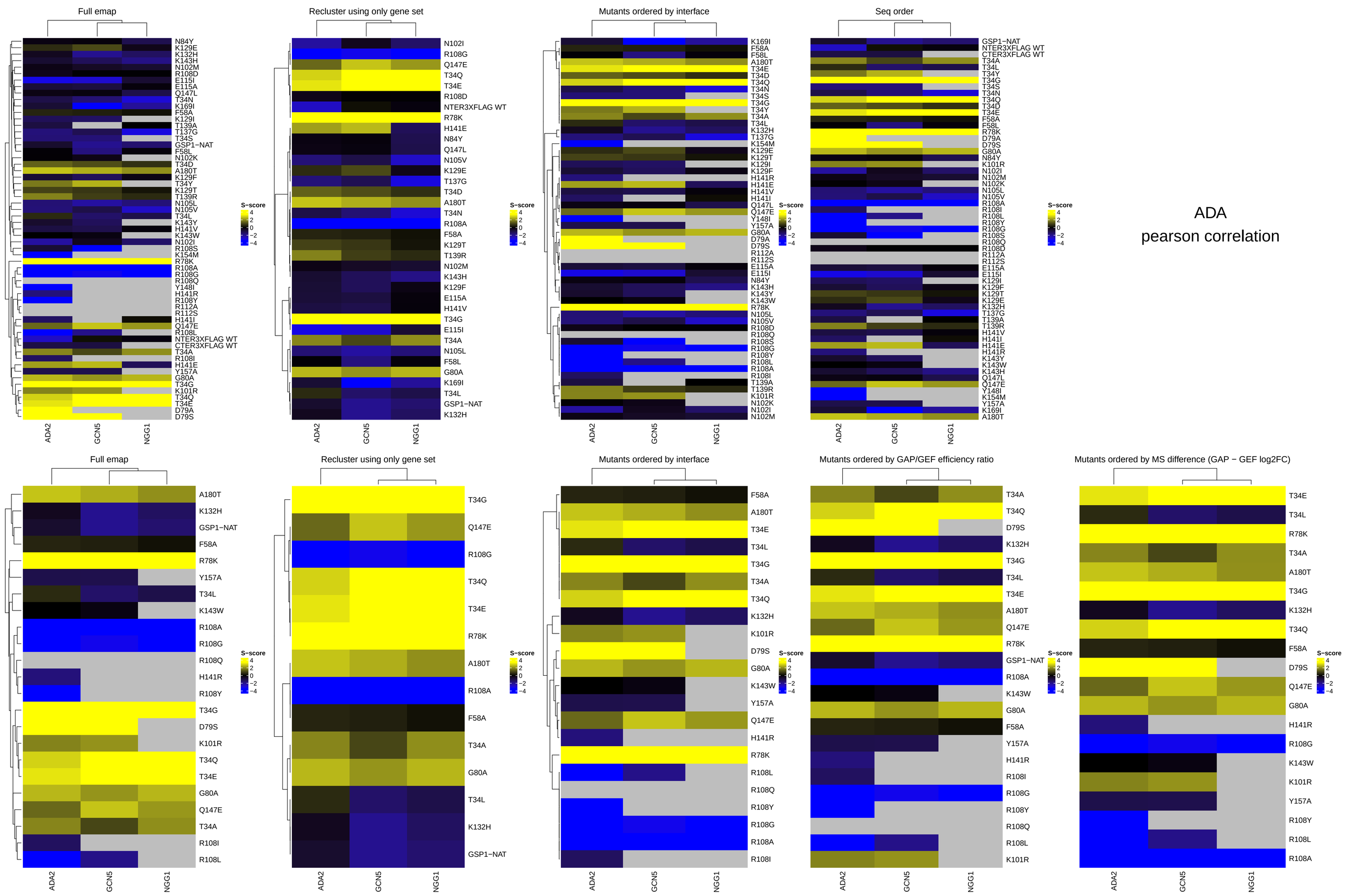
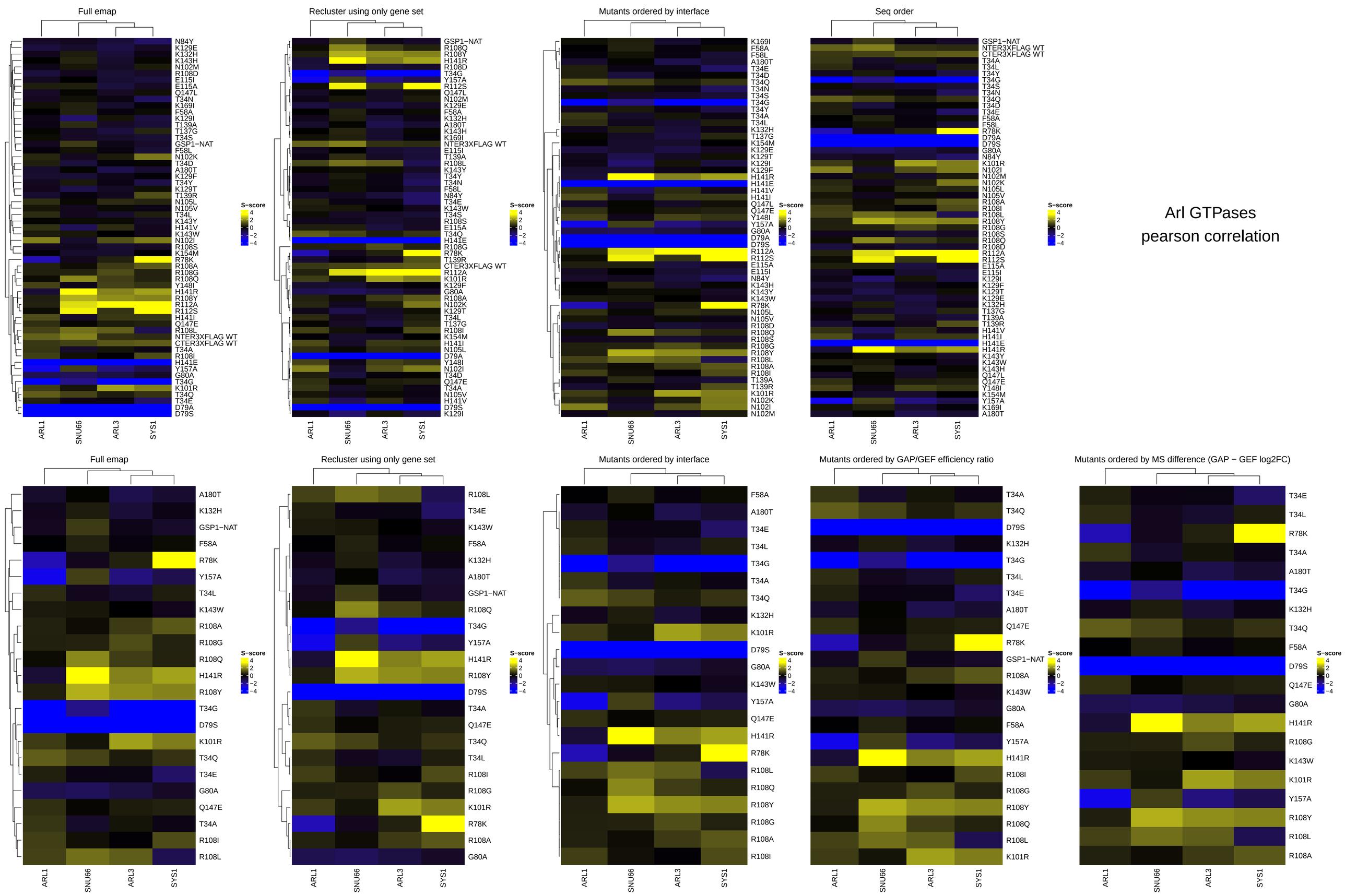
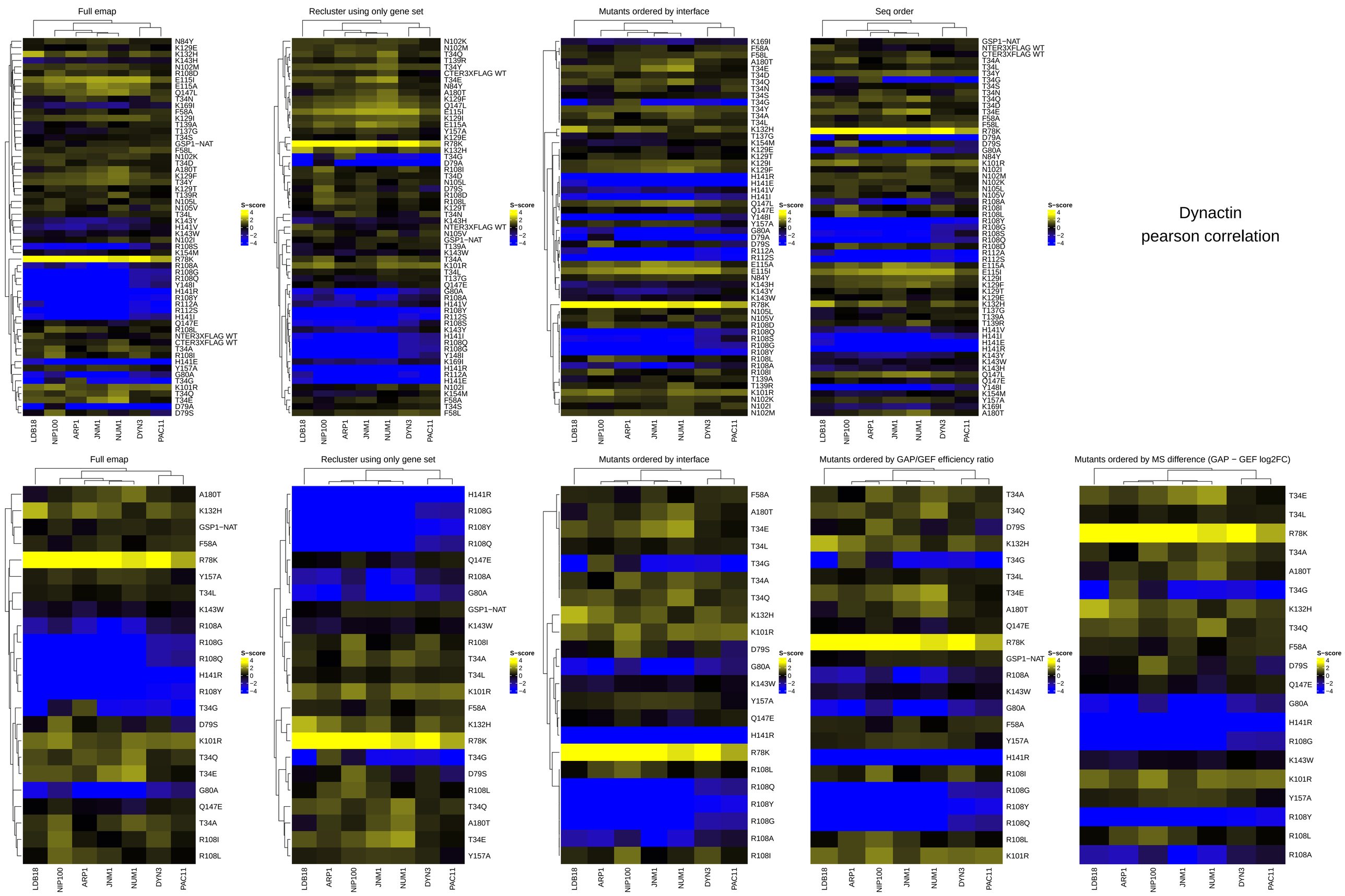
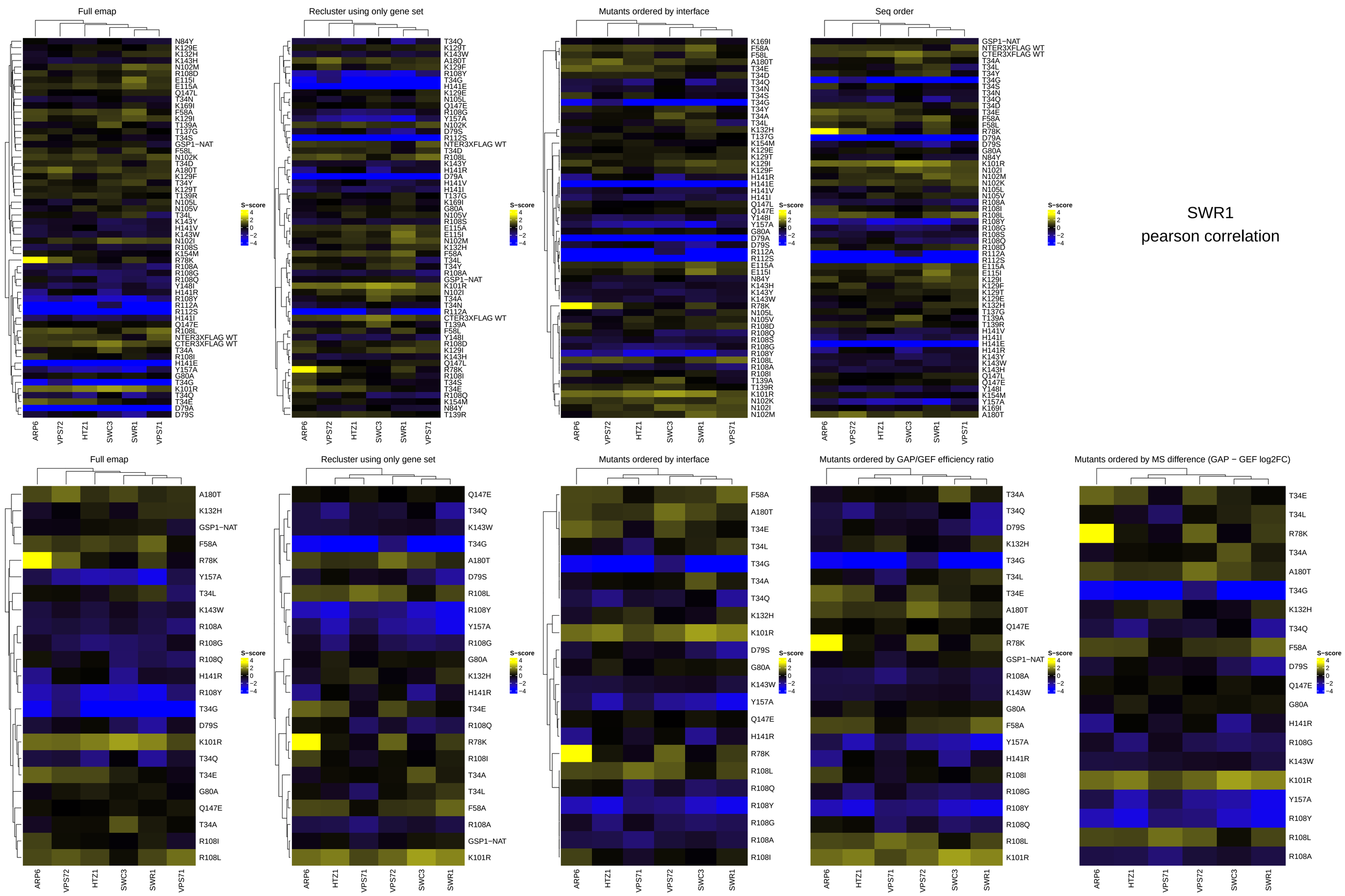
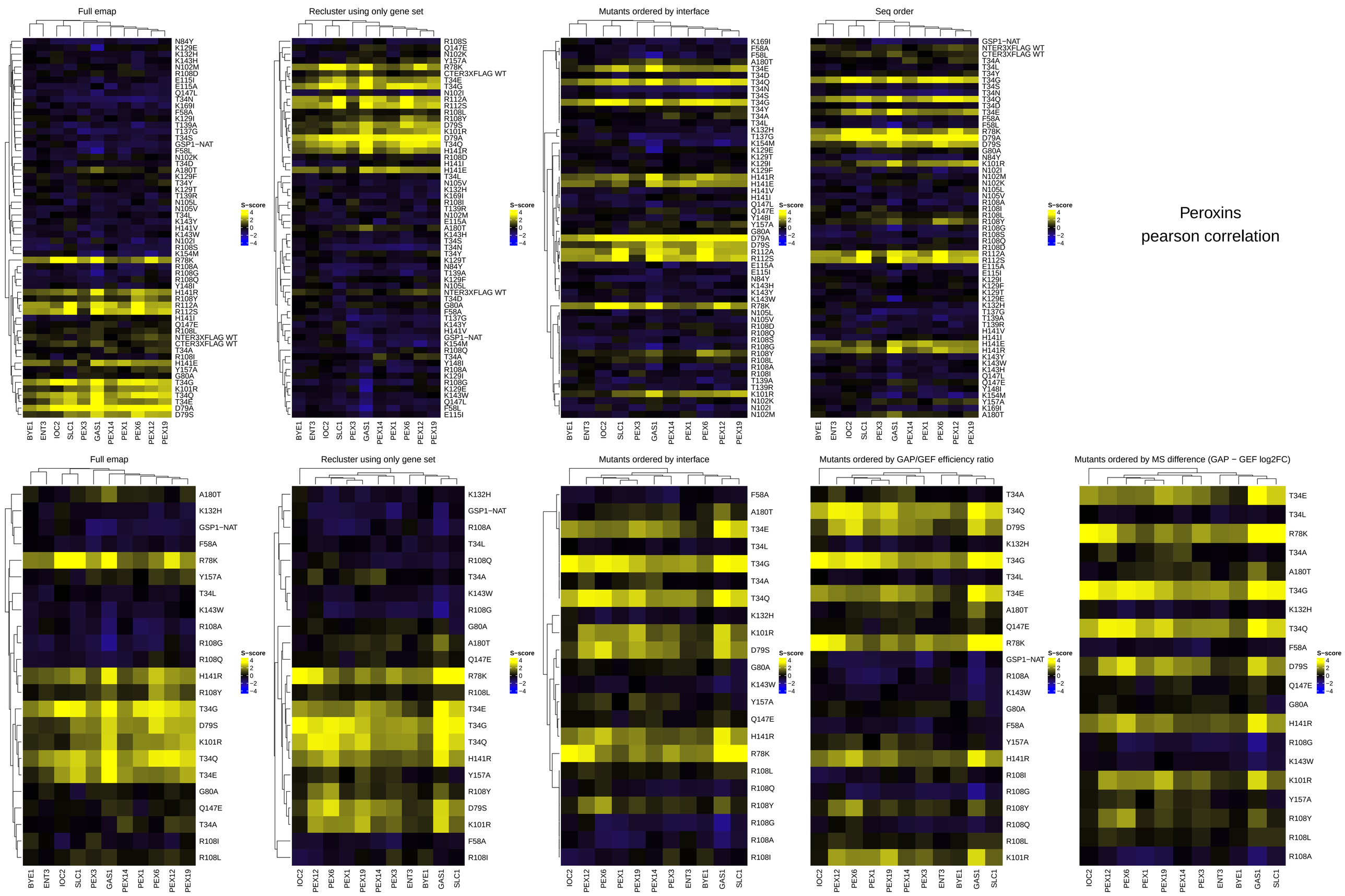
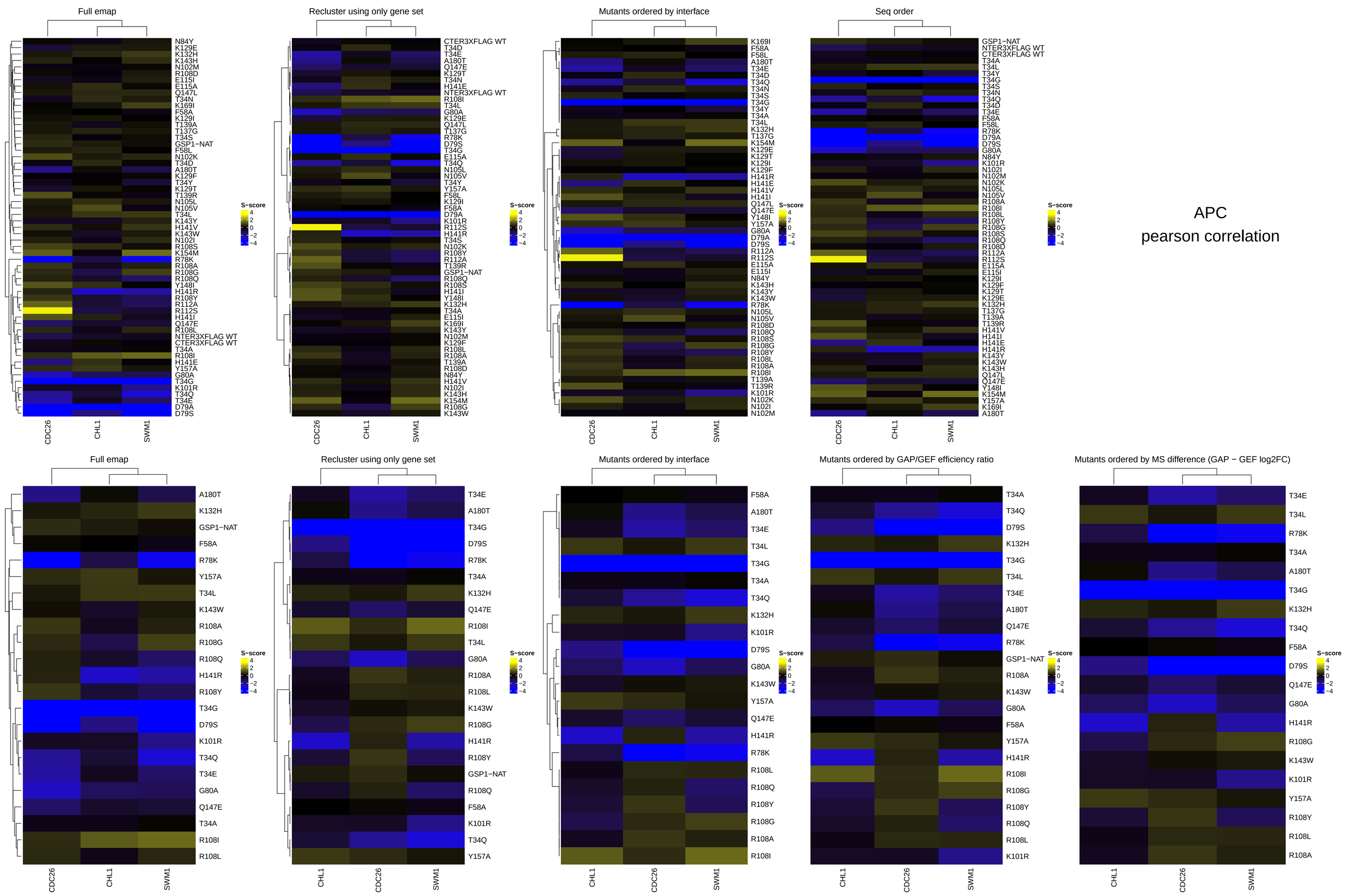

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ADA2
GCN5
NGG1
ADA
pearson correlation


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
ARL1
SNU66
ARL3
SYS1
Arl GTPases
pearson correlation

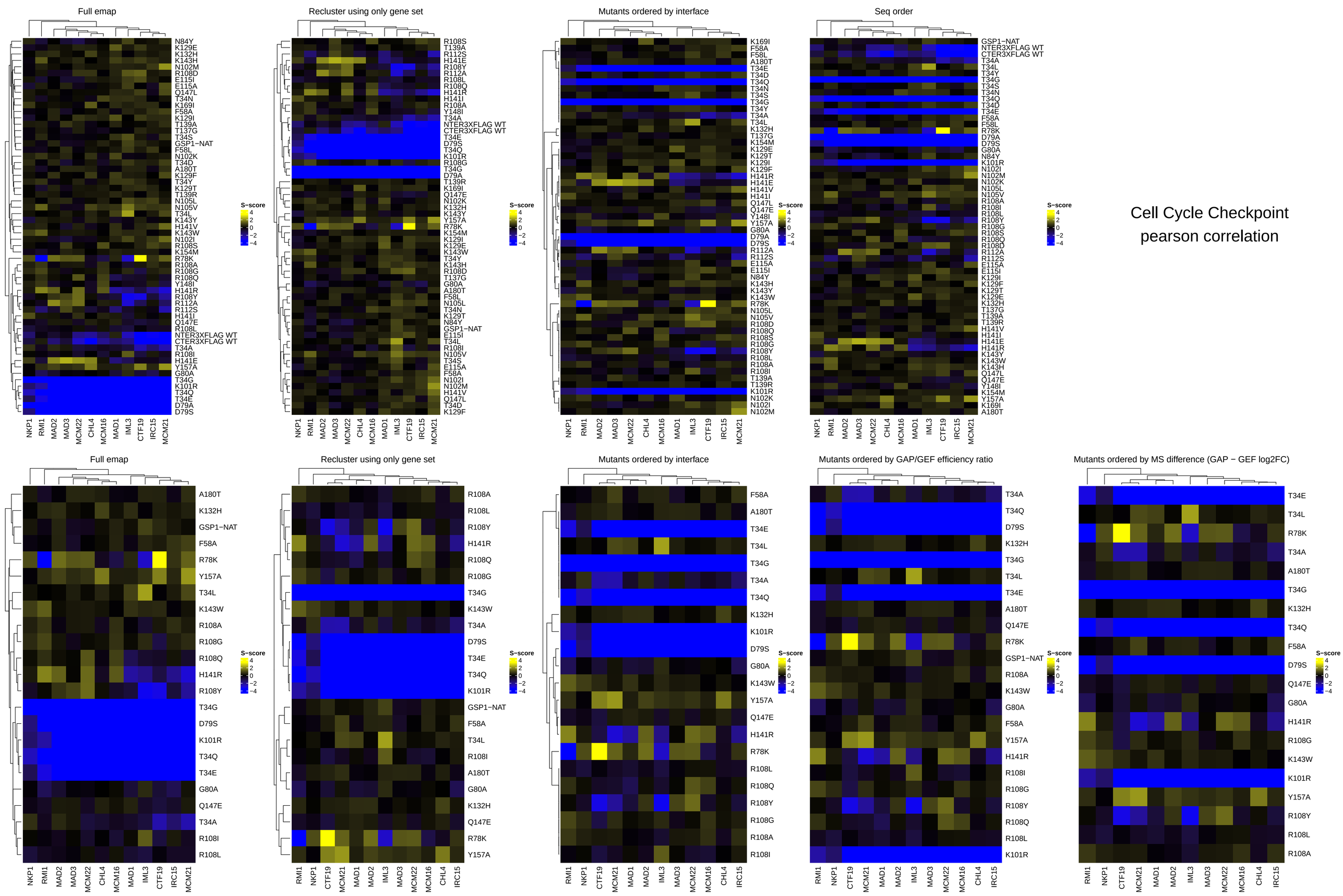

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
LDB18
NIP100
ARP1
JNM1
NUM1
DYN3
PAC11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


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
pearson correlation

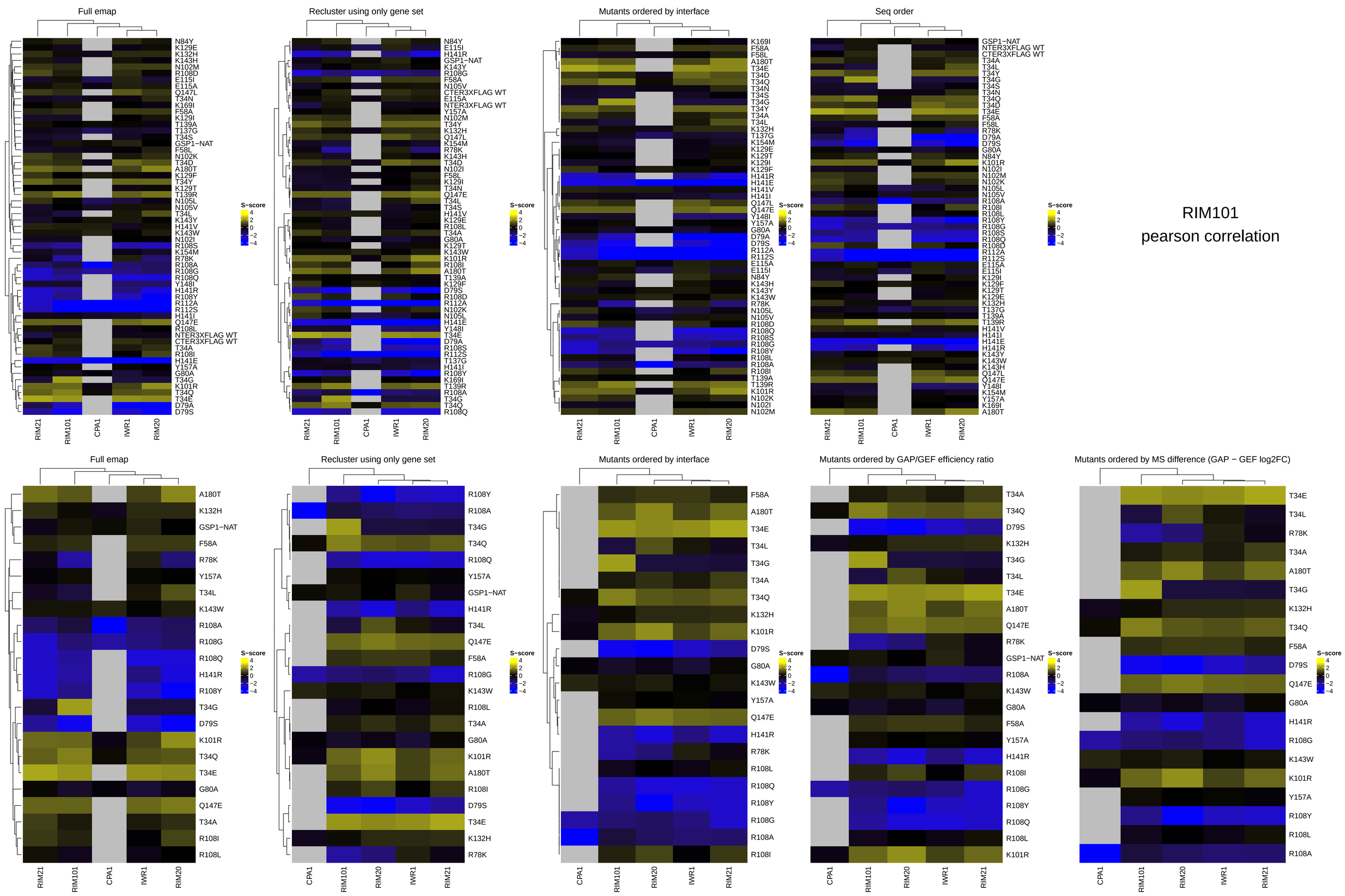

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
BYE1
ENT3
IOC2
SLC1
PEX3
GAS1
PEX14
PEX1
PEX6
PEX12
PEX19
Peroxins
pearson correlation



APC
pearson correlation



Cell Cycle Checkpoint
pearson correlation


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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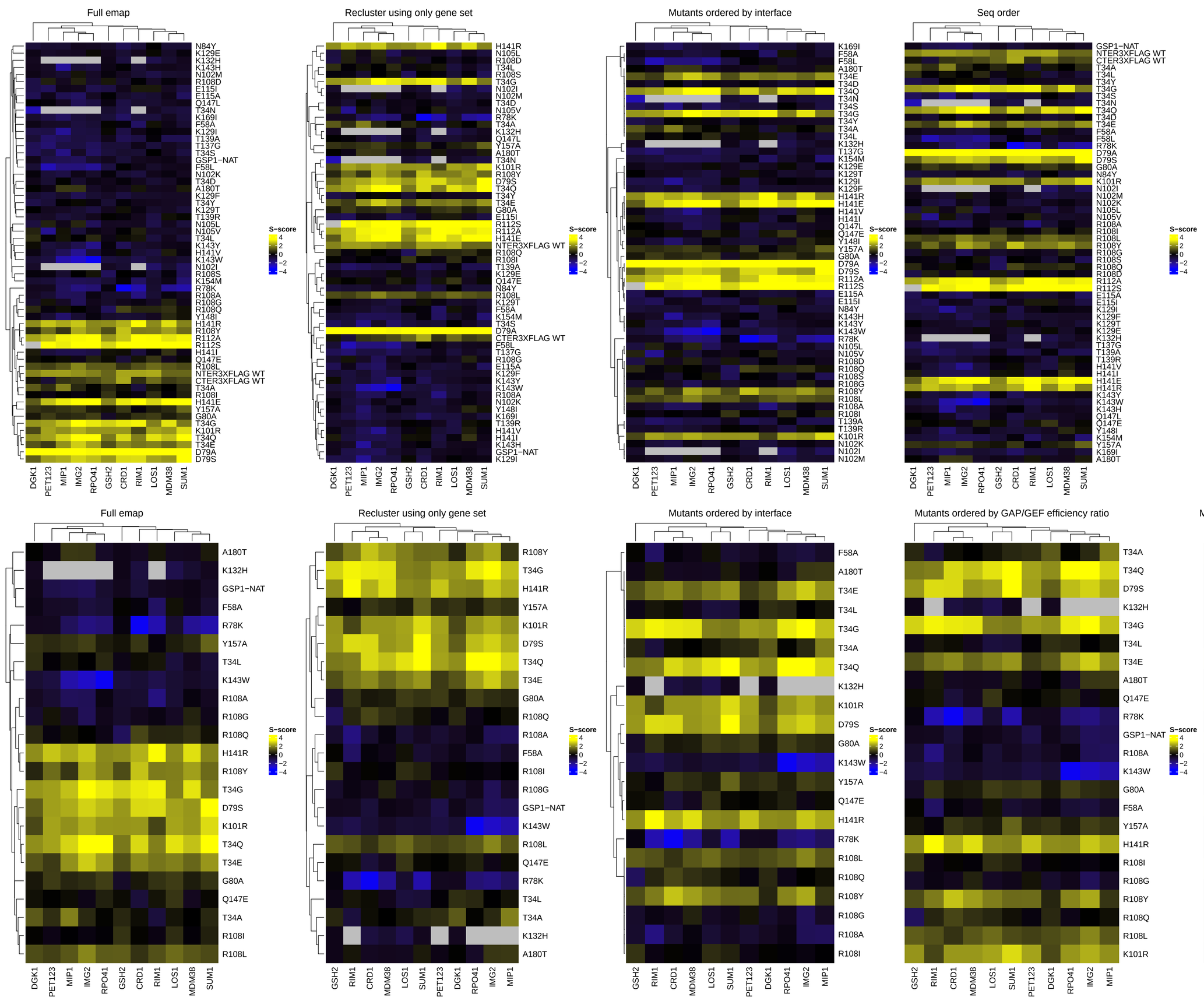
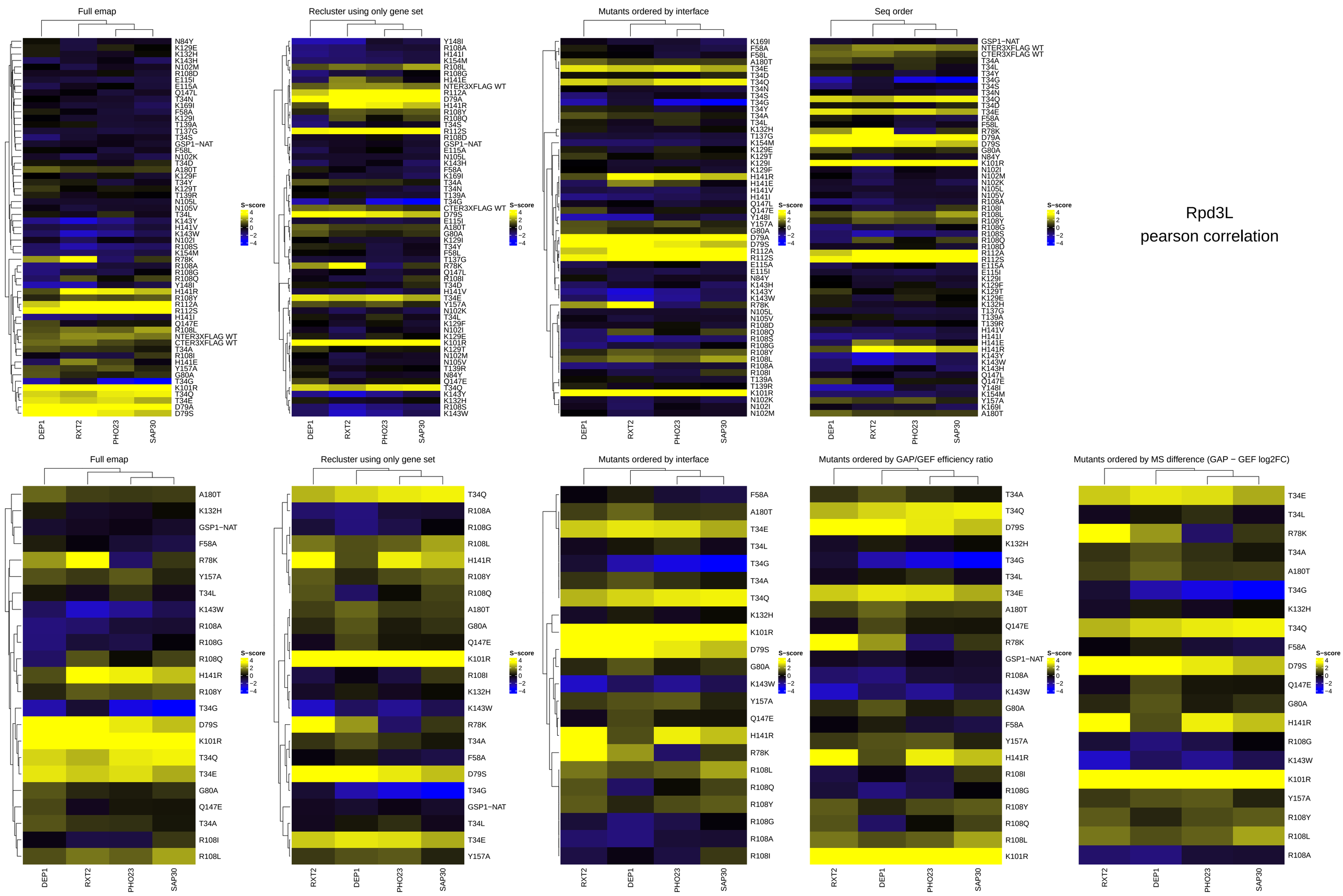
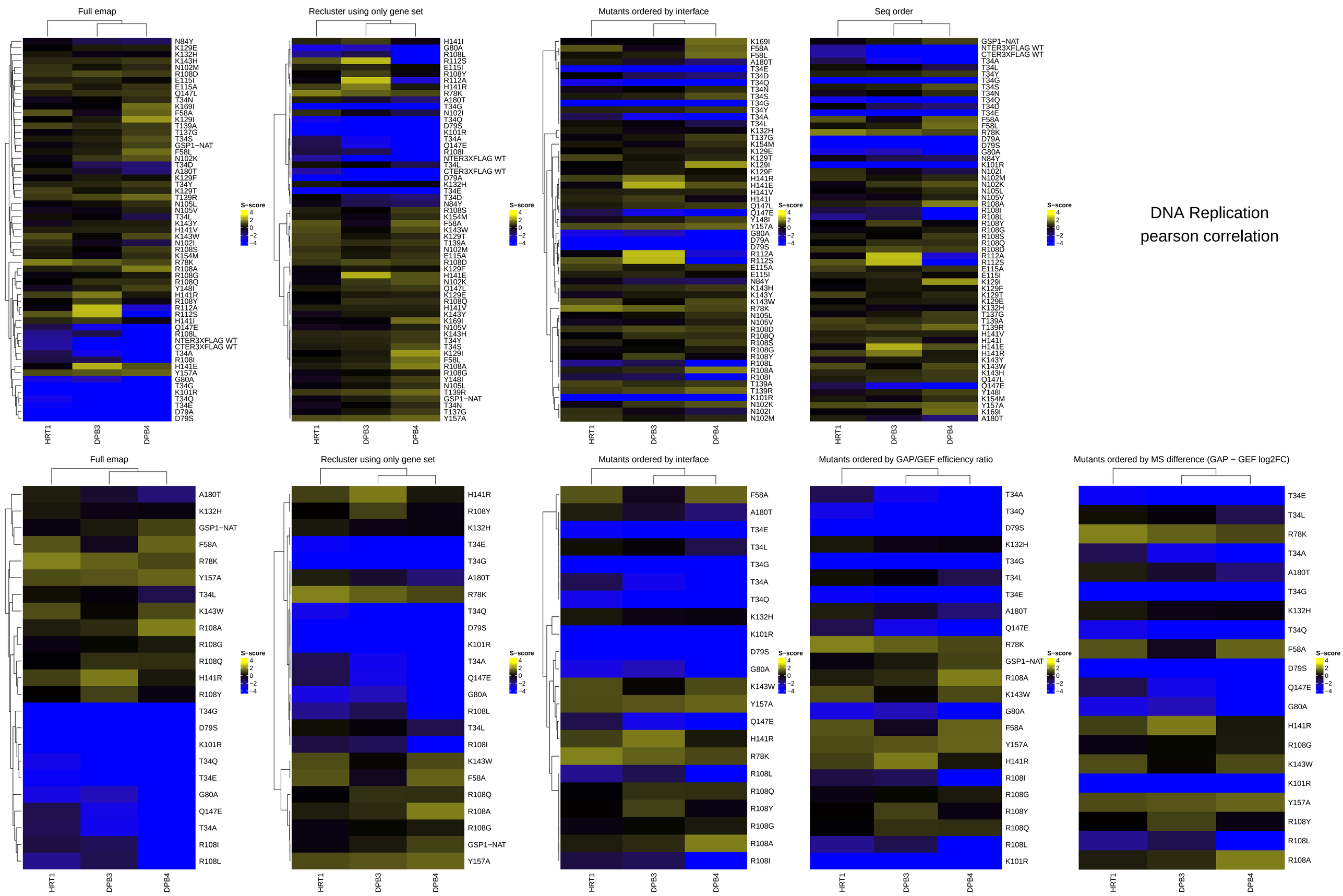
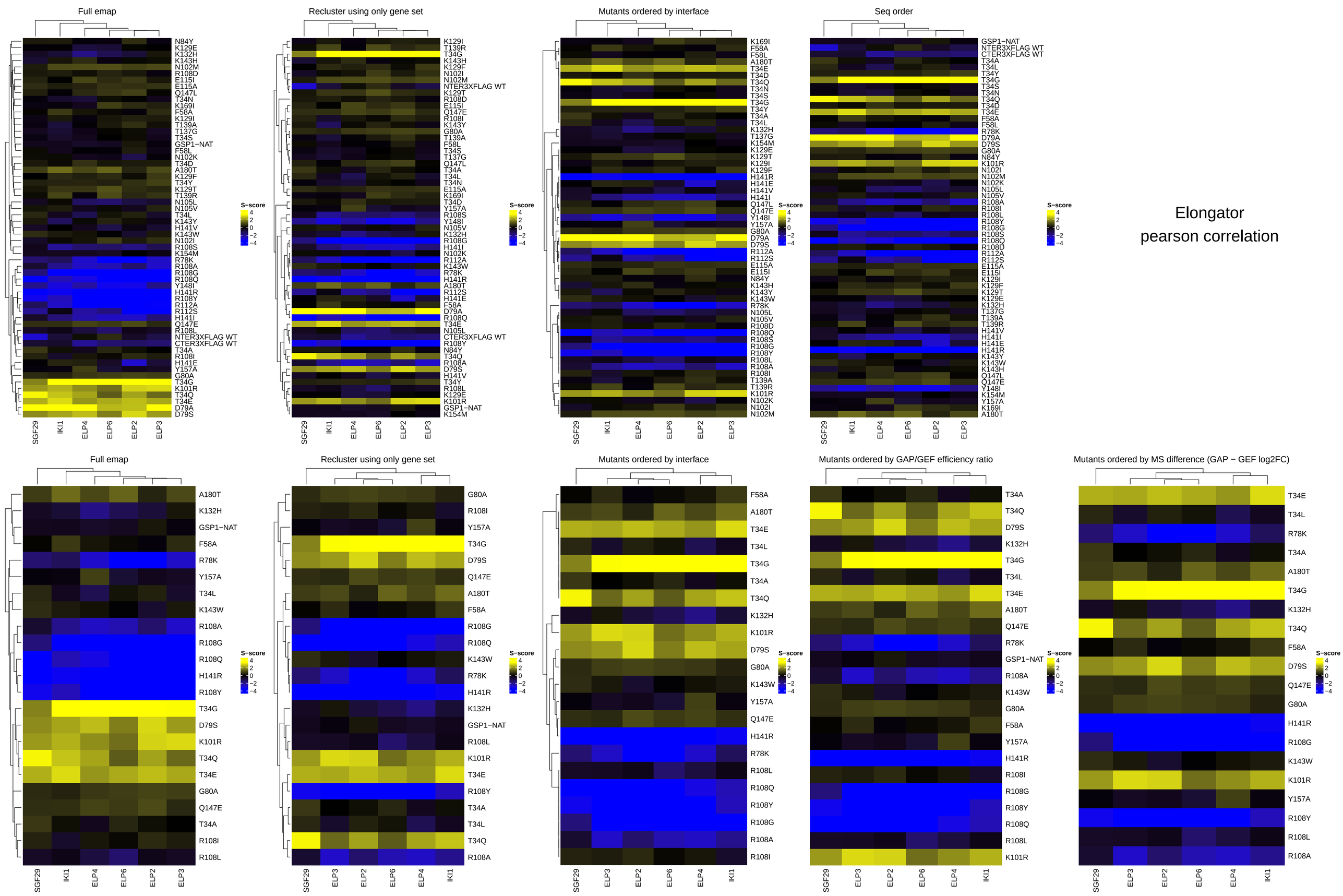
2
0
−2
−4
RIM21
RIM101
CPA1
IWR1
RIM20
RIM101
pearson correlation

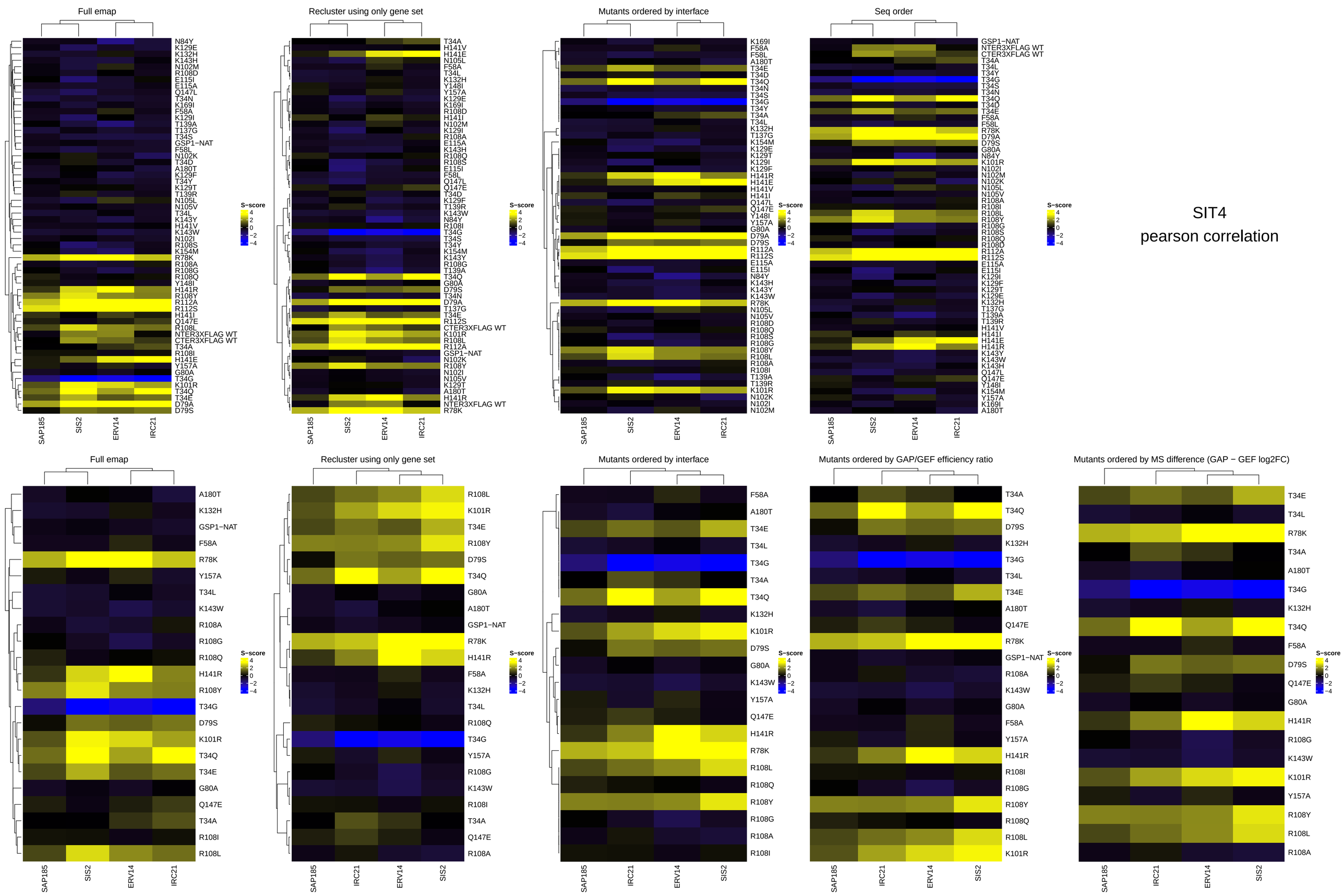


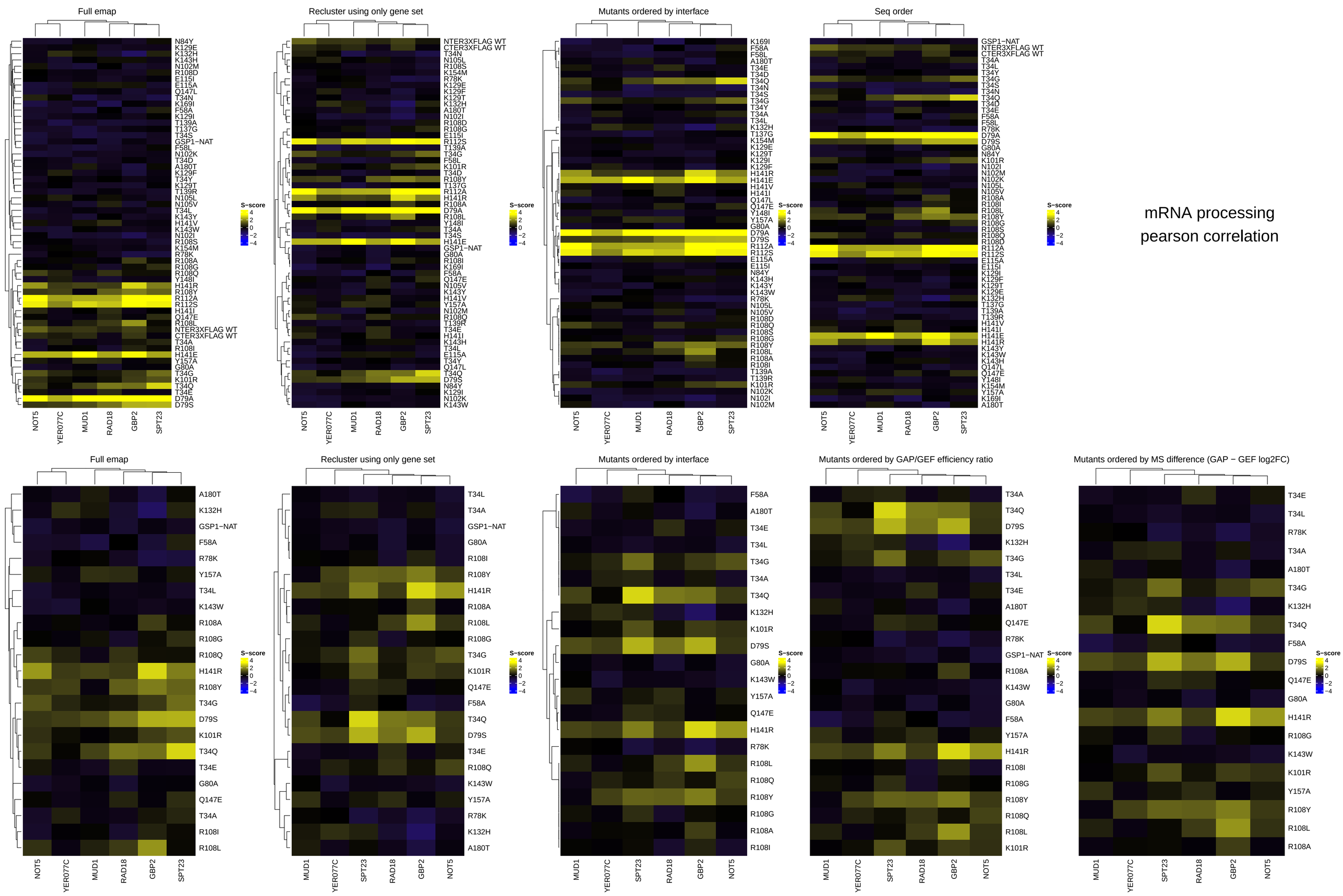
mitochondrial
pearson correlation


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
pearson correlation


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
pearson correlation


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Elongator
pearson correlation
S−score
4
2
0
−2
−4
SGF29
IKI1
ELP4
ELP6
ELP2
ELP3
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
SAP185
SIS2
ERV14
IRC21
SIT4
pearson correlation


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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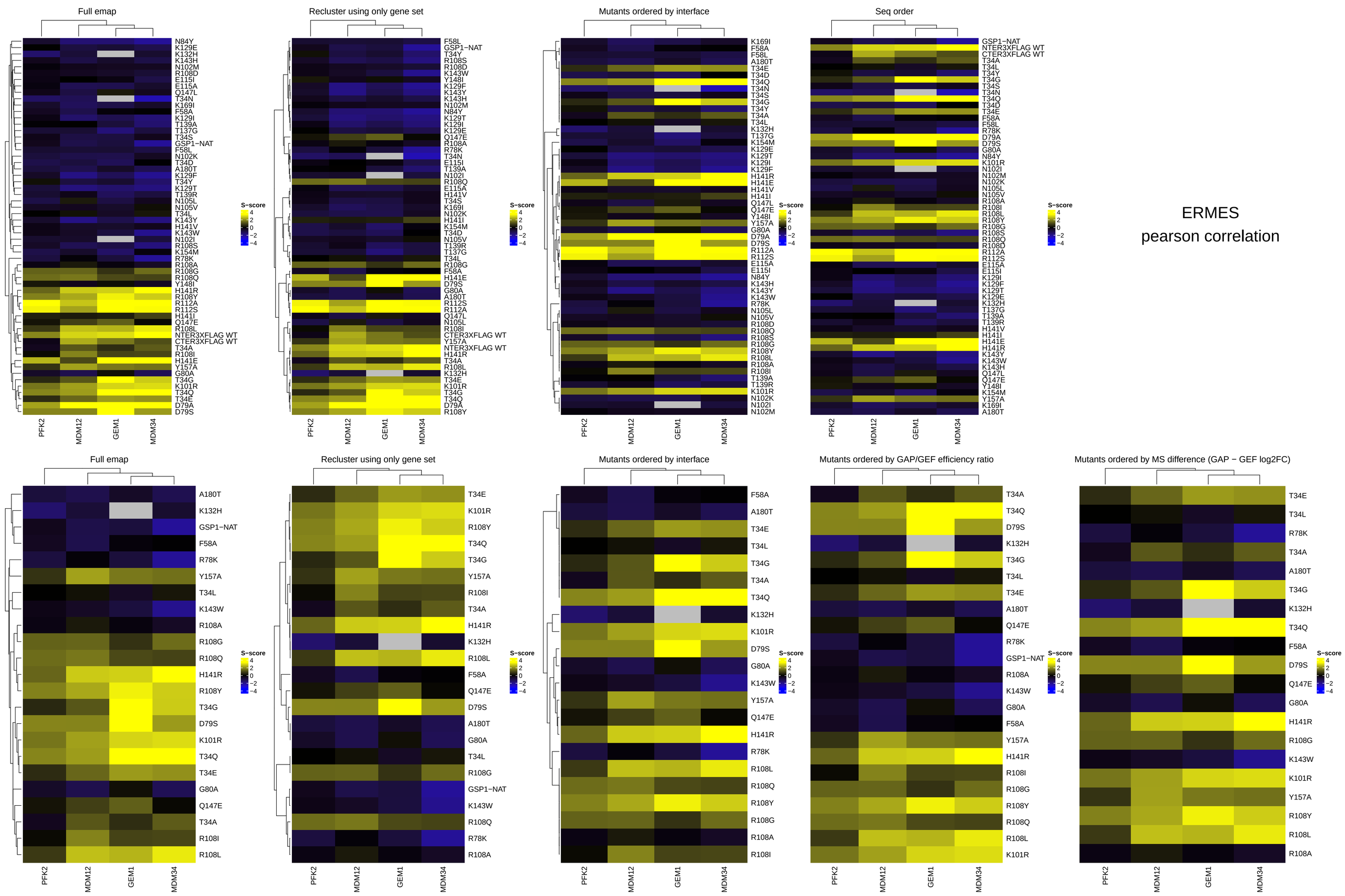
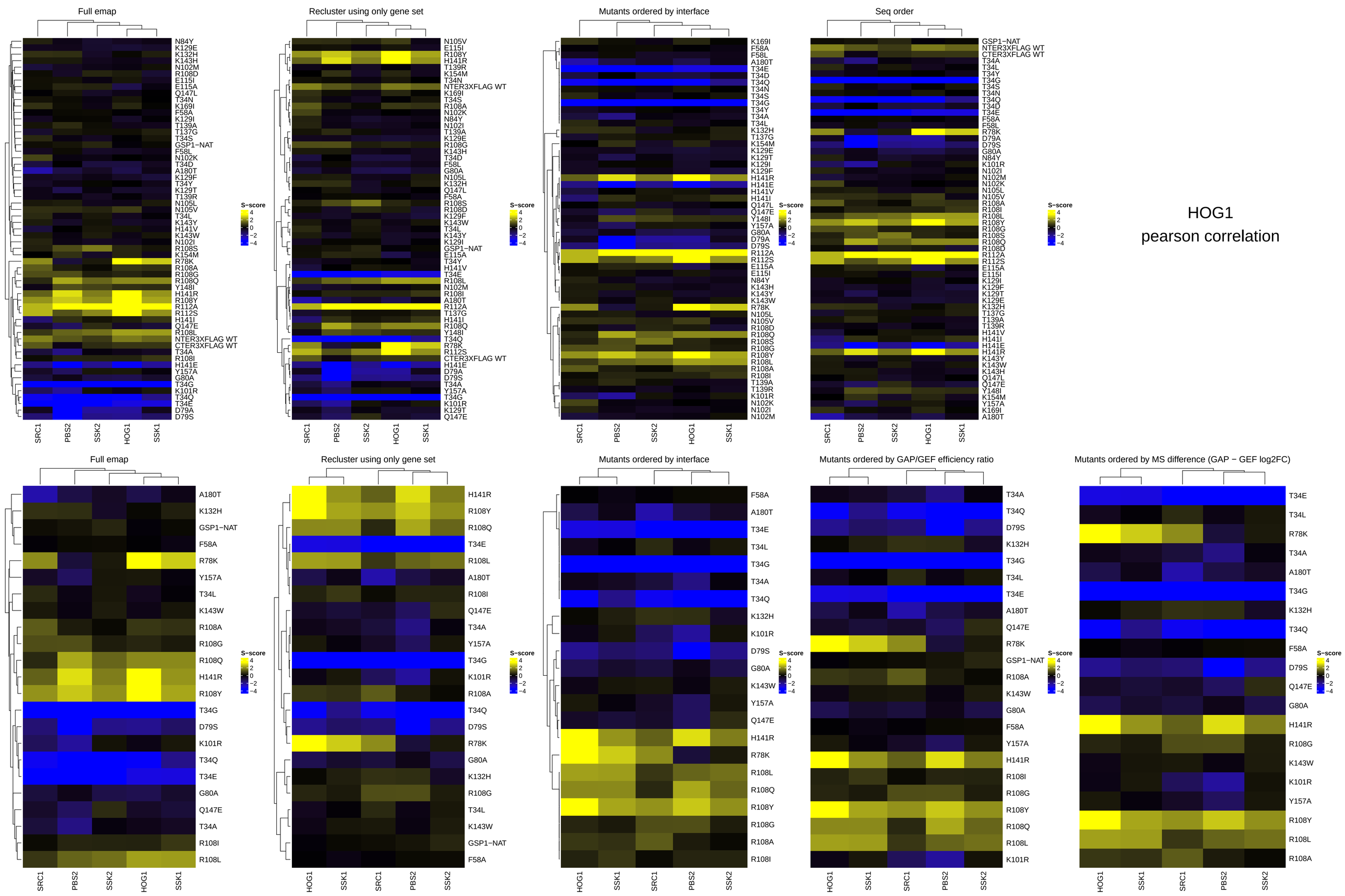
2
0
−2
−4
NOT5
YER077C
MUD1
RAD18
GBP2
SPT23
mRNA processing
pearson correlation


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
pearson correlation


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
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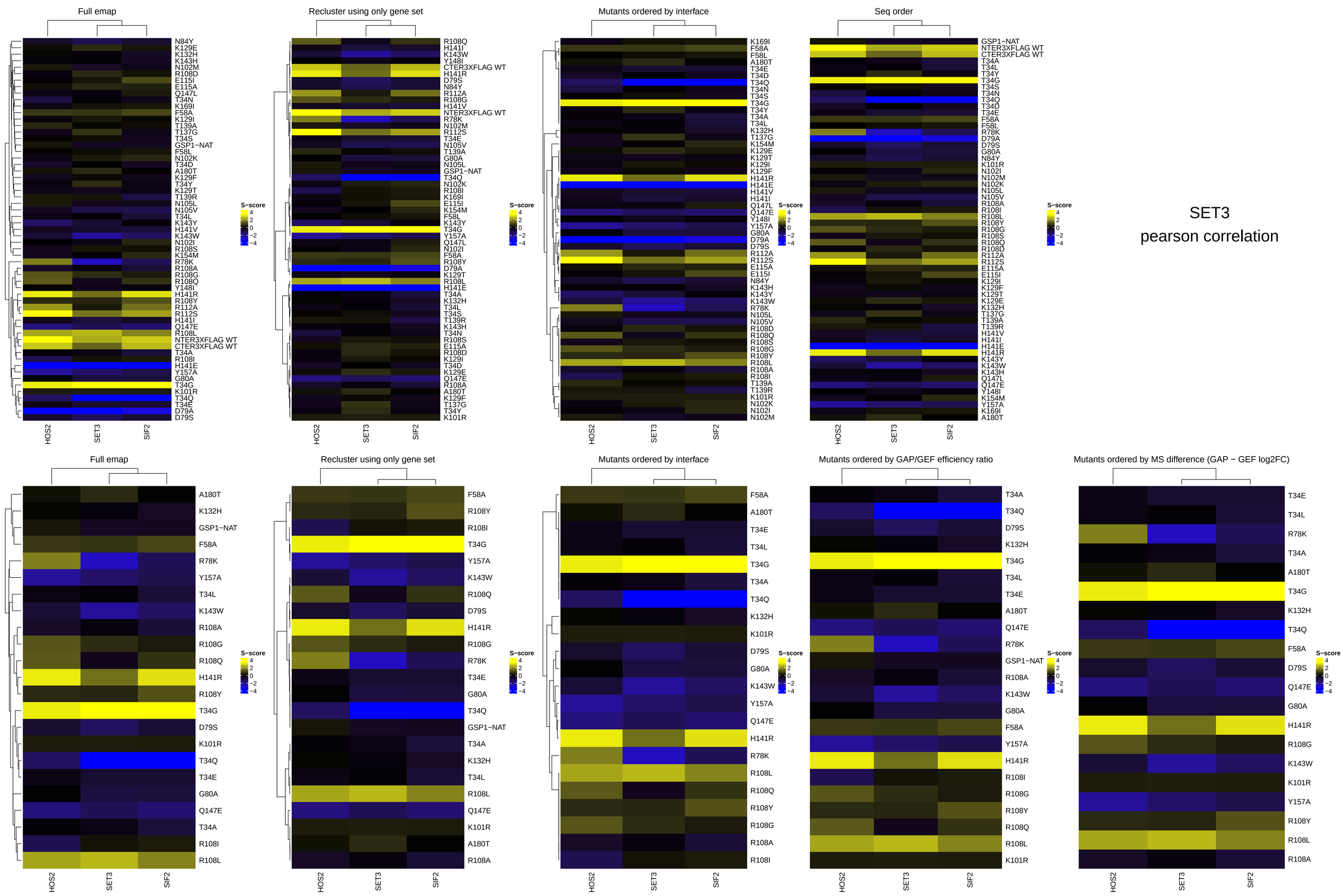
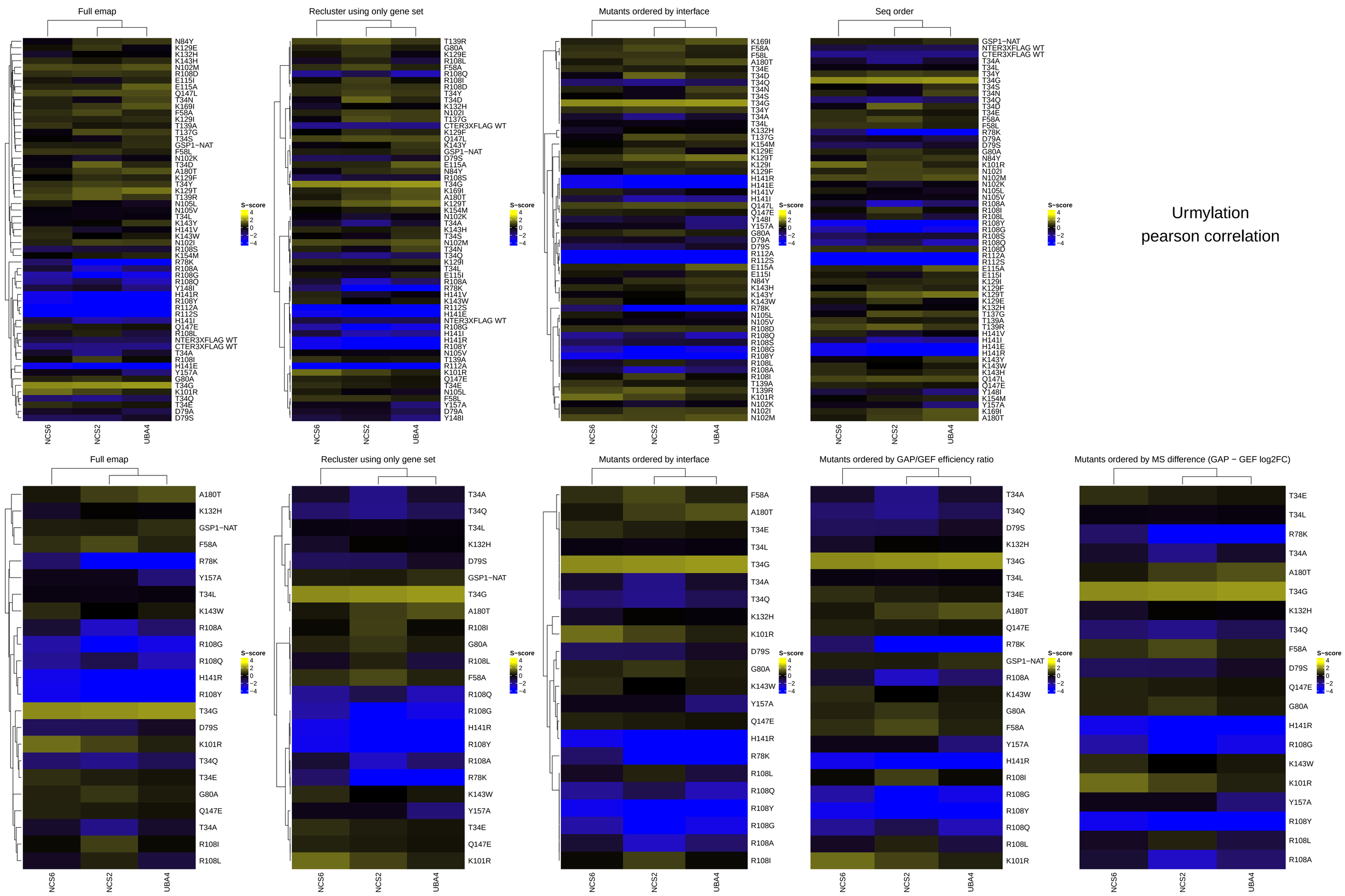
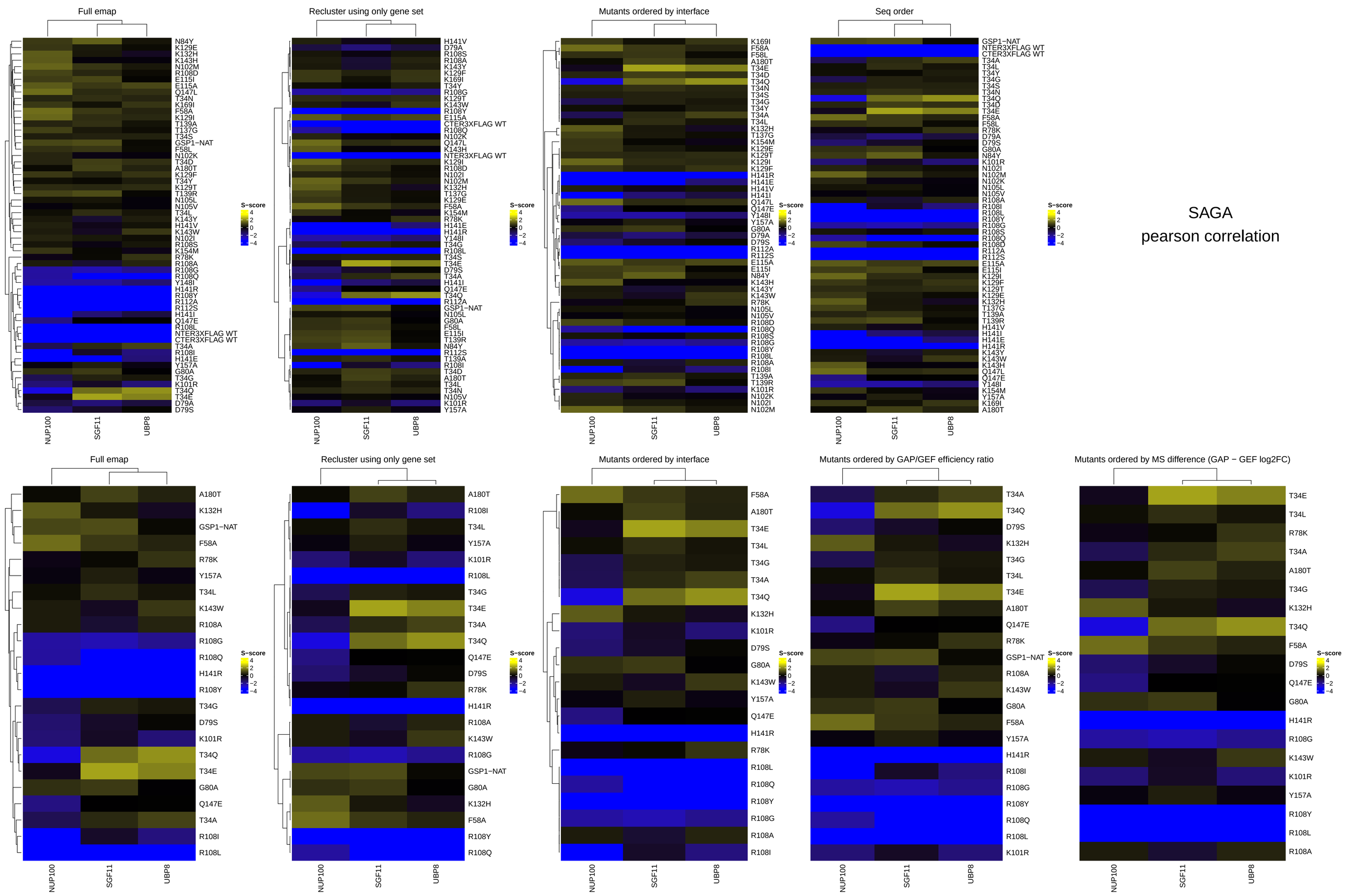
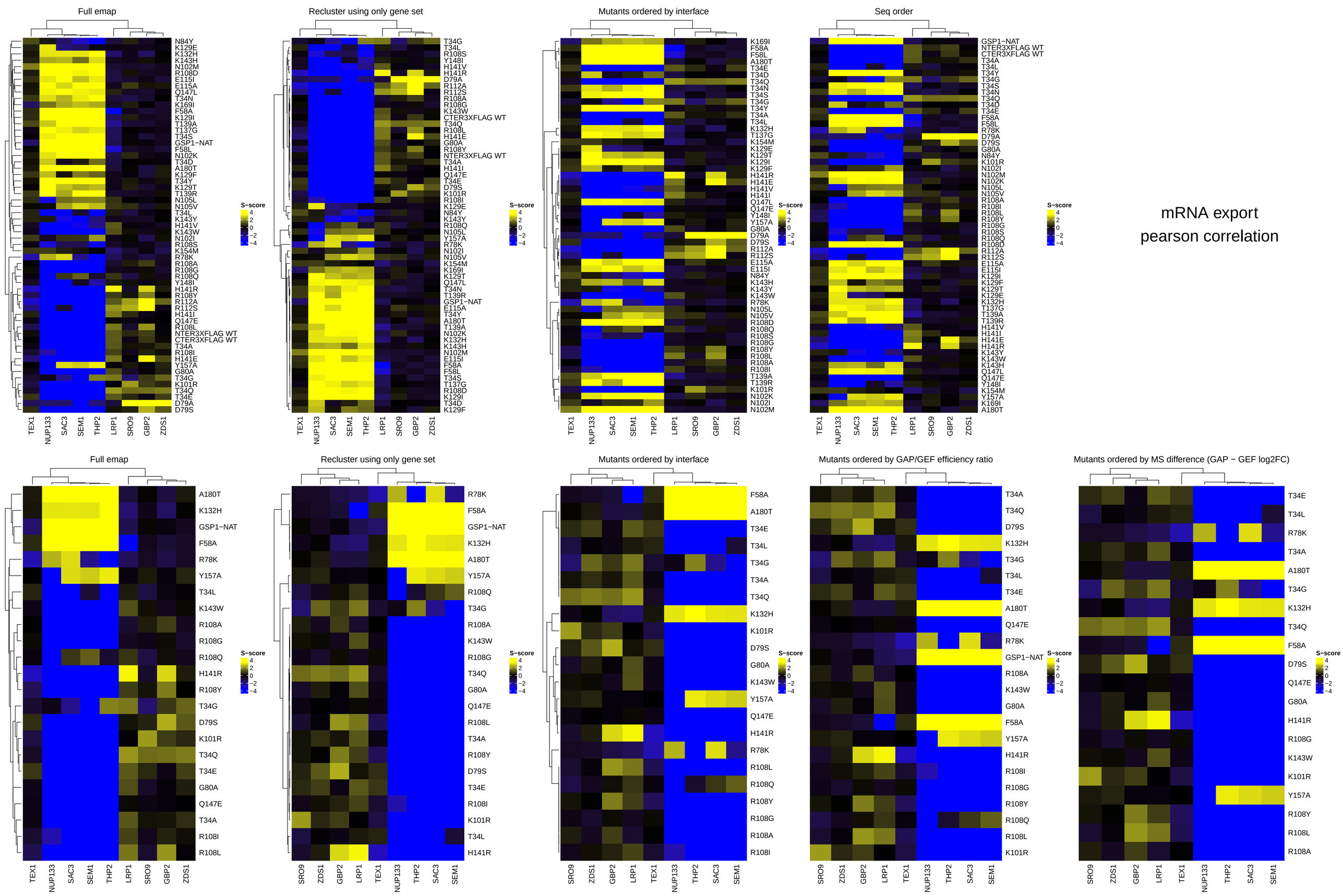
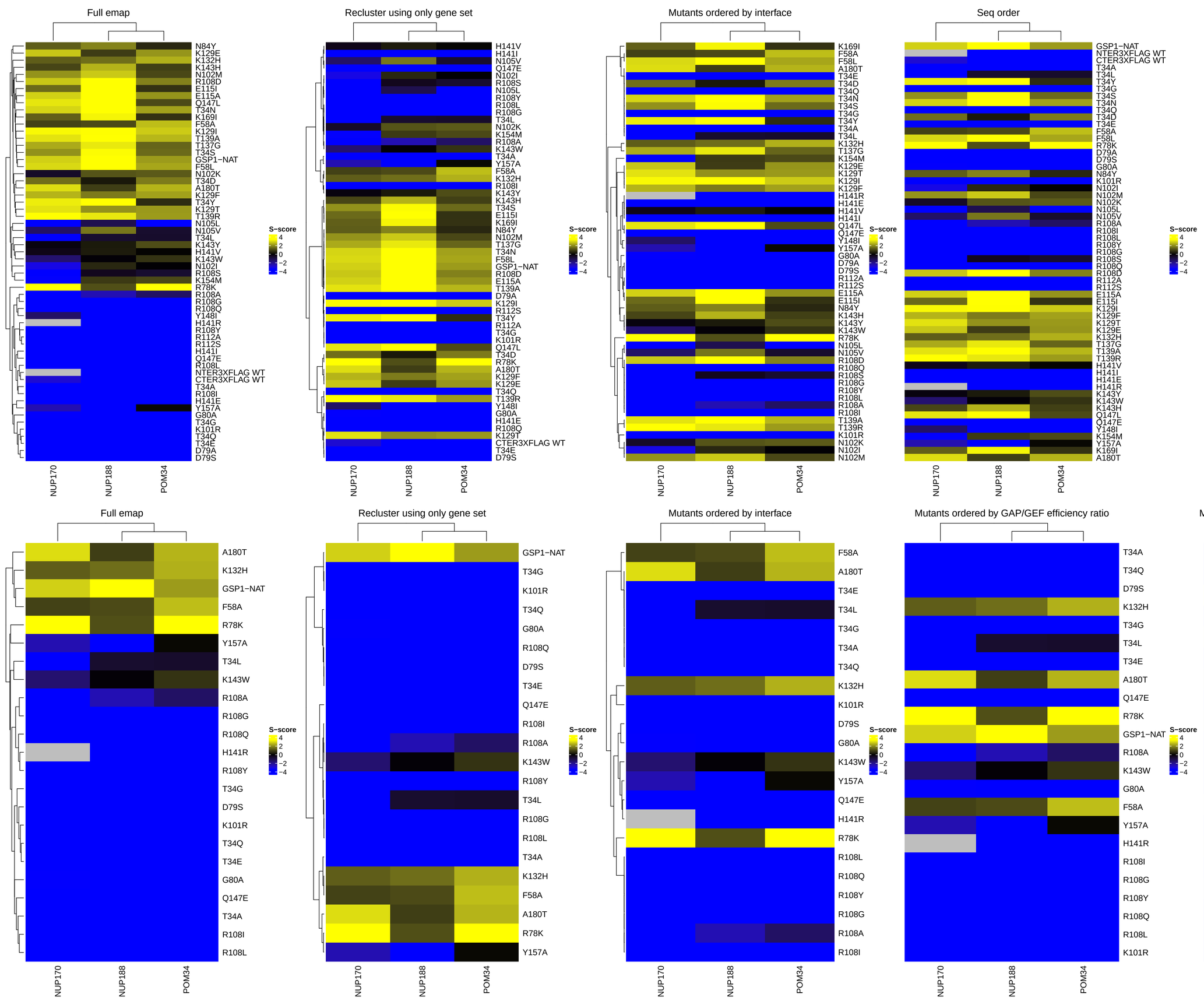
2
0
−2
−4
SRC1
PBS2
SSK2
HOG1
SSK1
HOG1
pearson correlation


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
pearson correlation

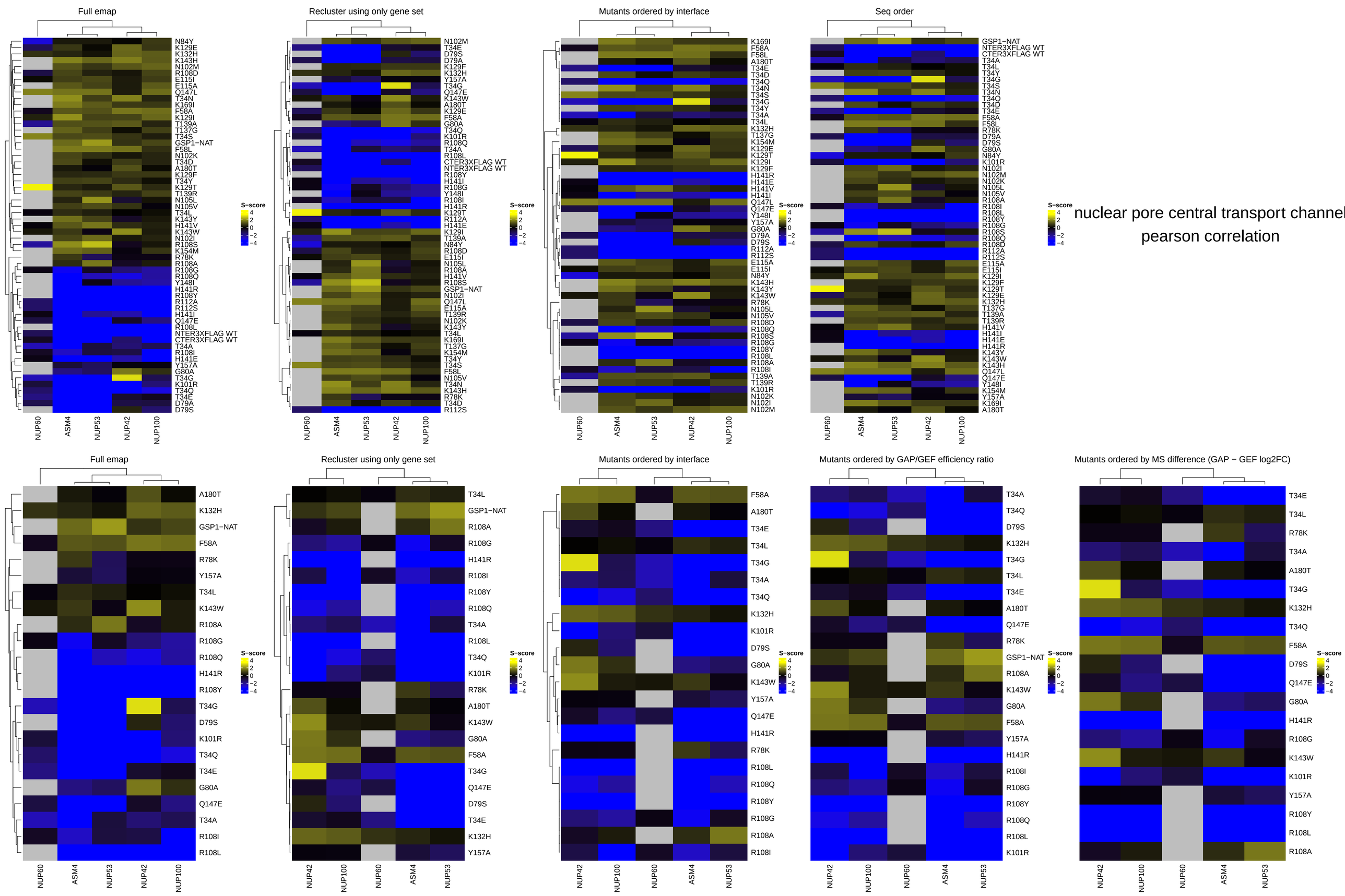

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
NCS6
NCS2
UBA4
Urmylation
pearson correlation

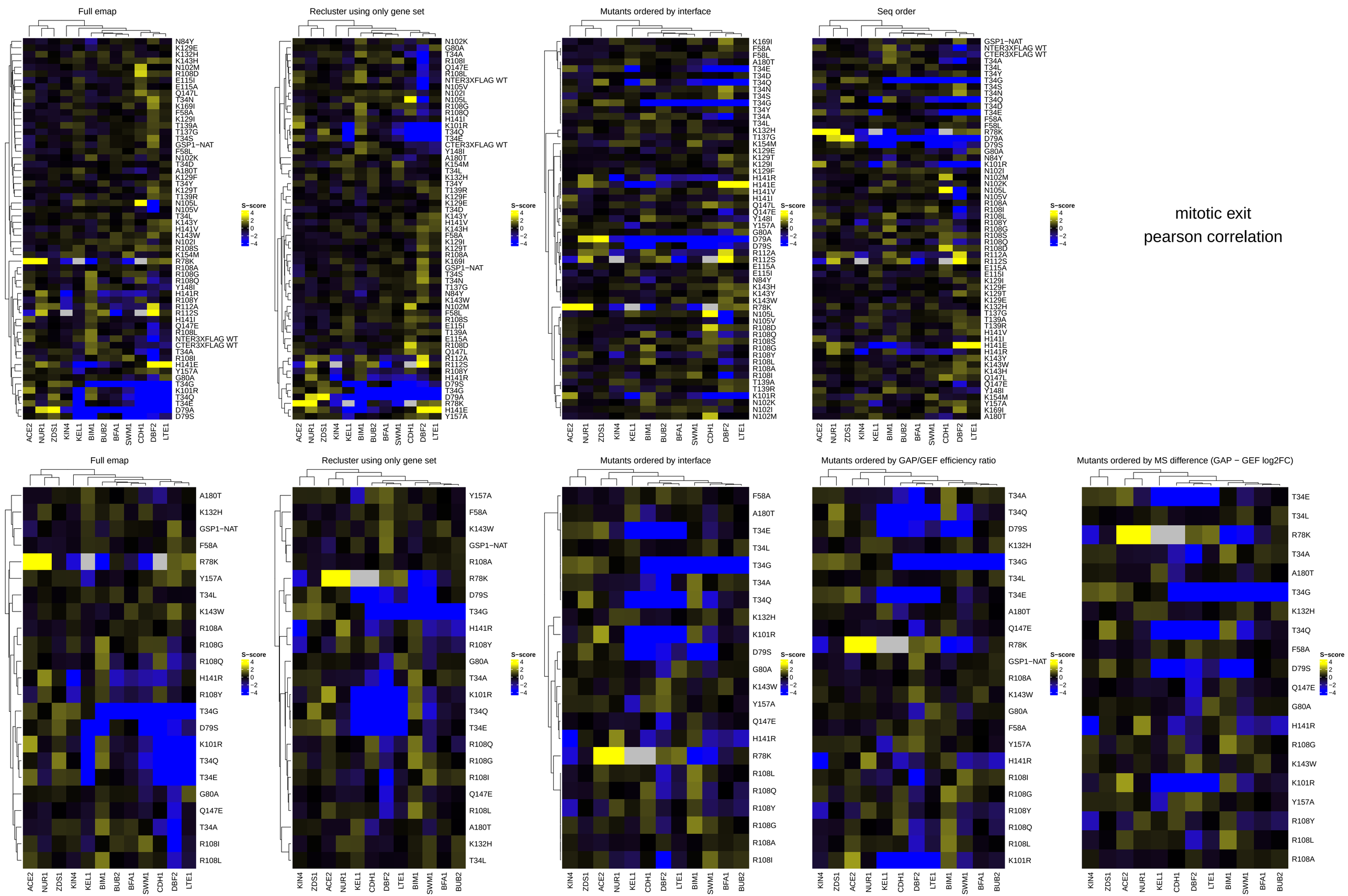

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
NUP100
SGF11
UBP8
SAGA
pearson correlation

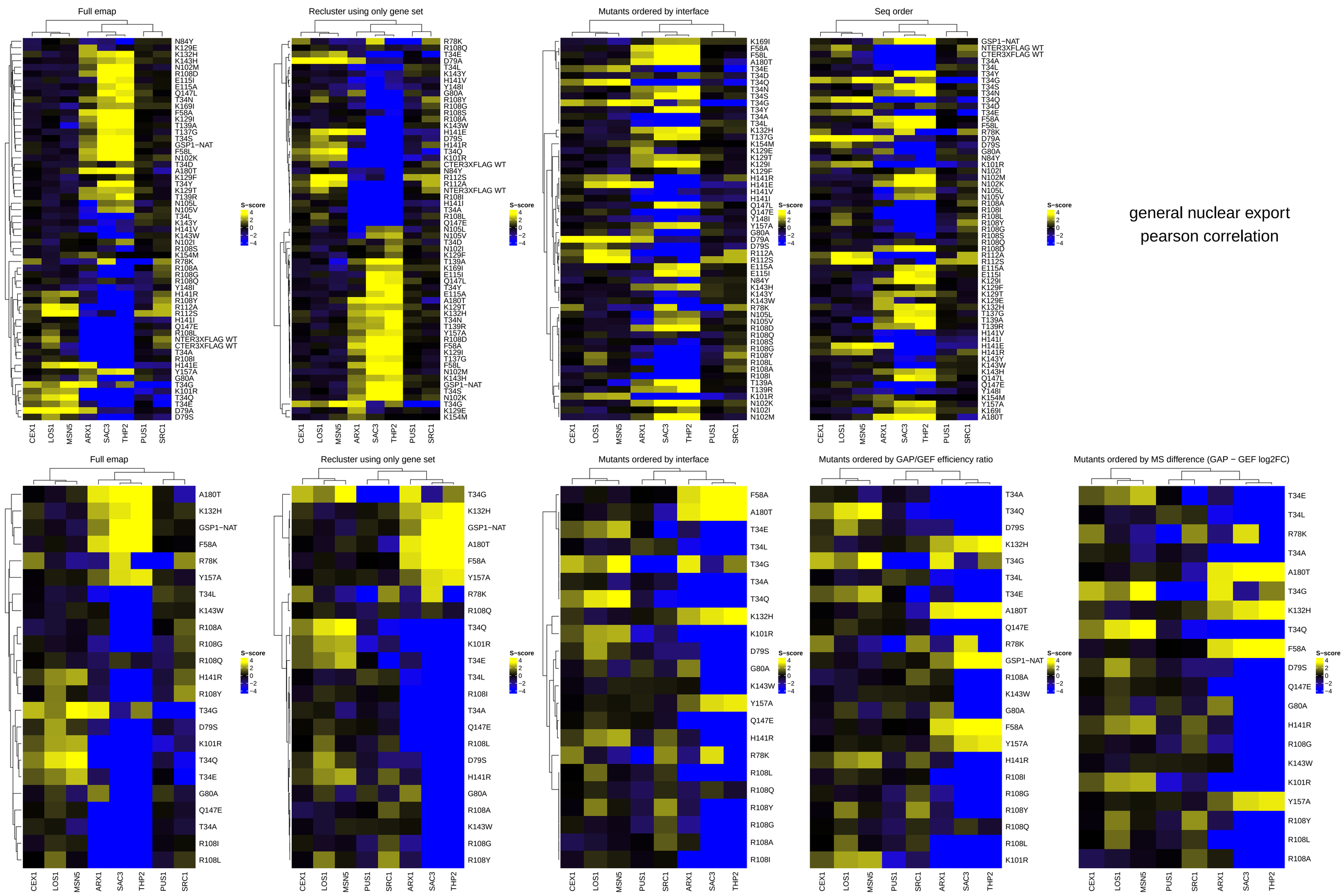

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TEX1
NUP133
SAC3
SEM1
THP2
LRP1
SRO9
GBP2
ZDS1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF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

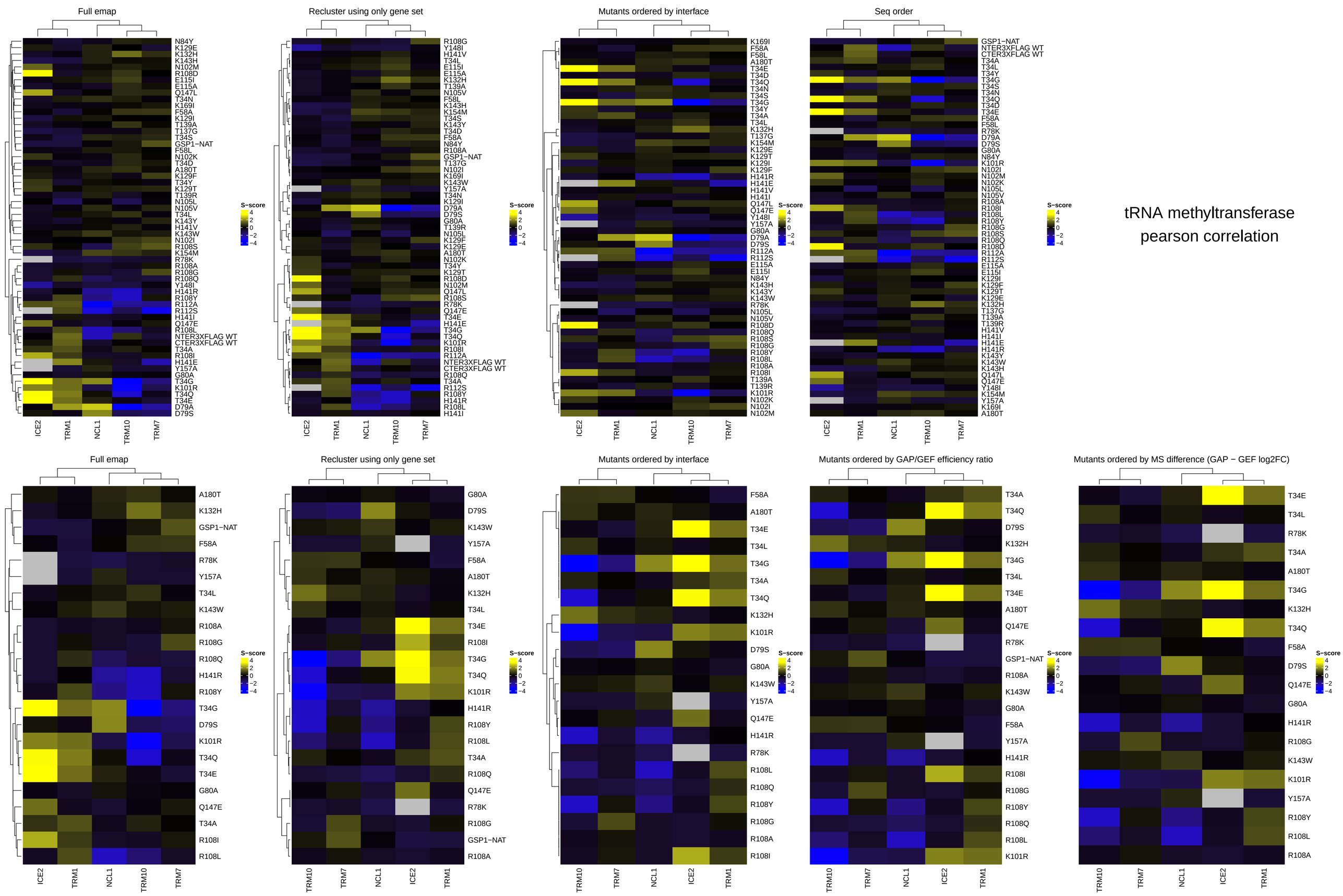


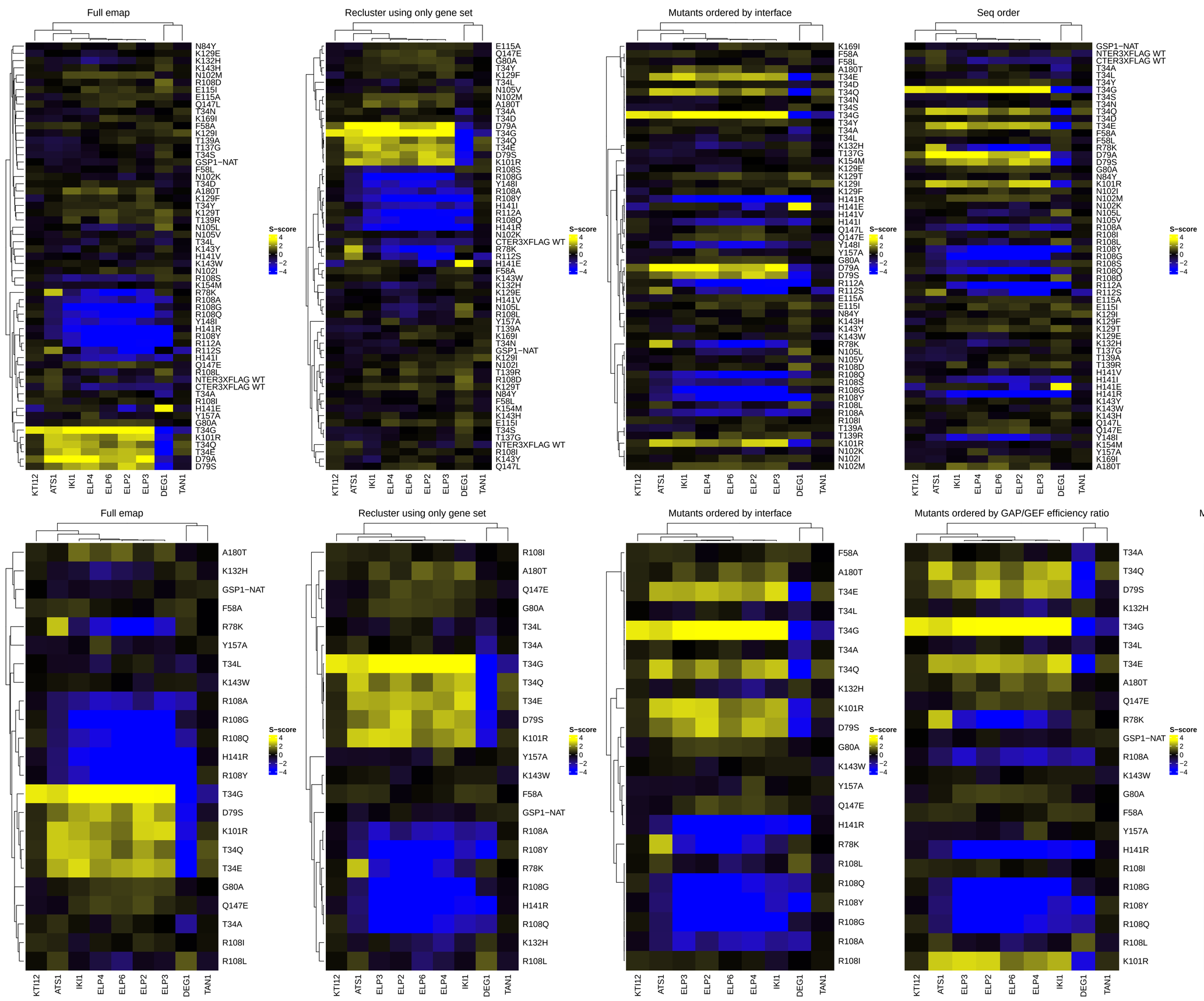
Inner NPC
pearson correlation


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
NUP60
ASM4
NUP53
NUP42
NUP100
nuclear pore central transport channel
pearson correlation

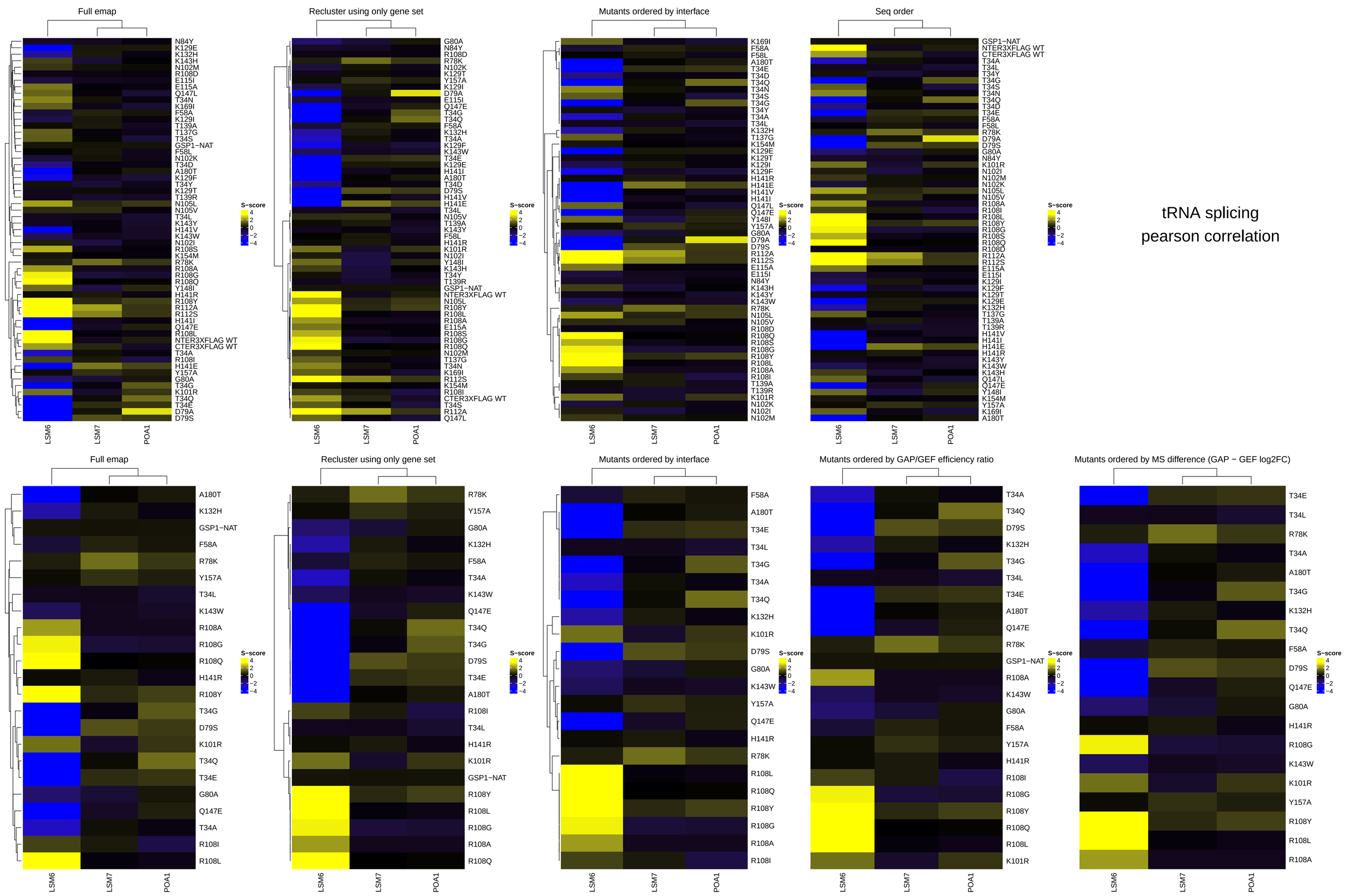

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
ACE2
NUR1
ZDS1
KIN4
KEL1
BIM1
BUB2
BFA1
SWM1
CDH1
DBF2
LTE1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference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


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
ARX1
SAC3
THP2
PUS1
SRC1
general nuclear export
pearson correlation

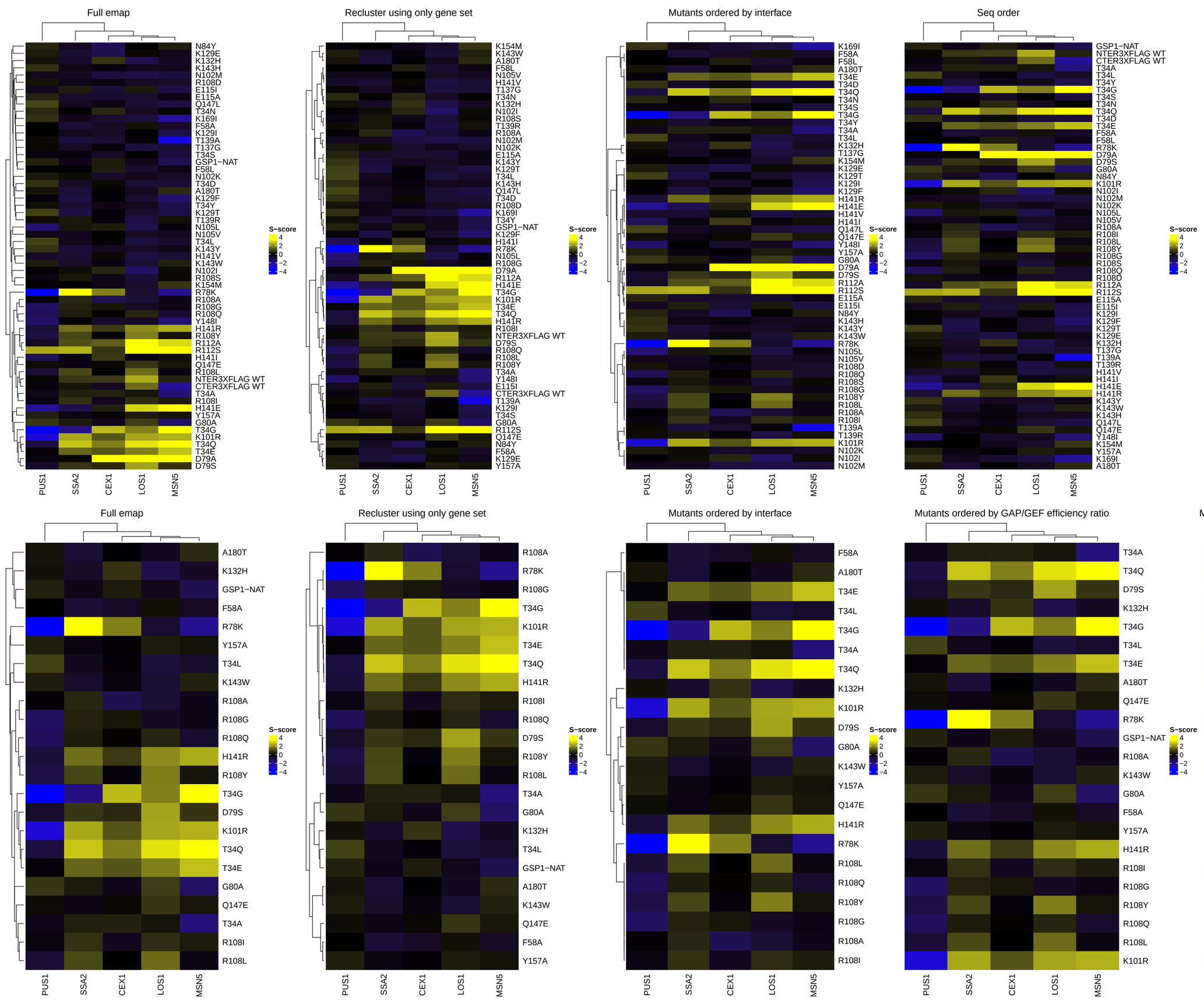

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ICE2
TRM1
NCL1
TRM10
TRM7
tRNA methyltransferase
pearson correlation



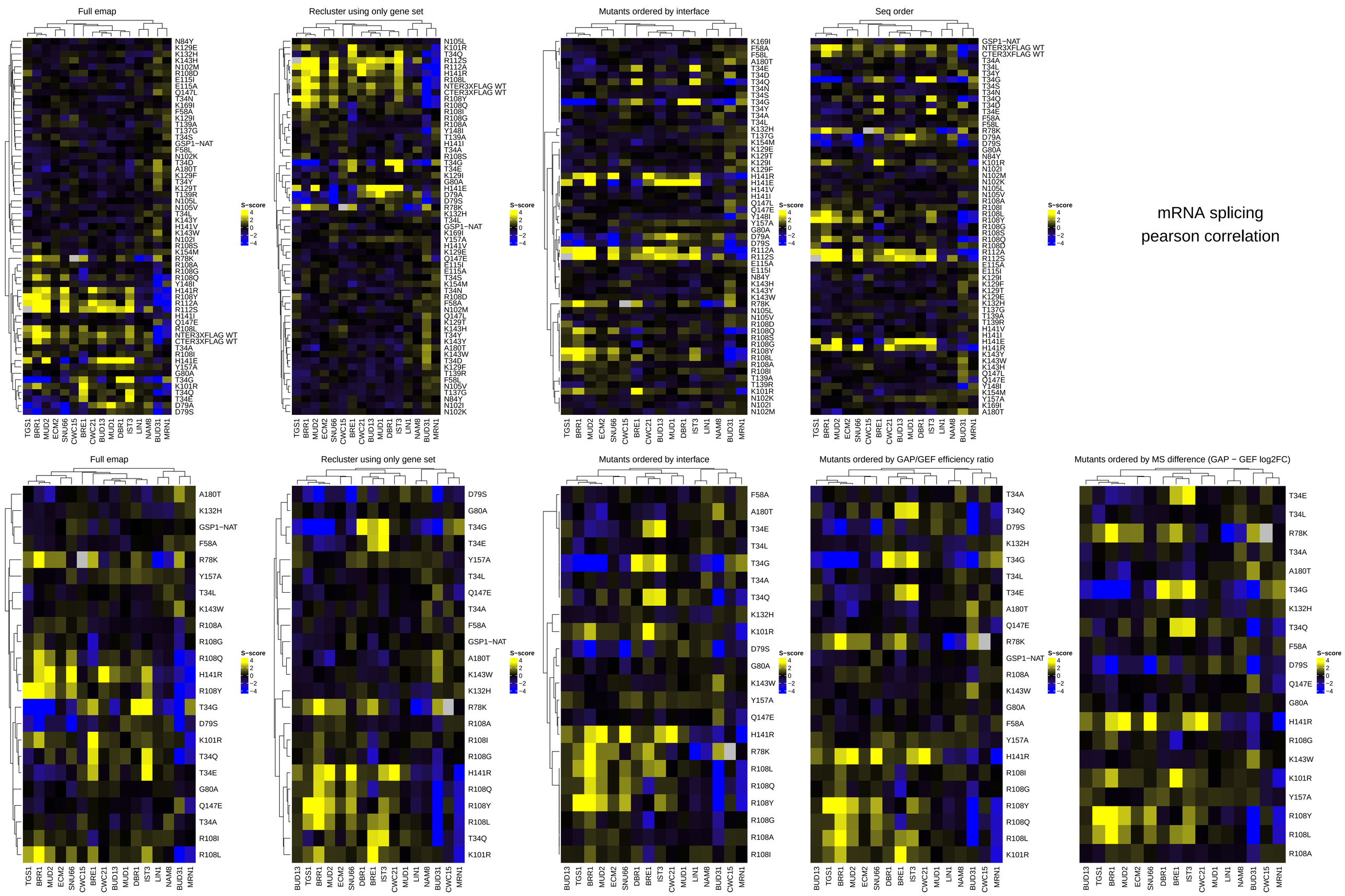
tRNA base modification
pearson correlation



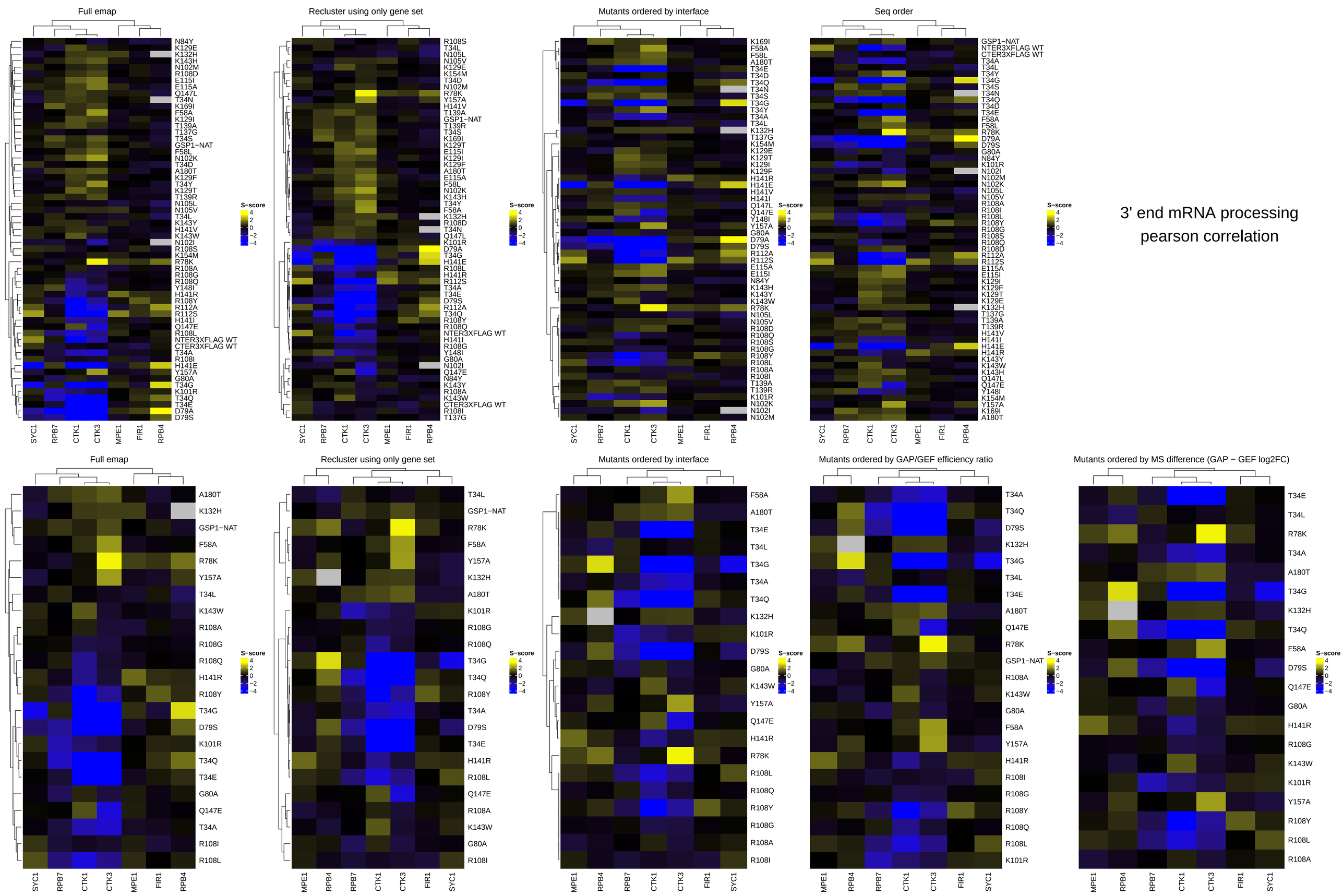
tRNA splicing
pearson correlation

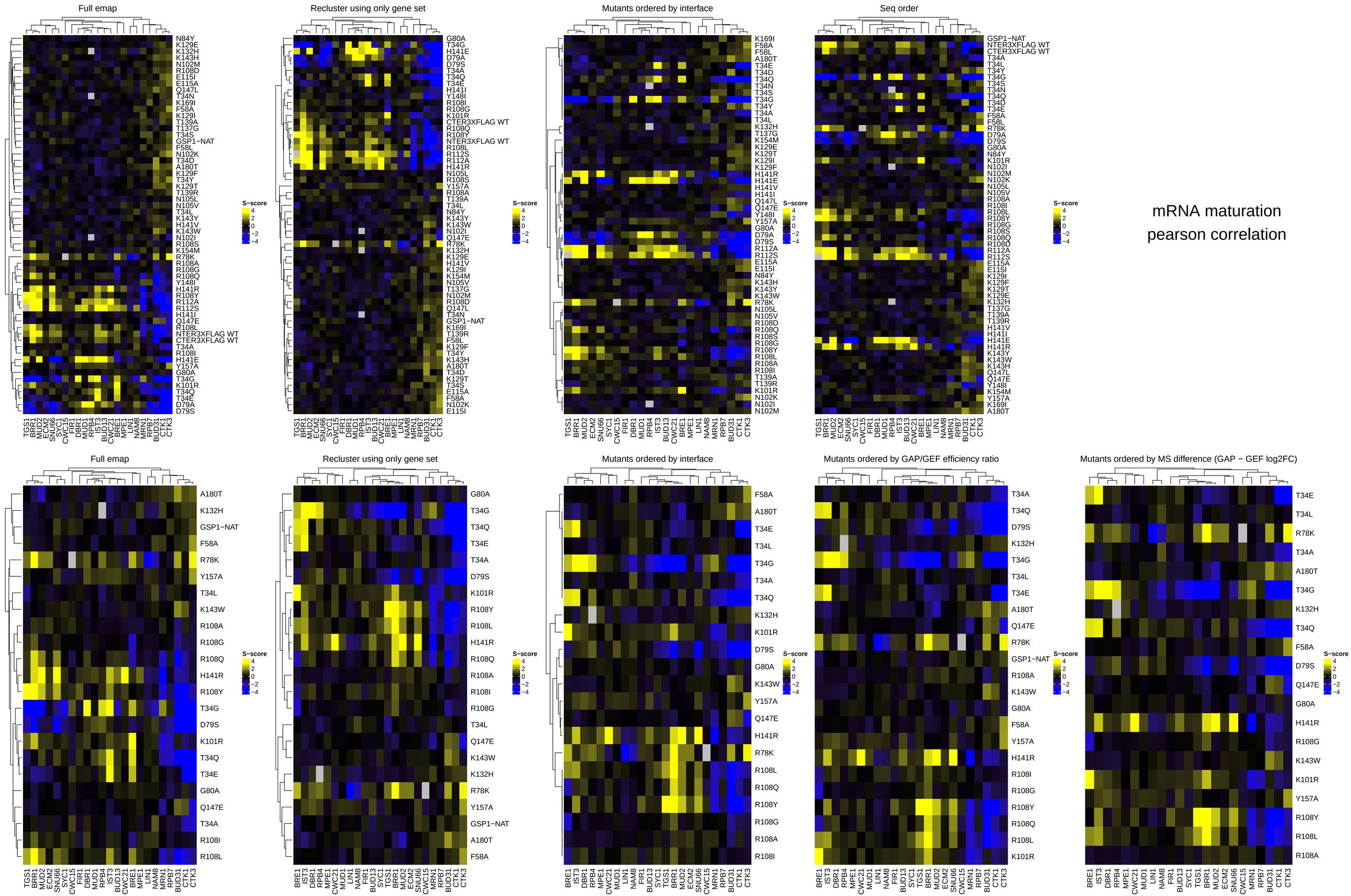


nuclear trasnport of tRNA
pearson correlation

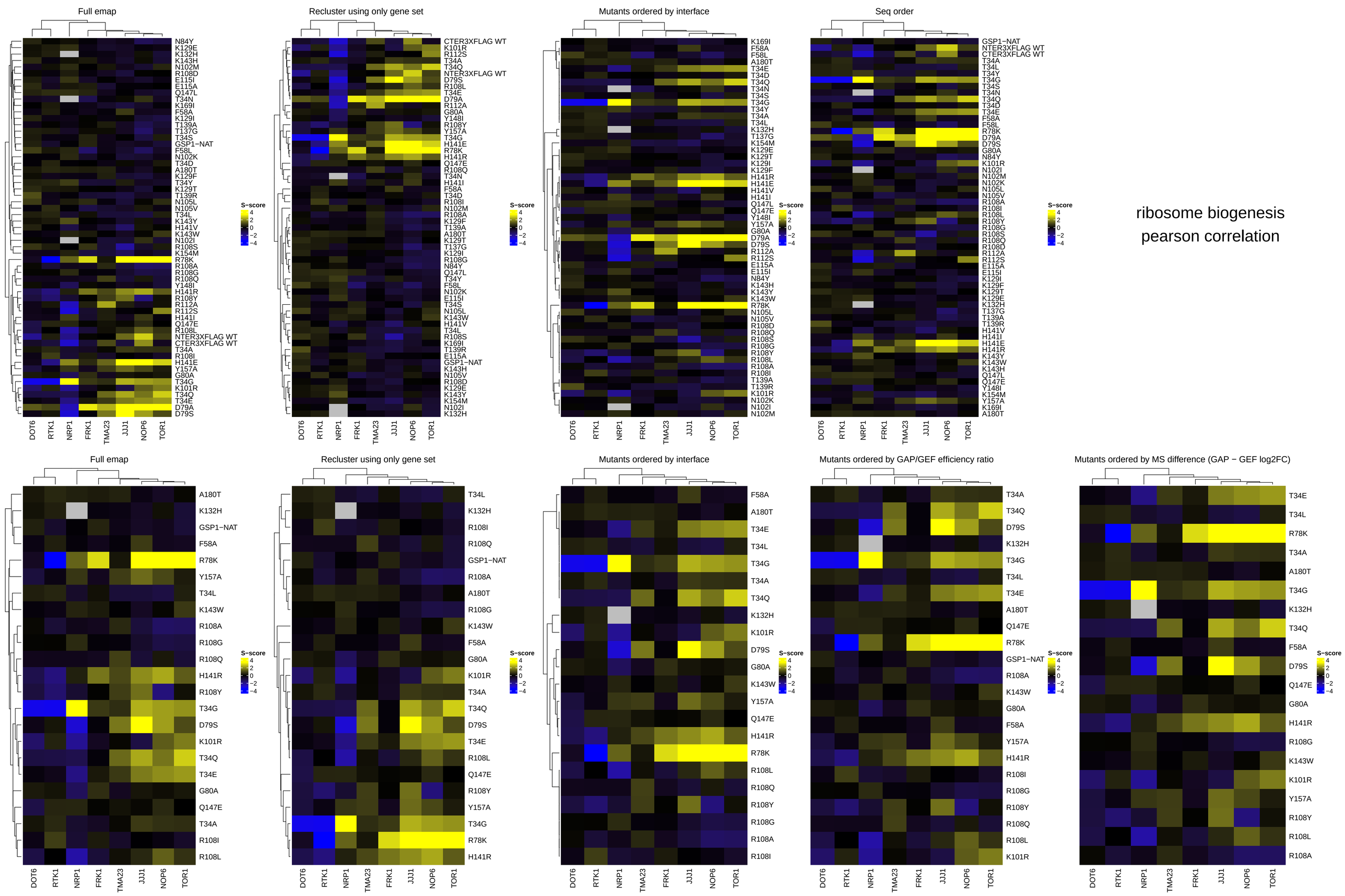


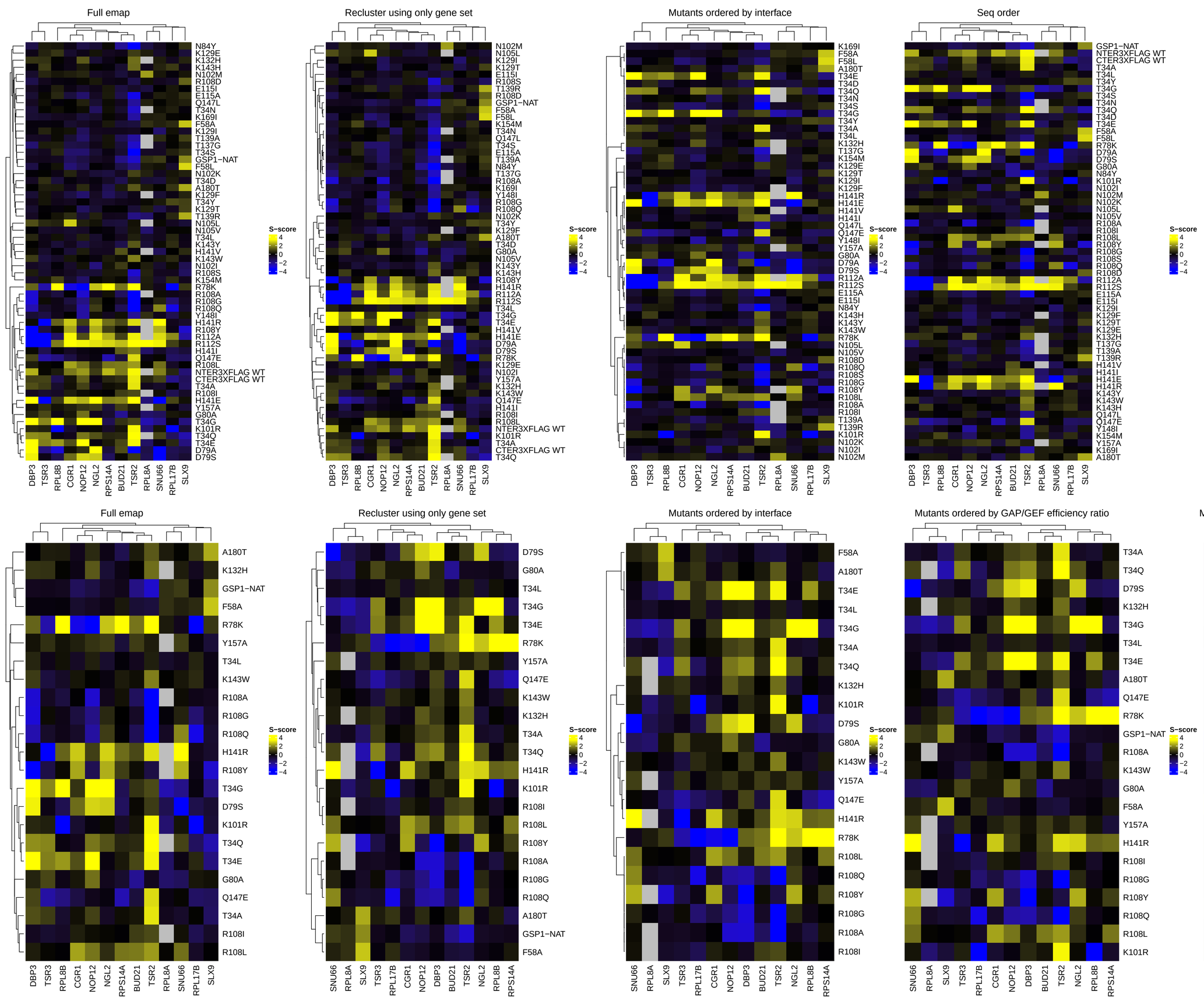
mRNA splicing
pearson correlation


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
pearson correlation

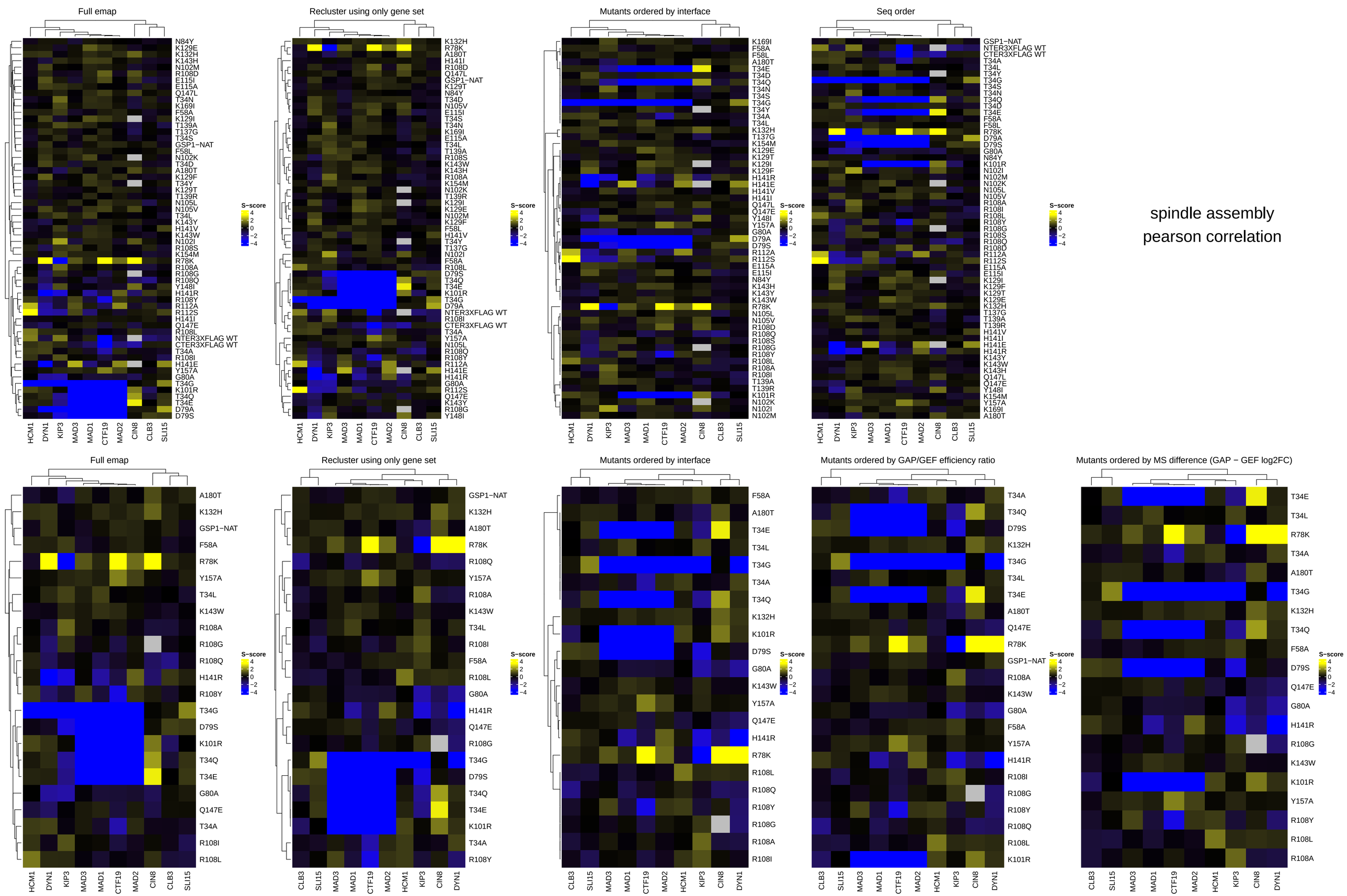


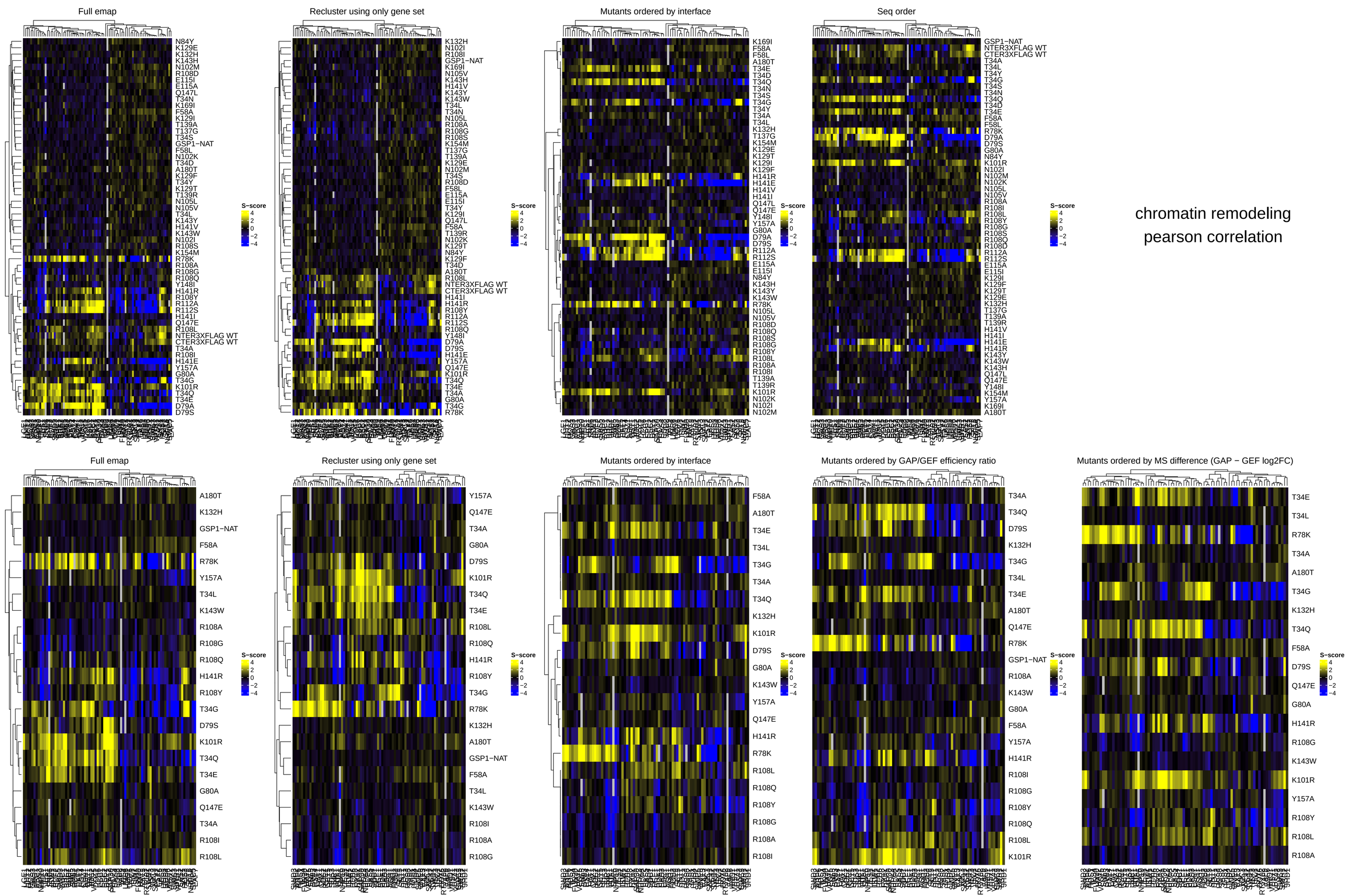
mRNA maturation
pearson correlation


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
pearson correlation

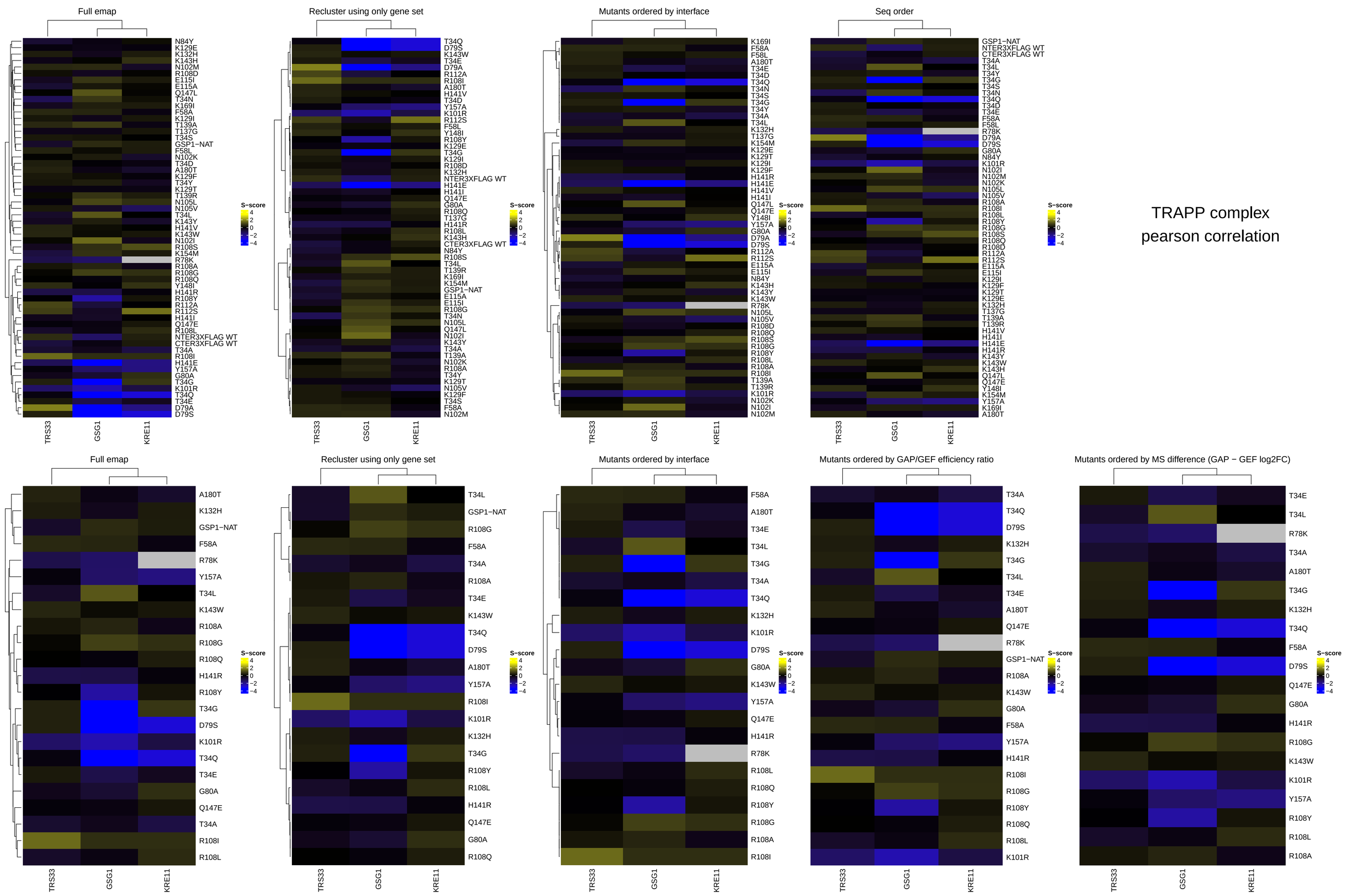


rRNA processing
pearson correlation

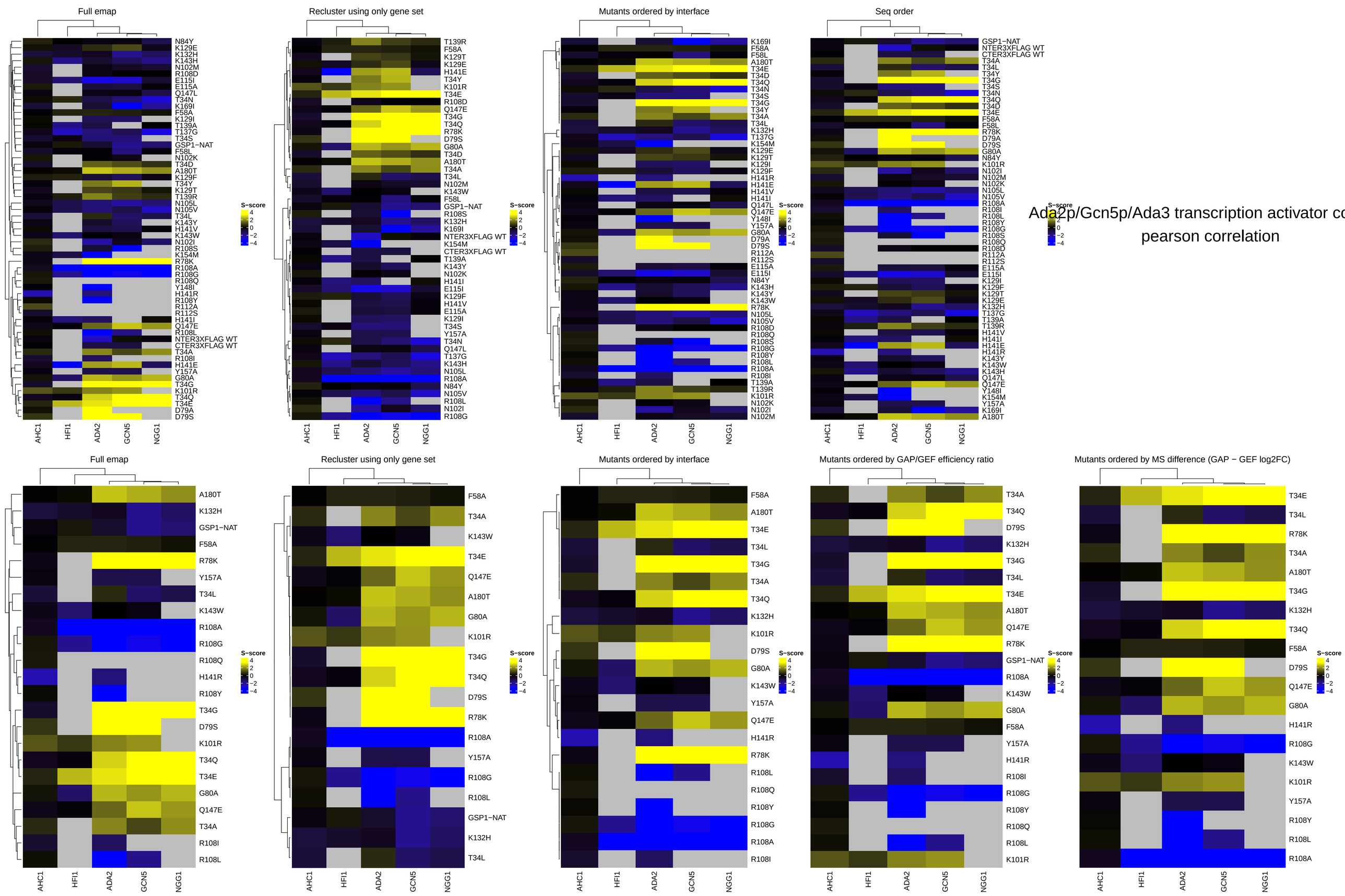

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
HCM1
DYN1
KIP3
MAD3
MAD1
CTF19
MAD2
CIN8
CLB3
SLI15
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP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

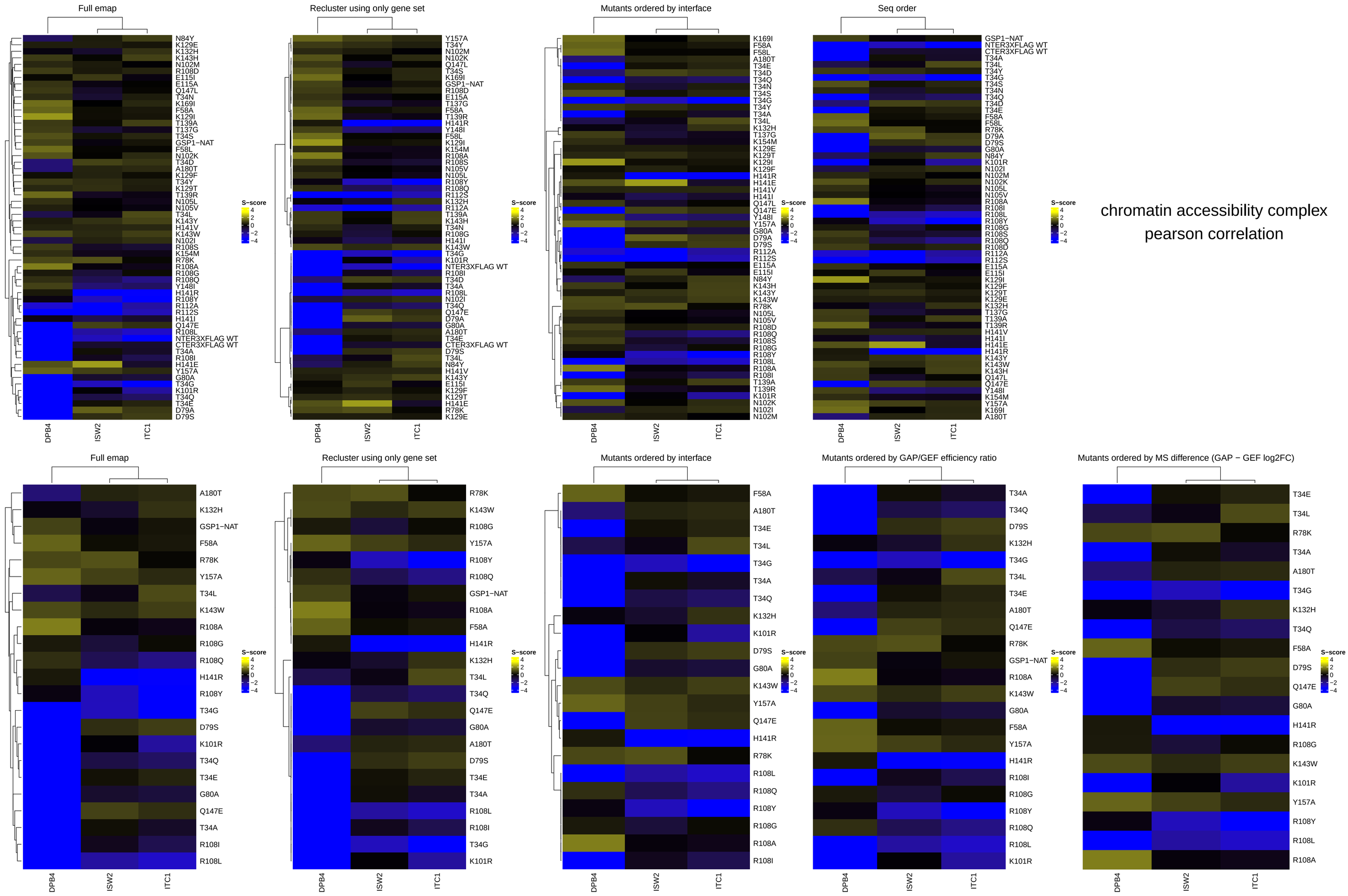


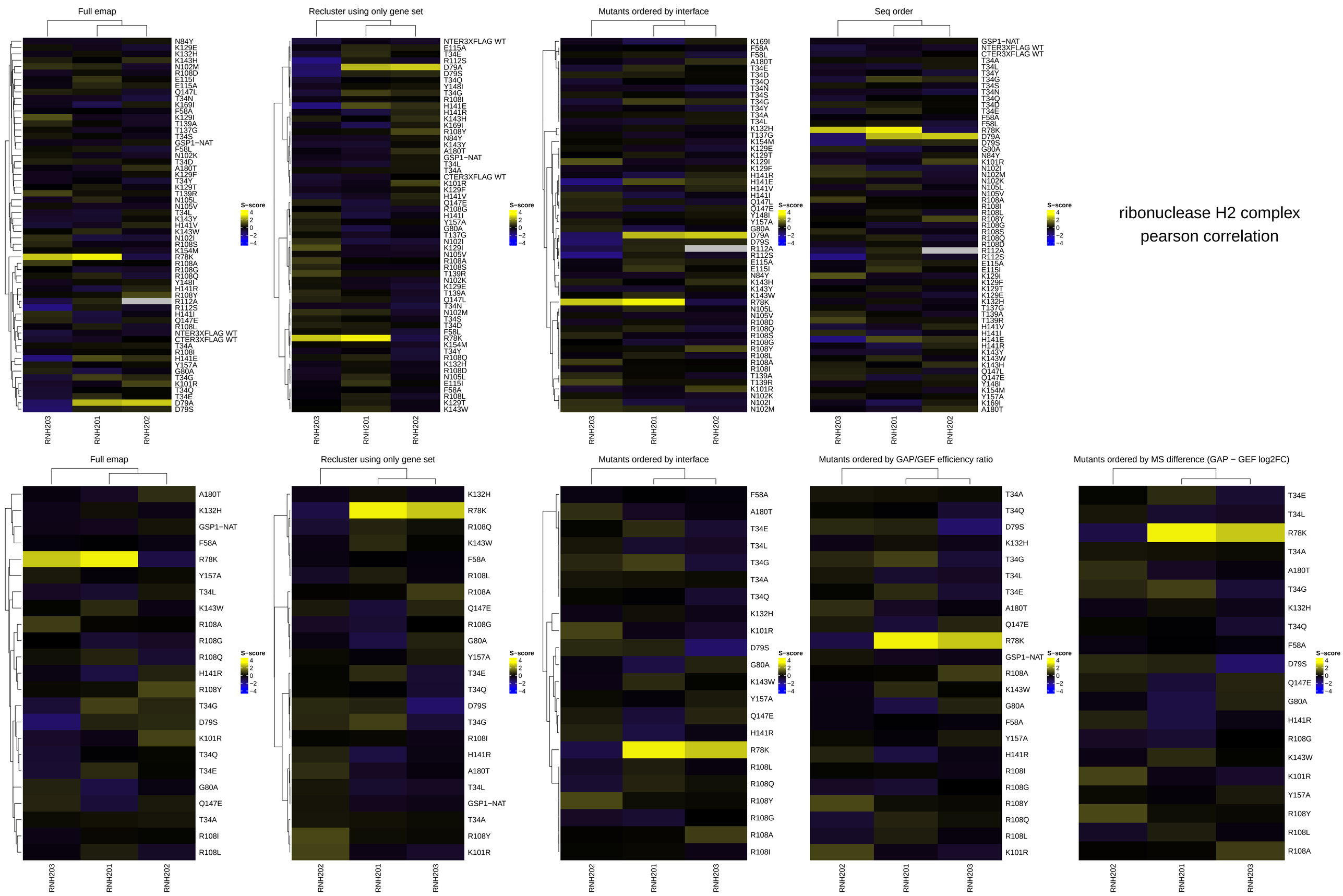
chromatin remodeling
pearson correlation

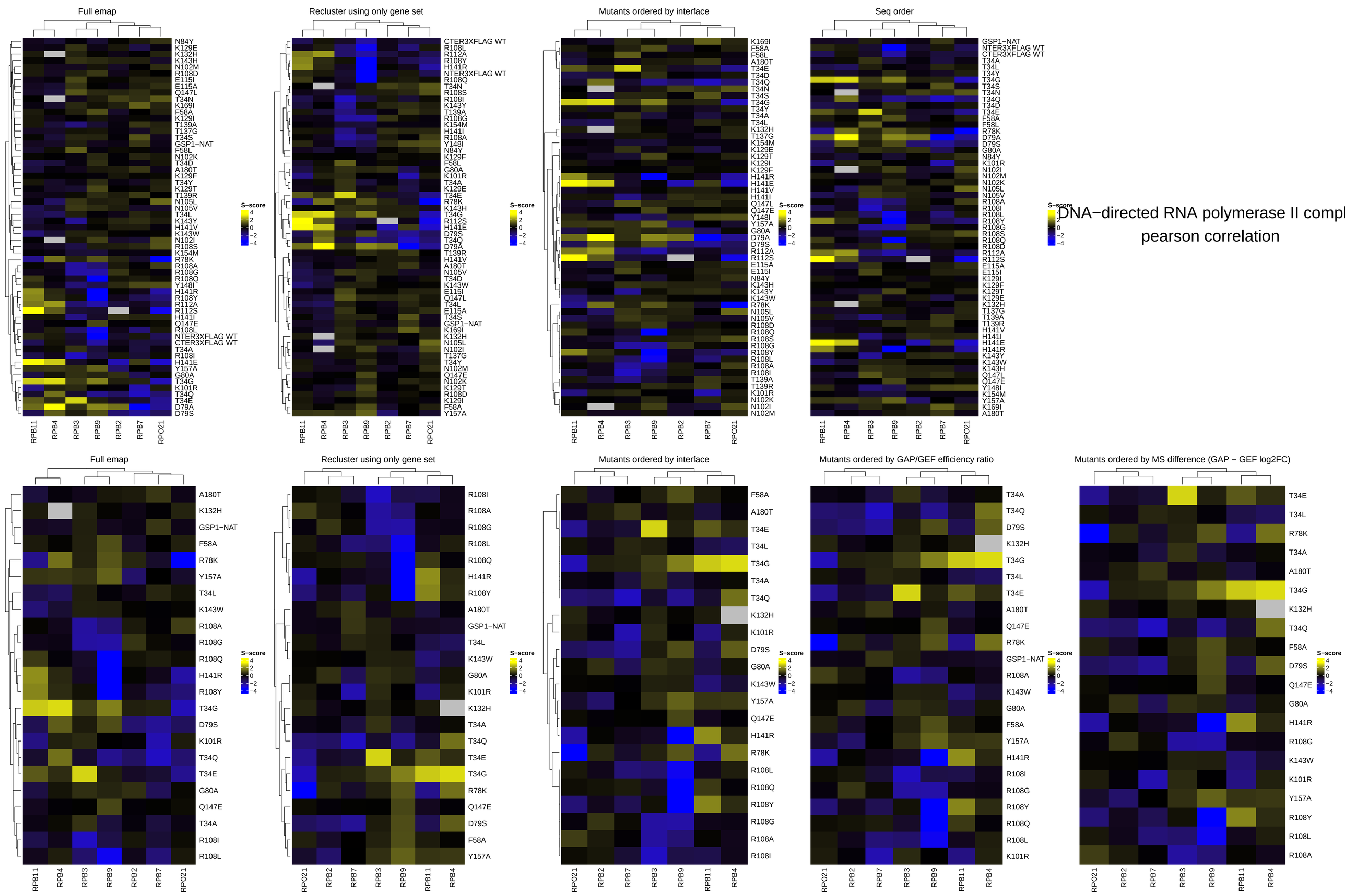


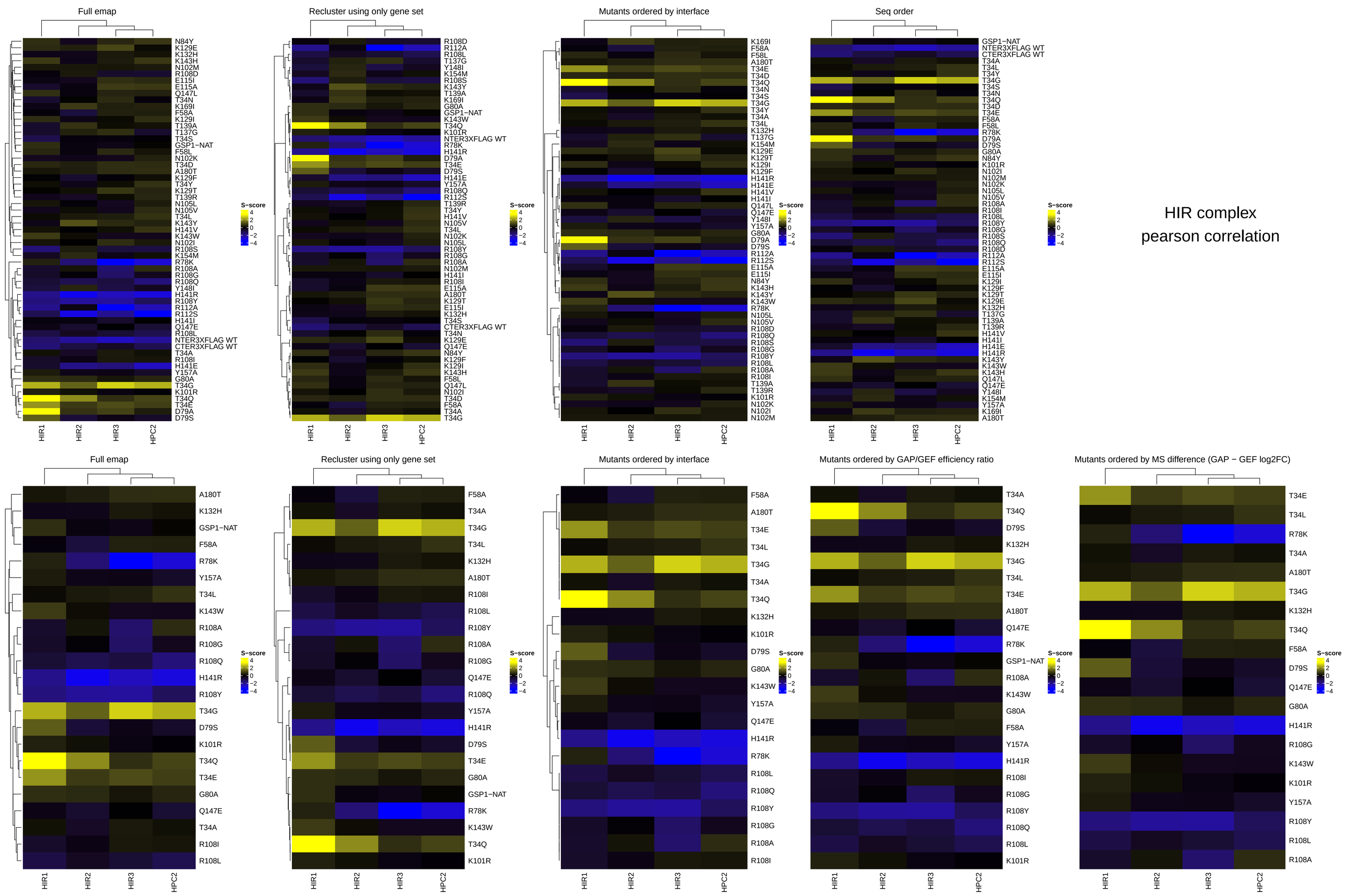
TRAPP complex
pearson correlation

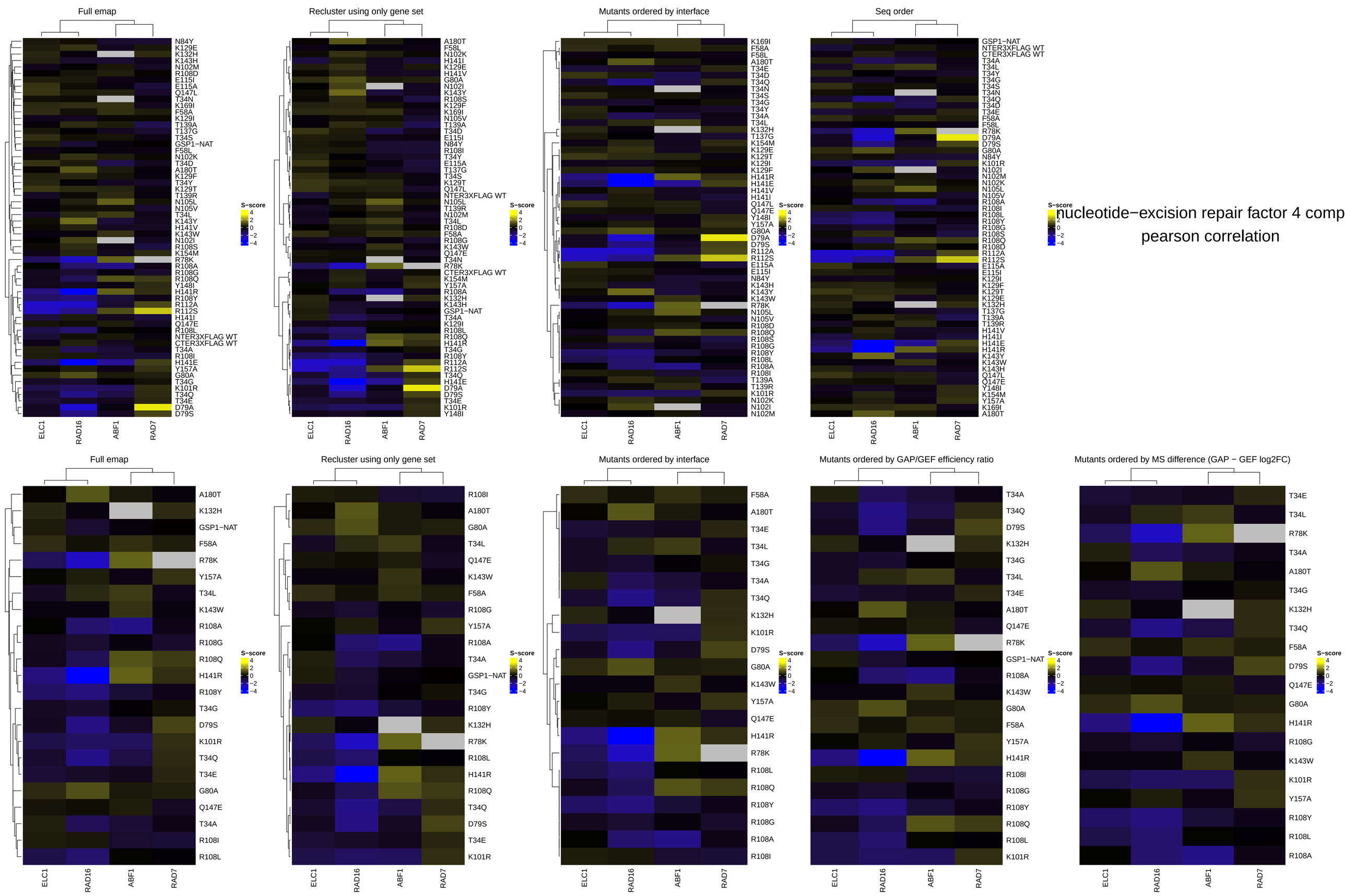

Ada2p/Gcn5p/Ada3 transcription activator co
pearson correlation
Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
AHC1
HFI1
ADA2
GCN5
NGG1

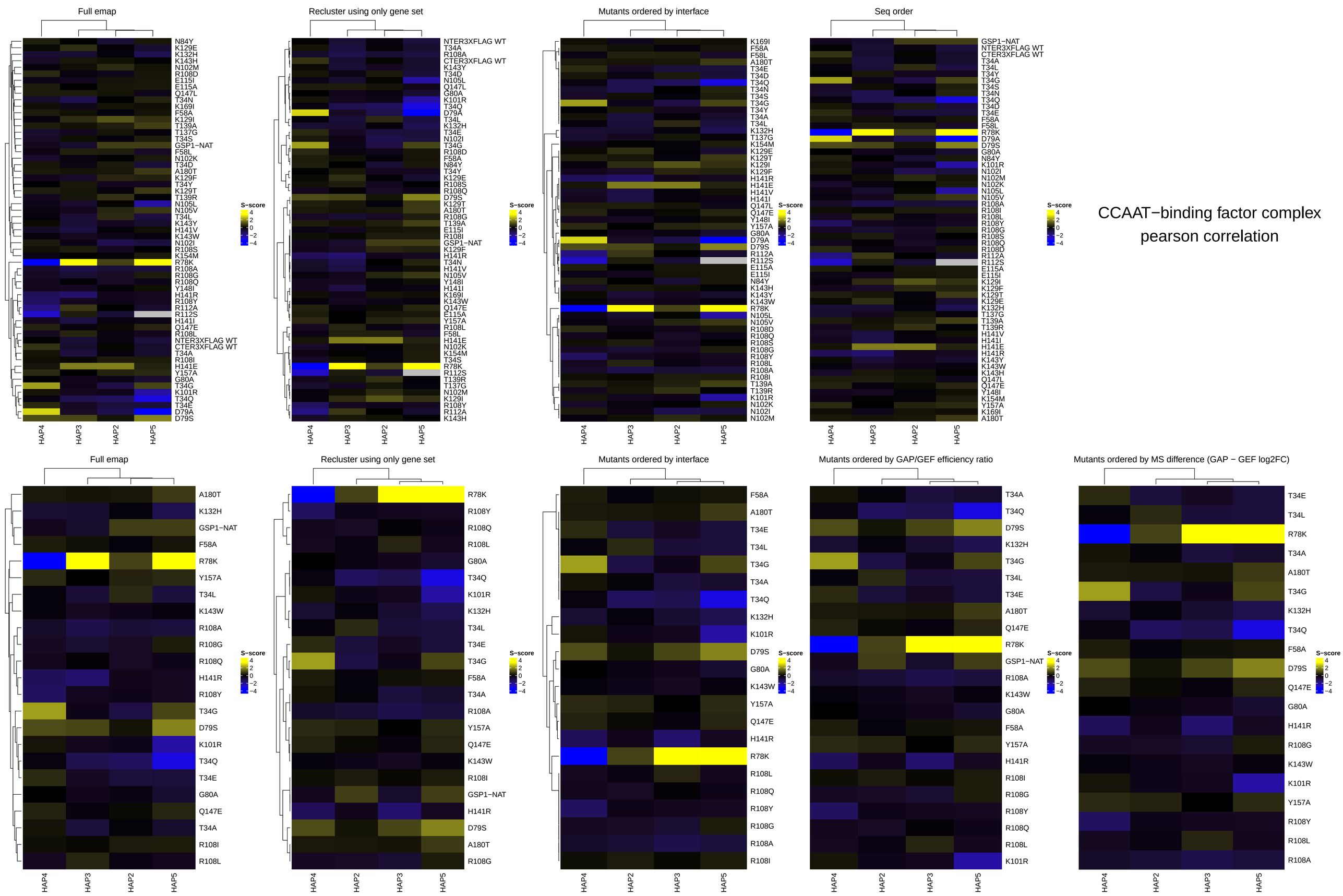

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
DPB4
ISW2
ITC1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
chromatin accessibility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

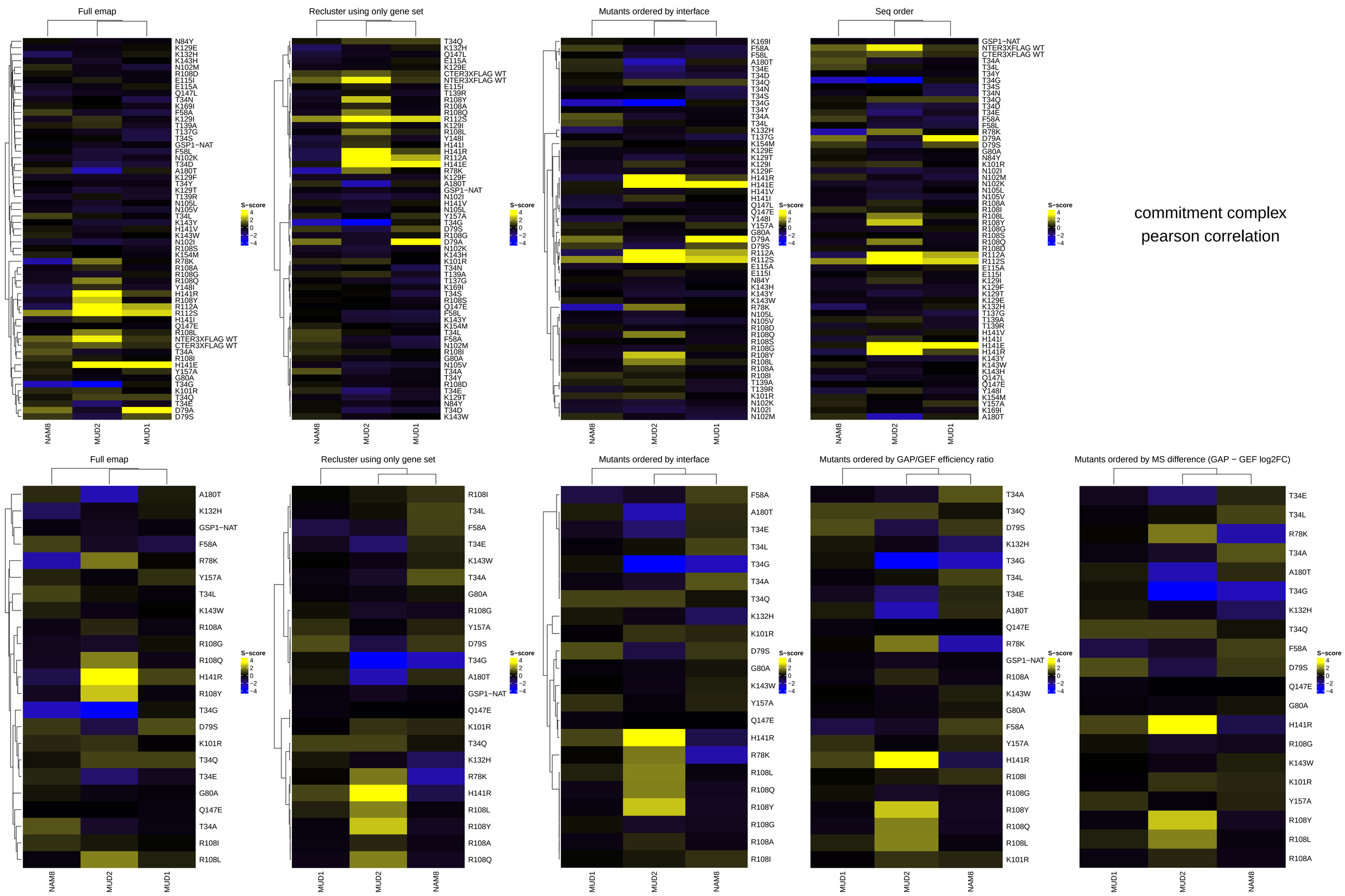

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
RNH203
RNH201
RNH202
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
ribonuclease H2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

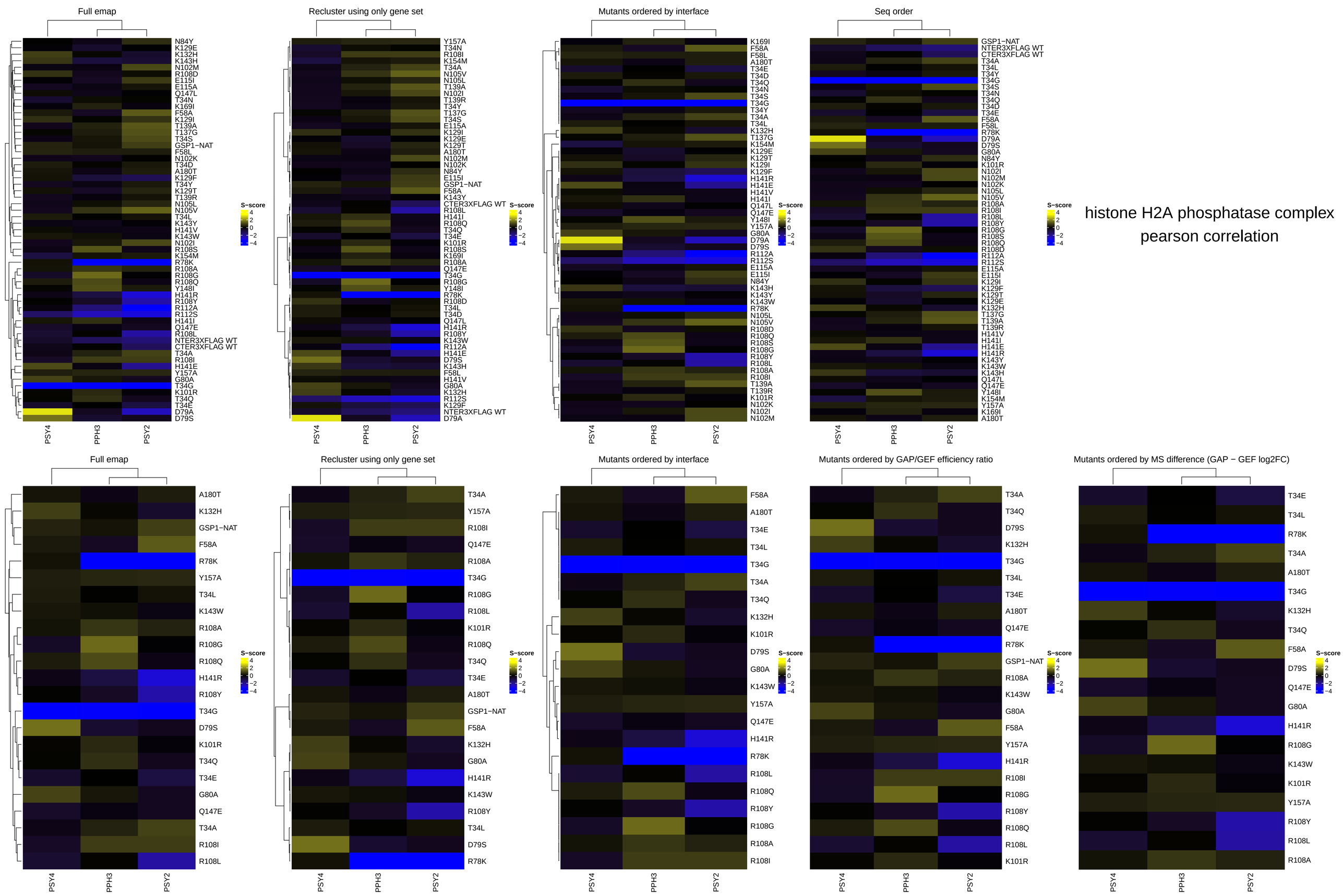

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
RPB11
RPB4
RPB3
RPB9
RPB2
RPB7
RPO21
DNA−directed RNA polymerase II compl
pearson correlation

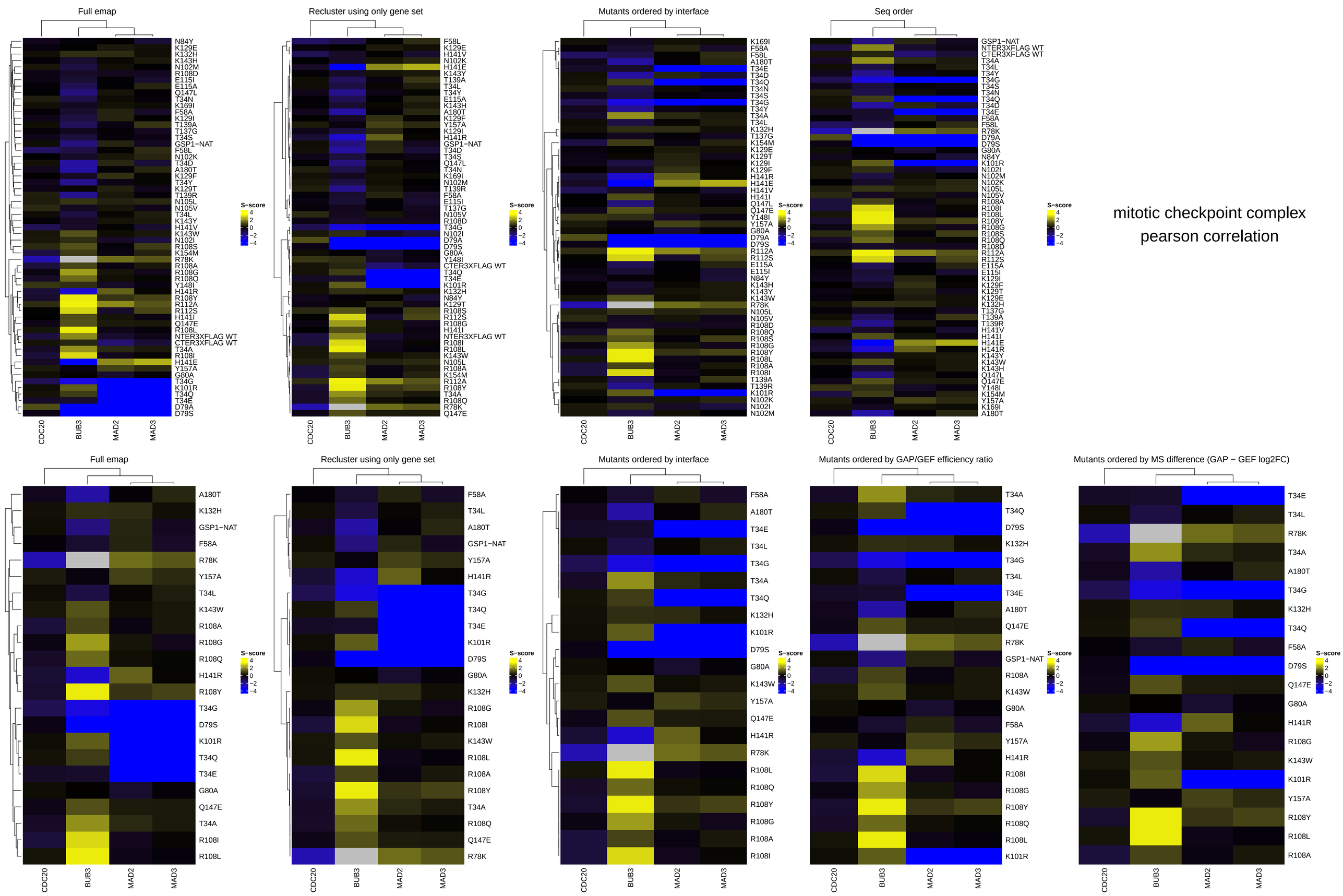

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HIR1
HIR2
HIR3
HPC2
HIR complex
pearson correlation

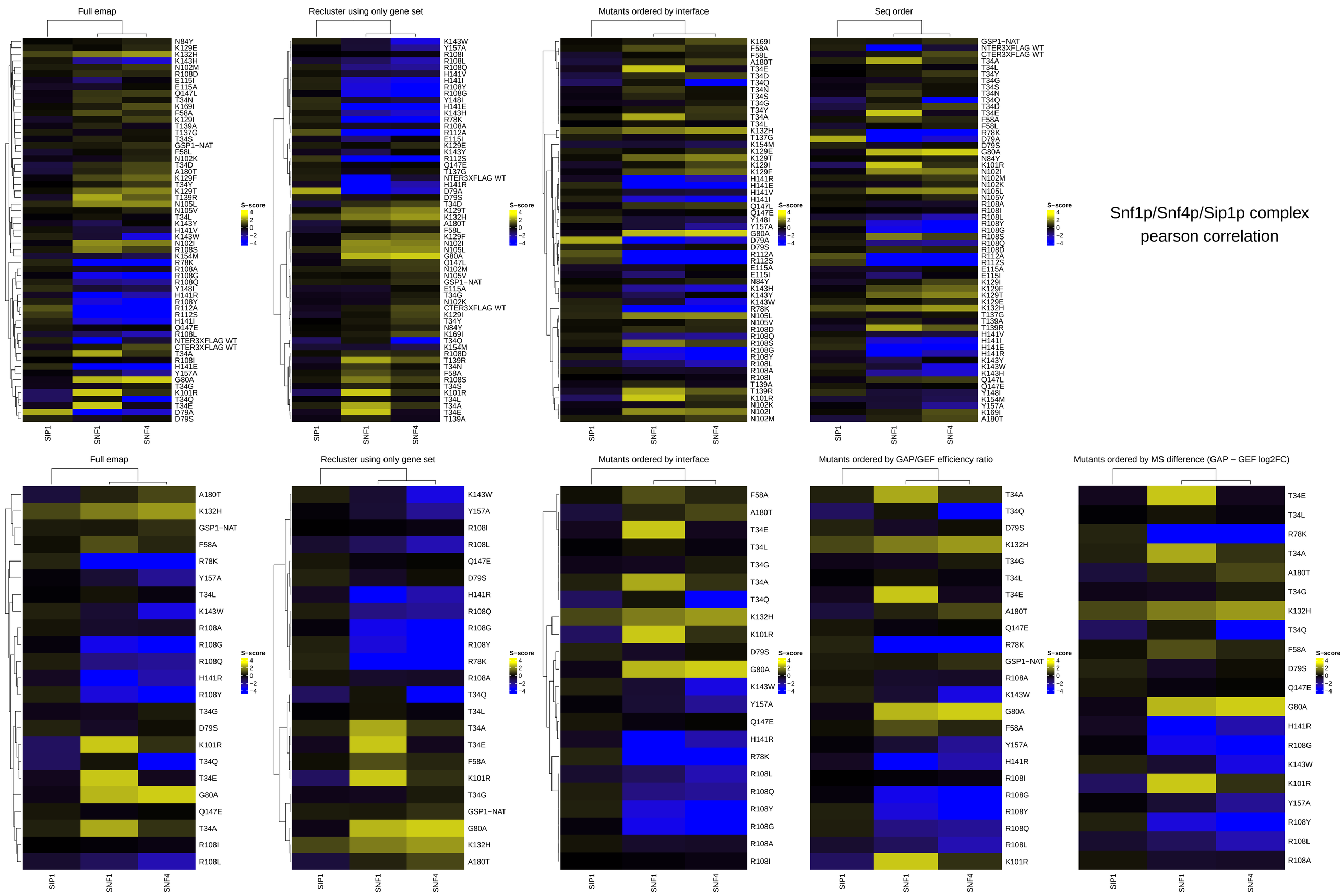

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
ELC1
RAD16
ABF1
RAD7
nucleotide−excision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

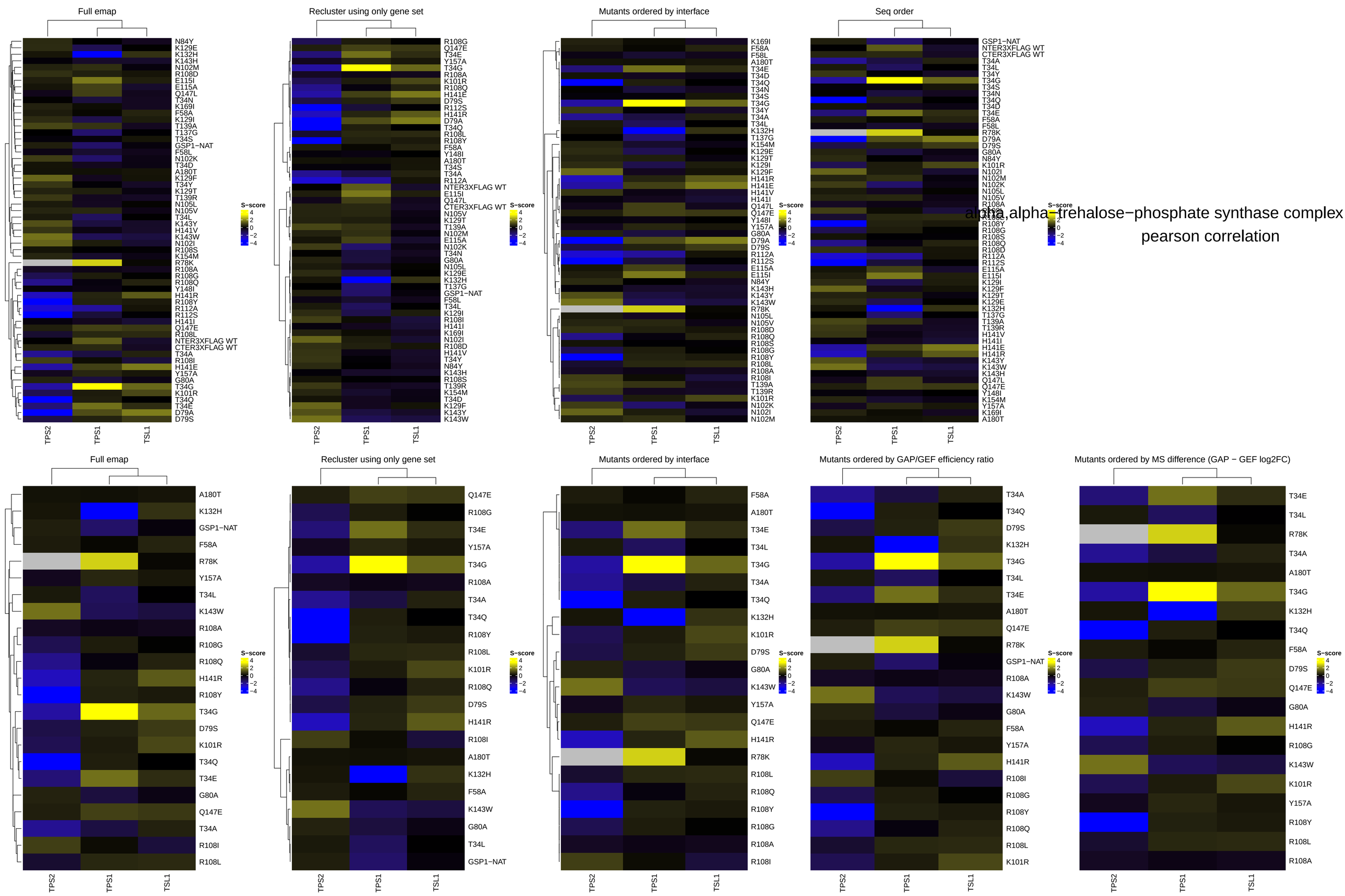

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
HAP4
HAP3
HAP2
HAP5
CCAAT−binding factor complex
pearson correlation

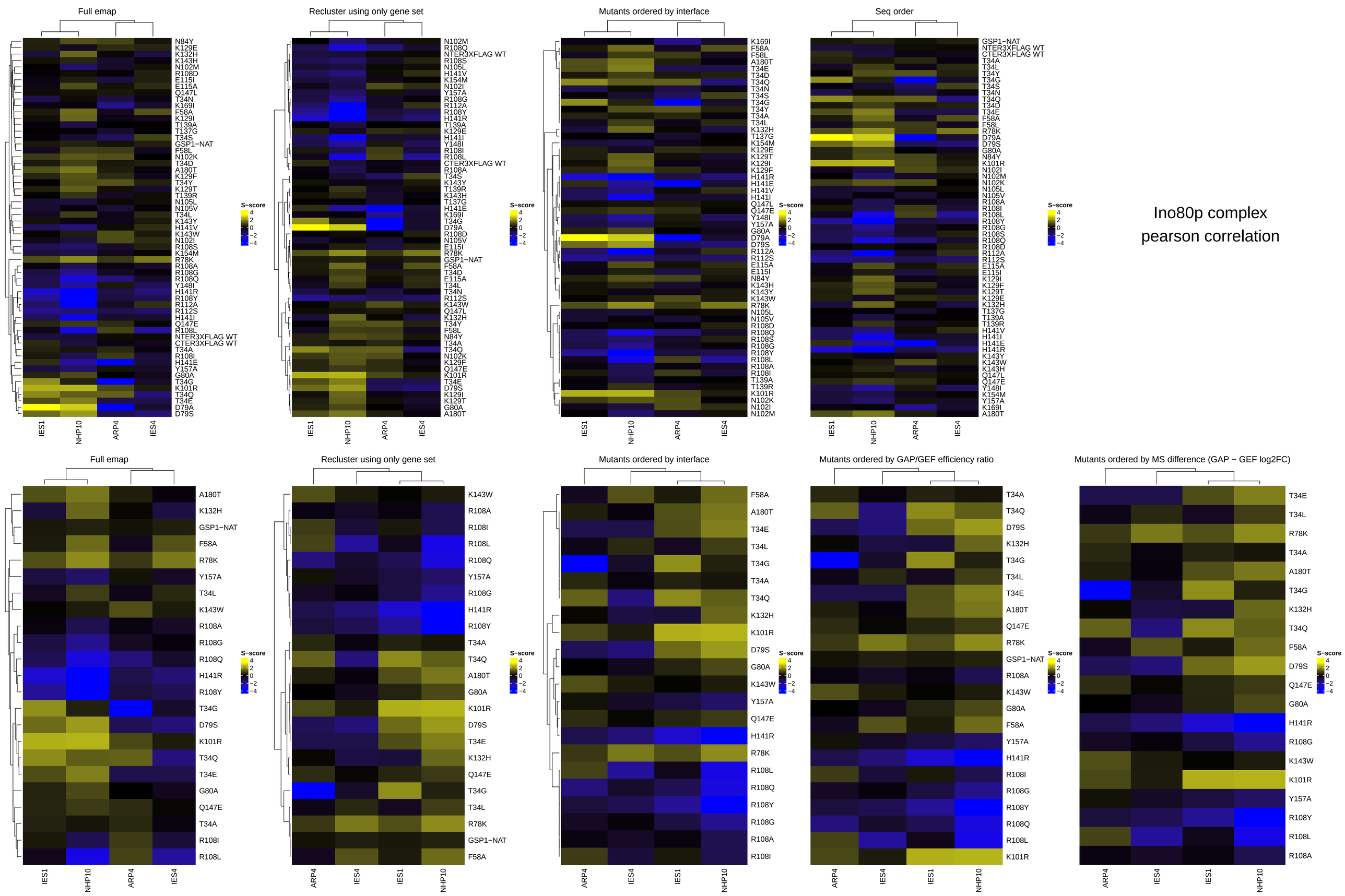

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
NAM8
MUD2
MUD1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
commitment complex
pearson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


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
pearson correlation

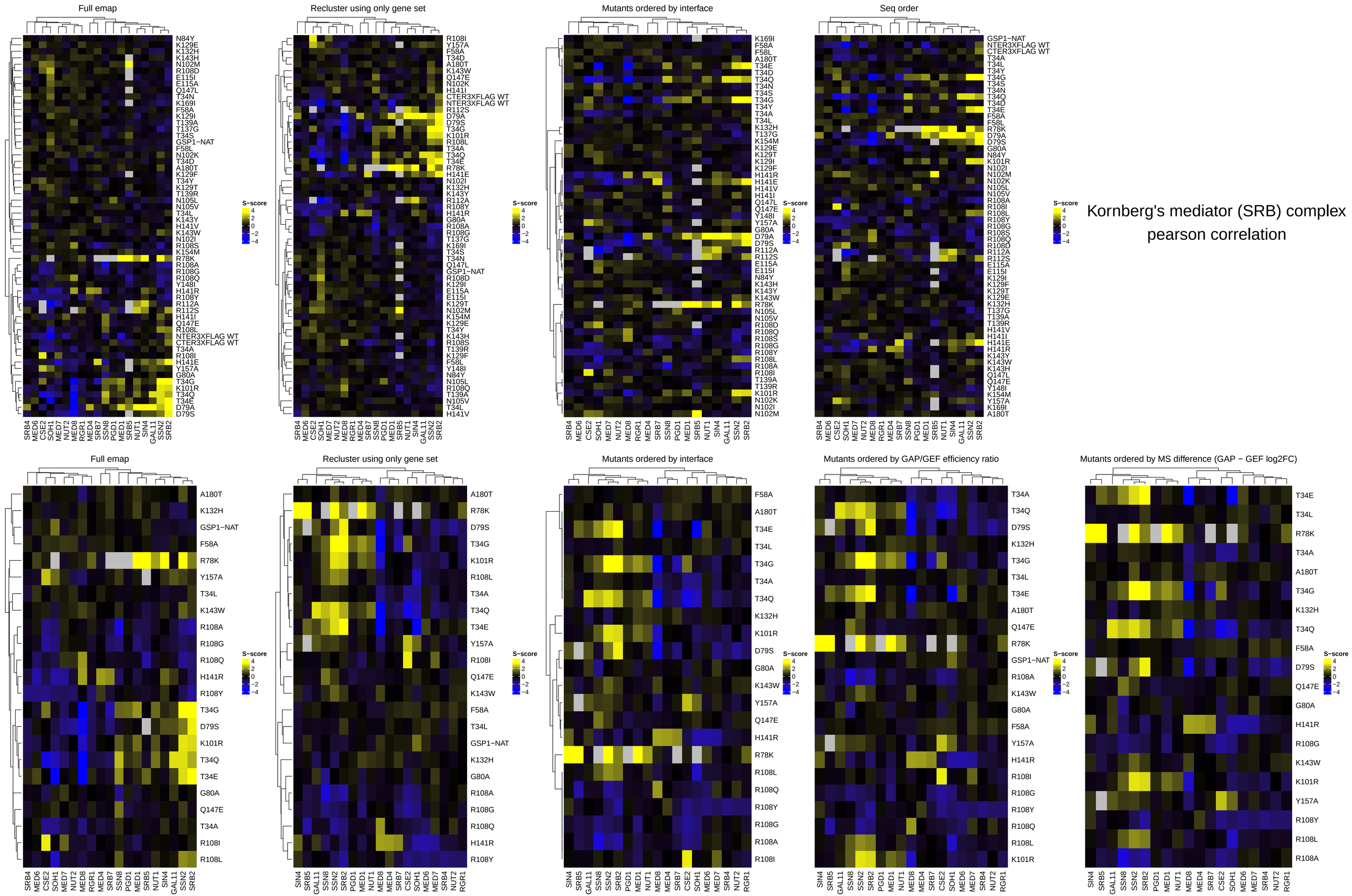

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CDC20
BUB3
MAD2
MAD3
mitotic checkpoint complex
pearson correlation


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
SIP1
SNF1
SNF4
Snf1p/Snf4p/Sip1p complex
pearson correlation

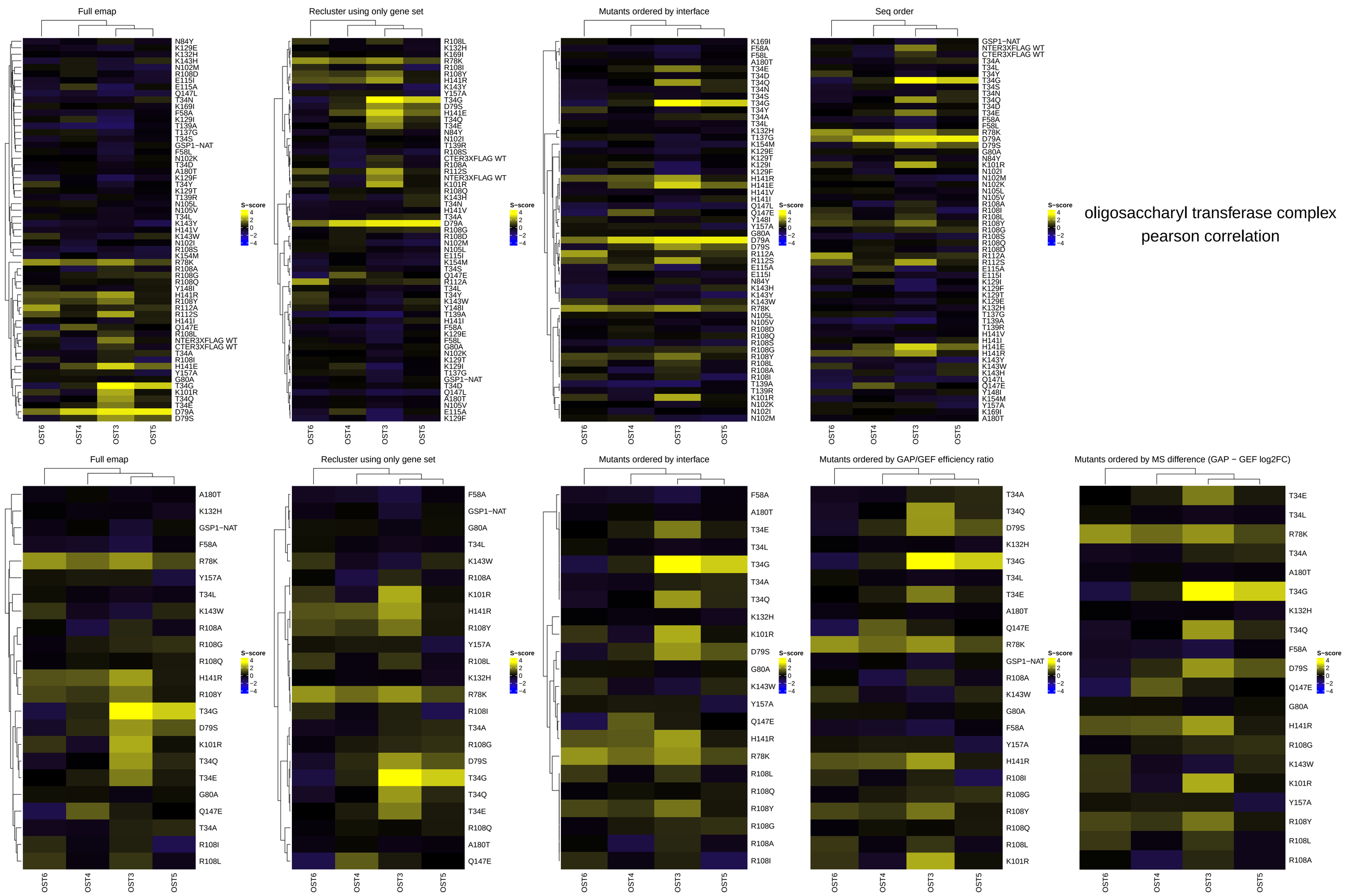

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
alpha,alpha−trehalose−phosphate synthase complex
pearson correlation
S−score
4
2
0
−2
−4
TPS2
TPS1
TSL1
Full emap
Recluster using only gene set
Mutants ordered by interface
Mutants ordered by GAP/GEF efficiency ratio
Mutants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

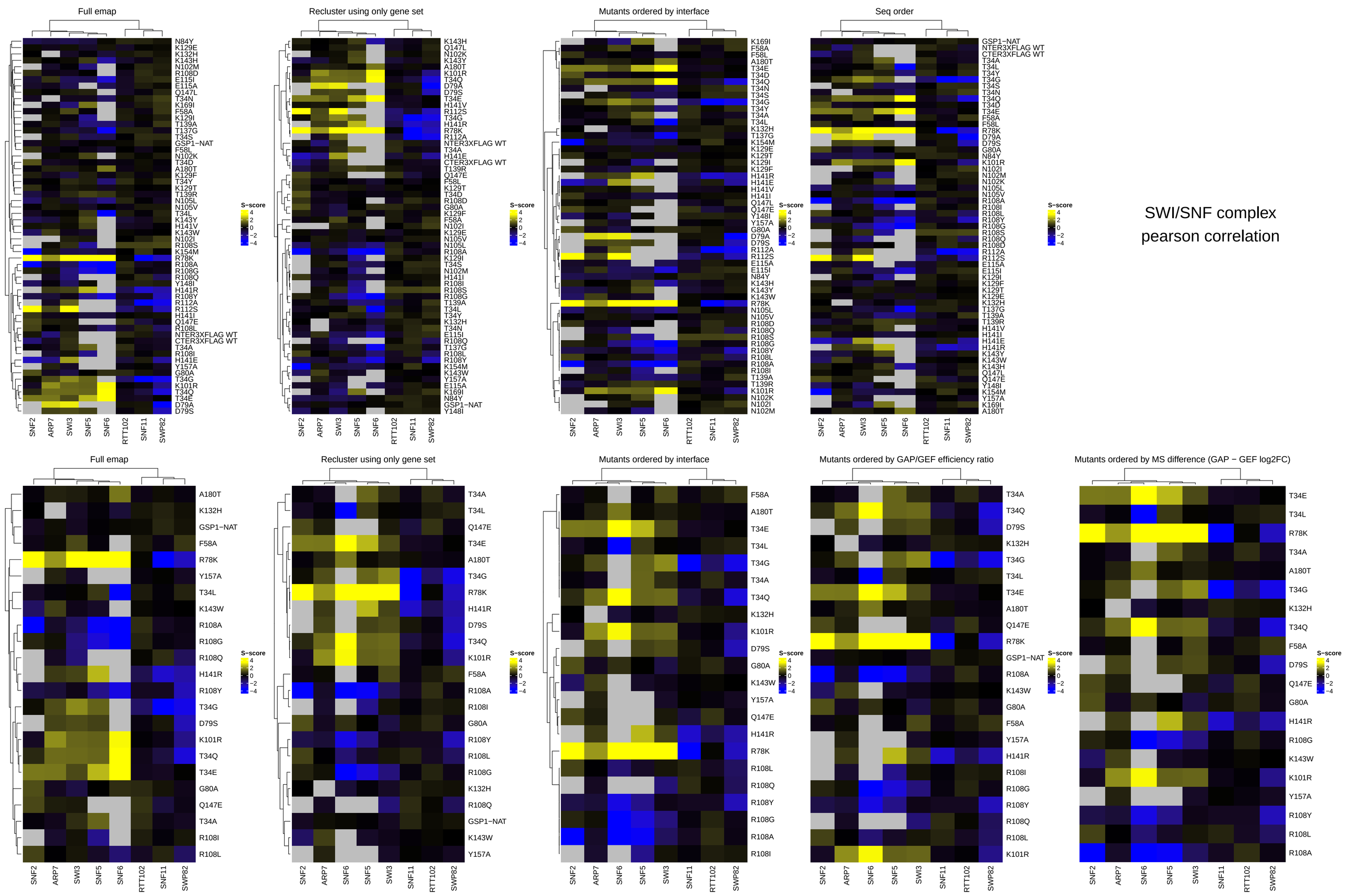


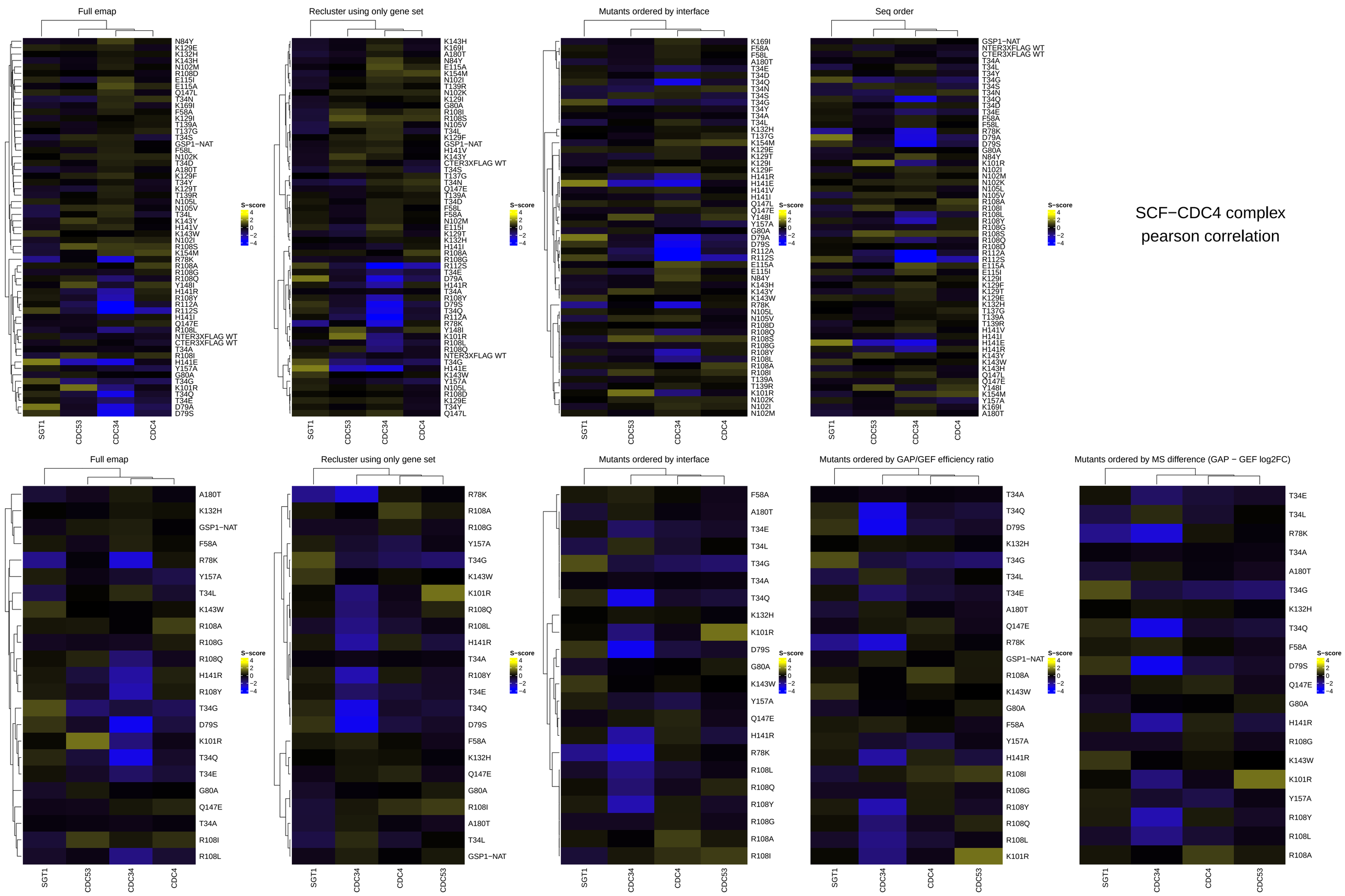
Ino80p complex
pearson correlation

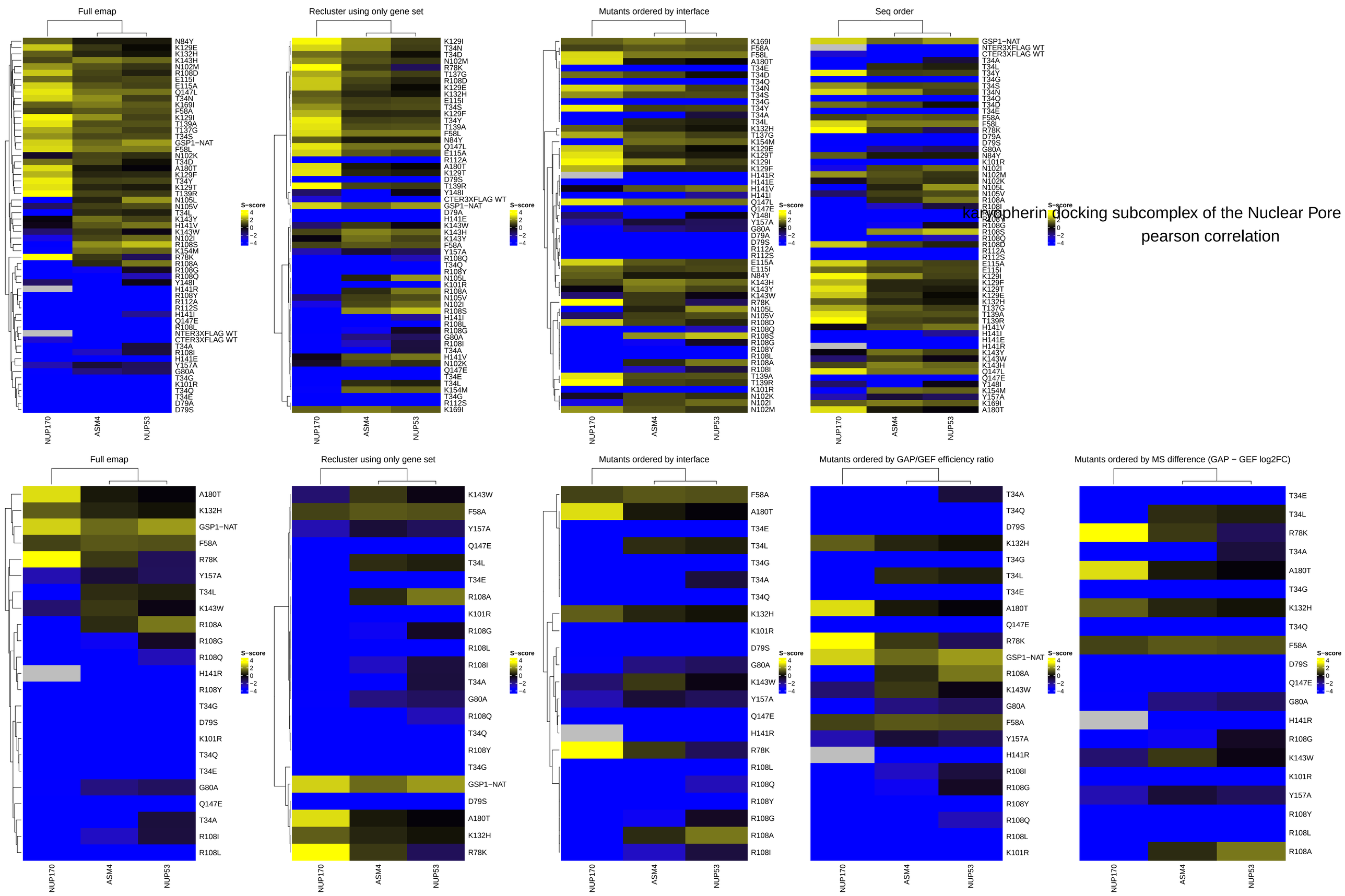


Kornberg's mediator (SRB) complex
pearson correlation


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
pearson correlation

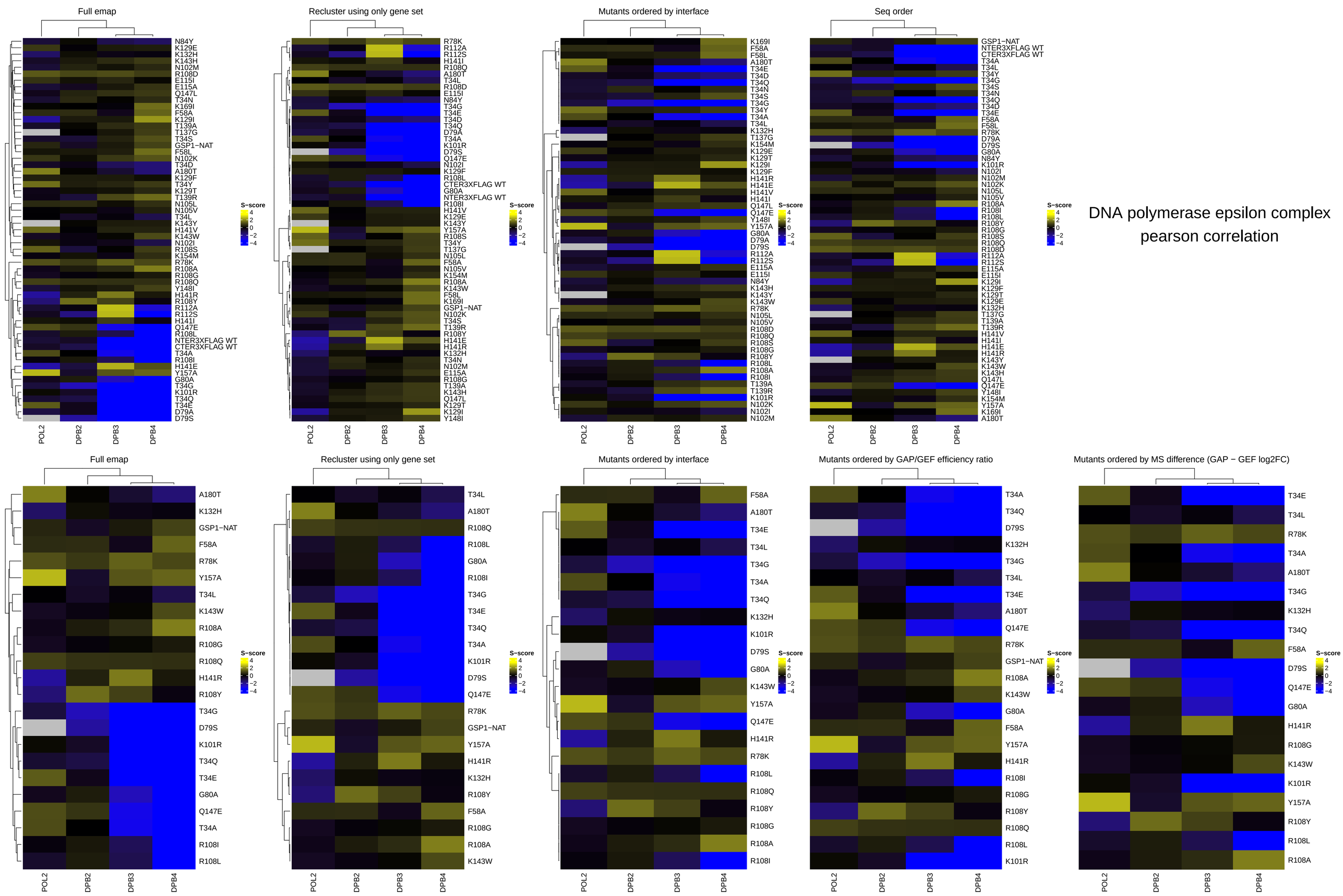

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SNF2
ARP7
SWI3
SNF5
SNF6
RTT102
SNF11
SWP82
SWI/SNF complex
pearson correlation

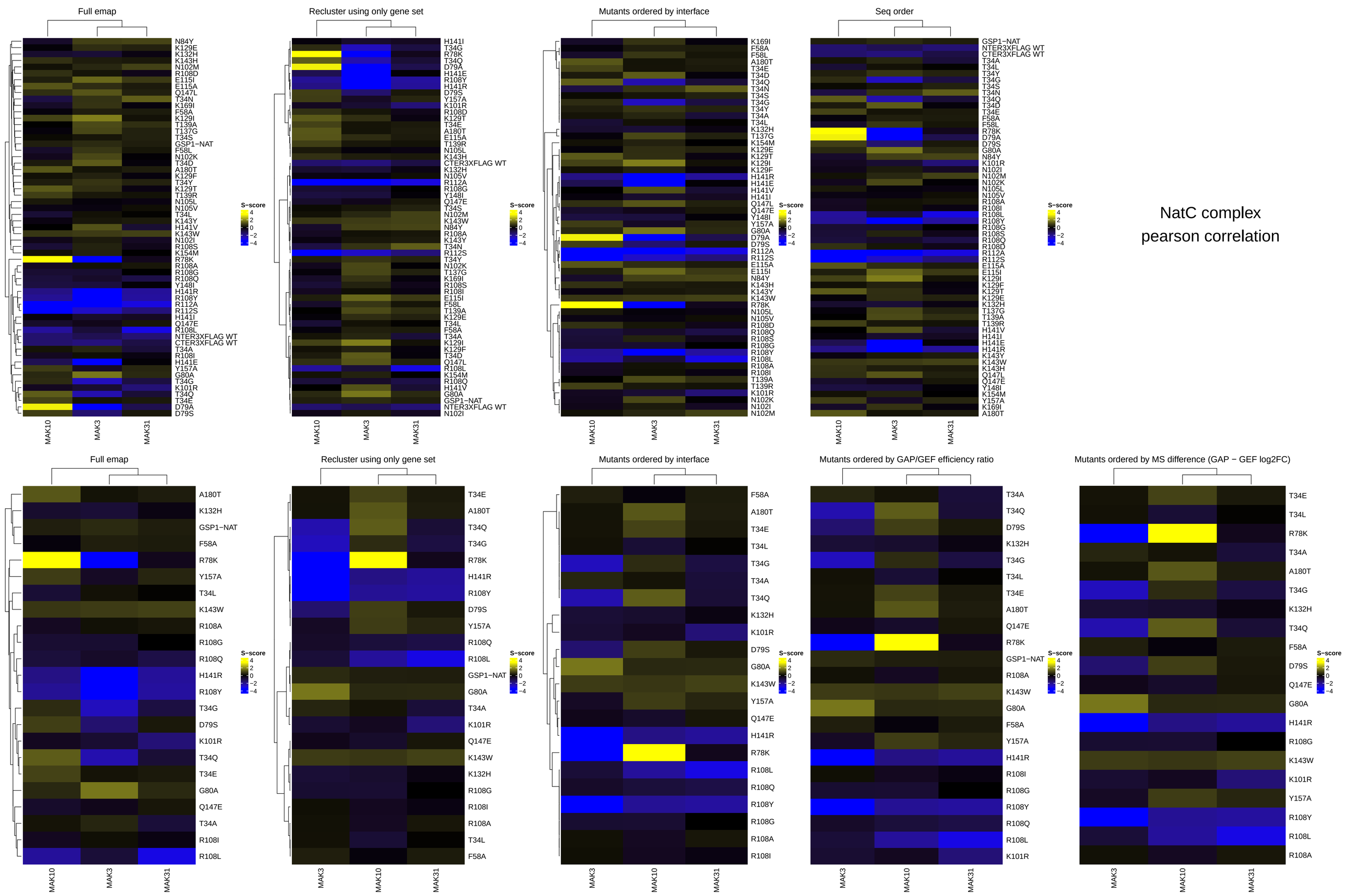

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
SGT1
CDC53
CDC34
CDC4
SCF−CDC4 complex
pearson correlation



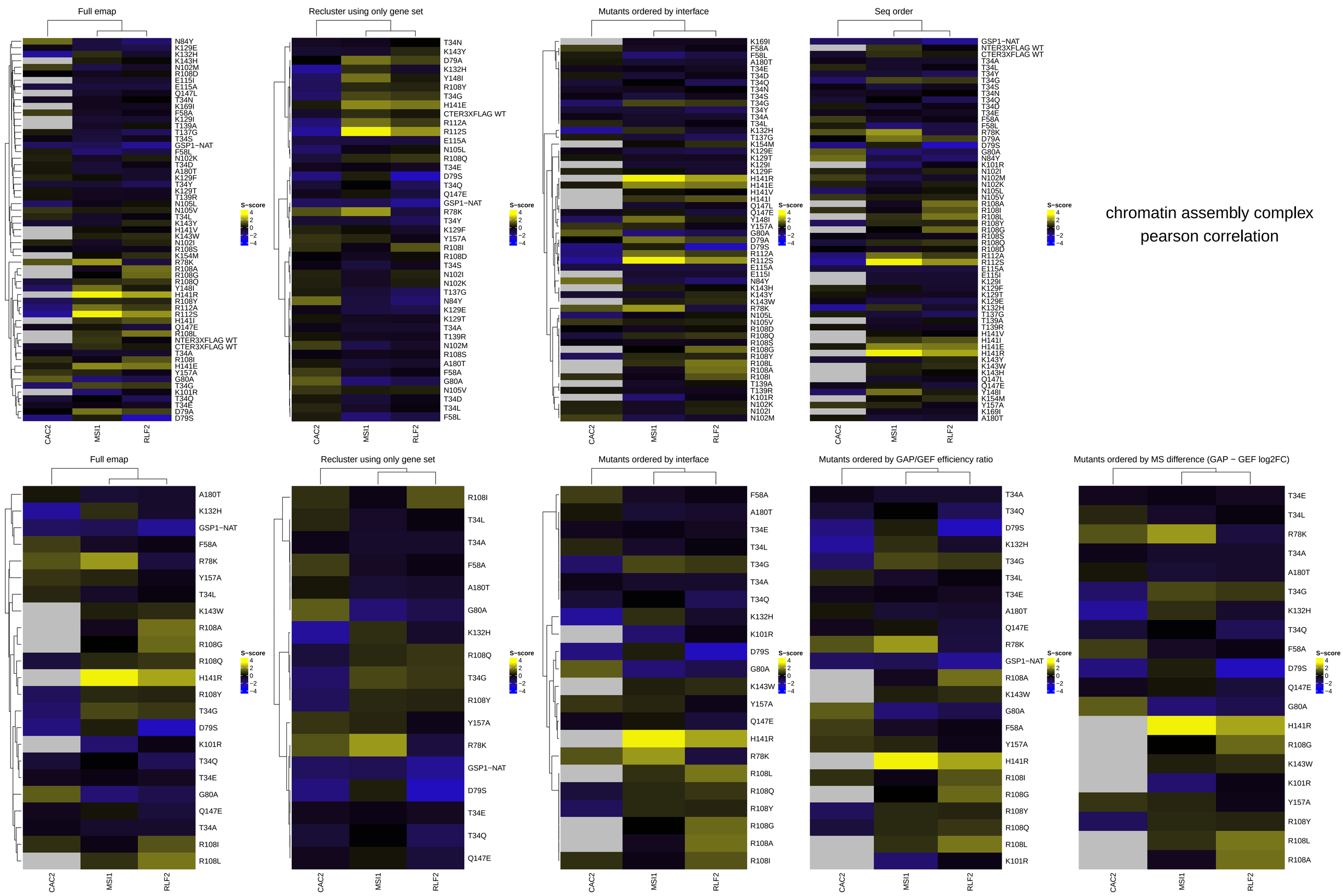
karyopherin docking subcomplex of the Nuclear Pore

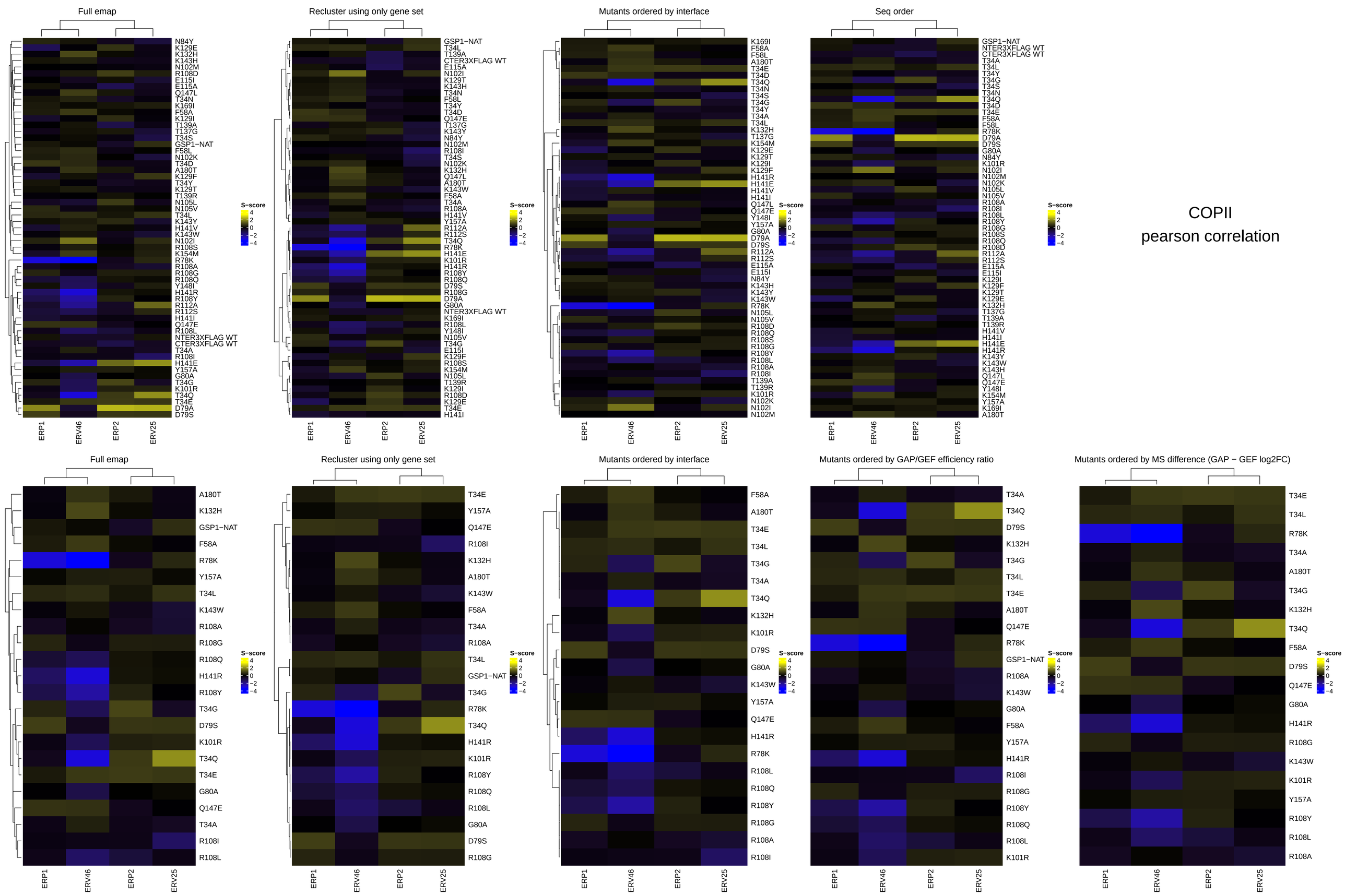
pearson correlation

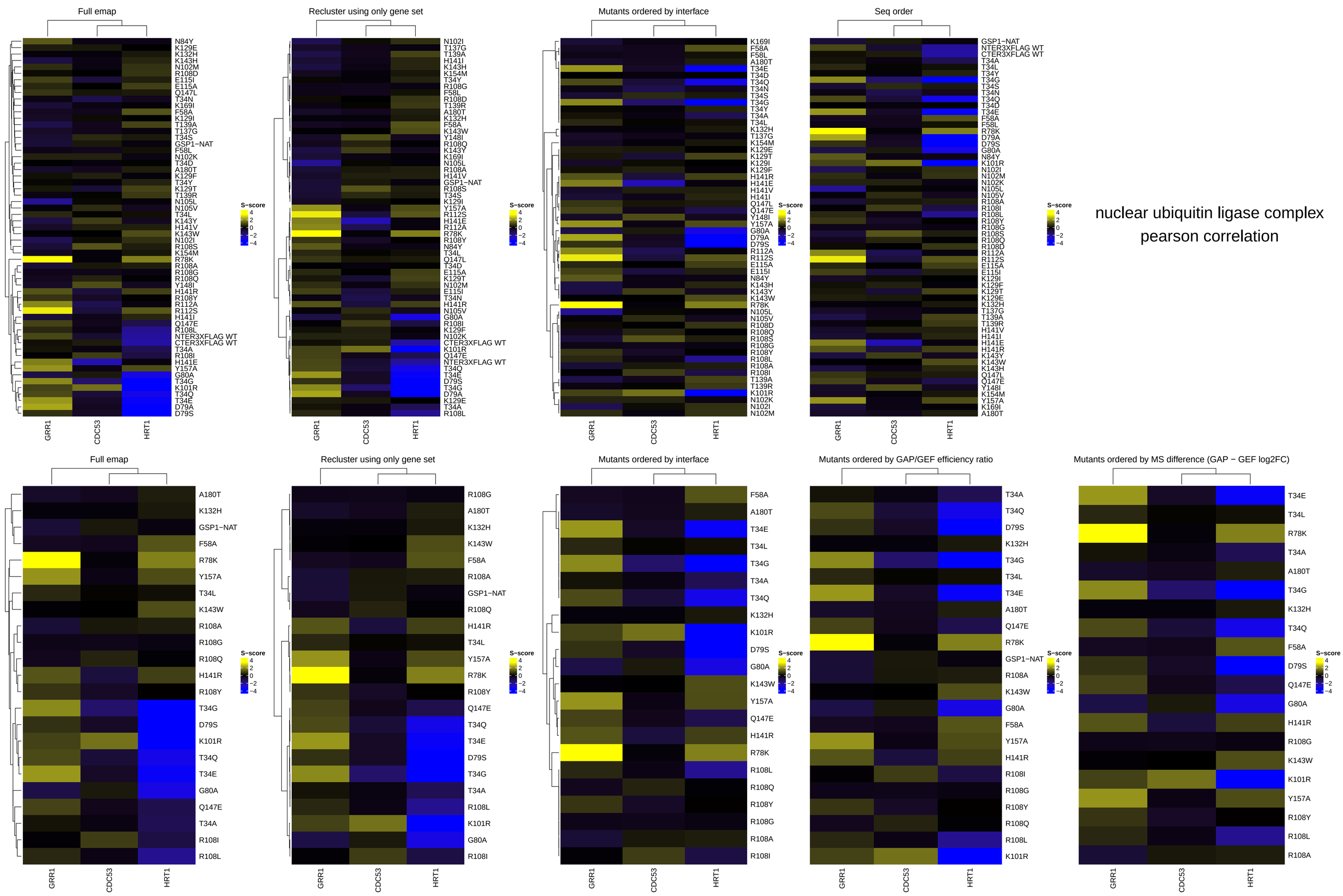

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
POL2
DPB2
DPB3
DPB4
DNA polymerase epsilon complex
pearson correlation



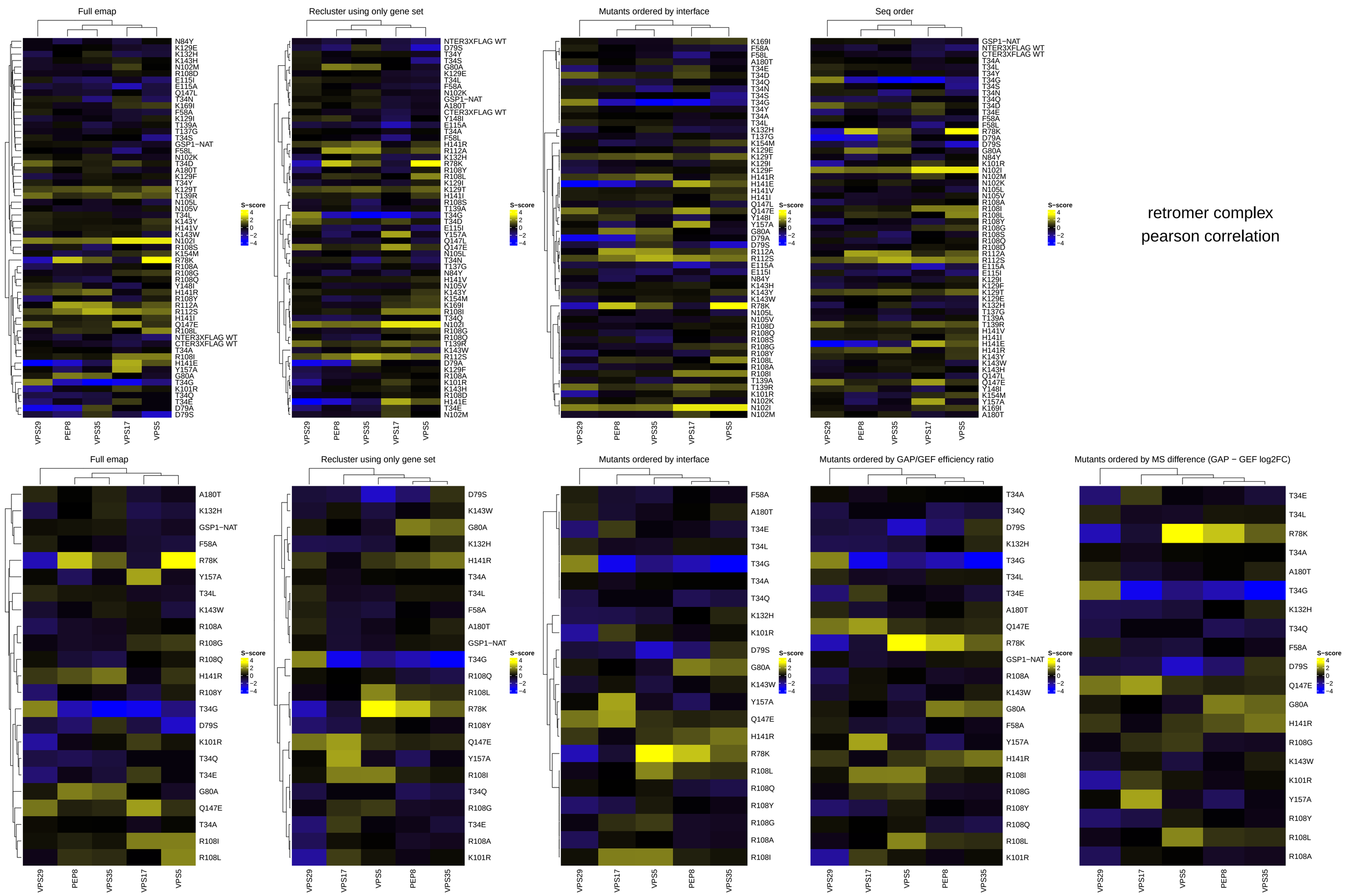
NatC complex
pearson correlation

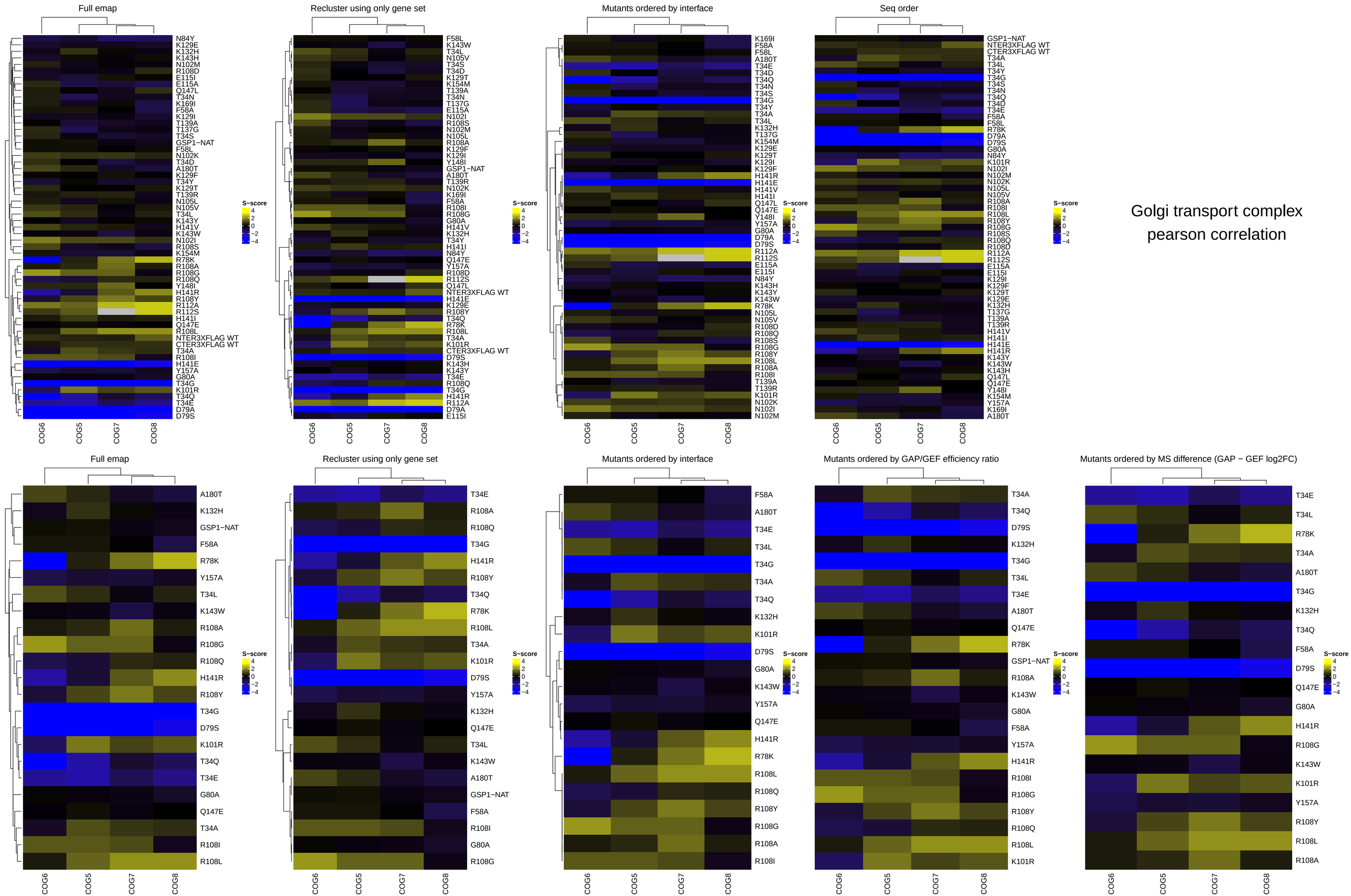

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
CAC2
MSI1
RLF2
chromatin assembly complex
pearson correlation


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
pearson correlation

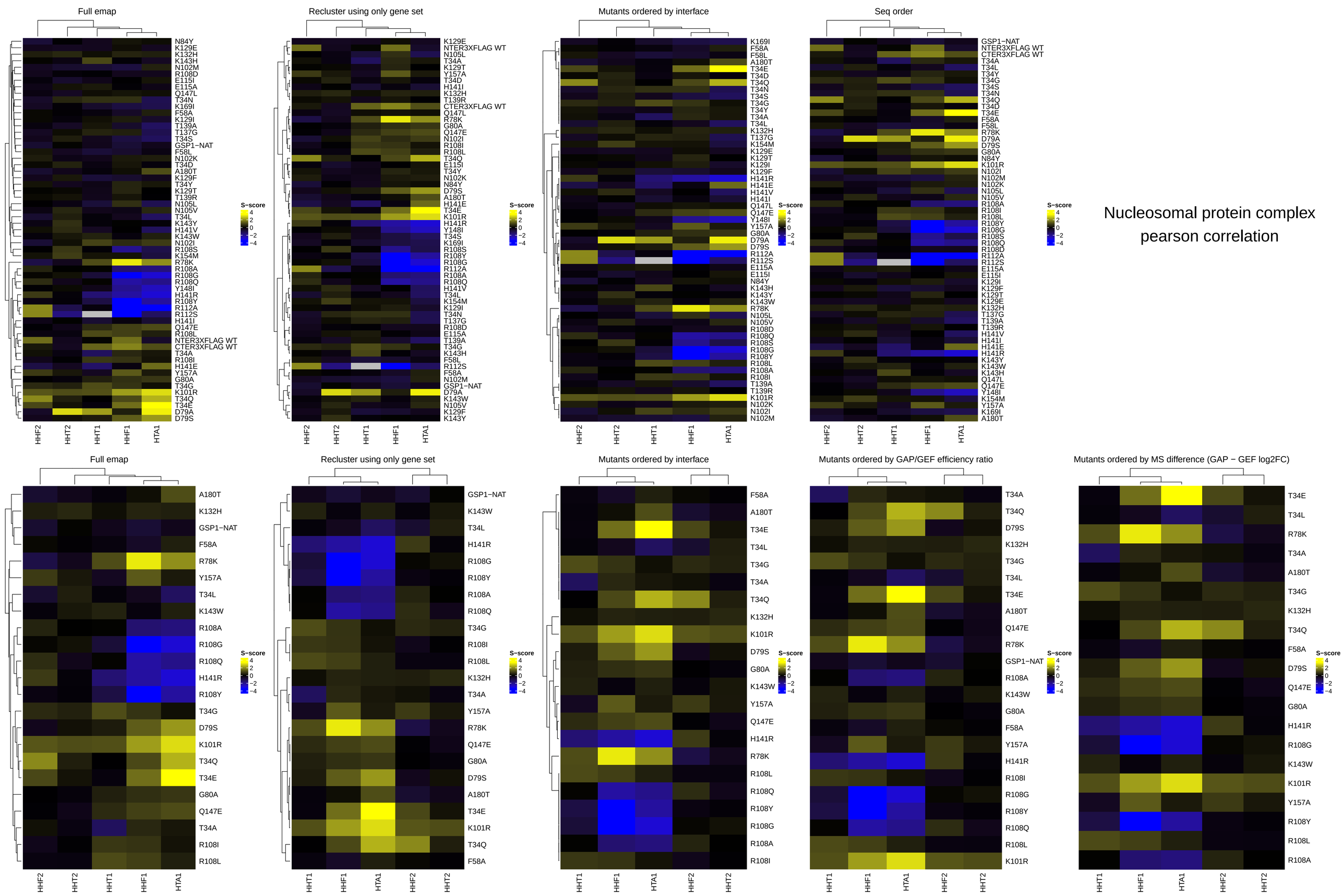


nuclear ubiquitin ligase complex
pearson correlation


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
PEP8
VPS35
VPS17
VPS5
retromer complex
pearson correlation



Golgi transport complex
pearson correlation


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
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
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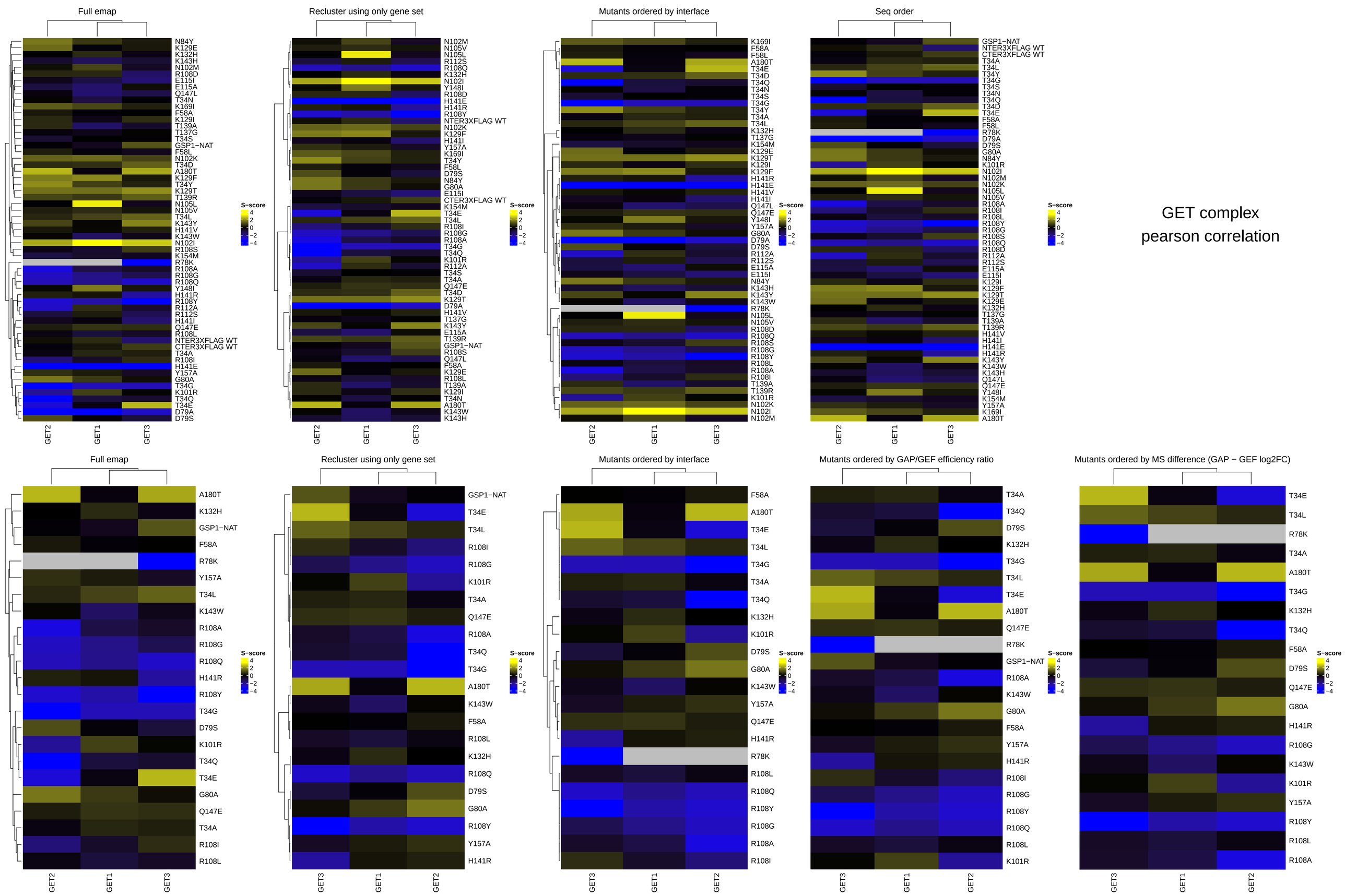
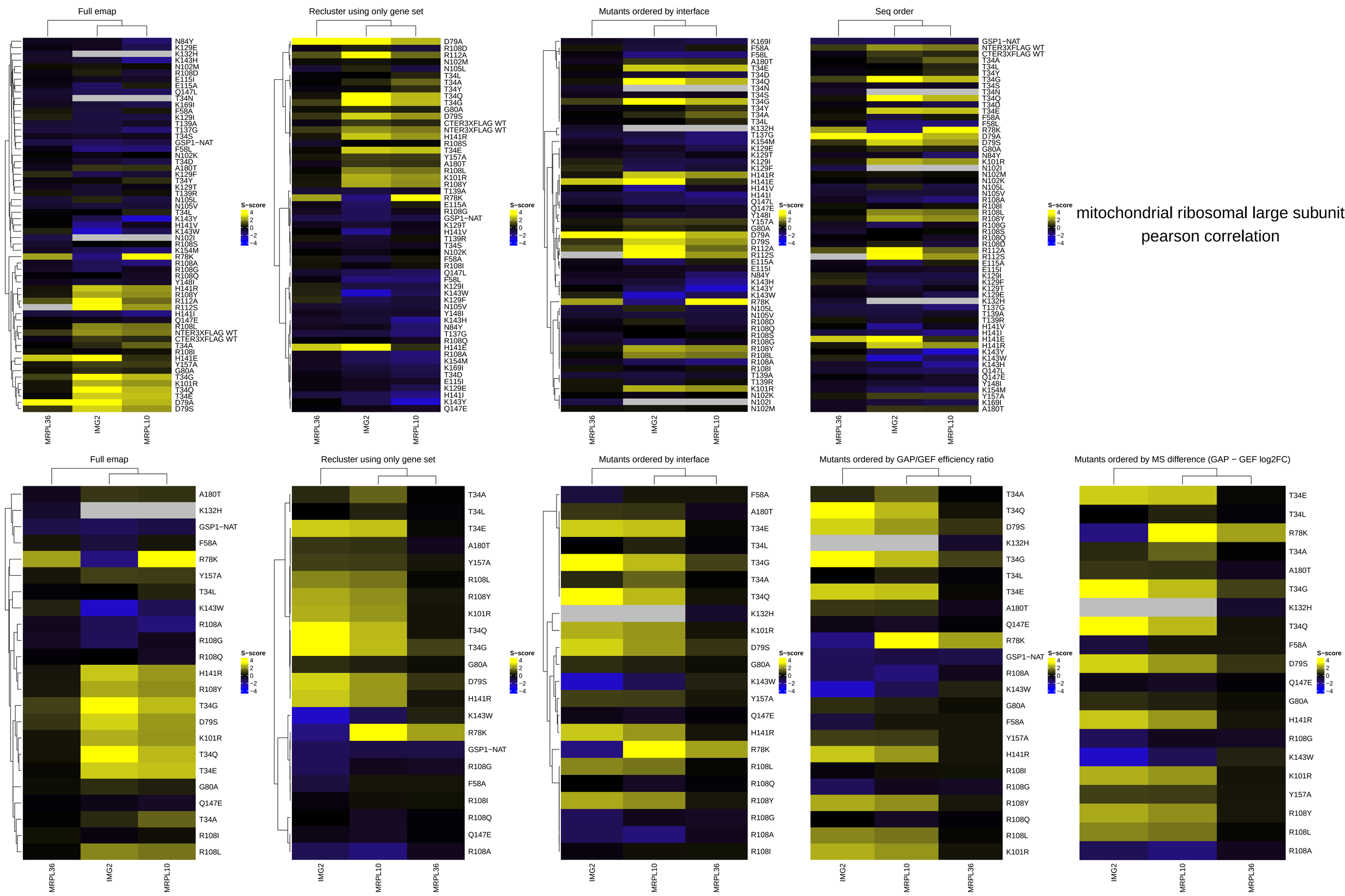
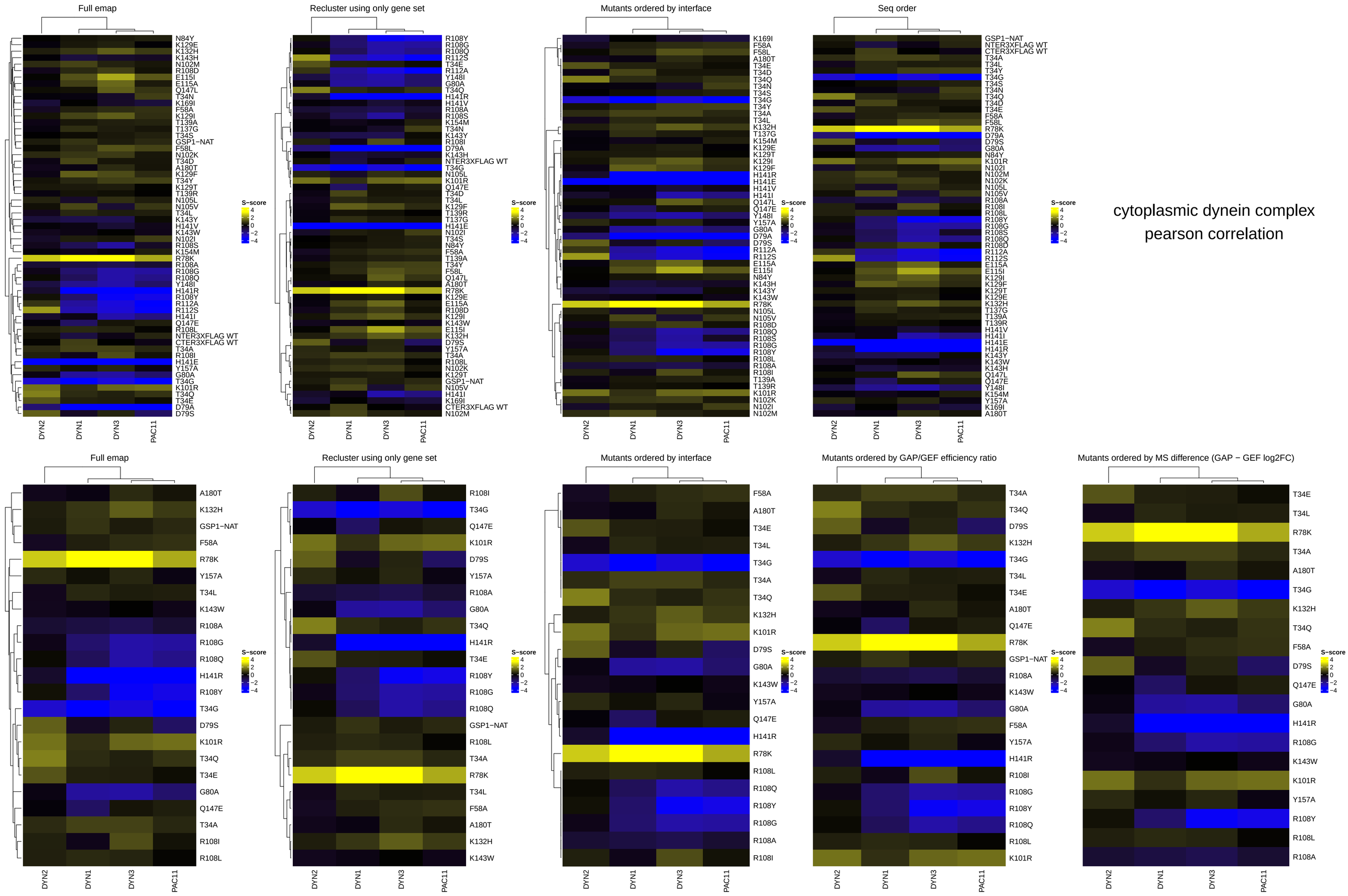
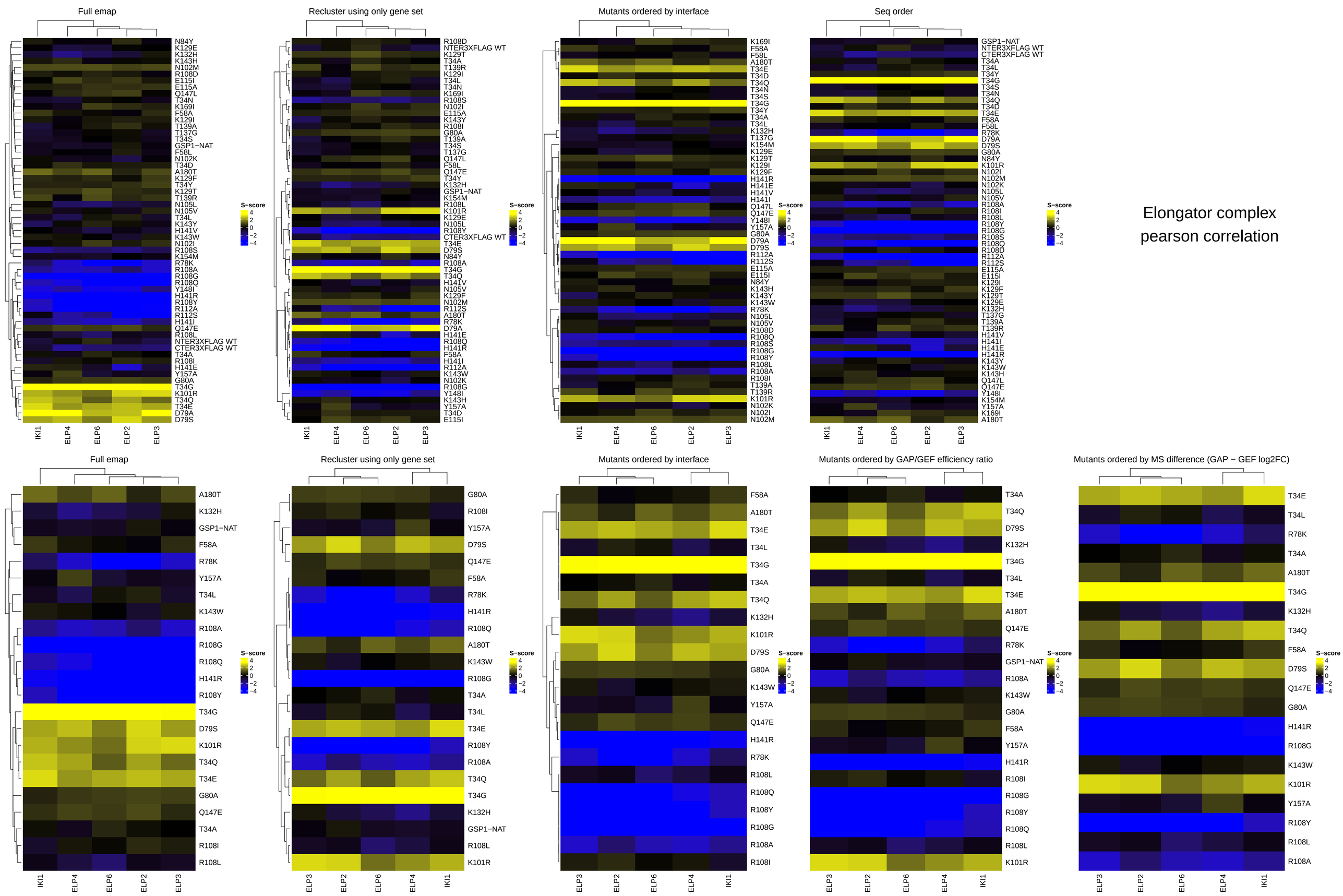
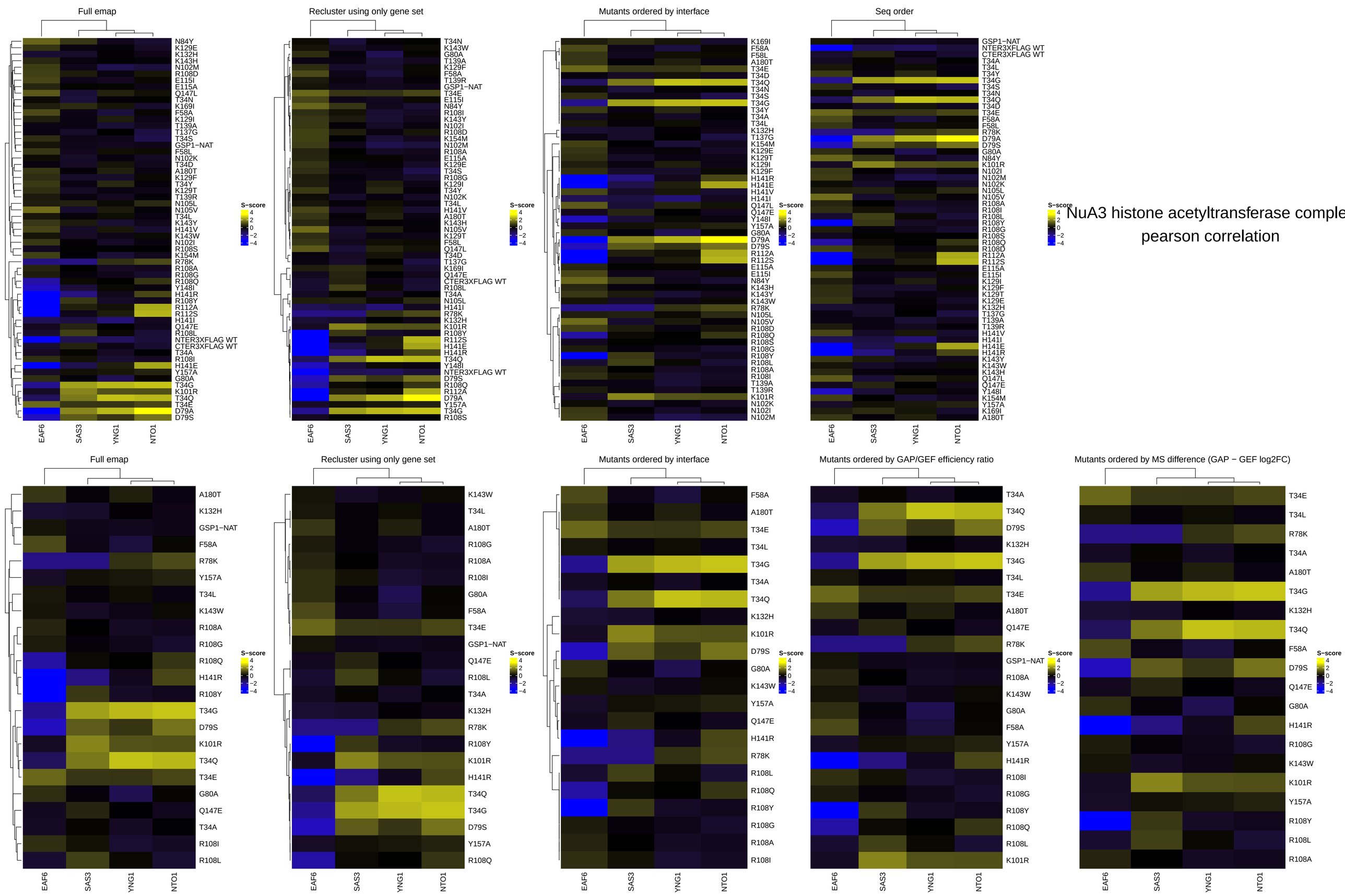
D79A
D79S
CTER3XFLAG WT
R78K
D79S
Nucleosomal protein complex
pearson correlation


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


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
pearson correlation


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
DYN2
DYN1
DYN3
PAC11
cytoplasmic dynein complex
pearson correlation


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
pearson correlation


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
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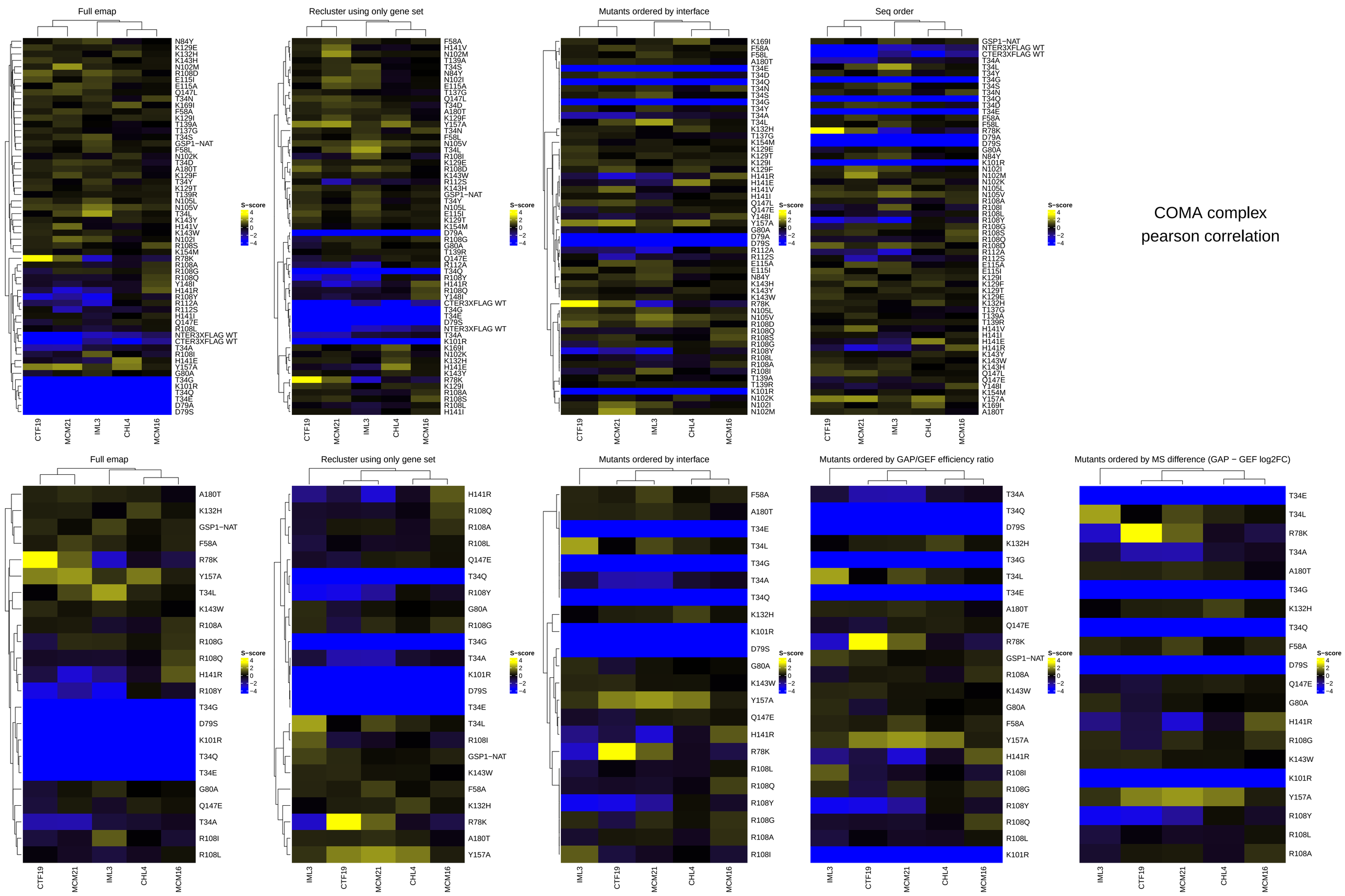
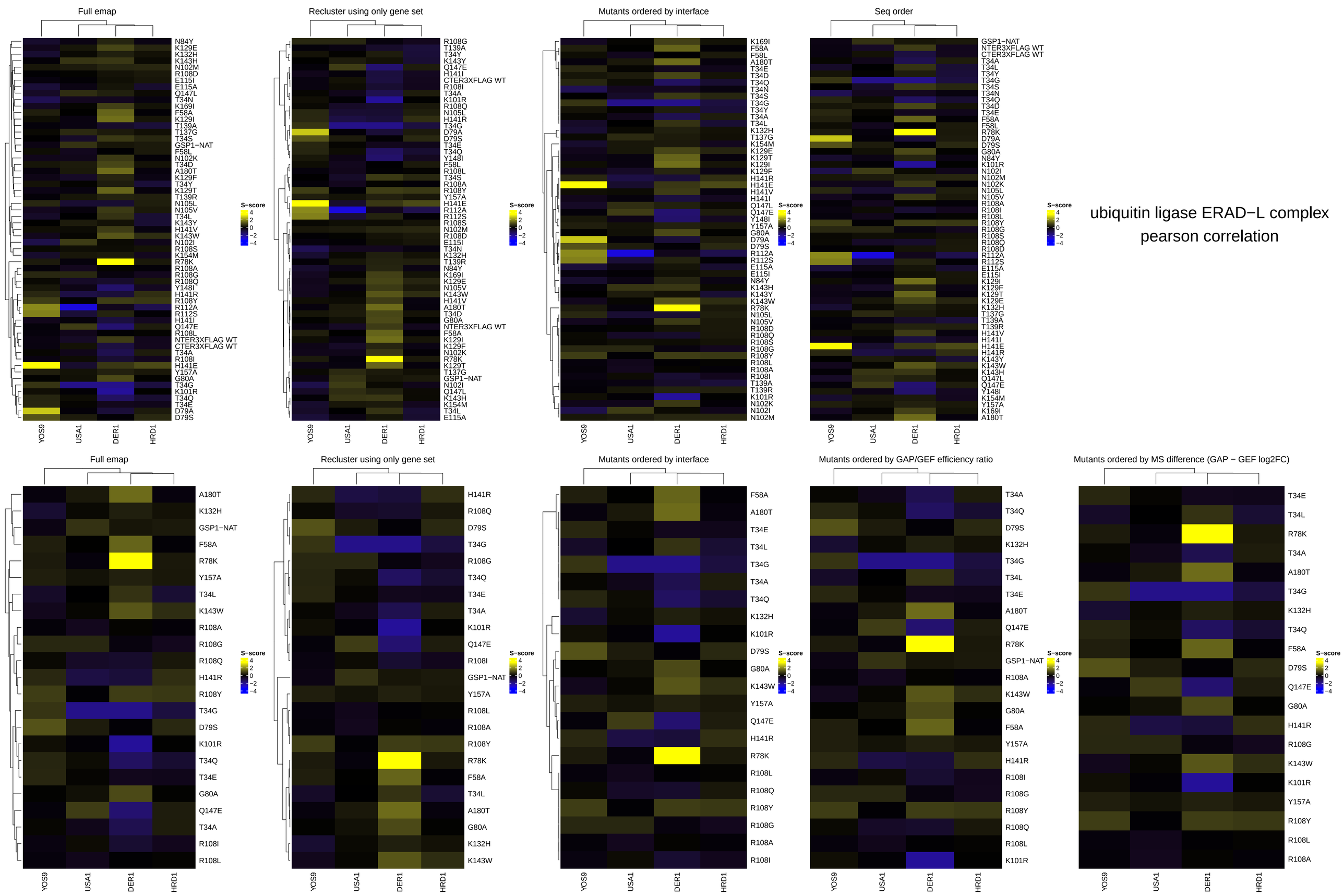
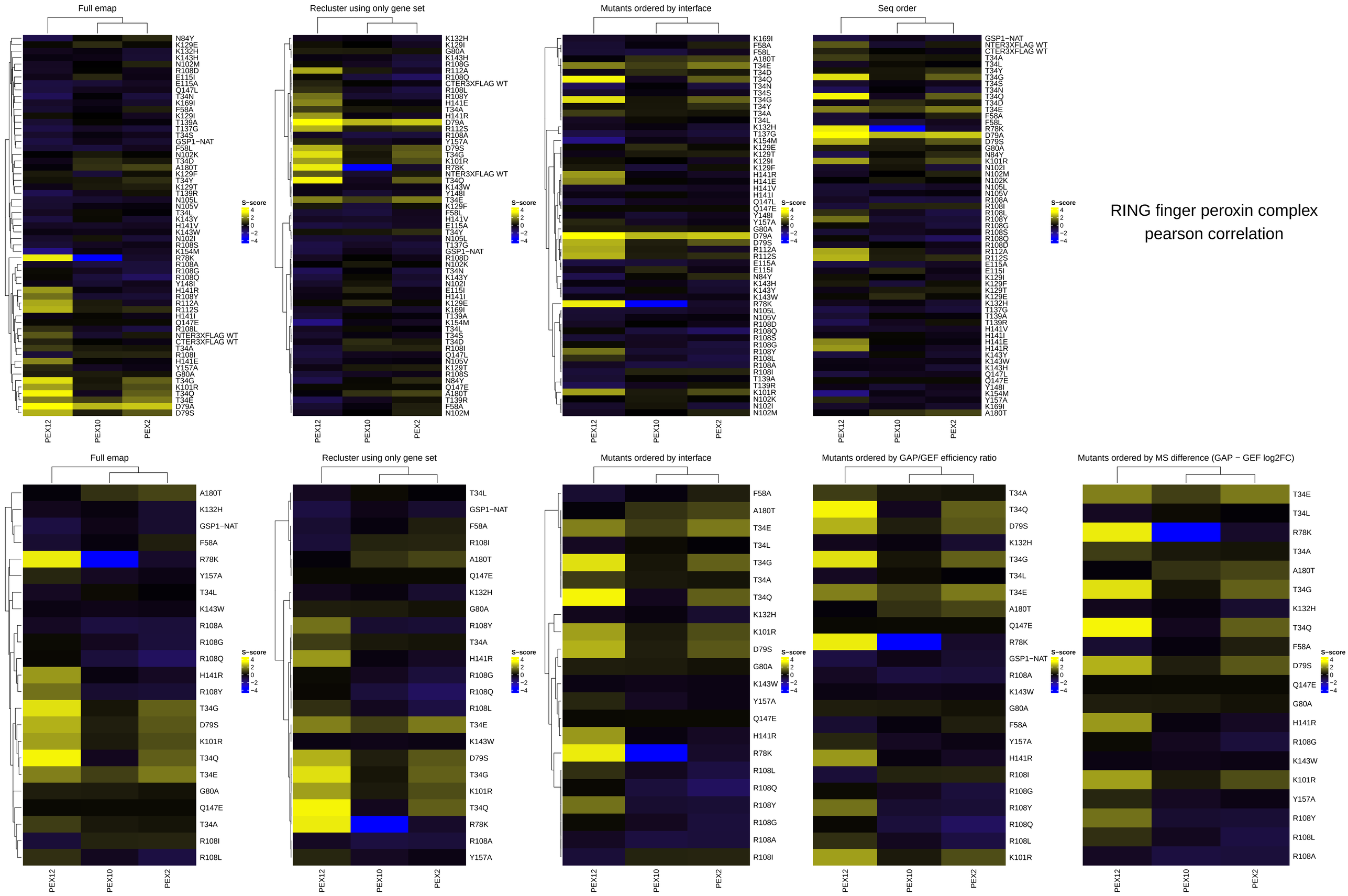
2
0
−2
−4
EAF6
SAS3
YNG1
NTO1
NuA3 histone acetyltransferase complex
pearson correlation

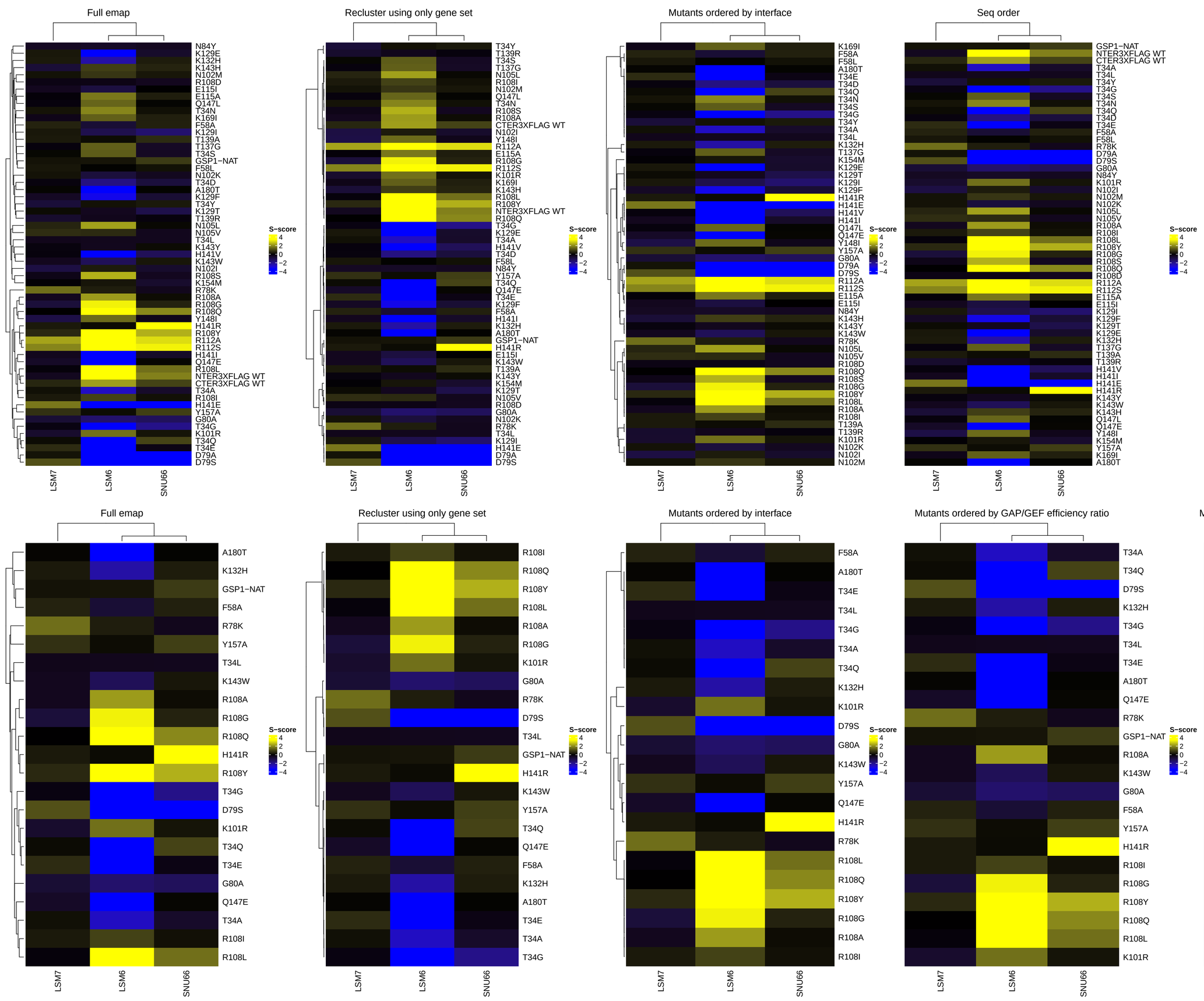


COMA complex
pearson correlation

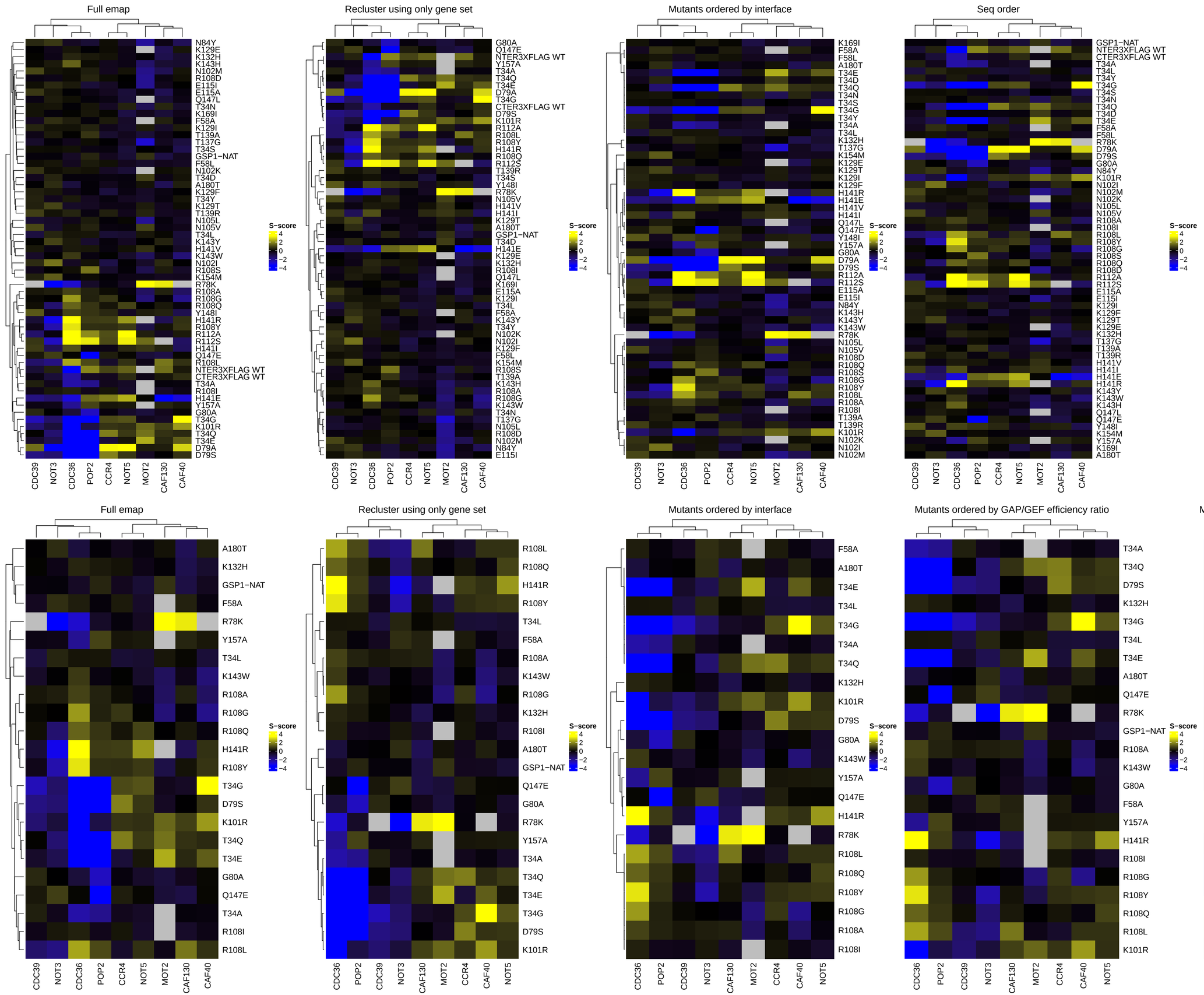

Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
YOS9
USA1
DER1
HRD1
ubiquitin ligase ERAD−L complex
pearson correlation



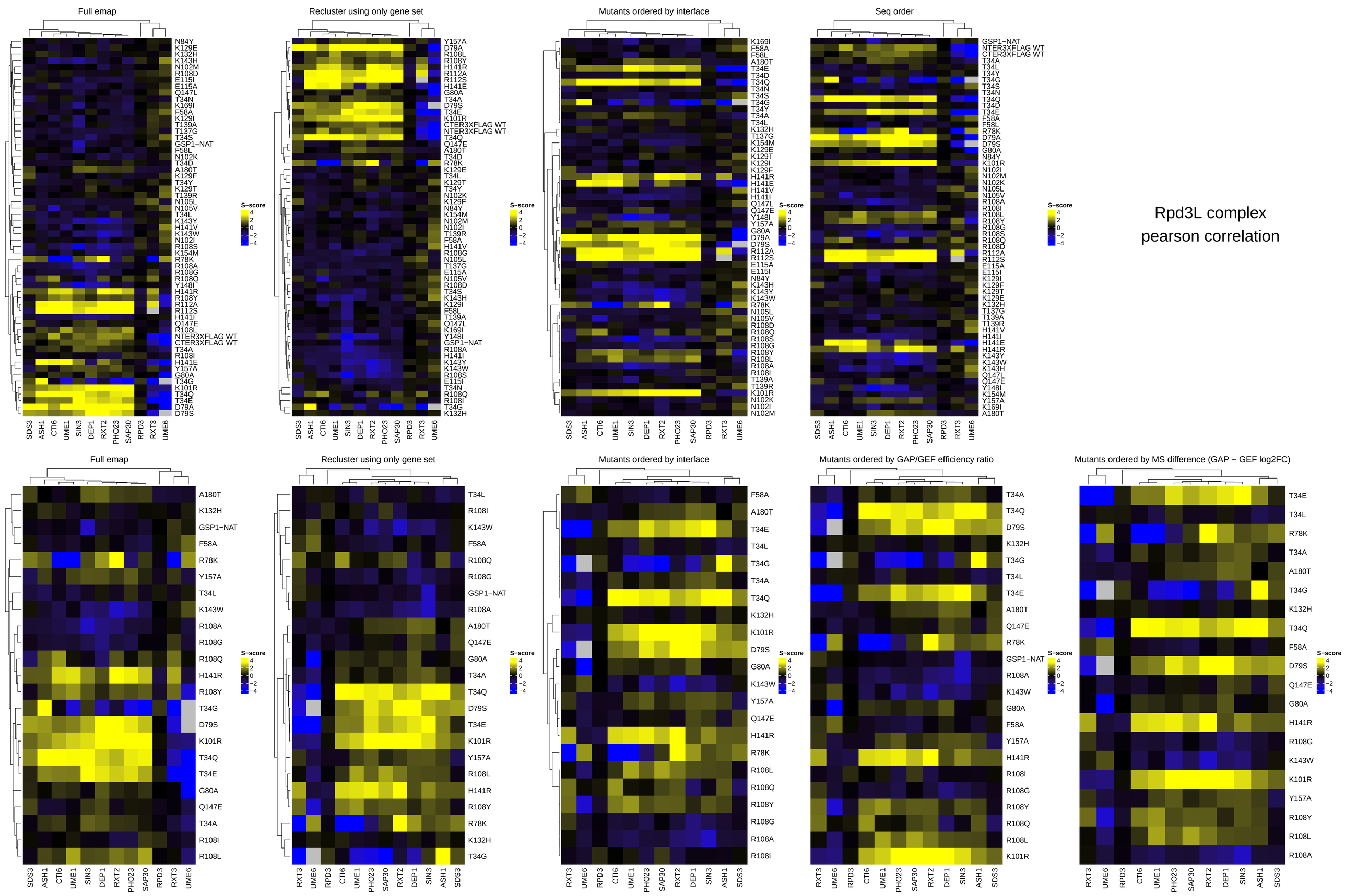
RING finger peroxin complex
pearson correlation



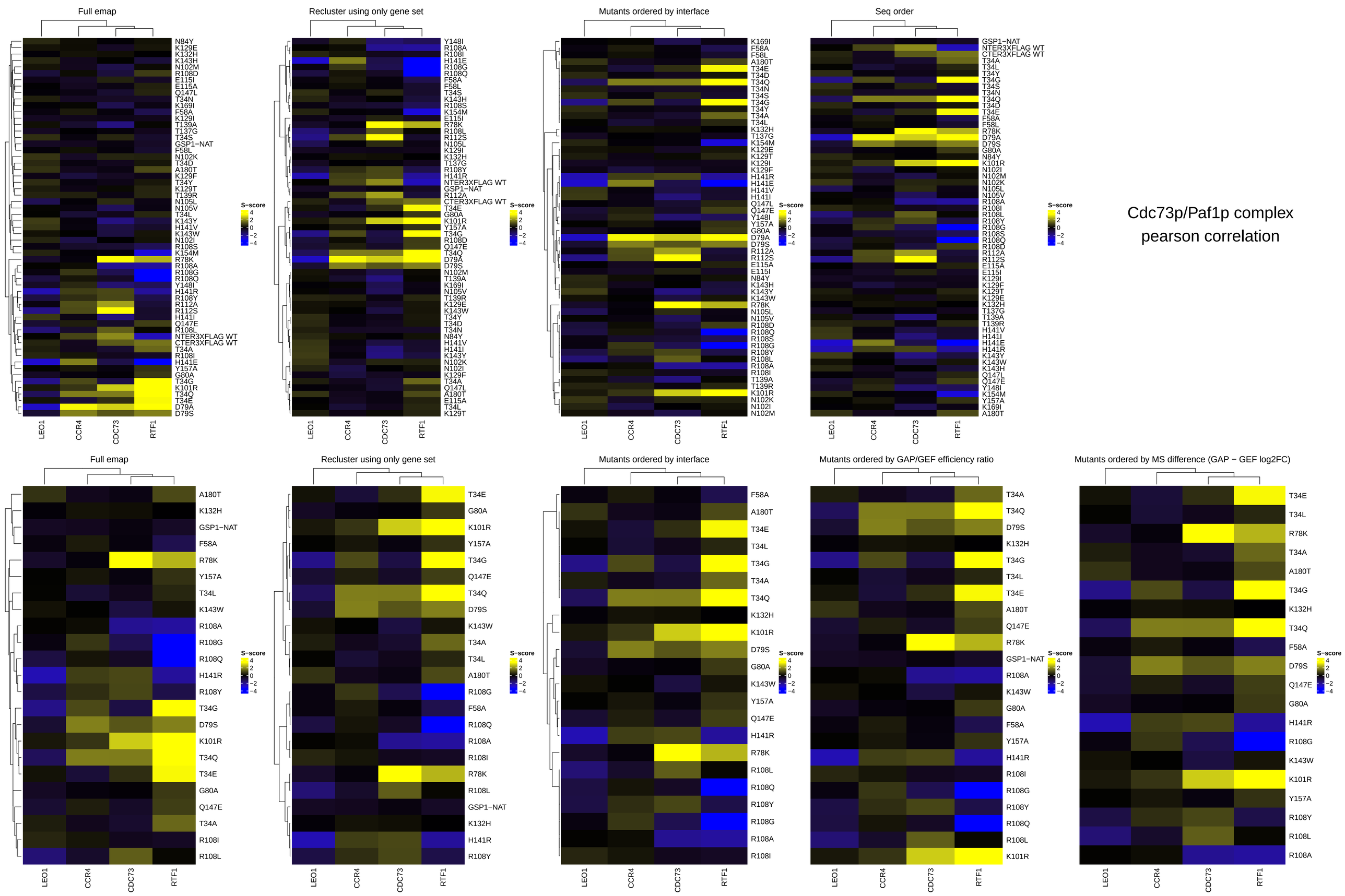
U4/U6 x U5 tri−snRNP complex
pearson correlation

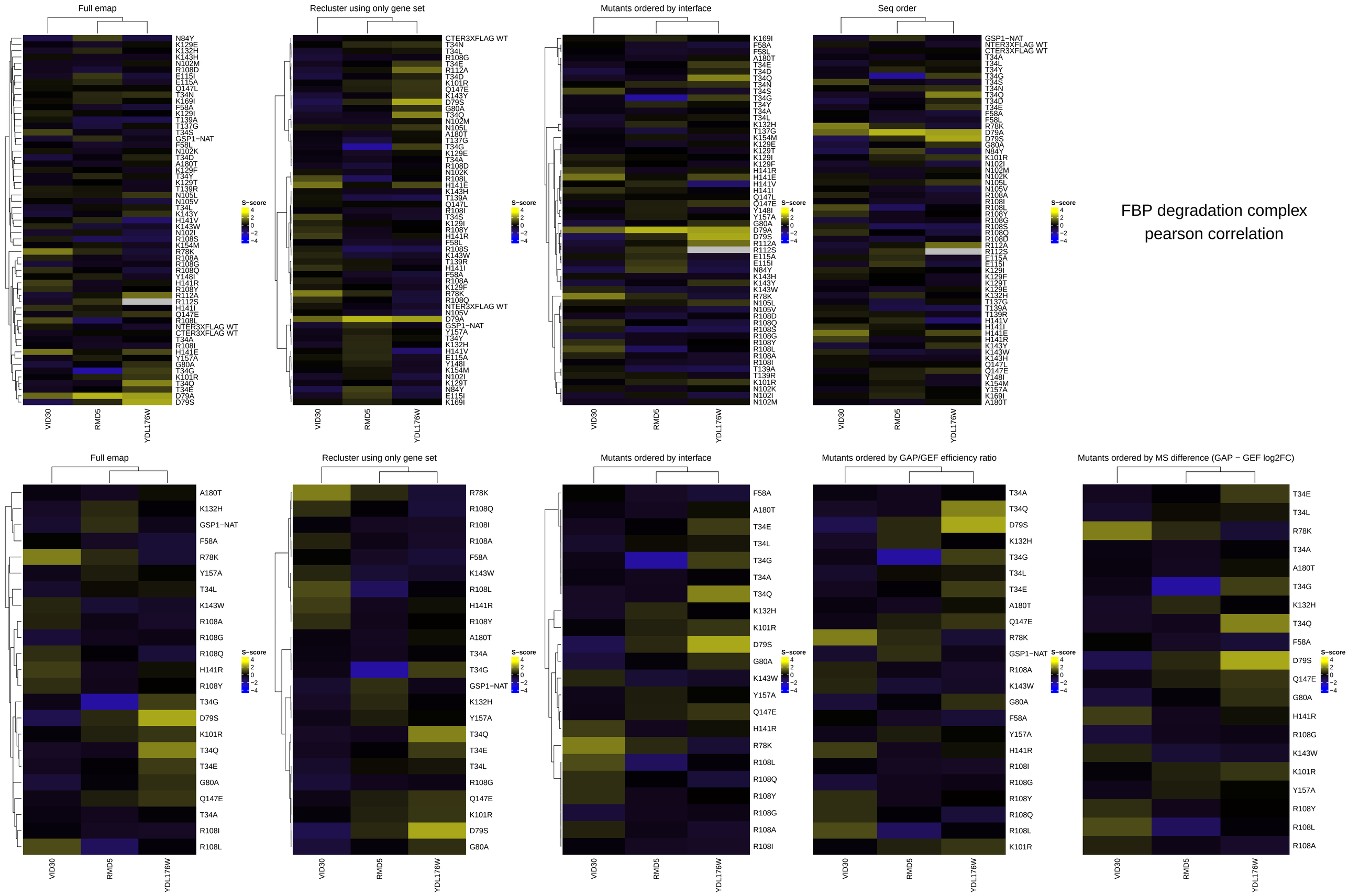


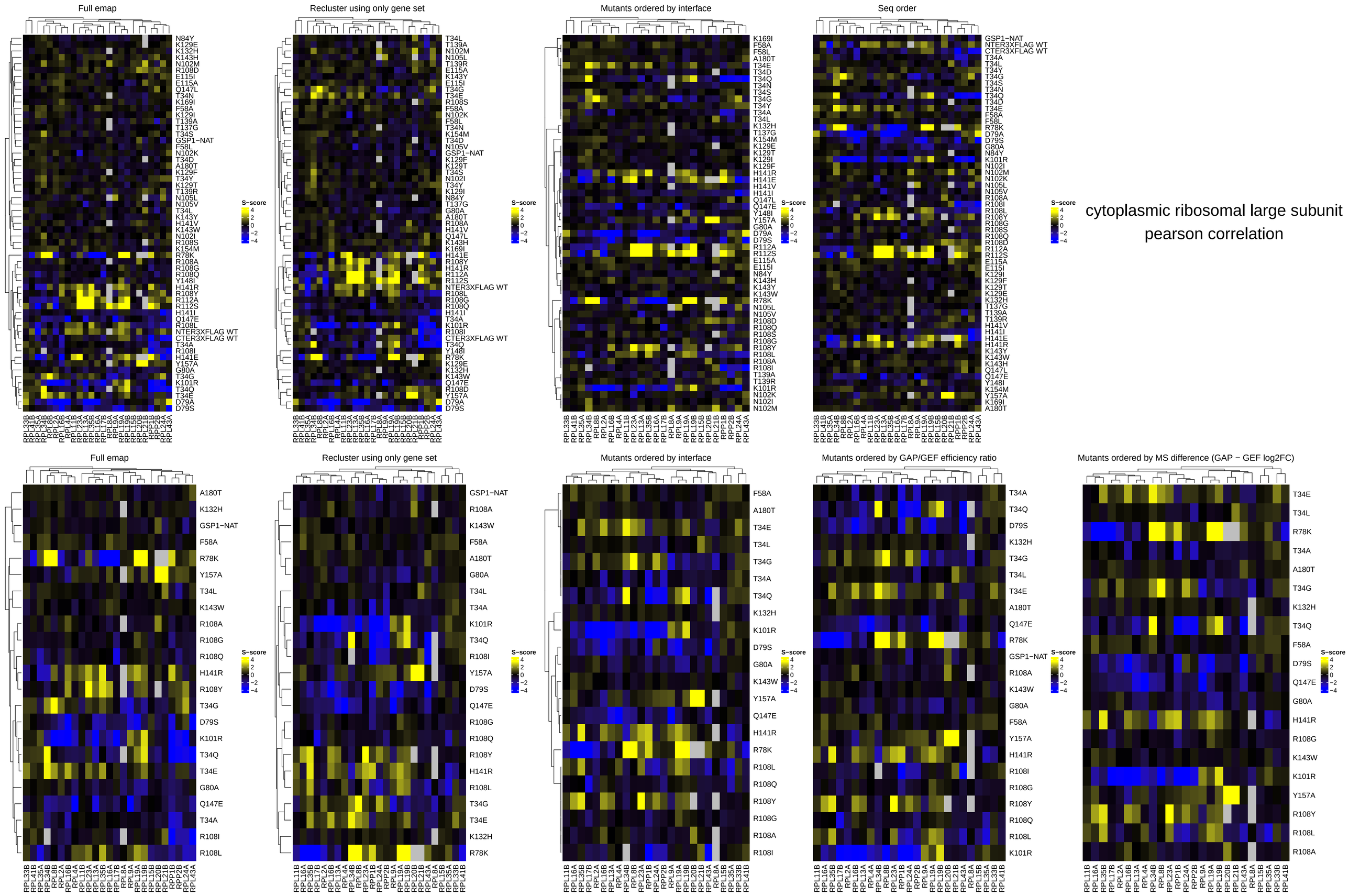
CCR4−NOT core complex
pearson correlation

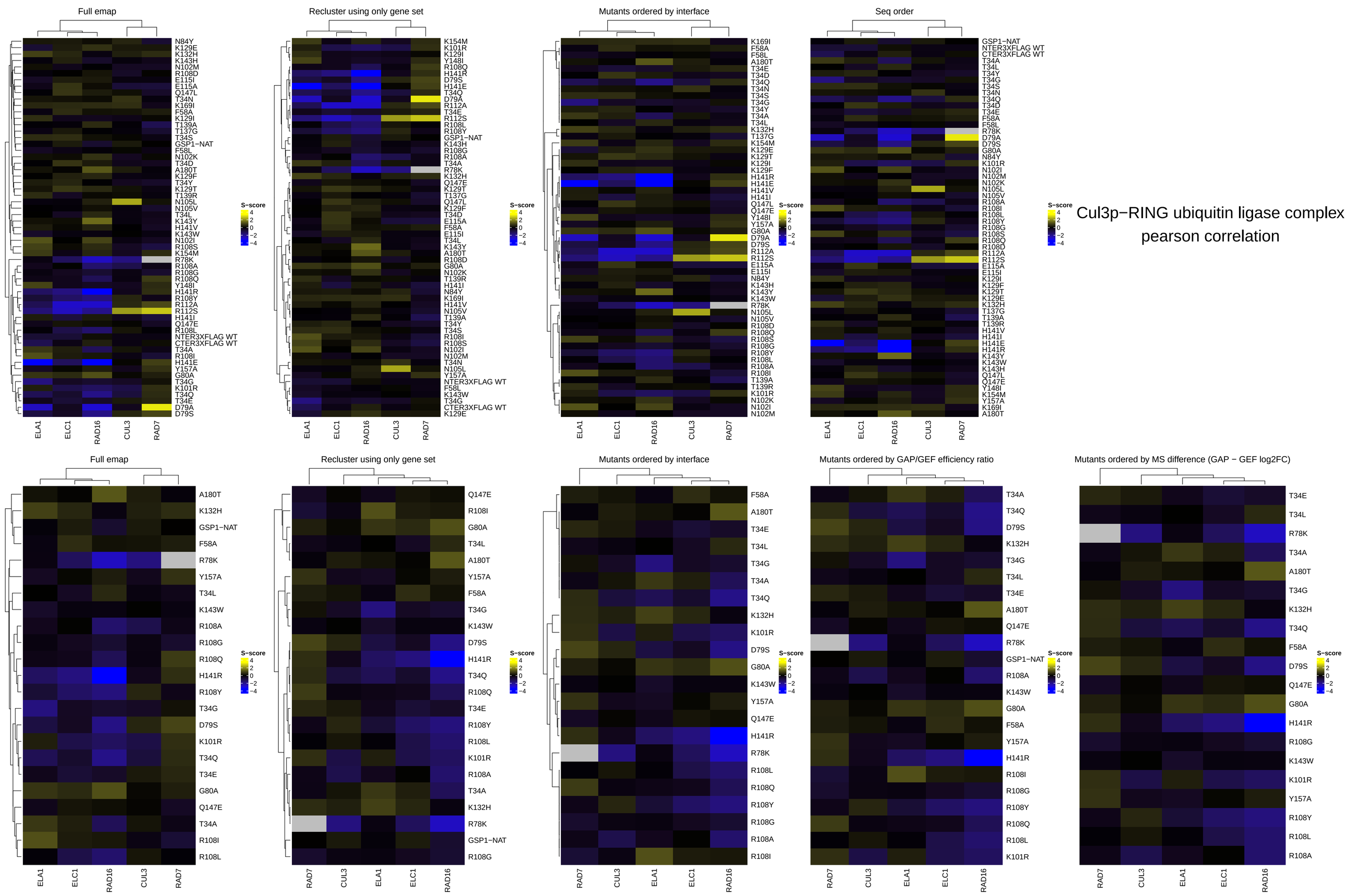


Rpd3L complex
pearson correlation


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
pearson correlation


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
VID30
RMD5
YDL176W
FBP degradation complex
pearson correlation


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
cytoplasmic ribosomal large subunit
pearson correlation


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)
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2
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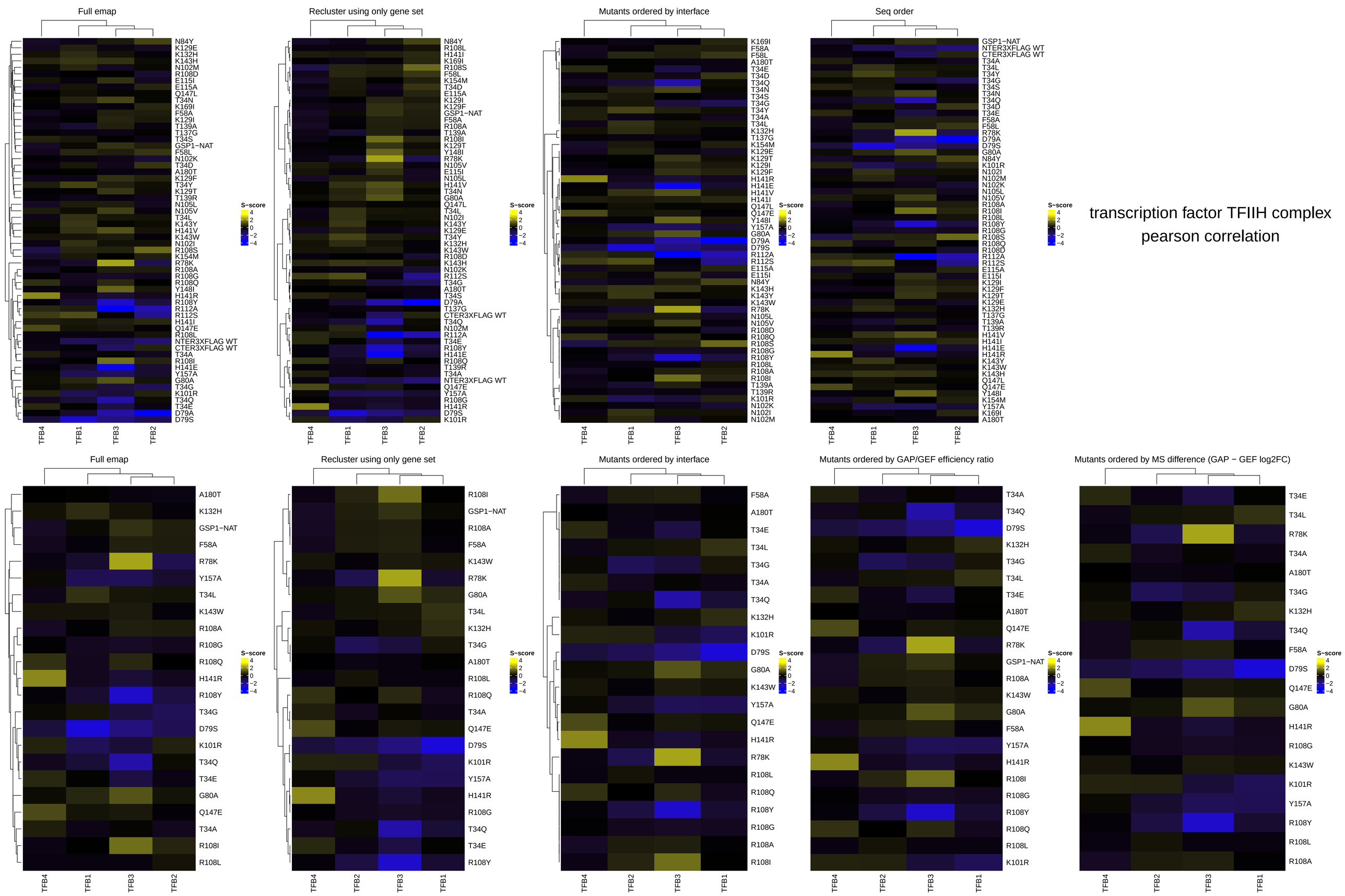
−2
−4
ELA1
ELC1
RAD16
CUL3
RAD7
Cul3p−RING ubiquitin ligase complex
pearson correlation


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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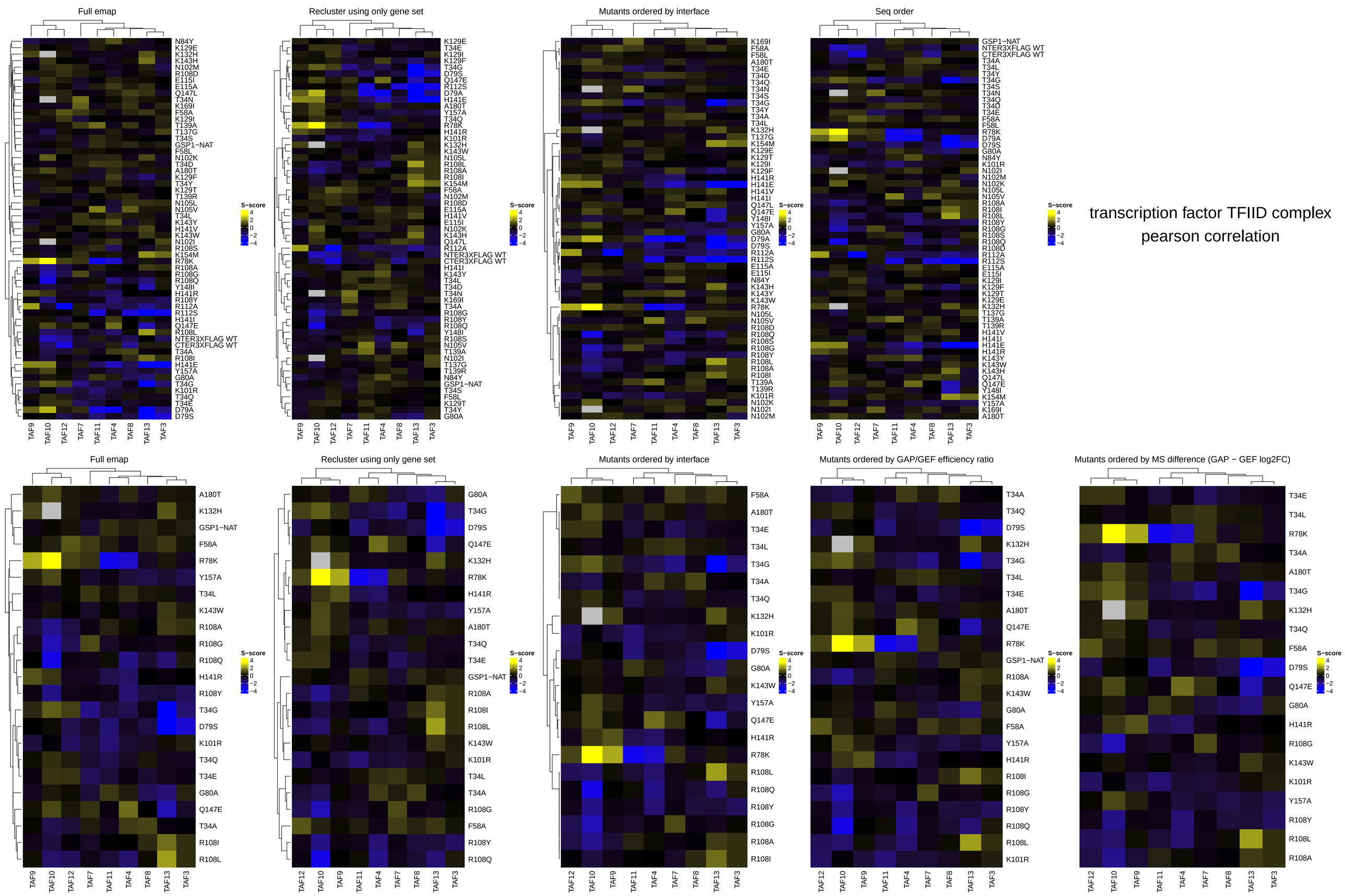
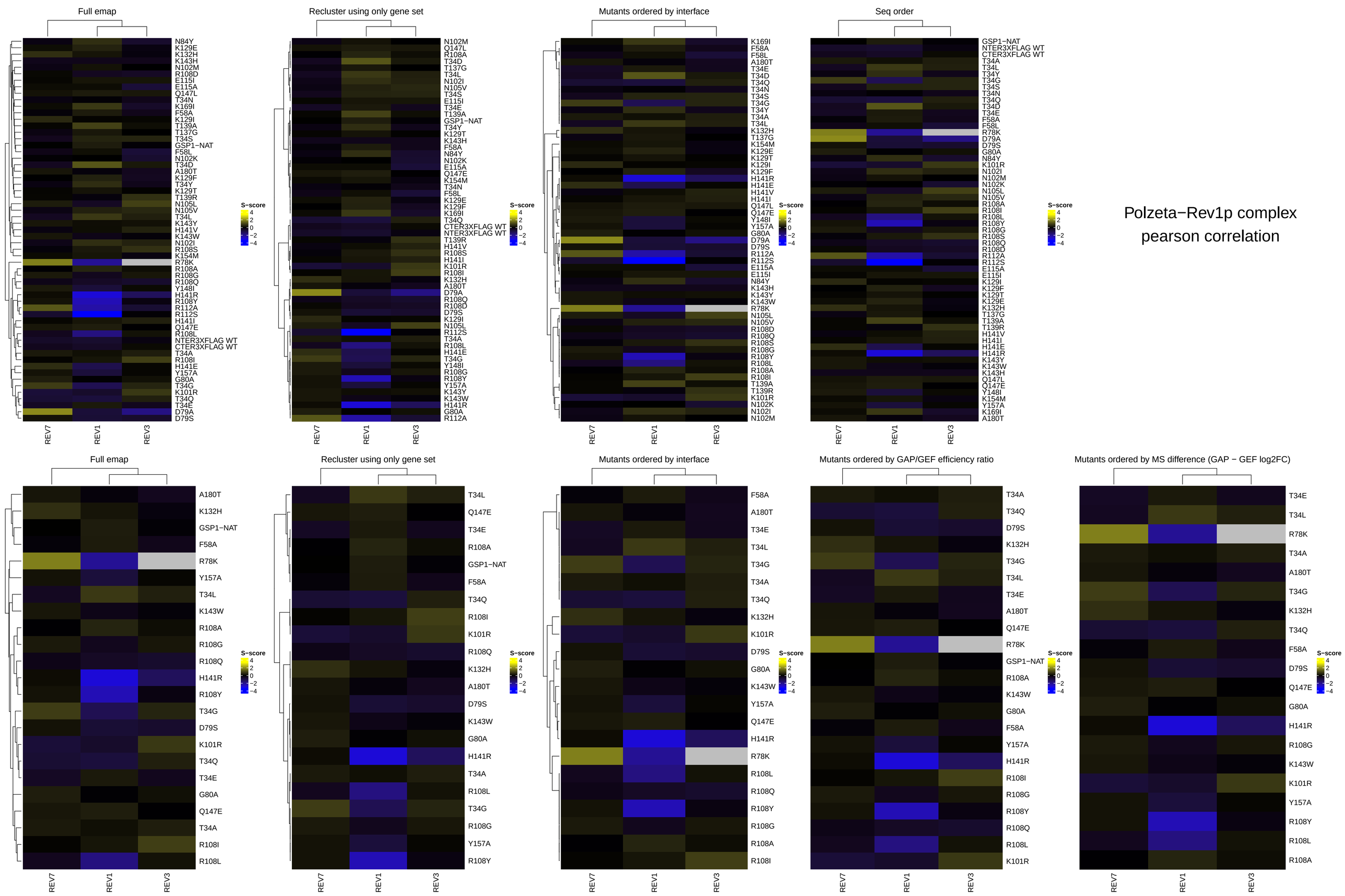
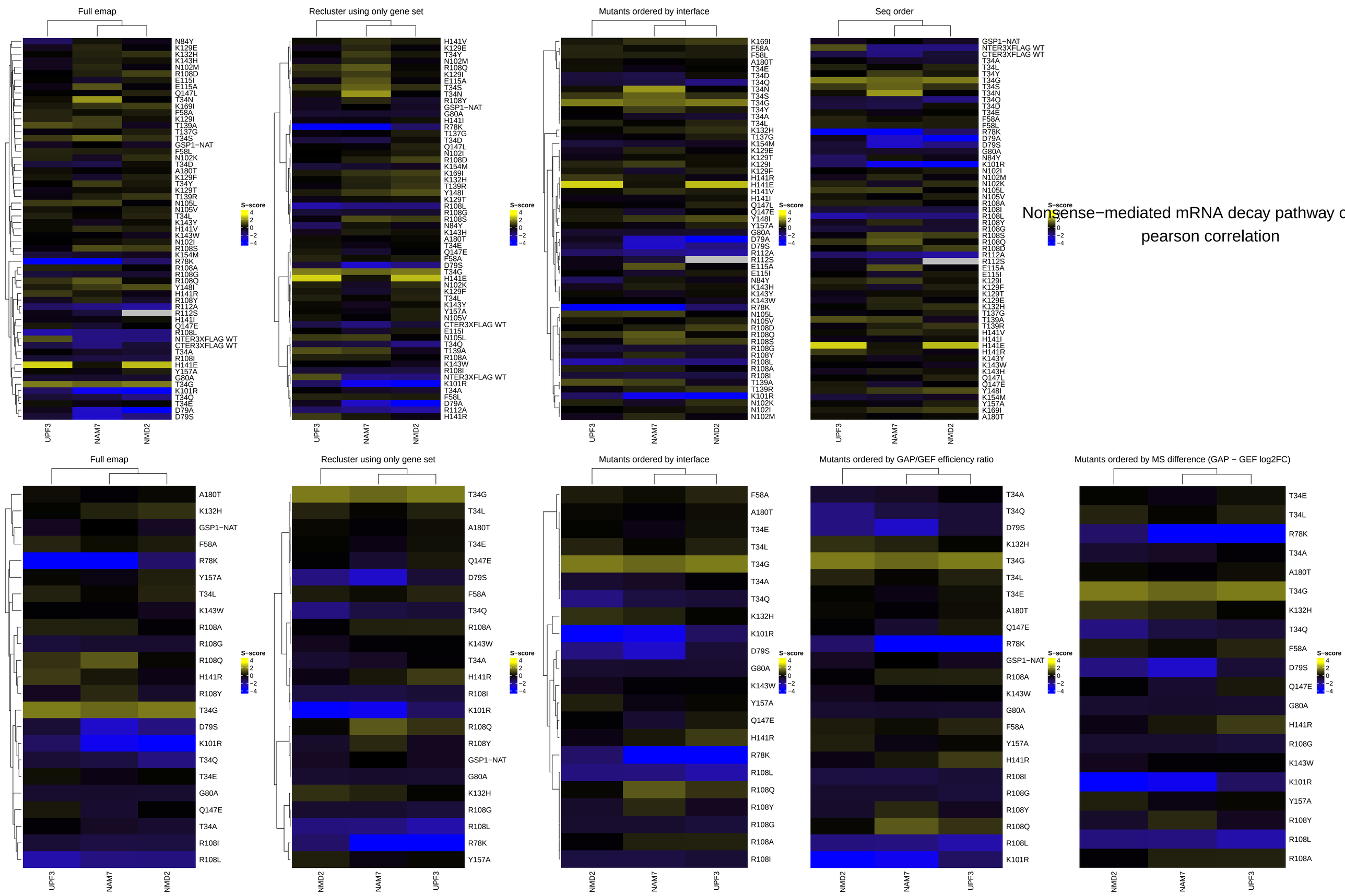
2
0
−2
−4
TFB4
TFB1
TFB3
TFB2
transcription factor TFIIH complex
pearson correlation


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
S−score
4
2
0
−2
−4
TAF9
TAF10
TAF12
TAF7
TAF11
TAF4
TAF8
TAF13
TAF3
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)
transcription factor TFIID complex
pearson correlation


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
pearson correlation


Nonsense−mediated mRNA decay pathway c
pearson correlation
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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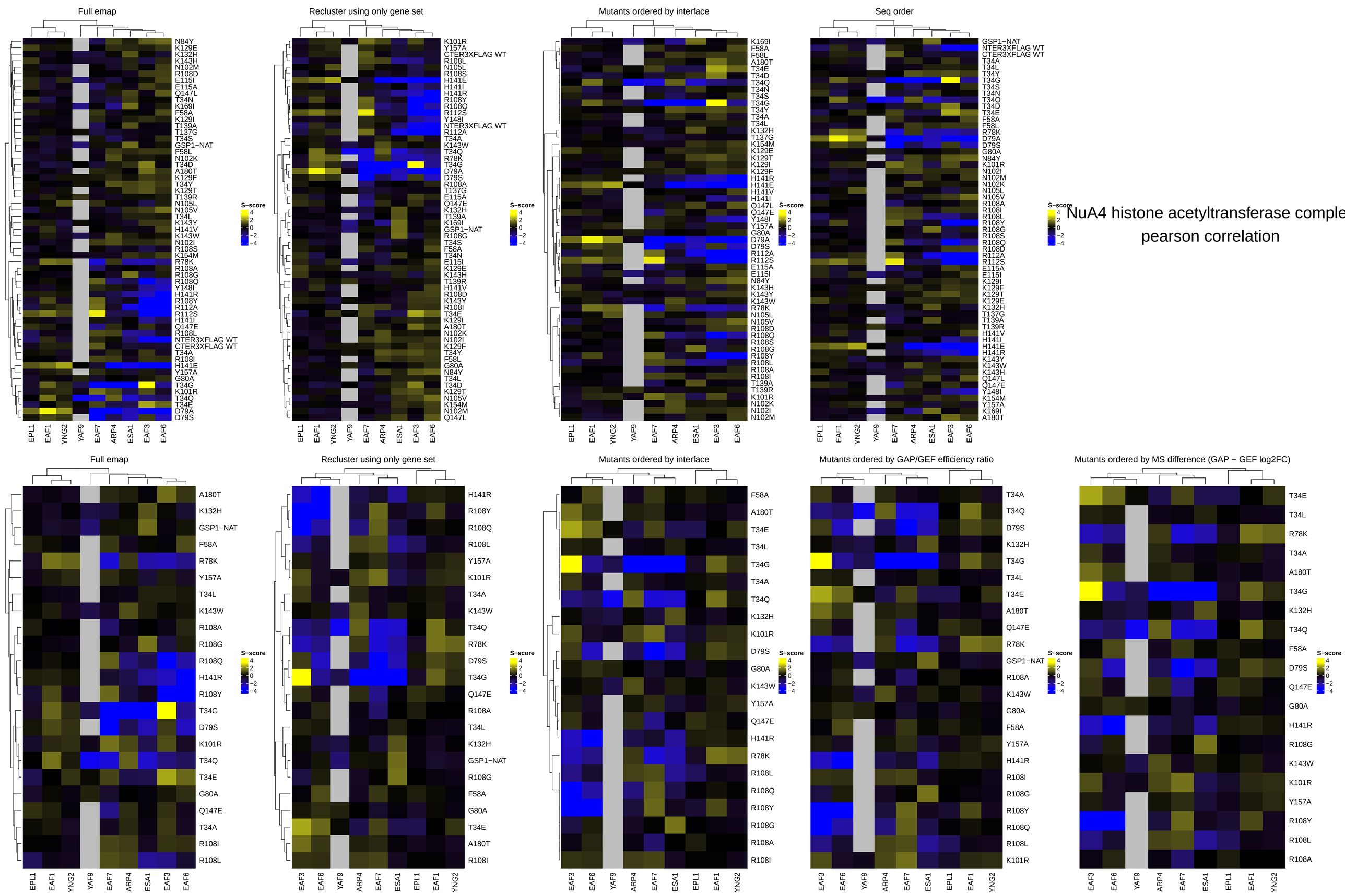
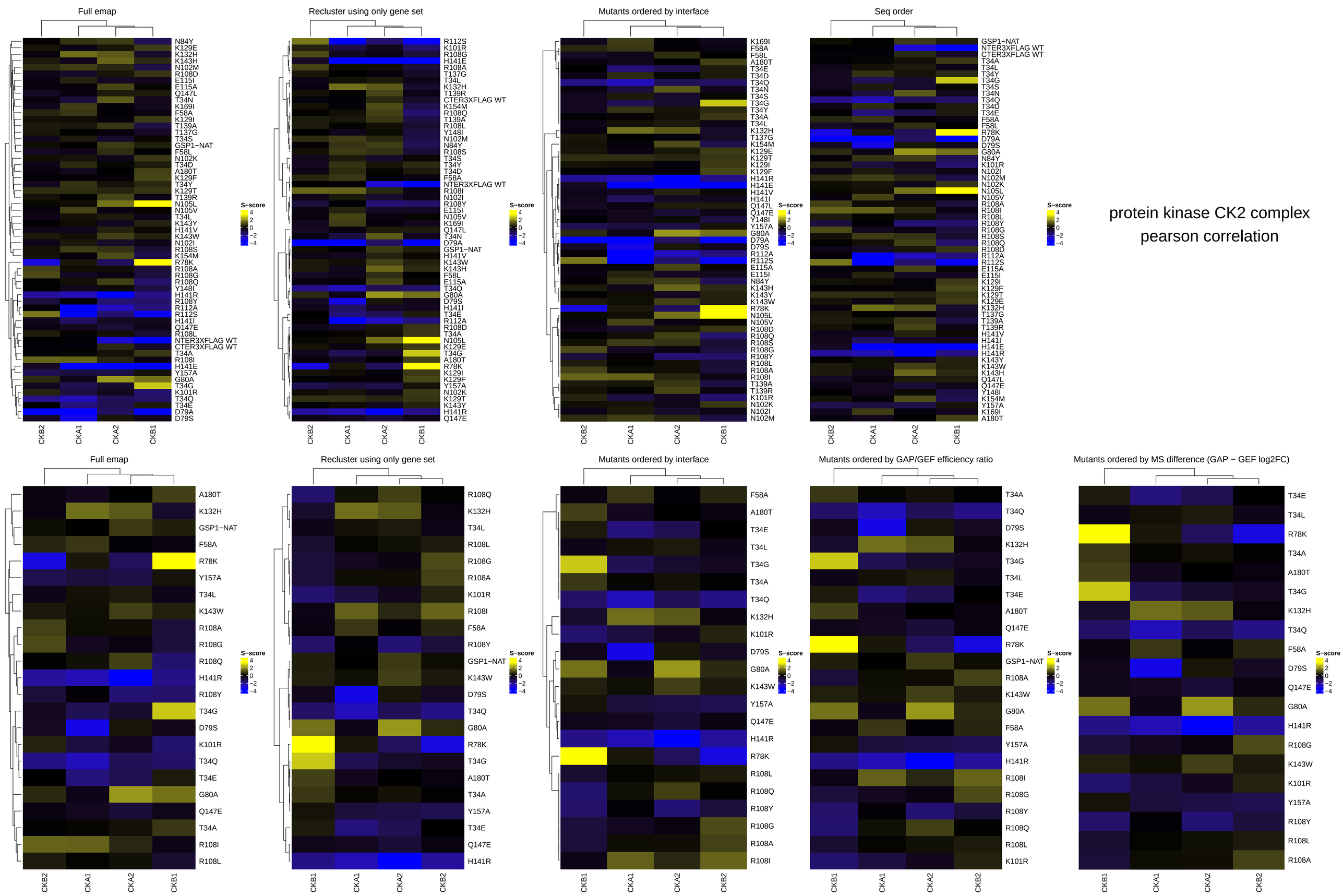
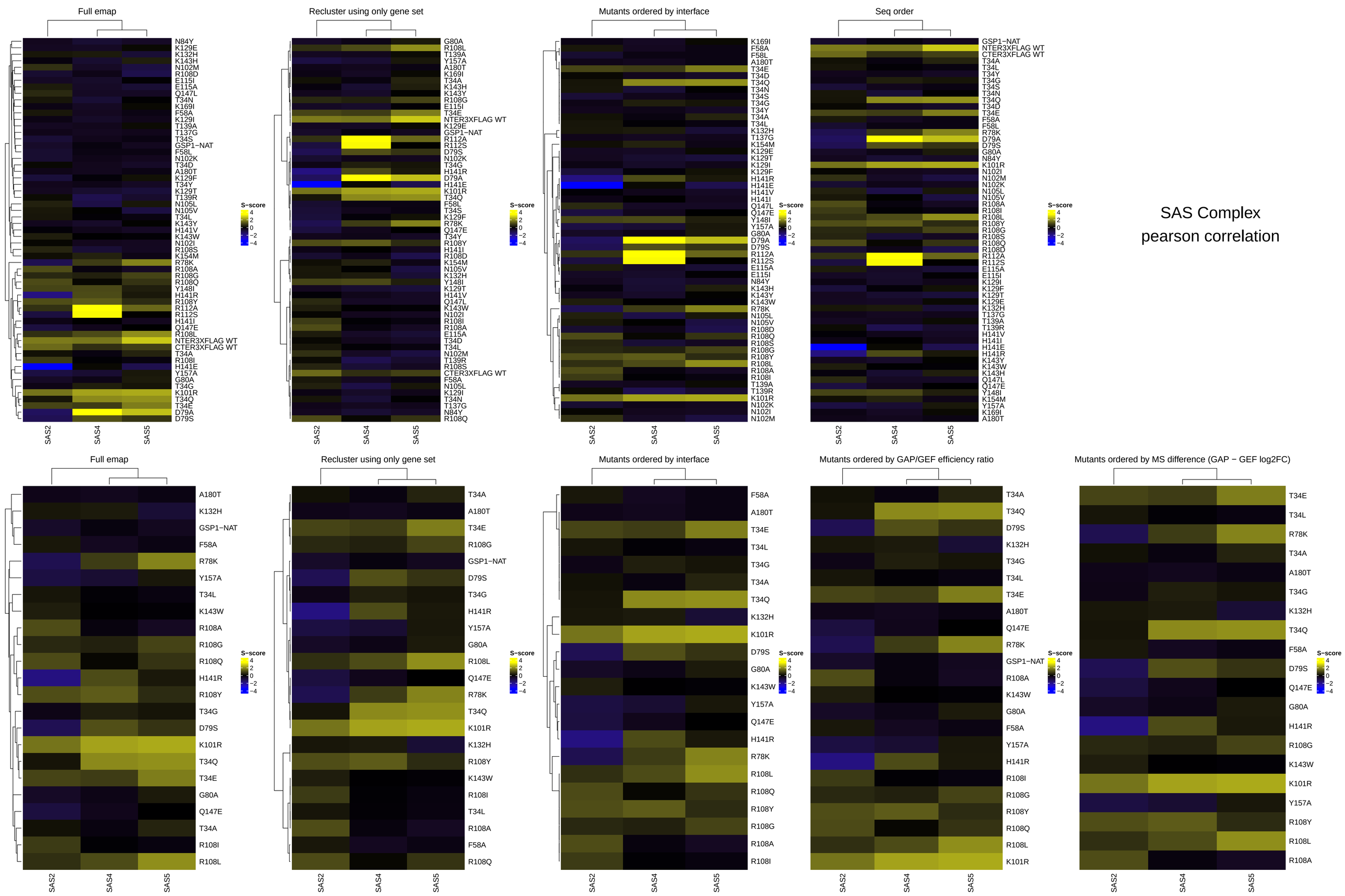
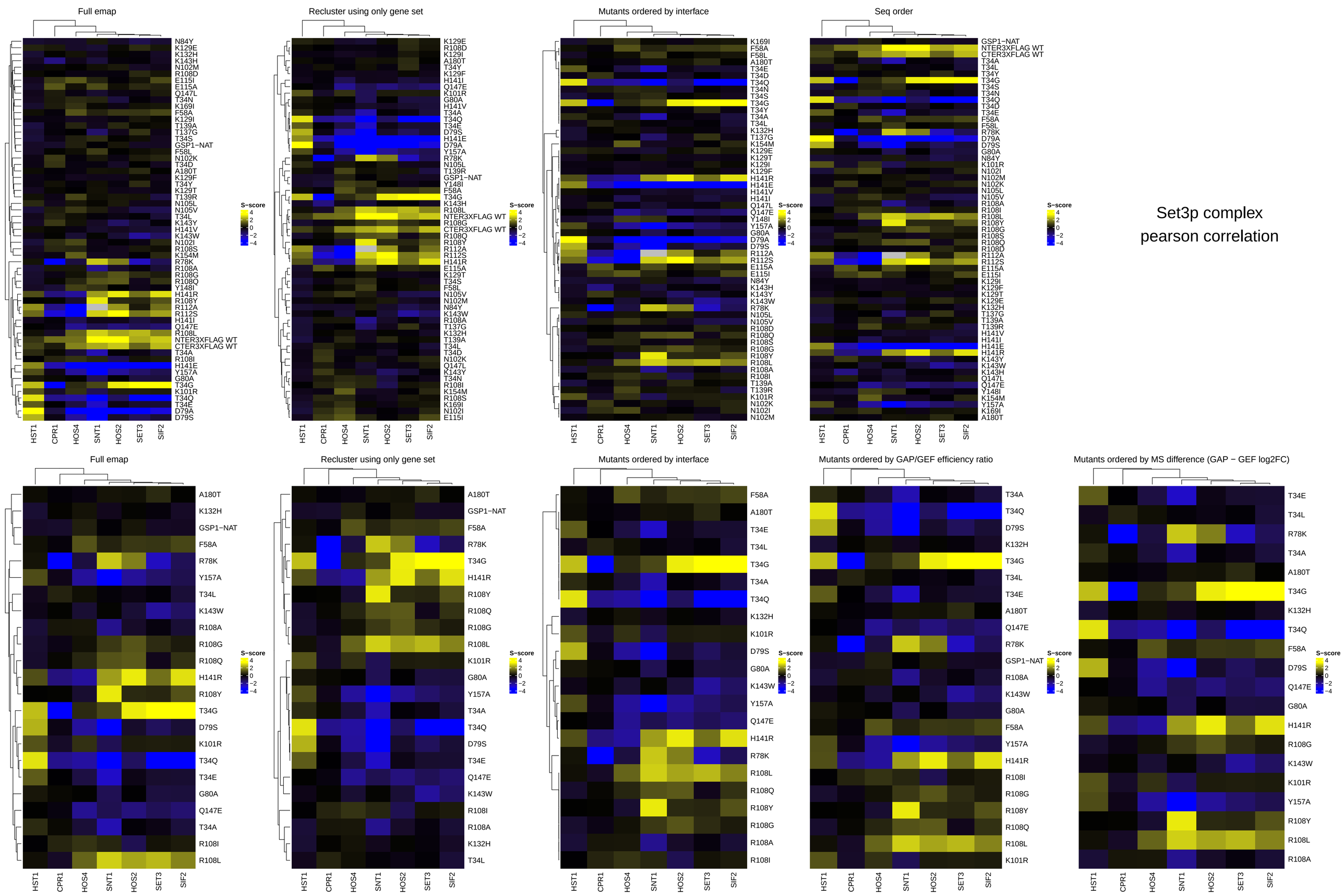
2
0
−2
−4
UPF3
NAM7
NMD2


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
EPL1
EAF1
YNG2
YAF9
EAF7
ARP4
ESA1
EAF3
EAF6
NuA4 histone acetyltransferase comple
pearson correlation


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
CKB2
CKA1
CKA2
CKB1
protein kinase CK2 complex
pearson correlation


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
pearson correlation


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
−4
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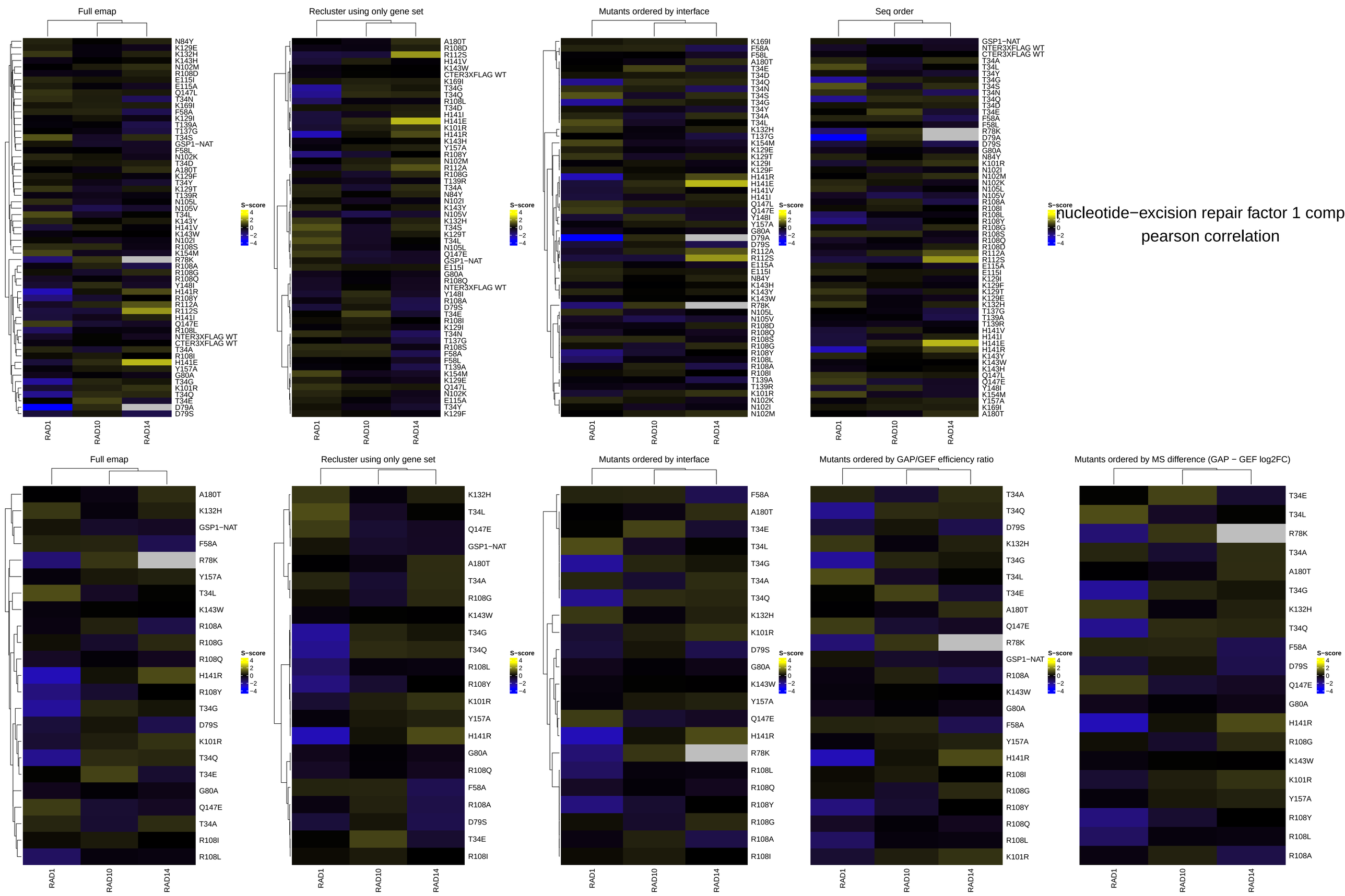
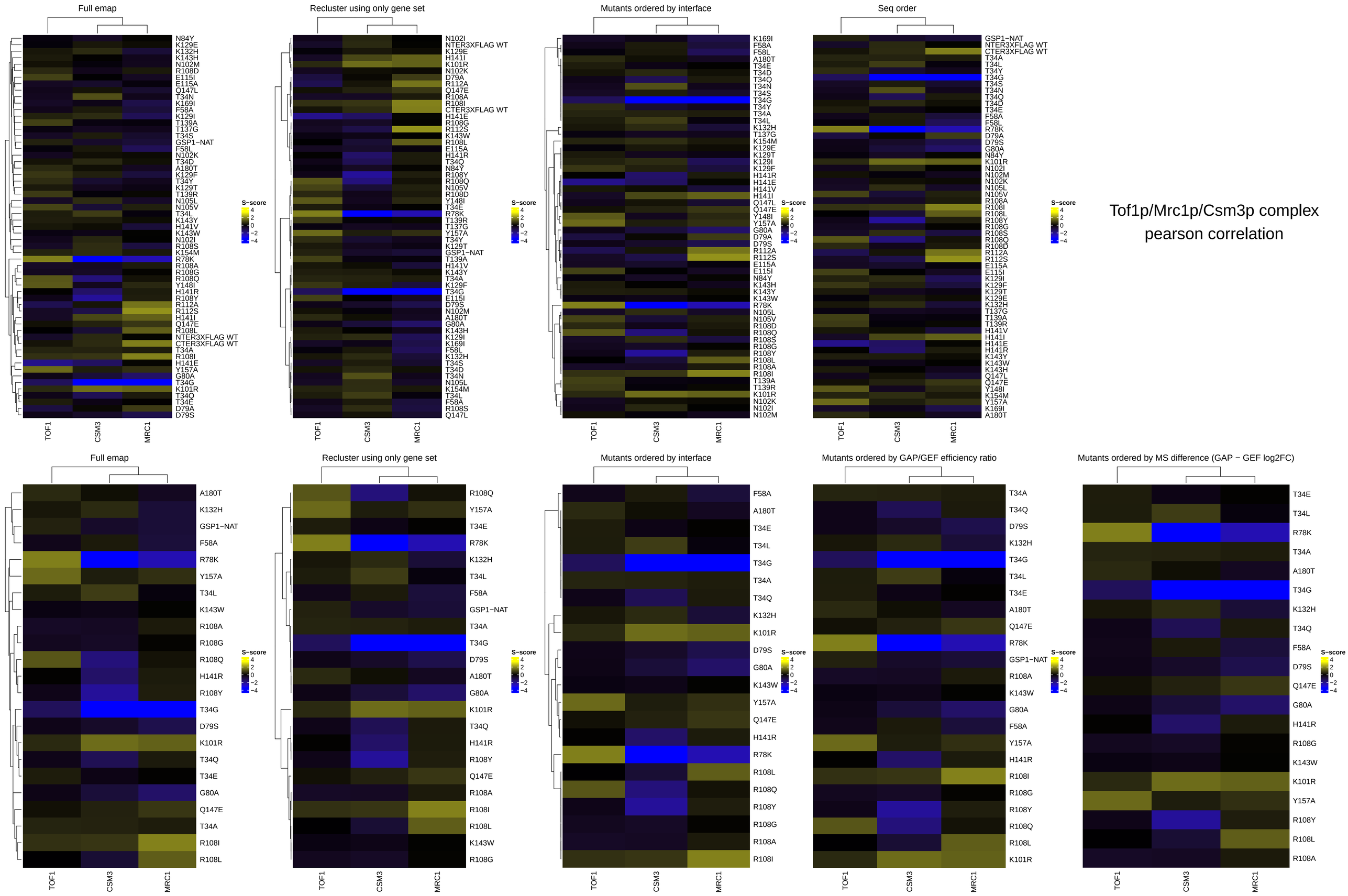
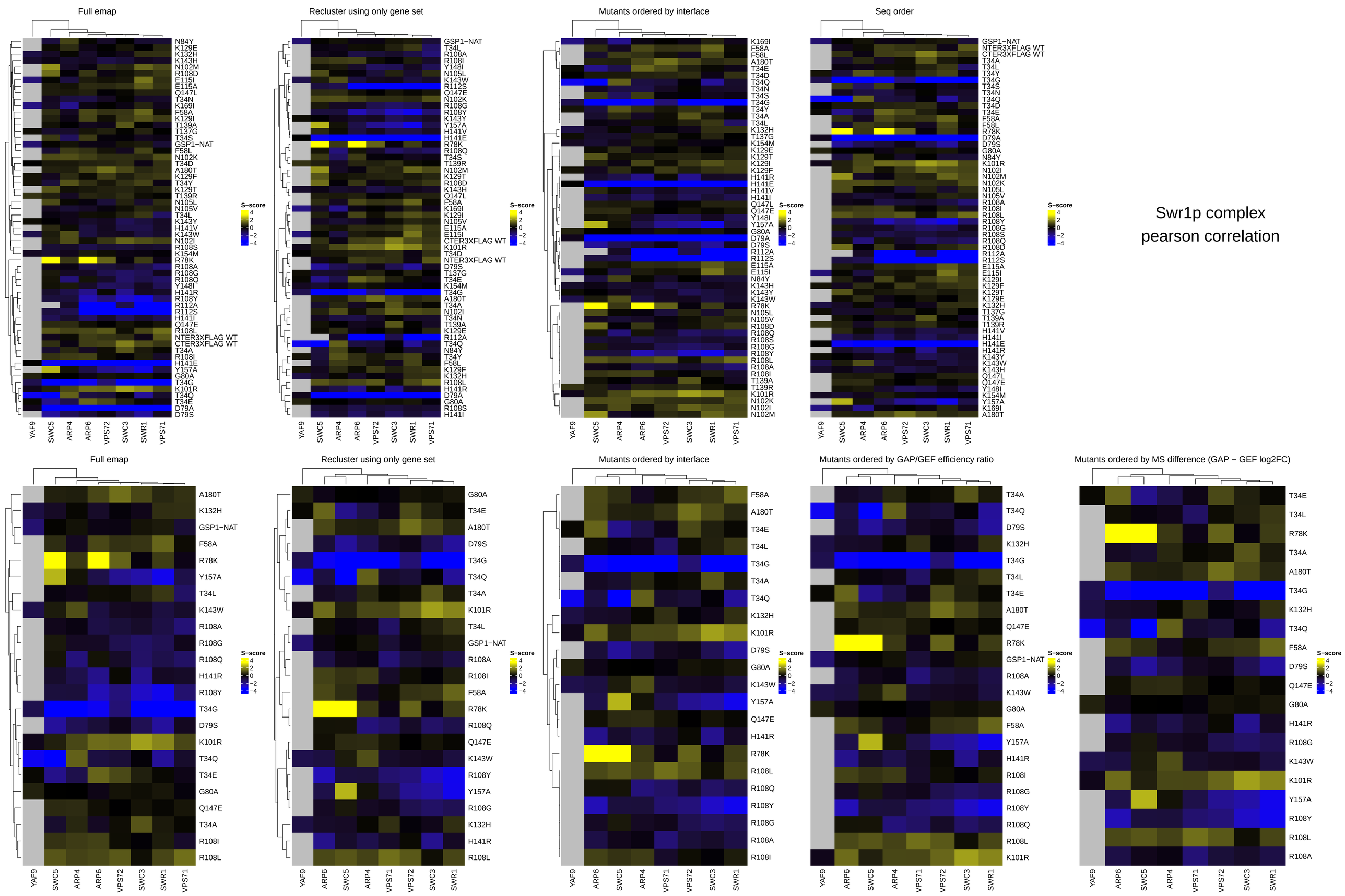
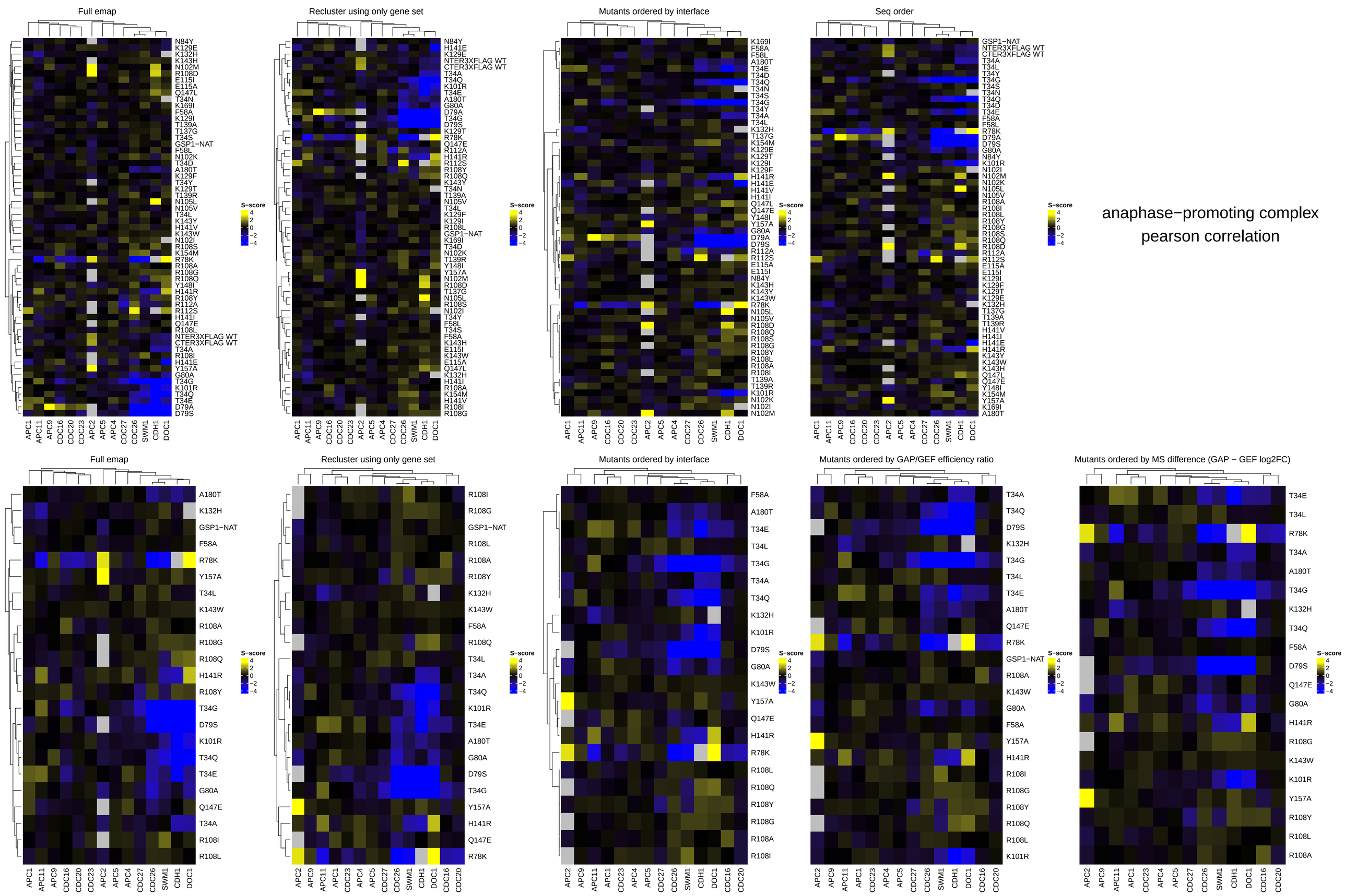
CPR1
HOS4
SNT1
HOS2
SET3
SIF2
Set3p complex
pearson correlation


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 comp
pearson correlation



Tof1p/Mrc1p/Csm3p complex
pearson correlation


Full emap
Recluster using only gene set
Mutants ordered by interface
Seq order
Swr1p complex
pearson correlation
S−score
4
2
0
−2
−4
YAF9
SWC5
ARP4
ARP6
VPS72
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)


Full emap
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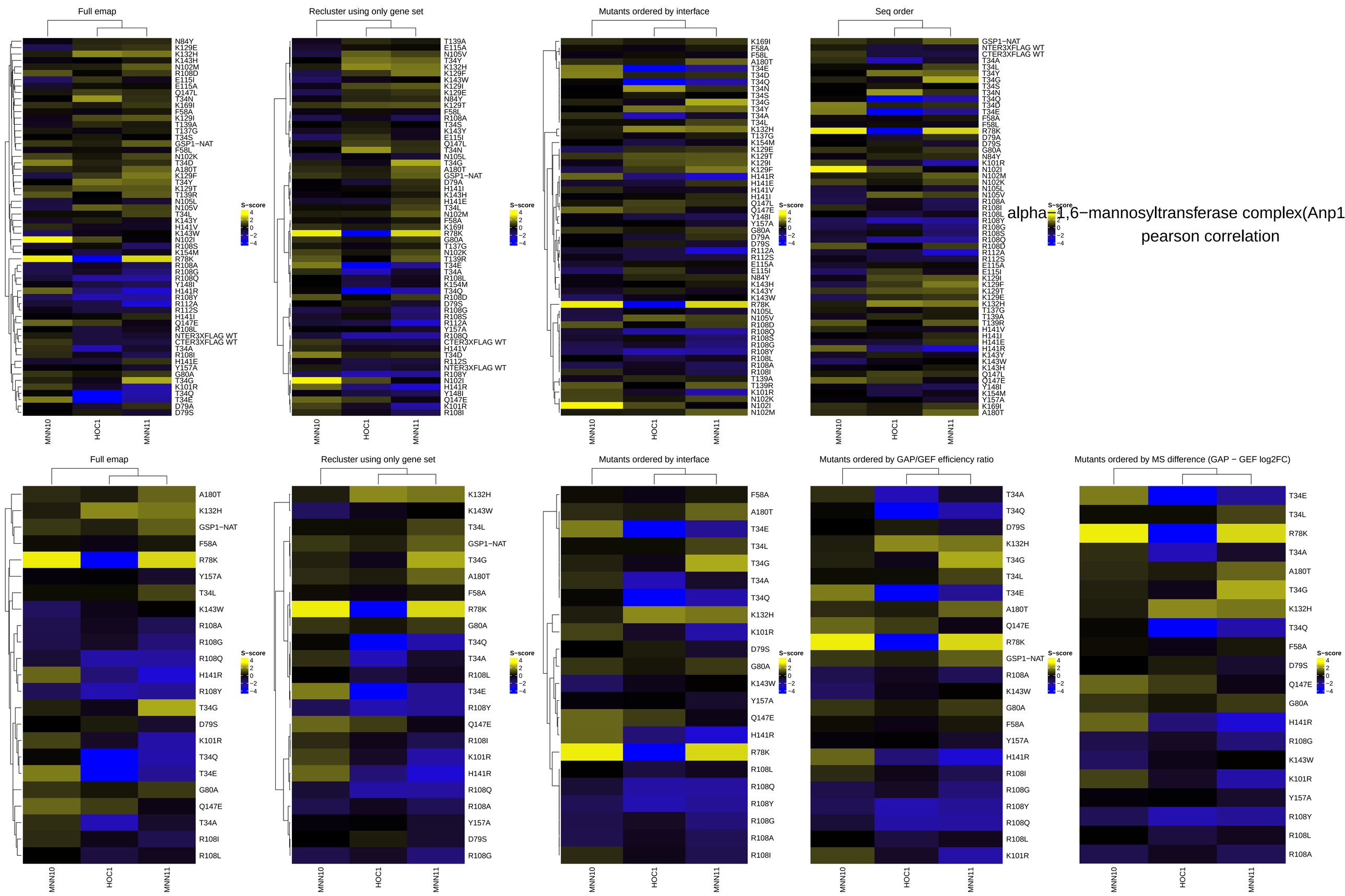
Mutants ordered by interface
Seq order
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
S−score
4
2
0
−2
−4
APC1 APC11 APC9 CDC16 CDC20 CDC23 APC2 APC5 APC4 CDC27 CDC26 SWM1 CDH1 DOC1
APC2 APC9 APC11 APC1 CDC23 APC4 APC5 CDC27 CDC26 SWM1 CDH1 DOC1 CDC16 CDC20
anaphase−promoting complex
pearson correlation


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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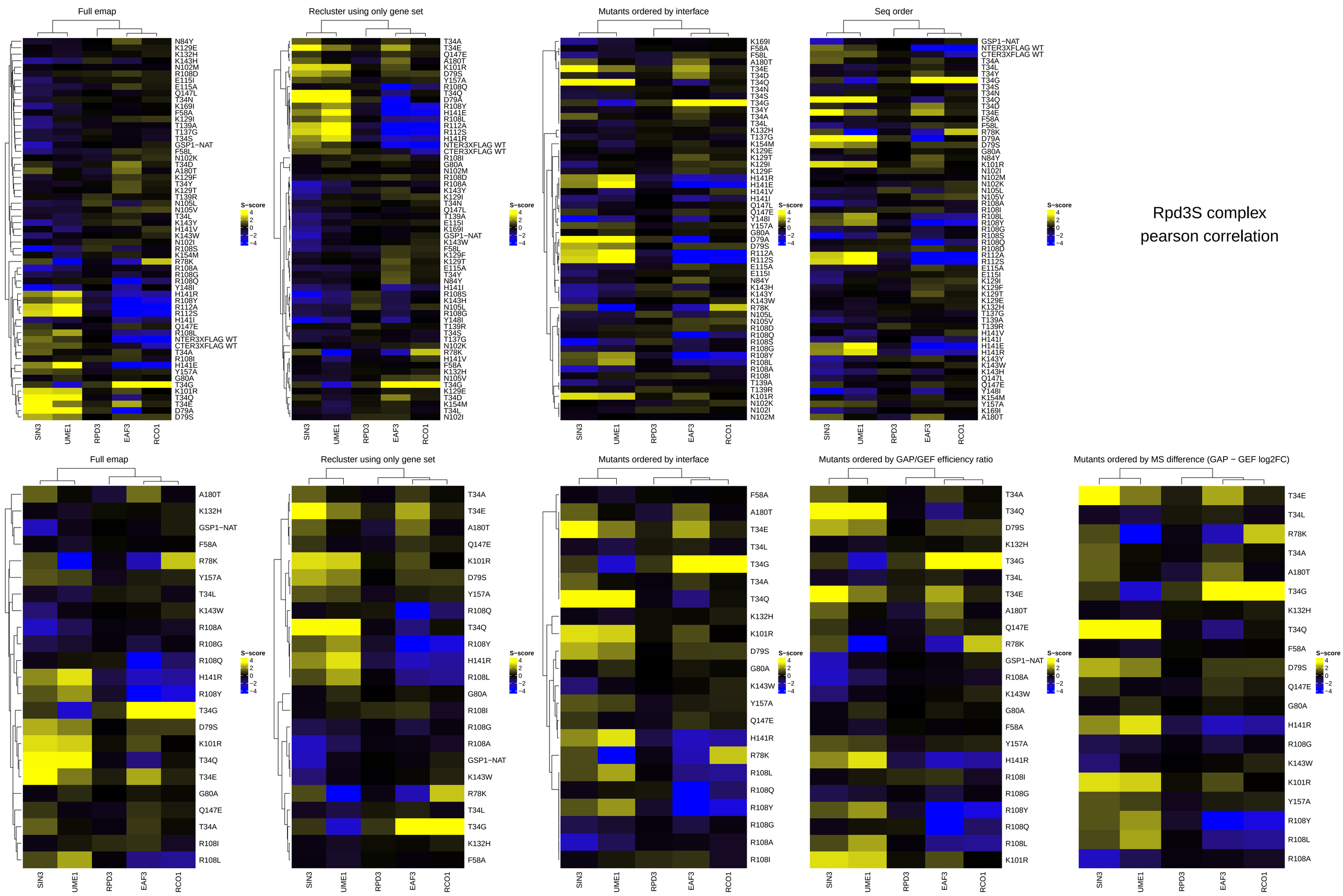
0
−2
−4
MNN10
HOC1
MNN11
alpha−1,6−mannosyltransferase complex(Anp1
pearson correlation


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)
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−2
−4
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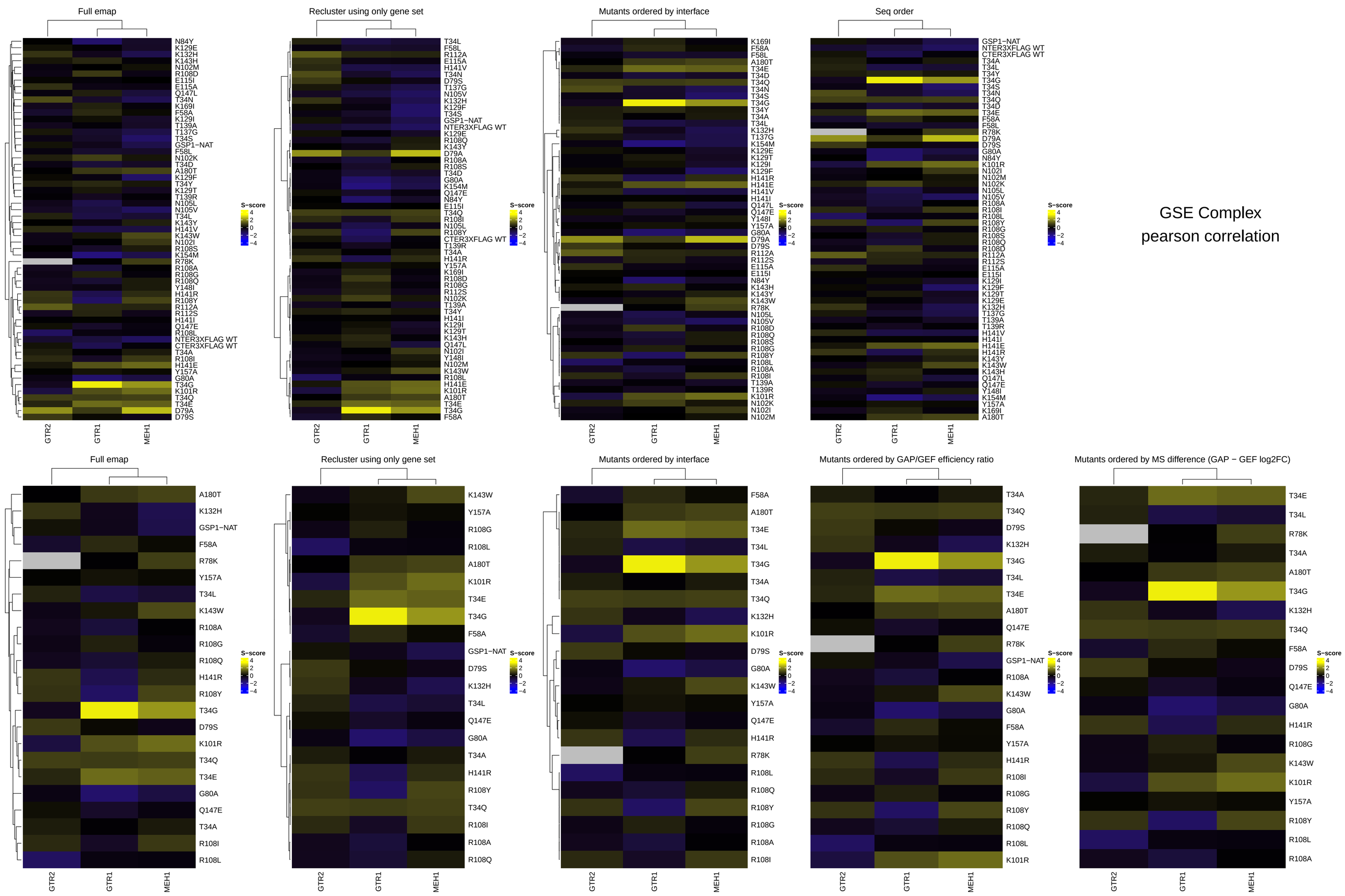
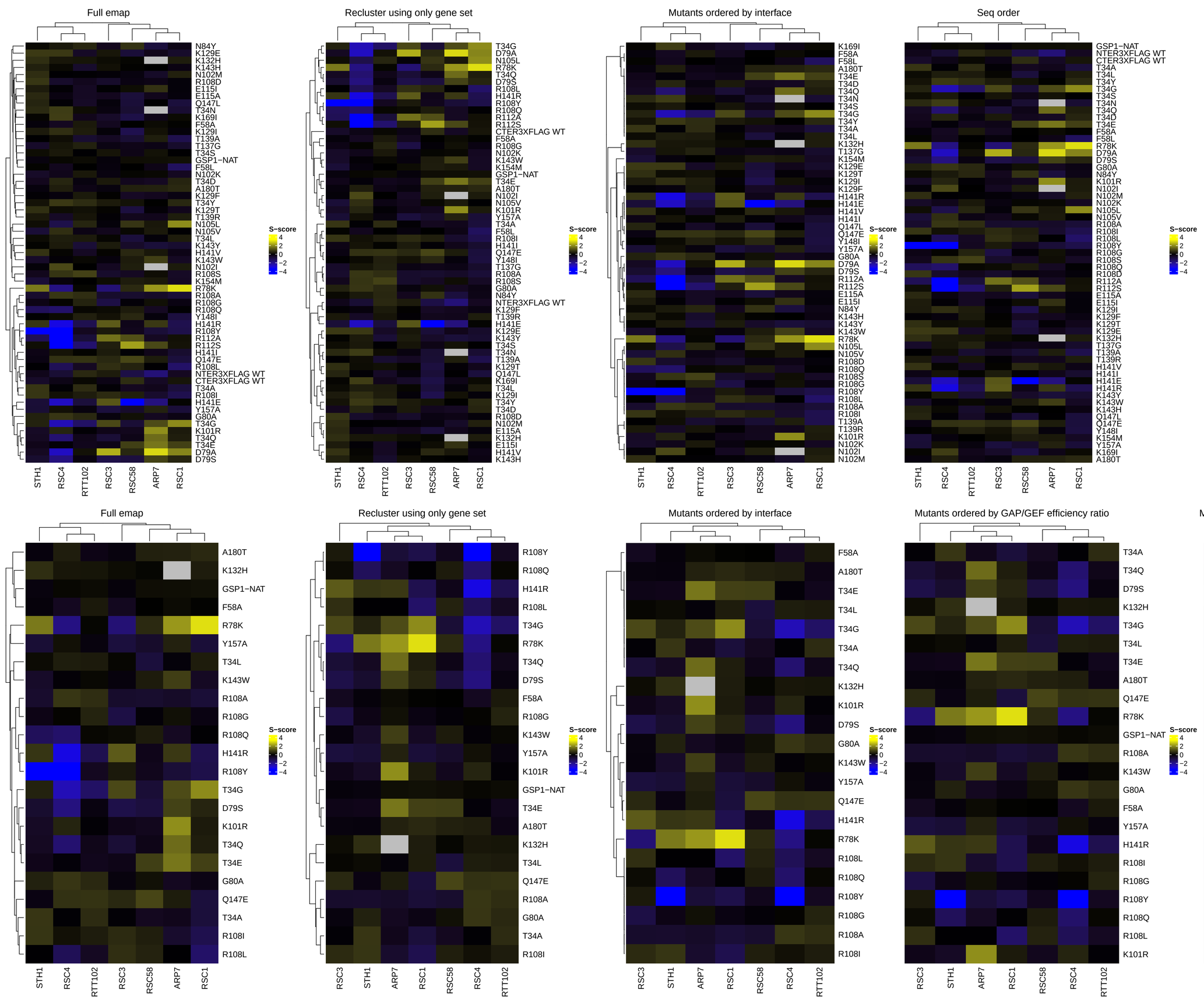
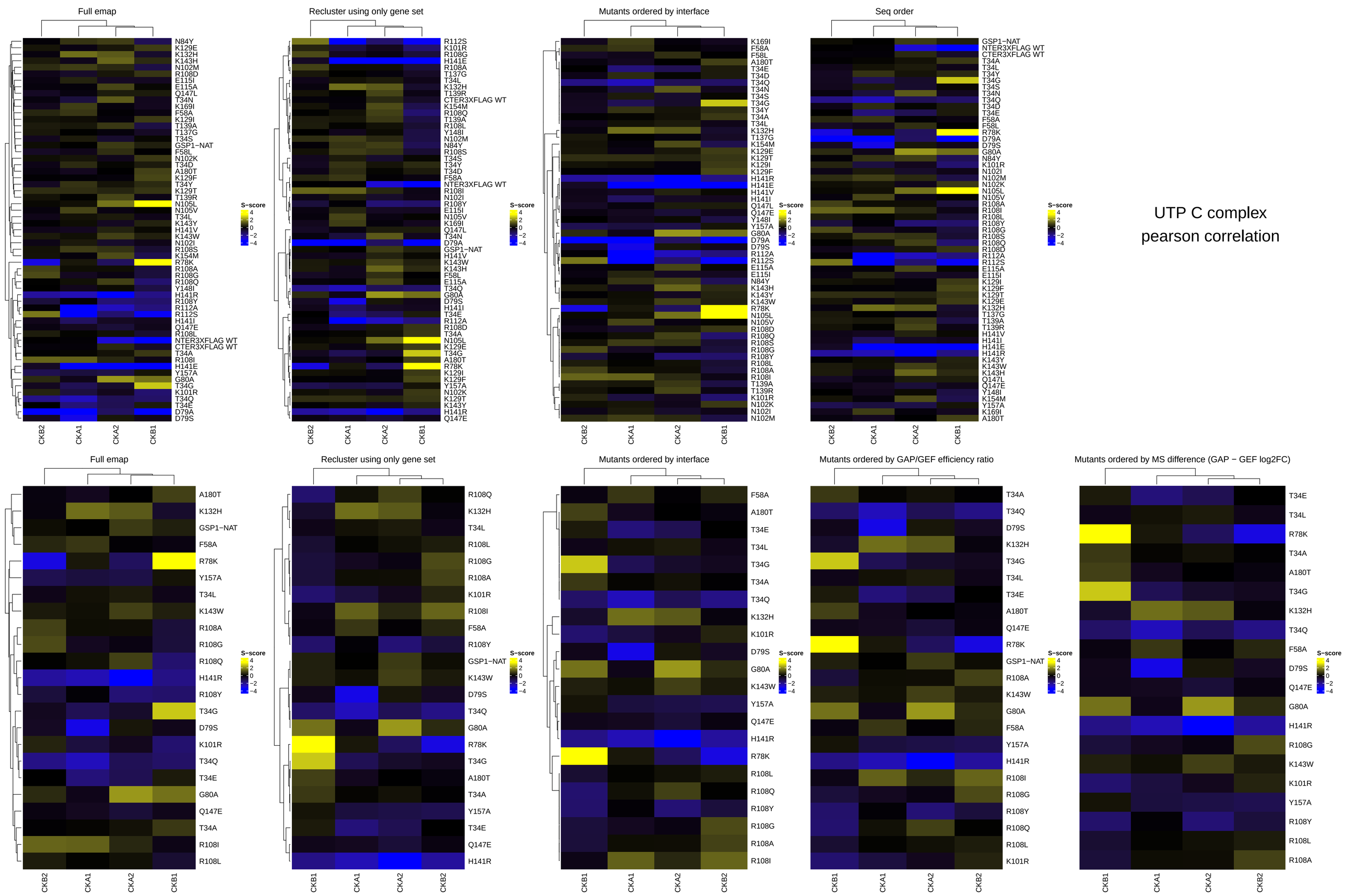
UME1
RPD3
EAF3
RCO1
Rpd3S complex
pearson correlation

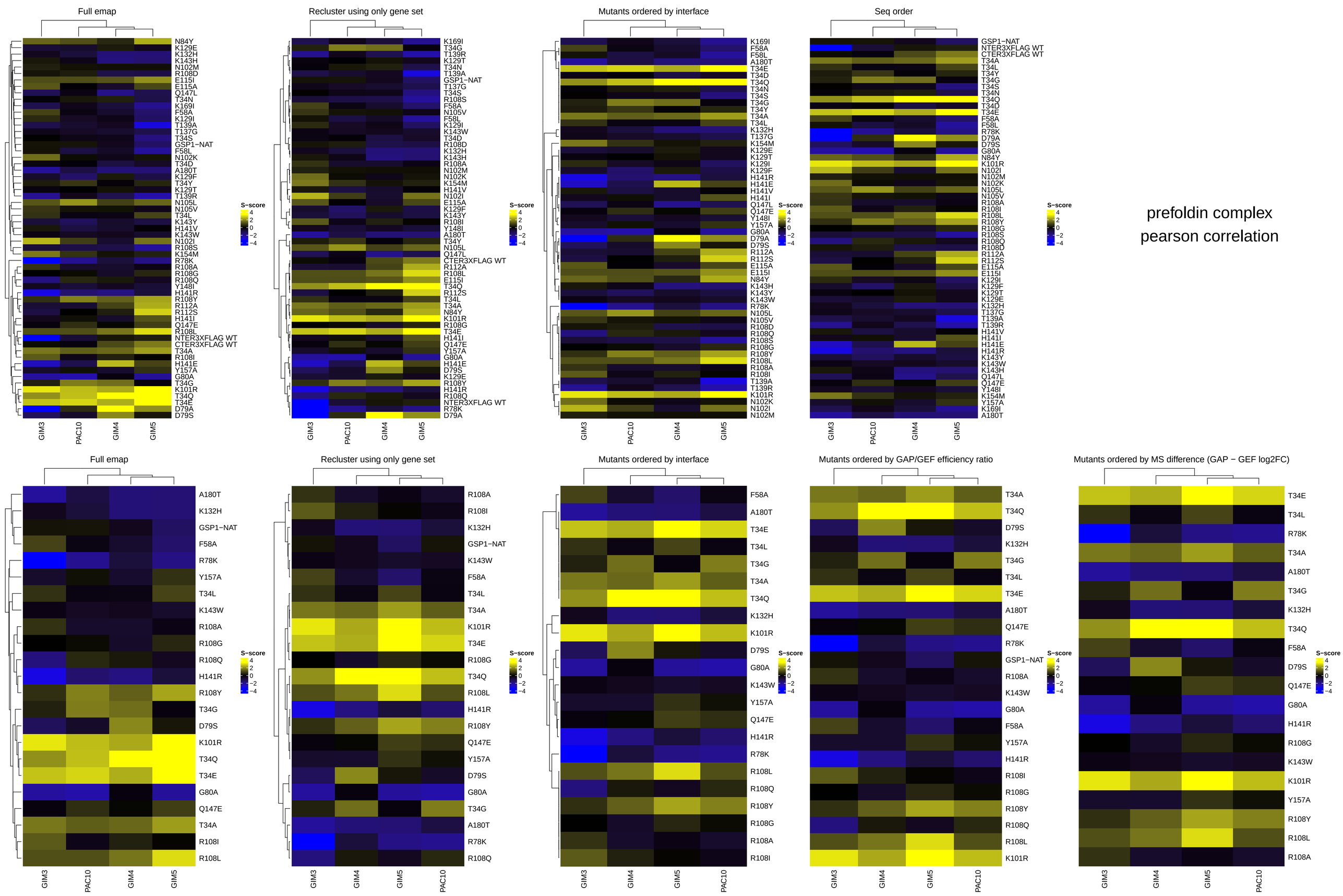


GSE Complex
pearson correlation



RSC complex
pearson correlation


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
CKB2
CKA1
CKA2
CKB1
UTP C complex
pearson correlation


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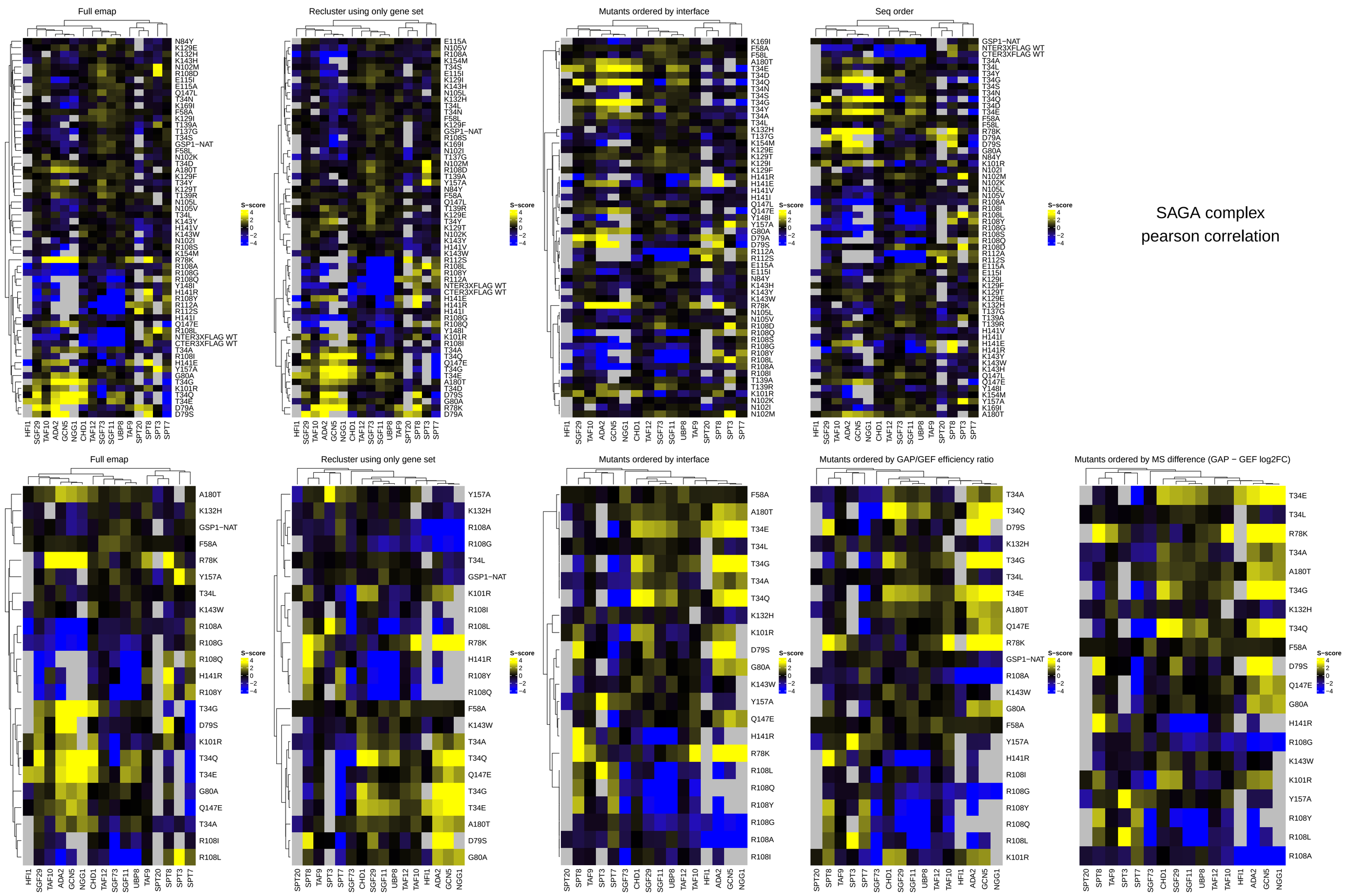
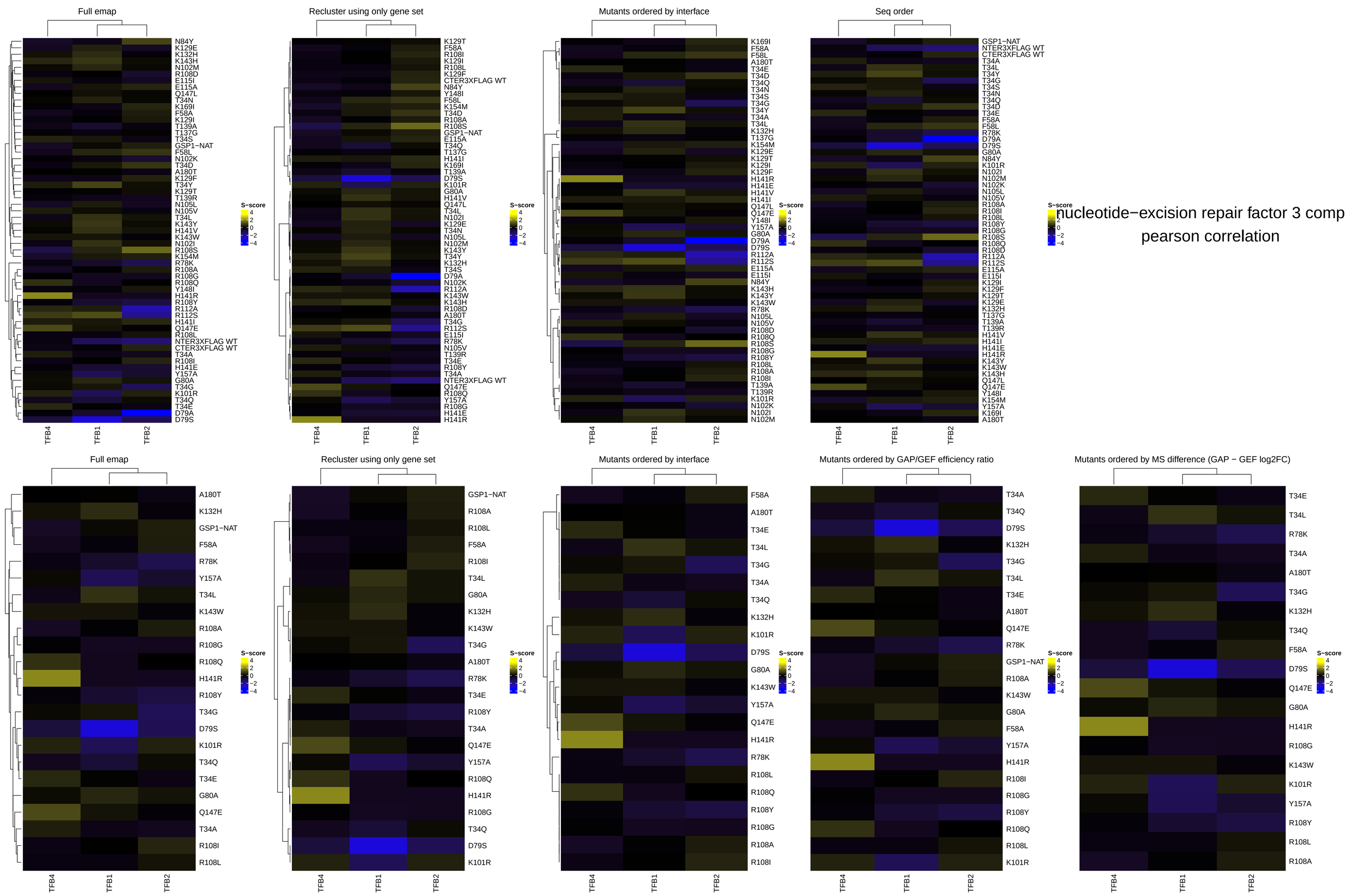
PAC10
GIM4
GIM5
Mutants ordered by GAP/GEF efficiency ratio
Mutants ordered by MS difference (GAP − GEF log2FC)
prefoldin complex
pearson correlation



SAGA complex
pearson correlation


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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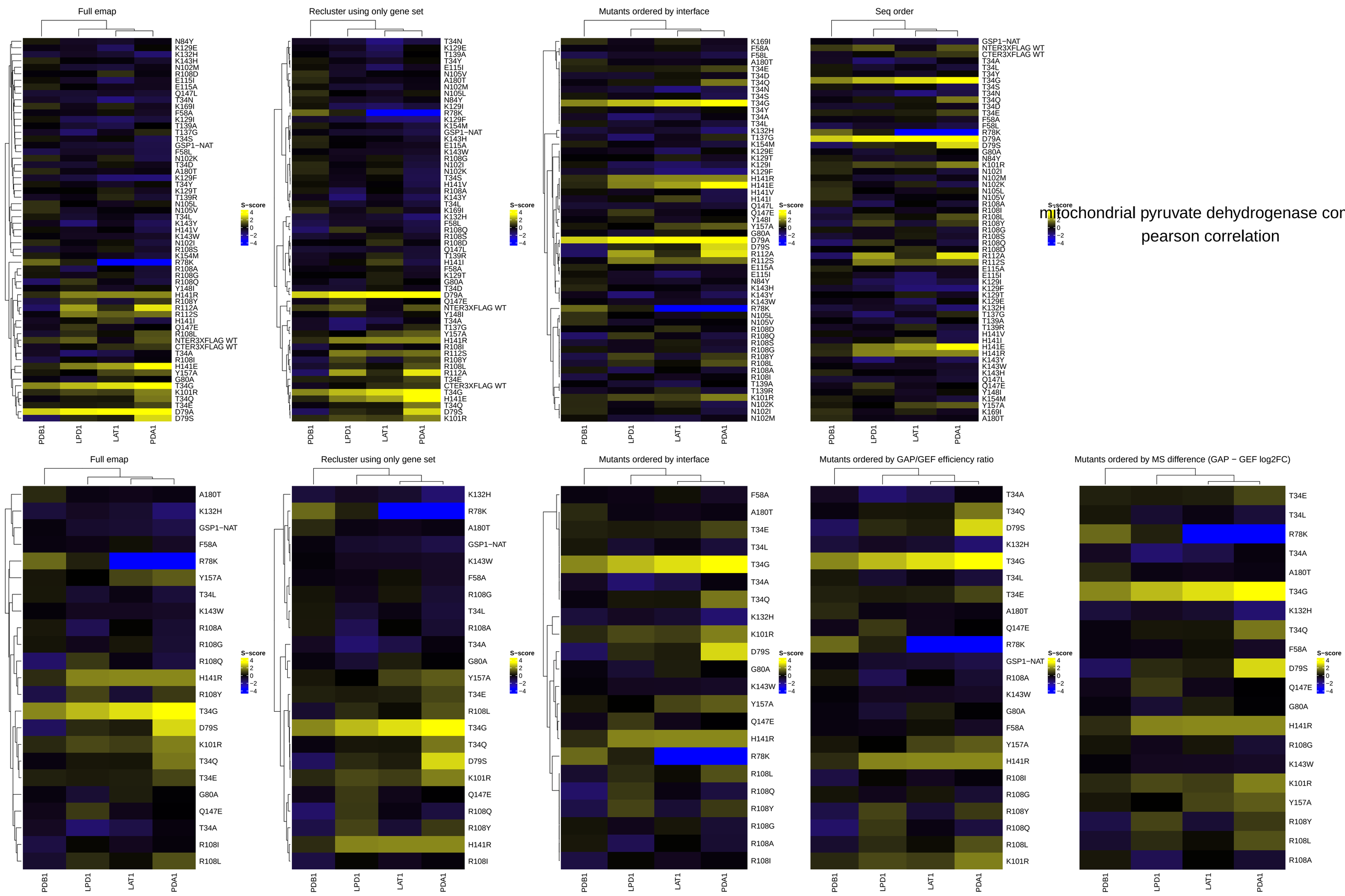
2
0
−2
−4
TFB4
TFB1
TFB2
nucleotide−excision repair factor 3 comp
pearson correlation


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
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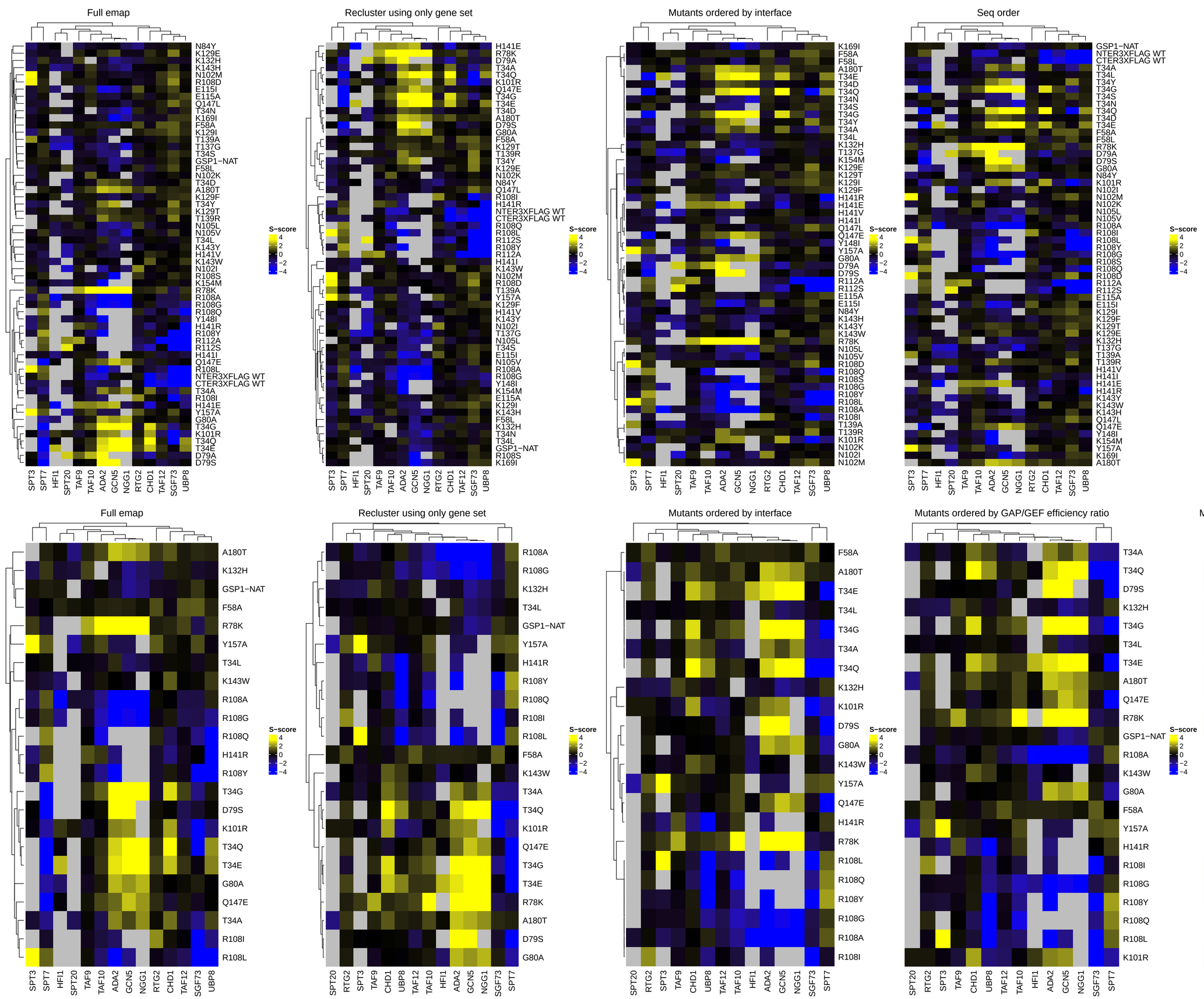
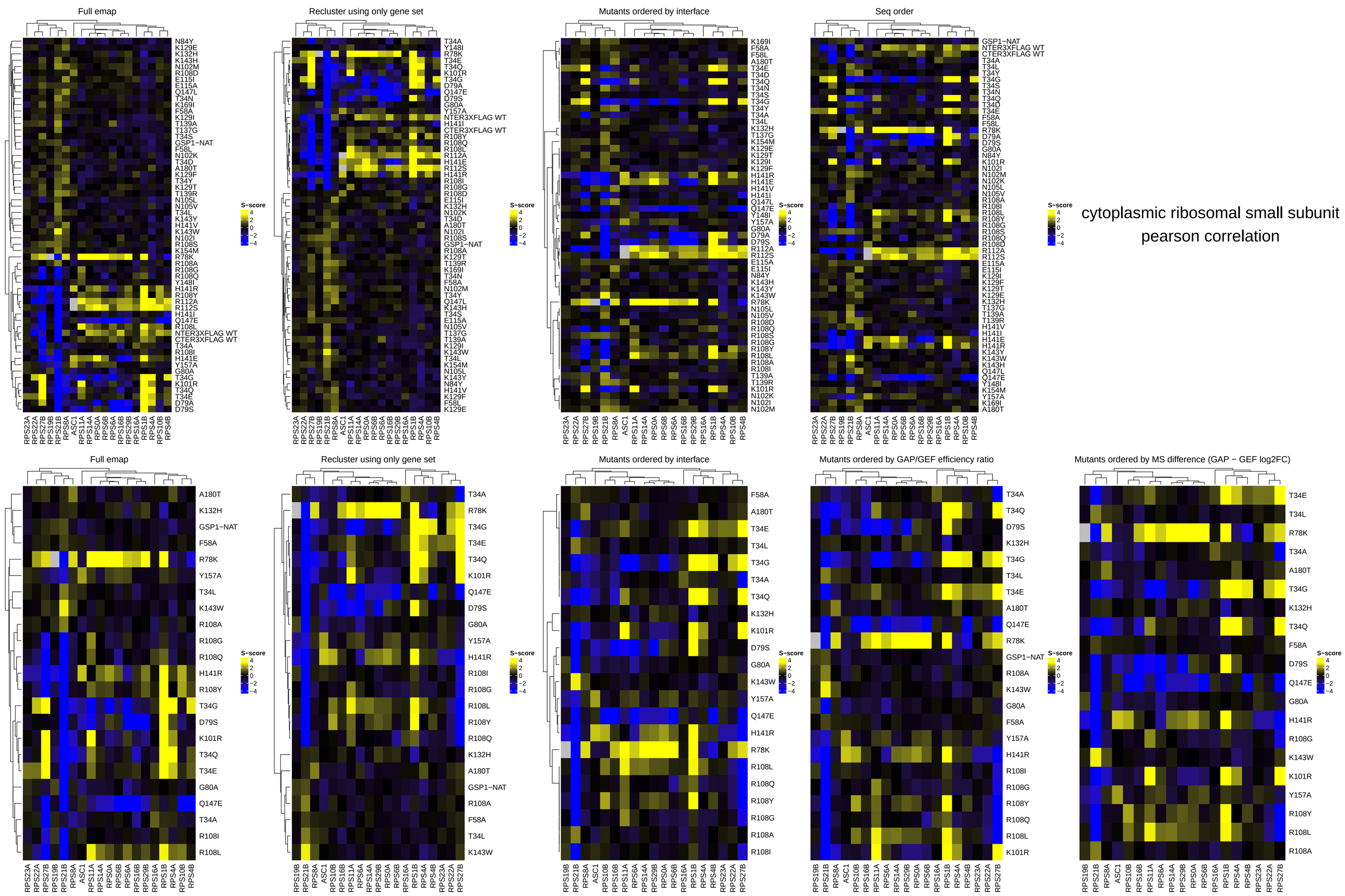
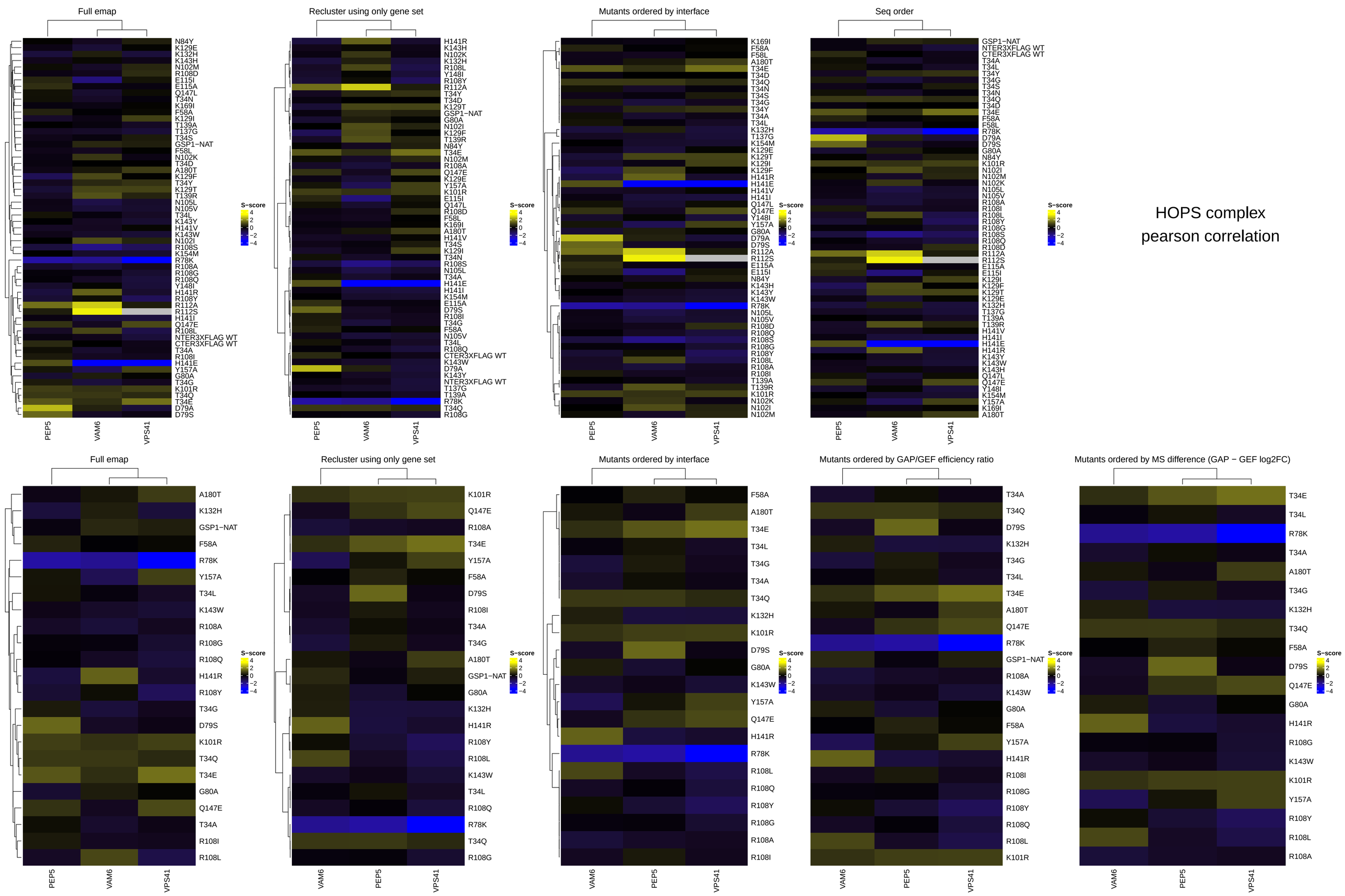
2
0
−2
−4
PDB1
LPD1
LAT1
PDA1
mitochondrial pyruvate dehydrogenase com
pearson correlation

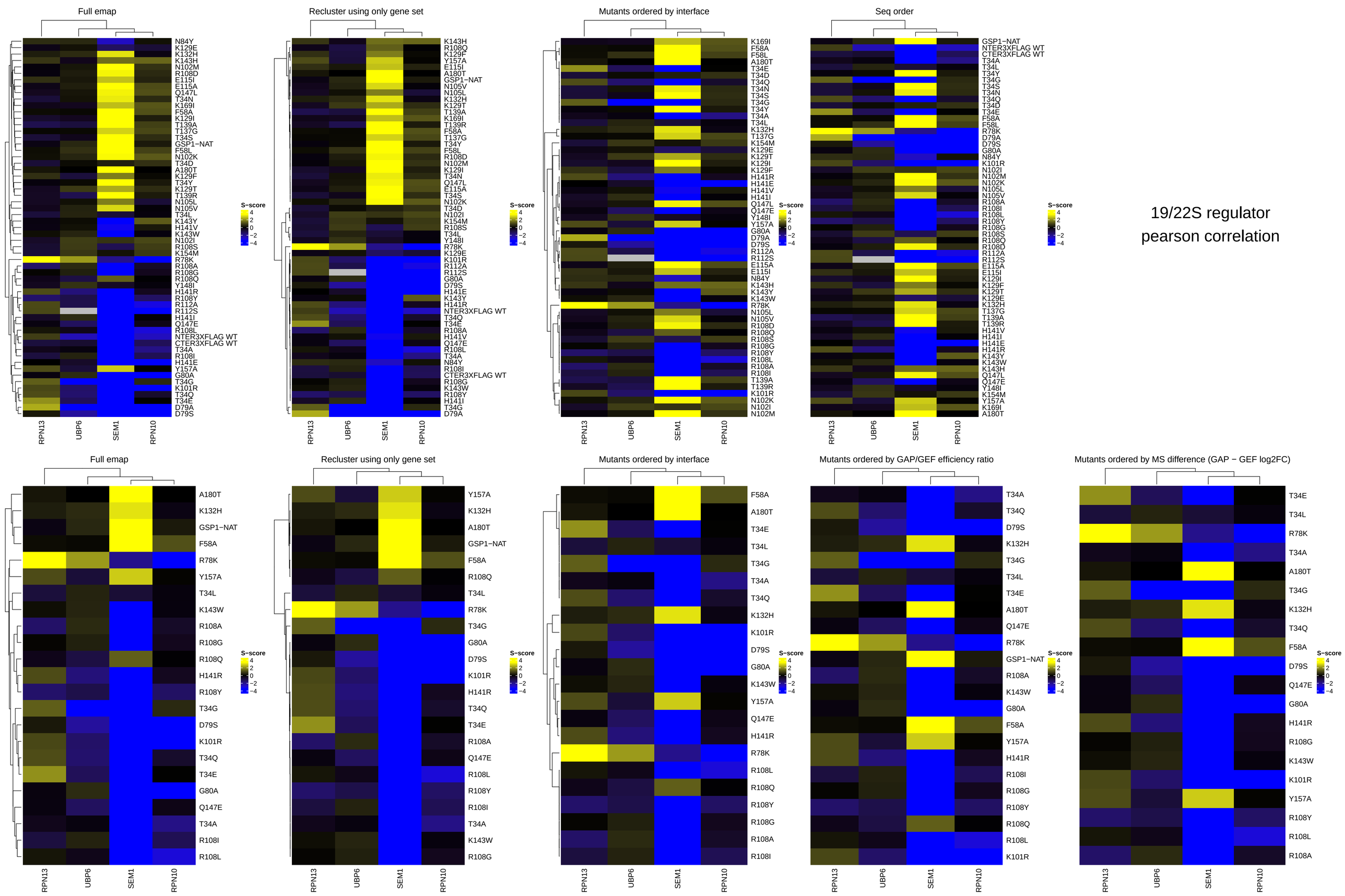


SLIK (SAGA−like) complex
pearson correlation

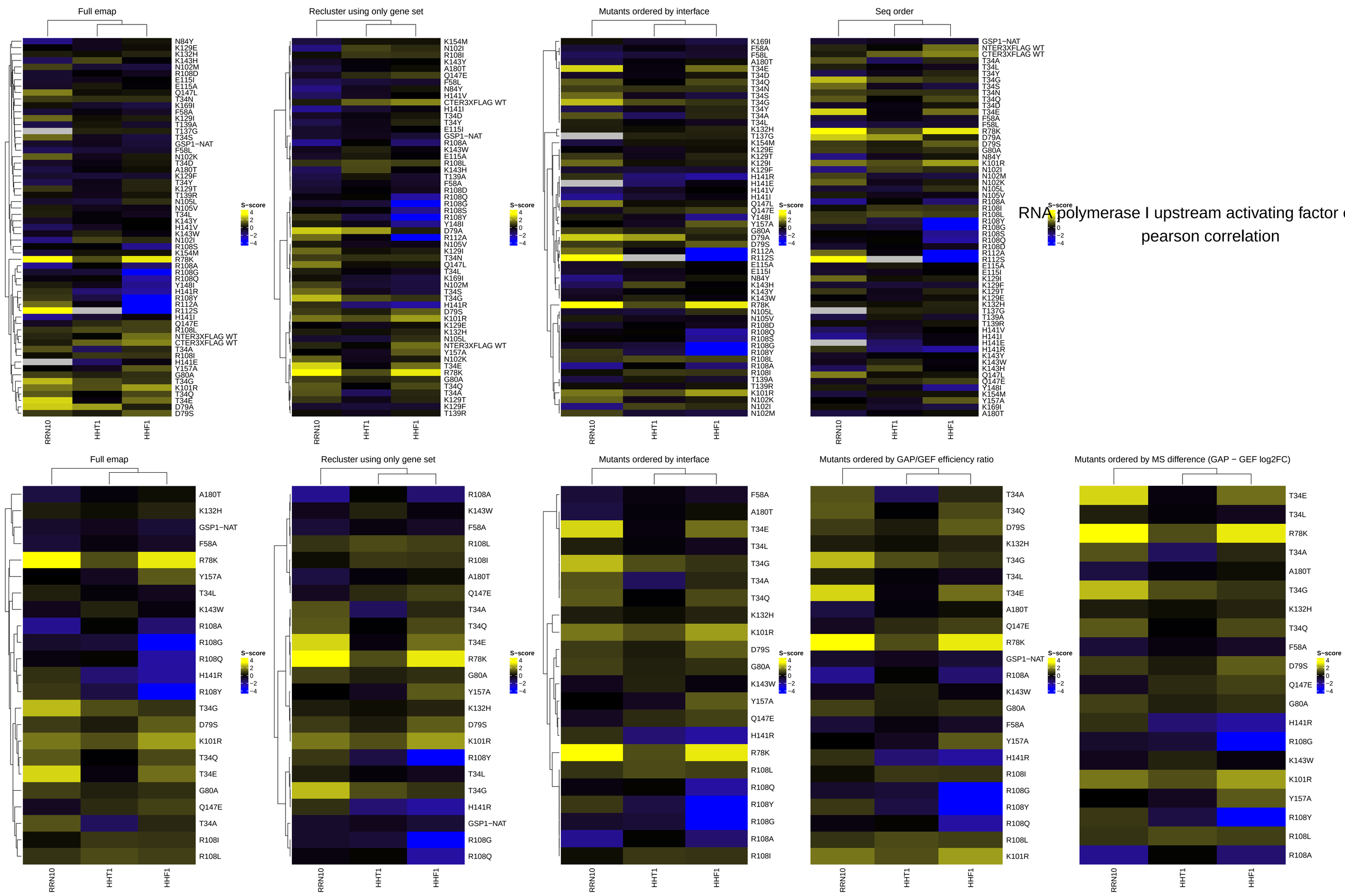


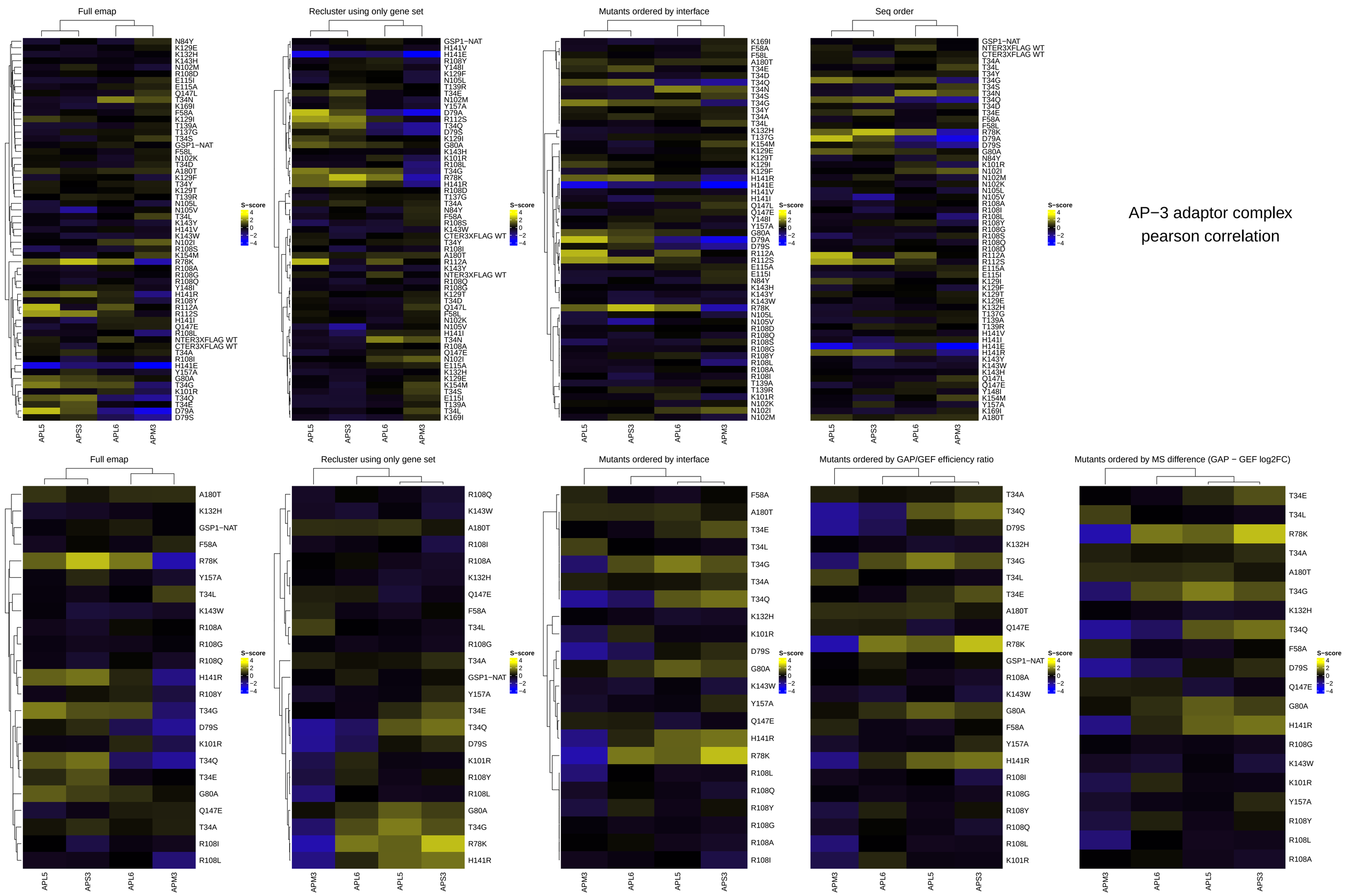
cytoplasmic ribosomal small subunit
pearson correlation


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
PEP5
VAM6
VPS41
HOPS complex
pearson correlation



19/22S regulator
pearson correlation


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
pearson correlation


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)
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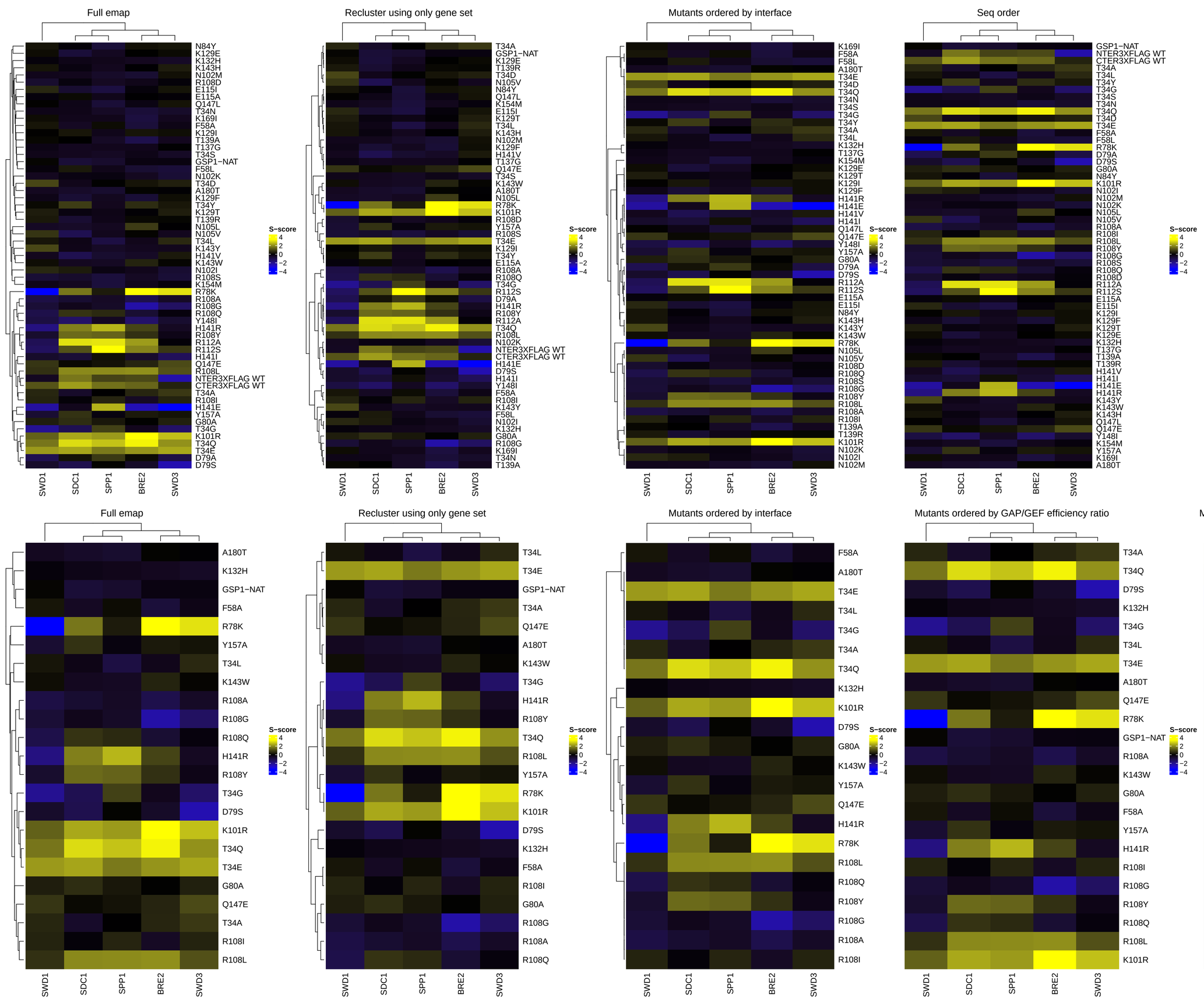
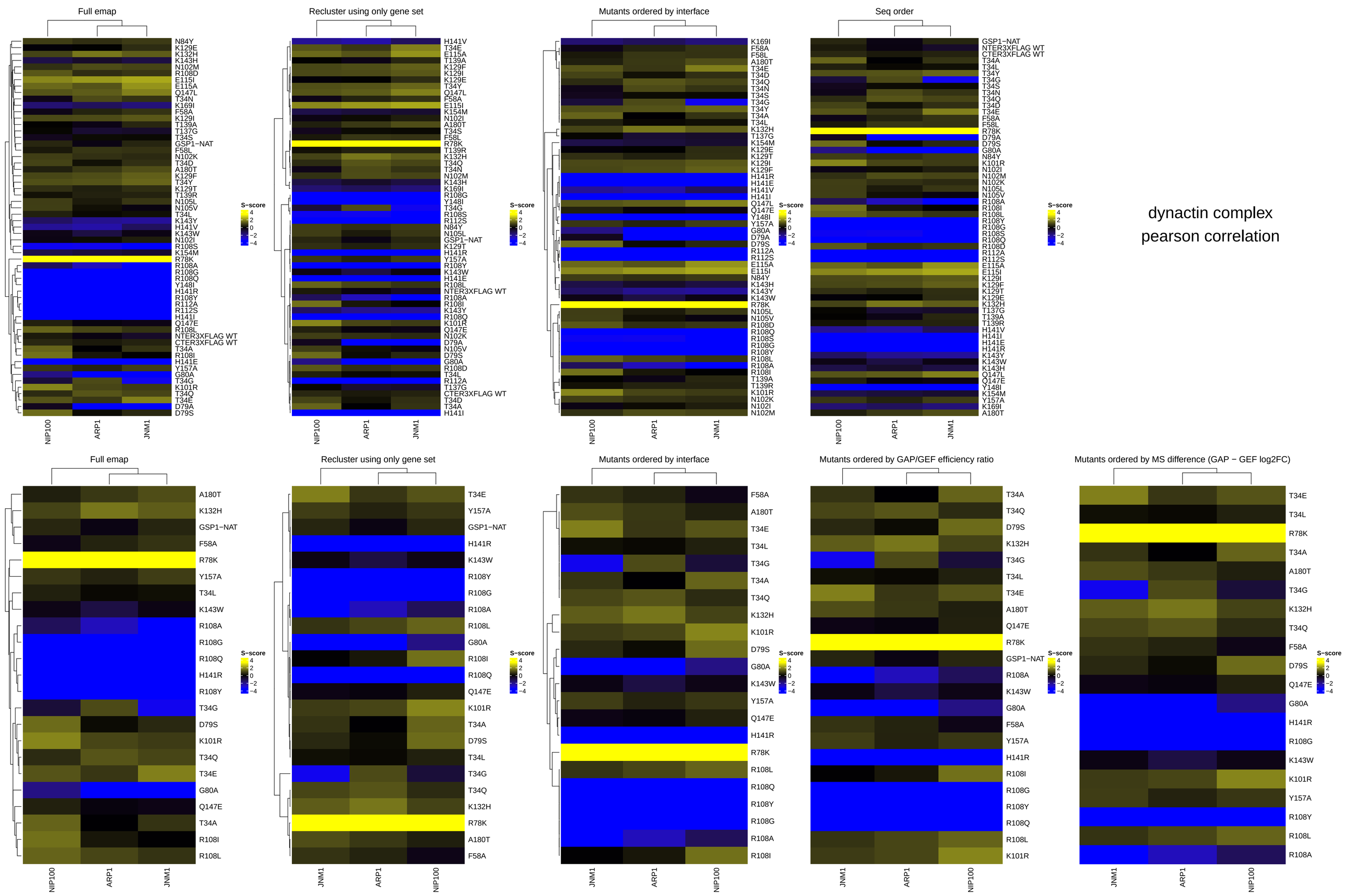
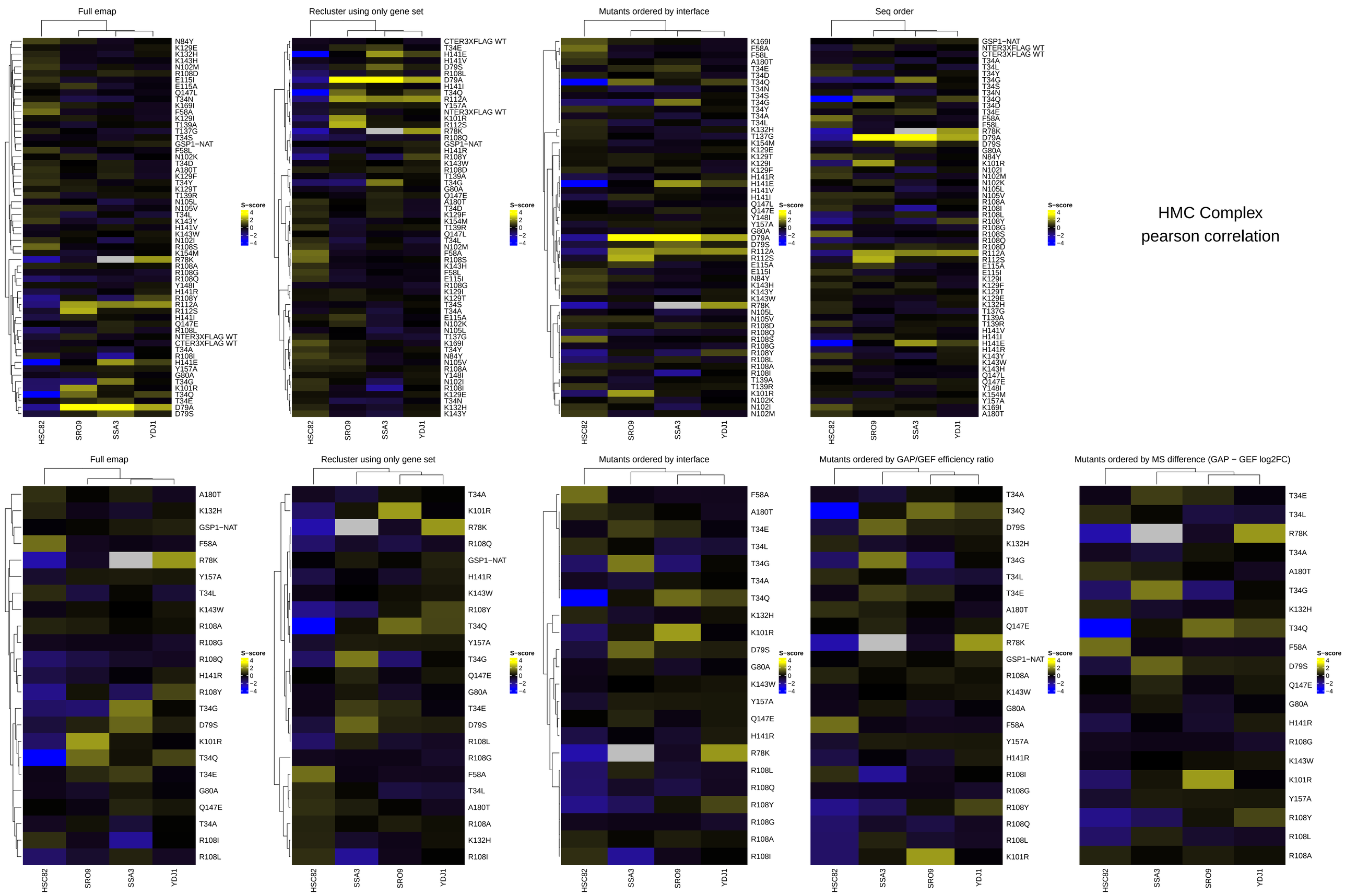
2
0
−2
−4
APL5
APS3
APL6
APM3
AP−3 adaptor complex
pearson correlation



COMPASS complex
pearson correlation


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
pearson correlation


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
pearson correlation