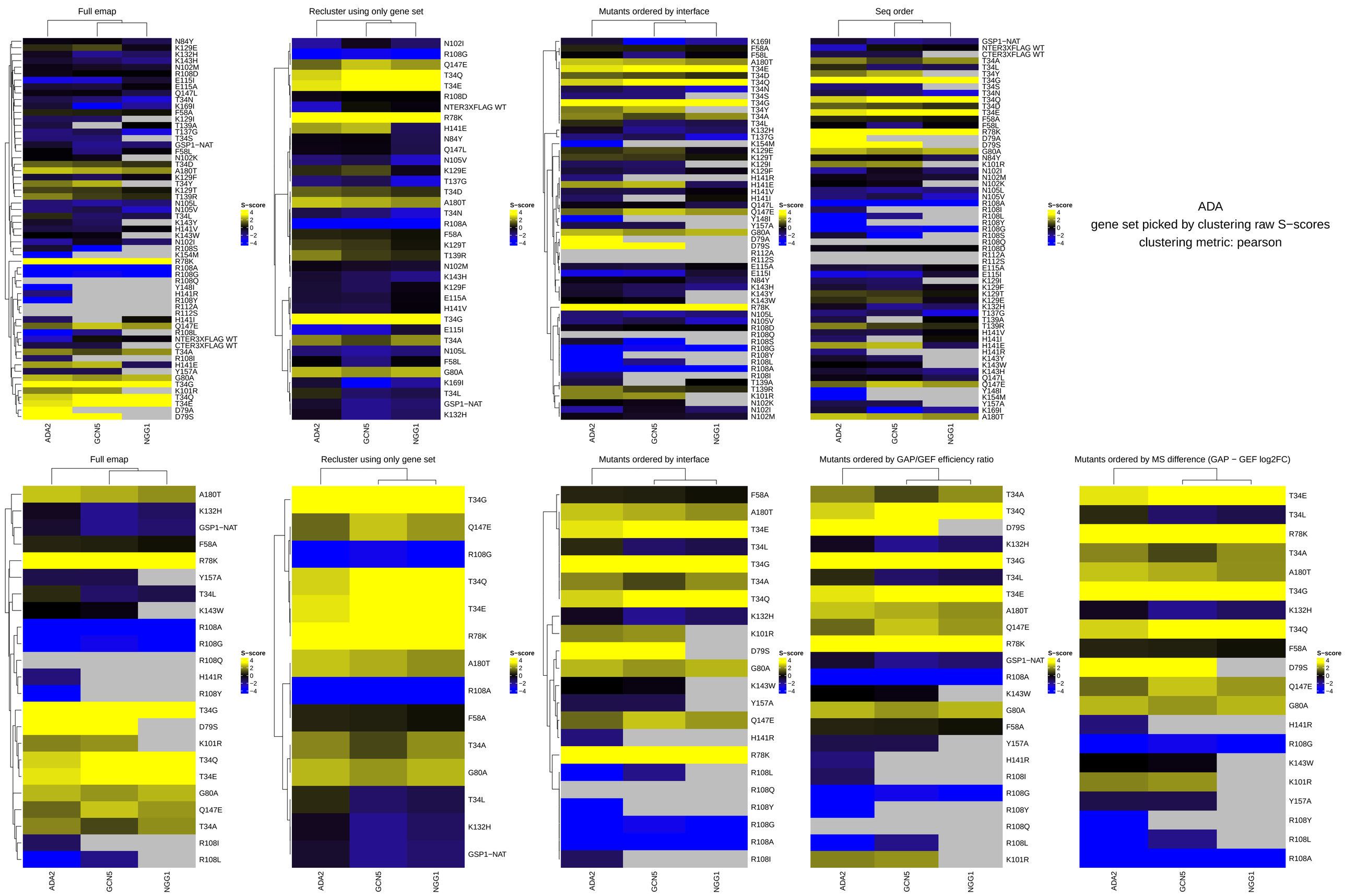
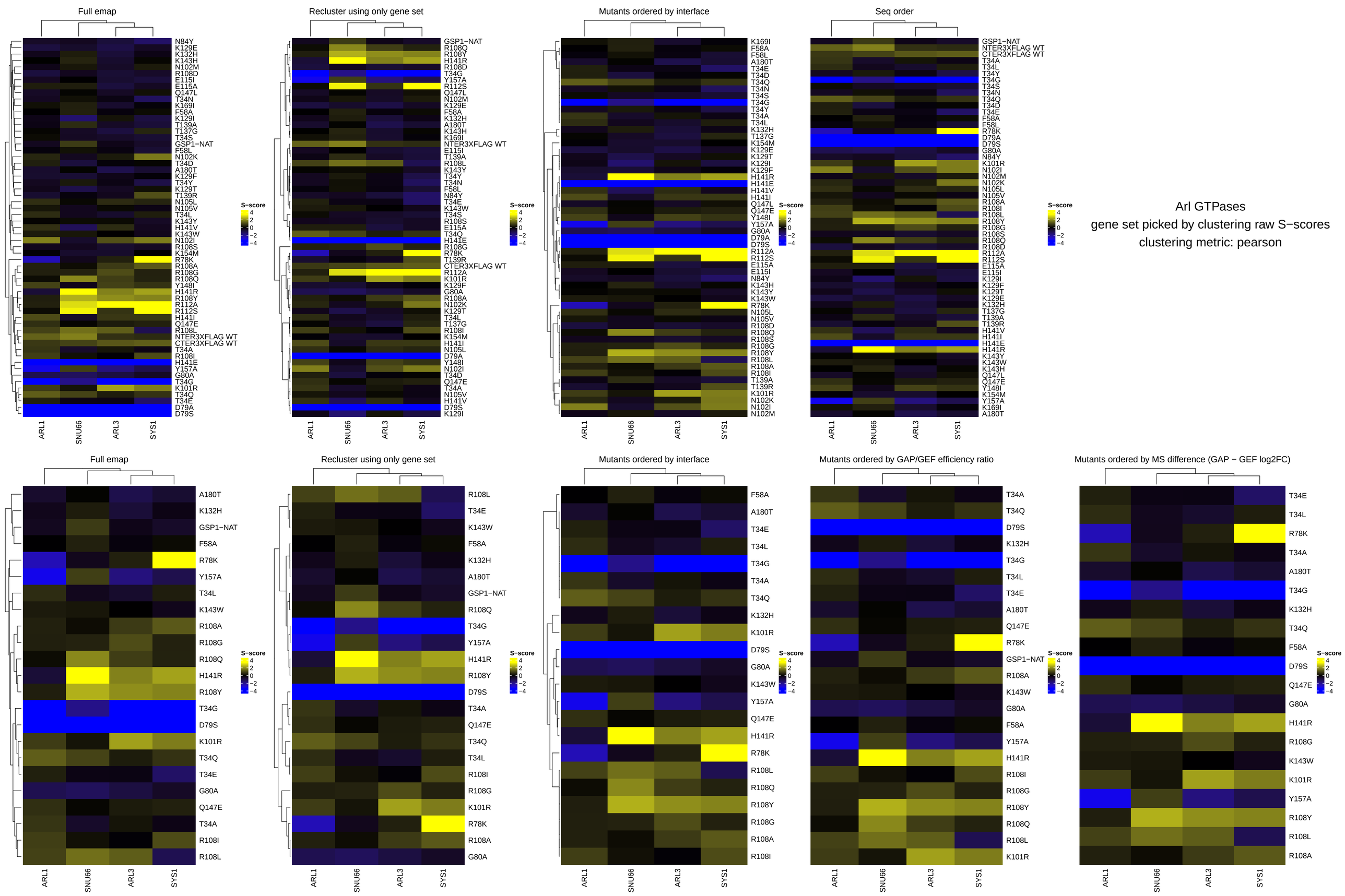
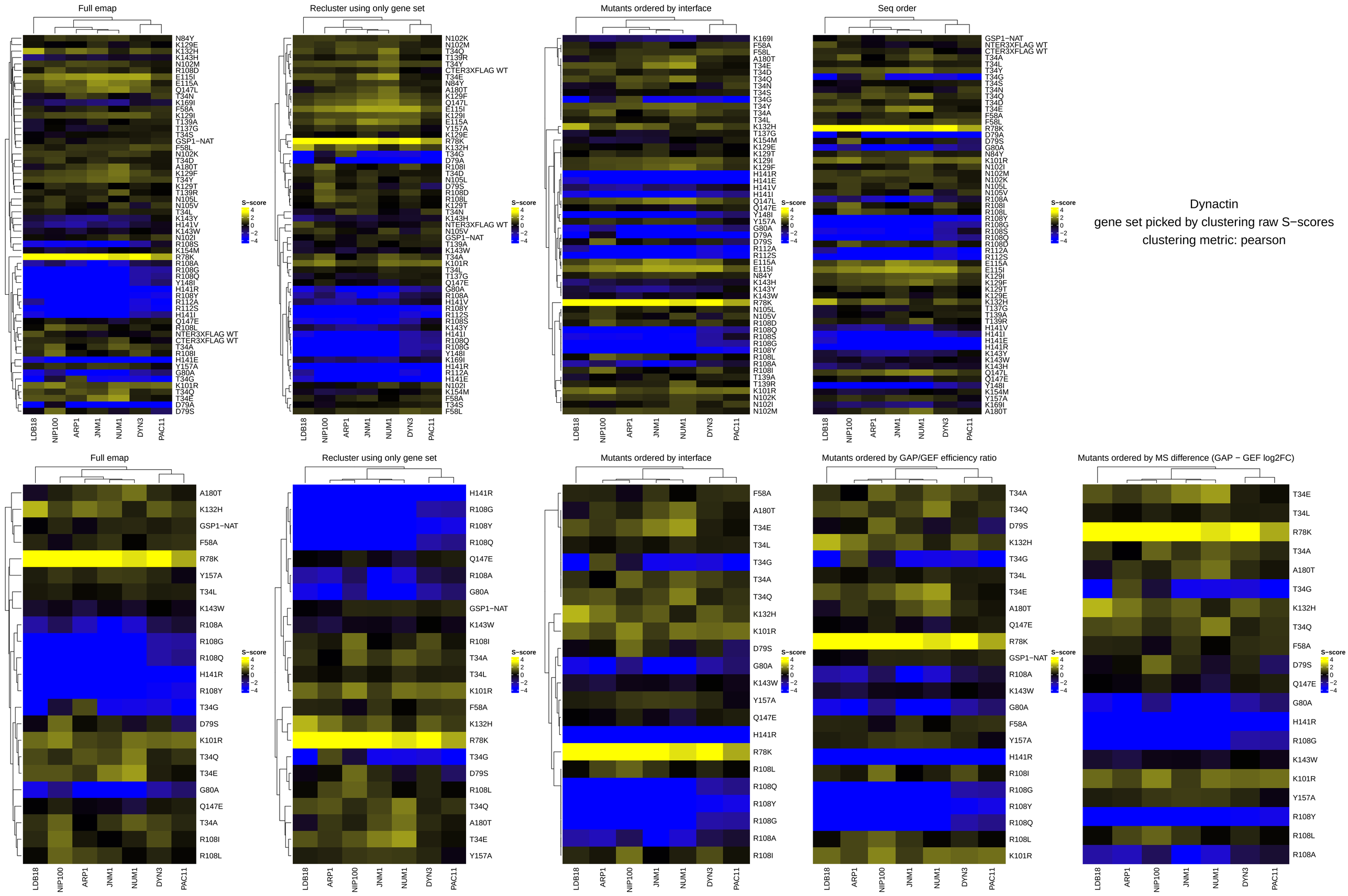
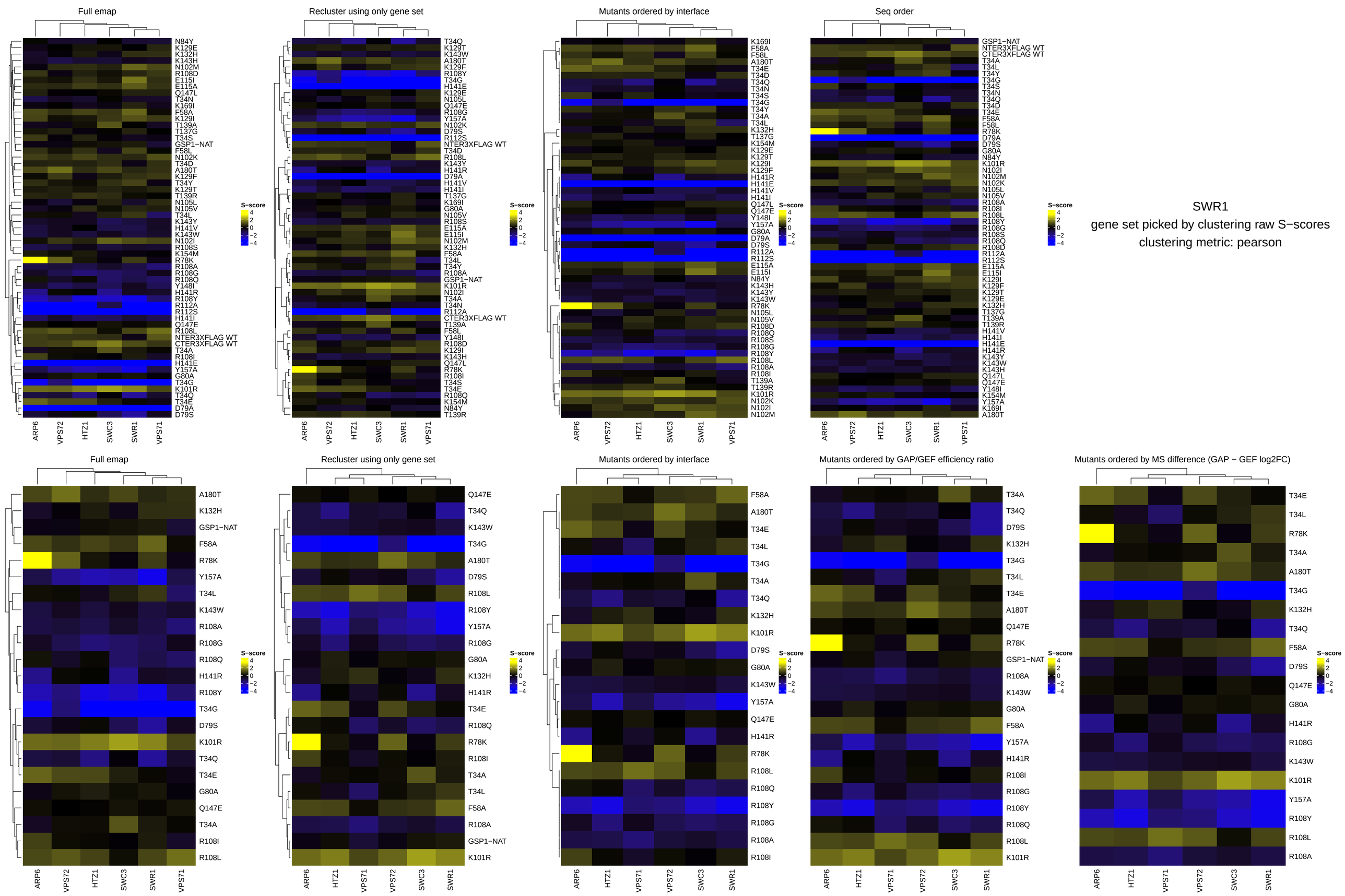
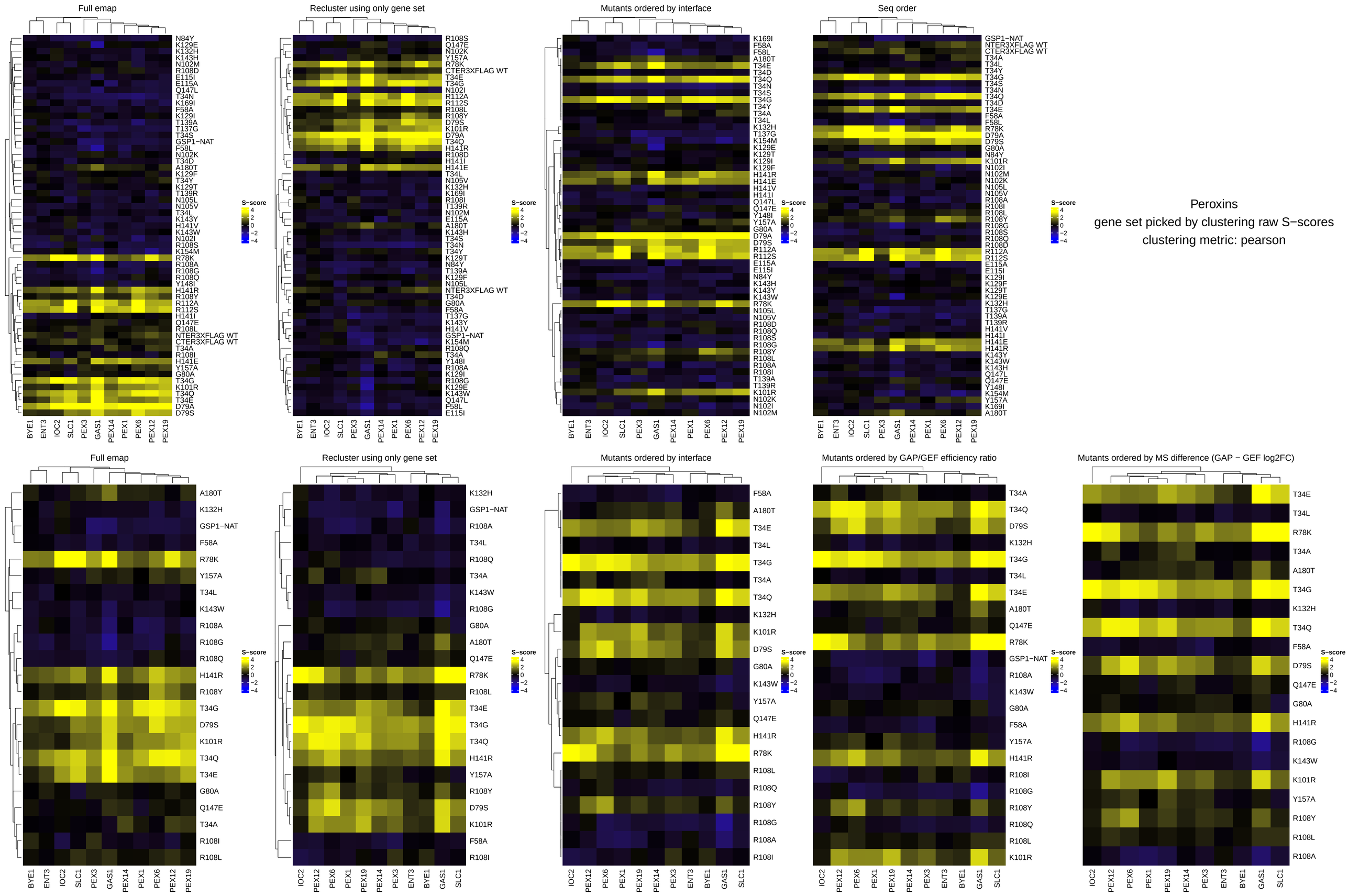
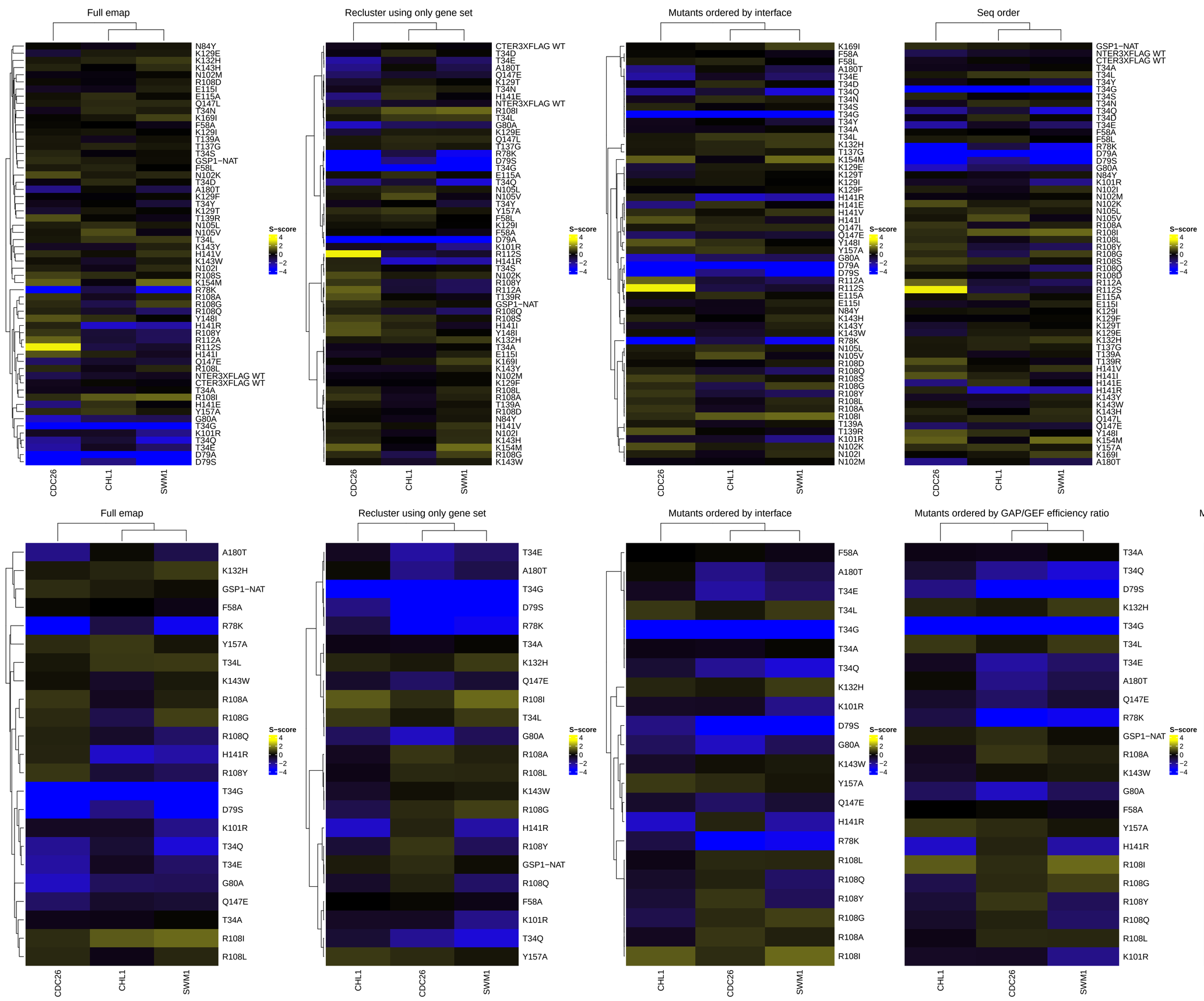

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ADA2
GCN5
NGG1
ADA
gene set picked by clustering raw S−scores
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
ARL1
SNU66
ARL3
SYS1
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)
Arl GTPases
gene set picked by clustering raw S−scores
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
LDB18
NIP100
ARP1
JNM1
NUM1
DYN3
PAC11
Dynactin
gene set picked by clustering raw S−scores
clustering metric: pearson


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
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: pearson

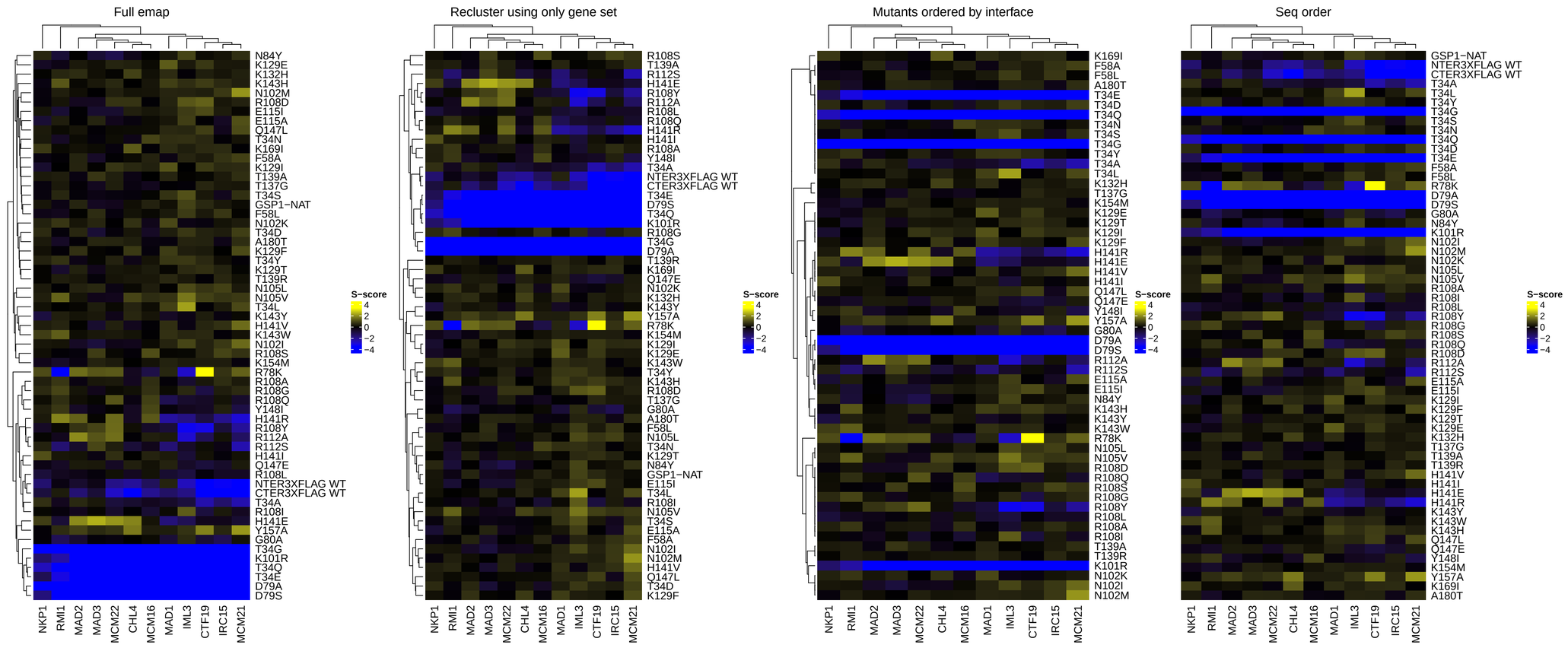

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
BYE1
ENT3
IOC2
SLC1
PEX3
GAS1
PEX14
PEX1
PEX6
PEX12
PEX19
Peroxins
gene set picked by clustering raw S−scores
clustering metric: pearson



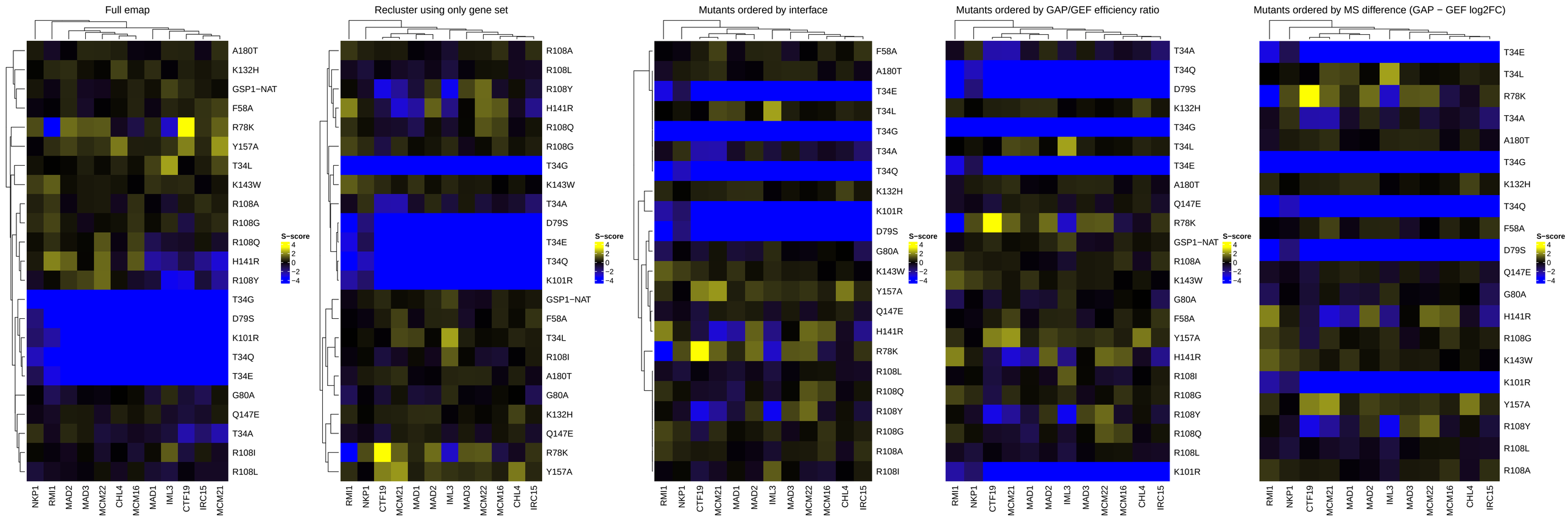
APC

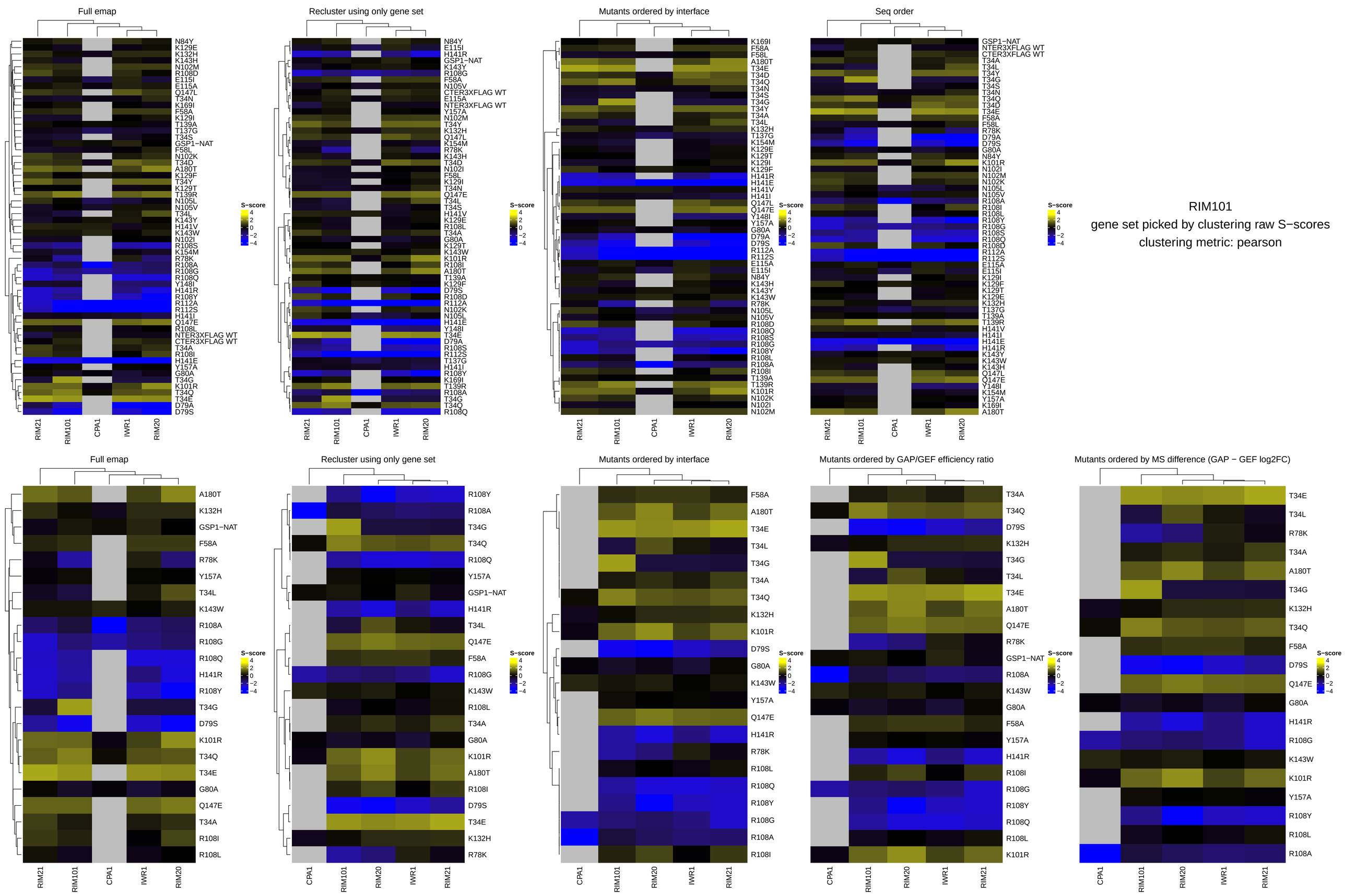
gene set picked by clustering raw S−scores

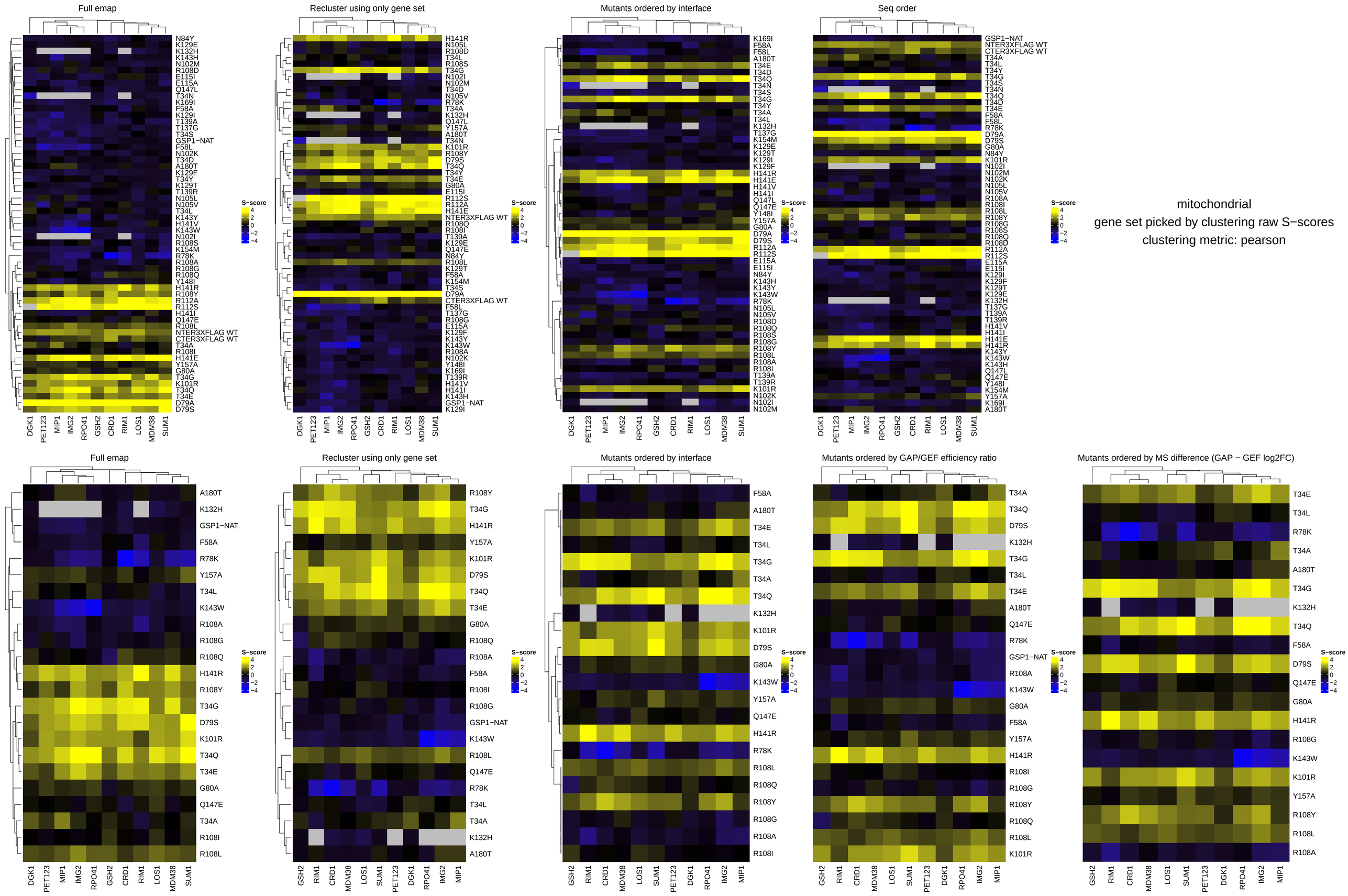
clustering metric: pearson

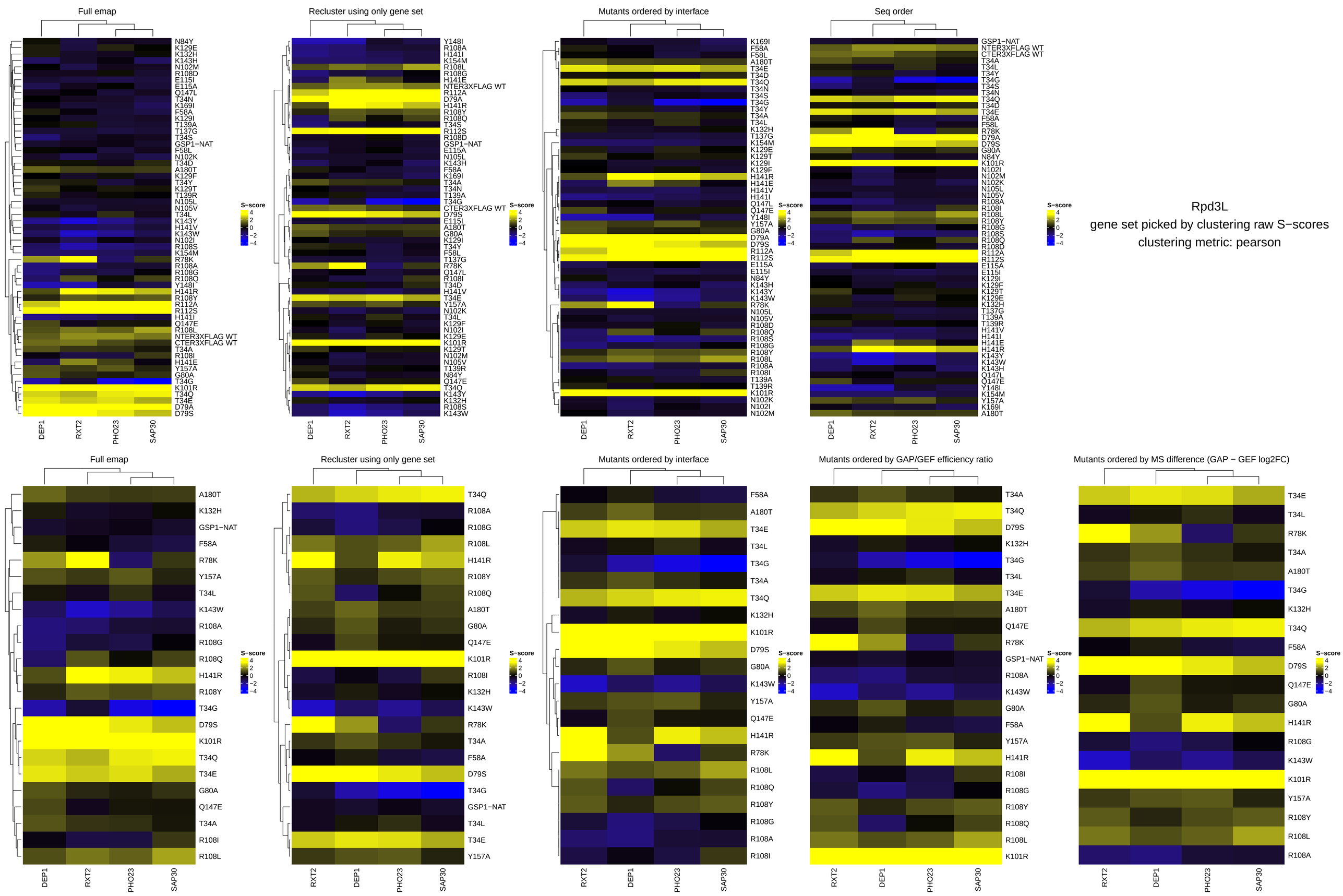


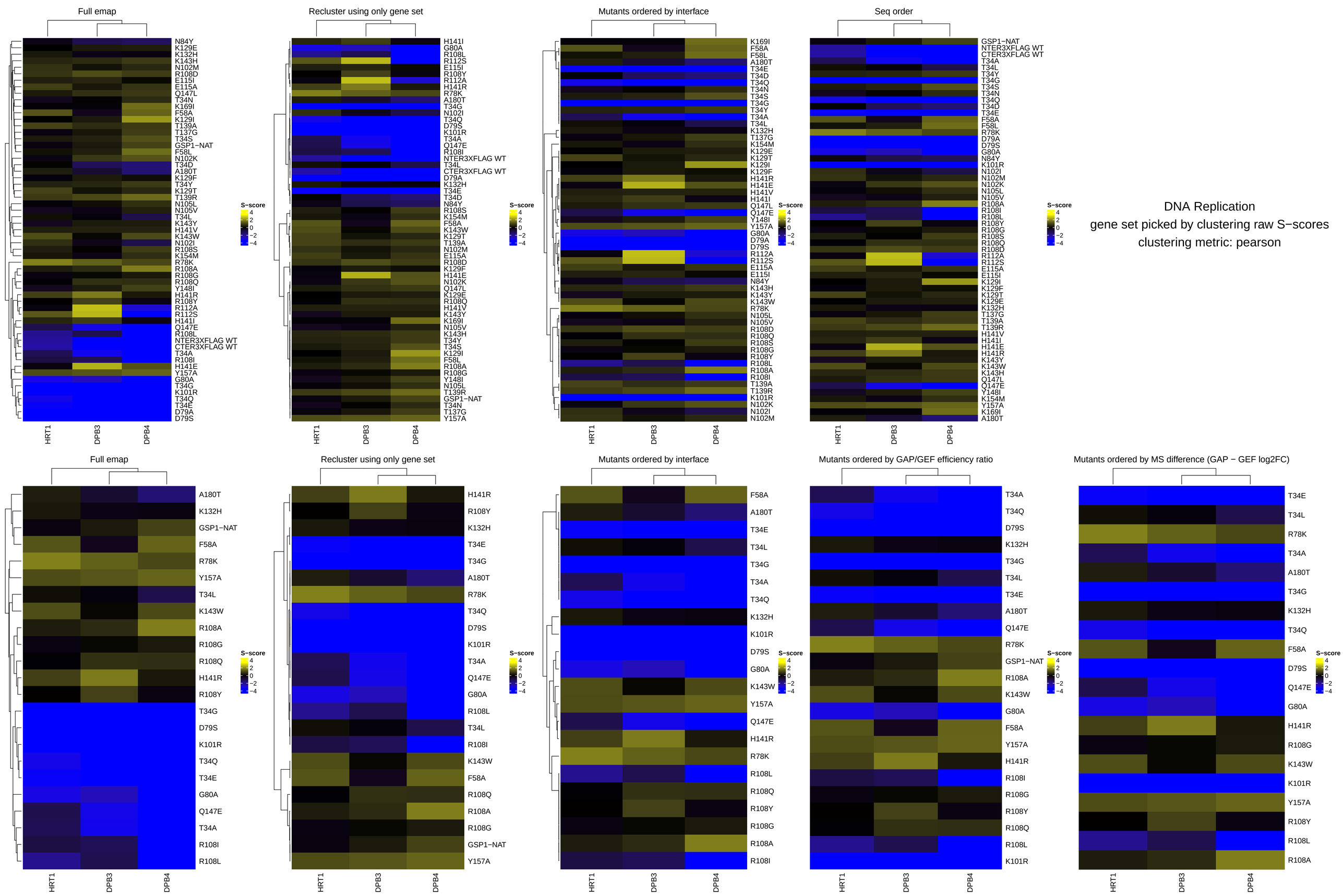
Cell Cycle Checkpoint
gene set picked by clustering raw S−scores
clustering metric: pearson

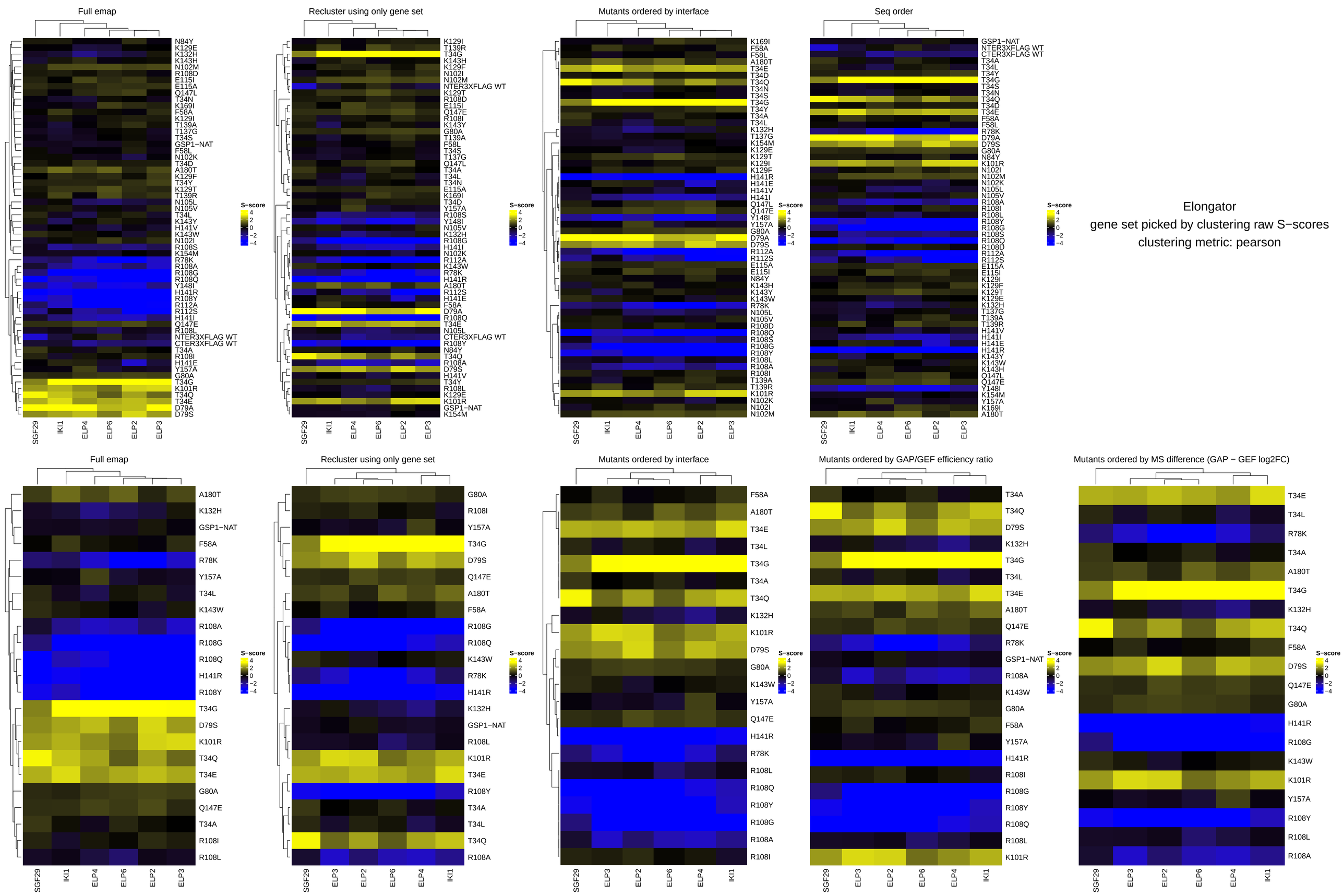


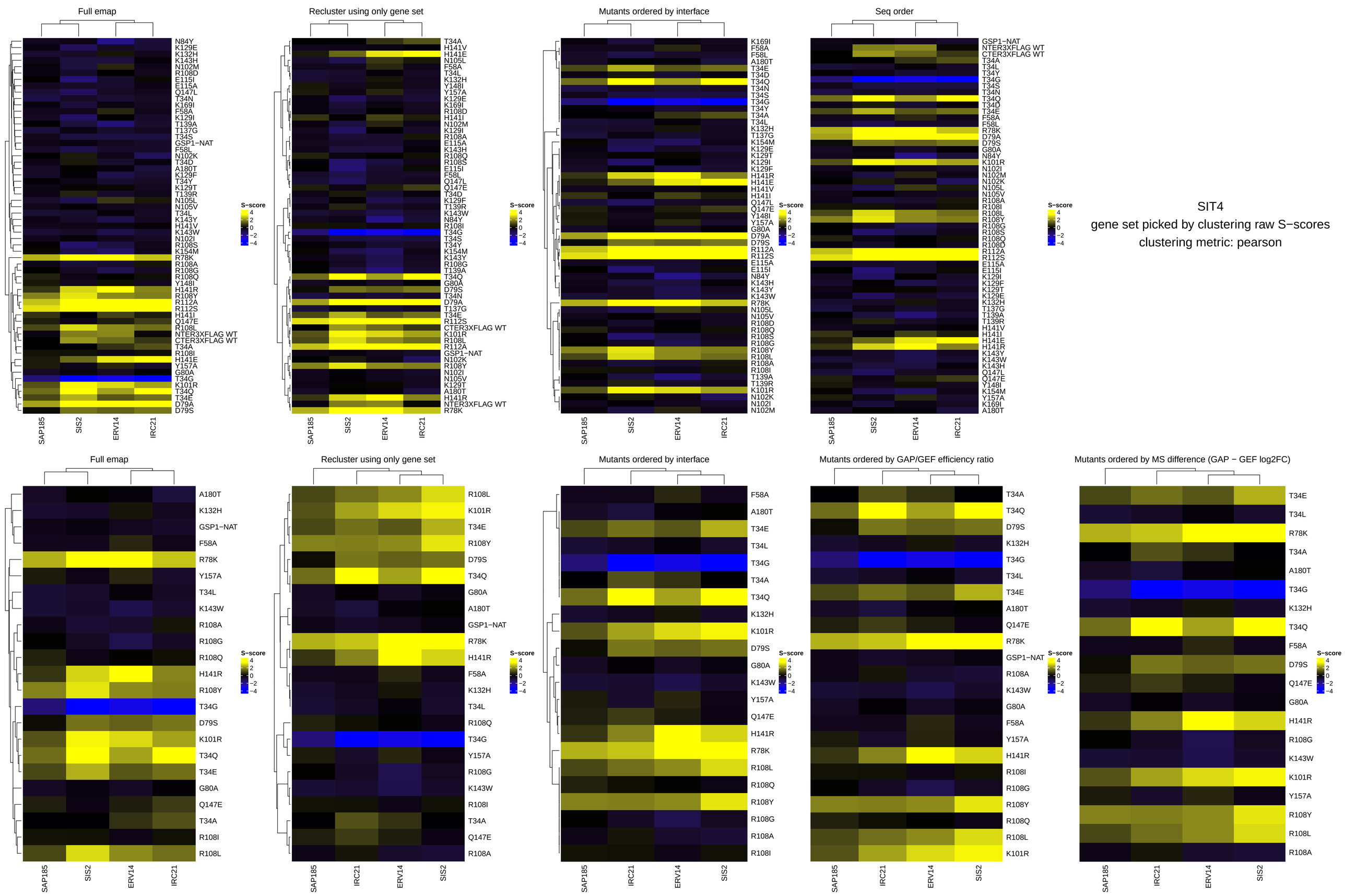

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RIM21
RIM101
CPA1
IWR1
RIM20
RIM101
gene set picked by clustering raw S−scores
clustering metric: pearson

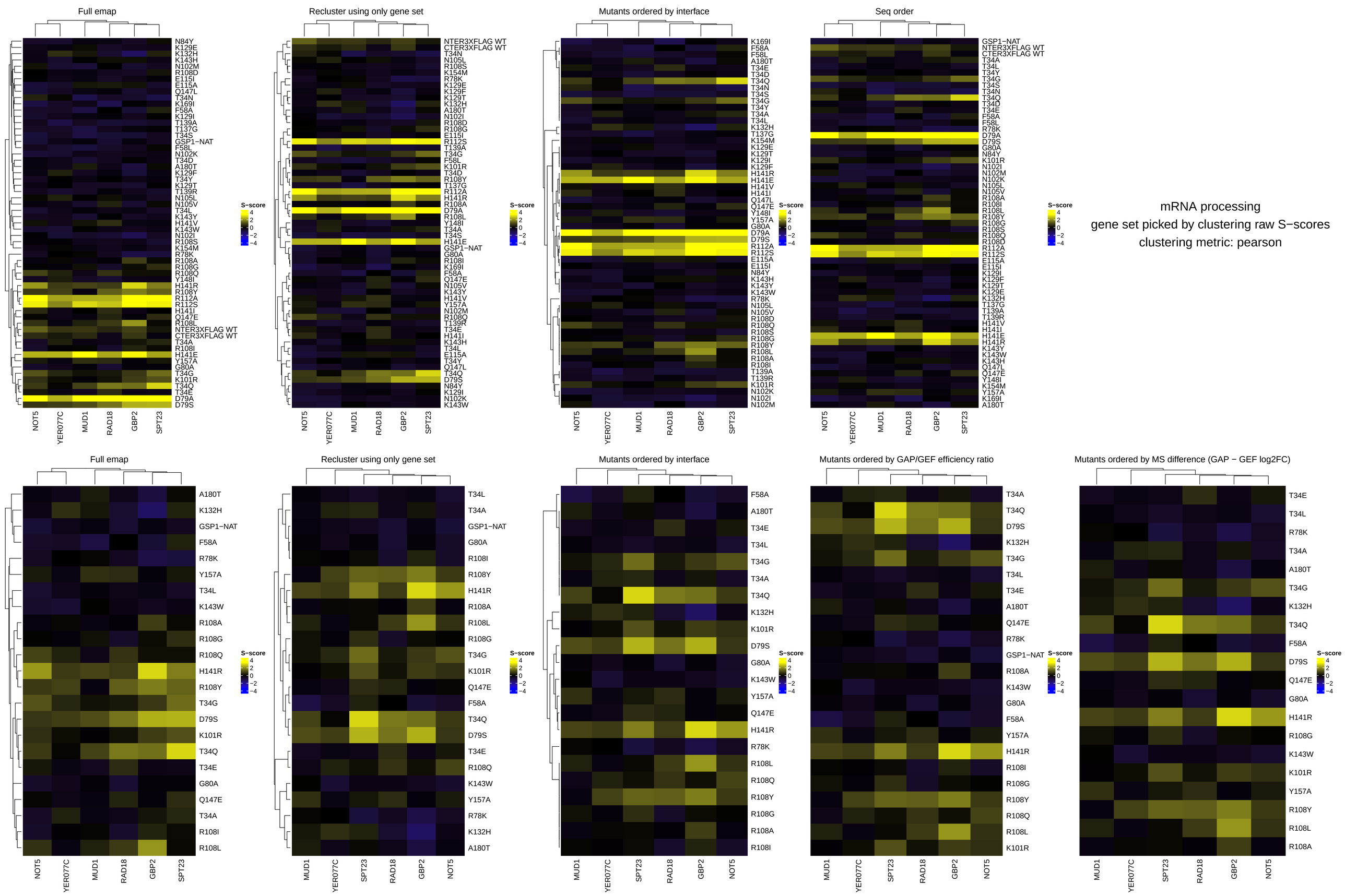

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
DGK1
PET123
MIP1
IMG2
RPO41
GSH2
CRD1
RIM1
LOS1
MDM38
SUM1
mitochondrial
gene set picked by clustering raw S−scores
clustering metric: pearson

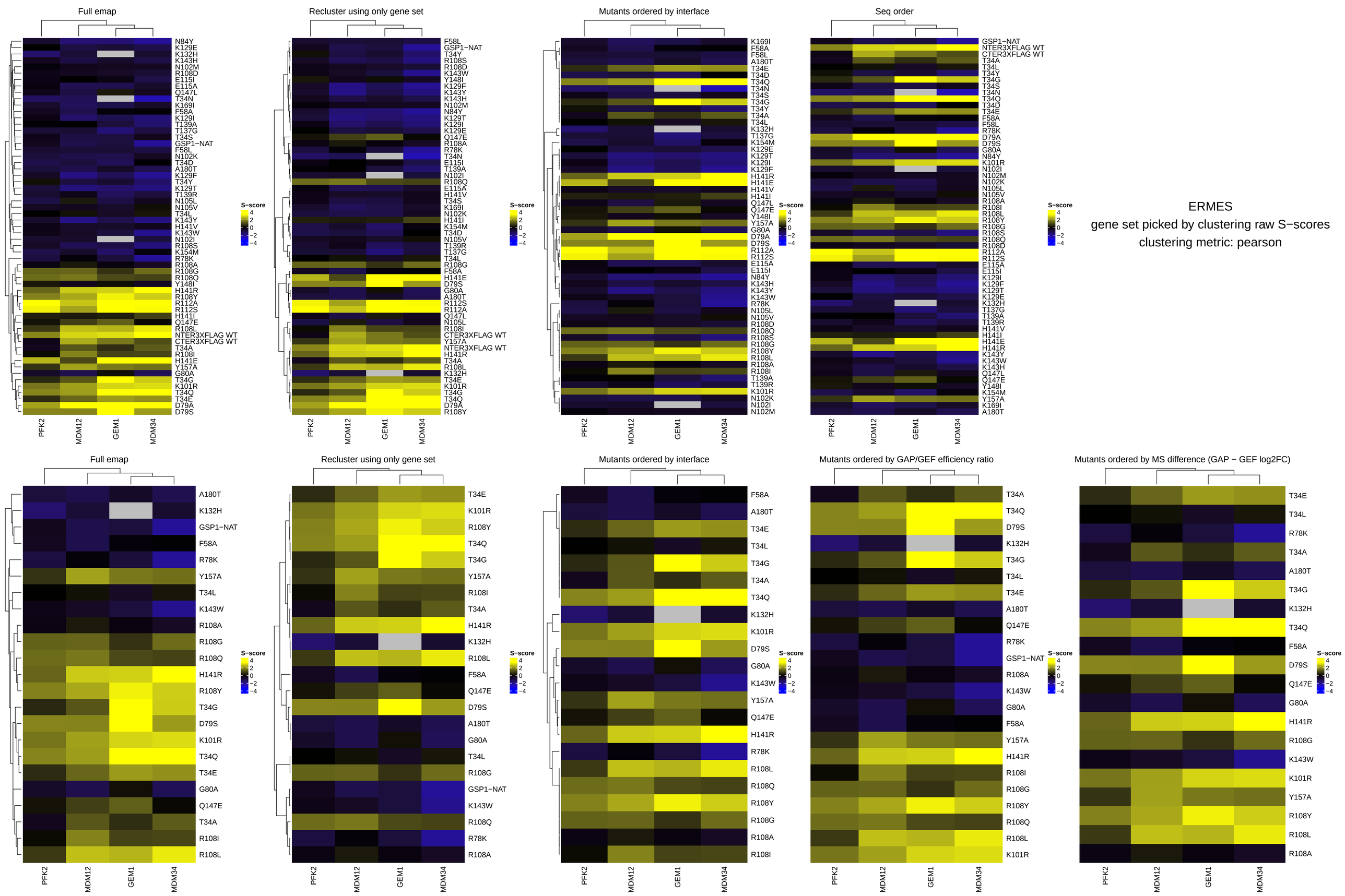

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
DEP1
RXT2
PHO23
SAP30
Rpd3L
gene set picked by clustering raw S−scores
clustering metric: pearson

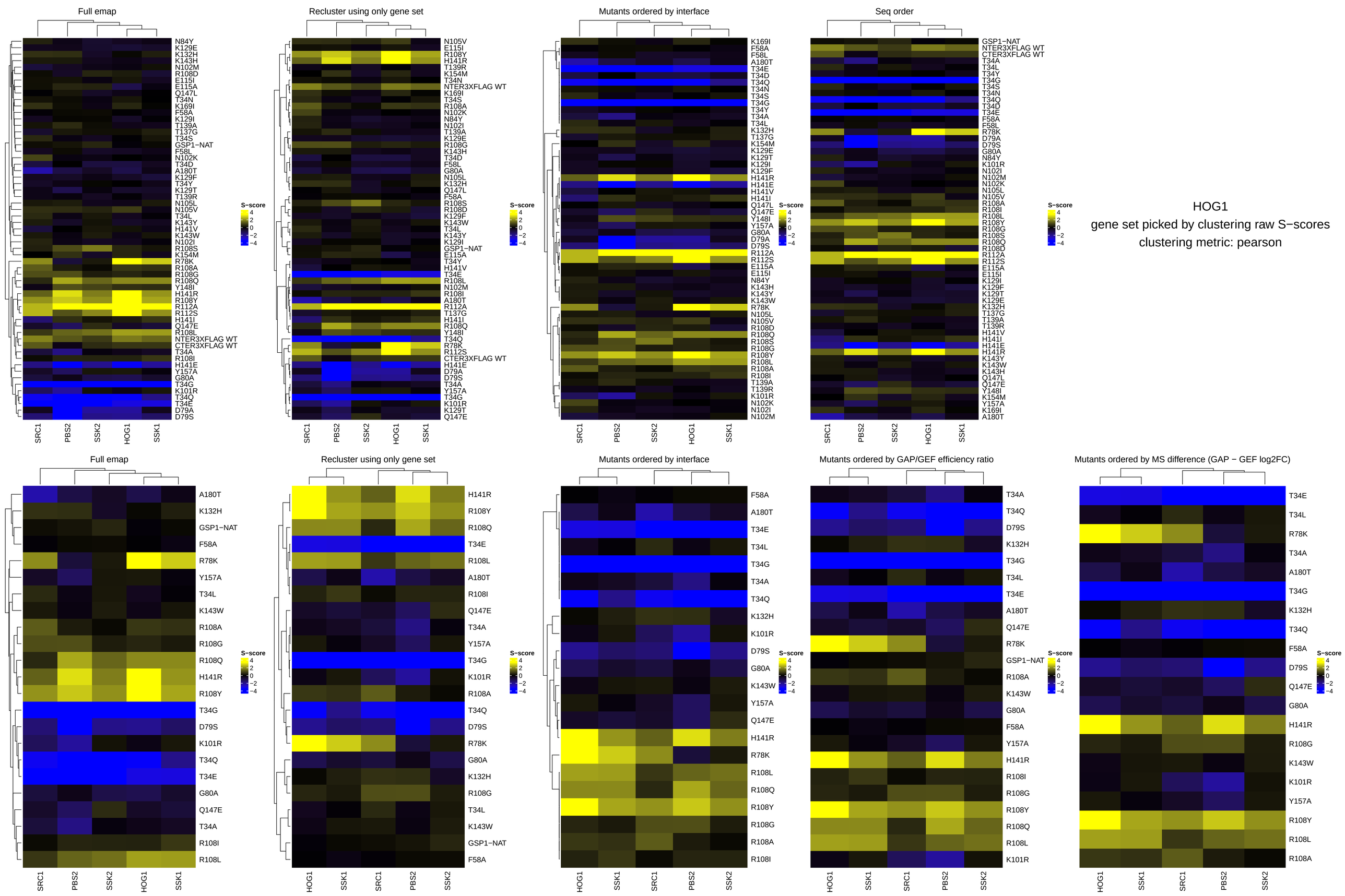

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HRT1
DPB3
DPB4
DNA Replication
gene set picked by clustering raw S−scores
clustering metric: pearson

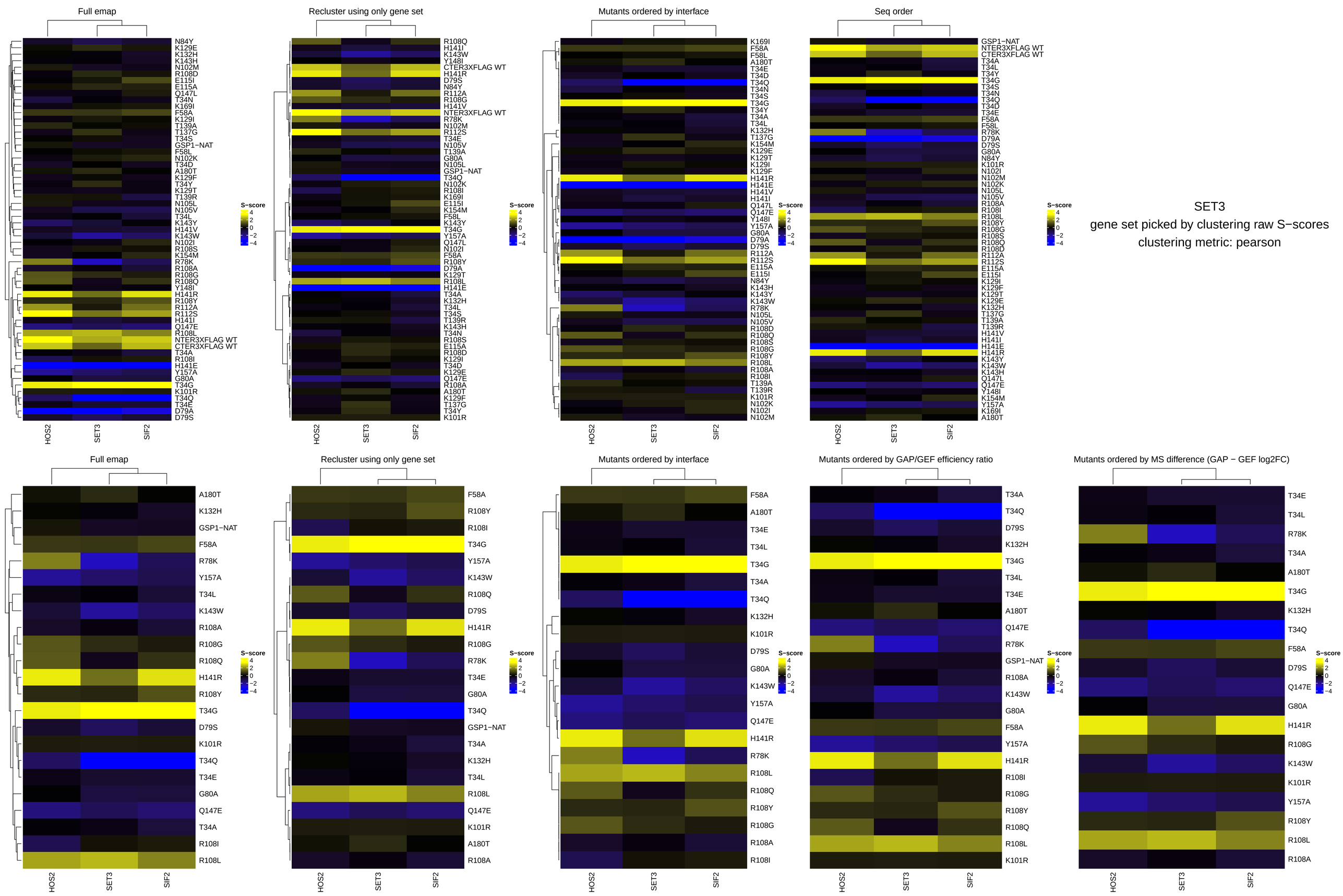

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
SGF29
IKI1
ELP4
ELP6
ELP2
ELP3
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
Elongator
gene set picked by clustering raw S−scores
clustering metric: pearson

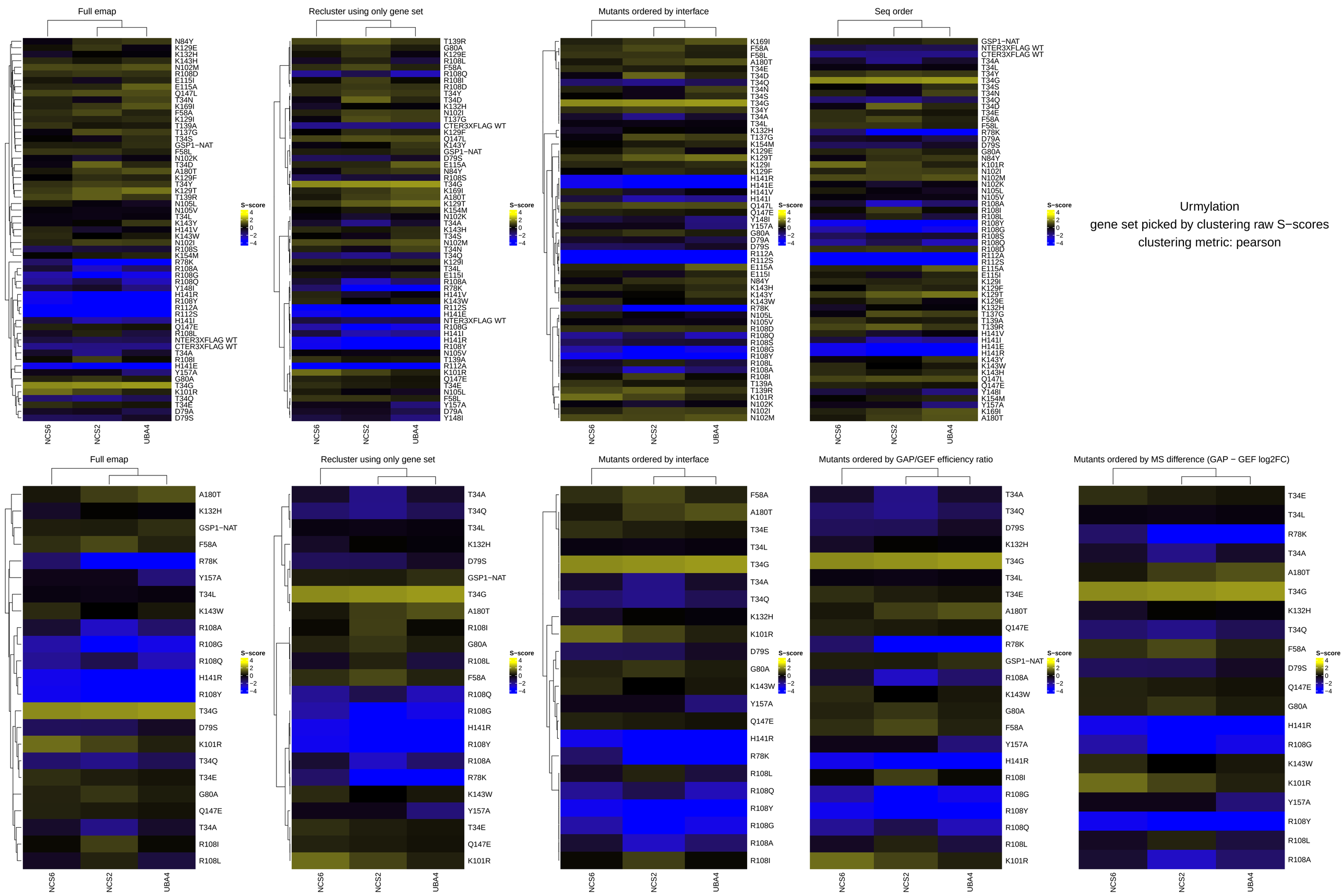

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SAP185
SIS2
ERV14
IRC21
SIT4
gene set picked by clustering raw S−scores
clustering metric: pearson

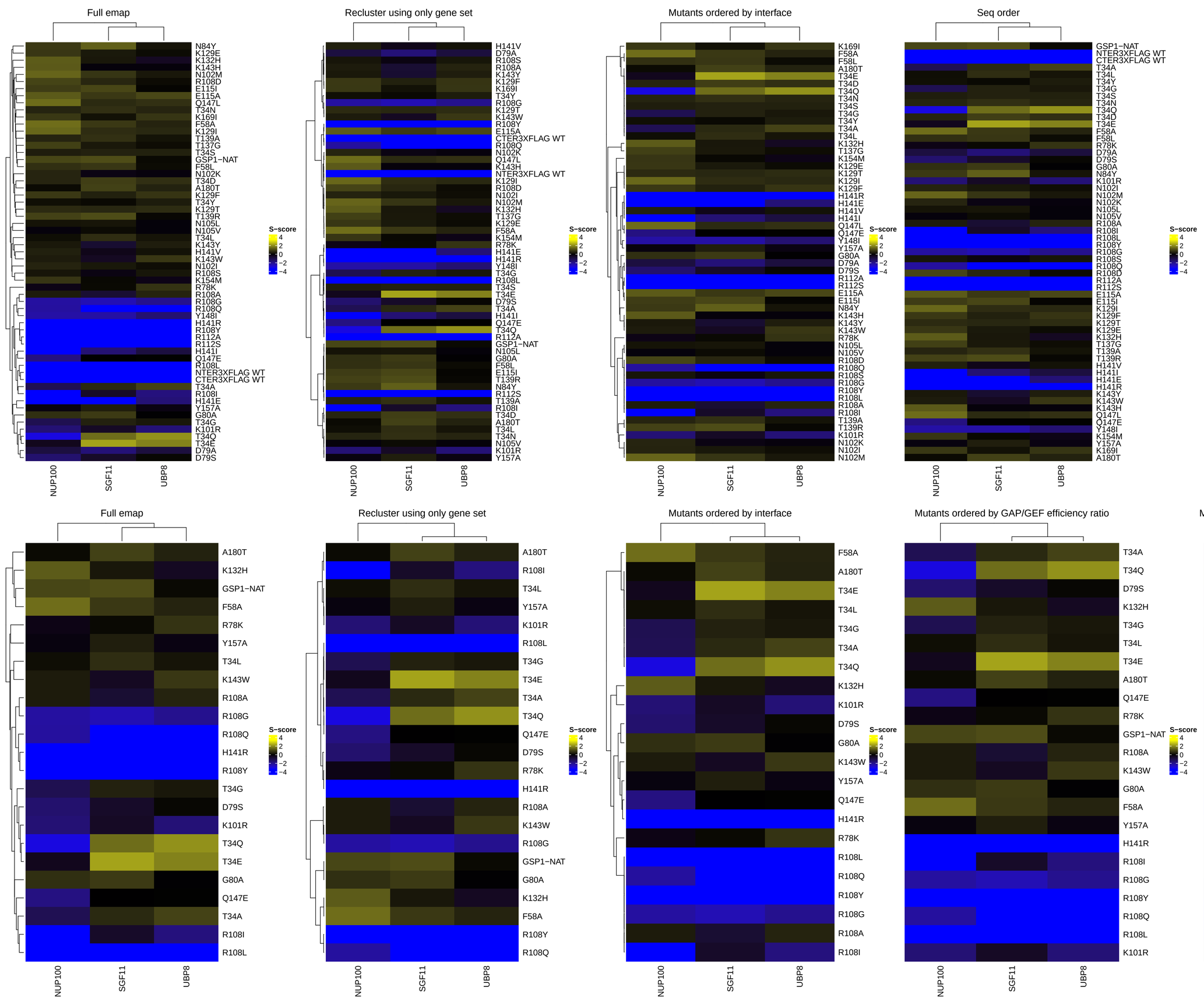

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
NOT5
YER077C
MUD1
RAD18
GBP2
SPT23
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
mRNA processing
gene set picked by clustering raw S−scores
clustering metric: pearson


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


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SRC1
PBS2
SSK2
HOG1
SSK1
HOG1
gene set picked by clustering raw S−scores
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HOS2
SET3
SIF2
SET3
gene set picked by clustering raw S−scores
clustering metric: pearson

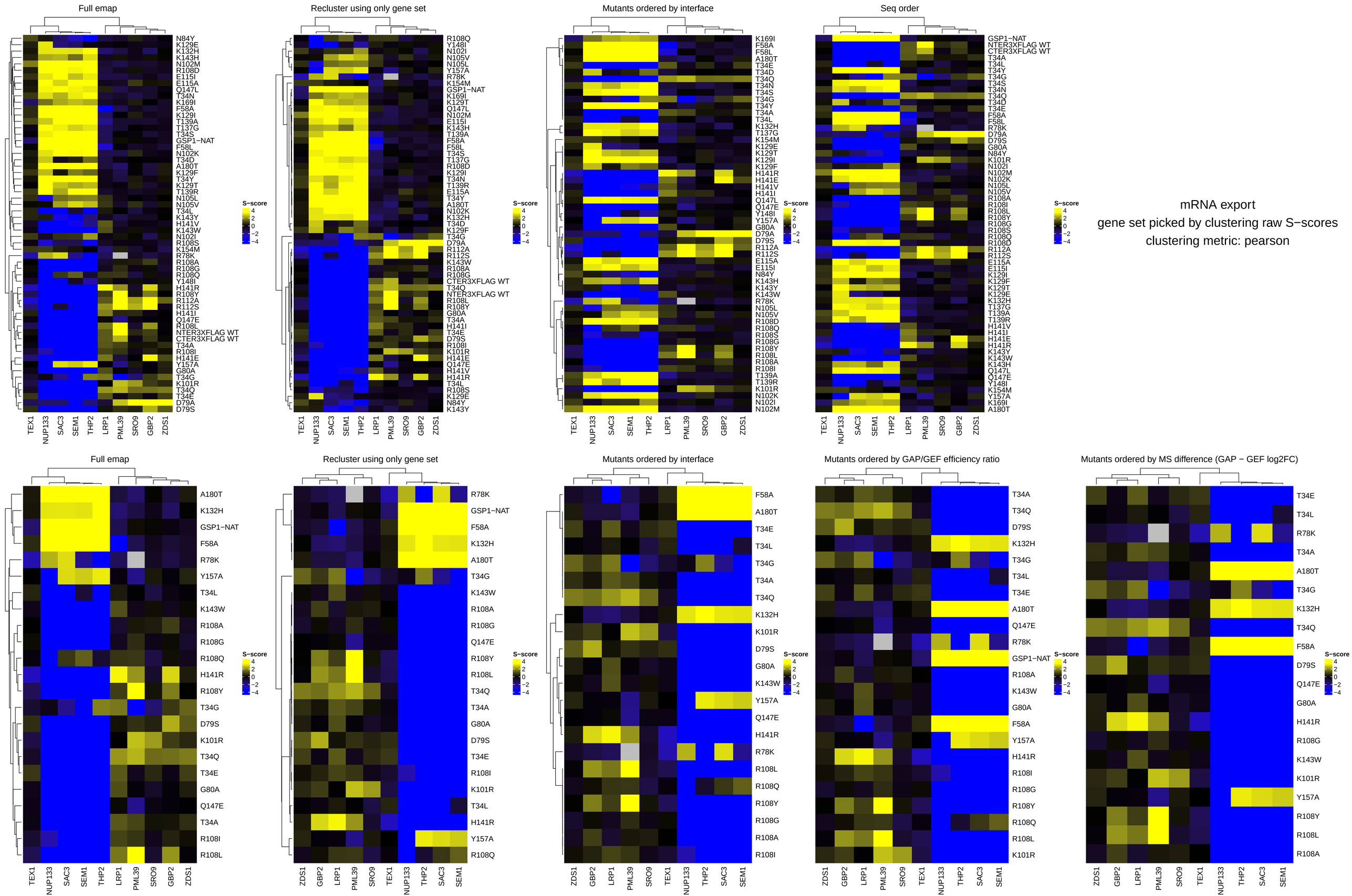

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
NCS6
NCS2
UBA4
Urmylation
gene set picked by clustering raw S−scores
clustering metric: pearson

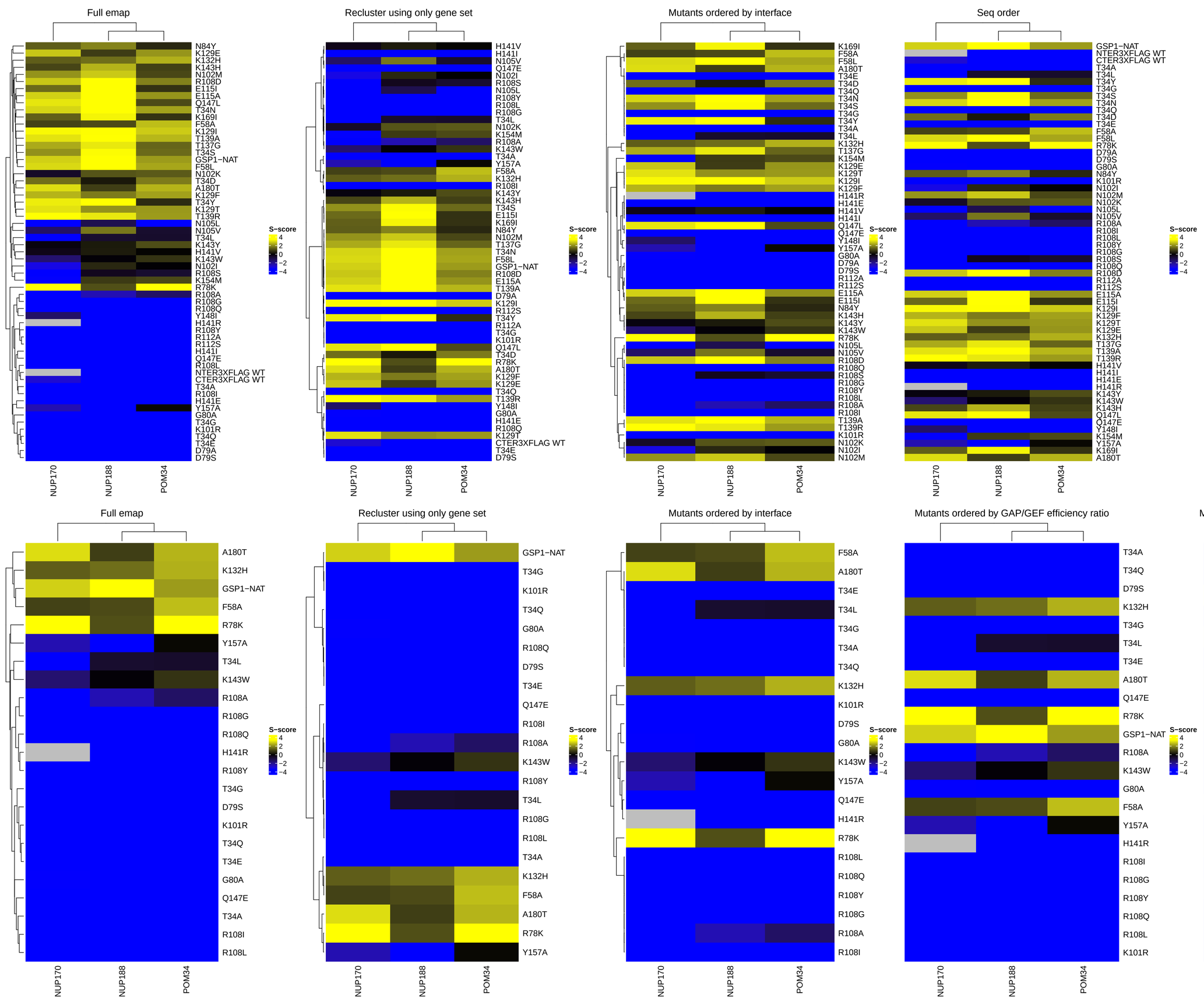


SAGA

gene set picked by clustering raw S−scores

clustering metric: pearson

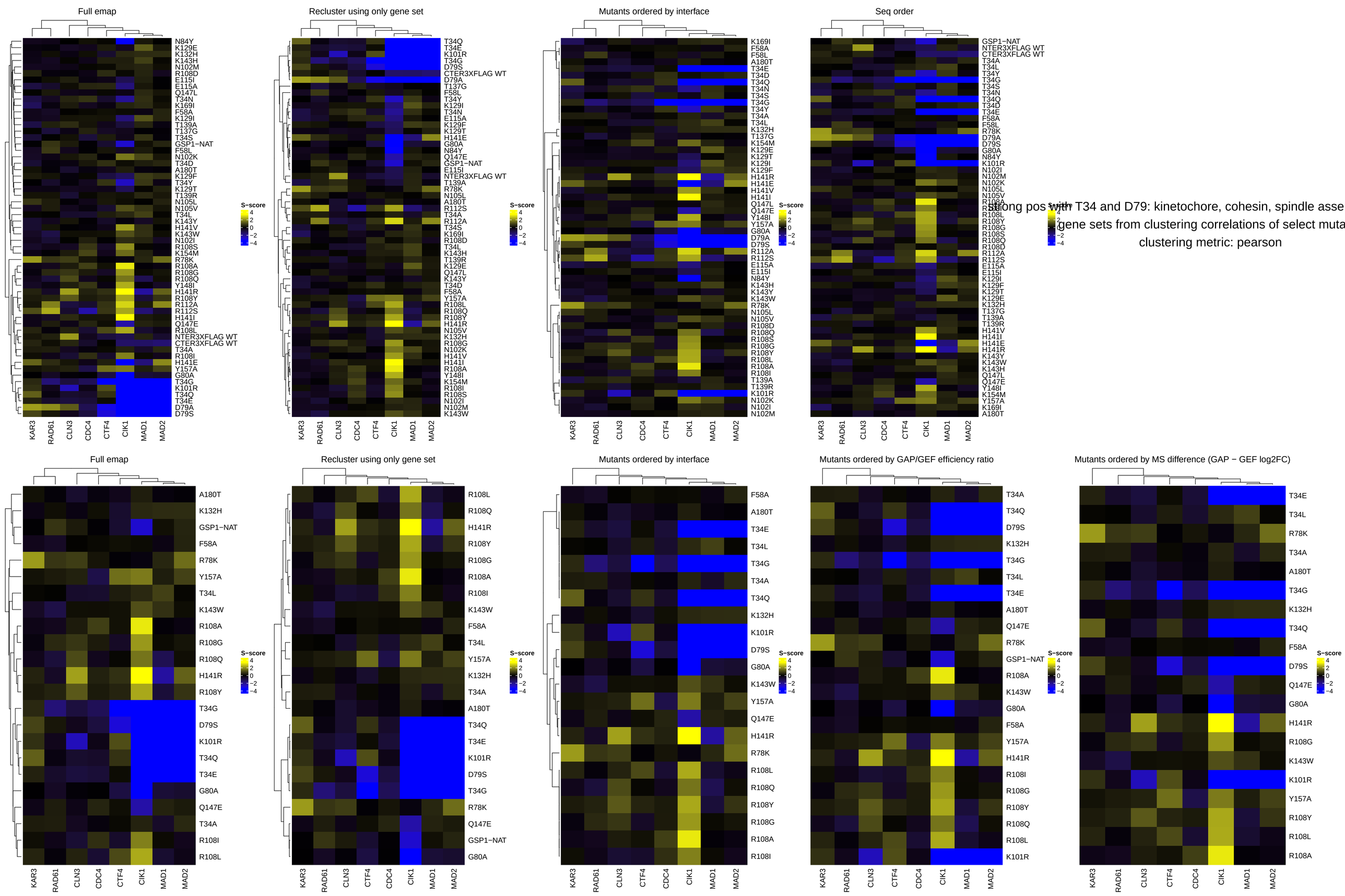

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TEX1
NUP133
SAC3
SEM1
THP2
LRP1
PML39
SRO9
GBP2
ZDS1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP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

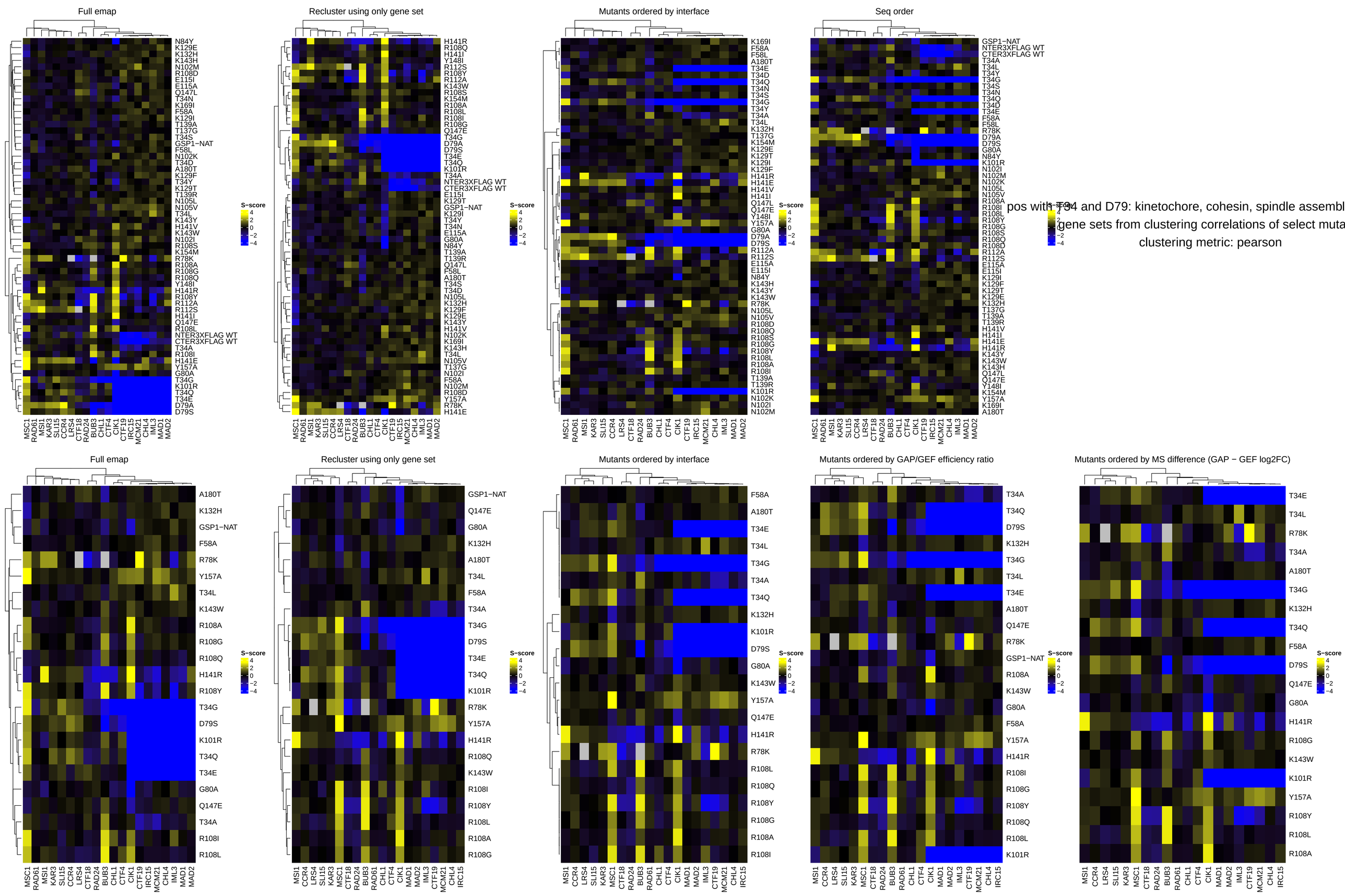


Inner NPC

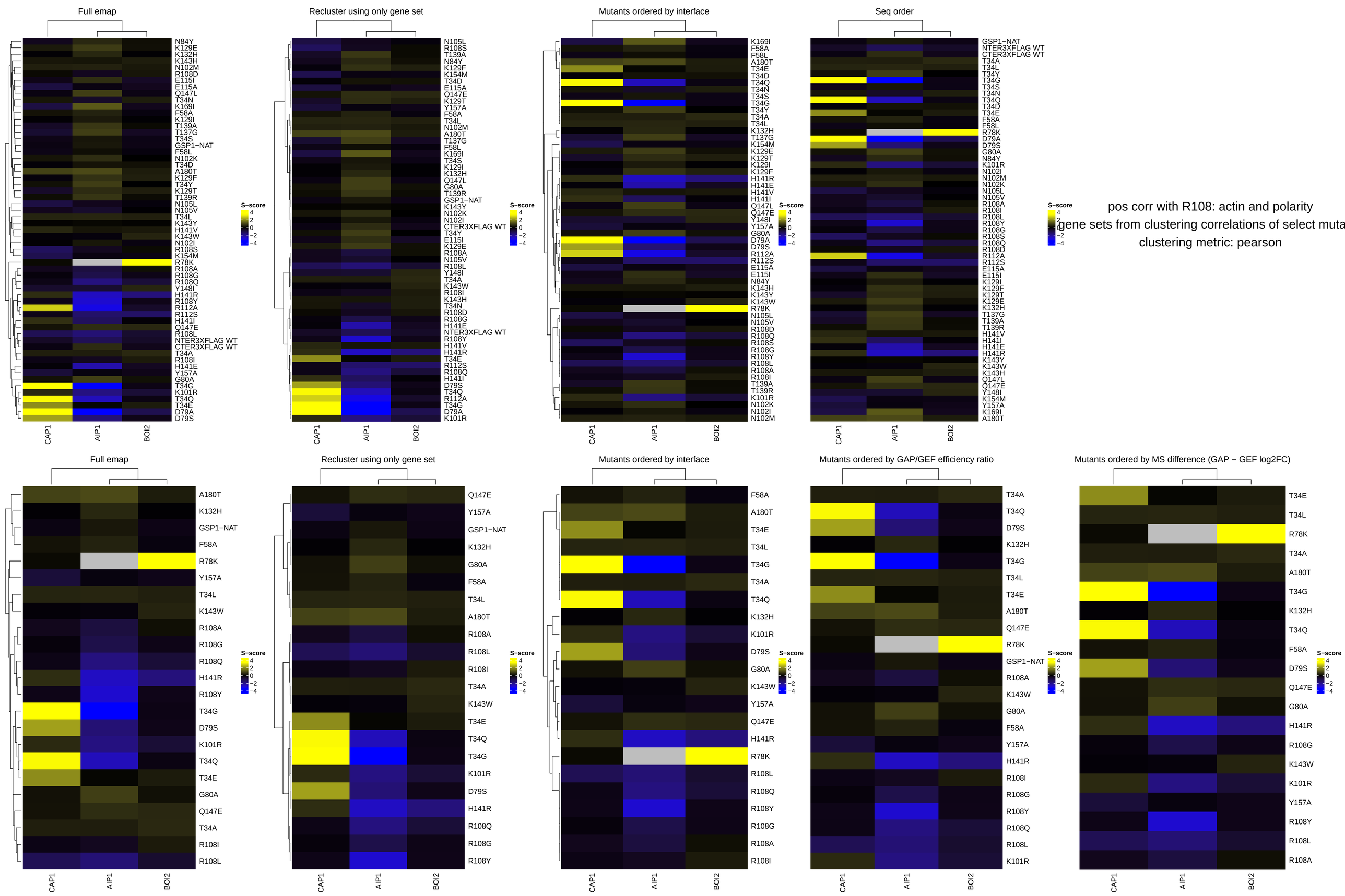
gene set picked by clustering raw S−scores

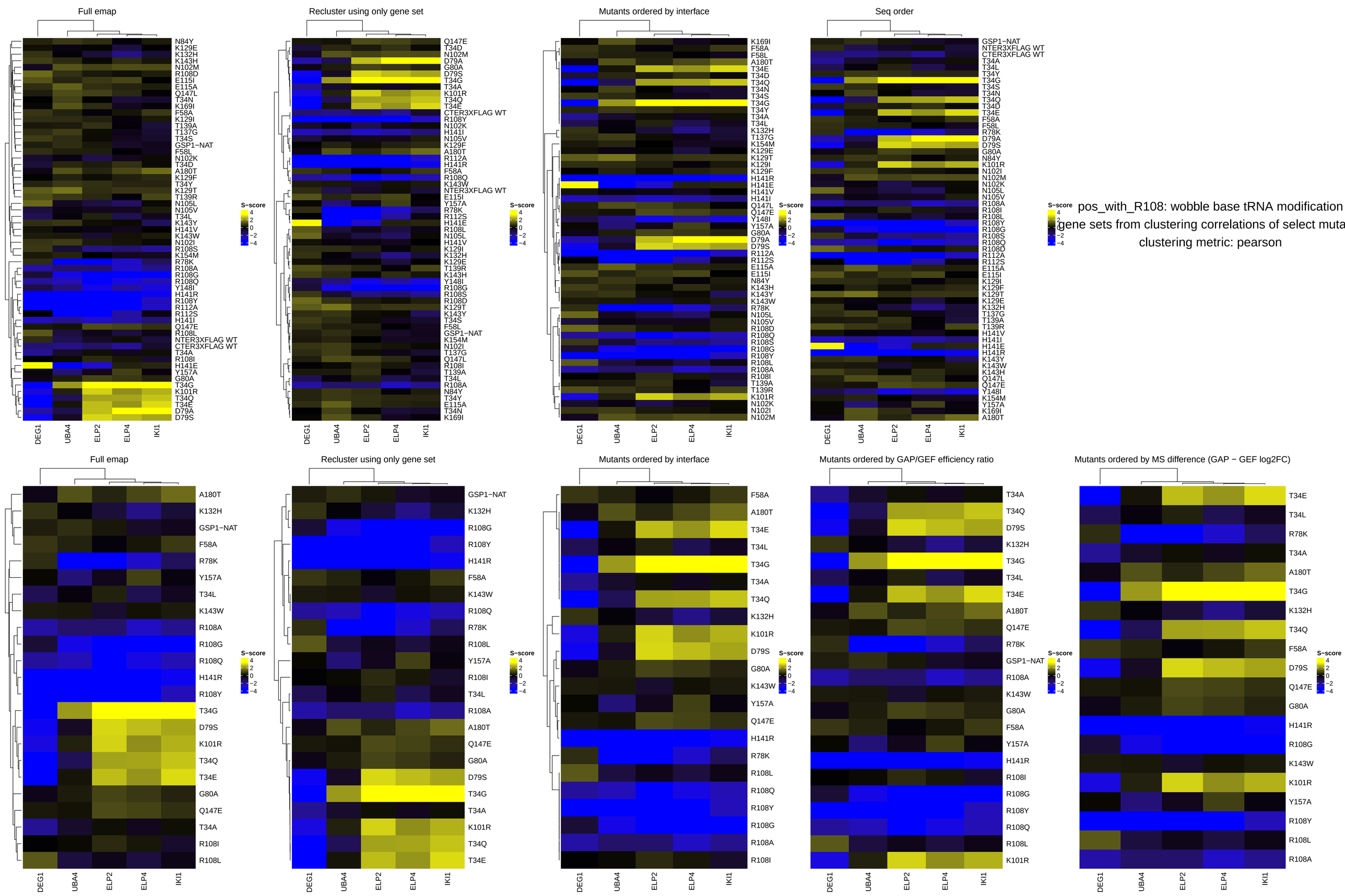
clustering metric: pearson

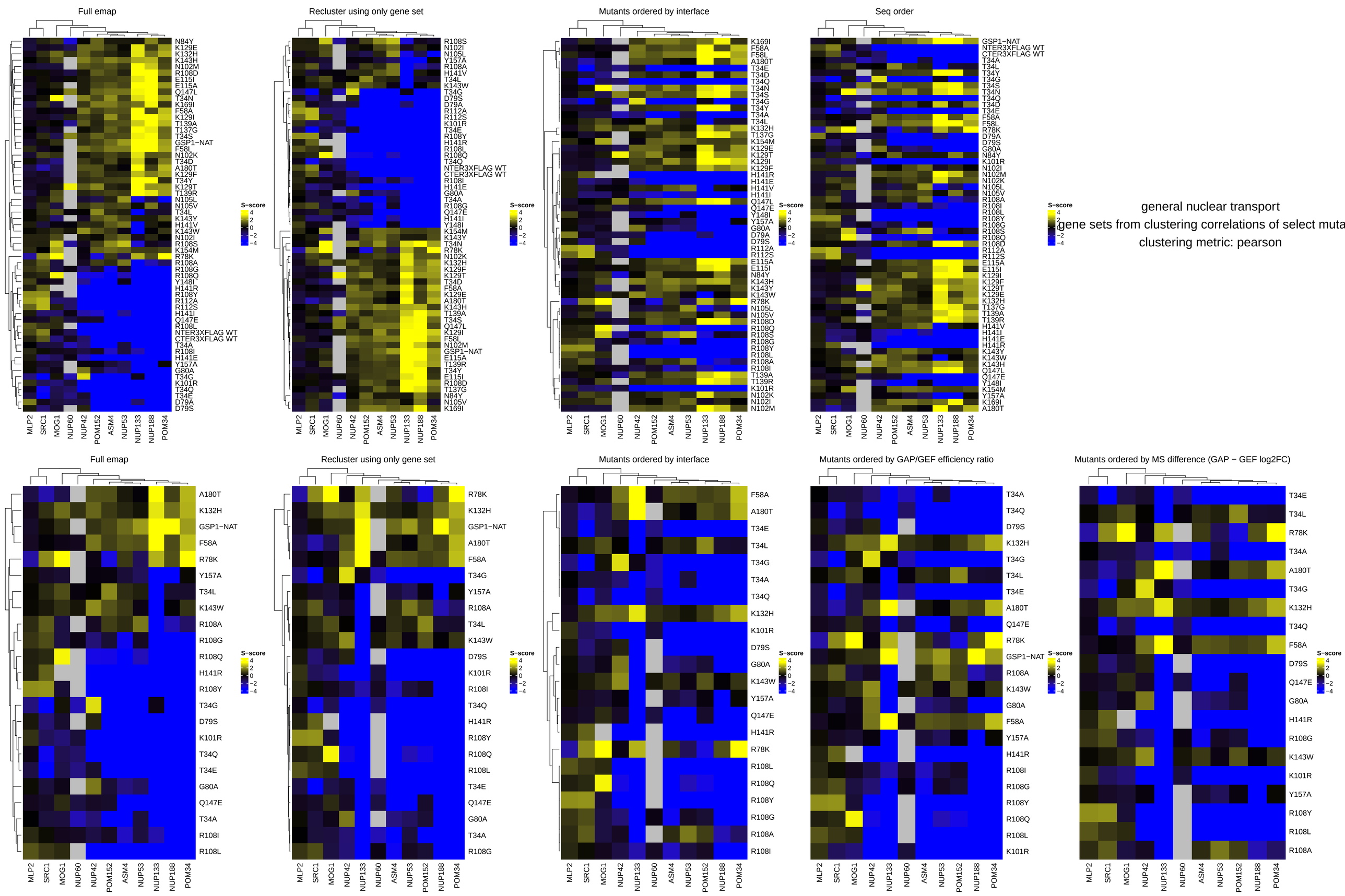

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
KAR3
RAD61
CLN3
CDC4
CTF4
CIK1
MAD1
MAD2
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
Strong pos with T34 and D79: kinetochore, cohesin, spindle asse
gene sets from clustering correlations of select muta
clustering metric: pearson



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


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
CAP1
AIP1
BOI2
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
pos corr with R108: actin and polarity
gene sets from clustering correlations of select muta
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
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: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
MLP2
SRC1
MOG1
NUP60
NUP42
POM152
ASM4
NUP53
NUP133
NUP188
POM34
N84Y
K129E
K132H
K143H
N102M
R108D
E115I
E115A
Q147L
T34N
K169I
F58A
K129I
T139A
T137G
T34S
GSP1−NAT
F58L
N102K
T34D
A180T
K129F
T34Y
K129T
T139R
N105L
N105V
T34L
K143Y
H141V
K143W
N102I
R108S
K154M
R78K
R108A
R108G
R108Q
Y148I
H141R
R108Y
R112A
R112S
H141I
Q147E
R108L
NTER3XFLAG WT
CTER3XFLAG WT
T34A
R108I
H141E
Y157A
G80A
T34G
K101R
T34Q
T34E
D79A
D79S
R108S
N102I
N105L
Y157A
R108A
H141V
T34L
K143W
T34G
D79S
D79A
R112A
R112S
K101R
T34E
R108Y
H141R
R108L
R108Q
T34Q
NTER3XFLAG WT
CTER3XFLAG WT
R108I
H141E
G80A
T34A
R108G
Q147E
H141I
Y148I
K154M
K143Y
T34N
R78K
N102K
K132H
K129F
K129T
T34D
F58A
K129E
A180T
K143H
T139A
T34S
Q147L
K129I
F58L
N102M
GSP1−NAT
E115A
T139R
T34Y
E115I
R108D
T137G
N84Y
N105V
K169I
K169I
F58A
F58L
A180T
T34E
T34D
T34Q
T34N
T34S
T34G
T34Y
T34A
T34L
K132H
T137G
K154M
K129E
K129T
K129I
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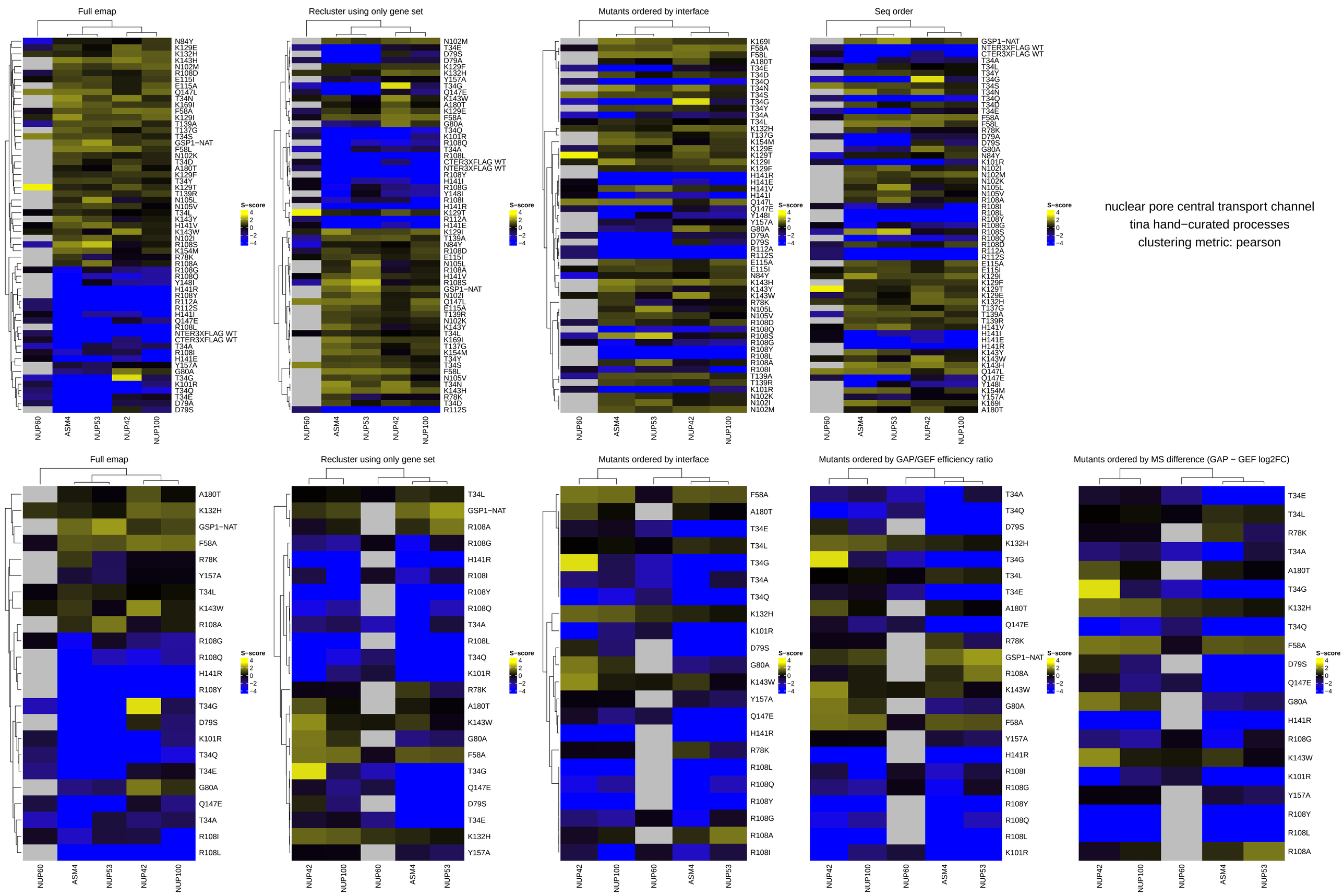
H141R
H141E
H141V
H141I
Q147L
Q147E
Y148I
Y157A
G80A
D79A
D79S
R112A
R112S
E115A
E115I
N84Y
K143H
K143Y
K143W
R78K
N105L
N105V
R108D
R108Q
R108S
R108G
R108Y
R108L
R108A
R108I
T139A
T139R
K101R
N102K
N102I
N102M
GSP1−NAT
NTER3XFLAG WT
CTER3XFLAG WT
T34A
T34L
T34Y
T34G
T34S
T34N
T34Q
T34D
T34E
F58A
F58L
R78K
D79A
D79S
G80A
N84Y
K101R
N102I
N102M
N102K
N105L
N105V
R108A
R108I
R108L
R108Y
R108G
R108S
R108Q
R108D
R112A
R112S
E115A
E115I
K129I
K129F
K129T
K129E
K132H
T137G
T139A
T139R
H141V
H141I
H141E
H141R
K143Y
K143W
K143H
Q147L
Q147E
Y148I
K154M
Y157A
K169I
A180T
general nuclear transport
gene sets from clustering correlations of select muta
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
A180T
K132H
GSP1−NAT
F58A
R78K
Y157A
T34L
K143W
R108A
R108G
R108Q
H141R
R108Y
T34G
D79S
K101R
T34Q
T34E
G80A
Q147E
T34A
R108I
R108L
R78K
K132H
GSP1−NAT
A180T
F58A
T34G
Y157A
R108A
T34L
K143W
D79S
K101R
R108I
T34Q
H141R
R108Y
R108Q
R108L
T34E
Q147E
G80A
T34A
R108G
F58A
A180T
T34E
T34L
T34G
T34A
T34Q
K132H
K101R
D79S
G80A
K143W
Y157A
Q147E
H141R
R78K
R108L
R108Q
R108Y
R108G
R108A
R108I
T34A
T34Q
D79S
K132H
T34G
T34L
T34E
A180T
Q147E
R78K
GSP1−NAT
R108A
K143W
G80A
F58A
Y157A
H141R
R108I
R108G
R108Y
R108Q
R108L
K101R
T34E
T34L
R78K
T34A
A180T
T34G
K132H
T34Q
F58A
D79S
Q147E
G80A
H141R
R108G
K143W
K101R
Y157A
R108Y
R108L
R108A
MLP2
SRC1
MOG1
NUP42
NUP133
NUP60
ASM4
NUP53
POM152
NUP188
POM34


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
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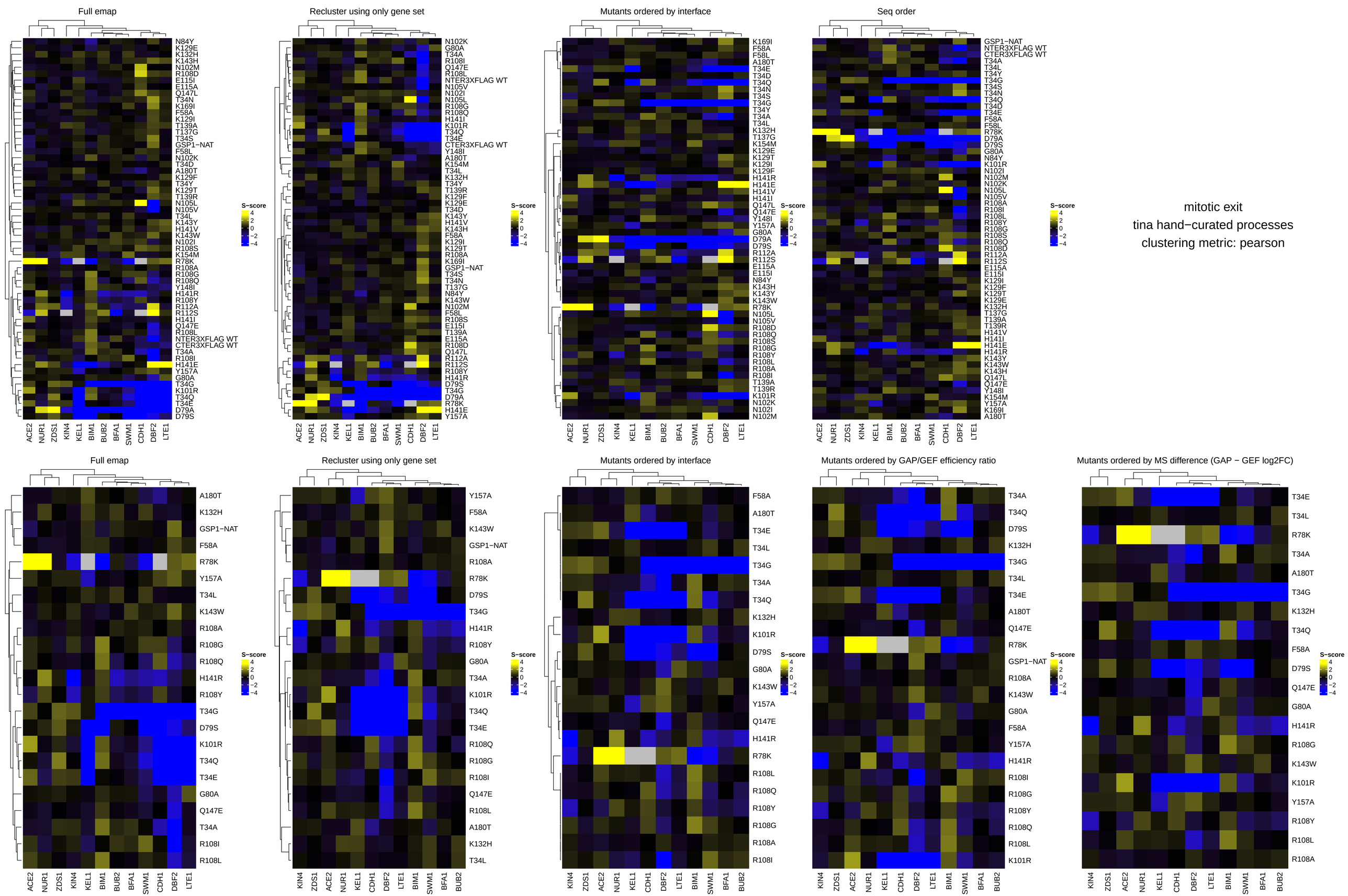
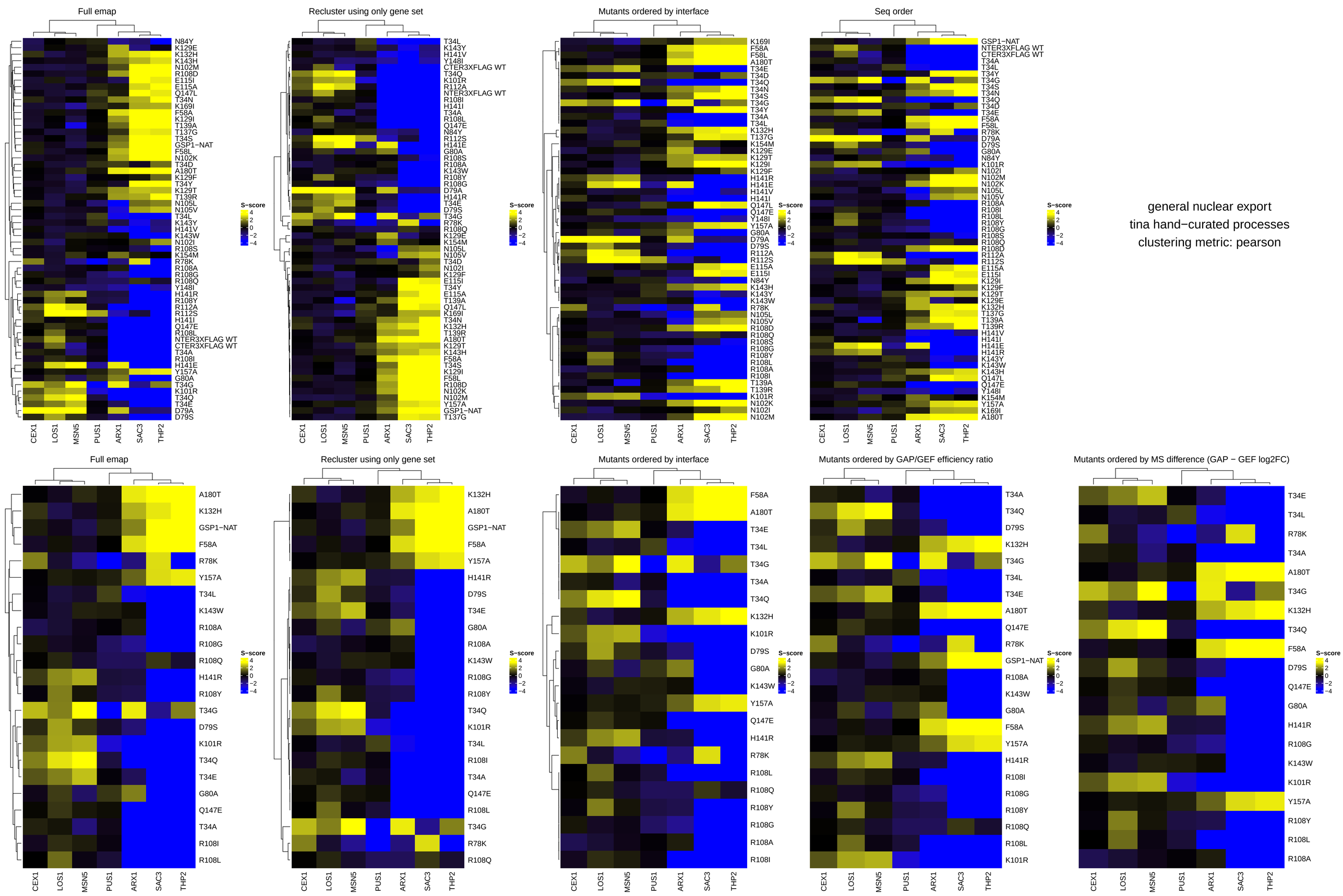
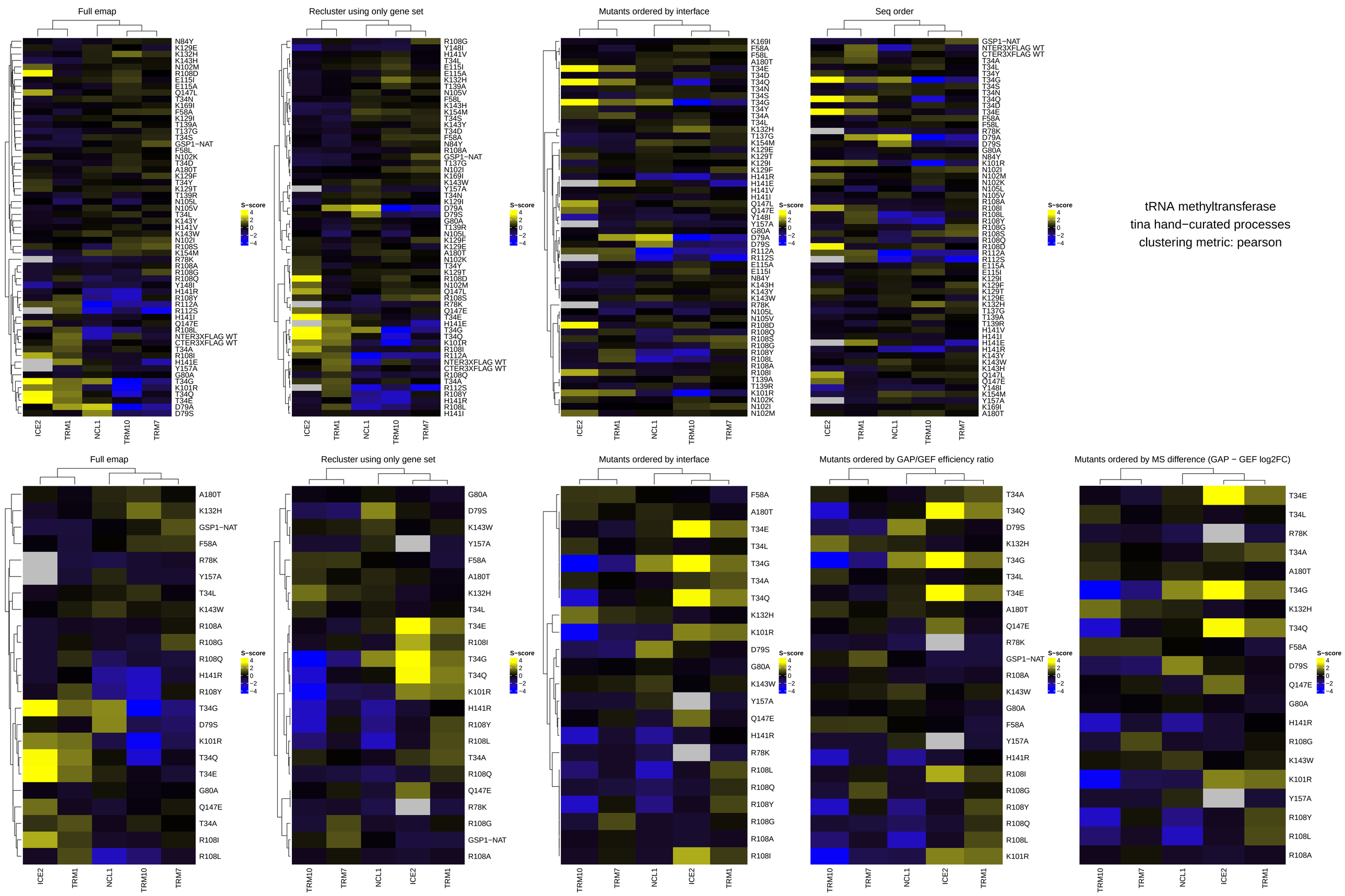
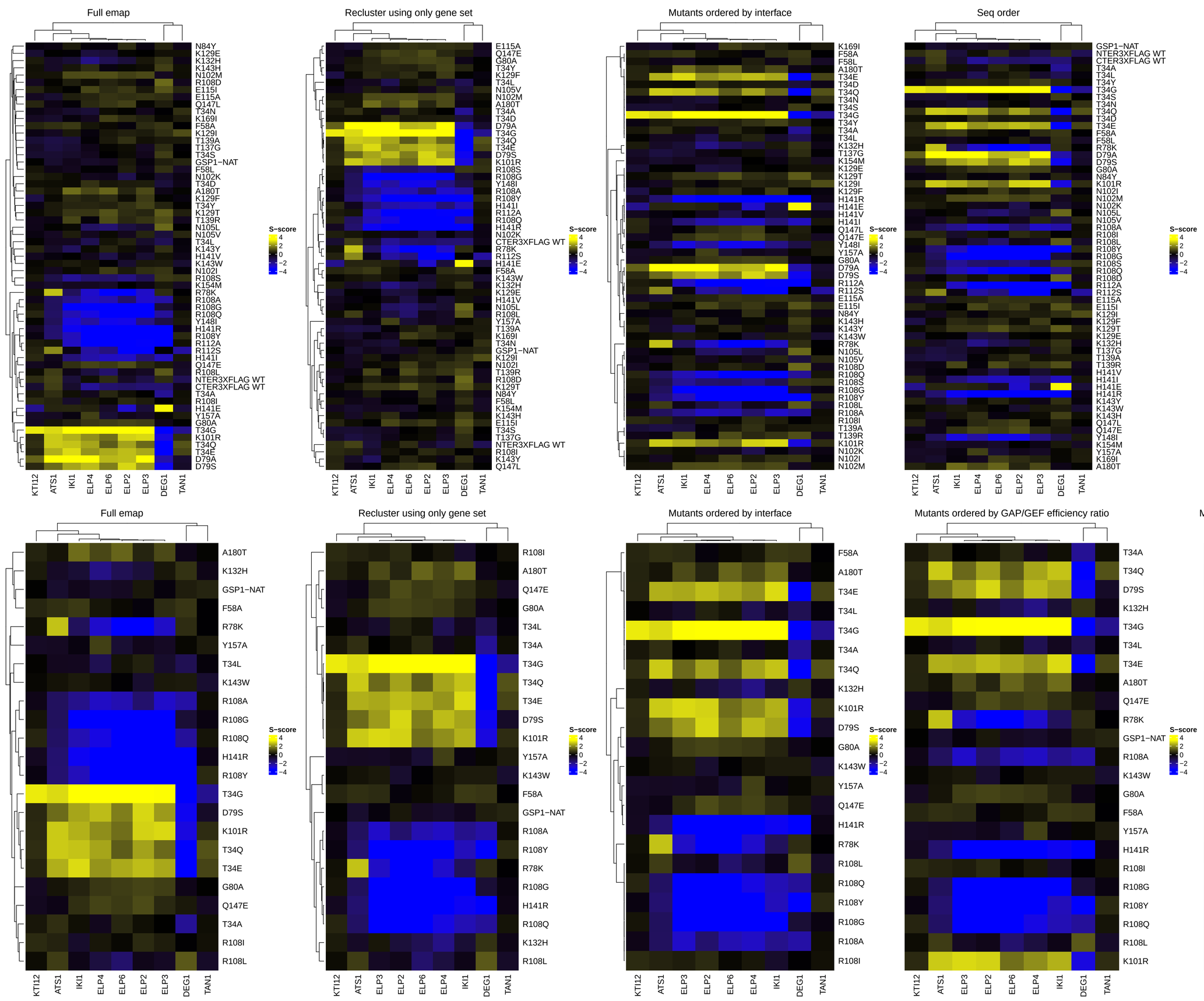
−2
−4
NUP60
ASM4
NUP53
NUP42
NUP100
nuclear pore central transport channel
tina hand−curated processes
clustering metric: pearson

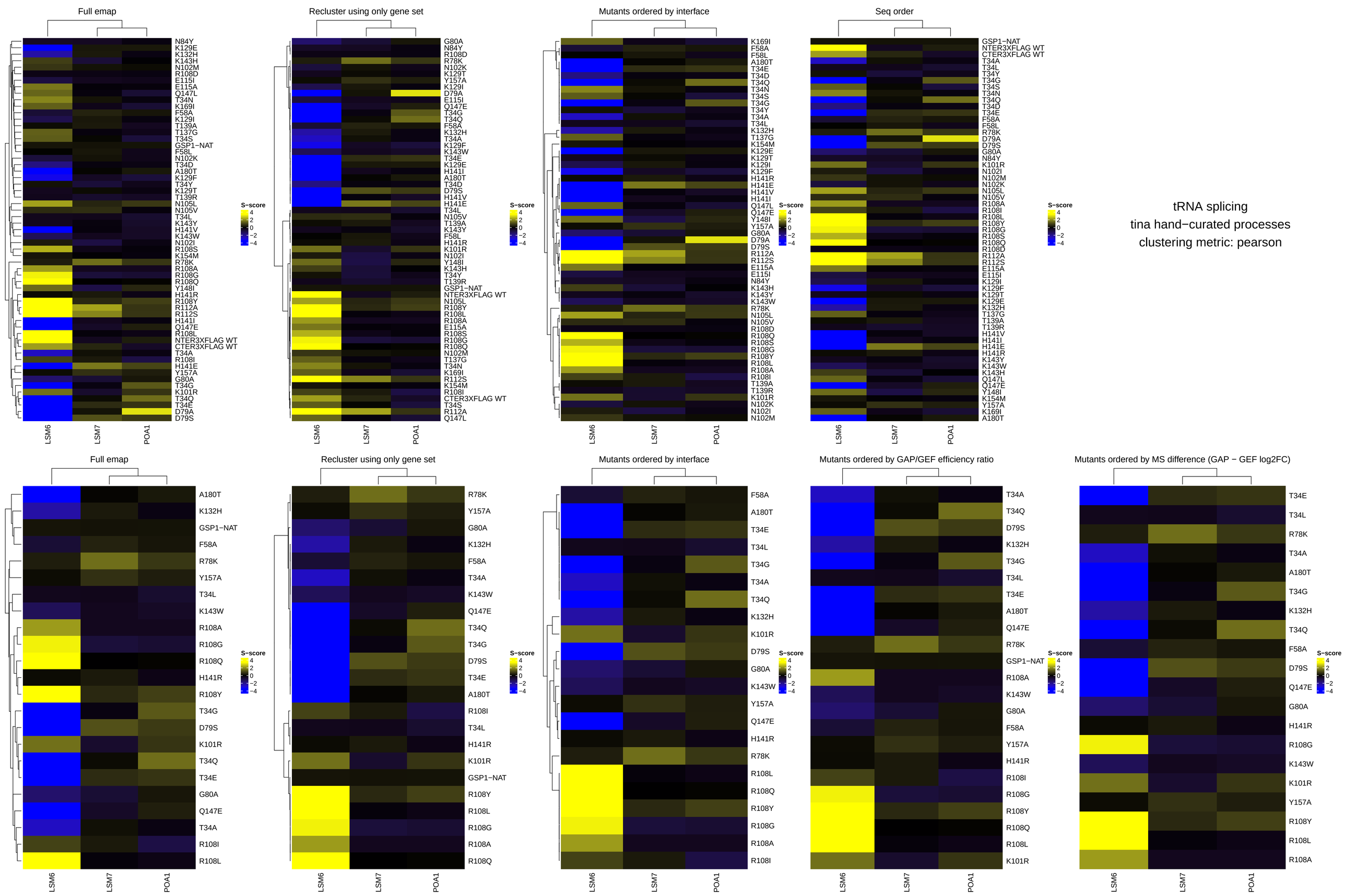

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ACE2
NUR1
ZDS1
KIN4
KEL1
BIM1
BUB2
BFA1
SWM1
CDH1
DBF2
LTE1
mitotic exit
tina hand−curated processes
clustering metric: pearson

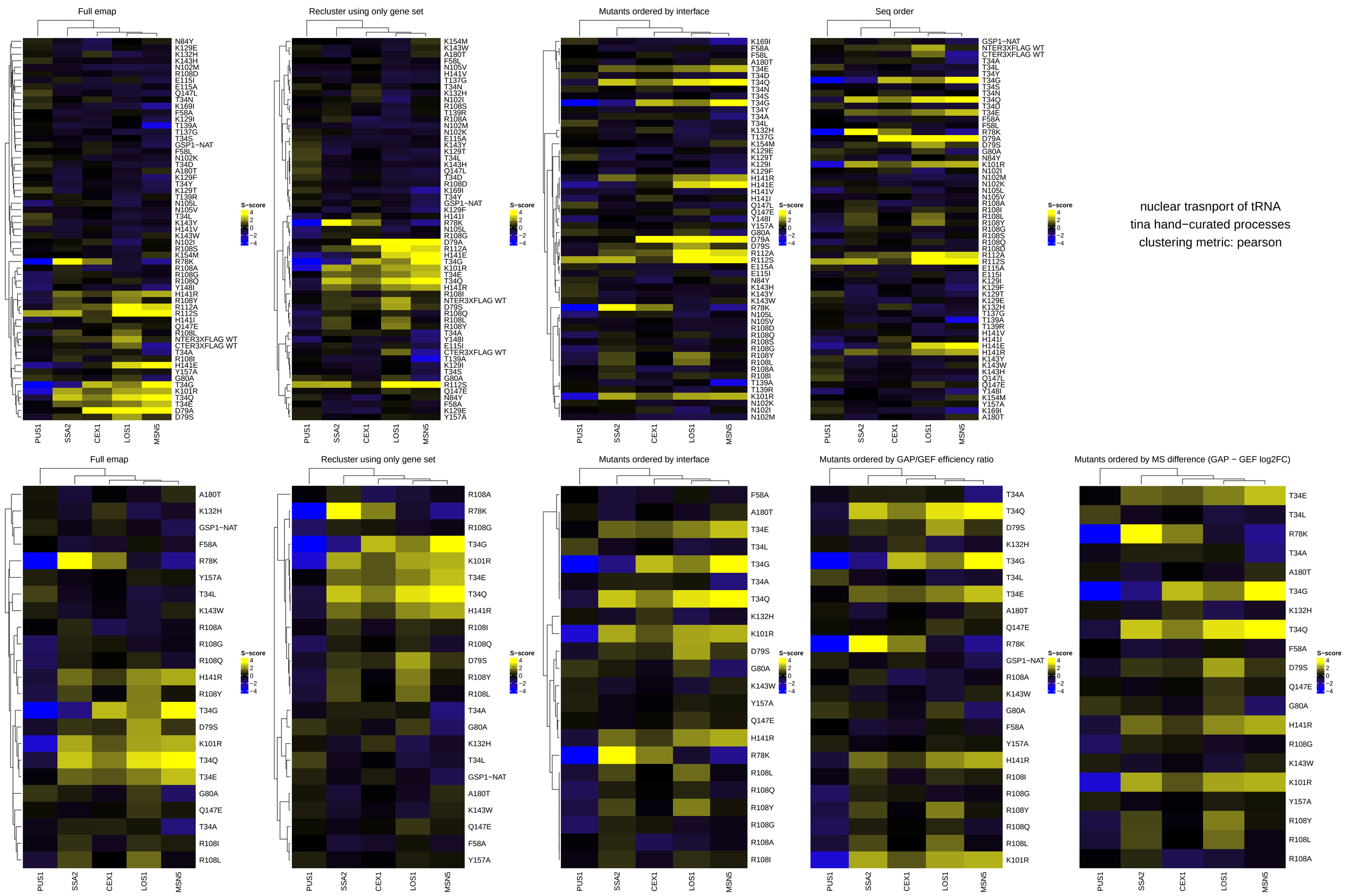

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CEX1
LOS1
MSN5
PUS1
ARX1
SAC3
THP2
general nuclear export
tina hand−curated processes
clustering metric: pearson

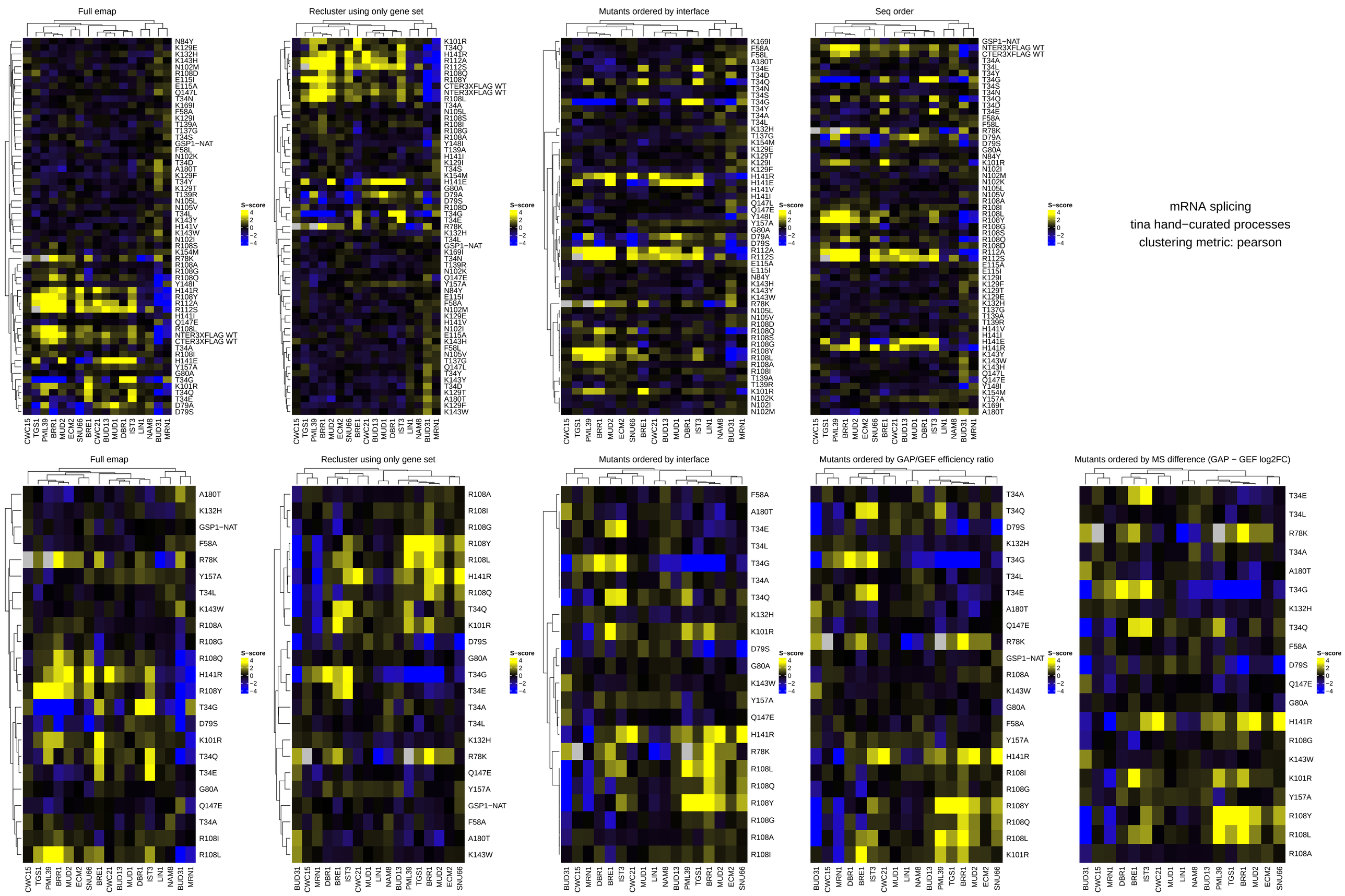

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
ICE2
TRM1
NCL1
TRM10
TRM7
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
tRNA methyltransferase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

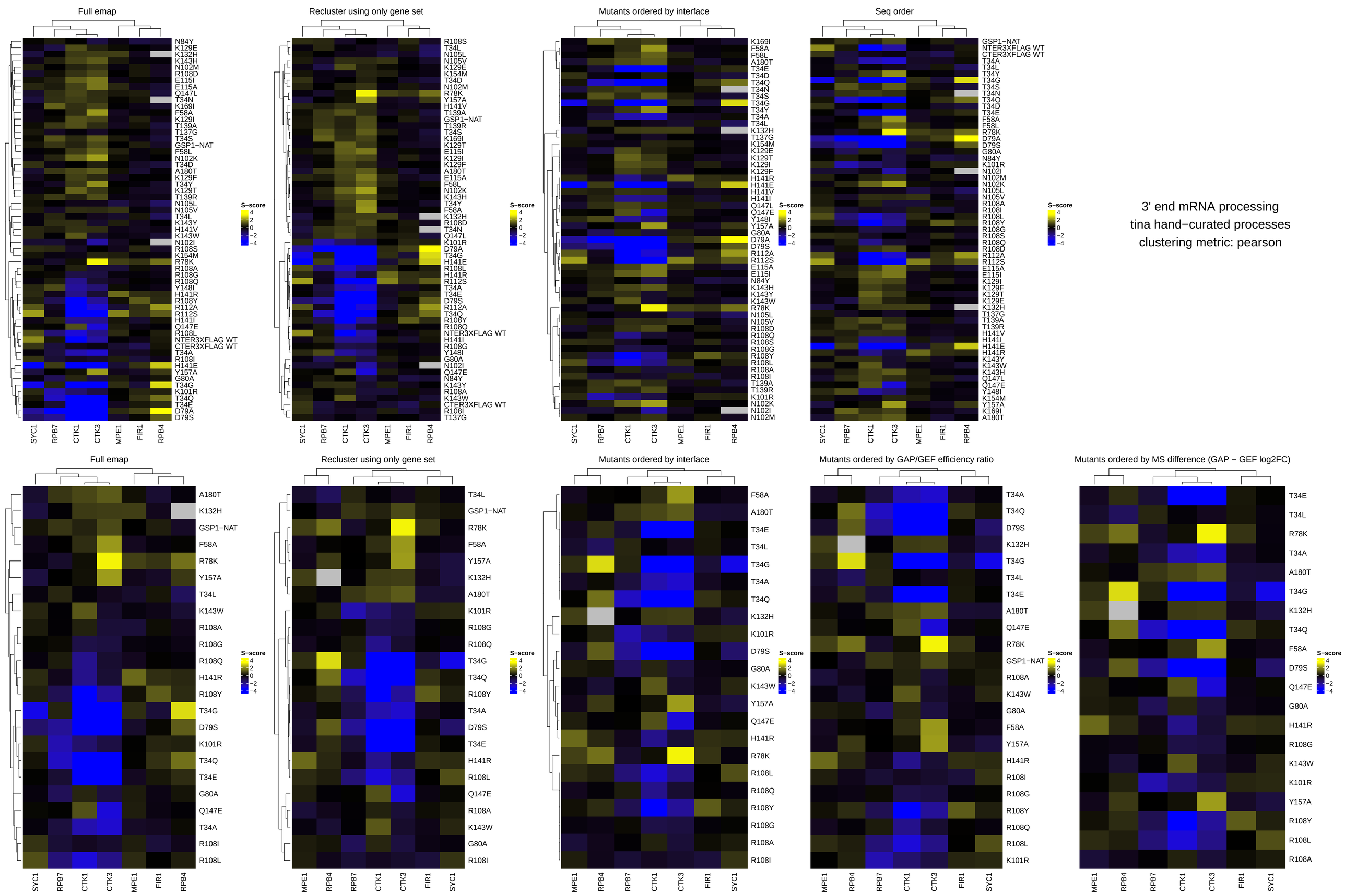


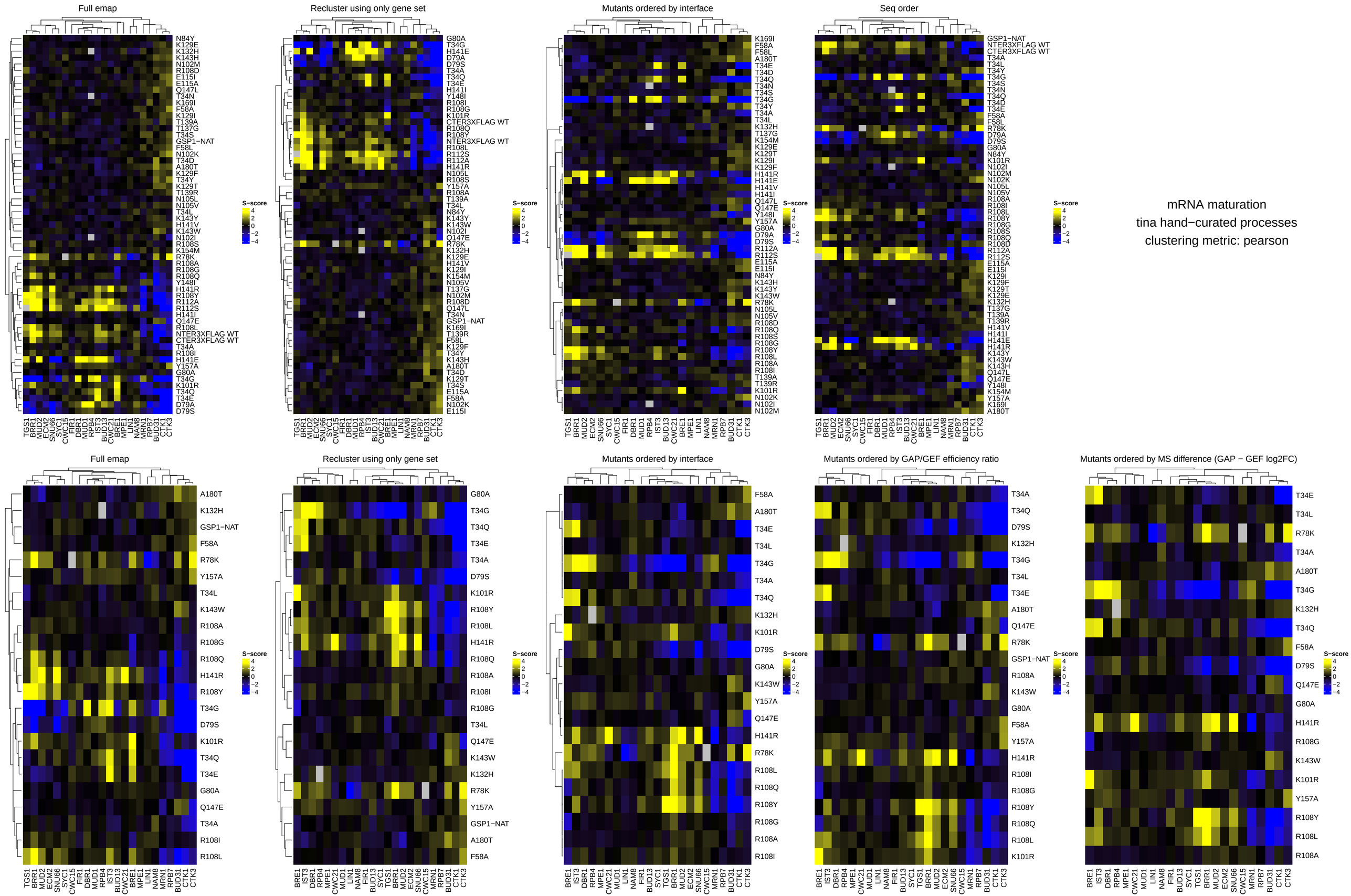
tRNA base modification
tina hand−curated processes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
LSM6
LSM7
POA1
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)
tRNA splicing
tina hand−curated processes
clustering metric: pearson

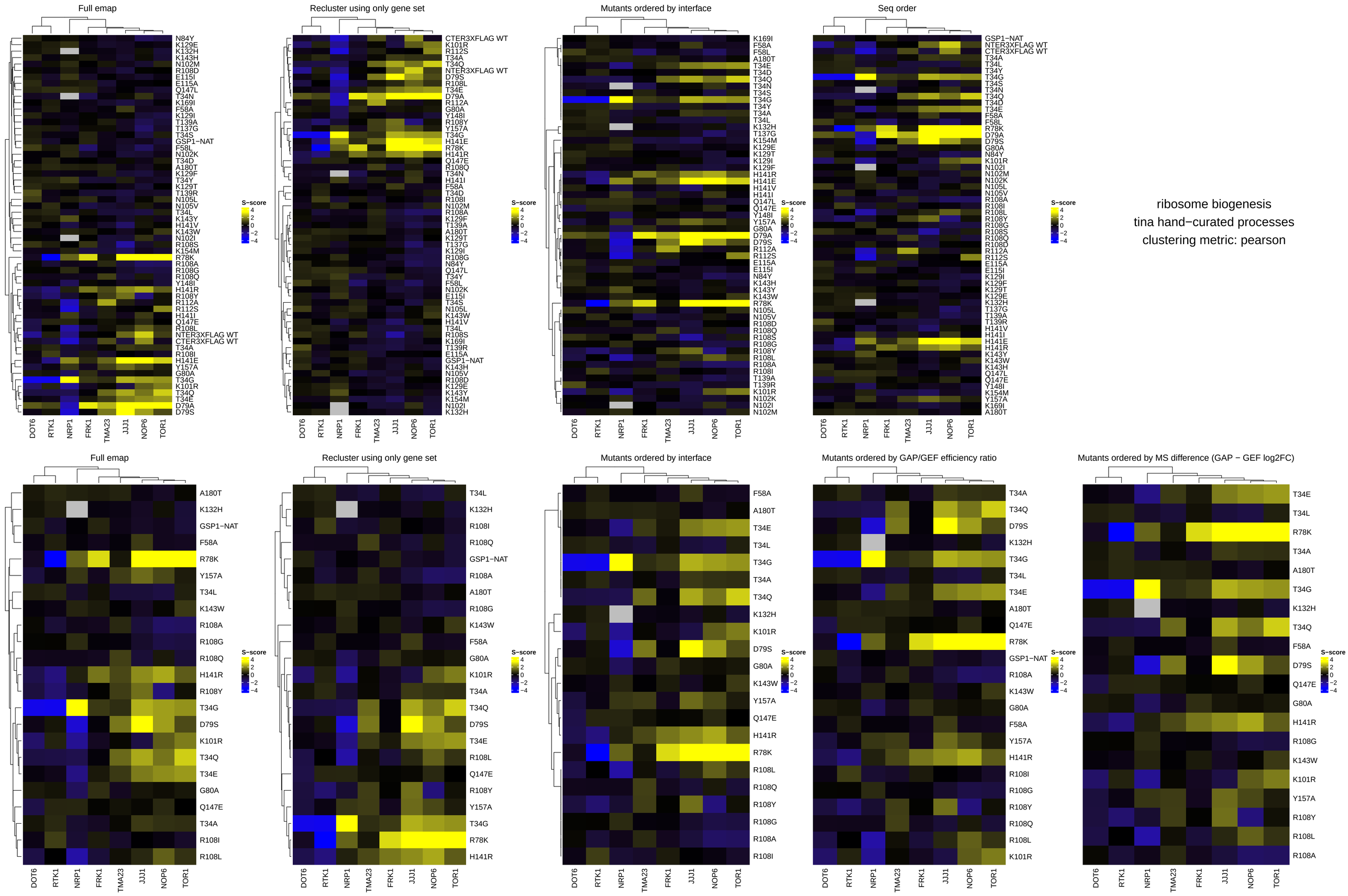

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PUS1
SSA2
CEX1
LOS1
MSN5
nuclear trasnport of tRNA
tina hand−curated processes
clustering metric: pearson

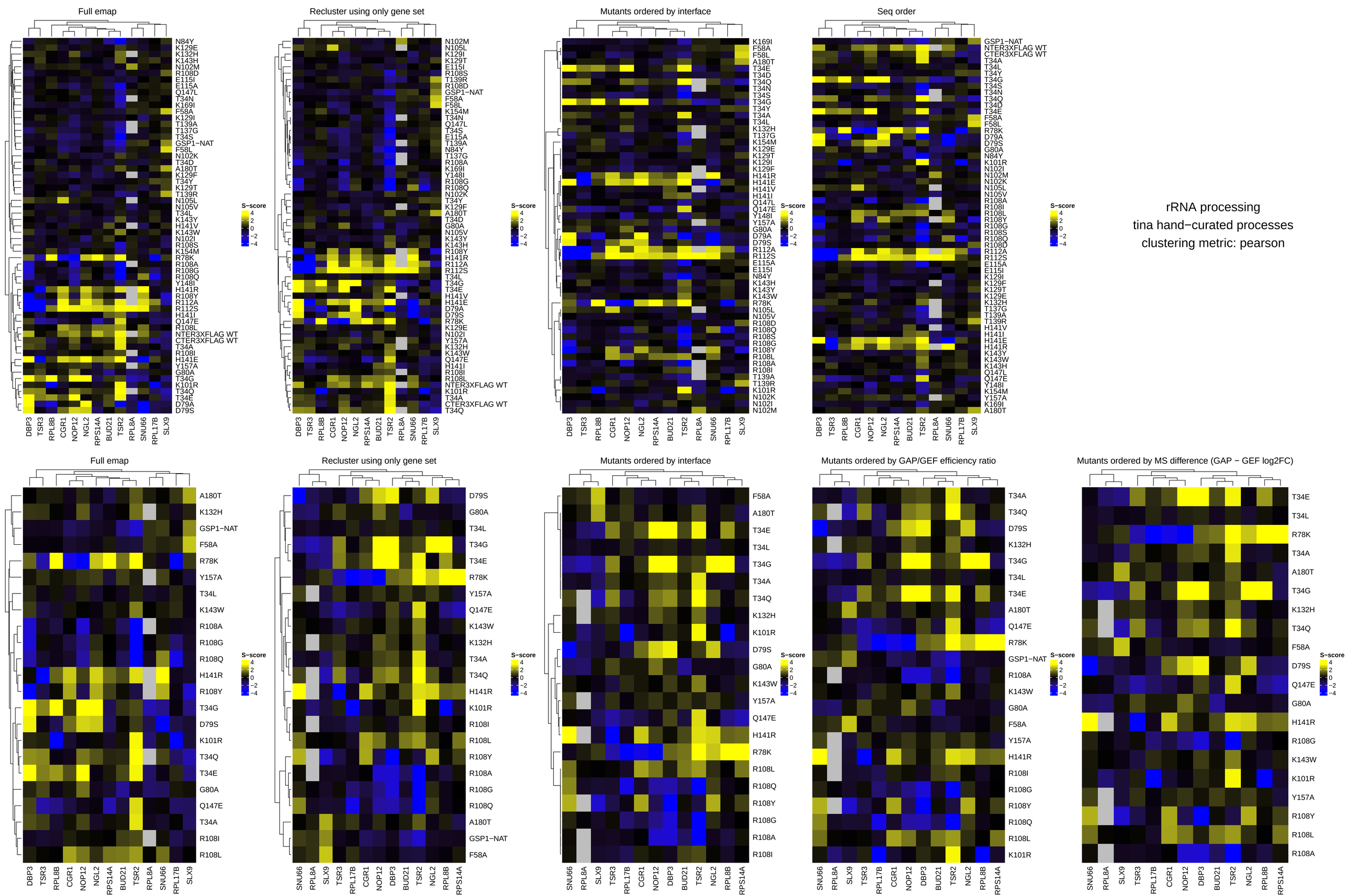

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CWC15 TGS1 PML39 BRR1 MUD2 ECM2 SNU66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

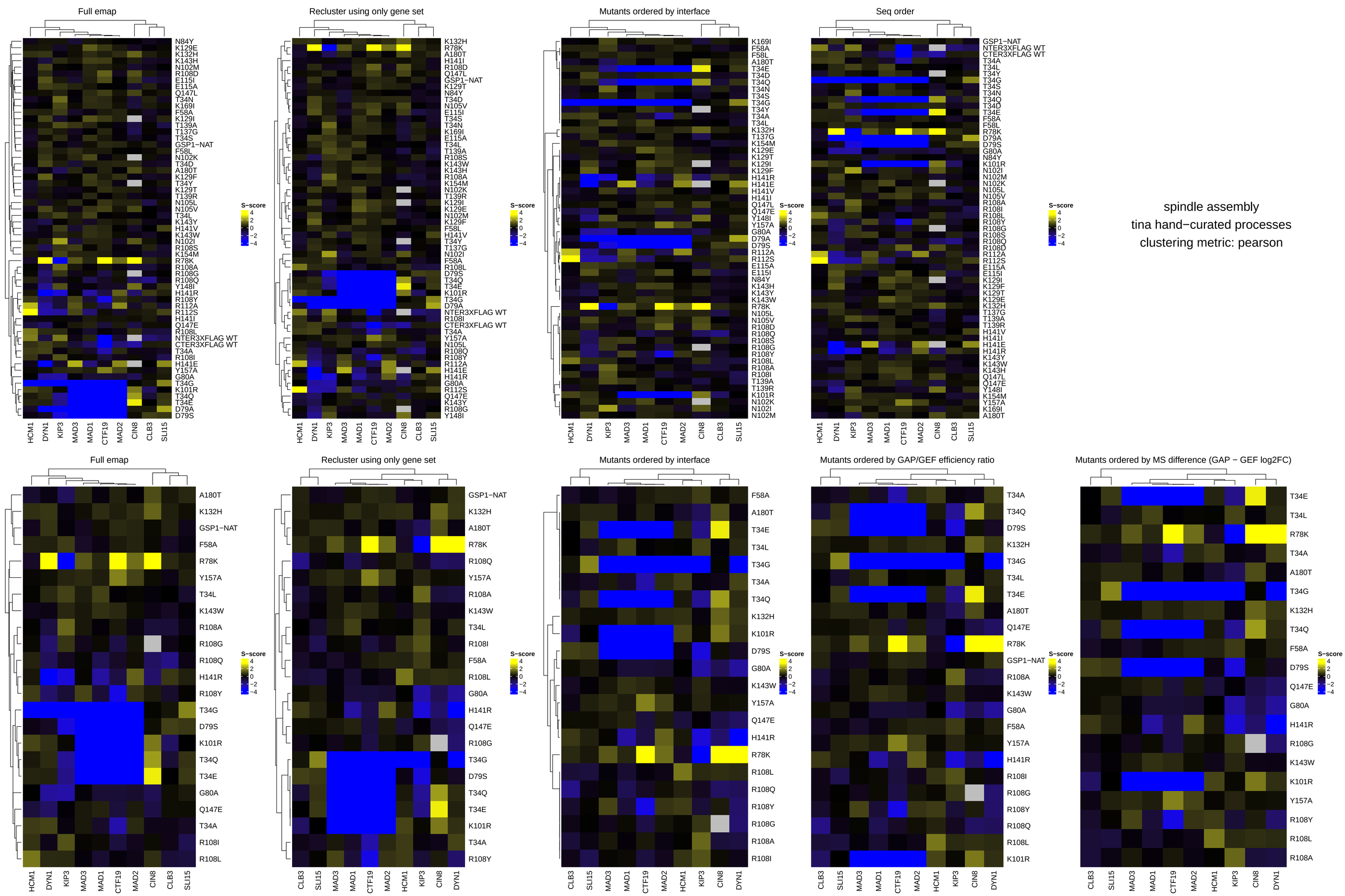

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SYC1
RPB7
CTK1
CTK3
MPE1
FIR1
RPB4
3' end mRNA processing
tina hand−curated processes
clustering metric: pearson

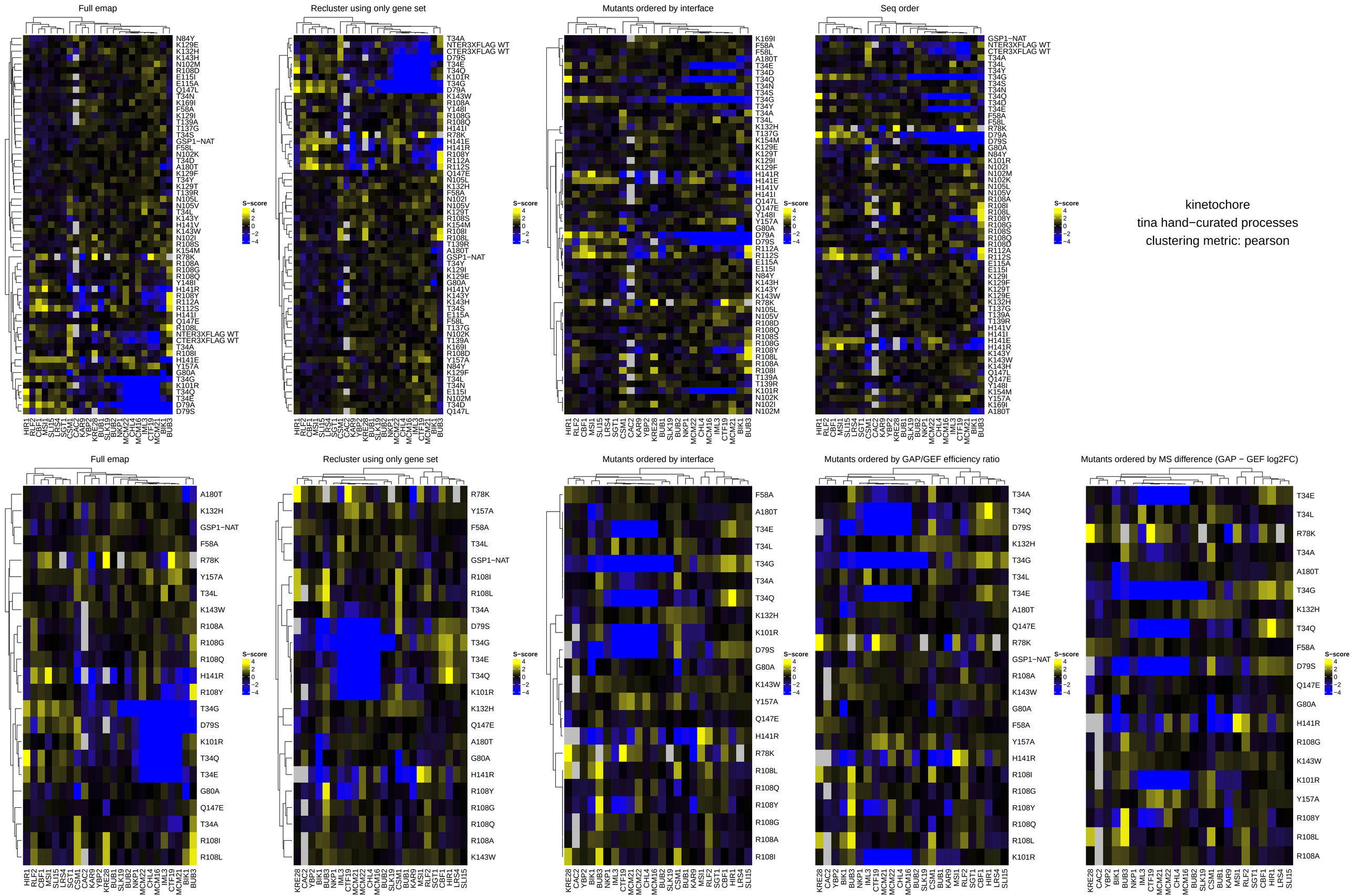


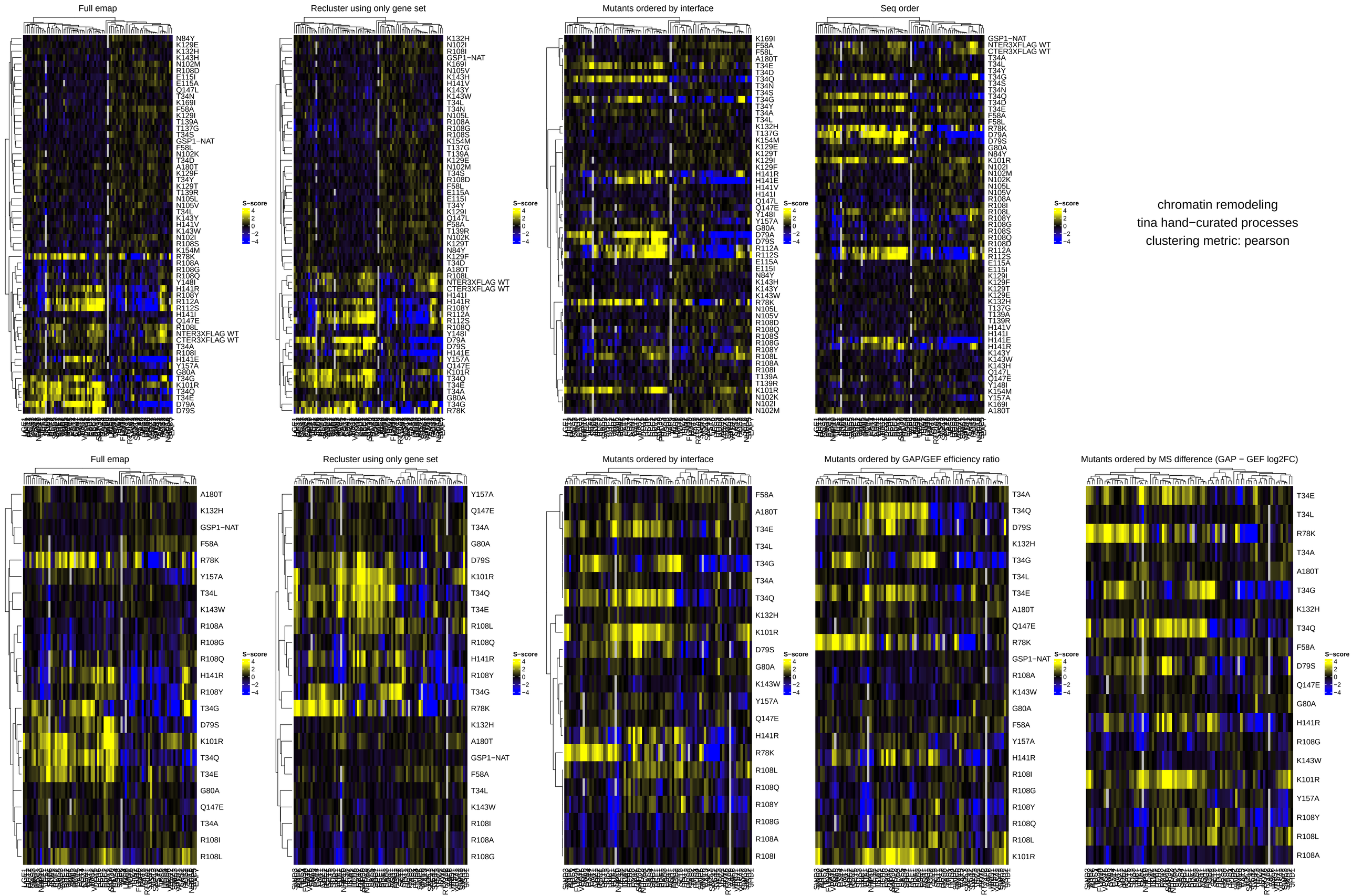
mRNA maturation
tina hand−curated processes
clustering metric: pearson

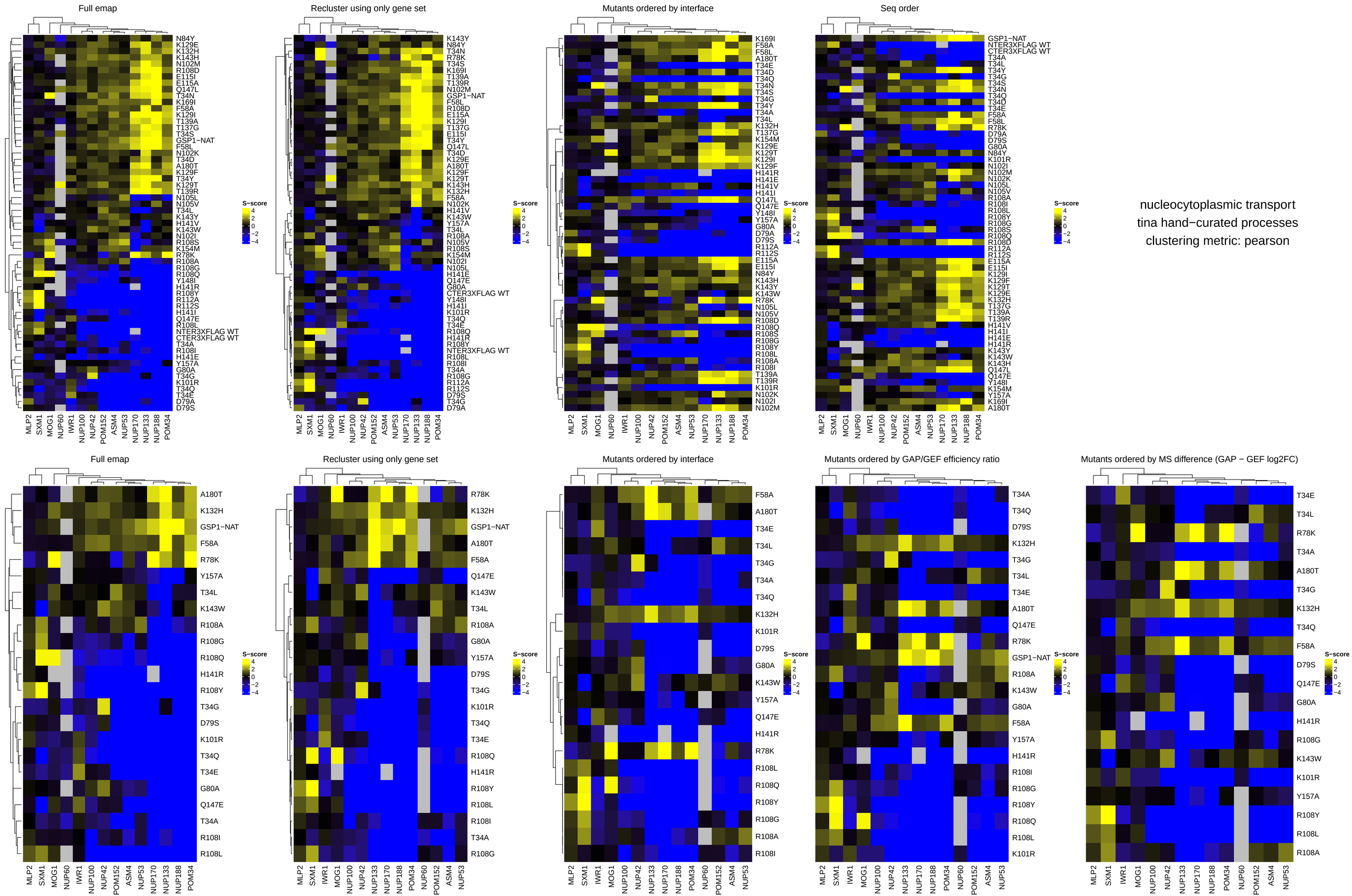

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
DOT6
RTK1
NRP1
FRK1
TMA23
JJJ1
NOP6
TOR1
ribosome biogenesis
tina hand−curated processes
clustering metric: pearson

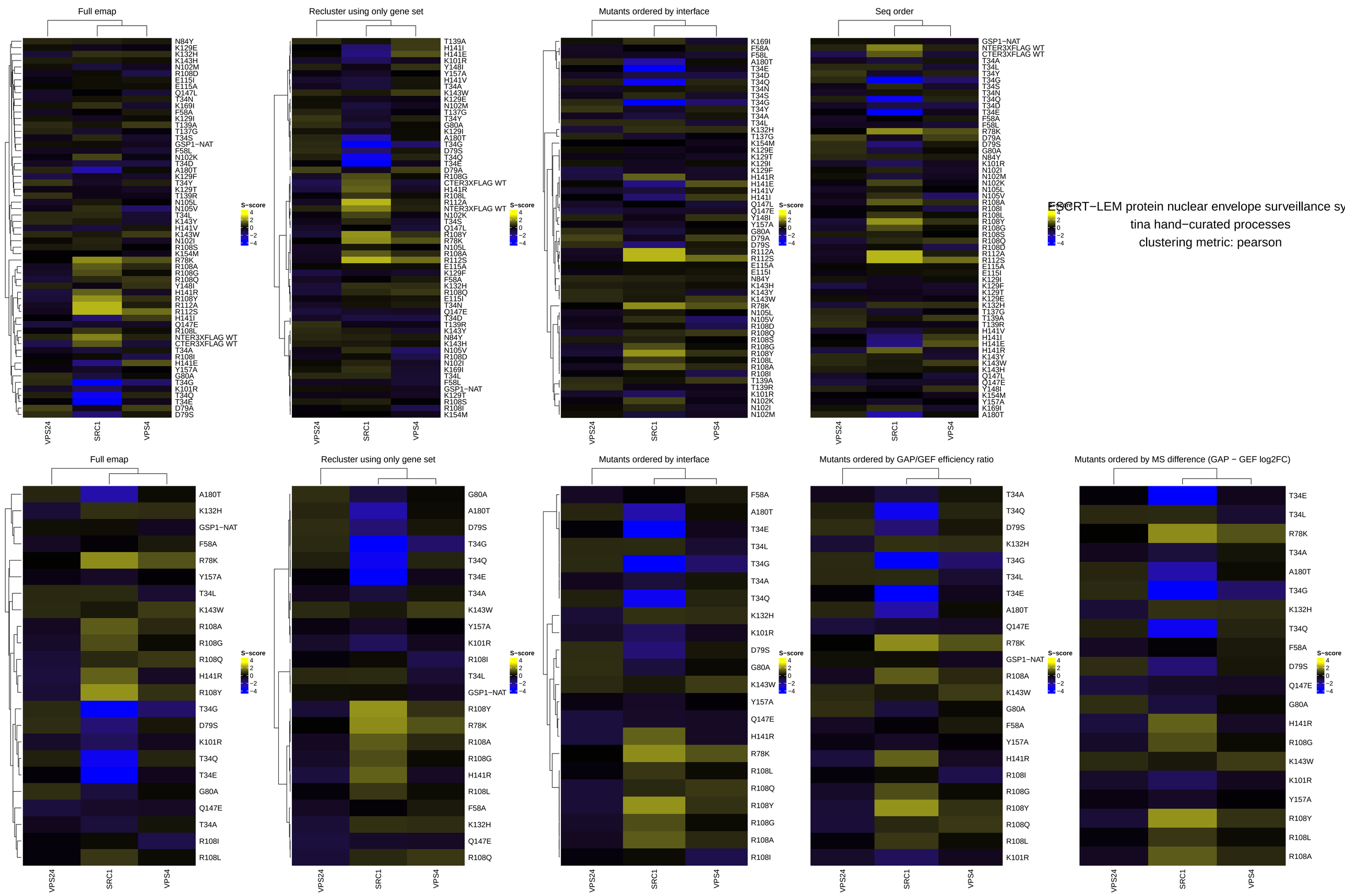

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
DBP3
TSR3
RPL8B
CGR1
NOP12
NGL2
RPS14A
BUD21
TSR2
RPL8A
SNU66
RPL17B
SLX9
rRNA processing
tina hand−curated processes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

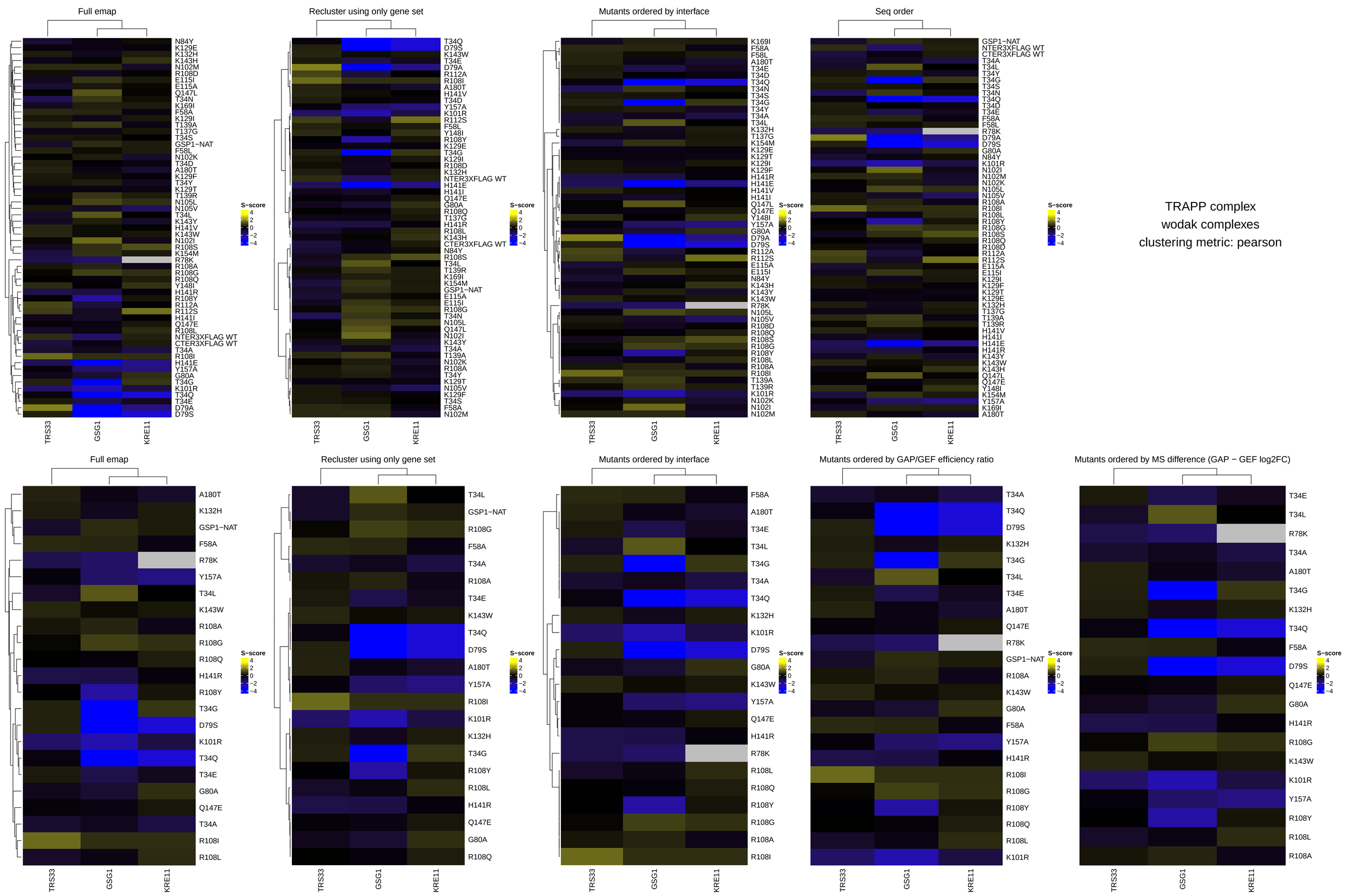

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
HCM1
DYN1
KIP3
MAD3
MAD1
CTF19
MAD2
CIN8
CLB3
SLI15
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
spindle assembly
tina hand−curated processes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
kinetochore
tina hand−curated processes
clustering metric: pearson
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

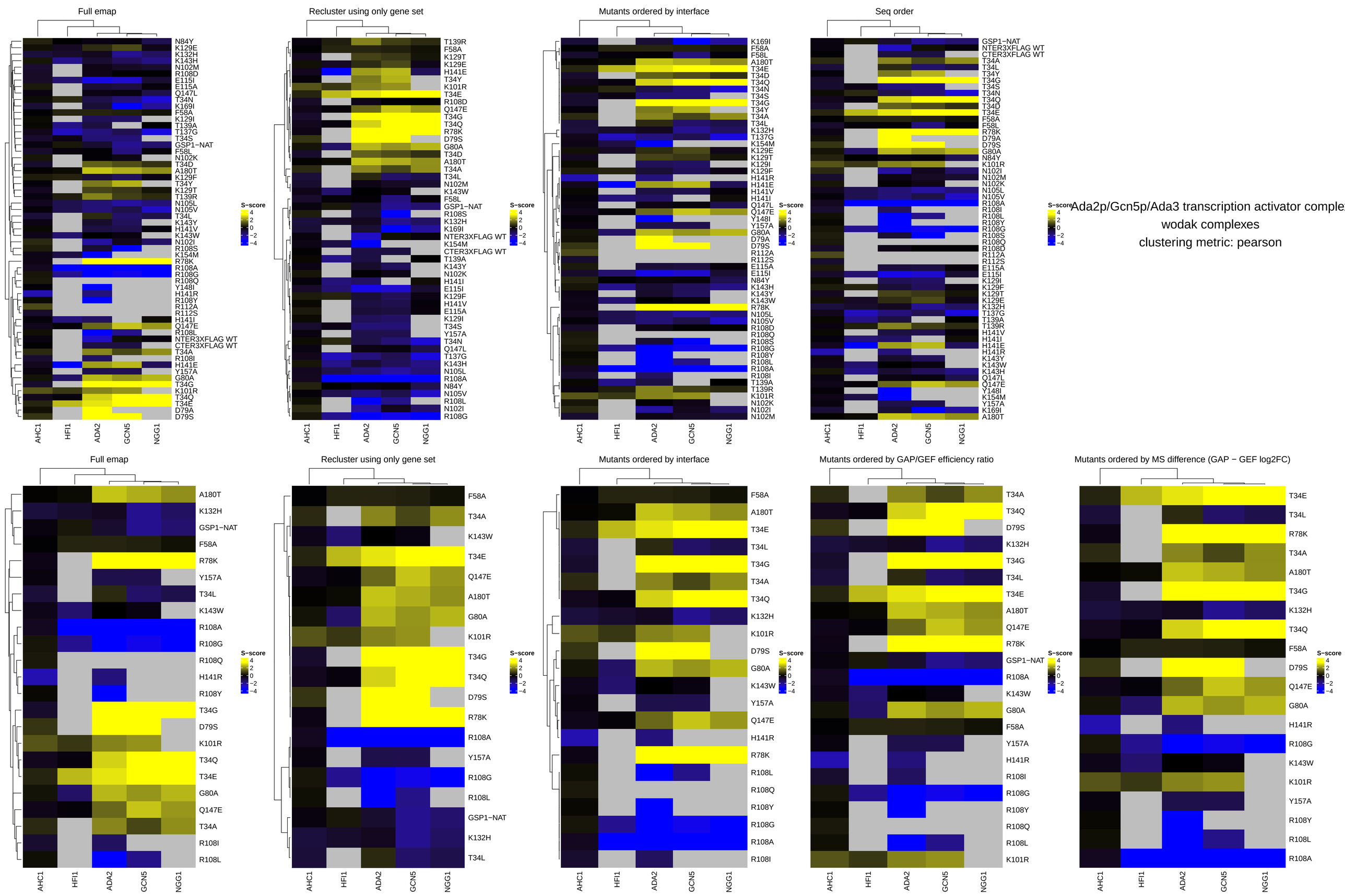

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
chromatin remodeling
tina hand−curated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

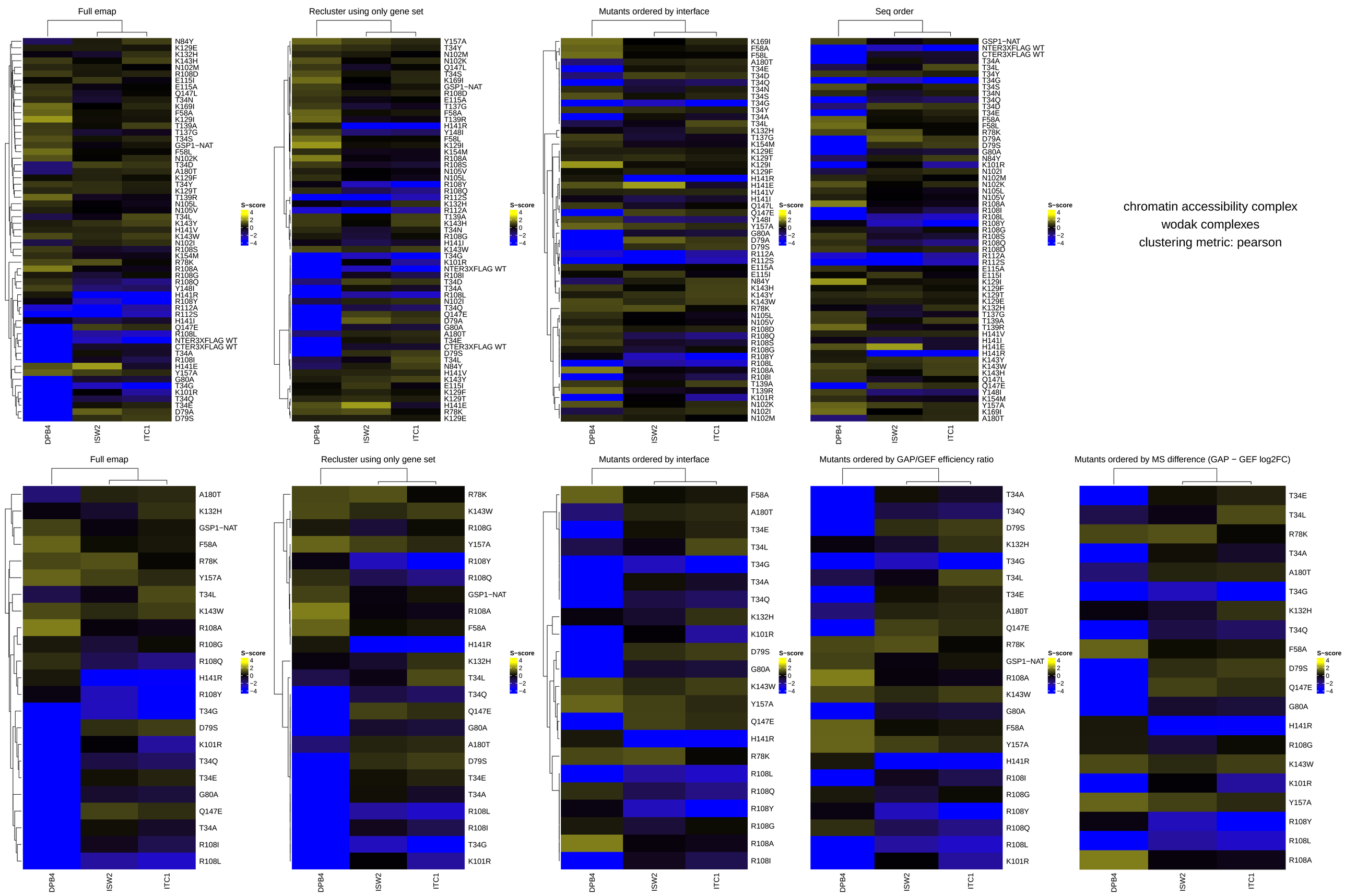

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
MLP2
SXM1
MOG1
NUP60
IWR1
NUP100
NUP42
POM152
ASM4
NUP53
NUP170
NUP133
NUP188
POM34
nucleocytoplasmic transport
tina hand−curated processes
clustering metric: pearson

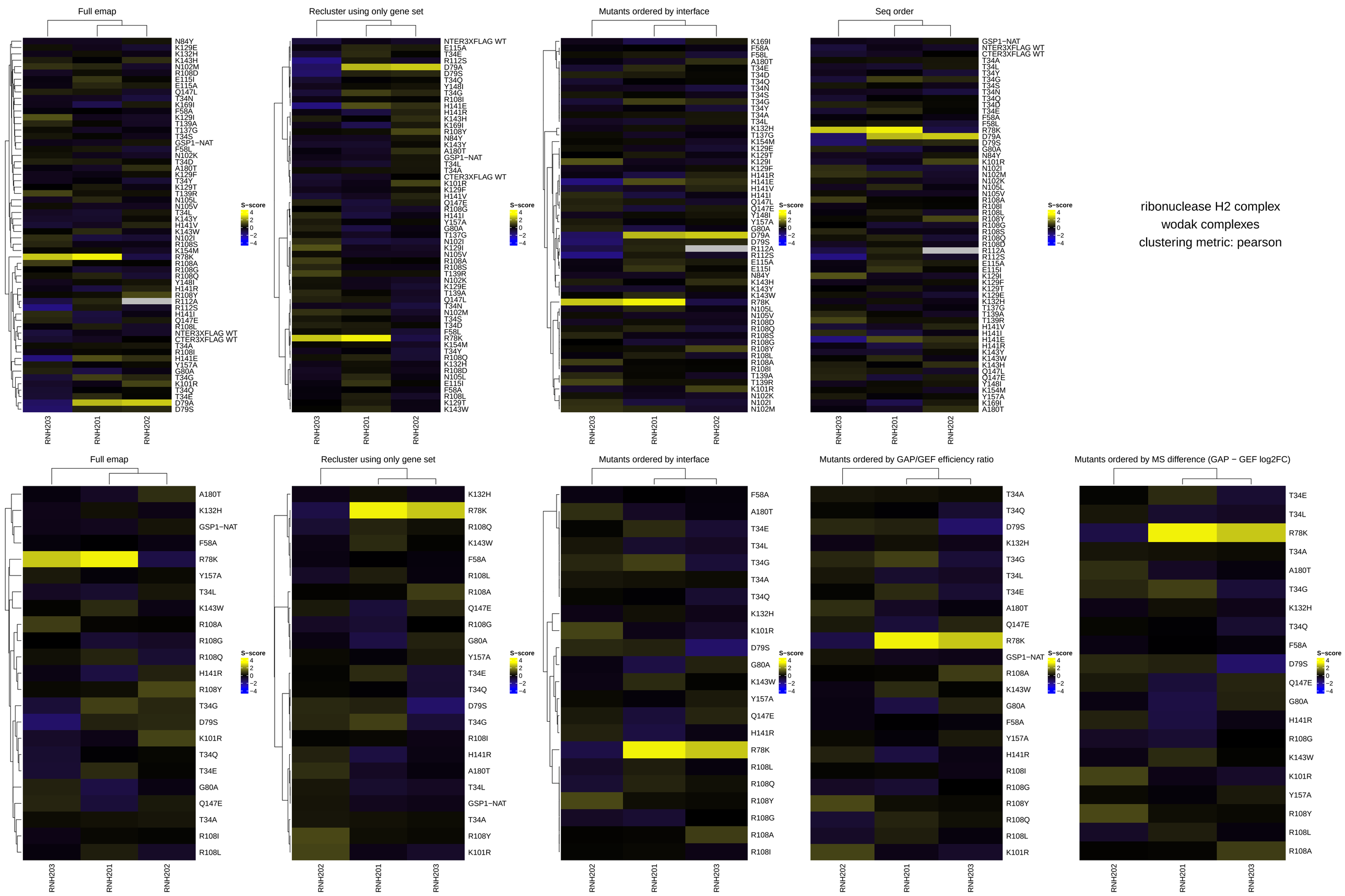

ESCRT−LEM protein nuclear envelope surveillance sy
tina hand−curated processes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4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

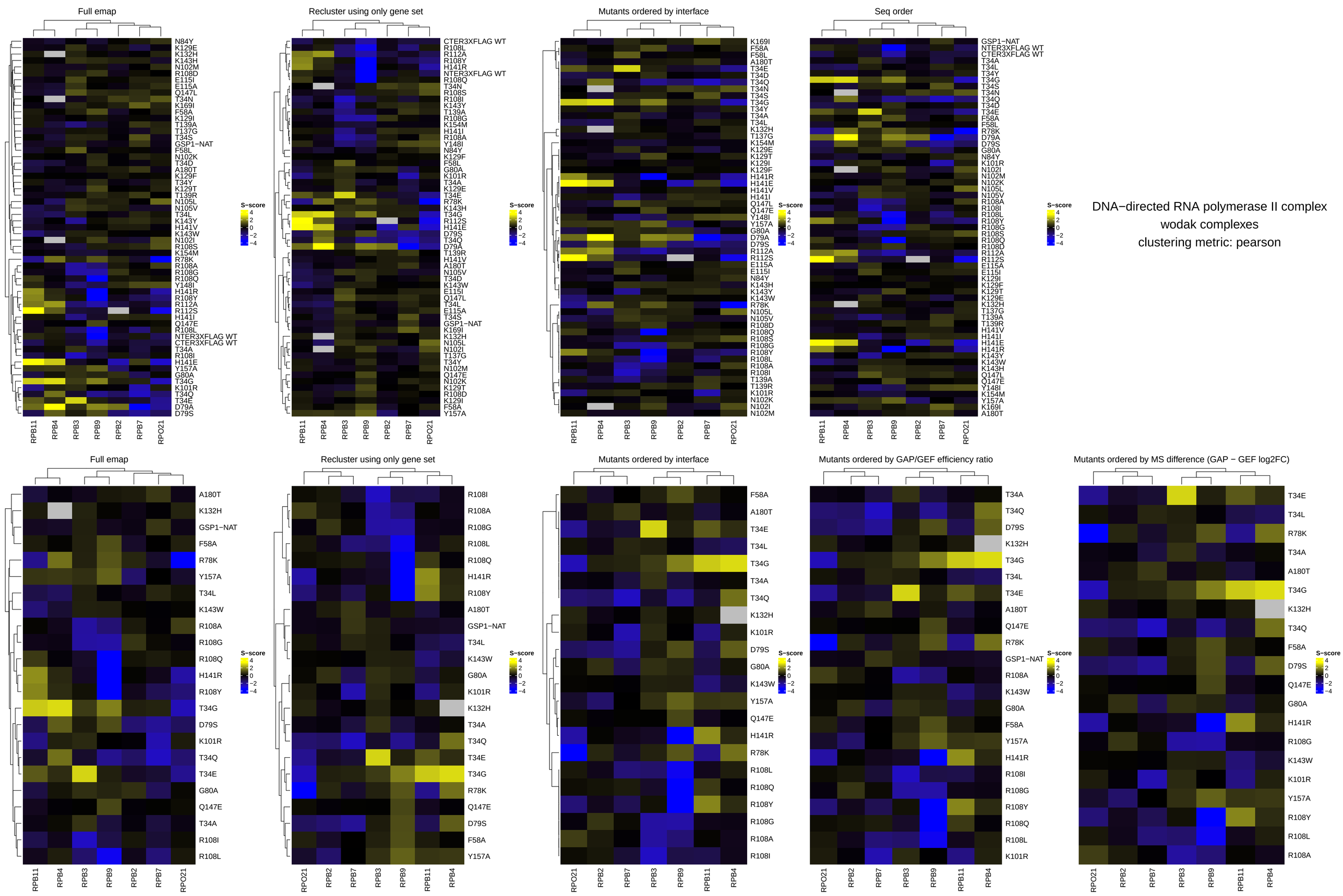


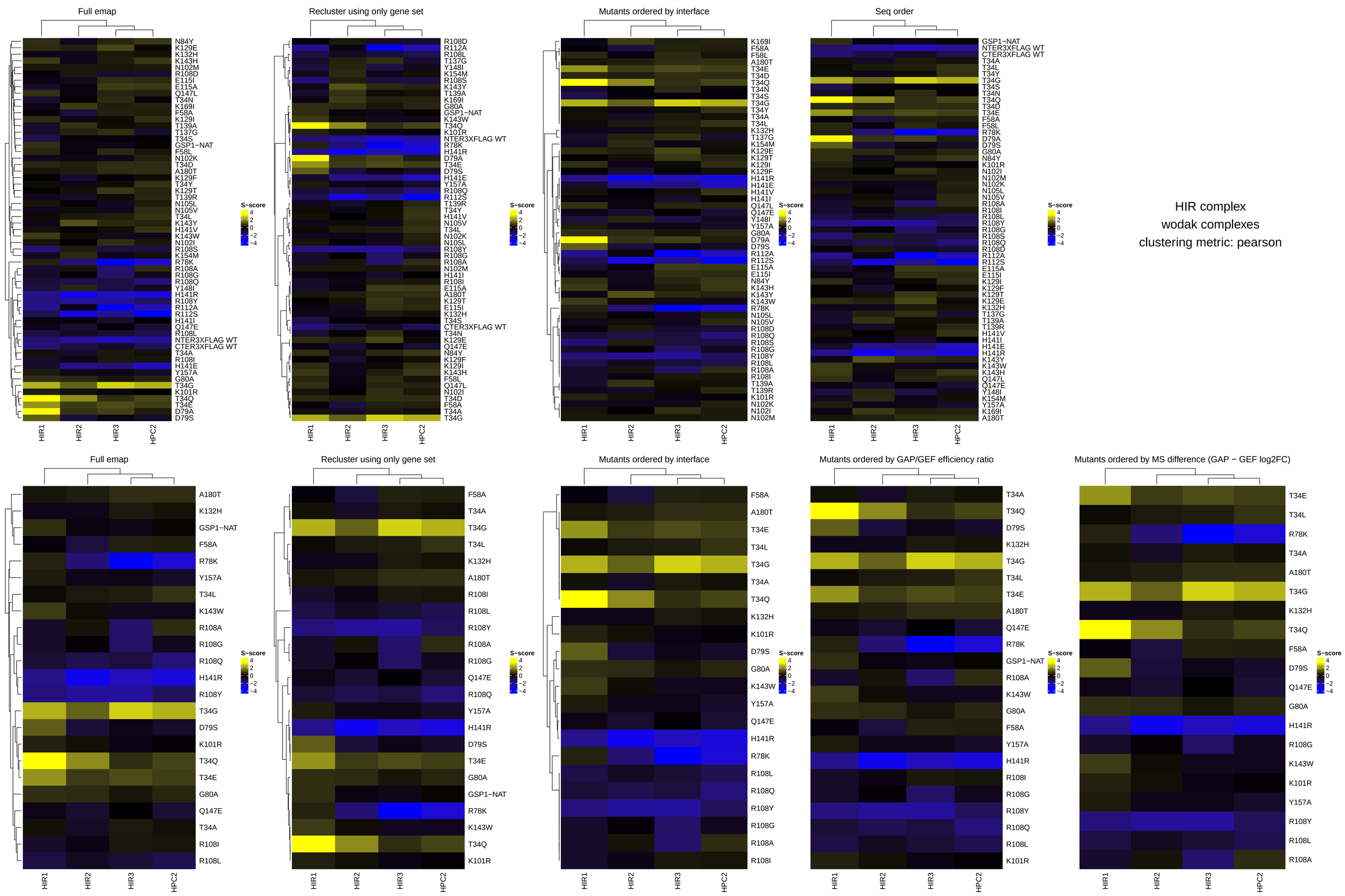
TRAPP complex
wodak complexes
clustering metric: pearson


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


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: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
RNH203
RNH201
RNH202
ribonuclease H2 complex
wodak complexes
clustering metric: pearson
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
RPB11
RPB4
RPB3
RPB9
RPB2
RPB7
RPO21
DNA−directed RNA polymerase II complex
wodak complexes
clustering metric: pearson


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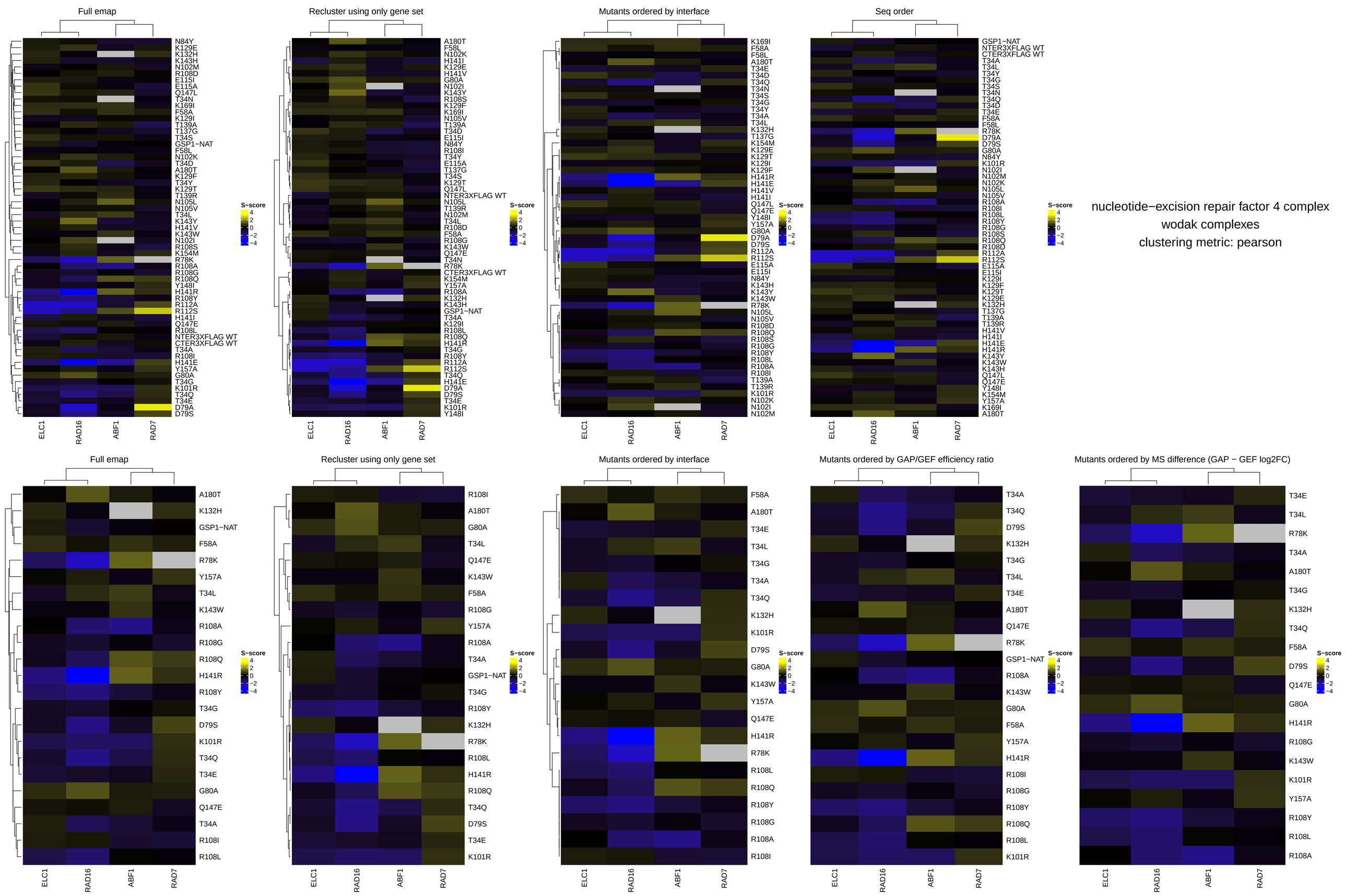
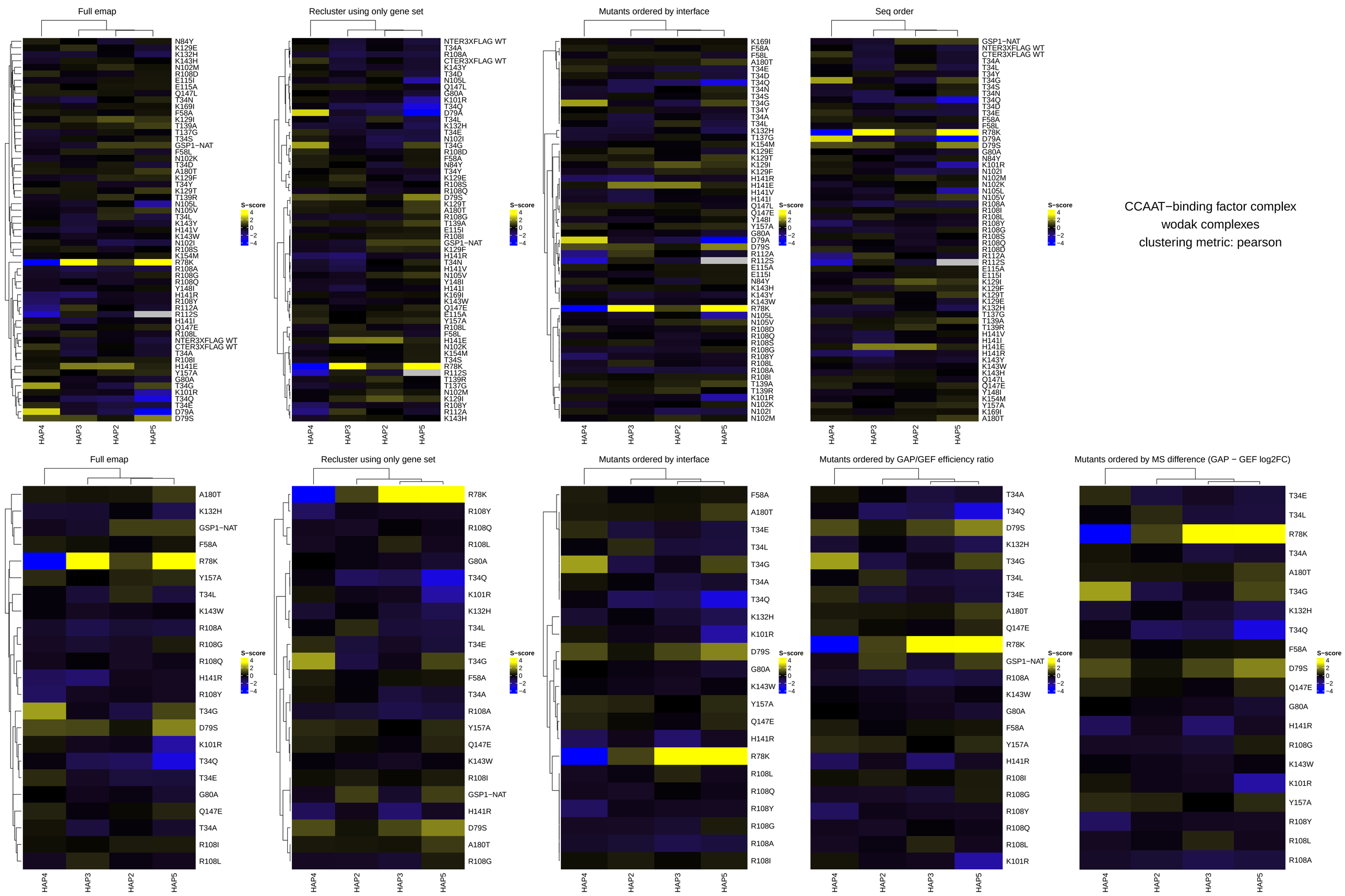
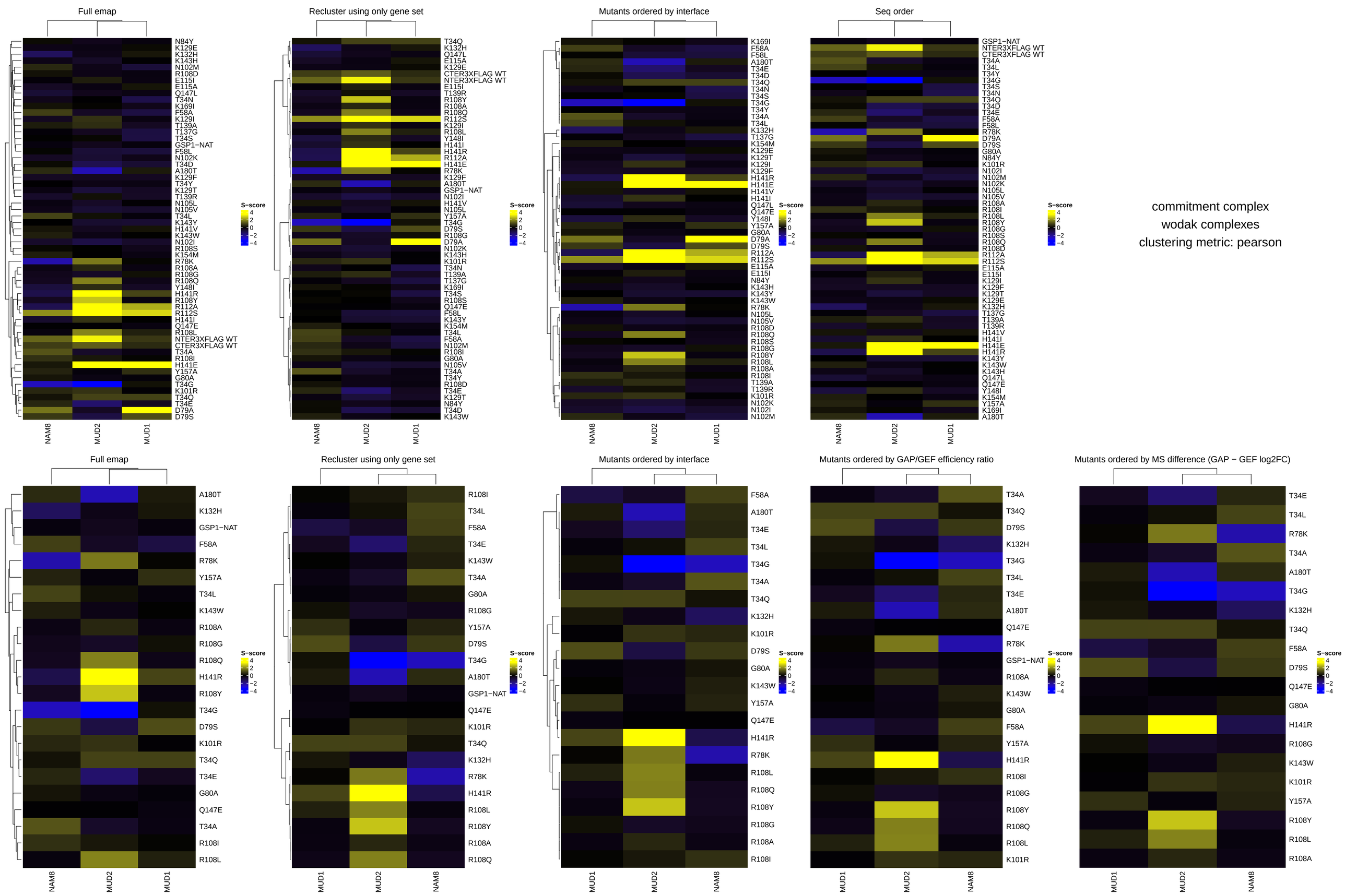
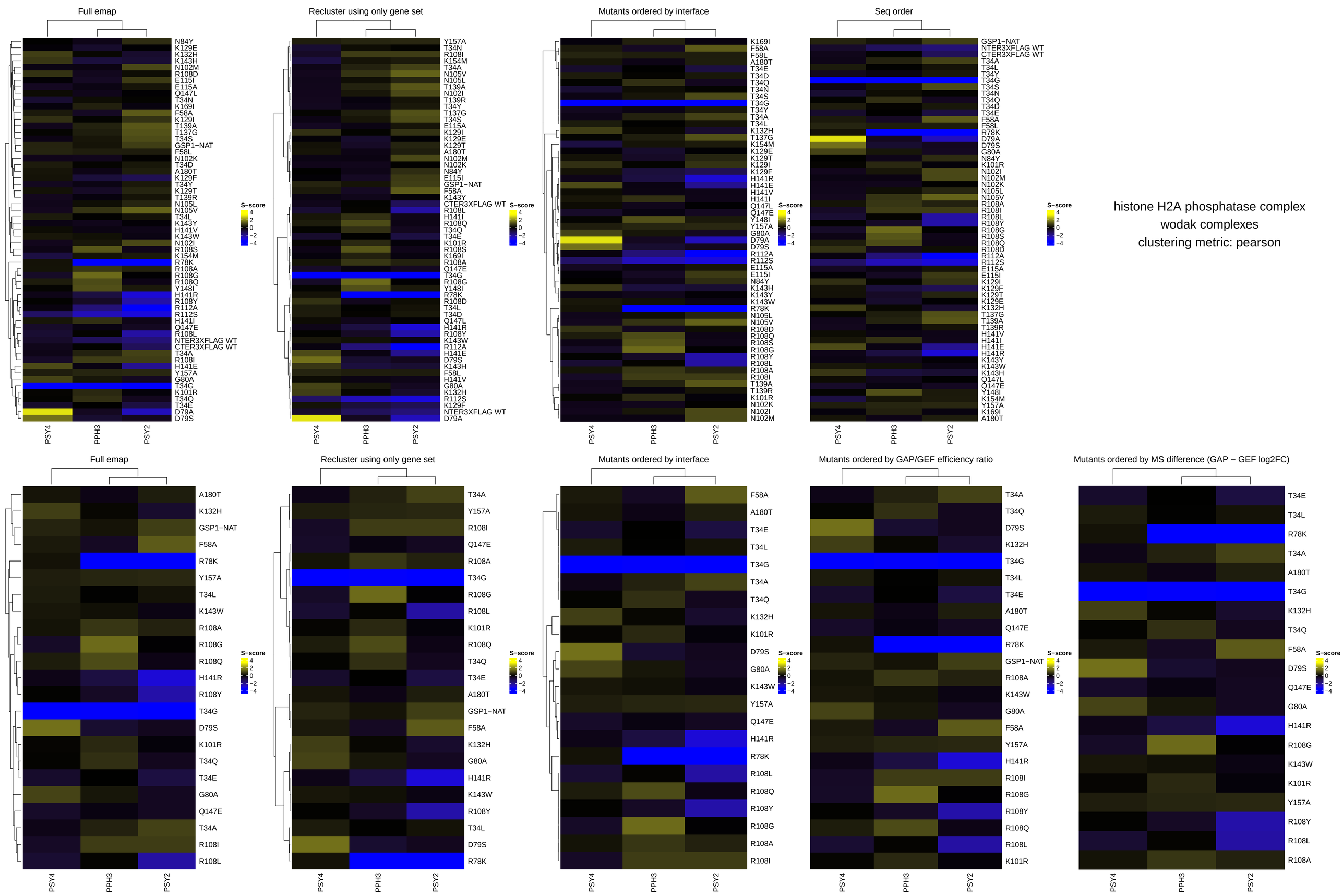
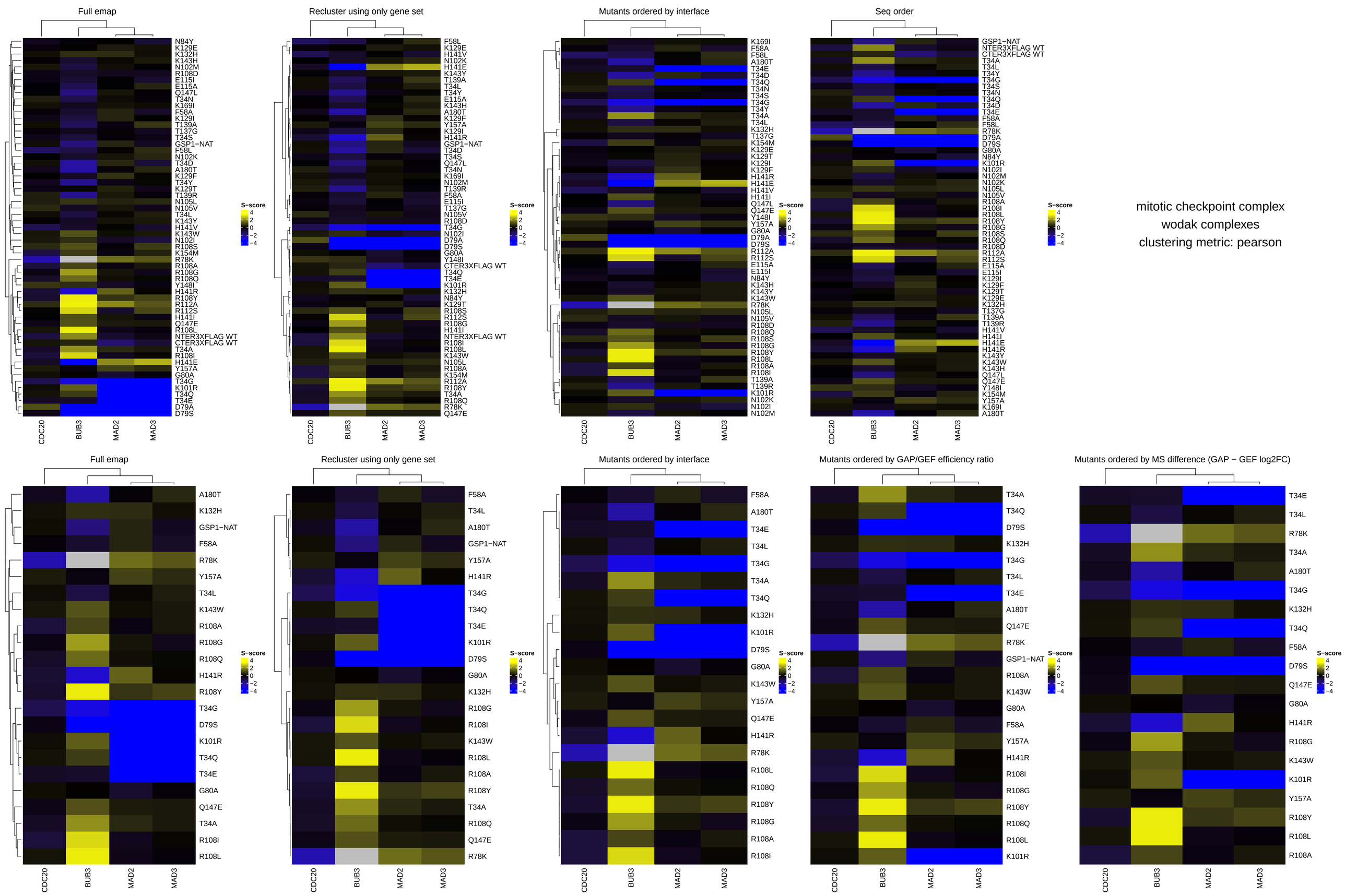
2
0
−2
−4
HIR1
HIR2
HIR3
HPC2
HIR complex
wodak complexes
clustering metric: pearson

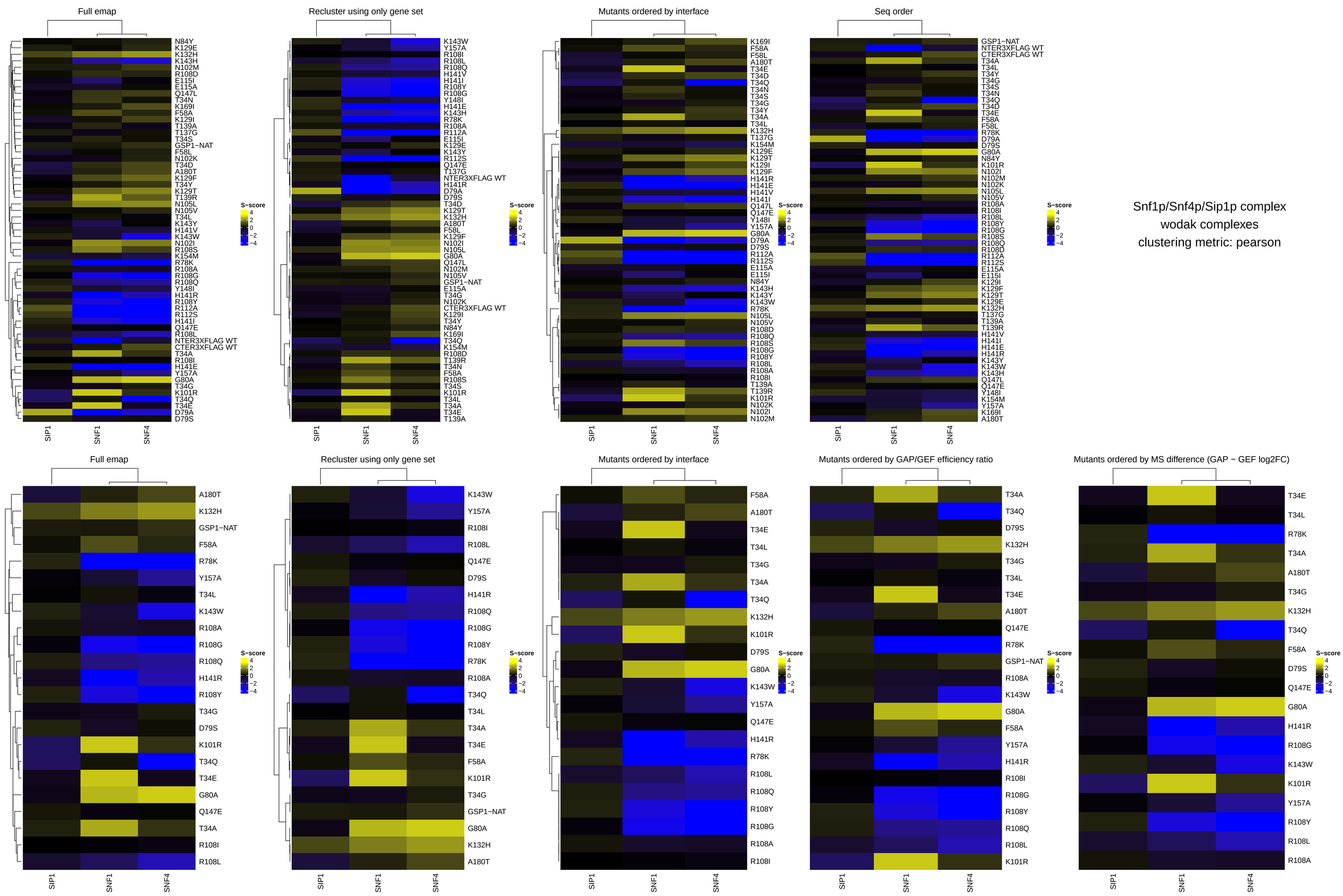

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ELC1
RAD16
ABF1
RAD7
nucleotide−excision repair factor 4 complex
wodak complexes
clustering metric: pearson

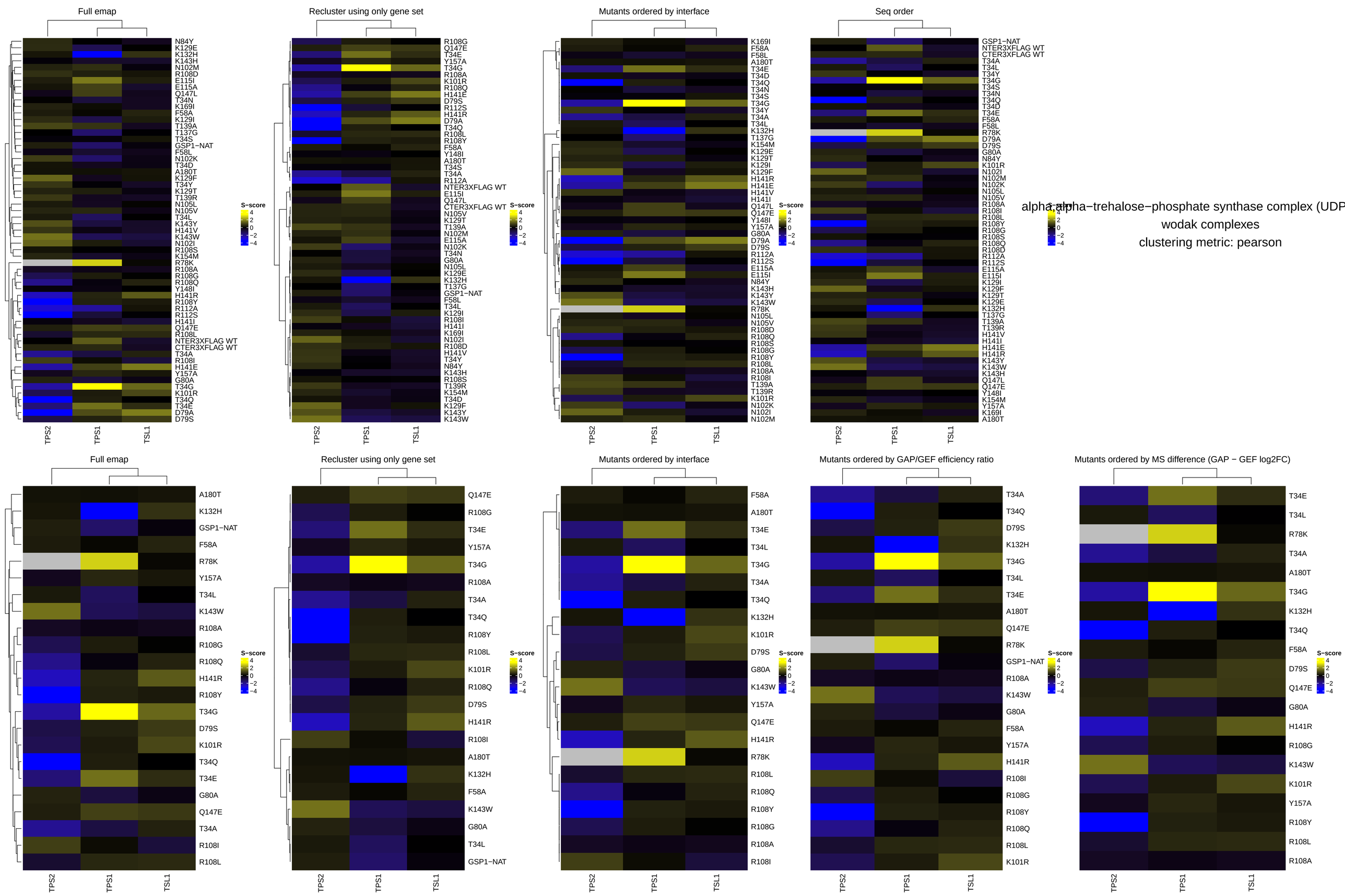

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HAP4
HAP3
HAP2
HAP5
CCAAT−binding factor complex
wodak complexes
clustering metric: pearson

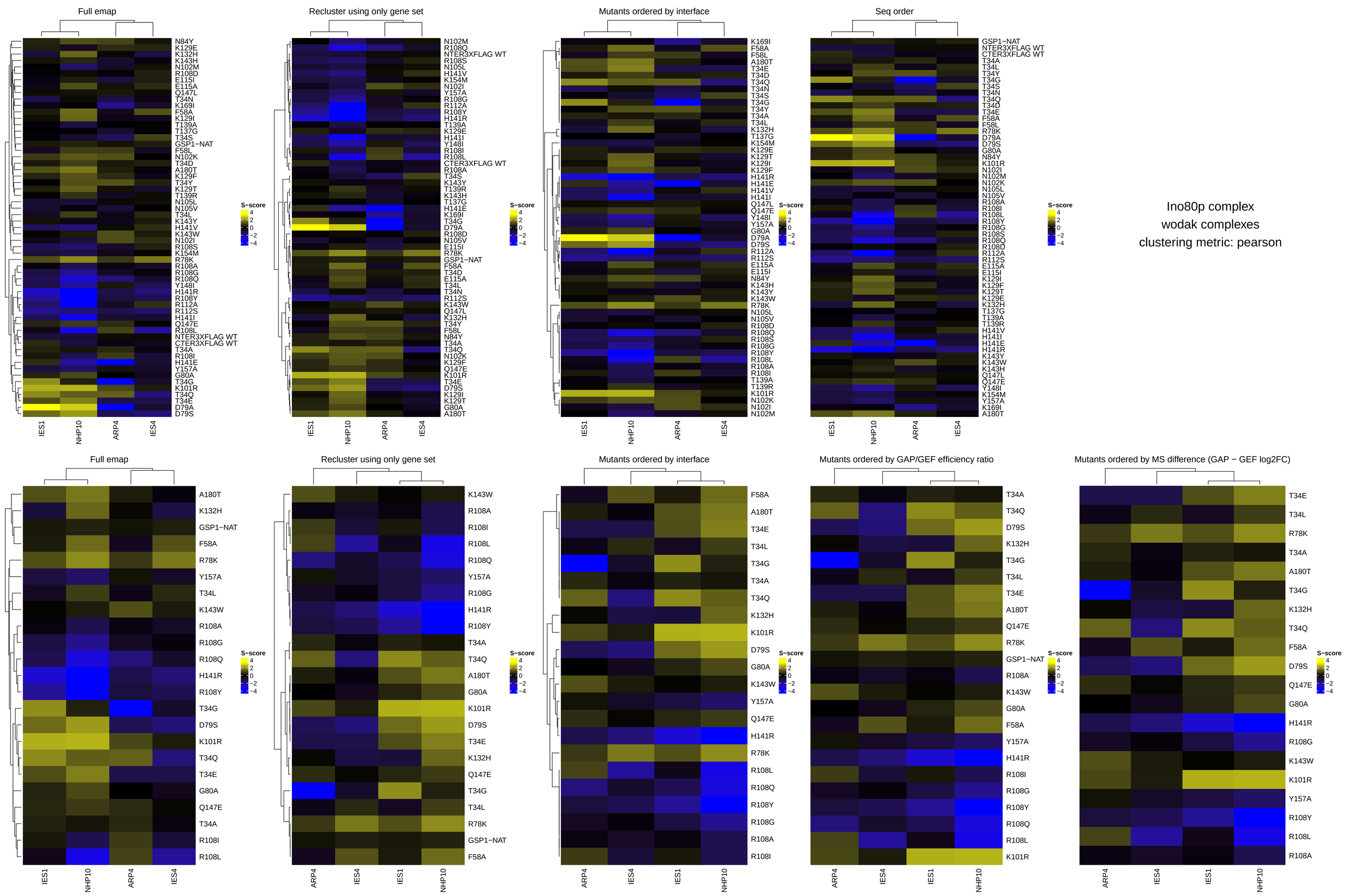

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
NAM8
MUD2
MUD1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
commitment complex
wodak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

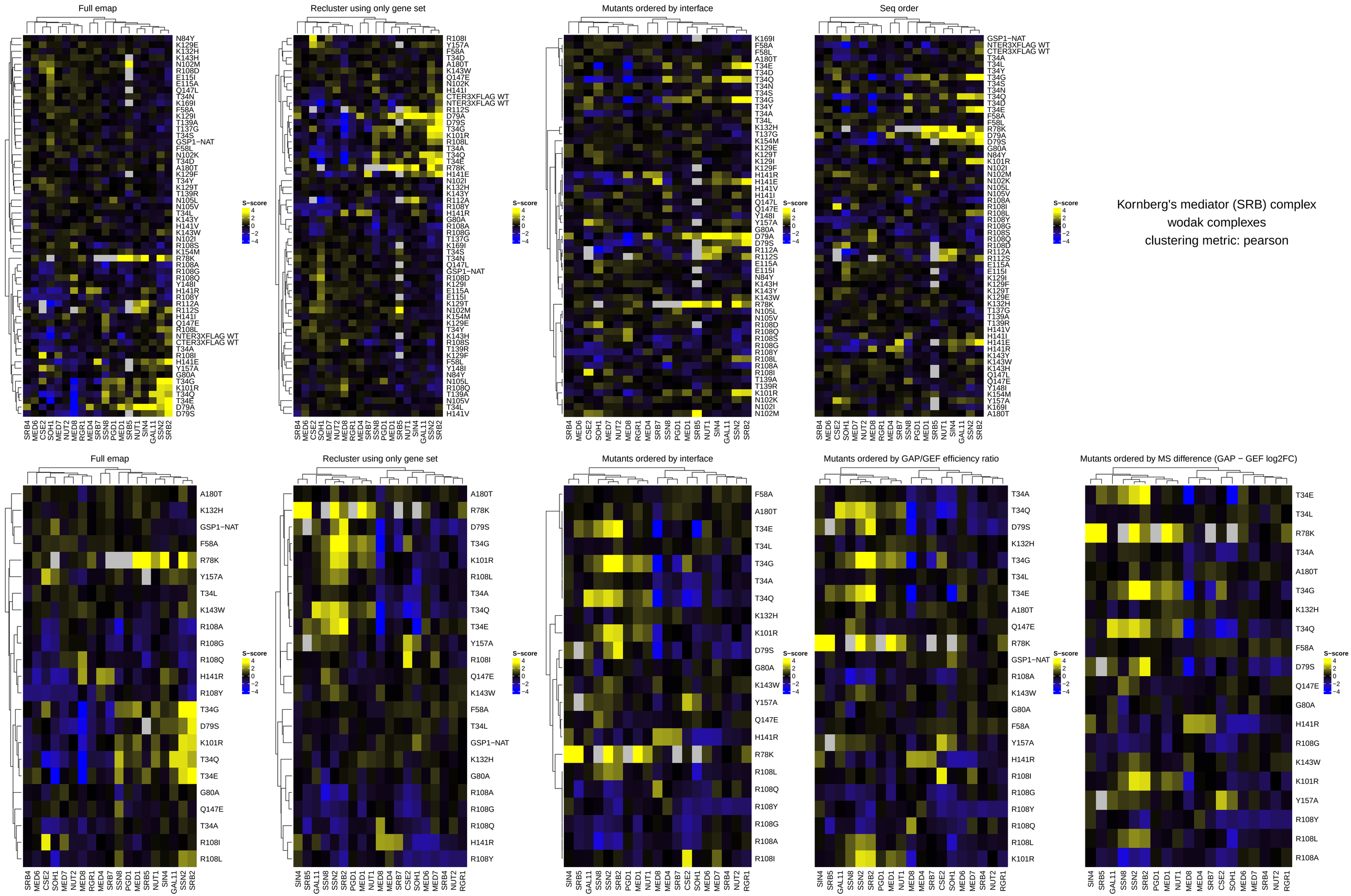

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PSY4
PPH3
PSY2
histone H2A phosphatase complex
wodak complexes
clustering metric: pearson

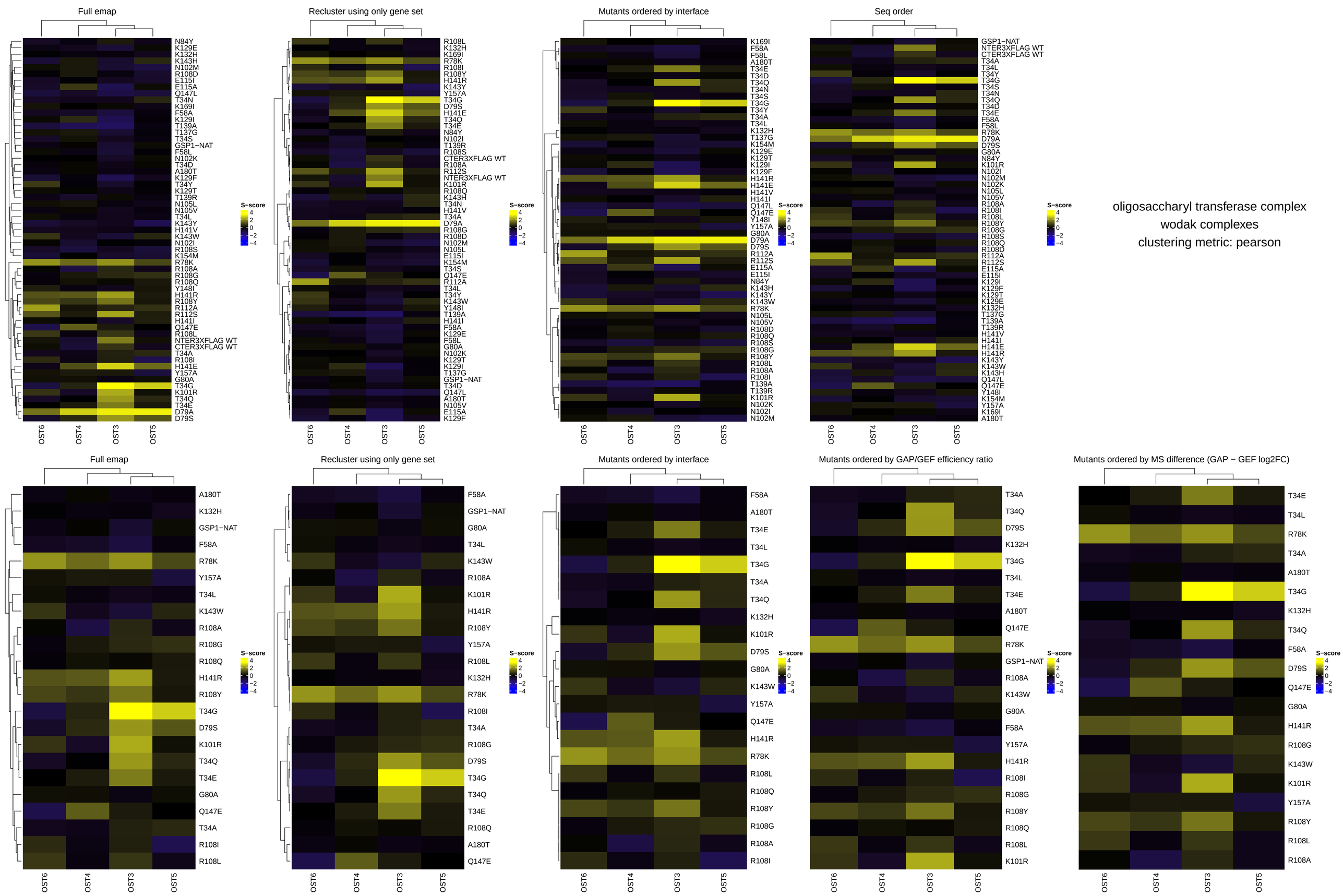

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CDC20
BUB3
MAD2
MAD3
mitotic checkpoint complex
wodak complexes
clustering metric: pearson

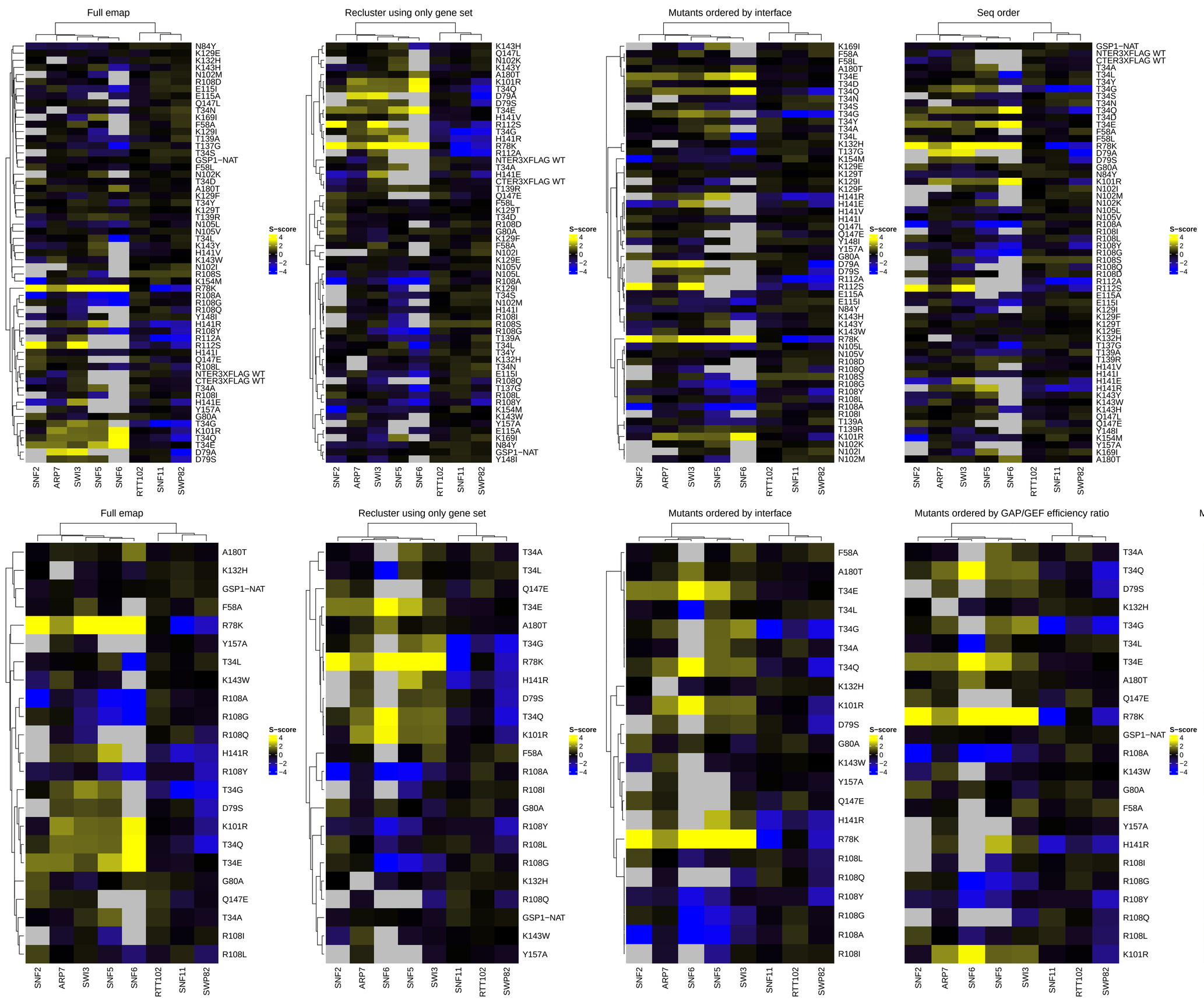

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SIP1
SNF1
SNF4
Snf1p/Snf4p/Sip1p complex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


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
alpha,alpha−trehalose−phosphate synthase complex (UDP
wodak complexes
clustering metric: pearson
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)

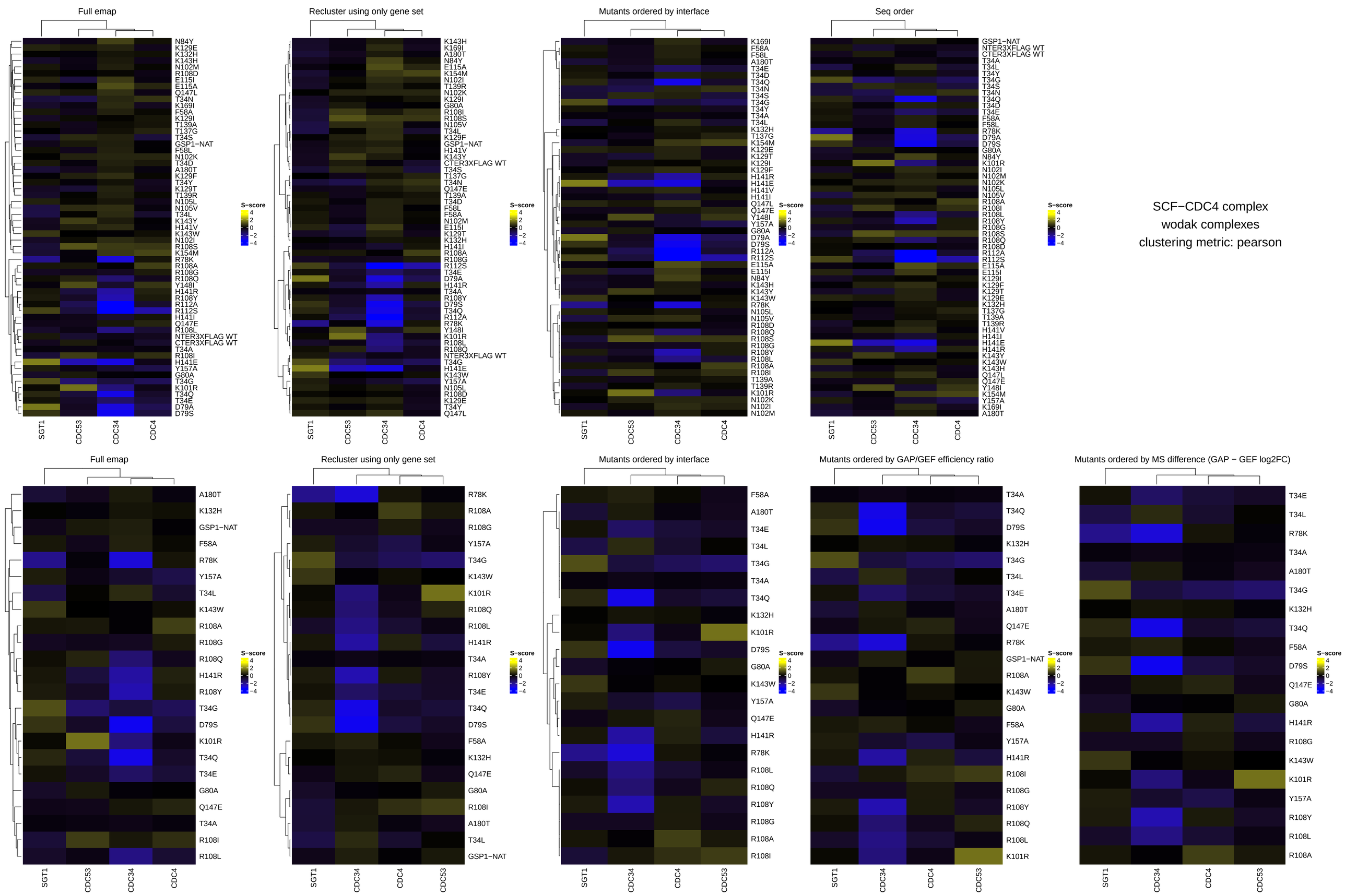

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
IES1
NHP10
ARP4
IES4
Ino80p complex
wodak complexes
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

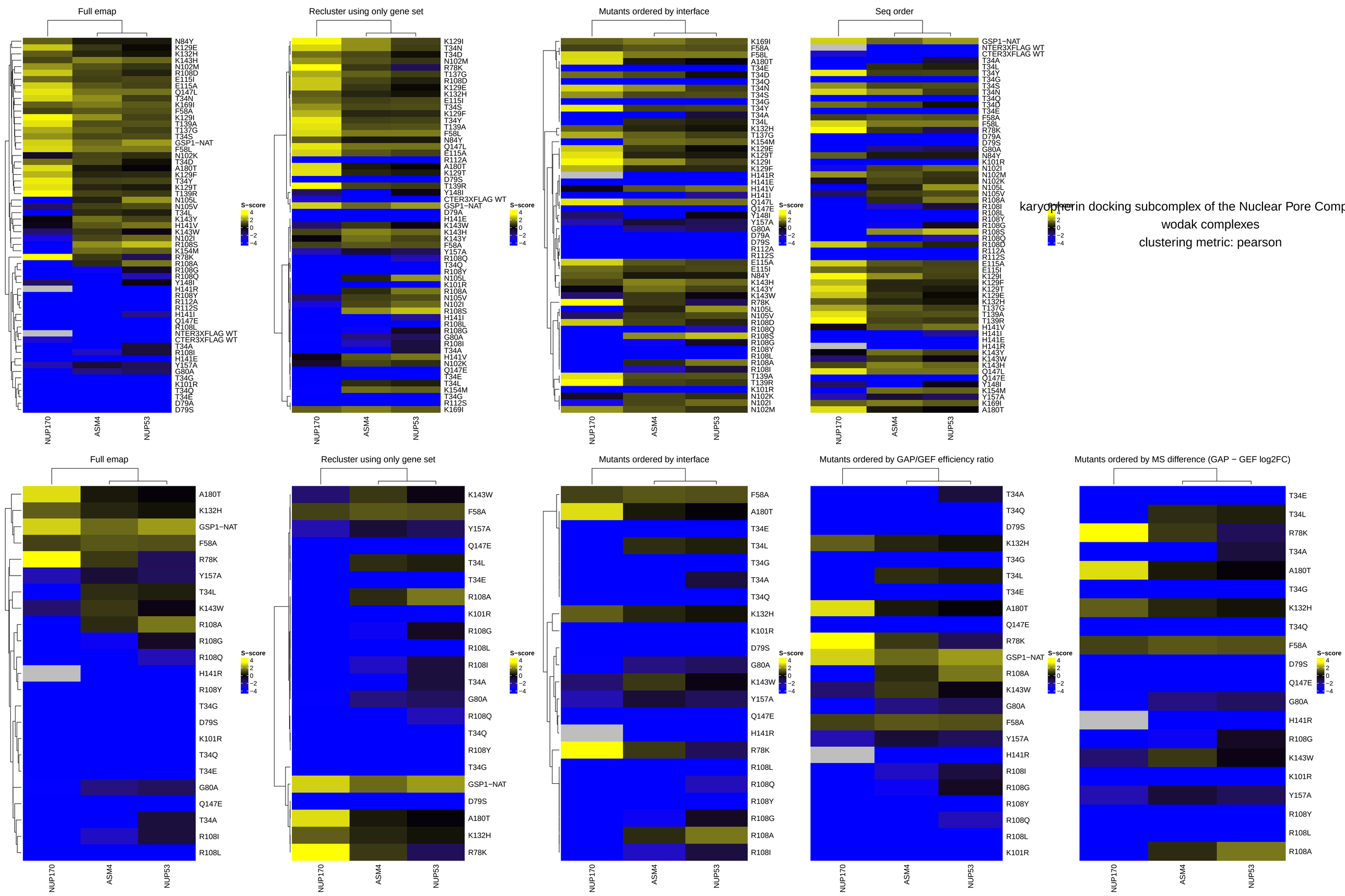

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SRB4 MED6 CSE2 SOH1 MED7 NUT2 MED8 RGR1 MED4 SRB7 SSN8 PGD1 MED1 SRB5 NUT1 SIN4 GAL11 SSN2 SRB2
Kornberg's mediator (SRB) complex
wodak complexes
clustering metric: pearson

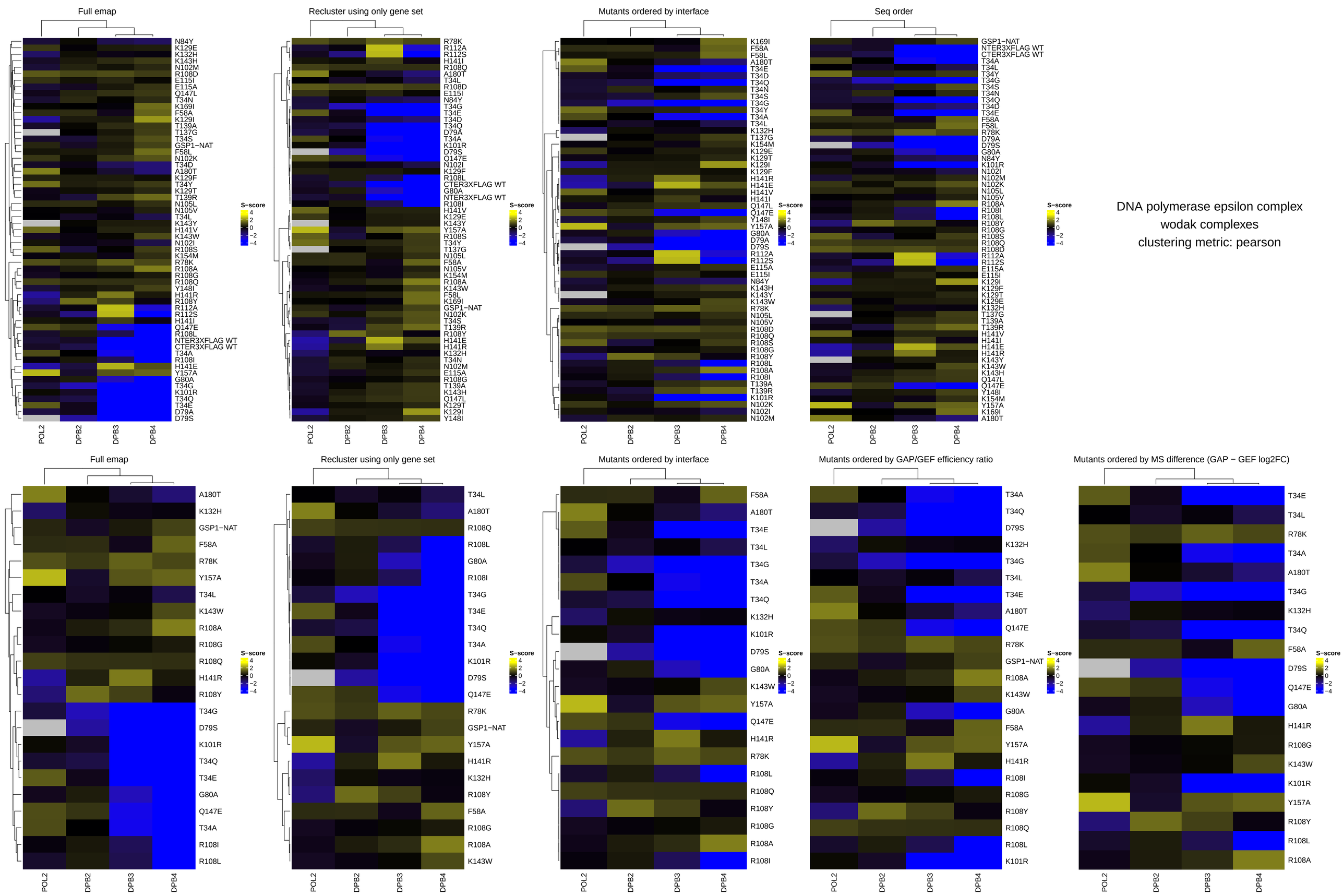

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
OST6
OST4
OST3
OST5
oligosaccharyl transferase complex
wodak complexes
clustering metric: pearson

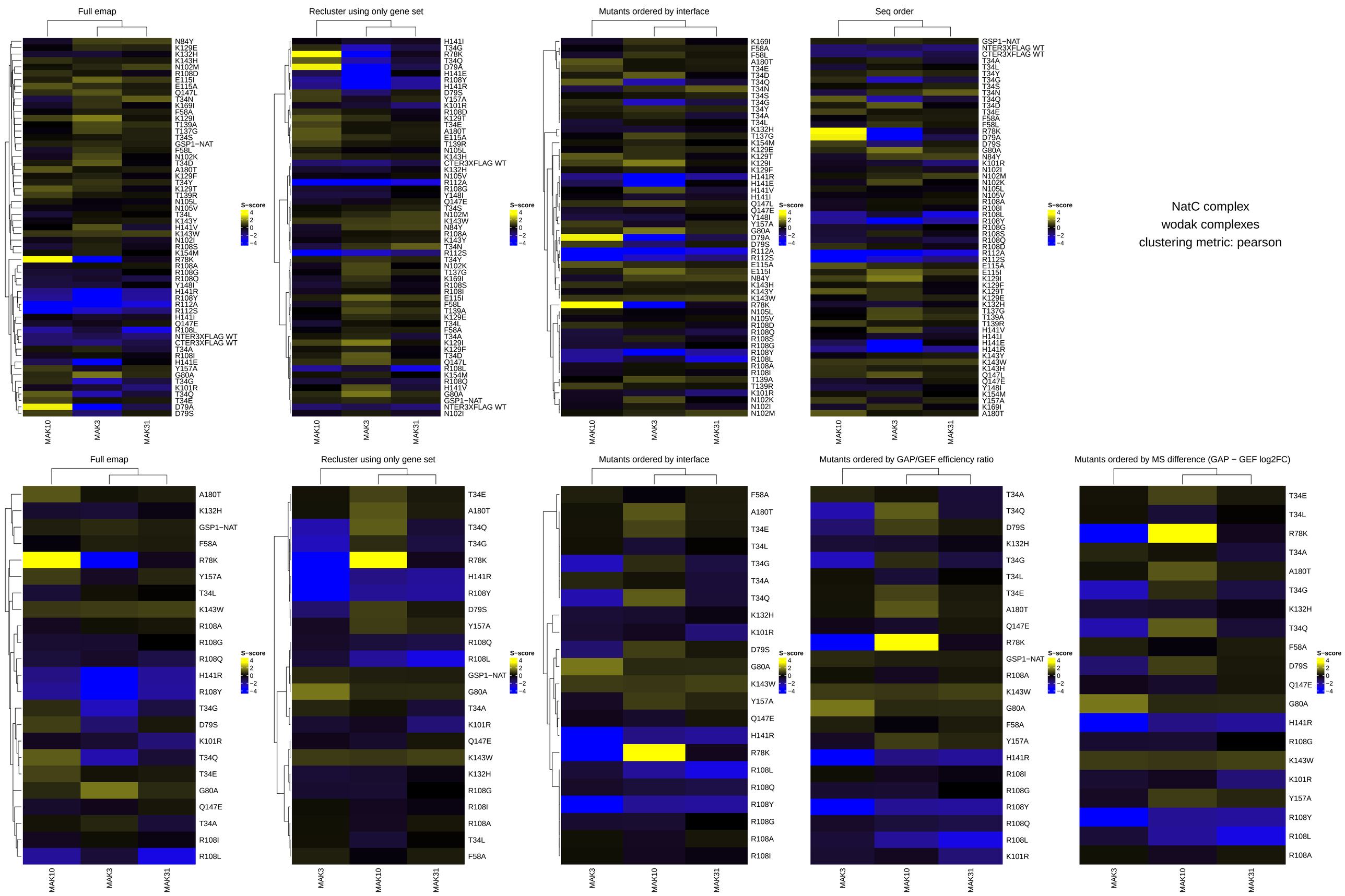


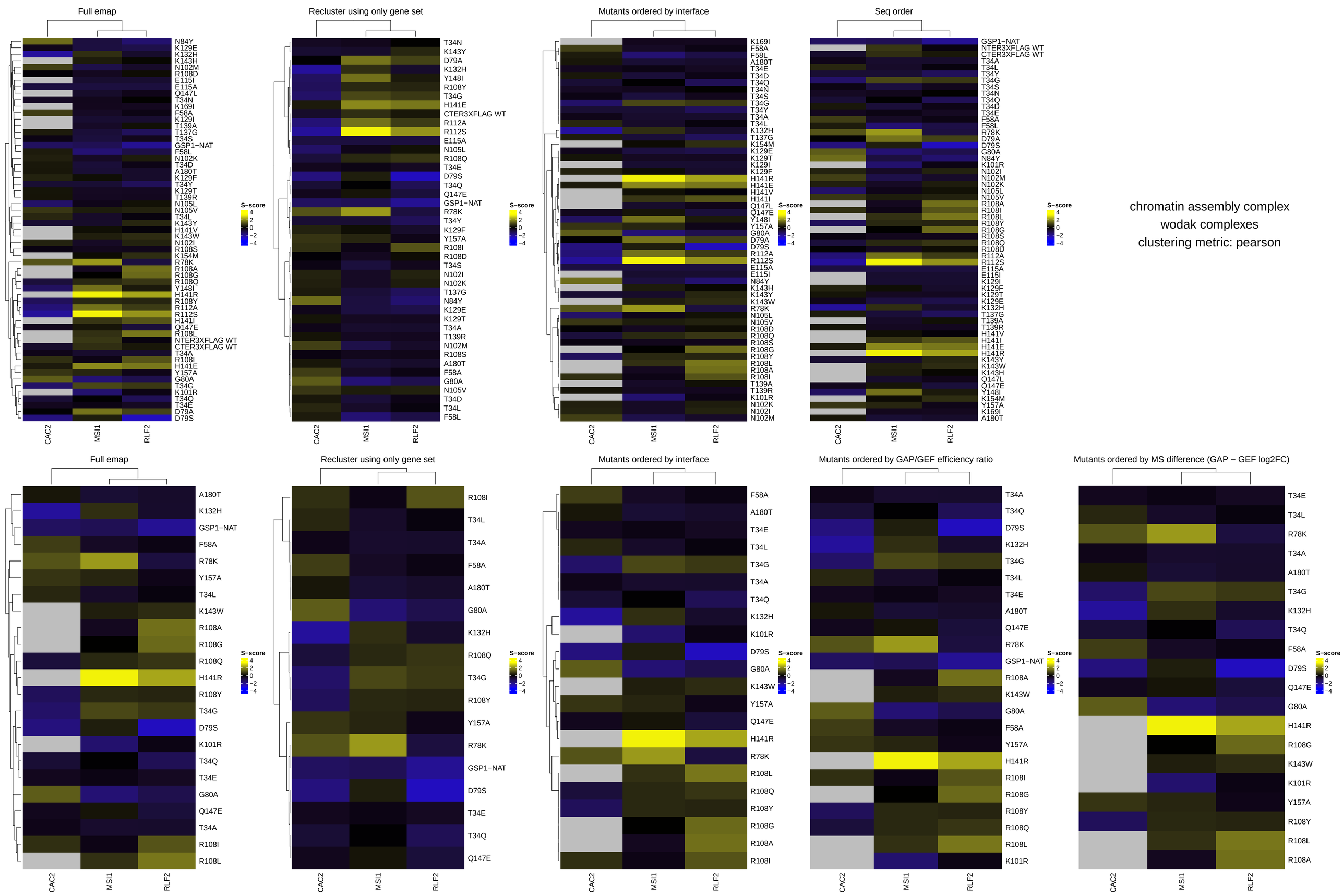
SWI/SNF complex
wodak complexes
clustering metric: pearson

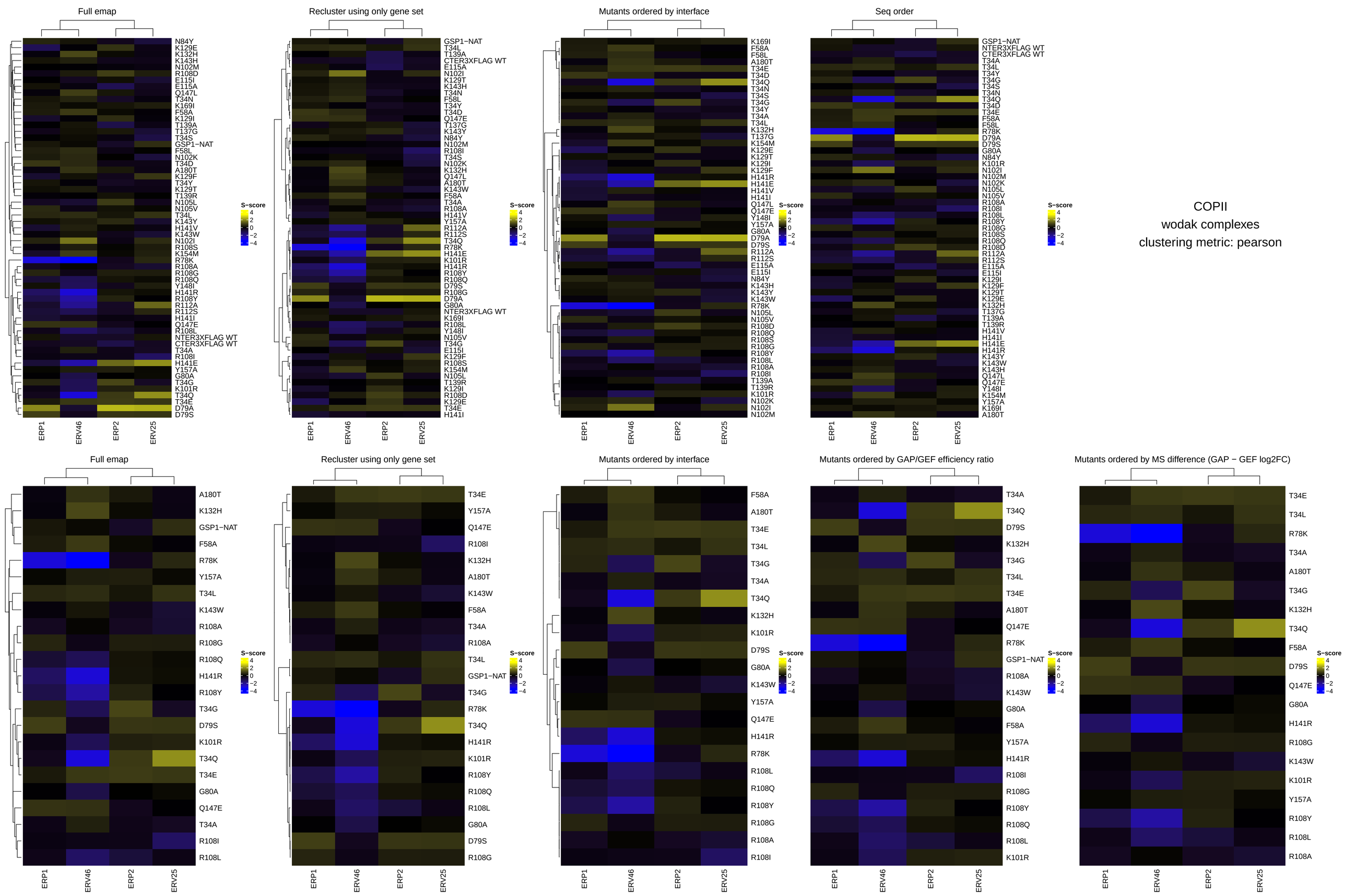

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SGT1
CDC53
CDC34
CDC4
SCF−CDC4 complex
wodak complexes
clustering metric: pearson

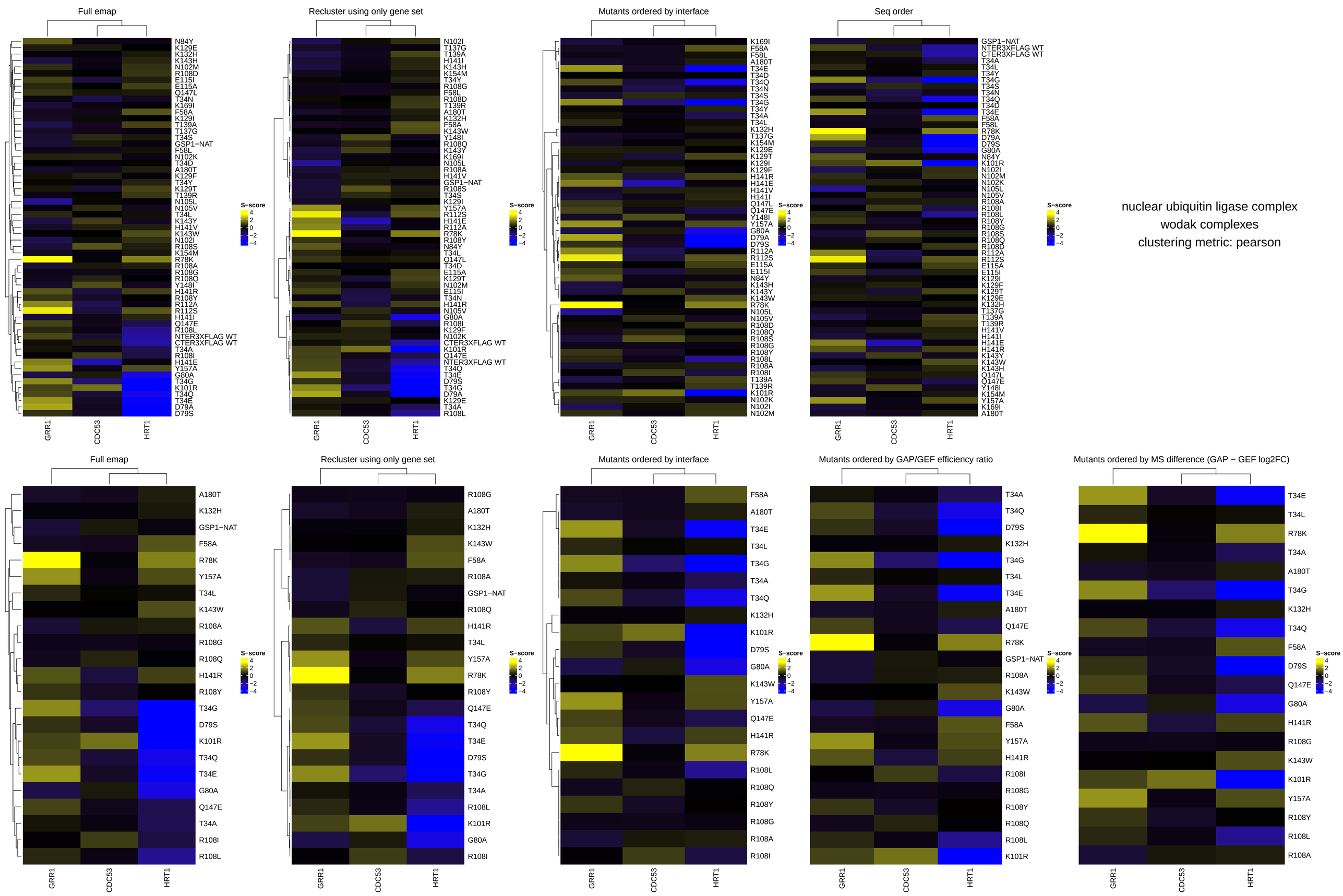

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
NUP170
ASM4
NUP53
karyopherin docking subcomplex of the Nuclear Pore Comp
wodak complexes
clustering metric: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

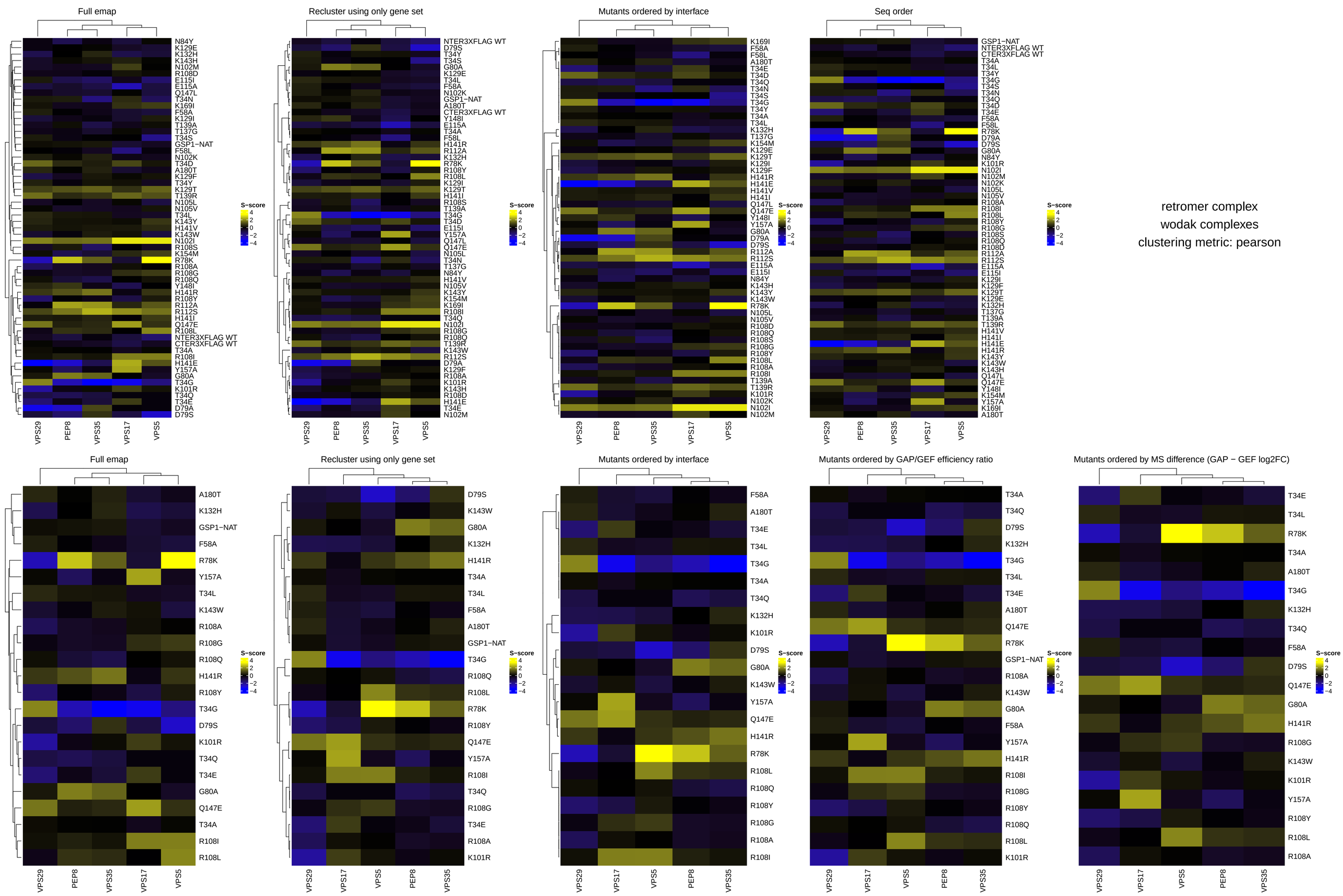

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
POL2
DPB2
DPB3
DPB4
DNA polymerase epsilon complex
wodak complexes
clustering metric: pearson

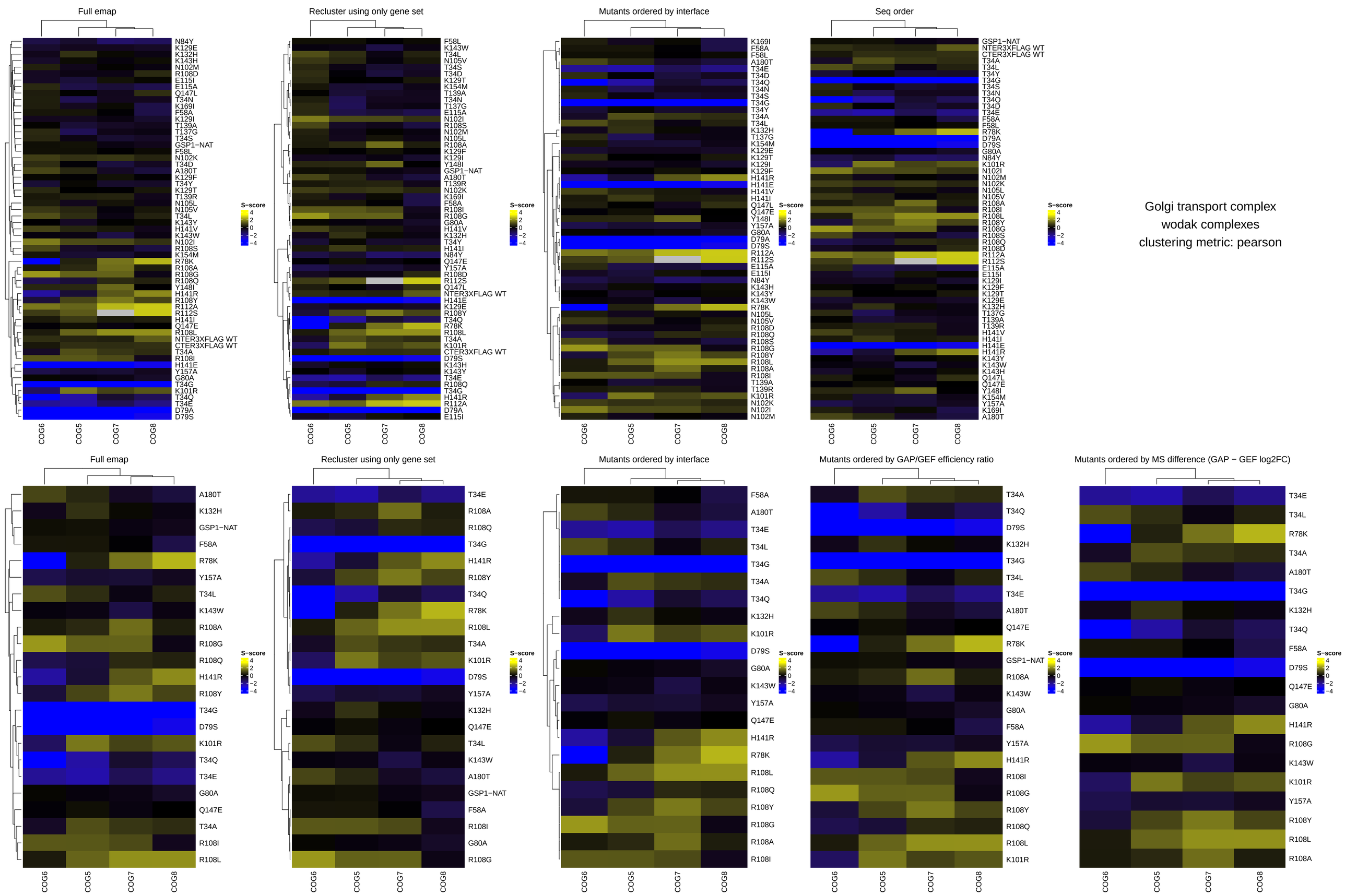

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
MAK10
MAK3
MAK31
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
NatC complex
wodak complexes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


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CAC2
MSI1
RLF2
N84Y K129E K132H K143H N102M R108D E115I E115A Q147L T34N K169I F58A K129I T139A T137G T34S GSP1−NAT F58L N102K T34D A180T K129F T34Y K129T T139R N105L N105V T34L K143Y H141V K143W N102I R108S K154M R78K R108A R108G R108Q Y148I H141R R108Y R112A R112S H141I Q147E R108L NTER3XFLAG WT CTER3XFLAG WT T34A R108I H141E Y157A G80A T34G K101R T34Q T34E D79A D79S
T34N K143Y D79A K132H Y148I R108Y T34G H141E CTER3XFLAG WT R112A R112S E115A N105L R108Q T34E D79S T34Q Q147E GSP1−NAT R78K T34Y K129F Y157A R108I R108D T34S N102I N102K T137G N84Y K129E K129T T34A T139R N102M R108S A180T F58A G80A N105V T34D T34L F58L
K169I F58A F58L A180T T34E T34D T34Q T34N T34S T34G T34Y T34A T34L K132H T137G K154M K129E K129T K129I K129F H141R H141E H141V H141I Q147L Q147E Y148I Y157A G80A D79A D79S R112A R112S E115A E115I N84Y K143H K143Y K143W R78K N105L N105V R108D R108Q R108S R108G R108Y R108L R108A R108I T139A T139R K101R N102K N102I N102M
GSP1−NAT NTER3XFLAG WT CTER3XFLAG WT T34A T34L T34Y T34G T34S T34N T34Q T34D T34E F58A F58L R78K D79A D79S G80A N84Y K101R N102I N102M N102K N105L N105V R108A R108I R108L R108Y R108G R108S R108Q R108D R112A R112S E115A E115I K129I K129F K129T K129E K132H T137G T139A T139R H141V H141I H141E H141R K143Y K143W K143H Q147L Q147E Y148I K154M Y157A K169I A180T
A180T K132H GSP1−NAT F58A R78K Y157A T34L K143W R108A R108G R108Q H141R R108Y T34G D79S K101R T34Q T34E G80A Q147E T34A R108I R108L
R108I T34L T34A F58A A180T G80A K132H R108Q T34G R108Y Y157A R78K GSP1−NAT D79S T34E T34Q Q147E
F58A A180T T34E T34L T34G T34A T34Q K132H K101R D79S G80A K143W Y157A Q147E H141R R78K R108L R108Q R108Y R108G R108A R108I
T34A T34Q D79S K132H T34G T34L T34E A180T Q147E R78K GSP1−NAT R108A K143W G80A F58A Y157A H141R R108I R108G R108Y R108Q R108L K101R
T34E T34L R78K T34A A180T T34G K132H T34Q F58A D79S Q147E G80A H141R R108G K143W K101R Y157A R108Y R108L R108A
chromatin assembly complex
wodak complexes
clustering metric: pearson

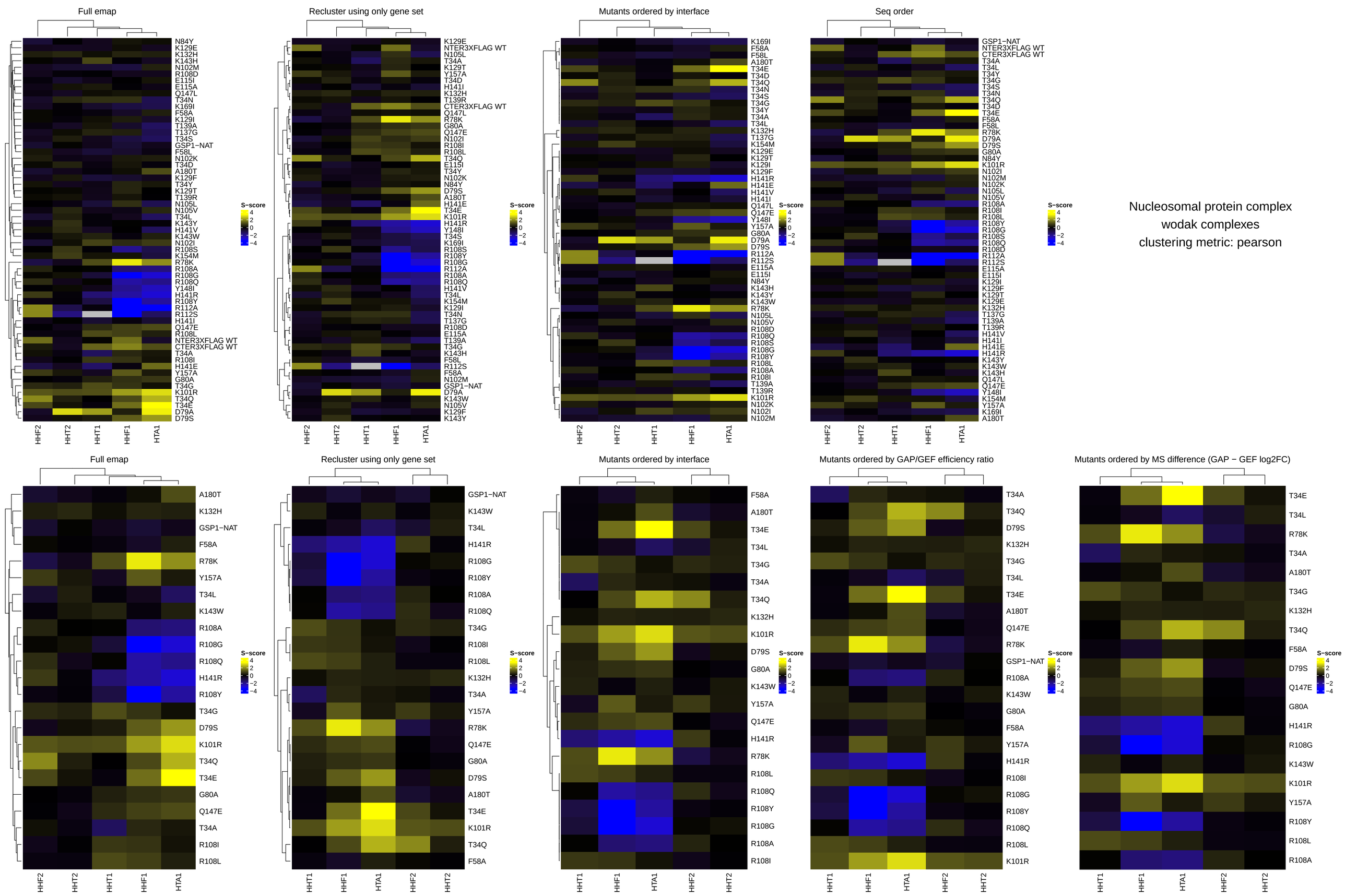

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ERP1
ERV46
ERP2
ERV25
COPII
wodak complexes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

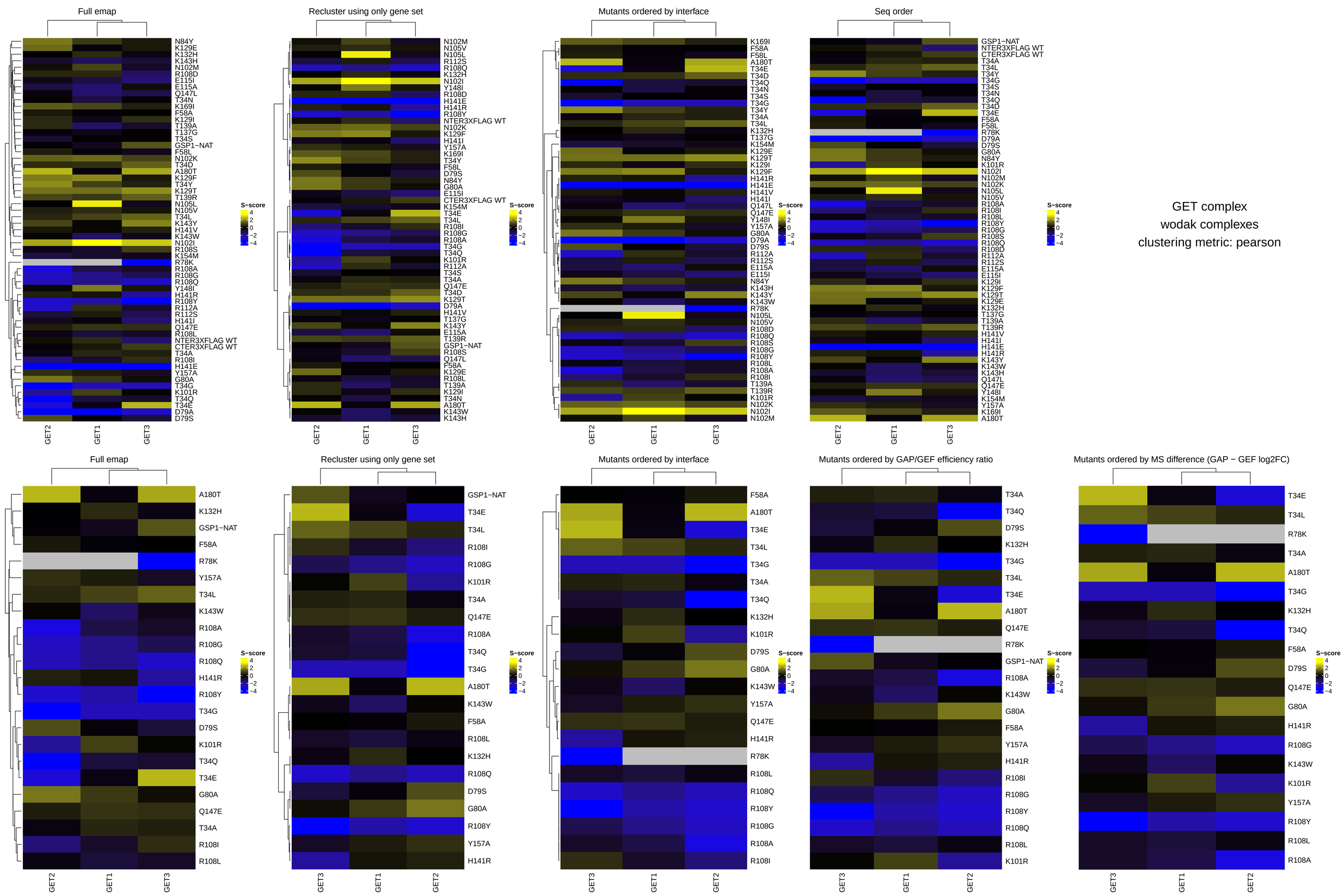

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
GRR1
CDC53
HRT1
nuclear ubiquitin ligase complex
wodak complexes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

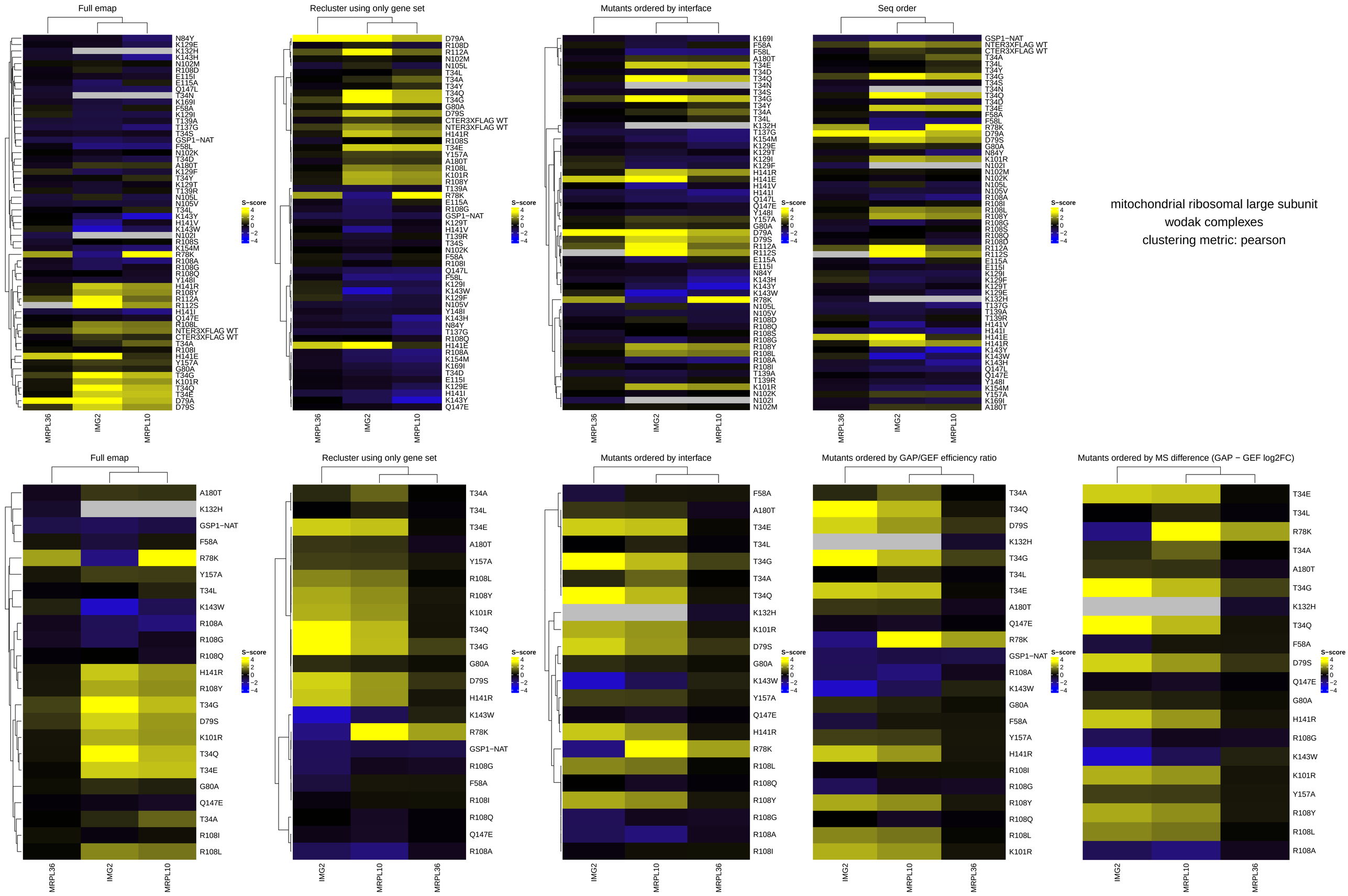

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
VPS29
PEP8
VPS35
VPS17
VPS5
retromer complex
wodak complexes
clustering metric: pearson
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

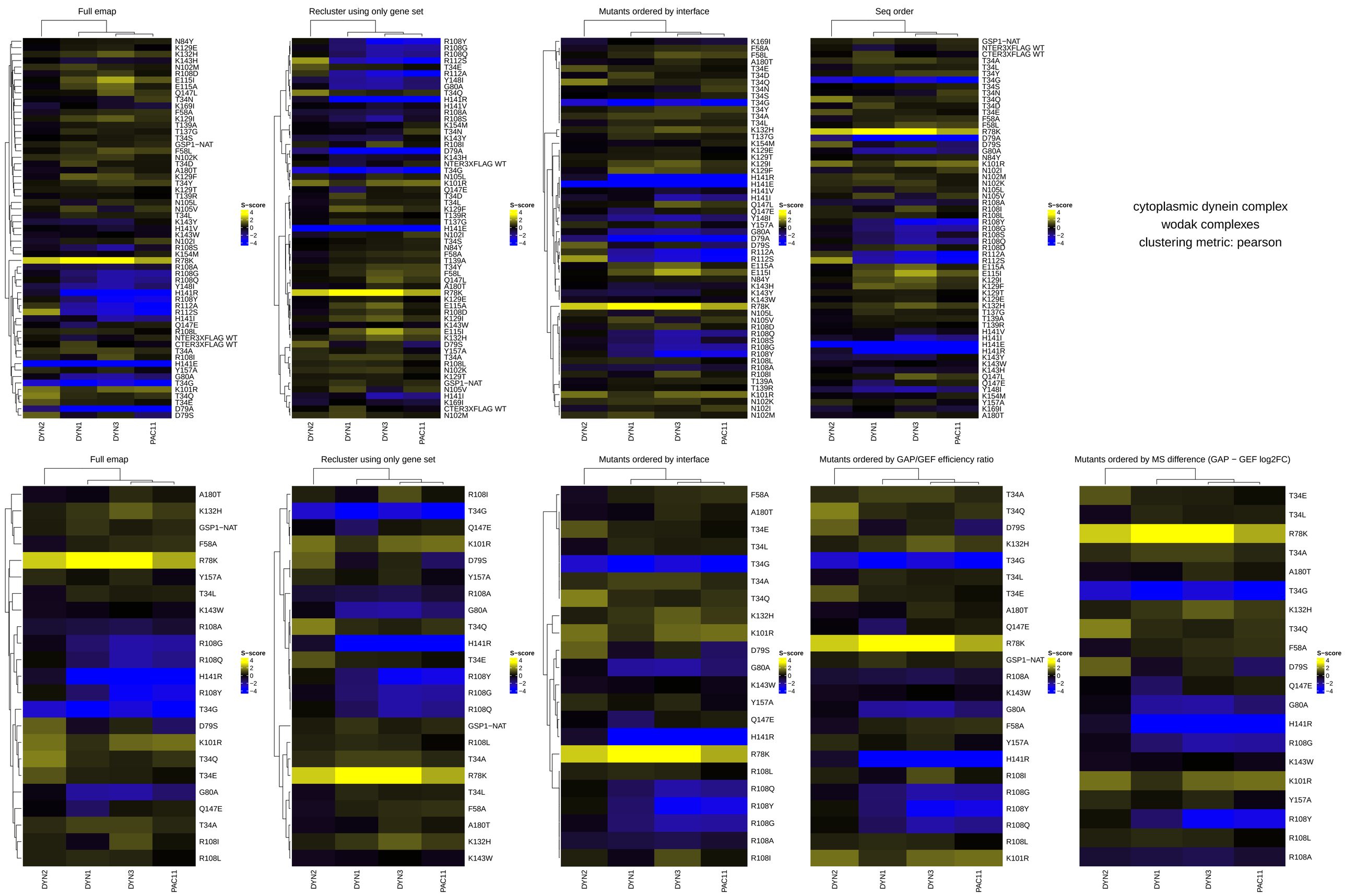


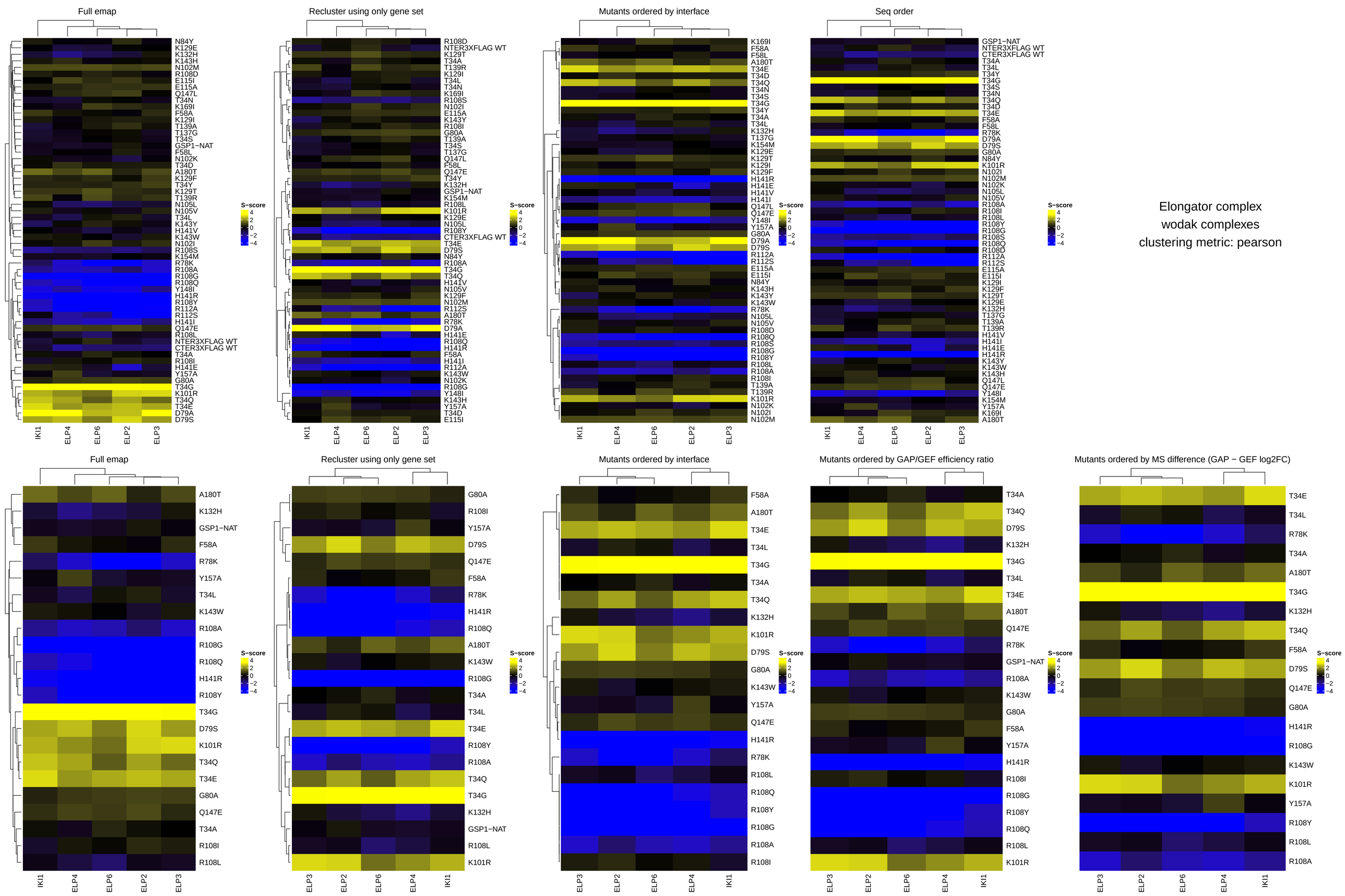
Golgi transport complex
wodak complexes
clustering metric: pearson

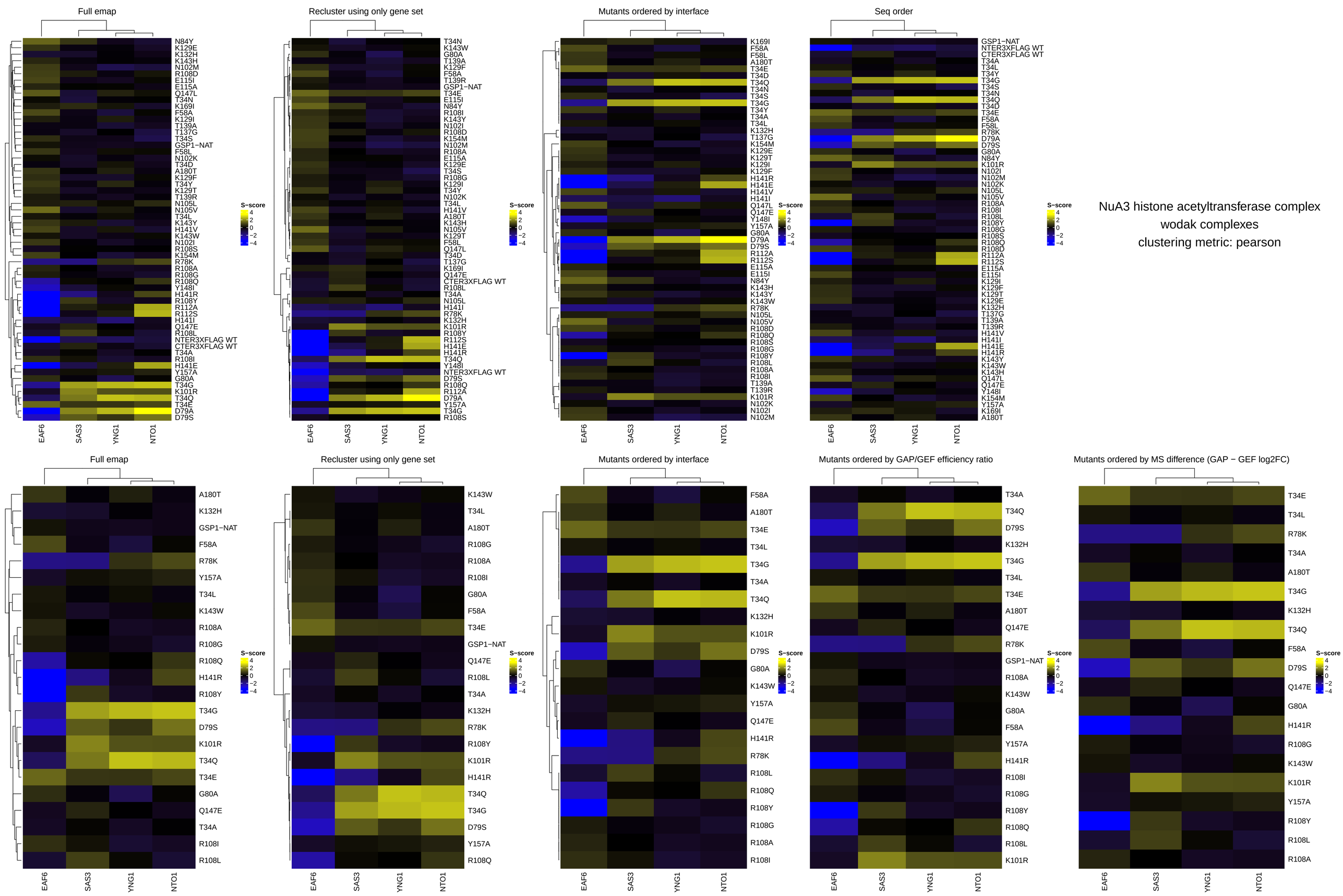

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HHF2
HHT2
HHT1
HHF1
HTA1
Nucleosomal protein complex
wodak complexes
clustering metric: pearson

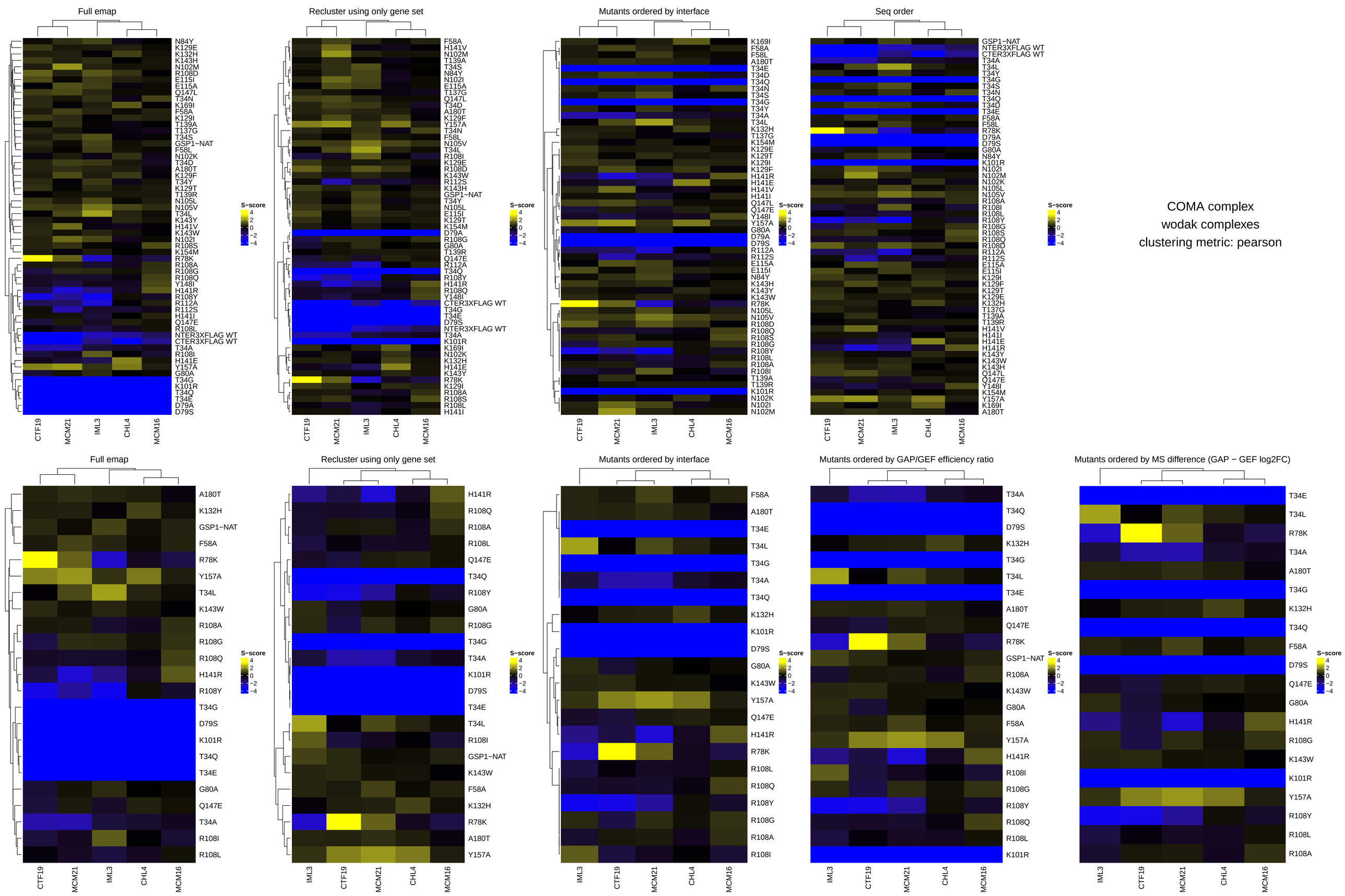

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
GET2
GET1
GET3
GET complex
wodak complexes
clustering metric: pearson

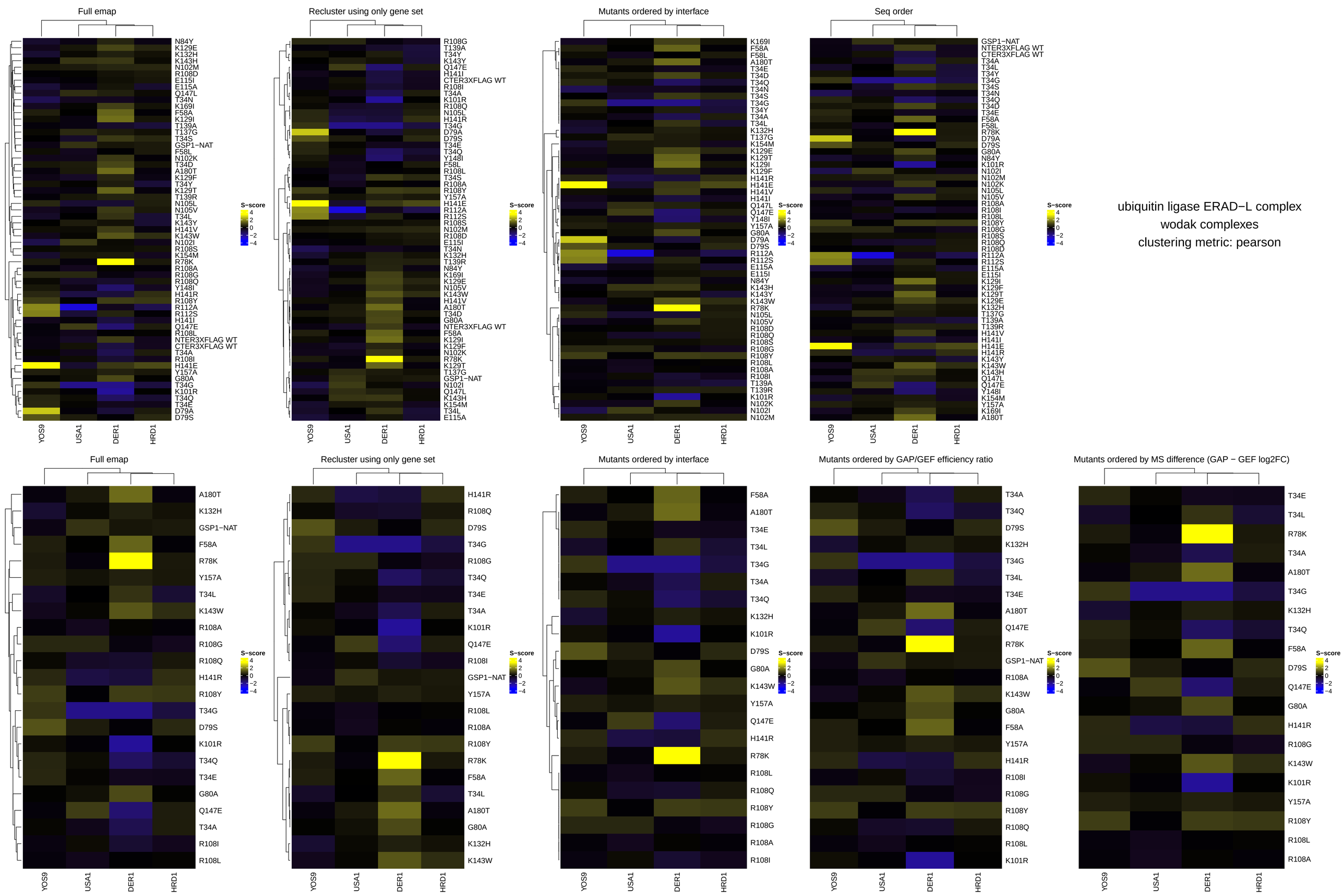

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
MRPL36
IMG2
MRPL10
mitochondrial ribosomal large subunit
wodak complexes
clustering metric: pearson

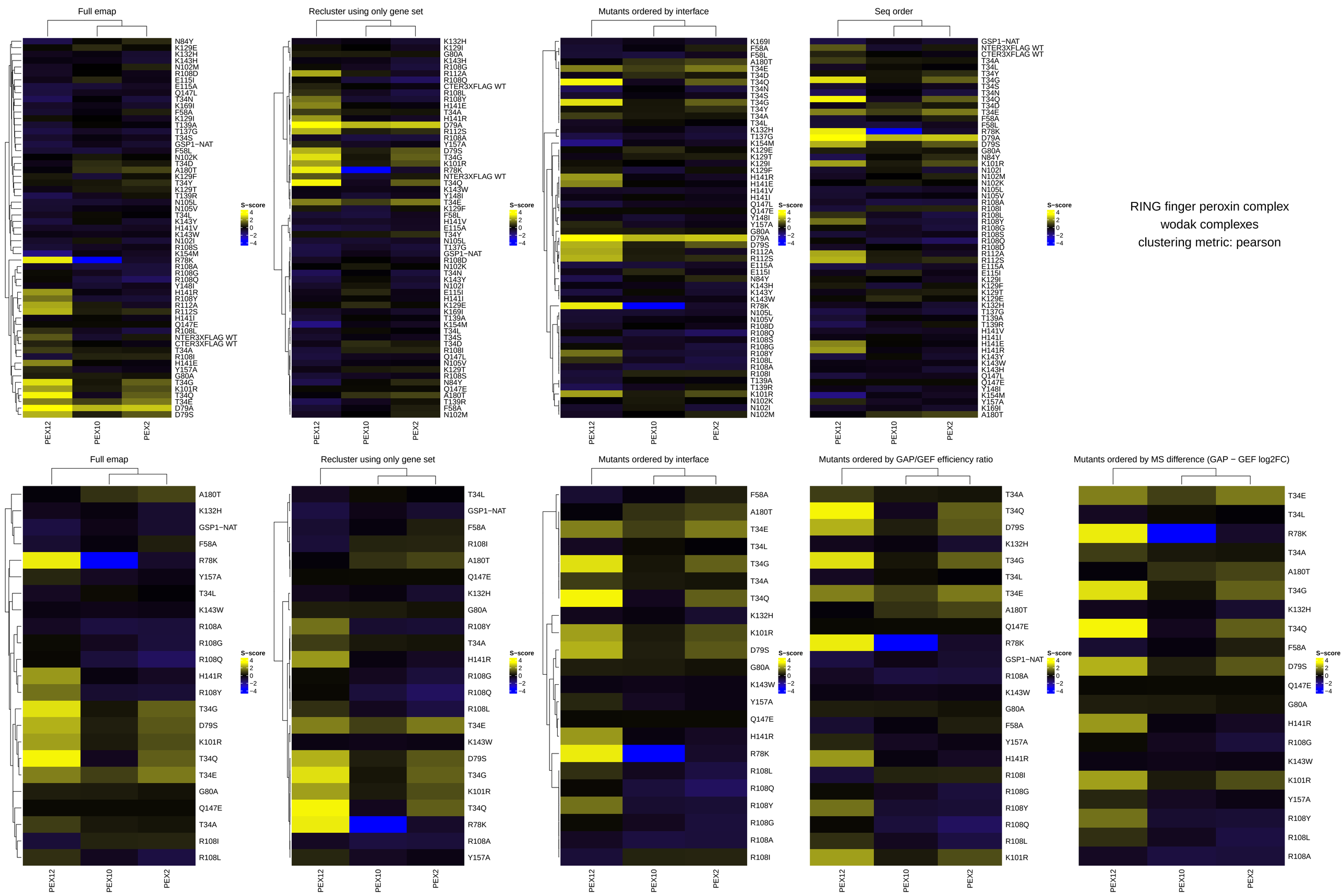

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
DYN2
DYN1
DYN3
PAC11
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
cytoplasmic dynein complex
wodak complexes
clustering metric: pearson

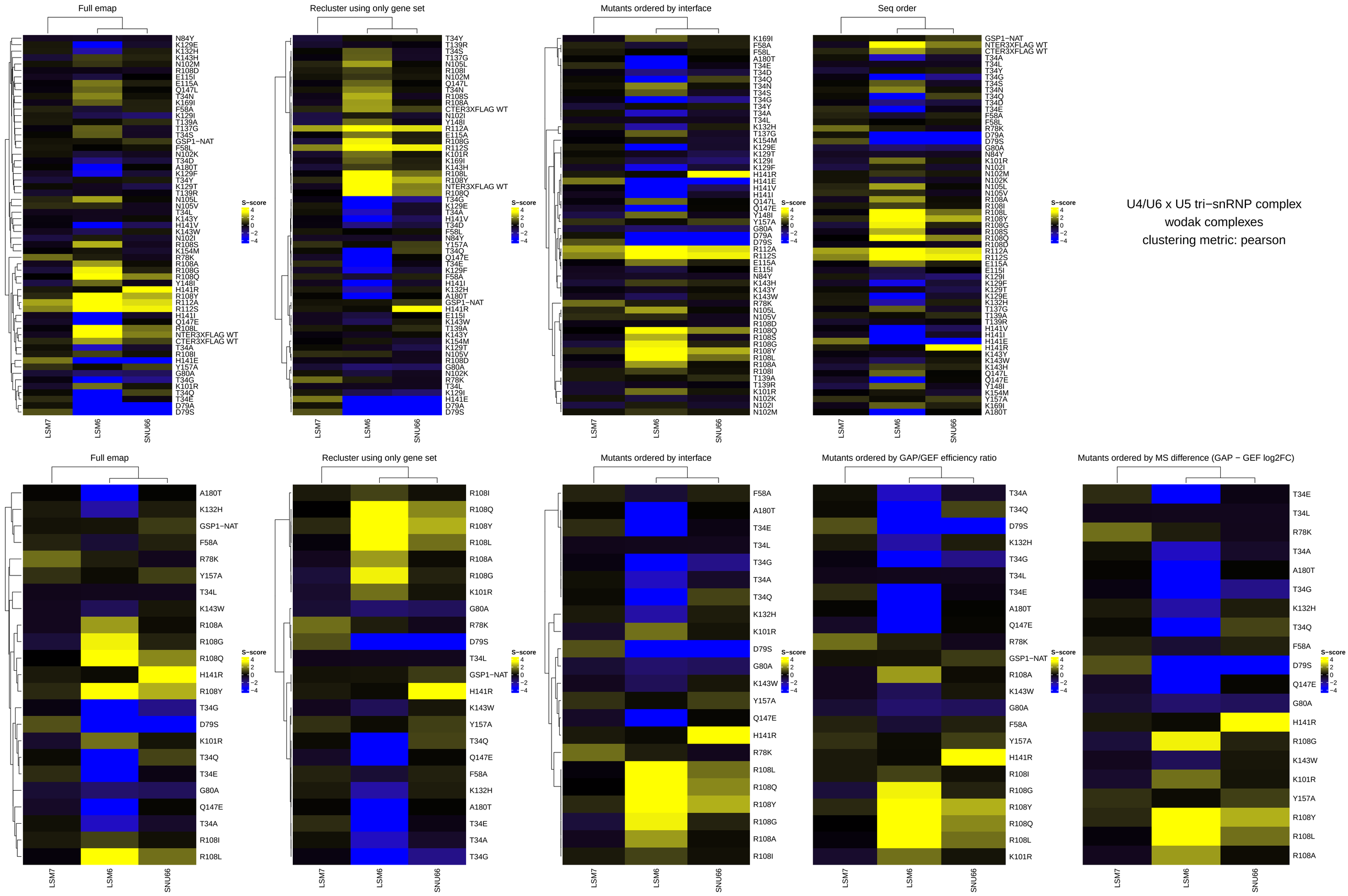

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
IKI1
ELP4
ELP6
ELP2
ELP3
Elongator complex
wodak complexes
clustering metric: pearson

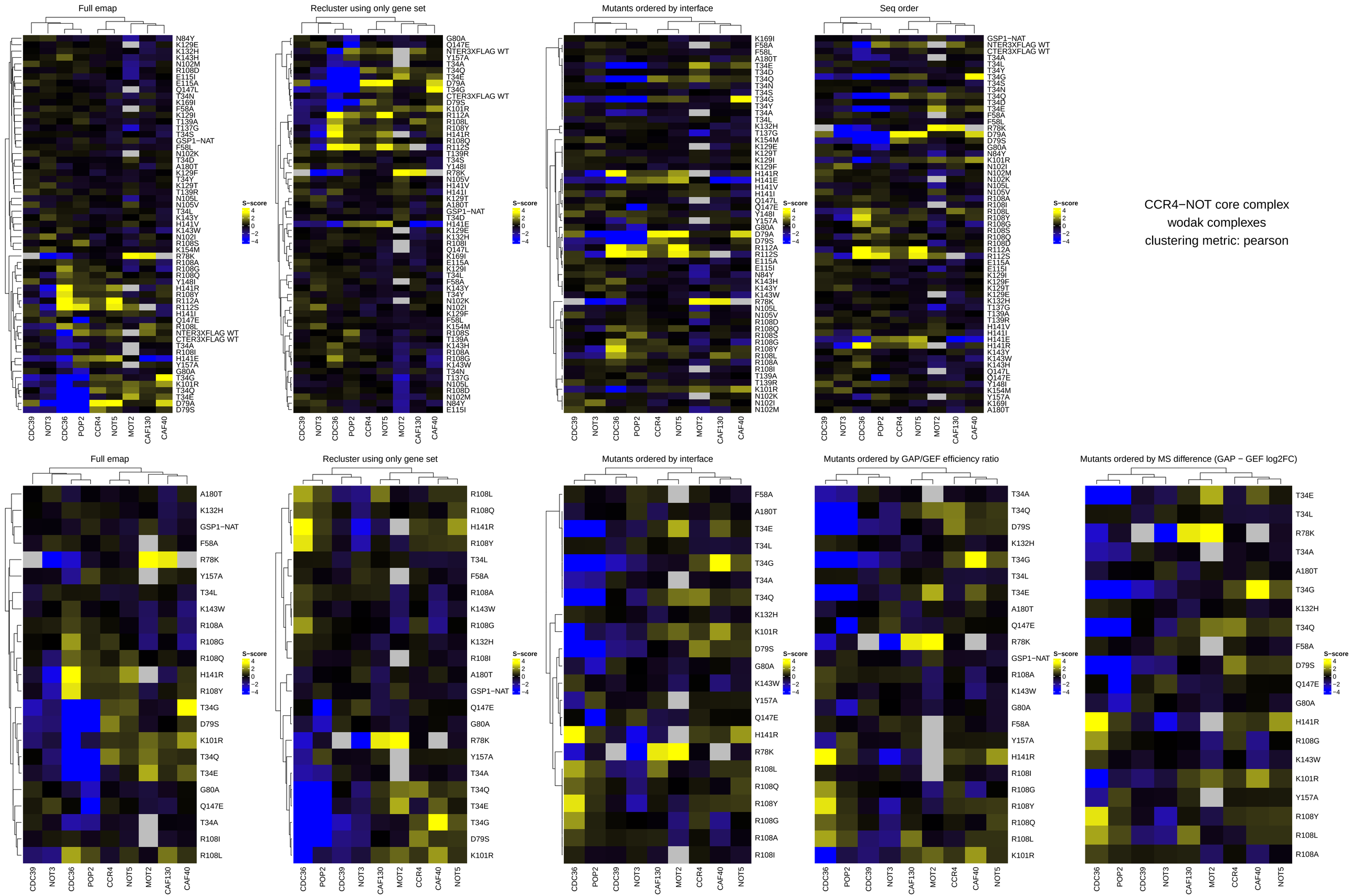

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
EAF6
SAS3
YNG1
NTO1
NuA3 histone acetyltransferase complex
wodak complexes
clustering metric: pearson

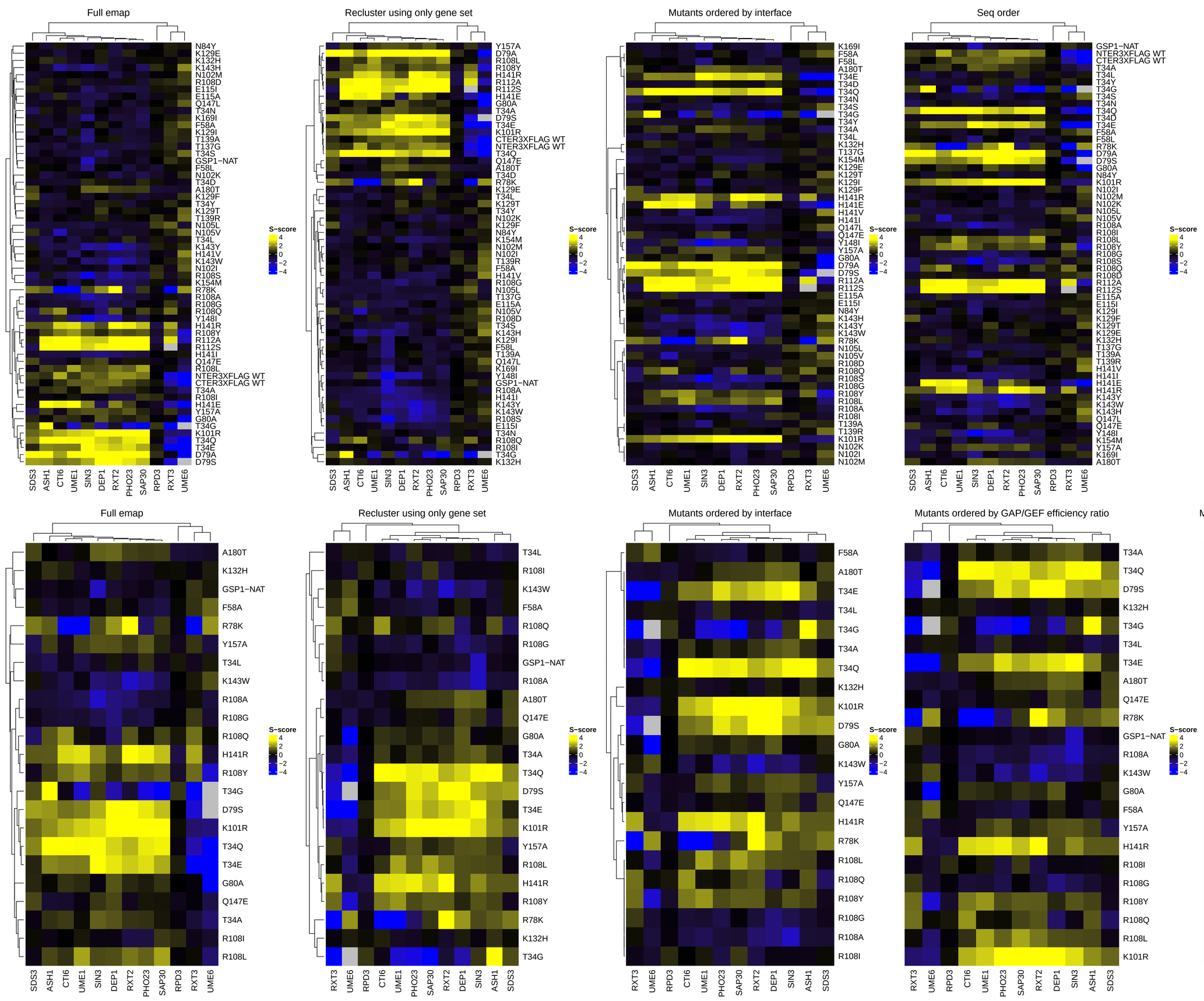

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CTF19
MCM21
IML3
CHL4
MCM16
COMA complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
YOS9
USA1
DER1
HRD1
ubiquitin ligase ERAD−L complex
wodak complexes
clustering metric: pearson

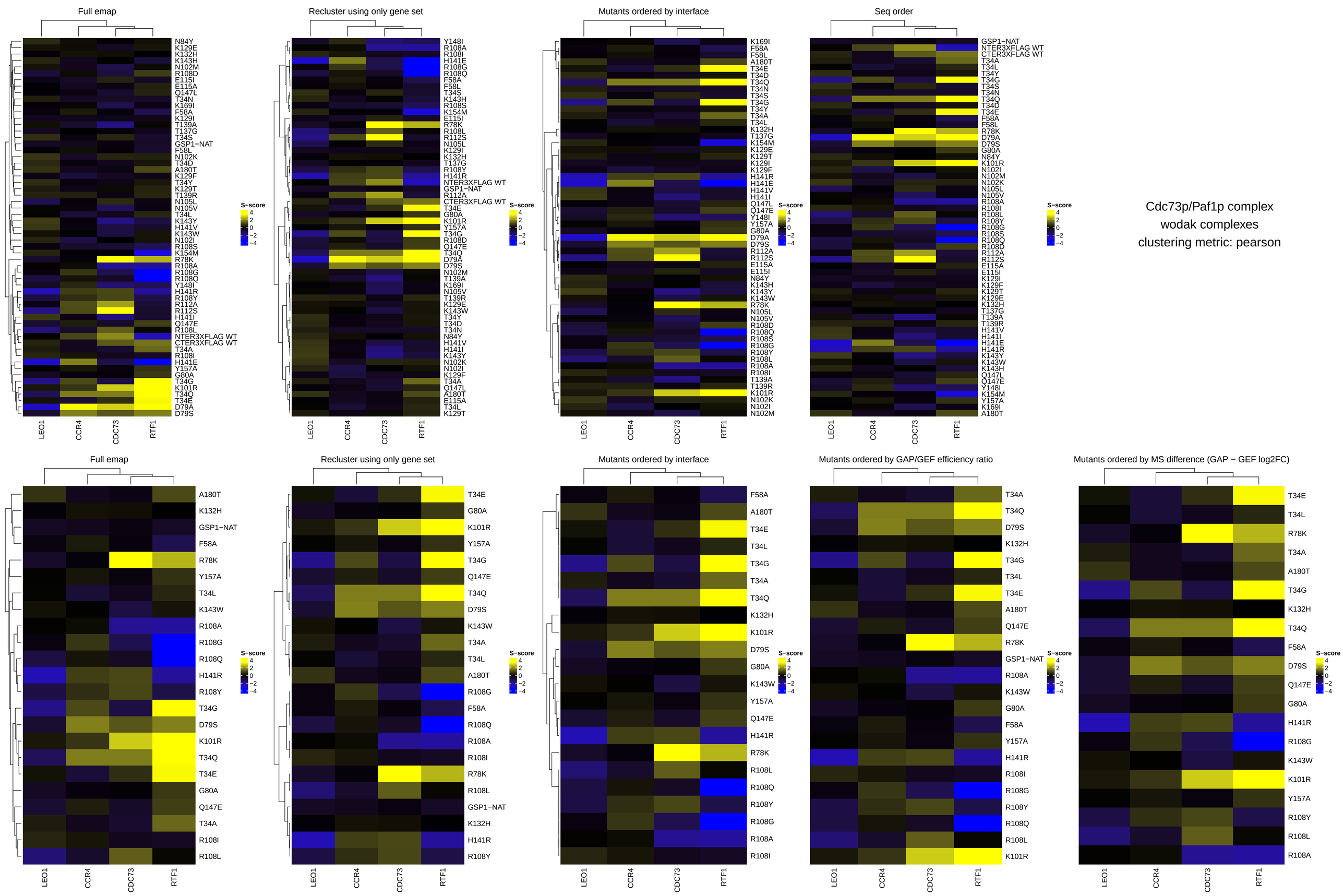

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
PEX12
PEX10
PEX2
RING finger peroxin complex
wodak complexes
clustering metric: pearson

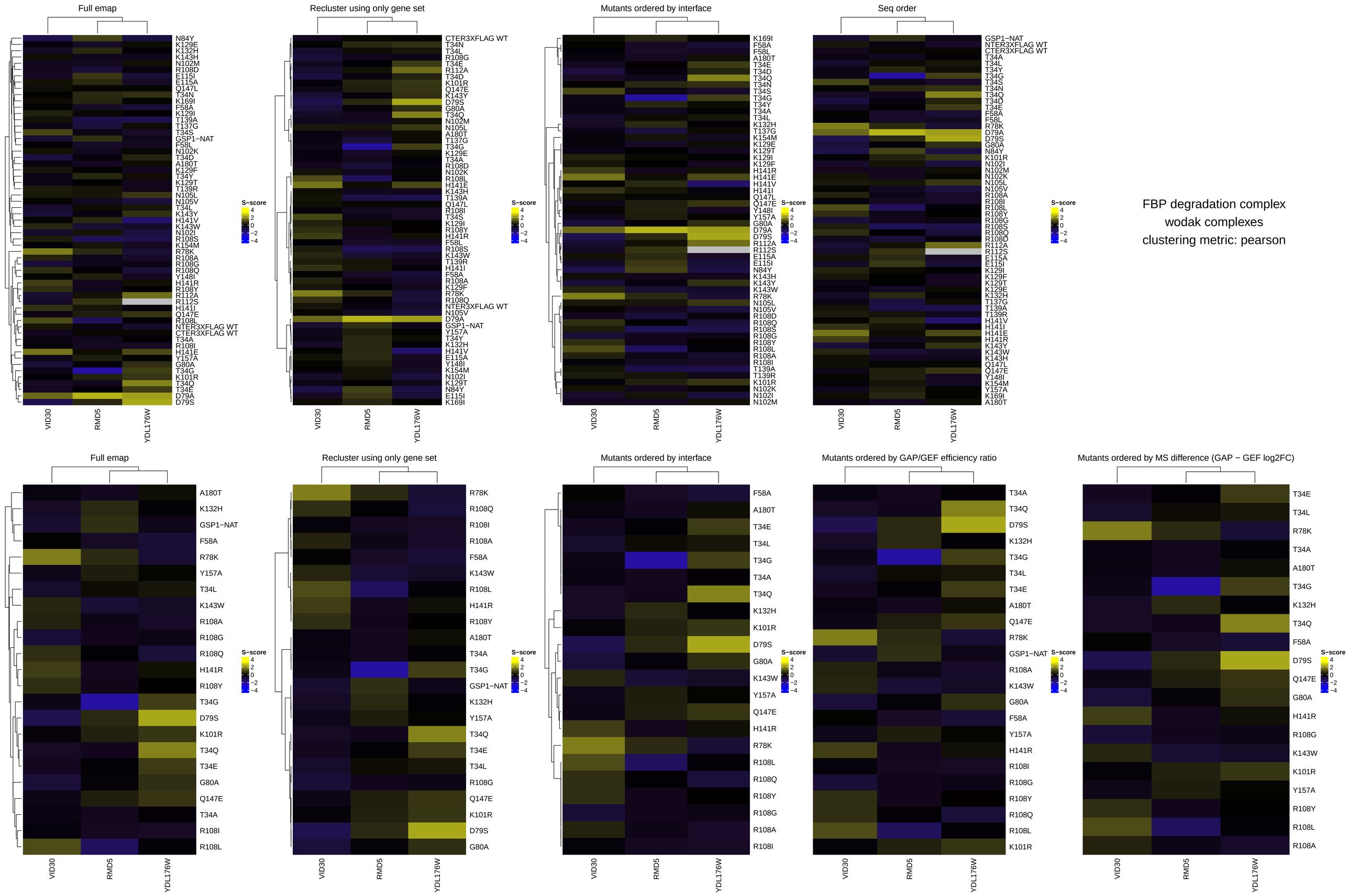

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
LSM7
LSM6
SNU66
U4/U6 x U5 tri−snRNP complex
wodak complexes
clustering metric: pearson

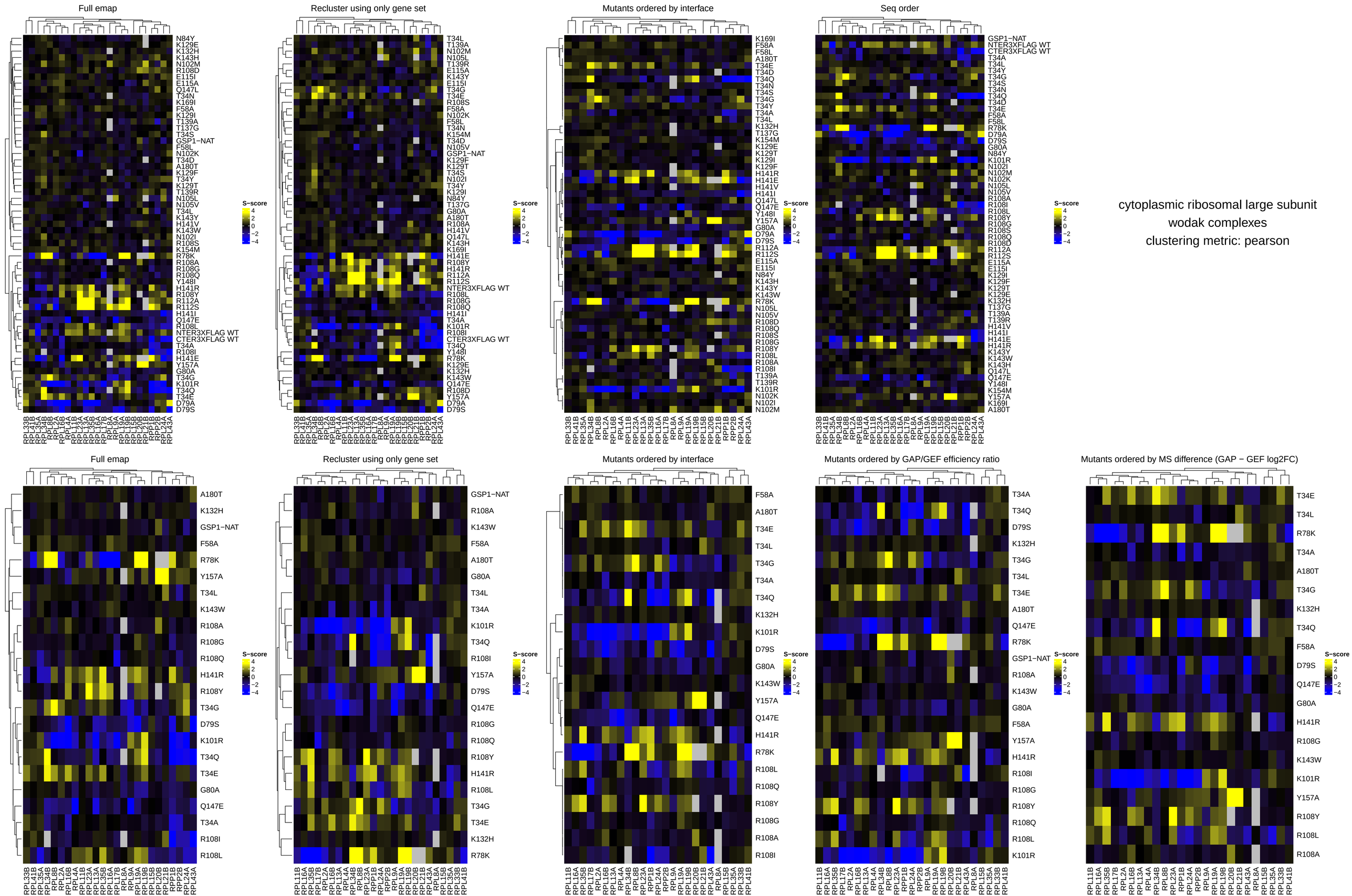

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CDC39
NOT3
CDC36
POP2
CCR4
NOT5
MOT2
CAF130
CAF40
CCR4−NOT core complex
wodak complexes
clustering metric: pearson

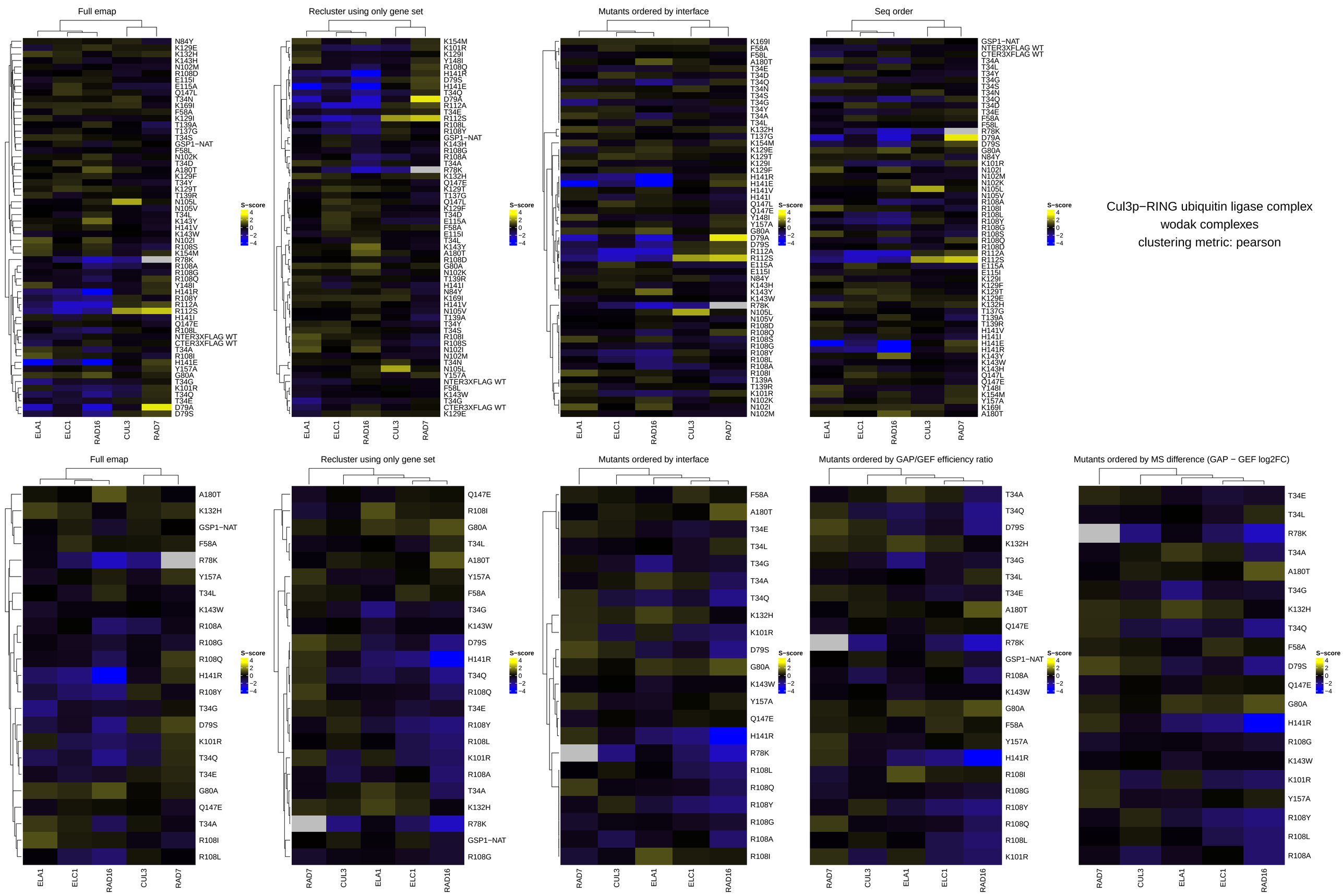


Rpd3L complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
LEO1
CCR4
CDC73
RTF1
Cdc73p/Paf1p complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
VID30
RMD5
YDL176W
FBP degradation complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
cytoplasmic ribosomal large subunit
wodak complexes
clustering metric: pearson


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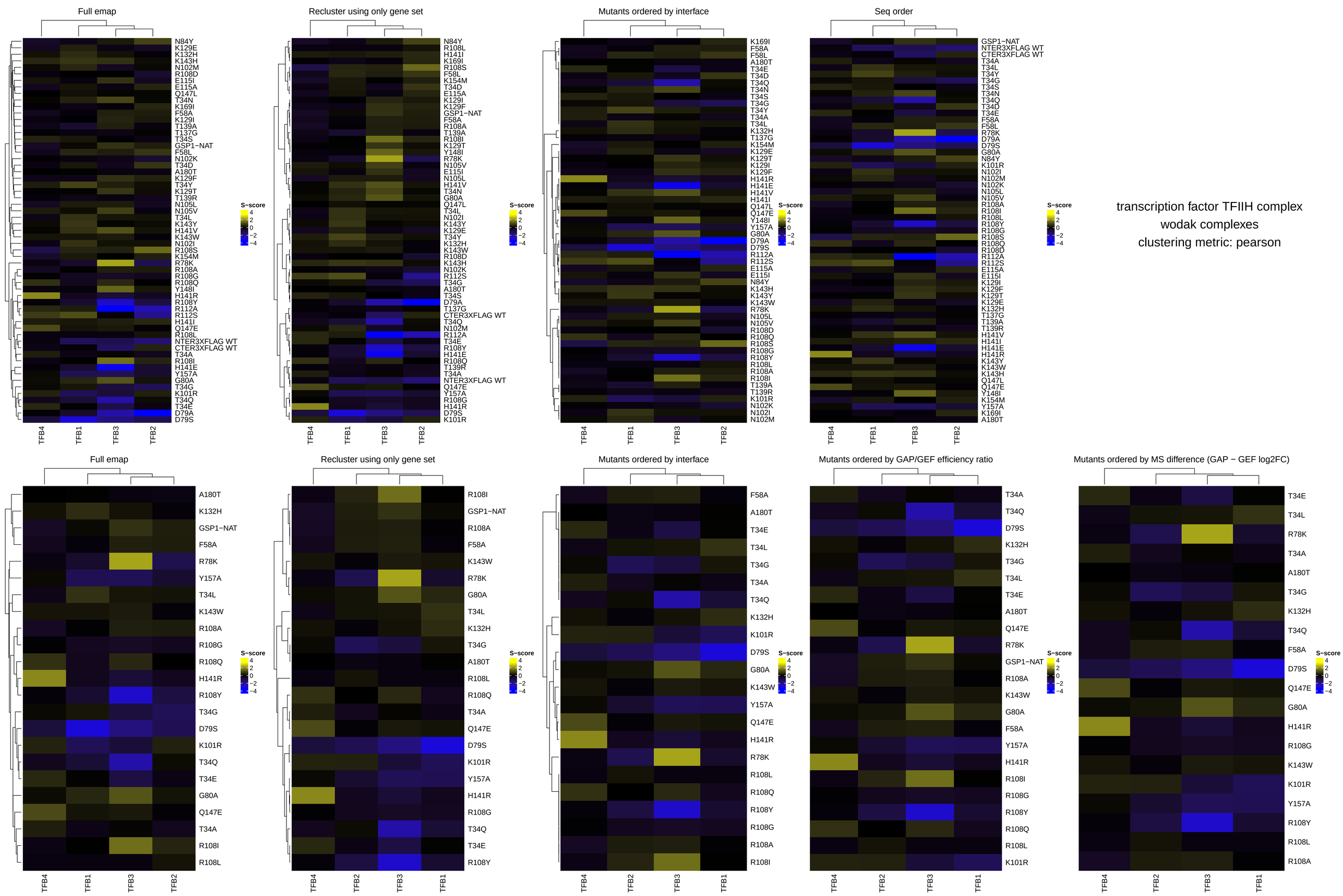
−2
−4
ELA1
ELC1
RAD16
CUL3
RAD7
Cul3p−RING ubiquitin ligase complex
wodak complexes
clustering metric: pearson


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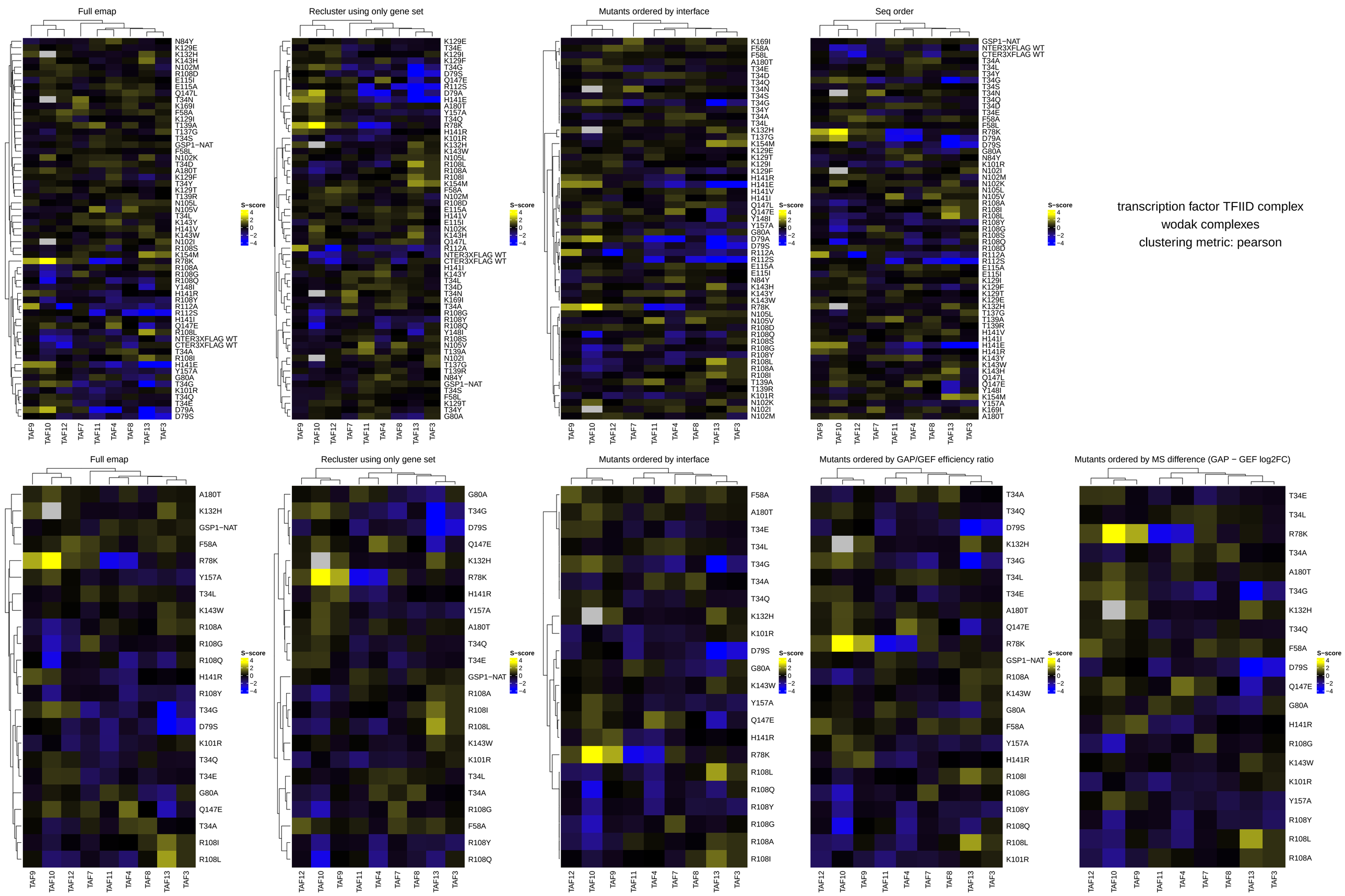
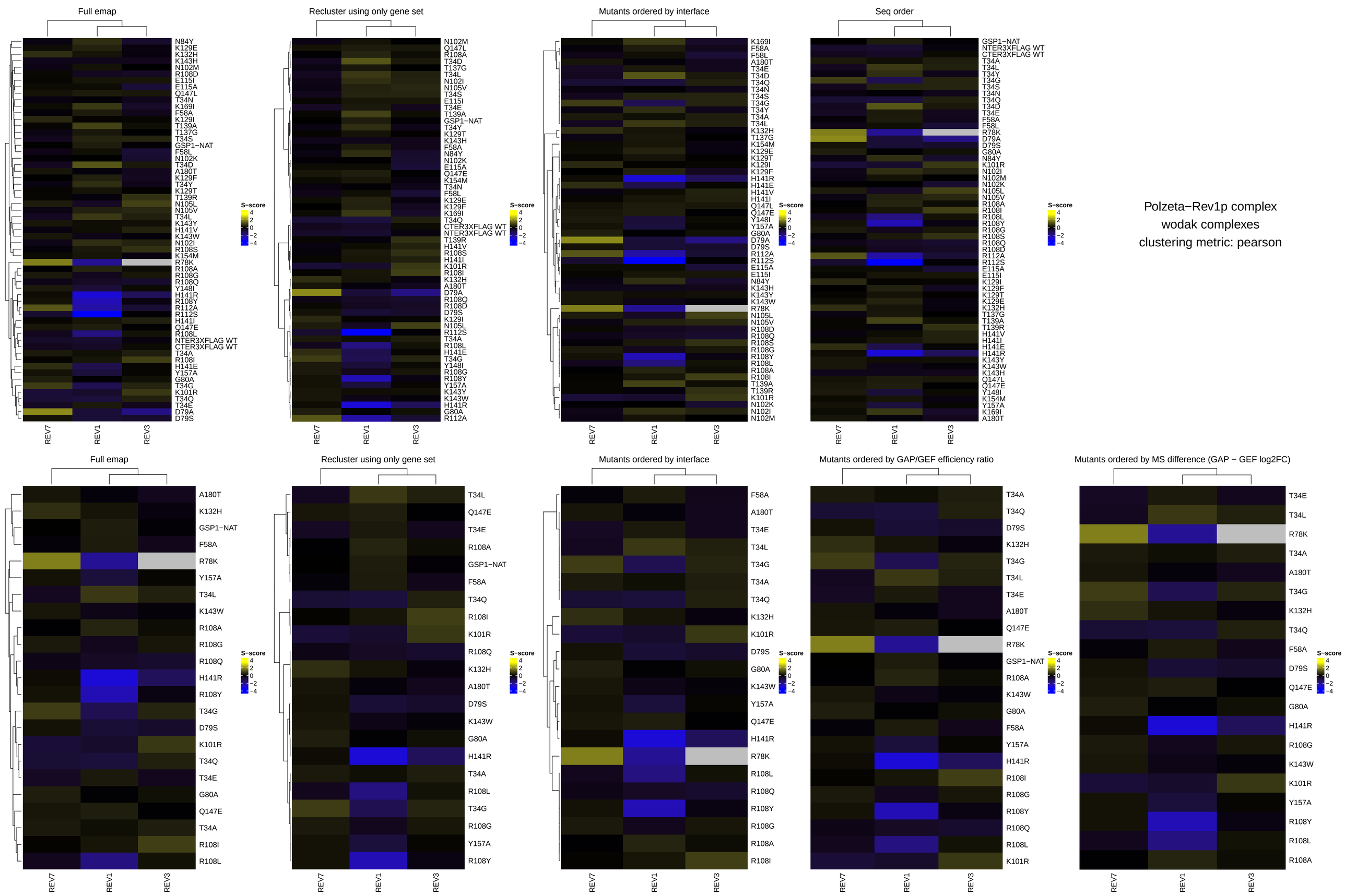
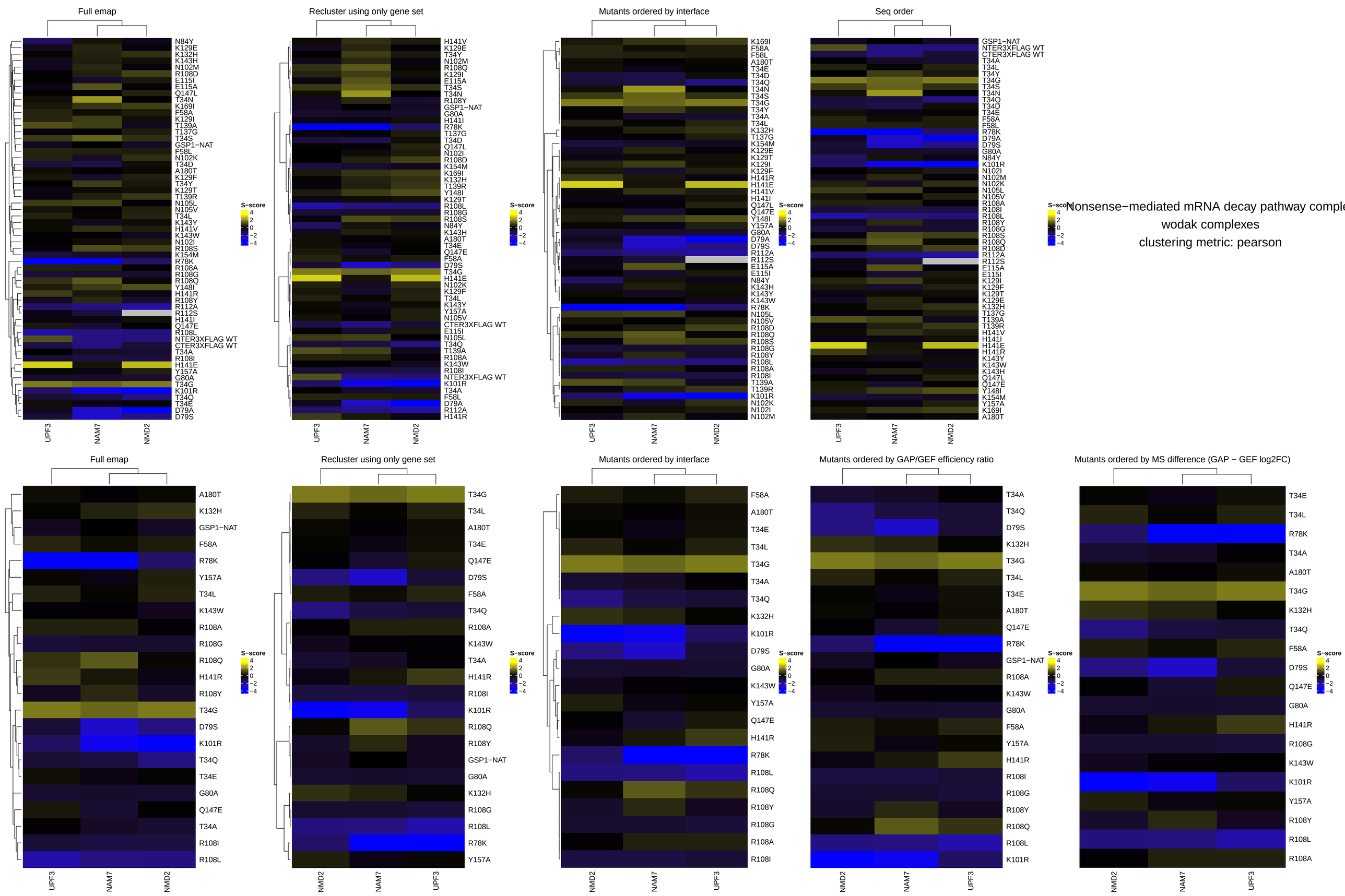
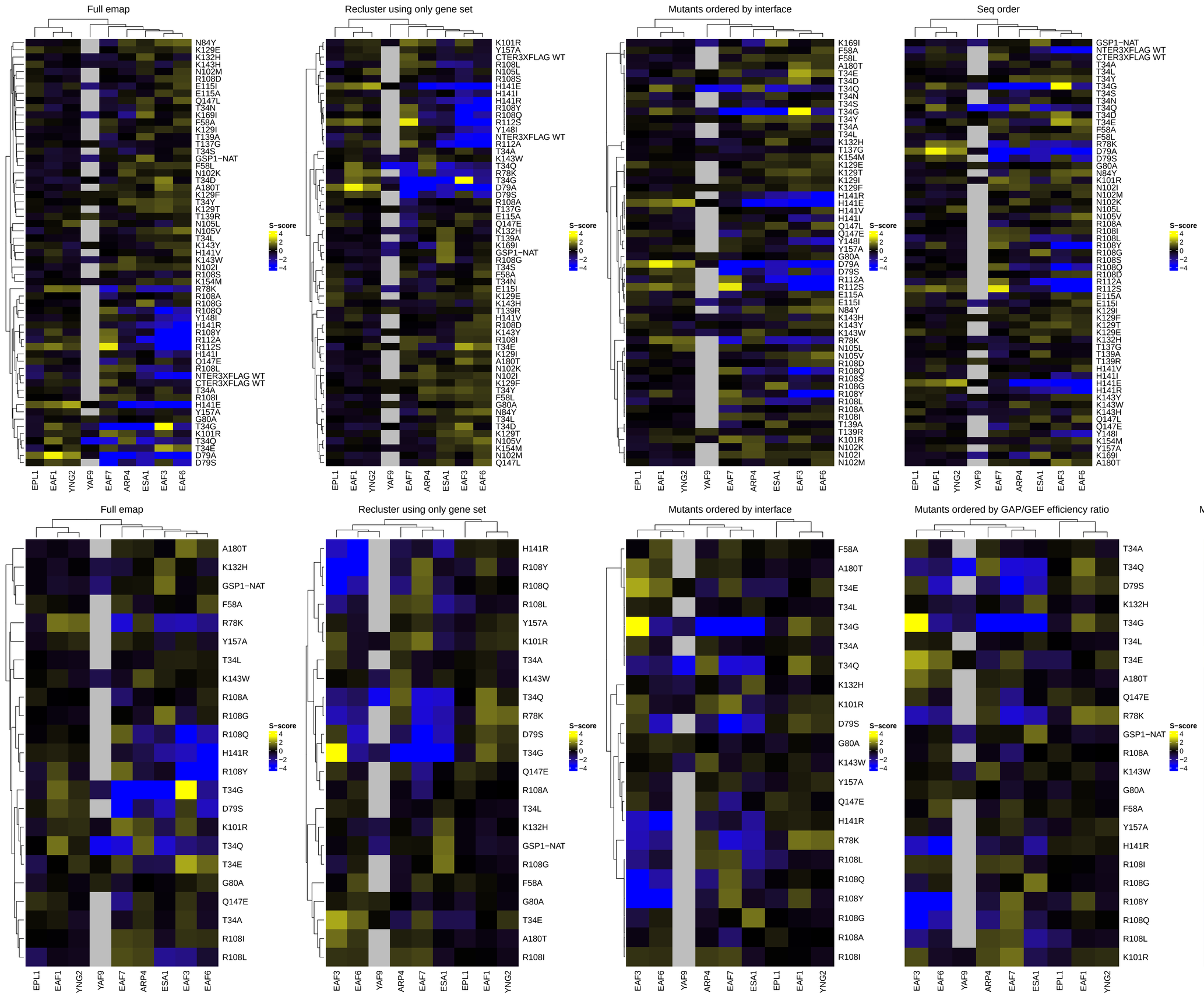
2
0
−2
−4
TFB4
TFB1
TFB3
TFB2
transcription factor TFIIH complex
wodak complexes
clustering metric: pearson



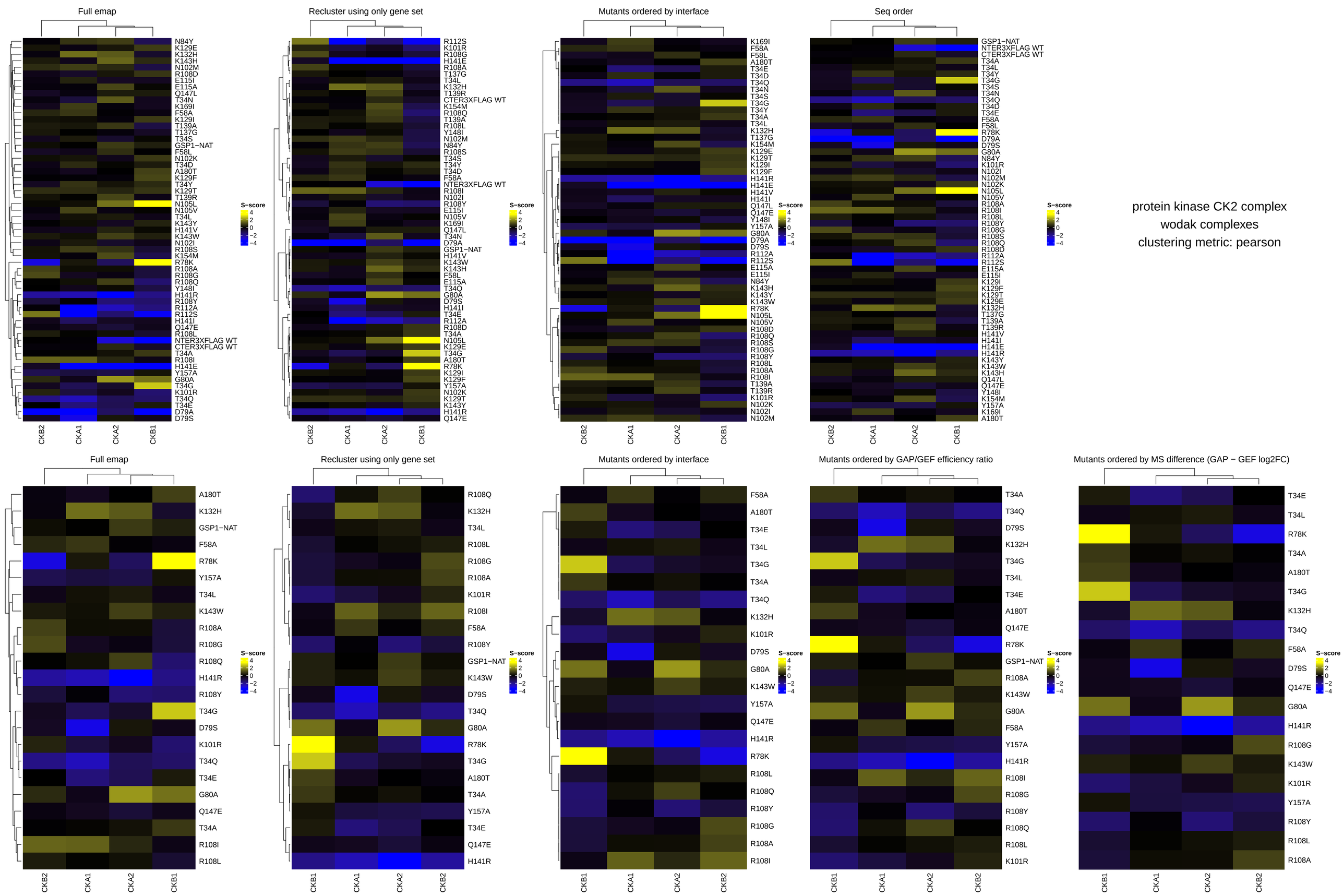
transcription factor TFIID complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
REV7
REV1
REV3
Polzeta−Rev1p complex
wodak complexes
clustering metric: pearson


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



NuA4 histone acetyltransferase complex
wodak complexes
clustering metric: pearson


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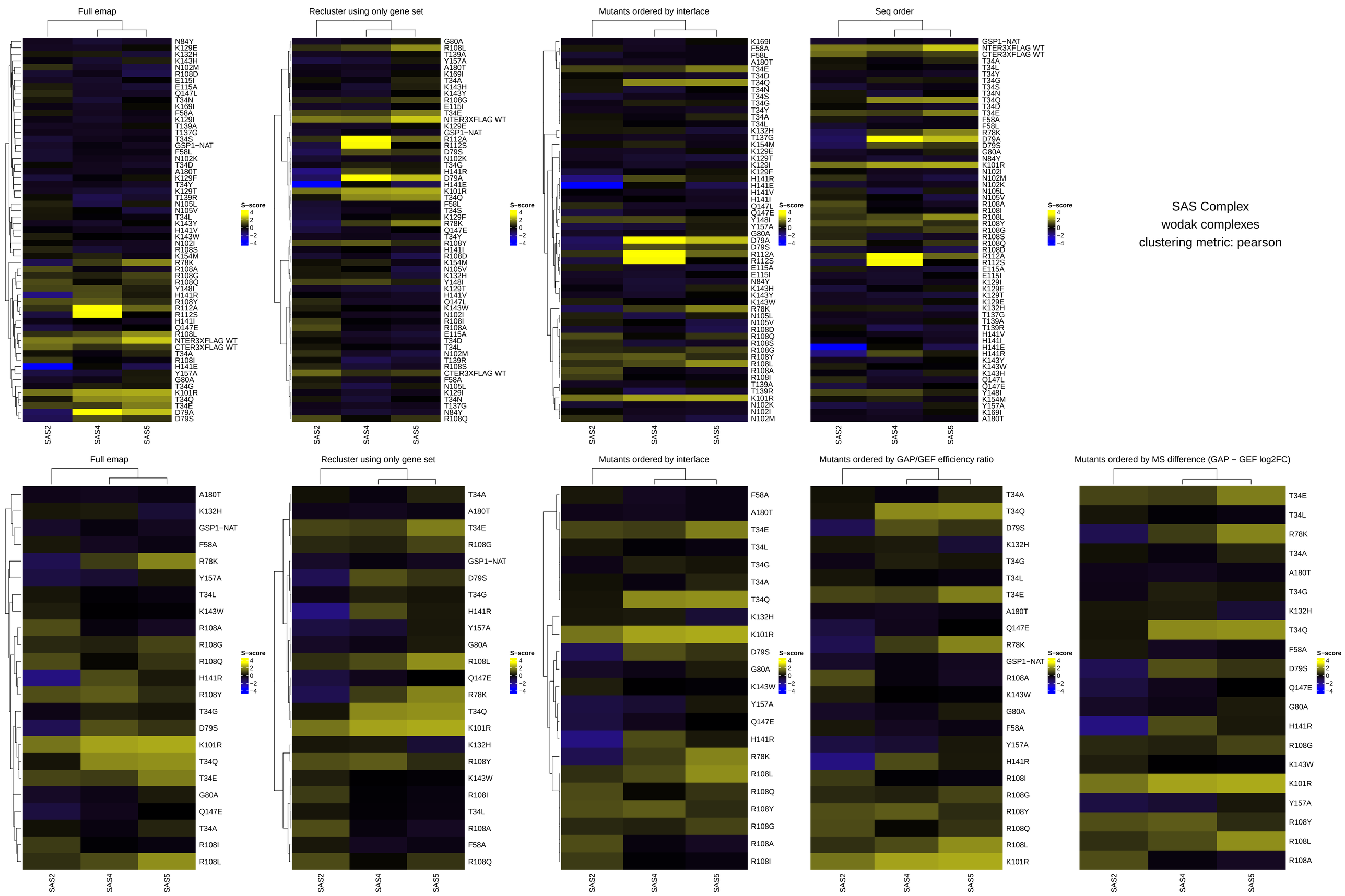
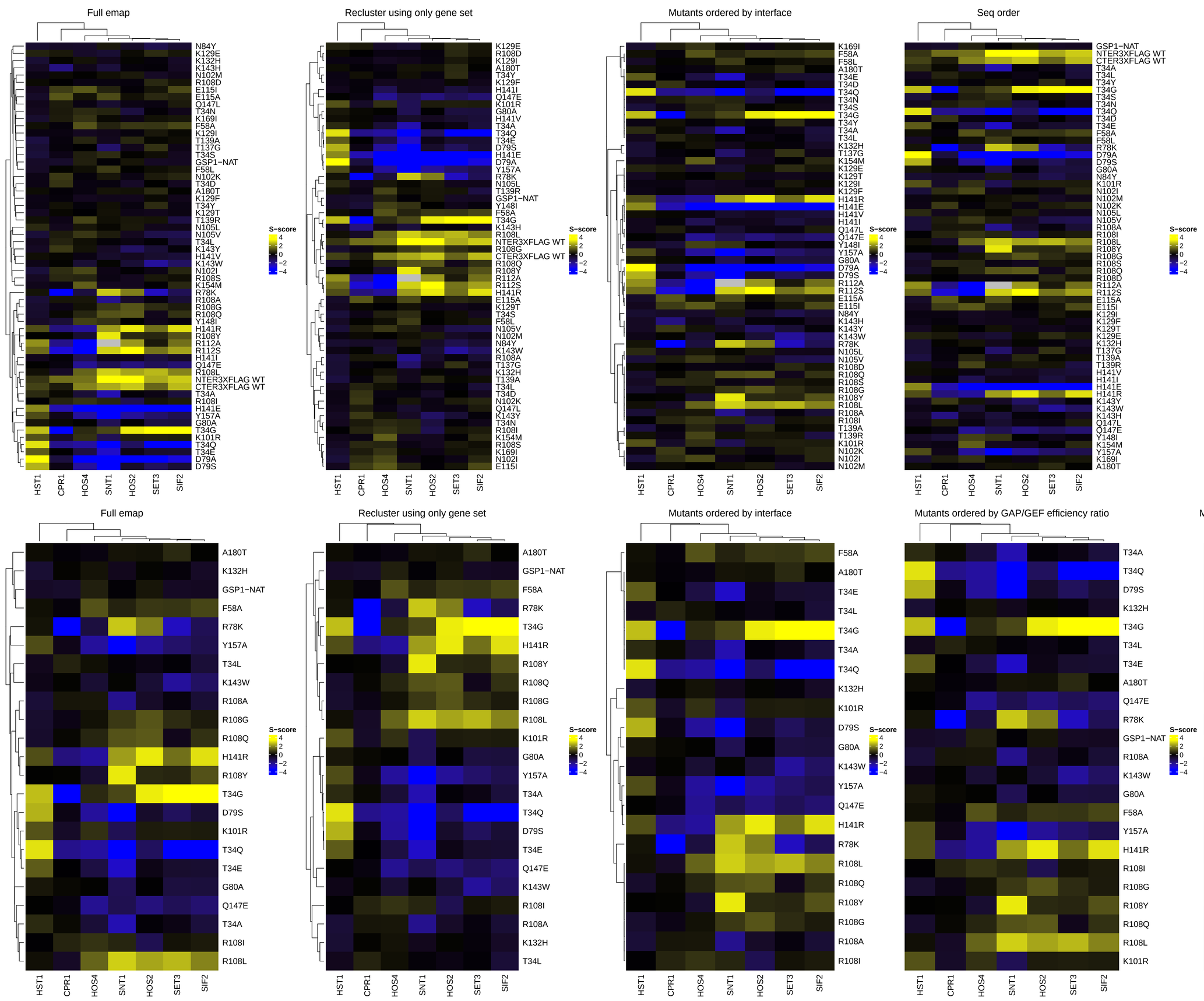
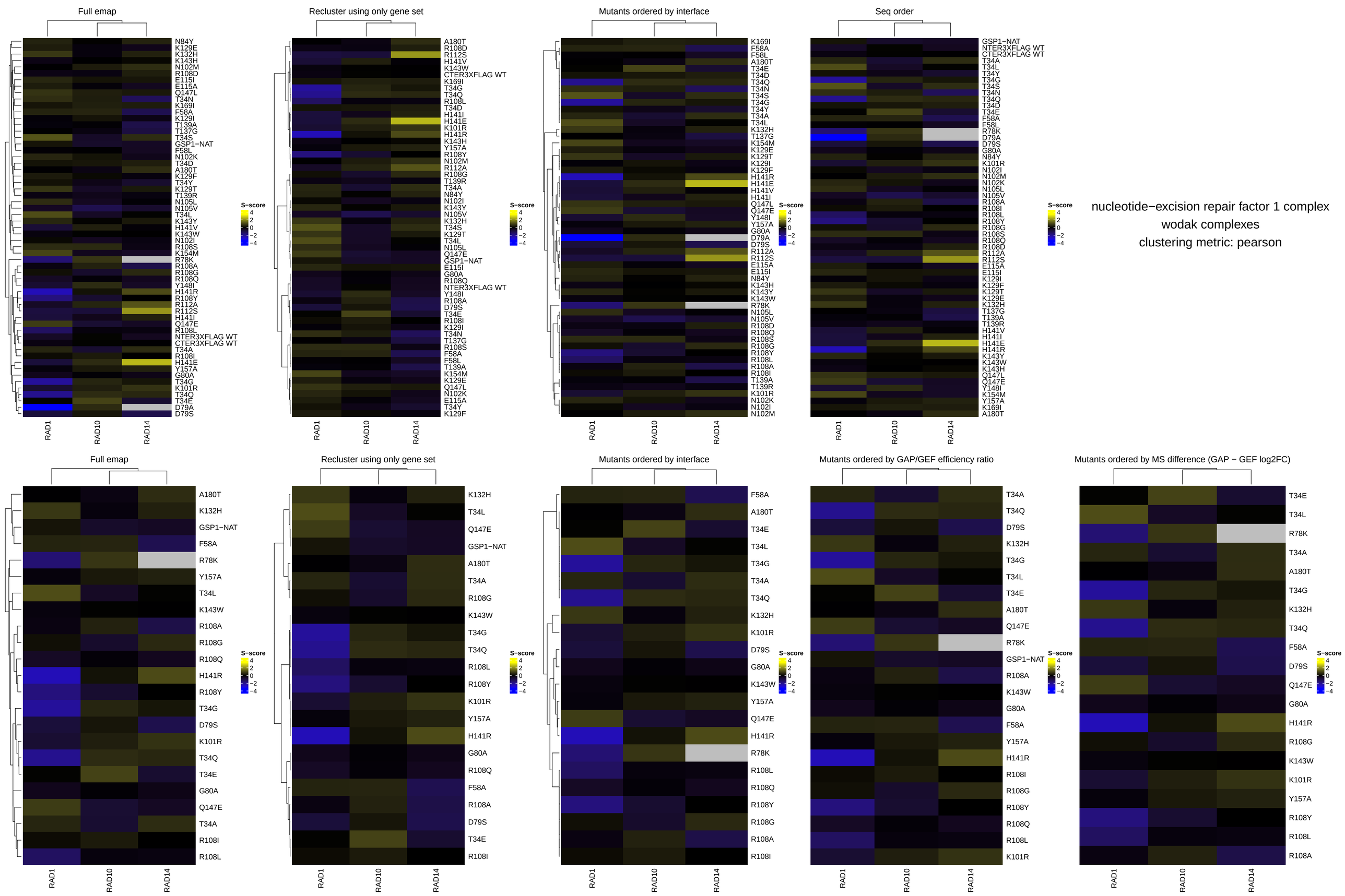
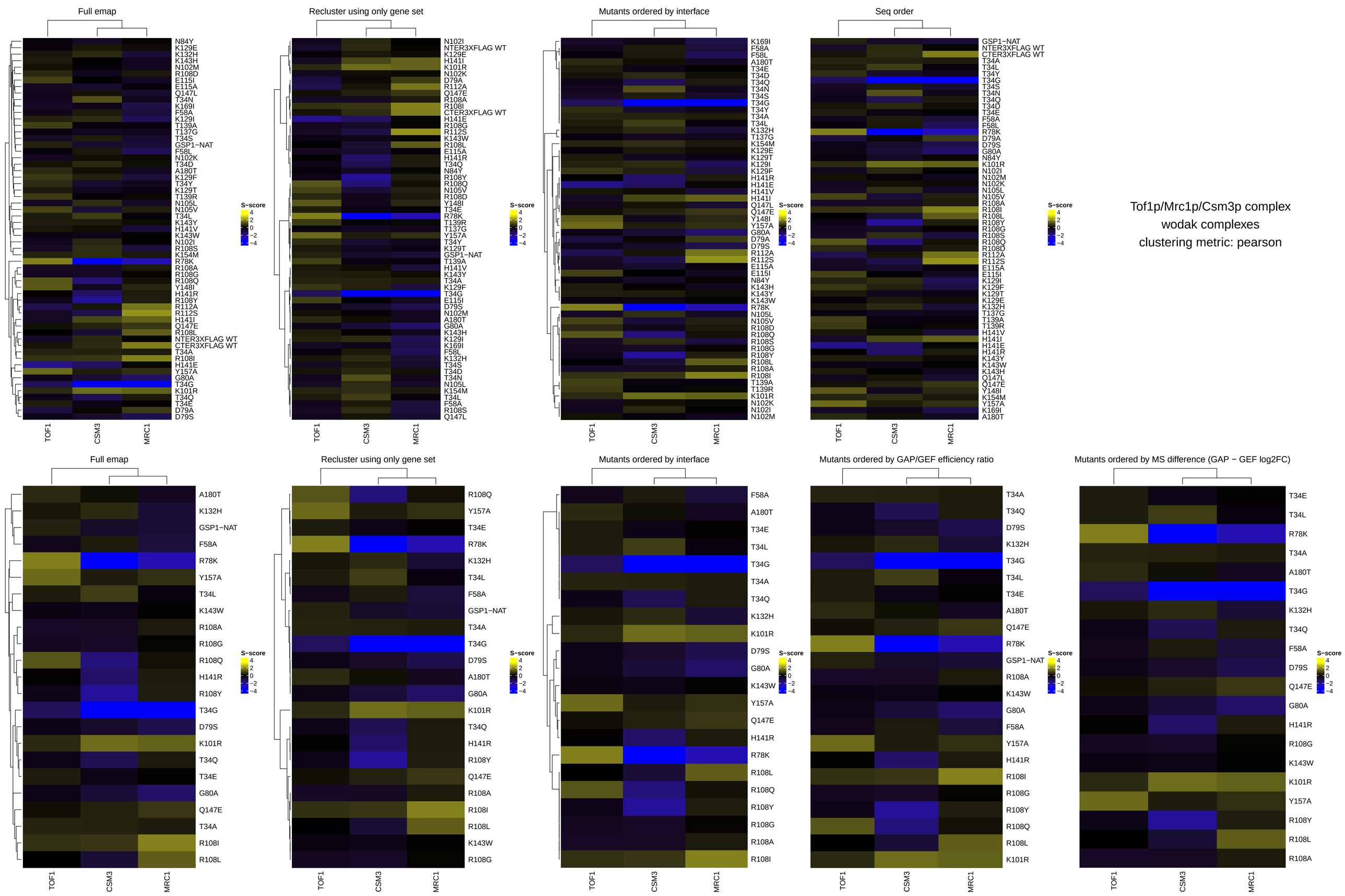
2
0
−2
−4
CKB2
CKA1
CKA2
CKB1
protein kinase CK2 complex
wodak complexes
clustering metric: pearson

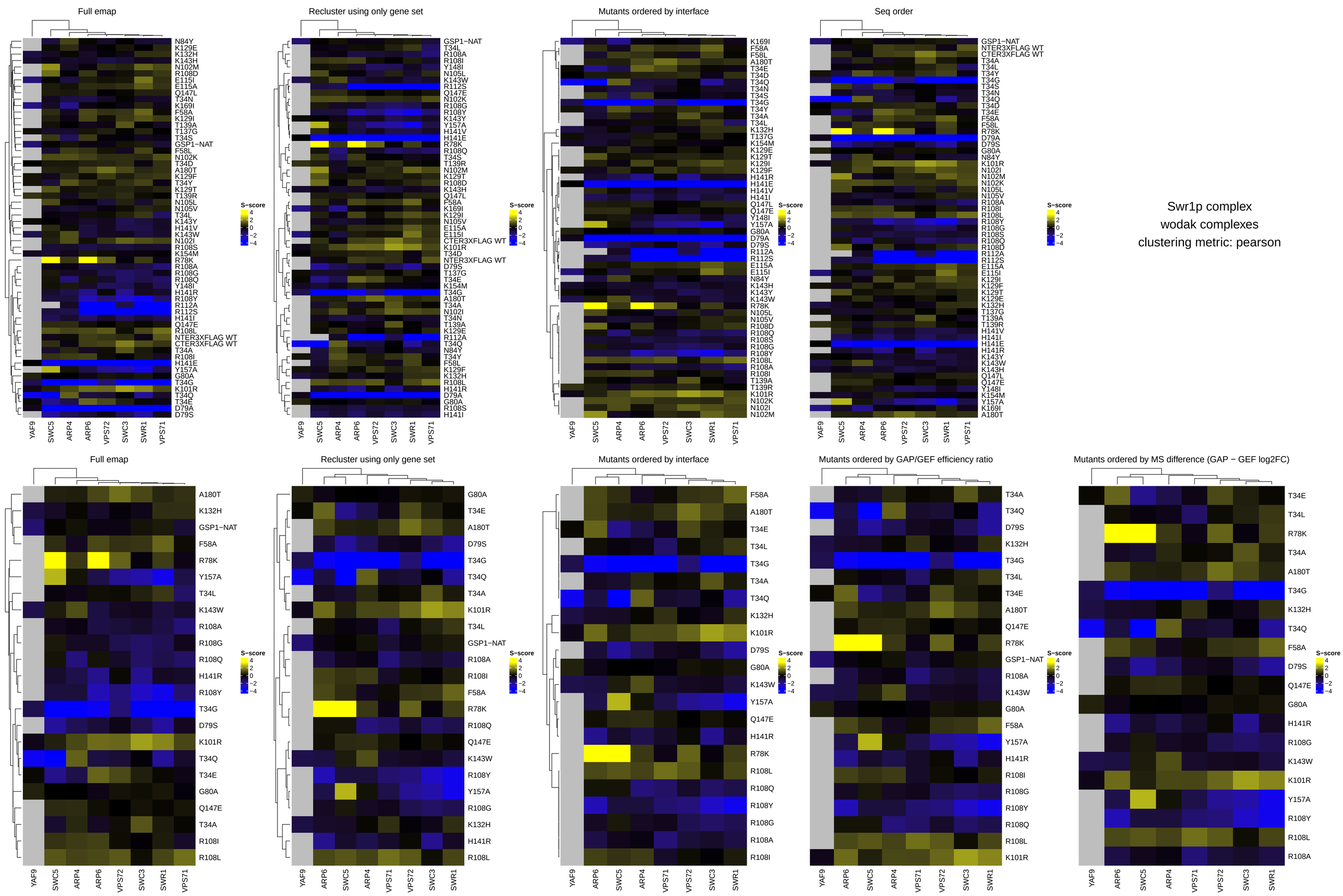

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SAS2
SAS4
SAS5
SAS Complex
wodak complexes
clustering metric: pearson

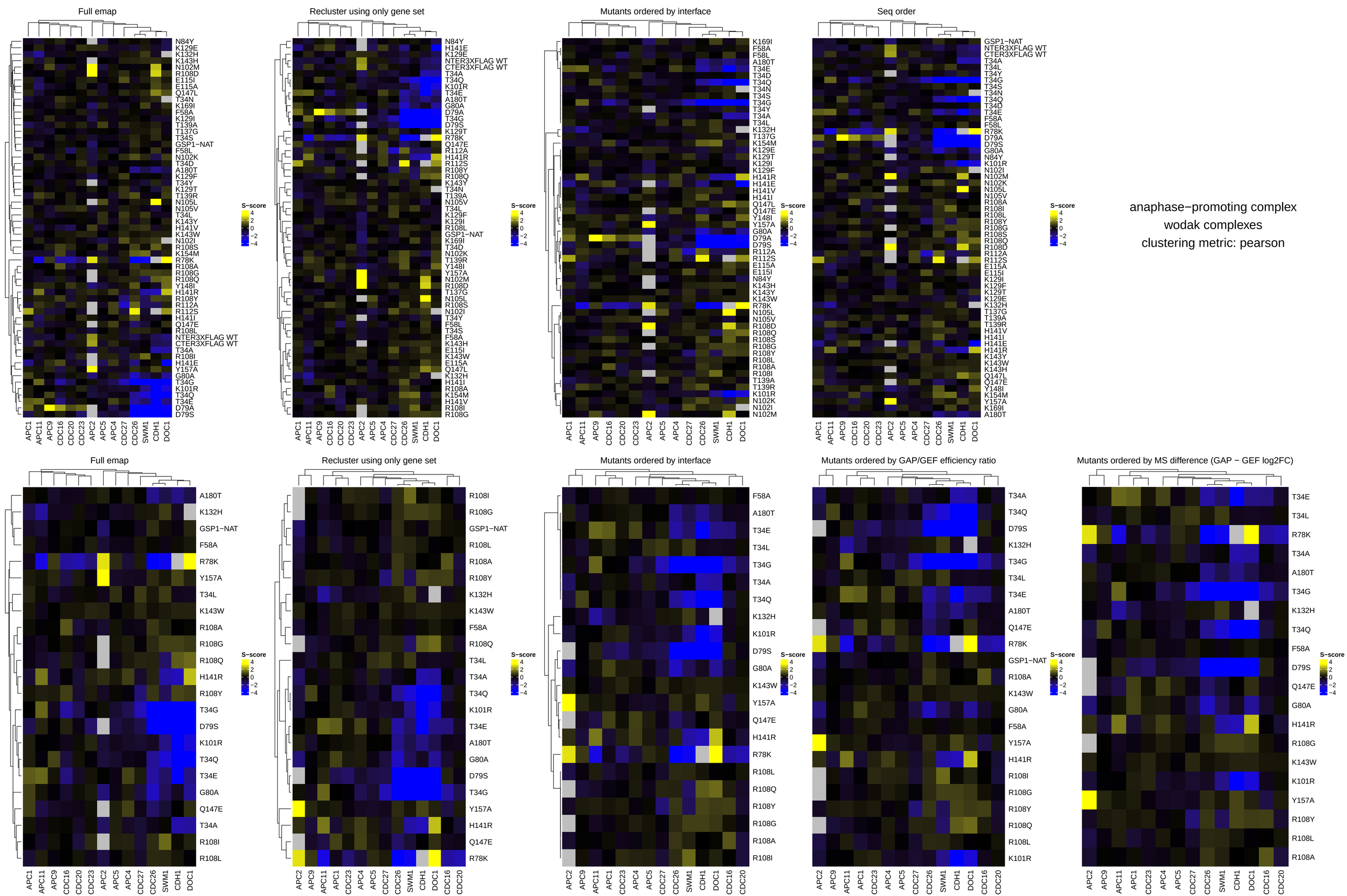


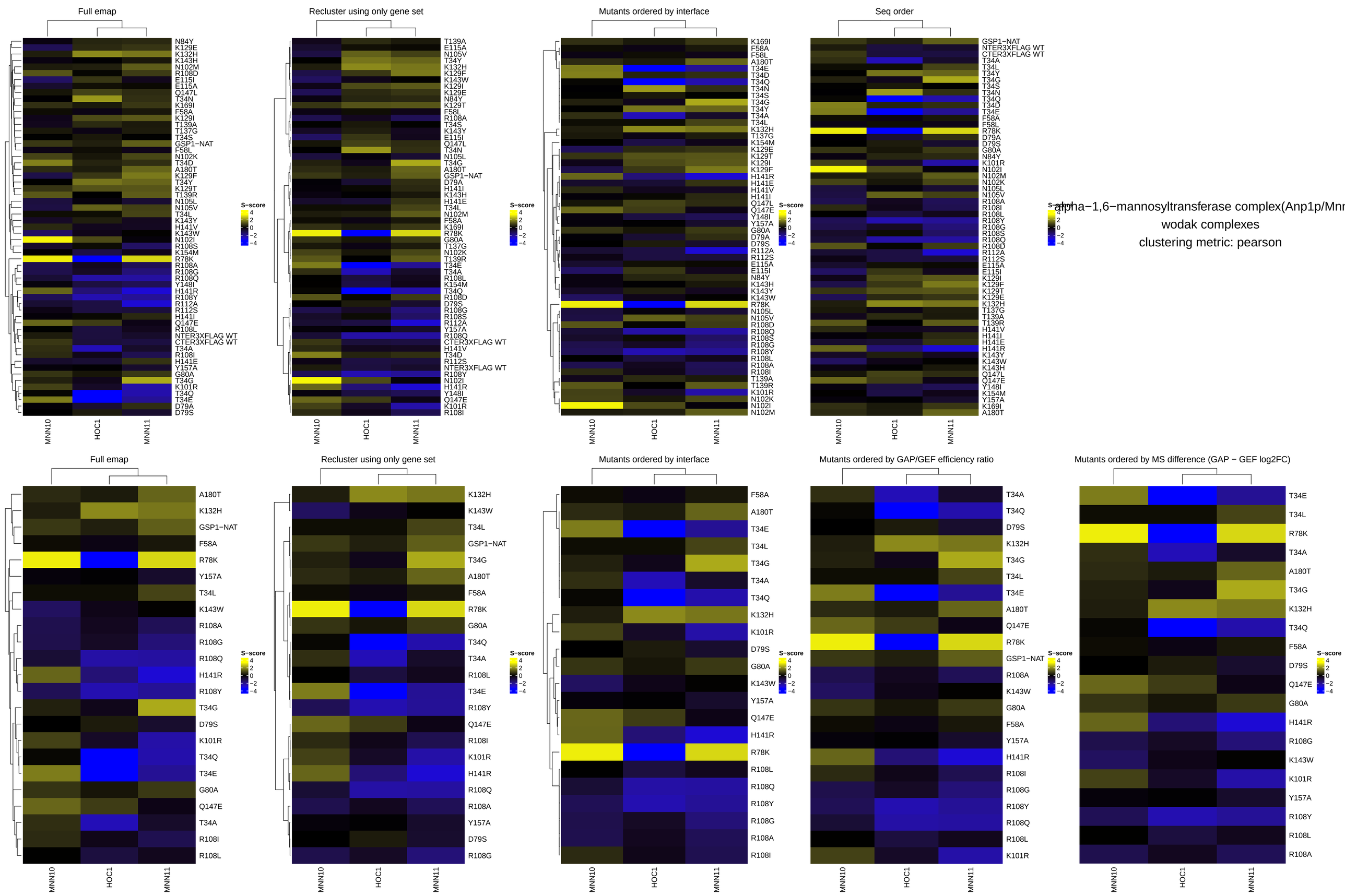
Set3p complex
wodak complexes
clustering metric: pearson

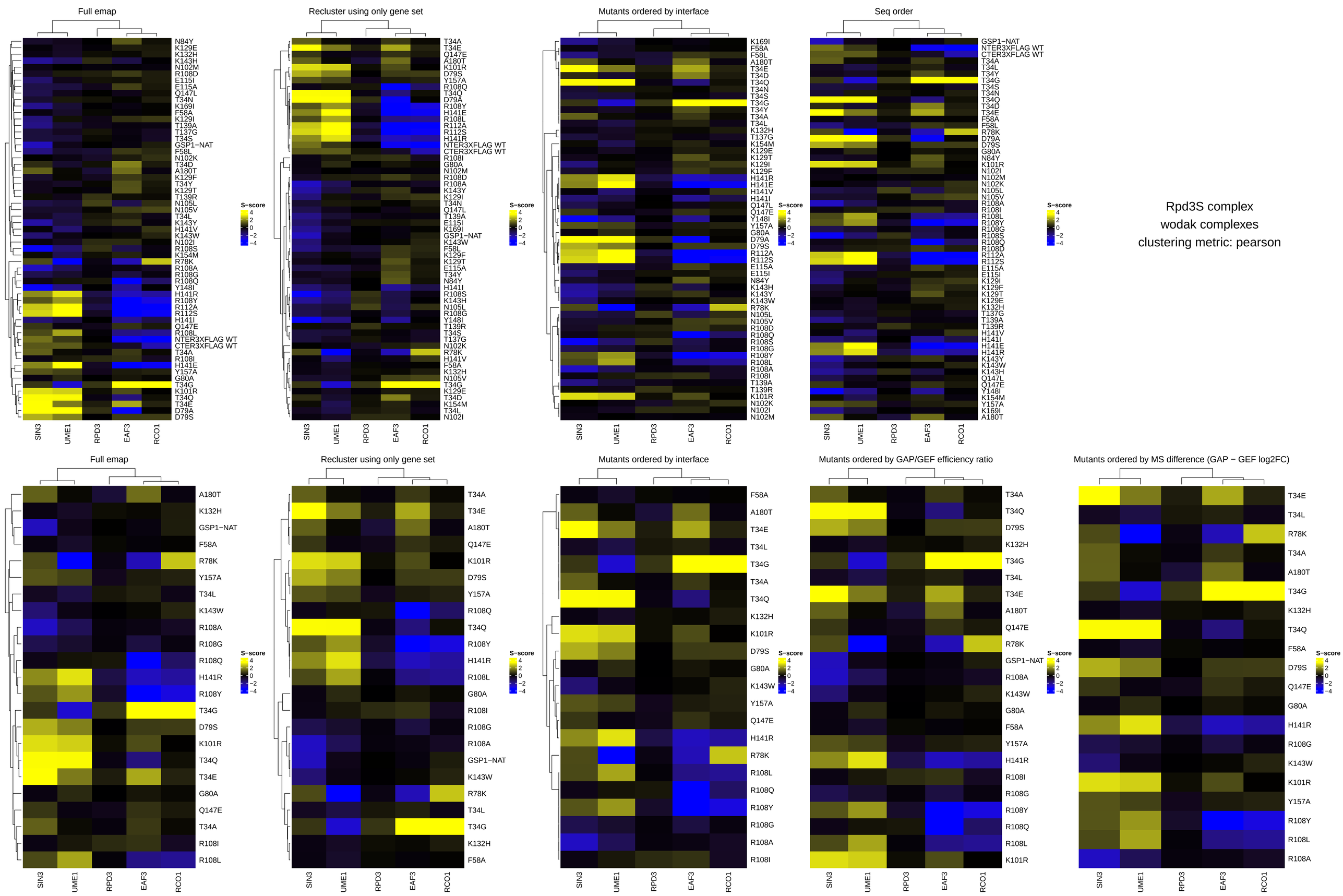

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RAD1
RAD10
RAD14
nucleotide−excision repair factor 1 complex
wodak complexes
clustering metric: pearson

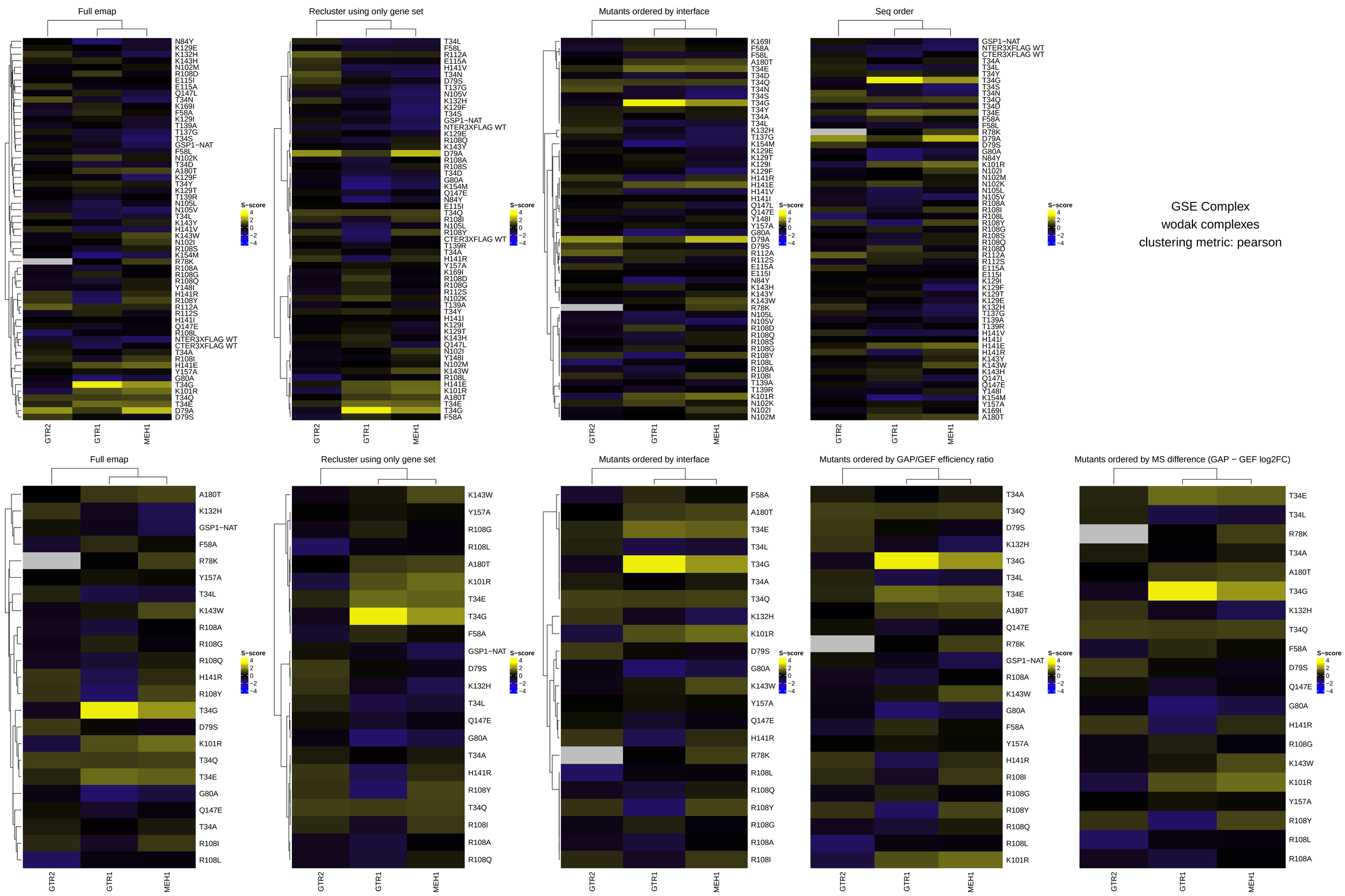

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
TOF1
CSM3
MRC1
Tof1p/Mrc1p/Csm3p complex
wodak complexes
clustering metric: pearson

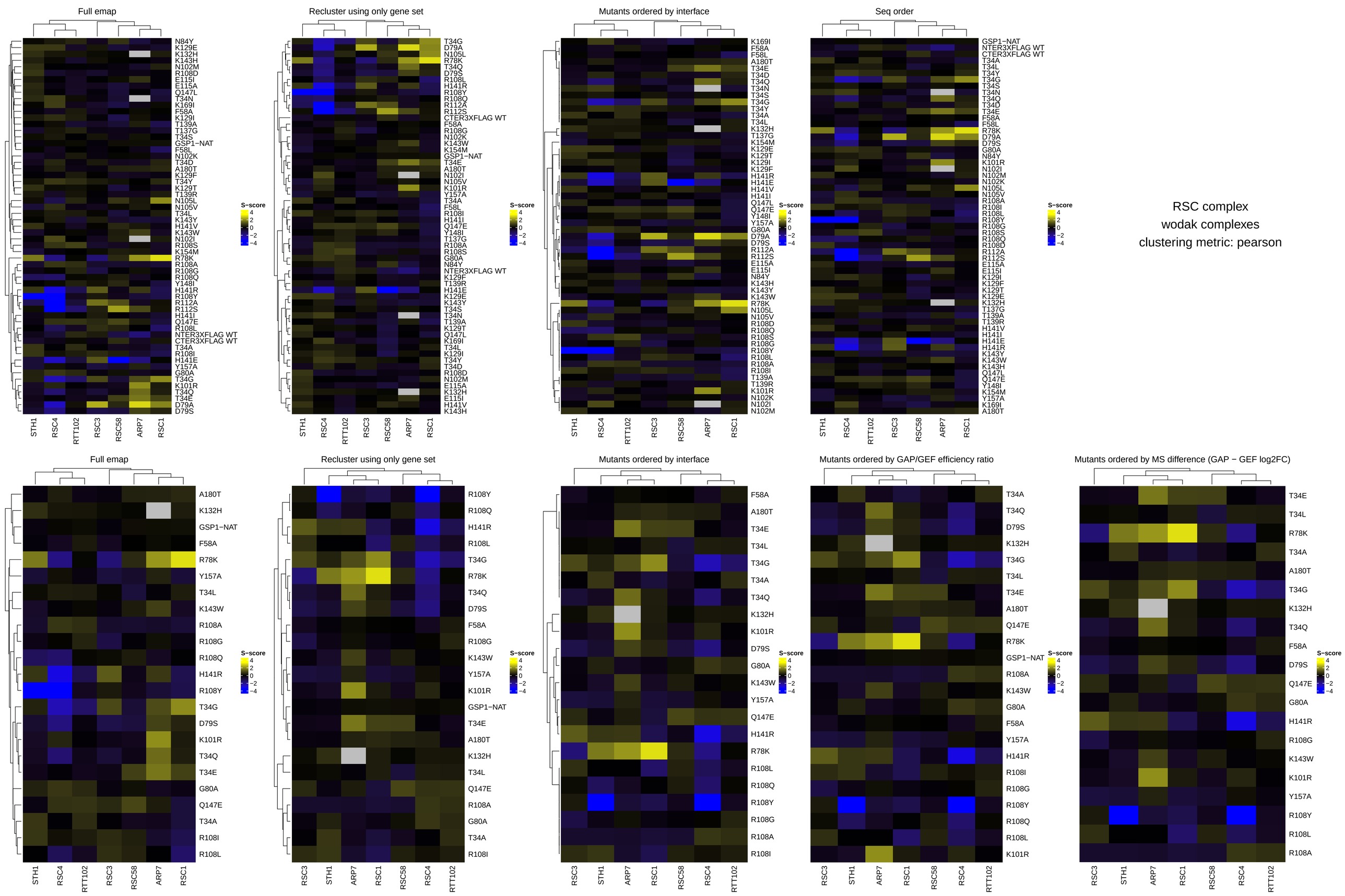

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
YAF9
SWC5
ARP4
ARP6
VPS72
SWC3
SWR1
VPS71
Swr1p complex
wodak complexes
clustering metric: pearson

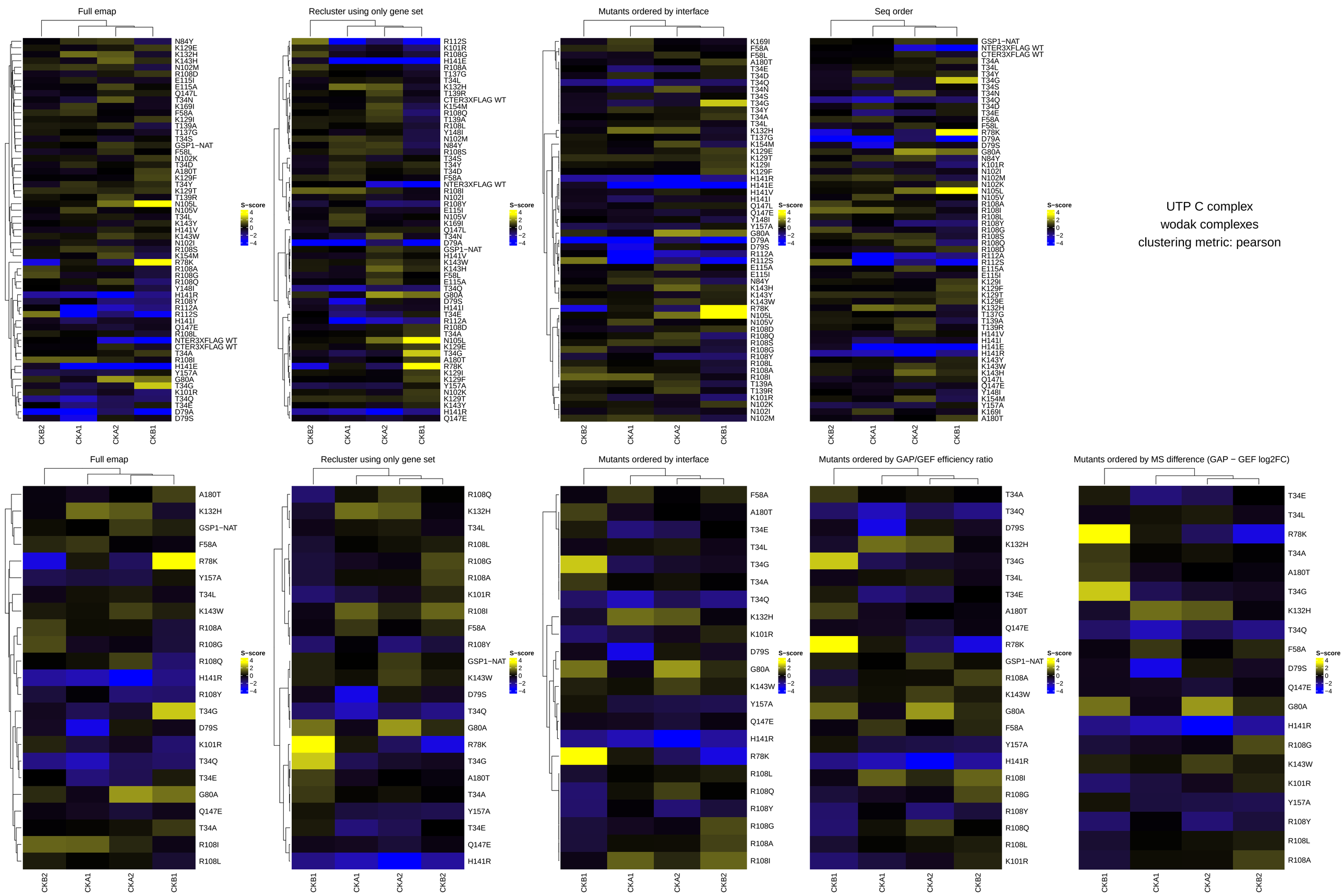

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
APC1 APC11 APC9 CDC16 CDC20 CDC23 APC2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

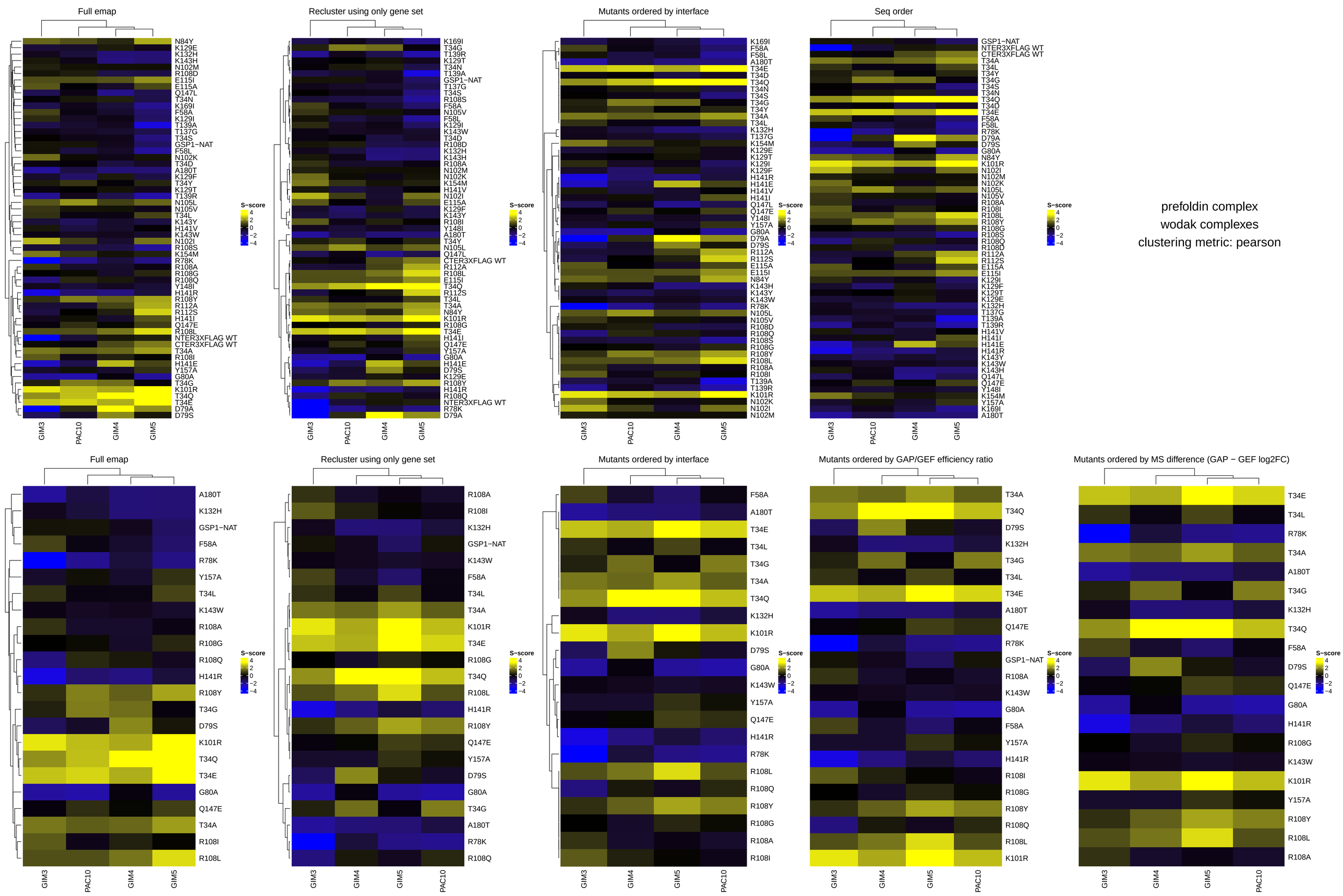

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
MNN10
HOC1
MNN11
alpha−1,6−mannosyltransferase complex(Anp1p/Mnn
wodak complexes
clustering metric: pearson

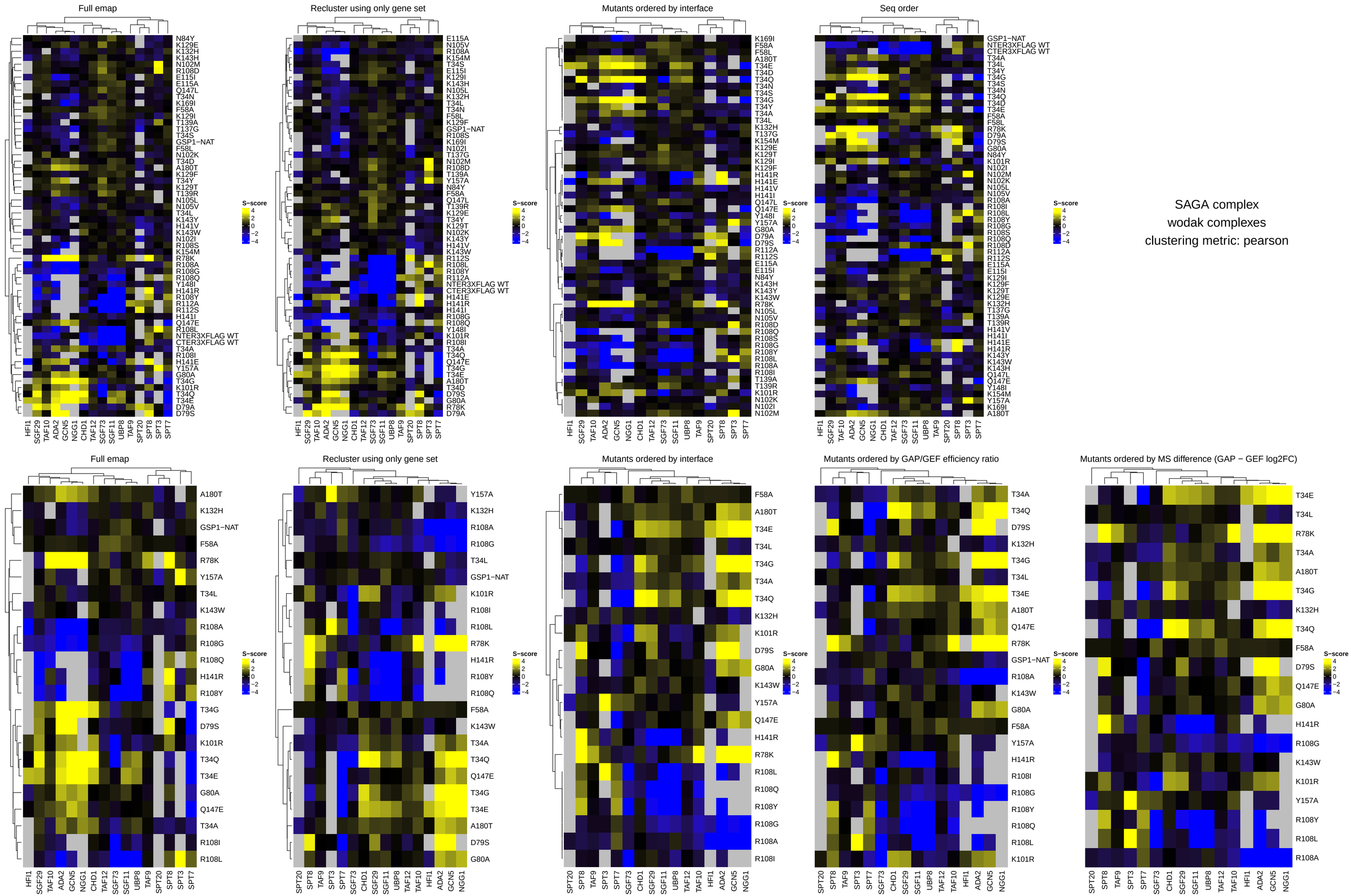

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SIN3
UME1
RPD3
EAF3
RCO1
Rpd3S complex
wodak complexes
clustering metric: pearson

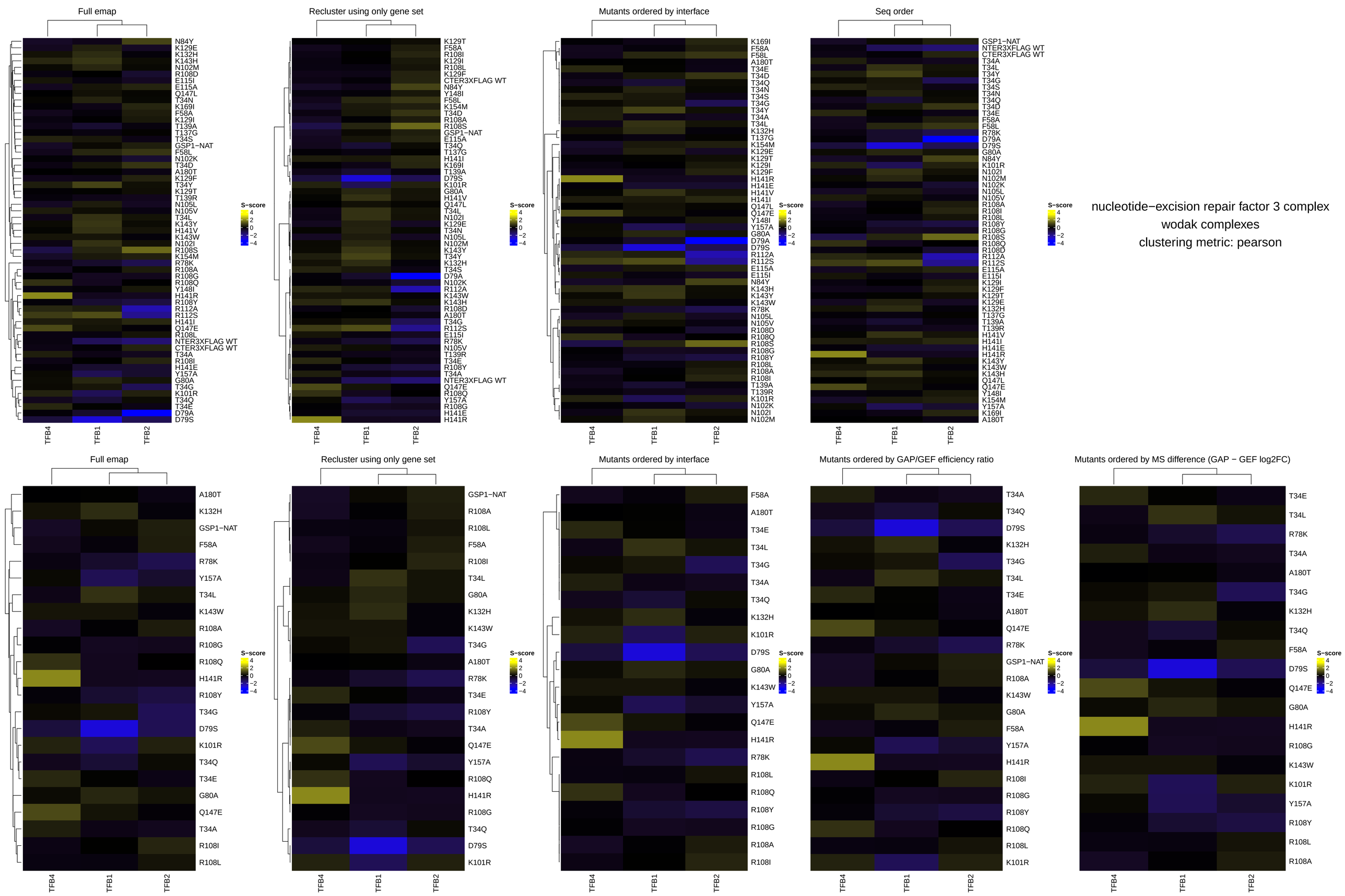

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
GTR2
GTR1
MEH1
GSE Complex
wodak complexes
clustering metric: pearson

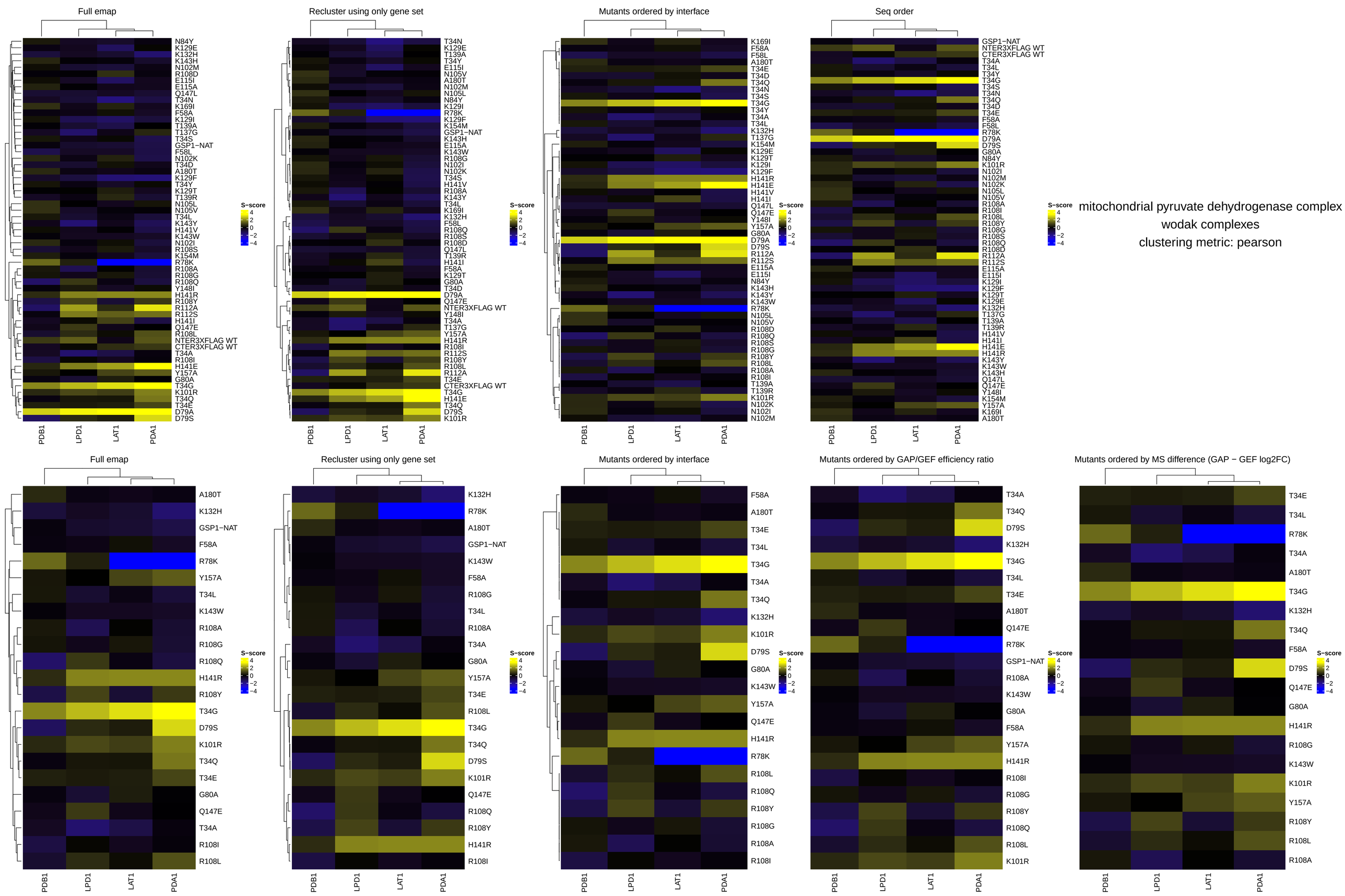

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
STH1
RSC4
RTT102
RSC3
RSC58
ARP7
RSC1
RSC complex
wodak complexes
clustering metric: pearson
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)

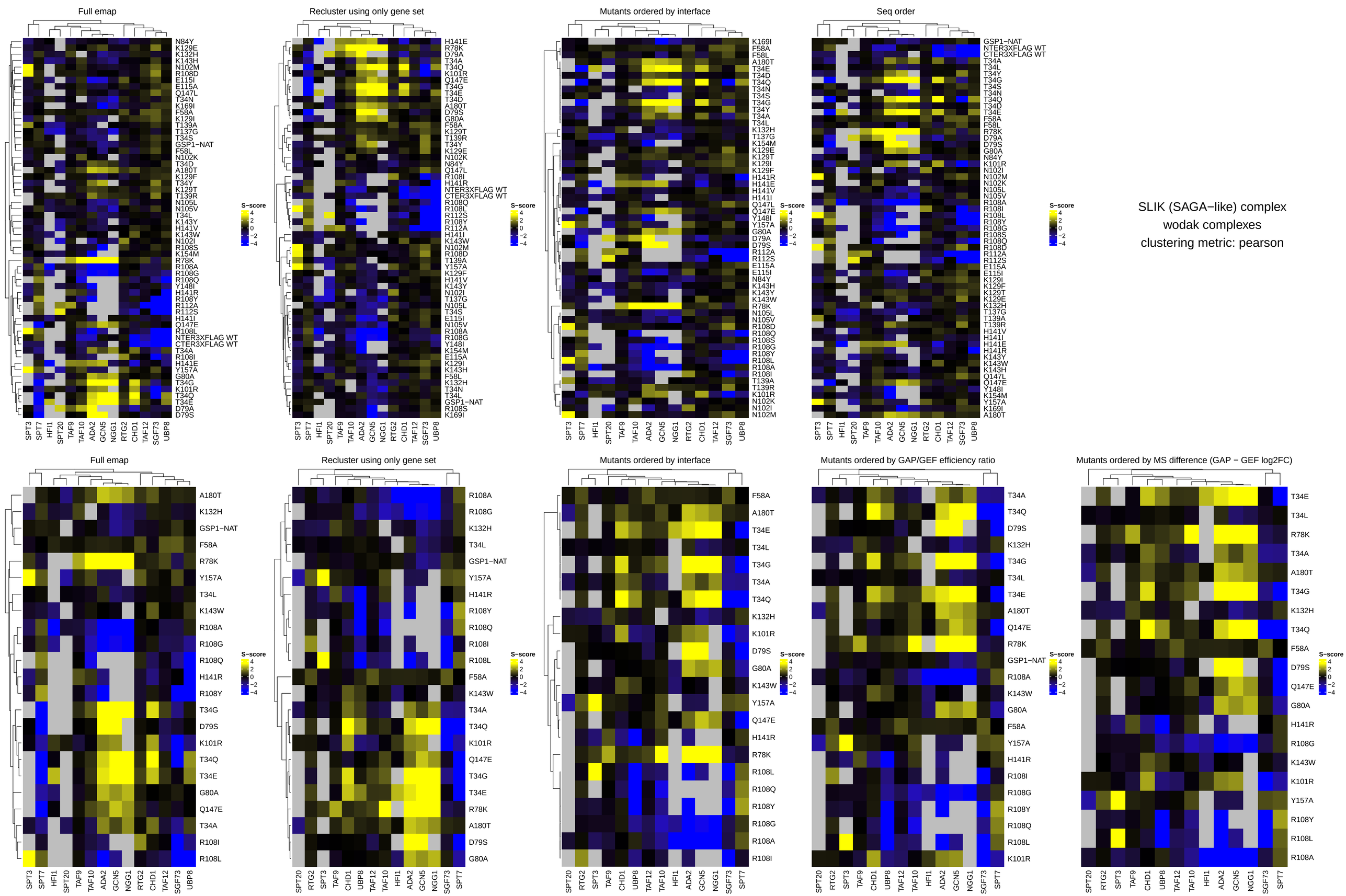

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CKB2
CKA1
CKA2
CKB1
UTP C complex
wodak complexes
clustering metric: pearson

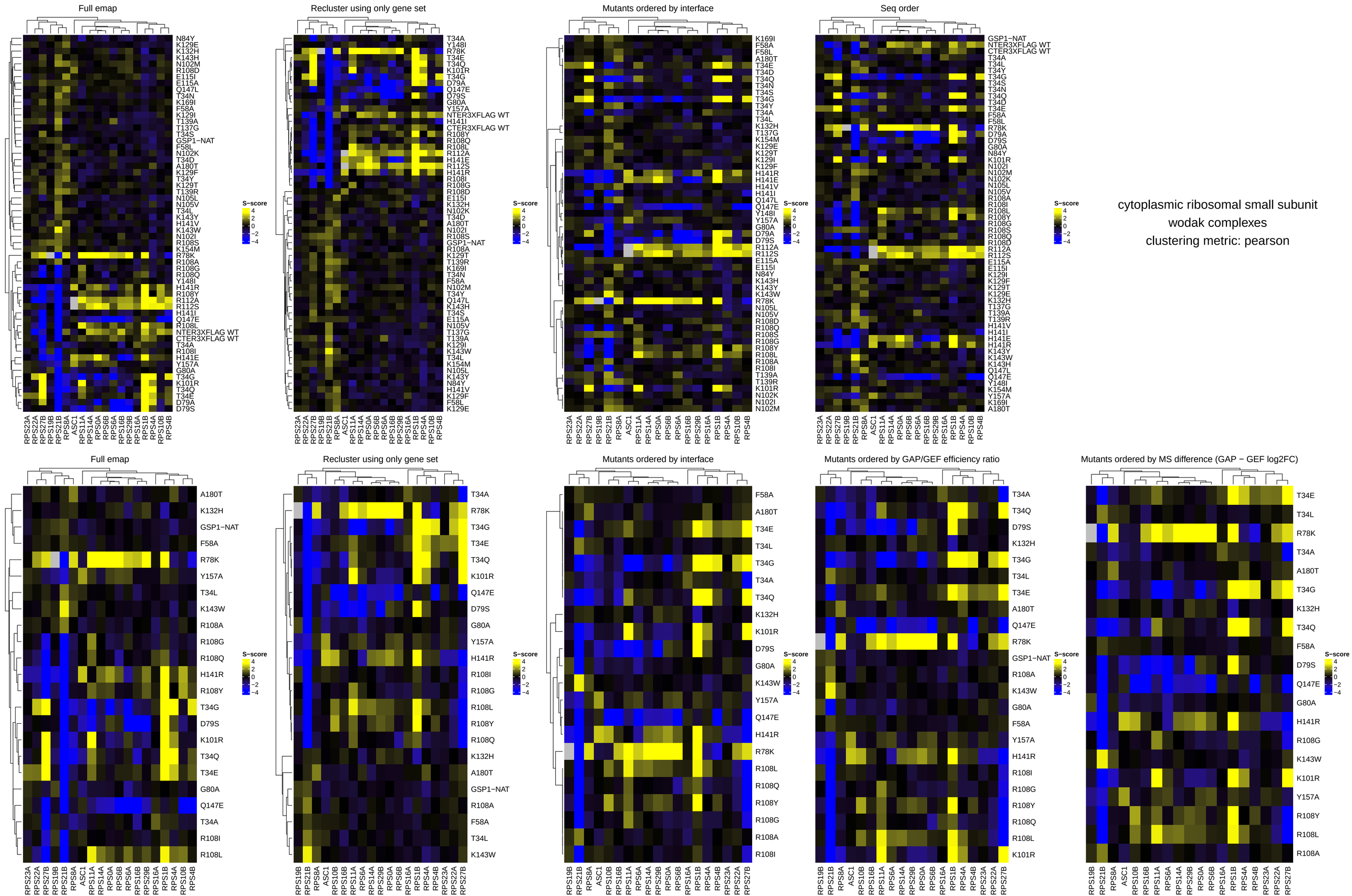

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
GIM3
PAC10
GIM4
GIM5
prefoldin complex
wodak complexes
clustering metric: pearson

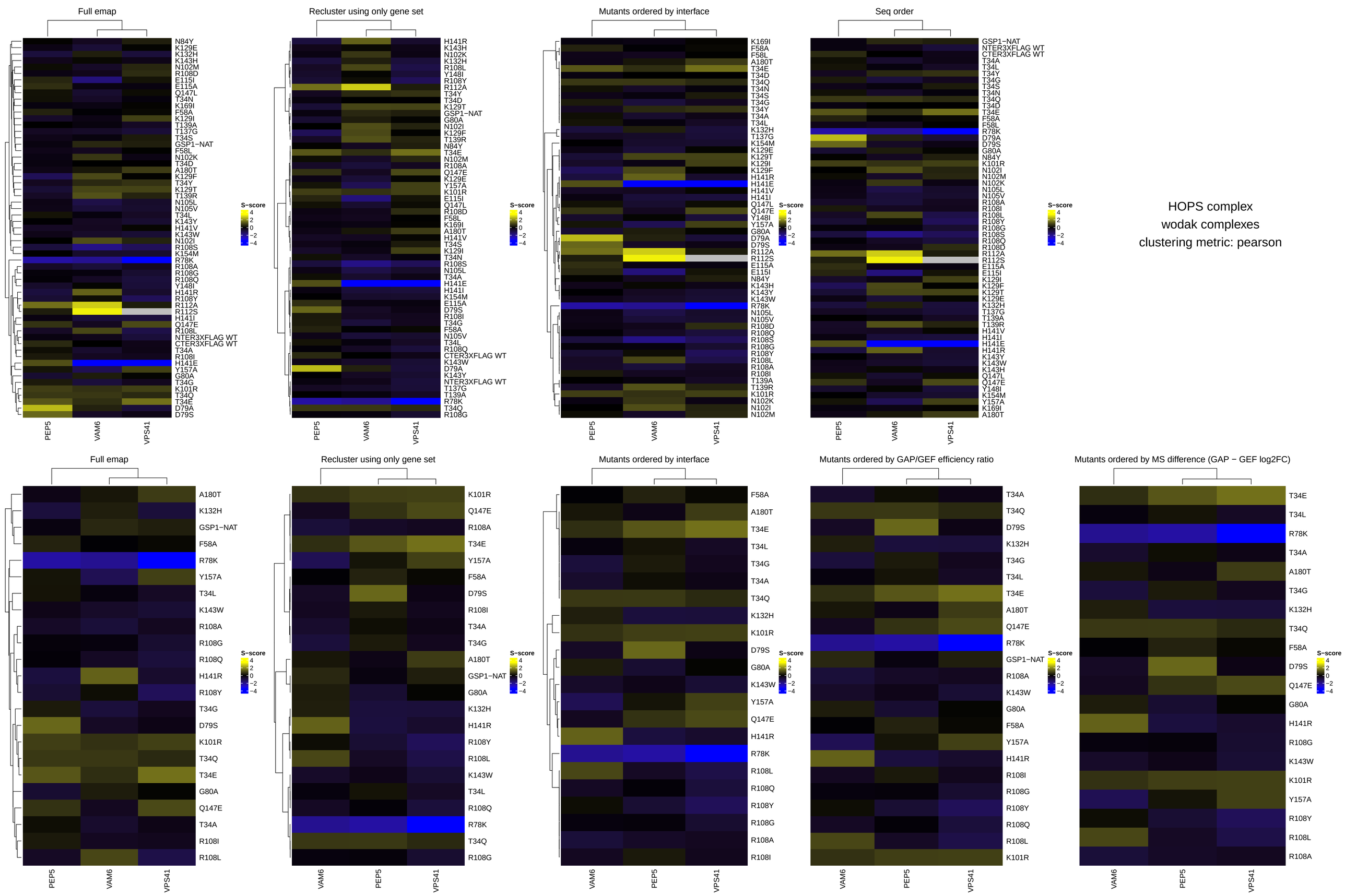

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HFI1 SGF29 TAF10 ADA2 GCN5 NGG1 CHD1 TAF12 SGF73 SGF11 UBP8 TAF9 SPT20 SPT8 SPT3 SPT7
SPT20 SPT8 TAF9 SPT3 SPT7 SGF73 CHD1 SGF29 SGF11 UBP8 TAF12 TAF10 HFI1 ADA2 GCN5 NGG1
SAGA complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TFB4
TFB1
TFB2
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: pearson


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


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SPT3 SPT7 HFI1 SPT20 TAF9 TAF10 ADA2 GCN5 NGG1 RTG2 CHD1 TAF12 SGF73 UBP8
SPT20 RTG2 SPT3 TAF9 CHD1 UBP8 TAF12 TAF10 HFI1 ADA2 GCN5 NGG1 SGF73 SPT7
SLIK (SAGA−like) complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RPS23A RPS22A RPS27B RPS19B RPS21B RPS8A ASC1 RPS11A RPS14A RPS0A RPS6B RPS6A RPS16B RPS29B RPS16A RPS1B RPS4A RPS10B RPS4B
cytoplasmic ribosomal small subunit
wodak complexes
clustering metric: pearson


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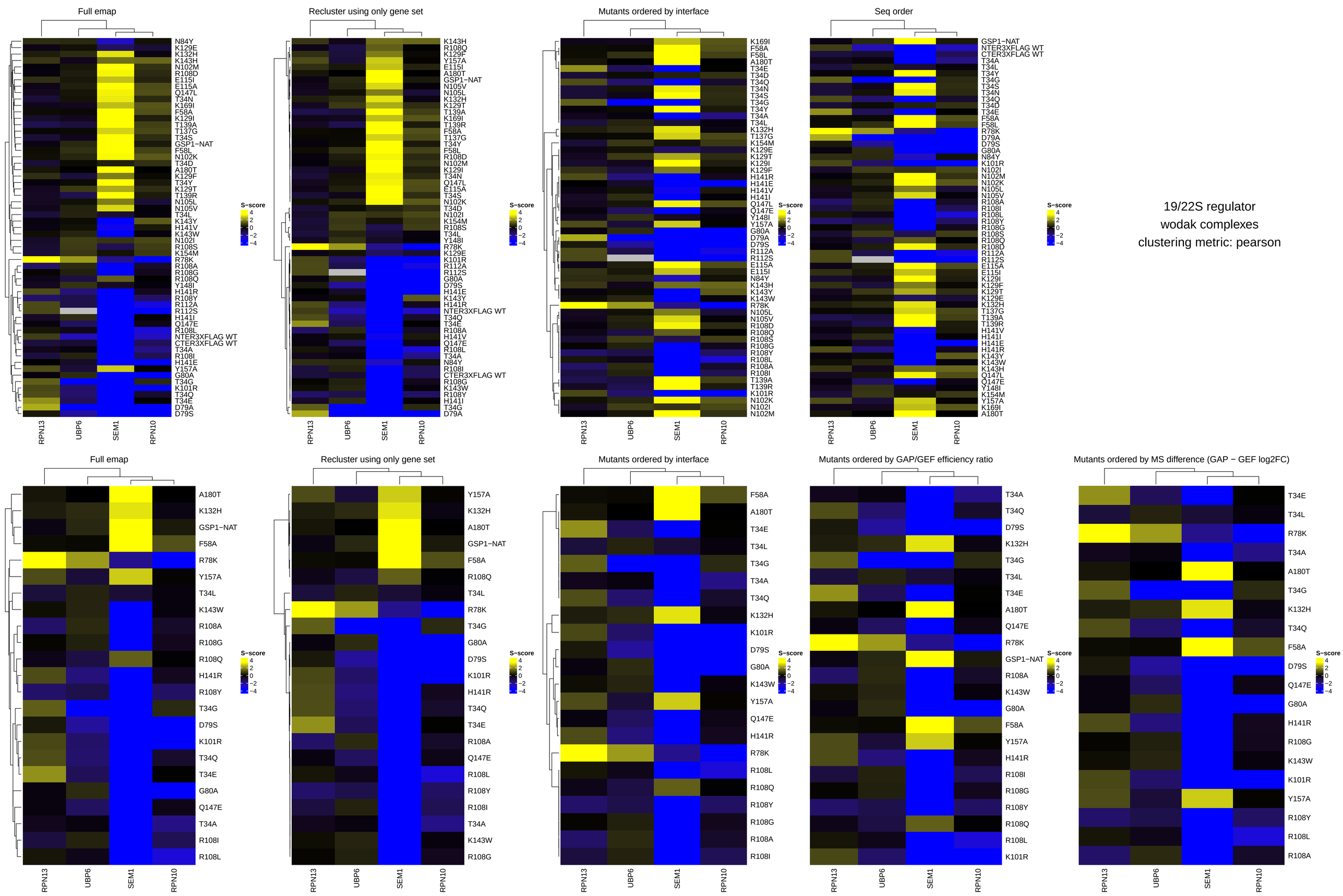
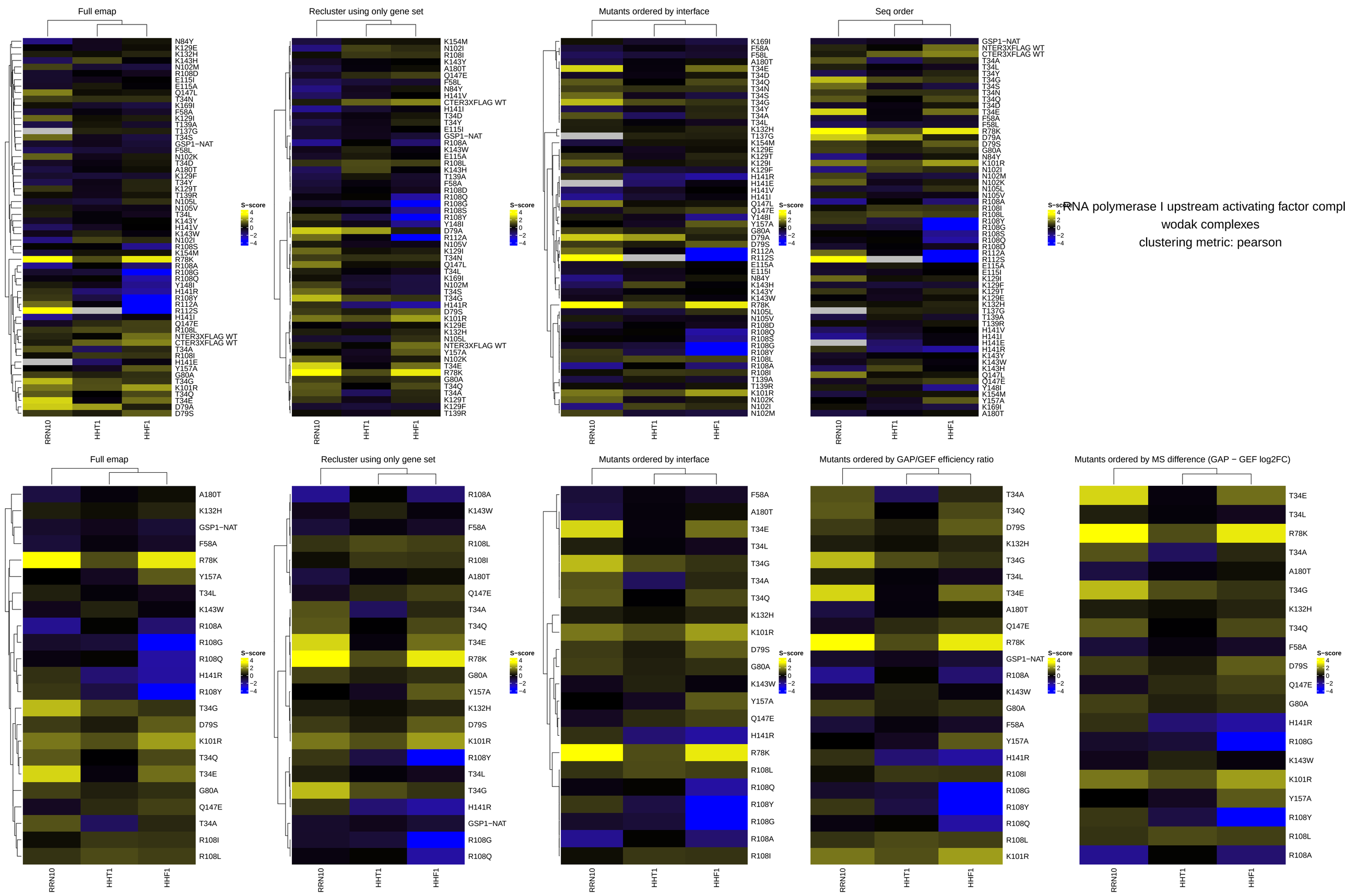
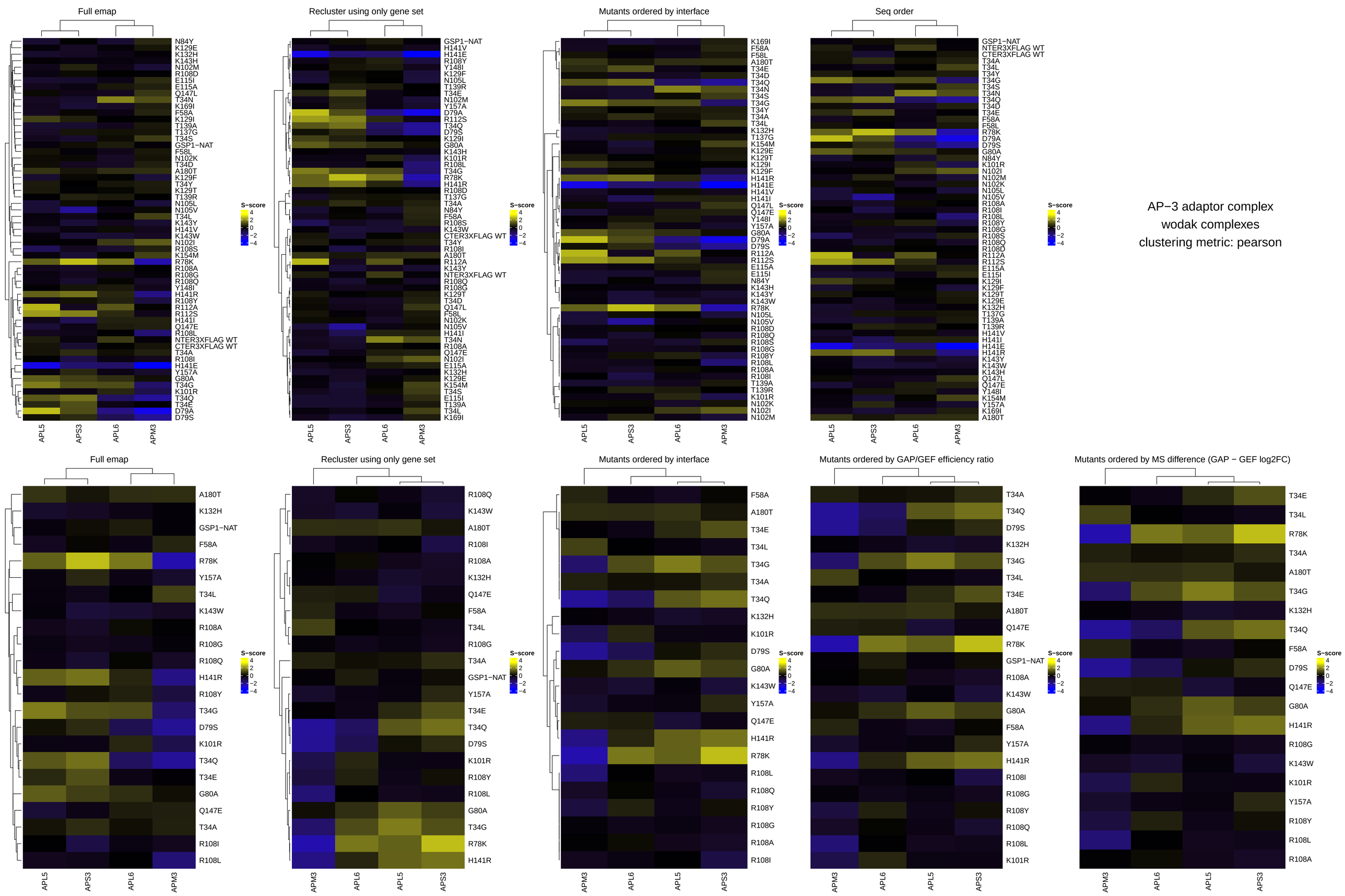
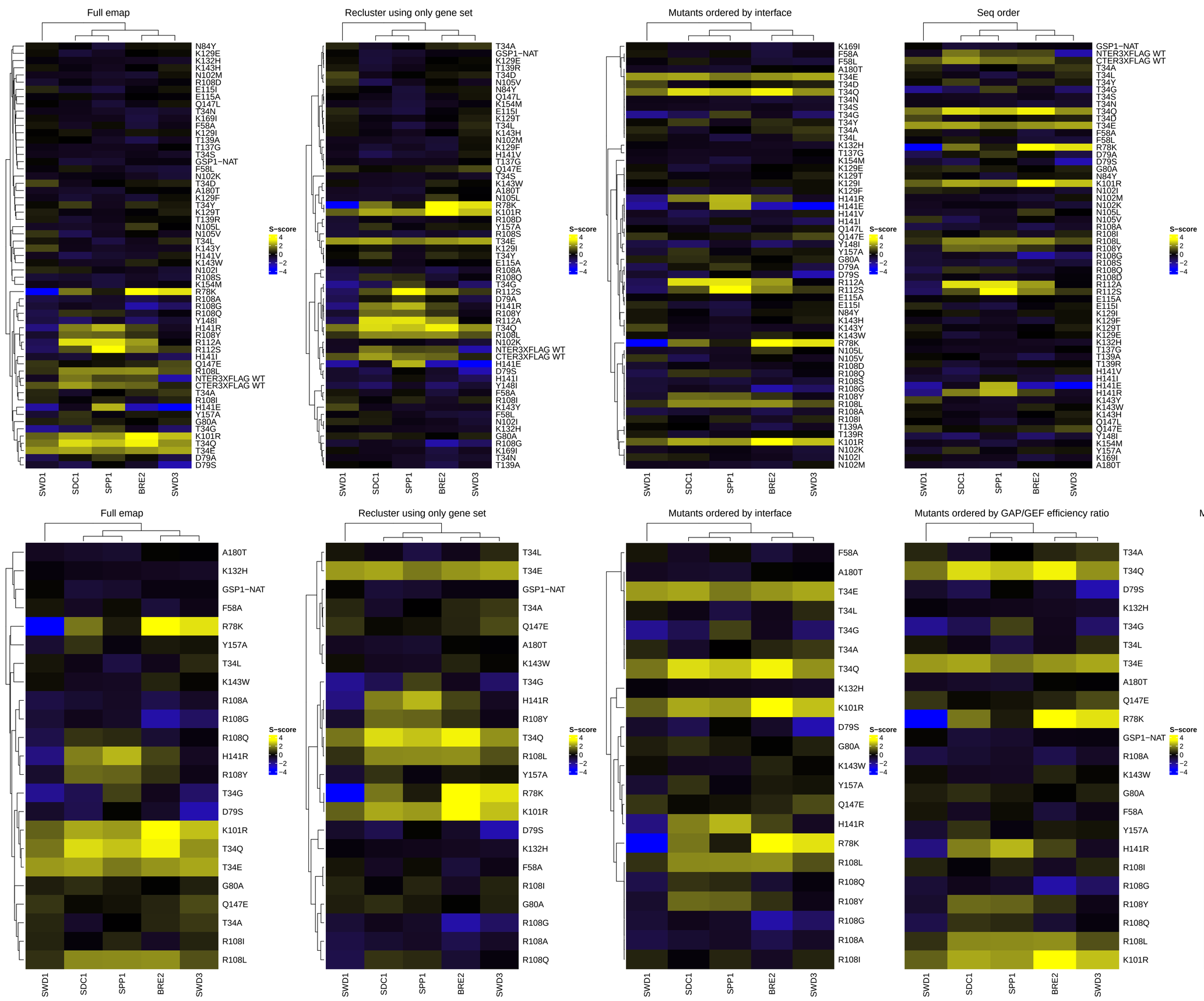
2
0
−2
−4
PEP5
VAM6
VPS41
HOPS complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
RPN13
UBP6
SEM1
RPN10
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
19/22S regulator
wodak complexes
clustering metric: pearson

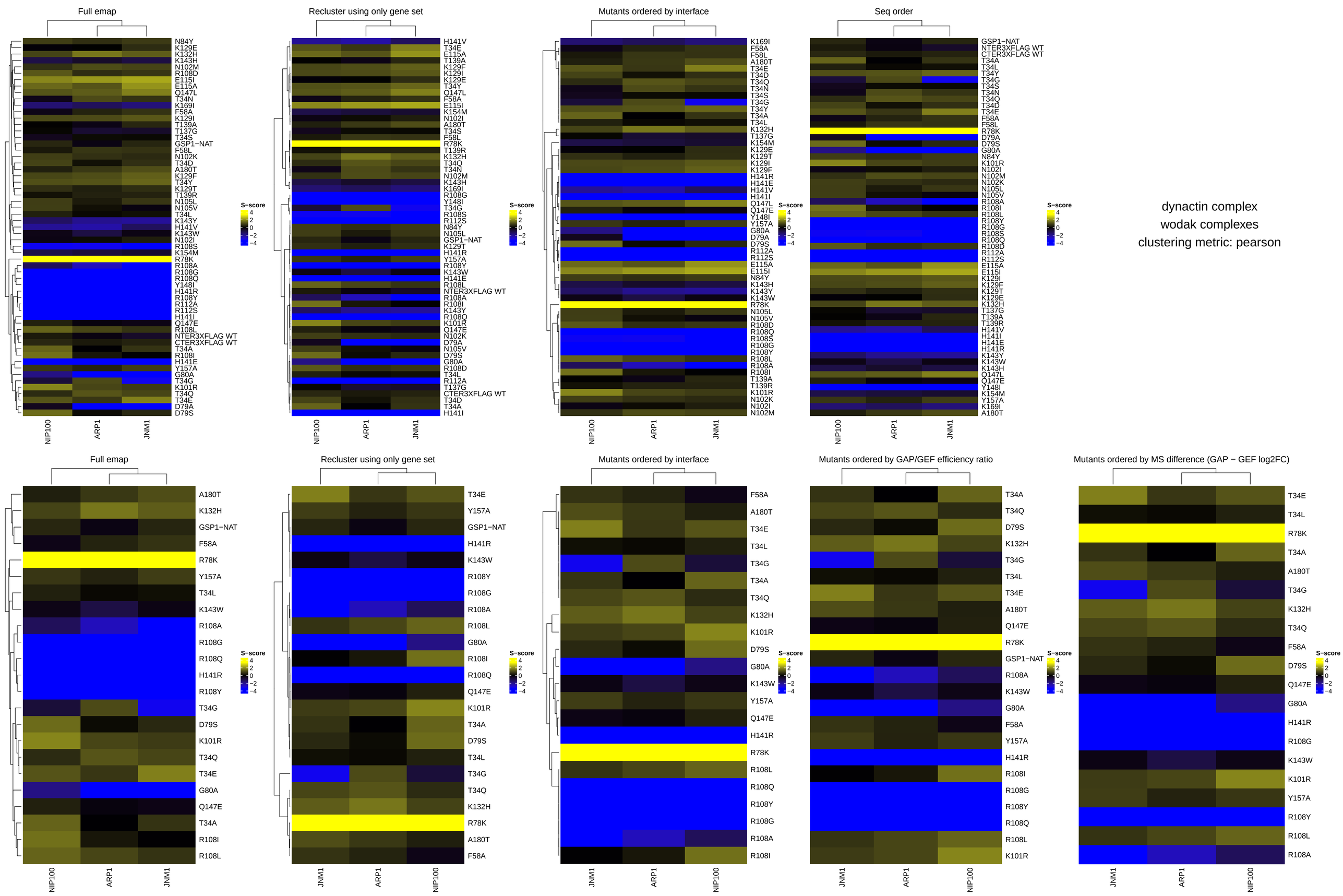


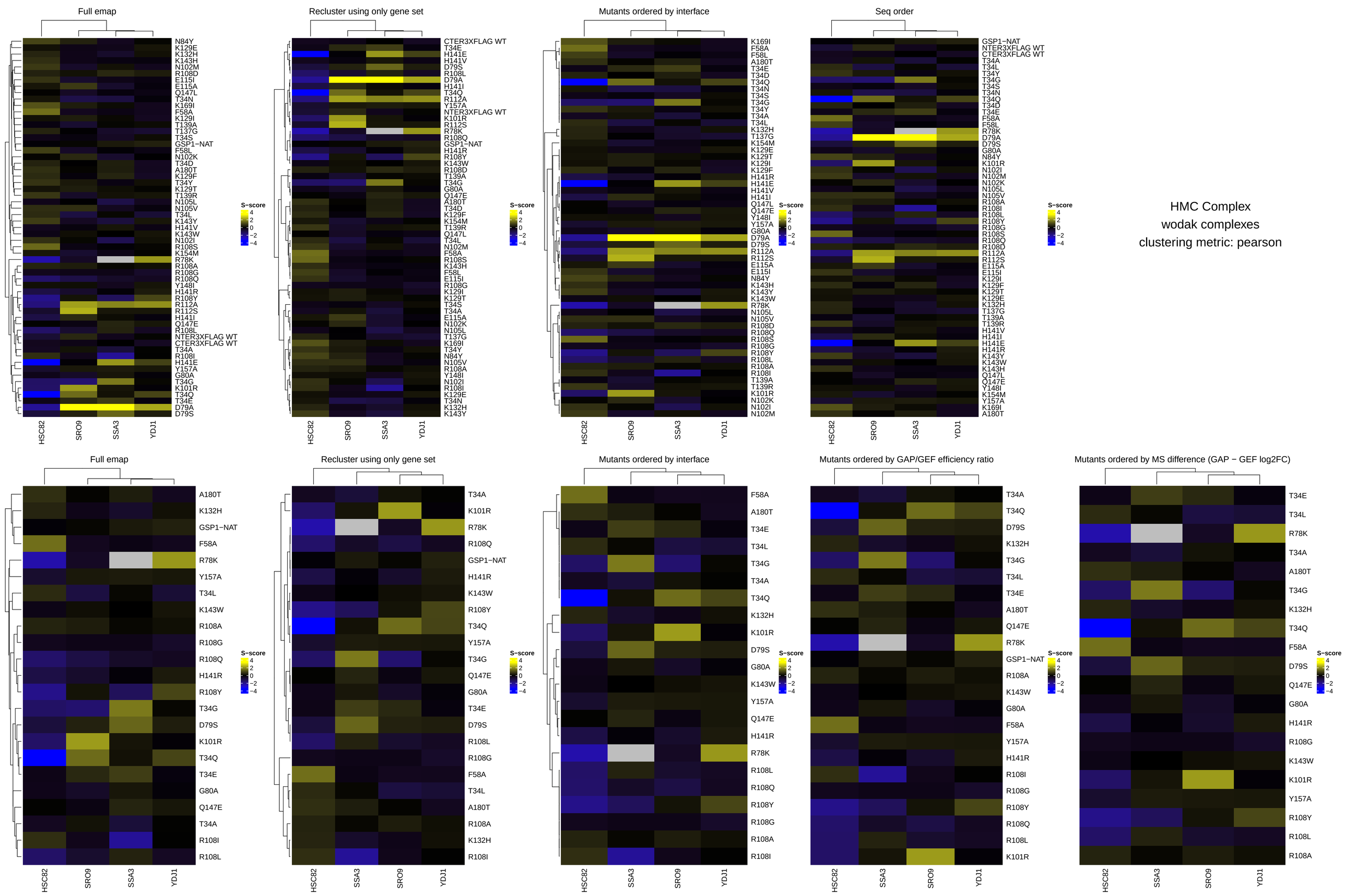
RNA polymerase I upstream activating factor compl
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
APL5
APS3
APL6
APM3
AP−3 adaptor complex
wodak complexes
clustering metric: pearson



COMPASS complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
NIP100
ARP1
JNM1
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)
dynactin complex
wodak complexes
clustering metric: pearson


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
HSC82
SRO9
SSA3
YDJ1
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)
HMC Complex
wodak complexes
clustering metric: pearson