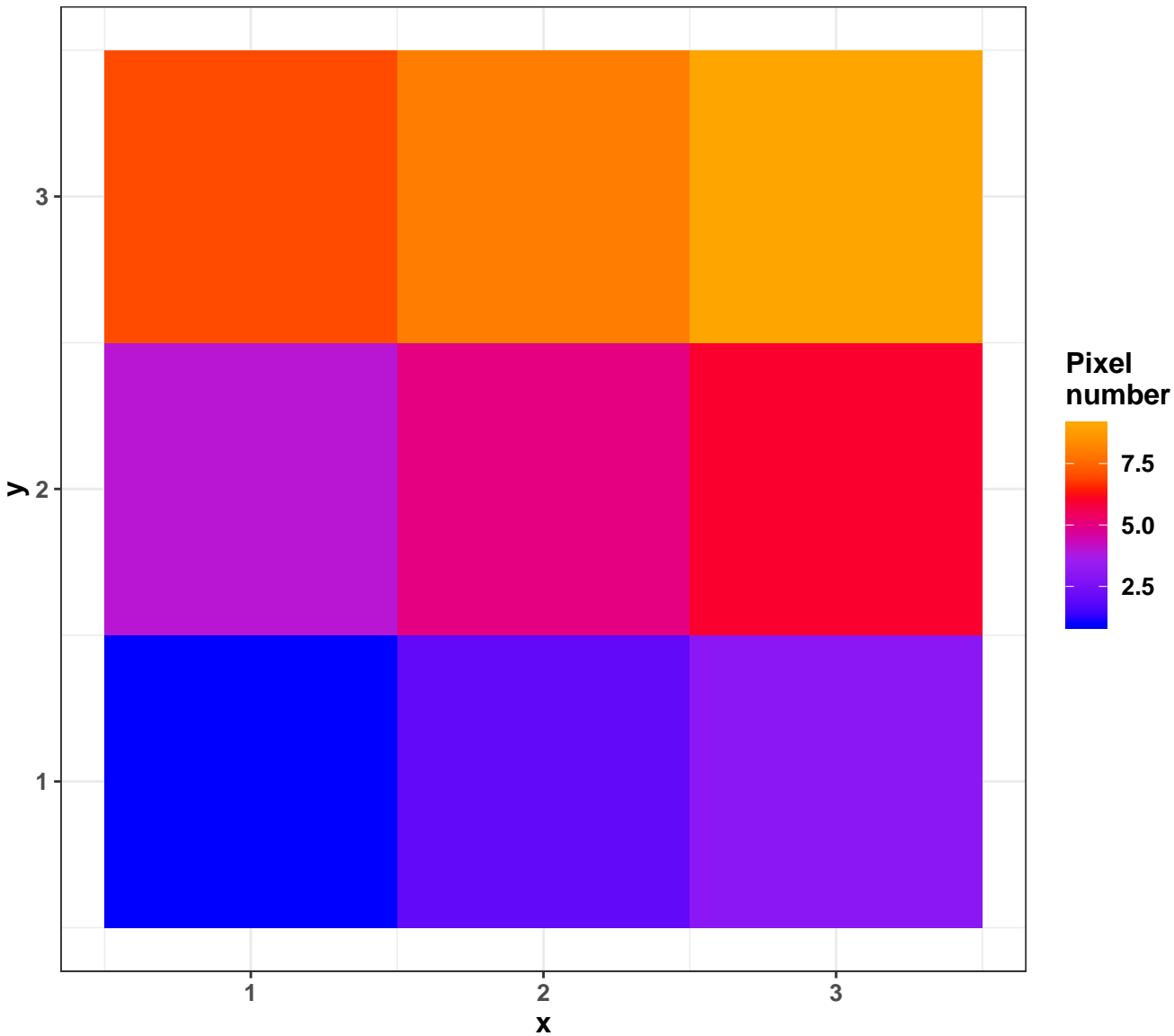


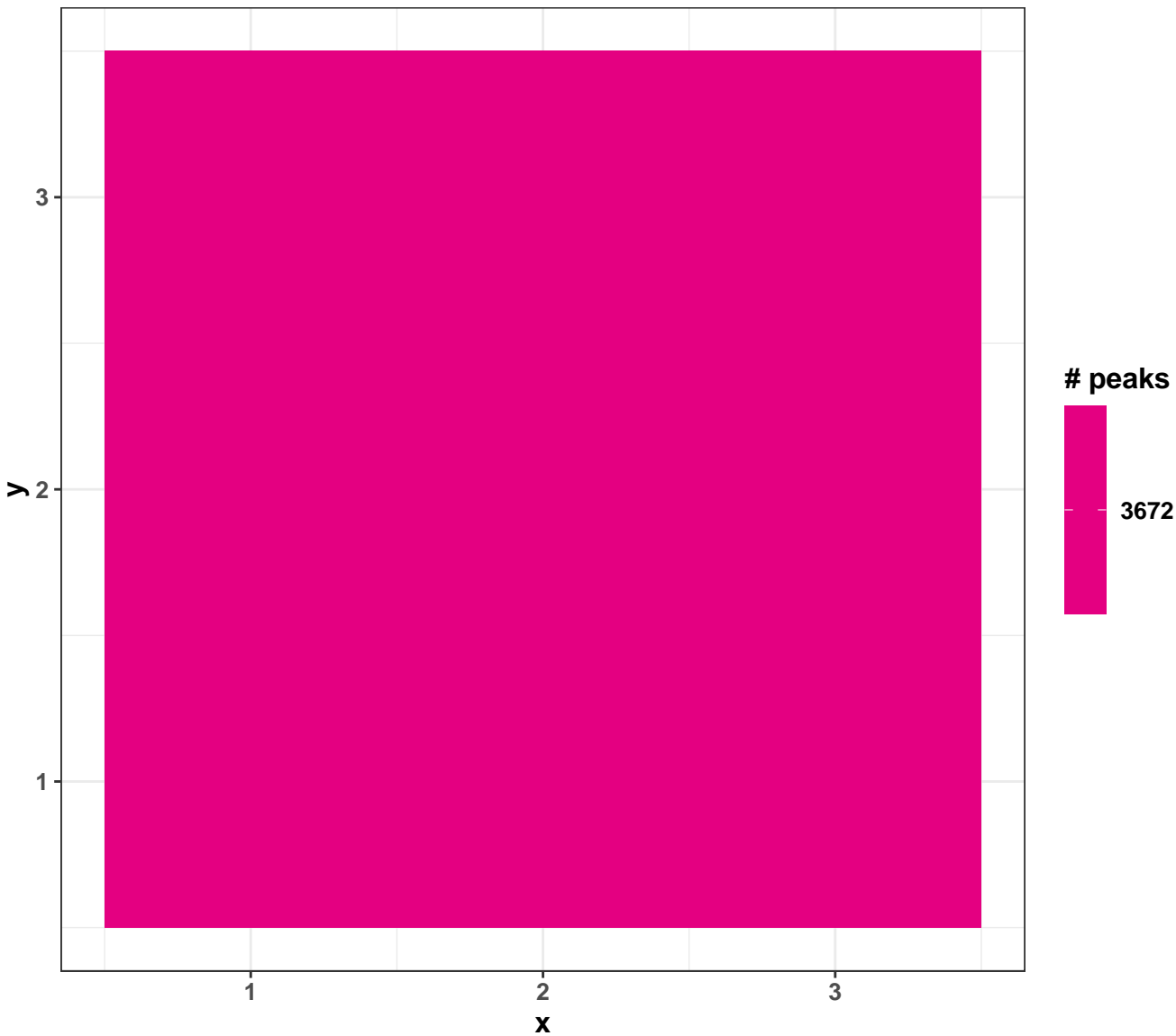
Testfile_analyze75

properties	values
Number of m/z features	3672
Range of m/z values	1199.47 – 1356.08
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	3 – 84
Number of NA intensities	0
Number of Inf intensities	0
Number of duplicated coordinates	0
Median of intensities	9
Intensities > 0	100 %
Number of empty spectra	0
Median TIC \pm sd	37005 \pm 5329
Median # peaks per spectrum \pm sd	3672 \pm 0
Centroided	FALSE
input m/z (#valid/#input) in None	0 / 0

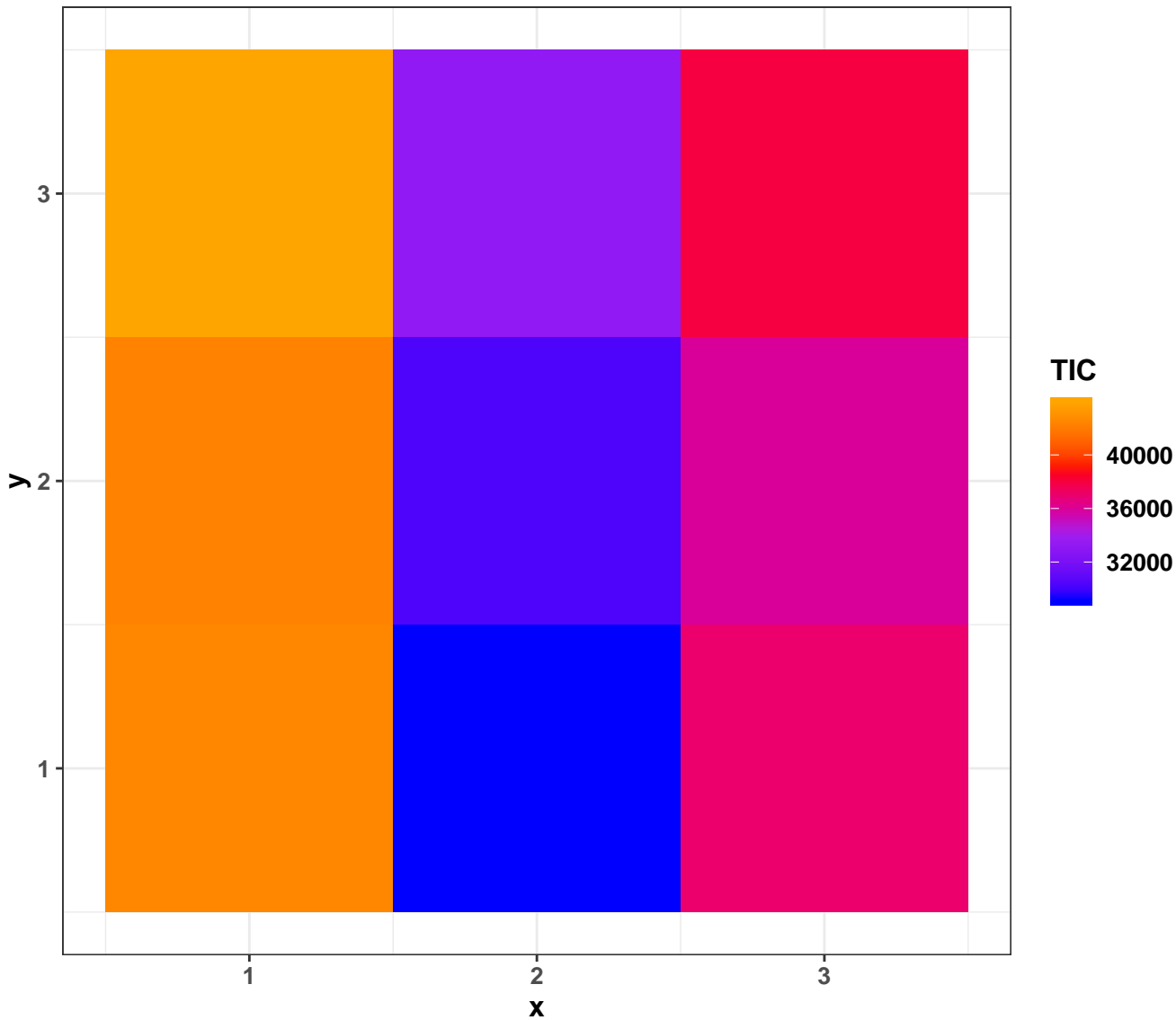
Pixel order



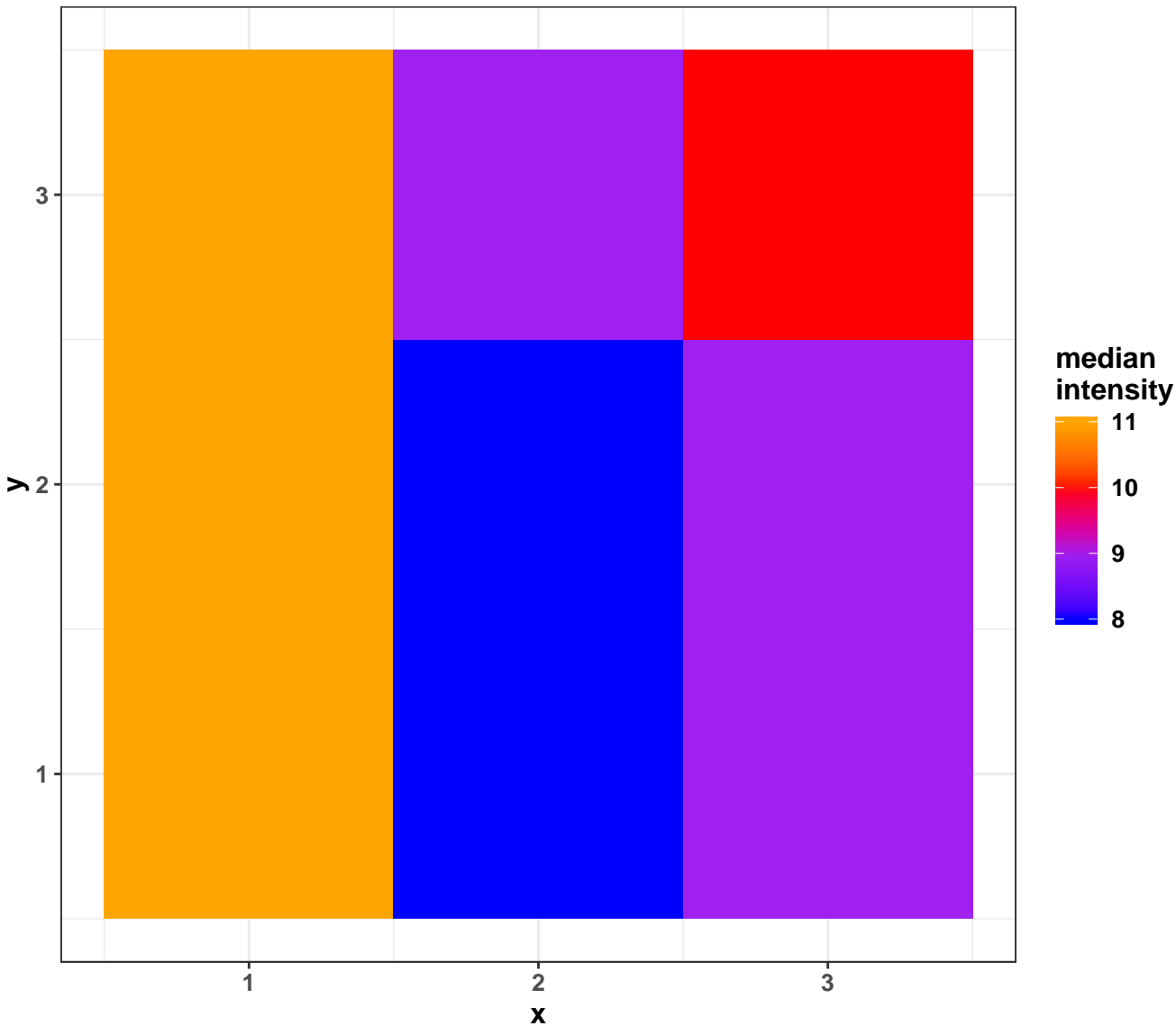
Number of peaks per spectrum



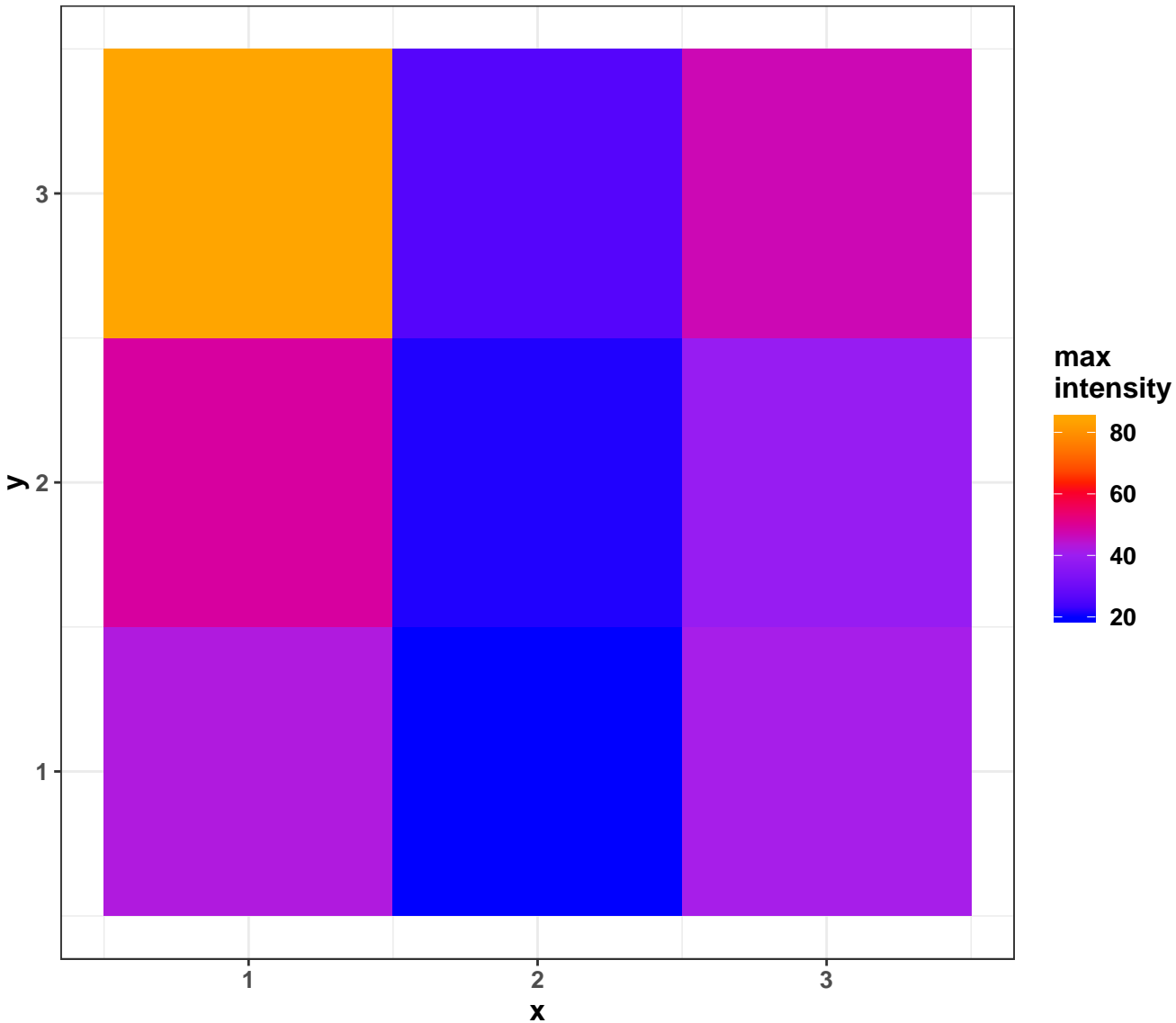
Total Ion Current



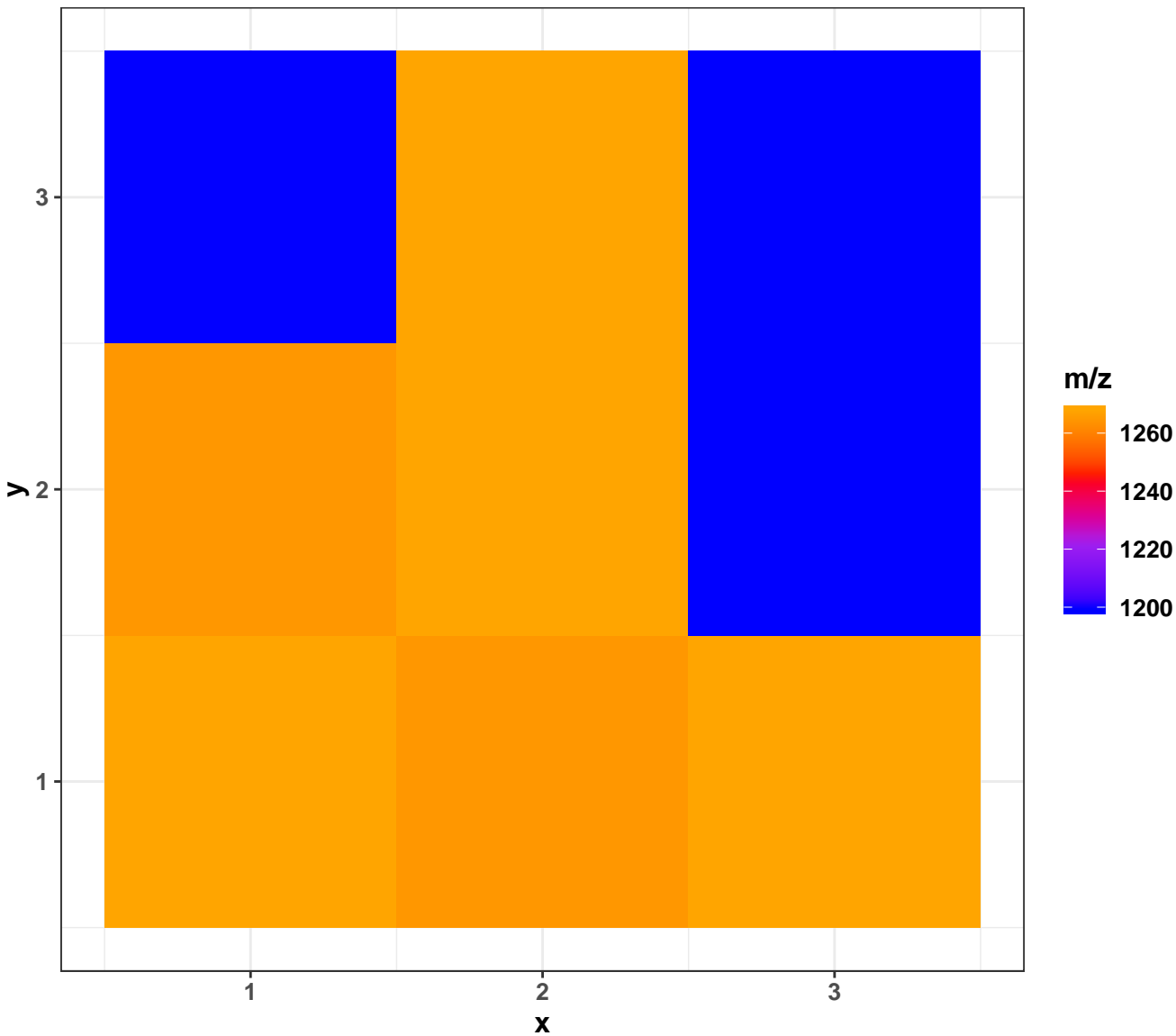
Median intensity per spectrum



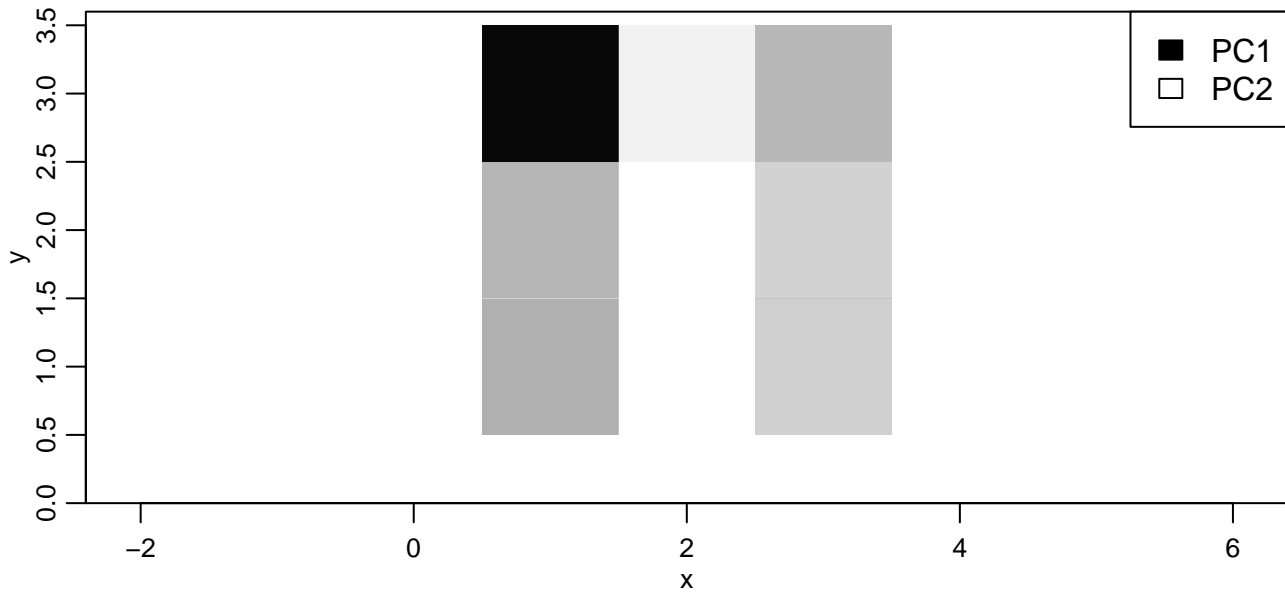
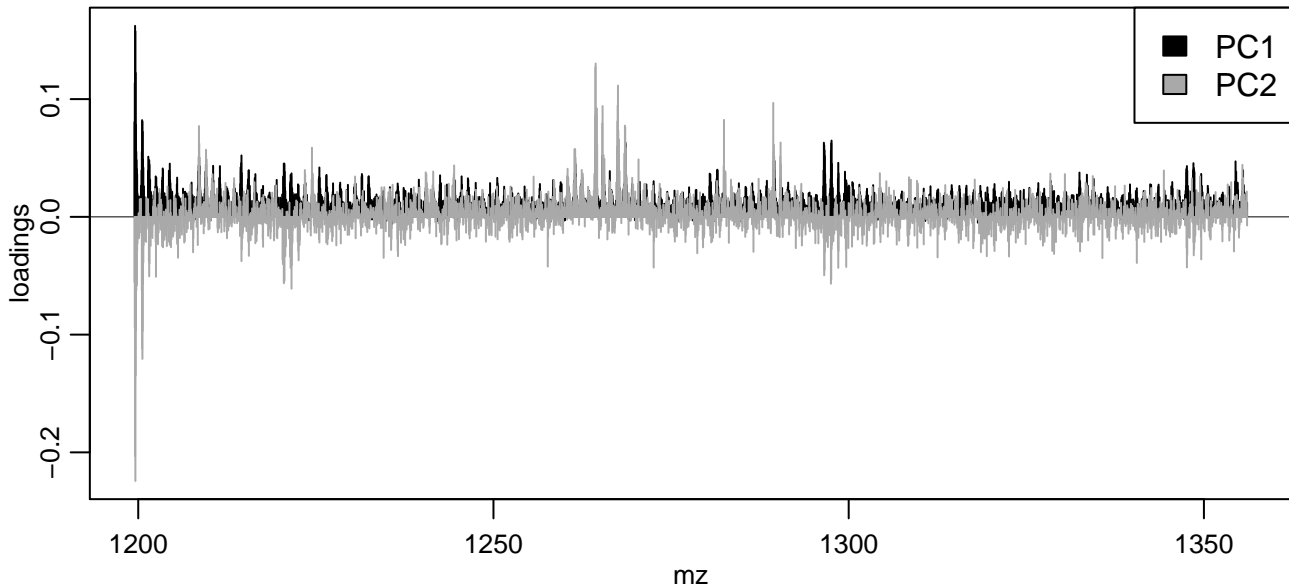
Maximum intensity per spectrum

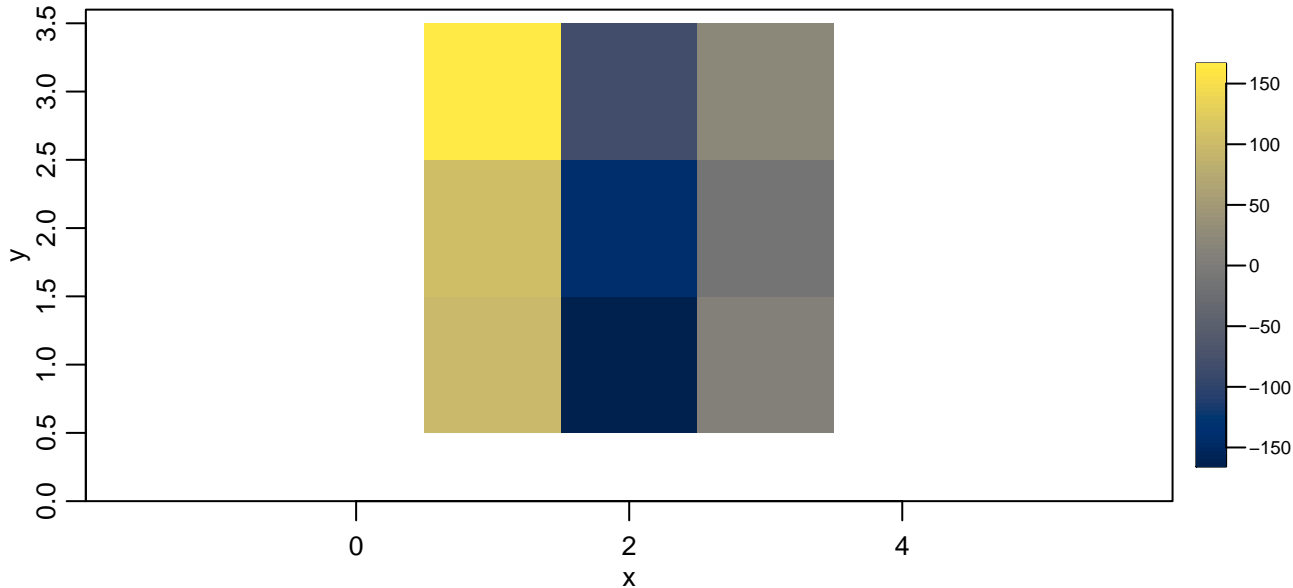
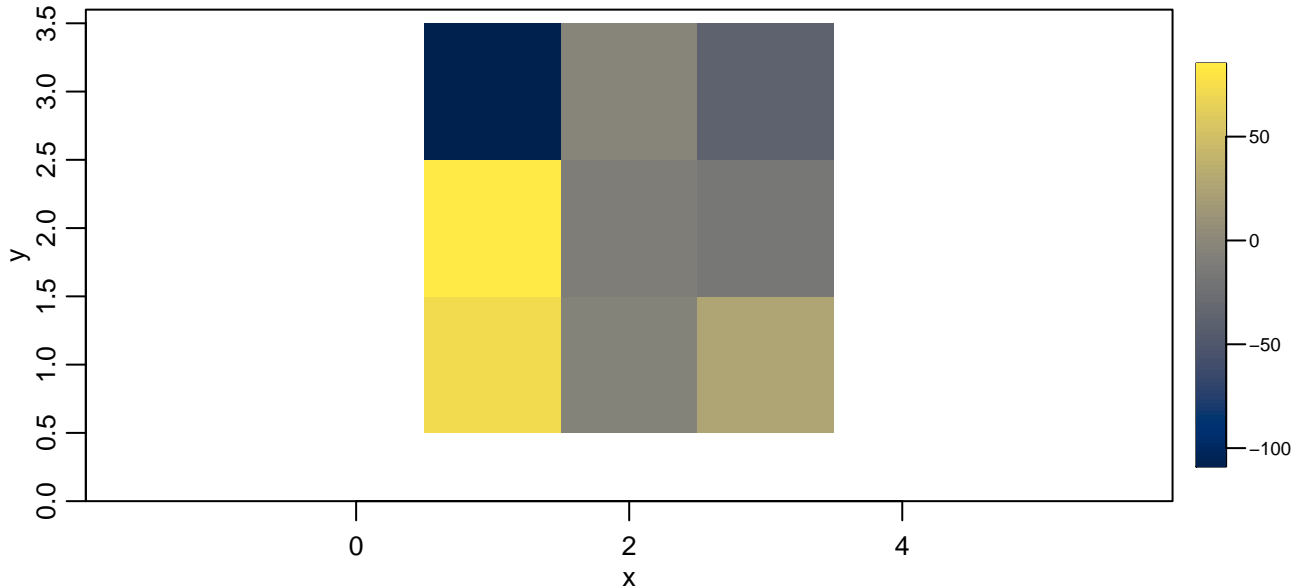


Most abundant m/z in each spectrum

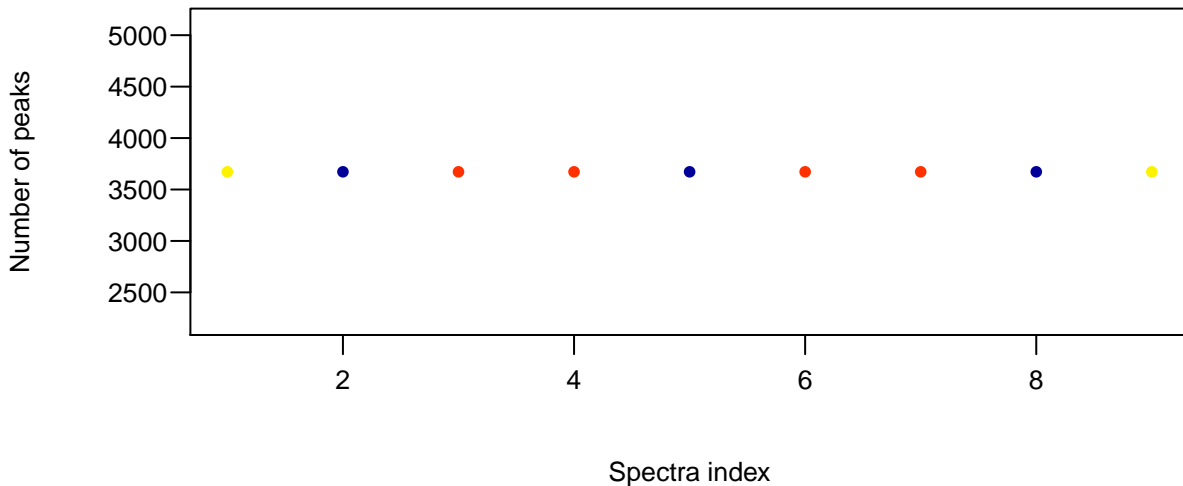


PCA for two components

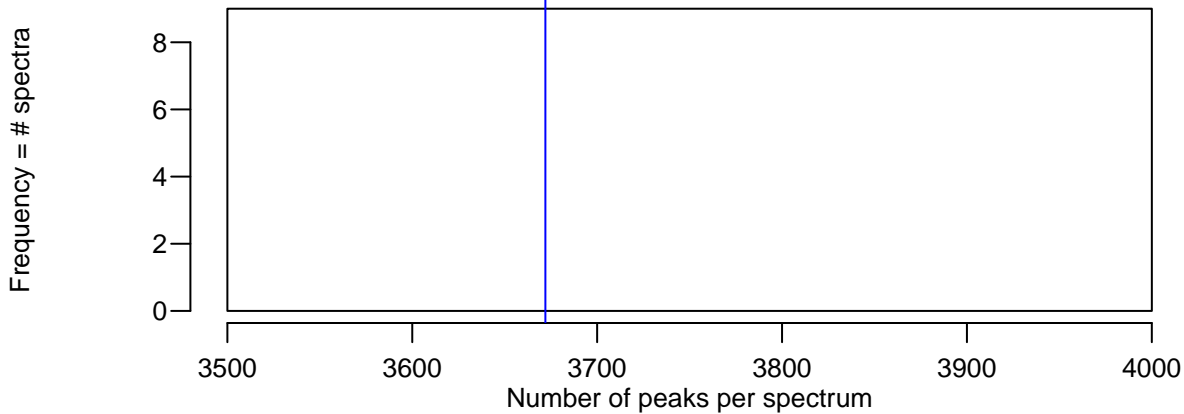


PC1**PC2**

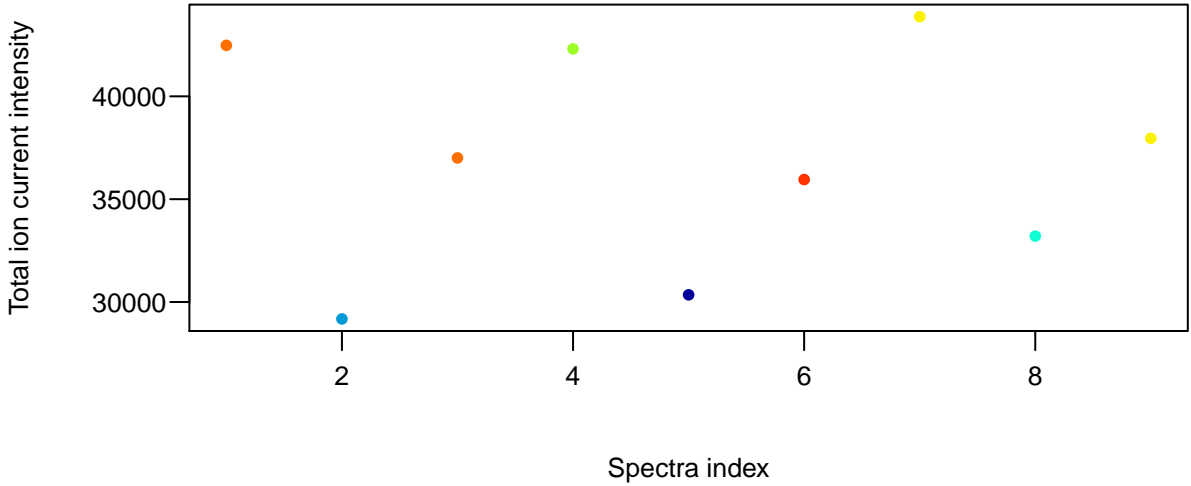
Number of peaks per spectrum



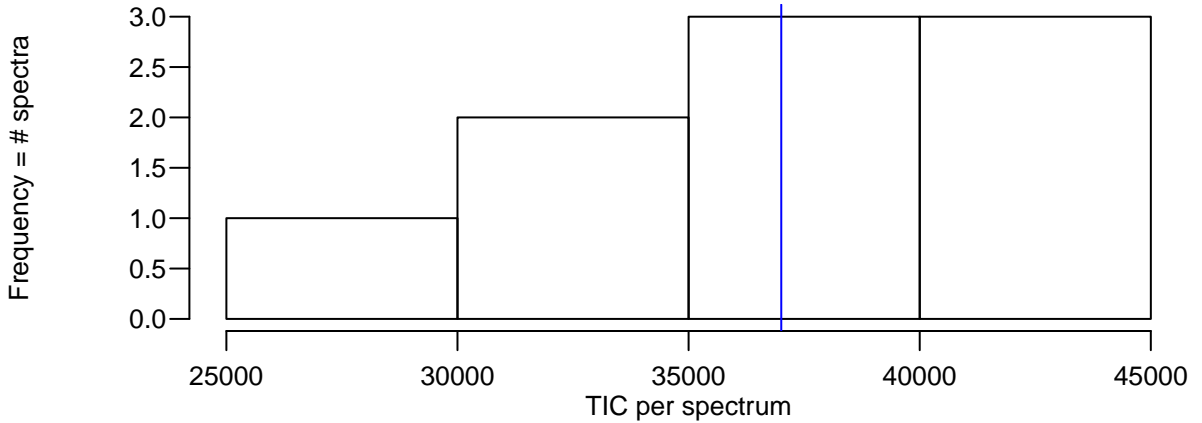
Number of peaks per spectrum



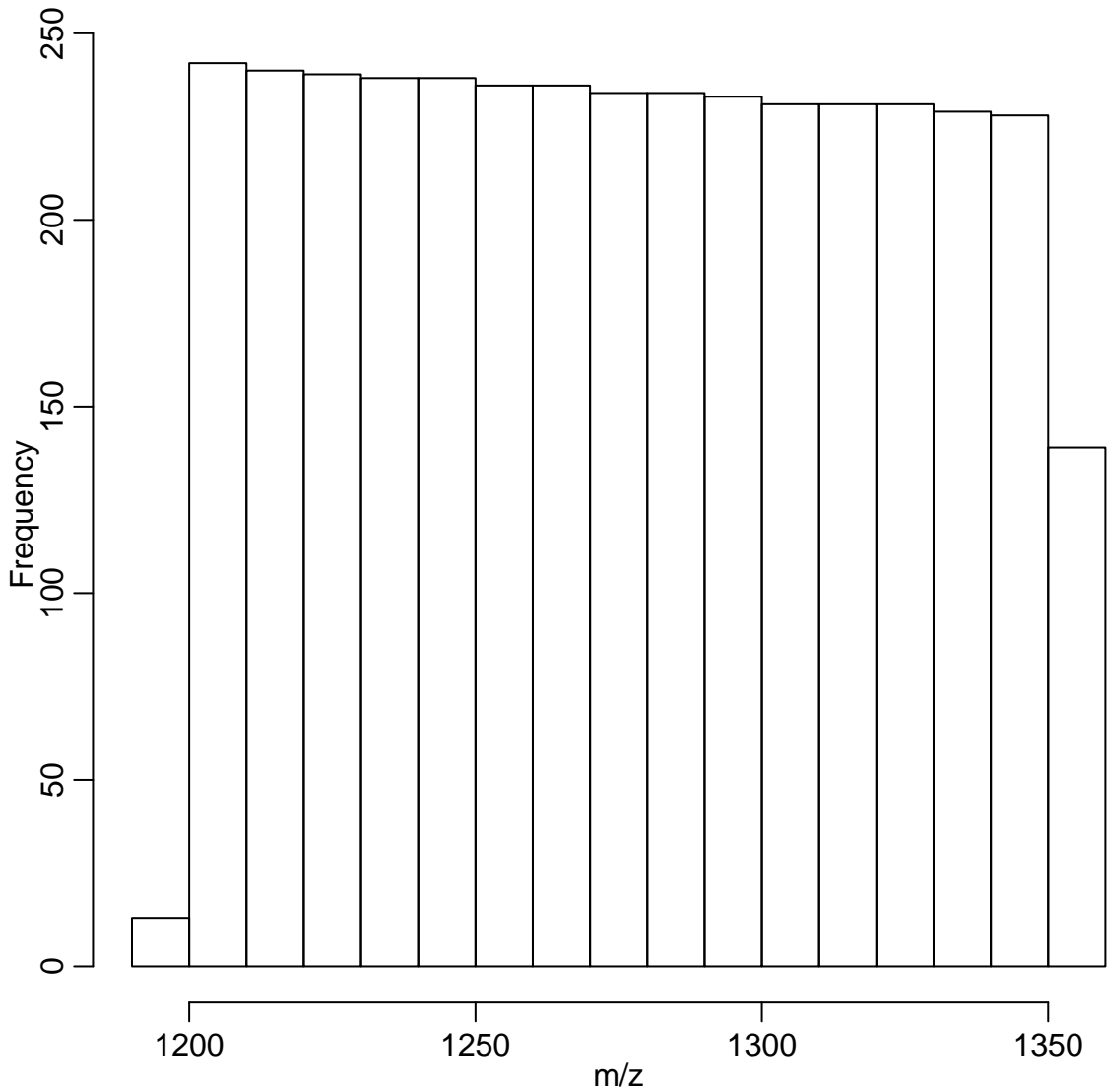
TIC per spectrum



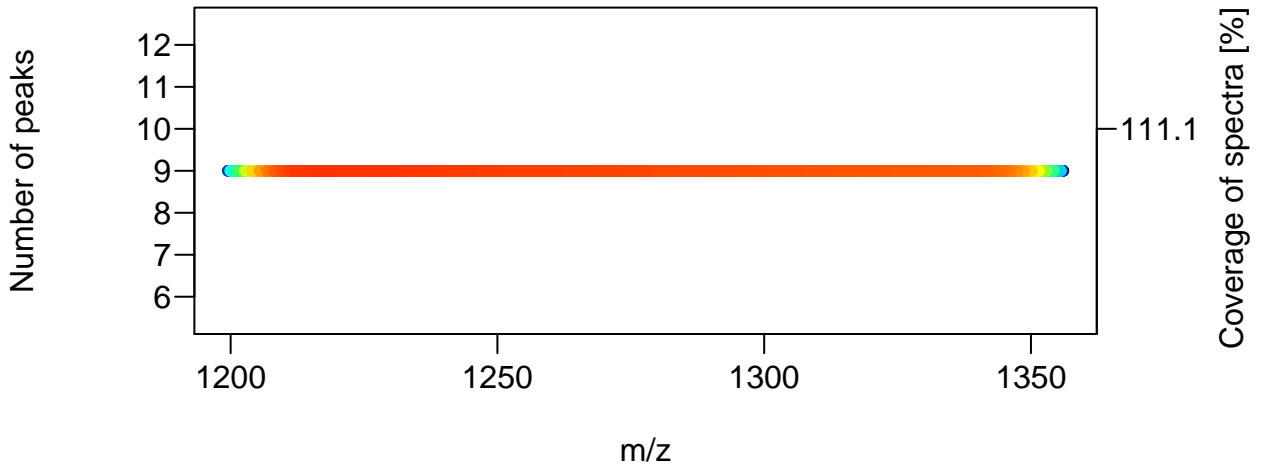
TIC per spectrum



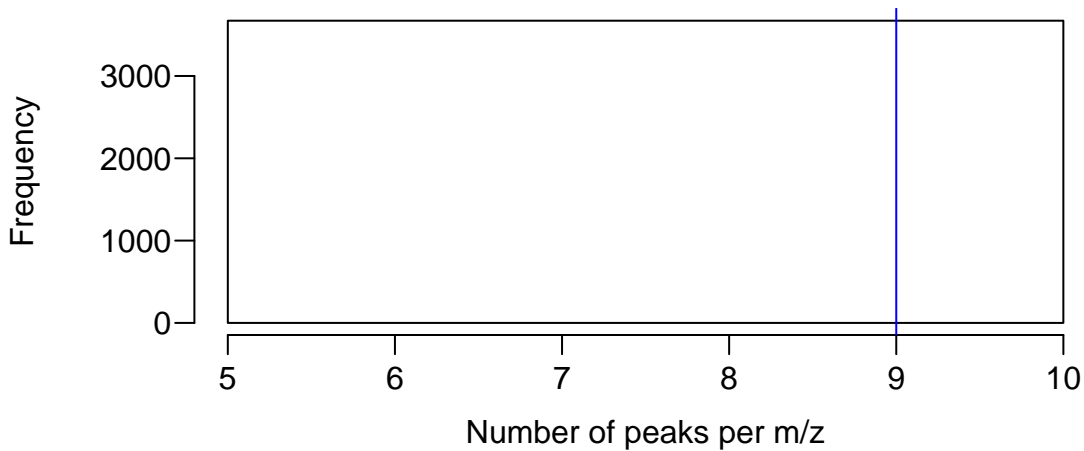
Histogram of m/z values



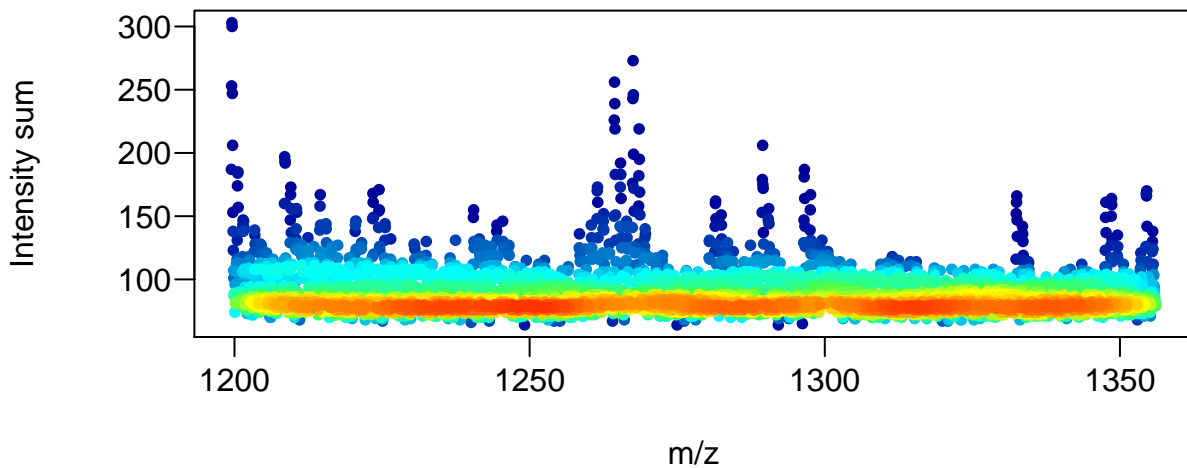
Number of peaks per m/z



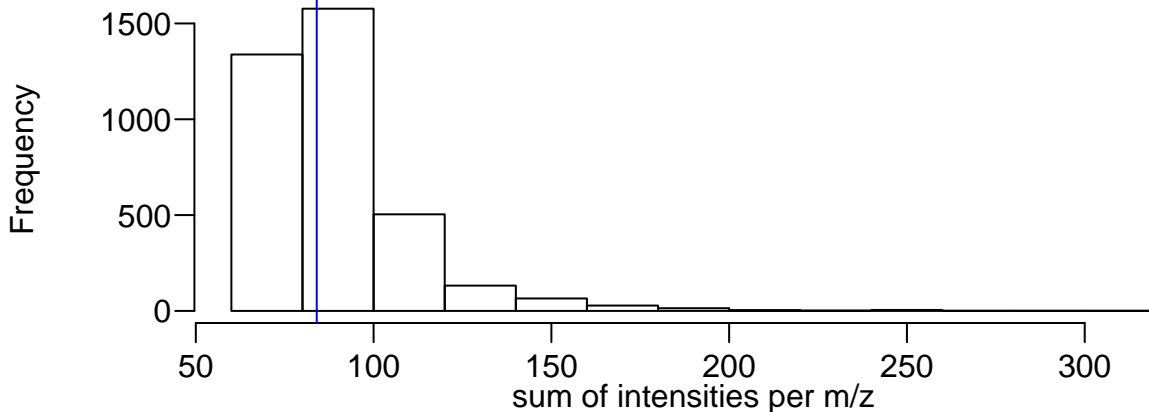
Number of peaks per m/z



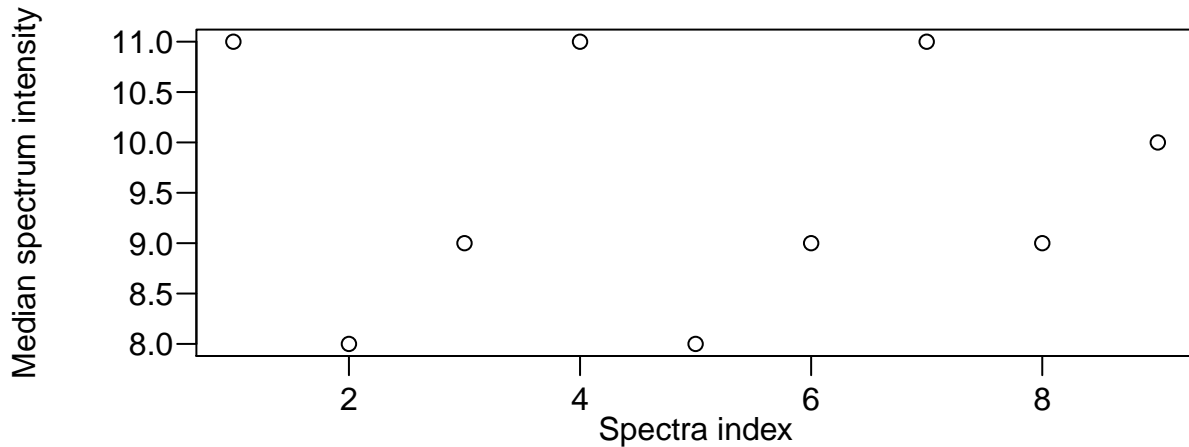
Sum of intensities per m/z



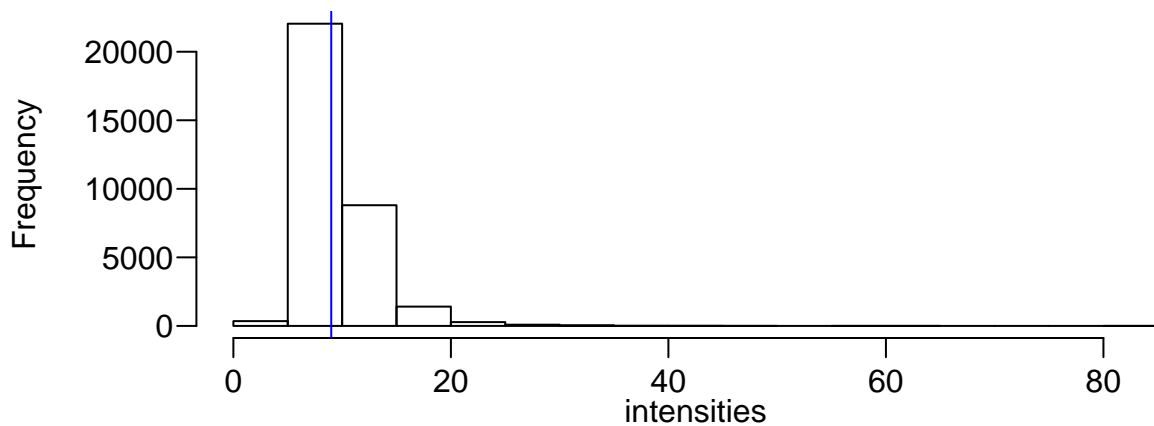
Sum of intensities per m/z



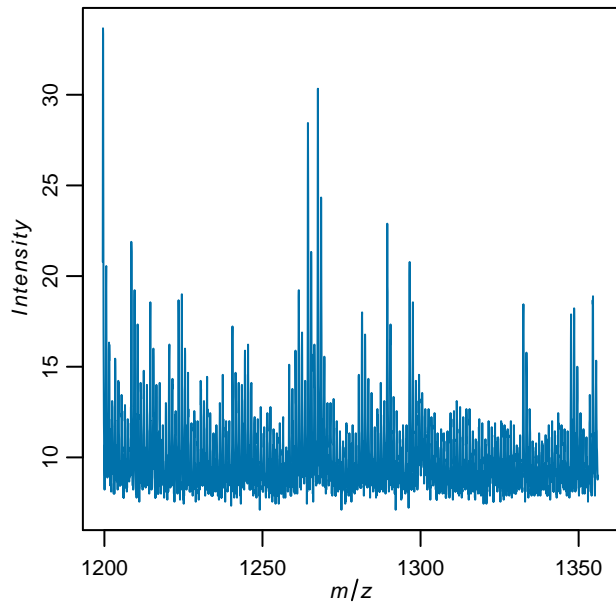
Median intensity per spectrum



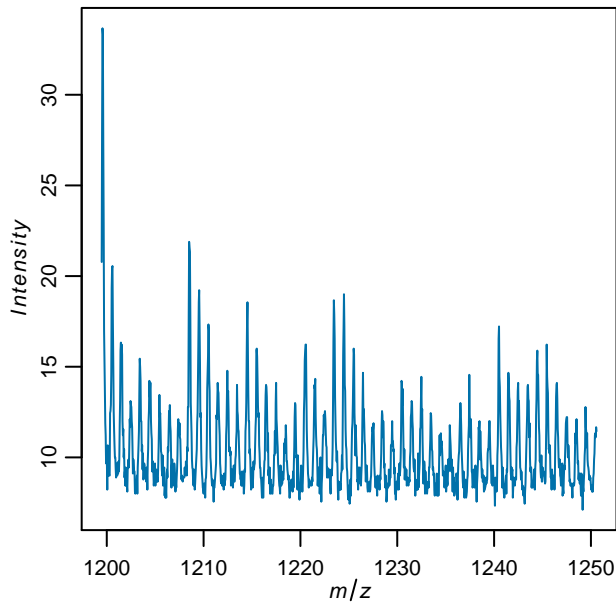
Intensity histogram



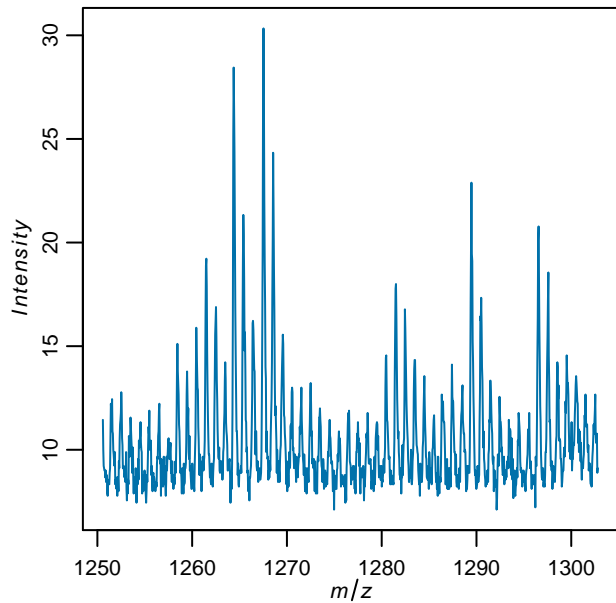
Average spectrum



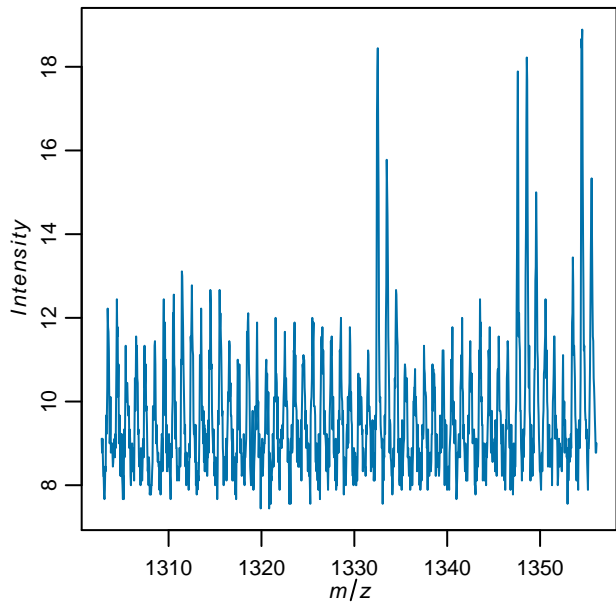
Zoomed average spectrum



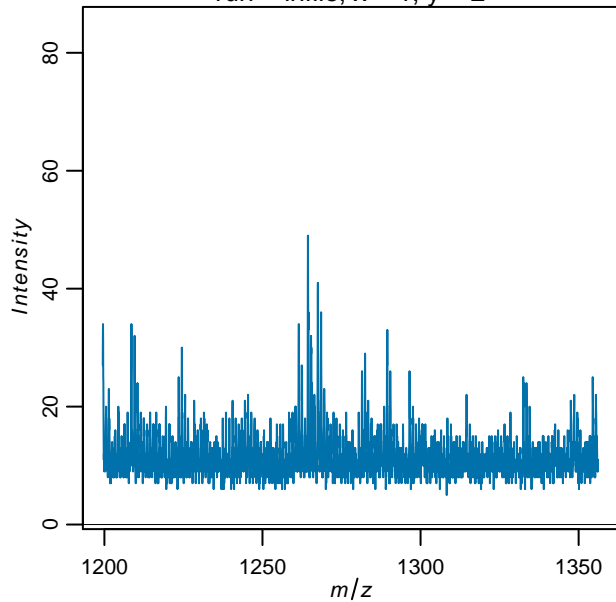
Zoomed average spectrum



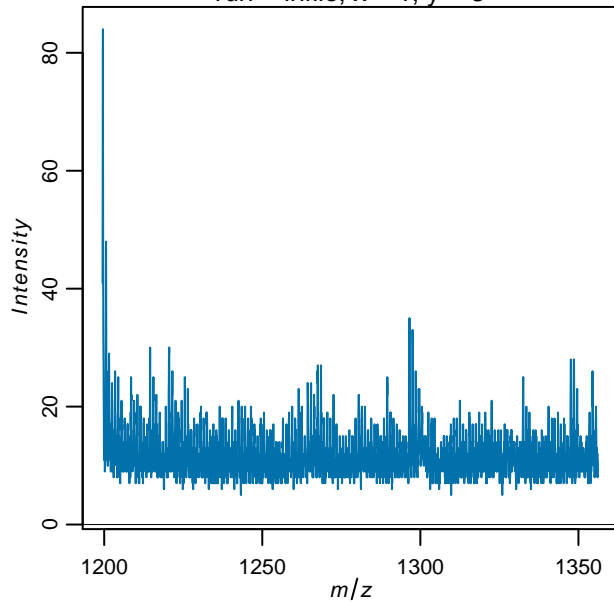
Zoomed average spectrum



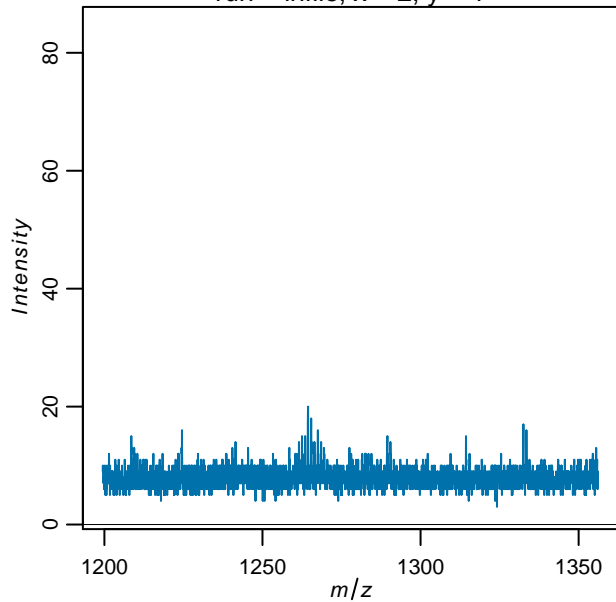
run = infile, x = 1, y = 2



run = infile, x = 1, y = 3



run = infile, x = 2, y = 1



run = infile, x = 3, y = 2

