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	100%
identified (total)	2,160	100%
identified (unique modified)	2,021	93.56%
identified (unique stripped)	1,926	89.17%

Table 1: Total number of quantified and identified peptides.

mod	specificity	number
Carbamidomethyl	C	205

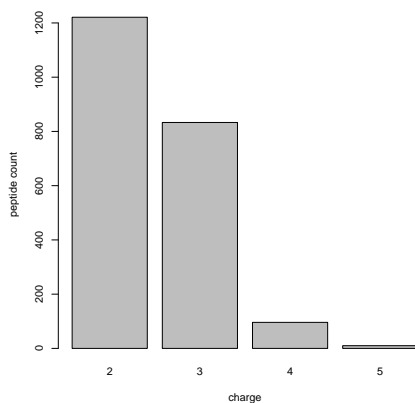Table 2: Statistics of modifications.

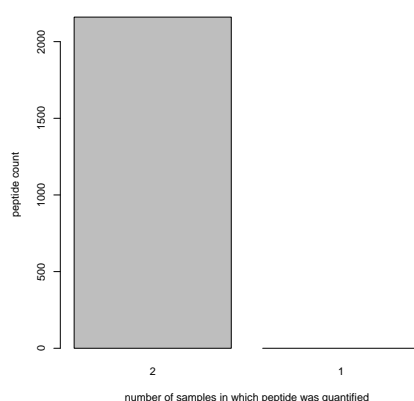Figure 1: Charge distribution of peptide quantifications.

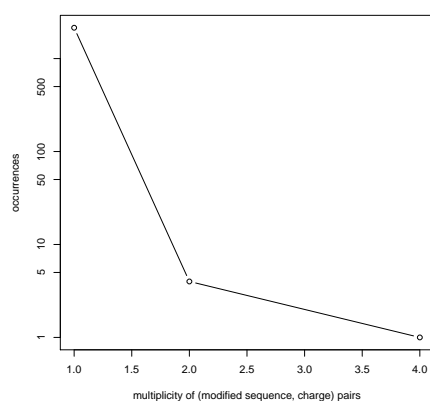Figure 2: Frequency plot of peptide quantifications.

Figure 3: (modified sequence, charge) pair multiplicity vs frequency plot. Each peptide feature (characterised by a (possibly) modified peptide sequence and a charge state) should ideally occur only once in the analysis. In other words, peptides of multiplicity 1 should have a very high frequency. The plot below should show a significant spike on the left and can be used as QC of the analysis.
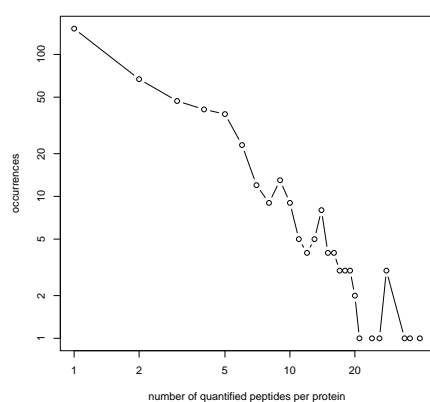

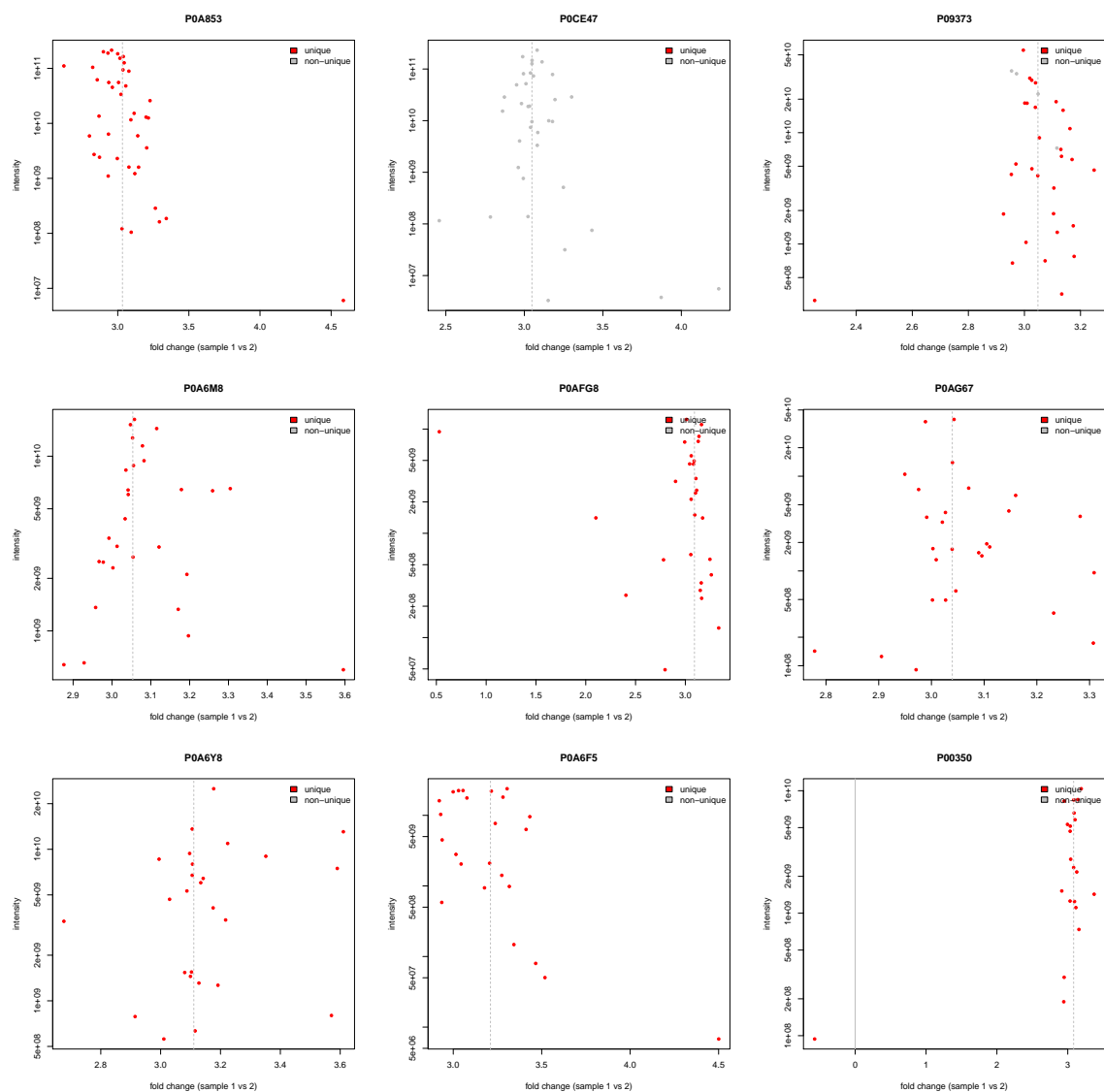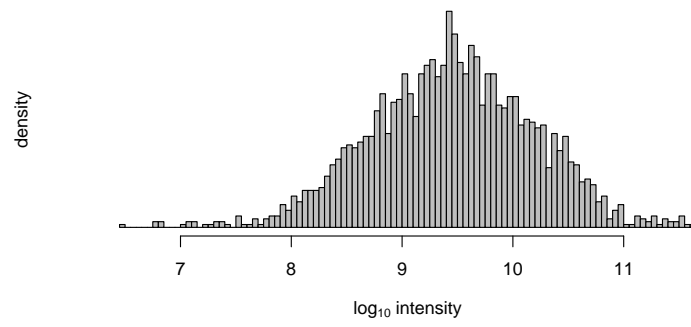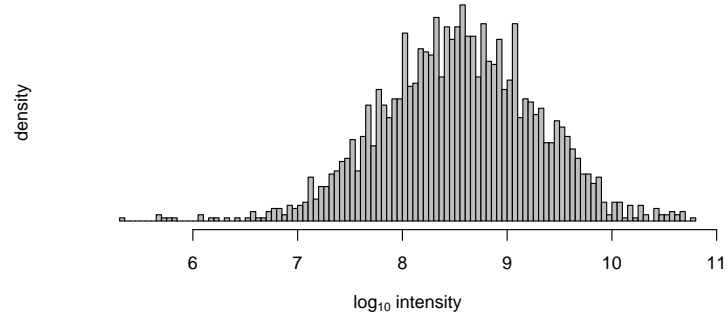Figure 4: Number of quantified peptides per protein.

Figure 5: Fold changes of peptide abundances 1 and 2. For proteins with the largest number of quantified peptides.

(a) peptide abundances 1, median(intensity) = $2, 858, 004, 992$

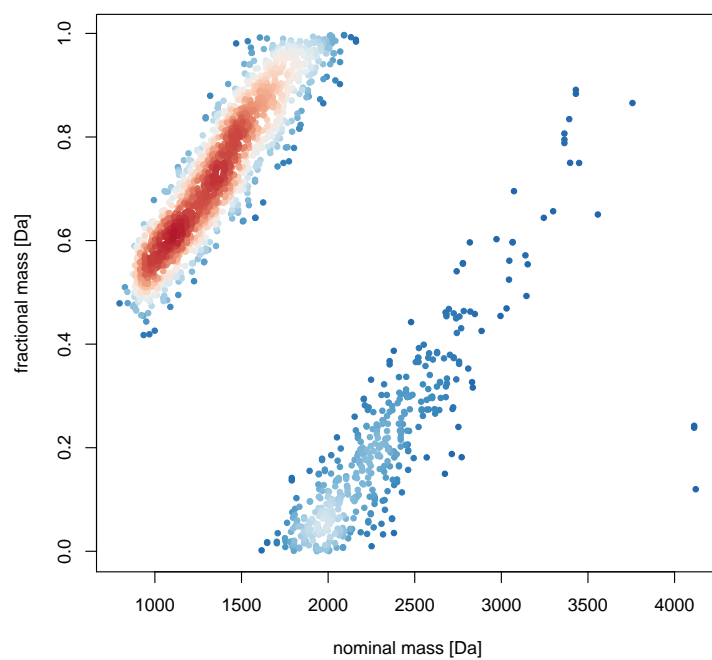(b) peptide abundances 2, median(intensity) = $348, 081, 008$

Figure 6: peptide abundance distributions.
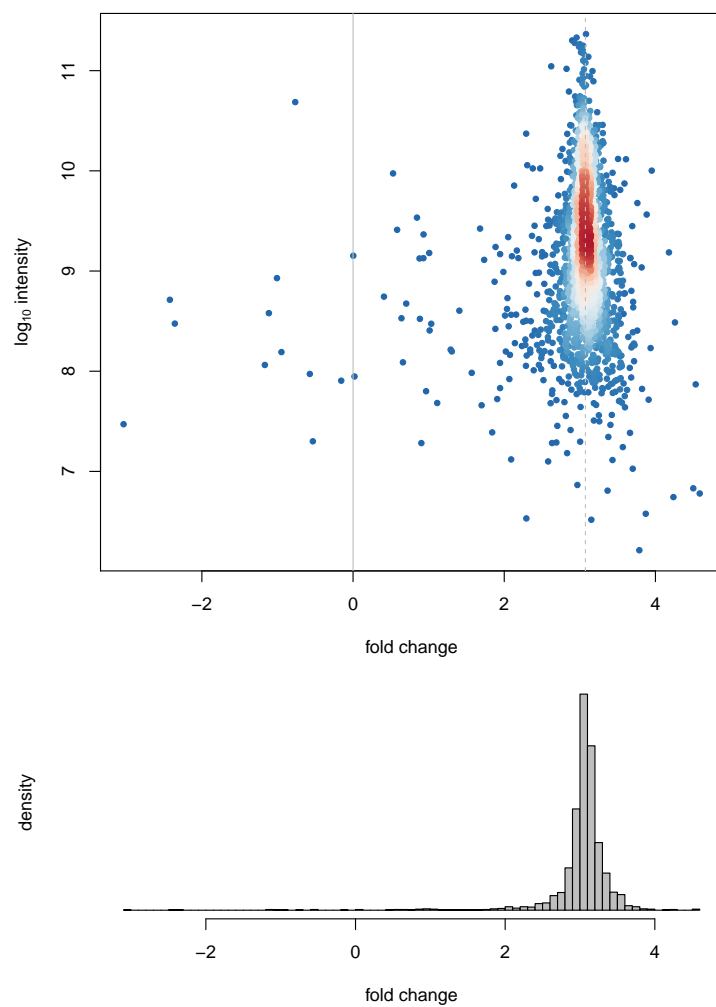
Figure 7: Kendrick nominal fractional mass plot

Figure 8: Fold changes of peptide abundances 1 and 2.
median(fc) = 3.0739   sd(fc) = 0.4645

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

Table 3: Peptides of interest. Please 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 4: Proteins of interest.