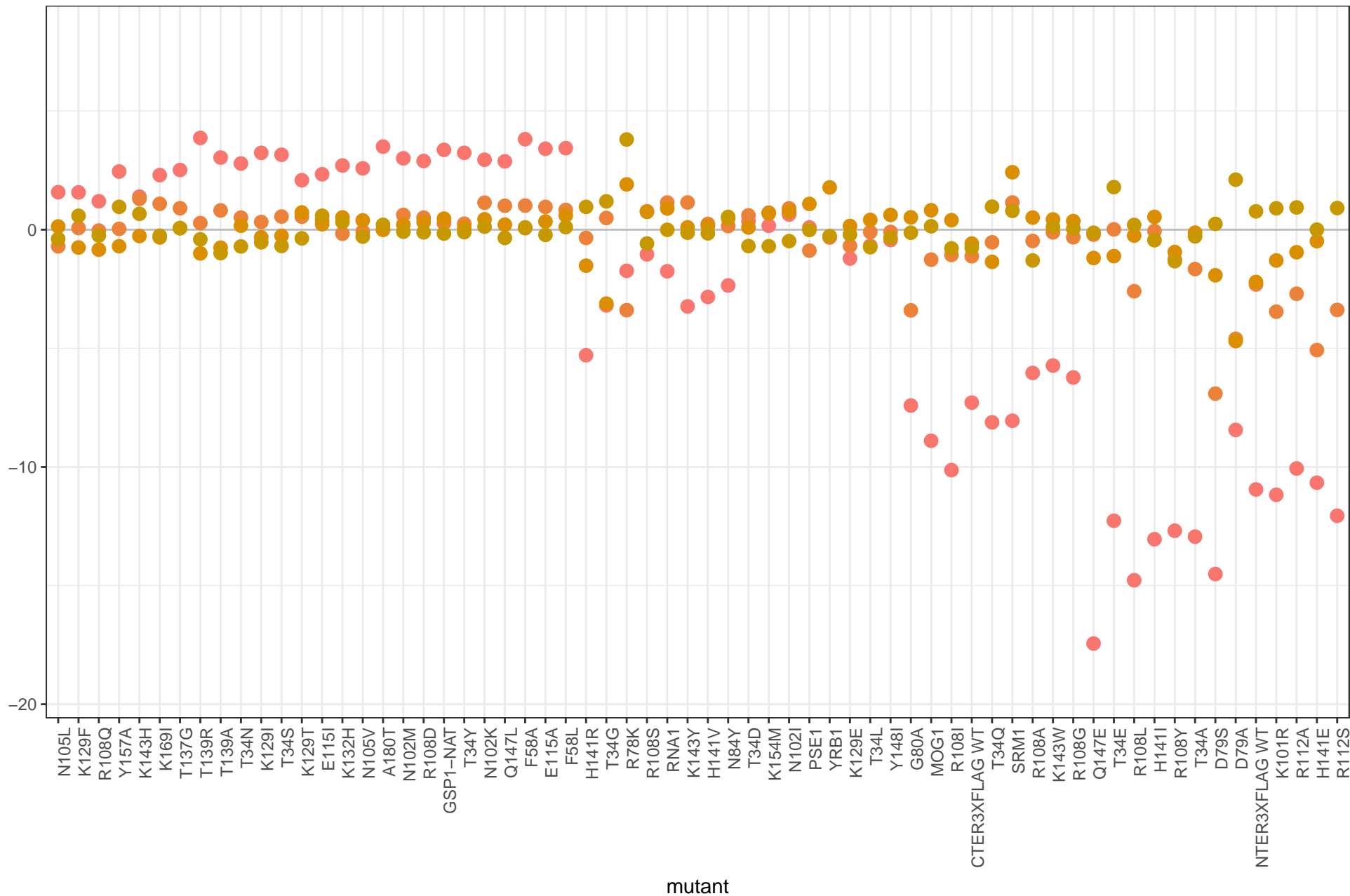


19/22S regulator

E-MAP score

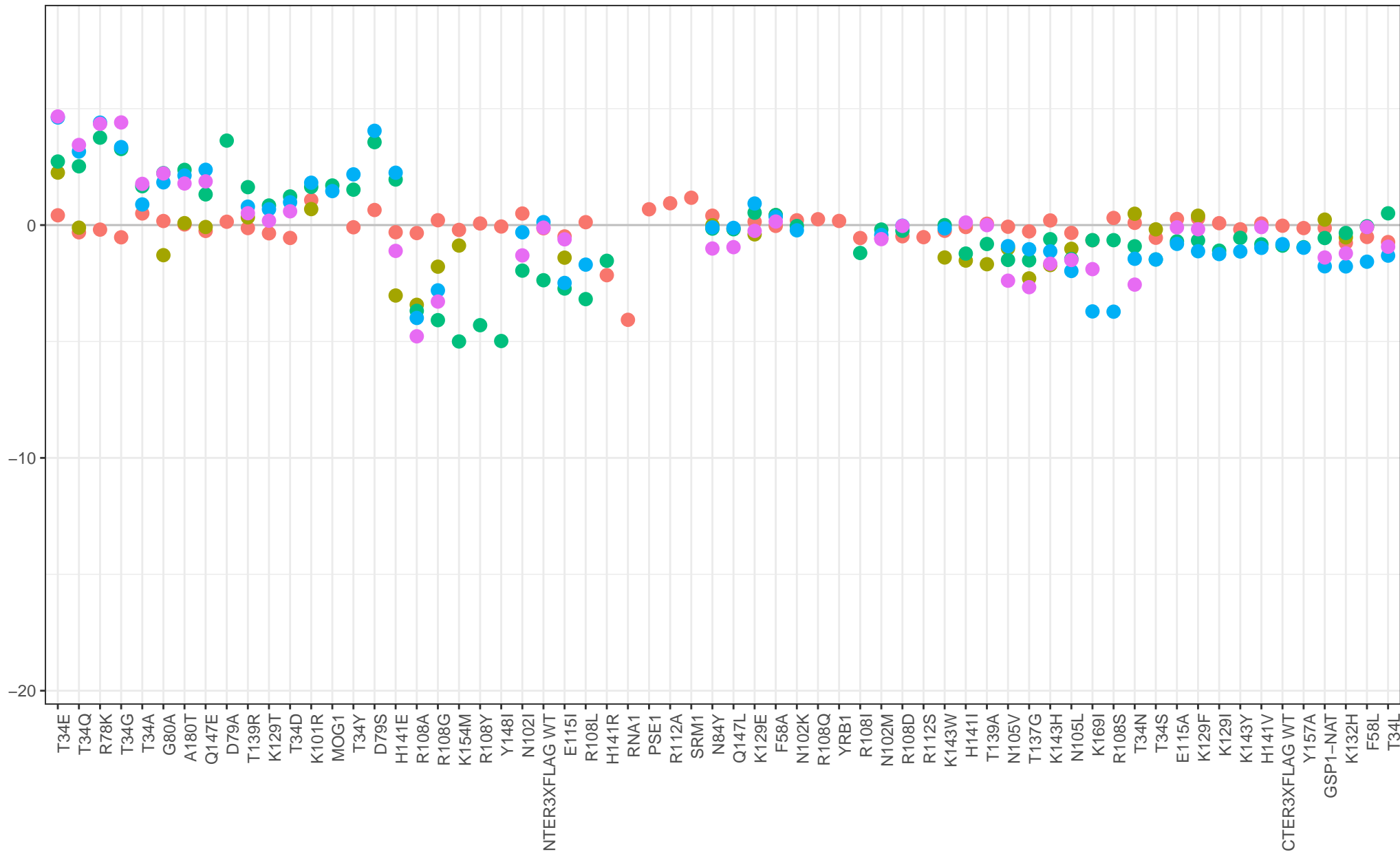


library gene

- SEM1
- RPN10
- UBP6
- RPN13
- RPT6
- RPT5
- RPT4
- RPT3
- RPT2
- RPT1
- RPN9
- RPN8
- RPN7
- RPN6
- RPN5
- RPN3
- RPN2
- RPN12
- RPN11
- RPN1
- ECM29
- NAS6

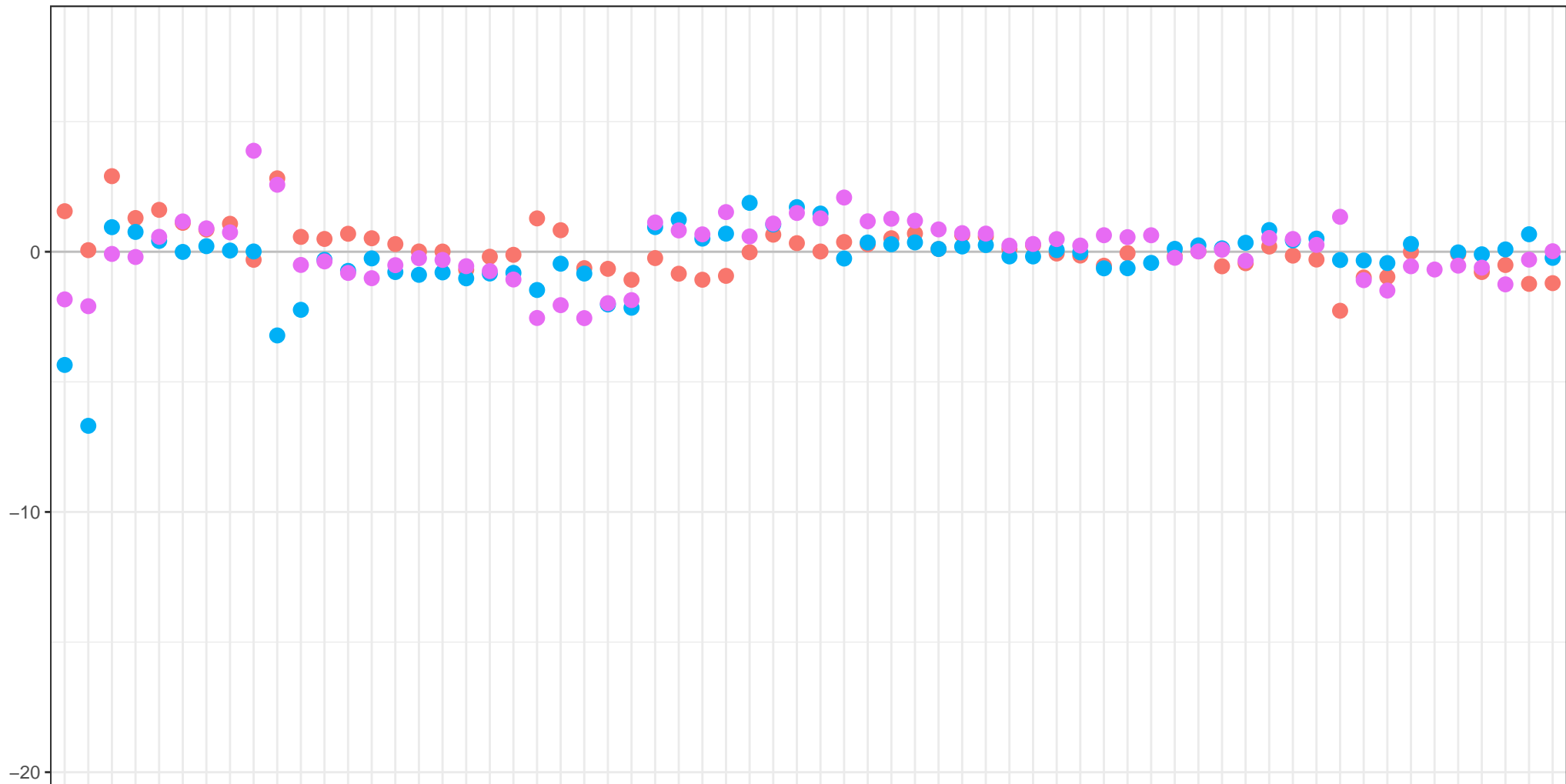
Ada2p/Gcn5p/Ada3 transcription activator complex

E-MAP score



alpha-1,6-mannosyltransferase complex(Anp1p/Mnn9p)

E-MAP score



library gene

- MNN10
- ANP1
- MNN9
- HOC1
- MNN11

mutant

alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)

E-MAP score

-20

-10

0

K132H
RNA1
R112A
SRM1
R78K
Q147L
E115A
NTER3XFLAG WT
E115I
Q147E
T137G
GSP1-NAT
T34L
YRB1
K129E
K129I
R108S
T34S
Y148I
MOG1
R108A
N105L
T34D
G80A
K154M
H141I
K143H
F58L
T34N
N102K
K143W
K143Y
T139A
CTER3XFLAG WT
N102M
K129T
N105V
N102I
R108I
K169I
N84Y
T139R
H141V
T34Y
K129F
PSE1
R108D
A180T
F58A
R108Q
T34A
R112S
R108Y
T34Q
D79S
K101R
R108G
R108L
Y157A
T34E
H141E
H141R
D79A
T34G

mutant

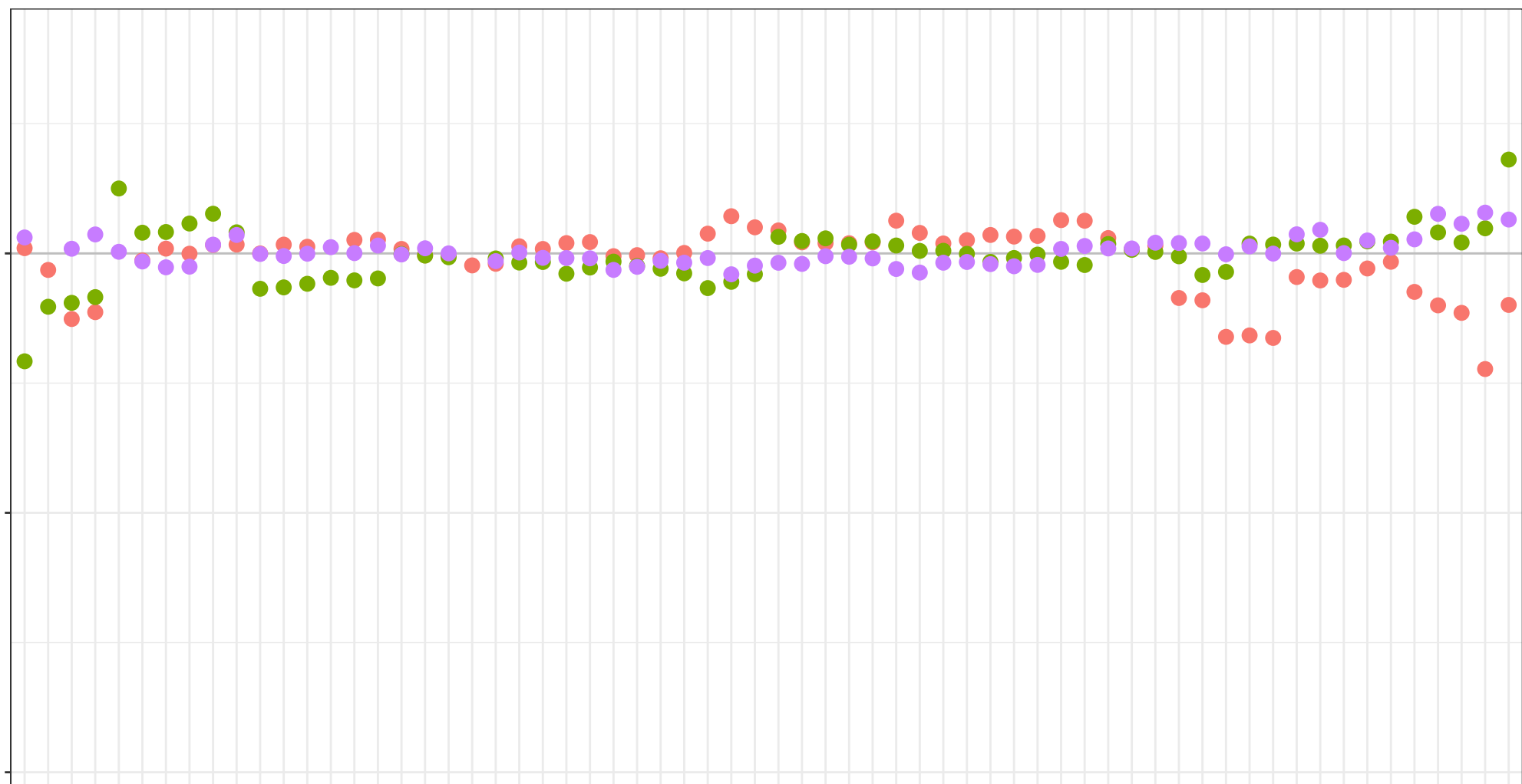
library gene

TPS2

TPS1

TPS3

TSL1



amino acid transport

E-MAP score

-20

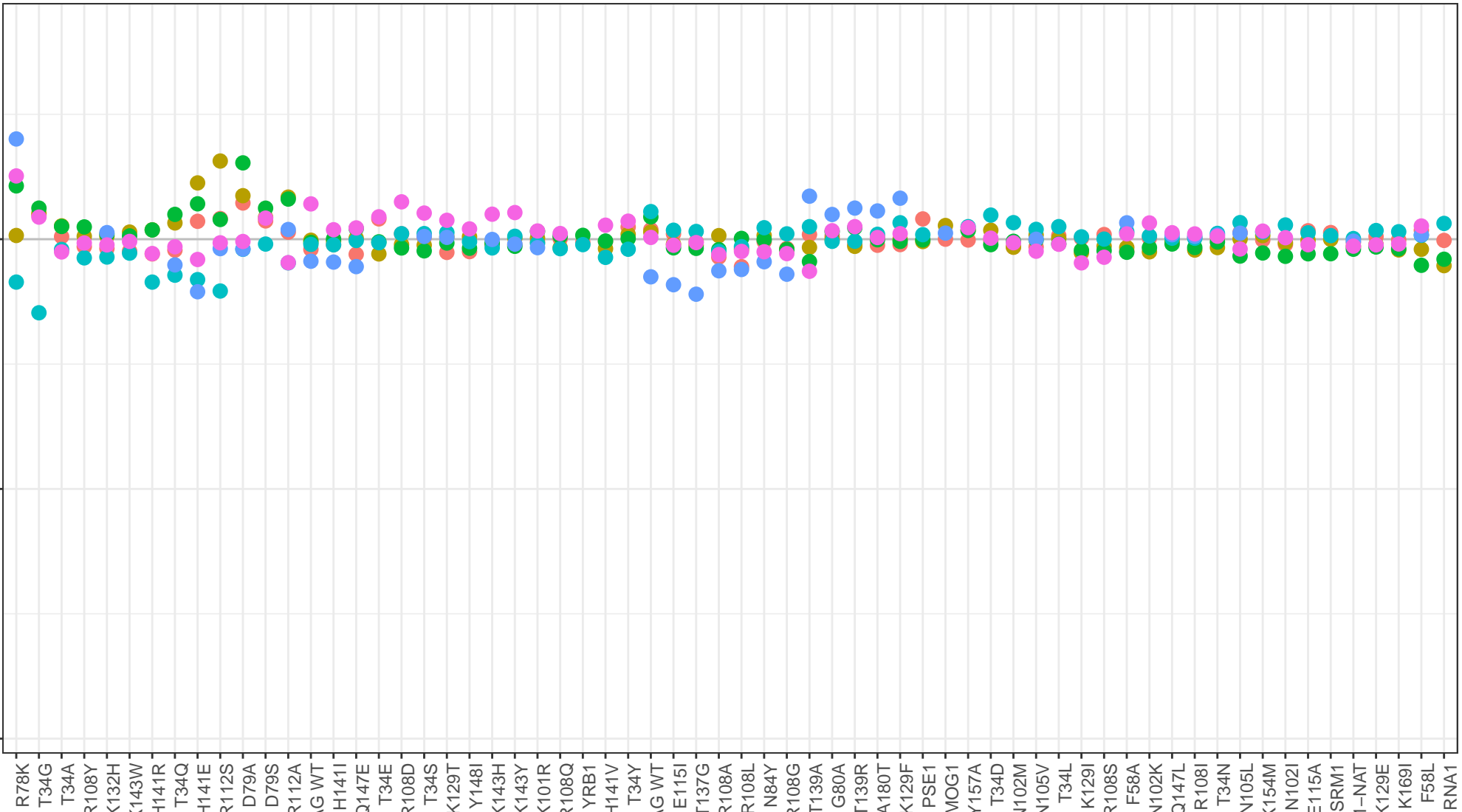
-10

0

mutant

library gene

- TAT1
- RHB1
- TAT2
- GNP1
- ALP1
- NPR2



anaphase-promoting complex

E-MAP score

-20

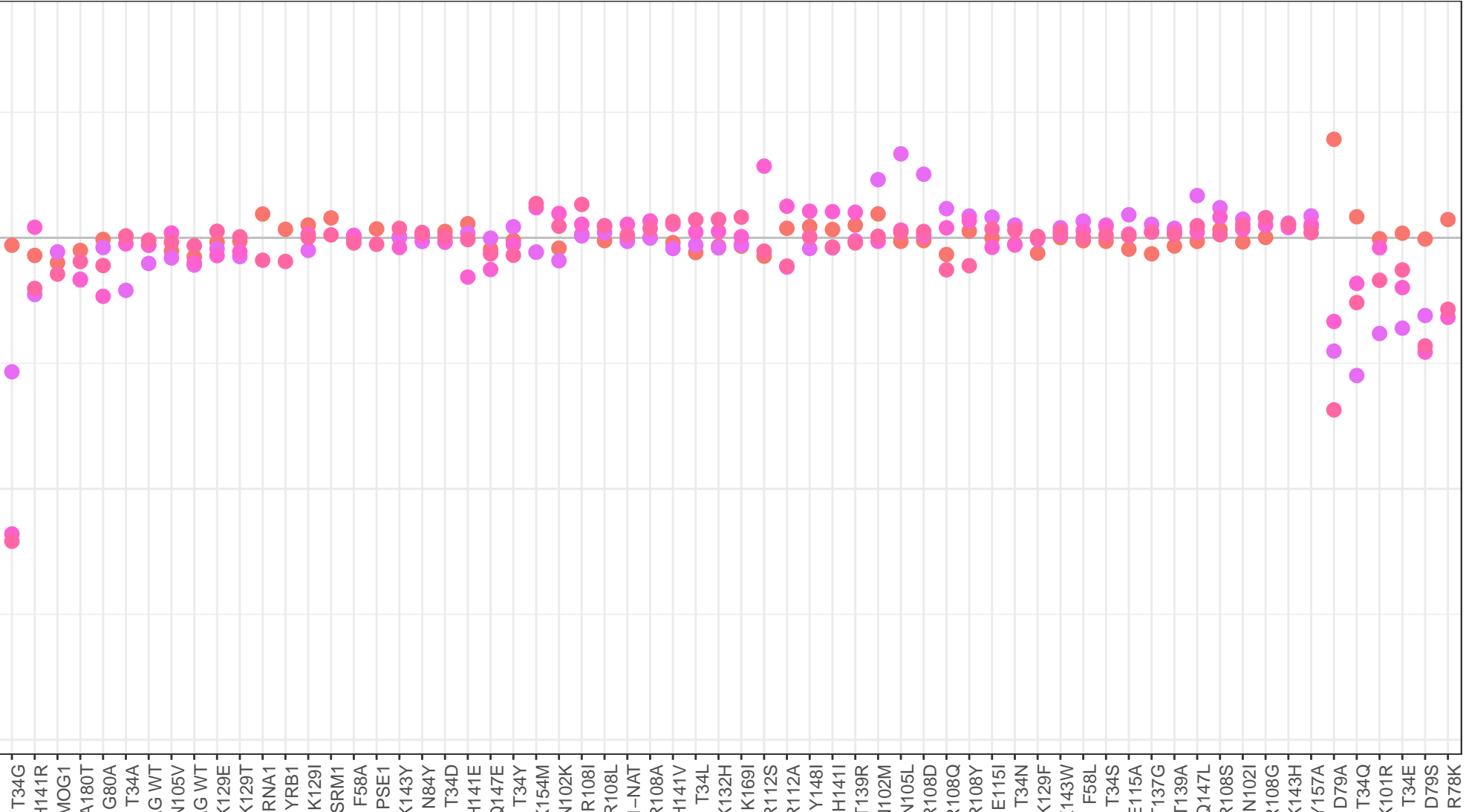
-10

0

mutant

library gene

- APC9
- MND2
- DOC1
- CDC27
- CDC23
- CDC20
- CDC16
- APC5
- APC4
- APC2
- APC1
- APC11
- CDH1
- CDC26
- SWM1



AP-3 adaptor complex

E-MAP score

-20

-10

0

mutant

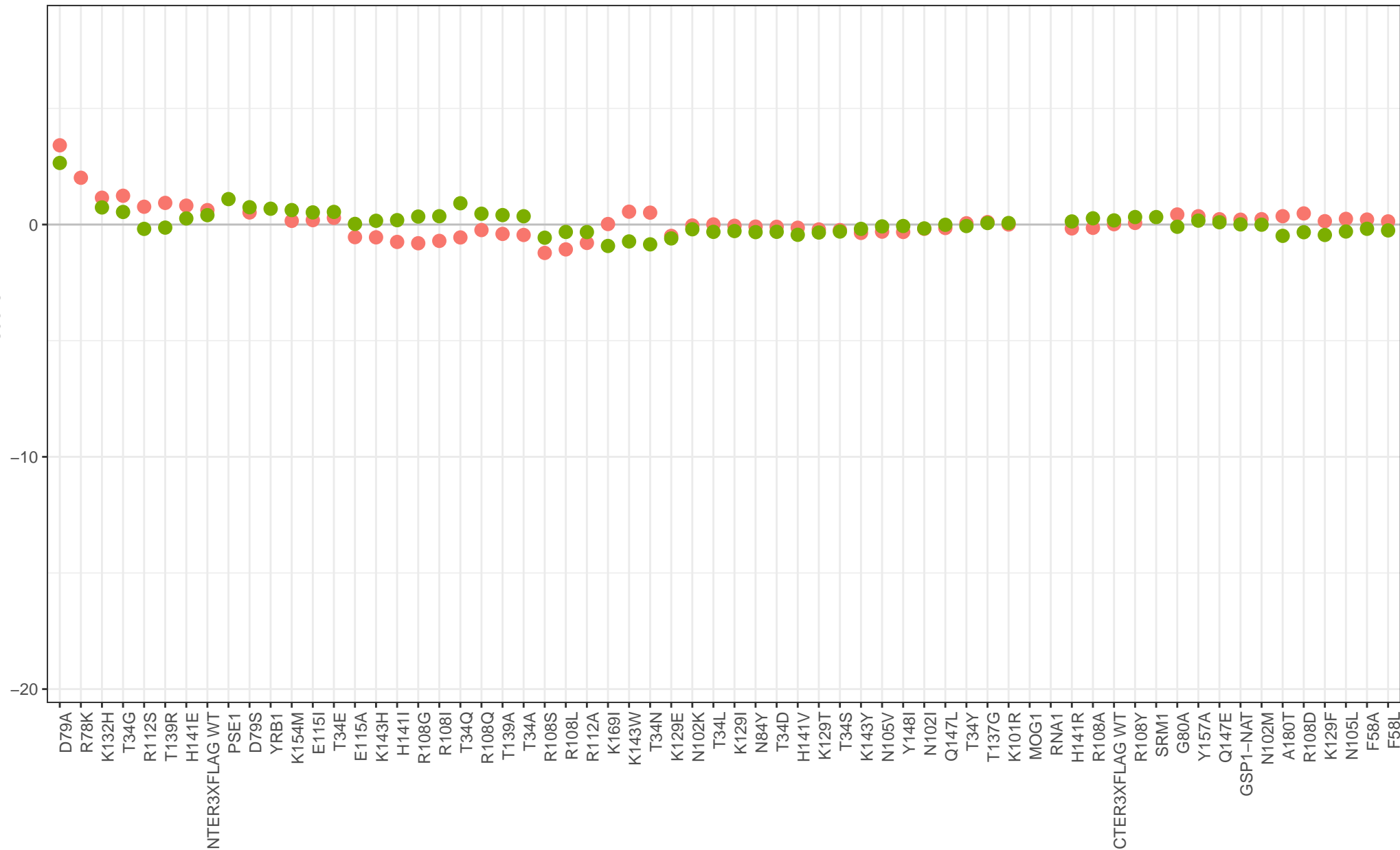
library gene

- APM3
- APL6
- APL5
- APS3

H141E YRB1 R78K R112S H141R T34G D79A D79S T34Q PSE1 R108L K101R R108Y N102M Y157A K129F N105L H141V MOG1 F58L N102K K143H R108D K169I E115I T139A K132H R108G K129E R108A E115A Q147E F58A T137G T34L K154M T34S CTER3XFLAG WT Q147L T34D H141I K143W K143Y R108I R108Q N105V RNA1 SRM1 N84Y R108S N102I T34N R112A G80A K129I T34E A180T T34A K129T T34Y NTER3XFLAG WT T139R GSP1-NAT Y148I

ARGR complex

E-MAP score



Bub1p/Bub3p complex

E-MAP score

0

-10

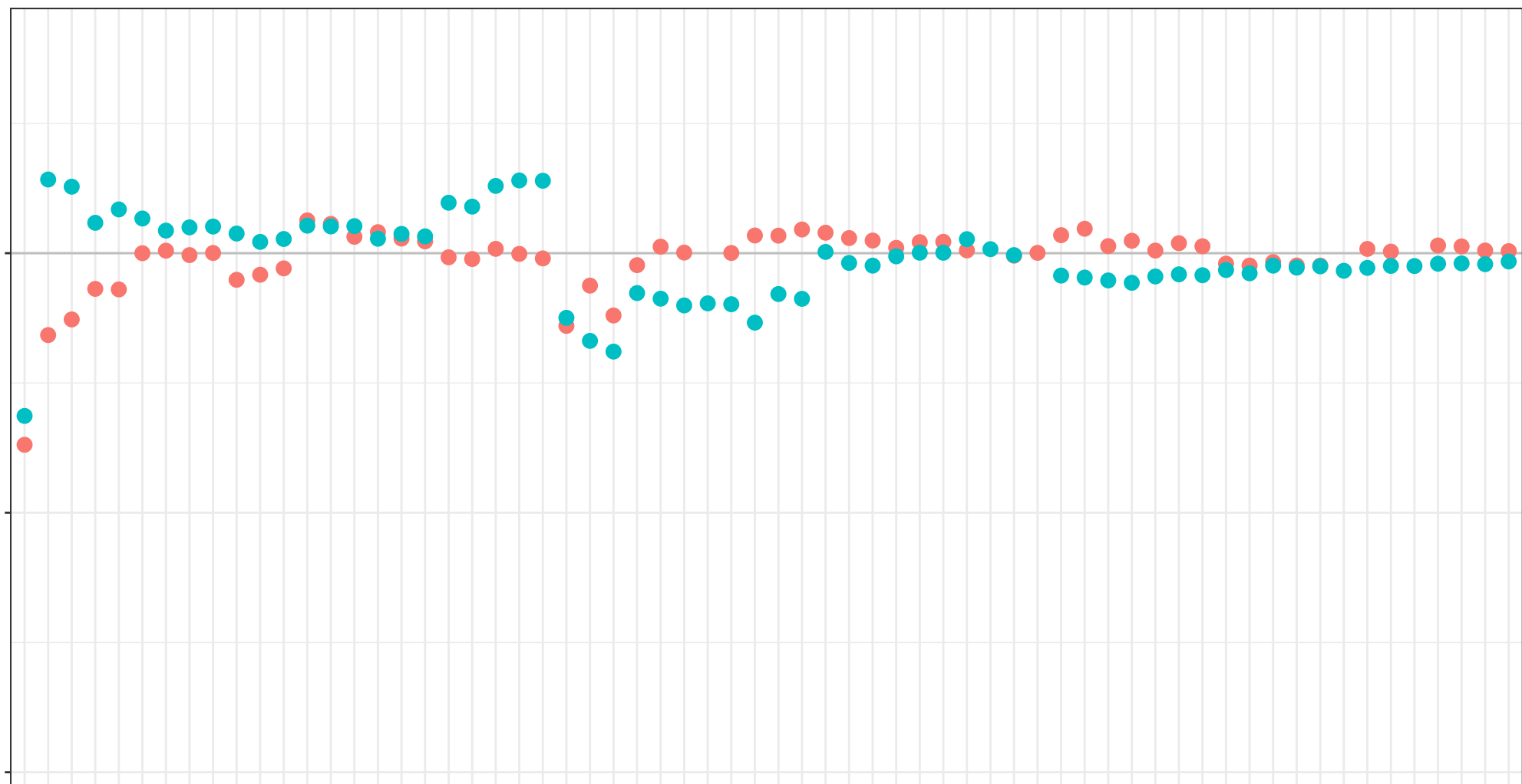
-20

D79A R112A R112S K101R NTER3XFLAG WT R108Q R108A H141I Q147E T34Q CTER3XFLAG WT Y148I MOG1 R108S K143W K132H K154M N105L R108G T34A R108I R108L R108Y H141R D79S H141E Q147L T34Y A180T PSE1 T34D T34G GSP1-NAT T139R K129T K169I R108D Y157A G80A K129E N102I SRM1 N84Y R78K T34L T34N E115A T139A F58L K129I N102M E115I T34S H141V K143H T34E RNA1 F58A N102K YRB1 K129F N105V K143Y T137G

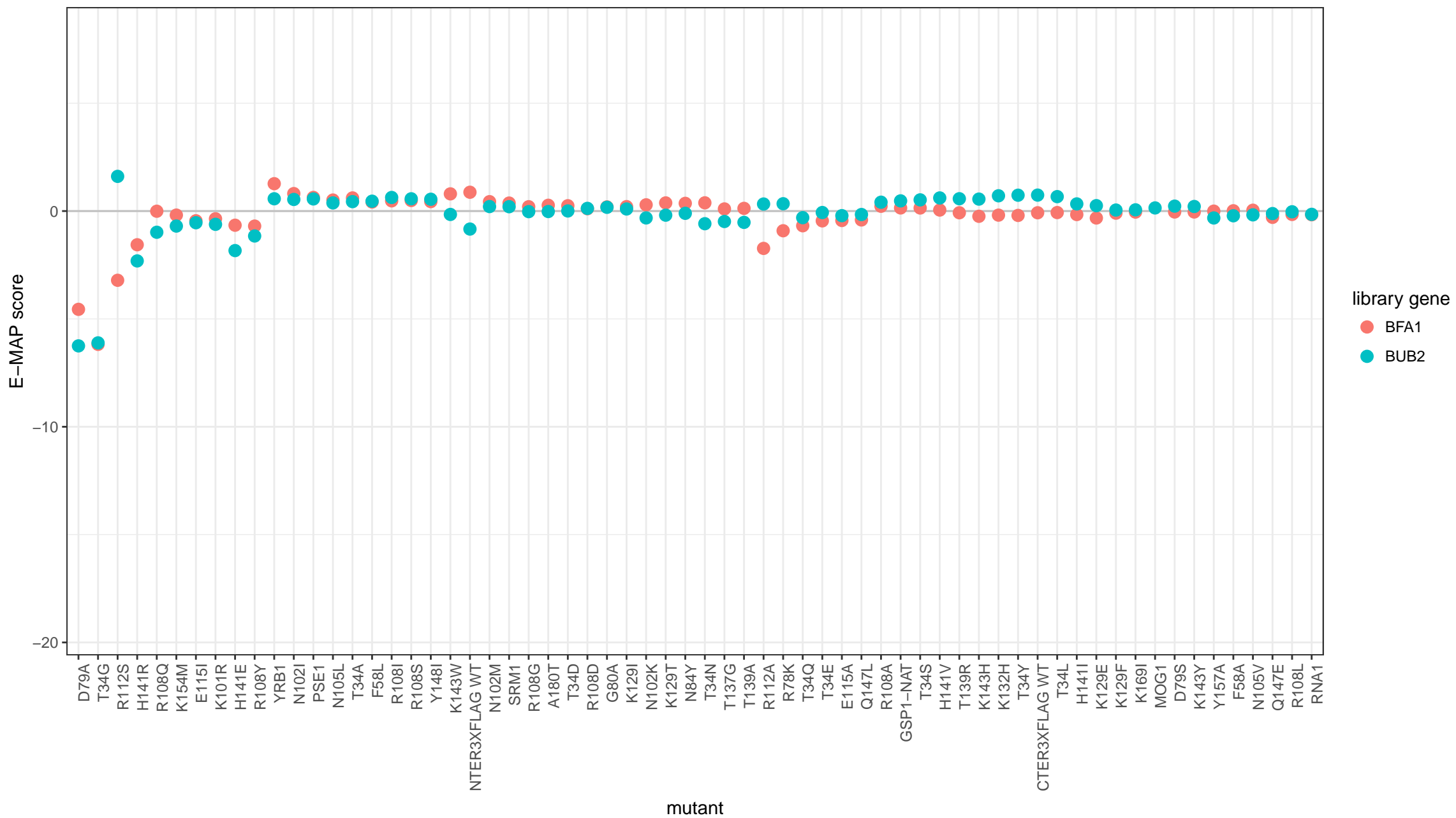
mutant

library gene

- BUB1
- BUB3



Bub2p/Bfa1p complex



calcineurin complex

E-MAP score

0

-10

-20

library gene

CNB1

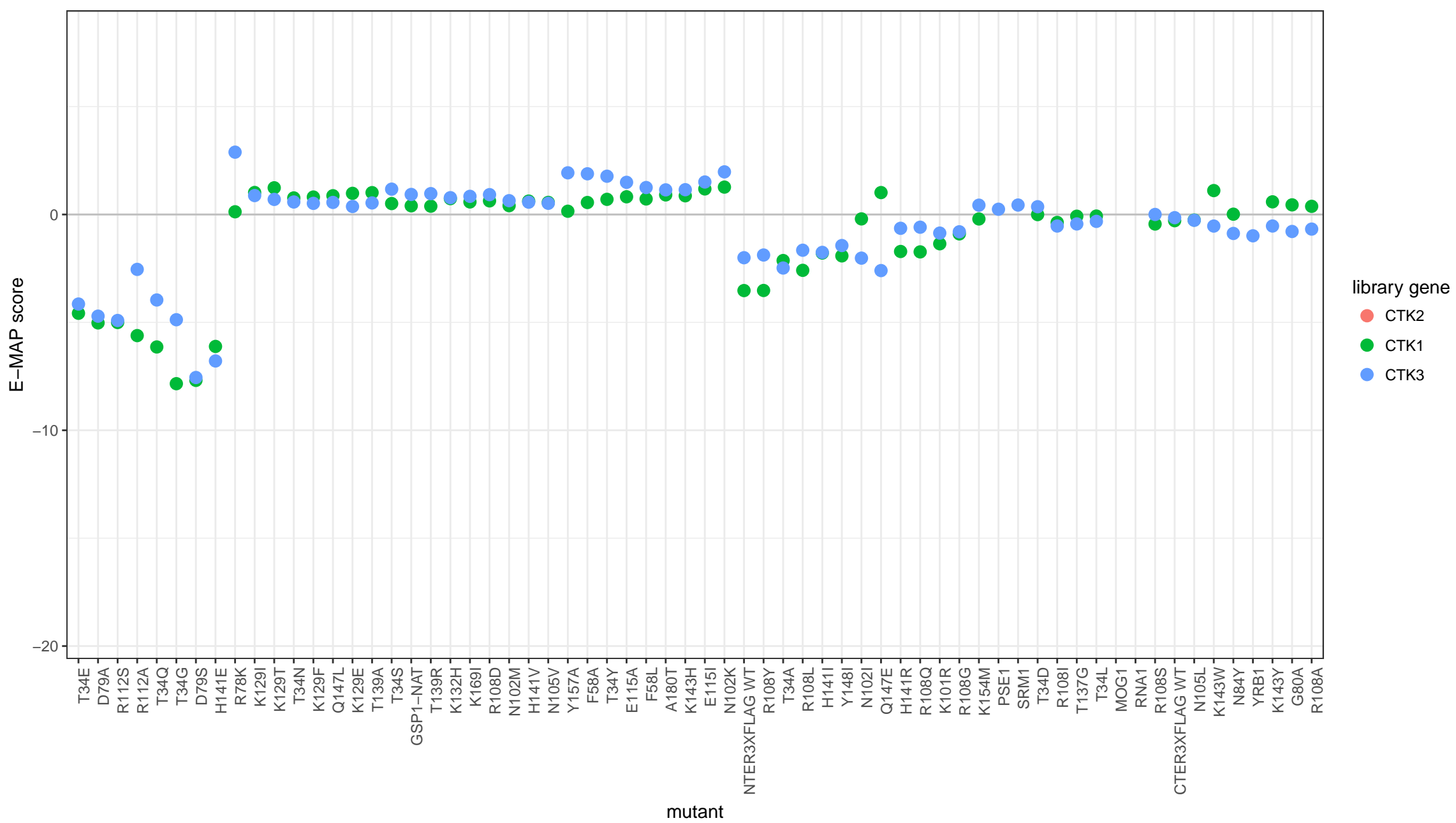
CMP2

CNA1

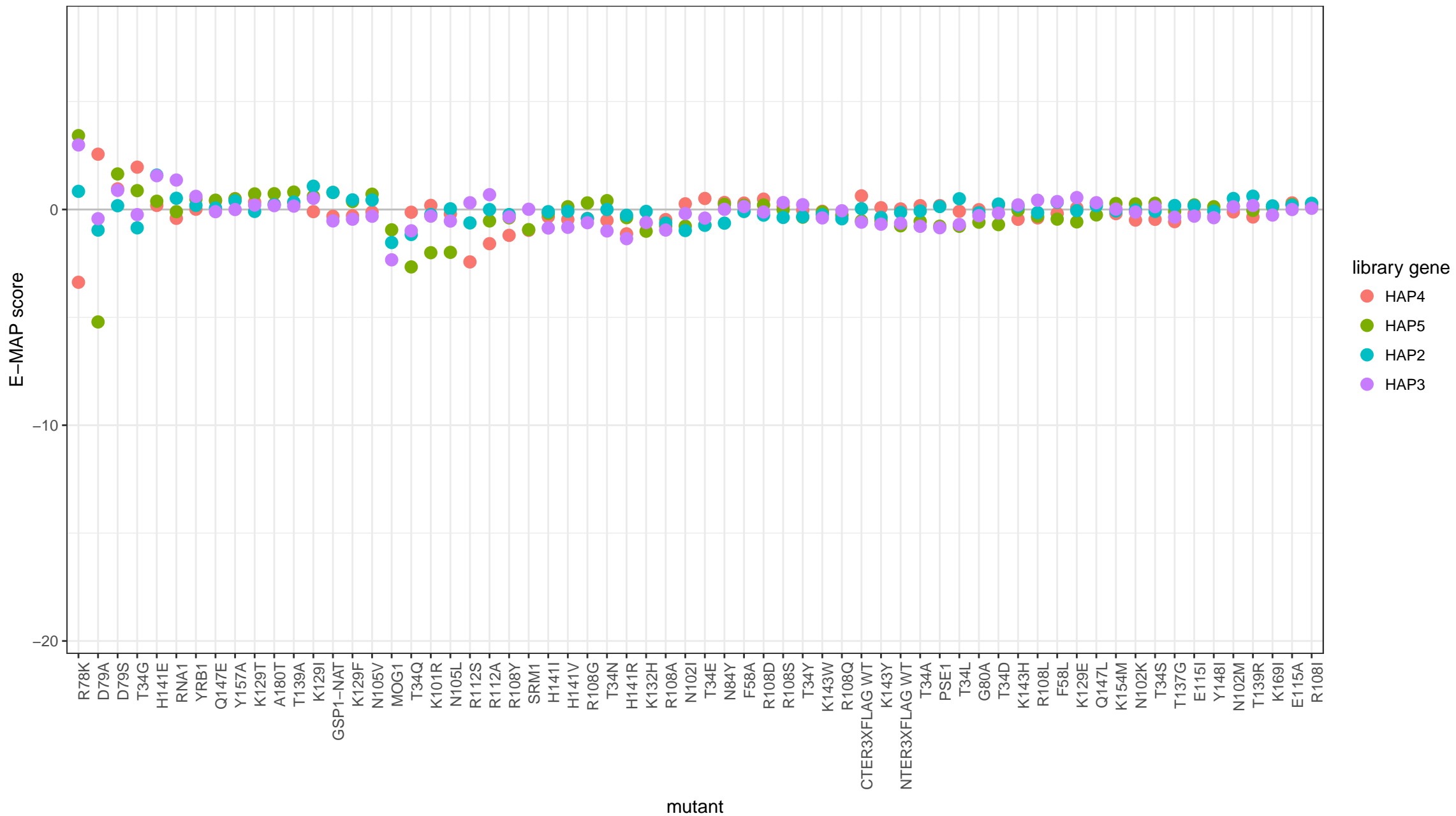
mutant

H141R
PSE1
N102K
T34Y
K129F
K132H
E115A
N102I
N105L
K143H
K143W
D79S
F58L
T34A
YRB1
K101R
R108I
Q147L
R112S
R78K
SRM1
NTER3XFLAG WT
RNA1
R108Q
T137G
T34E
K169I
T34Q
R108A
E115I
D79A
H141V
R108Y
A180T
Y157A
T139R
Q147E
Y148I
K129E
T139A
CTER3XFLAG WT
R112A
H141I
K154M
N102M
R108L
K129T
R108D
F58A
T34L
G80A
R108S
T34N
K143Y
T34G
K129I
T34S
GSP1-NAT
R108G
MOG1
N105V
N84Y
H141E
T34D

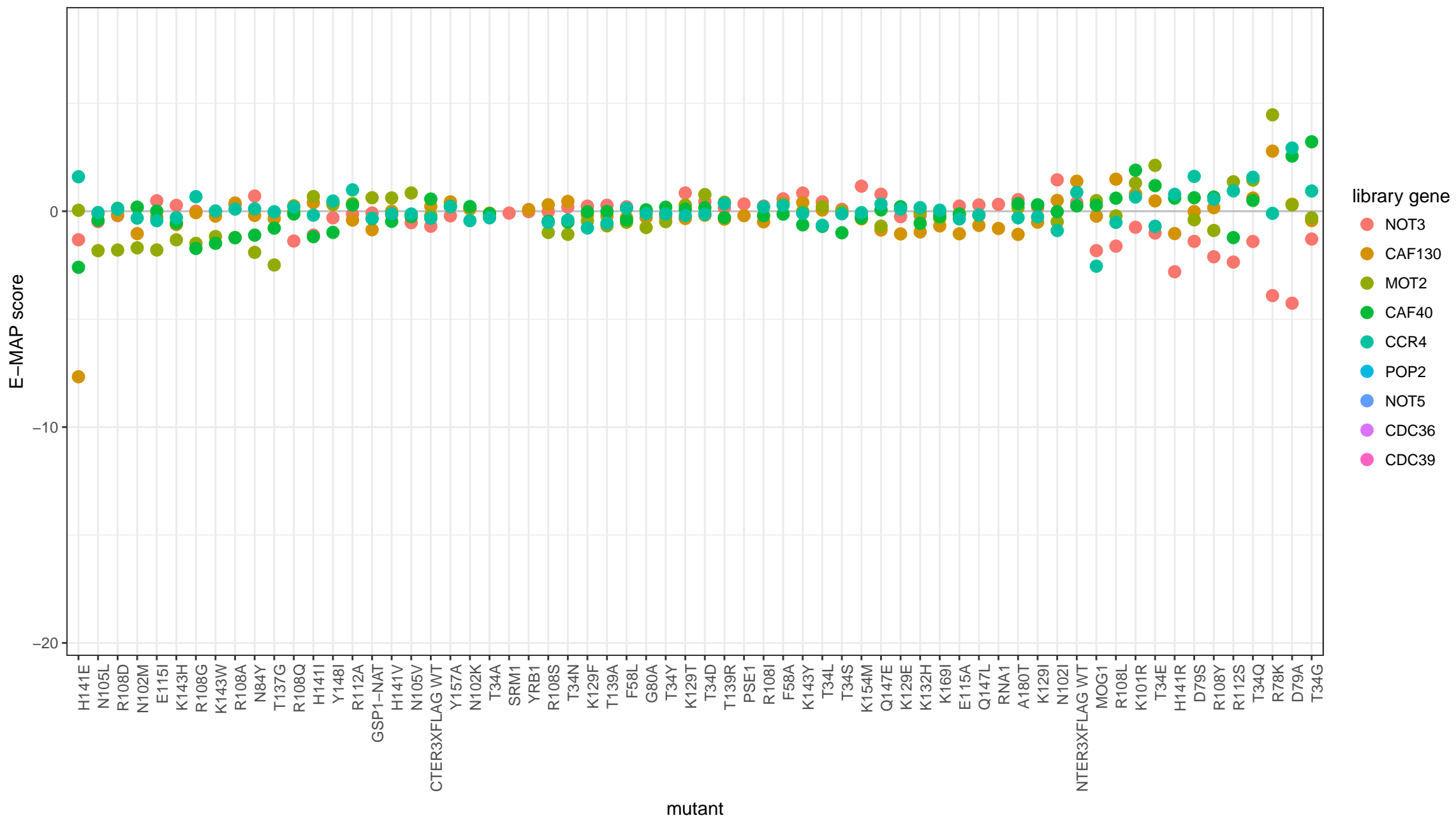
carboxy-terminal domain protein kinase complex



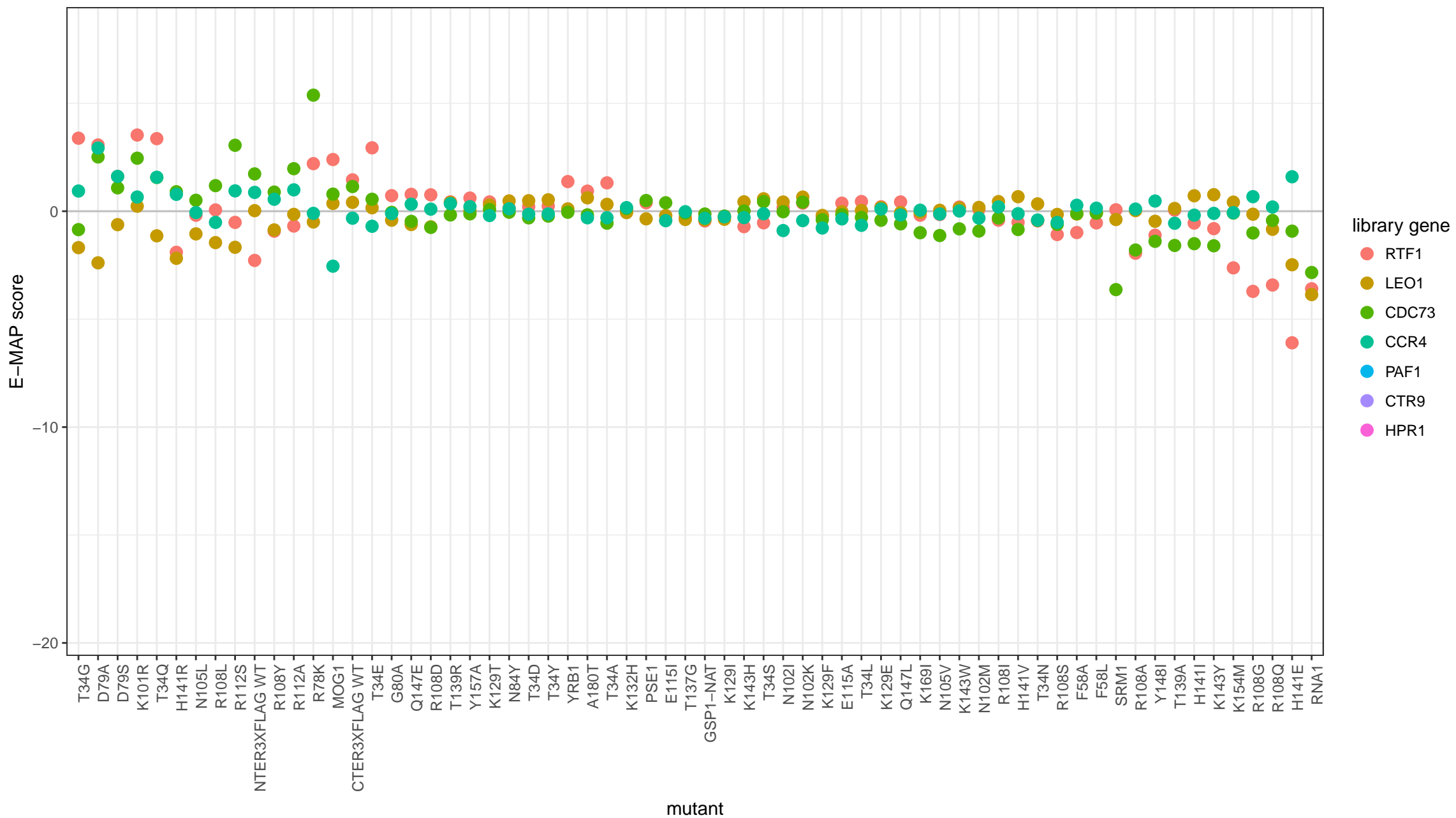
CCAAT-binding factor complex



CCR4–NOT core complex

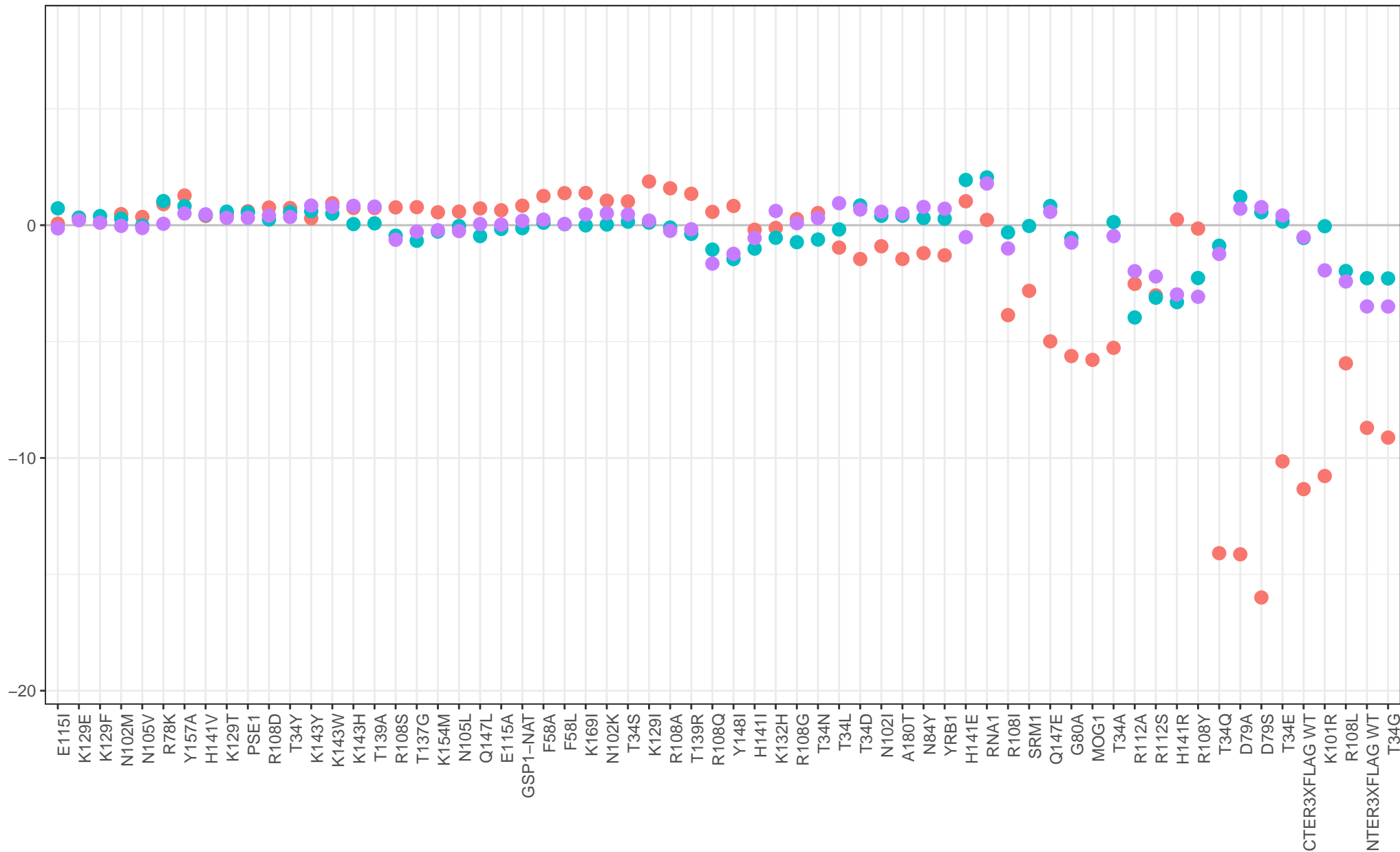


Cdc73p/Paf1p complex



chromatin accessibility complex

E-MAP score



chromatin assembly complex

E-MAP score

0

-10

-20

R112S
H141R
D79A
H141E
R78K
N105V
SRM1
K129F
Y157A
NTER3XFLAG WT
H141V
K143H
K132H
T34G
R112A
Y148I
H141I
R108L
R108I
R108A
R108G
N105L
CTER3XFLAG WT
R108Q
R108Y
PSE1
R108D
T139A
K143Y
T34N
K143W
K154M
MOG1
N102I
N102K
D79S
GSP1-NAT
G80A
N84Y
Q147E
RNA1
T34E
K169I
R108S
T34Q
K129E
E115A
T34Y
F58L
T137G
N102M
F58A
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K129T
T139R
A180T
E115I
K129I
T34A
T34S

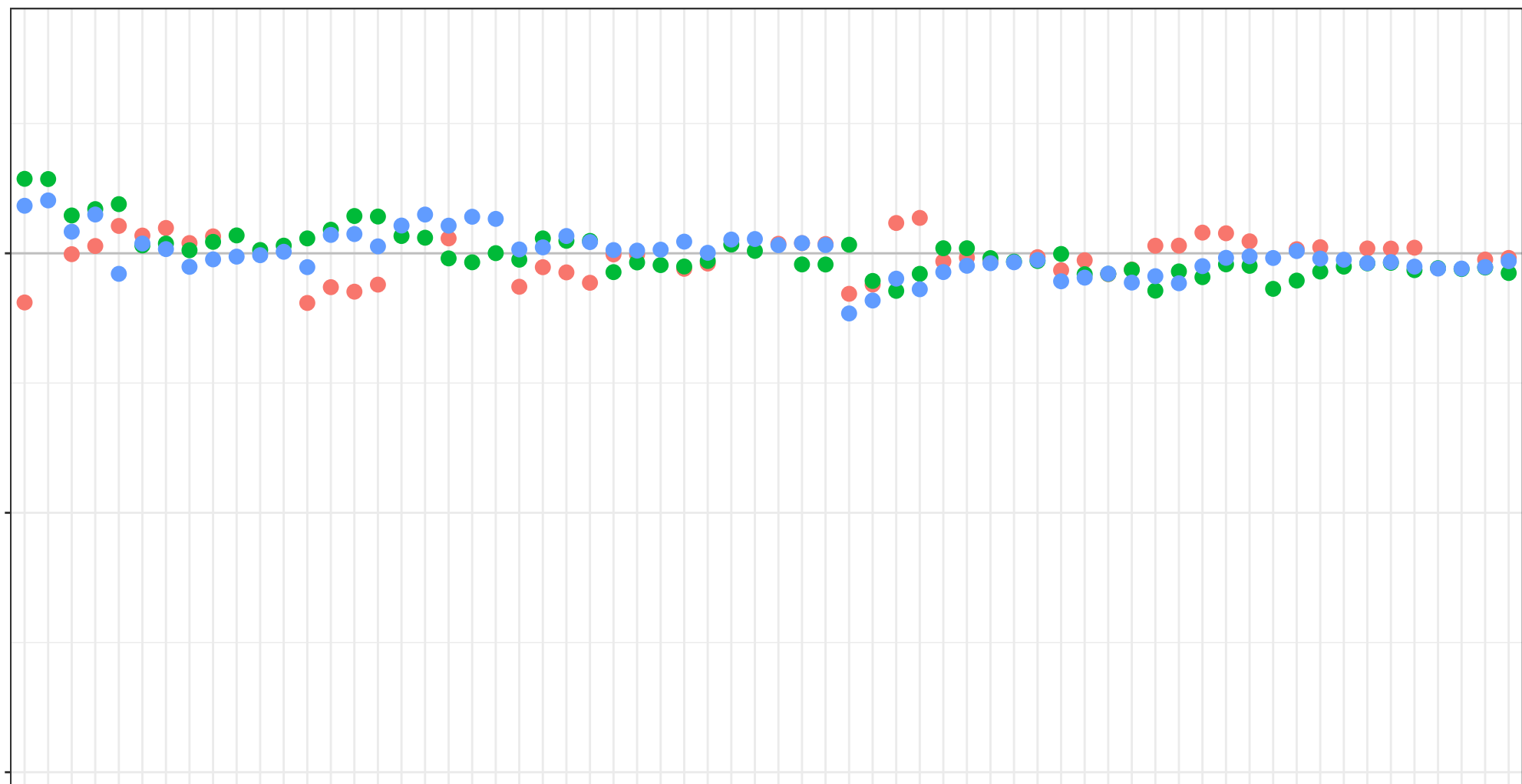
library gene

CAC2

MSI1

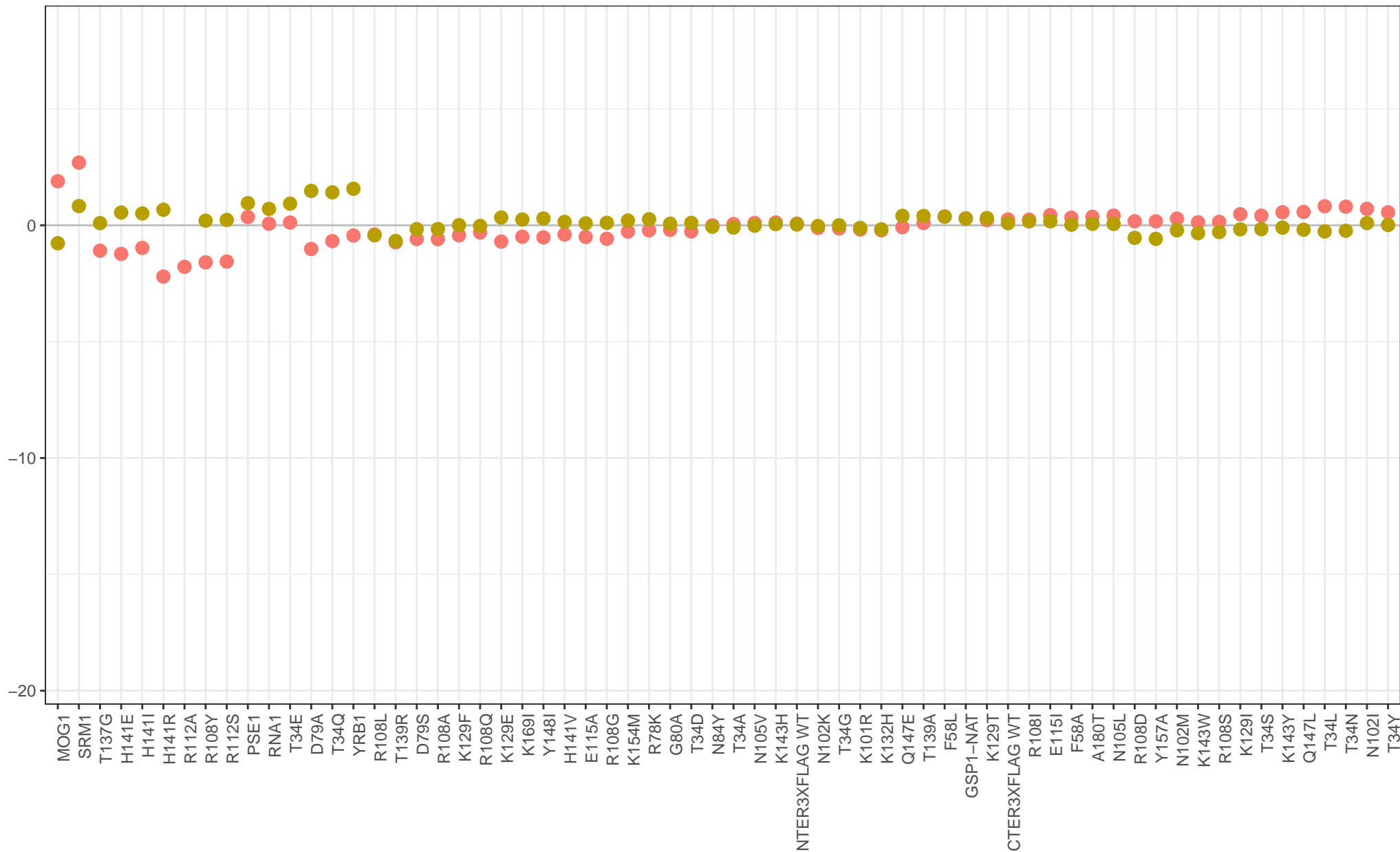
RLF2

mutant



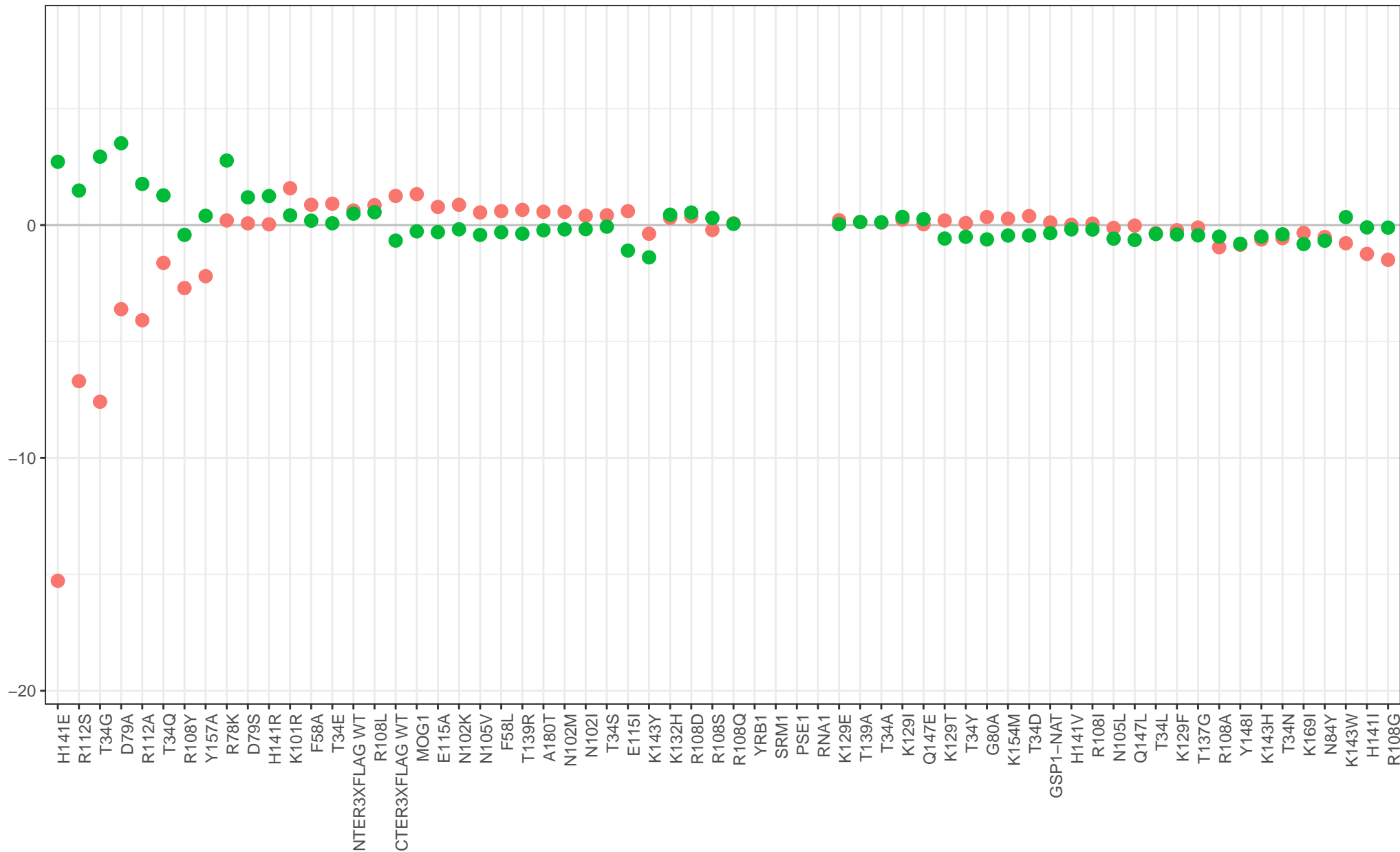
Chs5p/Arf-1binding proteins (ChAPs)

E-MAP score



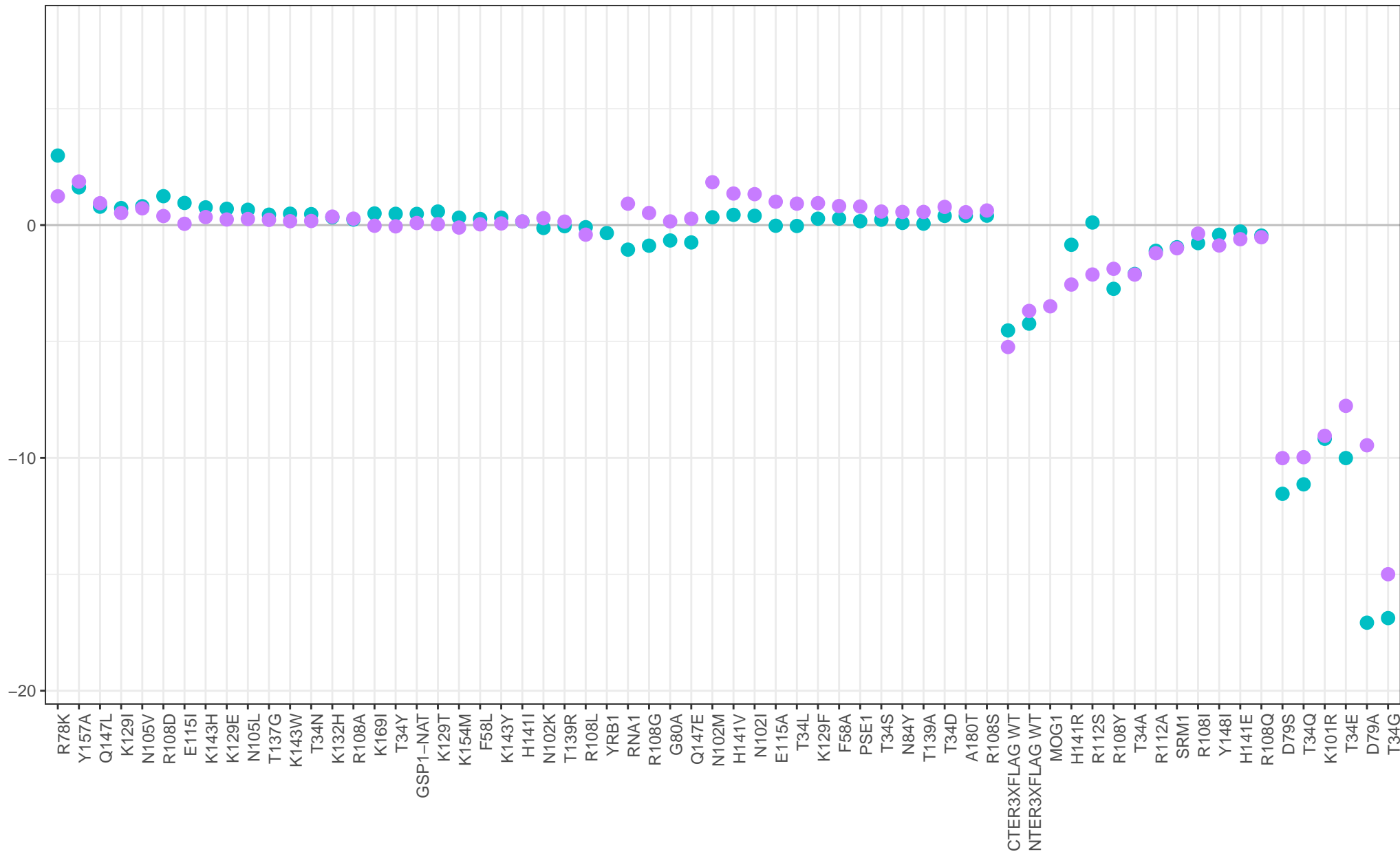
Chz1p/Htz1p/Htb1p complex

E-MAP score

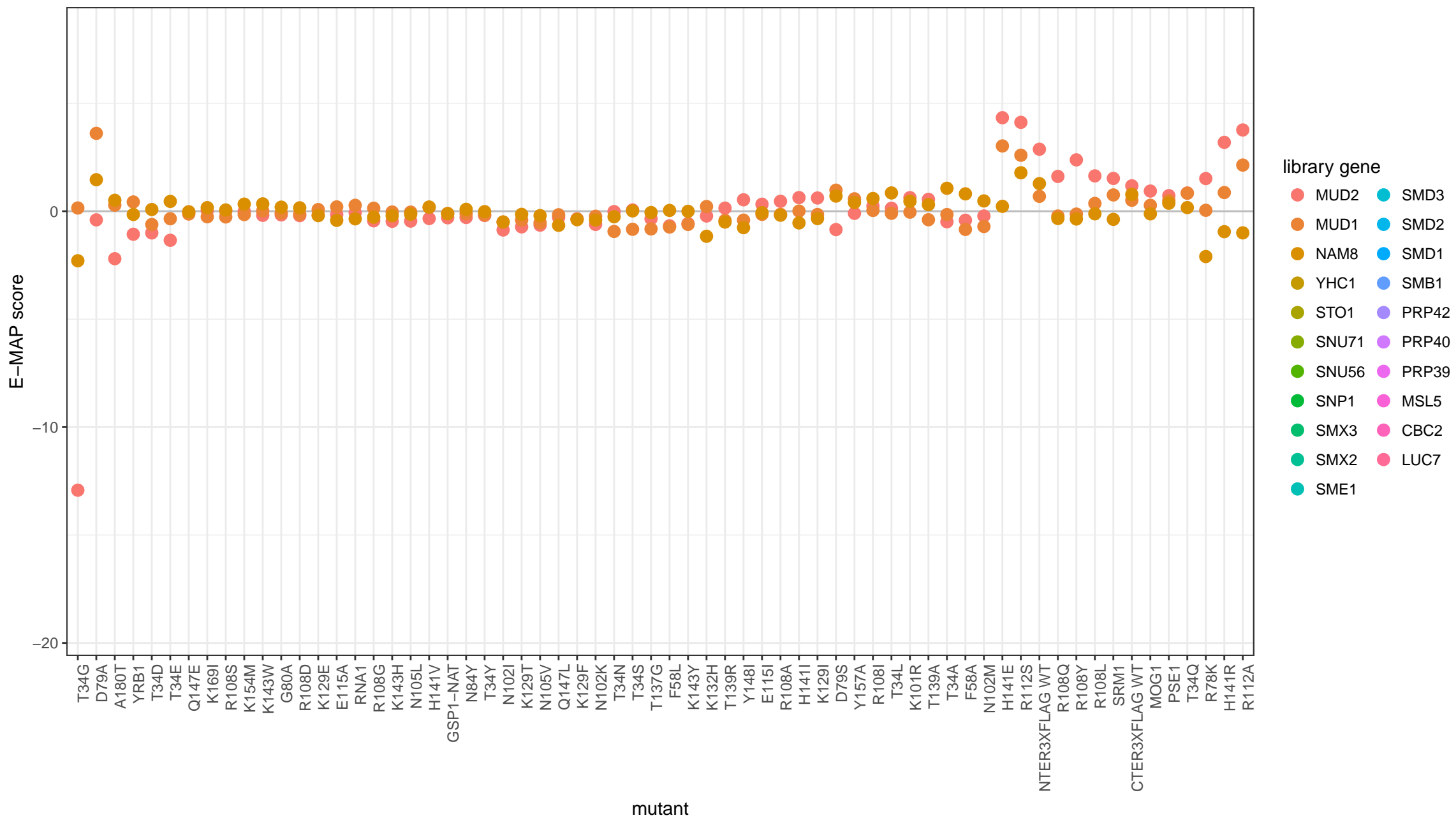


COMA complex

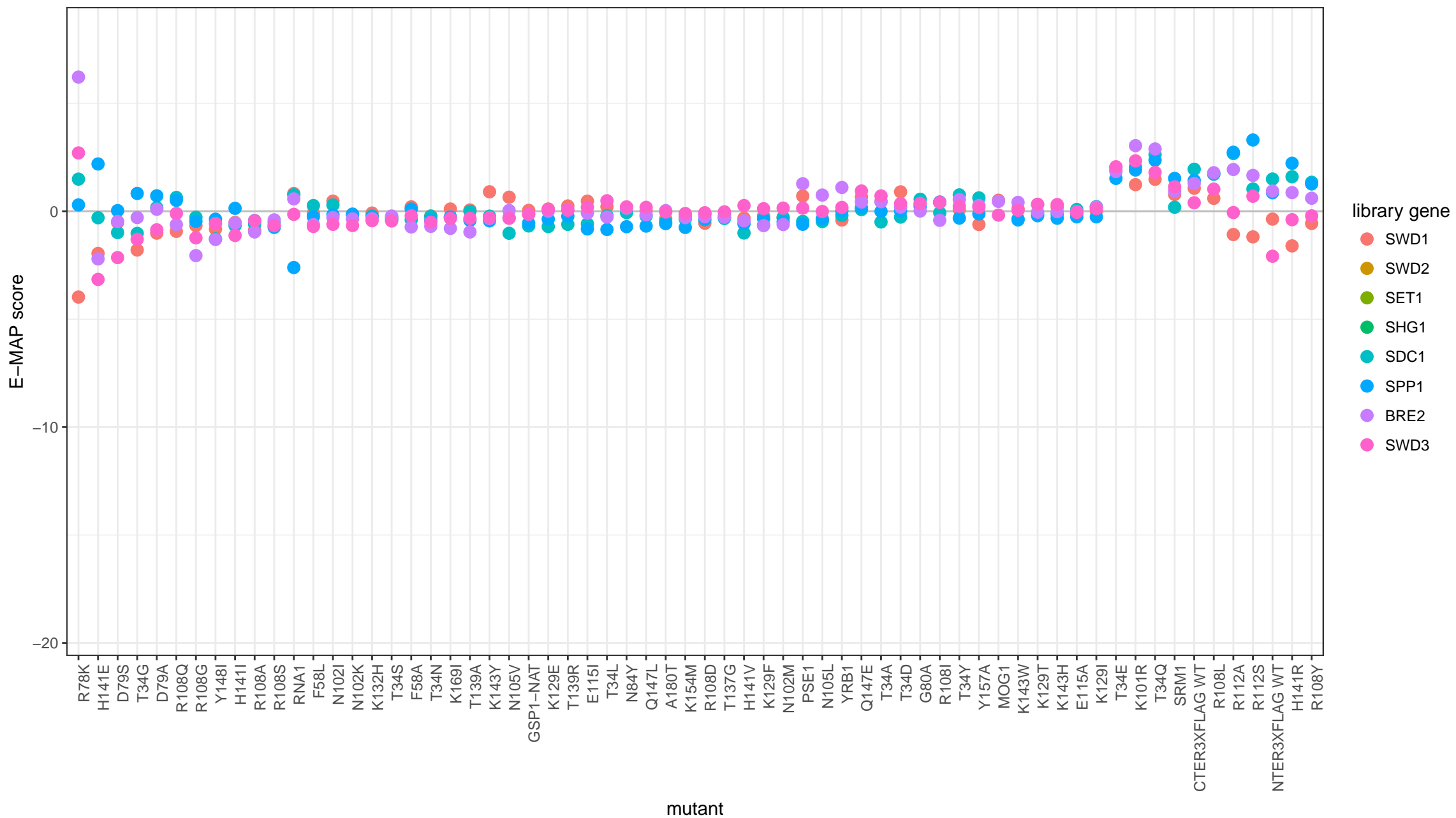
E-MAP score



commitment complex



COMPASS complex



COPII

E-MAP score

0

-10

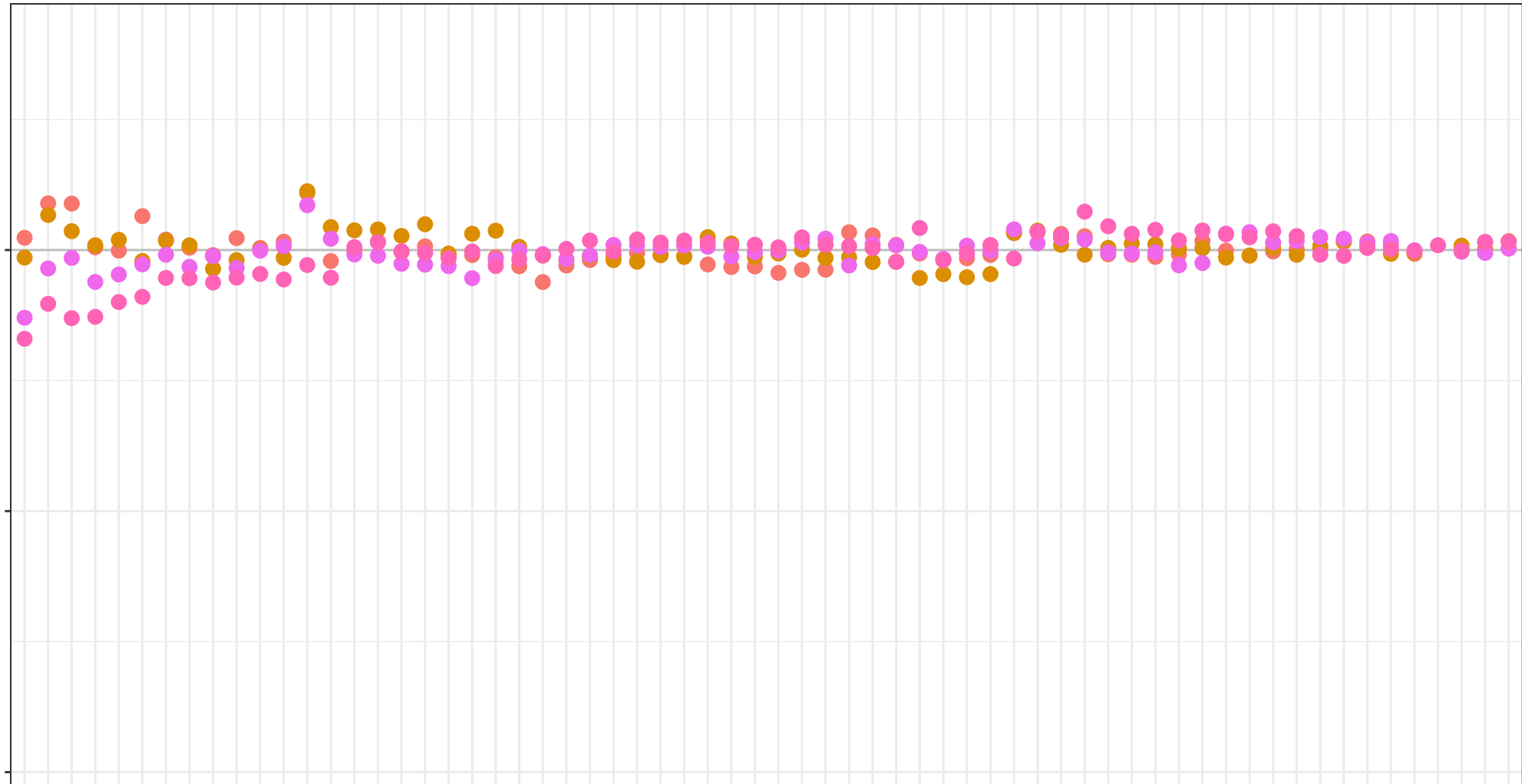
-20

R78K H141E T34Q H141R R108Y R112A K101R R108Q R108L R112S G80A Y148I D79A T34G PSE1 R108D K129I SRM1 H141I K129E N105L E115I R108I R108A T34A T34Y T34N K129T K143H K143Y T137G K143W T34S N102K N84Y K129F GSP1-NAT NTER3XFLAG WT RNA1 CTER3XFLAG WT E115A T139A D79S T34E T34L N102I K132H A180T Q147L H141V K154M Q147E T34D F58A F58L N105V R108G K169I YRB1 N102M MOG1 T139R R108S Y157A

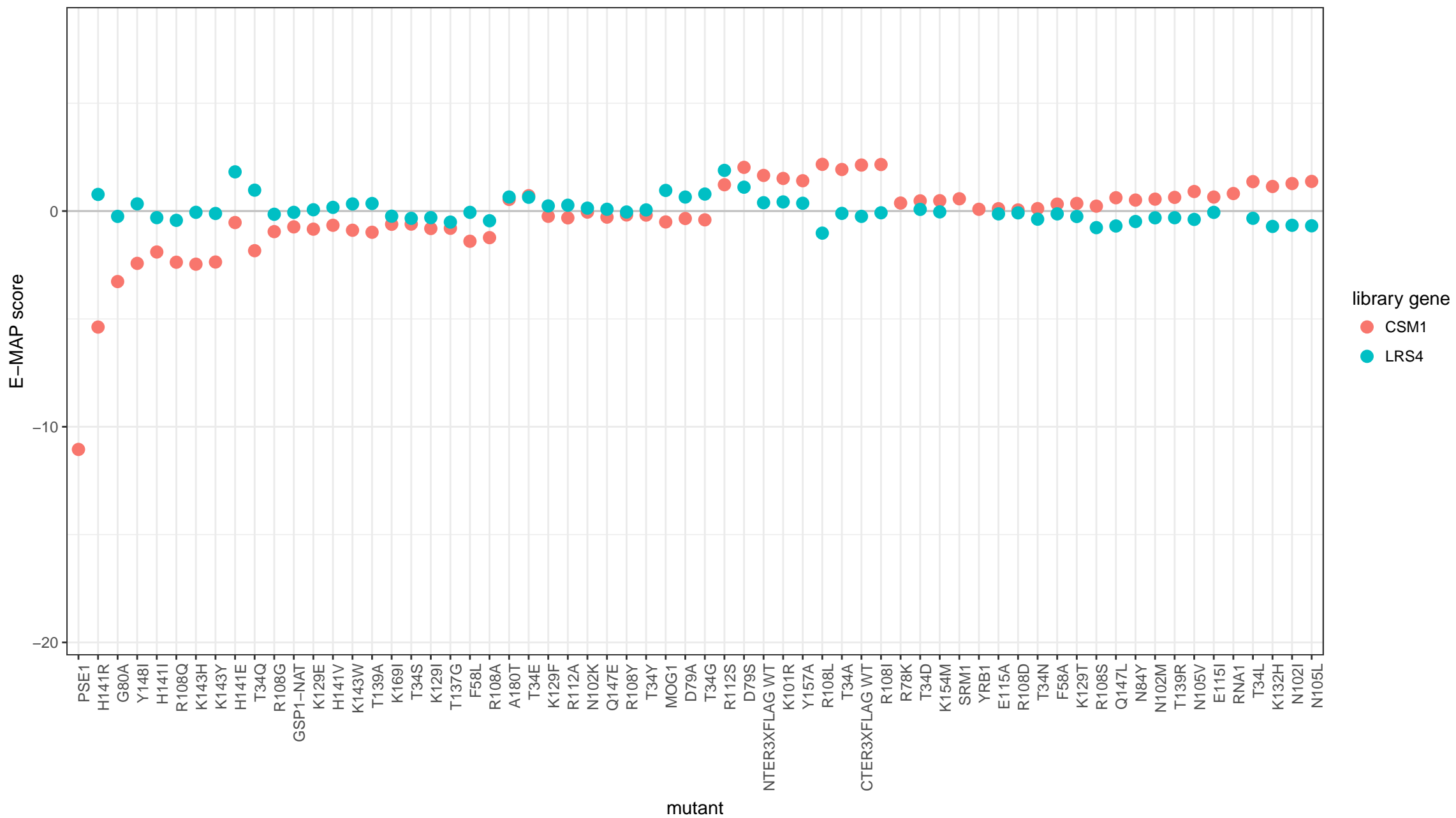
library gene

- ERV25
- ERP2
- SEC31
- SEC24
- SEC23
- SEC16
- SEC13
- EMP24
- SAR1
- ERP1
- ERV46

mutant



Csm1p/Lrs4p complex



Ctf3p protein complex

E-MAP score

0

-10

-20

D79A
T34G
N84Y
N102K
T34D
R108I
T34A
R108D
K143W
H141V
T139A
A180T
R112S
T137G
H141I
K129I
Y157A
K154M
N102M
T34Y
K129E
K143H
R108S
T34N
Y148I
R108A
R108G
K129T
T139R
R108L
K132H
Q147L
T34L
MOG1
K129F
K169I
T34S
F58L
G80A
K143Y
E115A
N102I
E115I
Q147E
F58A
N105V
GSP1-NAT
N105L
R108Y
R78K
RNA1
H141E
R112A
H141R
YRB1
PSE1
R108Q
T34Q
D79S
K101R
CTER3XFLAG WT
NTER3XFLAG WT
SRM1
T34E

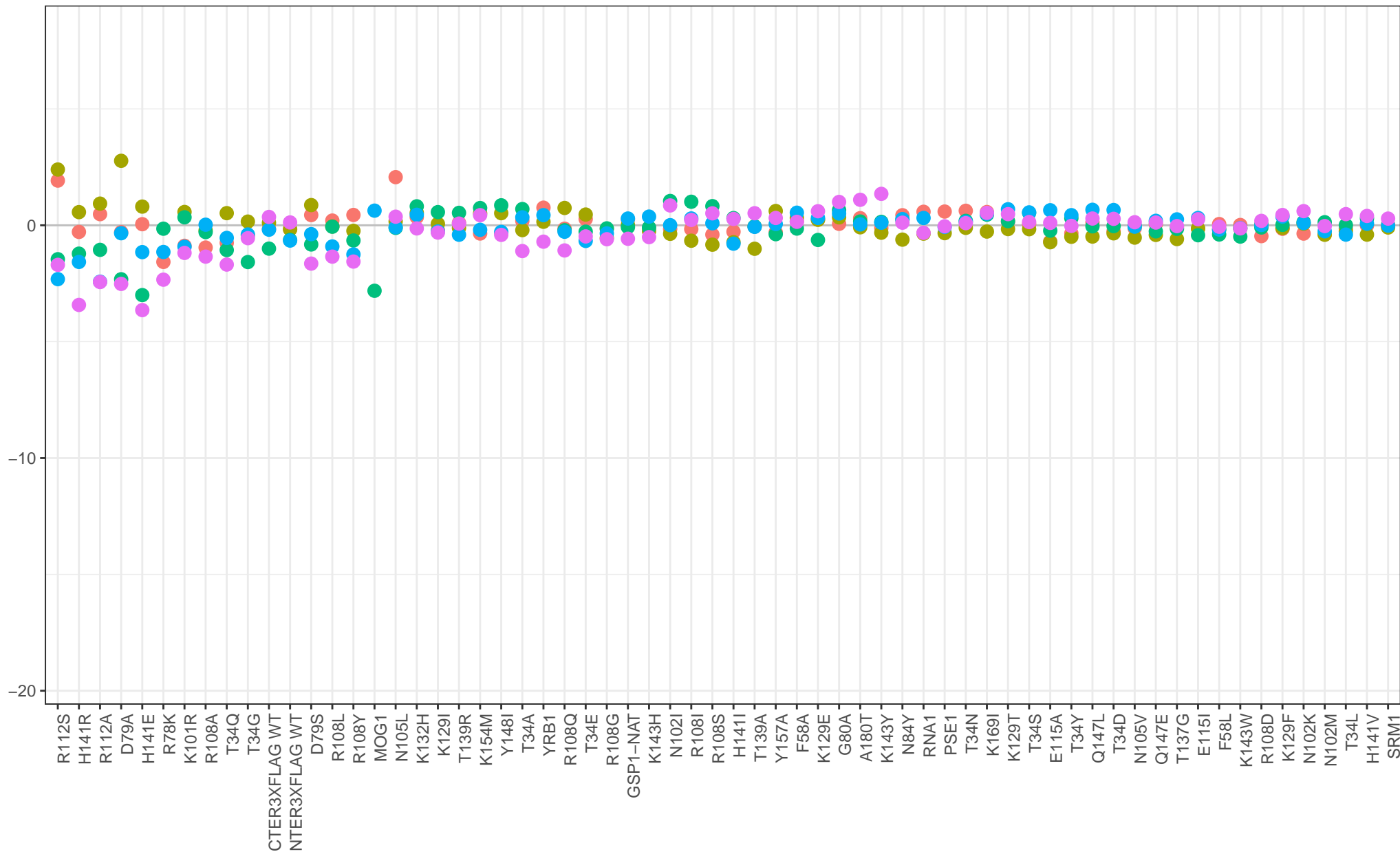
mutant

library gene

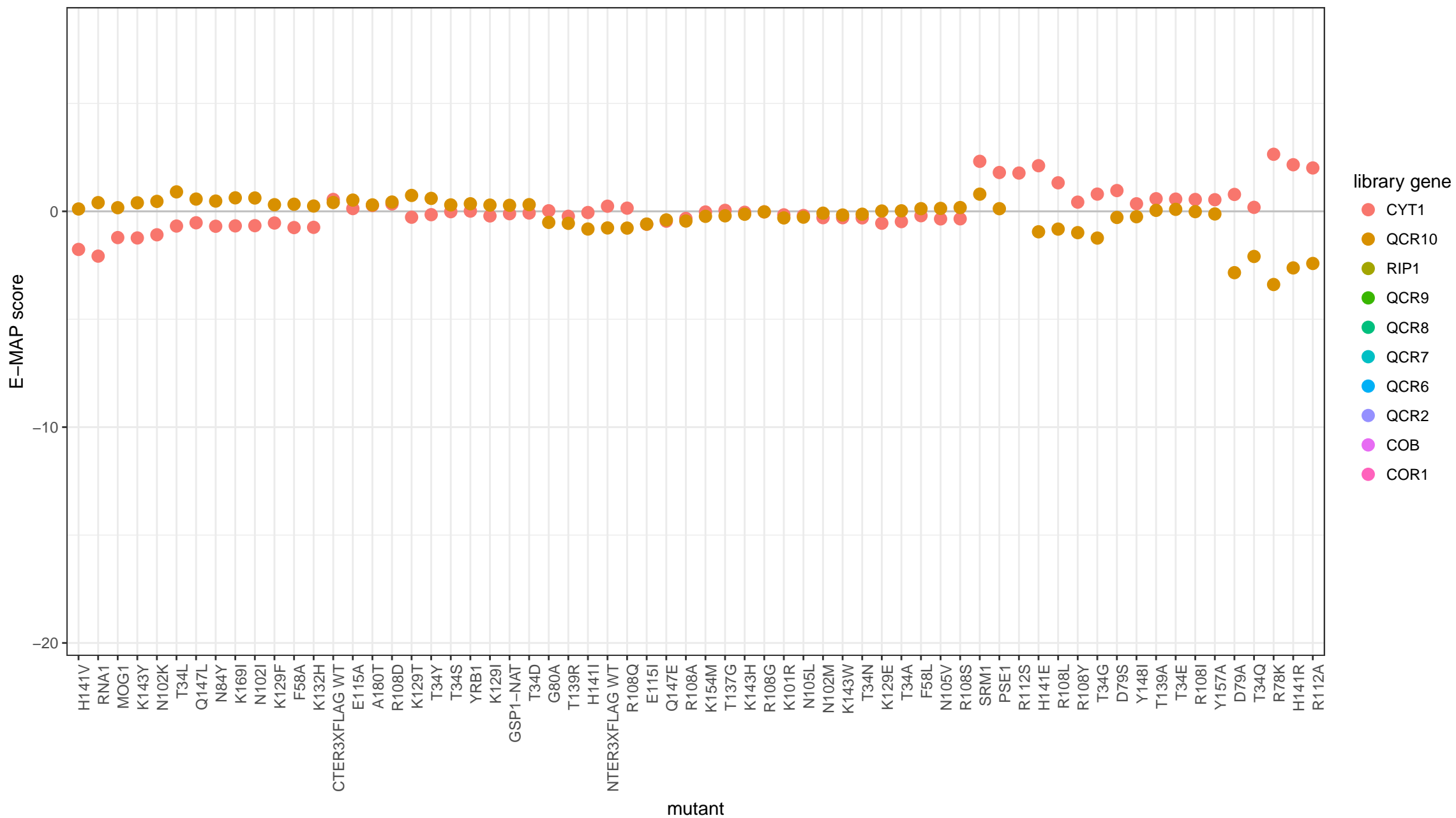
- CTF3
- MCM16
- MCM22

Cul3p-RING ubiquitin ligase complex

E-MAP score

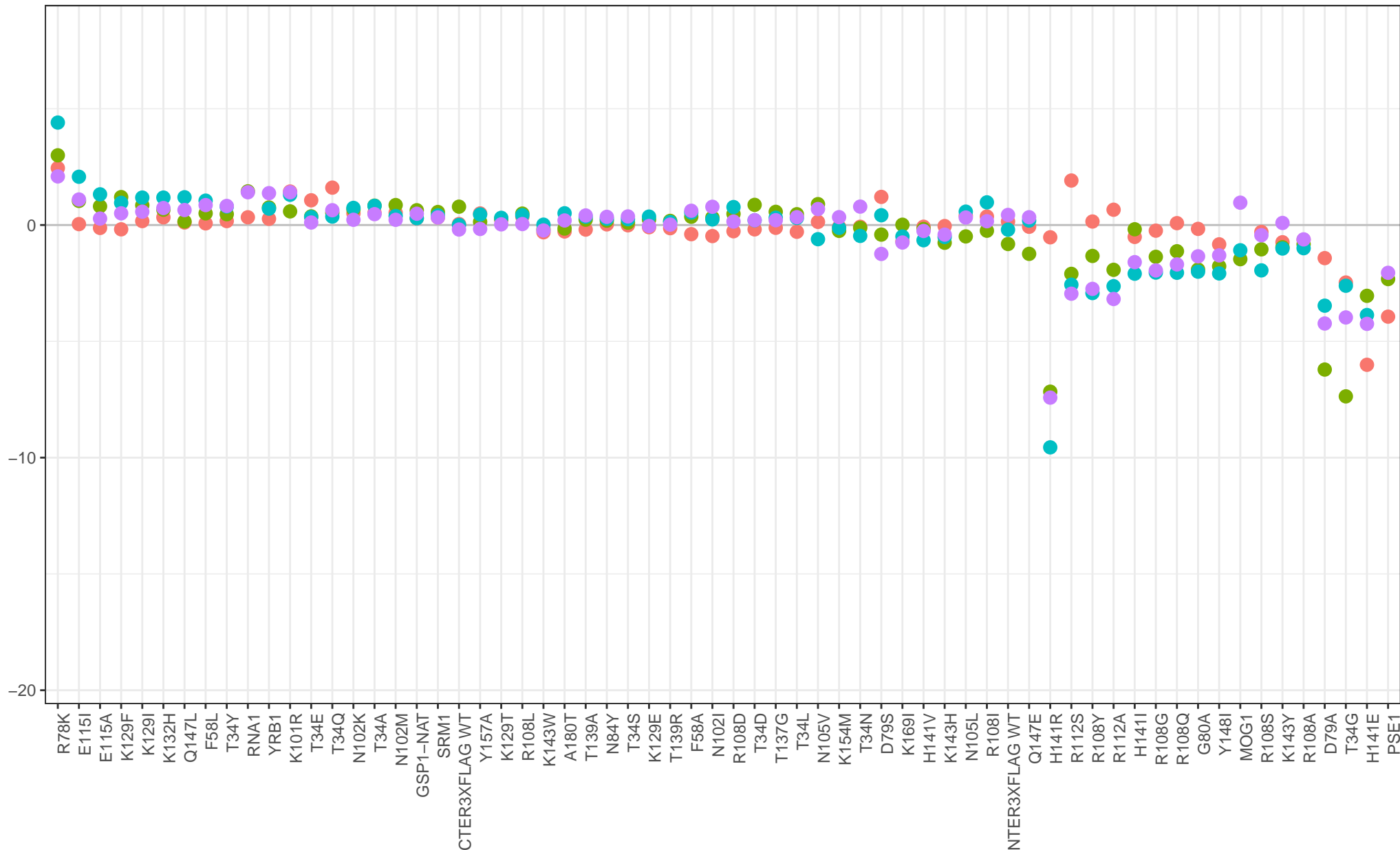


Cytochrome bc1 complex (Ubiquinol–cytochrome c reductase complex, complex III)



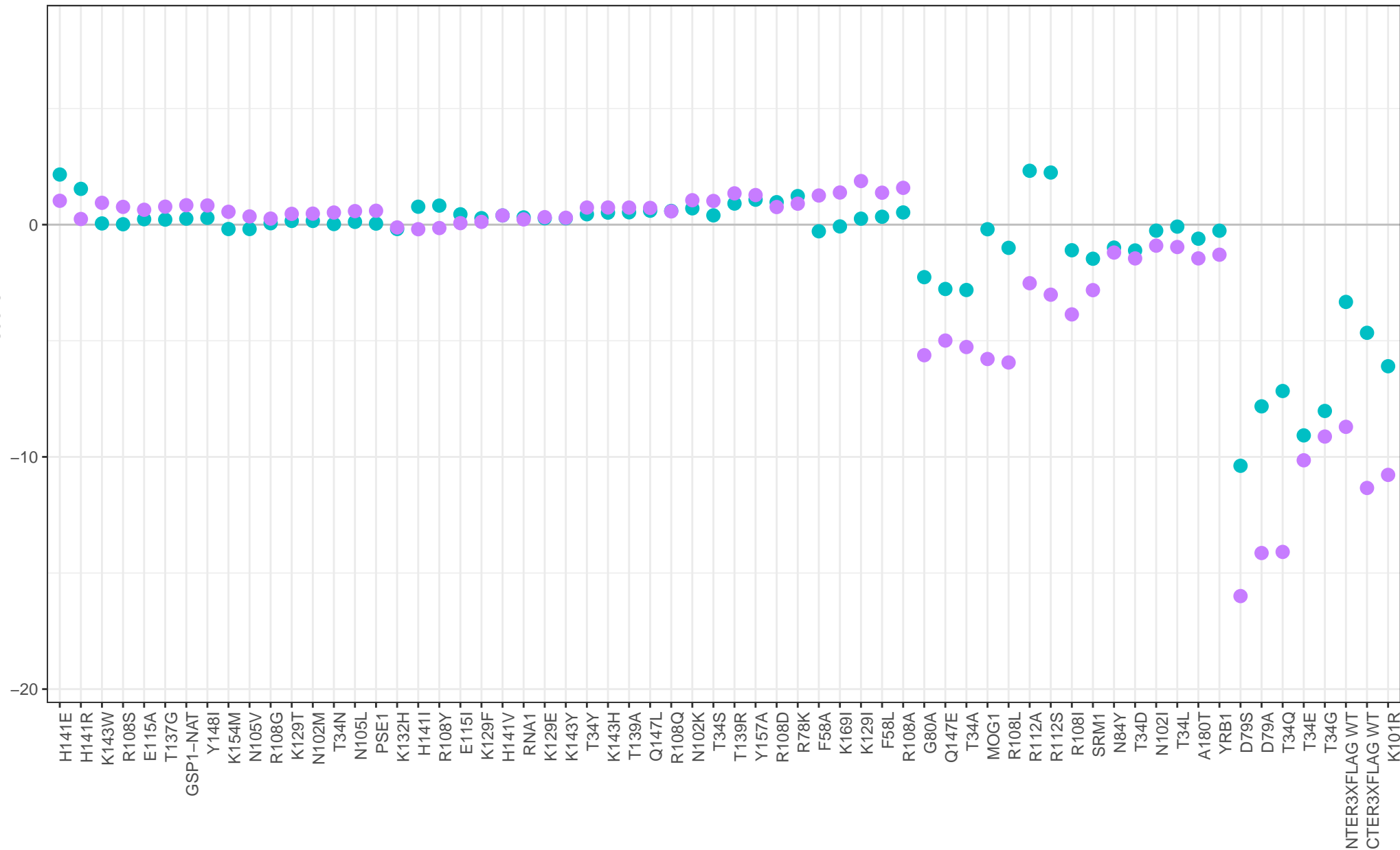
cytoplasmic dynein complex

E-MAP score



DNA polymerase epsilon complex

E-MAP score

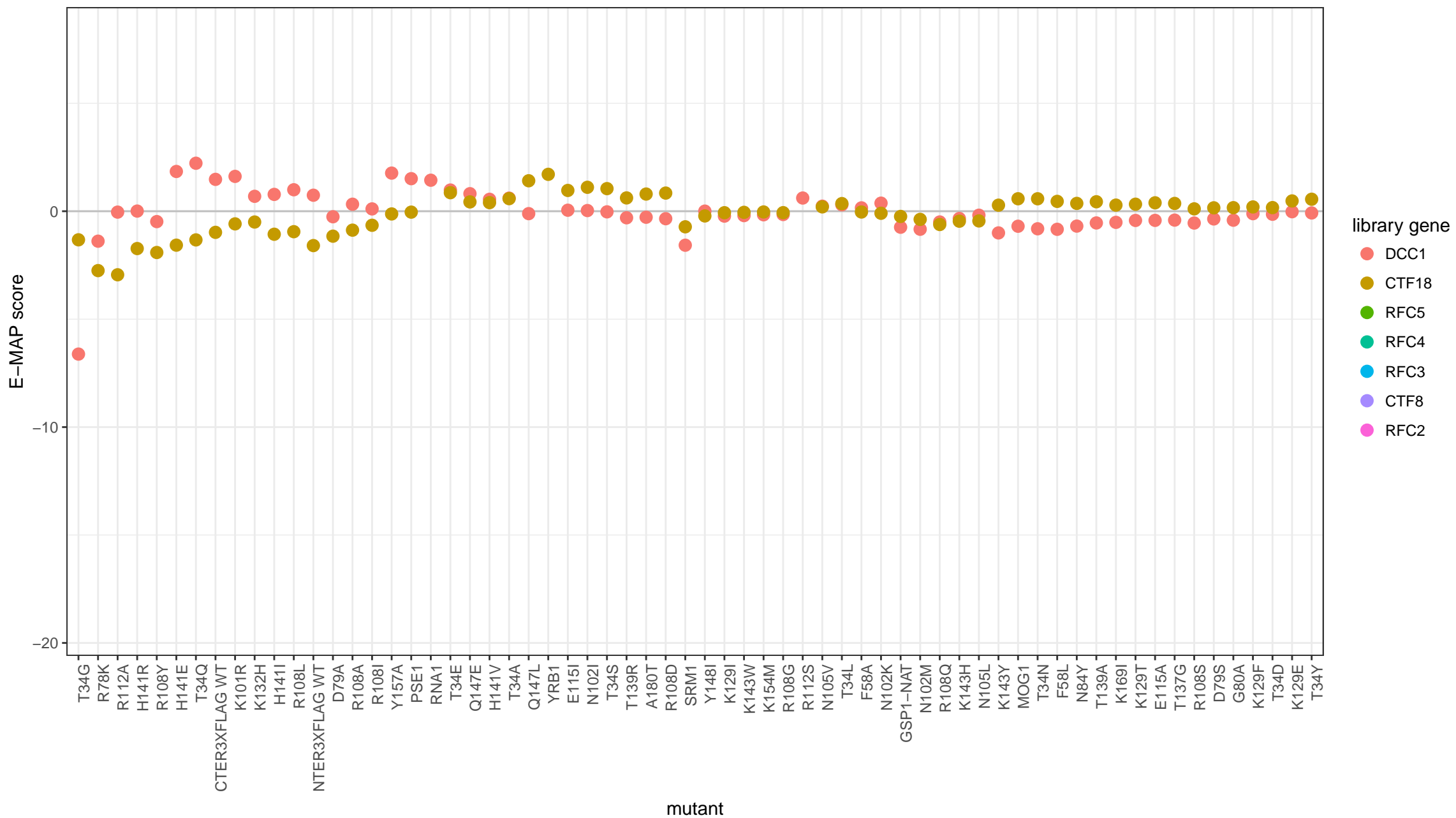


library gene

- DPB2
- POL2
- DPB3
- DPB4

mutant

DNA replication factor C complex (Ctf18p/Ctf8p/dcc1p)



DNA-directed RNA polymerase I complex

E-MAP score

-20

-10

0

D79A
R108Q
K101R
R108G
D79S
H141R
R108Y
T34Q
K129E
T34N
R108D
T139R
K129I
N84Y
T34S
F58L
T34D
GSP1-NAT
N102I
T137G
T139A
SRM1
K143H
CTER3XFLAG WT
H141V
T34L
K129F
N102M
K143W
E115I
K143Y
K129T
Q147L
K169I
E115A
G80A
PSE1
T34G
A180T
N105V
F58A
K154M
N105L
K132H
N102K
R108A
Y157A
T34A
Y148I
R108I
YRB1
T34Y
H141I
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R78K
MOG1
RNA1
T34E
Q147E
R108L

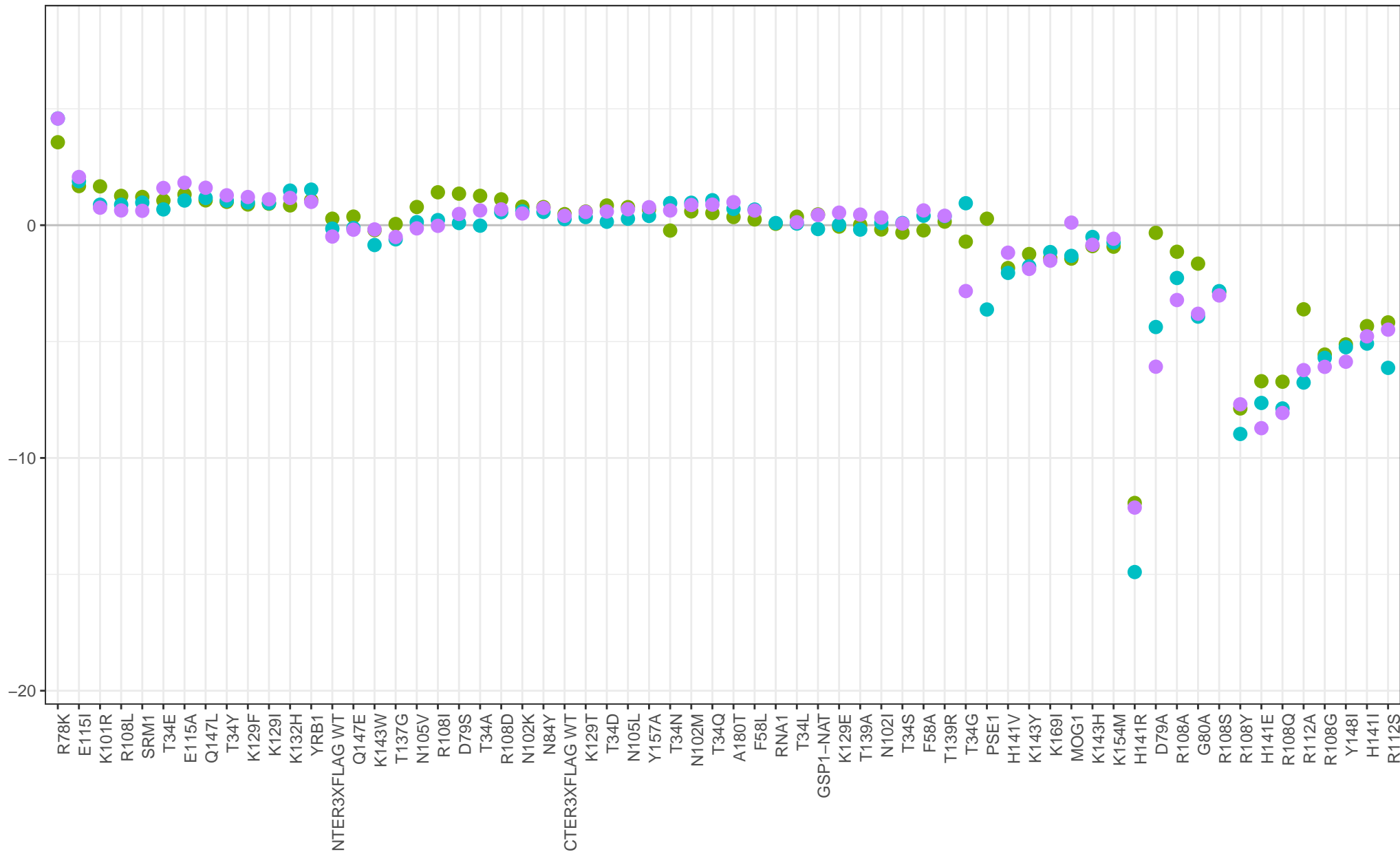
mutant

library gene

RPA34
RPA14
RPO26
RPC40
RPC19
RPC10
RPB8
RPB5
RPB10
RPA49
RPA43
RPA190
RPA12
RPA135

dynactin complex

E-MAP score



library gene

- ARP10
- NIP100
- ARP1
- JNM1

Ela1p/Elc1p complex

E-MAP score

-20

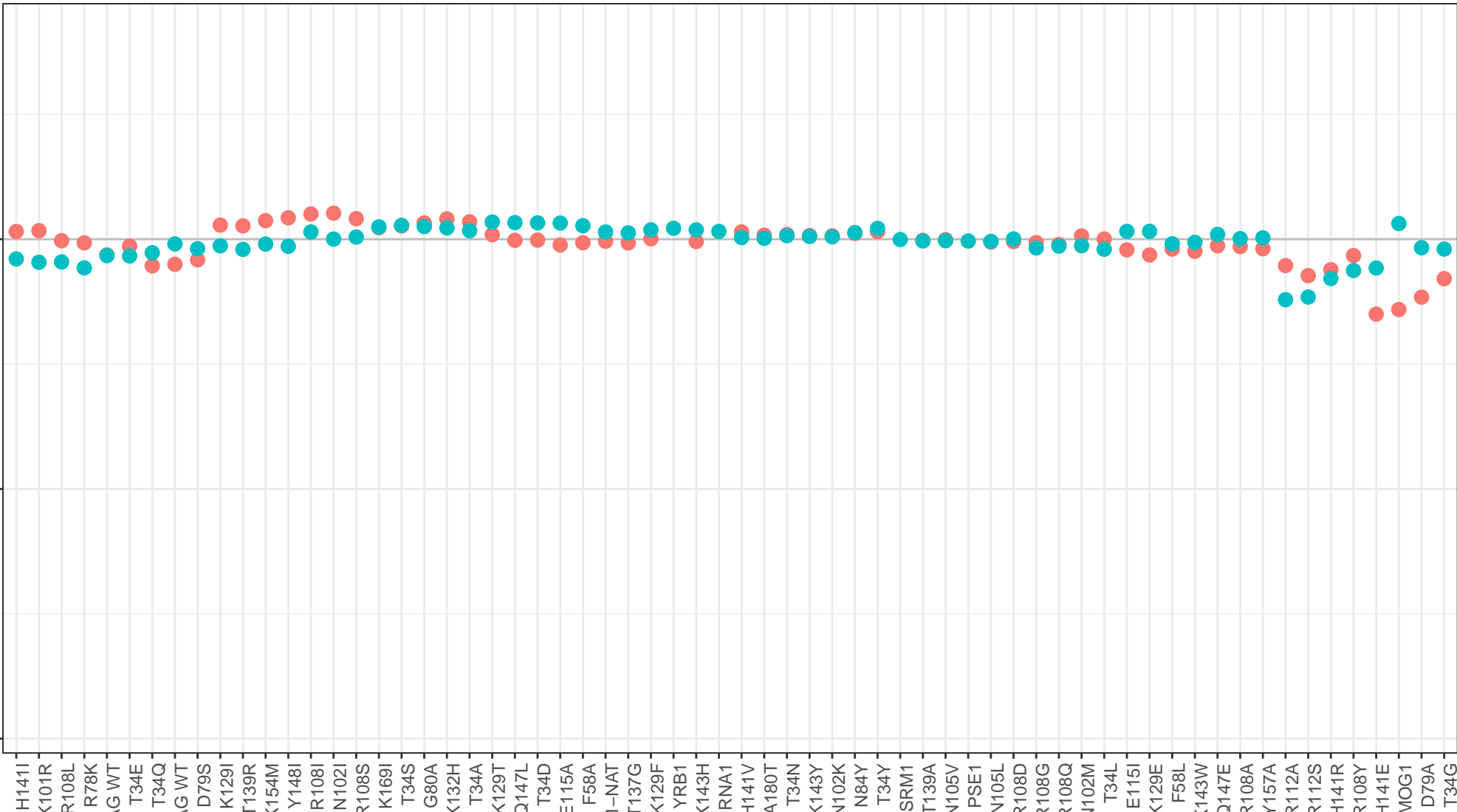
-10

0

mutant

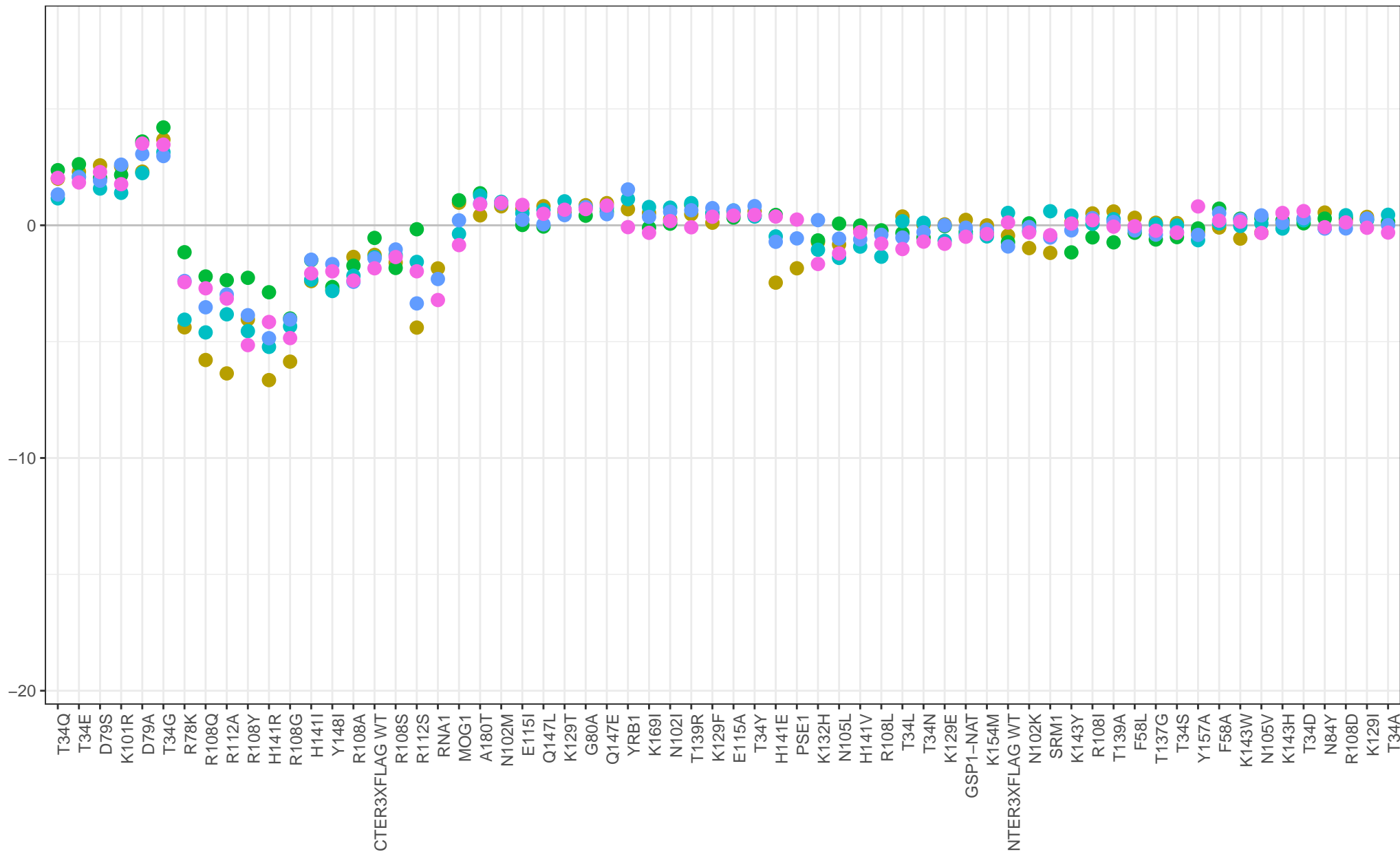
library gene

ELA1
ELC1



Elongator complex

E-MAP score



Erv41p/Erv46p complex

E-MAP score

-20

-10

0

mutant

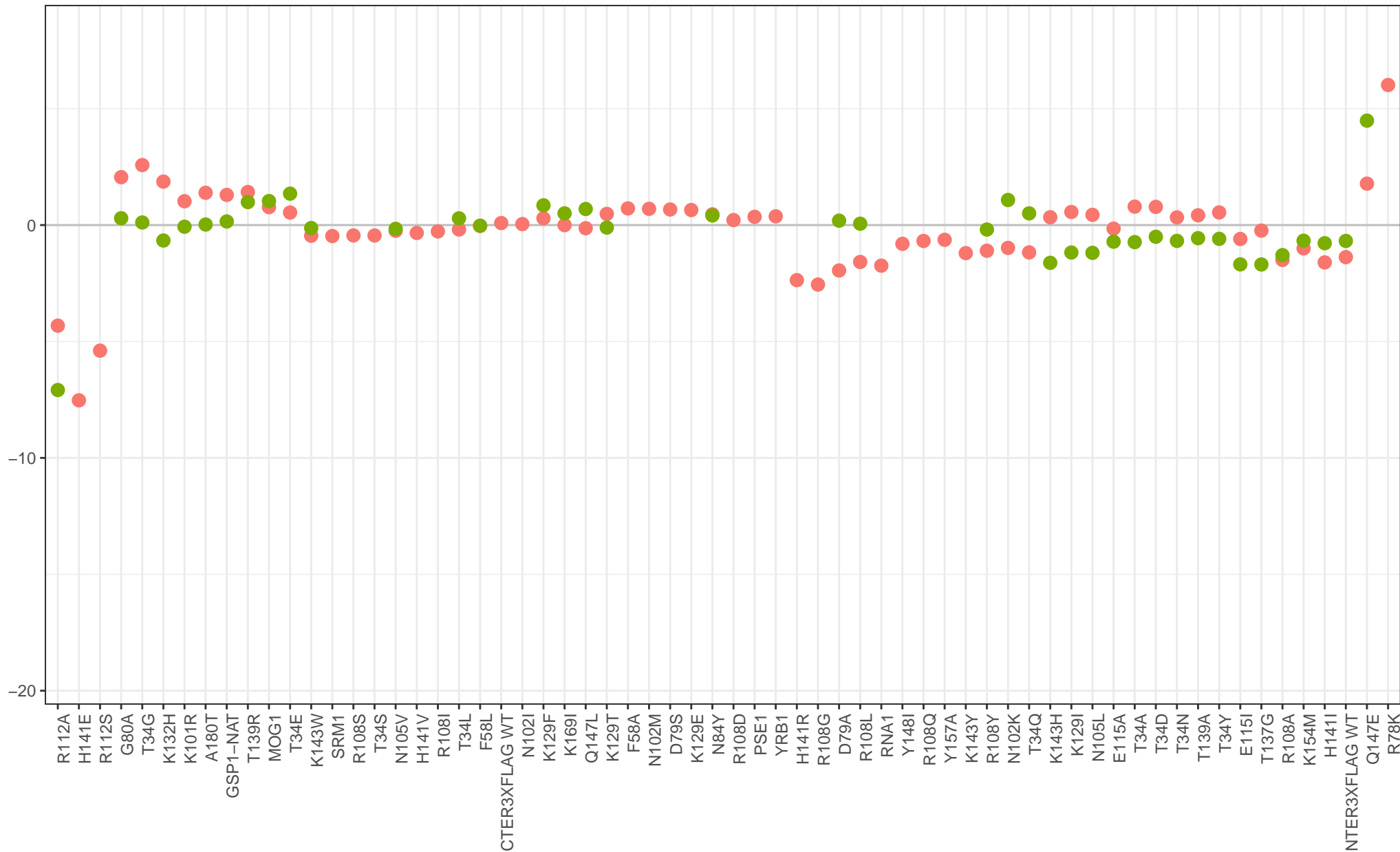
library gene

● ERV41
● ERV46

D79A
T34G
H141R
T34Q
H141E
R78K
N102I
K132H
N102K
Q147L
T34E
D79S
R108D
Y157A
K129I
T34Y
YRB1
E115I
R108I
R108G
E115A
SRM1
N102M
N105V
K129E
T139R
T34N
H141V
K143H
K143Y
R108S
MOG1
T139A
K129F
K169I
K154M
RNA1
A180T
F58A
T34D
Q147E
F58L
T34L
K129T
T34A
GSP1-NAT
PSE1
K143W
T137G
R108A
N84Y
T34S
N105L
H141I
CTER3XFLAG WT
NTER3XFLAG WT
R108Y
R112A
R108Q
R108L
Y148I
R112S
G80A
K101R

ESCRT I complex

E-MAP score



library gene

SRN2

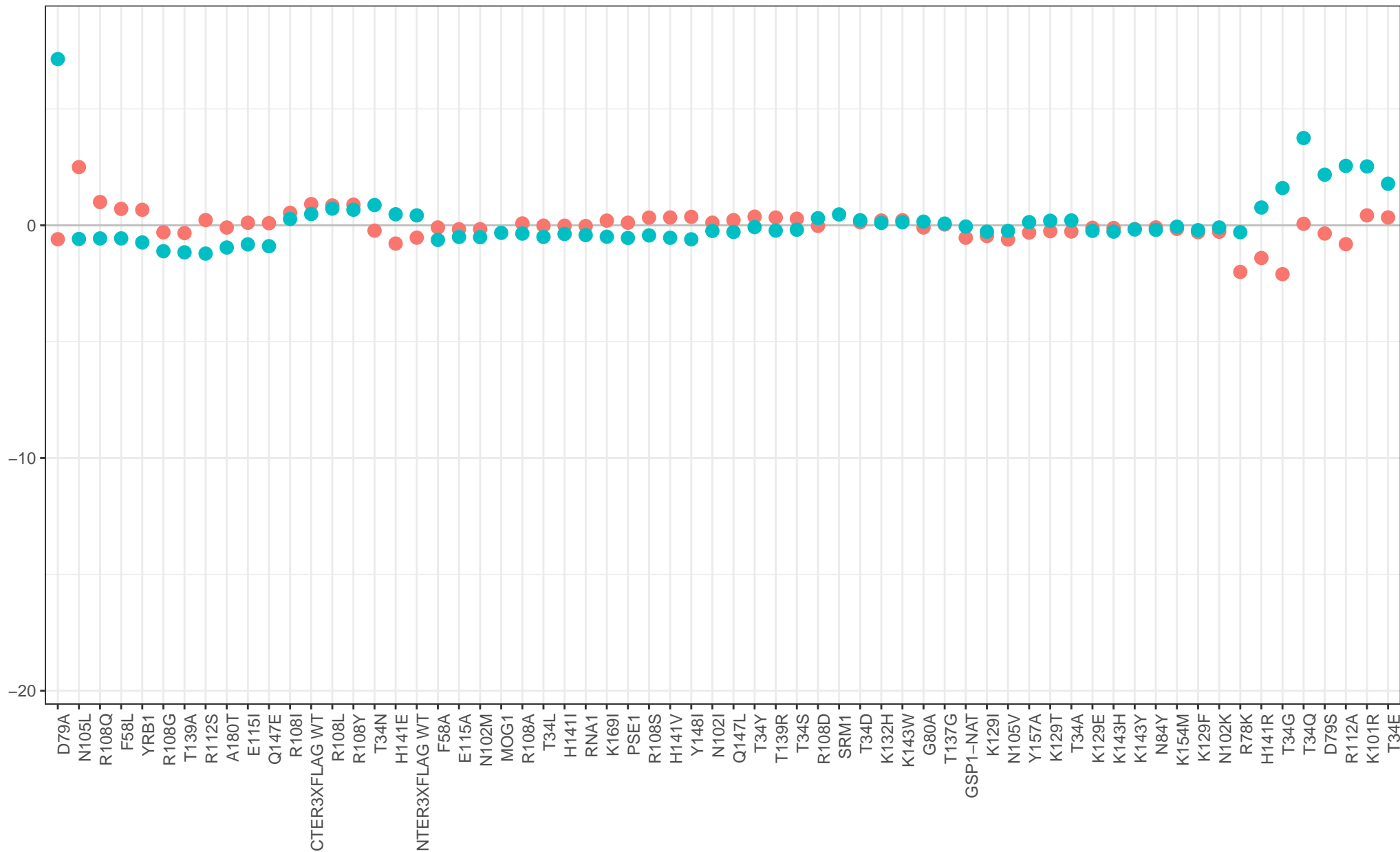
STP22

MVB12

VPS28

extracellular region

E-MAP score



library gene

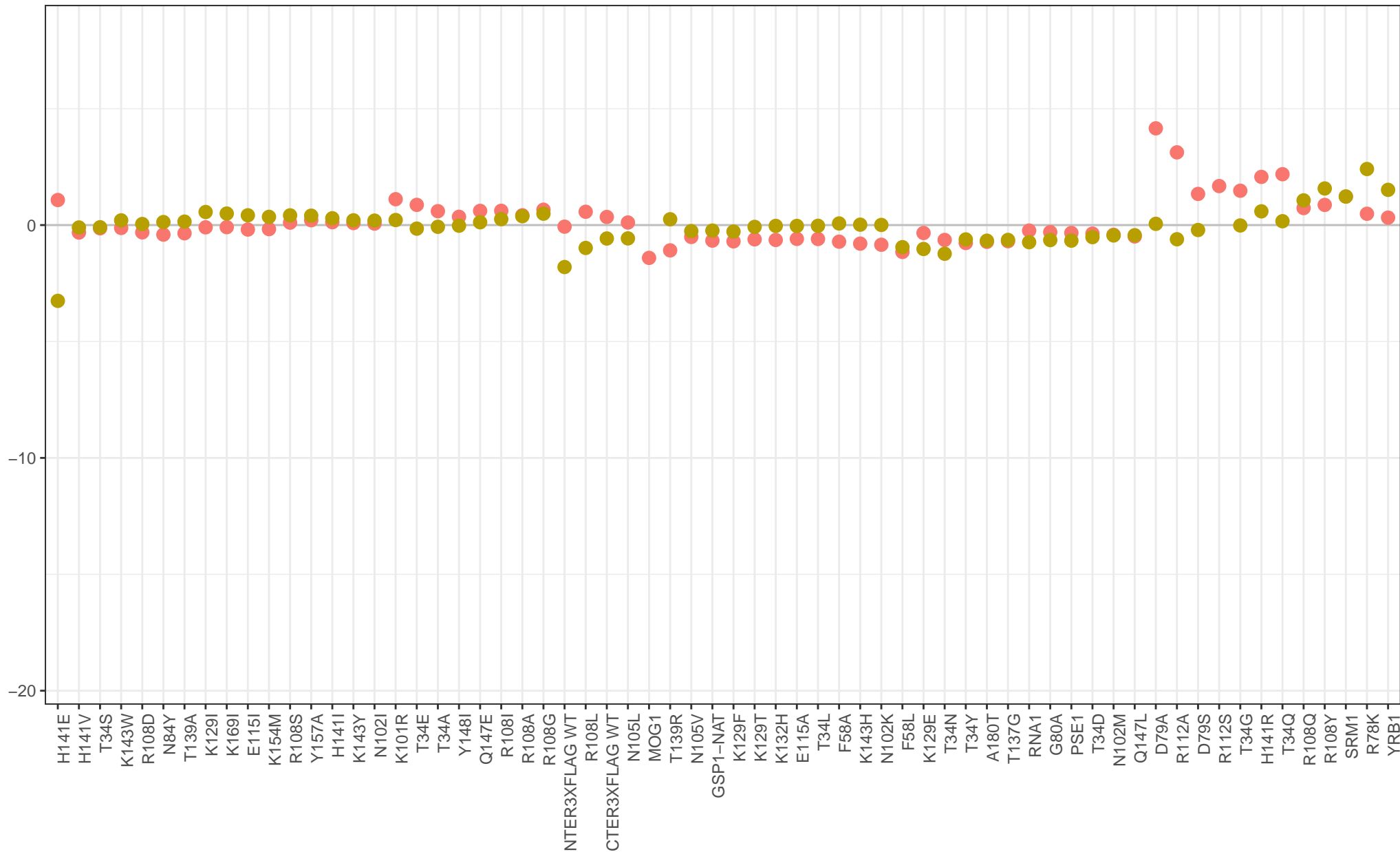
ACB1

PLB3

mutant

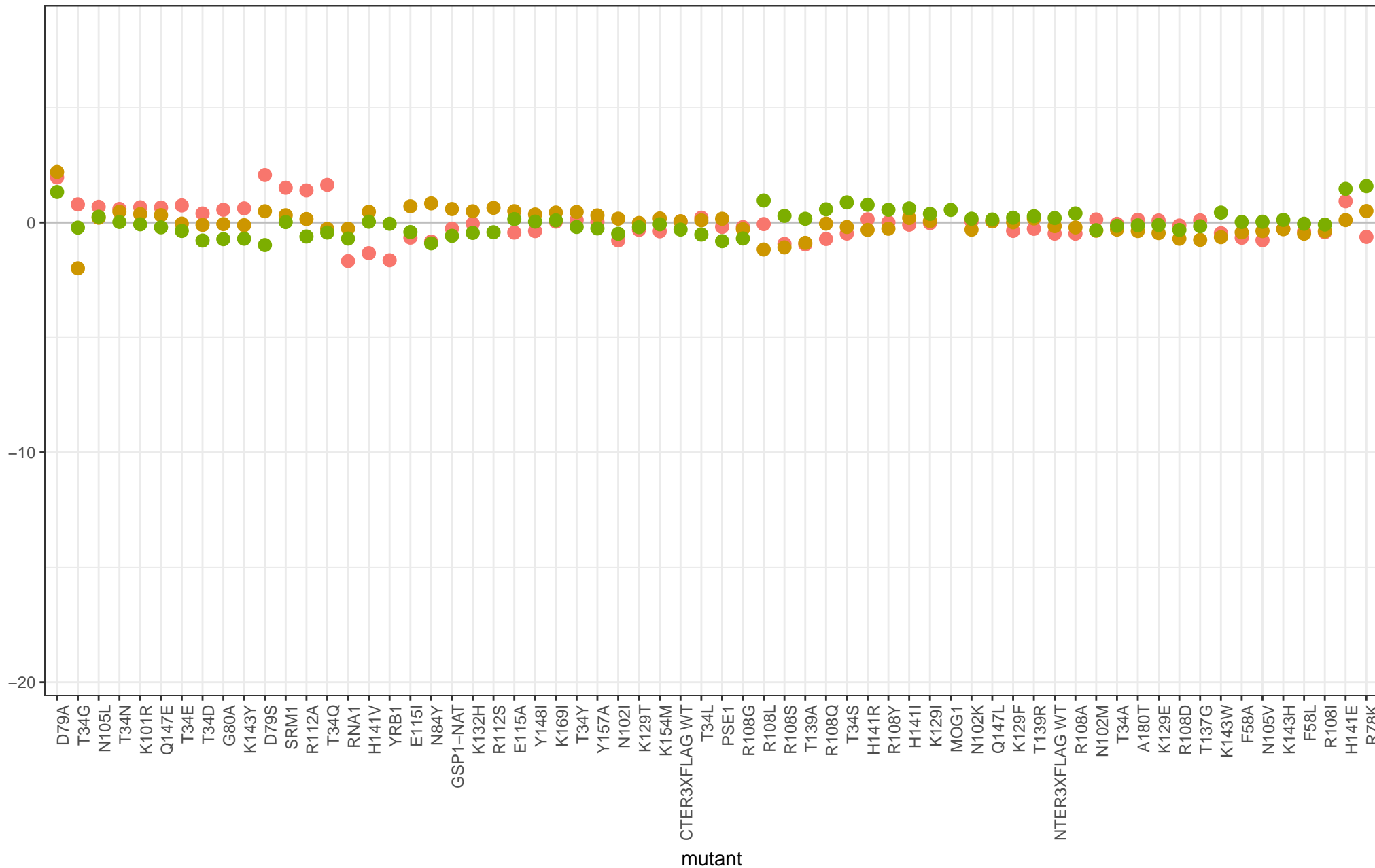
Far3p/Far7p/Far8p/Far9p/Far10p/Far11p complex

E-MAP score



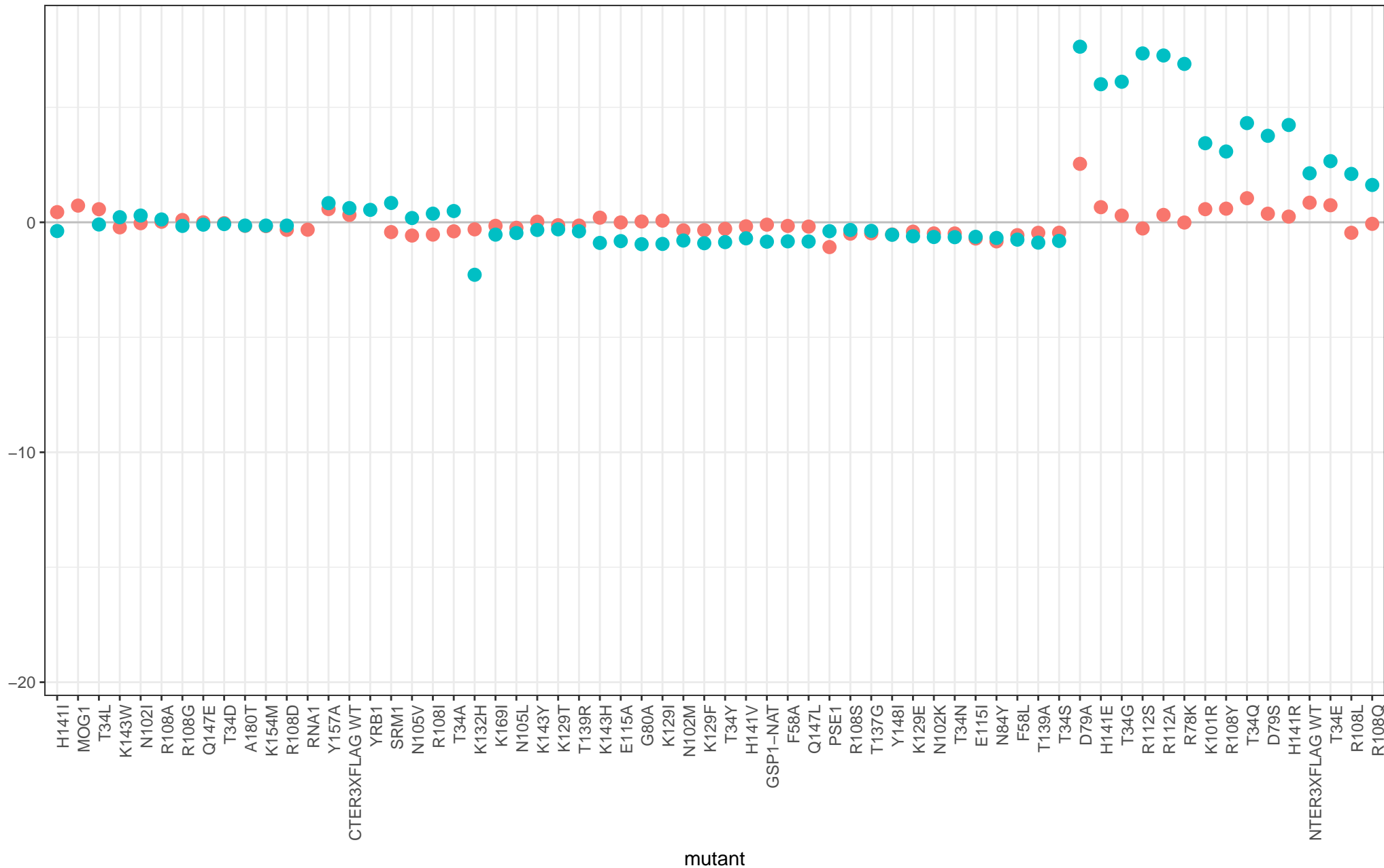
FBP degradation complex

E-MAP score



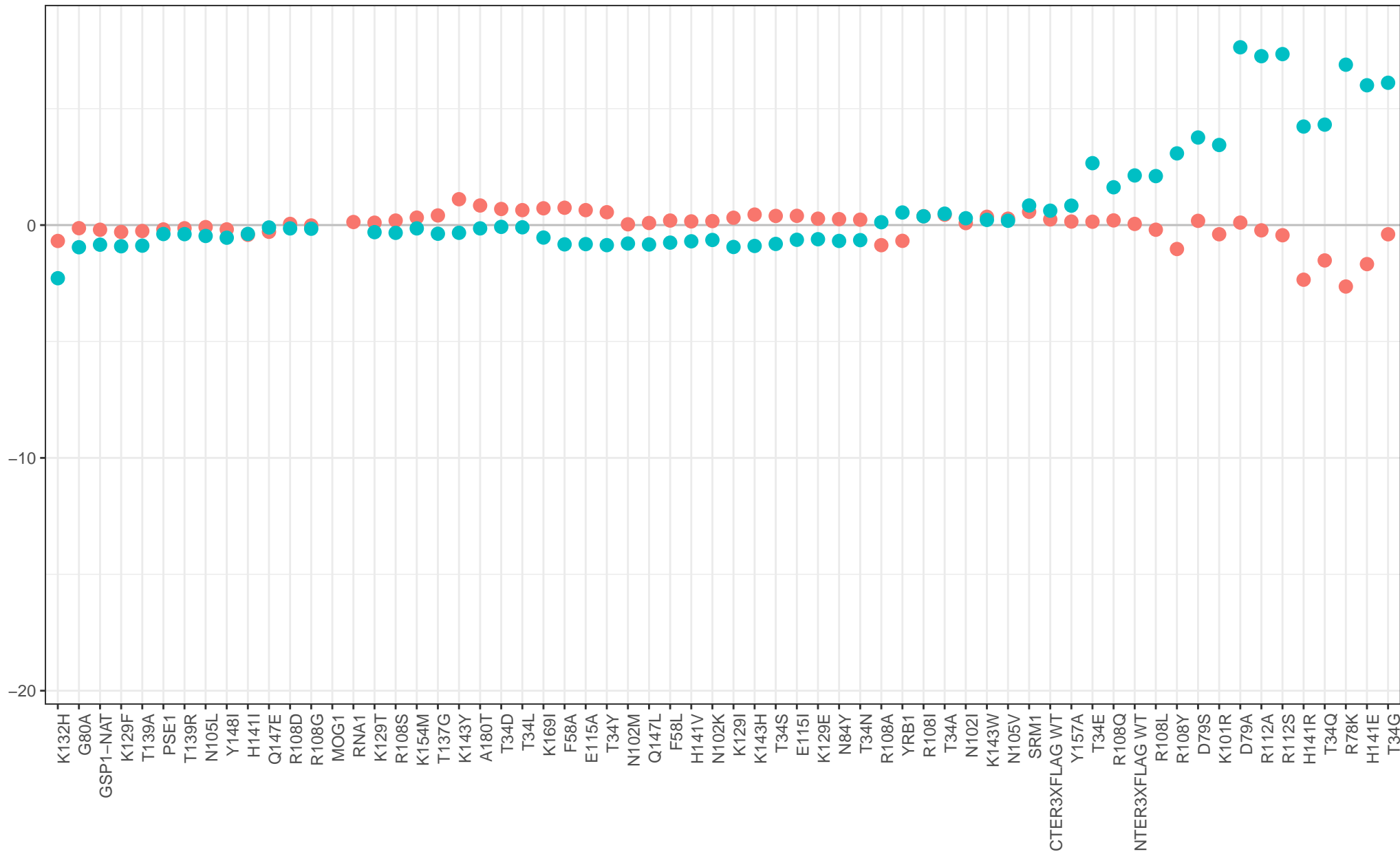
GAL3p/GAL80p complex

E-MAP score



GAL4p/GAL80p complex

E-MAP score



GARP complex

E-MAP score

-20

-10

0

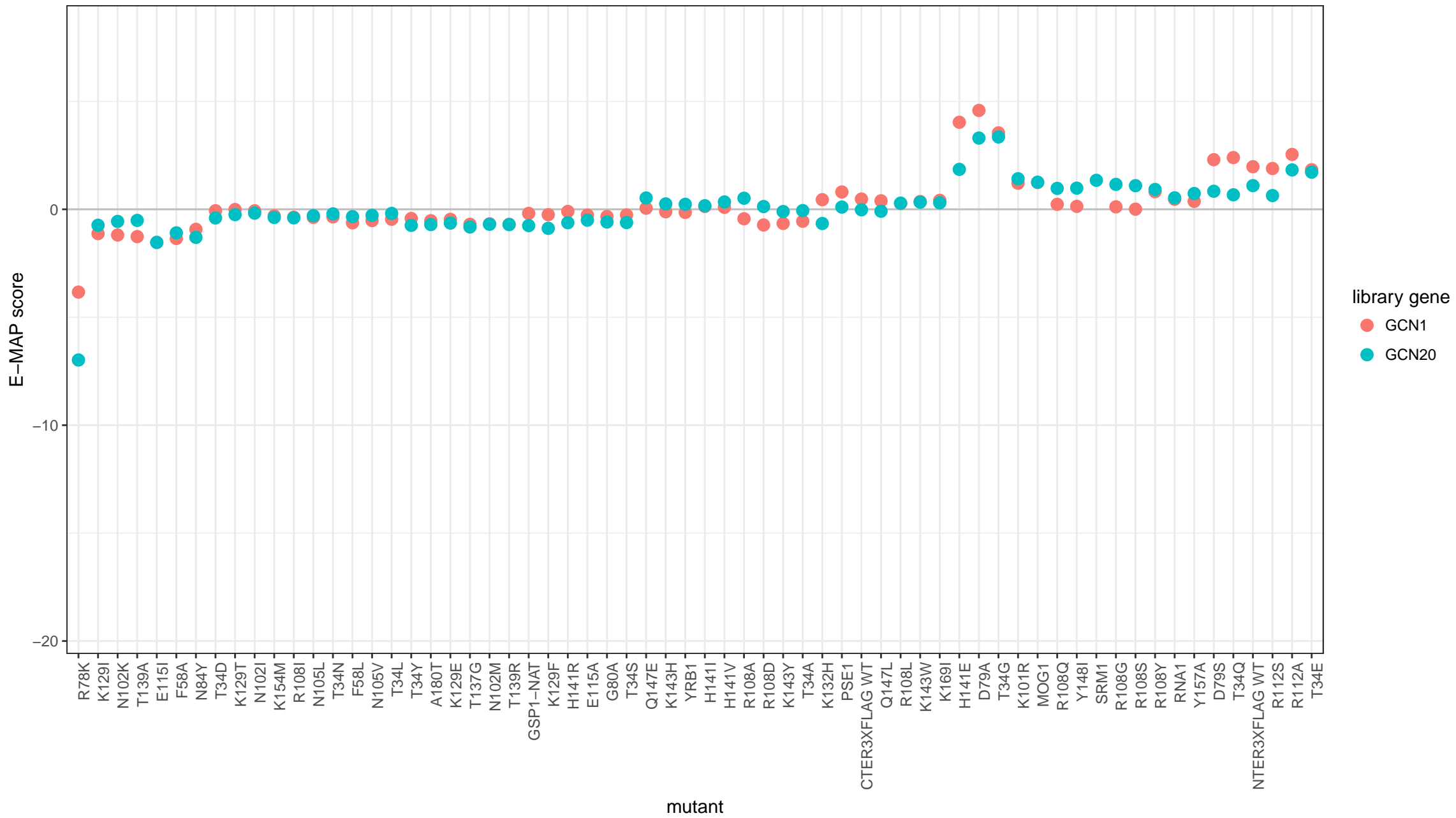
mutant

library gene

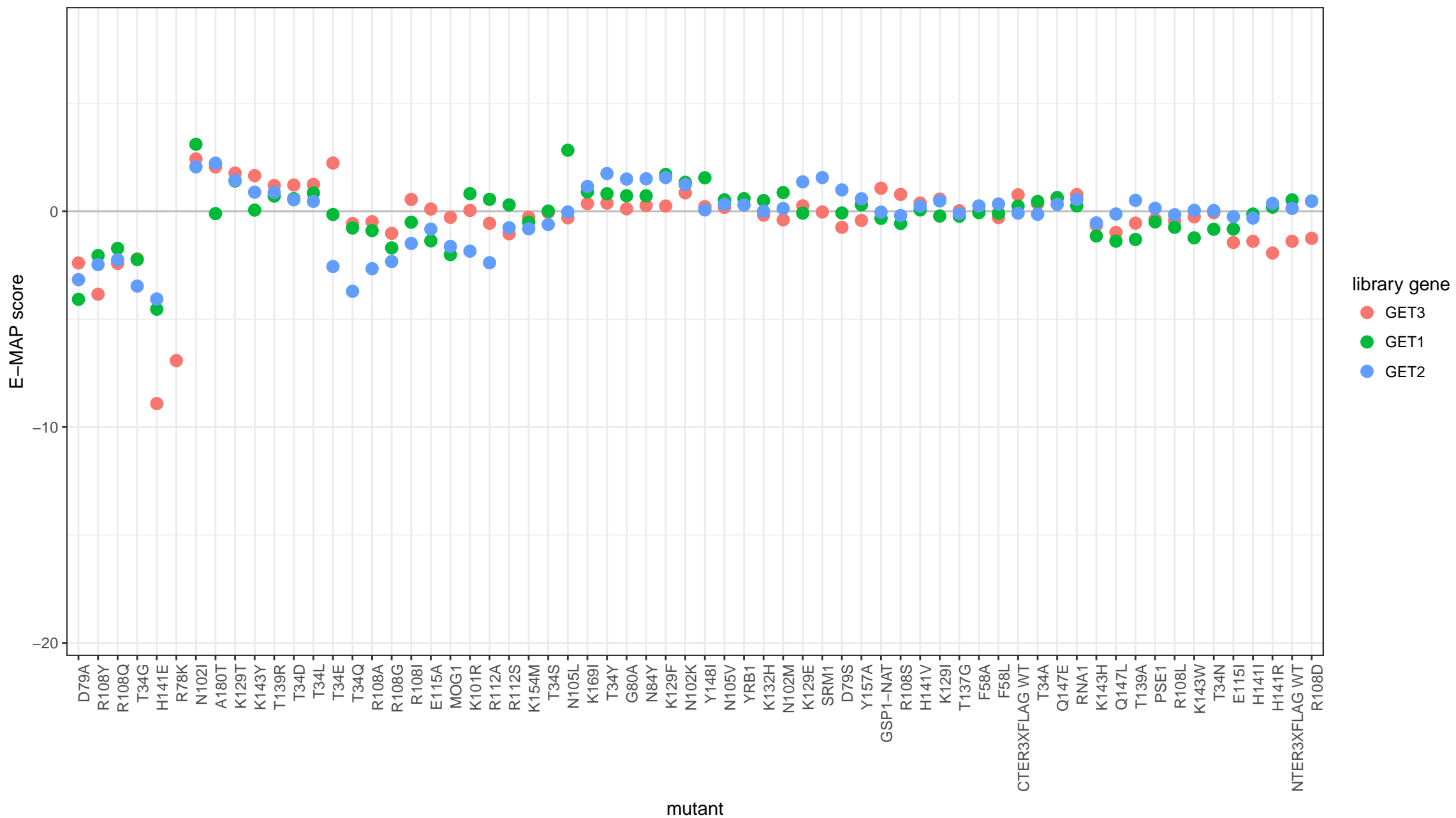
- VPS51
- VPS53
- VPS52
- VPS54

D79S H141E R78K T139R H141R R108Y R112A N102I R112S D79A NTER3XFLAG WT Y157A E115I K129E K154M K143H N84Y T34A K143W A180T K169I E115A R108S G80A T34S T34N R108A R108D R143Y T34G T139A T34Y F58L K129I CTER3XFLAG WT T34D YRB1 R108G T34L R108Q K101R Q147L N105L T34Q T137G MOG1 PSE1 SRM1 F58A K132H N102M H141V RNA1 GSP1-NAT T34E K129F K129T R108I N102K R108L Q147E Y148I H141I N105V

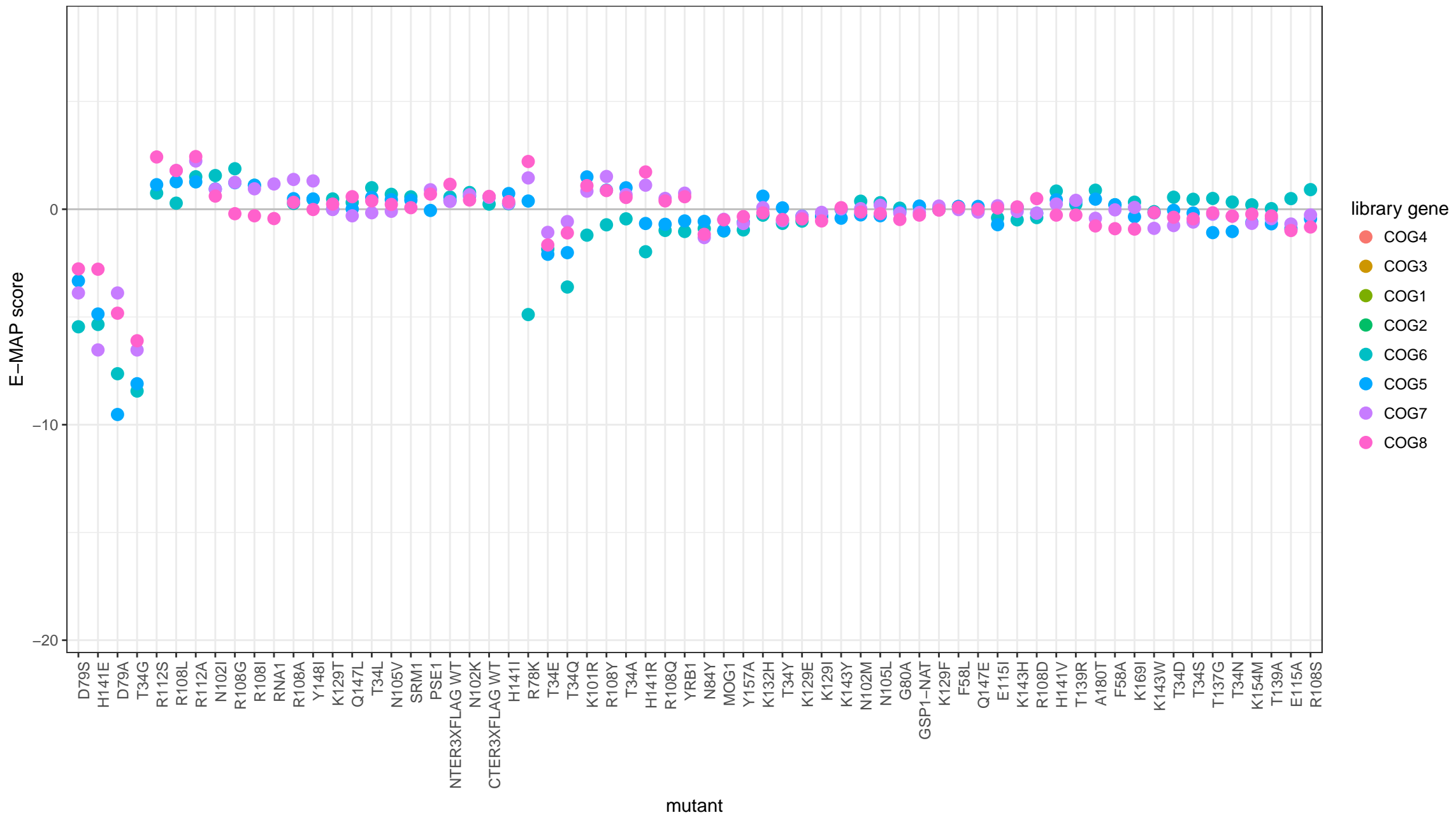
Gcn1p/Gcn20p complex



GET complex

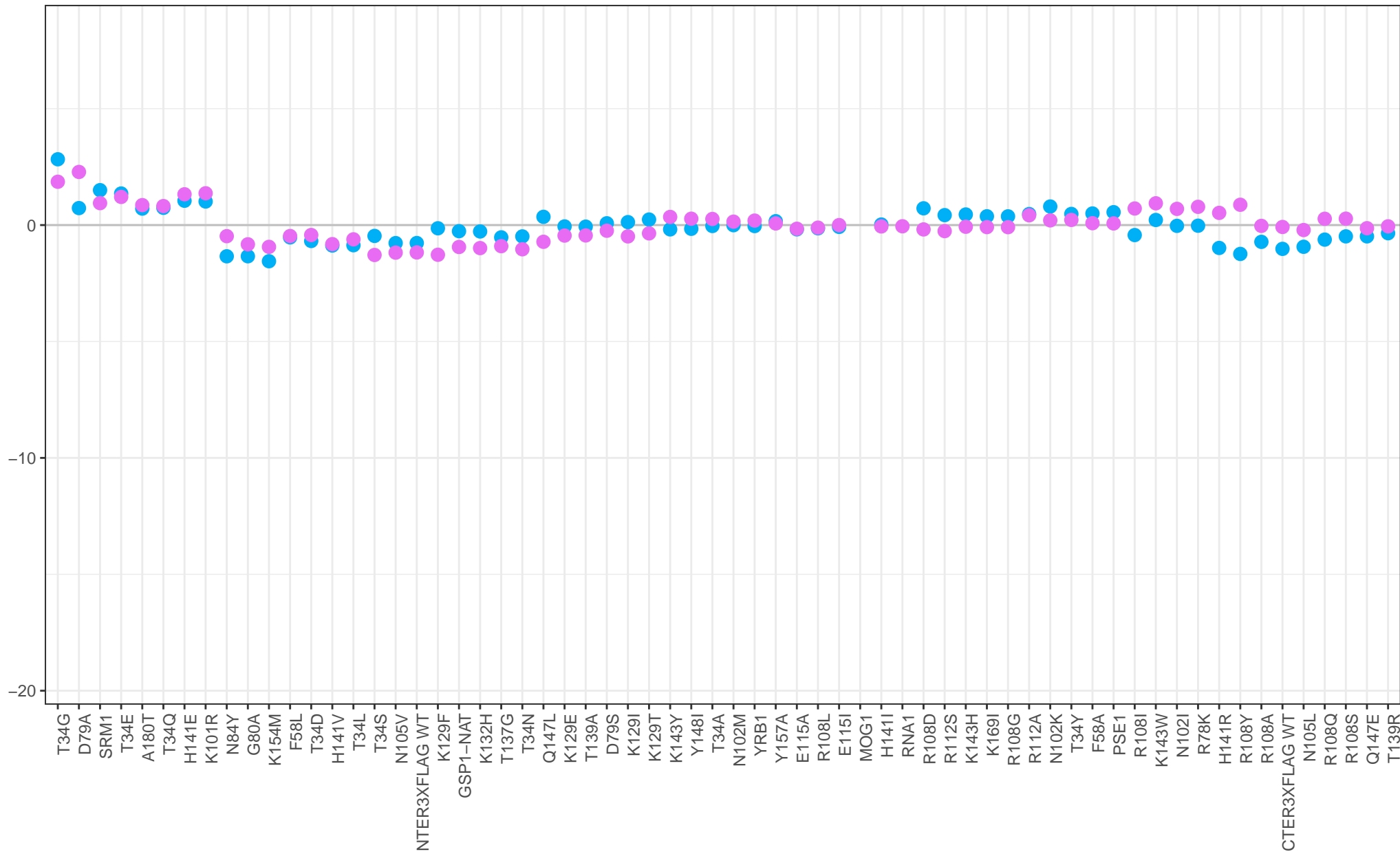


Golgi transport complex



GSE Complex

E-MAP score



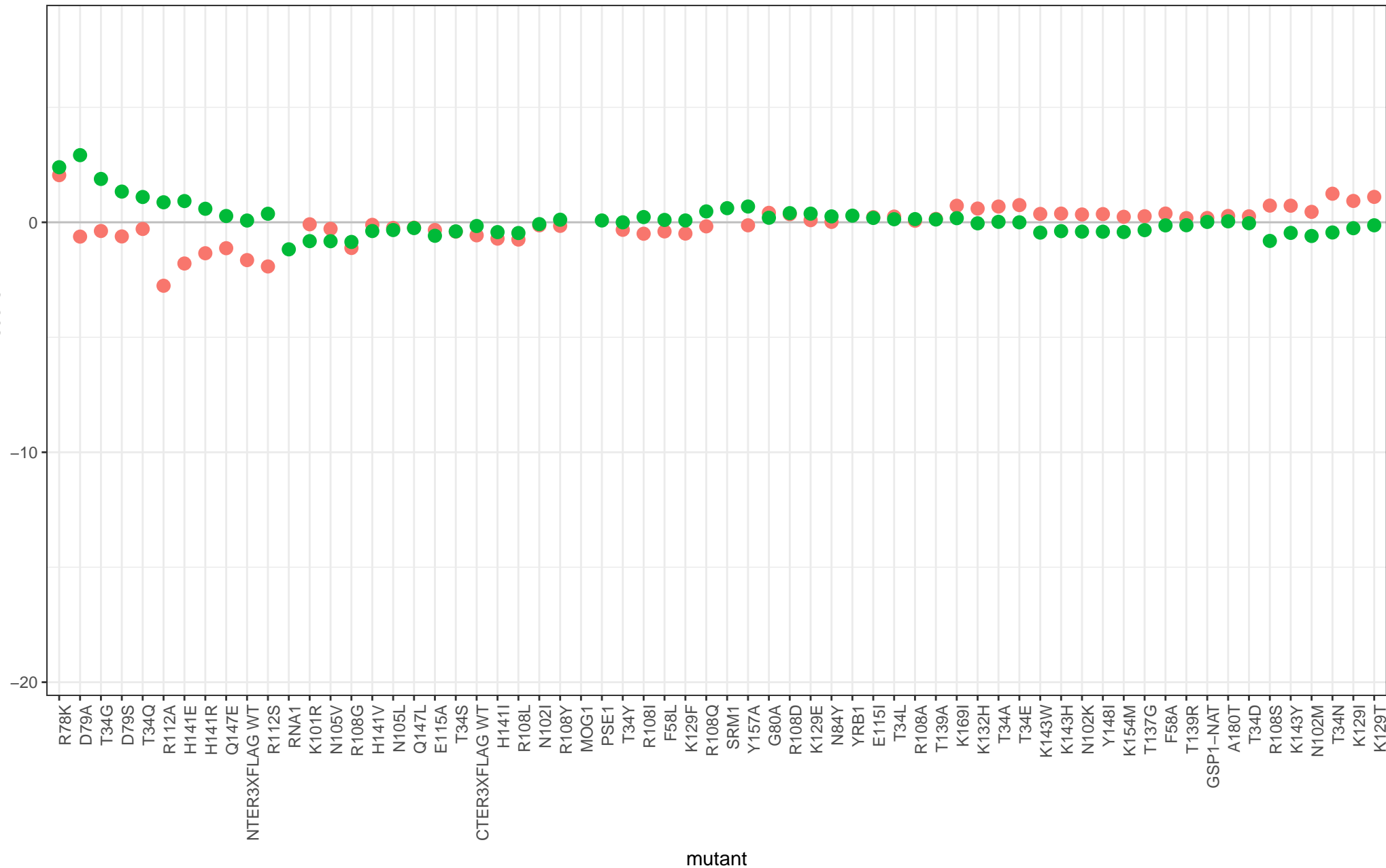
library gene

- SLM4
- GTR2
- LTV1
- GTR1
- MEH1

mutant

HAT-B complex

E-MAP score



library gene

HAT2

HAT1

HIF1

HIR complex

E-MAP score

-20

-10

0

mutant

library gene

HIR1

HIR2

HIR3

HPC2

H141R
R112S
R78K
R112A
H141E
NTER3XFLAG WT
R108Y
T34G
RNA1
T34E
D79A
T34Q
R108Q
CTER3XFLAG WT
R108L
R108S
R108D
R108G
Y148I
Q147E
T139R
K132H
R108I
F58A
K129F
T34A
T137G
T34N
MOG1
T34S
K154M
T139A
SRM1
K143Y
K169I
K129T
N102I
N102M
A180T
T34L
K129E
G80A
T34D
E115A
E115I
H141V
T34Y
F58L
Q147L
K129I
K143H
N84Y
YRB1
R108A
N102K
N105V
H141I
N105L
PSE1
D79S
Y157A
K143W
GSP1-NAT
K101R

histone H2A phosphatase complex

E-MAP score

-20

-10

0

R78K
T34G
RNA1
CTER3XFLAG WT
T34E
R108G
R108S
K101R
K169I
H141I
T34Q
R108Q
R108A
Y148I
F58A
N102M
E115I
N84Y
T137G
T139A
T34A
N102I
T34S
N105V
R108I
F58L
Y157A
GSP1-NAT
K129I
K143W
PSE1
T34D
T34L
R108D
A180T
K129T
K154M
T34N
N105L
T139R
E115A
T34Y
Q147E
K129E
N102K
K143Y
SRM1
MOG1
YRB1
H141V
Q147L
NTER3XFLAG WT
R108L
H141R
R108Y
R112A
R112S
D79A
D79S
G80A
K132H
H141E
K129F
K143H

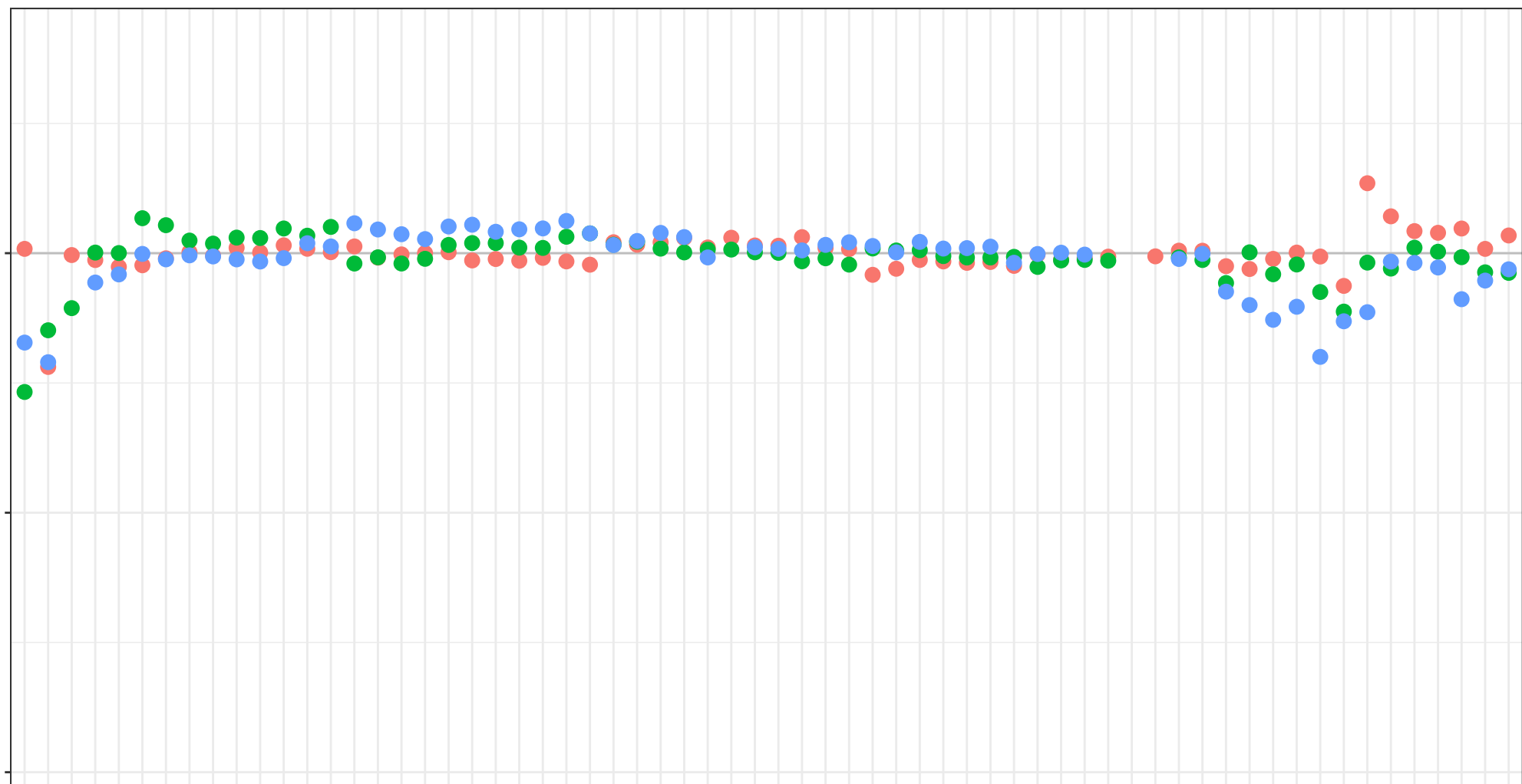
mutant

library gene

PSY4

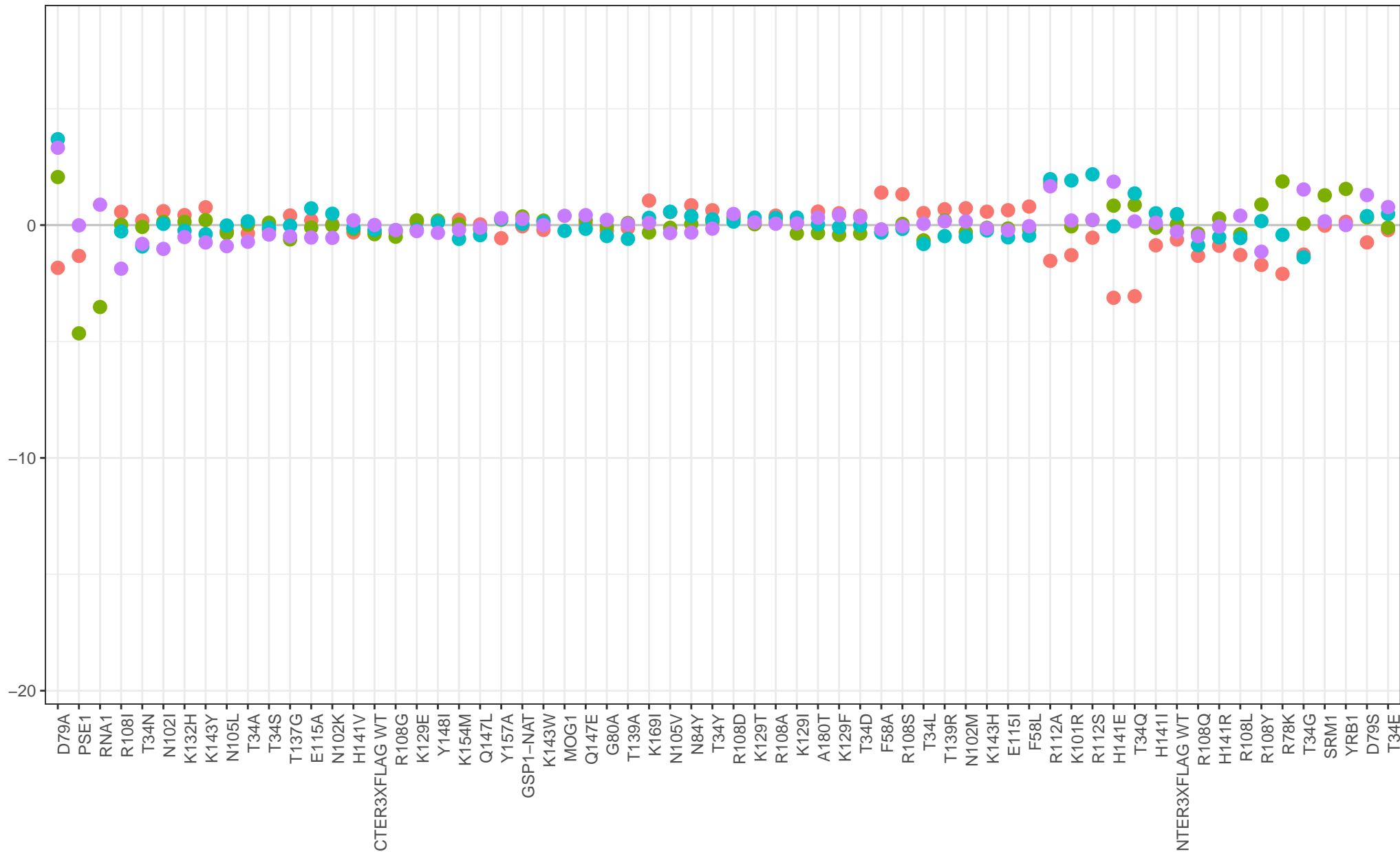
PPH3

PSY2



HMC Complex

E-MAP score



library gene

HSC82

YDJ1

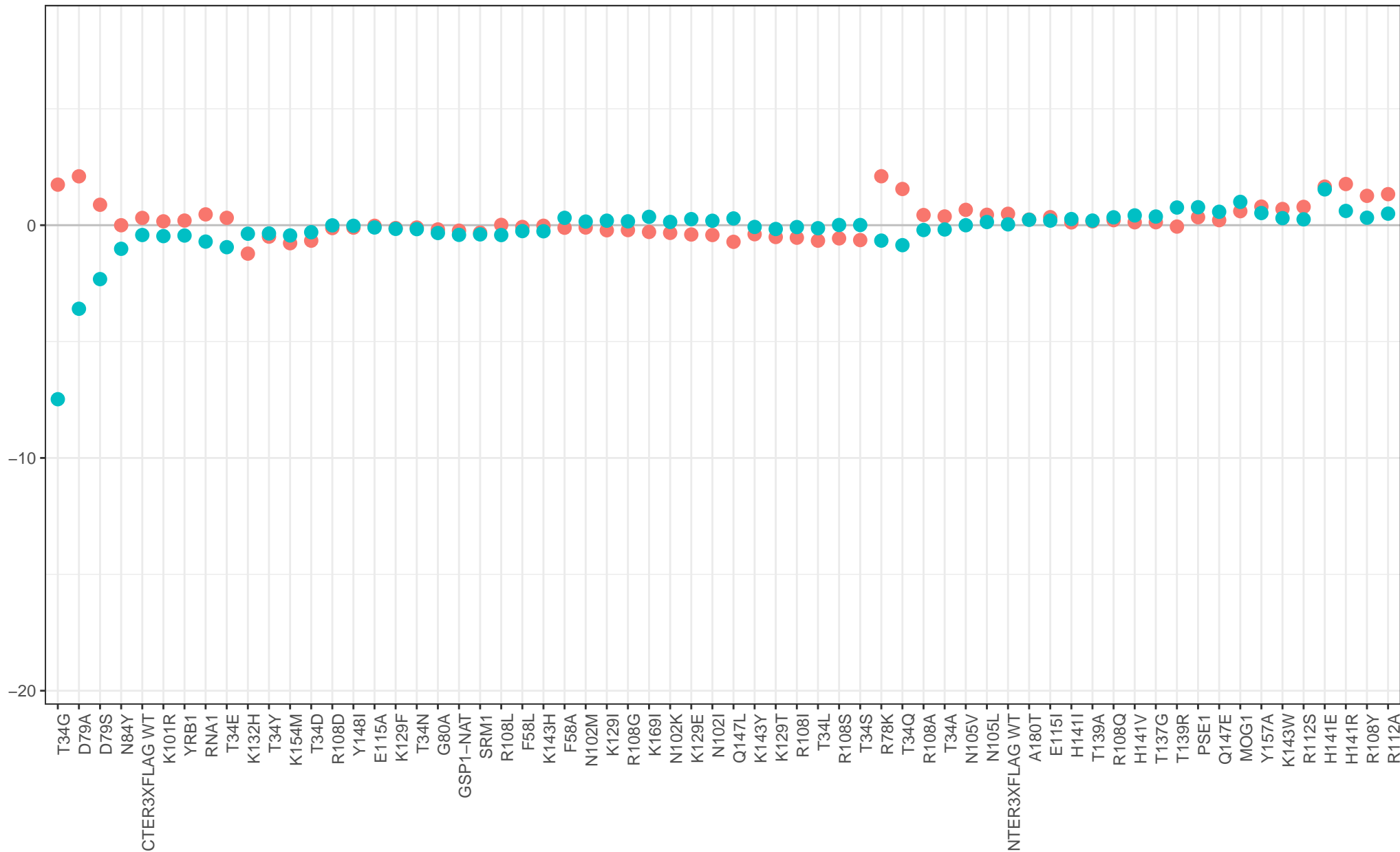
SRO9

SSA3

mutant

Holliday junction resolvase complex

E-MAP score



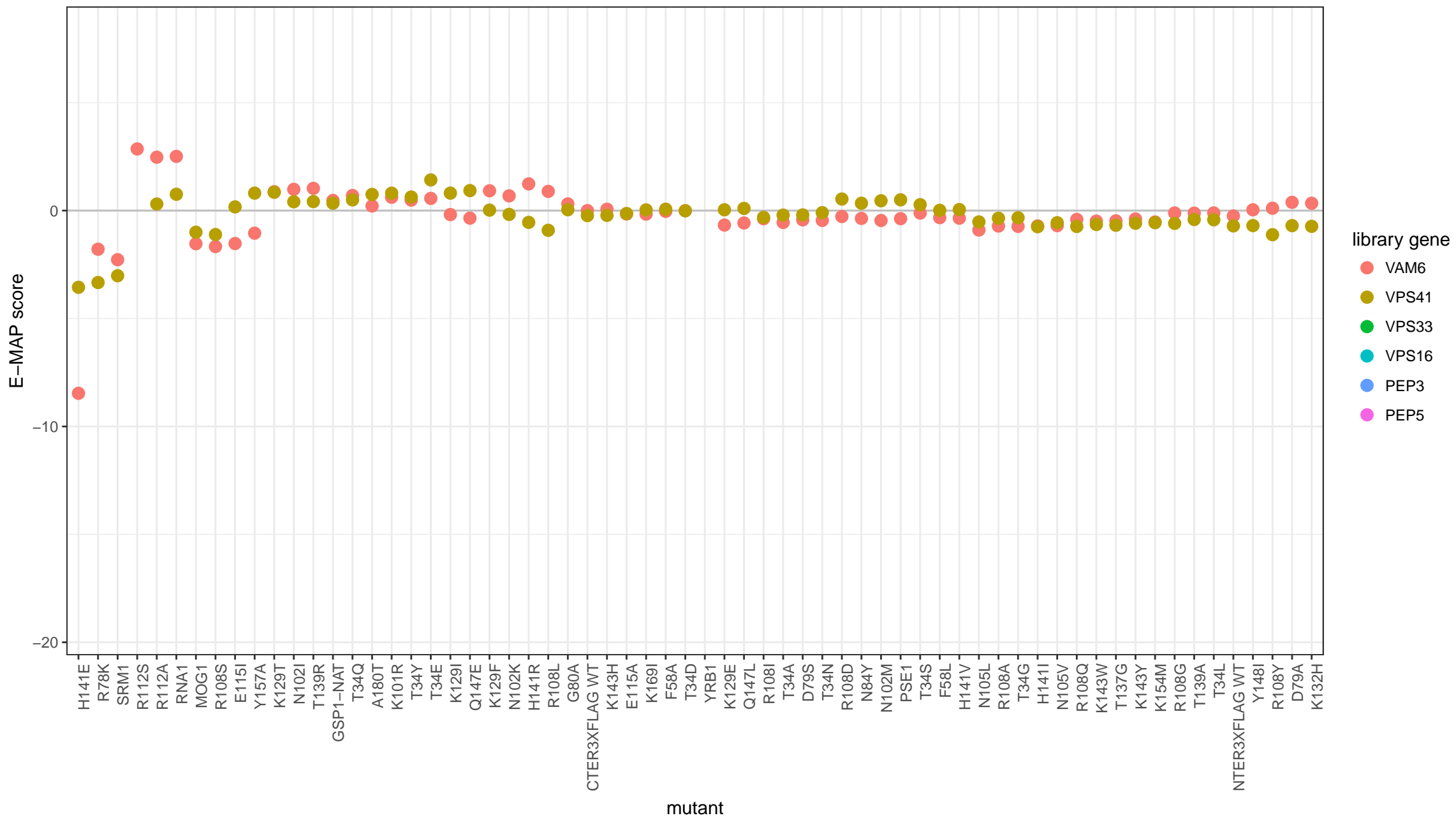
library gene

MMS4

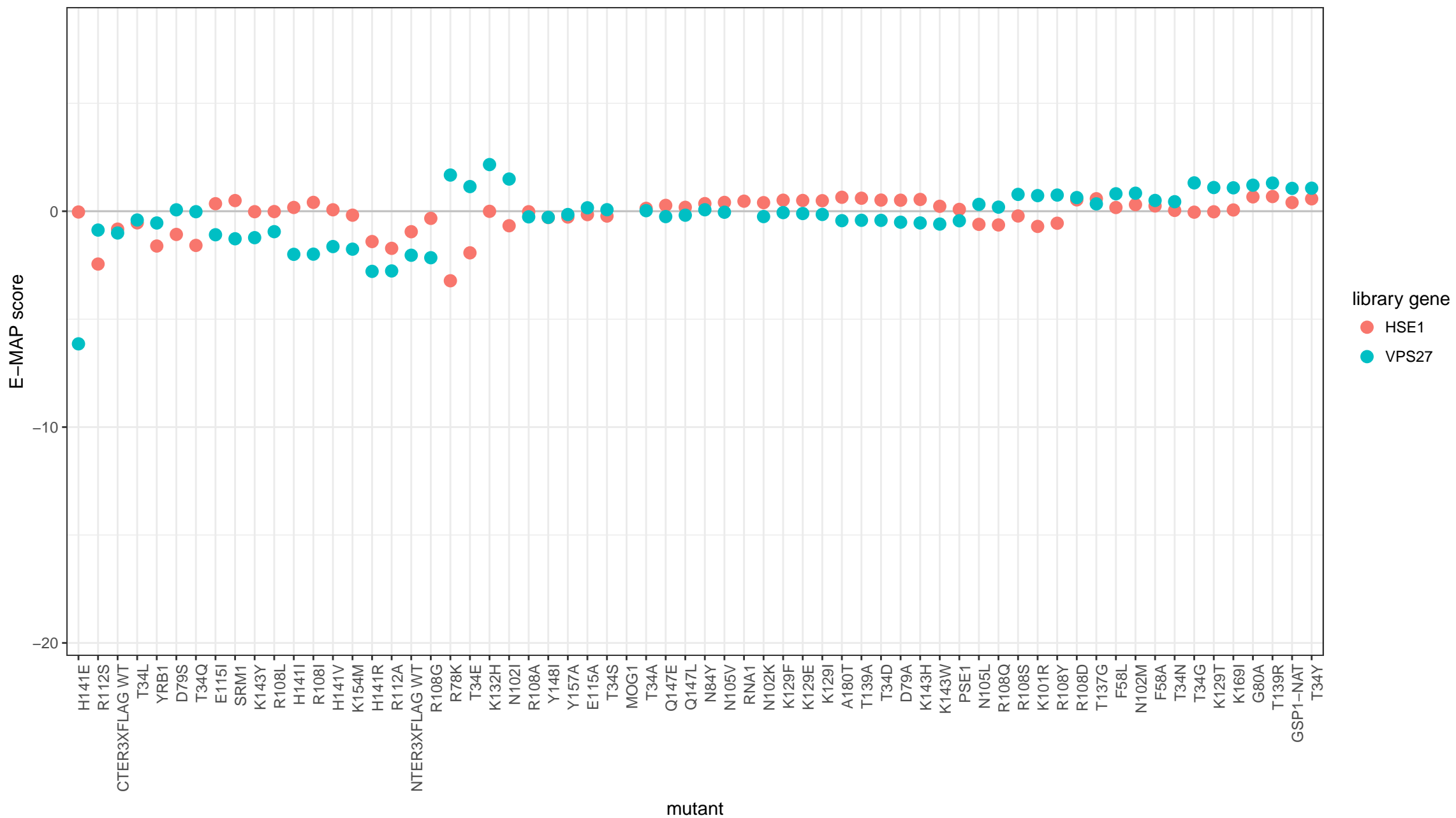
MUS81

mutant

HOPS complex

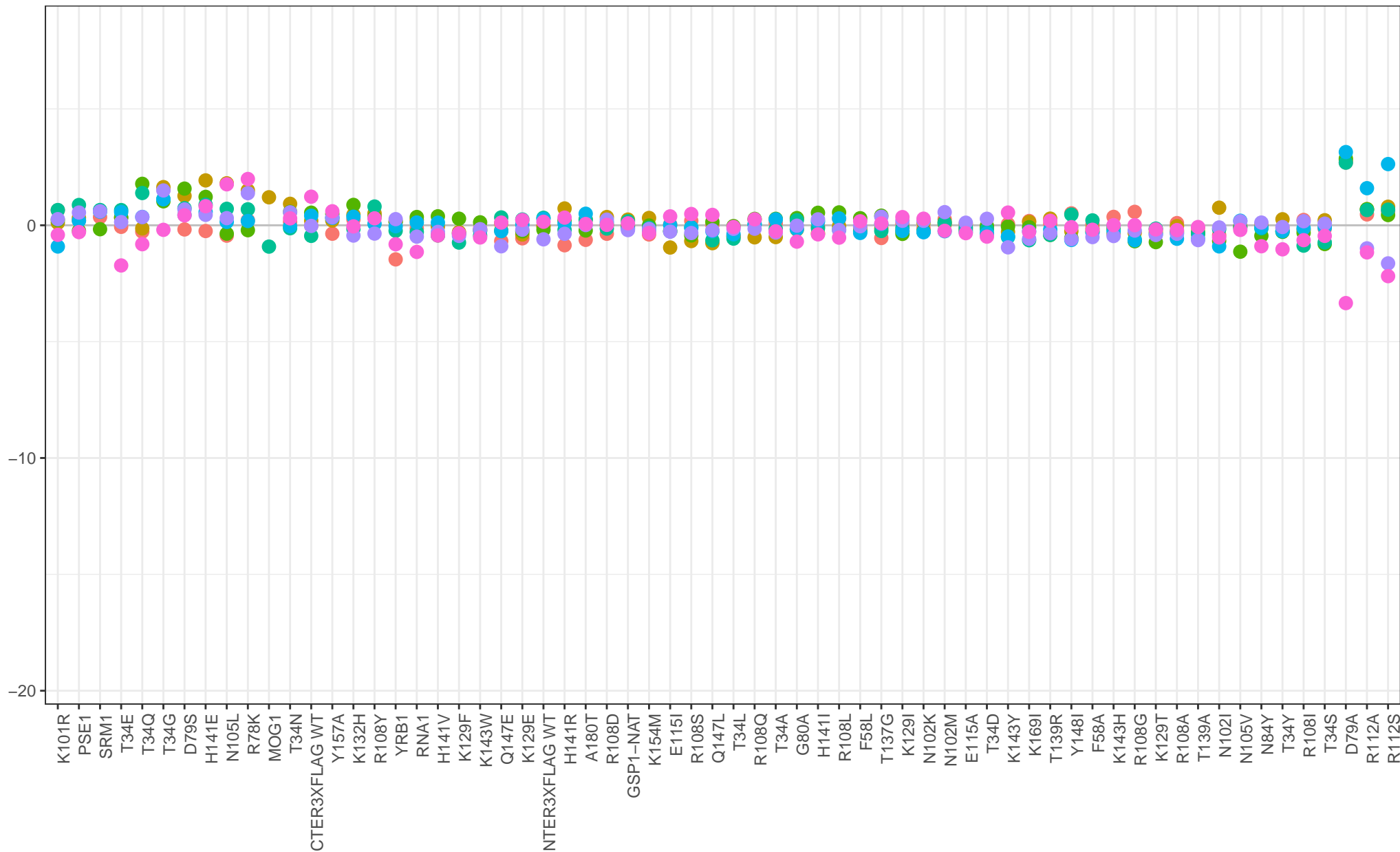


Hse1p/Vps27p complex



hydrolase activity, acting on glycosyl bonds

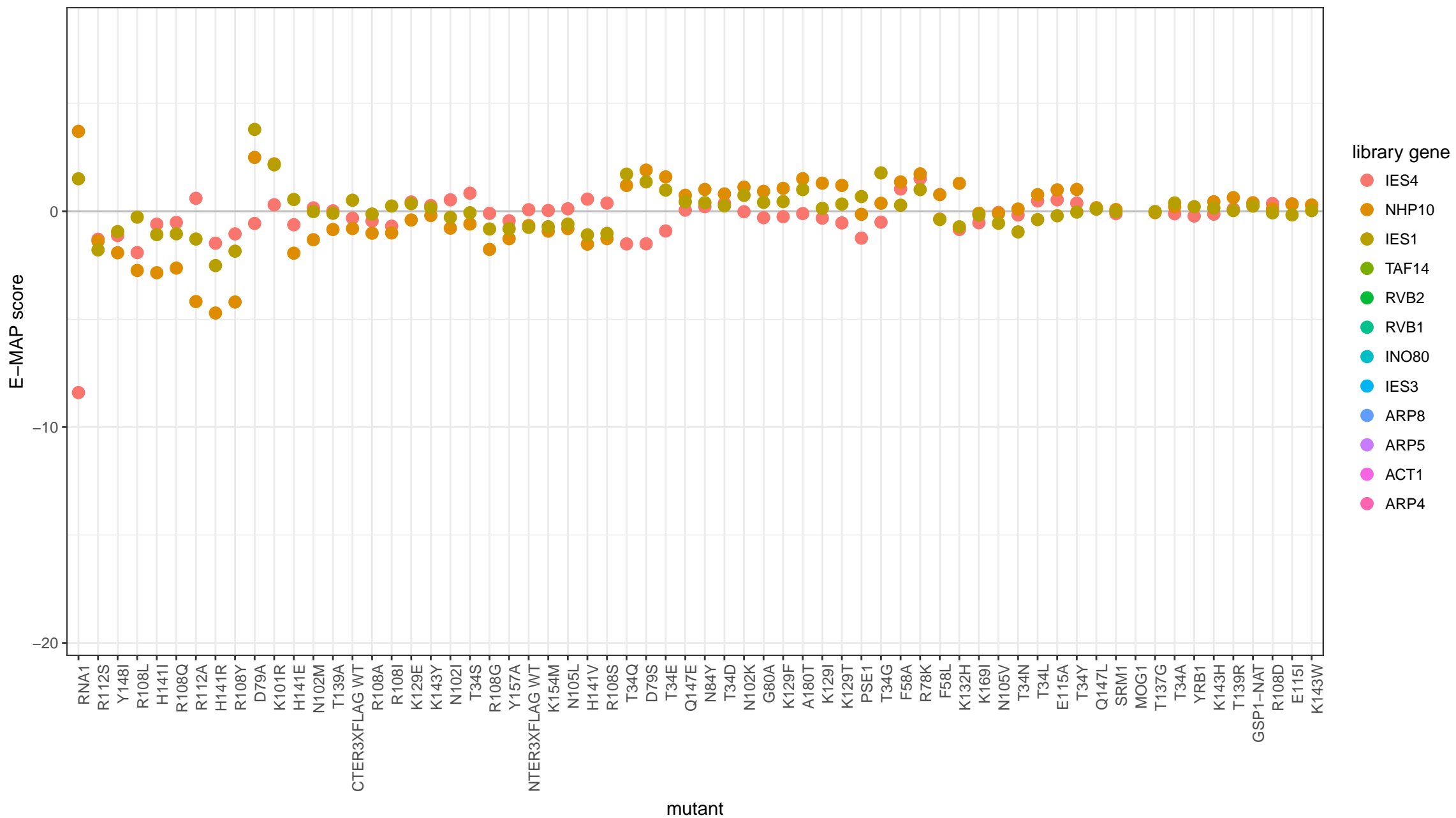
E-MAP score



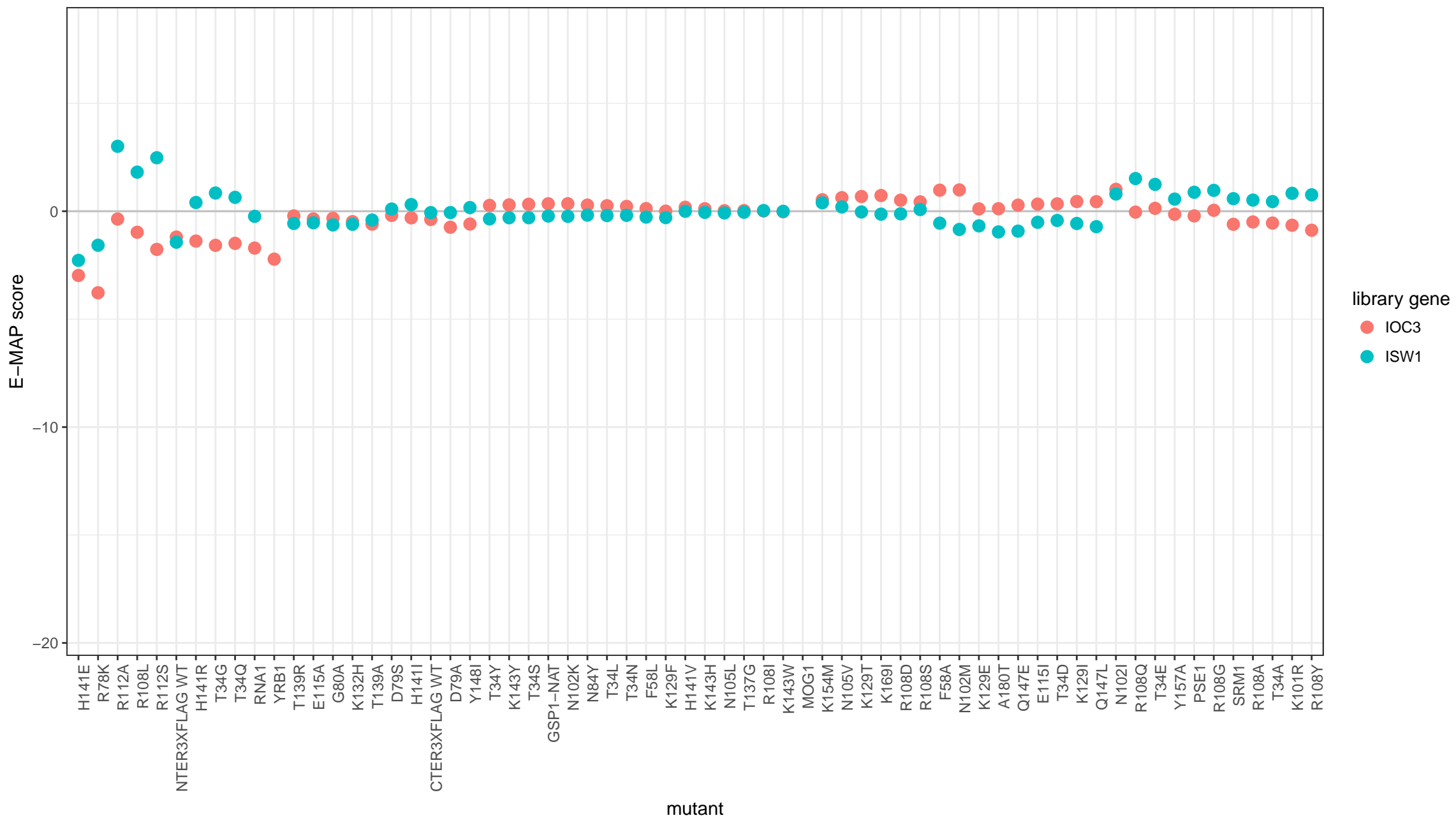
library gene

- GTB1
- CWH41
- MNL1
- POA1
- ROT2
- MNS1
- SCW11

Ino80p complex

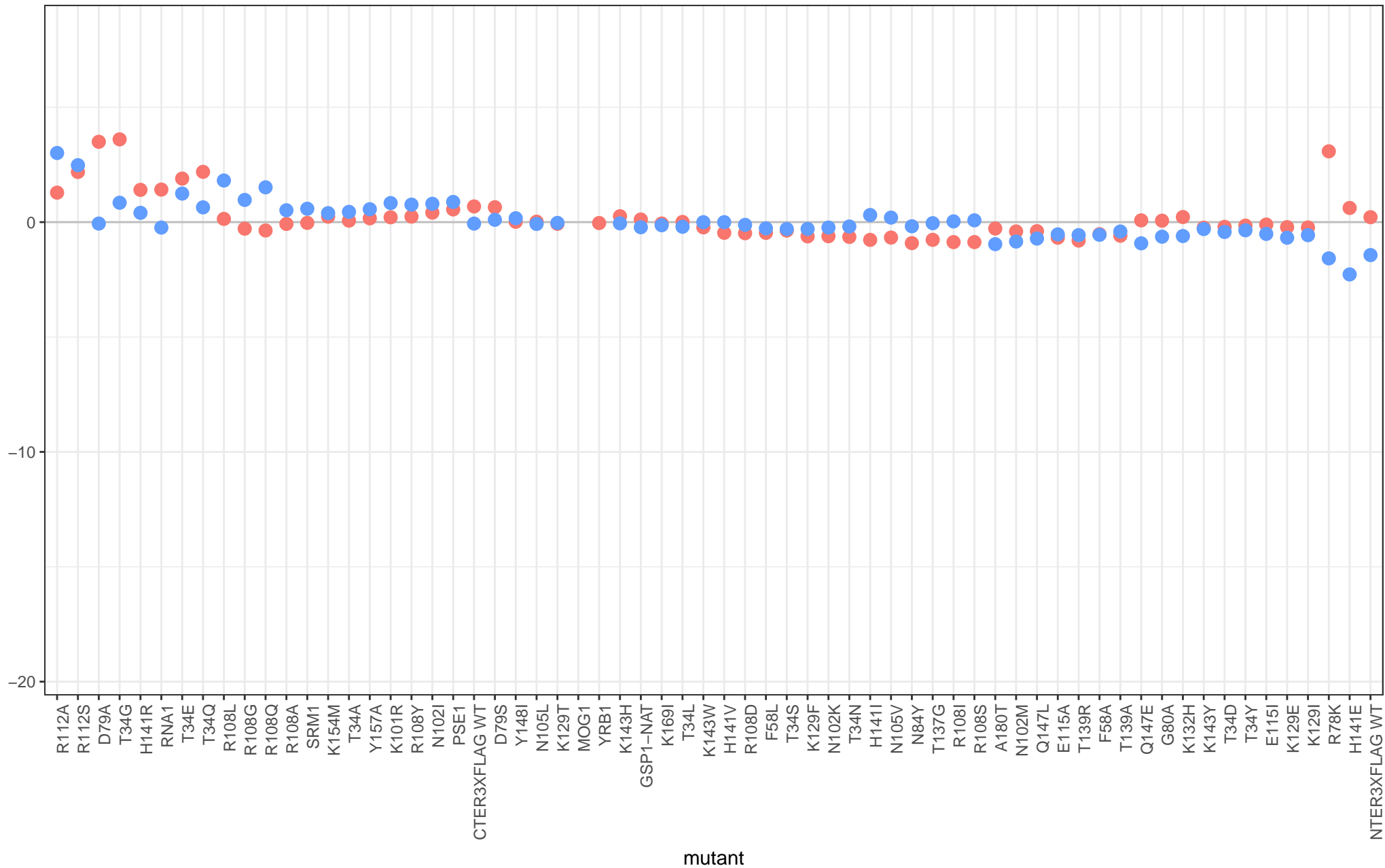


ISW1a complex

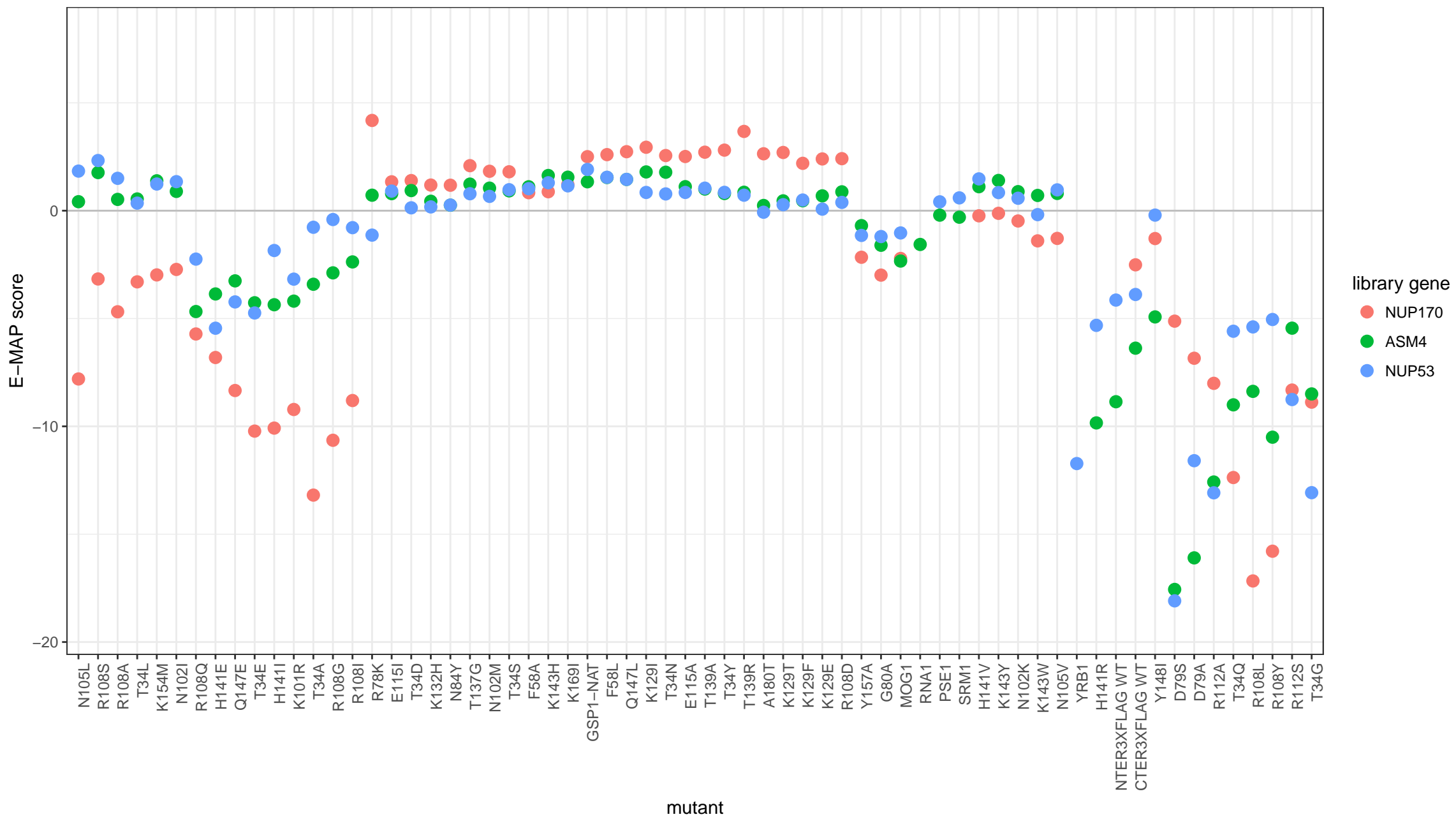


ISW1b complex

E-MAP score

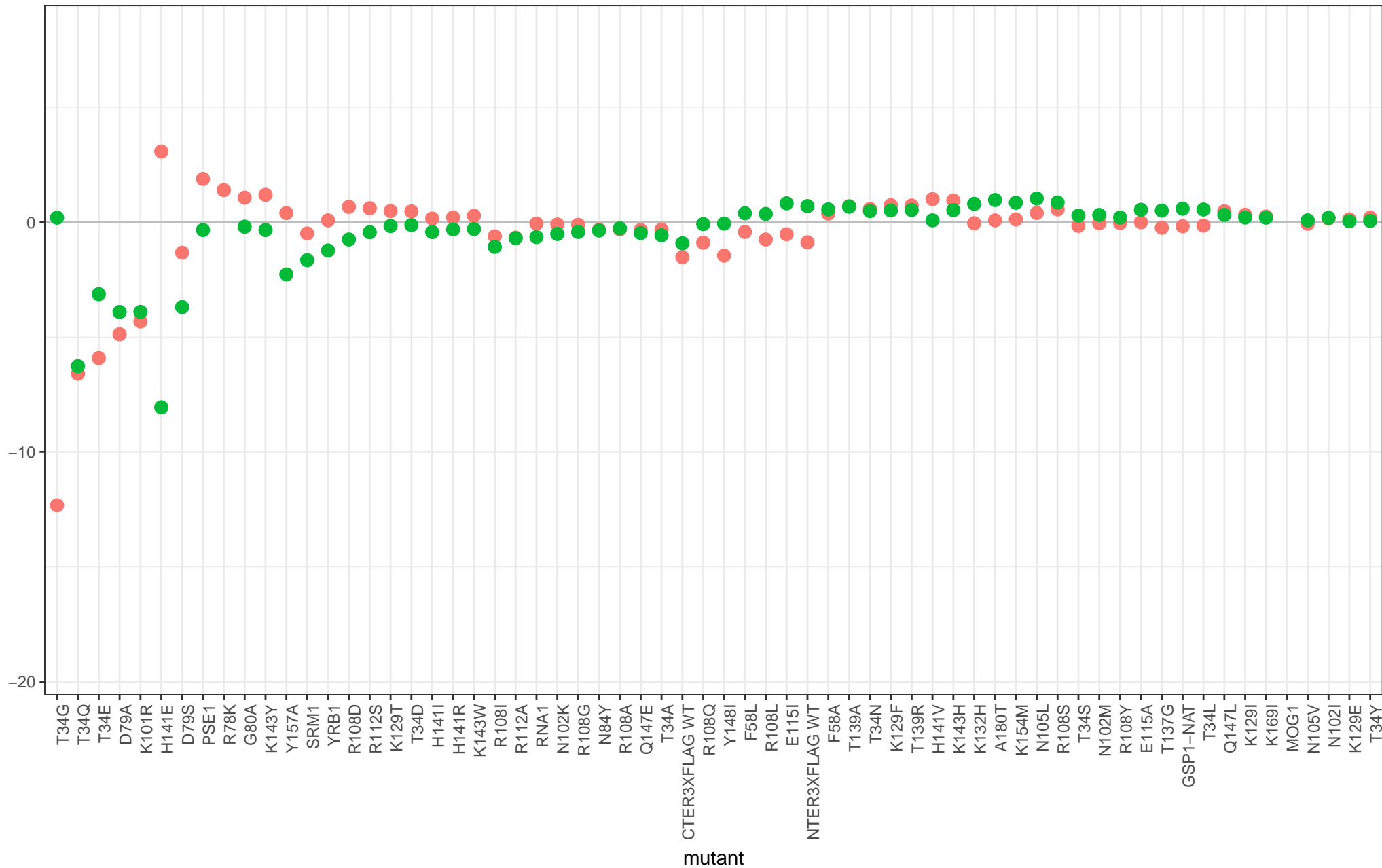


karyopherin docking subcomplex of the Nuclear Pore Complex (NPC)

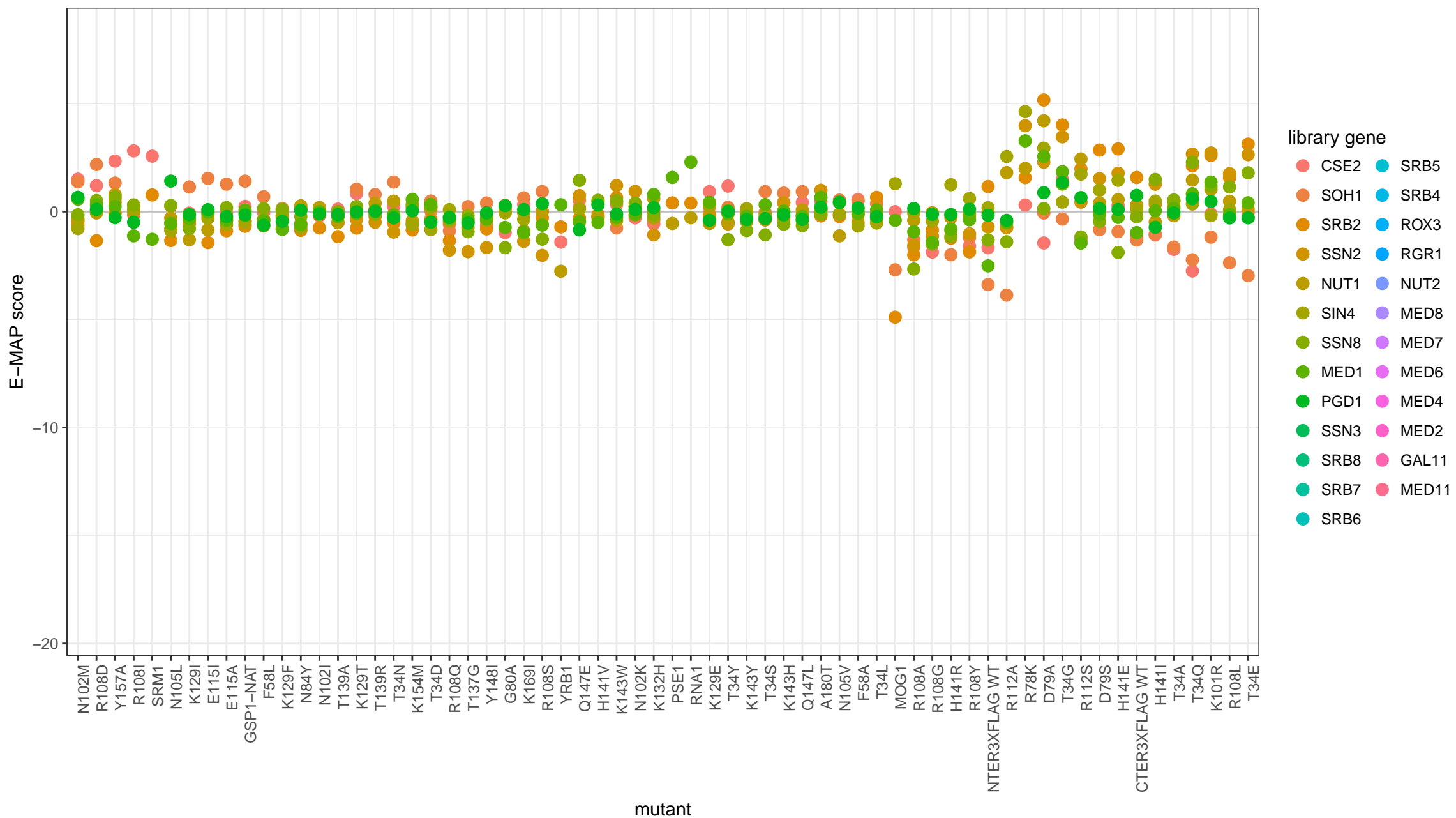


Kel1p/Kel2p/Lte1p complex

E-MAP score

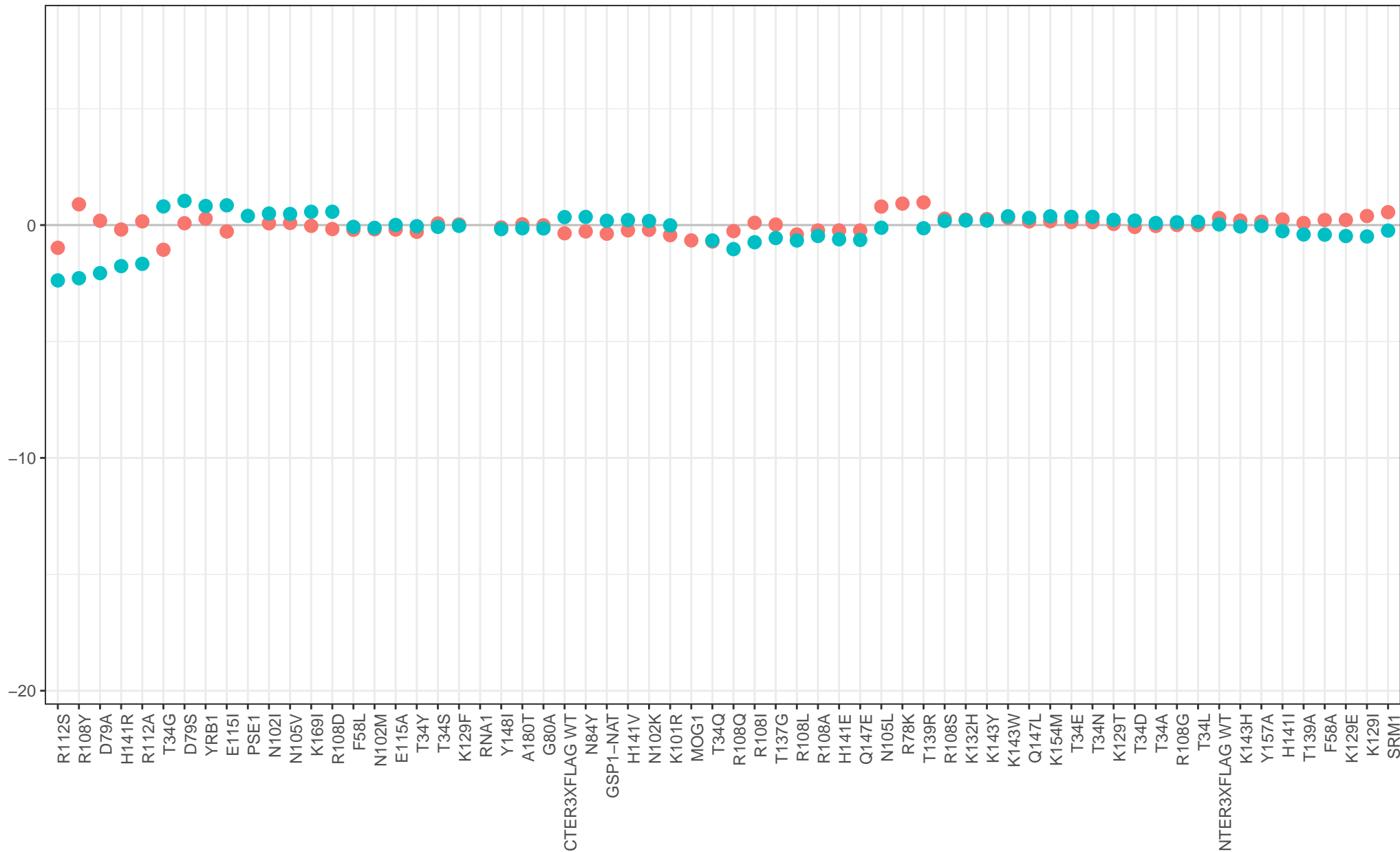


Kornberg's mediator (SRB) complex



Ku complex

E-MAP score



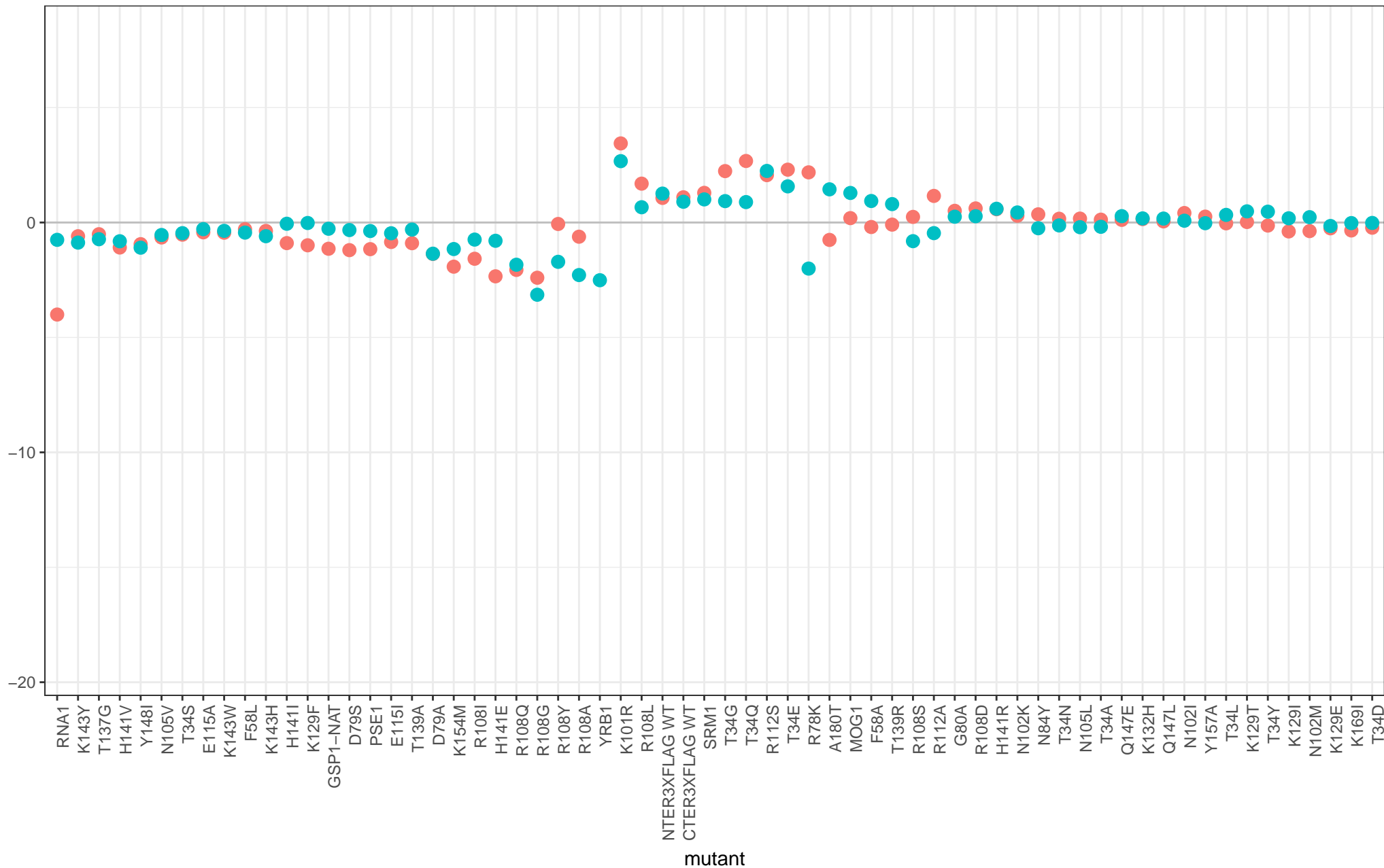
library gene

- YKU70
- YKU80

mutant

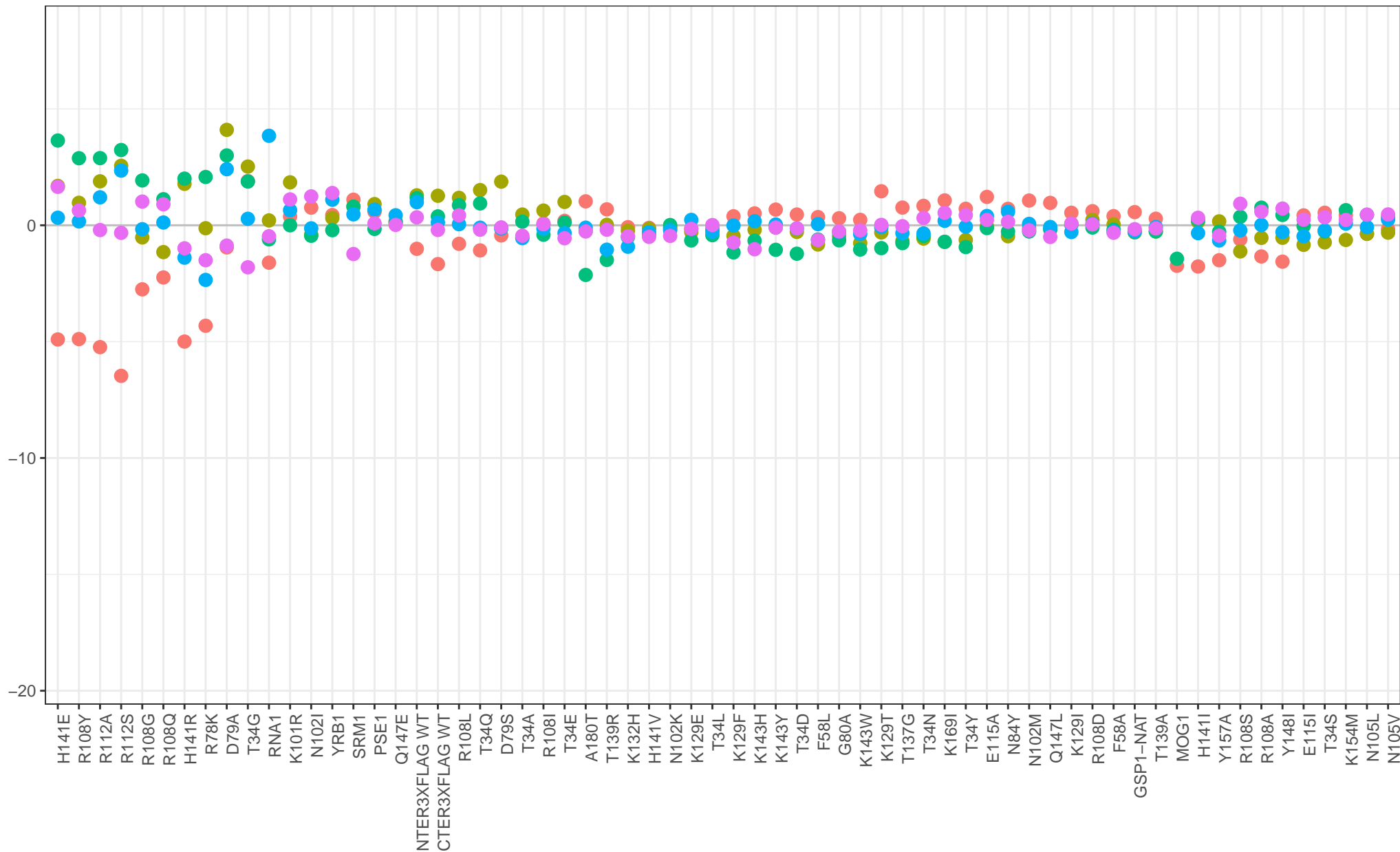
Lge1p/Bre1p complex

E-MAP score



ligase activity

E-MAP score

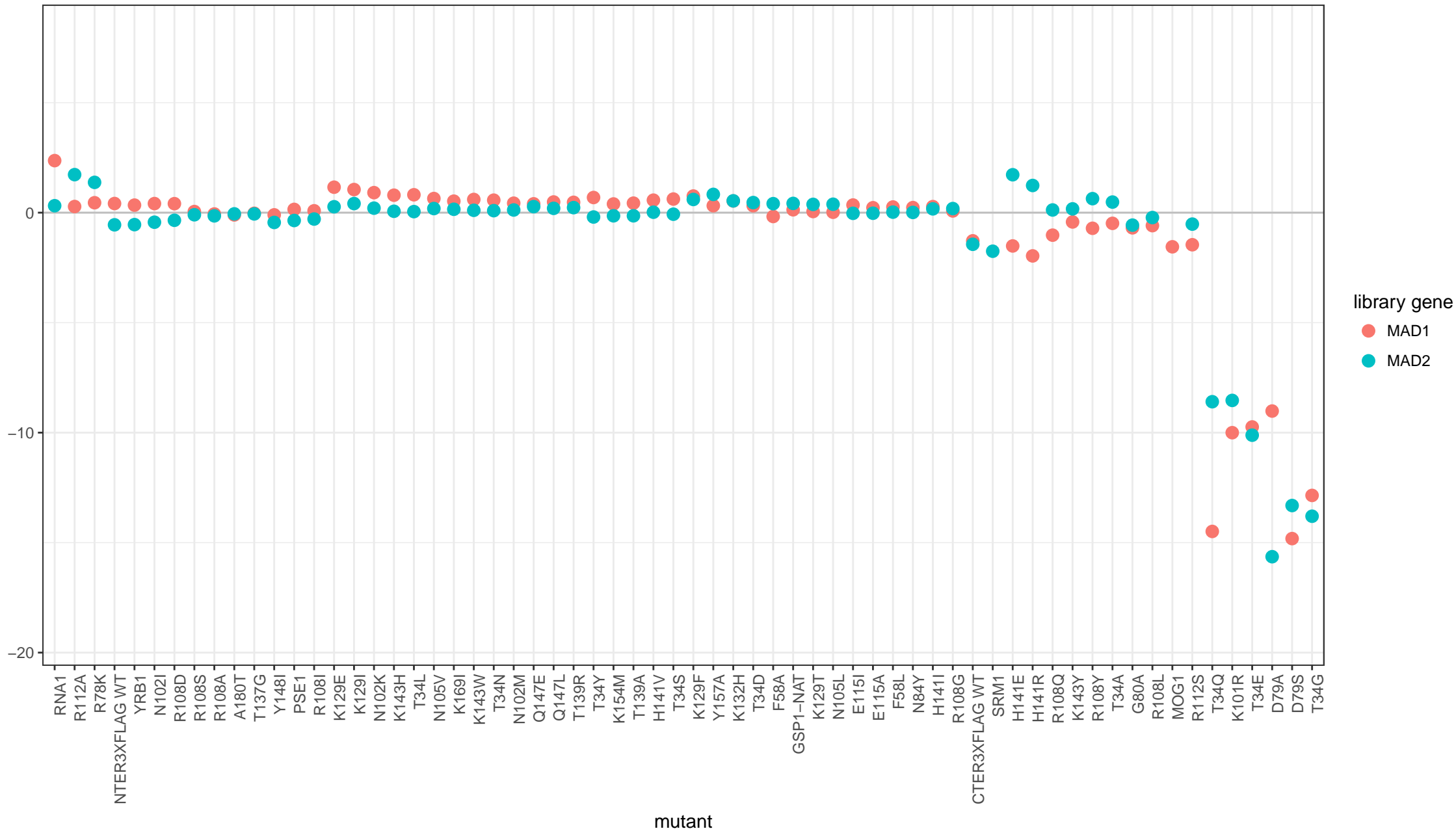


library gene

- UBA4
- GSH2
- UBA3
- AIM22
- FAT1

Mad1p/Mad2p complex

E-MAP score



MBF complex

E-MAP score

0

-10

-20

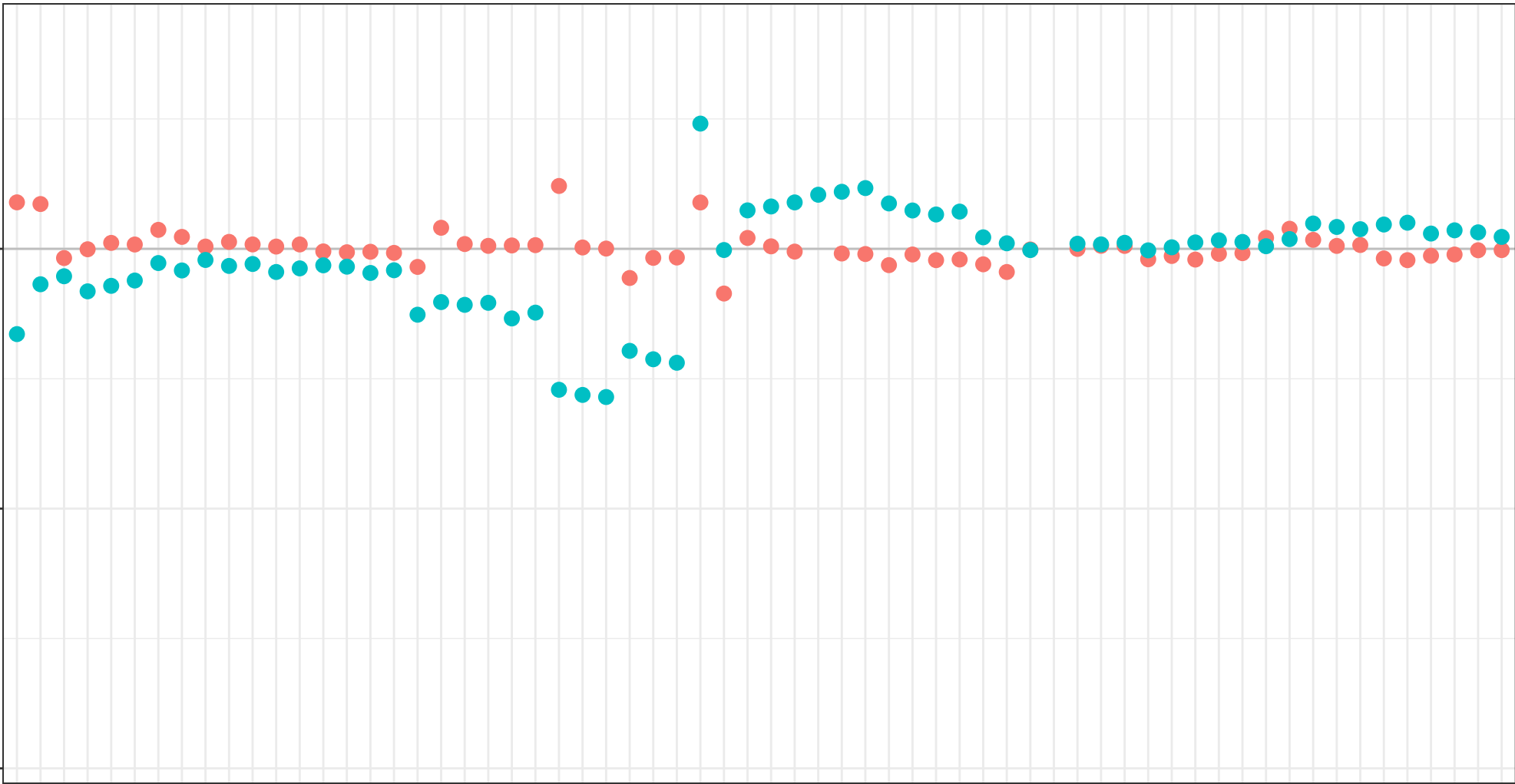
D79A
H141R
D79S
K129F
R108Q
T34E
NTER3XFLAG WT
R108S
F58L
CTER3XFLAG WT
PSE1
A180T
R108A
H141I
K154M
K129E
T34A
K101R
SRM1
RNA1
T34Q
R108G
R108I
H141E
R108Y
R112A
R112S
R108L
T34G
R78K
E115I
G80A
N102M
T34N
YRB1
K169I
T139R
T139A
T34Y
Q147L
T34S
H141V
K129T
K143W
MOG1
N102I
K143H
Y157A
K132H
N84Y
F58A
N105V
R108D
K143Y
Q147E
Y148I
E115A
GSP1-NAT
T137G
T34D
N102K
N105L
K129I
T34L

library gene

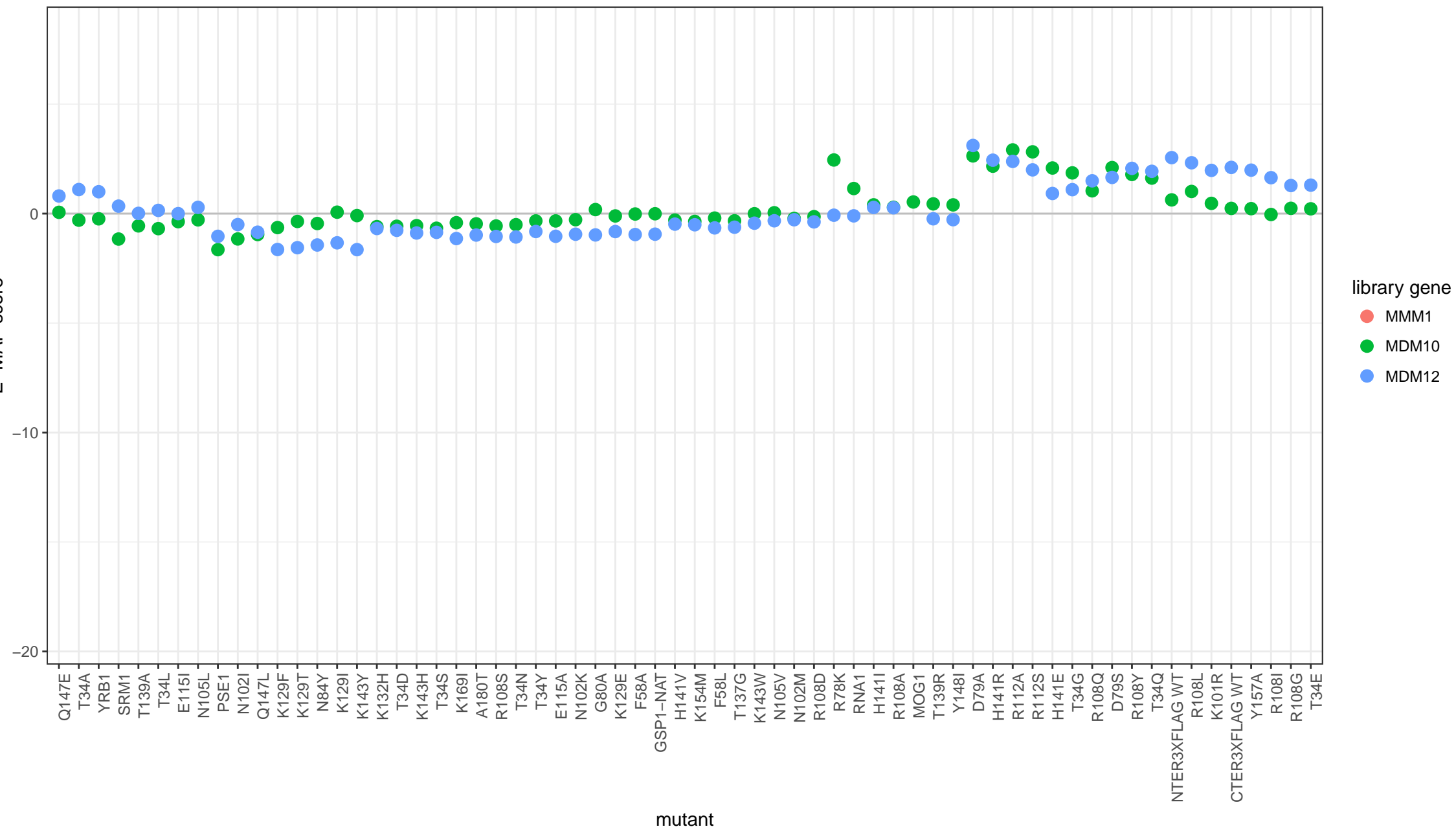
MBP1

SWI6

mutant

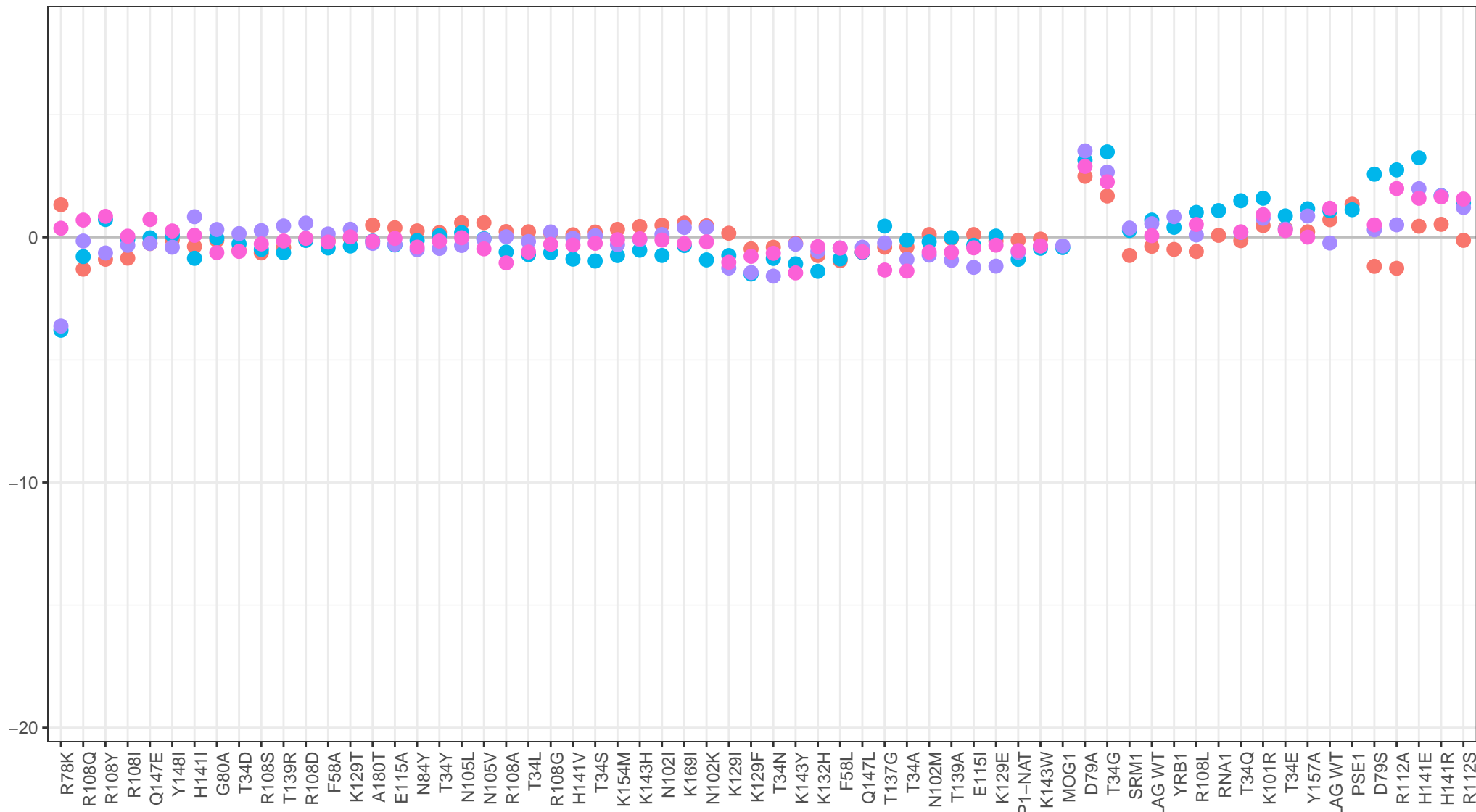


Mdm12p/Mmm1p/Mdm10p complex



mitochondrial pyruvate dehydrogenase complex

E-MAP score



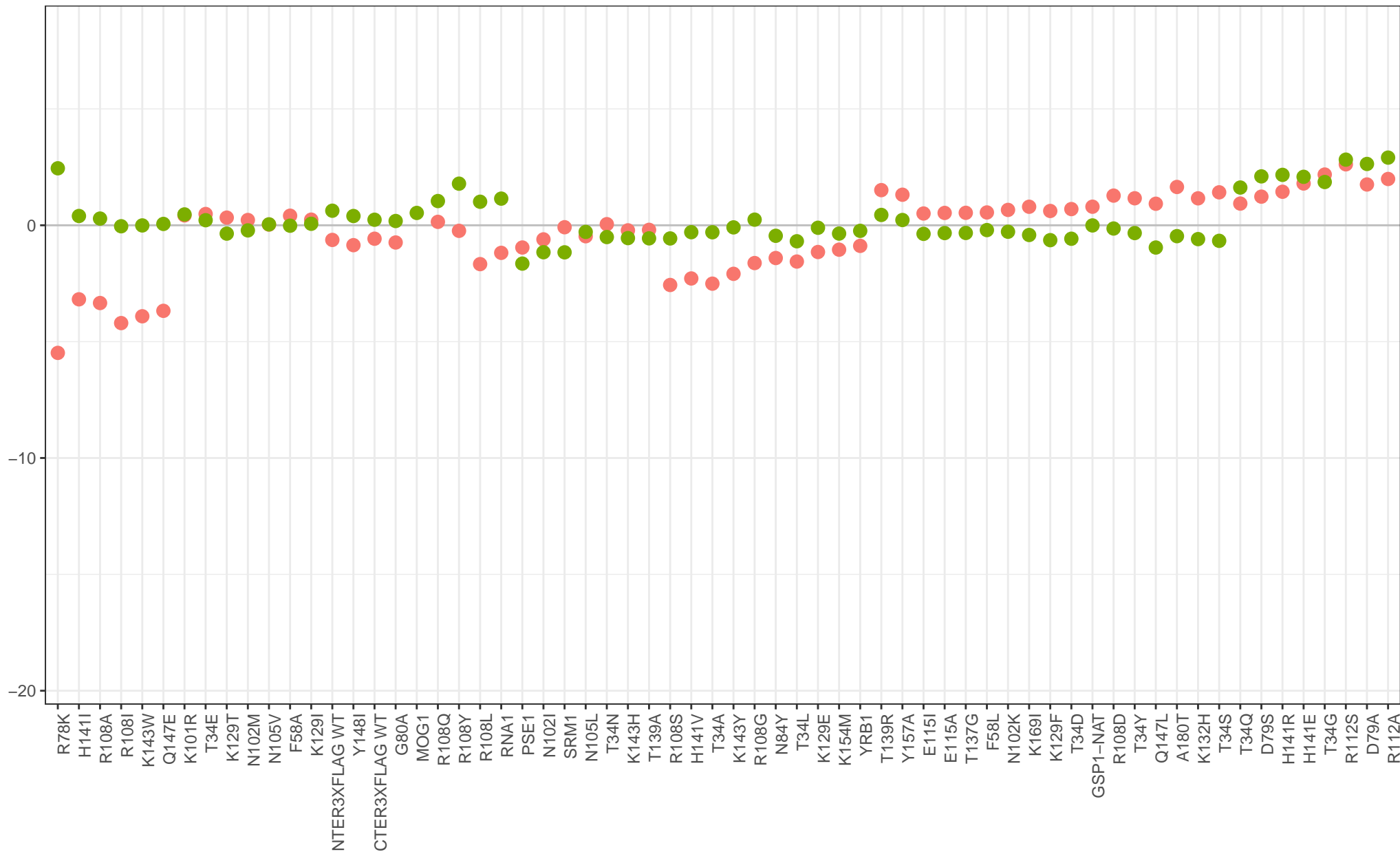
library gene

- PDB1
- PTC5
- PDX1
- PKP1
- PDA1
- LAT1
- LPD1

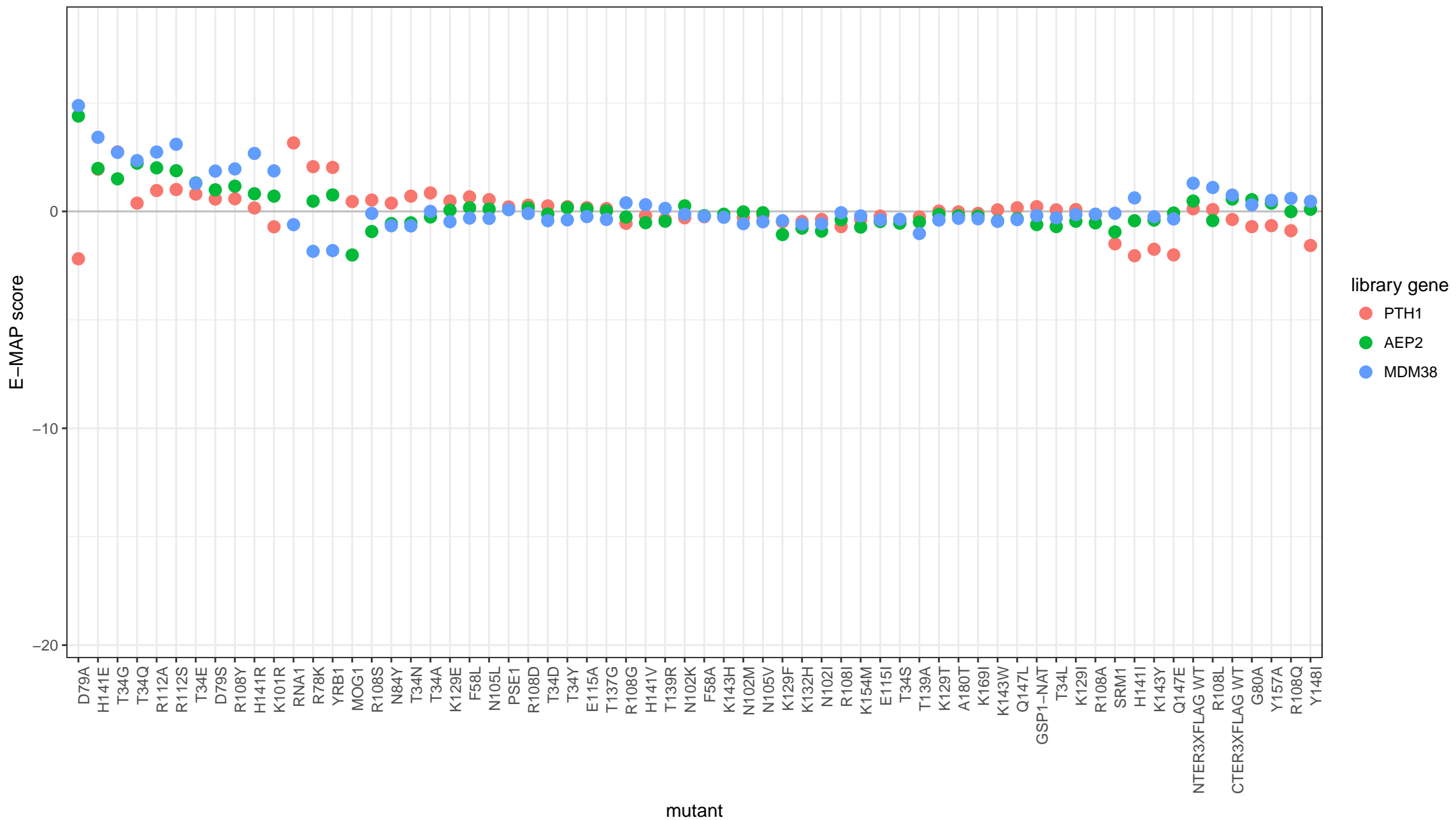
mutant

mitochondrial sorting and assembly machinery complex

E-MAP score

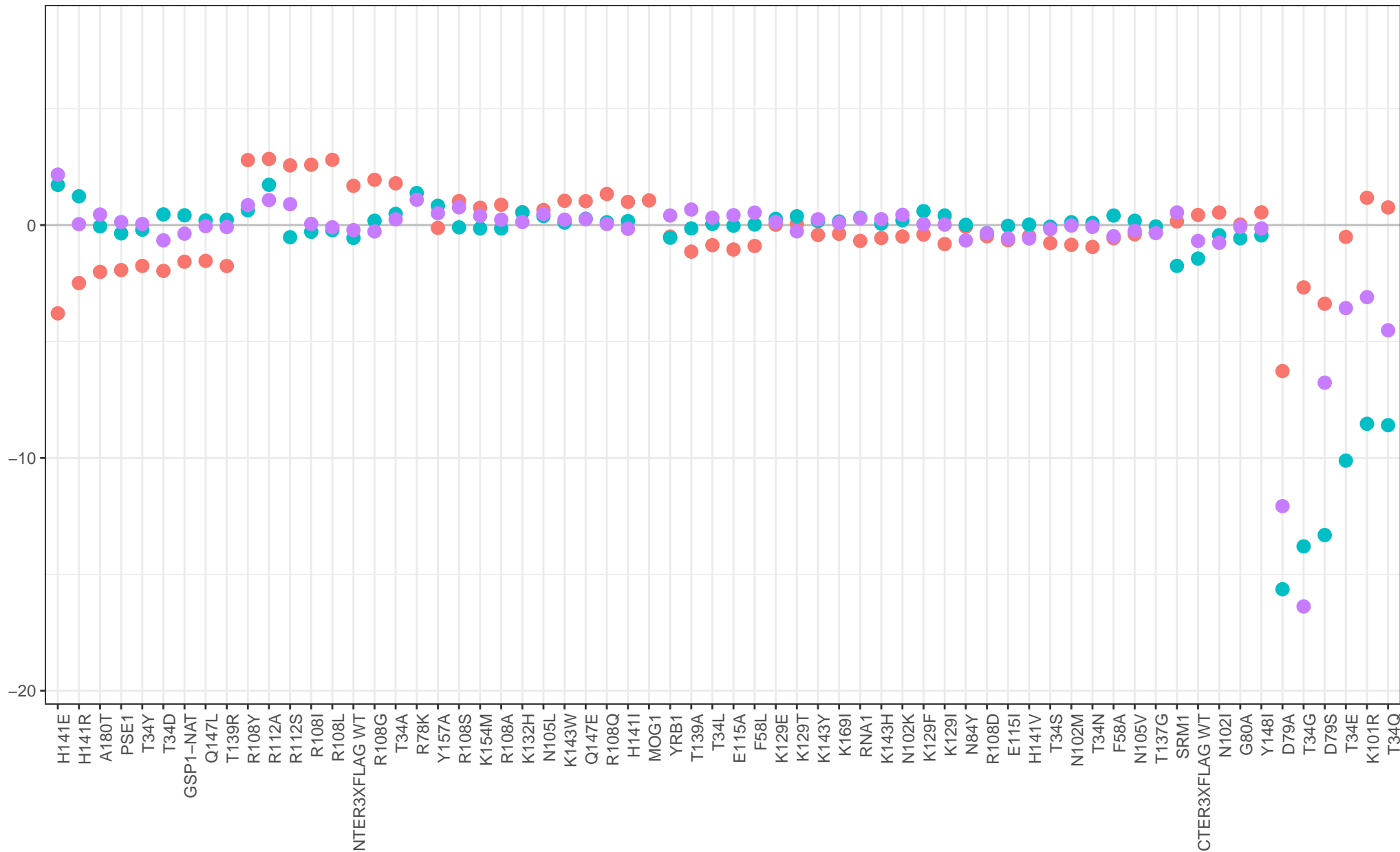


mitochondrial translation



mitotic checkpoint complex

E-MAP score

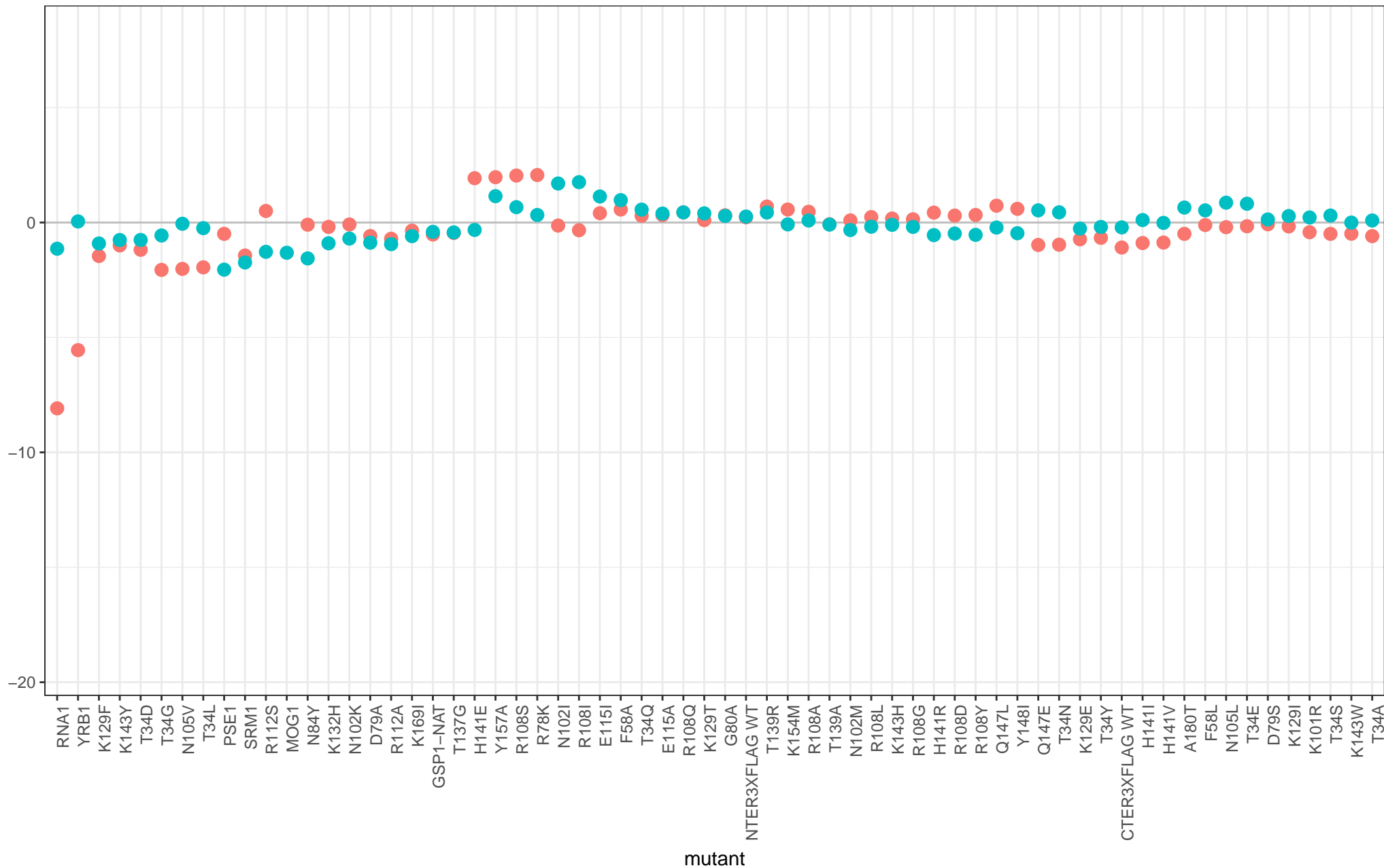


library gene

- BUB3
- CDC20
- MAD2
- MAD3

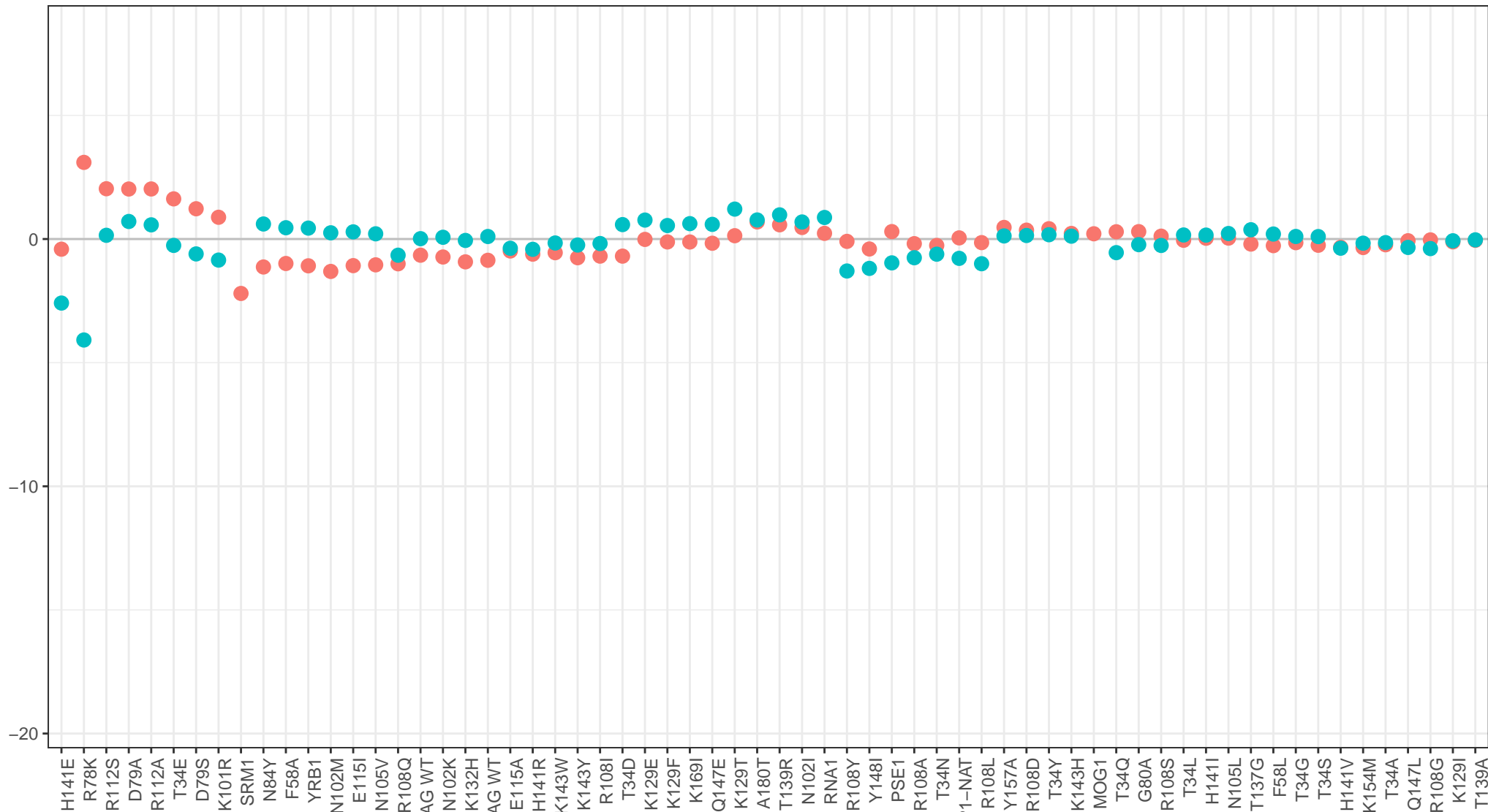
Mks1p/Rtg2p complex

E-MAP score



Mon1p/Ccz1p complex

E-MAP score



library gene

CCZ1

MON1

mutant

monopolin complex

E-MAP score

-20

-10

0

PSE1
H141R
G80A
Y148I
H141I
R108Q
K143H
K143Y
H141E
T34Q
R108G
GSP1-NAT
K129E
H141V
K143W
T139A
K169I
T34S
K129I
T137G
F58L
R108A
A180T
T34E
K129F
R112A
N102K
Q147E
R108Y
T34Y
MOG1
D79A
T34G
R112S
D79S
NTER3XFLAG WT
K101R
Y157A
R108L
T34A
CTER3XFLAG WT
R108I
R78K
T34D
K154M
SRM1
YRB1
E115A
R108D
T34N
F58A
K129T
R108S
Q147L
N84Y
N102M
T139R
N105V
E115I
RNA1
T34L
K132H
N102I
N105L

mutant

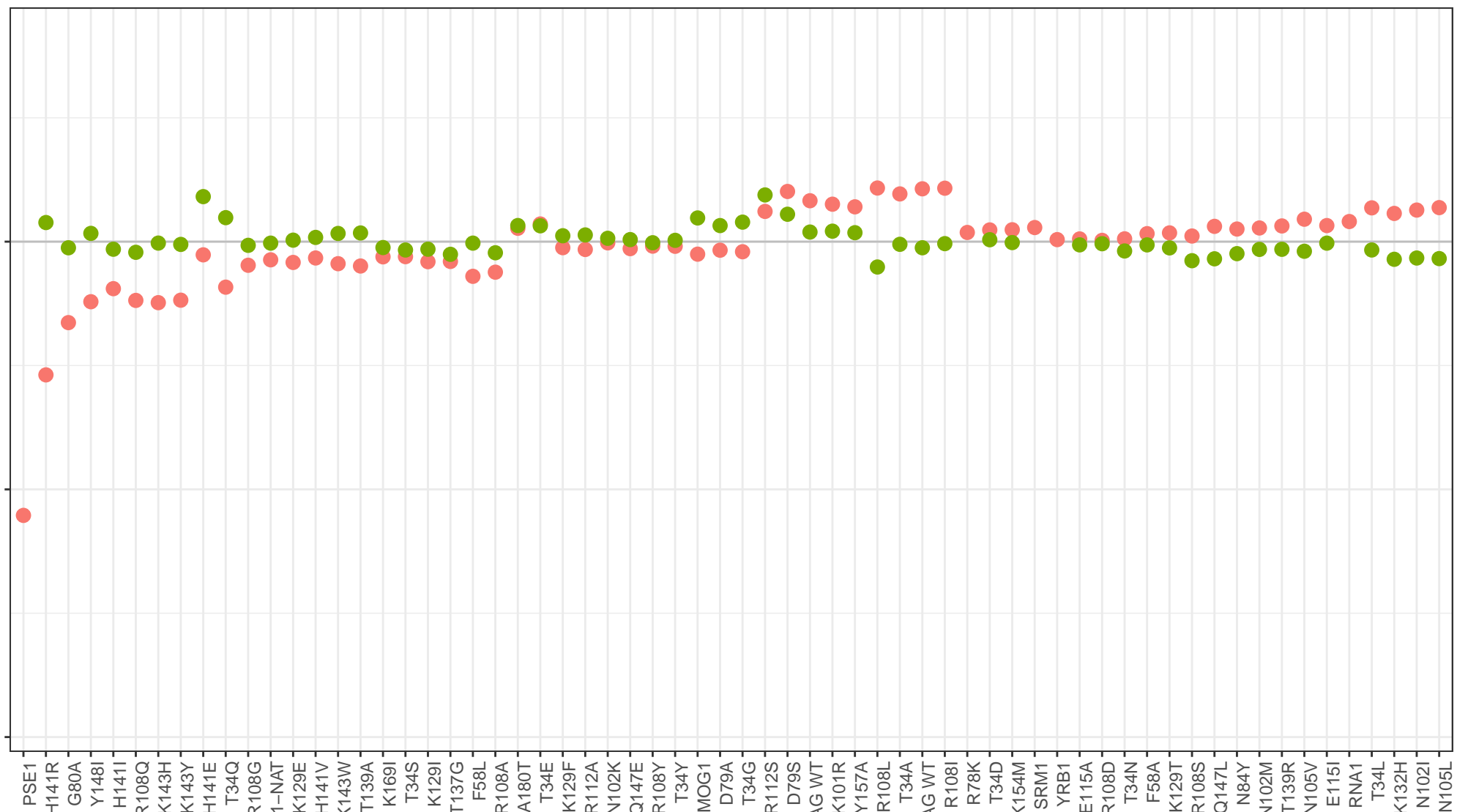
library gene

CSM1

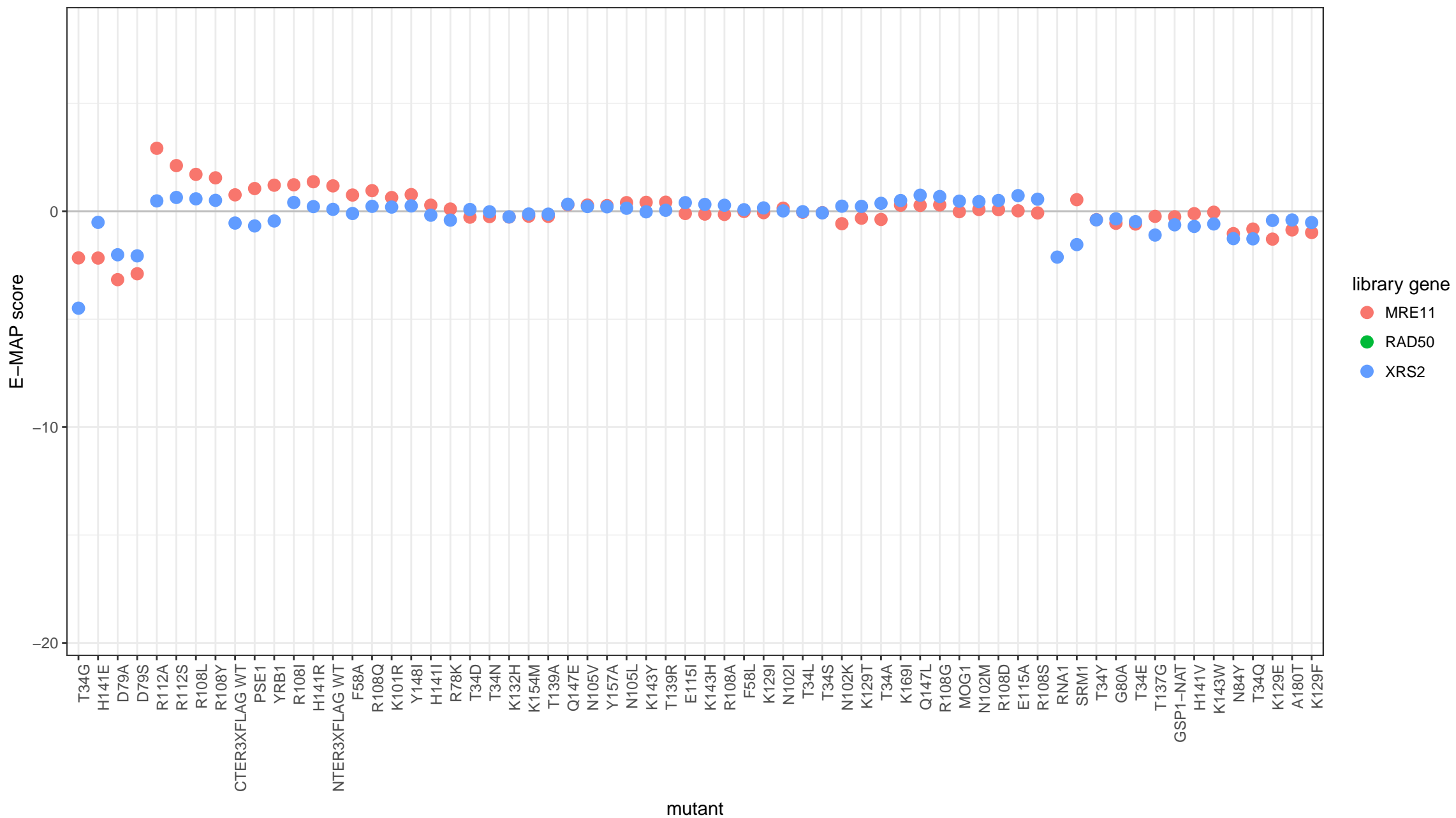
LRS4

HRR25

MAM1



MRX complex



MSH2p/MSH6p complex

E-MAP score

0

-10

-20

library gene

- MSH2
- MSH6

mutant

R108Q R108Y K132H N105L R108G NTER3XFLAG WT Y157A H141I SRM1 A180T K143W GSP1-NAT K129F N102M T139R R108D R108S R108A Y148I PSE1 RNA1 MOG1 T34D N102I K143Y YRB1 CTER3XFLAG WT T34Y Q147E T34S N102K N84Y T34A G80A R108I E115A K169I F58A N105V K154M K129E T137G H141V T34L F58L K143H K129I K129T T139A T34N E115I Q147L D79A R112S R78K T34G K101R T34E T34Q D79S R112A R108L H141E H141R

NatC complex

E-MAP score

-20

-10

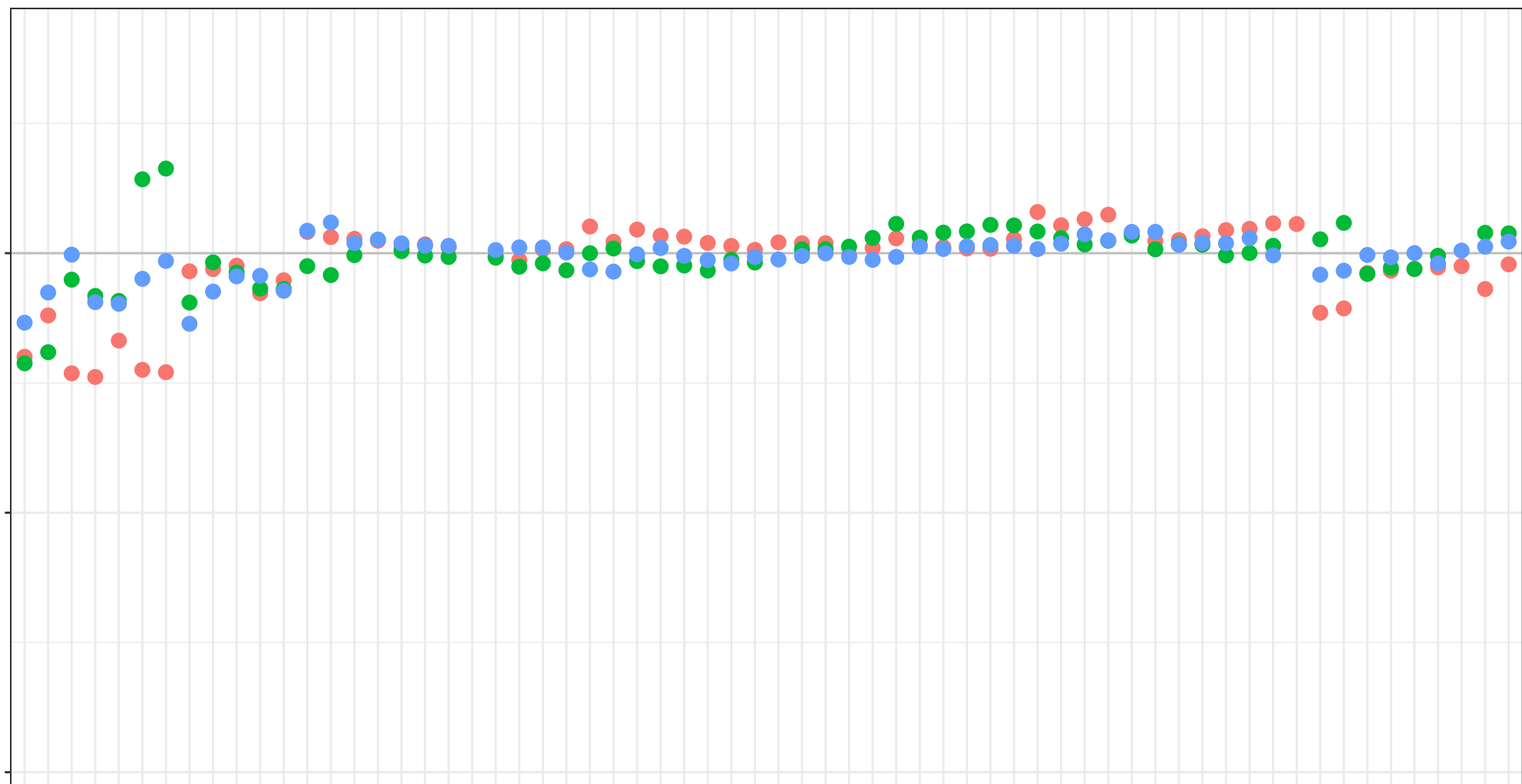
0

R112A
R112S
H141E
H141R
R108Y
D79A
R78K
R108L
K101R
R108Q
CTER3XFLAG WT
NTER3XFLAG WT
N84Y
T34N
K129E
PSE1
T34S
F58A
K143Y
MOG1
N105V
Q147E
R108A
T34L
H141V
T34A
N102K
F58L
K169I
R108S
N102I
R108I
RNA1
K129F
K154M
N105L
R108D
K129T
K143H
T139R
T34E
A180T
E115A
K129I
Q147L
E115I
G80A
K143W
N102M
GSP1-NAT
T34Y
T137G
T139A
T34D
YRB1
T34G
T34Q
Y148I
K132H
R108G
H141I
SRM1
D79S
Y157A

mutant

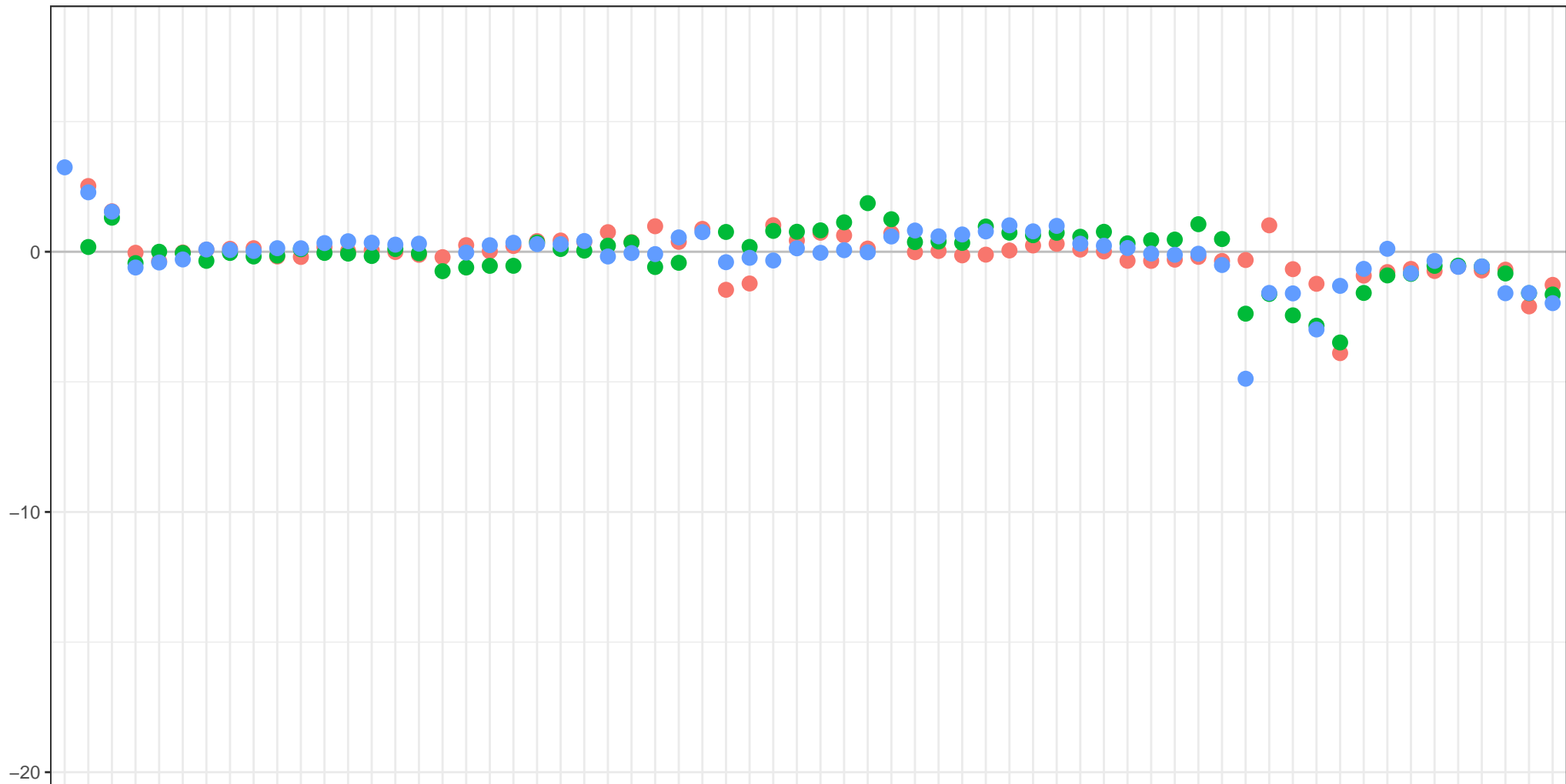
library gene

MAK3
MAK10
MAK31



Nonsense-mediated mRNA decay pathway complex

E-MAP score



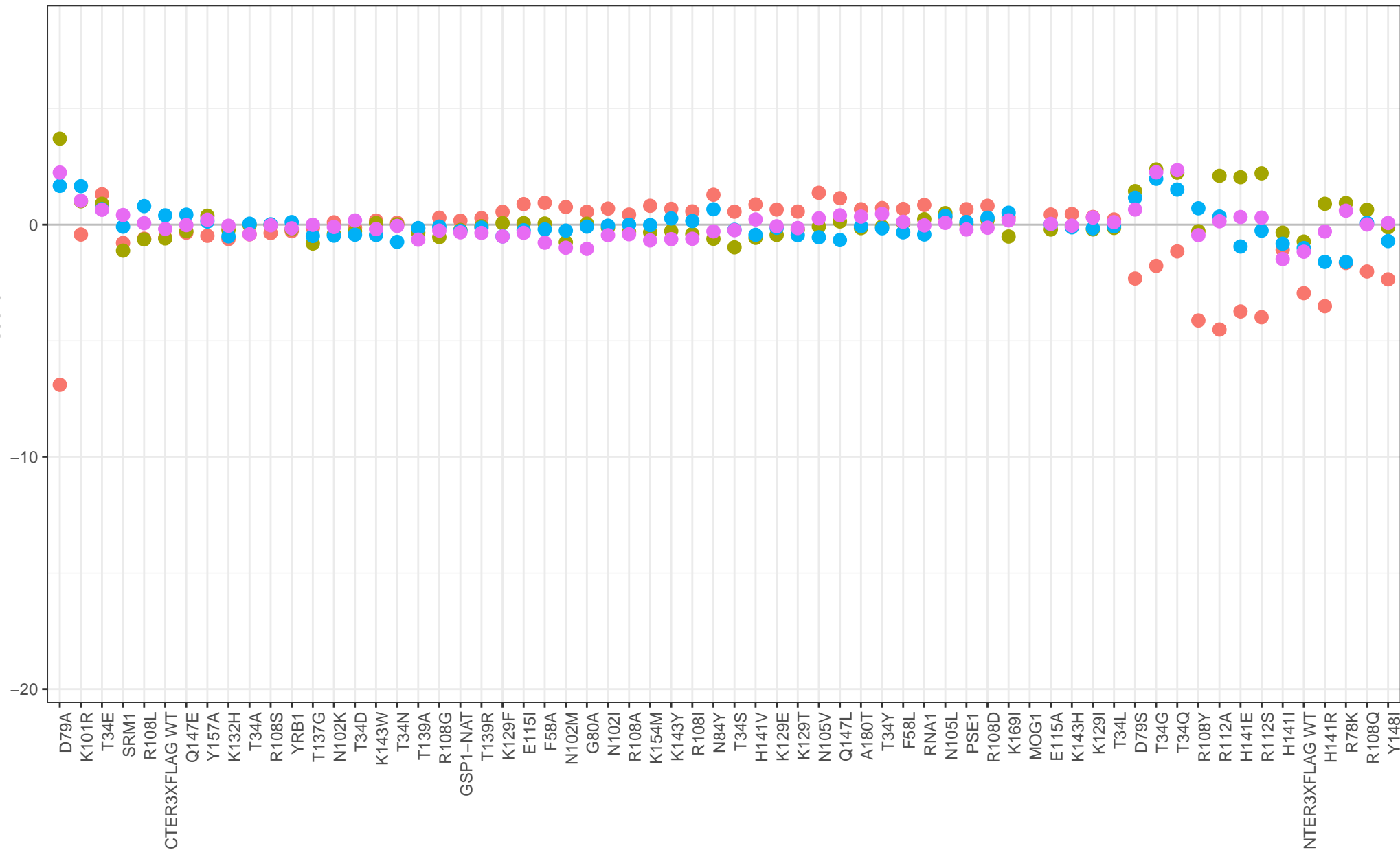
library gene

- UPF3
- NAM7
- NMD2

mutant

NuA3 histone acetyltransferase complex

E-MAP score



library gene

- EAF6
- NTO1
- TAF14
- SAS3
- YNG1

NuA4 histone acetyltransferase complex

E-MAP score

-20

-10

0

H141E R112S R108Y R112A R78K T34Q N105L R108S MOG1 R108G H141I R108L H141R Y148I NTER3XFLAG WT R108Q PSE1 SRM1 T34D E115A N84Y Q147E R108A T137G T139A T34A K132H K143W N102K T34L K129F K129I R108D T34Y F58L K129T H141V G80A T139R F58A N102I R108I N105V K154M K129E K143Y E115I GSP1-NAT K169I T34N N102M T34S K143H Q147L A180T T34E K101R CTER3XFLAG WT Y157A YRB1 D79A RNA1 D79S T34G

mutant

library gene

- EAF3
- EAF6
- EAF7
- EAF1
- YAF9
- YNG2
- TRA1
- SWC4
- ESA1
- EPL1
- EAF5
- ACT1
- ARP4

Nuclear exosome complex

E-MAP score

-20

-10

0

F58A F58L K101R D79A R78K K129T R108G N102I T34Y K169I R108A K143Y R108S E115I N84Y T34D A180T T34N T137G T34S K132H K154M T139A PSE1 K129I GSP1-NAT N102K H141R MOG1 K143W H141V T34A R108I T34E H141I H141E R108L T34G R112S T34Q R112A R108Q R108Y Y157A R108D N102M T139R D79S Q147E K129E E115A K129F K143H T34L Y148I N105L Q147L RNA1 SRM1 YRB1 CTER3XFLAG WT NTER3XFLAG WT G80A N105V

library gene

- LRP1
- RRP6
- SKI6
- RRP46
- RRP45
- RRP43
- RRP42
- RRP40
- RRP4
- MTR3
- CSL4
- DIS3

Nucleosomal protein complex

E-MAP score

0

-10

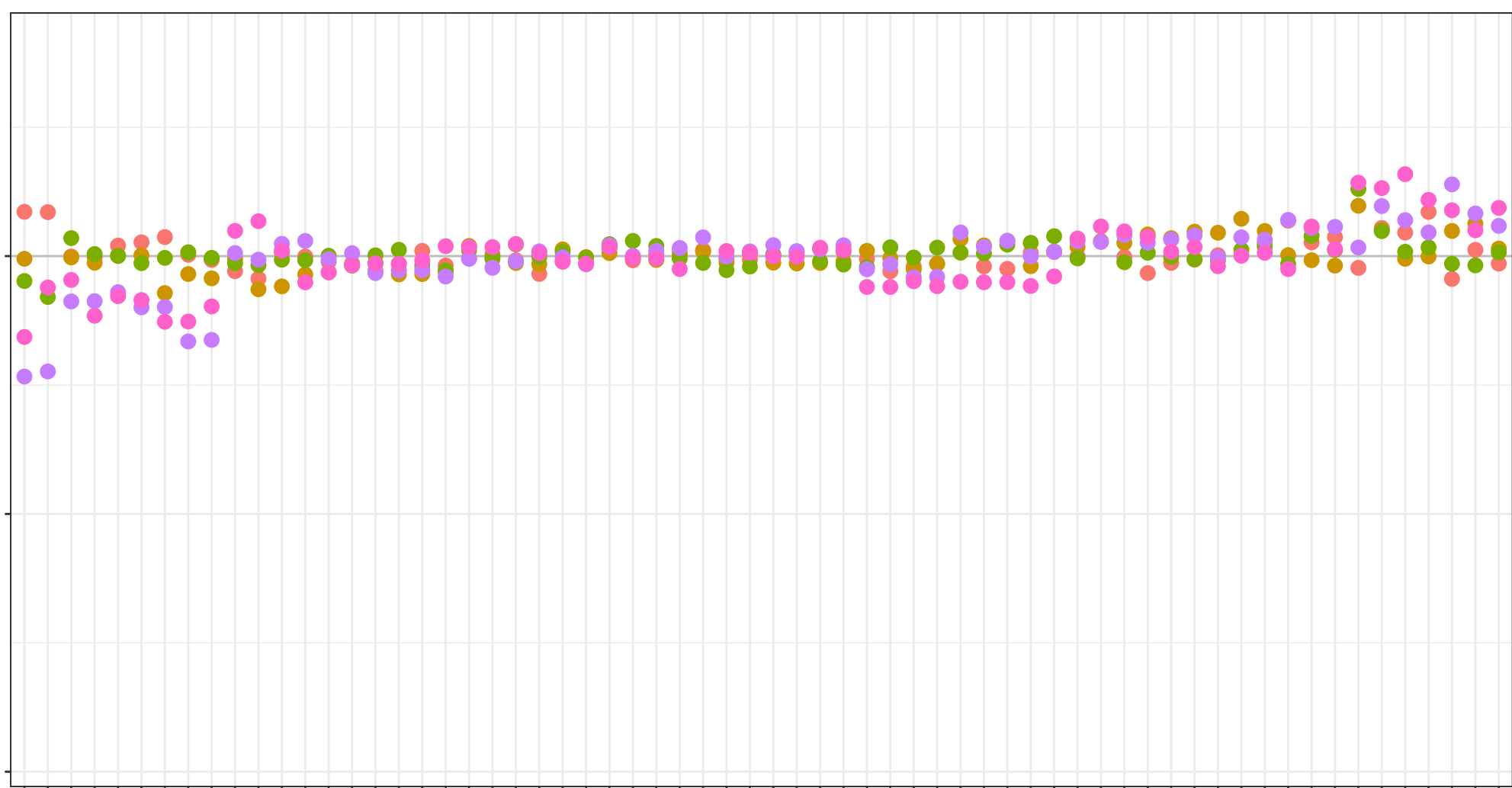
-20

R112A R112S R108S Y148I R108A R108Q R108R R108G R108Y A180T H141E T34A N105L H141I K129E GSP1-NAT K129F F58L N102M K143W F58A N105V N84Y E115A R108D K132H K143Y T34D K129I YRB1 E115I Q147L K129T T139R N102K T34Y T139A T34L K169I T34S RNA1 T137G T34N H141V K154M G80A PSE1 Q147E N102I R108I R108L K143H MOG1 T34G NTER3XFLAG WT SRM1 Y157A D79A K101R T34E T34Q R78K CTER3XFLAG WT D79S

mutant

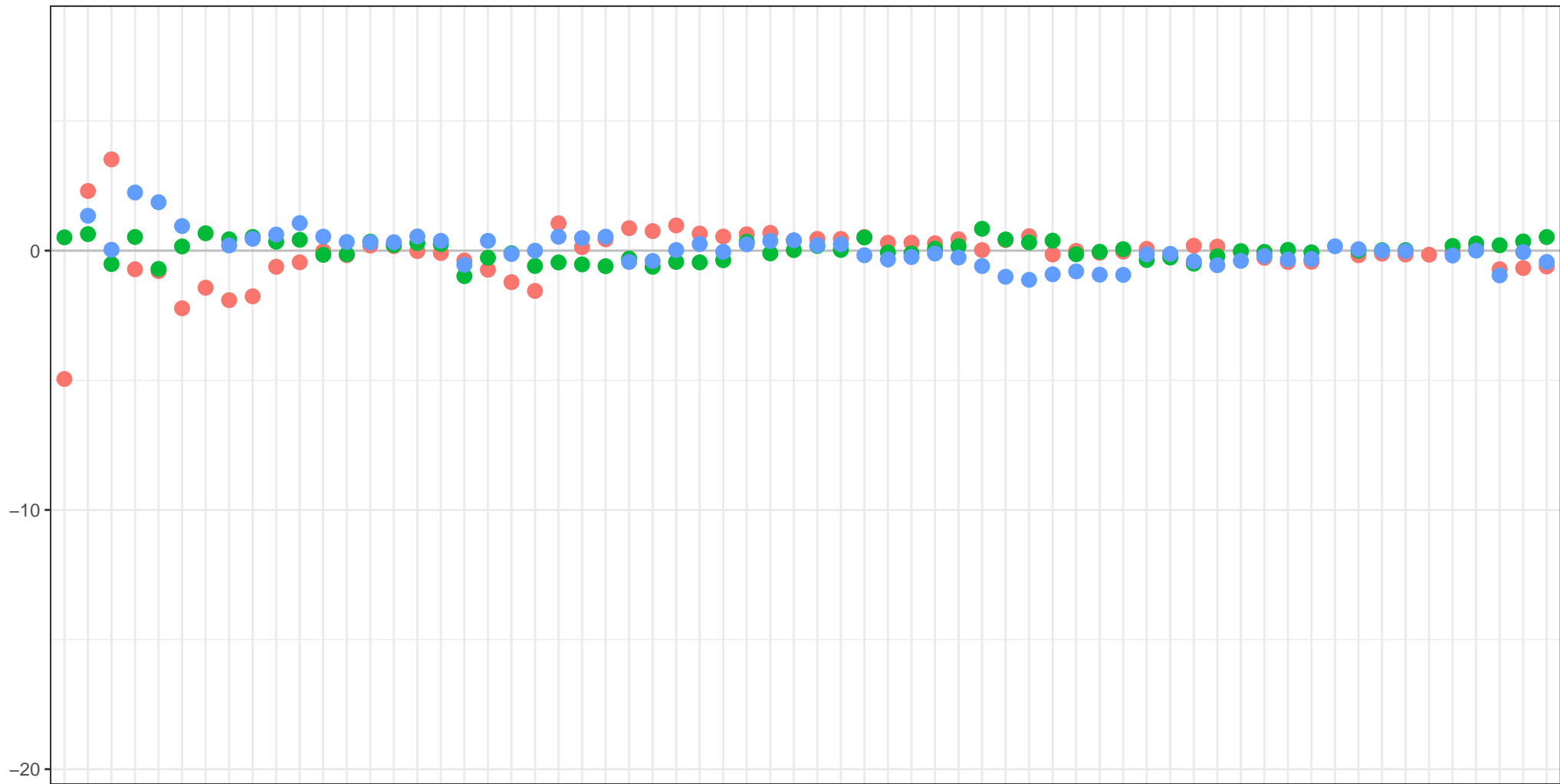
library gene

HHF2
HHT1
HHT2
HTB2
HTA2
HTB1
HHF1
HTA1



nucleotide-excision repair factor 1 complex

E-MAP score



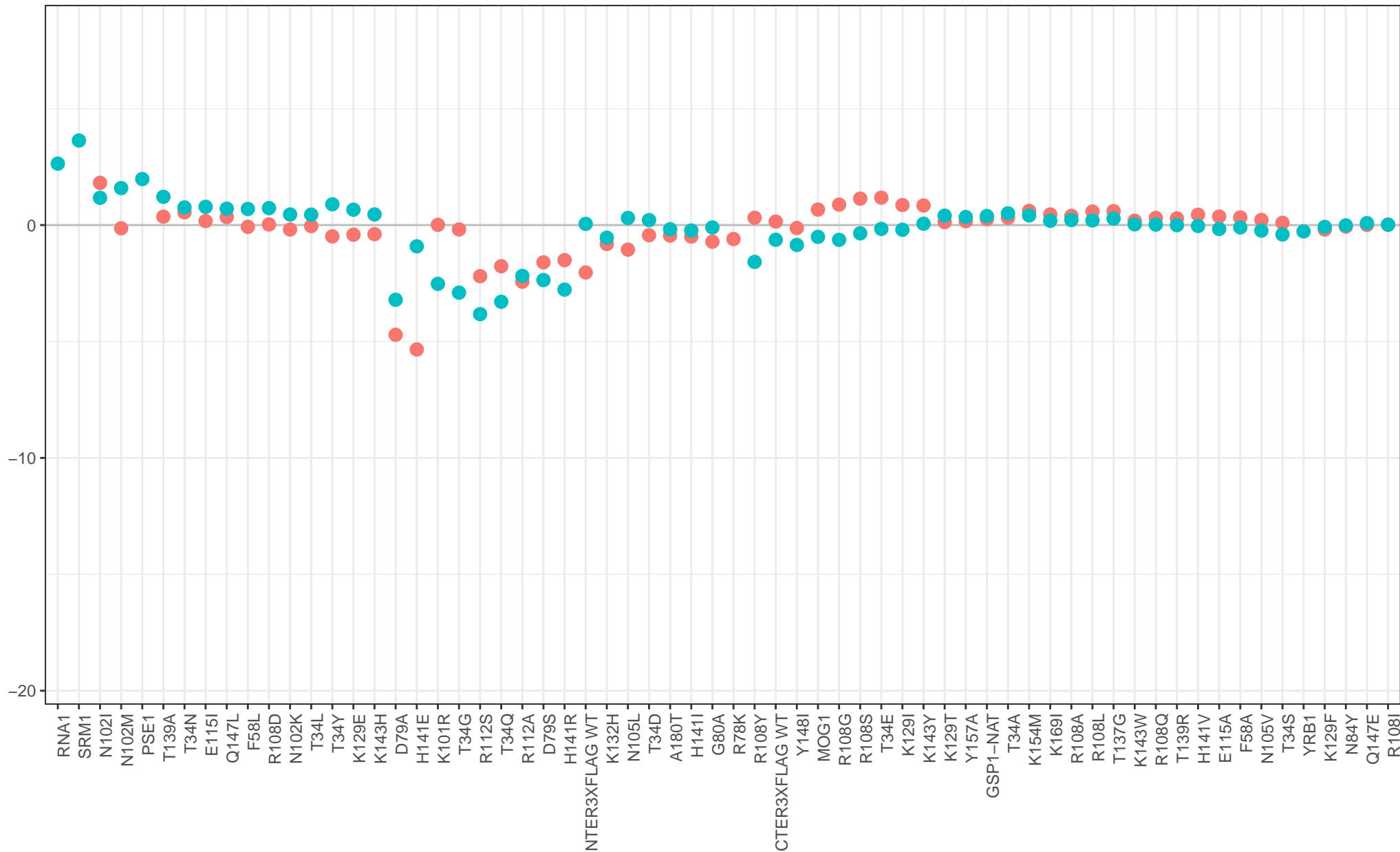
library gene

- RAD1
- RAD10
- RAD14

mutant

nucleotide–excision repair factor 2 complex

E-MAP score



library gene

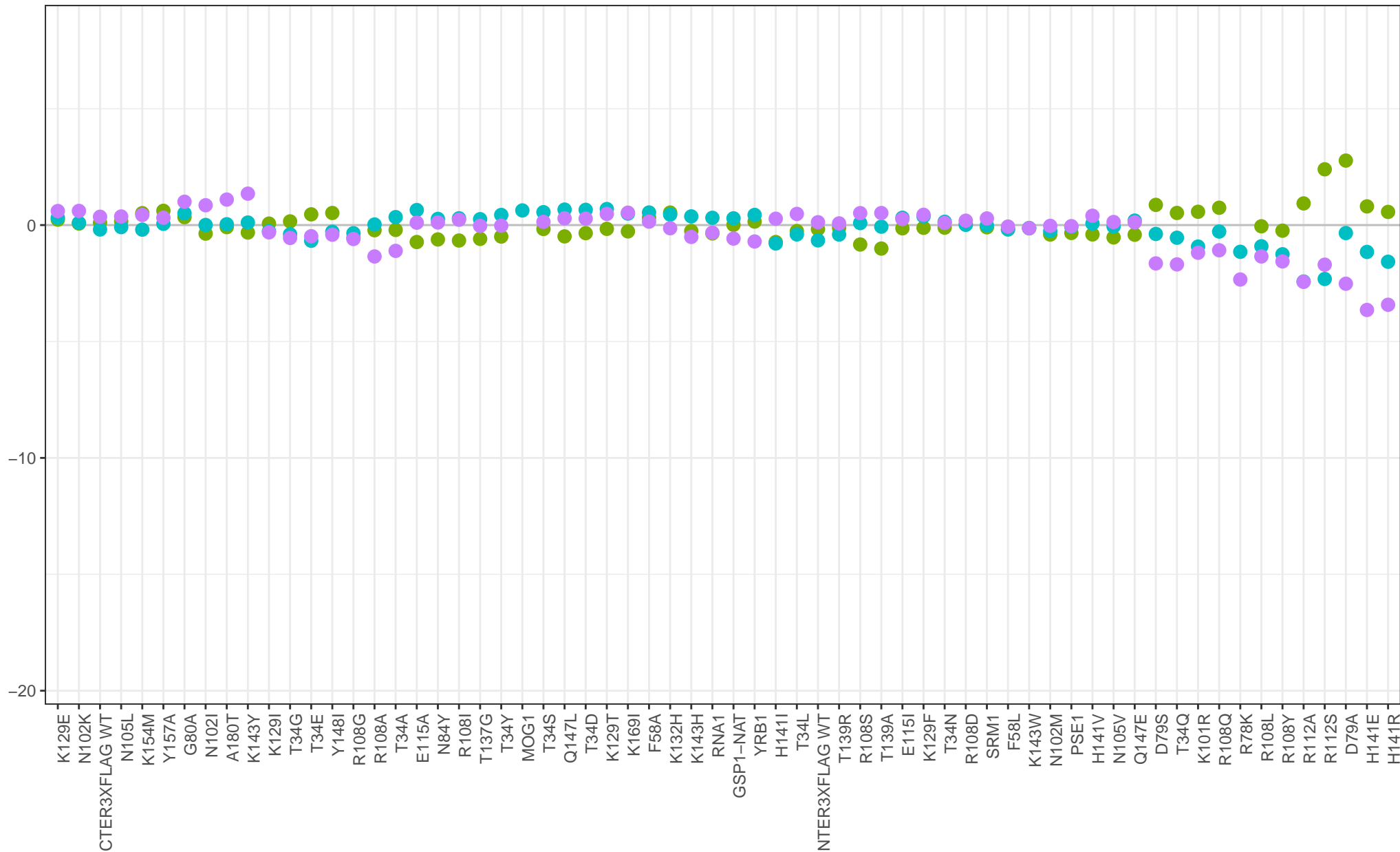
● RAD23

● RAD4

mutant

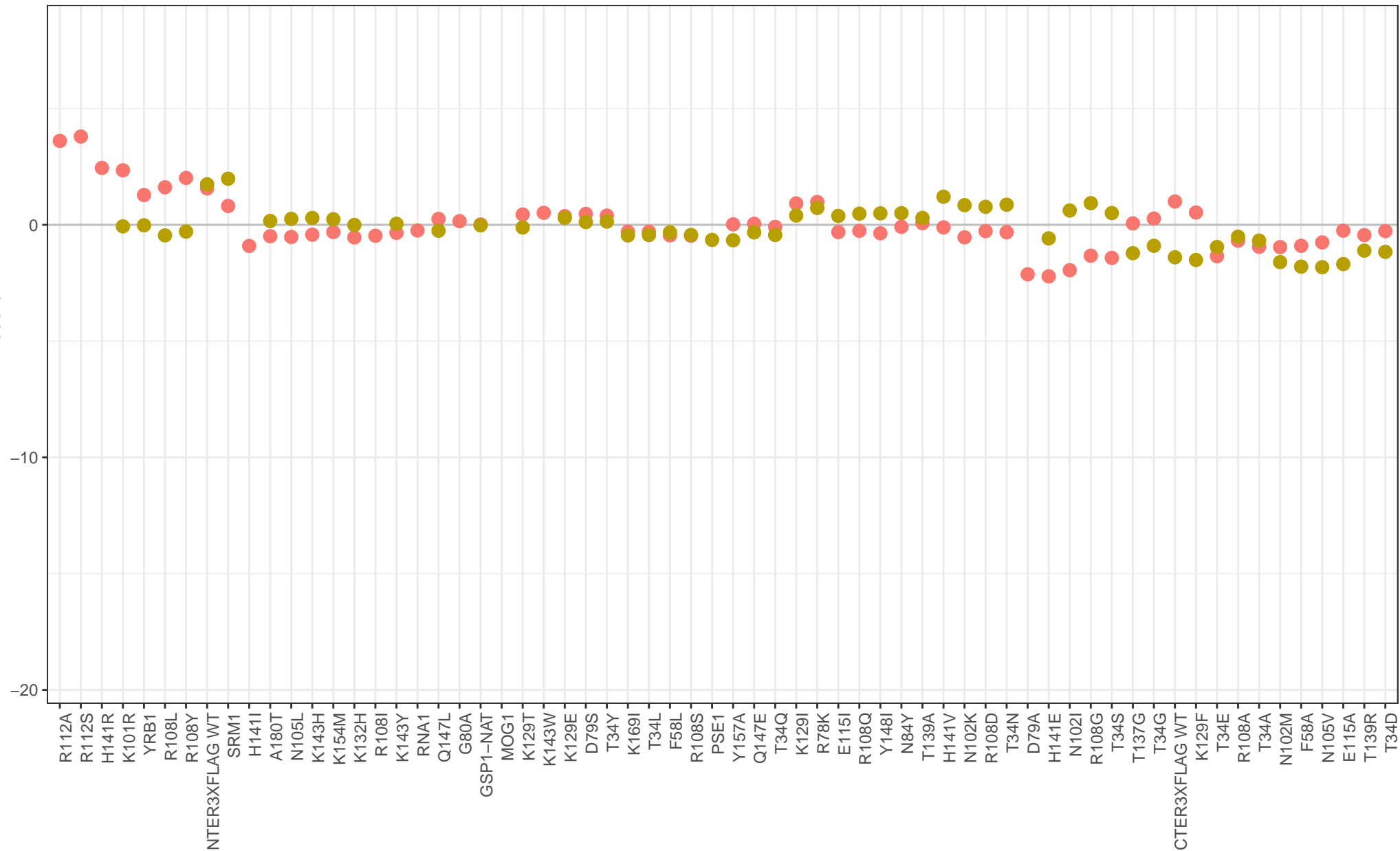
nucleotide–excision repair factor 4 complex

E-MAP score



OCA complex

E-MAP score



library gene

- SIW14
- OCA1
- YHL029C
- YDR067C
- OCA2
- YCR095C

oligosaccharide metabolic process

E-MAP score

-20

-10

0

mutant

library gene

- TPS2
- SNF5
- SNF6
- TPS1
- SWI3
- TSL1

R108Y R108A R108G K132H RNA1 T137G T34L K129I R108S N102M R108I A180T Q147E R108D F58A N105V CTER3XFLAG WT K129T NTER3XFLAG WT Q147L MOG1 Y157A K154M N84Y K129F G80A Y148I K143W GSP1-NAT K129E N102I K143Y N102K PSE1 H141V T139R K169I R108Q E115I E115A N105L T139A K143H T34Y R108L T34S T34N YRB1 H141I F58L T34D R78K R112S D79A H141E R112A SRM1 H141R D79S T34A T34G T34Q K101R T34E

oligosaccharyl transferase complex

E-MAP score

-20

-10

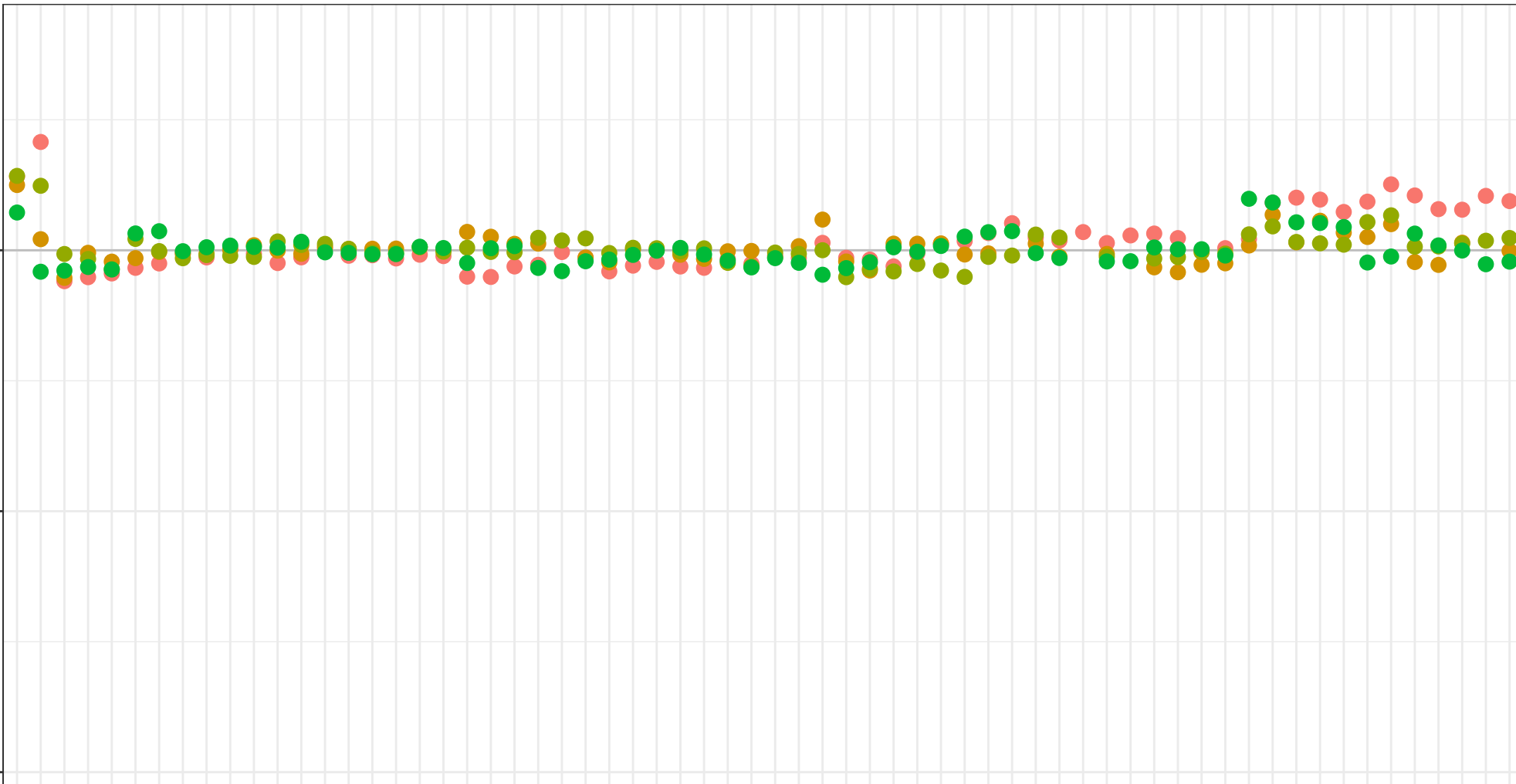
0

D79A T34G T139A K129F Q147L K143W T34Y K132H T34L K169I N105L H141I Y148I R108Q T34D A180T N105V G80A K129T E115A K129I T137G K143H PSE1 T34N F58A GSP1-NAT N102K F58L K129E E115I K154M H141V T34S Q147E K143Y R108S N102M R108D Y157A R108I R108L YRB1 R108G T34A MOG1 N84Y SRM1 CTER3XFLAG WT R108A N102I T139R T112A R78K R112S H141R R108Y D79S H141E K101R NTER3XFLAG WT T34E RNA1 T34Q

library gene

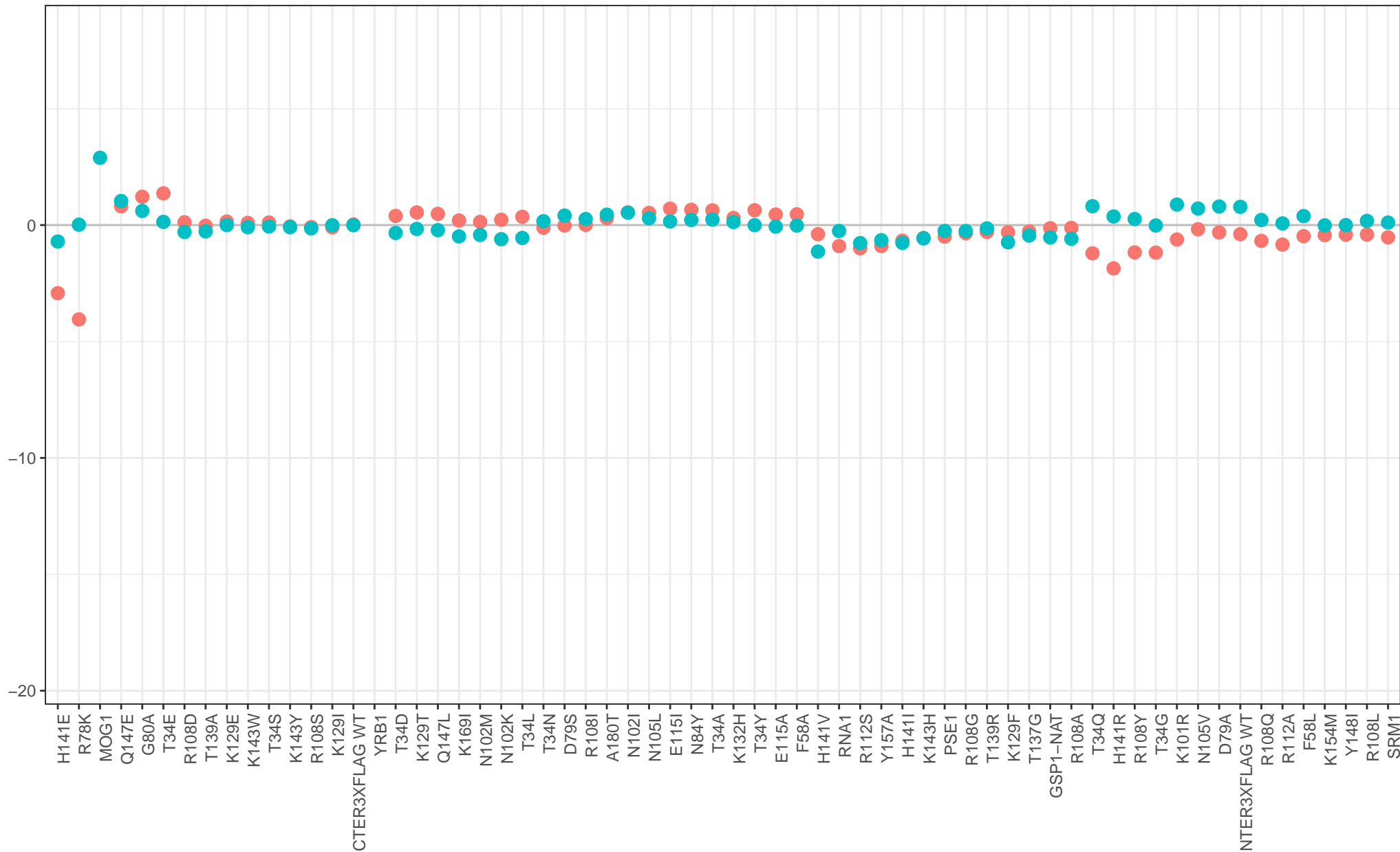
- OST3
- OST4
- OST5
- OST6
- WBP1
- SWP1
- STT3
- OST1
- OST2

mutant



other DNA repair complexes

E-MAP score



library gene

● RAD55

● RAD57

mutant

polarisome complex

E-MAP score

0

-10

-20

R78K N102K R108L R108A Y148I H141I H141R R108Y R108Q R108G R108S T139A E115I F58A K143W PSE1 K132H YRB1 Y157A GSP1-NAT K154M Q147L T137G T34N K143H K143Y G80A K169I N84Y T34L T34S T34Y N105L N102M F58L H141V K129E CTER3XFLAG WT K129T N105V RNA1 NTER3XFLAG WT T34A K129I R108D R108I MOG1 A180T E115A T139R K129F T34D N102I Q147E SRM1 H141E K101R R112A R112S D79A T34G T34Q D79S T34E

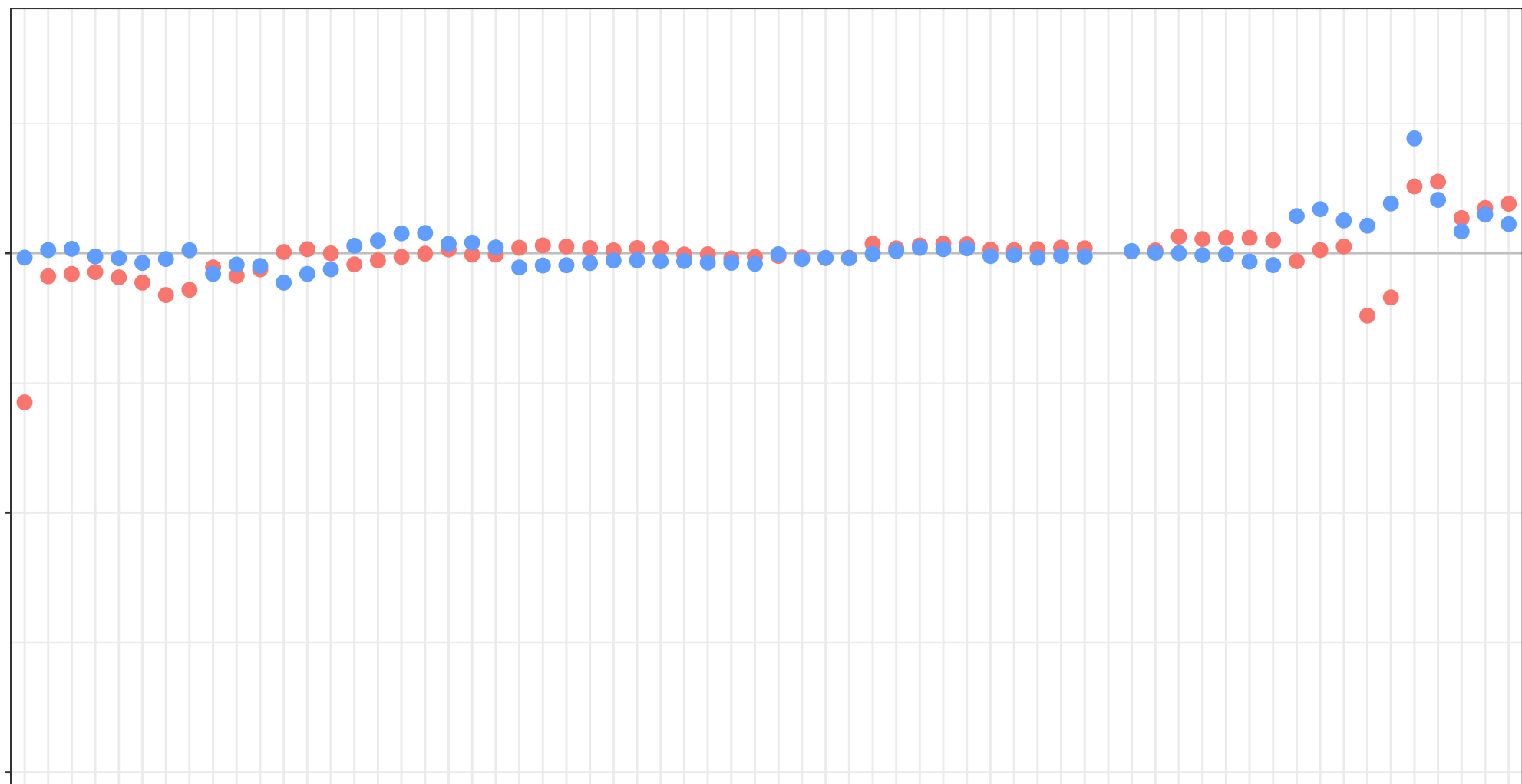
mutant

library gene

SPA2

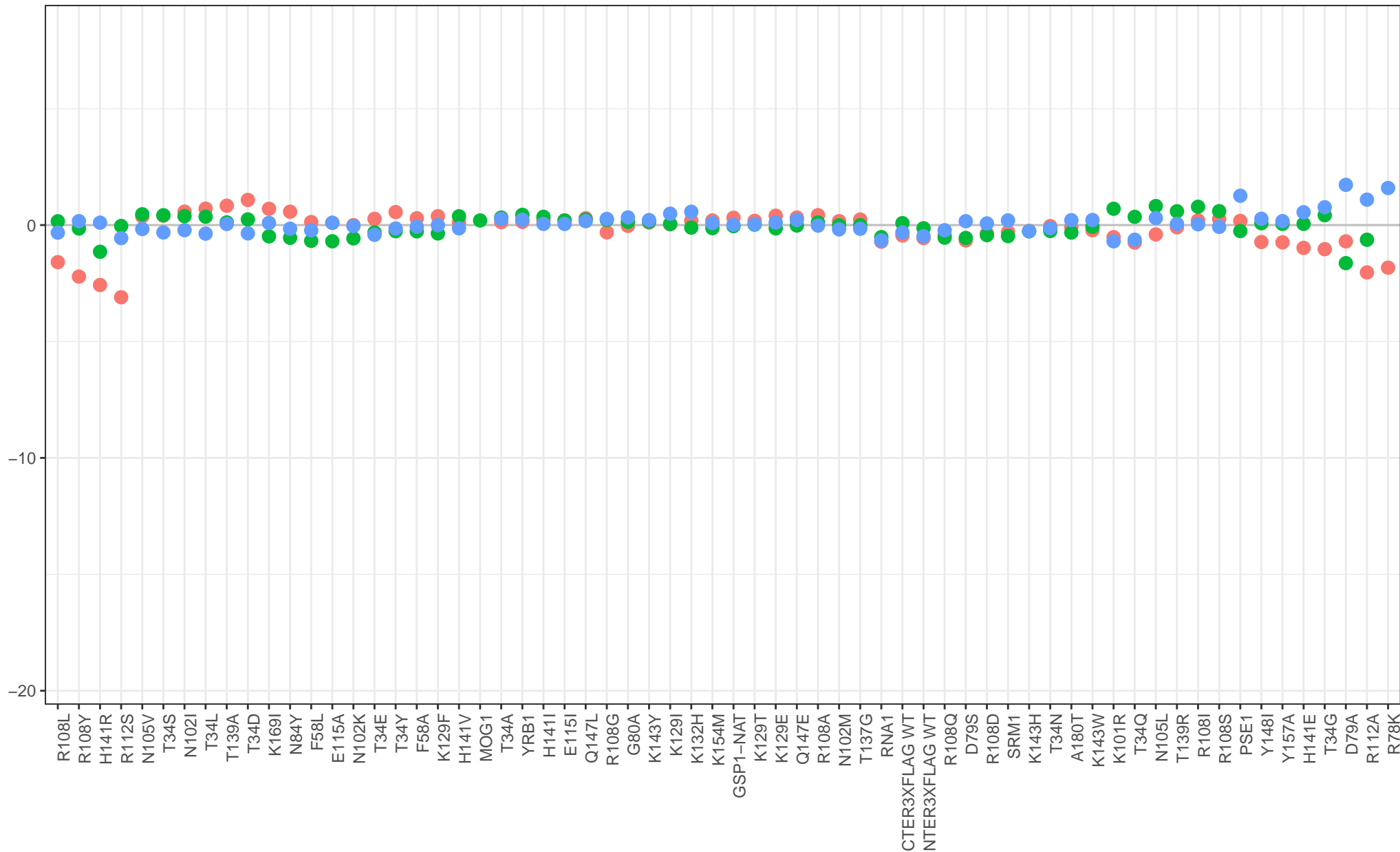
BUD6

PEA2



Polzeta-Rev1p complex

E-MAP score

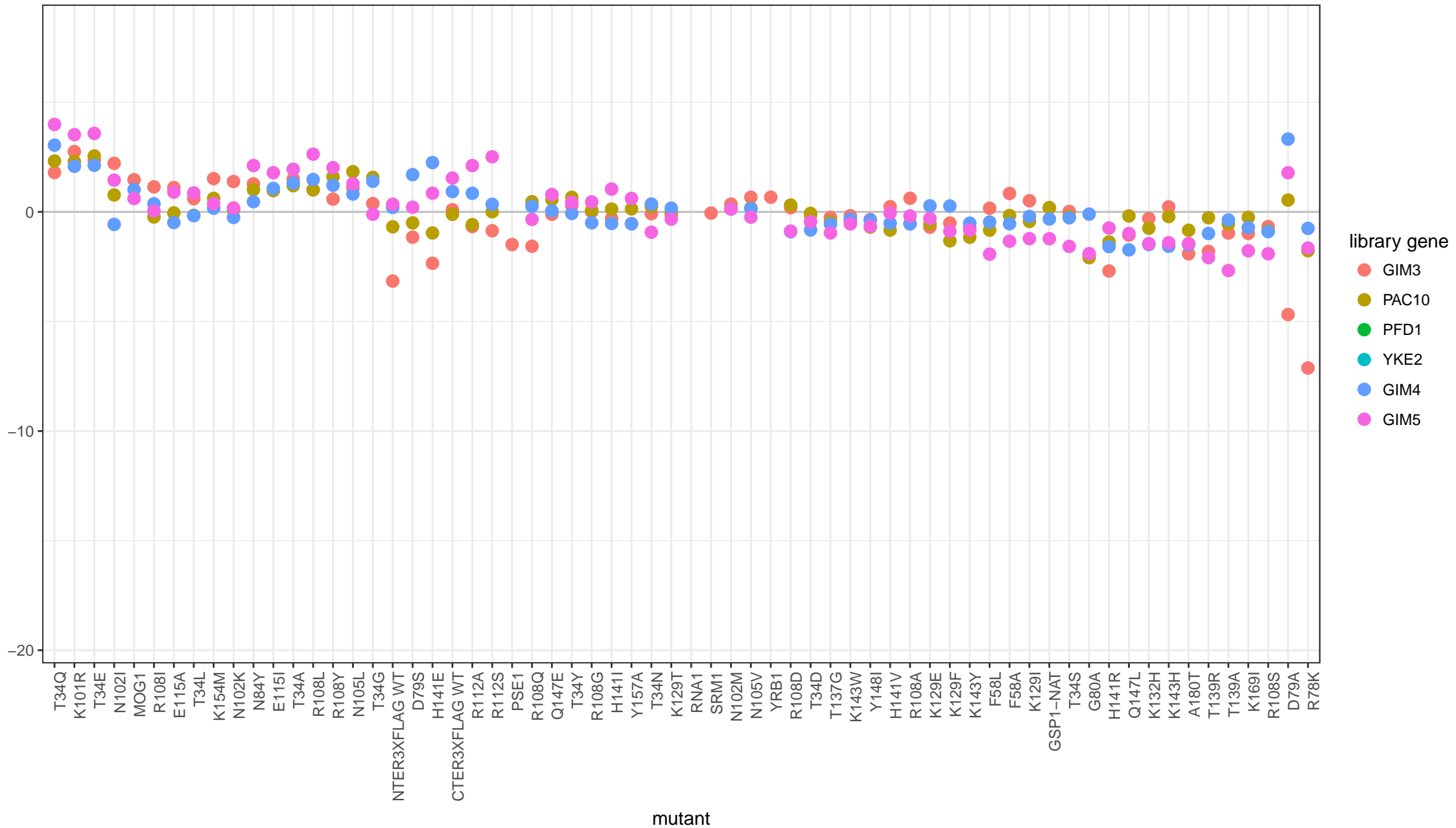


library gene

- REV1
- REV3
- REV7

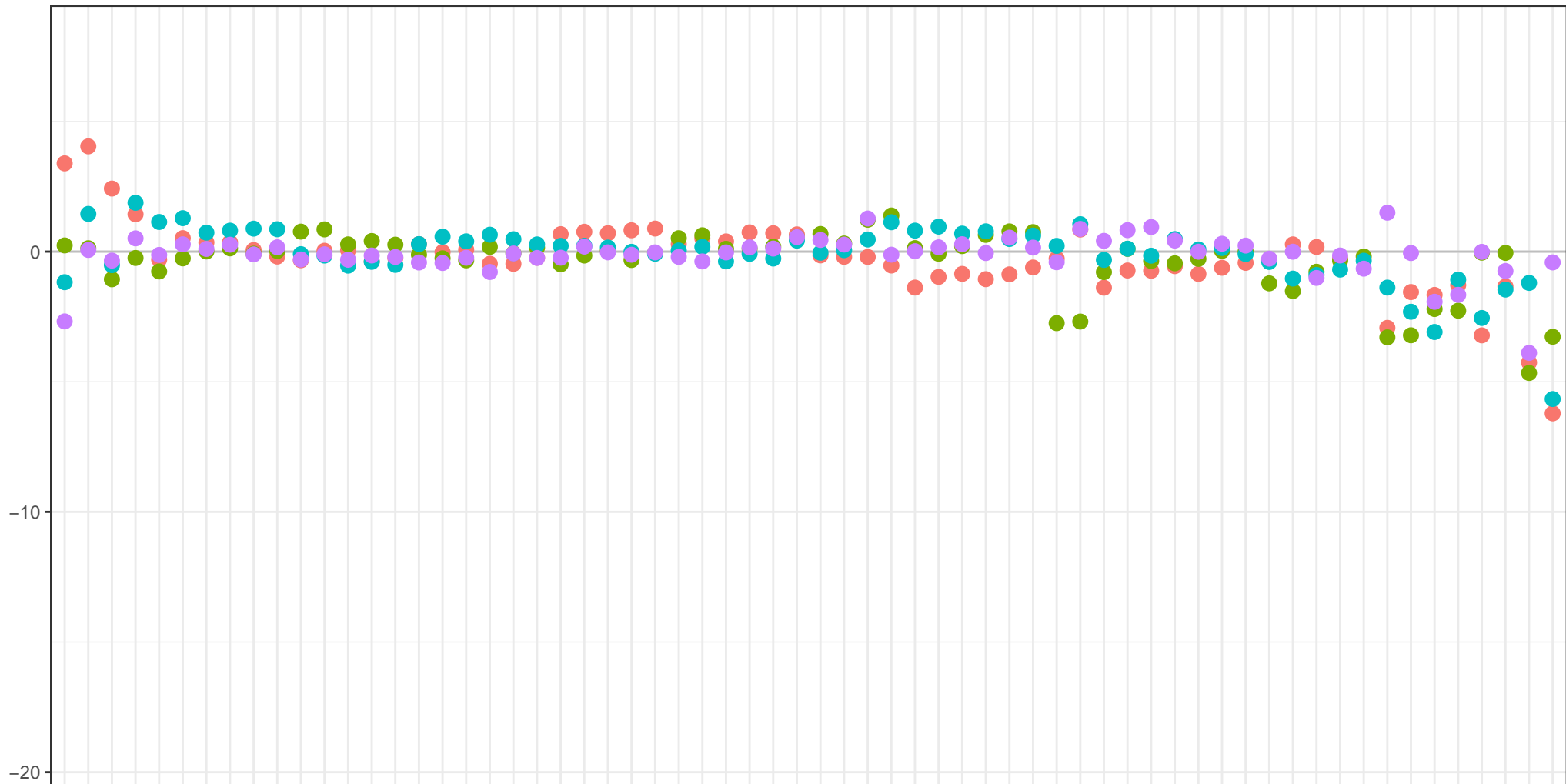
prefoldin complex

E-MAP score



protein kinase CK2 complex

E-MAP score

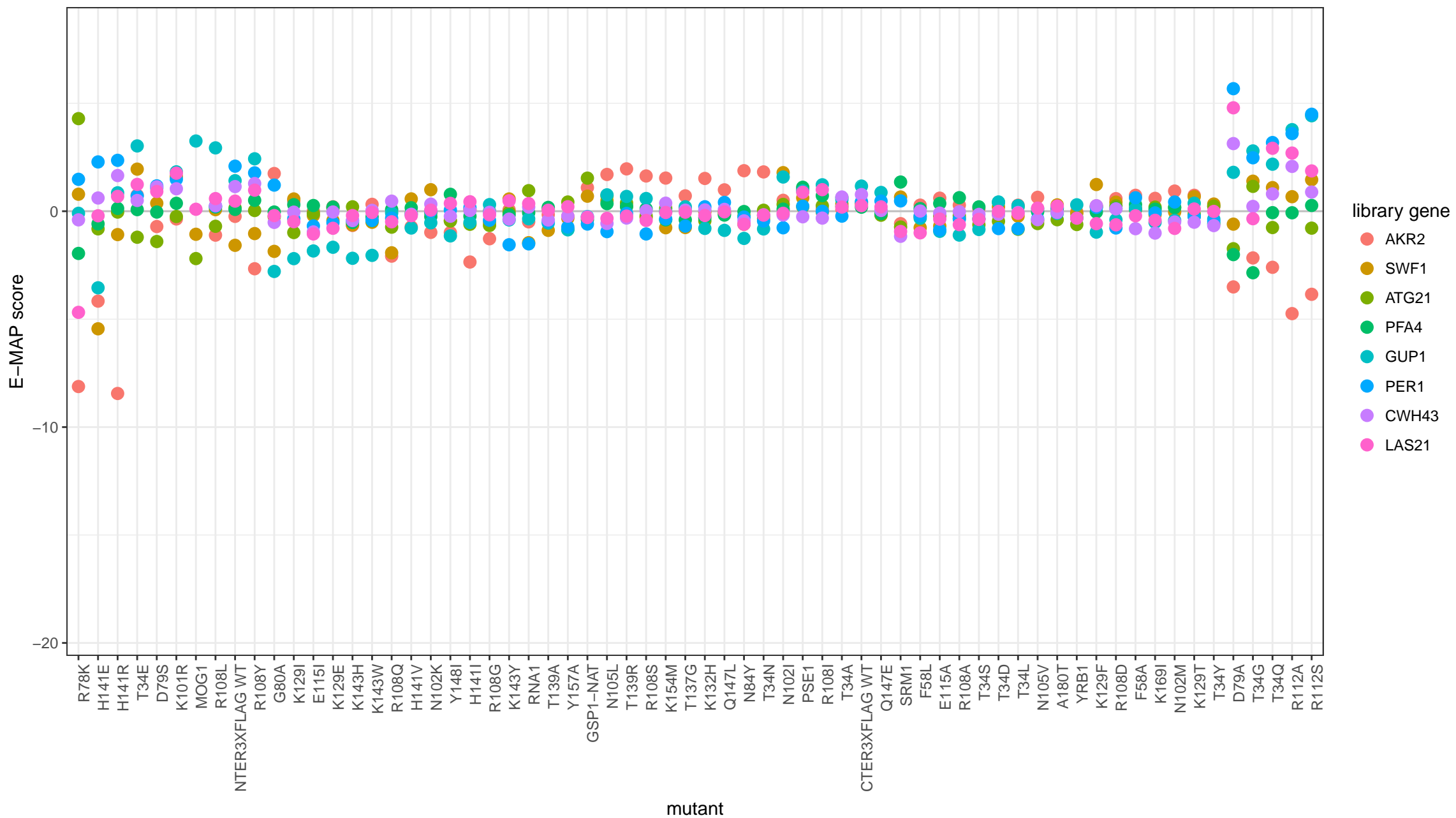


library gene

- CKB1
- CKA1
- CKA2
- CKB2

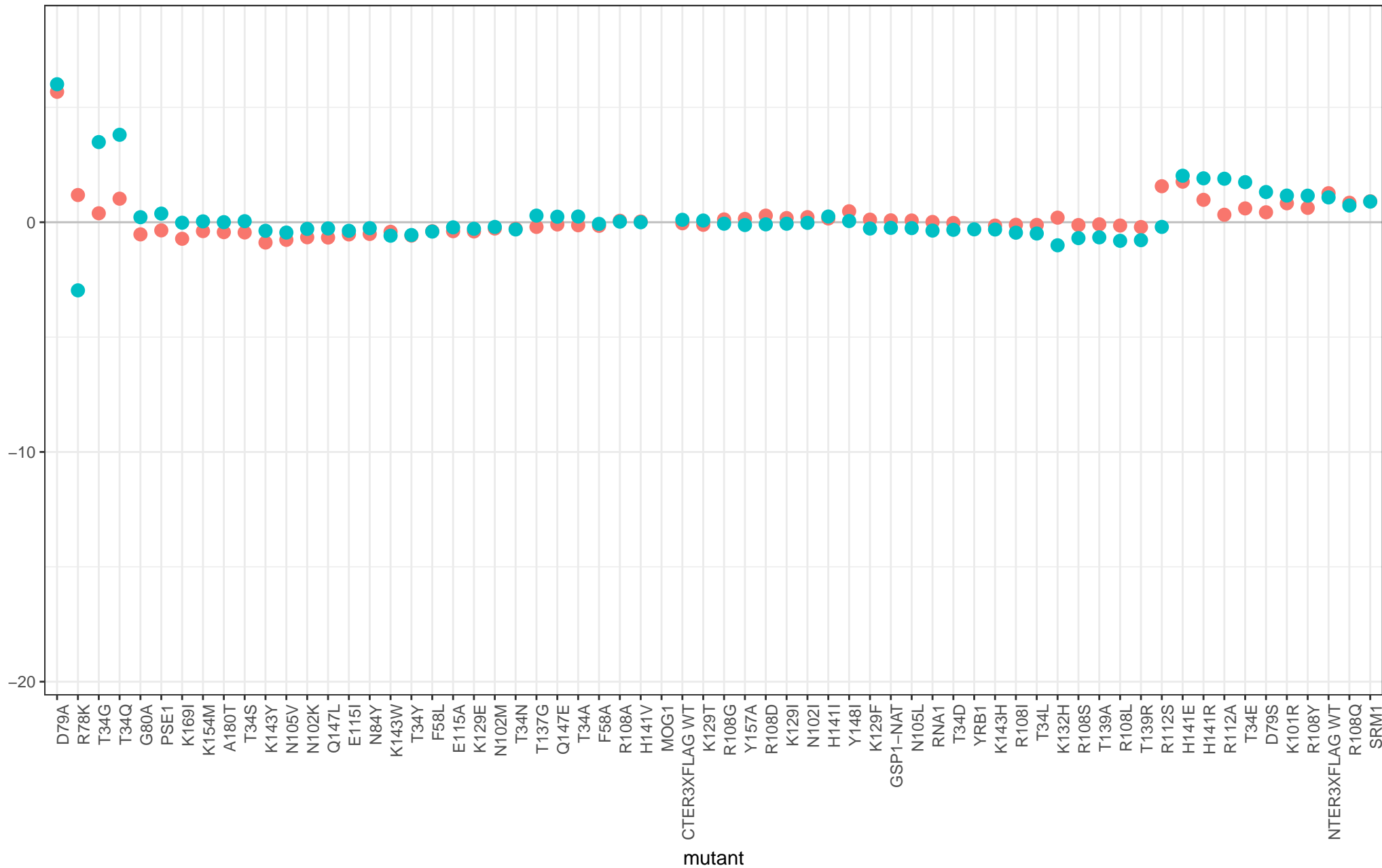
mutant

protein lipidation



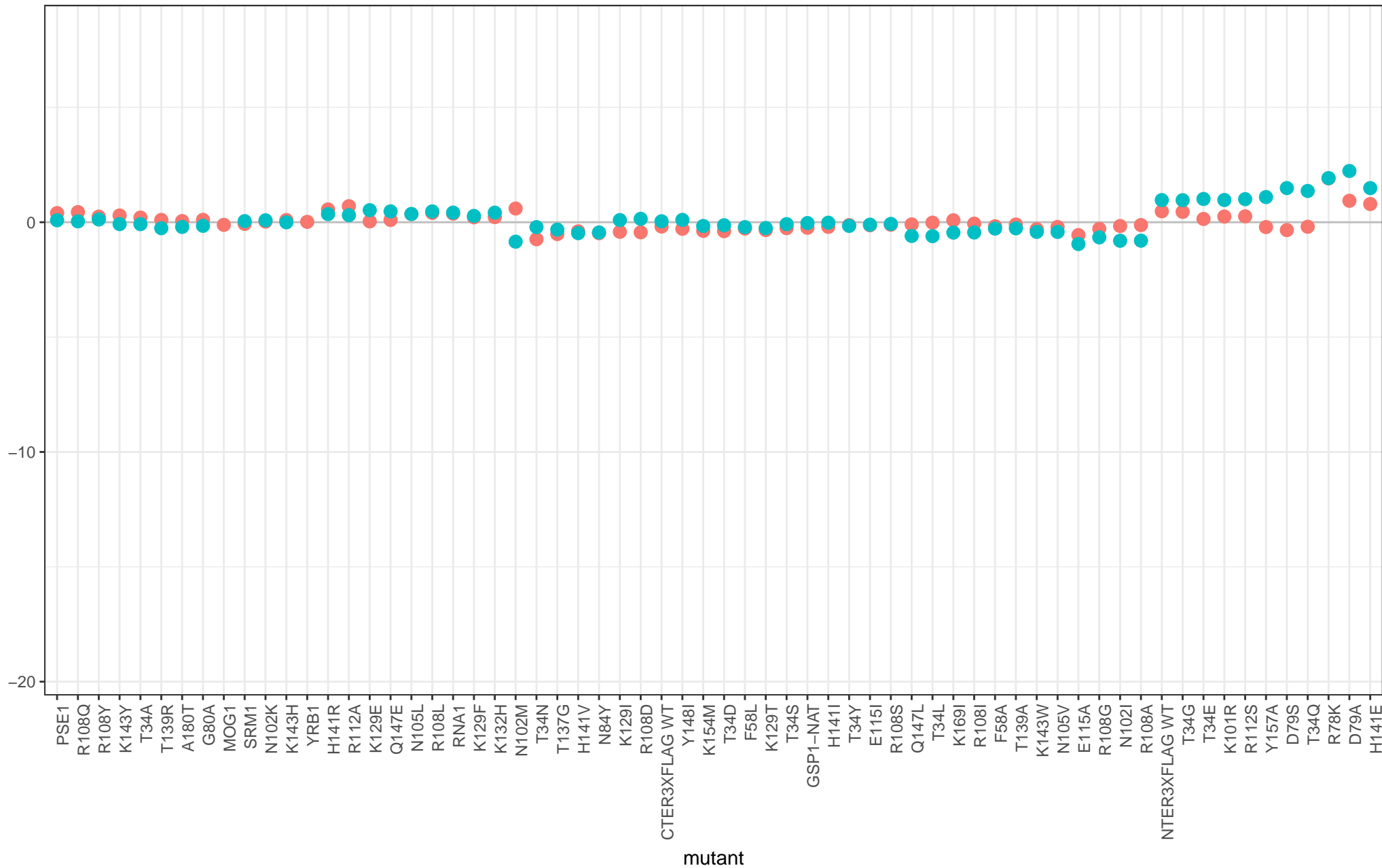
Protein O-mannosyltransferase(Pmt1p/Pmt2p)

E-MAP score



Protein O-mannosyltransferase(Pmt3p/Pmt5p)

E-MAP score



protein phosphatase type 2A complex (Rts1p)

E-MAP score

-20

-10

0

T34G
H141E
D79A
D79S
R78K
SRM1
K129E
Y157A
CTER3XFLAG WT
PSE1
RNA1
G80A
Q147E
H141R
H141I
R108G
N105L
R108Y
R112S
Y148I
R108S
T137G
R108L
E115A
T34D
K169I
T34E
R112A
T34A
F58A
T34L
F58L
Q147L
T139A
K132H
R108D
R108Q
K129F
GSP1-NAT
N84Y
A180T
N102M
N102I
NTER3XFLAG WT
T139R
N102K
K101R
YRB1
T34S
T34Y
K129T
E115I
K143Y
T34N
K129I
MOG1
R108I
T34Q
K143W
N105V
K154M
K143H
H141V
R108A

library gene

RTS1

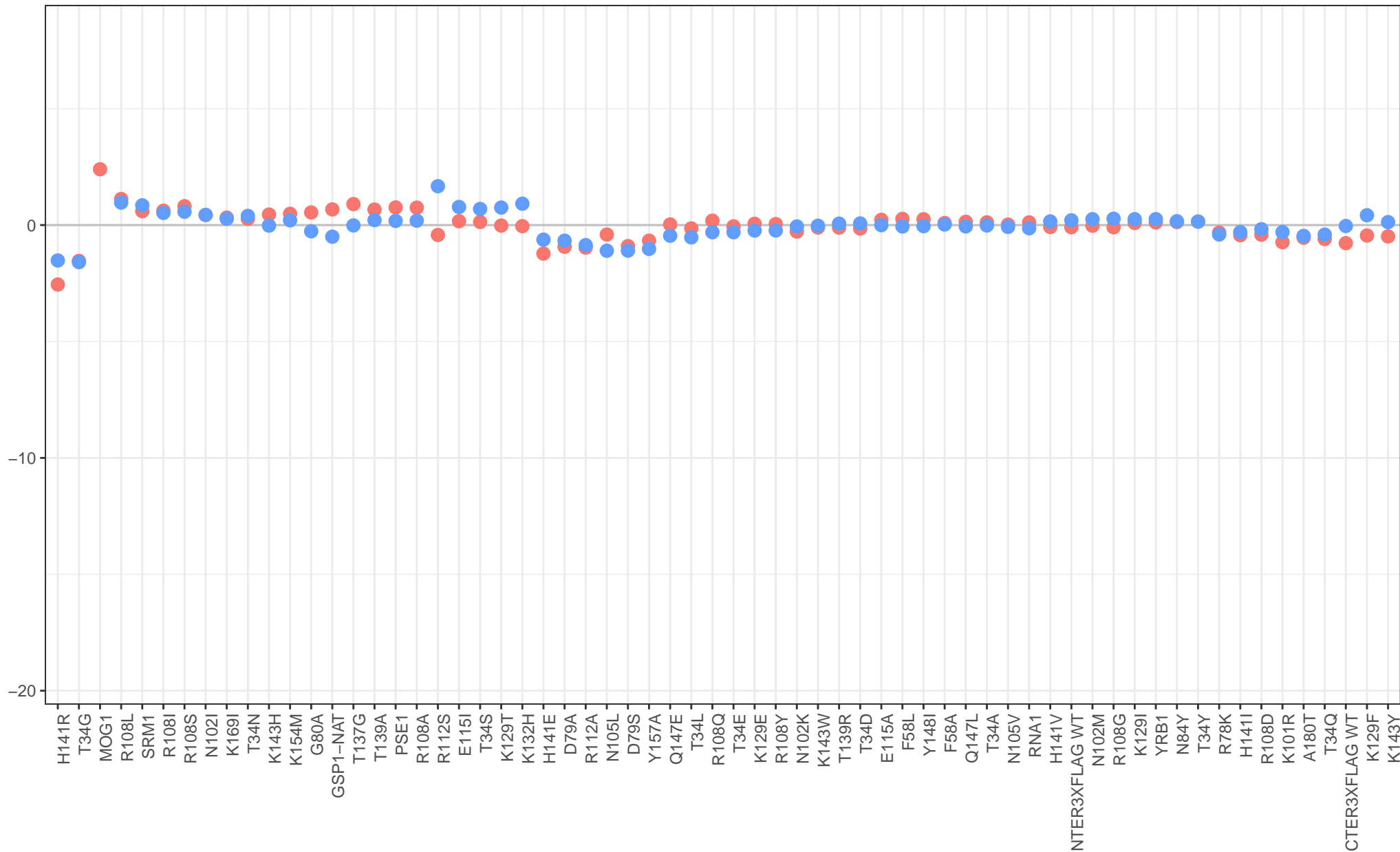
PPH21

TPD3

mutant

Rad17p/Ddc1p/Mec3p complex

E-MAP score



Rad6p/Rad18p complex

E-MAP score

0

-10

-20

library gene

RAD18

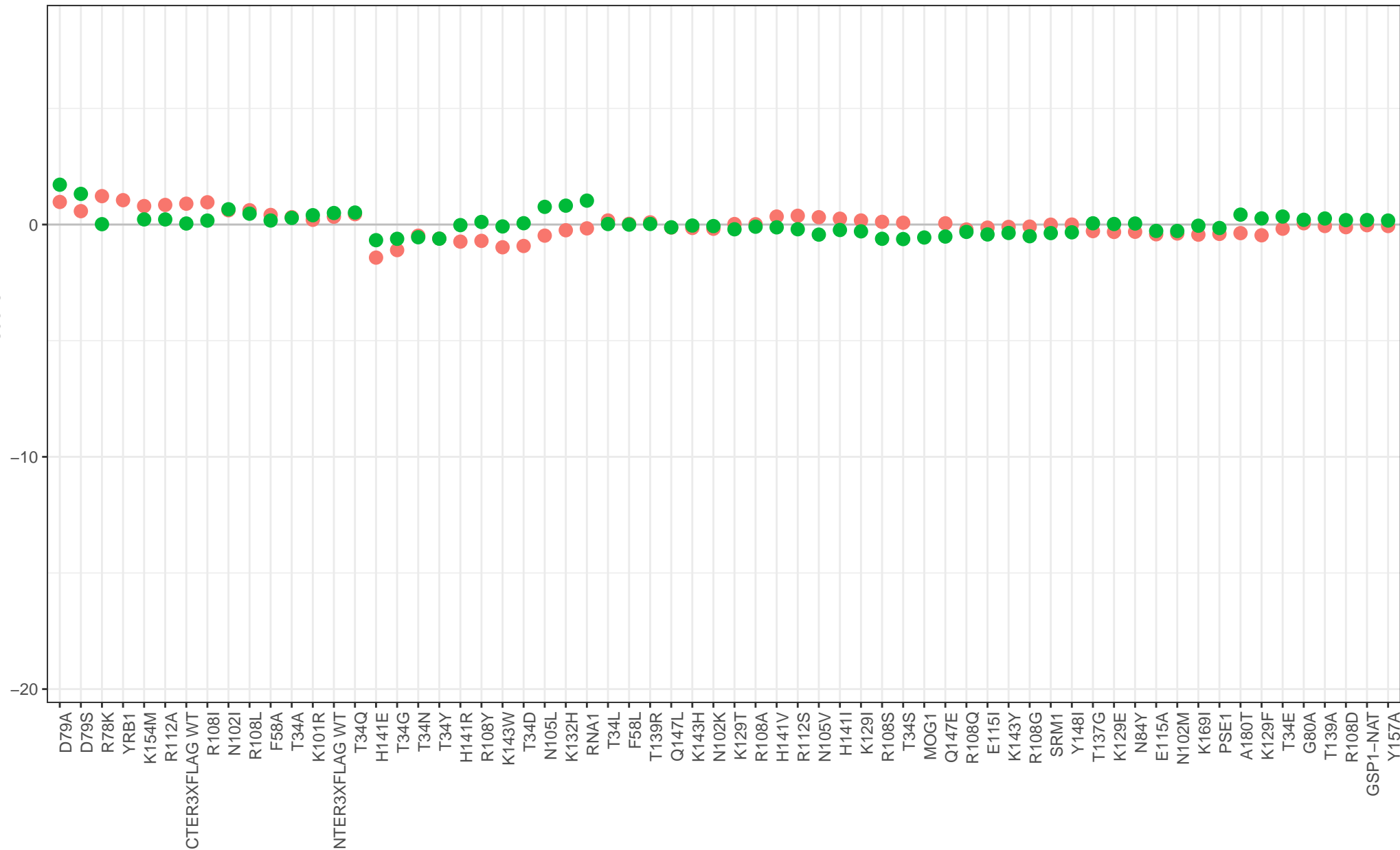
RAD6

mutant

D79S
T34Q
T34E
T34G
G80A
K129T
T34Y
A180T
T34A
R78K
K101R
Q147E
D79A
R112A
H141E
R112S
E115I
GSP1-NAT
T139A
K169I
T34S
F58L
T34N
K132H
T137G
Q147L
T139R
N84Y
T34L
K129F
R108D
T34D
N102K
K129E
N102I
CTER3XFLAG WT
F58A
K129I
YRB1
SRM1
PSE1
RNA1
K143W
N102M
K143Y
E115A
K143H
N105L
H141V
N105V
Y157A
MOG1
NTER3XFLAG WT
K154M
R108A
R108G
R108Q
Y148I
R108I
R108S
R108Y
H141R
H141I
R108L

RAVE complex

E-MAP score



library gene

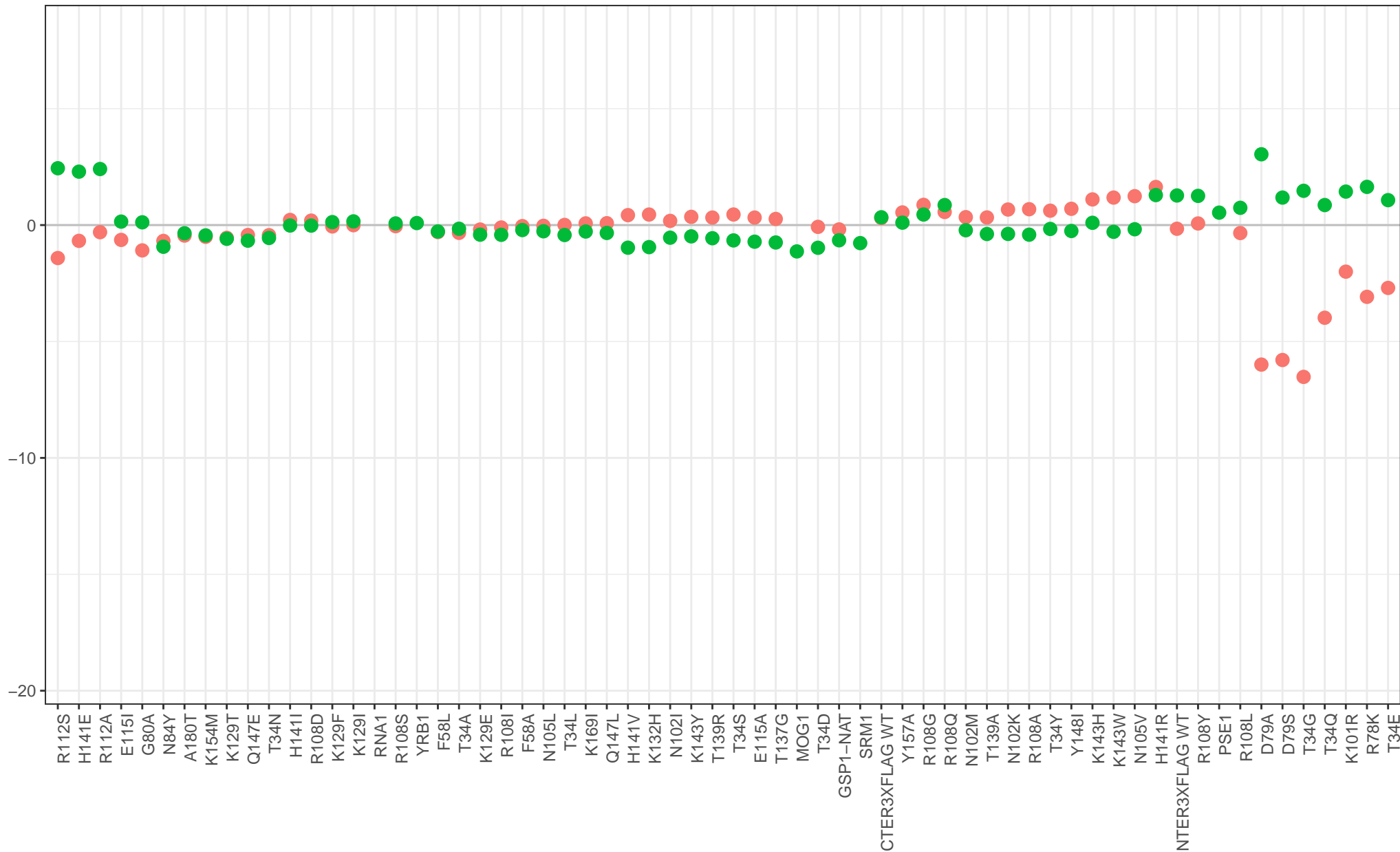
RAV1

RAV2

SKP1

RecQ helicase–Topo III complex

E-MAP score



RES complex

E-MAP score

0

-10

-20

H141E
R112S
T34E
T34Q
SRM1
R108L
R108Y
D79A
R112A
MOG1
NTER3XFLAG WT
CTER3XFLAG WT
H141R
T139A
H141I
K143H
K129F
T34A
A180T
T34D
GSP1-NAT
T139R
T34N
Y148I
PSE1
F58L
K143Y
G80A
Q147L
R108G
K129E
R108A
N102K
T34S
K129I
H141V
N105V
E115I
T34L
E115A
N102M
T137G
K132H
N102I
N84Y
Q147E
K129T
F58A
N105L
T34Y
K143W
R108S
RNA1
R108Q
R78K
K101R
Y157A
K154M
D79S
K169I
R108D
R108I
T34G
YRB1

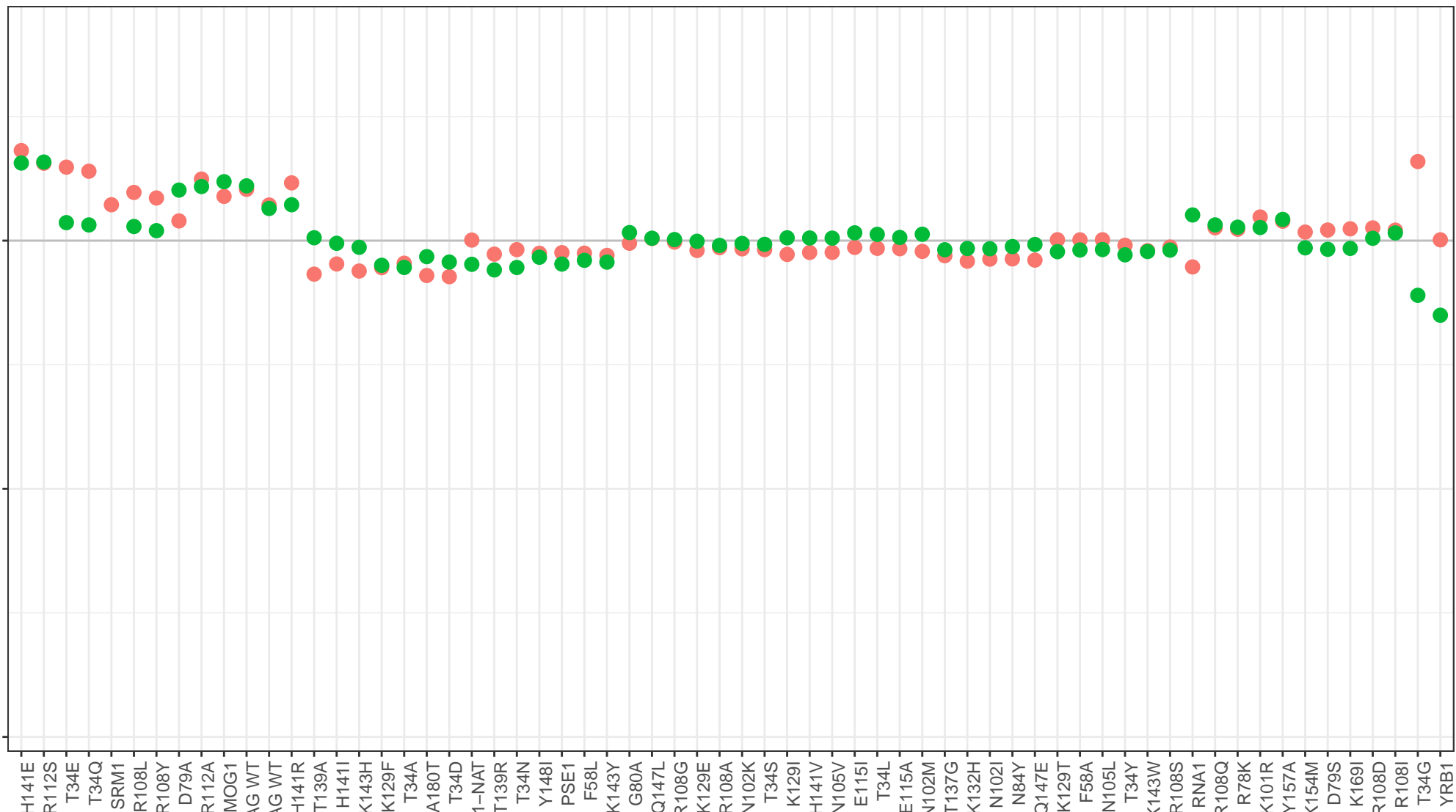
mutant

library gene

IST3

BUD13

PML1



retromer complex

E-MAP score

0

-10

-20

T34G
H141E
E115A
D79S
E115I
NTER3XFLAG WT
T34S
D79A
MOG1
RNA1
R108L
H141I
H141V
K143Y
K132H
K129I
R108Y
F58L
Y148I
CTER3XFLAG WT
F58A
K129E
T34Y
T34A
N102K
T34L
A180T
GSP1-NAT
Y157A
R108I
T34D
Q147E
T139R
T34N
YRB1
R108S
T139A
PSE1
K154M
K169I
R108G
N105V
R108Q
N84Y
T34Q
K101R
T34E
K143W
N105L
Q147L
T137G
K129F
R108A
N102M
K143H
R108D
N102I
R78K
G80A
H141R
SRM1
R112S
K129T
R112A

library gene

VPS29

VPS17

VPS5

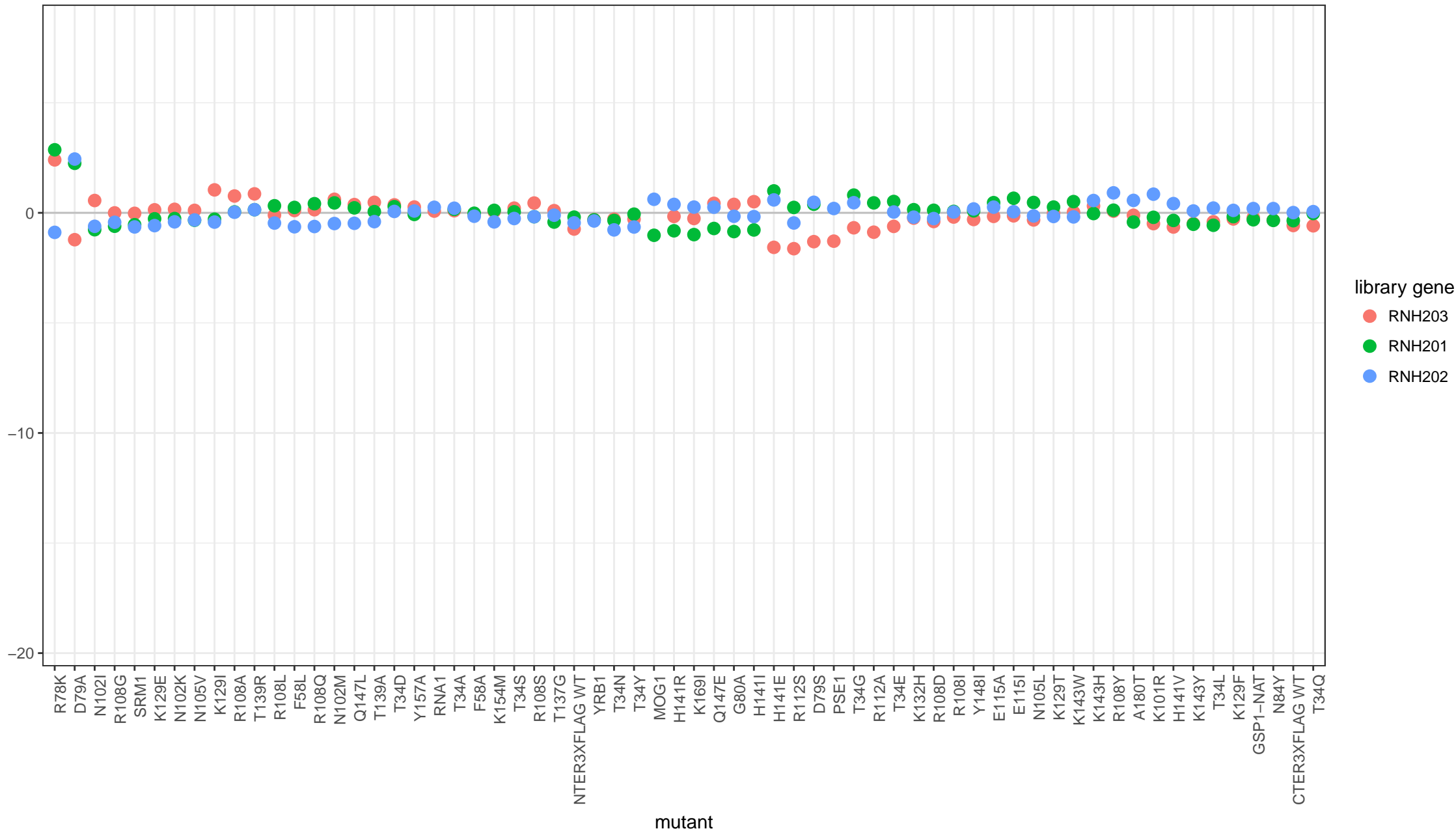
PEP8

VPS35

mutant

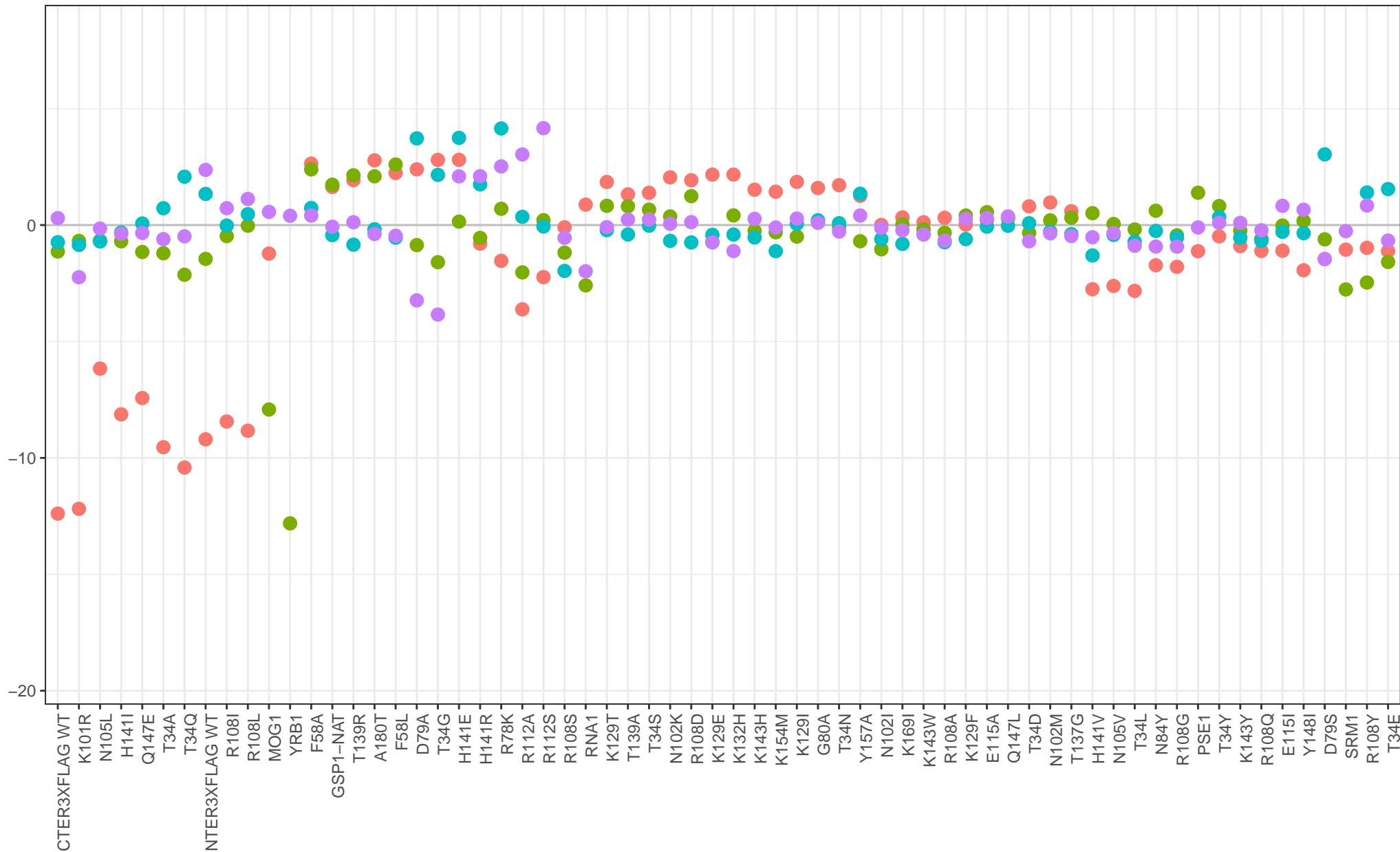
ribonuclease H2 complex

E-MAP score



ribosomal subunit export from nucleus

E-MAP score



library gene

ARX1

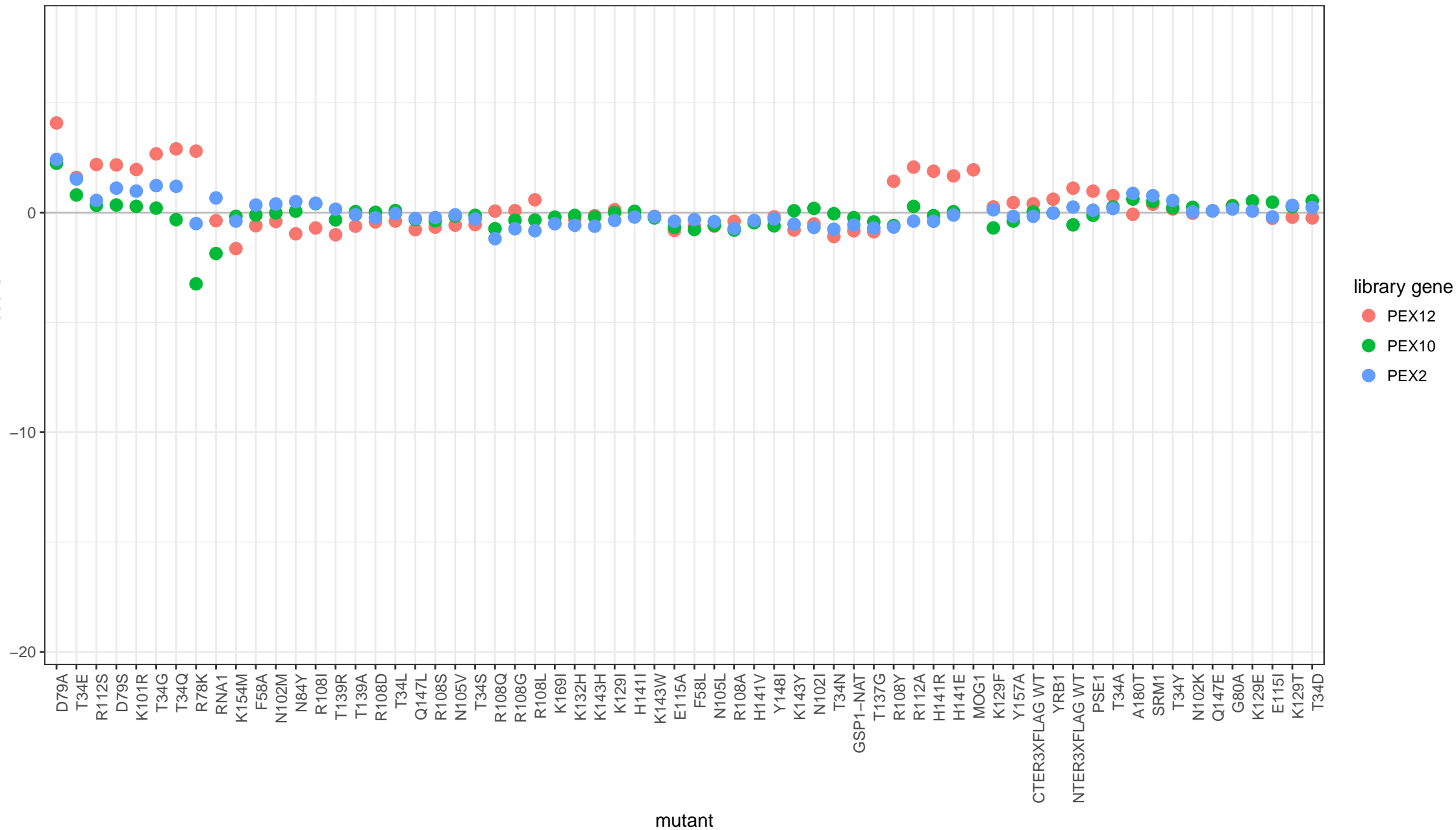
SLX9

JJJ1

YAR1

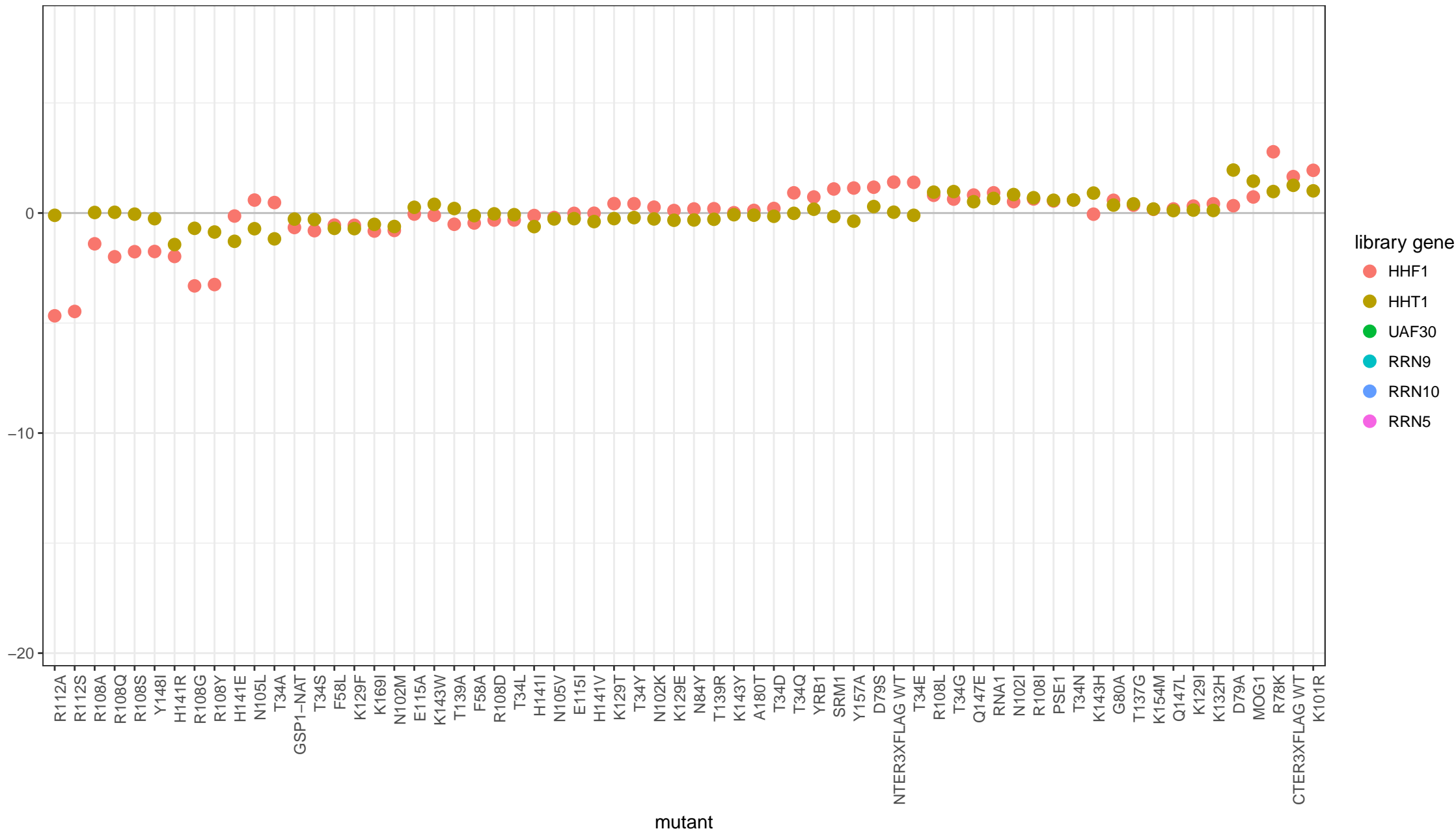
RING finger peroxin complex

E-MAP score



RNA polymerase I upstream activating factor complex

E-MAP score



Rot2p/Gtb1p complex

E-MAP score

0

-10

-20

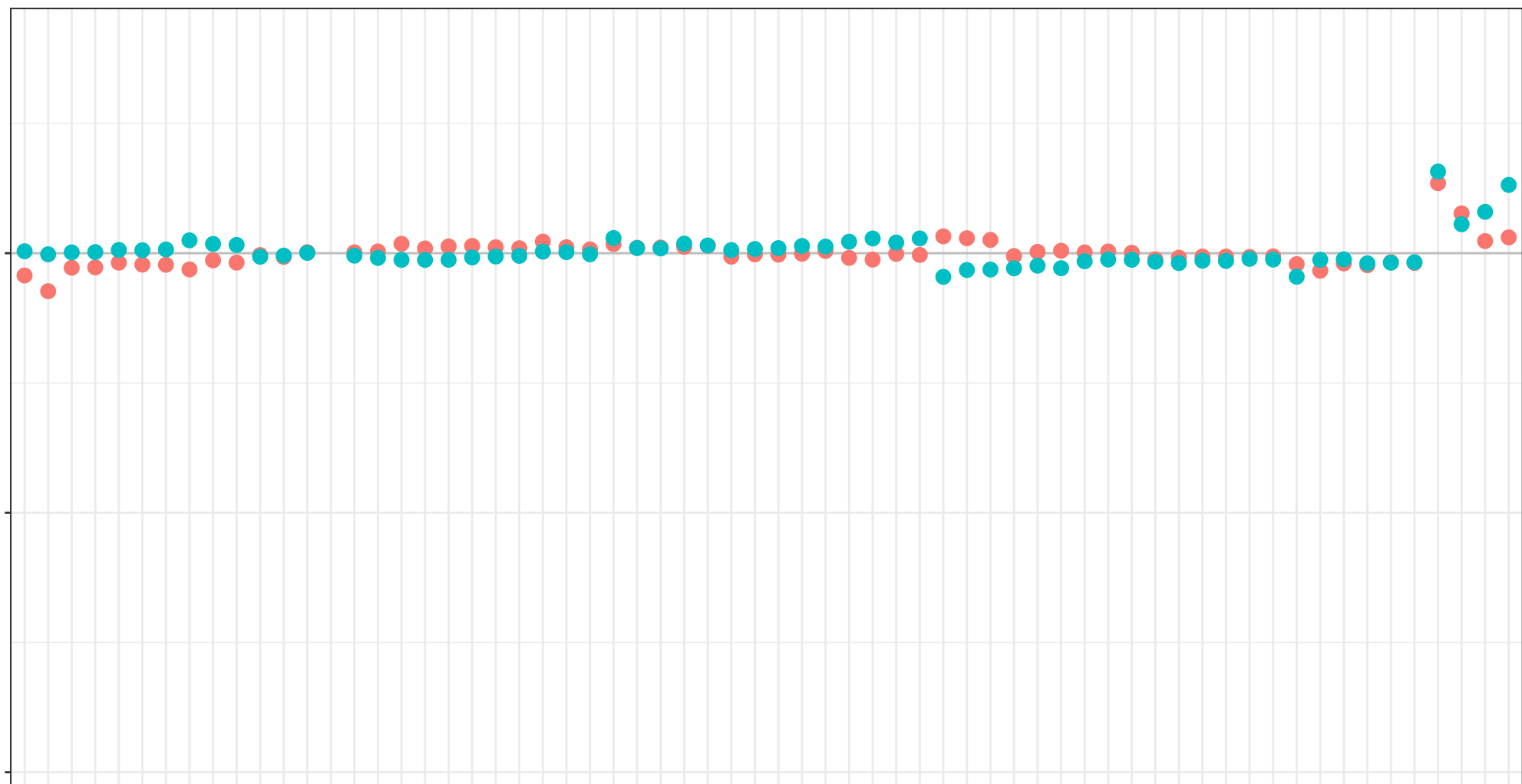
H141R YRB1 K129E T137G R108D H141V N105L A180T T34Q Y157A GSP1-NAT T34S E115I MOG1 N84Y T139R K143H K169I N102M G80A R108I R108S R108Y R108Q T34N SRM1 PSE1 R78K K132H R108L RNA1 H141I N105V NTER3XFLAG WT T34A D79S H141E CTER3XFLAG WT T34E K101R R108G Y148I T139A K143Y R108A F58A K129I Q147L F58L K129T E115A N102K K143W T34Y N102I Q147E K154M T34L K129F T34D D79A T34G R112A R112S

mutant

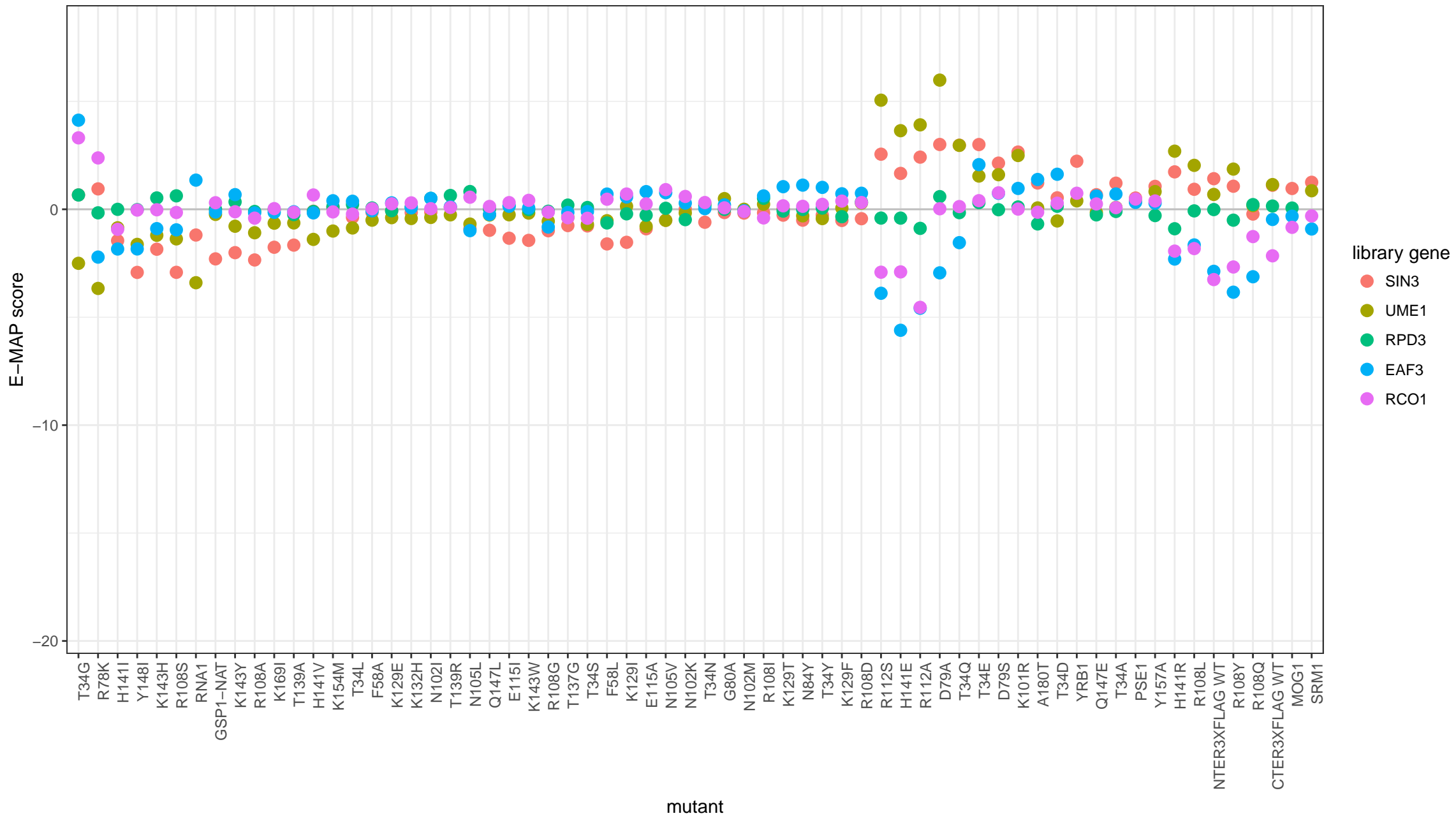
library gene

GTB1

ROT2

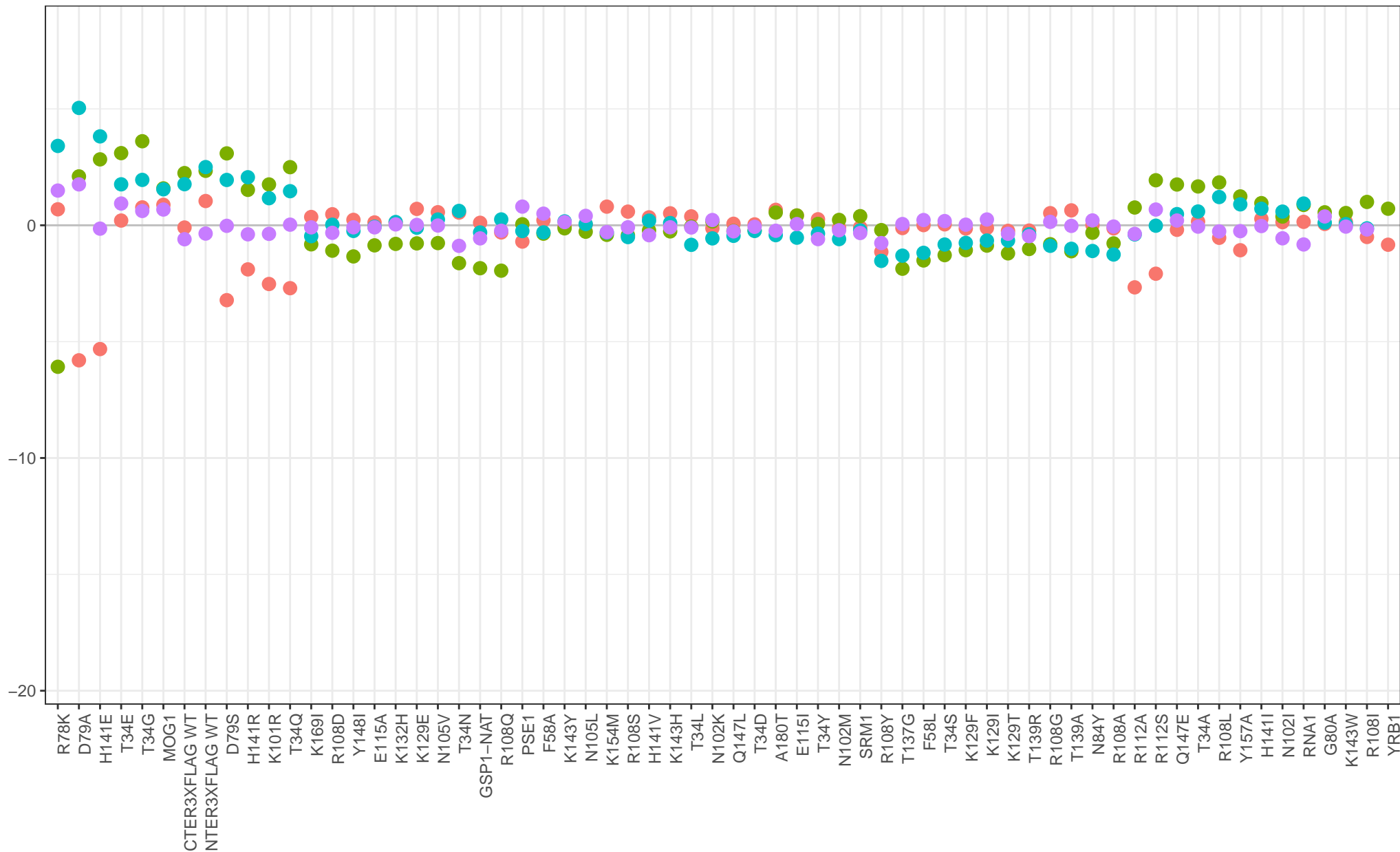


Rpd3S complex



rRNA binding

E-MAP score



library gene

MRT4

SSF1

NOP6

SSF2

mutant

RSC complex

E-MAP score

-20

-10

0

mutant

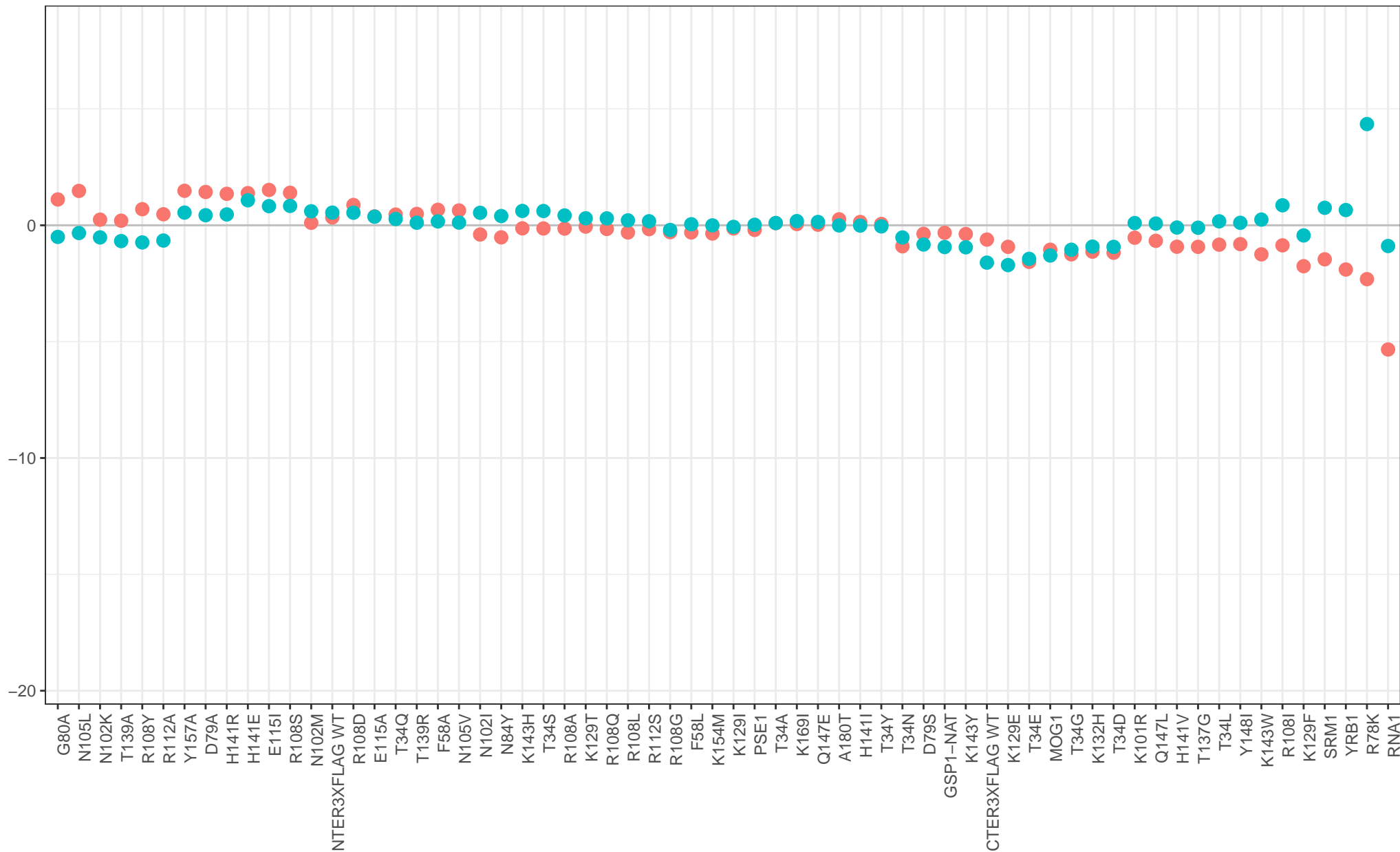
library gene

- RSC1
- RTT102
- STH1
- SFH1
- RSC9
- RSC8
- RSC6
- RSC58
- RSC4
- RSC30
- RSC3
- RSC2
- NPL6
- LDB7
- HTL1
- ARP7
- ARP9

F58L
R108L
H141R
K129E
K143Y
T139A
Q147L
R108Y
R108S
NTER3XFLAG WT
T137G
Q147E
R108A
T34A
R108I
Y148I
Y157A
K129T
N102K
K143W
K154M
H141I
T34N
T34Y
T34L
K132H
K139R
RNA1
SRM1
R108G
G80A
N84Y
K129F
K129I
F58A
YRB1
T34E
H141E
R112A
K169I
N105V
PSE1
R108D
E115A
E115I
H141V
K143H
CTER3XFLAG WT
GSP1-NAT
R108Q
MOG1
T34S
N102M
K101R
N102I
T34Q
A180T
D79S
T34D
R78K
D79A
N105L
R112S
T34G

Rtg1p/Rtg3p complex

E-MAP score



library gene

- RTG1
- RTG3

Rtt109p/Vps75p complex

E-MAP score

0

-10

-20

library gene

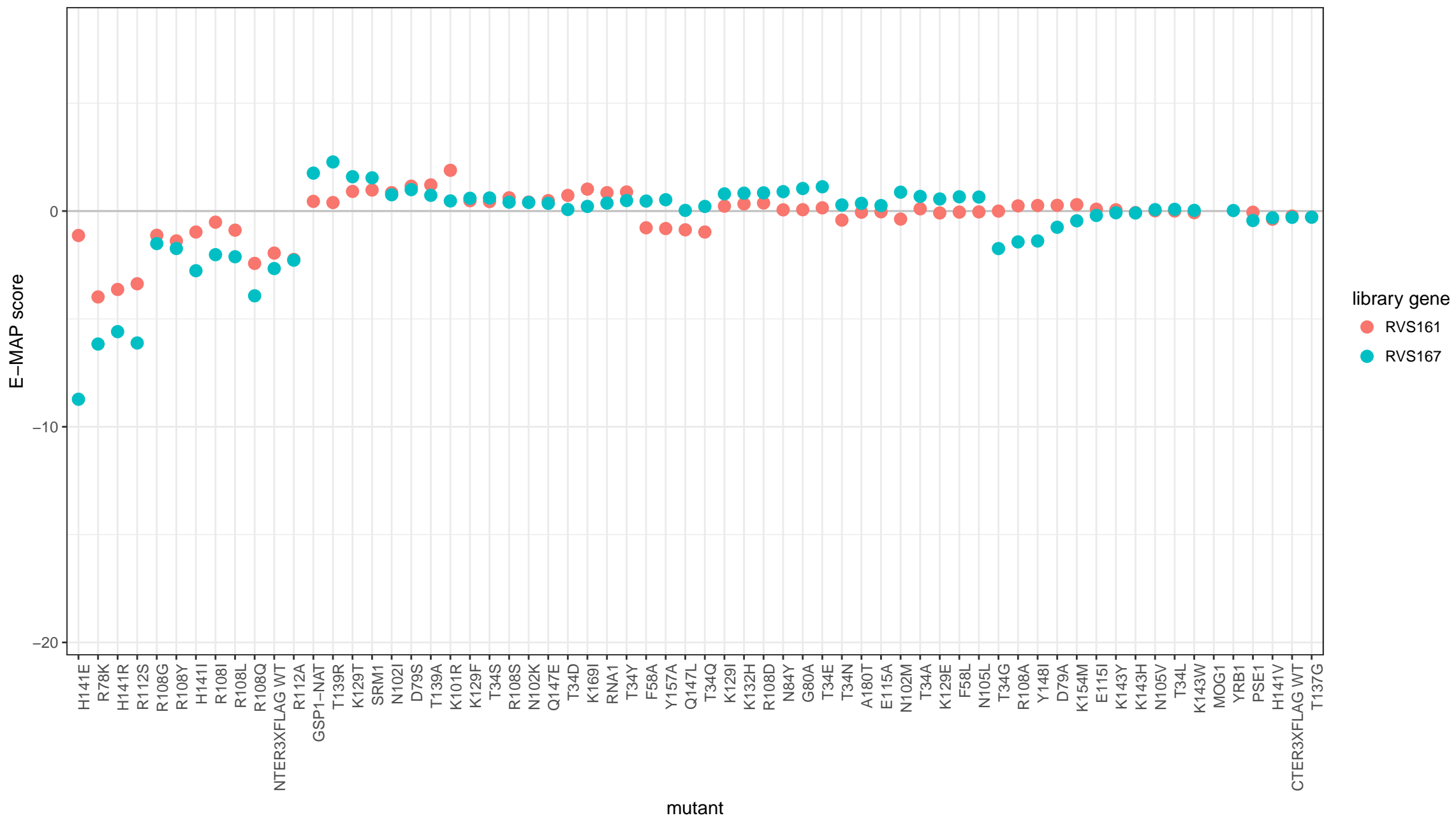
RTT109

VPS75

mutant

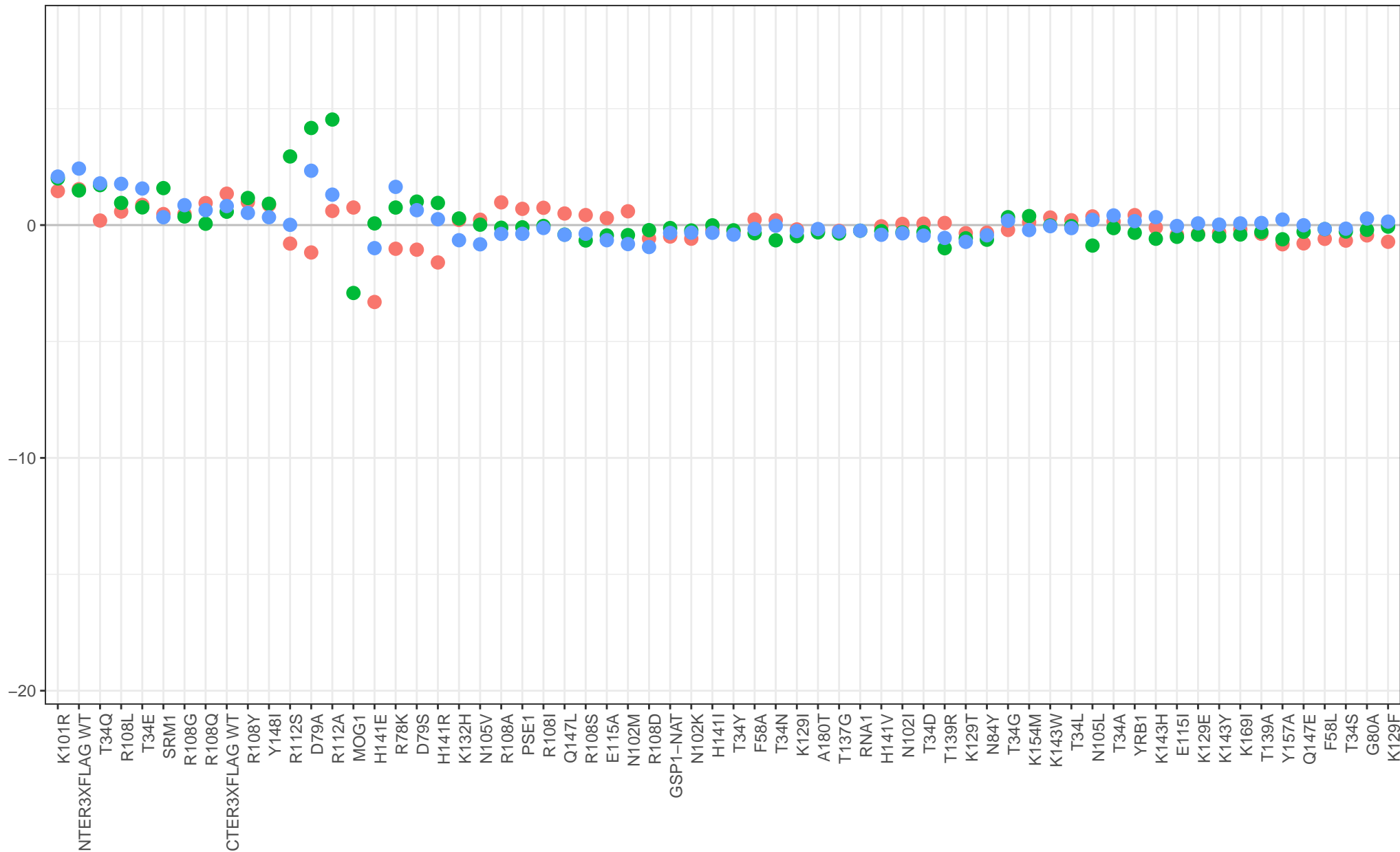
R78K
G80A
D79S
Y157A
NTER3XFLAG WT
R108Y
T34A
K101R
R108L
R112A
D79A
R112S
H141E
T34G
T34Q
H141R
T34E
SRM1
T34N
K143Y
R108A
K143W
K169I
R108G
PSE1
K143H
Q147L
Y148I
MOG1
YRB1
E115A
F58A
T137G
N102I
K132H
T139R
T34D
H141V
T139A
R108S
GSP1-NAT
H141I
N105V
R108I
K129E
K129I
A180T
RNA1
K154M
N84Y
T34Y
N102M
Q147E
N102K
E115I
R108D
CTER3XFLAG WT
R108Q
K129F
T34L
F58L
N105L
K129T
T34S

Rvs161p/Rvs167p complex



SAS Complex

E-MAP score



library gene

SAS2

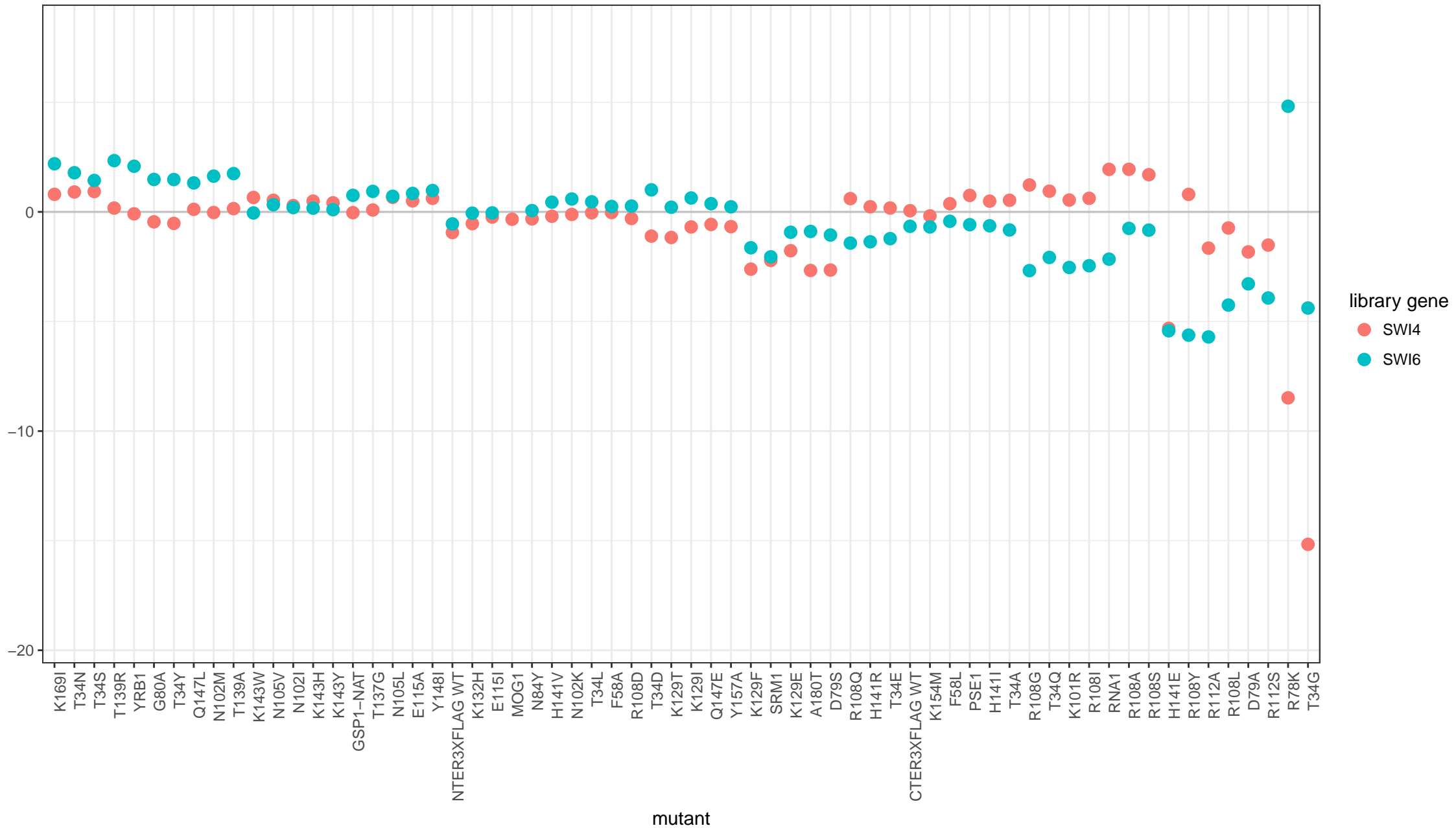
SAS4

SAS5

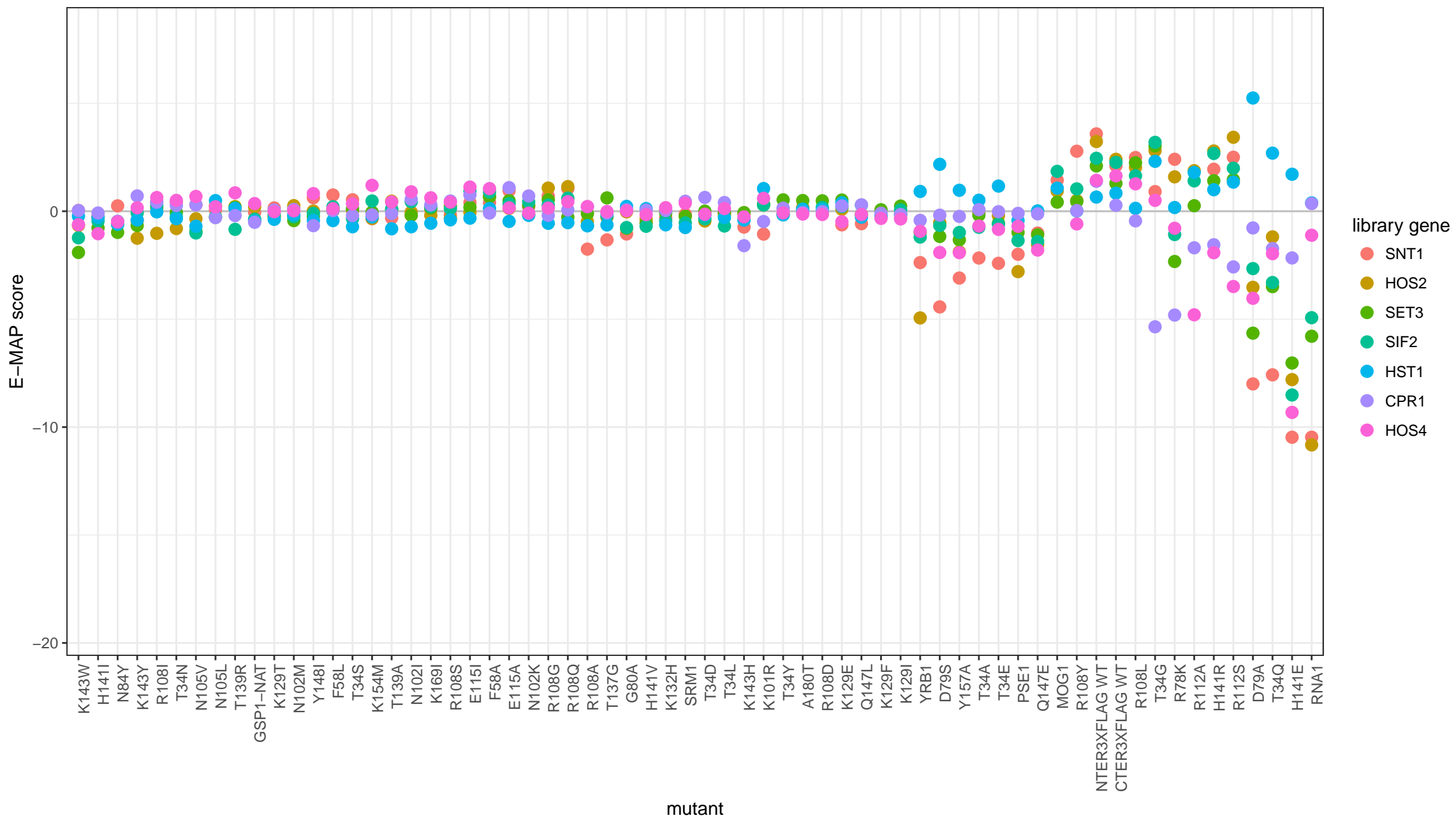
mutant

SBF complex

E-MAP score



Set3p complex



signal peptidase complex

E-MAP score

0

-10

-20

G80A
K129F
A180T
Y157A
YRB1
K129I
NTER3XFLAG WT
E115A
K129E
T137G
Q147E
F58A
R108D
T34A
E115I
K132H
R112S
D79S
H141R
K101R
R108I
R108S
K143W
PSE1
R112A
RNA1
CTER3XFLAG WT
K129T
T34E
T34Q
R108Q
SRM1
R108A
R108L
T34D
K143H
T34L
MOG1
N102M
R108Y
T139A
F58L
H141I
H141V
K169I
T34Y
Q147L
GSP1-NAT
R108G
K154M
N102K
N84Y
T139R
Y148I
K143Y
N102I
N105V
N105L
T34N
T34S
D79A
H141E
R78K
T34G

library gene

- SPC1
- SPC2
- SEC11
- SPC3

Ski Complex

E-MAP score

-20

-10

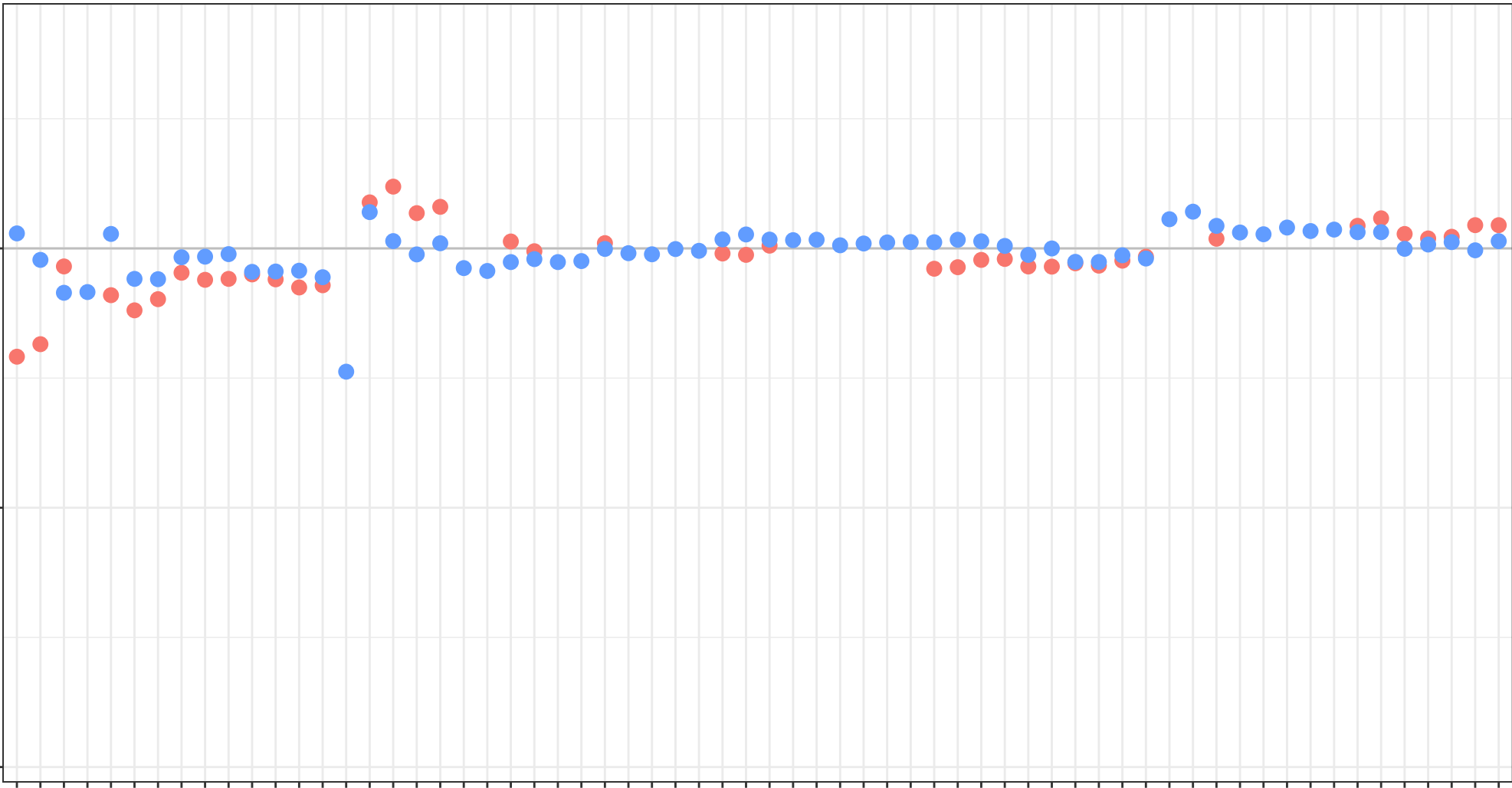
0

K143Y
R108S
K101R
R112A
F58A
D79S
R108L
YRB1
K143W
T137G
D79A
R112S
R108Y
RNA1
R78K
H141E
N84Y
Q147E
T34N
K132H
R108Q
N105L
T34A
K129F
N105V
Y148I
F58L
GSP1-NAT
CTER3XFLAG WT
R108A
N102K
T34E
H141I
K143H
NTER3XFLAG WT
T139A
R108D
K169I
Y157A
H141R
Q147L
K129E
T34Y
K154M
R108I
MOG1
PSE1
G80A
T34Q
SRM1
T34G
N102I
E115I
T34L
E115A
T139R
T34S
R108G
T34D
A180T
K129I
N102M
H141V
K129T

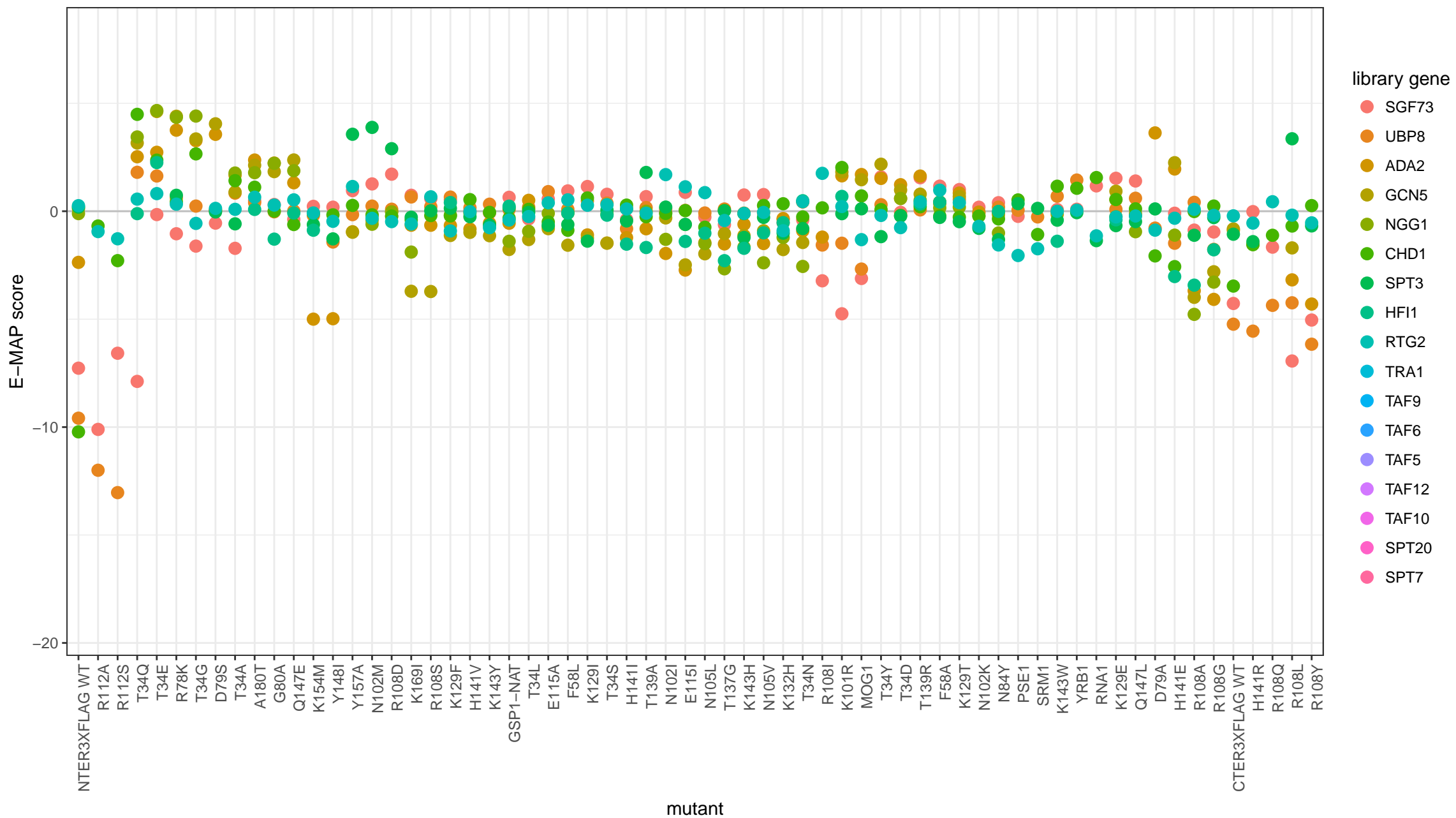
mutant

library gene

- SKI8
- SKI2
- SKI3

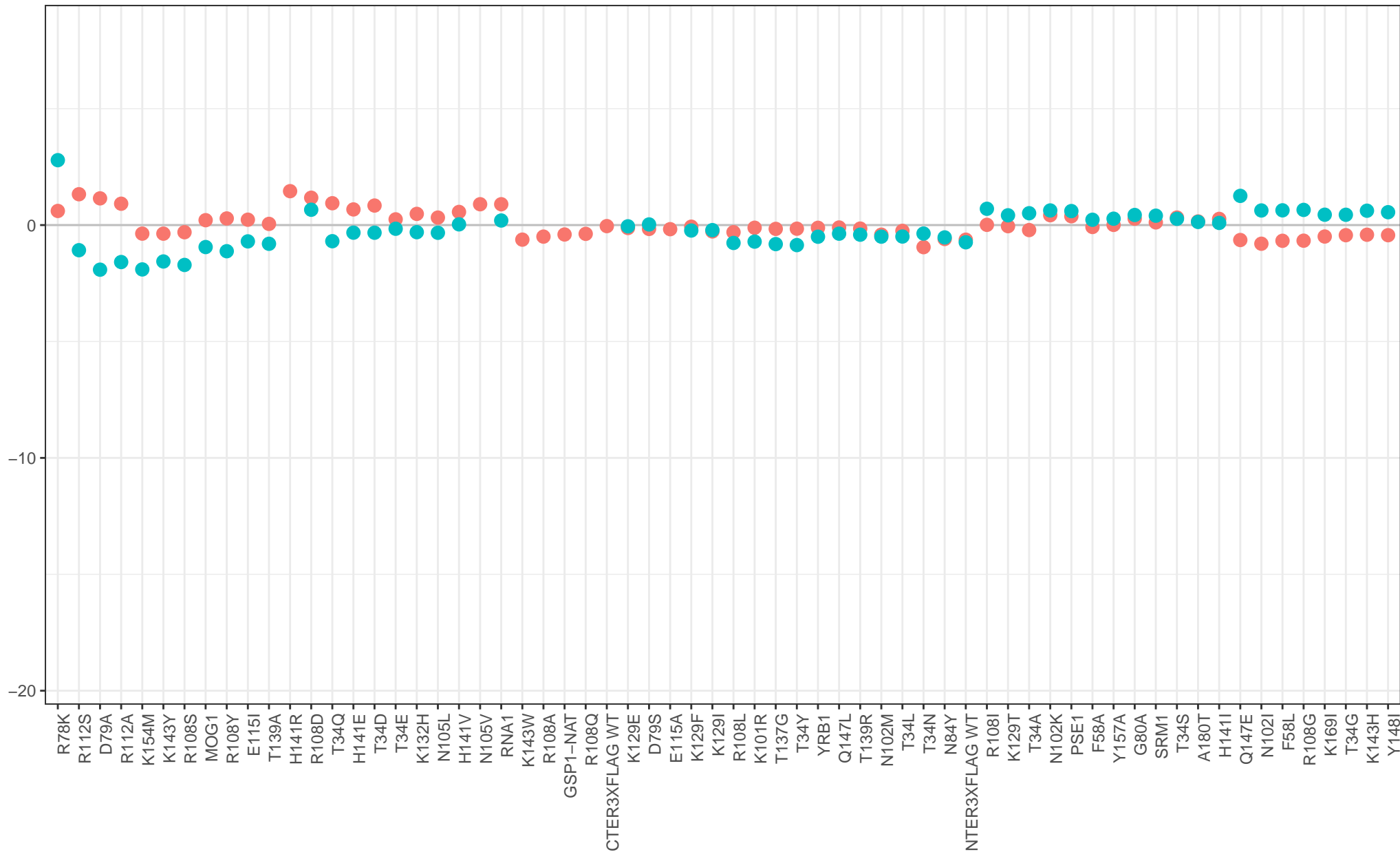


SLIK (SAGA-like) complex



Slx1p/Slx4p complex

E-MAP score



library gene

SLX1

SLX4

Slx5p/Slx8p complex

E-MAP score

0

-10

-20

library gene

SLX5

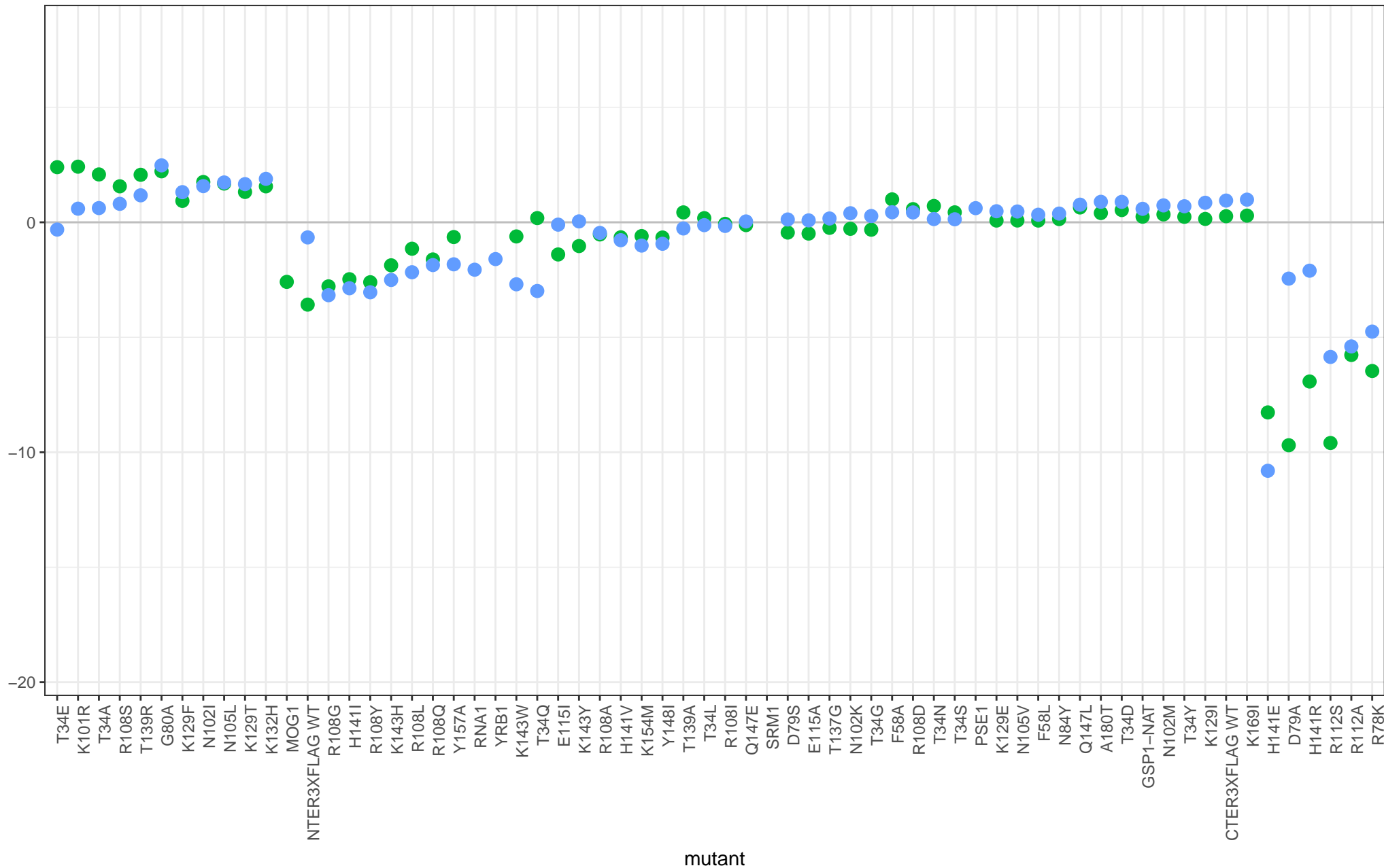
SLX8

mutant

D79A
K143W
R112A
NTER3XFLAG WT
D79S
E115I
H141E
MOG1
R108L
K143H
R112S
YRB1
N102I
H141V
Q147E
K129F
R108S
T34Y
Q147L
K154M
R108D
R108I
SRM1
F58A
CTER3XFLAG WT
K101R
T34G
H141R
Y157A
R108A
T139A
R108Q
R108G
T34E
T139R
K129E
T34L
T34A
T34S
K129I
H141I
N102M
K129T
K132H
N105L
RNA1
F58L
R108Y
Y148I
T34N
T34Q
PSE1
R78K
K143Y
N84Y
E115A
K169I
G80A
GSP1-NAT
N105V
A180T
T34D
N102K
T137G

Snf1p/Snf4p/Gal83p complex

E-MAP score

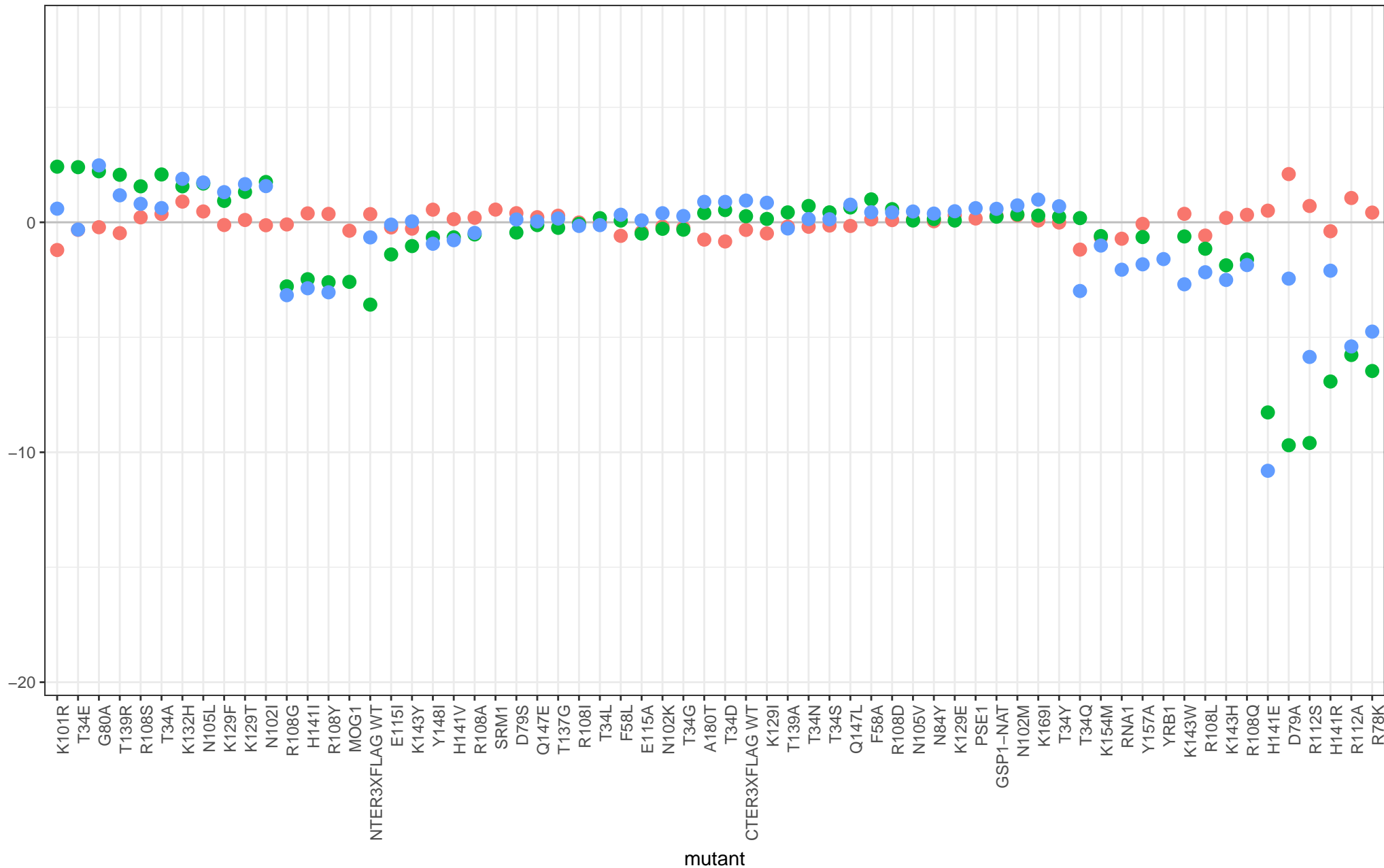


library gene

- GAL83
- SNF1
- SNF4

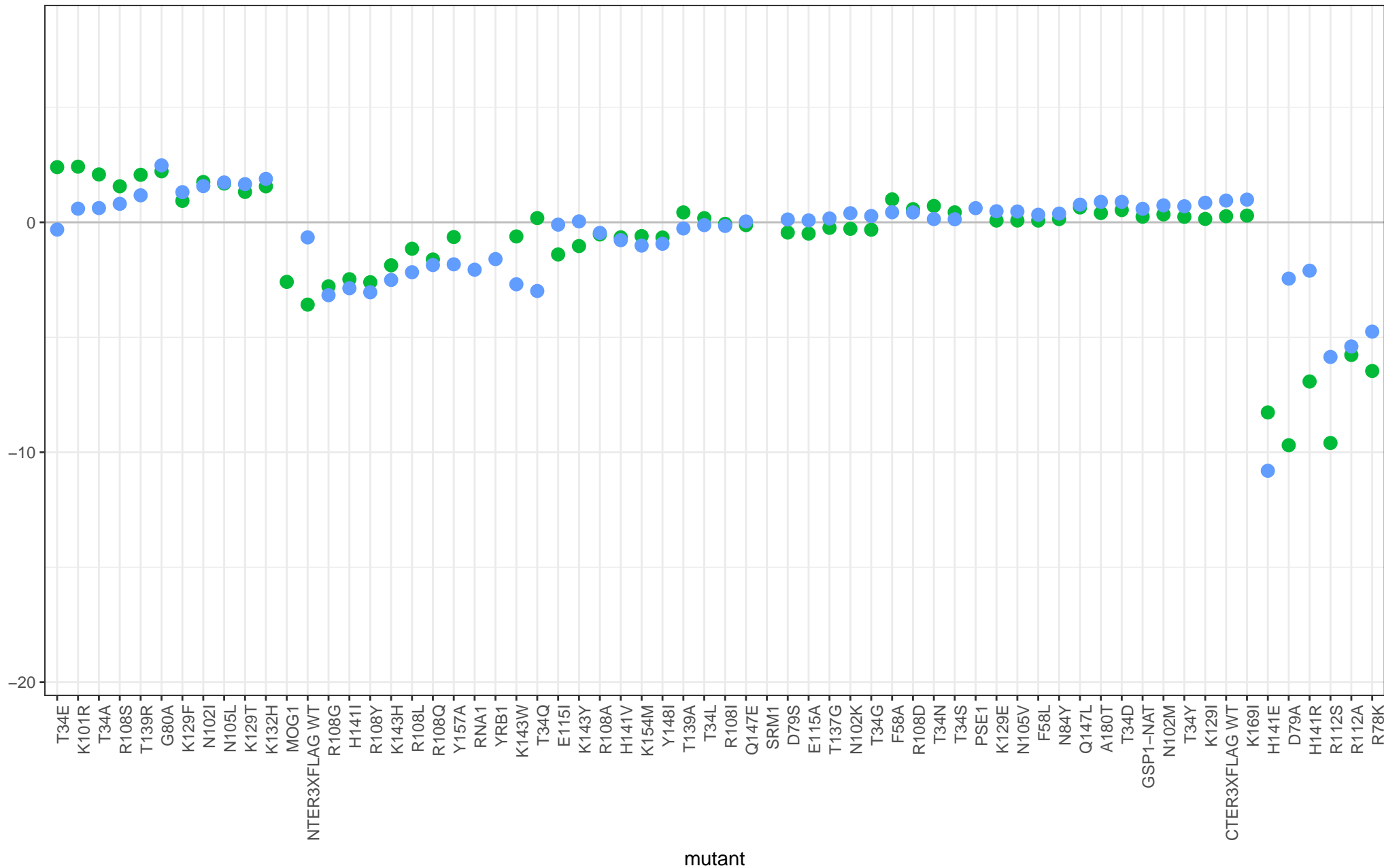
Snf1p/Snf4p/Sip1p complex

E-MAP score



Snf1p/Snf4p/Sip2p complex

E-MAP score



snoRNA processing

E-MAP score

-20

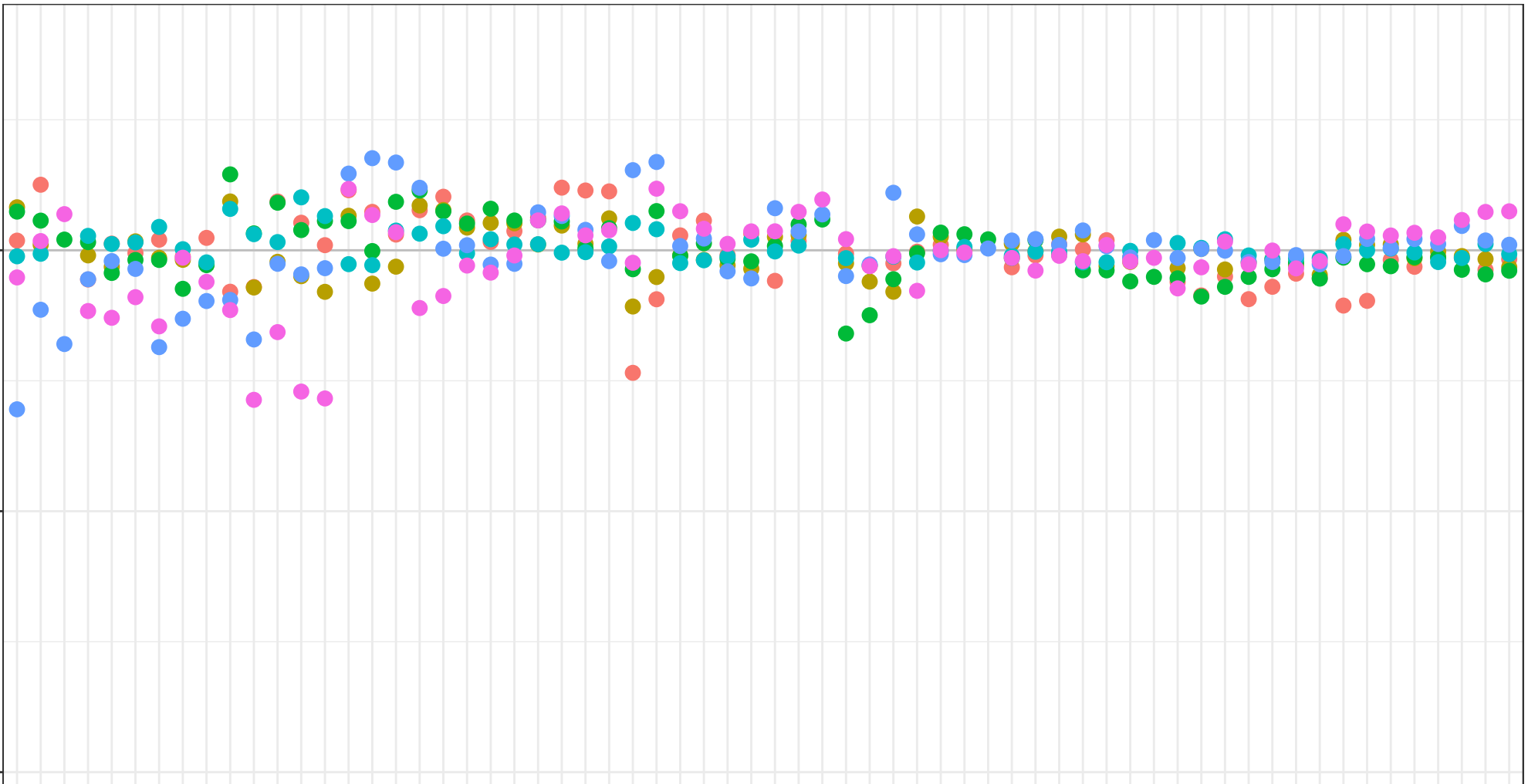
-10

0

mutant

library gene

- PAP2
- RRP6
- LRP1
- TRF5
- RTF1
- XRN1



Sum1p/Rfm1p/Hst1p complex

E-MAP score

-20

-10

0

CTER3XFLAG WT
NTER3XFLAG WT
Y157A
R108Y
R108L
RNA1
SRM1
G80A
T34A
Q147E
T139R
A180T
R108I
PSE1
R108Q
Y148I
MOG1
YRB1
F58A
N105L
K129E
K129I
T34D
H141V
R108D
R78K
N102K
K129F
T34Y
K143W
N102M
R108G
K132H
N105V
R108A
GSP1-NAT
K143H
H141I
Q147L
F58L
K143Y
K154M
E115A
R108S
N102I
T139A
E115I
T34N
K129T
T34L
T34S
T137G
K169I
N84Y
D79A
T34Q
H141E
R112S
D79S
R112A
T34G
K101R
H141R
T34E

mutant

library gene

RFM1

HST1

SUM1

Sur1p/Csg2p complex

E-MAP score

-20

-10

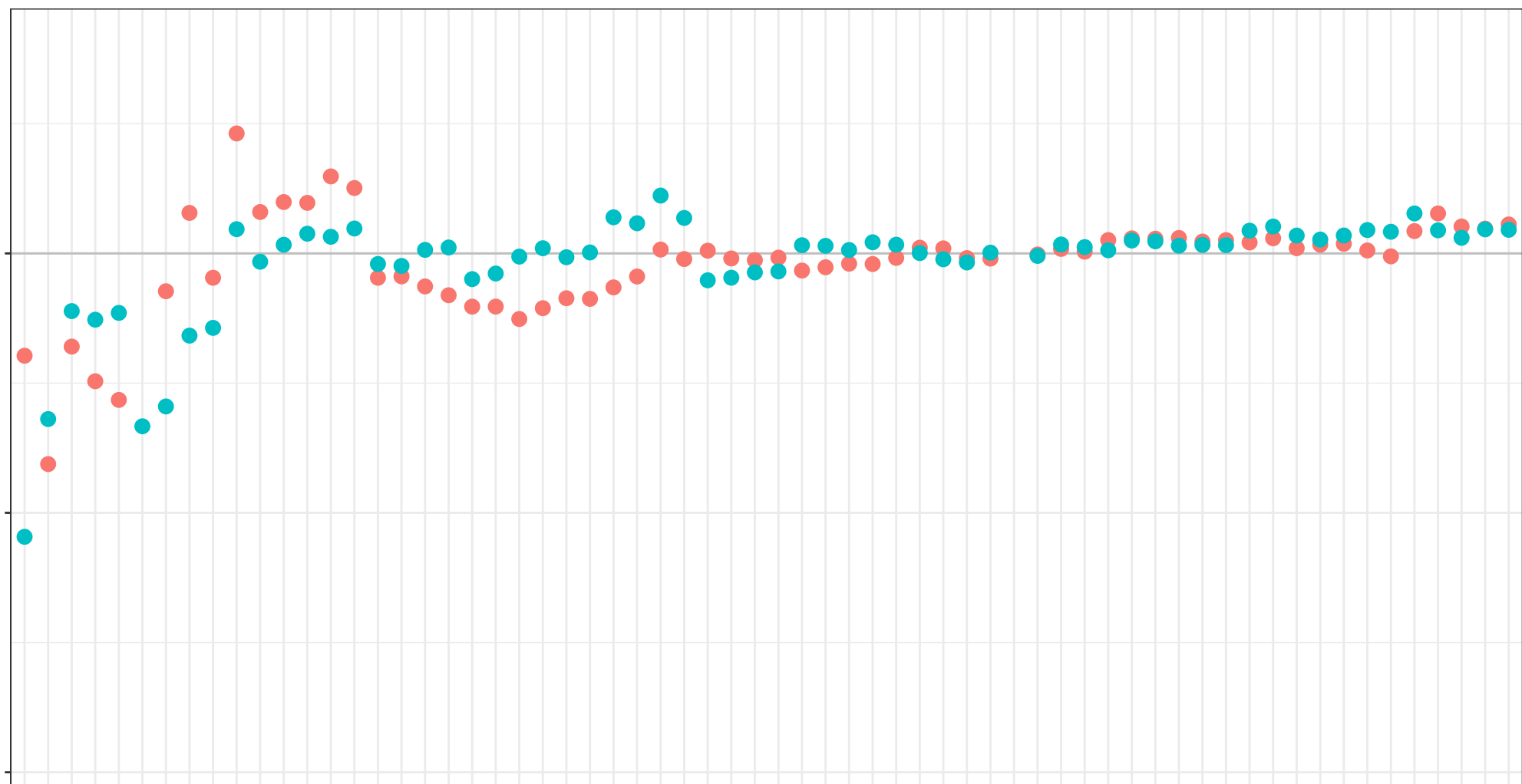
0

H141E D79S Y157A H141R R108Y R112A T34G D79A T34Q R78K T34Y N102M Q147E R108S R112S K129F R108A CTER3XFLAG WT YRB1 NTER3XFLAG WT R108G T34A R108Q H141I R108L N105L N105V K132H SRM1 RNA1 K129E A180T T34E PSE1 T34S Y148I E115A N84Y GSP1-NAT T34D N102I T34L MOG1 N102K K101R K169I K129T R108D T137G E115I K129I K143Y K108I T34N K154M G80A T139R H141V T139A K143W Q147L K143H F58A F58L

mutant

library gene

CSG2
SUR1



SWI/SNF complex

E-MAP score

-20

-10

0

mutant

CTER3XFLAG WT

NTER3XFLAG WT

R108S

N102M

K129I

R108I

T139A

T34S

E115A

T34N

H141I

K132H

K154M

N84Y

K129E

N105V

GSP1-NAT

R108D

Y157A

K143W

MOG1

T34D

T34L

K143H

T34Y

R108L

R108Y

R108A

R108G

E115I

T137G

N105L

RNA1

library gene

SWP82

SNF11

RTT102

TAF14

SWI1

SNF2

SNF12

ARP7

ARP9

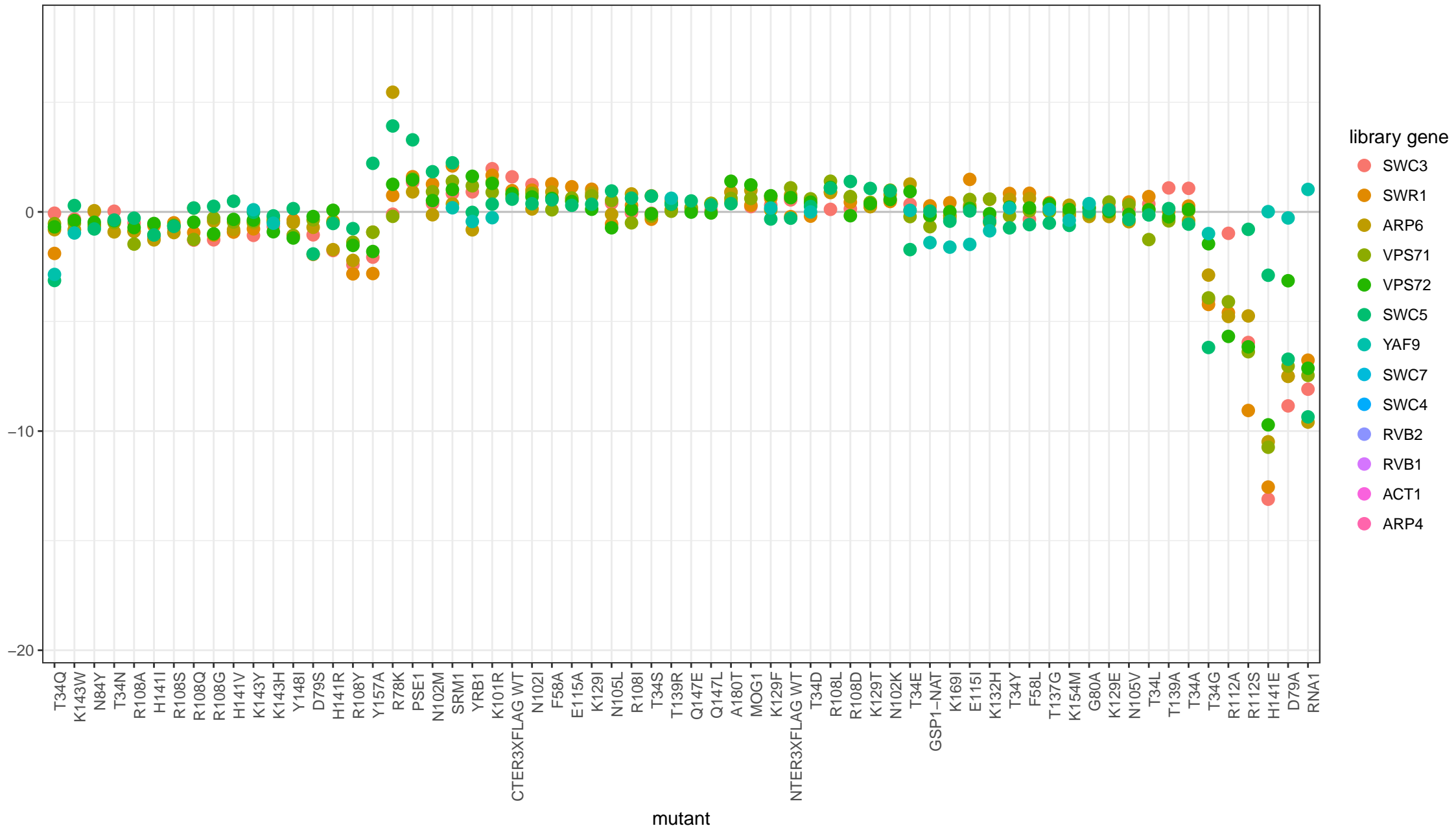
SNF6

SNF5

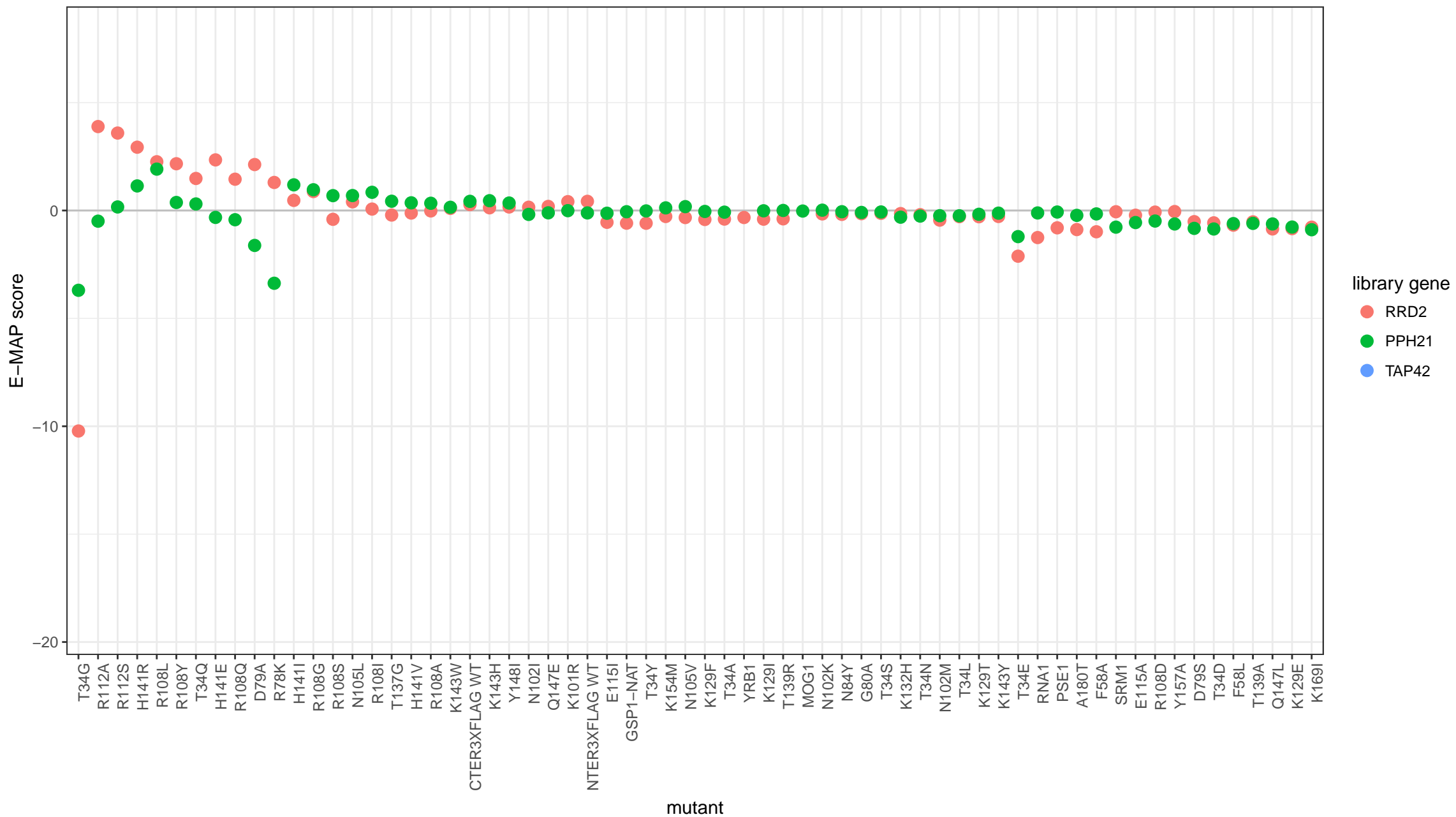
SWI3

Swr1p complex

E-MAP score

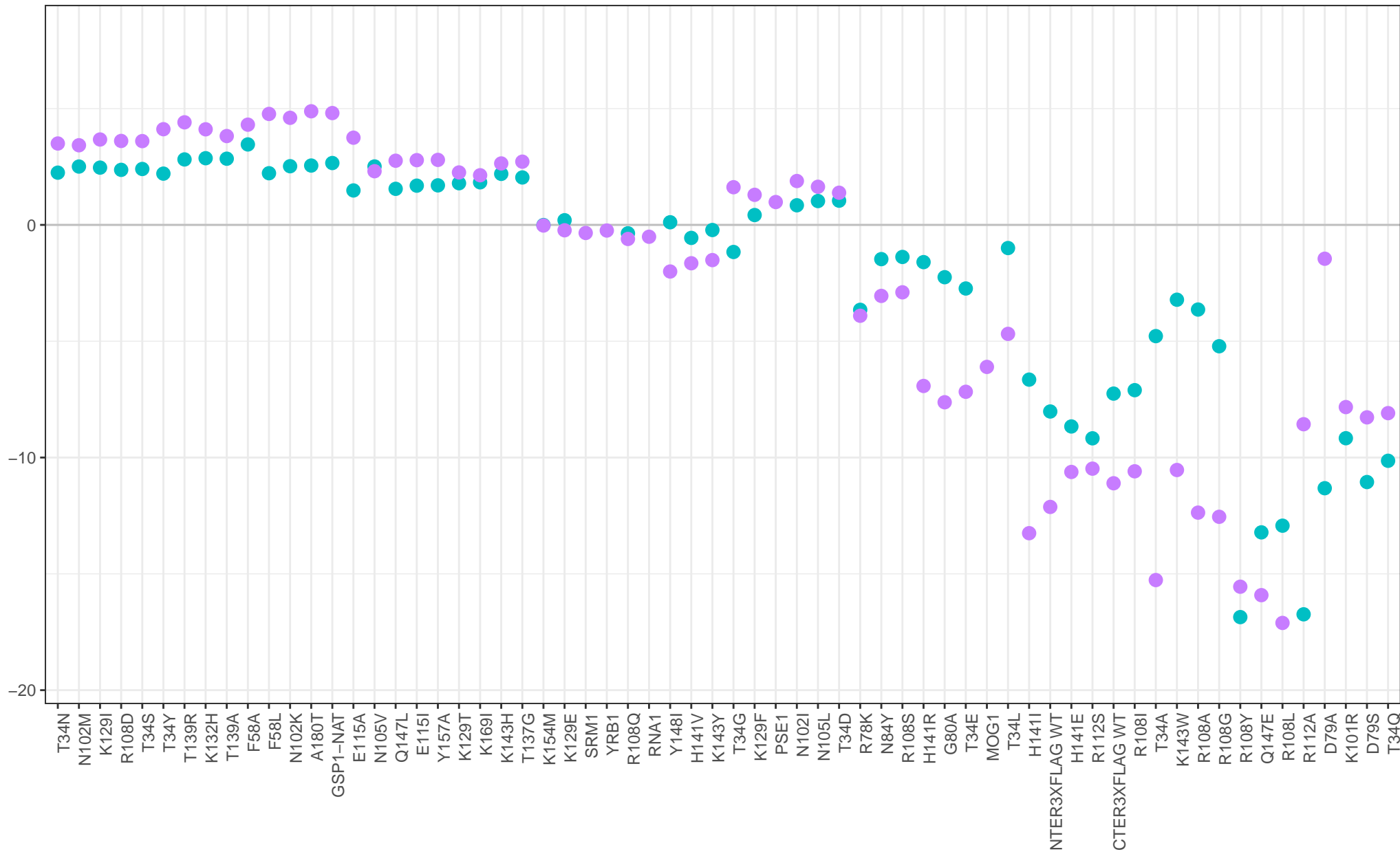


Tap42p/Pph21p/Rrd2p complex



THO complex

E-MAP score



library gene

- HPR1
- RLR1
- MFT1
- THP2

mutant

Tof1p/Mrc1p/Csm3p complex

E-MAP score

0

-10

-20

R108L R112S H141I R112A D79A MOG1 K101R CTER3XFLAG WT R108I Y157A N105V Y148I R108D T139A T139R H141V K132H K129F K129I T34N F58L T34S F58A Q147L N105L R108S T137G N84Y RNA1 K143W YRB1 R108A E115A R108G K129E SRM1 N102K N102I NTER3XFLAG WT Q147E K154M T34A K143Y T34D PSE1 T34L H141E R108Q R108Y H141R T34Q G80A D79S K169I GSP1-NAT T34Y A180T E115I K143H N102M K129T T34E R78K T34G

library gene

TOF1

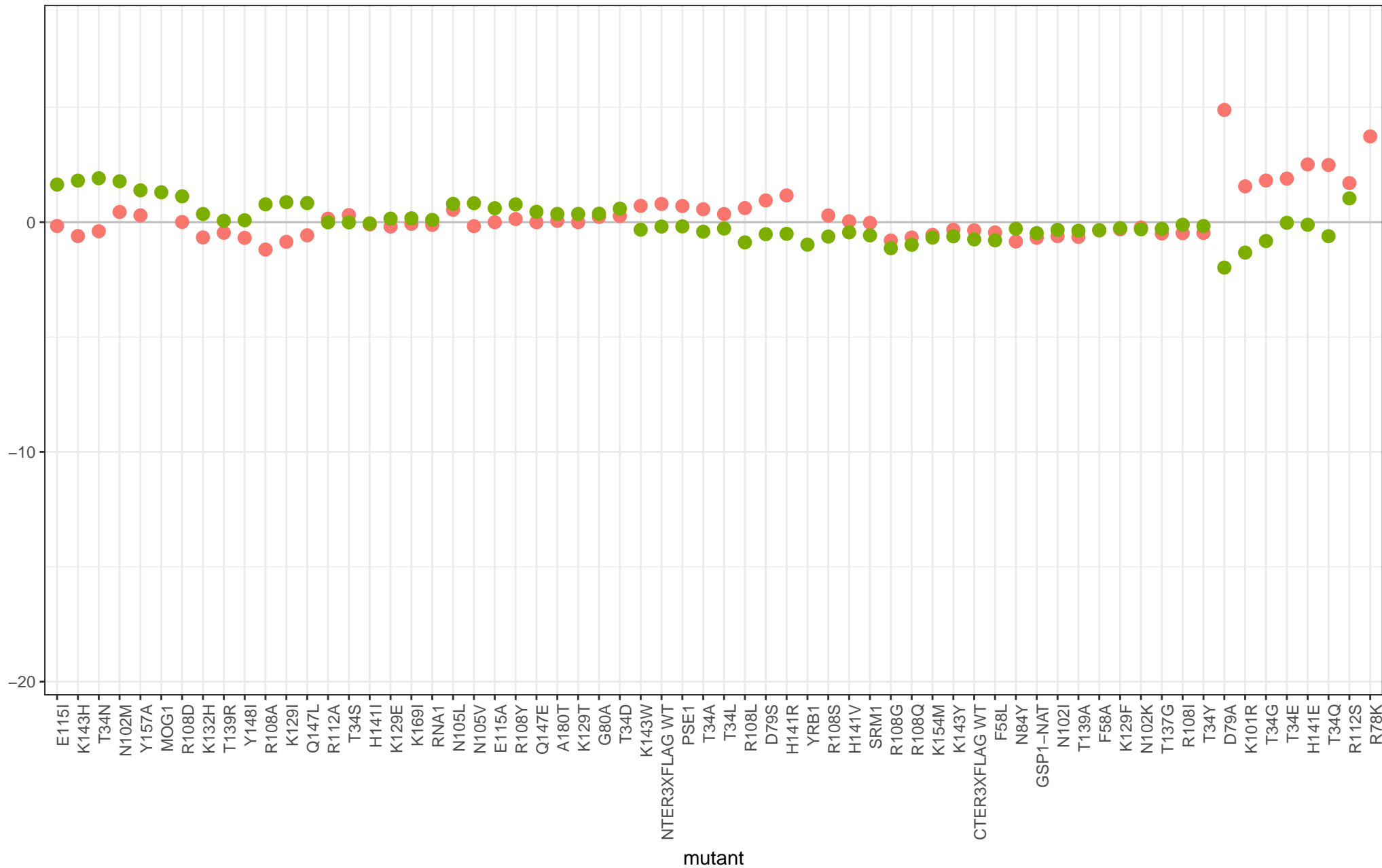
CSM3

MRC1

mutant

TORC 1 complex

E-MAP score



library gene

TOR1

TCO89

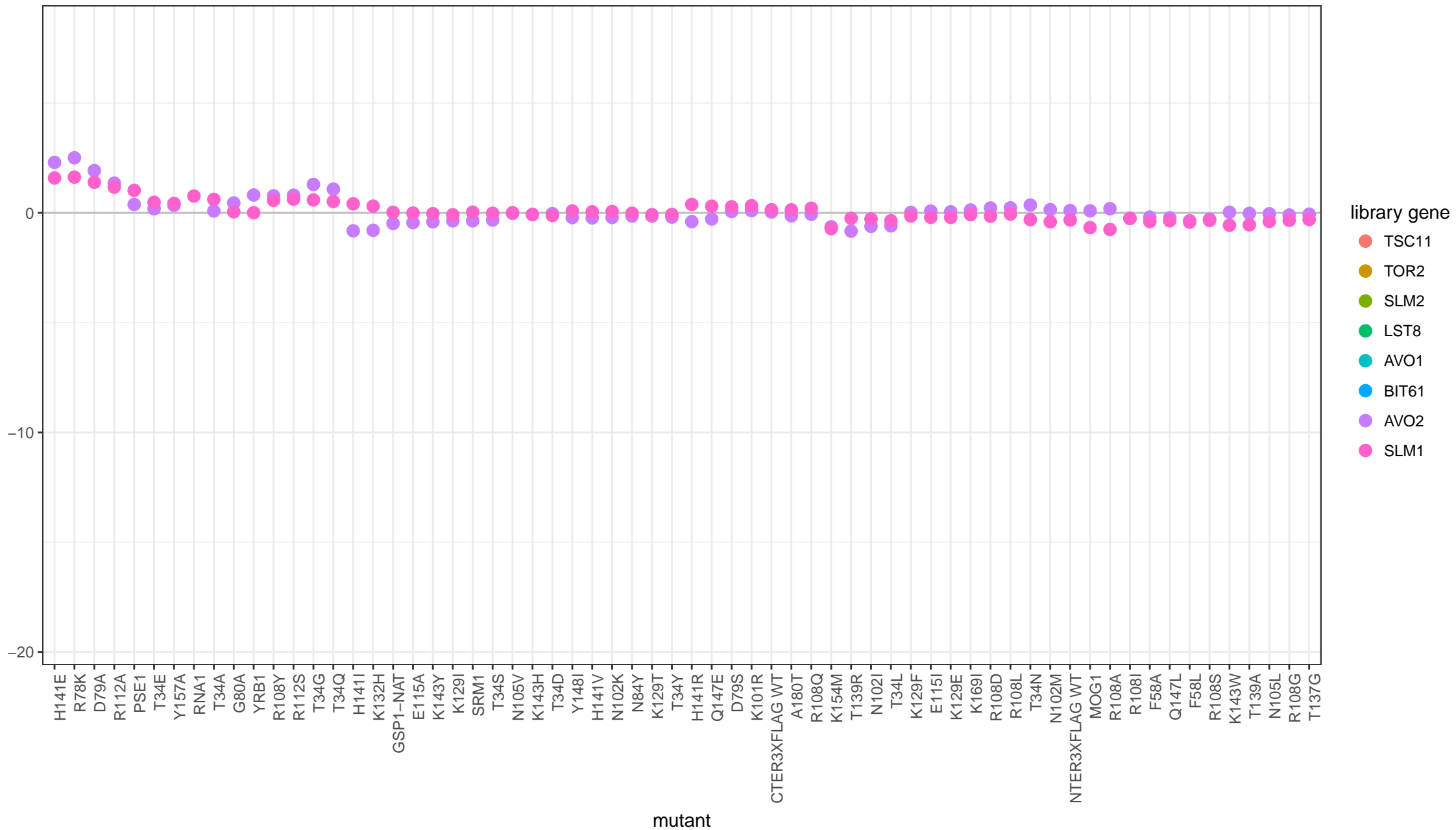
KOG1

LST8

mutant

TORC 2 complex

E-MAP score



TRAMP complex (Air1p)

E-MAP score

-20

-10

0

D79A
R78K
K169I
T137G
K129F
GSP1-NAT
T139R
T139A
T34G
R108Q
T34N
T34S
Y148I
D79S
K132H
NTER3XFLAG WT
R112S
T34E
R108L
T34A
Q147E
R108I
H141R
H141E
R112A
K101R
MOG1
CTER3XFLAG WT
K143W
T34L
R108Y
G80A
R108S
N84Y
H141I
N105V
R108G
E115I
K129E
N102I
R108A
H141V
T34Q
E115A
K143Y
K154M
YRB1
PSE1
RNA1
N105L
Y157A
A180T
N102M
K129T
F58L
N102K
K143H
T34D
K129I
Q147L
T34Y
F58A
R108D
SRM1

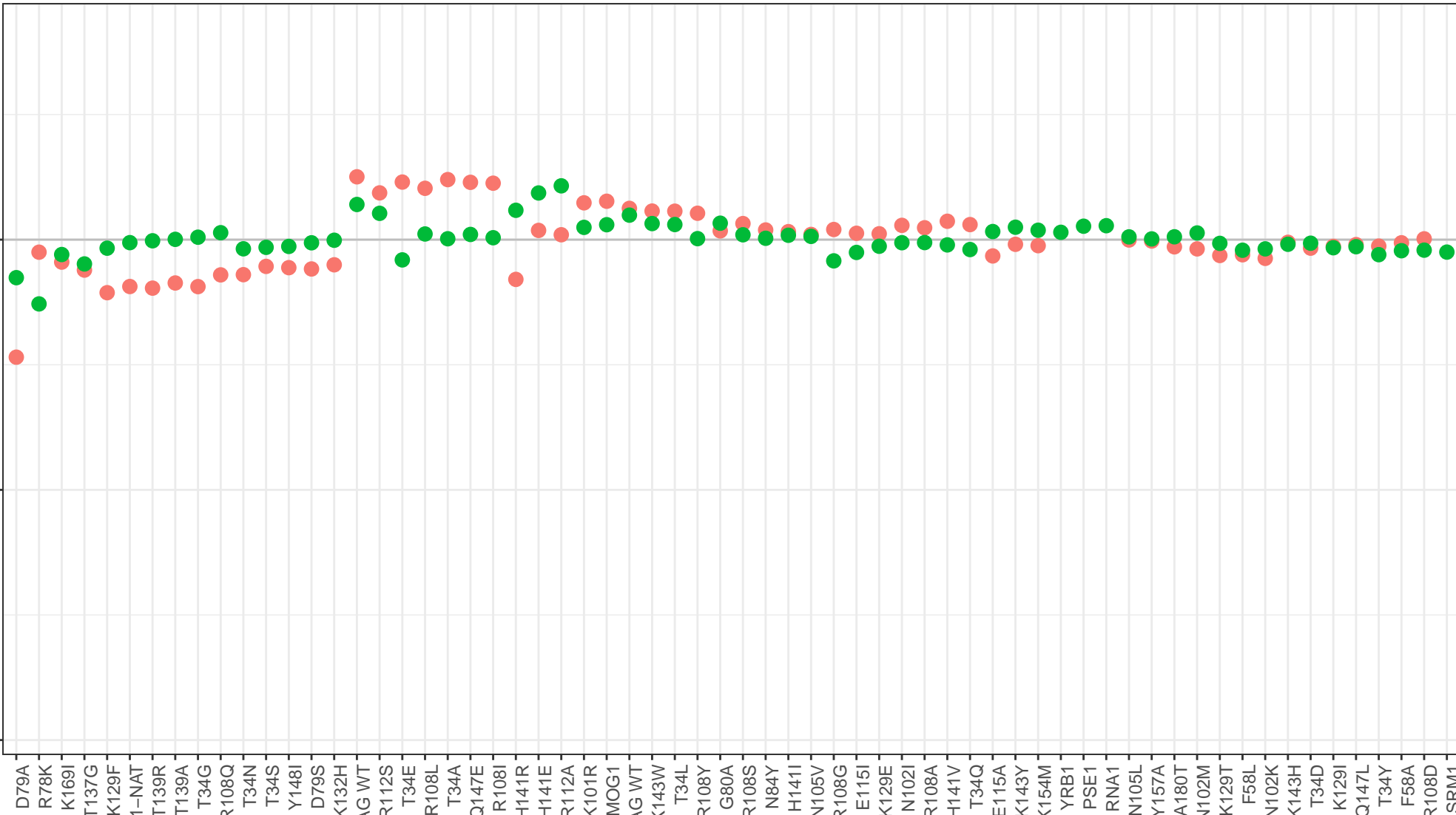
mutant

library gene

PAP2

AIR1

MTR4



TRAMP complex (Air2p)

E-MAP score

0

-10

-20

D79A
K101R
T34E
Q147E
R108I
R108L
R112S
NTER3XFLAG WT
T34A
CTER3XFLAG WT
R108Y
MOG1
K143W
T34L
H141E
E115I
SRM1
H141V
H141I
R108A
R108G
G80A
N105V
F58L
K129T
E115A
K132H
K169I
N102K
T34Y
Y157A
R108D
RNA1
A180T
K143Y
Q147L
Y148I
H141R
T139A
K129F
T34G
R108Q
T34N
GSP1-NAT
T139R
T34S
D79S
T137G
N102M
T34D
R78K
K129I
K154M
R112A
T34Q
N102I
R108S
K129E
N84Y
F58A
YRB1
N105L
K143H
PSE1

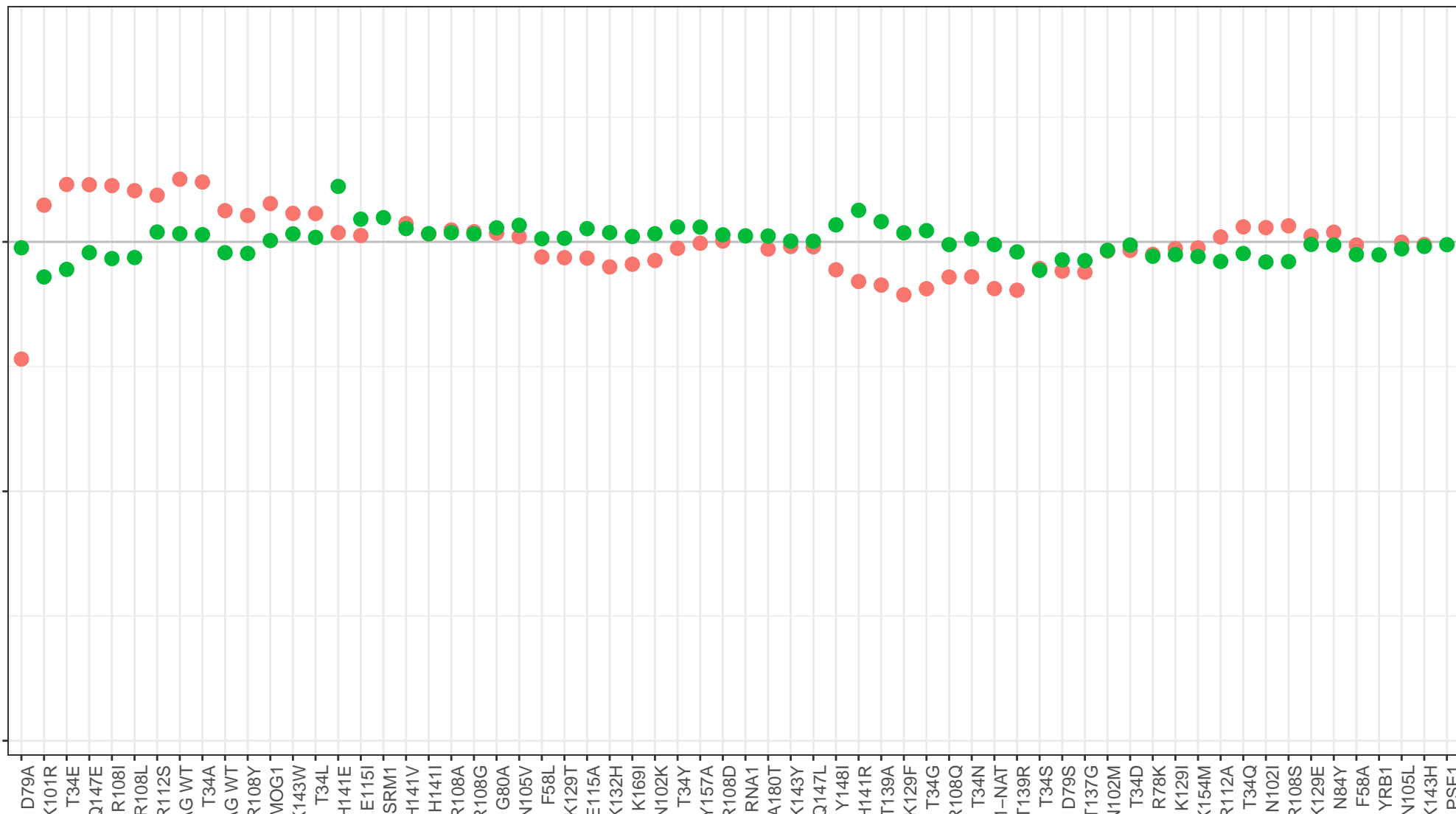
mutant

library gene

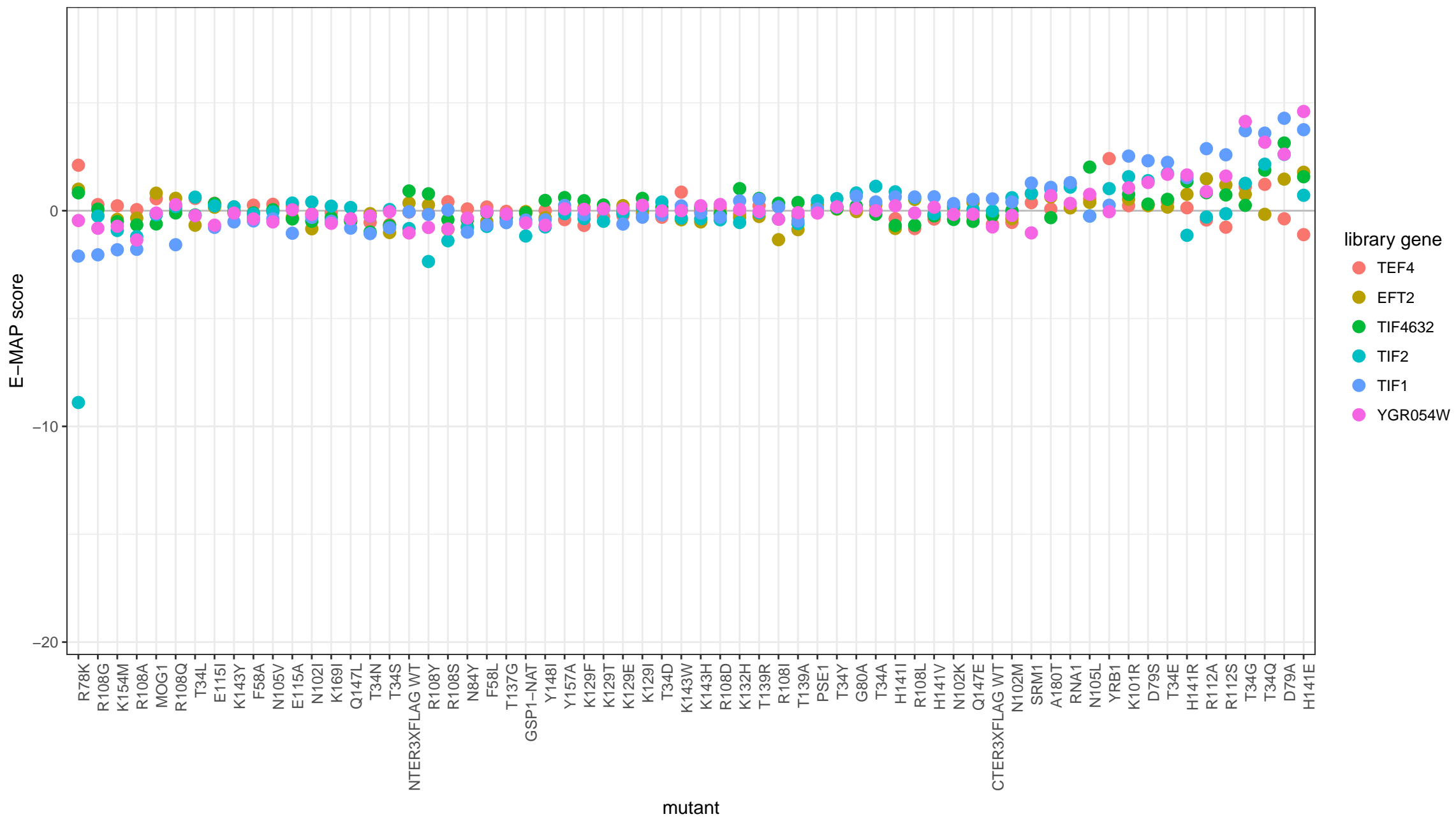
PAP2

AIR2

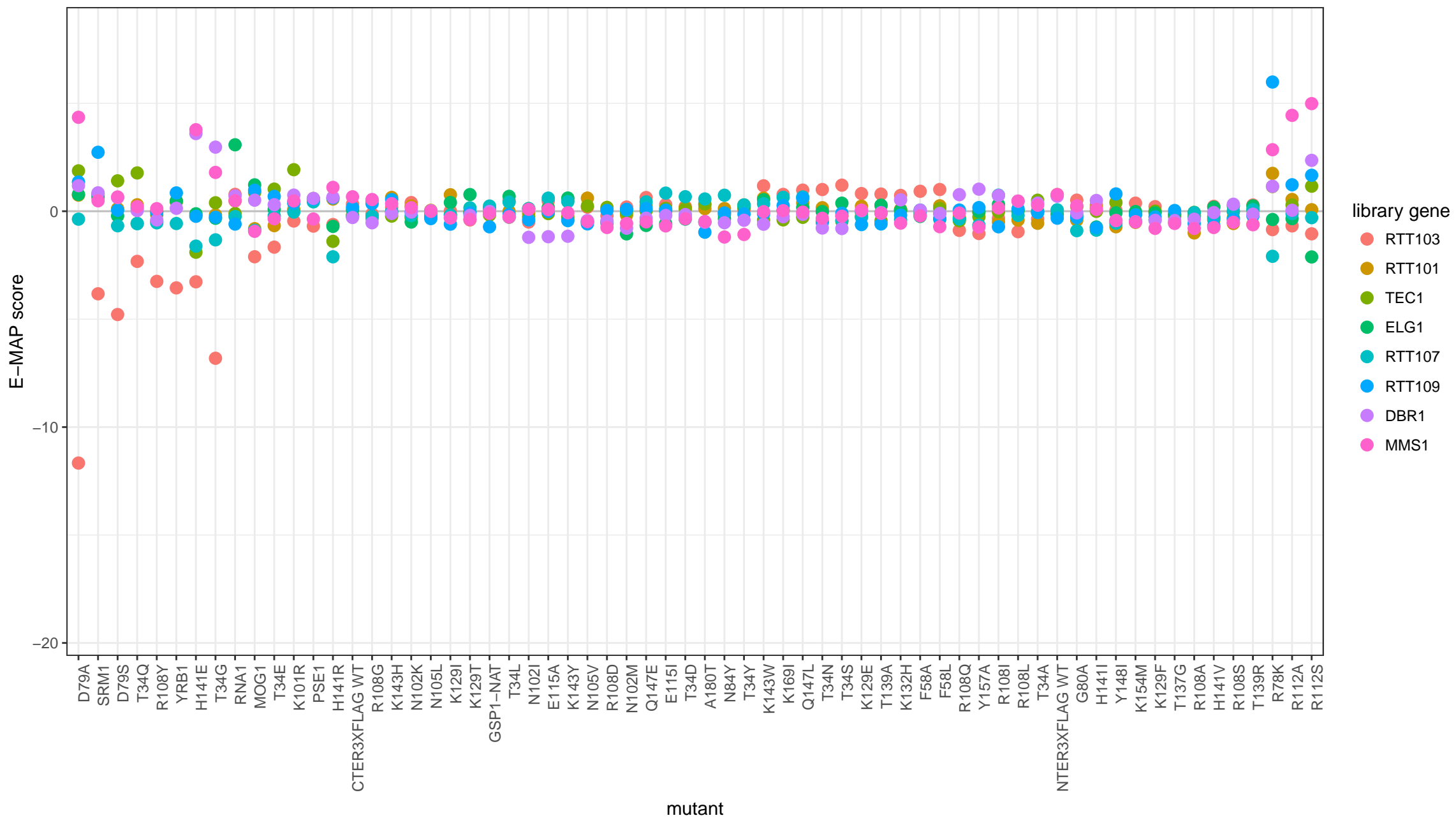
MTR4



translation factor activity, RNA binding

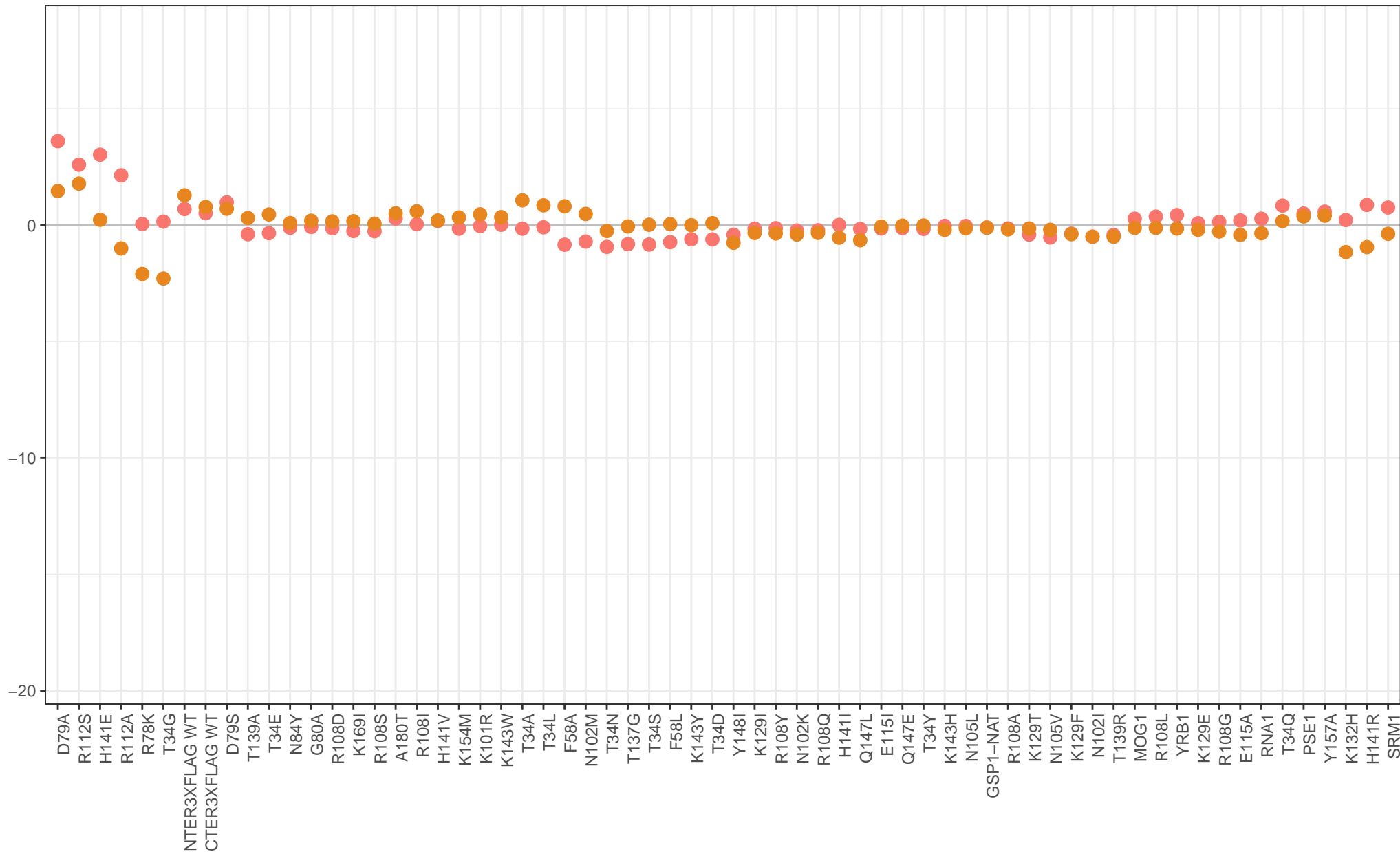


transposition



U1 snRNP complex

E-MAP score



library gene

- MUD1
- NAM8
- YHC1
- SNU71
- SNU56
- SNP1
- SMX3
- SMX2
- SME1
- SMD3
- SMD2
- SMD1
- SMB1
- PRP42
- PRP40
- LUC7
- PRP39

mutant

U2 snRNP complex

E-MAP score

0

-10

-20

mutant

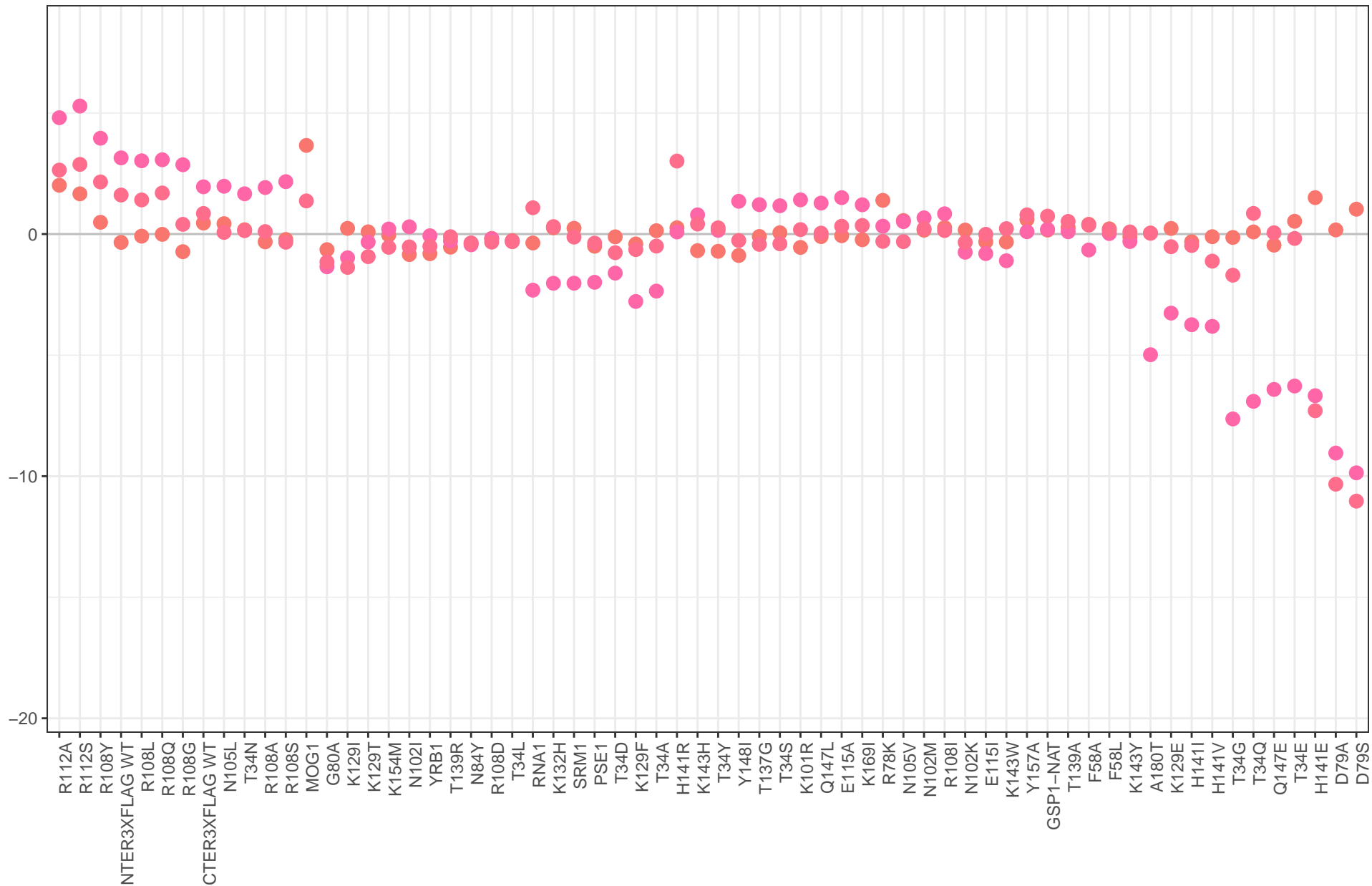
library gene

- IST3
- LEA1
- SMX3
- SMX2
- SME1
- SMD3
- SMD2
- SMD1
- SMB1
- RSE1
- PRP9
- PRP21
- PRP11
- MSL1
- HSH49
- HSH155
- CUS1
- CUS2

F58A
GSP1-NAT
K129T
R108G
YRB1
G80A
N105L
Q147L
K169I
R108I
R108D
K154M
R108Q
T139R
F58L
R108A
T34N
R108S
T34L
T137G
Y148I
RNA1
E115A
Q147E
T139A
A180T
T34D
K143H
H141I
K129F
N102I
T34A
K129I
K143Y
K132H
N84Y
PSE1
E115I
T34Y
H141V
K129E
K143W
N102K
T34S
N102M
N105V
D79A
H141E
R112S
T34E
T34G
R112A
T34Q
R108Y
H141R
NTER3XFLAG WT
R108L
CTER3XFLAG WT
MOG1
D79S
K101R
Y157A
R78K
SRM1

U4/U6 x U5 tri-snRNP complex

E-MAP score



library gene

- LSM7
- SPP381
- SNU23
- SNU13
- SNU114
- SMX3
- SMX2
- SME1
- SMD3
- SMD2
- SMD1
- SMB1
- PRP8
- PRP6
- PRP4
- PRP38
- PRP31
- PRP3
- PRP18
- LSM8
- LSM5
- LSM4
- LSM3
- LSM2
- BRR2
- DIB1
- LSM6
- SNU66

U6 snRNP complex

E-MAP score

-20

-10

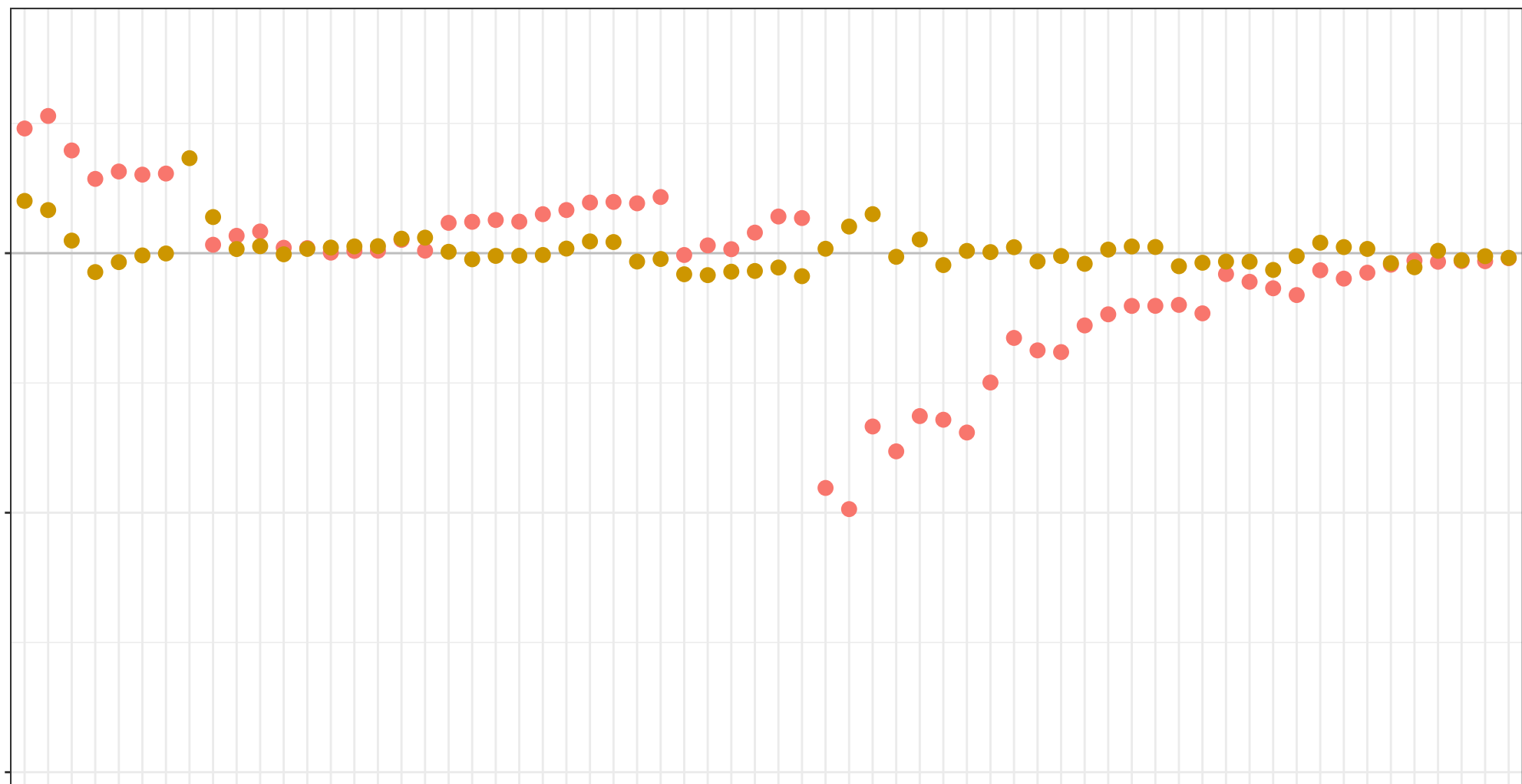
0

R112A
R112S
R108Y
R108G
NTER3XFLAG WT
R108L
R108Q
MOG1
R78K
N102M
R108I
K154M
GSP1-NAT
F58L
H141R
T139A
N105V
Y157A
T34S
K169I
Q147L
T137G
E115A
T34N
CTER3XFLAG WT
N105L
R108A
R108S
YRB1
N102I
T34Y
K143H
K101R
Y148I
D79A
D79S
H141E
T34G
T34E
Q147E
T34Q
A180T
K129E
H141I
H141V
K129F
T34A
K132H
SRM1
PSE1
RNA1
E115I
K143W
G80A
T34D
F58A
K129I
N102K
N84Y
T139R
K129T
T34L
K143Y
R108D

mutant

library gene

- LSM6
- LSM7
- PRP24
- LSM8
- LSM5
- LSM4
- LSM2
- LSM3



ubiquitin conjugating enzyme complex

E-MAP score

0

-10

-20

K101R
T34G
Y157A
R108L
H141V
SRM1
H141I
K154M
K143W
NTER3XFLAG WT
R108Y
CTER3XFLAG WT
R108G
R108D
T139A
E115I
K129E
K132H
K143H
R78K
T34Y
N102K
N102I
R108I
E115A
R108A
K169I
Y148I
GSP1-NAT
T139R
T34A
F58A
YRB1
A180T
K143Y
MOG1
G80A
Q147E
R108S
Q147L
T34L
K129F
T137G
RNA1
PSE1
R108Q
K129T
N105V
N105L
F58L
K129I
N102M
T34N
T34D
N84Y
T34S
D79A
D79S
H141E
T34Q
H141R
T34E
R112A
R112S

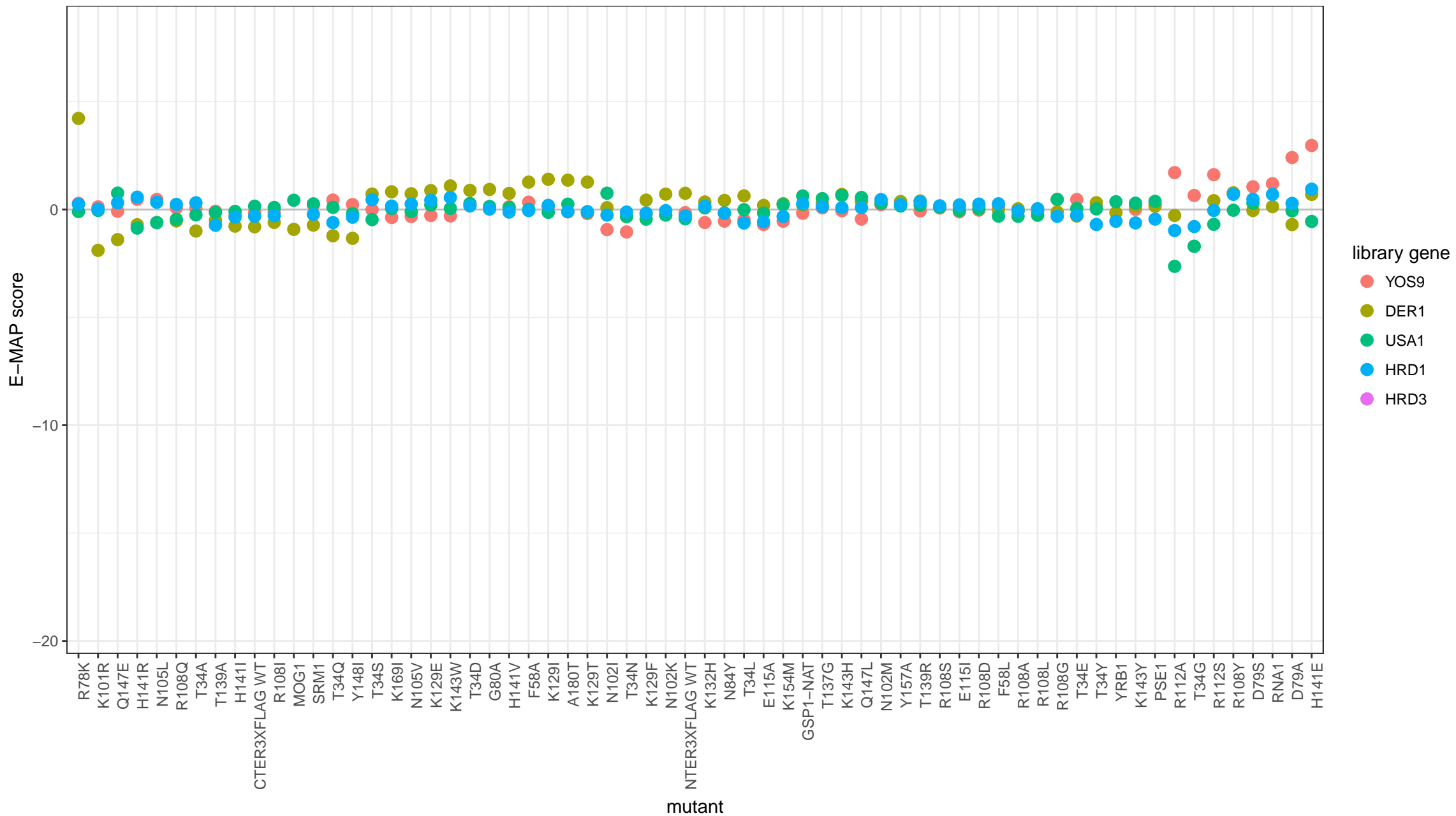
mutant

library gene

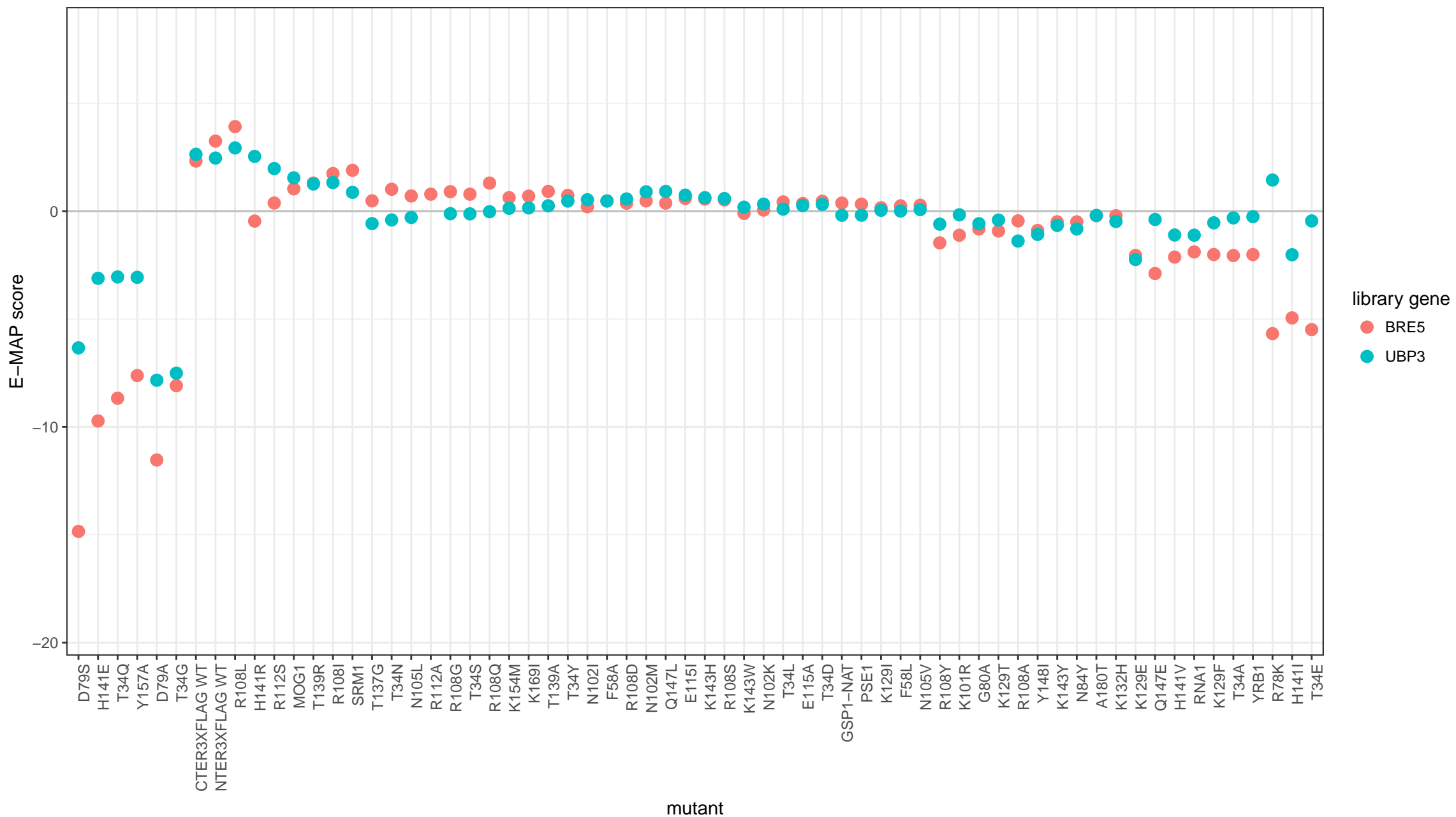
MMS2

UBC13

ubiquitin ligase ERAD-L complex



Ubp3p/Bre5p complex



Ume6p/Ime1p complex

E-MAP score

0

-10

-20

R112S H141R R108G R108Y R112A MOG1 Q147E R108L T34A K101R SRM1 T137G R108A Y157A K129E T34D A180T R108I F58L T34N N105L YRB1 K143W N102I F58A H141V K143H R78K N105V RNA1 K143Y N102M T34S T139R K129T Q147L GSP1-NAT T139A E115I T34G Y148I D79S R108Q K129F R108D K129I N102K PSE1 K169I E115A R108S K132H N84Y T34L T34Y H141I K154M D79A NTER3XFLAG WT CTER3XFLAG WT T34Q H141E G80A T34E

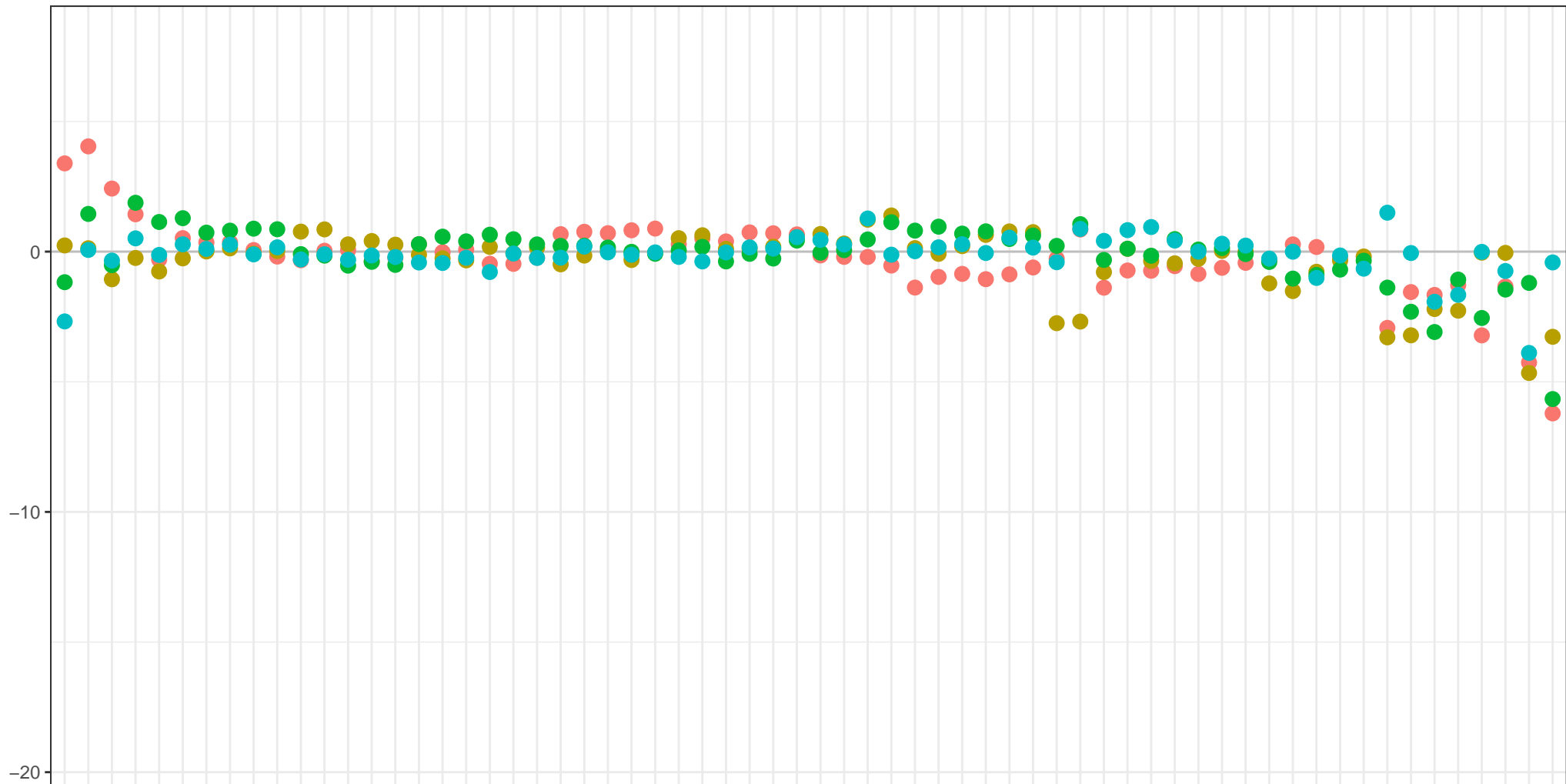
library gene

IME1
UME6

mutant

UTP C complex

E-MAP score

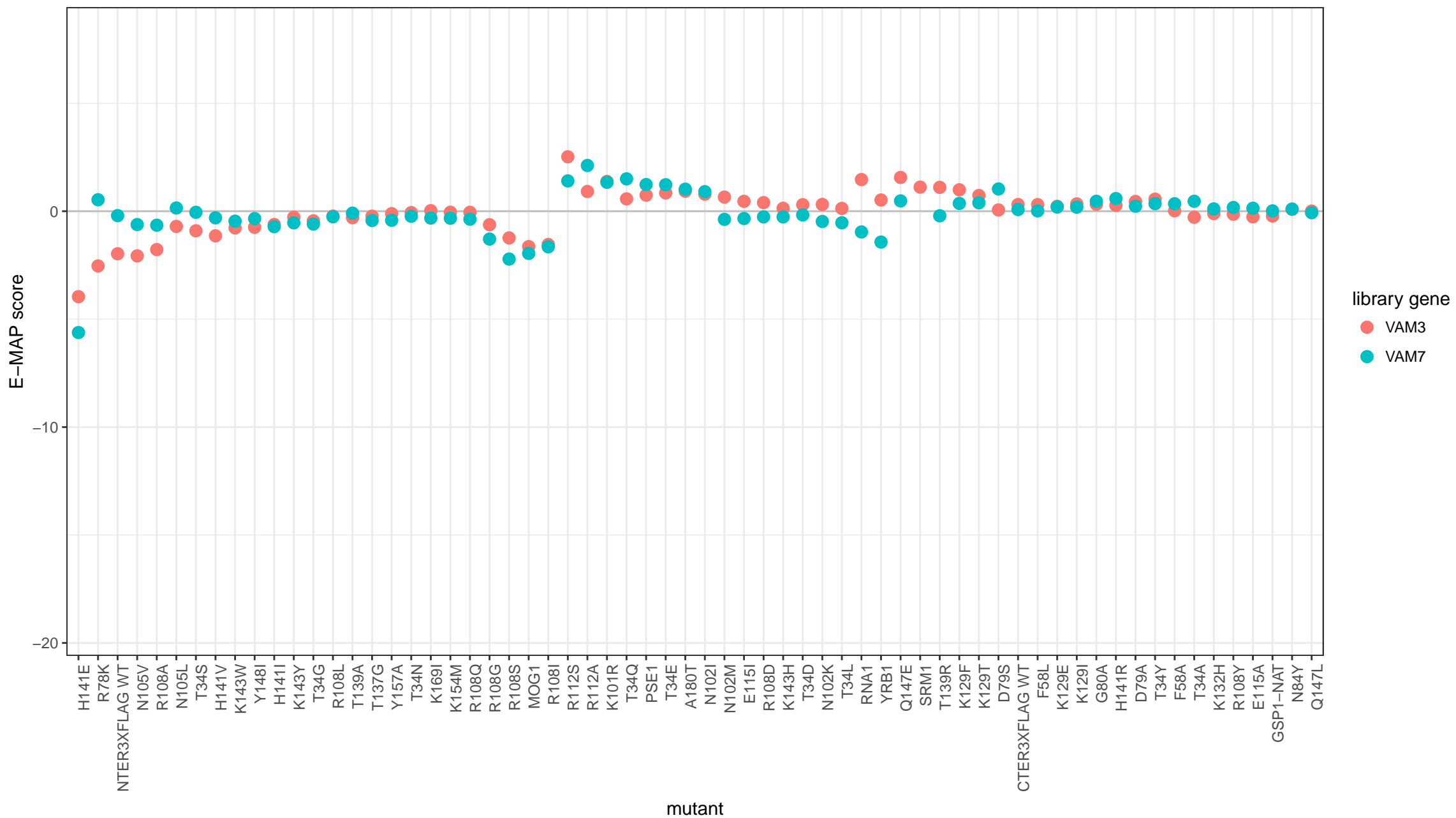


library gene

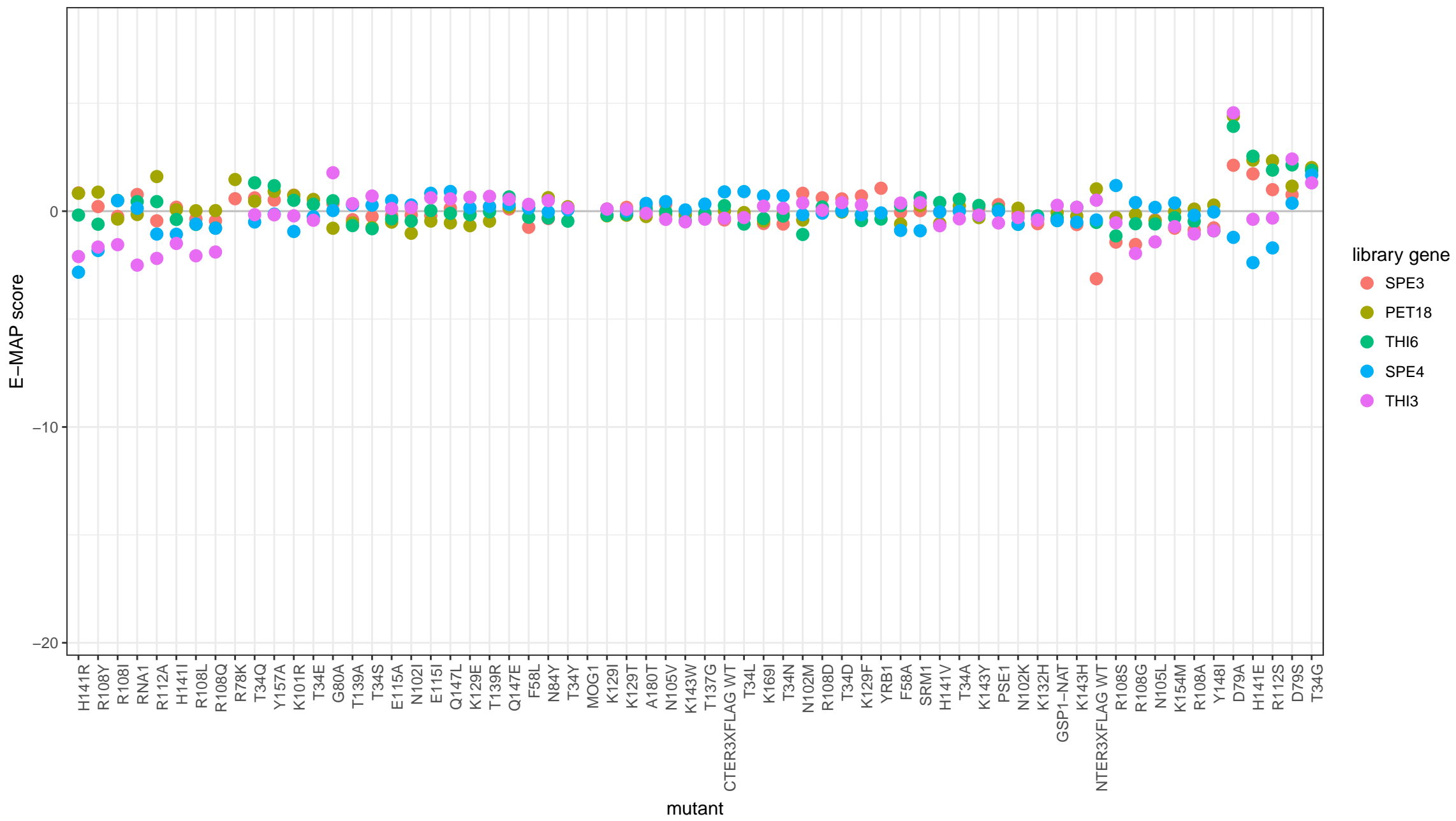
- CKB1
- CKA1
- CKA2
- CKB2
- RRP7
- UTP22

mutant

Vam3p/Vam7 vacuolar tSNARE complex

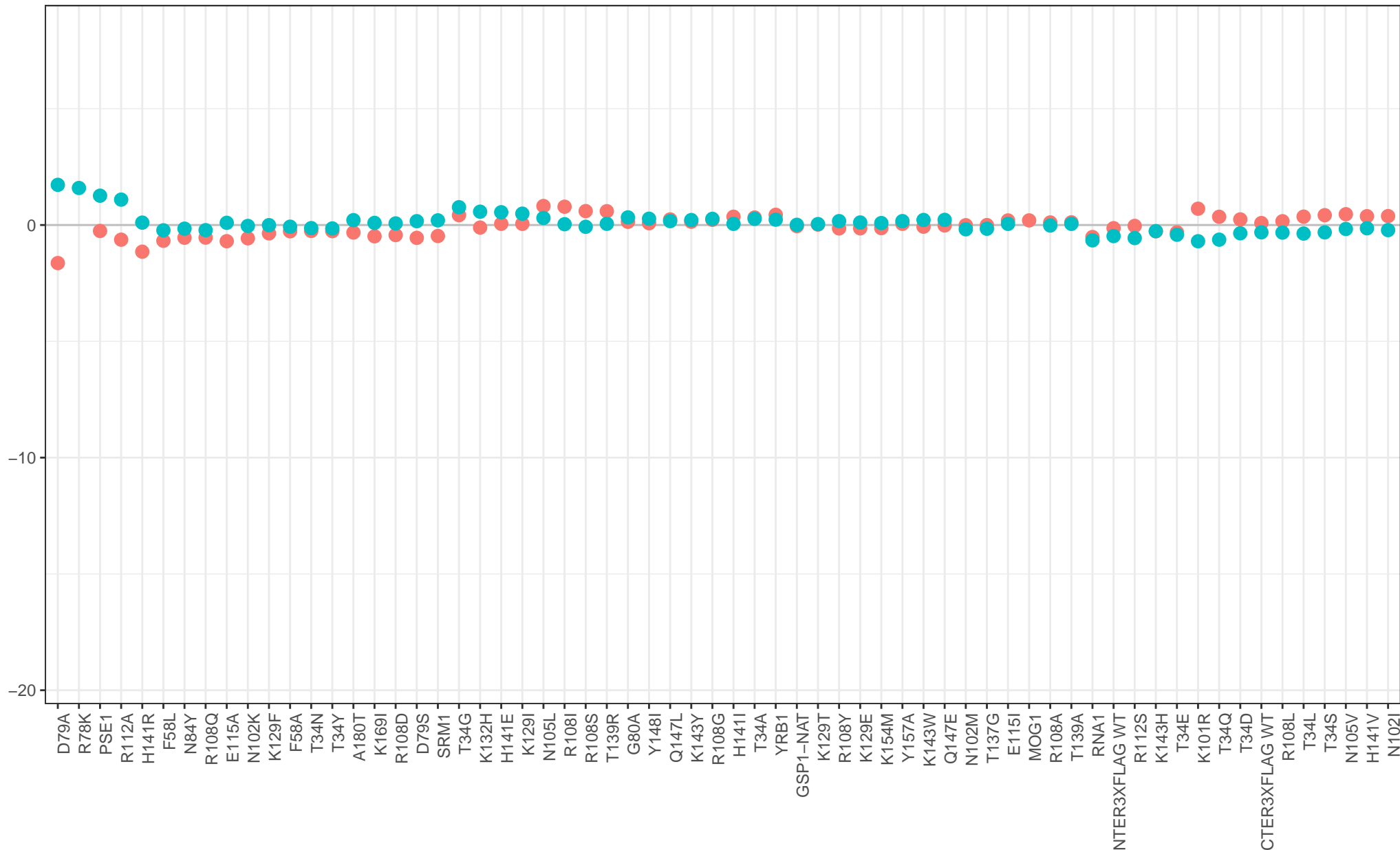


vitamin metabolic process



zeta DNA polymerase complex

E-MAP score



library gene

REV3

REV7

mutant