cBioPortal Tutorial #7: Pathways

Explore genomics data in the context of pathways

Last update: January 26, 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*

[1] Bahceci et al. "PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data", Bioinformatics, 2017
[2] The Cancer Genome Atlas Program

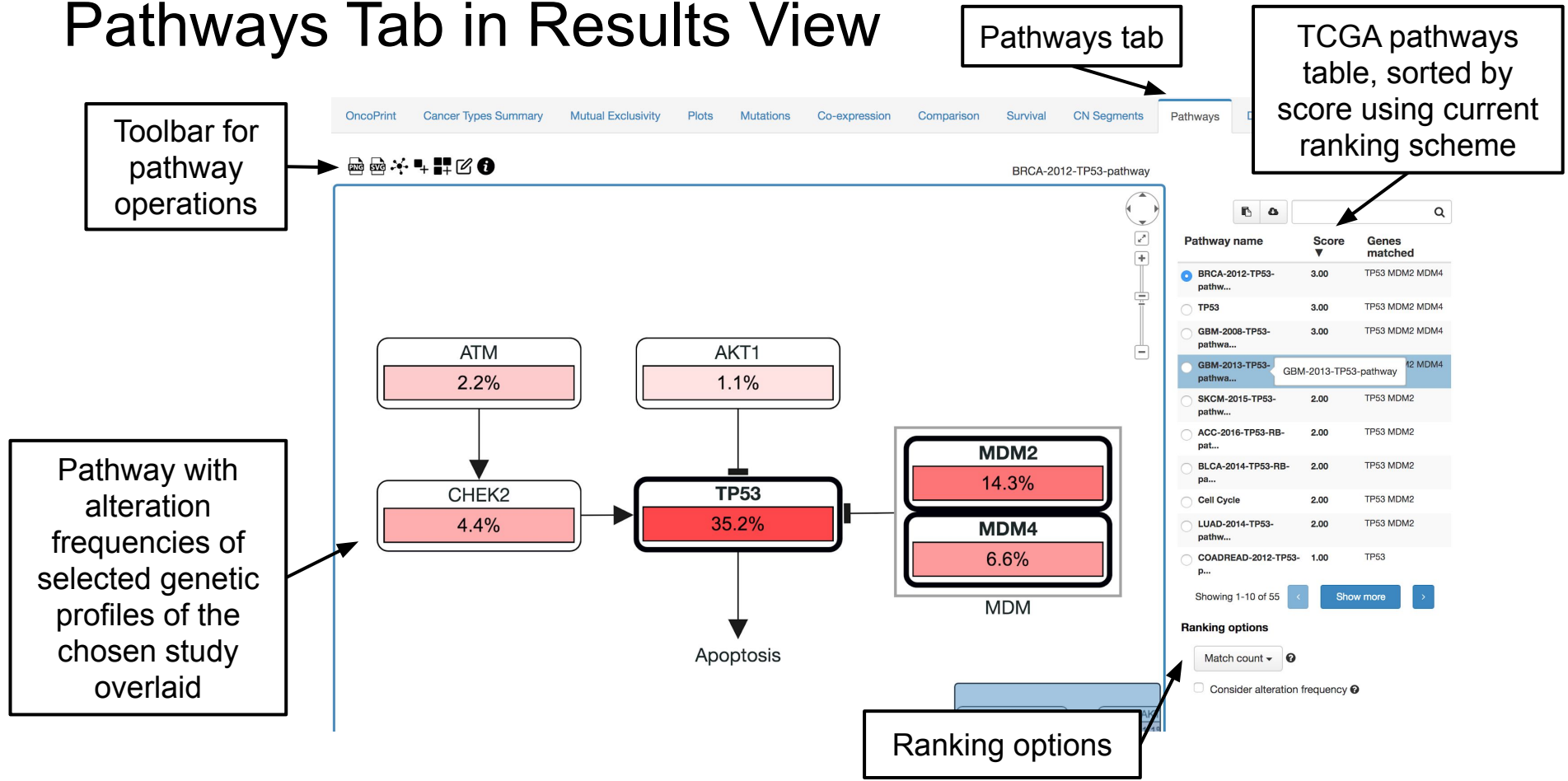
Pathways Tab in Results View

- 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 Tutorial #2: Single Study Query

Link to this page

Pathways Tab in Results View



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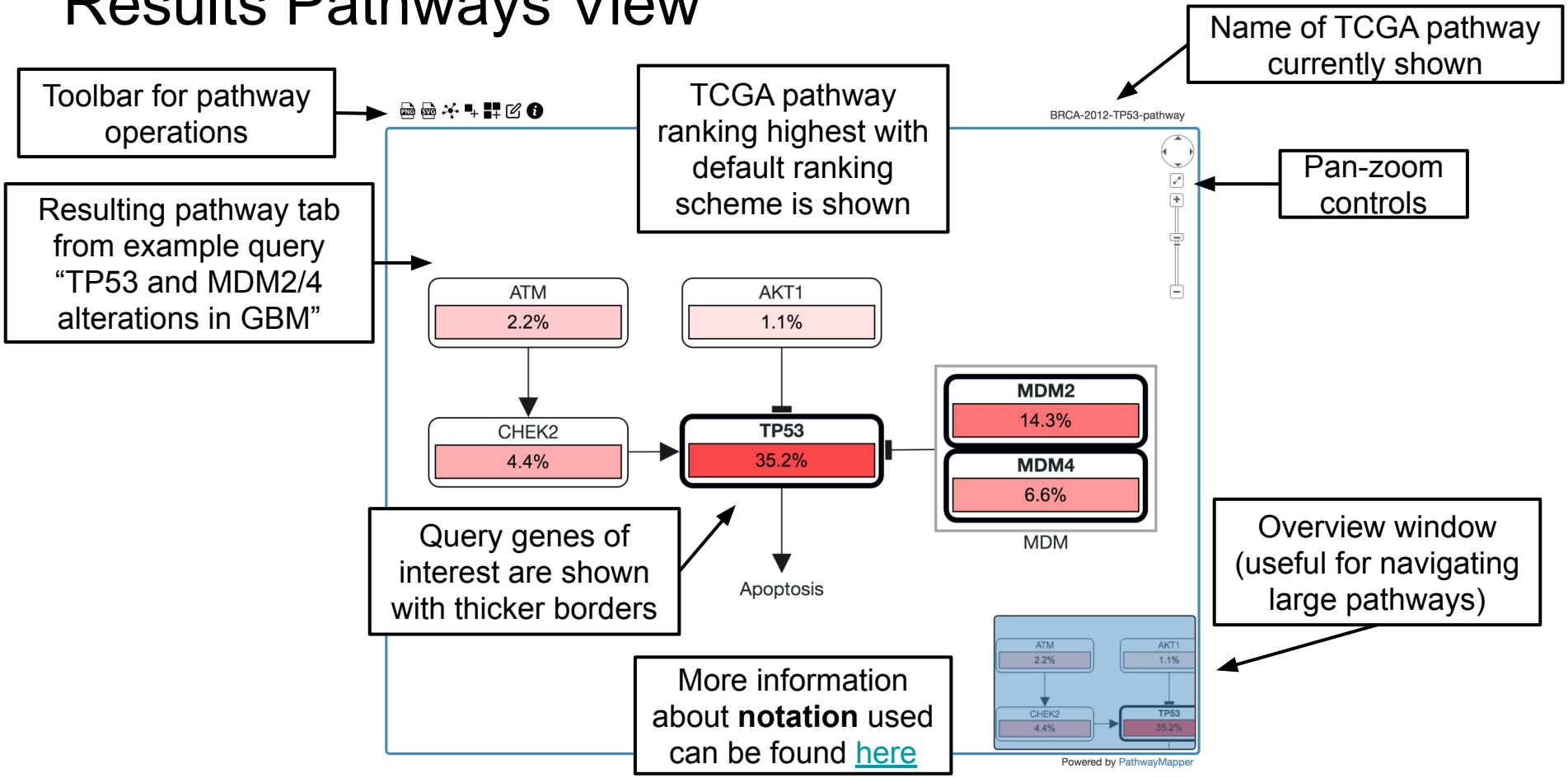
Results Pathways View



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Results Pathways View Toolbar

Buttons on the toolbar provide useful operations

Save current pathway as PNG

Save current pathway as SVG

Perform incremental layout, respecting current positions

Add selected genes to query

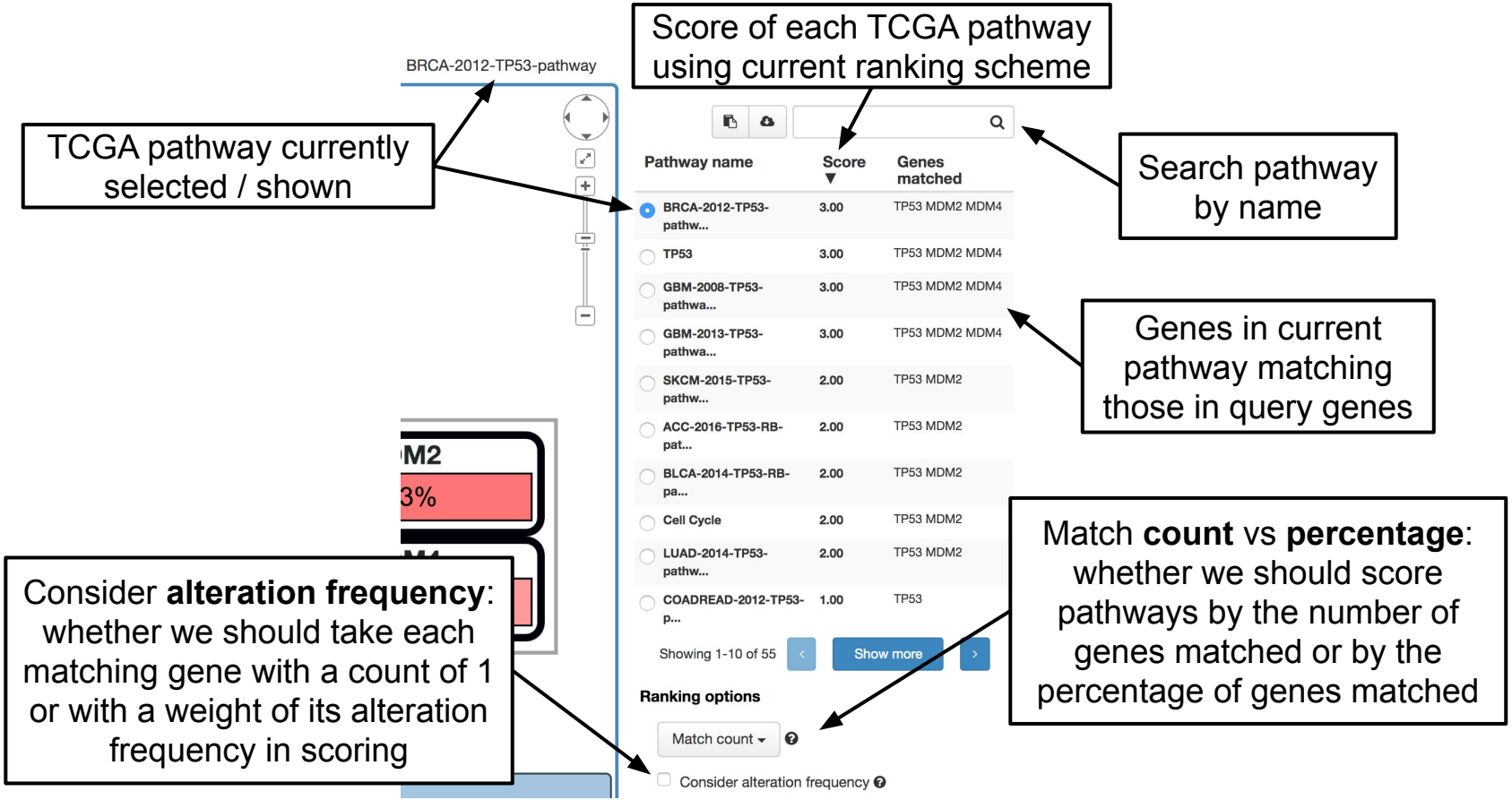
Add all valid genes in this pathway to query

Edit pathway with PathwayMapper editor

Quick help with a link to detailed documentation

Link to this page

Results Pathways Table & Ranking Options



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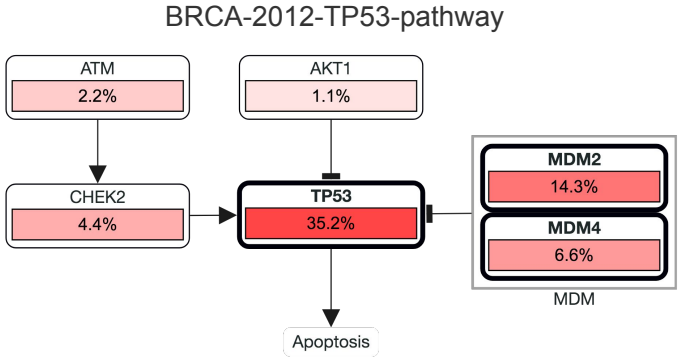
Results Pathways View Ranking Options

- 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.
  - 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**.

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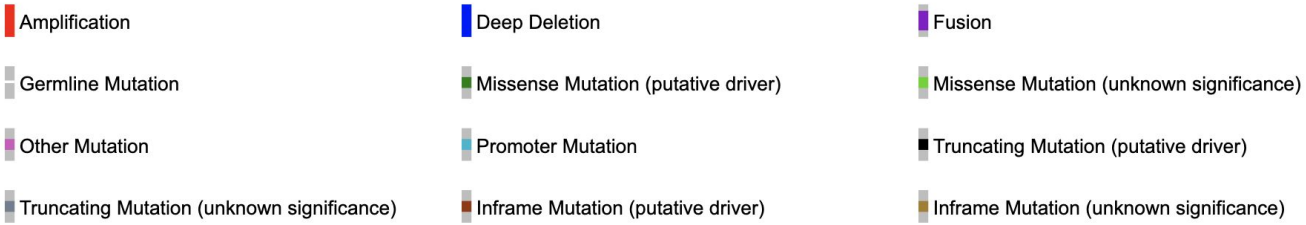
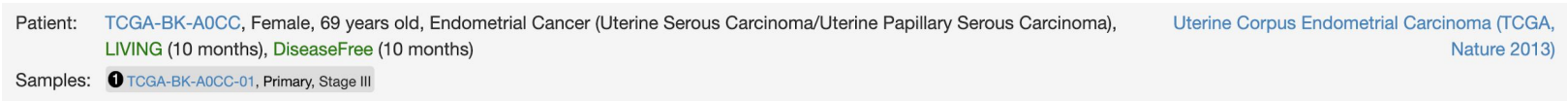
Pathways Tab in Patient View

- 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

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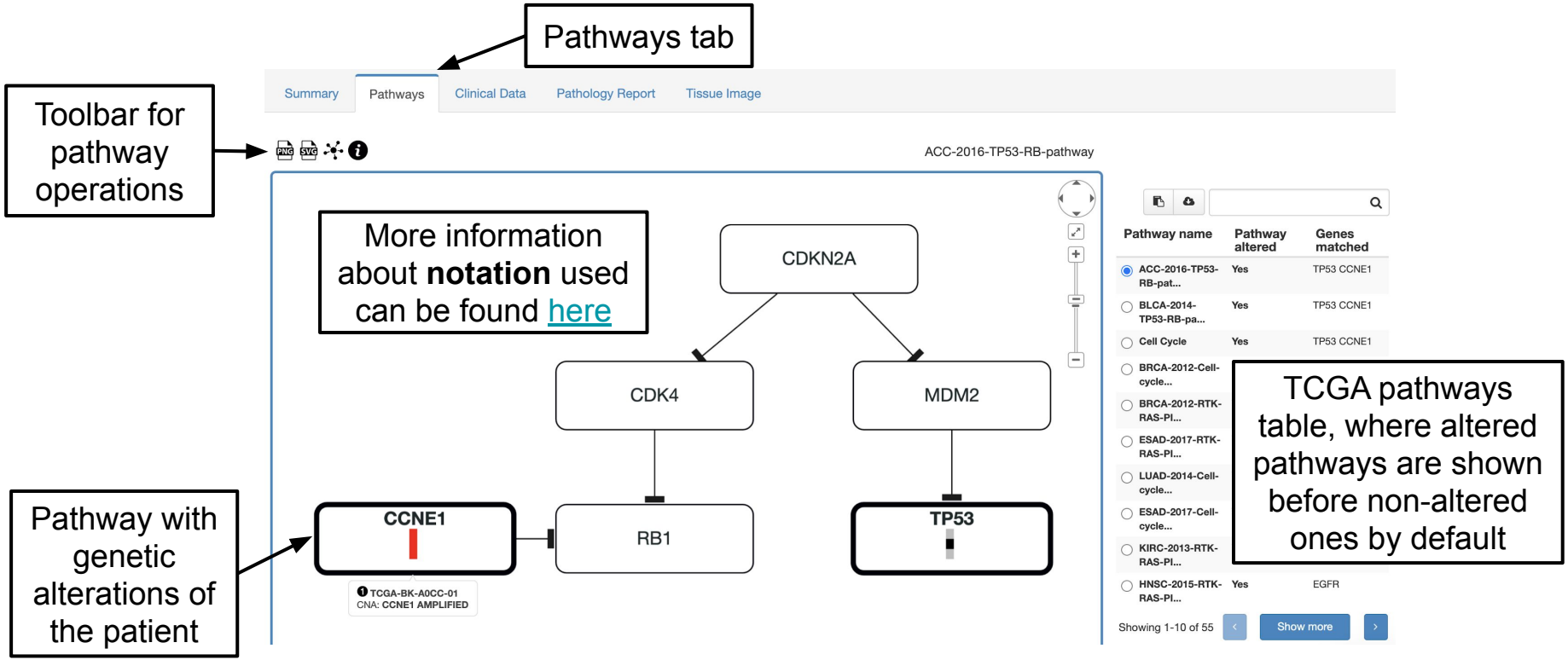
Patient Pathways View



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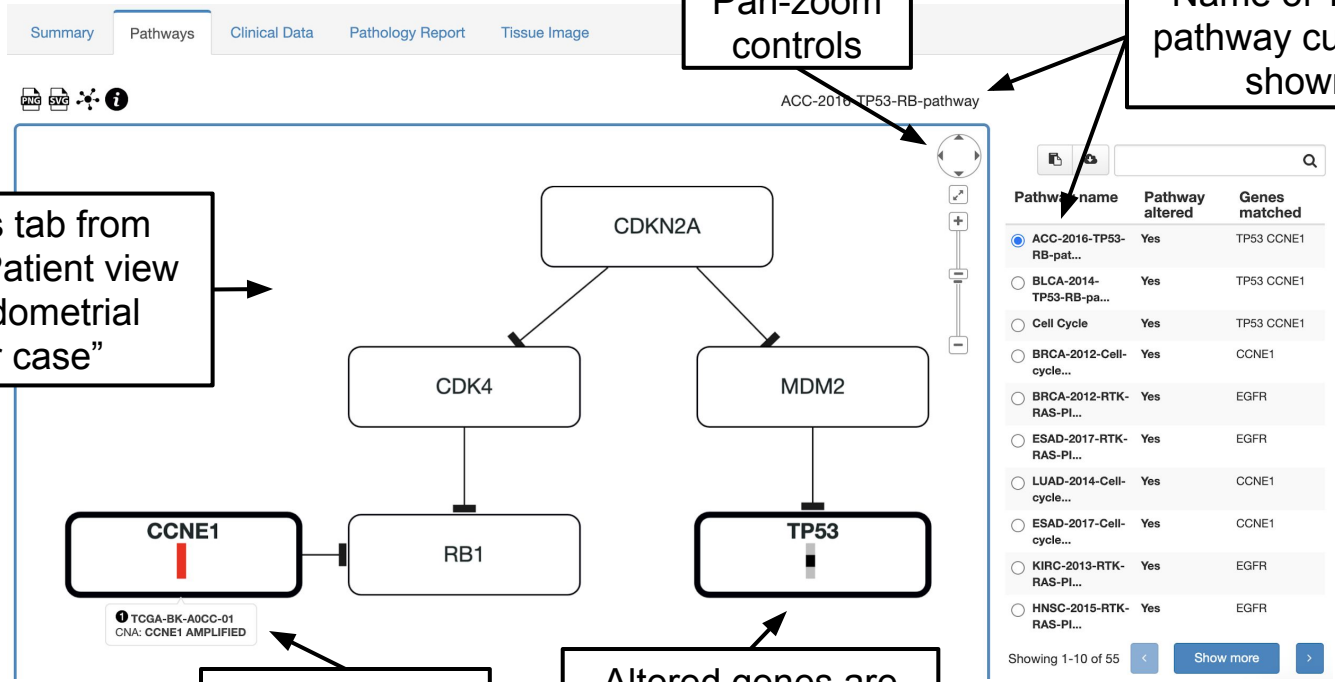
Patient Pathways View



Pan-zoom controls

Name of TCGA pathway currently shown

Pathways tab from example “Patient view of an endometrial cancer case”

Mouse over to see alteration details

Altered genes are shown with thicker borders

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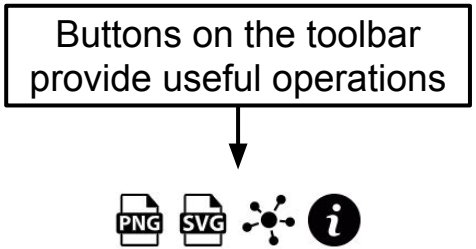
Patient Pathways View



PNG Save current pathway as PNG

SVG Save current pathway as SVG

Perform incremental layout, respecting current positions

Quick help with a link to detailed documentation

Link to this page

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.

Questions?
Check out our other tutorials
or email us at:
cbioportal@googlegroups.com