



Guide for calculate the T-test value between cell lines in Morpheus.

1- Load the .csv file obtained from Cellprofiler and previously edited with the python code.

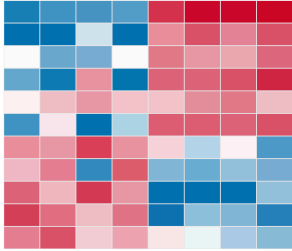


All data is processed on your computer and never sent to any server.

My Computer | [URL](#) | [Dropbox](#) | [Preloaded Datasets](#)



or Copy and Paste Clipboard Data, Drag and Drop



MORPHEUS

Versatile matrix visualization and analysis software

View your dataset as a heat map, then explore the interactive tools in Morpheus. Cluster, create new annotations, search, filter, sort, display charts, and more.

30,000+ users
100,000+ matrices analyzed.

If you use Morpheus for published work, please cite:
Morpheus, <https://software.broadinstitute.org/morpheus>

2- Select in red the metadata columns, which are the rows with the names starting in “Image_”. In green will be the first column with the features measured.

Open

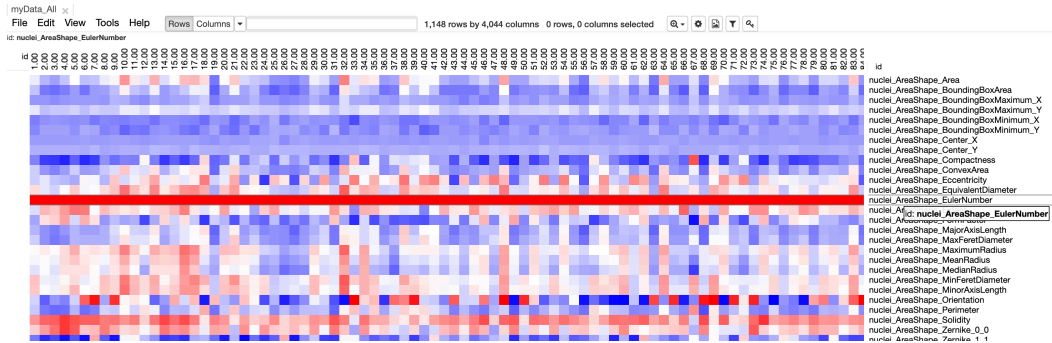
Click the table cell containing the first data row and column.

- Data Matrix
- Column Annotations
- Row Annotations

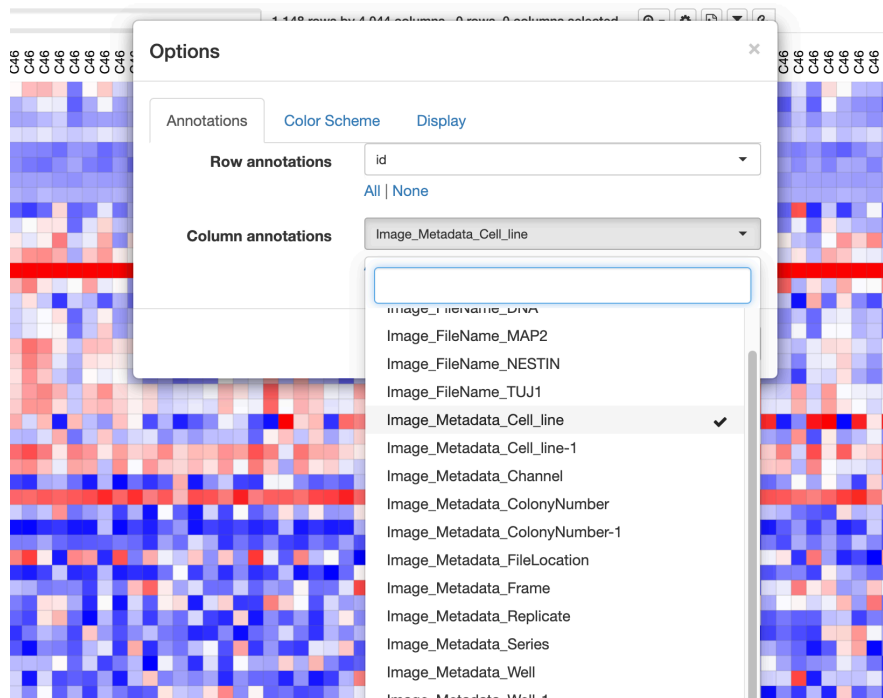
	BROAD	BROAD	BROAD	BROAD	BROAD	BROAD
Image_PathN	/Users/lanos/	/Users/lanos/	/Users/lanos/	/Users/lanos/	/Users/lanos/	/Users/lanos/
Image_PathN	/Users/lanos/	/Users/lanos/	/Users/lanos/	/Users/lanos/	/Users/lanos/	/Users/lanos/
	BROAD	BROAD	BROAD	BROAD	BROAD	BROAD
nuclei_AreaSi	4273	3586	3338	3822	4528	3743
nuclei_AreaSi	7470	5467	5183	5624	6399	5304
nuclei_AreaSi	151	151	147	150	152	152
nuclei_AreaSi	159	147	150	150	153	147
nuclei_AreaSi	68	74	76	74	73	74
nuclei_AreaSi	69	76	77	76	72	79
nuclei_AreaSi	111.0308916	110.8870607	111.5844817	111.3390894	111.7170936	112.2067
nuclei_AreaSi	113.0175520	112.7203011	112.9517675	112.8992673	112.0916519	111.7170
nuclei_AreaSi	2.958022041	2.049078786	1.985119122	1.769106576	2.475260861	1.833828

OK Cancel

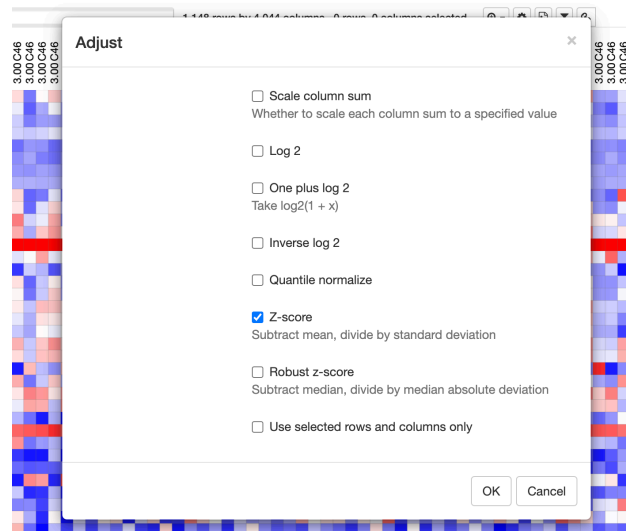
3- You will get something like the image below. Where the rows corresponds to the features and the columns correspond to each organid ID. Since this, doesn't give us enough information, we can display the data to show in the columns, like cell line, replicate, well, etc.



4- Select the gear and click in the tab “Annotations”, then select any metadata that you are interesting in see difference. In this case, will be “Cell_line”.



5- In Tools, go to adjust to normalize the scales of the data, then everything will be in a range between 0 to 1. Tools->Adjust->Z-score

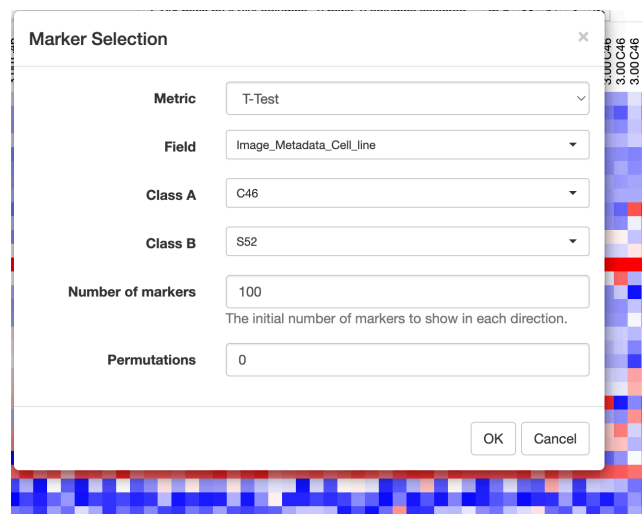


6-No we can calculate the T-test values for the groups desired.

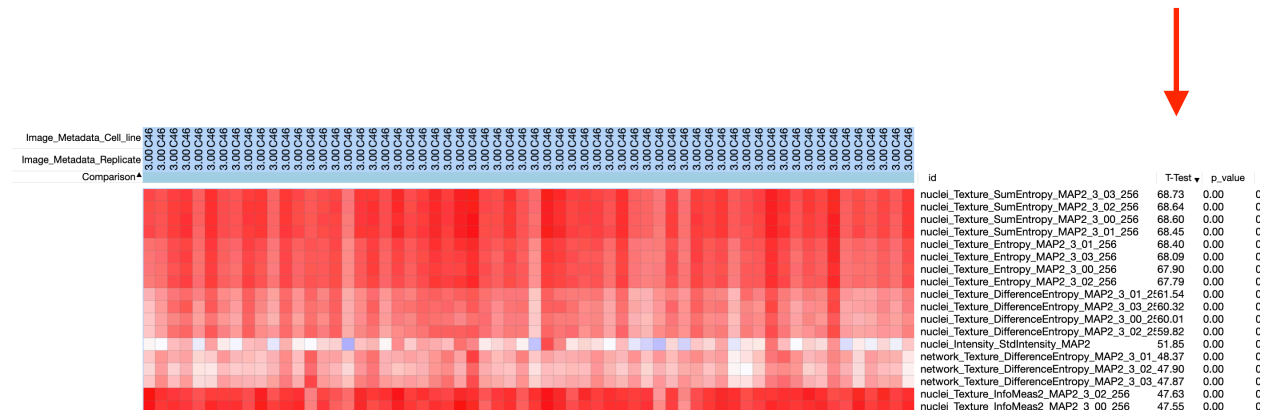
In tools, go to Marker Selection. In the Metric you should select T-test, the field, is the metadata that you want to compare. In this case “cell_line”.

Class A will be the cell line of one group (e.g: WT). Could be one or as many as you want in that group.

Class B, the second group, e.g, mutant.



7- The result will be displayed like the image below. Then, you can sort the T-test values by the absolute values, which will give you the features with more difference. If is positive will be a difference in the same direction and if is negative will be a difference in an opposite direction. All the p_values are pretty low, then many of all the features measured are possible to use for the PCA.



8- To zoom out, go to the lens and select Fit to the Windows.