

**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)

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# Main Components of the NG-CHM Viewer

The image shows a screenshot of the NG-CHM Viewer interface. At the top left is the MD Anderson Cancer Center logo. The main area displays a heatmap with a dendrogram on the left and top. The heatmap is color-coded with red, green, and blue. 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; 'Covariate bars (which can be added or subtracted) and can be discrete or continuous' points to the horizontal bars above the heatmap; 'Image Details Window' points to a panel on the right showing mutation data; 'Covariate Details Window' points to another panel on the right showing clinical data; 'Axis locks' points to lock icons on the left; 'Heat Map itself' points to the main heatmap area; 'Navigator Window' points to a small overview window on the right; and 'Row (e.g., gene) Dendrogram' points to the left dendrogram.

**Action Menus (see index)**

**Column (e.g., sample) Dendrogram**

**Covariate bars (which can be added or subtracted) and can be discrete or continuous**

**Image Details Window**

**Covariate Details Window**

**Axis locks**

**Heat Map itself**

**Navigator Window**

**Row (e.g., gene) Dendrogram**

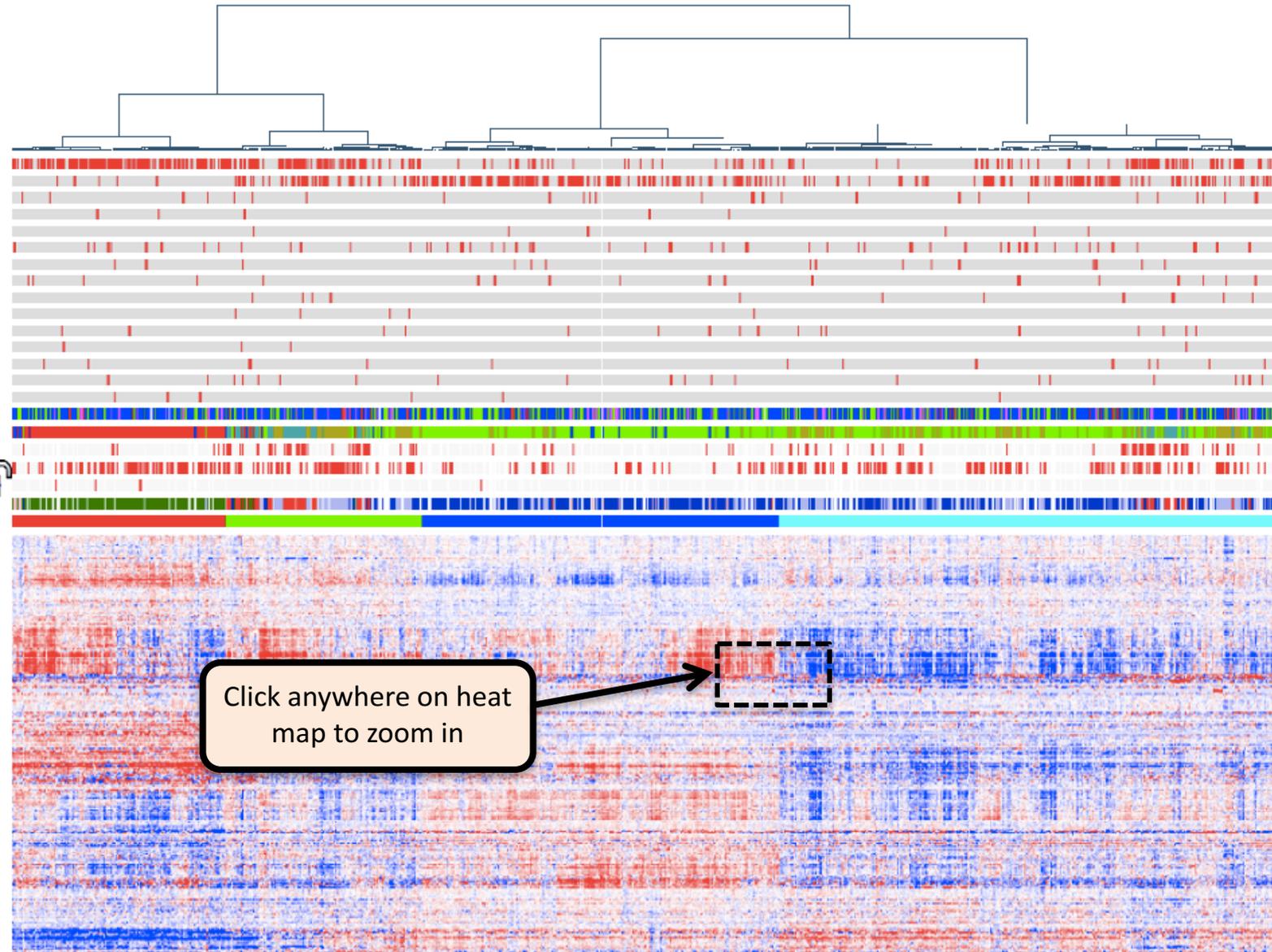
**Image Details**

Column (Data):  
Column (Display):  
Row (Data):  
Row (Display):  
Value:

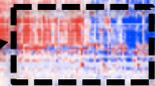
**Covariate Details**

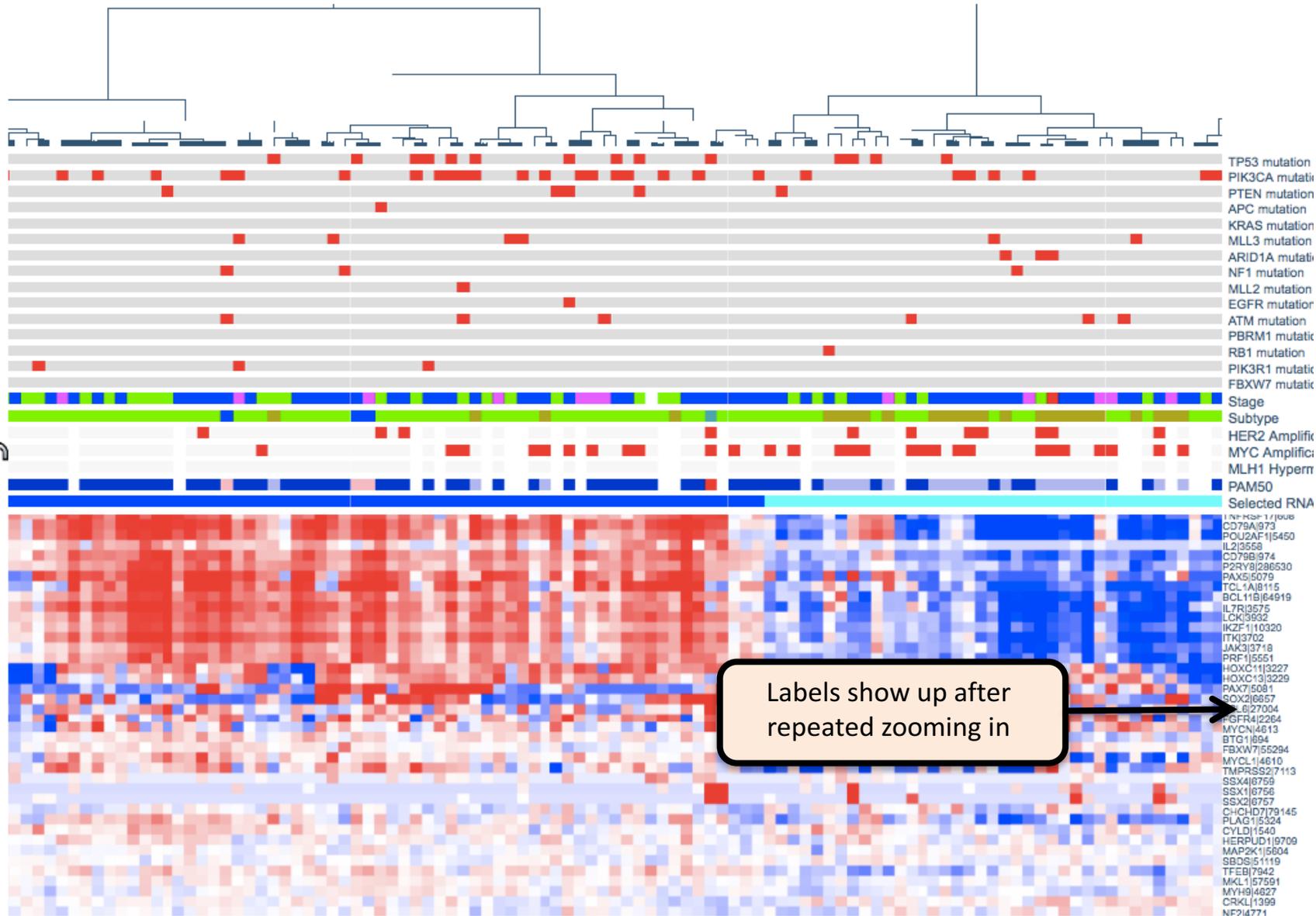
PIK3CA mutatio  
PTEN mutatio  
APC mutatio  
KRAS mutatio  
MLL3 mutatio  
ARID1A mutatio  
NF1 mutatio  
MLL2 mutatio  
EGFR mutatio  
ATM mutatio  
PBRM1 mutatio  
RB1 mutatio  
PIK3R1 mutatio  
GNAW1 mutatio  
Stage  
Subtype  
HER2 Amplific  
MYC Amplifica  
MLH1 Hyperme  
PAM50  
Selected RNA

**Navigator**

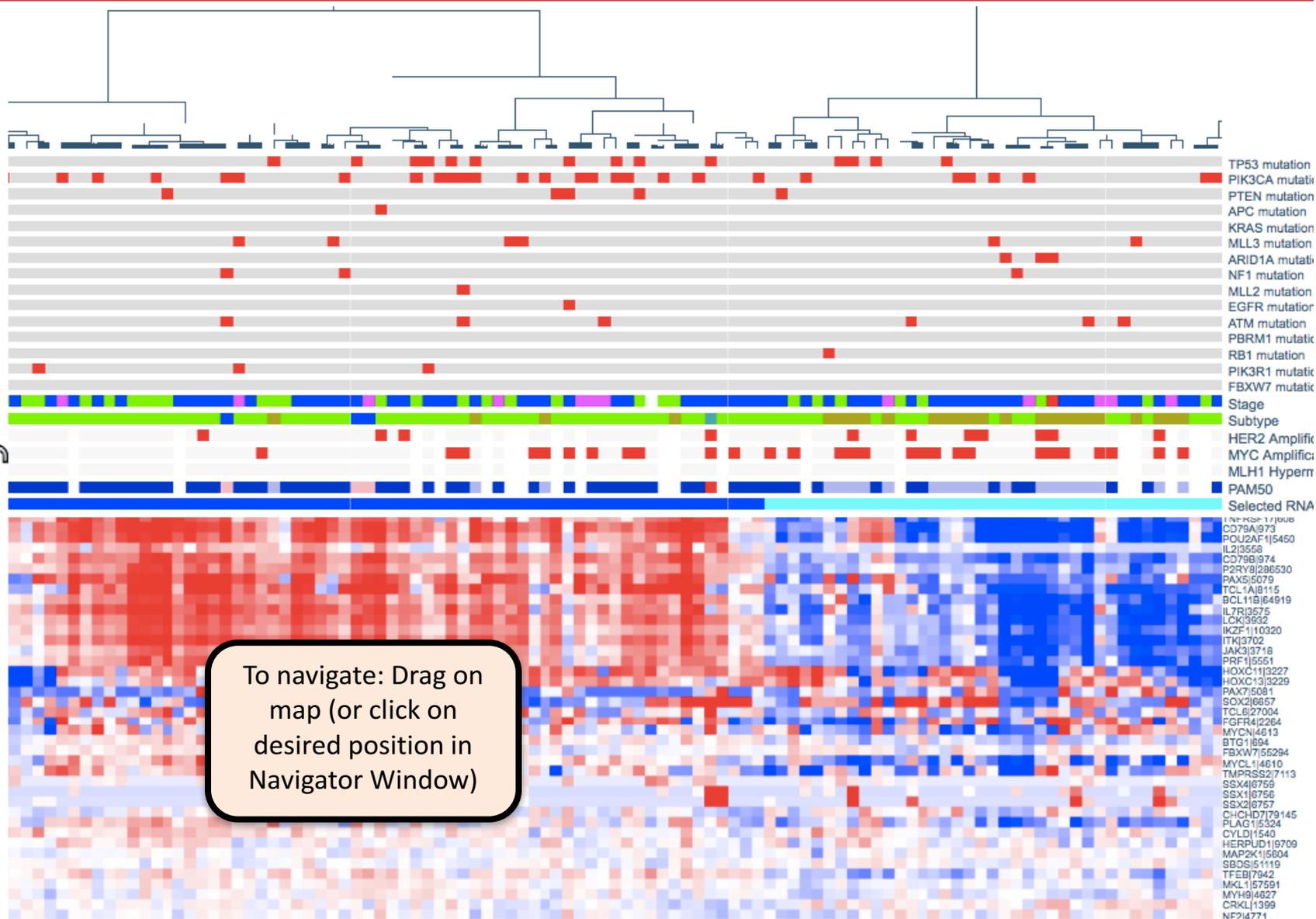


Click anywhere on heat map to zoom in

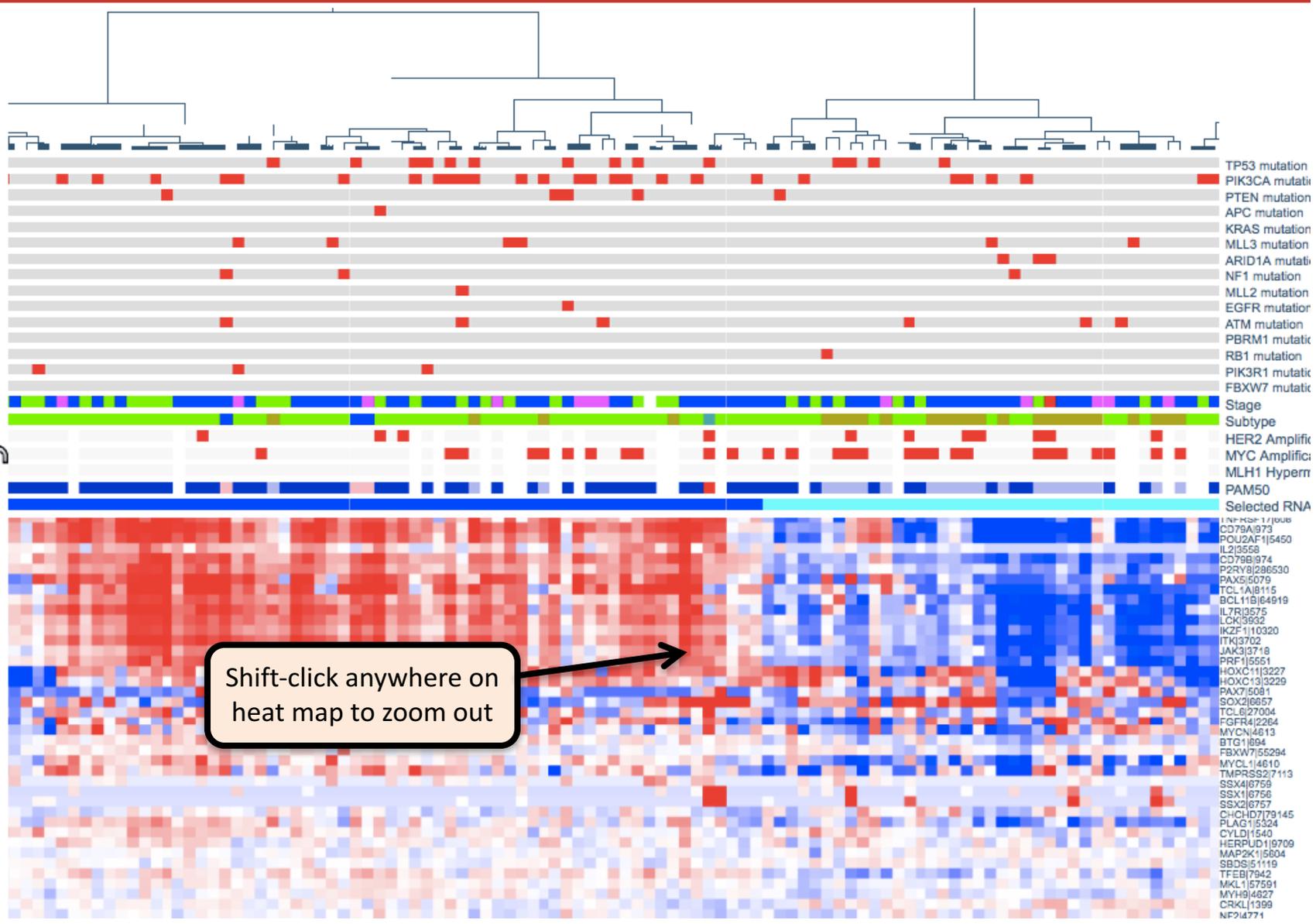




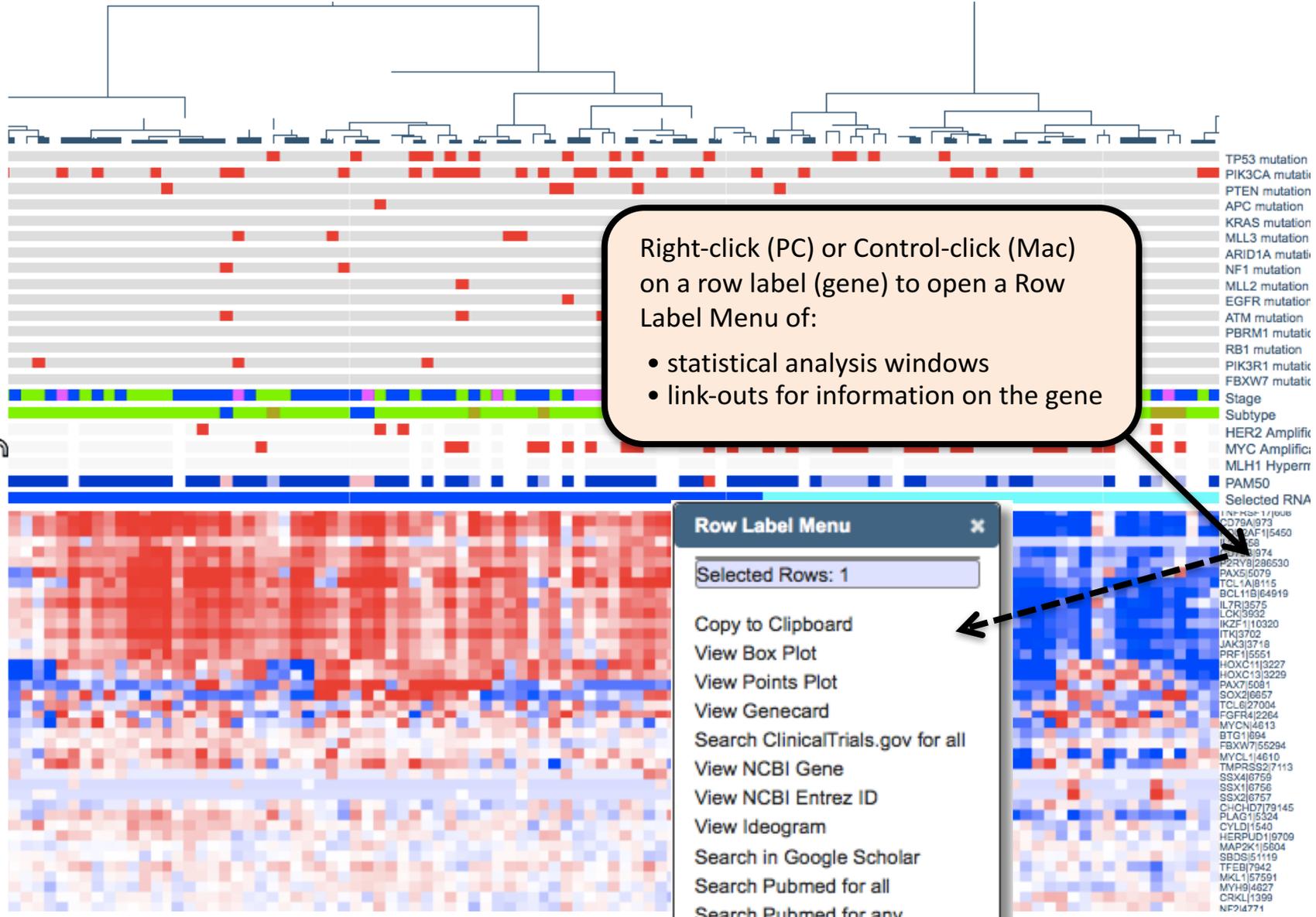
Labels show up after repeated zooming in



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

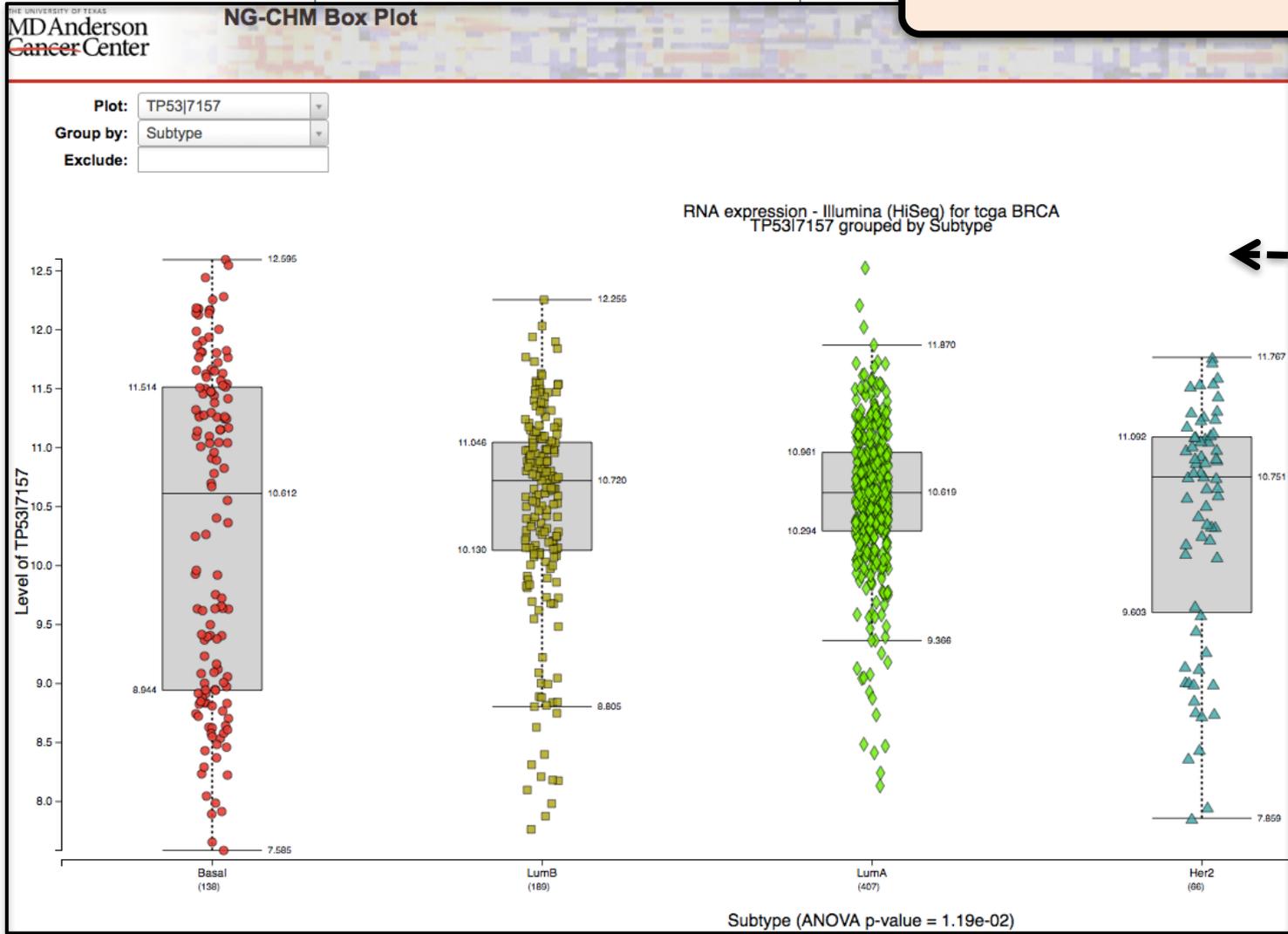
**Row Label Menu** [X]

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](#)

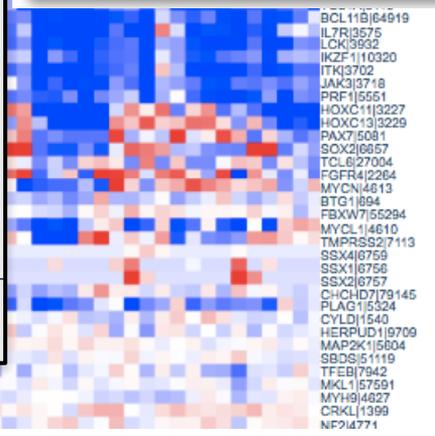
Select "View Box Plot" from Menu



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



# NG-CHM Points Plot

ing the TCGA Pan-Cancer freezeV4 data.

Plot: TP53I7157

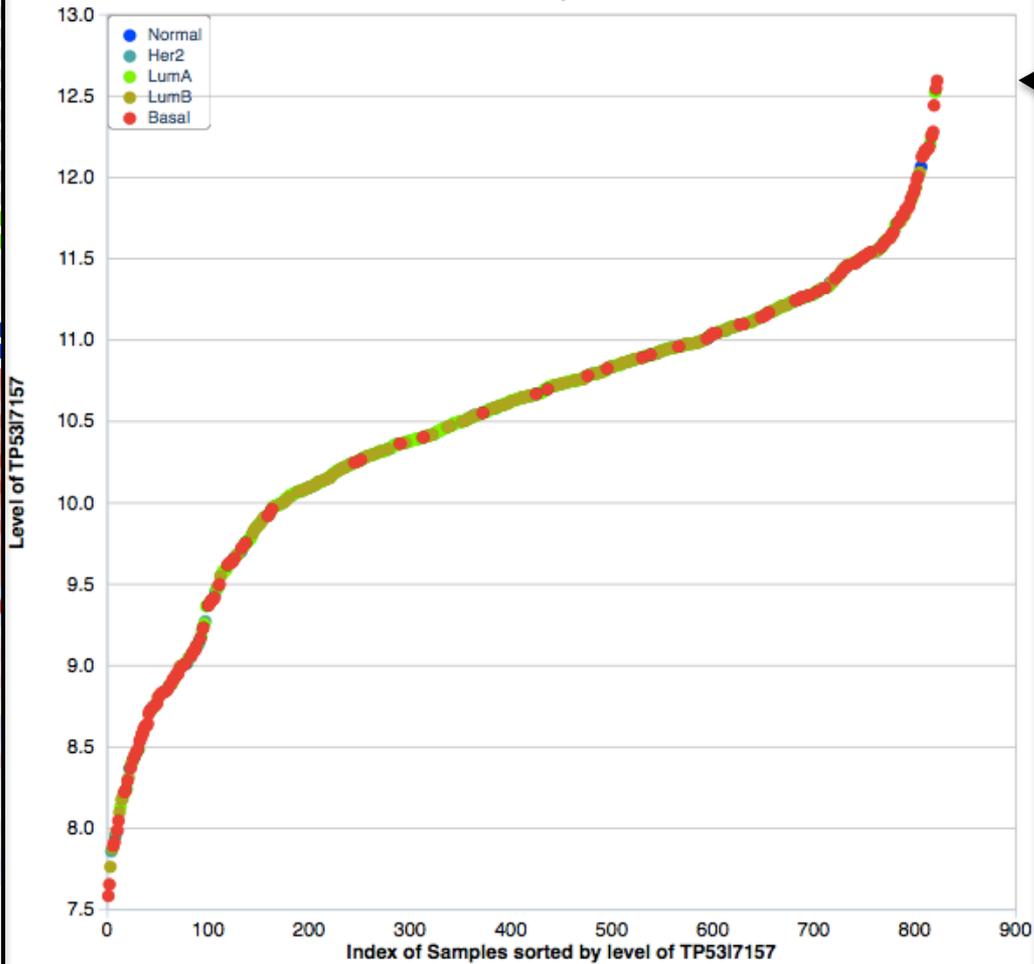
Group by: Subtype

Threshold:

True Positives:

False Positives:

RNA expression - Illumina (HiSeq) for tcga BRCA  
 TP53I7157



**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

Zoom Reset Zoom Out Zoom In ?

■ gene1  
■ Oncogene  
■ Suppressor



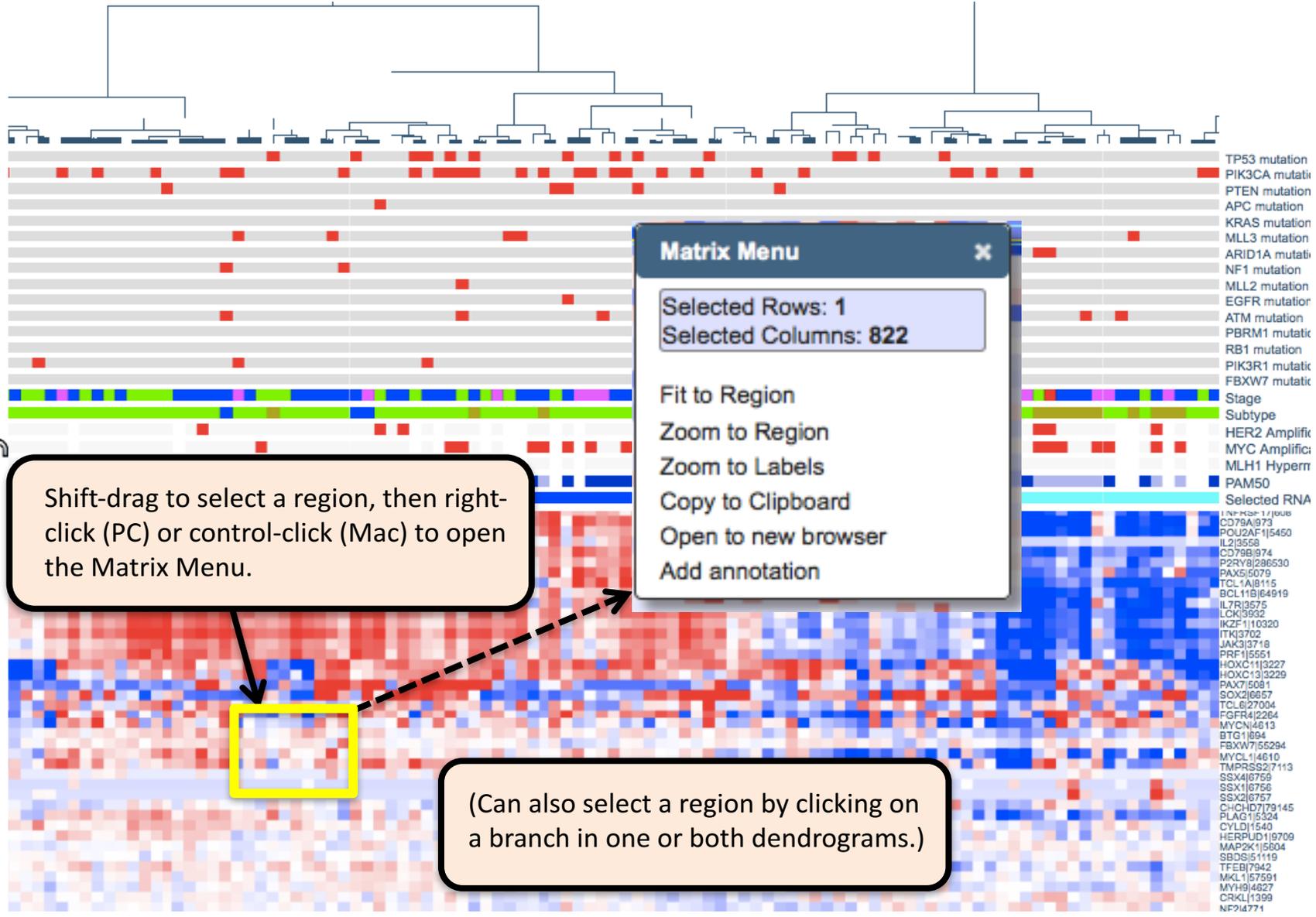
**Ideogram Viewer key features**

- 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 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



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

**Matrix Menu** x

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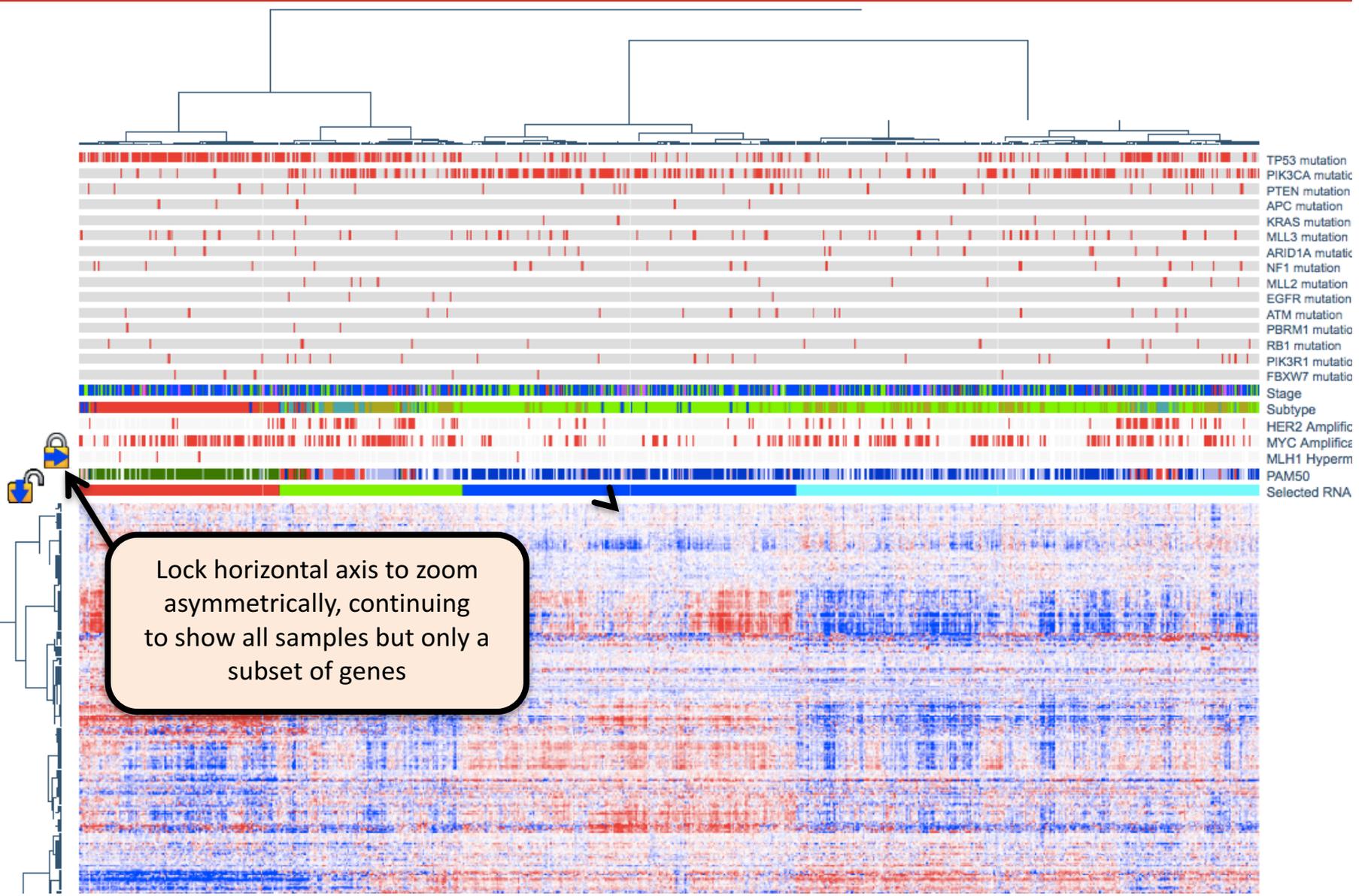
Selected Rows: 1  
 Selected Columns: 822

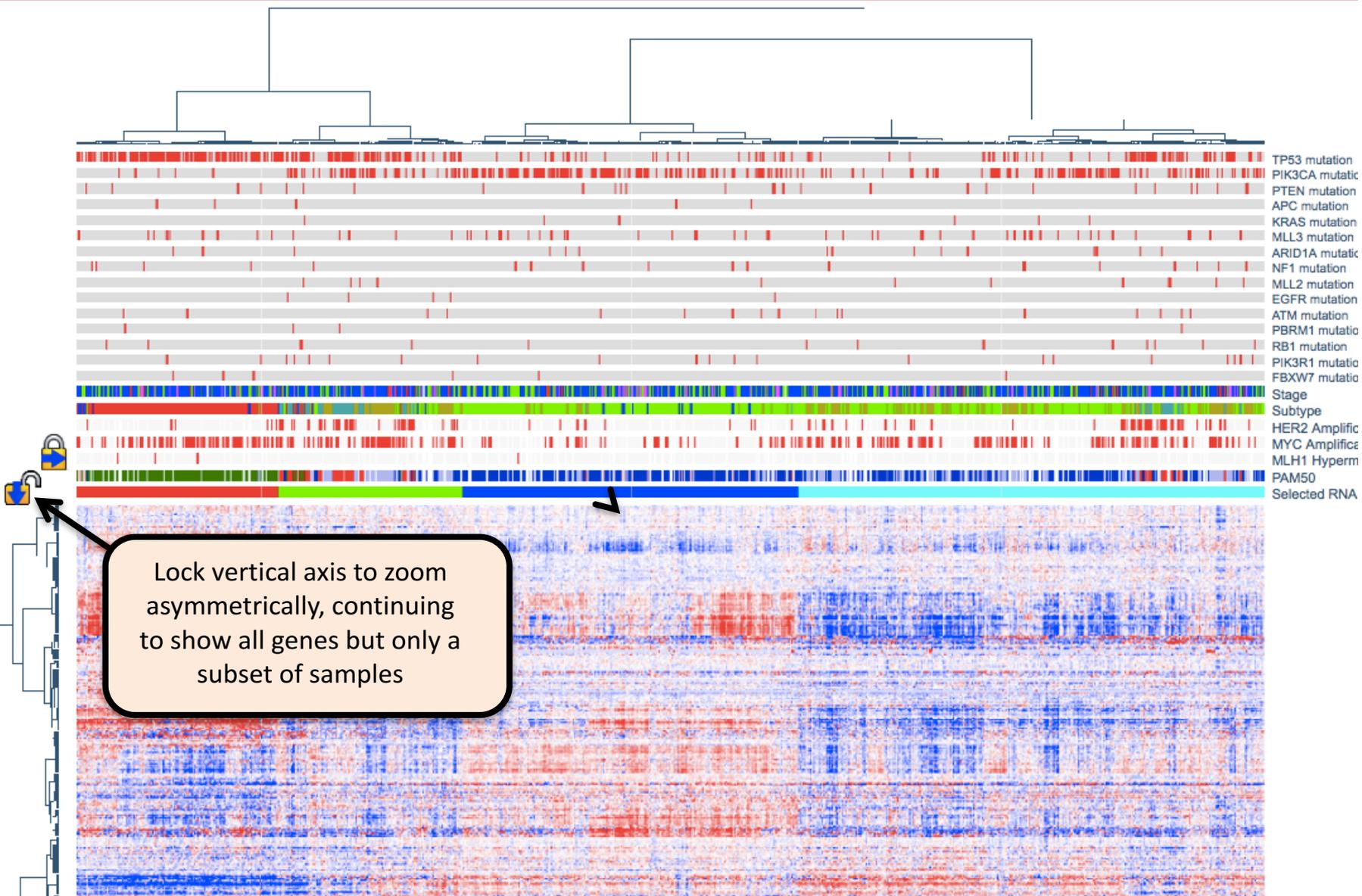
---

Fit to Region  
 Zoom to Region  
 Zoom to Labels  
 Copy to Clipboard  
 Open to new browser  
 Add annotation

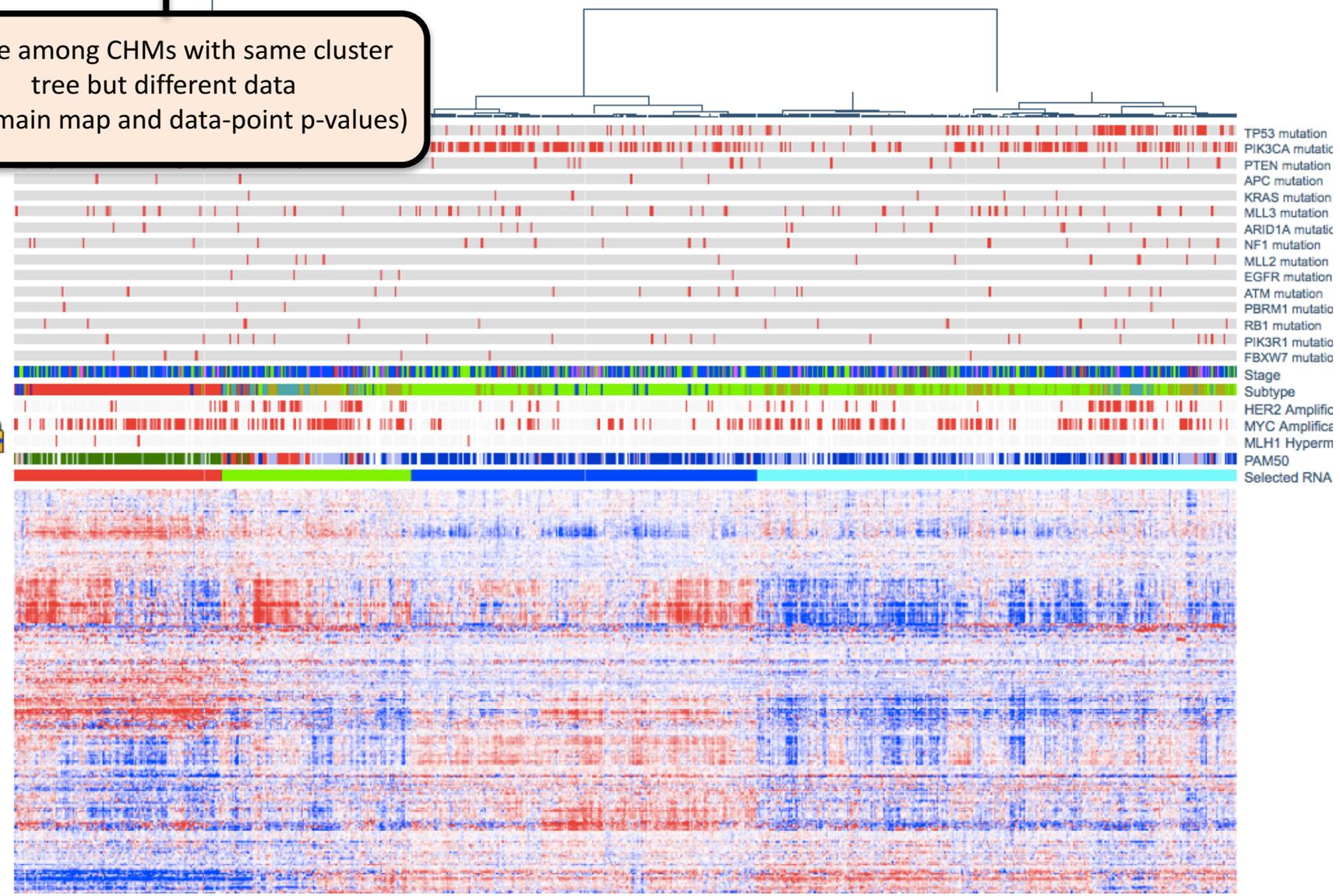
(Can also select a region by clicking on a branch in one or both dendrograms.)

- TP53 mutation
- PIK3CA mutati
- PTEN mutation
- APC mutation
- KRAS mutation
- MLL3 mutation
- ARID1A mutati
- NF1 mutation
- MLL2 mutation
- EGFR mutator
- ATM mutation
- PBRM1 mutat
- RB1 mutation
- PIK3R1 mutati
- FBXW7 mutati
- Stage
- Subtype
- HER2 Amplific
- MYC Amplific
- MLH1 Hyperm
- PAM50
- Selected RNA
- LNFBKSF11008
- CD79A/973
- POU2AF1/5450
- IL2/3558
- CD79B/974
- P2RY8/286530
- PAX5/6079
- TCL1A/8115
- BCL11B/64919
- IL7R/3575
- LCK/9592
- IKZF1/10320
- ITK/3702
- JAK3/3718
- PRF1/5551
- HOXC11/3227
- HOXC13/3229
- PAX7/6081
- SOX2/6657
- TCL6/27004
- FGFR4/2264
- MYCN/4513
- BTG1/694
- FBXW7/55294
- MYCL1/4610
- TMPRSS2/7113
- SSX4/6759
- SSX1/6756
- SSX2/6757
- CHCHD7/79145
- PLAG1/5324
- CYLD/1540
- HERPJD1/9709
- MAP2K1/5804
- SBDS/51119
- TFEB/7942
- MKL1/57591
- MYH9/4627
- CRKL/1399
- NF2/4774

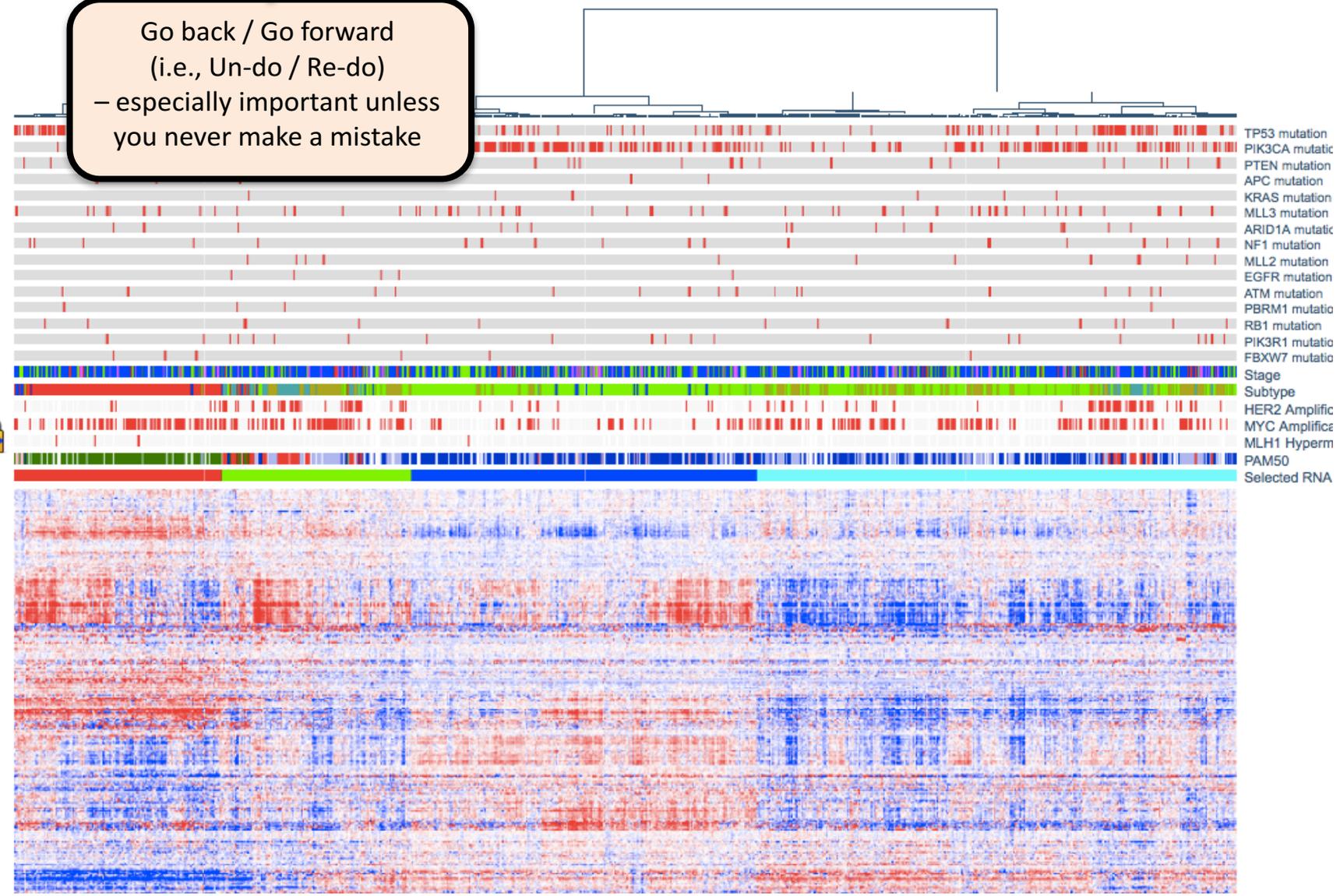




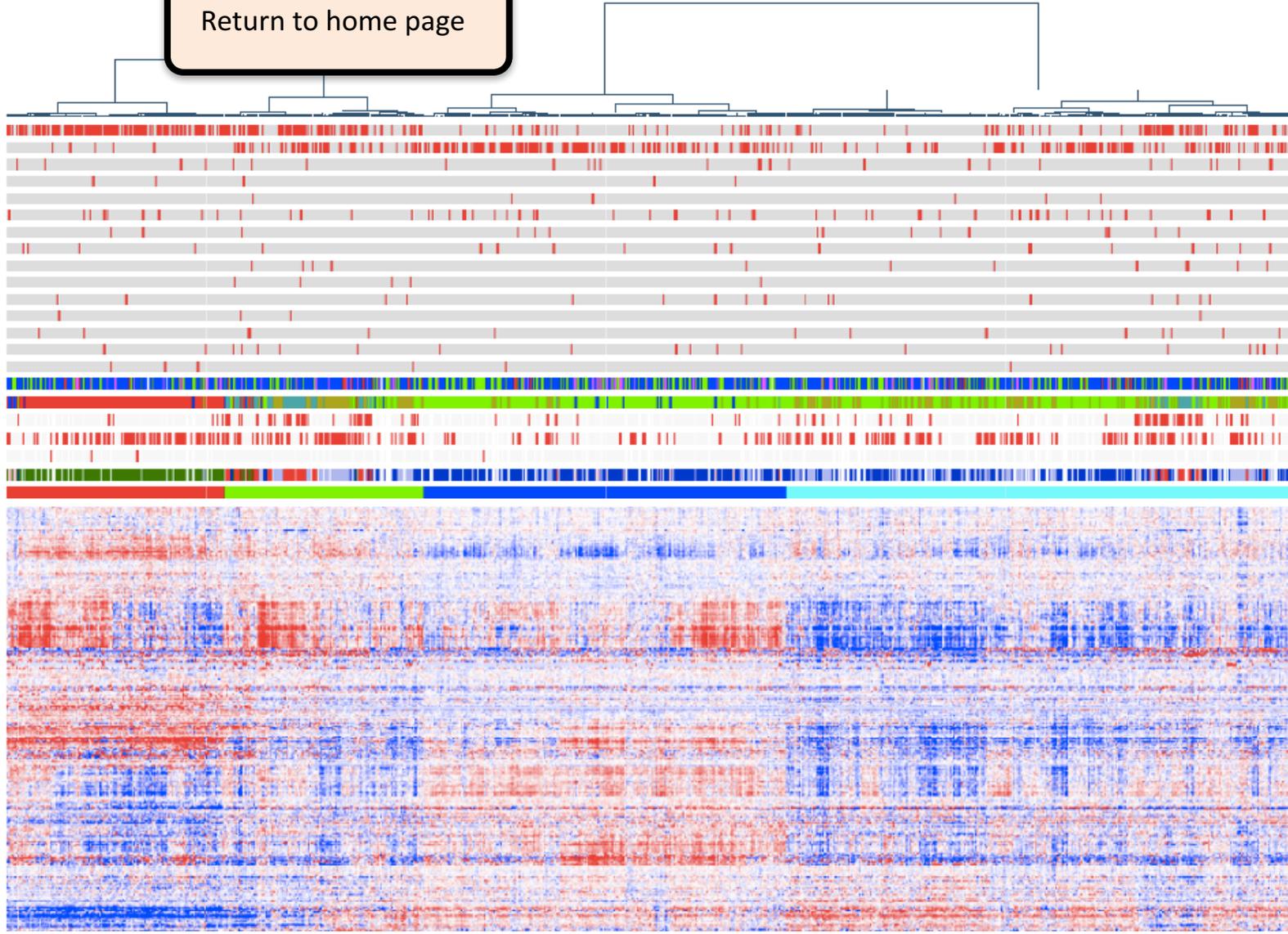
Toggle among CHMs with same cluster tree but different data (e.g., main map and data-point p-values)



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

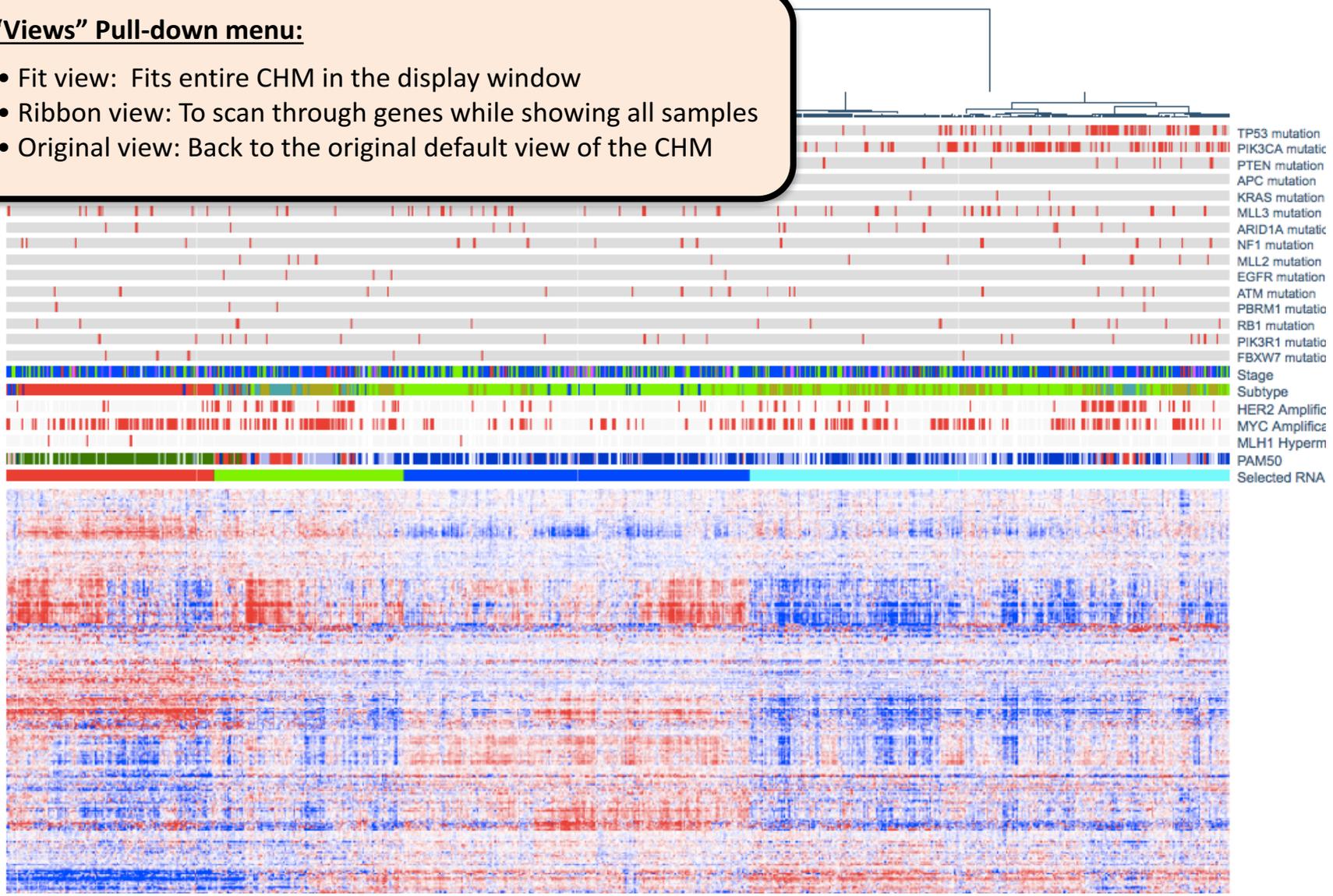


Return to home page



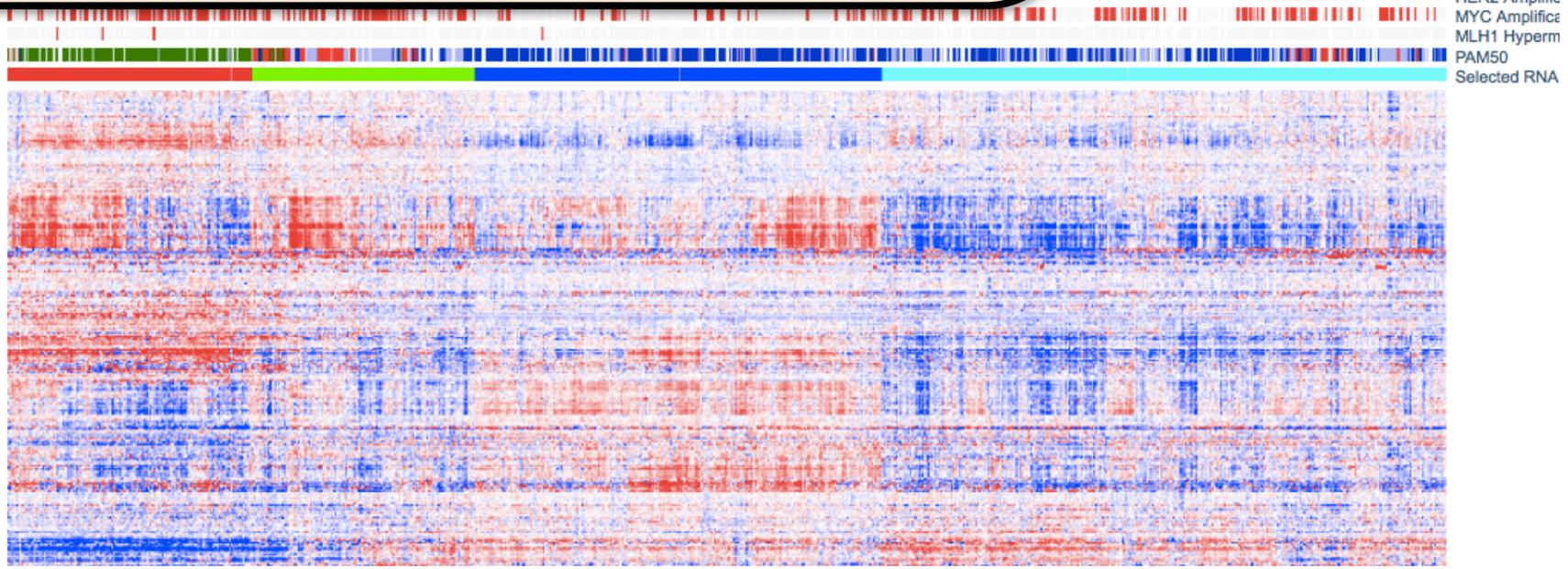
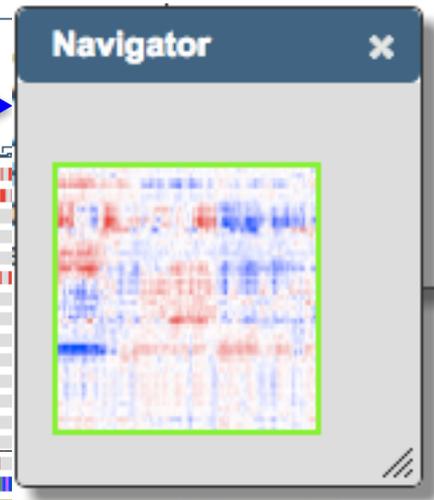
**“Views” Pull-down menu:**

- 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



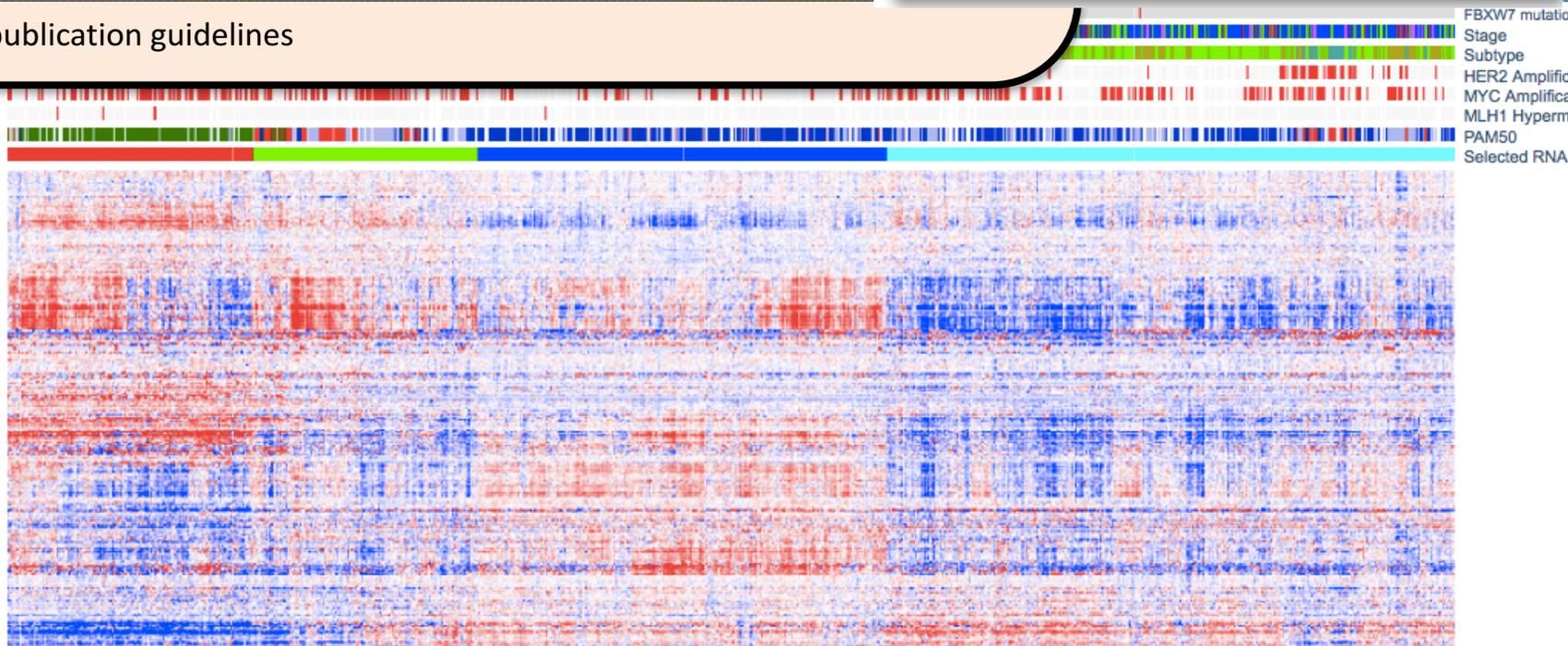
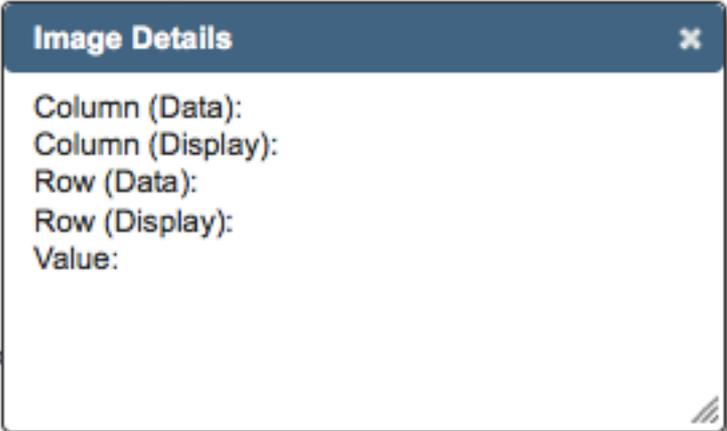
**“Dialogs” menu for opening movable, resizable windows:**

- 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*
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  - Credits
- 
- TCGA publication guidelines

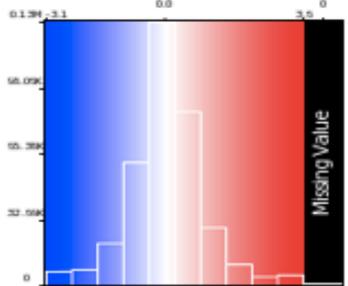
### Color Scheme

**Define New Custom Color Scheme:**

Select Color Scheme Type:  
linear

Color	Break Point	Add / Remove
	-10.184	+/-
	1.370	+/-
	12.924	+/-
<b>Missing Value Color</b>		

Render Preview



**Select Color Scheme to Render:**

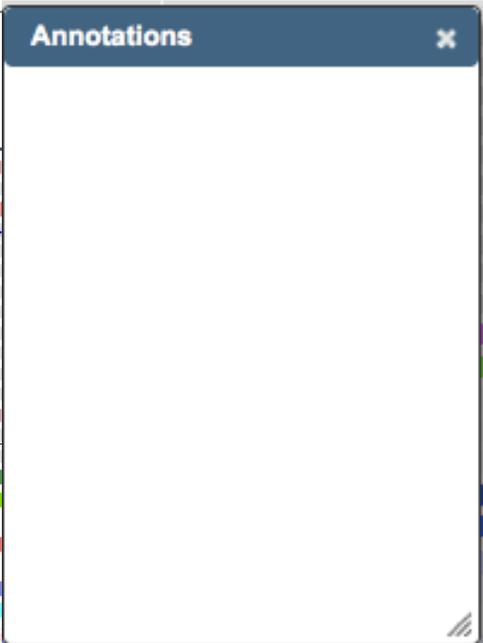
Permanent Color Schemes

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



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

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  - Image details: *row/column/value data*
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  - 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*
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The image shows a software interface with a main heatmap and several dialog boxes. The 'Annotations' dialog box is open on the right side, showing a white area for text input. A blue arrow points from the 'Annotations' item in the list to this dialog box. The main heatmap below shows a color scale from blue to red, with a dendrogram on the left side. There are also some smaller dialog boxes or controls at the top left of the heatmap area.

**“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

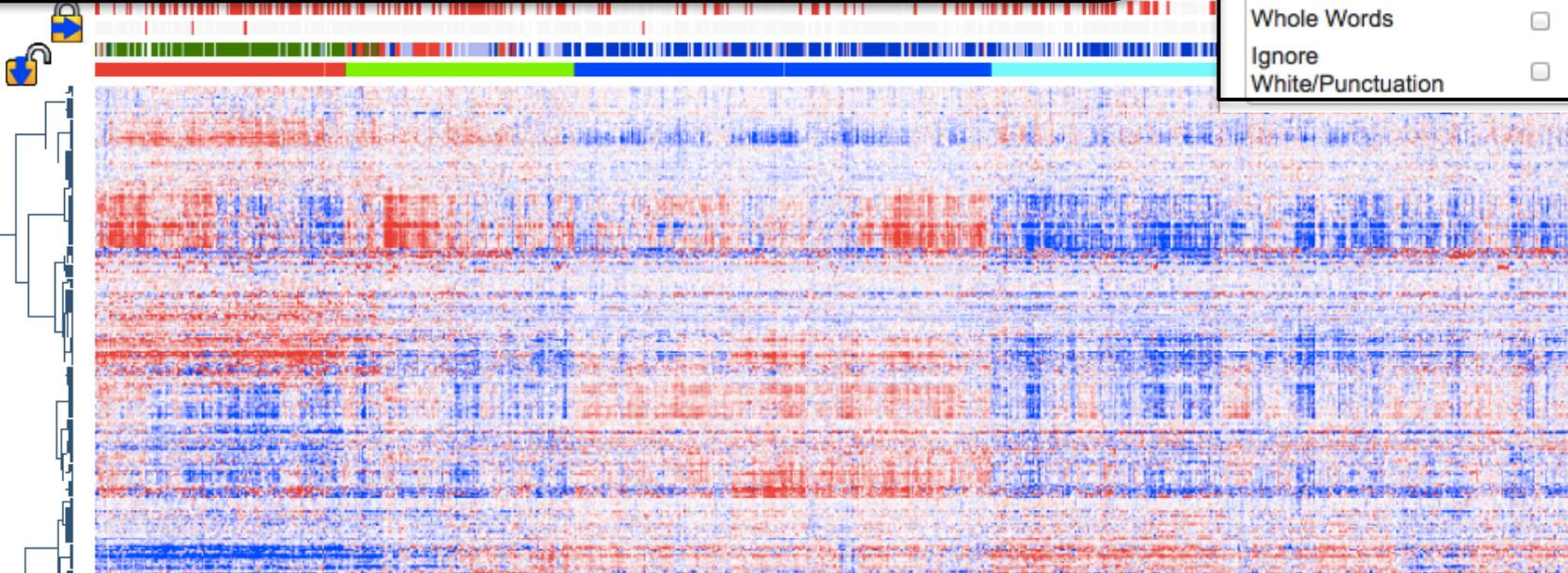
**Advanced Search** ✕

Column Search Term:

Row Search Term:

Search Options:

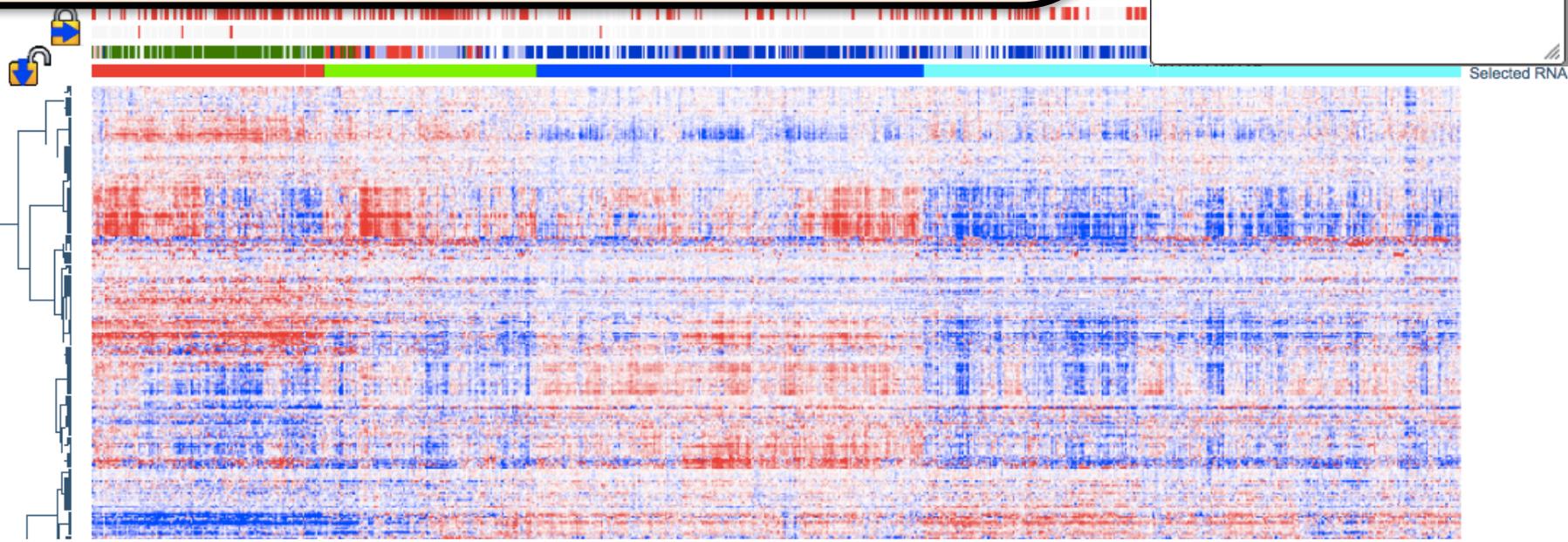
Search Syntax	Column	Row
Simple	<input checked="" type="radio"/>	<input checked="" type="radio"/>
Regular Expression	<input type="radio"/>	<input type="radio"/>
Case Sensitive	<input type="checkbox"/>	<input type="checkbox"/>
Whole Words	<input type="checkbox"/>	<input type="checkbox"/>
Ignore White/Punctuation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

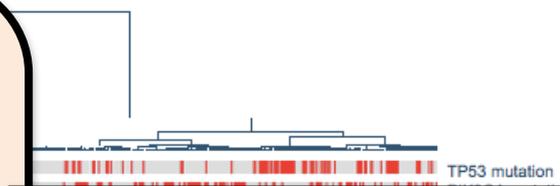
A dialog box titled "Covariate Details" with a close button (X) in the top right corner. The dialog box is currently empty. It is positioned over a heatmap visualization. An arrow from the text "Mouse-over for details on covariate bars and their distributions" in the list points to this dialog box.





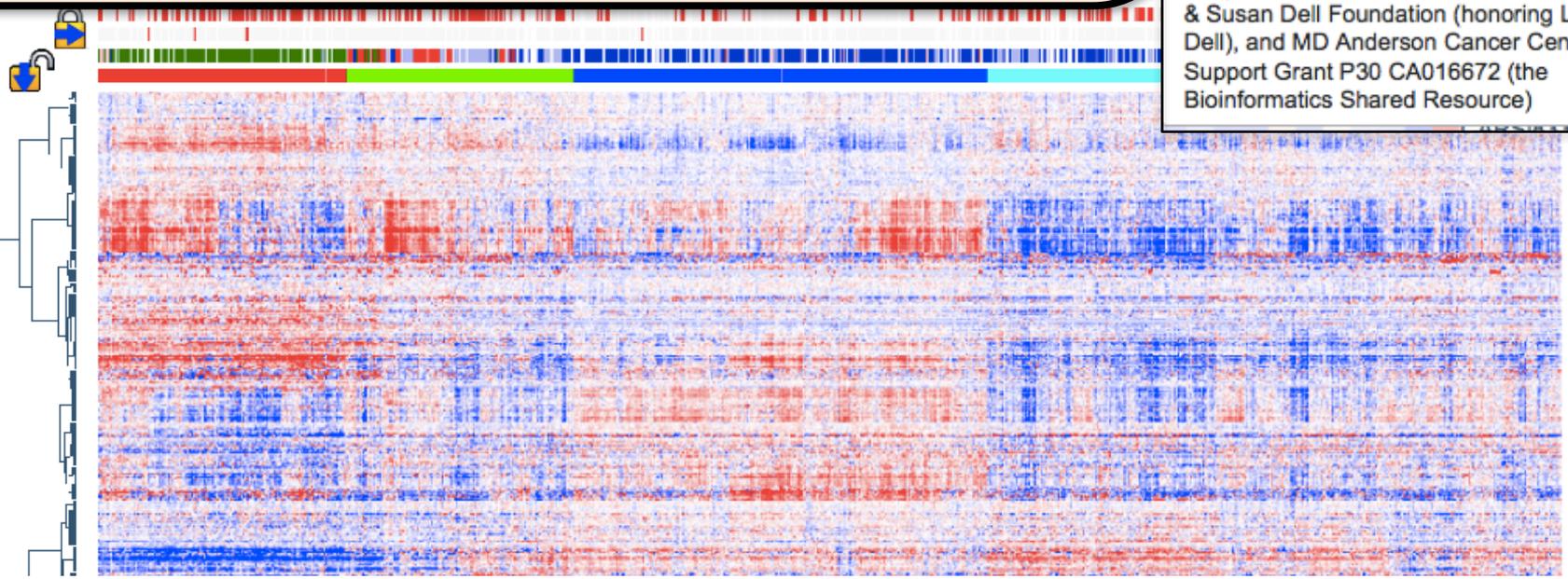
**“Dialogs” menu for opening movable, resizable windows:**

- 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
- 
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**About NG-CHM** ✕

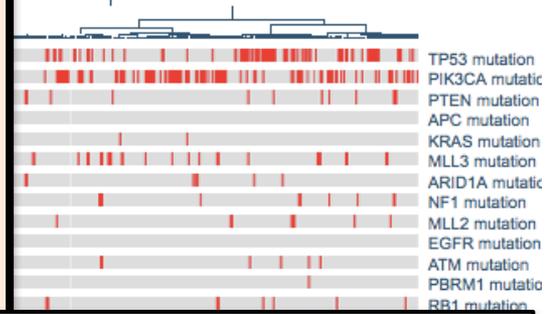
Developed by the MD Anderson Cancer Center Department of Bioinformatics and Computational Biology, SRA International, and In Silico Solutions. This work was supported in part by U.S. National Cancer Institute (NCI; MD Anderson TCGA Genome Data Analysis Center) grant numbers CA143883 and CA083639, the 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:**

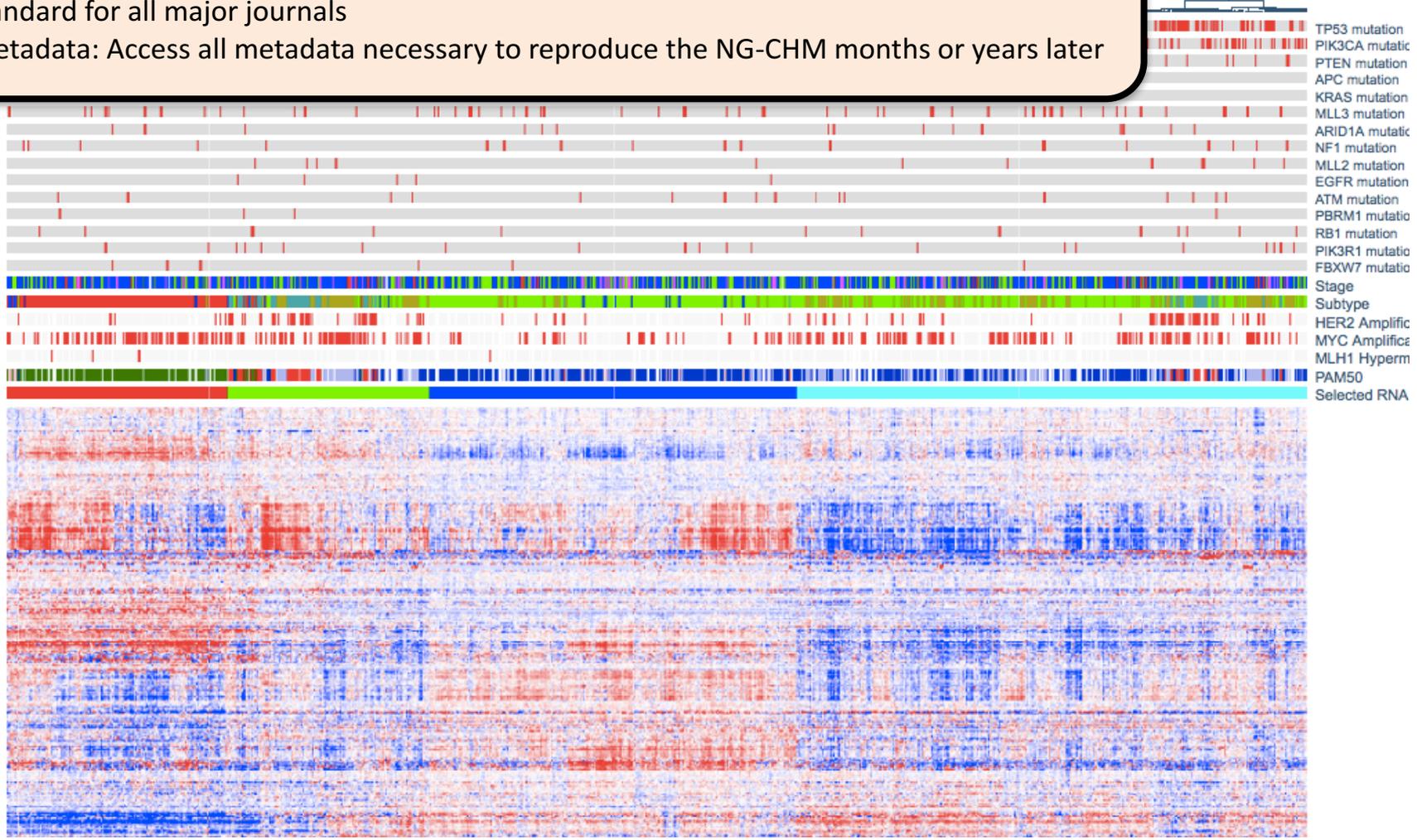
- Navigator
- Image details: *row/column/value data*
- Color Schemes: *create and/or change color scheme on the fly*
- Annotations
- Advanced search: *Advanced syntax/row/column searches*
- Covariate details: *Mouse-over for details on covariate bars and their distributions*
- Covariate control panel: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

• TCGA publication guidelines



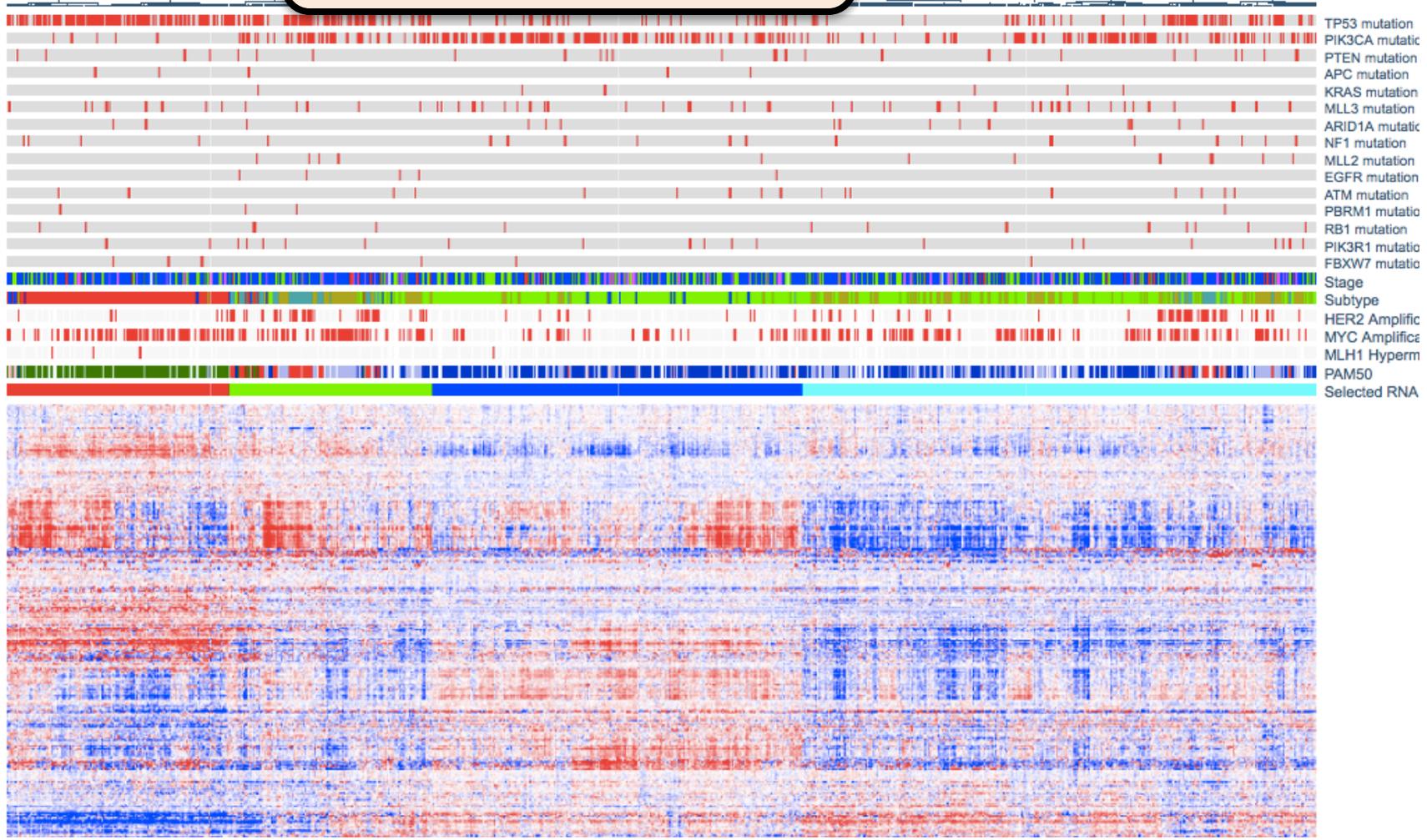
**“Miscellaneous” menu:**

- 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

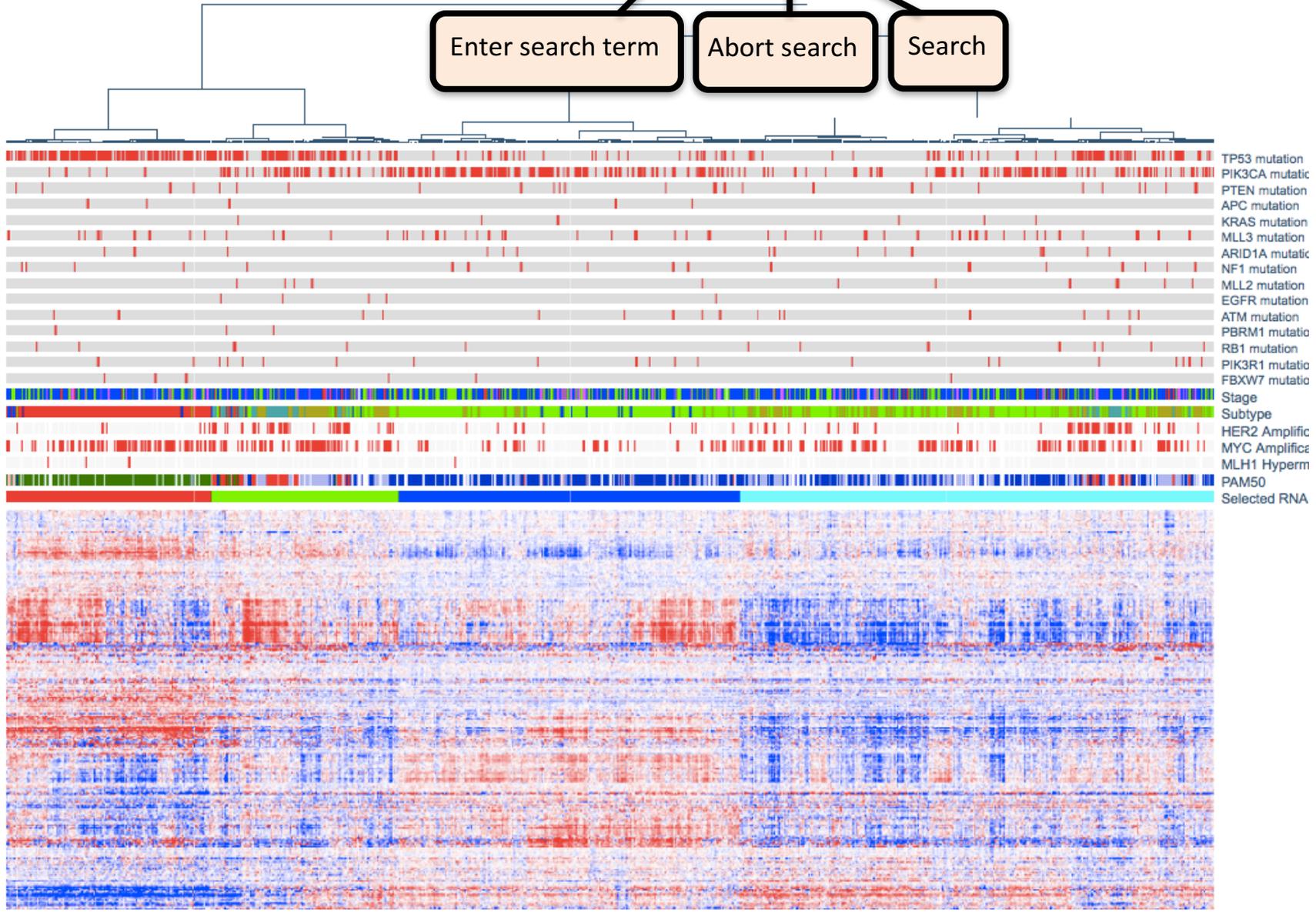


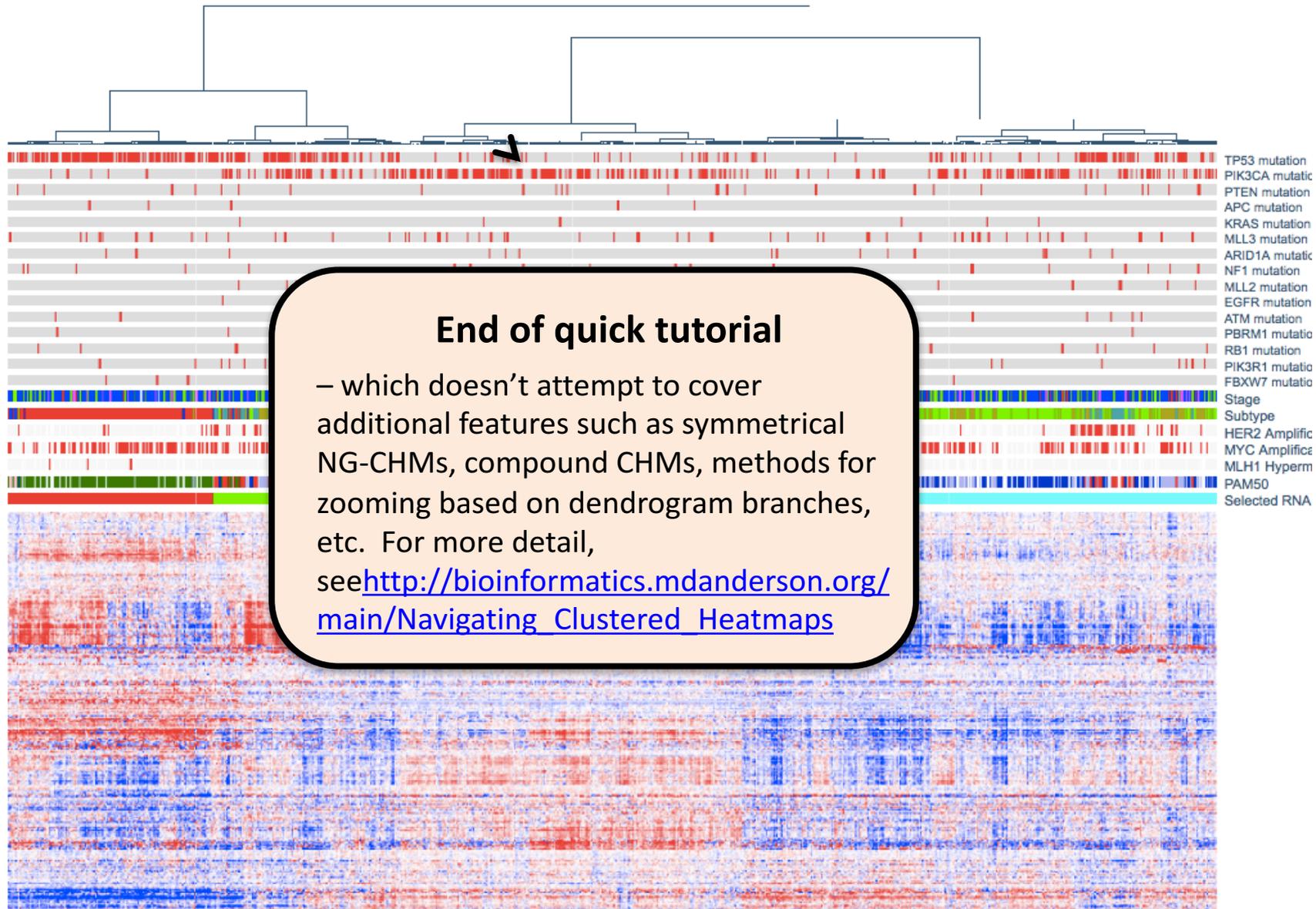
**“?” menu:**

- Basic instructions for first-time users



Enter search term    Abort search    Search





**End of quick tutorial**

– which doesn't attempt to cover additional features such as symmetrical NG-CHMs, compound CHMs, methods for zooming based on dendrogram branches, etc. For more detail, see [http://bioinformatics.mdanderson.org/main/Navigating Clustered Heatmaps](http://bioinformatics.mdanderson.org/main/Navigating_Clustered_Heatmaps)