

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 ($H + \text{median}(H:L) * L$).

peptide pairs	=	9,910
median(fc)	=	-1.8904
sd(fc)	=	0.9416

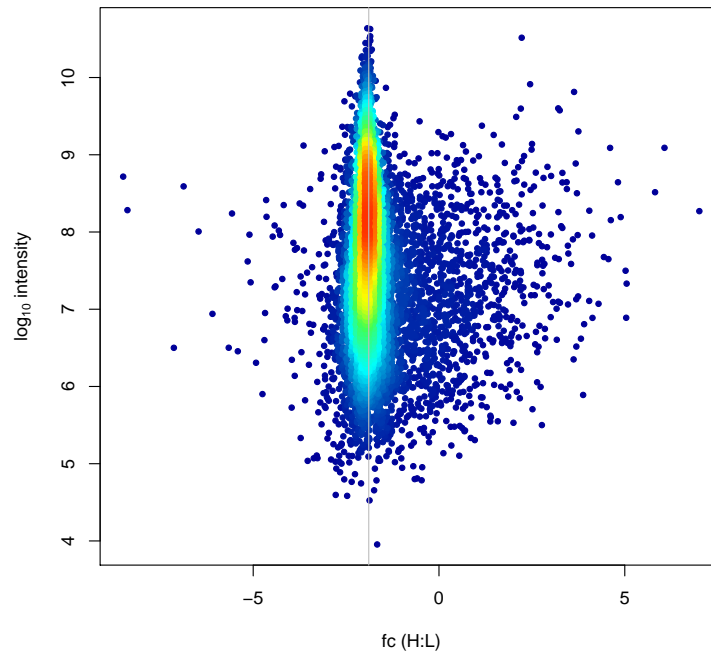


Figure 1: Heavy-to-light fold change vs normalised intensity

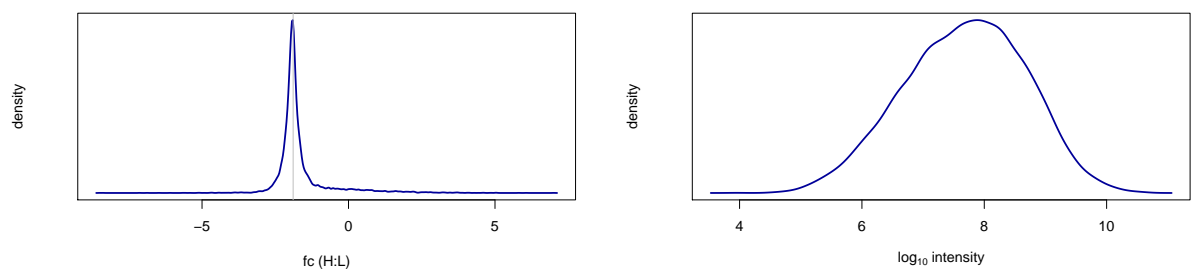


Figure 2: densities of heavy-to-light fold changes and normalised intensities