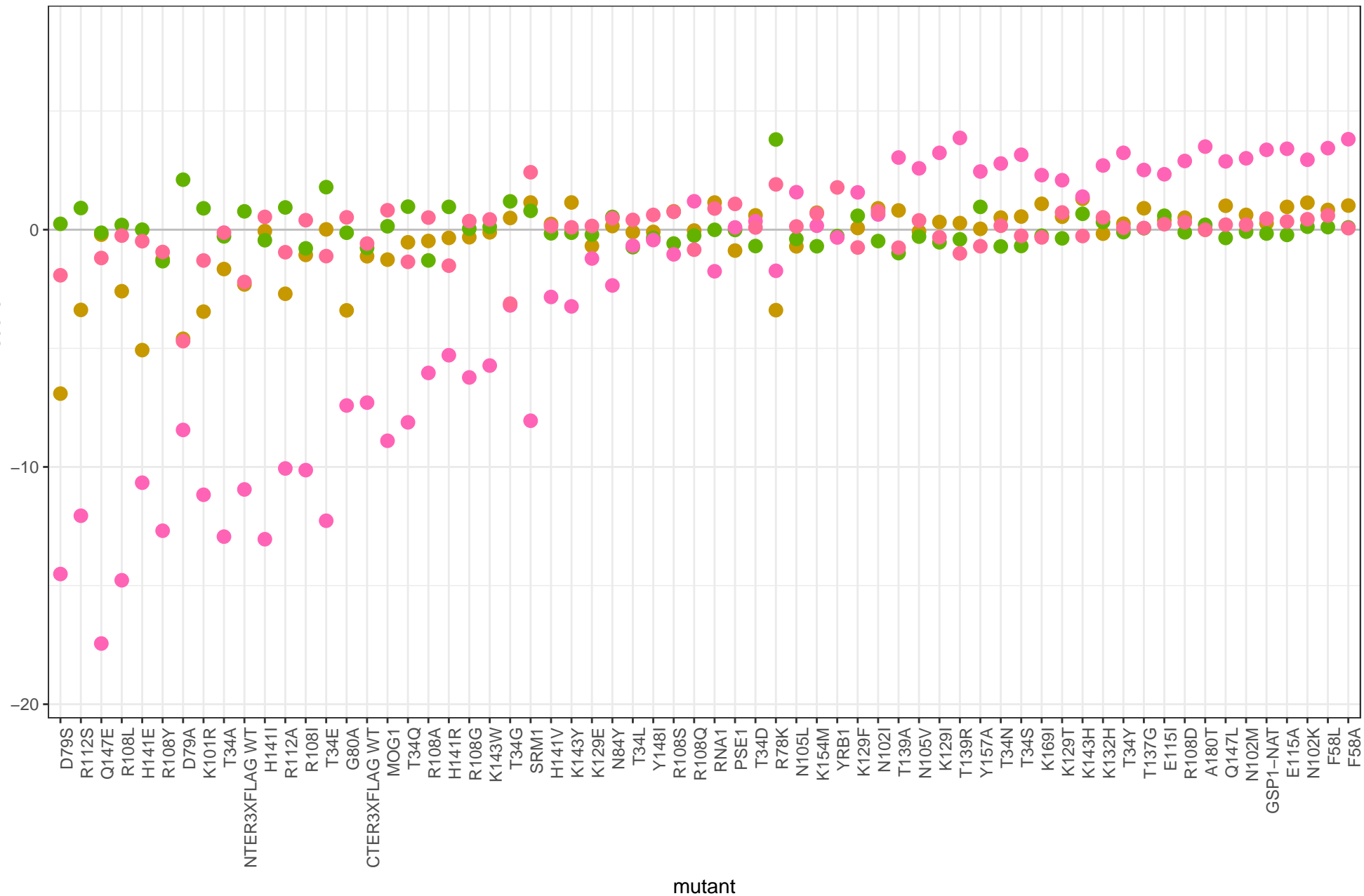
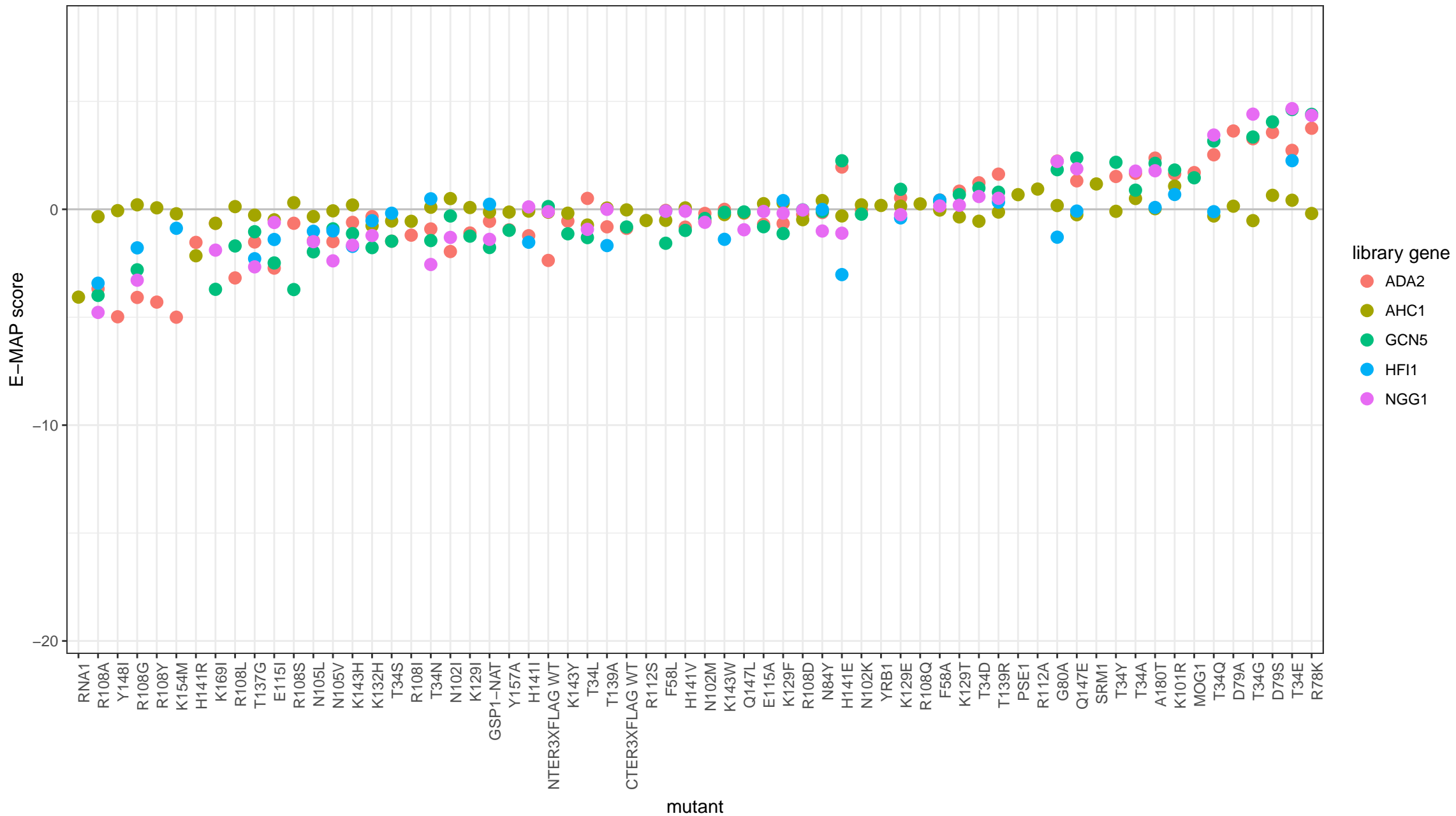


19/22S regulator

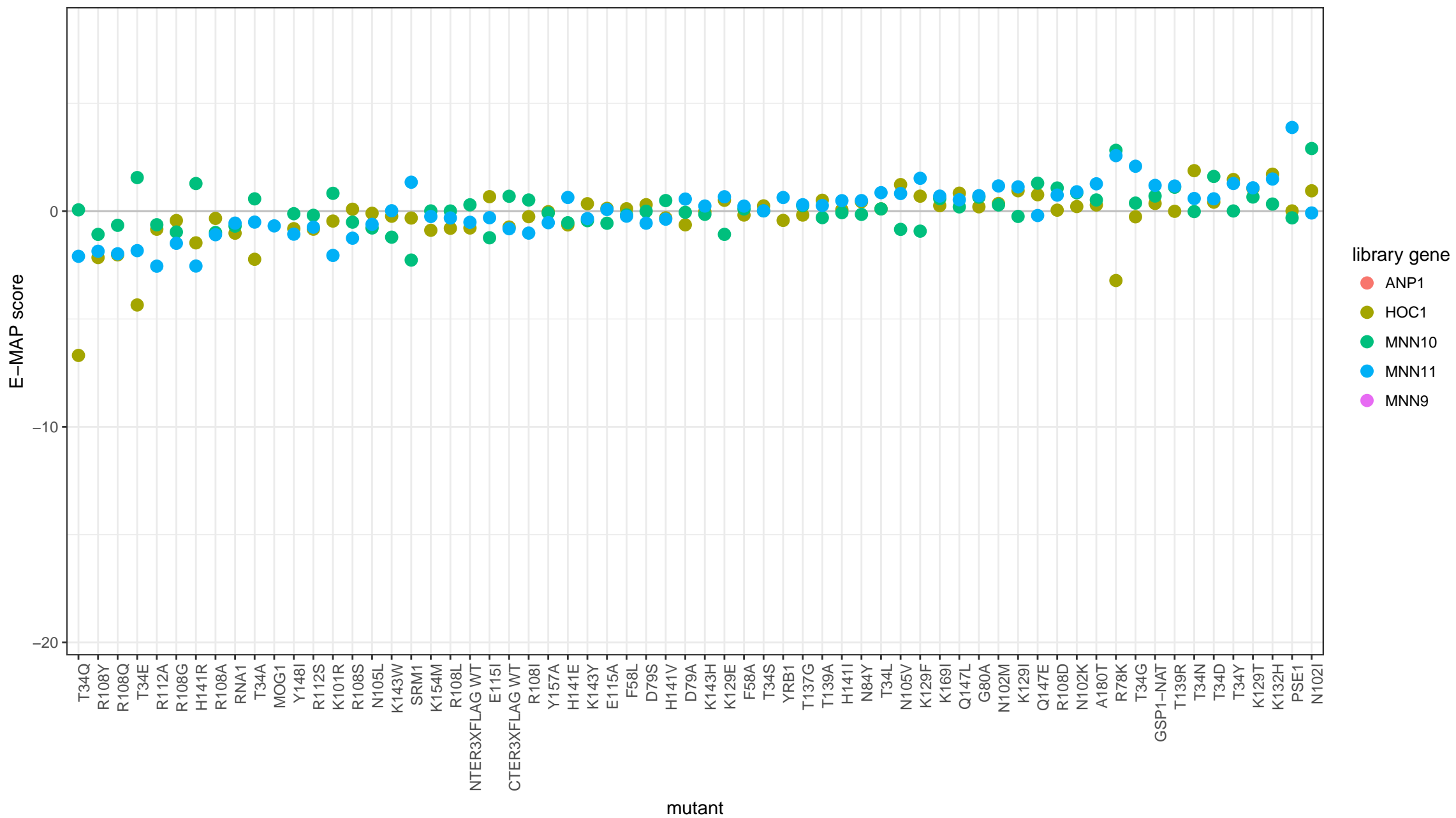
E-MAP score



Ada2p/Gcn5p/Ada3 transcription activator complex

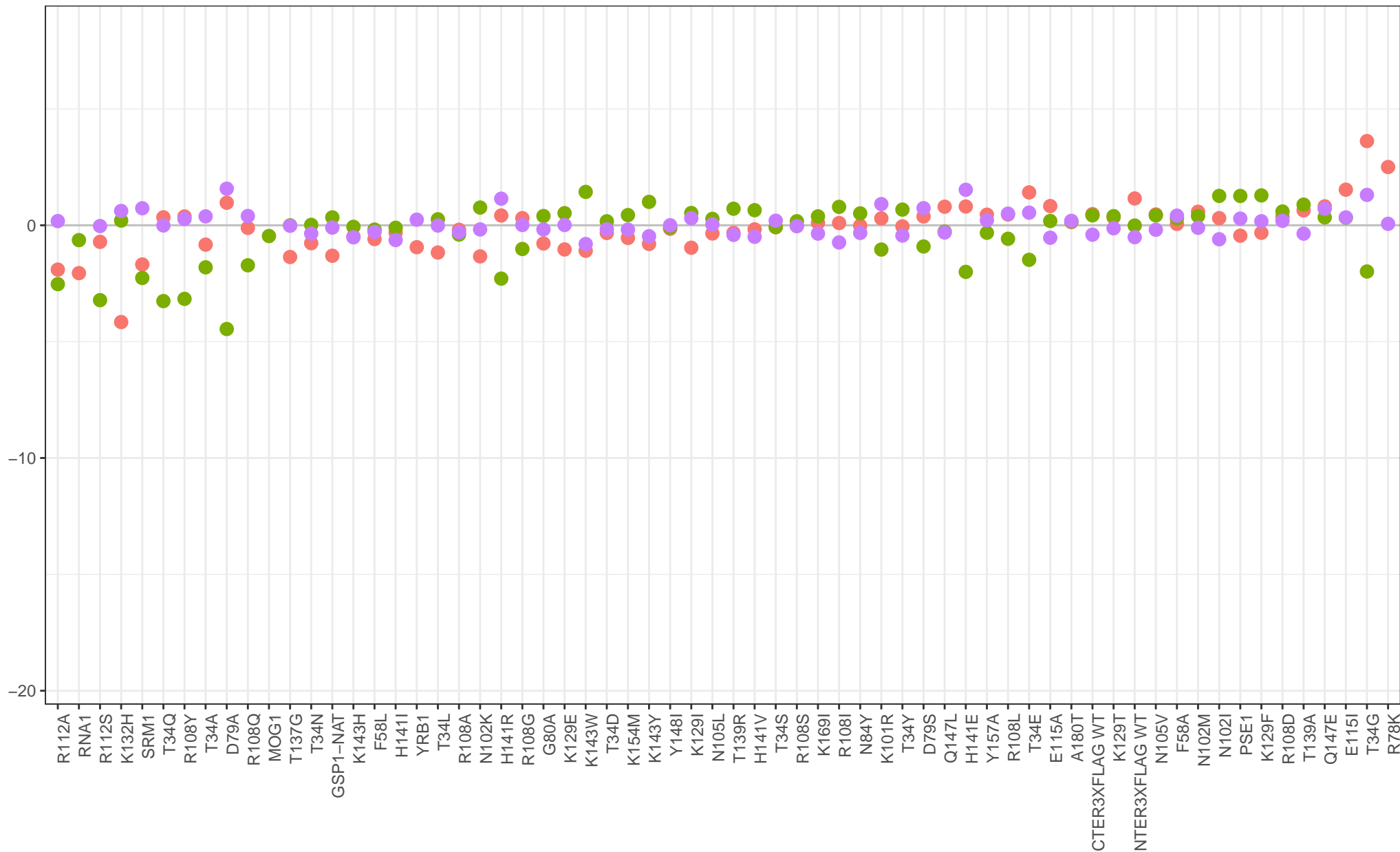


alpha-1,6-mannosyltransferase complex(Anp1p/Mnn9p)



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

E-MAP score



library gene

TPS1

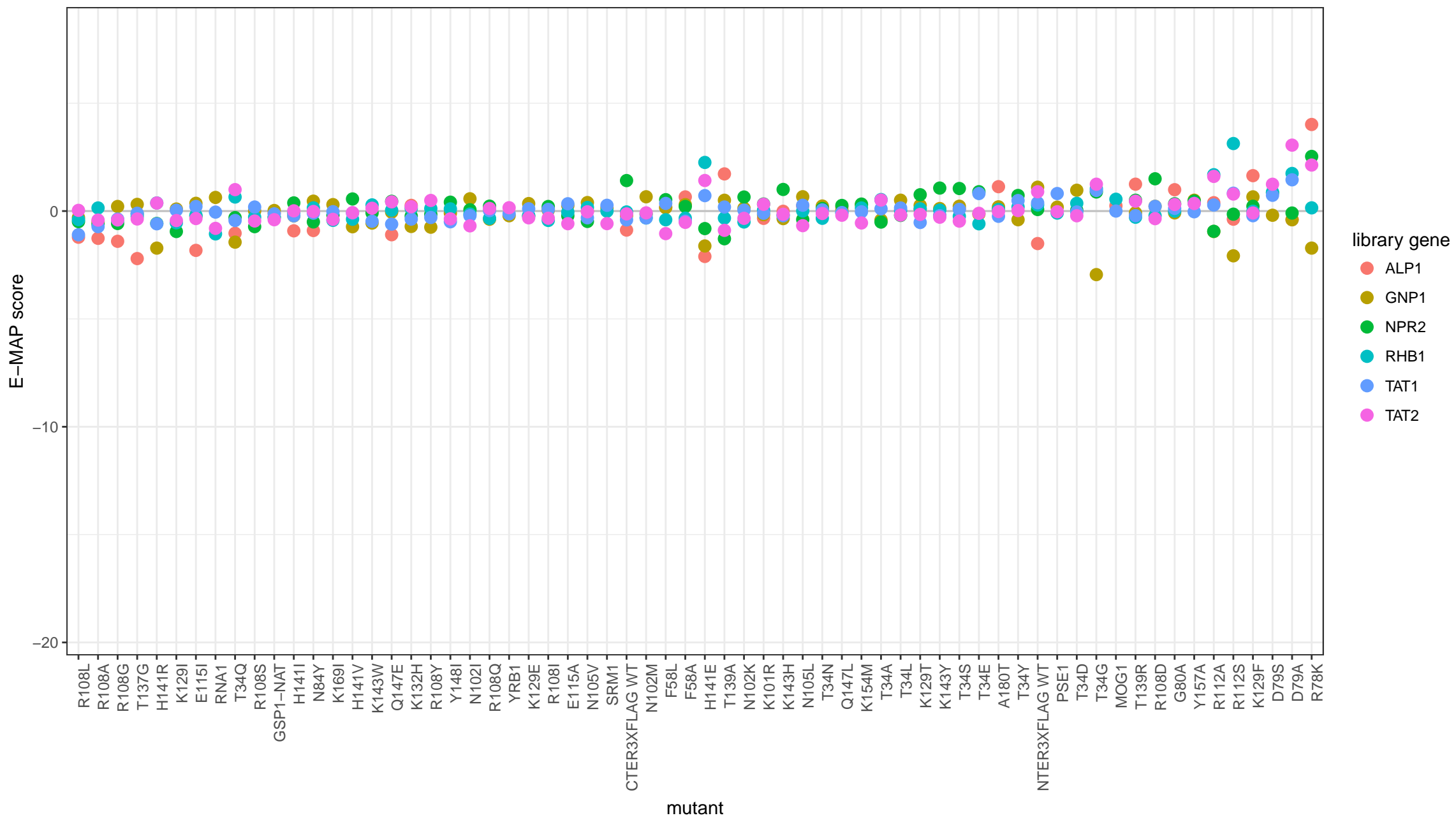
TPS2

TPS3

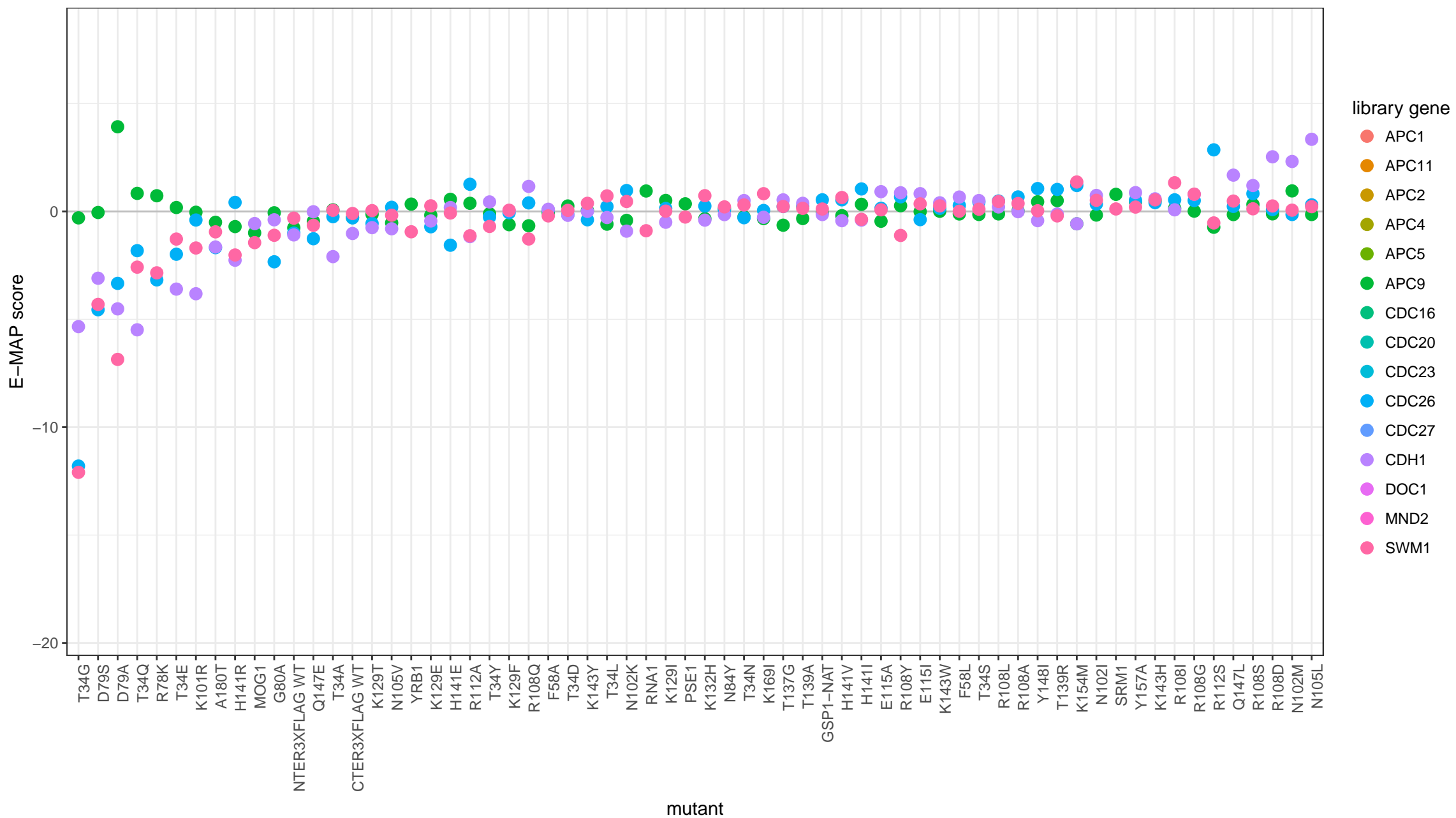
TSL1

mutant

amino acid transport



anaphase-promoting complex



AP-3 adaptor complex

E-MAP score

-20

-10

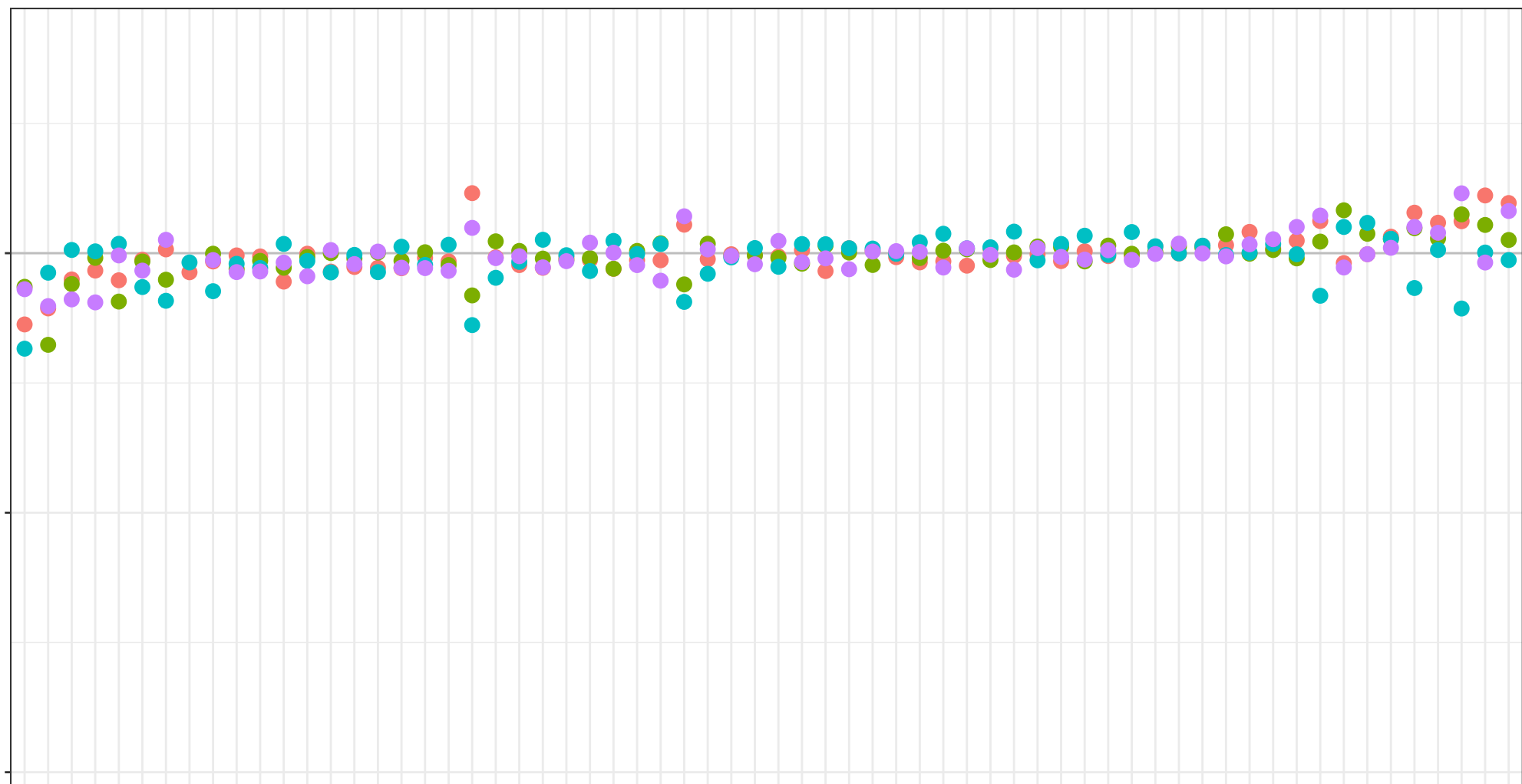
0

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

mutant

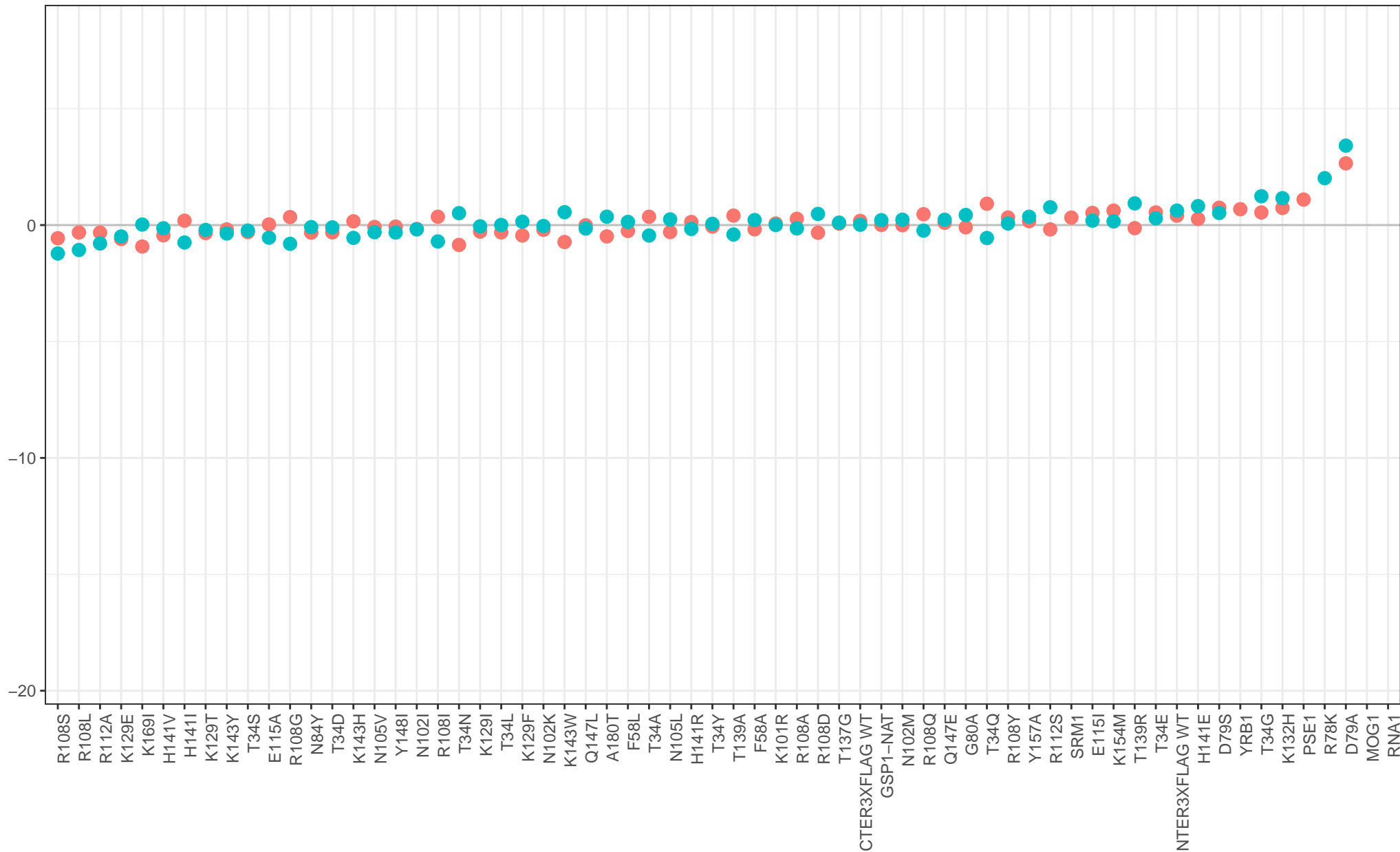
library gene

- APL5
- APL6
- APM3
- APS3



ARGR complex

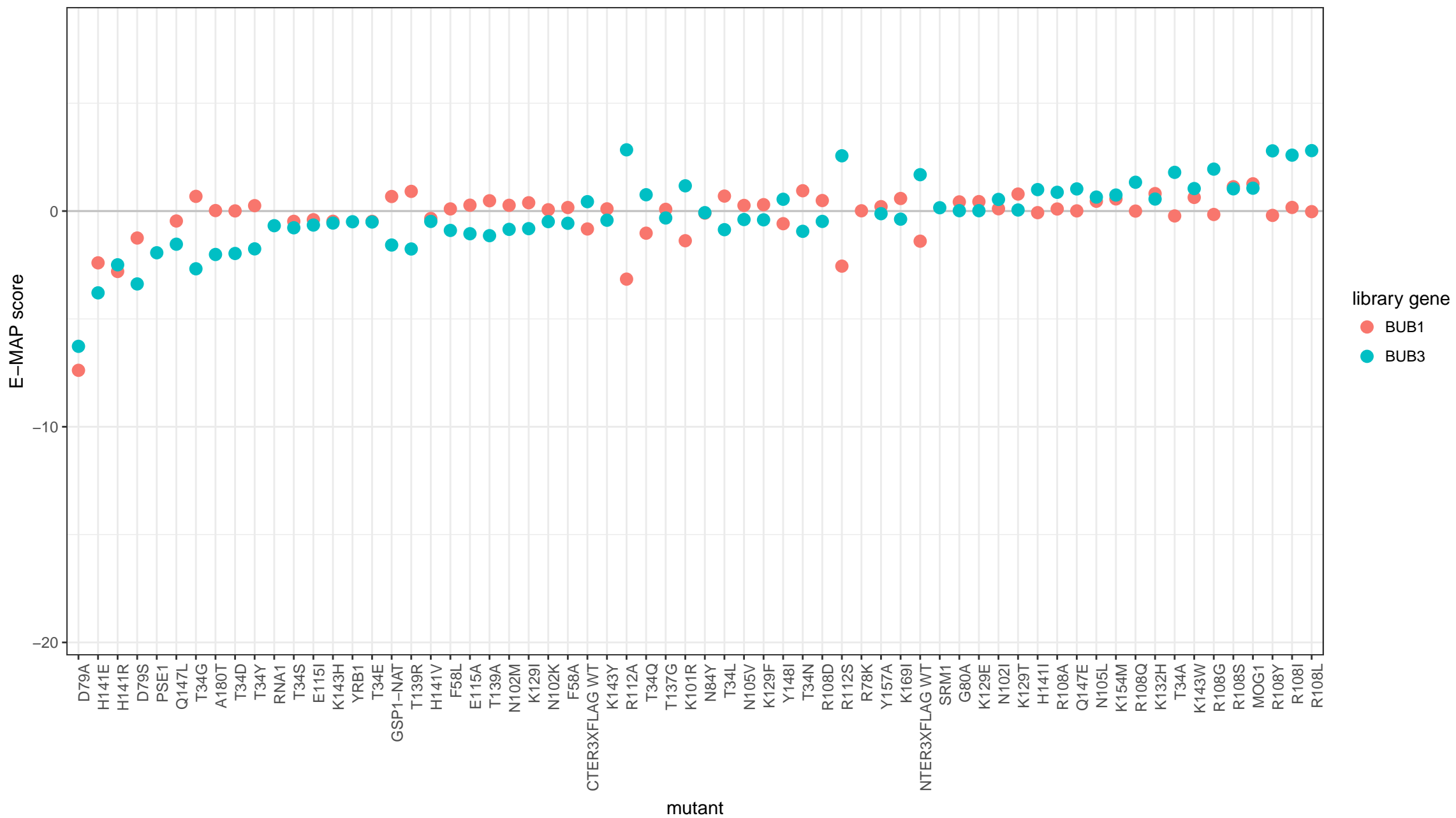
E-MAP score



library gene

- ARG80
- ARG81
- ARG82
- MCM1

Bub1p/Bub3p complex



Bub2p/Bfa1p complex

E-MAP score

-20

-10

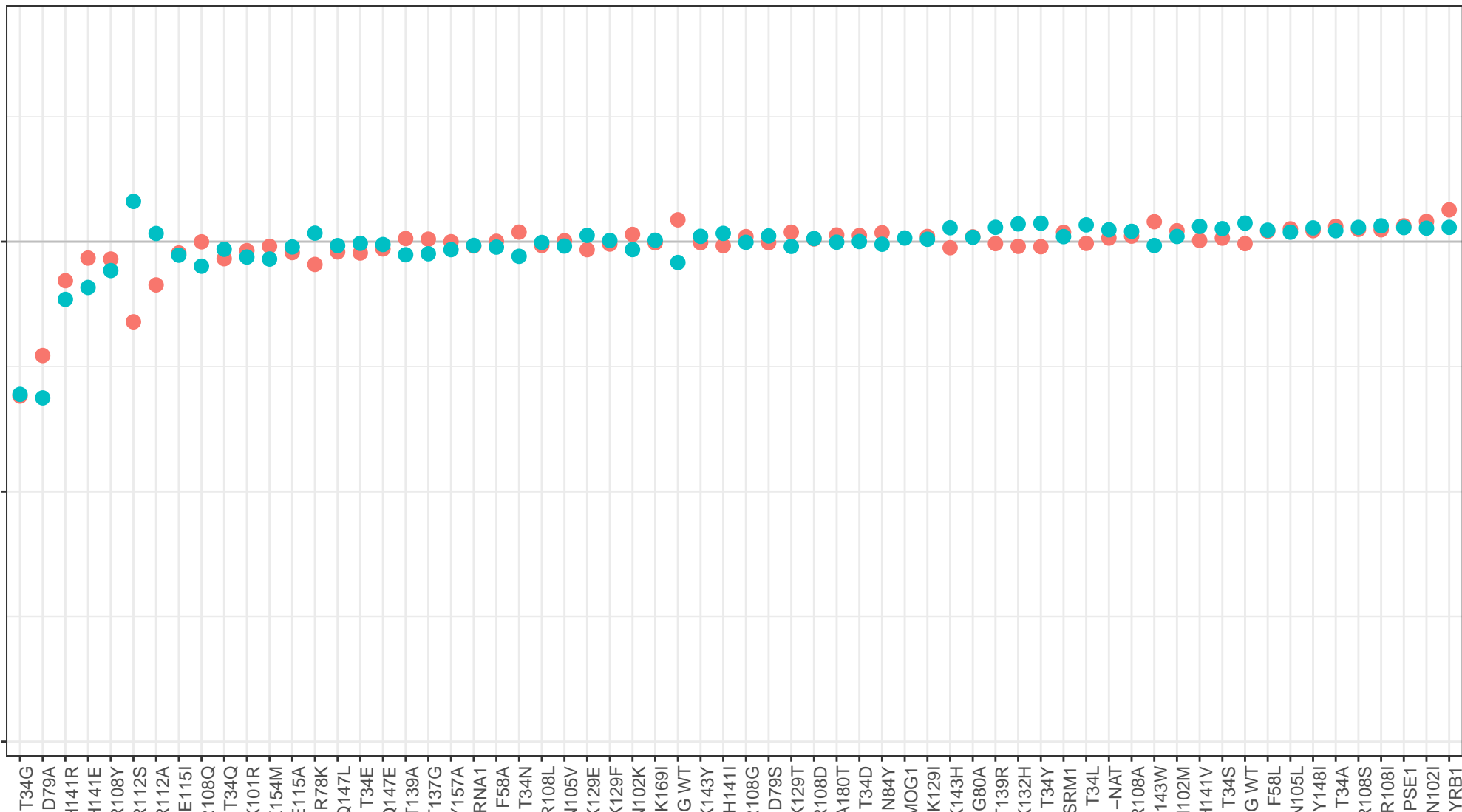
0

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

mutant

library gene

BFA1
BUB2



calcineurin complex

E-MAP score

-20

-10

0

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

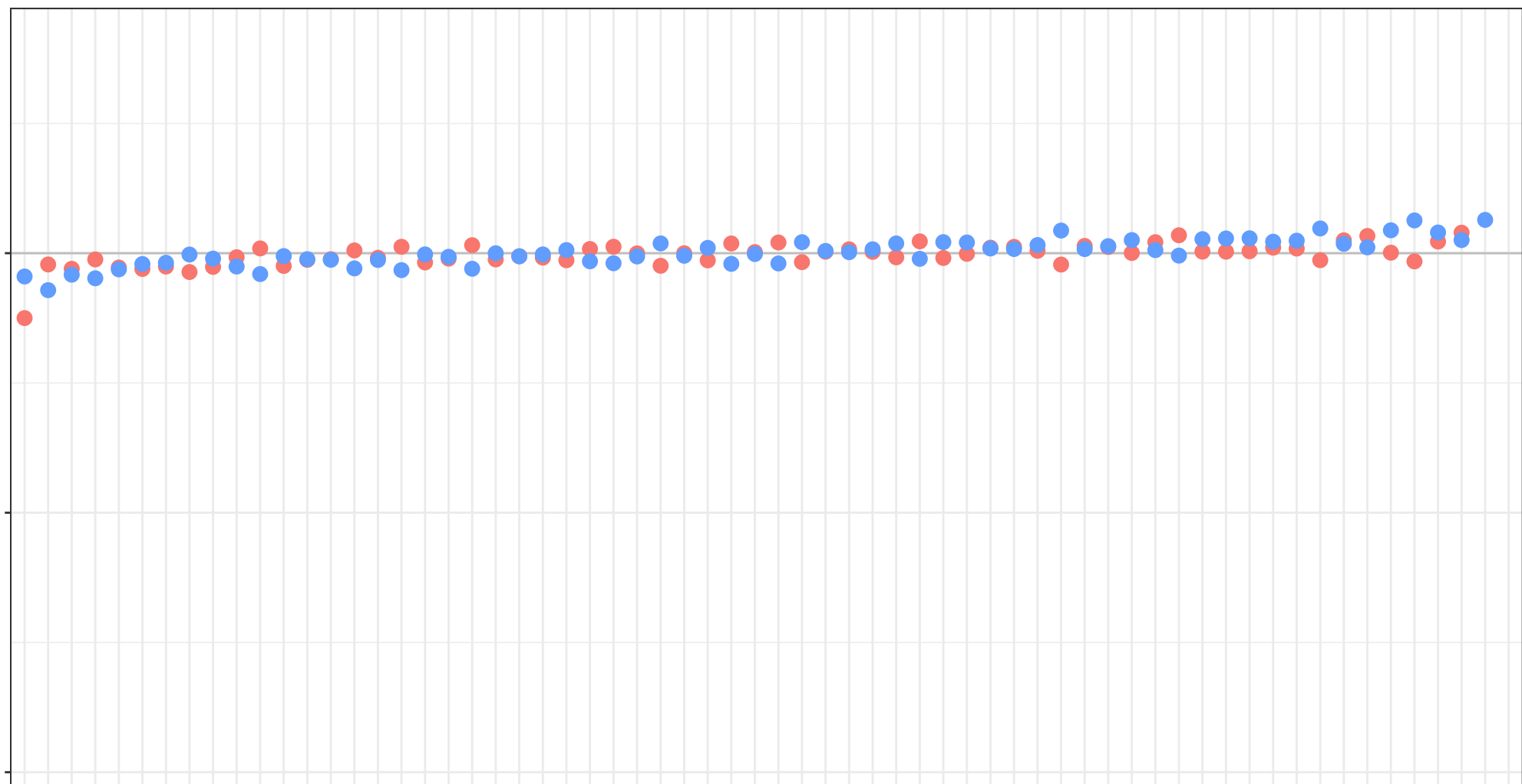
mutant

library gene

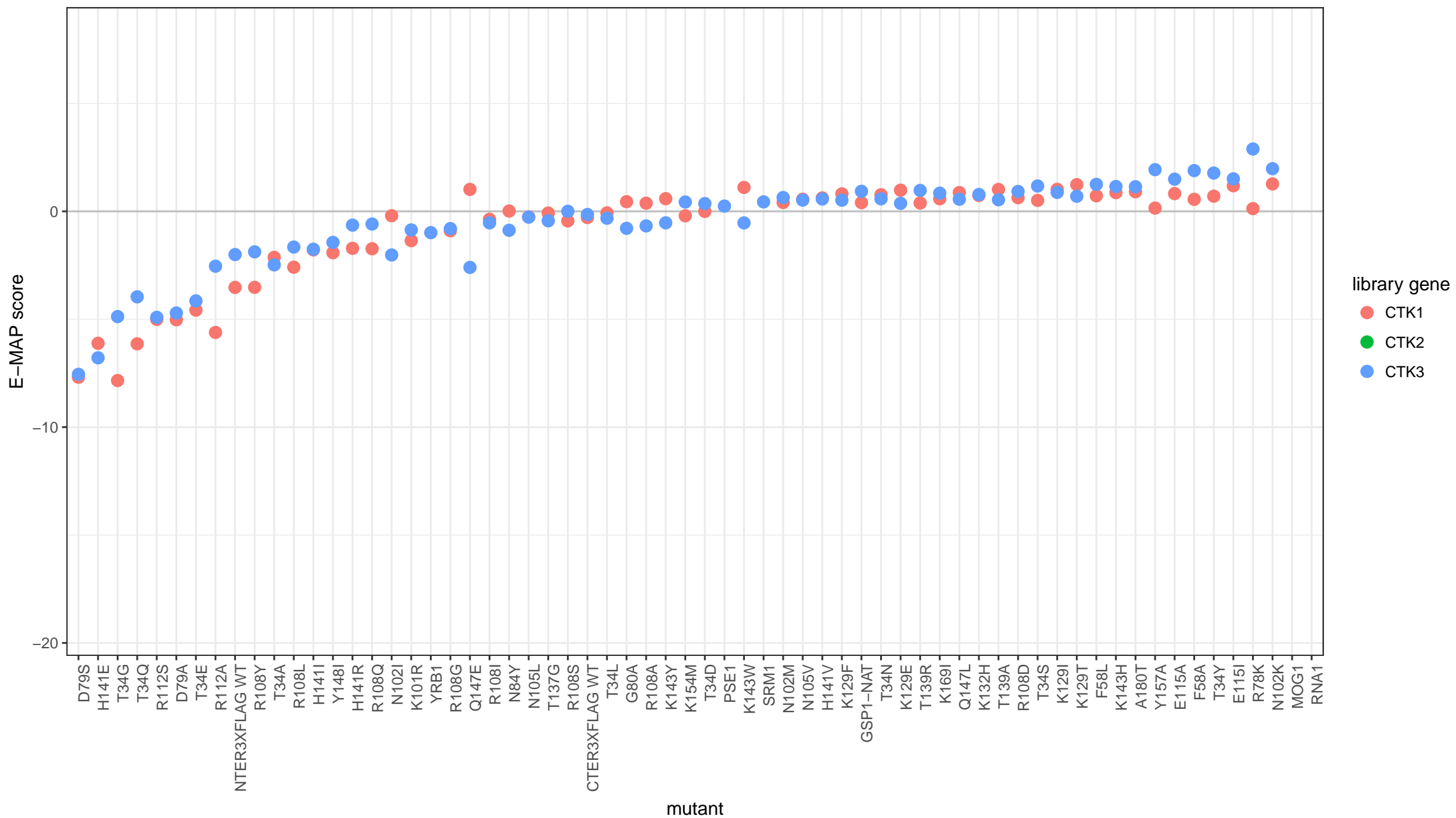
CMP2

CNA1

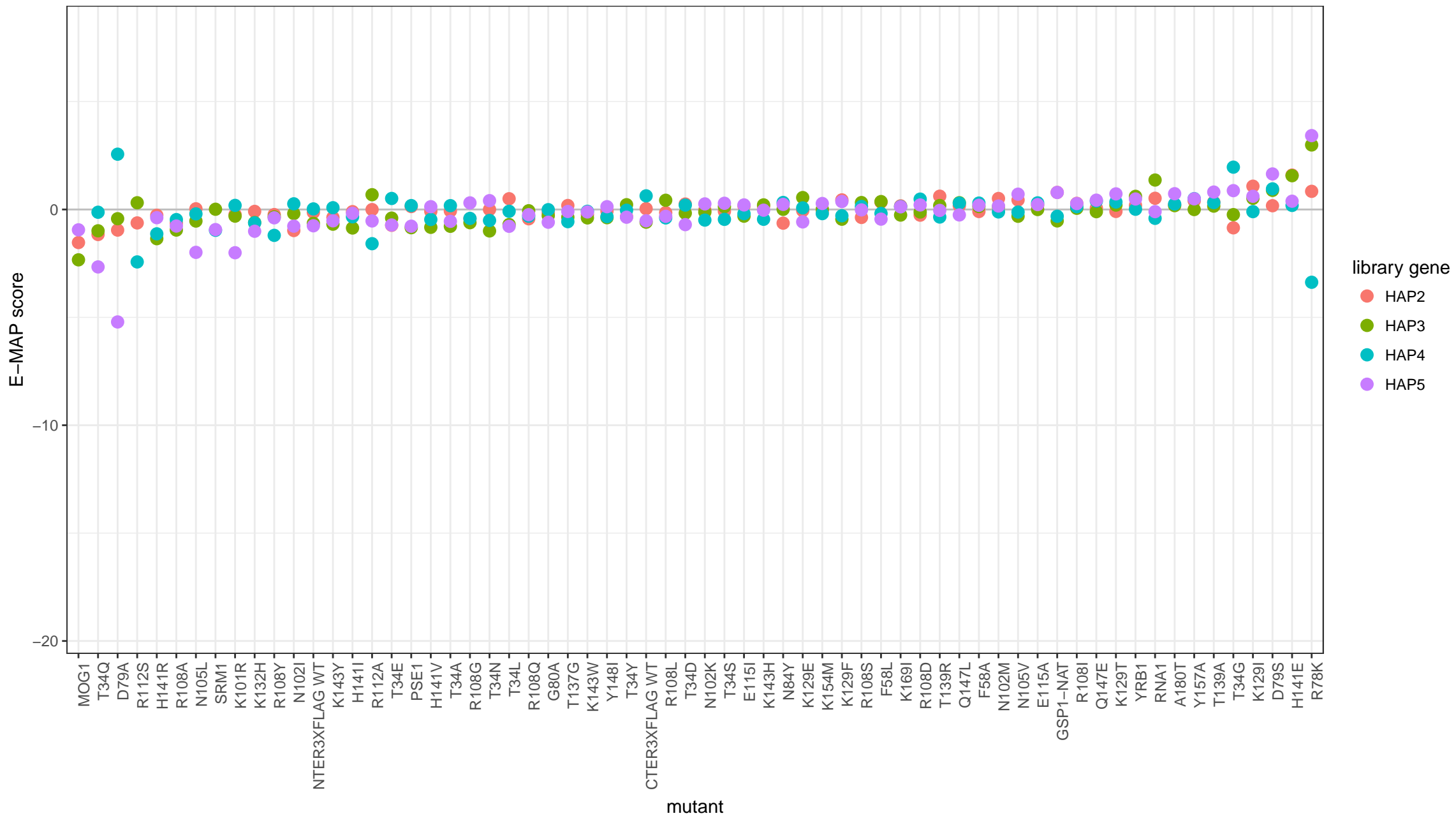
CNB1



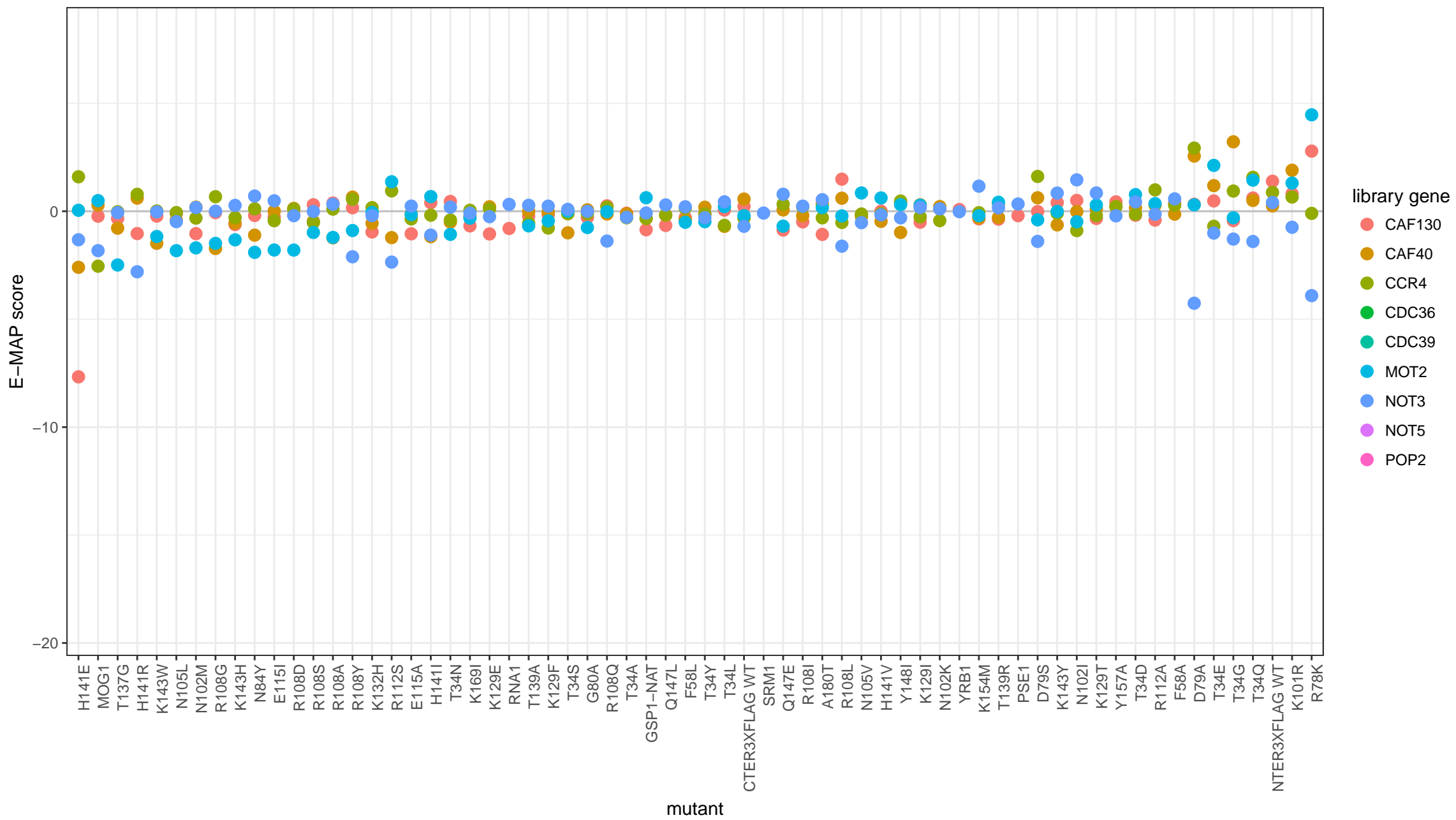
carboxy-terminal domain protein kinase complex



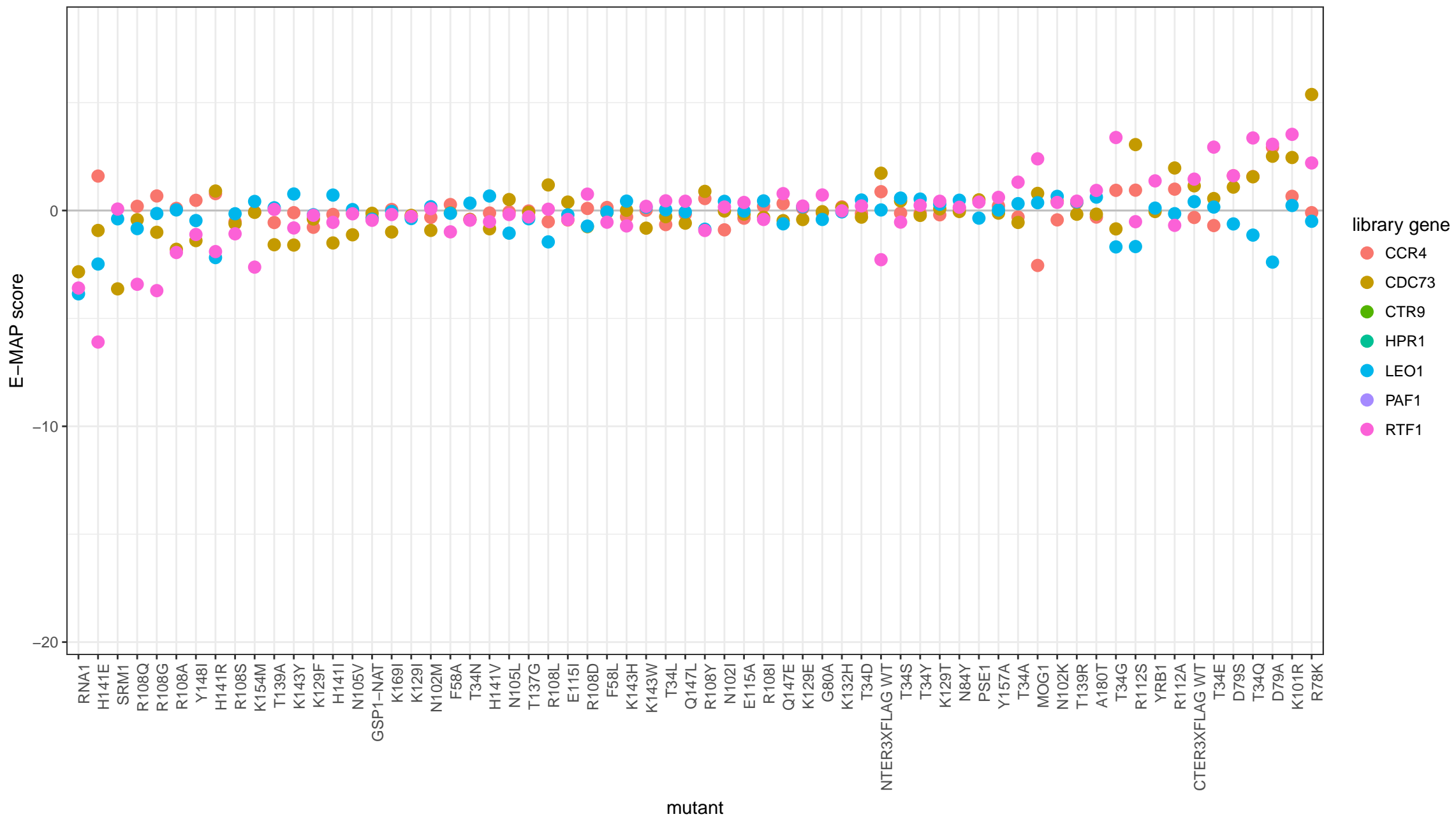
CCAAT-binding factor complex



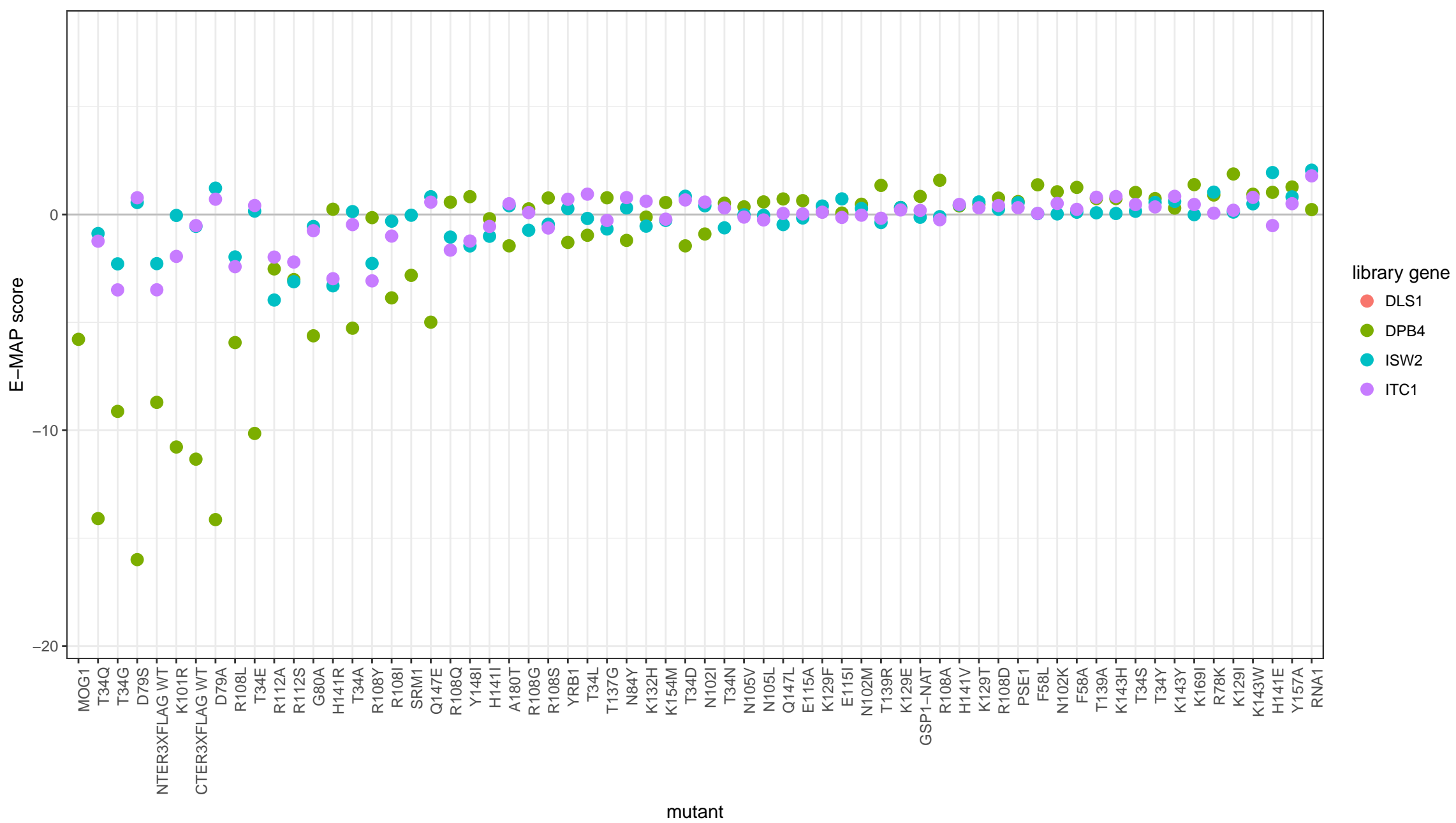
CCR4–NOT core complex



Cdc73p/Paf1p complex



chromatin accessibility complex



chromatin assembly complex

E-MAP score

-20

-10

0

mutant

library gene

CAC2

MSI1

RLF2

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

Chs5p/Arf-1binding proteins (ChAPs)

E-MAP score

-20

-10

0

mutant

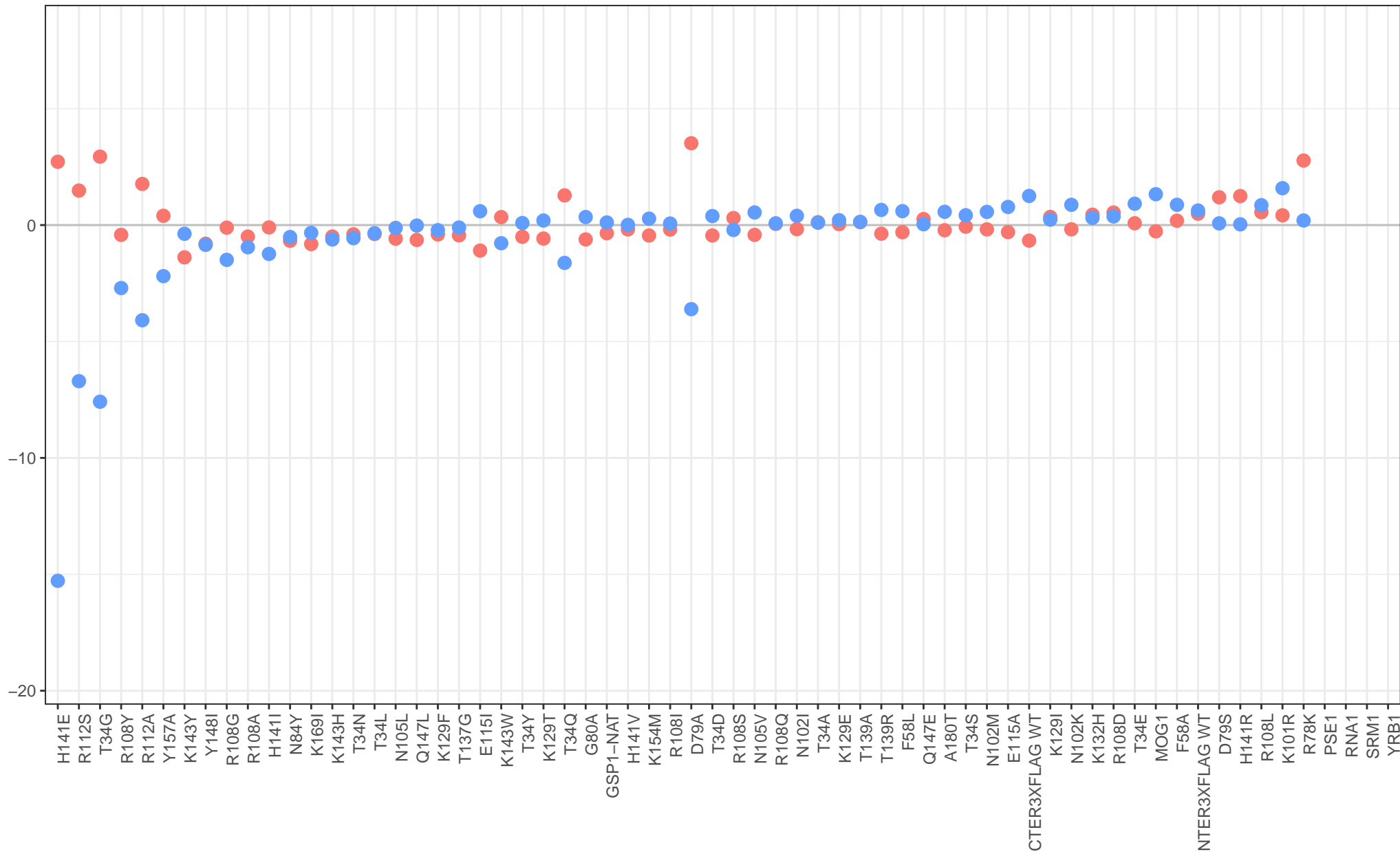
library gene

- ARF1
- BCH1
- BCH2
- BUD7
- CHS5
- CHS6

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

Chz1p/Htz1p/Htb1p complex

E-MAP score



library gene

- CHZ1
- HTB1
- HTZ1

mutant

COMA complex

E-MAP score

0

-10

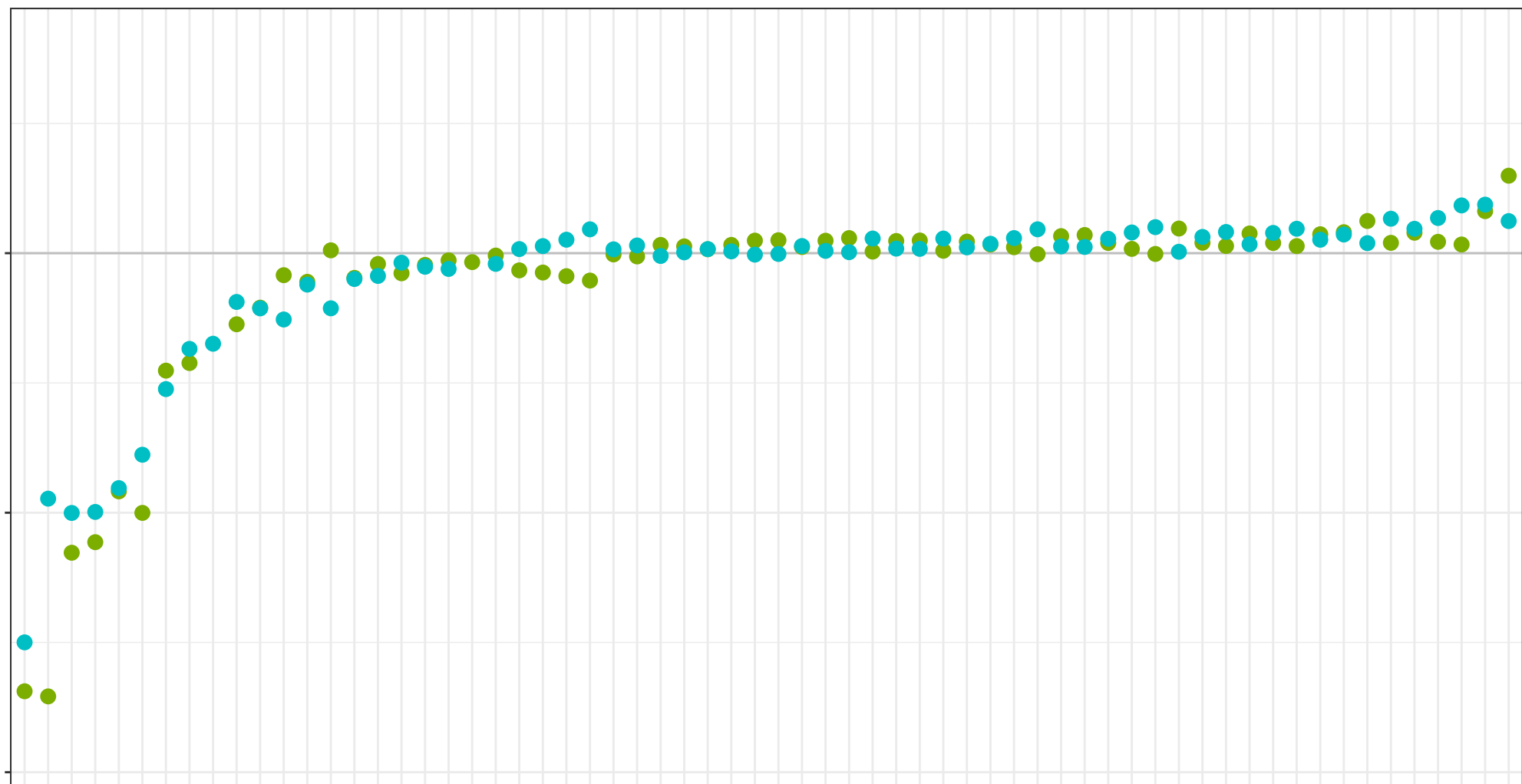
-20

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

mutant

library gene

- AME1
- CTF19
- MCM21
- OKP1



commitment complex

E-MAP score

-20

-10

0

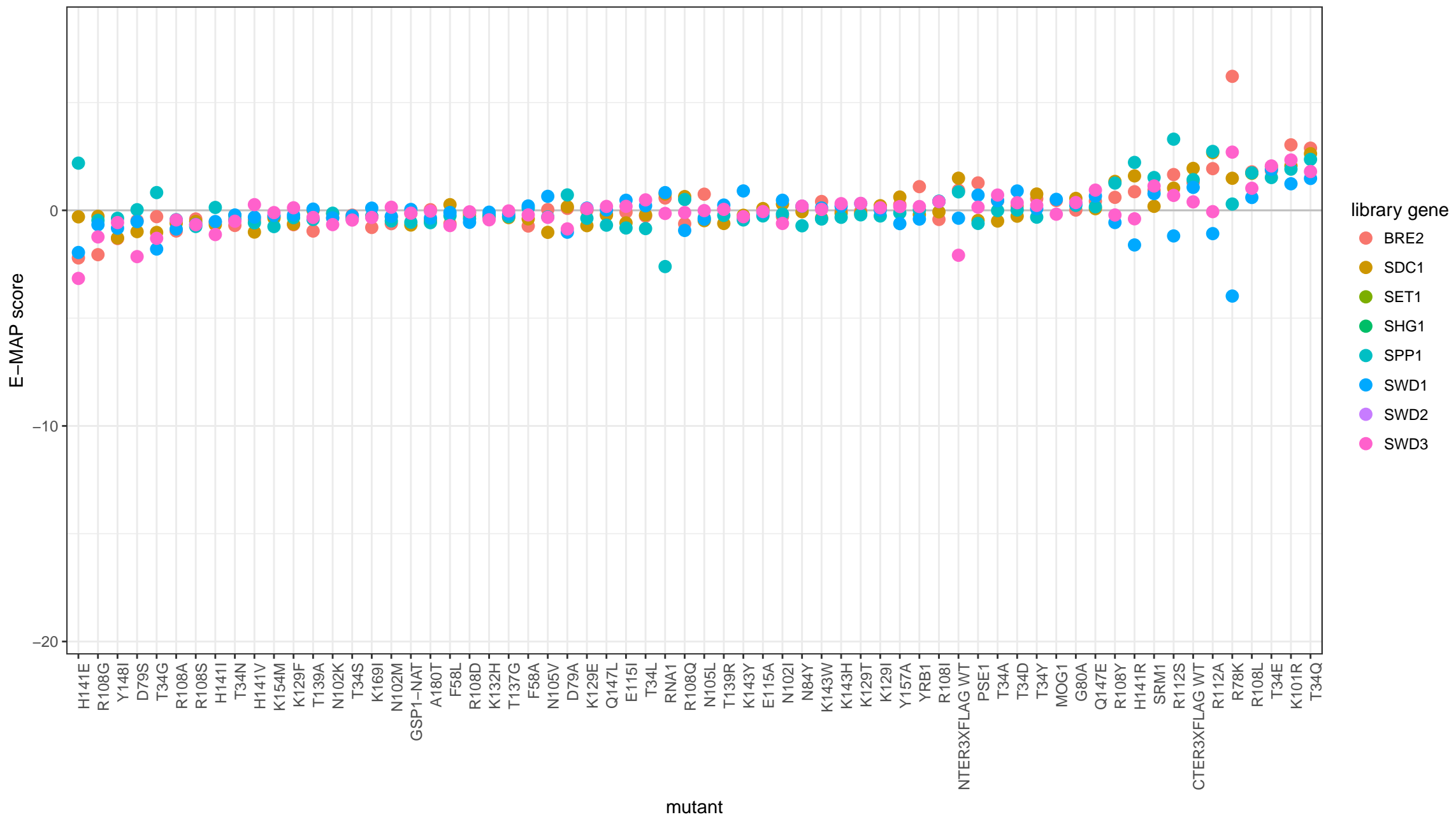
mutant

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

library gene

- CBC2
- LUC7
- MSL5
- MUD1
- MUD2
- NAM8
- PRP39
- PRP40
- PRP42
- SMB1
- SMD1
- SMD2
- SMD3
- SME1
- SMX2
- SMX3
- SNP1
- SNU56
- SNU71
- STO1
- YHC1

COMPASS complex



COPII

E-MAP score

-20

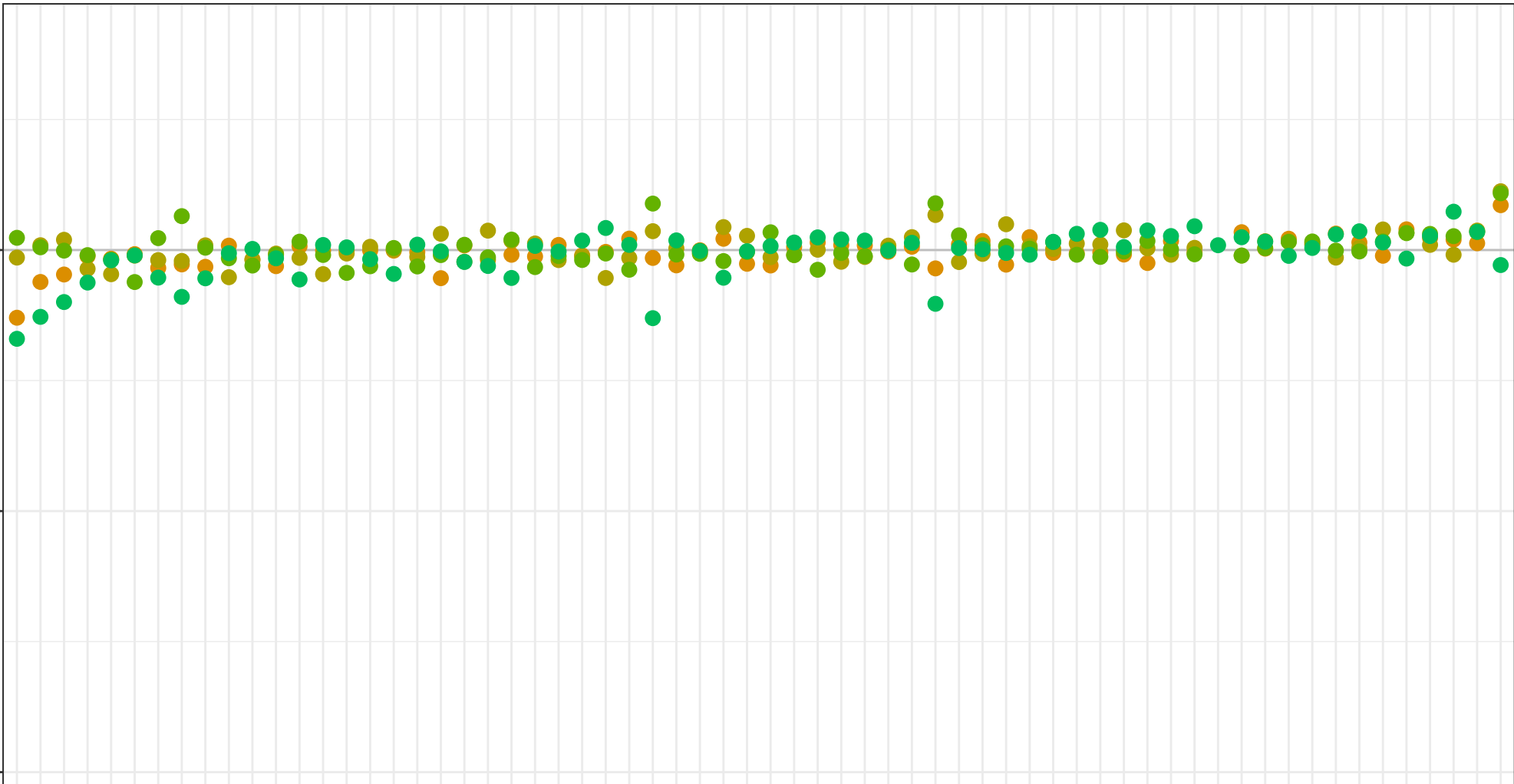
-10

0

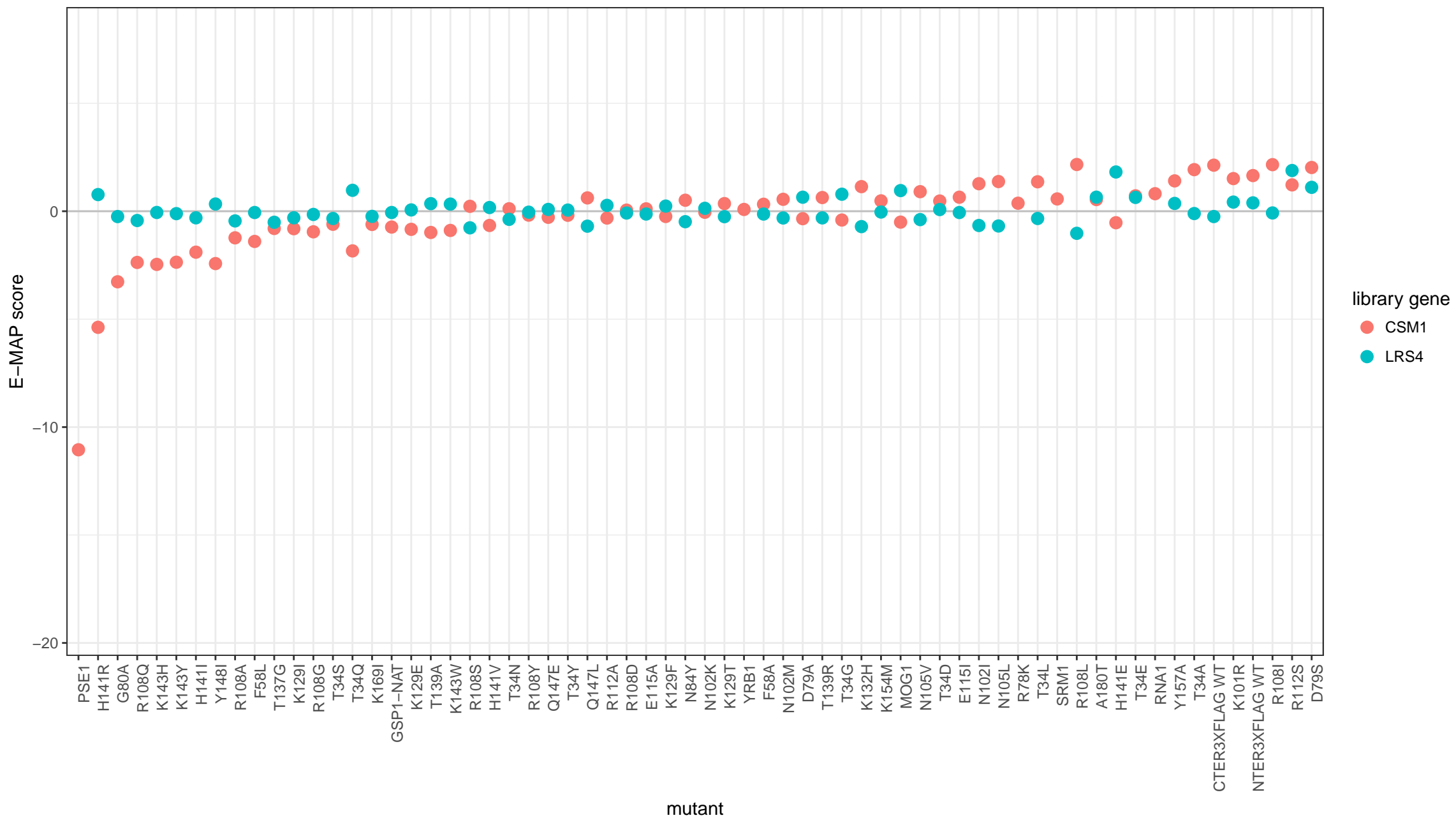
mutant

library gene

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



Csm1p/Lrs4p complex



Ctf3p protein complex

E-MAP score

0

-10

-20

library gene

CTF3

MCM16

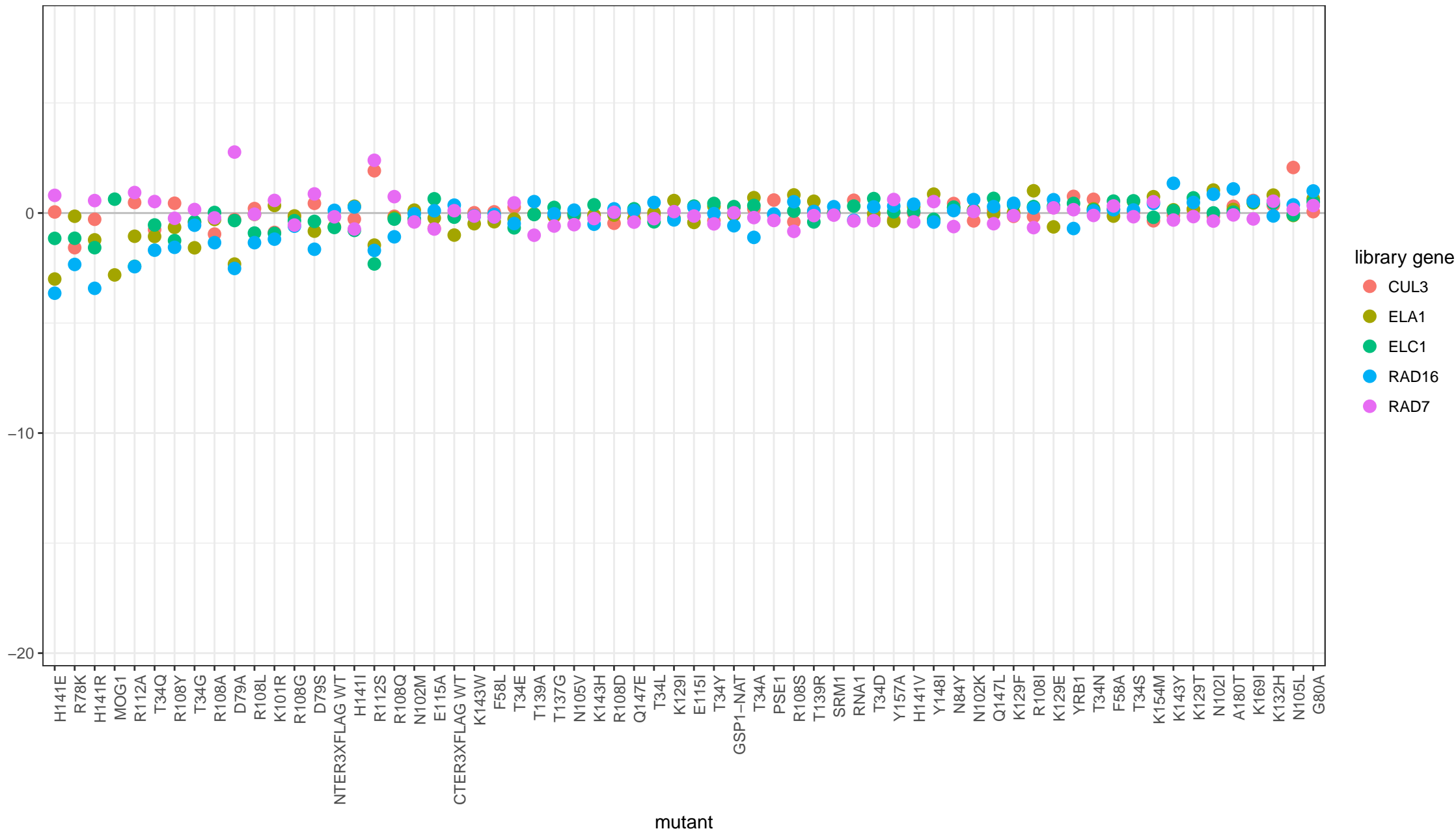
MCM22

mutant

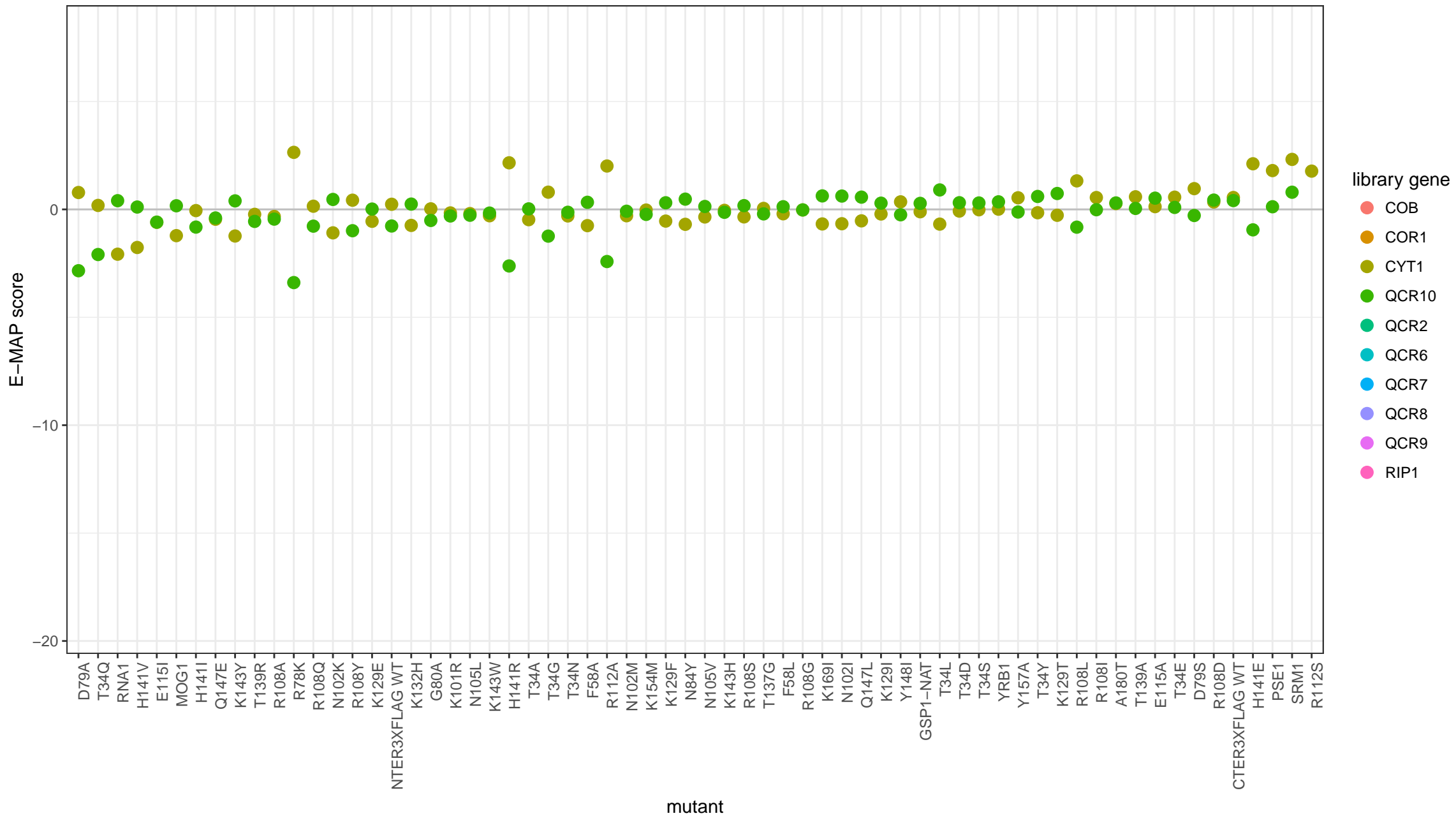
T34G
D79A
T34Q
K101R
D79S
T34E
SRM1
CTER3XFLAG WT
NTER3XFLAG WT
R108I
T34A
N84Y
T34D
E115I
N102K
Q147E
E115A
K169I
N102I
K129F
T34S
F58L
G80A
K143Y
T137G
R112S
GSP1-NAT
RNA1
N105L
Q147L
T34L
K132H
R78K
K143W
N105V
R108L
A180T
H141V
T139A
F58A
T139R
K154M
K129T
K129E
N102M
T34Y
R108D
K143H
R108G
R108A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

Cul3p-RING ubiquitin ligase complex

E-MAP score



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



cytoplasmic dynein complex

E-MAP score

-20

-10

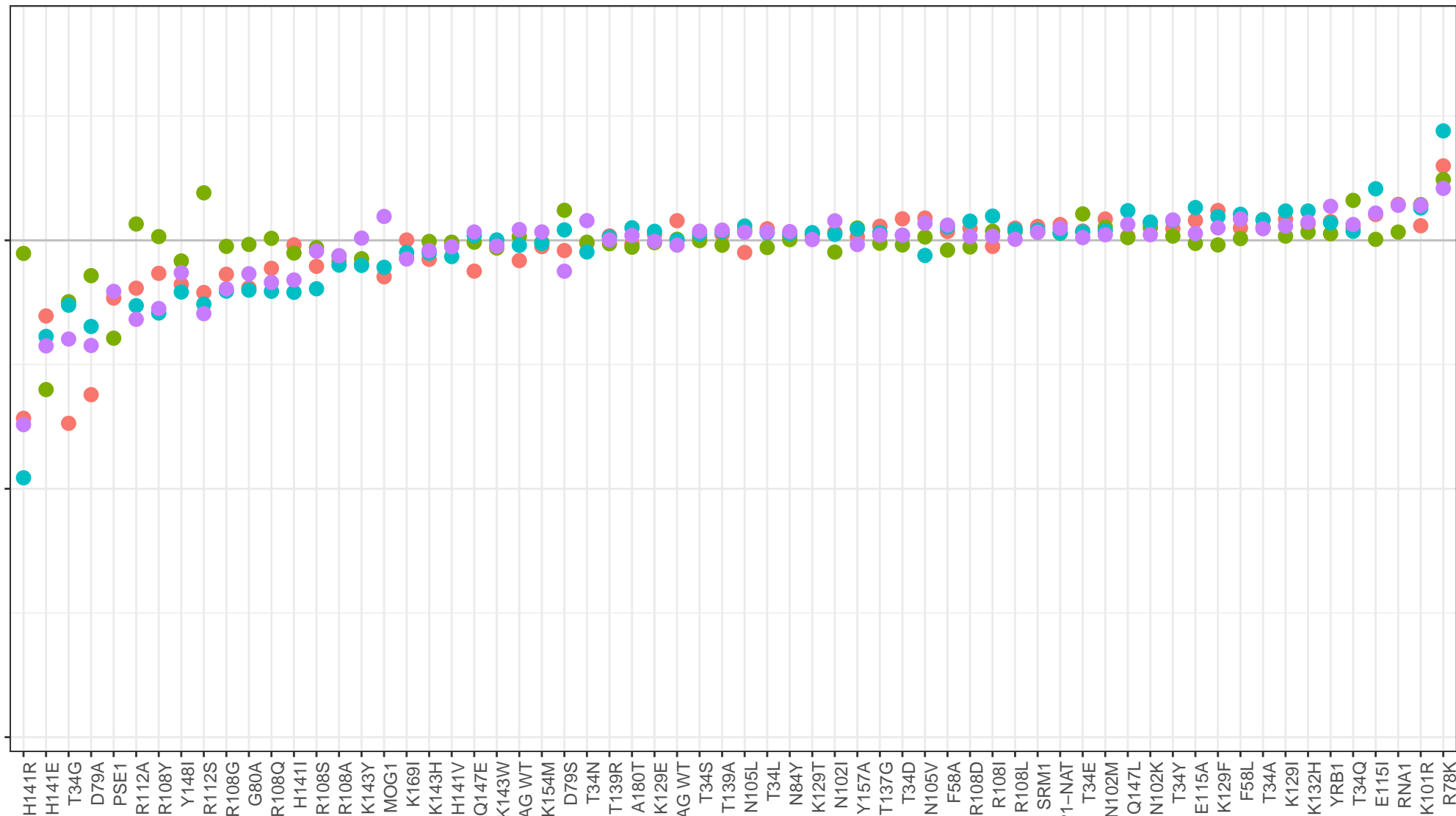
0

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

mutant

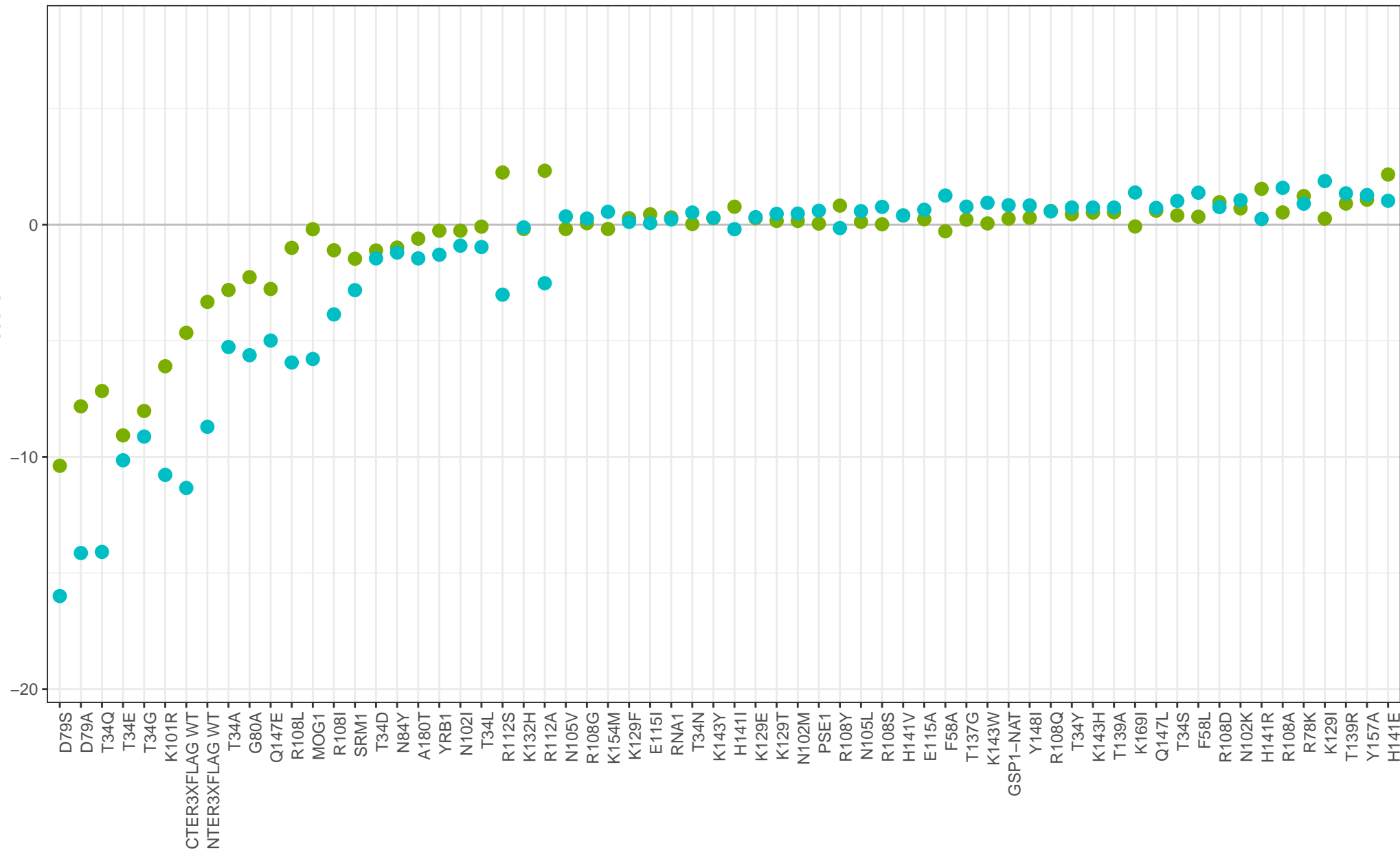
library gene

DYN1
DYN2
DYN3
PAC11



DNA polymerase epsilon complex

E-MAP score

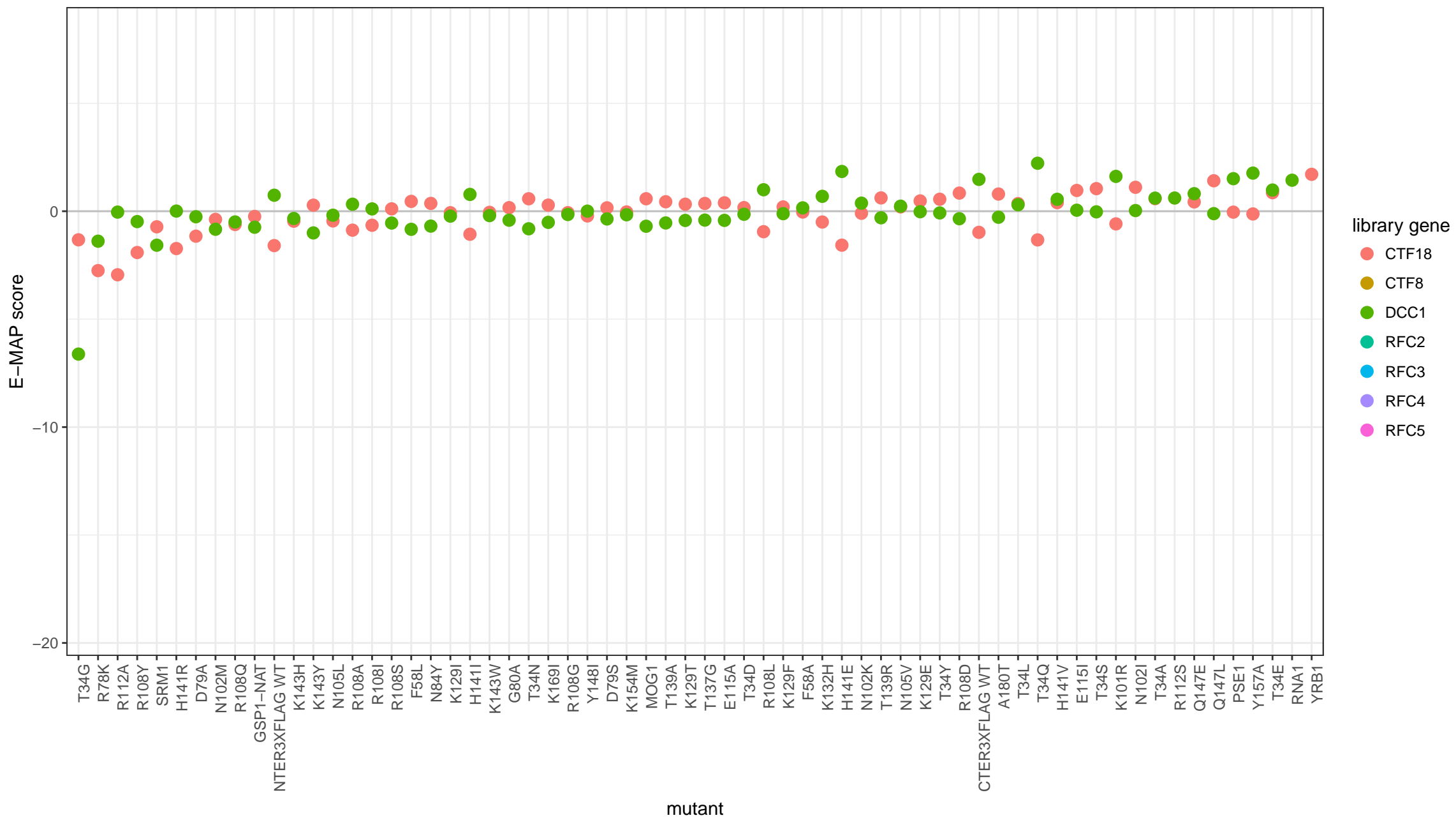


library gene

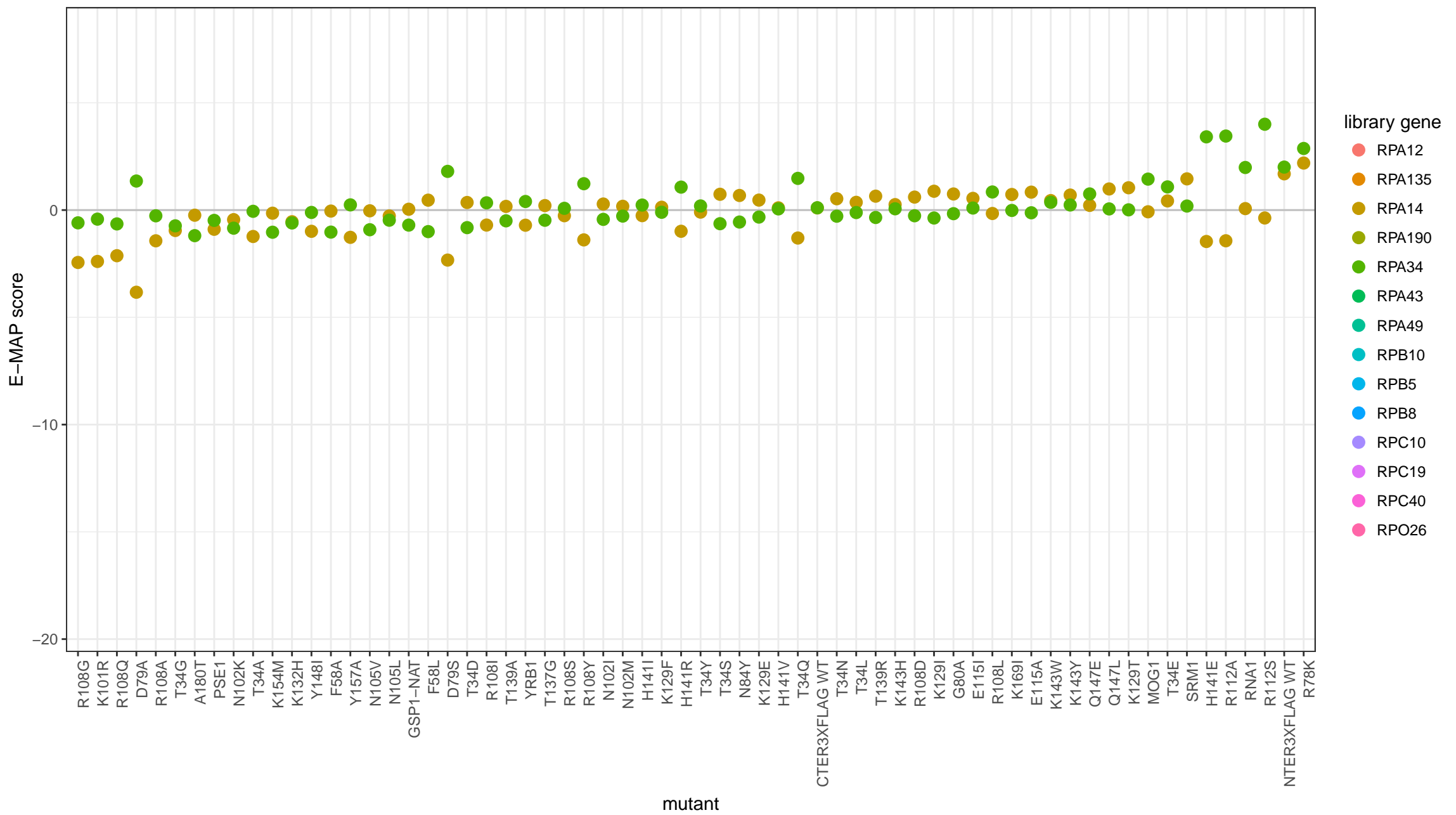
- DPB2
- DPB3
- DPB4
- POL2

mutant

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

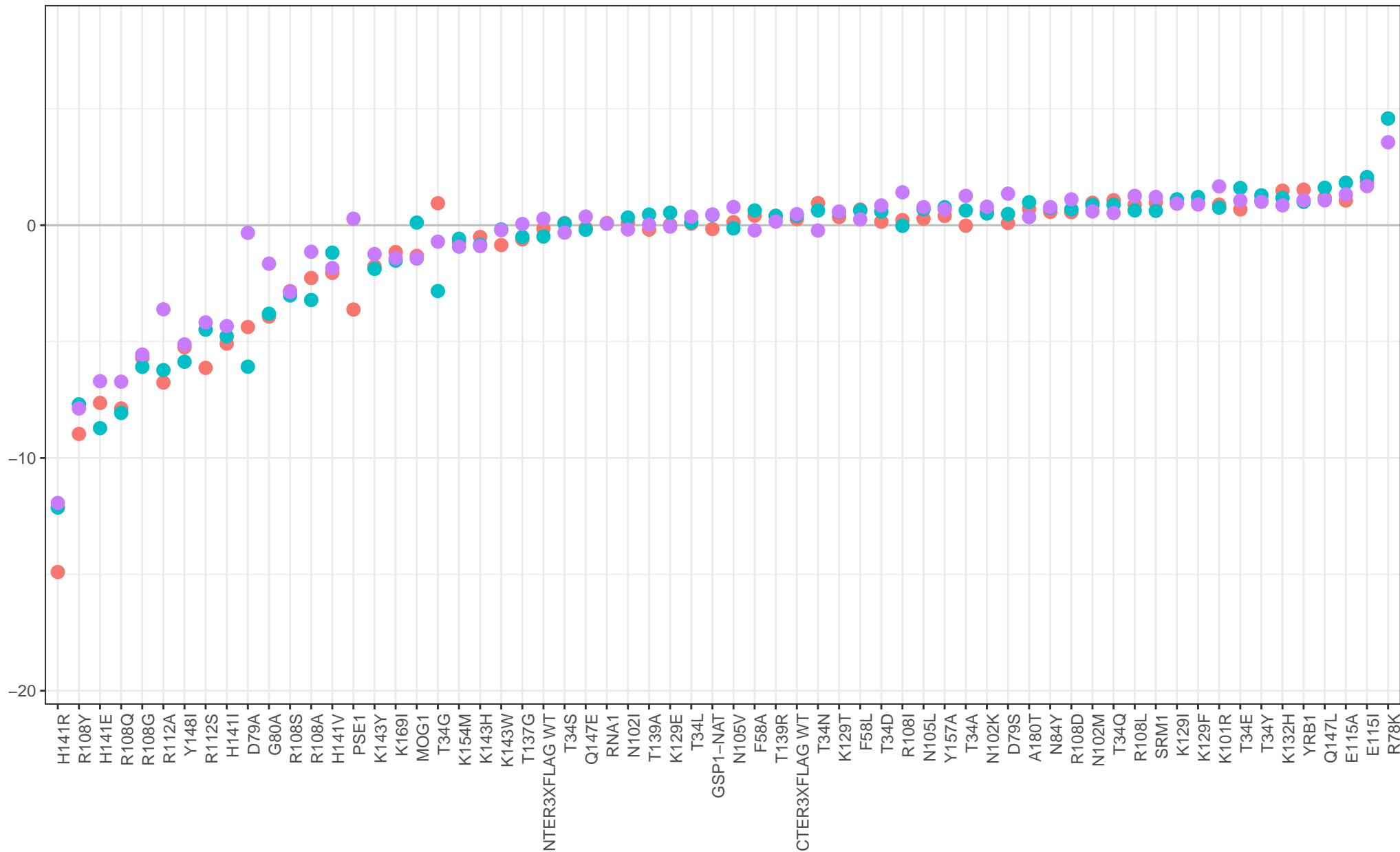


DNA-directed RNA polymerase I complex



dynactin complex

E-MAP score



Elc1p/Elc1p complex

E-MAP score

-20

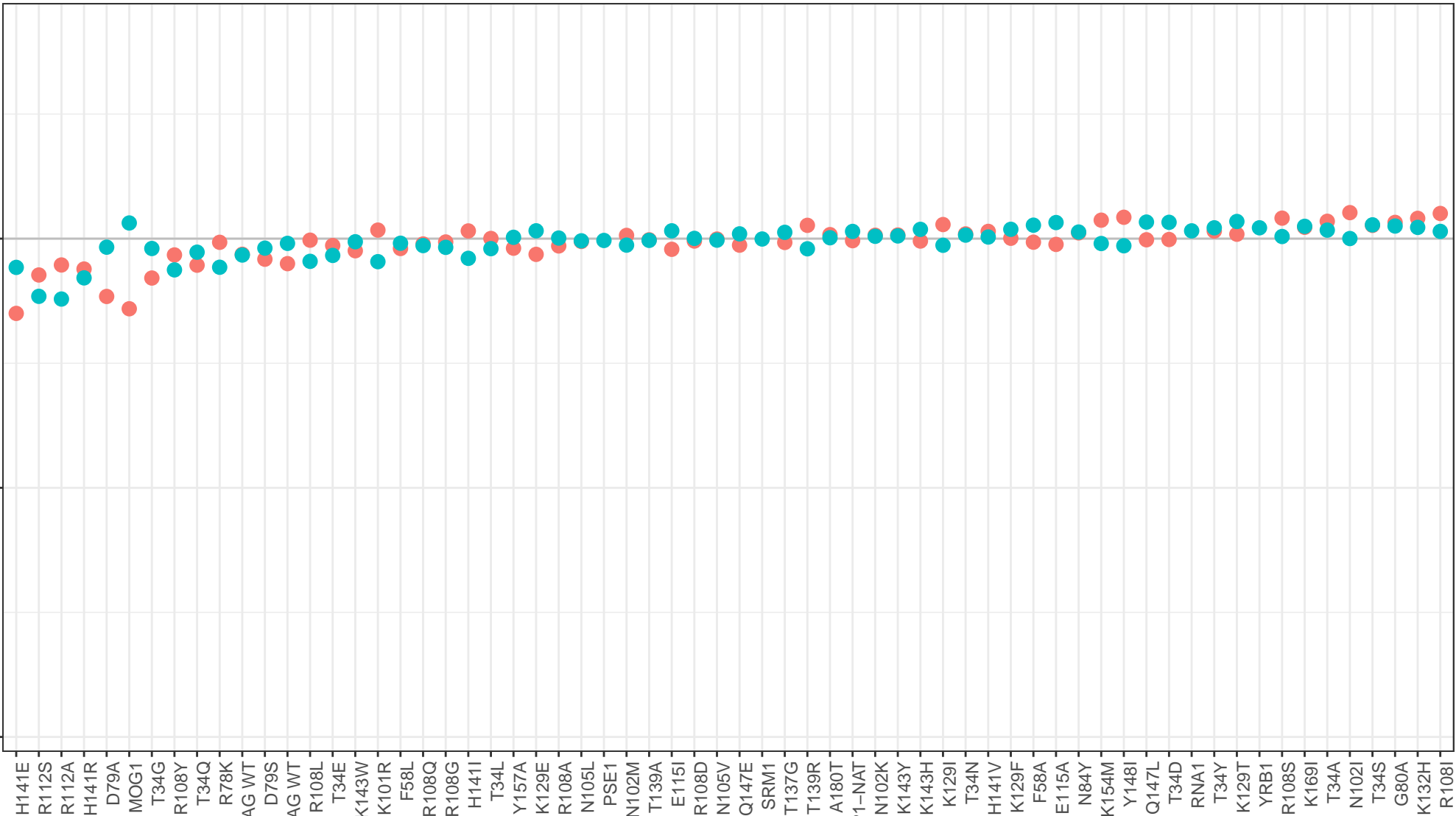
-10

0

mutant

library gene

ELA1
ELC1



Elongator complex

E-MAP score

-20

-10

0

mutant

library gene

- ELP2
- ELP3
- ELP4
- ELP6
- IKI1
- IKI3

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

Erv41p/Erv46p complex

E-MAP score

-20

-10

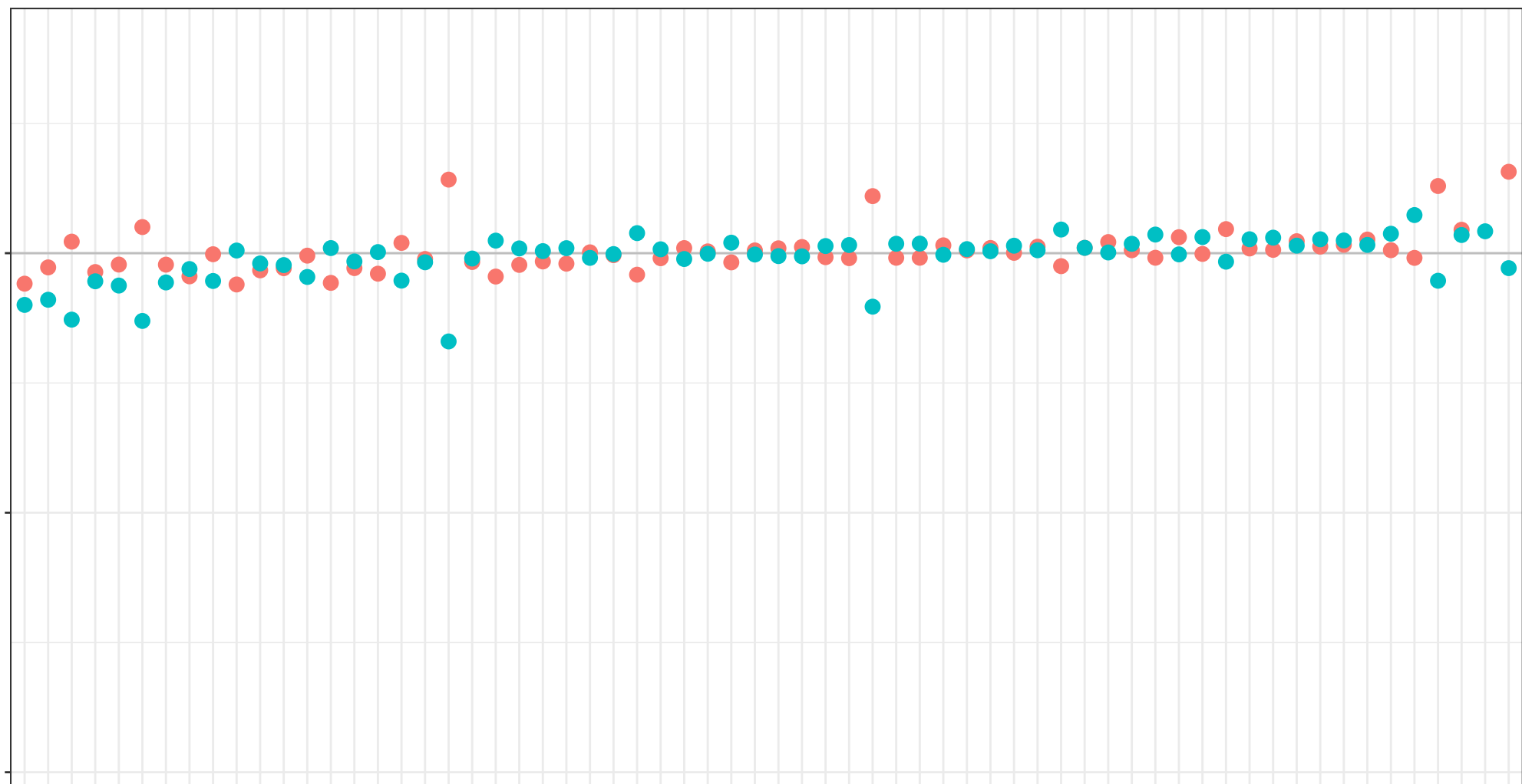
0

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

mutant

library gene

ERV41
ERV46



ESCRT I complex

E-MAP score

-20

-10

0

mutant

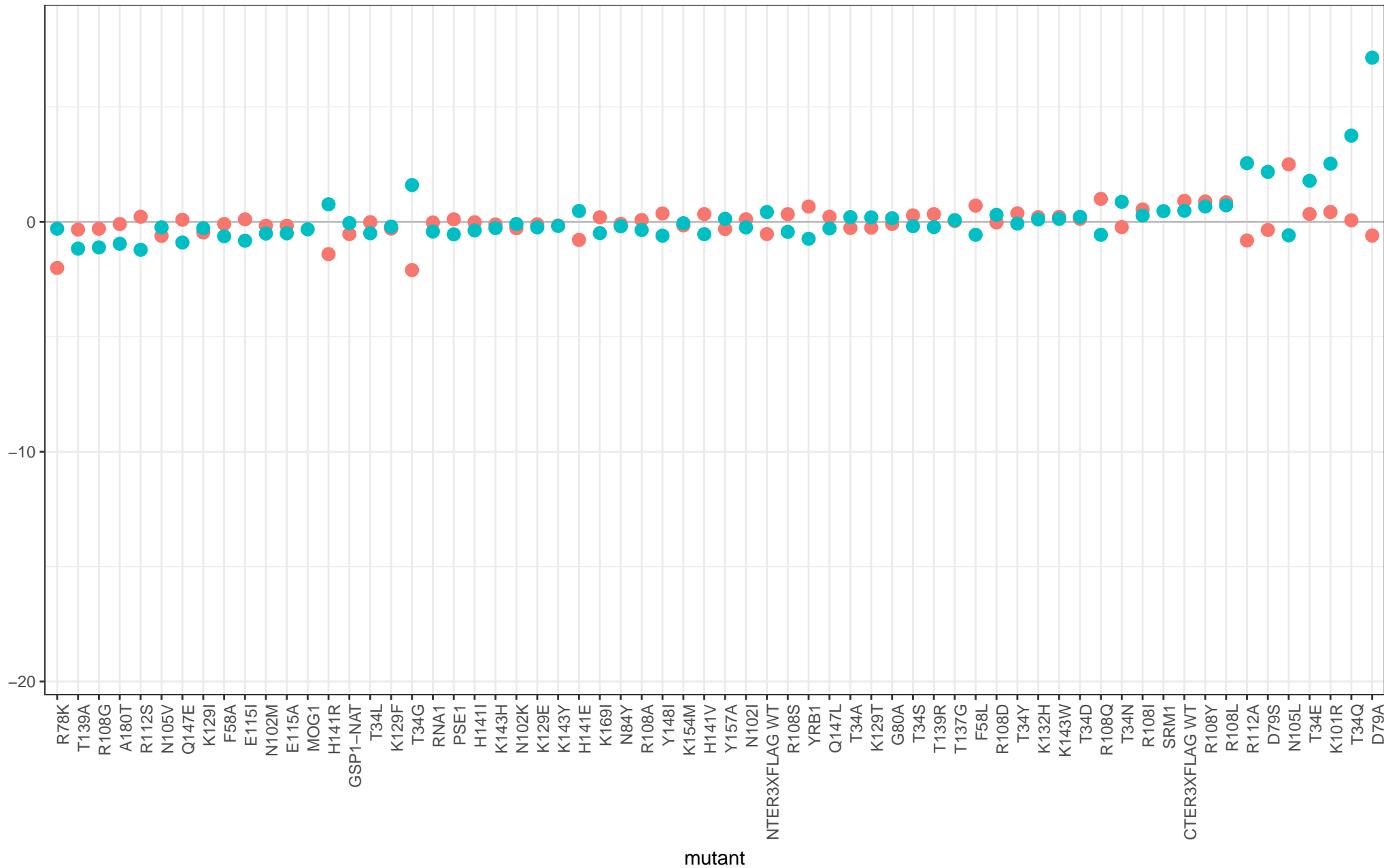
library gene

- MVB12
- SRN2
- STP22
- VPS28

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

extracellular region

E-MAP score



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

E-MAP score

-20

-10

0

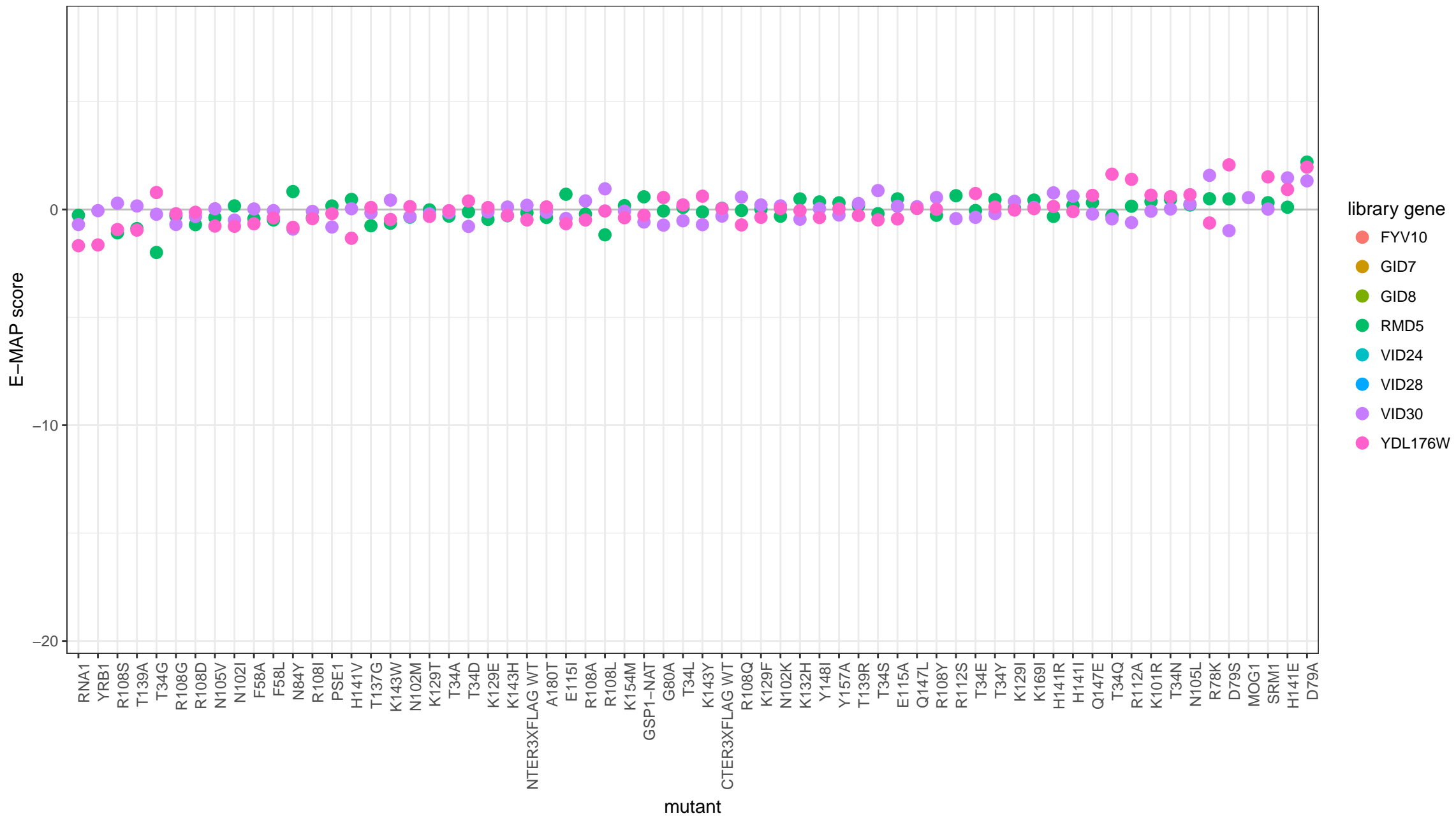
MOG1
H141E
F58L
T34N
NTER3XFLAG WT
A180T
T34Y
K129E
T137G
PSE1
K129F
RNA1
G80A
Q147L
GSP1-NAT
T34D
N102M
N102K
T139R
K143H
N105V
K129T
K132H
F58A
E115A
T34L
N105L
H141V
R108L
N84Y
R108D
T34S
CTER3XFLAG WT
T139A
K143W
K154M
E115I
N102I
K143Y
Y148I
K169I
H141I
K129I
R108S
T34A
Y157A
T34E
Q147E
R108A
R108I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

mutant

library gene

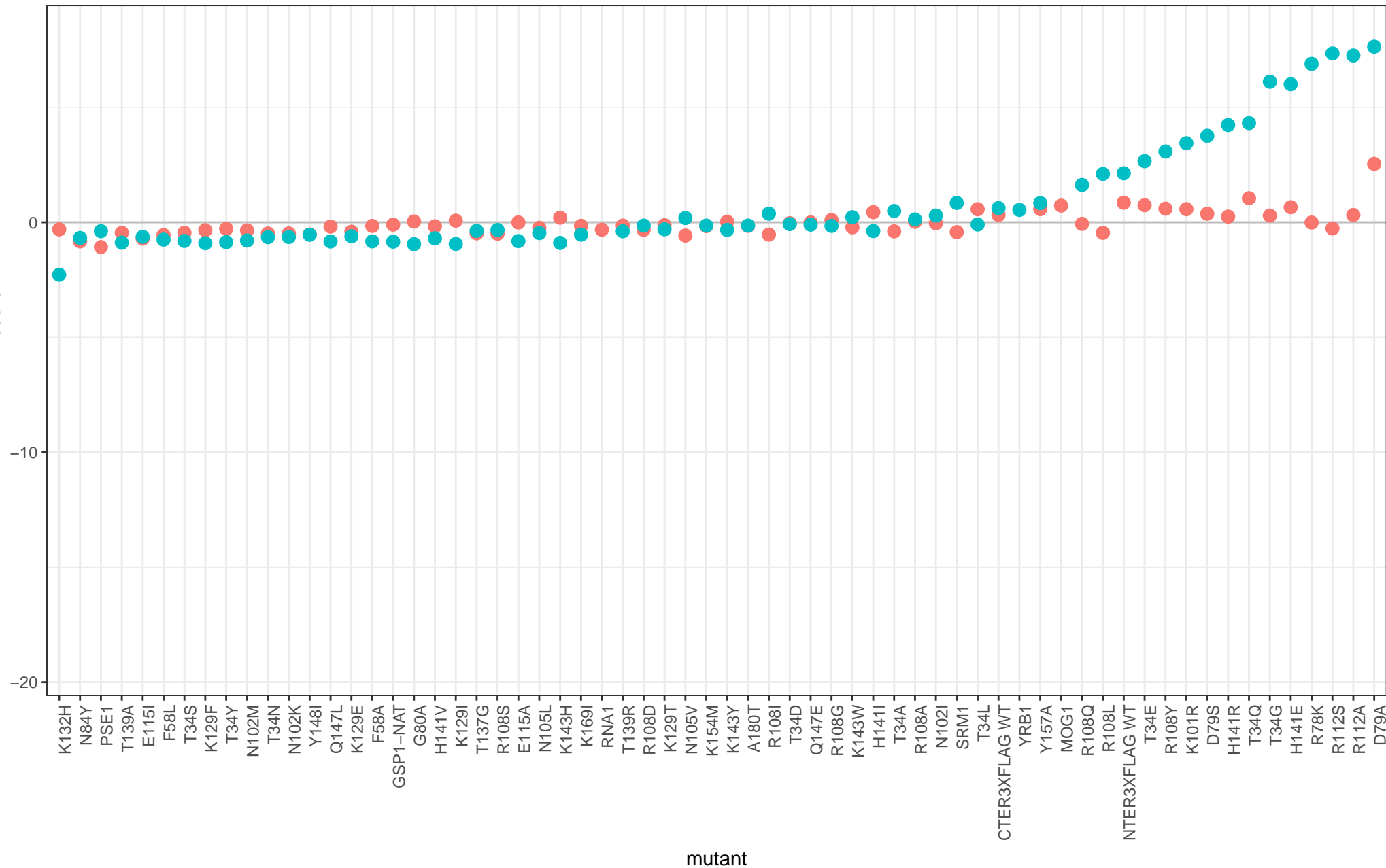
- FAR10
- FAR11
- FAR3
- FAR7
- FAR8
- VPS64

FBP degradation complex



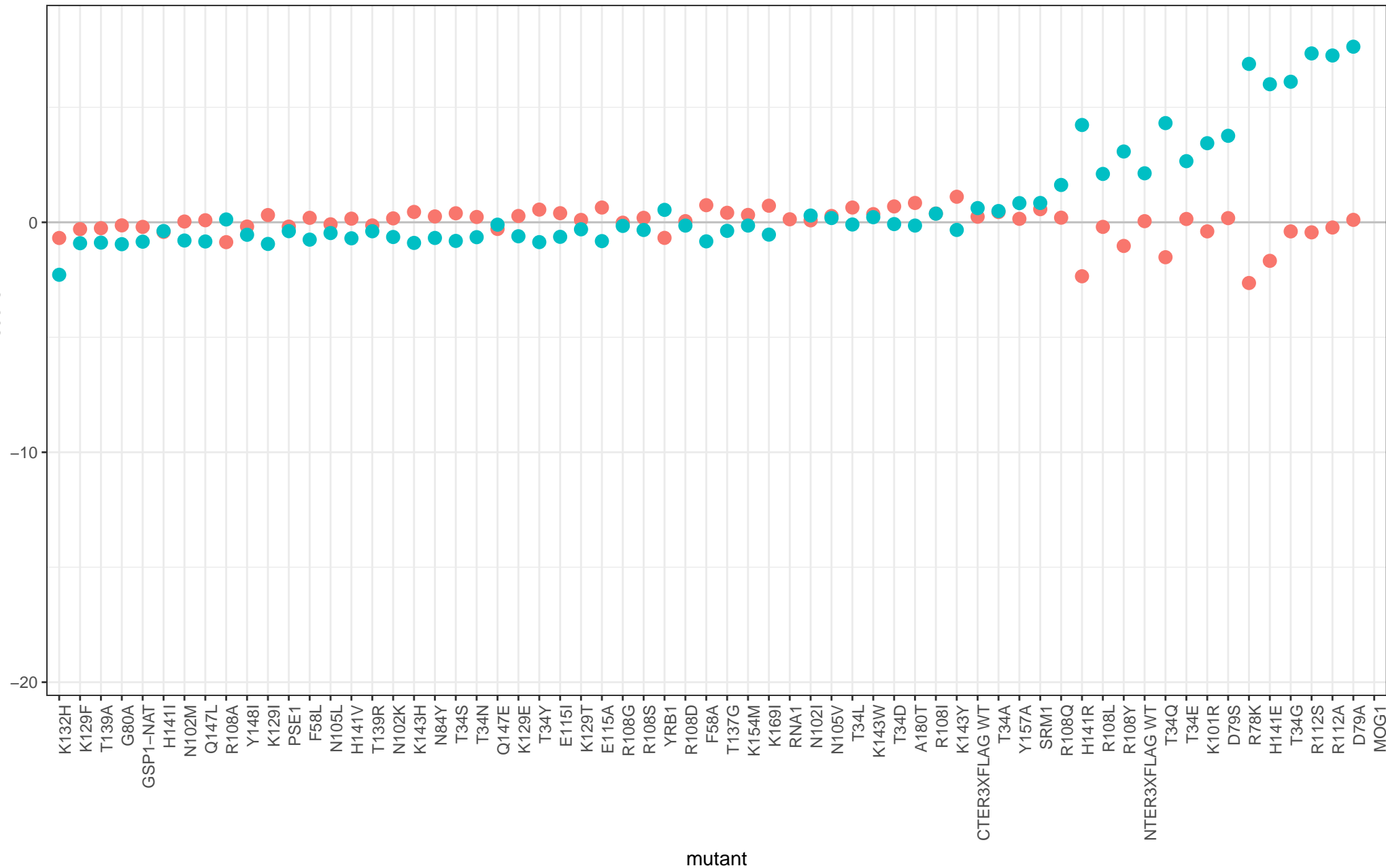
GAL3p/GAL80p complex

E-MAP score



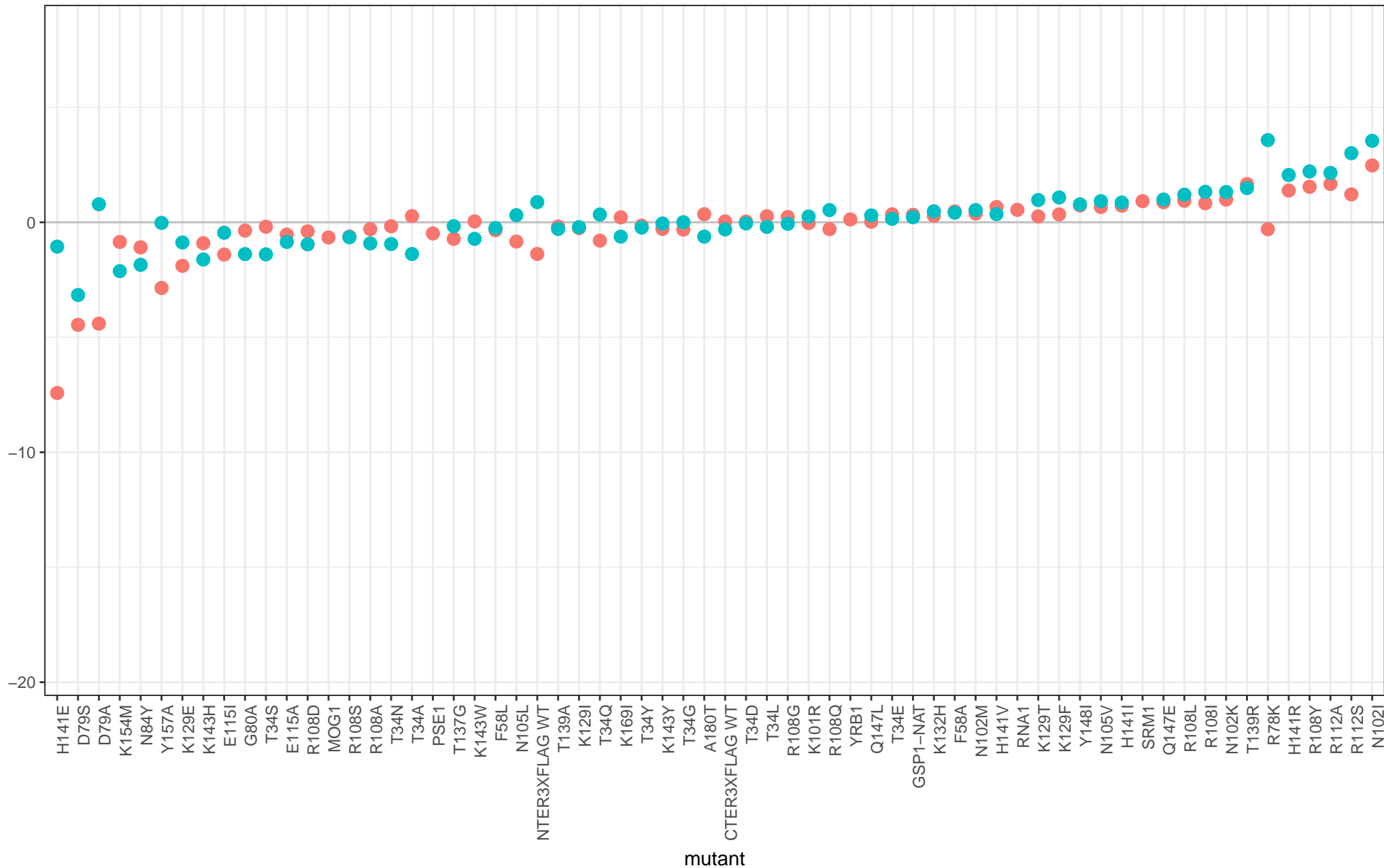
GAL4p/GAL80p complex

E-MAP score

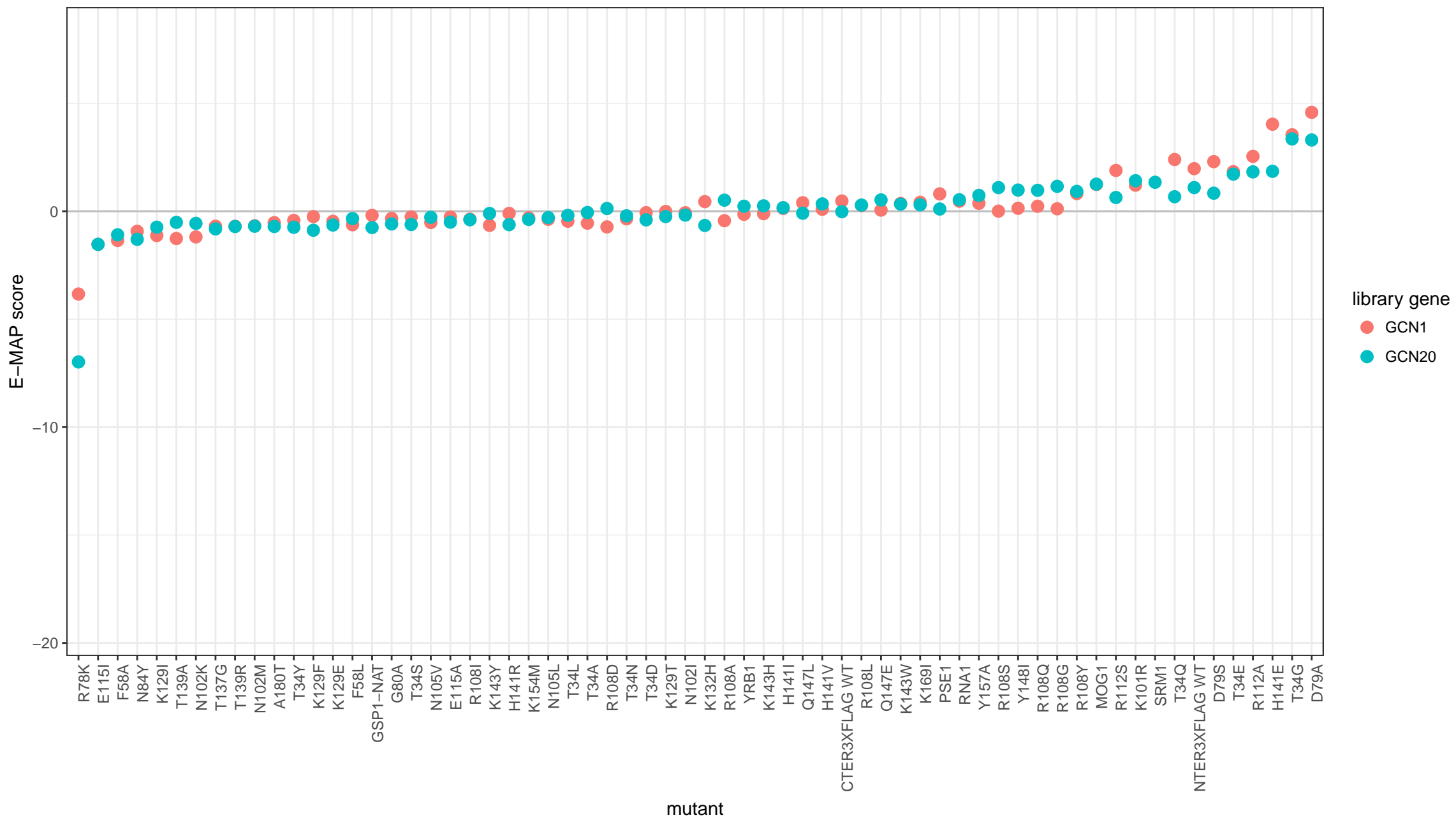


GARP complex

E-MAP score



Gcn1p/Gcn20p complex



GET complex

E-MAP score

-20

-10

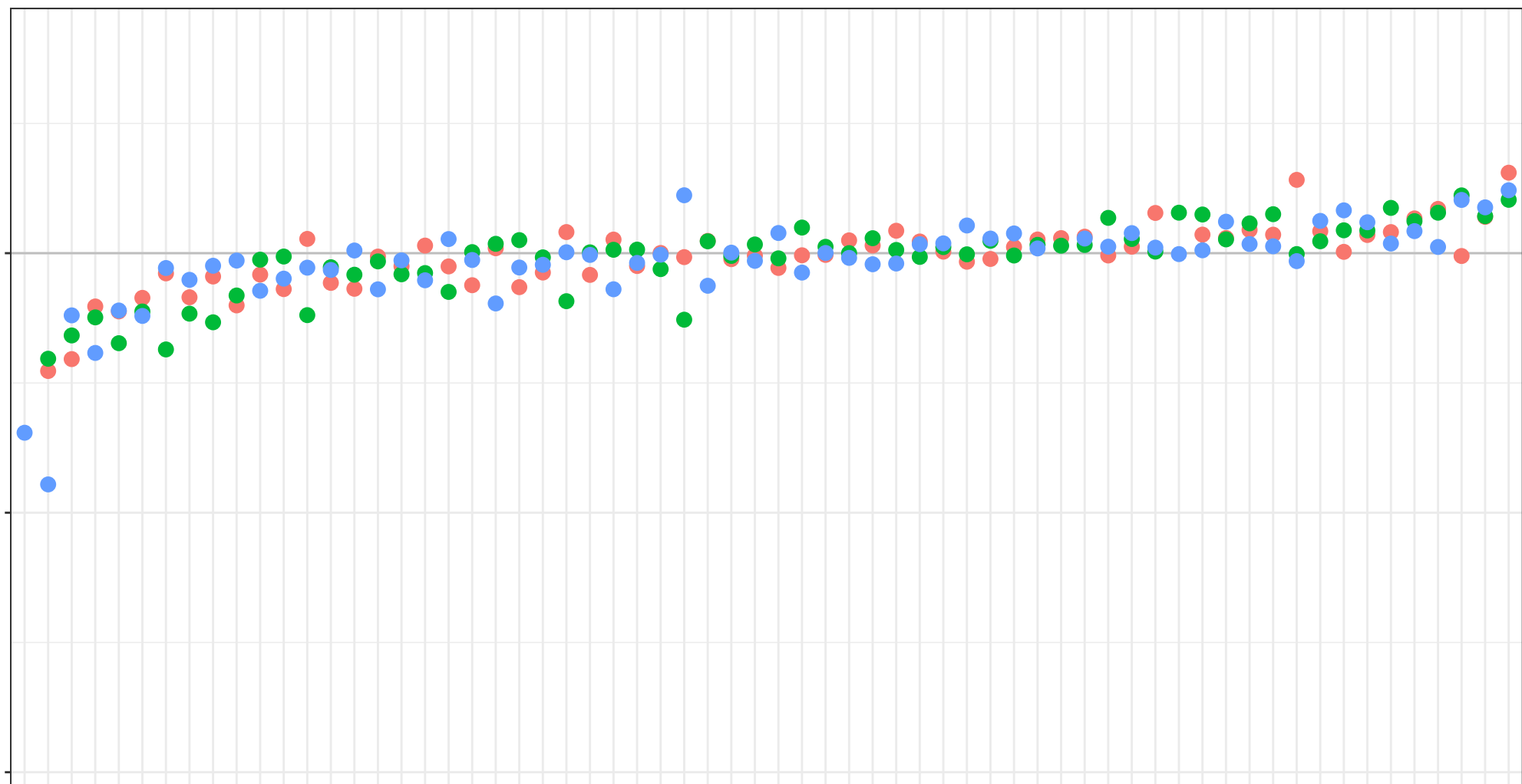
0

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

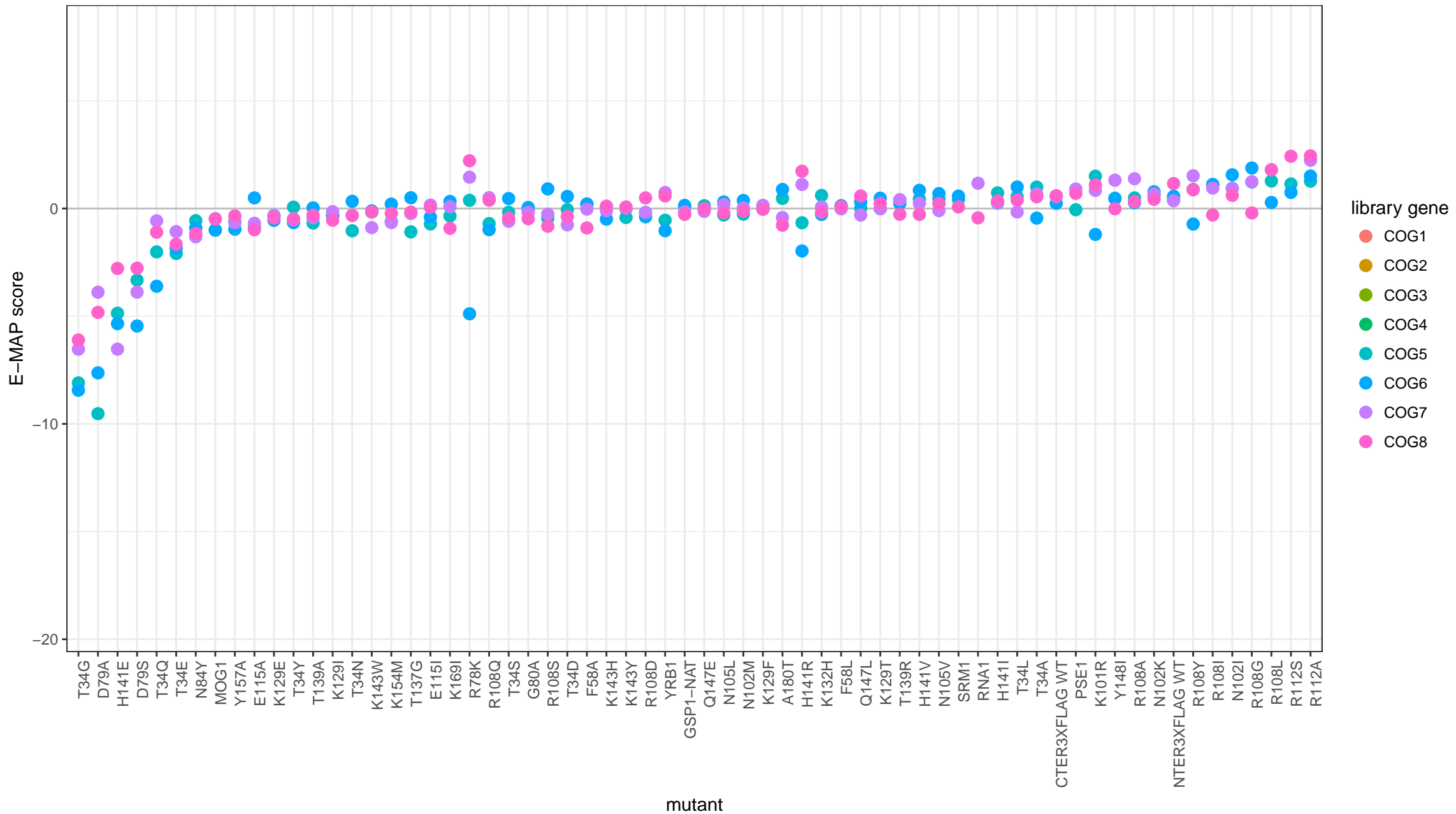
mutant

library gene

GET1
GET2
GET3

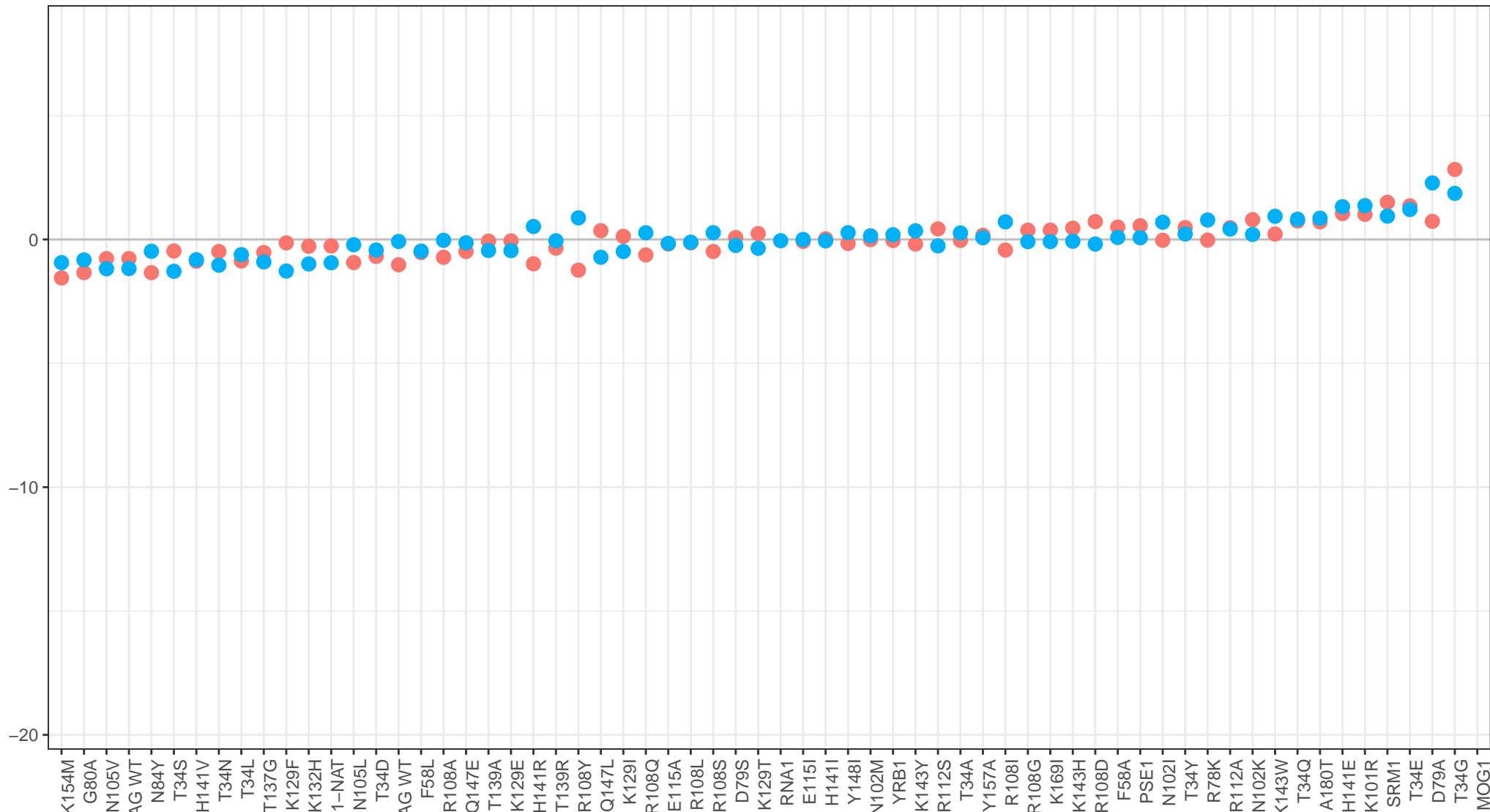


Golgi transport complex



GSE Complex

E-MAP score



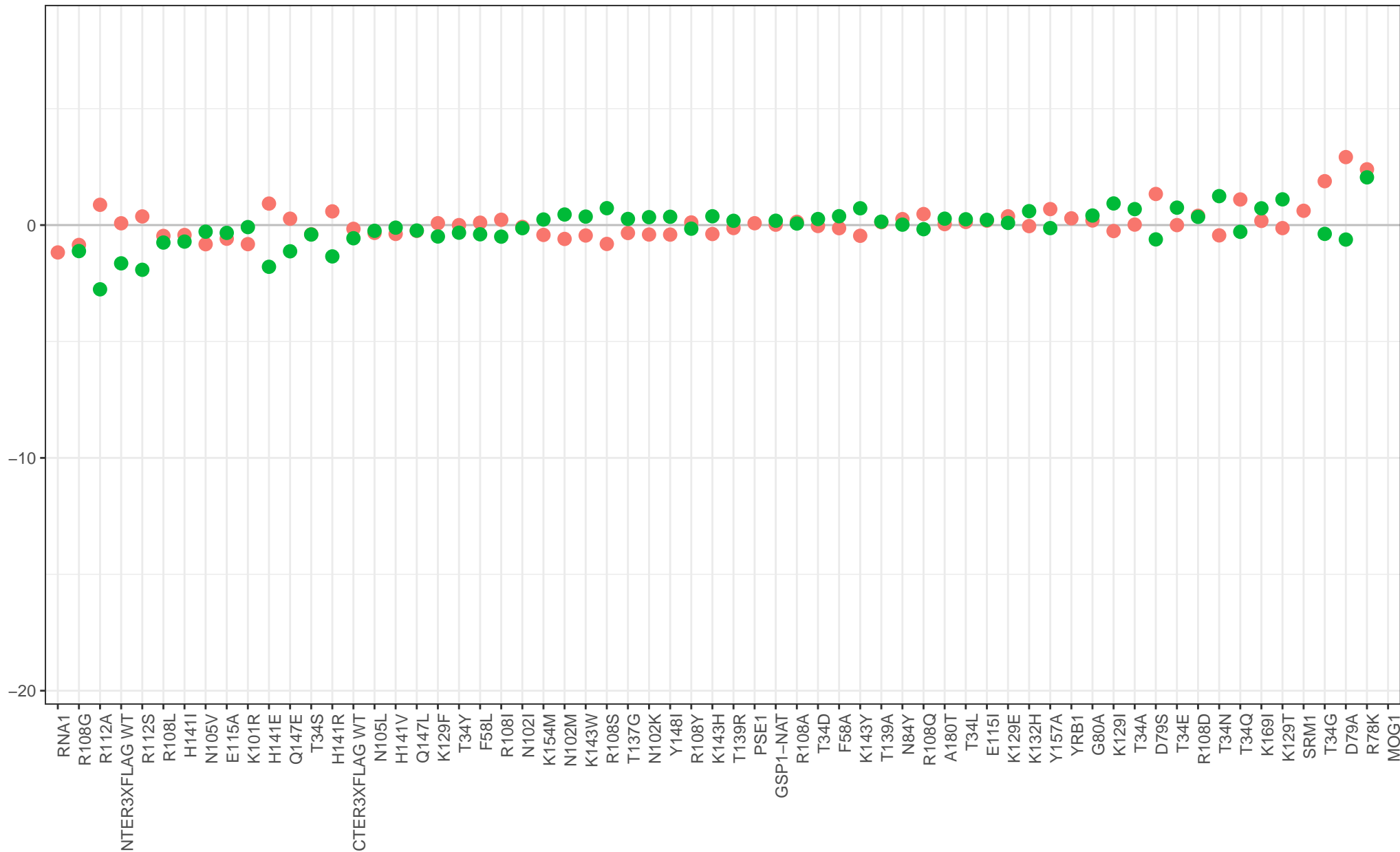
mutant

library gene

- GTR1
- GTR2
- LTV1
- MEH1
- SLM4

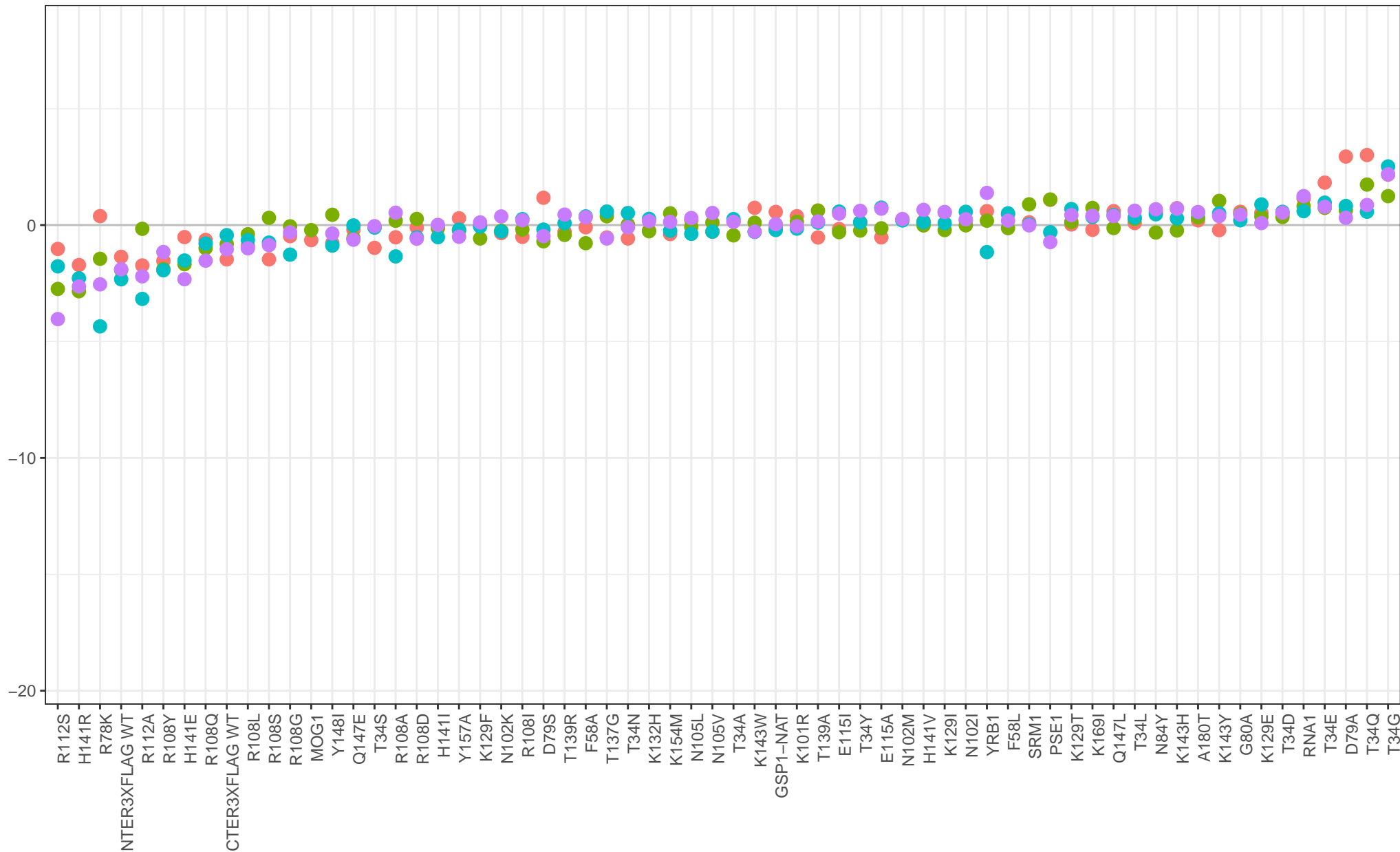
HAT-B complex

E-MAP score



HIR complex

E-MAP score

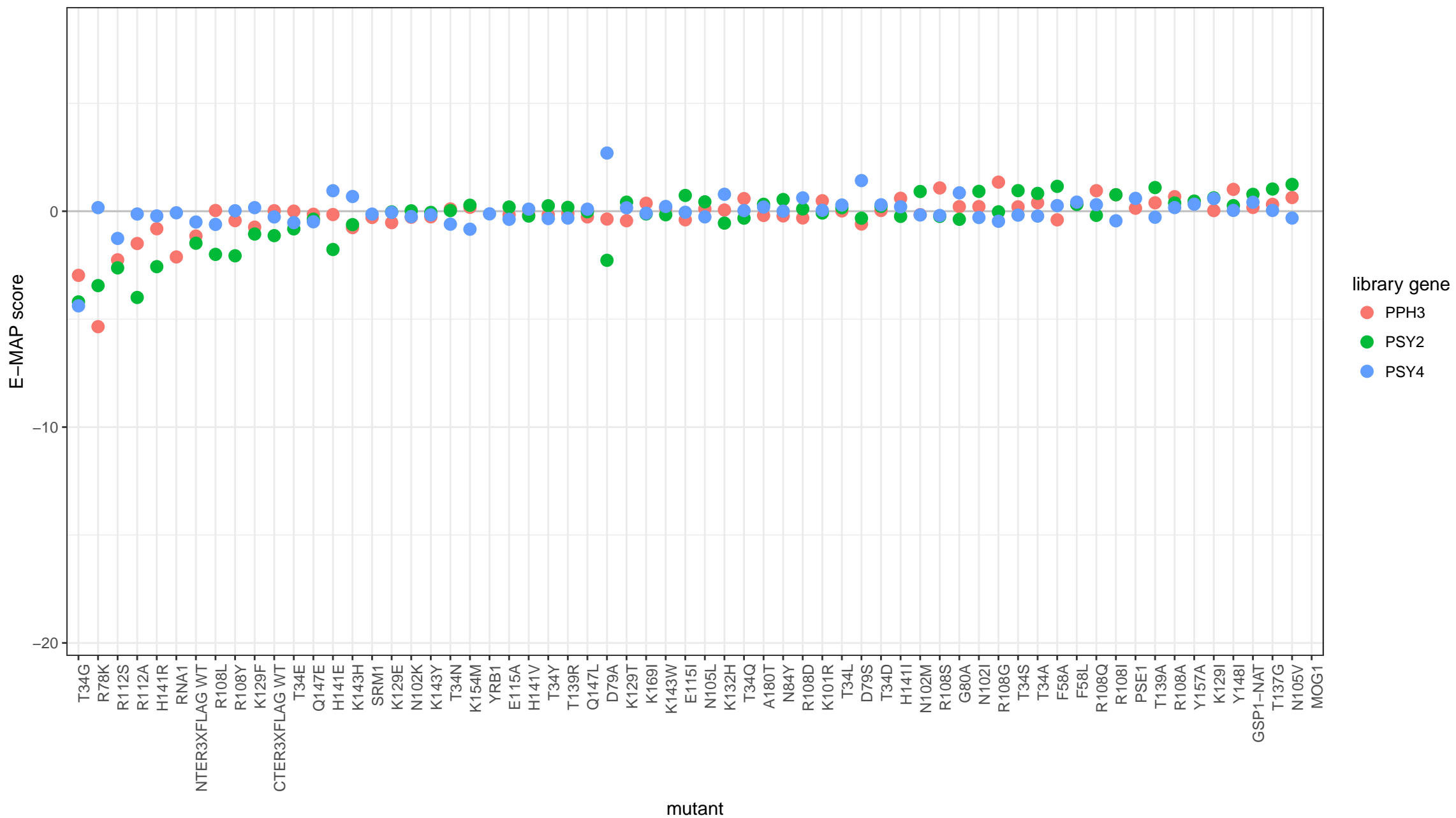


library gene

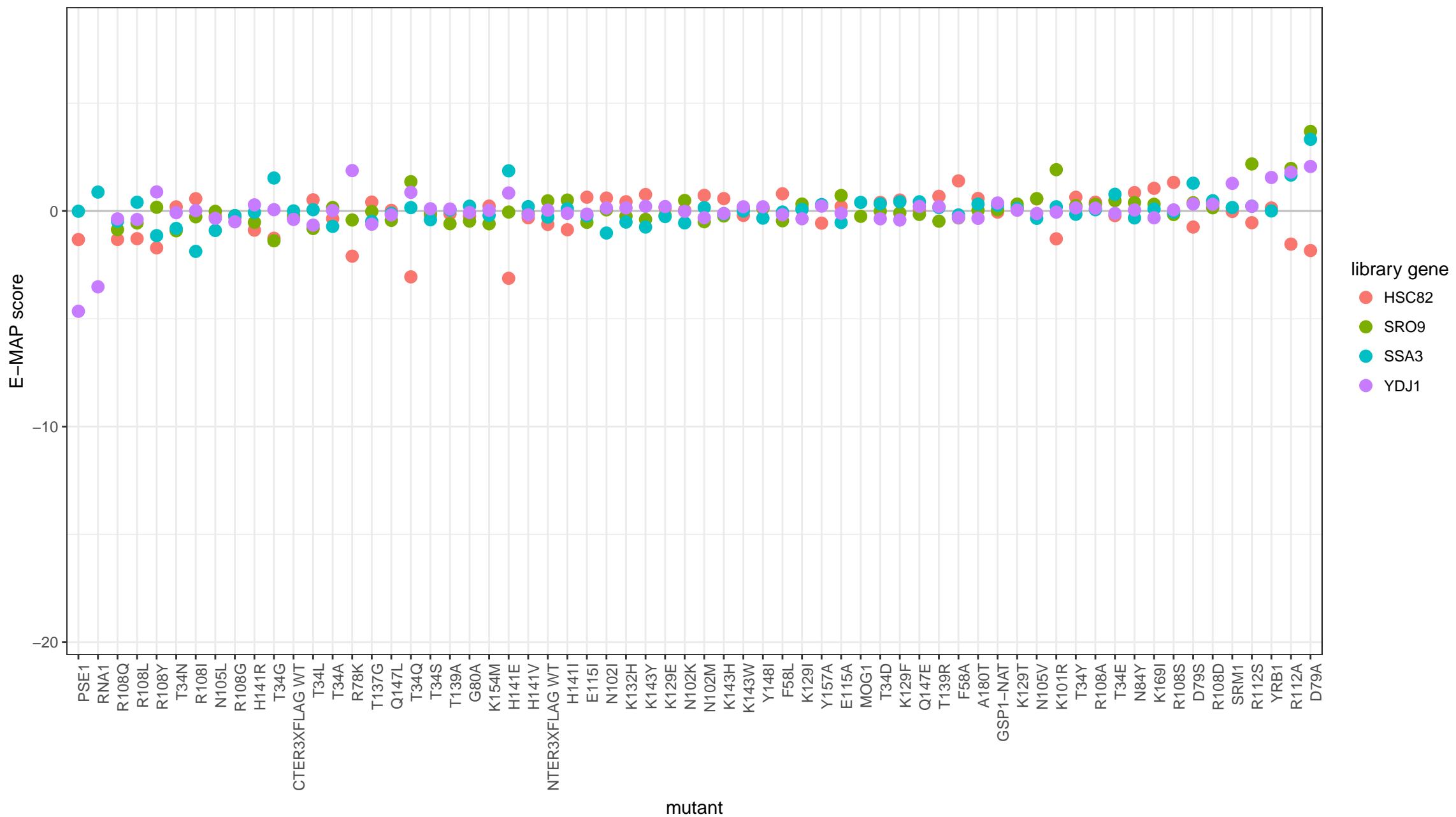
- HIR1
- HIR2
- HIR3
- HPC2

mutant

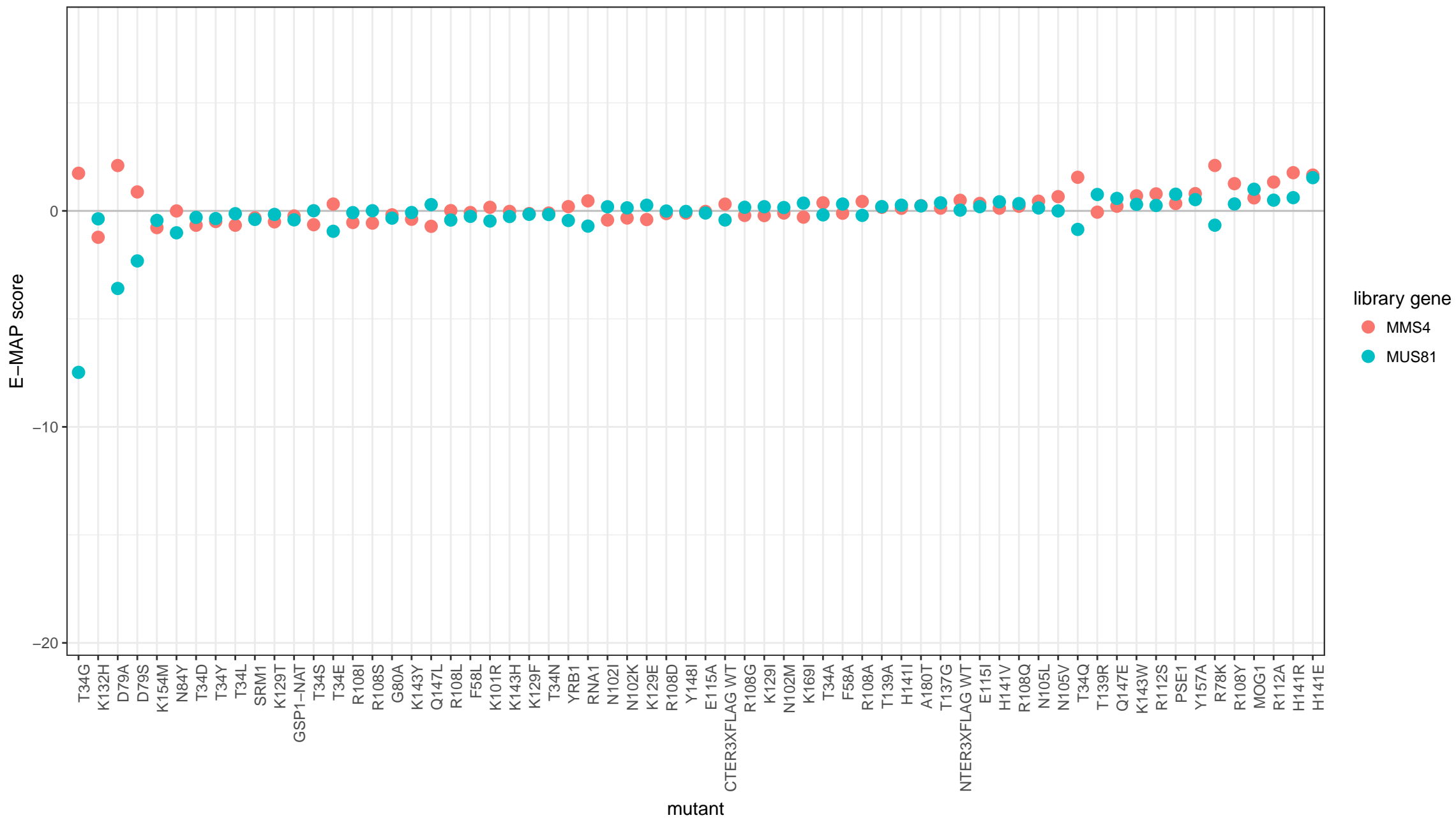
histone H2A phosphatase complex



HMC Complex



Holliday junction resolvase complex



HOPS complex

E-MAP score

-20

-10

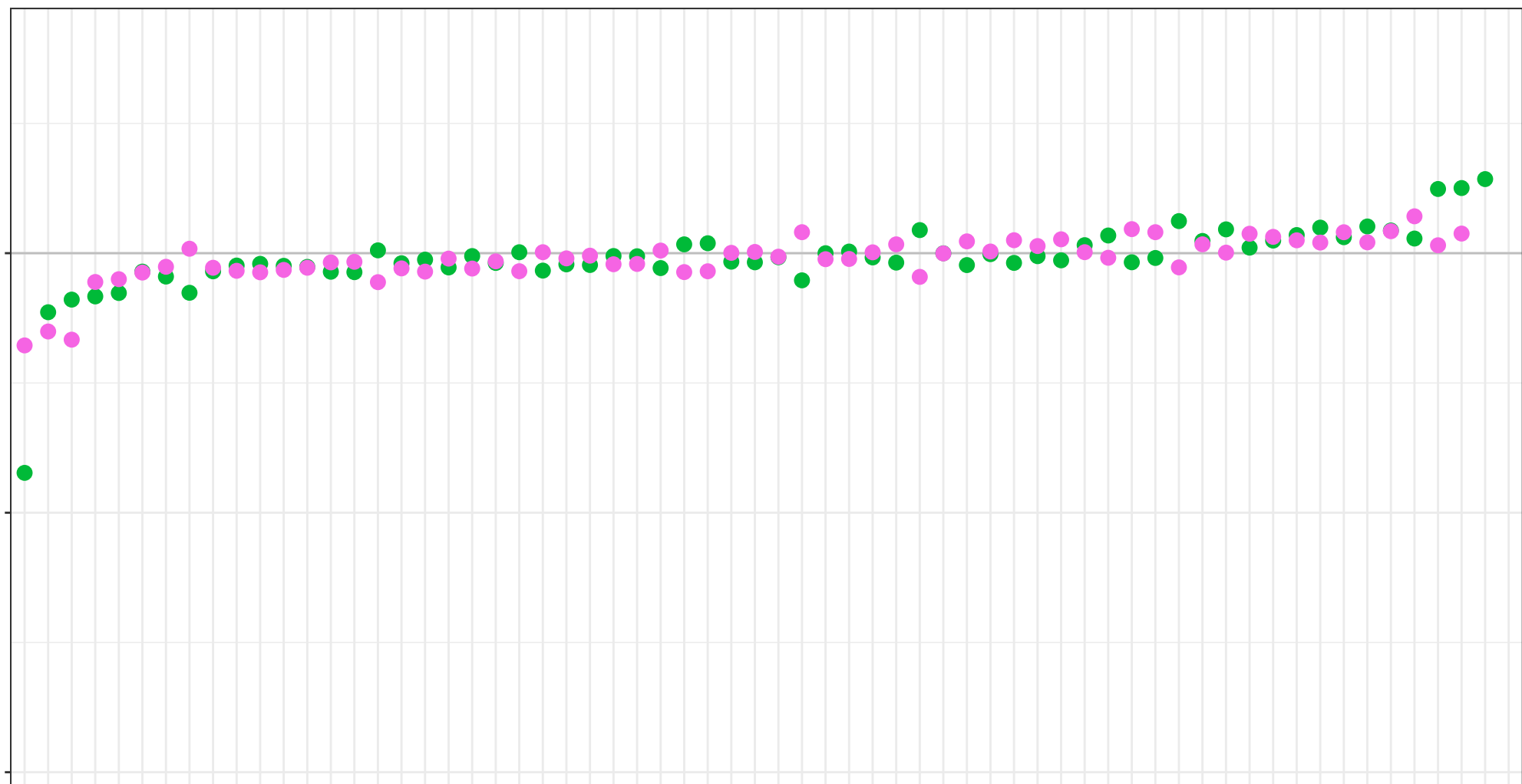
0

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

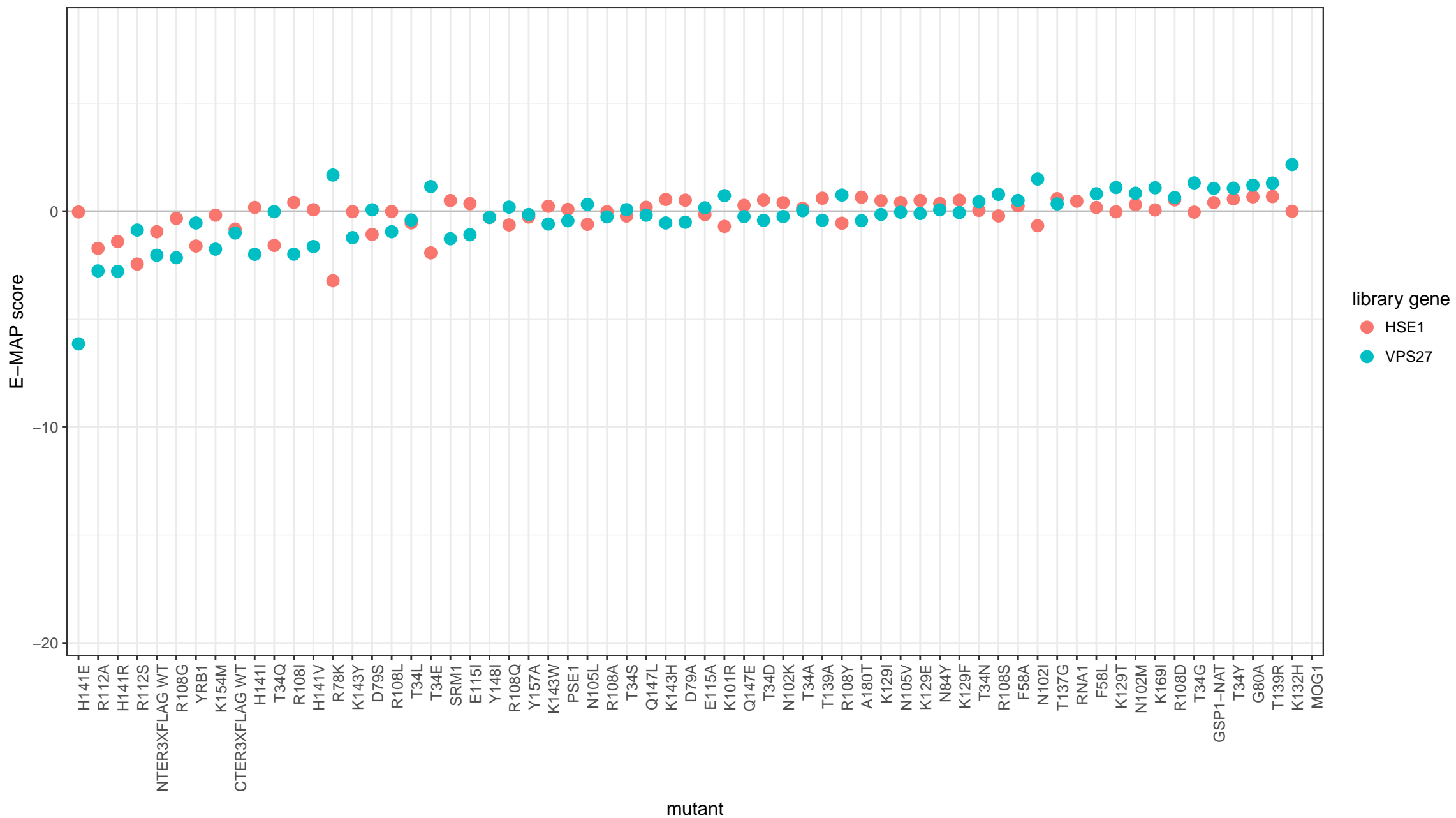
mutant

library gene

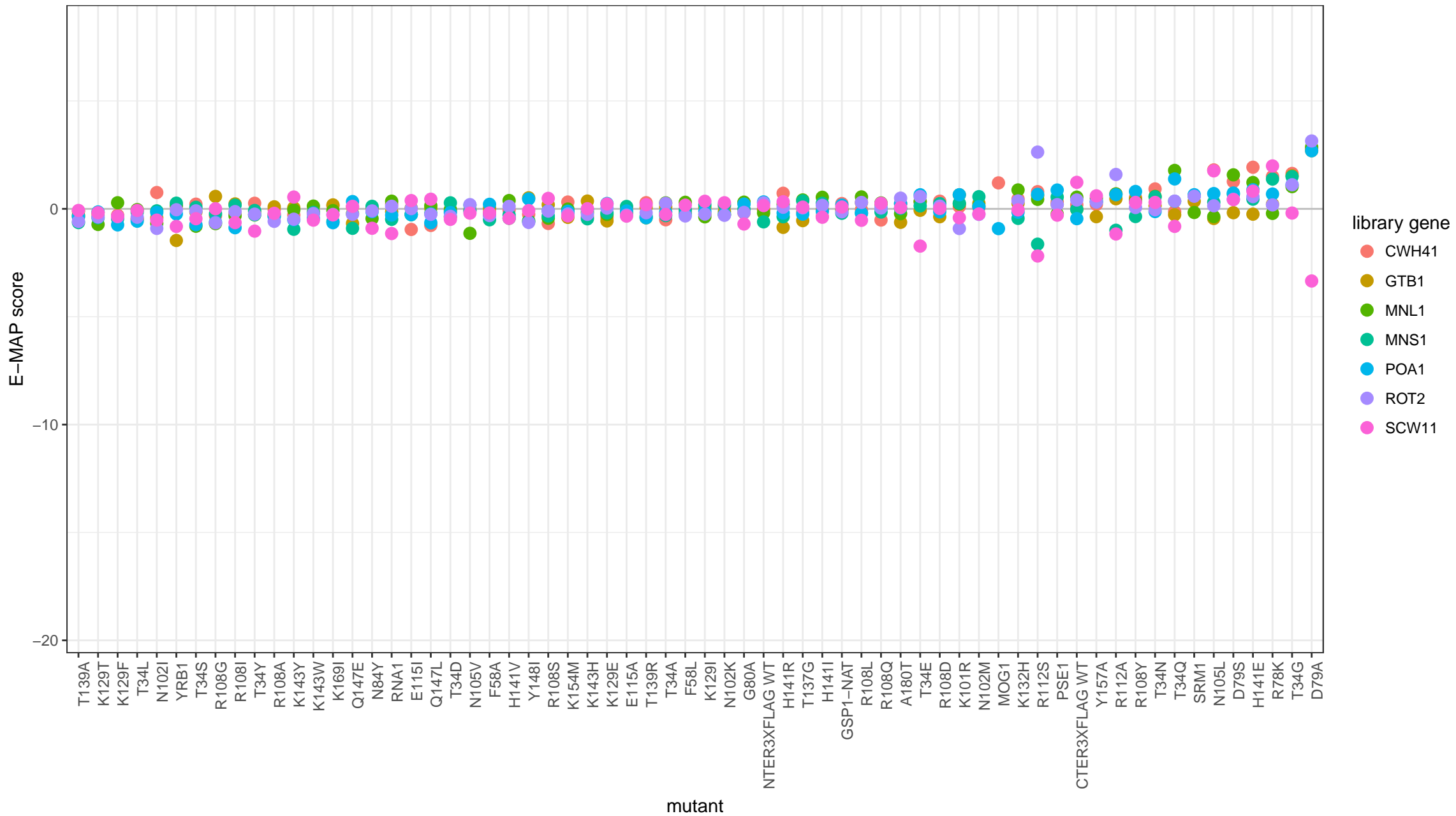
- PEP3
- PEP5
- VAM6
- VPS16
- VPS33
- VPS41



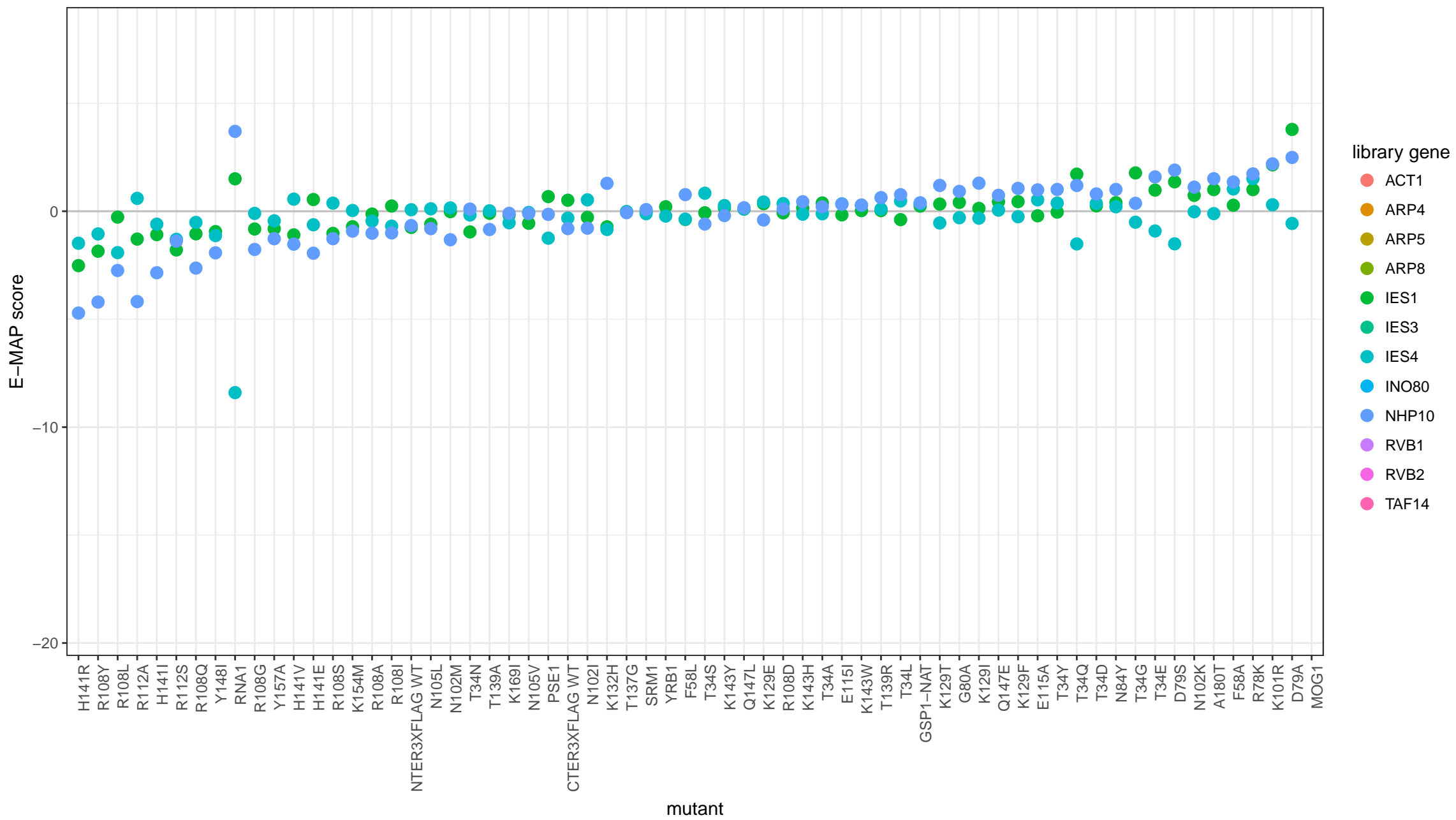
Hse1p/Vps27p complex



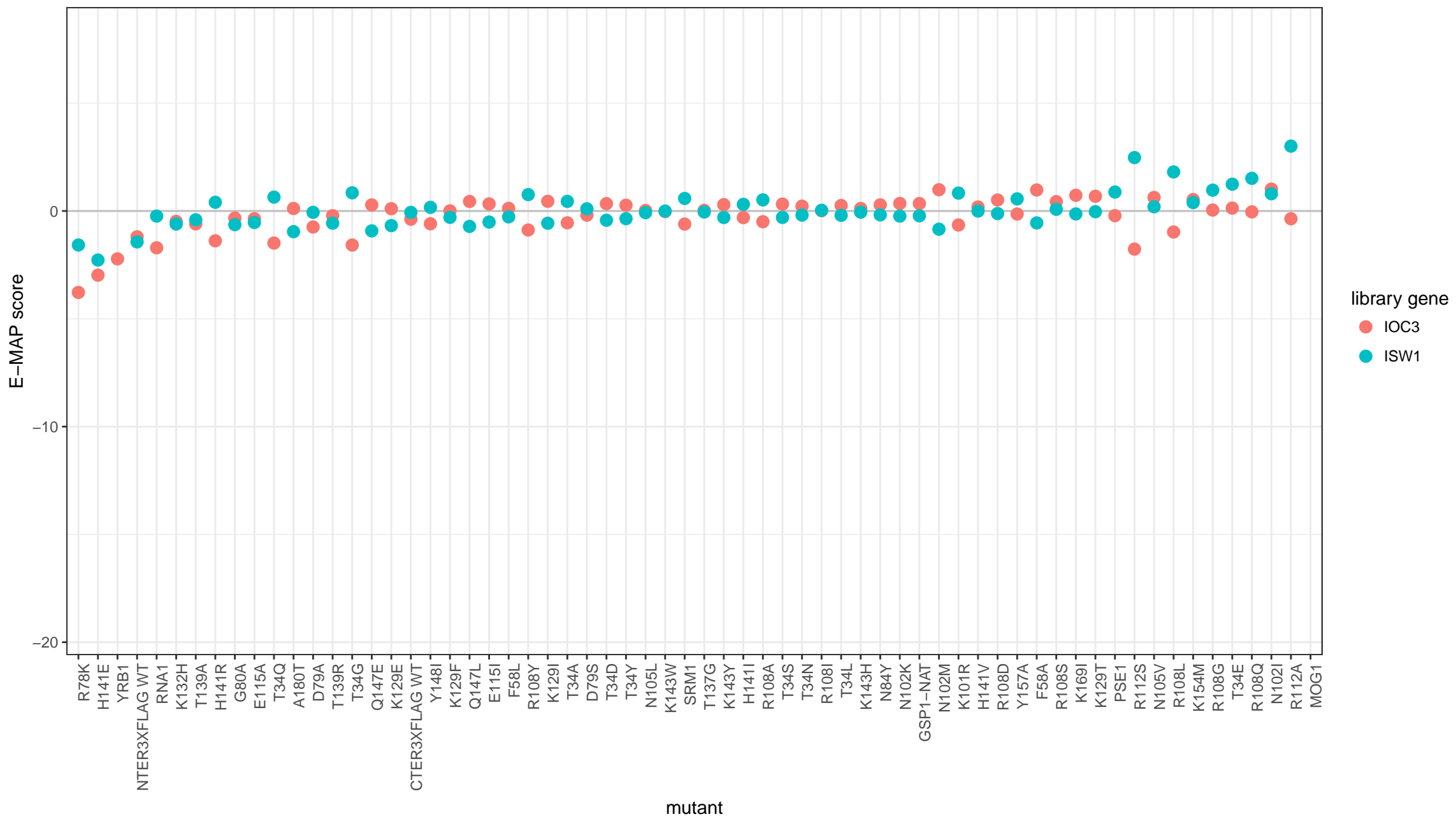
hydrolase activity, acting on glycosyl bonds



Ino80p complex



ISW1a complex



ISW1b complex

E-MAP score

0

-10

-20

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

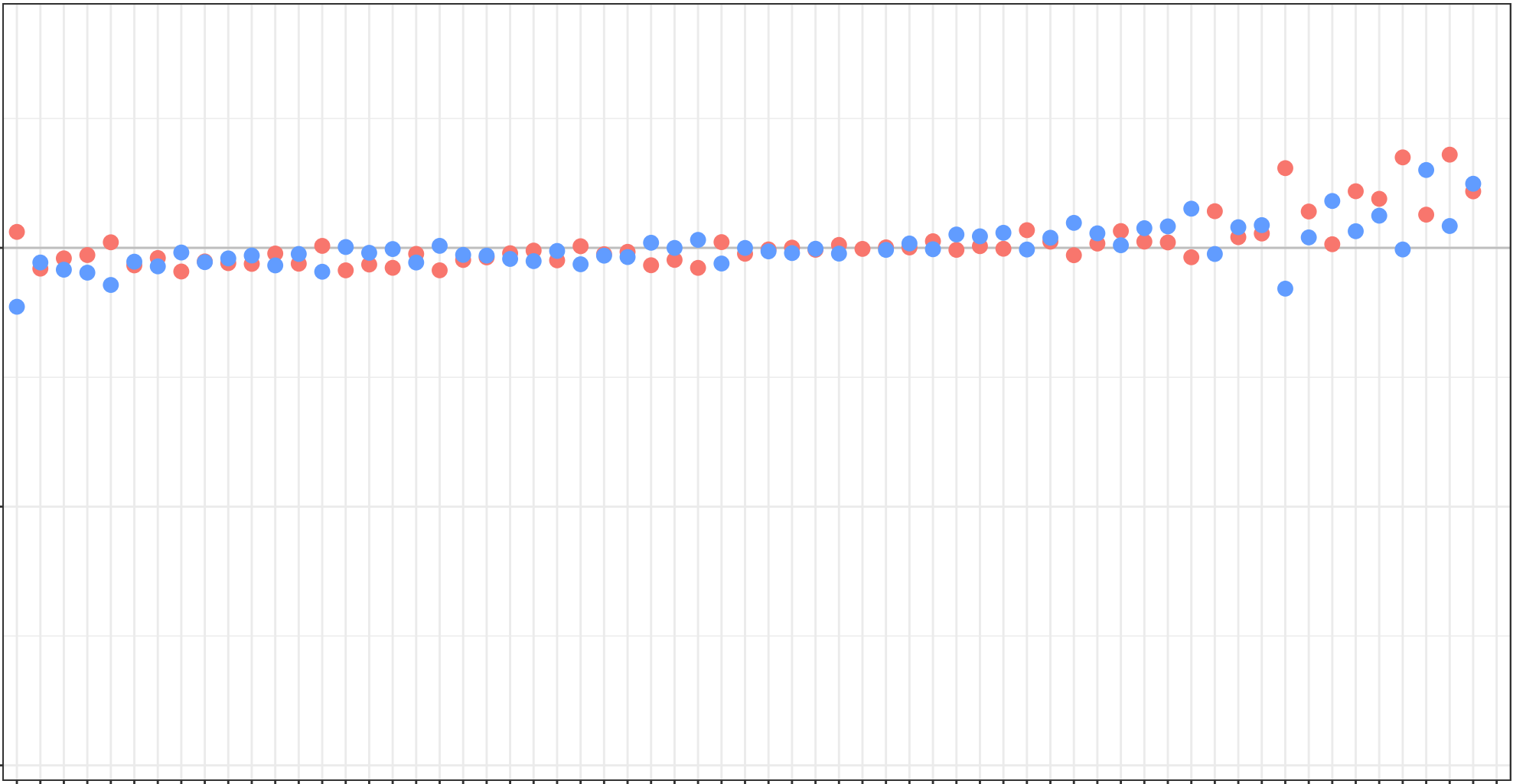
mutant

library gene

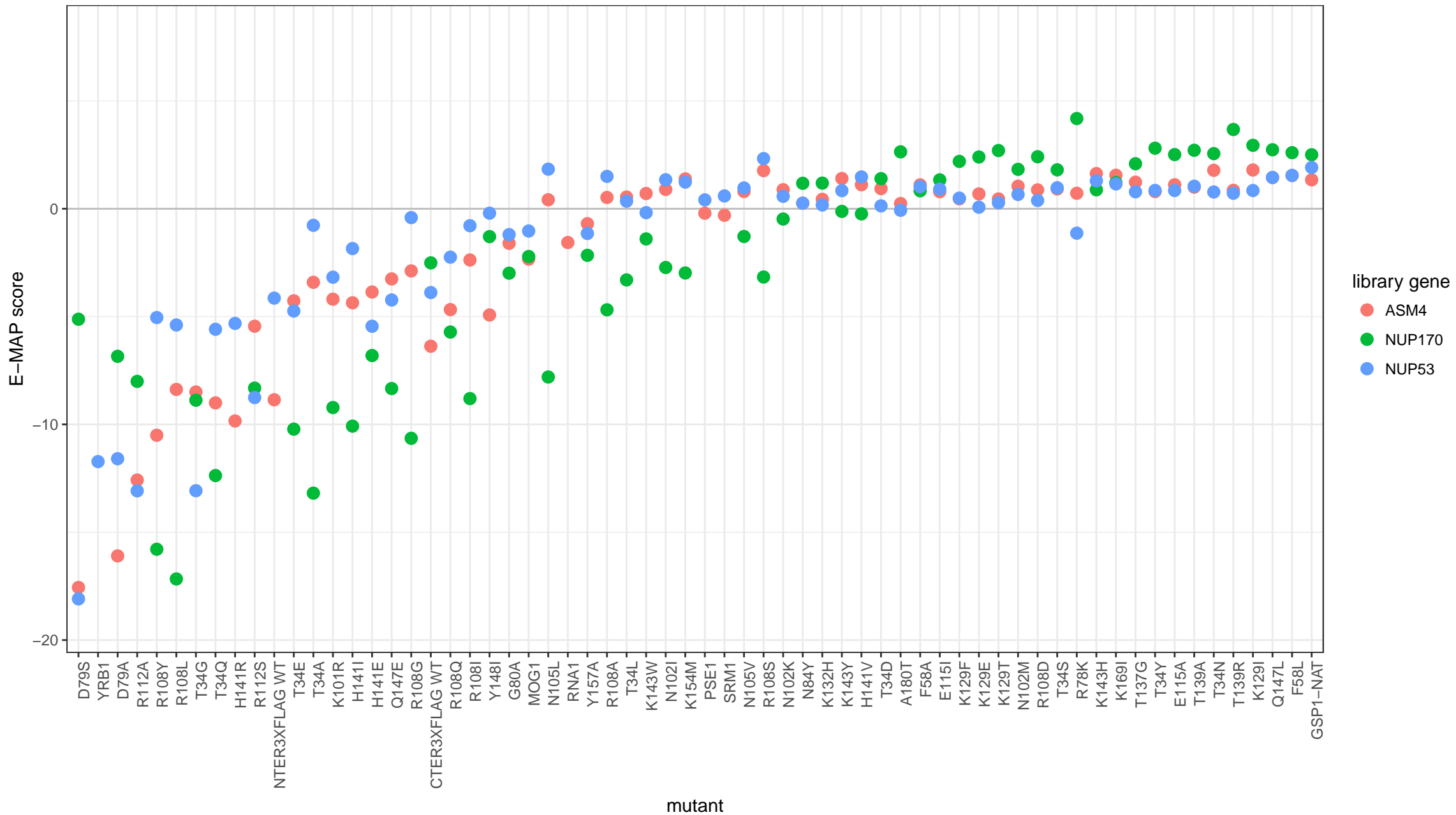
IOC2

IOC4

ISW1



karyopherin docking subcomplex of the Nuclear Pore Complex (NPC)



Kel1p/Kel2p/Lte1p complex

E-MAP score

-20

-10

0

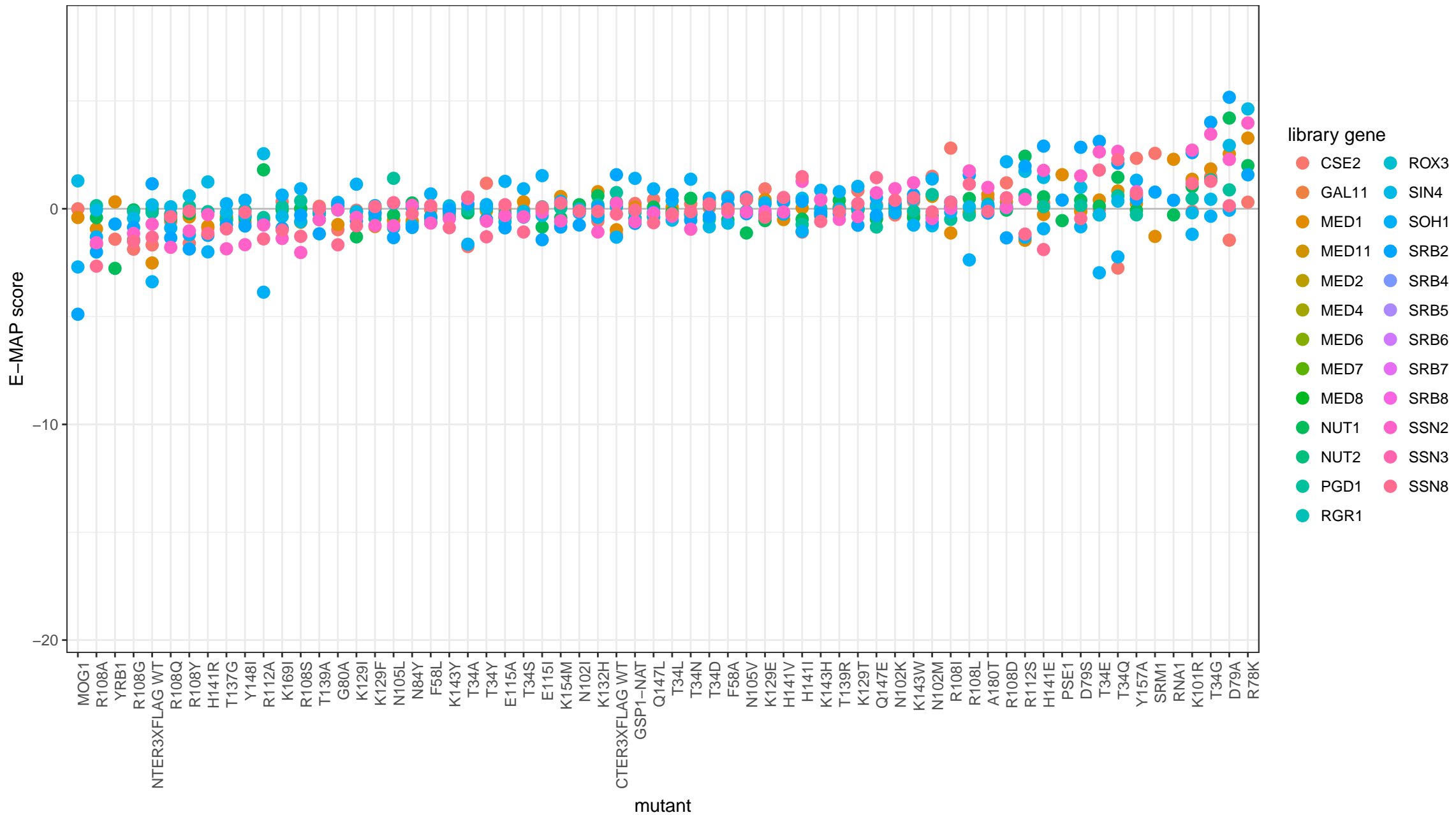
mutant

library gene

KEL1
KEL2
LTE1

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

Kornberg's mediator (SRB) complex



Ku complex

E-MAP score

-20

-10

0

mutant

library gene

YKU70
YKU80

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

Lge1p/Bre1p complex

E-MAP score

-20

-10

0

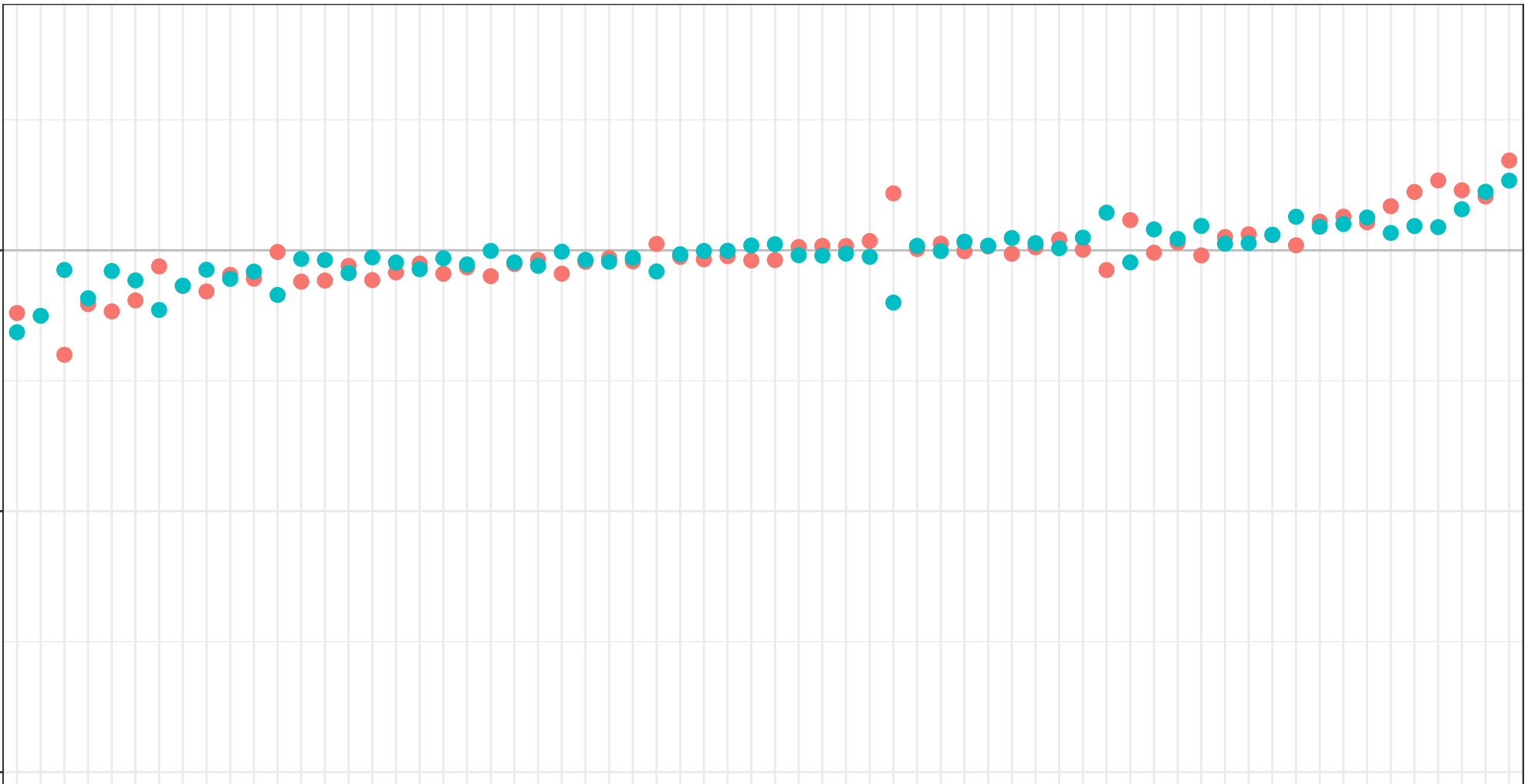
R108G
YRB1
RNA1
R108Q
H141E
K154M
R108A
D79A
R108I
Y148I
H141V
R108Y
D79S
PSE1
K143Y
GSP1-NAT
E115I
T137G
T139A
N105V
K129F
T34S
K143H
H141I
K143W
F58L
E115A
R108S
K129E
K169I
T34D
K129I
N102M
T34A
N105L
T34N
N84Y
R78K
Q147L
Y157A
T34L
K132H
T34Y
Q147E
N102I
K129T
A180T
R112A
T139R
N102K
F58A
G80A
R108D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

mutant

library gene

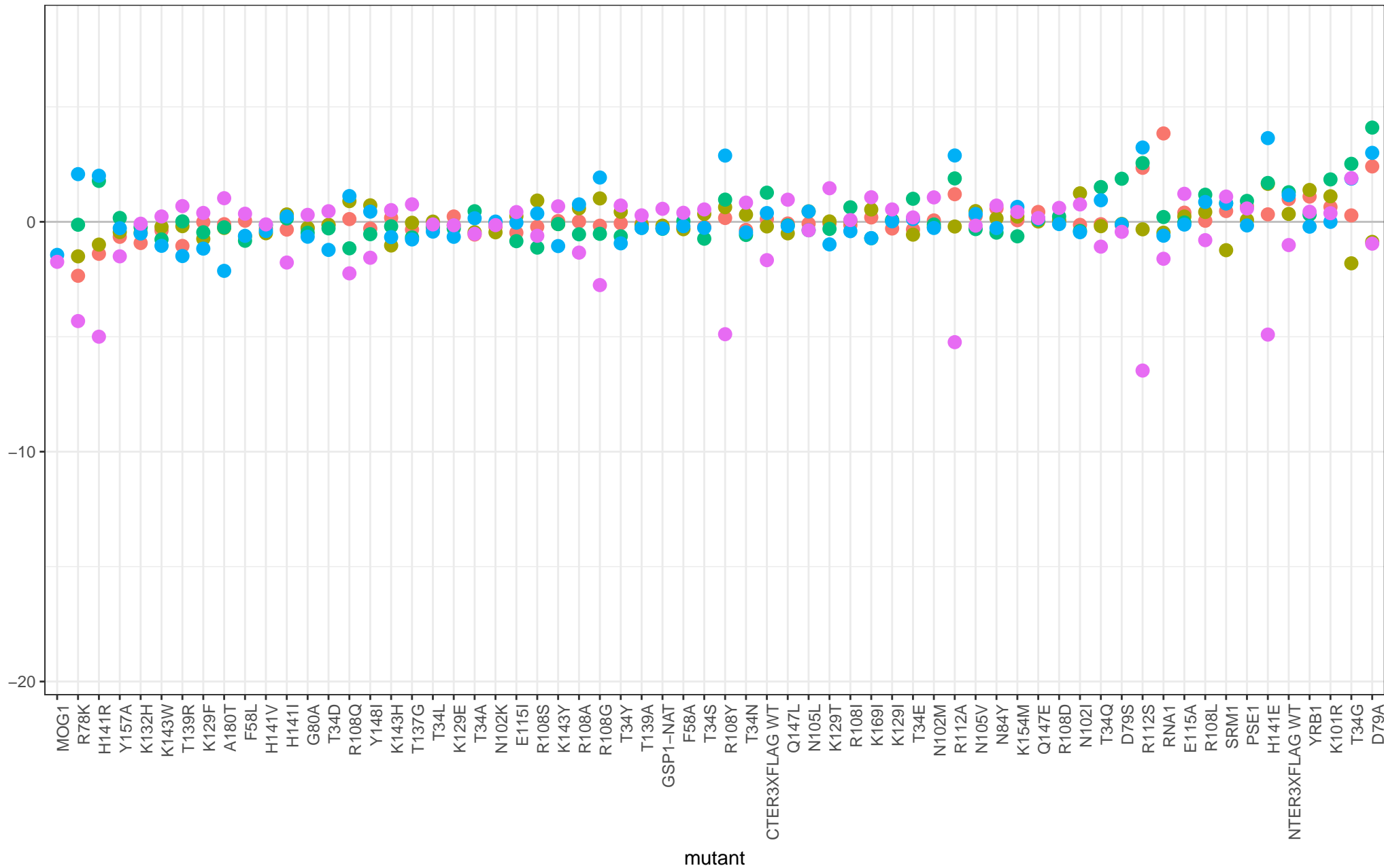
BRE1

LGE1



ligase activity

E-MAP score



Mad1p/Mad2p complex

E-MAP score

0

-10

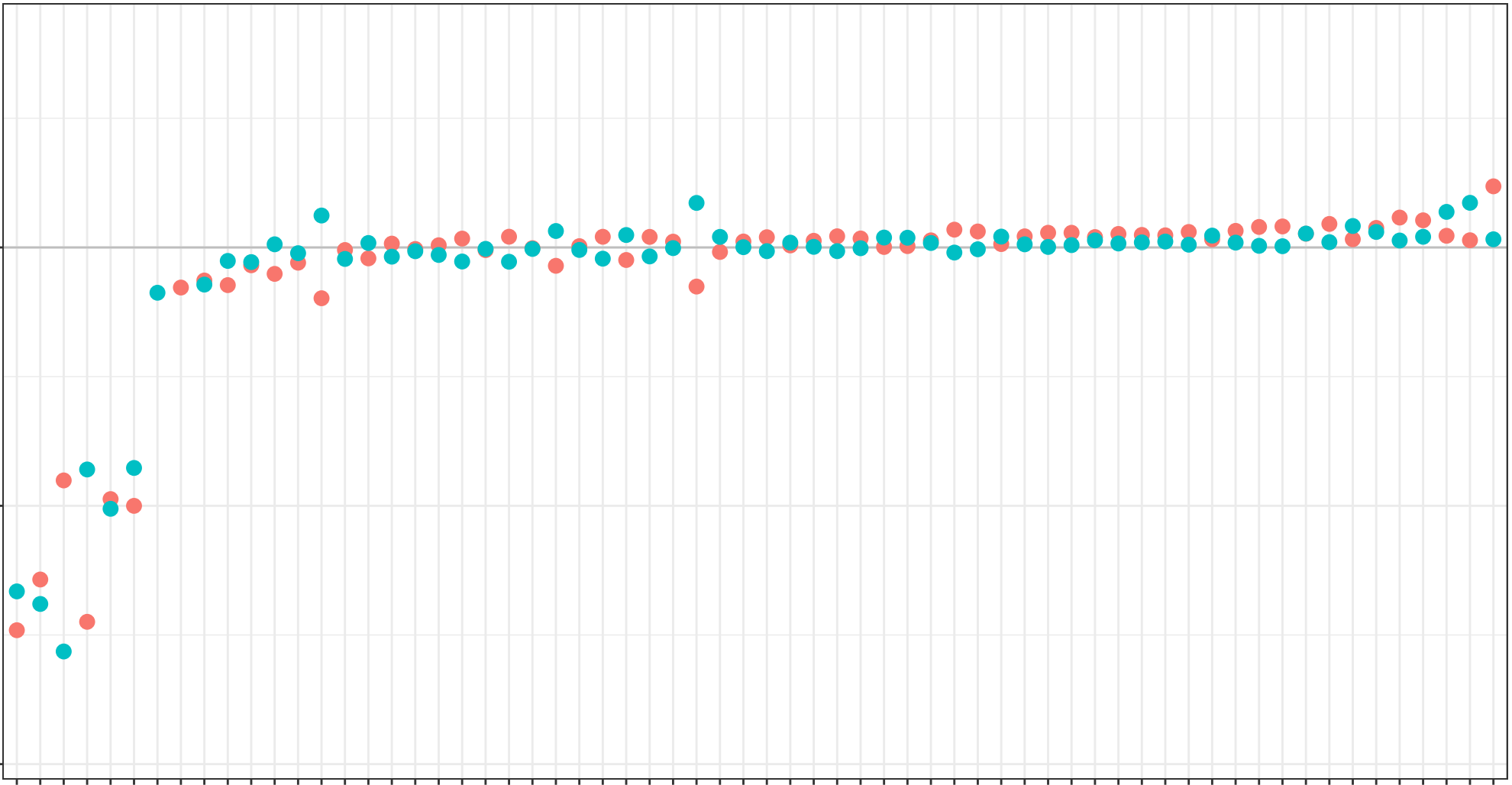
-20

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

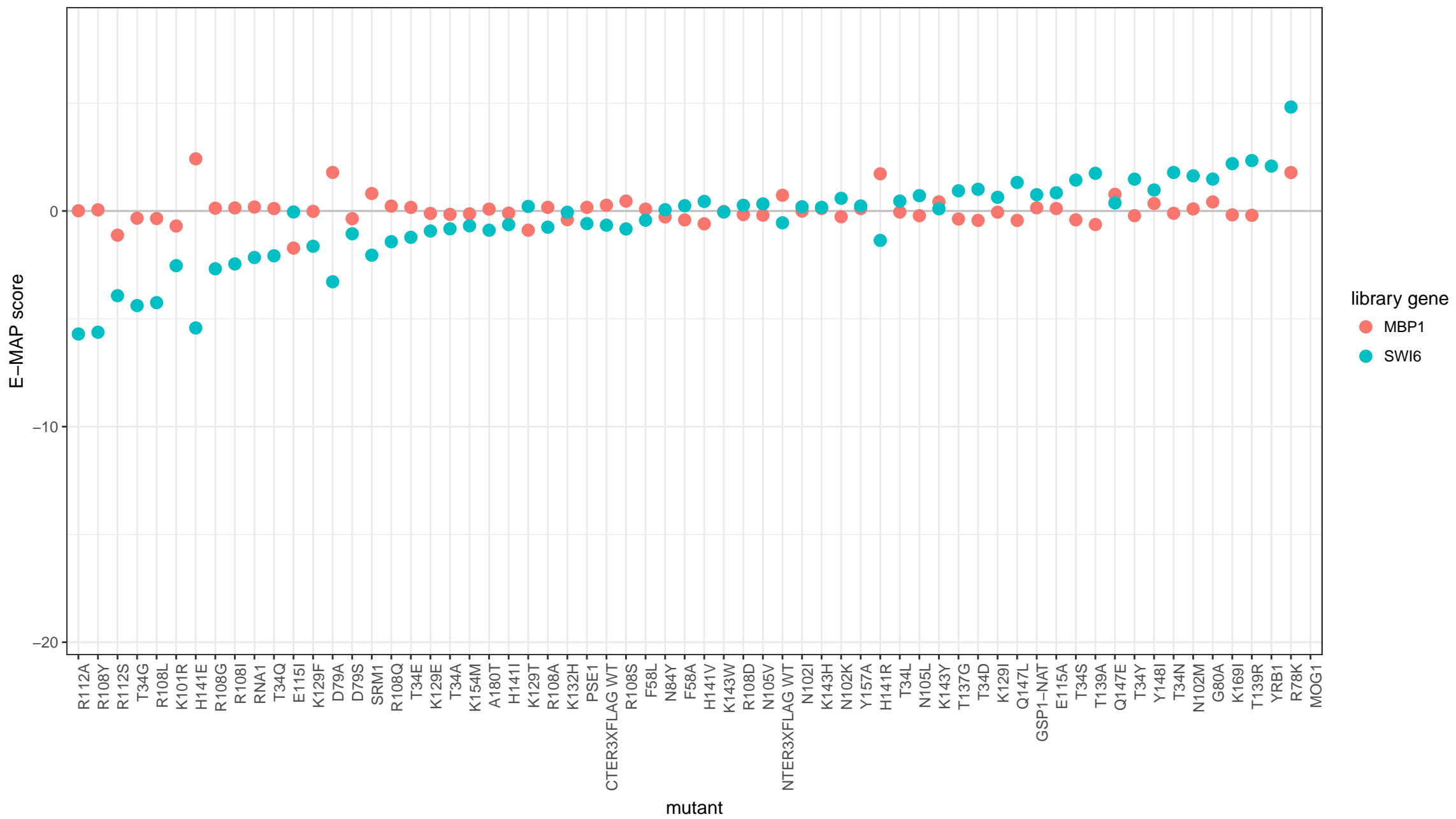
mutant

library gene

MAD1
MAD2



MBF complex



Mdm12p/Mmm1p/Mdm10p complex

E-MAP score

0

-10

-20

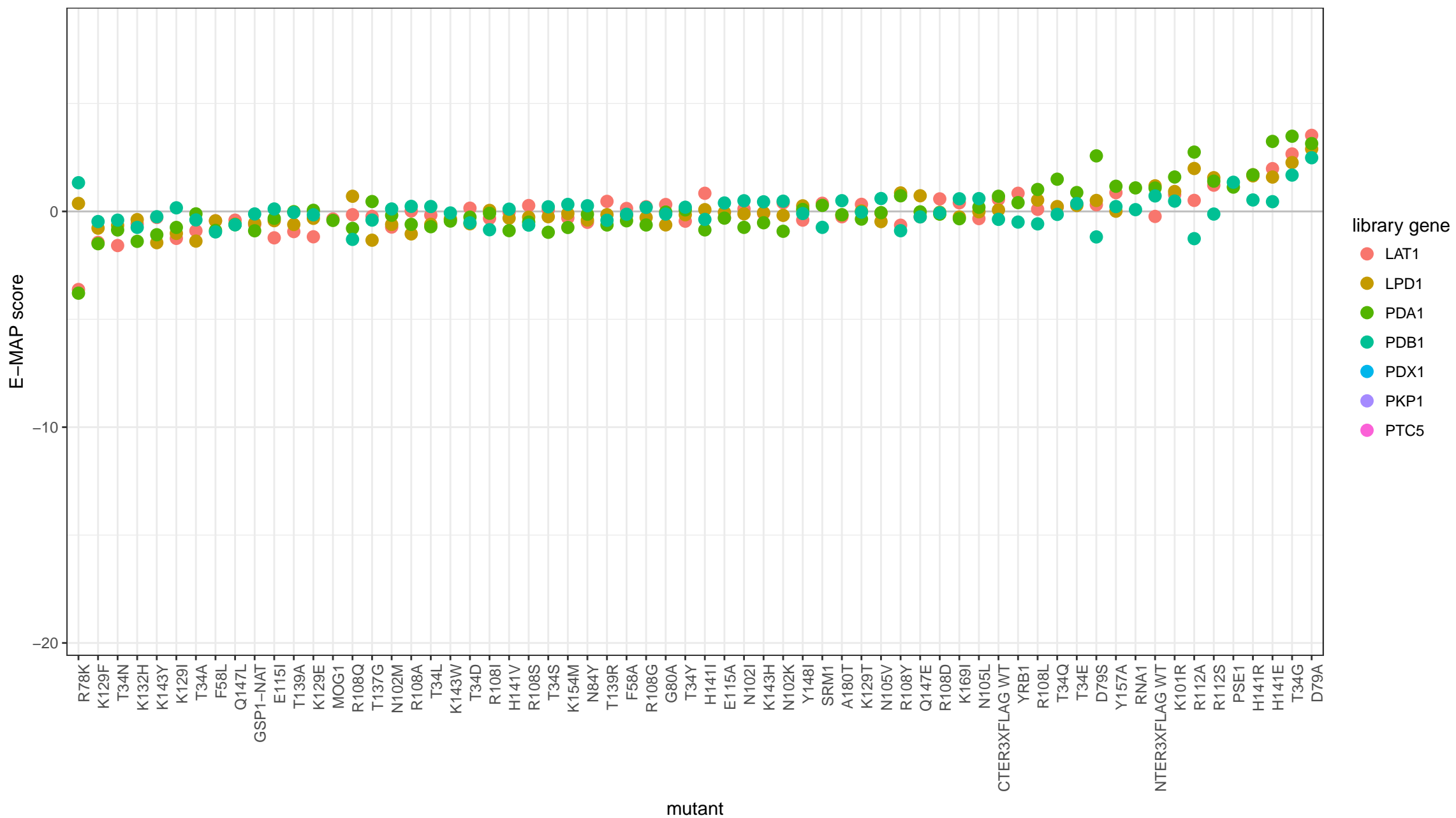
PSE1
K129F
K129T
N84Y
Q147L
K143Y
N102I
R108S
T34N
K169I
T34S
A180T
K143H
E115A
T34D
K132H
K129I
N102K
T34Y
F58A
T137G
GSP1-NAT
K129E
K154M
F58L
SRM1
G80A
H141V
T139A
T34L
R108D
N102M
K143W
E115I
N105V
N105L
Y148I
T139R
R108A
H141I
YRB1
T34A
Q147E
RNA1
MOG1
T34E
R108G
R108I
Y157A
CTER3XFLAG WT
R78K
K101R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

mutant

library gene

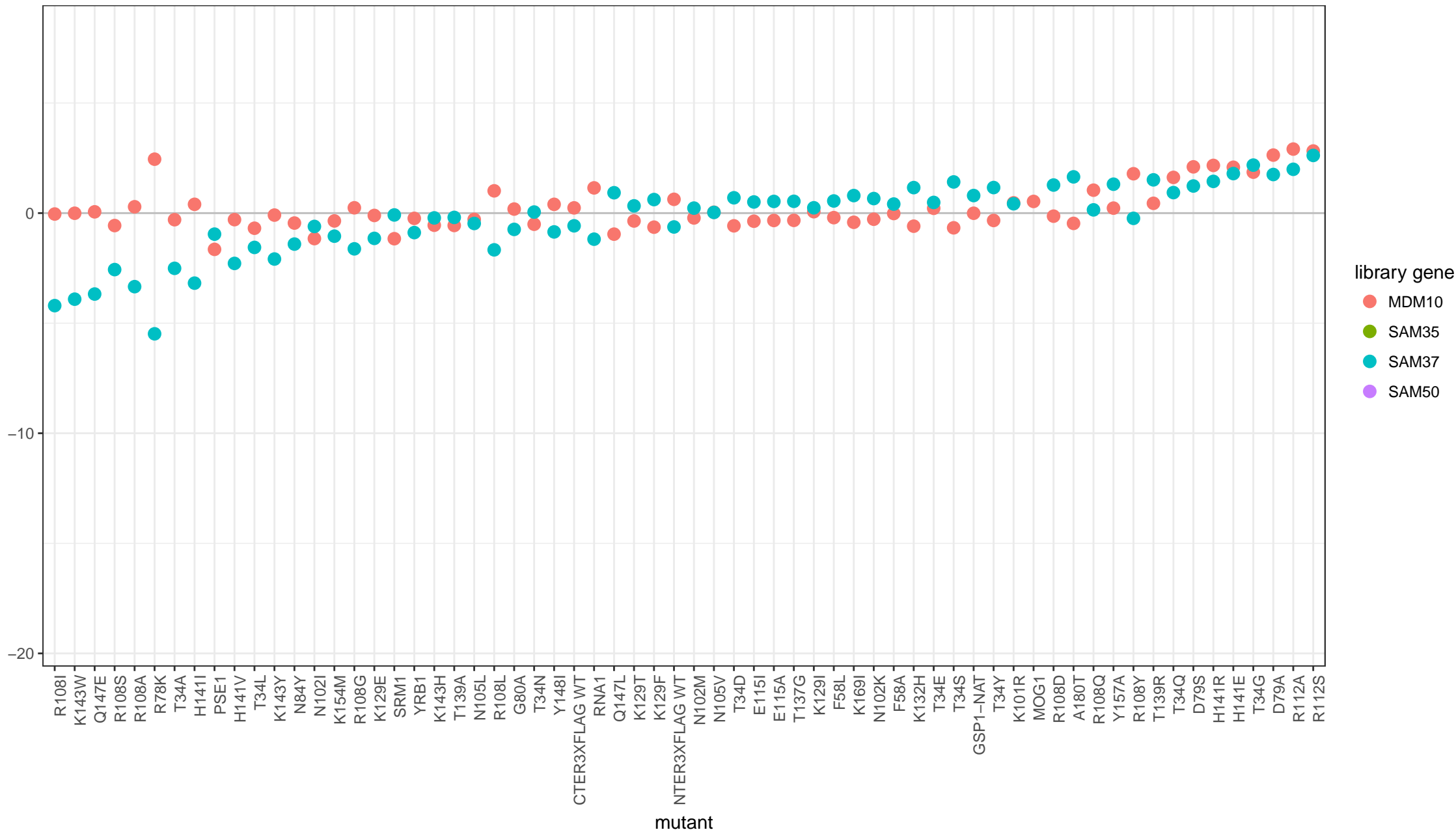
- MDM10
- MDM12
- MMM1

mitochondrial pyruvate dehydrogenase complex

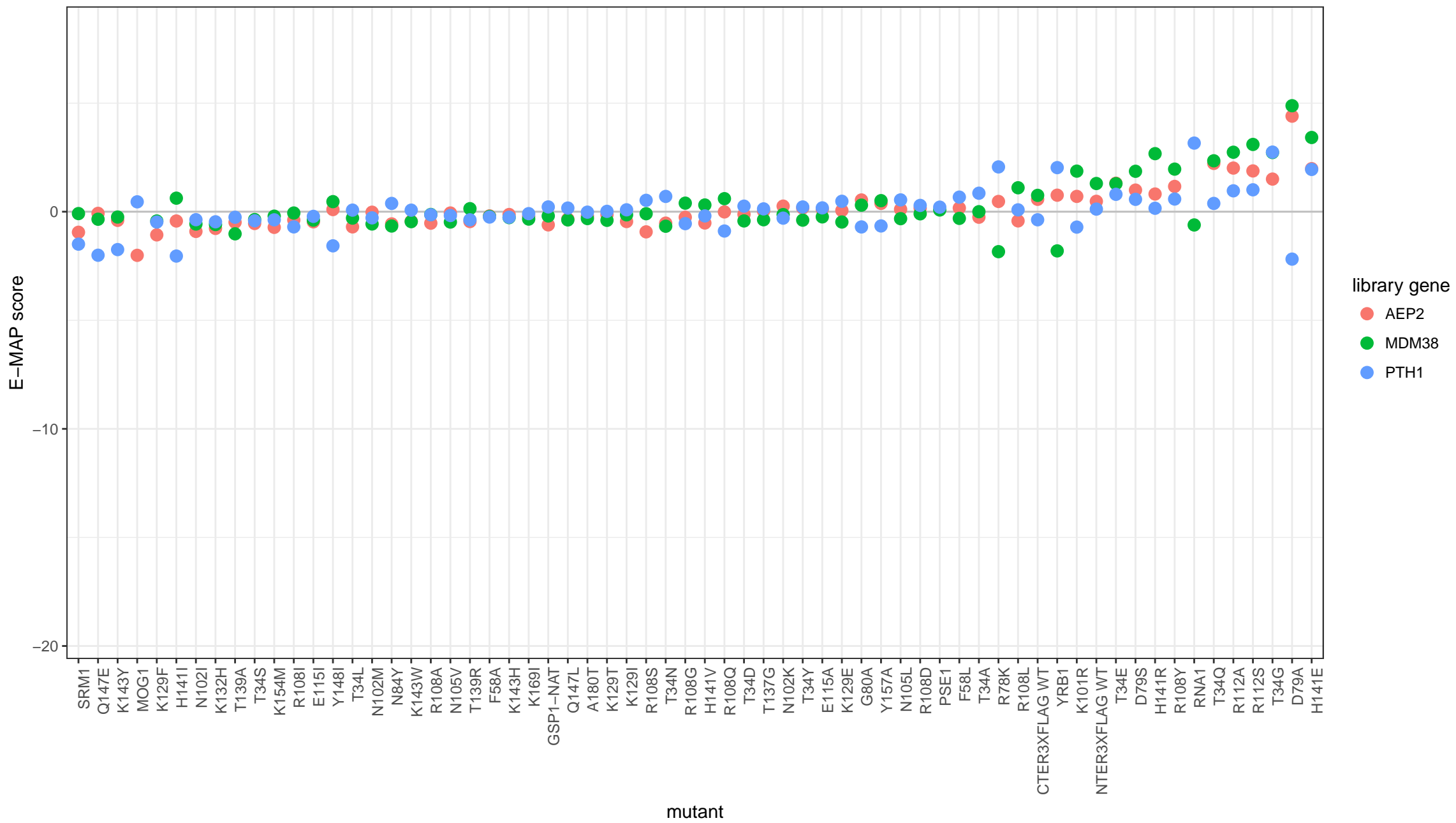


mitochondrial sorting and assembly machinery complex

E-MAP score

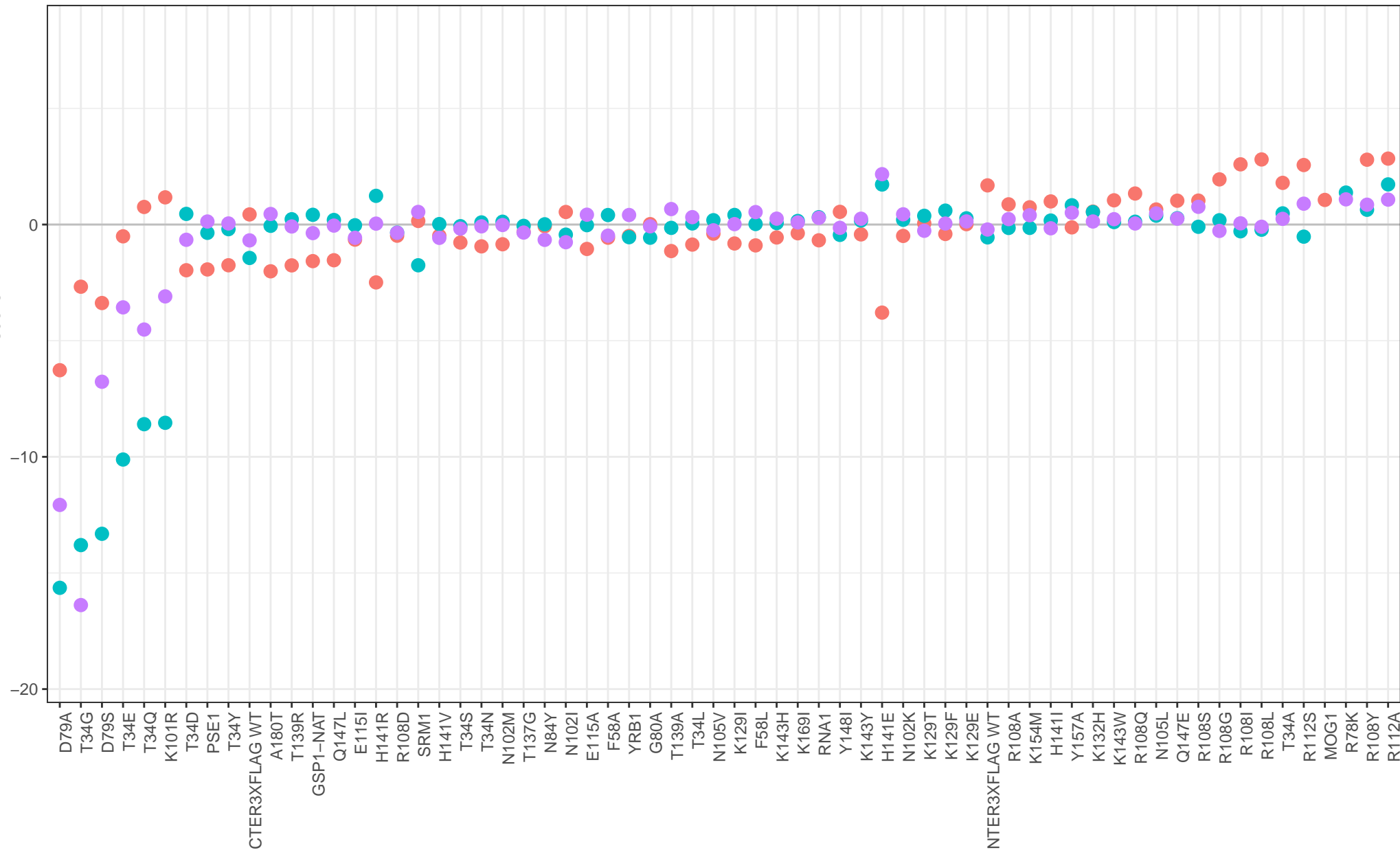


mitochondrial translation



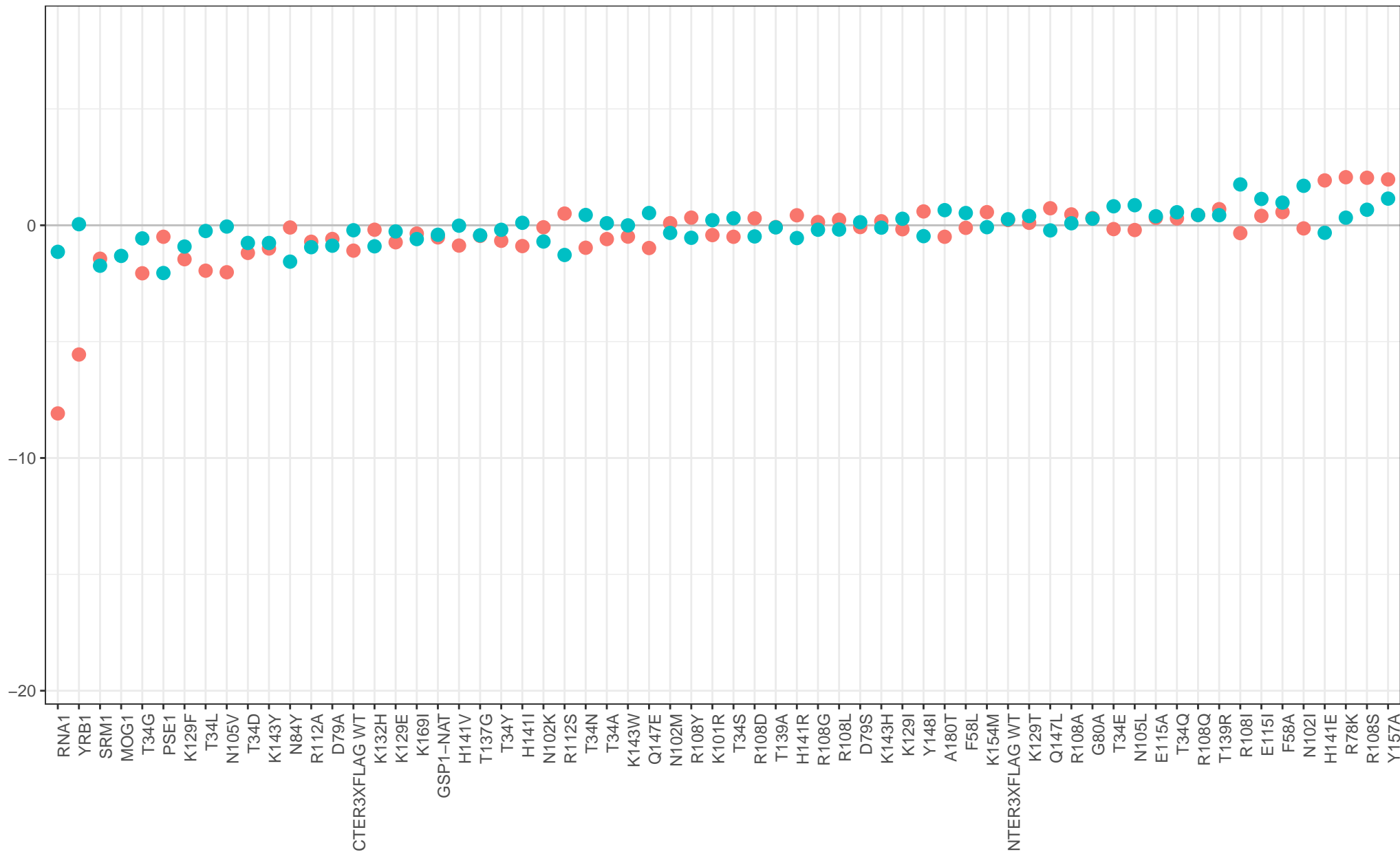
mitotic checkpoint complex

E-MAP score



Mks1p/Rtg2p complex

E-MAP score



library gene

MKS1

RTG2

Mon1p/Ccz1p complex

E-MAP score

-20

-10

0

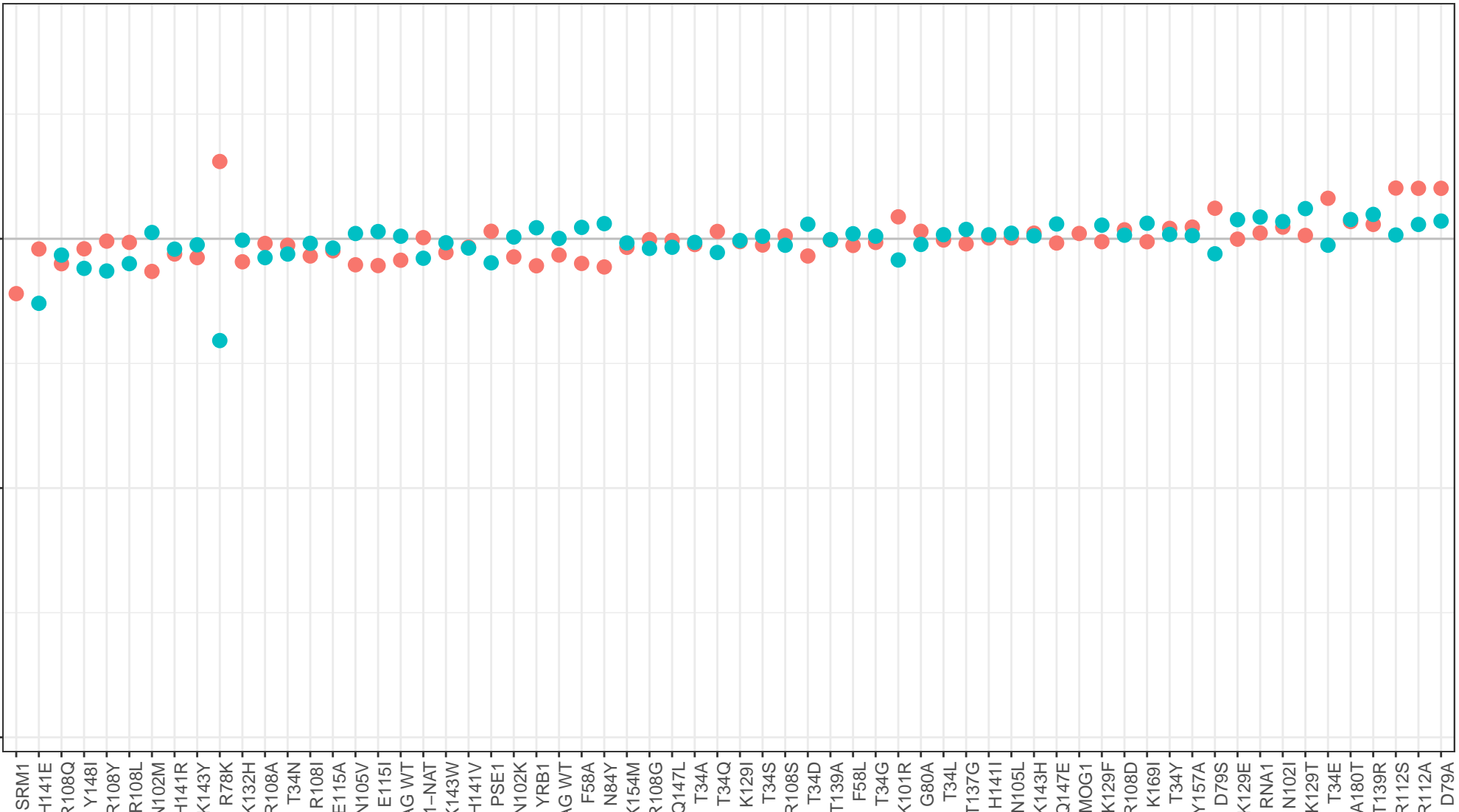
SRM1
H141E
R108Q
Y148I
R108Y
R108L
N102M
H141R
K143Y
R78K
K132H
R108A
T34N
R108I
E115A
N105V
E115I
NTER3XFLAG WT
GSP1-NAT
K143W
H141V
PSE1
N102K
YRB1
CTER3XFLAG WT
F58A
N84Y
K154M
R108G
Q147L
T34A
T34Q
K129I
T34S
R108S
T34D
T139A
F58L
T34G
K101R
G80A
T34L
T137G
H141I
N105L
K143H
Q147E
MOG1
K129F
R108D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

mutant

library gene

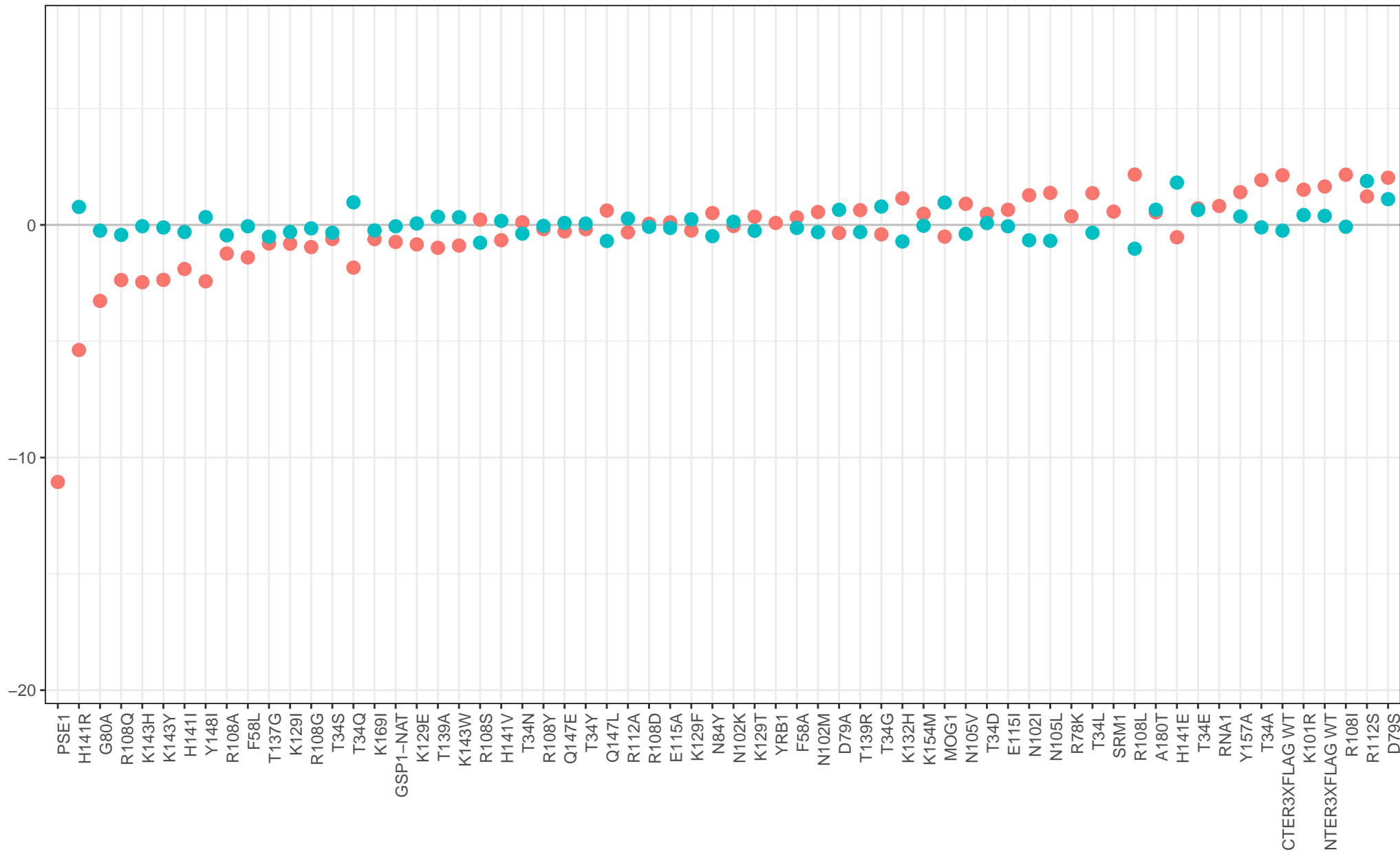
CCZ1

MON1



monopolin complex

E-MAP score



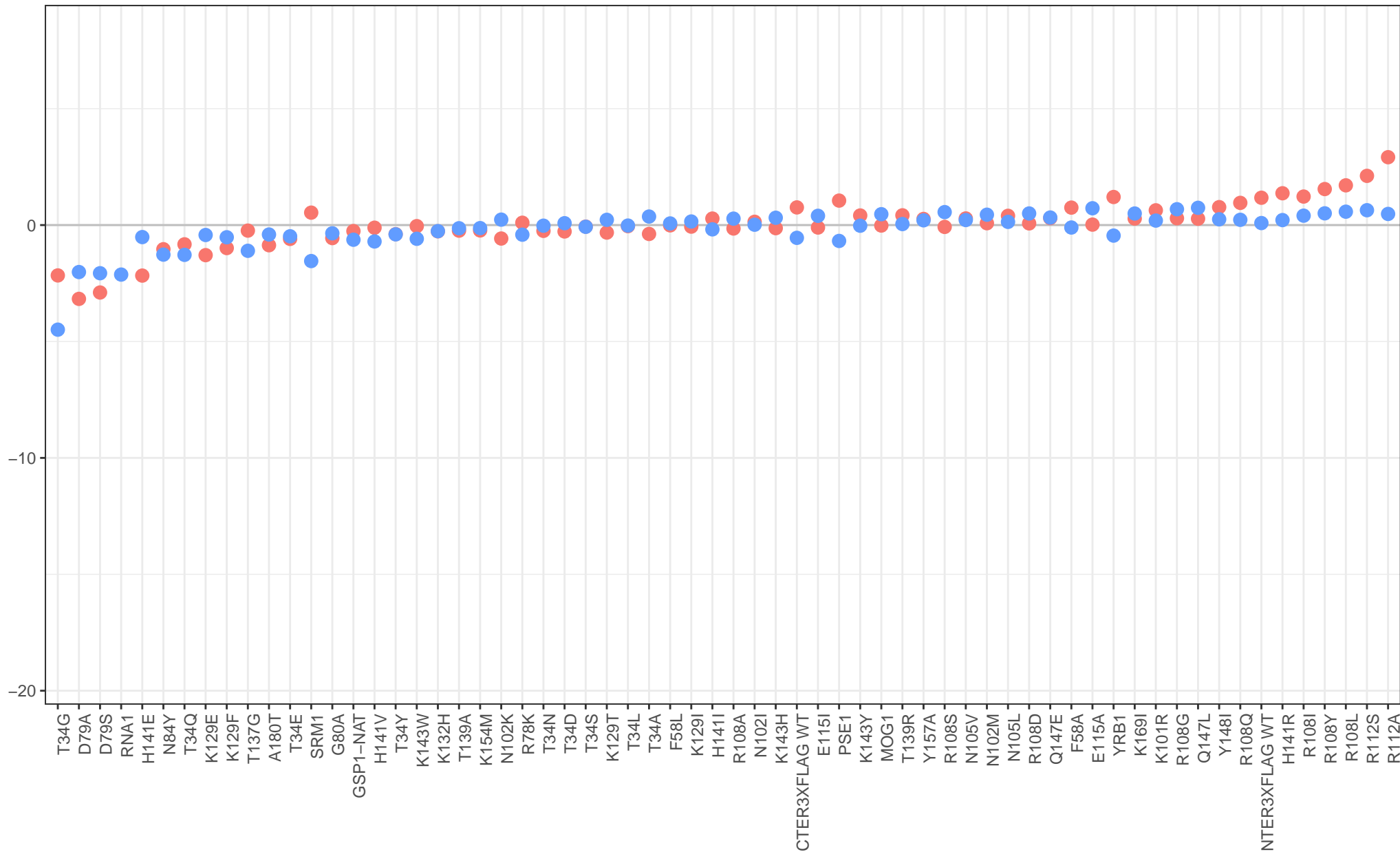
library gene

- CSM1
- HRR25
- LRS4
- MAM1

mutant

MRX complex

E-MAP score



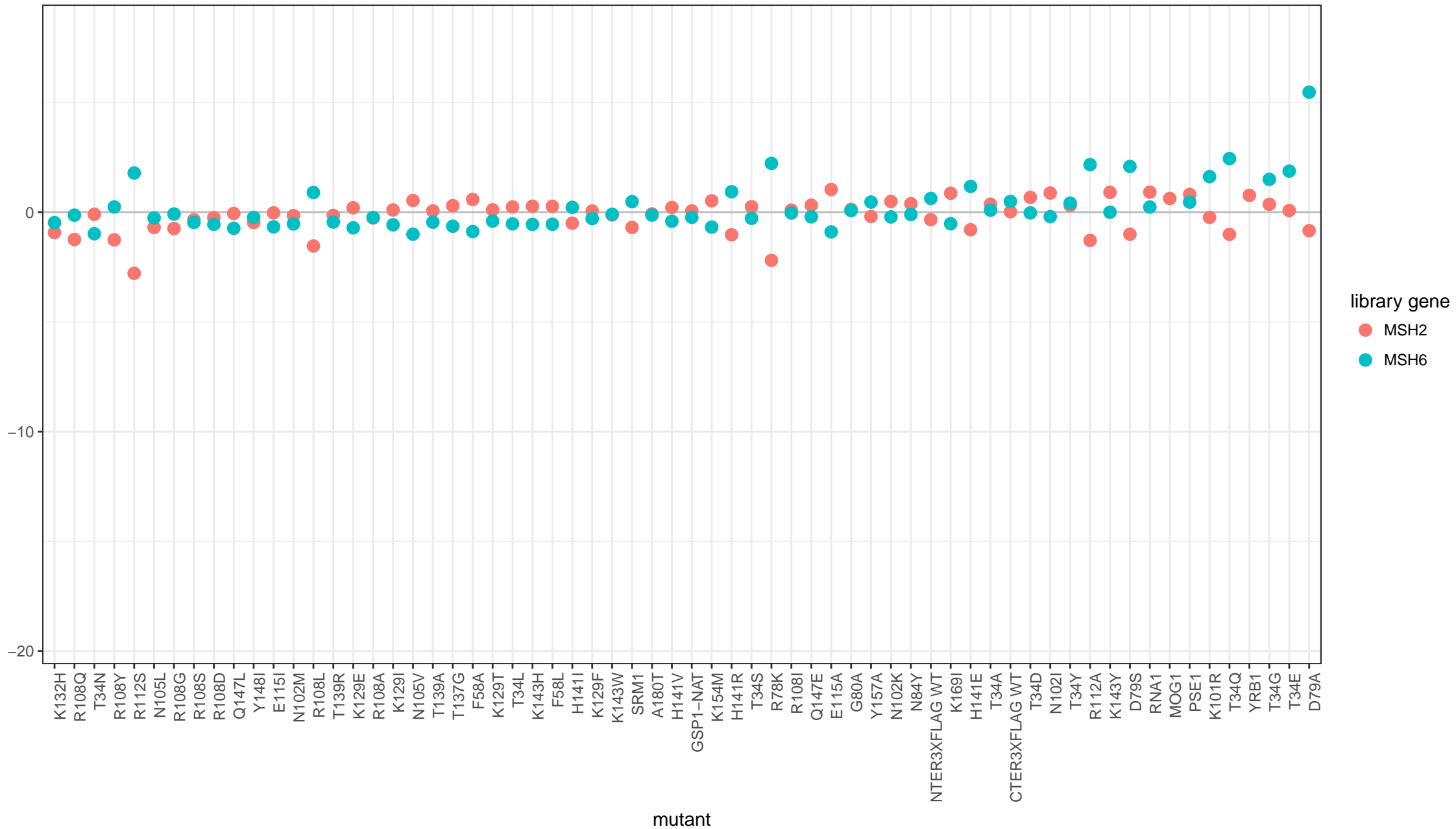
library gene

- MRE11
- RAD50
- XRS2

mutant

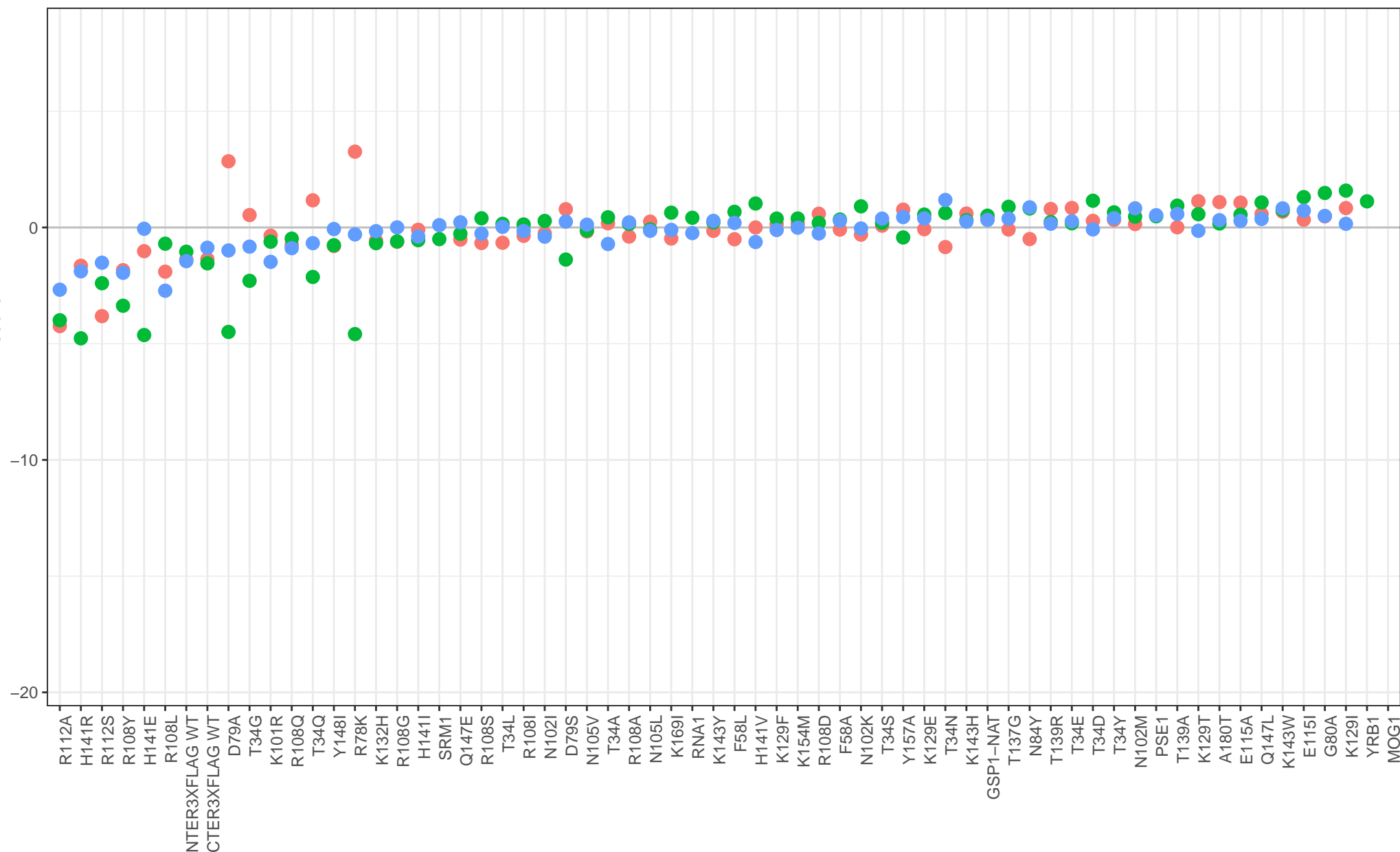
MSH2p/MSH6p complex

E-MAP score



NatC complex

E-MAP score



library gene

- MAK10
- MAK3
- MAK31

Nonsense-mediated mRNA decay pathway complex

E-MAP score

-20

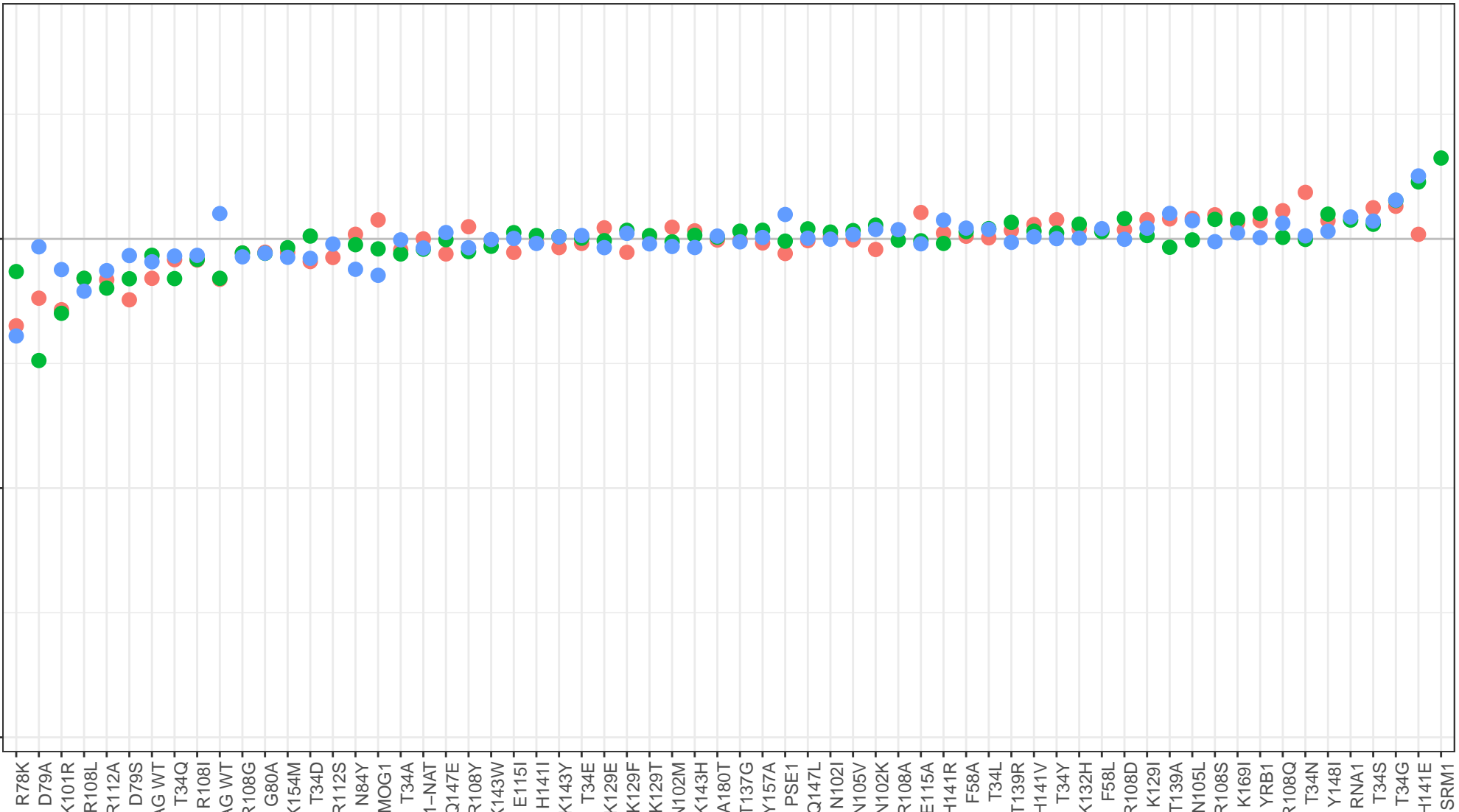
-10

0

mutant

library gene

NAM7
NMD2
UPF3



NuA3 histone acetyltransferase complex

E-MAP score

-20

-10

0

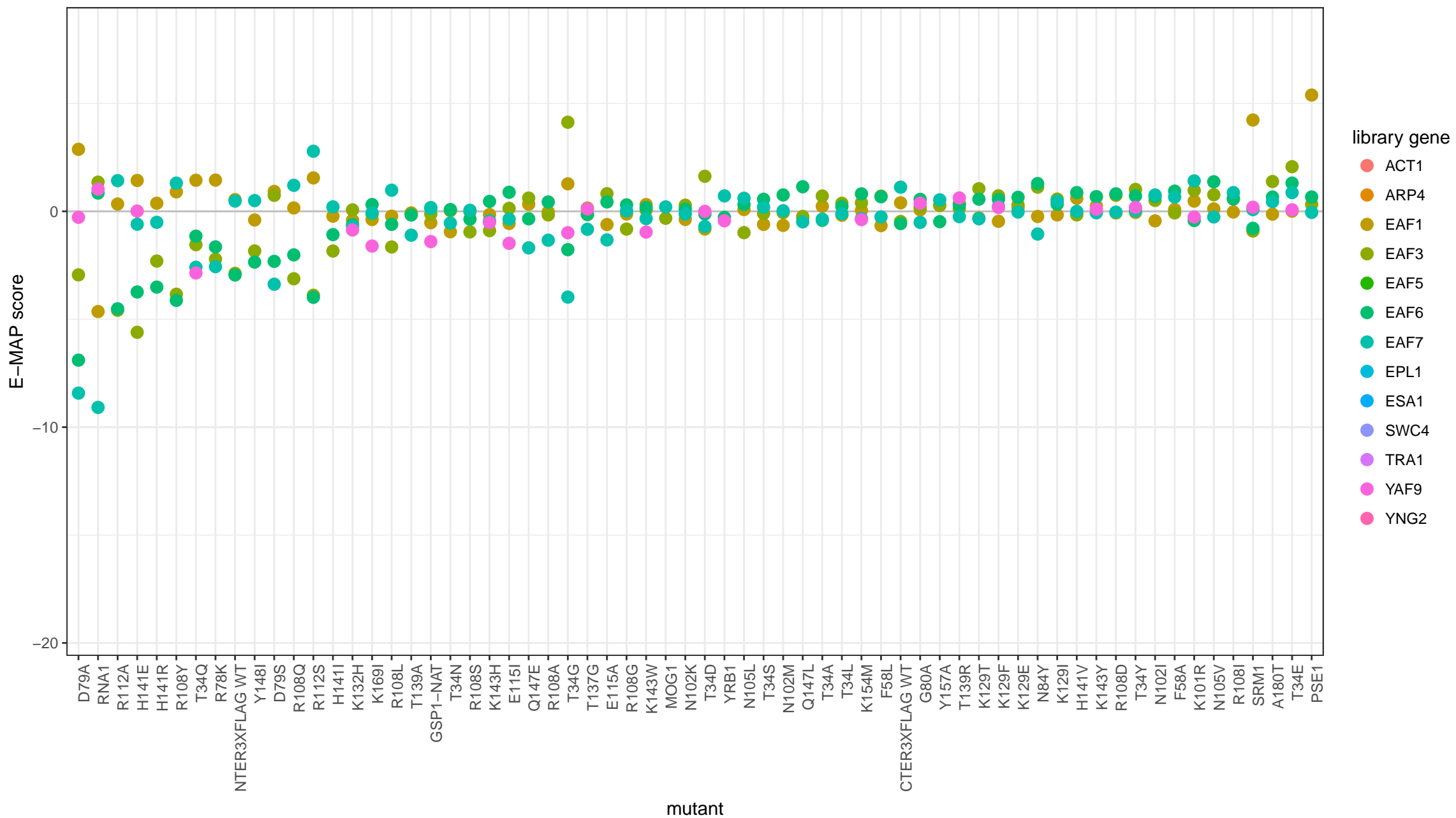
mutant

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

library gene

- EAF6
- NTO1
- SAS3
- TAF14
- YNG1

NuA4 histone acetyltransferase complex



Nuclear exosome complex

E-MAP score

-20

-10

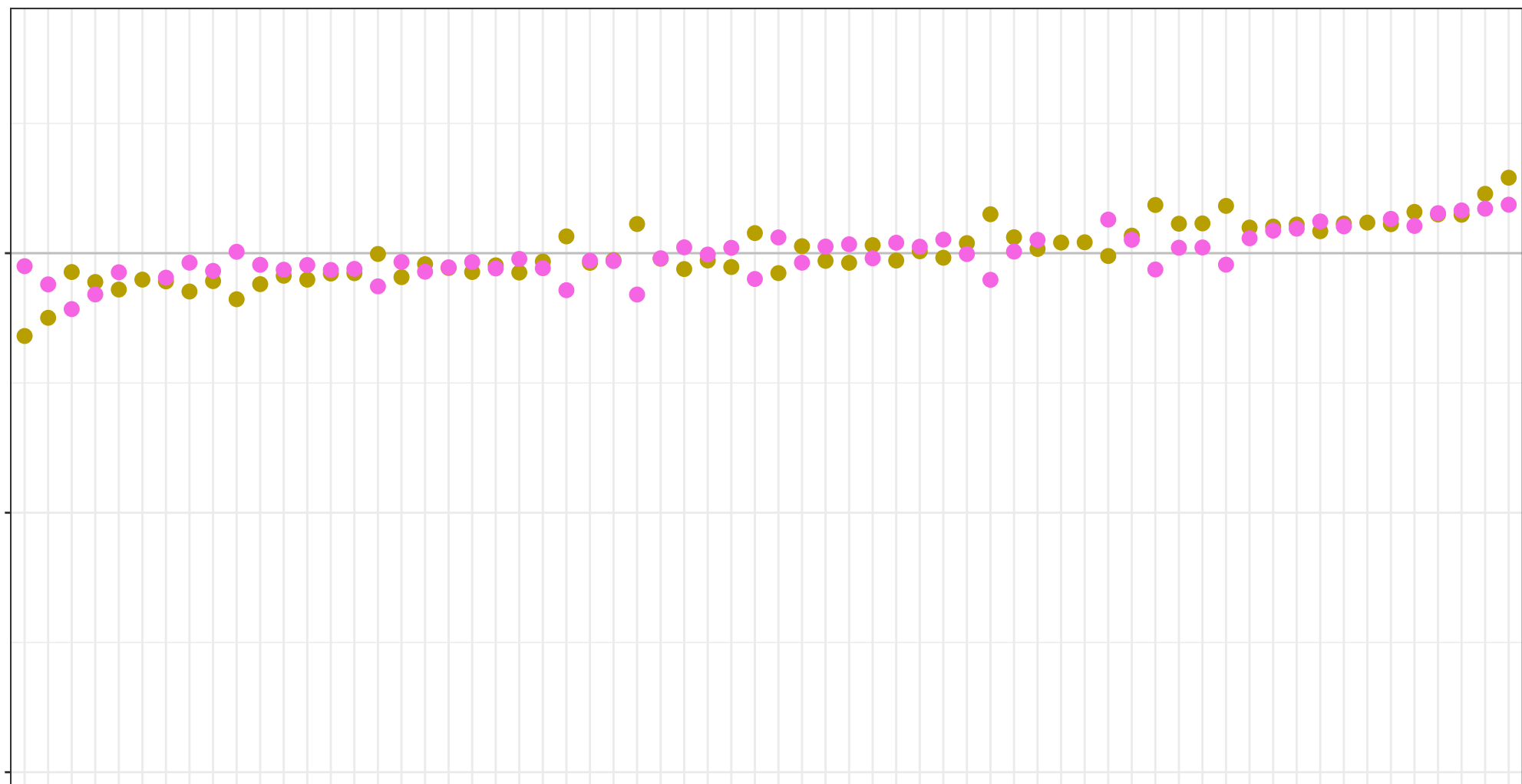
0

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

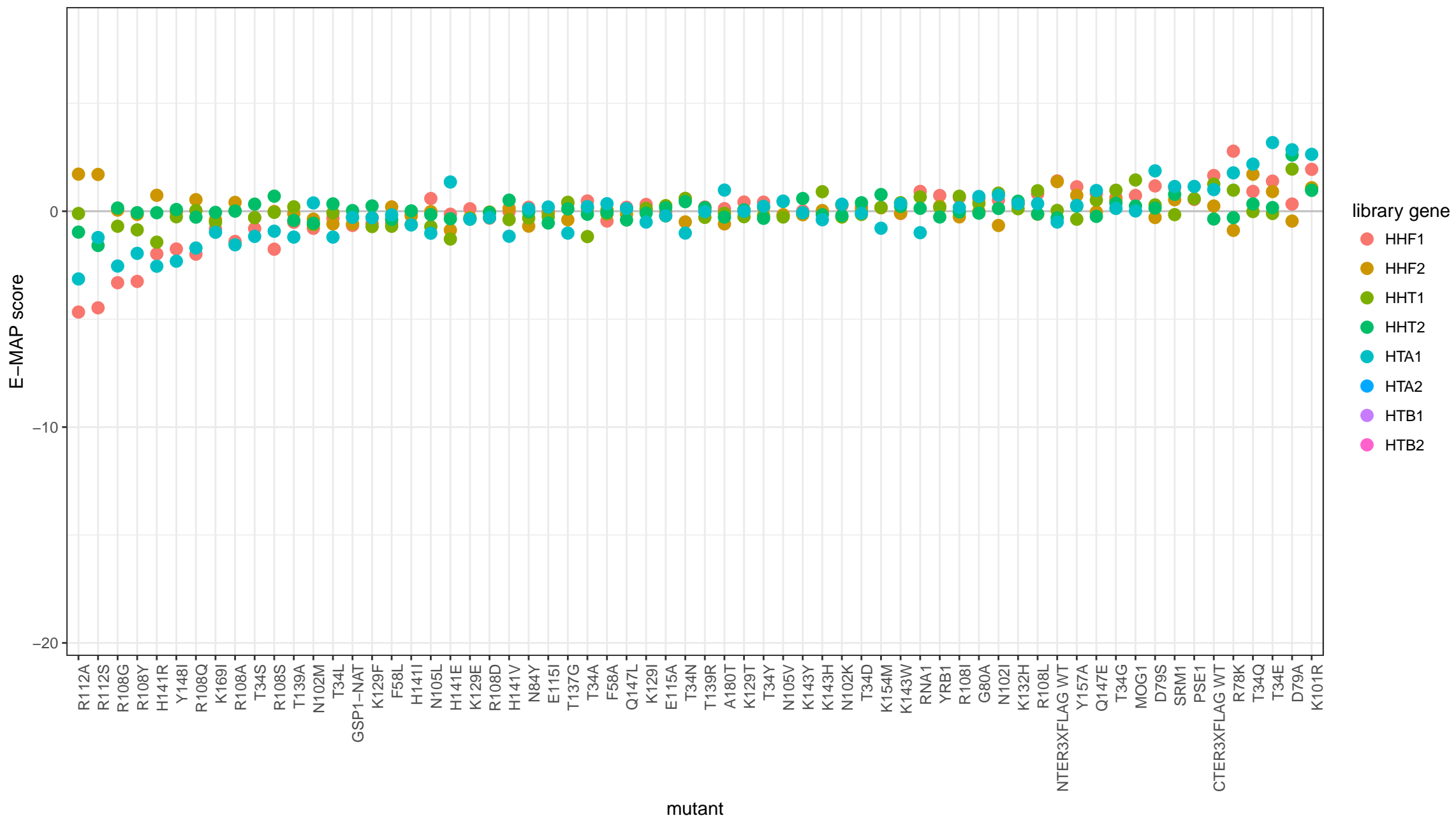
mutant

library gene

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

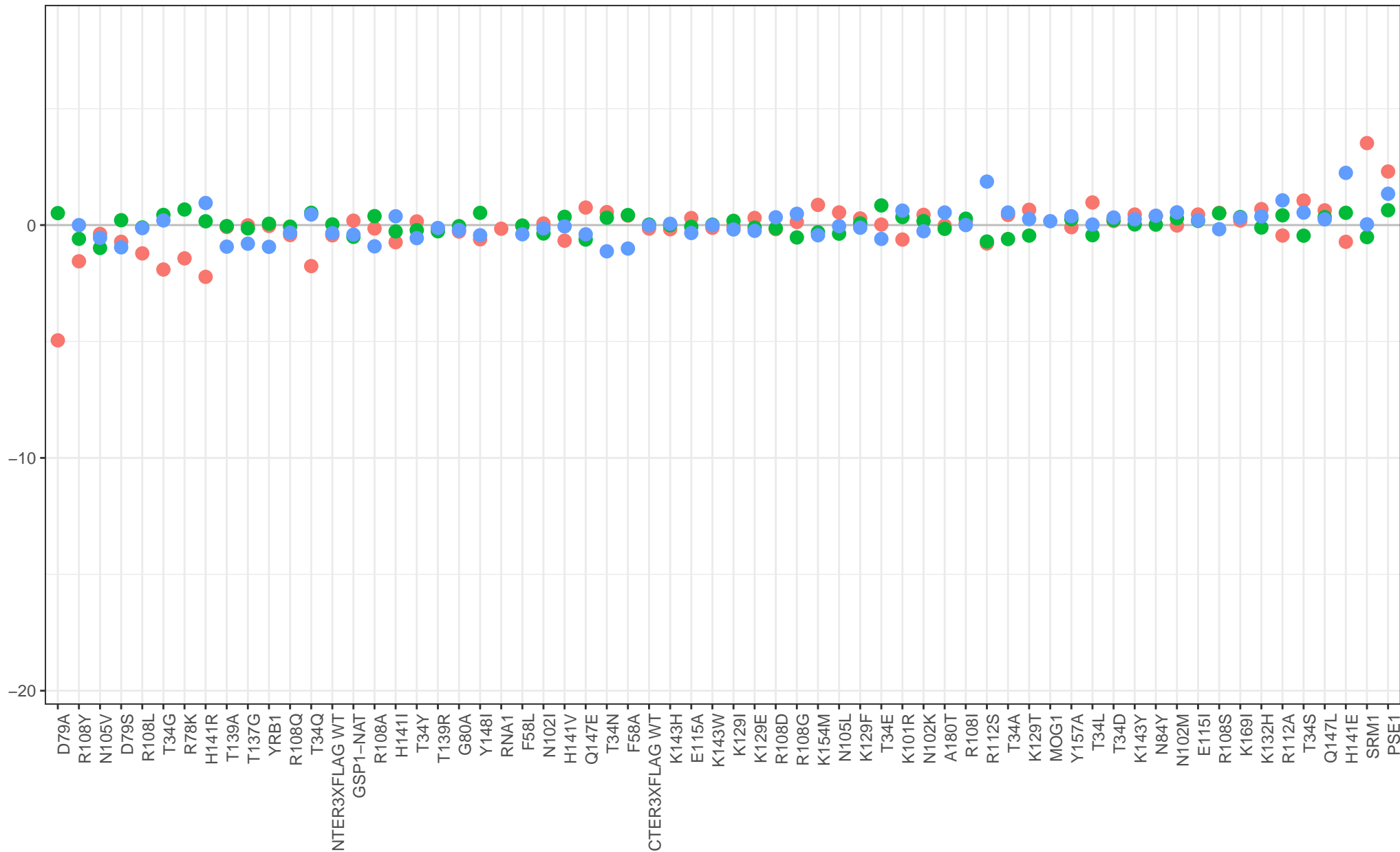


Nucleosomal protein complex



nucleotide–excision repair factor 1 complex

E-MAP score



mutant

nucleotide-excision repair factor 2 complex

E-MAP score

-20

-10

0

mutant

library gene

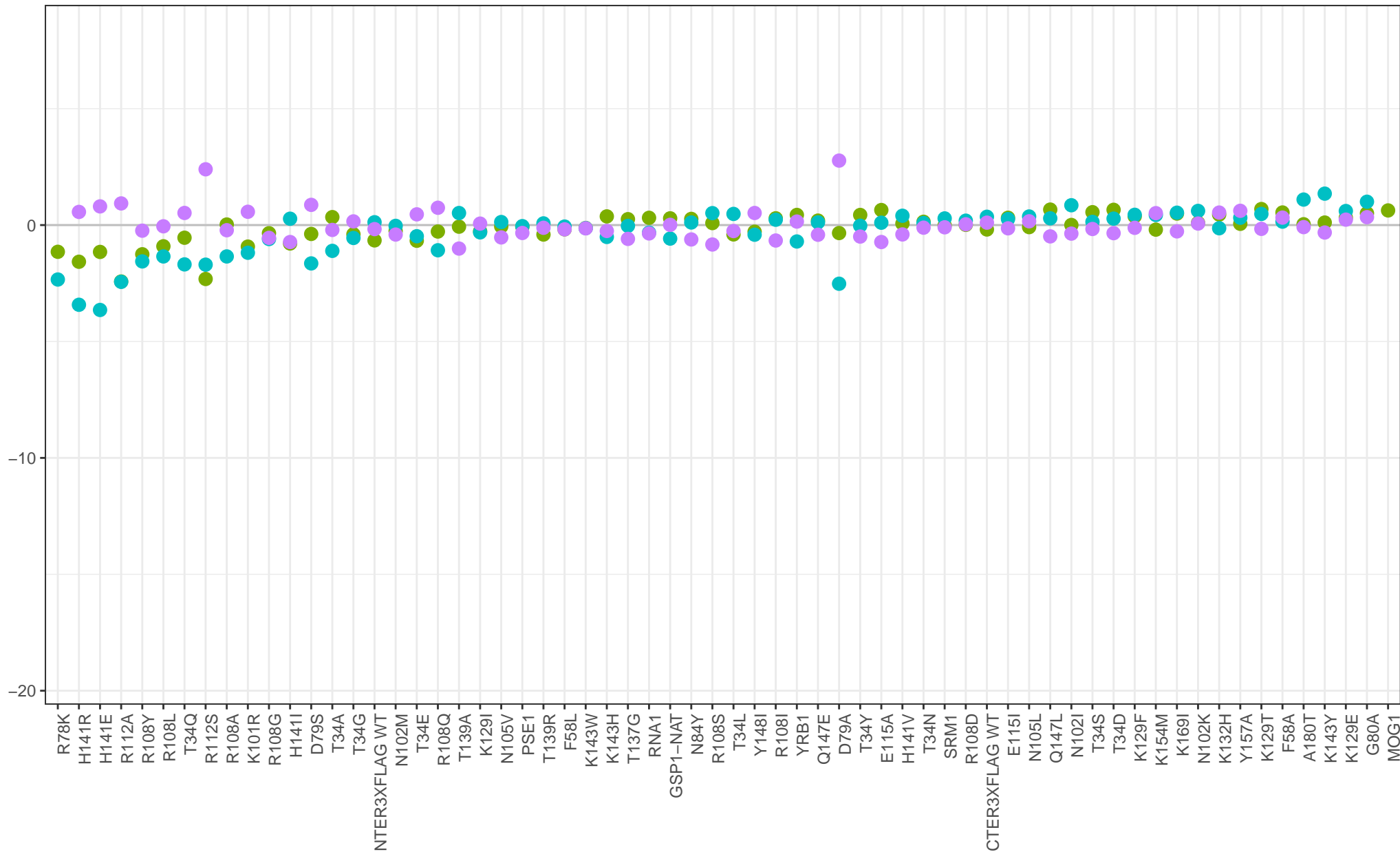
RAD23

RAD4

D79A H141E R112S T34Q R112A H141R D79S T34G K101R NTER3XFLAG WT K132H R108Y R78K Y148I G80A N105L H141I A180T YRB1 CTER3XFLAG WT T34S K129F T34D N84Y N105V R108I K143H Q147E M0G1 E115A K143W F58A R108G K129E N102K T139R R108Q T34L H141V T34Y Y157A K129T R108A F58L K169I GSP1-NAT K129I R108D R108L R108S T34A T137G K143Y E115I T34E K154M Q147L T34N N102M T139A N102I PSE1 RNA1 SRM1

nucleotide-excision repair factor 4 complex

E-MAP score



OCA complex

E-MAP score

-20

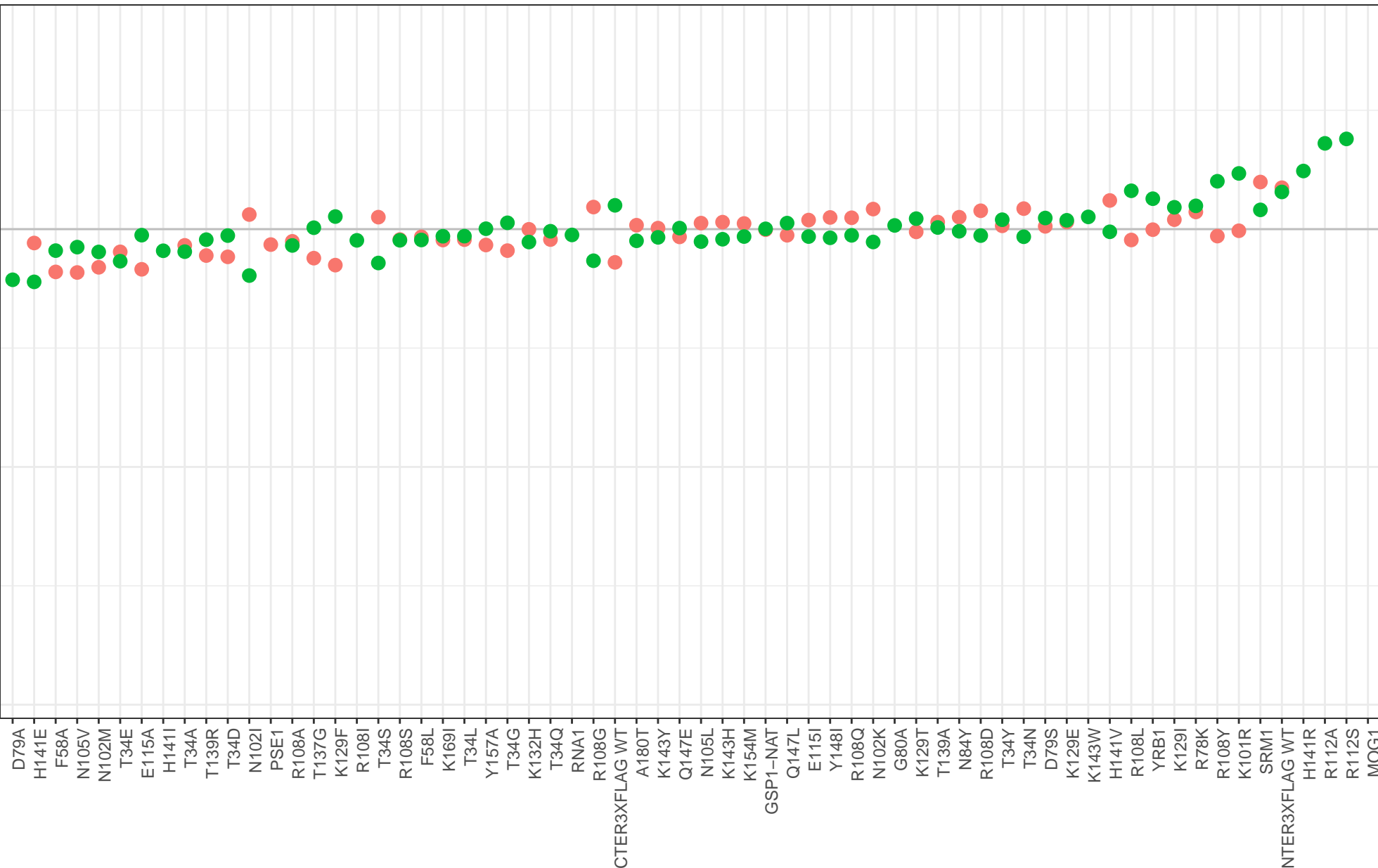
-10

0

mutant

library gene

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



oligosaccharide metabolic process

E-MAP score

-20

-10

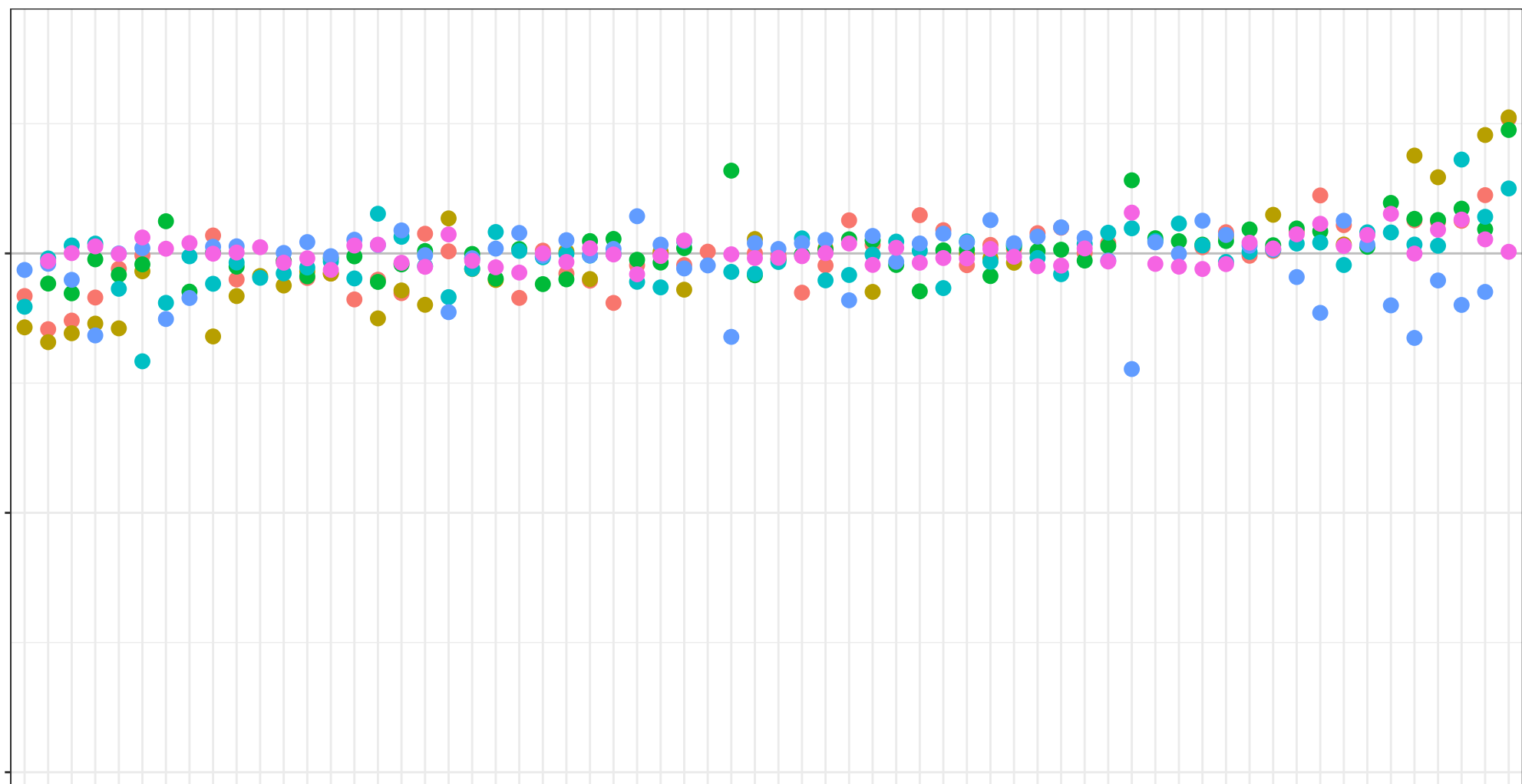
0

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

mutant

library gene

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



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

OST2

● OCT2

● 0054

● OST5

- OST6

- STT3

- SWP1

1000

other DNA repair complexes

E-MAP score

0

-10

-20

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

GSP1-NAT

CTER3XFLAG WT

NTER3XFLAG WT

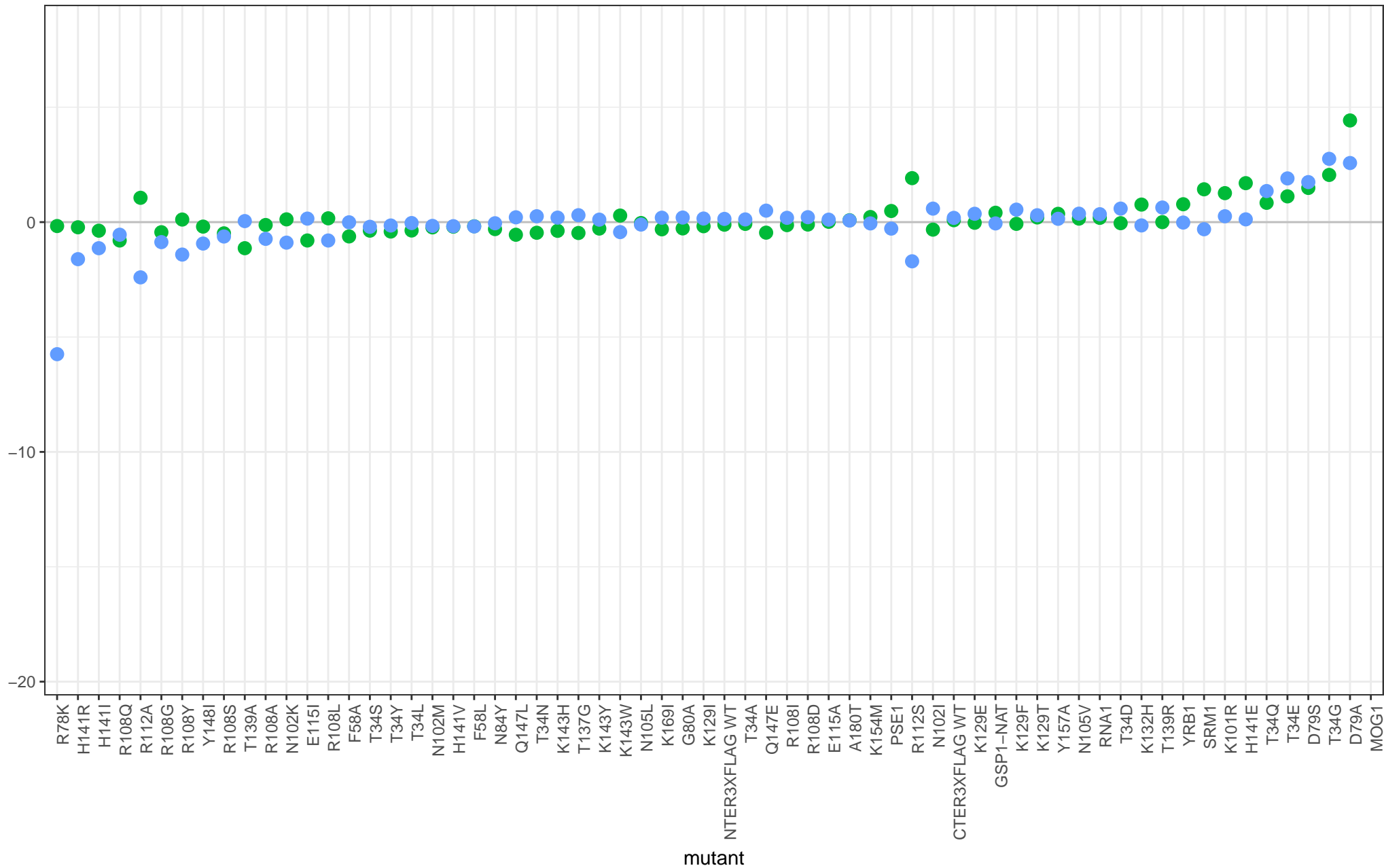
mutant

library gene

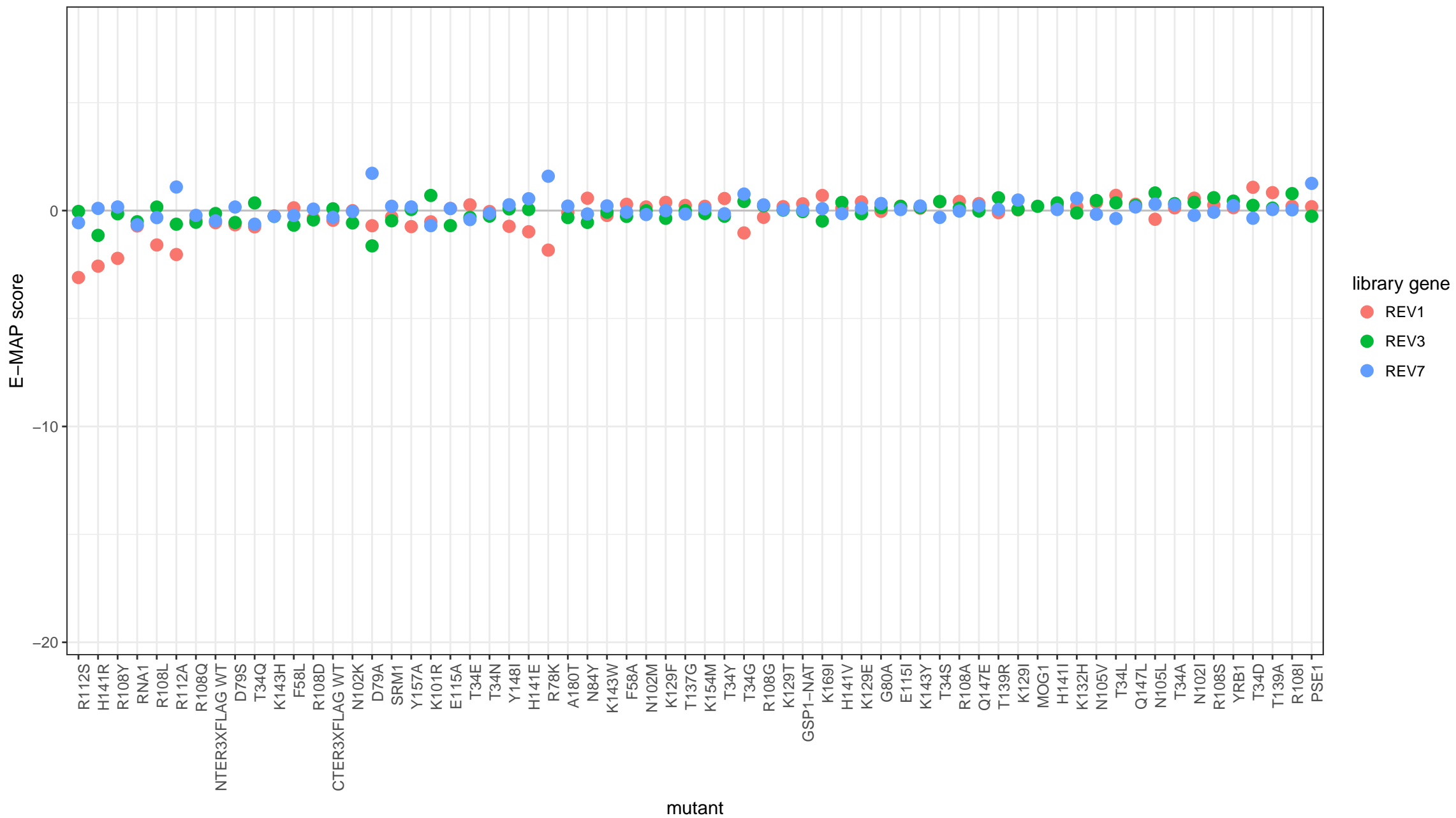
● RAD55
● RAD57

polarisome complex

E-MAP score

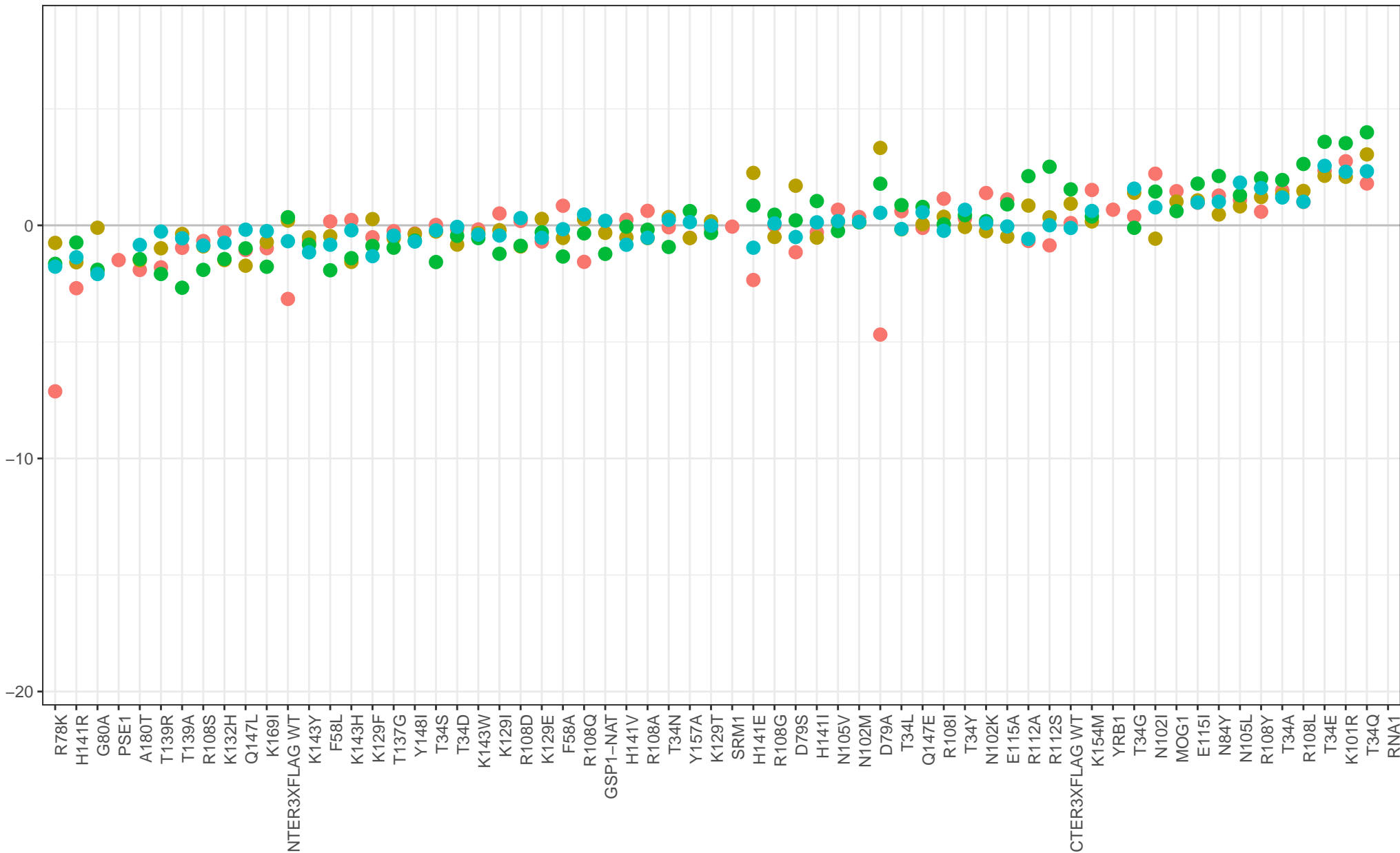


Polzeta-Rev1p complex



prefoldin complex

E-MAP score



library gene

- GIM3
- GIM4
- GIM5
- PAC10
- PFD1
- YKE2

mutant

protein kinase CK2 complex

E-MAP score

0

-10

-20

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

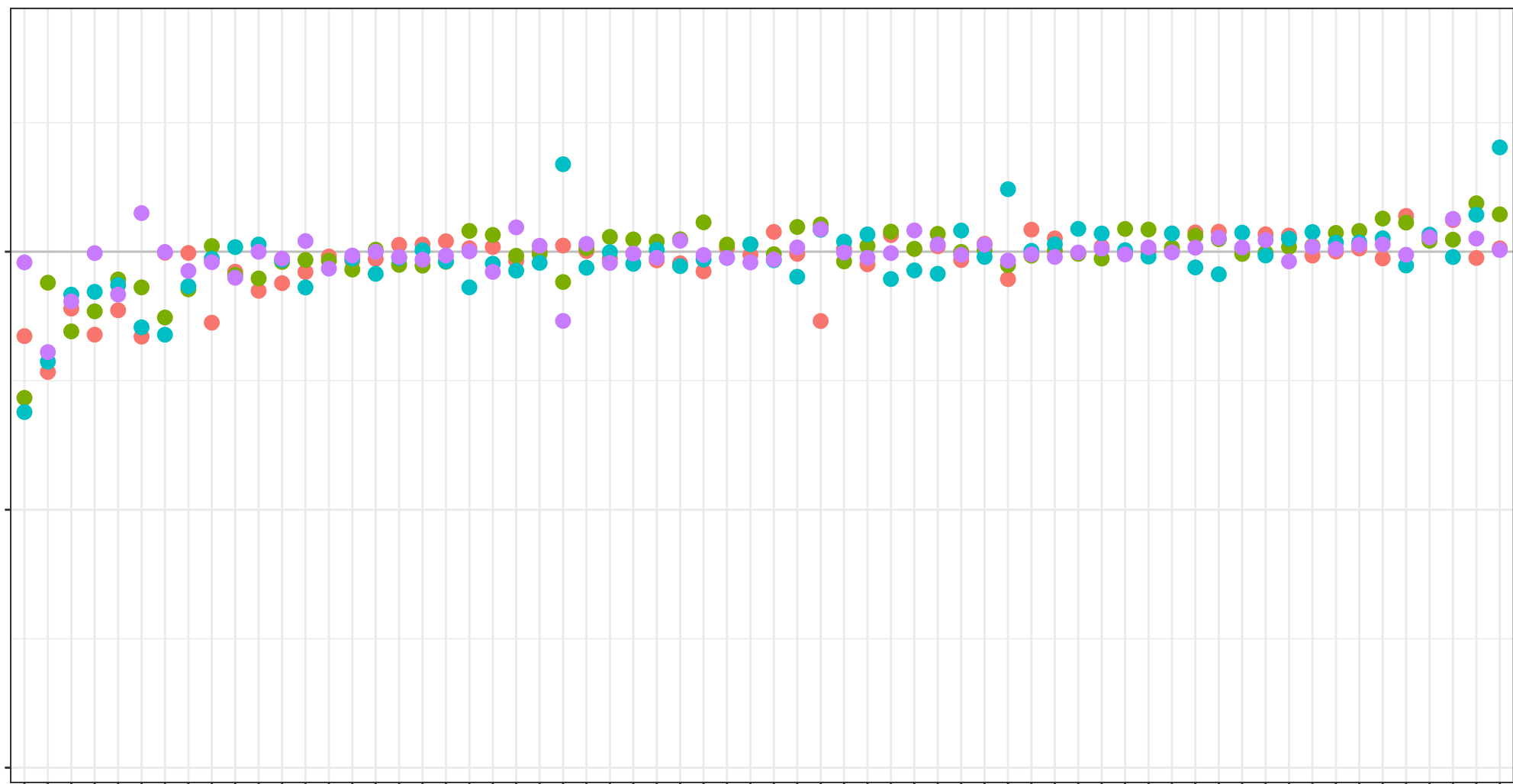
NTER3XFLAG WT

CTER3XFLAG WT

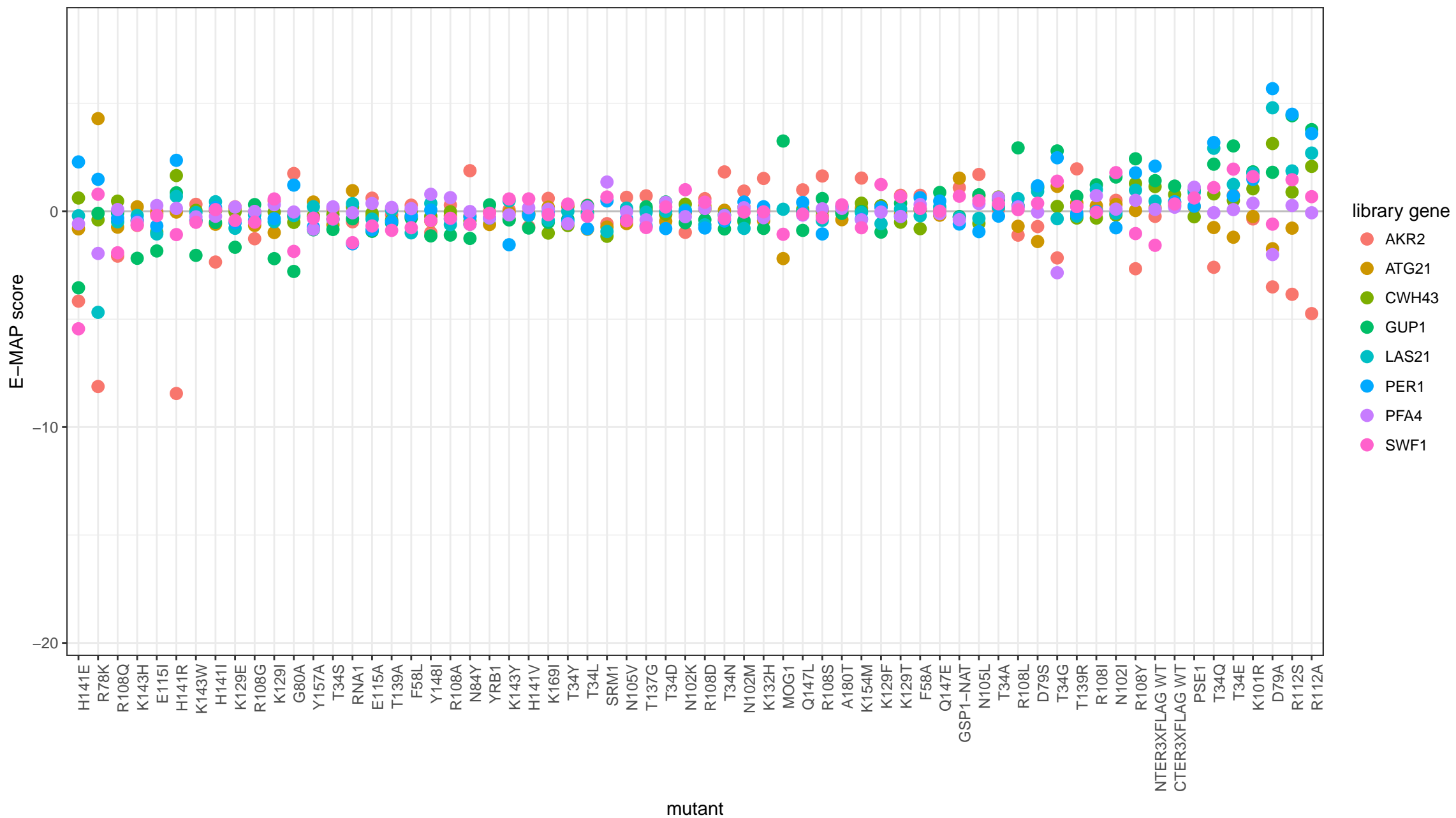
mutant

library gene

- CKA1
- CKA2
- CKB1
- CKB2

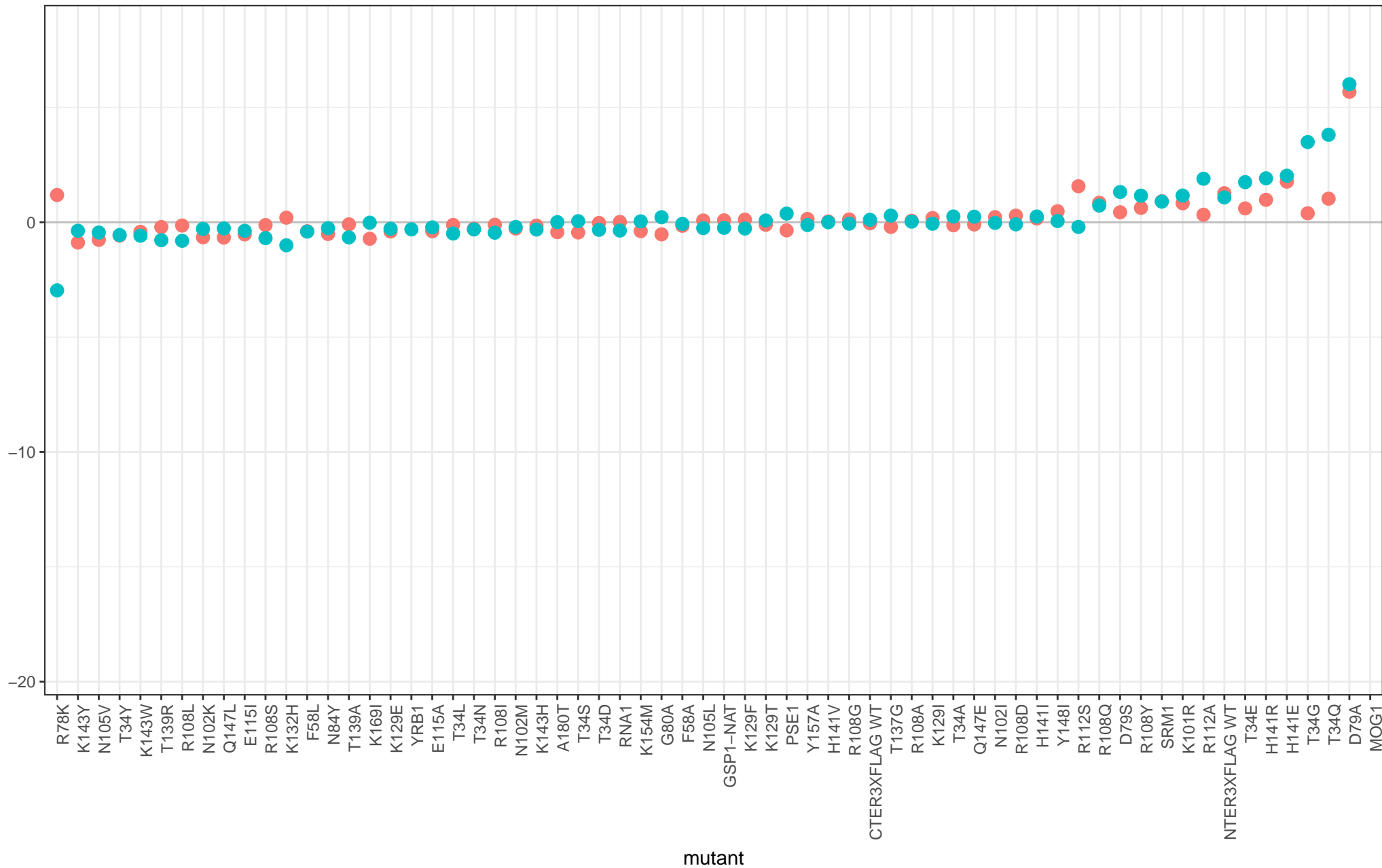


protein lipidation



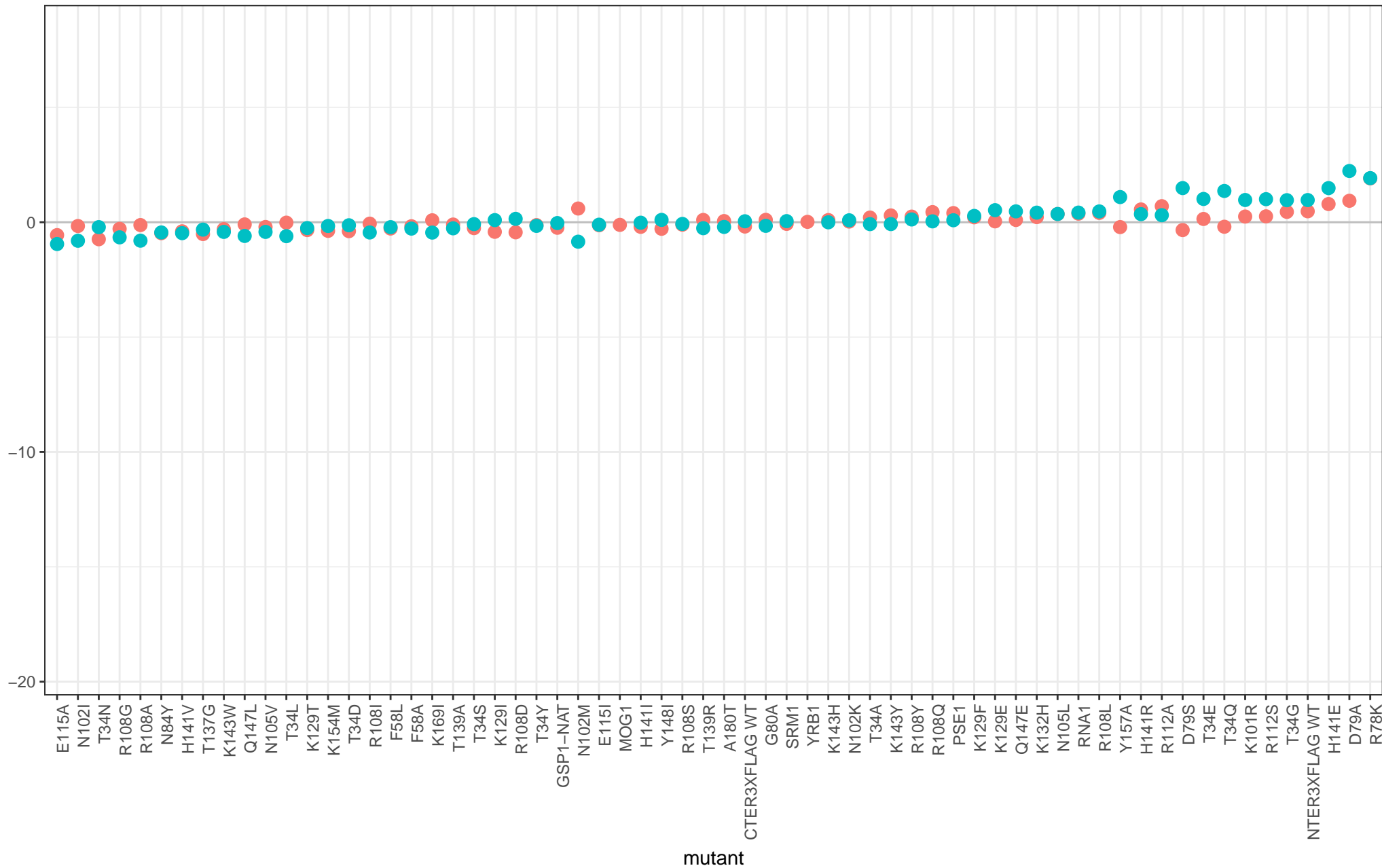
Protein O-mannosyltransferase(Pmt1p/Pmt2p)

E-MAP score



Protein O-mannosyltransferase(Pmt3p/Pmt5p)

E-MAP score



protein phosphatase type 2A complex (Rts1p)

E-MAP score

-20

-10

0

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

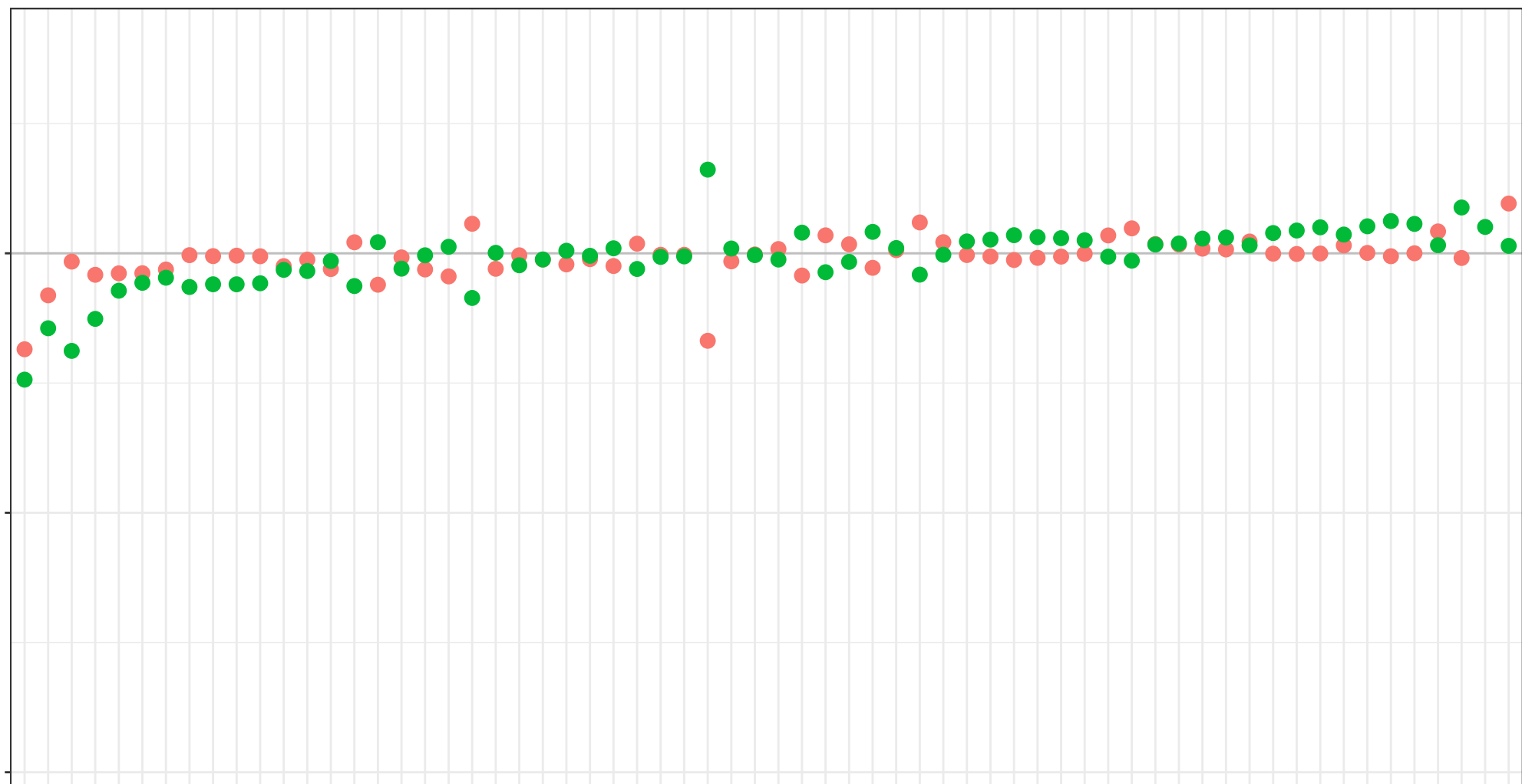
mutant

library gene

PPH21

RTS1

TPD3



Rad17p/Ddc1p/Mec3p complex

E-MAP score

0

-10

-20

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

mutant

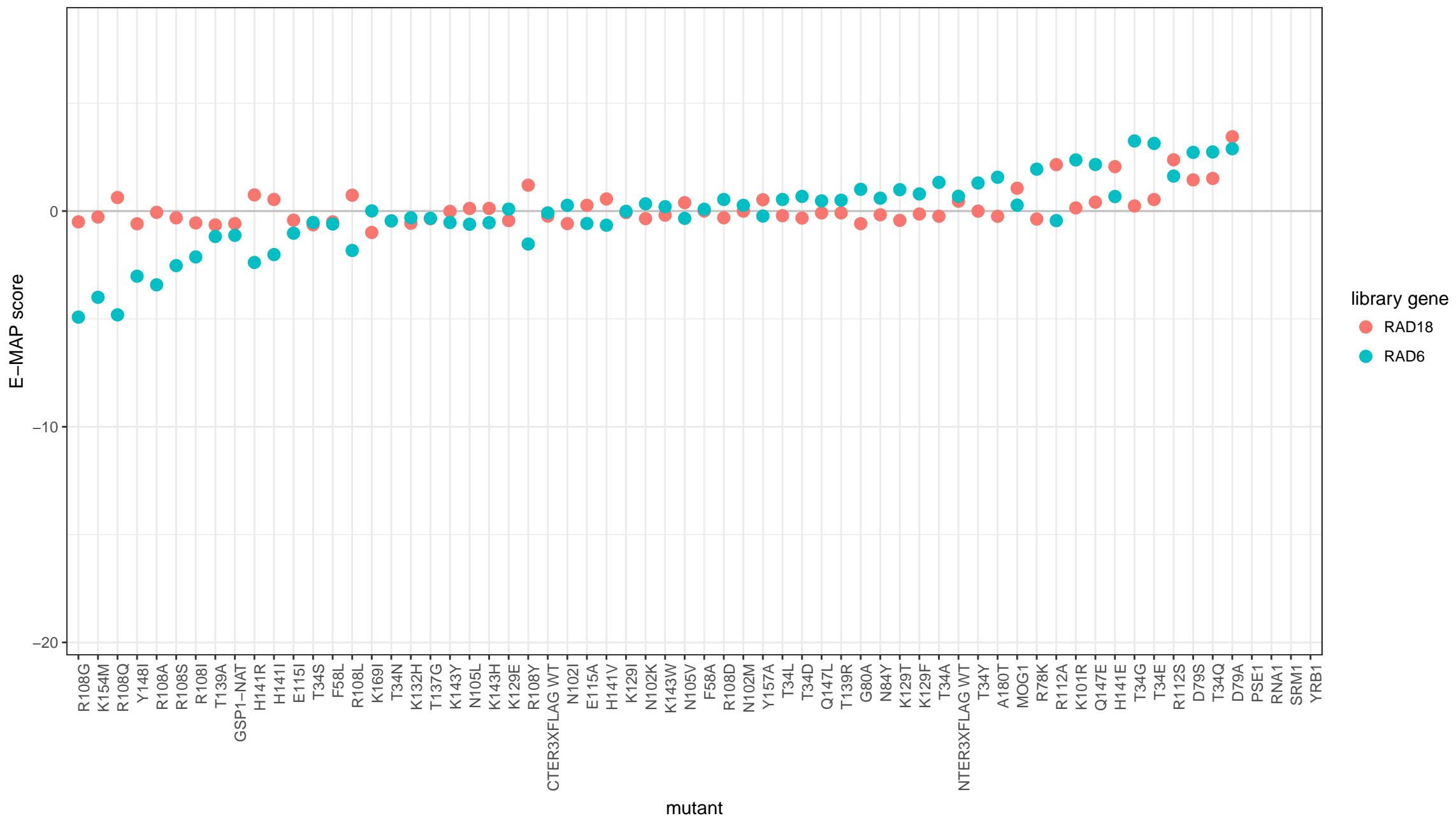
library gene

DDC1

MEC3

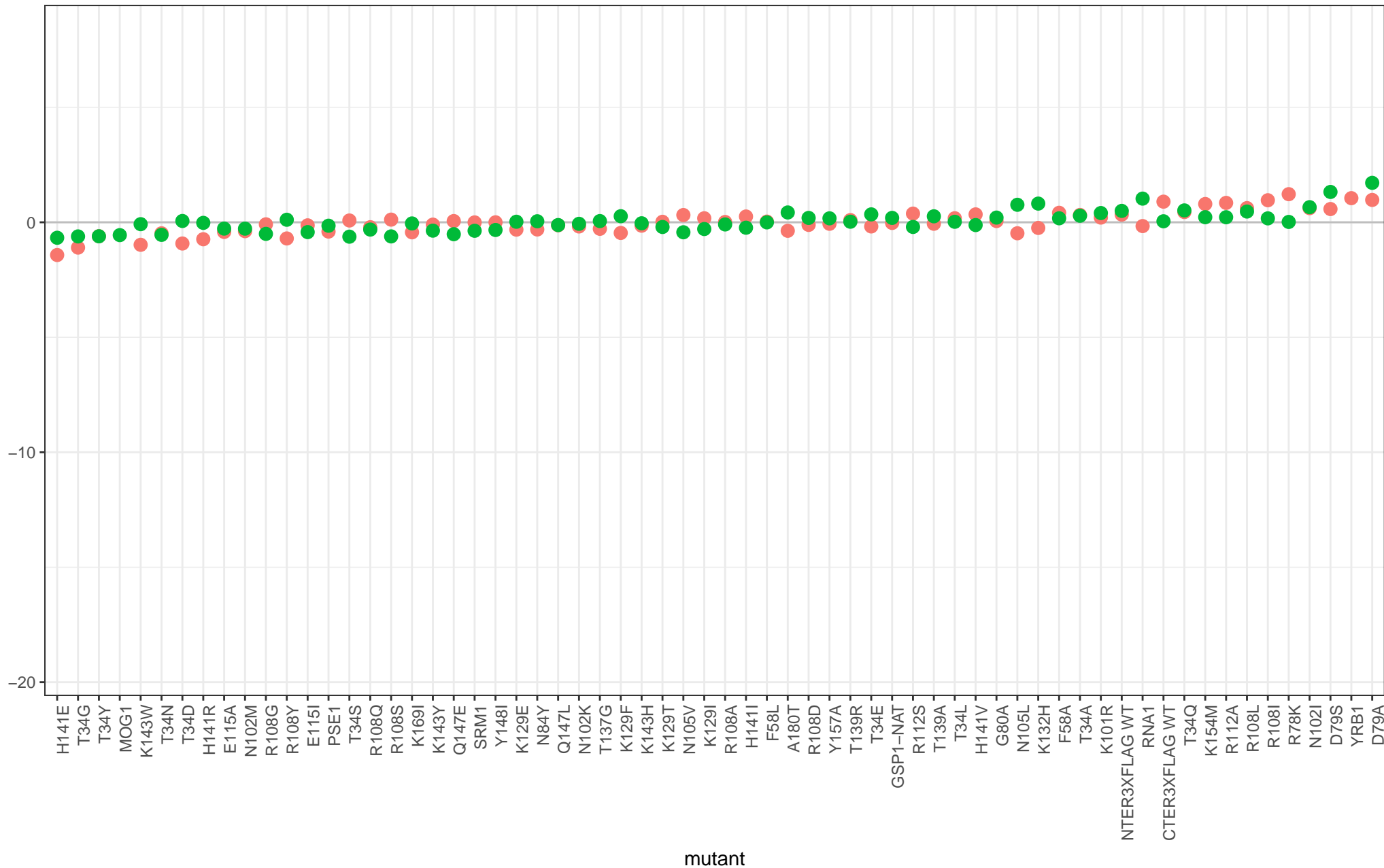
RAD17

Rad6p/Rad18p complex



RAVE complex

E-MAP score

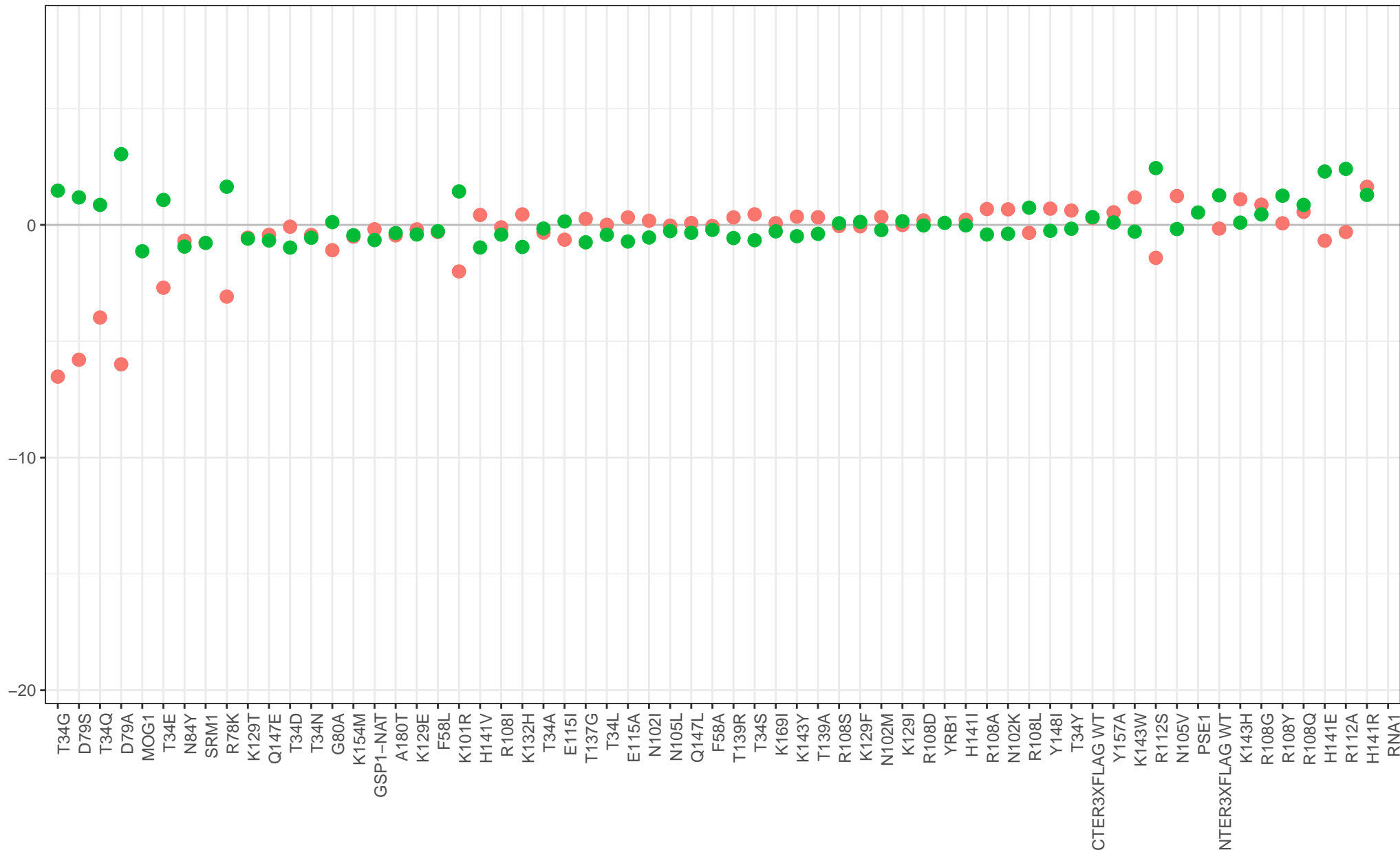


library gene

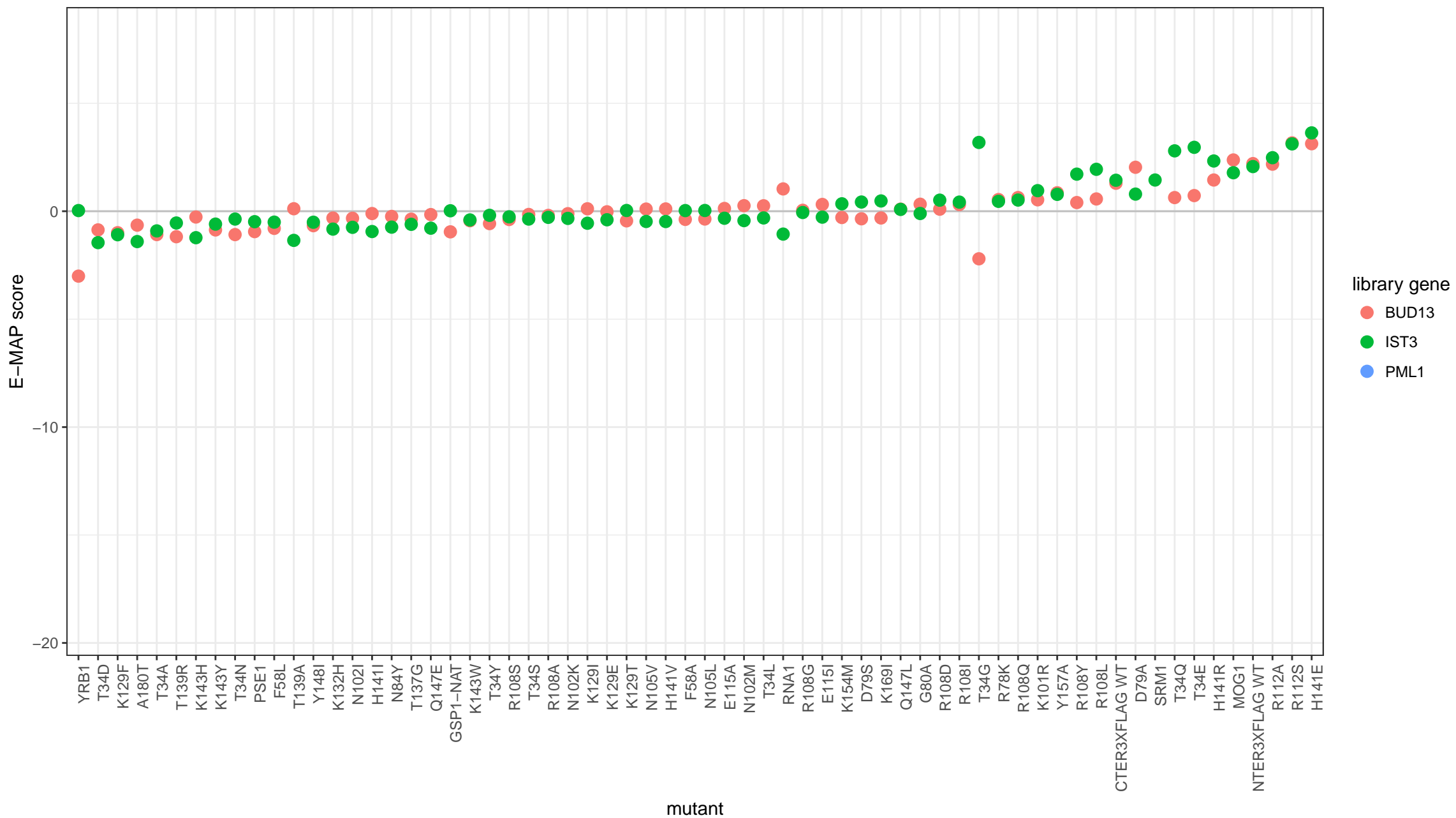
- RAV1
- RAV2
- SKP1

RecQ helicase–Topo III complex

E-MAP score



RES complex



retromer complex

E-MAP score

0

-10

-20

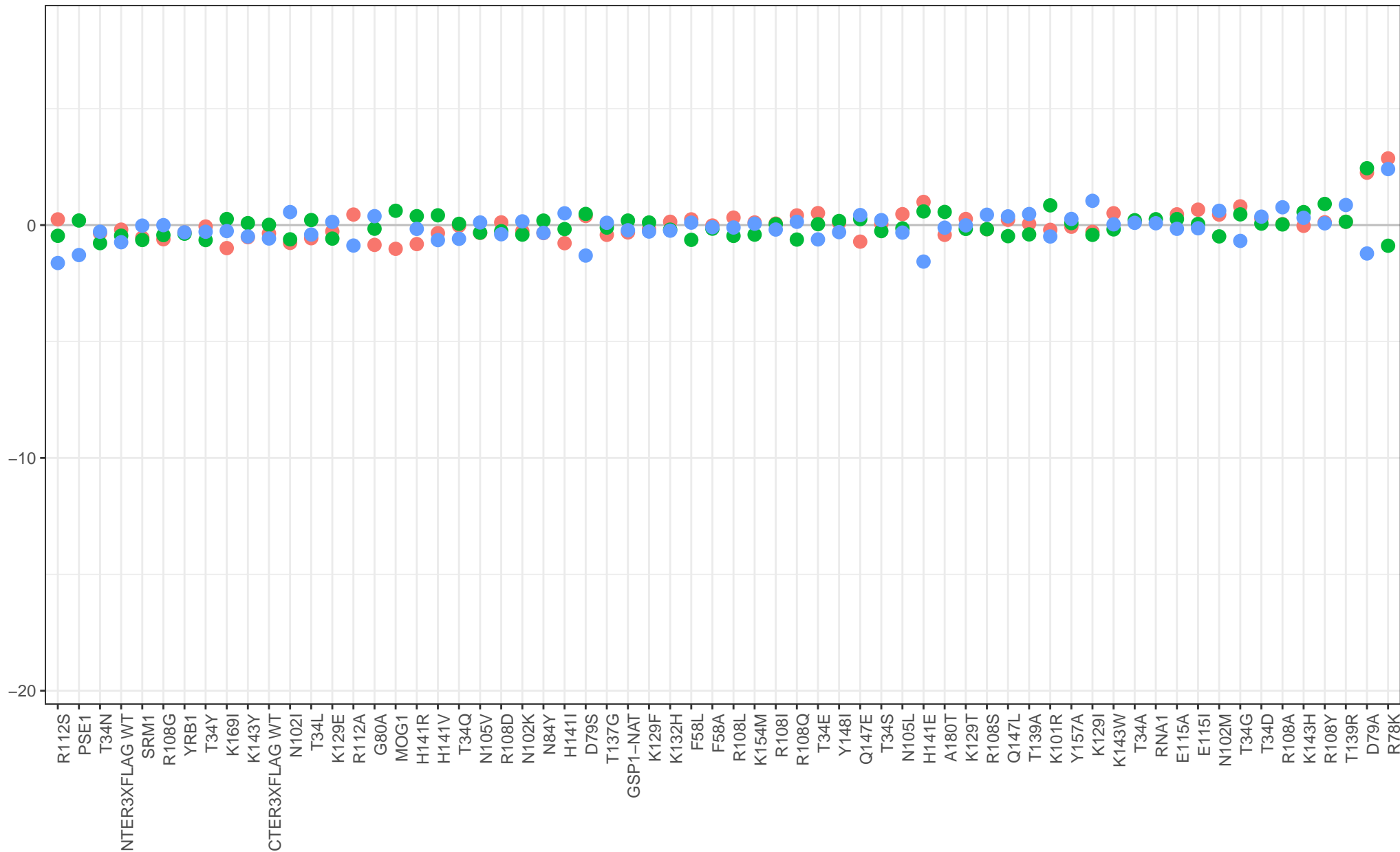
T34G
MOG1
E115A
D79S
D79A
H141E
E115I
NTER3XFLAG WT
T34Q
K132H
R108Y
F58L
Q147L
N84Y
CTER3XFLAG WT
R108S
R108A
T34E
T34S
N105L
T34N
K129I
R108Q
T139A
T137G
F58A
K129E
K101R
K143W
N105V
K129F
GSP1-NAT
N102M
R108D
K154M
YRB1
Y148I
T34A
A180T
T34L
K143H
PSE1
T34Y
N102K
R108G
Y157A
RNA1
K169I
H141V
K143Y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

library gene

- PEP8
- VPS17
- VPS29
- VPS35
- VPS5

ribonuclease H2 complex

E-MAP score

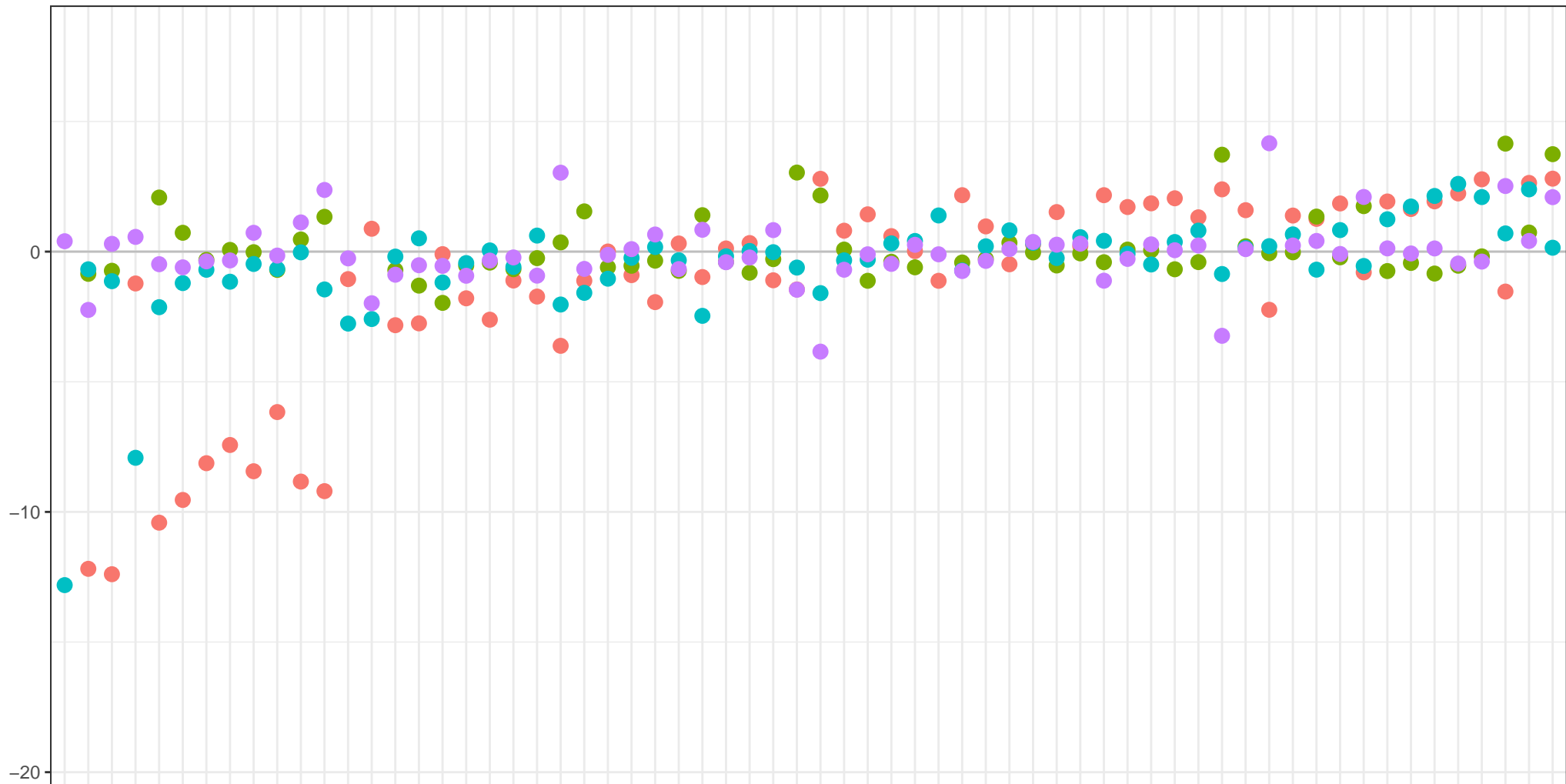


library gene

- RNH201
- RNH202
- RNH203

ribosomal subunit export from nucleus

E-MAP score



library gene

ARX1

JJJ1

SLX9

YAR1

mutant

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

RING finger peroxin complex

E-MAP score

0

-10

-20

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

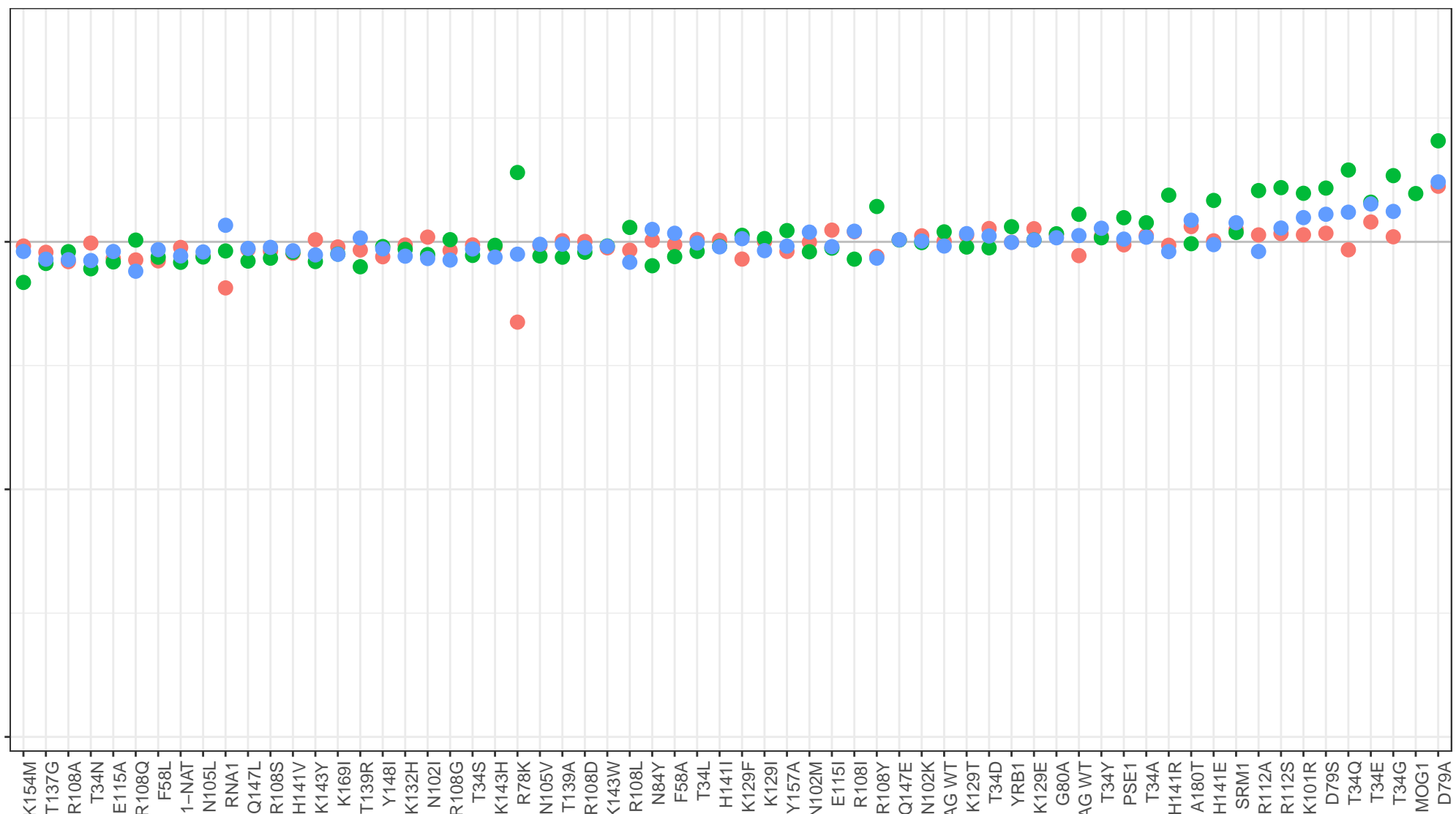
mutant

library gene

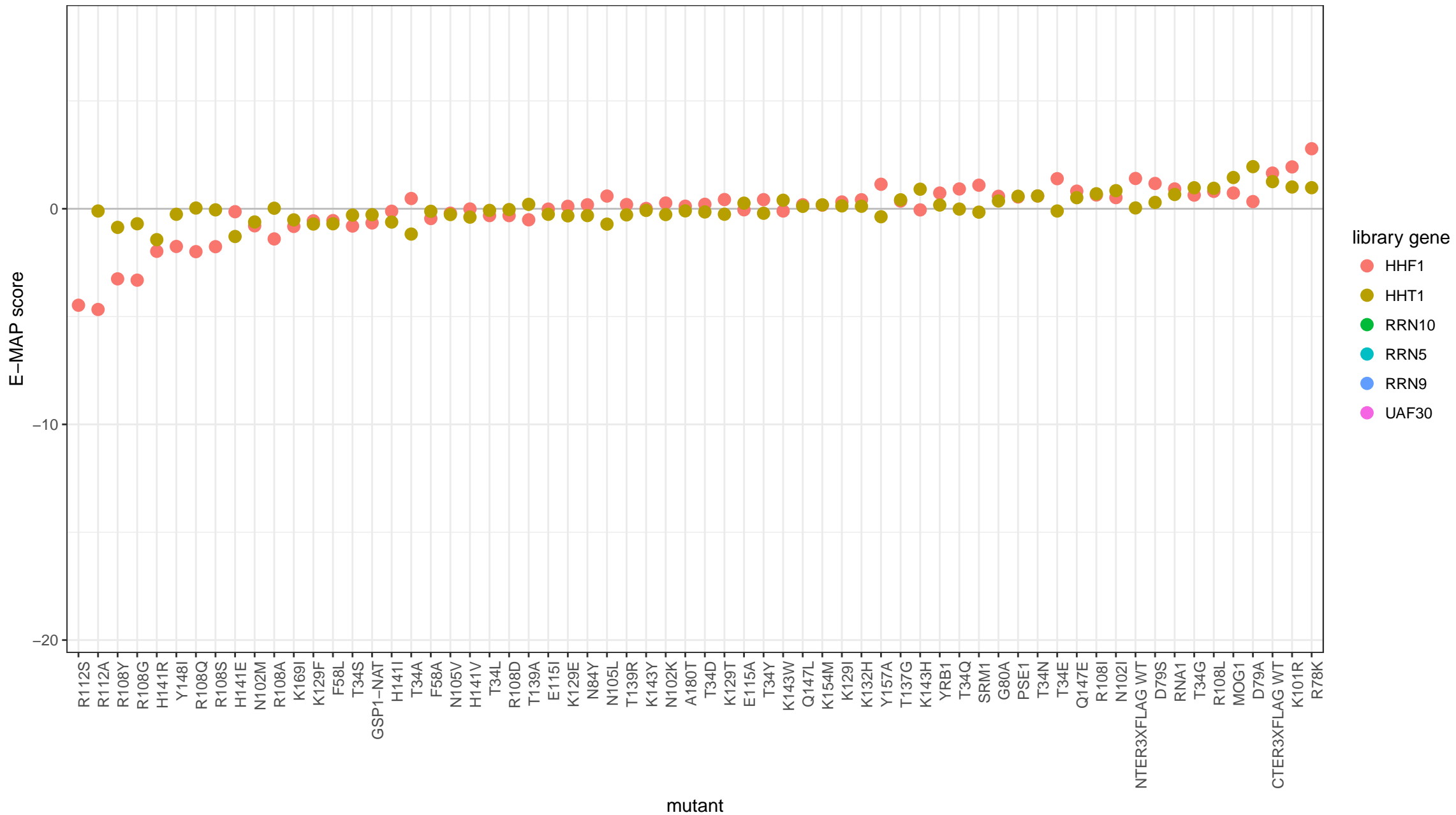
PEX10

PEX12

PEX2

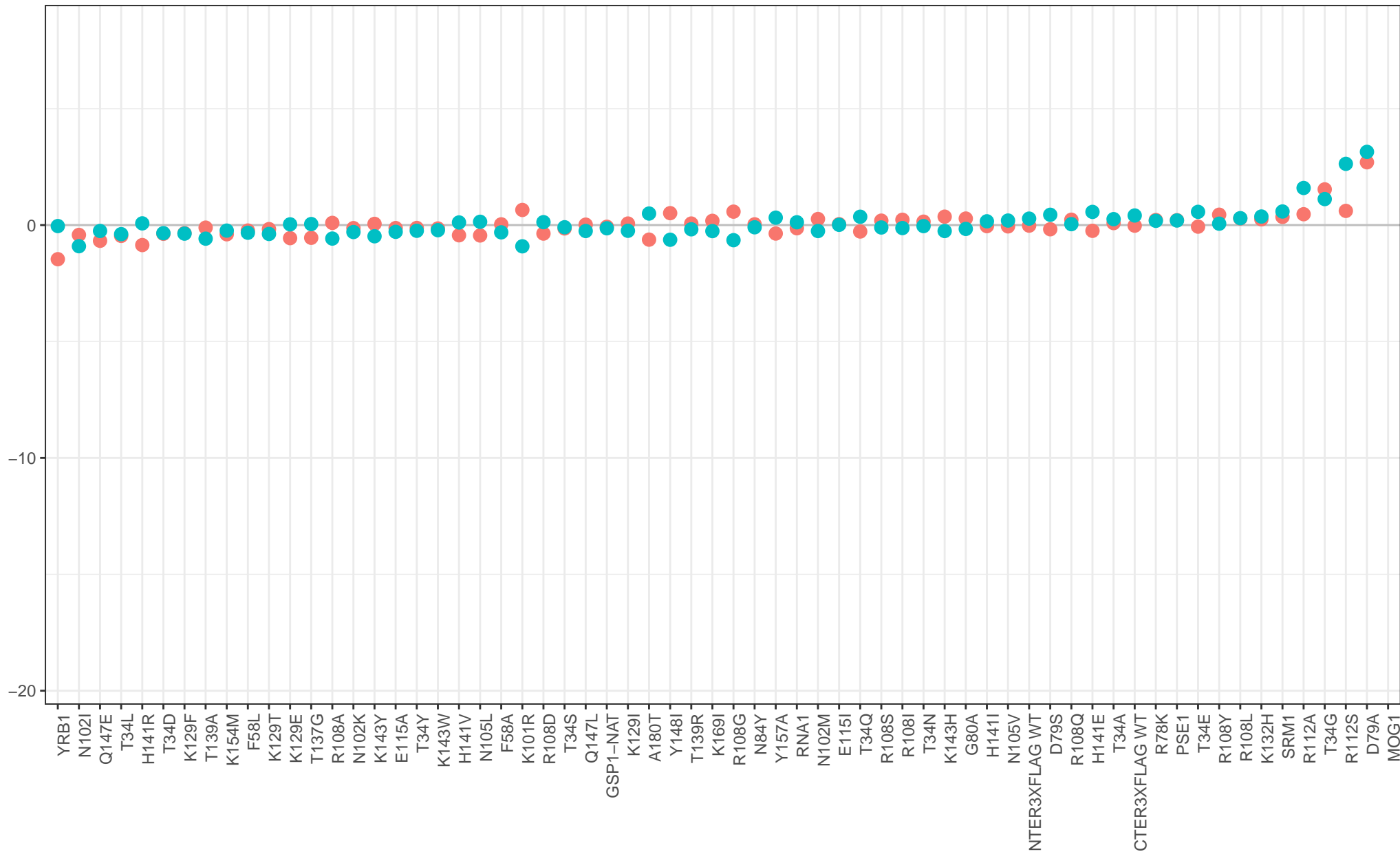


RNA polymerase I upstream activating factor complex



Rot2p/Gtb1p complex

E-MAP score



Rpd3S complex

E-MAP score

0

-10

-20

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

library gene

EAF3

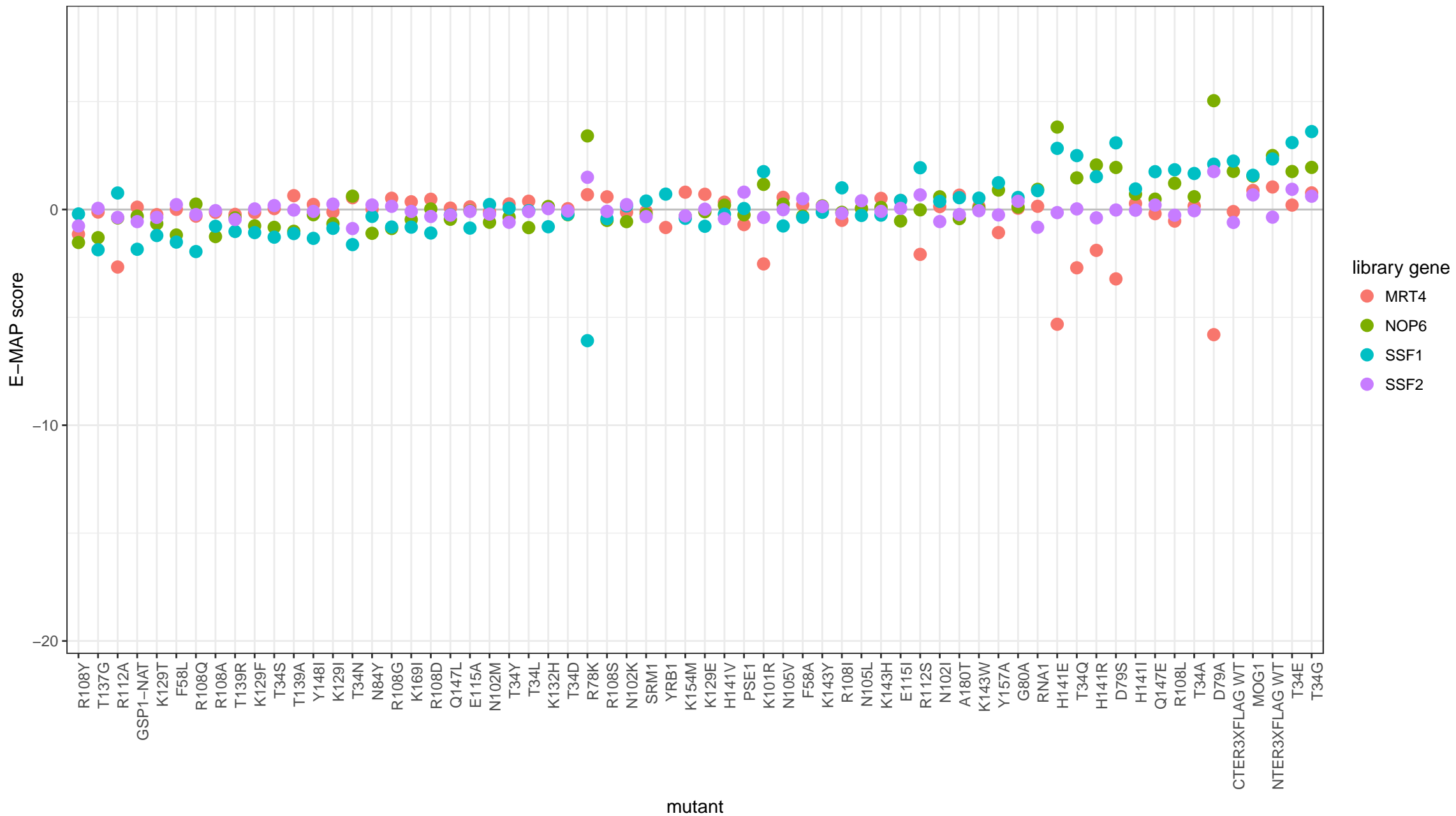
RCO1

RPD3

SIN3

UME1

rRNA binding



RSC complex

E-MAP score

0

-10

-20

mutant

library gene

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

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

Rtg1p/Rtg3p complex

E-MAP score

0

-10

-20

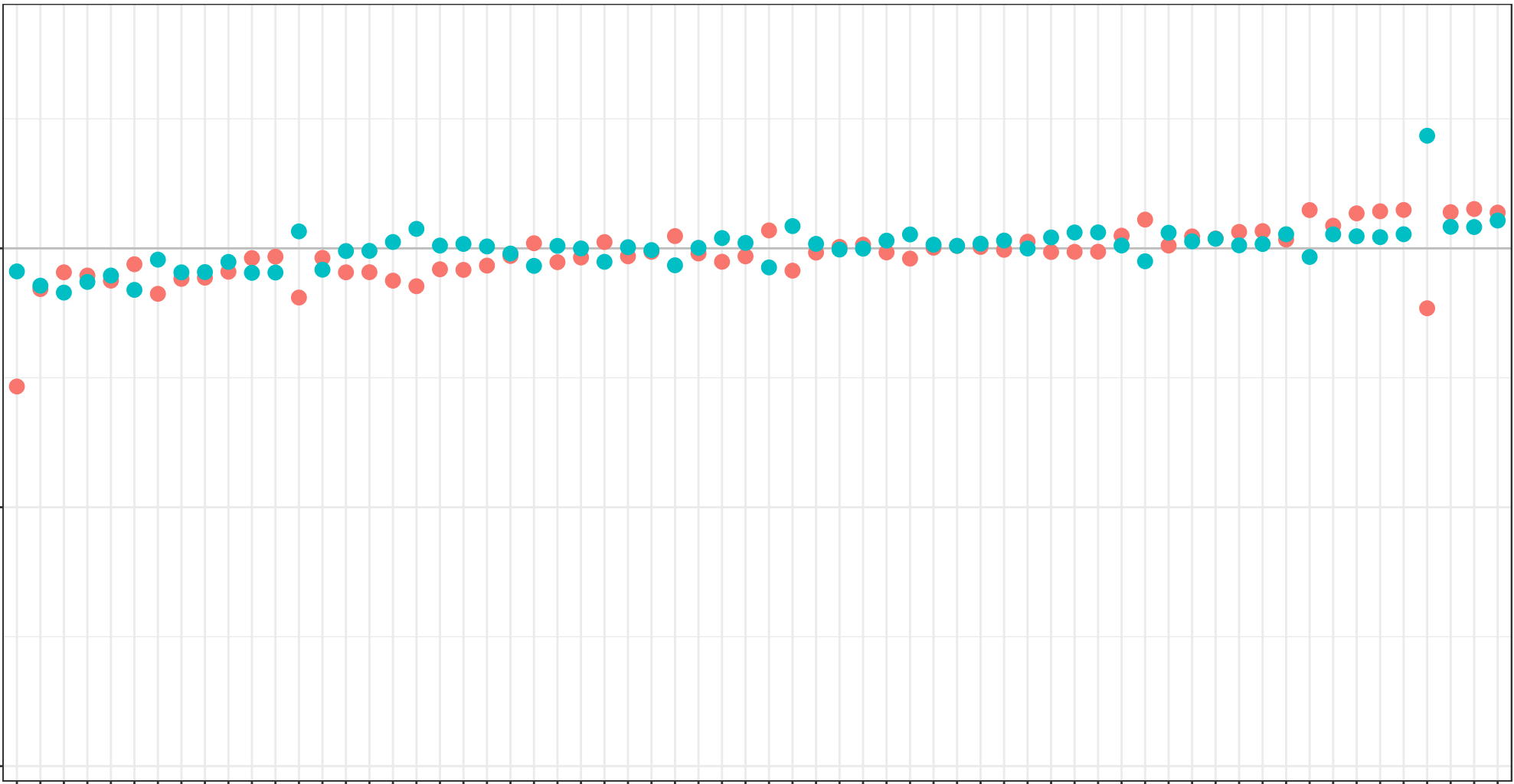
RNA1
T34E
K129E
MOG1
T34G
CTER3XFLAG WT
K129F
T34D
K132H
T34N
K143Y
GSP1-NAT
YRB1
D79S
T137G
H141V
K143W
SRM1
Y148I
T34L
Q147L
R108G
T139A
K101R
K154M
N102K
F58L
K129I
R112A
PSE1
N84Y
R108L
R108Y
R108I
R112S
T34Y
H141I
R108Q
N102I
Q147E
T34A
K169I
K129T
A180T
R108A
T34S
K143H
T139R
G80A
N102M
T34Q
E115A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

mutant

library gene

RTG1

RTG3



Rtt109p/Vps75p complex

E-MAP score

0

-10

-20

mutant

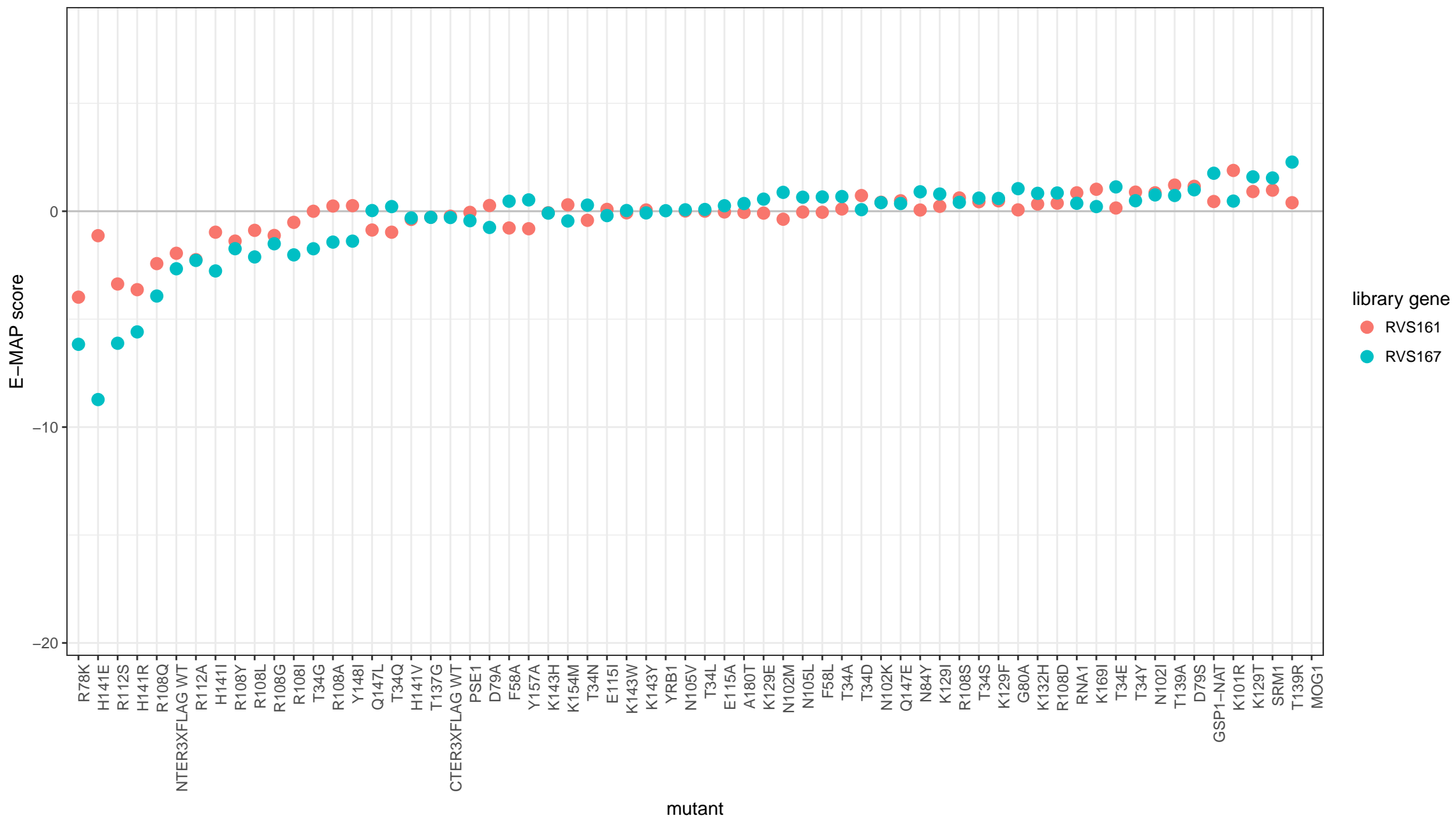
library gene

RTT109

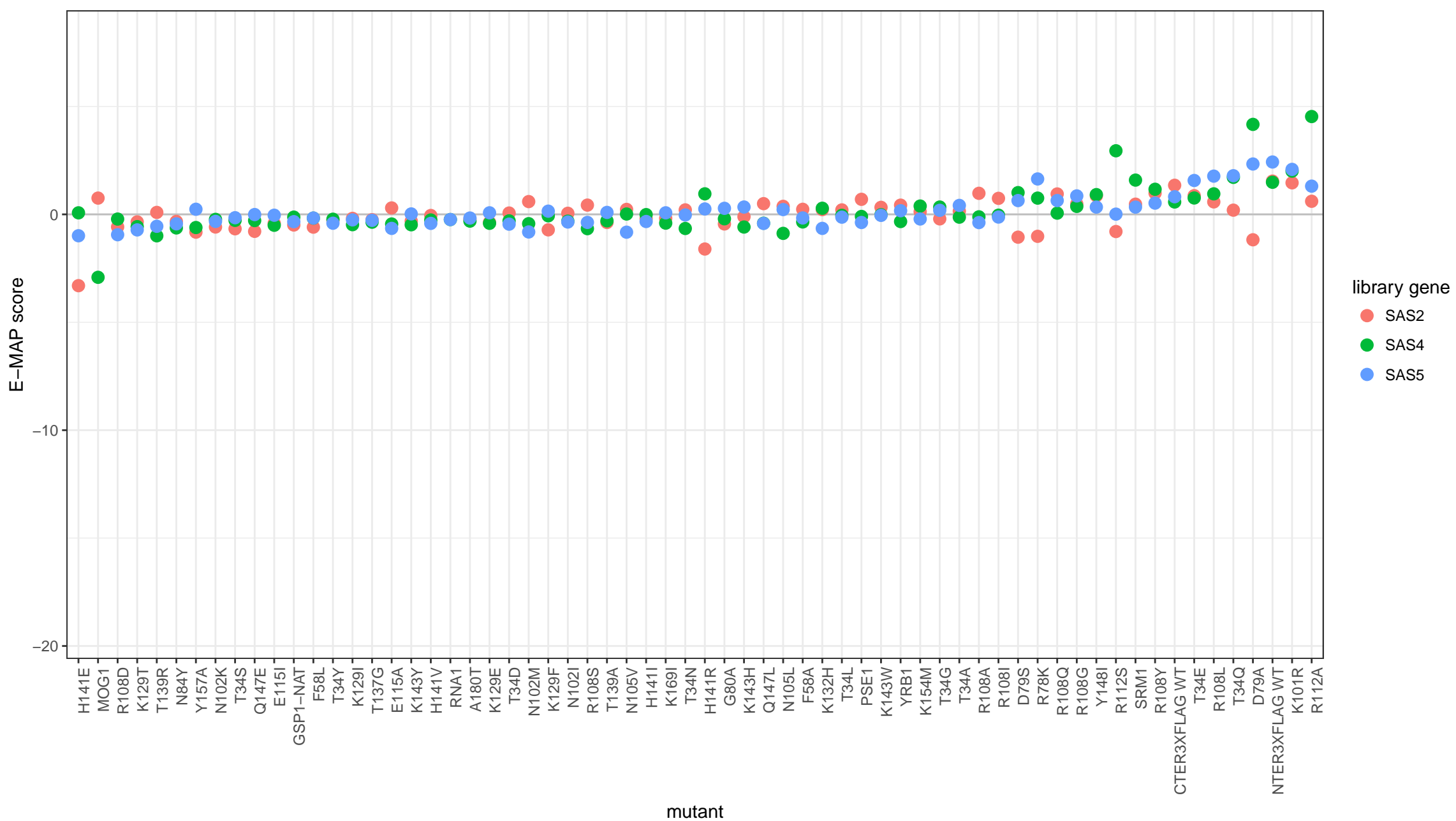
VPS75

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

Rvs161p/Rvs167p complex

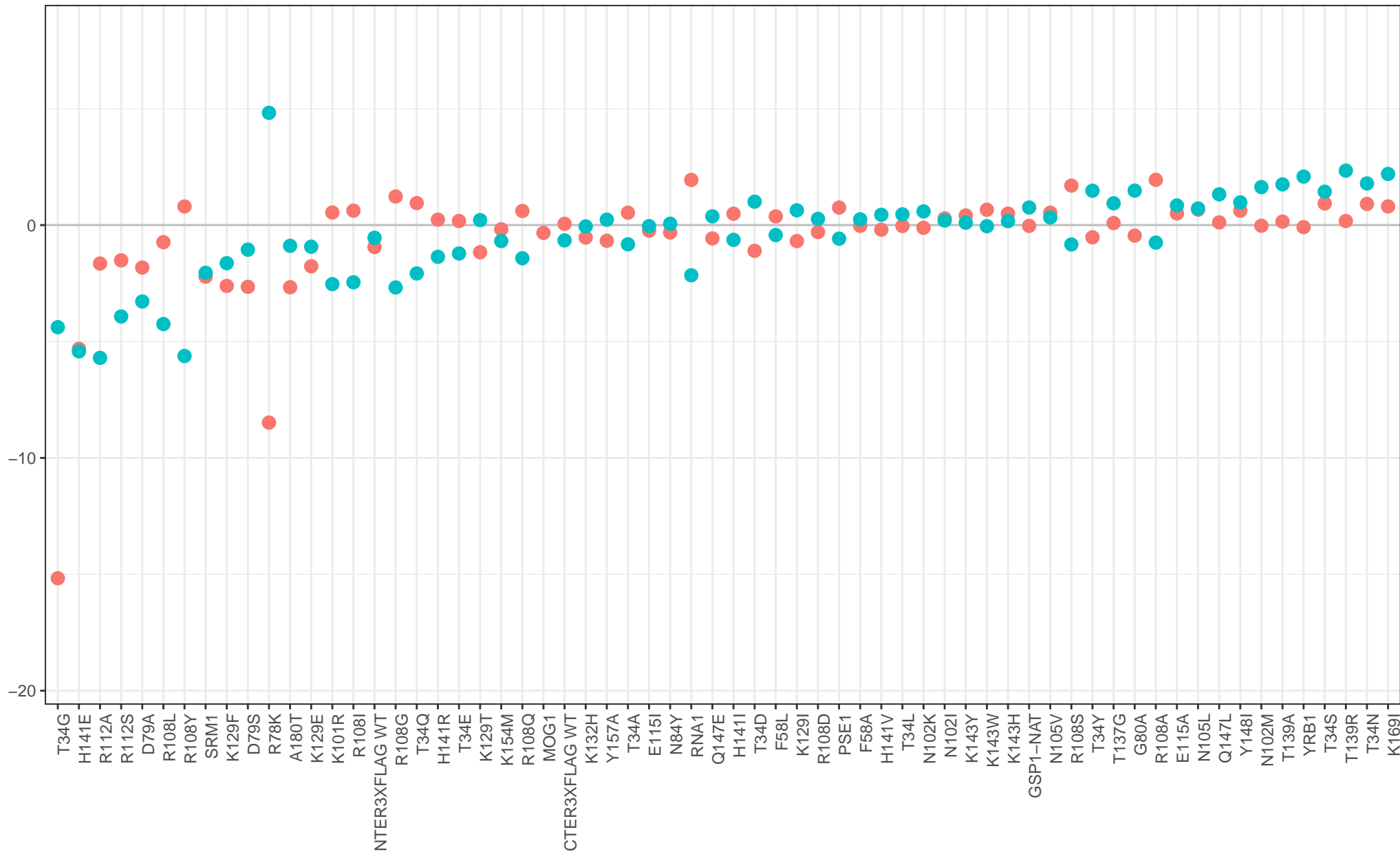


SAS Complex



SBF complex

E-MAP score



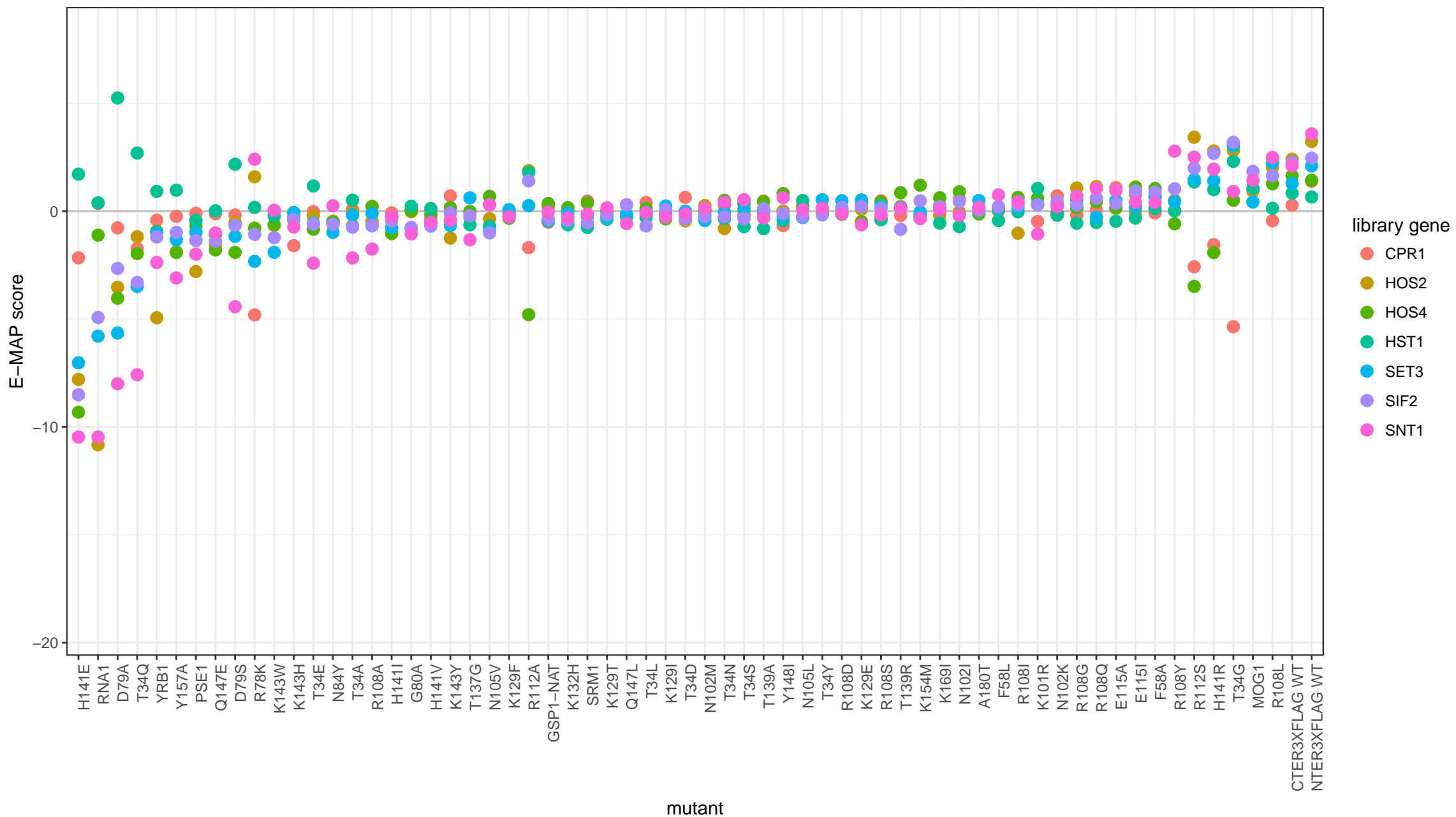
library gene

SWI4

SWI6

mutant

Set3p complex



signal peptidase complex

E-MAP score

0

-10

-20

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

library gene

SEC11

SPC1

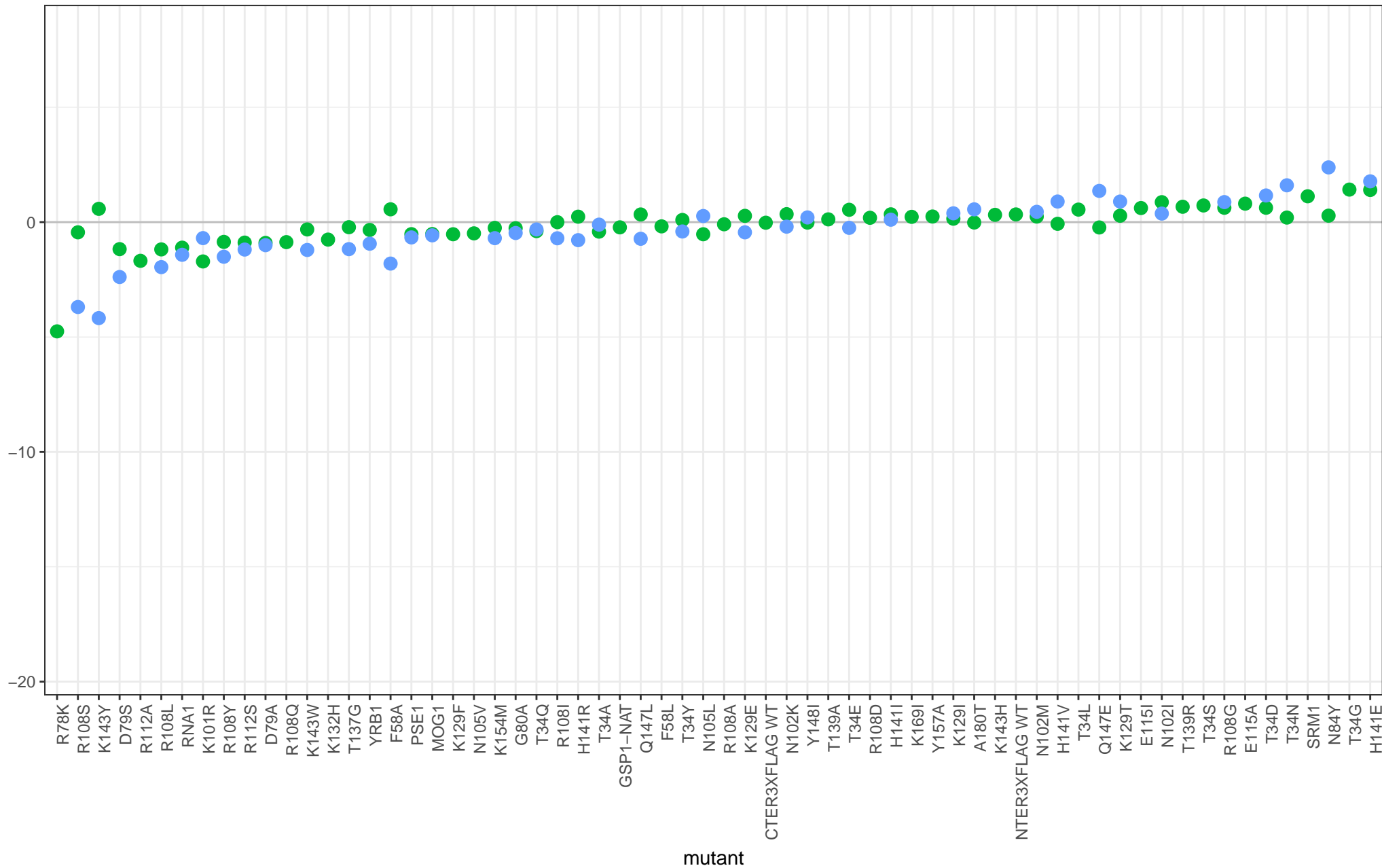
SPC2

SPC3

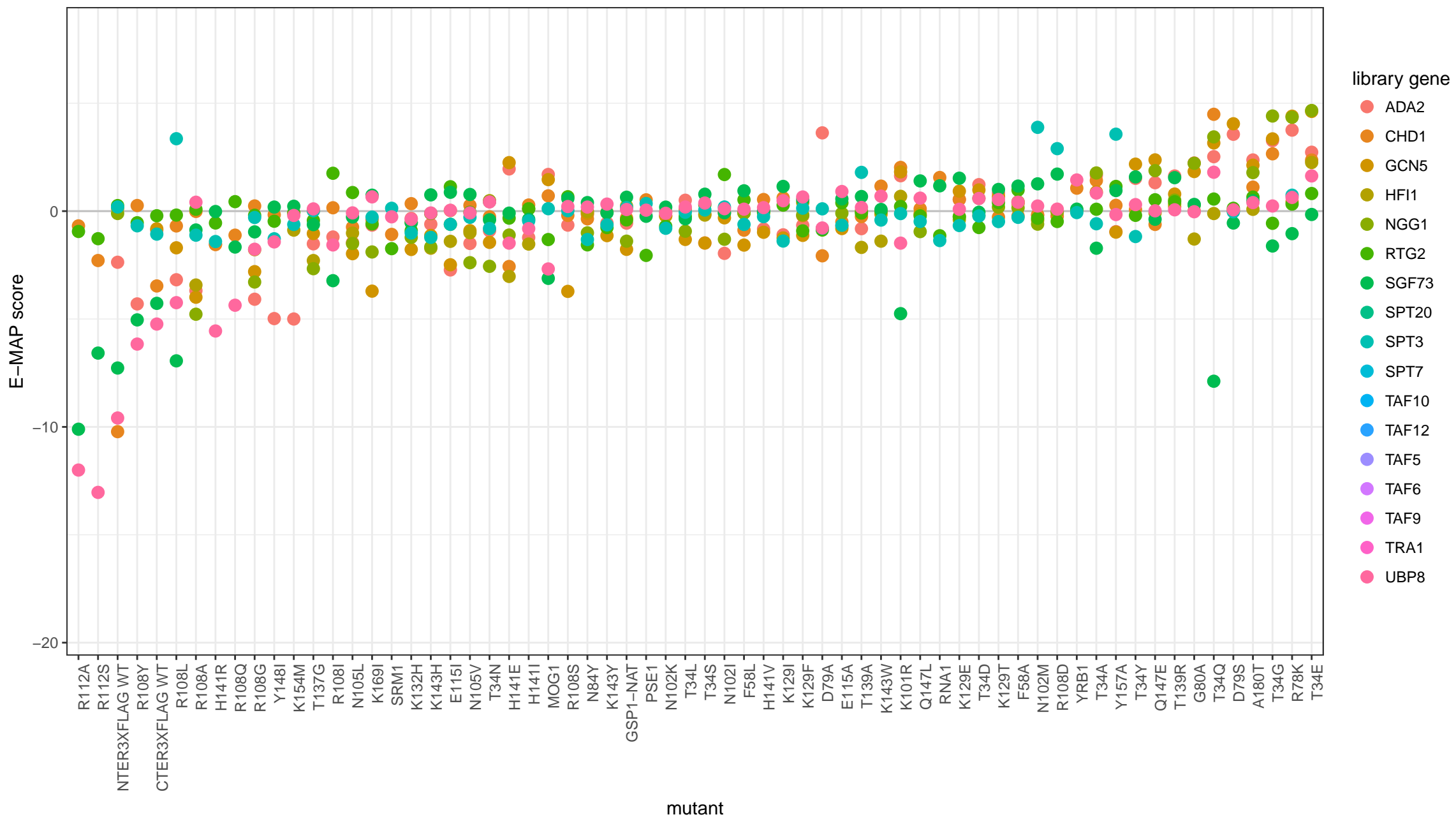
mutant

Ski Complex

E-MAP score



SLIK (SAGA-like) complex



Slx1p/Slx4p complex

E-MAP score

0

-10

-20

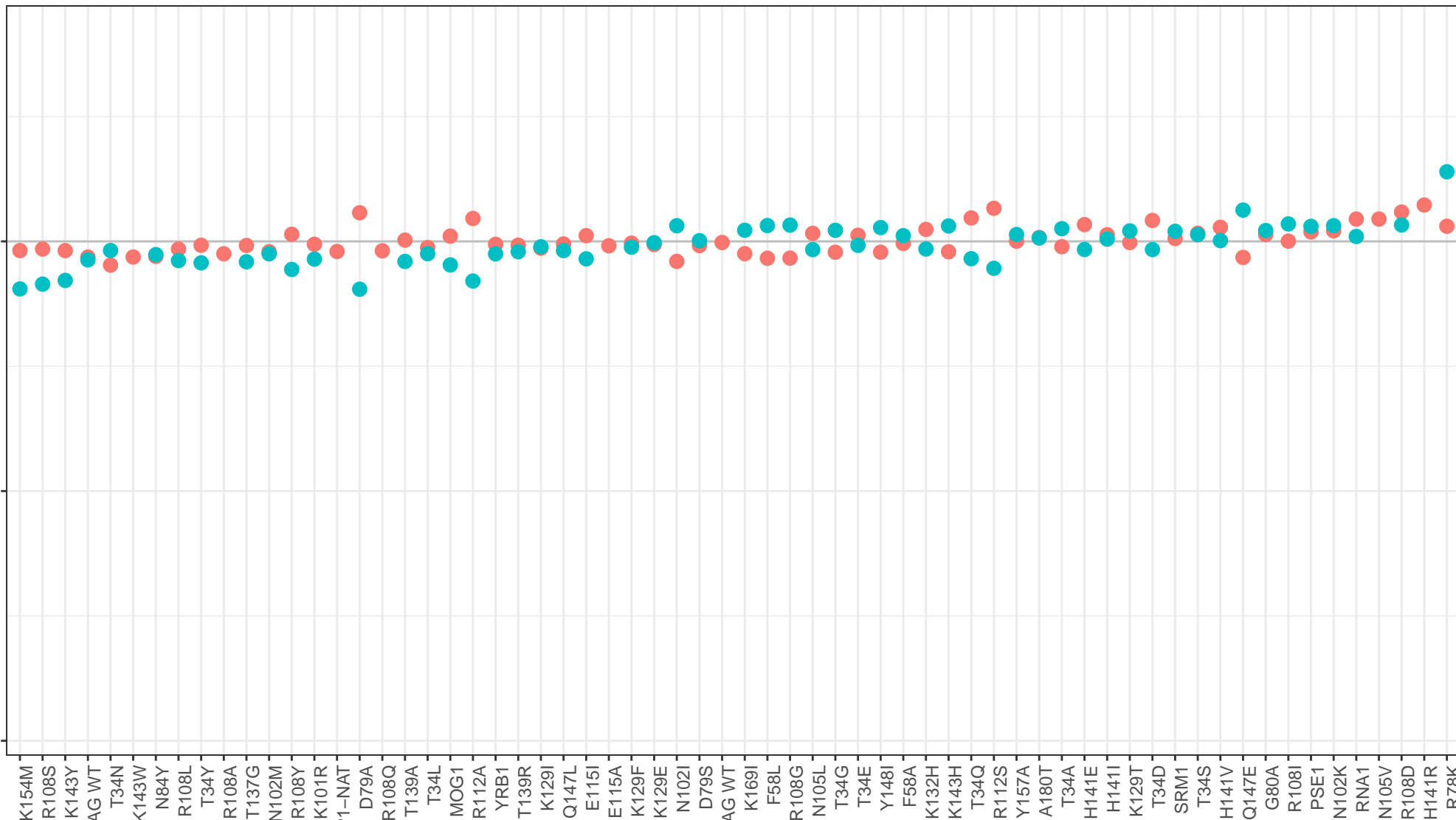
K154M
R108S
K143Y
NTER3XFLAG WT
T34N
K143W
N84Y
R108L
T34Y
R108A
T137G
N102M
R108Y
K101R
GSP1-NAT
D79A
R108Q
T139A
T34L
MOG1
R112A
YRB1
T139R
K129I
Q147L
E115I
E115A
K129F
K129E
N102I
D79S
CTER3XFLAG WT
K169I
F58L
R108G
N105L
T34G
T34E
Y148I
F58A
K132H
K143H
T34Q
R112S
Y157A
A180T
T34A
H141E
H141I
K129T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

mutant

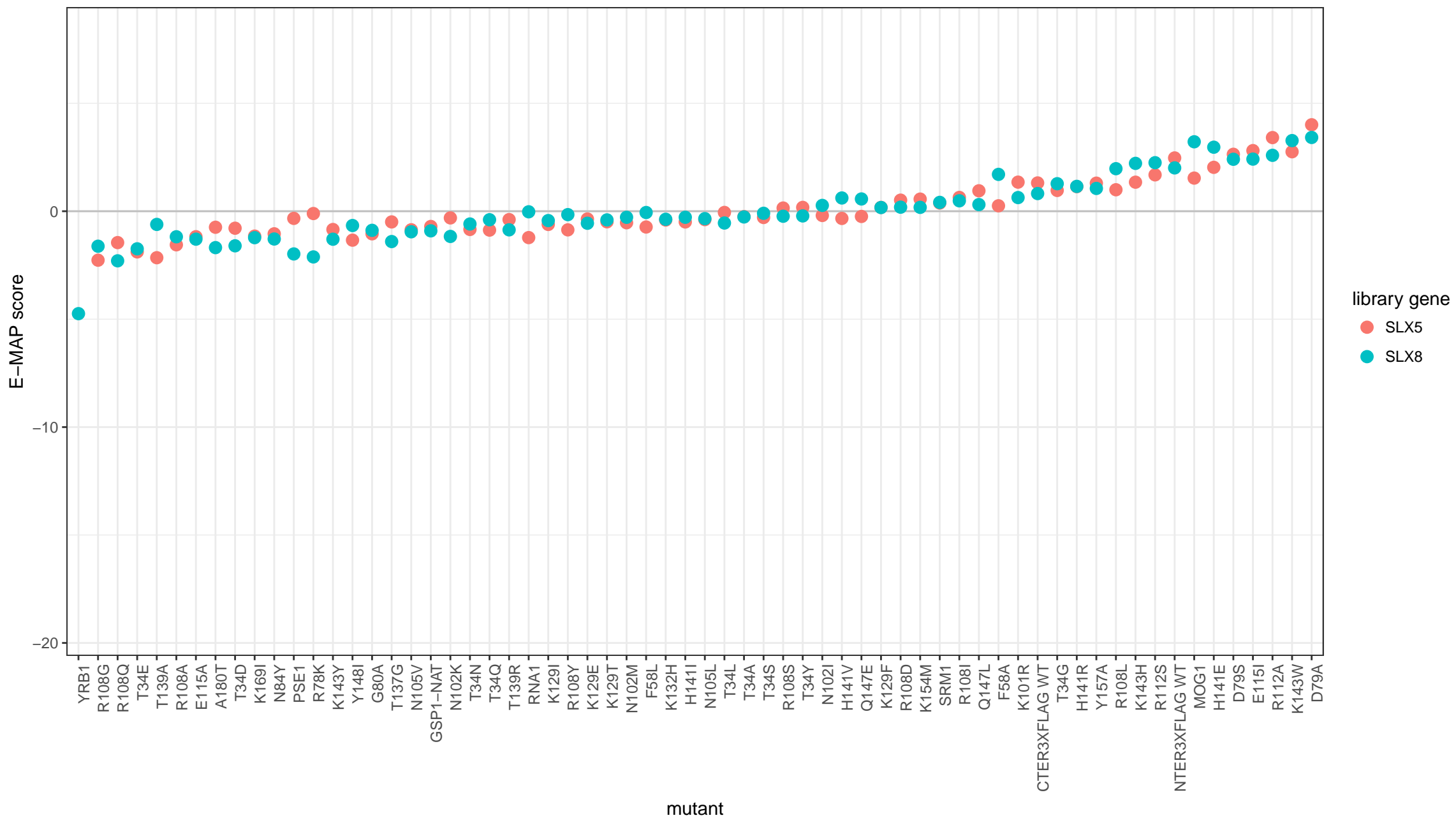
library gene

SLX1

SLX4



Slx5p/Slx8p complex



Snf1p/Snf4p/Gal83p complex

E-MAP score

-20

-10

0

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

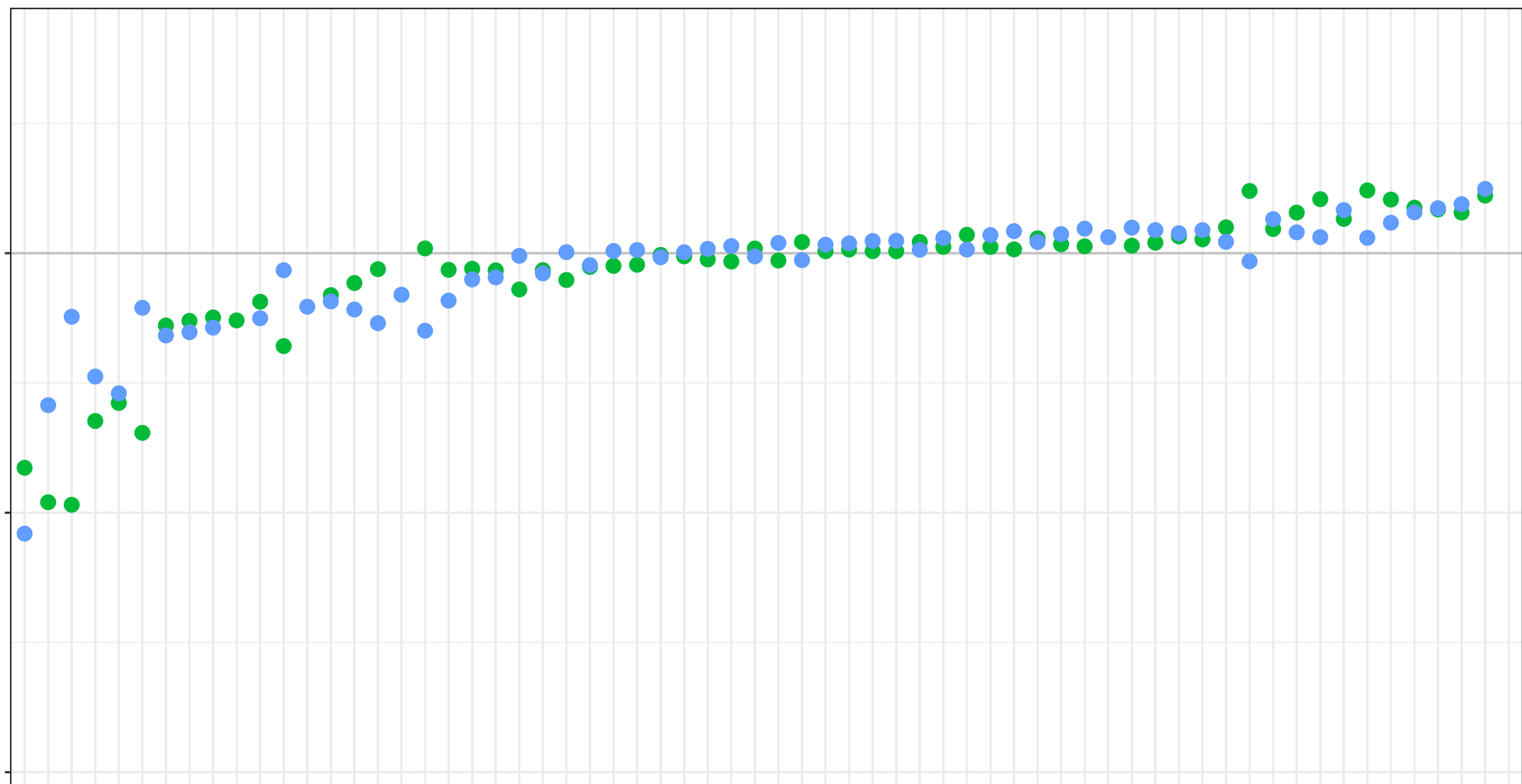
mutant

library gene

GAL83

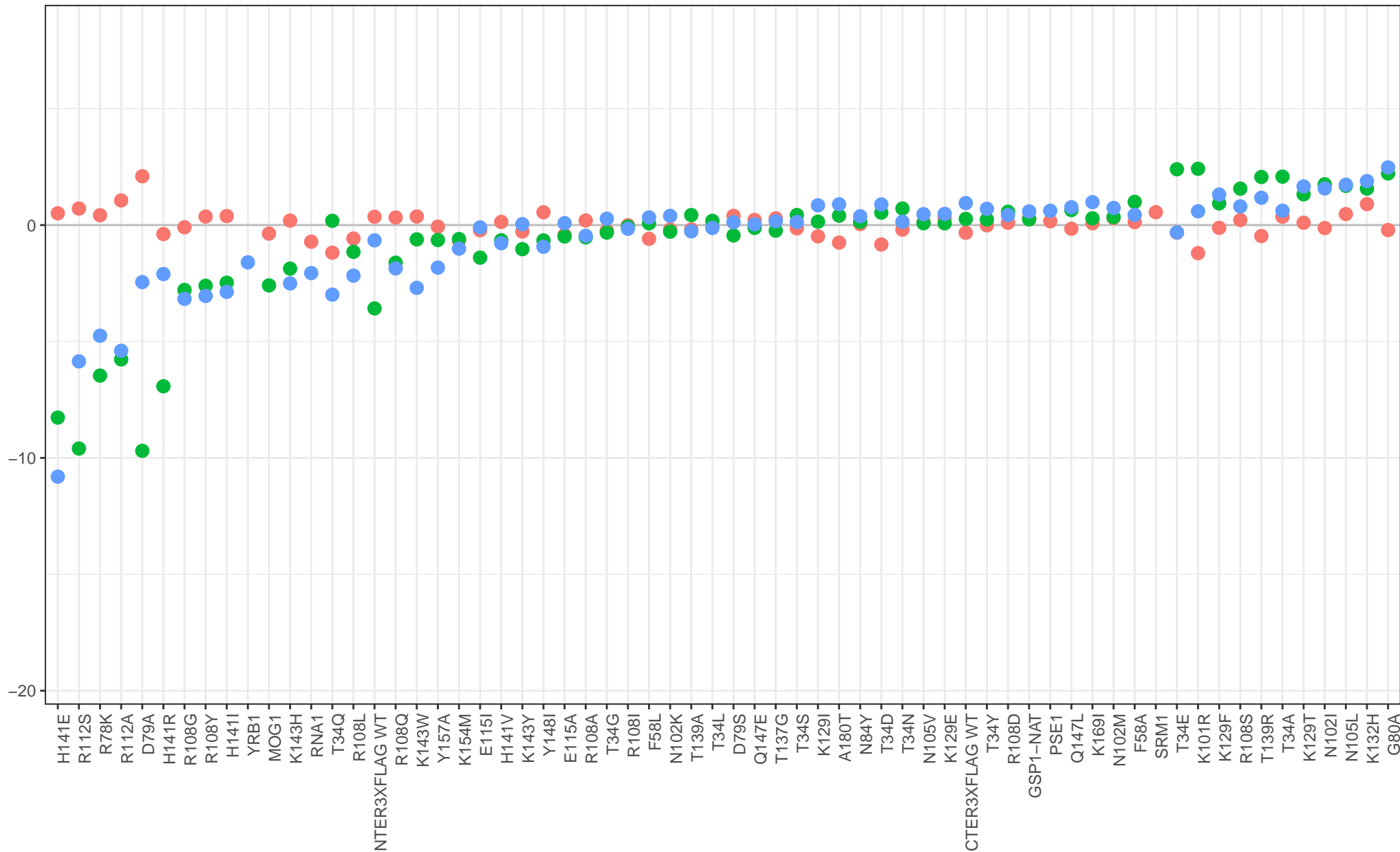
SNF1

SNF4



Snf1p/Snf4p/Sip1p complex

E-MAP score



Snf1p/Snf4p/Sip2p complex

E-MAP score

-20

-10

0

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

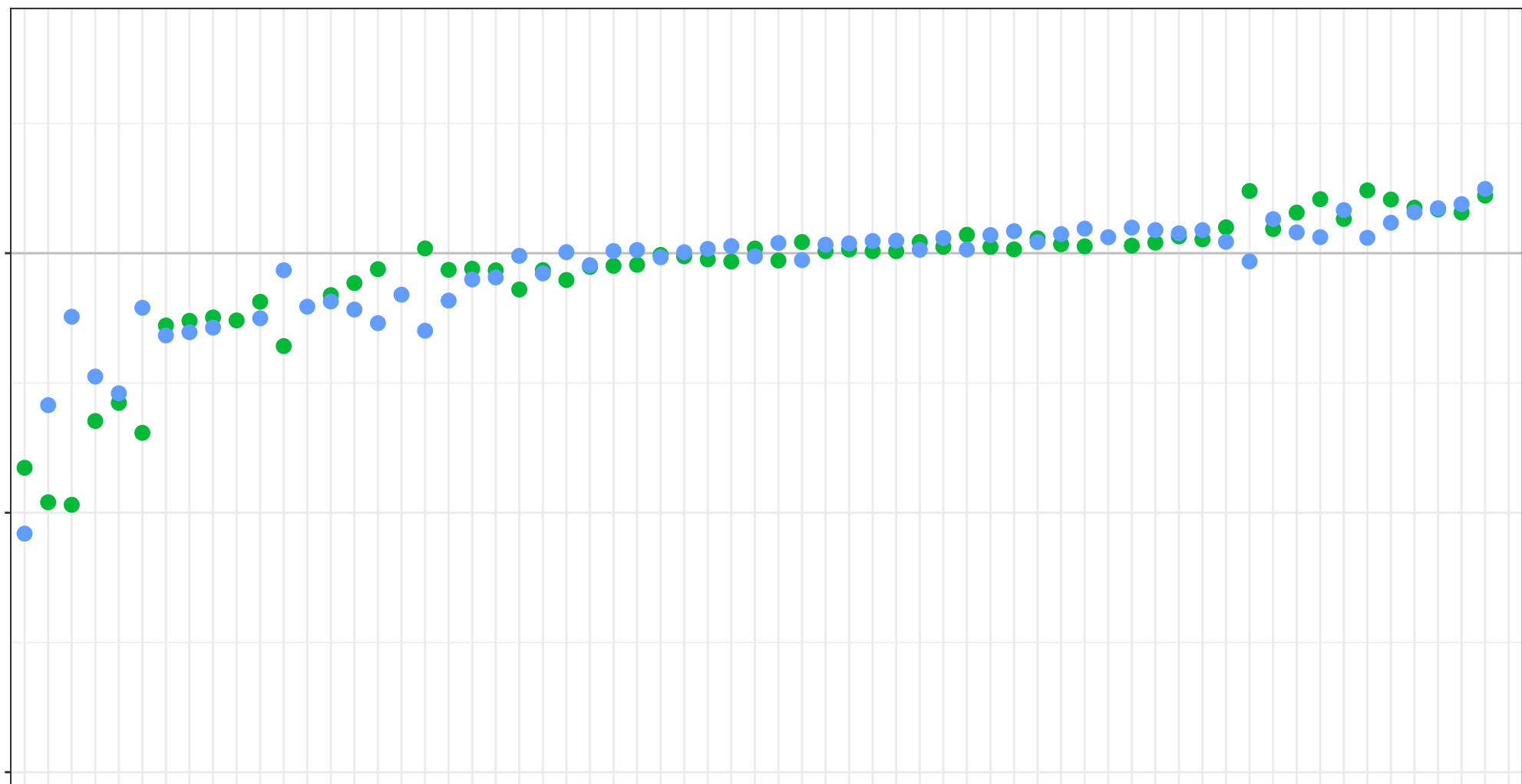
mutant

library gene

SIP2

SNF1

SNF4



snoRNA processing

E-MAP score

-20

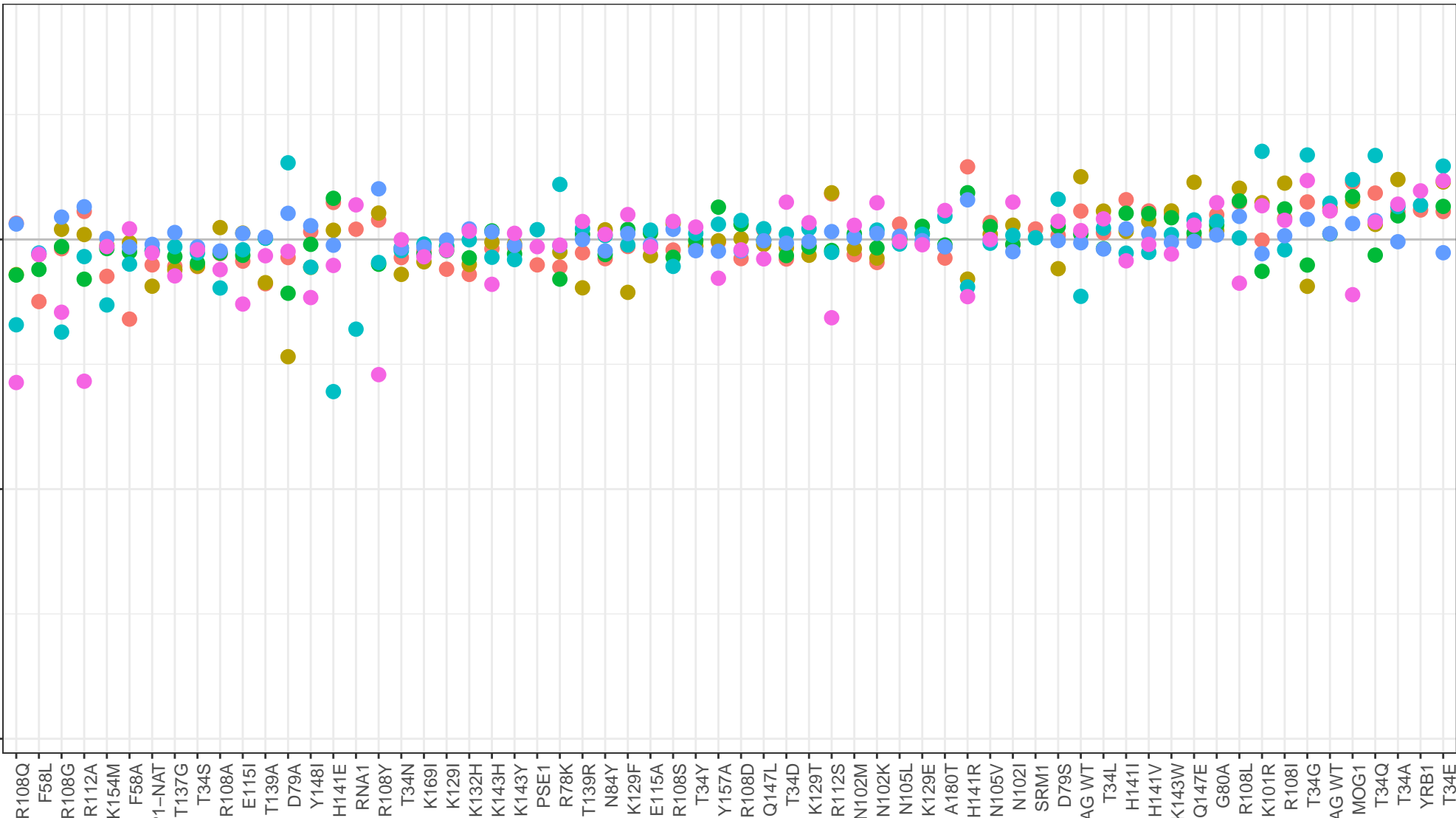
-10

0

mutant

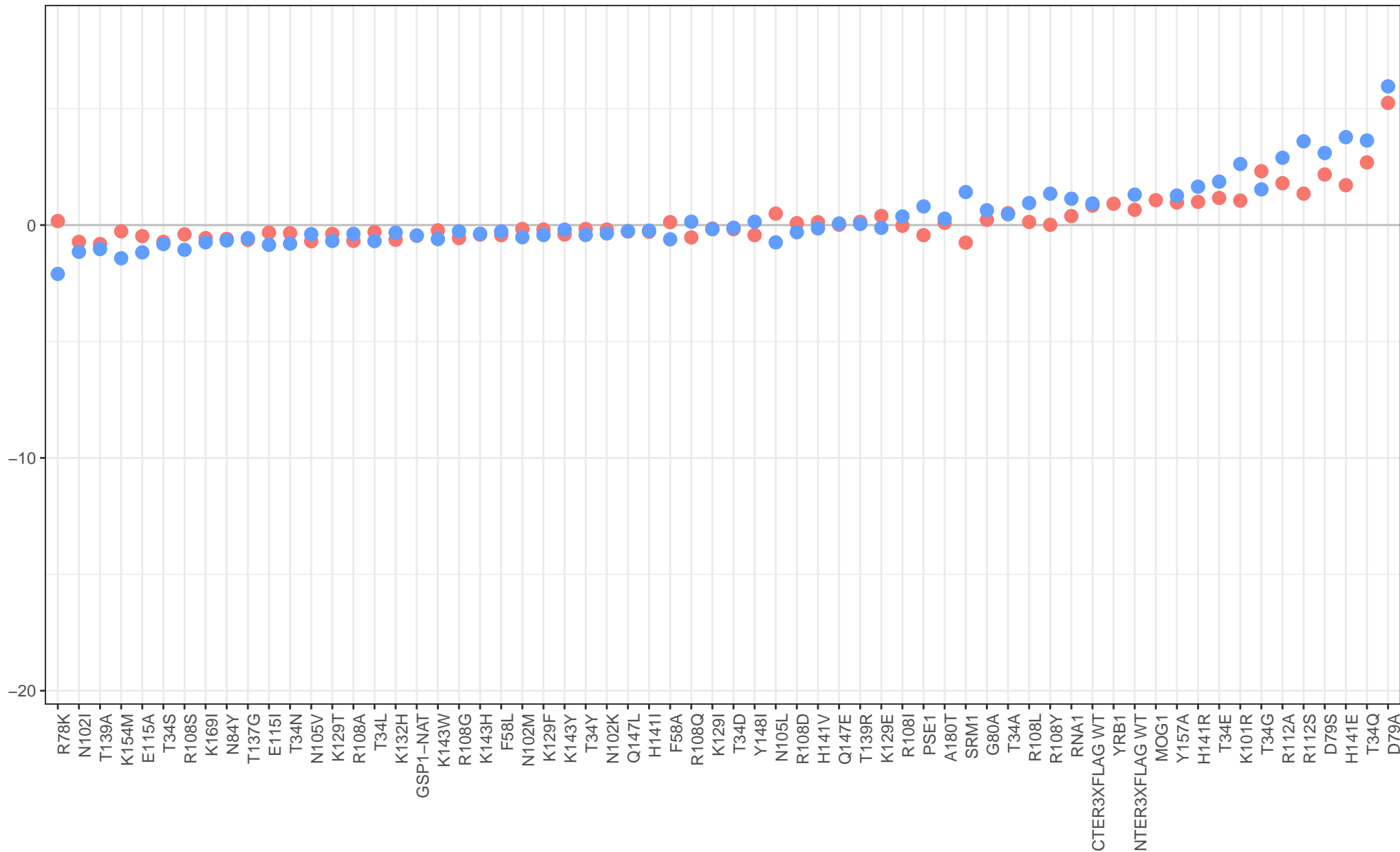
library gene

LRP1
PAP2
RRP6
RTF1
TRF5
XRN1



Sum1p/Rfm1p/Hst1p complex

E-MAP score



library gene

HST1

RFM1

SUM1

mutant

Sur1p/Csg2p complex

E-MAP score

-20

-10

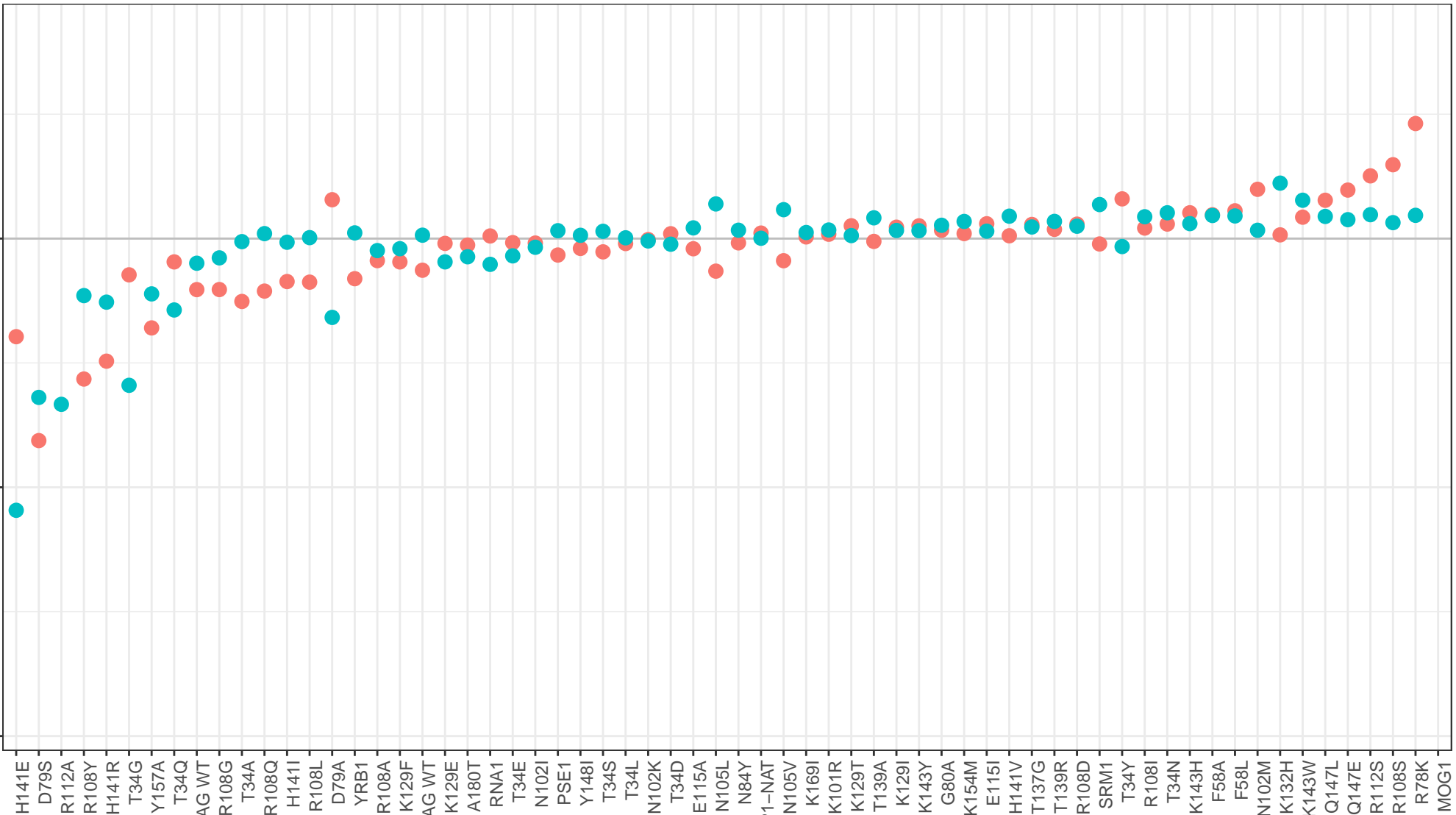
0

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

mutant

library gene

CSG2
SUR1



SWI/SNF complex

E-MAP score

-20

-10

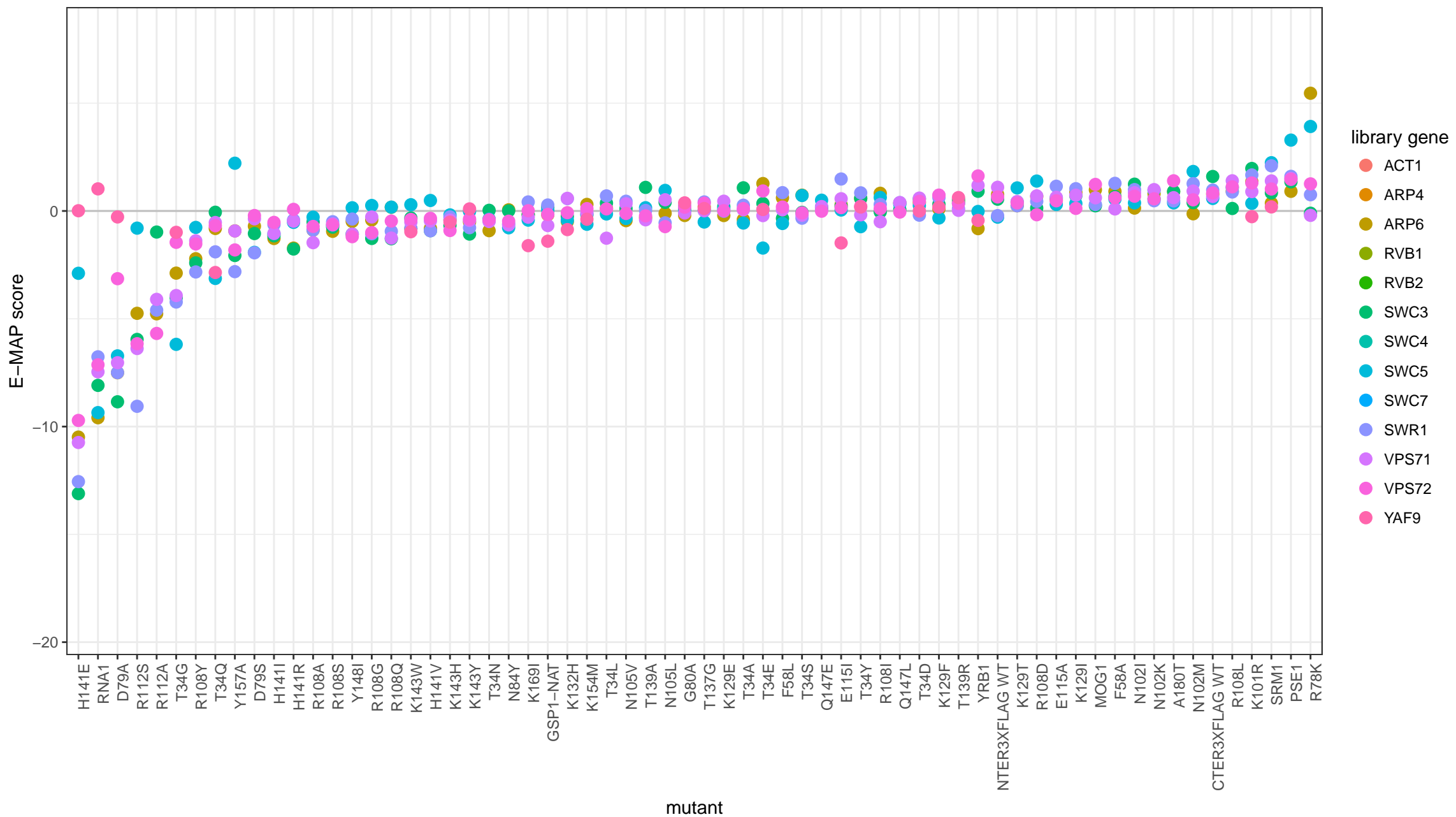
0

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

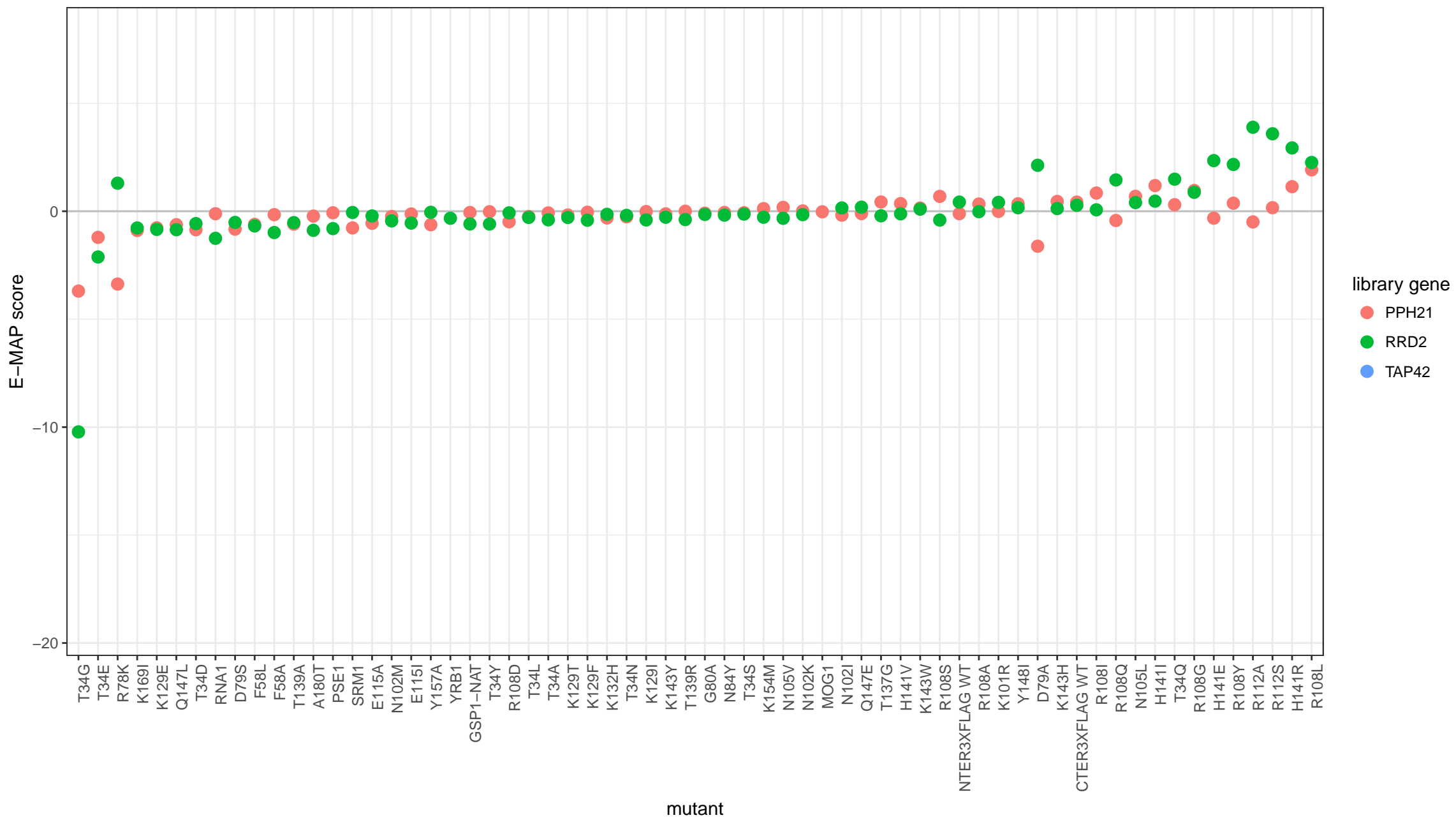
library gene

- ARP7
- ARP9
- RTT102
- SNF11
- SNF12
- SNF2
- SNF5
- SNF6
- SWI1
- SWI3
- SWP82
- TAF14

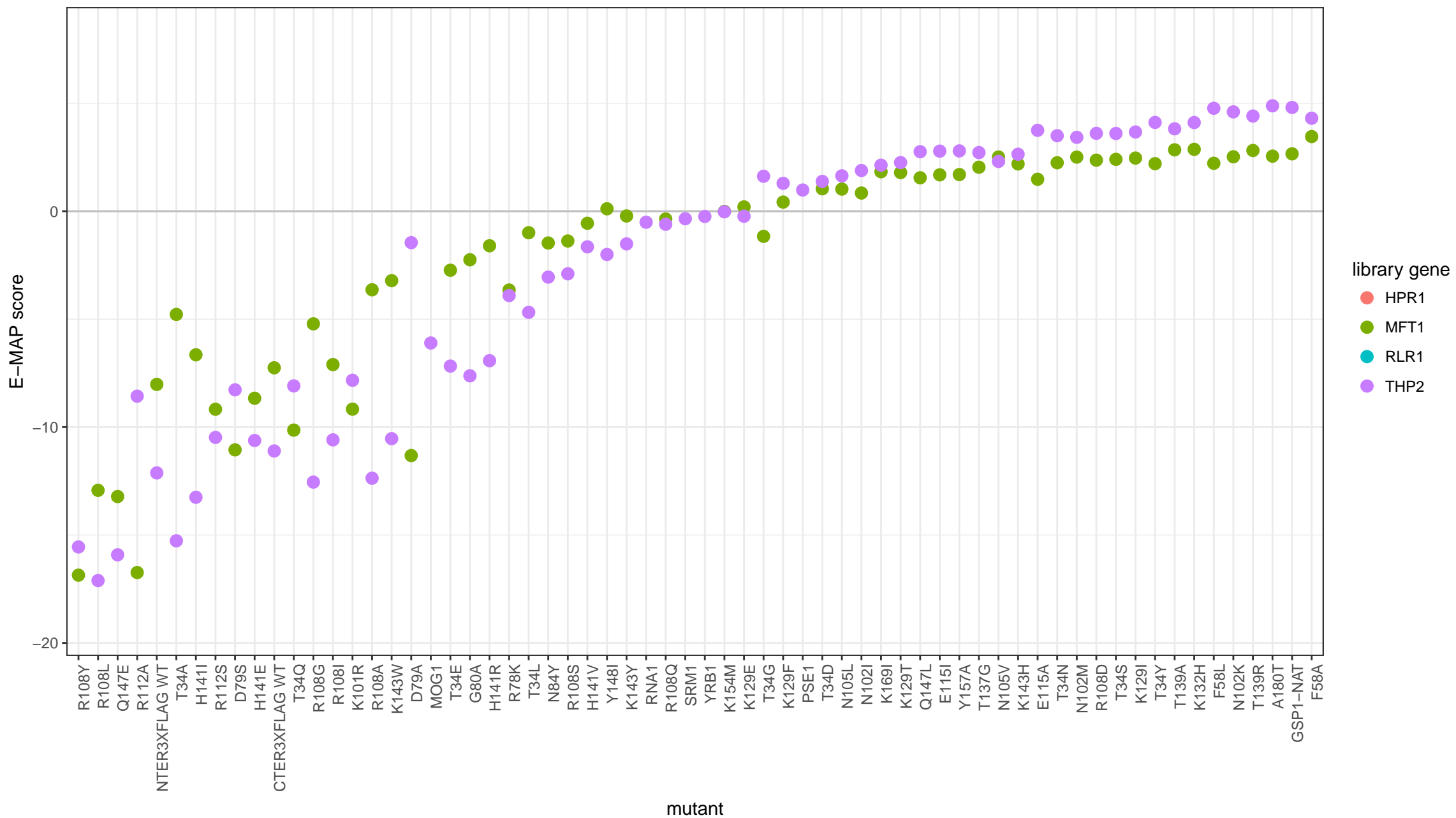
Swr1p complex



Tap42p/Pph21p/Rrd2p complex

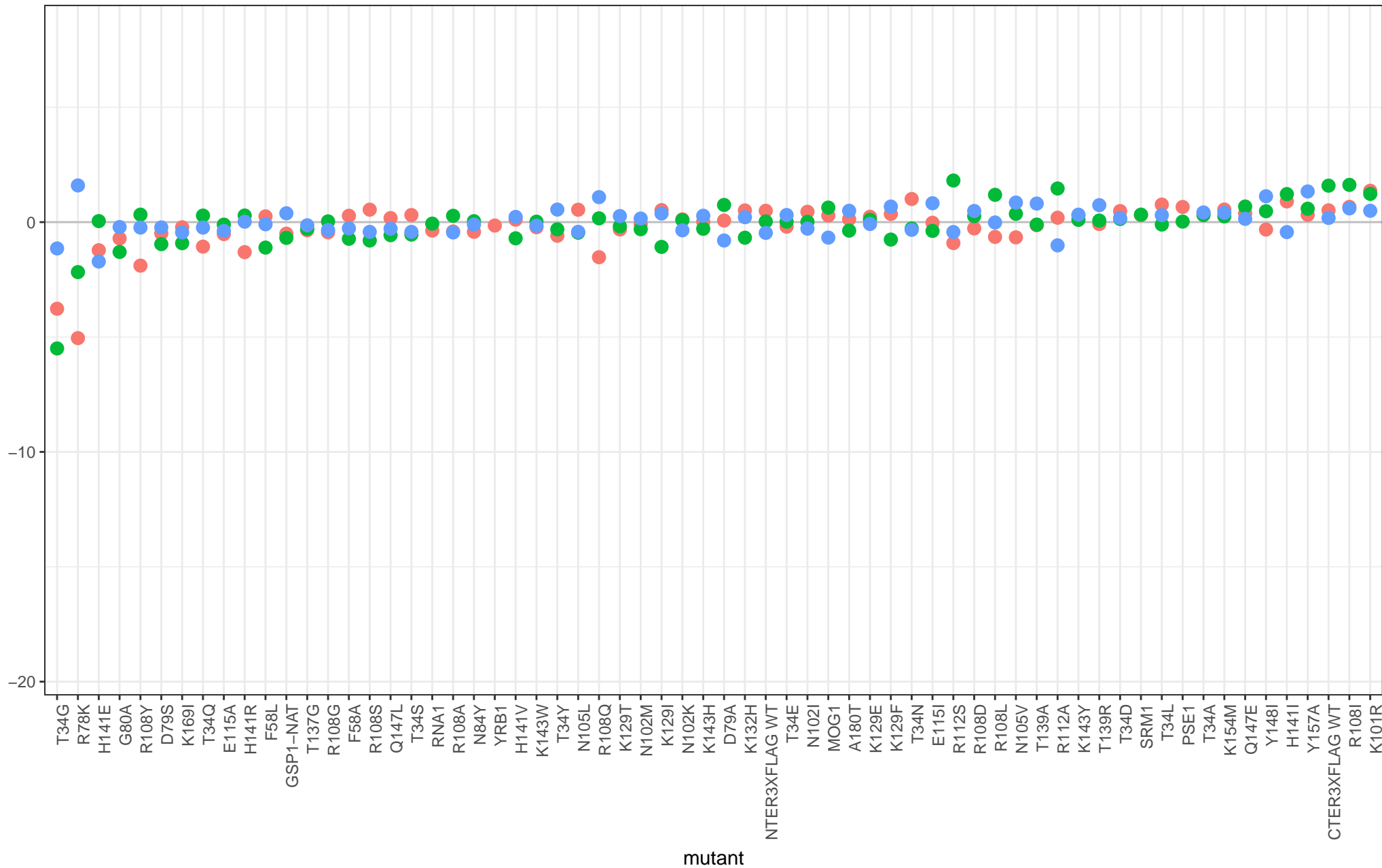


THO complex



Tof1p/Mrc1p/Csm3p complex

E-MAP score



TORC 1 complex

E-MAP score

0

-10

-20

mutant

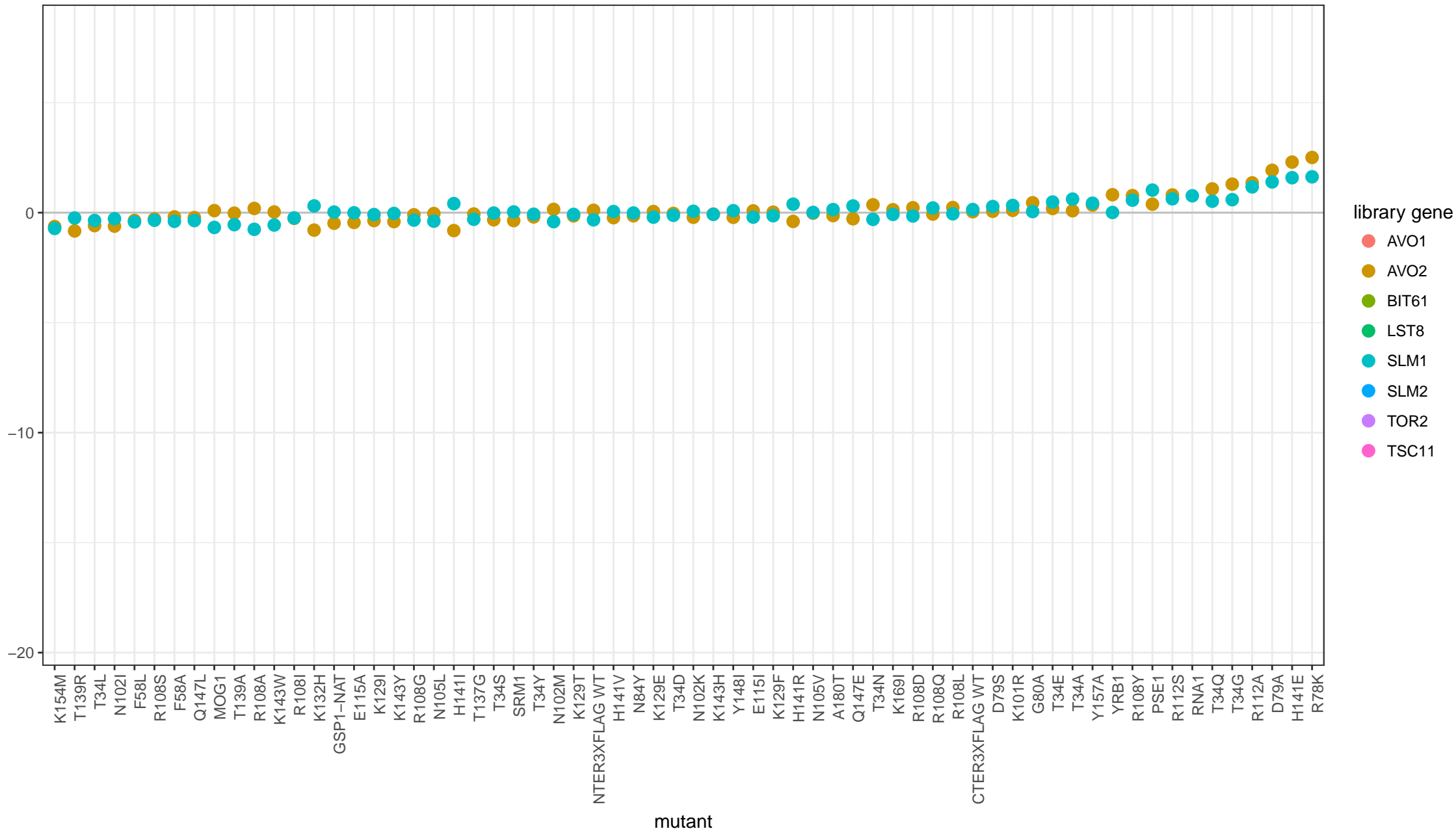
library gene

- KOG1
- LST8
- TCO89
- TOR1

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

TORC 2 complex

E-MAP score



TRAMP complex (Air1p)

E-MAP score

0

-10

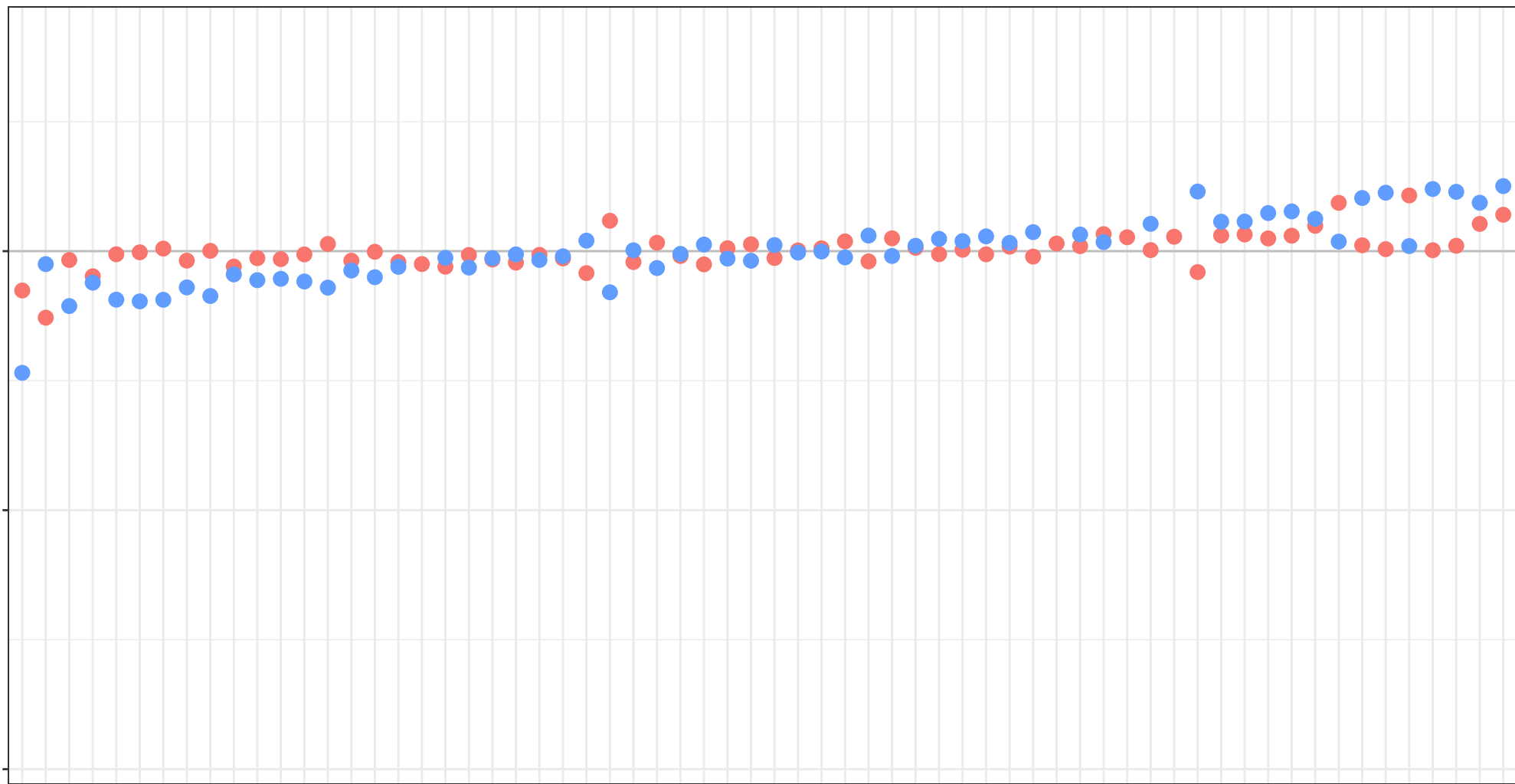
-20

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

mutant

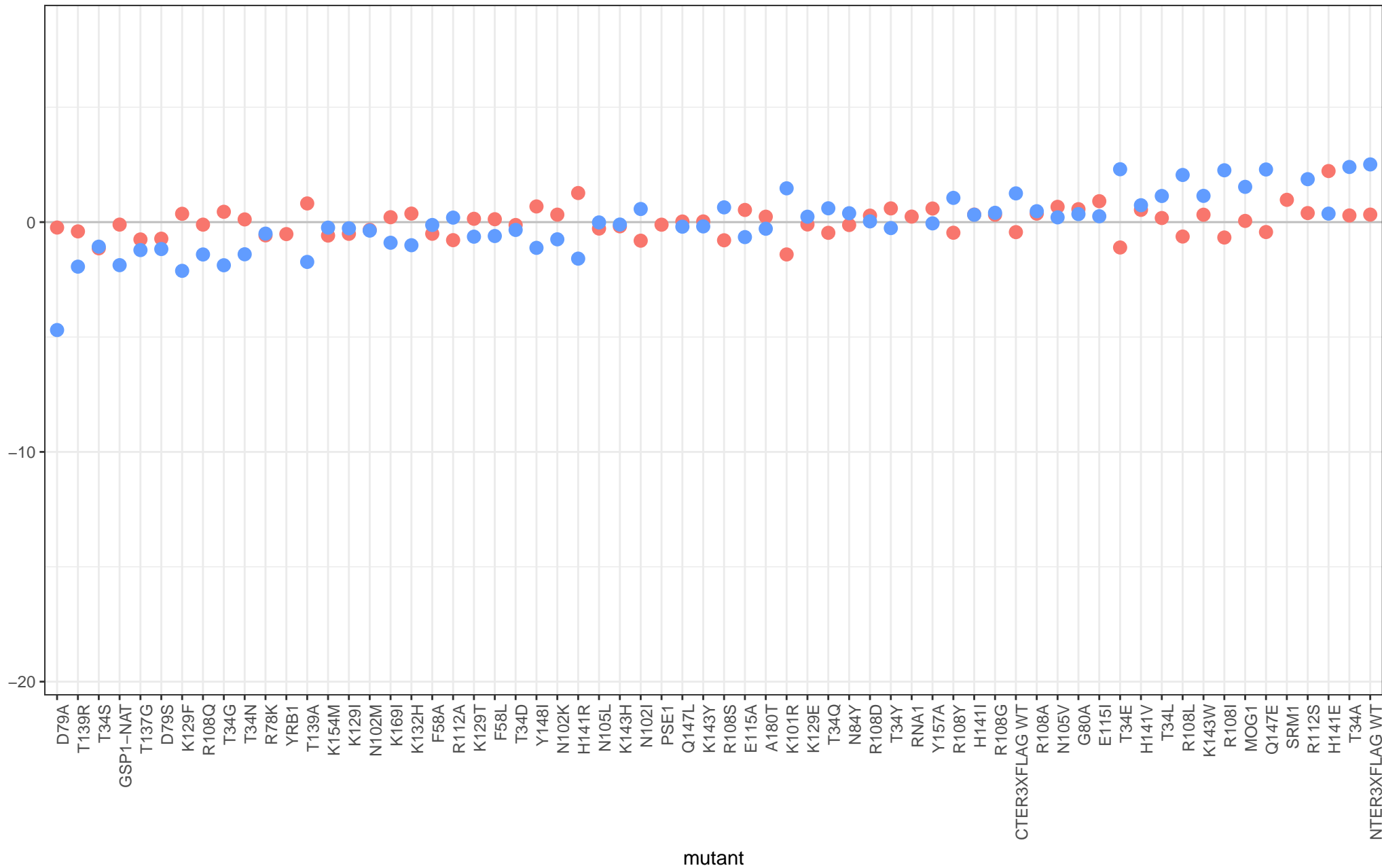
library gene

- AIR1
- MTR4
- PAP2



TRAMP complex (Air2p)

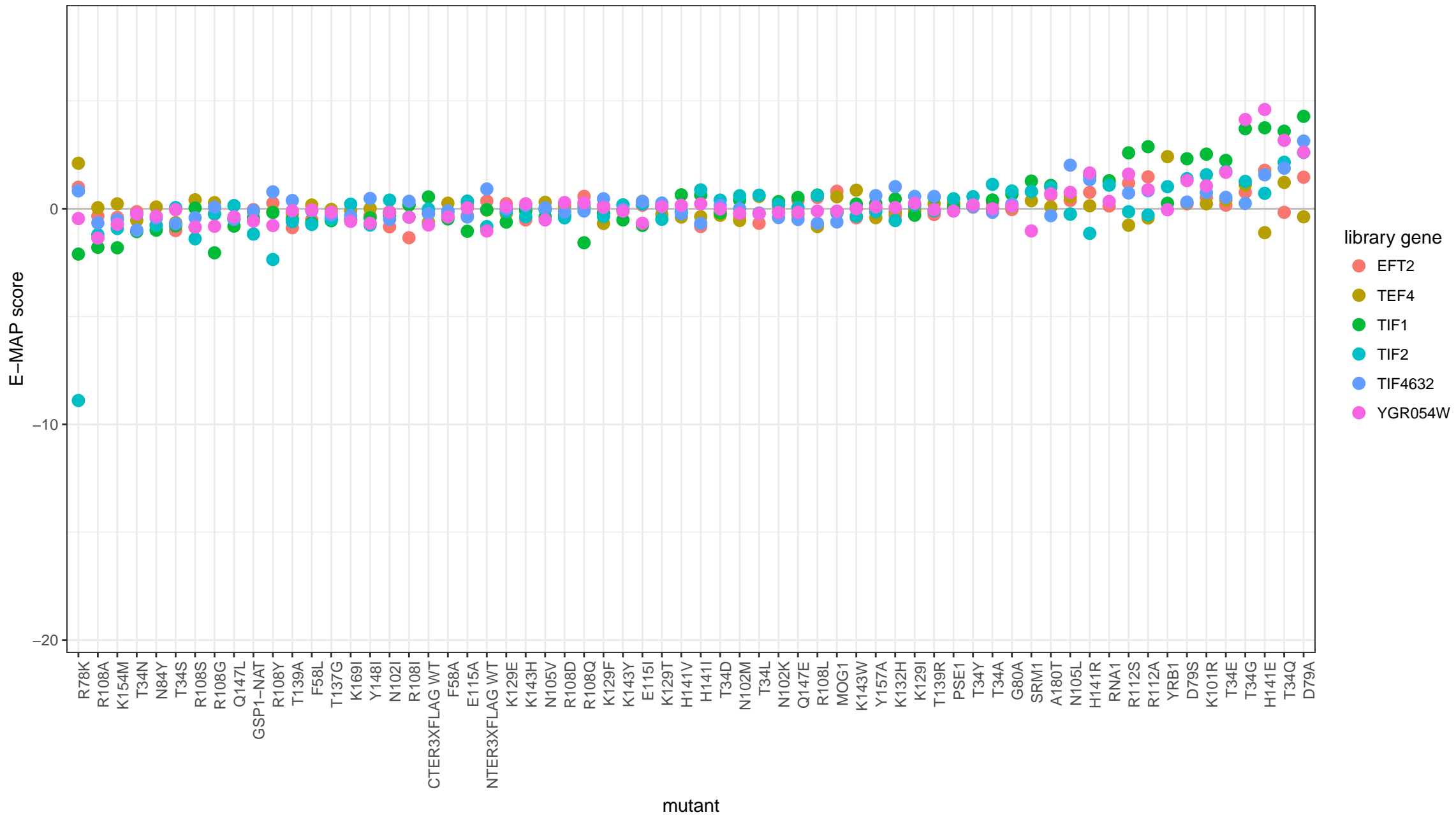
E-MAP score



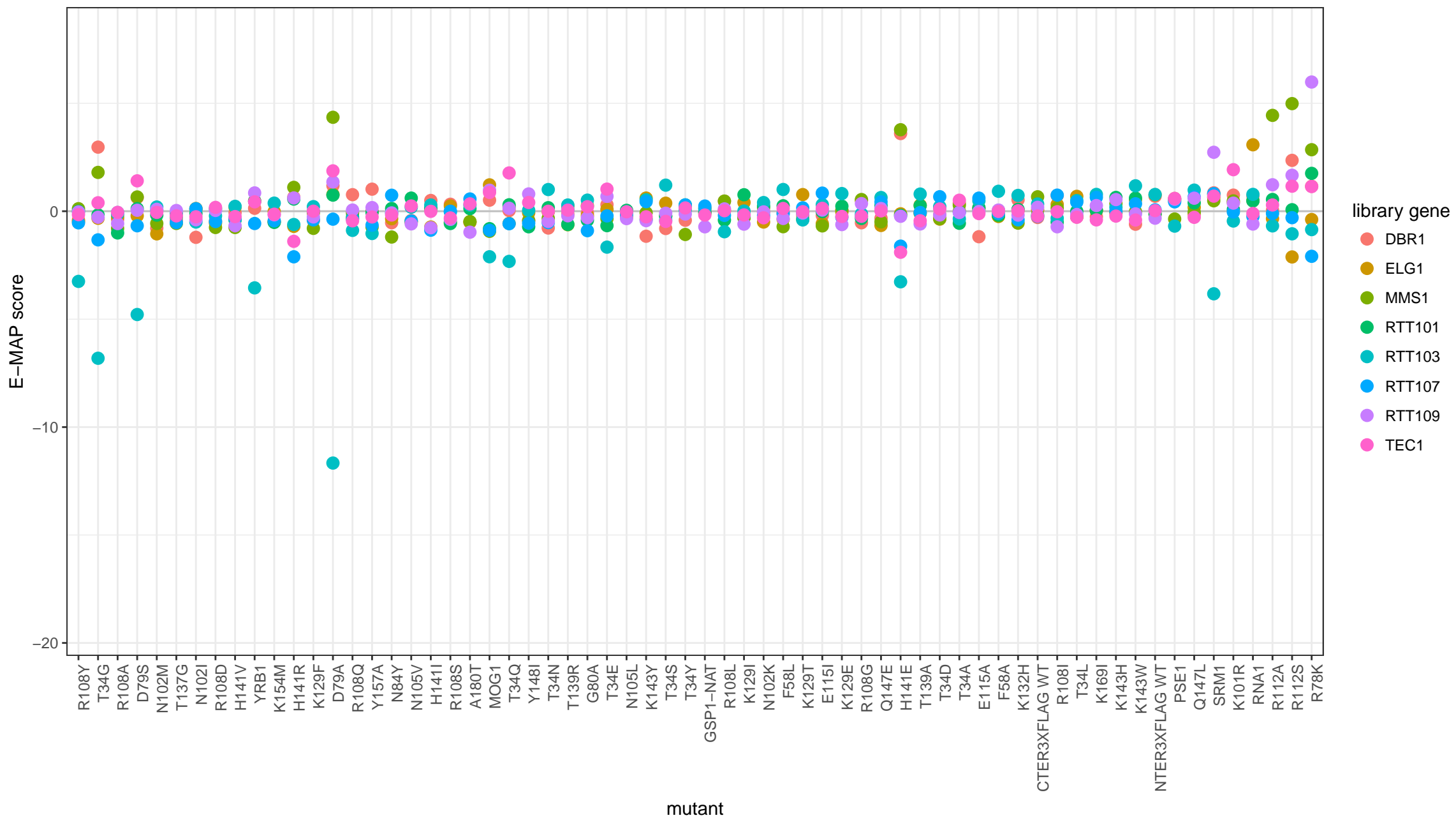
library gene

- AIR2
- MTR4
- PAP2

translation factor activity, RNA binding



transposition



U1 snRNP complex

E-MAP score

-20

-10

0

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

library gene

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

U2 snRNP complex

E-MAP score

-20

-10

0

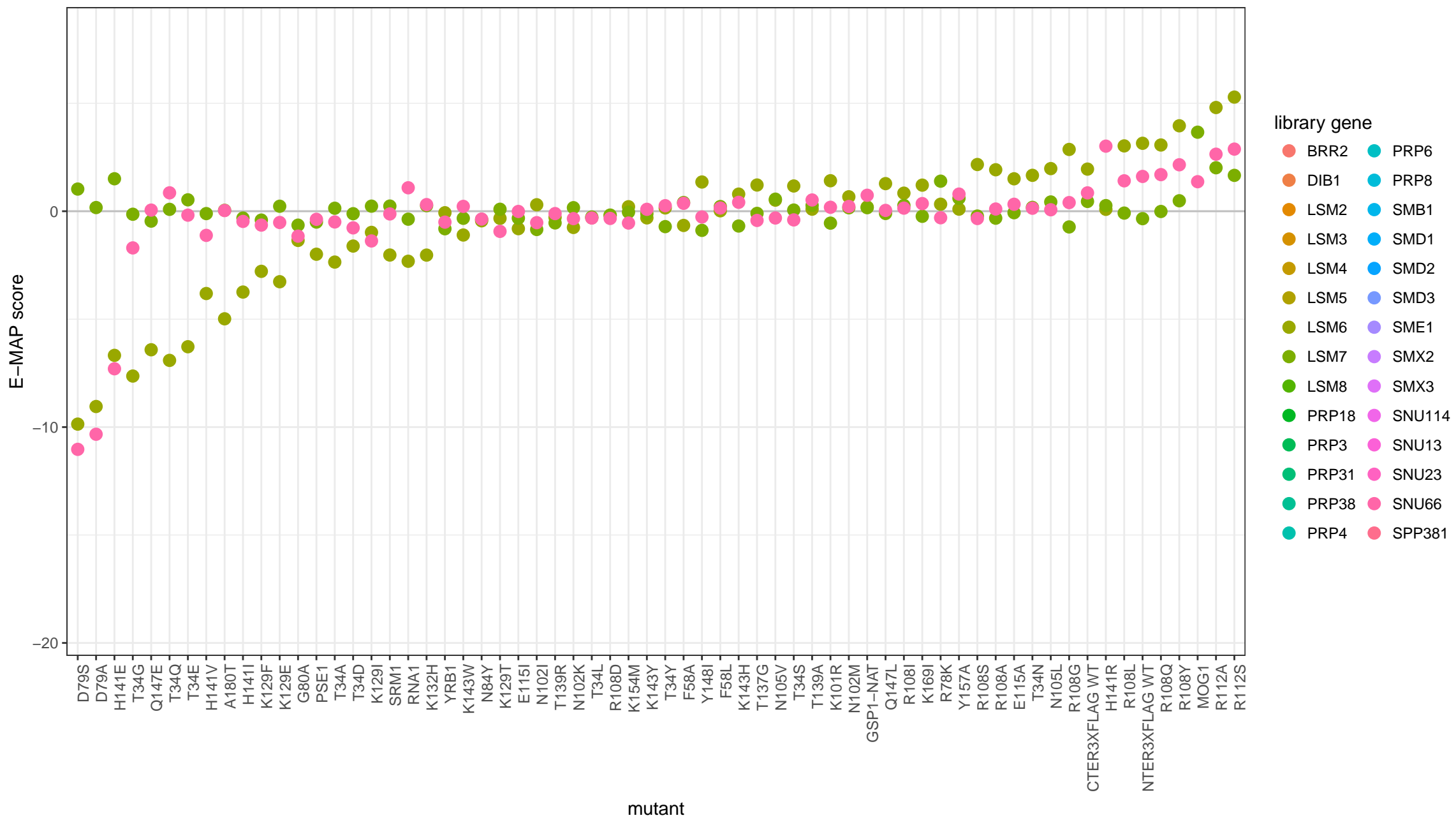
T139R
T139A
T34D
A180T
H141I
Y148I
K129F
K143H
T137G
T34L
N84Y
R108S
F58L
K132H
T34A
T34N
R108A
K129I
K143Y
N105V
N102I
T34S
N102K
N102M
H141V
R108G
K143W
YRB1
R108I
K129E
K169I
GSP1-NAT
G80A
K129T
Q147E
F58A
E115I
PSE1
Q147L
N105L
R108D
K154M
RNA1
T34Y
R108Q
E115A
D79S
R108Y
K101R
Y157A
CTER3XFLAG WT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

mutant

library gene

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

U4/U6 x U5 tri-snRNP complex



U6 snRNP complex

E-MAP score

-20

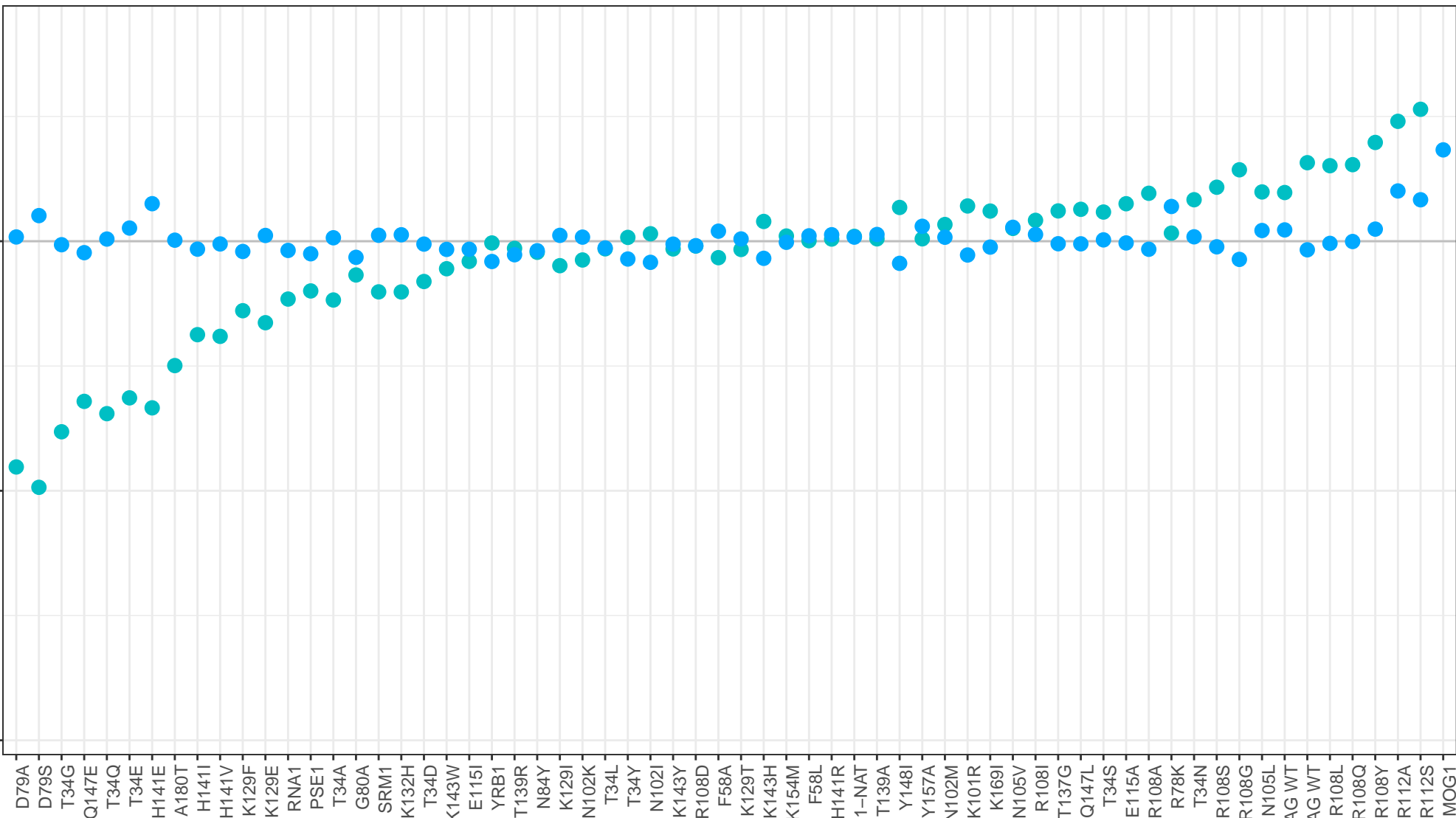
-10

0

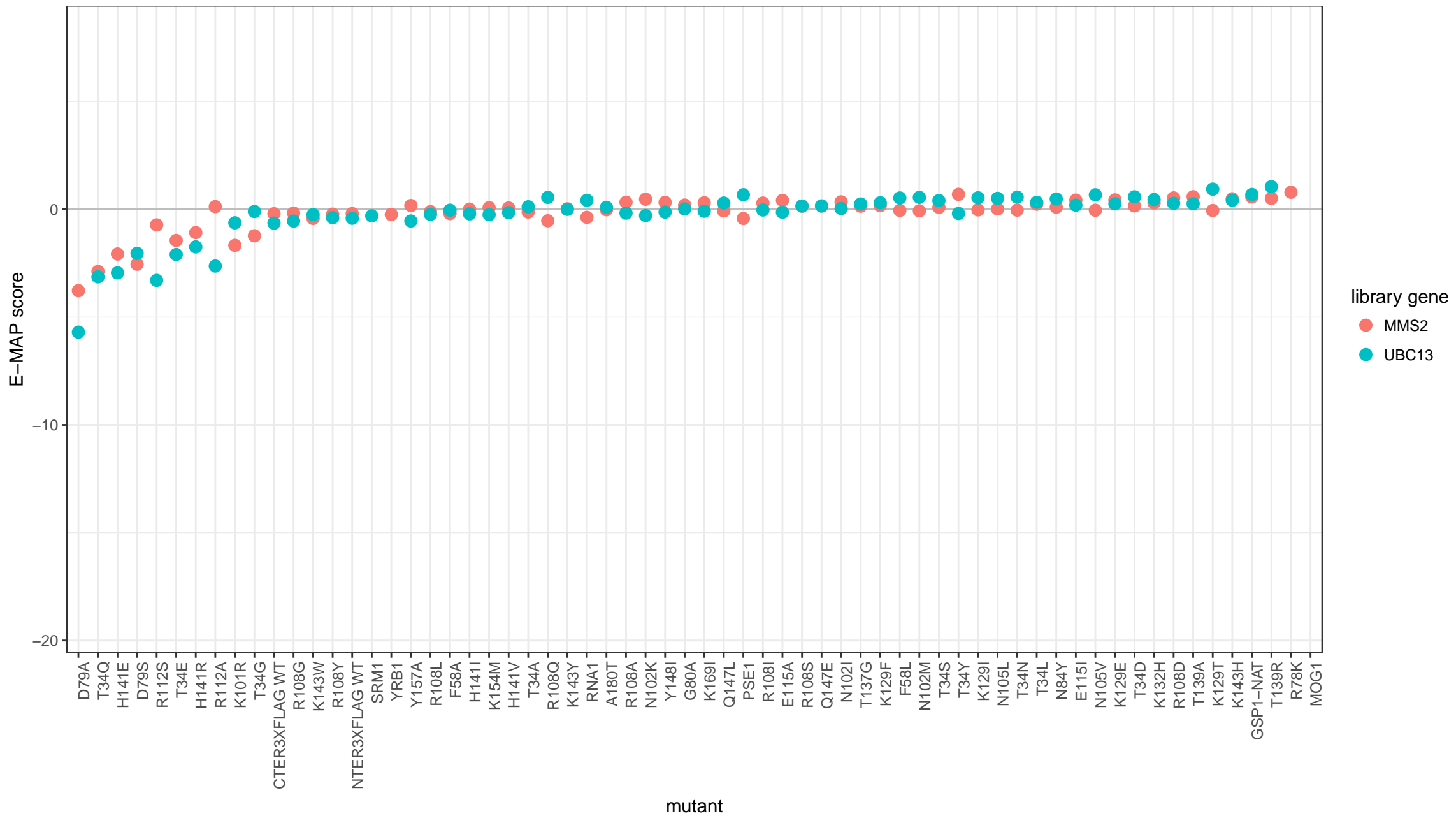
mutant

library gene

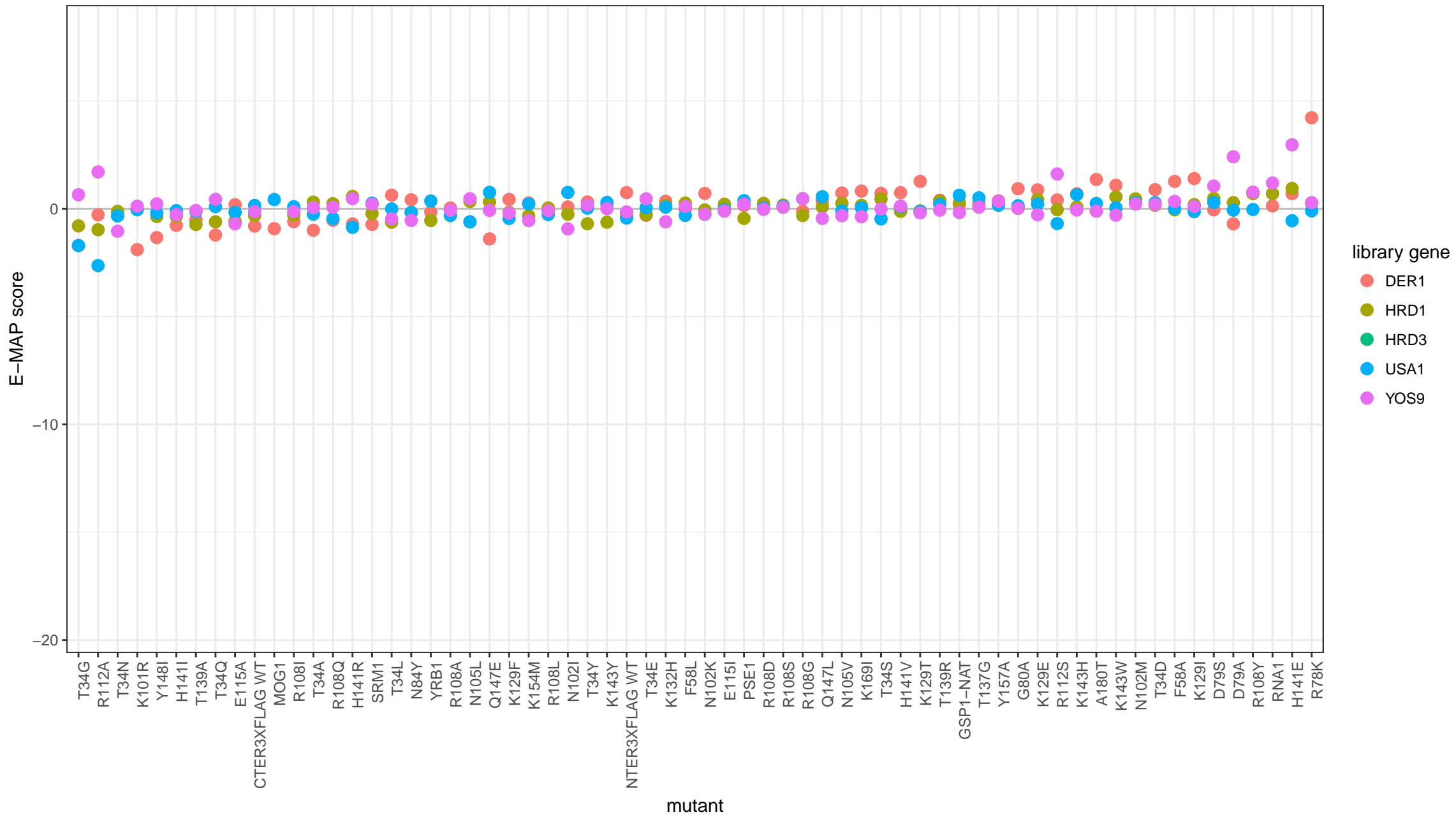
- LSM2
- LSM3
- LSM4
- LSM5
- LSM6
- LSM7
- LSM8
- PRP24



ubiquitin conjugating enzyme complex



ubiquitin ligase ERAD-L complex



Ubp3p/Bre5p complex

E-MAP score

-20

-10

0

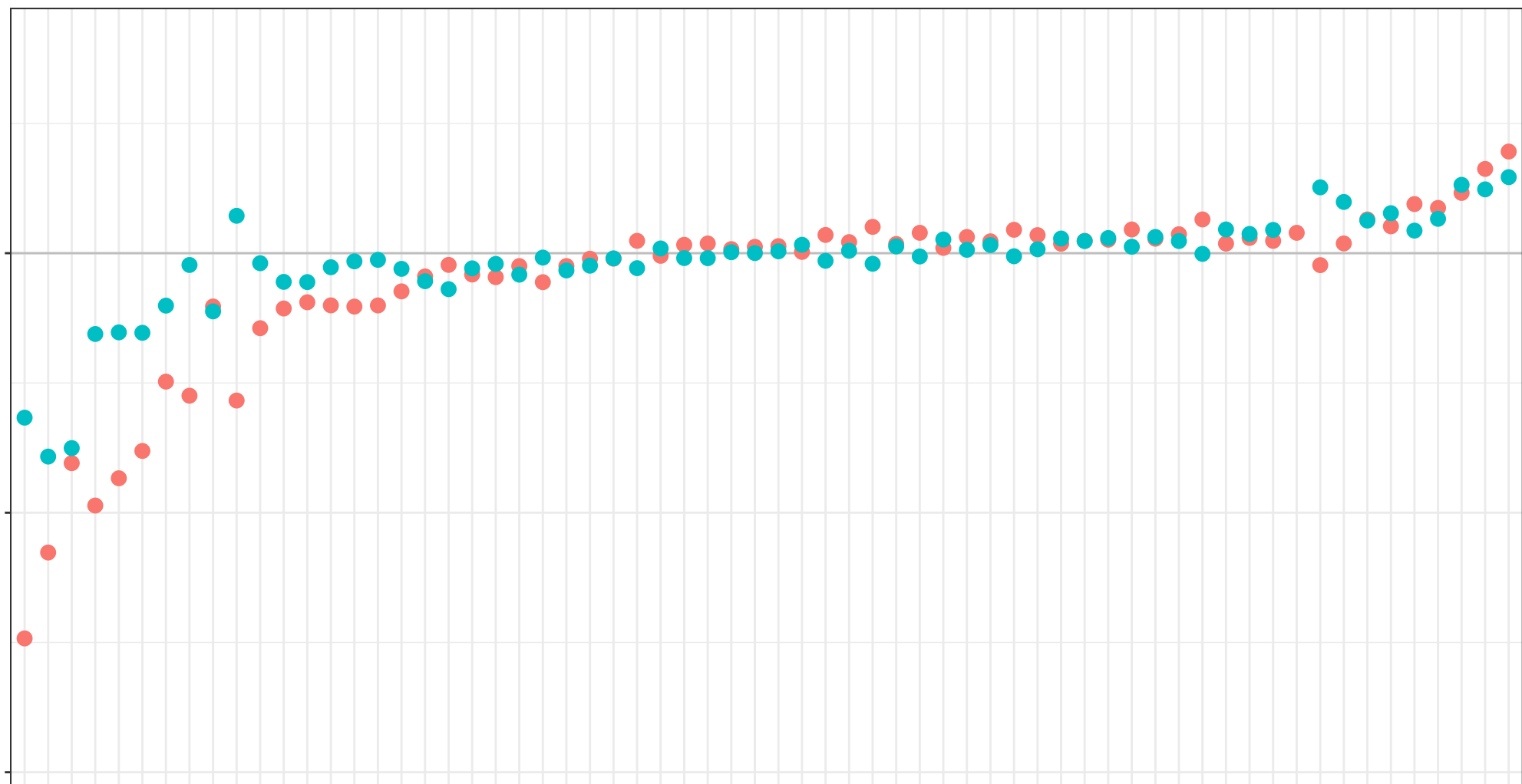
D79S
D79A
T34G
H141E
T34Q
Y157A
H141I
T34E
K129E
R78K
Q147E
H141V
RNA1
K129F
T34A
YRB1
R108Y
Y148I
R108A
G80A
K129T
N84Y
K101R
K143Y
K132H
A180T
T137G
K143W
PSE1
GSP1-NAT
K129I
F58L
N105V
N102K
N105L
T34L
T34N
E115A
T34S
N102I
K154M
T34D
R108G
K169I
R108D
F58A
R108S
T139A
K143H
T34Y
R108Q
Q147L
E115I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

mutant

library gene

BRE5

UBP3



Ume6p/Ime1p complex

E-MAP score

0

-10

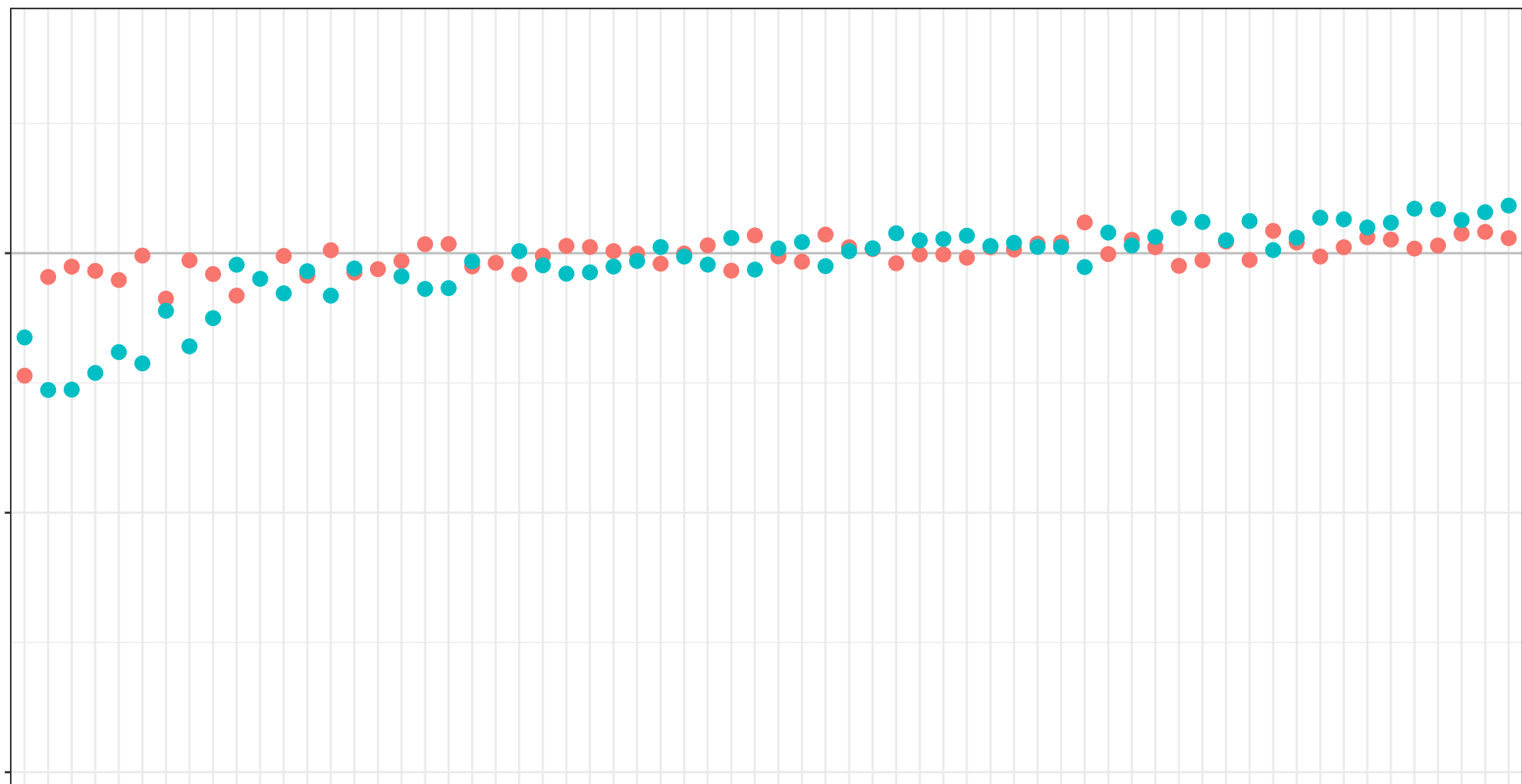
-20

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

mutant

library gene

IME1
UME6



UTP C complex

E-MAP score

-20

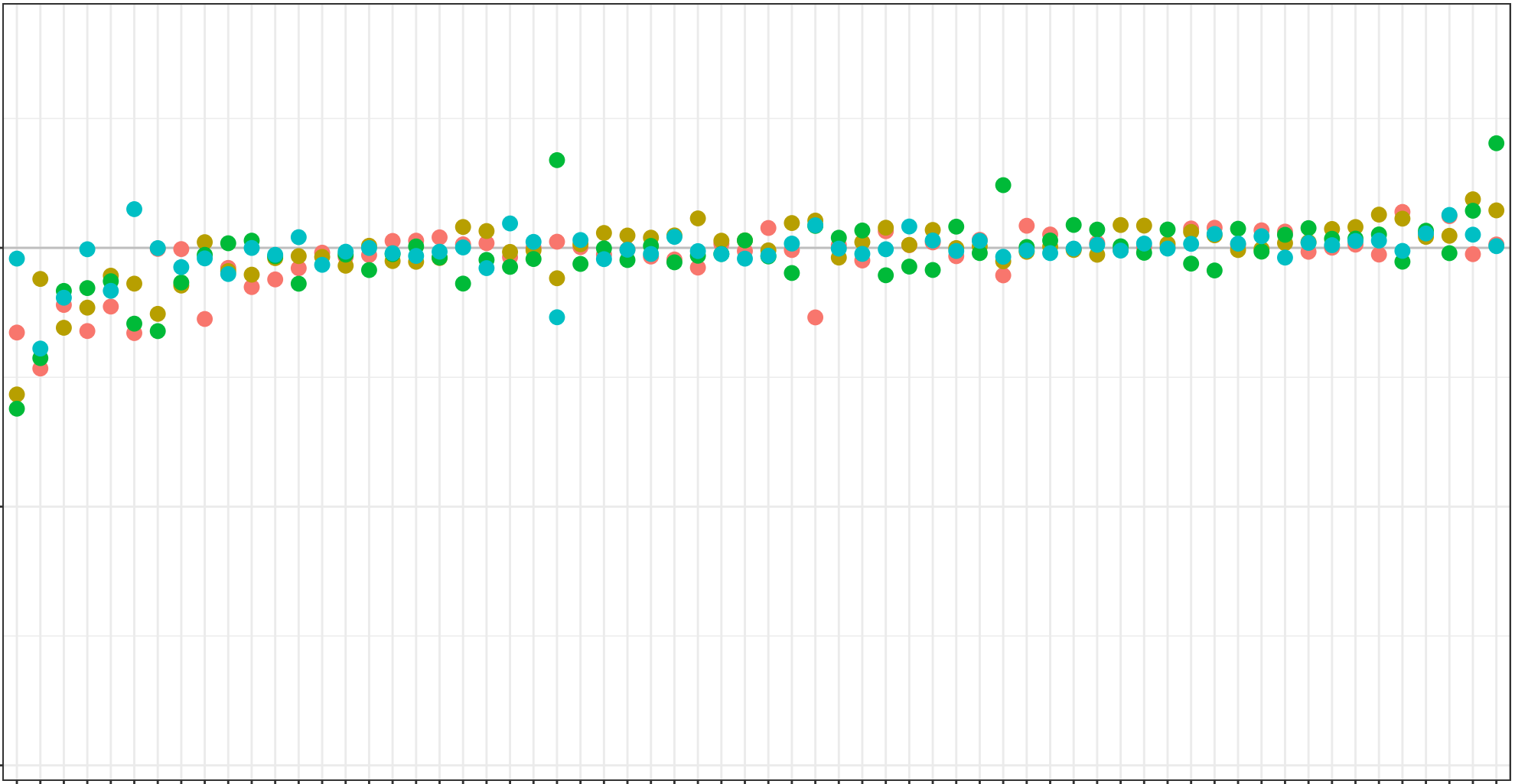
-10

0

H141E D79A H141R R112A T34Q R112S NTER3XFLAG WT R108Y D79S Y157A T34E H141I K101R SRM1 Q147E Y148I N102I T34S E115I R108Q MOG1 R108G T137G R78K R108L F58L CTER3XFLAG WT H141V YRB1 T34N T34L Q147L Q169I K154M RNA1 K143Y R108D N84Y R108A T139A A180T PSE1 T34G N105V T34D K129F N102K E115A T139R T34A R108S N102M K129I F58A T34Y K129E GSP1-NAT K143W K143H K132H K129T R108I G80A N105L

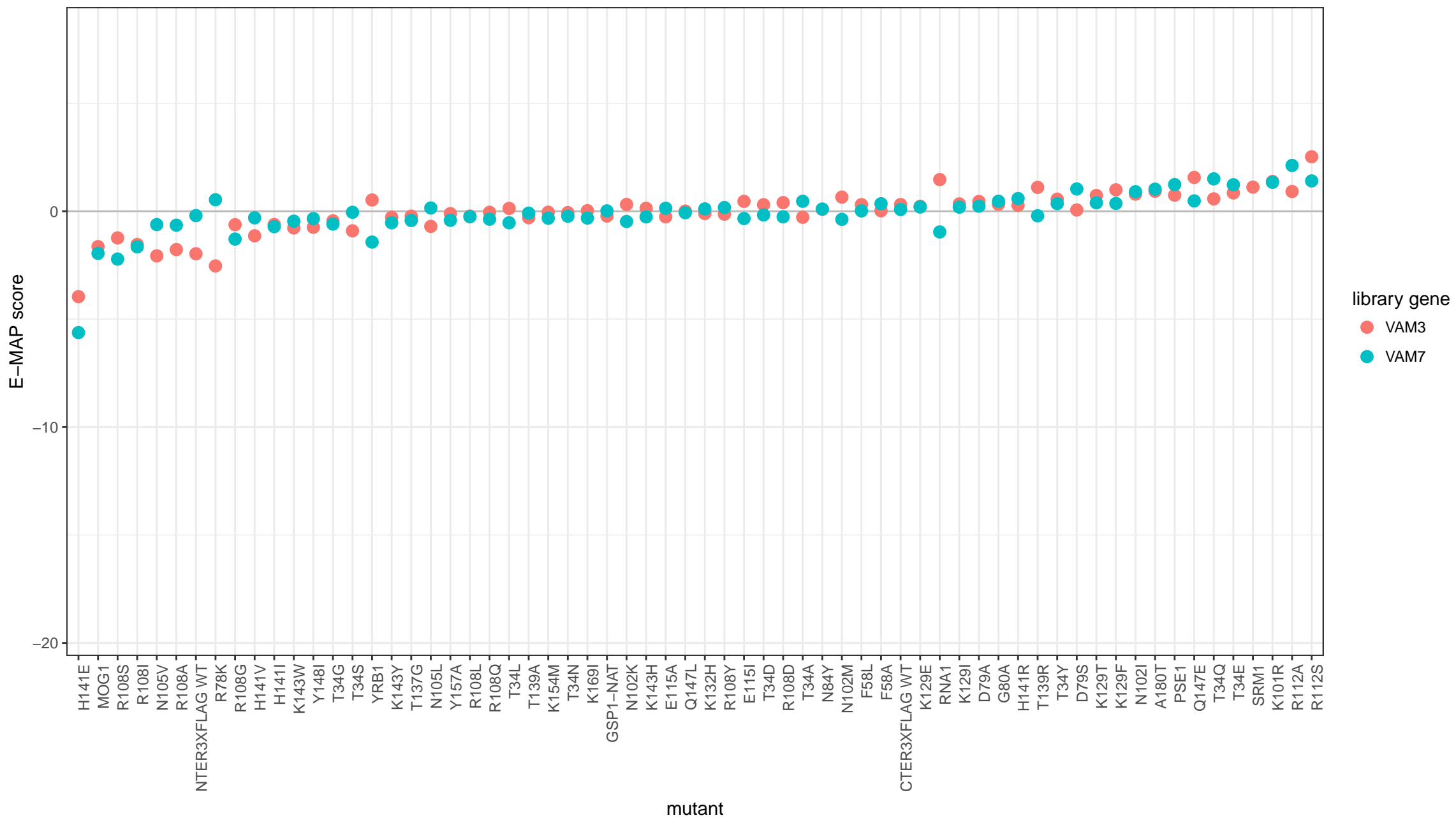
library gene

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



mutant

Vam3p/Vam7 vacuolar tSNARE complex



vitamin metabolic process

E-MAP score

0

-10

-20

R108Q R108G R108L R141R R108Y R141I R105L N105L NTER3XFLAG WT R108A Y148I R108S K132H R112A N102K K154M RNA1 N102I R108I K143W K143H K143H GSP1-NAT T139A F58A H141V T34S T137G E115A N102M K169I F58L K143Y T34L K129E K129I PSE1 T34N K129T T34Y N105V K129F A180T SRM1 CTER3XFLAG WT N84Y T34A T139R R108D T34E E115I K101R T34D Q147L YRB1 T34Q Q147E G80A Y157A R112S H141E R78K D79S T34G D79A MOG1

library gene

PET18

SPE3

SPE4

THI3

THI6

mutant

zeta DNA polymerase complex

E-MAP score

0

-10

-20

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

mutant

library gene

REV3
REV7

