

a **COAD**

Diagram illustrating the network structure of mutations in COAD (Colon Adenocarcinoma). The network shows nodes representing mutations, connected by edges. The nodes are color-coded based on the computation value:

- Increased computation (Green):** G61L, G12S, G12C, G12V, G12D.
- Reduced computation (Blue):** G12A, A146T, A146V, G13D.

The legend indicates that green lines represent increased computation and blue lines represent reduced computation. The network shows a complex interplay of these mutations, with G12D and G13D being highly connected nodes.

Network diagram showing gene-gene interactions. Nodes are colored by $-\log(p\text{-value})$ and connected by blue lines. Key nodes include G12V, G12D, G12C, G13D, and G146T. A color scale at the bottom indicates $-\log(p\text{-value})$ from 5.0 to 15.0.

Pathway	G12D	G12V	G13D
PPI of YWHAZ (hub)	10	0	0
Hedgehog signaling pathway	2	0	0
Focal Adhesion	10	0	0
Beta-catenin phosphorylation cascade	2	0	0
PPI of SMAD2 (TF)	10	0	0
PI3K-Akt signaling pathway	10	0	0
Targets of ATM (kinase)	10	0	0
Hippo signaling pathway	0	5	0
Wnt signaling pathway	0	3	0
mTOR signaling pathway	0	3	5
Developmental Biology	10	0	5
Apoptosis	0	0	2
Cellular senescence	0	0	1

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Biological Pathway	Enrichment Level (Relative)
RAC1/PAK1/p38/MMP2 Pathway	Low
PPI of CTNNB1 (hub)	Medium
positive regulation of MAPK cascade	Medium
PPI of MYC (TF)	High
PPI of PRKACA (hub)	Medium
PI3K-Akt signaling pathway	Medium-Low
Focal Adhesion	Medium-Low
Pathways Regulating Hippo Signaling	Low
Apelin signaling pathway	Low
Wnt signaling pathway	High
PPI of PRKCA (hub)	Very High
Chromatin Remodeling by hSWI/ SNF ATP-dependent Complexes	Very Low

Pathway	G12D	G12R	G12V	Q61H
Wnt signaling pathway	2	2	0	0
PPI of MYC (TF)	2	2	0	0
Targets of PRKACA (kinase)	2	0	2	0
calcium ion transport	0	0	4	0
PPI of SMAD2 (TF)	2	0	2	4
PPI of SMAD3 (TF)	0	2	0	4
TGF-beta Signaling Pathway	2	0	0	1
PPI of SMAD1 (TF)	0	0	0	1

Gene	Percentage
KRAS G12D	8%
KRAS other	22%
MAGEC1	6%
AMER1	4%
TGIF1	2%

e

4
2

KRAS G12D 8%

KRAS other 22%

SDK1 8%

SCN10A 2%

TRPM2 2%

DICER1 2%

200 400

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

Figure 1 consists of two panels. The top panel is a heatmap showing the presence (black) or absence (white) of SMAD3, SMAD2, and SMAD1 binding events across 15 genomic regions. The bottom panel is a stacked bar chart showing the distribution of computation events for SMAD3 (red), SMAD2 (yellow), and SMAD1 (blue) across the same 15 genomic regions. The y-axis for the bar chart ranges from 0.00 to 1.00.

Genomic Region	SMAD3 (Red)	SMAD2 (Yellow)	SMAD1 (Blue)
ACVR1B	0.60	0.10	0.30
COL5A1	0.55	0.15	0.30
SMARCA4	0.35	0.35	0.30
TP53	0.28	0.22	0.50
TGFBR1	0.28	0.17	0.55
TGFBR2	0.22	0.33	0.45
ARID1A	0.22	0.28	0.50
SMAD4	0.22	0.25	0.53
APOB	0.15	0.40	0.45
GNAS	0.18	0.32	0.50
BRCA2	0.15	0.25	0.60
DYNCH1	0.00	0.68	0.32
GLI3	0.10	0.28	0.62
SETD2	0.00	0.32	0.68
FLNA	0.15	0.15	0.70