Report for PEP Section in mzTab File
example_3

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

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

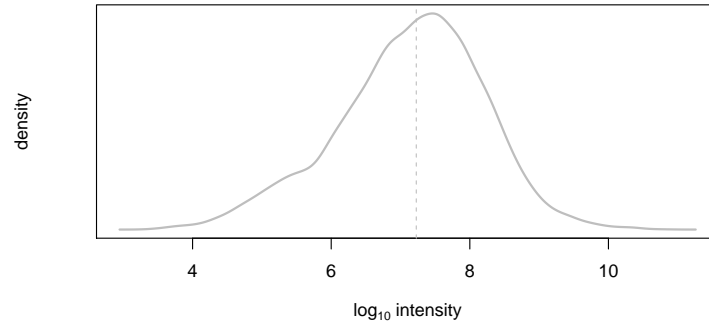Table 1: Total number of quantified and identified peptides.

Peptides of Interest

Sequence	Accession	Charge	Retention Time	m/z
no sequences reported				

Proteins of Interest

Sequence	Accession	Charge	Retention Time	m/z
	no accessions reported			

modifications statistics

modification	specificity	number
no mods reported		

(a) peptide abundances 1, median(intensity) = $16, 881, 700$
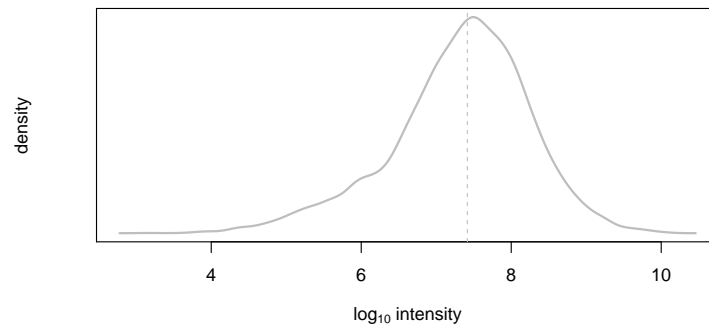
(b) peptide abundances 2, median(intensity) = $26, 020, 850$
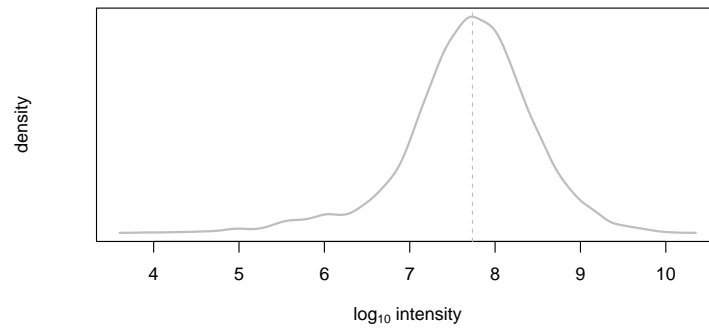
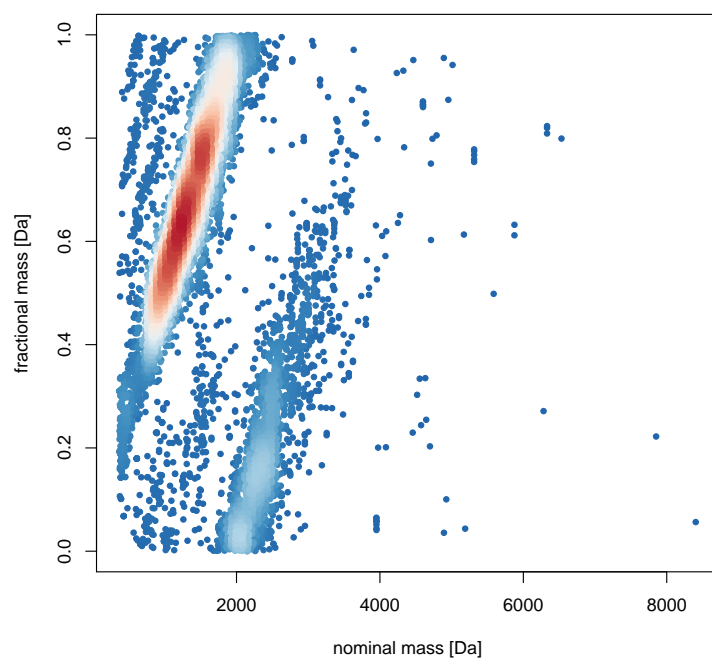(c) peptide abundances 3, median(intensity) = $54, 309, 500$

Figure 1: peptide abundance distributions.

Figure 2: Kendrick nominal fractional mass plot

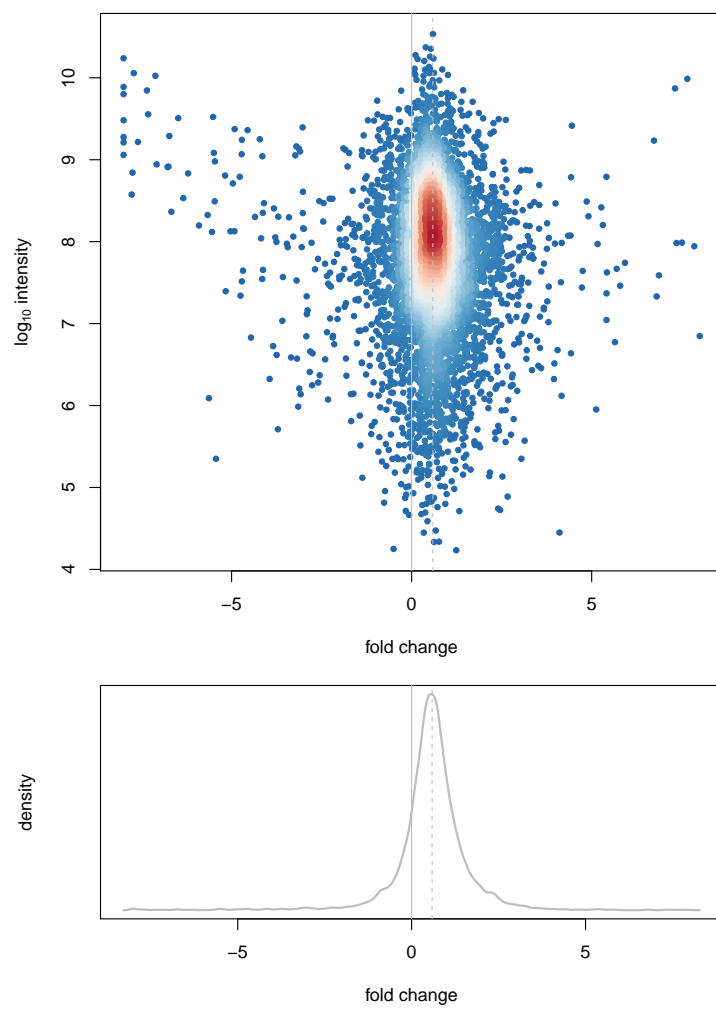Figure 3: Fold changes of peptide abundances 1 and 2.
median(fc) = 0.589   sd(fc) = 1.1158

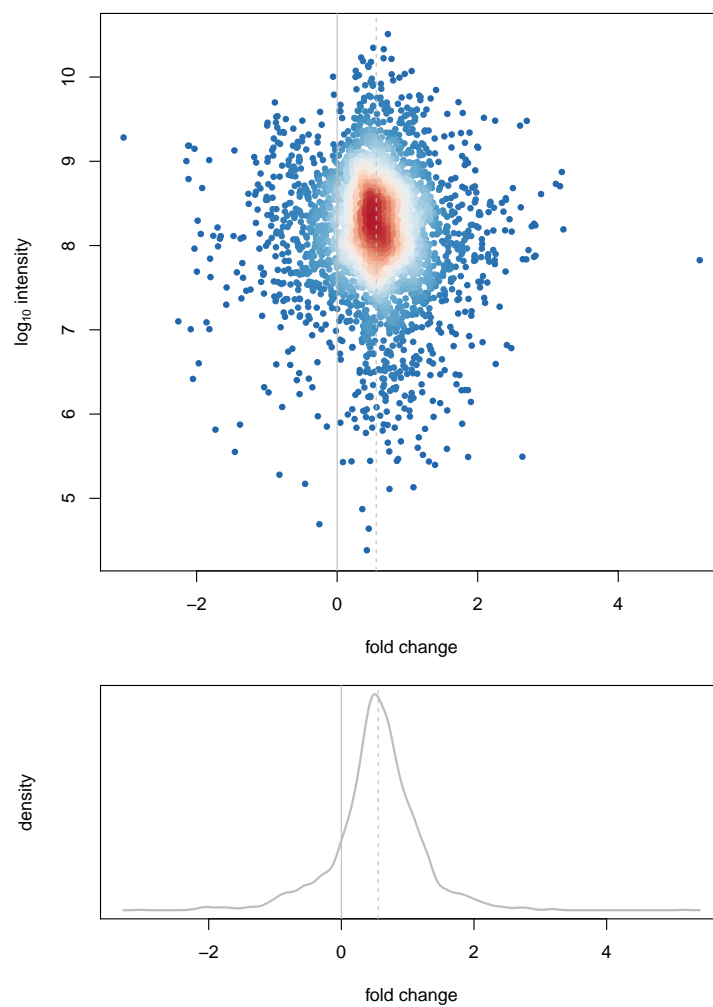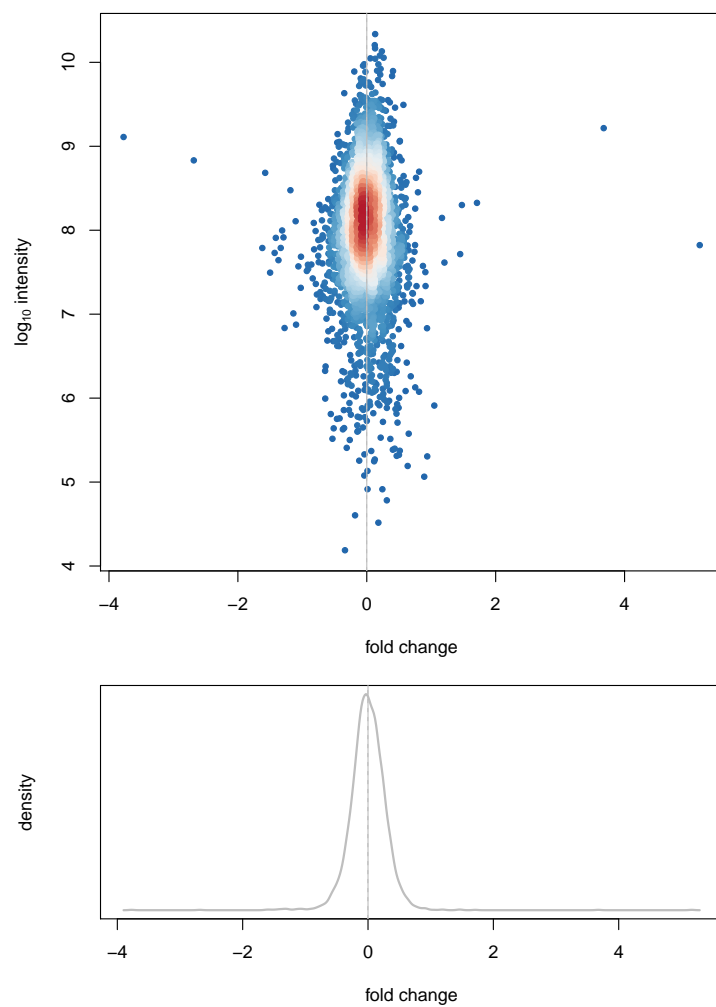Figure 4: Fold changes of peptide abundances 1 and 3.
median(fc) = 0.5559   sd(fc) = 0.6453

Figure 5: Fold changes of peptide abundances 2 and 3.
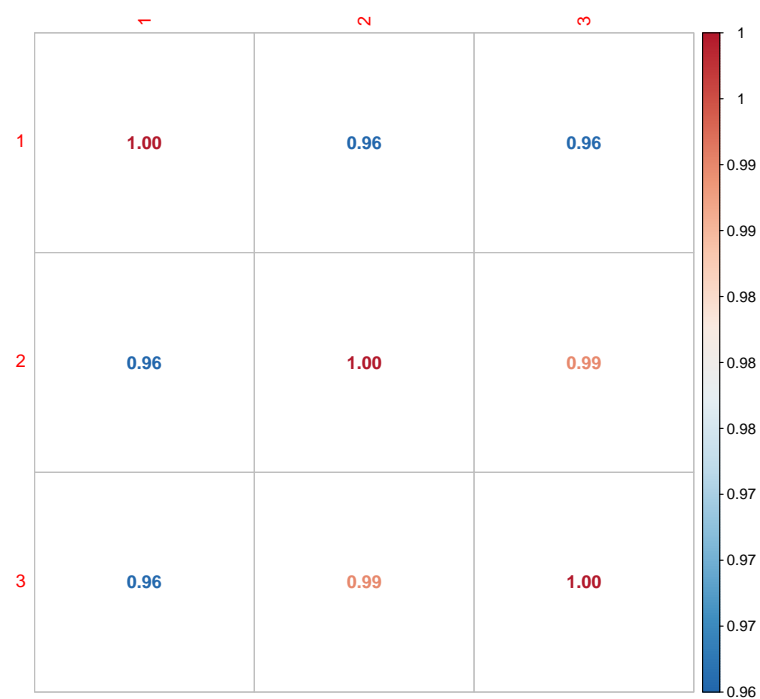median(fc) = −0.0025   sd(fc) = 0.3047
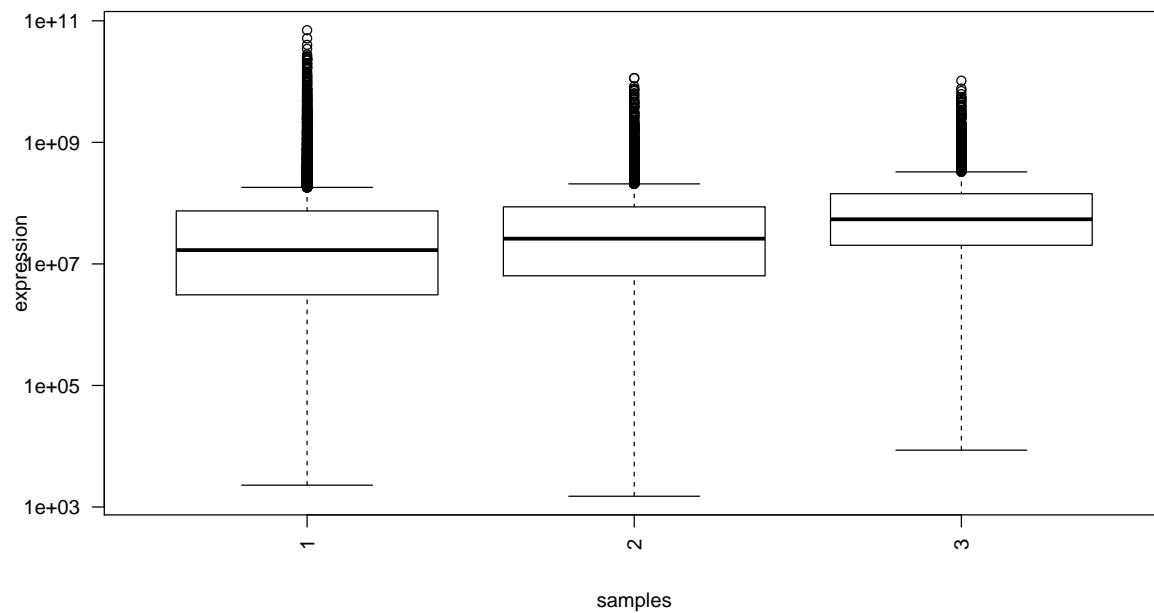
Figure 6: Correlation of all peptide abundances.

Figure 7: Boxplot of all peptide abundances.