

cBioPortal Tutorial #7: Pathways

Explore genomics data in the context of pathways

Tutorial Objectives

- Motivate viewing cancer genomics data in context of pathways
- Locate cBioPortal Pathways tab
- Introduce pathway view components
- Detail pathway view toolbar operations
 - Save as static images
 - Perform layout
 - Expand query genes
 - Edit pathway with PathwayMapper editor
 - Get help on notation
- Walk through different pathway ranking options
- 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 tab in cBioPortal allows you to overlay alteration data from your study of interest on TCGA pathways consisting of your genes of interest
- Start with *TP53* and *MDM2/4* alterations in “Glioblastoma (TCGA, Nature 2008)” as an example

[1] Bahceci et al. “[PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data](#)”, Bioinformatics, 2017

[2] [The Cancer Genome Atlas Program](#)

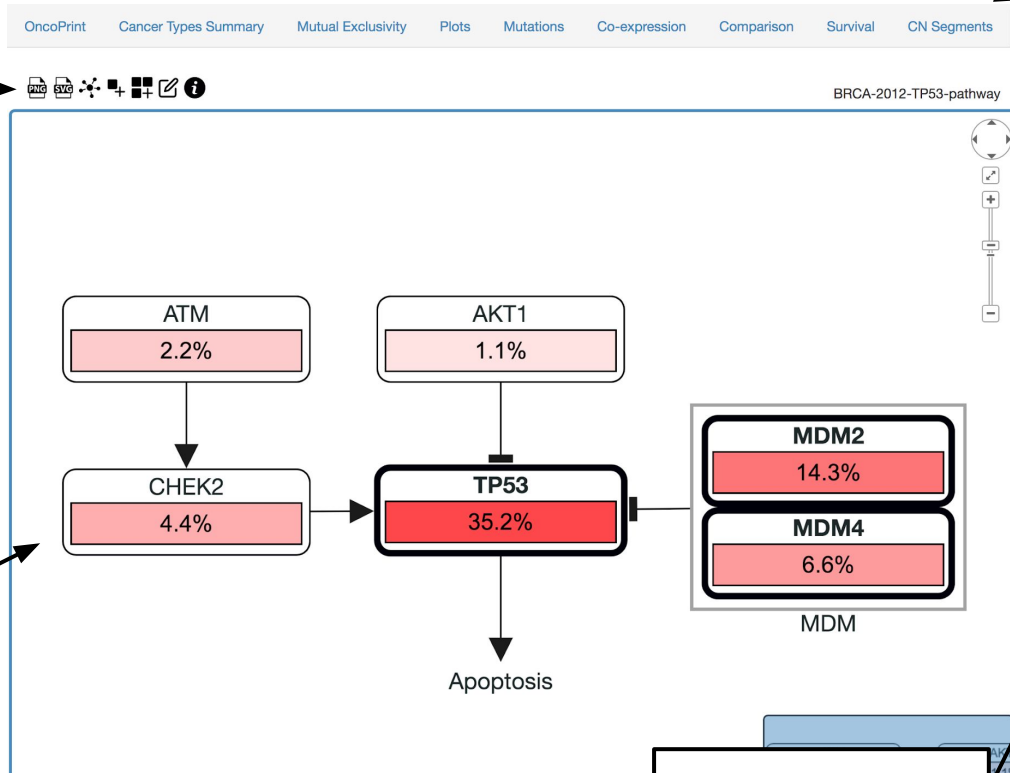
cBioPortal Pathways Tab

Toolbar for pathway operations

Pathways tab

TCGA pathways table, sorted by score using current ranking scheme

Pathway with alteration frequencies of selected genetic profiles of the chosen study overlaid



Ranking options

Pathway name	Score	Genes matched
<input checked="" type="radio"/> BRCA-2012-TP53-pathw...	3.00	TP53 MDM2 MDM4
<input type="radio"/> TP53	3.00	TP53 MDM2 MDM4
<input type="radio"/> GBM-2008-TP53-pathwa...	3.00	TP53 MDM2 MDM4
<input checked="" type="radio"/> GBM-2013-TP53-pathwa...	2.00	TP53 MDM2 MDM4
<input type="radio"/> SKCM-2015-TP53-pathw...	2.00	TP53 MDM2
<input type="radio"/> ACC-2016-TP53-RB-pa...	2.00	TP53 MDM2
<input type="radio"/> BLCA-2014-TP53-RB-pa...	2.00	TP53 MDM2
<input type="radio"/> Cell Cycle	2.00	TP53 MDM2
<input type="radio"/> LUAD-2014-TP53-pathw...	2.00	TP53 MDM2
<input type="radio"/> COADREAD-2012-TP53-p...	1.00	TP53

Showing 1-10 of 55 [Show more](#)

Ranking options

[?](#)

☐ Consider alteration frequency [?](#)

Pathway View

Toolbar for pathway operations



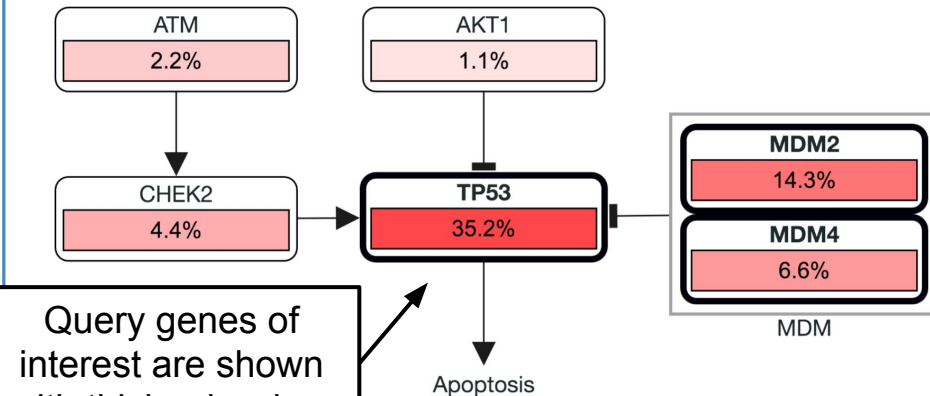
Resulting pathway tab from example query "TP53 and MDM2/4 alterations in GBM"

TCGA pathway ranking highest with default ranking scheme is shown

Name of TCGA pathway currently shown

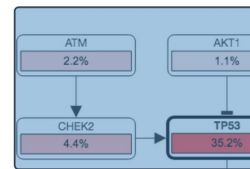
BRCA-2012-TP53-pathway

Pan-zoom controls



More information about **notation** used can be found [here](#)

Overview window (useful for navigating large pathways)



Powered by PathwayMapper

Pathway 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](#)

Pathway Table & Ranking Options

BRCA-2012-TP53-pathway

TCGA pathway currently selected / shown

Score of each TCGA pathway using current ranking scheme

Search pathway by name

Pathway name	Score	Genes matched
<input checked="" type="radio"/> BRCA-2012-TP53-pathw...	3.00	TP53 MDM2 MDM4
<input type="radio"/> TP53	3.00	TP53 MDM2 MDM4
<input type="radio"/> GBM-2008-TP53-pathwa...	3.00	TP53 MDM2 MDM4
<input type="radio"/> GBM-2013-TP53-pathwa...	3.00	TP53 MDM2 MDM4
<input type="radio"/> SKCM-2015-TP53-pathw...	2.00	TP53 MDM2
<input type="radio"/> ACC-2016-TP53-RB-pat...	2.00	TP53 MDM2
<input type="radio"/> BLCA-2014-TP53-RB-pa...	2.00	TP53 MDM2
<input type="radio"/> Cell Cycle	2.00	TP53 MDM2
<input type="radio"/> LUAD-2014-TP53-pathw...	2.00	TP53 MDM2
<input type="radio"/> COADREAD-2012-TP53-p...	1.00	TP53

Genes in current pathway matching those in query genes

Consider **alteration frequency**: whether we should take each matching gene with a count of 1 or with a weight of its alteration frequency in scoring

Match count vs percentage: whether we should score pathways by the number of genes matched or by the percentage of genes matched

Showing 1-10 of 55 [Show more](#)

Ranking options

Match count ☐ Consider alteration frequency ☐

3%

Pathways tab in cBioPortal was 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:

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