# Triple TAILS Report
example

This report is based on 3,556 quantified peptide features provided in the `mzTab` input file. Some peptide sequences have been quantified multiple times (multiple charge states, different fractions). In the following analysis, we will choose the most intense peptide quantifications and focus on the subset of 1,845 (51.88%) unique peptide sequences. 351 of those peptides are mapped very close to N- or C-terminus (less than 6 amino acid positions) which leaves us with 1,494 quantified peptides.

|	number of peptides with $fc \to -\infty$	number of peptides with fc unchanged	number of peptides with $fc \to +\infty$	total number of peptides
H:L	341	1,032	121	1,494
H:M	125	1,247	122	1,494
M:L	311	1,089	94	1,494

Table 1: Number of peptides for which both or none of the two labelled forms were detected (fc unchanged), or only one of them ($fc \to \pm\infty$).
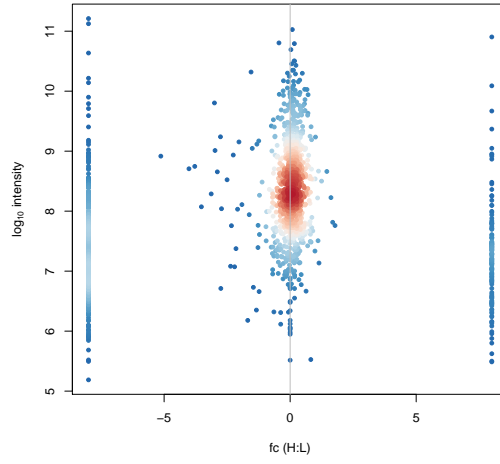
(a) H:L (341 peptides no Heavy, 1,032 peptides Light and Heavy, 121 peptides no Light)
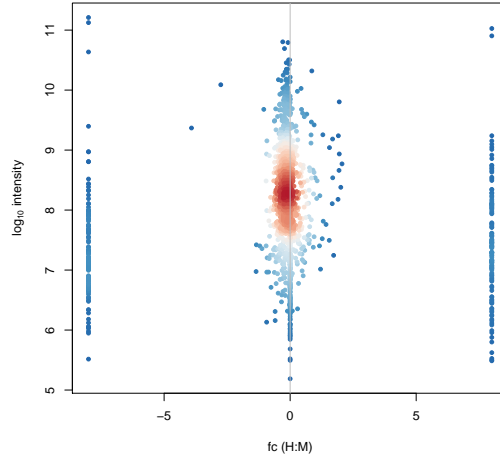
(b) H:M (125 peptides no Heavy, 1,247 peptides Medium and Heavy, 122 peptides no Medium)
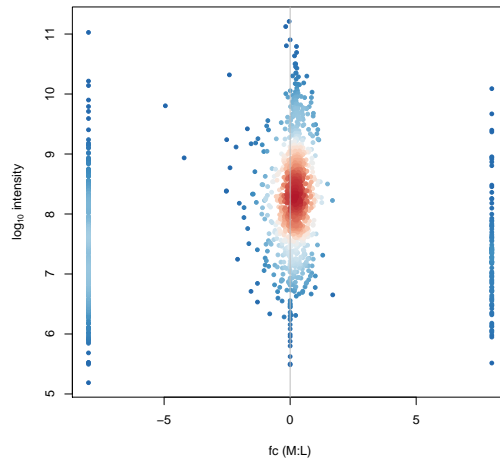
(c) M:L (311 peptides no Medium, 1,089 peptides Light and Medium, 94 peptides no Light)

Figure 1: Fold change vs log intensity for the set of 1,494 unique peptides. Infinite fold changes (fc $\rightarrow \pm\infty$) are mapped to fc $= \pm 10$. The colour gradient reflects the density of the scatter plot.
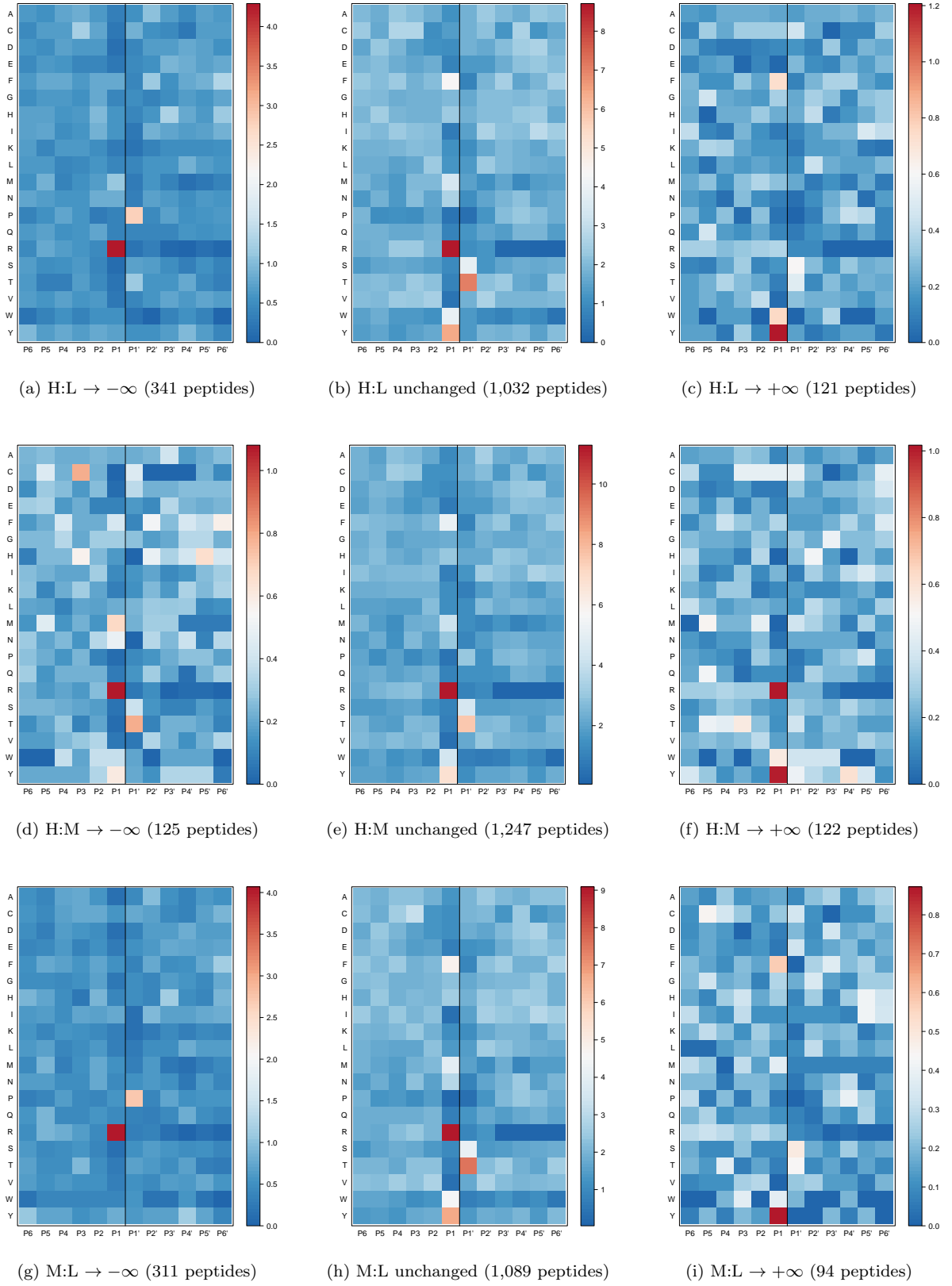
Figure 2: Amino acid frequencies fingerprints for the nine subsets listed in Table 1. For example, figure (g) depicts the fingerprint of peptides detected in light (L) but absent in medium (M).