

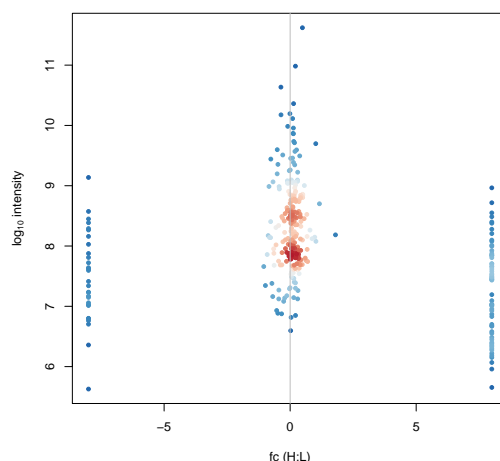
Double TAILS Report

example

This report is based on 850 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 598 (70.35%) unique peptide sequences. 286 of those peptides are mapped very close to N- or C-terminus (less than 6 amino acid positions) which leaves us with 312 quantified peptides.

	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	29	222	61	312

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 (29 peptides no Heavy, 222 peptides Light and Heavy, 61 peptides no Light)

Figure 1: Fold change vs log intensity for the set of 312 unique peptides. Infinite fold changes ($fc \rightarrow \pm\infty$) are mapped to $fc = \pm 8$. The colour gradient reflects the density of the scatter plot.

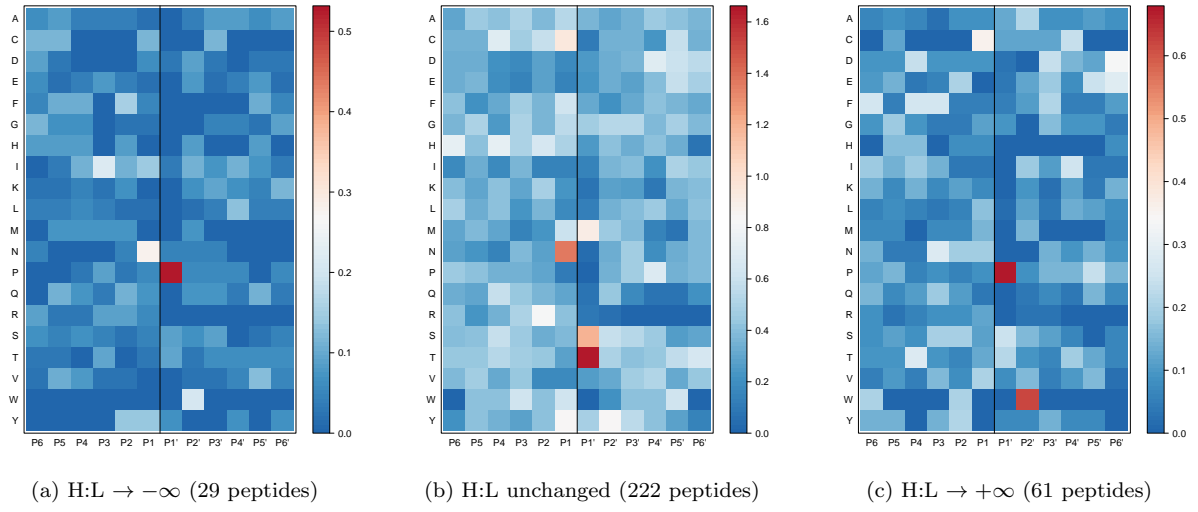


Figure 2: Amino acid frequencies fingerprints for the nine subsets listed in Table 1. For example, figure (g) depicts the fingerprint of peptides detected in light (L) but absent in medium (M).