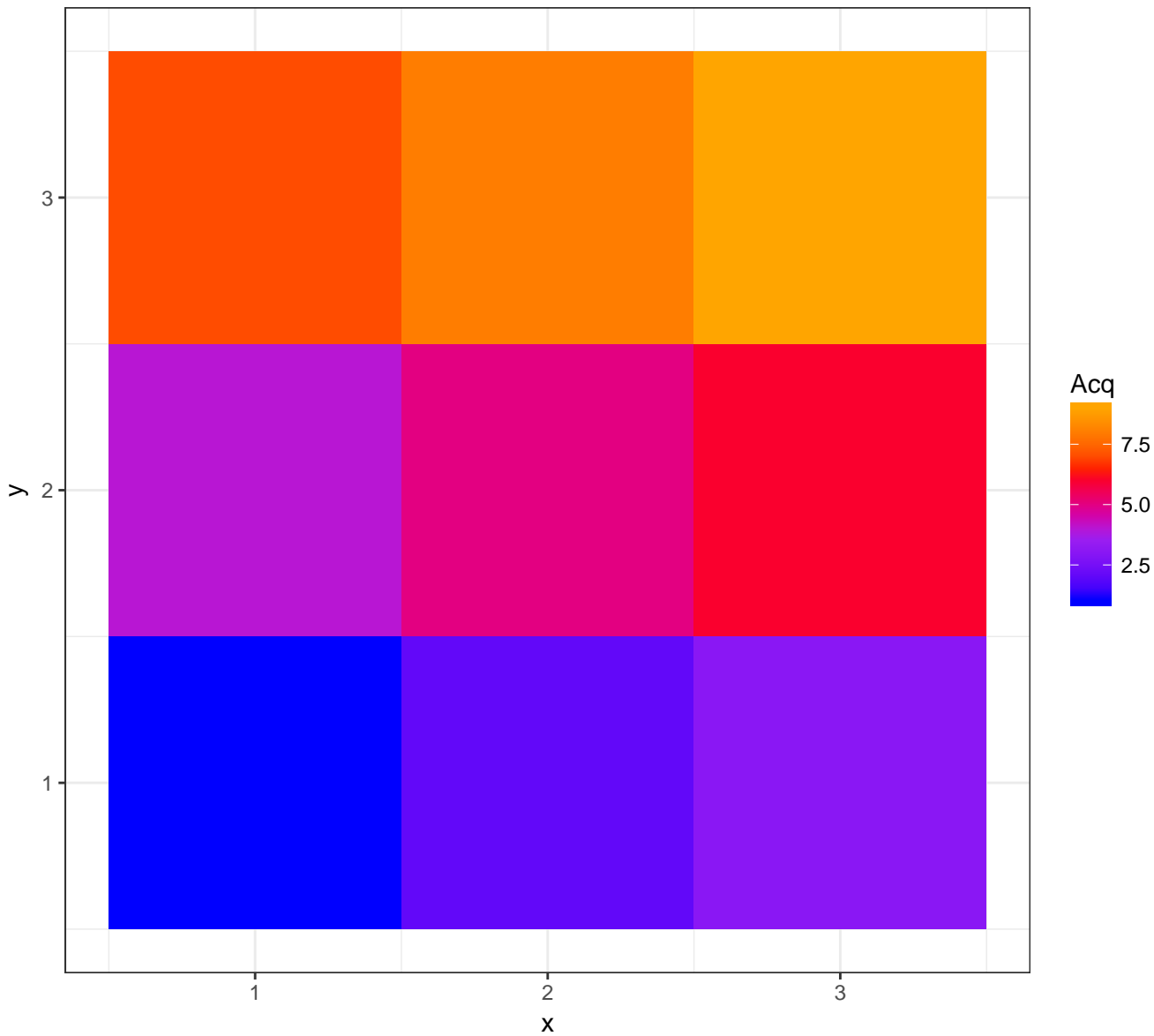


# Quality control of MSI data

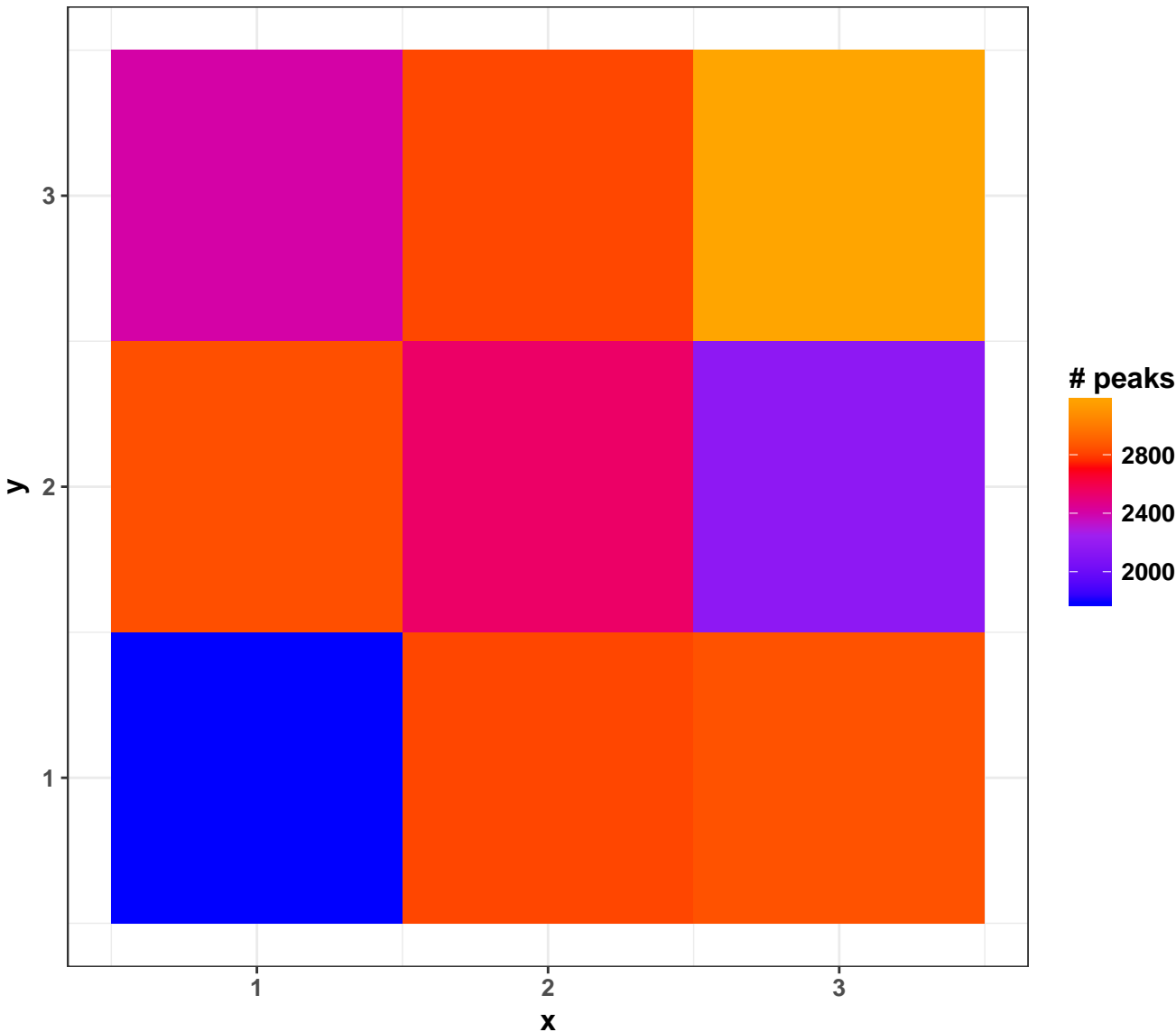
Filename: Testfile\_rdata

properties	values
Number of mz features	8399
Range of mz values [Da]	100.08 – 799.92
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	0 – 318.82
Median of intensities	0
Intensities > 0	30.92 %
Number of zero TICs	0
Preprocessing	
Normalization	tic
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
# peptides in None	0 / 0
# calibrants in None	0 / 0

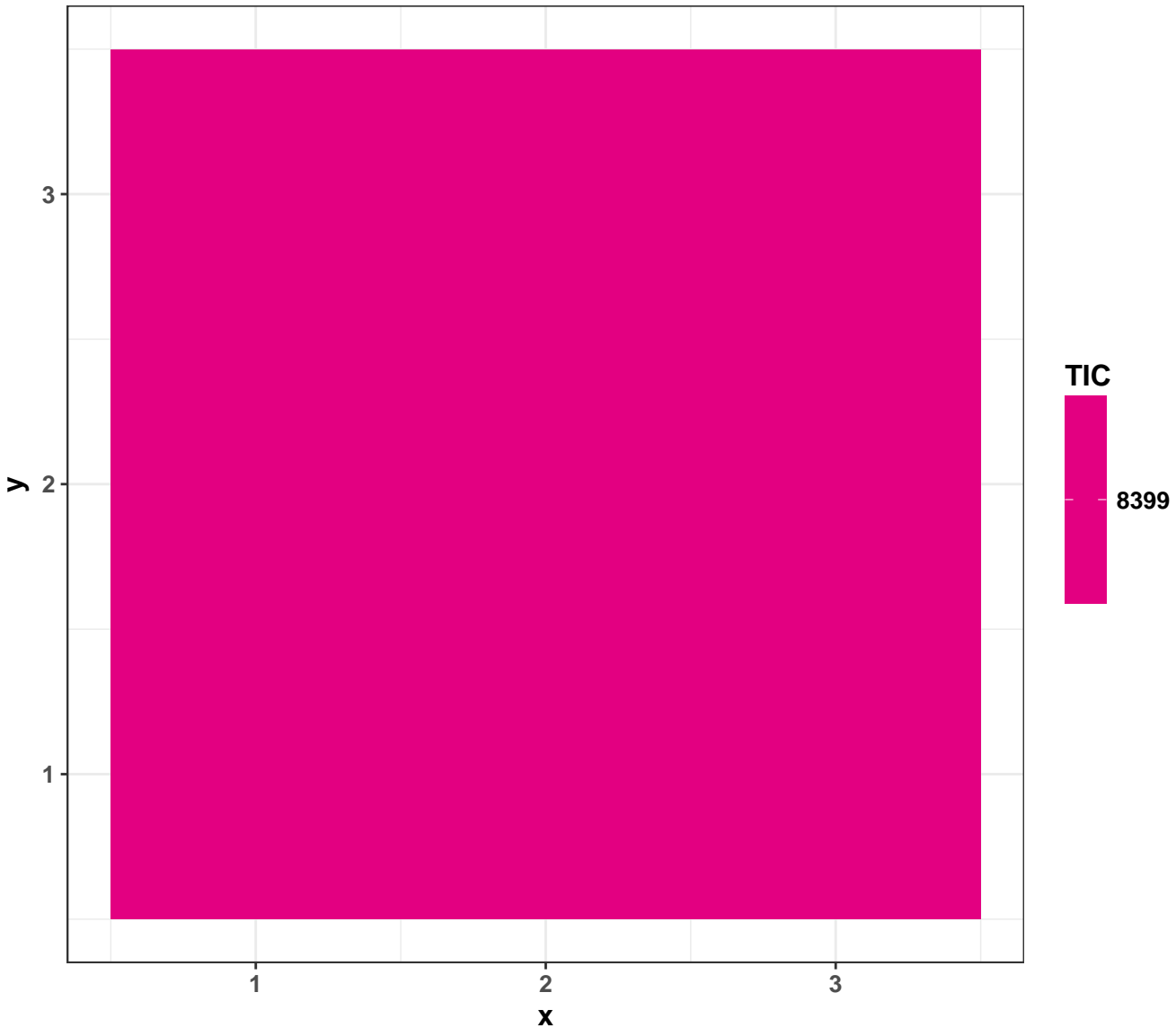
# Order of Acquisition



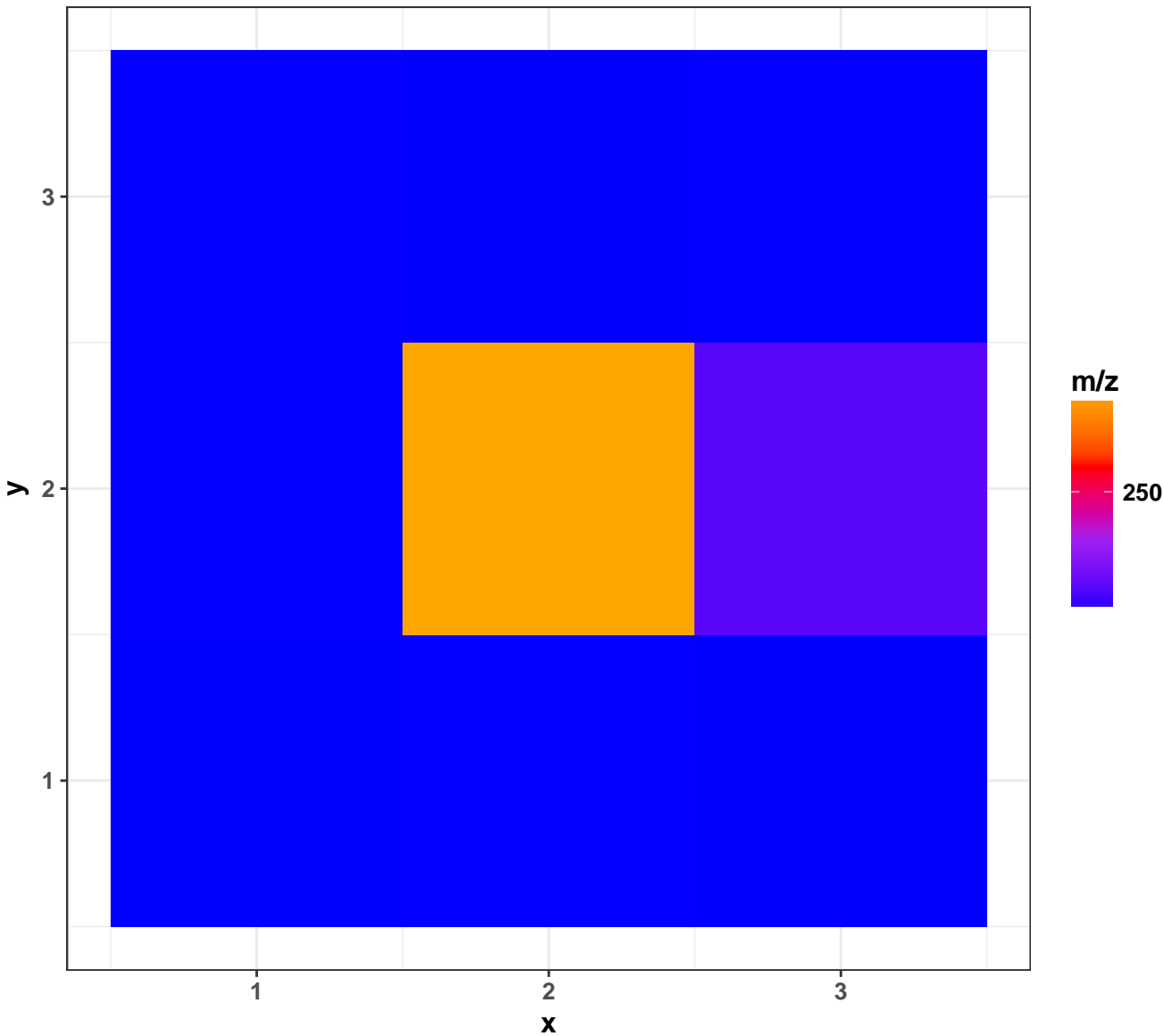
# Number of peaks per pixel



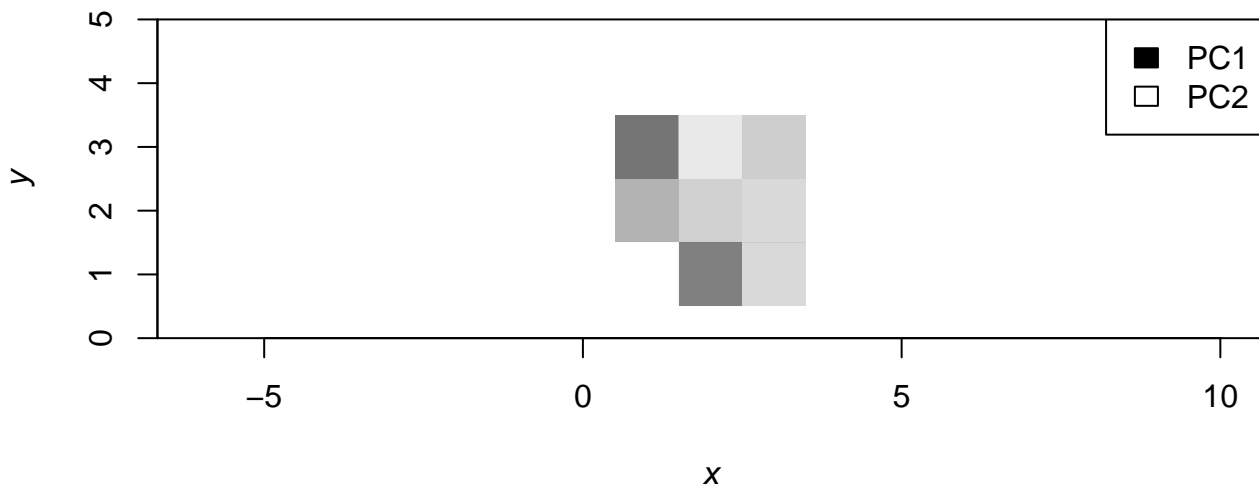
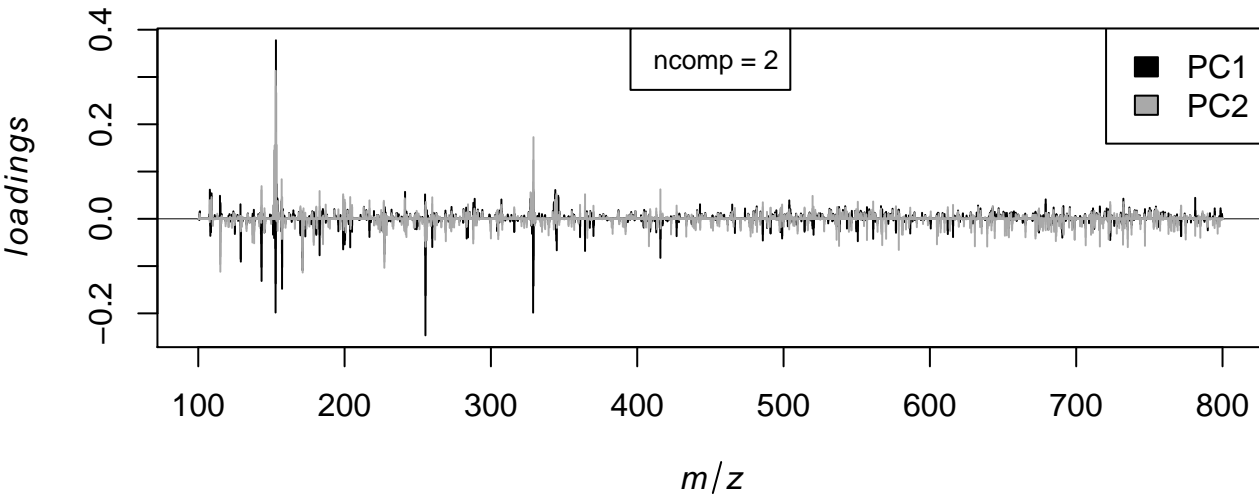
# Total Ion Chromatogram



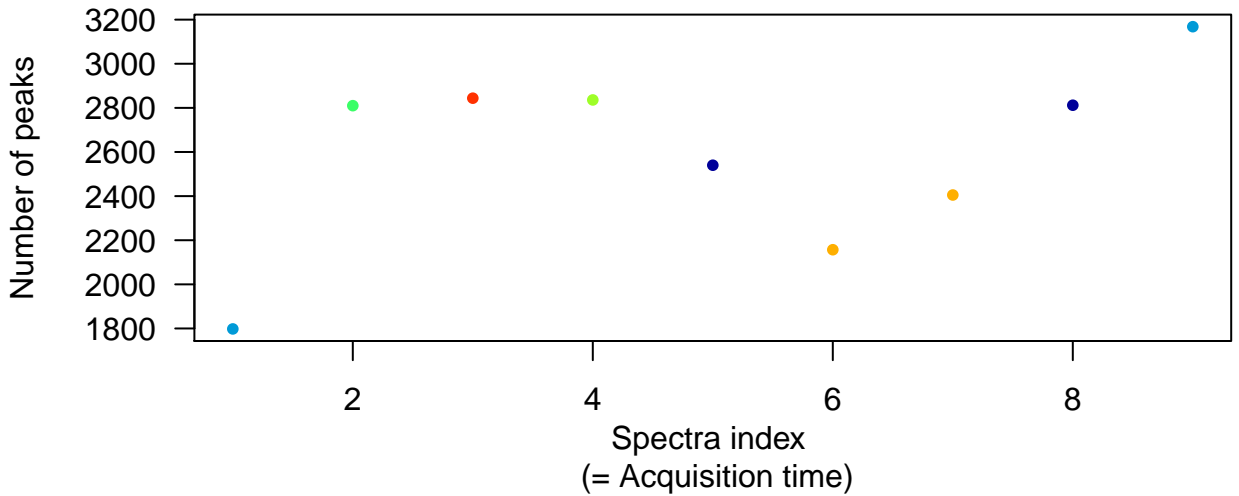
# Most abundant m/z in each pixel



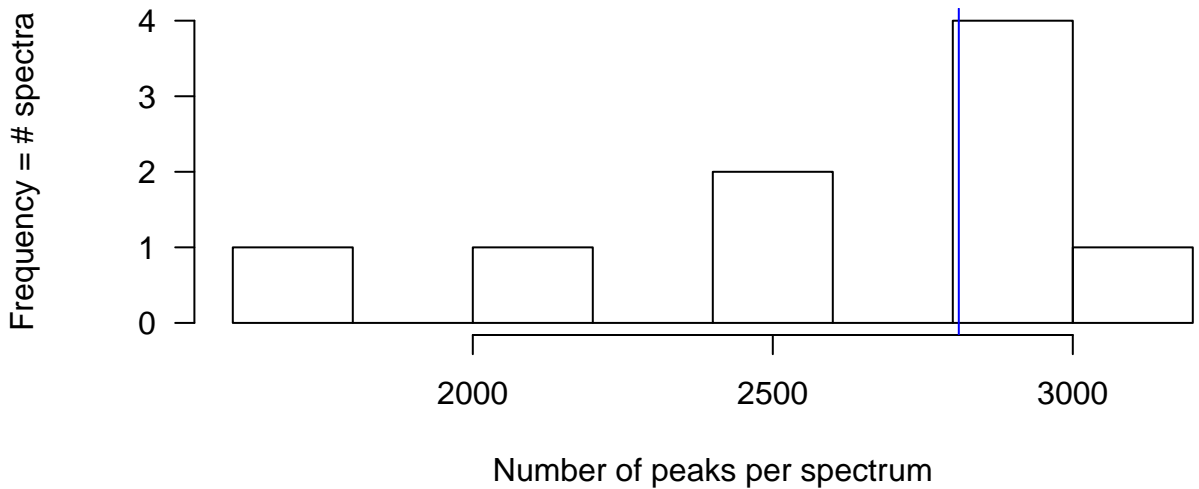
# PCA for two components



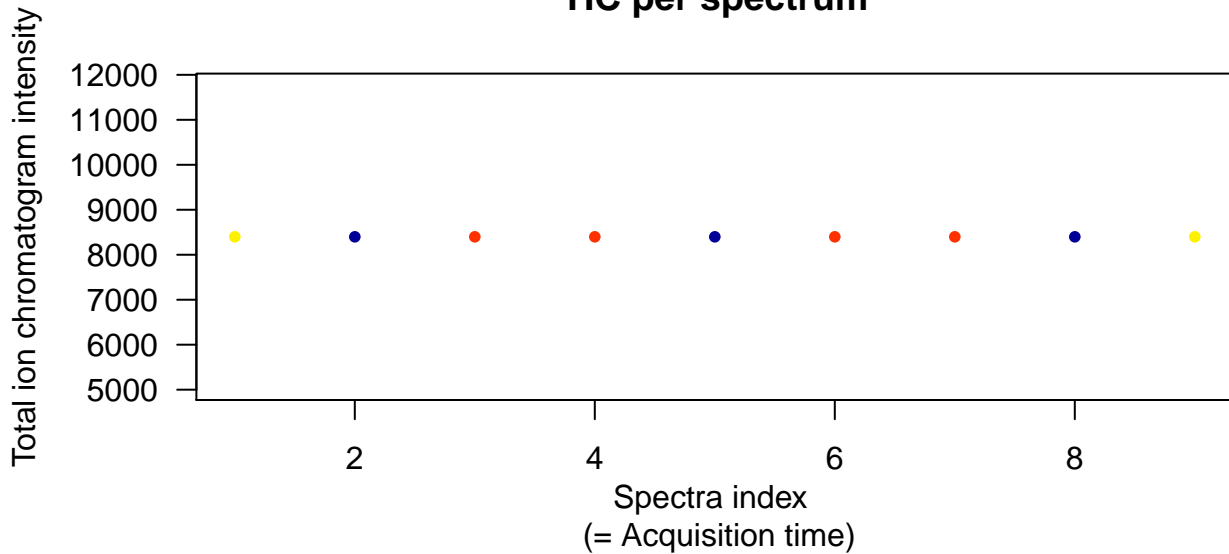
## Number of peaks per spectrum



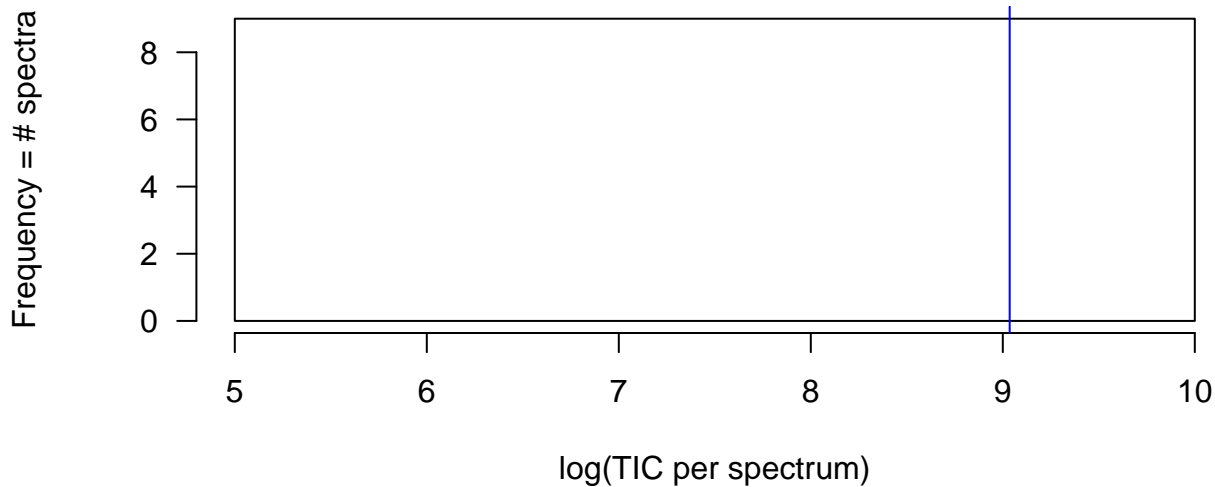
## Number of peaks per spectrum



### TIC per spectrum

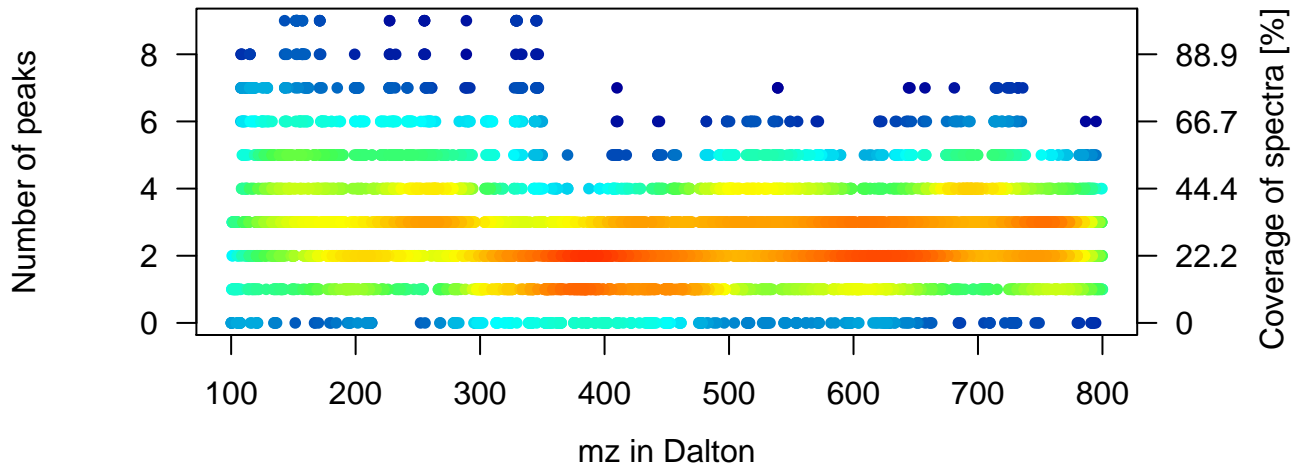


### TIC per spectrum

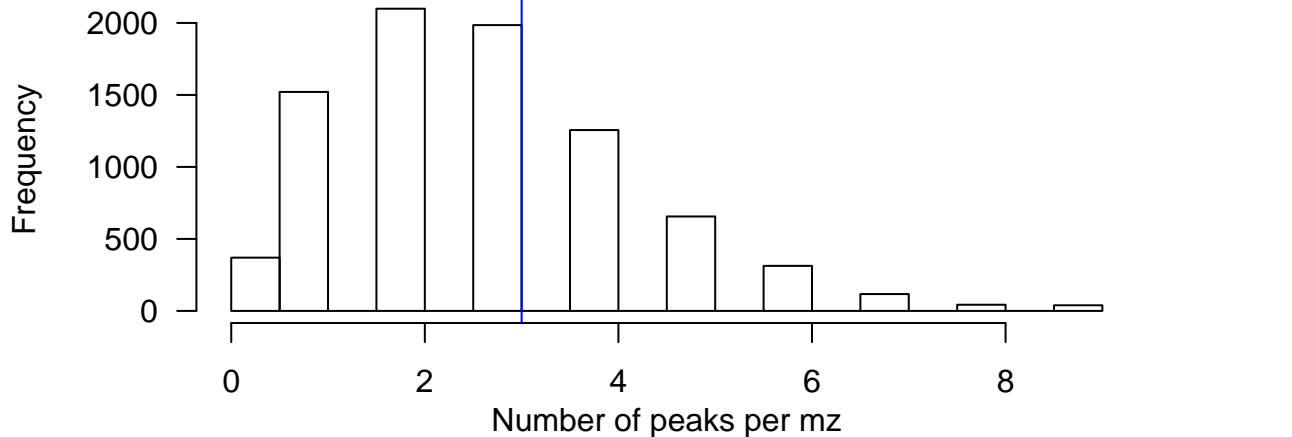




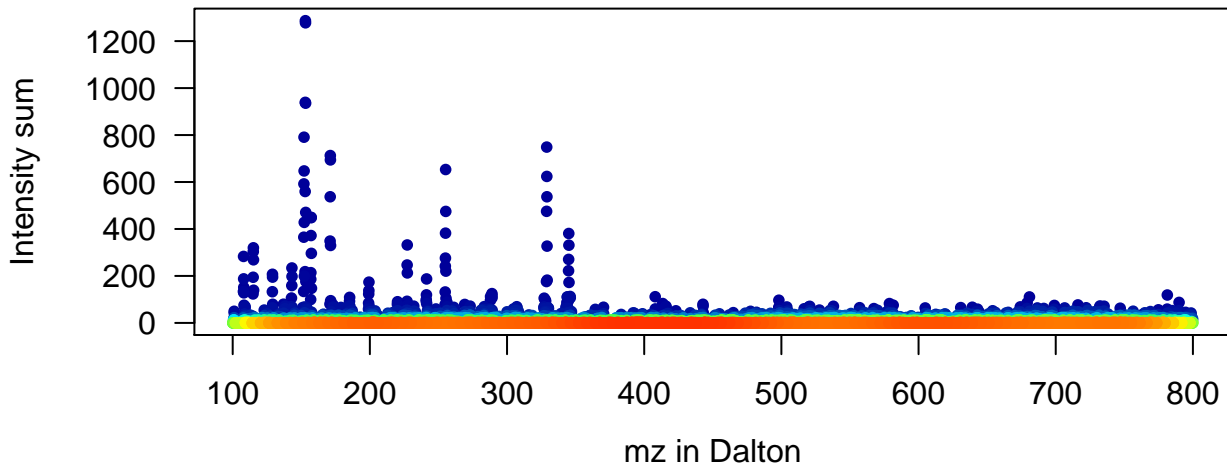
## Number of peaks per mz



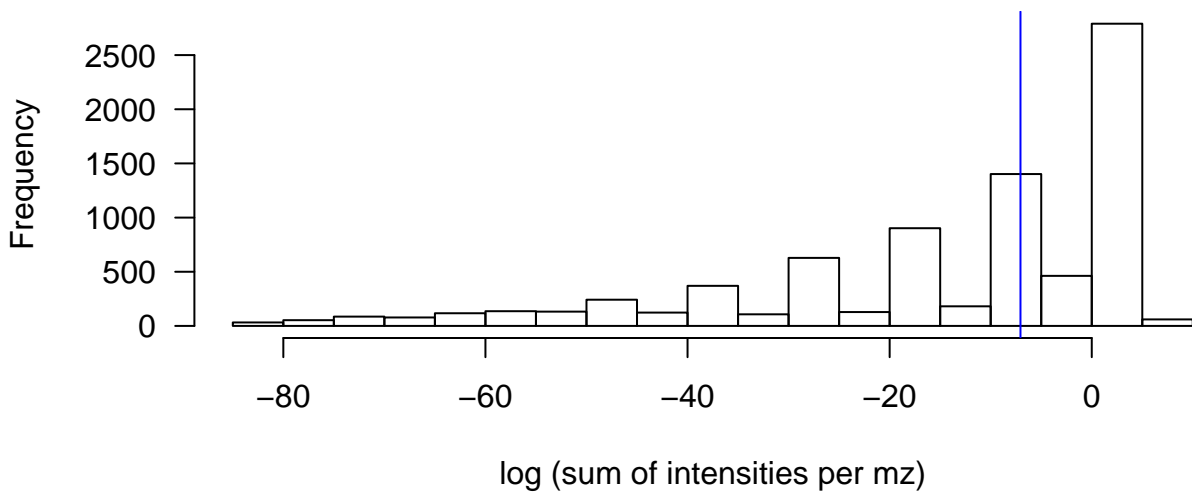
## Number of peaks per mz



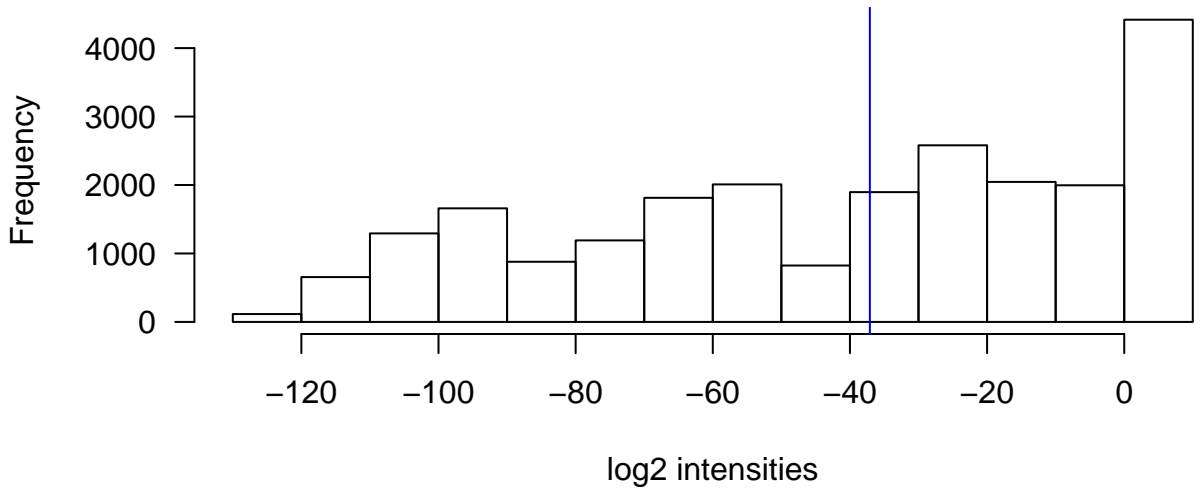
### Sum of intensities per mz



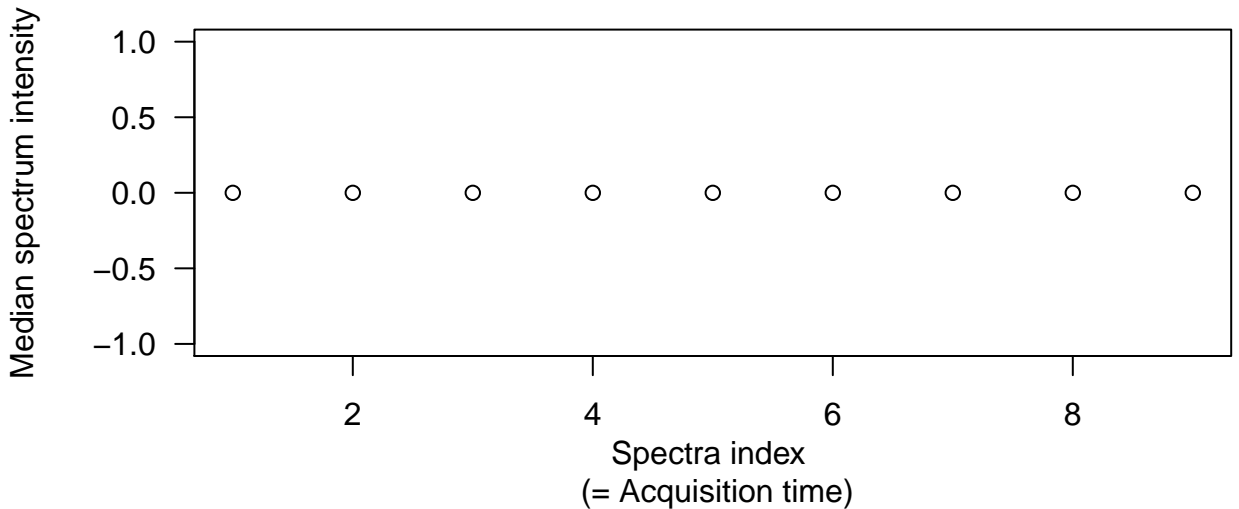
### Sum of intensities per mz



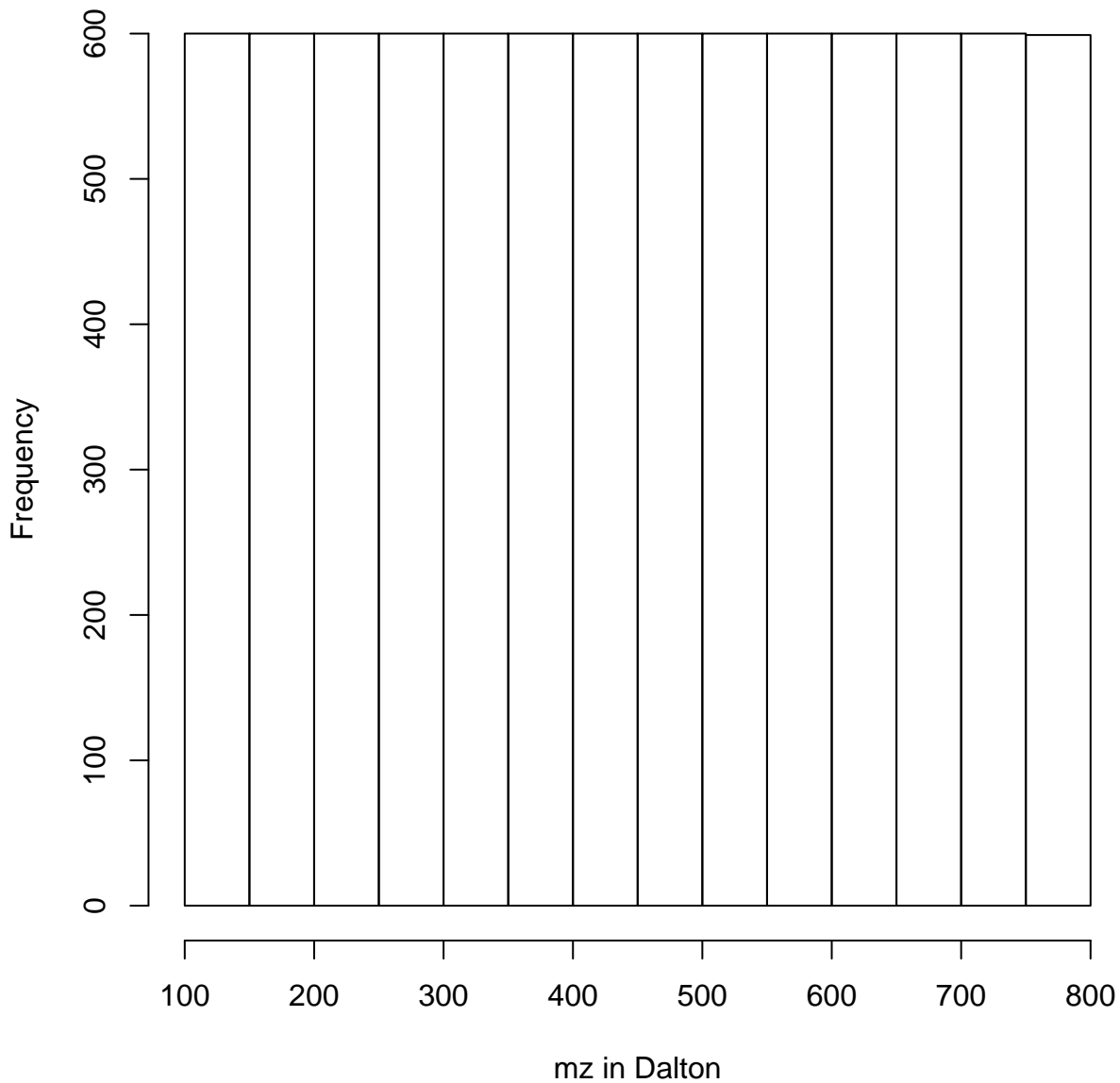
## Log2-transformed intensities



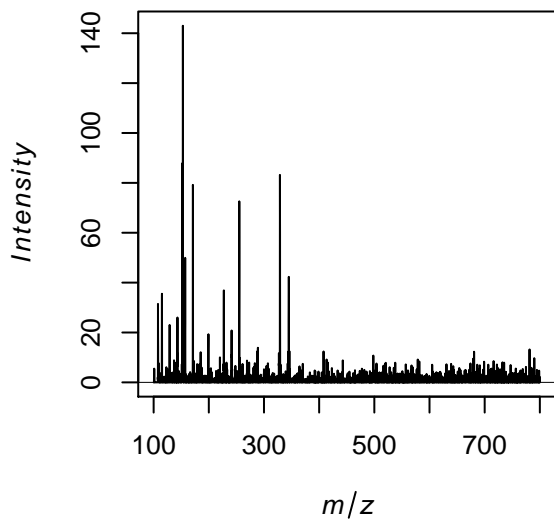
## Median intensity per spectrum



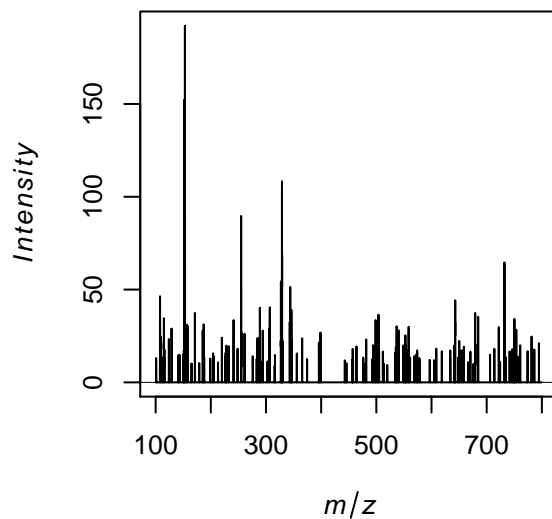
# Histogram of mz values



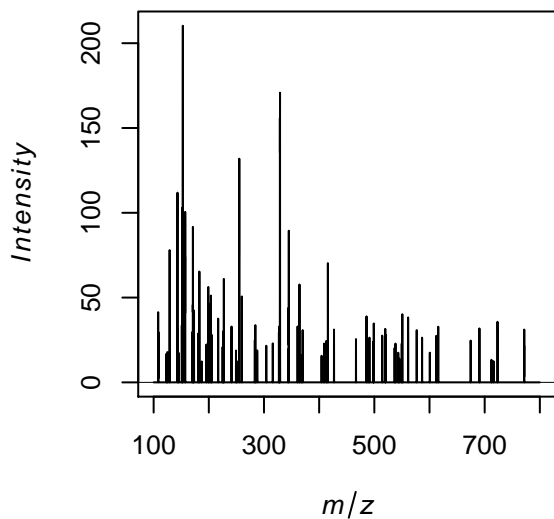
**Average spectrum**



**Spectrum in middle of acquisition**



**Spectrum at x = 1, y = 1**



**Spectrum at x = 3, y = 2**

