

**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:**

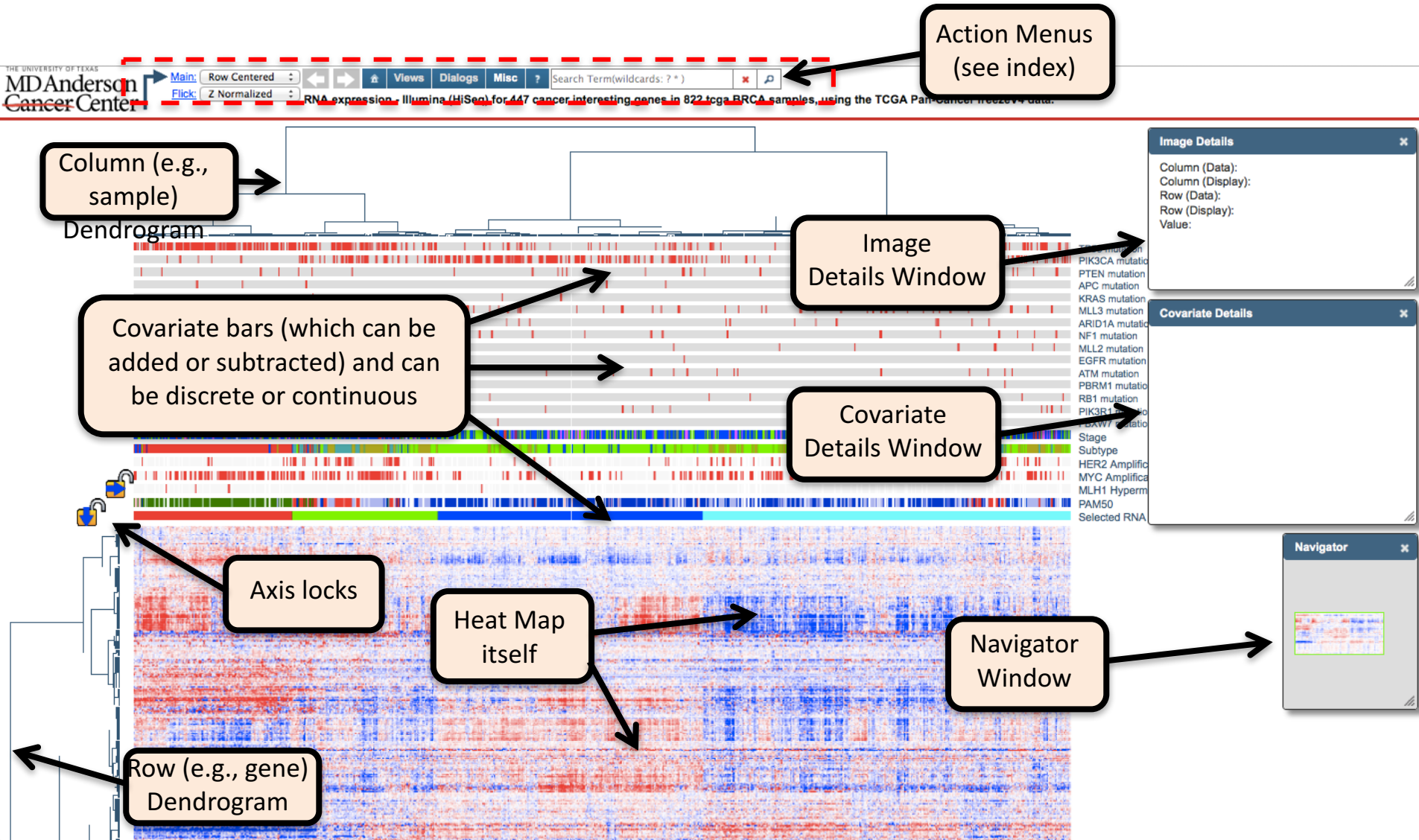
- A TCGA mRNA expression (rows) vs. samples (columns) NG-CHM for breast cancer (as part of our TCGA NG-CHM Compendium: <http://bioinformatics.mdanderson.org/TCGA/NGCHMPortal/>)
- The specific map: [http://bioinformatics.mdanderson.org/chm/chm.html?name=tcga\\_rnaseq\\_brca\\_v1.0\\_gene\\_sample&collectionHome=http%3A%2F%2Fbioinformatics.mdanderson.org%2FTCGA%2FNGCHMPortal%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)

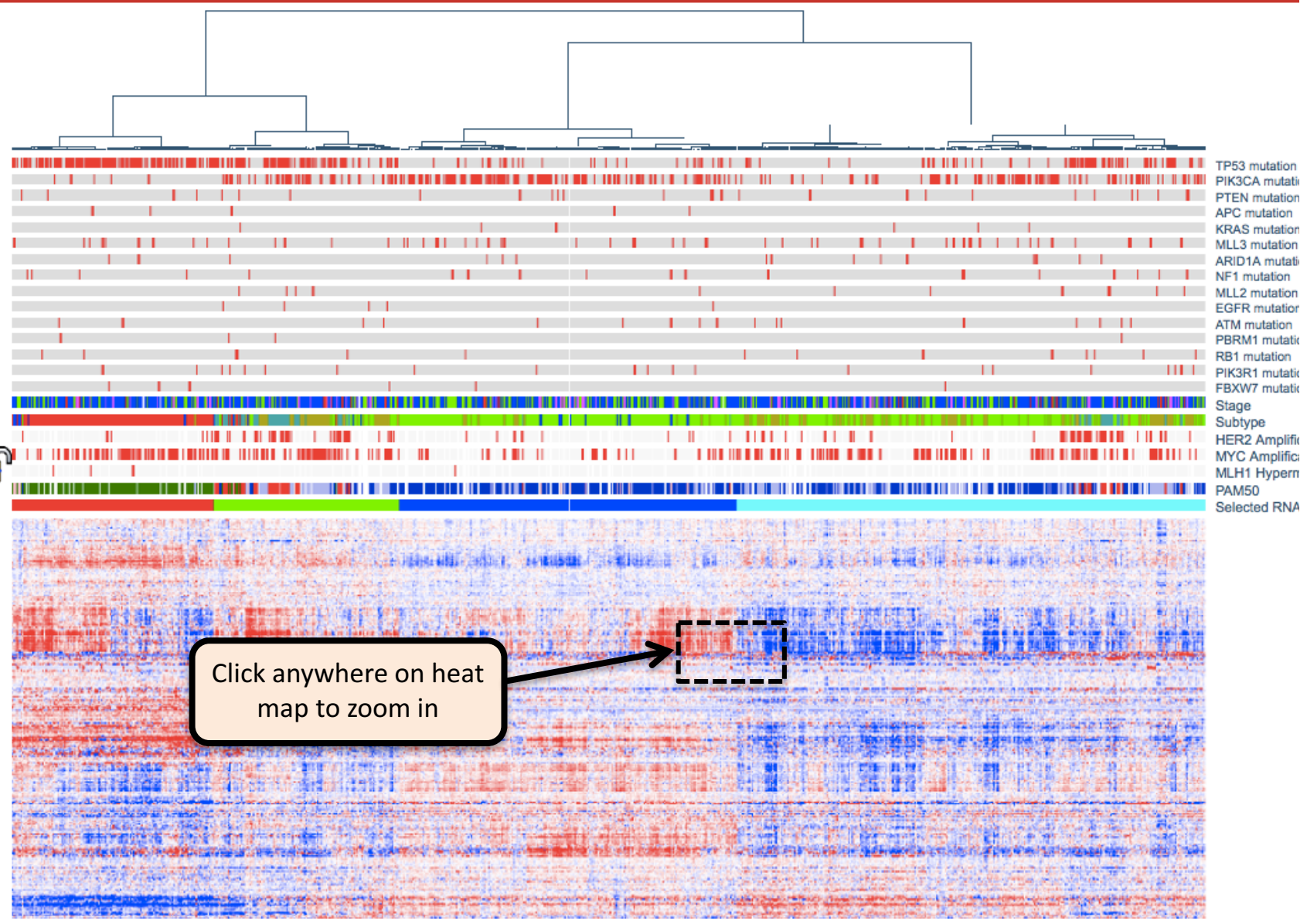
# Index of Slides (with live links to them)

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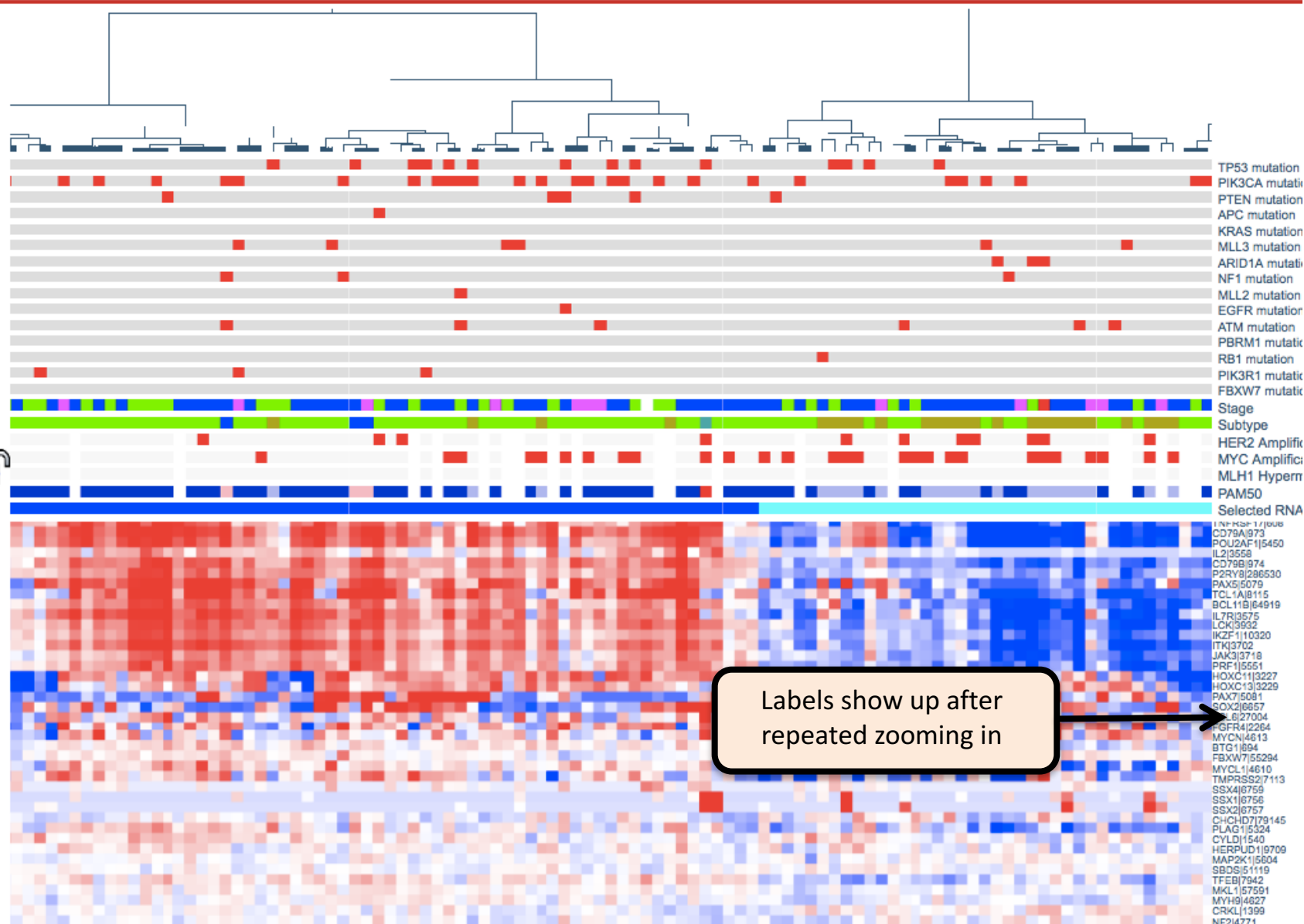
Slide 1: <a href="#">Title Slide</a>	Slide 18: <a href="#">Views Menu</a>
Slide 2: <a href="#">Index of slides</a>	Slides 19 – 26: Dialogs Menu
Slide 3: <a href="#">Annotated summary screen shot</a>	Slide 19: <a href="#">Navigator Window</a>
Slide 4: <a href="#">Zooming in</a>	Slide 20: <a href="#">Image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

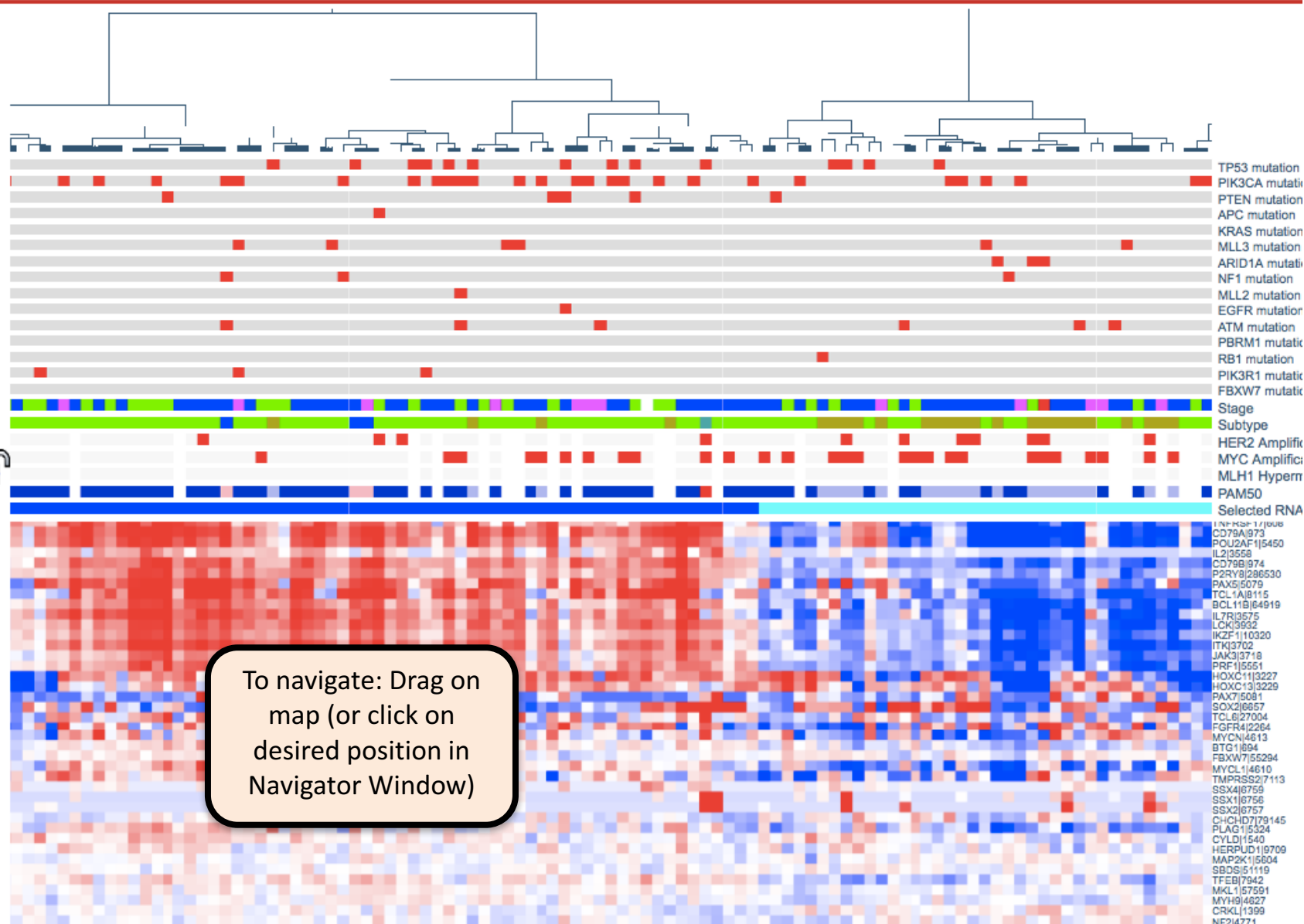
# Main Components of the NG-CHM Viewer

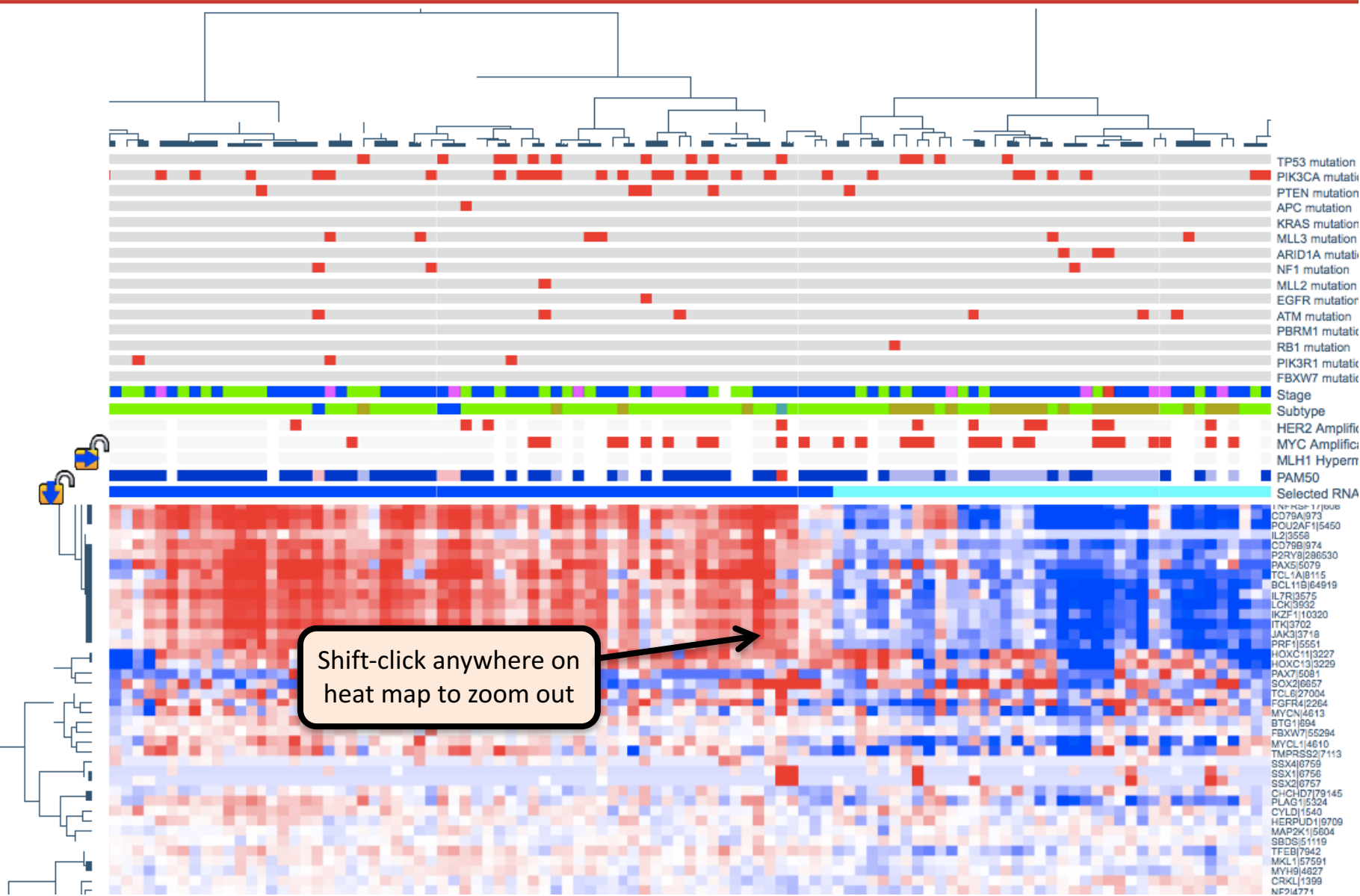


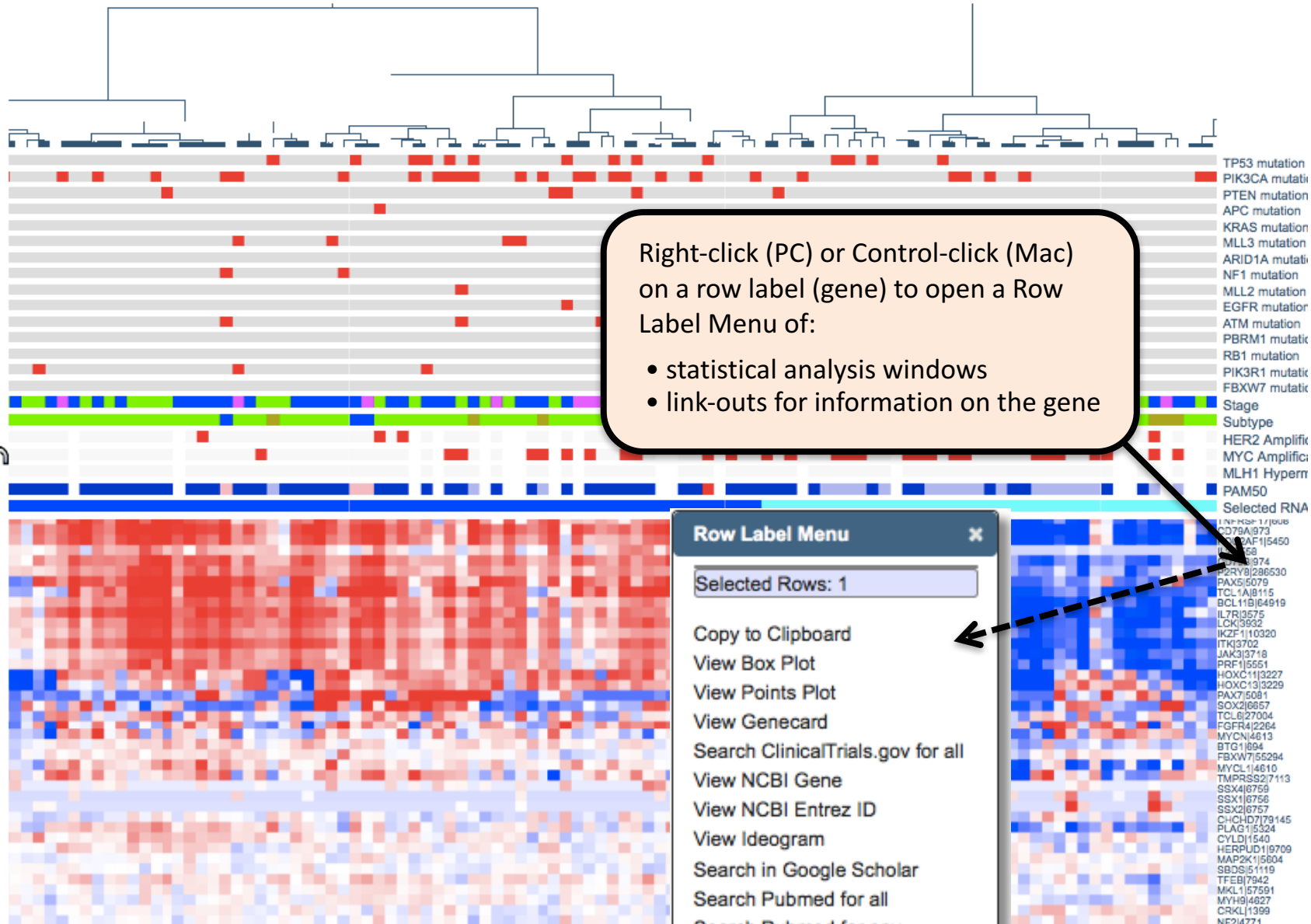






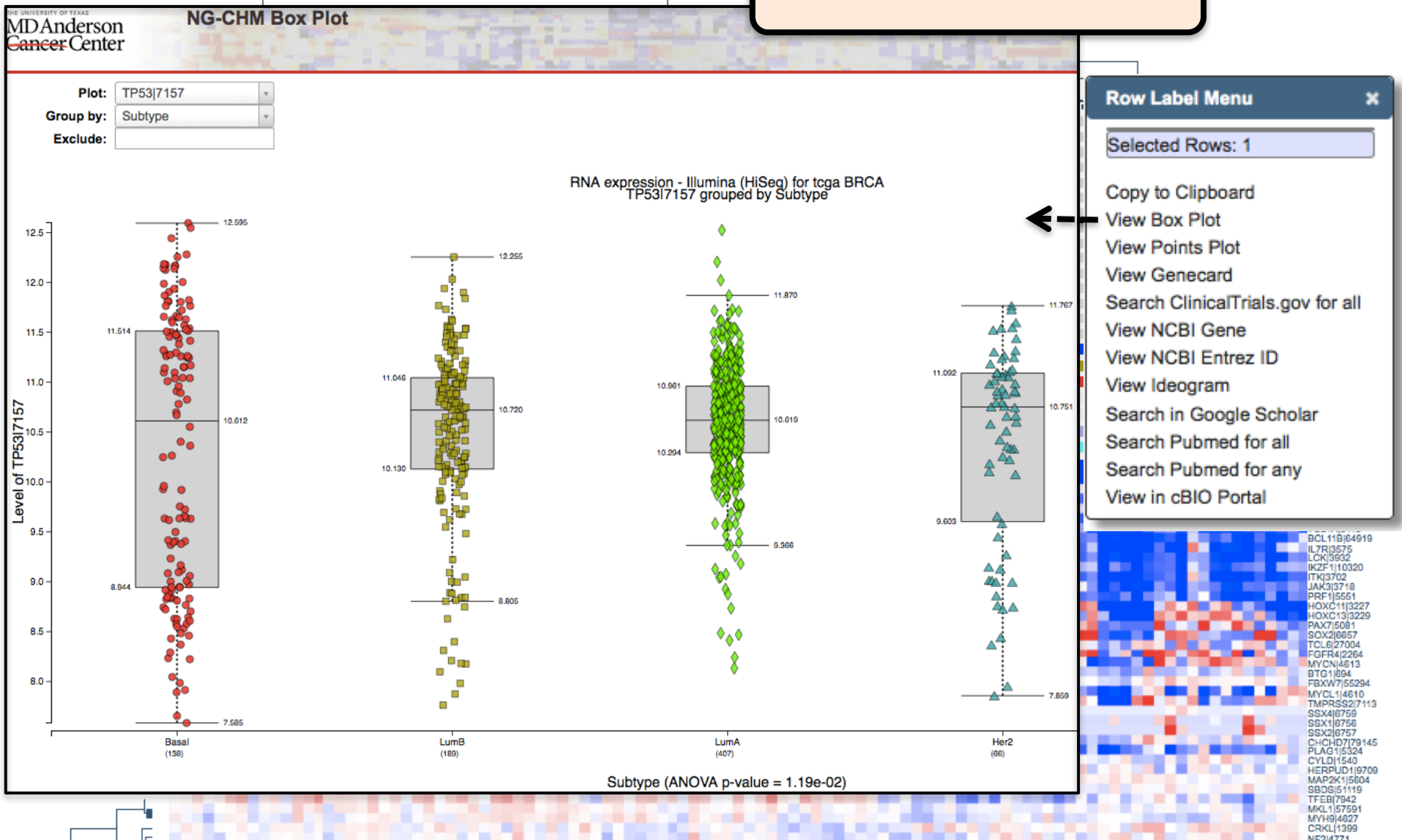








Select "View Box Plot" from Menu



[Back to Index Slide](#)

Plot: TP53I7157

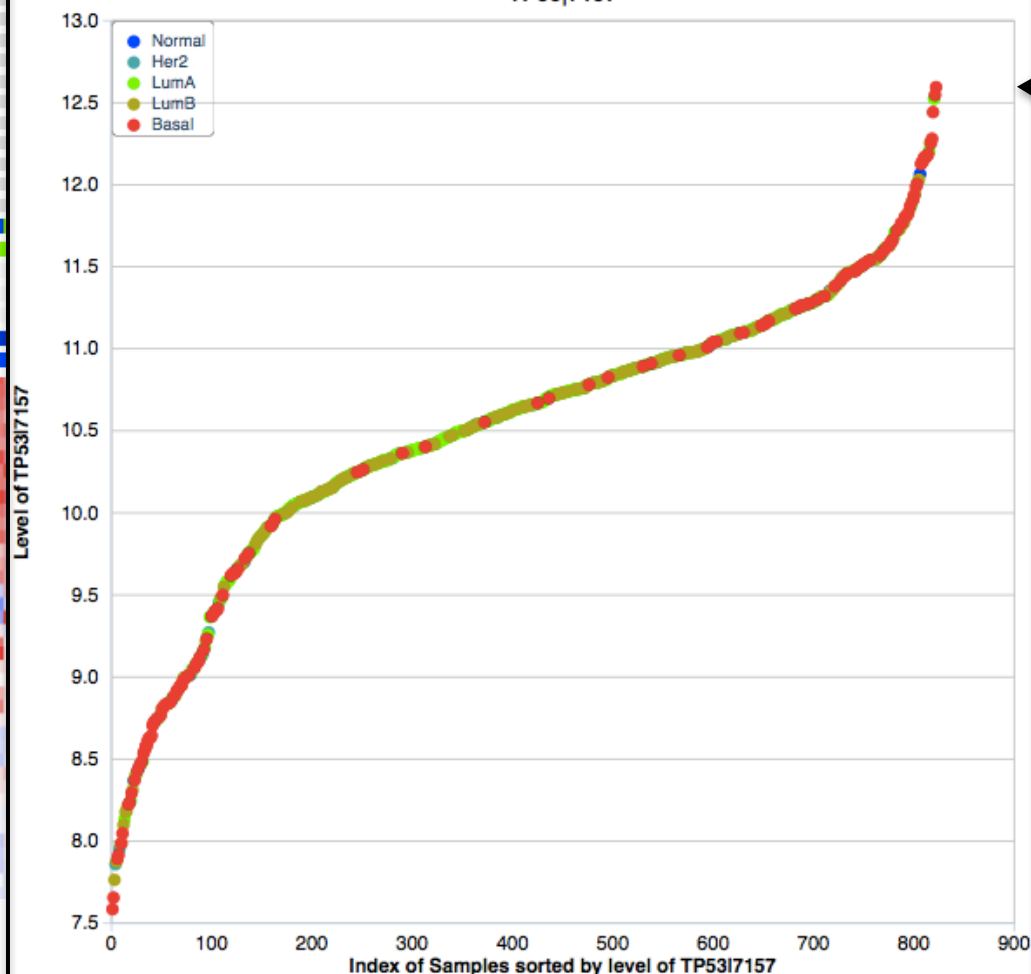
Group by: Subtype

Threshold:

True Positives:

False Positives:

RNA expression - Illumina (HiSeq) for tcga BRCA  
TP53I7157



## 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|64519  
IL7R|3575  
LCK|5532  
IKZF1|10320  
ITK|3702  
JAK3|3718  
PRF1|5551  
HOXC11|3227  
HOXC13|3229  
PAX7|5081  
SOX2|6657  
TCL6|27004  
PGFR4|2264  
MYCN|4613  
BTG1|694  
FBXW7|55294  
MYCL1|4610  
TMPRSS2|7113  
SSX4|6759  
SSX1|6756  
SSX2|6757  
CHCHD7|79145  
PLAG1|5324  
CYLD|1540  
HERPUD1|9709  
MAP2K1|5604  
SBD5|5119  
TFEB|7942  
MKL1|57591  
MYH9|4627  
CRKL|1399  
NFI4771

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## Ideogram Viewer

gene1  
Oncogene  
Suppressor

Zoom Reset

Zoom Out

Zoom In



### Ideogram Viewer key features

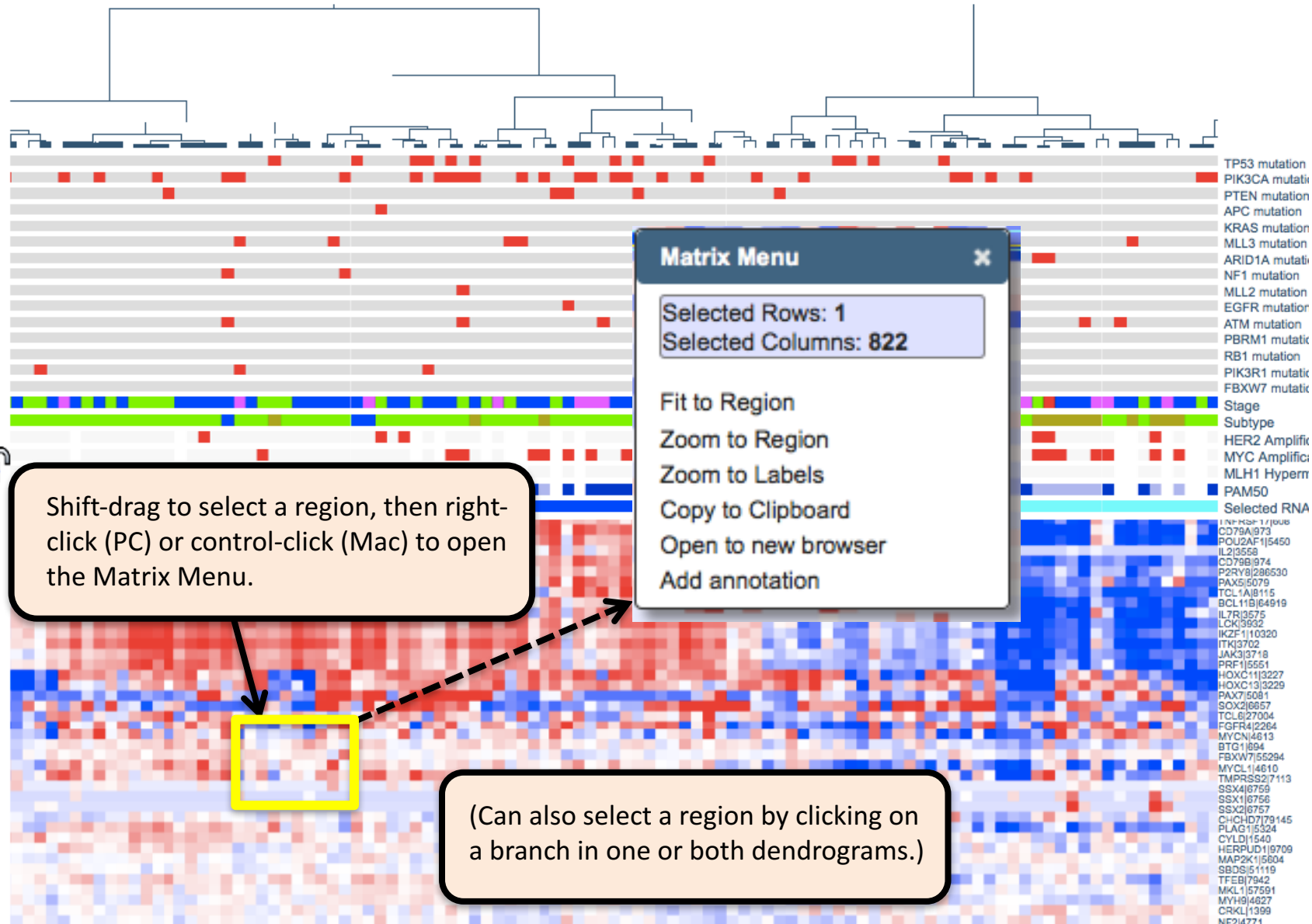
- **Zoom In** : Double-clicking or mouse scroll wheel, or use Zoom In button, or drag the control end on the zoom indicator
- **Zoom Out** : Shift-double-clicking or mouse scroll wheel, or use Zoom Out button, or drag the control end on the zoom indicator
- **Reset zoom** : Use Zoom Reset button to restore 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.

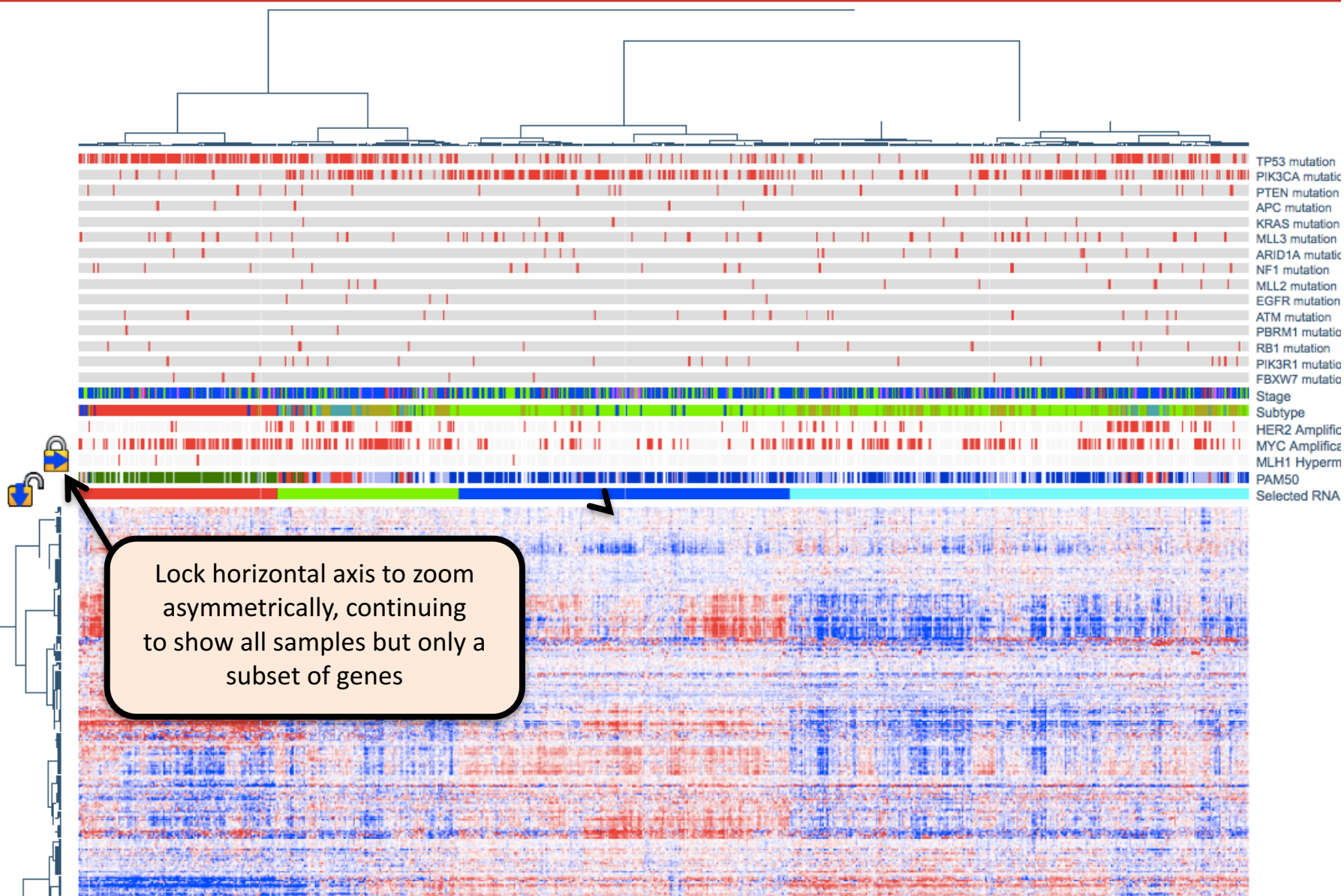
Link-out to an interactive ideogram viewer to show chromosome location(s) of one or more user-selected genes. The viewer has link-outs to other resources, including the UCSC Genome Browser

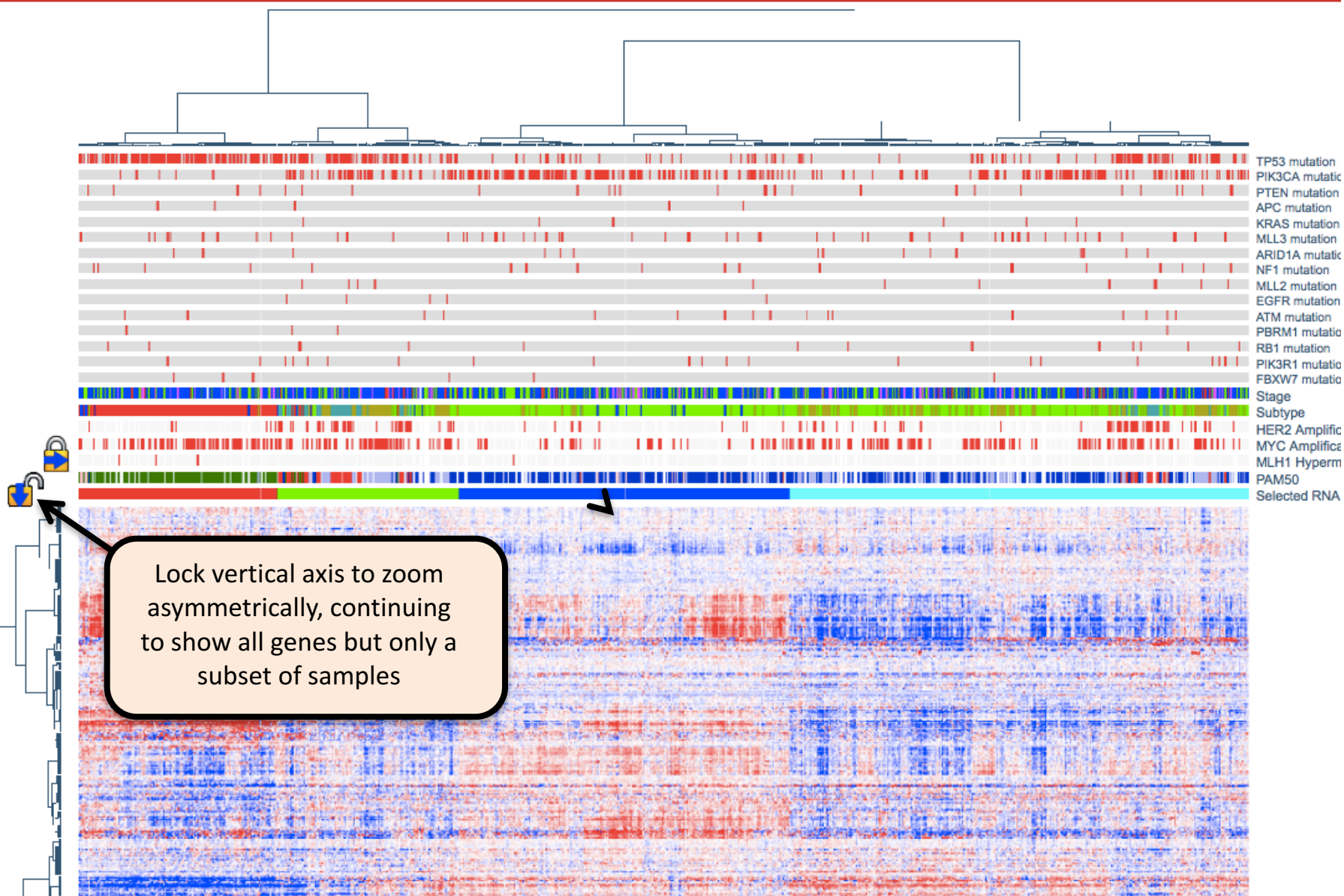
View GeneCards  
Search ClinicalTrials.gov for all  
View NCBI Gene  
View NCBI Entrez ID  
View Ideogram  
Search in Google Scholar  
Search Pubmed for all  
Search Pubmed for any  
View in cBio Portal

[Back to Index Slide](#)



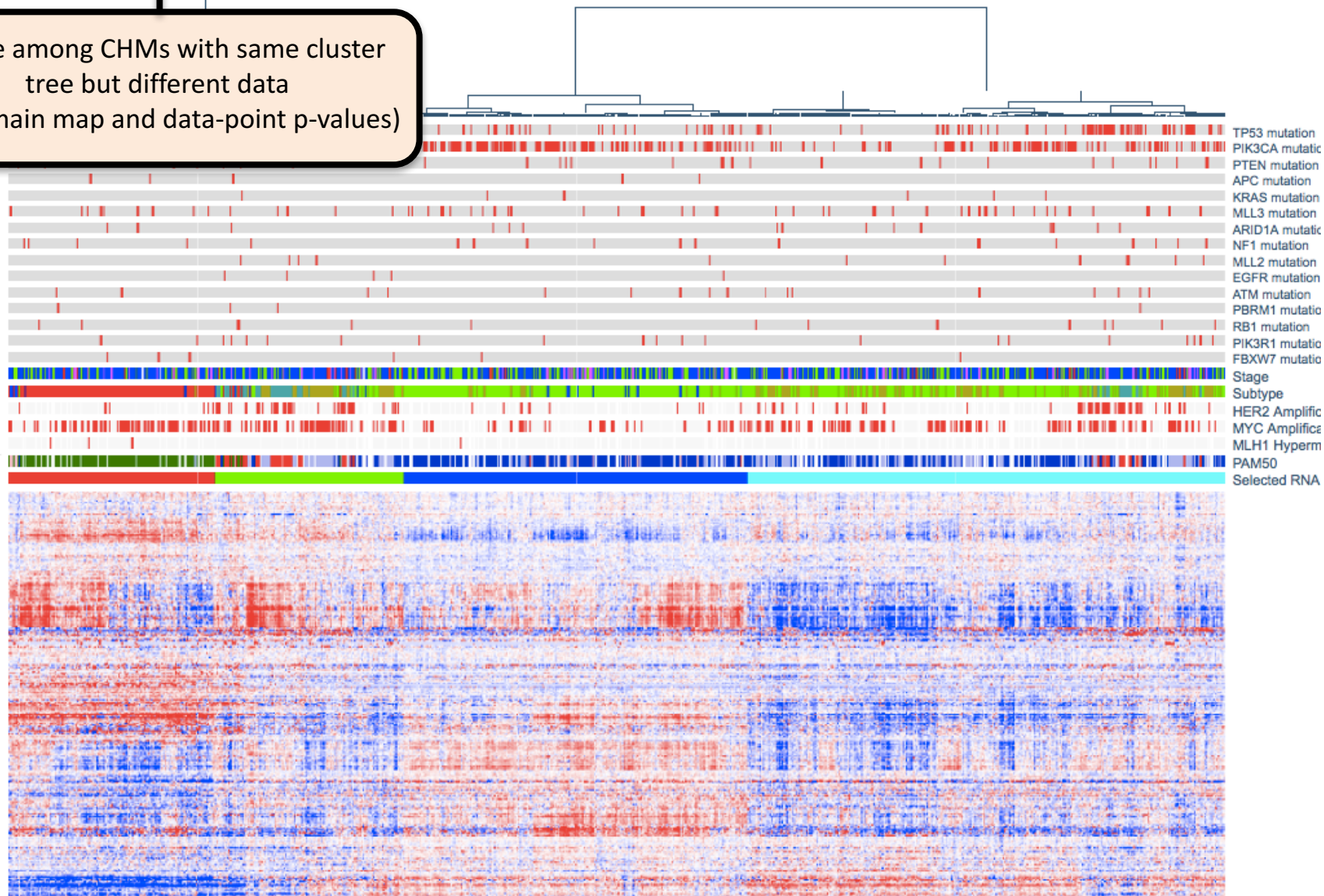




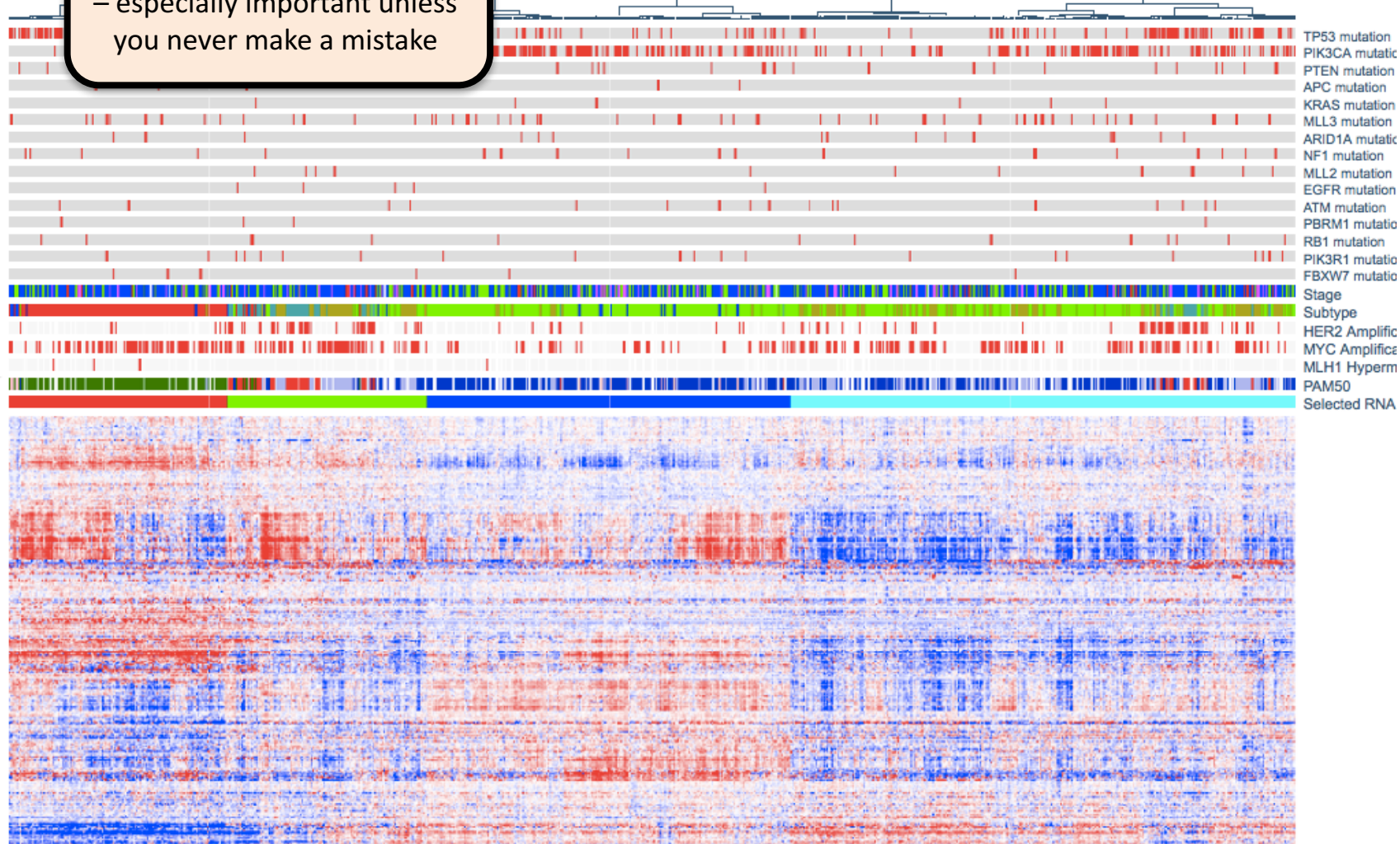




Toggle among CHMs with same cluster tree but different data (e.g., main map and data-point p-values)

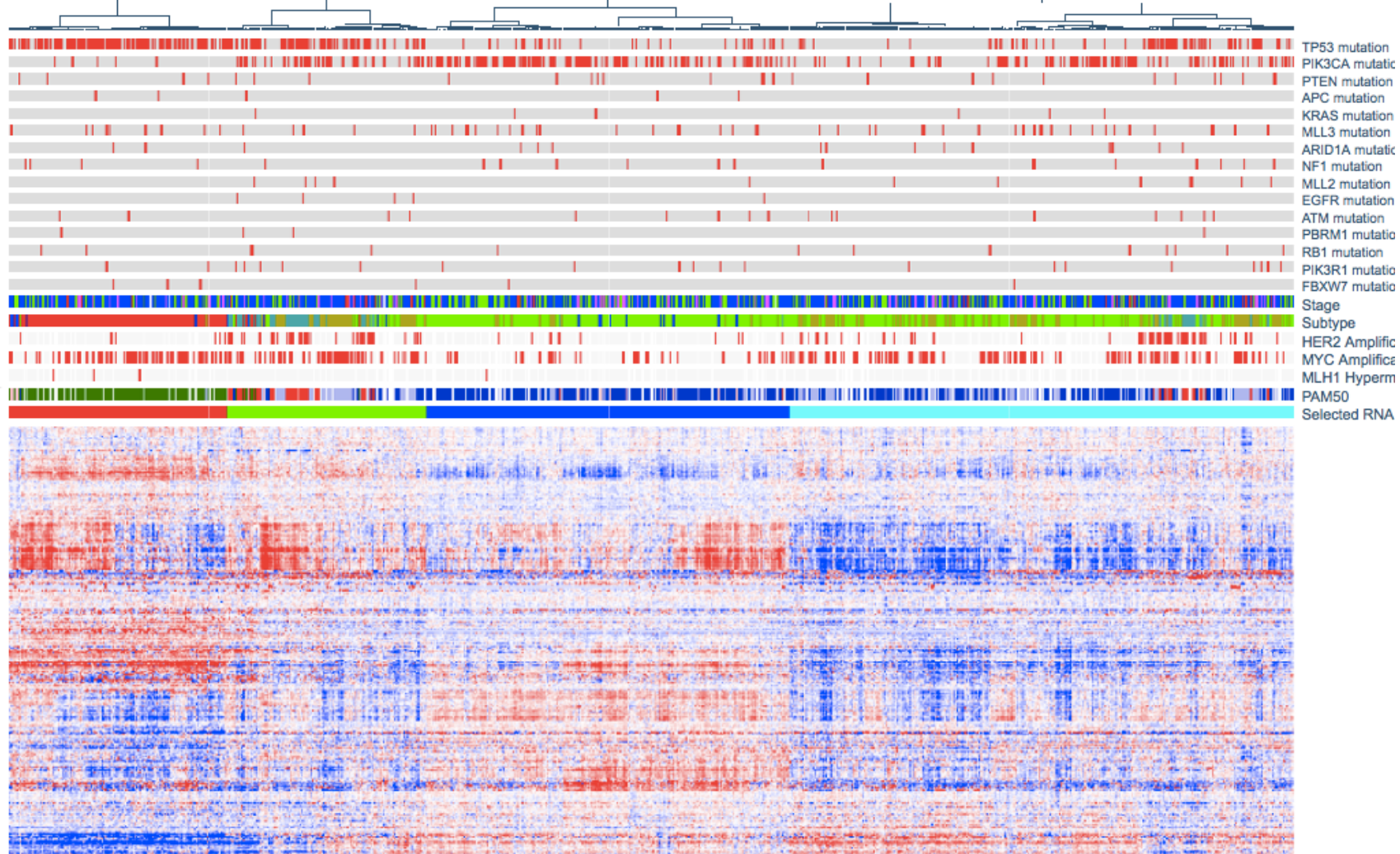


Go back / Go forward  
(i.e., Un-do / Re-do)  
– especially important unless  
you never make a mistake



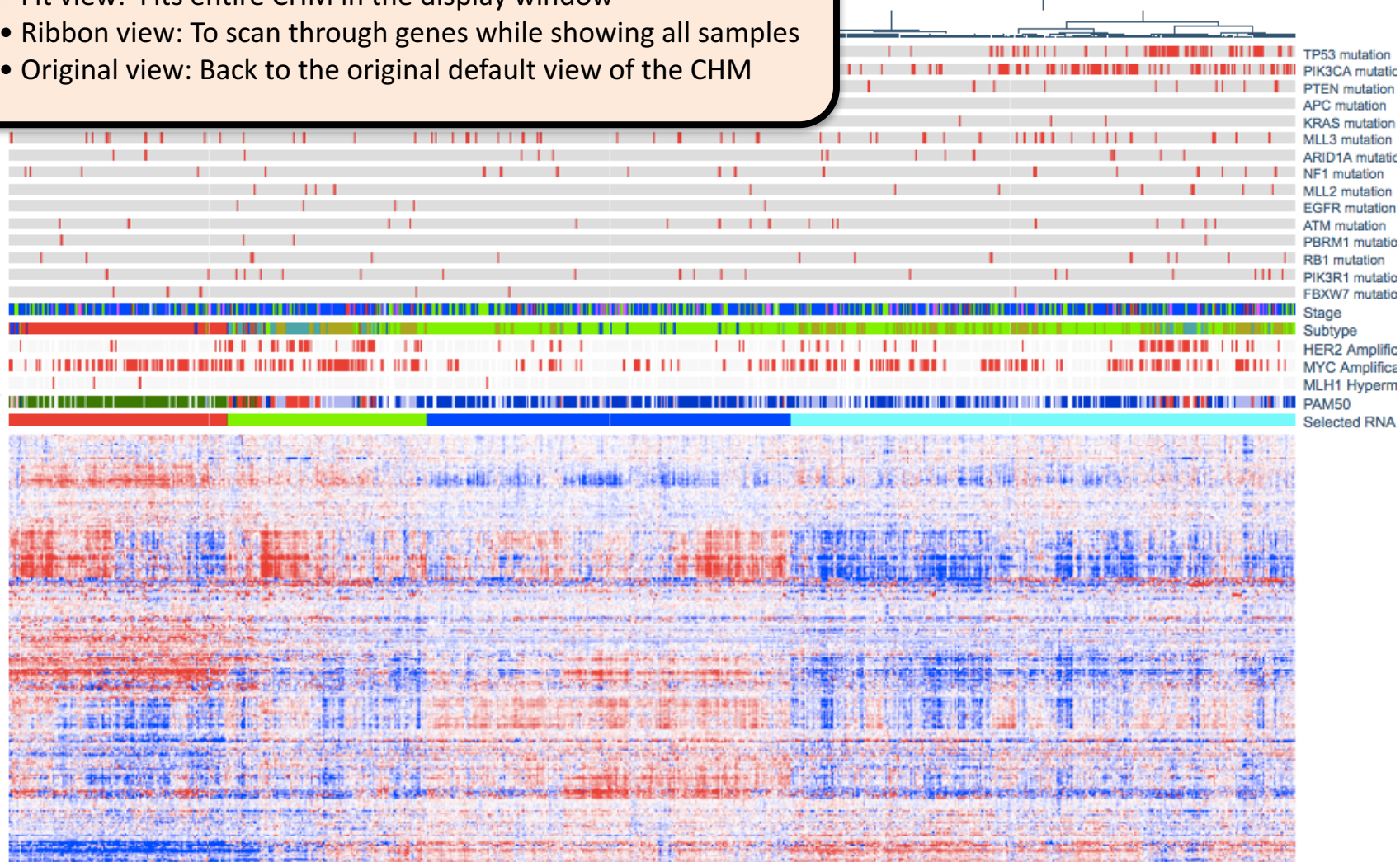


Return to home page



### “Views” Pull-down menu:

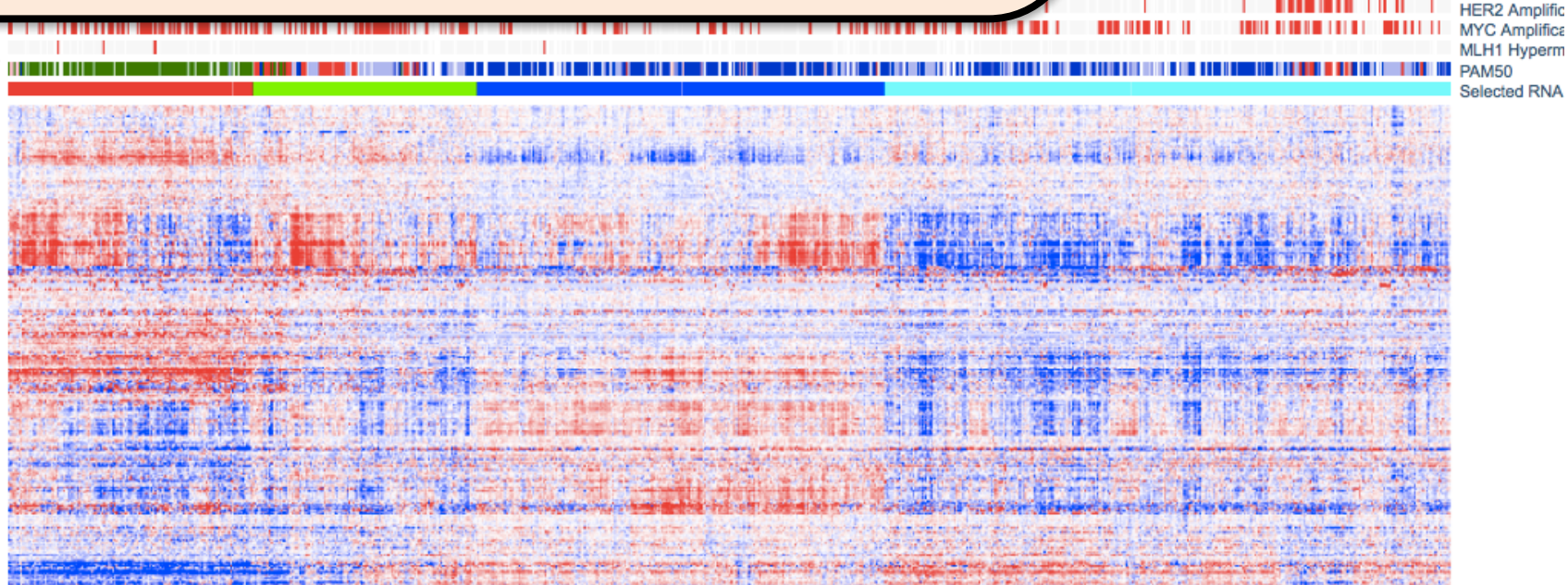
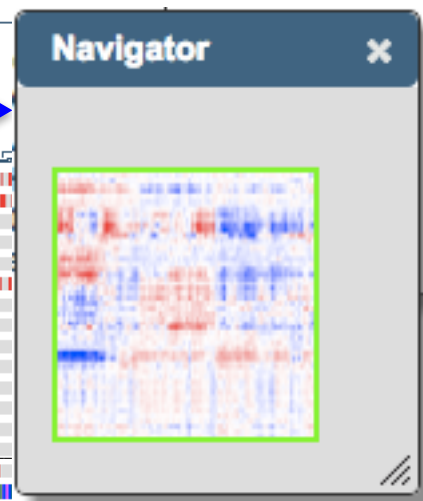
- Fit view: Fits entire CHM in the display window
- Ribbon view: To scan through genes while showing all samples
- Original view: Back to the original default view of the CHM





## "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

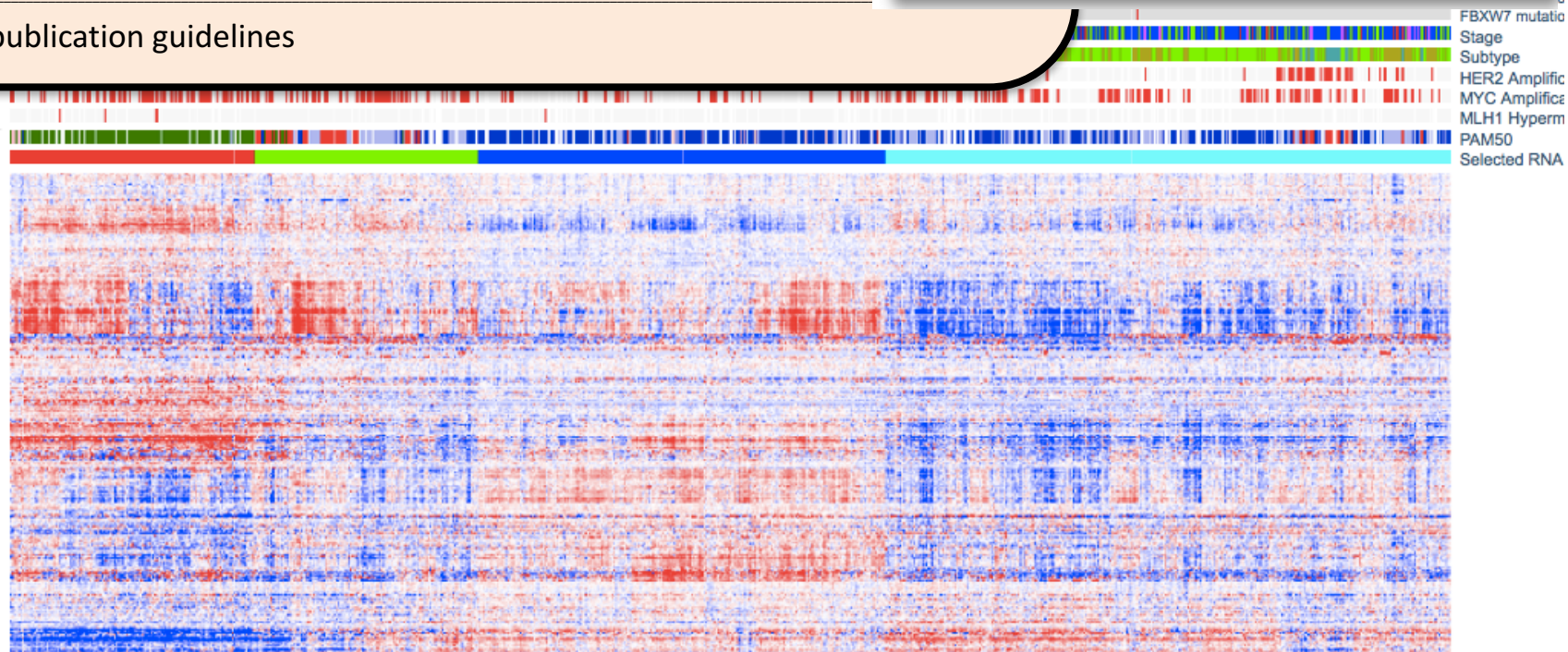


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### Image Details

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





## "Dialogs" menu for opening movable, resizable windows:





- Navigator
  - Image details: *row/column/value data*
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Color Scheme

Define New Custom Color Scheme:

Select Color Scheme Type:

linear

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

Render Preview

Select Color Scheme to Render:

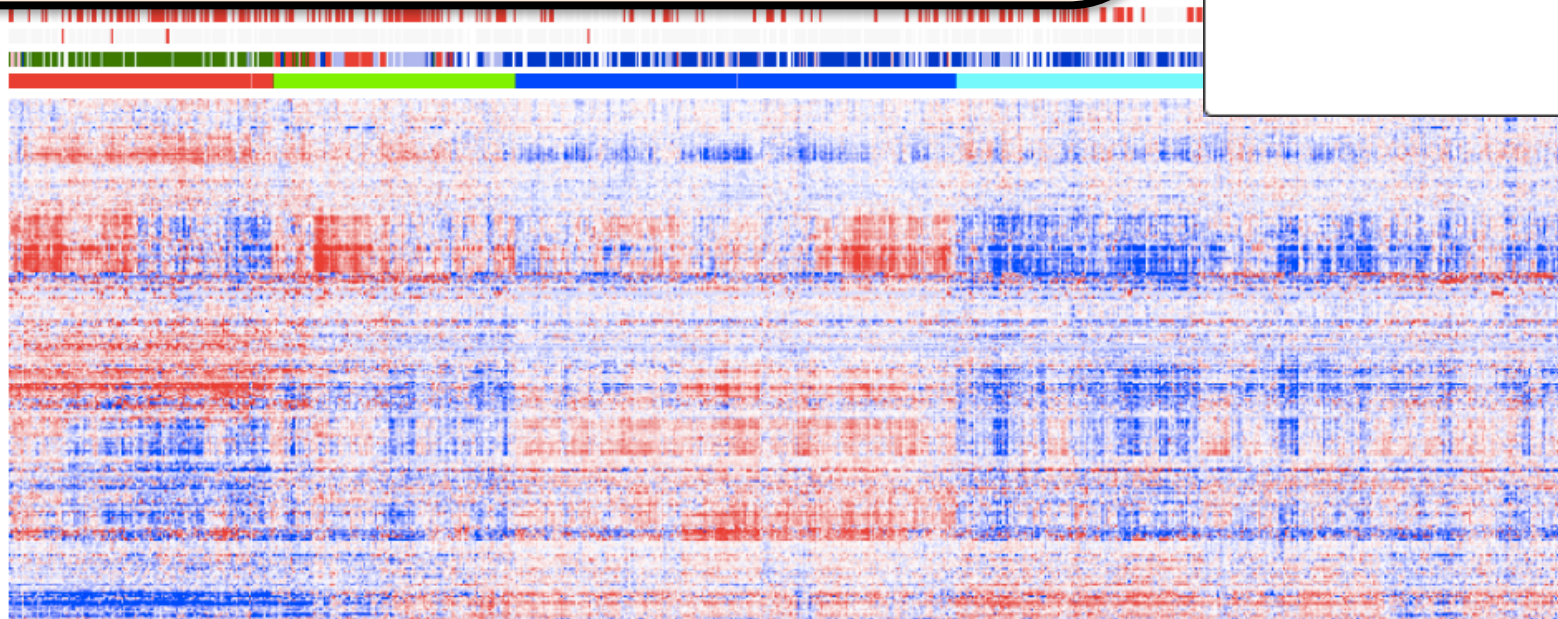
Permanent Color Schemes

cm1 (-3.1249442...3.5524044)

cm2 (-2.5...2.5)

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Advanced Search ×

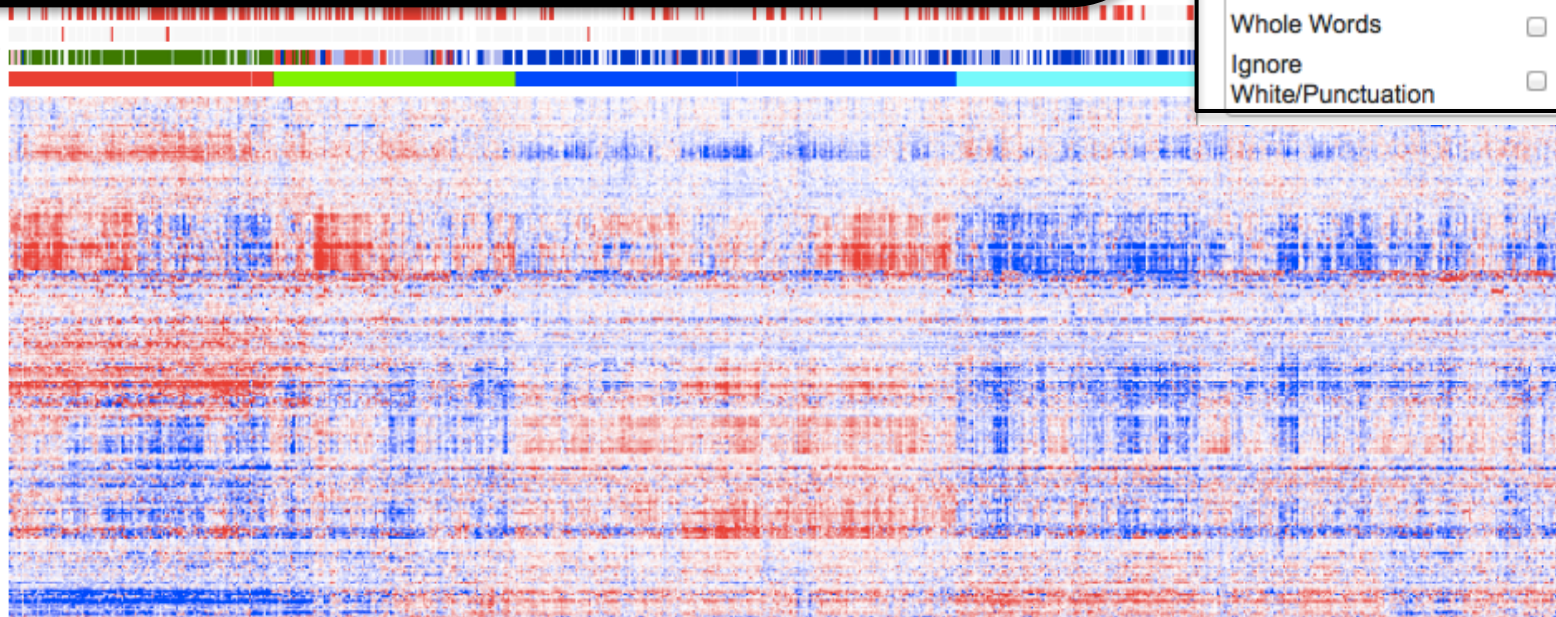
Column Search Term:

Row Search Term: 🔒

Search All

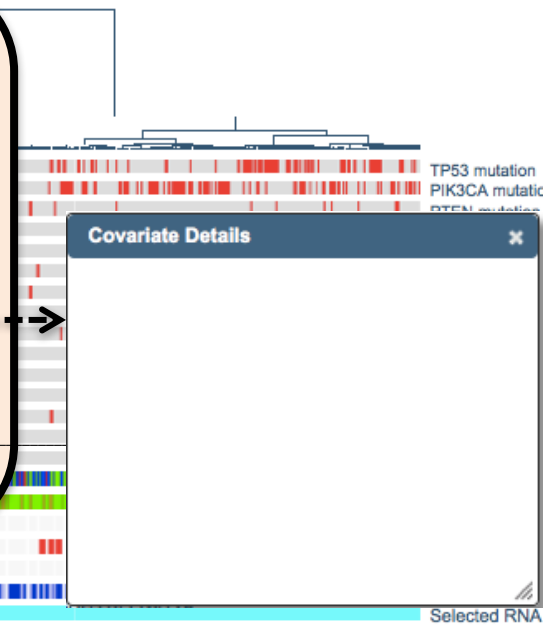
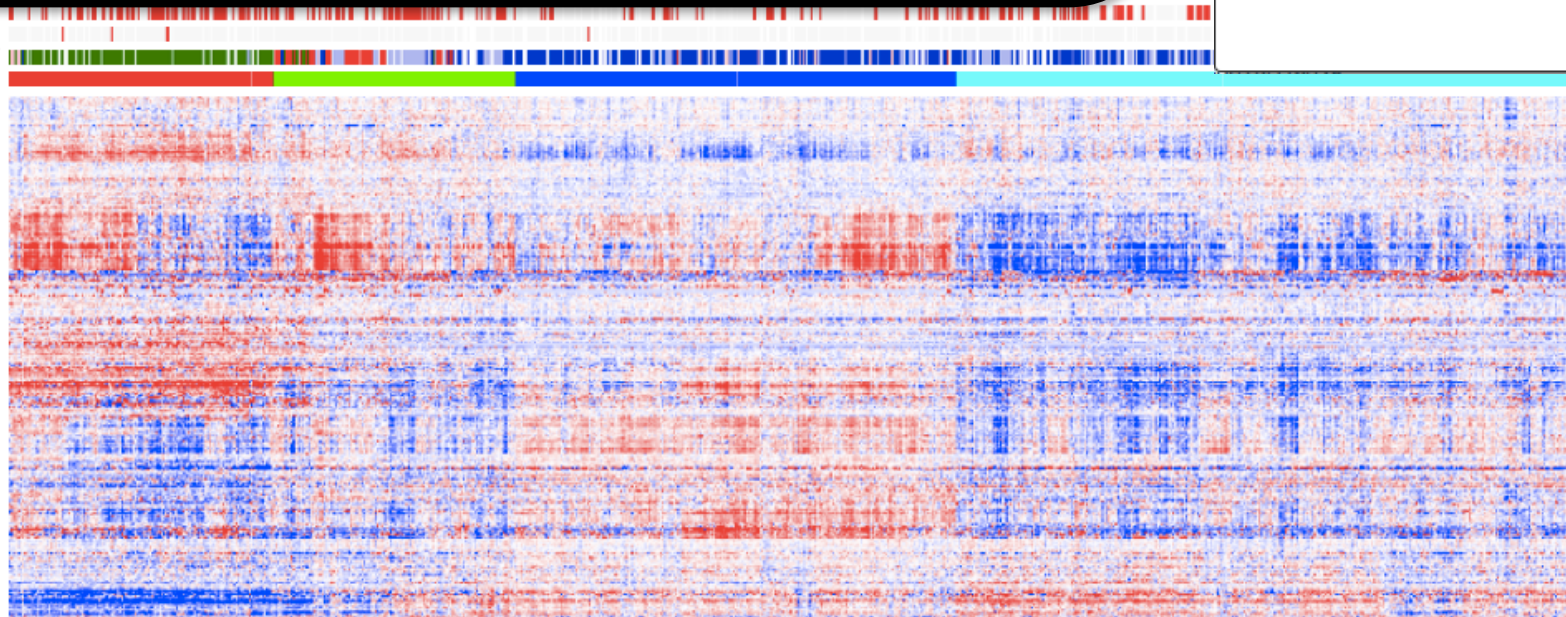
Search Options:

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:

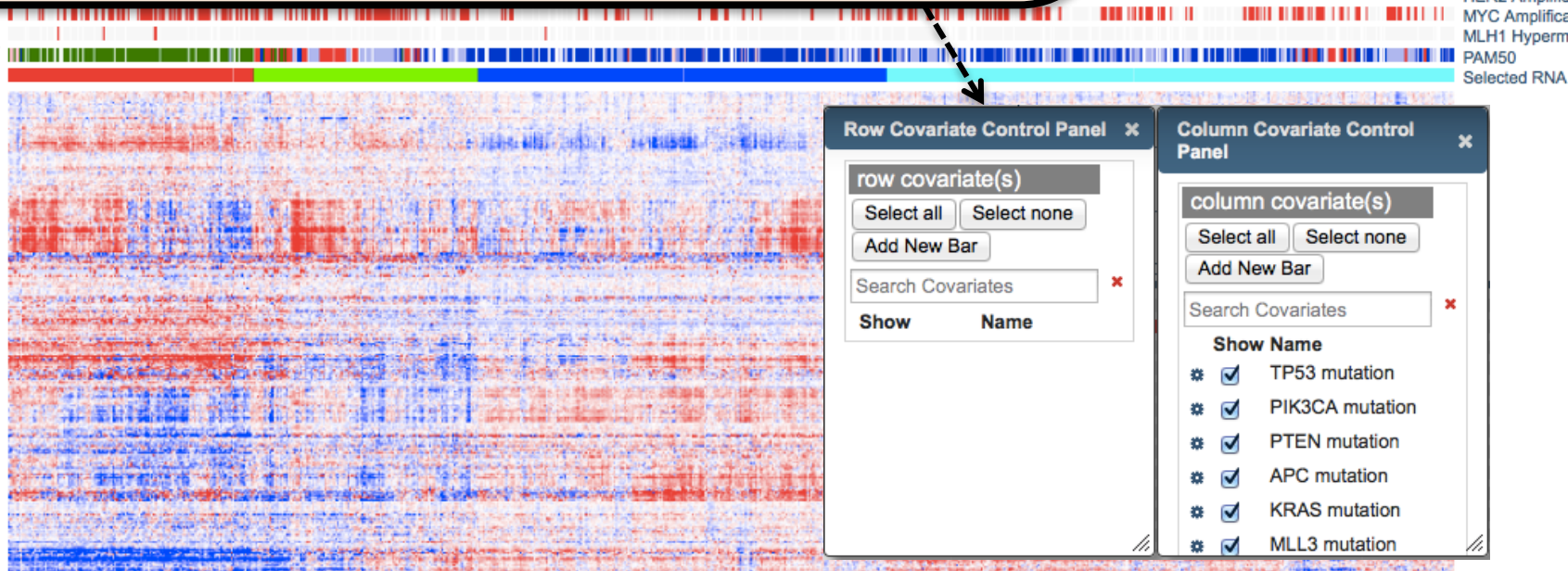
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  - Covariate control panel: Hide, show, subtract, or add *row or column covariate bars*
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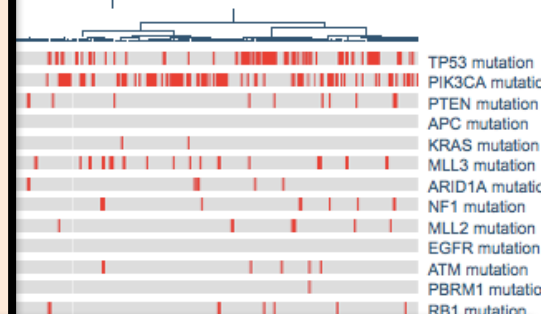
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### About NG-CHM

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)

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## 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

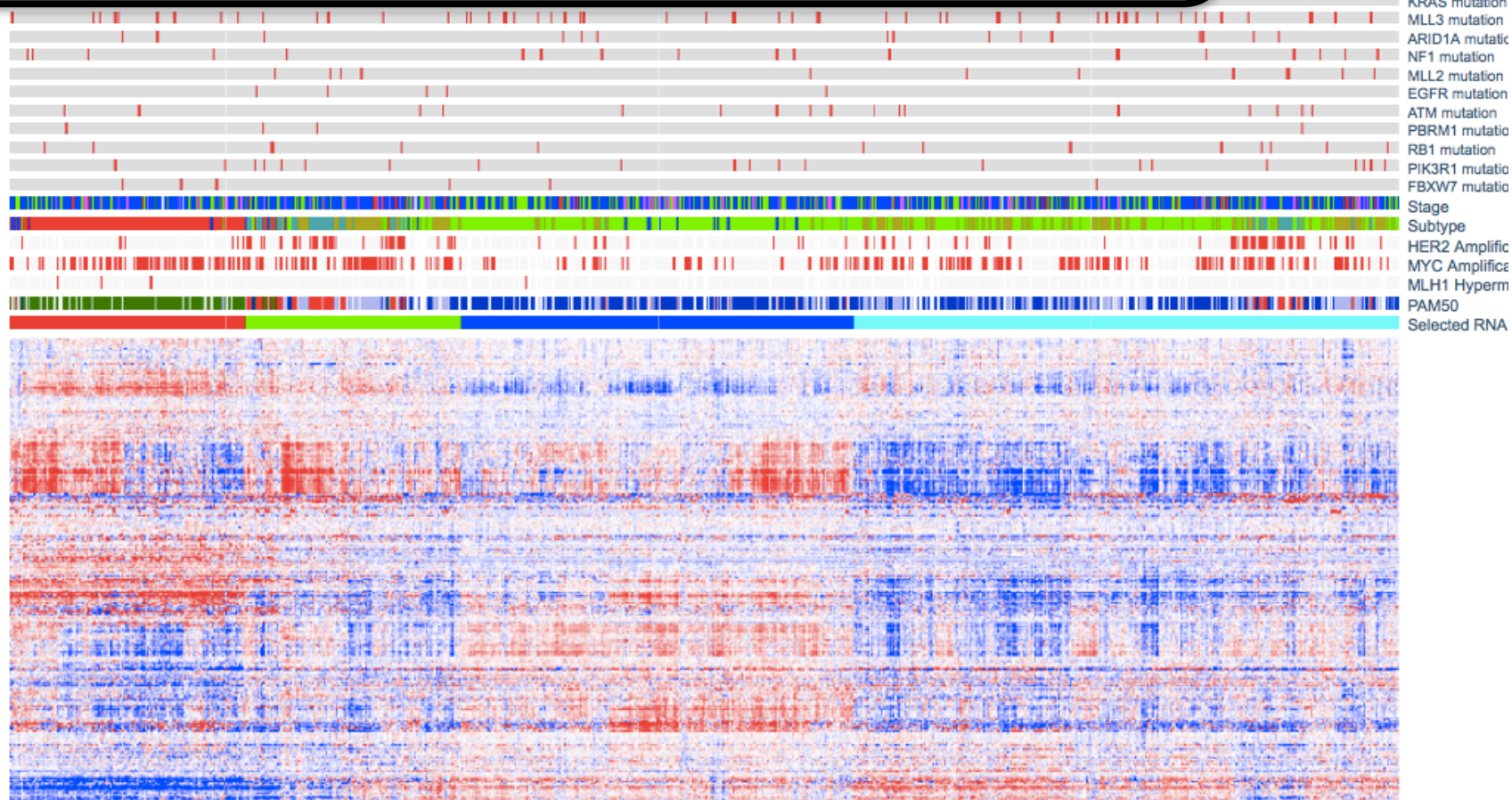
Last Updated: September 30, 2014

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.*



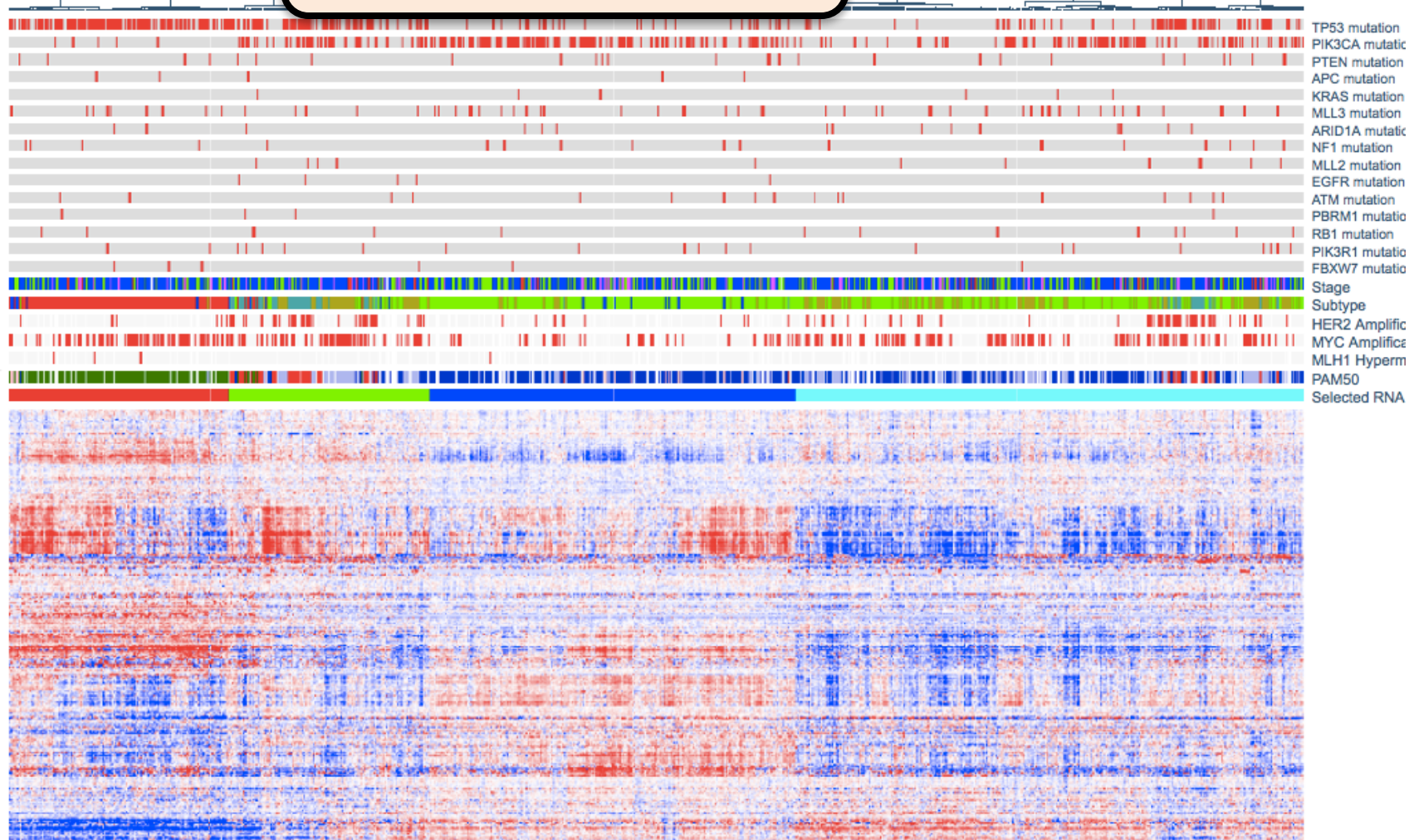
### “Miscellaneous” menu:

- 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

