Functional analysis

Miscellaneous

Quality control

Relative quantification

S
stats

artmsQuantification(“config.yaml”)

Input Files

keys.txt

evidence.txt

contrast.txt

config.yaml

TXT FILES	- quantification-results.txt
	- quantification-results-annotated.txt
	- Normalized abundance
	  * results_ModelQC.txt
	  * results_RunlevelData.txt
	  * results-mss-groupQuant.txt
	  * results-mss-normalized.txt
	  * results-mss-sampleQuant.txt
	- results_sampleSize.txt
	- results_experimentPower.txt

PDF FILES	- results-heatmap.pdf - results-peptidecounts-perBait.pdf - results-peptidecounts.pdf - results-sign.pdf - results-volcano.pdf

artMS

Analytical R Tools for Mass Spectrometry

http://artms.org

artMS

Analytical R Tools for Mass Spectrometry

http://artms.org

Bioconductor

Input Files

- evidence.txt
- keys.txt
- contrast.txt
- config.yaml

Quality control

Relative quantification

Functional analysis

Miscellaneous

artmsQuantification("config.yaml")

TXT FILES

- quantification-results.txt
- quantification-results-annotated.txt
- Normalized abundance
  - * results_ModelQC.txt
  - * results_RunlevelData.txt
  - * results-mss-groupQuant.txt
  - * results-mss-normalized.txt
  - * results-mss-sampleQuant.txt
- results_sampleSize.txt
- results_experimentPower.txt

PDF FILES

- results-heatmap.pdf
- results-peptidecounts-perBait.pdf
- results-peptidecounts.pdf
- results-sign.pdf
- results-volcano.pdf

artMS

Analytical R Tools for Mass Spectrometry

http://artms.org

Bioconductor

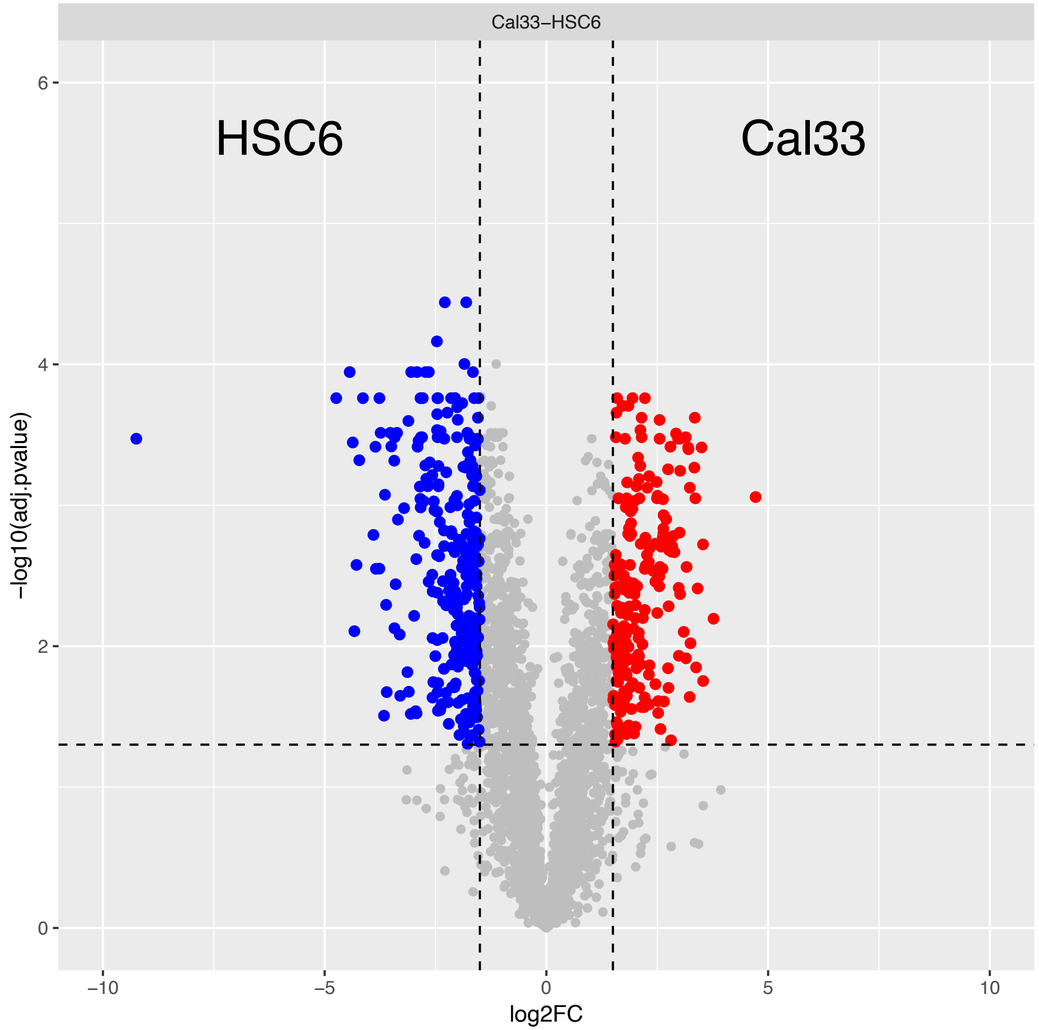
Input Files

- evidence.txt
- keys.txt
- contrast.txt
- config.yaml

Quality control

Relative quantification

Functional analysis

Miscellaneous

artmsQuantification("config.yaml")