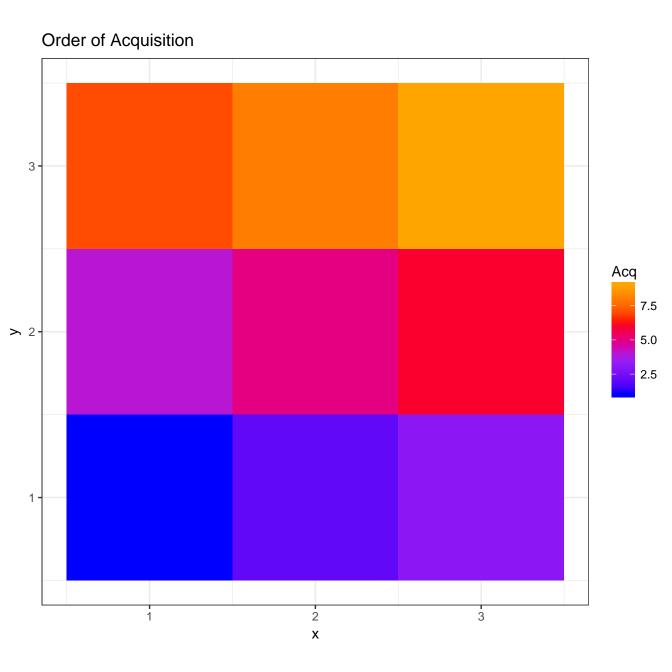
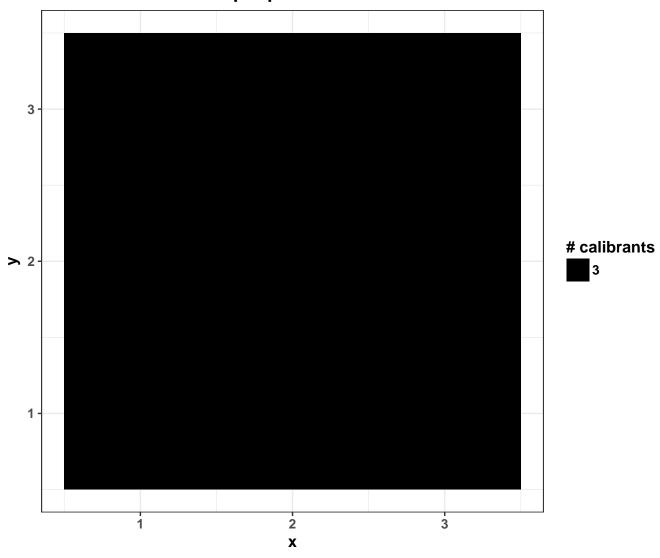
Quality control of MSI data

Filename: Testfile_analyze75

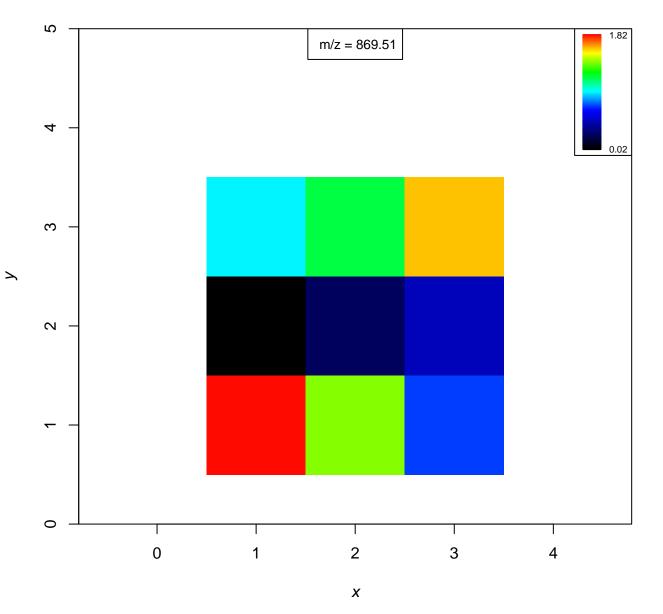
properties	values
Number of mz features	58031
Range of mz values [Da]	699.75 – 1916.29
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	0 – 146
Median of intensities	0
Intensities > 0	28.02 %
Number of zero TICs	0
Preprocessing	
Normalization	FALSE
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
# peptides in inputpeptides.txt	2/3
# calibrants in inputcalibrantfile2.txt	3/3



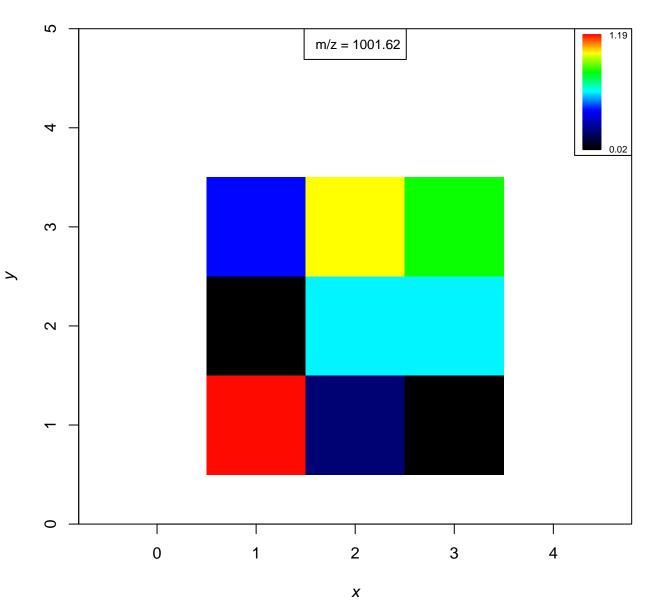
Number of calibrants per pixel



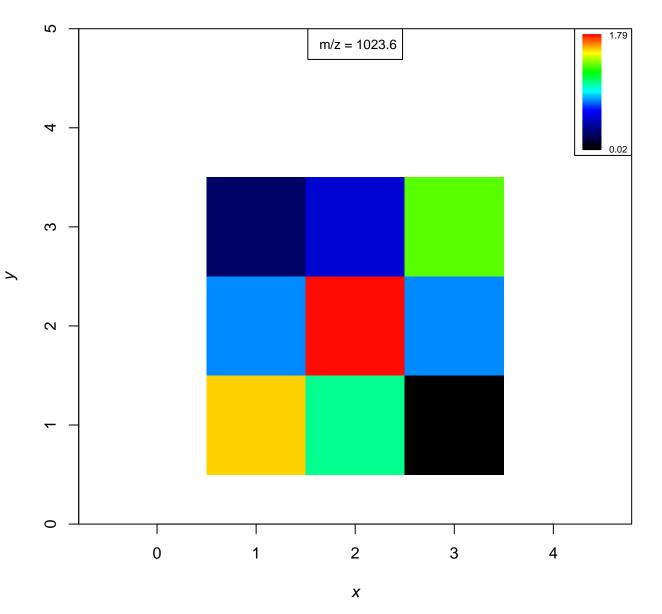
mass1 (869.51 ± 0.5 Da)



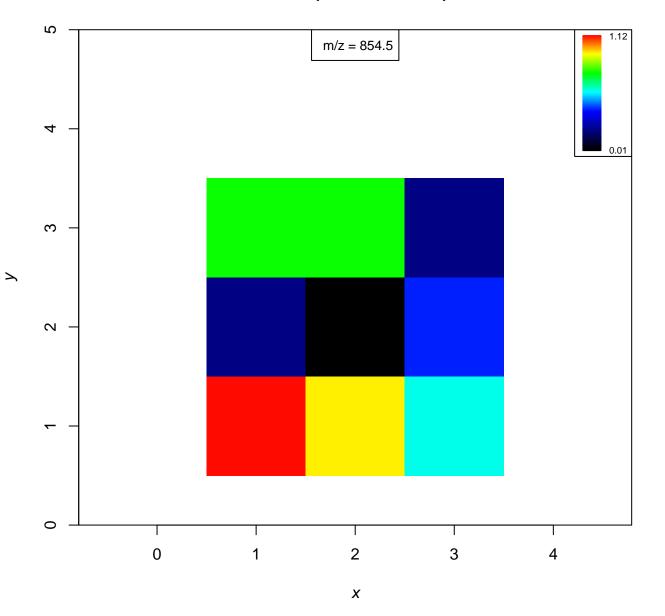
mass2 (1001.62 ± 0.5 Da)



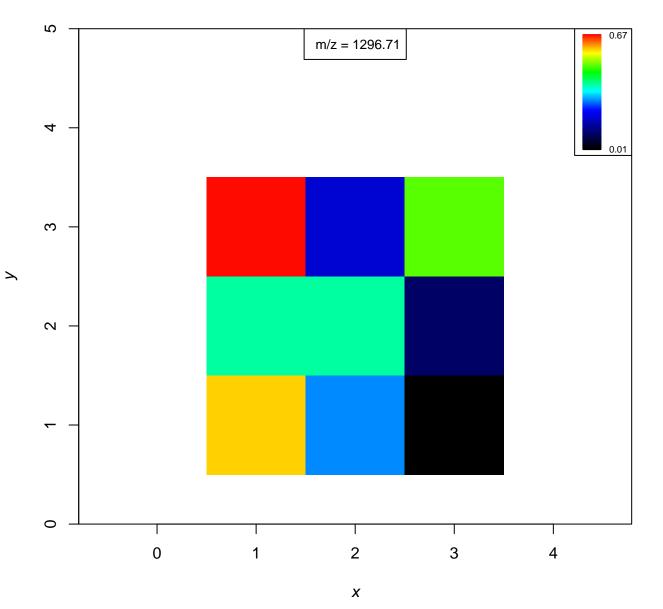
mass3 (1023.6 ± 0.5 Da)



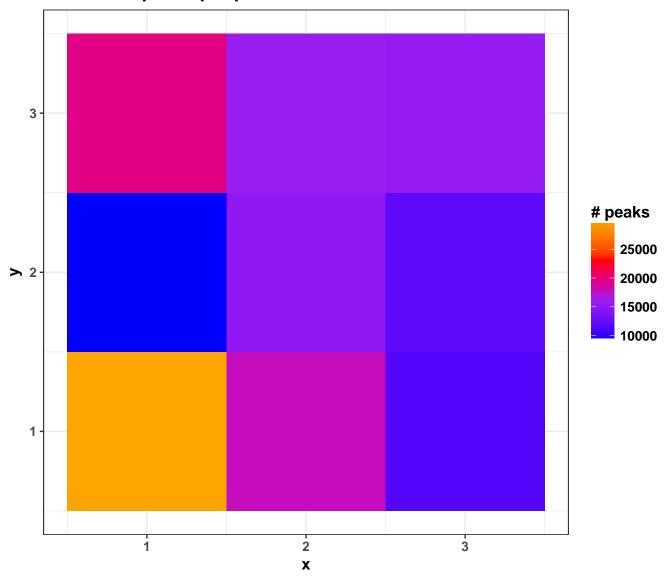
854.5 (854.5 ± 0.5 Da)



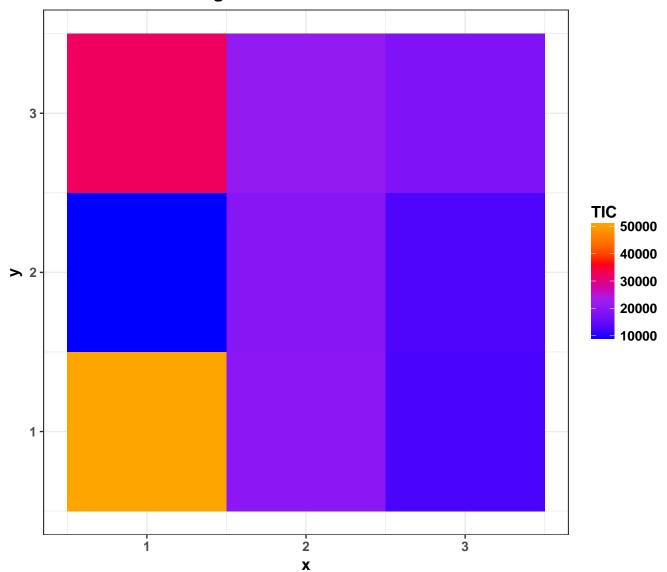
1296.7 (1296.7 ± 0.5 Da)



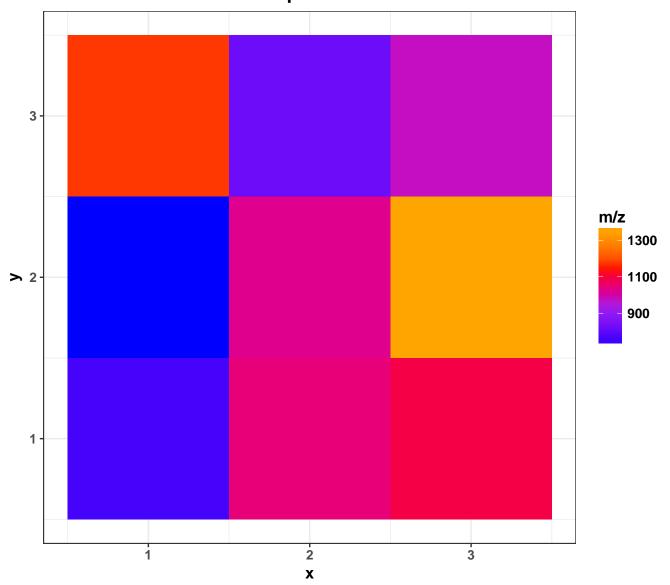
Number of peaks per pixel



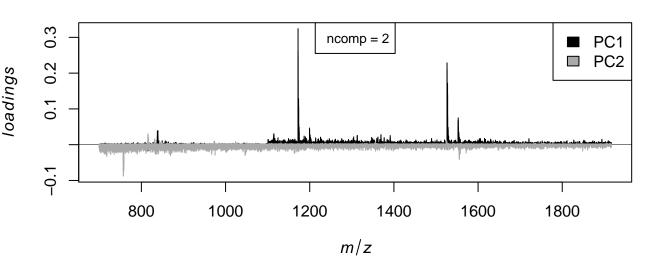


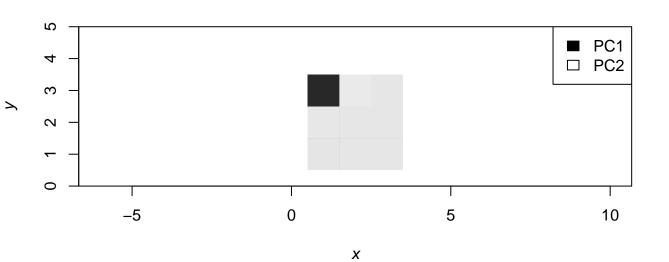


Most abundant m/z in each pixel

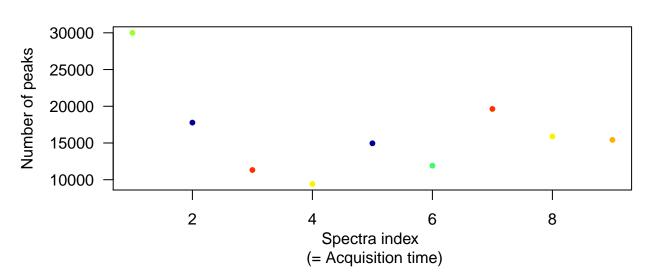


PCA for two components

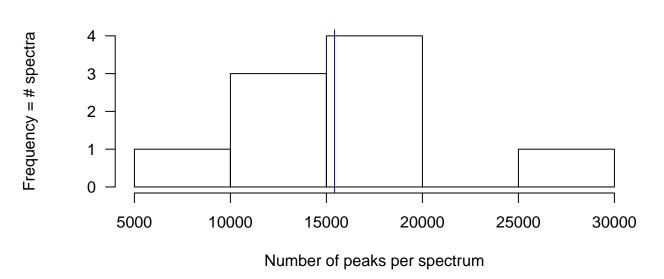


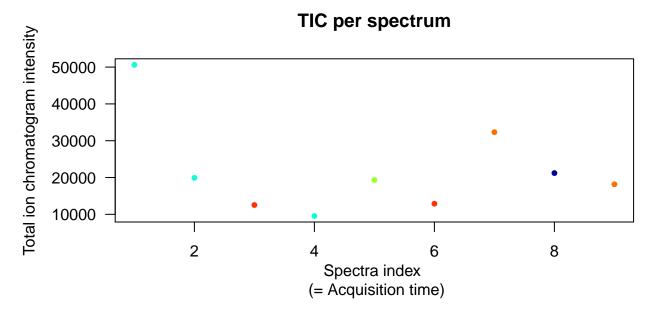


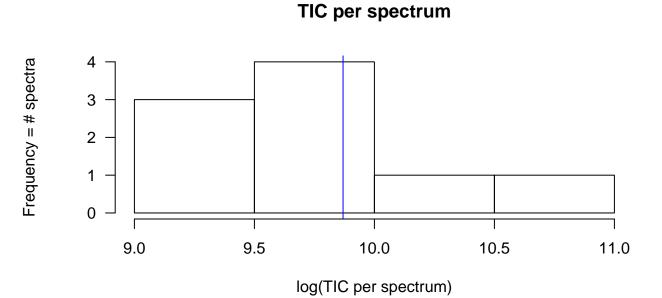
Number of peaks per spectrum



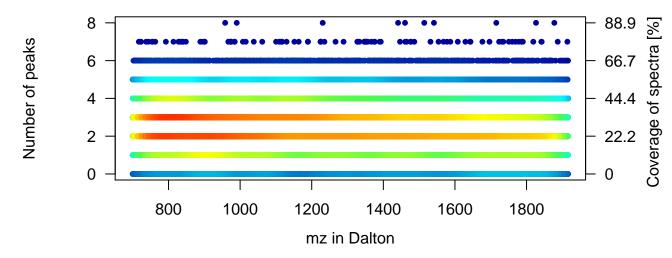
Number of peaks per spectrum



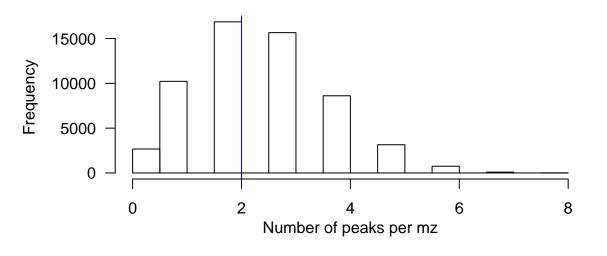




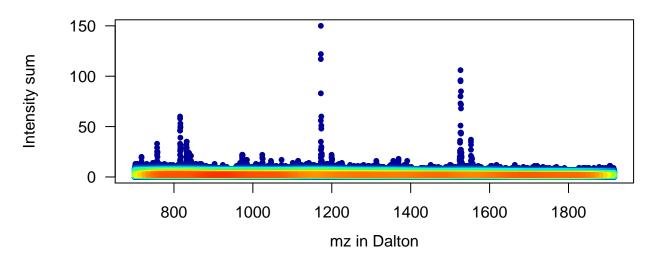
Number of peaks per mz



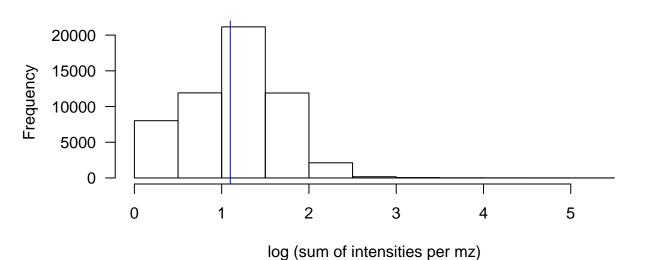
Number of peaks per mz



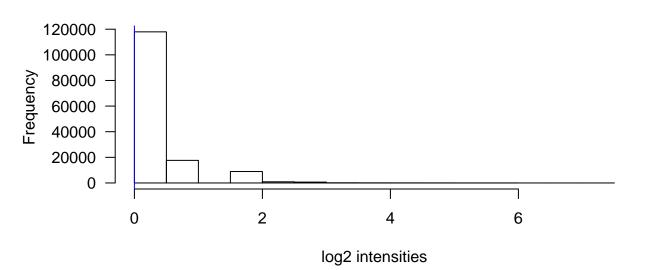
Sum of intensities per mz



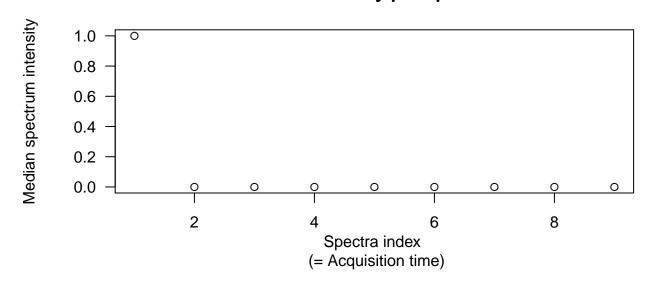
Sum of intensities per mz



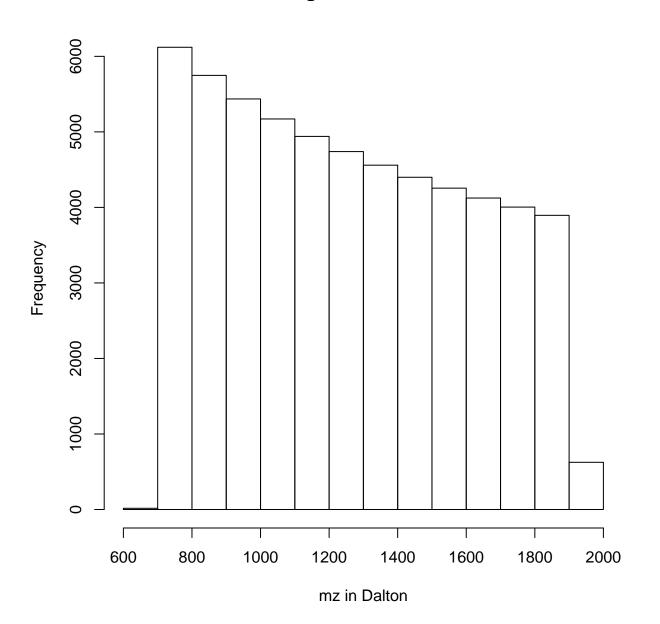
Log2-transformed intensities

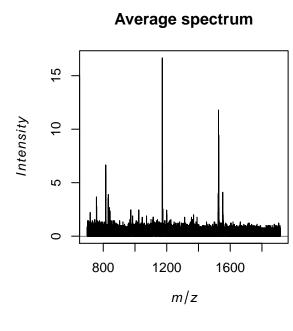


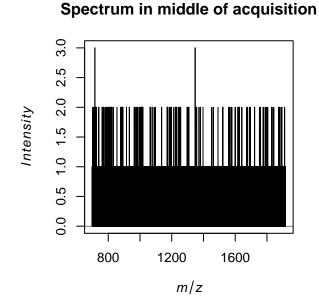
Median intensity per spectrum

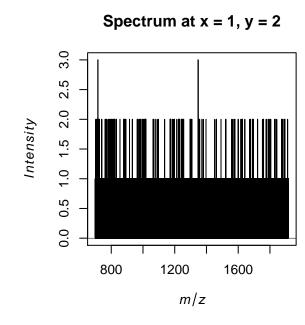


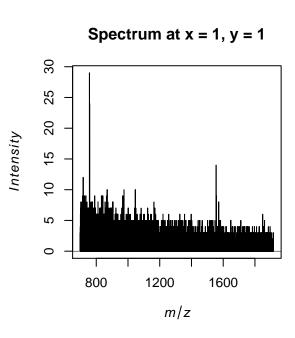
Histogram of mz values



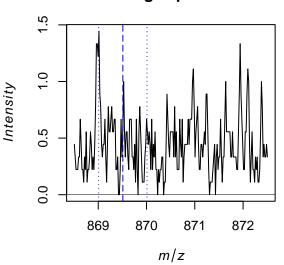




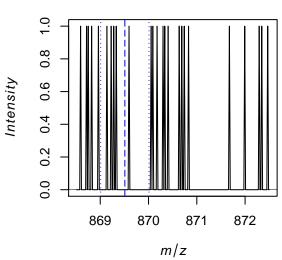




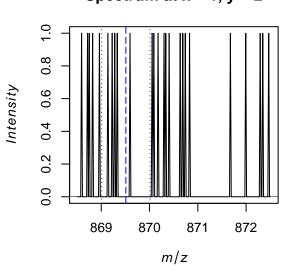




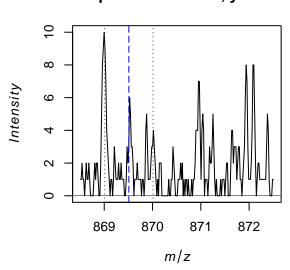
pixel in middle of acquisition



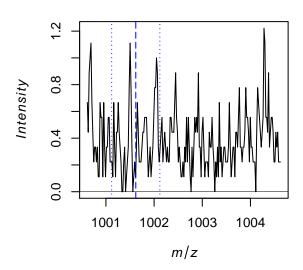
Spectrum at x = 1, y = 2



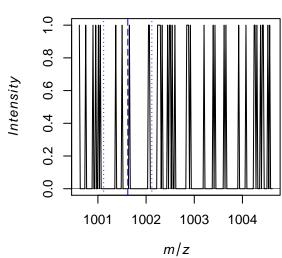
Spectrum at x = 1, y = 1



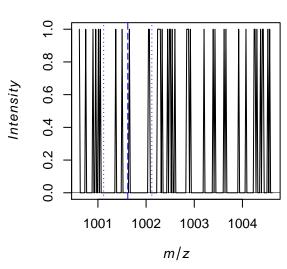
average spectrum



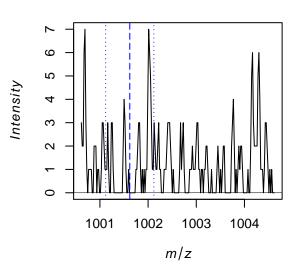
pixel in middle of acquisition



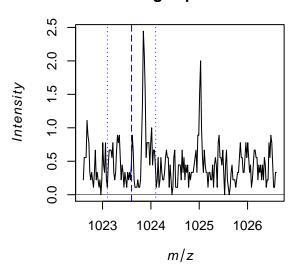
Spectrum at x = 1, y = 2



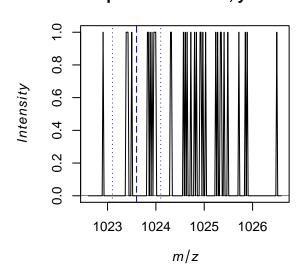
Spectrum at x = 1, y = 1



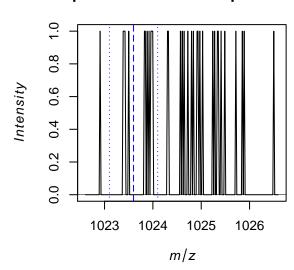
average spectrum



Spectrum at x = 1, y = 2



pixel in middle of acquisition



Spectrum at x = 1, y = 1

