artMS
Analytical R Tools for Mass Spectrometry
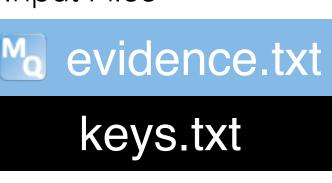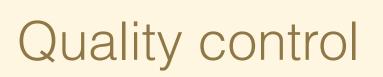
http://artms.org

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Input Files

evidence.txt

keys.txt

Quality control
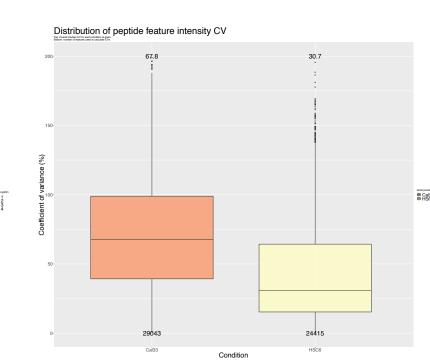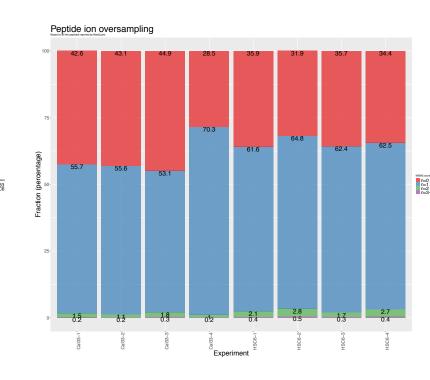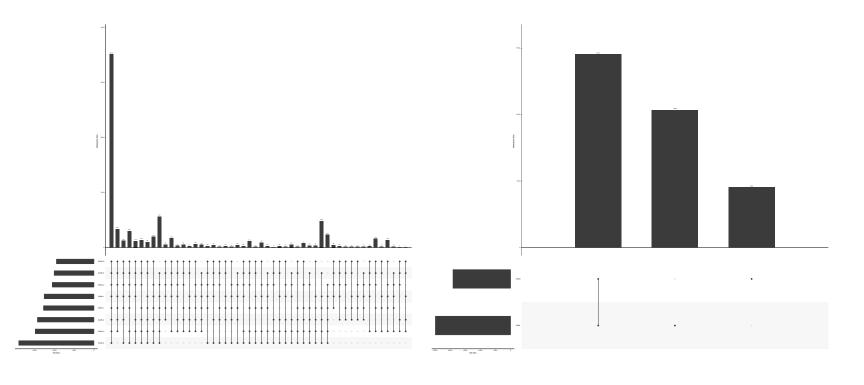
artmsQualityControlEvidenceBasic()
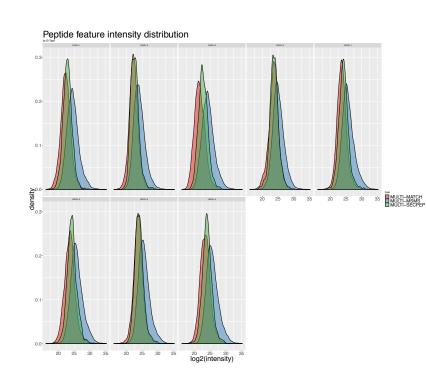
artmsQualityControlEvidenceExtended()

- Charge State Distribution
- ID overlap
- Peptide Ion Statistics
- Precursor Mass Error
- Precursor m/z error
- Frequency Peptide Detection
- Peptide Intensity CV
- Peptide Statistics
- Peptide Ion oversampling
- Protein detection frequency
- Protein Statistics / CV
- PCA
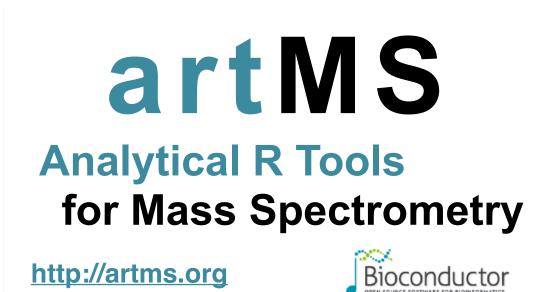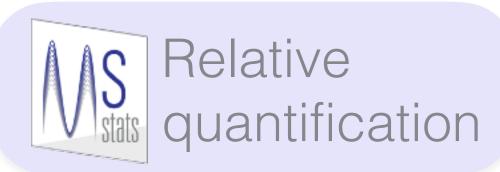- Peptide-spectrum matches
- MaxQuant Type statistics

Relative quantification

Functional analysis

Miscellaneous

artmsEvidenceToSAINTq()
artmsEvidenceToSaintExpress()

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summary.txt

keys.txt

Quality control

artmsQualityControlEvidenceBasic()
artmsQualityControlEvidenceExtended()
artmsQualityControlSummaryExtended()

- MS1 scan counts
- MS2 scan counts
- MS2 identification rate
- Isotope Pattern counts

Relative quantification

Functional analysis

Miscellaneous

```
> artmsQualityControlSummaryExtended(summary_file = "summary.txt",
+                                    keys_file = "keys.txt")
```