

**This slide deck introduces many, but by no means all, features of Next-Generation clustered Heat Maps (NG-CHMs). For concreteness, it's based on:**

- A TCGA mRNA expression (rows) vs. samples (columns) NG-CHM for breast cancer (as part of our TCGA NG-CHM Compendium: <http://bioinformatics.mdanderson.org/TCGA/NGCHMPortal/>)
- The specific map: [http://bioinformatics.mdanderson.org/chm/chm.html?name=tcga\\_rnaseq\\_brca\\_v1.0\\_gene\\_sample&collectionHome=http%3A%2F%2Fbioinformatics.mdanderson.org%2FTCGA%2FNGCHMPortal%3Fview%3D0%26p0DiseaseInput%3Dbrca](http://bioinformatics.mdanderson.org/chm/chm.html?name=tcga_rnaseq_brca_v1.0_gene_sample&collectionHome=http%3A%2F%2Fbioinformatics.mdanderson.org%2FTCGA%2FNGCHMPortal%3Fview%3D0%26p0DiseaseInput%3Dbrca) (too long, sorry)
- If you have a large monitor or two monitors, you might want to open the breast cancer map in a separate window to explore while you're going through the tutorial.
- Each index entry on slide 2 link to the corresponding slide – which links back to slide 2.
- Note: not all features are pertinent to any given map in the compendium (e.g., a gene-name link-out to GeneCards wouldn't be pertinent to for a copy number variation map).
- A more complete, detailed tutorial plus other videos can be found at [http://bioinformatics.mdanderson.org/main/Navigating\\_Clustered\\_Heatmaps](http://bioinformatics.mdanderson.org/main/Navigating_Clustered_Heatmaps)

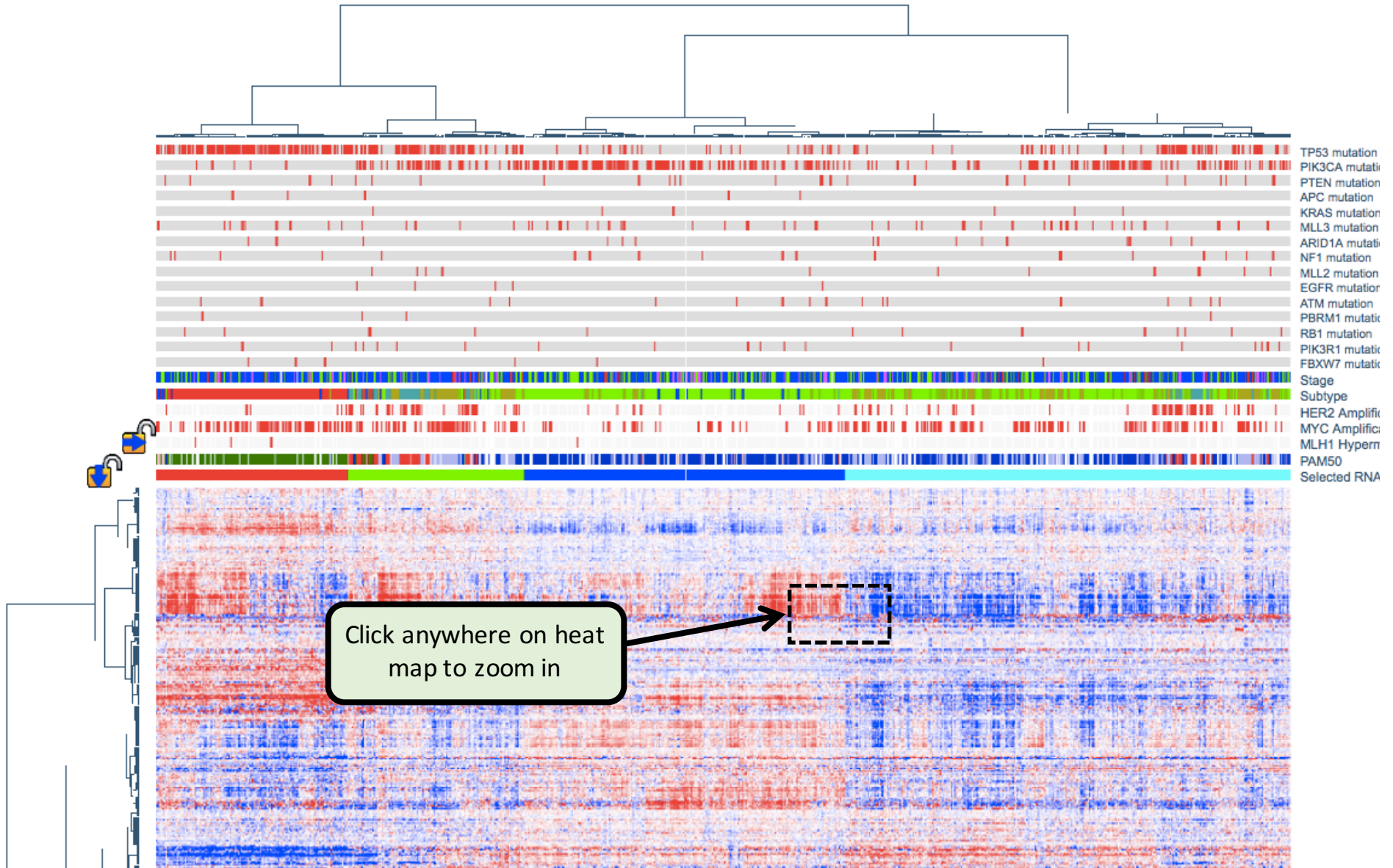
# Index of Slides (with live links to them)

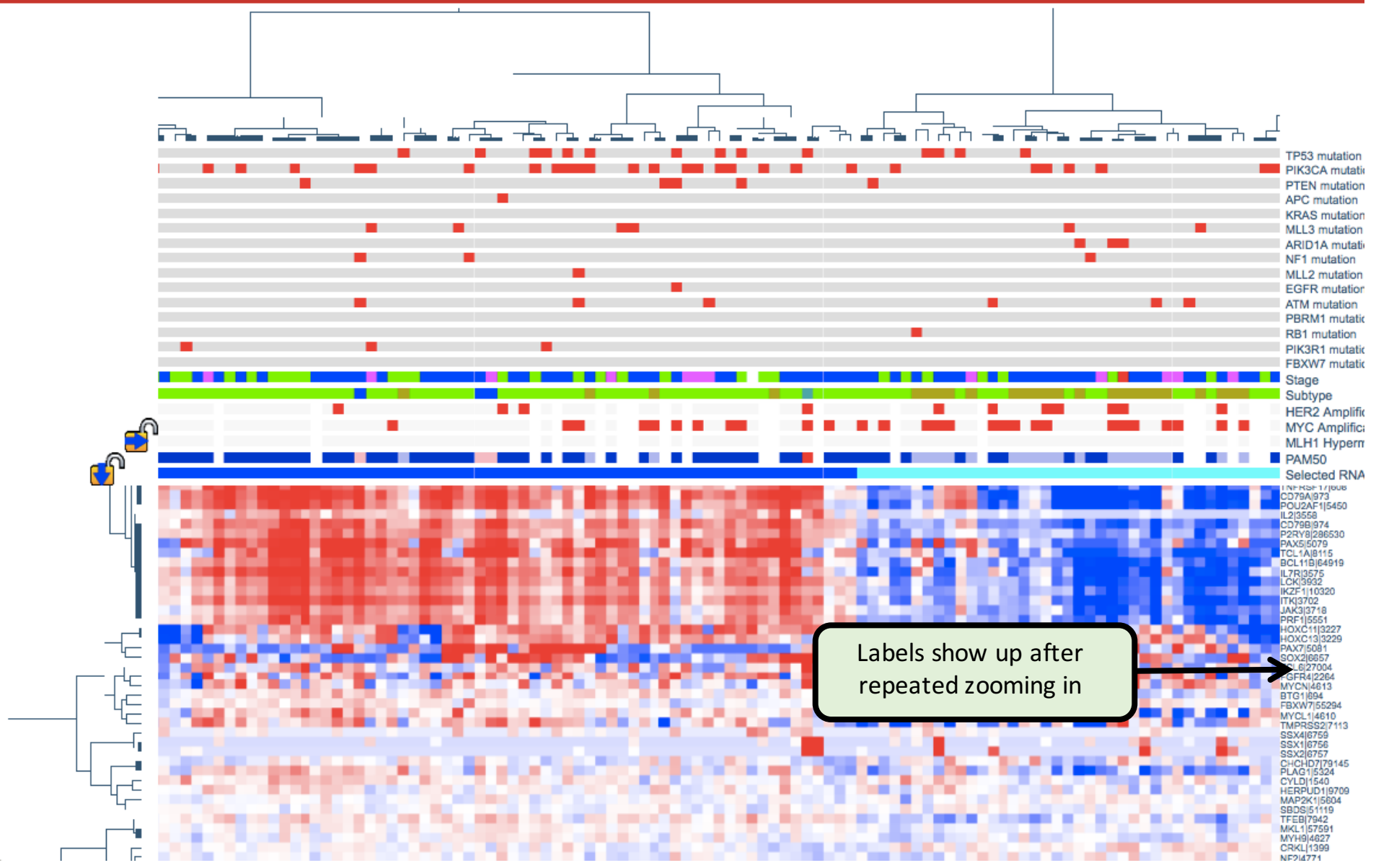
---

- Slide 1: [Title Slide](#)
- Slide 2: [Index of slides](#)
- Slide 3: [Annotated summary screen shot](#)
- Slide 4: [Zooming in](#)
- Slide 5: [Gene labels show up](#)
- Slide 6: [Navigating in the map](#)
- Slide 7: [Zooming out](#)
- Slide 8: [The Row Label Menu](#)
- Slide 9: [Link to Box plot](#)
- Slide 10: [Link to Distribution plot](#)
- Slide 11: [Link to Ideogram](#)
- Slide 12: [The Matrix Menu](#)
- Slide 13: [The horizontal axis lock](#)
- Slide 14: [The vertical axis lock](#)
- Slide 15: [Toggling among CHMs](#)
- Slide 16: [Go back/Go forward \(i.e., Un-do/Re-do\)](#)
- Slide 17: [Return to home page](#)
- Slide 18: [Views Menu](#)
- Slides 19 – 26: Dialogs Menu
- Slide 19: [Navigator Window](#)
- Slide 20: [Image Details Window](#)
- Slide 21: [Color scheme change on the fly](#)
- Slide 22: [Annotations](#)
- Slide 23: [Advanced search](#)
- Slide 24: [Covariate Bar Details](#)
- Slide 25: [Covariate Bar Control Panels](#)
- Slide 26: [Credits](#)
- Slide 27: [TCGA publication guidelines](#)
- Slide 28: Miscellaneous menu
- Slide 28: [PDF maker](#)
- Slide 28: [Metadata for reproducibility](#)
- Slide 29: [? Menu \(basic instructions\)](#)
- Slide 30: [Search \(enter term/abort search/search\)](#)
- Slide 31: [End of Quick Tutorial](#)

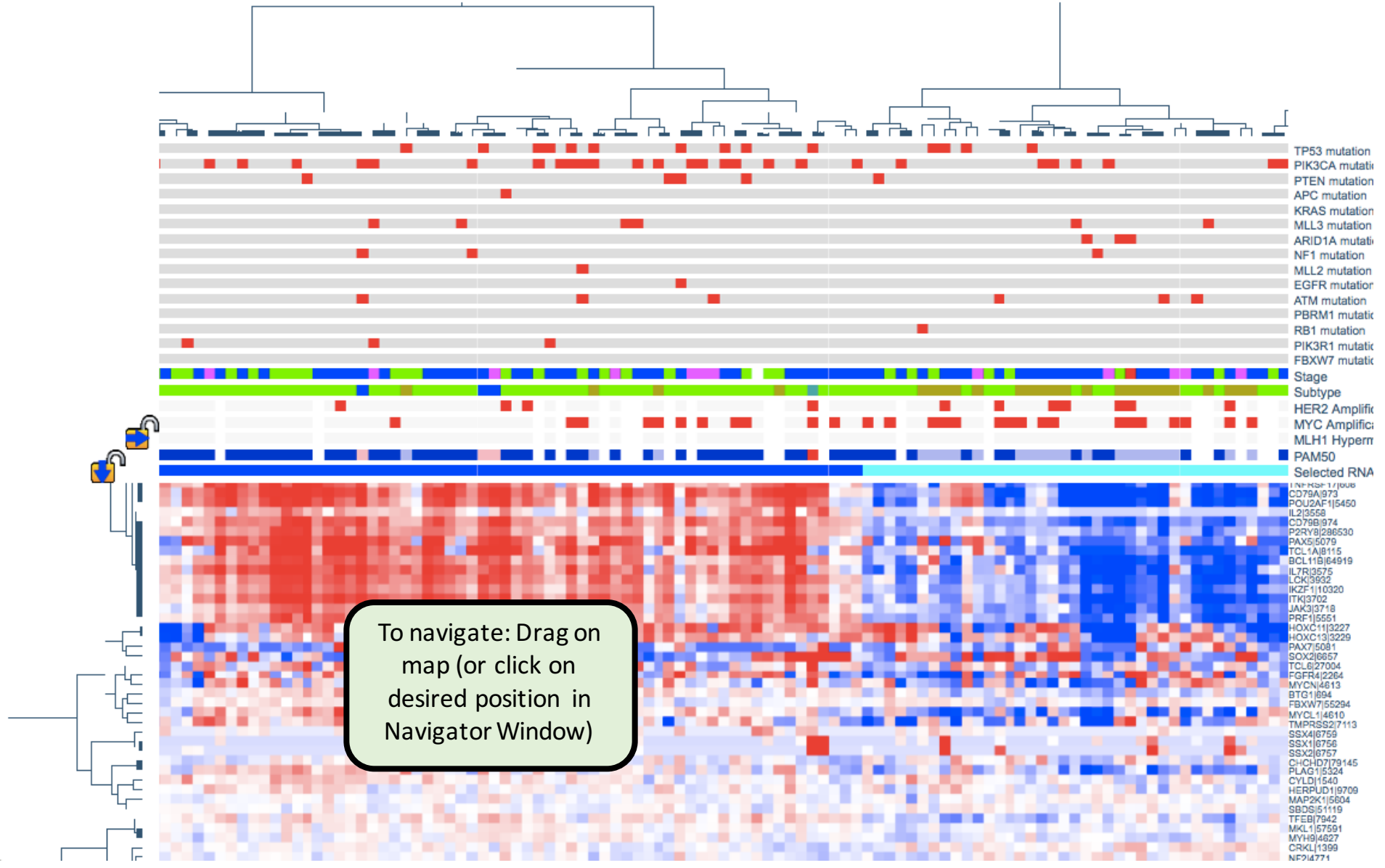
# Main Components of the NG-CHM Viewer

The image shows a screenshot of the NG-CHM Viewer interface. At the top, there is a navigation bar with the MD Anderson Cancer Center logo, a search bar, and menu options like 'Main', 'Views', 'Dialogs', and 'Misc'. The main area displays a heatmap with a dendrogram at the top and a gene list on the right. Several callout boxes with arrows point to specific features: 'Action Menus (see index)' points to the top navigation bar; 'Column (e.g., sample) Dendrogram' points to the top dendrogram; 'Image Details Window' points to a window showing 'Column (Data):', 'Column (Display):', 'Row (Data):', 'Row (Display):', and 'Value:'; 'Covariate bars (which can be added or subtracted) and can be discrete or continuous' points to the colored bars above the heatmap; 'Covariate Details Window' points to a window showing a list of covariates like 'PIK3CA mutatio', 'PTEN mutatio', 'APC mutatio', etc.; 'Axis locks' points to a lock icon on the left; 'Heat Map itself' points to the main heatmap; 'Navigator Window' points to a window showing a small overview of the heatmap; and 'Row (e.g., gene) Dendrogram' points to the dendrogram on the left side of the heatmap.

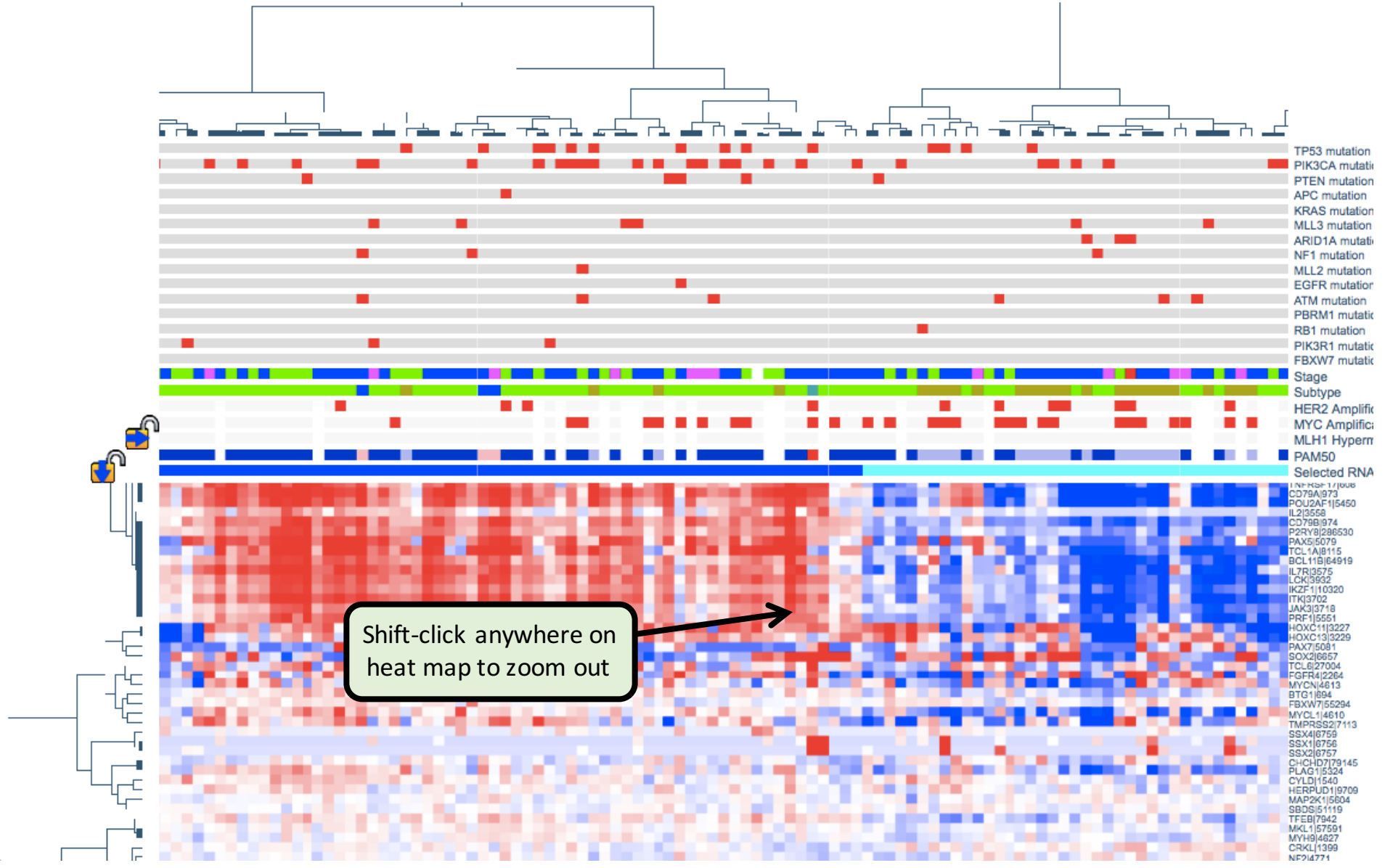




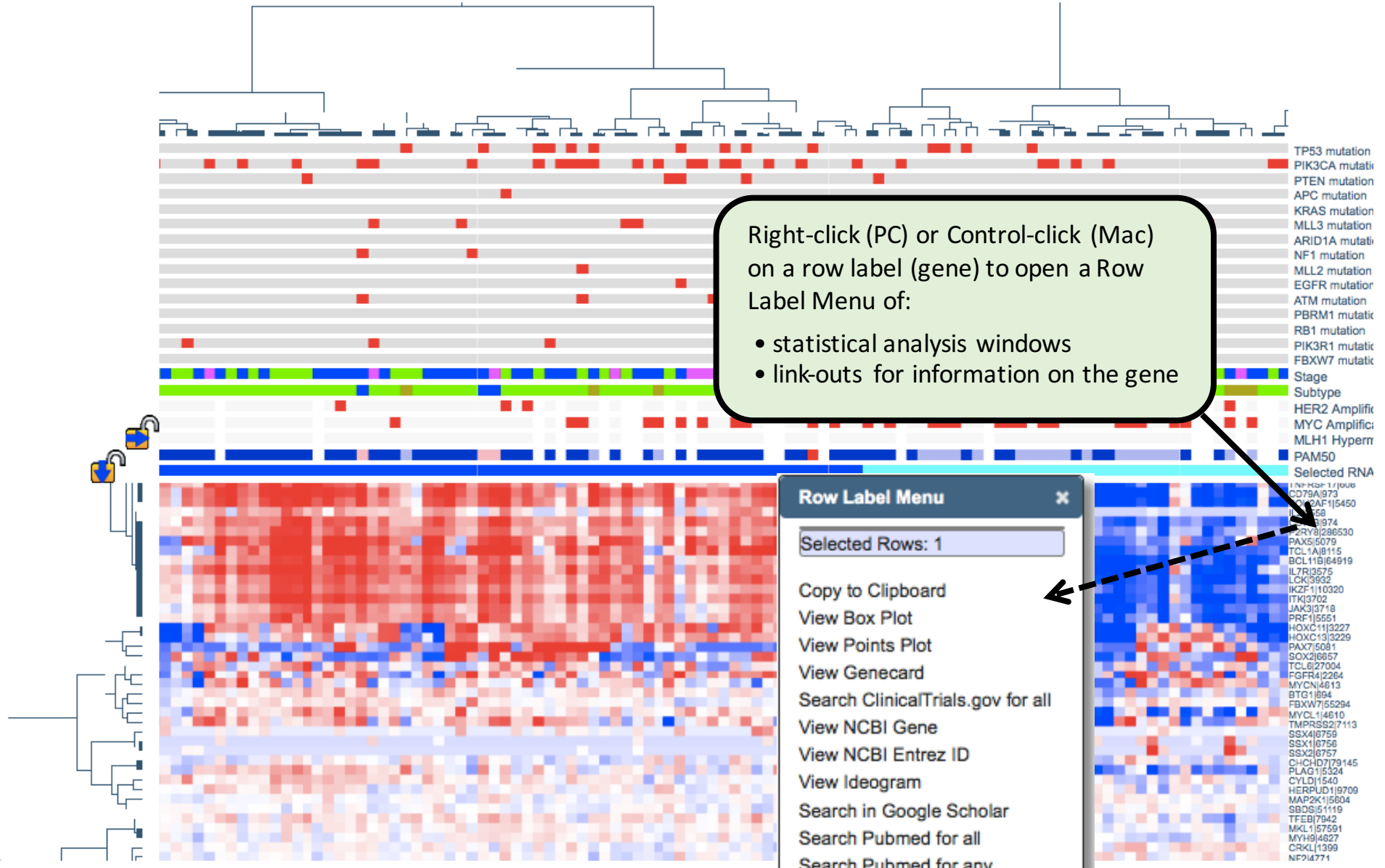
Labels show up after repeated zooming in



To navigate: Drag on map (or click on desired position in Navigator Window)



Shift-click anywhere on heat map to zoom out



Right-click (PC) or Control-click (Mac) on a row label (gene) to open a Row Label Menu of:

- statistical analysis windows
- link-outs for information on the gene

**Row Label Menu** [X]

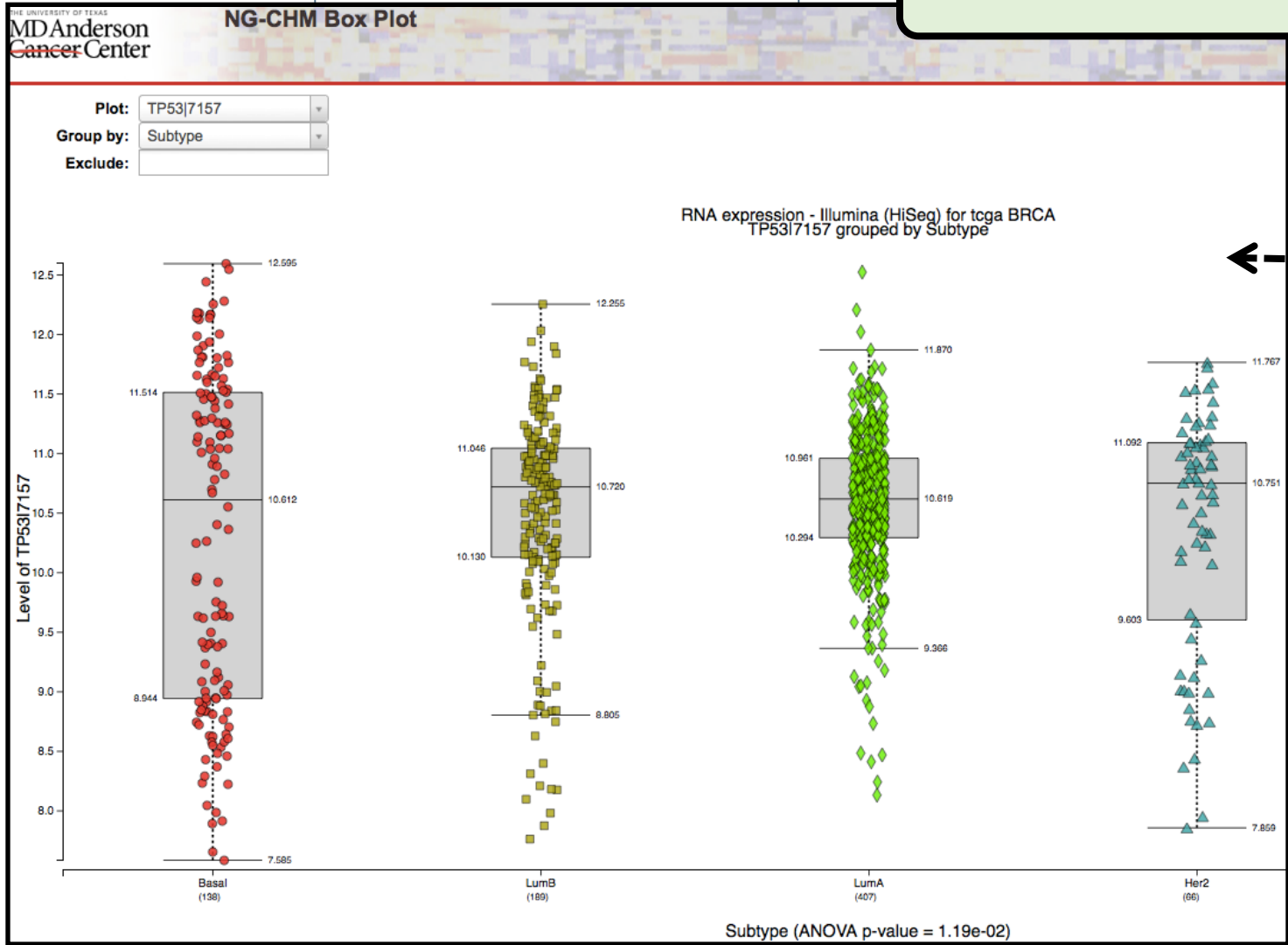
Selected Rows: 1

- Copy to Clipboard
- View Box Plot
- View Points Plot
- View Genecard
- Search ClinicalTrials.gov for all
- View NCBI Gene
- View NCBI Entrez ID
- View Ideogram
- Search in Google Scholar
- Search Pubmed for all
- Search Pubmed for any
- View in cBio Portal

[Back to Index Slide](#)



Select "View Box Plot" from Menu



Row Label Menu

Selected Rows: 1

- Copy to Clipboard
- View Box Plot
- View Points Plot
- View Genecard
- Search ClinicalTrials.gov for all
- View NCBI Gene
- View NCBI Entrez ID
- View Ideogram
- Search in Google Scholar
- Search Pubmed for all
- Search Pubmed for any
- View in cBIO Portal

BCL11B 64919
IL7R 3575
LCK 3509
IKZF1 10320
ITK 3702
JAK3 3718
PRF 15551
HOXC11 3227
HOXC13 3229
PAX7 5081
SOX2 6657
TCL6 27004
FSFR4 2264
MYCN 4813
BTG1 894
FBXW7 55294
MYCL1 4810
TMPPRSS2 7113
SSX4 6759
SSX1 6756
SSX2 6757
CHCHD7 79145
PLAG1 5324
CYLD 1540
HERPUD1 9709
MAP2K1 5604
SBD5 5119
TFEB 7942
MKL1 57591
MYH9 4927
CRKL 1399
NF94 771

Plot: TP53|7157

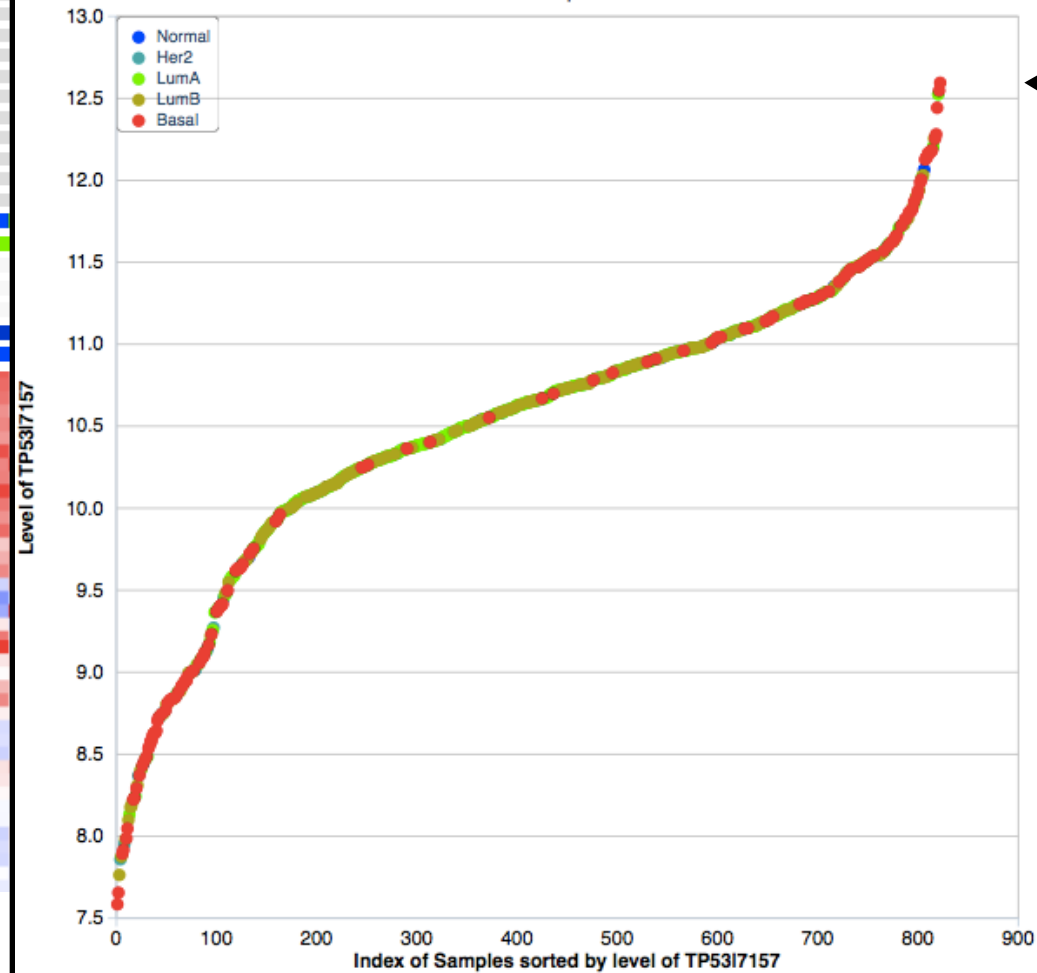
Group by: Subtype

Threshold:

True Positives:

False Positives:

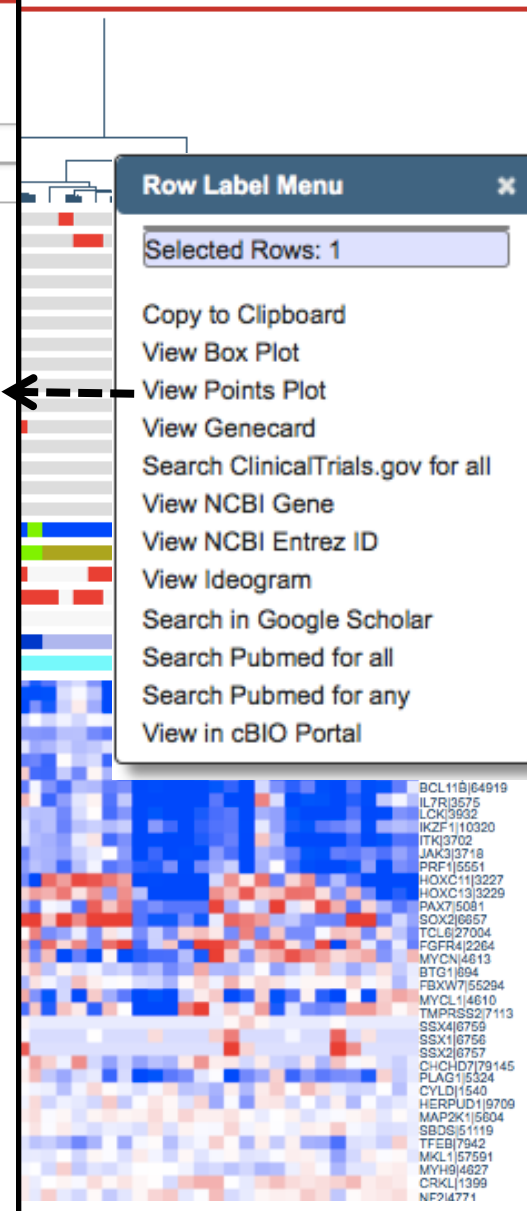
RNA expression - Illumina (HiSeq) for tcga BRCA  
 TP53|7157



**Row Label Menu** [X]

Selected Rows: 1

- Copy to Clipboard
- View Box Plot
- View Points Plot
- View Genecard
- Search ClinicalTrials.gov for all
- View NCBI Gene
- View NCBI Entrez ID
- View Ideogram
- Search in Google Scholar
- Search Pubmed for all
- Search Pubmed for any
- View in cBIO Portal



[Back to Index Slide](#)

# Ideogram Viewer

gene1  
Oncogene  
Suppressor

Zoom Reset Zoom Out Zoom In



### Ideogram Viewer key features

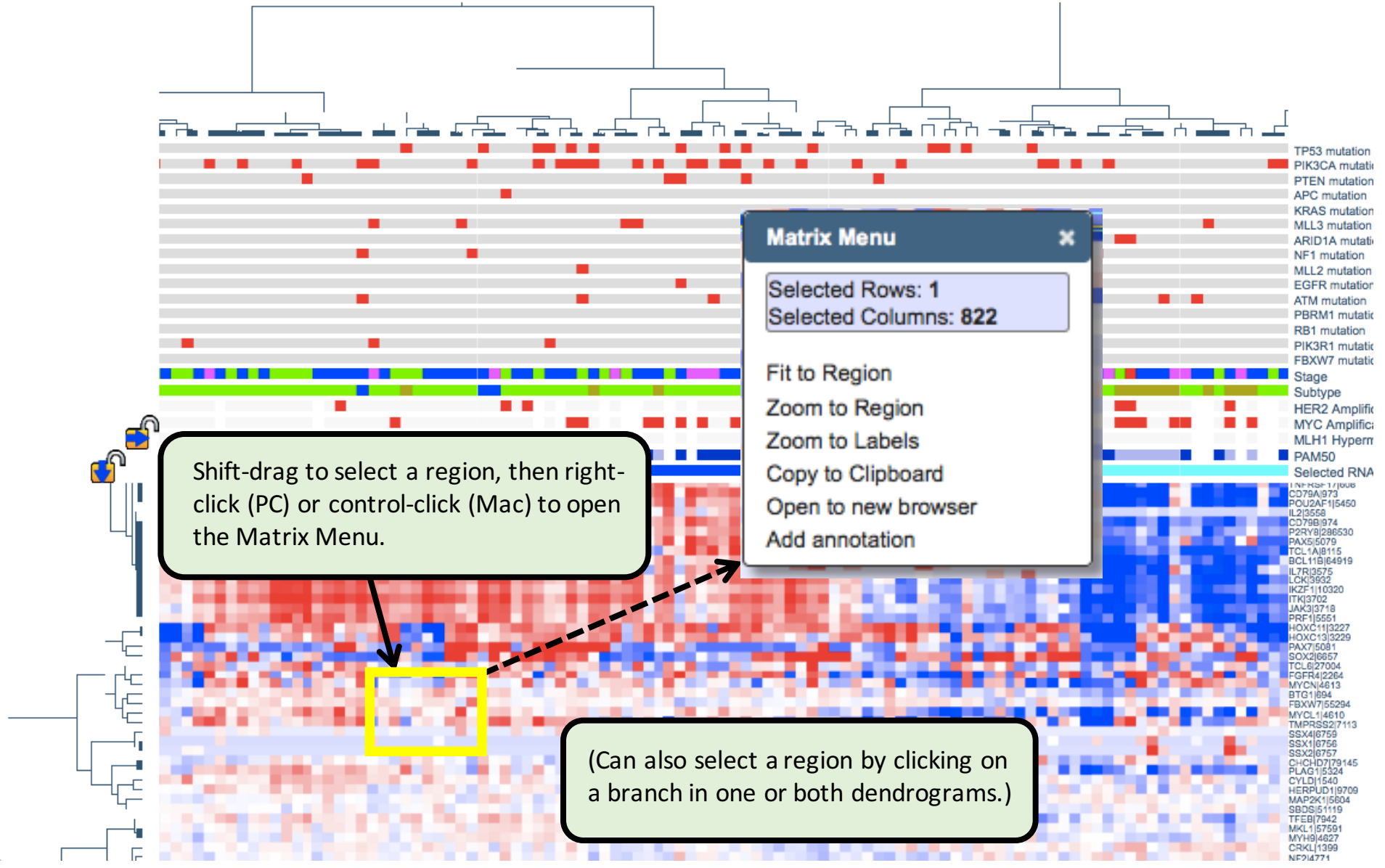
- **Zoom In** : Double-clicking or mouse scroll wheel, or use Zoom In button, or drag the control end on the zoom indicator
- **Zoom Out** : Shift-double-clicking or mouse scroll wheel, or use Zoom Out button, or drag the control end on the zoom indicator
- **Reset zoom** : Use Zoom Reset button to restore the original zoom level
- **Pan** : Click and drag across the ideogram area, or drag the content rectangle on the zoom indicator horizontally
- **Select a region** : on a chromosome press the shift key, the cursor turns to crosshair style, left mouse down, move the cursor to select a region of your interest, release the mouse
- **Display Oncogene and Suppressor** : Click the item in the legend

Please see [documentation page](#) for more information.

Link-out to an interactive ideogram viewer to show chromosome location(s) of one or more user-selected genes. The viewer has link-outs to other resources, including the UCSC Genome Browser

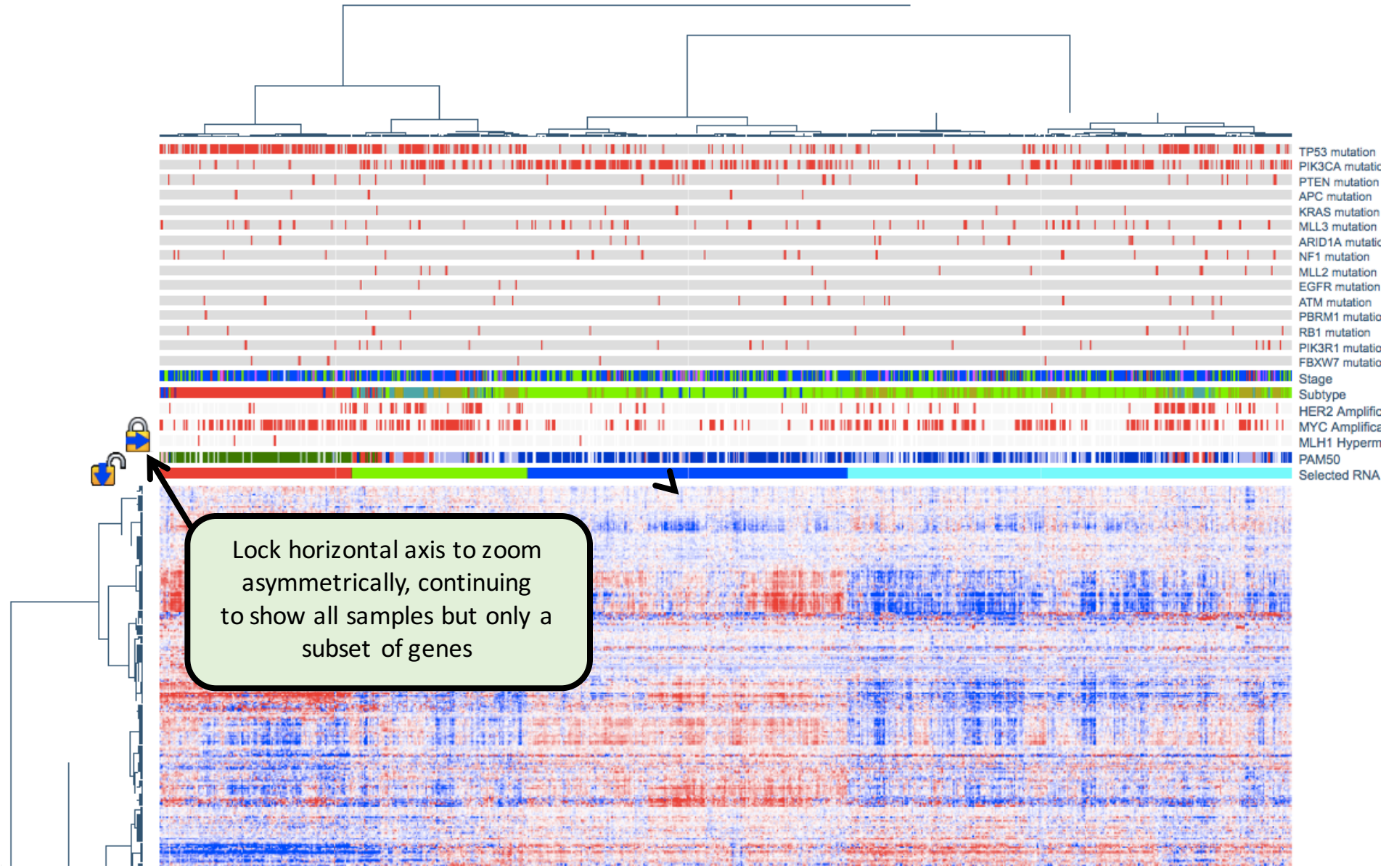
- View GeneCards
- Search ClinicalTrials.gov for all
- View NCBI Gene
- View NCBI Entrez ID
- View Ideogram
- Search in Google Scholar
- Search Pubmed for all
- Search Pubmed for any
- View in cBIO Portal

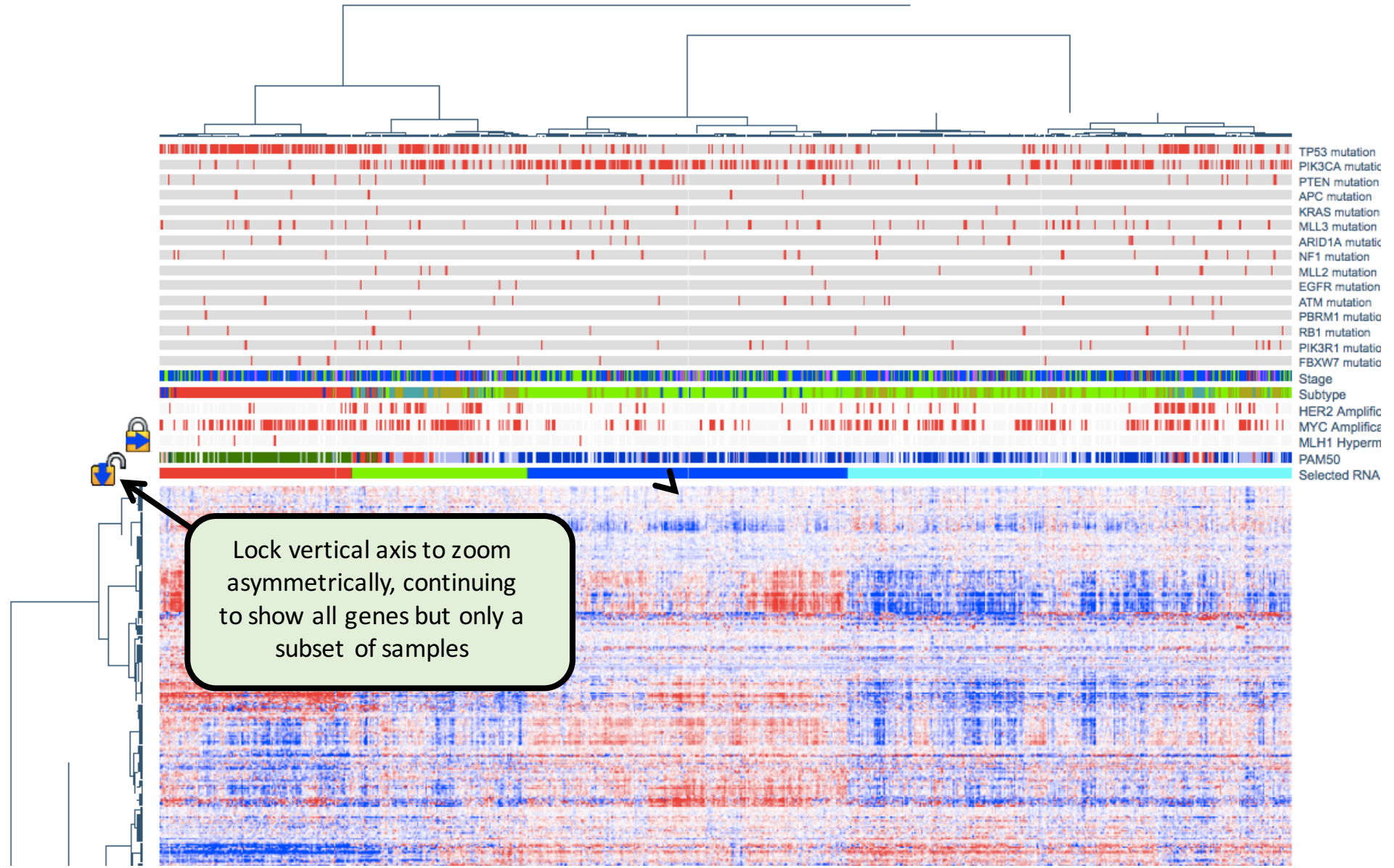
[Back to Index Slide](#)



Shift-drag to select a region, then right-click (PC) or control-click (Mac) to open the Matrix Menu.

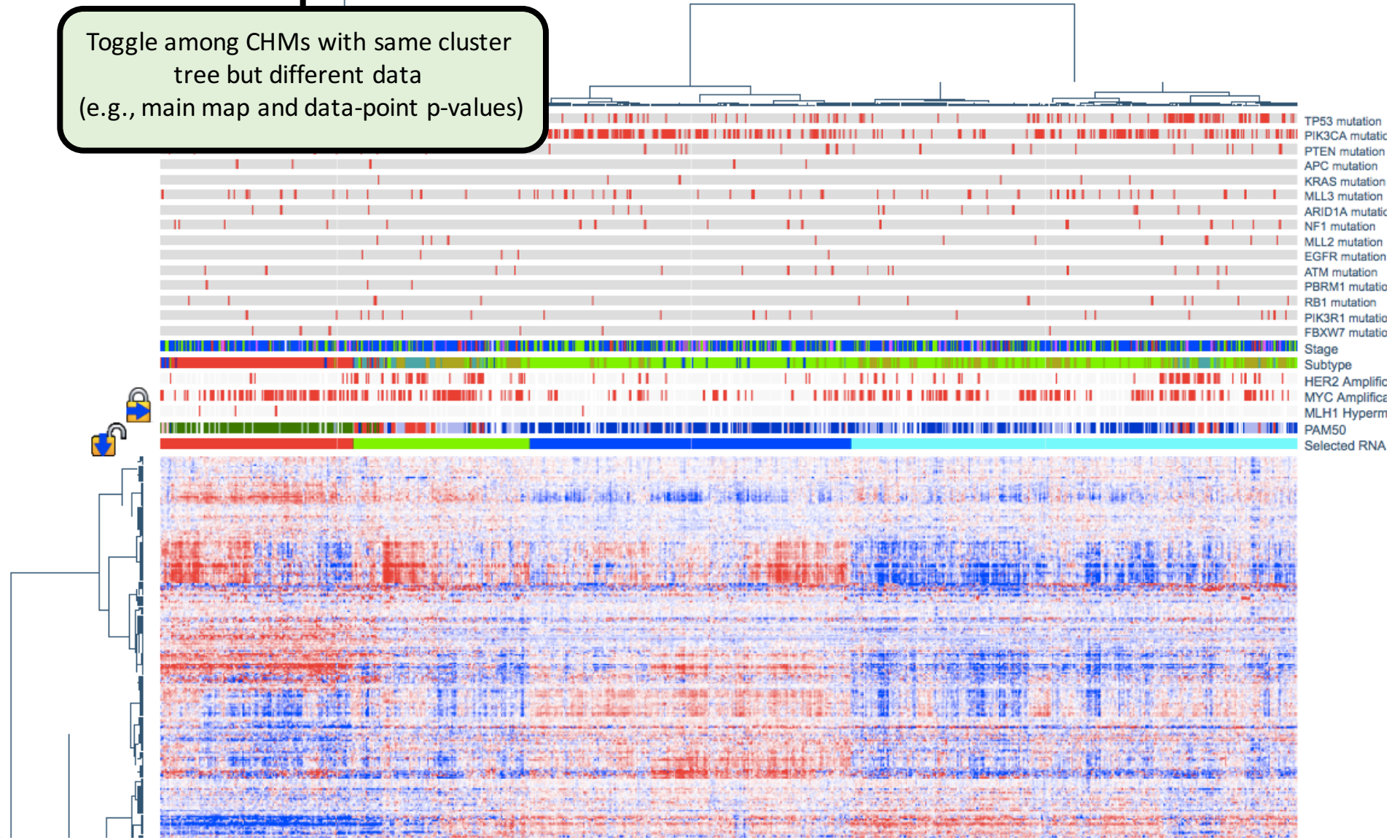
(Can also select a region by clicking on a branch in one or both dendrograms.)



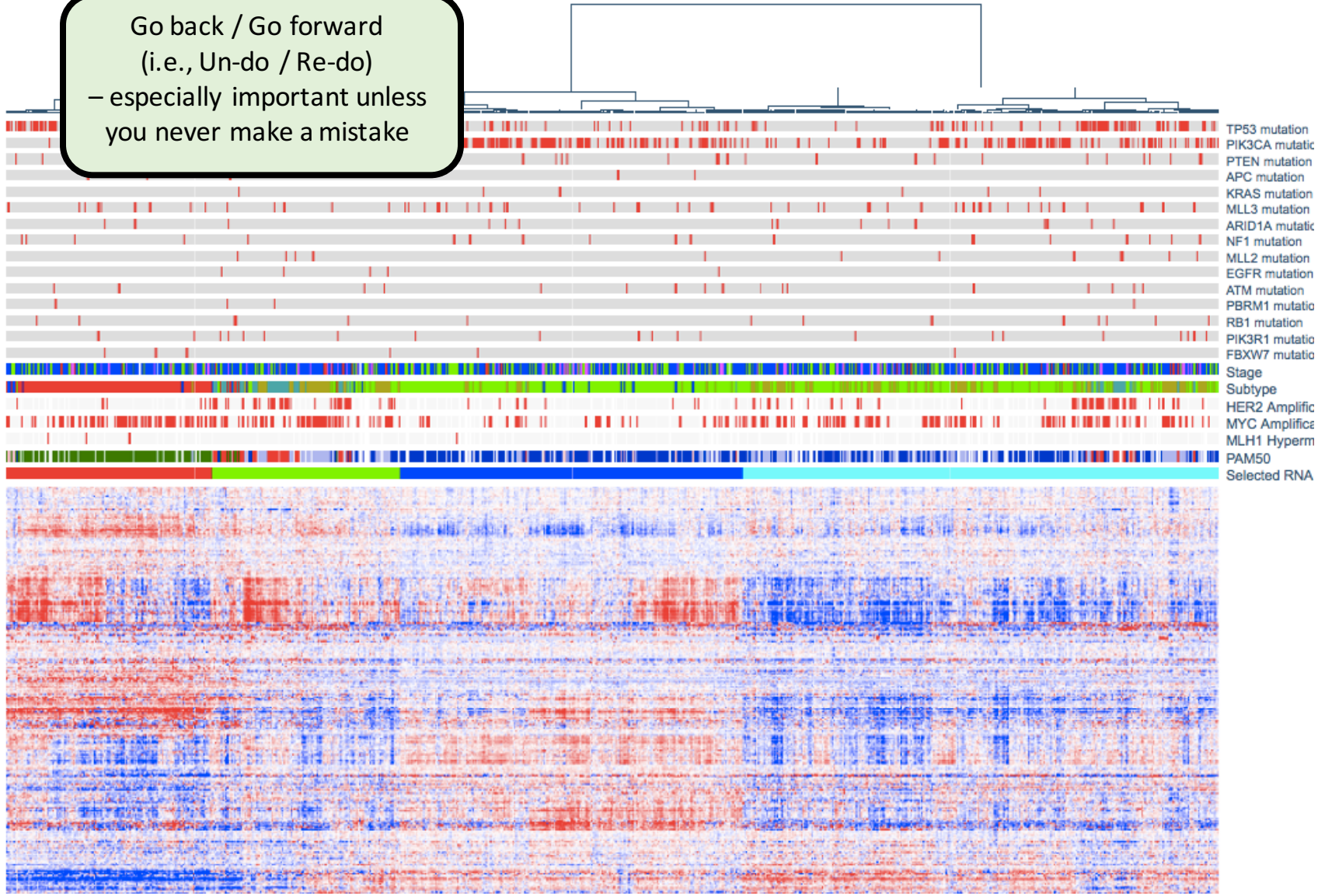


Lock vertical axis to zoom asymmetrically, continuing to show all genes but only a subset of samples

Toggle among CHMs with same cluster tree but different data (e.g., main map and data-point p-values)

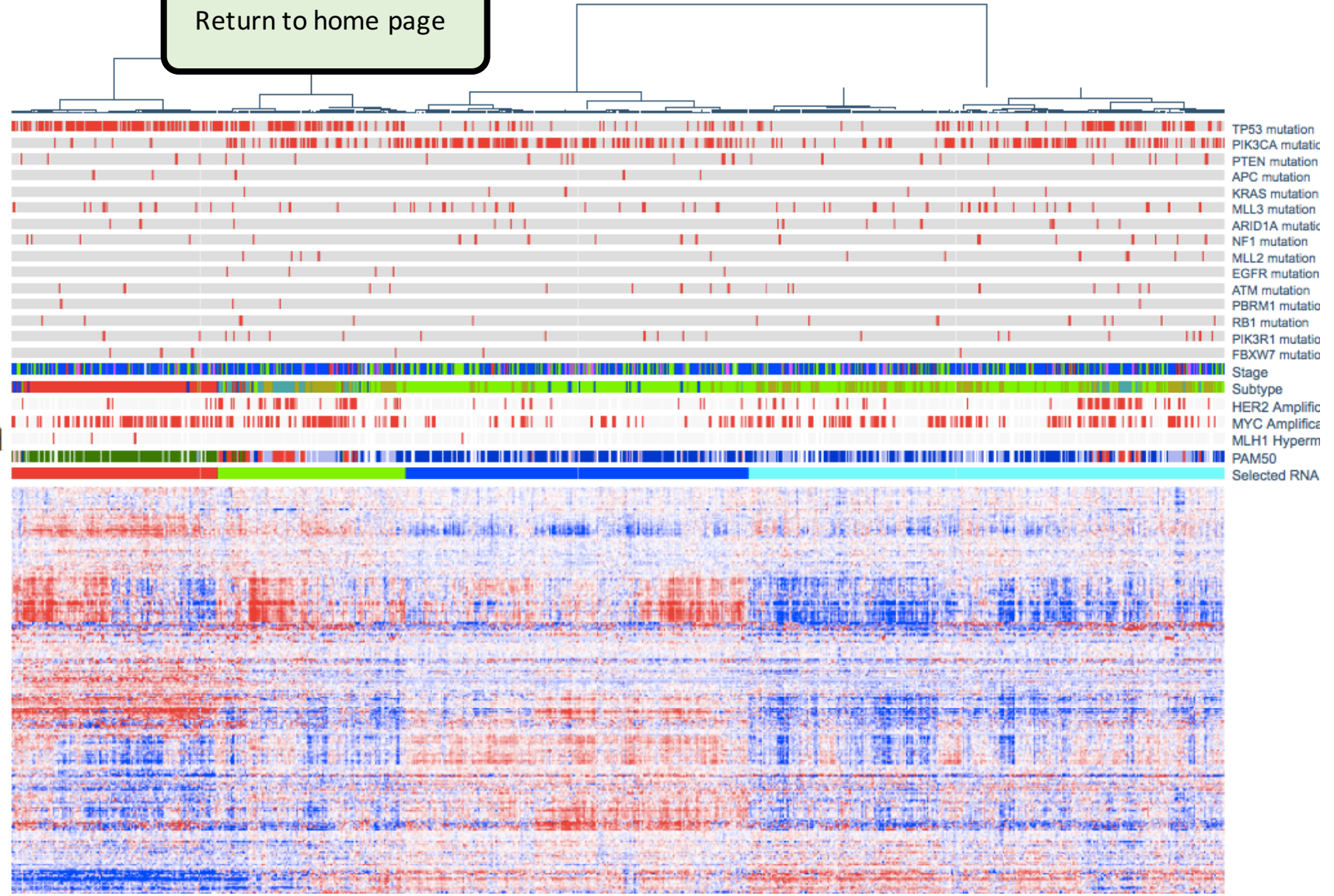


Go back / Go forward  
(i.e., Un-do / Re-do)  
- especially important unless  
you never make a mistake



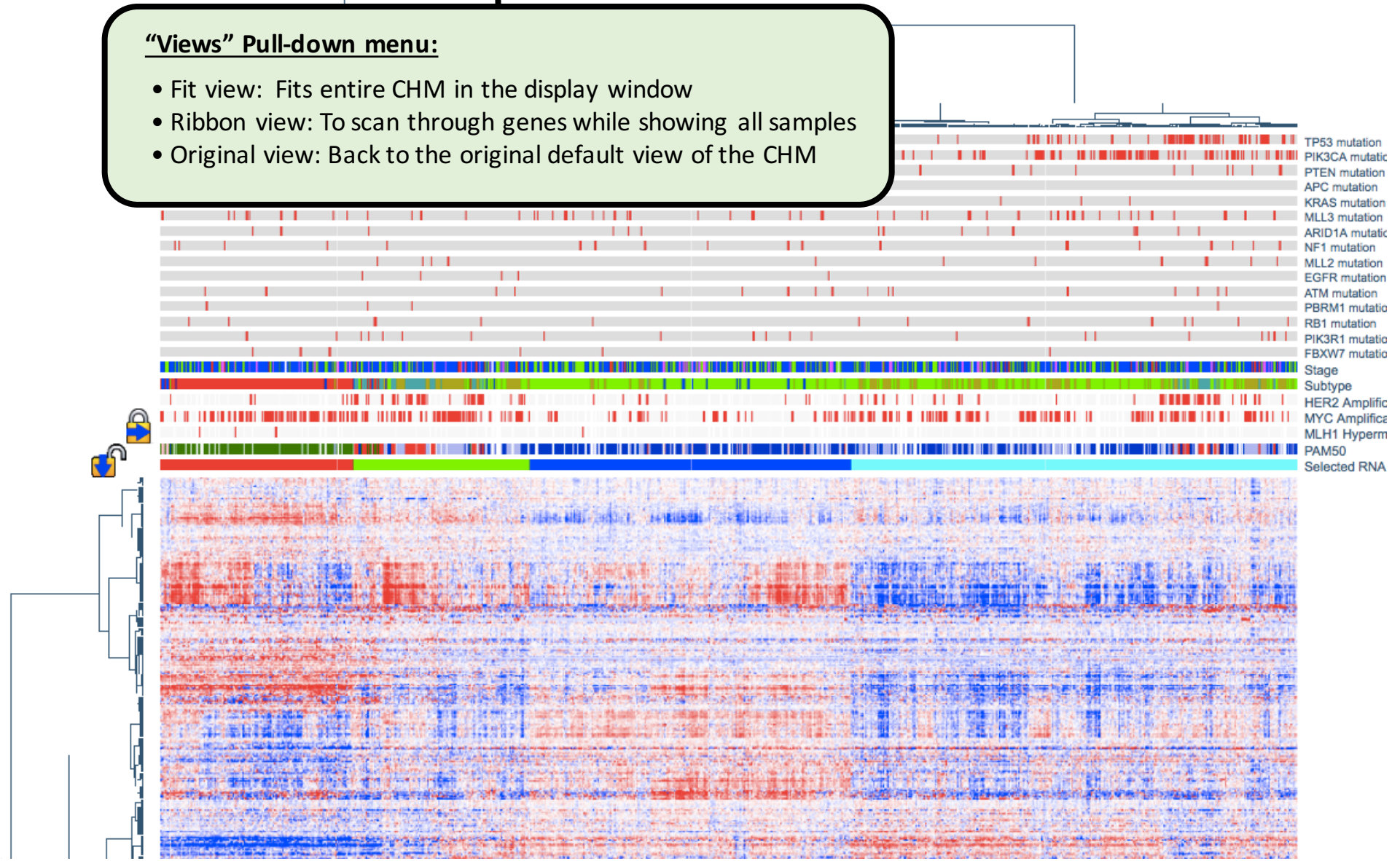


Return to home page



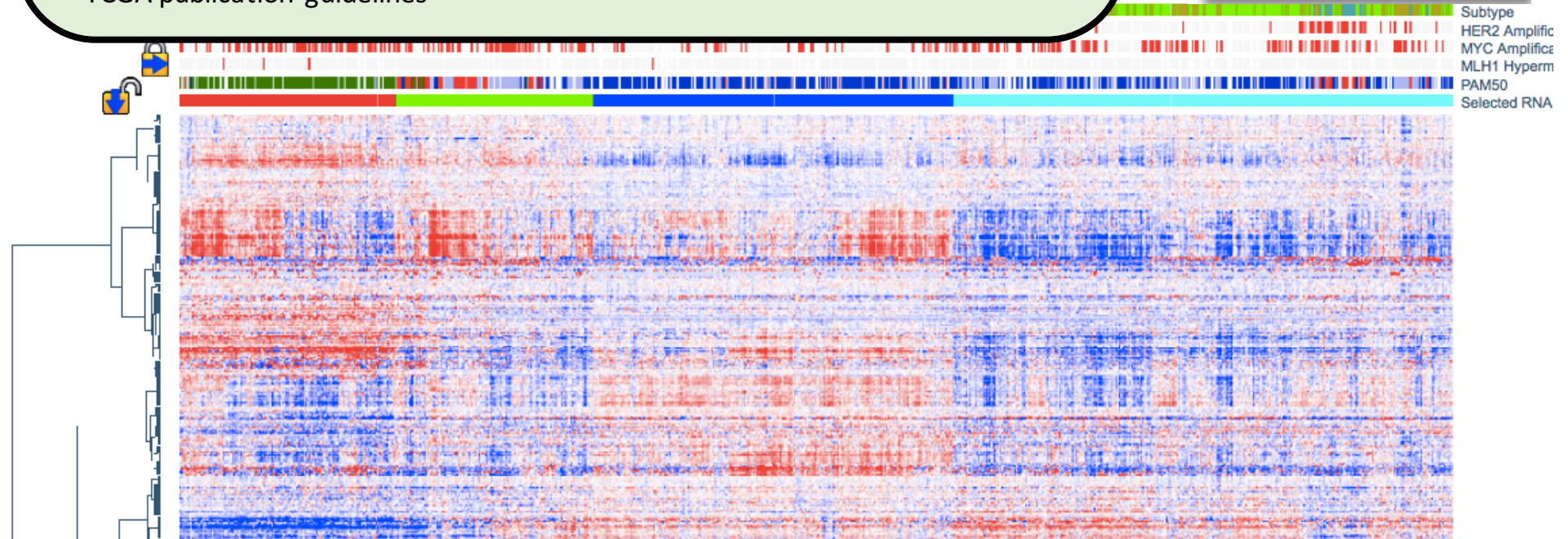
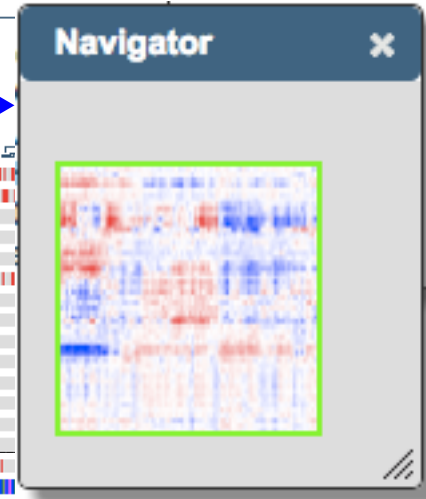
**“Views” Pull-down menu:**

- Fit view: Fits entire CHM in the display window
- Ribbon view: To scan through genes while showing all samples
- Original view: Back to the original default view of the CHM



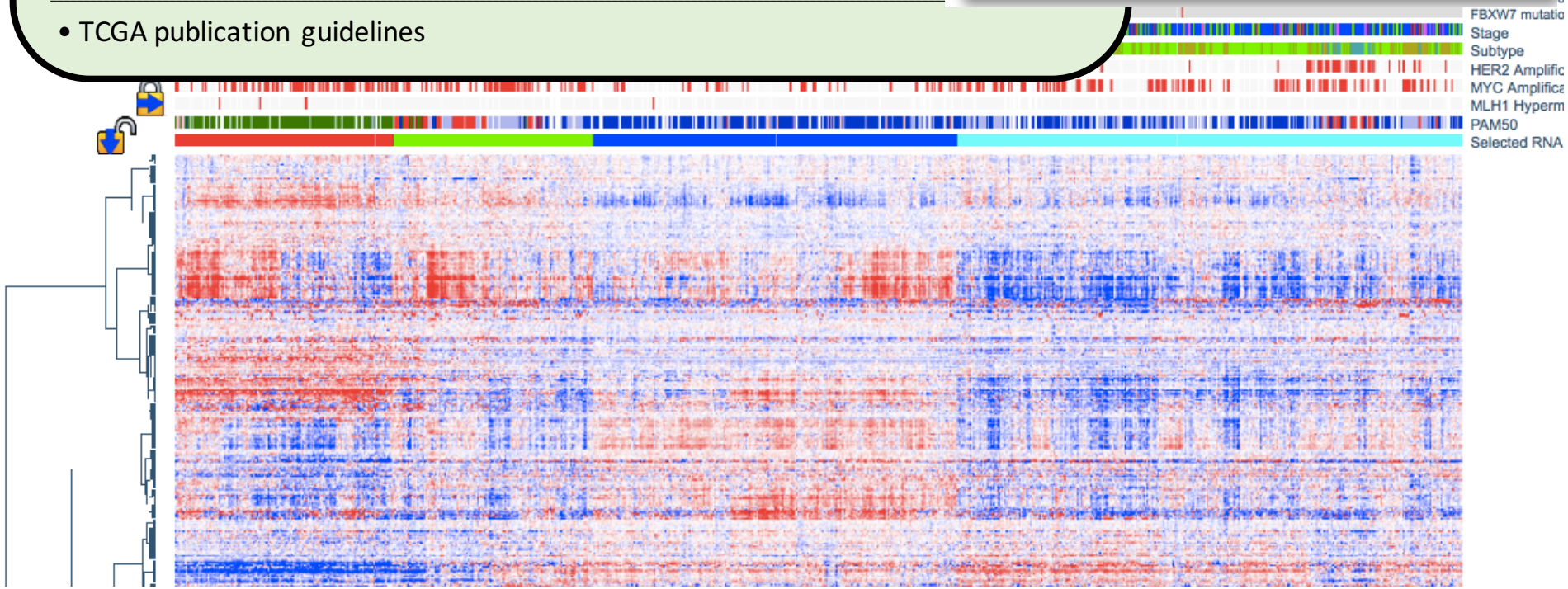
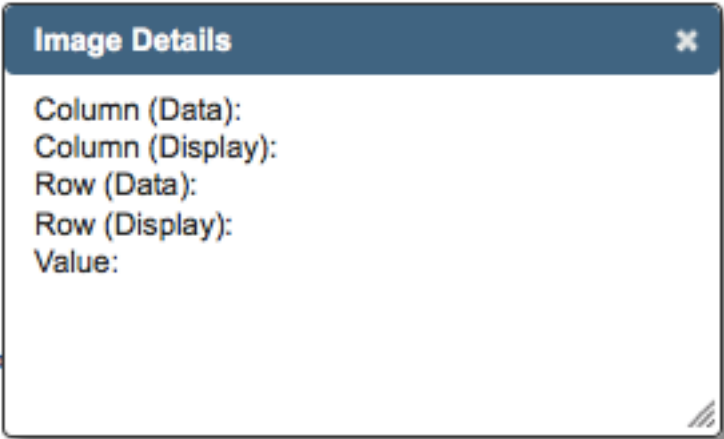
**“Dialogs” menu for opening movable, resizable windows:**

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panel: *Select or add row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines



**“Dialogs” menu for opening movable, resizable windows:**

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their a*
  - Covariate control panel: *Select or add row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines



**“Dialogs” menu for opening movable, resizable windows:**

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panel: *Select or add row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines

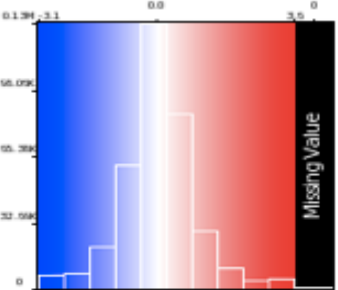
### Color Scheme

**Define New Custom Color Scheme:**

Select Color Scheme Type:  
linear

Color	Break Point	Add / Remove
<span style="display: inline-block; width: 15px; height: 15px; background-color: blue; border: 1px solid black;"></span>	-10.184	+ / -
<span style="display: inline-block; width: 15px; height: 15px; background-color: white; border: 1px solid black;"></span>	1.370	+ / -
<span style="display: inline-block; width: 15px; height: 15px; background-color: red; border: 1px solid black;"></span>	12.924	+ / -
<b>Missing Value Color</b>	<span style="display: inline-block; width: 15px; height: 15px; background-color: black; border: 1px solid black;"></span>	

Render Preview



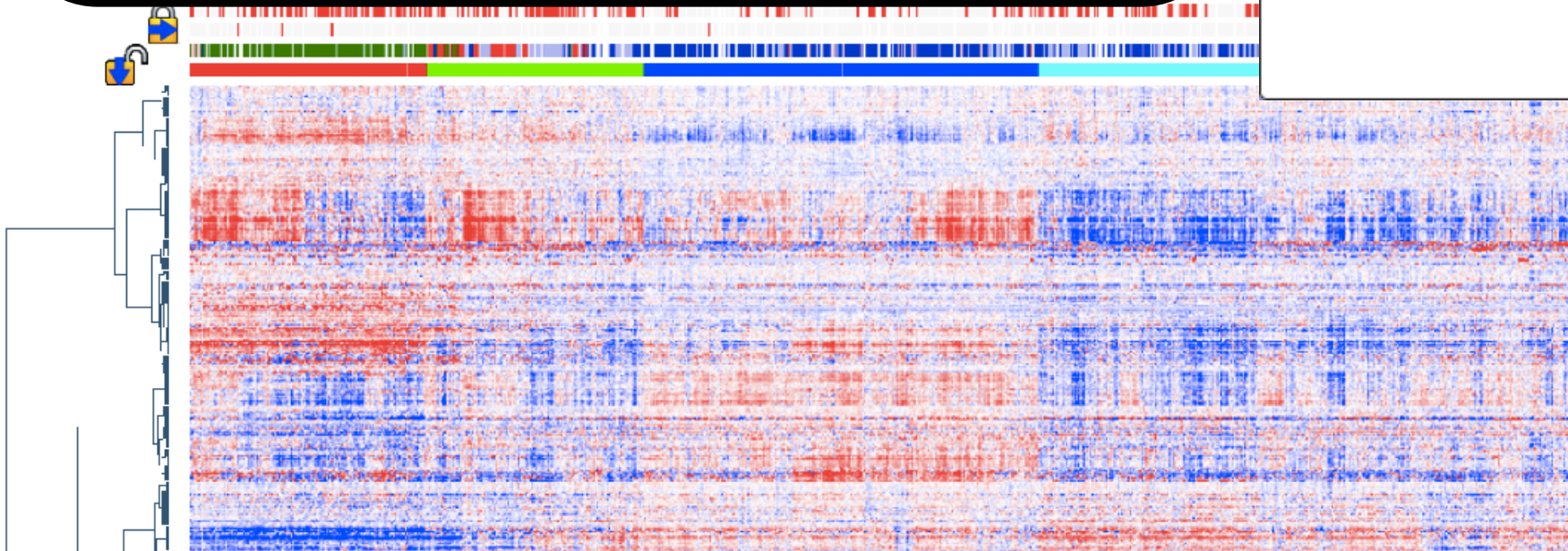
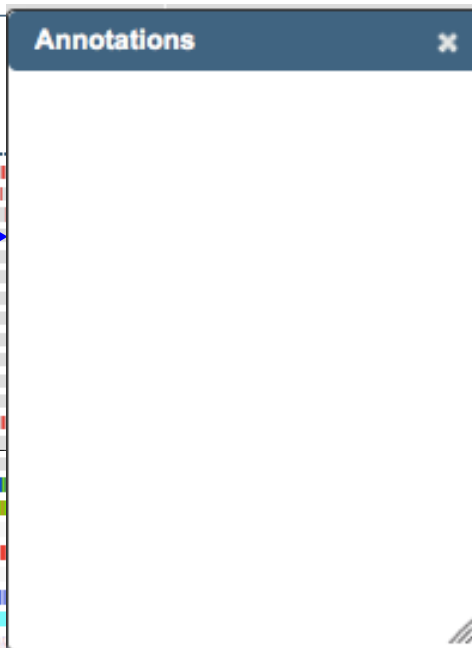
Select Color Scheme to Render:

Permanent Color Schemes

- cm1 | (-3.1249442...3.5524044)
- cm2 | (-2.5...2.5)

### “Dialogs” menu for opening movable, resizable windows:

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panel: *Select or add row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines




**“Dialogs” menu for opening movable, resizable windows:**

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panel: *Select or add row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines

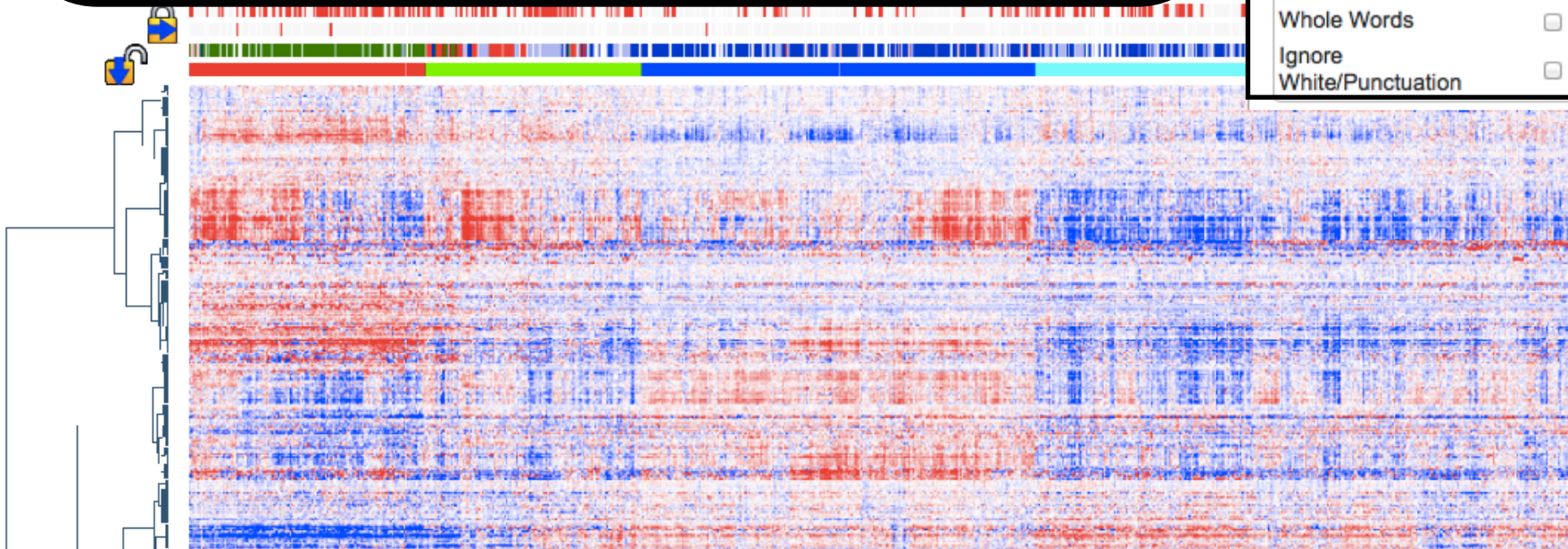
**Advanced Search** ✕

Column Search Term:

Row Search Term: 

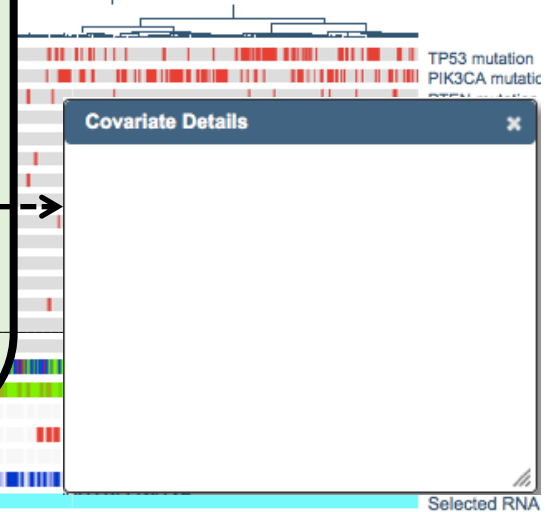
Search Options:

Search Syntax	Column	Row
Simple	<input checked="" type="radio"/>	<input checked="" type="radio"/>
Regular Expression	<input type="radio"/>	<input type="radio"/>
Case Sensitive	<input type="checkbox"/>	<input type="checkbox"/>
Whole Words	<input type="checkbox"/>	<input type="checkbox"/>
Ignore White/Punctuation	<input type="checkbox"/>	<input type="checkbox"/>



**“Dialogs” menu for opening movable, resizable windows:**

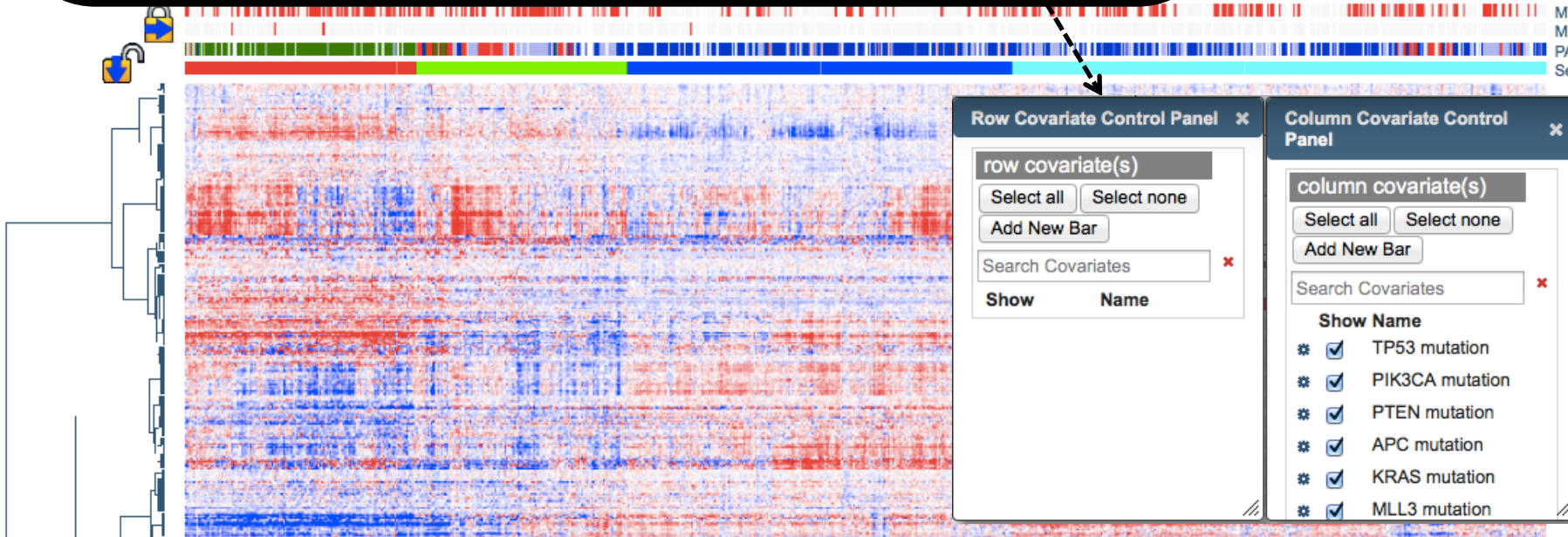
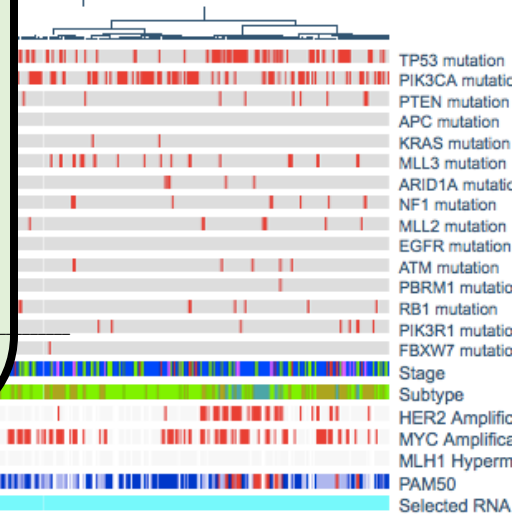
- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panel: Hide, show, subtract, or add *row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines





**“Dialogs” menu for opening movable, resizable windows:**

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panels: Hide, show, subtract, or add *row or column covariate bars*
  - Credits
- 
- TCGA publication guidelines



**“Dialogs” menu for opening movable, resizable windows:**

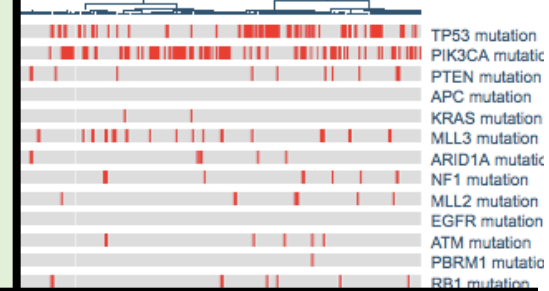
- Navigator
- Image details: *row/column/value data*
- Color Schemes: *create and/or change color scheme on the fly*
- Annotations
- Advanced search: *Advanced syntax/row/column searches*
- Covariate details: *Mouse-over for details on covariate bars and their distributions*
- Covariate control panel: *Select or add row or column covariate bars*
- Credits
- TCGA publication guidelines


**About NG-CHM**

Developed by the MD Anderson Cancer Center Department of Bioinformatics and Computational Biology, SRA International, and In Silico Solutions. This work was supported in part by U.S. National Cancer Institute (NCI; MD Anderson TCGA Genome Data Analysis Center) grant numbers CA143883 and CA083639, the Mary K. Chapman Foundation, the Michael & Susan Dell Foundation (honoring Lorraine Dell), and MD Anderson Cancer Center Support Grant P30 CA016672 (the Bioinformatics Shared Resource)

**“Dialogs” menu for opening movable, resizable windows:**

- Navigator
  - Image details: *row/column/value data*
  - Color Schemes: *create and/or change color scheme on the fly*
  - Annotations
  - Advanced search: *Advanced syntax/row/column searches*
  - Covariate details: *Mouse-over for details on covariate bars and their distributions*
  - Covariate control panel: *Select or add row or column covariate bars*
  - Credits
- TCGA publication guidelines →



**The Cancer Genome Atlas**  Understanding genomics to improve cancer care

Search

Home About Cancer Genomics Cancers Selected for Study Research Highlights Publications

Home > Publications > Publication Guidelines

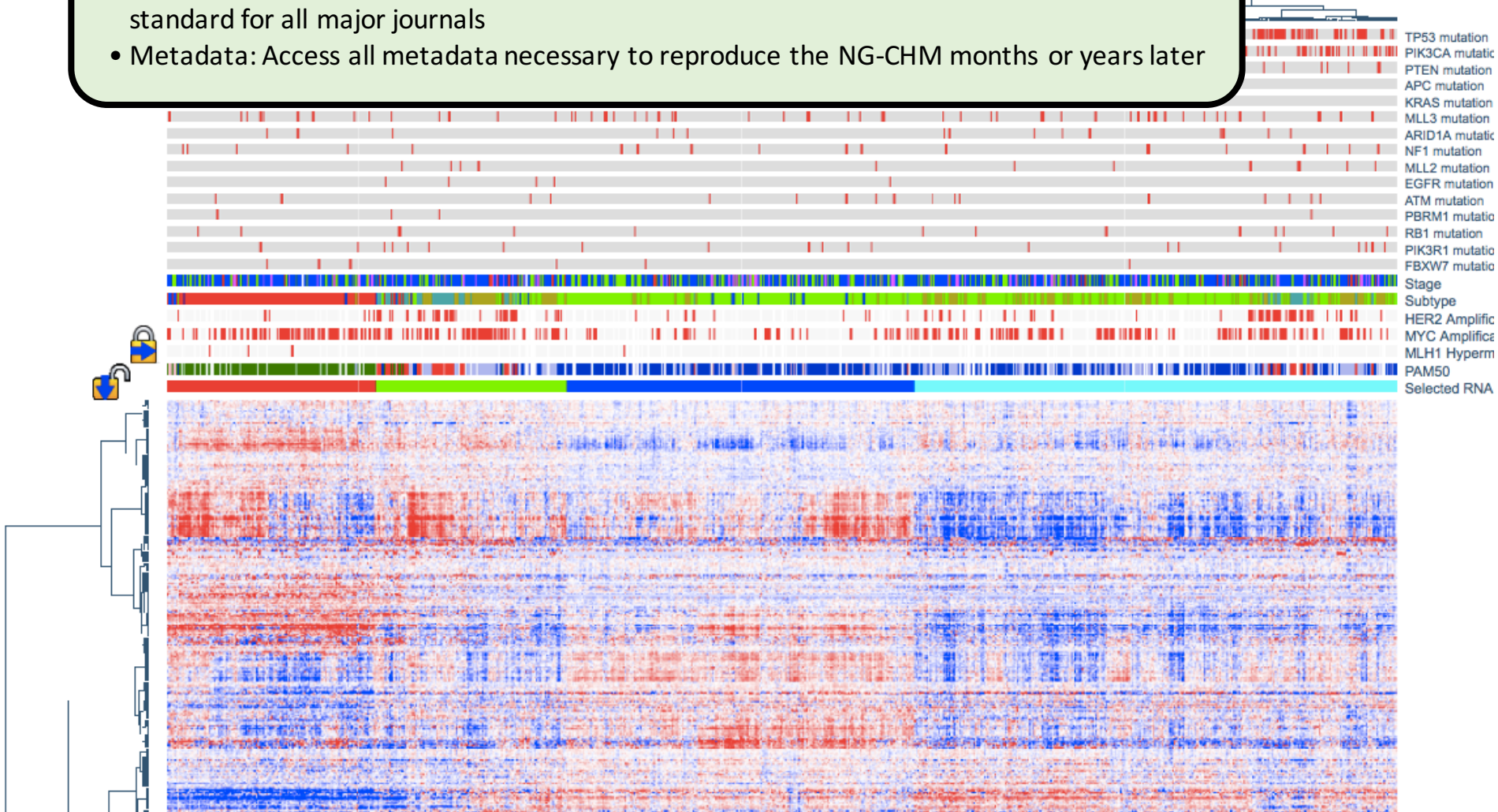
## Publication Guidelines

Last Updated: September 30, 2014

TCGA is a community resource project and data are made available rapidly after generation for community research use. To act in accord with the Fort Lauderdale principles and support the continued prompt public release of large-scale genomic data prior to publication, researchers who plan to prepare reports (publications or presentations) containing descriptions of TCGA data that would be of comparable scope to an initial TCGA comprehensive, global analysis publication, and journal editors or conference organizers who receive such reports, are encouraged to coordinate their independent reports with TCGA's publication schedule. *Specifically, comparable scope is defined as global genome-wide analysis of TCGA data from more than one platform OR analysis of data from a single platform across more than one tumor type under moratorium. Publications or presentations involving such analyses are restricted prior to the TCGA publication moratorium release date as described further below.*

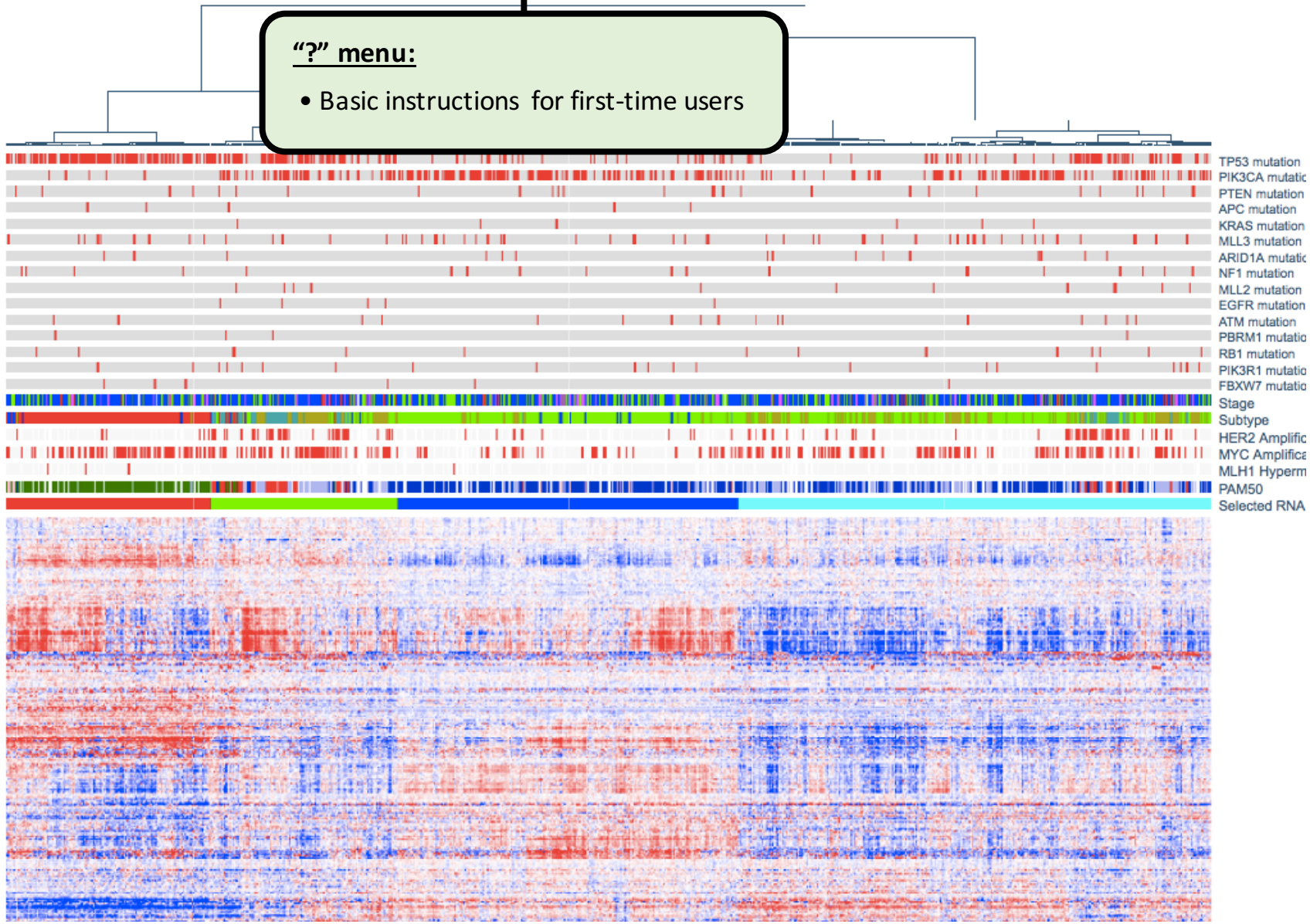
**“Miscellaneous” menu:**

- PDF: Produces high-resolution PDF (of current state of image) that meets publication standard for all major journals
- Metadata: Access all metadata necessary to reproduce the NG-CHM months or years later



**“?” menu:**

- Basic instructions for first-time users



Enter search term Abort search Search

