Report for PEP Section in mzTab File

example_4

The PEP section of the mzTab file contains 1,335 quantified peptide features.

Peptides of Interest

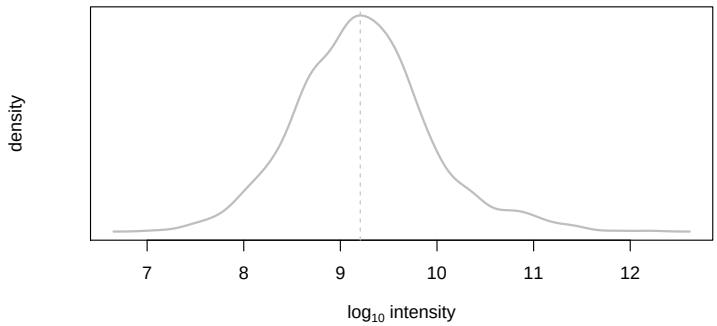
Sequence	Accession	Charge	Retention Time	m/z
SSAAPPPPPR	STD_01	2	1659.92	493.77
HVLTSIGEK	STD_03	2	2127.71	496.29
IGDYAGIK	STD_05	2	3096.71	422.74
TASEFDSAIAQDK	STD_06	2	4266.53	695.83
SAAGAFGPELSR	STD_07	2	4457.27	586.80
ELGQSGVDTYLQTK	STD_08	2	5741.14	773.90
GLILVGGYGTR	STD_09	2	6431.53	558.33
GILFVGSGVSGGEEGAR	P52209	2	6780.92	796.41
GILFVGSGVSGGEEGAR	P52209	2	6781.34	801.41
SFANQPLEVVYSK	STD_11	2	6787.30	745.39
ELASGLSFPVGFK	STD_14	2	9083.08	680.37

Proteins of Interest

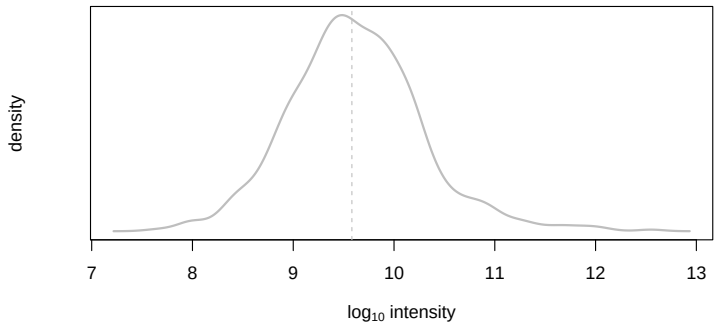
Sequence	Accession	Charge	Retention Time	m/z
INQEELASGTPPARFPK	O15117	3	4675.29	618.99

modifications statistics

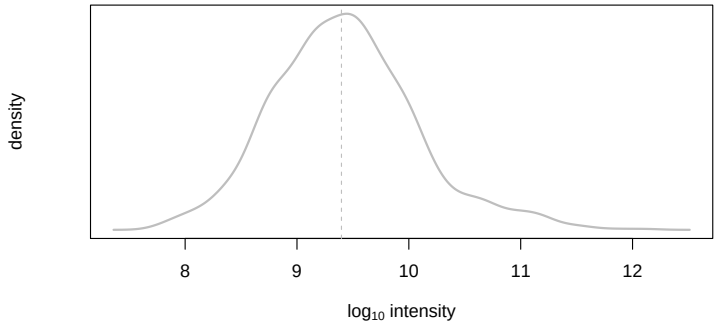
mod	specificity	number
Oxidation	M	179
Methylthio	C	150
Label:13C(6)15N(2)	K	6
Label:13C(6)15N(4)	R	4



(a) peptide abundances 1, median(intensity) $= 1,605,469,952$



(b) peptide abundances 2, median(intensity) $= 3,819,539,968$



(c) peptide abundances 3, median(intensity) $= 2,497,959,936$

Figure 1: peptide abundance distributions.

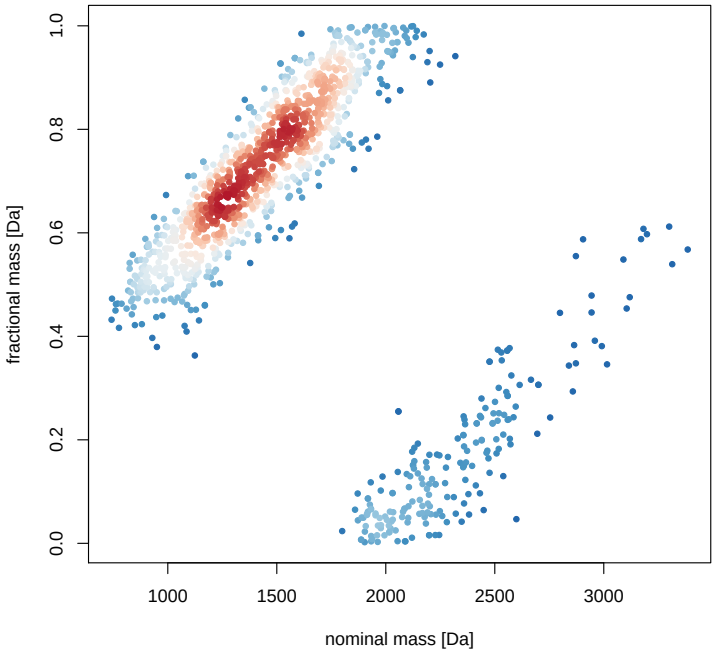


Figure 2: Kendrick nominal fractional mass plot

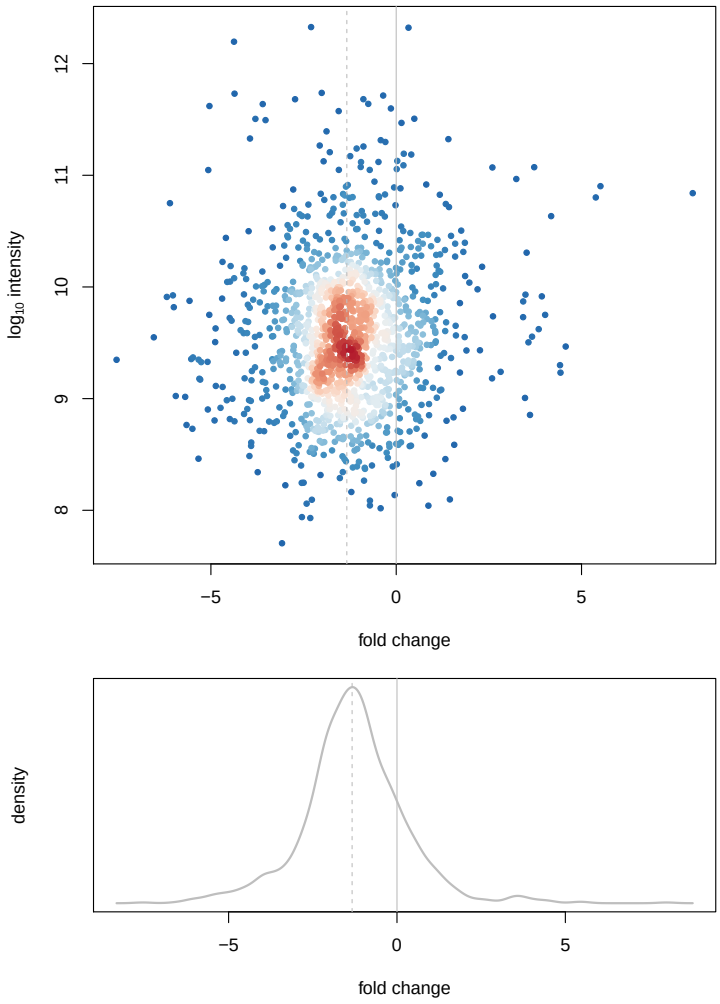


Figure 3: Fold changes of peptide abundances 1 and 2.
median(fc) = −1.3328 sd(fc) = 1.5445

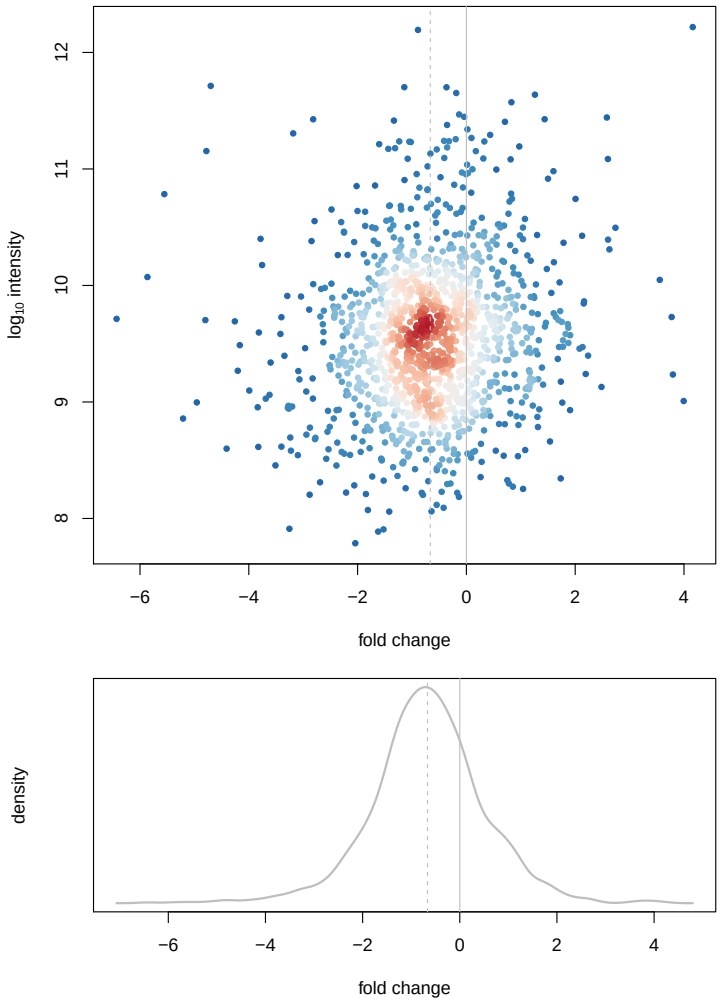


Figure 4: Fold changes of peptide abundances 1 and 3.
median(fc) = −0.6641 sd(fc) = 1.1804

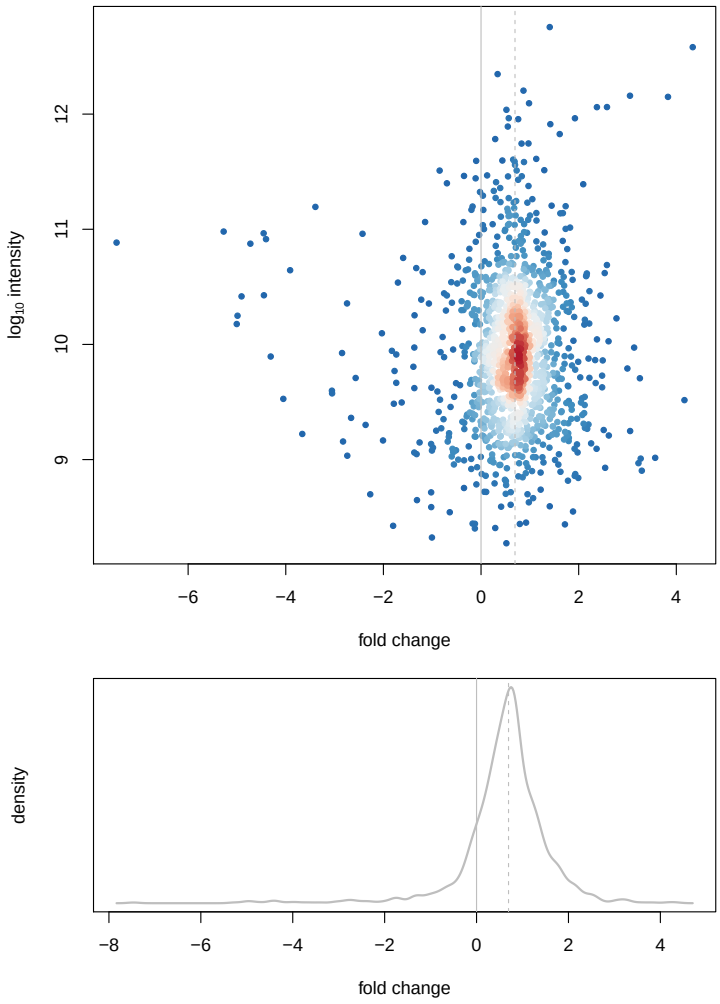


Figure 5: Fold changes of peptide abundances 2 and 3.
median(fc) = 0.6958 sd(fc) = 0.9636

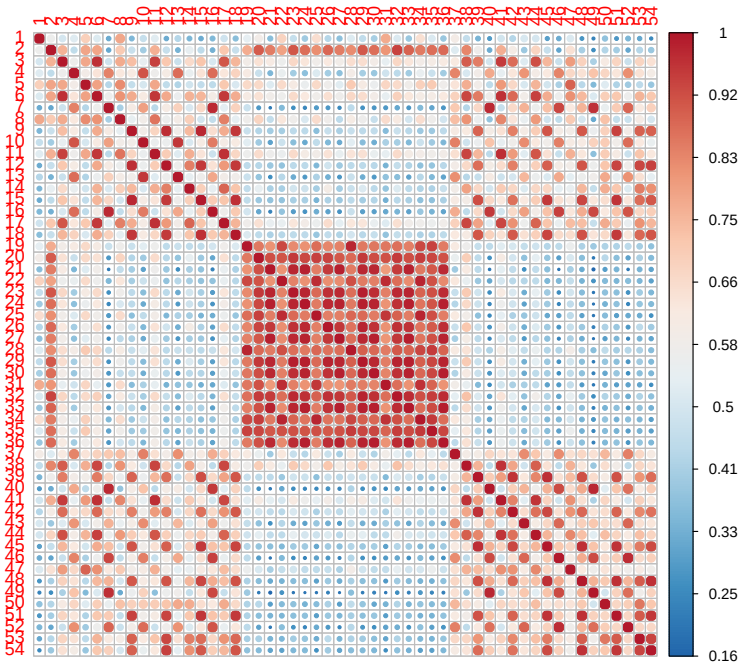


Figure 6: Correlation of all peptide abundances.

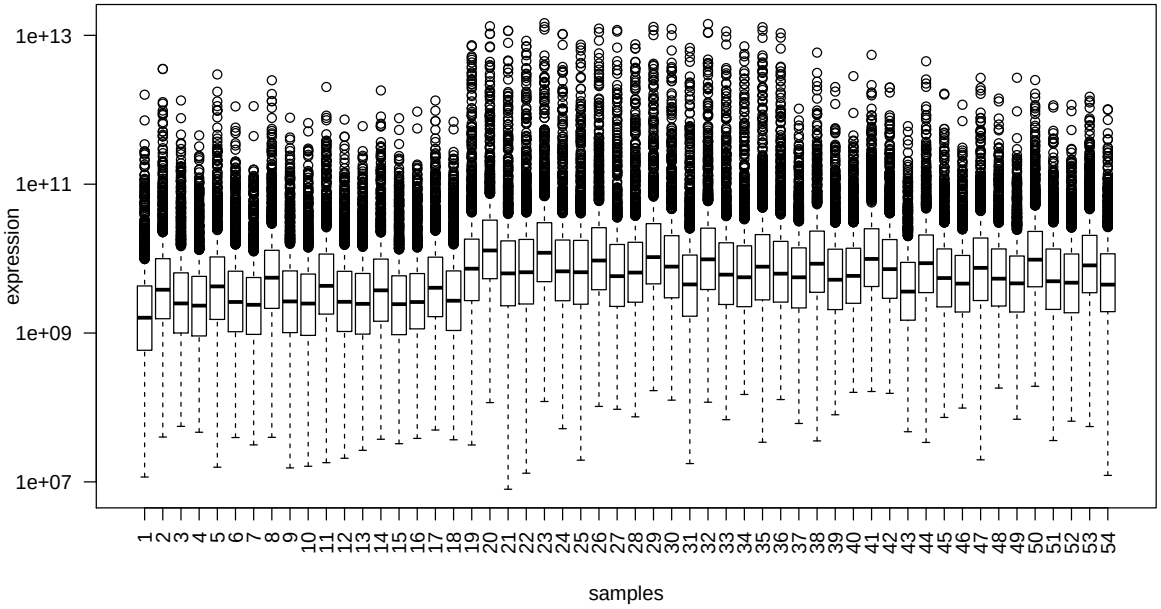


Figure 7: Boxplot of all peptide abundances.