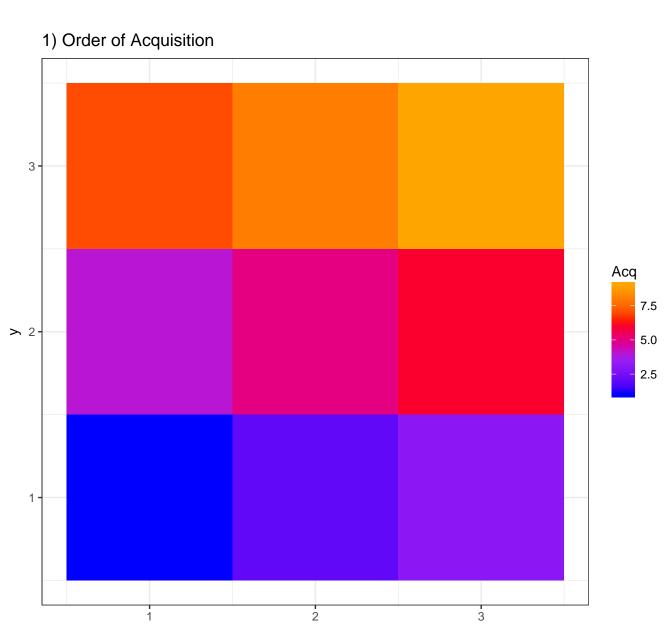
Quality control of MSI data

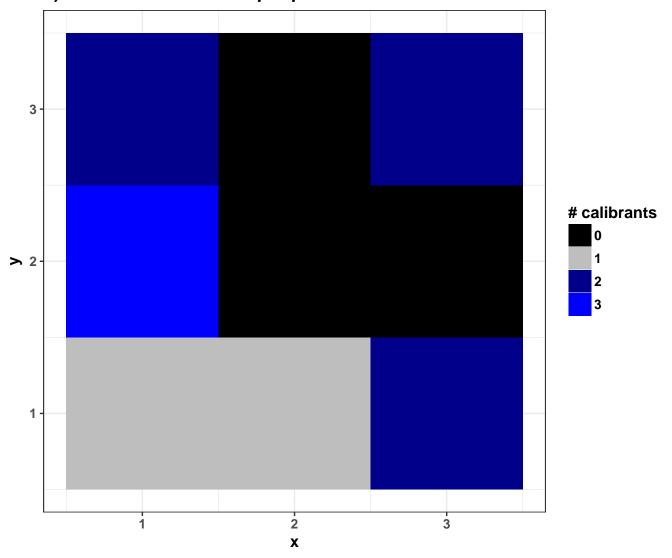
Filename: Testfile_rdata

properties	values
Number of mz features	8399
Range of mz values [Da]	100.08 - 799.92
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	0 – 318.82
Median of intensities	0
Intensities > 0	30.92 %
Number of zero TICs	0
Preprocessing	
Normalization	tic
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
# peptides in inputpeptides.csv	2/3
# calibrants in inputcalibrantfile1.txt	2/3

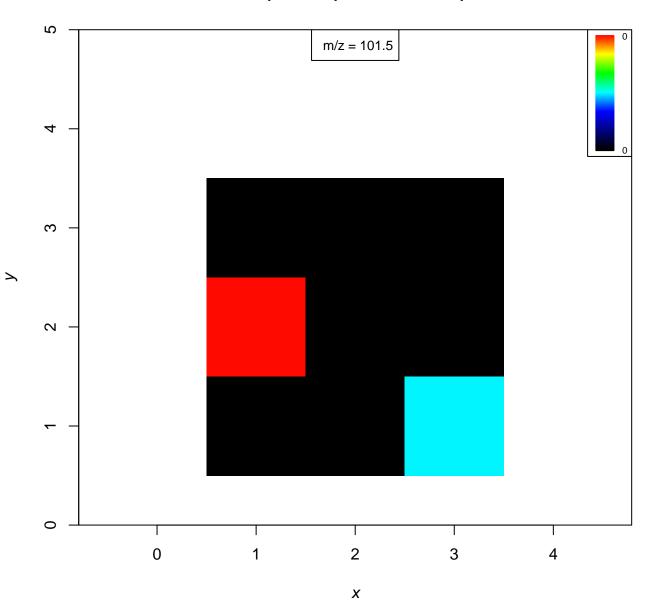


Х

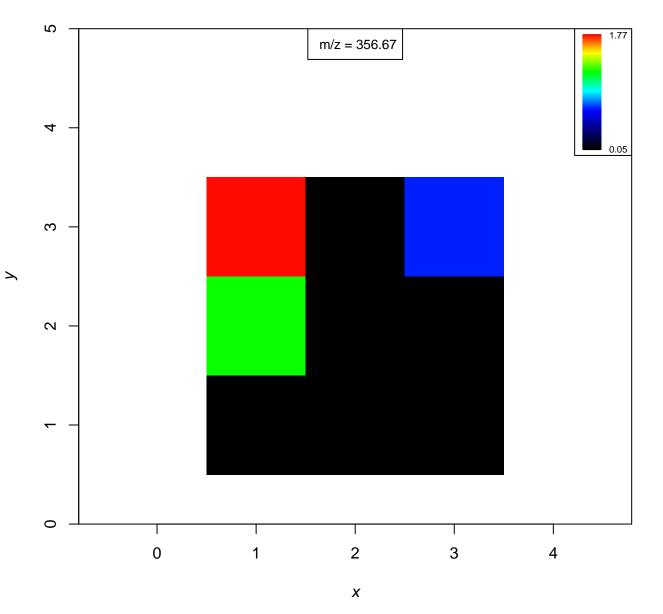
2) Number of calibrants per pixel



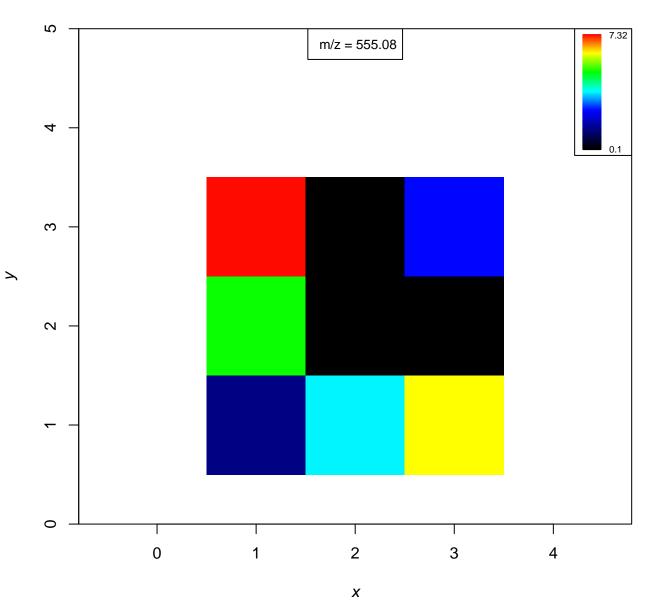
3A) 101.5 (101.5 ± 0.1 Da)



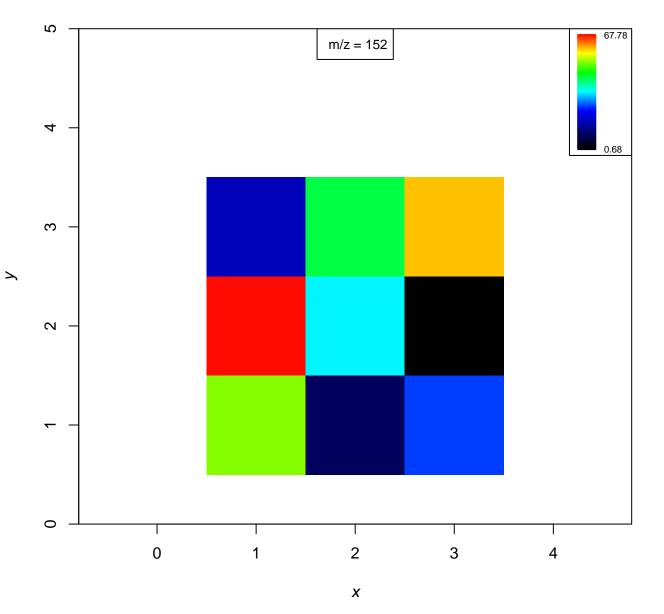
3B) 356.7 (356.7 ± 0.1 Da)



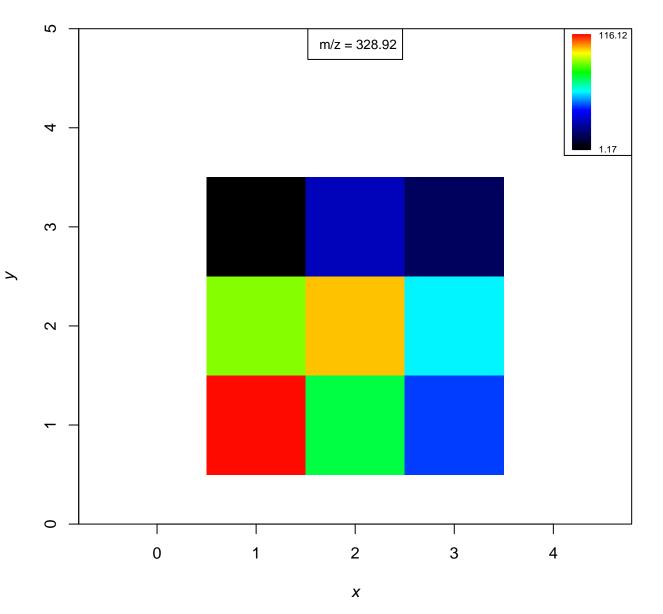
3C) 555.1 (555.1 ± 0.1 Da)



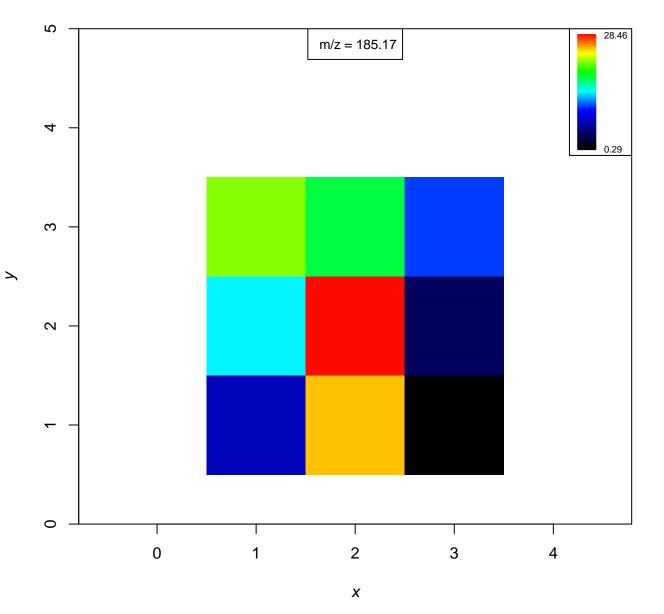
3D) mass1 (152 ± 0.1 Da)



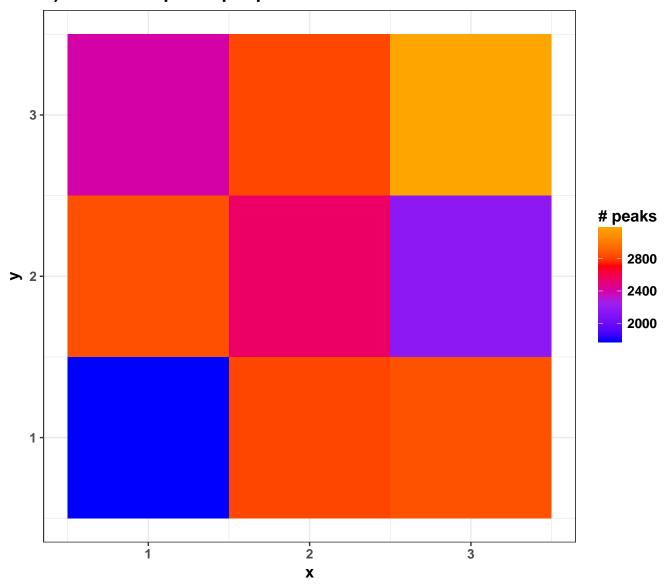
3E) mass2 (328.9 ± 0.1 Da)



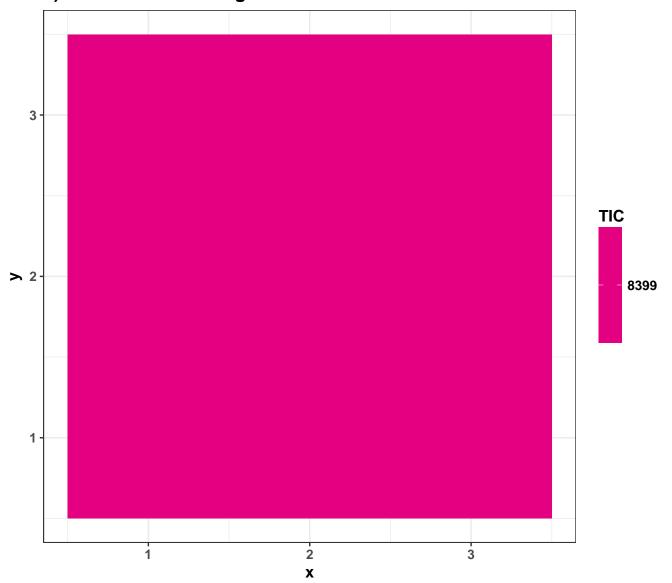
3F) mass3 (185.2 ± 0.1 Da)



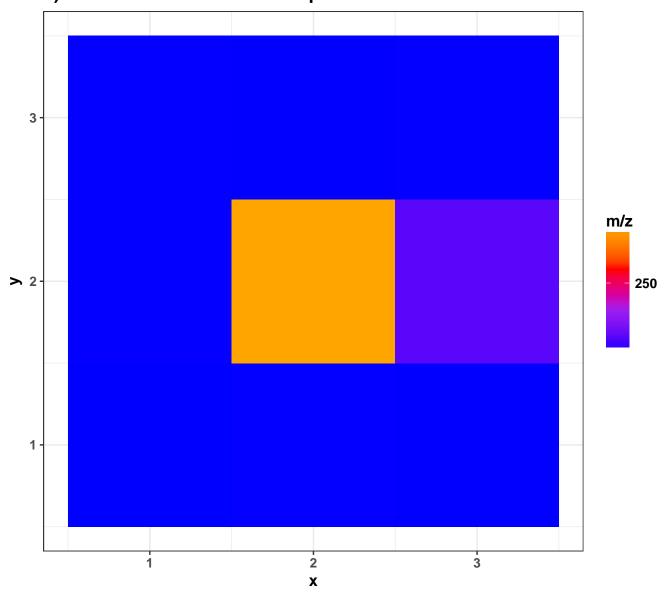
4) Number of peaks per pixel



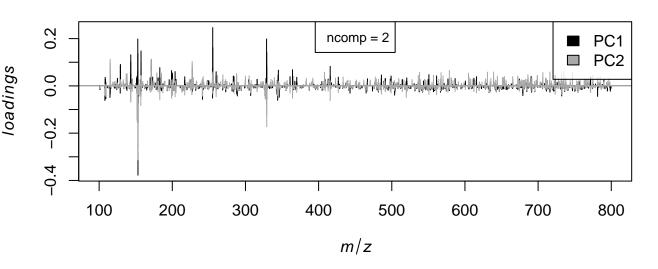
5) Total Ion Chromatogram

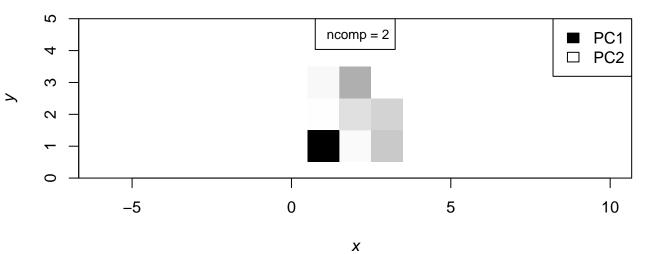


6) Most abundant m/z in each pixel

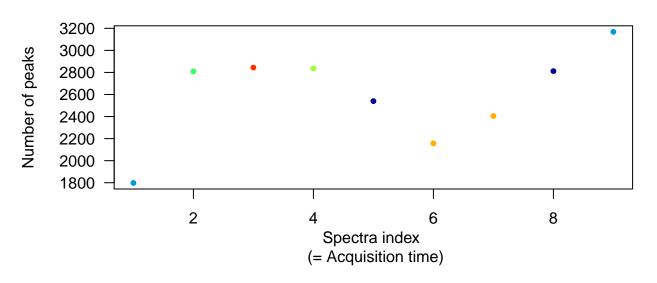


7) PCA for two components

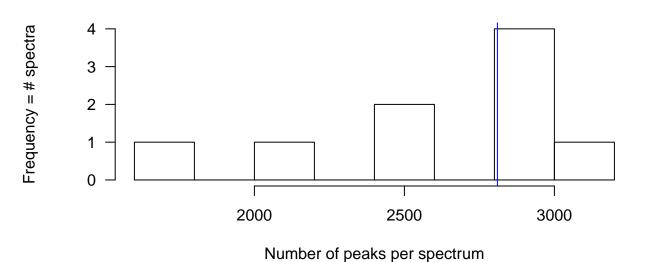


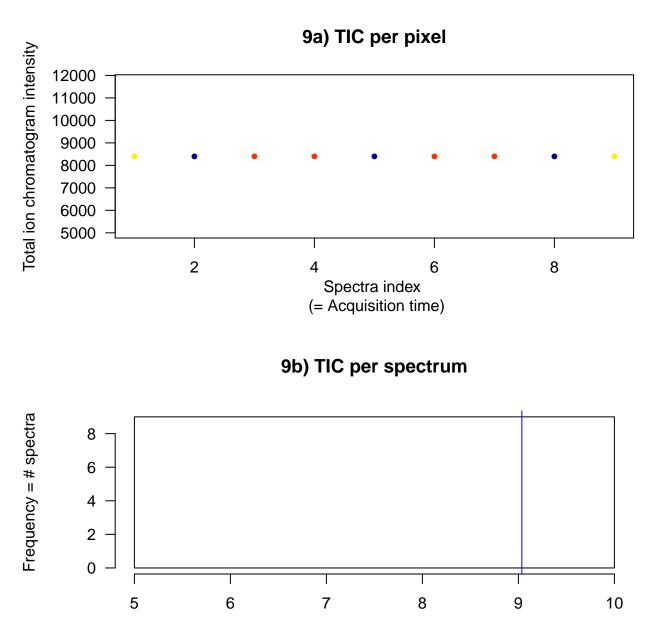


8a) Number of peaks per spectrum



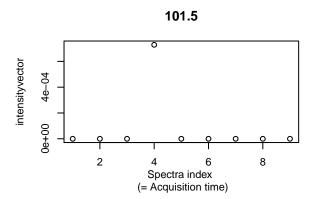
8b) Number of peaks per spectrum

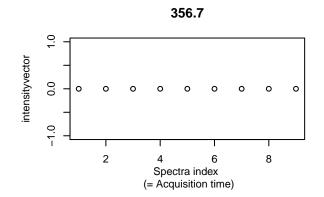


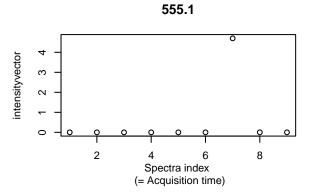


log(TIC per spectrum)

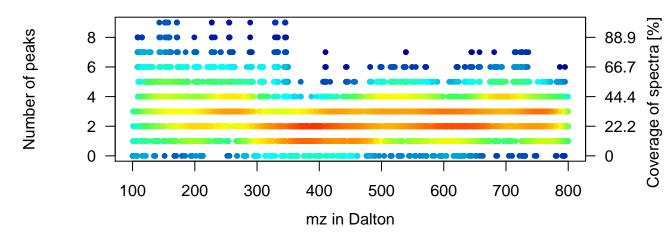
10) intensity of calibrants over acquisition



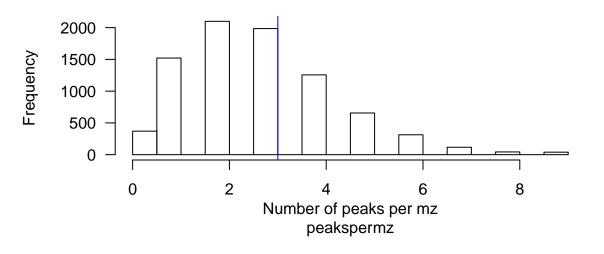




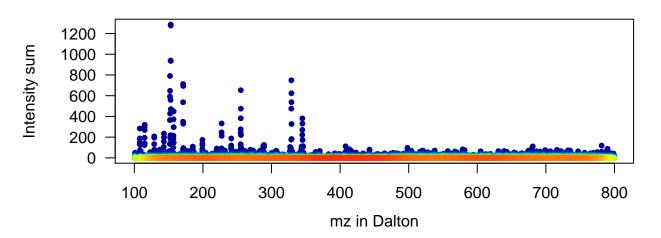
11a) Number of peaks for each mz



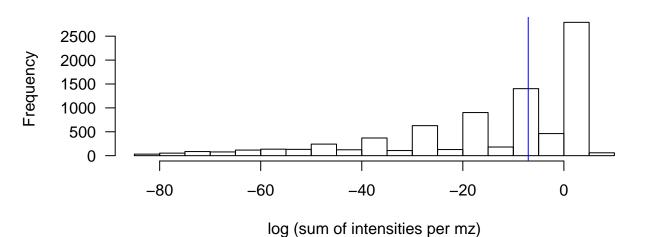
11b) Number of peaks per mz



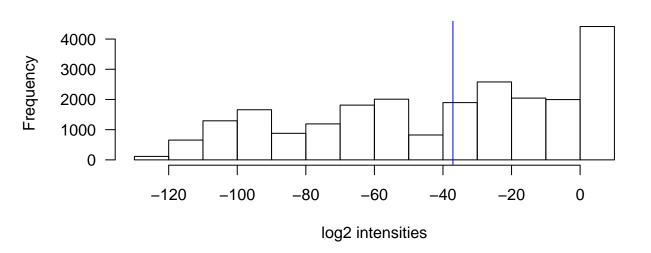
12a) Sum of all peak intensities for each mz



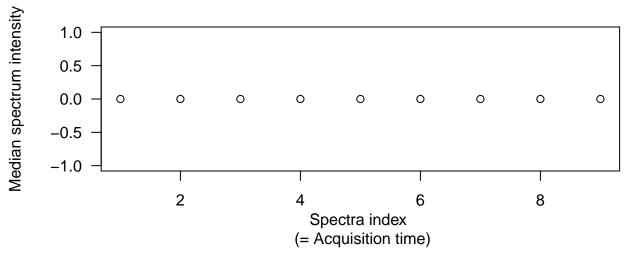
12b) Sum of intensities per mz



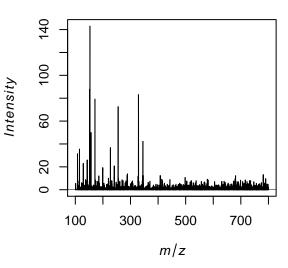
13a) Log2-transformed intensities





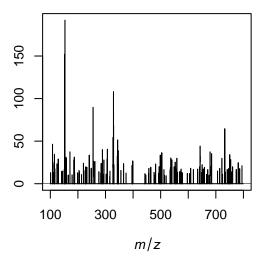


Average spectrum



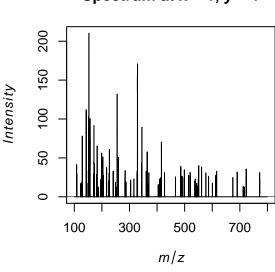
Intensity

Intensity

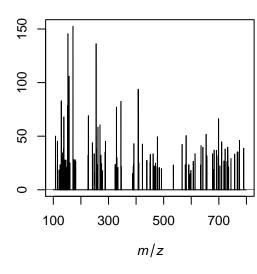


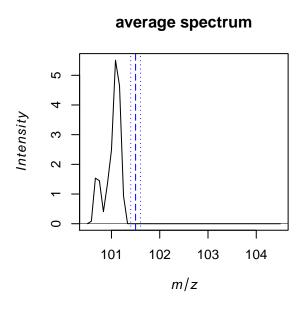
Spectrum in middle of acquisition

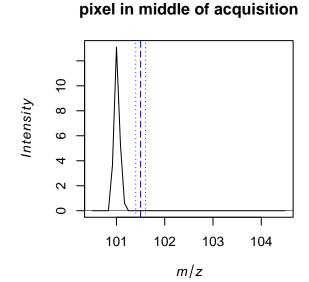
Spectrum at x = 1, y = 1

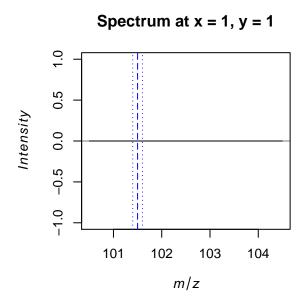


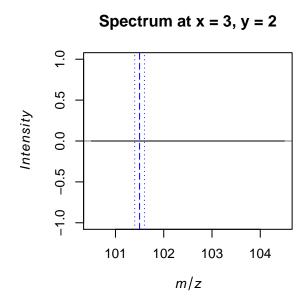
Spectrum at x = 3, y = 2







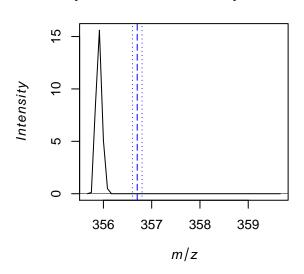




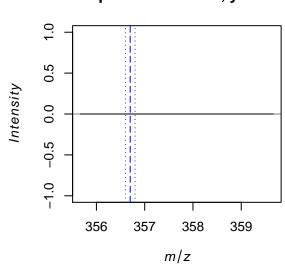


356 357 358 359 m/z

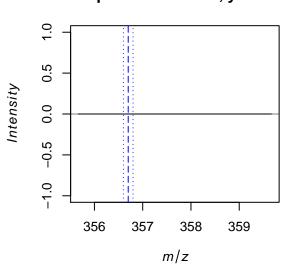
pixel in middle of acquisition



Spectrum at x = 1, y = 1

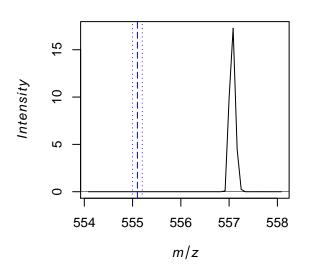


Spectrum at x = 3, y = 2

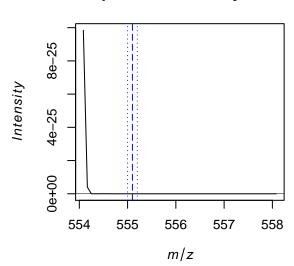




pixel in middle of acquisition



Spectrum at x = 1, y = 1



Spectrum at x = 3, y = 2

