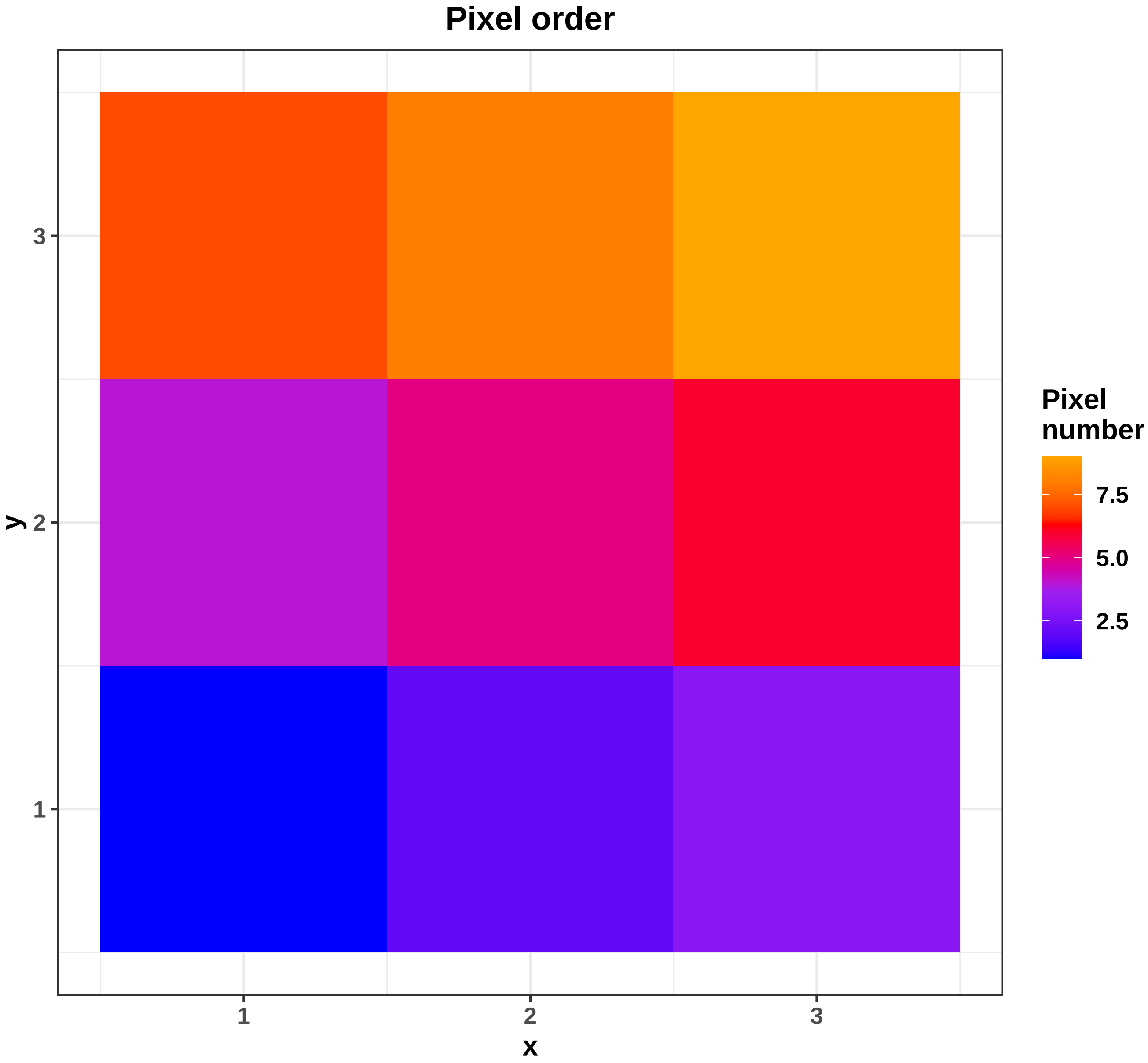
Testfile_analyze75

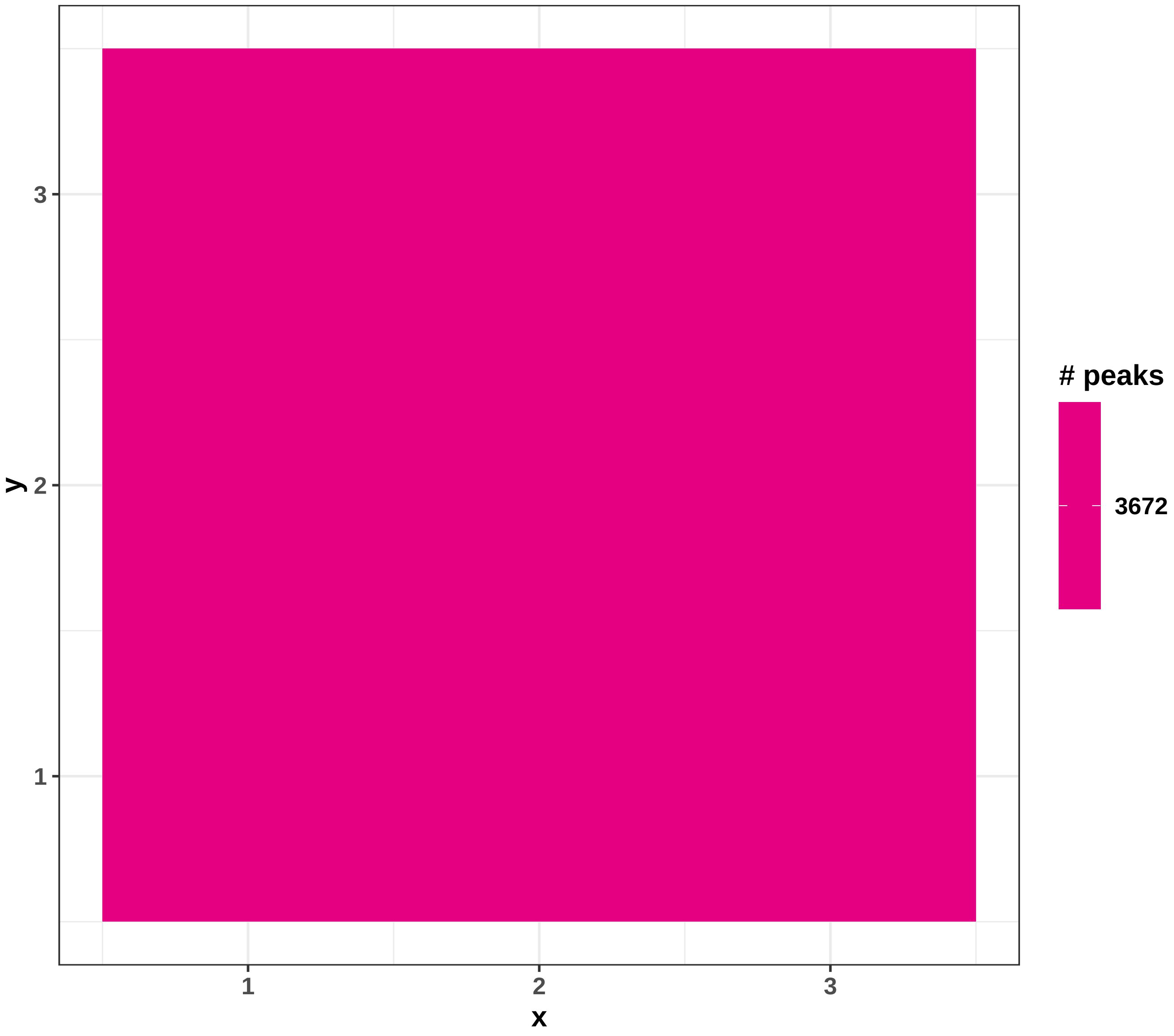
properties	values
Number of m/z features	3672
Range of m/z values	1199.47 − 1356.08
Number of pixels	9
Range of x coordinates	1 − 3
Range of y coordinates	1 − 3
Range of intensities	3 − 84
Number of NA intensities	0
Number of Inf intensities	0
Number of duplicated coordinates	0
Median of intensities	9
Intensities > 0	100 %
Number of empty spectra	0
Median TIC ± sd	37005 ± 5329
Median # peaks per spectrum ± sd	3672 ± 0
maximum m/z window size	0.04
Centroided	FALSE
input m/z (#valid/#input) in None	0 / 0


Pixel order
y
3
2
1
x
1
2
3
Pixel number
7.5
5.0
2.5

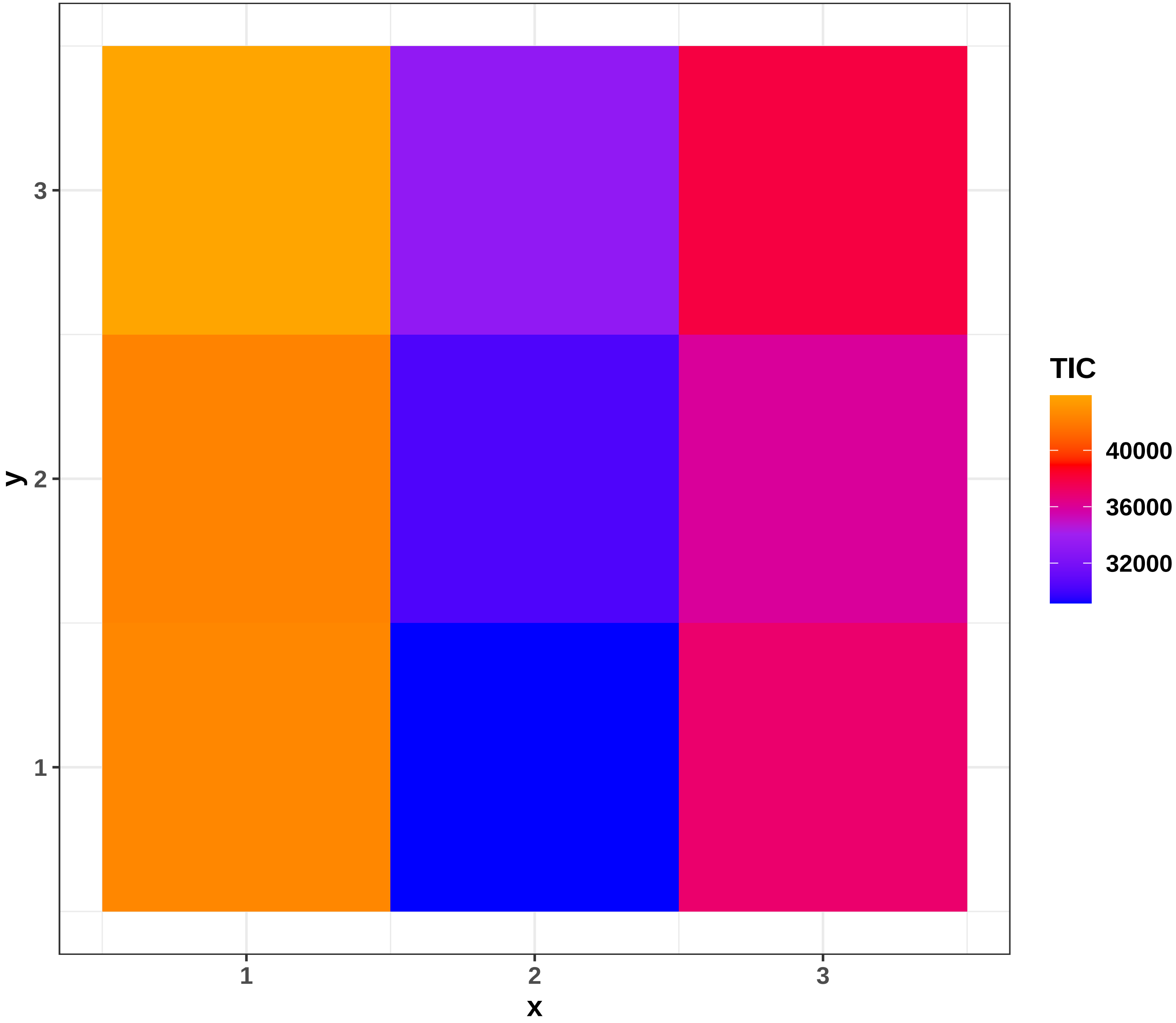
The input calibrant m/z were not provided
or outside the m/z range.

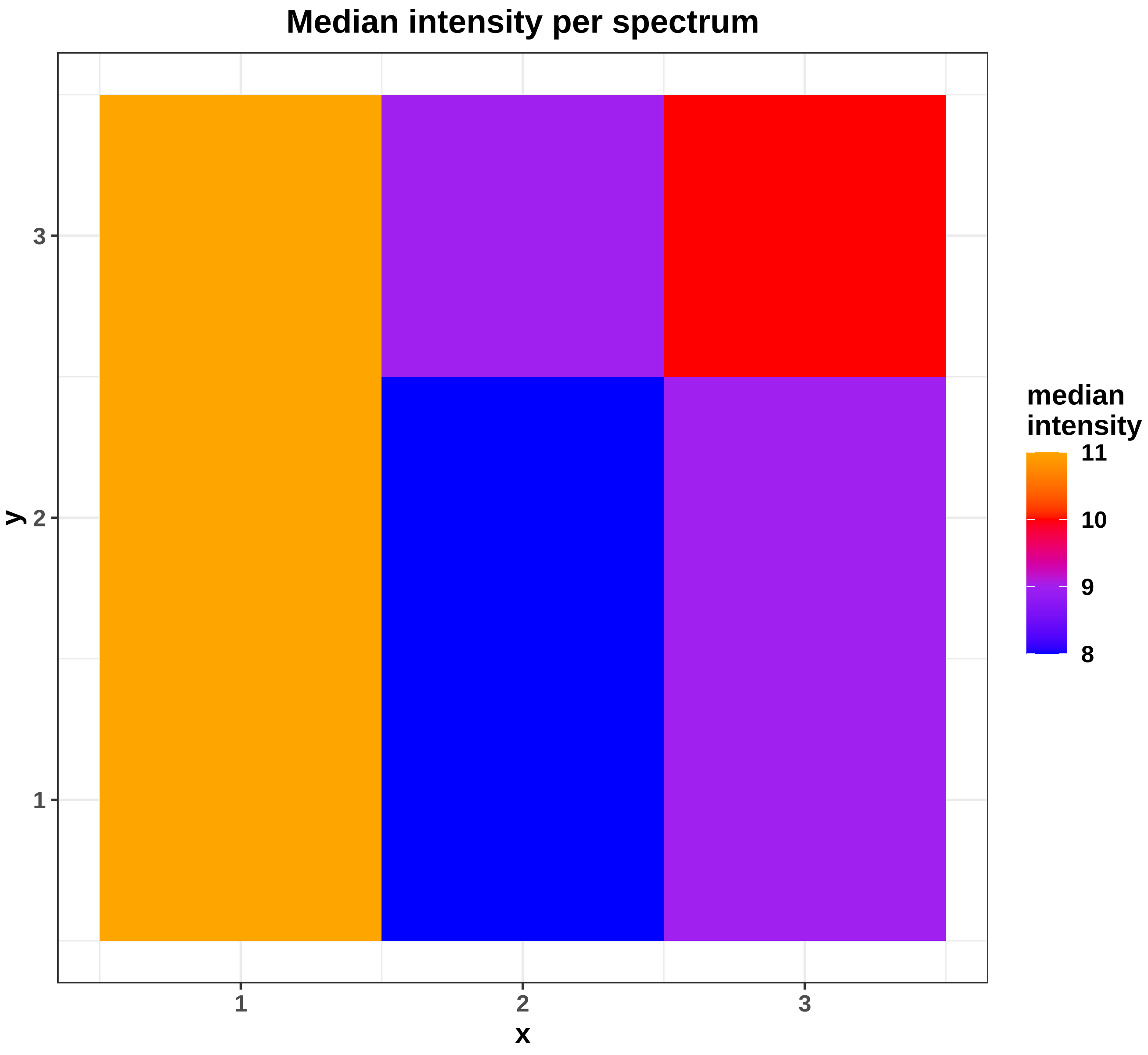
The input peptide and calibrant m/z were not provided or outside the m/z range.

Number of peaks per spectrum

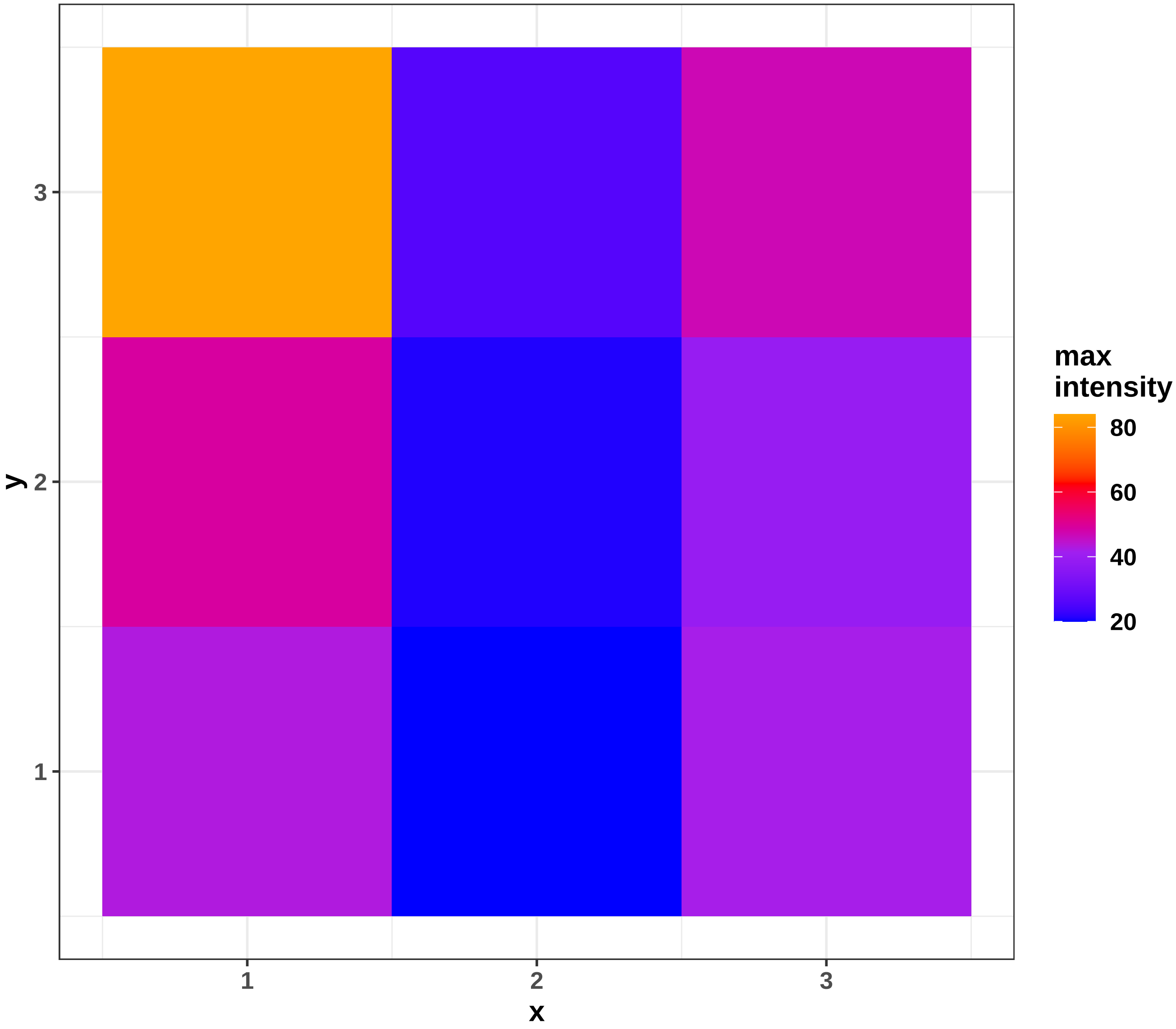


Total Ion Current

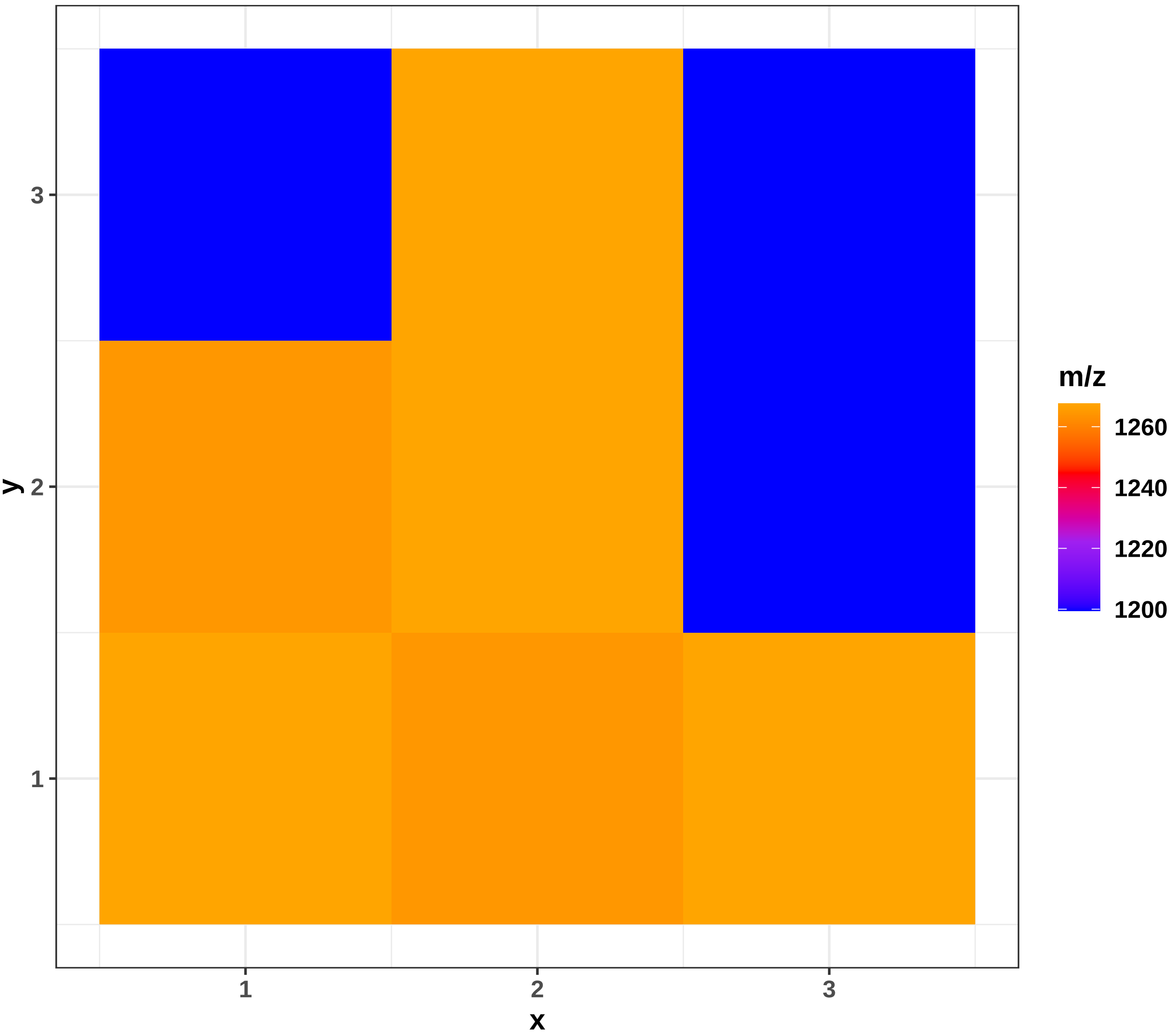


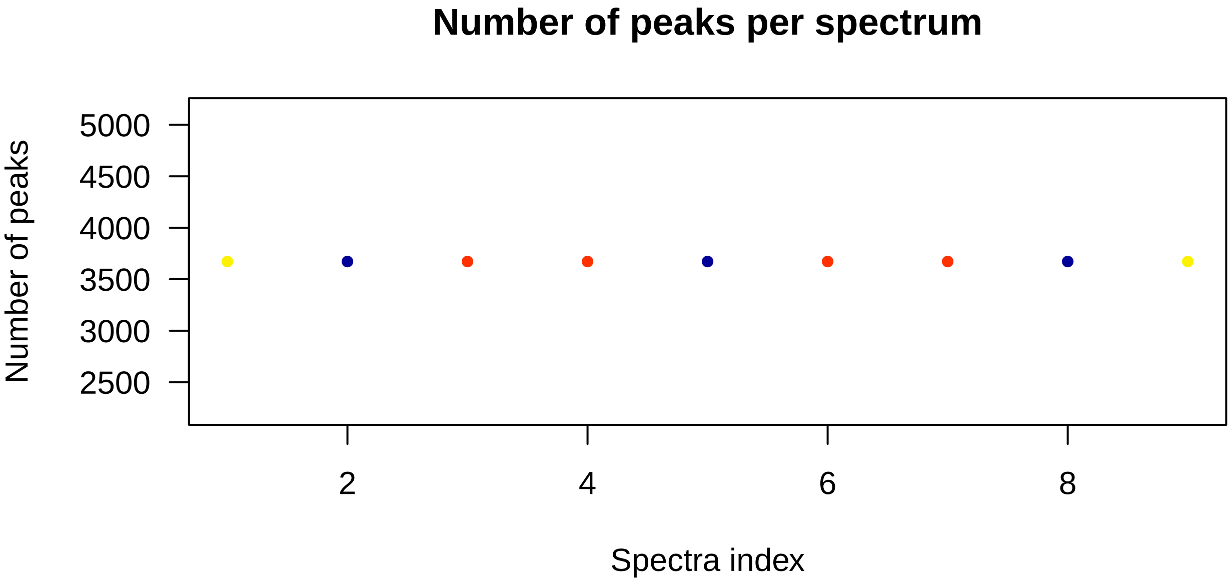

Median intensity per spectrum
y
3
2
1
x
1
2
3
median intensity
11
10
9
8

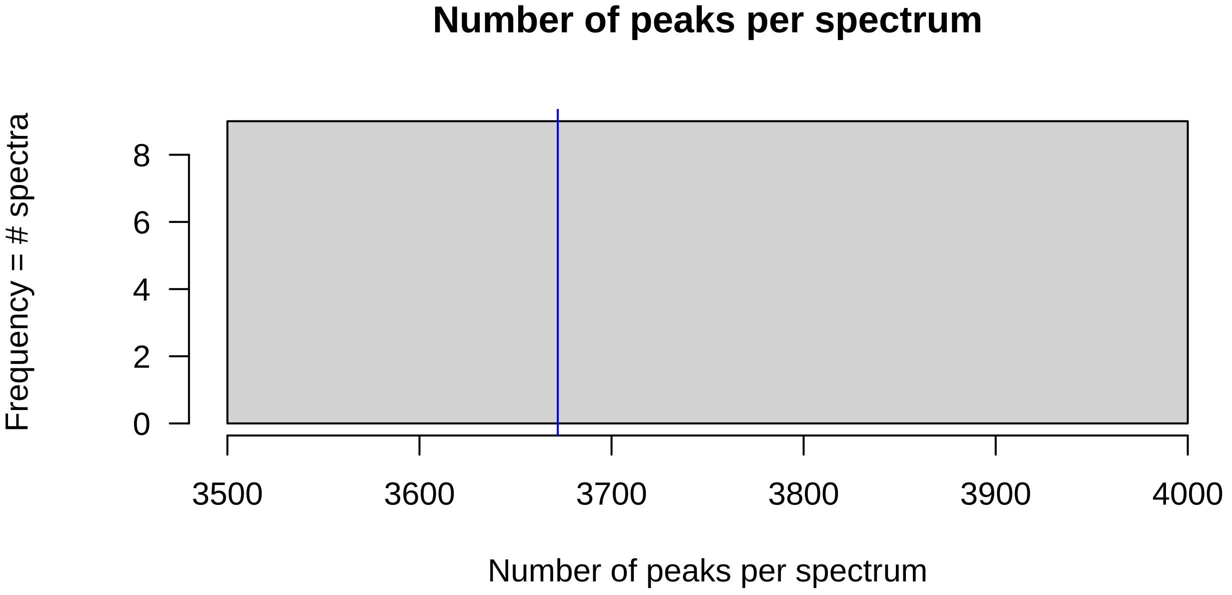
Maximum intensity per spectrum

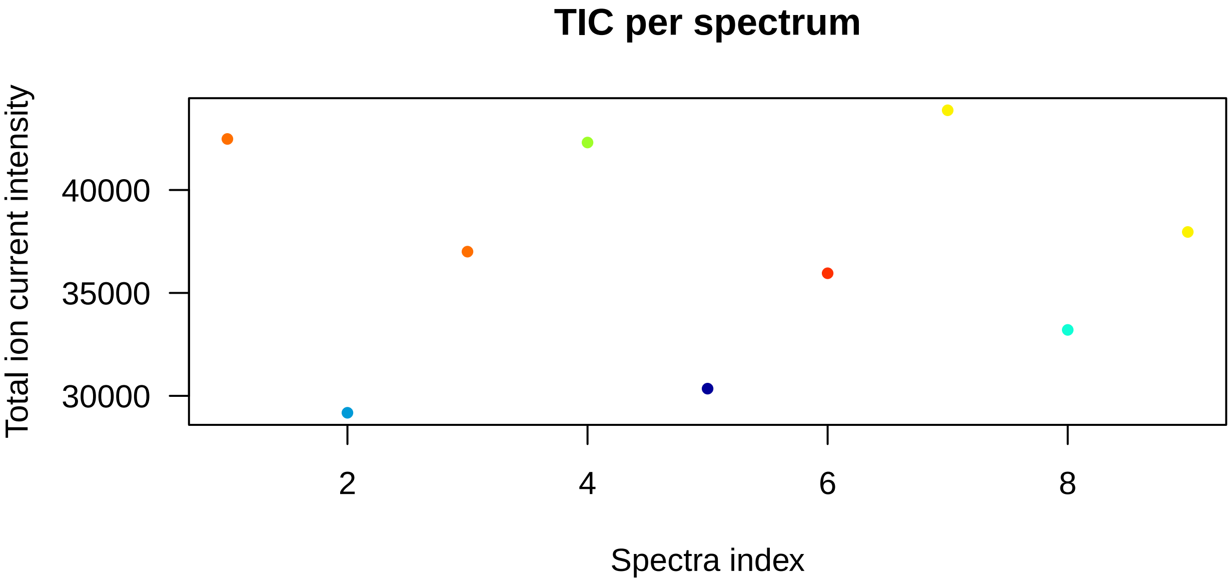


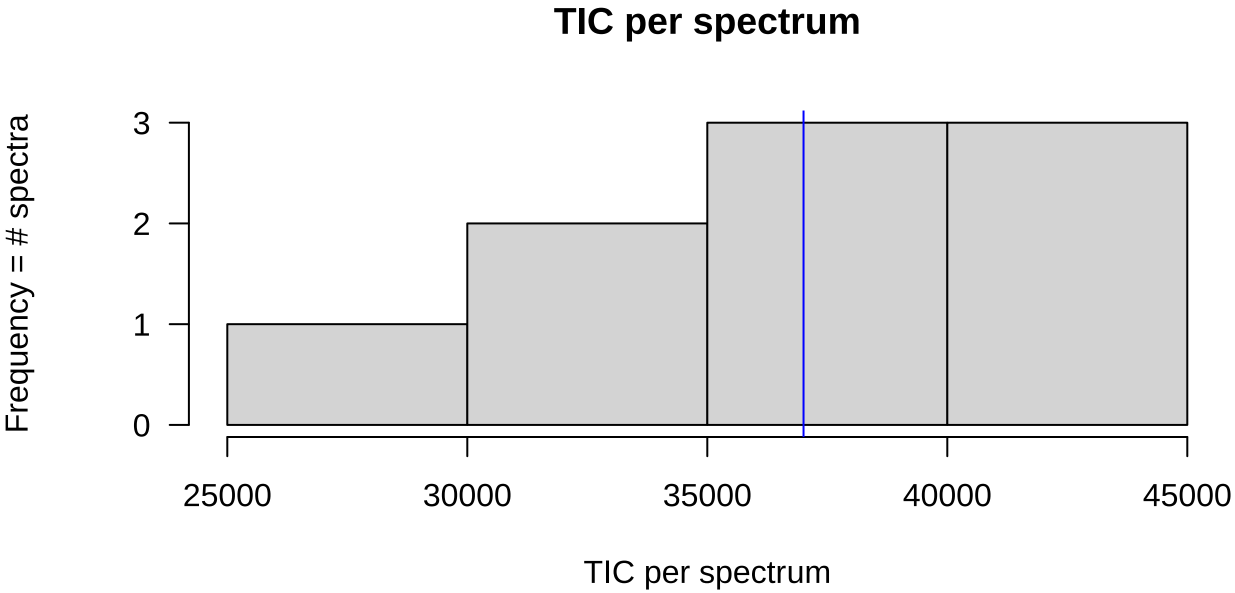
Most abundant m/z in each spectrum

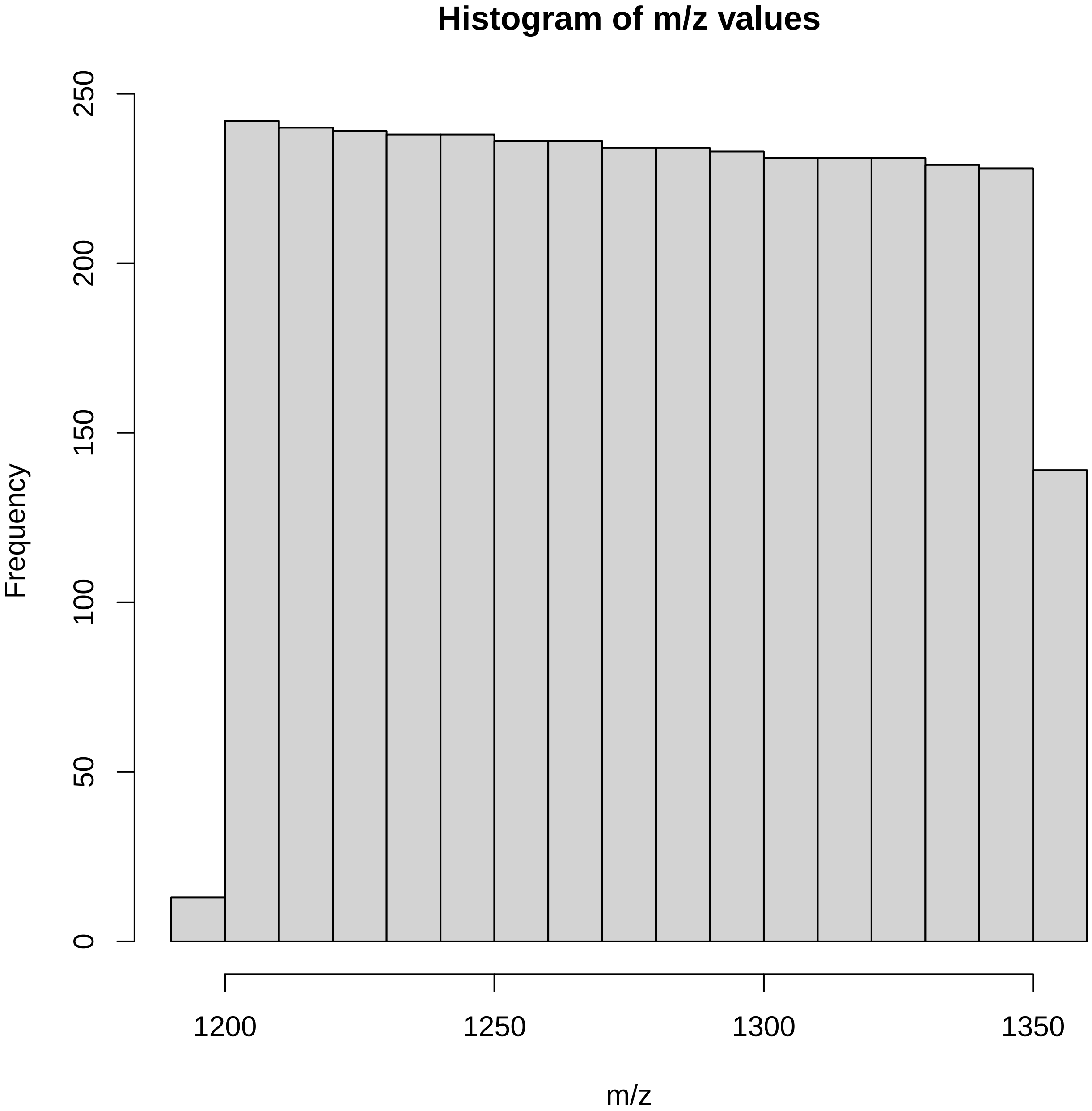


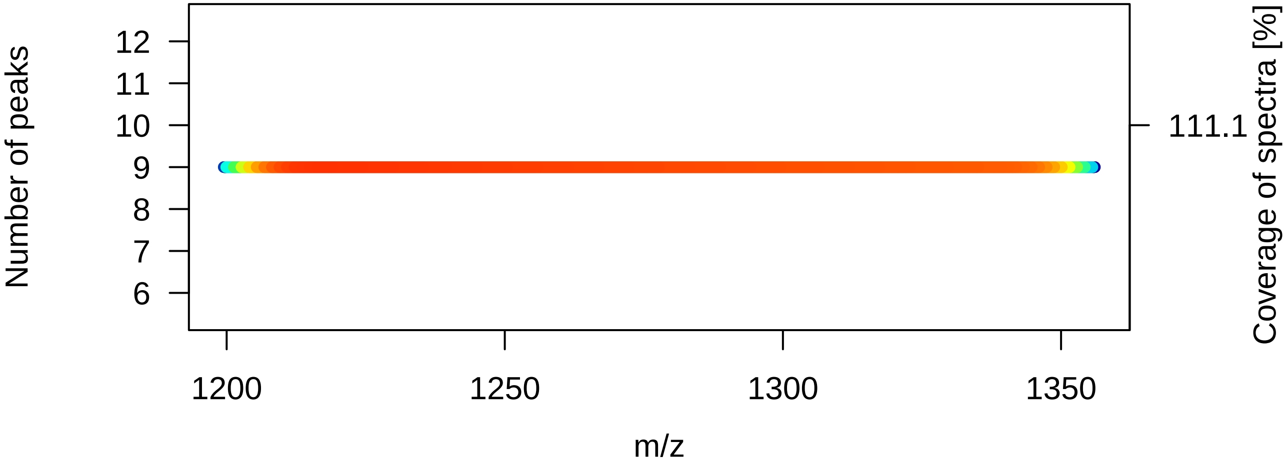

Number of peaks per spectrum
Number of peaks
5000
4500
4000
3500
3000
2500
2
4
6
8
Spectra index


Number of peaks per spectrum
Frequency = # spectra
8
6
4
2
0
3500
3600
3700
3800
3900
4000
Number of peaks per spectrum

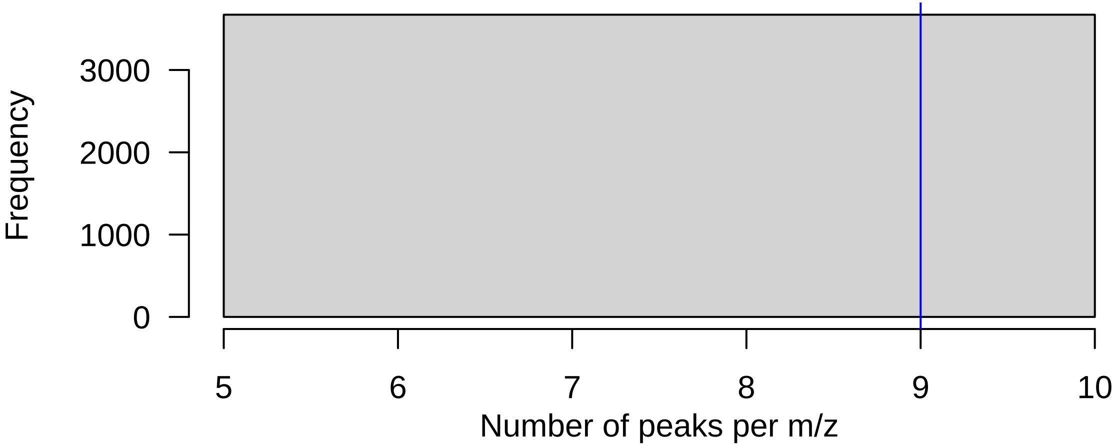

TIC per spectrum
Total ion current intensity
40000
35000
30000
2
4
6
8
Spectra index


TIC per spectrum
Frequency = # spectra
3
2
1
0
25000
30000
35000
40000
45000
TIC per spectrum

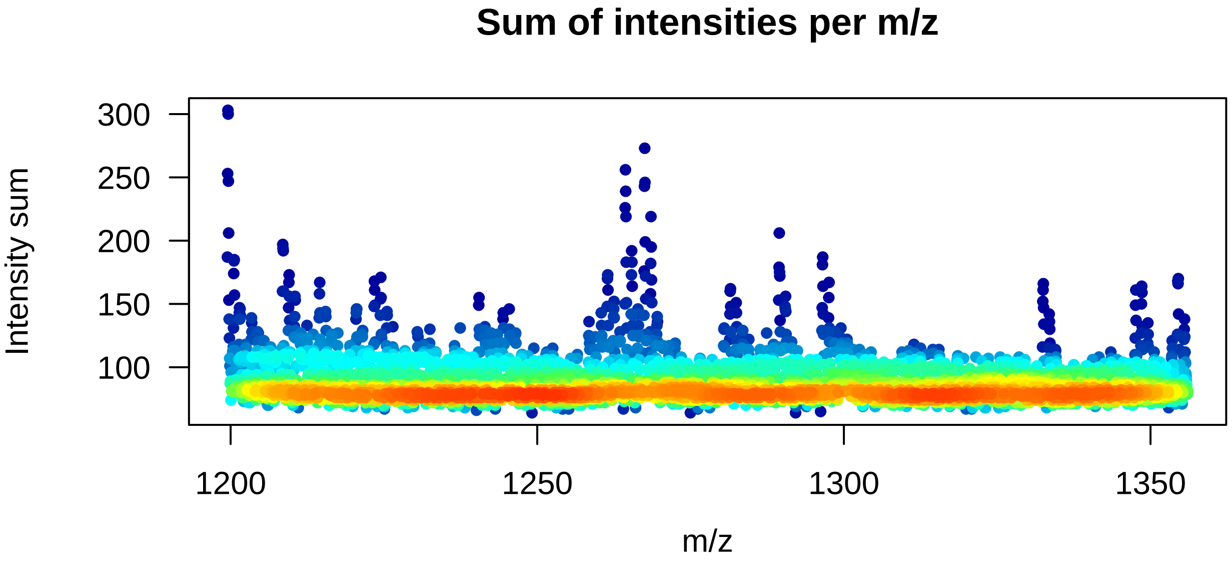

Histogram of m/z values
Frequency
0
50
100
150
200
250
1200
1250
1300
1350
m/z



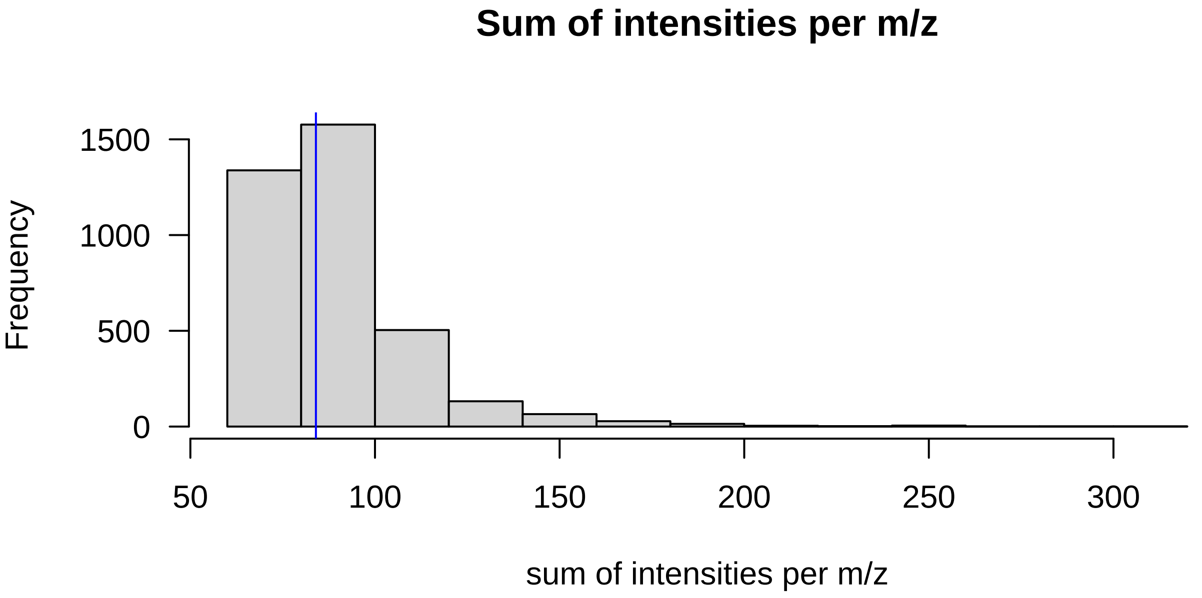
Number of peaks per m/z



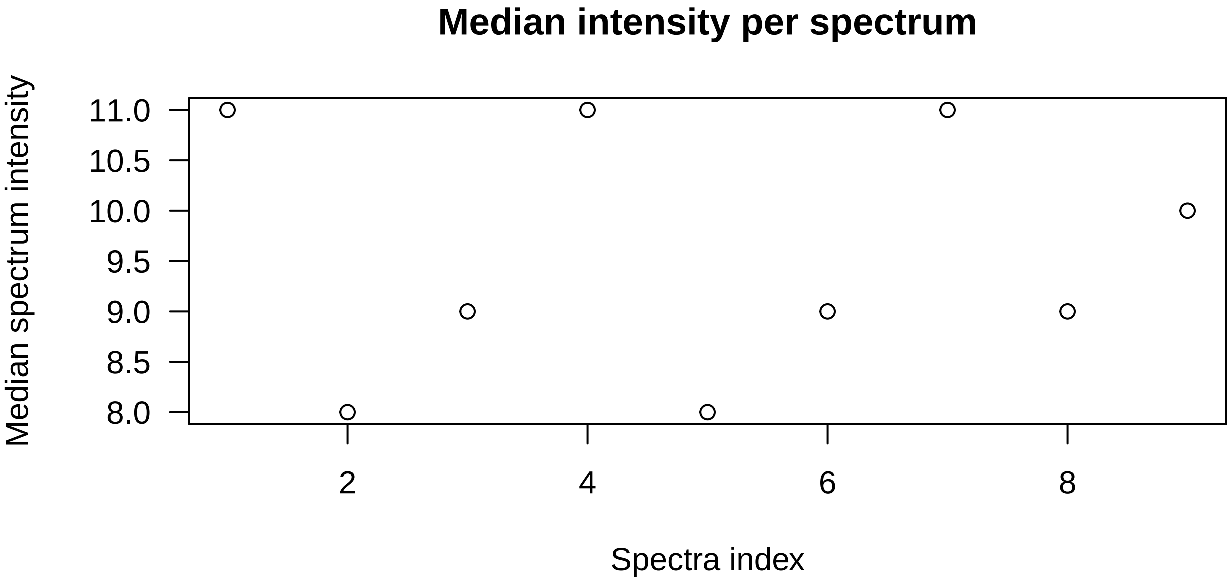
Number of peaks per m/z

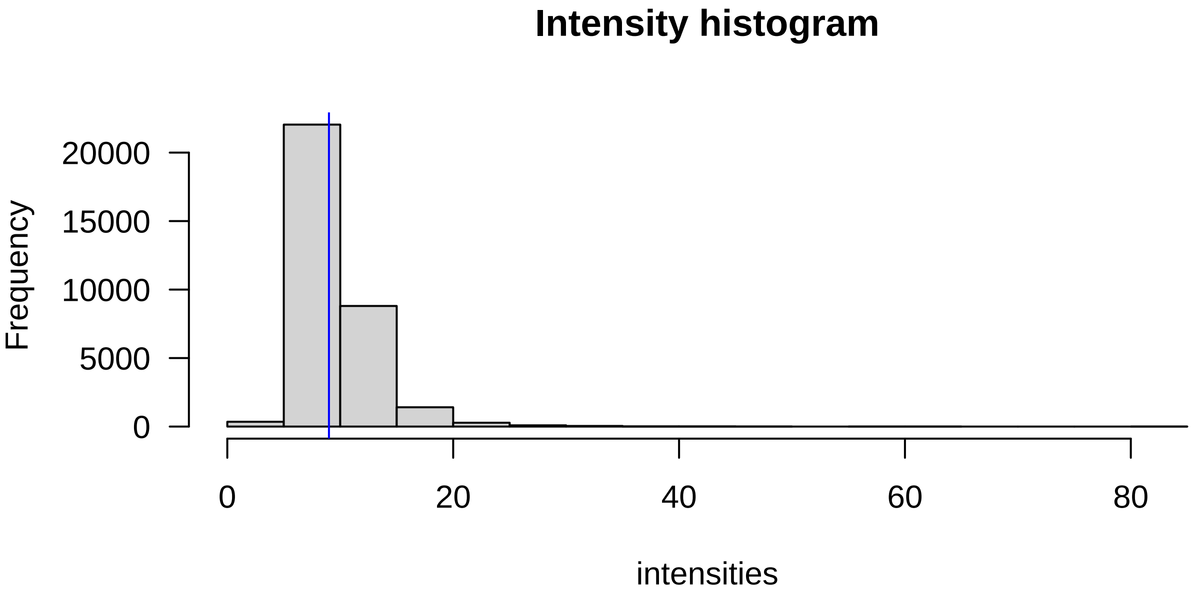


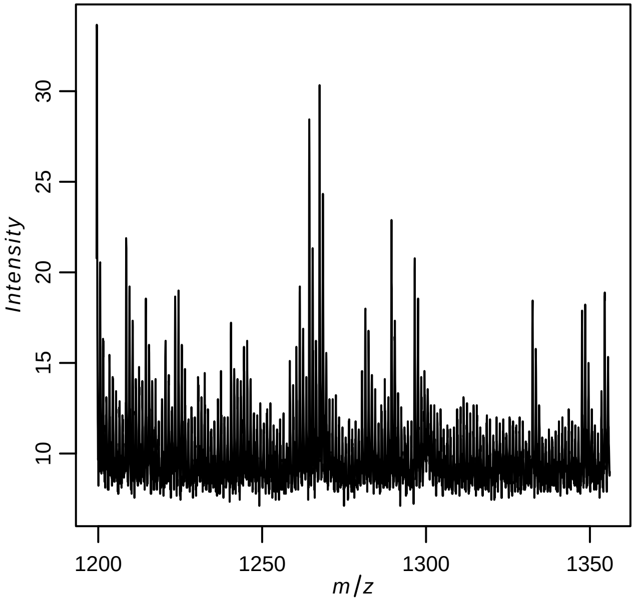
Sum of intensities per m/z

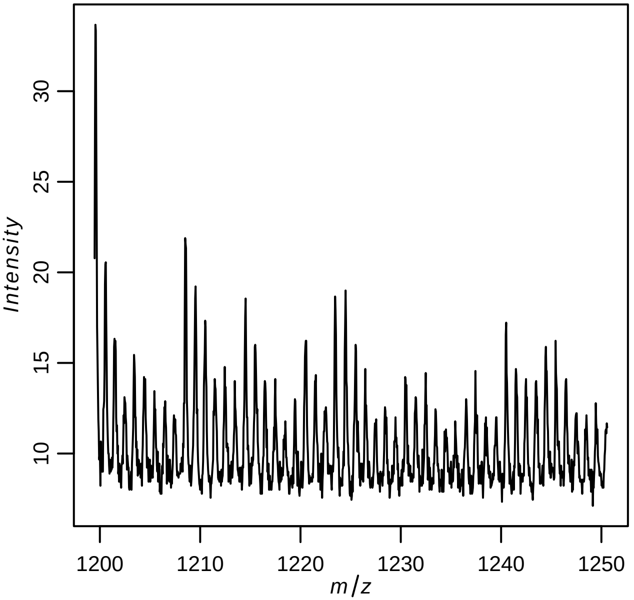


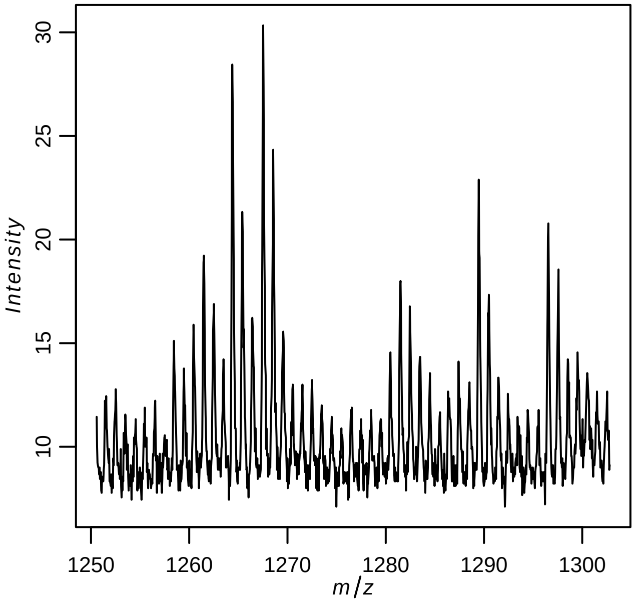
Sum of intensities per m/z

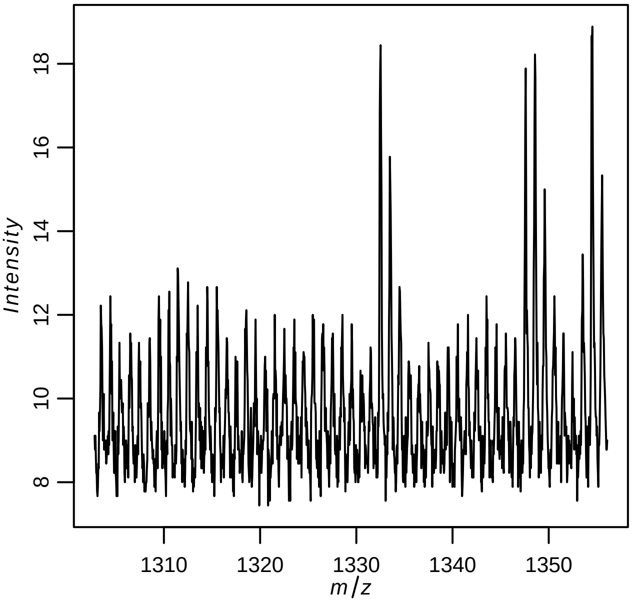

Median intensity per spectrum

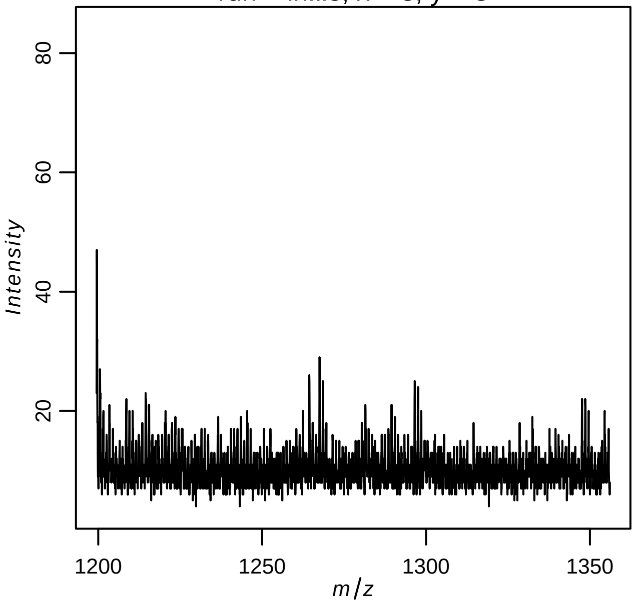

Intensity histogram

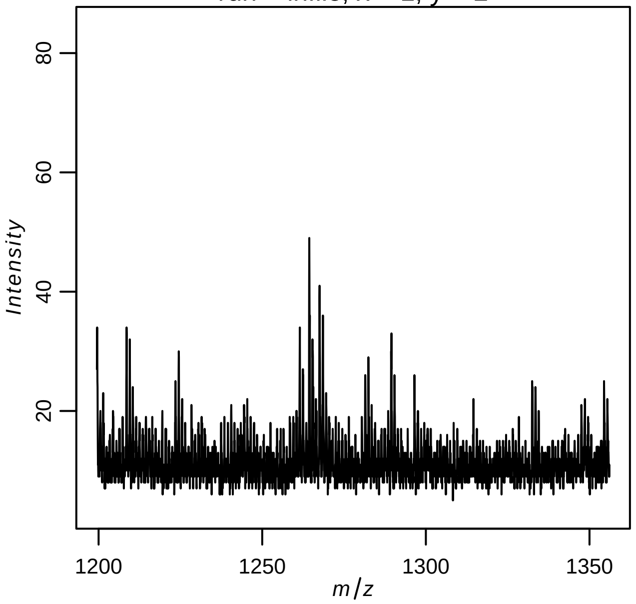

Average spectrum

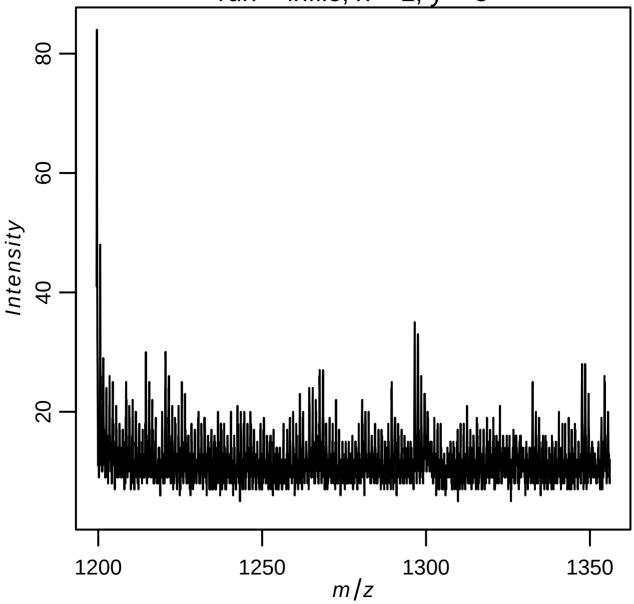

Zoomed average spectrum

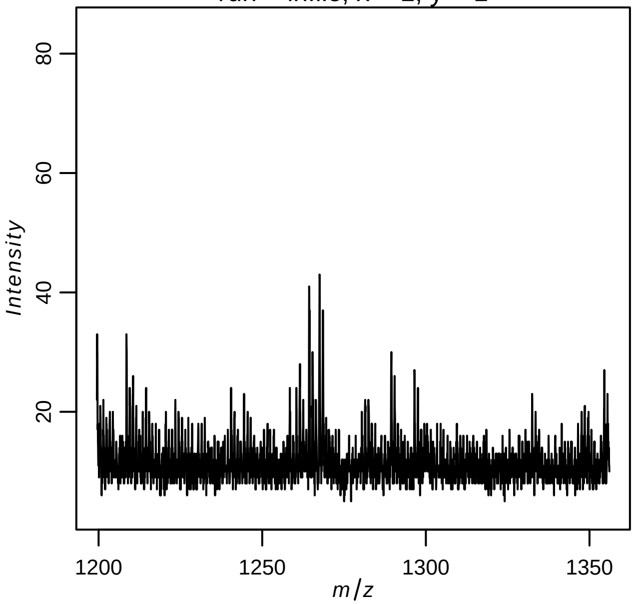

Zoomed average spectrum


Zoomed average spectrum


run = infile, x = 3, y = 3


run = infile, x = 1, y = 2


run = infile, x = 1, y = 3


run = infile, x = 1, y = 1