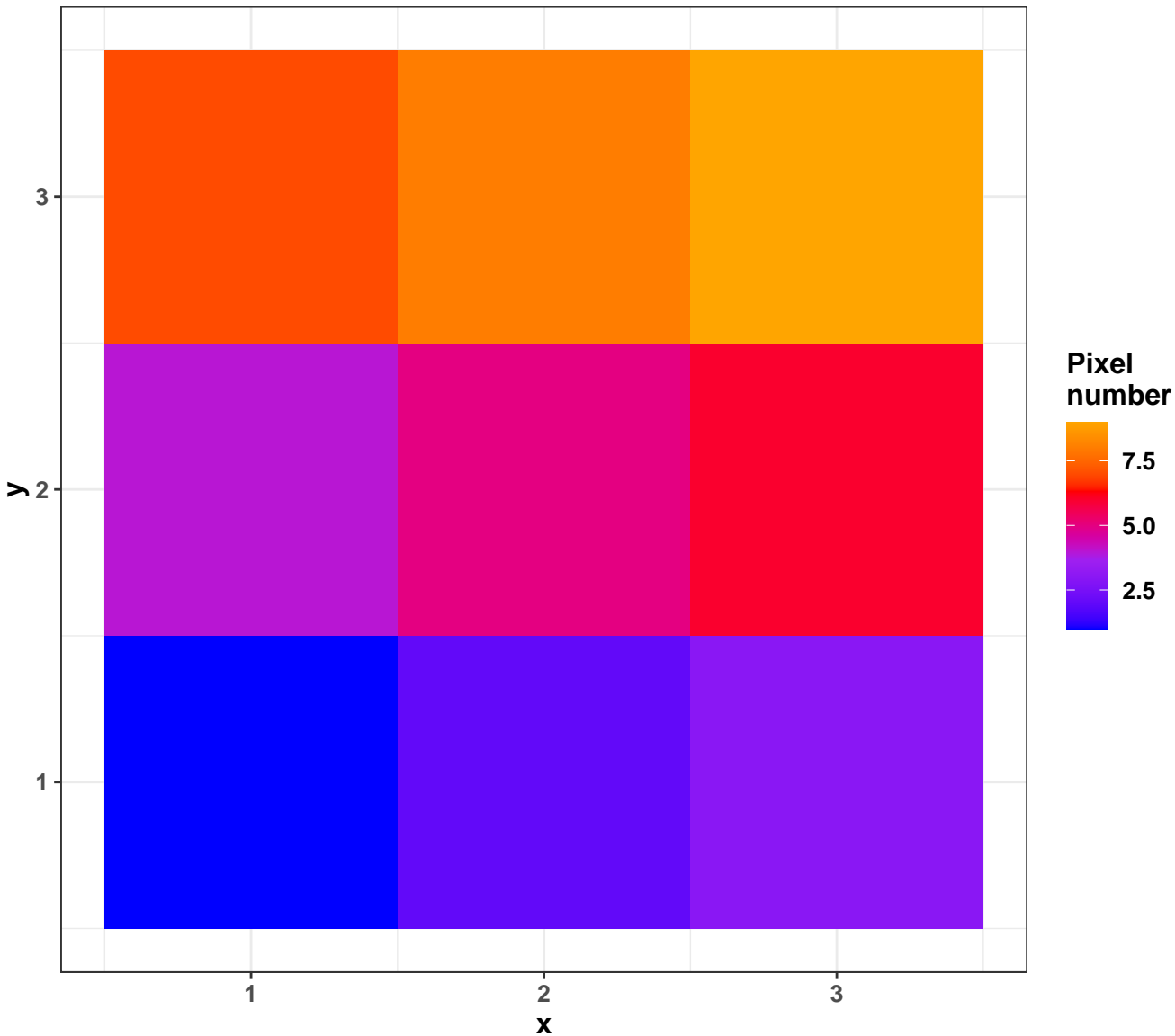


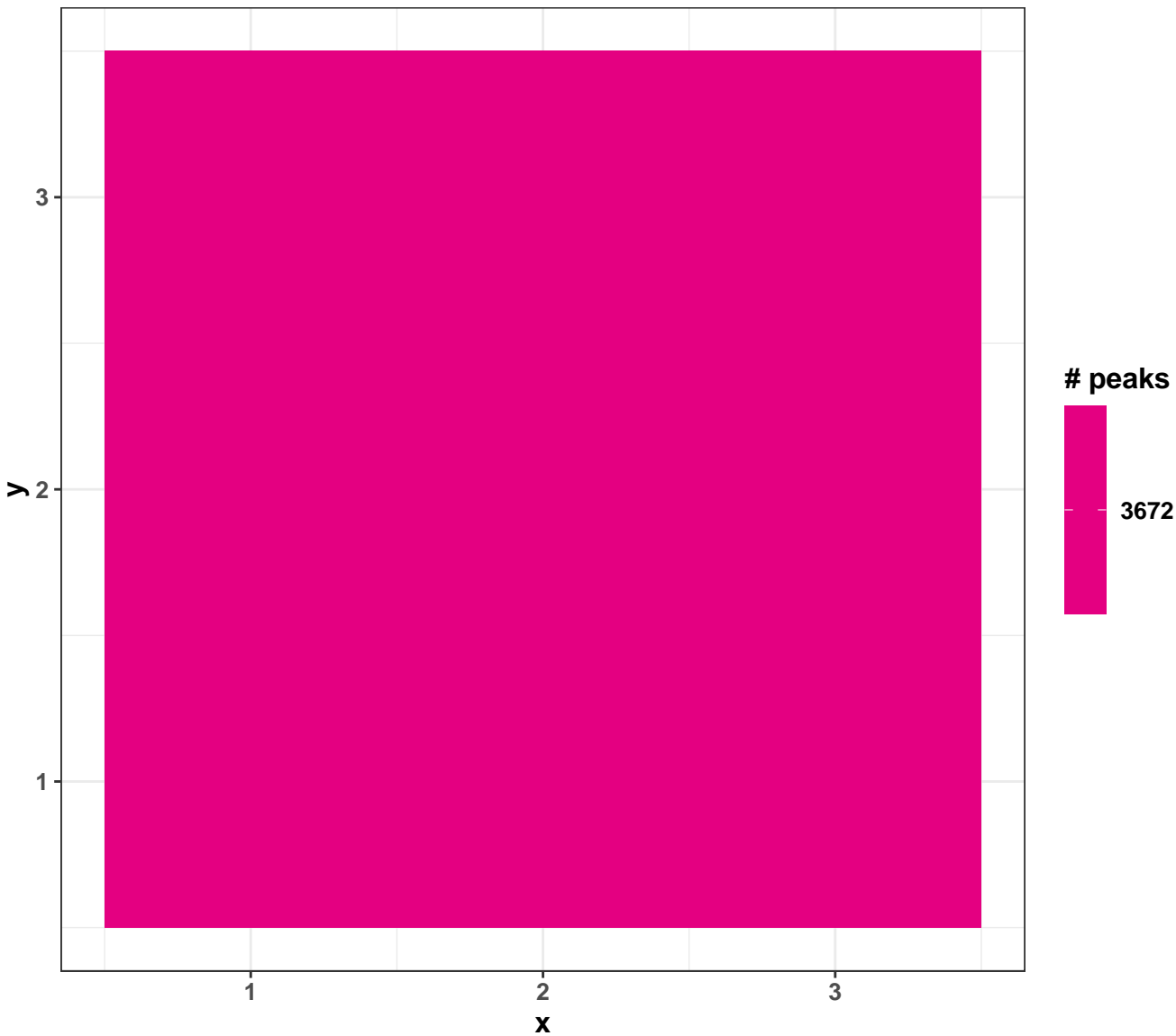
## Testfile\_analyze75

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 ± sd	37005 ± 5329
Median # peaks per spectrum ± sd	3672 ± 0
Centroided	FALSE
input m/z (#valid/#input) in None	0 / 0

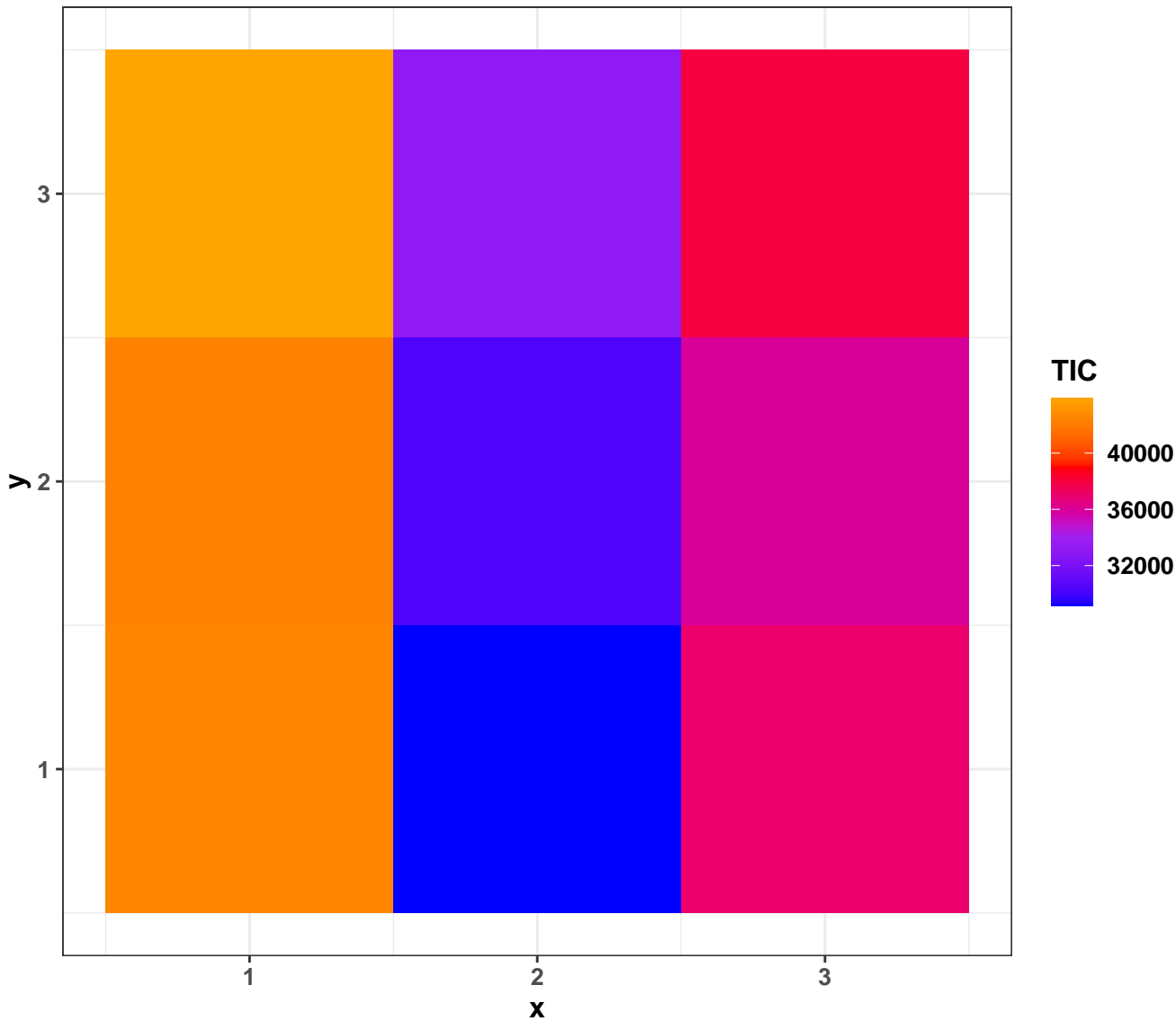
# Pixel order



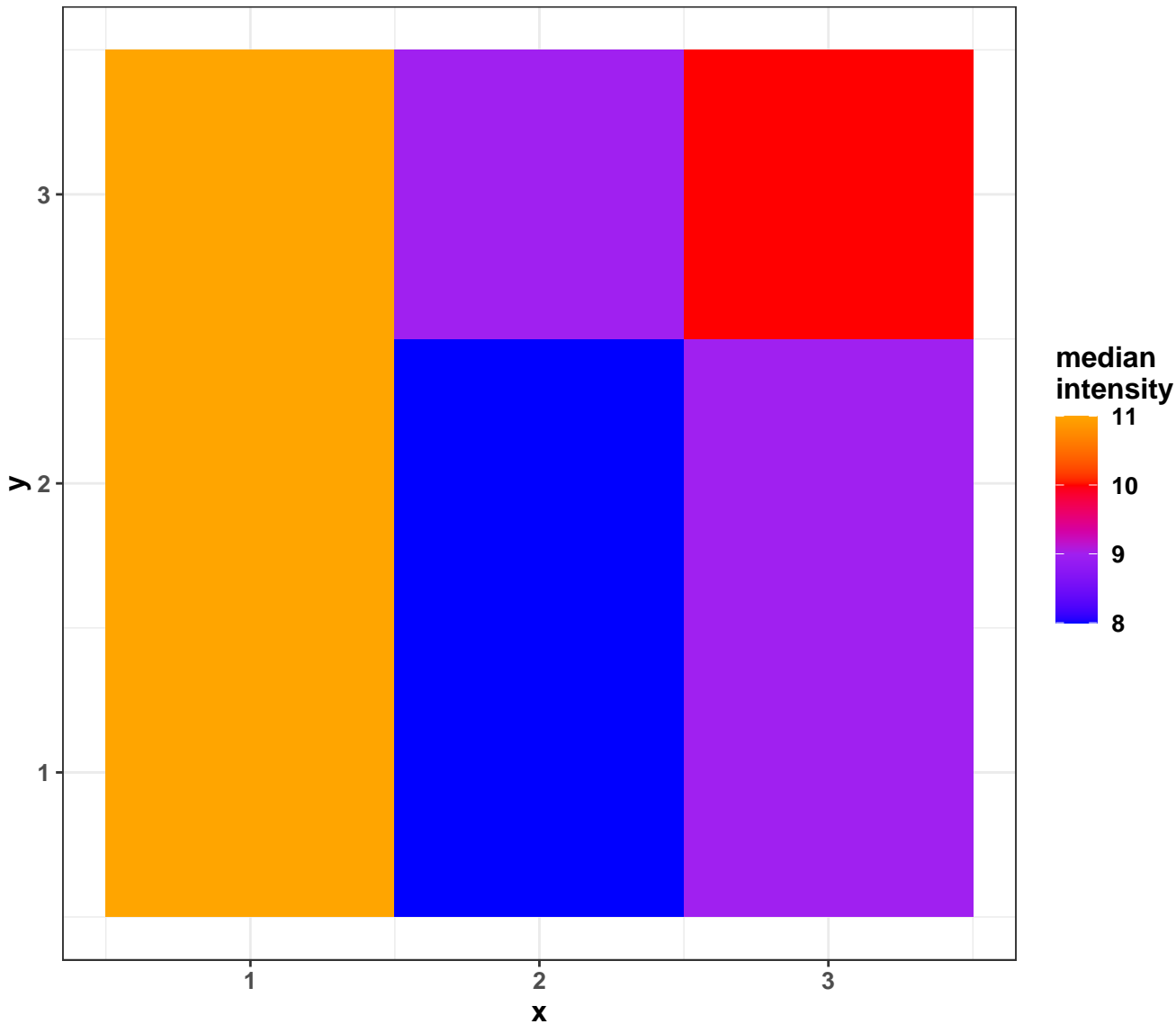
# Number of peaks per spectrum



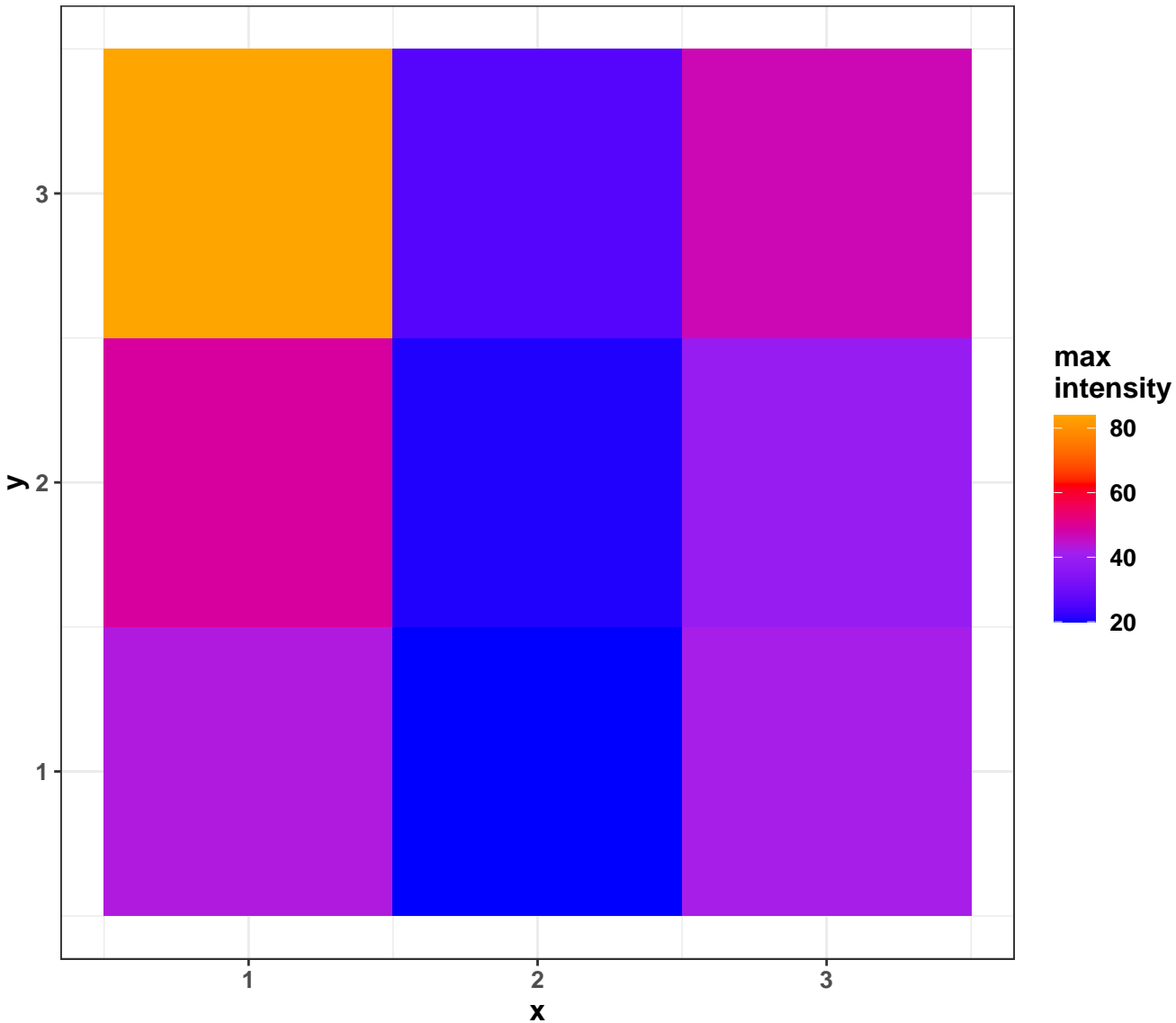
# Total Ion Current



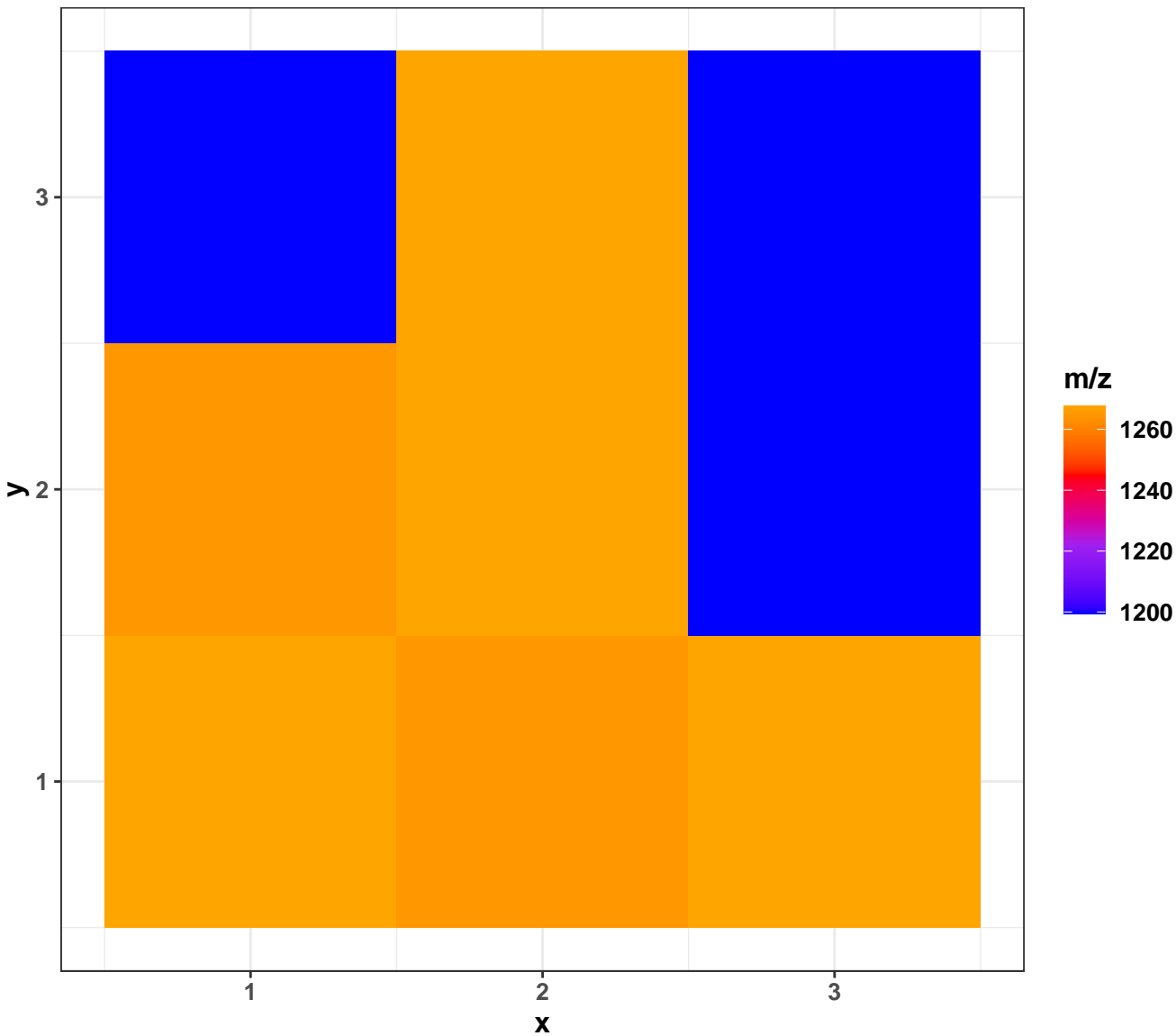
Median intensity per spectrum



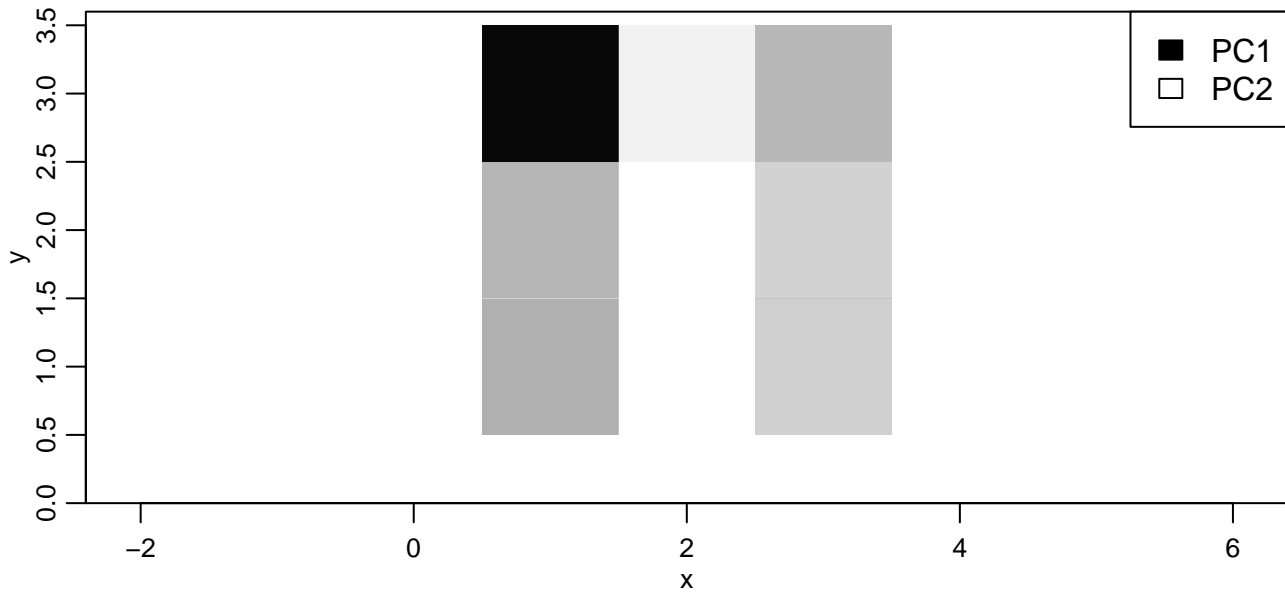
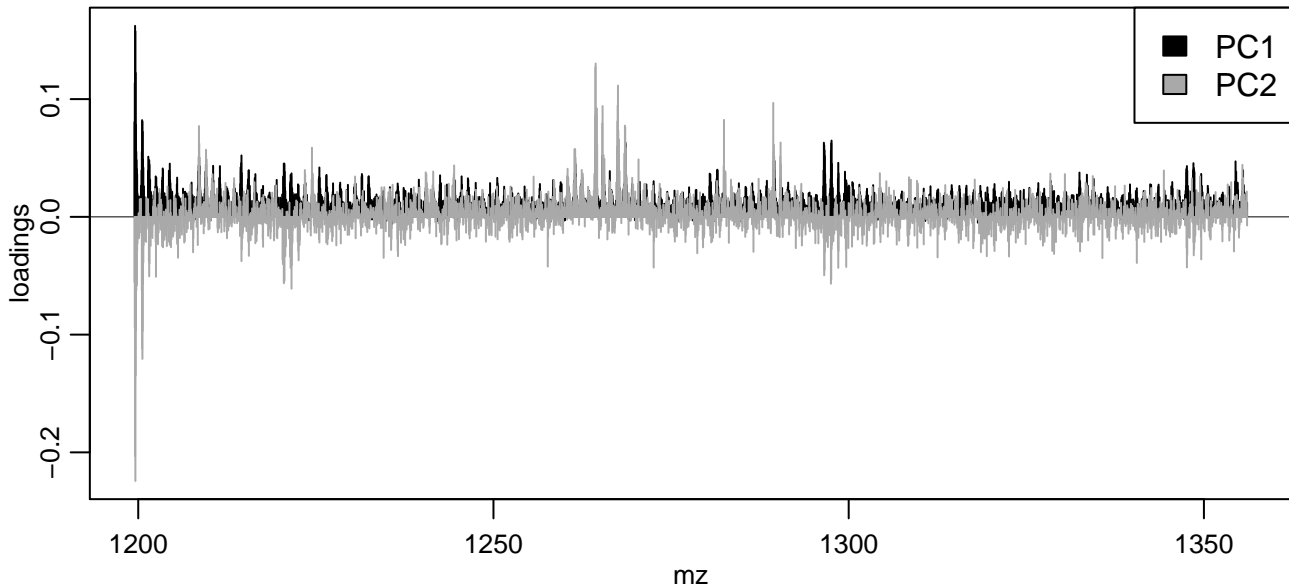
# Maximum intensity per spectrum



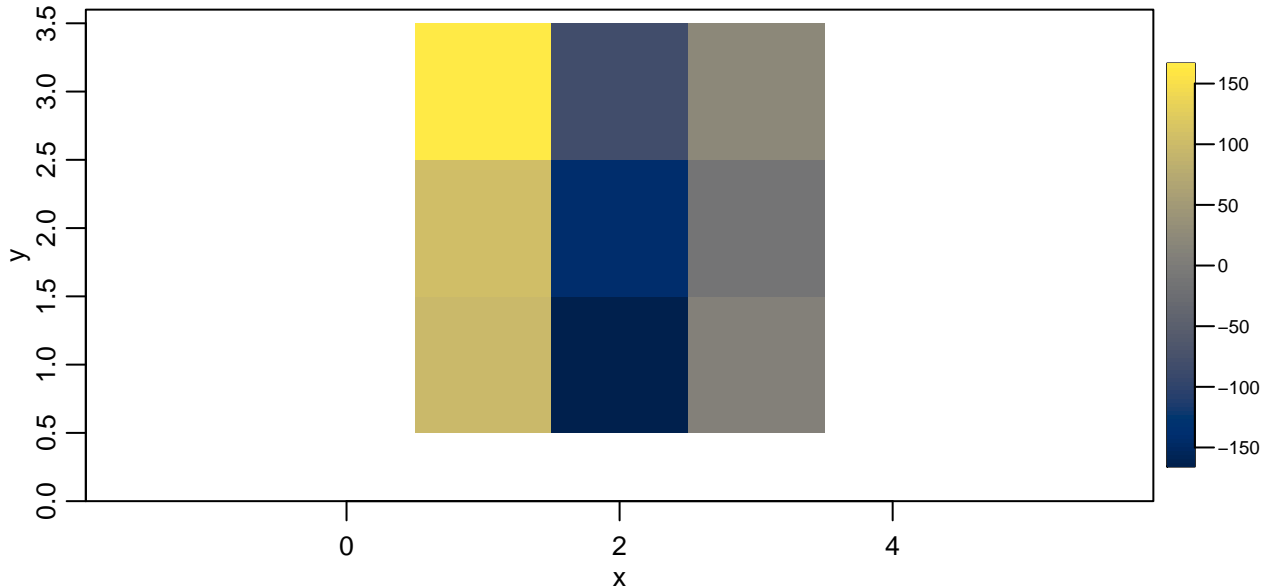
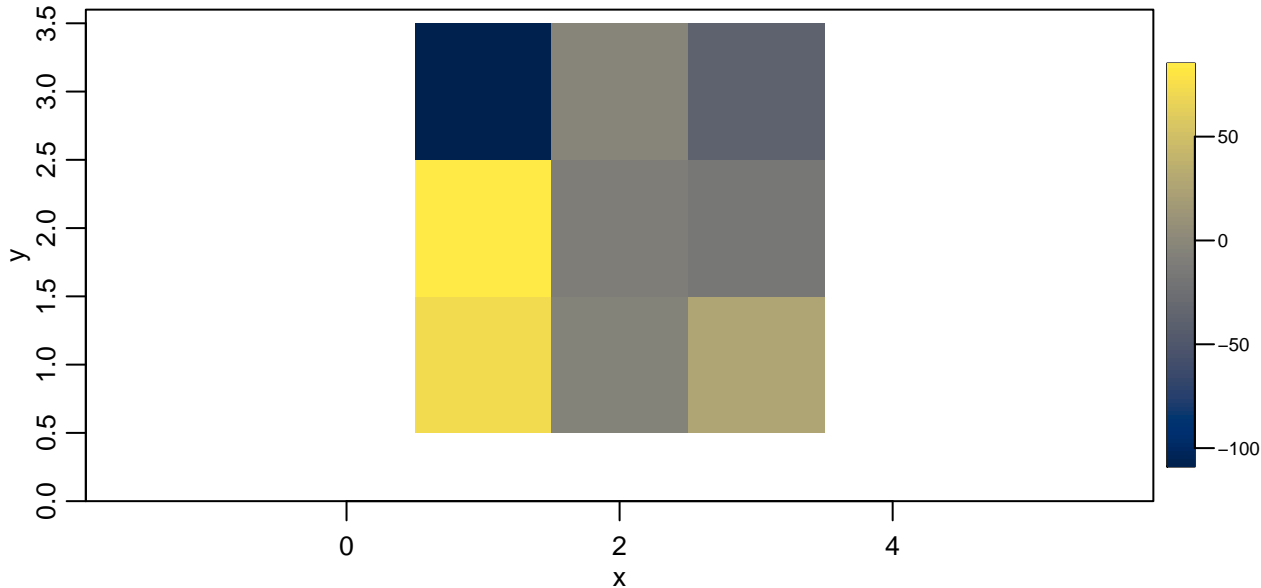
# Most abundant m/z in each spectrum



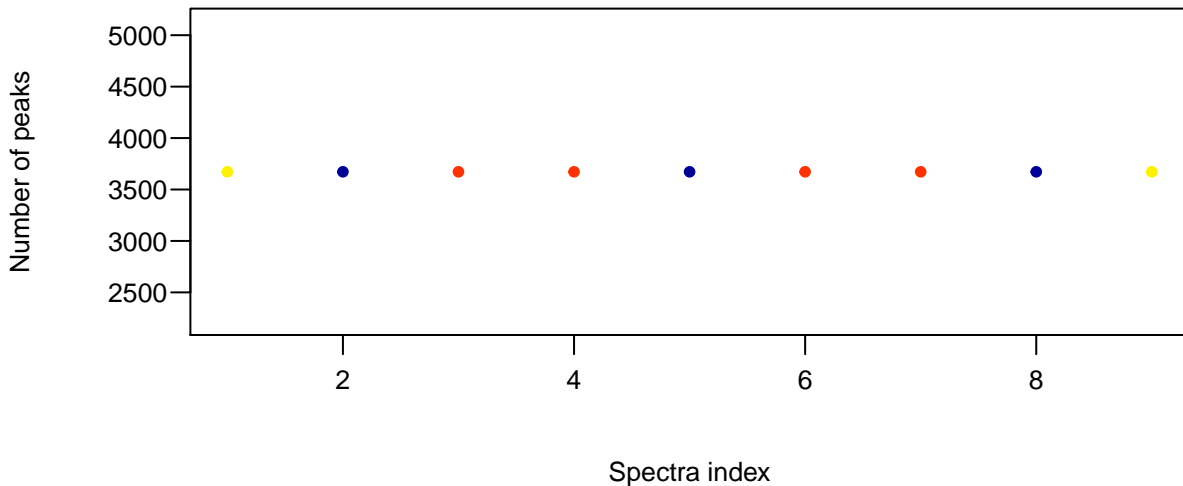
# PCA for two components



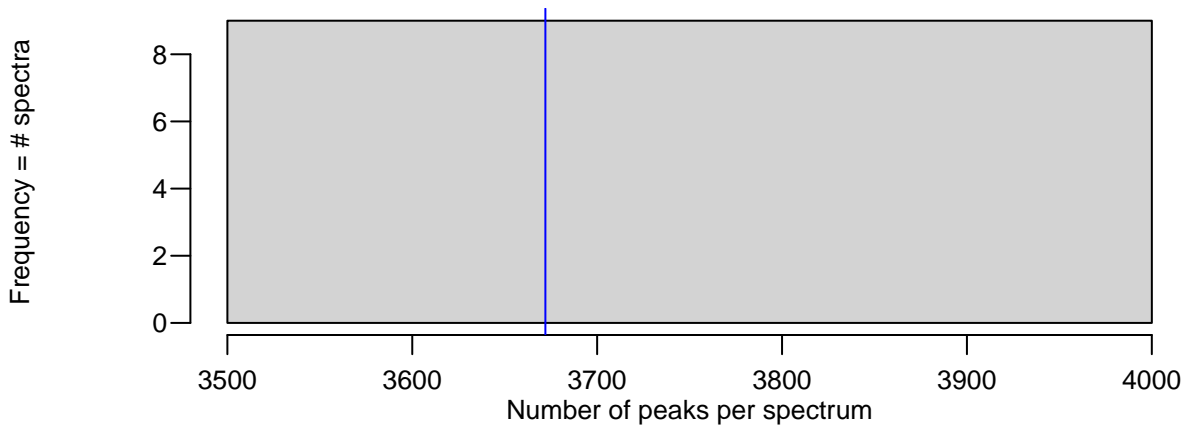


**PC1****PC2**

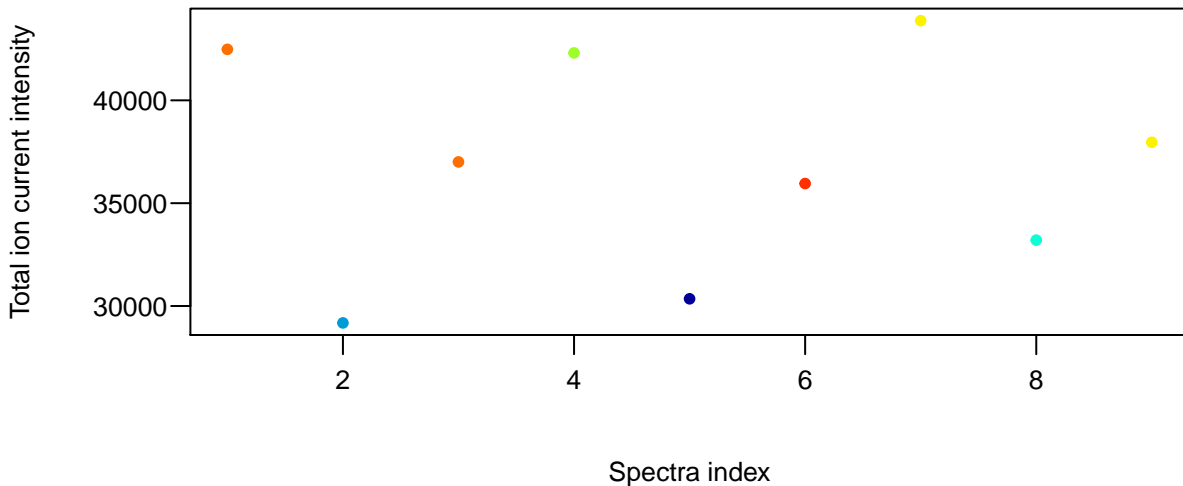
## Number of peaks per spectrum



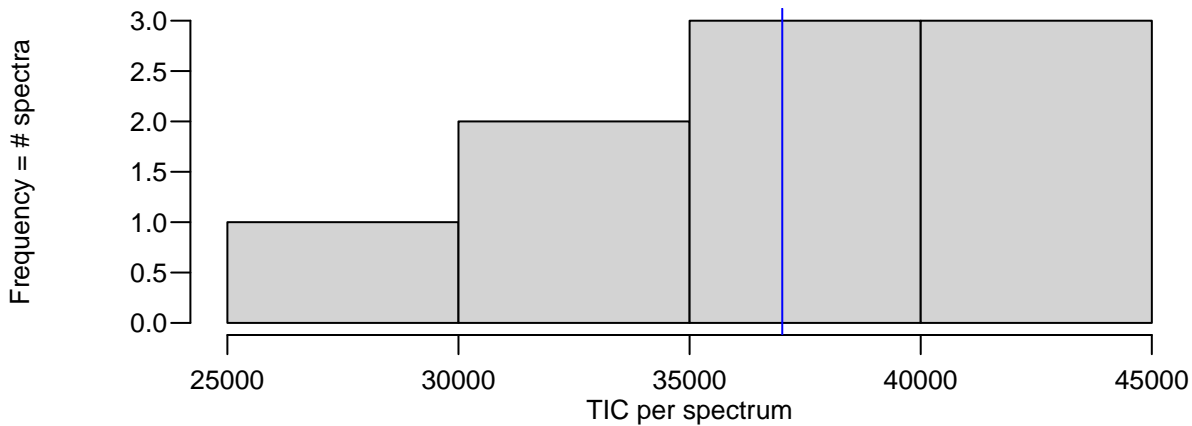
## Number of peaks per spectrum



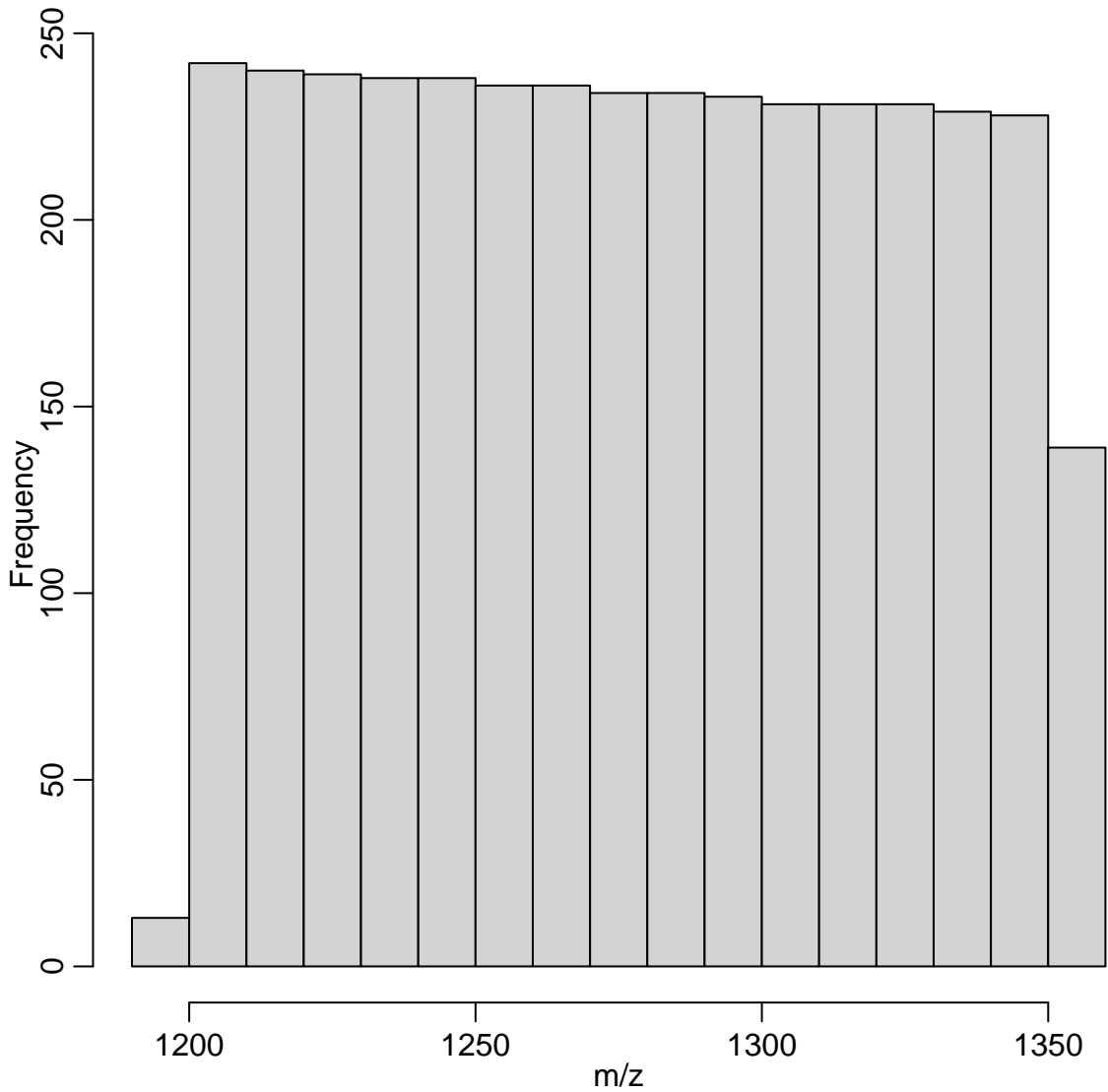
## TIC per spectrum



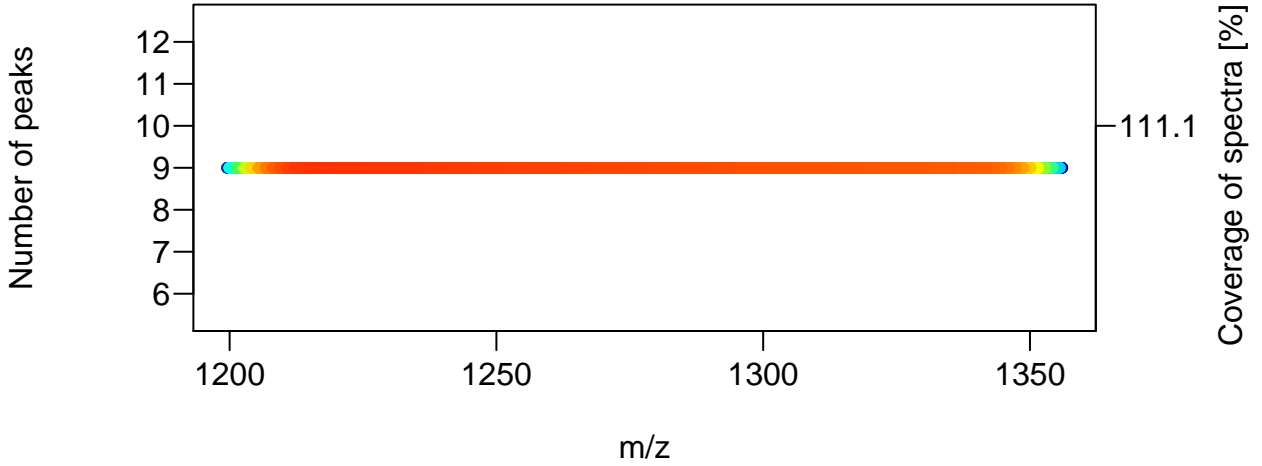
## TIC per spectrum



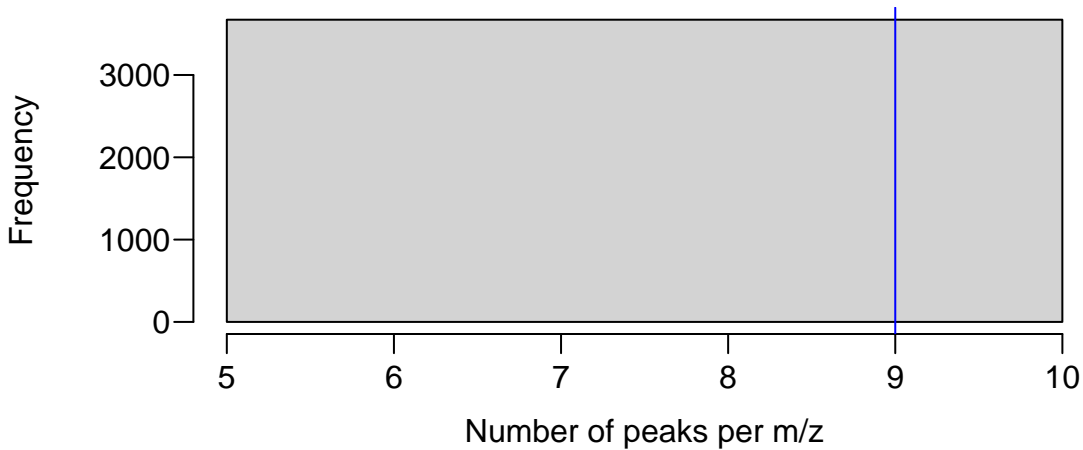
# Histogram of m/z values



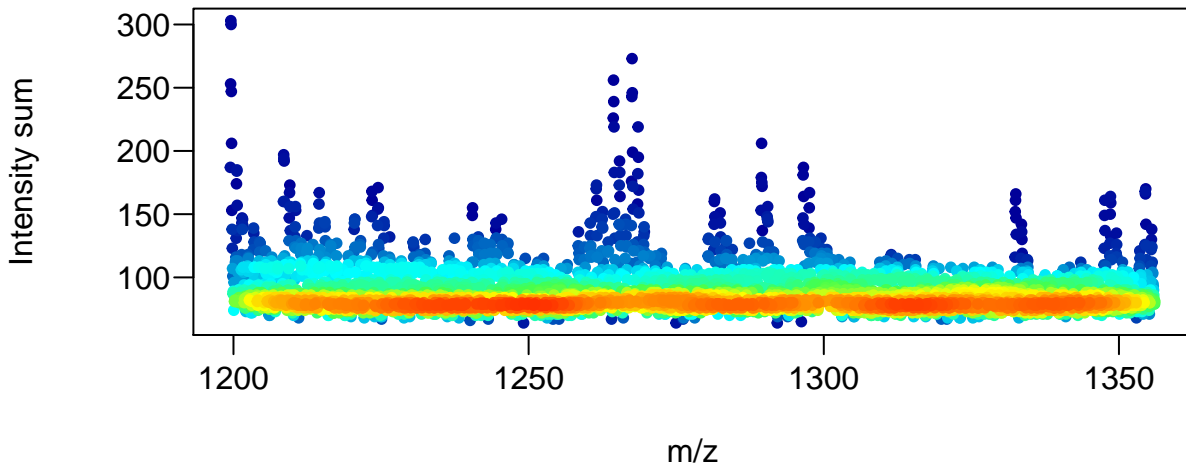
## Number of peaks per m/z



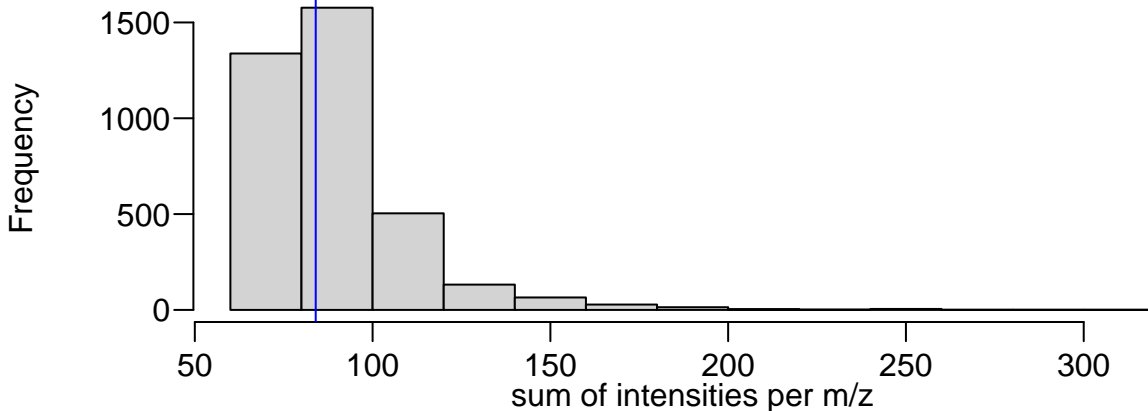
## Number of peaks per m/z



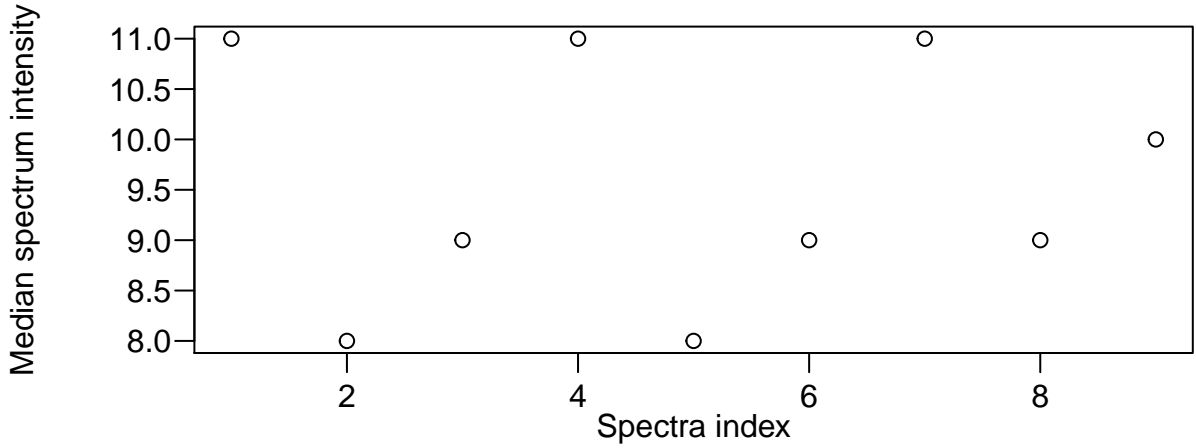
### Sum of intensities per m/z



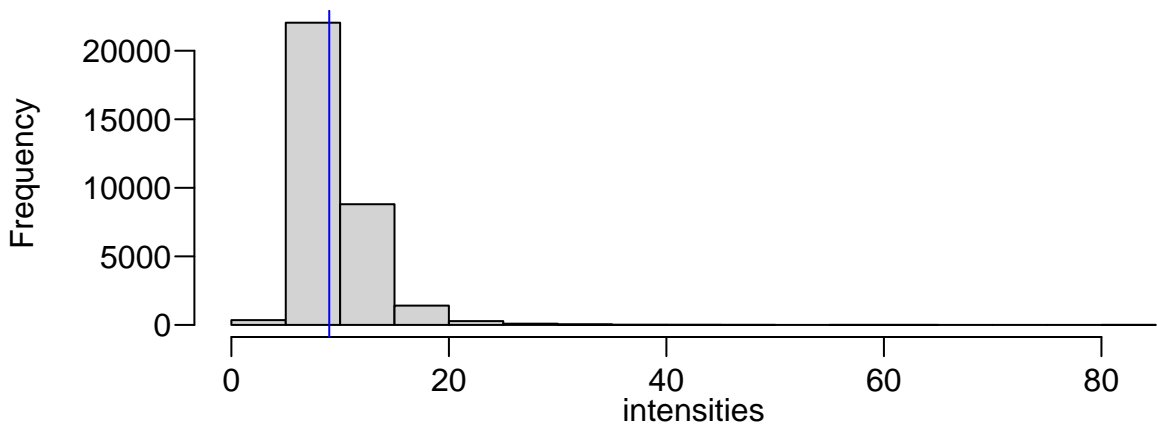
### Sum of intensities per m/z



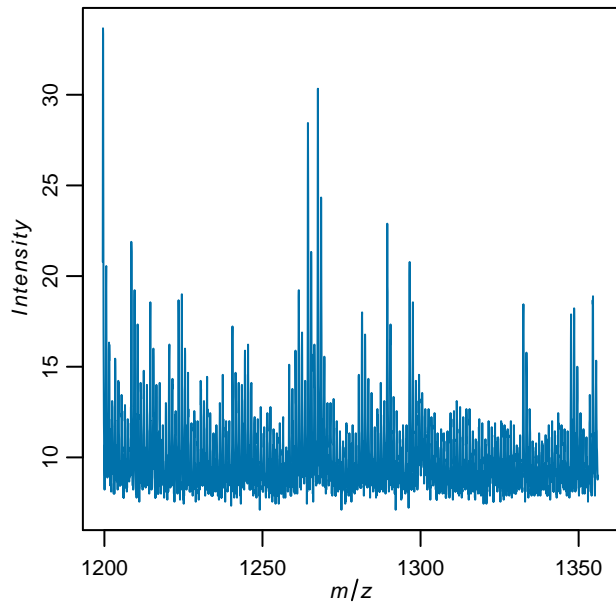
## Median intensity per spectrum



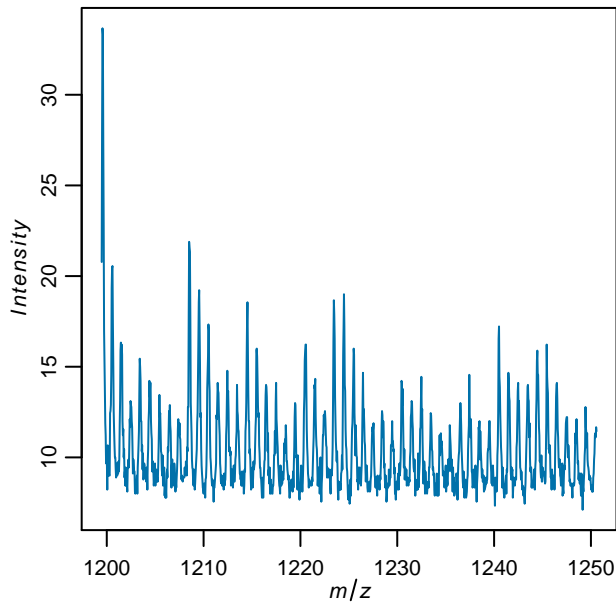
## Intensity histogram



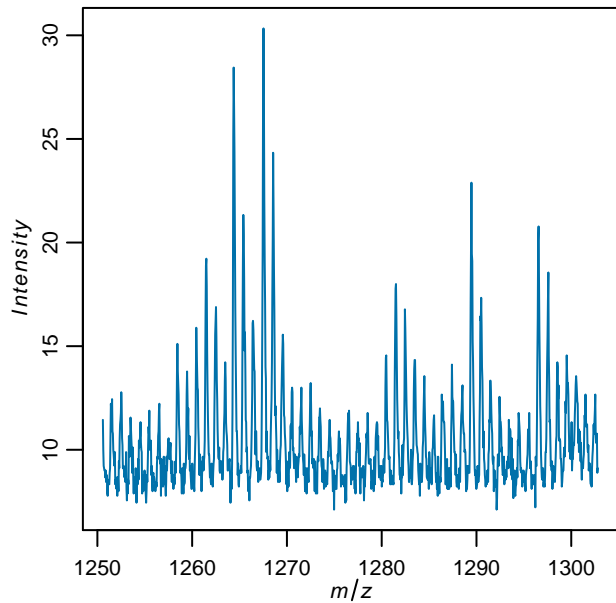
### Average spectrum



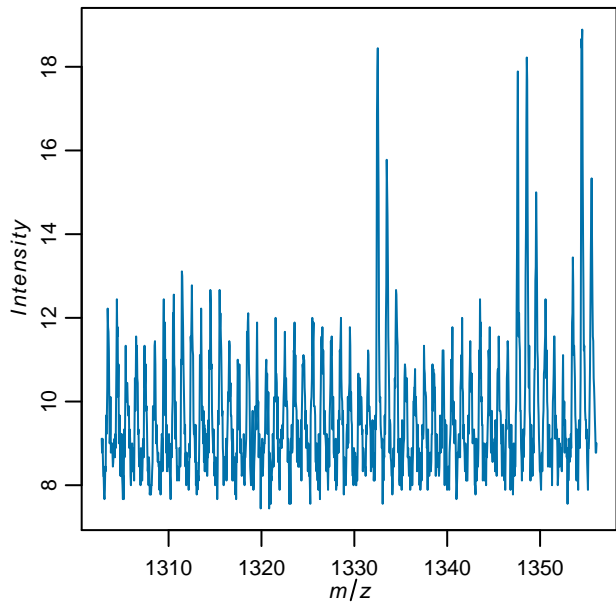
### Zoomed average spectrum



### Zoomed average spectrum

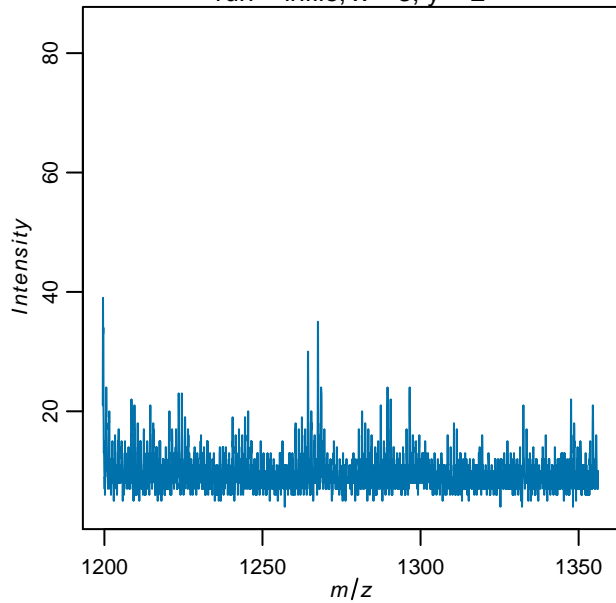


### Zoomed average spectrum

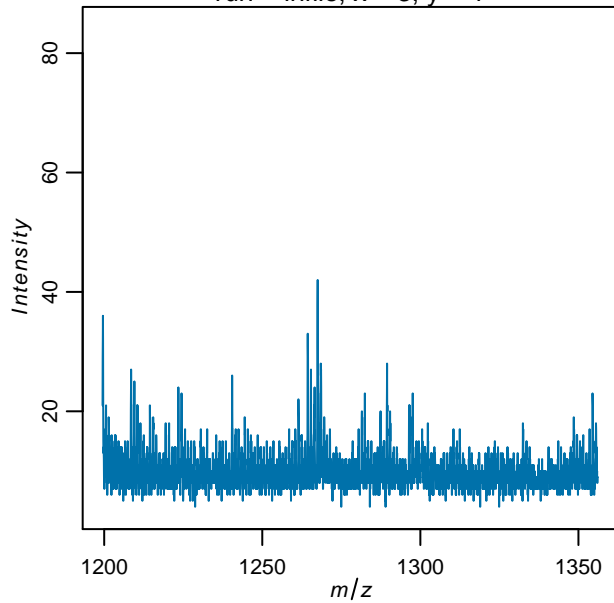




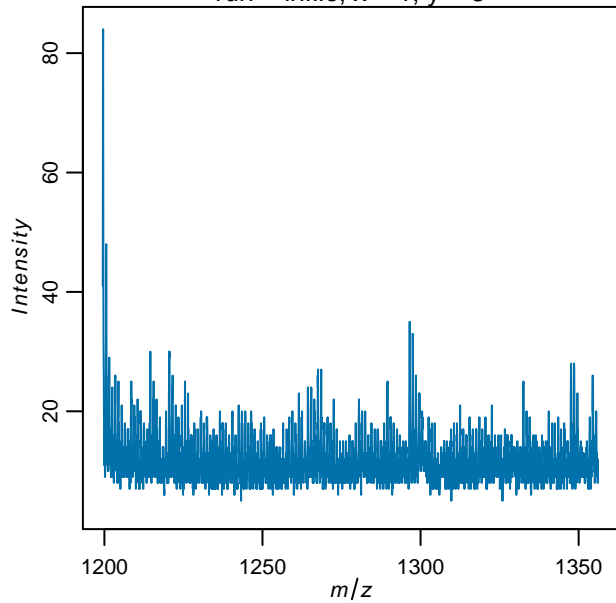
run = infile, x = 3, y = 2



run = infile, x = 3, y = 1



run = infile, x = 1, y = 3



run = infile, x = 1, y = 2

