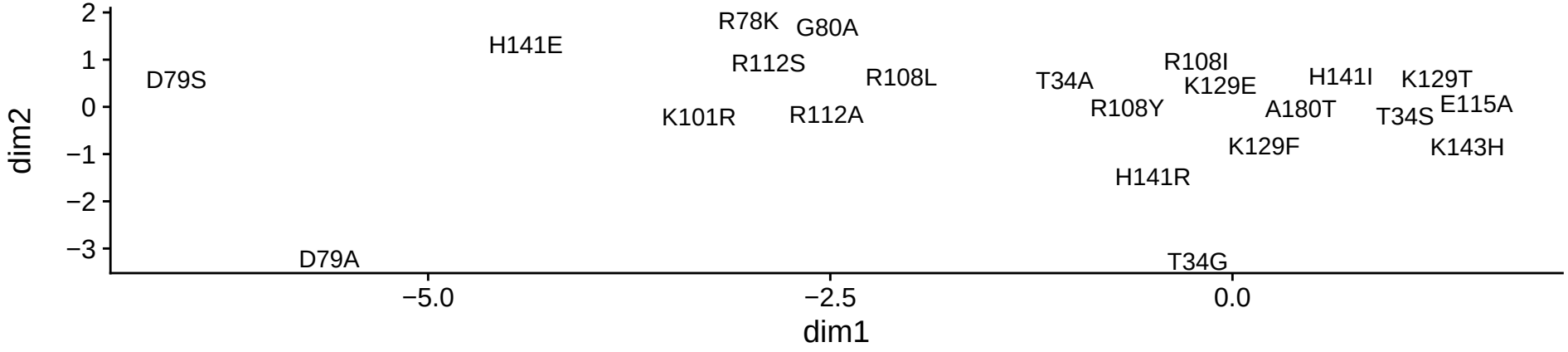
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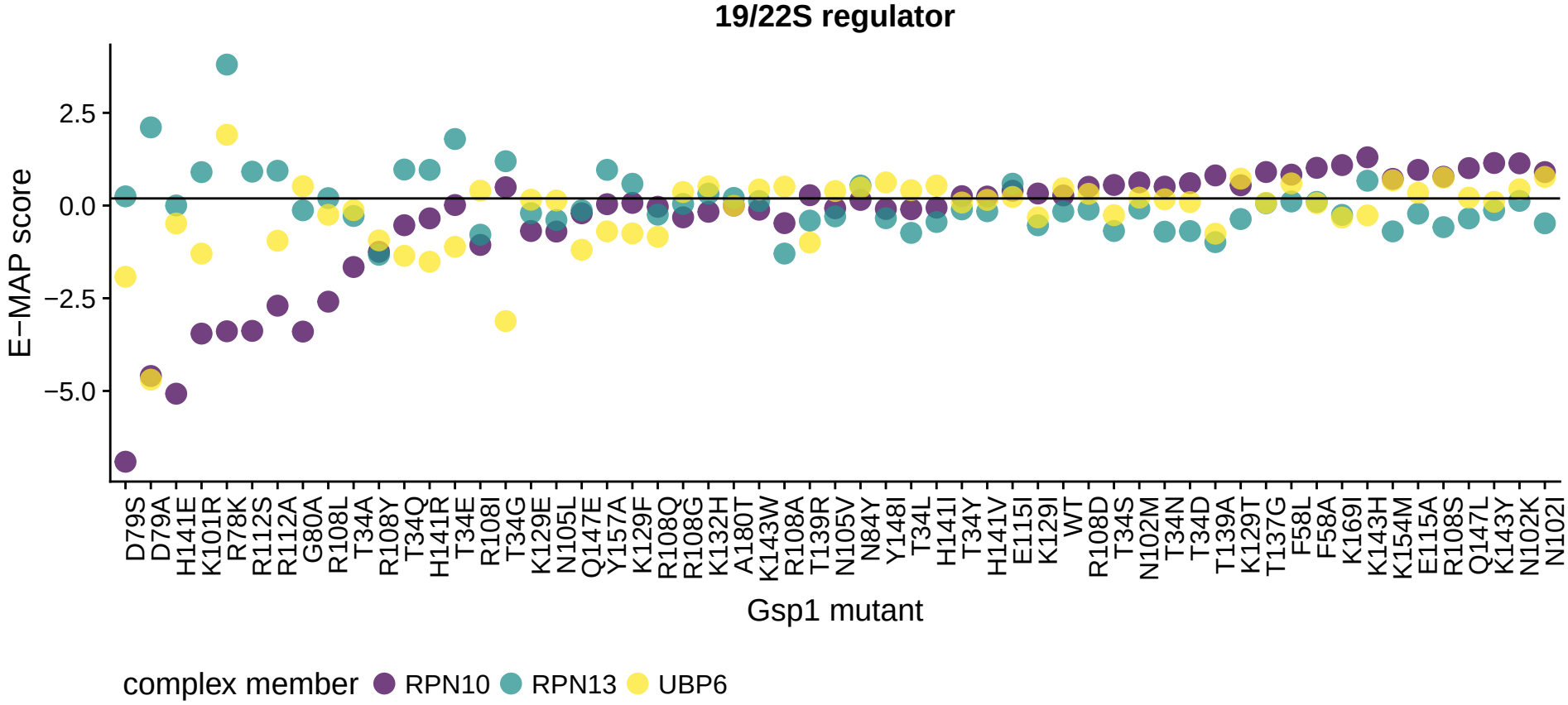
dim1
2
1
0
−1
−2
−3
−5.0
−2.5
0.0
D79S
D79A
H141E
R78K
G80A
R112S
R108L
K101R
R112A
T34A
R108I
K129E
H141I
K129T
R108Y
A180T
T34S
E115A
K129F
K143H
H141R
T34G


19/22S regulator
E−MAP score
2.5
0.0
−2.5
−5.0
D79S
D79A
H141E
K101R
R78K
R112S
R112A
G80A
R108L
T34A
R108Y
T34Q
H141R
T34E
R108I
T34G
K129E
N105L
Q147E
Y157A
K129F
R108Q
R108G
K132H
A180T
K143W
R108A
T139R
N105V
N84Y
Y148I
T34L
H141I
T34Y
H141V
E115I
K129I
WT
R108D
T34S
N102M
T34N
T34D
T139A
K129T
T137G
F58L
F58A
K169I
K143H
K154M
E115A
R108S
Q147L
K143Y
N102K
N102I
Gsp1 mutant
complex member
RPN10
RPN13
UBP6