# cBioPortal Tutorial #7: Pathways

Explore genomics data in the context of pathways

Last update: February 15, 2021

### **Tutorial Objectives**

- Motivate viewing cancer genomics data in context of pathways
- Locate cBioPortal Pathways tabs in Results or Patient views
- Introduce pathway view components
- Detail pathway view toolbar operations
  - Save as static images
  - Perform layout
  - Expand query genes [Results view only]
  - Edit pathway with PathwayMapper editor [Results view only]
  - Get help on notation
- Walk through different pathway ranking options [Results view only]
- List technology behind the component

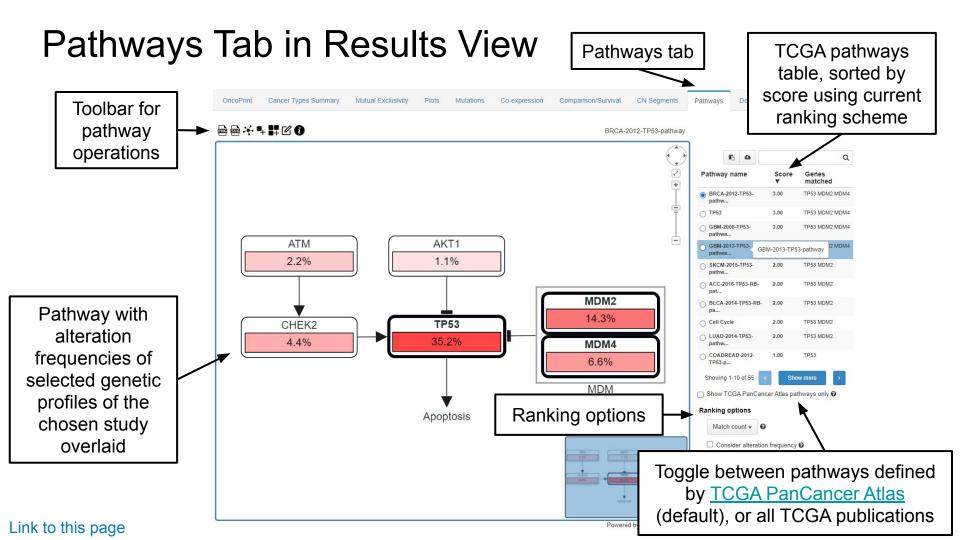
### Motivation for Pathways View

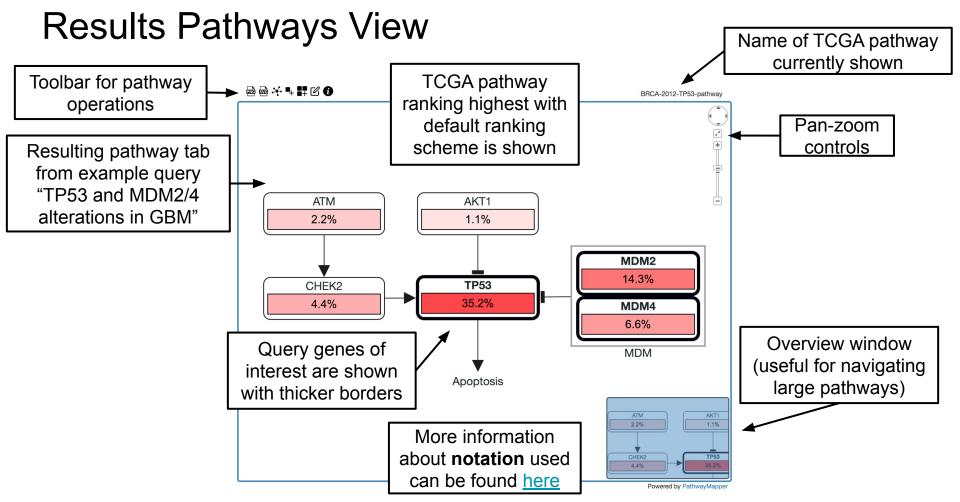
- Genomic alterations in cancer often affect a relatively small number of signaling pathways involved in cell proliferation, cell growth, apoptosis and DNA repair, among others [1]
- The Cancer Genome Atlas (TCGA), an effort to comprehensively characterize genomic alterations in more than 20 tumor types, produced a number of publications with hand-drawn pathways summarizing such alterations [2]
- Pathways tabs in cBioPortal overlay alteration data from your study or patient of interest on TCGA pathways while highlighting your genes of interest.
- The Pathways tab is available in Results view and Patient view

### Pathways Tab in Results View

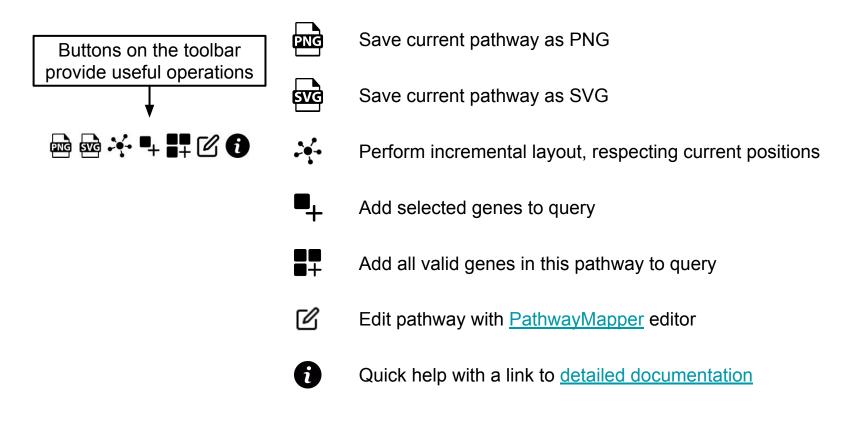
- One may be interested in viewing genetic alterations in a particular study in the context of pathways
- Start with Results view in TP53 and MDM2/4 alterations in "Glioblastoma (TCGA, Nature 2008)" as an example

Not sure how to run a query to get to Results View? Review <u>Tutorial #2: Single Study Query</u>

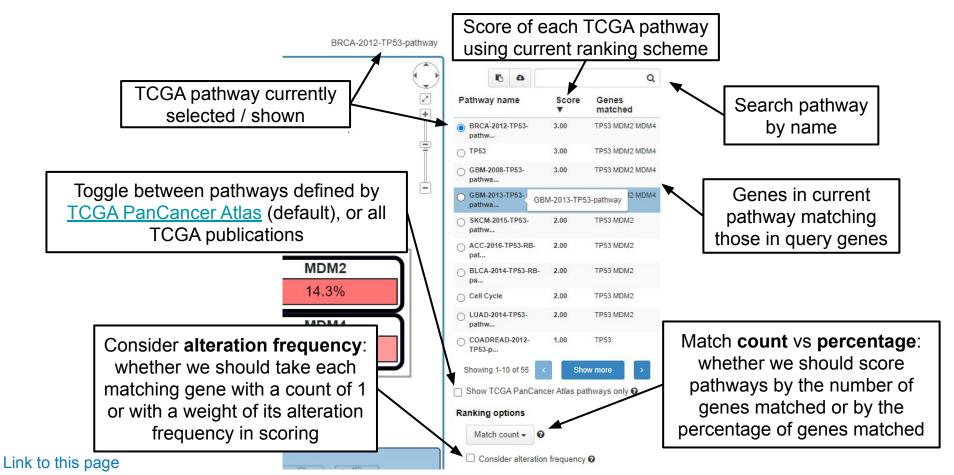




### Results Pathways View Toolbar



### Results Pathways Table & Ranking Options



### Results Pathways View Ranking Options

 When a query gene is in a particular pathway, we consider it "matching".

#### Example:

- Query genes: TP53, MDM2, MDM4
- Pathway: BRCA-2012-TP53-pathway (see on the right)

#### 

#### Match count vs percentage:

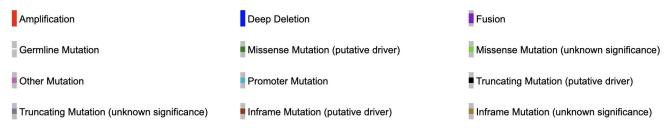
- Count the query genes matching and rank pathways based on this count. The score in our example is 3 as all three genes are in the pathway.
- $\circ$  Take the ratio of query genes matching to total number of genes in the pathway. The score in our example is 3 / 6 = 50%.

#### Consider alteration frequency:

• When checked, each matching gene will not contribute to the score as 1 unit but with its alteration frequency of that gene. The score in our example is 35.2+14.3+6.6 = **56.1**.

### Pathways Tab in Patient View

 One may be interested in viewing following types of genetic alterations of a patient in the context of pathways



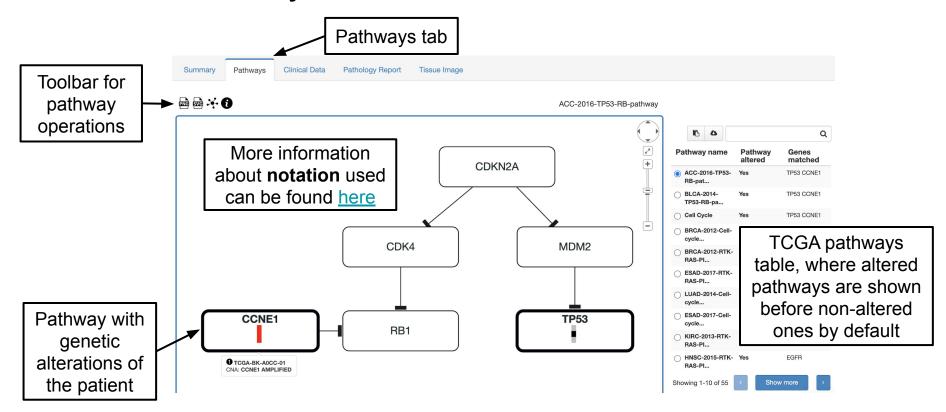
Putative driver and unknown significance annotations are based on data from OncoKB and CancerHotspots.org.

 Start with "Patient view of an endometrial cancer case (TCGA, Nature 2013)" as an example

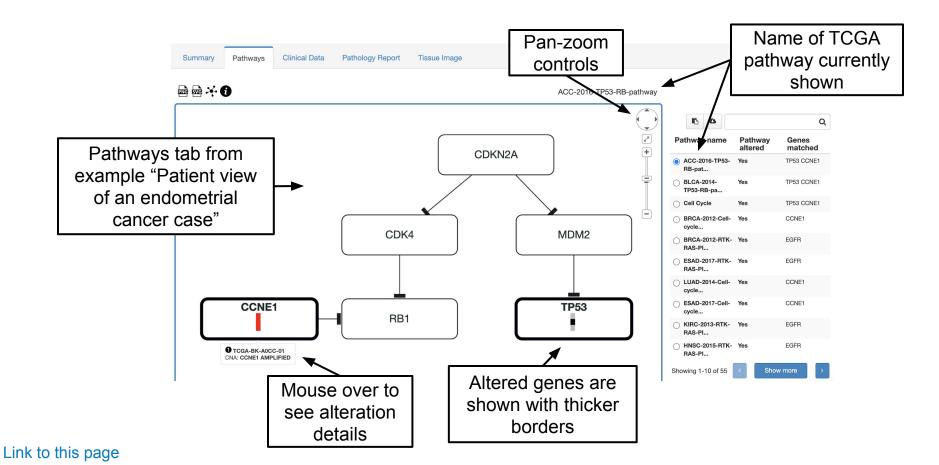


Not sure how to get to patient view? Review Tutorial #3: Patient View

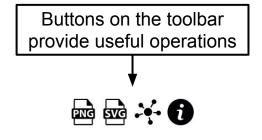
### Patient Pathways View



### Patient Pathways View



### Patient Pathways View





Save current pathway as PNG



Save current pathway as SVG



Perform incremental layout, respecting current positions



Quick help with a link to <u>detailed documentation</u>

Pathways tabs in cBioPortal were built using a viewer only edition of PathwayMapper, which in turn was based on Cytoscape.js, a fully featured graph library in pure JavaScript.

## or email us at:

Questions?

Check out our other tutorials

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