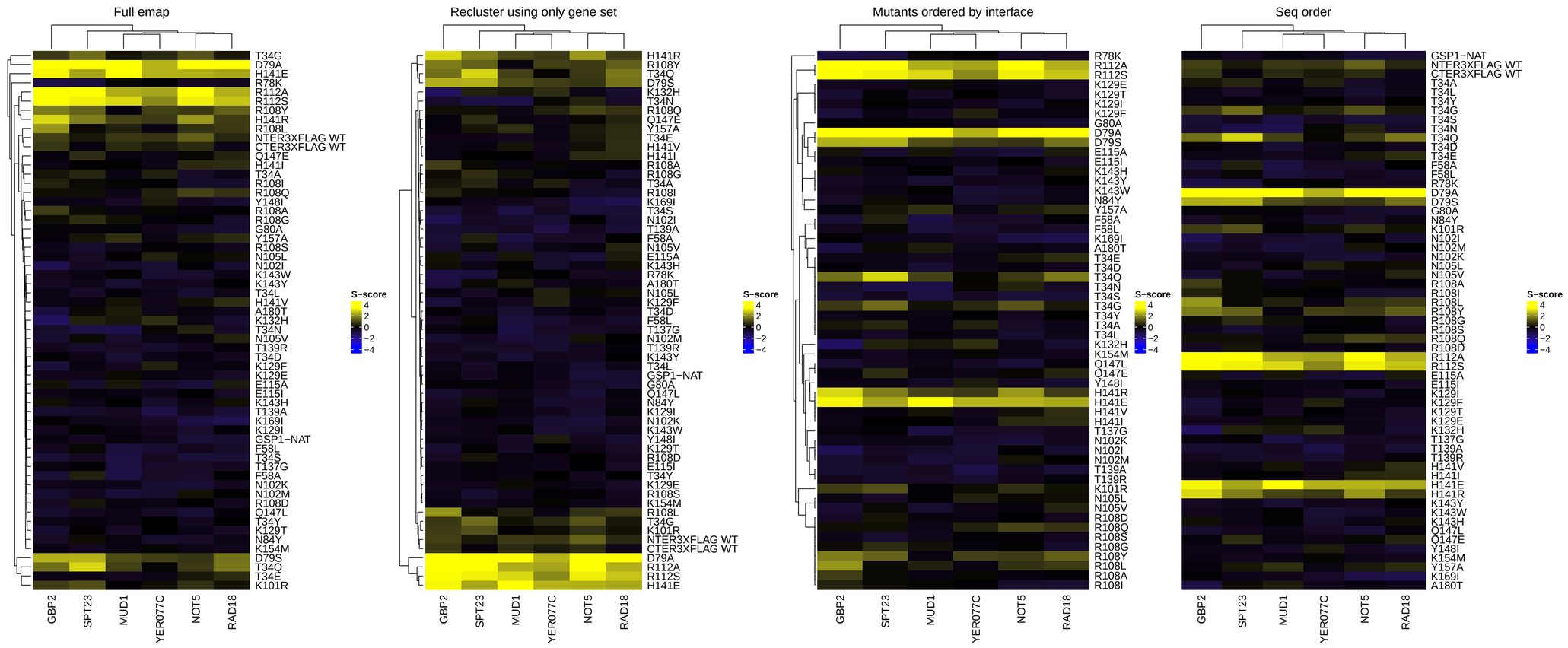


Elongator

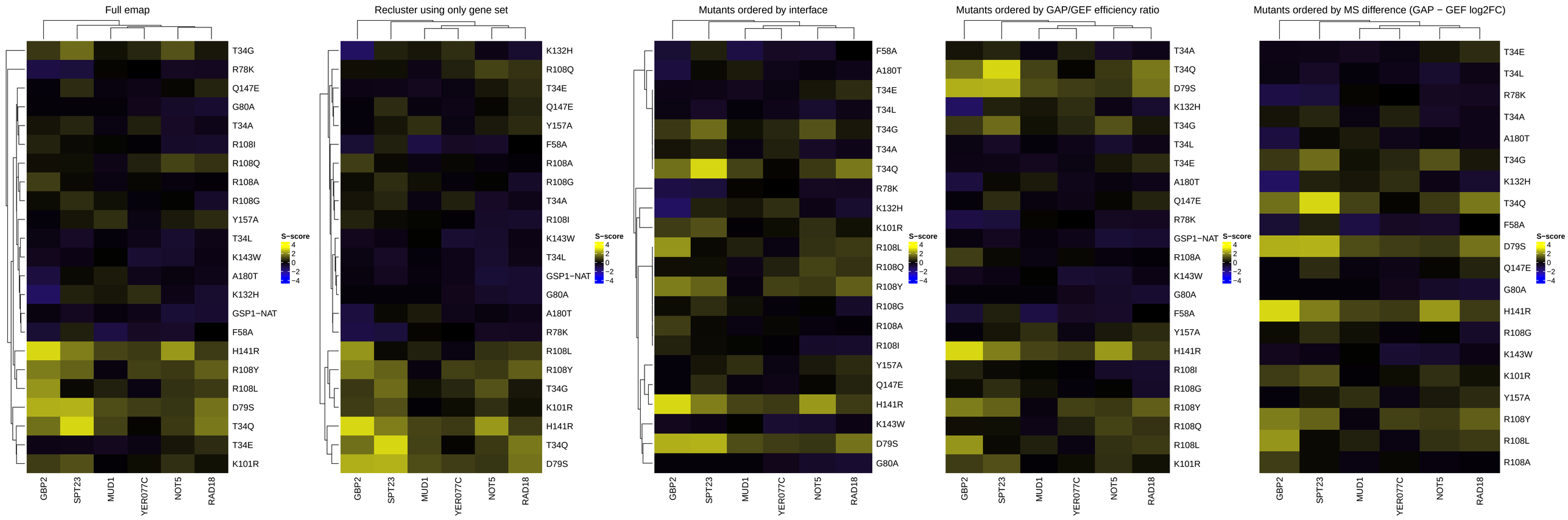
gene set picked by clustering raw S−scores

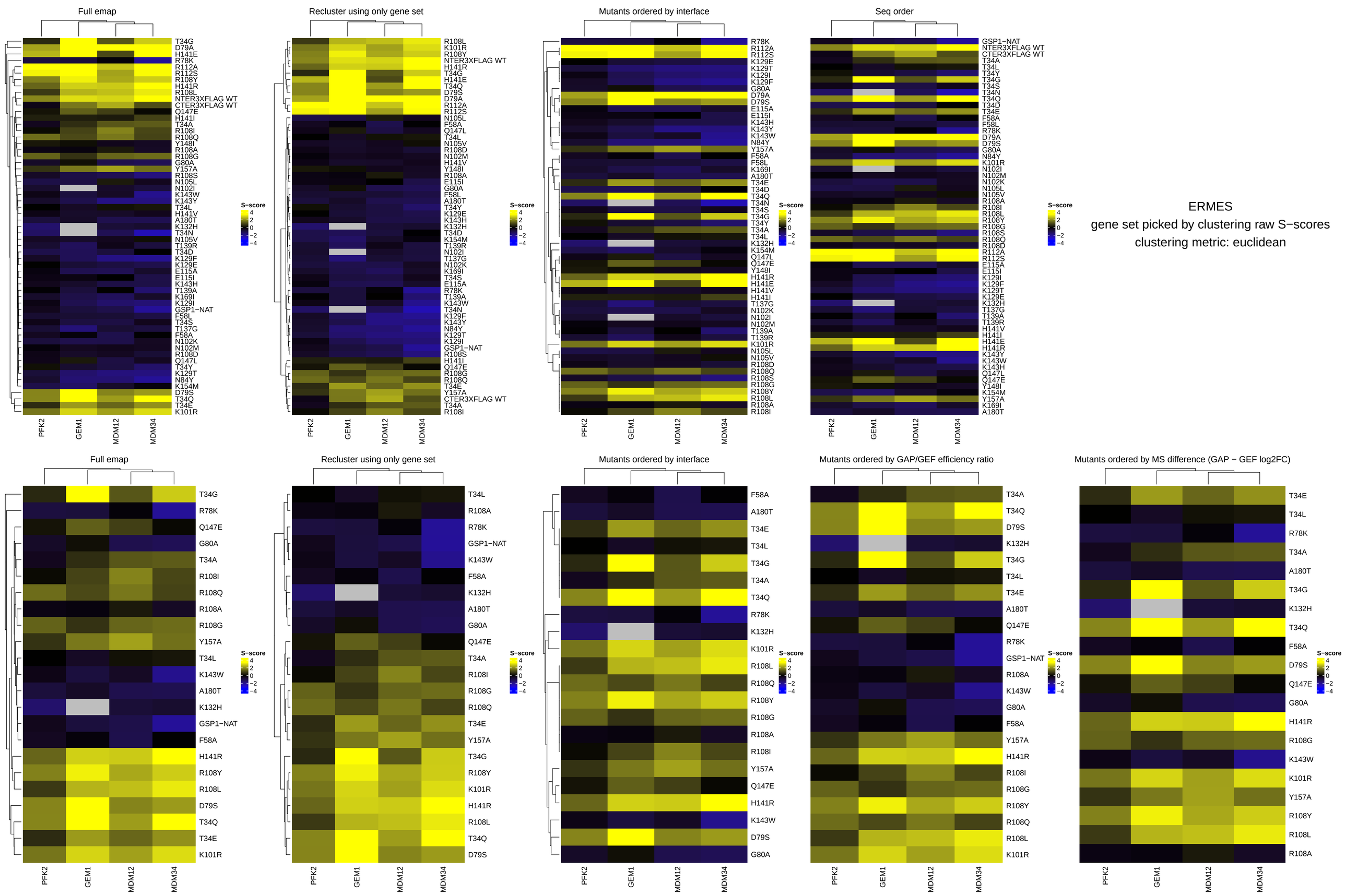
clustering metric: euclidean

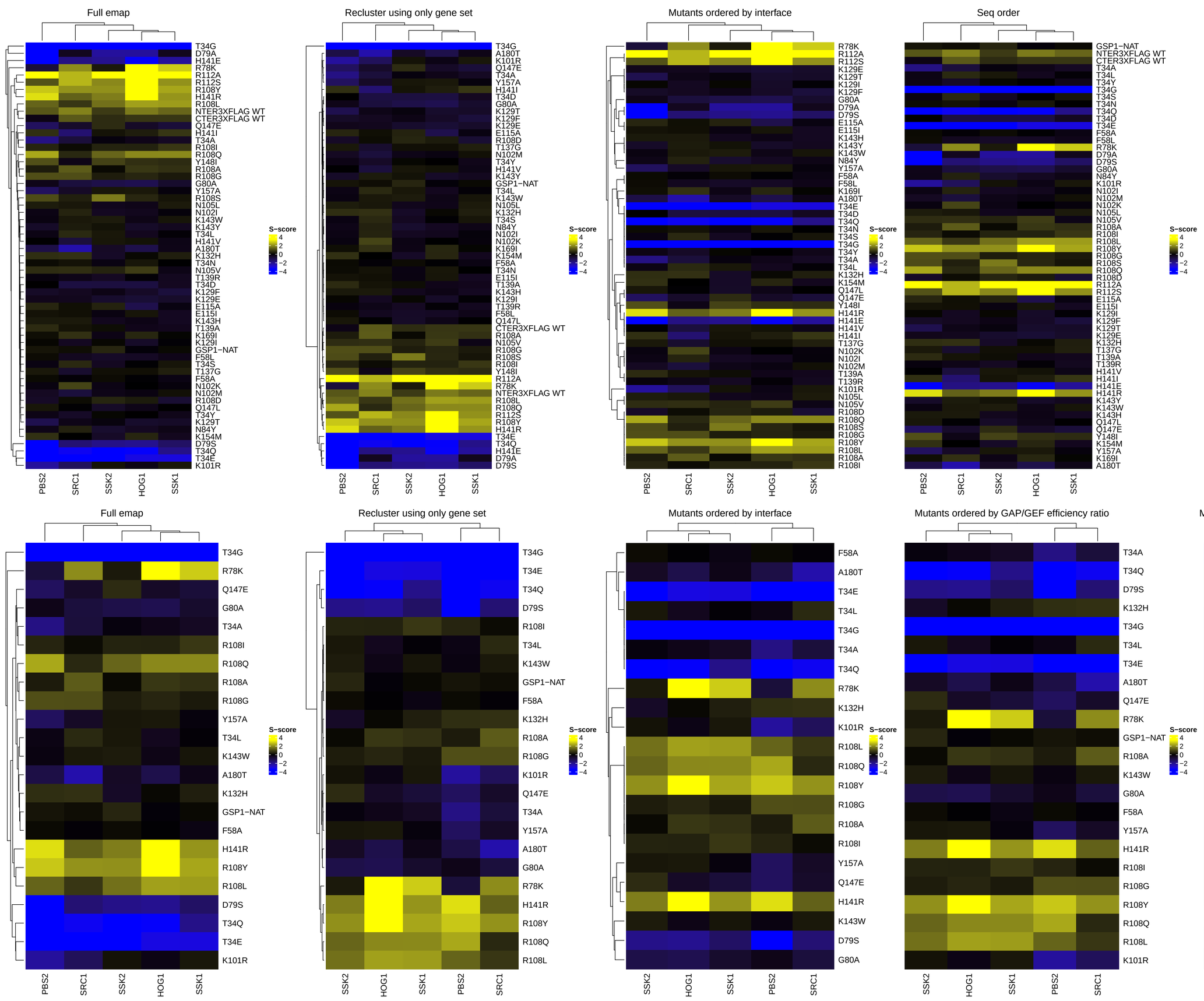

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SAP185
SIS2
ERV14
IRC21
SIT4
gene set picked by clustering raw S−scores
clustering metric: euclidean



mRNA processing
gene set picked by clustering raw S−scores
clustering metric: euclidean



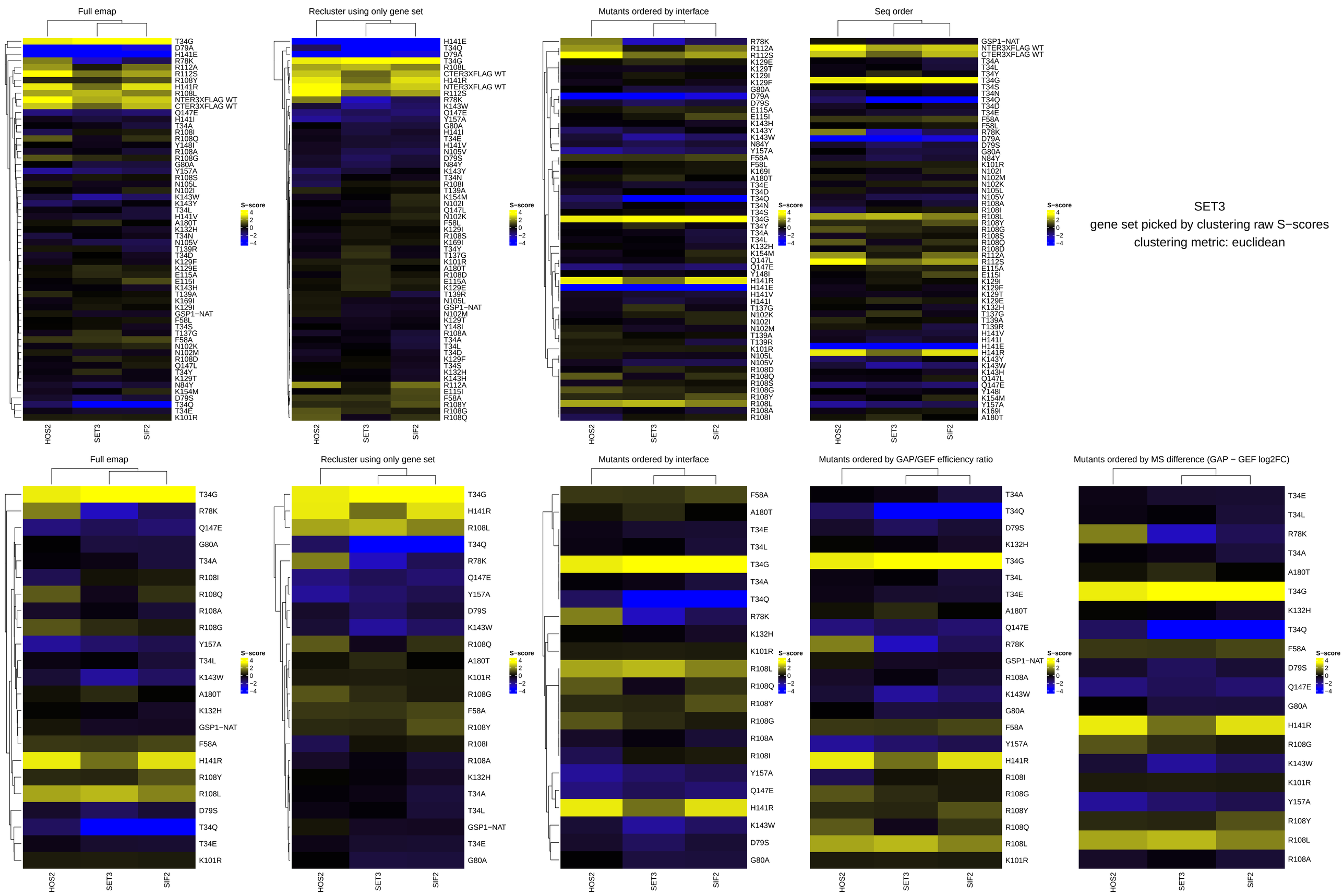

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PFK2
GEM1
MDM12
MDM34
ERMES
gene set picked by clustering raw S−scores
clustering metric: euclidean

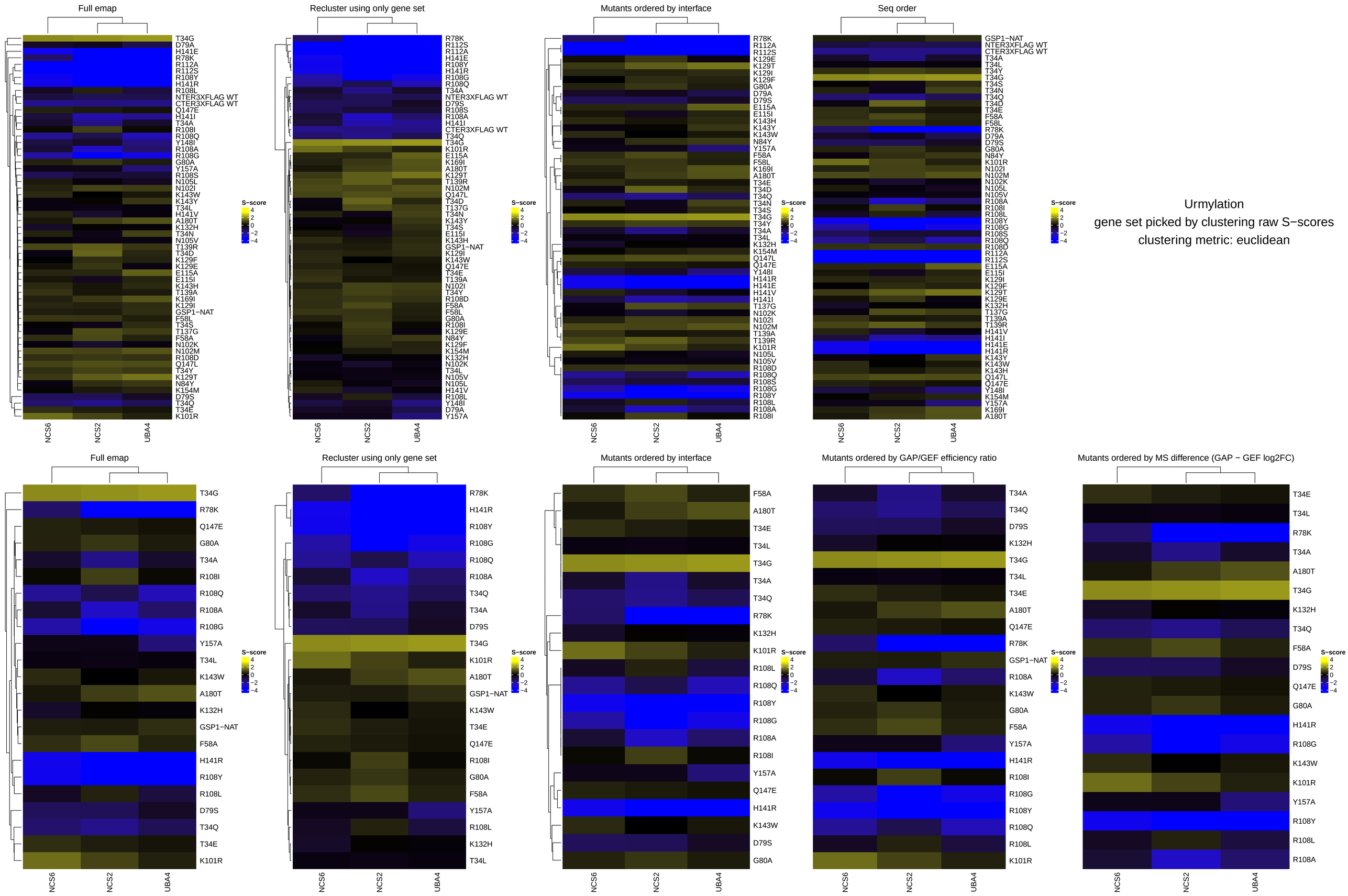


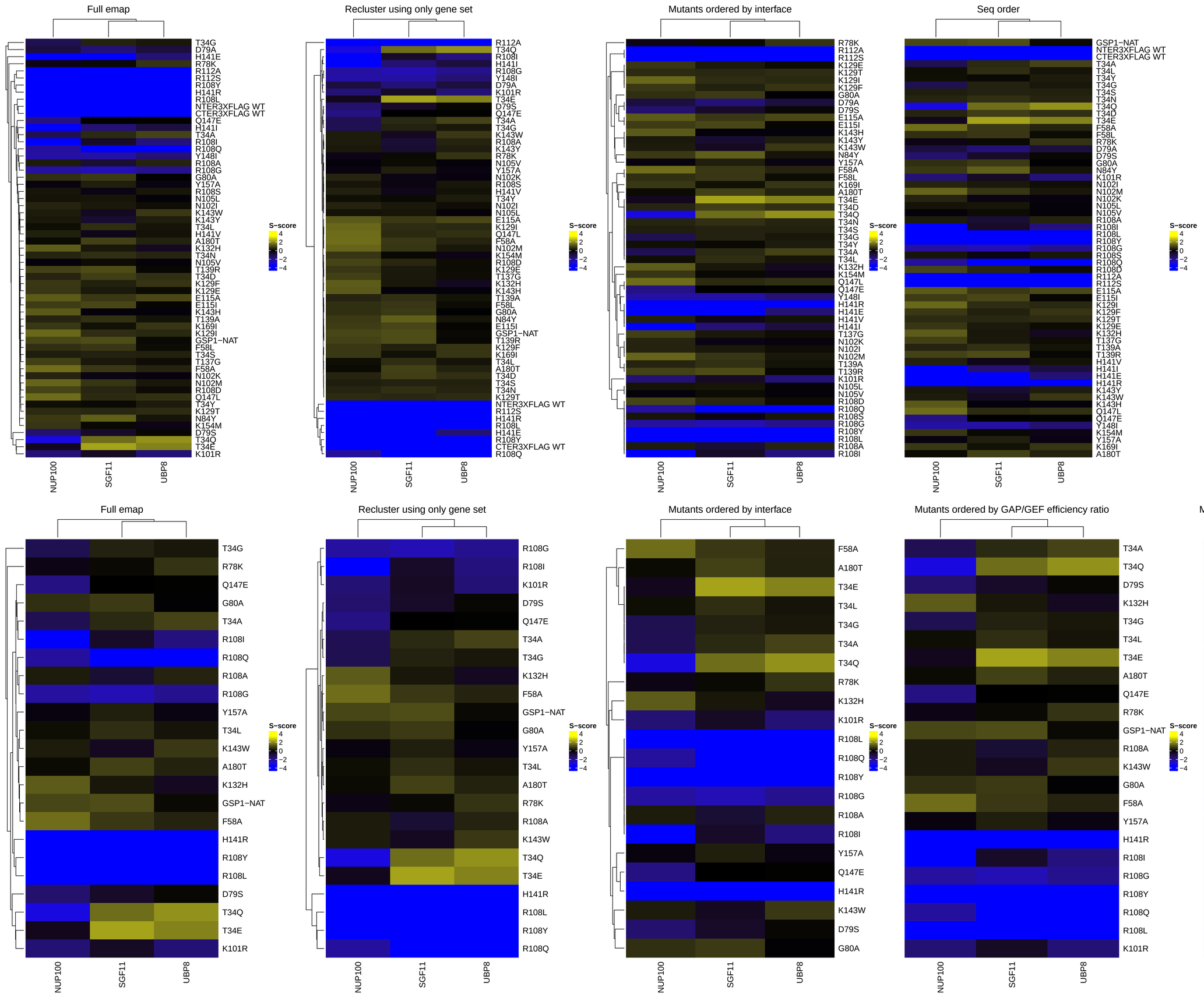
HOG1

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
4
2
0
−2
−4
HOS2
SET3
SIF2
SET3
gene set picked by clustering raw S−scores
clustering metric: euclidean

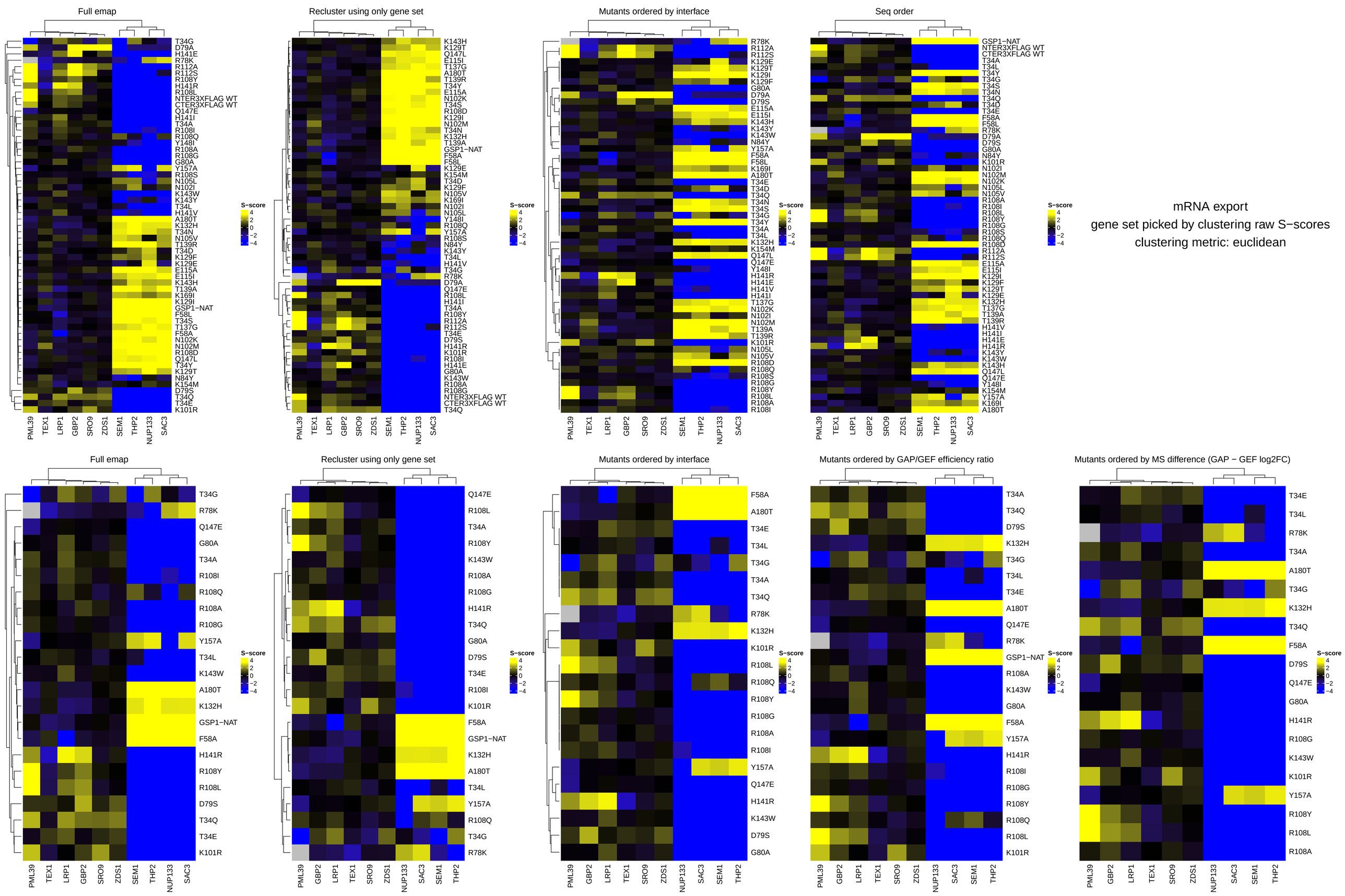

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
NCS6
NCS2
UBA4
Urmylation
gene set picked by clustering raw S−scores
clustering metric: euclidean

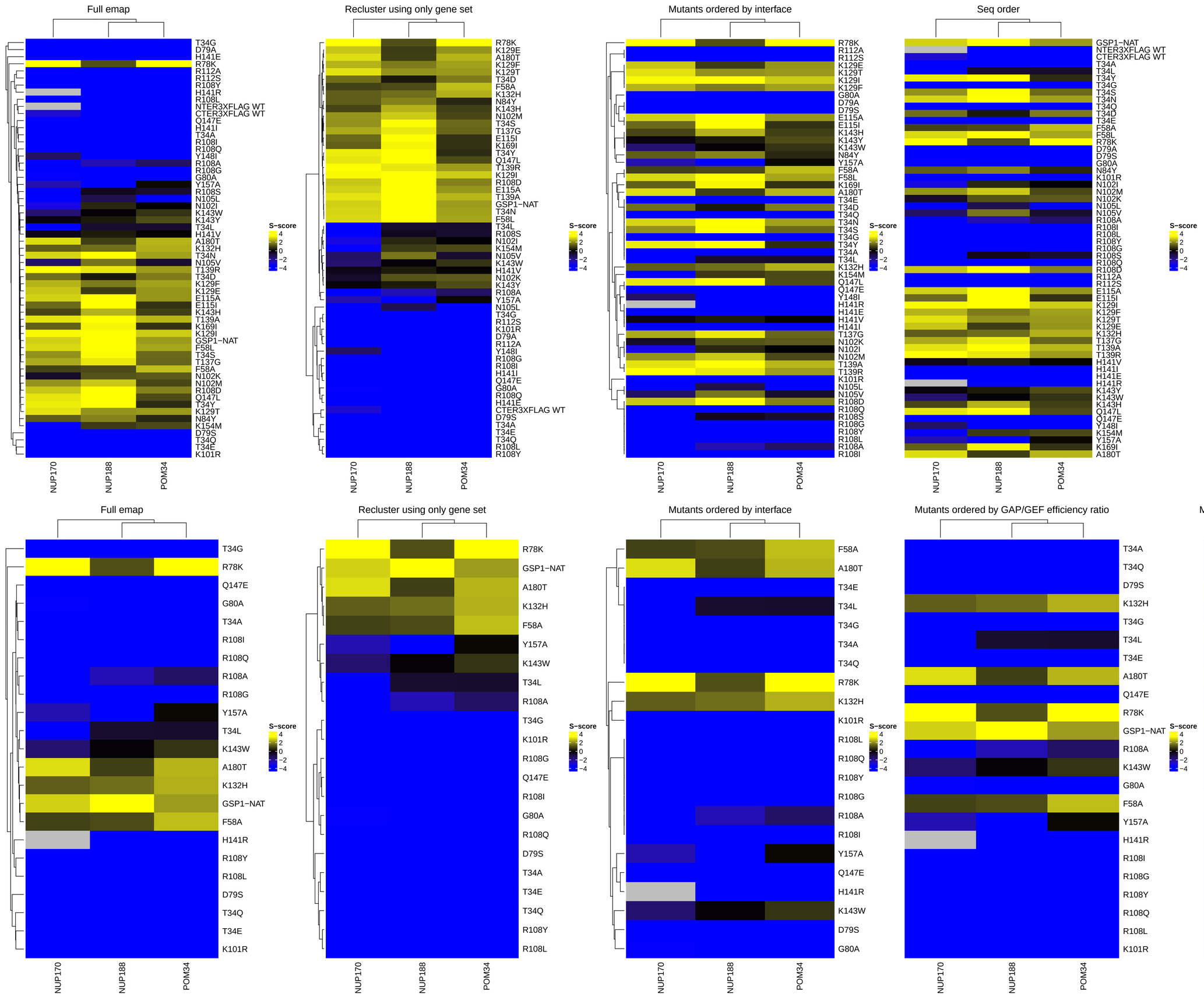


SAGA

gene set picked by clustering raw S−scores

clustering metric: euclidean

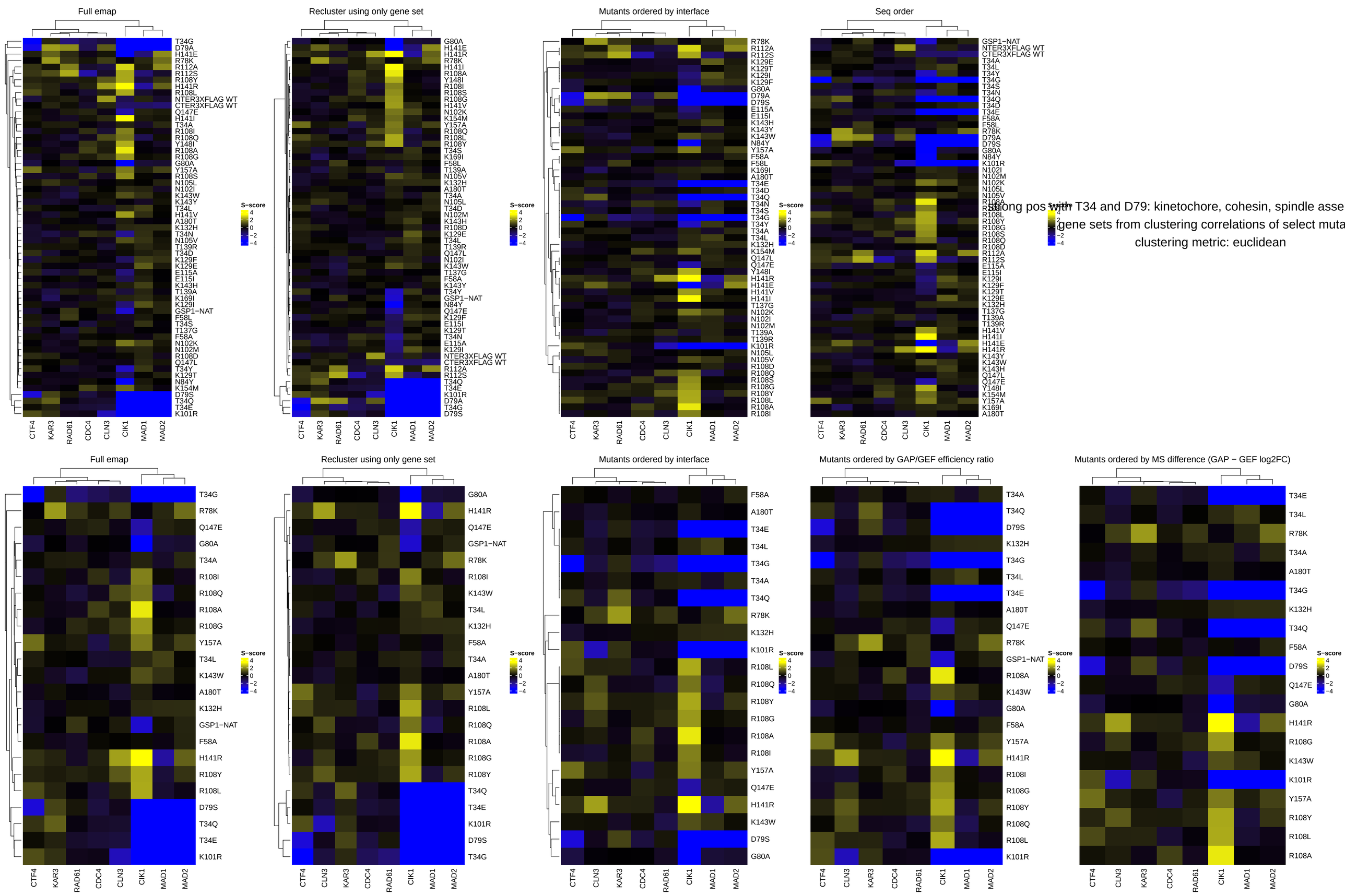

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PML39
TEX1
LRP1
GBP2
SRO9
ZDS1
SEM1
THP2
NUP133
SAC3
mRNA export
gene set picked by clustering raw S−scores
clustering metric: euclidean



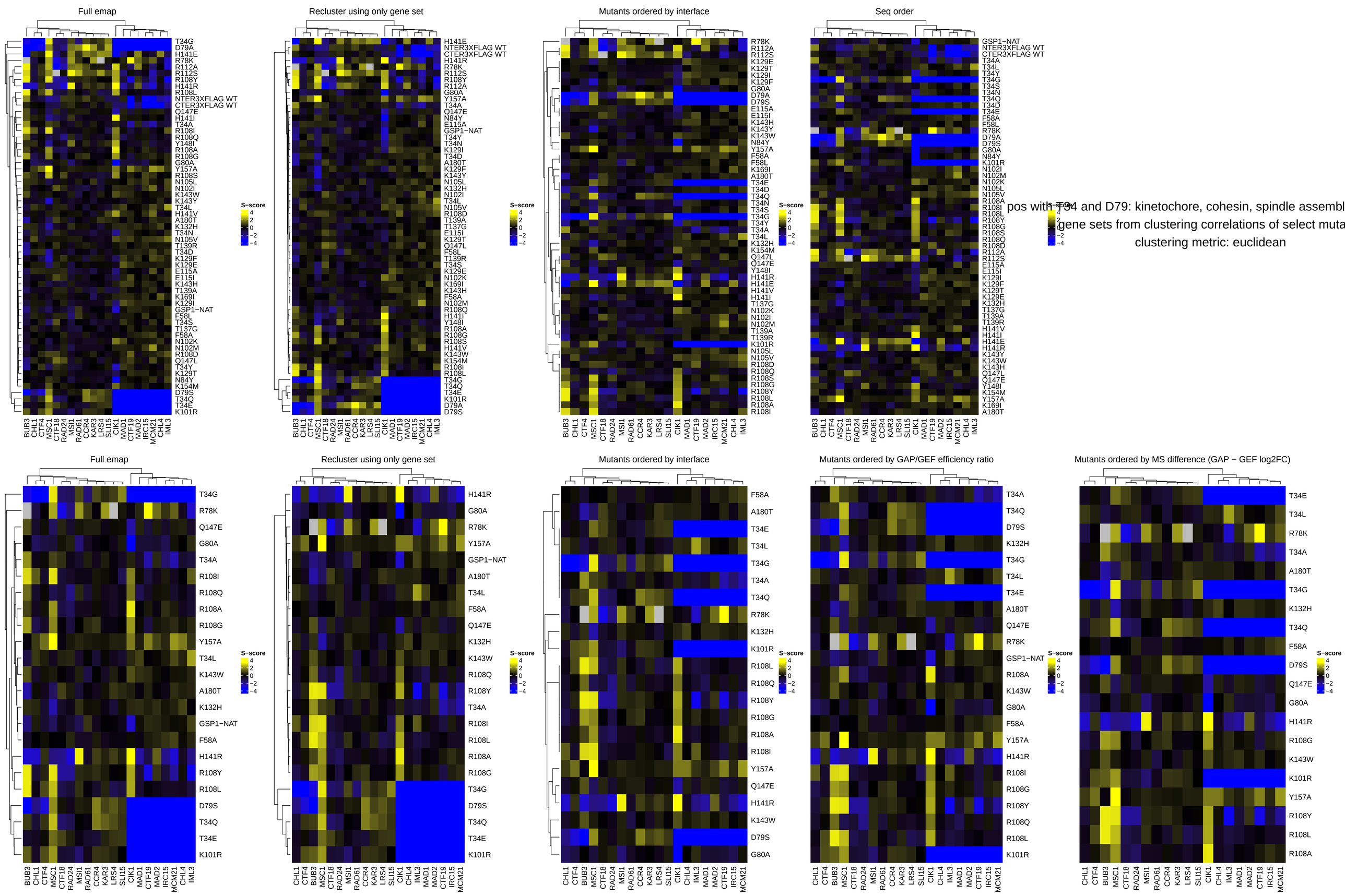
Inner NPC

gene set picked by clustering raw S−scores

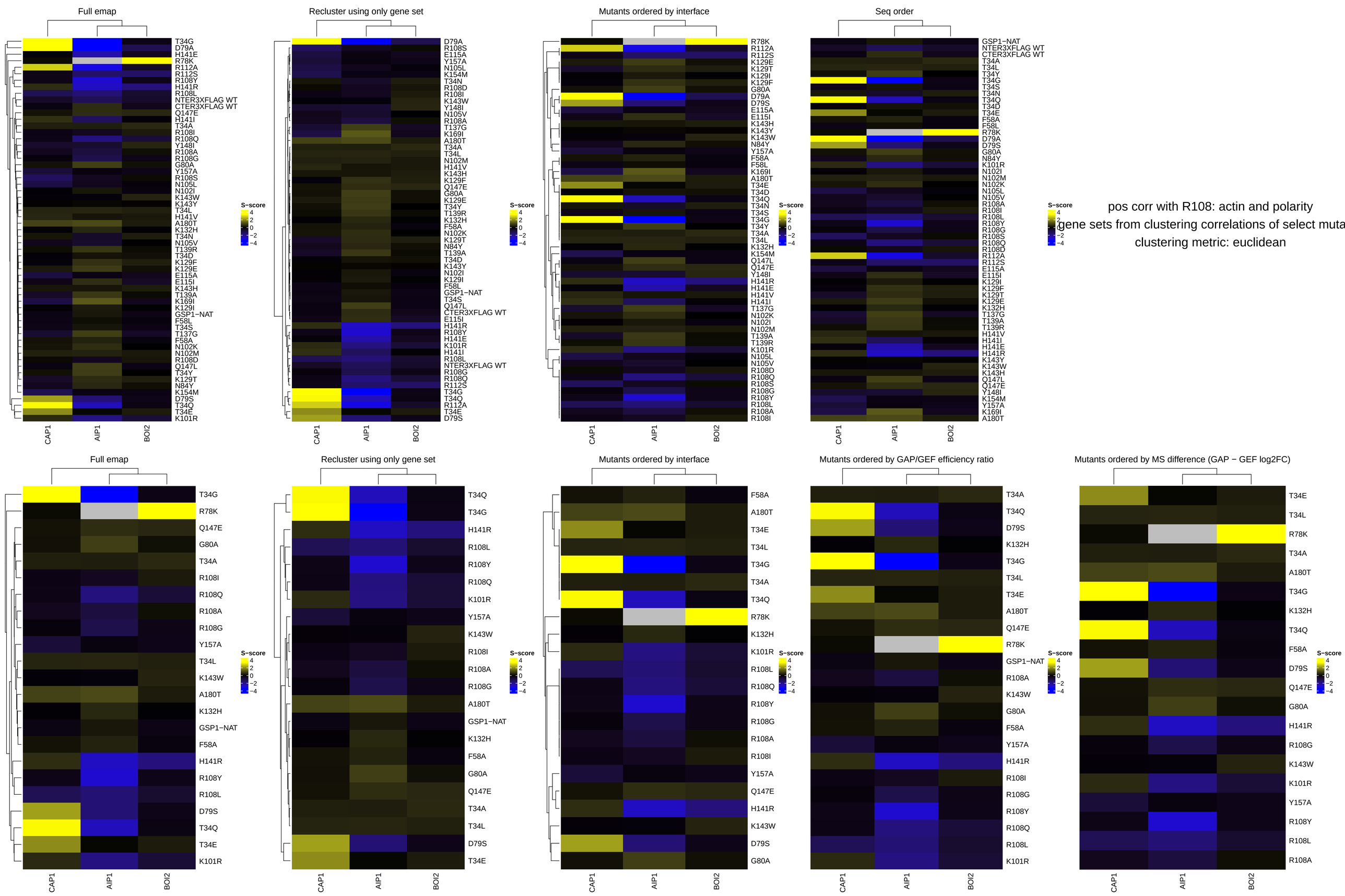
clustering metric: euclidean

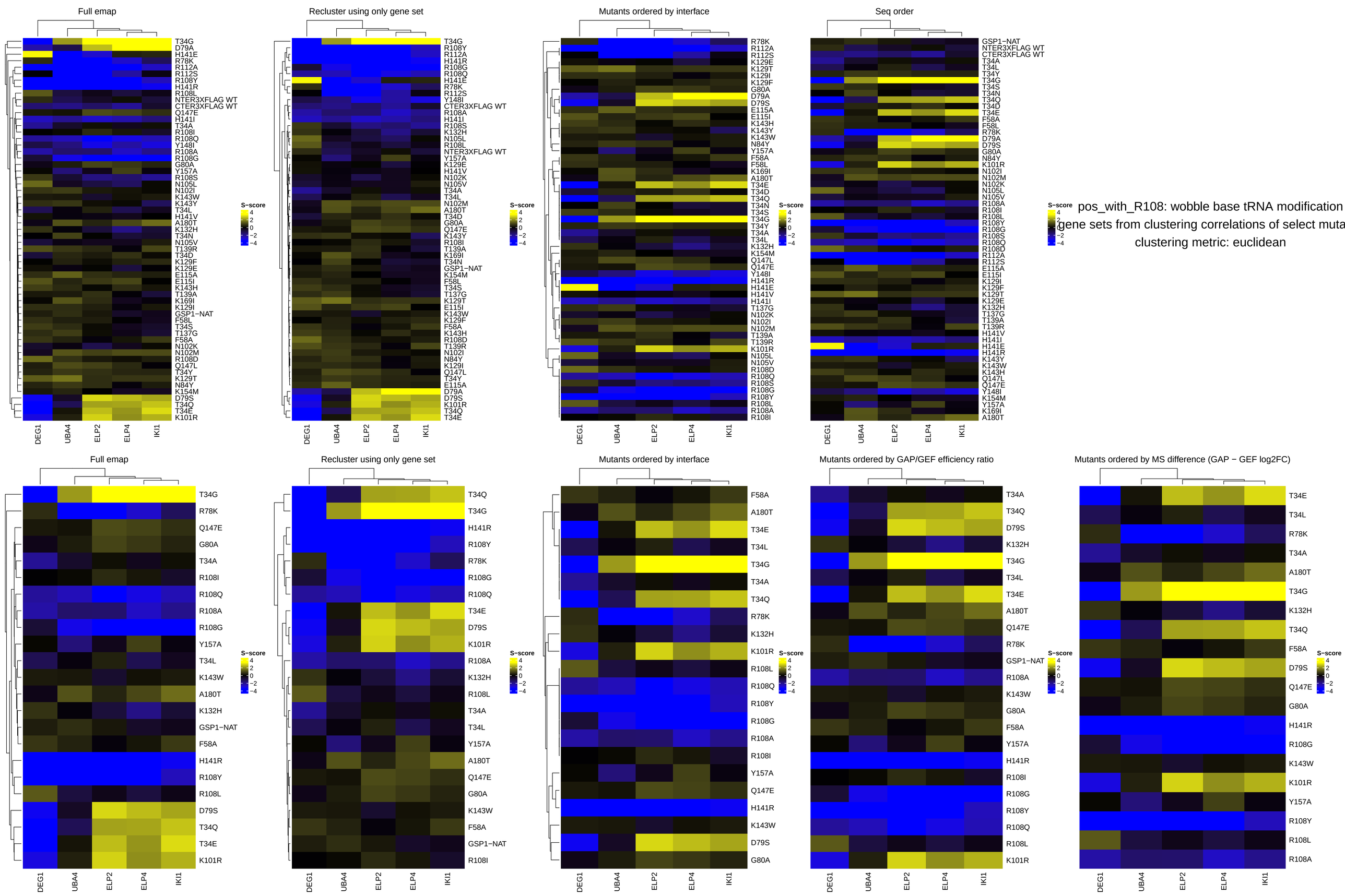


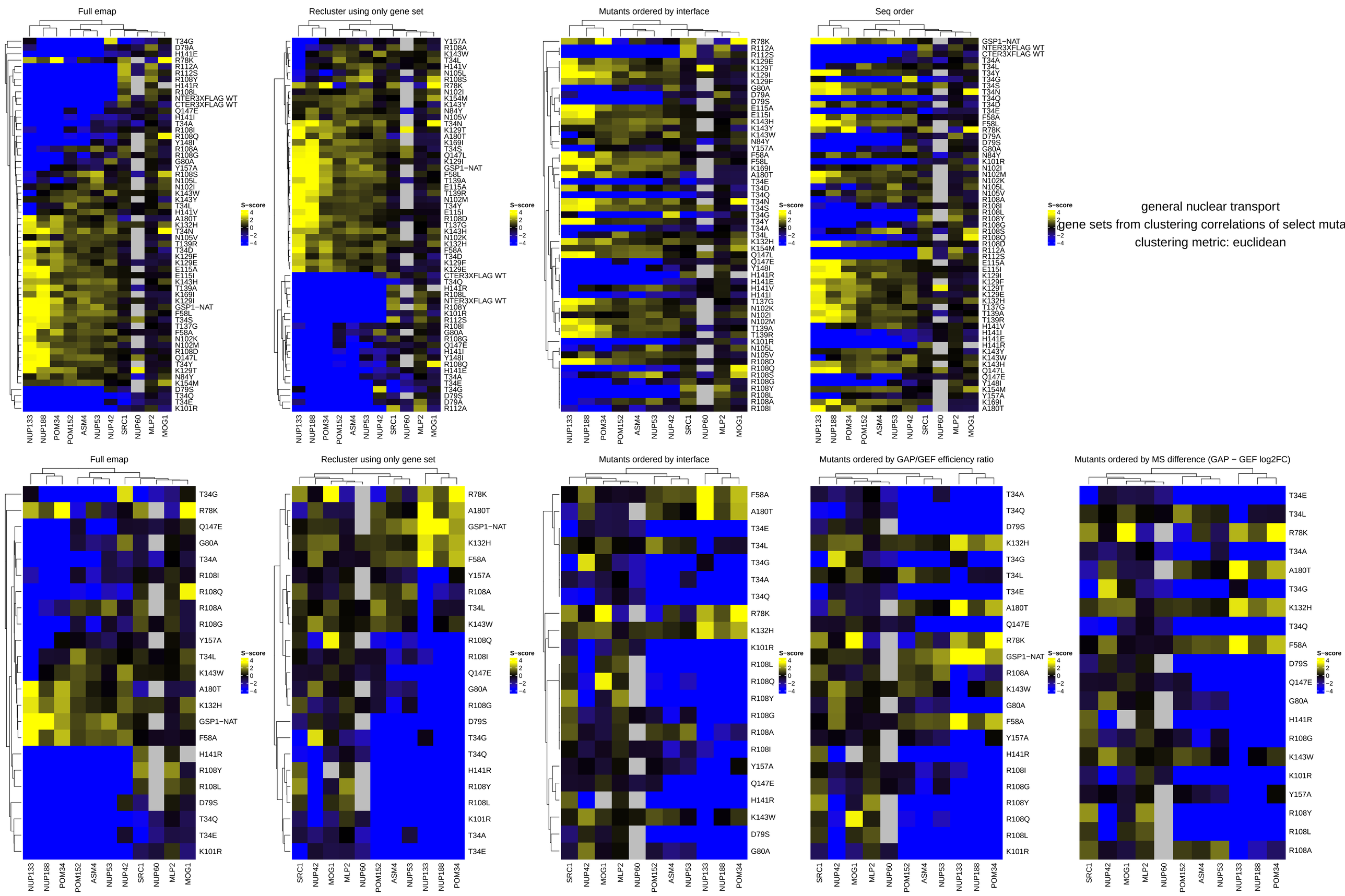
Strong pos with T34 and D79: kinetochore, cohesin, spindle asse
gene sets from clustering correlations of select muta
clustering metric: euclidean

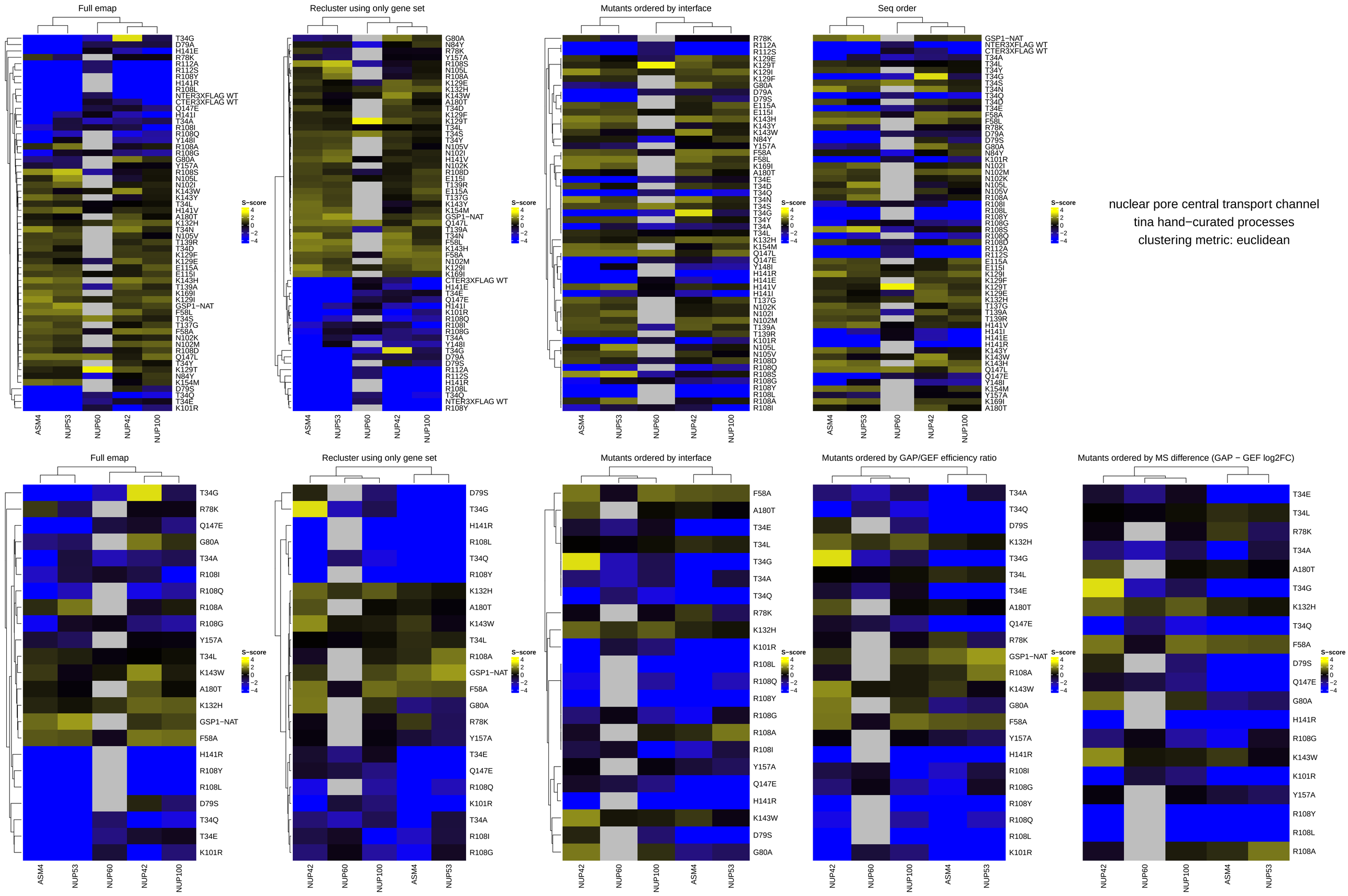


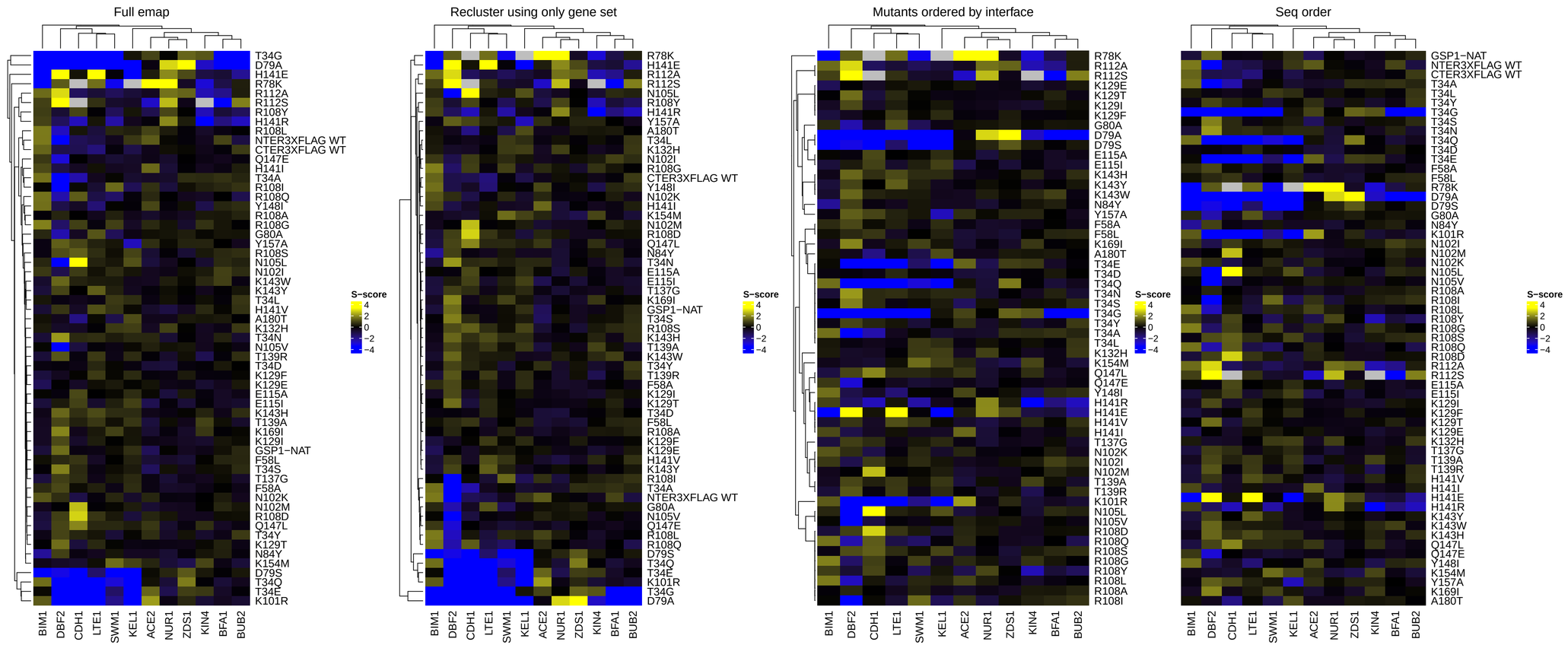
pos with T34 and D79: kinetochore, cohesin, spindle assembl
gene sets from clustering correlations of select muta
clustering metric: euclidean


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
4
2
0
−2
−4
CAP1
AIP1
BOI2
pos corr with R108: actin and polarity
gene sets from clustering correlations of select muta
clustering metric: euclidean

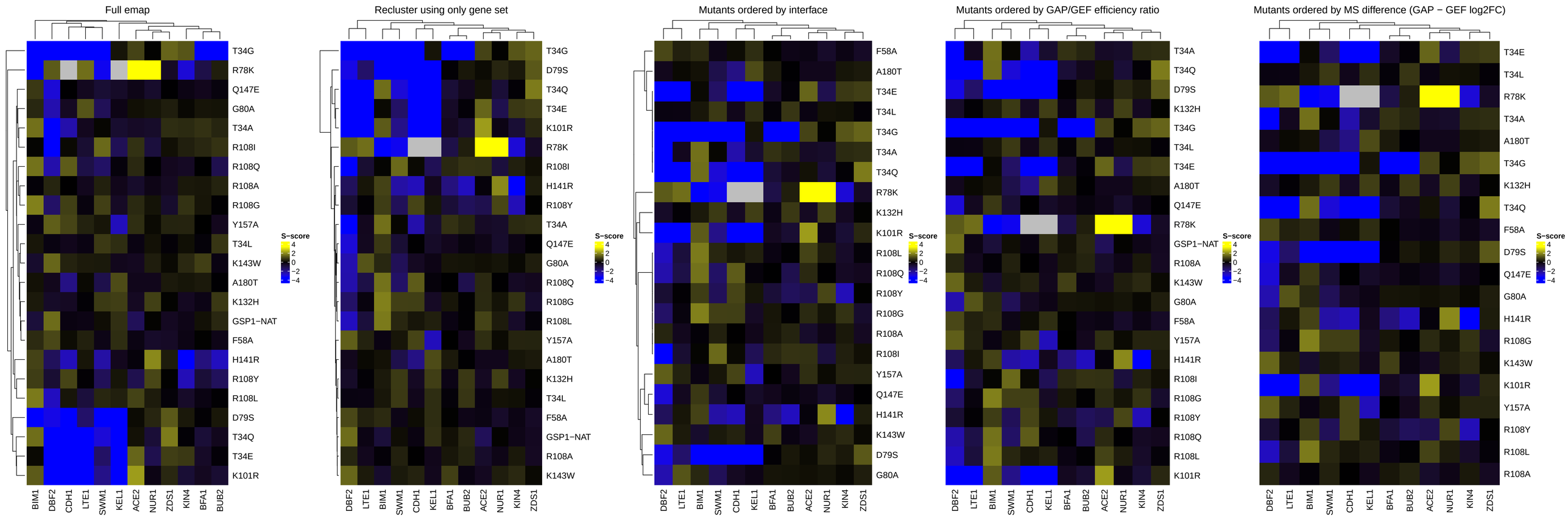

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
DEG1
UBA4
ELP2
ELP4
IKI1
pos_with_R108: wobble base tRNA modification
gene sets from clustering correlations of select muta
clustering metric: euclidean

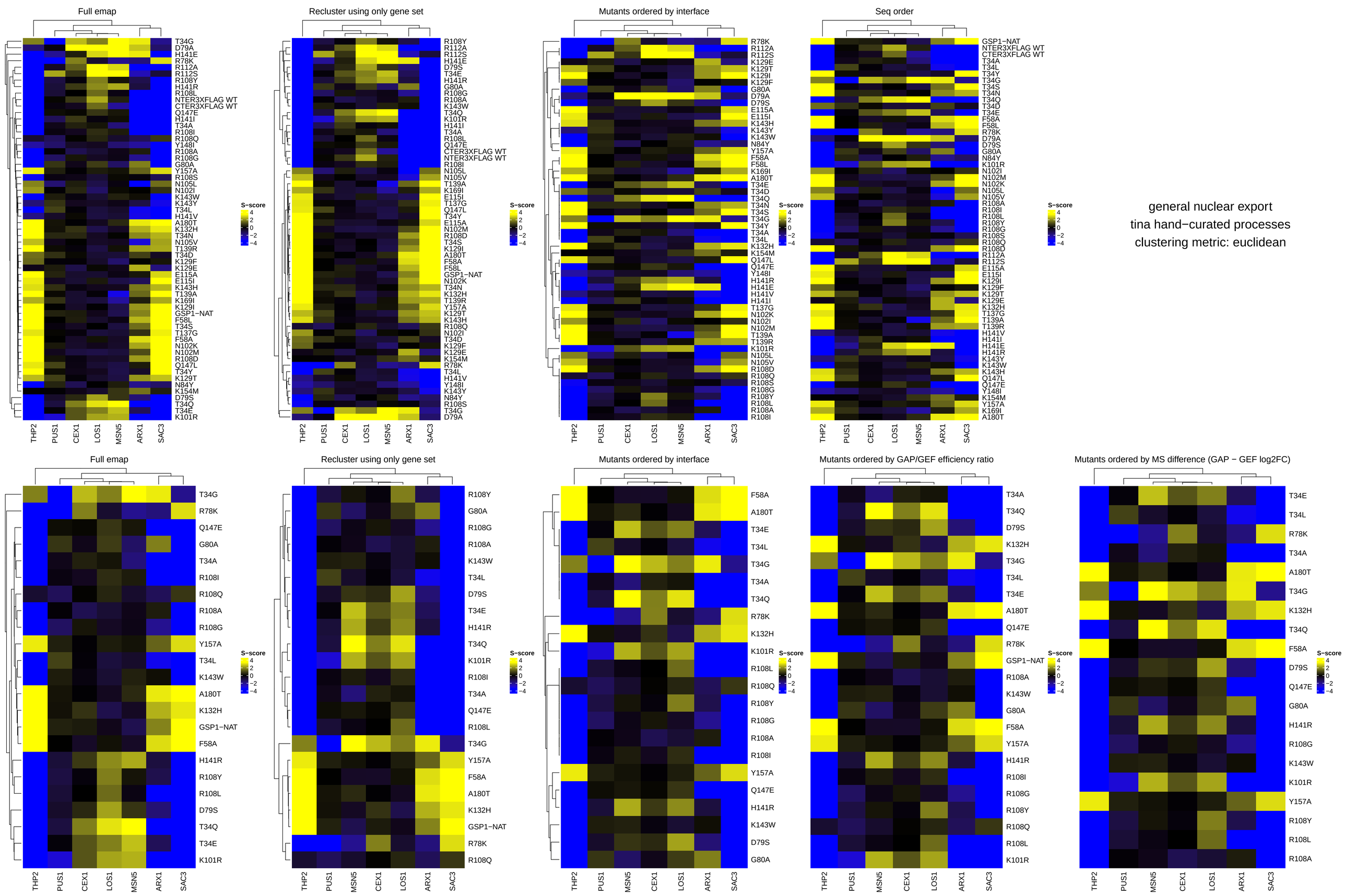

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
NUP133
NUP188
POM34
POM152
ASM4
NUP53
NUP42
SRC1
NUP60
MLP2
MOG1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
general nuclear transport
gene sets from clustering correlations of select muta
clustering metric: euclidean

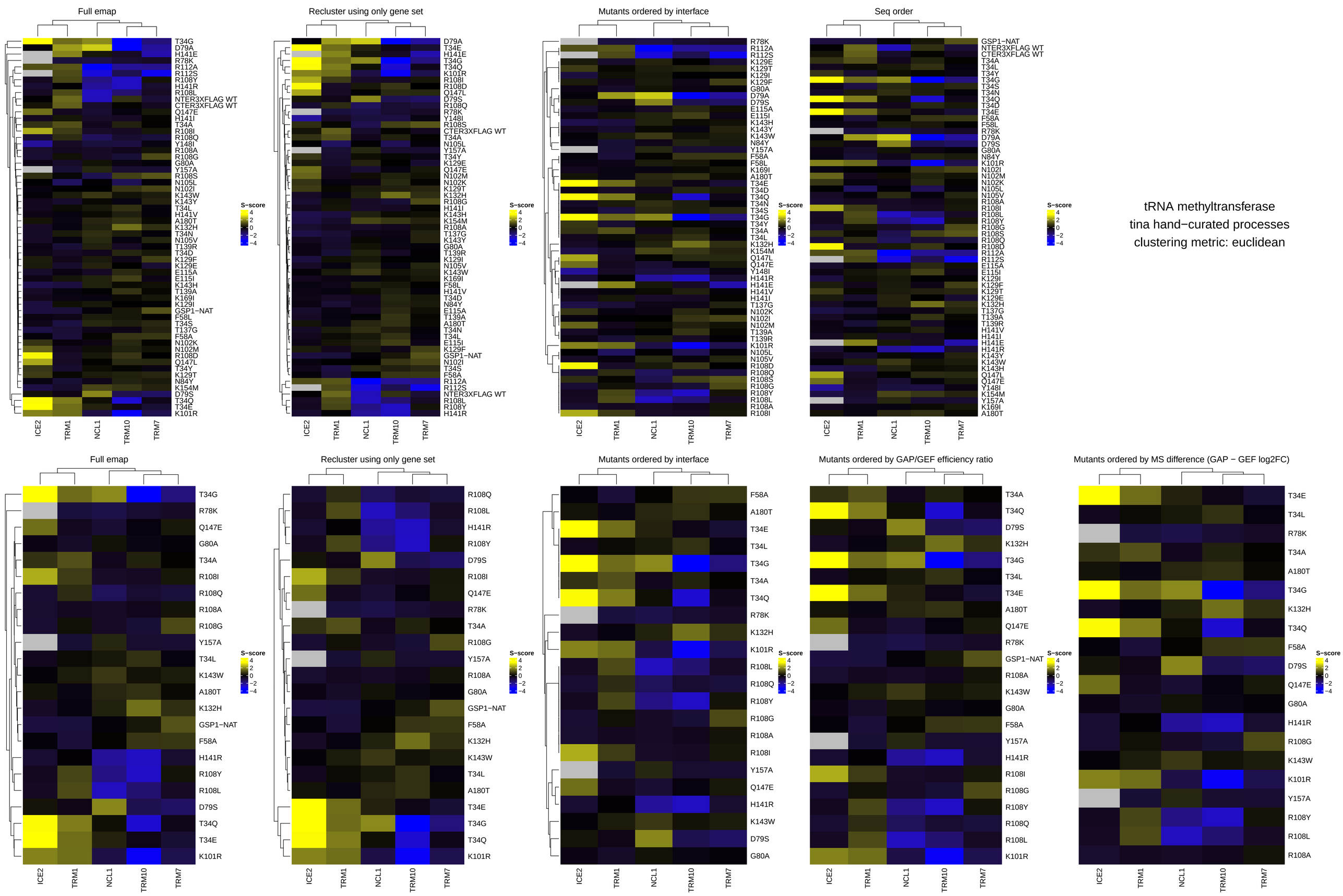

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ASM4
NUP53
NUP60
NUP42
NUP100
nuclear pore central transport channel
tina hand−curated processes
clustering metric: euclidean

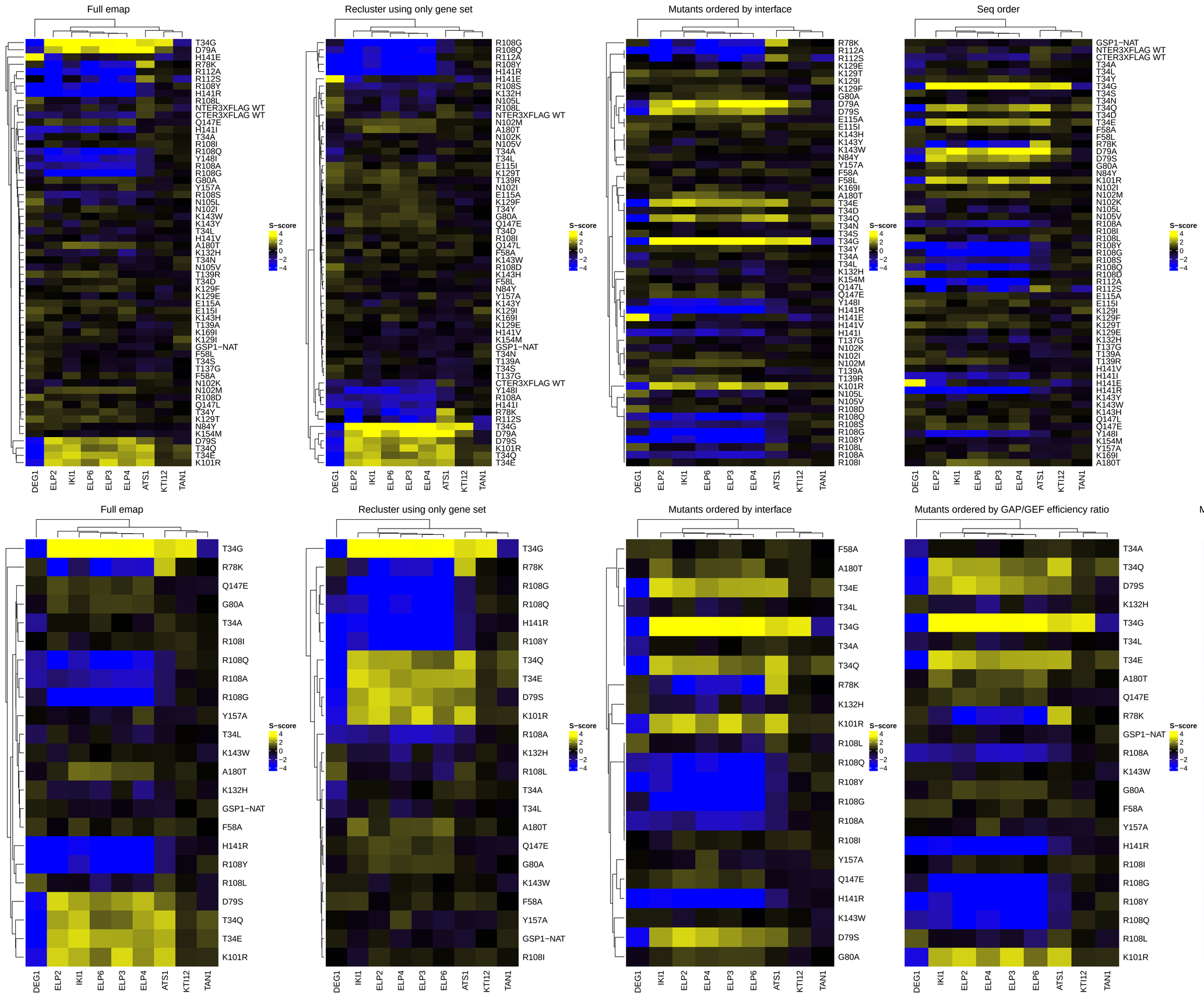


mitotic exit
tina hand−curated processes
clustering metric: euclidean

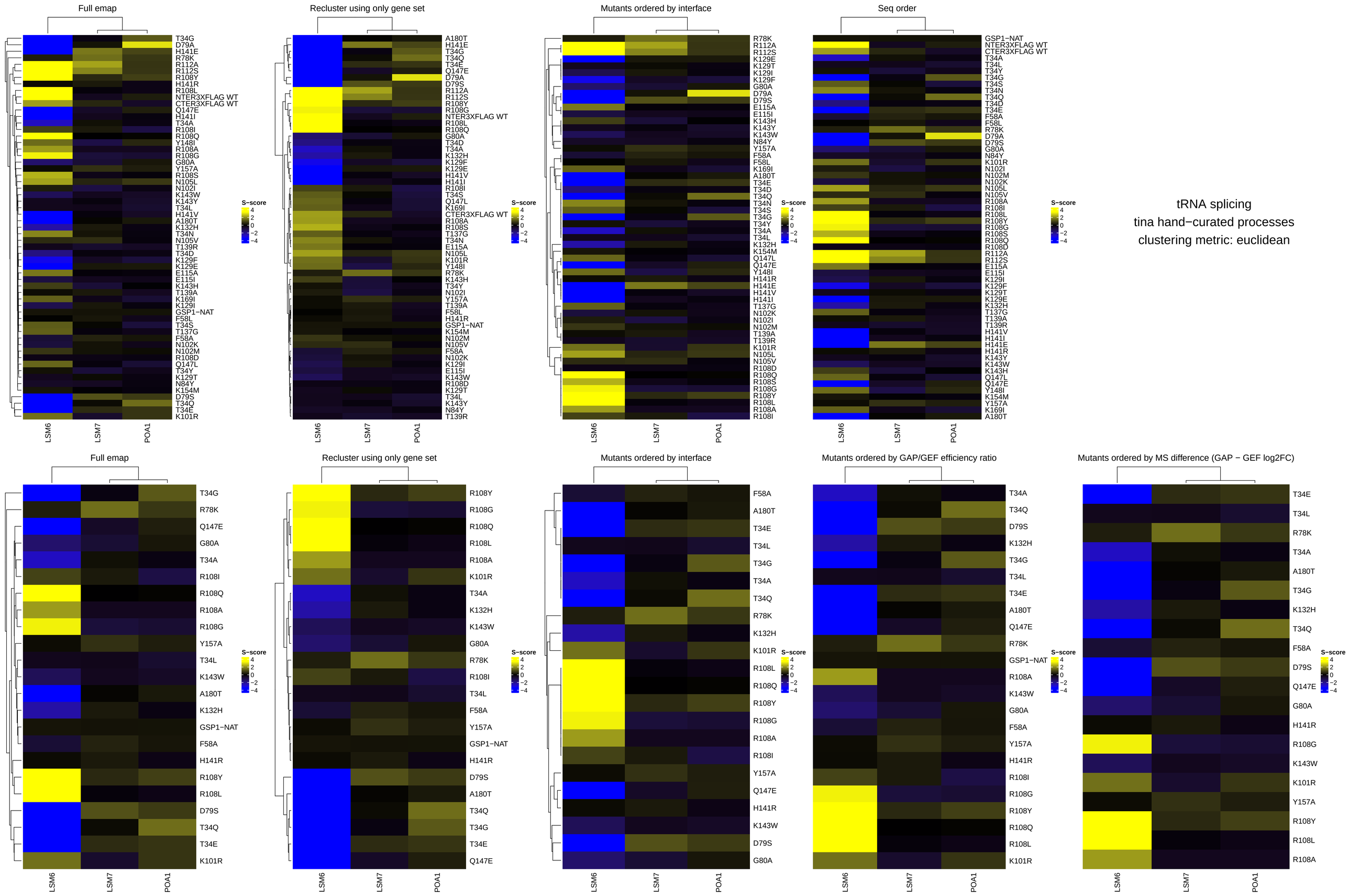


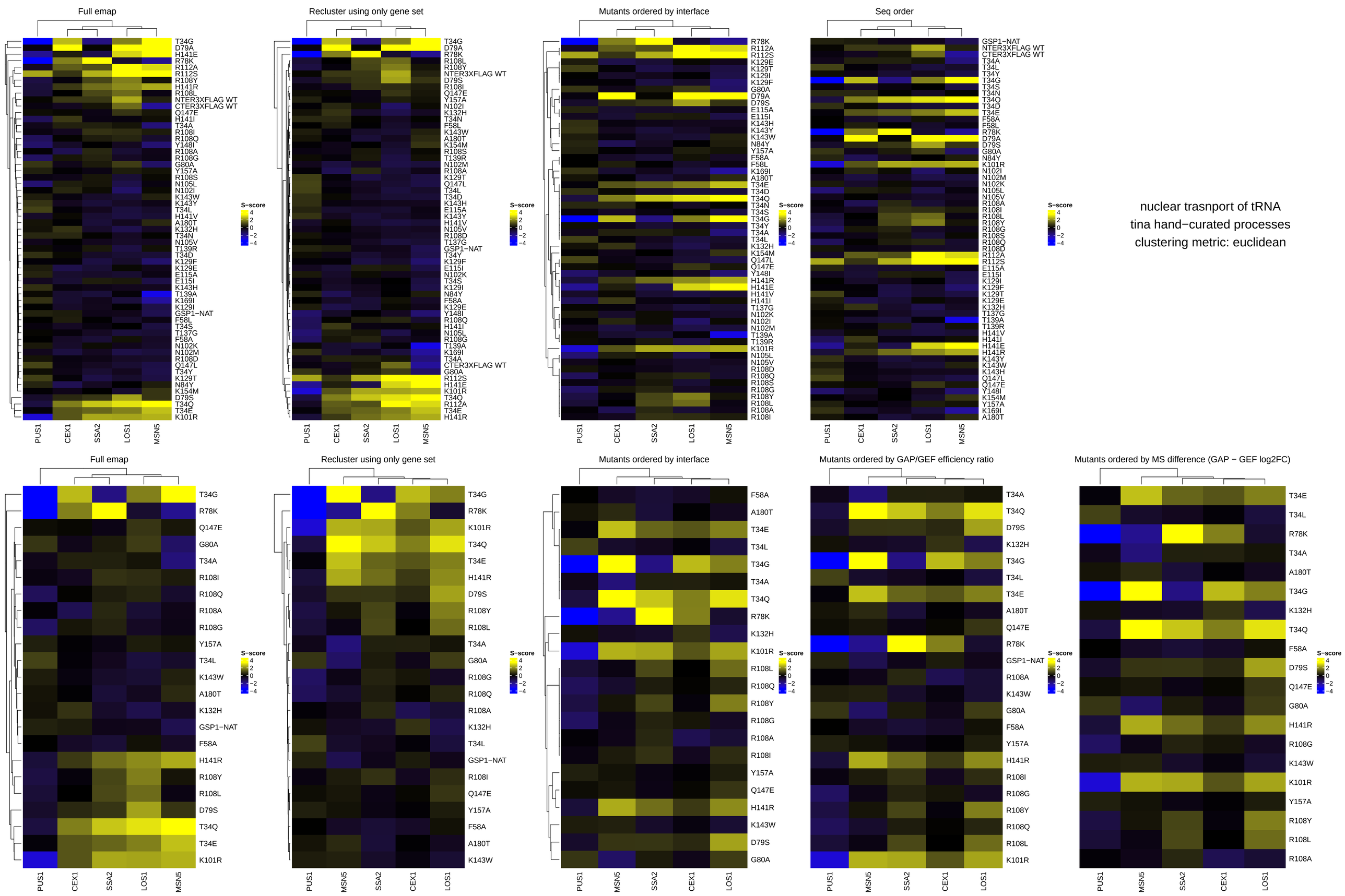

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
THP2
PUS1
CEX1
LOS1
MSN5
ARX1
SAC3
general nuclear export
tina hand−curated processes
clustering metric: euclidean

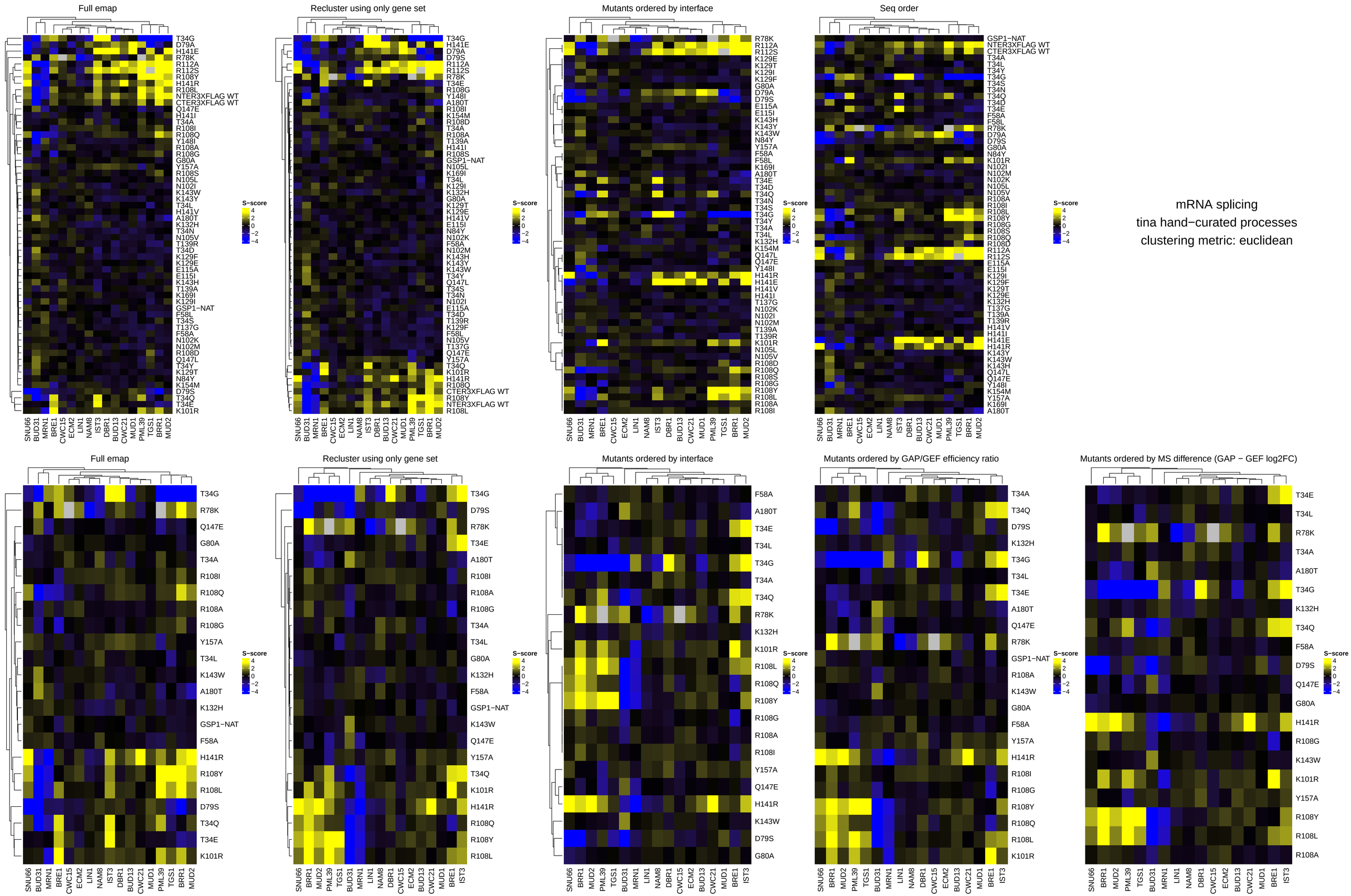

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ICE2
TRM1
NCL1
TRM10
TRM7
tRNA methyltransferase
tina hand−curated processes
clustering metric: euclidean

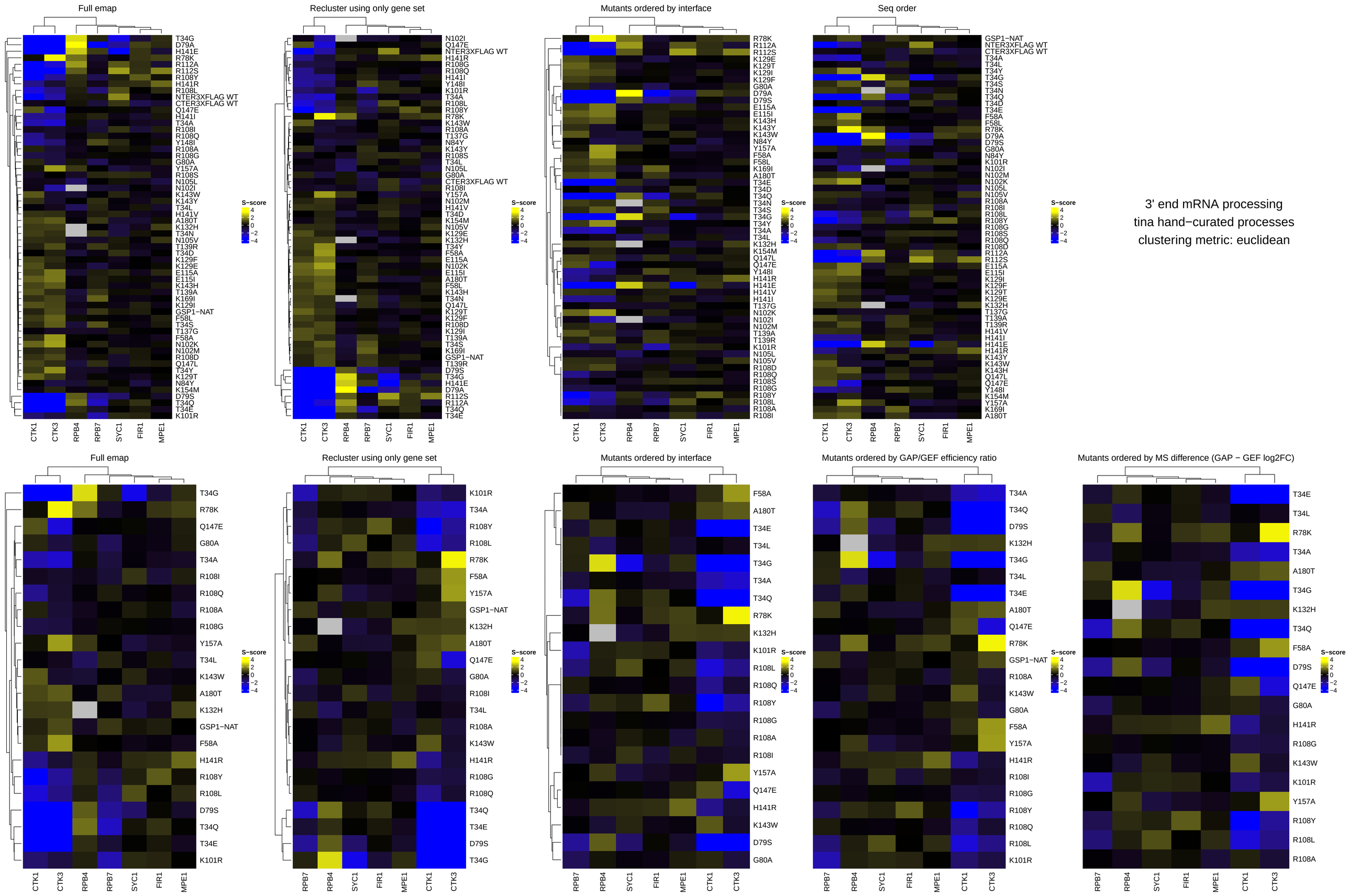


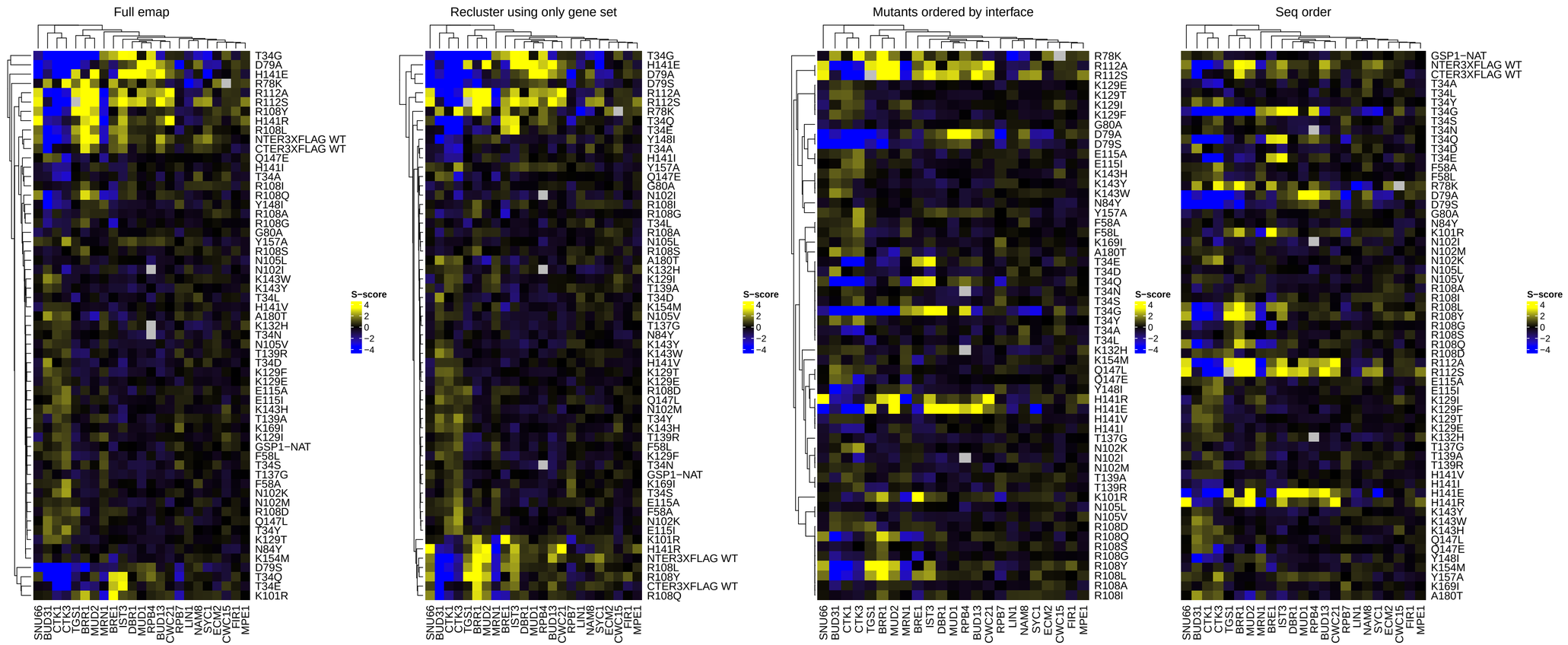
tRNA base modification
tina hand−curated processes
clustering metric: euclidean


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
4
2
0
−2
−4
LSM6
LSM7
POA1
tRNA splicing
tina hand−curated processes
clustering metric: euclidean

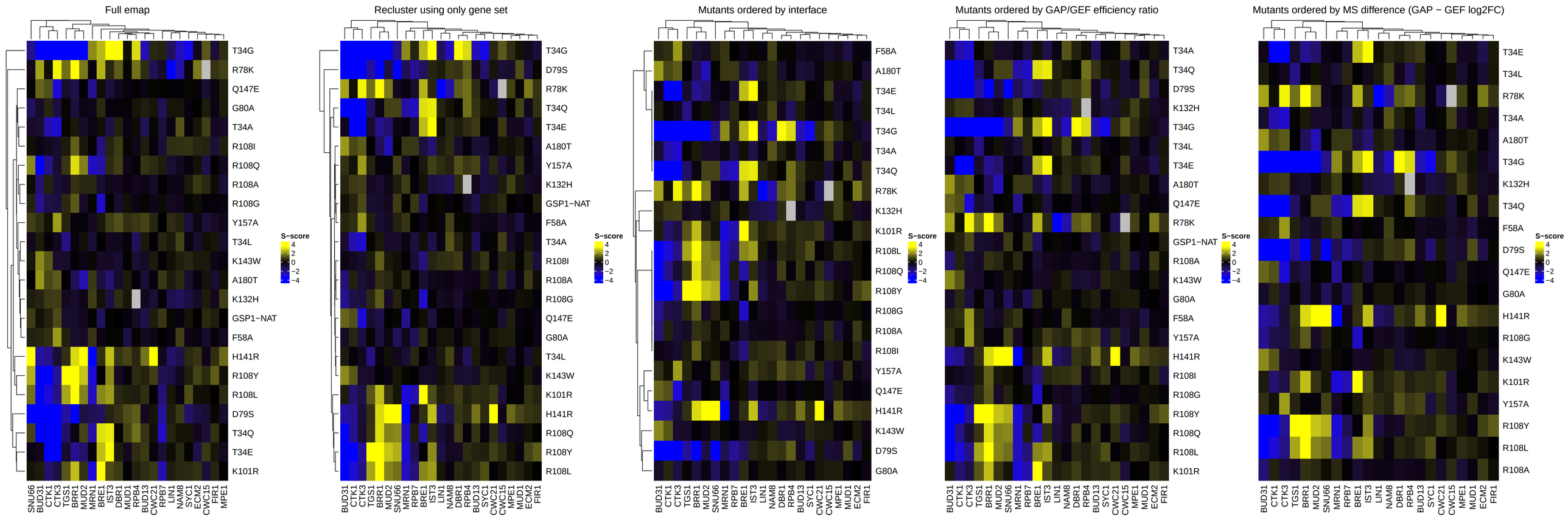

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PUS1
CEX1
SSA2
LOS1
MSN5
nuclear trasnport of tRNA
tina hand−curated processes
clustering metric: euclidean

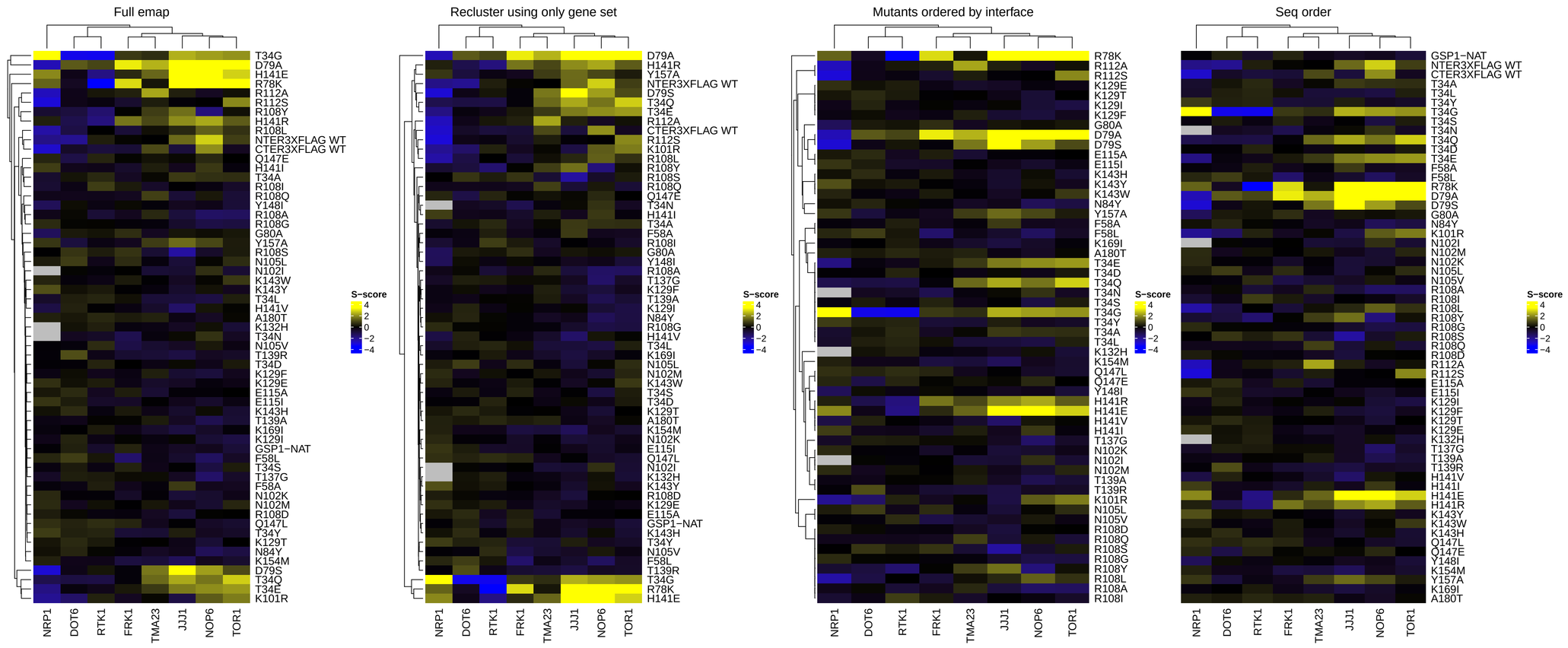

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
SNU66
BUD31
MRN1
BRE1
CWC15
ECM2
LIN1
NAM8
IST3
DBR1
BUD13
CWC21
MUD1
PML39
TGS1
BRR1
MUD2
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
mRNA splicing
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
4
2
0
−2
−4
CTK1
CTK3
RPB4
RPB7
SYC1
FIR1
MPE1
3' end mRNA processing
tina hand−curated processes
clustering metric: euclidean

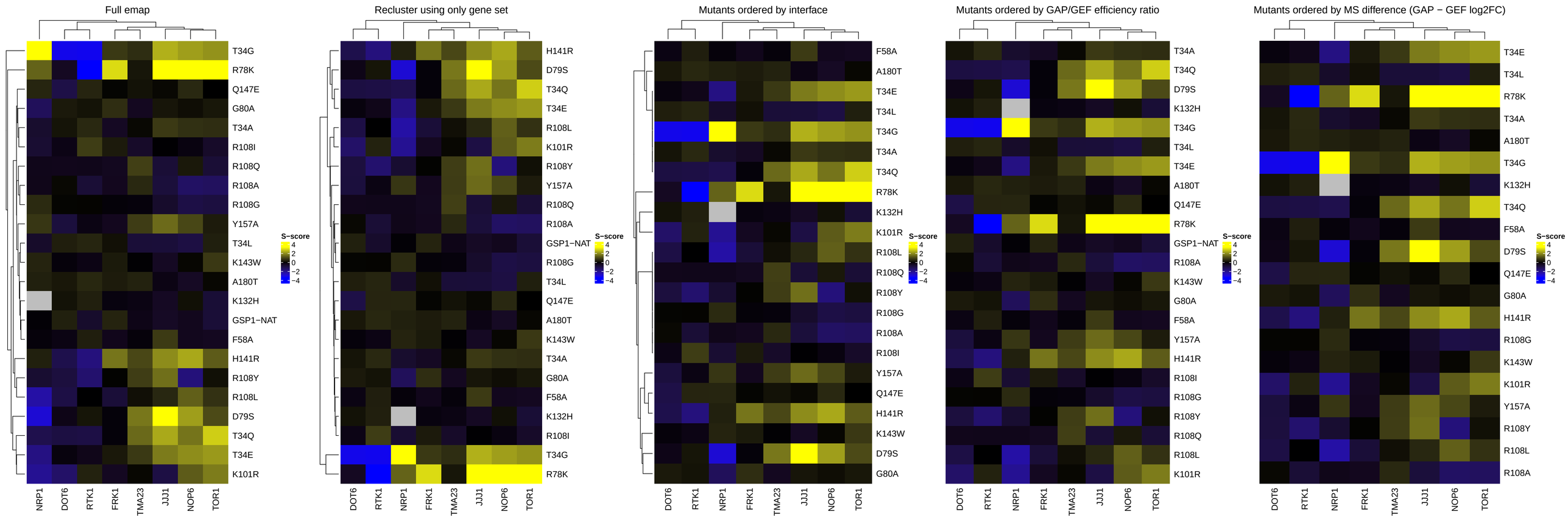


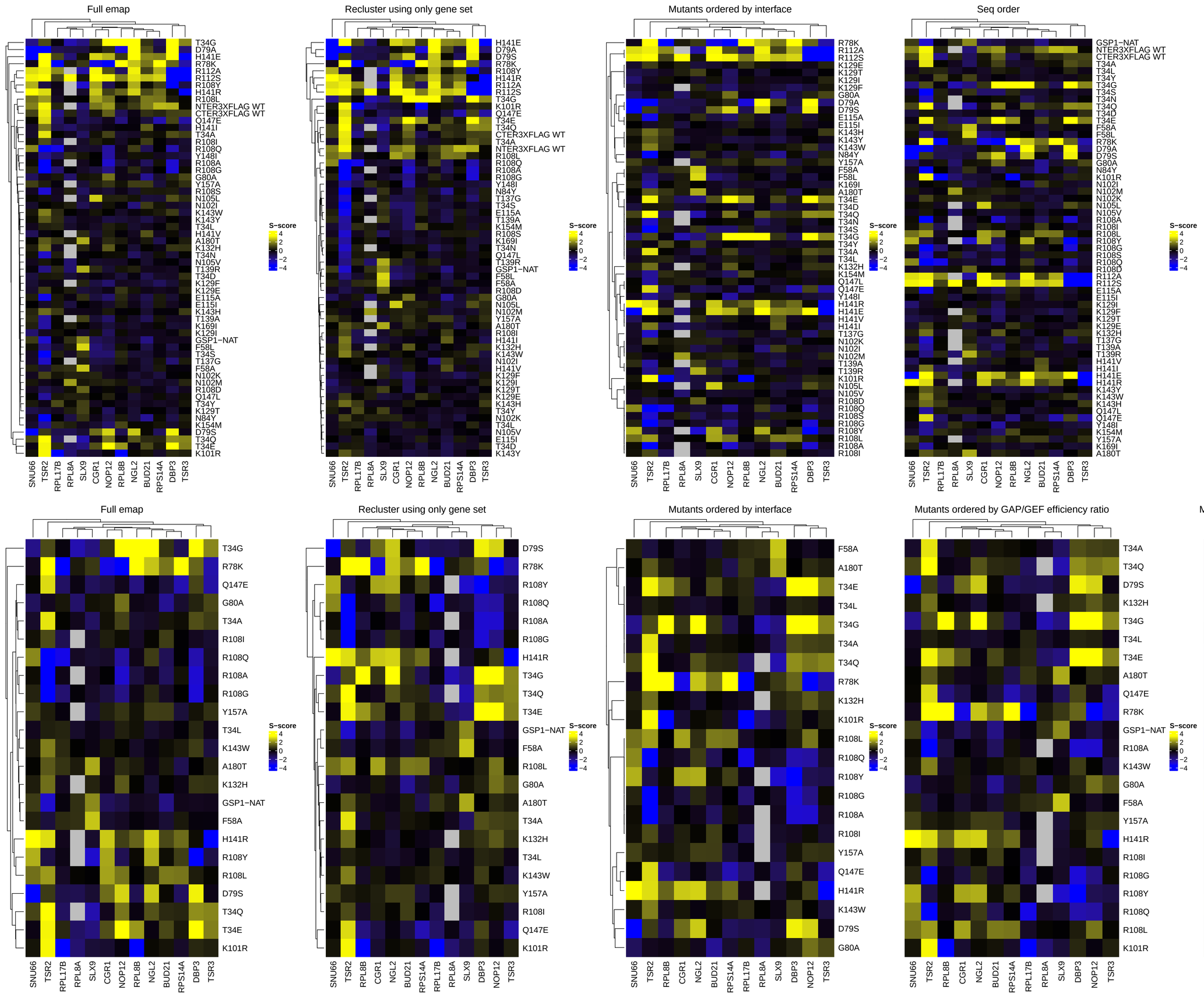
mRNA maturation
tina hand−curated processes
clustering metric: euclidean



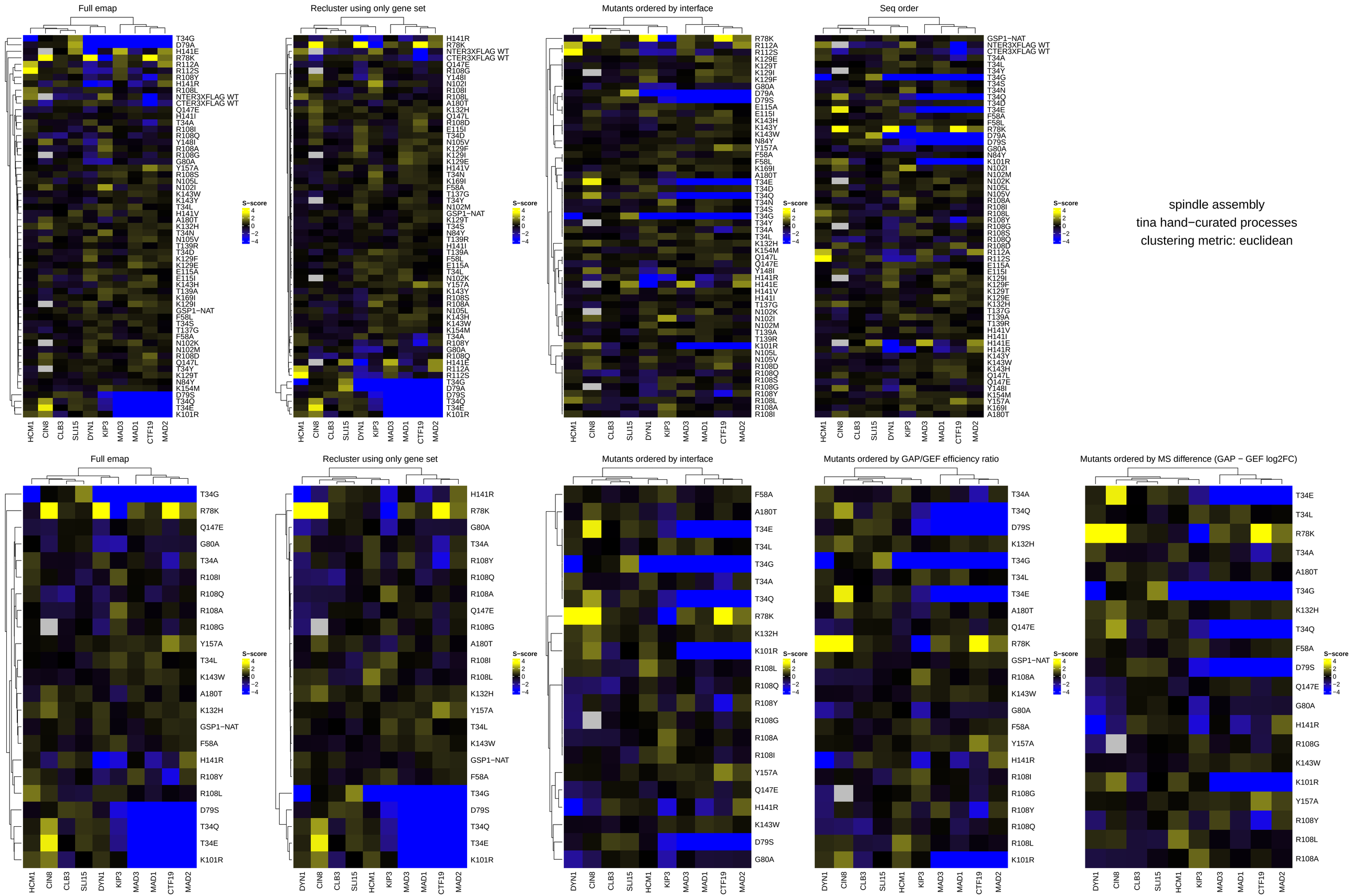


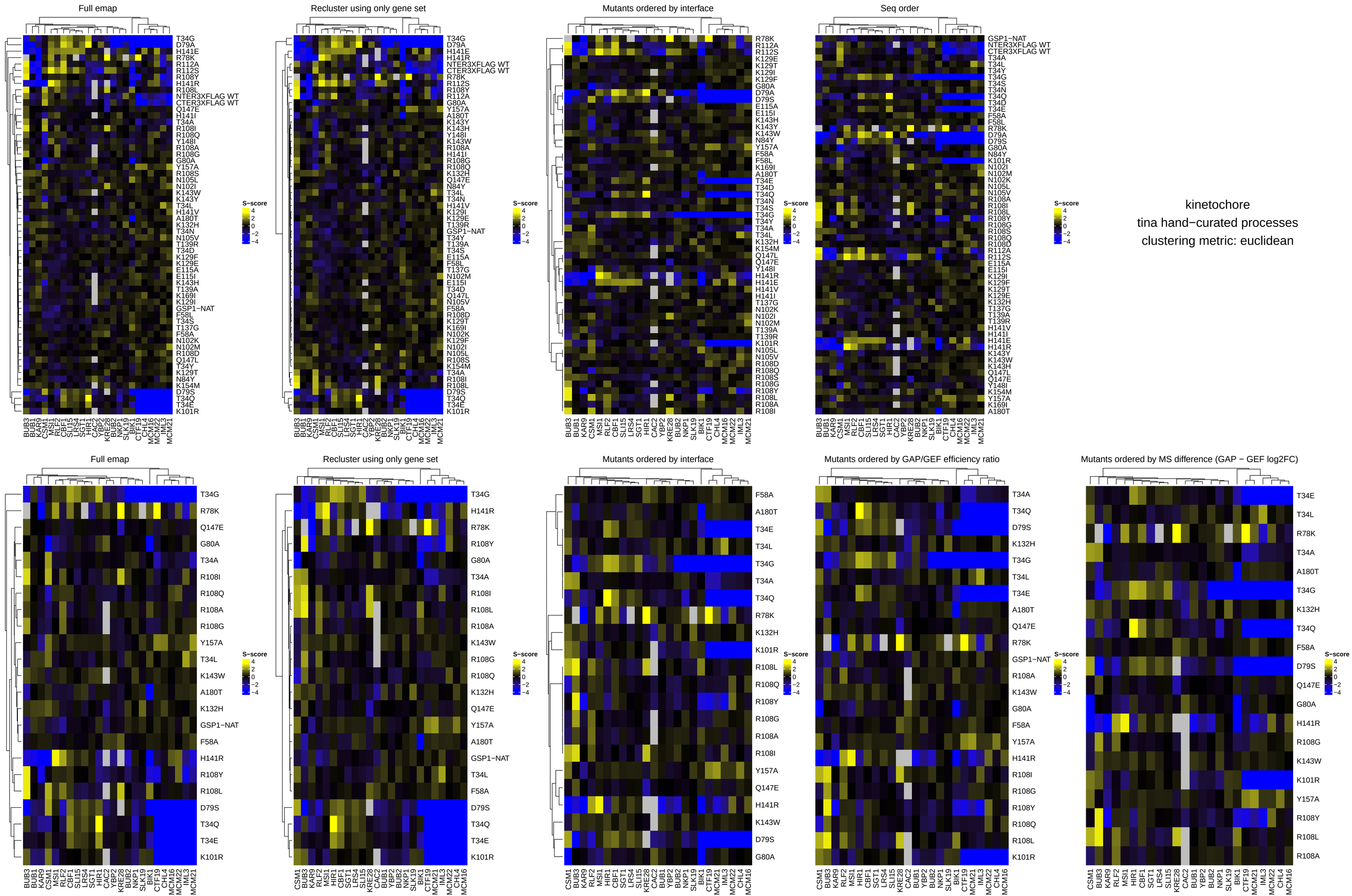
ribosome biogenesis
tina hand−curated processes
clustering metric: euclidean

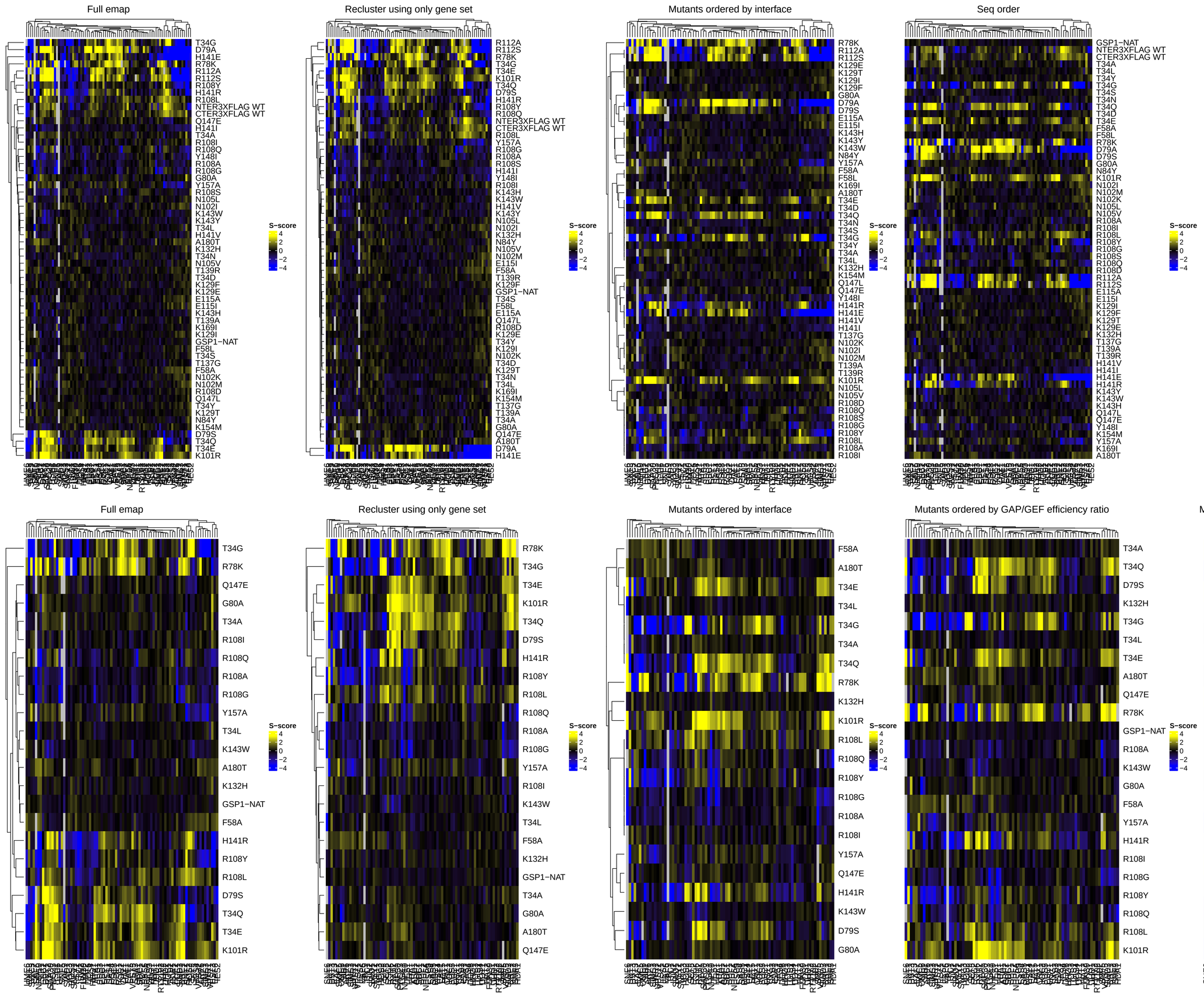




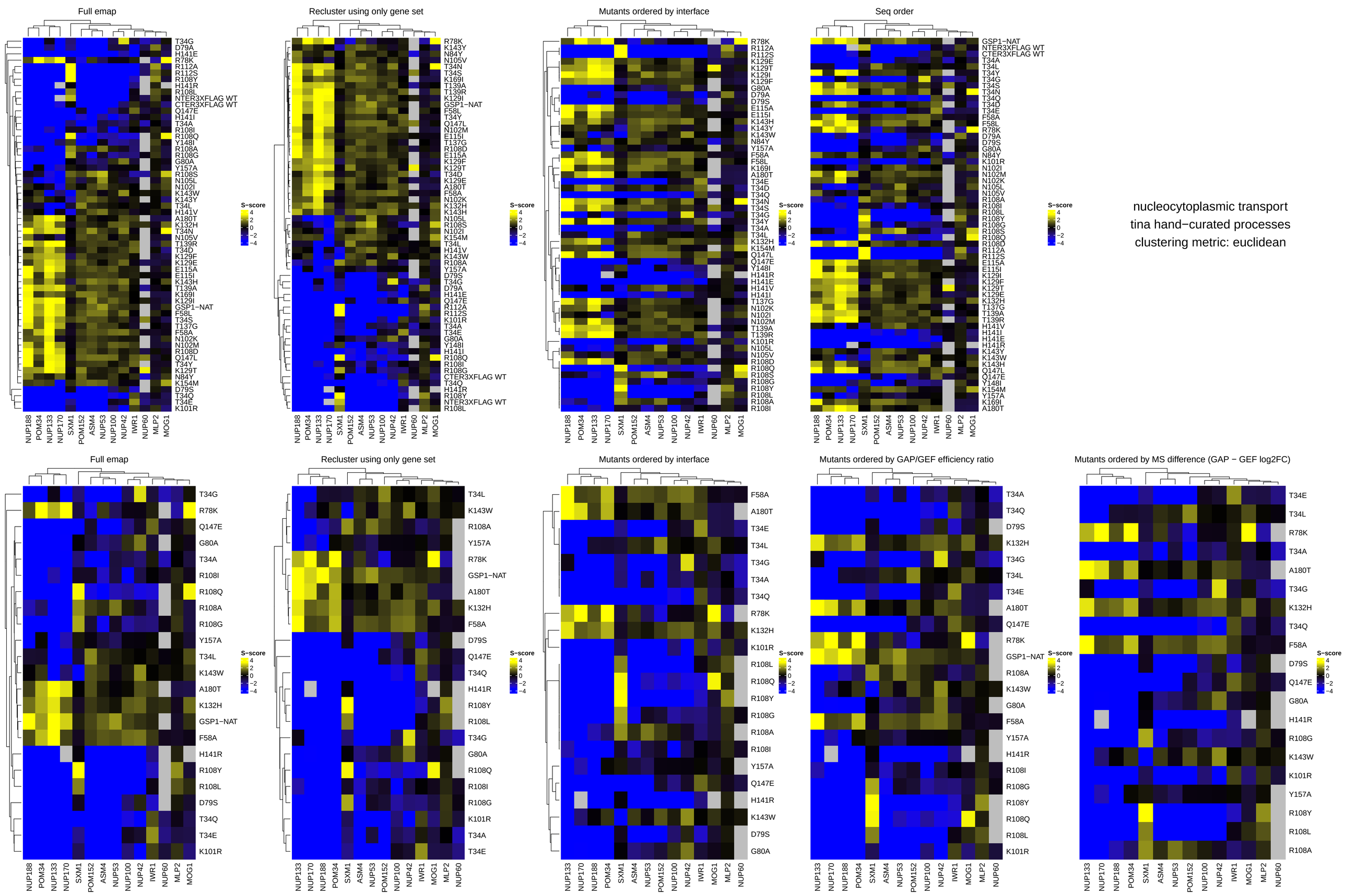
rRNA processing
tina hand−curated processes
clustering metric: euclidean


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
4
2
0
−2
−4
HCM1
CIN8
CLB3
SLI15
DYN1
KIP3
MAD3
MAD1
CTF19
MAD2
spindle assembly
tina hand−curated processes
clustering metric: euclidean

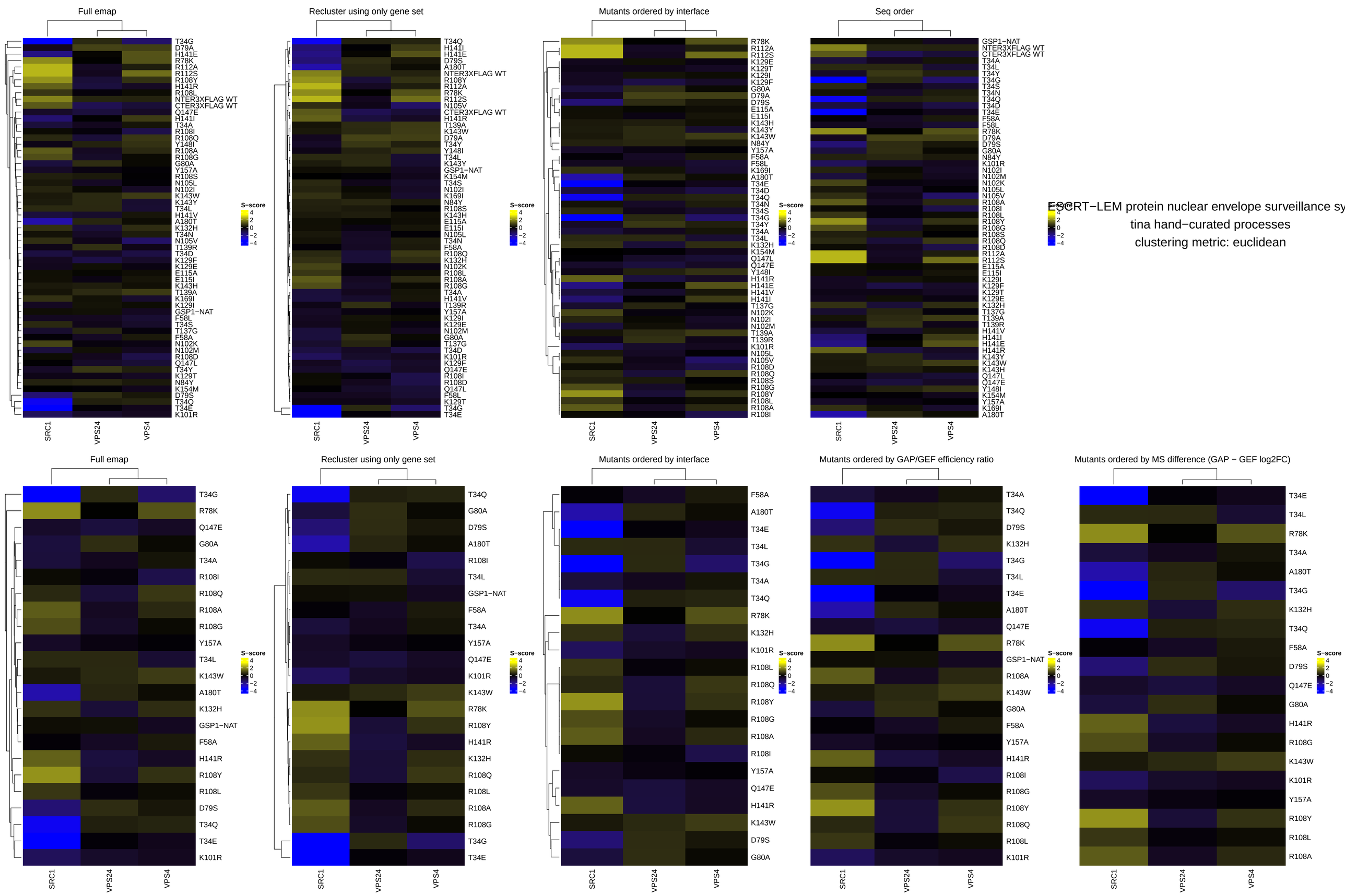

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
kinetochore
tina hand−curated processes
clustering metric: euclidean

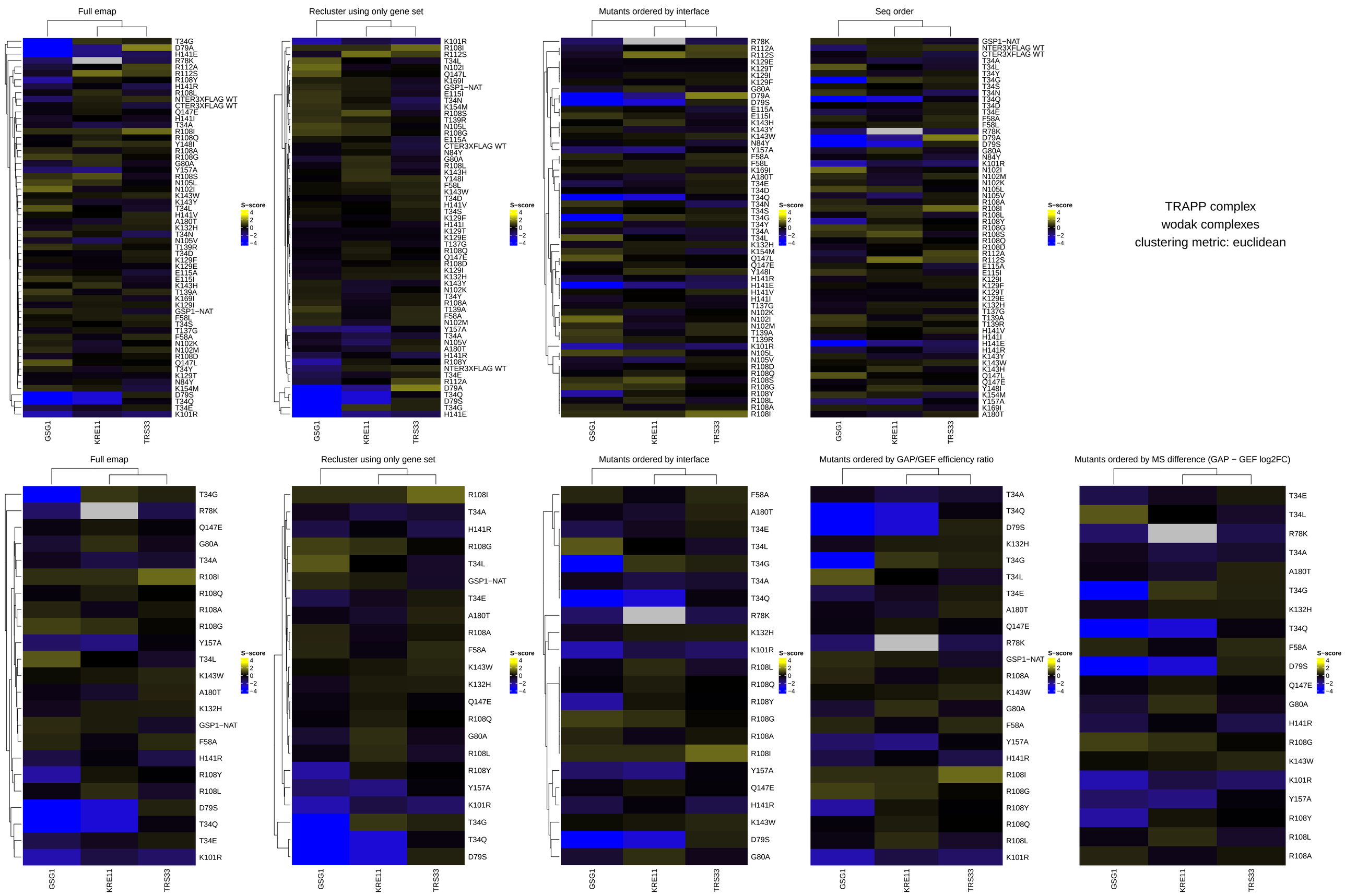


chromatin remodeling
tina hand−curated processes
clustering metric: euclidean

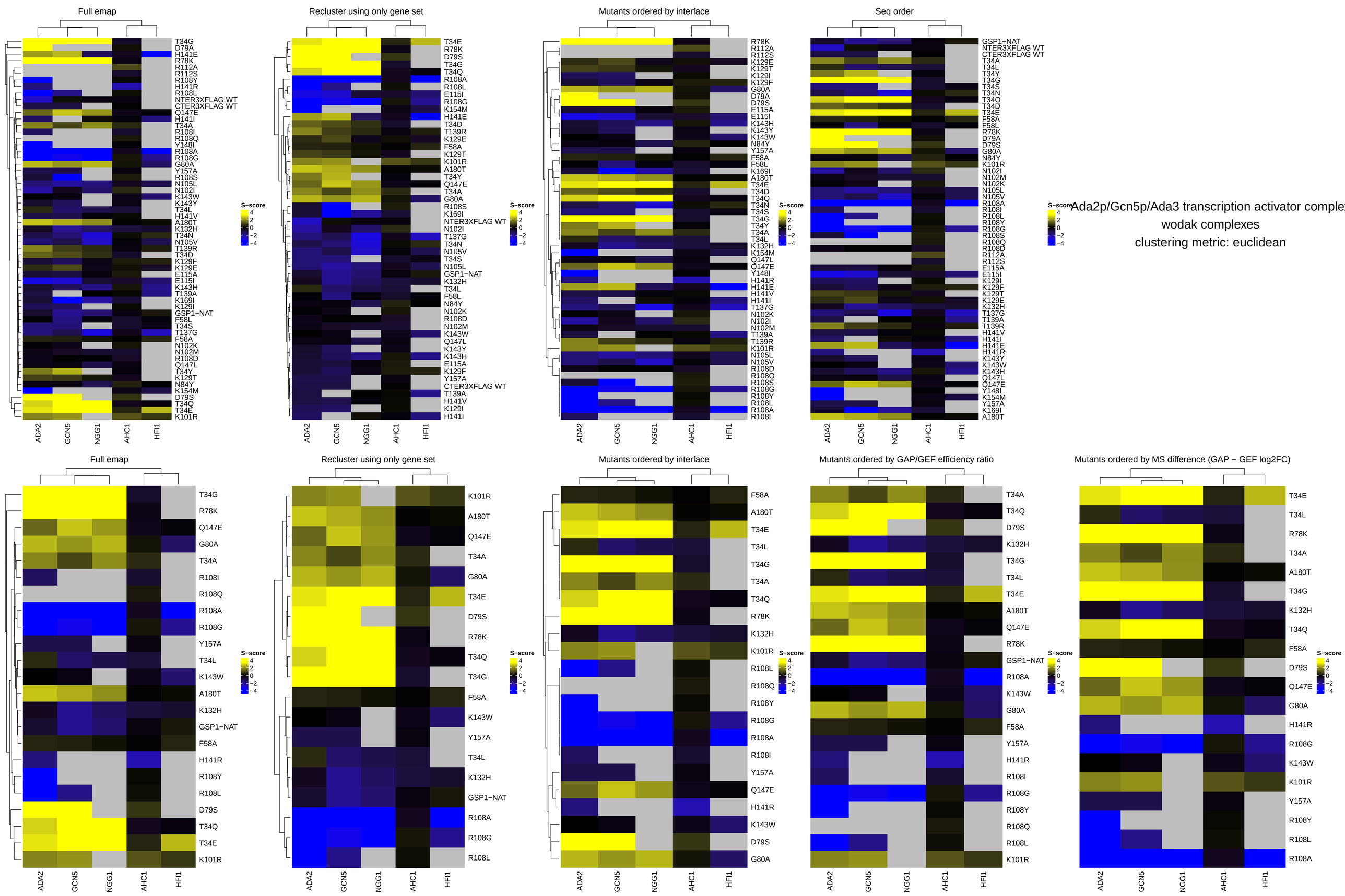


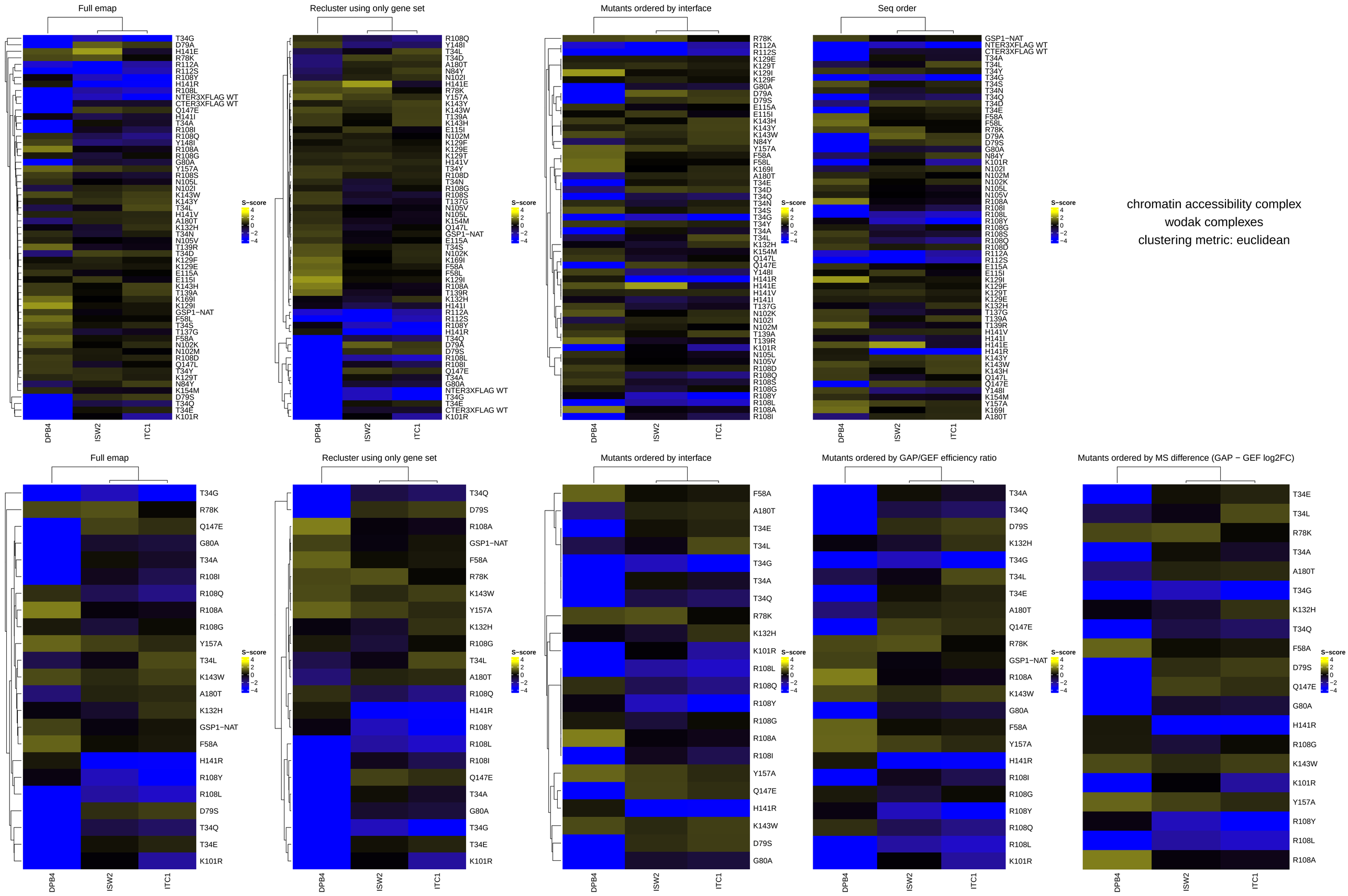
nucleocytoplasmic transport
tina hand−curated processes
clustering metric: euclidean

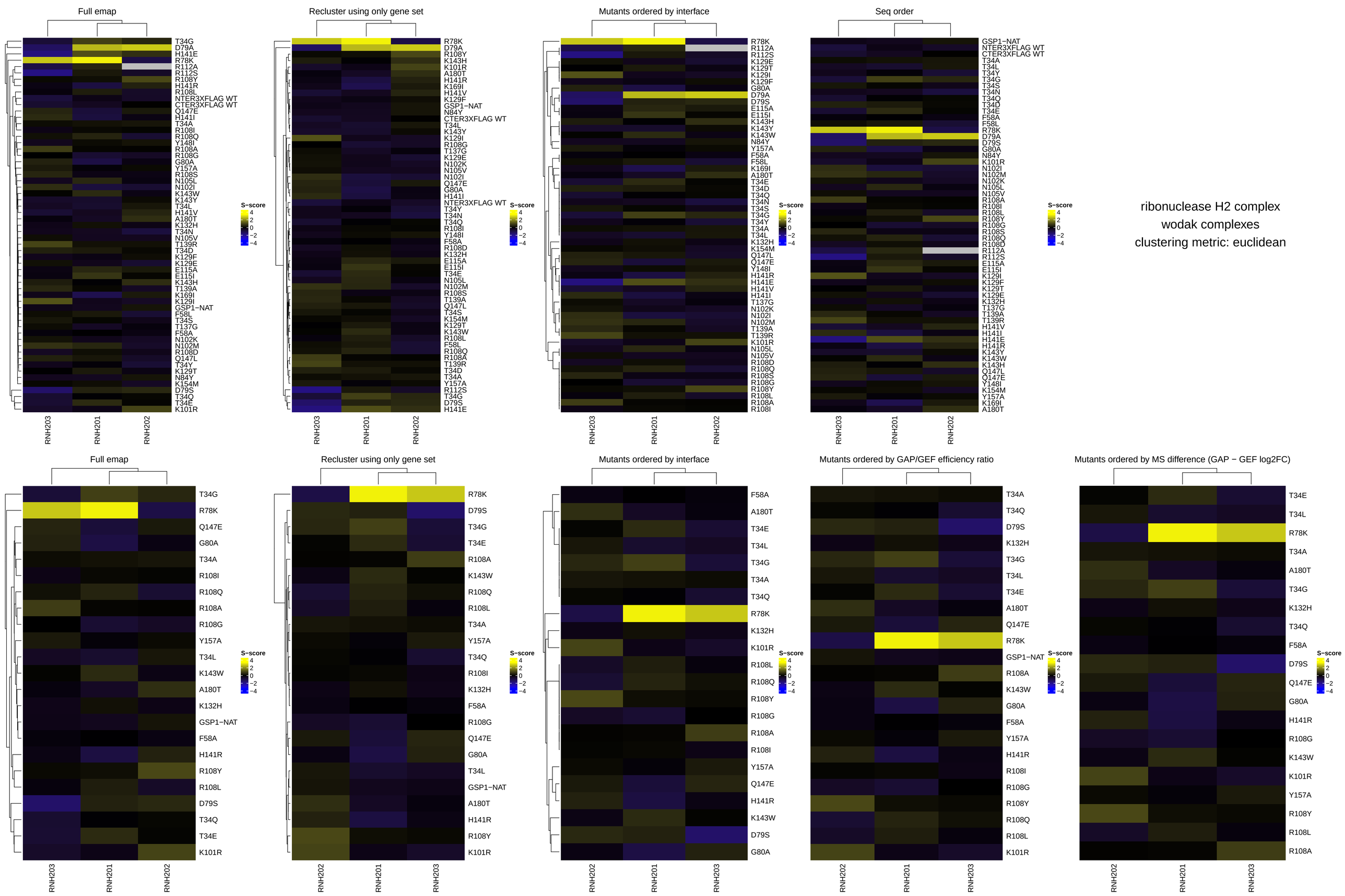

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
ESCRT−LEM protein nuclear envelope surveillance sy
tina hand−curated processes
clustering metric: euclidean
S−score
4
2
0
−2
−4
SRC1
VPS24
VPS4
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

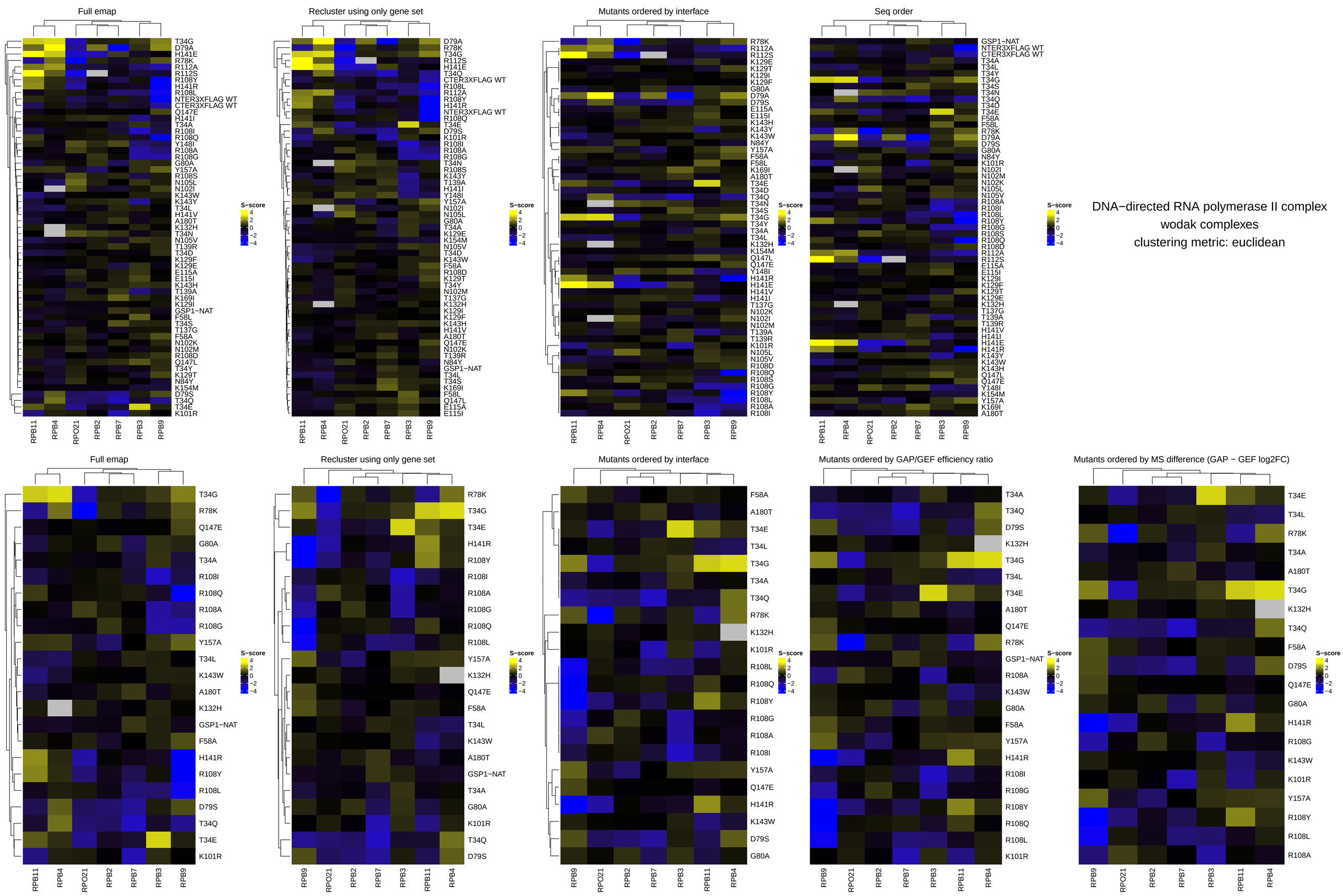


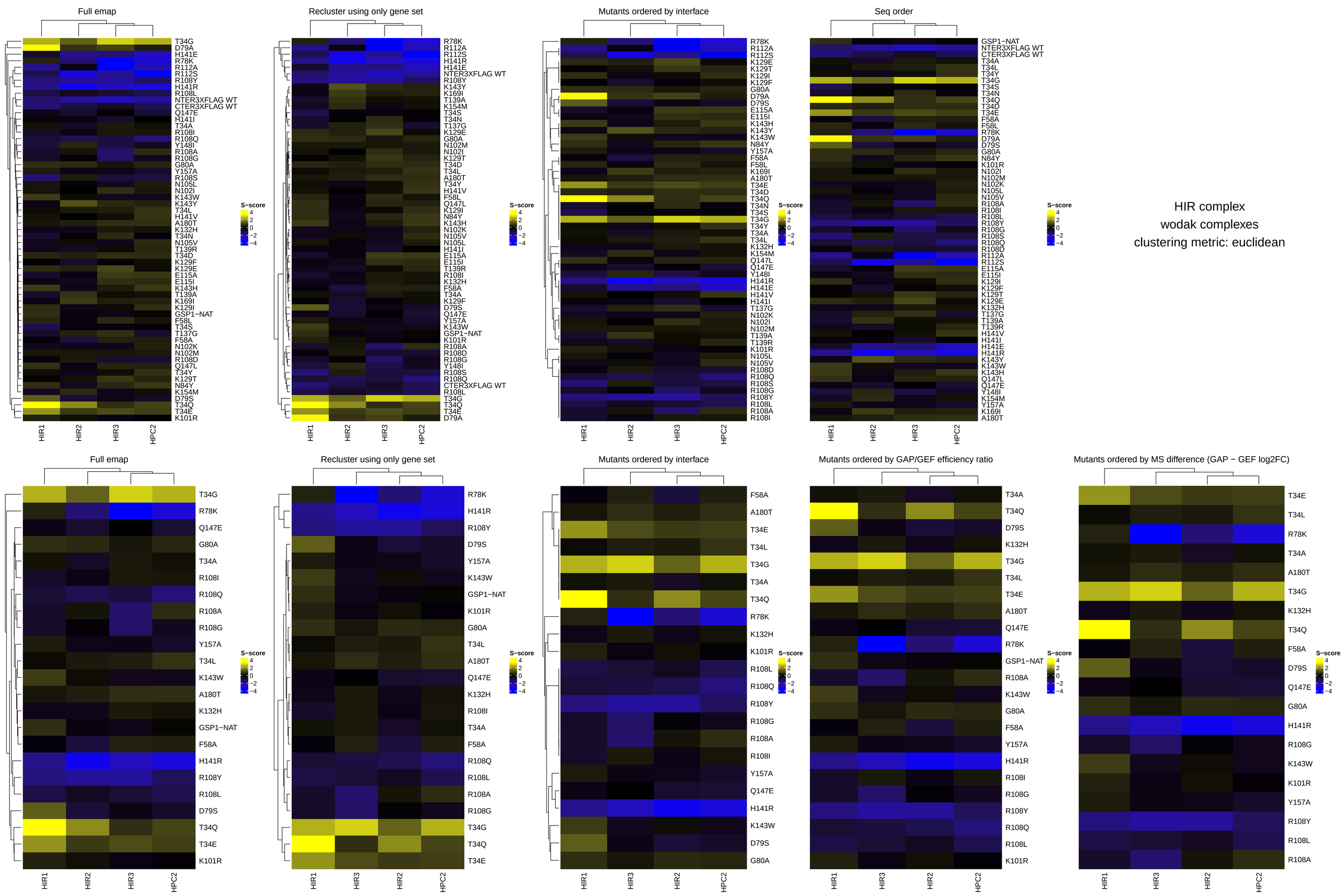
TRAPP complex
wodak complexes
clustering metric: euclidean

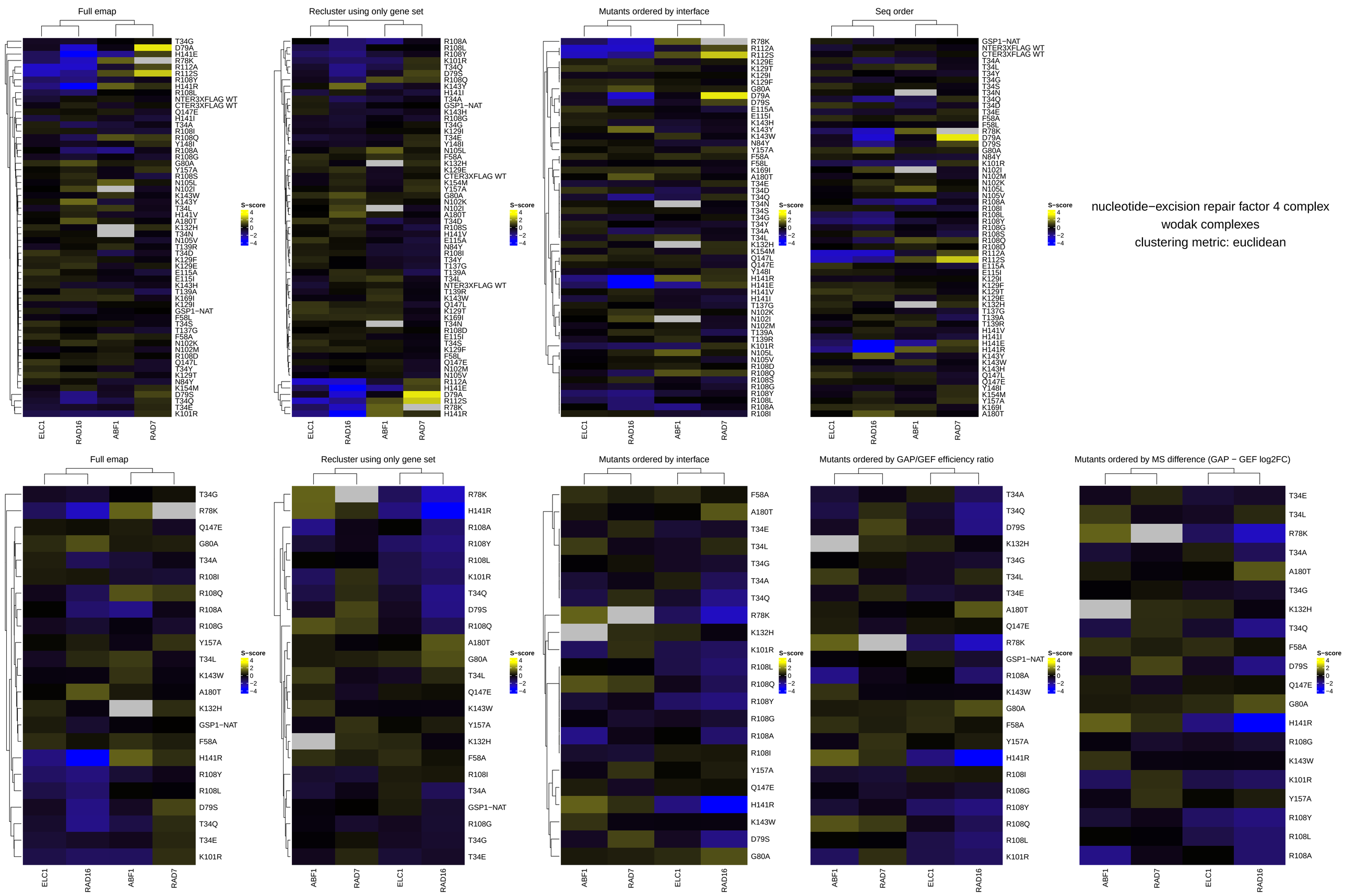

Ada2p/Gcn5p/Ada3 transcription activator complex
wodak complexes
clustering metric: euclidean
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ADA2
GCN5
NGG1
AHC1
HFI1

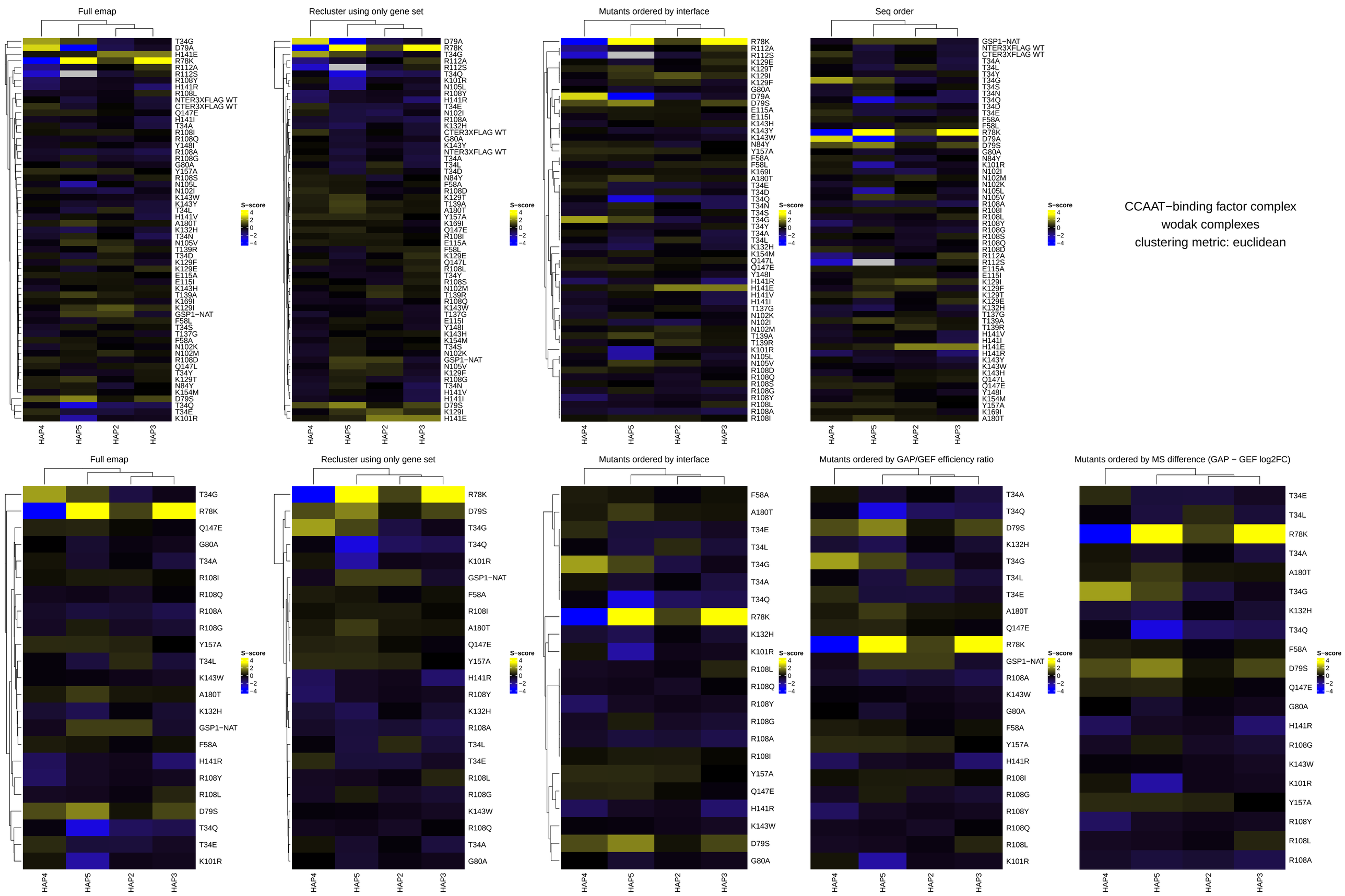

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
DPB4
ISW2
ITC1
chromatin accessibility complex
wodak complexes
clustering metric: euclidean

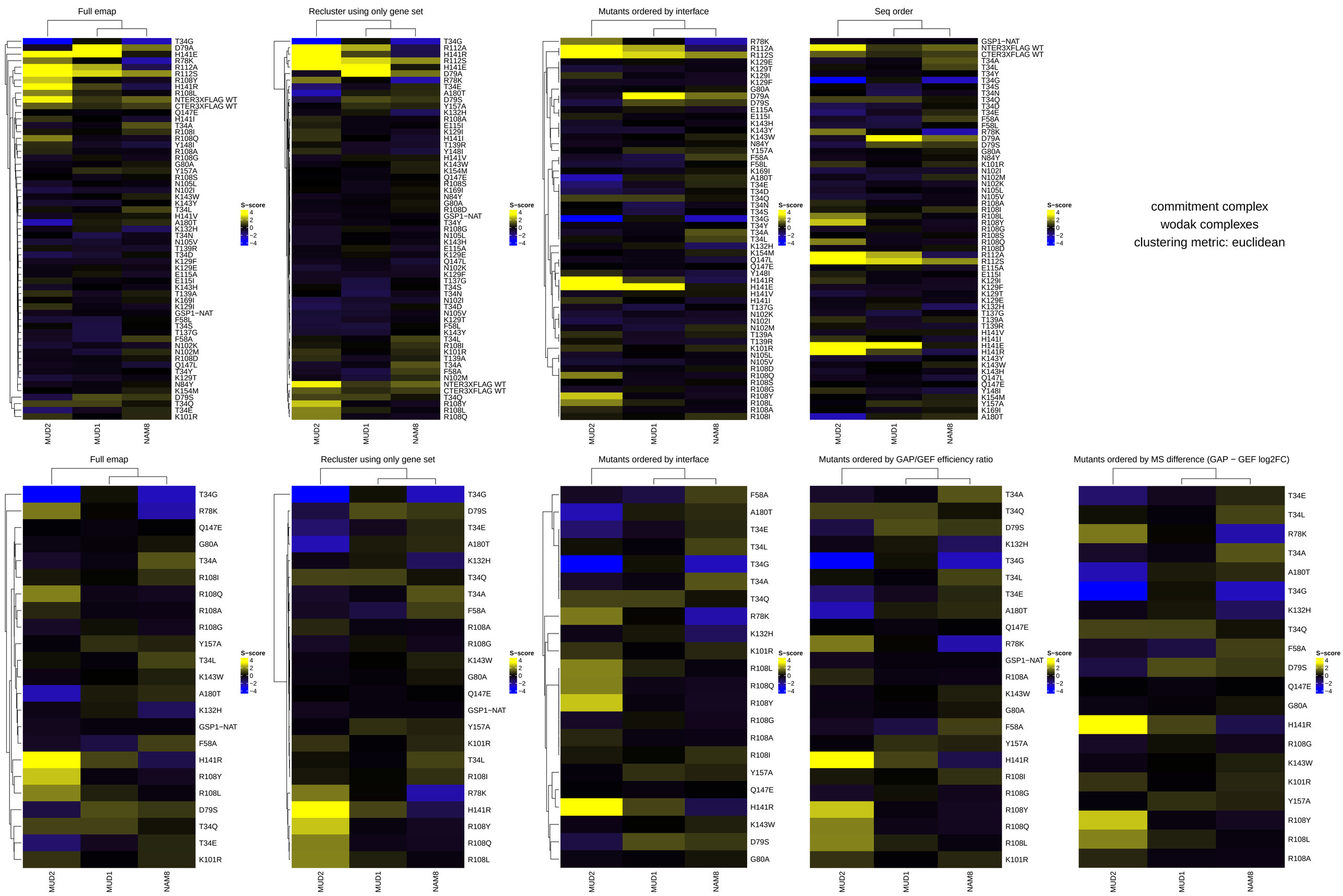

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RNH203
RNH201
RNH202
ribonuclease H2 complex
wodak complexes
clustering metric: euclidean

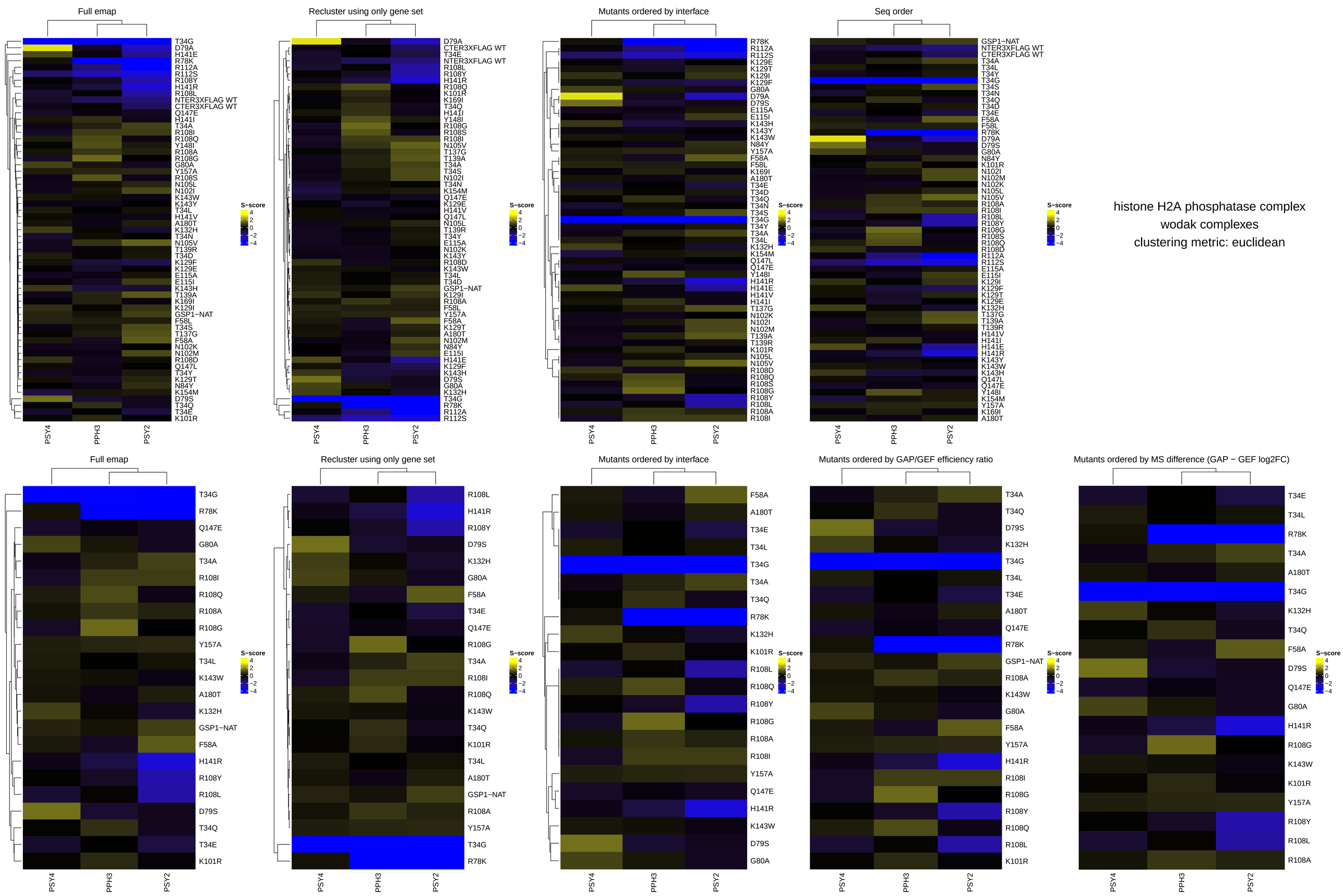

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
RPB11
RPB4
RPO21
RPB2
RPB7
RPB3
RPB9
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
DNA−directed RNA polymerase II complex
wodak complexes
clustering metric: euclidean

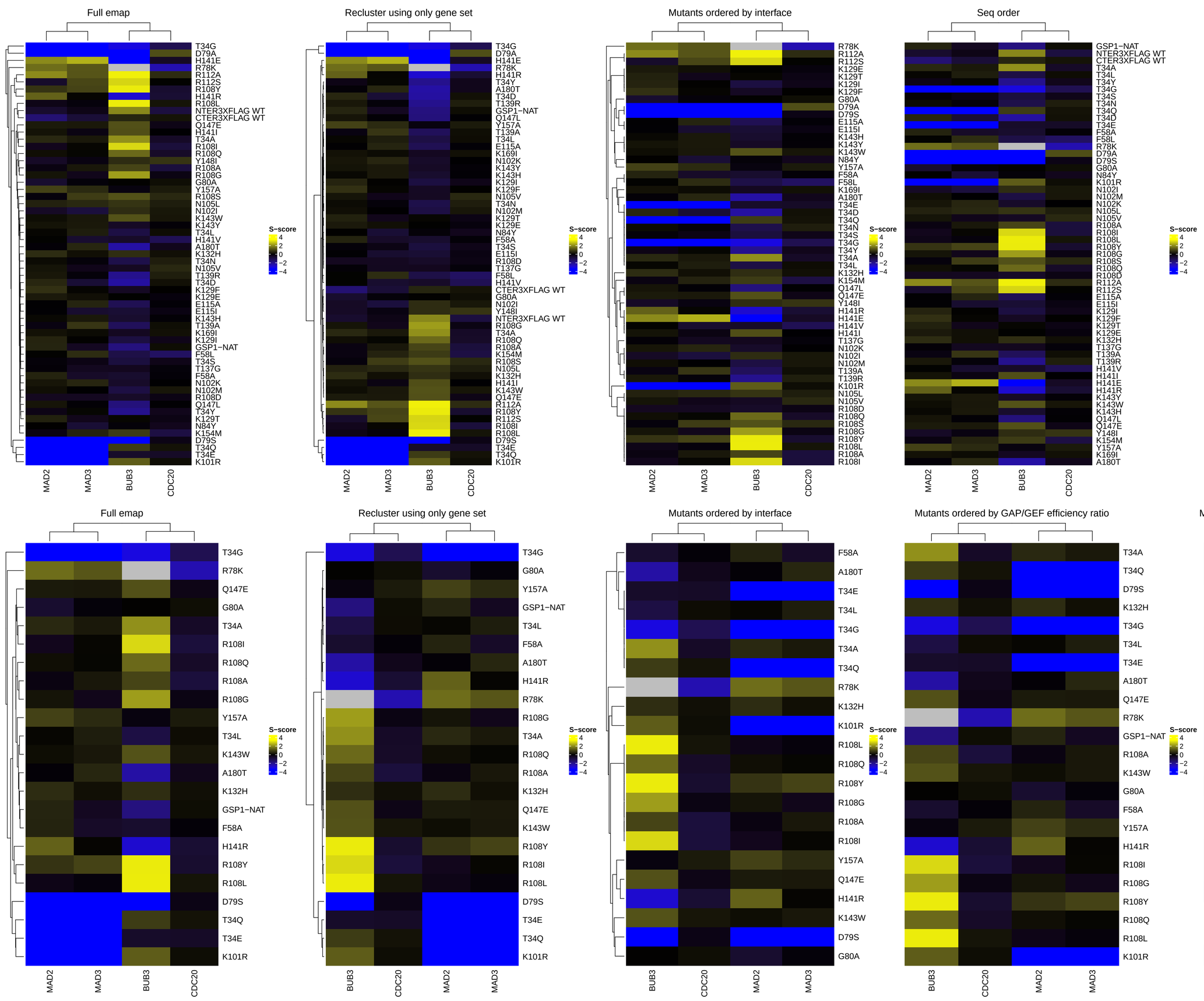

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HIR1
HIR2
HIR3
HPC2
HIR complex
wodak complexes
clustering metric: euclidean


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
4
2
0
−2
−4
ELC1
RAD16
ABF1
RAD7
nucleotide−excision repair factor 4 complex
wodak complexes
clustering metric: euclidean

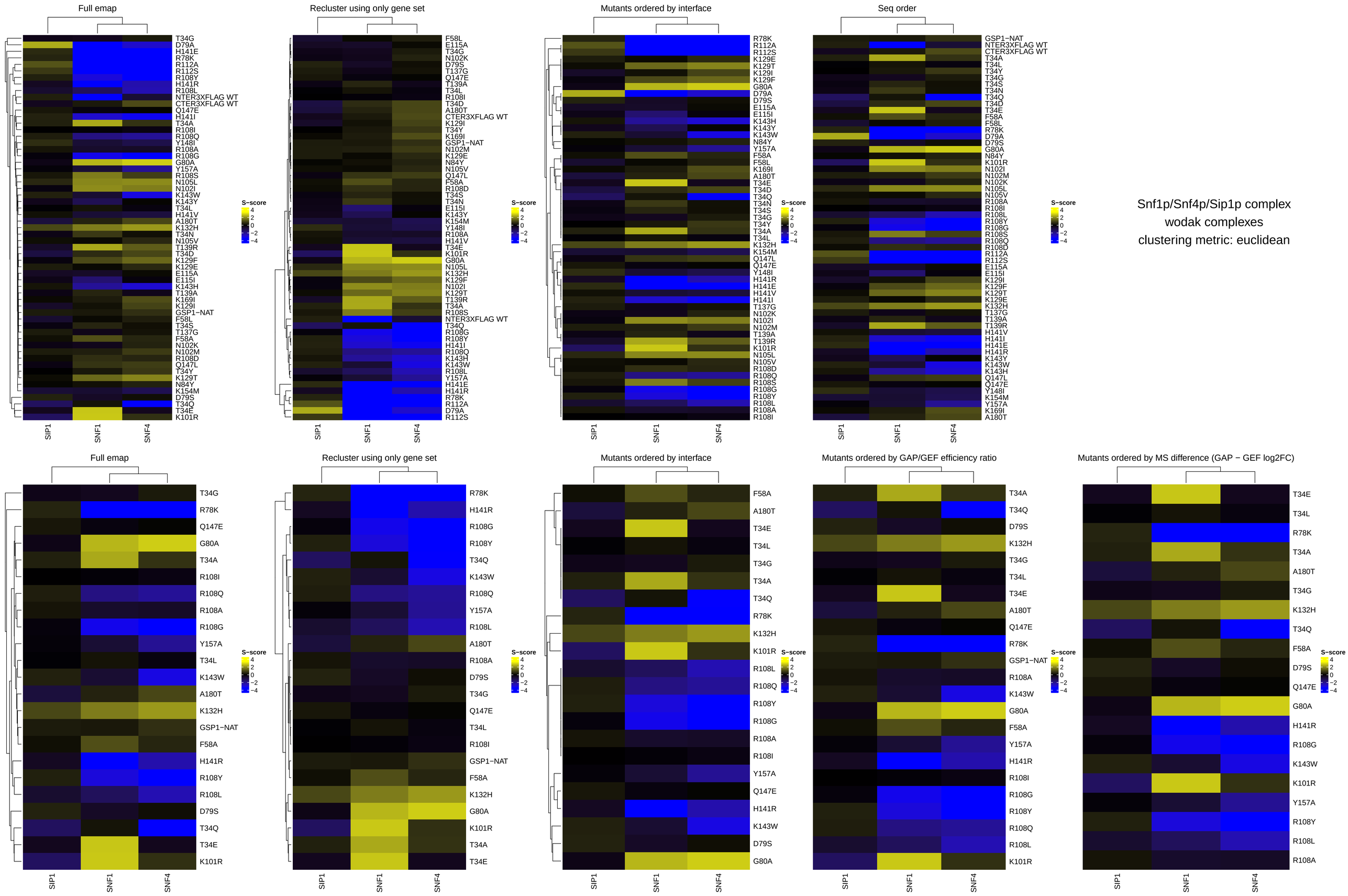

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HAP4
HAP5
HAP2
HAP3
CCAAT−binding factor complex
wodak complexes
clustering metric: euclidean

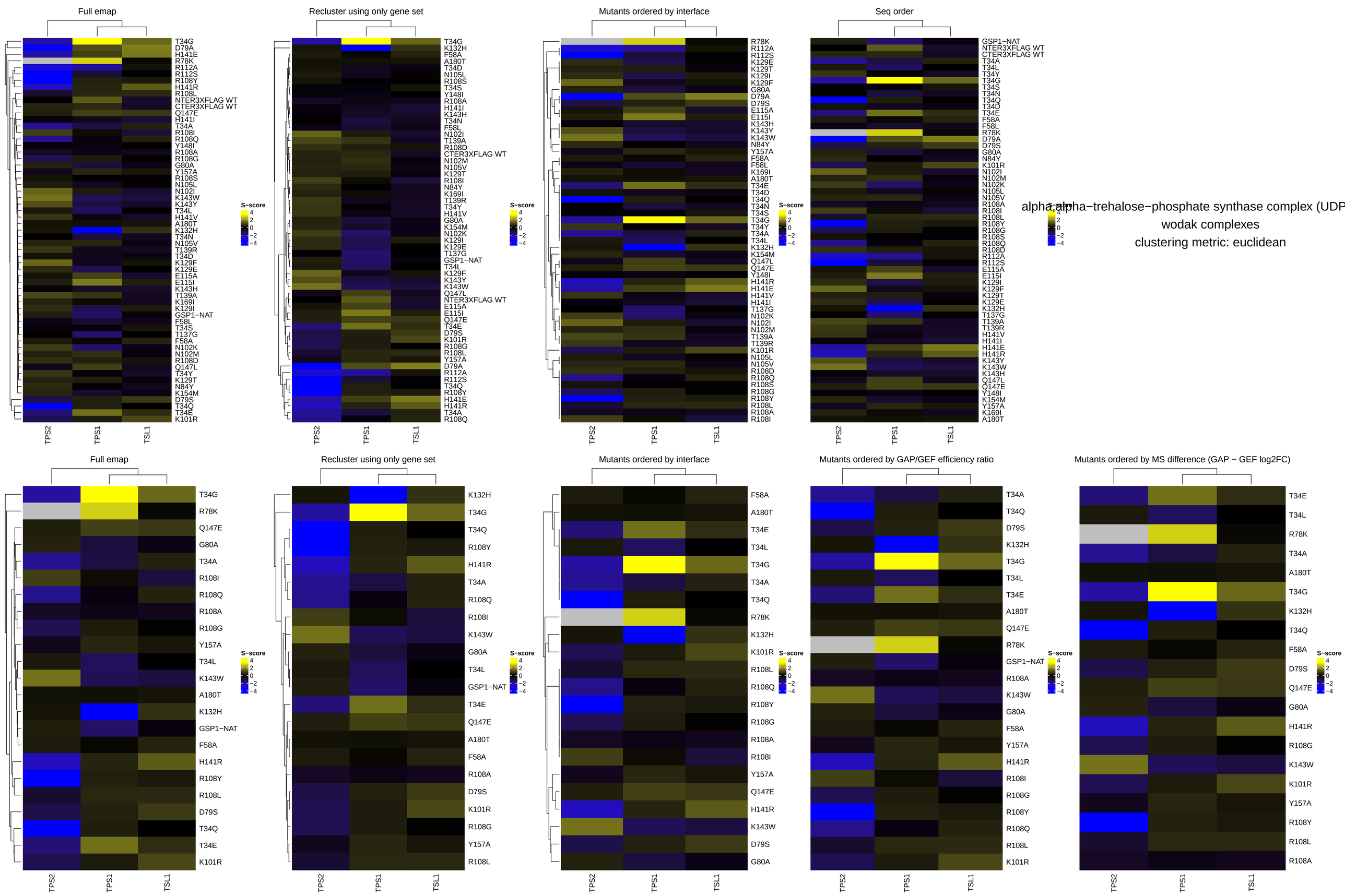

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
MUD2
MUD1
NAM8
commitment complex
wodak complexes
clustering metric: euclidean

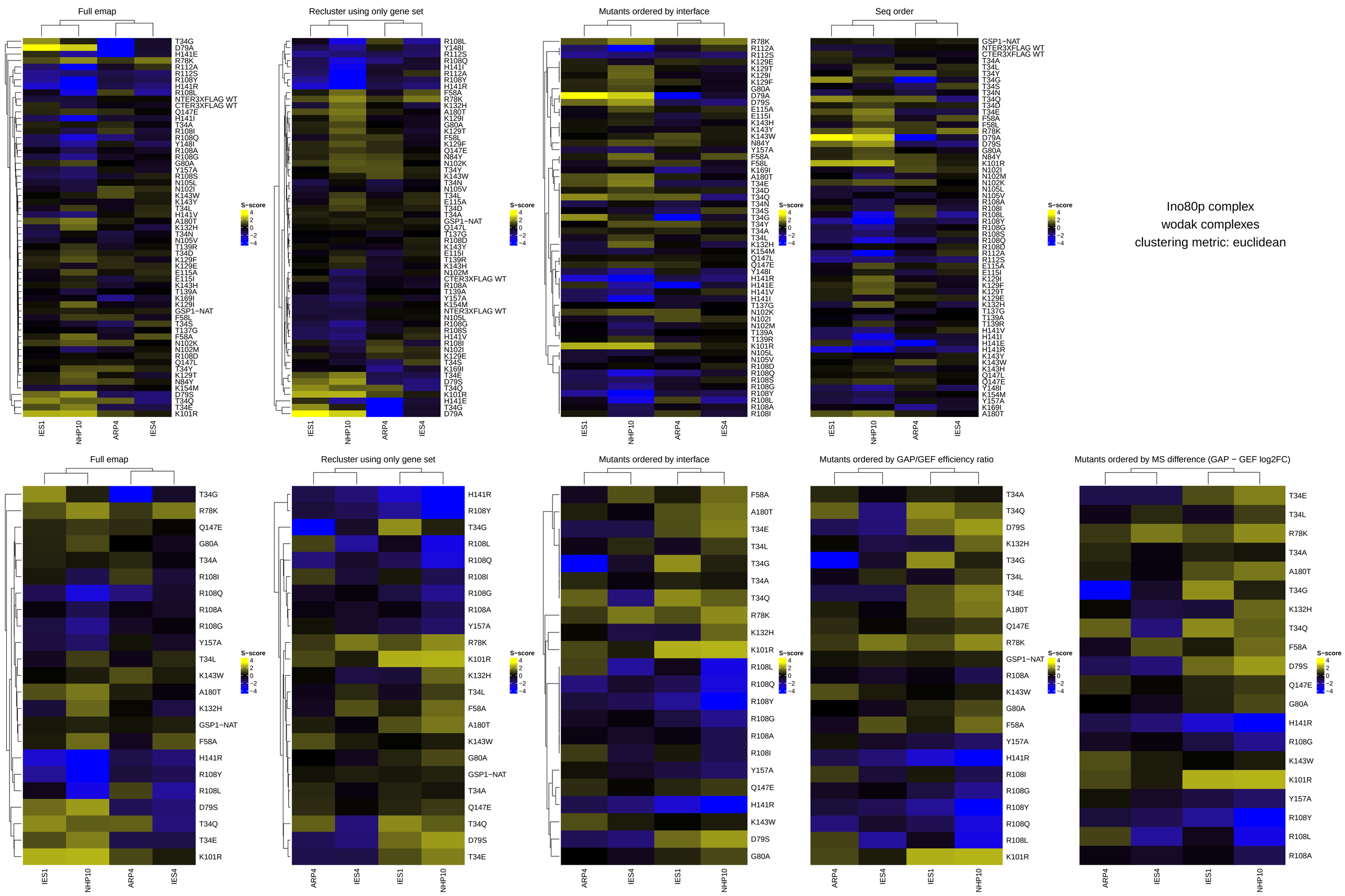

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PSY4
PPH3
PSY2
histone H2A phosphatase complex
wodak complexes
clustering metric: euclidean

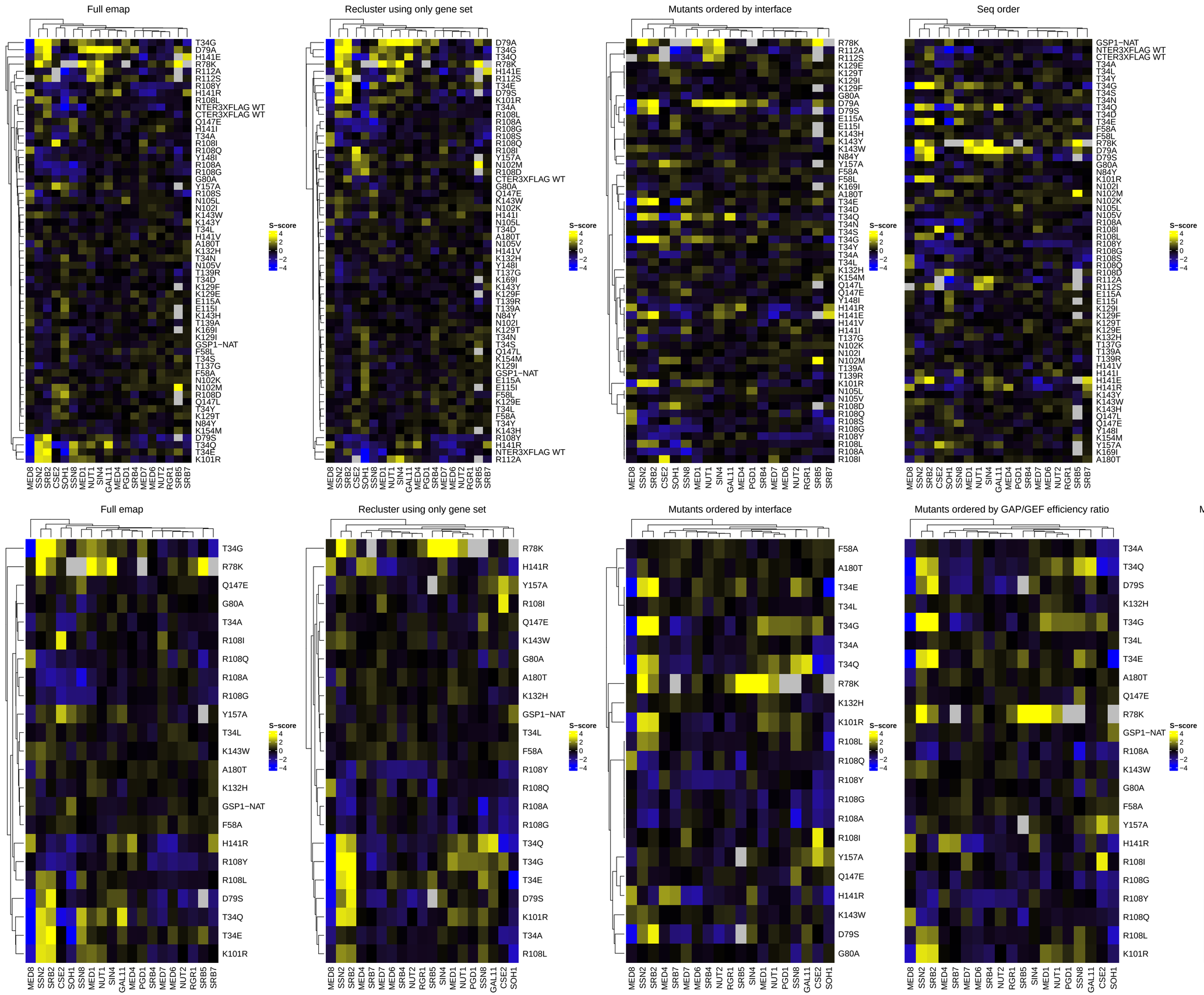


mitotic checkpoint complex
wodak complexes
clustering metric: euclidean

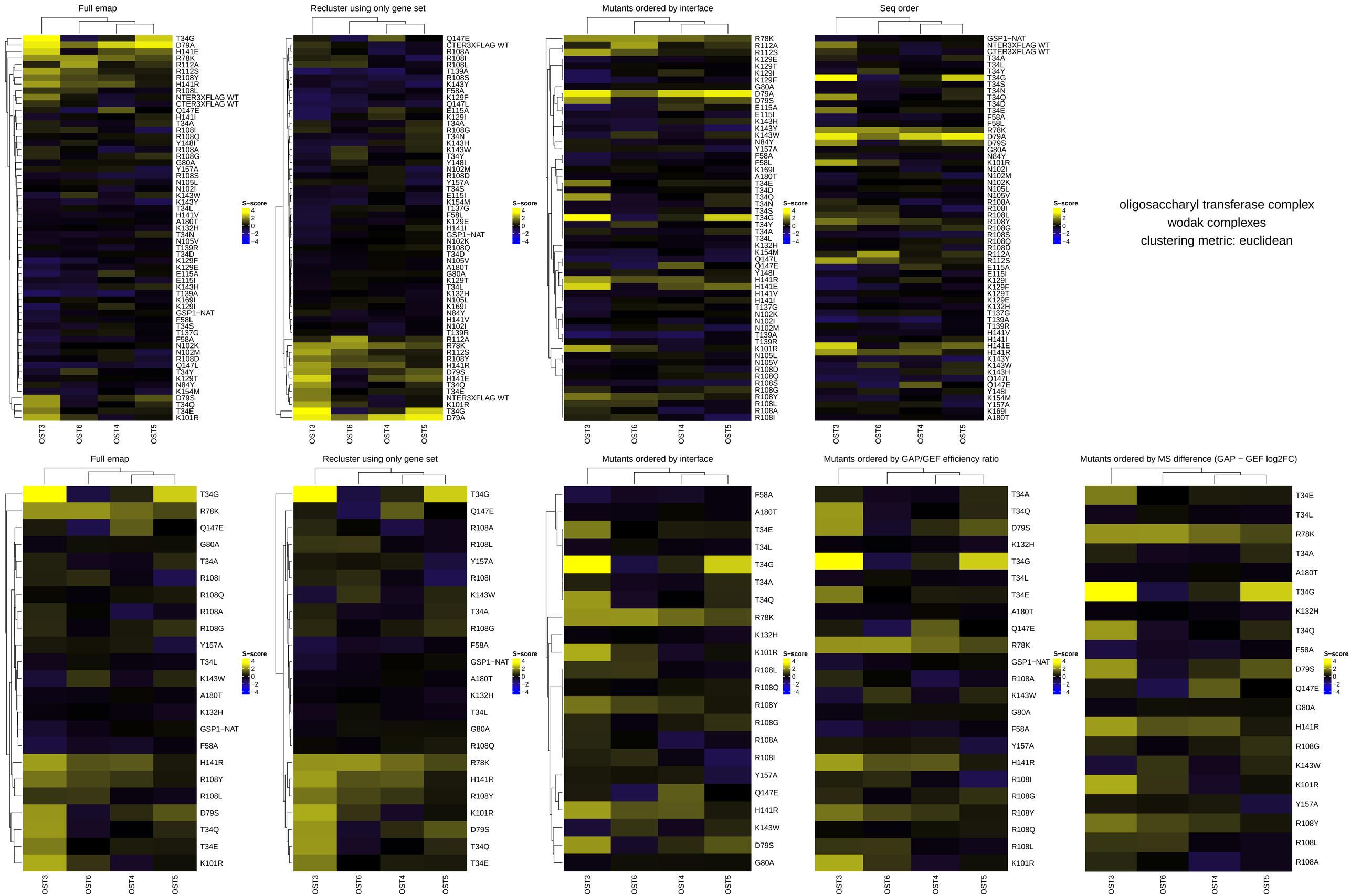

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SIP1
SNF1
SNF4
Snf1p/Snf4p/Sip1p complex
wodak complexes
clustering metric: euclidean

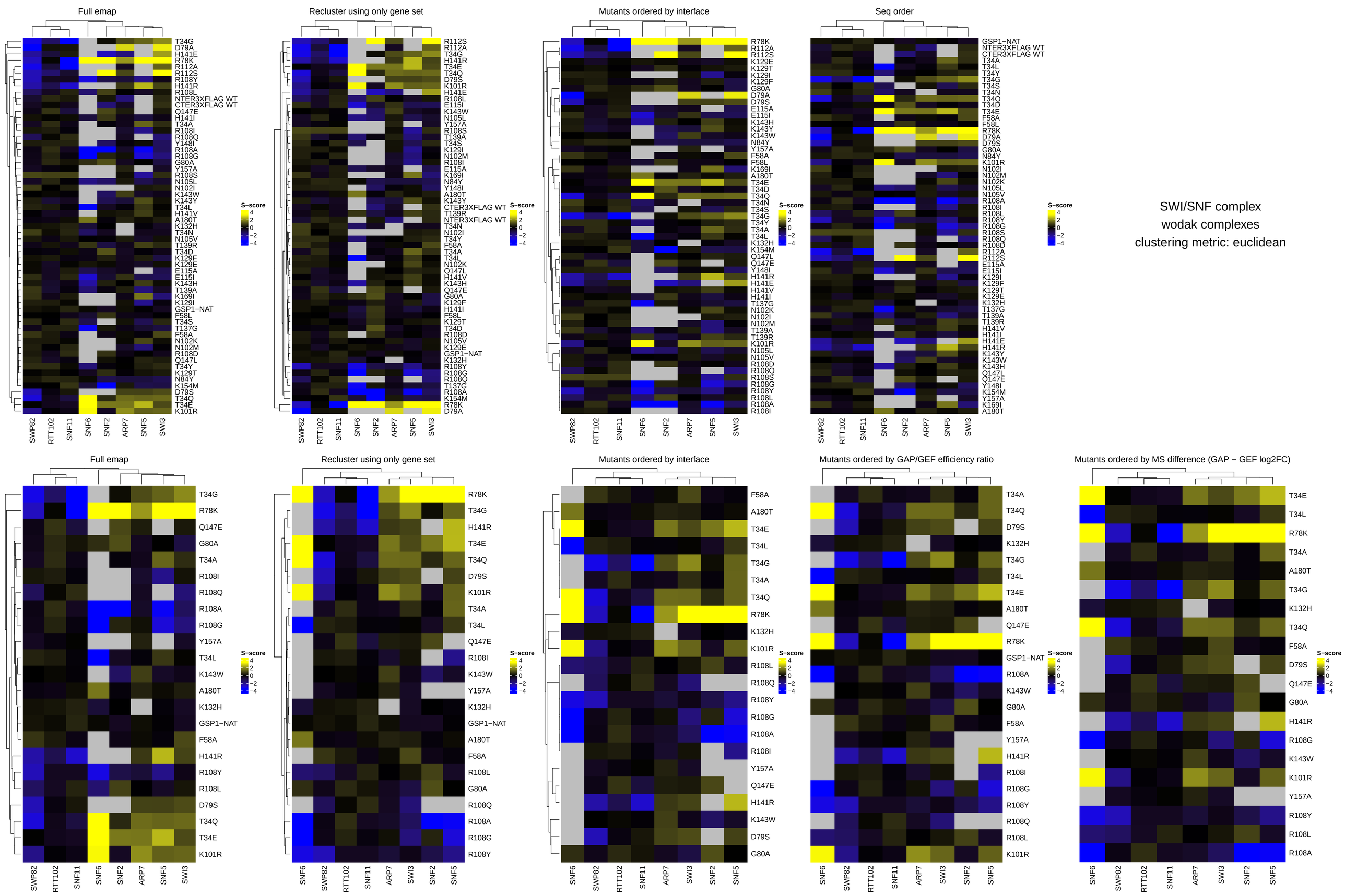

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
alpha,alpha−trehalose−phosphate synthase complex (UDP
wodak complexes
clustering metric: euclidean
S−score
4
2
0
−2
−4
TPS2
TPS1
TSL1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)


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
4
2
0
−2
−4
IES1
NHP10
ARP4
IES4
Ino80p complex
wodak complexes
clustering metric: euclidean

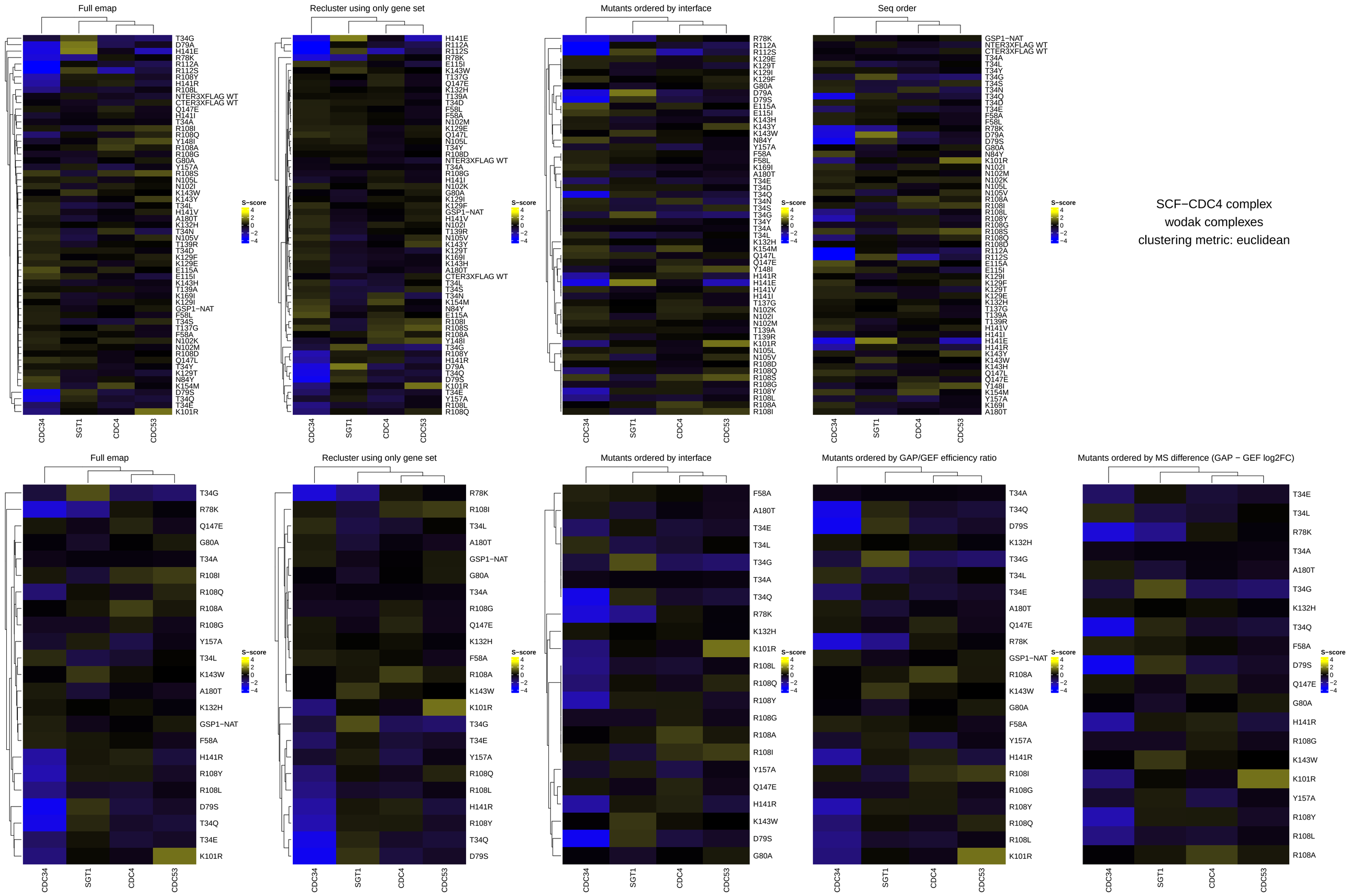


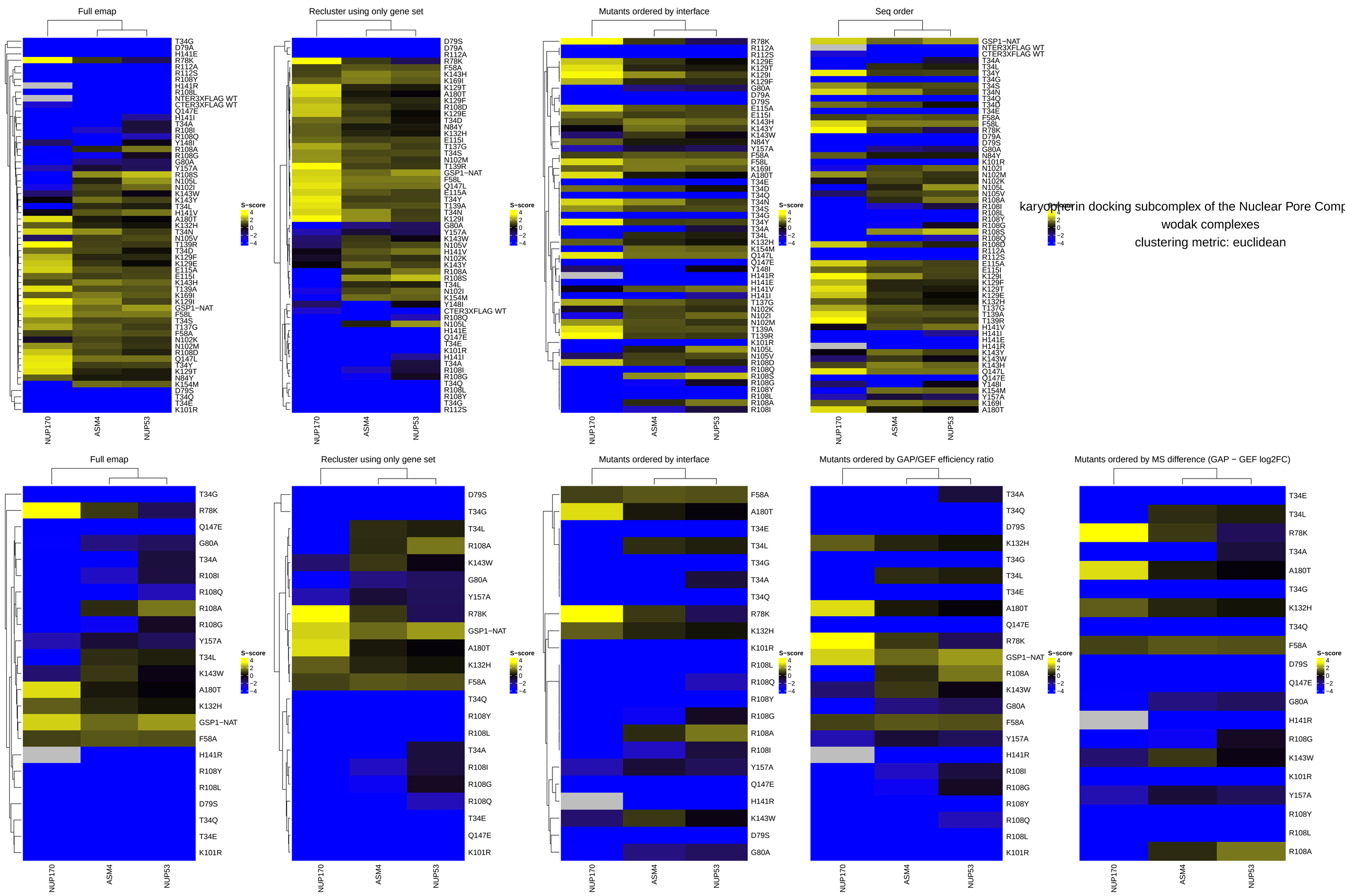
Kornberg's mediator (SRB) complex
wodak complexes
clustering metric: euclidean

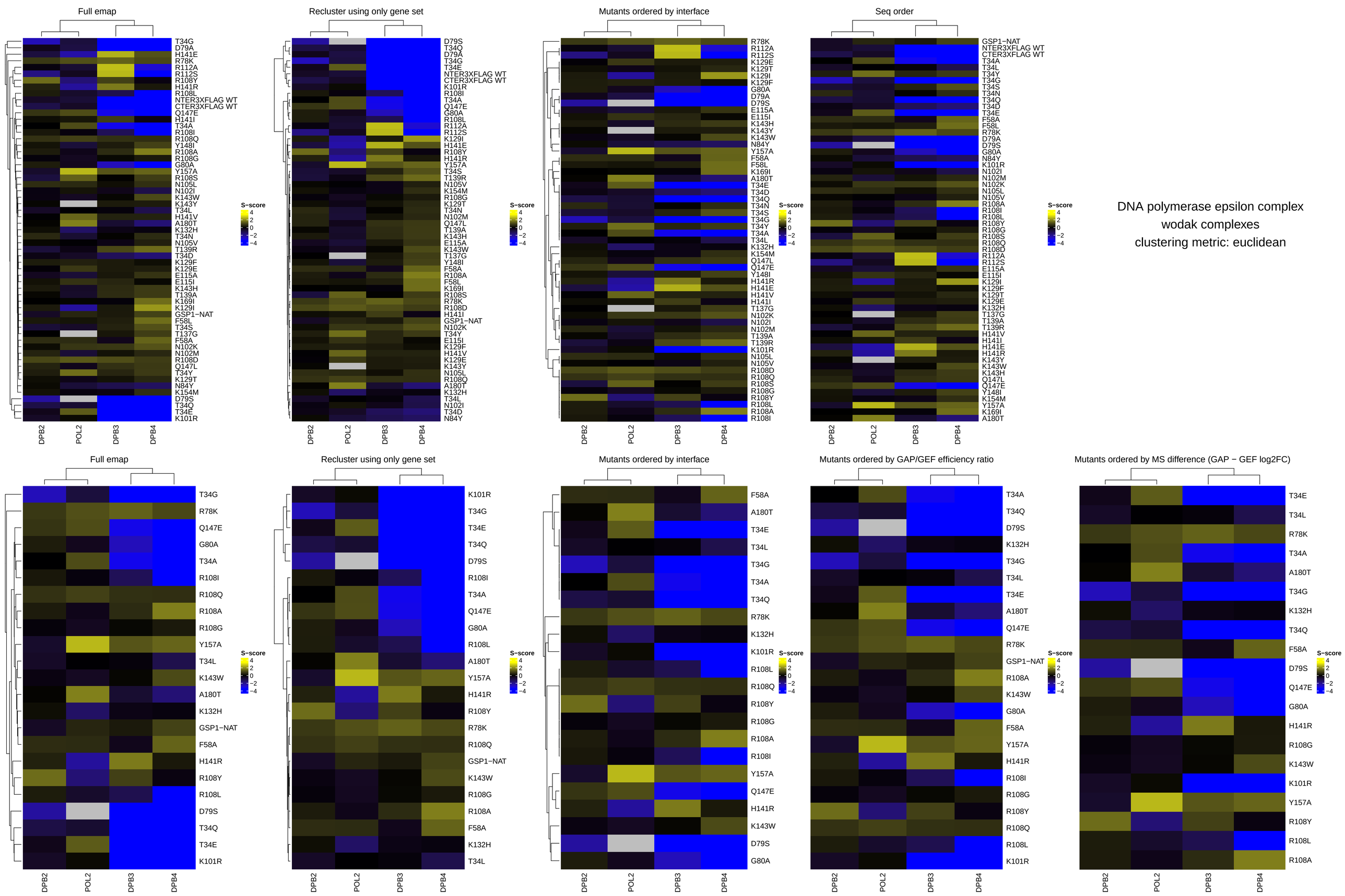

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
OST3
OST6
OST4
OST5
oligosaccharyl transferase complex
wodak complexes
clustering metric: euclidean

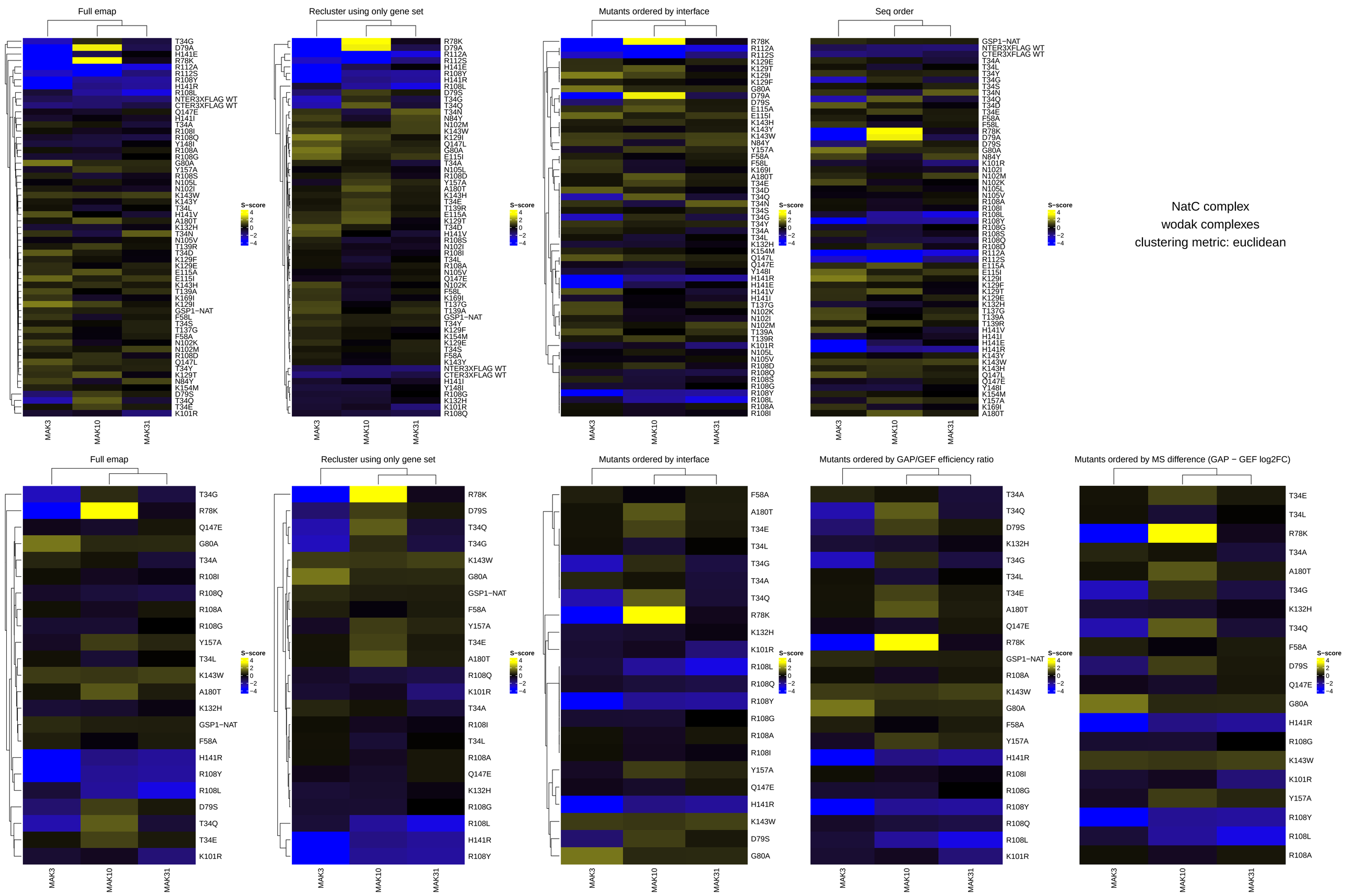


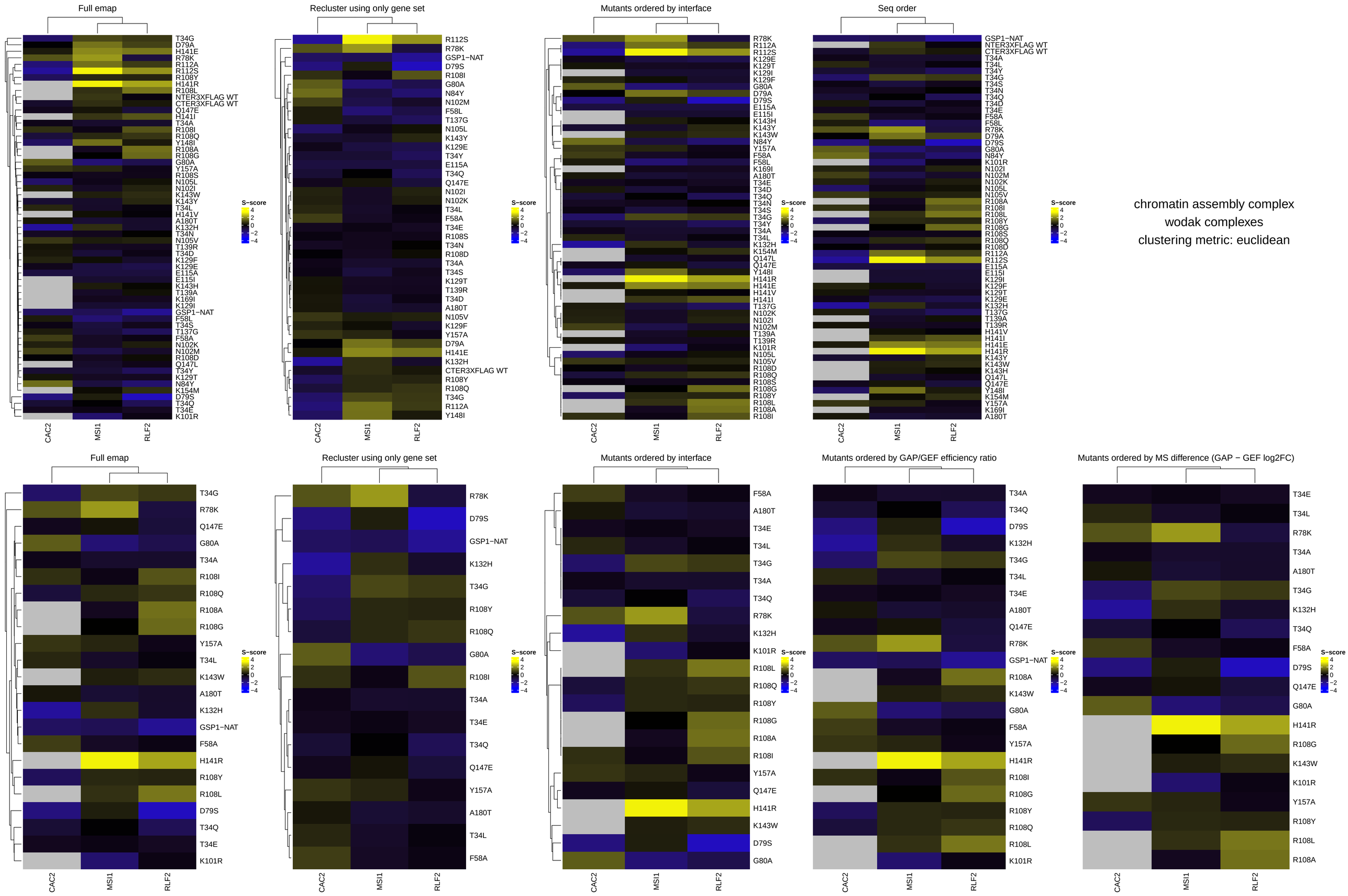
SWI/SNF complex
wodak complexes
clustering metric: euclidean

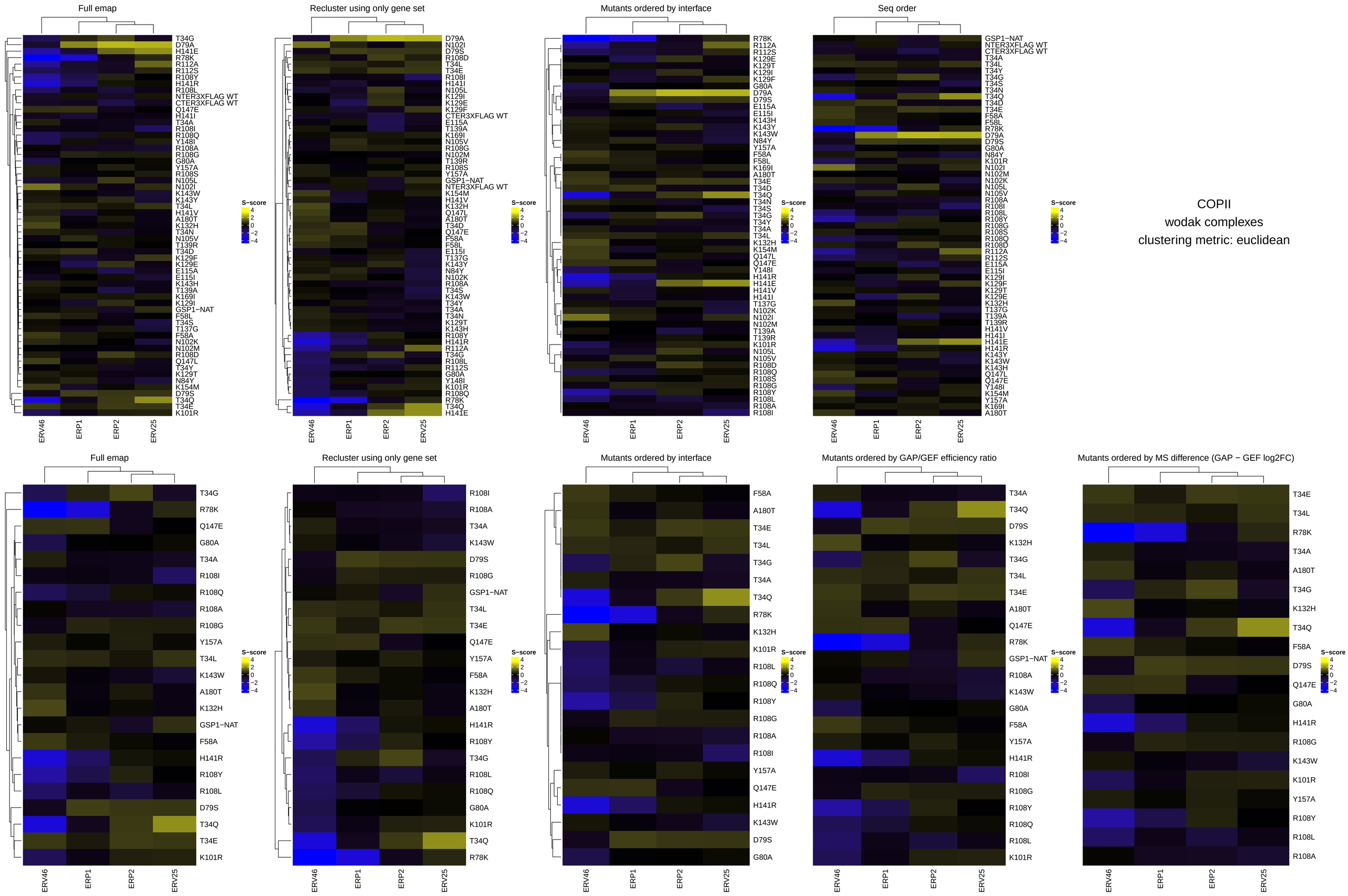

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CDC34
SGT1
CDC4
CDC53
SCF−CDC4 complex
wodak complexes
clustering metric: euclidean

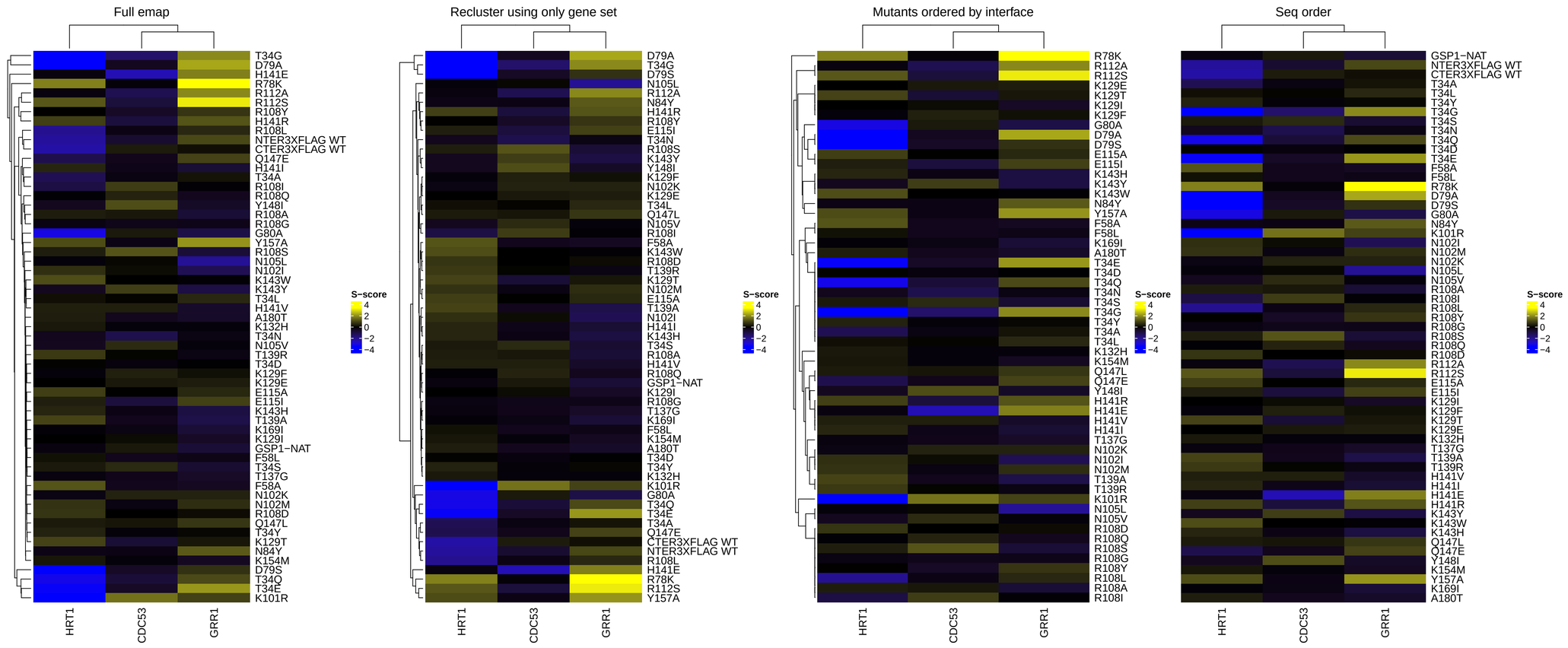

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
NUP170
ASM4
NUP53
karyopherin docking subcomplex of the Nuclear Pore Comp
wodak complexes
clustering metric: 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
4
2
0
−2
−4
DPB2
POL2
DPB3
DPB4
DNA polymerase epsilon complex
wodak complexes
clustering metric: euclidean

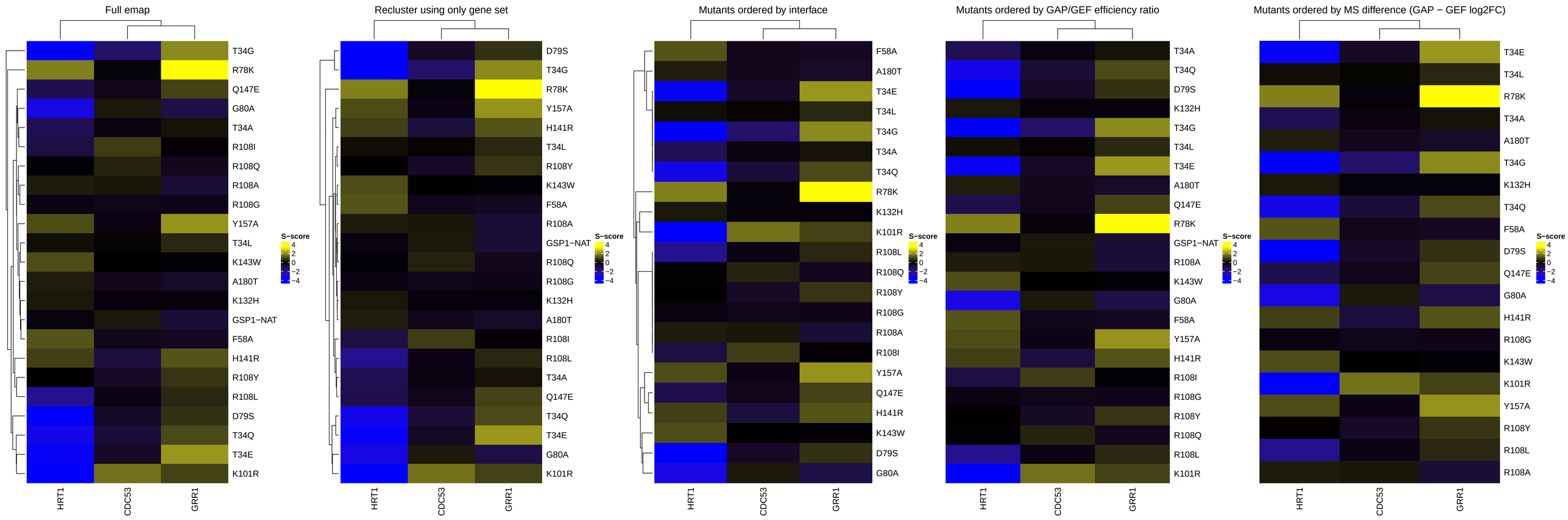

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
MAK3
MAK10
MAK31
NatC complex
wodak complexes
clustering metric: euclidean

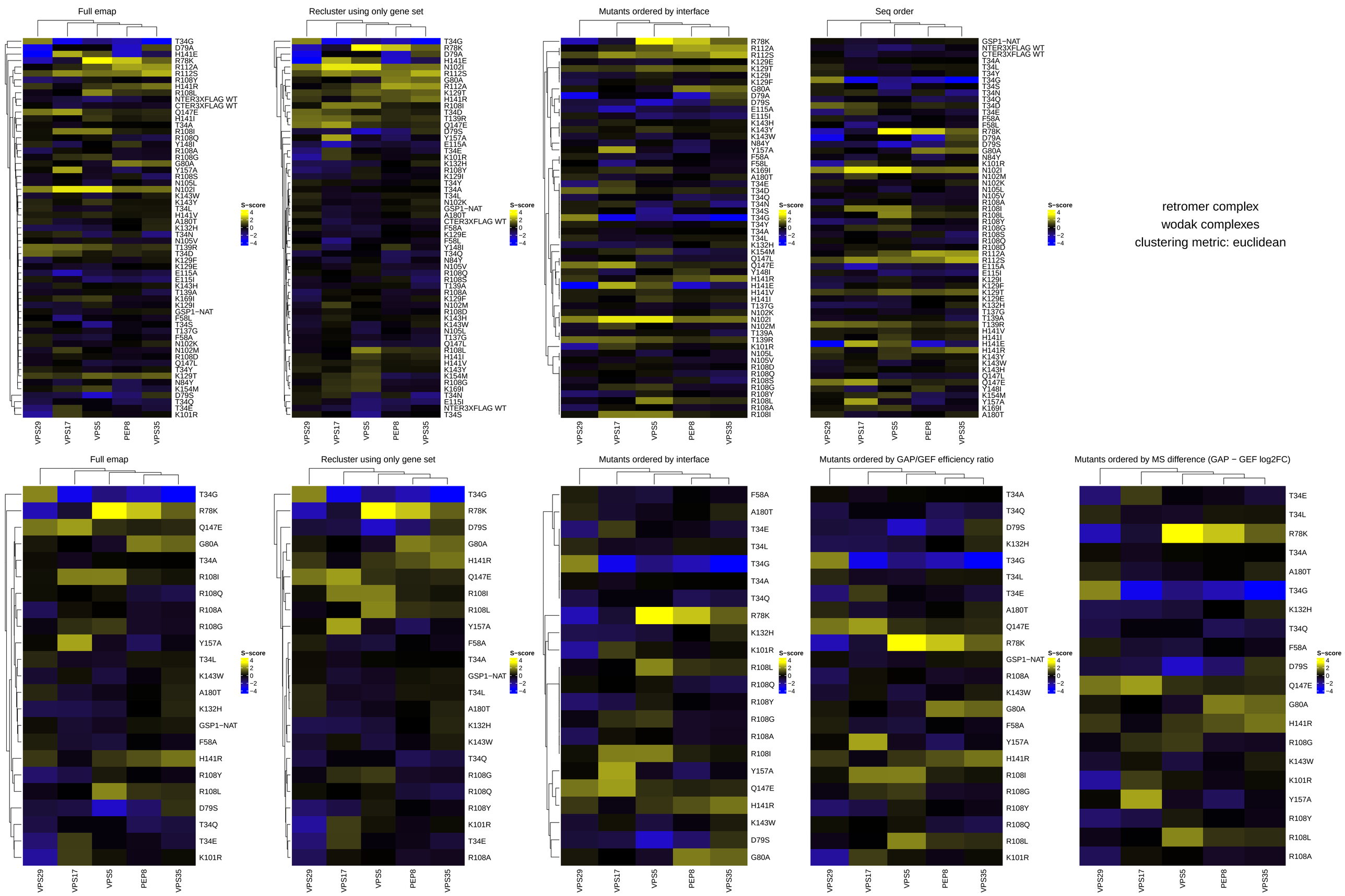

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CAC2
MSI1
RLF2
chromatin assembly complex
wodak complexes
clustering metric: euclidean

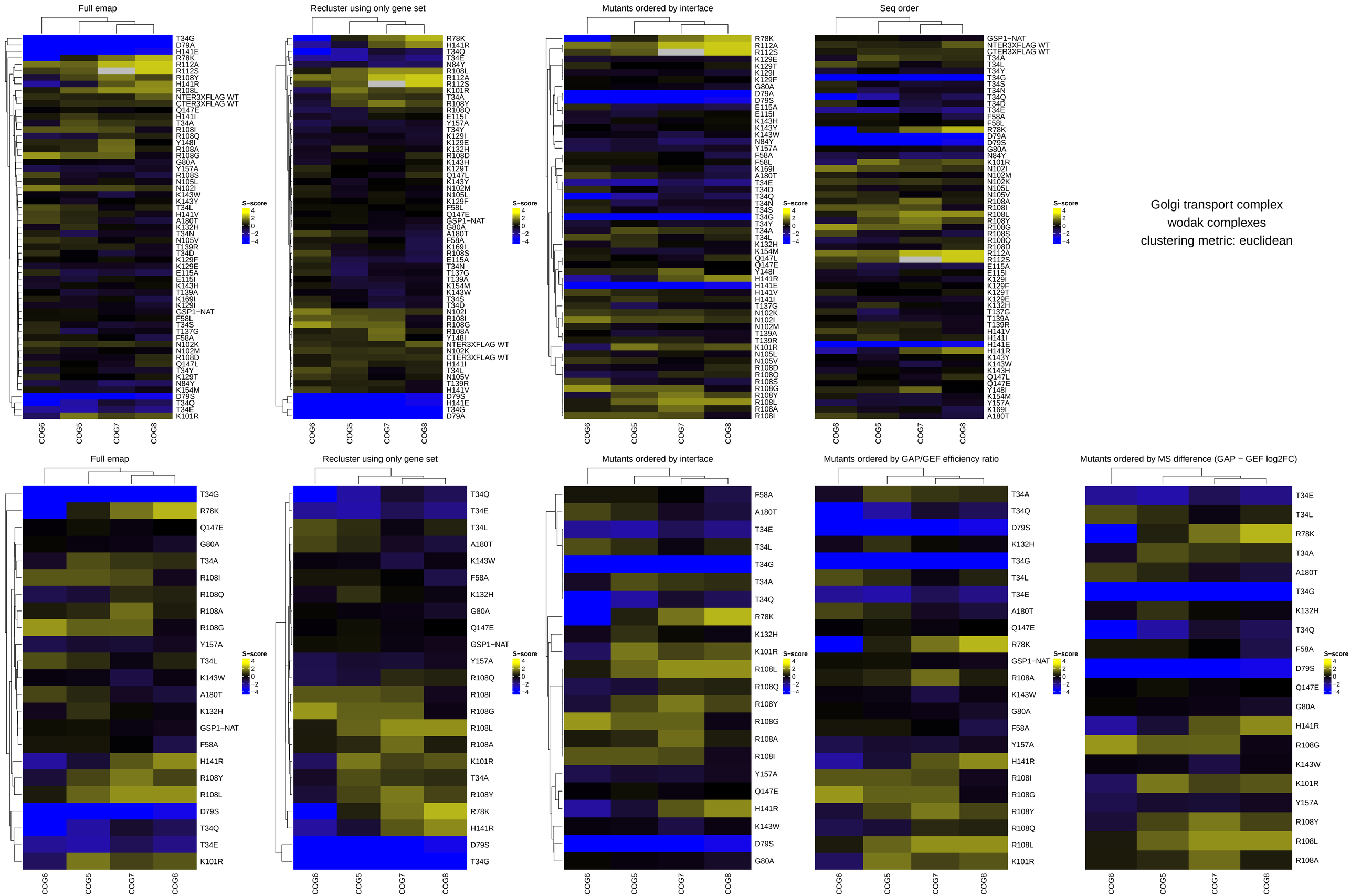

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ERV46
ERP1
ERP2
ERV25
COPII
wodak complexes
clustering metric: euclidean



nuclear ubiquitin ligase 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
4
2
0
−2
−4
VPS29
VPS17
VPS5
PEP8
VPS35
retromer 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
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2
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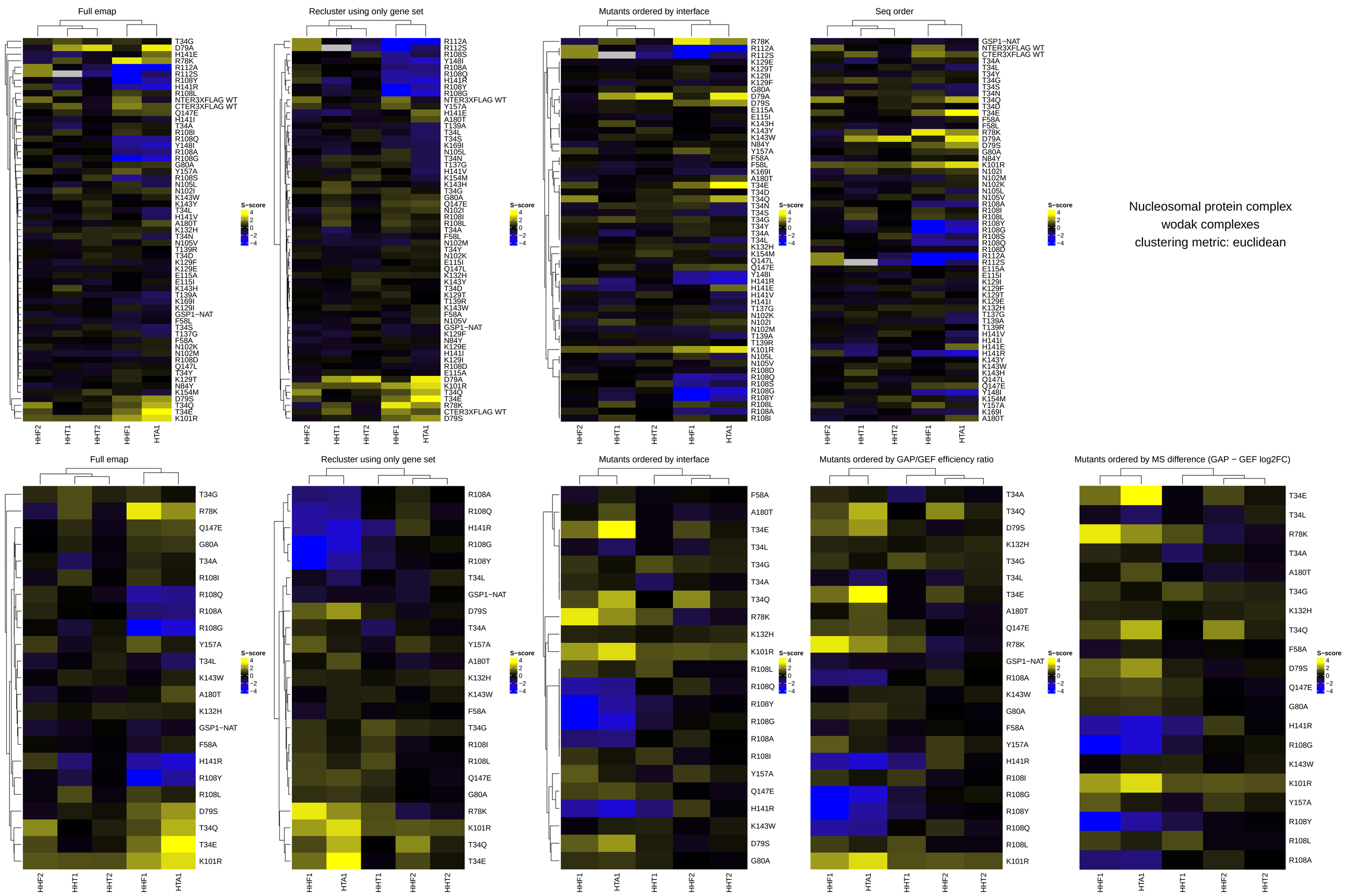
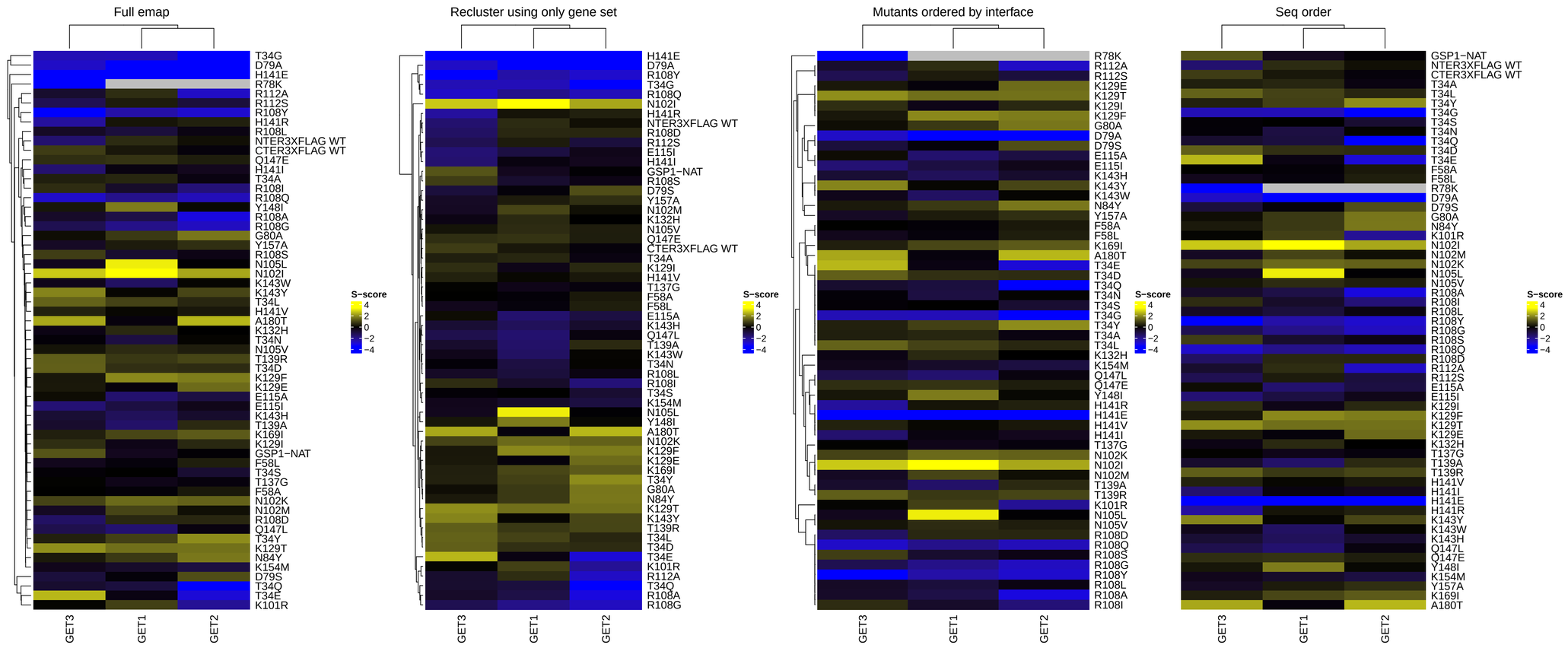
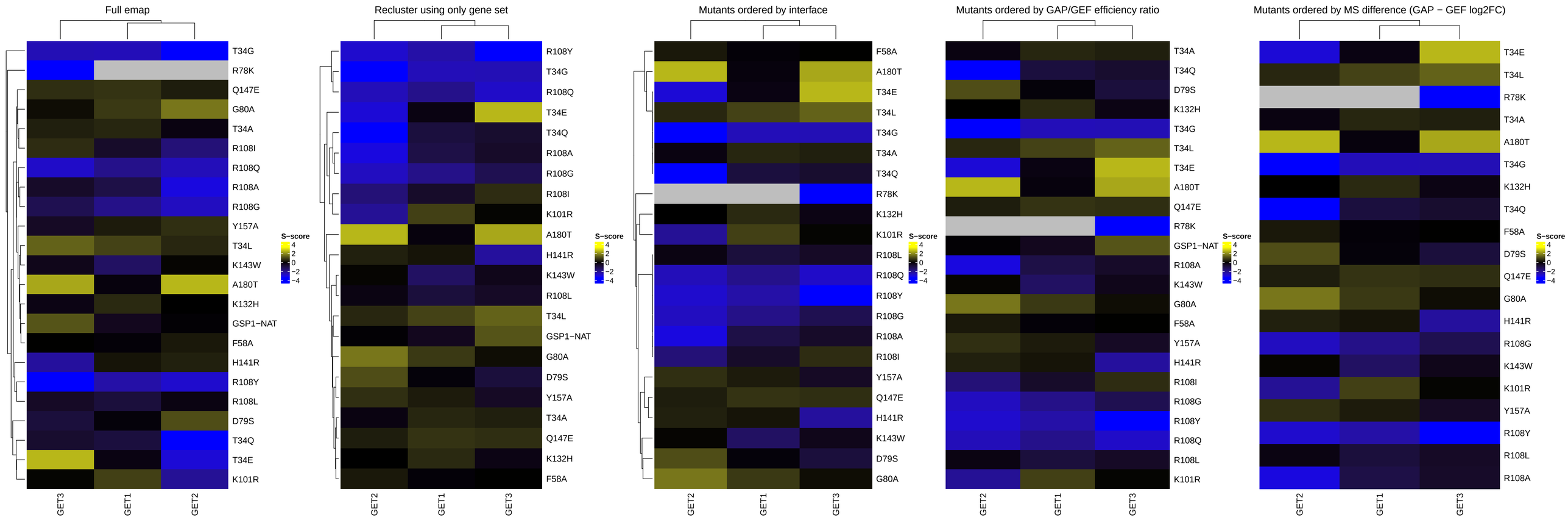
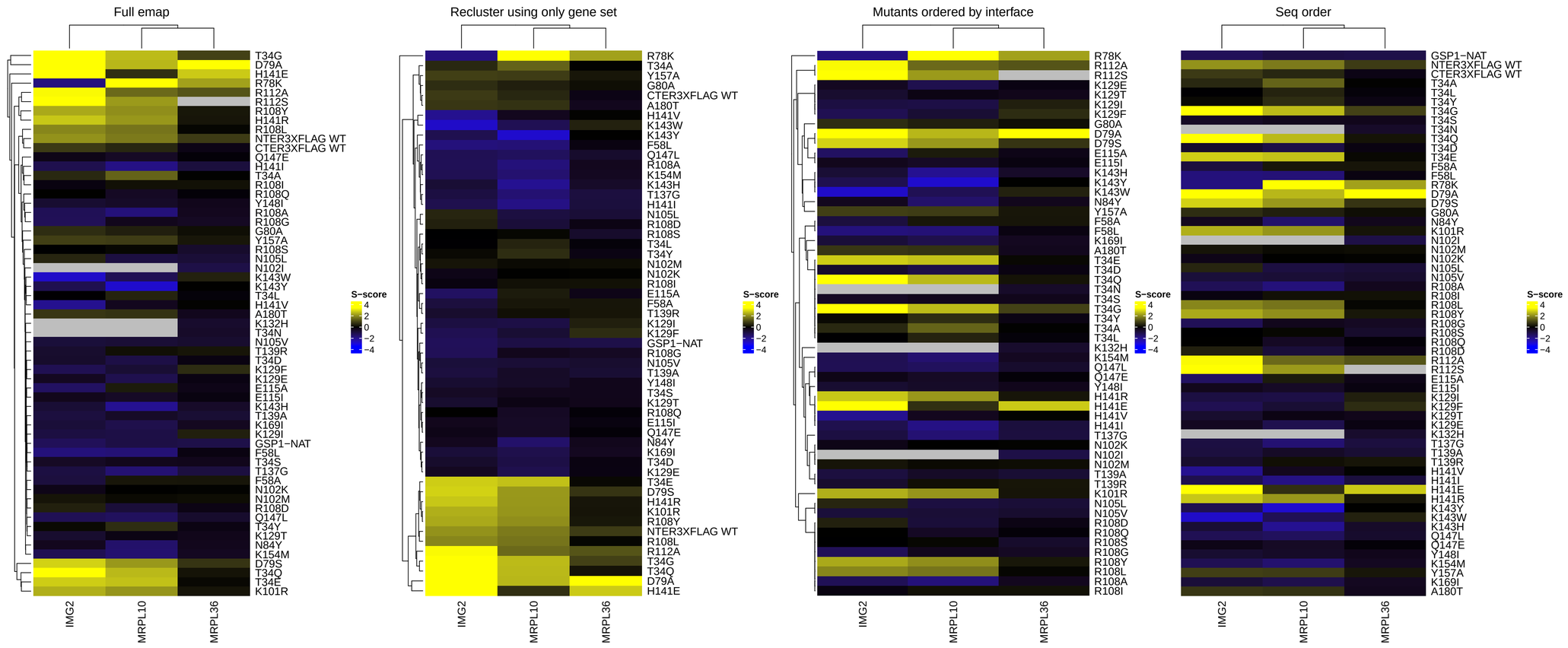
−2
−4
COG6
COG5
COG7
COG8
Golgi transport complex
wodak complexes
clustering metric: euclidean


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
4
2
0
−2
−4
HHF2
HHT1
HHT2
HHF1
HTA1
Nucleosomal protein complex
wodak complexes
clustering metric: euclidean

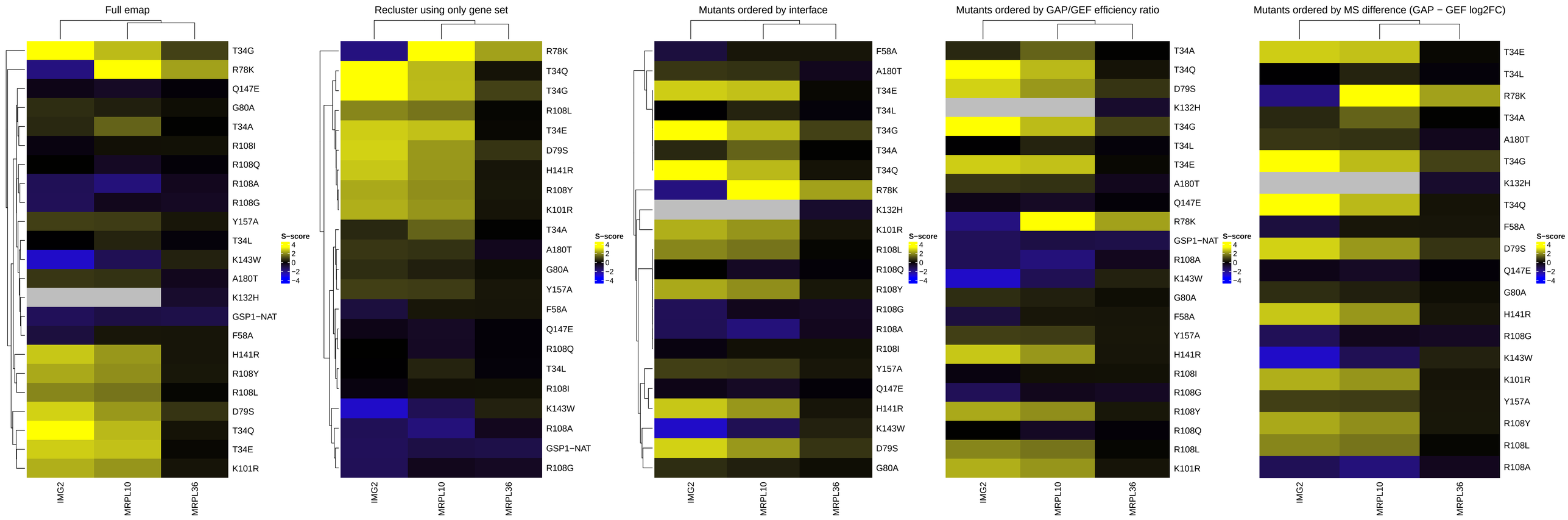


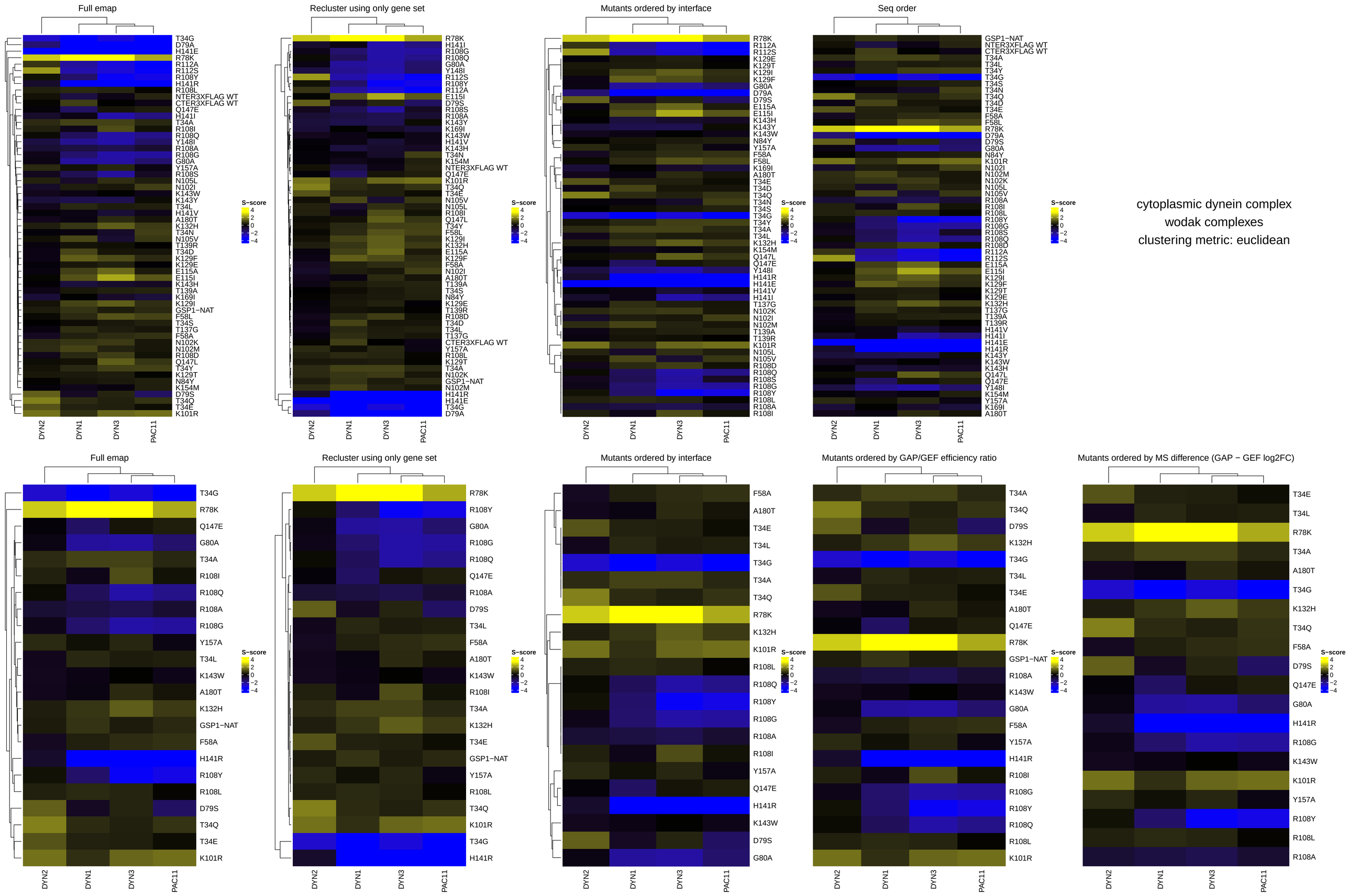
GET complex
wodak complexes
clustering metric: euclidean



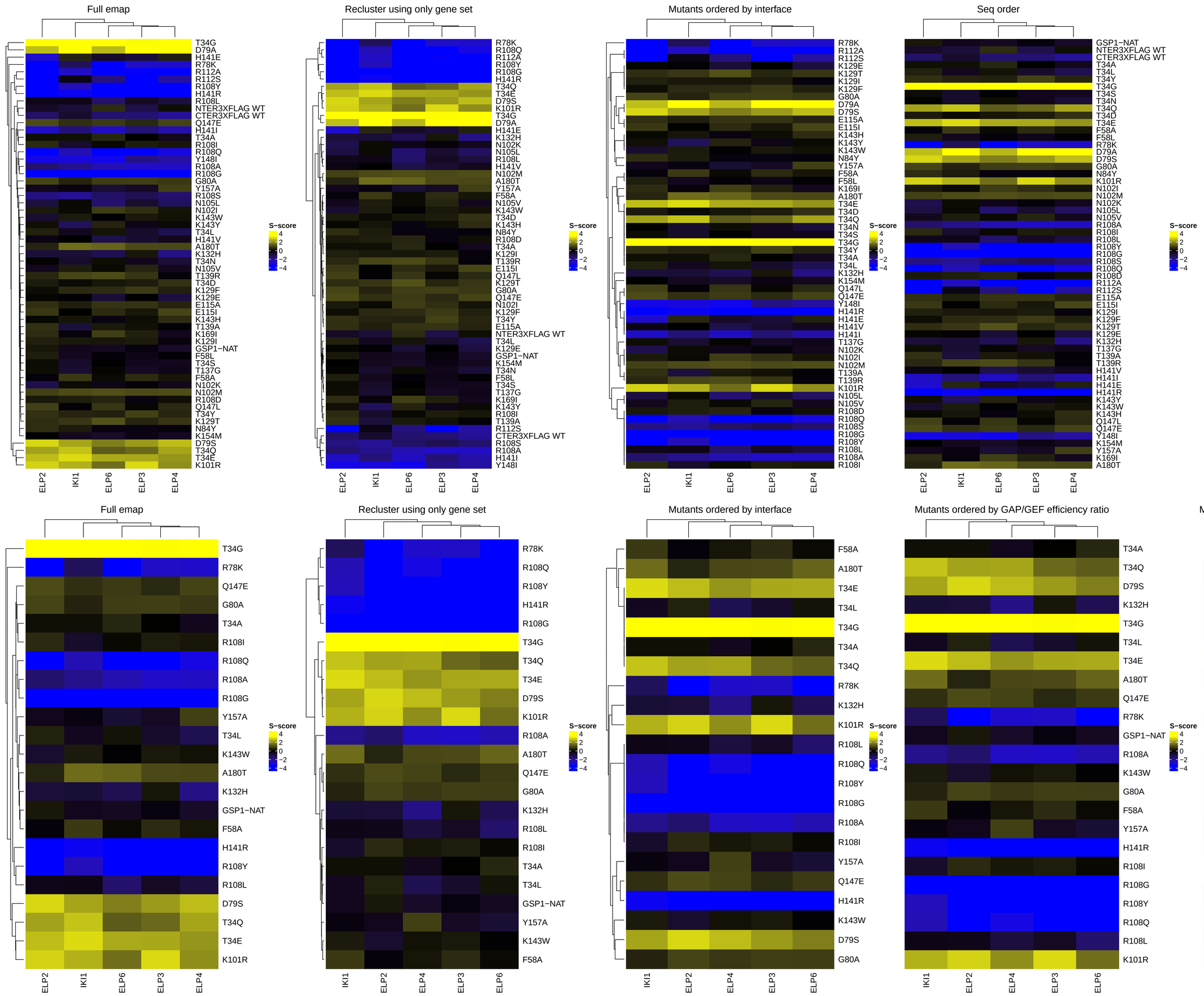


mitochondrial ribosomal large subunit
wodak complexes
clustering metric: euclidean

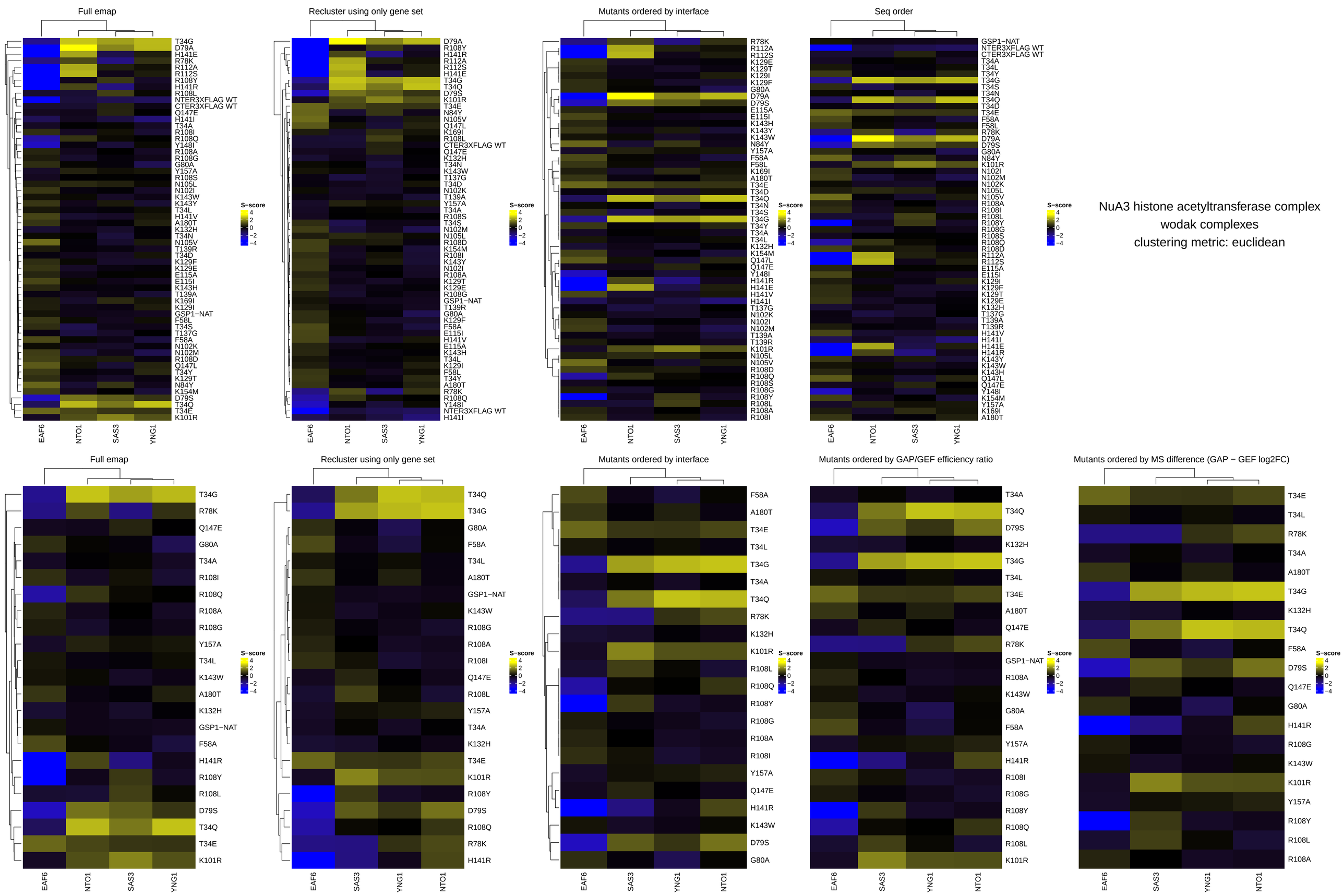


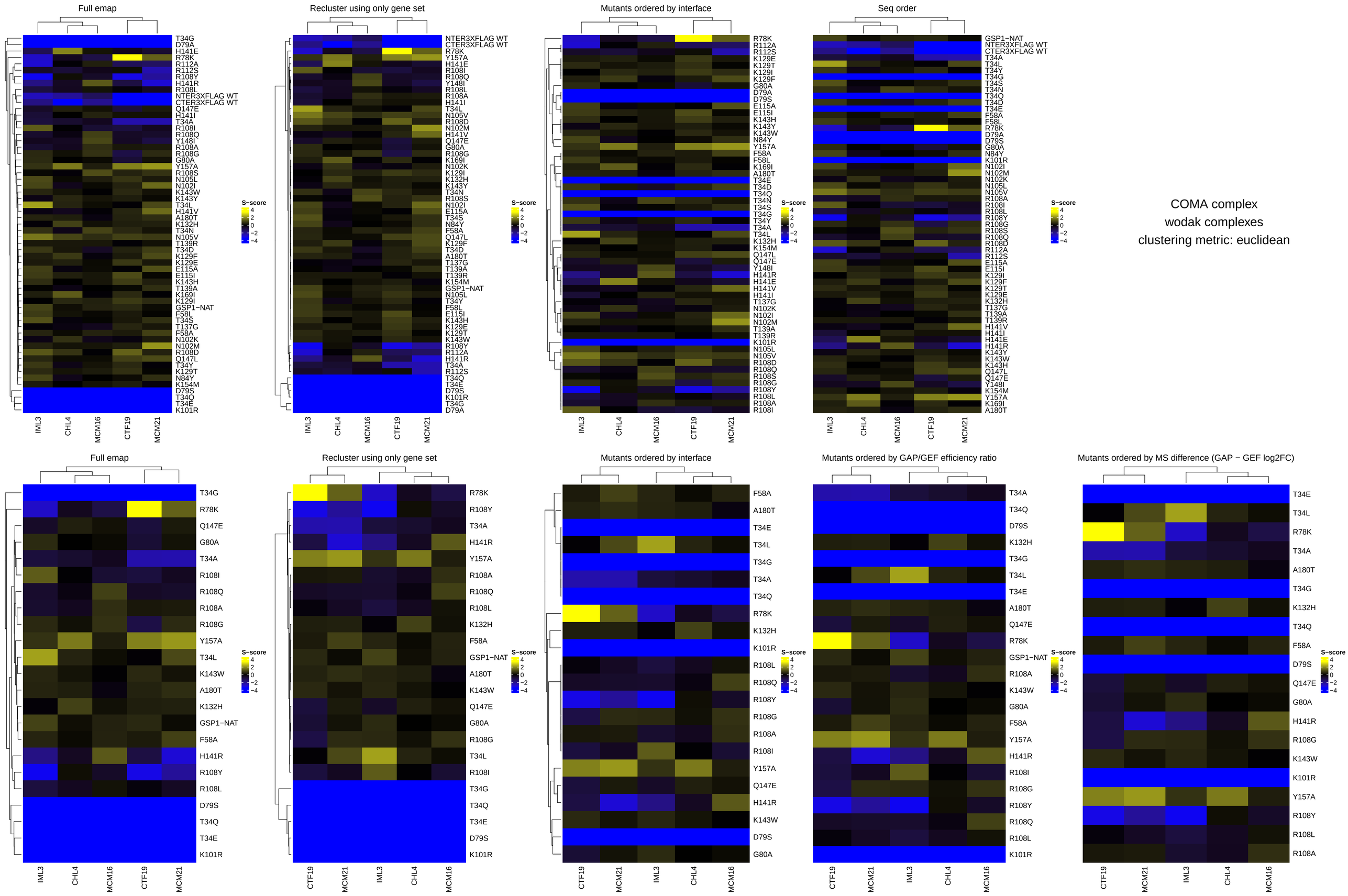


cytoplasmic dynein complex
wodak complexes
clustering metric: euclidean



Elongator 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
4
2
0
−2
−4
EAF6
NTO1
SAS3
YNG1
NuA3 histone acetyltransferase 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
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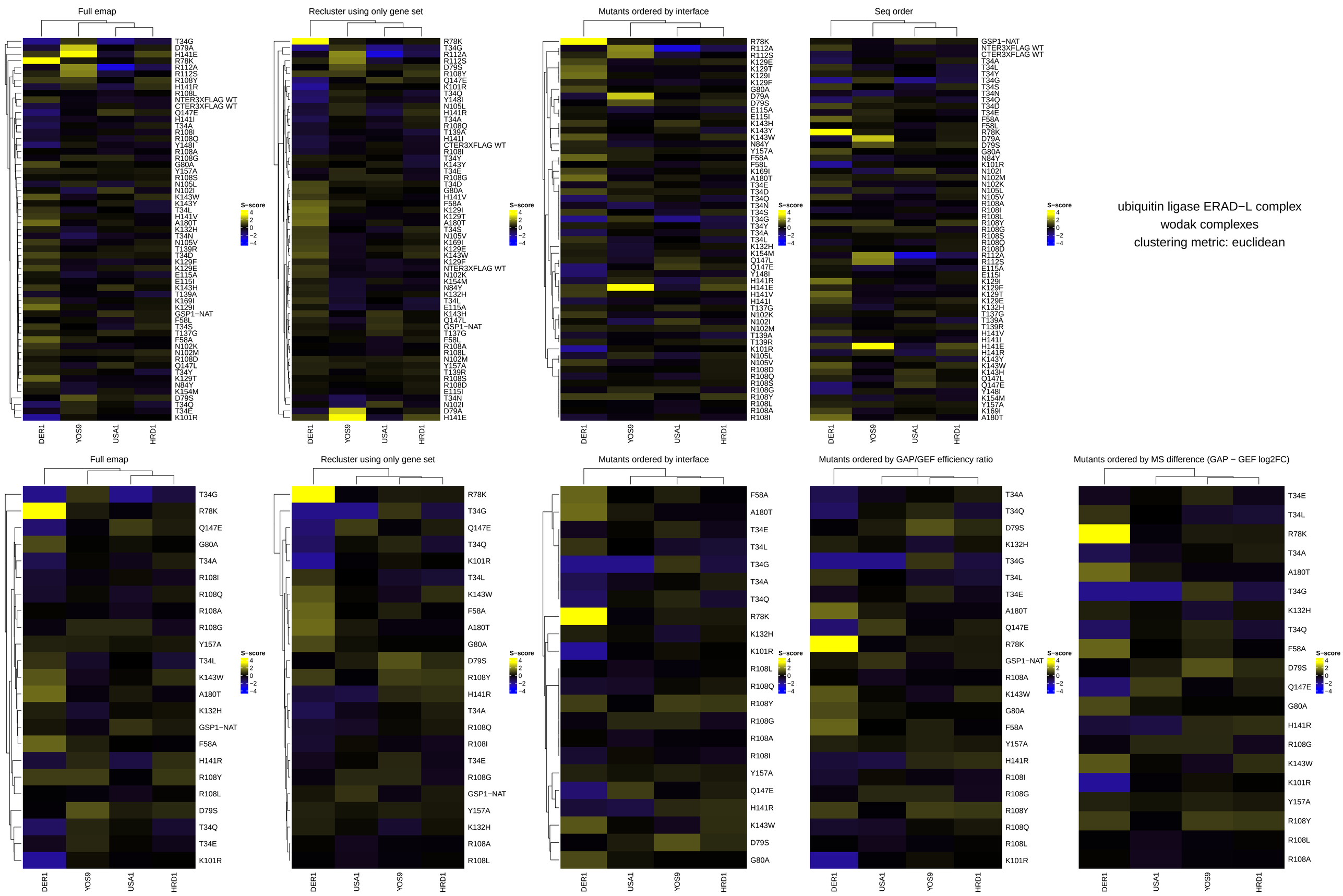
2
0
−2
−4
IML3
CHL4
MCM16
CTF19
MCM21
COMA complex
wodak complexes
clustering metric: euclidean


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
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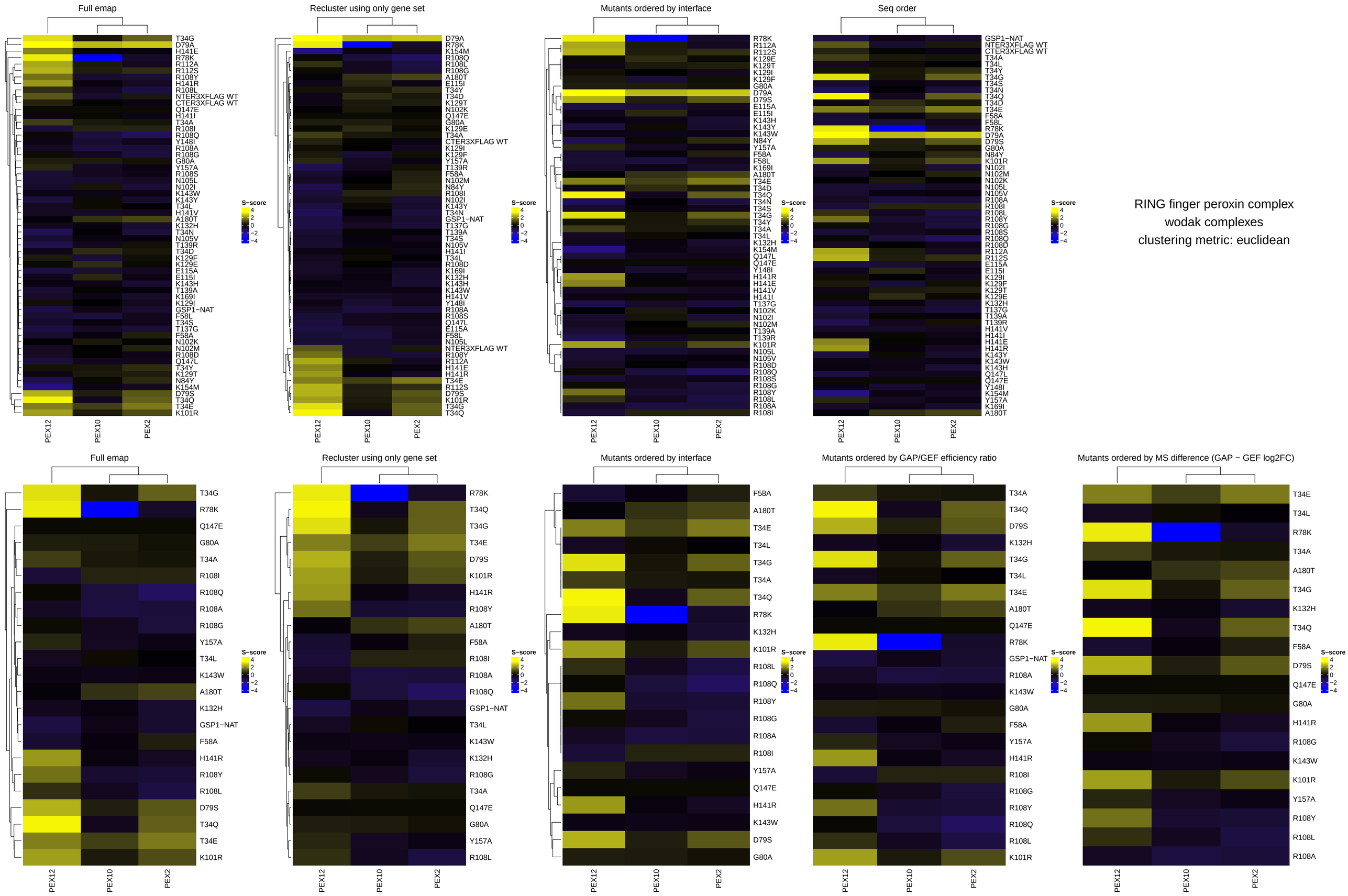
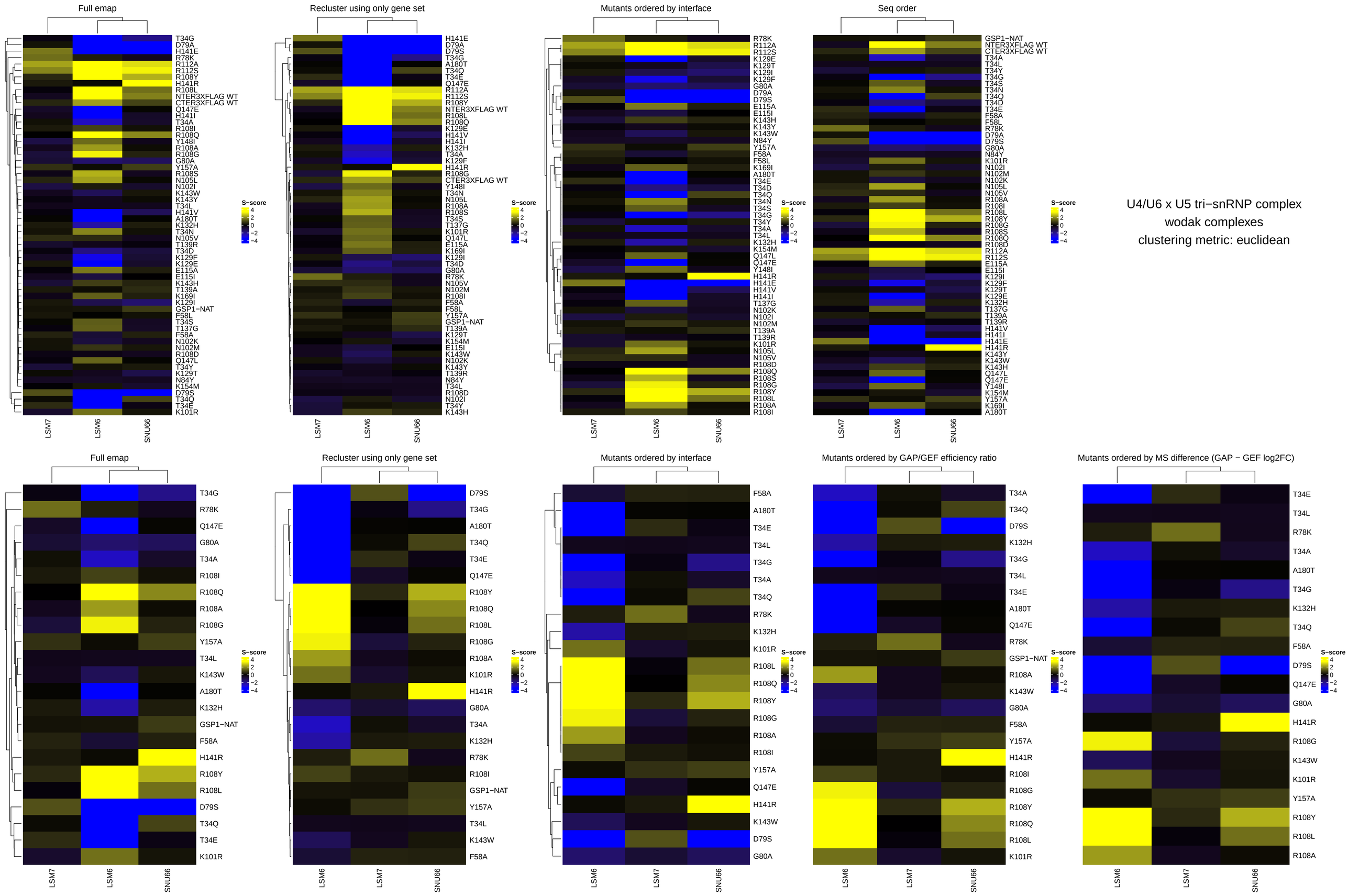
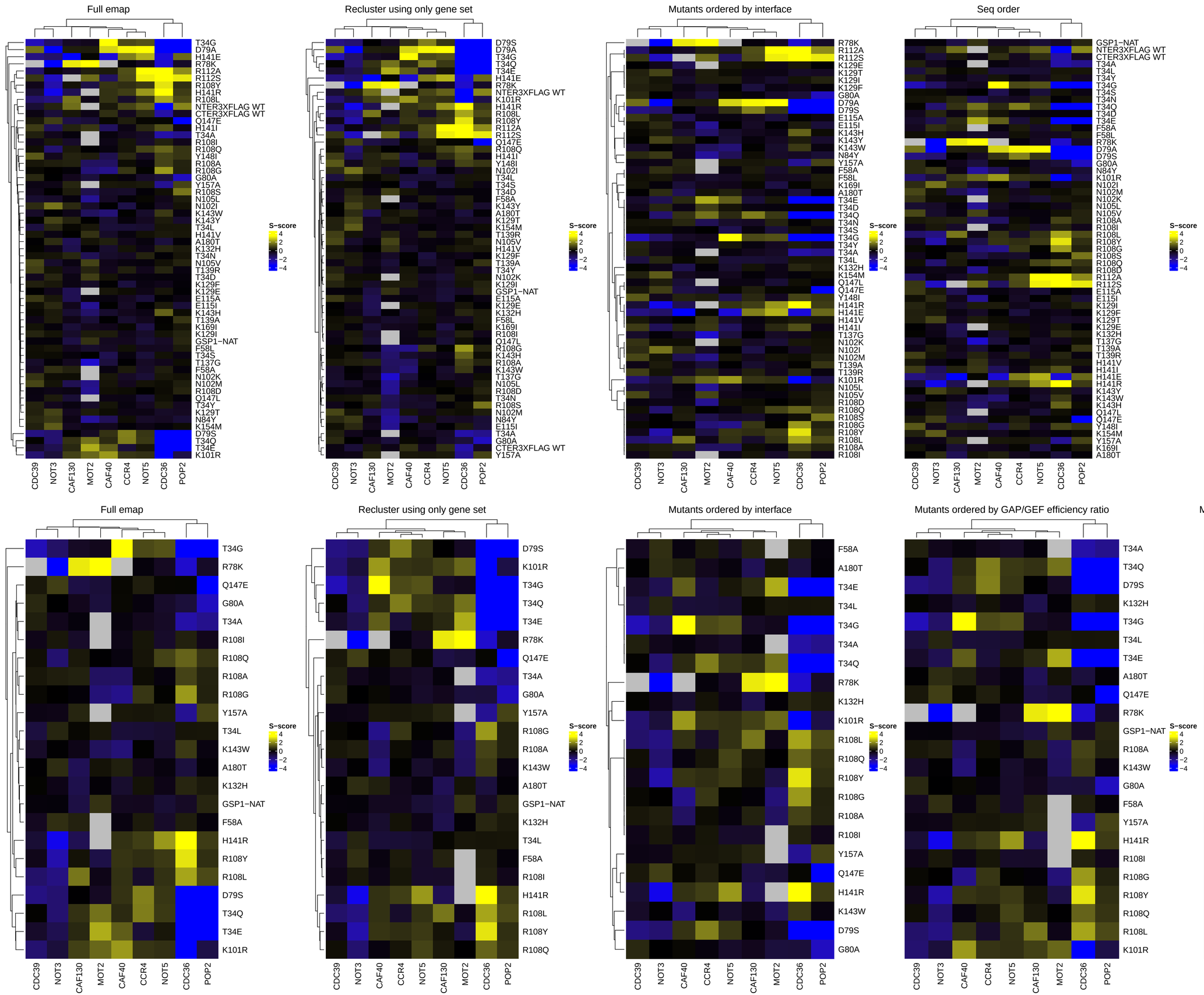
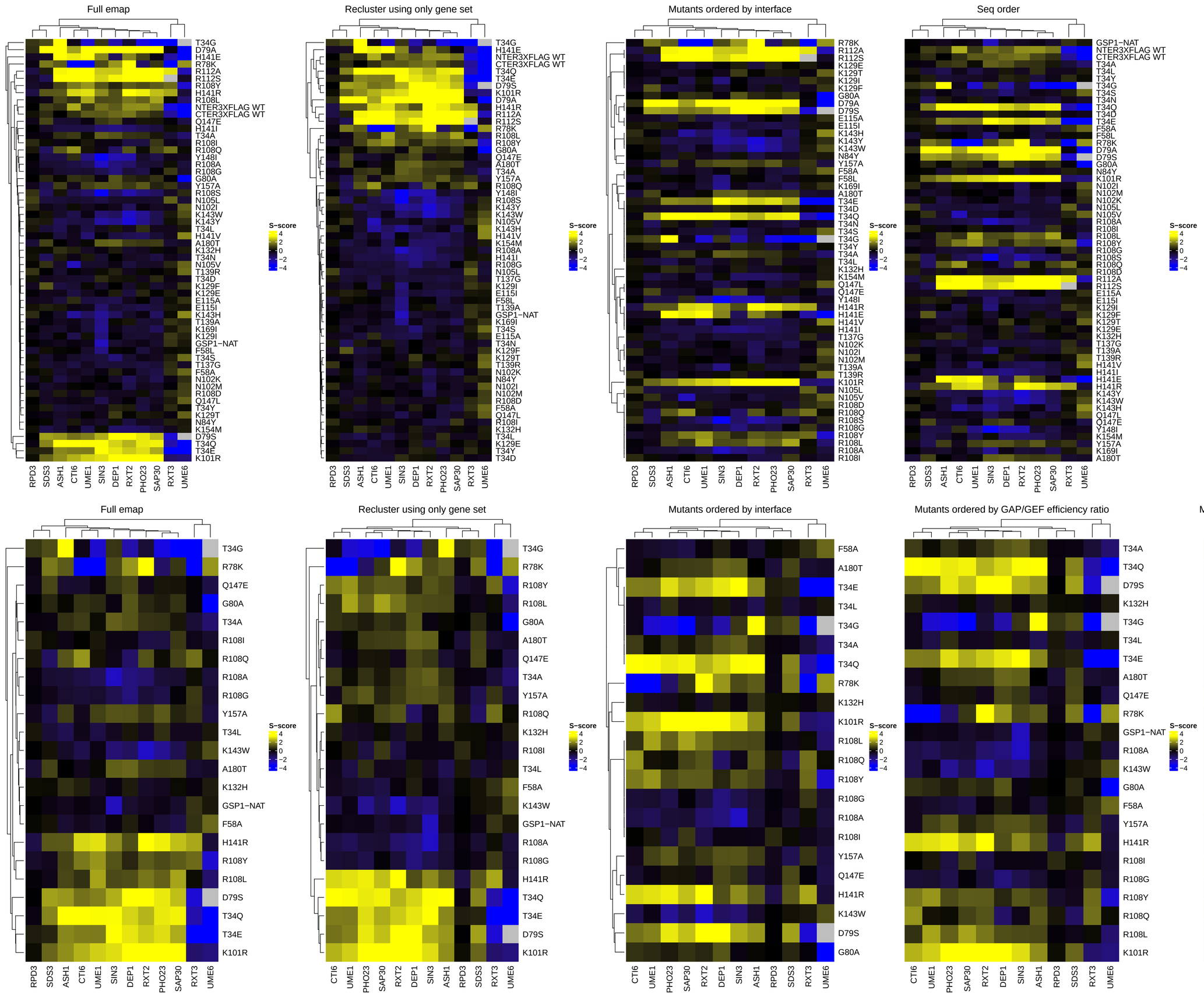
2
0
−2
−4
DER1
YOS9
USA1
HRD1
ubiquitin ligase ERAD−L complex
wodak complexes
clustering metric: euclidean


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
4
2
0
−2
−4
PEX12
PEX10
PEX2
RING finger peroxin complex
wodak complexes
clustering metric: euclidean

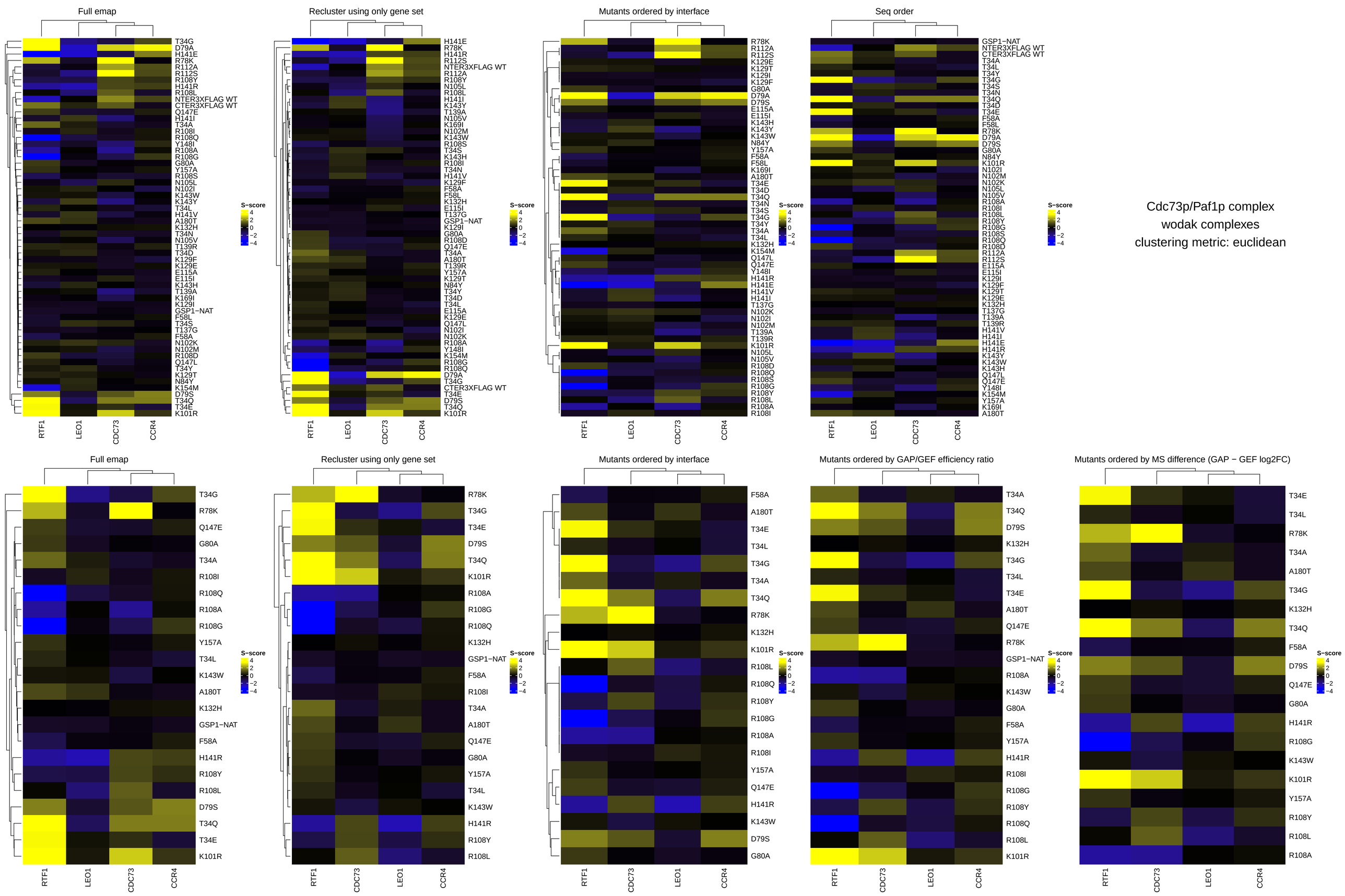

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
LSM7
LSM6
SNU66
U4/U6 x U5 tri−snRNP complex
wodak complexes
clustering metric: euclidean

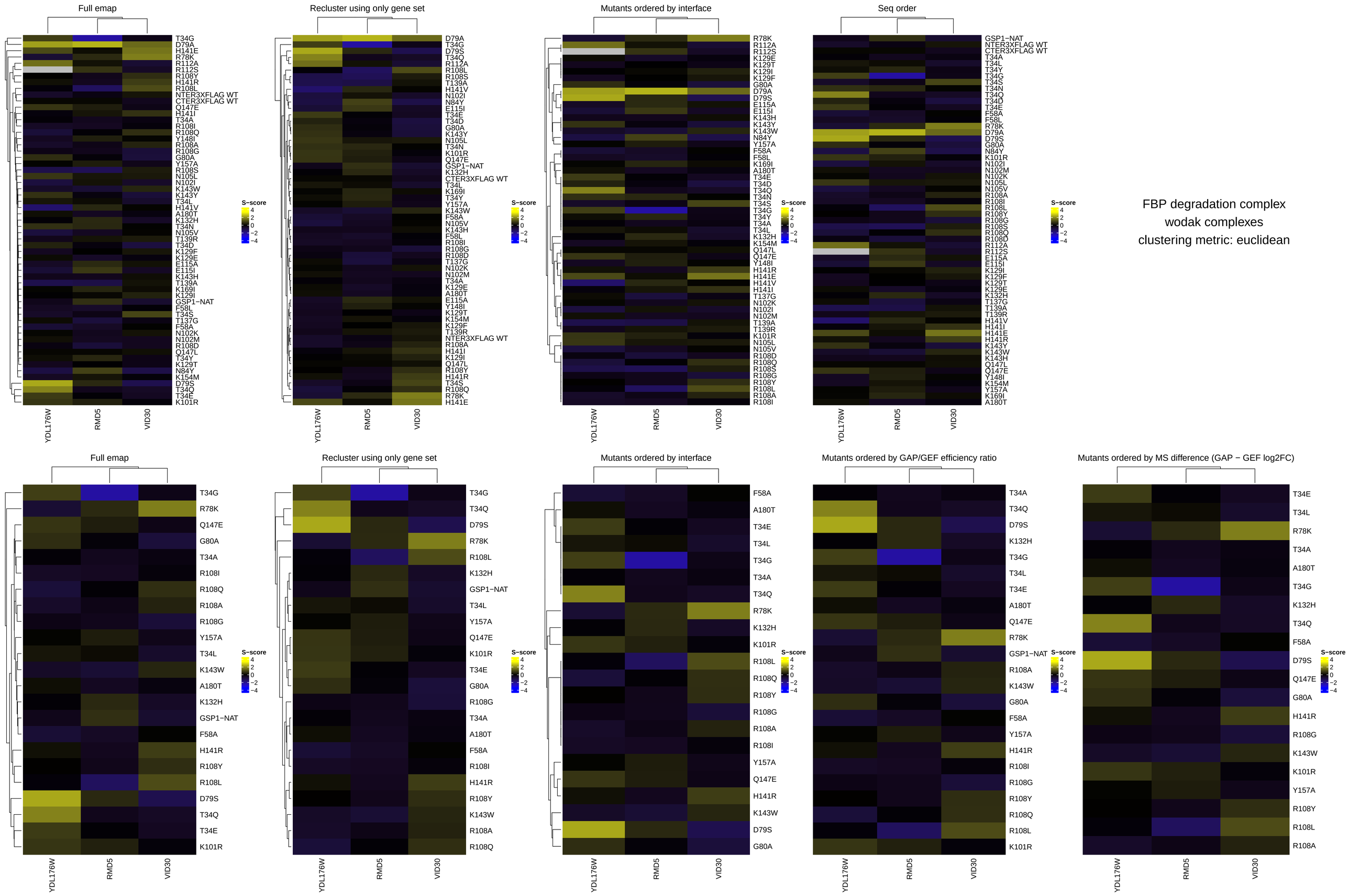


CCR4−NOT core complex
wodak complexes
clustering metric: euclidean



Rpd3L 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
4
2
0
−2
−4
RTF1
LEO1
CDC73
CCR4
Cdc73p/Paf1p 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
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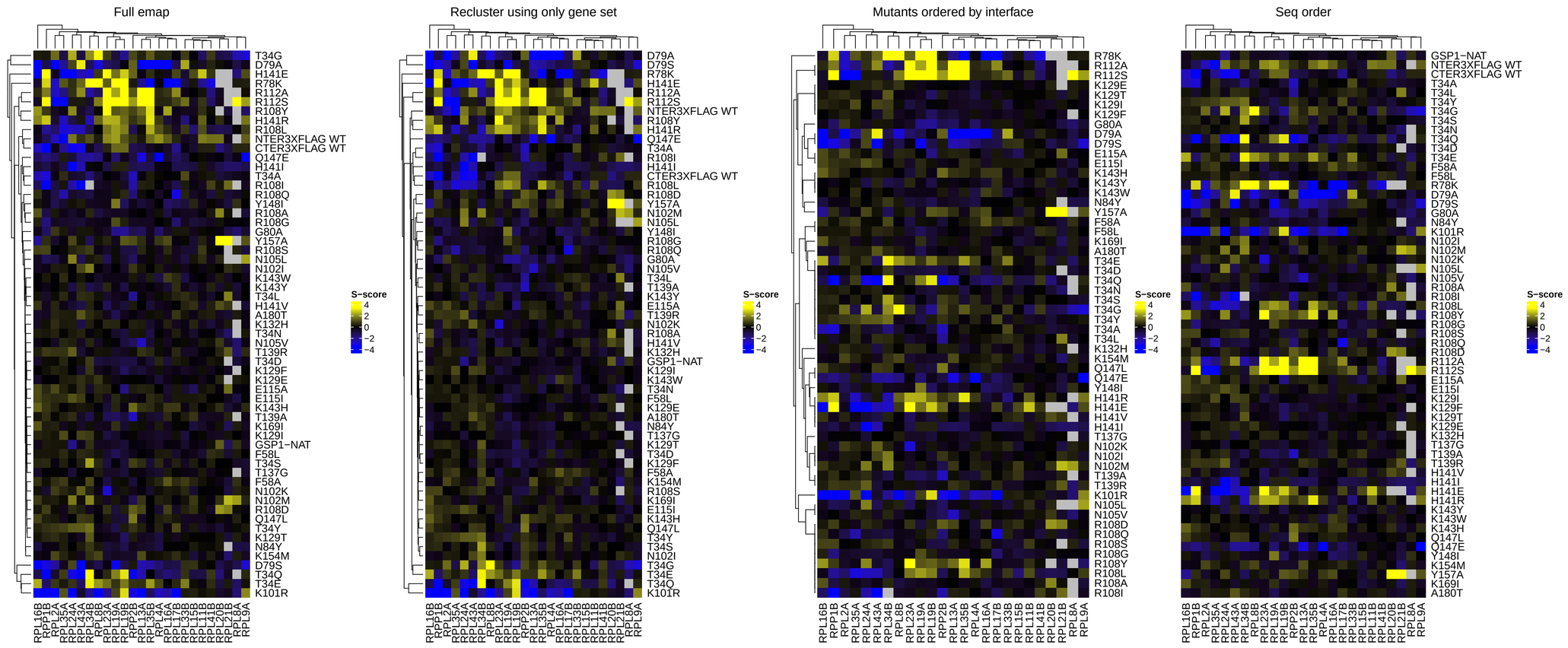
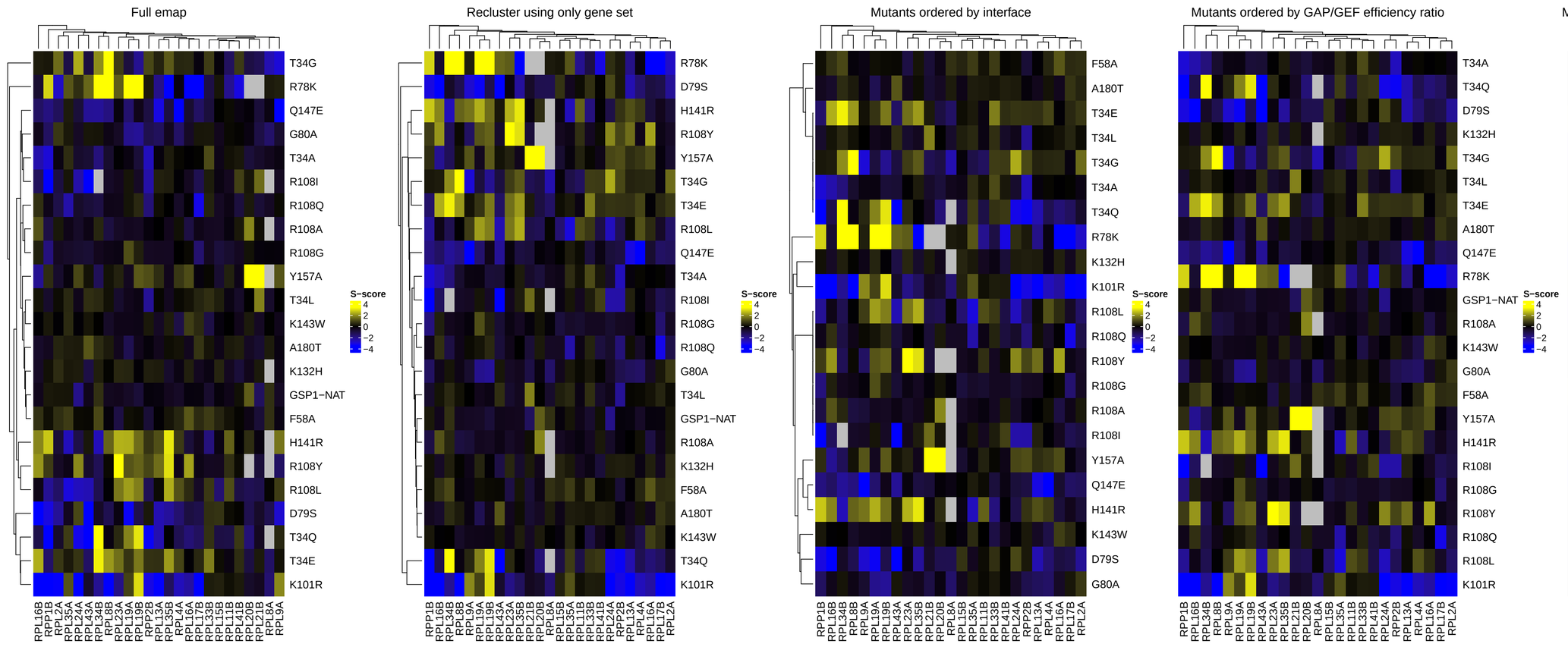
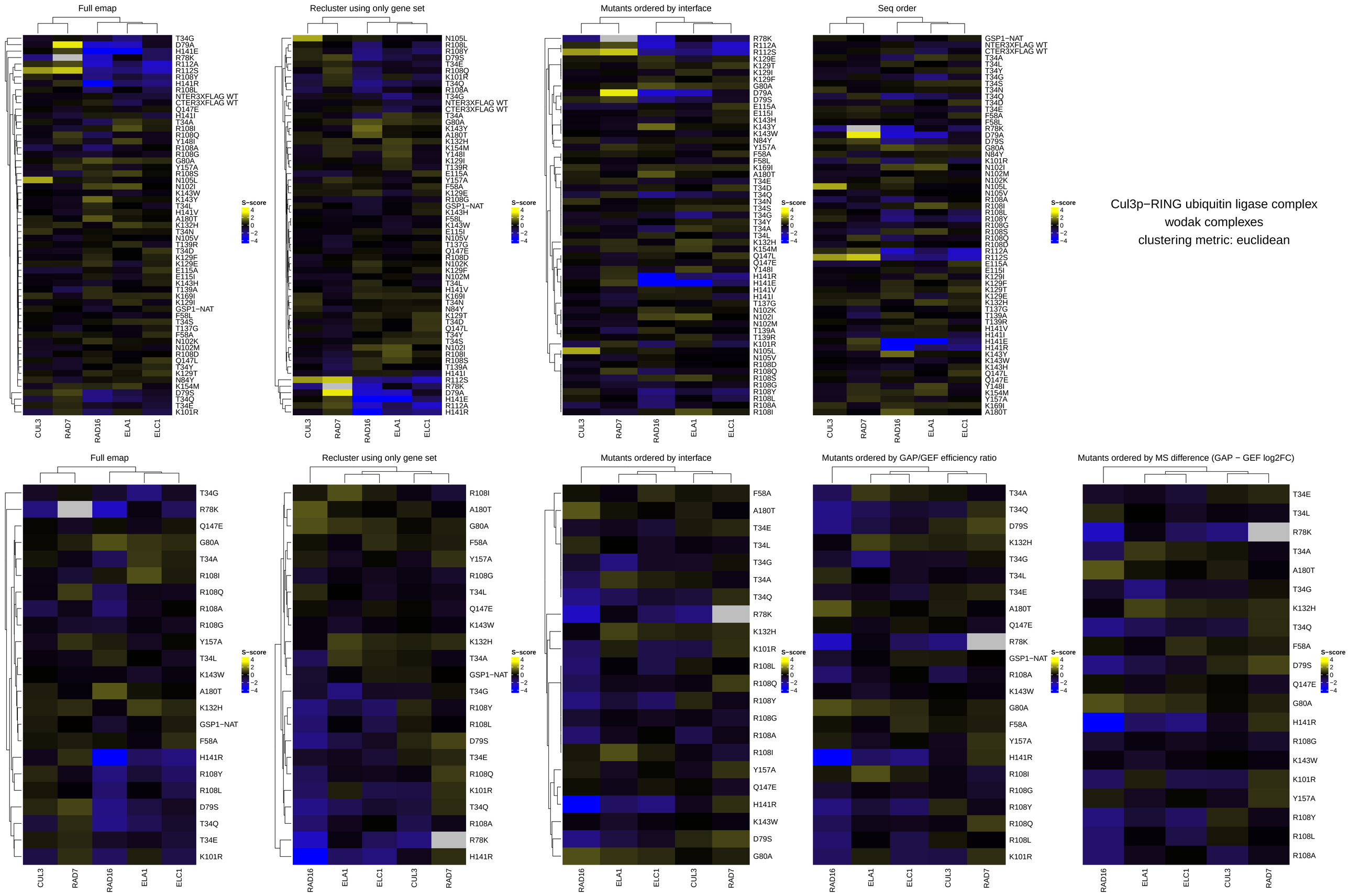
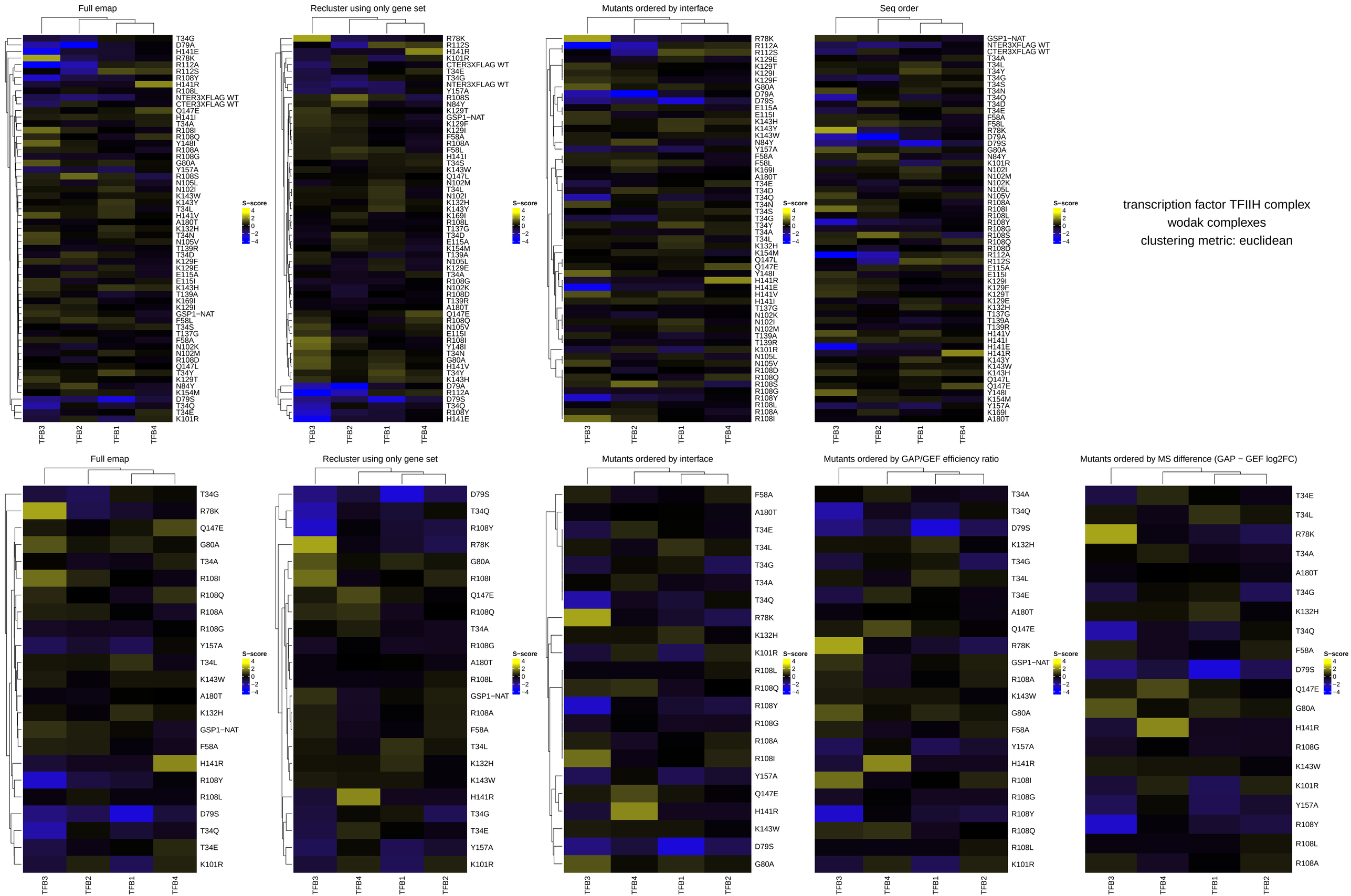
2
0
−2
−4
YDL176W
RMD5
VID30
FBP degradation complex
wodak complexes
clustering metric: euclidean

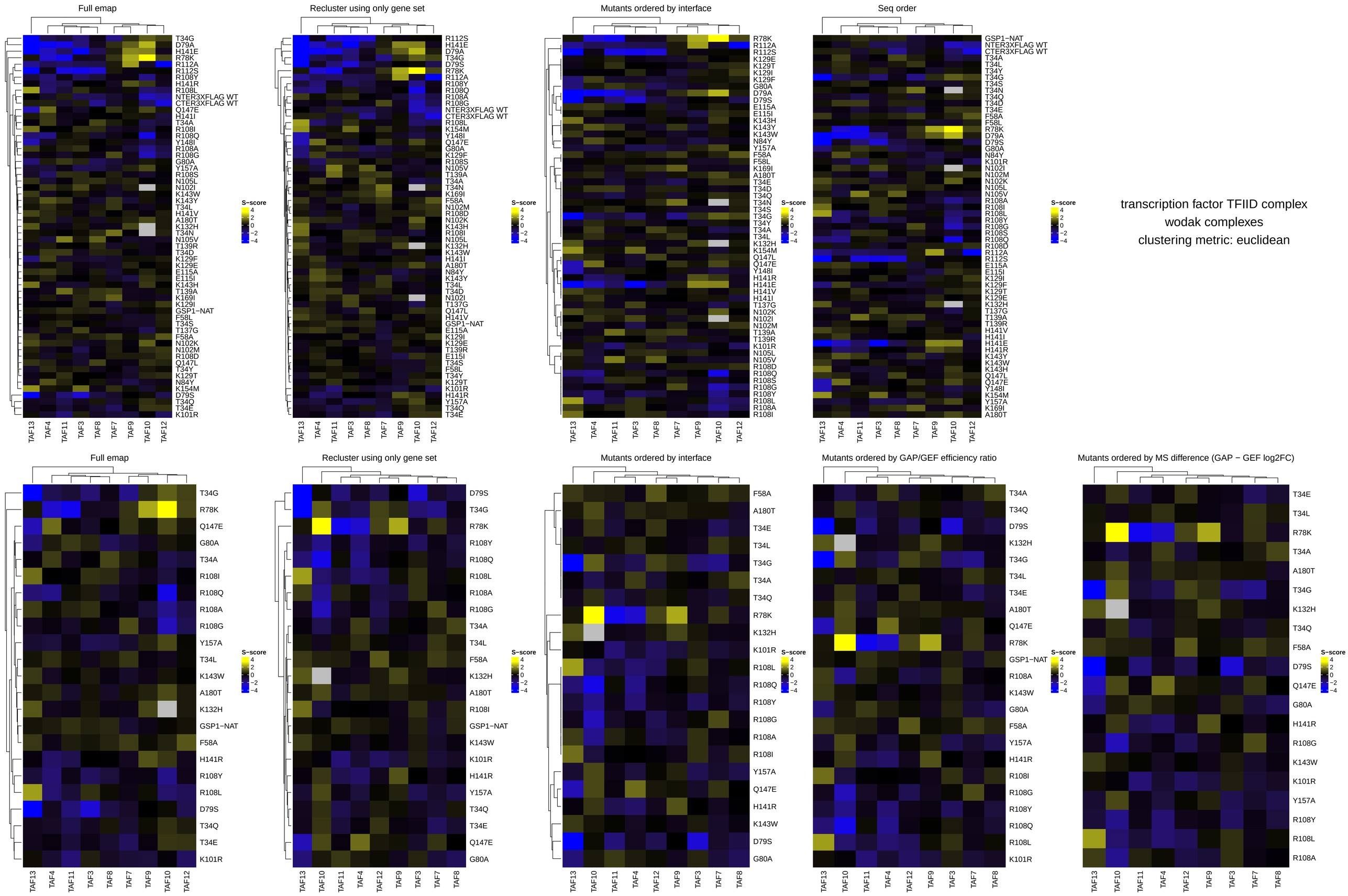


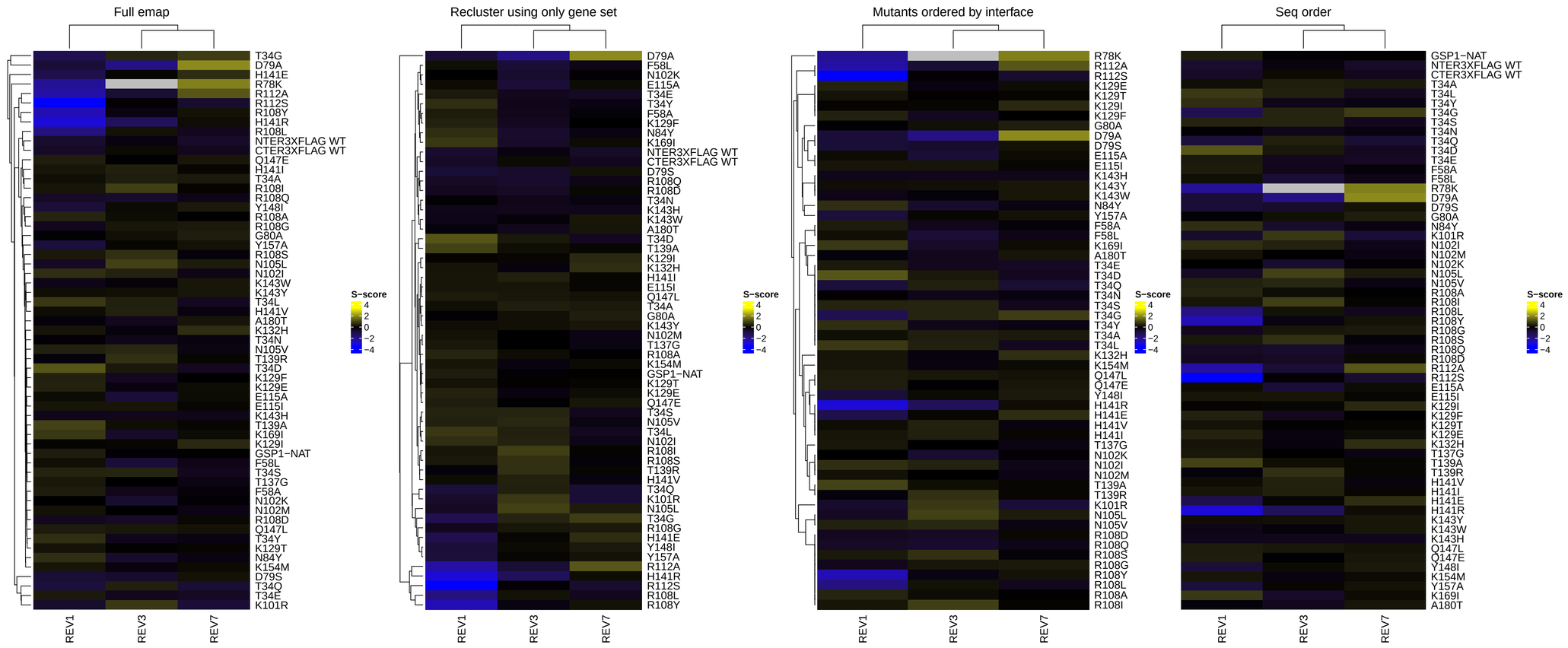


cytoplasmic ribosomal large subunit
wodak complexes
clustering metric: euclidean

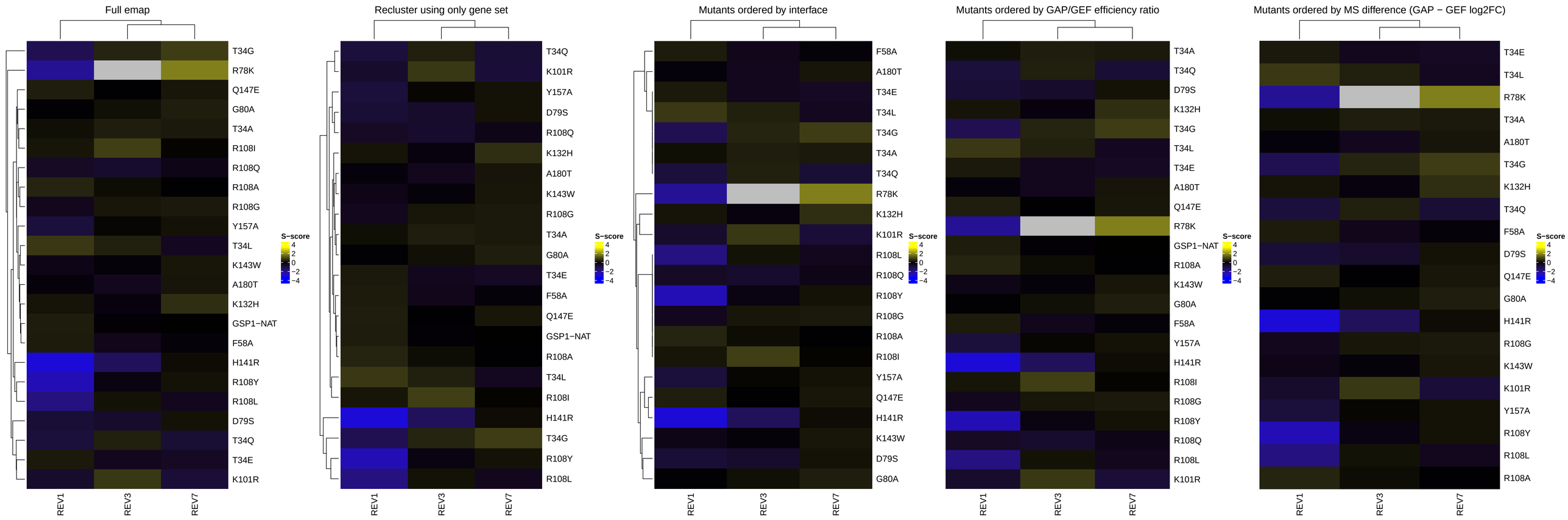

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CUL3
RAD7
RAD16
ELA1
ELC1
Cul3p−RING ubiquitin ligase complex
wodak complexes
clustering metric: euclidean

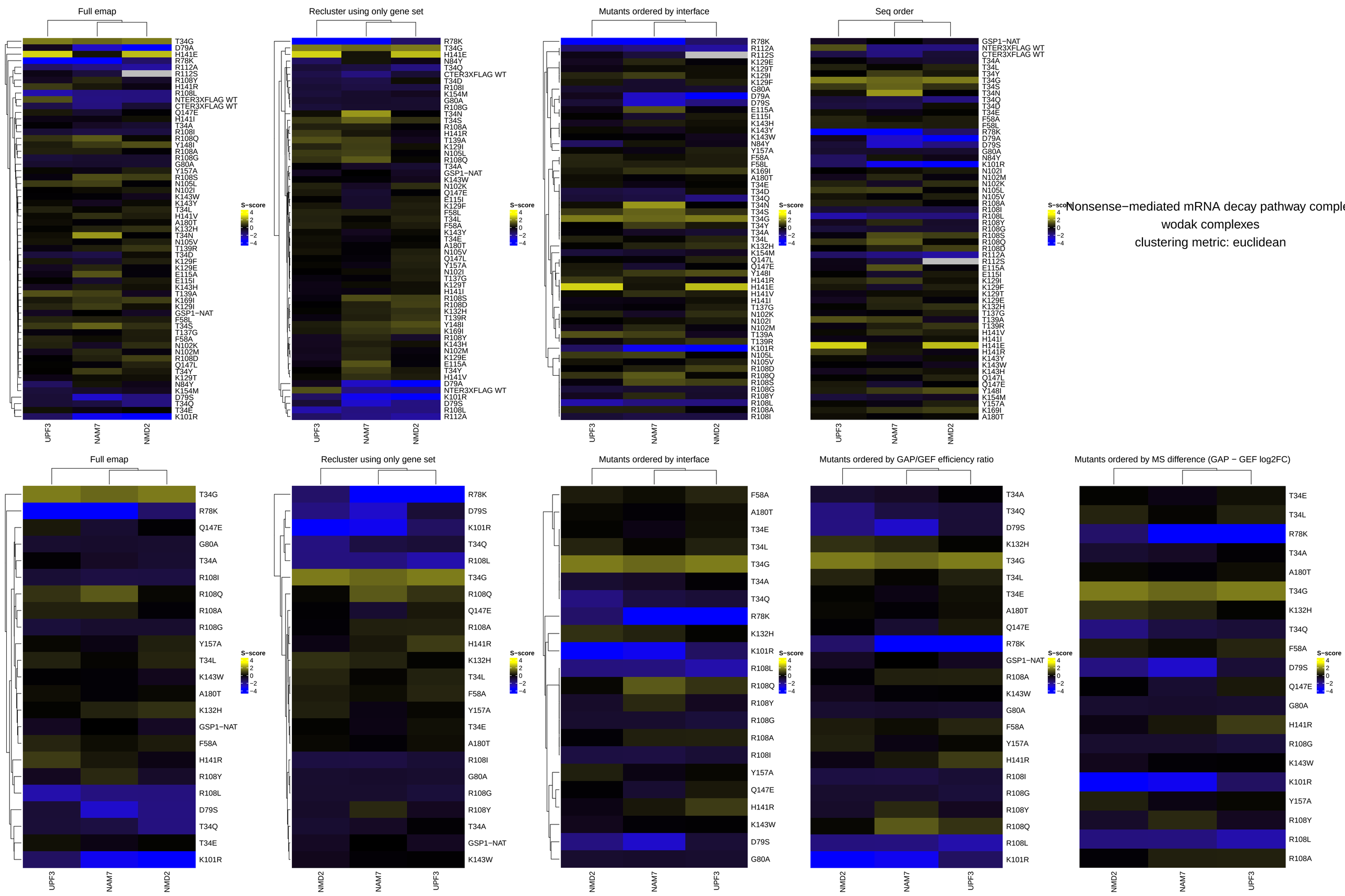

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TFB3
TFB2
TFB1
TFB4
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
transcription factor TFIIH complex
wodak complexes
clustering metric: euclidean

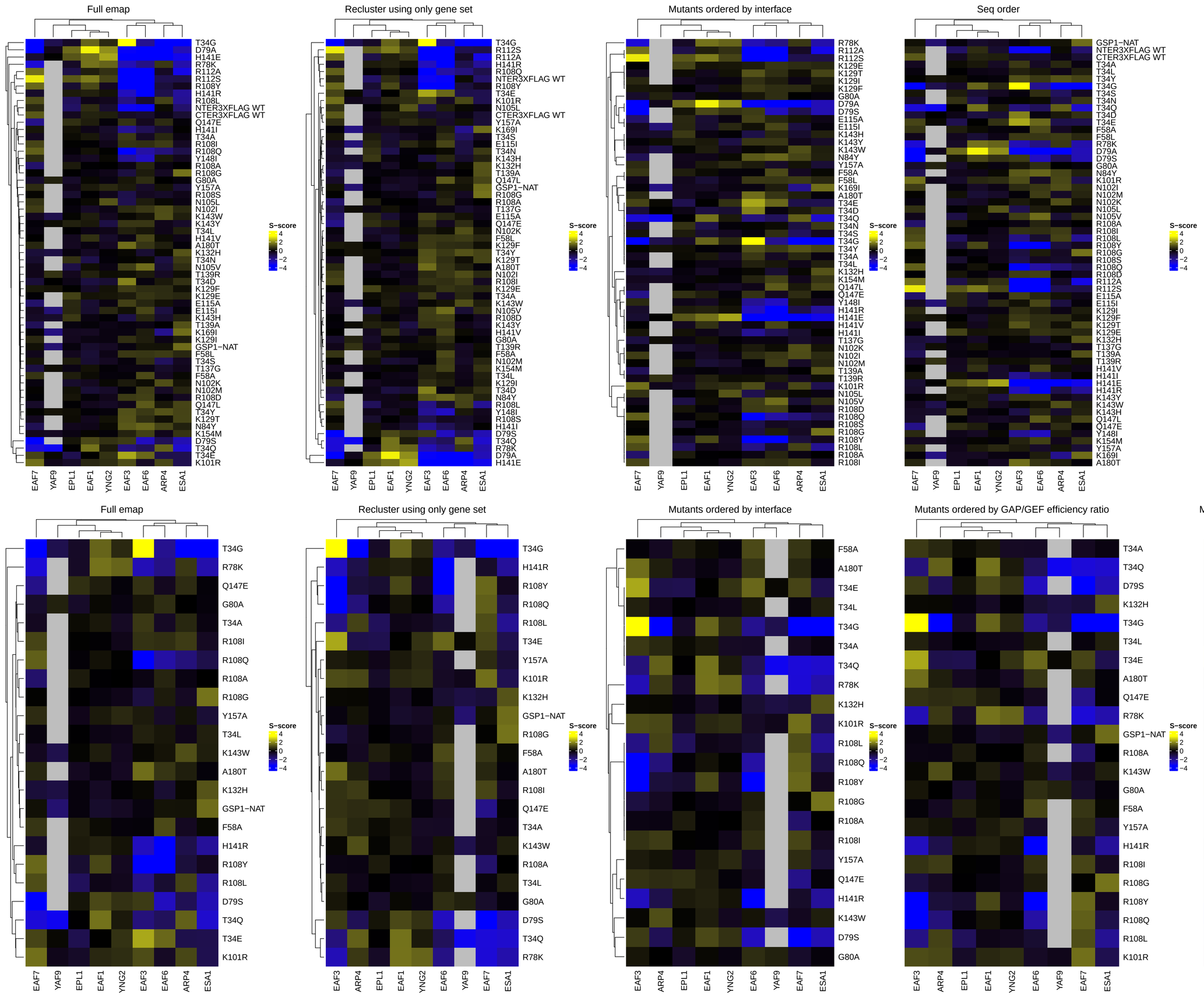

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TAF13
TAF4
TAF11
TAF3
TAF8
TAF7
TAF9
TAF10
TAF12
transcription factor TFIID complex
wodak complexes
clustering metric: euclidean
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)



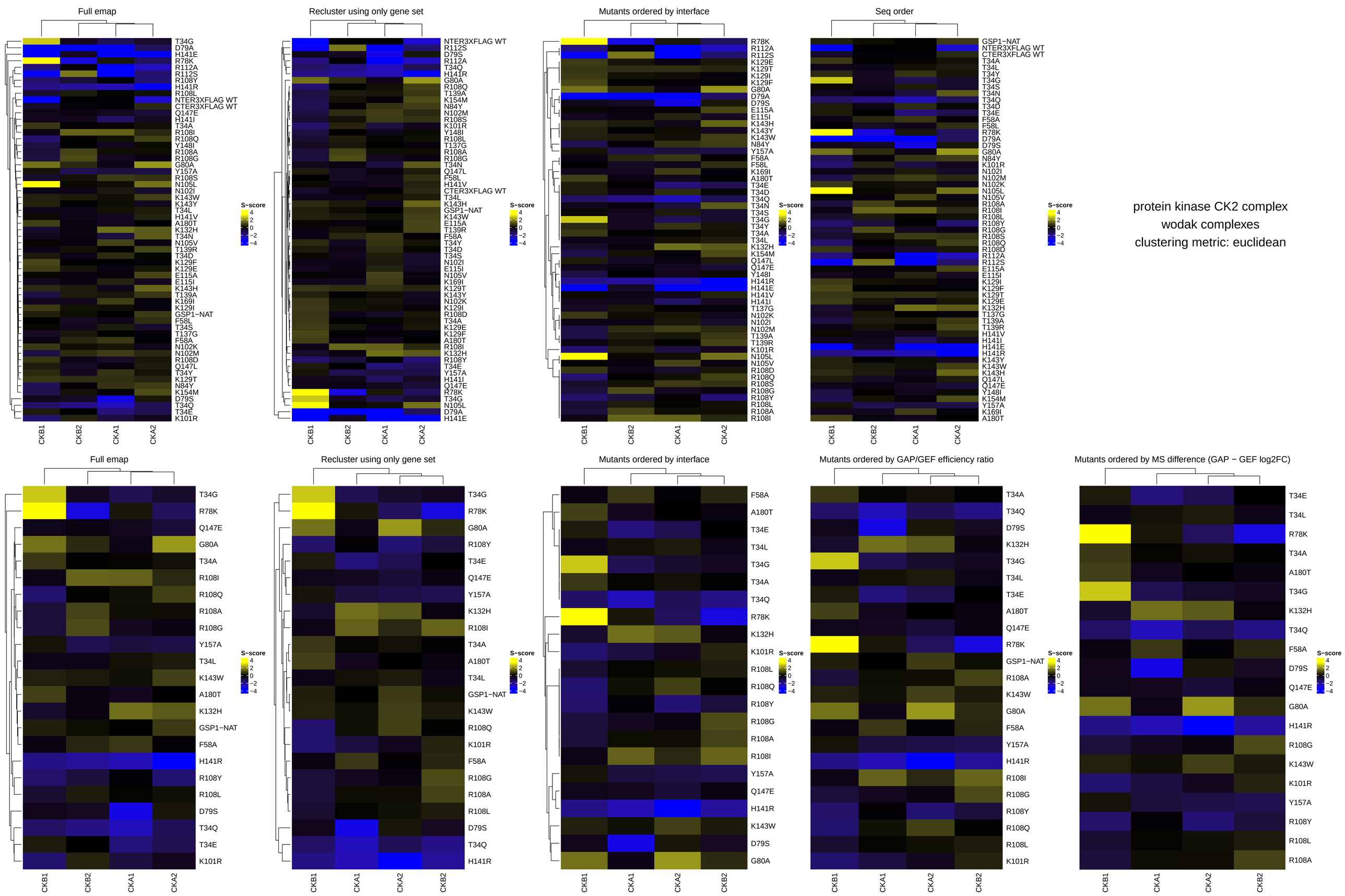
Polzeta−Rev1p complex
wodak complexes
clustering metric: euclidean

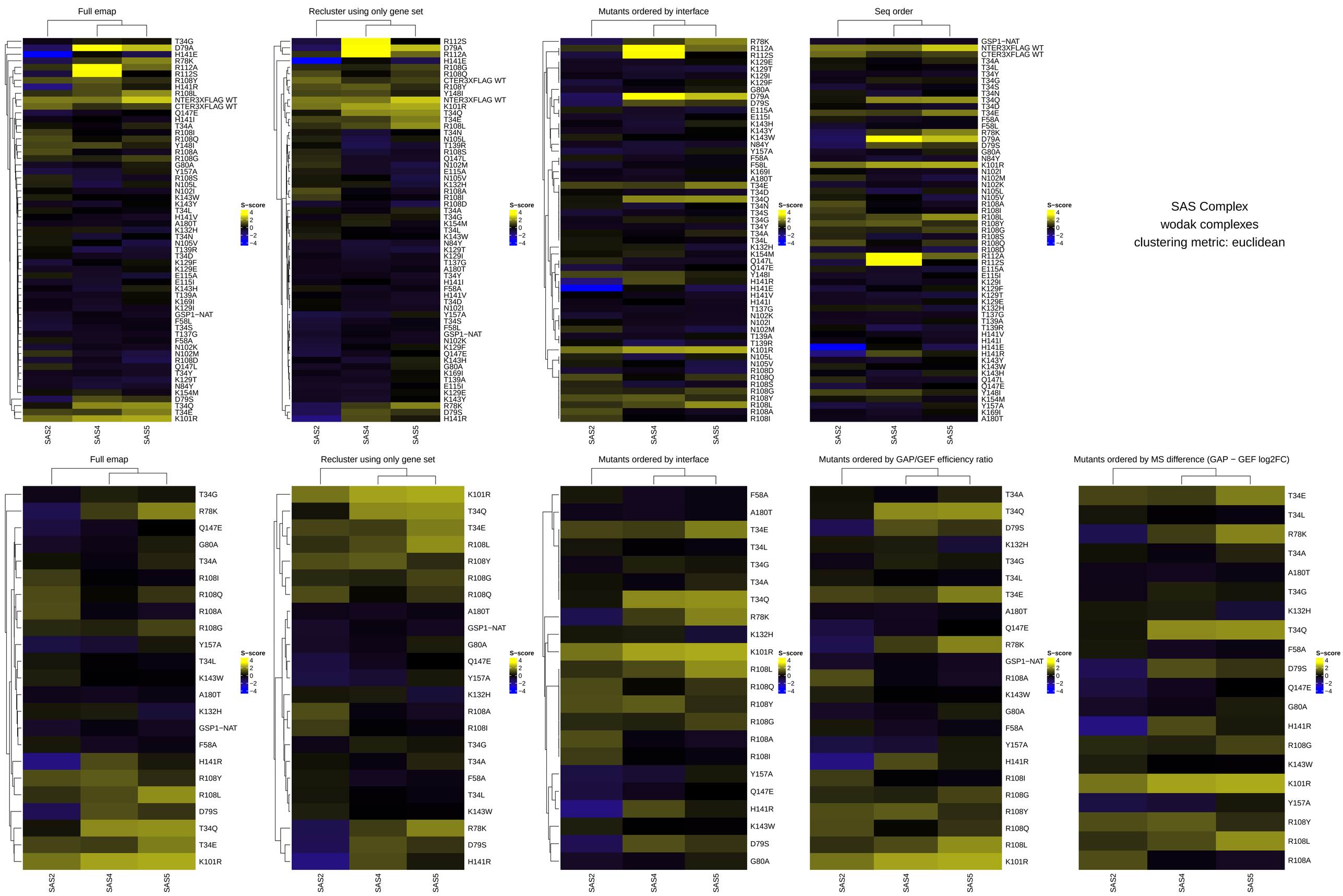


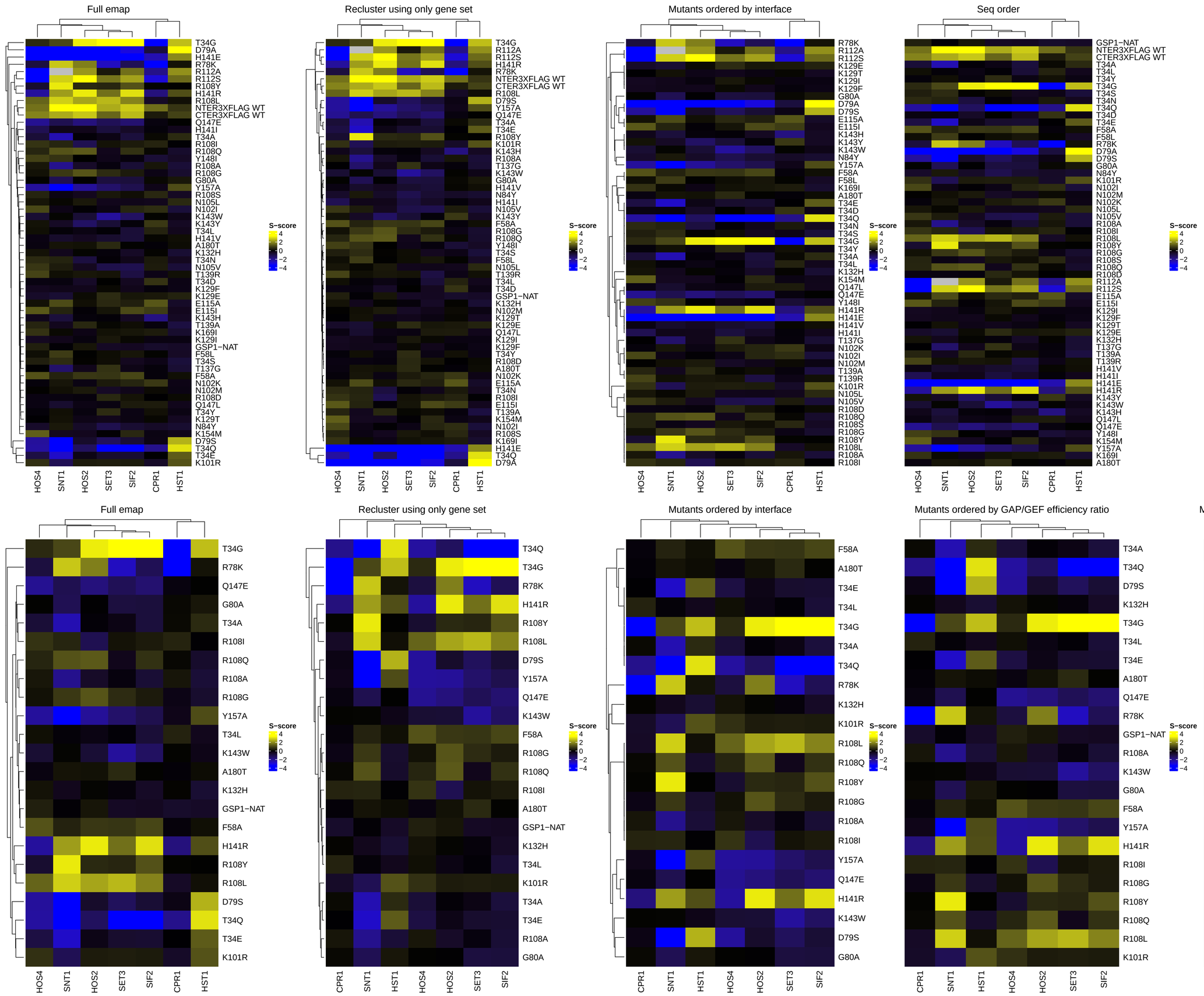

Nonsense−mediated mRNA decay pathway comple
wodak complexes
clustering metric: euclidean
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
UPF3
NAM7
NMD2



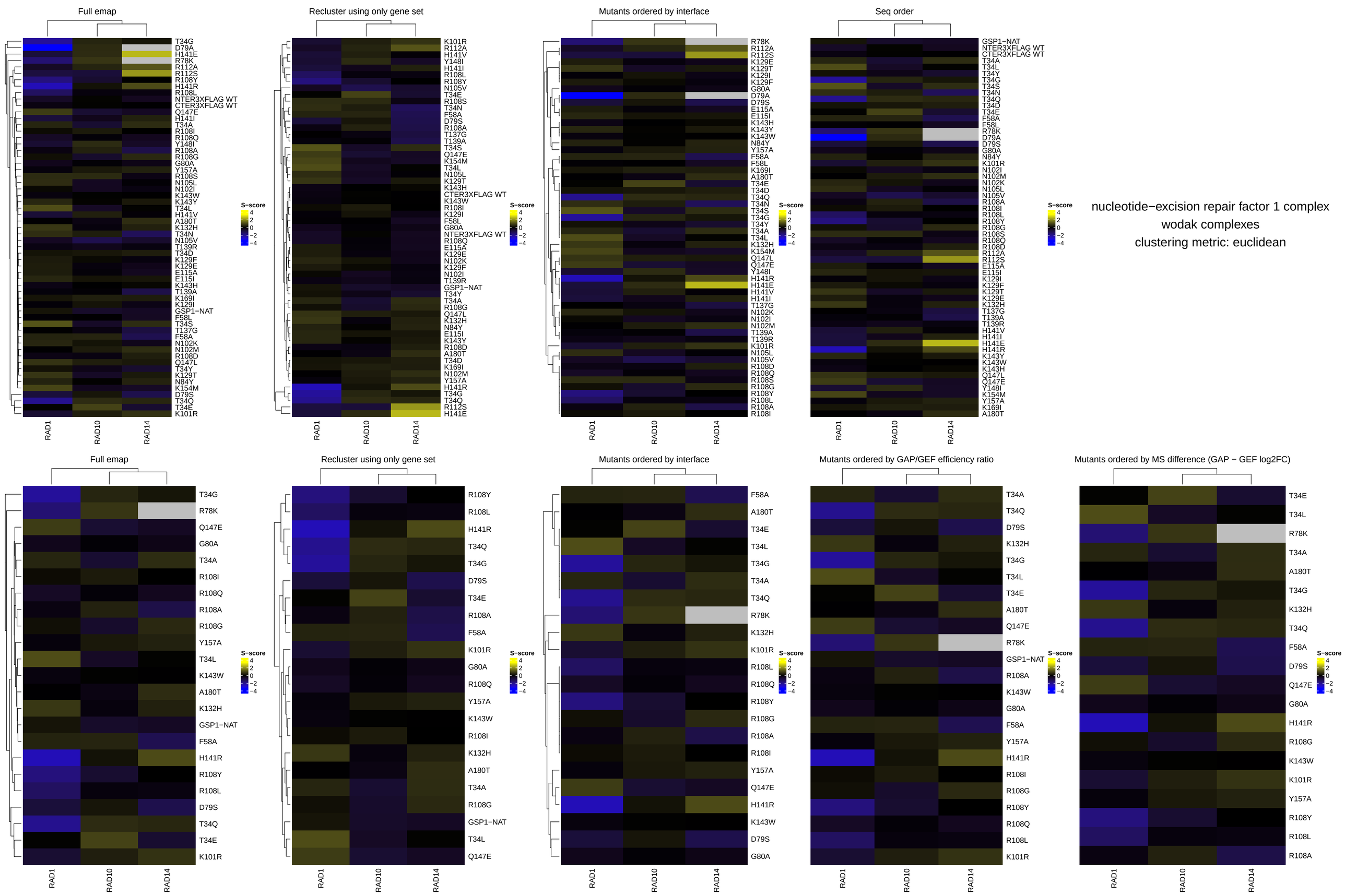
NuA4 histone acetyltransferase complex
wodak complexes
clustering metric: euclidean

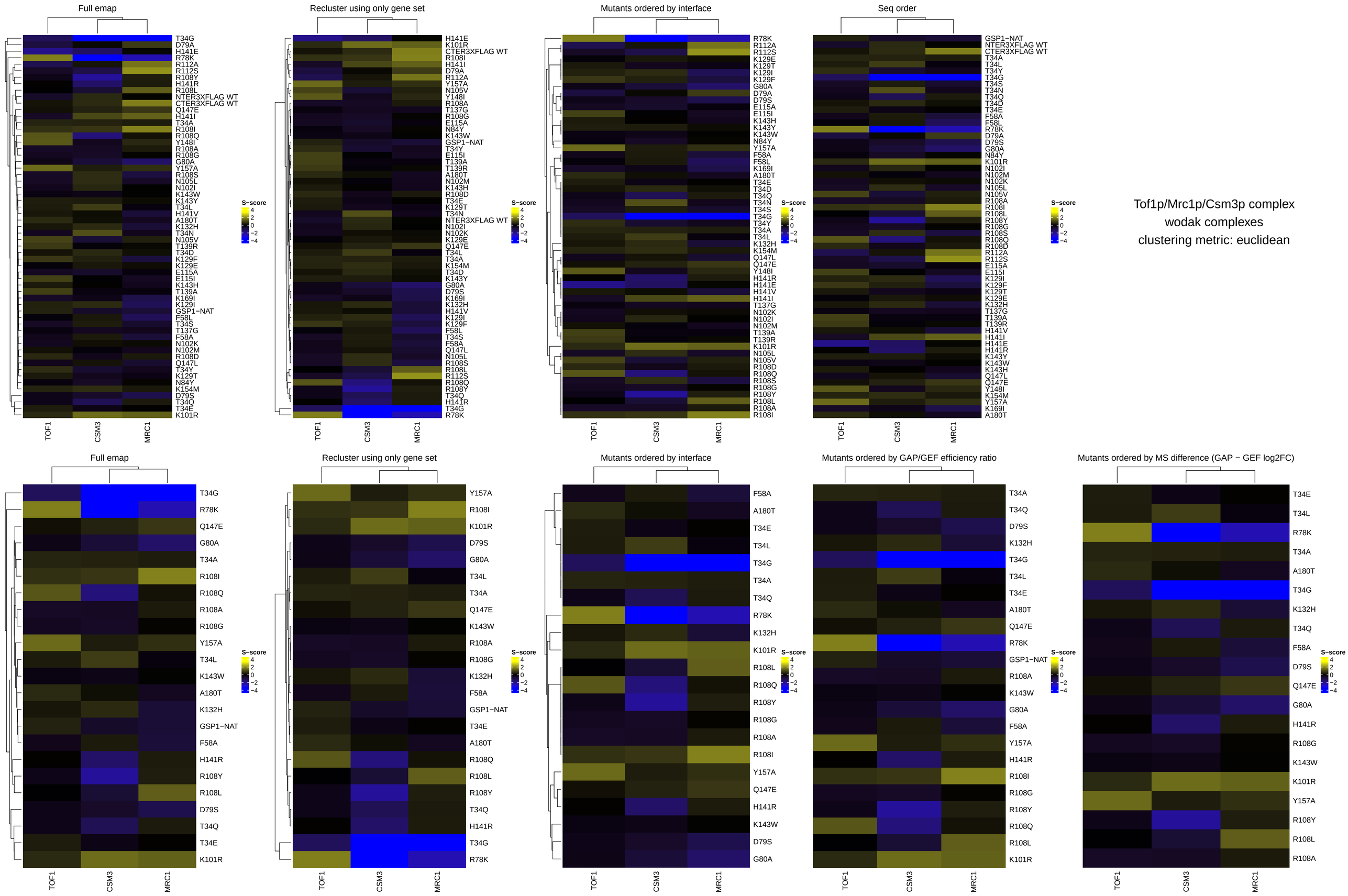

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CKB1
CKB2
CKA1
CKA2
protein kinase CK2 complex
wodak complexes
clustering metric: euclidean

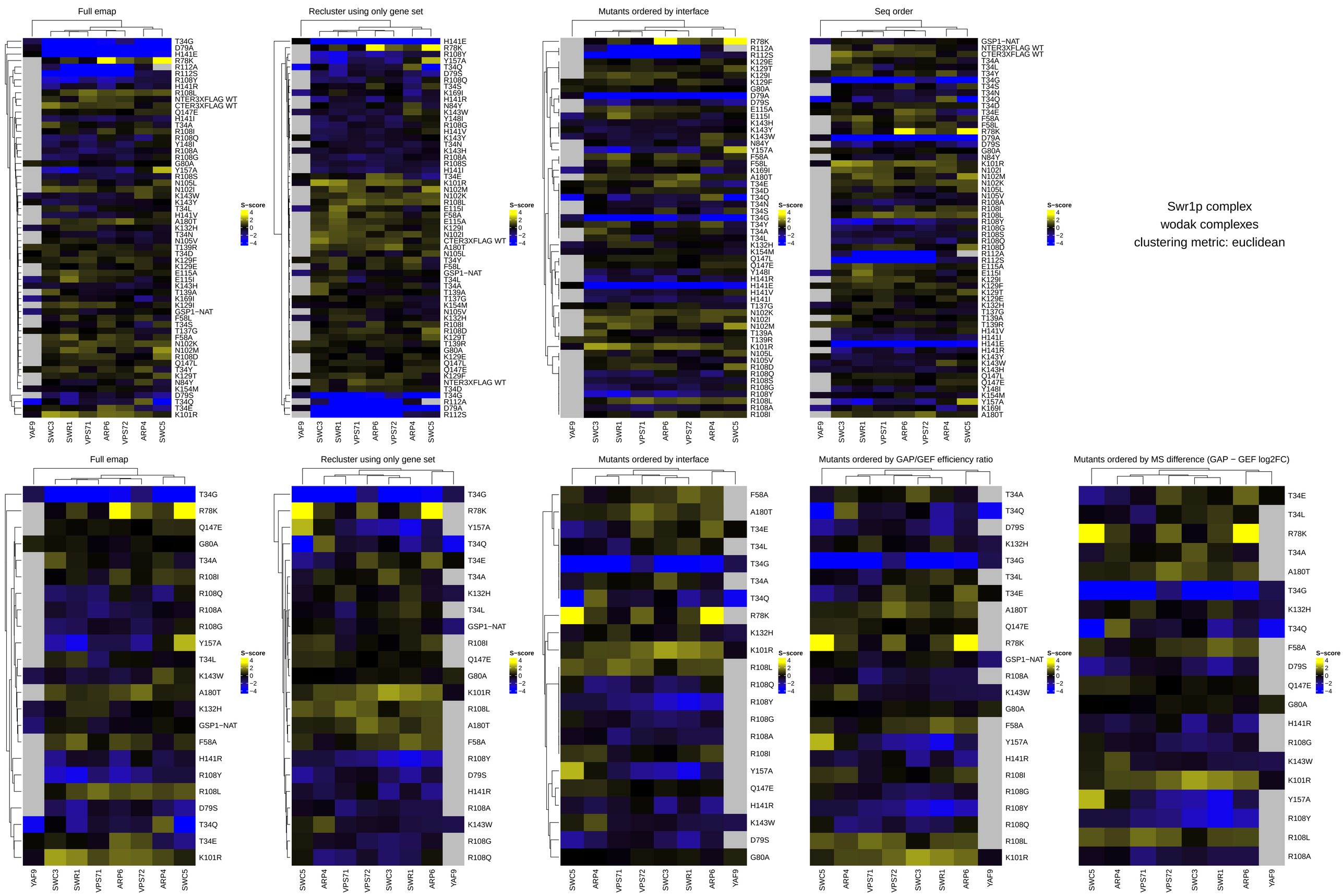

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SAS2
SAS4
SAS5
SAS Complex
wodak complexes
clustering metric: euclidean

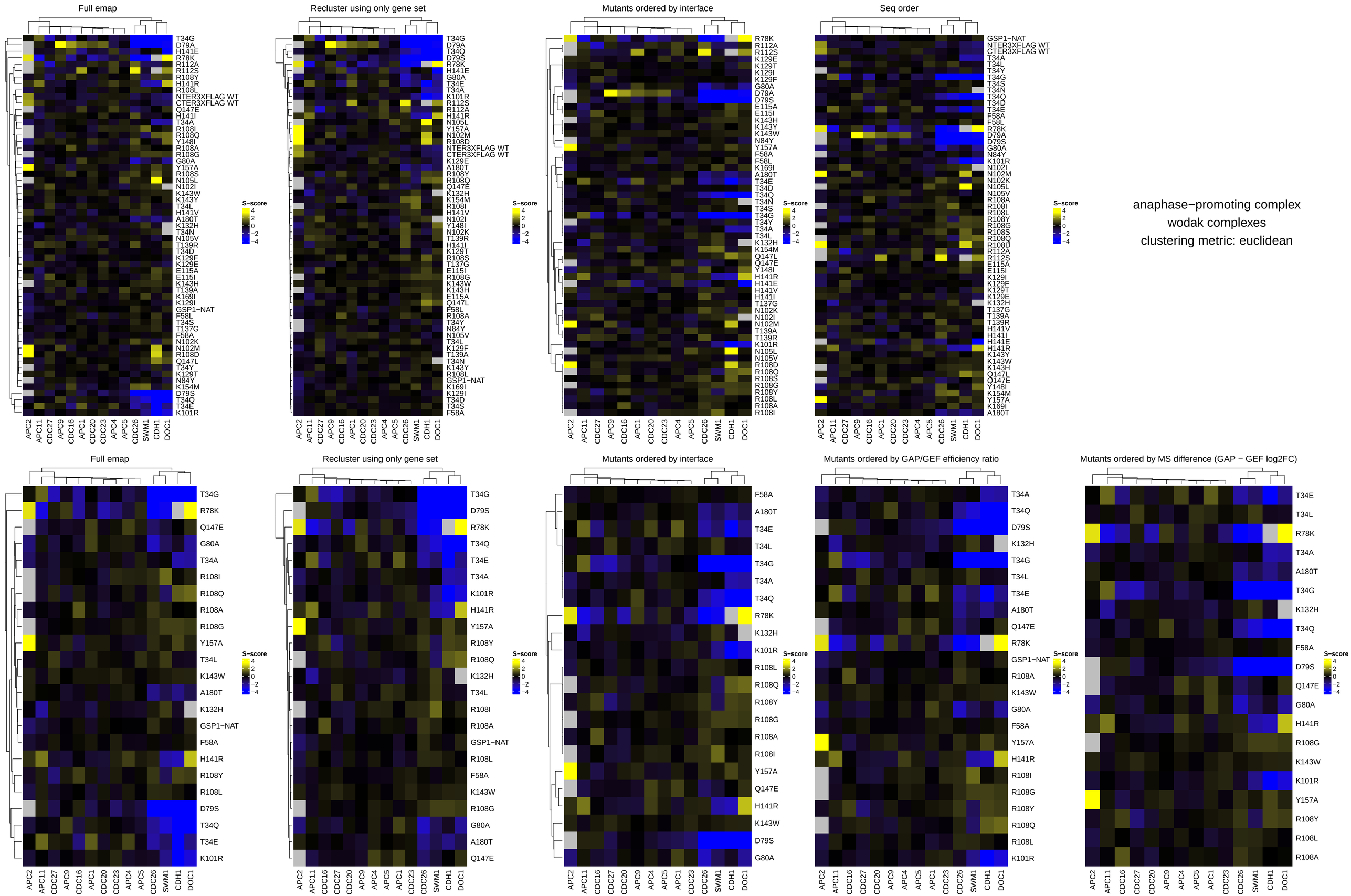


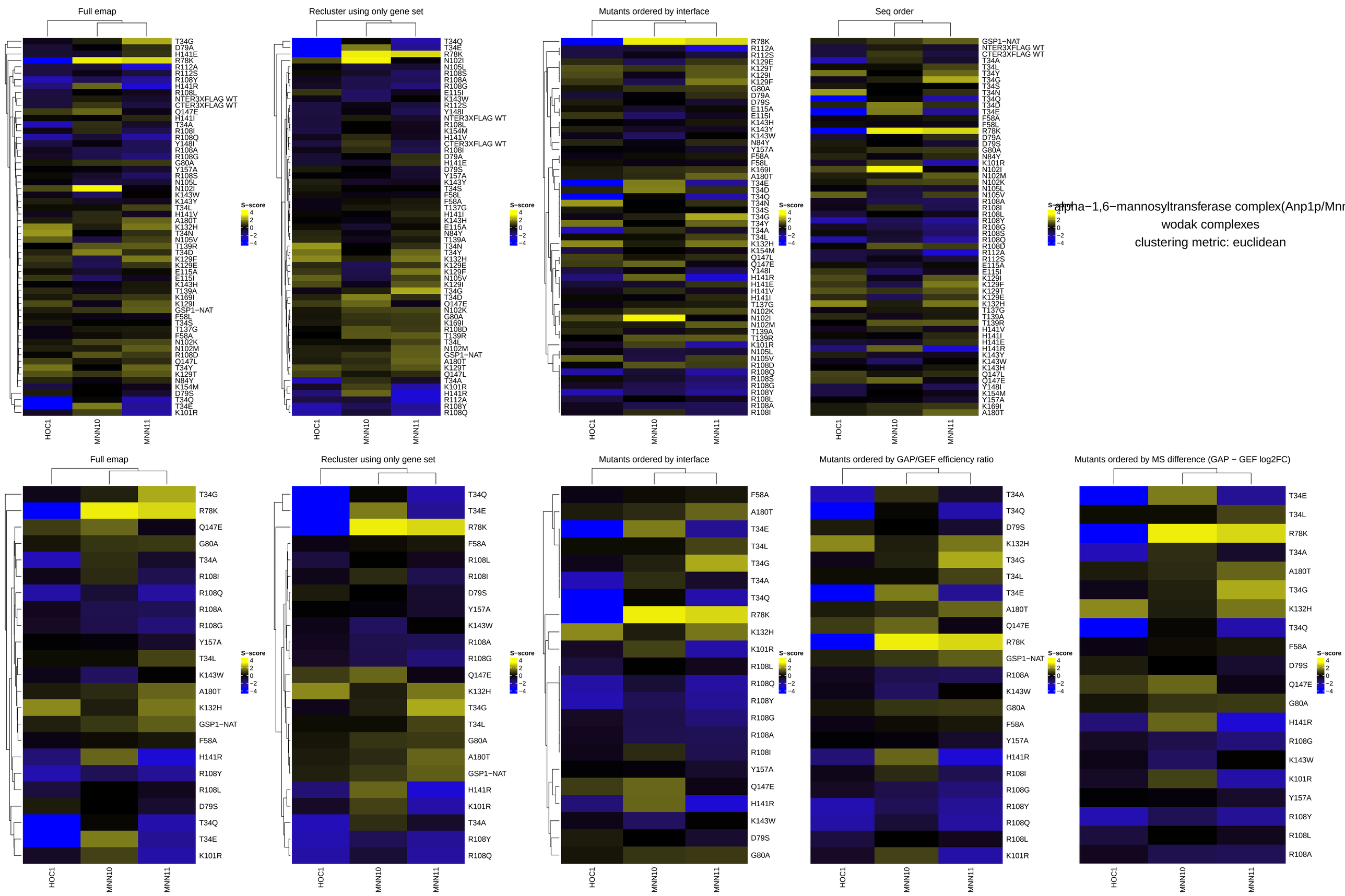
Set3p complex
wodak complexes
clustering metric: euclidean

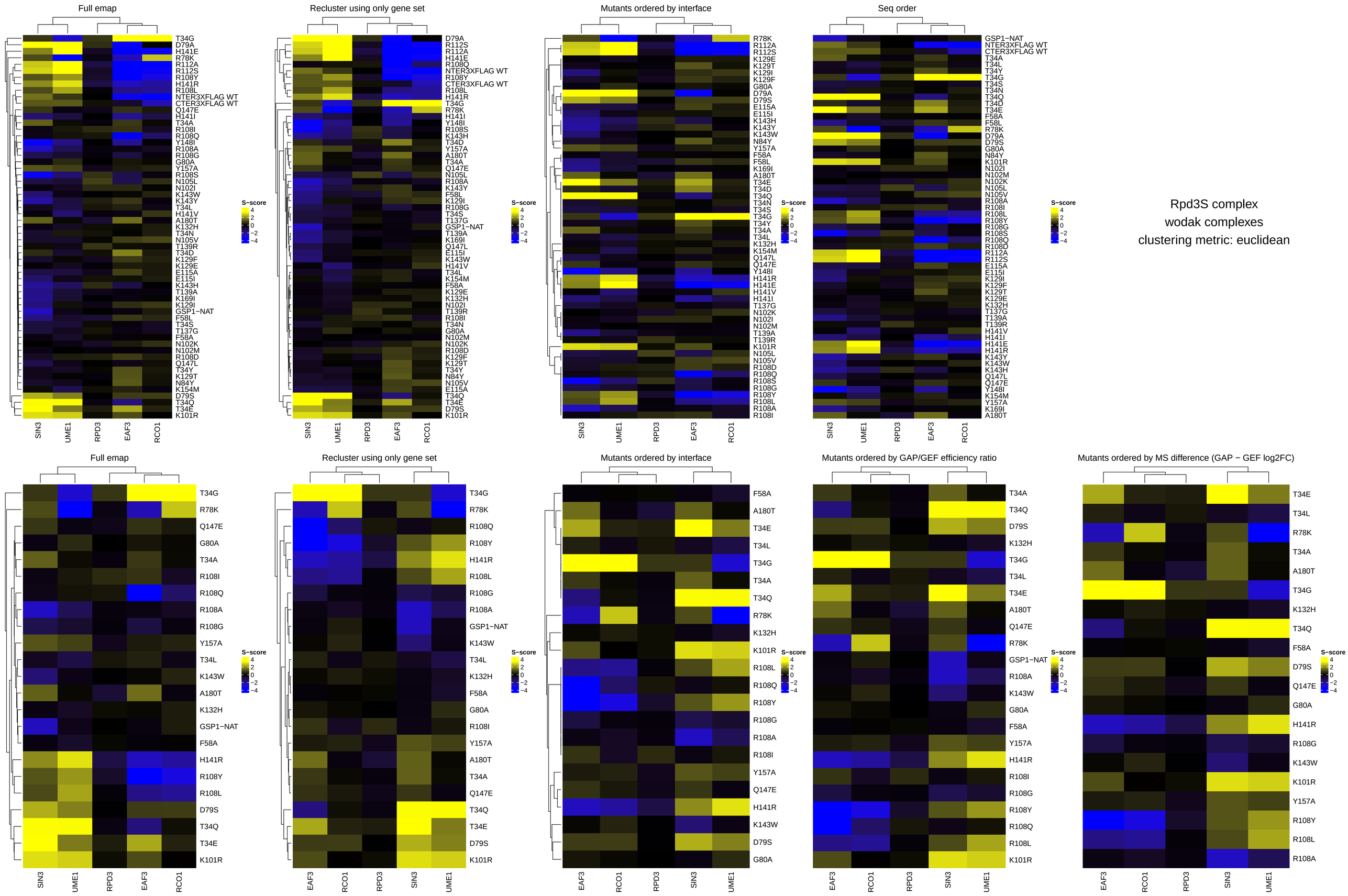

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RAD1
RAD10
RAD14
nucleotide−excision repair factor 1 complex
wodak complexes
clustering metric: euclidean

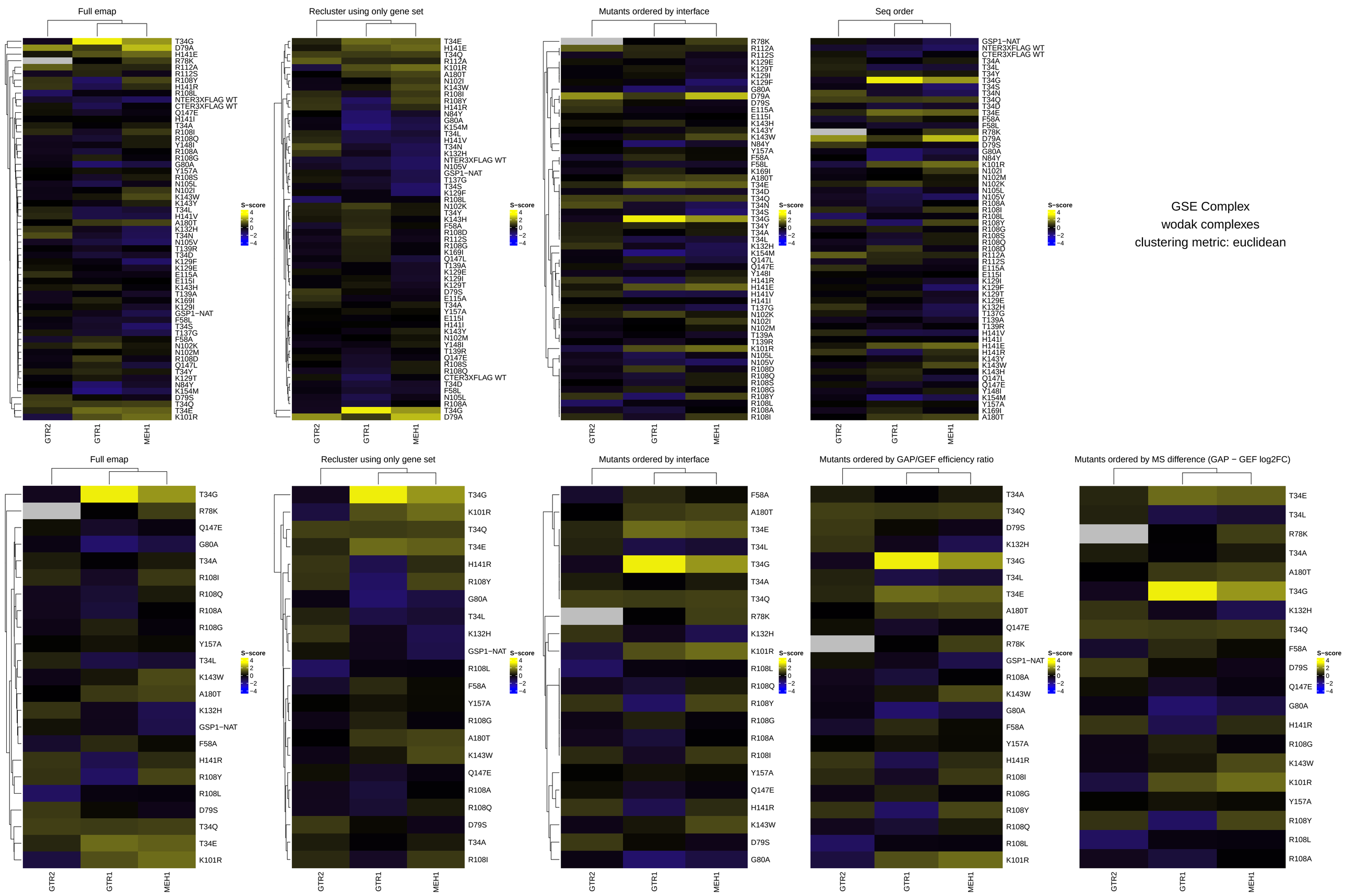

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
TOF1
CSM3
MRC1
Tof1p/Mrc1p/Csm3p complex
wodak complexes
clustering metric: euclidean


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
4
2
0
−2
−4
YAF9
SWC3
SWR1
VPS71
ARP6
VPS72
ARP4
SWC5
Swr1p complex
wodak complexes
clustering metric: euclidean

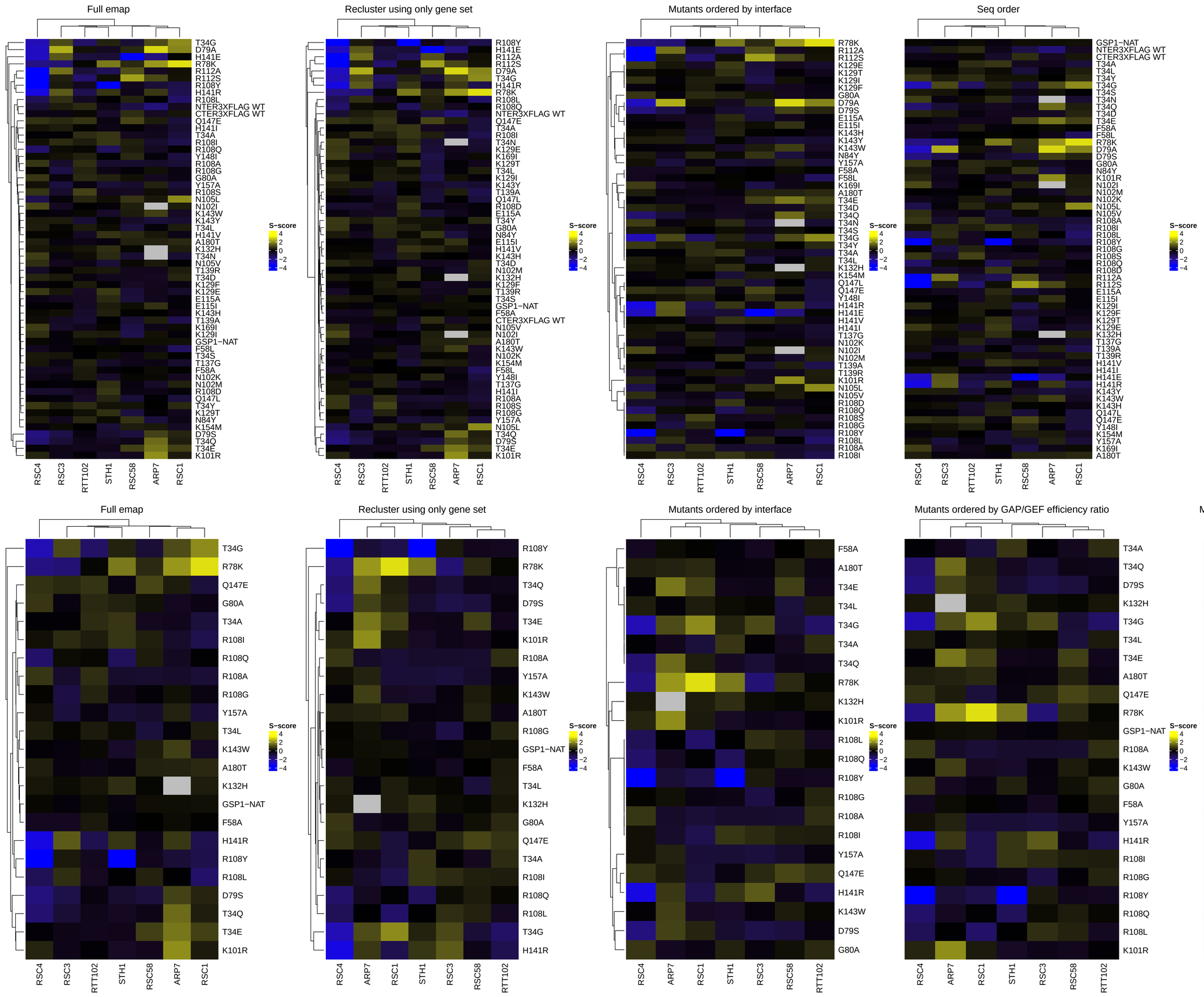

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
APC2
APC11
CDC27
APC9
CDC16
APC1
CDC20
CDC23
APC4
APC5
CDC26
SWM1
CDH1
DOC1
anaphase−promoting complex
wodak 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
4
2
0
−2
−4
HOC1
MNN10
MNN11
alpha−1,6−mannosyltransferase complex(Anp1p/Mnn
wodak complexes
clustering metric: euclidean

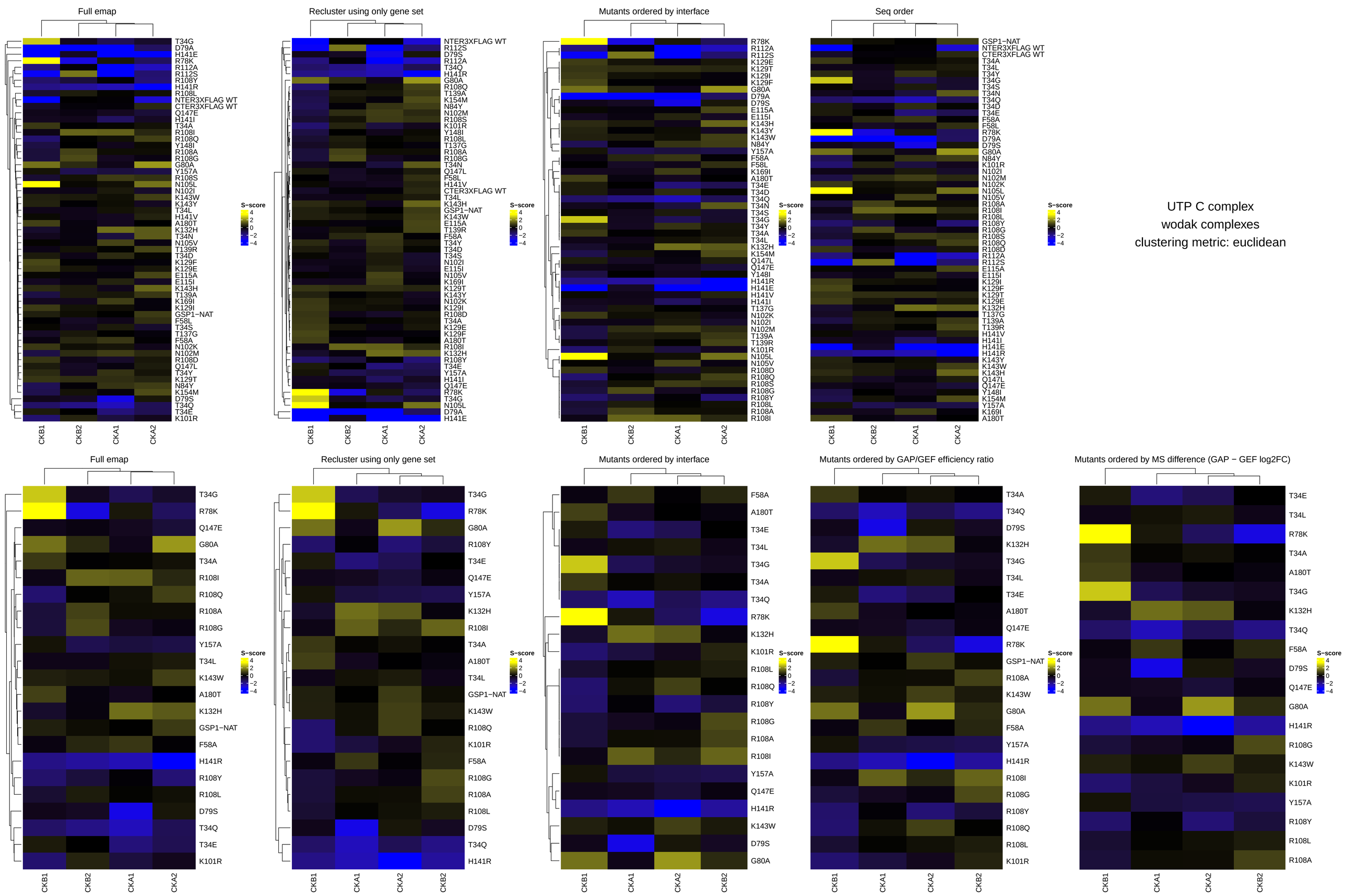

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SIN3
UME1
RPD3
EAF3
RCO1
Rpd3S complex
wodak complexes
clustering metric: euclidean

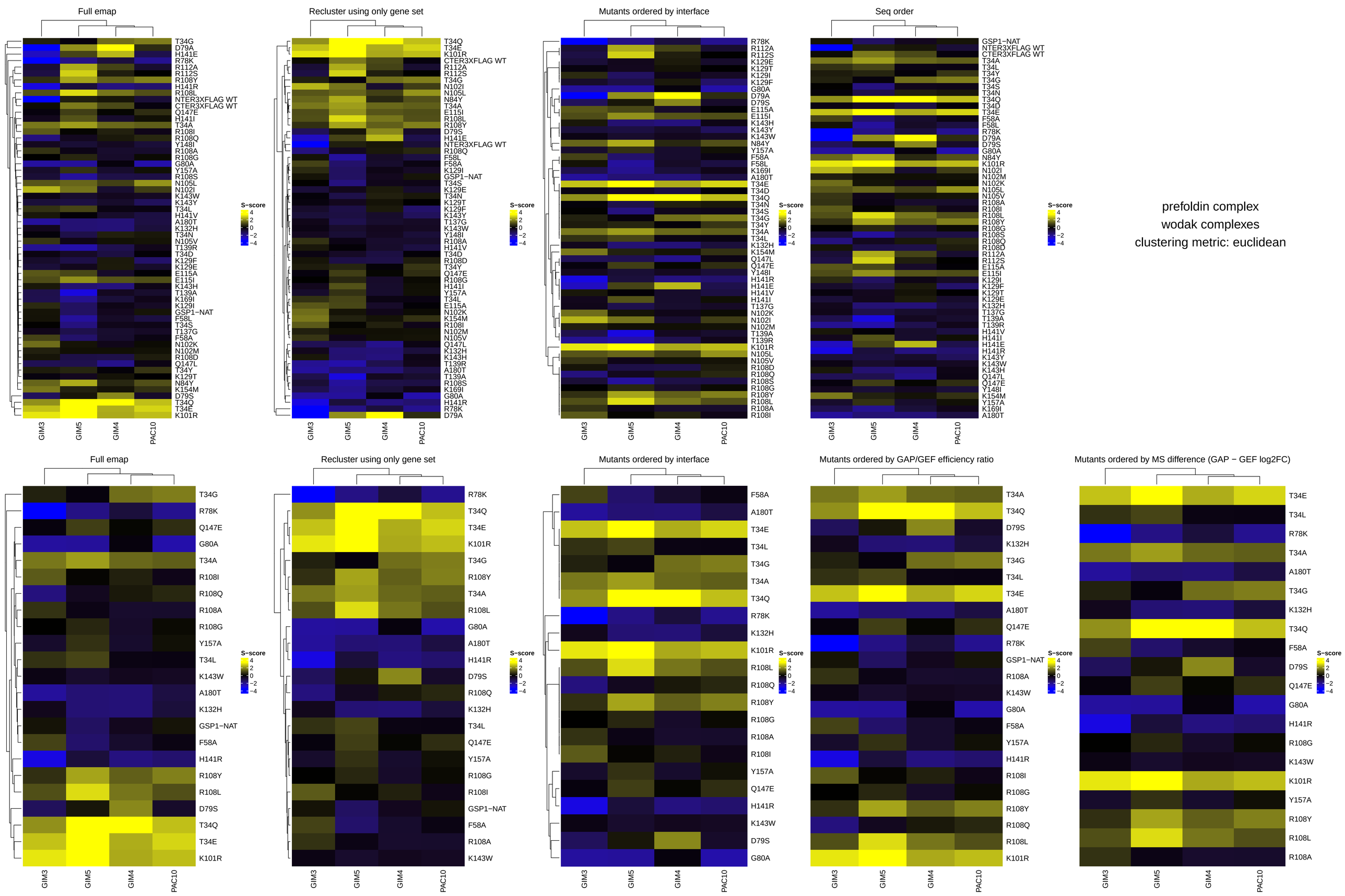


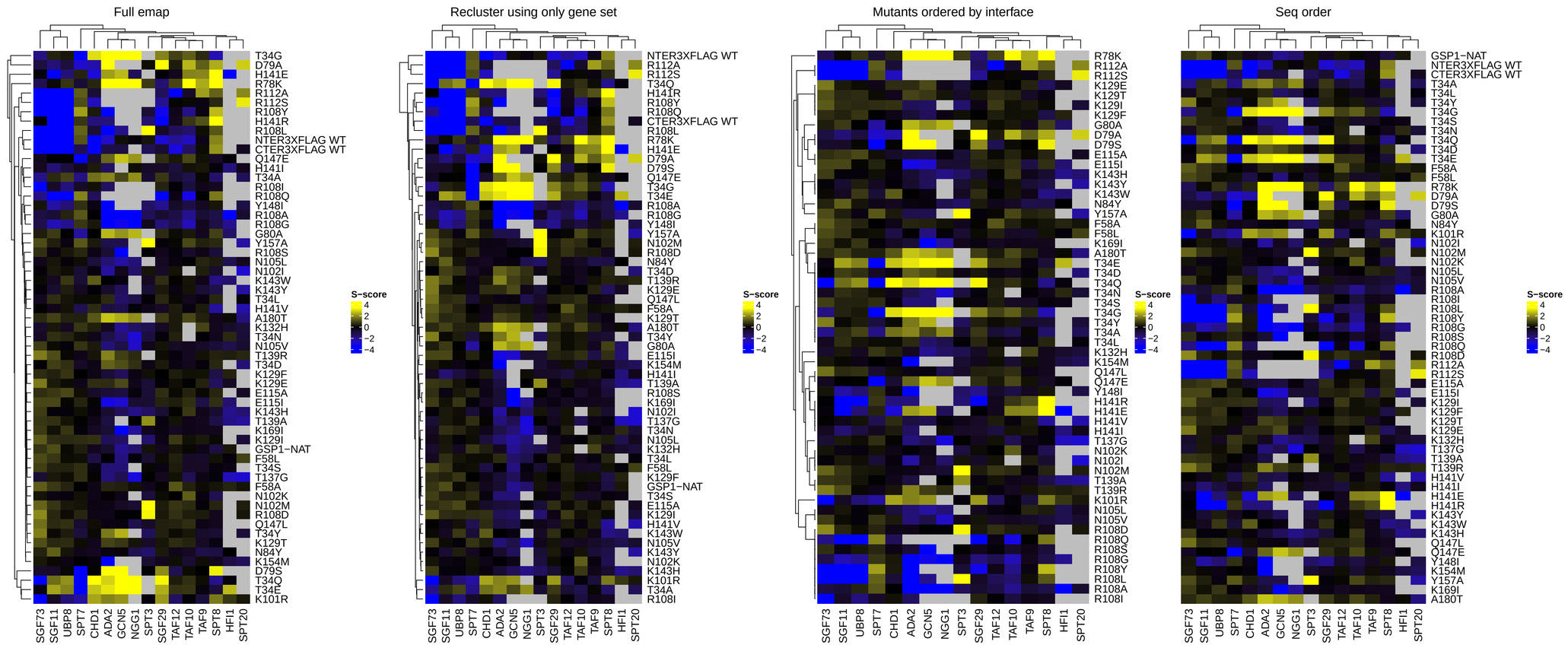
GSE Complex
wodak complexes
clustering metric: euclidean



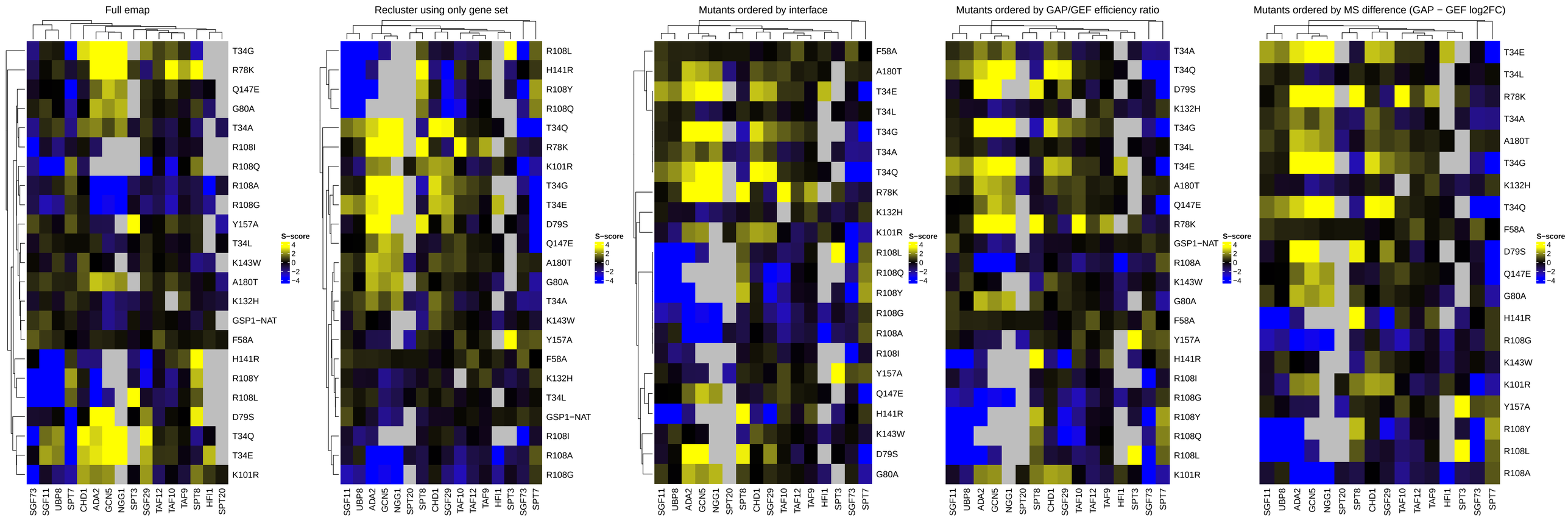
RSC complex
wodak complexes
clustering metric: euclidean

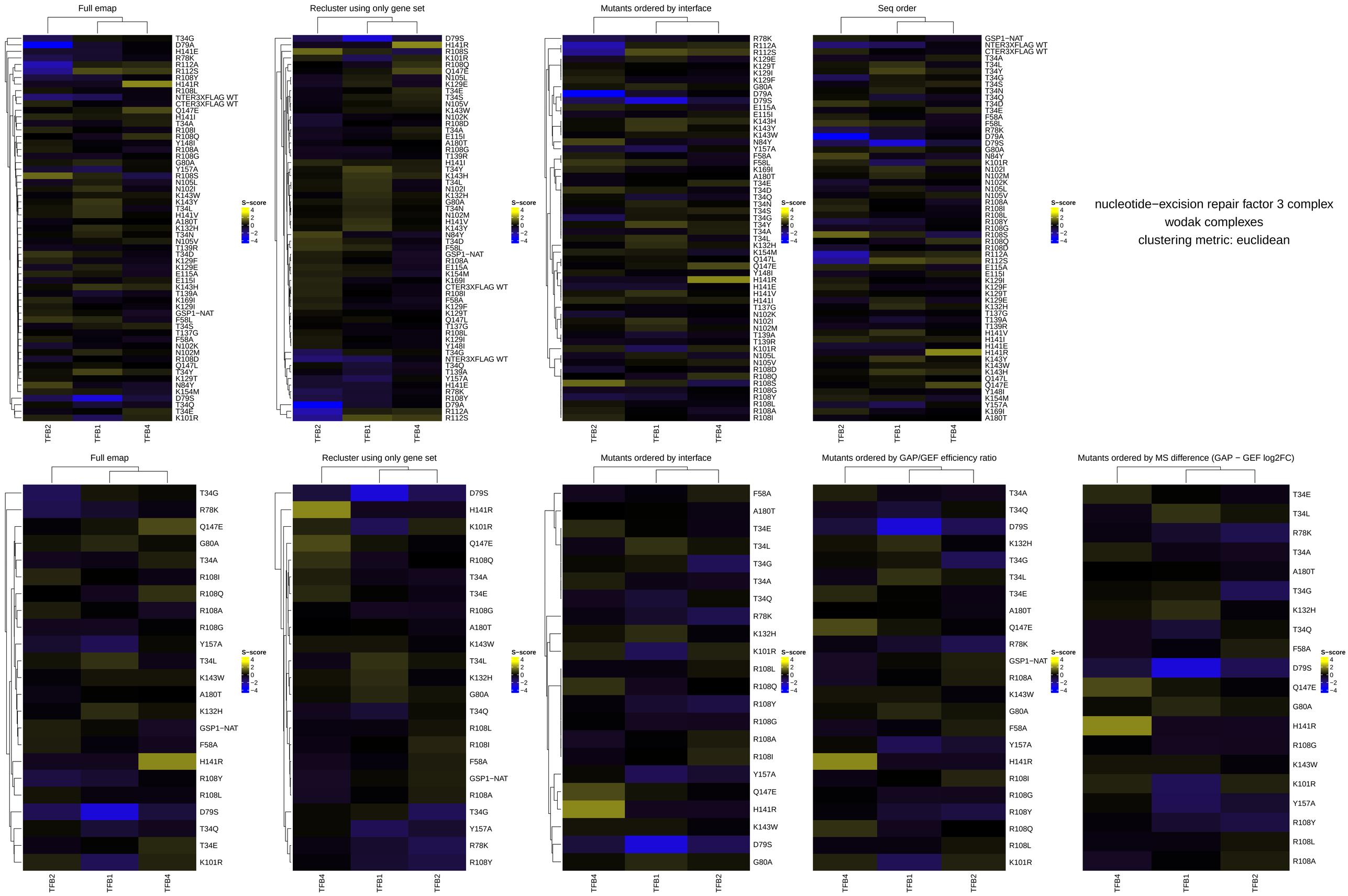

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CKB1
CKB2
CKA1
CKA2
UTP C complex
wodak complexes
clustering metric: euclidean

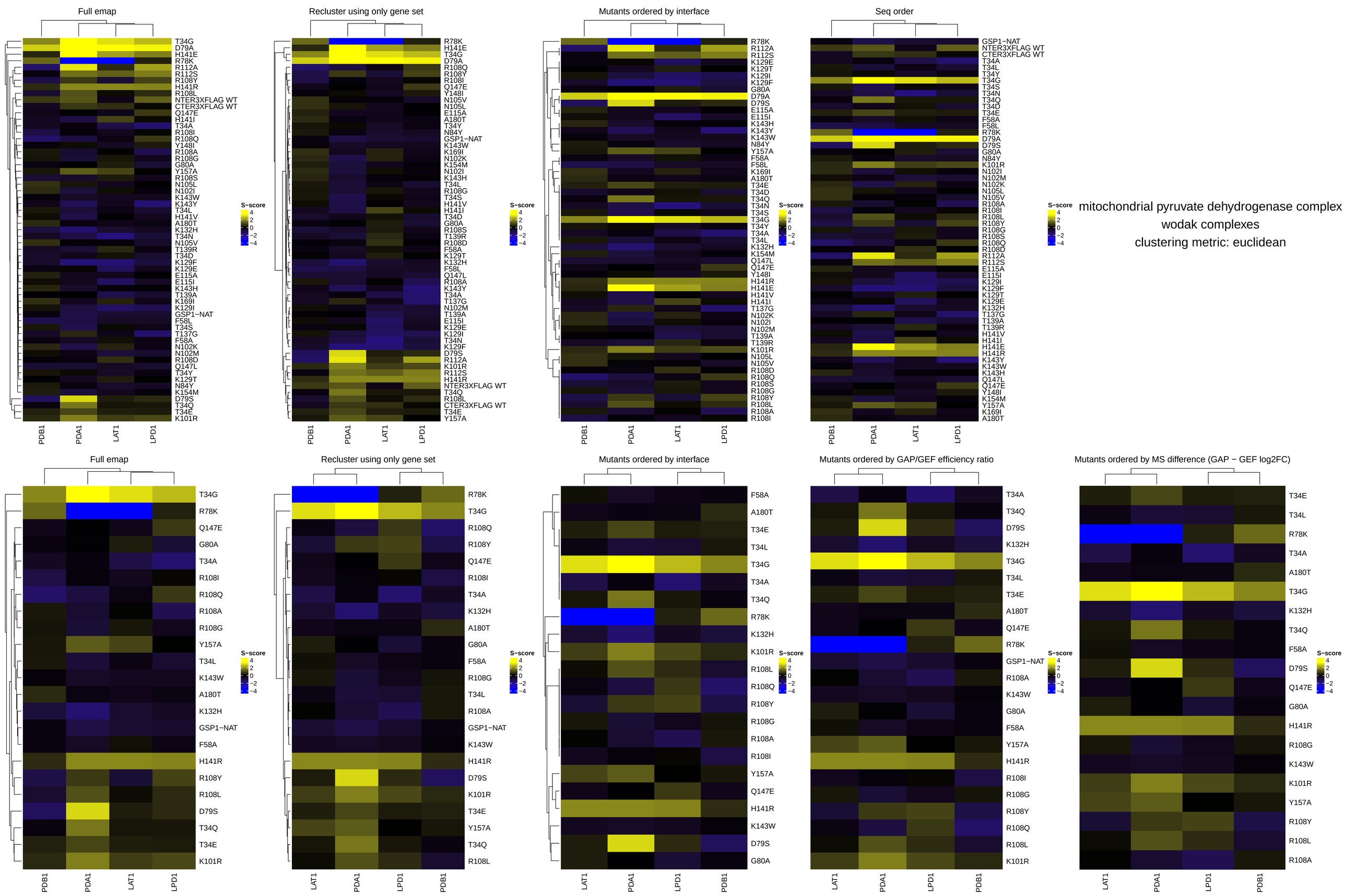

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
GIM3
GIM5
GIM4
PAC10
prefoldin complex
wodak complexes
clustering metric: euclidean

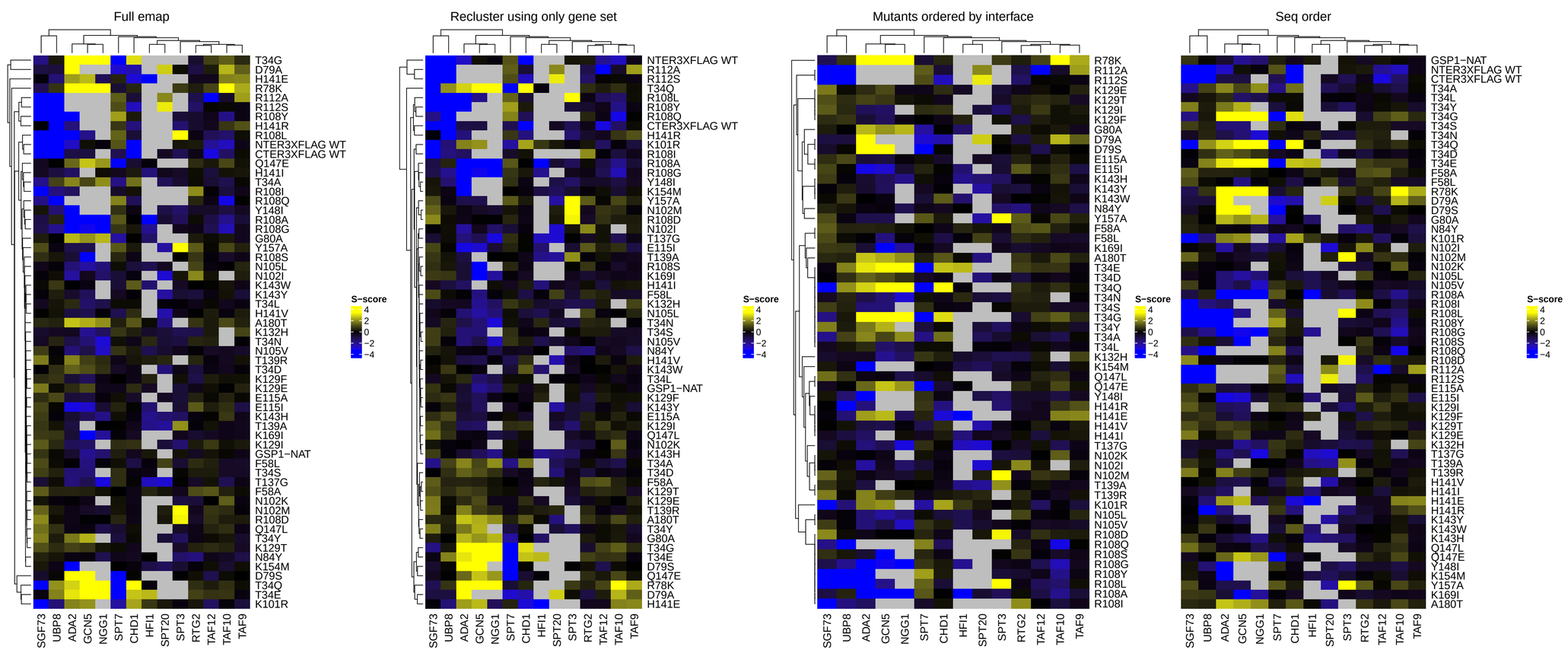


SAGA complex
wodak complexes
clustering metric: euclidean

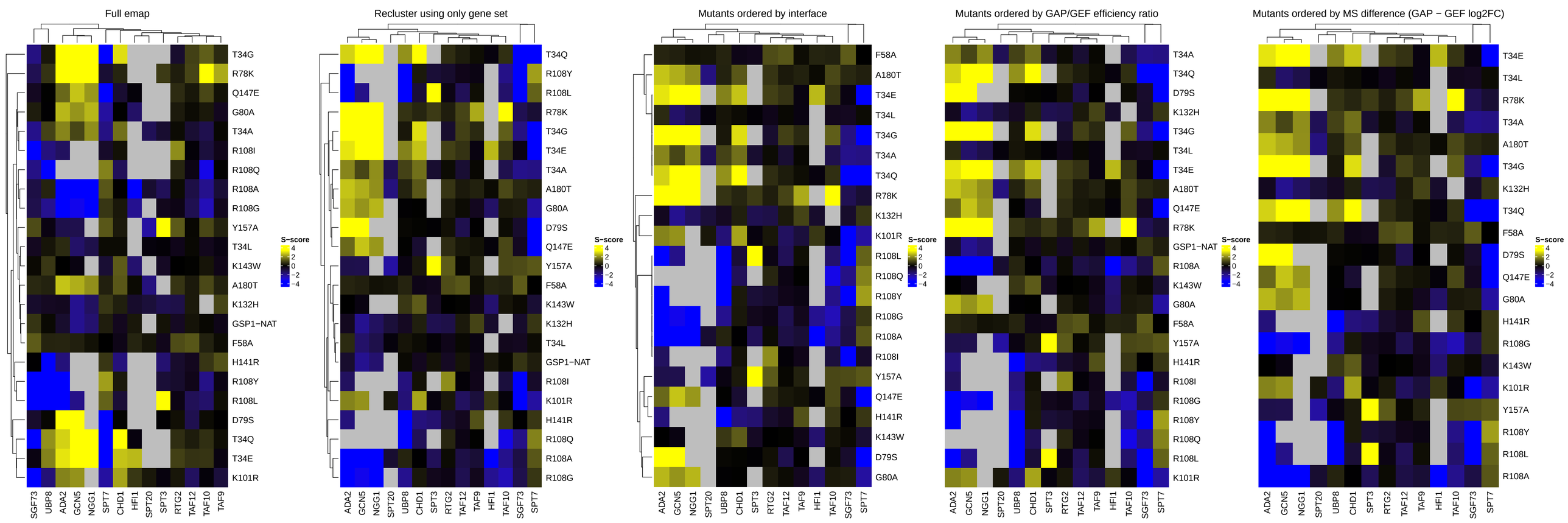


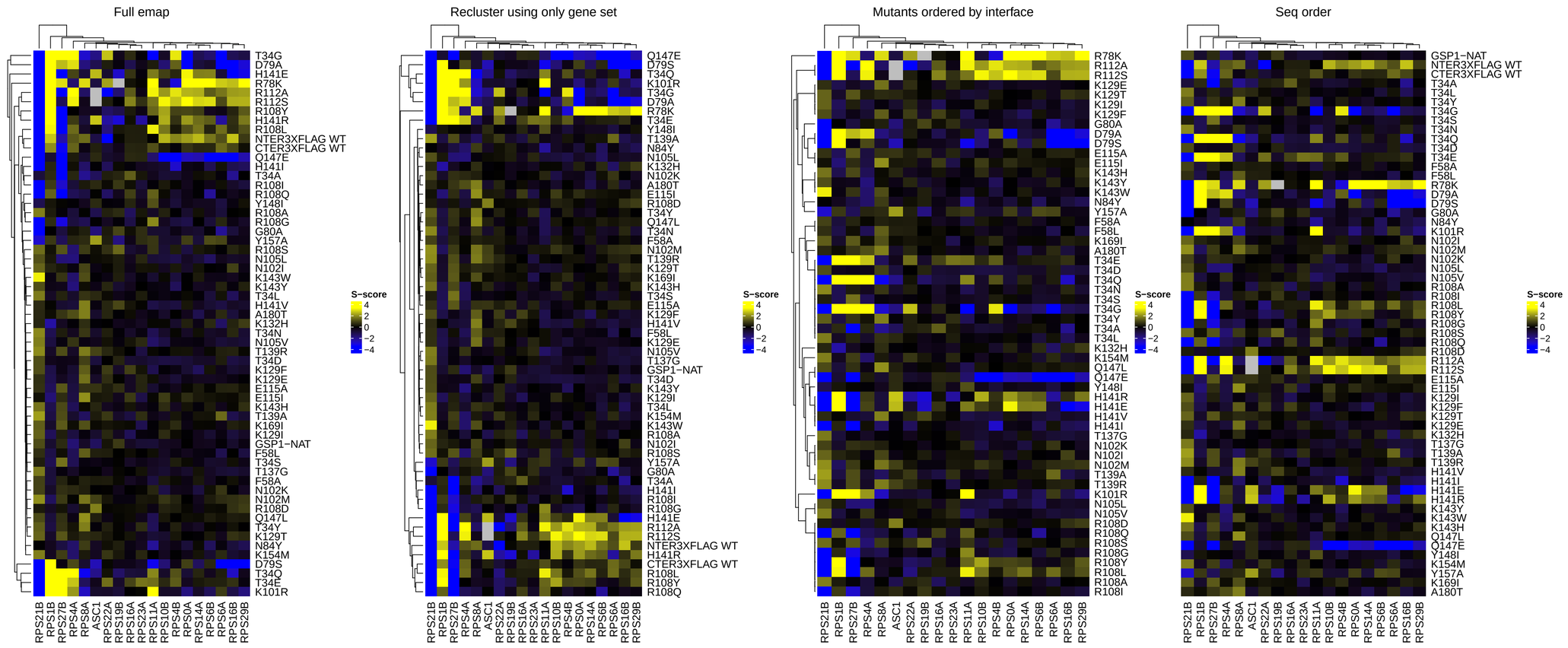

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TFB2
TFB1
TFB4
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
nucleotide−excision repair factor 3 complex
wodak complexes
clustering metric: euclidean

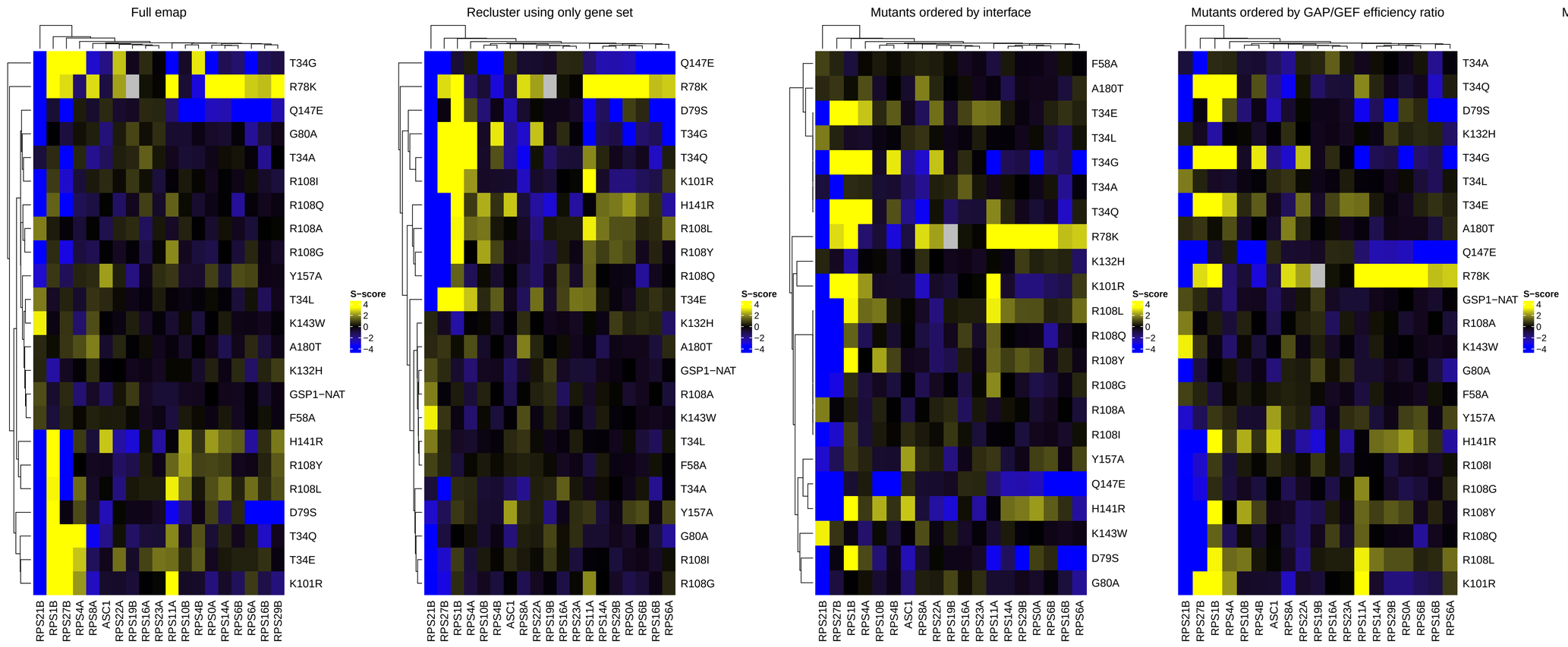

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PDB1
PDA1
LAT1
LPD1
mitochondrial pyruvate dehydrogenase complex
wodak complexes
clustering metric: euclidean



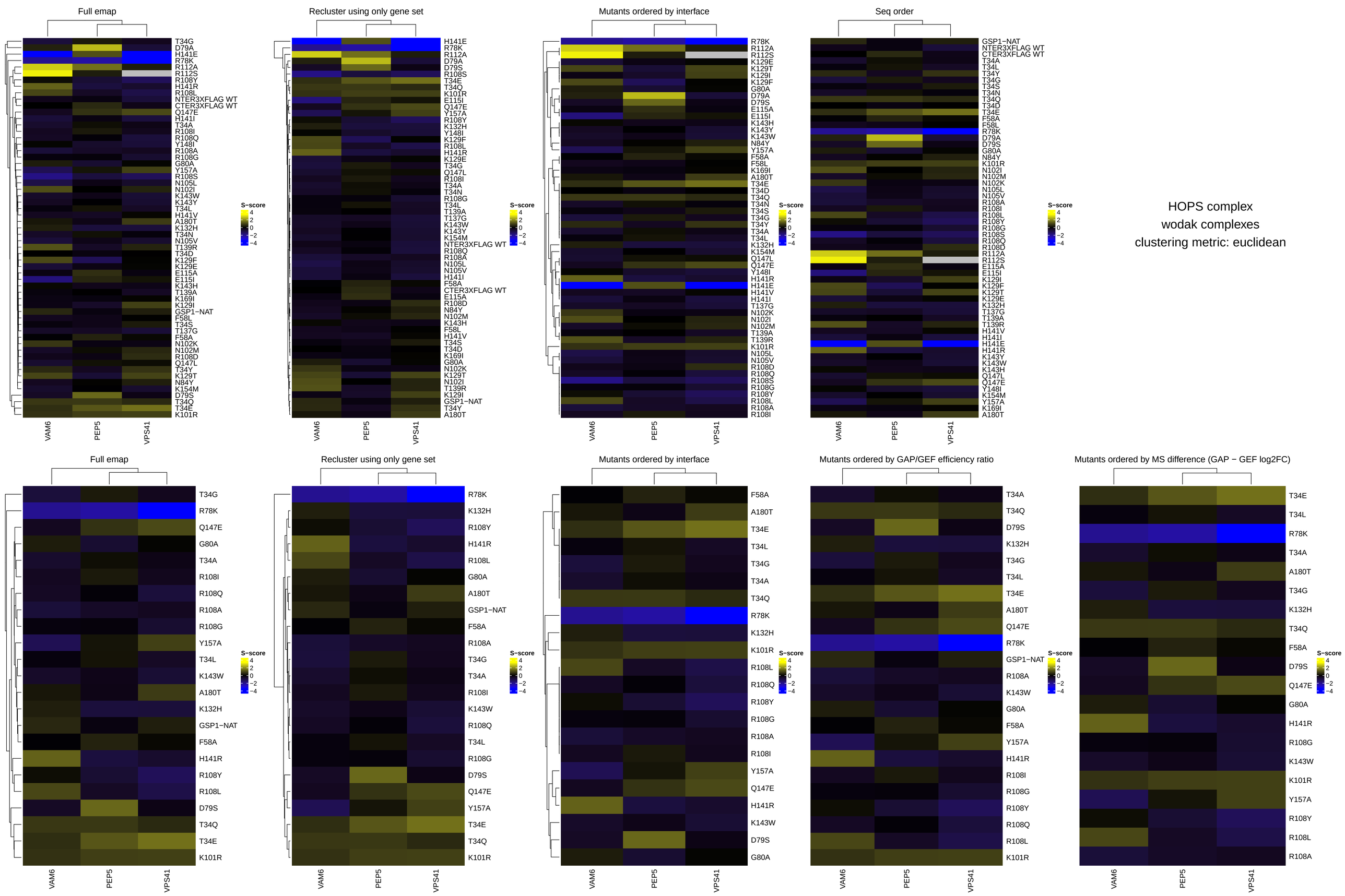
SLIK (SAGA−like) complex
wodak complexes
clustering metric: euclidean

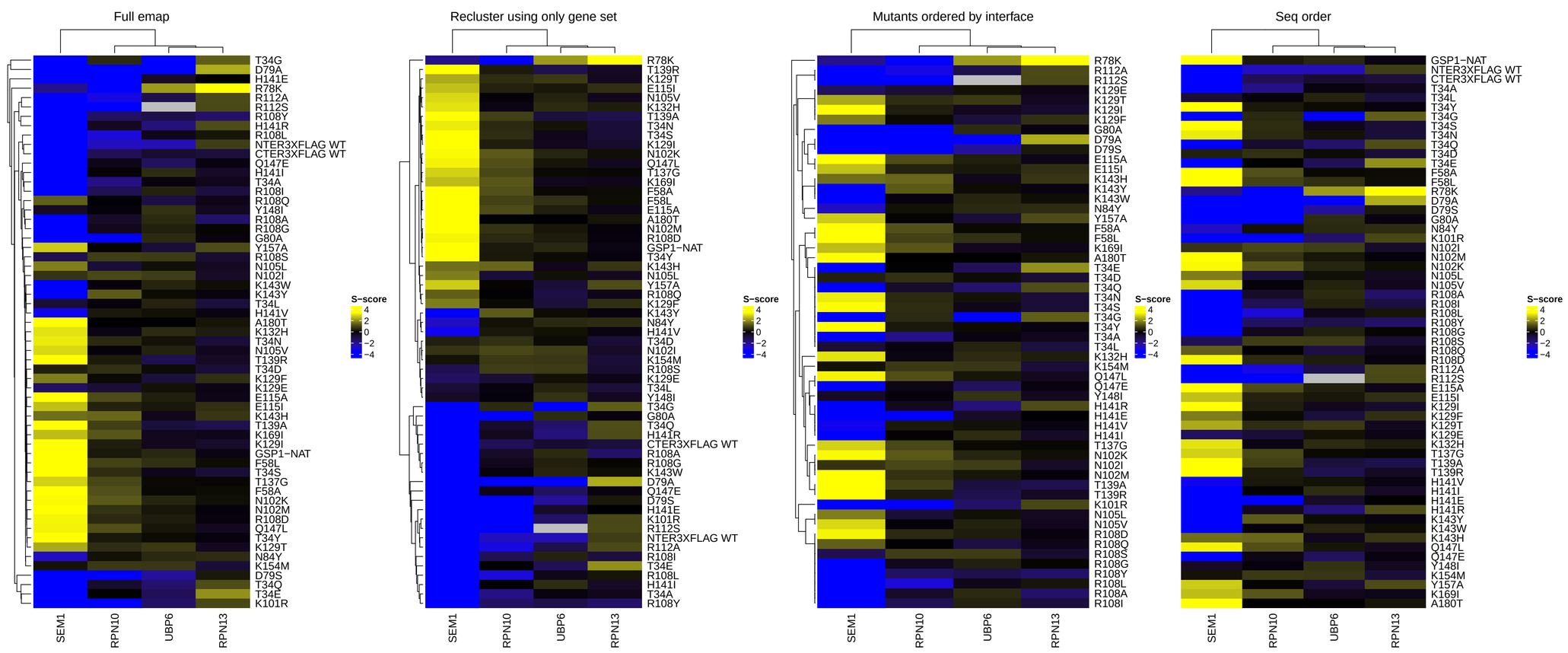




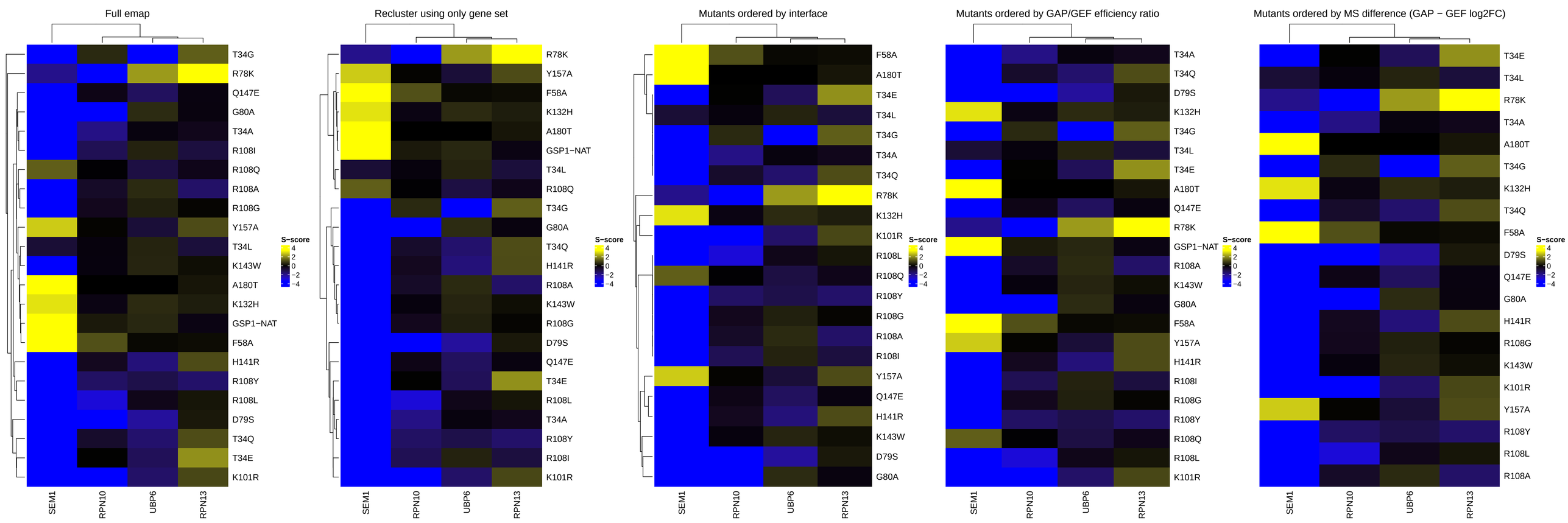


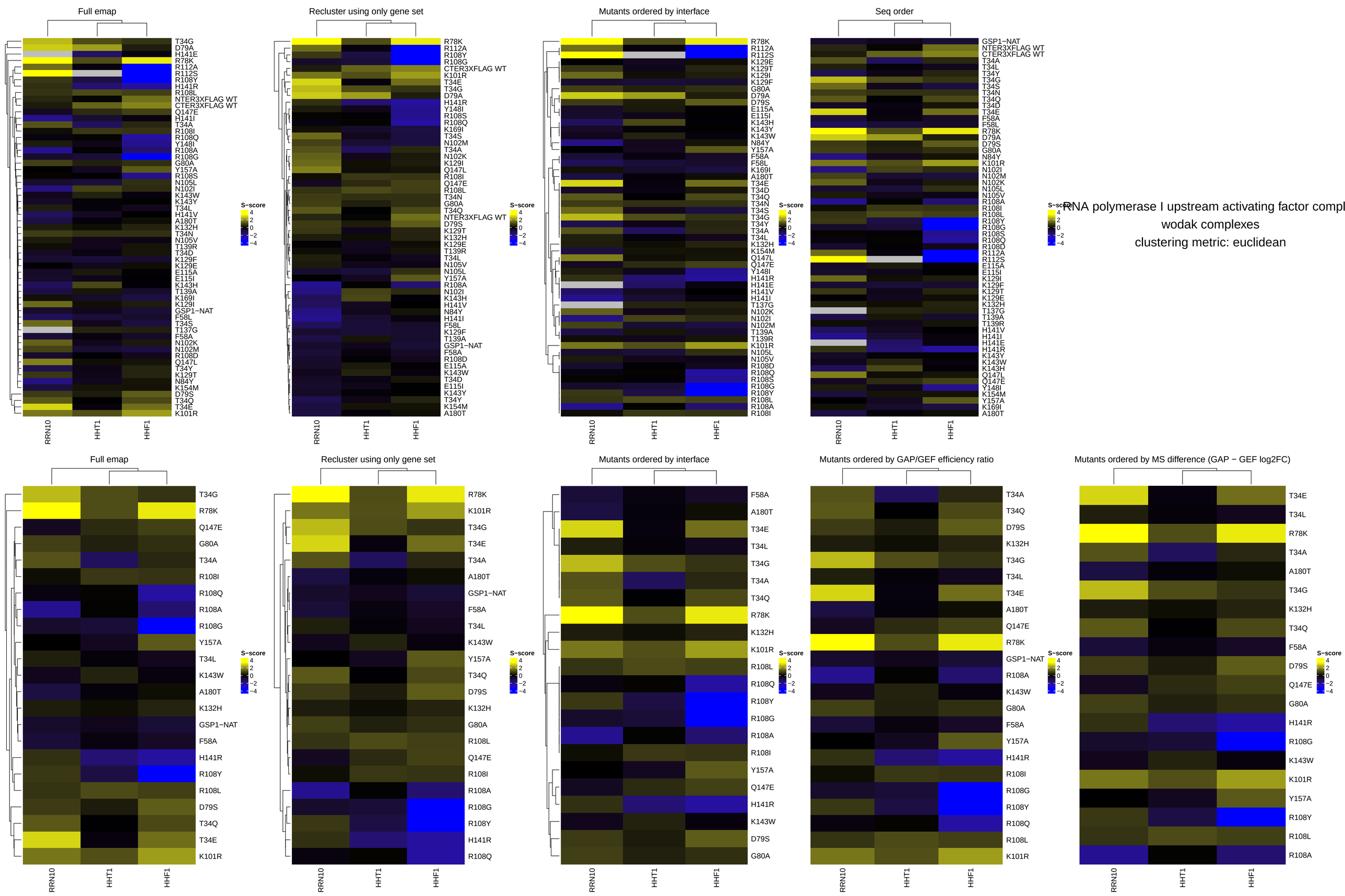
cytoplasmic ribosomal small subunit
wodak complexes
clustering metric: euclidean

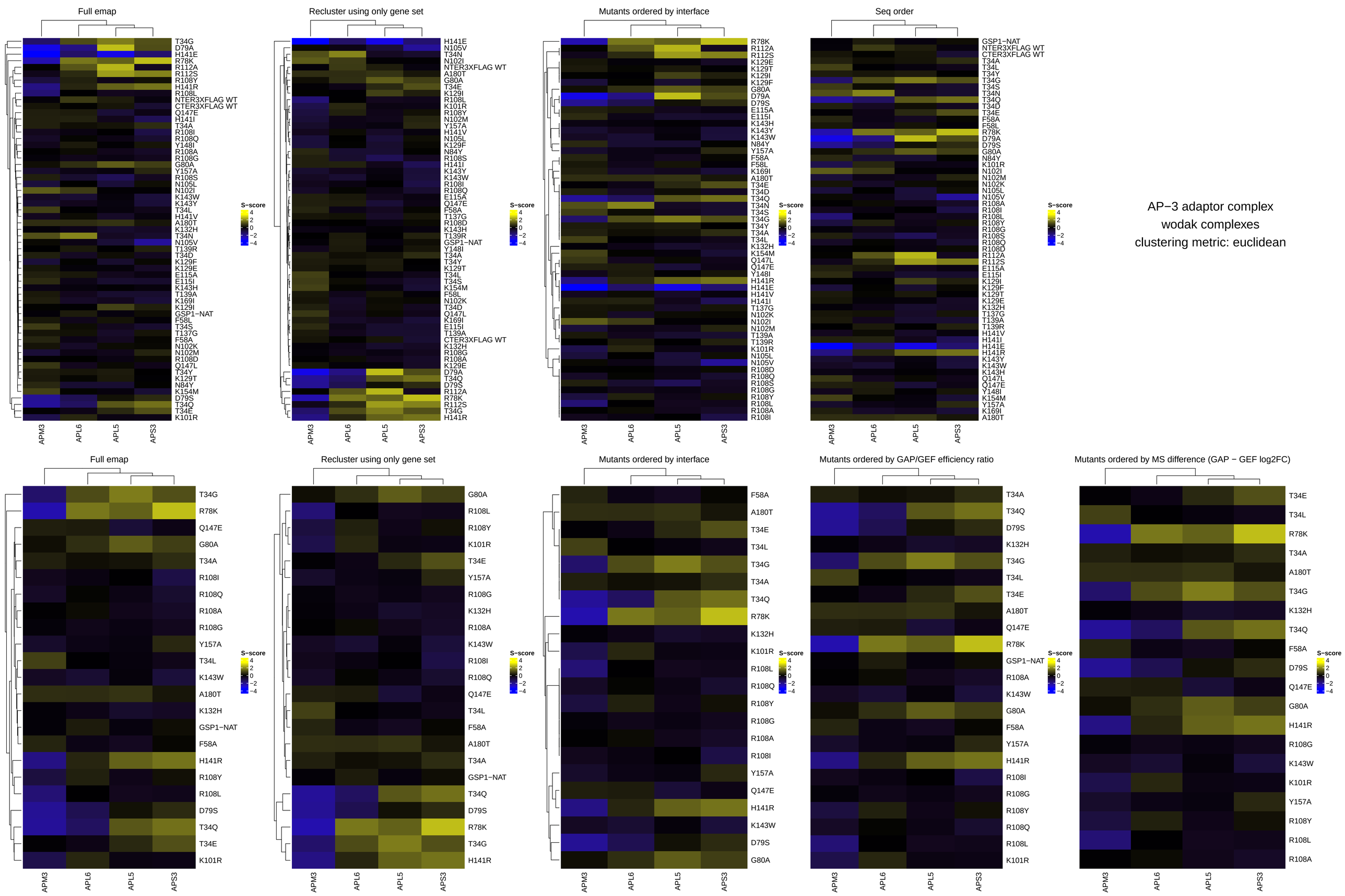

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
VAM6
PEP5
VPS41
HOPS complex
wodak complexes
clustering metric: euclidean

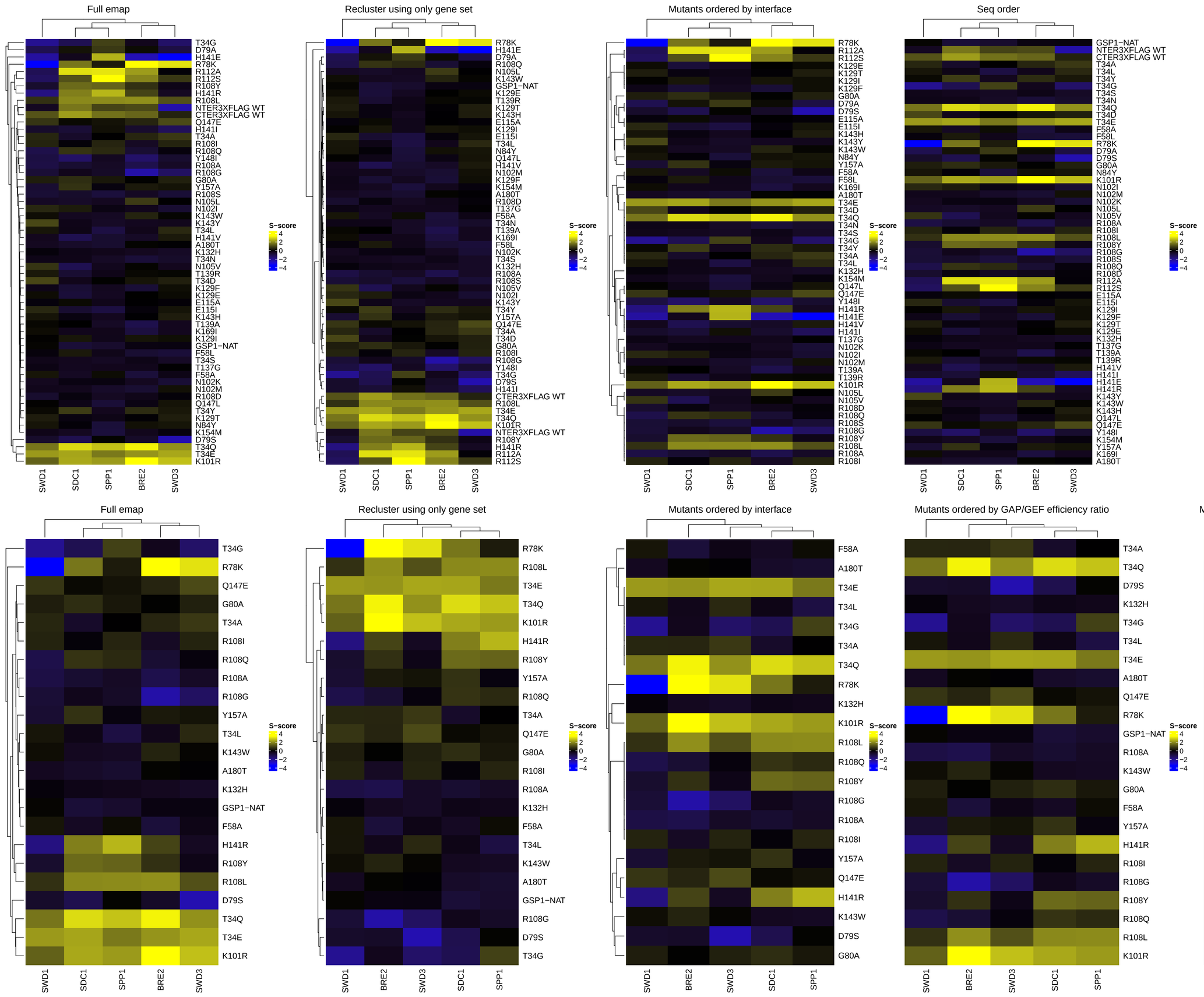


19/22S regulator
wodak complexes
clustering metric: euclidean

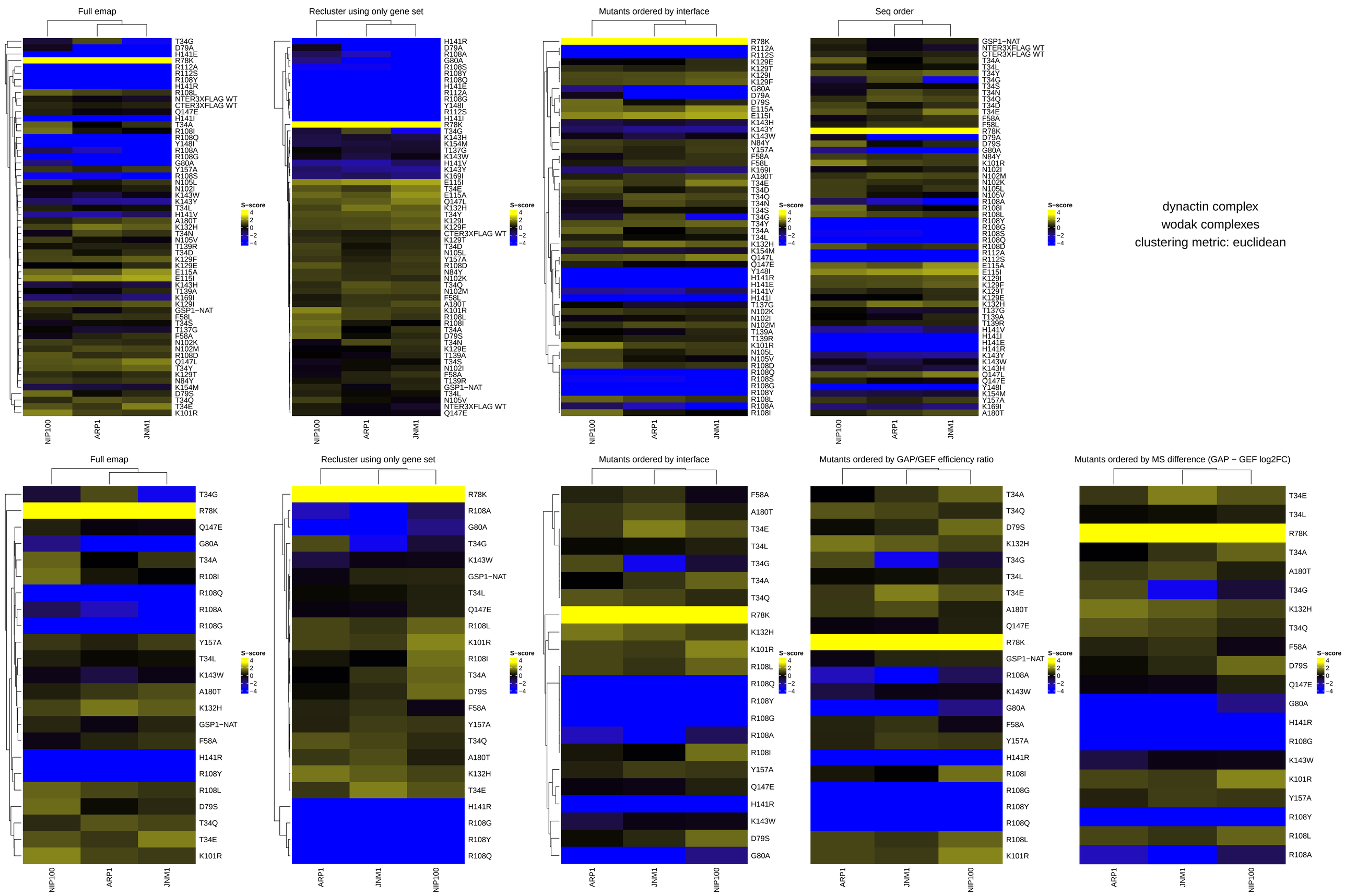


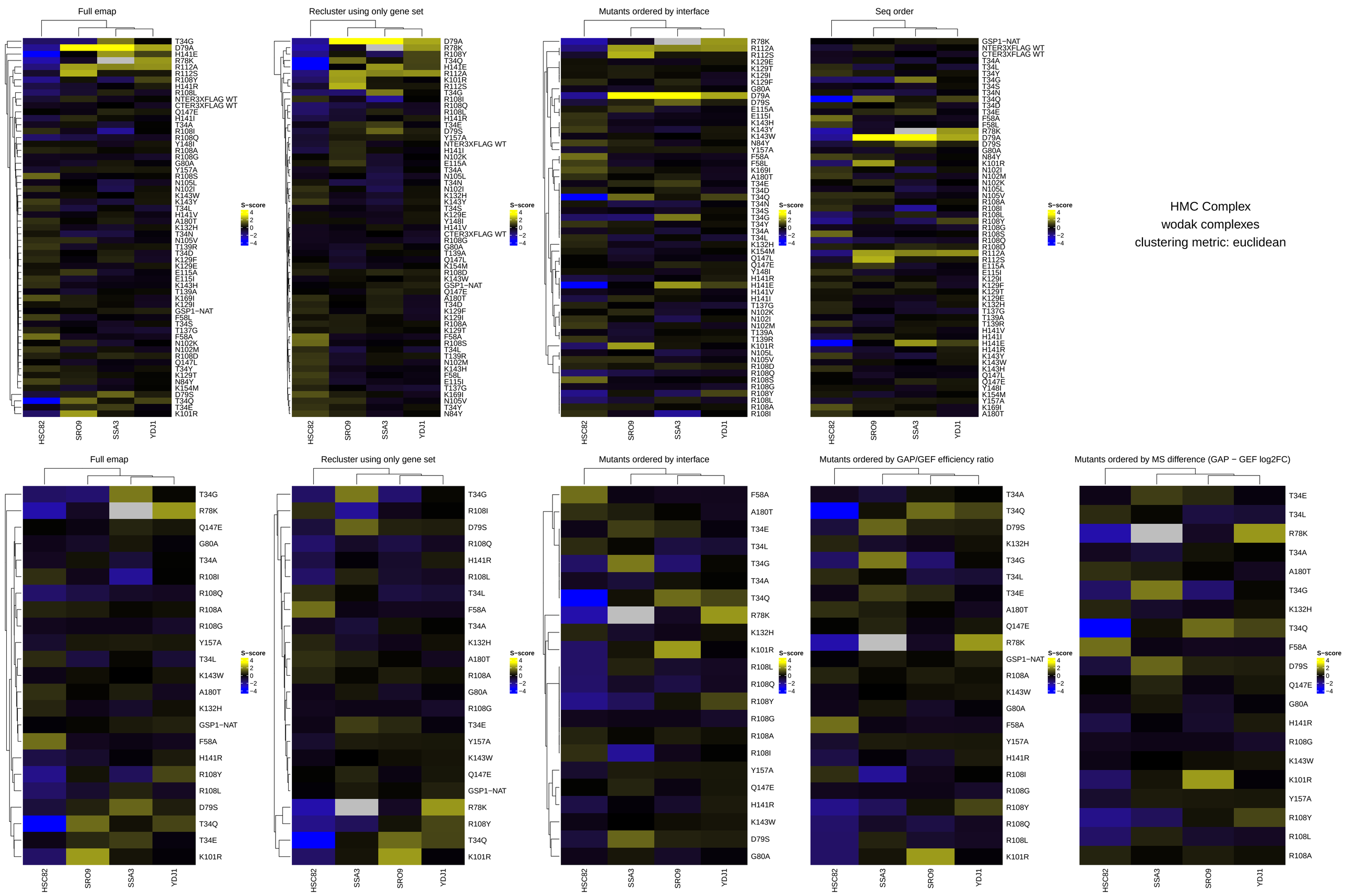

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RRN10
HHT1
HHF1
RNA polymerase I upstream activating factor compl
wodak complexes
clustering metric: euclidean


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
4
2
0
−2
−4
APM3
APL6
APL5
APS3
AP−3 adaptor complex
wodak complexes
clustering metric: euclidean



COMPASS complex
wodak complexes
clustering metric: euclidean


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
NIP100
ARP1
JNM1
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
dynactin 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
4
2
0
−2
−4
HSC82
SRO9
SSA3
YDJ1
HMC Complex
wodak complexes
clustering metric: euclidean