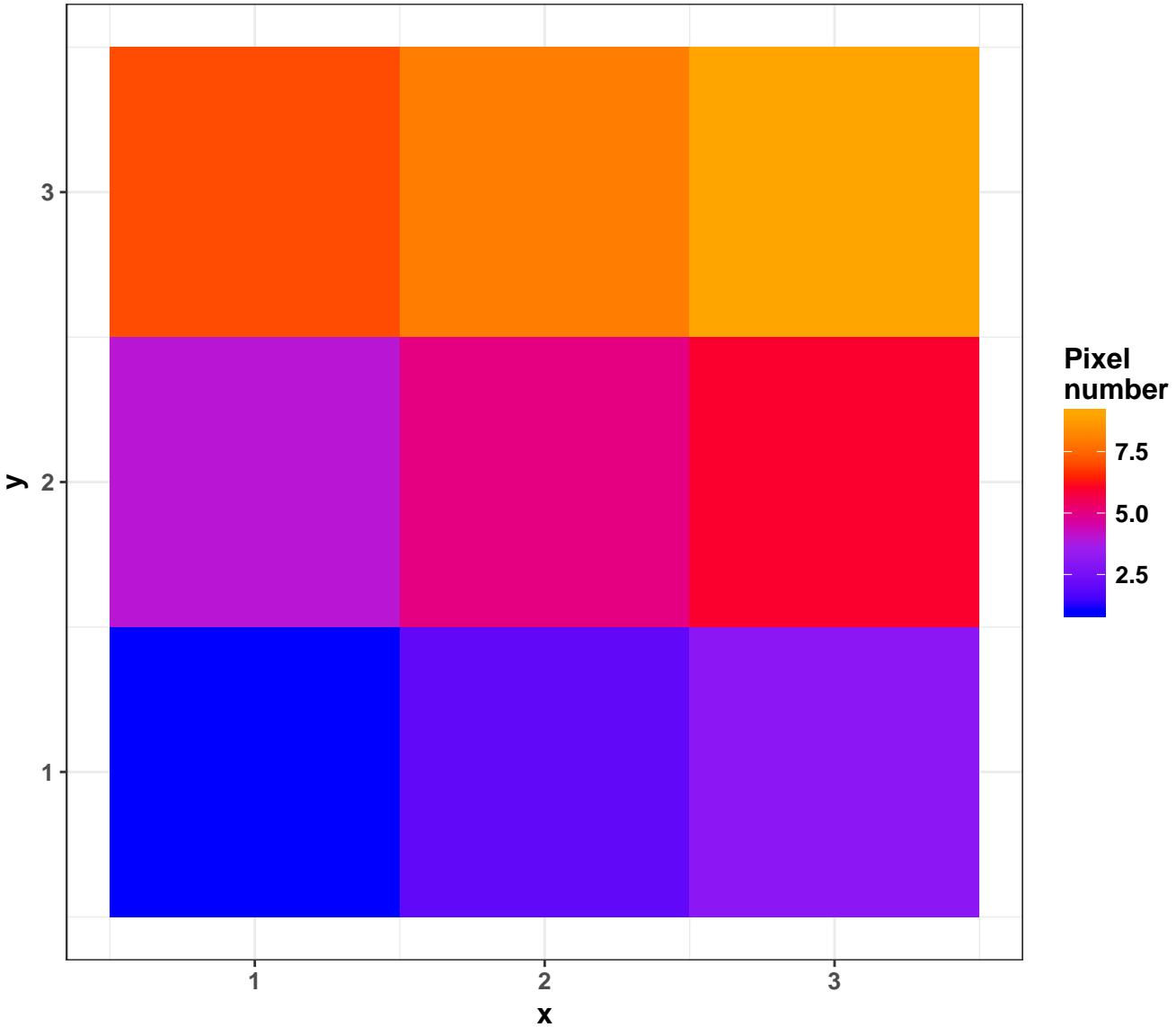


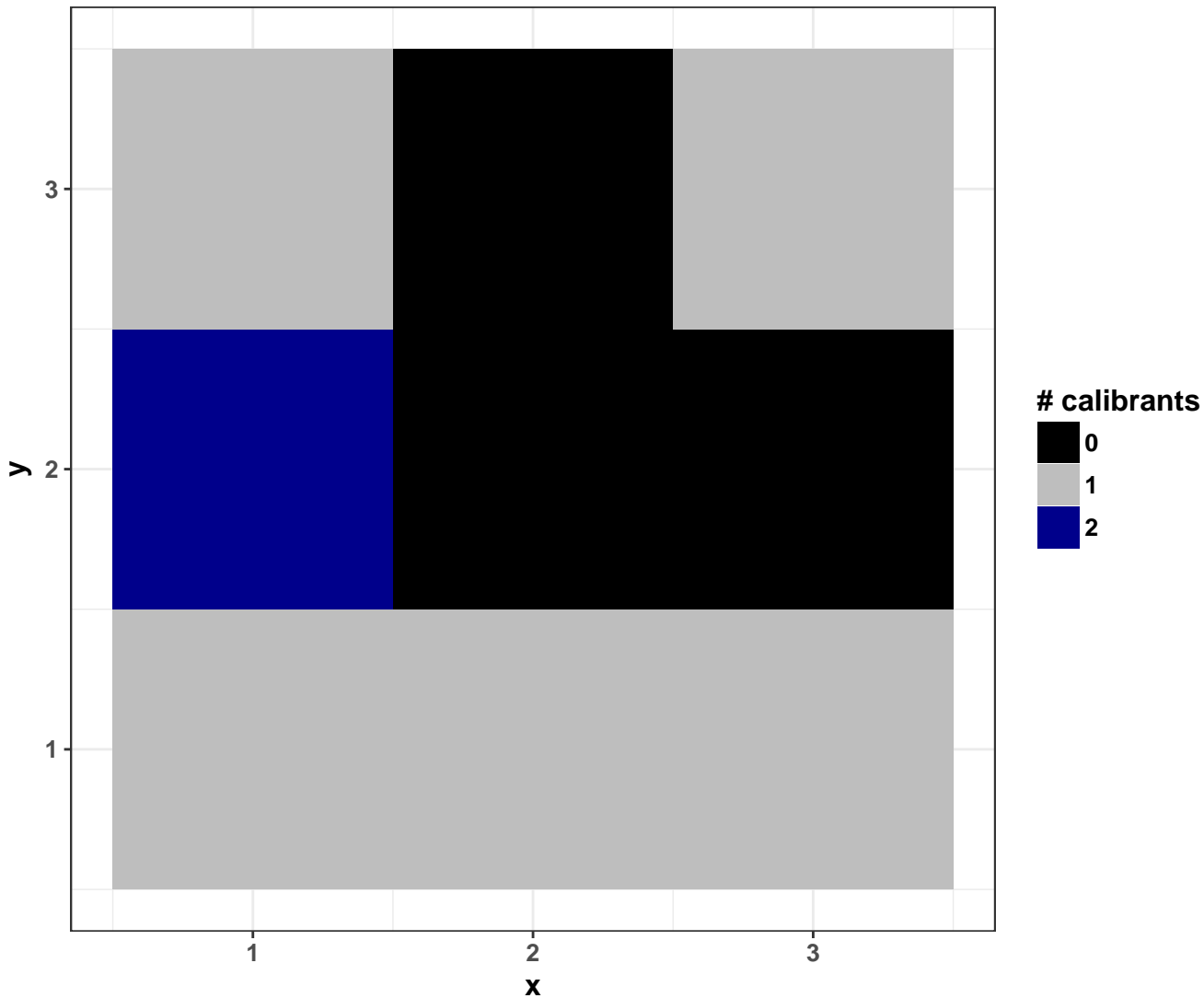
Testfile_imzml

| 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

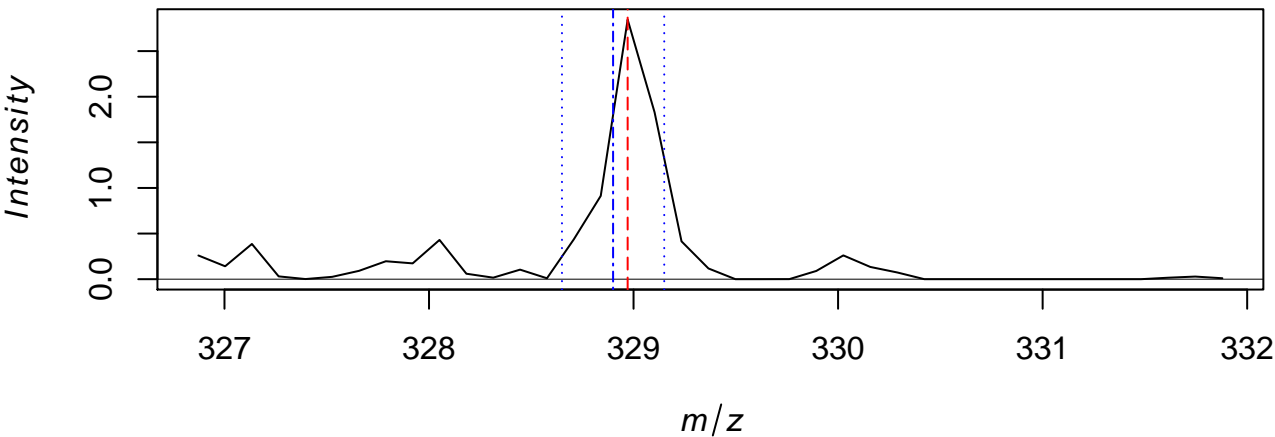


Number of calibrants per pixel (± 100 ppm)

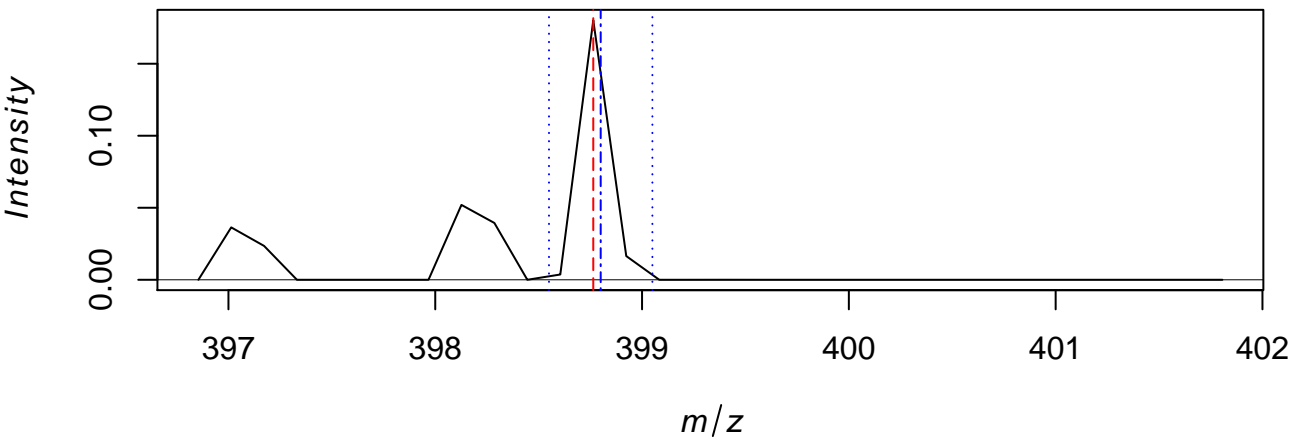


Control of fold change plot

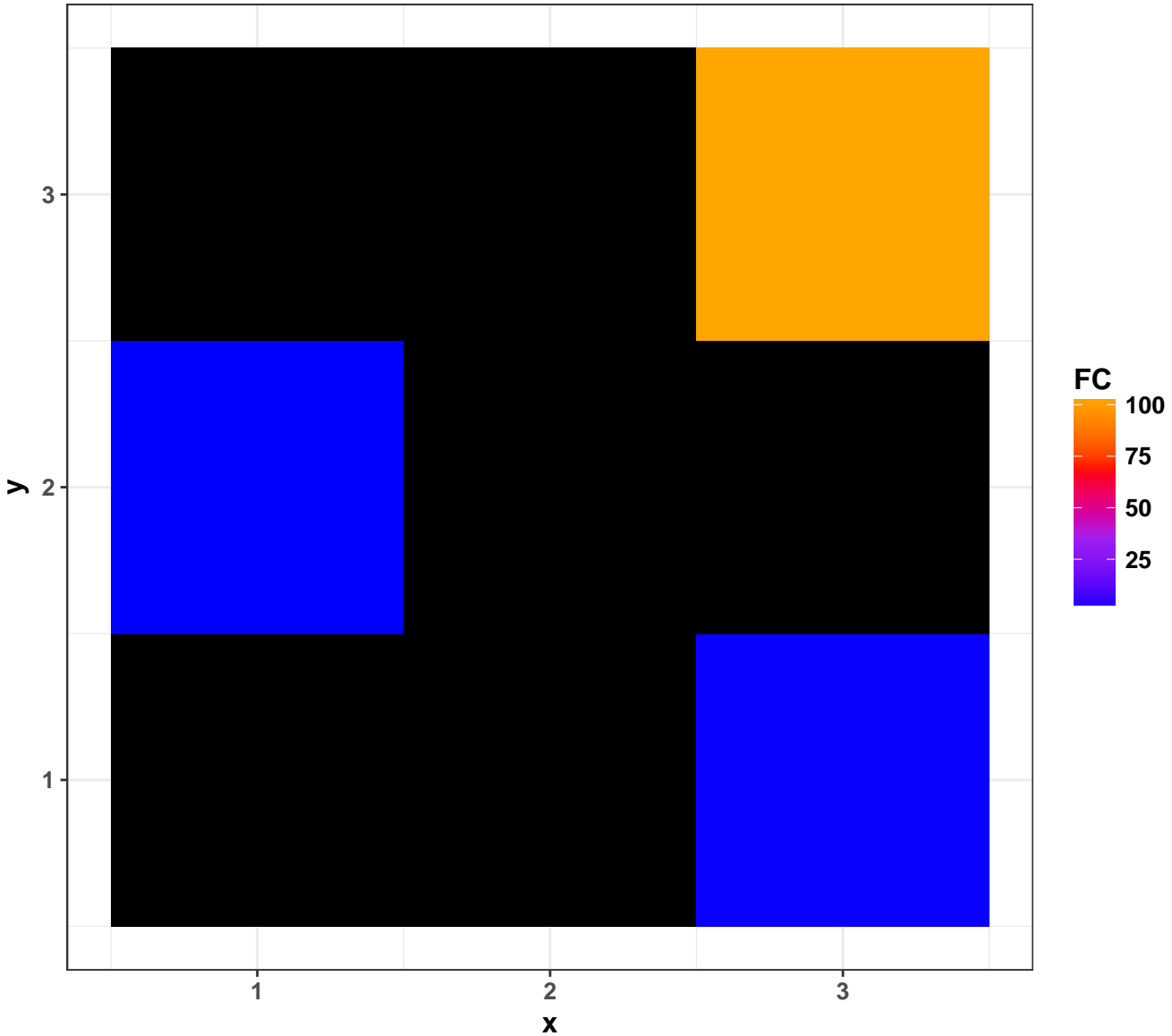
average spectrum 328.9 Da



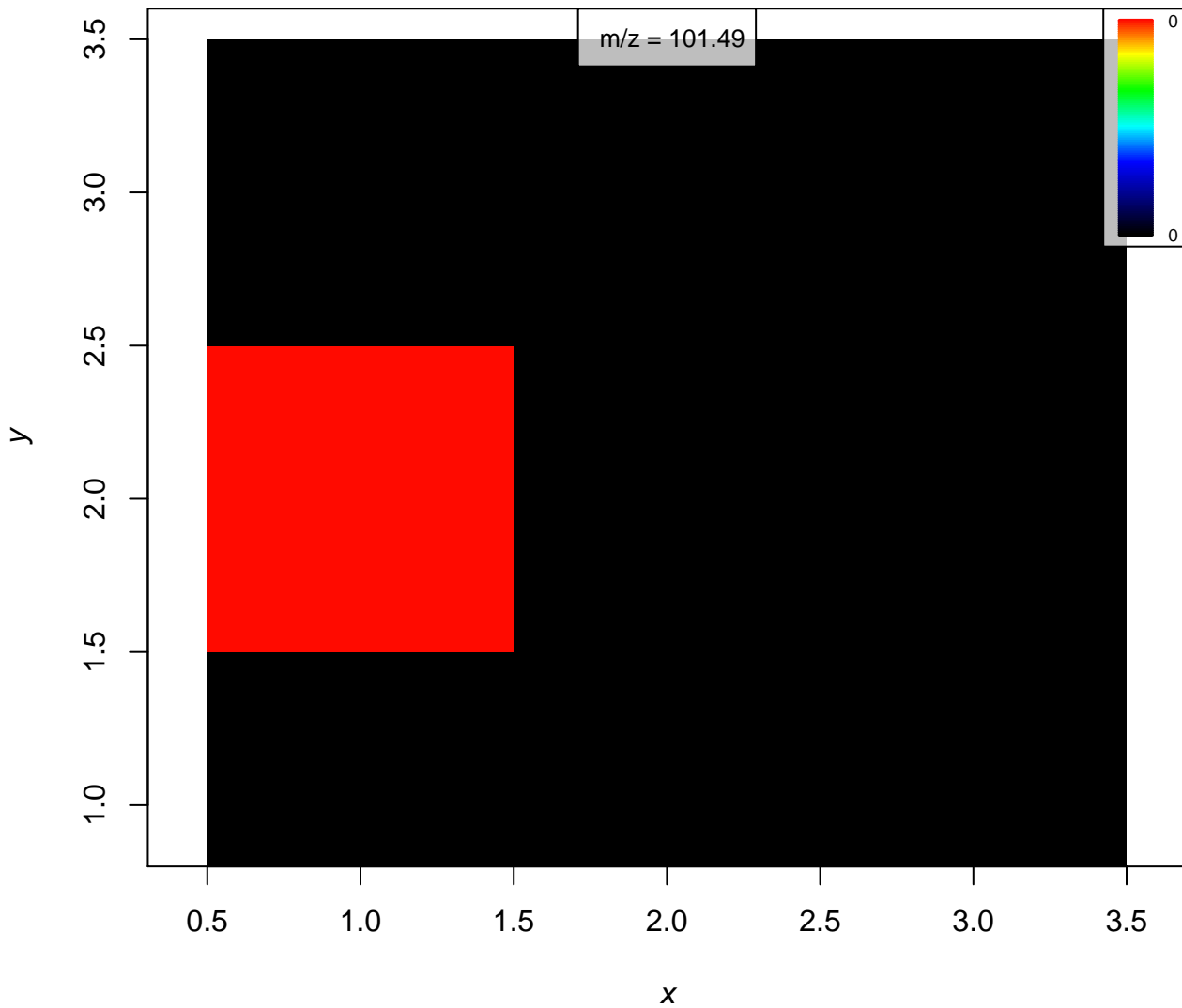
average spectrum 398.8 Da



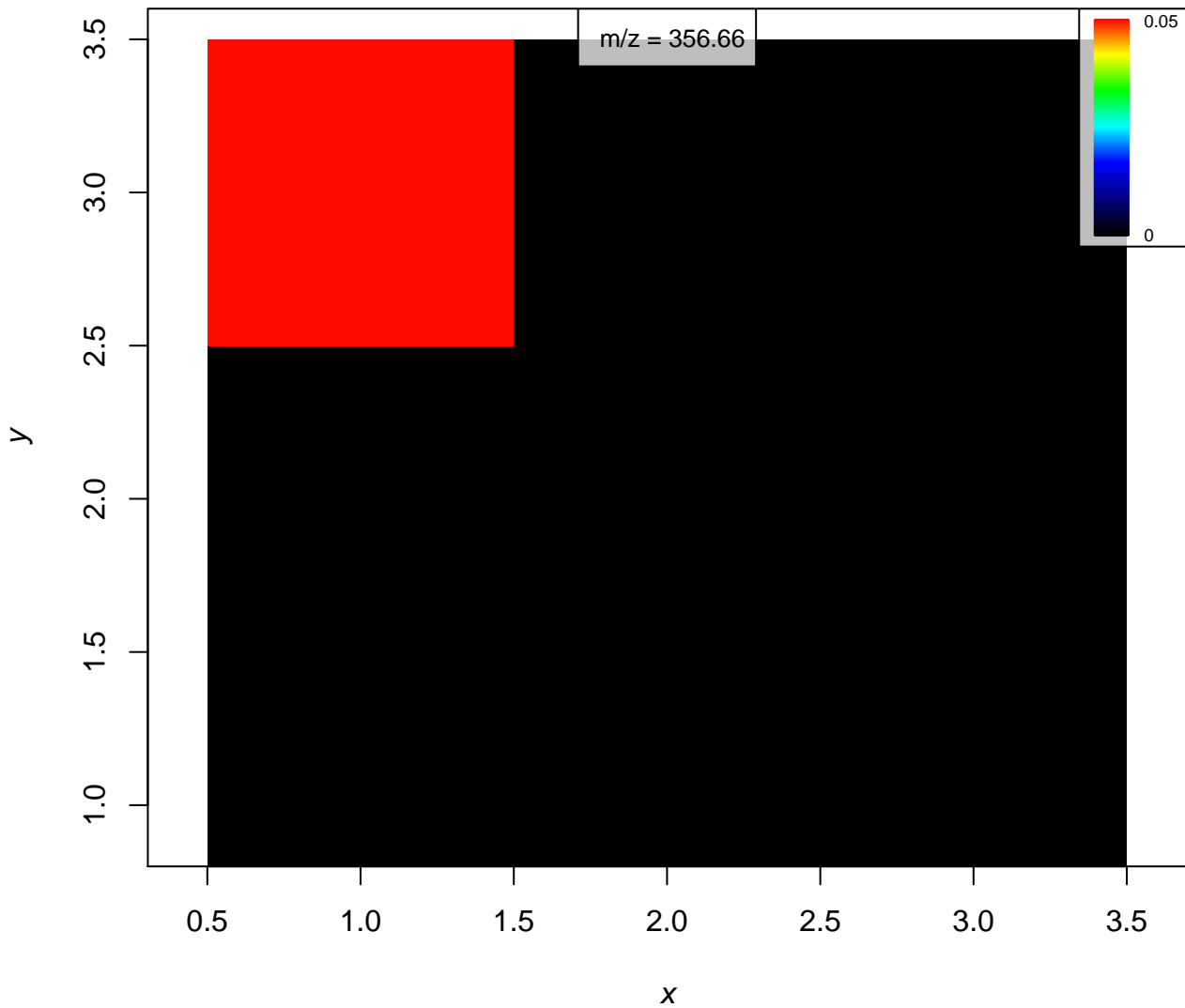
Ratio of mass1 (328.9) / mass2 (398.8)



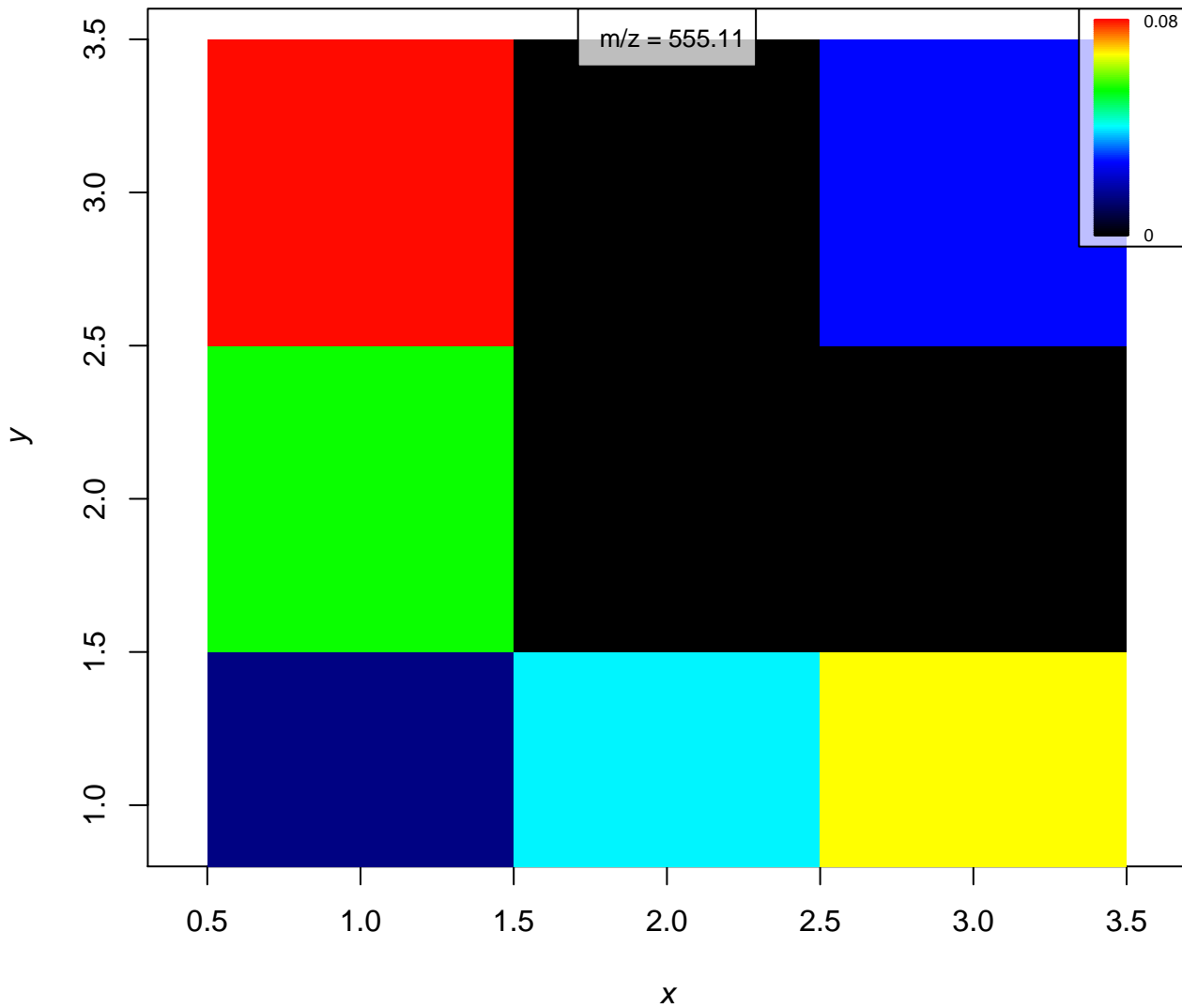
101.5: 101.5 (± 100 ppm)



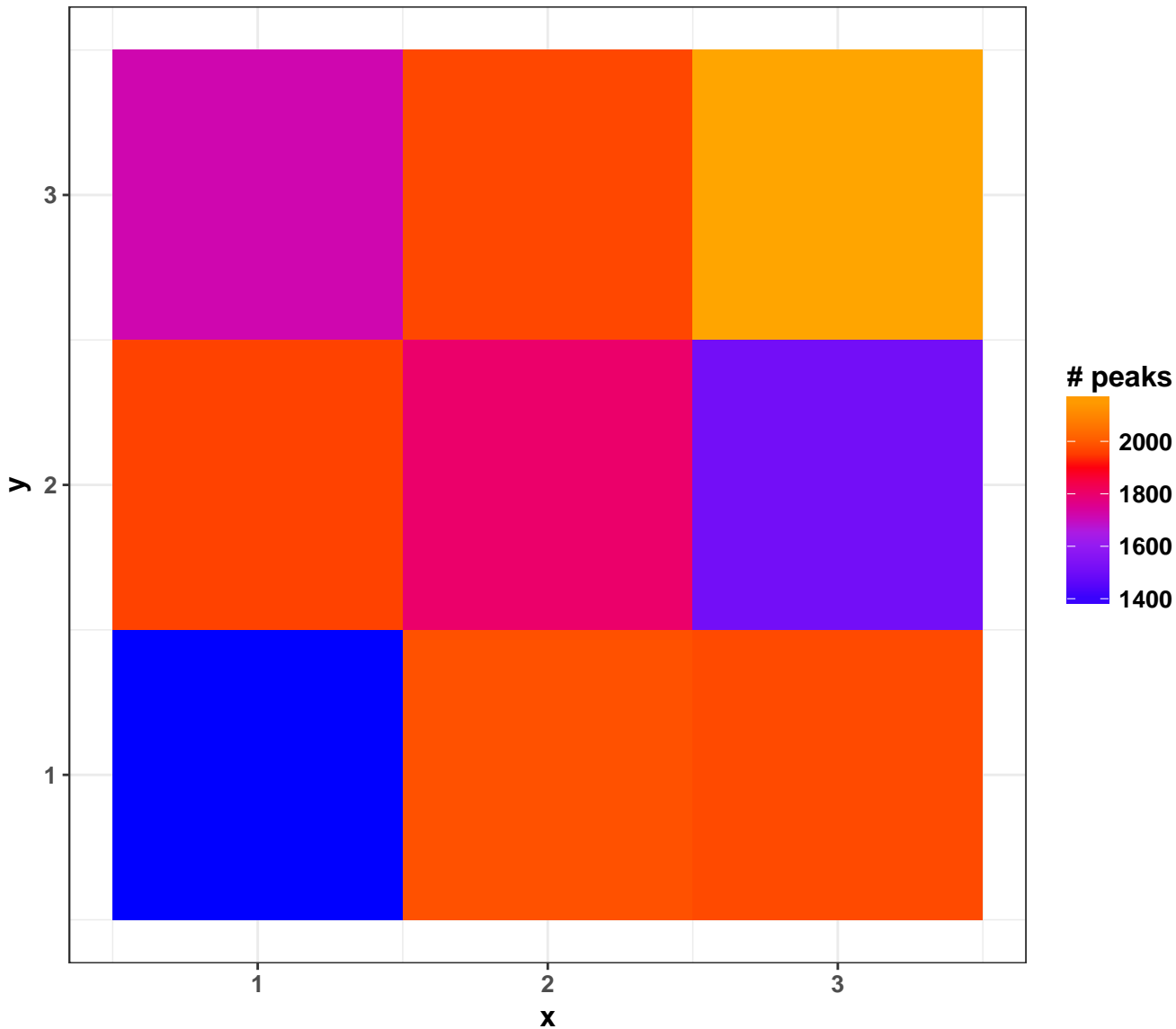
356.7: 356.7 (± 100 ppm)



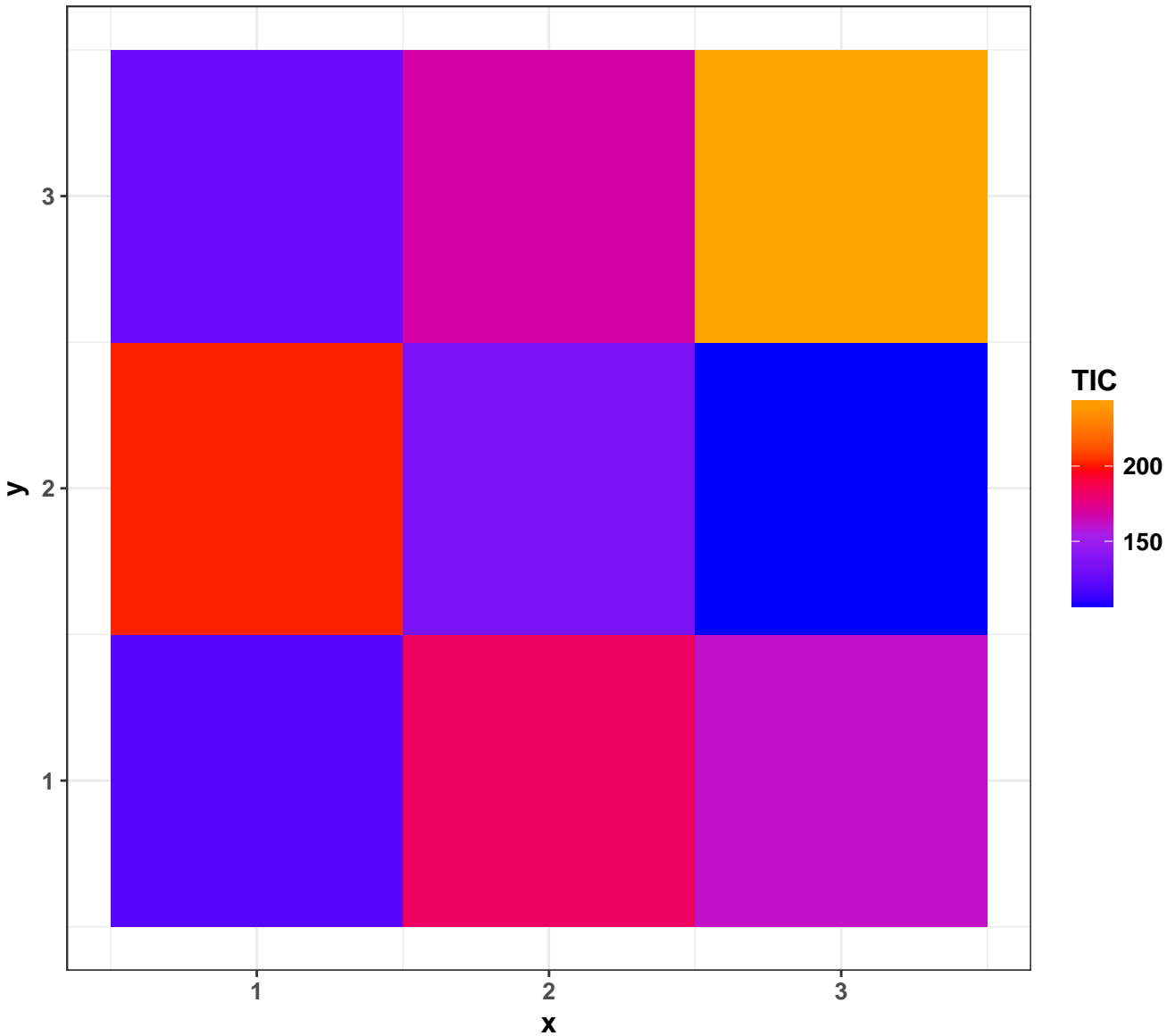
555.1: 555.1 (± 100 ppm)



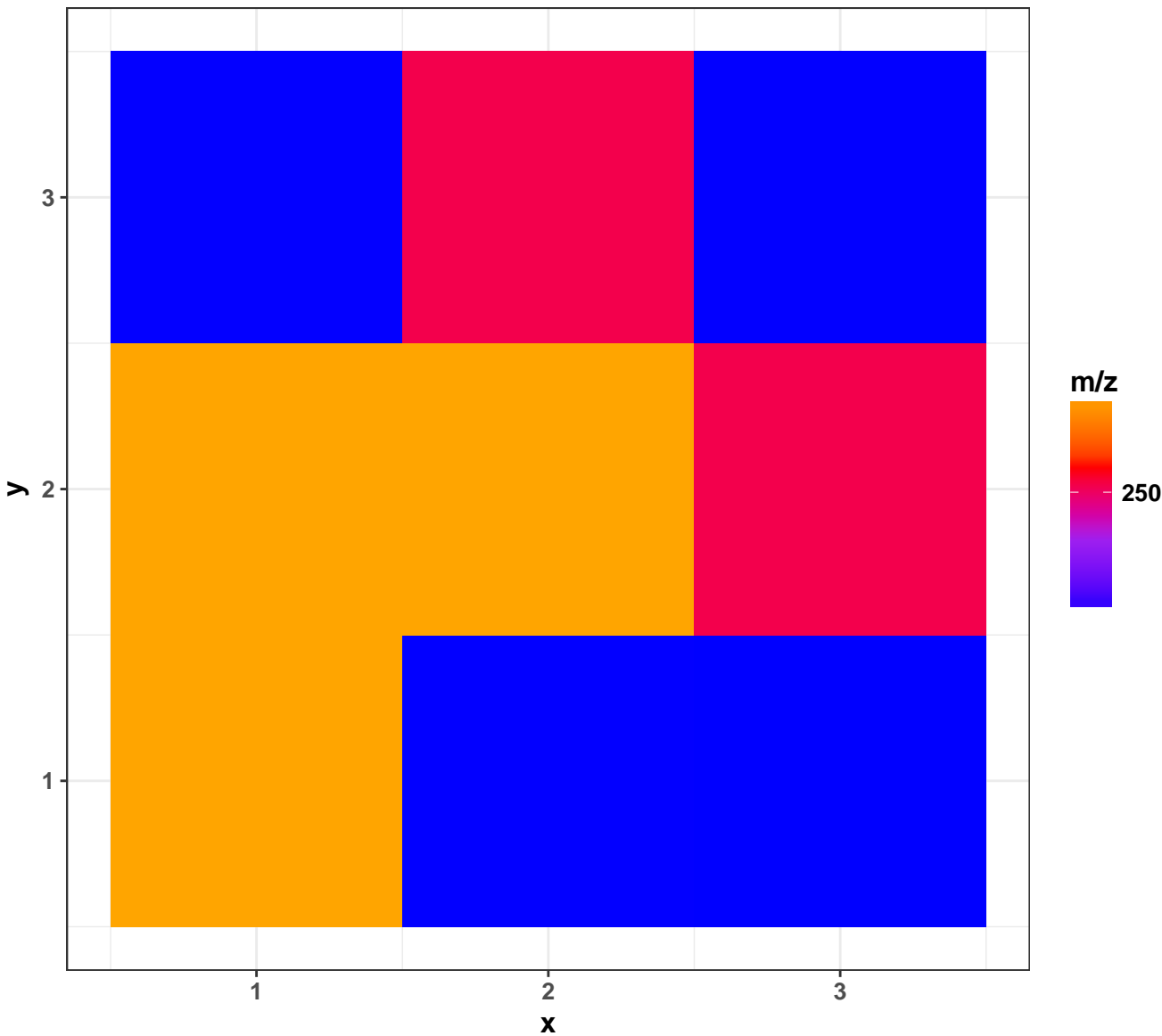
Number of peaks per spectrum



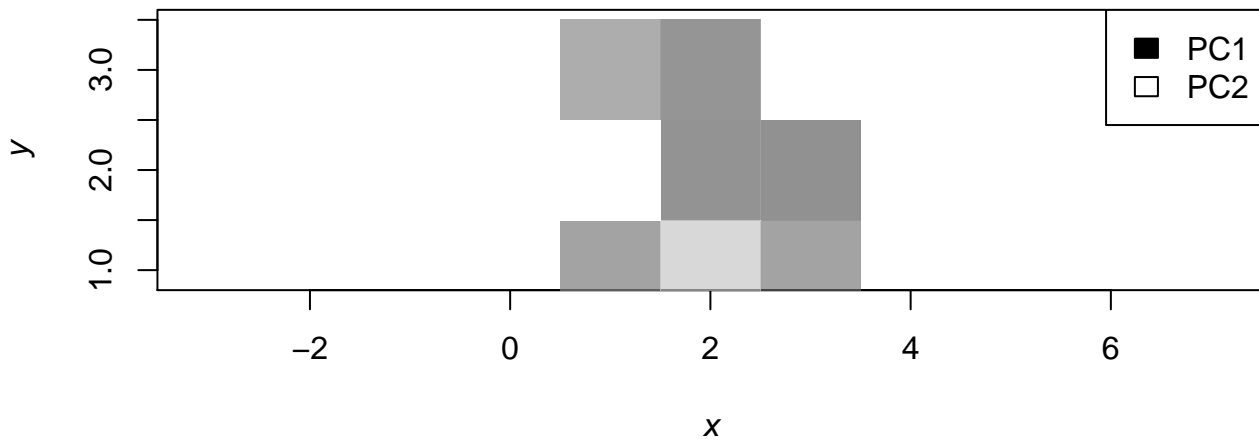
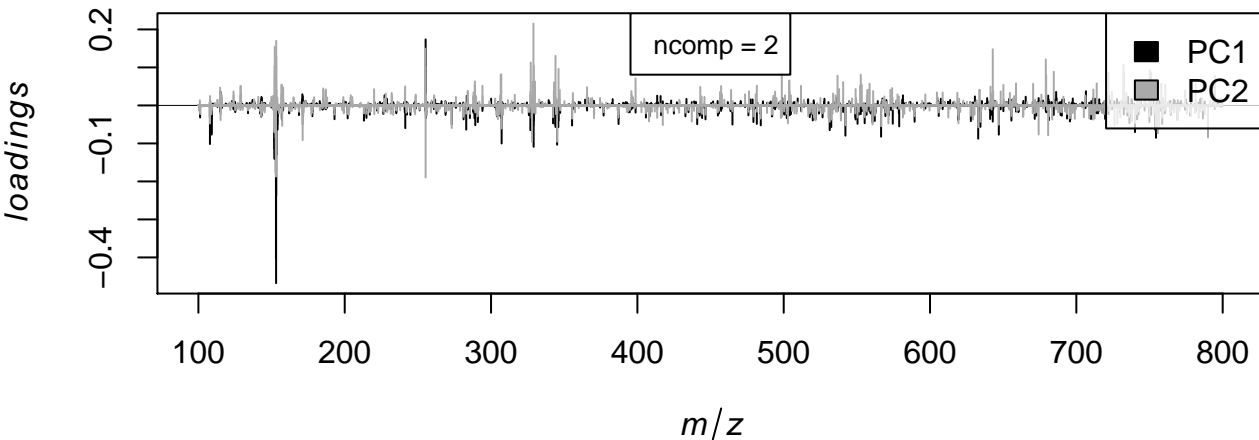
Total Ion Chromatogram



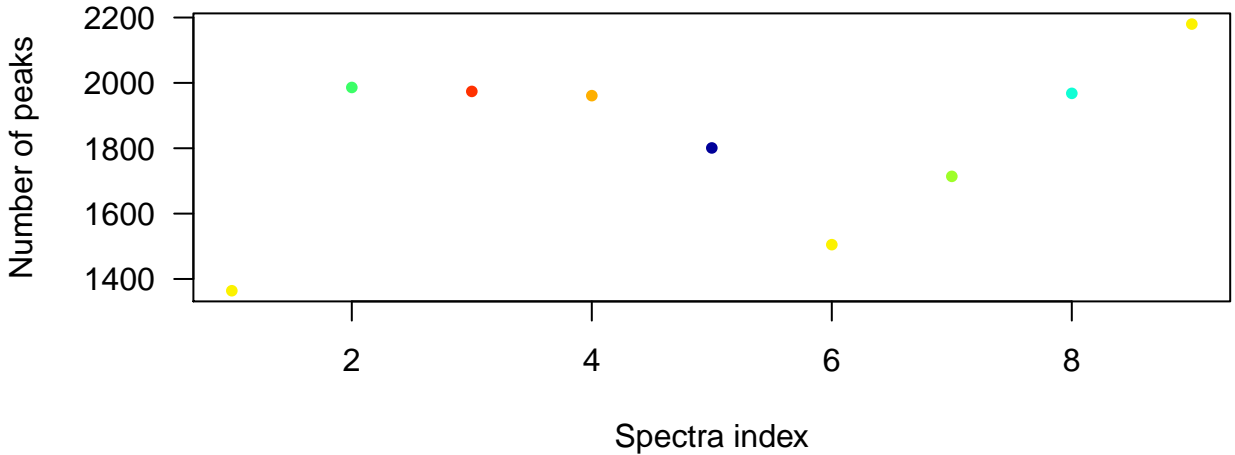
Most abundant m/z in each spectrum



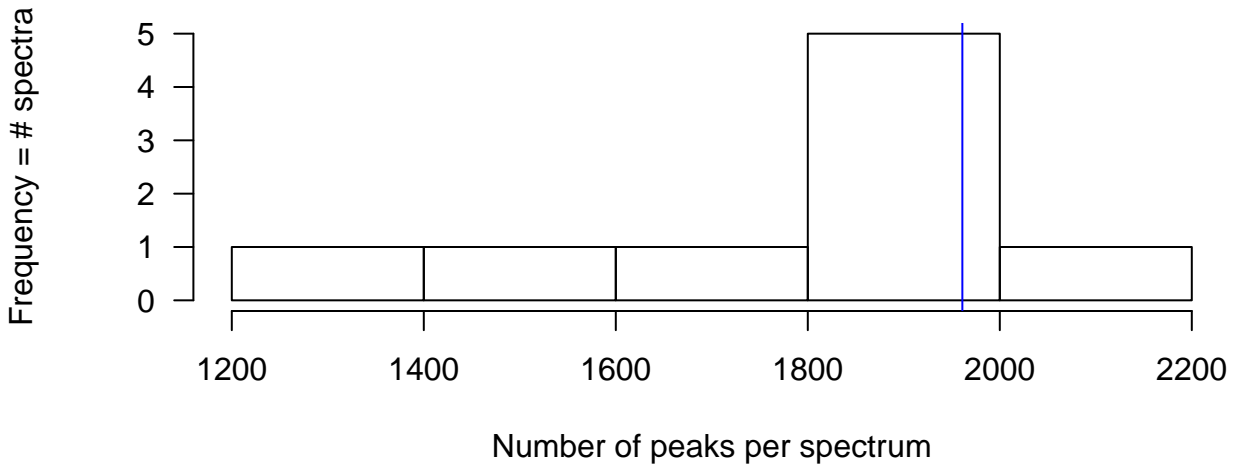
PCA for two components



Number of peaks per spectrum

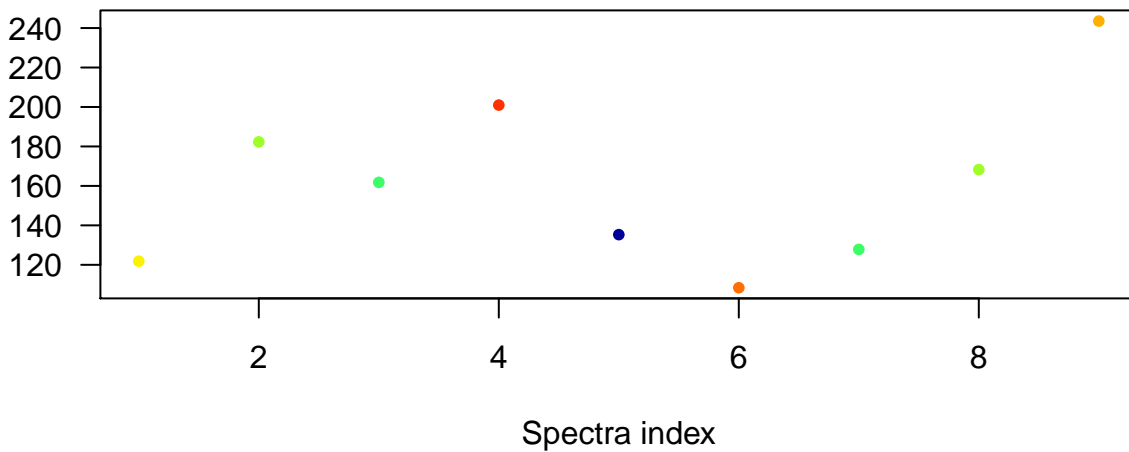


Number of peaks per spectrum



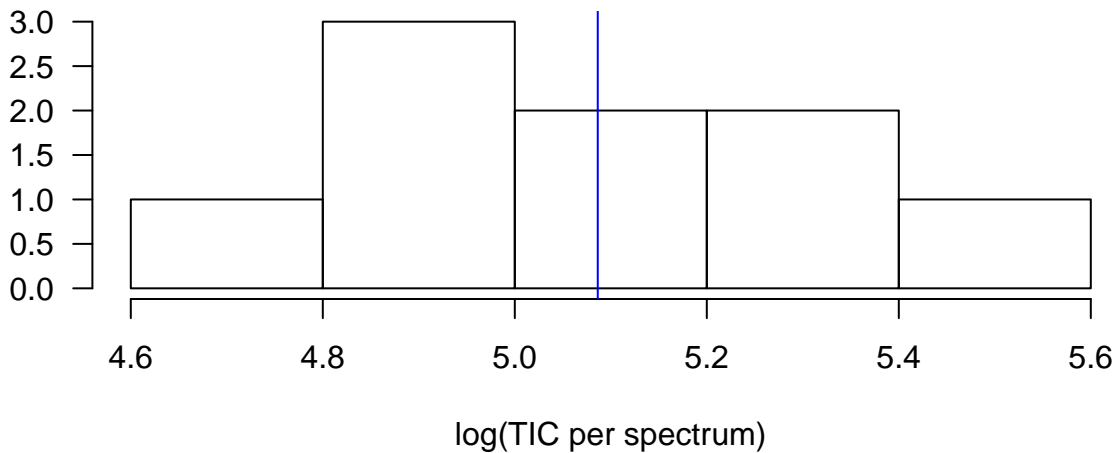
Total ion chromatogram intensity

TIC per spectrum

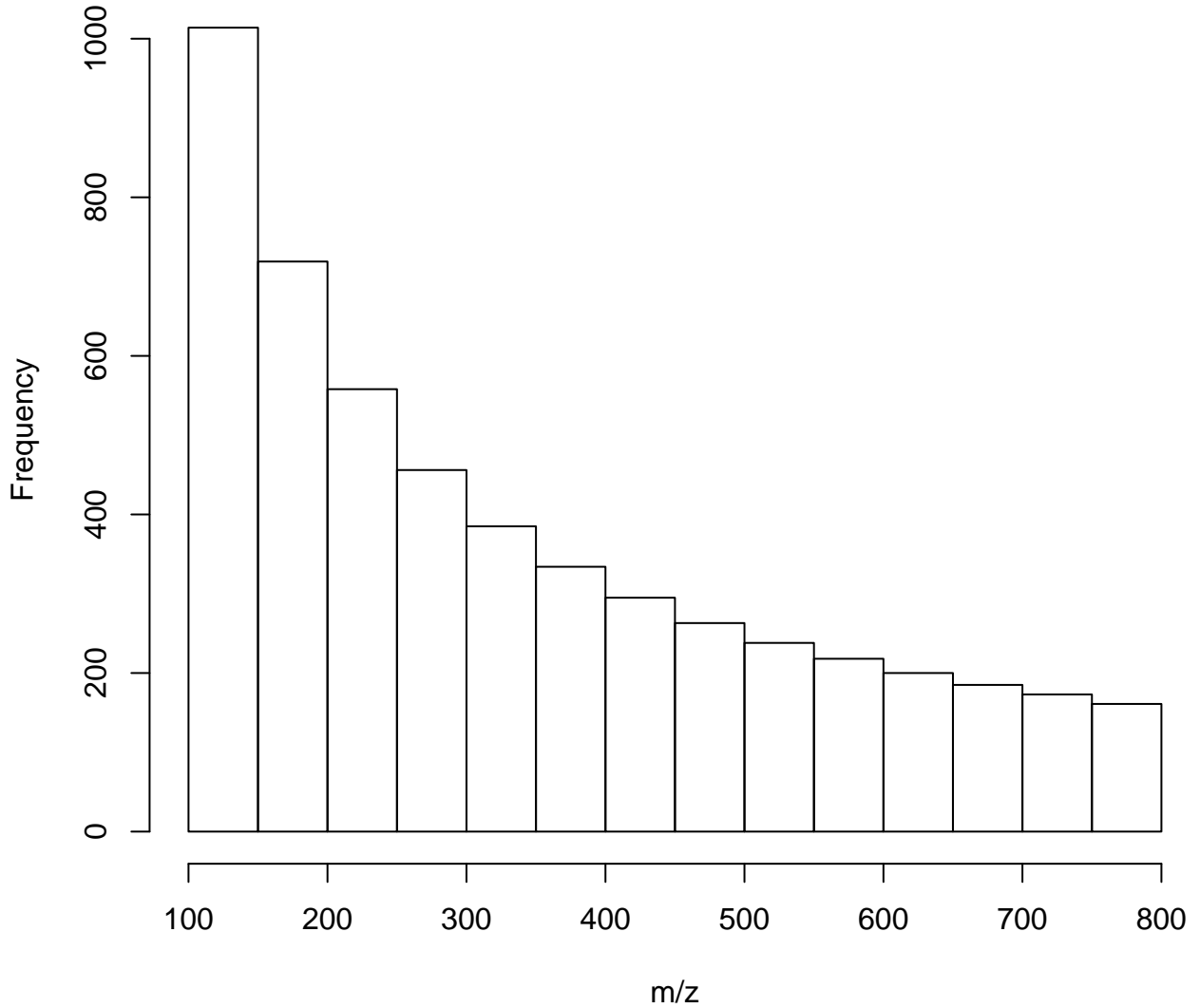


Frequency = # spectra

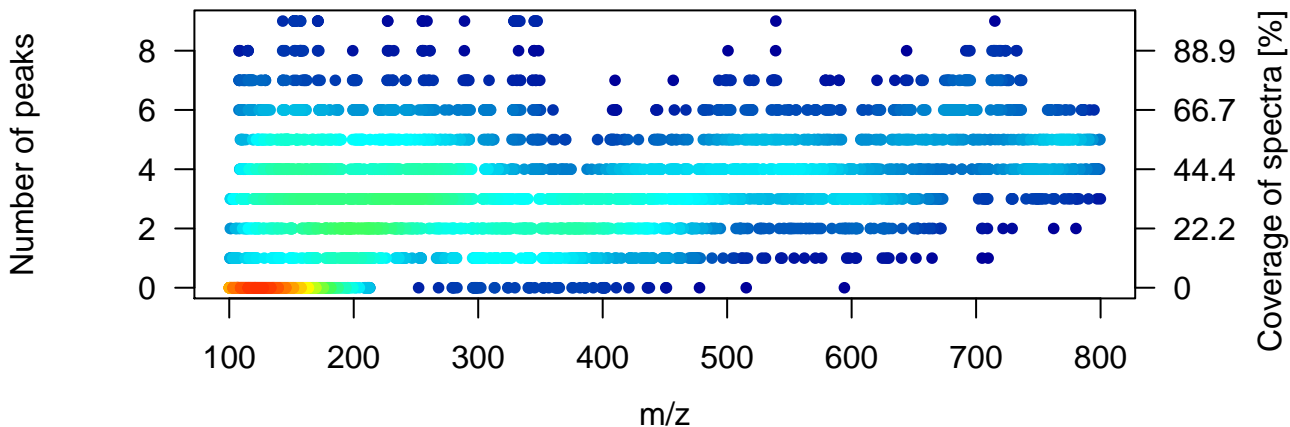
TIC per spectrum



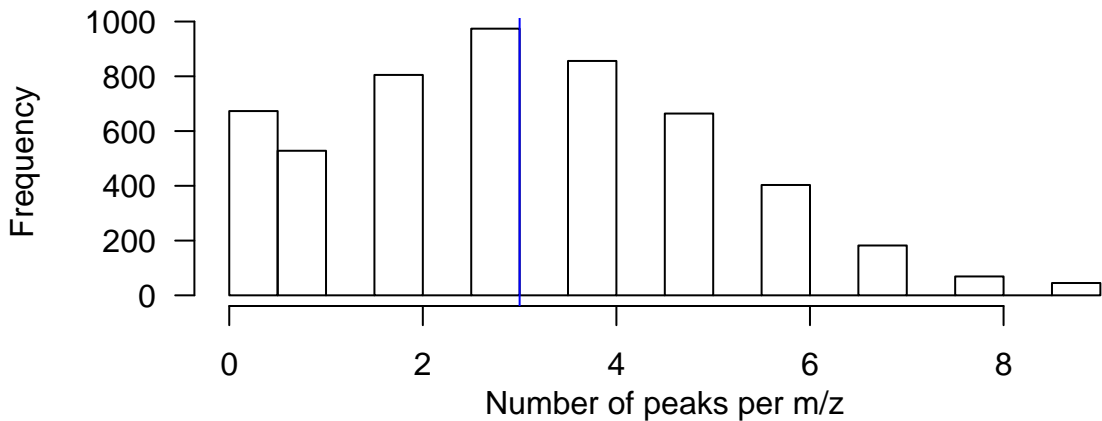
Histogram of m/z values



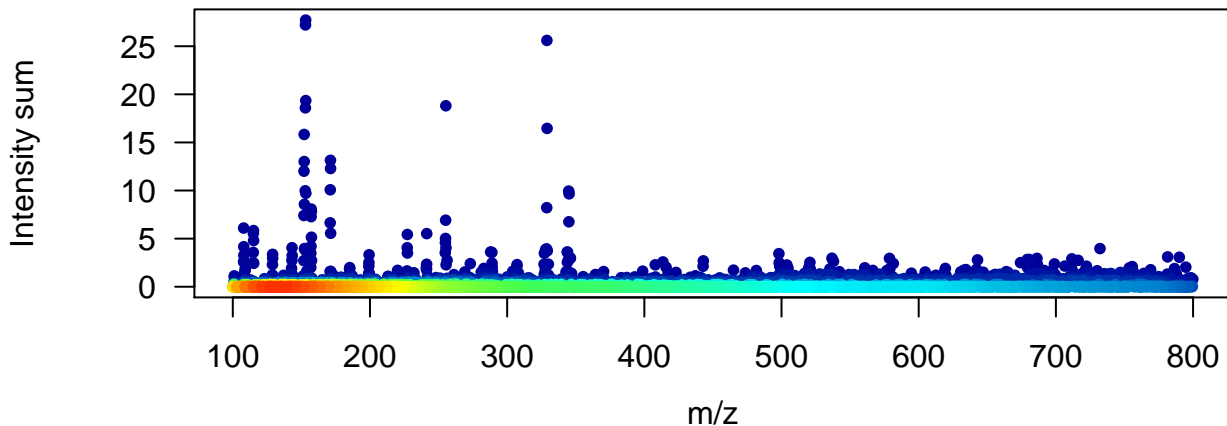
Number of peaks per m/z



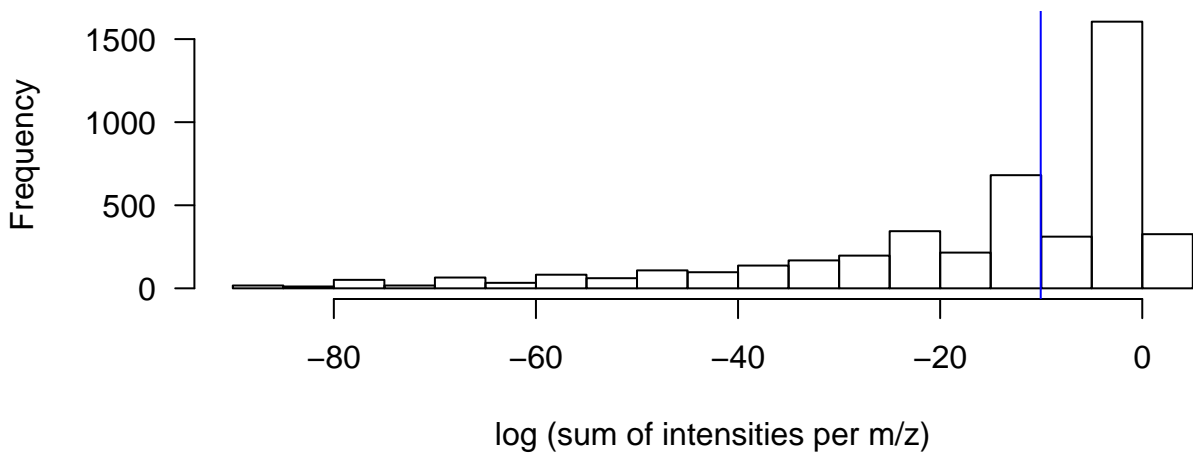
Number of peaks per m/z



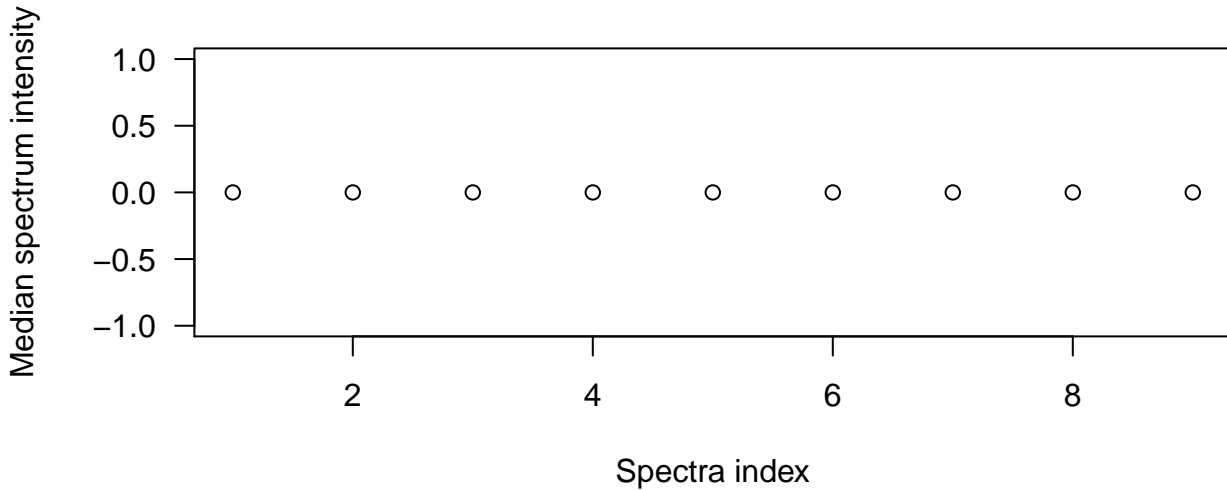
Sum of intensities per m/z



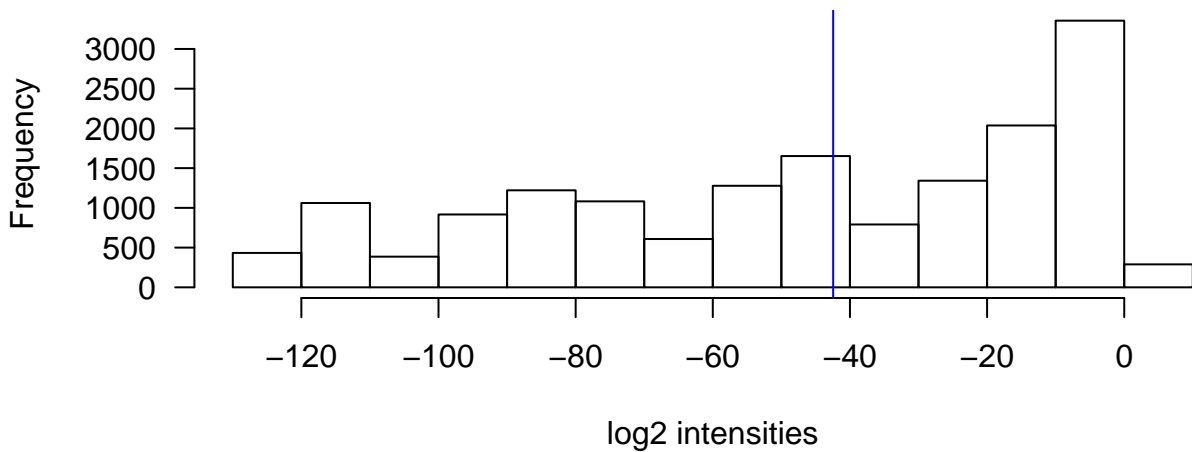
Sum of intensities per m/z



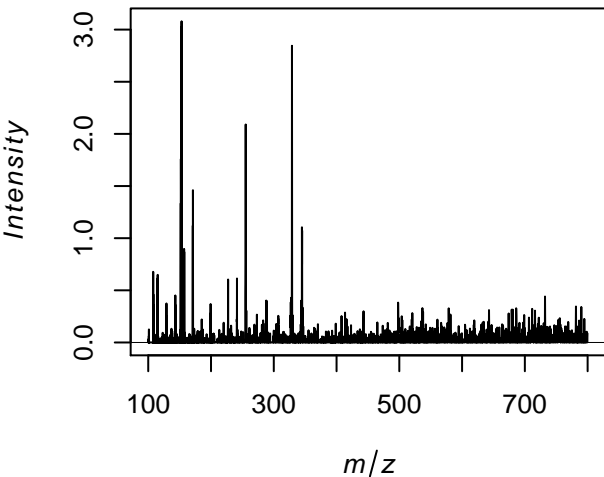
Median intensity per spectrum



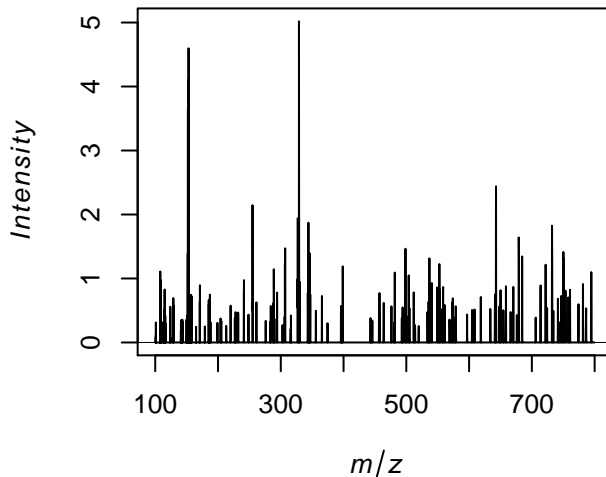
Log2-transformed intensities



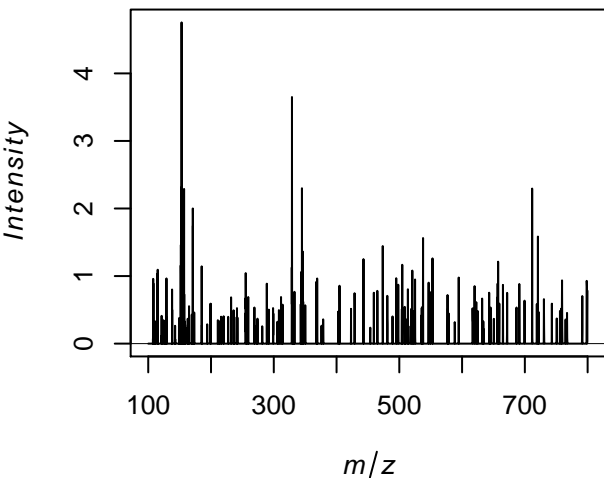
Average spectrum



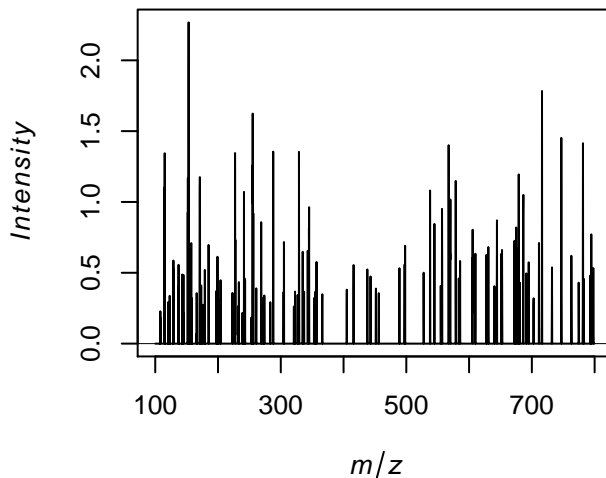
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

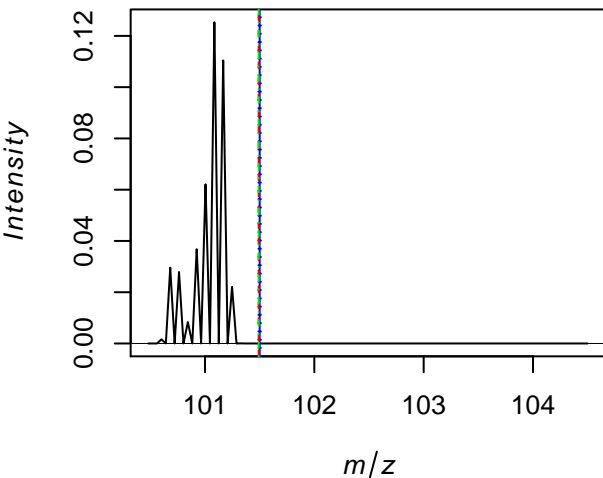


theor. m/z: 101.5

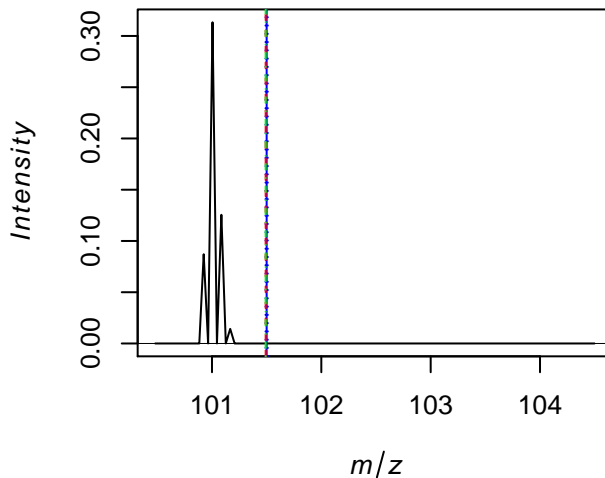
most abundant m/z: 101.491

closest m/z: 101.491

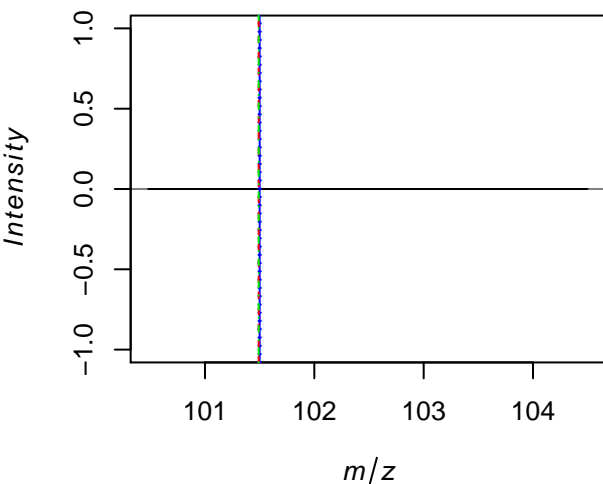
average spectrum



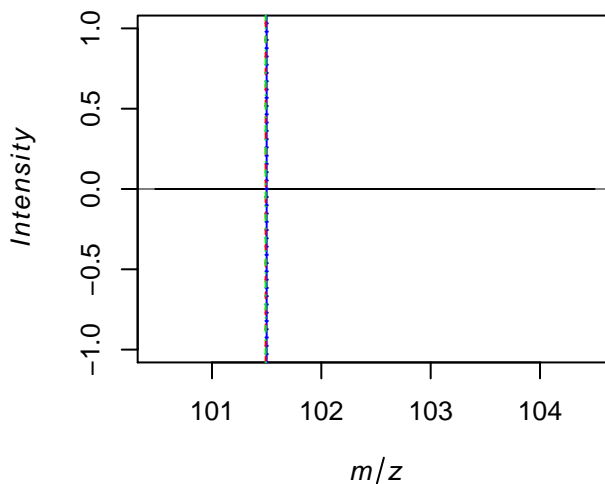
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

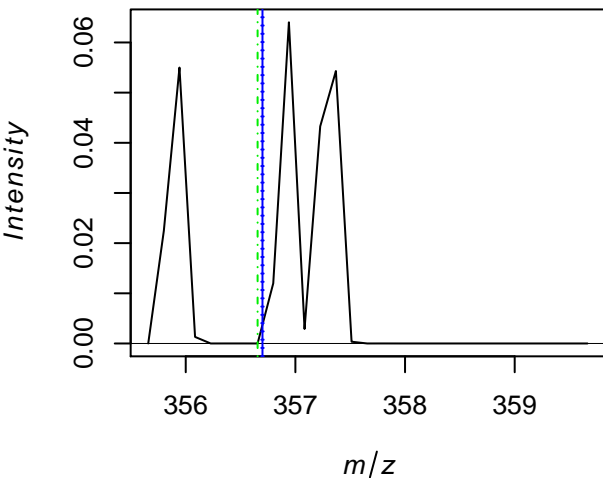


theor. m/z: 101.5

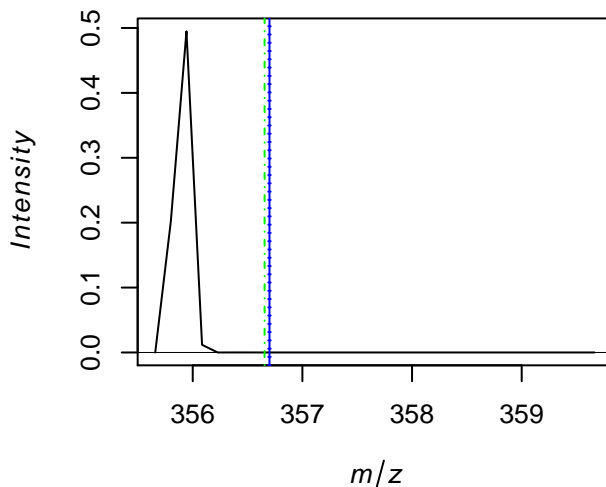
most abundant m/z: NA

closest m/z: 356.6555

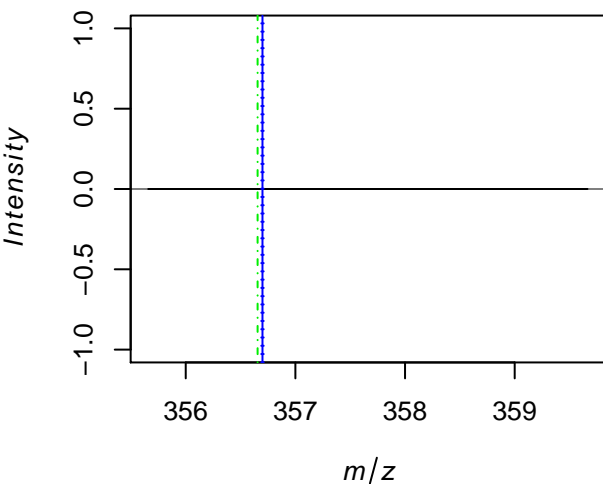
average spectrum



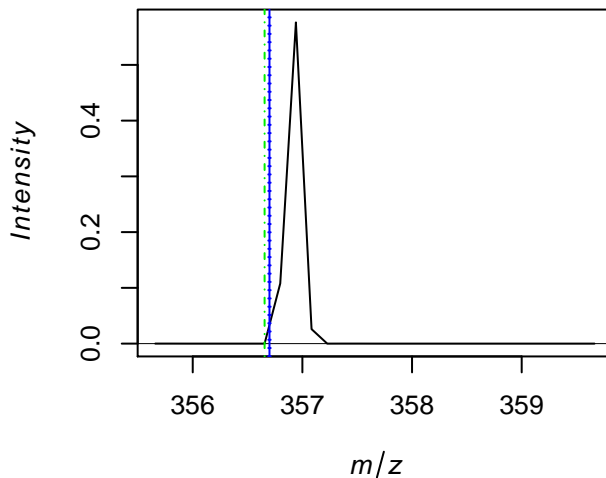
Spectrum at x = 1, y = 2



Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

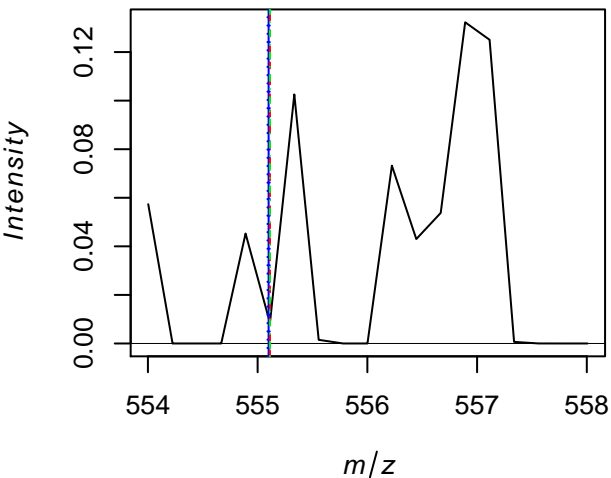


theor. m/z: 101.5

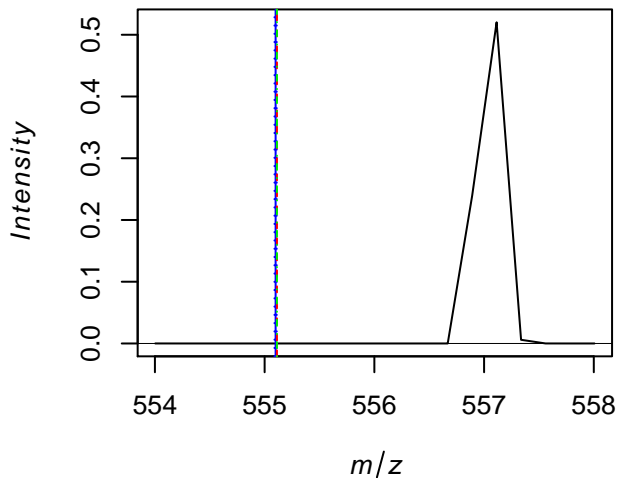
most abundant m/z: 555.1122

closest m/z: 555.1122

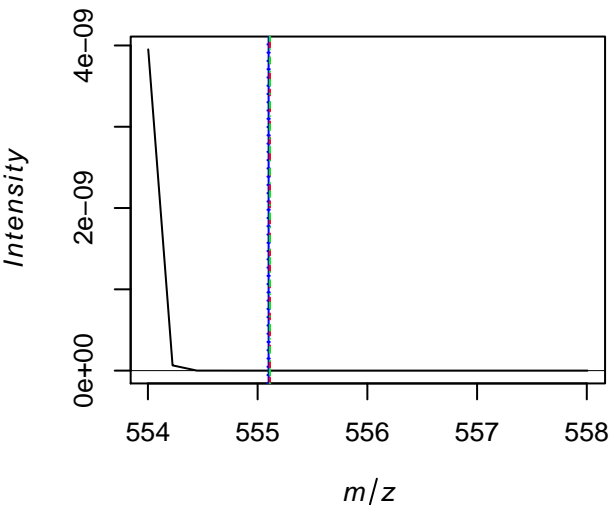
average spectrum



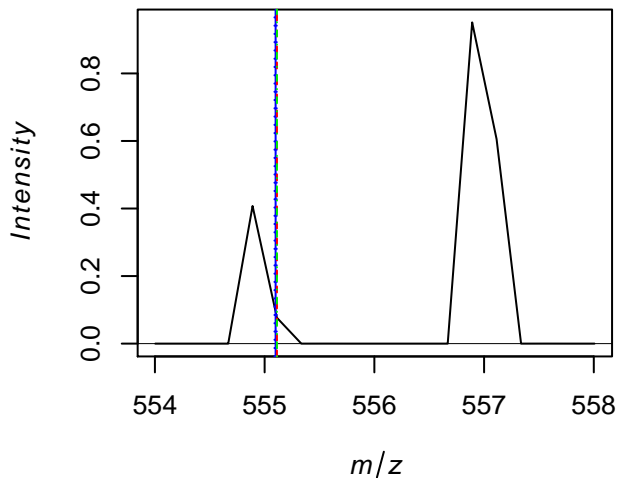
Spectrum at x = 1, y = 2



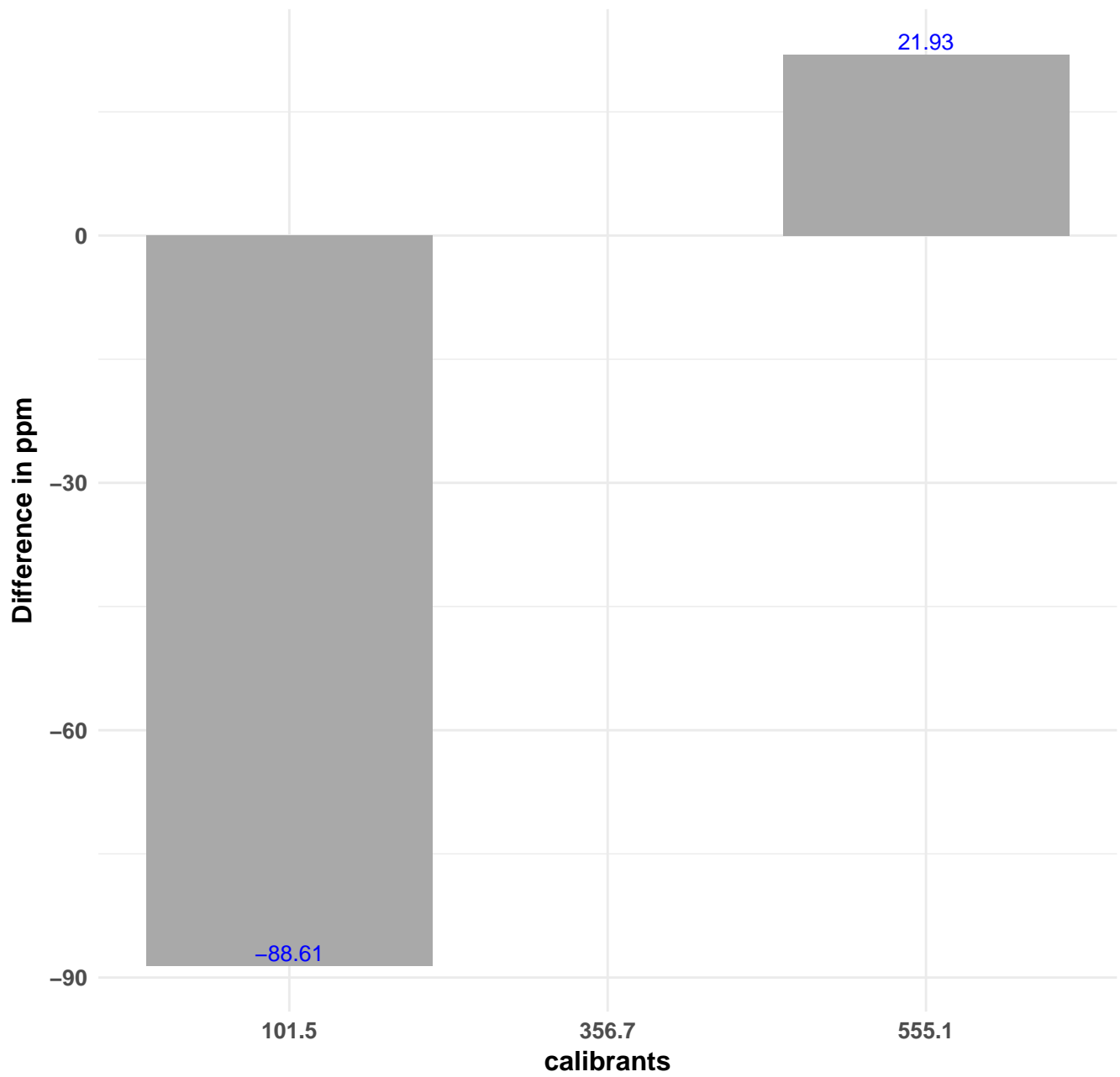
Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3

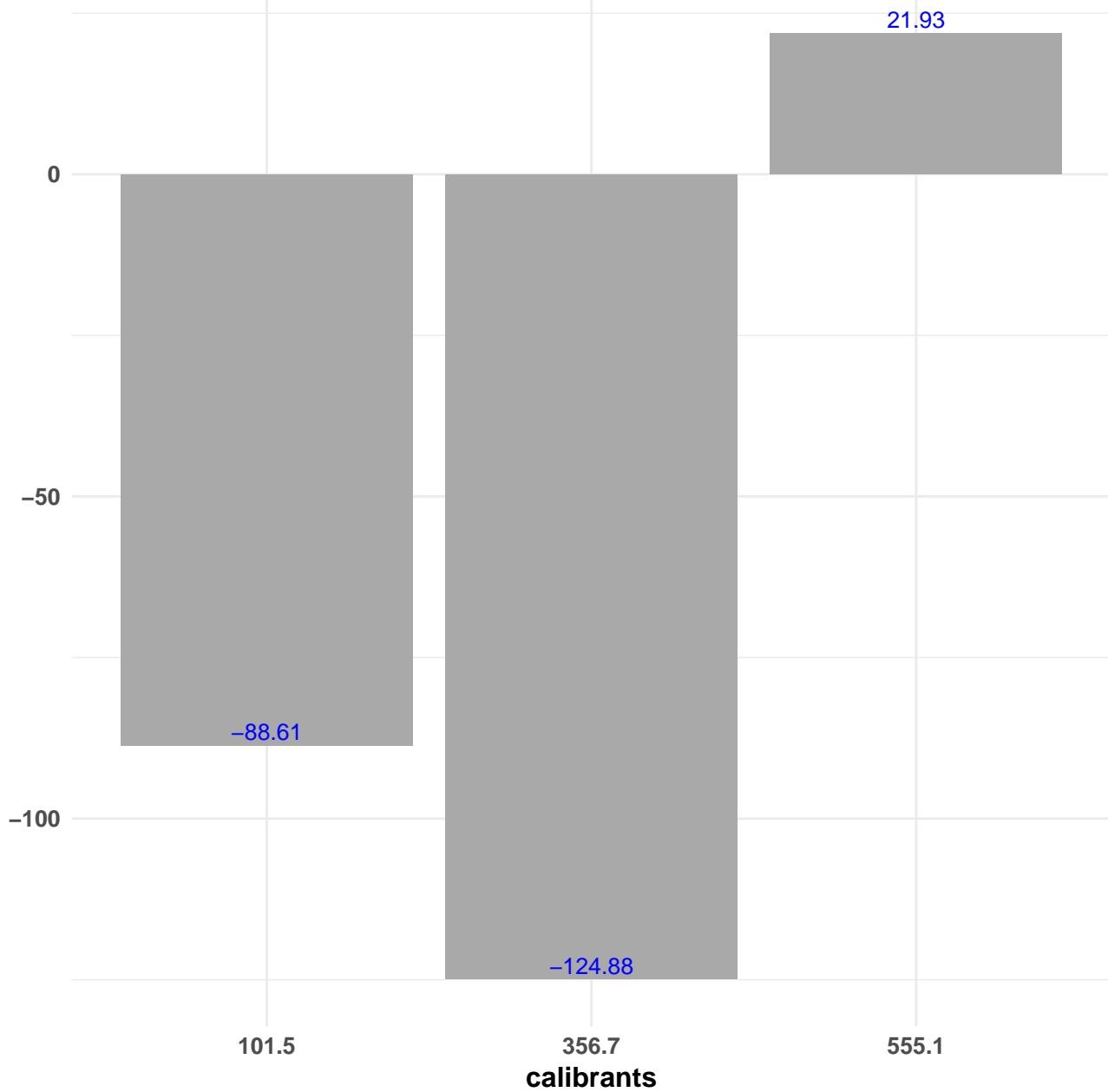


Difference m/z with max. average intensity vs. theor. calibrant m/z



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

Difference in ppm



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

