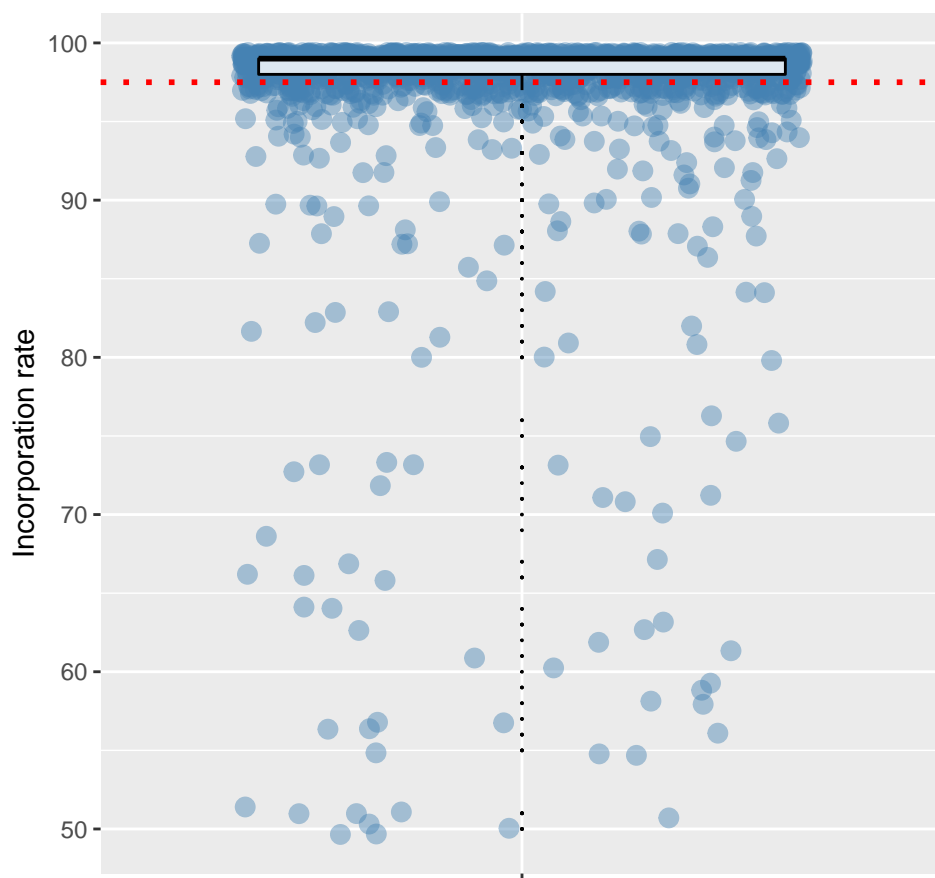# 15N labelling experiment

Arnoud Groen

November 26, 2020

1 15N incorporation rate

```
## Object of class "QcMetric"
##  Name: 15N incorporation rate
##  Status: TRUE
##  QC threshold: 97.5
##  Incorporation rate
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   50.00   98.00   99.00   97.04   99.00   99.00
```
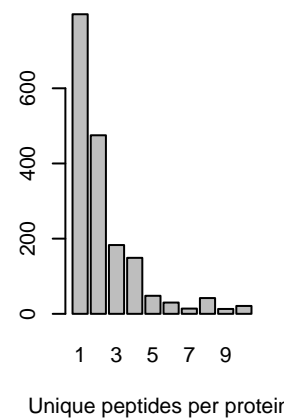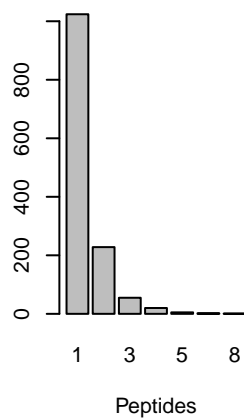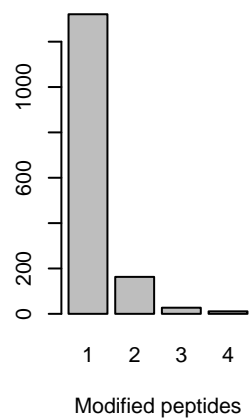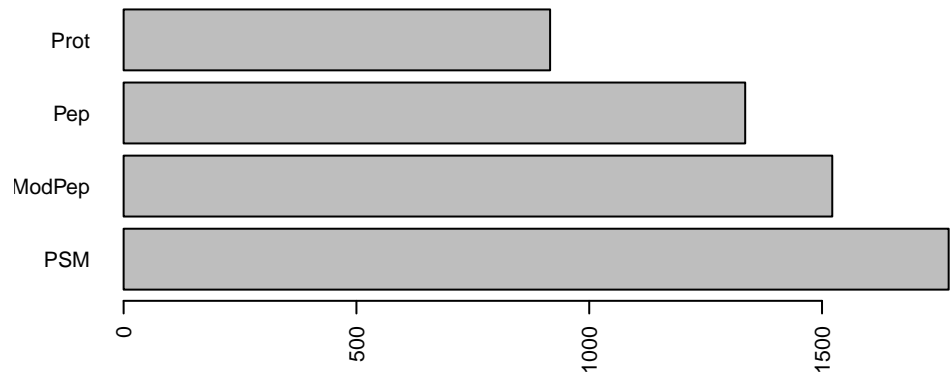
2 Log2 fold-changes

```
## Object of class "QcMetric"
##  Name: Log2 fold-changes
##  Status: TRUE
##  QC thresholds: -0.5 0.5
##  * PSM log2 fold-changes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -5.7641 -0.3164  0.2087  0.3536  0.8242 10.3712
##  * Modified peptide log2 fold-changes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -5.7641 -0.3306  0.1946  0.3393  0.8001 10.3712
##  * Peptide log2 fold-changes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -5.7268 -0.3285  0.1854  0.3317  0.7934 10.3712
##  * Protein log2 fold-changes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -3.4621 -0.3273  0.1942  0.3344  0.7902 10.3712
```
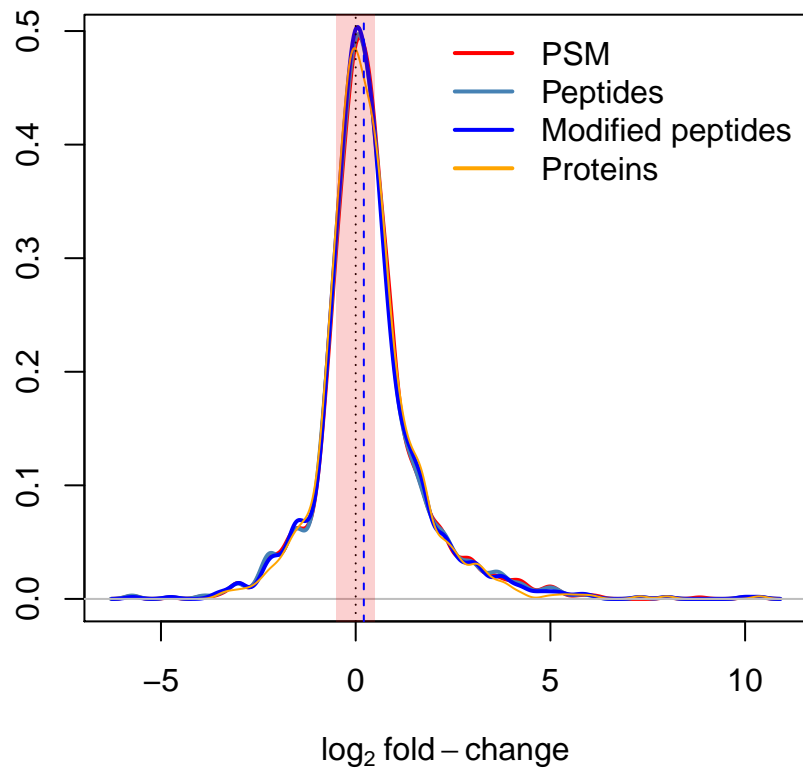
3 Number of features

```
## Object of class "QcMetric"
##  Name: Number of features
##  Status: NA
##    PSM ModPep    Pep    Prot
##   1772    1522   1335    916
```

4   QC summary

	name	status
1	15N incorporation rate	TRUE
2	Log2 fold-changes	TRUE
3	Number of features	

5   Session information

- R version 4.0.0 (2020-04-24), `x86_64-pc-linux-gnu`

- Locale: `LC_CTYPE=en_US.UTF-8`, `LC_NUMERIC=C`, `LC_TIME=fr_FR.UTF-8`, `LC_COLLATE=en_US.UTF-8`, `LC_MONETARY=fr_FR.UTF-8`, `LC_MESSAGES=en_US.UTF-8`, `LC_PAPER=fr_FR.UTF-8`, `LC_NAME=C`, `LC_ADDRESS=C`, `LC_TELEPHONE=C`, `LC_MEASUREMENT=fr_FR.UTF-8`, `LC_IDENTIFICATION=C`

- Running under: `Ubuntu 18.04.5 LTS`

- Matrix products: default

- BLAS: `/usr/lib/x86_64-linux-gnu/libf77blas.so.3.10.3`

- LAPACK: `/usr/lib/x86_64-linux-gnu/atlas/liblapack.so.3.10.3`

- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, stats4, utils

- Other packages: affy 1.68.0, Biobase 2.50.0, BiocGenerics 0.36.0, gcrma 2.62.0, genefilter 1.72.0, ggplot2 3.3.2, MSnbase 2.16.0, mzR 2.24.1, ProtGenerics 1.23.1, qcmetrics 1.28.0, Rcpp 1.0.5, S4Vectors 0.28.0, simpleaffy 2.66.0, xtable 1.8-4, yaqcaffy 1.50.0

- Loaded via a namespace (and not attached): affyio 1.60.0, annotate 1.68.0, AnnotationDbi 1.52.0, BiocManager 1.30.10, BiocParallel 1.24.1, Biostrings 2.58.0, bit 4.0.4, bit64 4.0.5, blob 1.2.1, codetools 0.2-16, colorspace 2.0-0, compiler 4.0.0, crayon 1.3.4, DBI 1.1.0, digest 0.6.27, doParallel 1.0.16, dplyr 1.0.2, ellipsis 0.3.1, evaluate 0.14, farver 2.0.3, foreach 1.5.1, generics 0.1.0, glue 1.4.2, grid 4.0.0, gtable 0.3.0, highr 0.8, httr 1.4.2, impute 1.64.0, IRanges 2.24.0, iterators 1.0.13, knitr 1.30, labeling 0.4.2, lattice 0.20-41, lifecycle 0.2.0, limma 3.46.0, magrittr 2.0.1, MALDIquant 1.19.3, MASS 7.3-53, Matrix 1.2-18, memoise 1.1.0, munsell 0.5.0, mzID 1.28.0, ncdf4 1.17, Nozzle.R1 1.1-1, pander 0.6.3, pcaMethods 1.82.0, pillar 1.4.7, pkgconfig 2.0.3, plyr 1.8.6, preprocessCore 1.52.0, purrr 0.3.4, R6 2.5.0, rlang 0.4.8, RSQLite 2.2.1, scales 1.1.1, splines 4.0.0, stringi 1.5.3, stringr 1.4.0, survival 3.2-7, tibble 3.0.4, tidyselect 1.1.0, tools 4.0.0, vctrs 0.3.5, vsn 3.58.0, withr 2.3.0, xfun 0.19, XML 3.99-0.5, XVector 0.30.0, zlibbioc 1.36.0