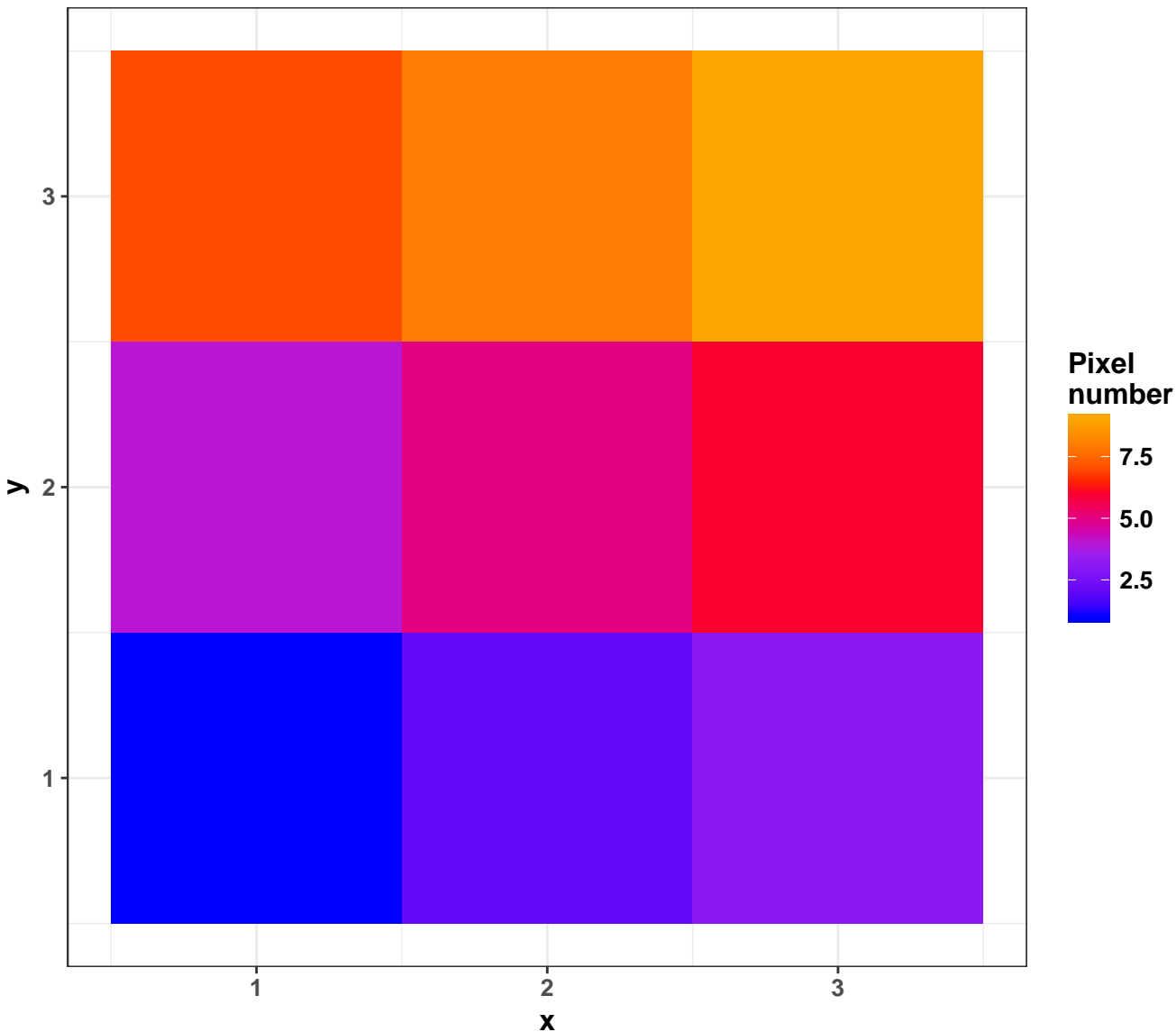


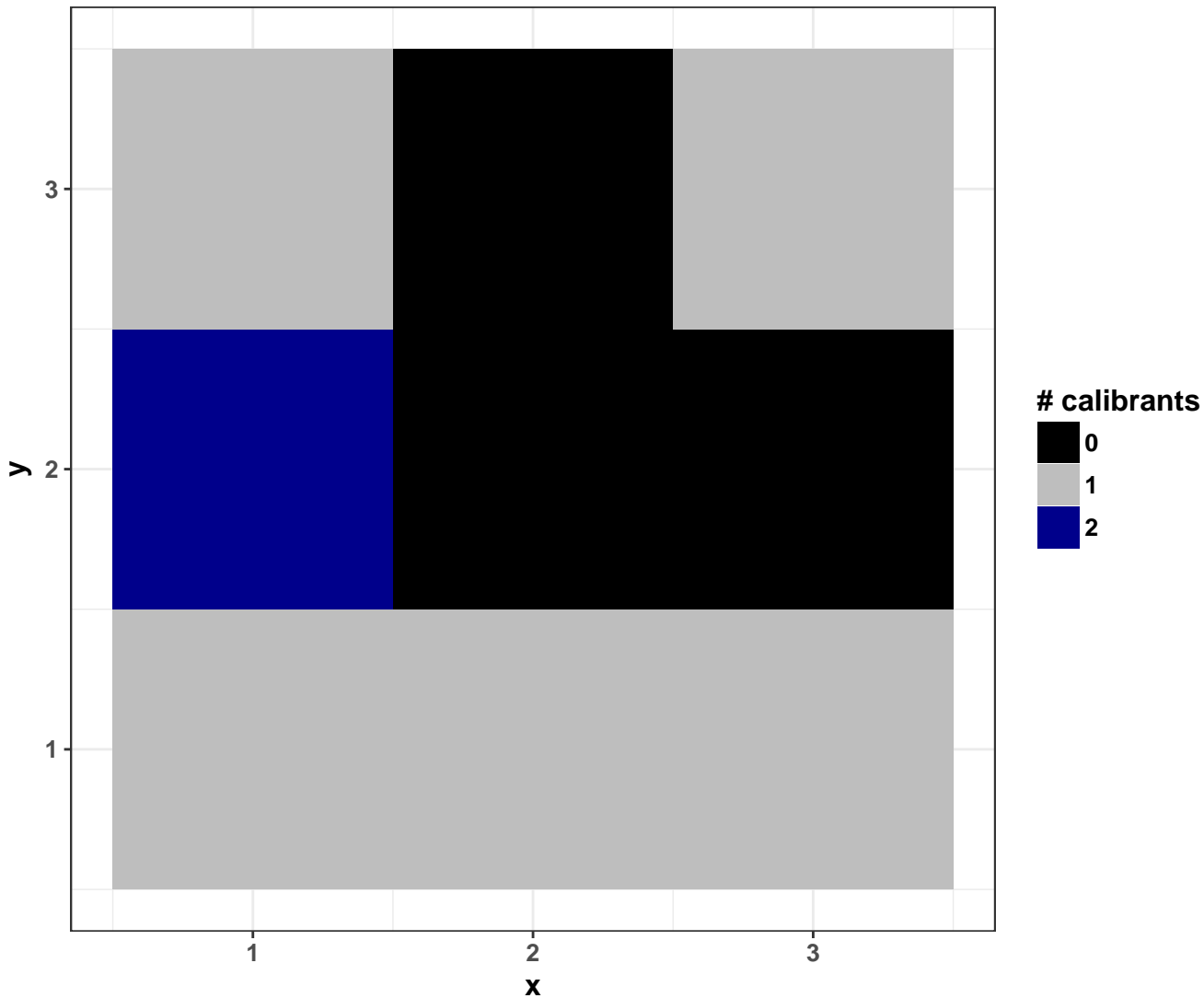
Testfile_imzml

properties	values
Number of m/z features	5199
Range of m/z values	100 – 799.81
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	0 – 9.24
Median of intensities	0
Intensities > 0	35.16 %
Number of empty spectra	0
Median TIC	161.81
Median # peaks per spectrum	1961
Normalization	FALSE
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
calibrants (#valid/#input) in inputcalibrantfile1.txt	3 / 3

Pixel order

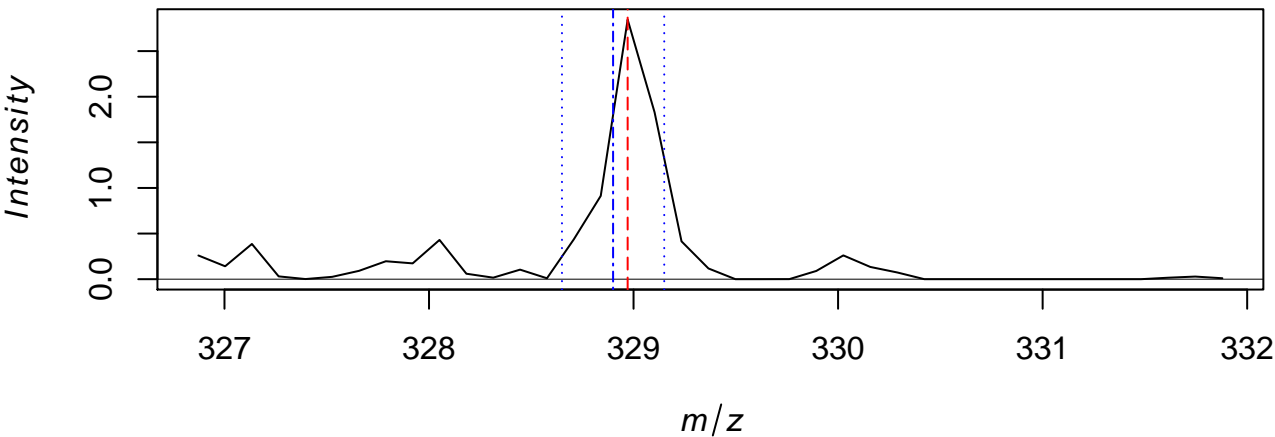


Number of calibrants per pixel (± 100 ppm)

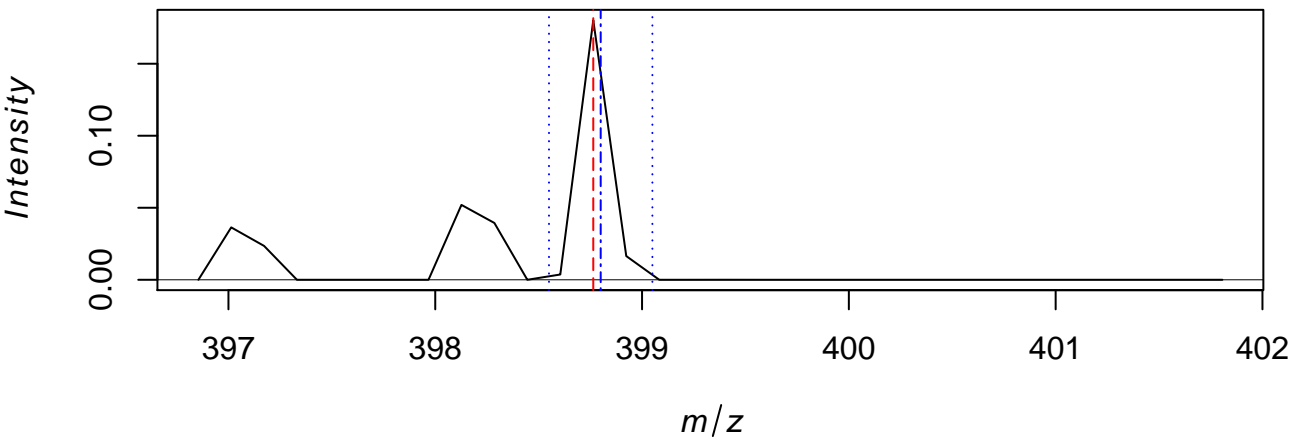


Control of fold change plot

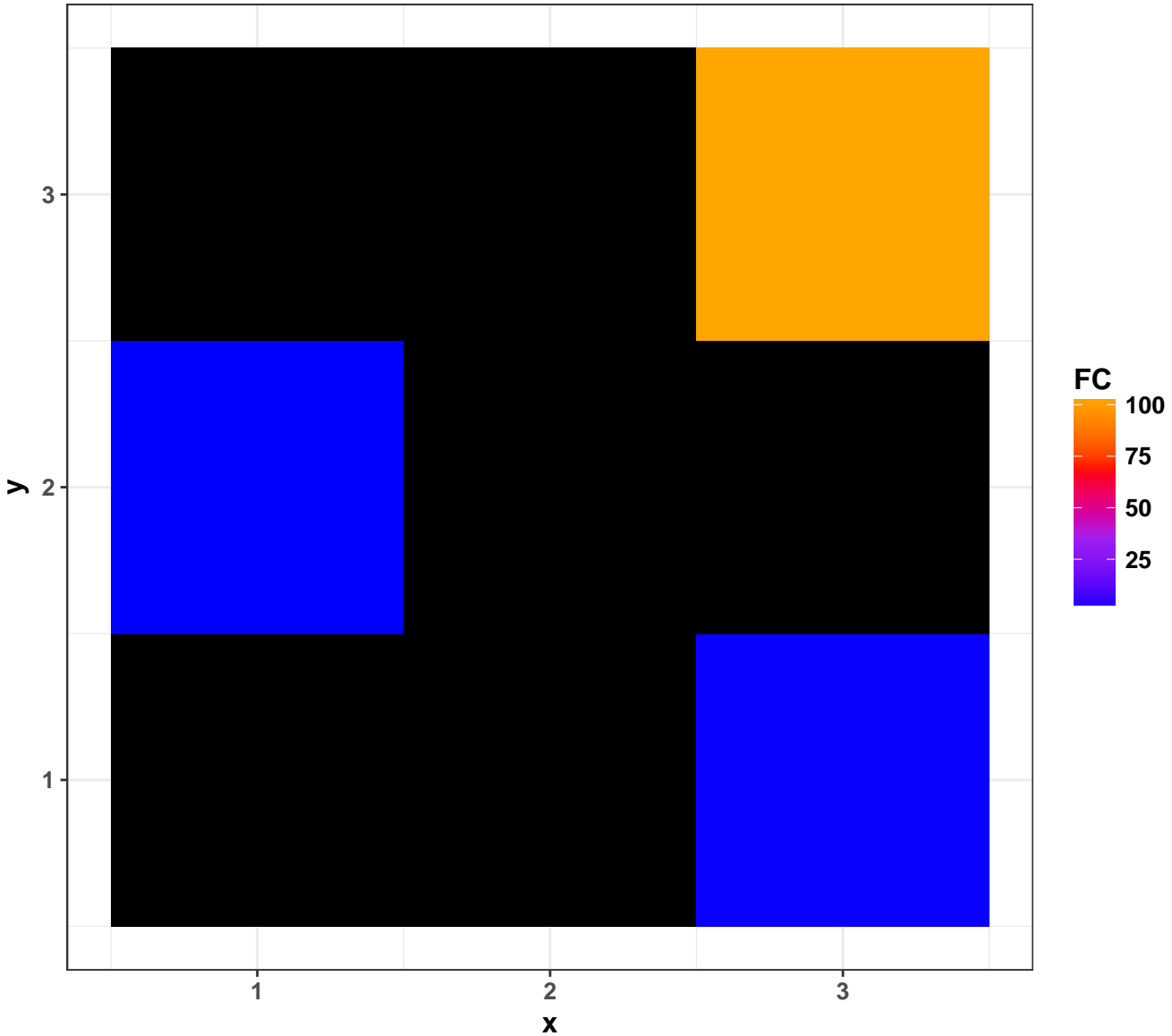
average spectrum 328.9 Da



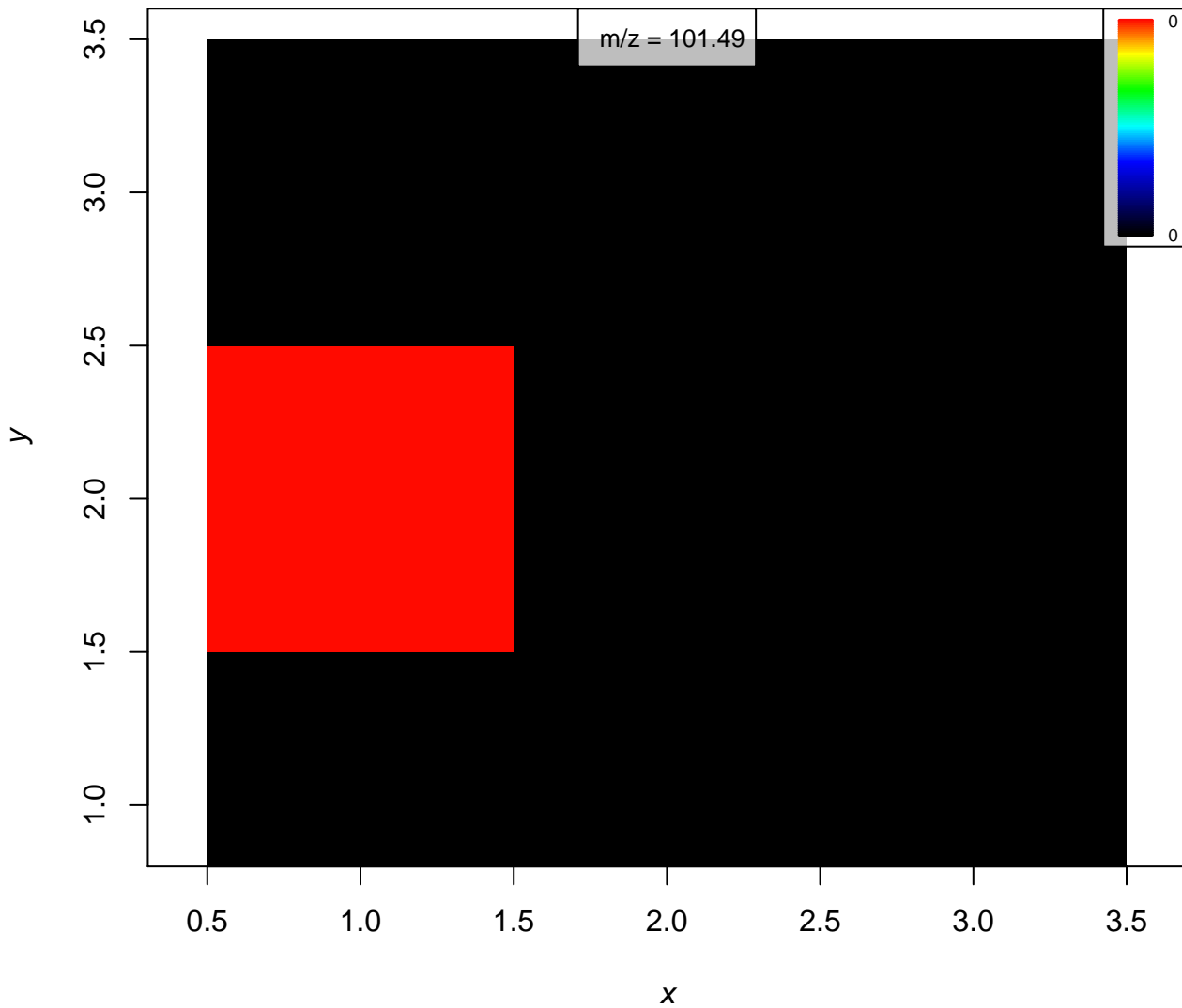
average spectrum 398.8 Da



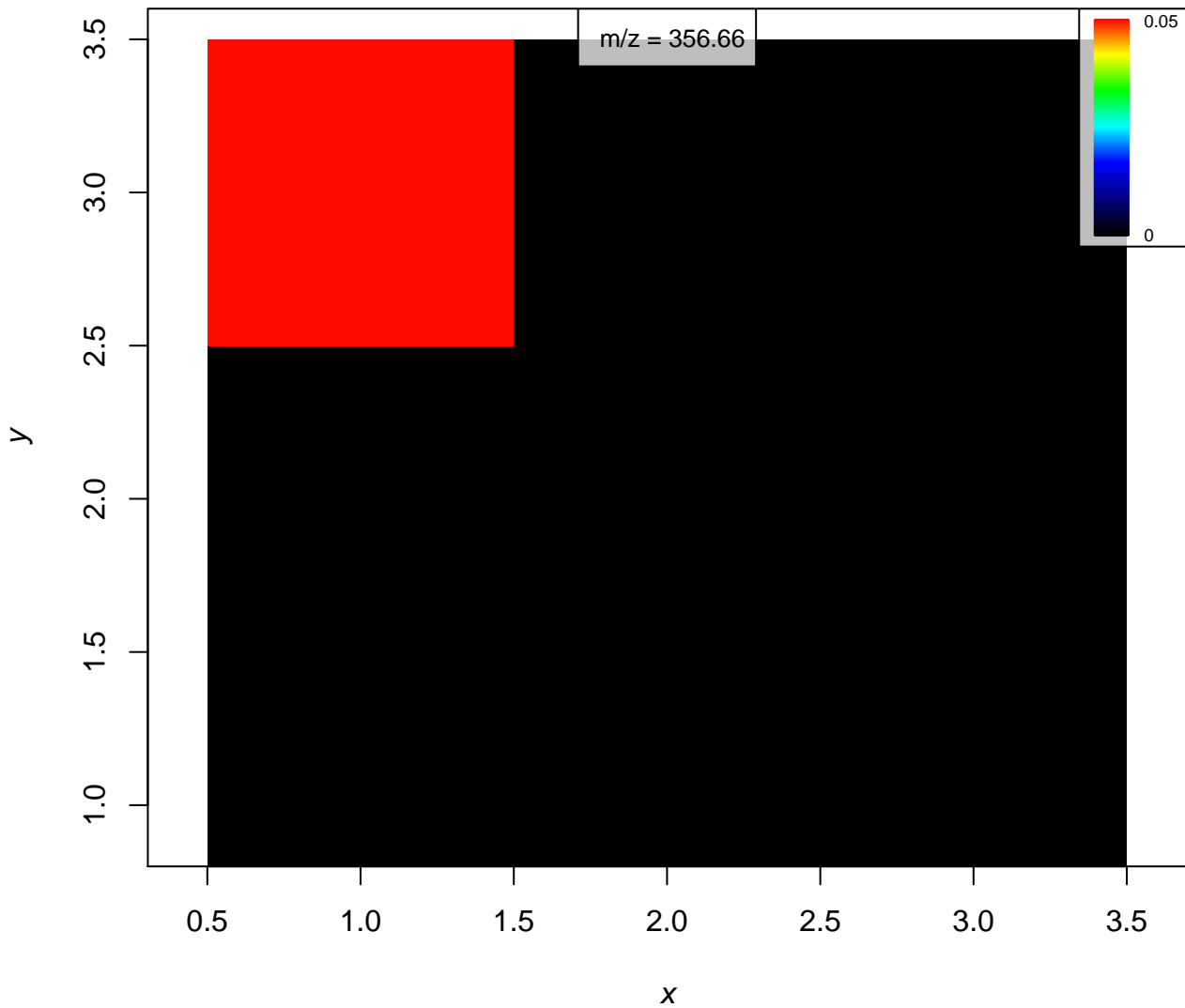
Ratio of mass1 (328.9) / mass2 (398.8)



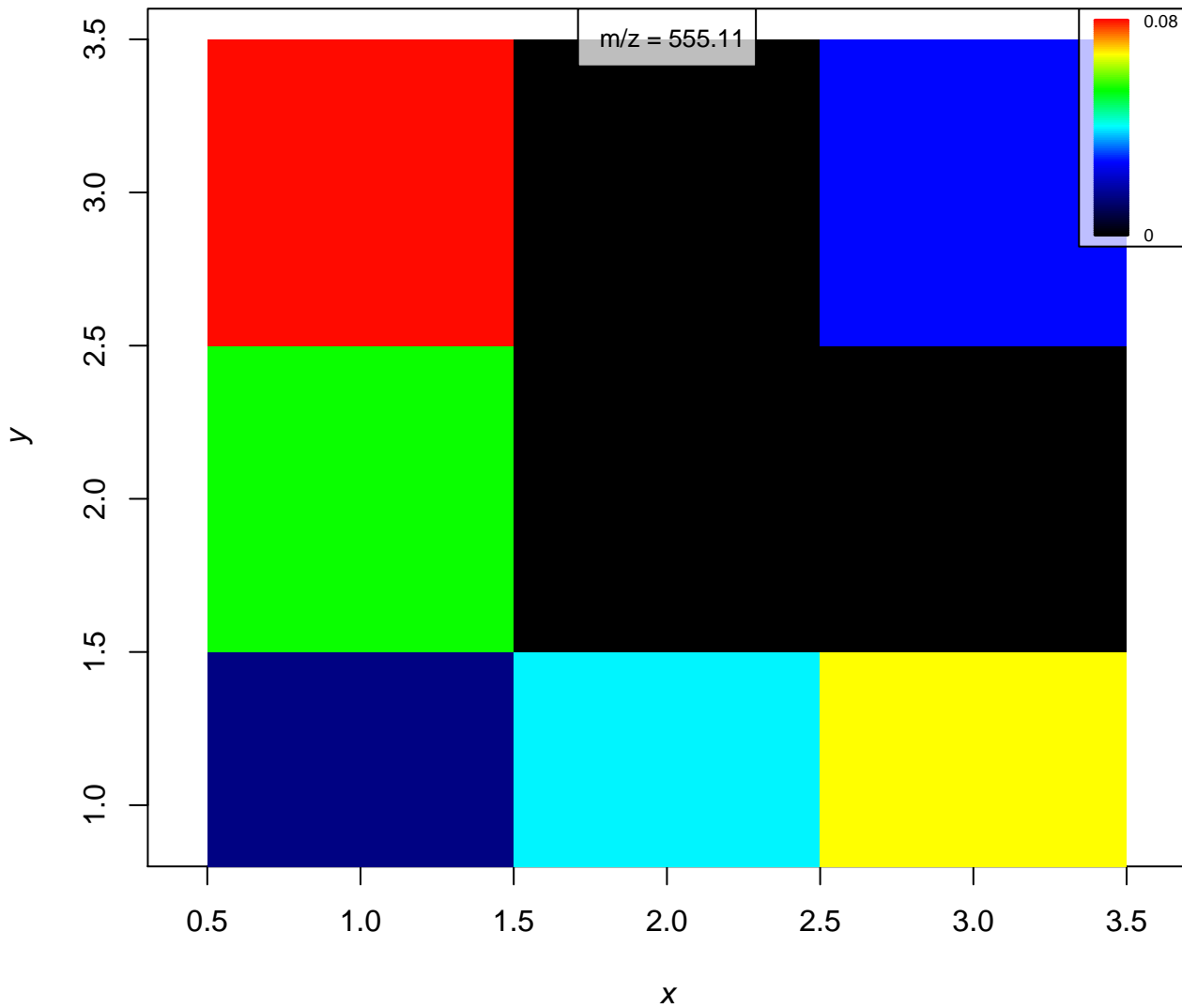
101.5: 101.5 (± 100 ppm)



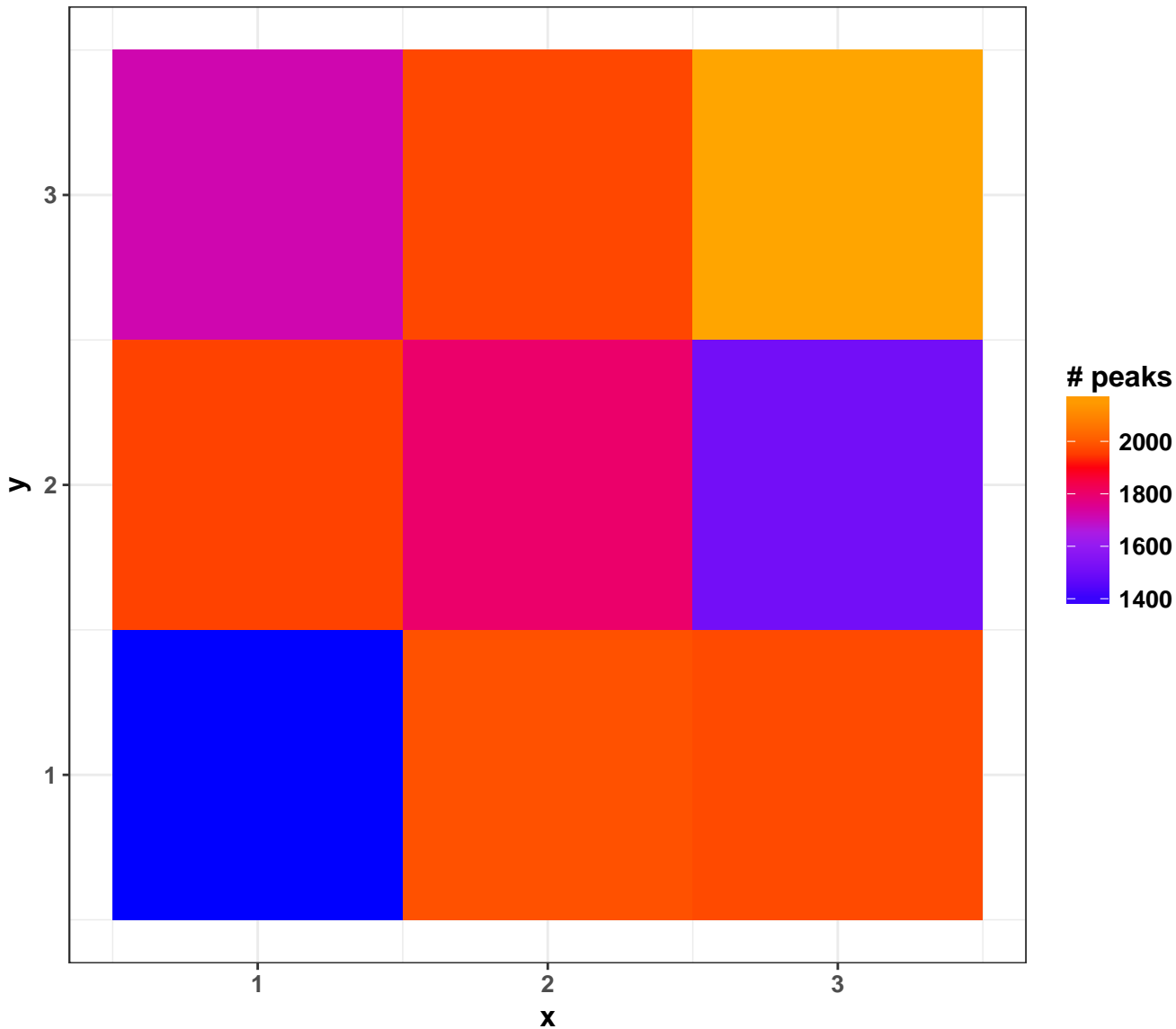
356.7: 356.7 (± 100 ppm)



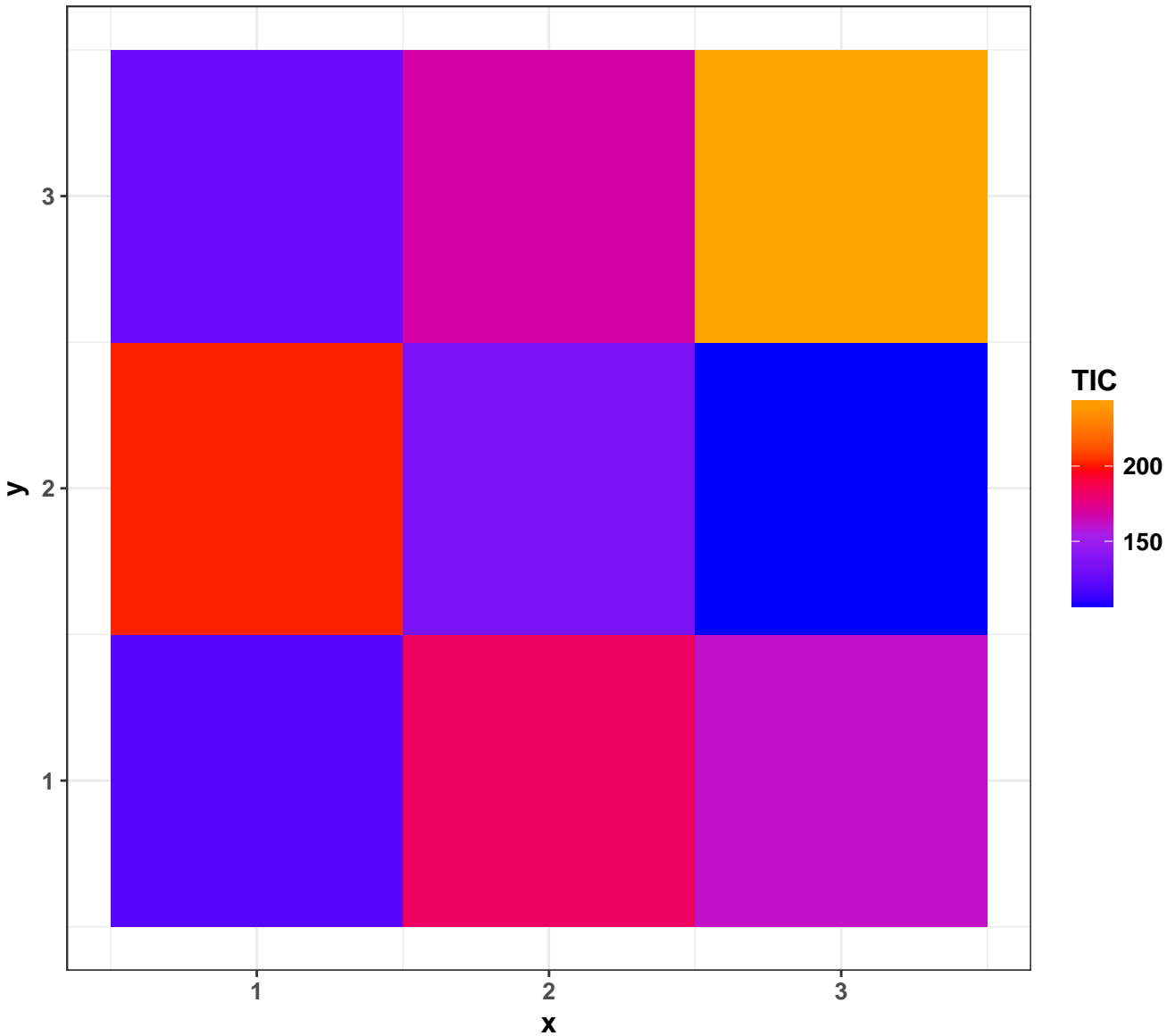
555.1: 555.1 (± 100 ppm)



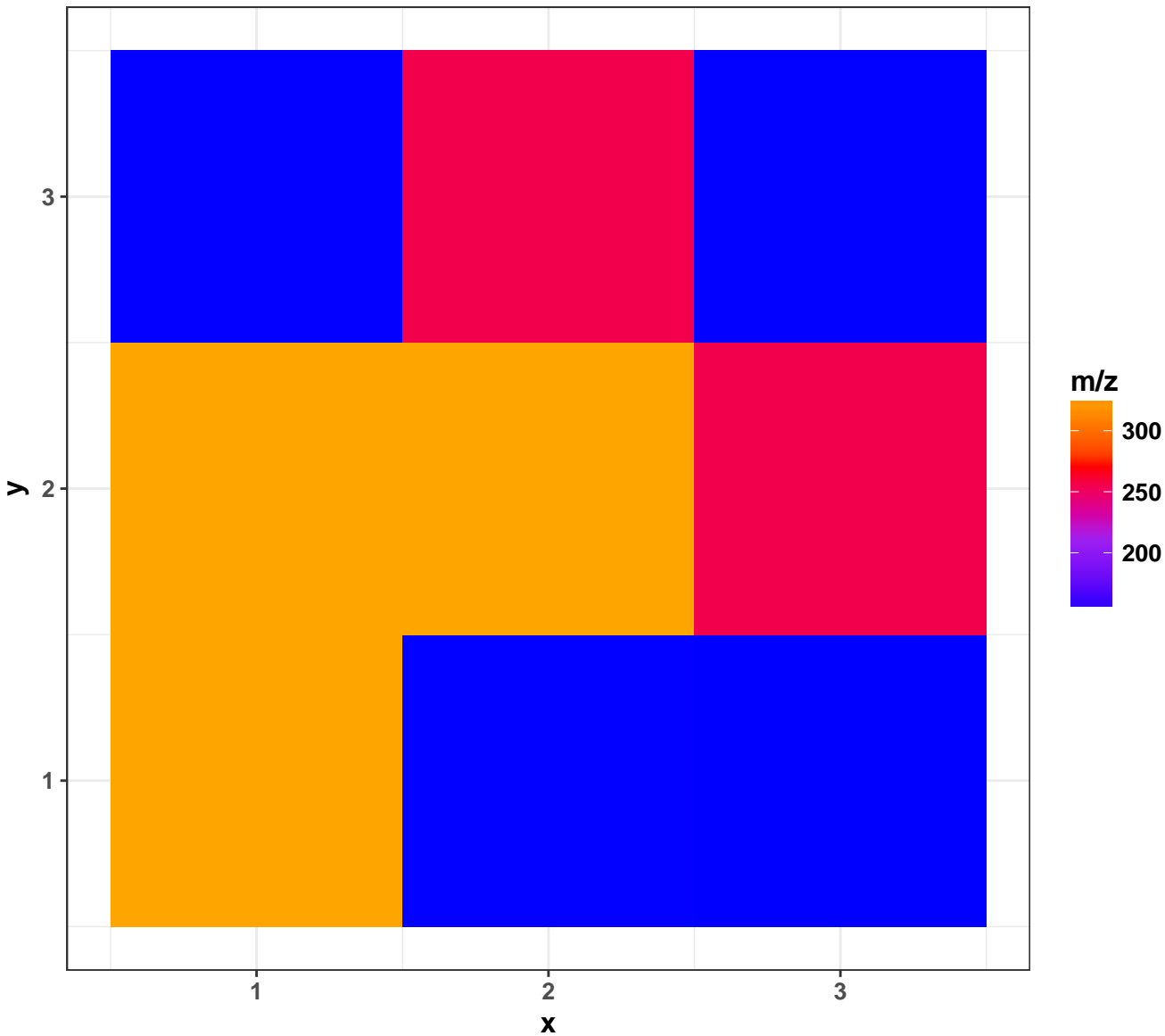
Number of peaks per spectrum



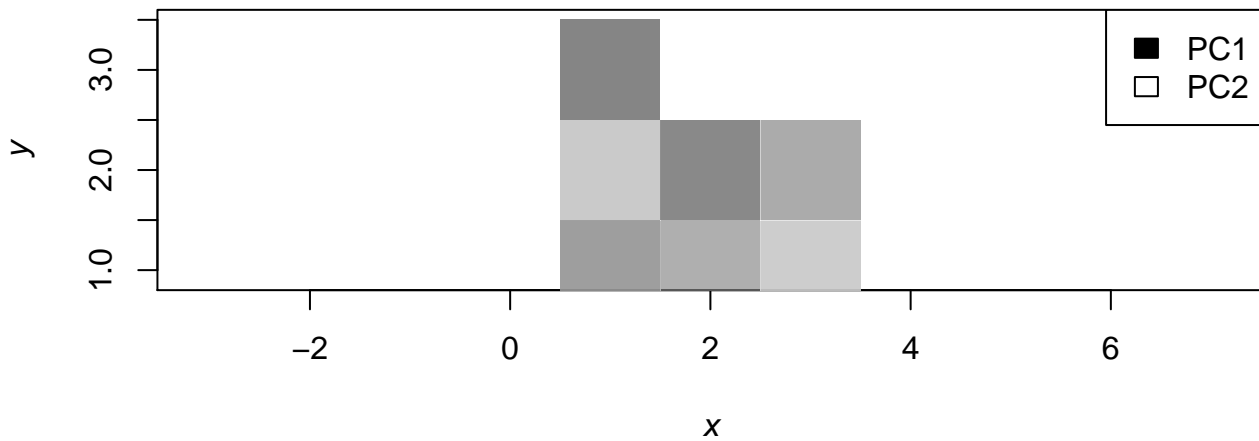
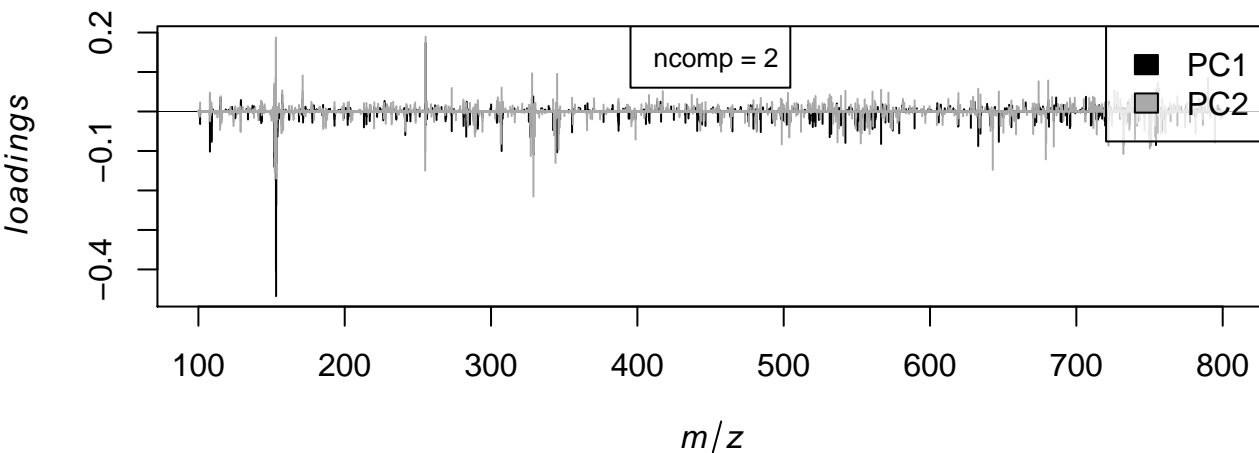
Total Ion Chromatogram



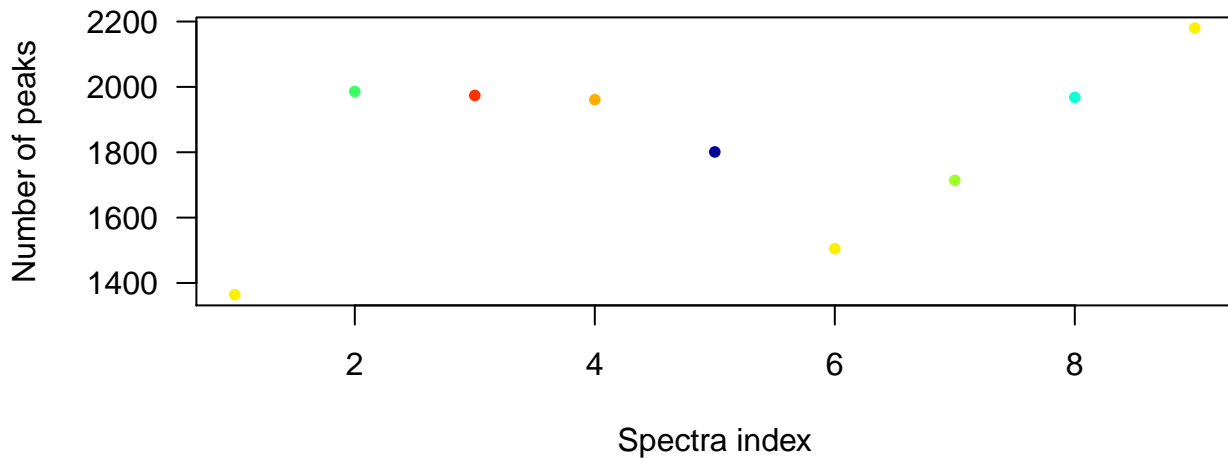
Most abundant m/z in each spectrum



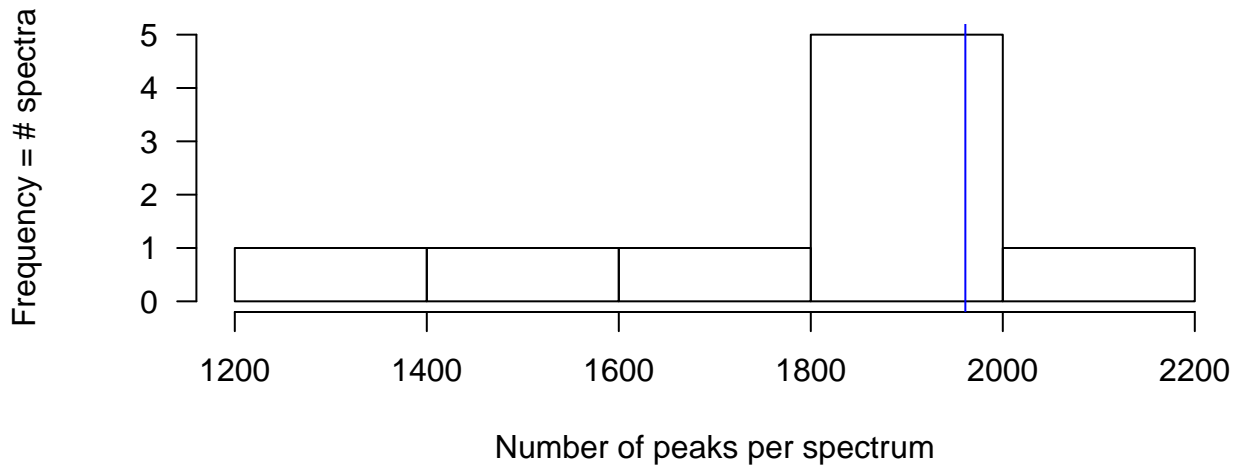
PCA for two components



Number of peaks per spectrum

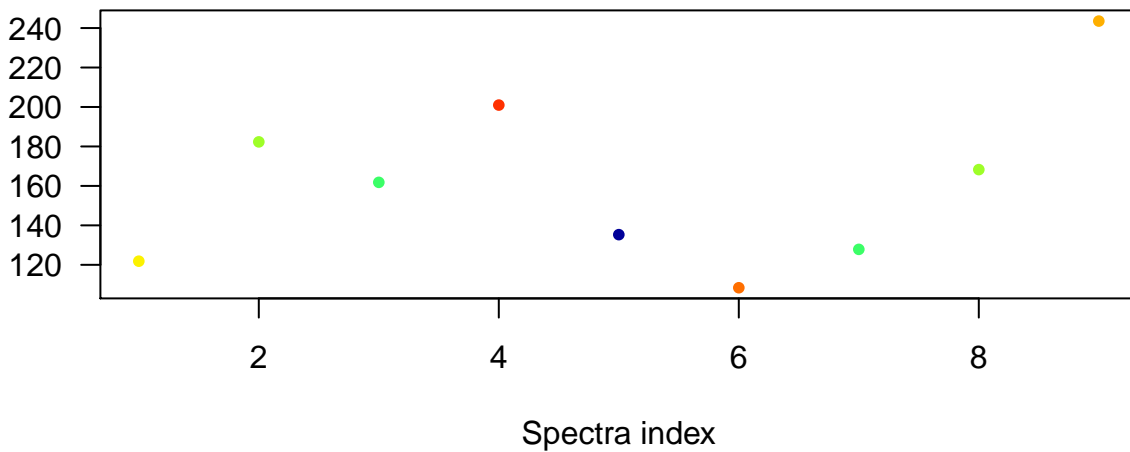


Number of peaks per spectrum



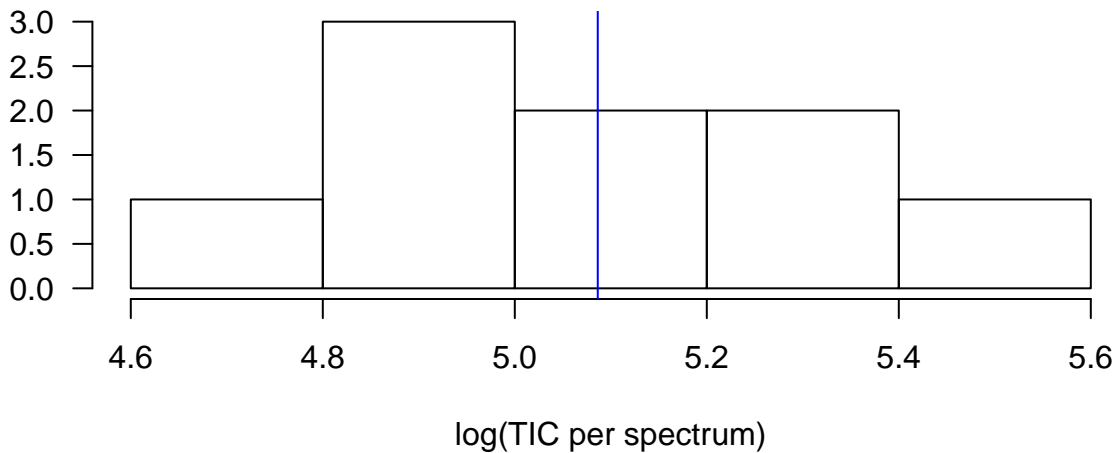
Total ion chromatogram intensity

TIC per spectrum

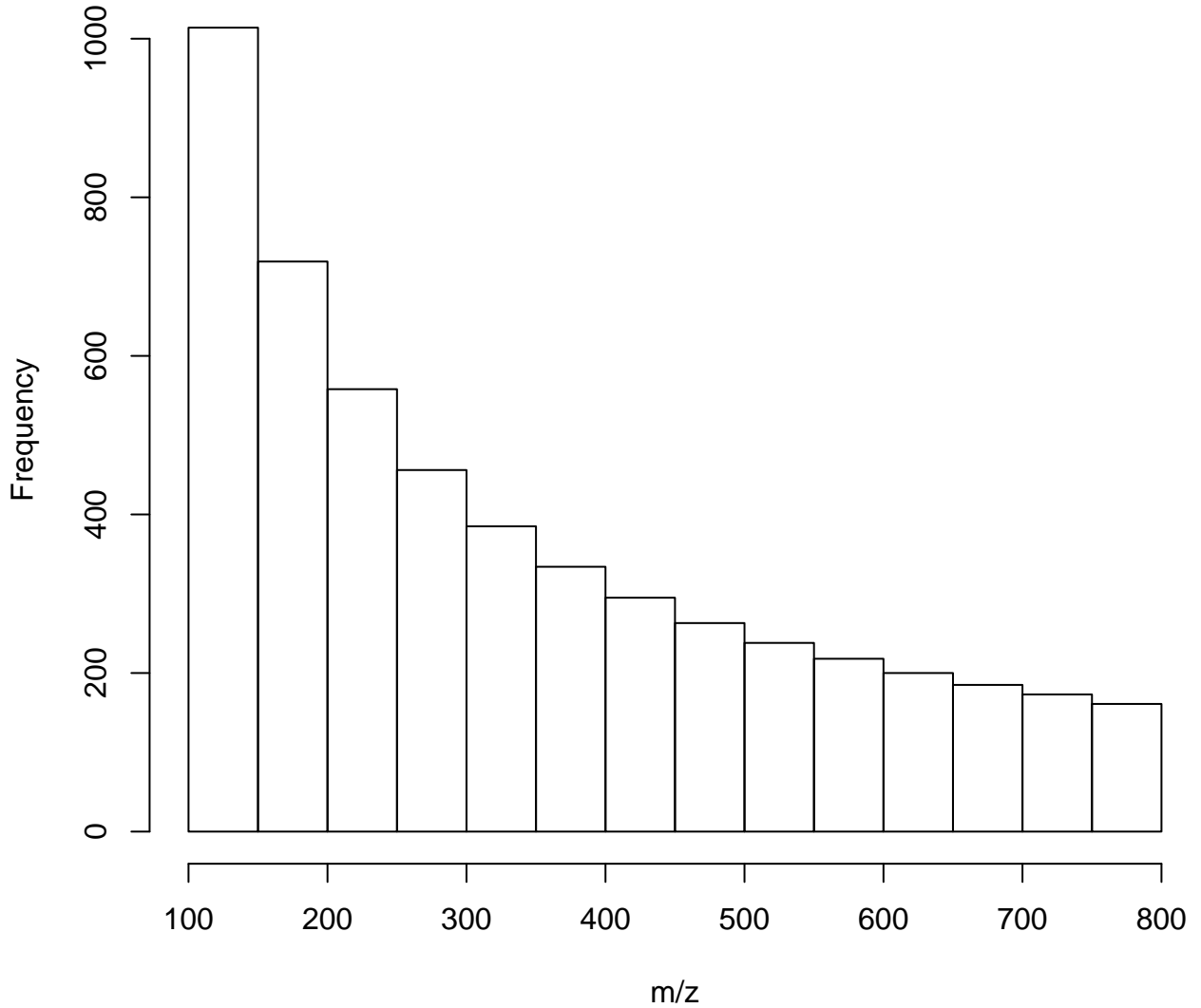


Frequency = # spectra

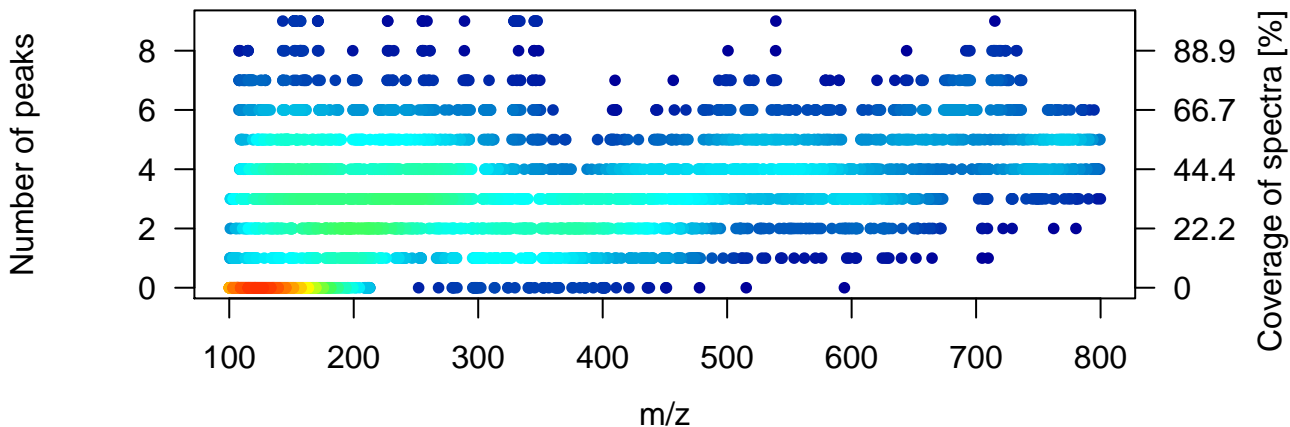
TIC per spectrum



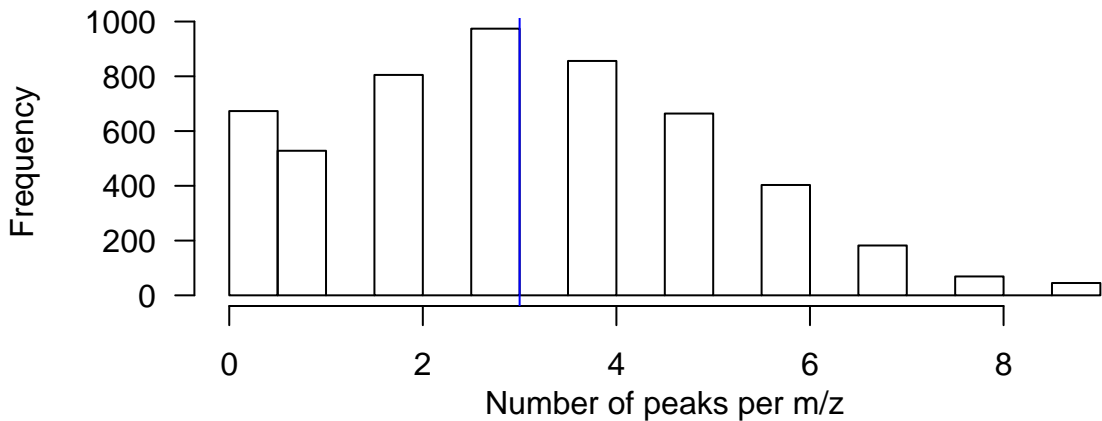
Histogram of m/z values



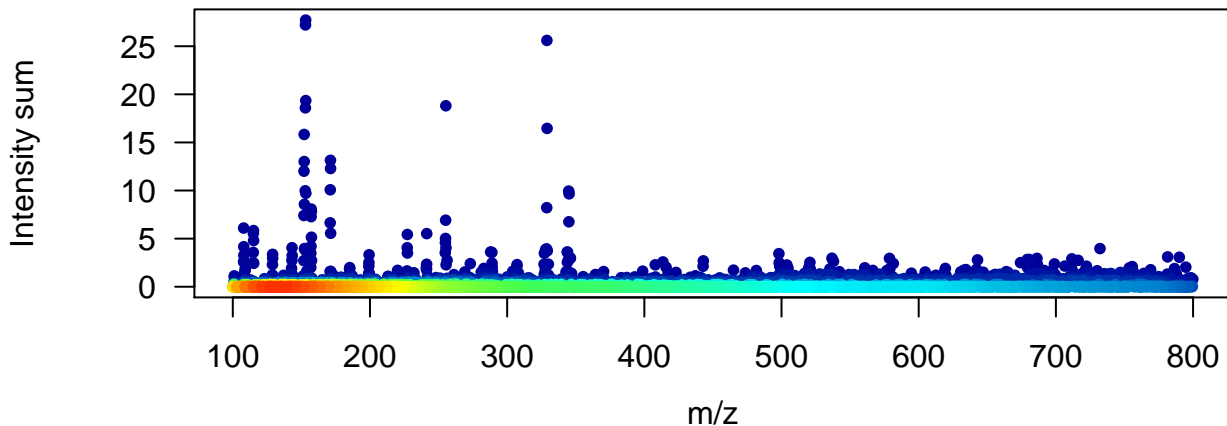
Number of peaks per m/z



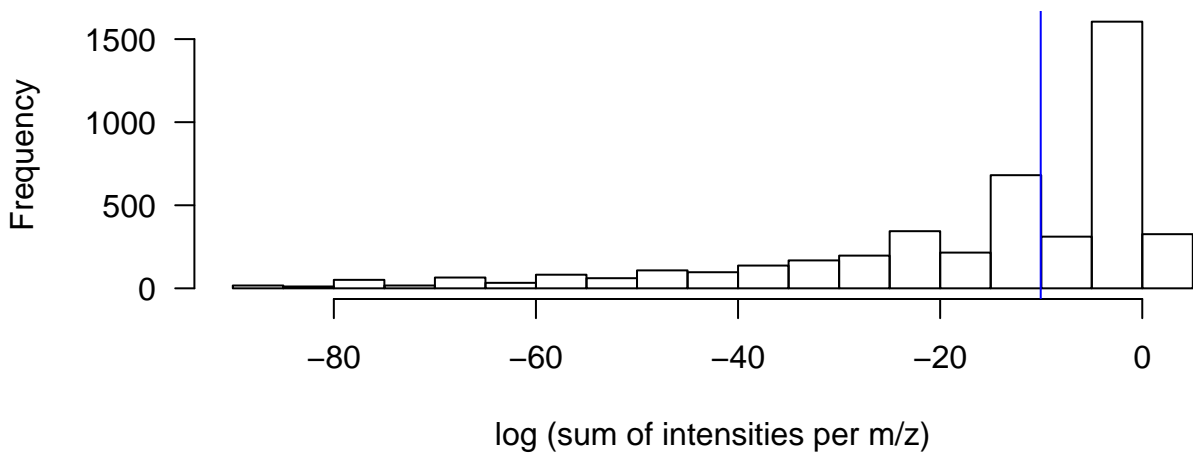
Number of peaks per m/z



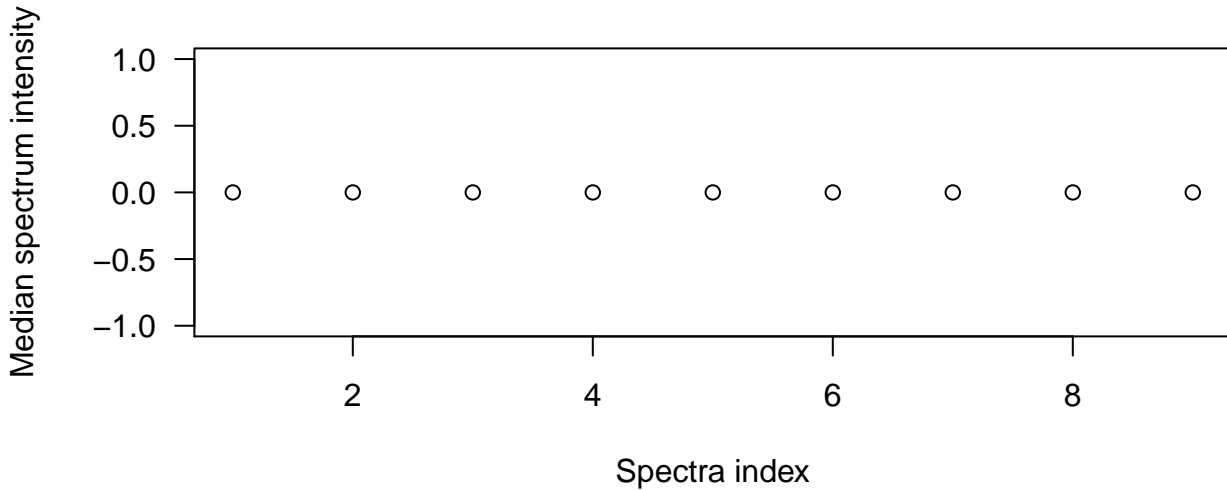
Sum of intensities per m/z



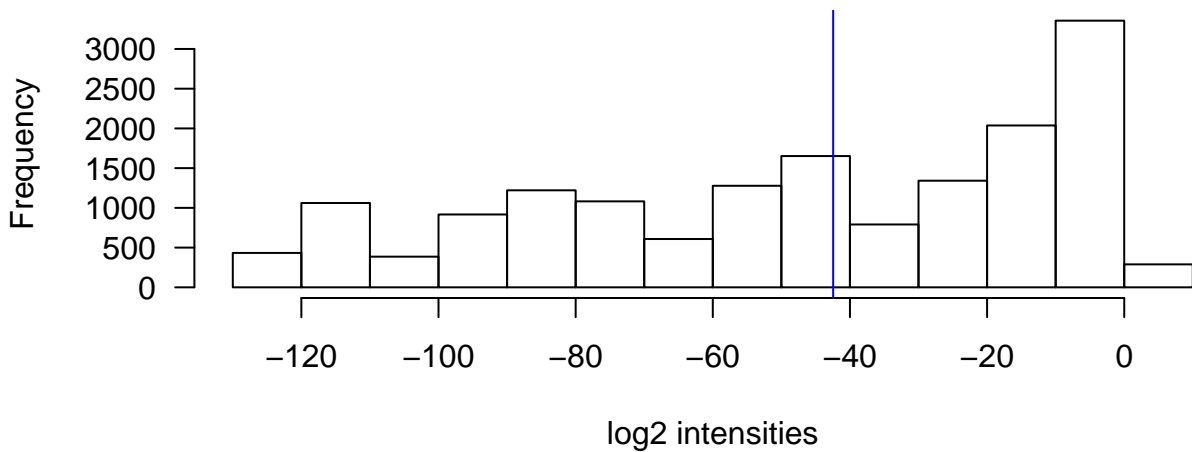
Sum of intensities per m/z



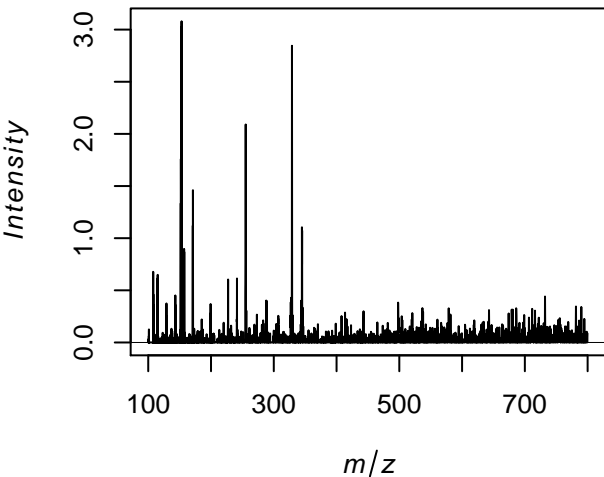
Median intensity per spectrum



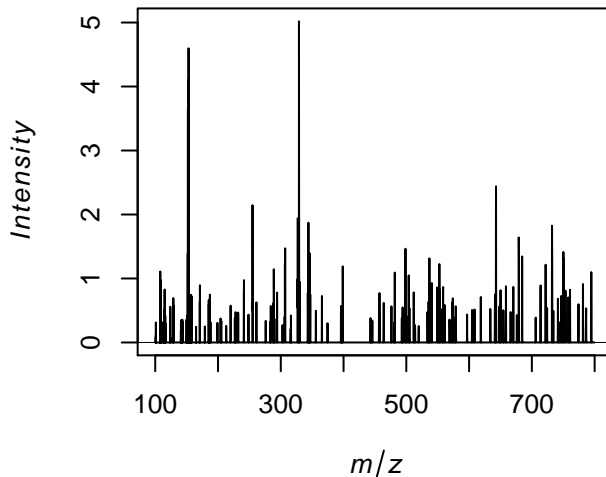
Log2-transformed intensities



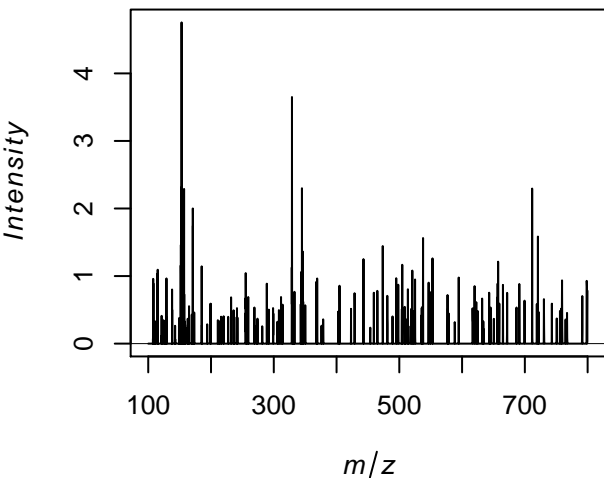
Average spectrum



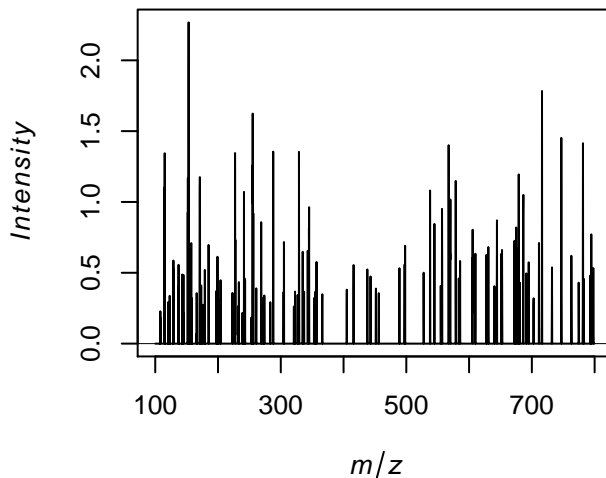
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

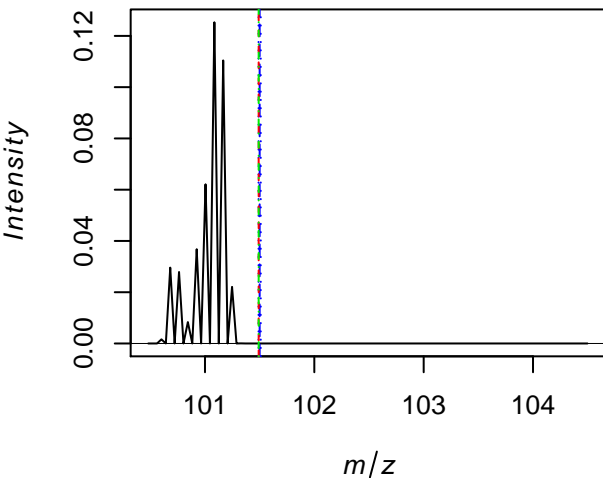


theor. m/z: 101.5

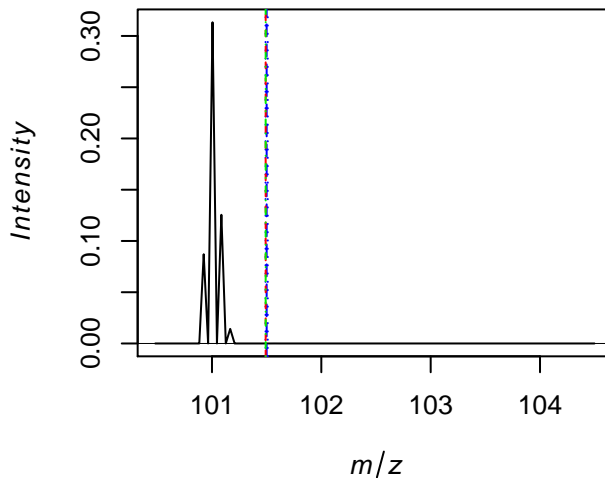
most abundant m/z: 101.491

closest m/z: 101.491

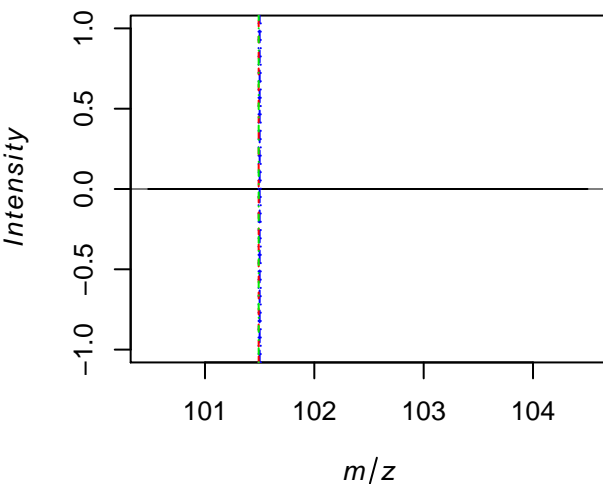
average spectrum



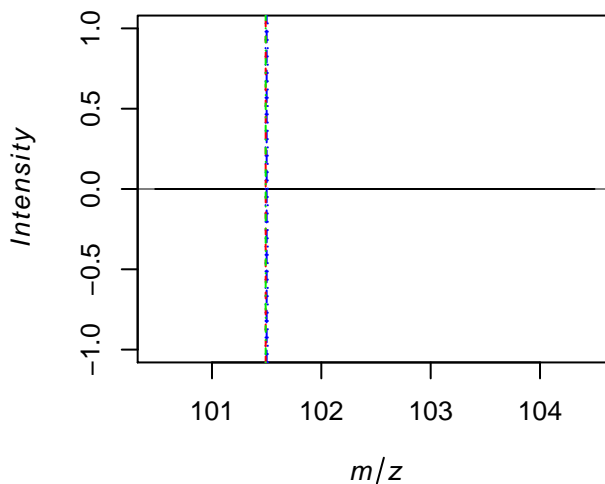
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

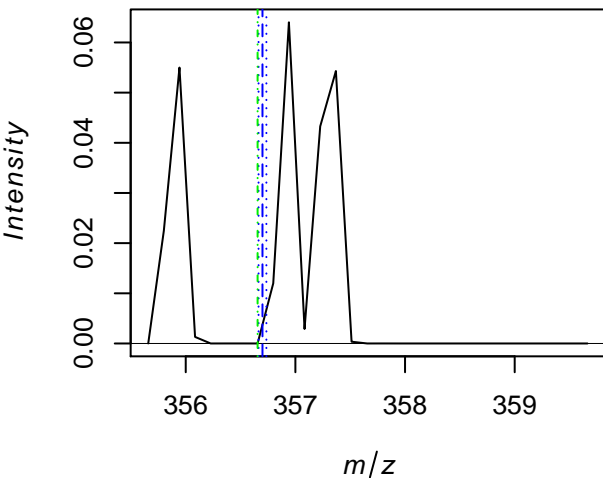


theor. m/z: 356.7

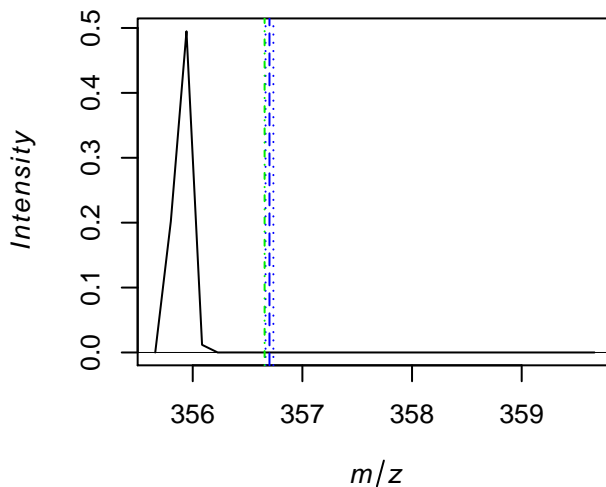
most abundant m/z: NA

closest m/z: 356.6555

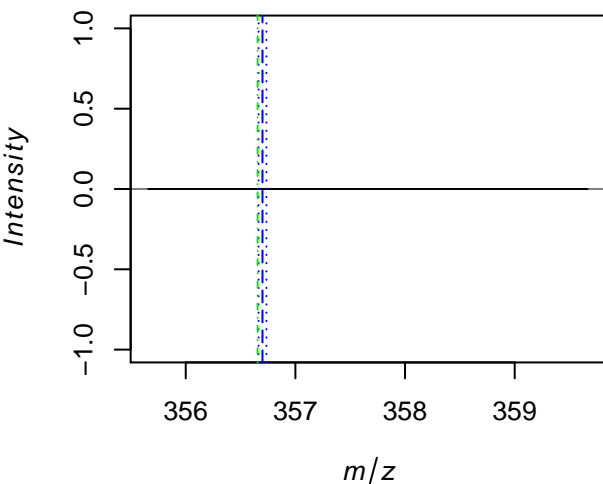
average spectrum



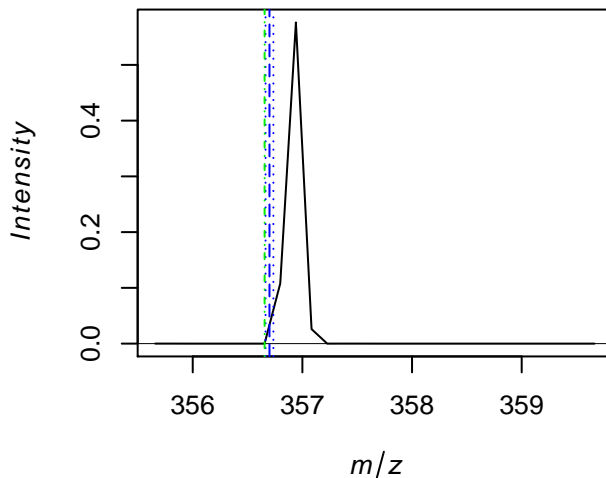
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

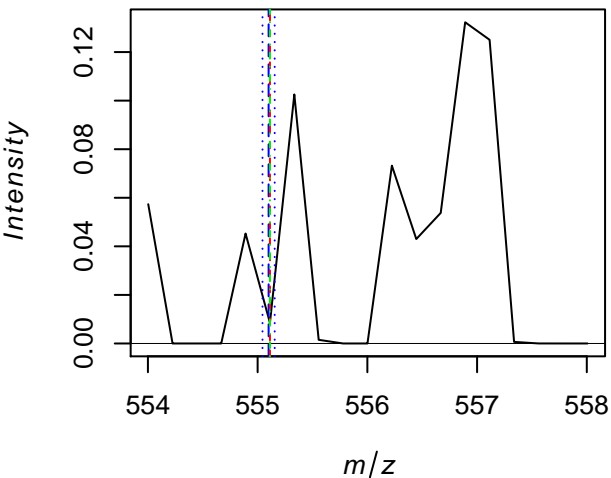


theor. m/z: 555.1

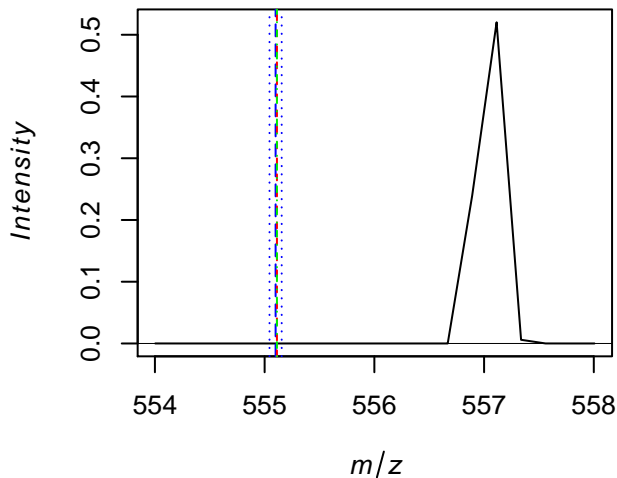
most abundant m/z: 555.122

closest m/z: 555.122

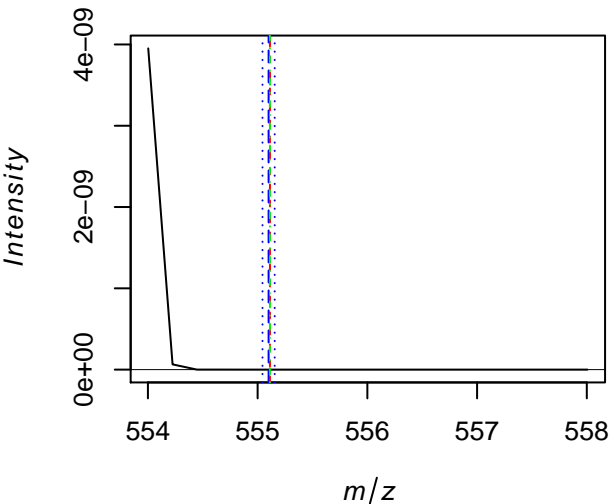
average spectrum



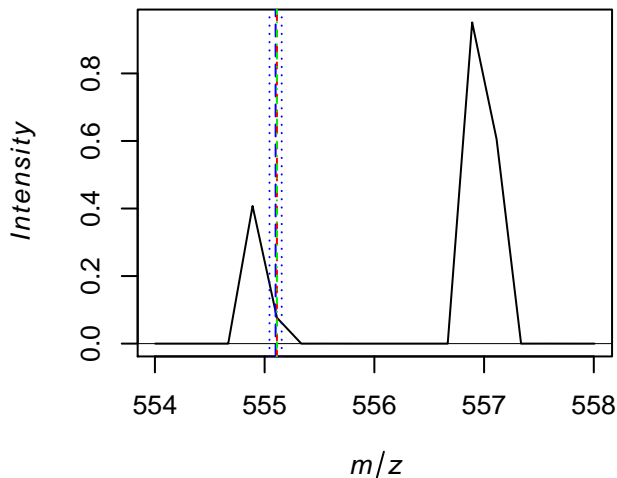
Spectrum at x = 1, y = 2



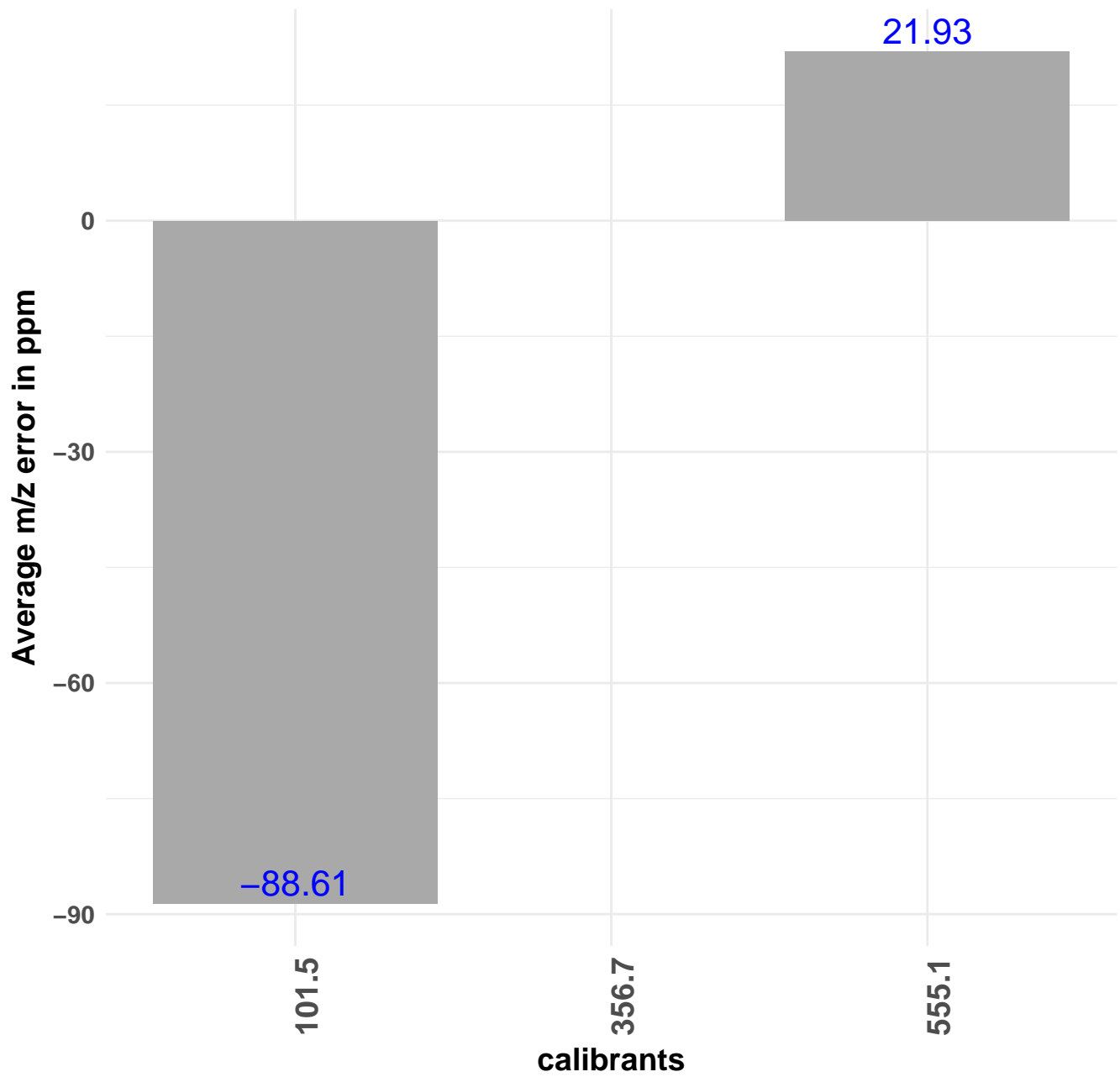
Spectrum at x = 2, y = 1



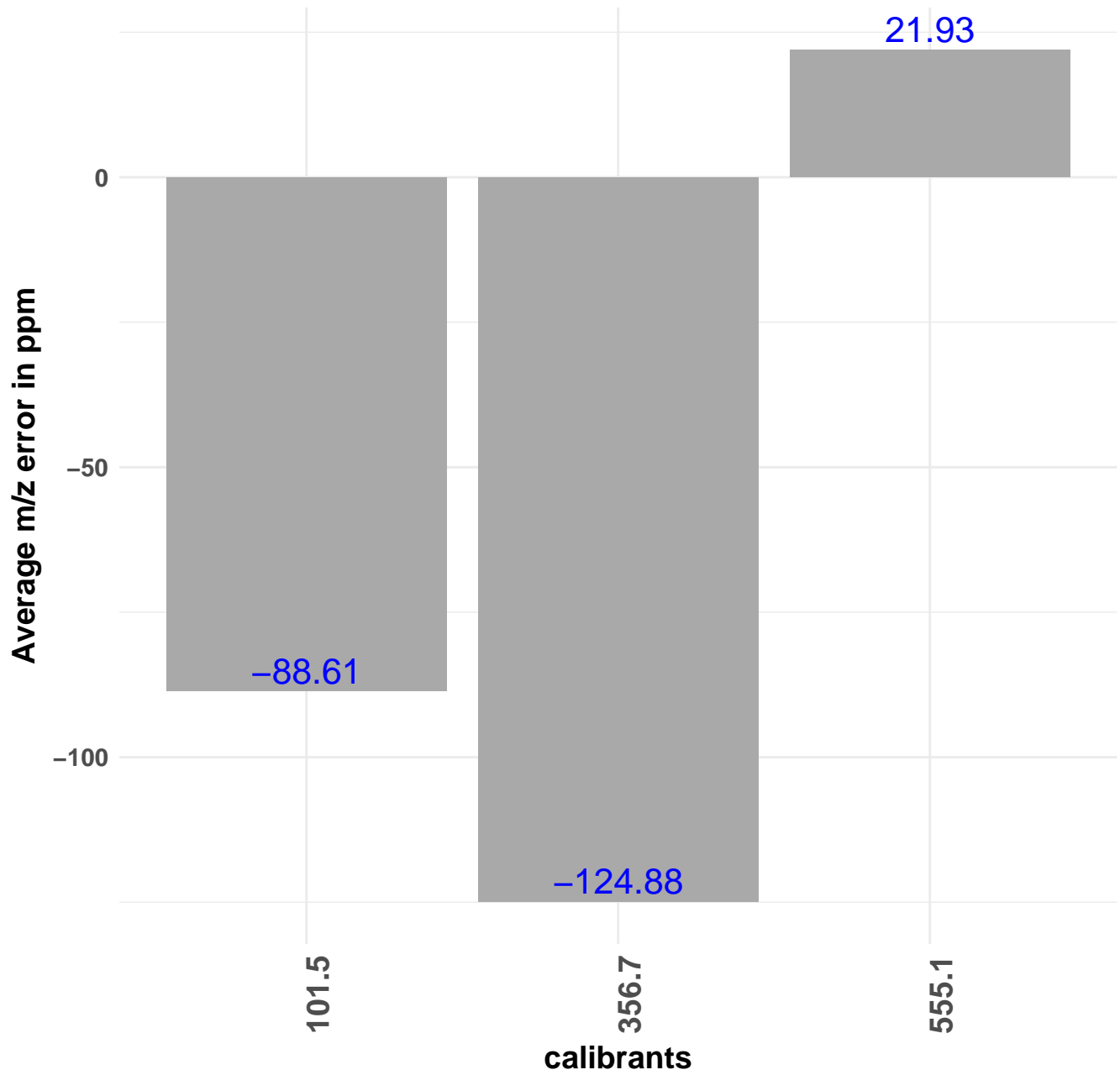
Spectrum at x = 1, y = 3



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)

