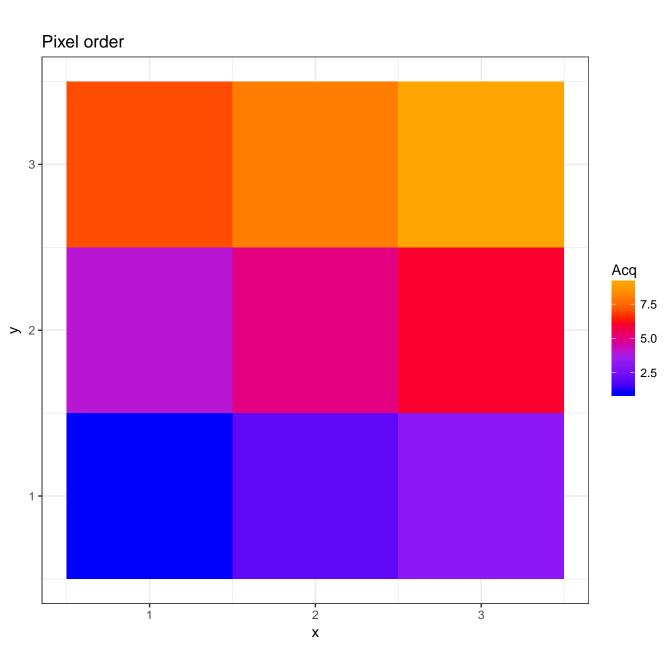
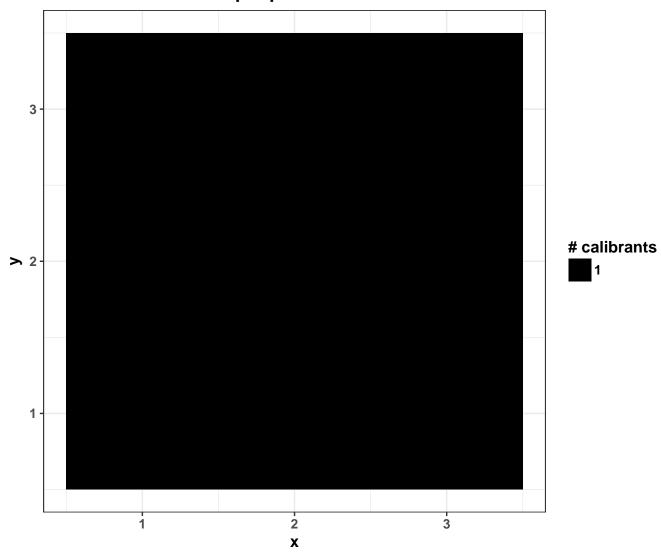
# Testfile\_analyze75

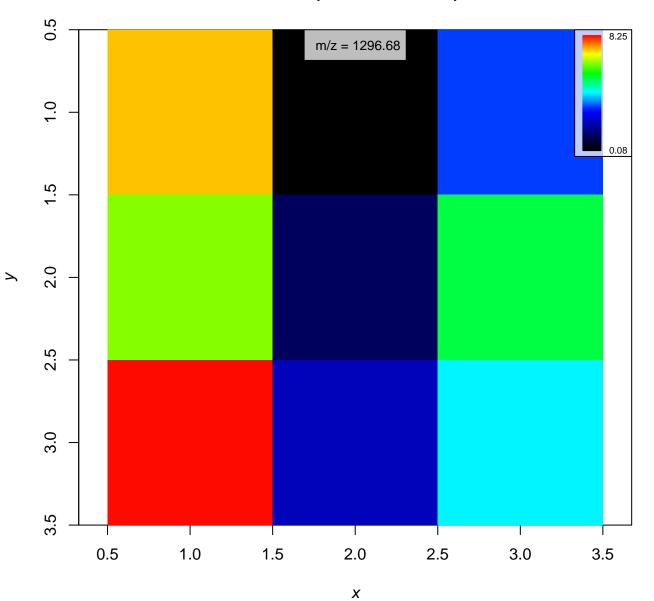
properties	values
Number of m/z features	3672
Range of m/z values [Da]	1199.47 – 1356.08
Number of pixels	9
Range of x coordinates	1 – 3
Range of y coordinates	1 – 3
Range of intensities	3 – 84
Median of intensities	9
Intensities > 0	100 %
Number of zero TICs	0
Median TIC	37005
Median # peaks per spectrum	3672
Normalization	FALSE
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
# peptides in inputpeptides.txt	1 / 6
# calibrants in inputcalibrantfile2.txt	1/3



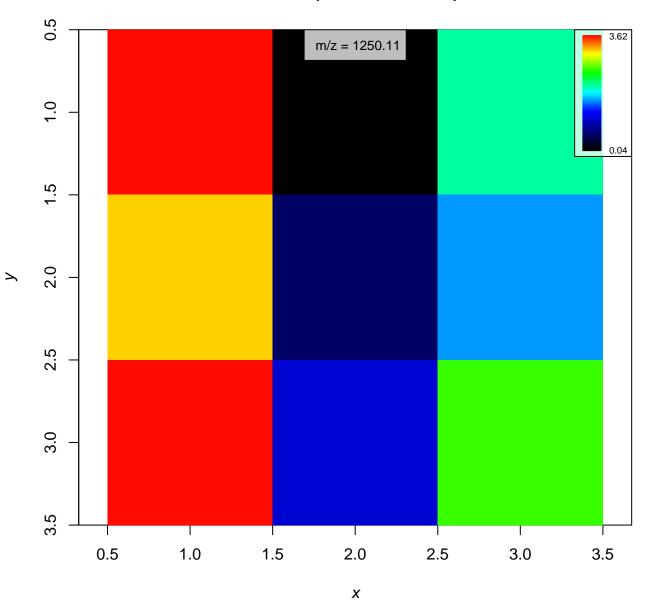
# Number of calibrants per pixel



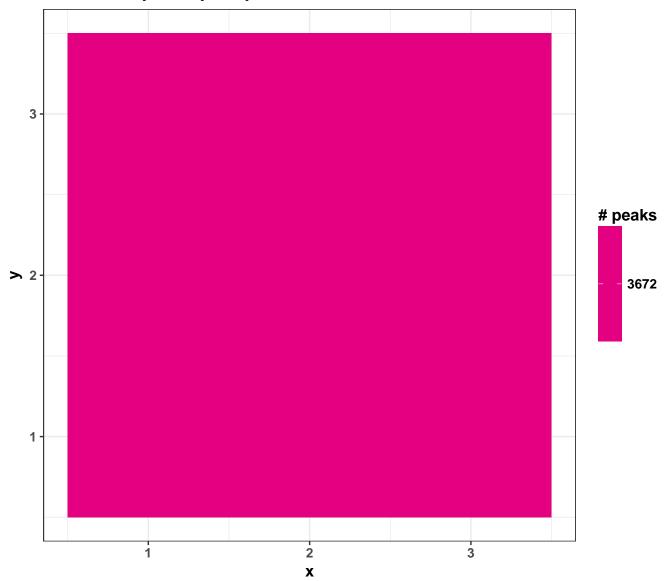
# mass3 (1296.7 ± 0.5 Da)



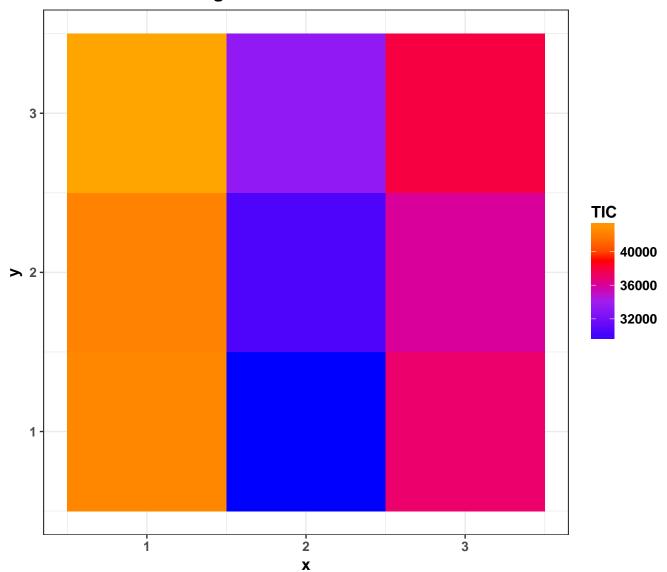
# 1250.1 (1250.1 ± 0.5 Da)



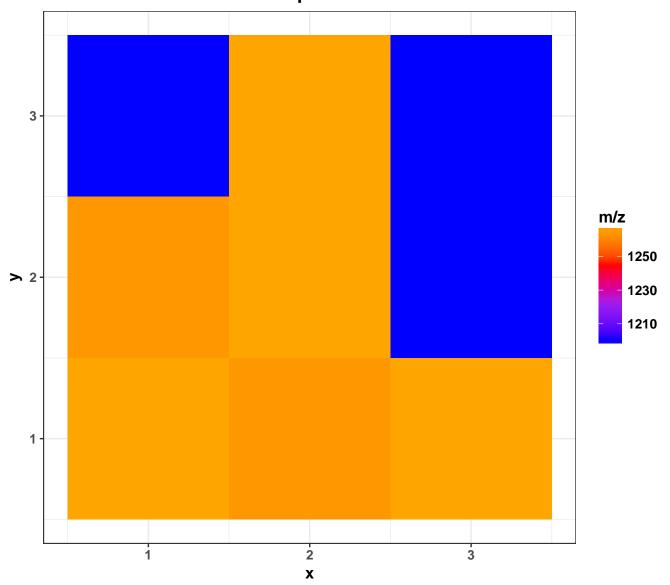
# Number of peaks per spectrum



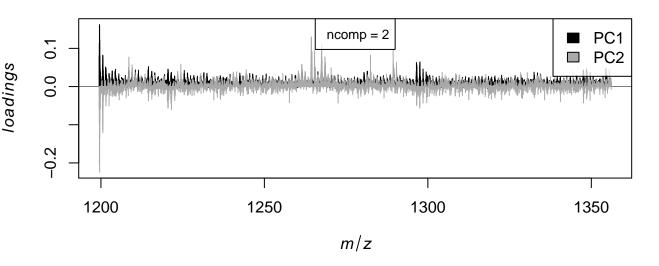


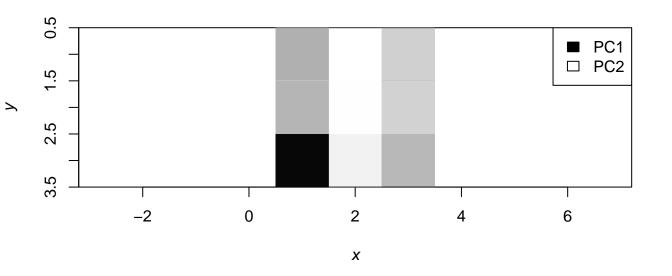


# Most abundant m/z in each spectrum

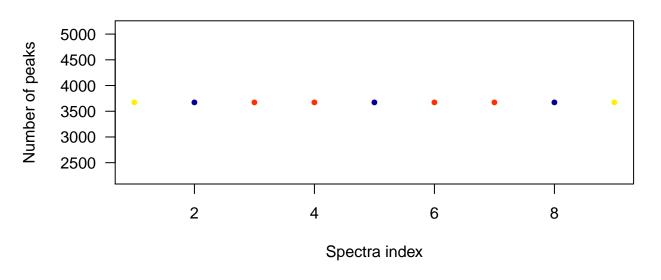


#### **PCA** for two components

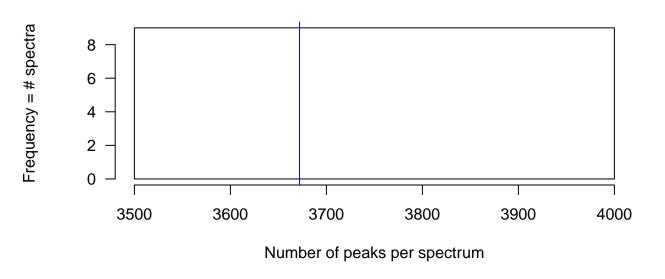


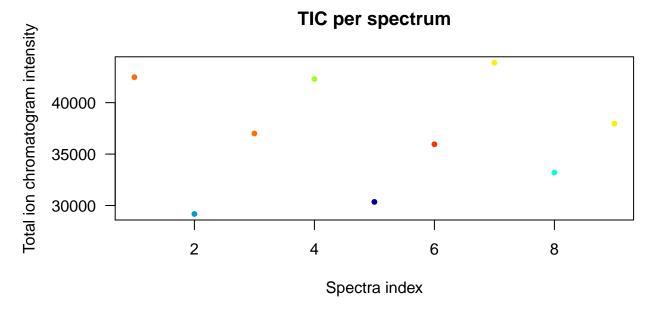


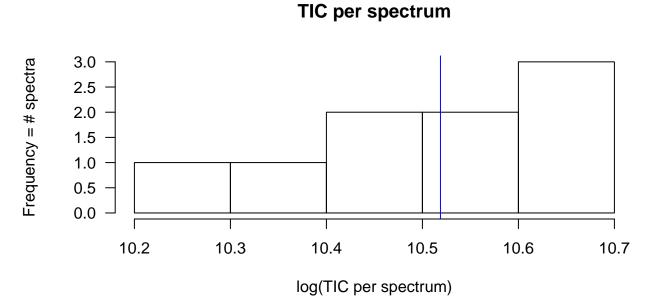
#### Number of peaks per spectrum



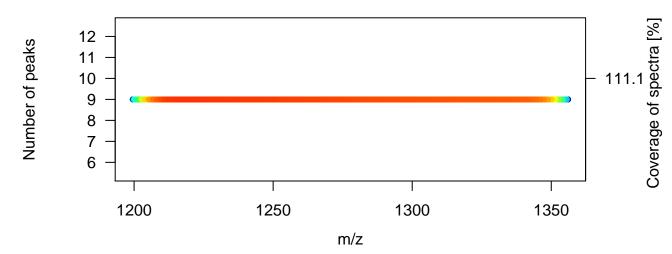
#### Number of peaks per spectrum



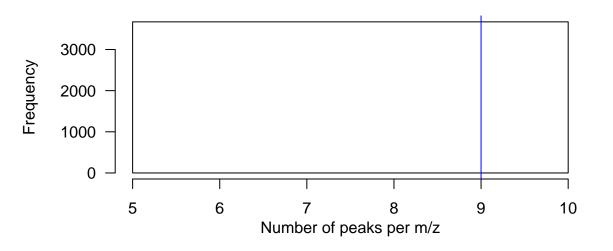




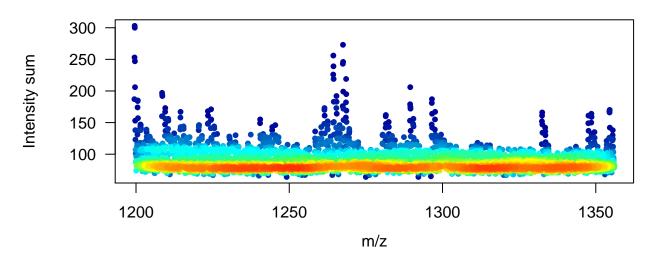
#### Number of peaks per m/z



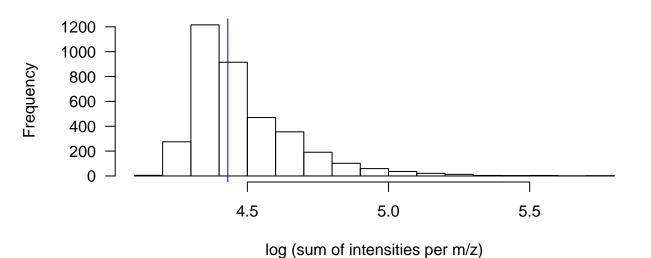




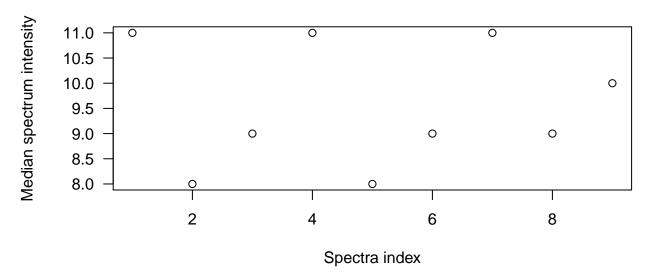
#### Sum of intensities per m/z



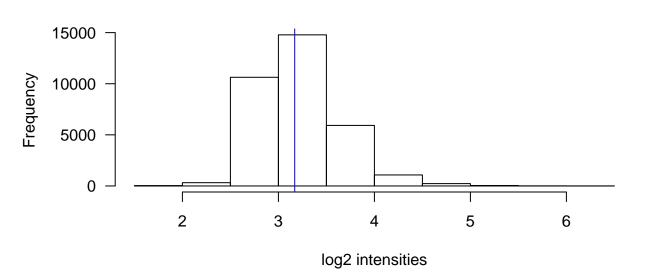
#### Sum of intensities per m/z



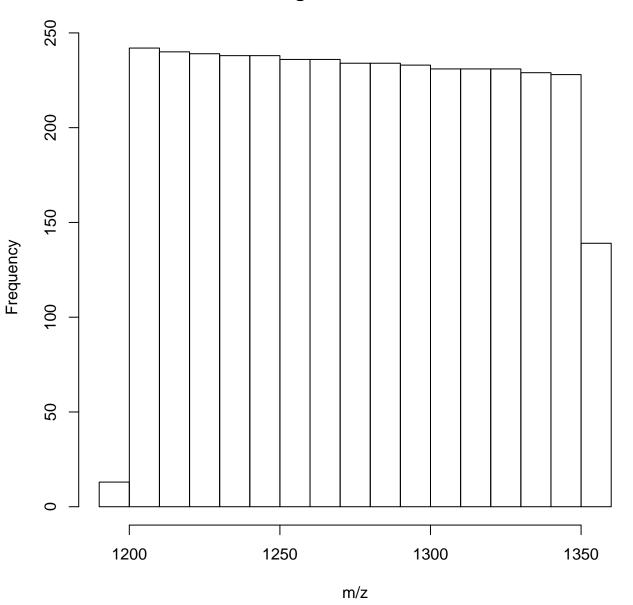
#### Median intensity per spectrum

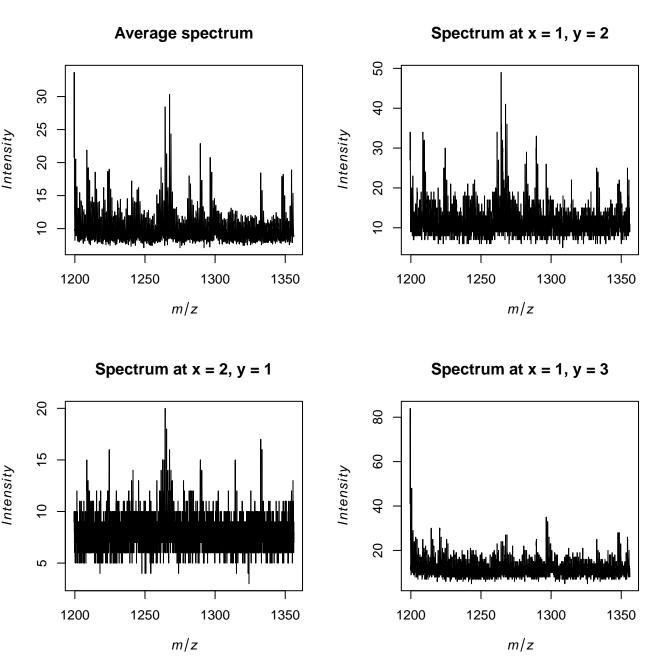


#### Log2-transformed intensities

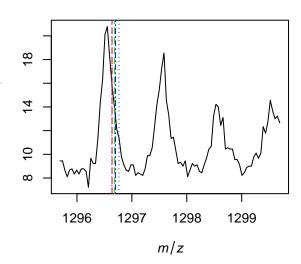


# Histogram of m/z values



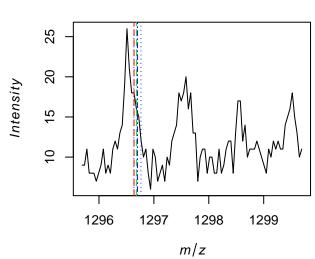




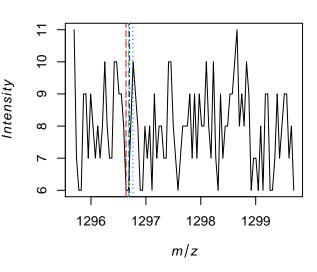


Intensity

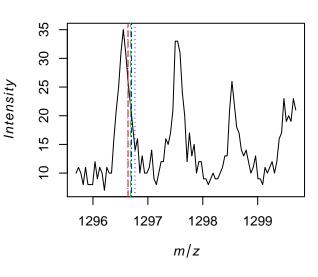
Spectrum at x = 1, y = 2

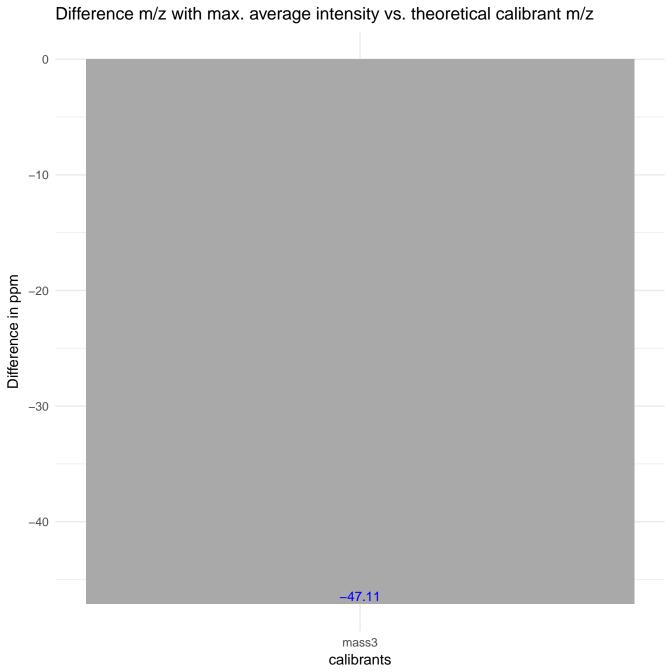


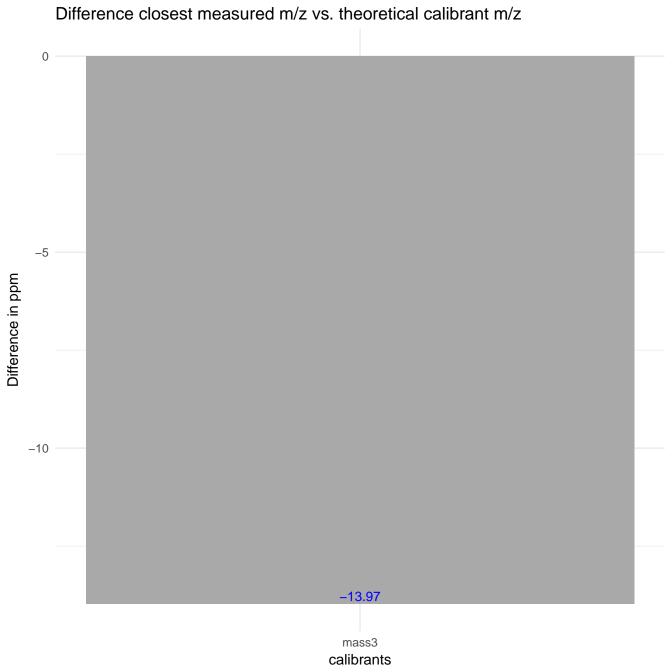
Spectrum at x = 2, y = 1



Spectrum at x = 1, y = 3







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

