Report for PEP Section in mzTab File
example_3

The PEP section of the mzTab file contains $13,936$ quantified peptide features measured in 3 samples.

	number of peptides
quantified	13,936
identified (total)	0
identified (unique modified)	0
identified (unique stripped)	0

Table 1: Total number of quantified and identified peptides.

modified sequence	accession	charge	retention time	m/z
no sequences reported				

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 accessions reported			

Table 3: Proteins of interest.

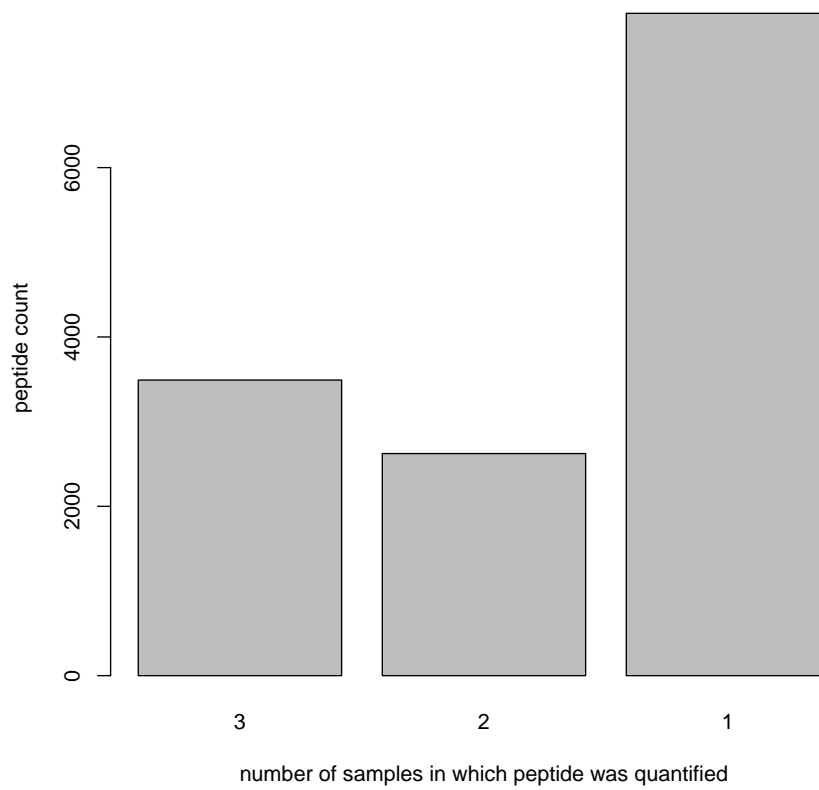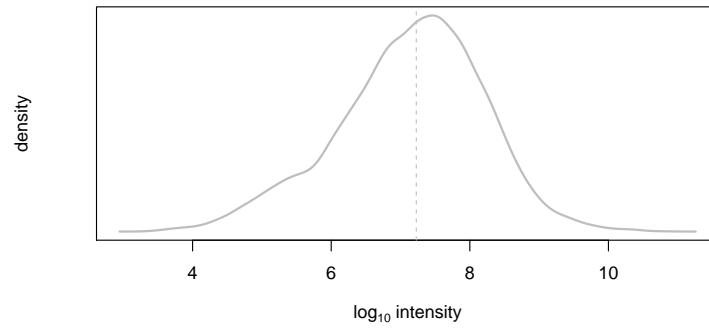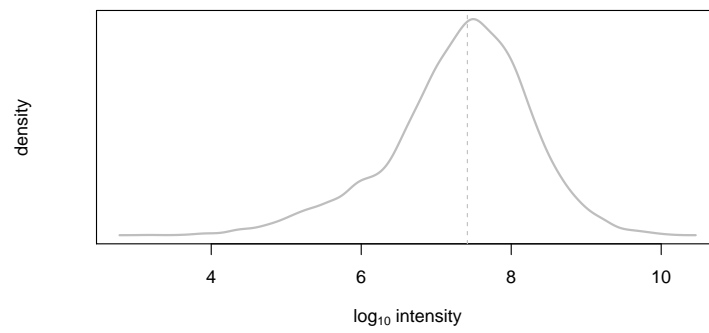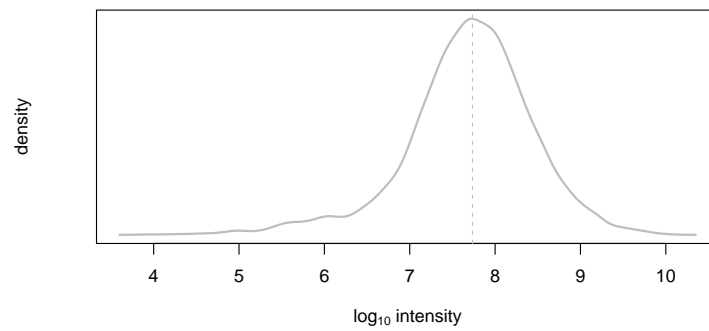| modification	specificity	number
no mods reported		

Table 4: Statistics of modifications.

Figure 1: Frequency plot of peptide quantifications.

(a) peptide abundances 1, median(intensity) $= 16,881,700$

(b) peptide abundances 2, median(intensity) $= 26,020,850$

(c) peptide abundances 3, median(intensity) $= 54,309,500$

Figure 2: peptide abundance distributions.

Figure 3: Kendrick nominal fractional mass plot

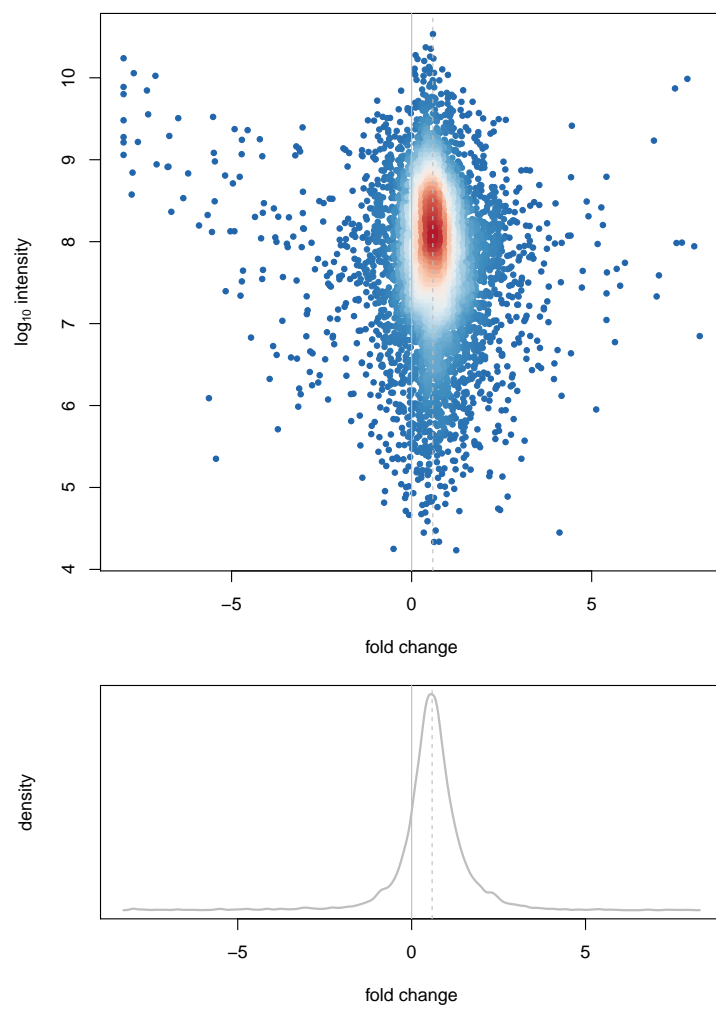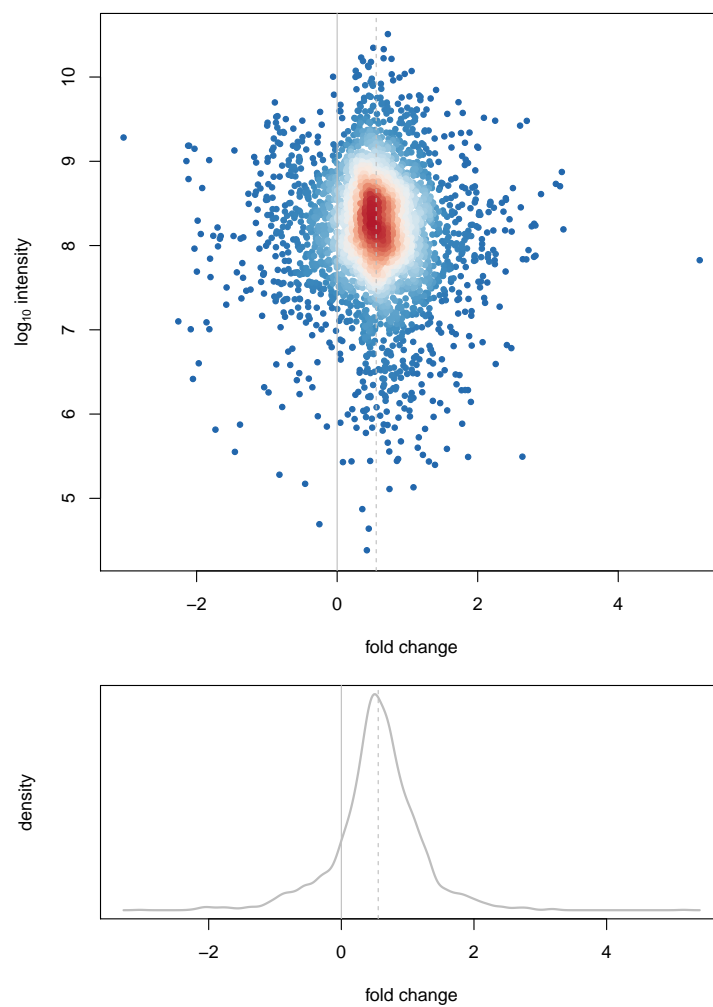Figure 4: Fold changes of peptide abundances 1 and 2.
median(fc) = 0.589   sd(fc) = 1.1158

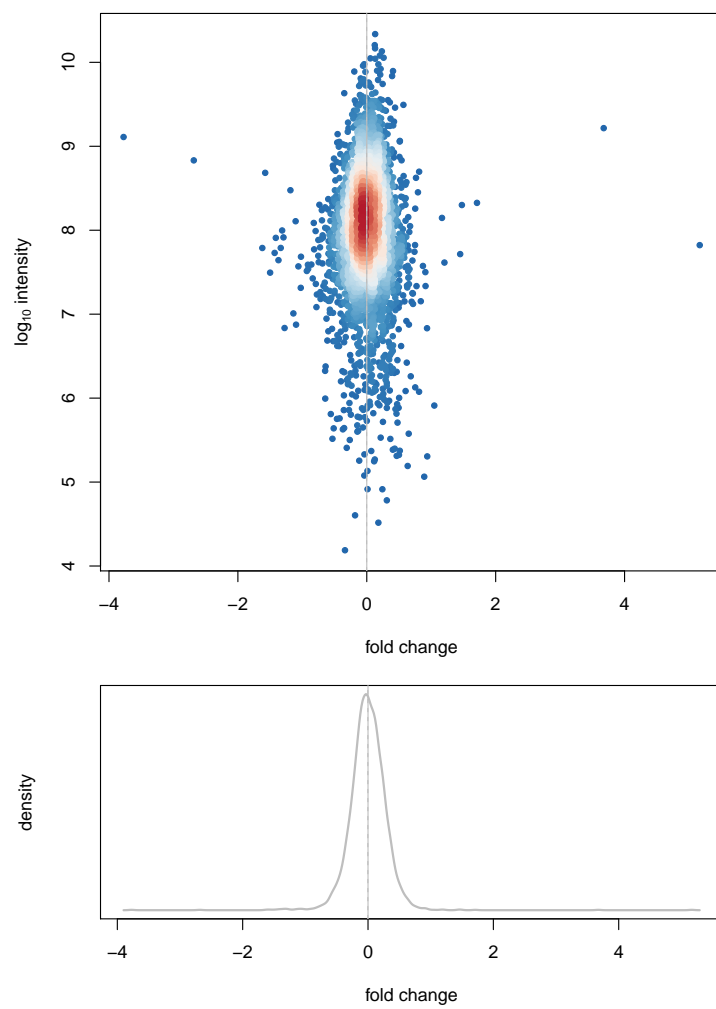Figure 5: Fold changes of peptide abundances 1 and 3.
median(fc) = 0.5559   sd(fc) = 0.6453

Figure 6: Fold changes of peptide abundances 2 and 3.
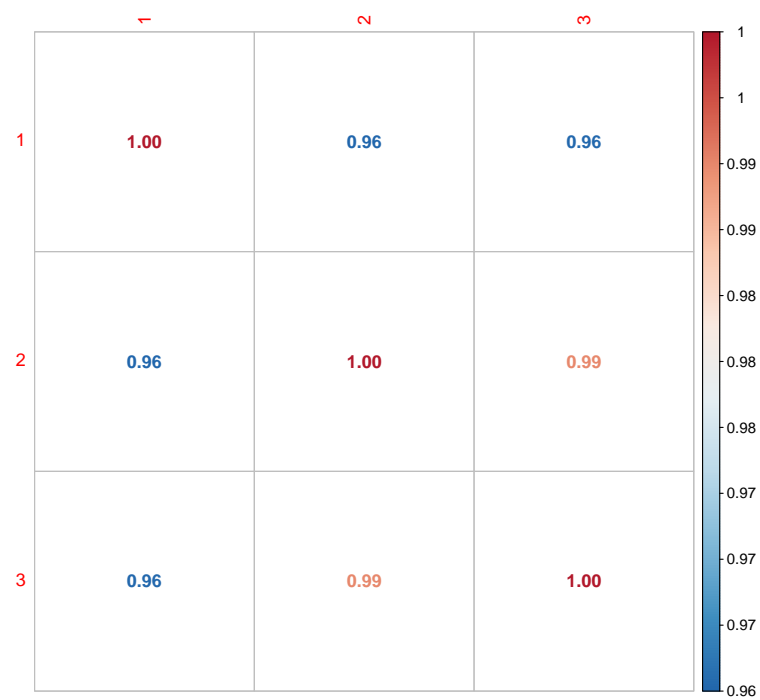median(fc) = −0.0025   sd(fc) = 0.3047

Figure 7: Pearson rank correlation of all peptide abundances. (min correlation = 0.962, median correlation = 0.9925, max correlation = 1)

Figure 8: Boxplot of all peptide abundances.