

artMS

Analytical R Tools
for Mass Spectrometry

<http://artms.org>



Input Files



evidence.txt

+

keys.txt

+

contrast.txt

Configuration

config.yaml

Quality control

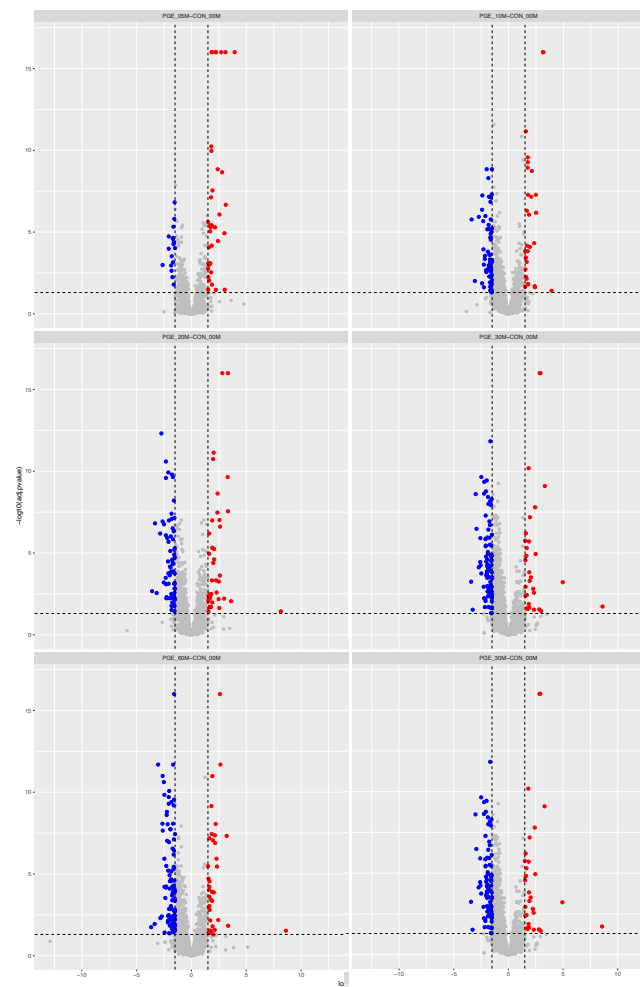


Relative
quantification

Functional analysis

Miscellaneous

Relative quantification
between conditions



A-B
A-C
A-D
D-E
D-F
D-G
etc

- Several conditions: **A, B, C, D, E, F, G**
- 4 biological replicates each

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Quality control



Relative
quantification

Functional analysis

Miscellaneous

Configuration

config.yaml

```
config-phglobal.yaml x
1 files:
2   evidence: evidence.txt
3   keys: keys.txt
4   contrasts: contrast.txt
5   summary: summary.txt
6   output: phglobal_results/phglobal-results.txt
7 qc:
8   basic: 1
9   extended: 1
10  extendedSummary: 1
11 data:
12  enabled: 1
13  fractions:
14    enabled: 0
15  silac:
16    enabled: 0
17  filters:
18    enabled: 1
19    contaminants: 1
20    protein_groups: remove
21    modifications: PH
22  sample_plots: 1
23 msstats:
24  enabled: 1
25  msstats_input:
26  profilePlots: none
27  normalization_method: equalizeMedians
28  normalization_reference:
29  summaryMethod: TMP
30  censoredInt: NA
31  cutoffCensored: minFeature
32  MBimpute: 1
33  feature_subset: all
34 output_extras:
35  enabled: 1
36  annotate:
37    enabled: 1
38    species: HUMAN
39  plots:
40    volcano: 1
41    heatmap: 1
42    LFC: -0.58 0.58
43    FDR: 0.05
44    heatmap_cluster_cols: 0
45    heatmap_display: log2FC
```