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.

modification	specificity	number
no mods reported		

Table 2: Statistics of modifications.

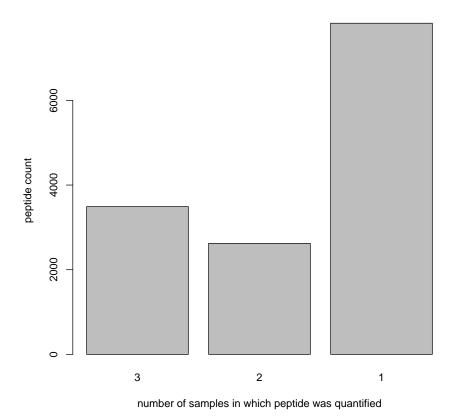
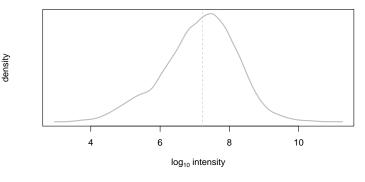
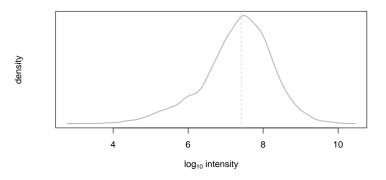


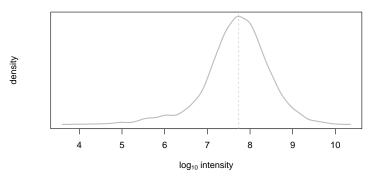
Figure 1: Frequency plot of peptide quantifications.



(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

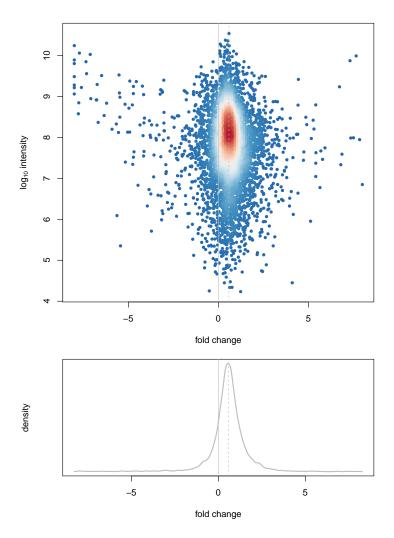


Figure 4: Fold changes of peptide abundances 1 and 2. $\mathrm{median(fc)} = 0.589 \qquad \mathrm{sd(fc)} = 1.1158$

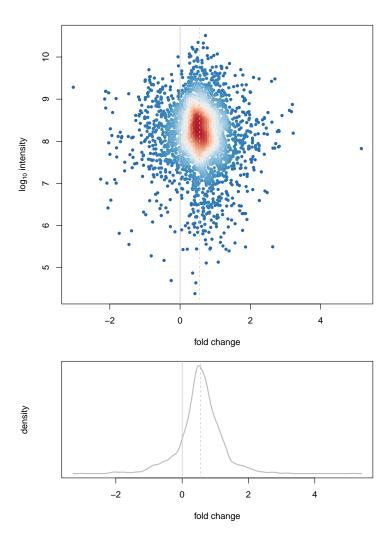


Figure 5: Fold changes of peptide abundances 1 and 3. $median(fc) = 0.5559 \qquad sd(fc) = 0.6453$

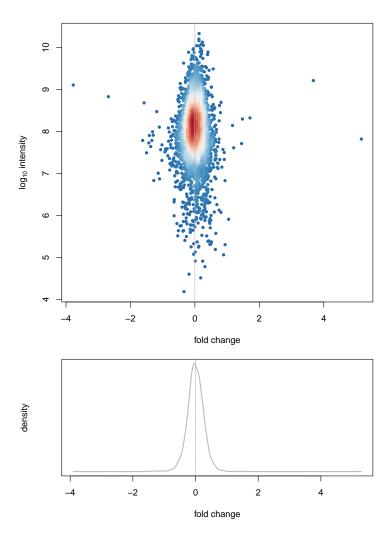


Figure 6: Fold changes of peptide abundances 2 and 3. $median(fc) = -0.0025 \qquad sd(fc) = 0.3047$

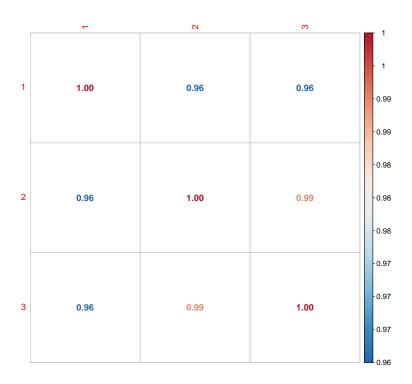


Figure 7: Pearson correlation of all peptide abundances. (min correlation = 0.962, median correlation = 0.9925, max correlation = 1)

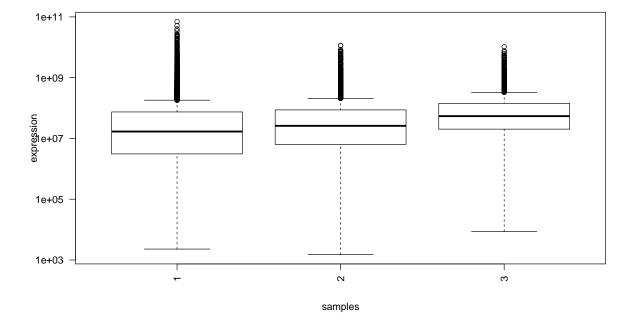


Figure 8: Boxplot of all peptide abundances.

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

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 accessions reported			

Table 4: Proteins of interest.