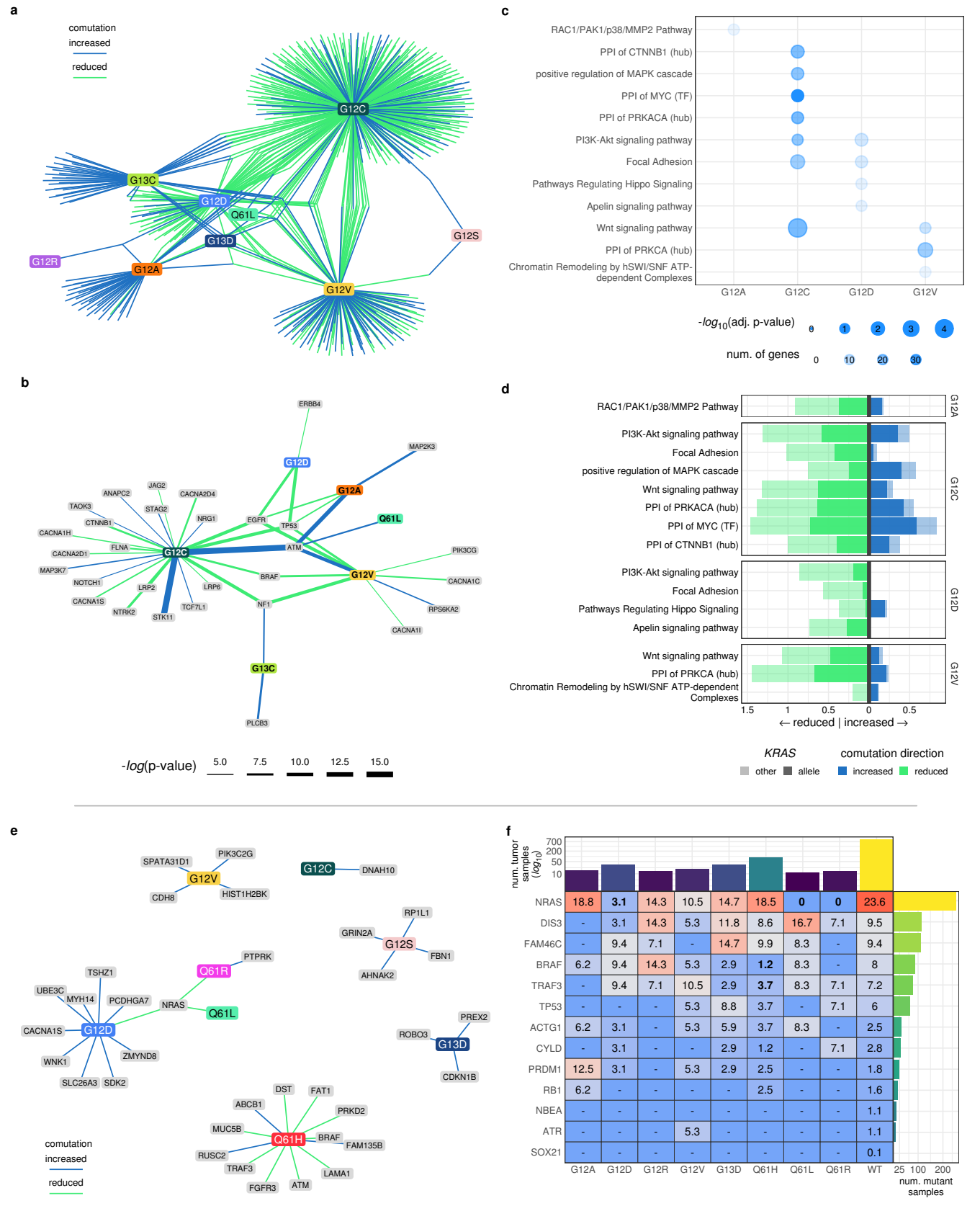
a
comutation
increased
reduced
G12C
G13C
G12D
Q61L
G13D
G12S
G12R
G12A
G12V
b
ERBB4
MAP2K3
G12D
G12A
Q61L
JAG2
ANAPC2
CACNA2D4
TAOK3
STAG2
NRG1
EGFR
TP53
CTNNB1
CACNA1H
FLNA
G12C
ATM
PIK3CG
CACNA2D1
MAP3K7
BRAF
G12V
CACNA1C
NOTCH1
LRP2
LRP6
CACNA1S
NF1
RPS6KA2
NTRK2
TCF7L1
STK11
CACNA1I
G13C
PLCB3
-log(p-value)
5.0
7.5
10.0
12.5
15.0
c
RAC1/PAK1/p38/MMP2 Pathway
PPI of CTNNB1 (hub)
positive regulation of MAPK cascade
PPI of MYC (TF)
PPI of PRKACA (hub)
PI3K-Akt signaling pathway
Focal Adhesion
Pathways Regulating Hippo Signaling
Apelin signaling pathway
Wnt signaling pathway
PPI of PRKCA (hub)
Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes
G12A
G12C
G12D
G12V
-log10(adj. p-value)
0
1
2
3
4
num. of genes
0
10
20
30
d
RAC1/PAK1/p38/MMP2 Pathway
G12A
PI3K-Akt signaling pathway
Focal Adhesion
positive regulation of MAPK cascade
Wnt signaling pathway
PPI of PRKACA (hub)
PPI of MYC (TF)
PPI of CTNNB1 (hub)
G12C
PI3K-Akt signaling pathway
Focal Adhesion
Pathways Regulating Hippo Signaling
Apelin signaling pathway
G12D
Wnt signaling pathway
PPI of PRKCA (hub)
Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes
G12V
1.5
1
0.5
0
0.5
← reduced | increased →
KRAS
other
allele
comutation direction
increased
reduced
e
SPATA31D1
PIK3C2G
G12V
CDH8
HIST1H2BK
G12C
DNAH10
RP1L1
GRIN2A
G12S
FBN1
AHNAK2
PTPRK
Q61R
TSHZ1
UBE3C
MYH14
PCDHGA7
NRAS
Q61L
CACNA1S
G12D
WNK1
ZMYND8
SLC26A3
SDK2
PREX2
ROBO3
G13D
CDKN1B
DST
FAT1
ABCB1
PRKD2
MUC5B
Q61H
BRAF
FAM135B
RUSC2
TRAF3
LAMA1
FGFR3
ATM
comutation
increased
reduced
f
num. tumor samples (log10)
700
200
50
10
NRAS 18.8 3.1 14.3 10.5 14.7 18.5 0 0 23.6
DIS3 - 3.1 14.3 5.3 11.8 8.6 16.7 7.1 9.5
FAM46C - 9.4 7.1 - 14.7 9.9 8.3 - 9.4
BRAF 6.2 9.4 14.3 5.3 2.9 1.2 8.3 - 8
TRAF3 - 9.4 7.1 10.5 2.9 3.7 8.3 7.1 7.2
TP53 - - - 5.3 8.8 3.7 - 7.1 6
ACTG1 6.2 3.1 - 5.3 5.9 3.7 8.3 - 2.5
CYLD - 3.1 - - 2.9 1.2 - 7.1 2.8
PRDM1 12.5 3.1 - 5.3 2.9 2.5 - - 1.8
RB1 6.2 - - - - 2.5 - - 1.6
NBEA - - - - - - - - 1.1
ATR - - - 5.3 - - - - 1.1
SOX21 - - - - - - - - 0.1
G12A G12D G12R G12V G13D Q61H Q61L Q61R WT
25 100 200
num. mutant samples