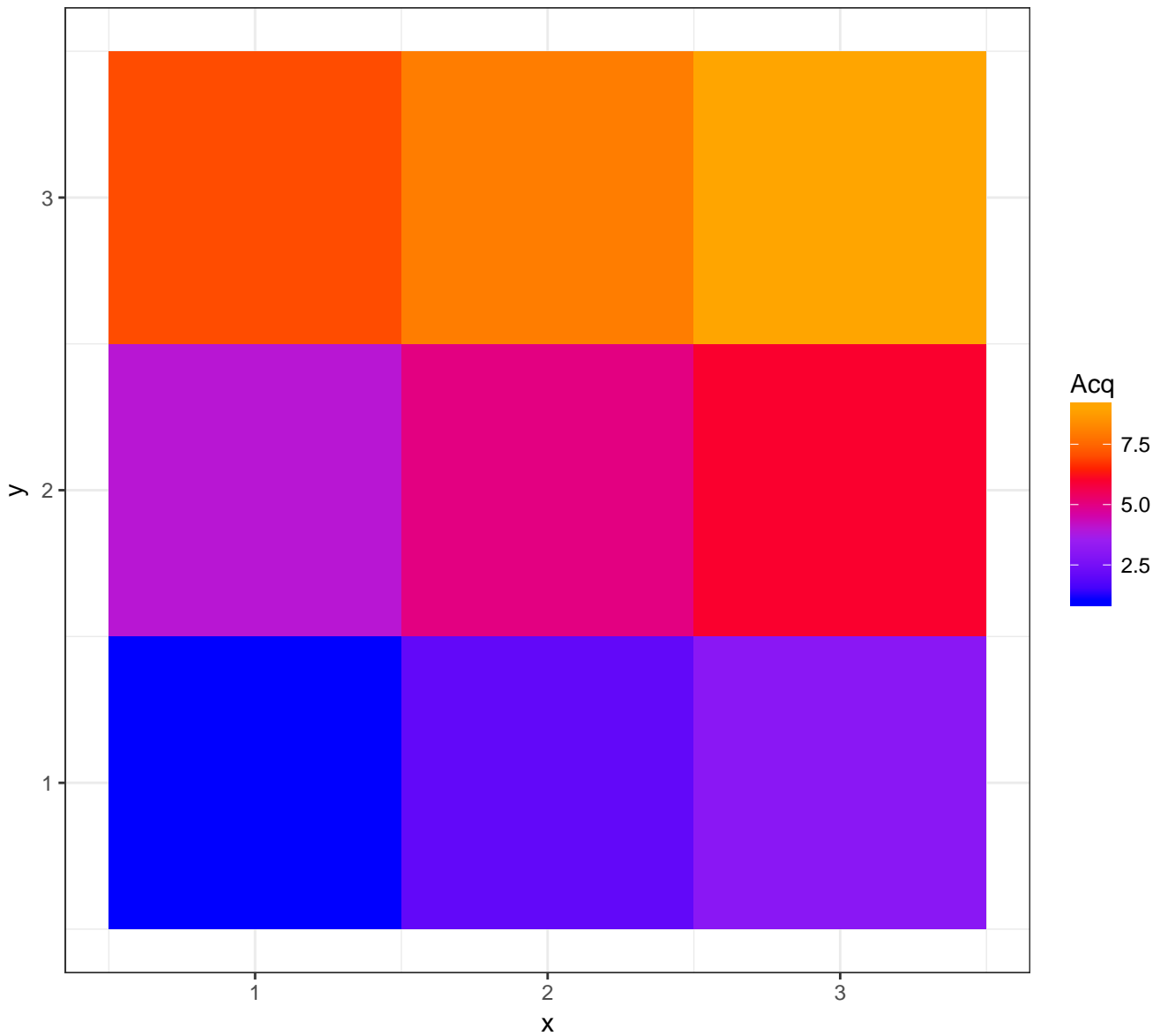


# Quality control of MSI data

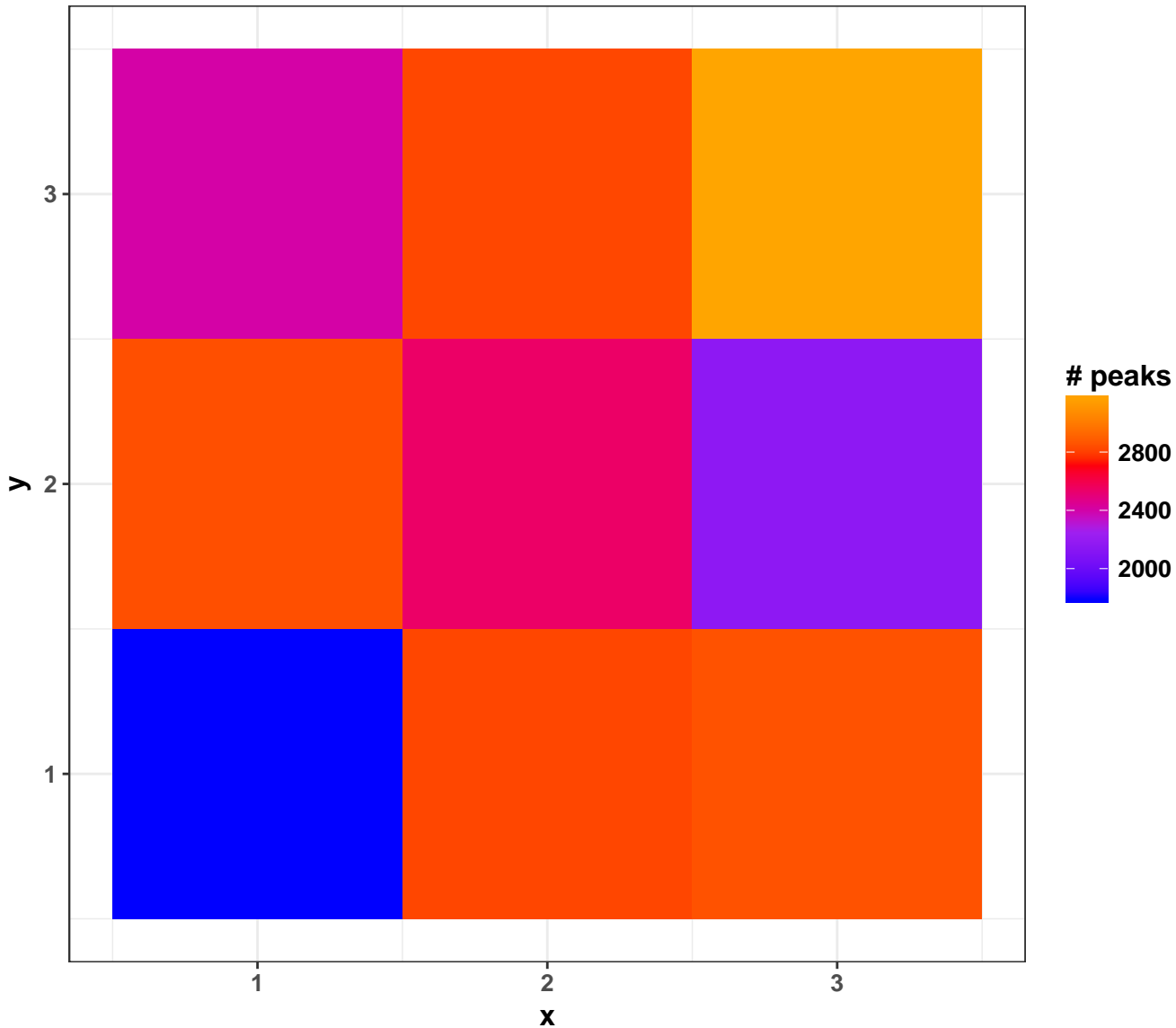
Filename: Testfile\_rdata

| 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 None      | 0 / 0           |
| # calibrants in None    | 0 / 0           |

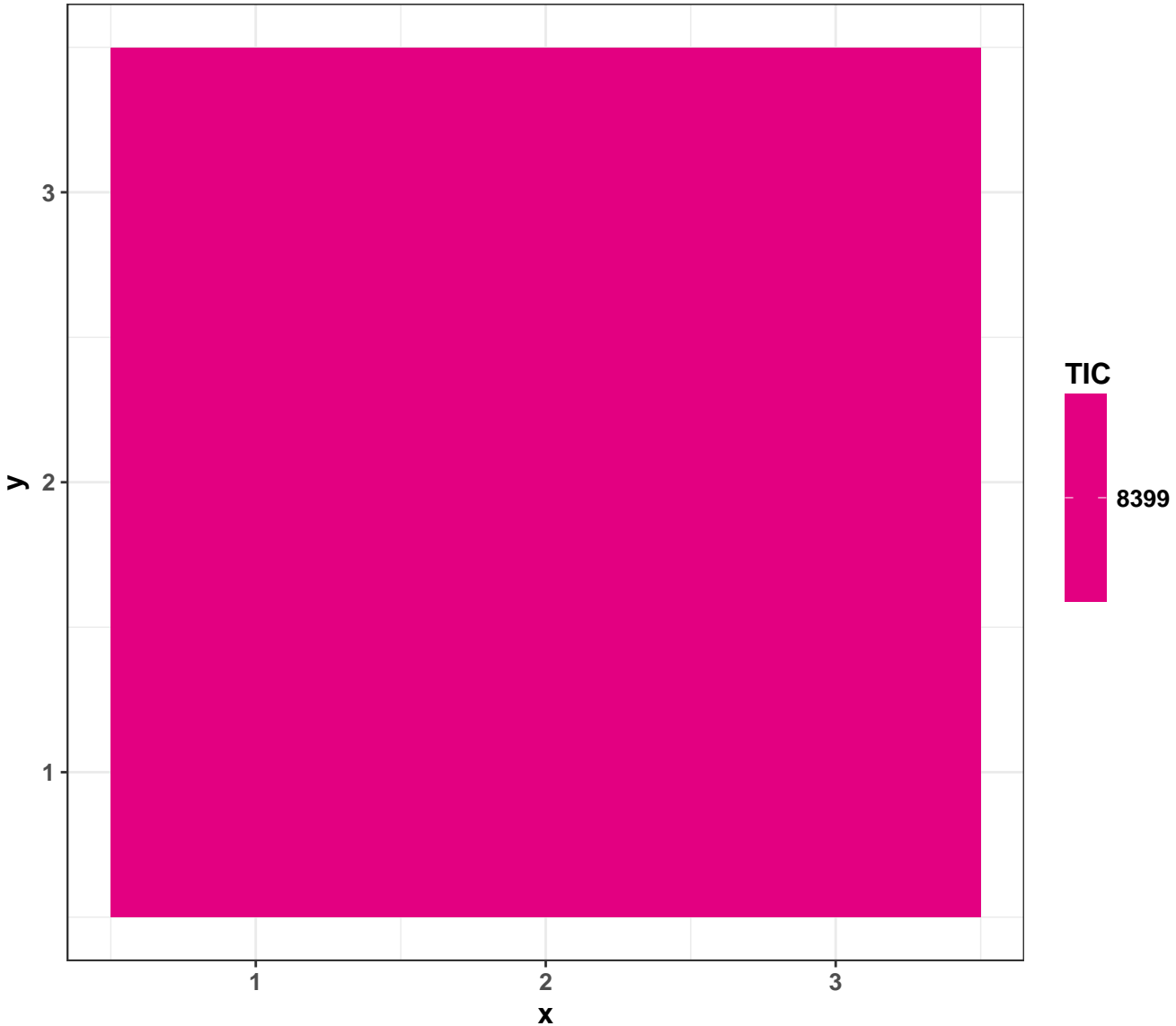
# 1) Order of Acquisition



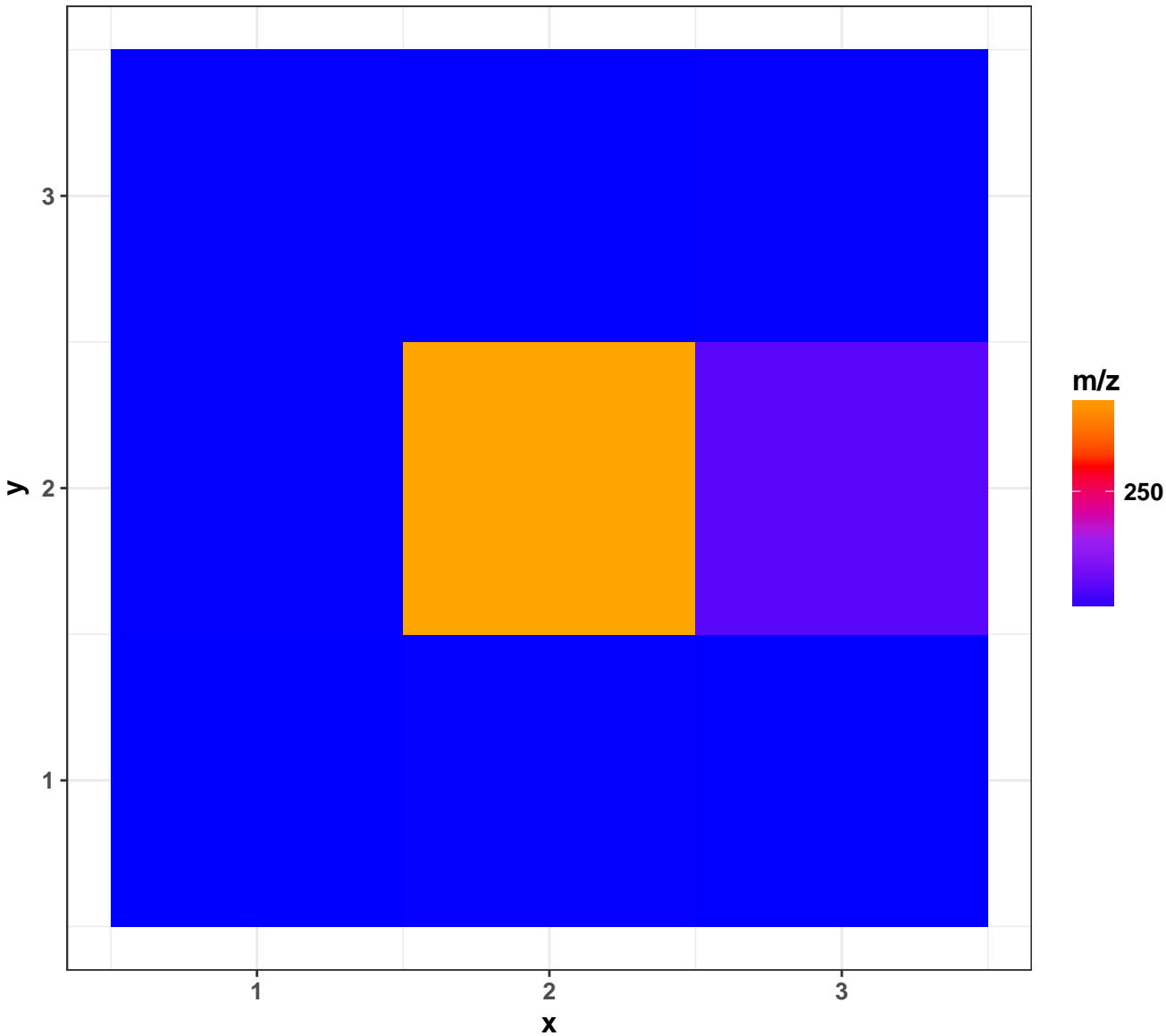
#### 4) Number of peaks per pixel



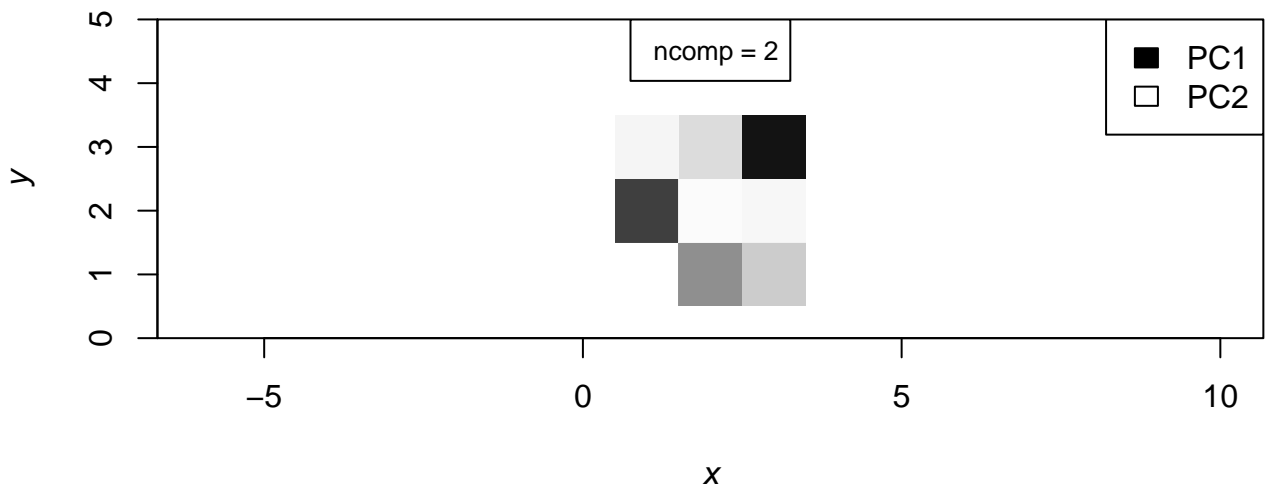
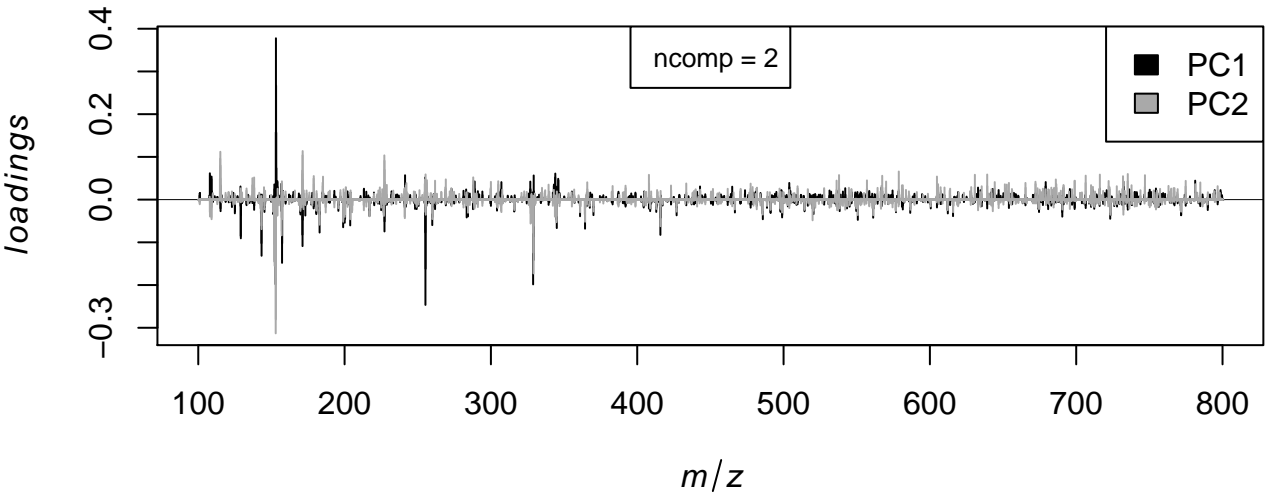
## 5) Total Ion Chromatogram



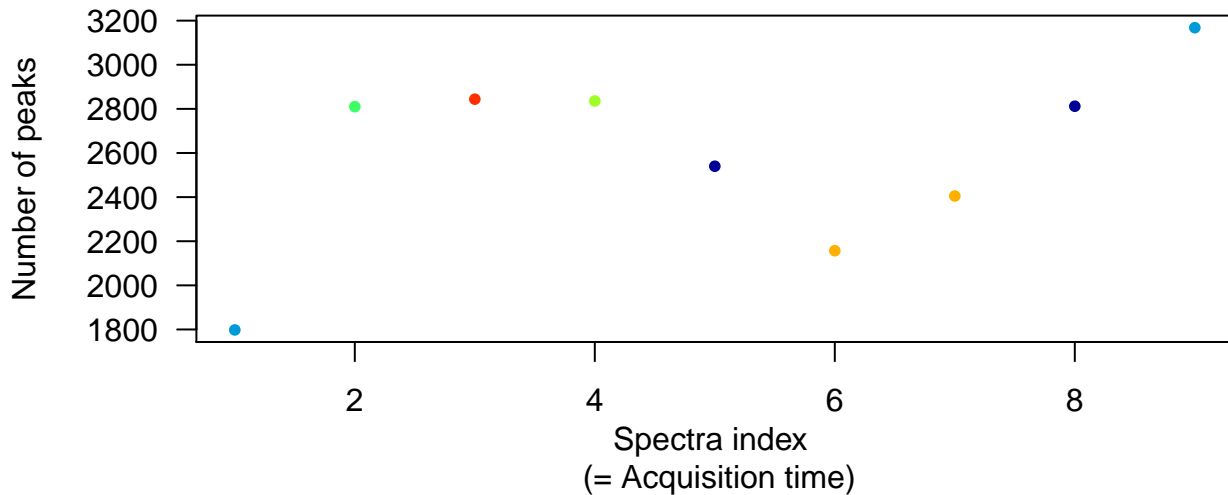
## 6) Most abundant m/z in each pixel



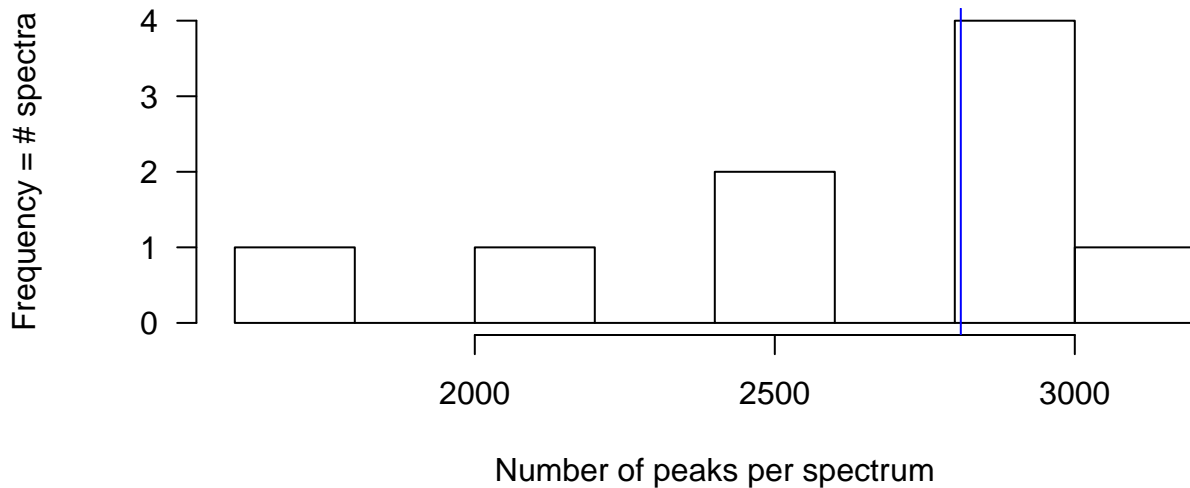
## 7) PCA for two components



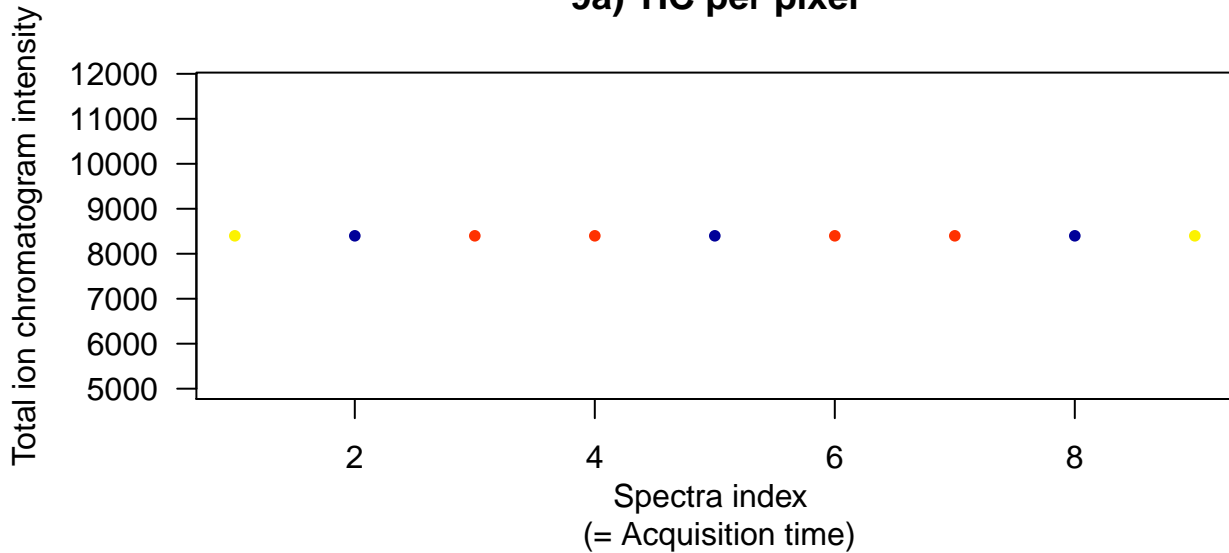
### 8a) Number of peaks per spectrum



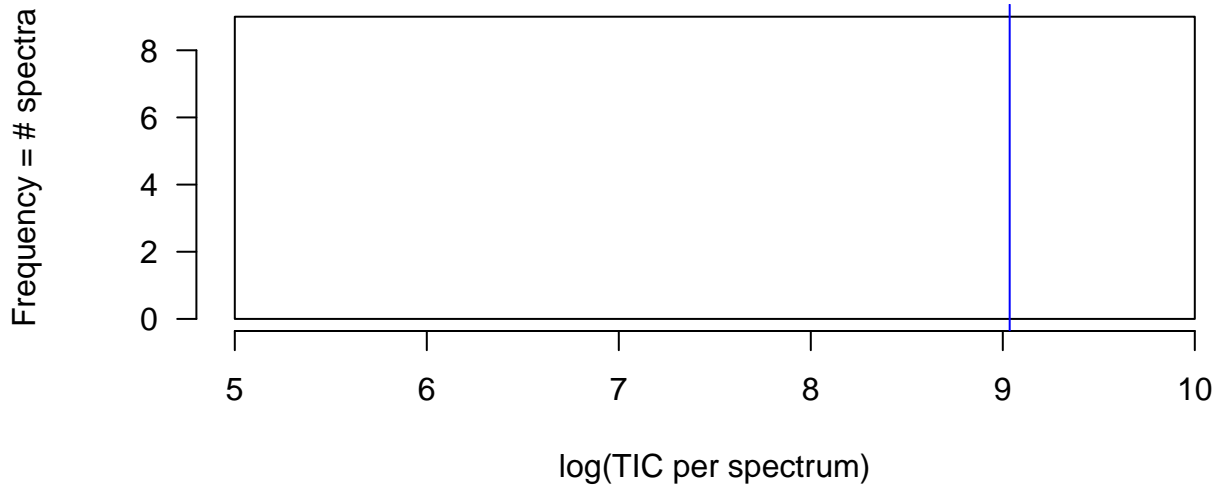
### 8b) Number of peaks per spectrum



### 9a) TIC per pixel

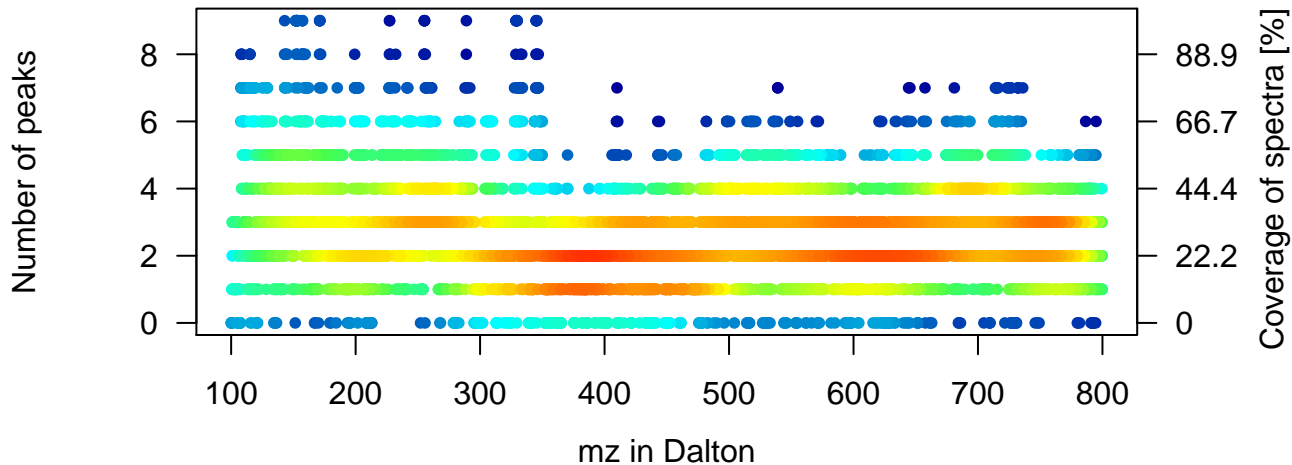


### 9b) TIC per spectrum

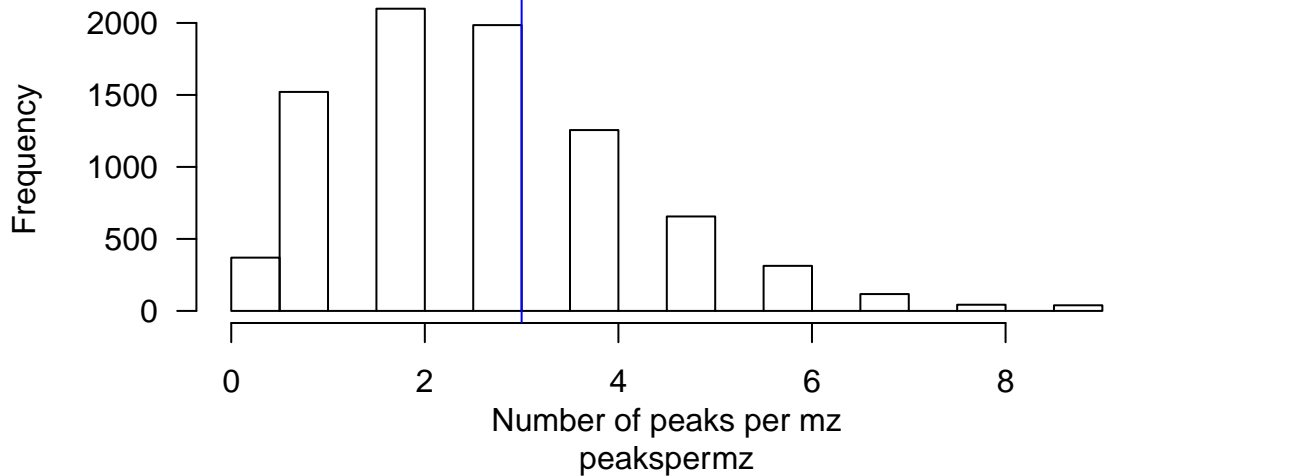




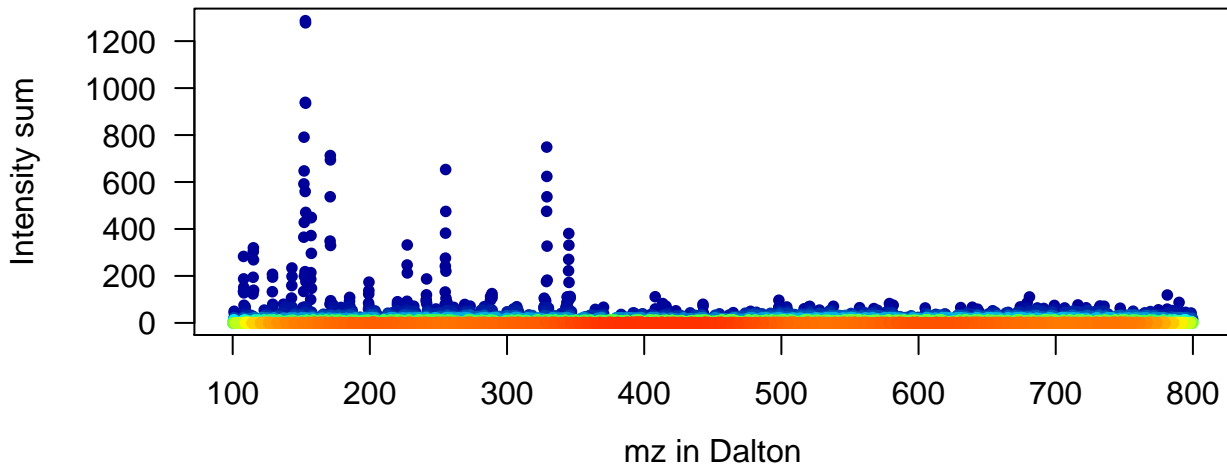
### 11a) Number of peaks for each mz



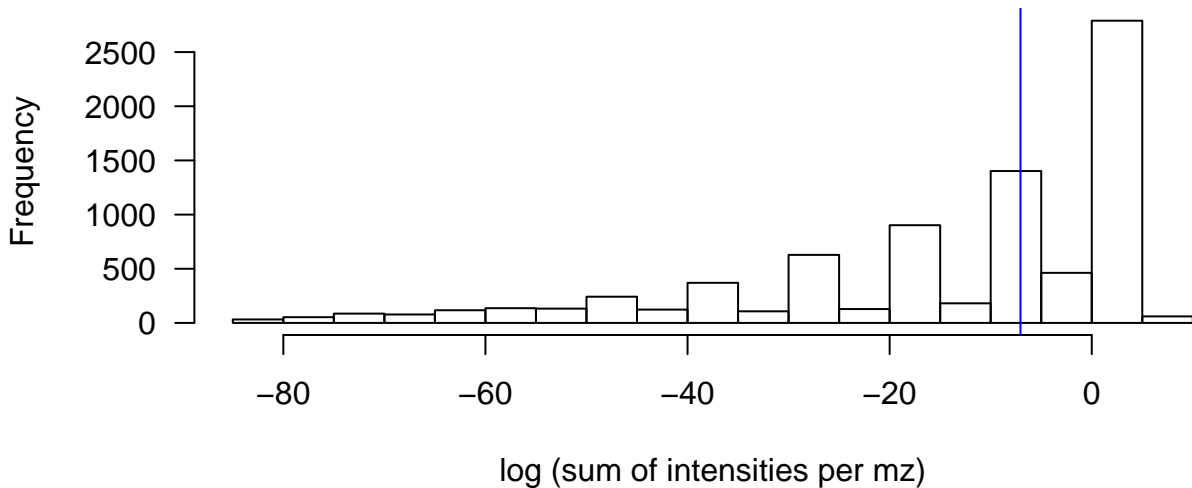
### 11b) Number of peaks per mz



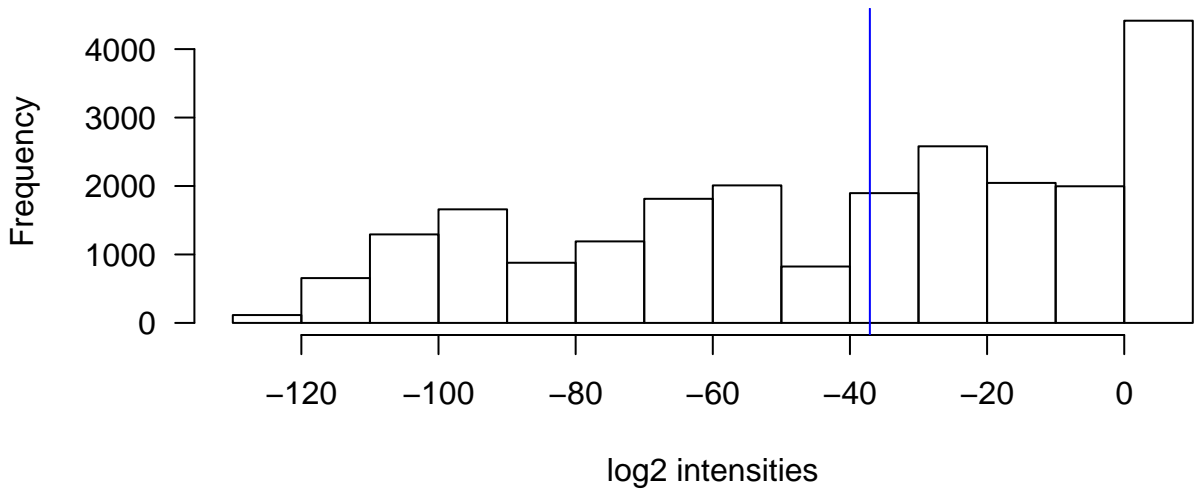
**12a) Sum of all peak intensities for each mz**



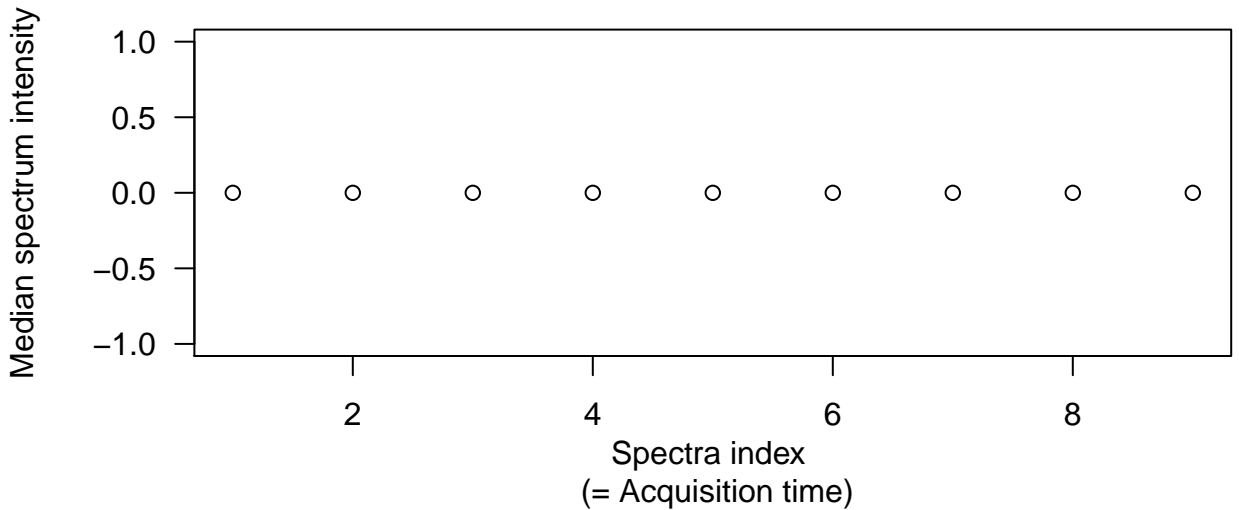
**12b) Sum of intensities per mz**



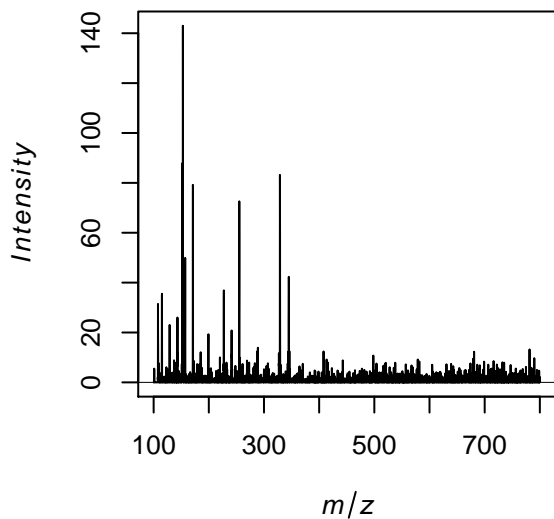
### 13a) Log2-transformed intensities



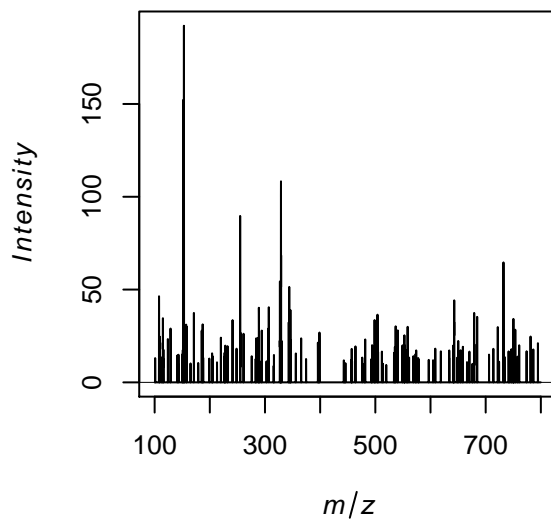
### 13b) Median intensity per spectrum



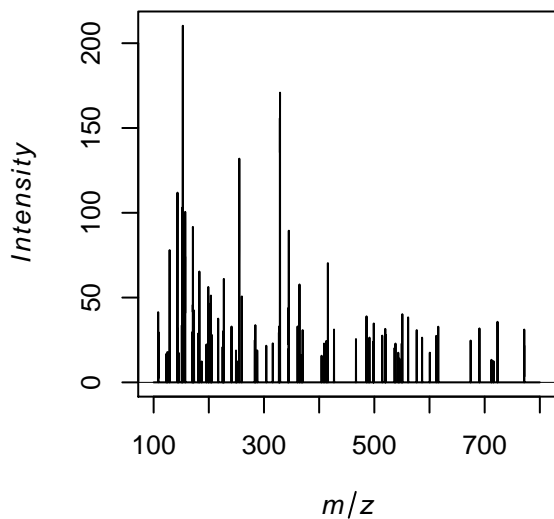
**Average spectrum**



**Spectrum in middle of acquisition**



**Spectrum at x = 1, y = 1**



**Spectrum at x = 3, y = 2**

