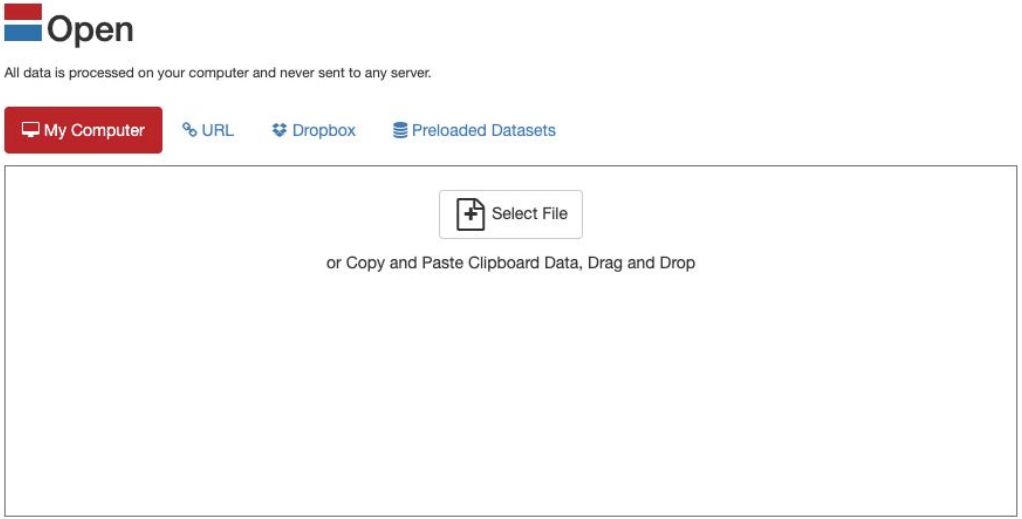
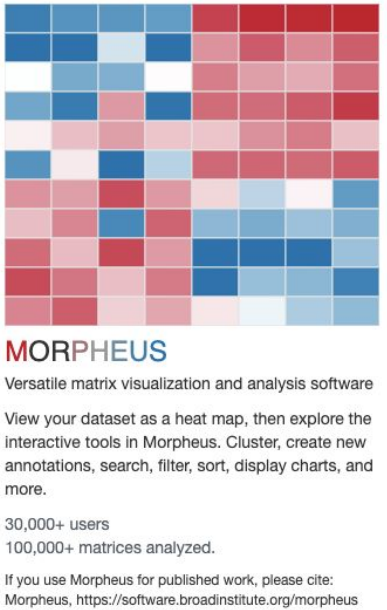
Introduction to exploring morphological profile data with Morpheus

Beth Cimini

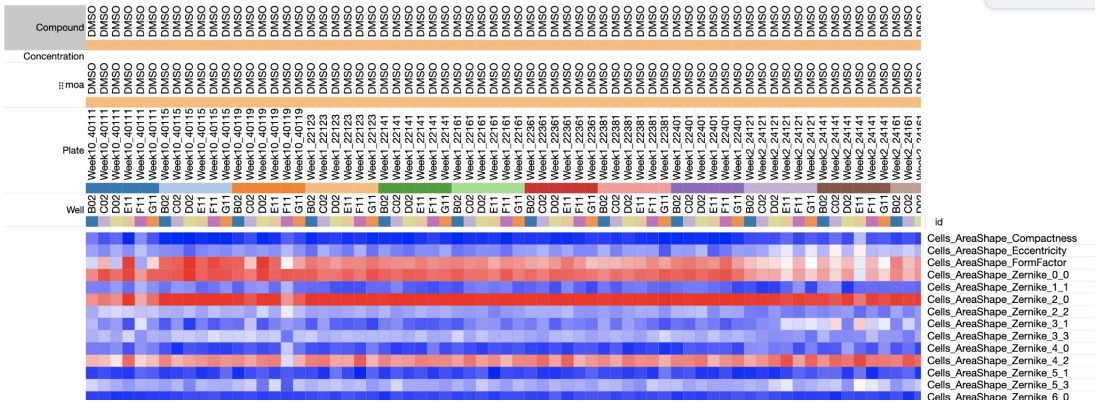
Morpehus - https://software.broadinstitute.org/morpheus/

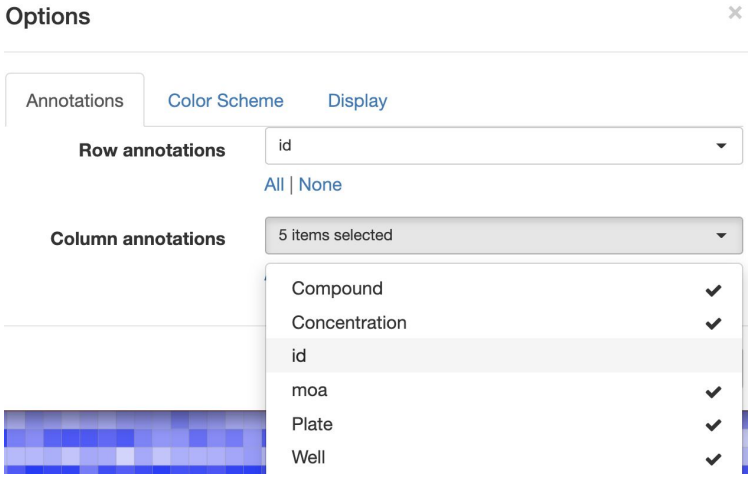




Drag and drop CSVs, GCTs, or Morpheus- created JSON files

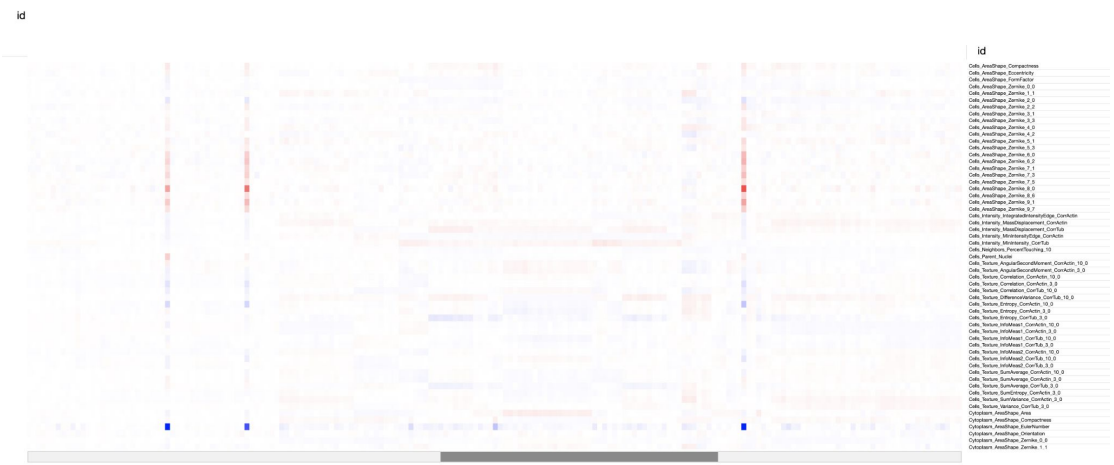
1 - Change column annotations to something useful

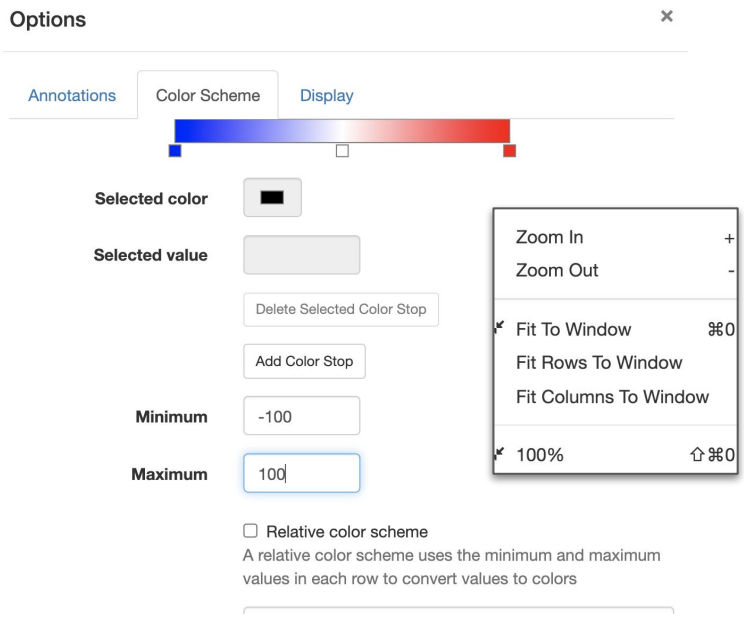




⚙ Options -> Annotation, optionally then right click each annotation to add color

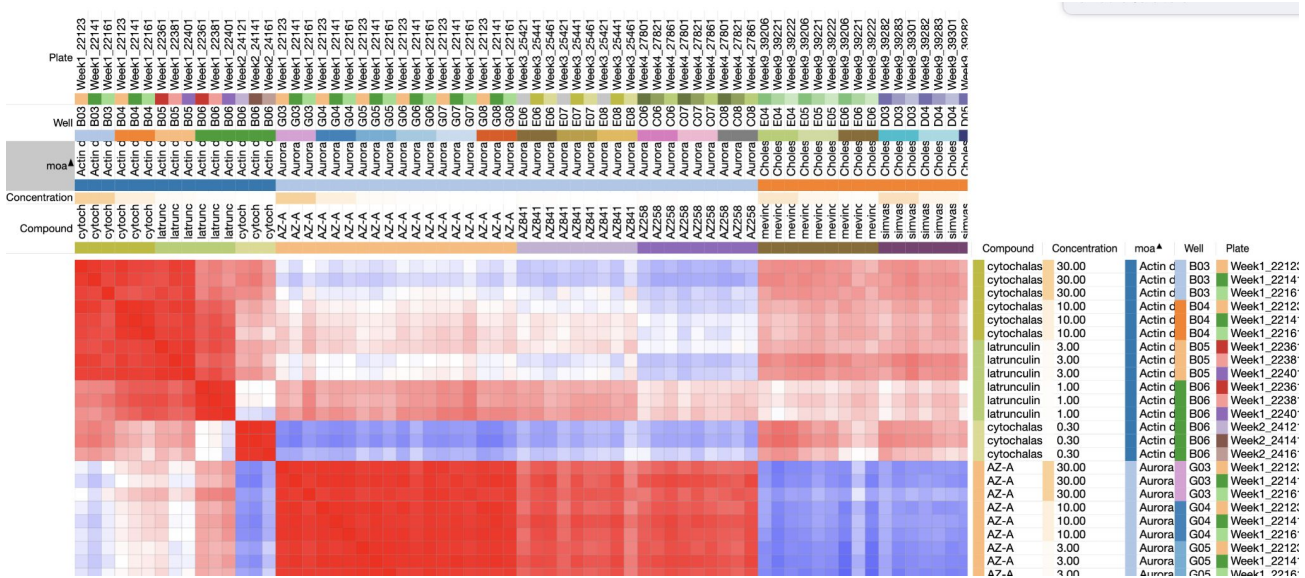
2 - Change color displays to make it easier to look for aberrant rows/columns

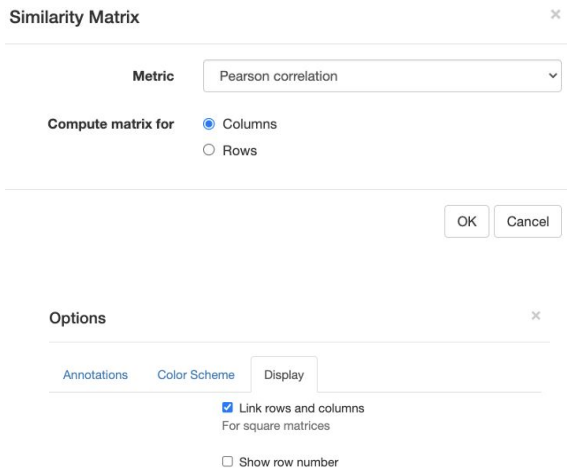




Options -> Color Scheme, then uncheck “Relative color scheme” and set minimum and maximum to -100 and 100. Close, and then zoom to “fit to window”. Be sure to return display to “Relative color scheme” before continuing.

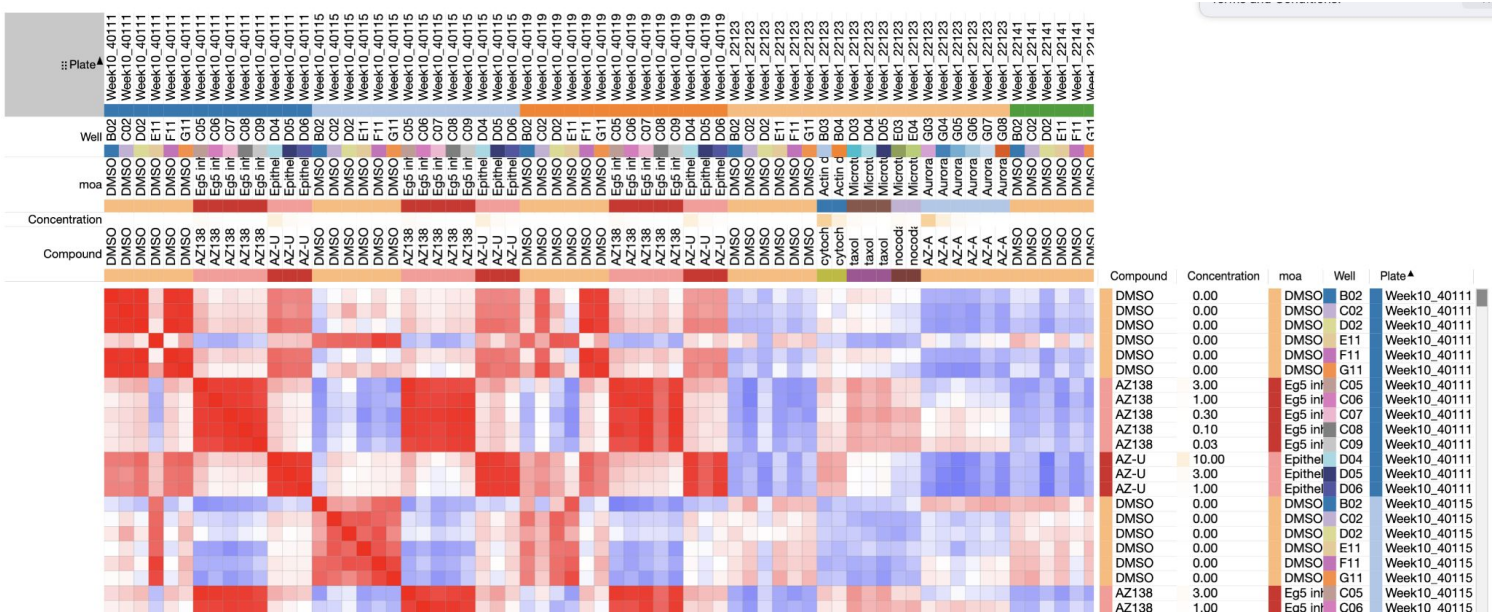
3 - Create a similarity matrix and link the rows and columns





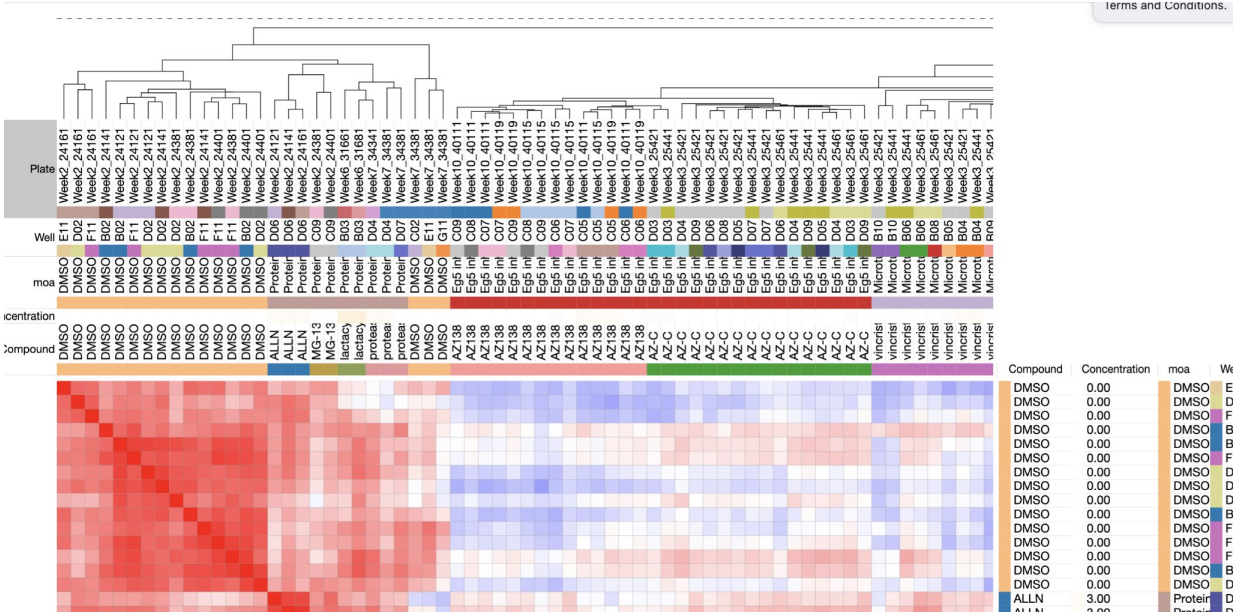
Tools -> Similarity Matrix -> Pearson/Columns then ⚙ Options -> Display -> Link rows and columns. 🔍 | Zoom in and out as needed.

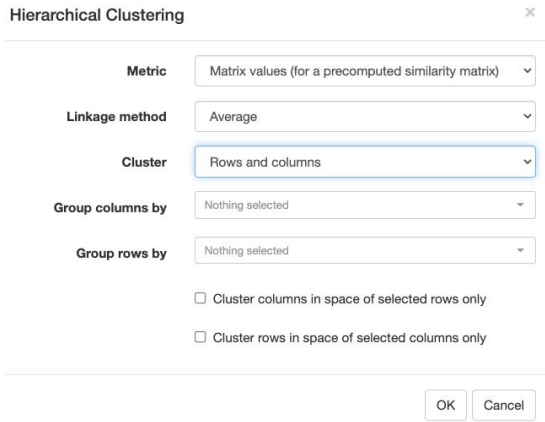
4 - Create a similarity matrix, look clustering by plate



Change sorting by clicking the variable you want to sort by. Holding shift before clicking an additional variable (or variables) will allow you to sort by multiple variables, with the sorting tier indicated by a number next to the arrow.

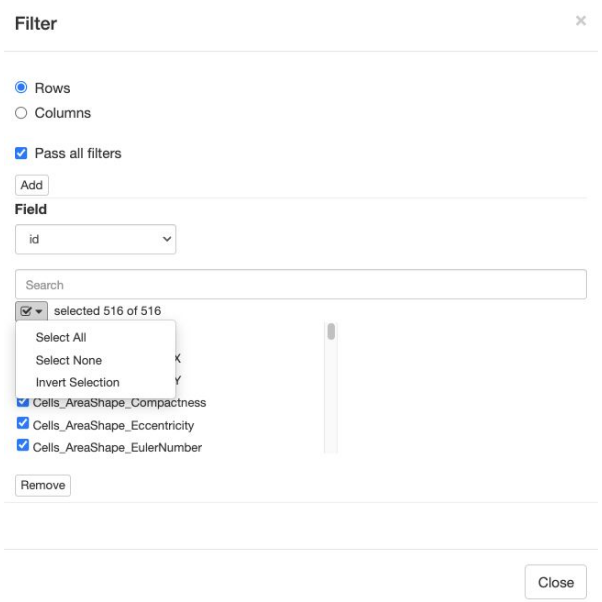
5 - Look at the clustering of the similarity matrix

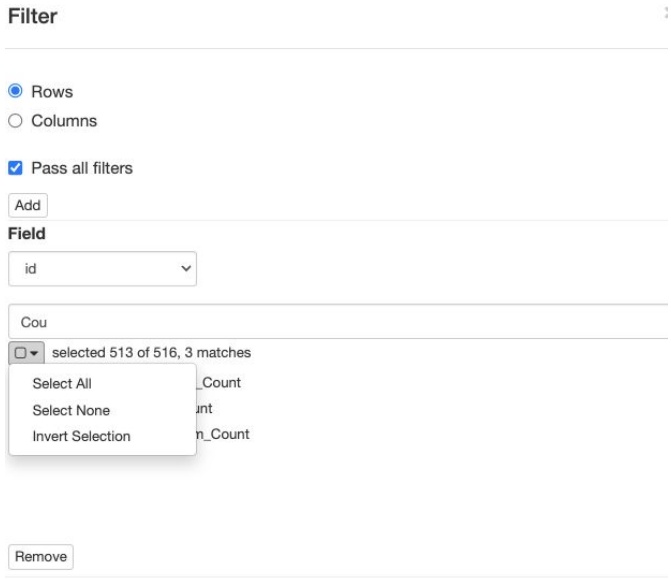




Tools -> Hierarchical Clustering -> Precomputed similarity matrix/ Rows and columns

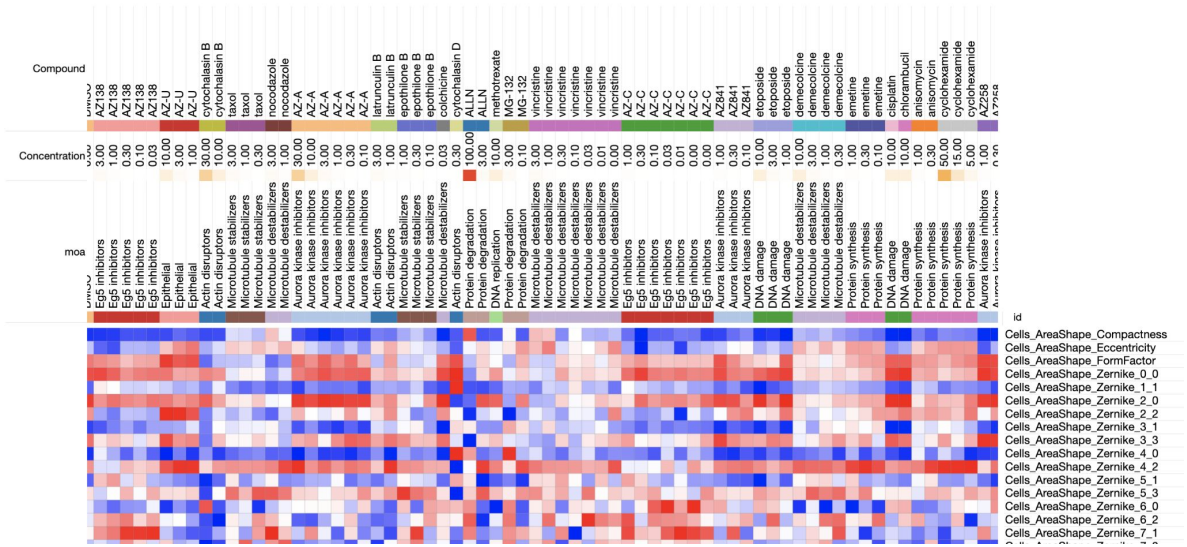
6 - Filter out troubling features

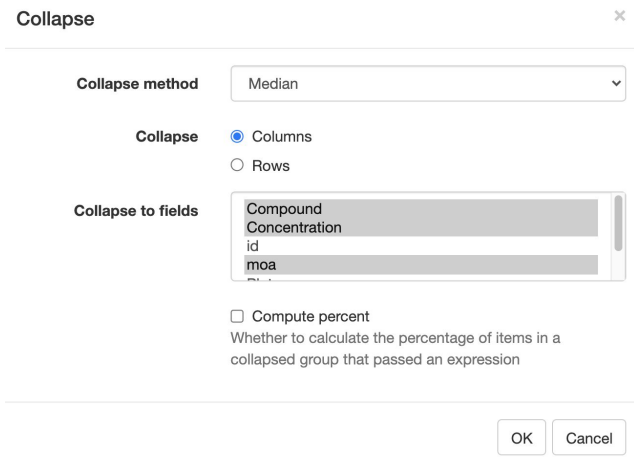




Tools -> Filter -> Rows -> Add -> Select all, then type enough of the feature name you want to remove and uncheck it or hit “Select None”. Hit close when done.

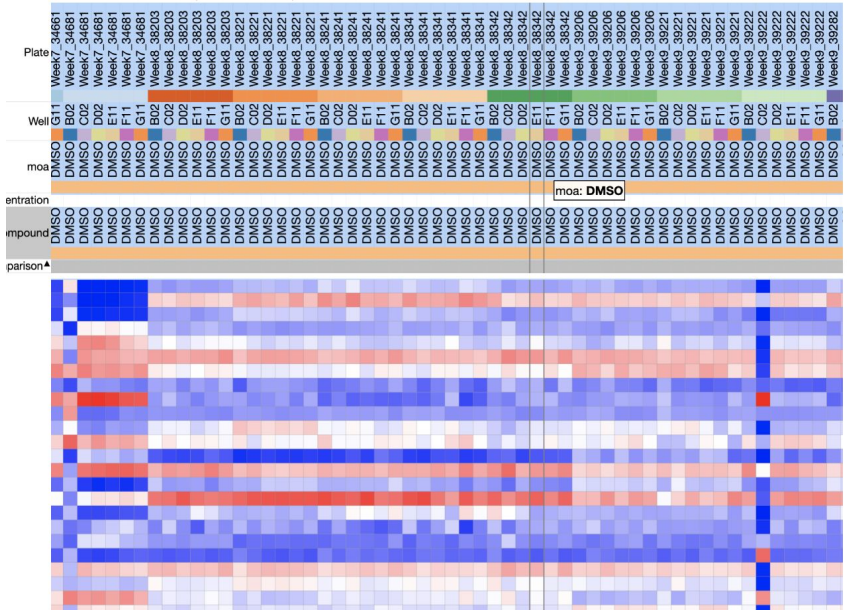
7 - Collapse all replicates to make it easier to look at MOA associations



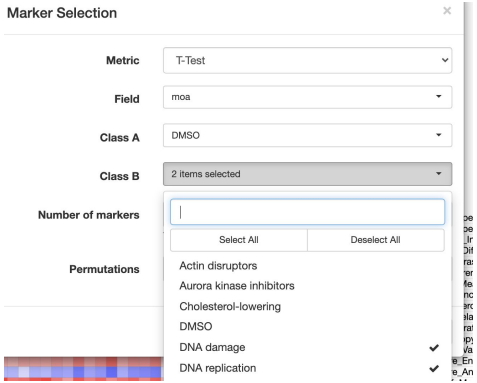


From feature data -> Tools -> Collapse -> Median/Columns/Compound,Concentration, and moa (hold shift to select multiple options), then follow previous instructions to create a similarity matrix on the collapsed data

8 - See which features drive particular strong phenotypes

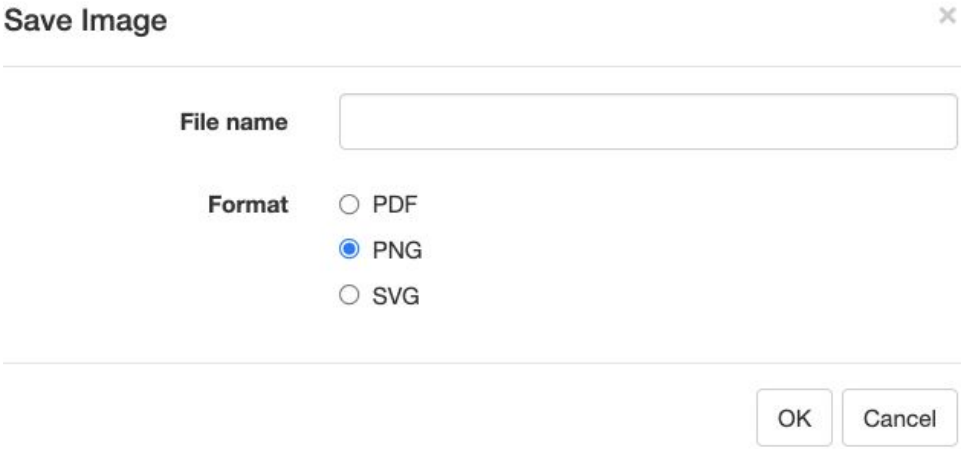


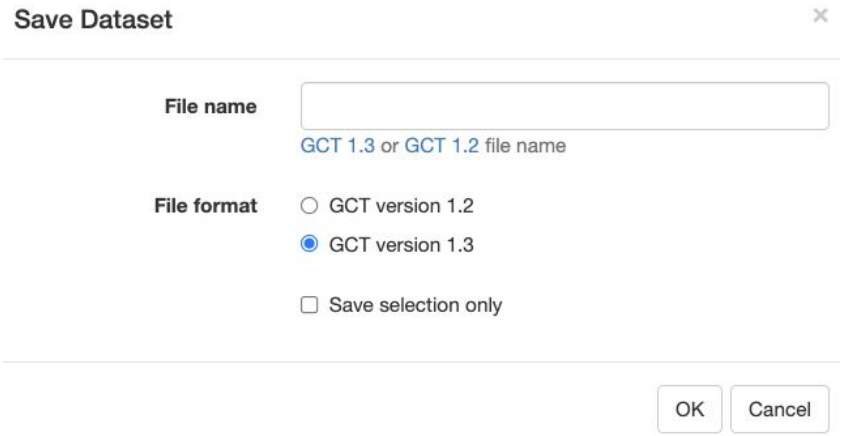
id	T-Test	p_value	FDR(BH)
Cytoplasm_AreaShape_Area	-15.45	0.00	0.00
Cytoplasm_AreaShape_Zernike_2_0	-10.67	0.00	0.00
Cytoplasm_Intensity_IntegratedIntensity_CorrActin	-13.12	0.00	0.00
Cytoplasm_Texture_DifferenceVariance_CorrActin_10_0	10.90	0.00	0.00
Nuclei_Texture_Contrast_CorrActin_10_0	11.83	0.00	0.00
Nuclei_Texture_DifferenceVariance_CorrDAPI_10_0	12.00	0.00	0.00
Nuclei_Texture_InfoMeas2_CorrTub_10_0	12.21	0.00	0.00
Nuclei_Texture_Variance_CorrDAPI_3_0	10.51	0.00	0.00
Nuclei_Neighbors_PercentTouching_20	10.65	0.00	0.00
Nuclei_Texture_Correlation_CorrDAPI_10_0	-11.11	0.00	0.00
Cells_Intensity_IntegratedIntensityEdge_CorrActin	-9.95	0.00	0.00
Nuclei_Texture_Entropy_CorrActin_3_0	9.98	0.00	0.00
Nuclei_Texture_SumVariance_CorrTub_3_0	9.20	0.00	0.00
Cytoplasm_Texture_Entropy_CorrActin_3_0	9.58	0.00	0.00
Cytoplasm_Texture_AngularSecondMoment_CorrActin_3_0	-9.11	0.00	0.00
Nuclei_Texture_InfoMeas1_CorrTub_10_0	-8.45	0.00	0.00
Nuclei_Neighbors_SecondClosestDistance_20	-8.63	0.00	0.00
Cytoplasm_AreaShape_Zernike_3_1	8.21	0.00	0.00
Cytoplasm_Texture_Contrast_CorrTub_10_0	8.00	0.00	0.00
Nuclei_Texture_AngularSecondMoment_CorrDAPI_3_0	-8.35	0.00	0.00
Nuclei_Texture_Variance_CorrDAPI_10_0	8.02	0.00	0.00
Cells_Intensity_MassDisplacement_CorrActin	-8.31	0.00	0.00
Cells_Texture_Entropy_CorrActin_3_0	7.77	0.00	0.00



Back to feature data -> Tools -> Marker Selection -> T-Test, Field is moa, Class A is DMSO, Class B are DNA damage and DNA replication, then sort by FDR

9 - Optionally save out your data





File -> Save Image allows you to save an image of the current tab in the format of your choice. File -> Save Dataset saves a GCT file of the DATA of your current tab. File -> Save Session saves the data AND settings (annotations, sortings, etc) of your current tab in a JSON file.