

# 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				

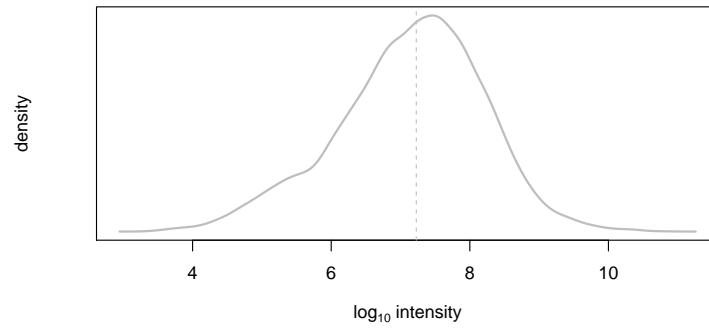
Table 3: Proteins of interest.

### modifications statistics

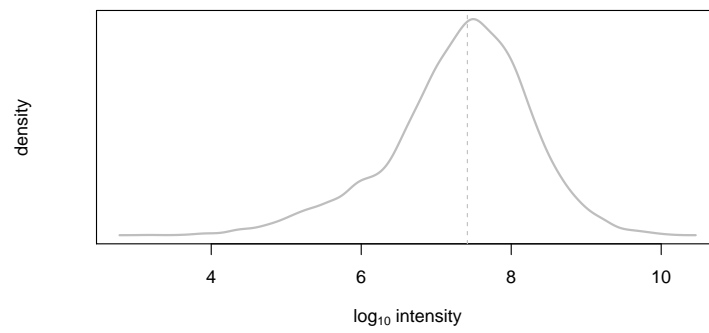
modification	specificity	number
no mods reported		



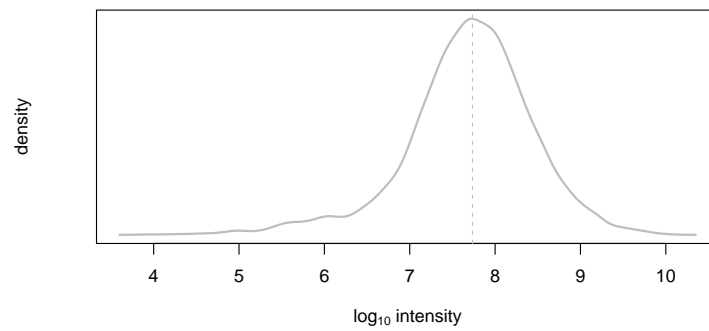
Figure 1: Frequency plot of peptide quantifications.



(a) peptide abundances 1,  $\text{median}(\text{intensity}) = 16,881,700$



(b) peptide abundances 2,  $\text{median}(\text{intensity}) = 26,020,850$



(c) peptide abundances 3,  $\text{median}(\text{intensity}) = 54,309,500$

Figure 2: peptide abundance distributions.



Figure 3: Kendrick nominal fractional mass plot

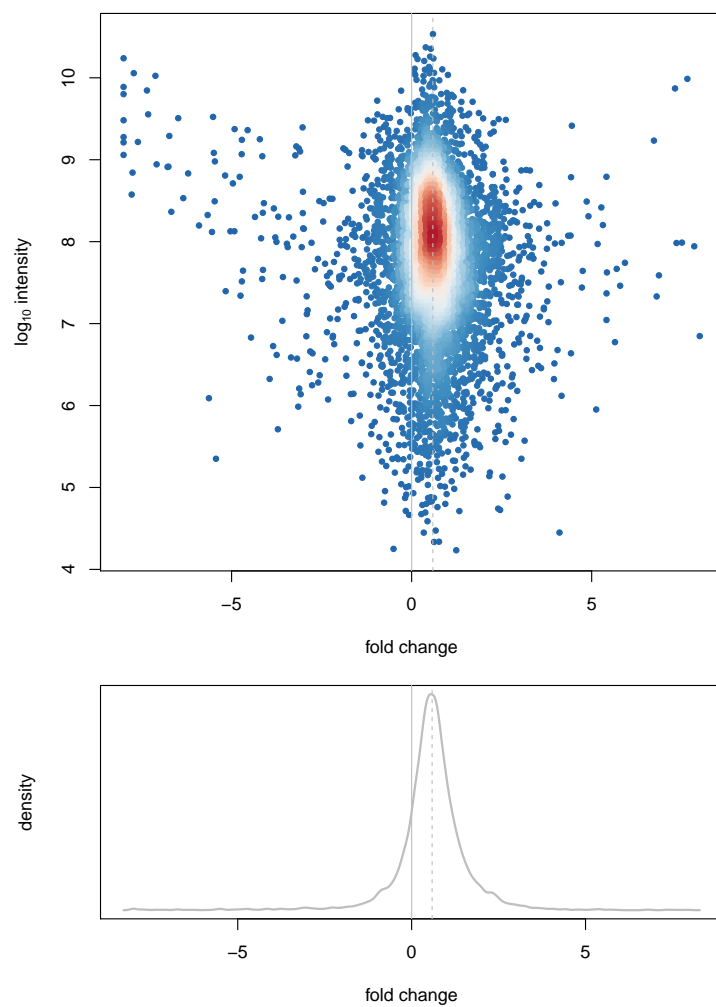


Figure 4: Fold changes of peptide abundances 1 and 2.  
 $\text{median}(\text{fc}) = 0.589$        $\text{sd}(\text{fc}) = 1.1158$

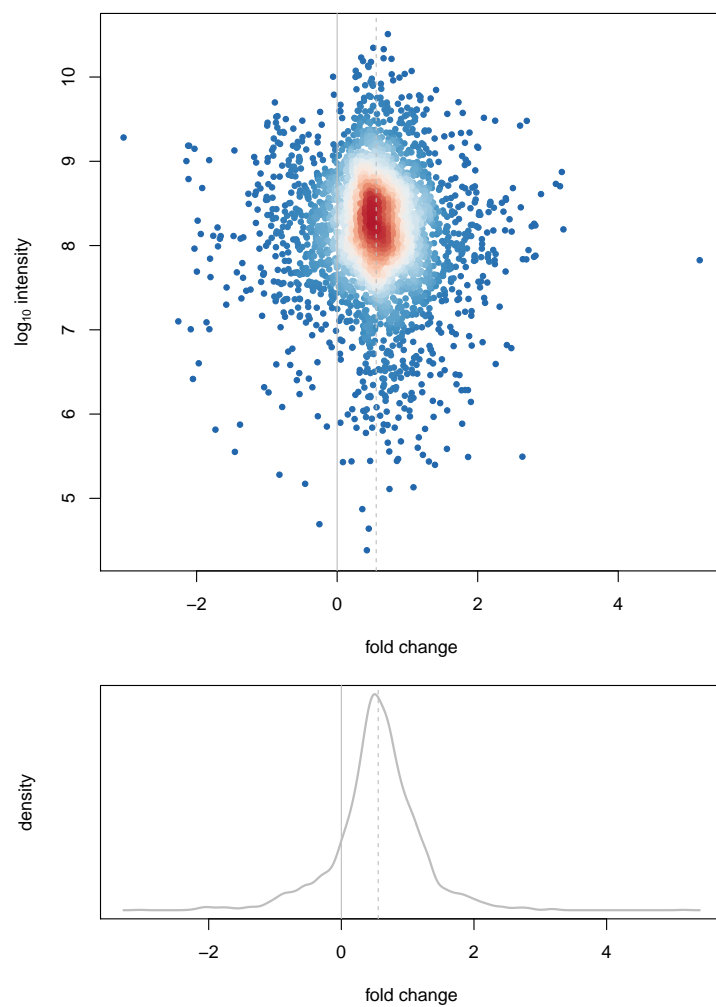


Figure 5: Fold changes of peptide abundances 1 and 3.  
 $\text{median}(\text{fc}) = 0.5559$        $\text{sd}(\text{fc}) = 0.6453$

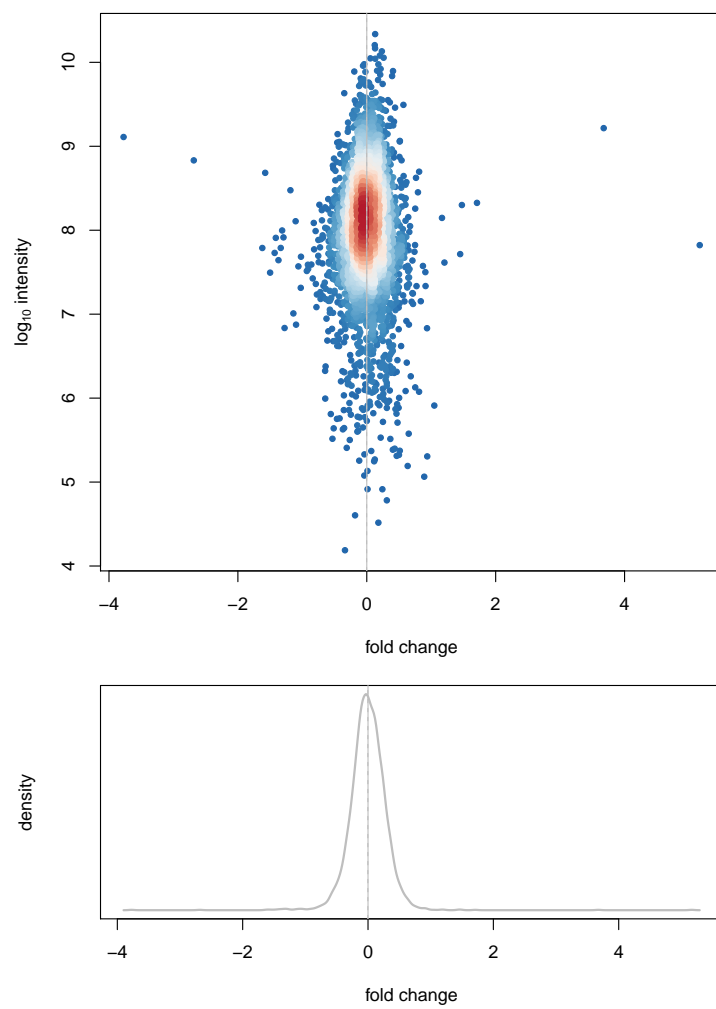


Figure 6: Fold changes of peptide abundances 2 and 3.  
 $\text{median}(\text{fc}) = -0.0025$        $\text{sd}(\text{fc}) = 0.3047$

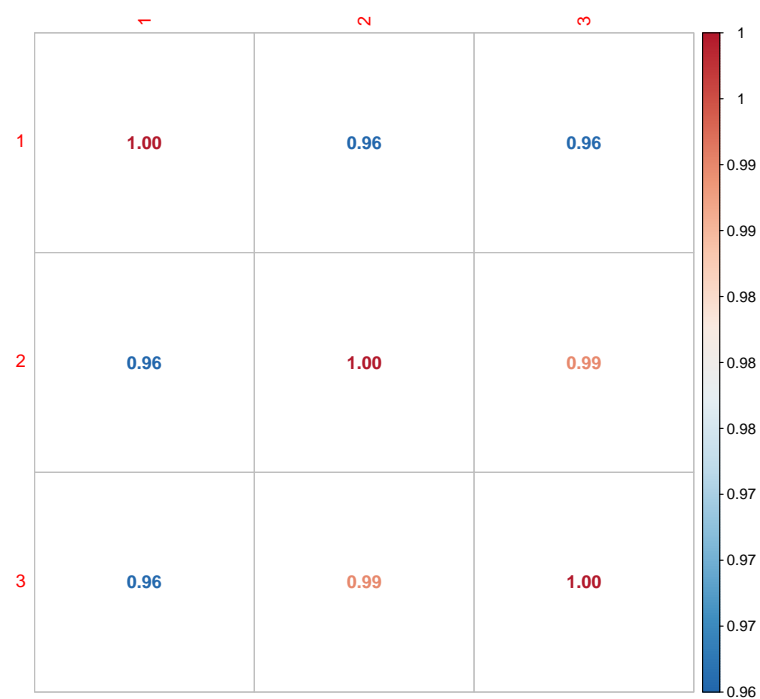


Figure 7: Correlation of all peptide abundances.

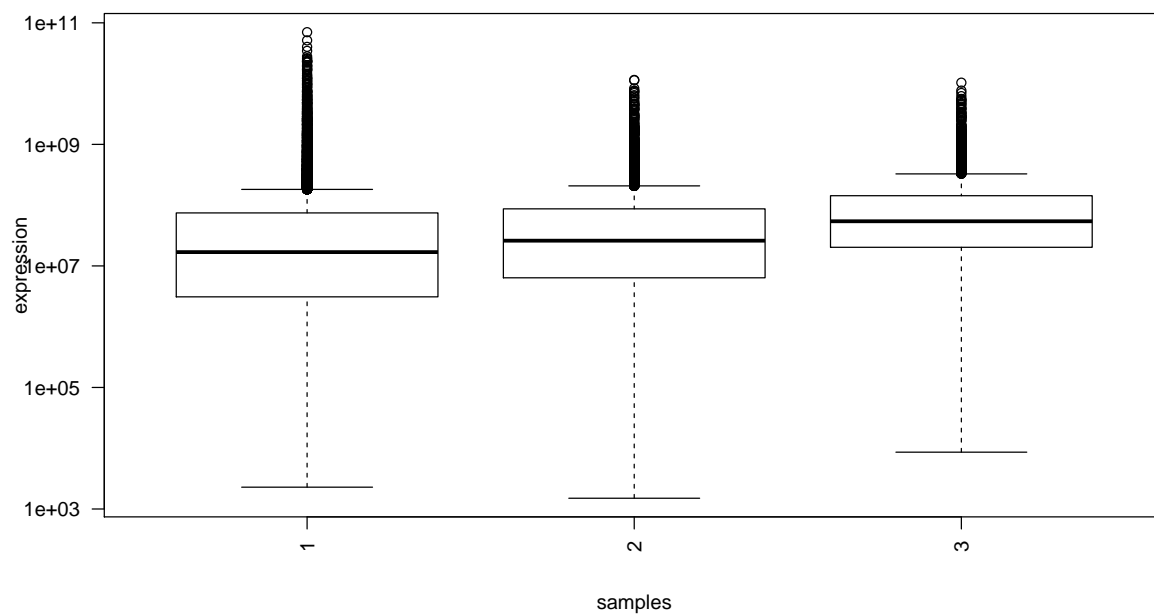


Figure 8: Boxplot of all peptide abundances.