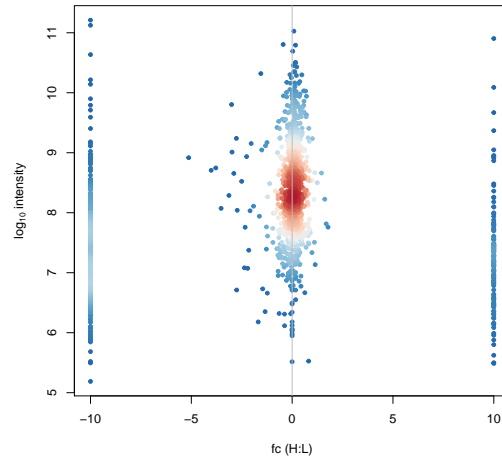


Triple TAILS Report

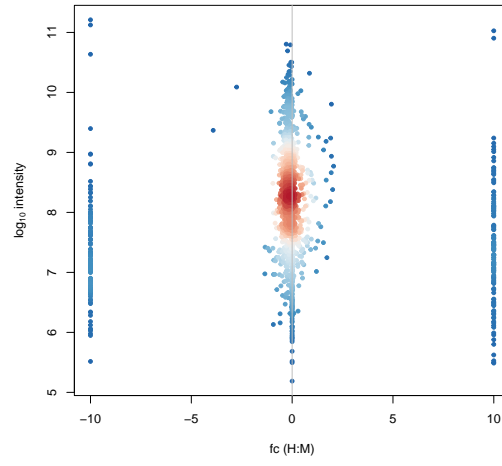
This report is based on 3,558 quantified peptide features provided in the **mzTab** input file. Some peptide sequences have been quantified multiple times (multiple charge states, different fractions). In the following analysis, we will choose the most intense peptide quantifications and focus on the subset of 1,847 (51.91%) unique peptide sequences.

	number of peptides with $fc \rightarrow -\infty$	number of peptides with fc unchanged	number of peptides with $fc \rightarrow +\infty$	total number of peptides
H:L	341	1,032	121	1,847
H:M	125	1,247	122	1,847
M:L	311	1,089	94	1,847

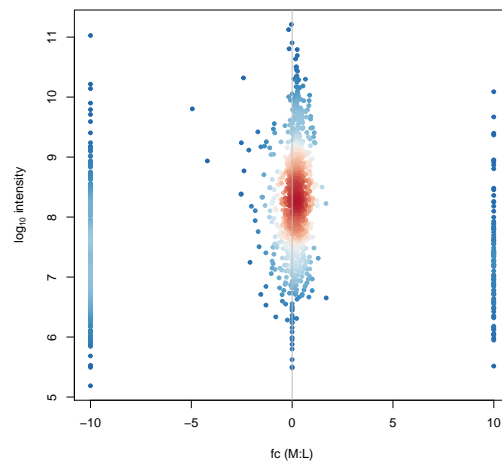
Table 1: Number of peptides for which both or none of the two labelled forms were detected (fc unchanged), or only one of them ($fc \rightarrow \pm\infty$).



(a) H:L 341

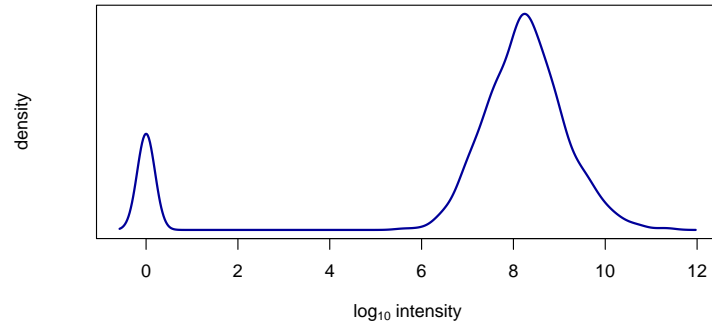


(b) H:M

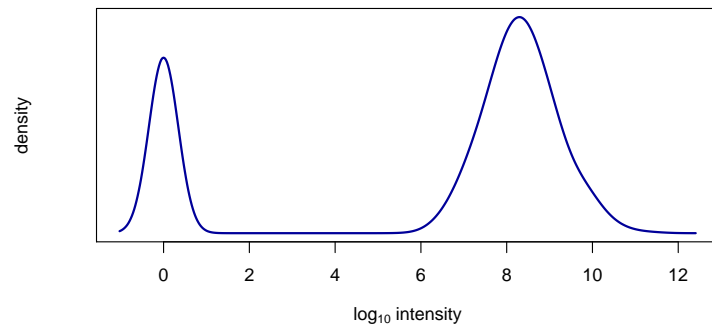


(c) M:L

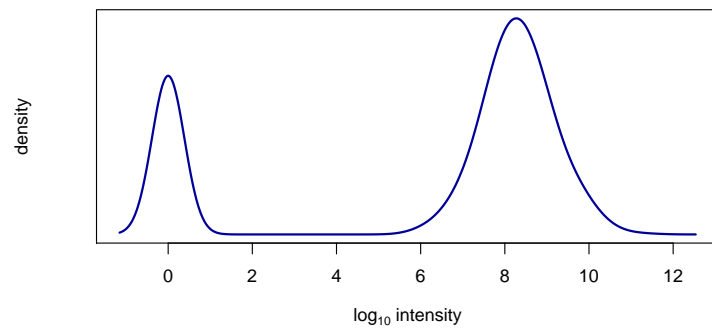
Figure 1: Fold change vs log intensity for the set of 1,847 unique peptides. Infinite fold changes ($fc \rightarrow \pm\infty$) are mapped to $fc = \pm 10$. The colour gradient reflects the density of the scatter plot.



(a) Plot of density intensities for `peptide_abundance_study_variable[1]`



(b) Plot of density intensities for `peptide_abundance_study_variable[2]`



(c) Plot of density intensity for `peptide_abundance_study_variable[3]`

Figure 2: Plots of peptide densities with different intensities

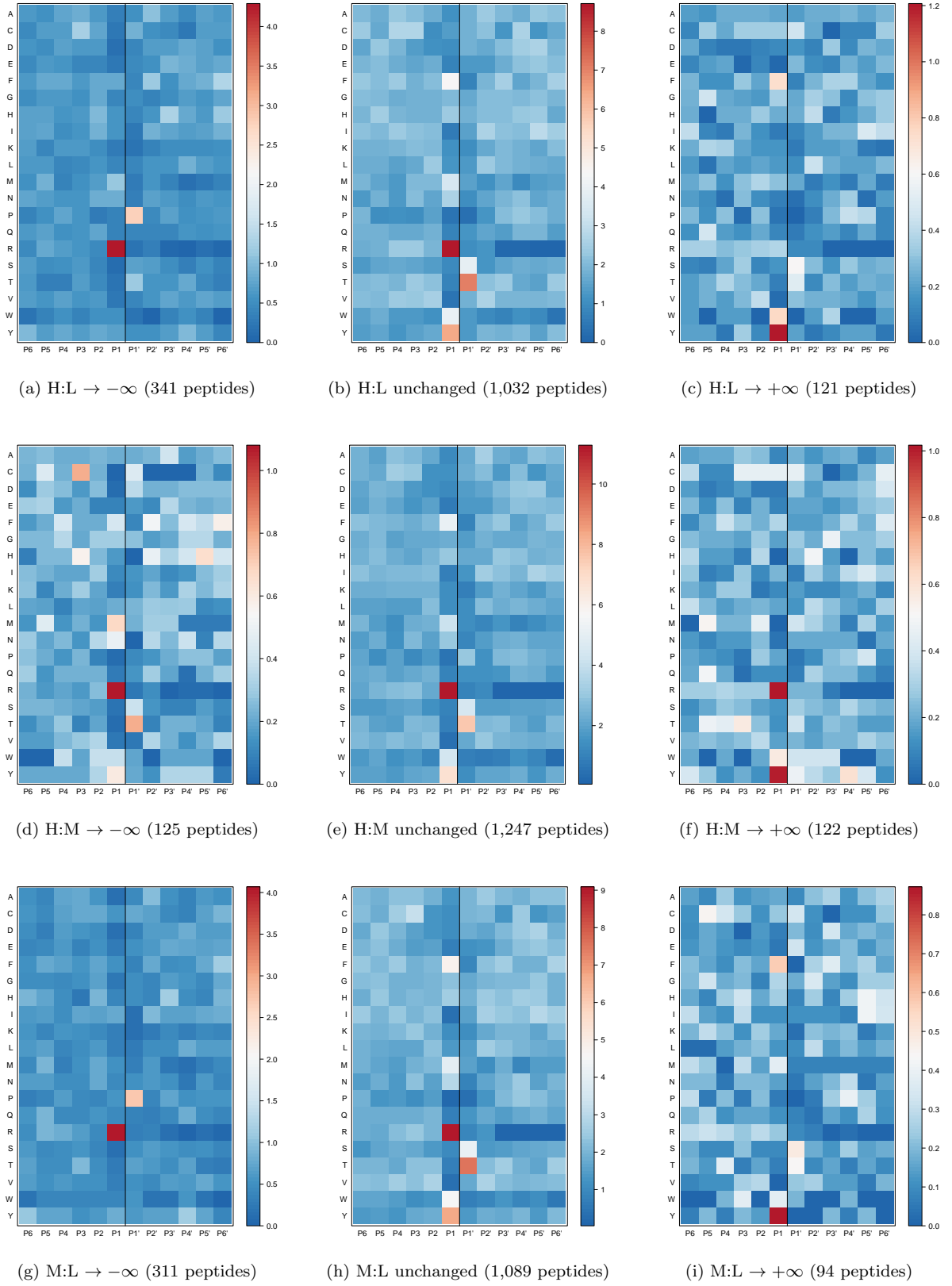


Figure 3: Amino acid frequencies fingerprints for the nine subsets listed in Table 1. For example, figure (g) depicts the fingerprint of peptides detected in light (L) but absent in medium (M).