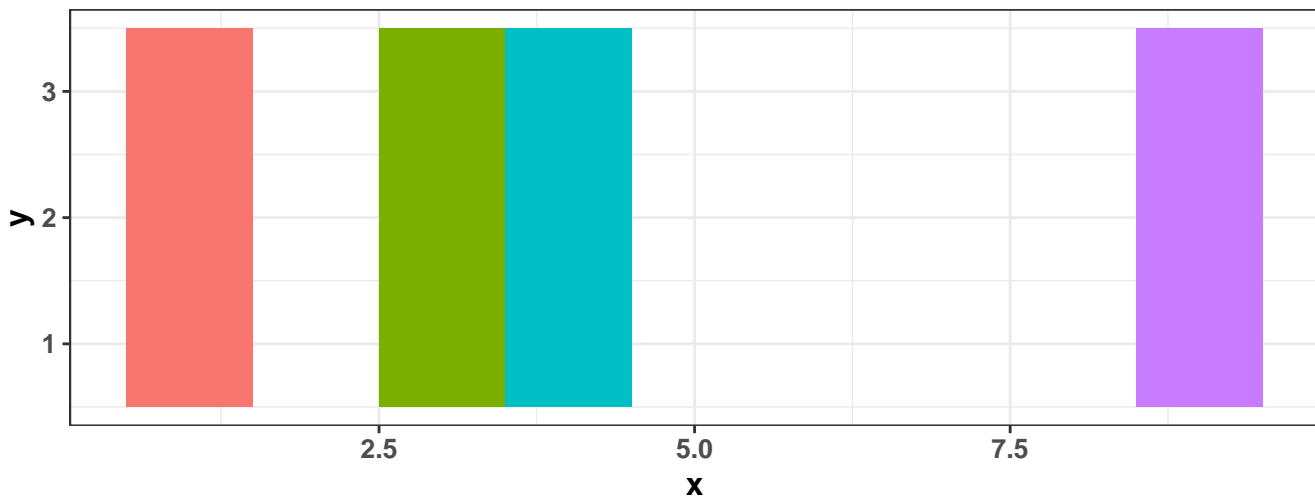


## Testfile\_rdata

properties	values
Number of m/z features	8399
Range of m/z values	100.08 – 799.92
Number of pixels	12
Range of x coordinates	1 – 9
Range of y coordinates	1 – 3
Range of intensities	0 – 9.24
Median of intensities	0
Intensities > 0	31.29 %
Number of empty spectra	0
Median TIC $\pm$ sd	161.8 $\pm$ 47
Median # peaks per spectrum $\pm$ sd	2811 $\pm$ 424
Centroided	FALSE
calibrants (#valid/#input) in inputcalibrantfile1.tabular	3 / 3

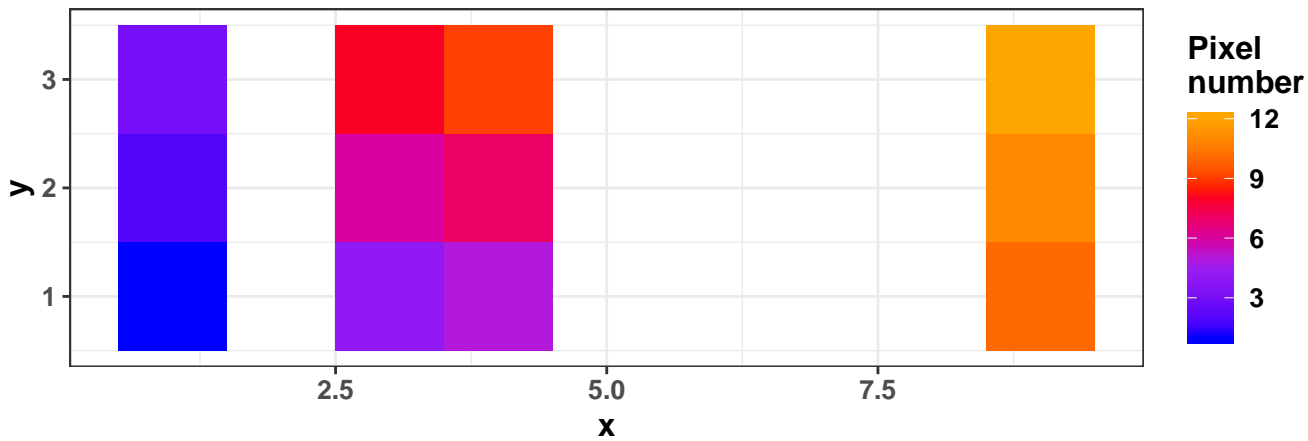
## Spatial orientation of pixel annotations



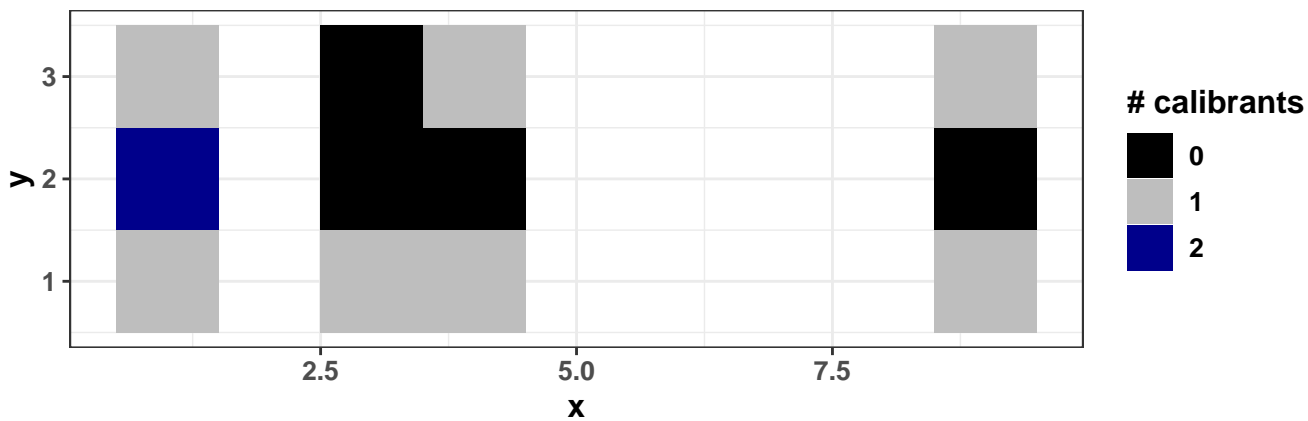
### annotation

column1 column2 column3 column4

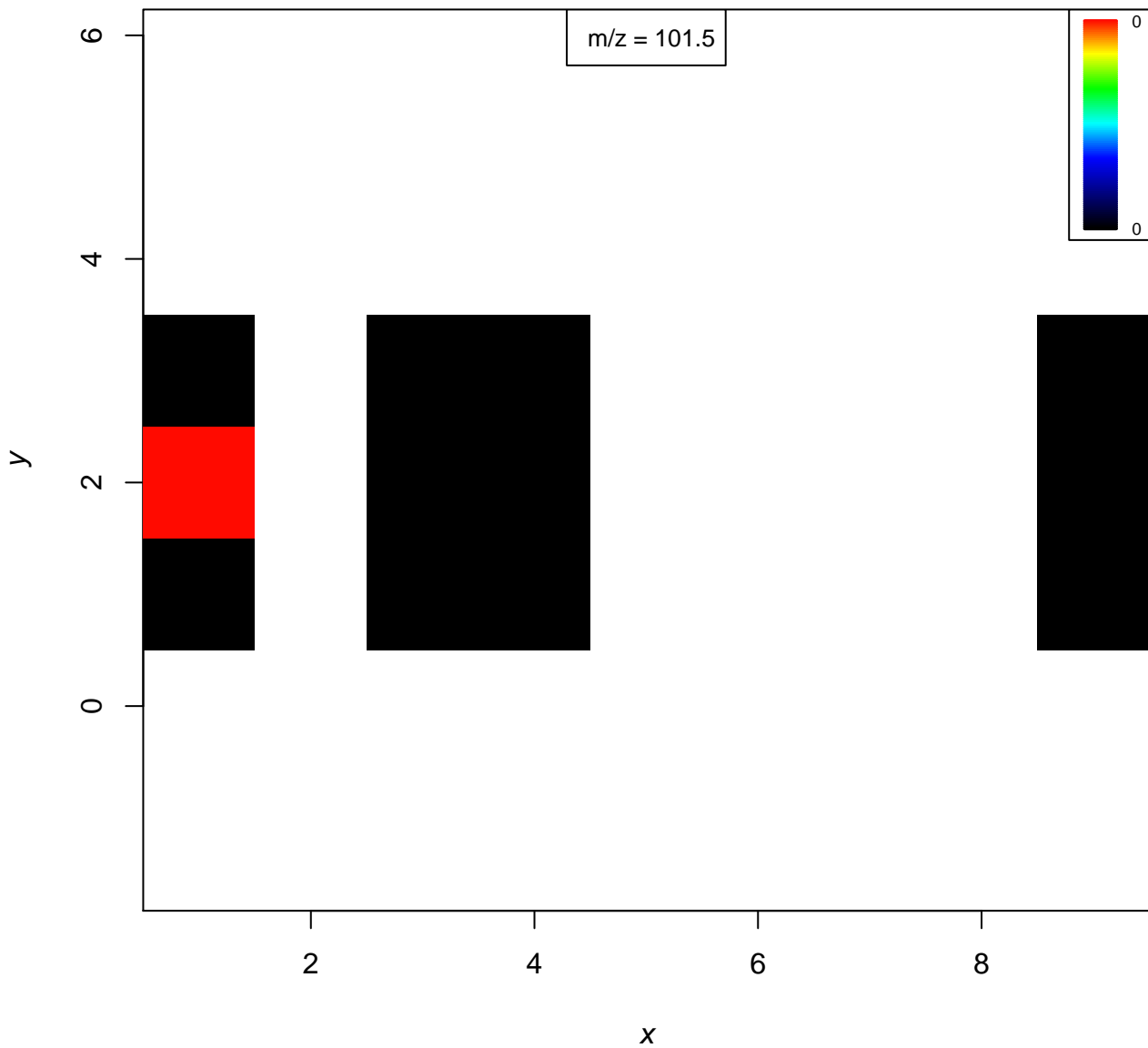
### Pixel order



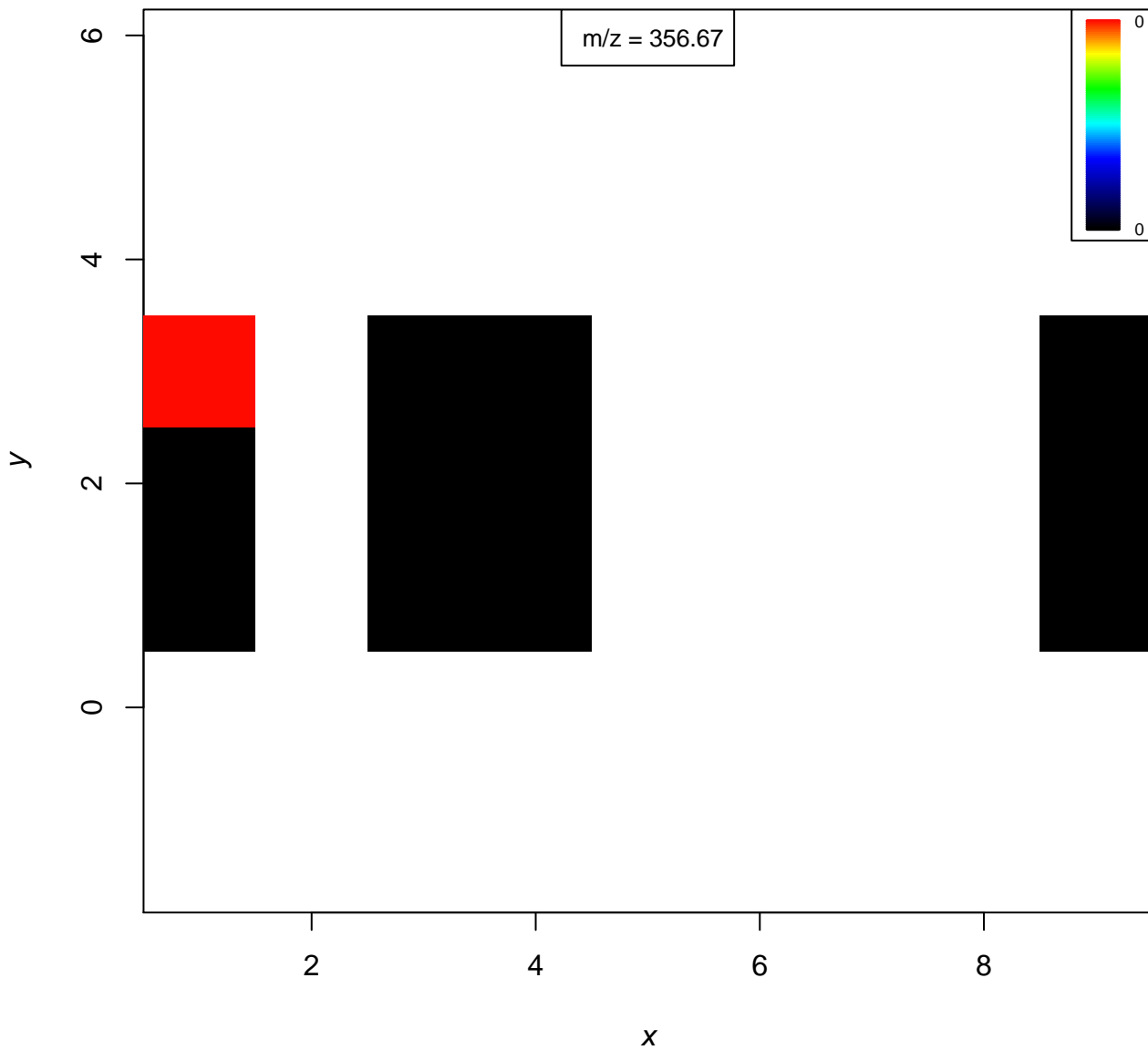
Number of calibrants per pixel ( $\pm 100$  ppm)



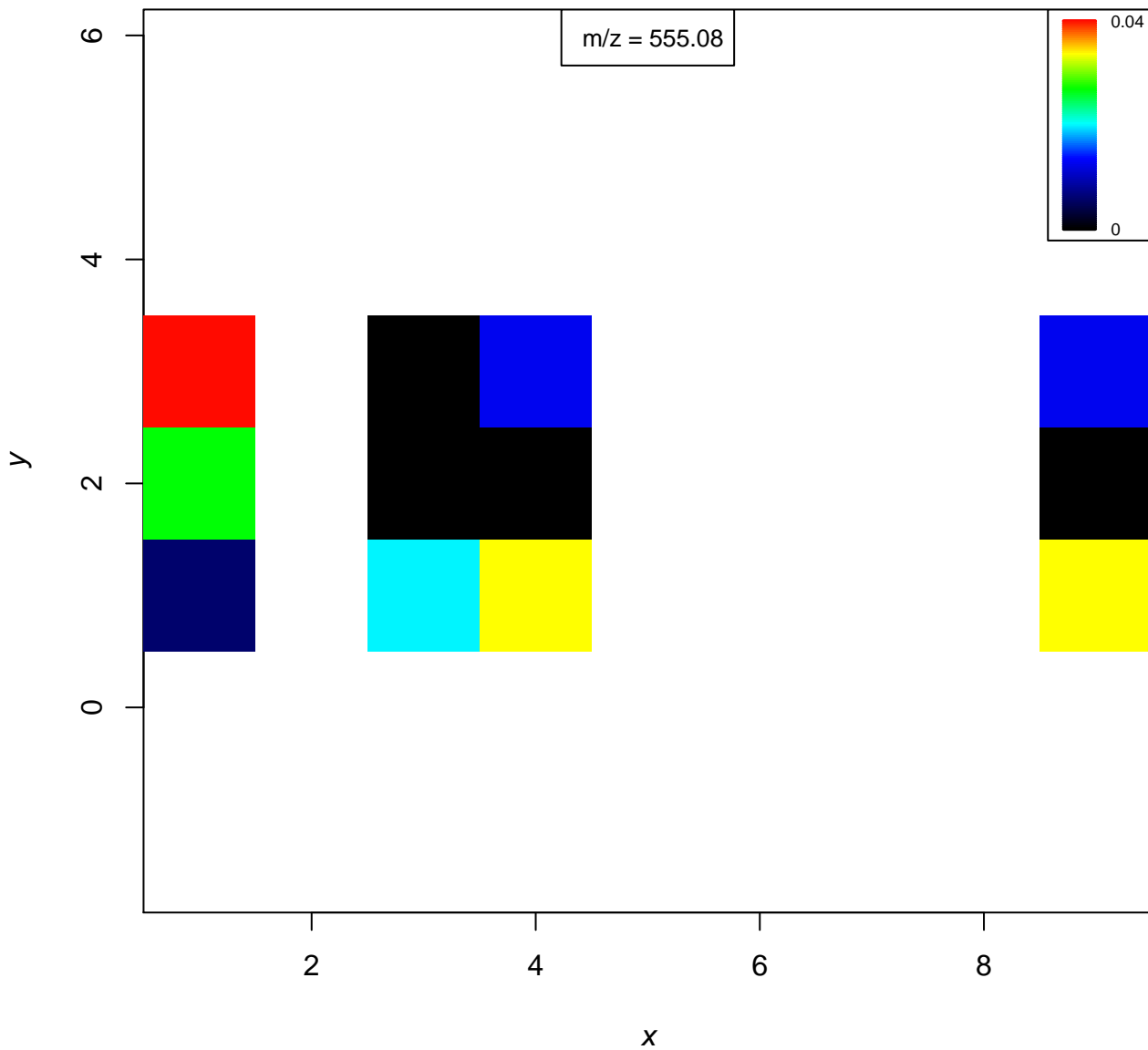
# 101.5: 101.5 ( $\pm 100$ ppm)



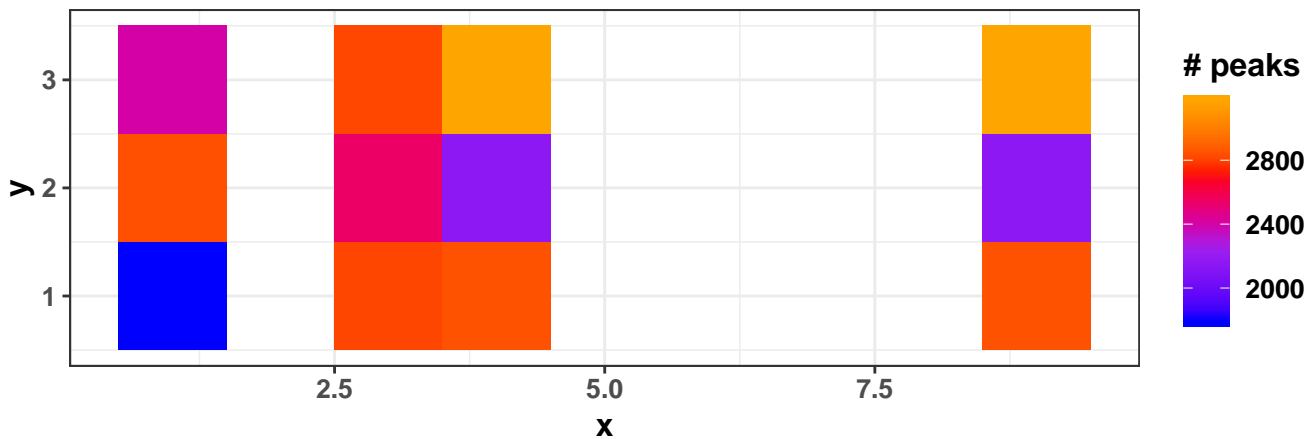
356.7: 356.7 ( $\pm 100$  ppm)



# 555.1: 555.1 ( $\pm 100$ ppm)

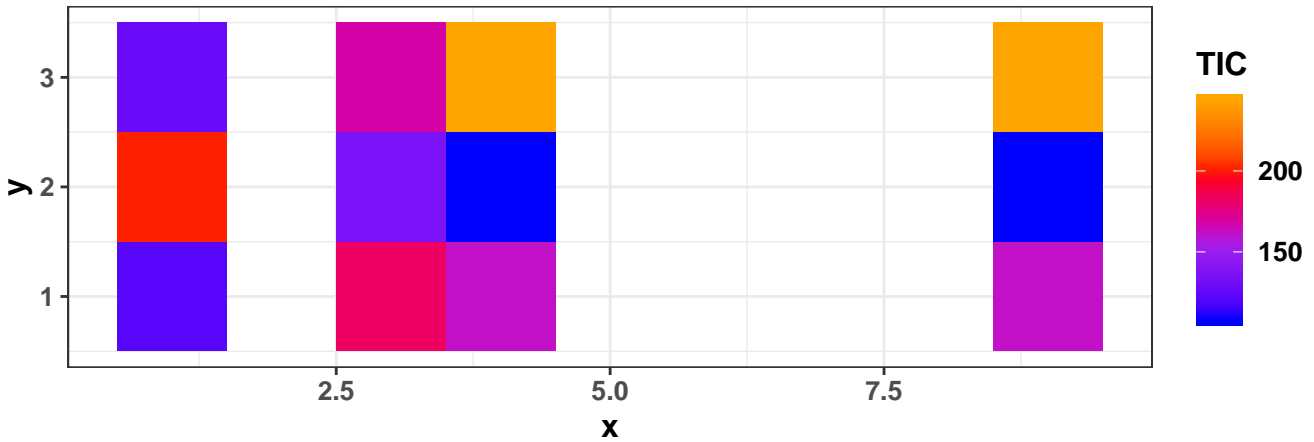


### Number of peaks per spectrum

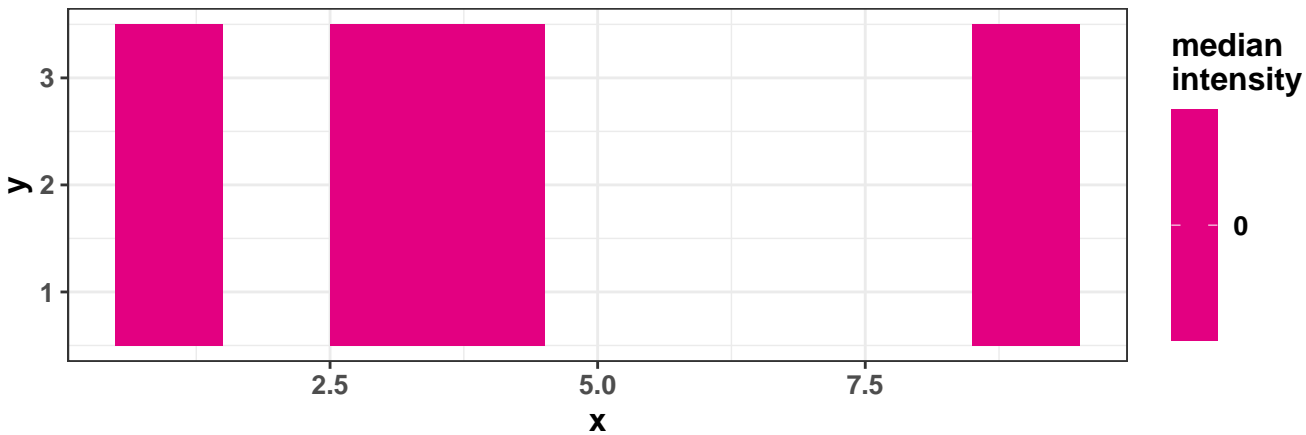




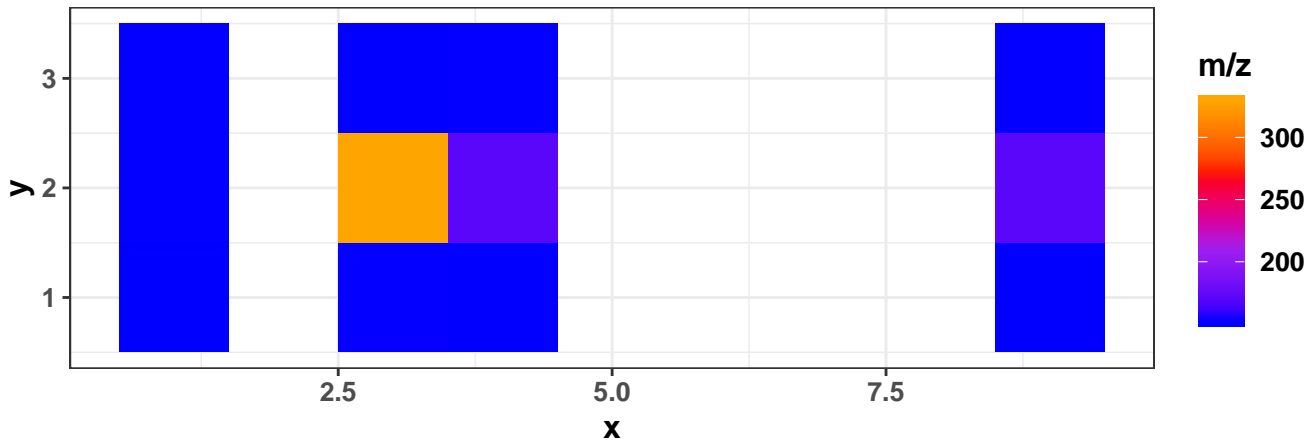
# Total Ion Chromatogram



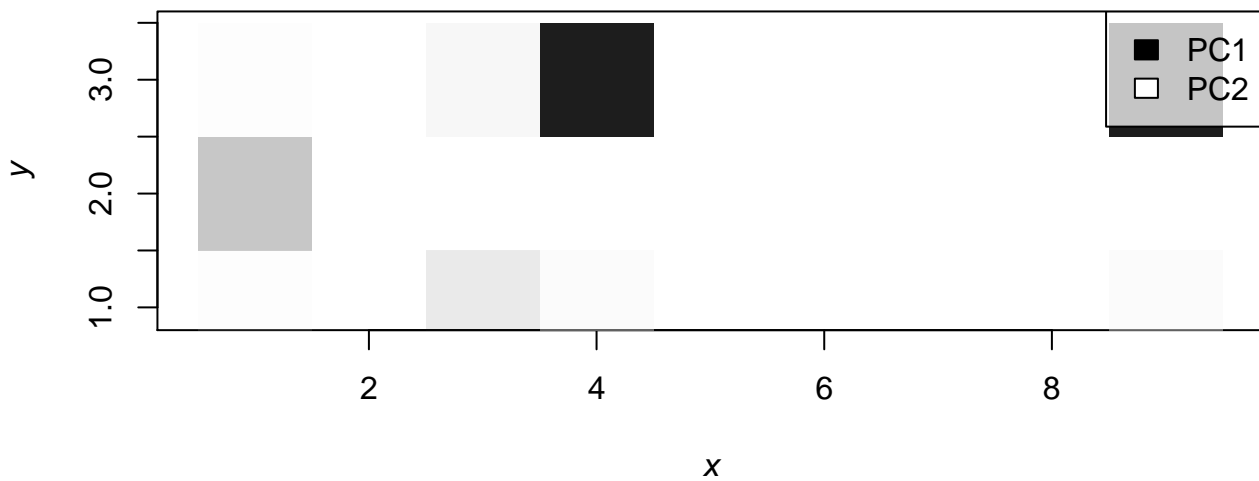
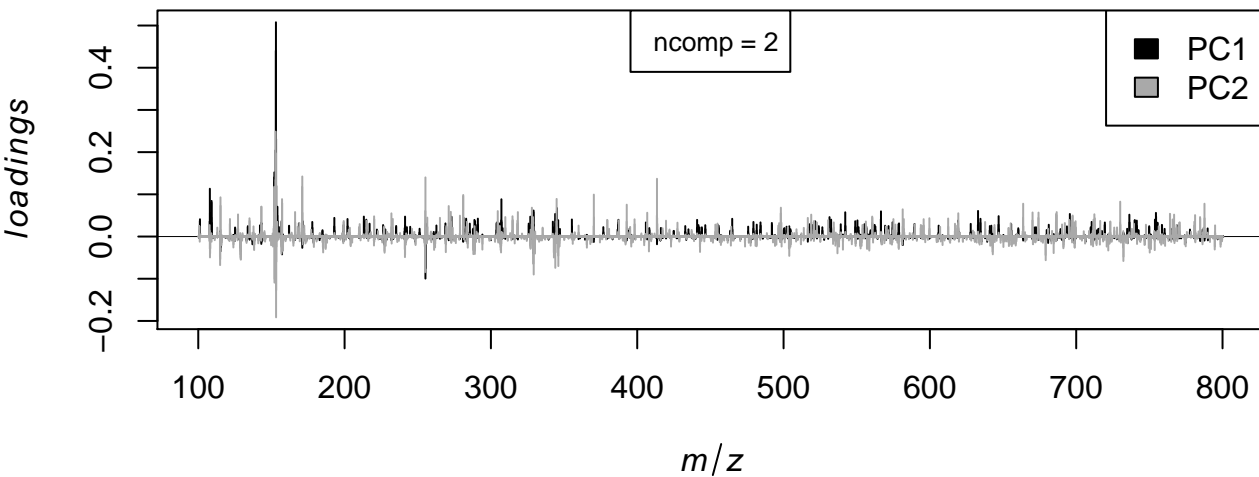
### Median intensity per pixel



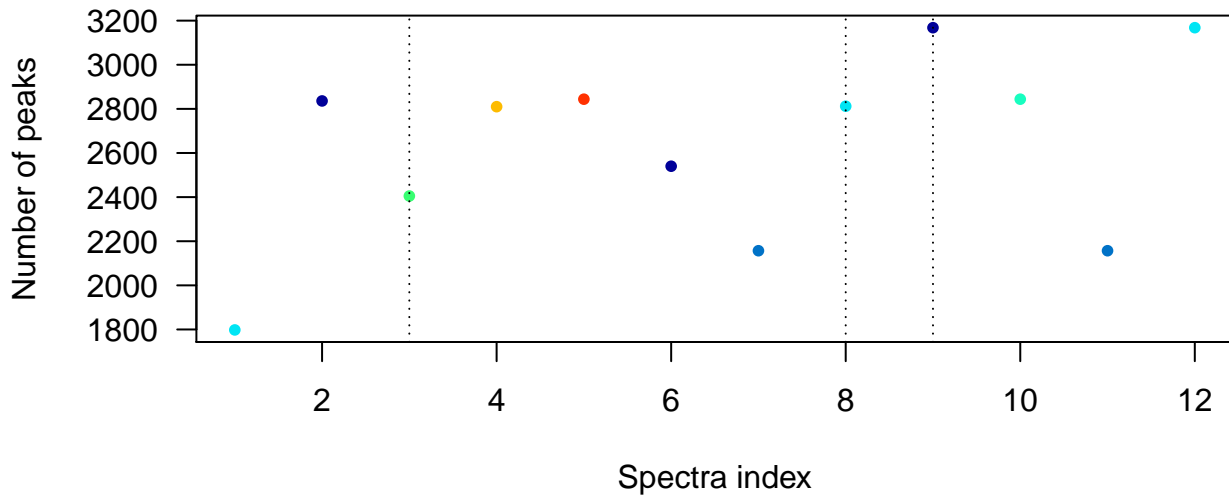
### Most abundant m/z in each spectrum



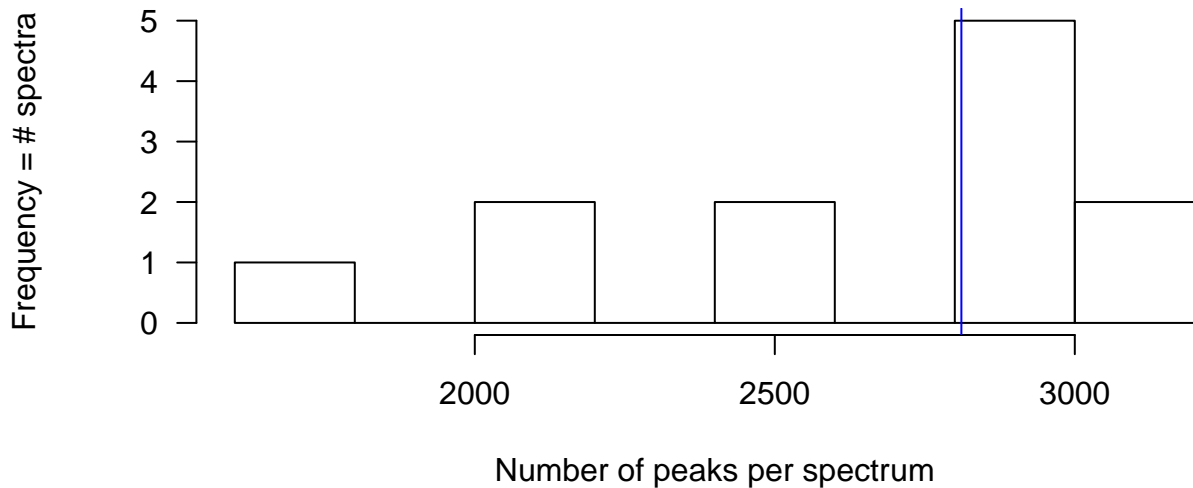
# PCA for two components



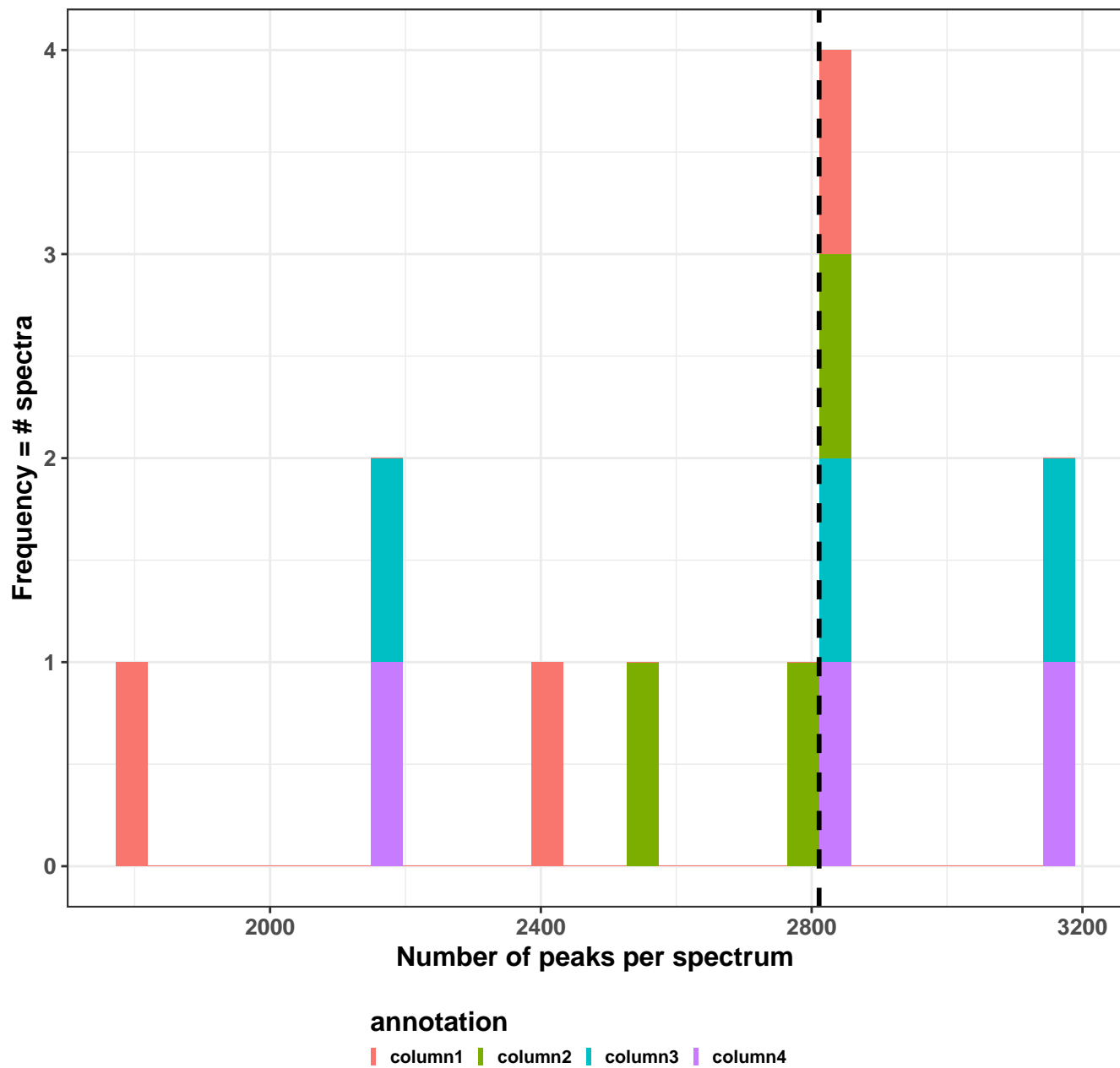
### Number of peaks per spectrum



### Number of peaks per spectrum

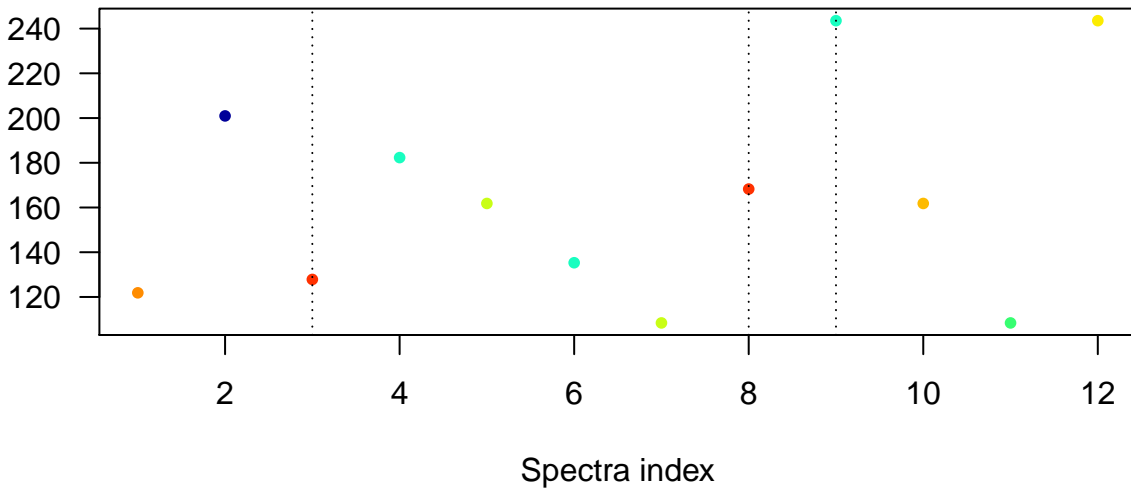


# Number of peaks per spectrum and annotation group



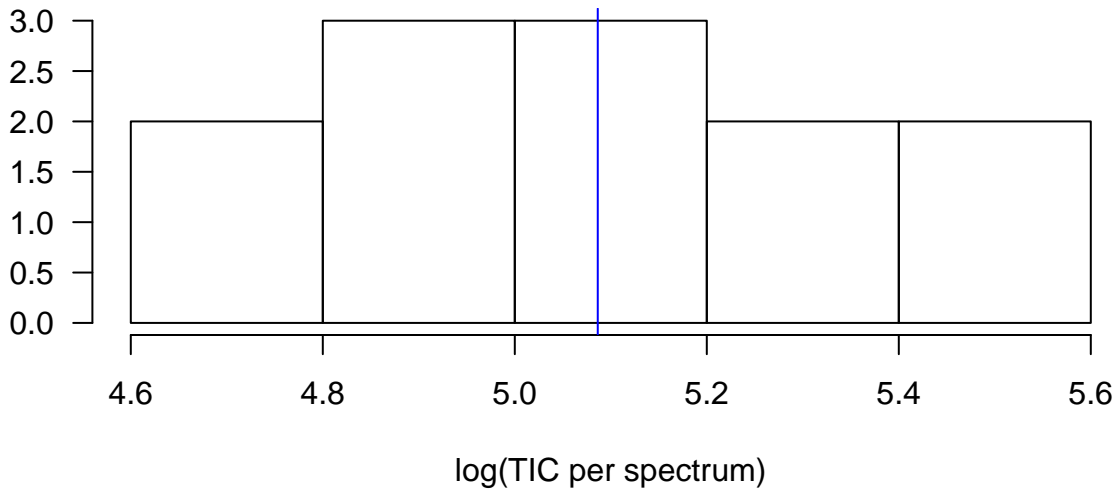
### TIC per spectrum

Total ion chromatogram intensity

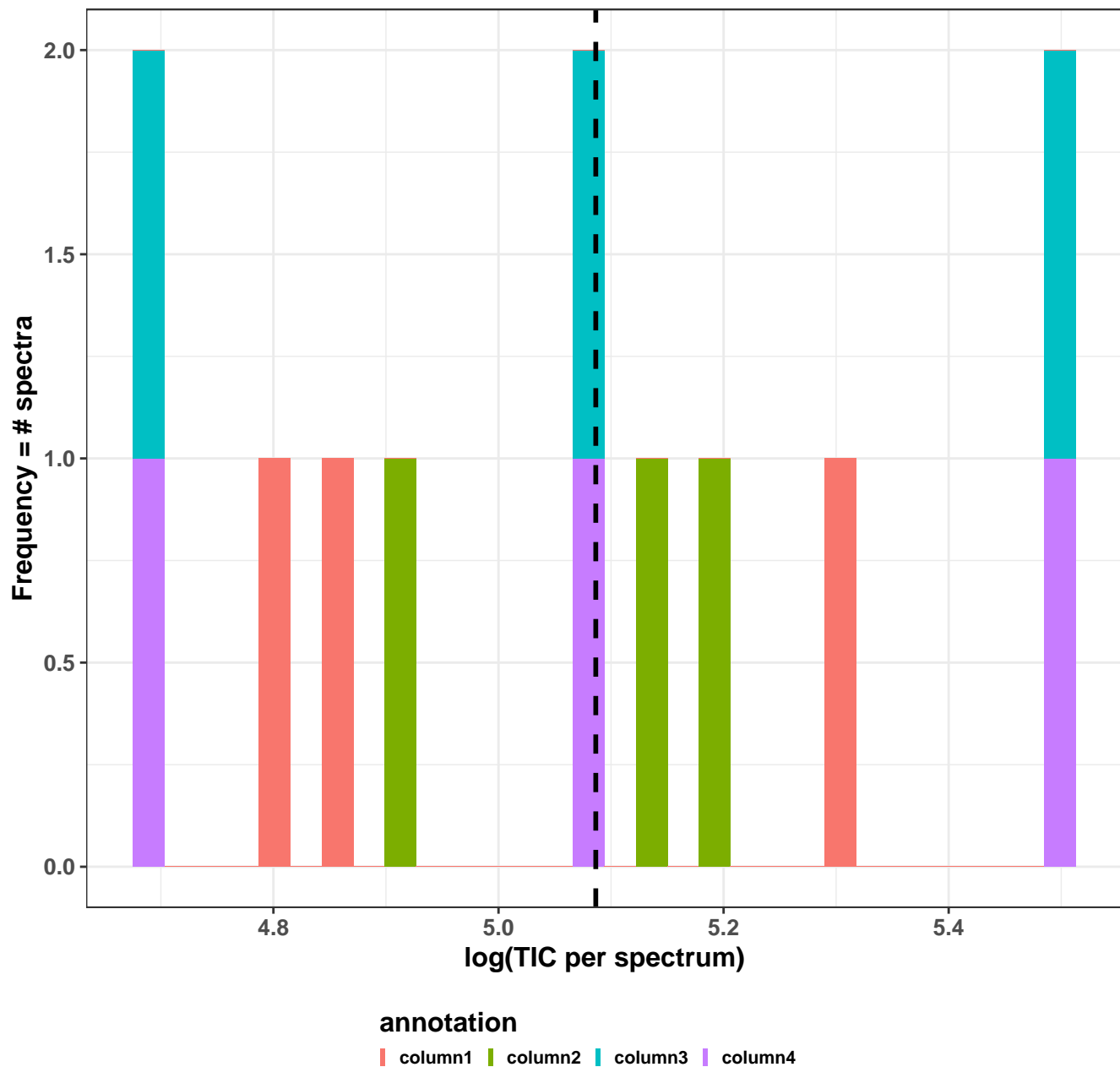


### TIC per spectrum

Frequency = # spectra

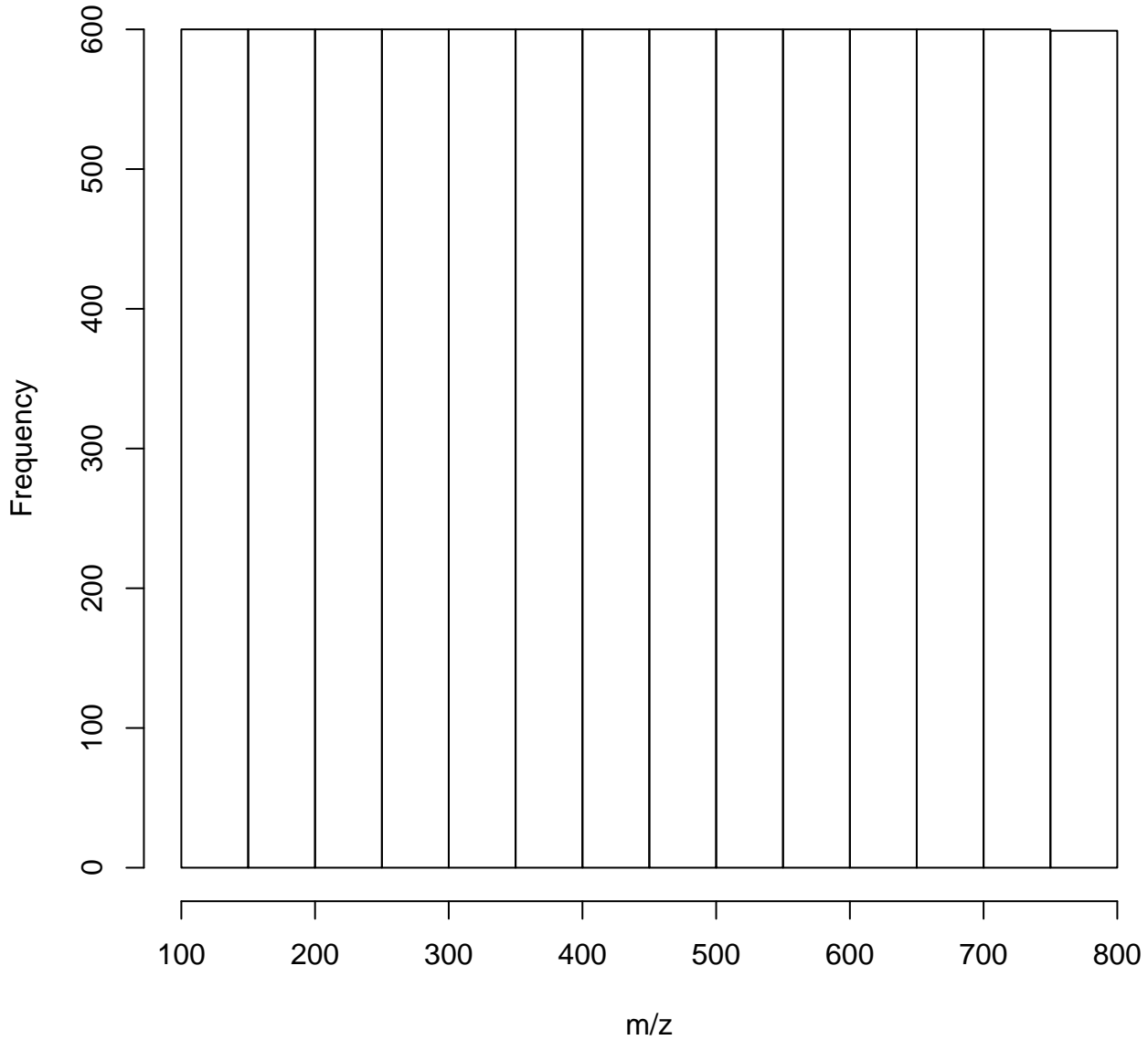


# TIC per spectrum and annotation group

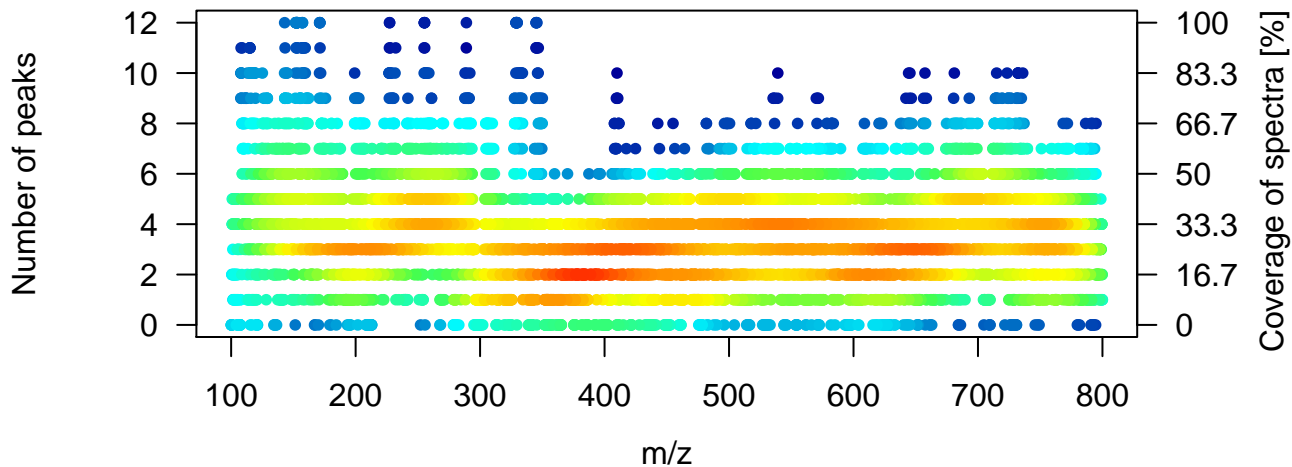




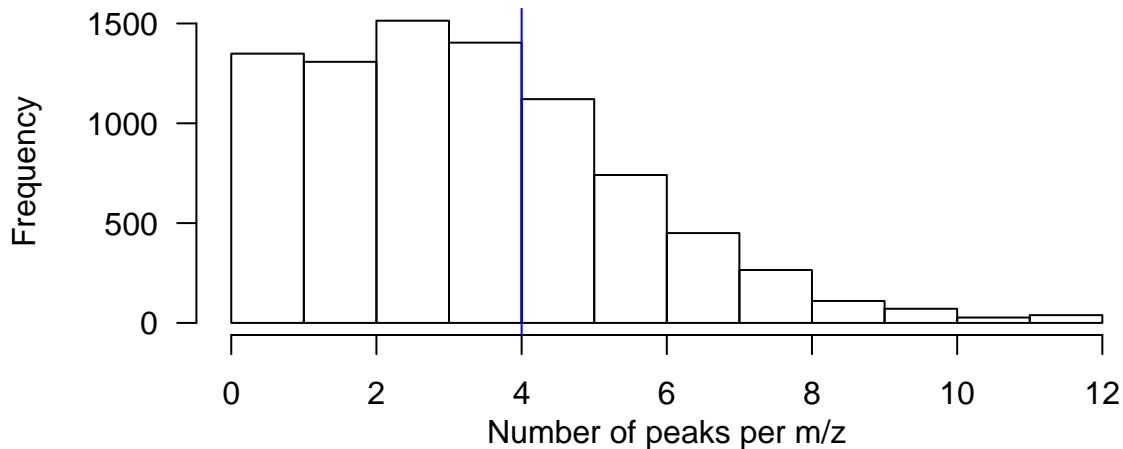
# Histogram of m/z values



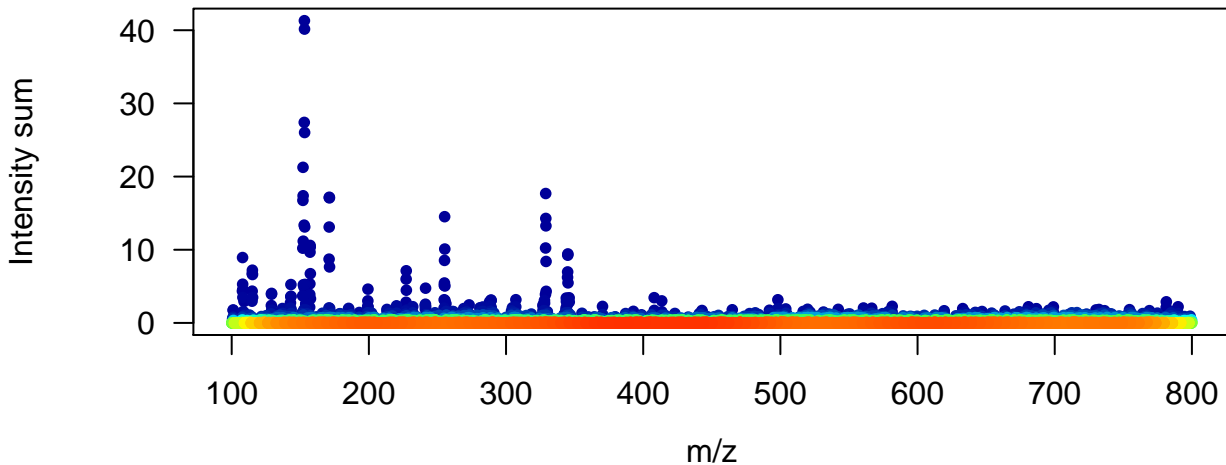
### Number of peaks per m/z



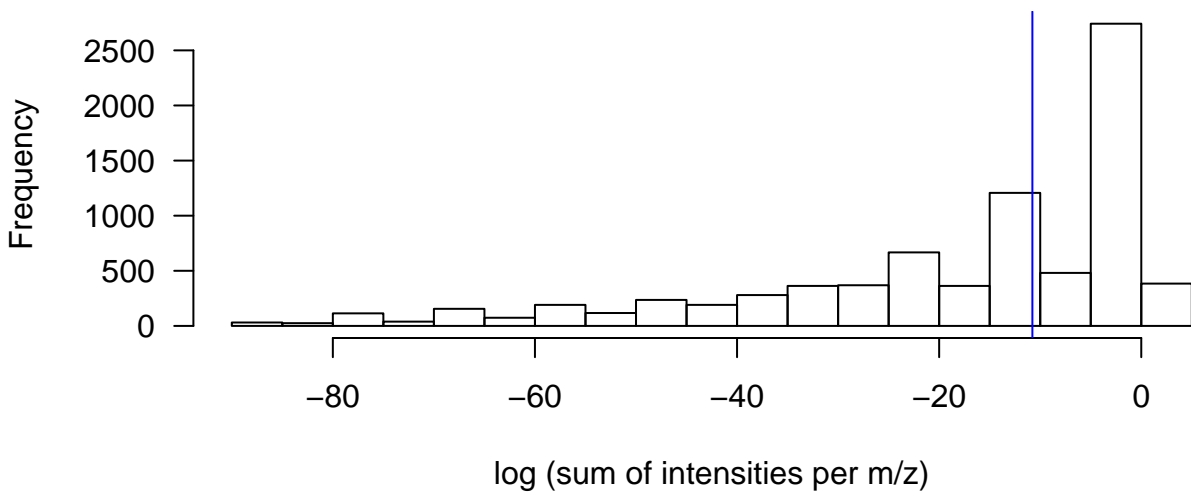
### Number of peaks per m/z



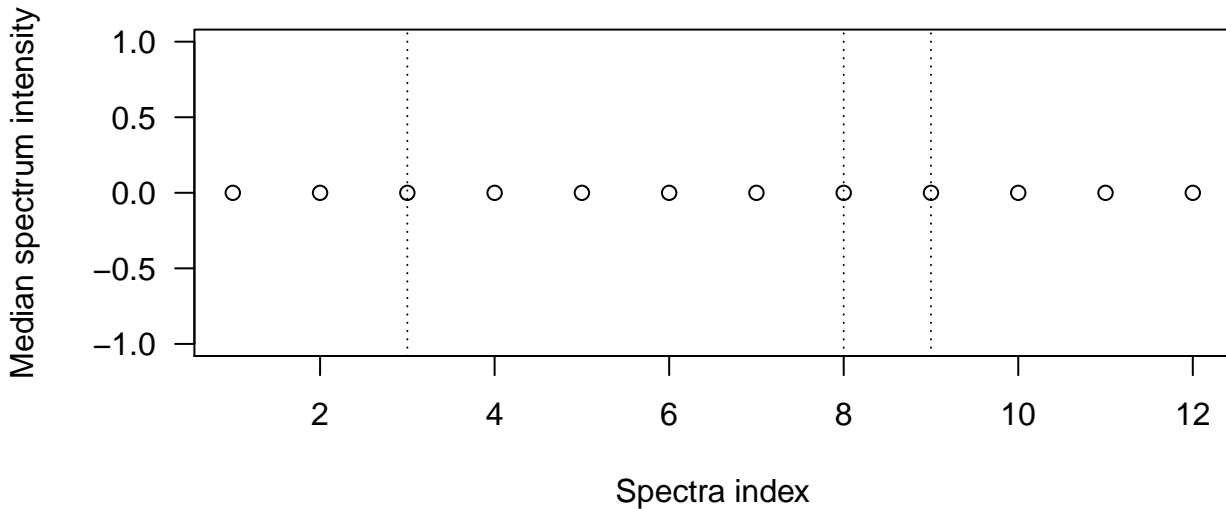
### Sum of intensities per m/z



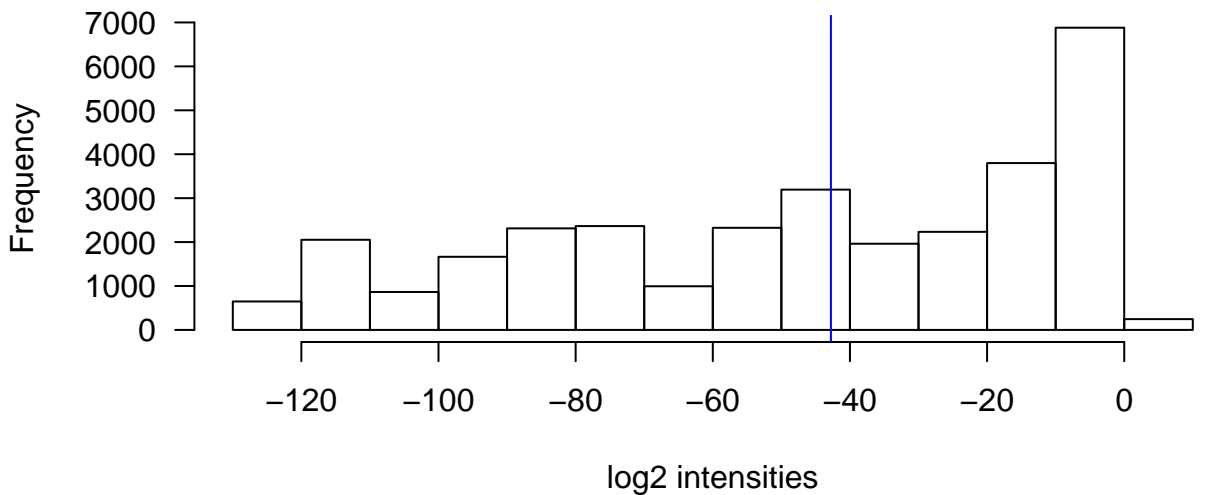
### Sum of intensities per m/z



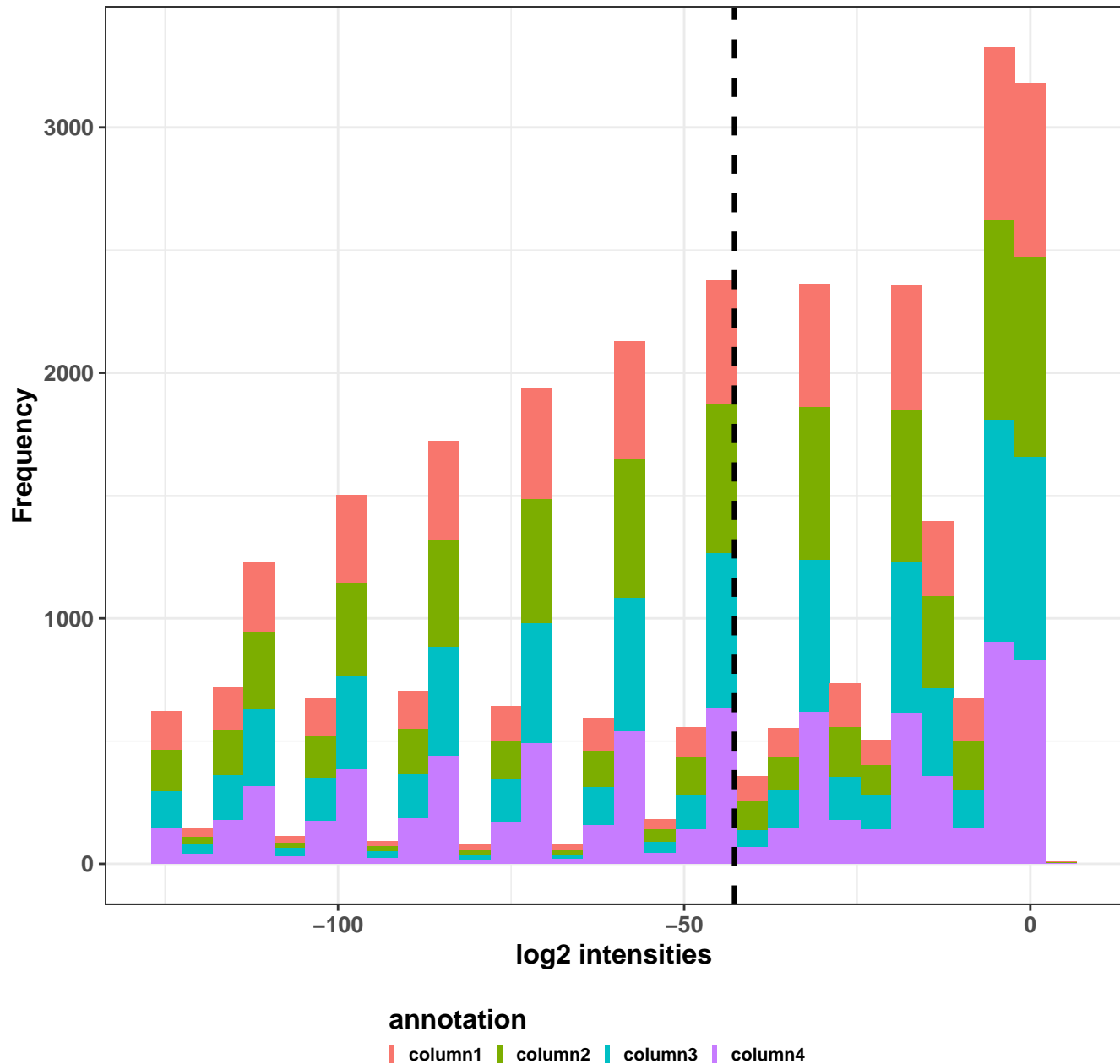
## Median intensity per spectrum



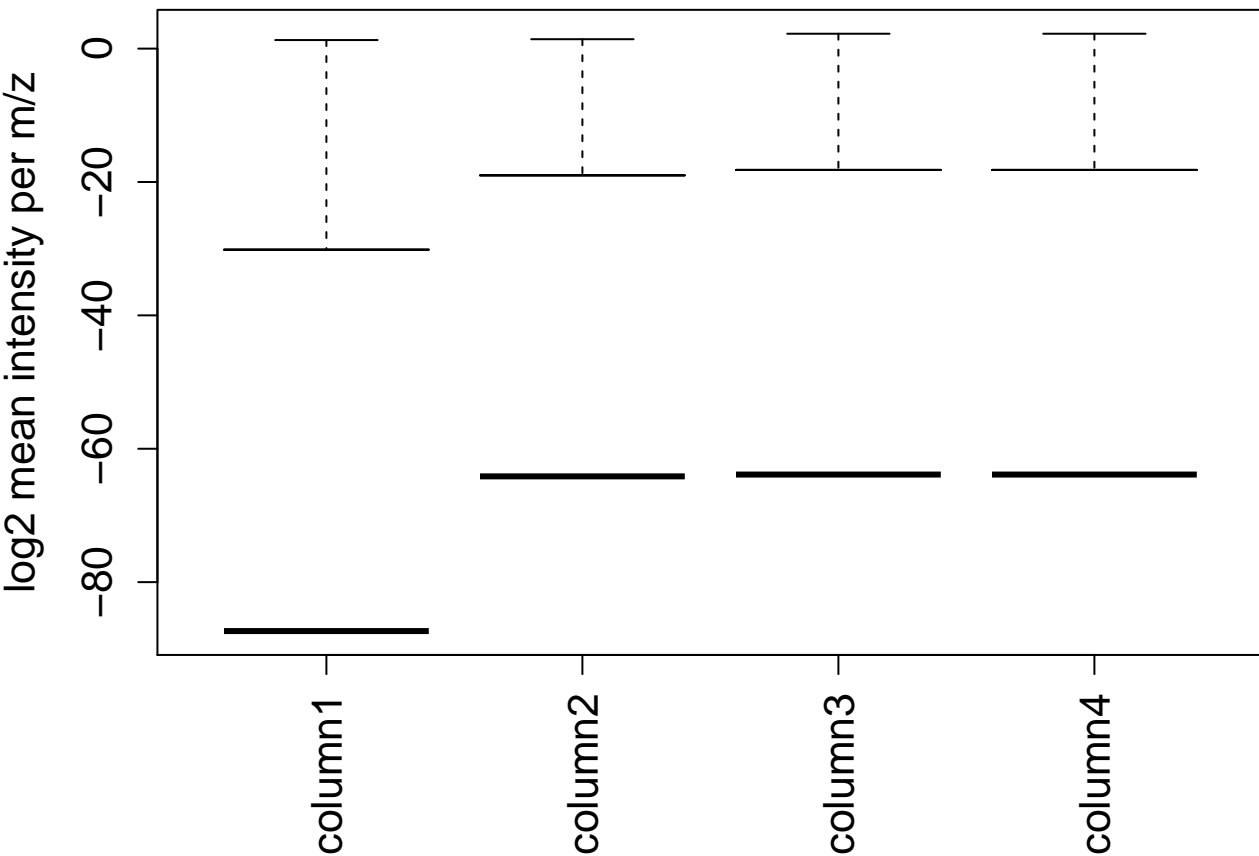
## Log2-transformed intensities



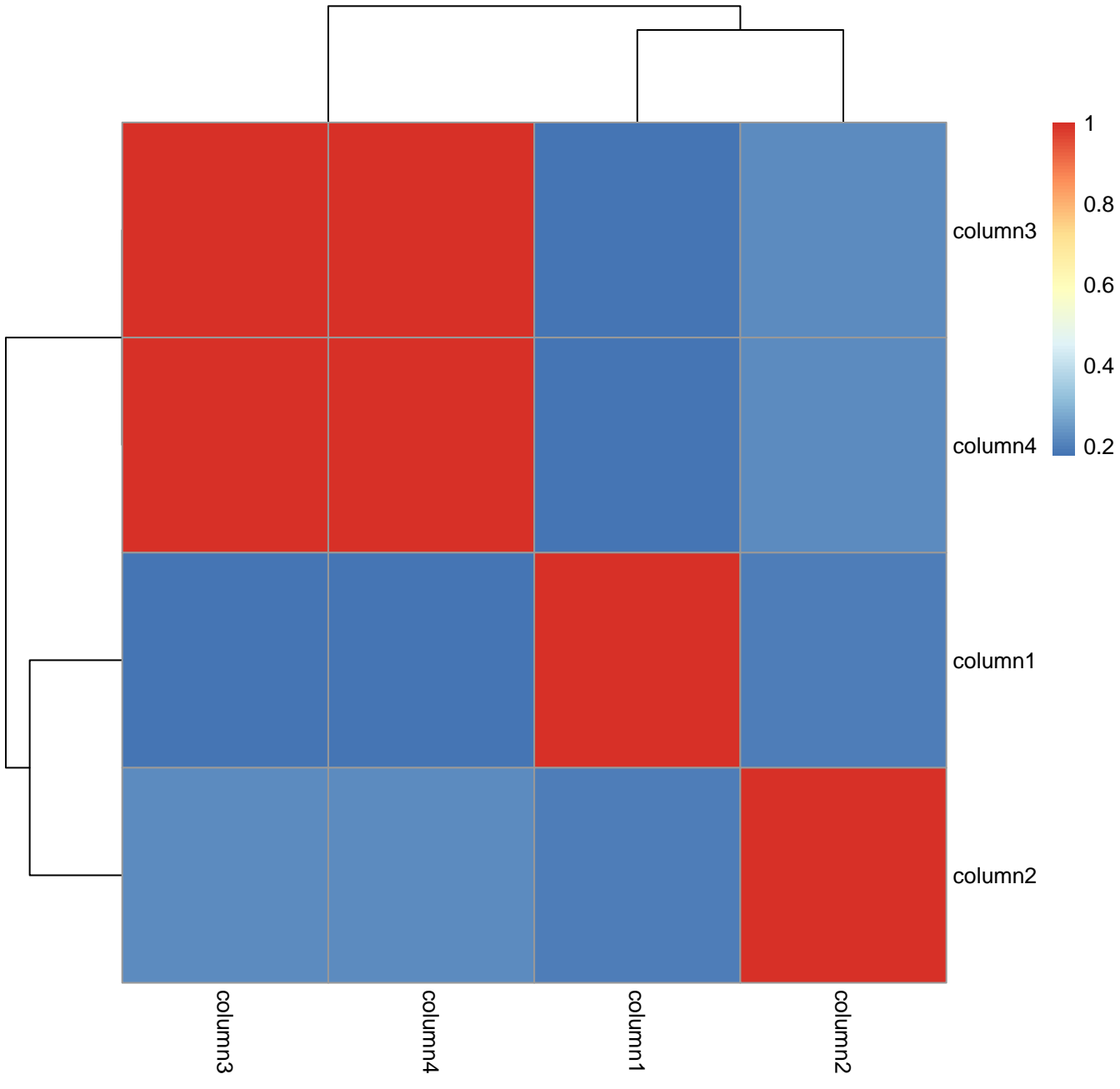
# Log2-transformed intensities per sample



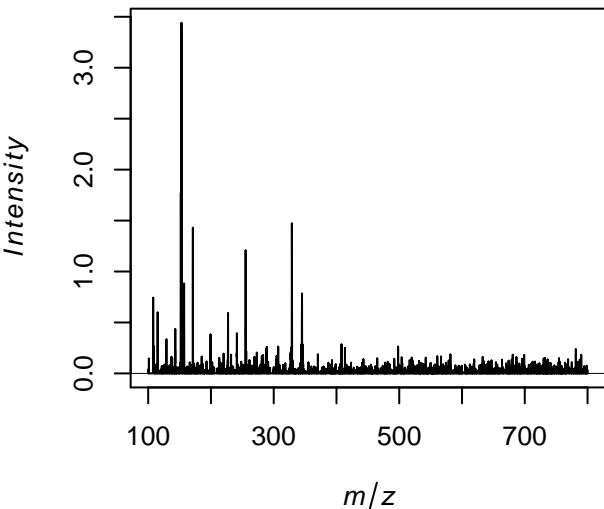
# Mean m/z intensities per annotation group



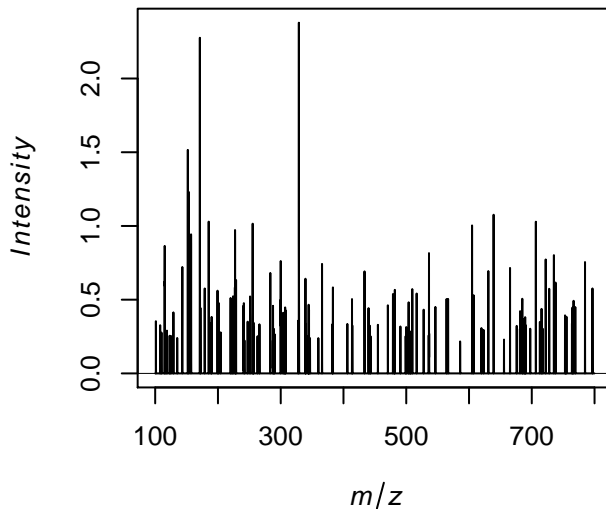
Pearson correlation on mean intensities



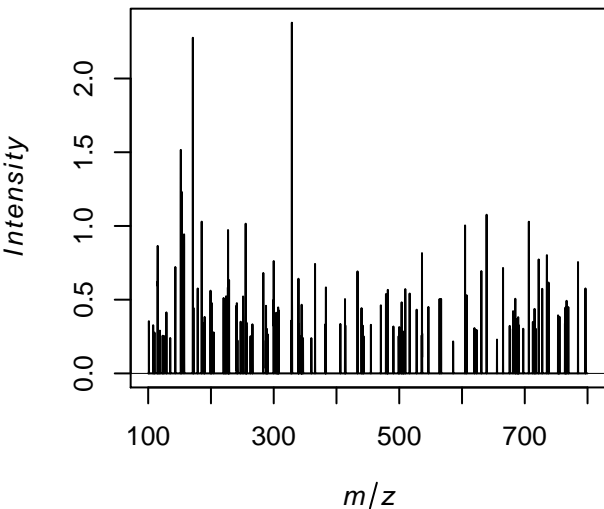
**Average spectrum**



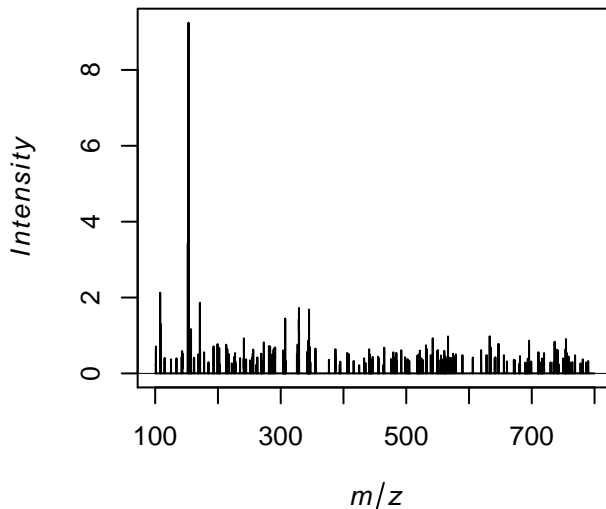
**Spectrum at x = 3, y = 2**



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



**Spectrum at x = 9, y = 3**



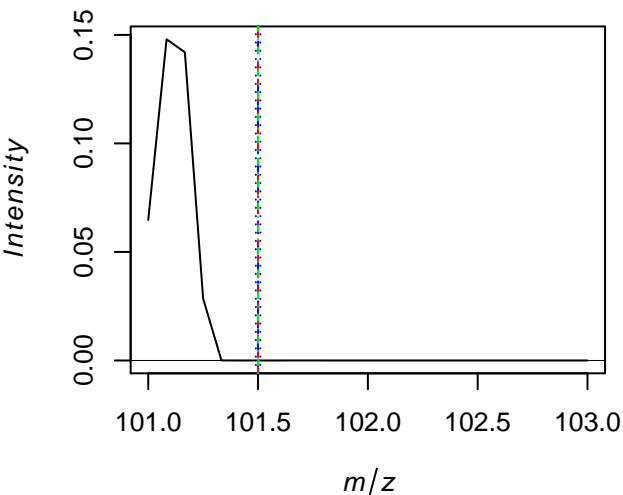


theor. m/z: 101.5

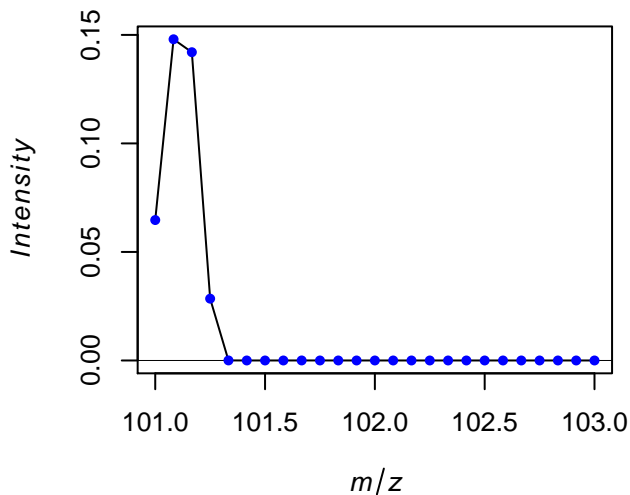
most abundant m/z: 101.5

closest m/z: 101.5

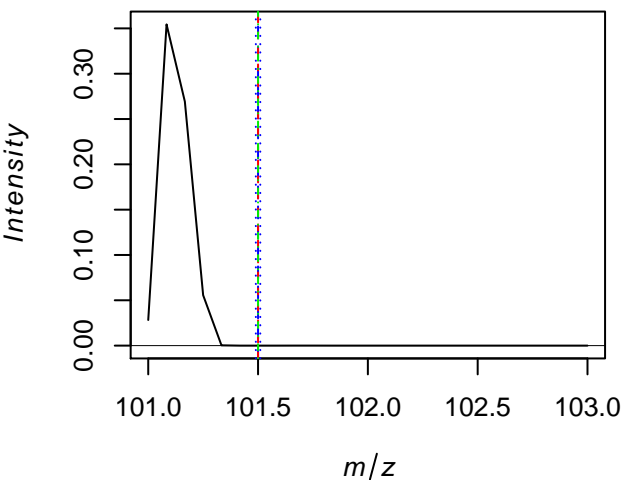
Average spectrum



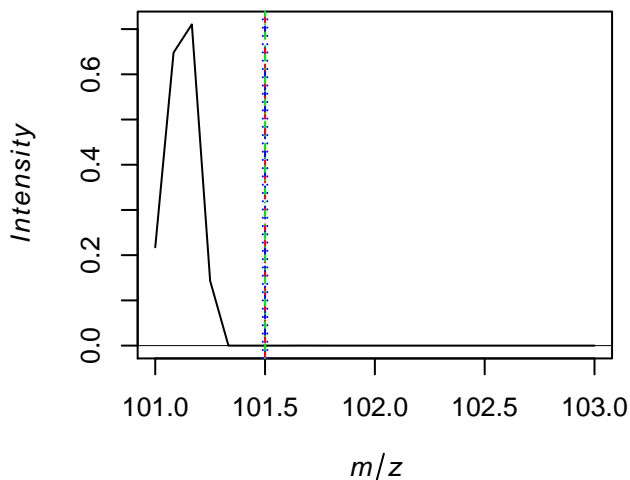
Average spectrum with data points



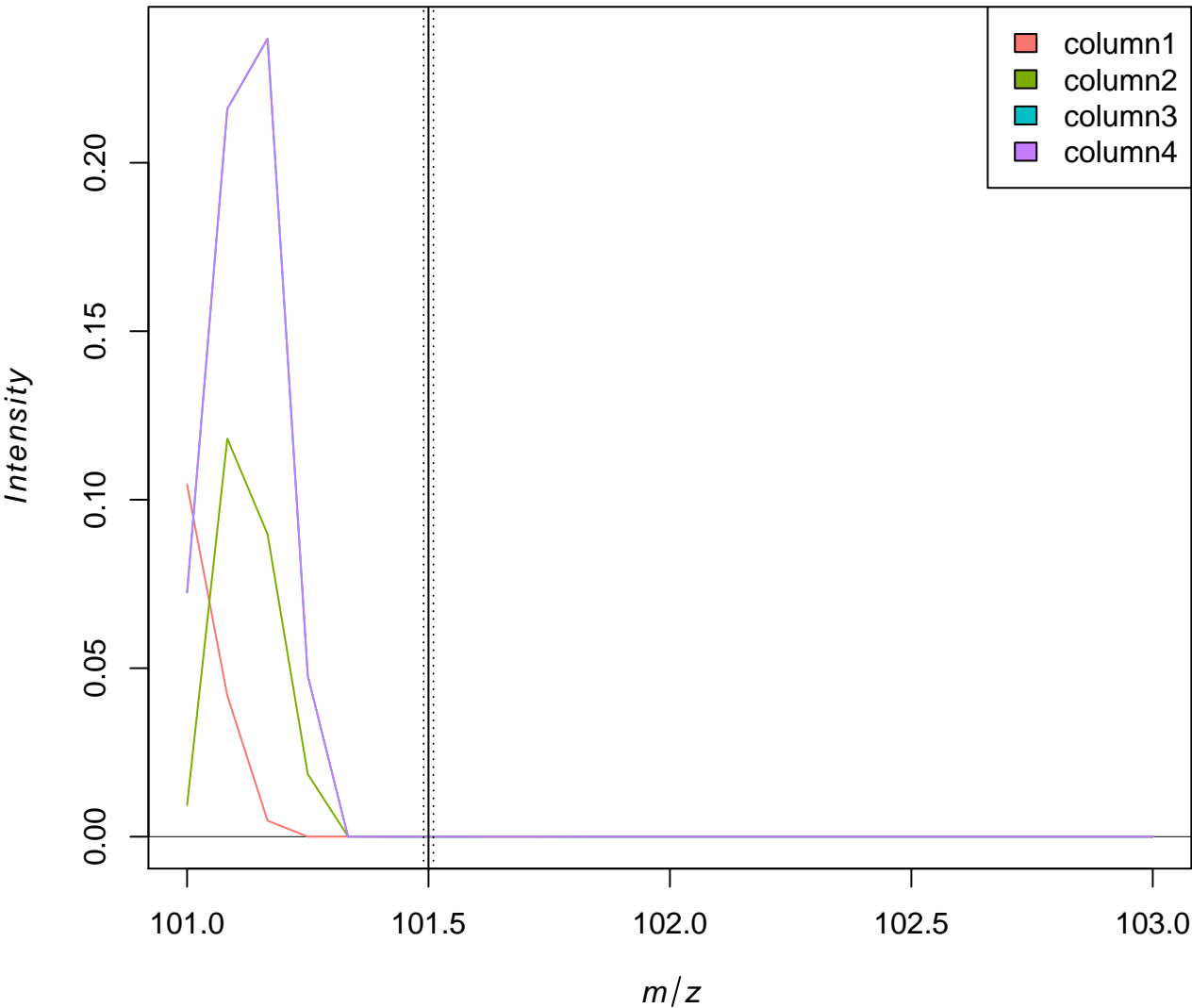
Spectrum at x = 3, y = 2



Spectrum at x = 9, y = 3



# Average spectrum per annotation group

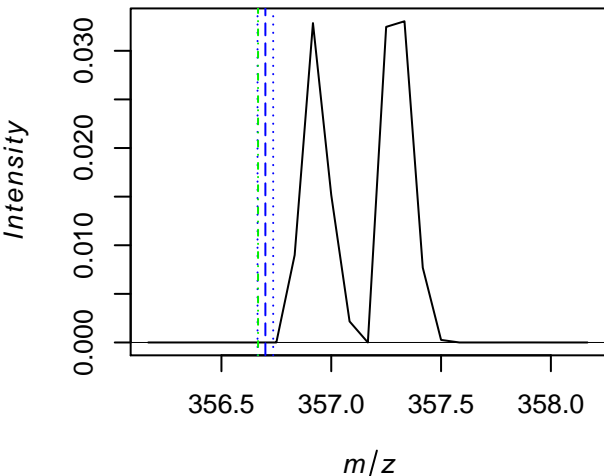


theor. m/z: 356.7

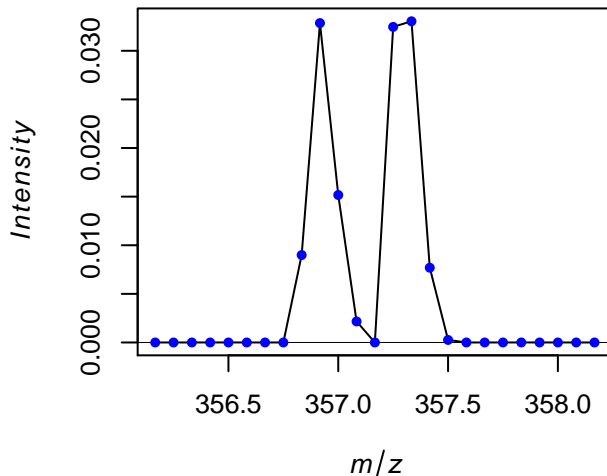
most abundant m/z: NA

closest m/z: 356.667

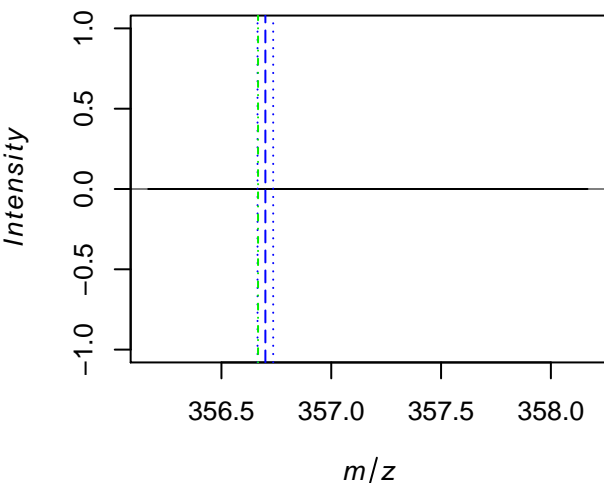
Average spectrum



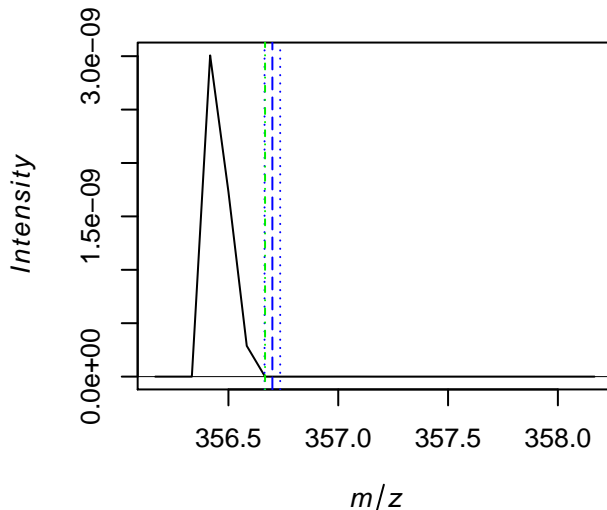
Average spectrum with data points



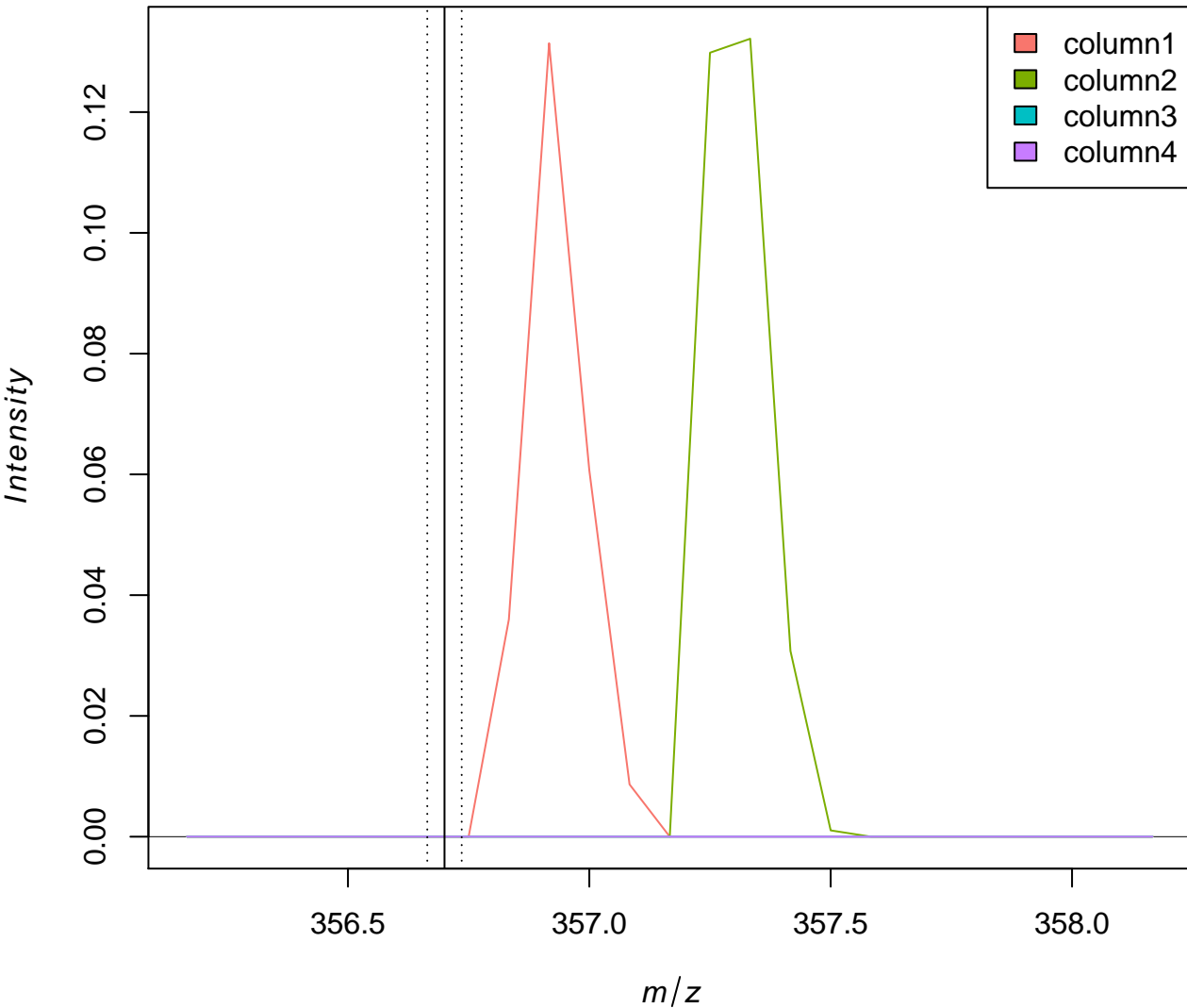
Spectrum at x = 3, y = 2



Spectrum at x = 9, y = 3



# Average spectrum per annotation group

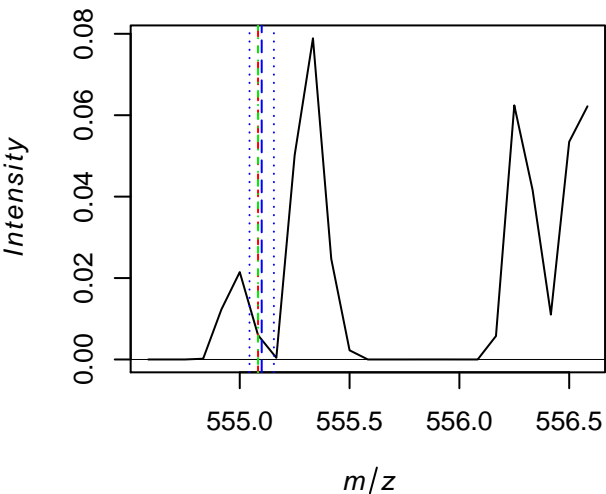


theor. m/z: 555.1

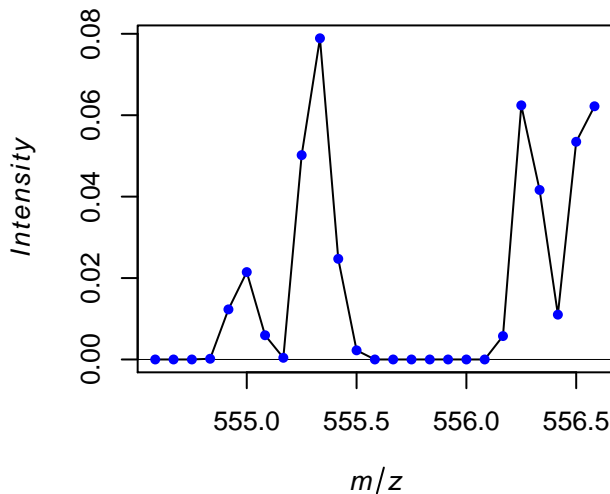
most abundant m/z: 555.0834

closest m/z: 555.0834

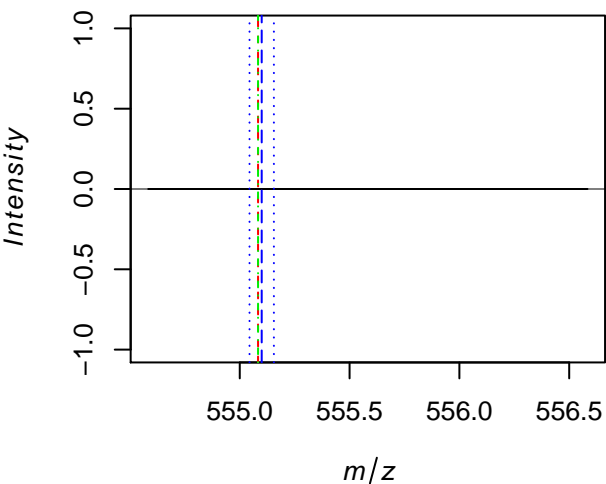
Average spectrum



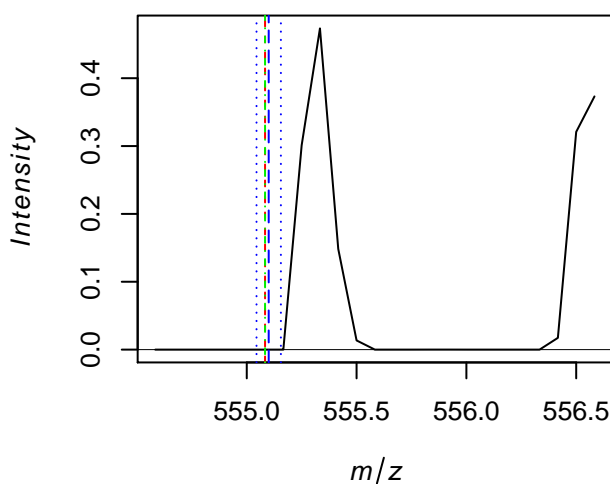
Average spectrum with data points



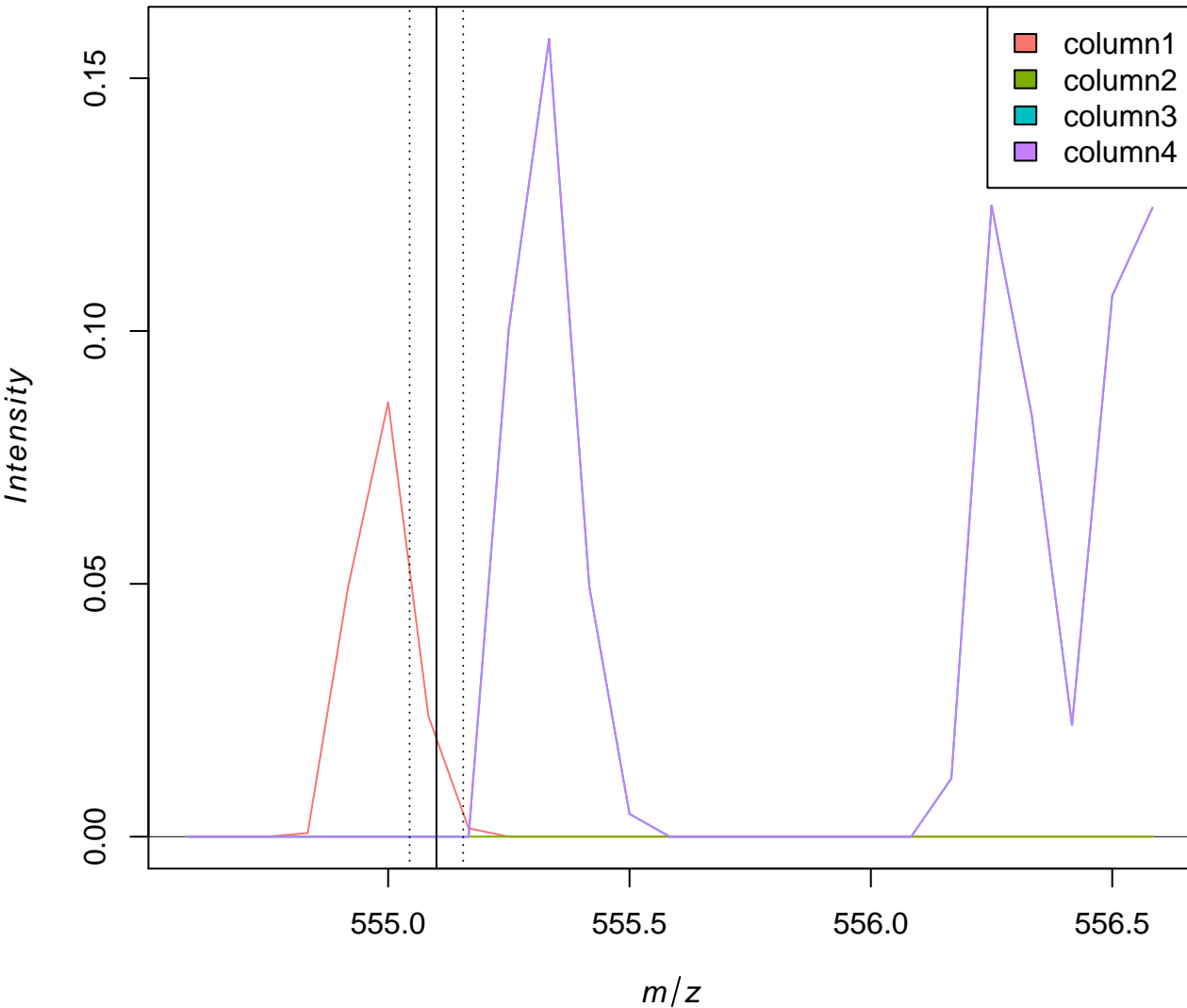
Spectrum at x = 3, y = 2



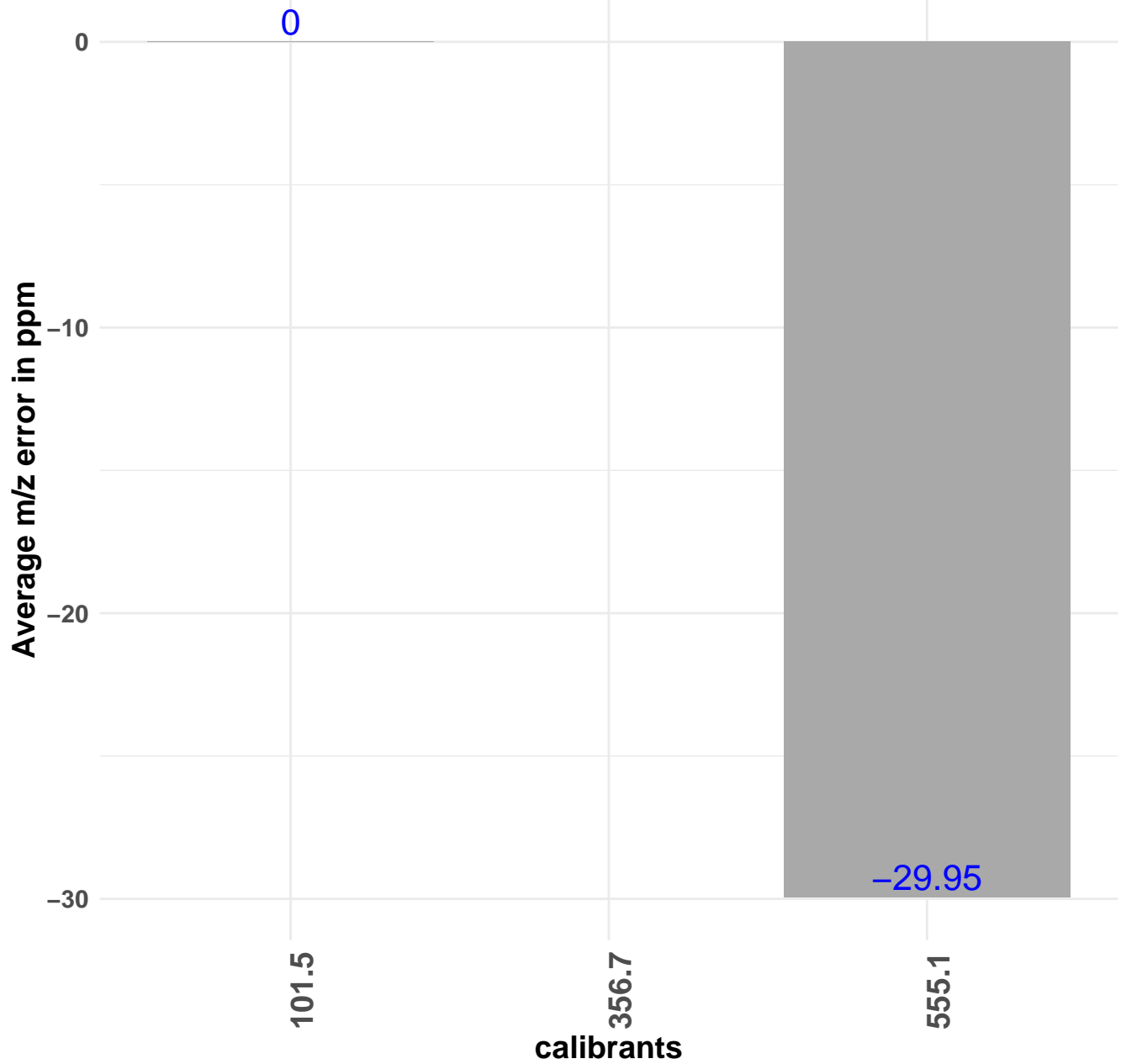
Spectrum at x = 9, y = 3



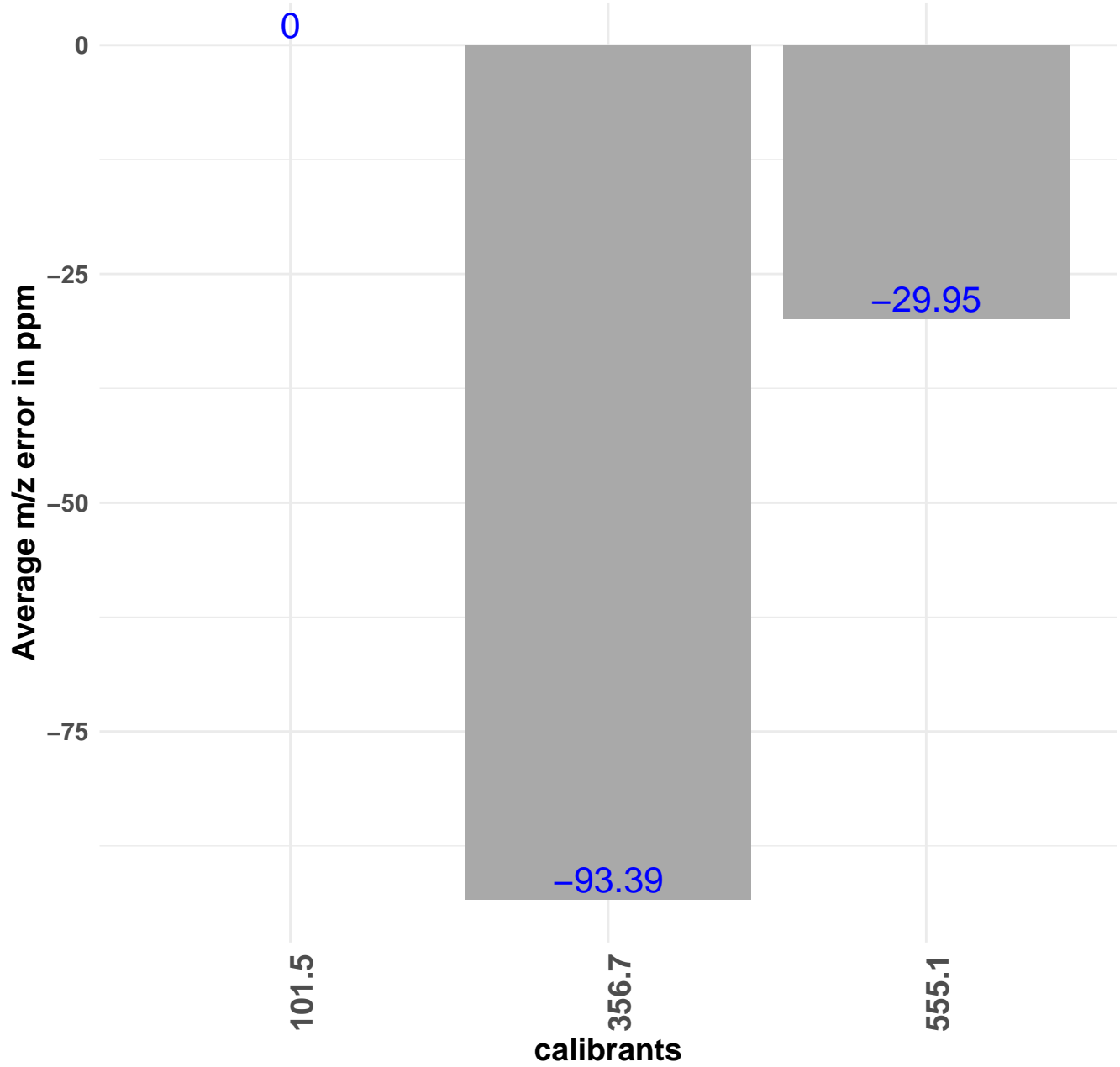
# Average spectrum per annotation group



# Average m/z error (max. average intensity vs. theor. calibrant m/z)



# Average m/z error (closest measured m/z vs. theor. calibrant m/z)





# Difference m/z with max. average intensity vs. theor. m/z (per spectrum)

