

Select plot variables

Select sample(s)

Nothing selected

Select gene group(s)

Nothing selected

If No group(s) selected, resulted plot will be for all the genes.

Number of genes to plot

✓ # top variable genes (By standard deviation)

✗ All genes

# top variable genes to show

500

Cluster by

✗ Raw value

✓ Z-Score

Display value

✗ Raw value

✓ Z-Score

Row options

Row names

✓ TRUE

✗ FALSE

Row names font size

5

Row cluster

✓ K-means

✗ Gene groups

# of row clusters (k-means)

1

Row cluster label prefix

Clust\_

Row cluster (within the cluster)

✓ TRUE

✗ FALSE

Row dendogram

✓ TRUE

✗ FALSE

Row cluster border

✓ TRUE

✗ FALSE

Add standard deviation heatmap

✓ TRUE

✗ FALSE

Sort by standard deviation

✓ TRUE

✗ FALSE

Column options

Column names

✓ TRUE

✗ FALSE

Column names font size

10

Column cluster

✓ K-means

✗ Sample groups

# of column clusters (k-means)

1

Column cluster label prefix

Clust\_

Column cluster (within the cluster)

✓ TRUE

✗ FALSE

Column dendogram

✓ TRUE

✗ FALSE

Column annotation

✗ Sample groups

✗ Boxplot

Column annotaion height

1

Legend options

Legend name

Value

Legend position

✓ T

✗ B

✗ L

✗ R

Legend direction

✗ H

✓ V

Heatmap Colors

Low

#004E63

Middle

white

High

#BD1717


Heatmap scale

Minimum

-1.5

Maximum

1.5

 Plot