

**a** **COAD**

Diagram illustrating the network structure of mutations in COAD (Colon Adenocarcinoma). The network shows nodes representing mutations, connected by lines indicating interactions. The nodes are color-coded and labeled: G61L (green), G12A (orange), G12S (pink), G12C (dark blue), G12D (blue), G12V (yellow), A146T (olive), G13D (dark blue), and A146V (purple). The network is divided into two main clusters: a green cluster (G61L, G12S, G12C, G12V) and a blue cluster (G12A, G12D, G13D, A146V). The green cluster is connected to the blue cluster by a few lines. The green cluster is labeled 'increased' and the blue cluster is labeled 'reduced'.

computation

increased

reduced

Network diagram showing interactions between various genes and proteins. The nodes are colored by their  $-\log(p\text{-value})$  and labeled with their gene names. The diagram shows a central cluster of nodes including G12V, G12D, G12C, G13D, and A146V, with other nodes like CACNA1E, Q61H, LRP2, SMAD3, G12S, CTNNB1, ABCC1, SMC1B, GLI3, ARHGAP5, SMO, TP53, APC, NRAS, PIK3CA, BRAF, TTN, RICTOR, MAP3K1, and PORCN also connected to the central cluster.

**COAD**

- PPI of YWHAZ (hub)
- Hedgehog signaling pathway
- Focal Adhesion
- Beta-catenin phosphorylation cascade
- PPI of SMAD2 (TF)
- PI3K-Akt signaling pathway
- Targets of ATM (kinase)
- Hippo signaling pathway
- Wnt signaling pathway
- mTOR signaling pathway
- Developmental Biology
- Apoptosis
- Cellular senescence

**LUAD**

- 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

**PAAD**

- Wnt signaling pathway
- PPI of MYC (TF)
- Targets of PRKACA (kinase)
- calcium ion transport
- PPI of SMAD2 (TF)
- PPI of SMAD3 (TF)
- TGF-beta Signaling Pathway
- PPI of SMAD1 (TF)

num. of genes: 10, 20, 30

$-\log_{10}(\text{adj. p-value})$ : 2, 3, 4

**e**

4  
2  
0

KRAS G12D 8%  
KRAS other 22%  
SDK1 8%  
SCN10A 2%  
TRPM2 2%  
DICER1 2%

0 200 400

missense    frame shift del.    frame shift ins.    nonsense    in-frame ins.    splice site

	G12A	G12D	G12R	G12V	G13D	Q61H	Q61L	Q61R	WT
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