Report for single duplex experiment

The analysis identified 9,910 peptide pairs with the following fold changes (fc = $\log_2$ H: L) and normalised intensities (H + median(H:L) * L).

$$
\begin{aligned}
\text{peptide pairs} &= 9,910 \\
\text{median(fc)} &= -1.8904 \\
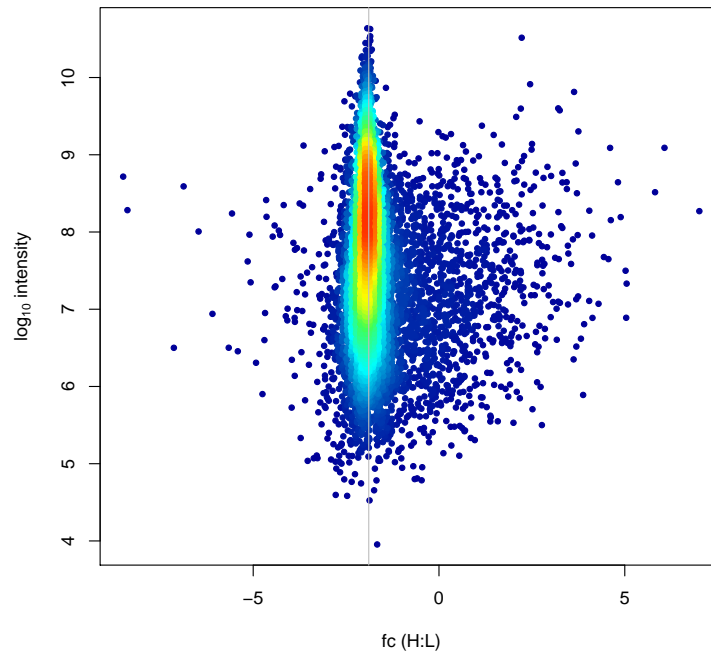\text{sd(fc)} &= 0.9416
\end{aligned}
$$

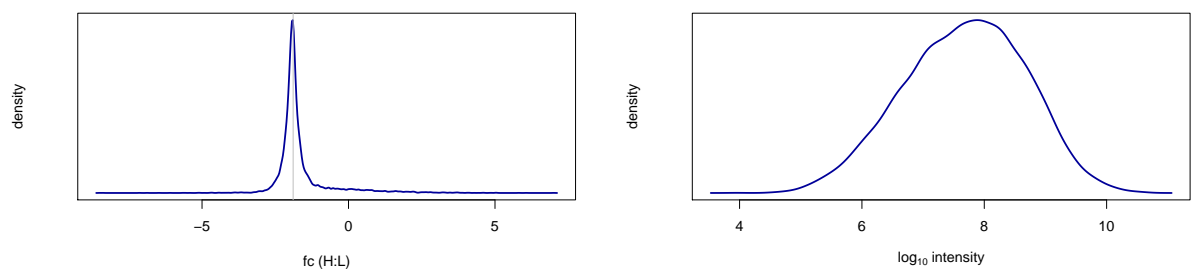Figure 1: Heavy-to-light fold change vs normalised intensity

Figure 2: densities of heavy-to-light fold changes and normalised intensities