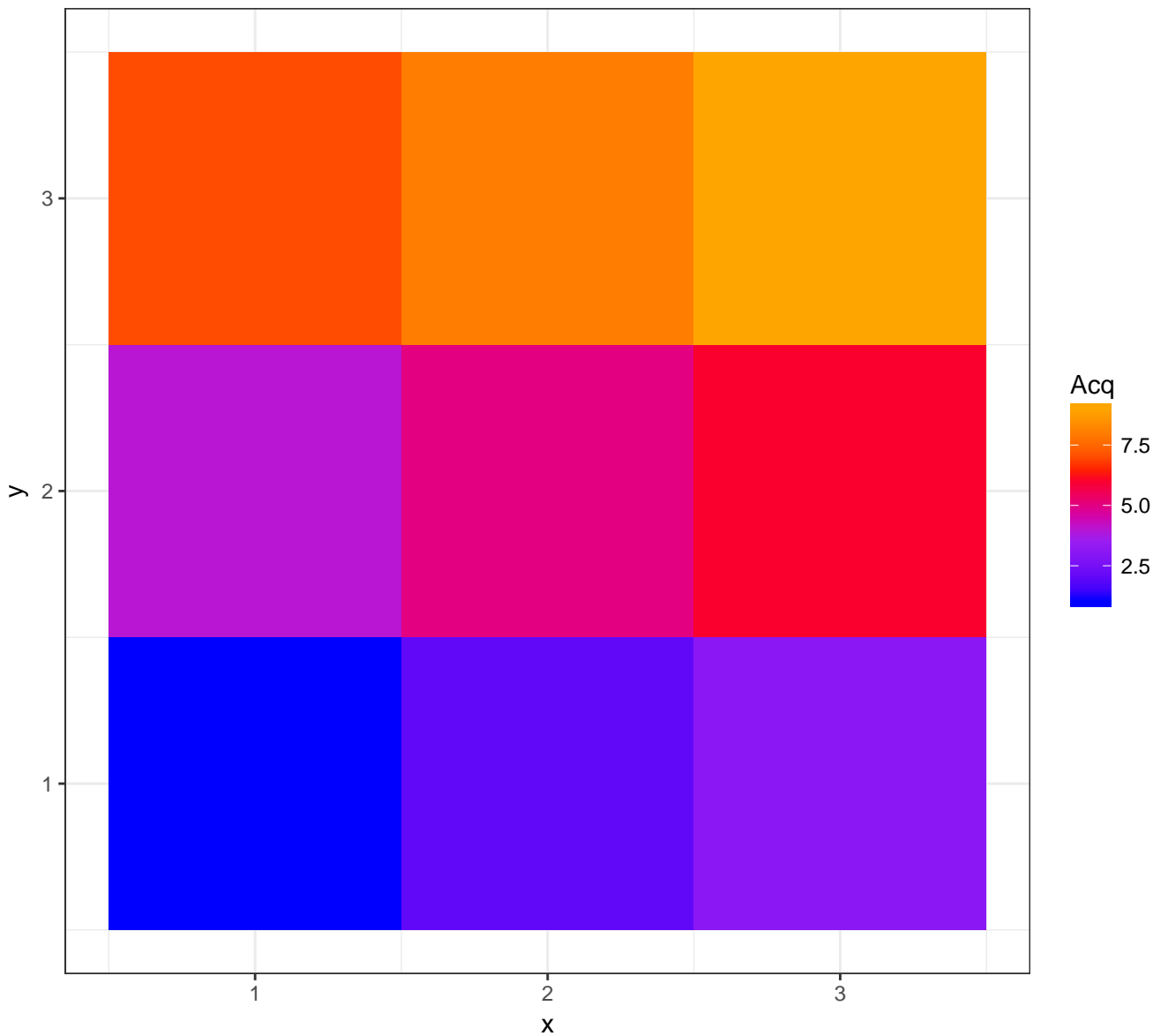


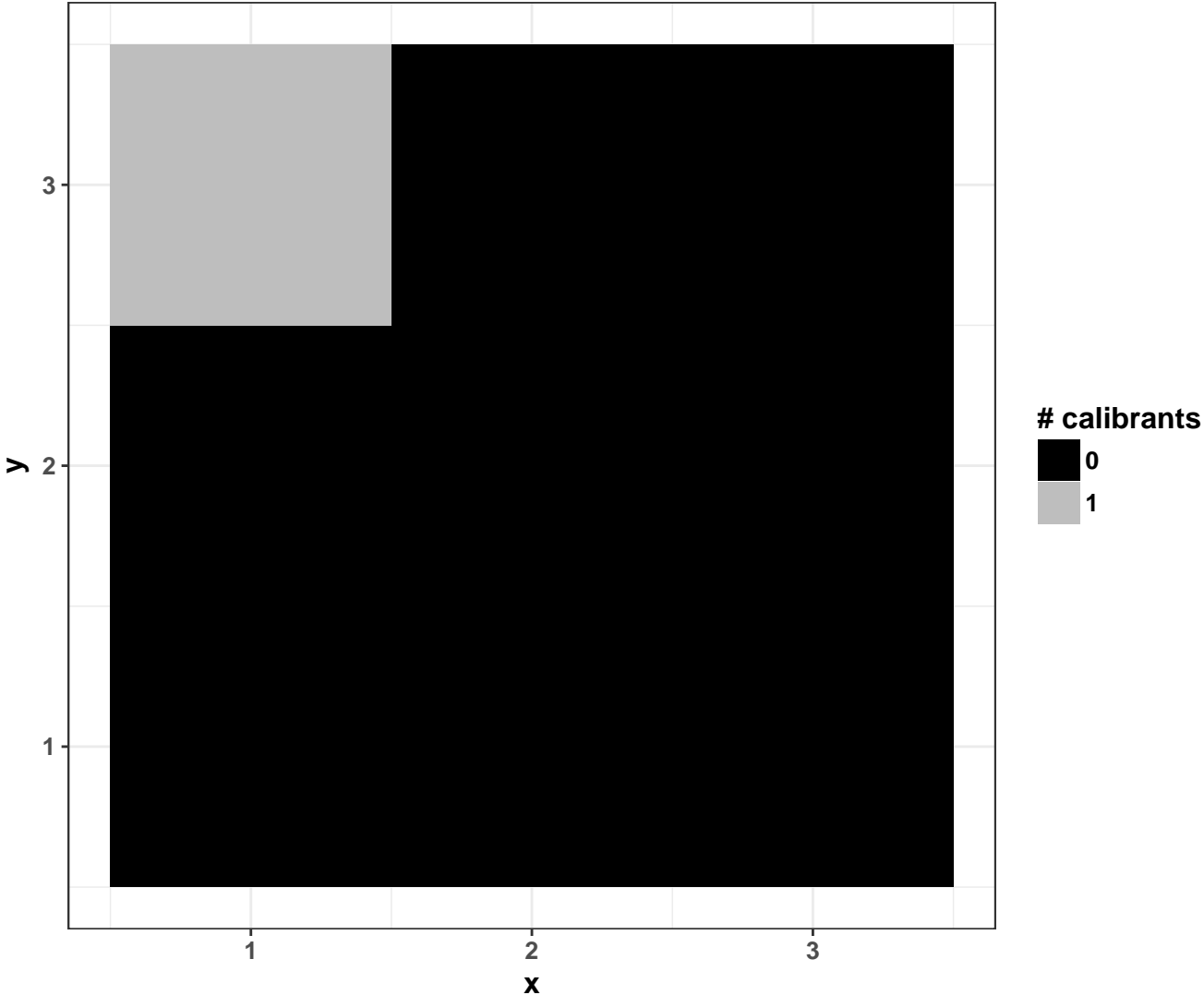
Testfile_imzml

properties	values
Number of m/z features	1199
Range of m/z values [Da]	300.08 – 399.92
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	0 – 2.59
Median of intensities	0
Intensities > 0	26.17 %
Number of zero TICs	0
Median TIC	24.4319108750771
Median # peaks per spectrum	323
Normalization	FALSE
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
# peptides in inputpeptides.txt	1 / 6
# calibrants in inputcalibrantfile1.txt	1 / 3

Pixel order

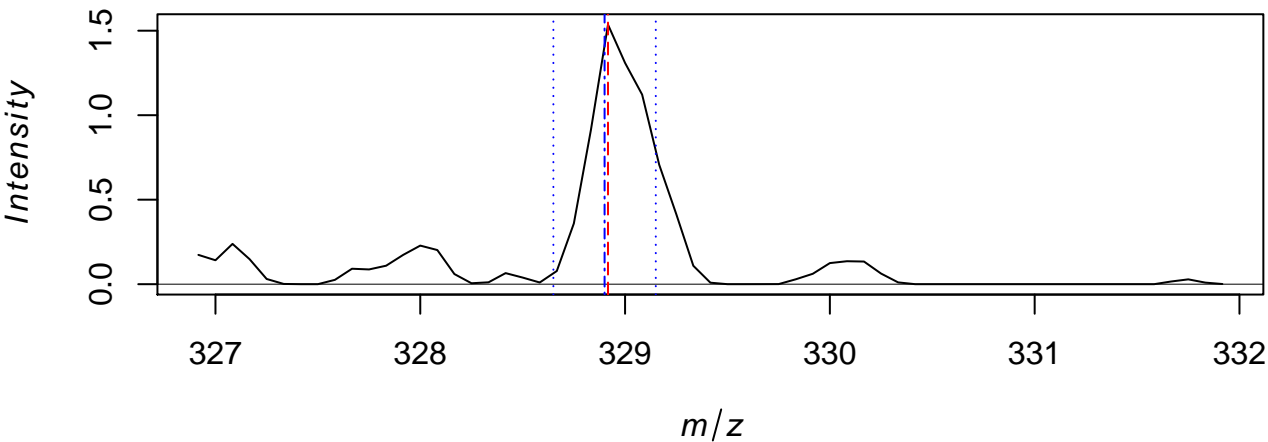


Number of calibrants per pixel

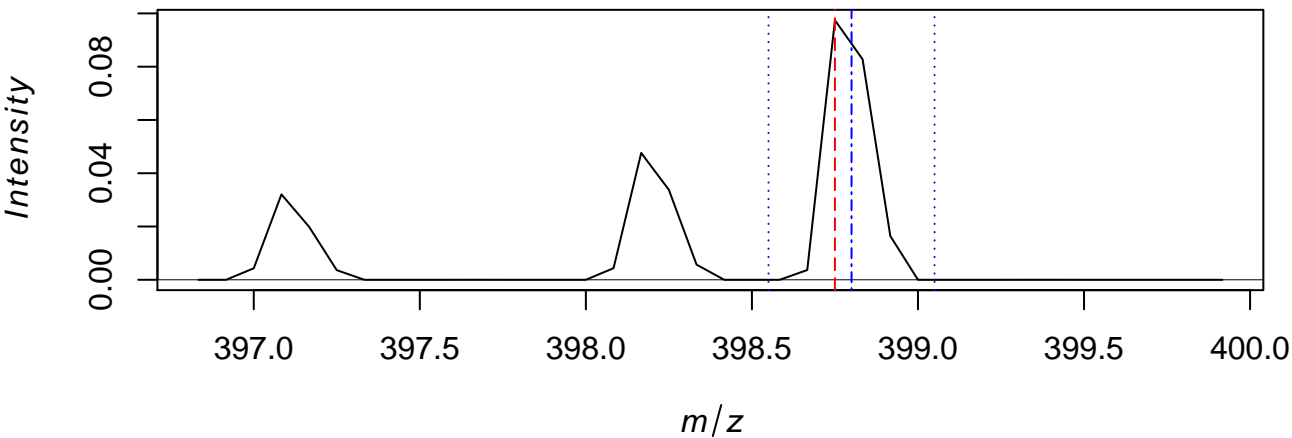


Control of fold change plot

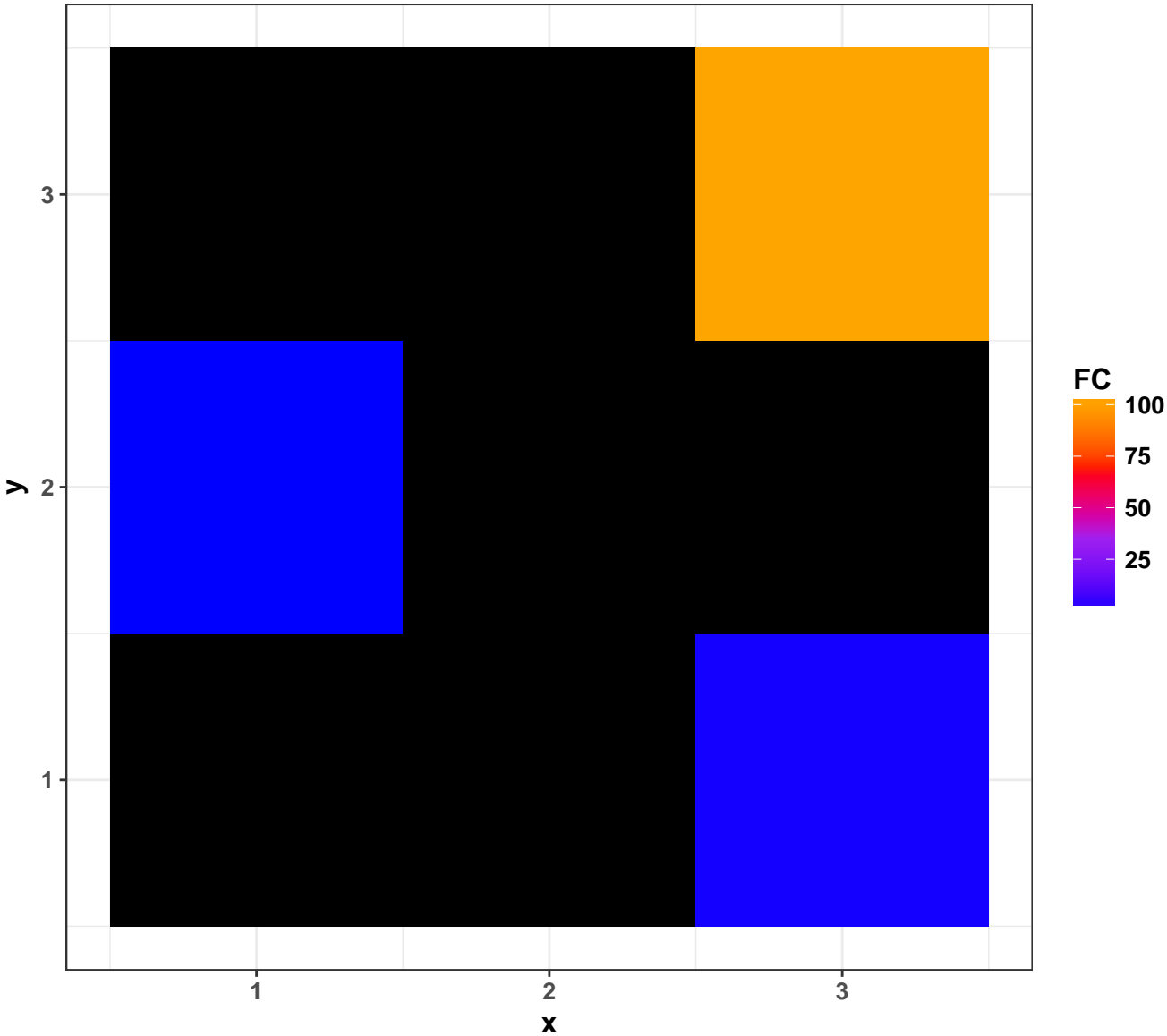
average spectrum 328.9 Da



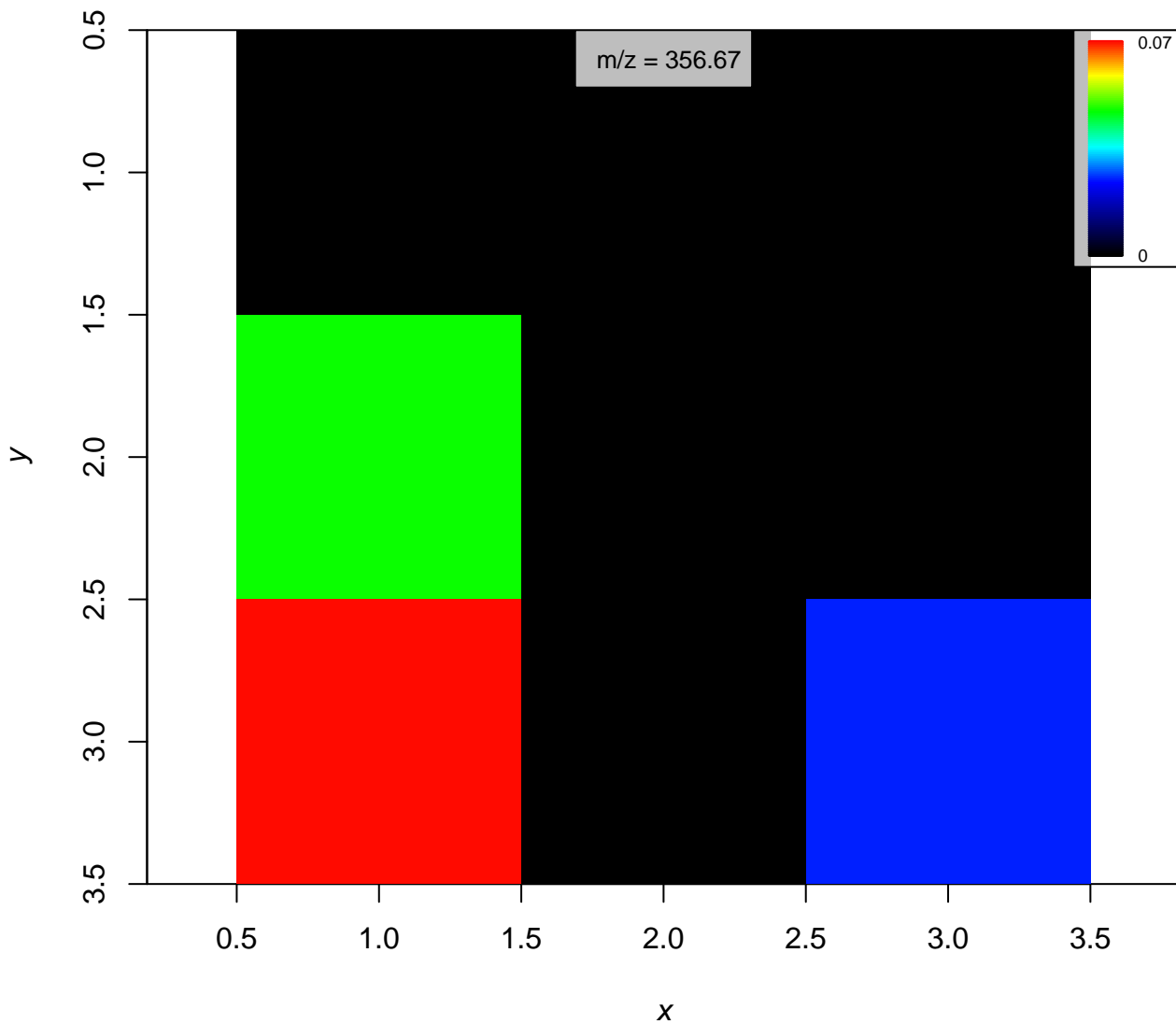
average spectrum 398.8 Da



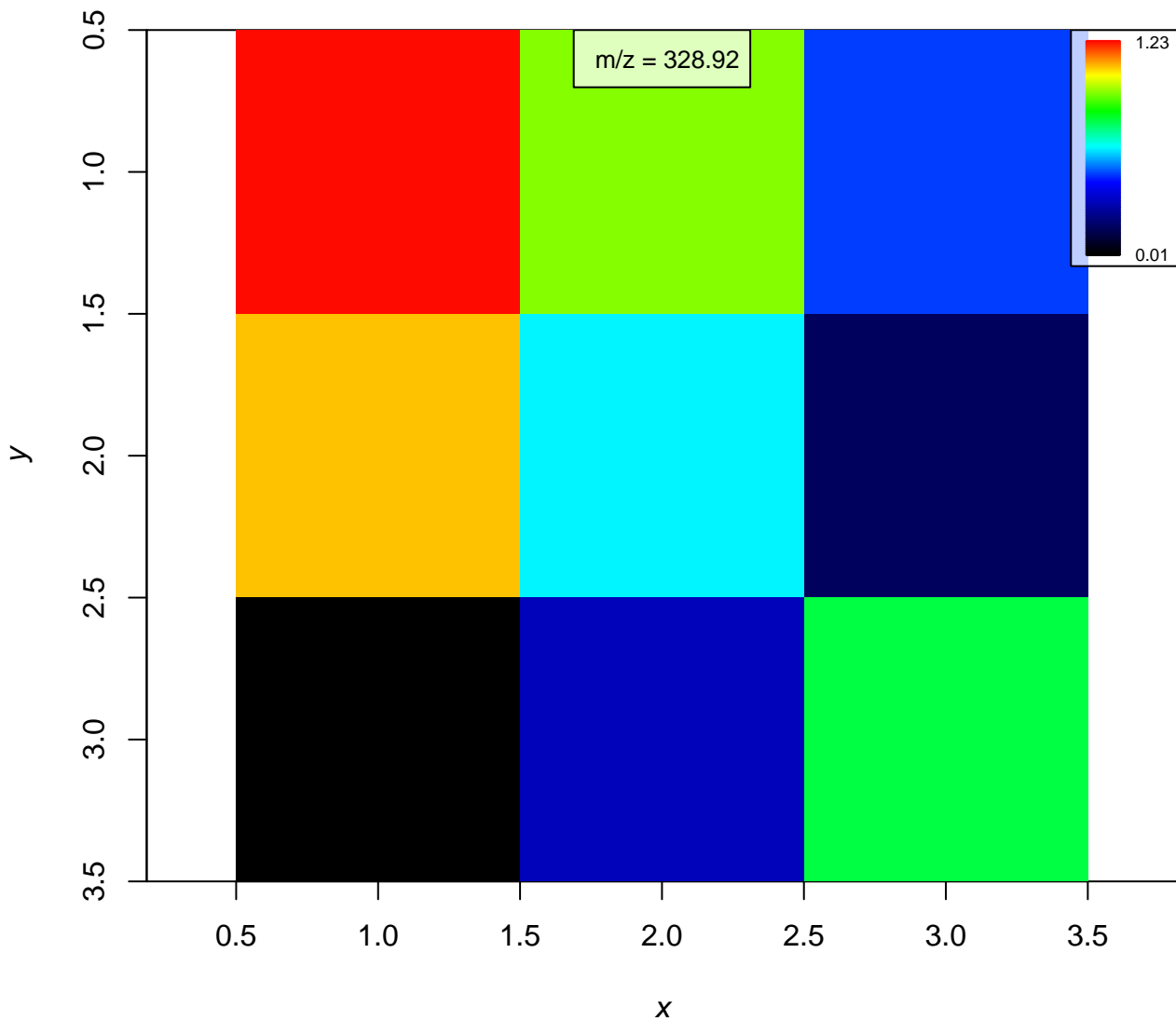
Ratio of mass1 (328.9) / mass2 (398.8)



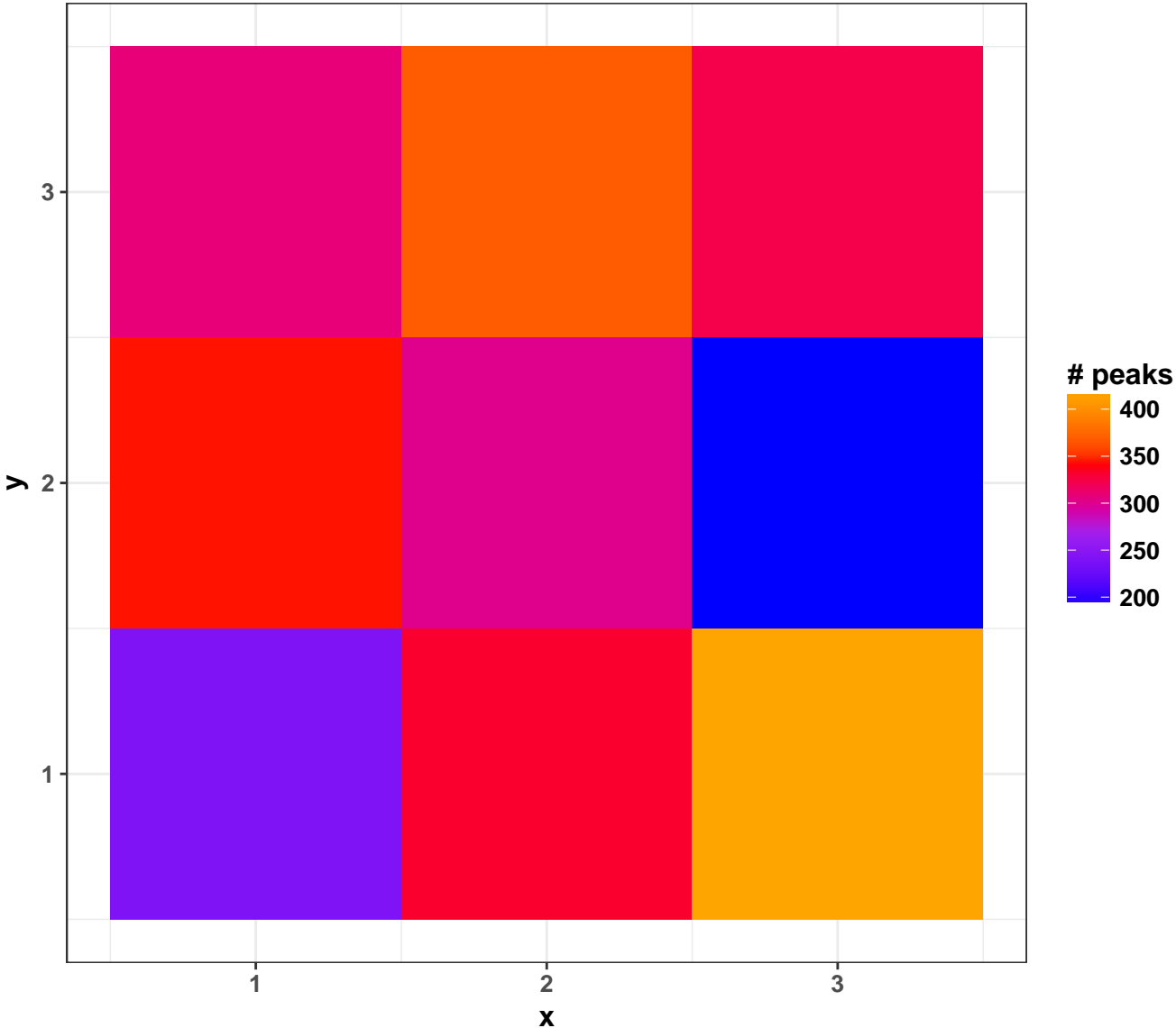
356.7 (356.7 \pm 0.25 Da)



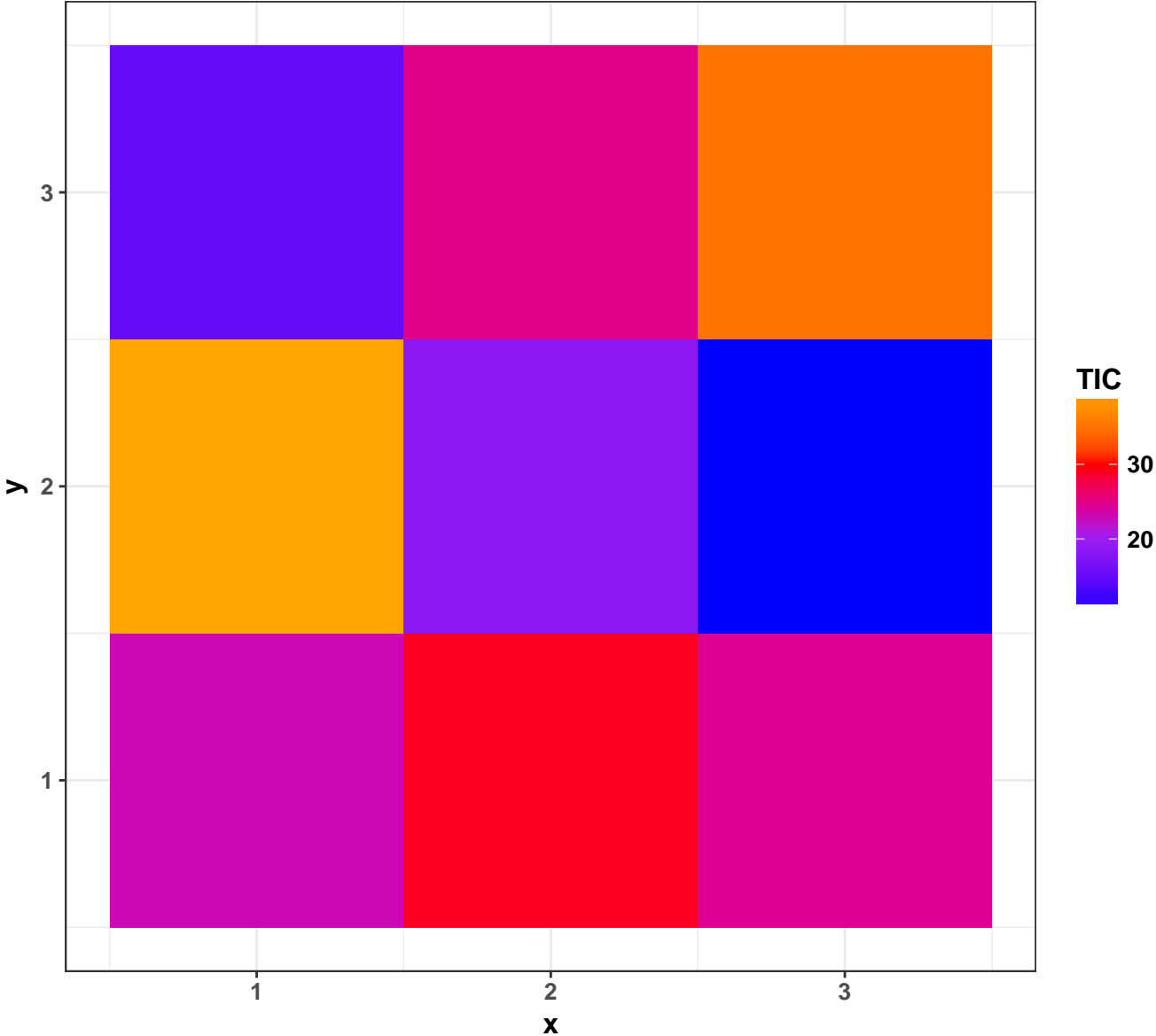
328.9 (328.9 \pm 0.25 Da)



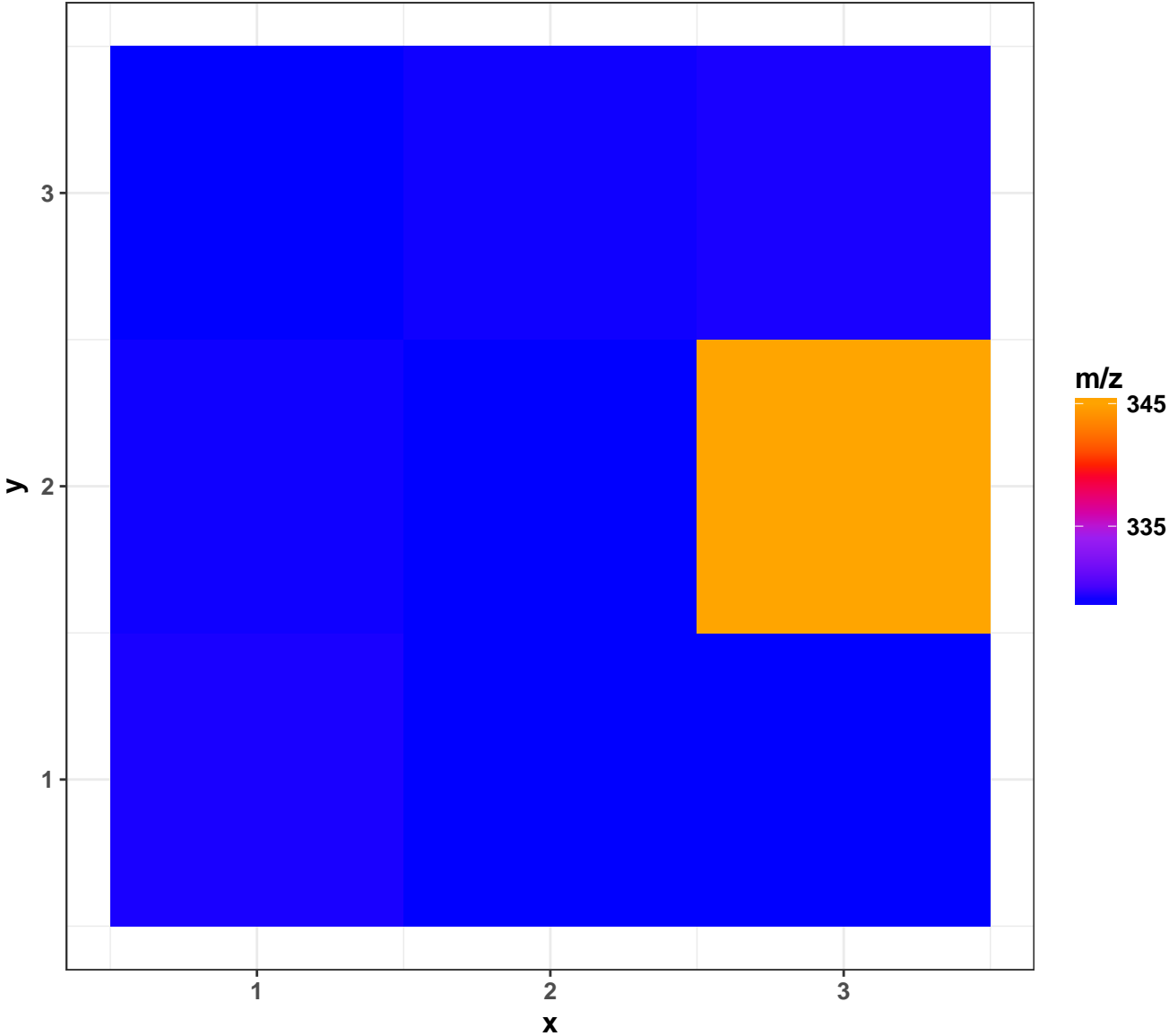
Number of peaks per spectrum



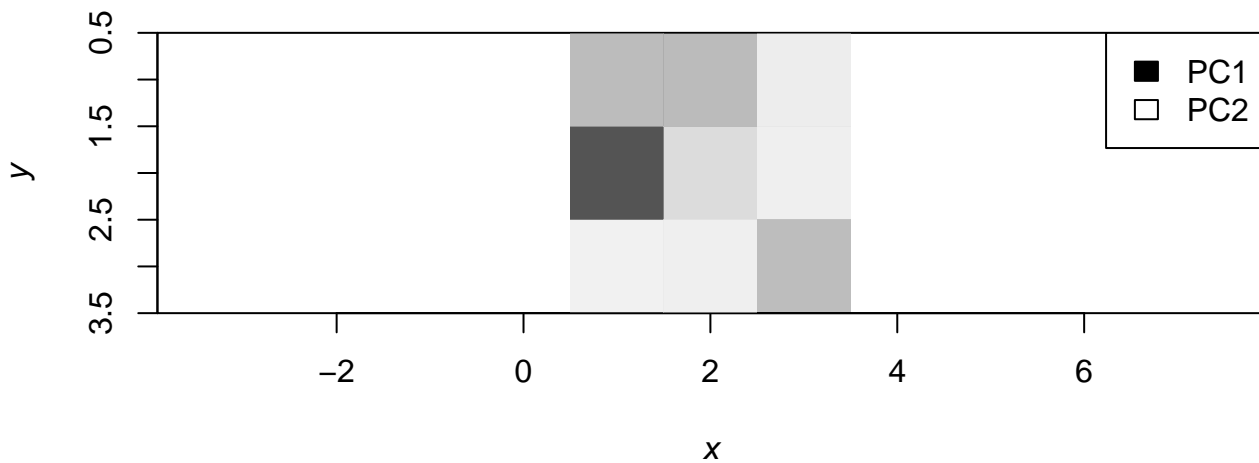
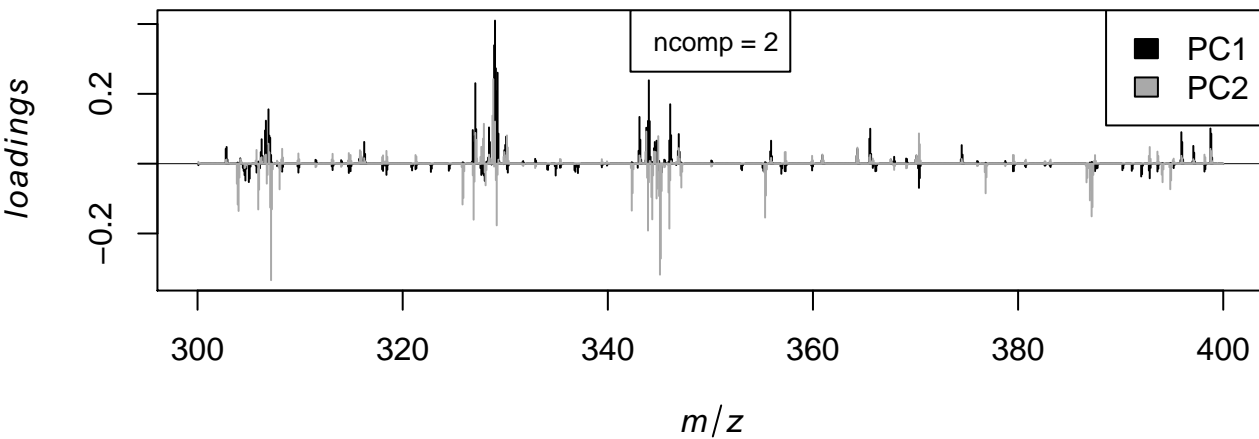
Total Ion Chromatogram



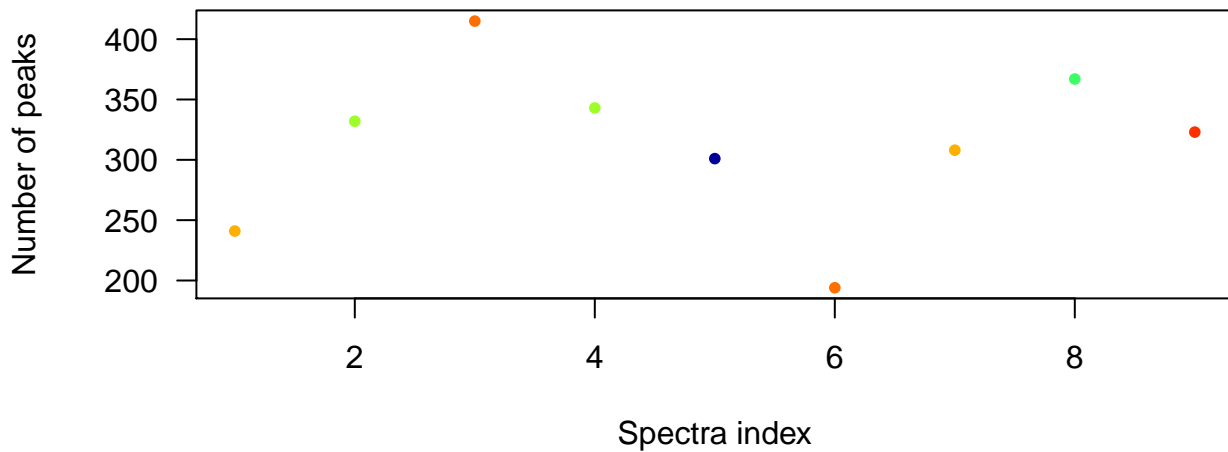
Most abundant m/z in each spectrum



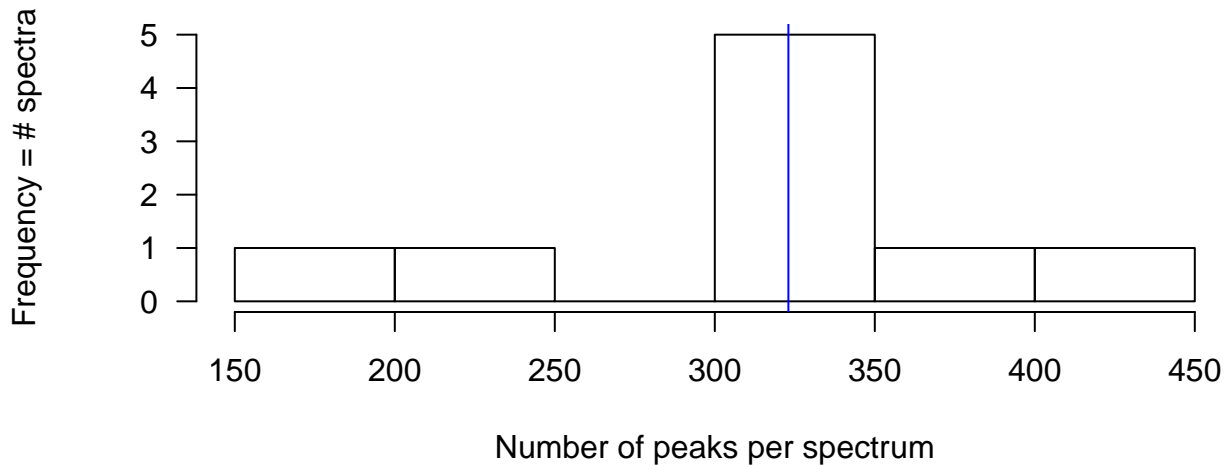
PCA for two components

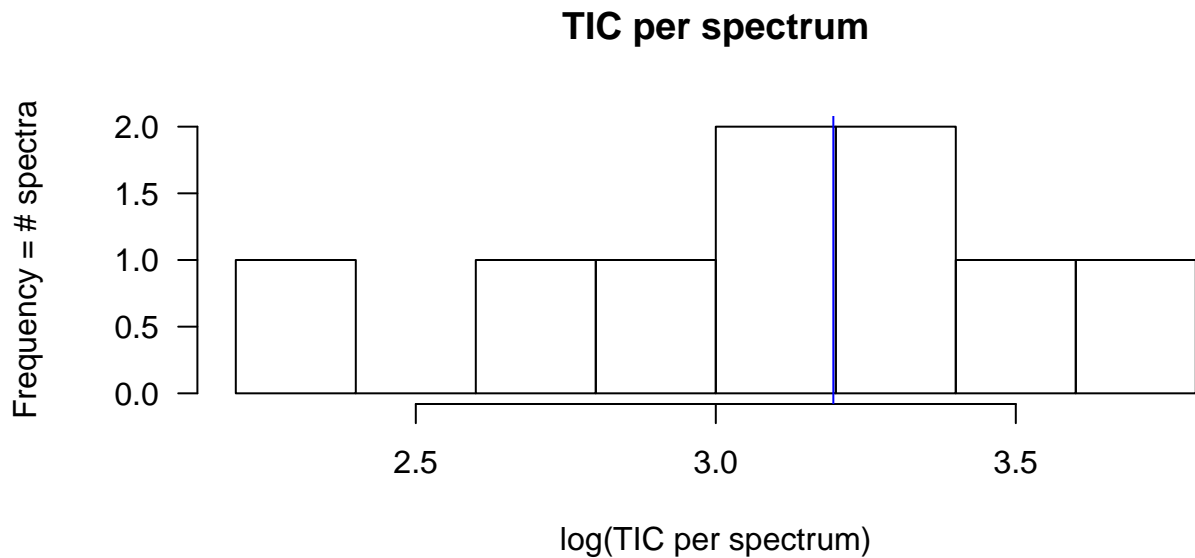
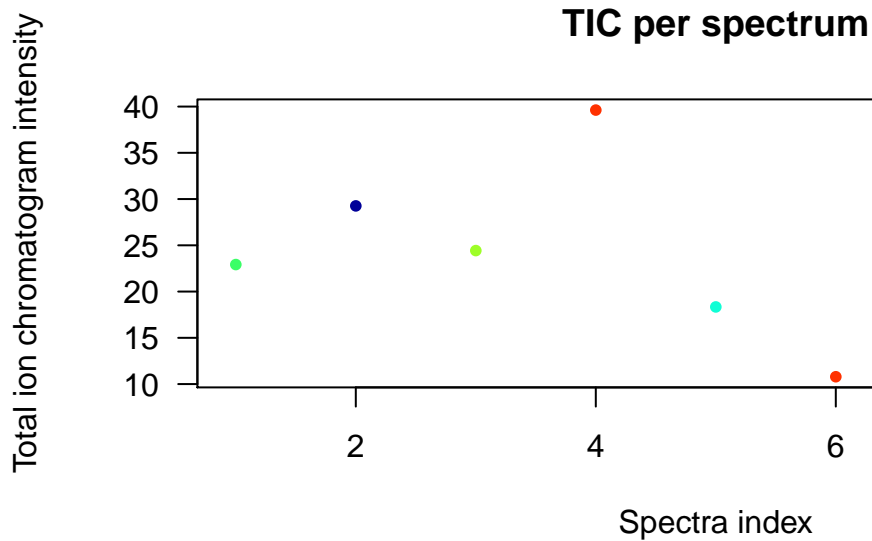


Number of peaks per spectrum

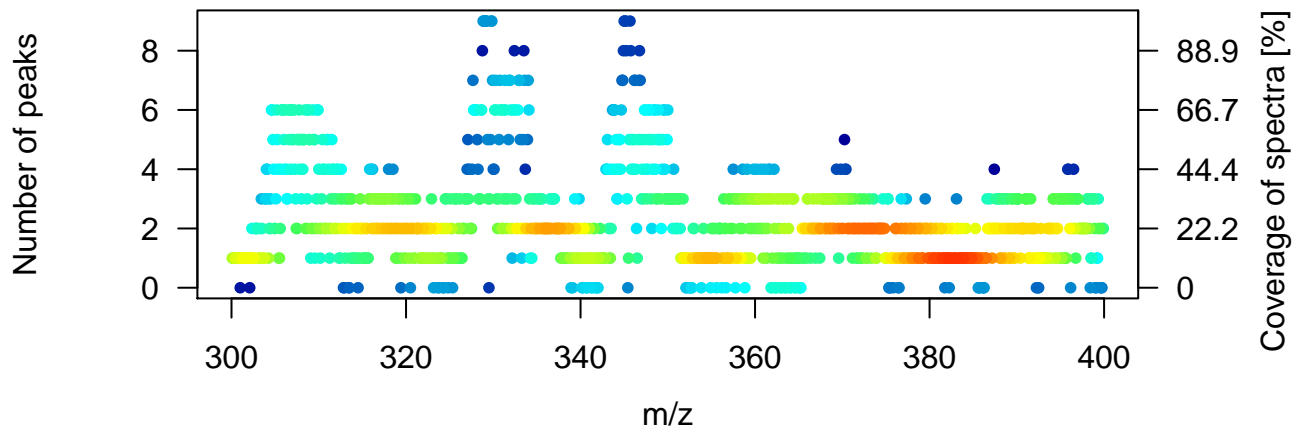


Number of peaks per spectrum

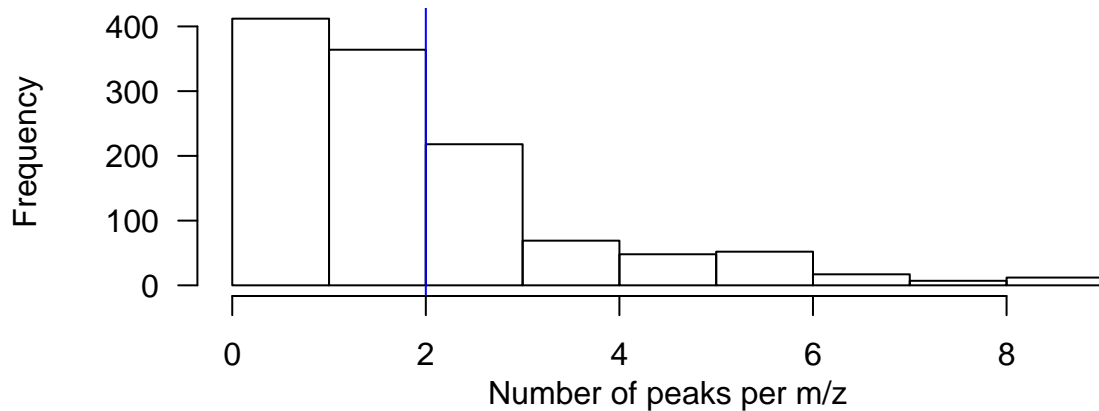




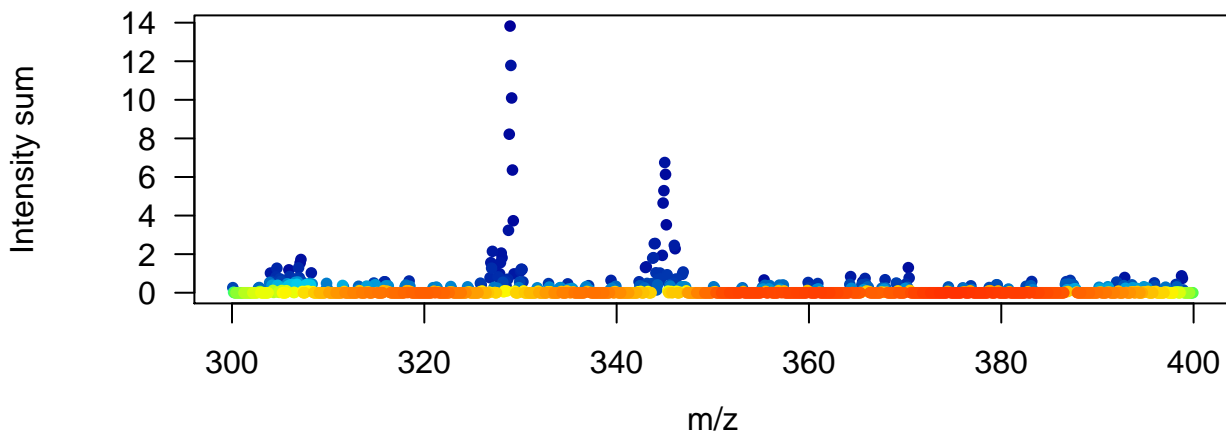
Number of peaks per m/z



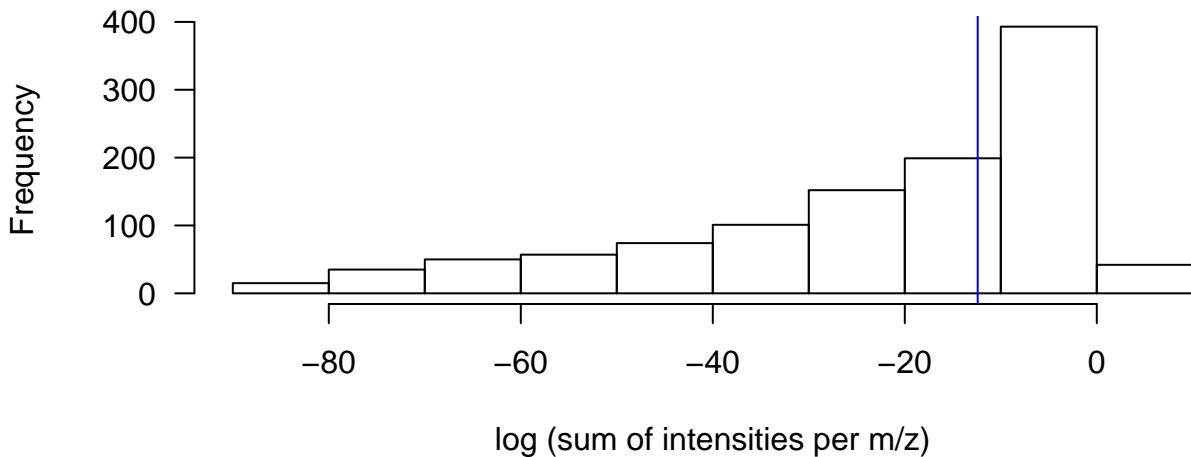
Number of peaks per m/z



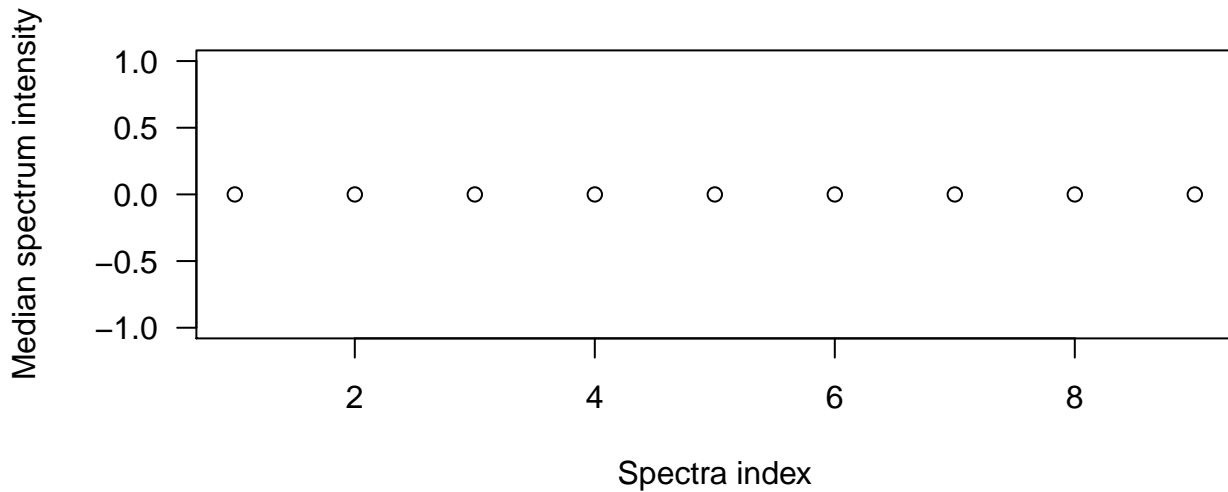
Sum of intensities per m/z



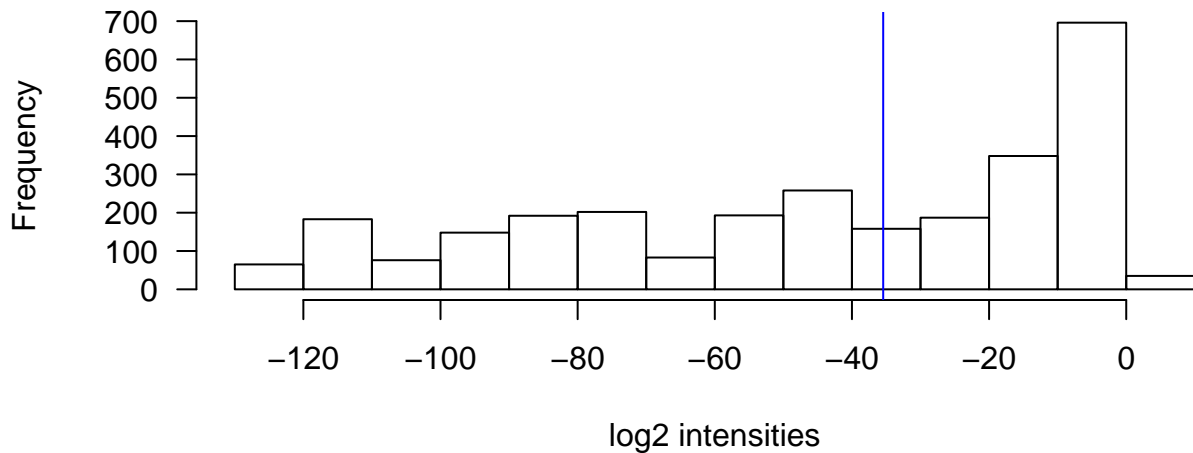
Sum of intensities per m/z



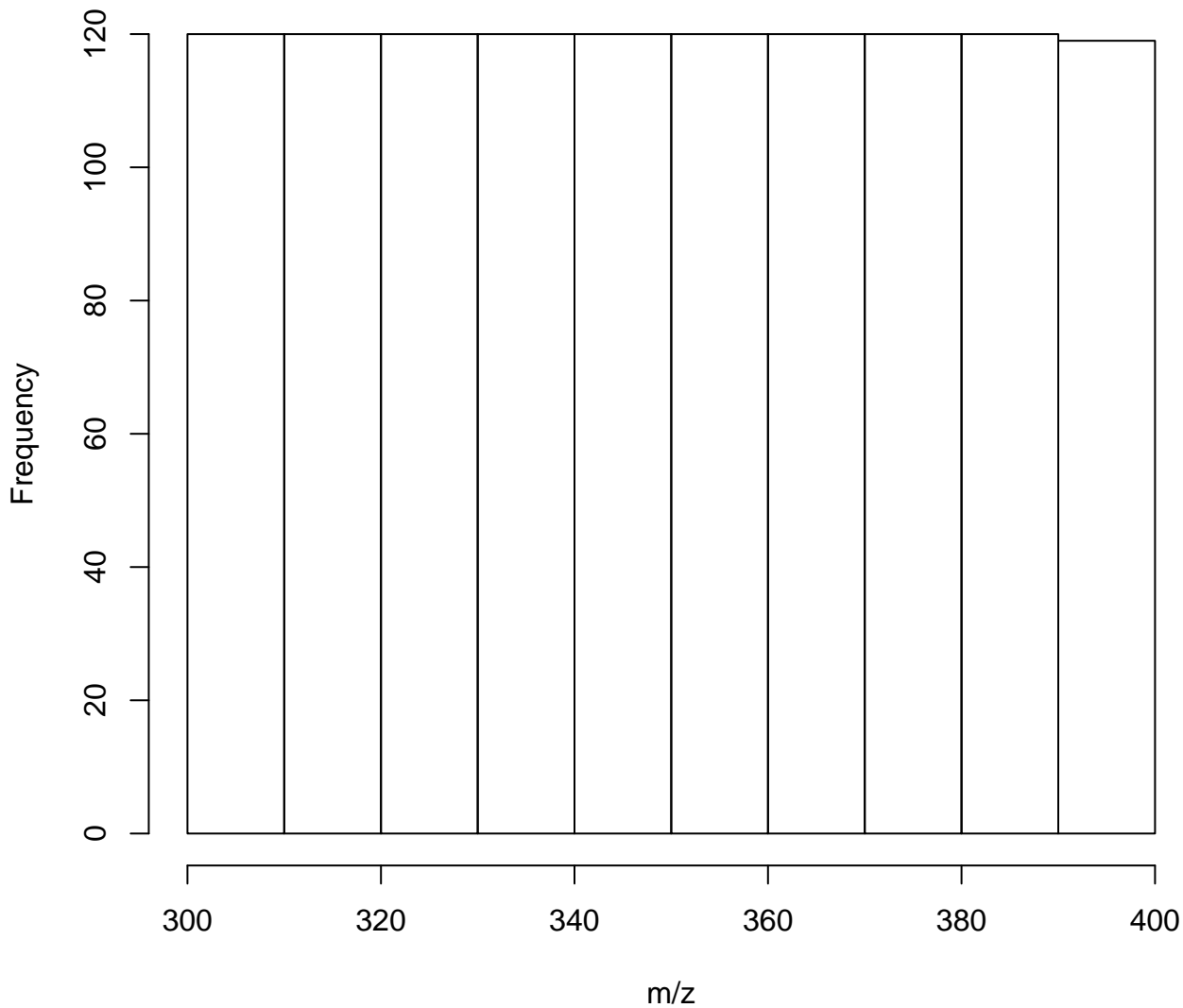
Median intensity per spectrum



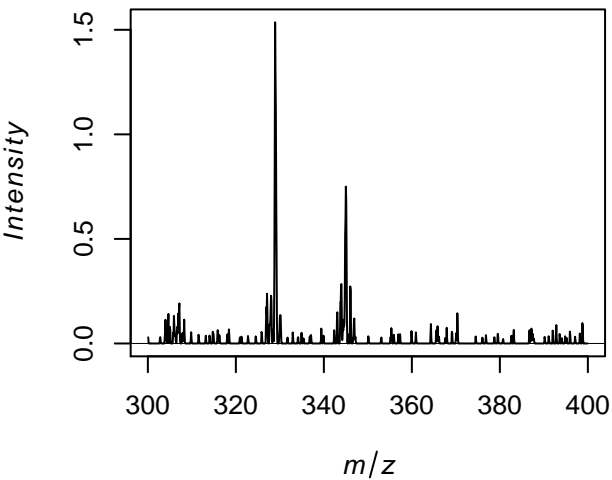
Log2-transformed intensities



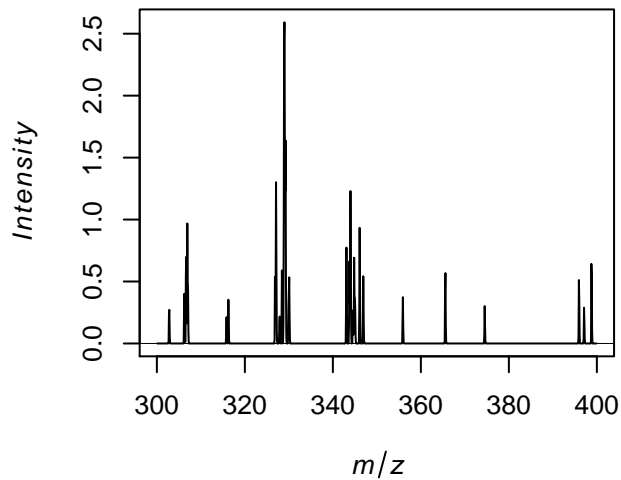
Histogram of m/z values



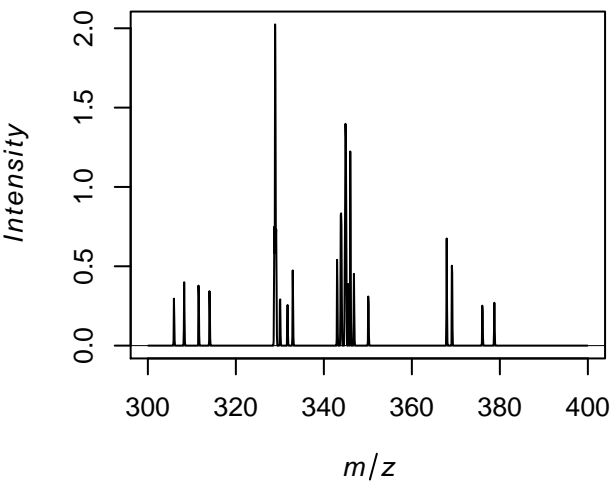
Average spectrum



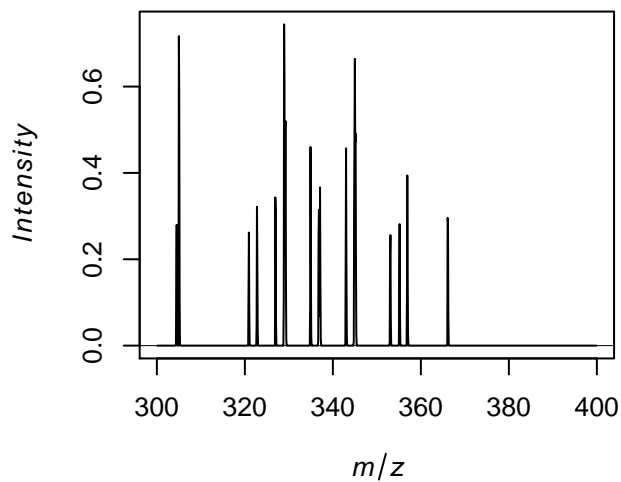
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

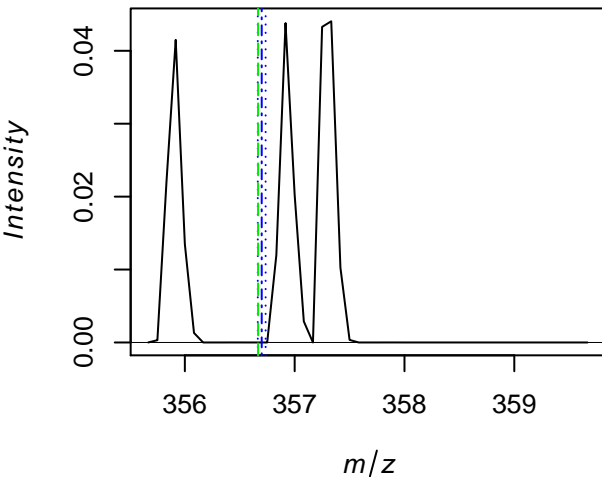


theor. m/z: 356.7

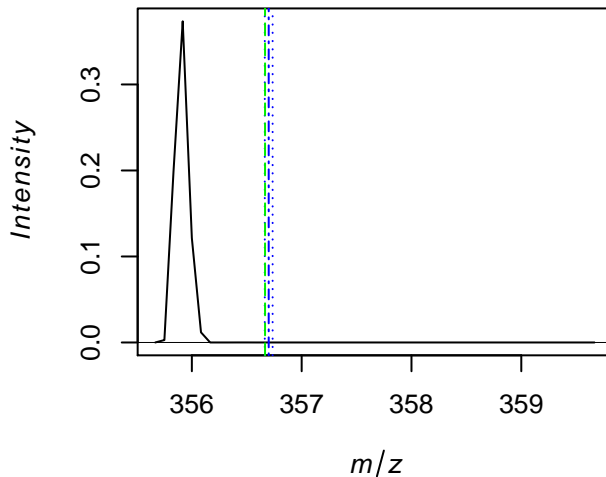
most abundant m/z: NA

closest m/z: 356.6667

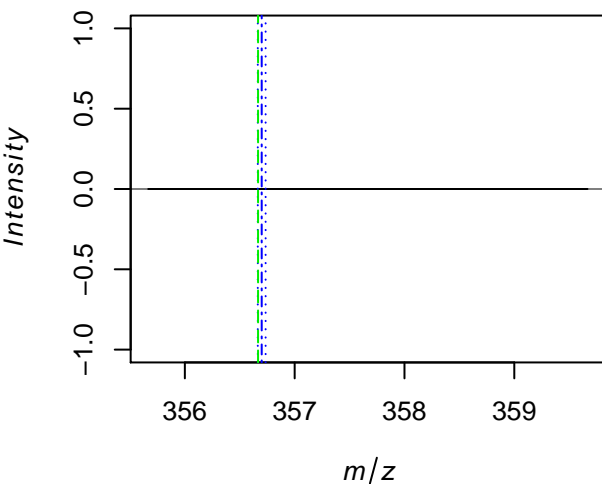
average spectrum



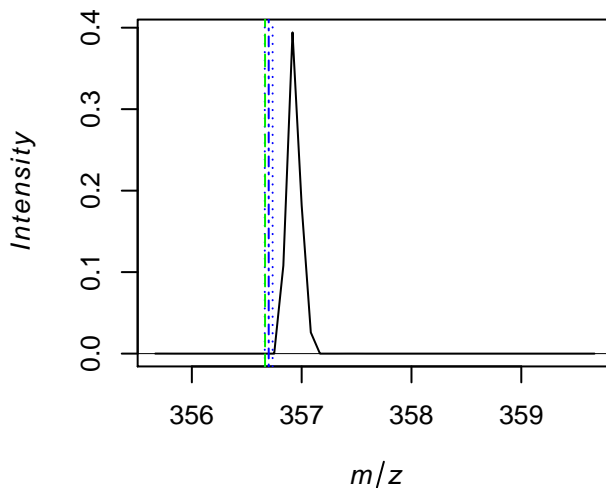
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3



Difference closest measured m/z vs. theoretical calibrant m/z

