

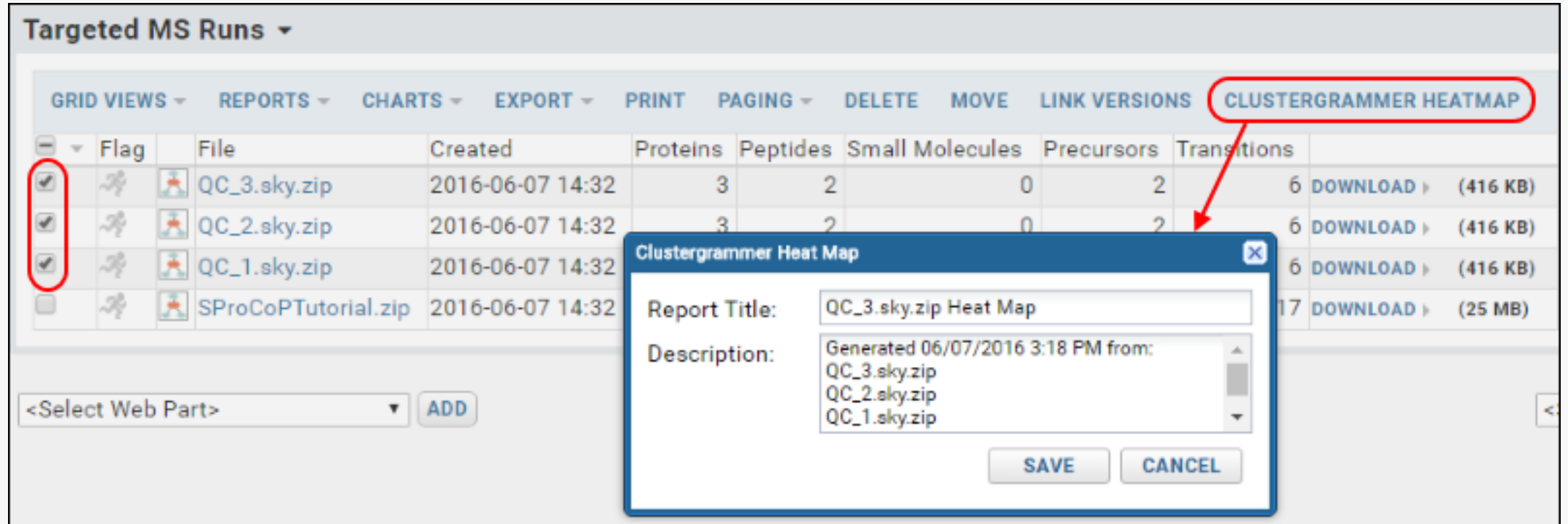
## Panorama: Clustergrammer Heat Maps

Clustergrammer is a free visualization service and open source project provided by the [Ma'ayan Lab at the Icahn School of Medicine at Mount Sinai](#). LabKey has leveraged their APIs to generate heat maps for TargetedMS expression matrices using the free web service version of Clustergrammer. The basics for the desired usage is to look for up-regulated or down-regulated proteins, via their constituent peptides, in targeted mass spec data.

To use the tool, the user navigates to a LabKey folder which has TargetedMS runs upload, selects the runs of interest, and initiates the Clustergrammer heat map generation tool from the 'Clustergrammer Heatmap' button on the data grid button bar. One thing to note is that this tool is third-party and any data/heat-maps are publicly accessible.

### Technologies Used

- **Data source:** runs uploaded to TargetedMS assay
- **Code location:** TargetedMS module in the LabKey subversion repository
- **Tools/packages:** Clustergrammer web service version (built using JavaScript D3.js library)
- **Features:** selection of subsets of runs to be included; heat map allows zoom, pan, reorder, search, and filter
- **Accessibility:** link report viewable from Data Views webpart
- **Developer(s):** Ian Sigmon, LabKey



The screenshot displays the 'Targeted MS Runs' interface. At the top, there is a navigation bar with options: GRID VIEWS, REPORTS, CHARTS, EXPORT, PRINT, PAGING, DELETE, MOVE, LINK VERSIONS, and CLUSTERGRAMMER HEATMAP (highlighted with a red circle). Below this is a table with columns: Flag, File, Created, Proteins, Peptides, Small Molecules, Precursors, Transitions, and a download link. The first three rows are selected, indicated by checked checkboxes in the Flag column. A dialog box titled 'Clustergrammer Heat Map' is open, showing the Report Title as 'QC\_3.sky.zip Heat Map' and the Description as 'Generated 06/07/2016 3:18 PM from: QC\_3.sky.zip, QC\_2.sky.zip, QC\_1.sky.zip'. The dialog has 'SAVE' and 'CANCEL' buttons.

Flag	File	Created	Proteins	Peptides	Small Molecules	Precursors	Transitions	Download
<input checked="" type="checkbox"/>	QC_3.sky.zip	2016-06-07 14:32	3	2	0	2	6	DOWNLOAD (416 KB)
<input checked="" type="checkbox"/>	QC_2.sky.zip	2016-06-07 14:32	3	2	0	2	6	DOWNLOAD (416 KB)
<input checked="" type="checkbox"/>	QC_1.sky.zip	2016-06-07 14:32					6	DOWNLOAD (416 KB)
<input type="checkbox"/>	SProCoPTutorial.zip	2016-06-07 14:32					17	DOWNLOAD (25 MB)

Zoom, scroll, and click buttons to interact with the clustergram.



Row Order

- Alphabetically
- Cluster
- Rank by Sum
- Rank by Variance

Column Order

- Alphabetically
- Cluster
- Rank by Sum
- Rank by Variance

Gene

Opacity Slider

Row Group Size

Column Group Size

Top rows sum: all

Top rows variance: all

- H3K4me3 - B10005
- H3K4ac1 - B10007
- H3K27ac1K39me3
- H3K27ac1K39me2
- H3K9ac1K14ac1
- H3K18ac1K23ac1
- H3K9me3 - B10
- H3K18ac1K23ac1
- H3K4me3 - B10003
- H3K27me3K39me2
- H3K9me3K14ac1
- H3K27me3K39me0
- H3K27me3K39me0
- H3K27me3K39me0
- H3K9me3K14ac1
- H3K9me3K14ac1
- H3K27me3K39me3
- H3K27me3K39me1
- H3K27me3K39me0
- H3K27me3K39me0
- H3K79me1 - B10
- H3K79me1 - B10
- H3K9me3K14ac1
- H3K9me3K14ac1
- H3K27me3K39me2
- H3K27me3K39me2
- H3K27me3K39me2
- H3K27me3K39me2
- H3K27me3K39me1
- H3K4me3 - B10005
- H3K4me1 - B10004
- H3K9me3H41-49
- H3K9me3H41-49
- H3K9me3K14ac1
- H3K18ac1K23ac1
- H3K27me3K39me3
- H3K79me2 - B10
- H3K27ac1K39me1
- H3K27ac1K39me0
- H3K27me3K39me1
- H3K9me3S18ph1K
- H3K9me3S18ph1K
- H3K9me3S18ph1K
- H3K9me3S18ph1K
- H3K9me3S18ph1K
- H3K9me3S18ph1K
- H3K27me3K39me3
- H3K9me1 - B10
- H3K54ac1 - B10058
- H3K9me3S18ph1K
- H3K9me3S18ph1K
- H3K18ac1K23ac1
- H3K9me2 - B10

