

Report for PEP Section in mzTab File

example_2

The PEP section of the **mzTab** file contains 2,160 quantified peptide features measured in 2 samples.

	number of peptides
quantified	2,160
identified (total)	2,160
identified (unique modified)	2,021
identified (unique stripped)	1,926

Table 1: Total number of quantified and identified peptides.

modified sequence	accession	charge	retention time	m/z
no matching sequences found				

Table 2: Peptides of interest. Note that the script requires a vector of *stripped* peptides sequences, but in the above table we list the *modified* peptide sequences.

modified sequence	accession	charge	retention time	m/z
no matching accessions found				

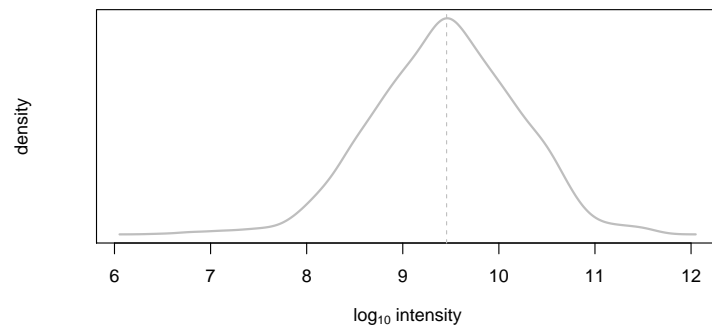
Table 3: Proteins of interest.

modifications statistics

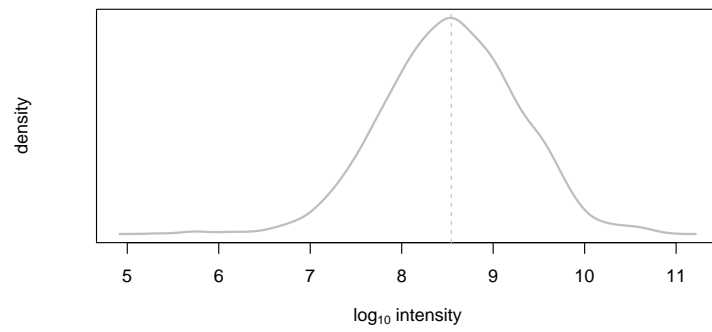
mod	specificity	number
Carbamidomethyl	C	205



Figure 1: Frequency plot of peptide quantifications.



(a) peptide abundances 1, $\text{median}(\text{intensity}) = 2,858,004,992$



(b) peptide abundances 2, $\text{median}(\text{intensity}) = 348,081,008$

Figure 2: peptide abundance distributions.

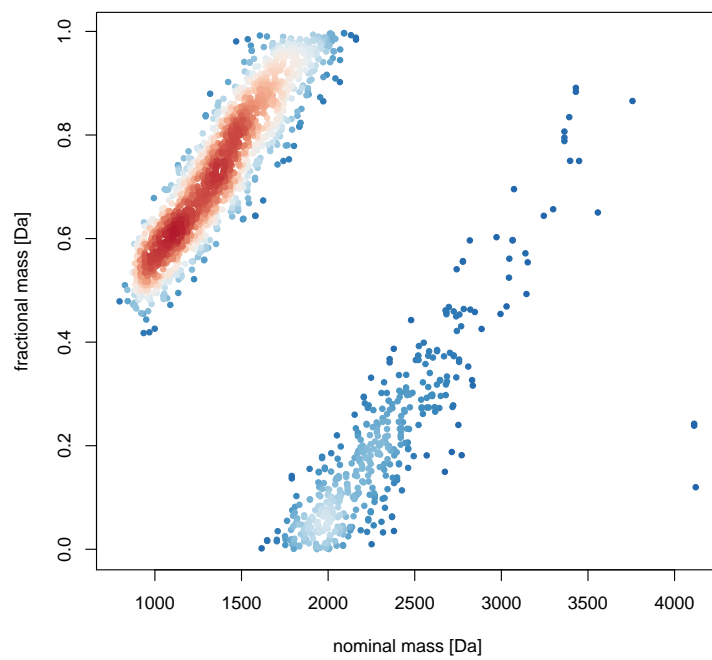


Figure 3: Kendrick nominal fractional mass plot

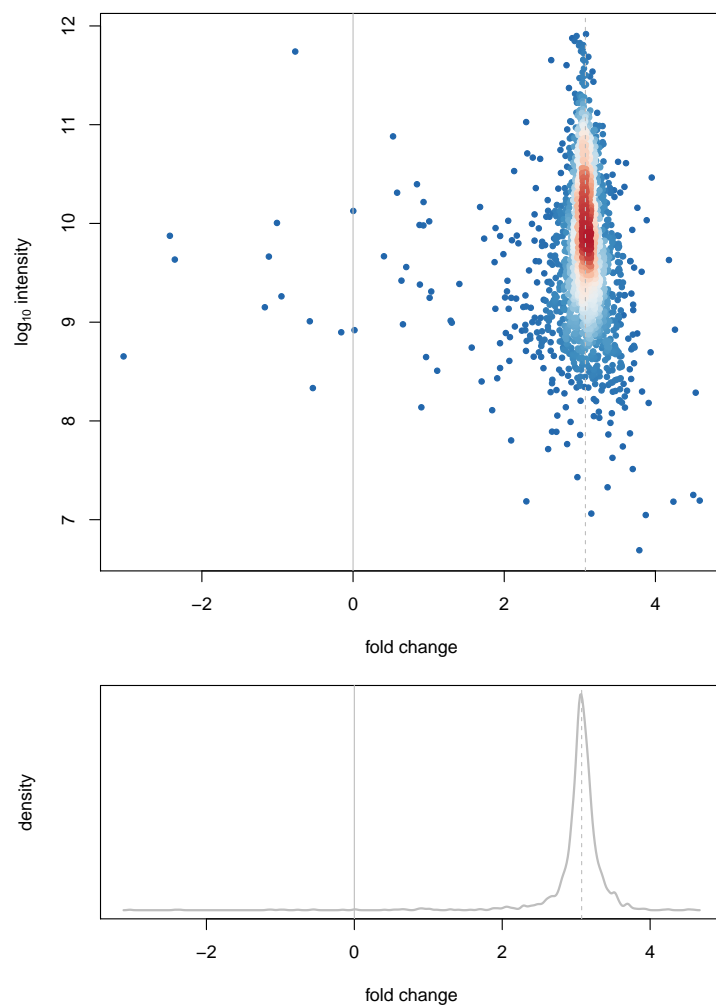


Figure 4: Fold changes of peptide abundances 1 and 2.
 $\text{median}(\text{fc}) = 3.0739$ $\text{sd}(\text{fc}) = 0.4645$