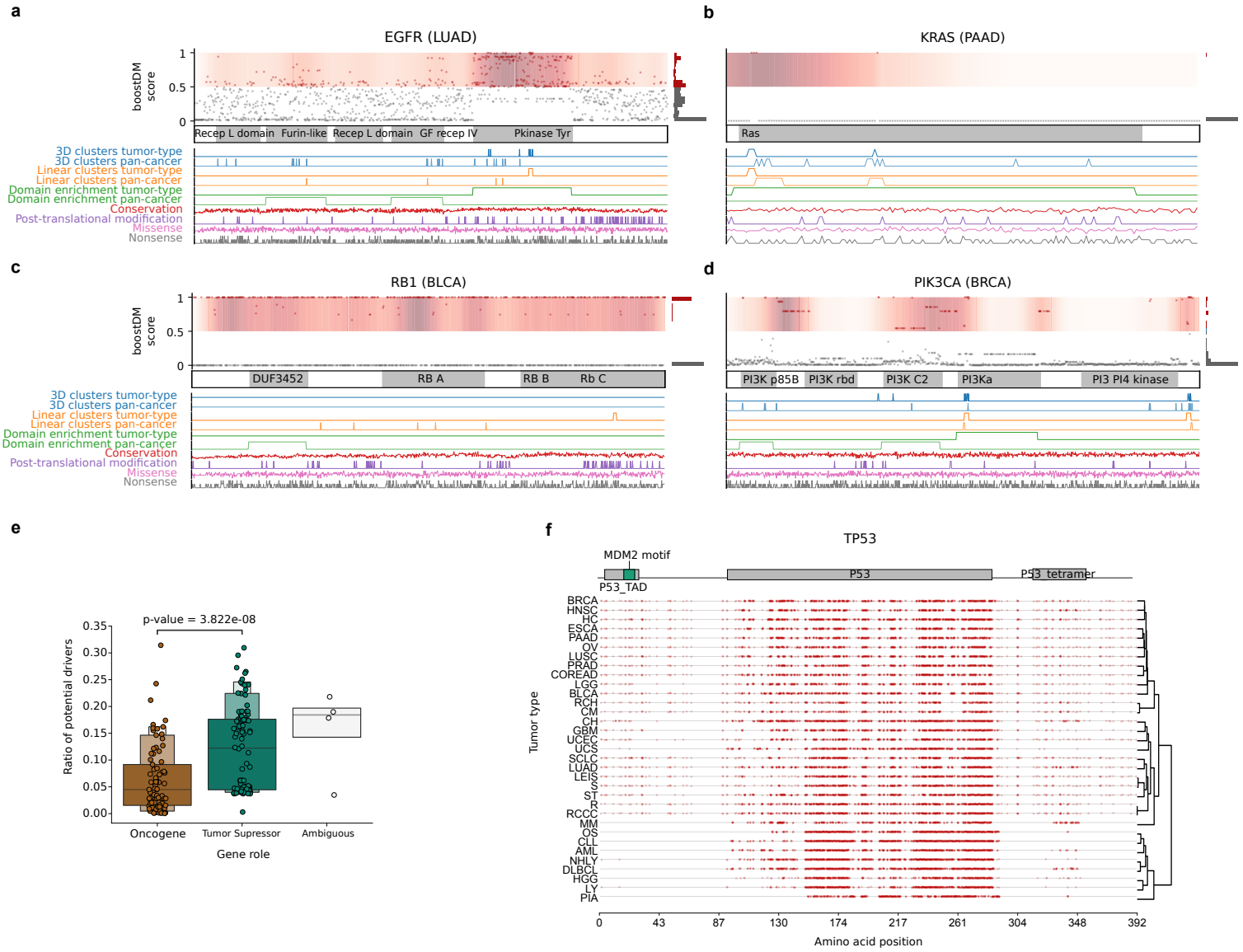
a
EGFR (LUAD)
boostDM score
1
0.5
0
Recep L domain
Furin-like
Recep L domain
GF recep IV
Pkinase Tyr
3D clusters tumor-type
3D clusters pan-cancer
Linear clusters tumor-type
Linear clusters pan-cancer
Domain enrichment tumor-type
Domain enrichment pan-cancer
Conservation
Post-translational modification
Missense
Nonsense
b
KRAS (PAAD)
Ras
c
RB1 (BLCA)
boostDM score
1
0.5
0
DUF3452
RB A
RB B
Rb C
3D clusters tumor-type
3D clusters pan-cancer
Linear clusters tumor-type
Linear clusters pan-cancer
Domain enrichment tumor-type
Domain enrichment pan-cancer
Conservation
Post-translational modification
Missense
Nonsense
d
PIK3CA (BRCA)
PI3K p85B
PI3K rbd
PI3K C2
PI3Ka
PI3 PI4 kinase
e
p-value = 3.822e-08
Ratio of potential drivers
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Oncogene
Tumor Supressor
Ambiguous
Gene role
f
TP53
MDM2 motif
P53_TAD
P53
P53_tetramer
Tumor type
BRCA
HNSC
HC
ESCA
PAAD
OV
LUSC
PRAD
COREAD
LGG
BLCA
RCH
CM
CH
GBM
UCEC
UCS
SCLC
LUAD
LEIS
S
ST
R
RCCC
MM
OS
CLL
AML
NHLY
DLBCL
HGG
LY
PIA
0
43
87
130
174
217
261
304
348
392
Amino acid position