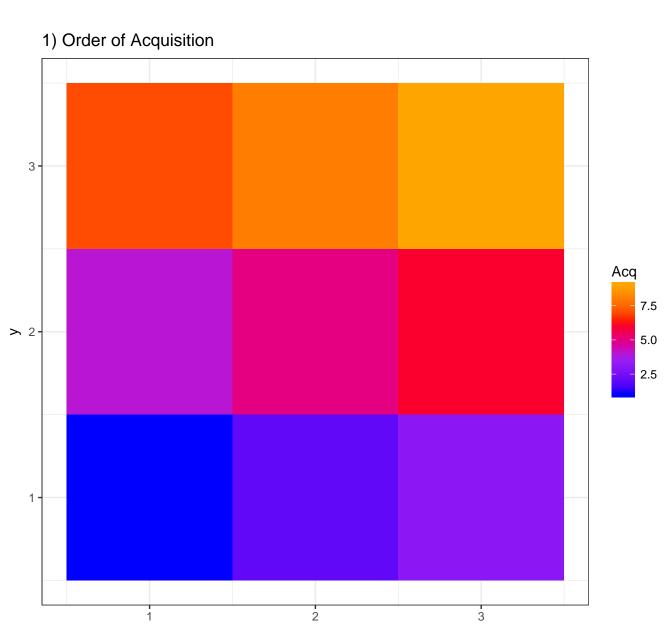
# Quality control of MSI data

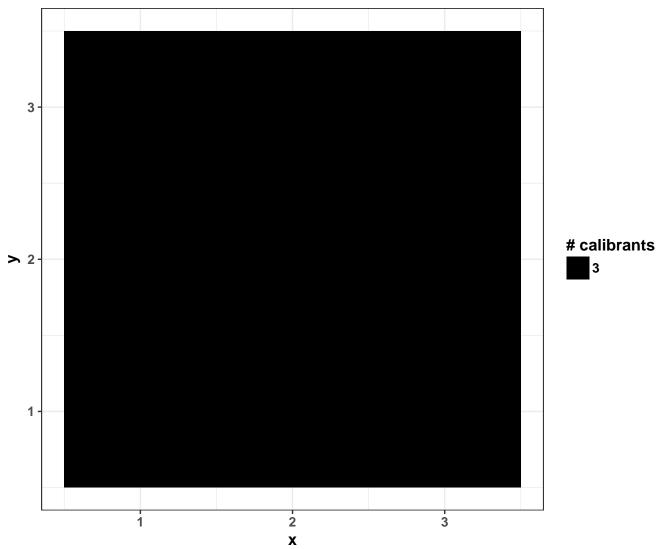
Filename: Testfile\_analyze75

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	2/3

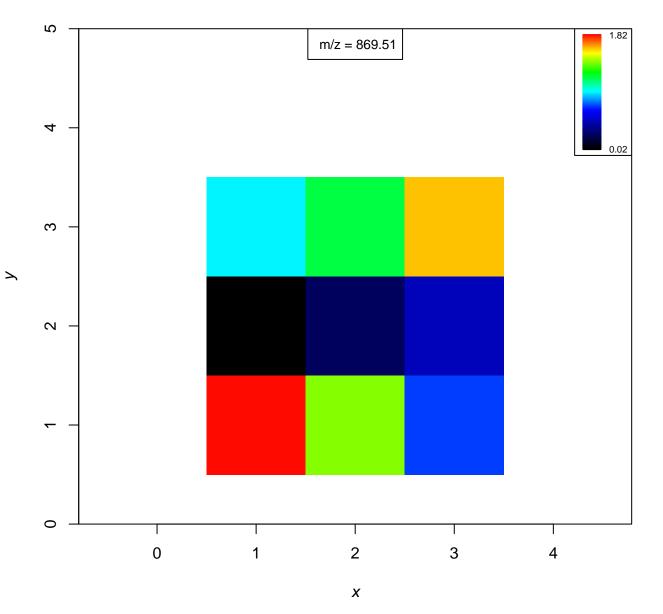


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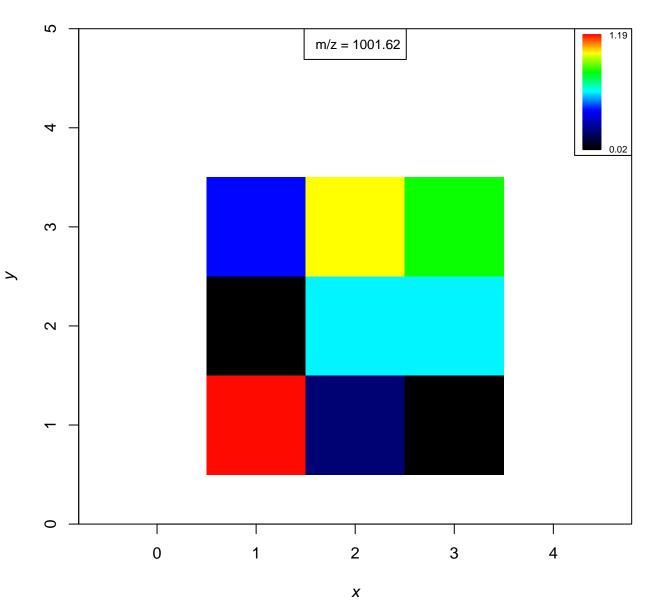
# 2) Number of calibrants per pixel



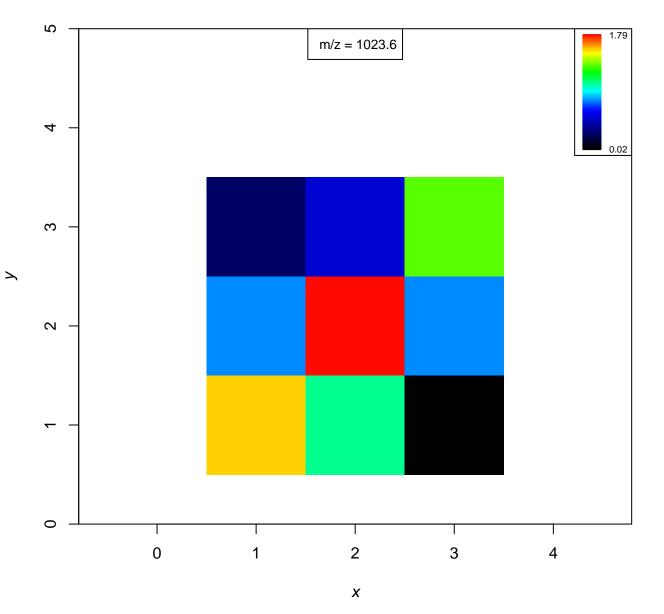
# 3A) mass1 (869.51 ± 0.5 Da)



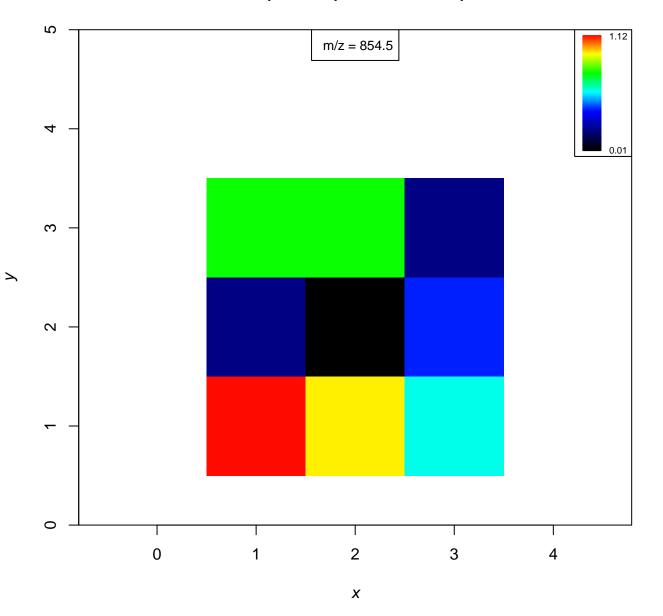
## 3B) mass2 (1001.62 ± 0.5 Da)



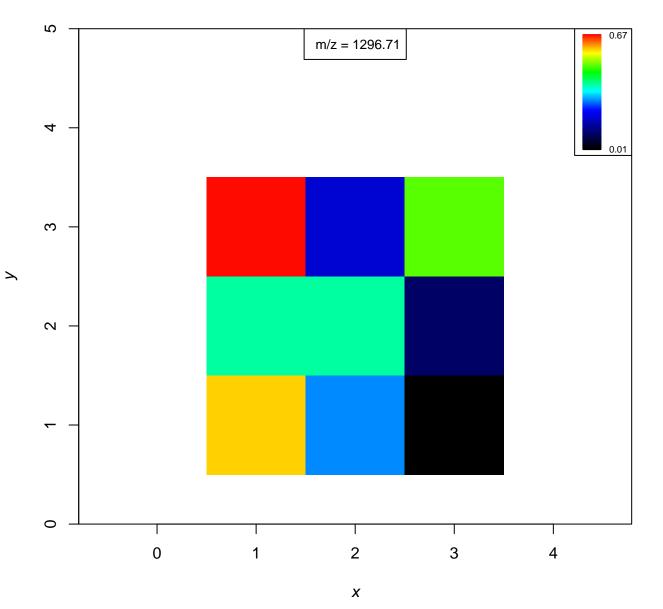
# 3C) mass3 (1023.6 ± 0.5 Da)



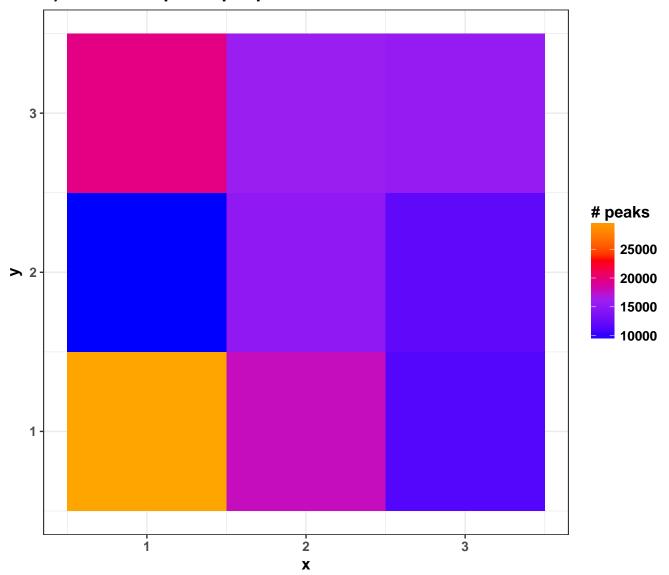
3D) 854.5 (854.5 ± 0.5 Da)



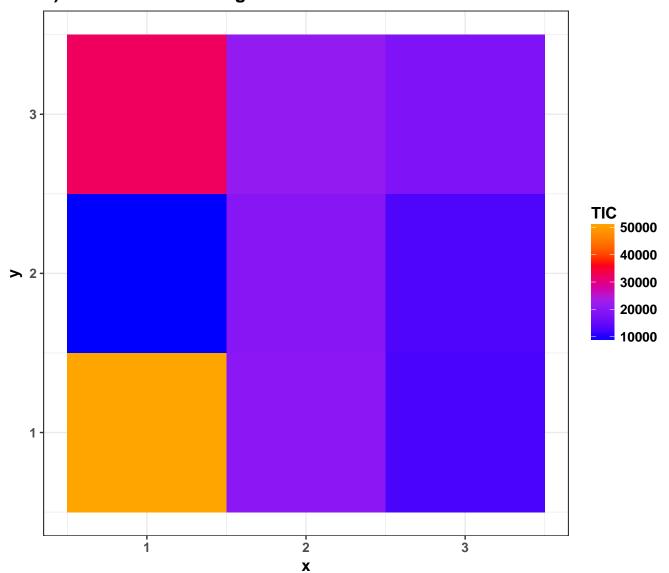
3E) 1296.7 (1296.7 ± 0.5 Da)



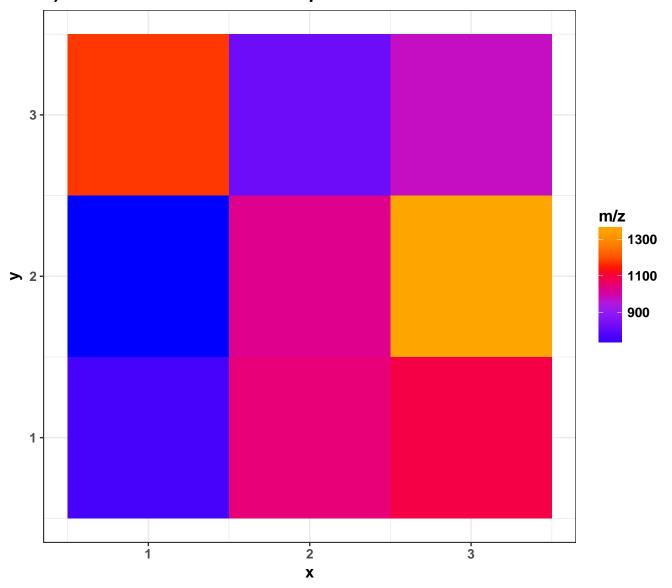
# 4) Number of peaks per pixel



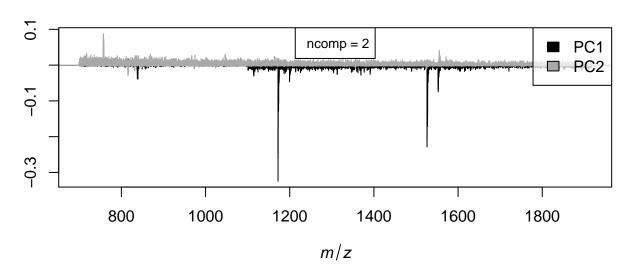
# 5) Total Ion Chromatogram



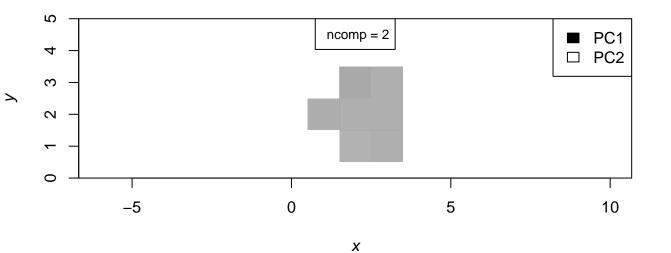
# 6) Most abundant m/z in each pixel



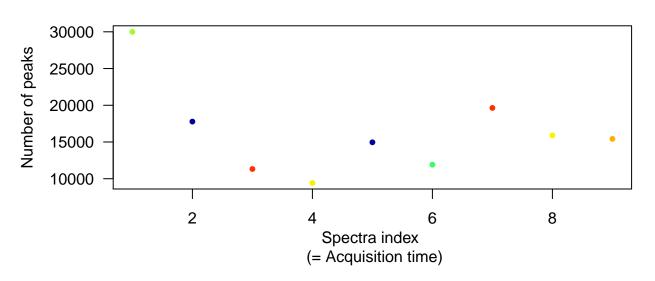
# 7) PCA for two components



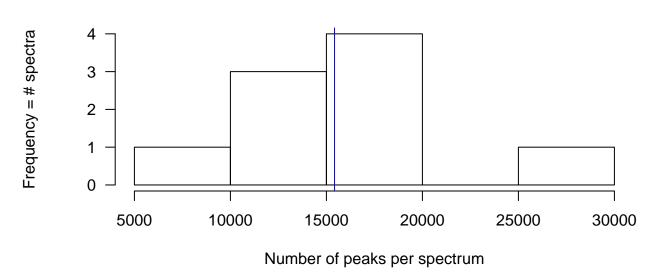
loadings

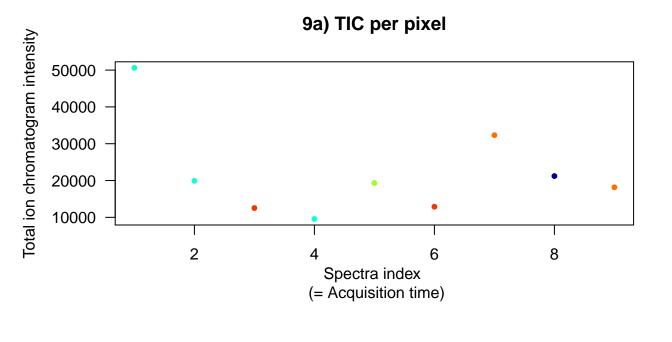


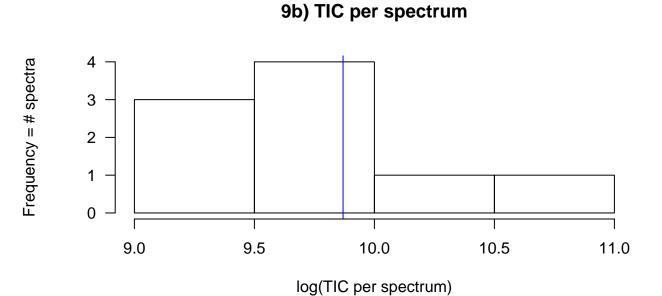
#### 8a) Number of peaks per spectrum



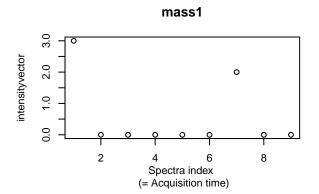
#### 8b) Number of peaks per spectrum

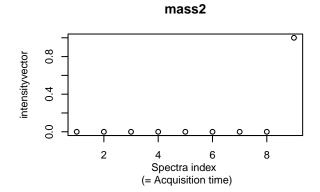


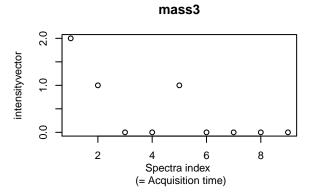




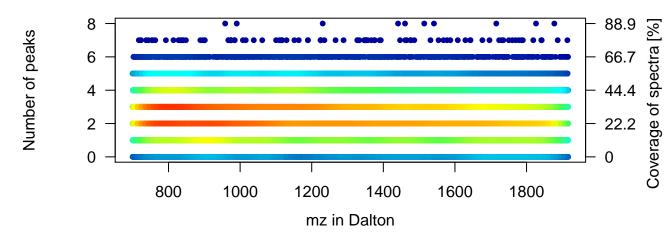
#### 10) intensity of calibrants over acquisition



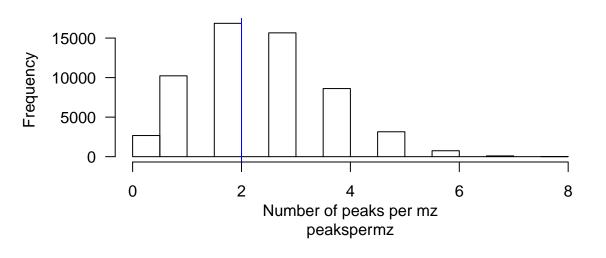




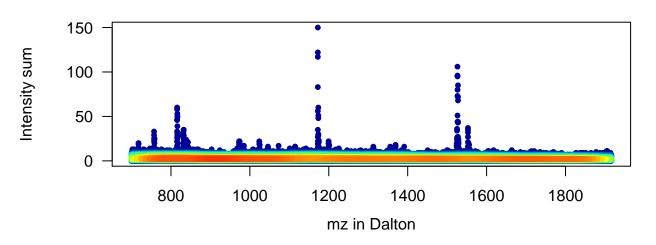
#### 11a) Number of peaks for each mz



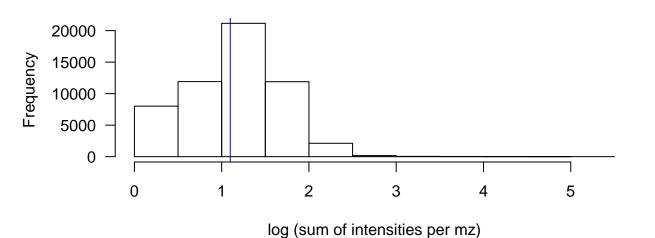
#### 11b) Number of peaks per mz



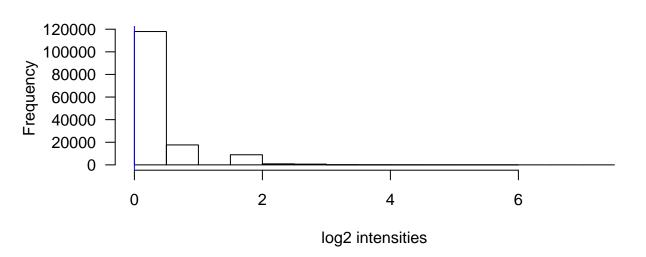
#### 12a) Sum of all peak intensities for each mz



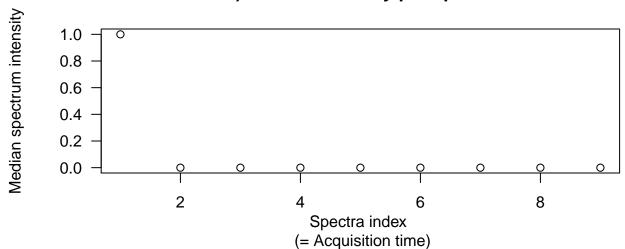
### 12b) Sum of intensities per mz



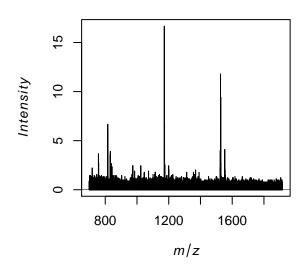
#### 13a) Log2-transformed intensities



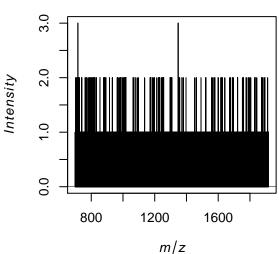




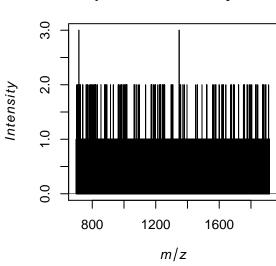
#### Average spectrum

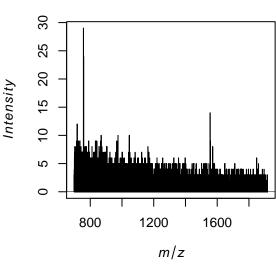


# Spectrum in middle of acquisition

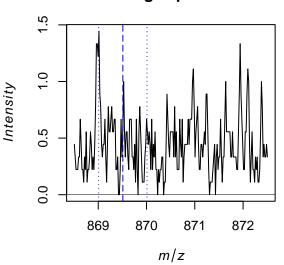


#### Spectrum at x = 1, y = 2

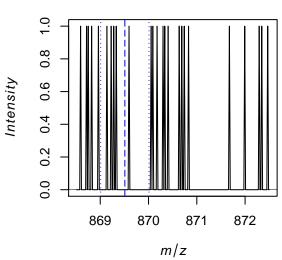




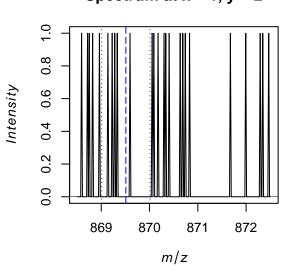


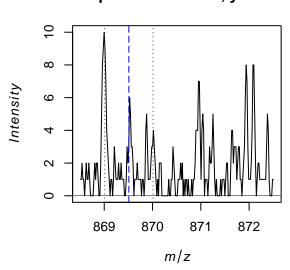


### pixel in middle of acquisition

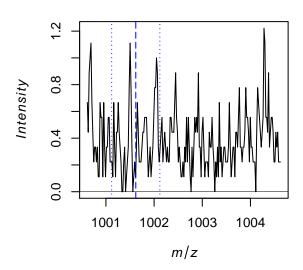


#### Spectrum at x = 1, y = 2

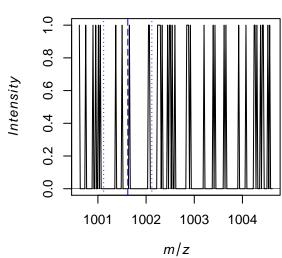




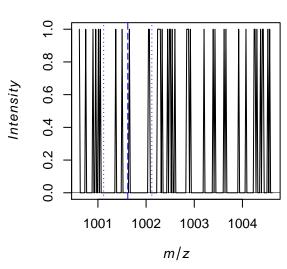
average spectrum

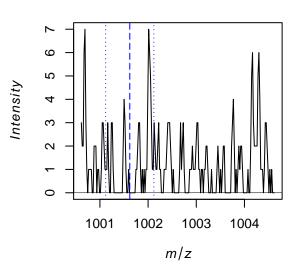


## pixel in middle of acquisition

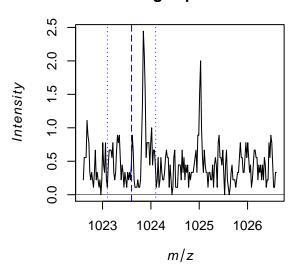


#### Spectrum at x = 1, y = 2

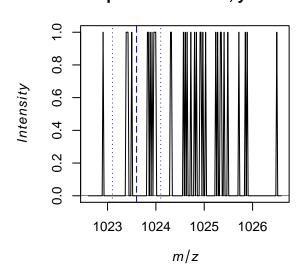




#### average spectrum



## Spectrum at x = 1, y = 2



#### pixel in middle of acquisition

