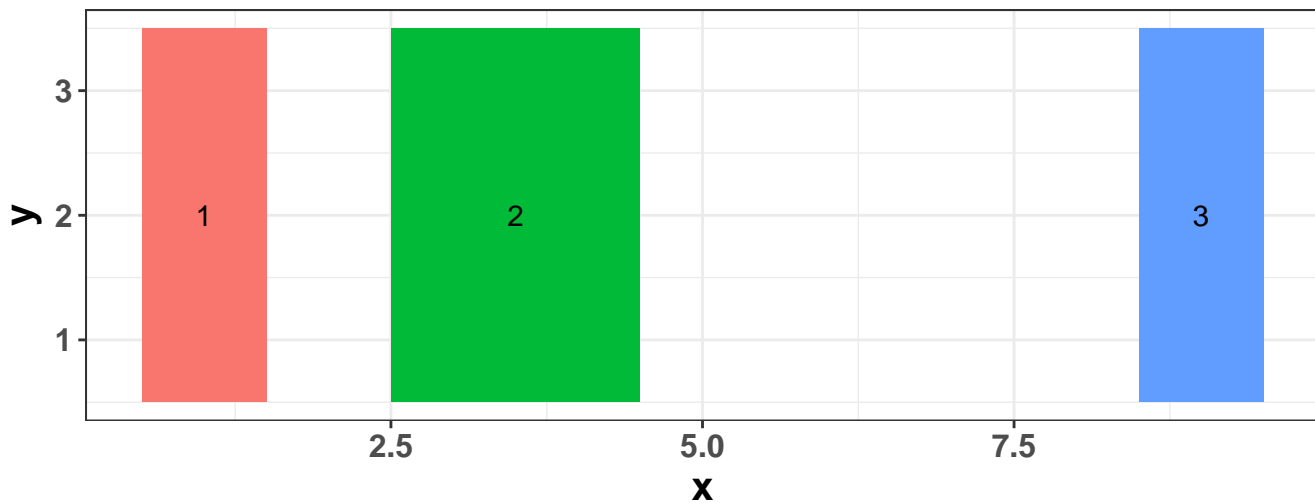


Testfile_rdata

properties	values
Number of m/z features	8399
Range of m/z values [Da]	100.08 – 799.92
Number of pixels	12
Range of x coordinates	1 – 9
Range of y coordinates	1 – 3
Range of intensities	0 – 9.24
Median of intensities	0
Intensities > 0	31.29 %
Number of zero TICs	0
Median TIC	161.809190448268
Median # peaks per spectrum	2811
Normalization	FALSE
Smoothing	FALSE
Baseline reduction	FALSE
Peak picking	FALSE
Centroided	FALSE
# peptides in None	0 / 0
# calibrants in None	0 / 0

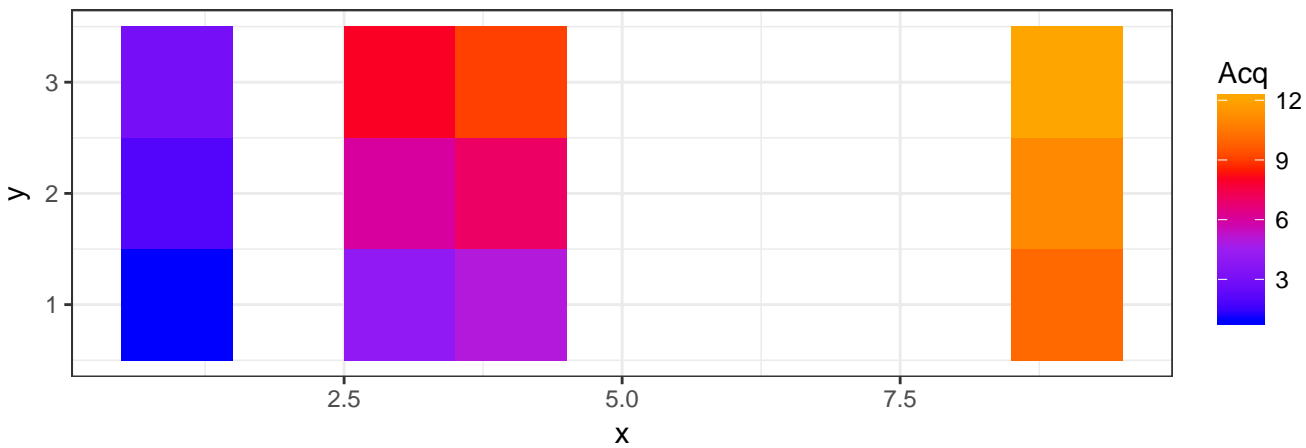
Spatial orientation of combined data



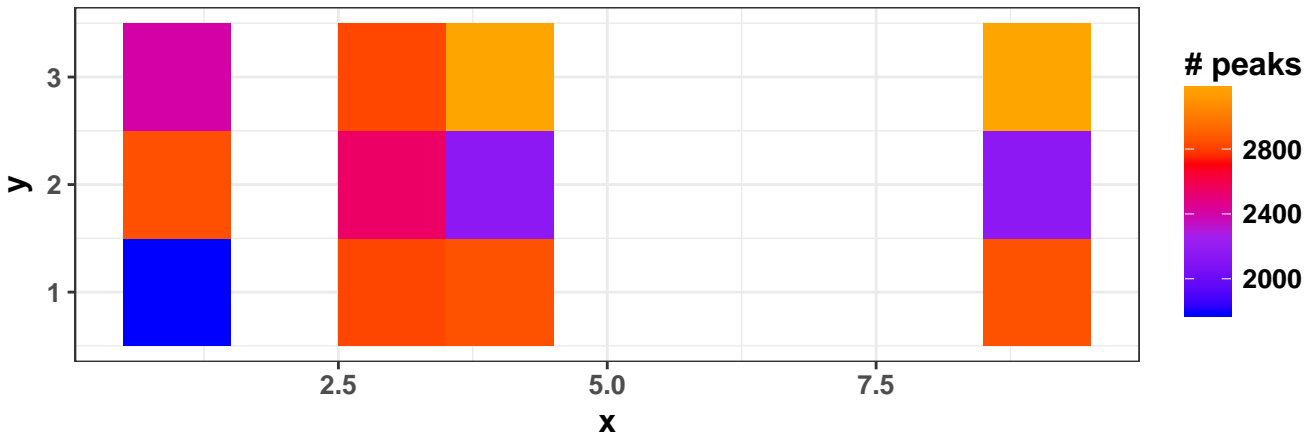
sample_name

1_File1 2_File2 3_File3

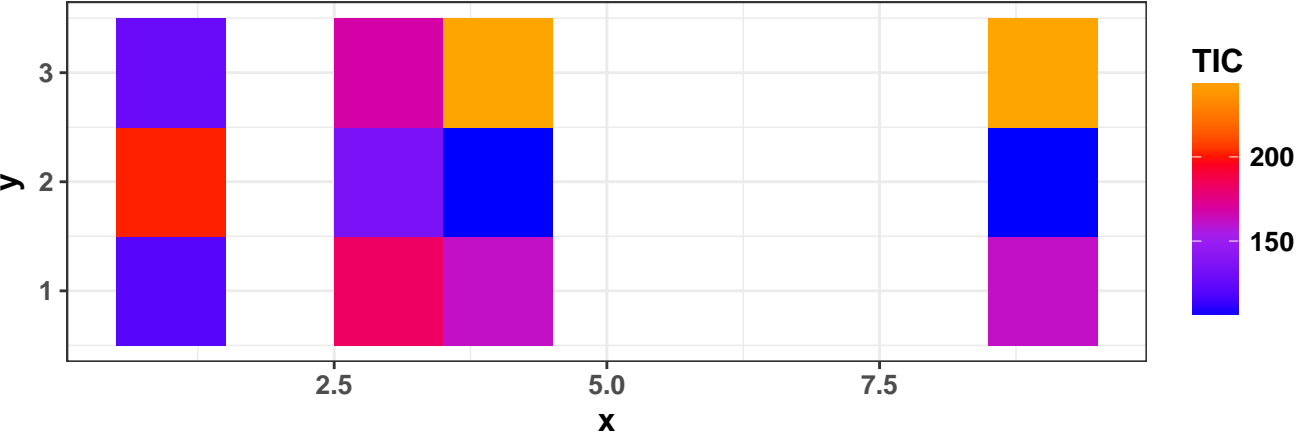
Pixel order



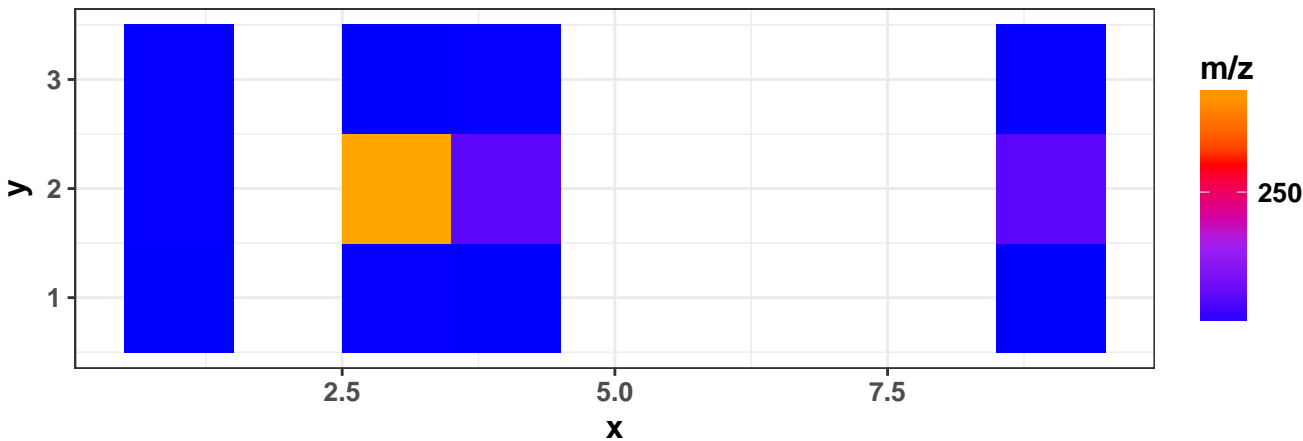
Number of peaks per spectrum



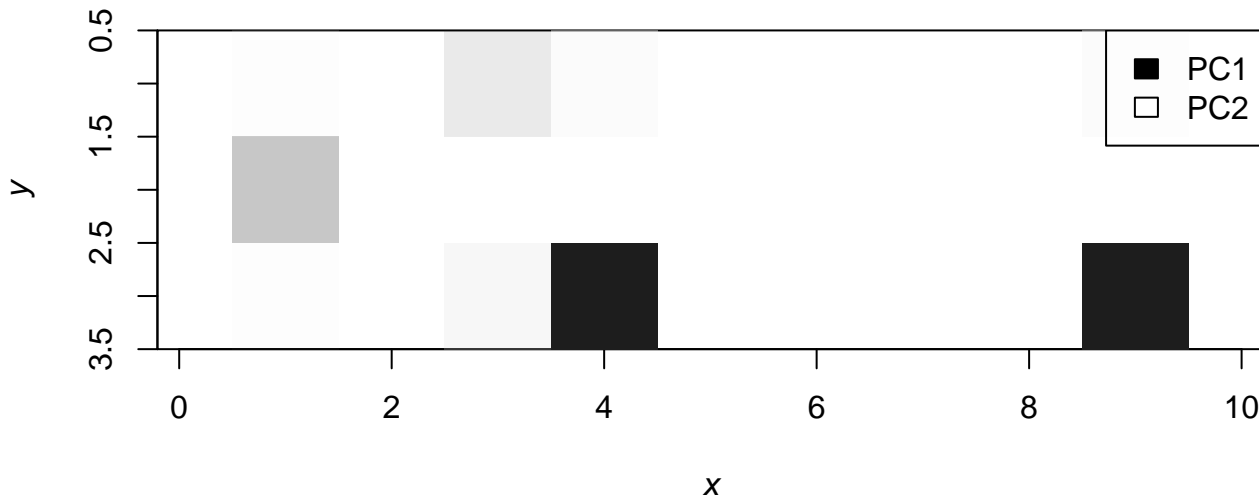
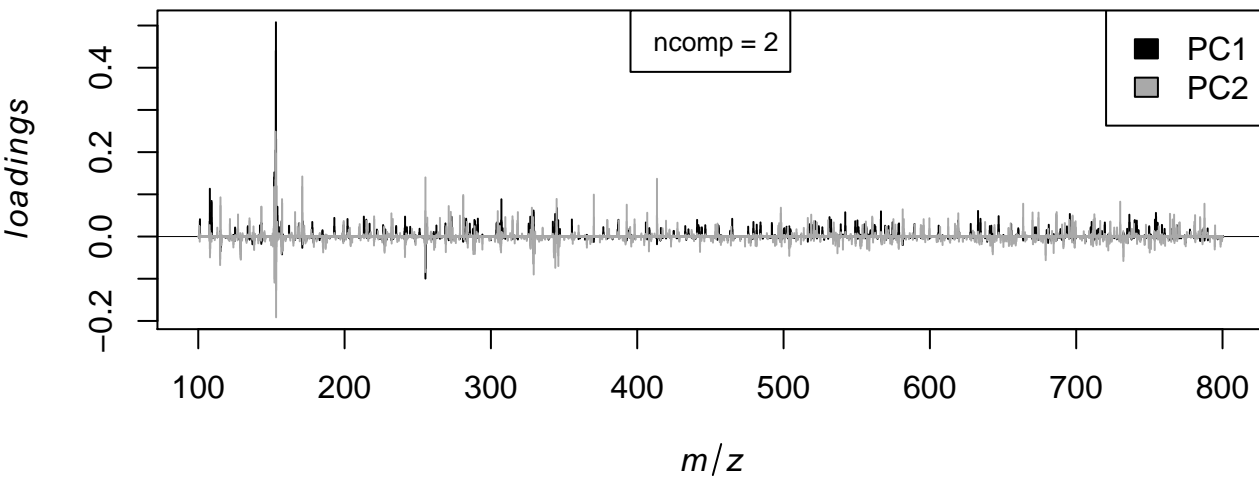
Total Ion Chromatogram



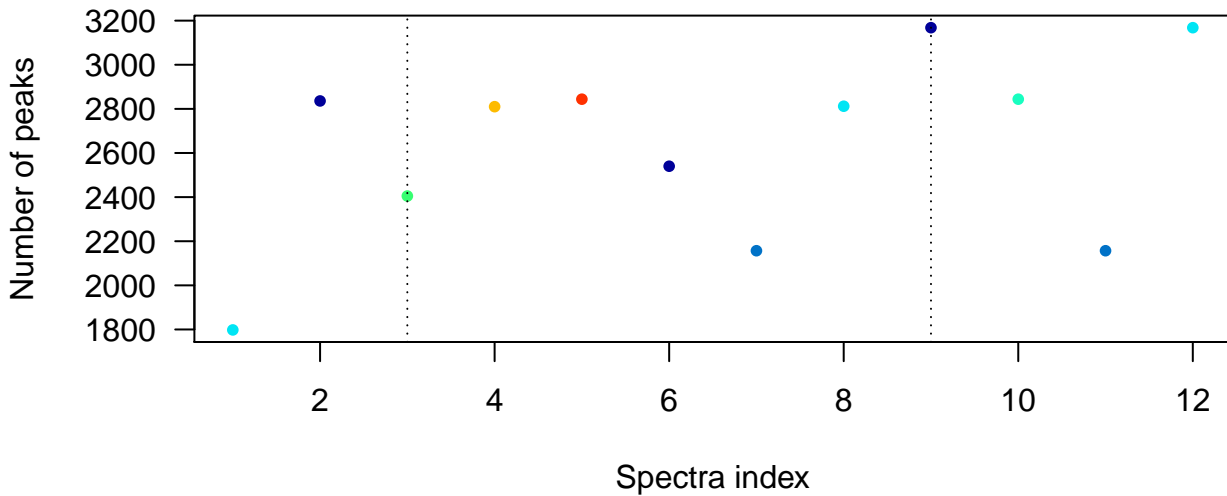
Most abundant m/z in each spectrum



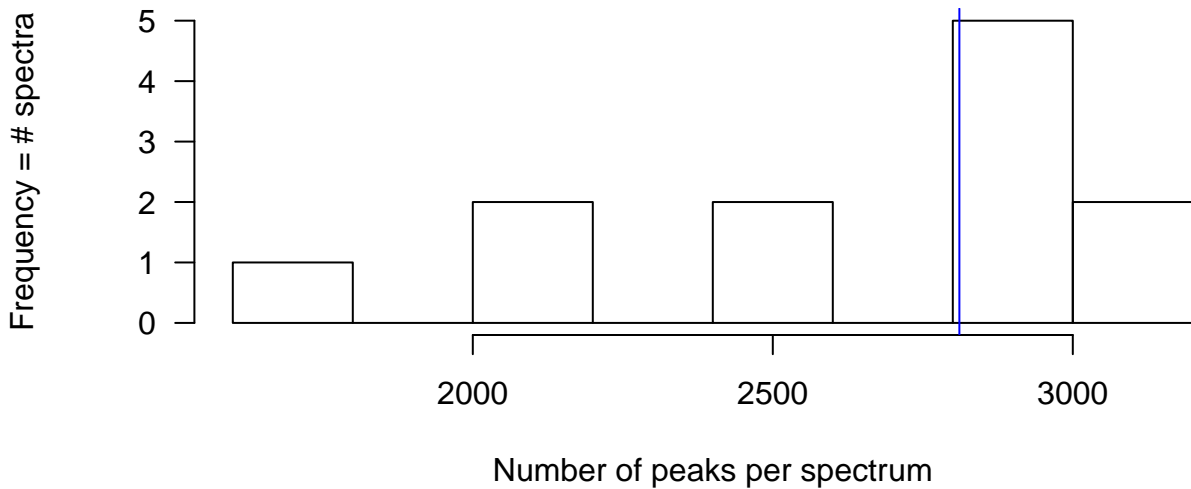
PCA for two components



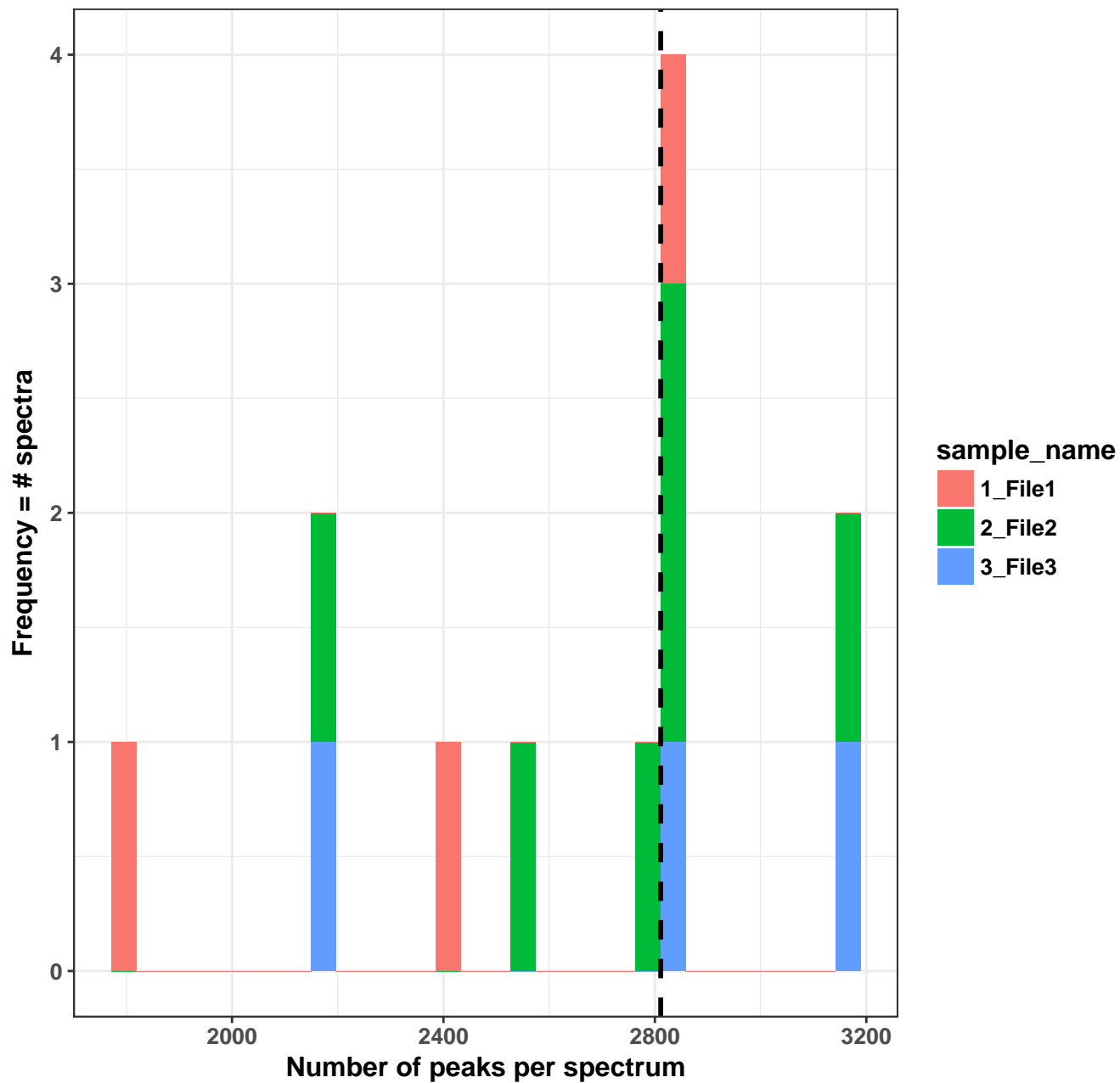
Number of peaks per spectrum



Number of peaks per spectrum

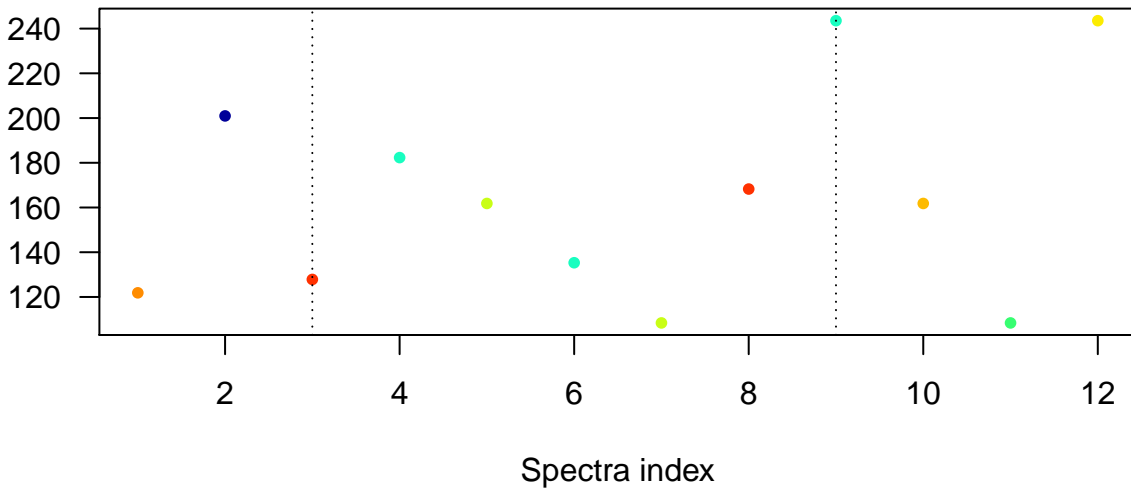


Number of peaks per spectrum and sample



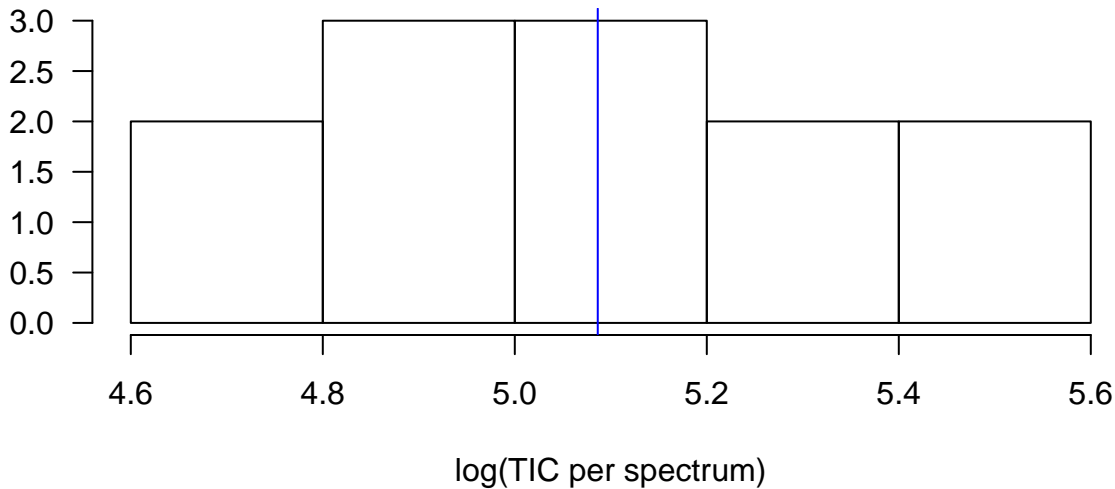
TIC per spectrum

Total ion chromatogram intensity

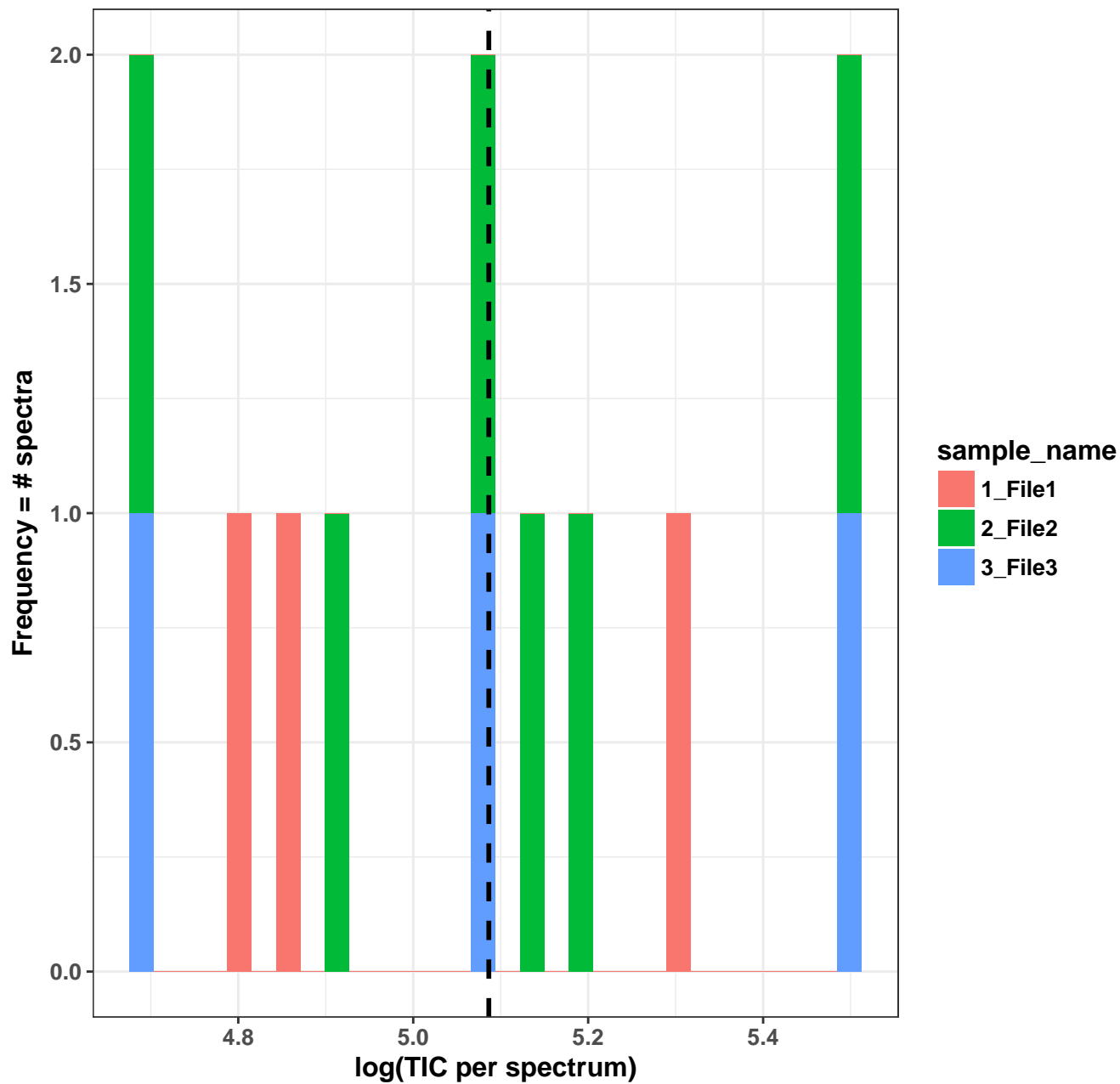


TIC per spectrum

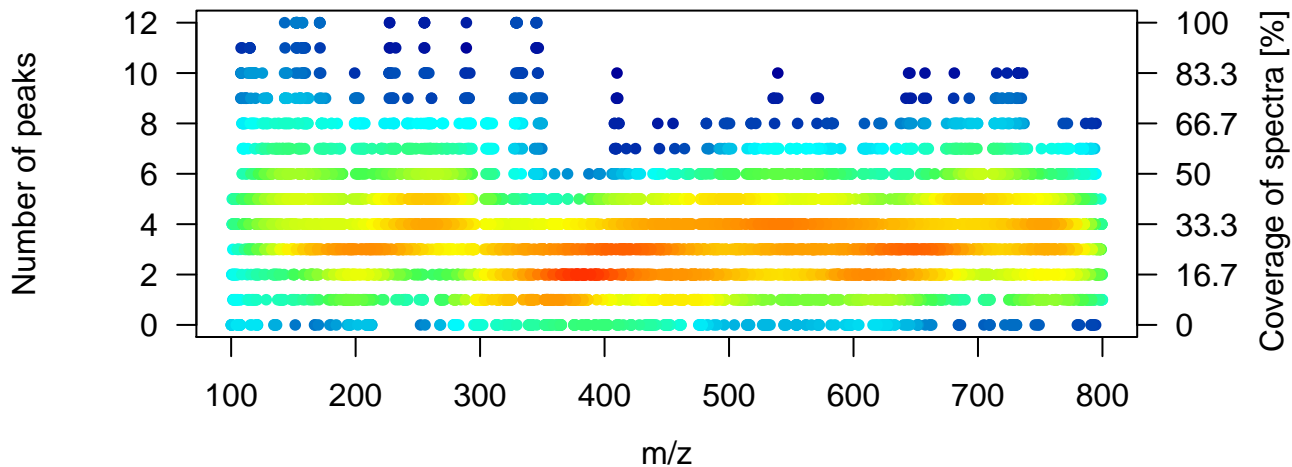
Frequency = # spectra



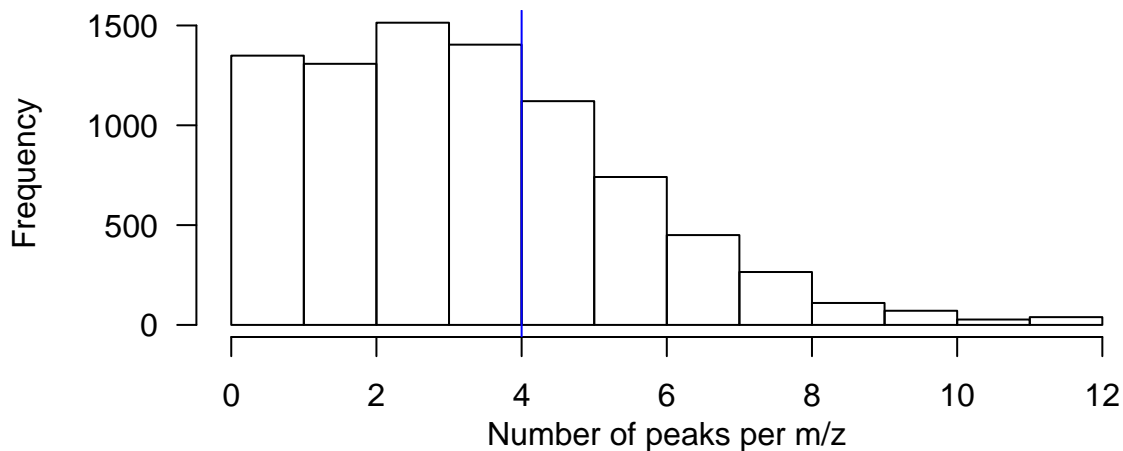
TIC per spectrum and sample



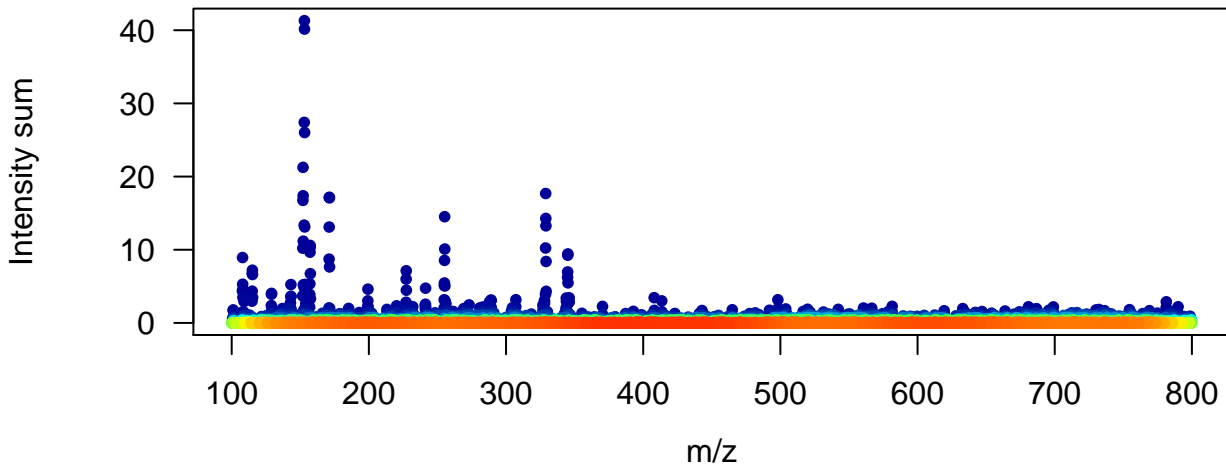
Number of peaks per m/z



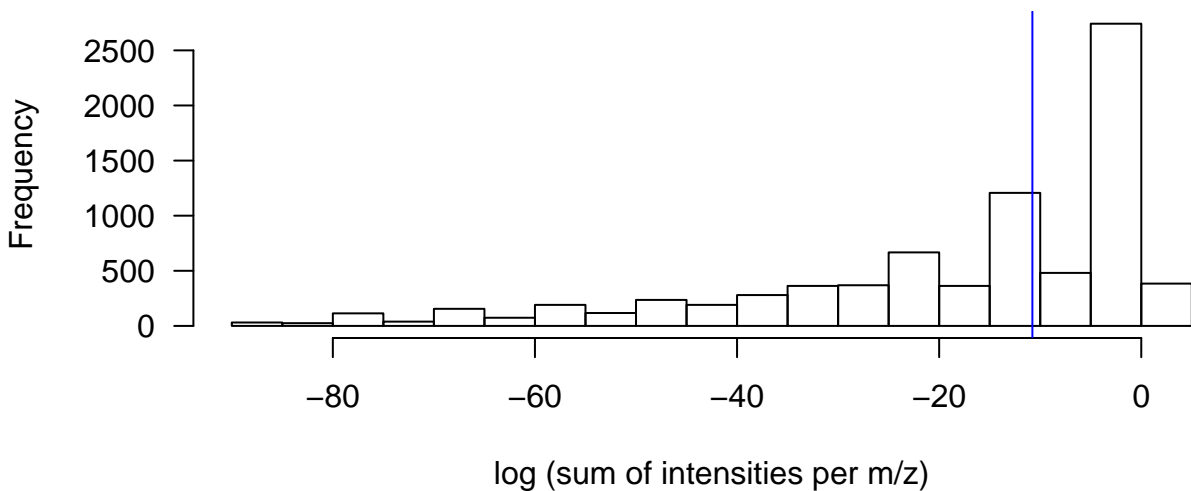
Number of peaks per m/z



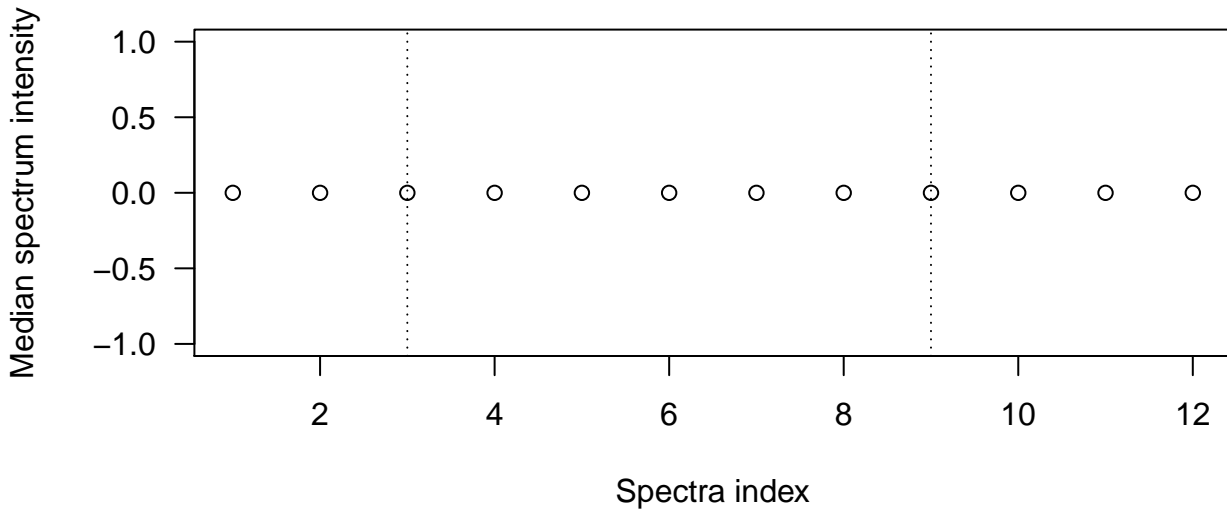
Sum of intensities per m/z



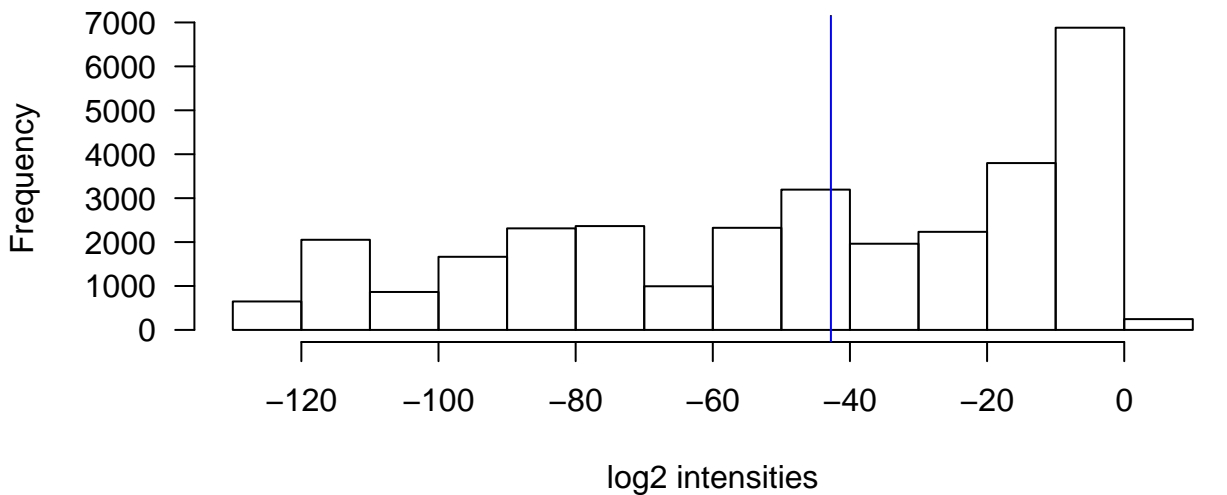
Sum of intensities per m/z



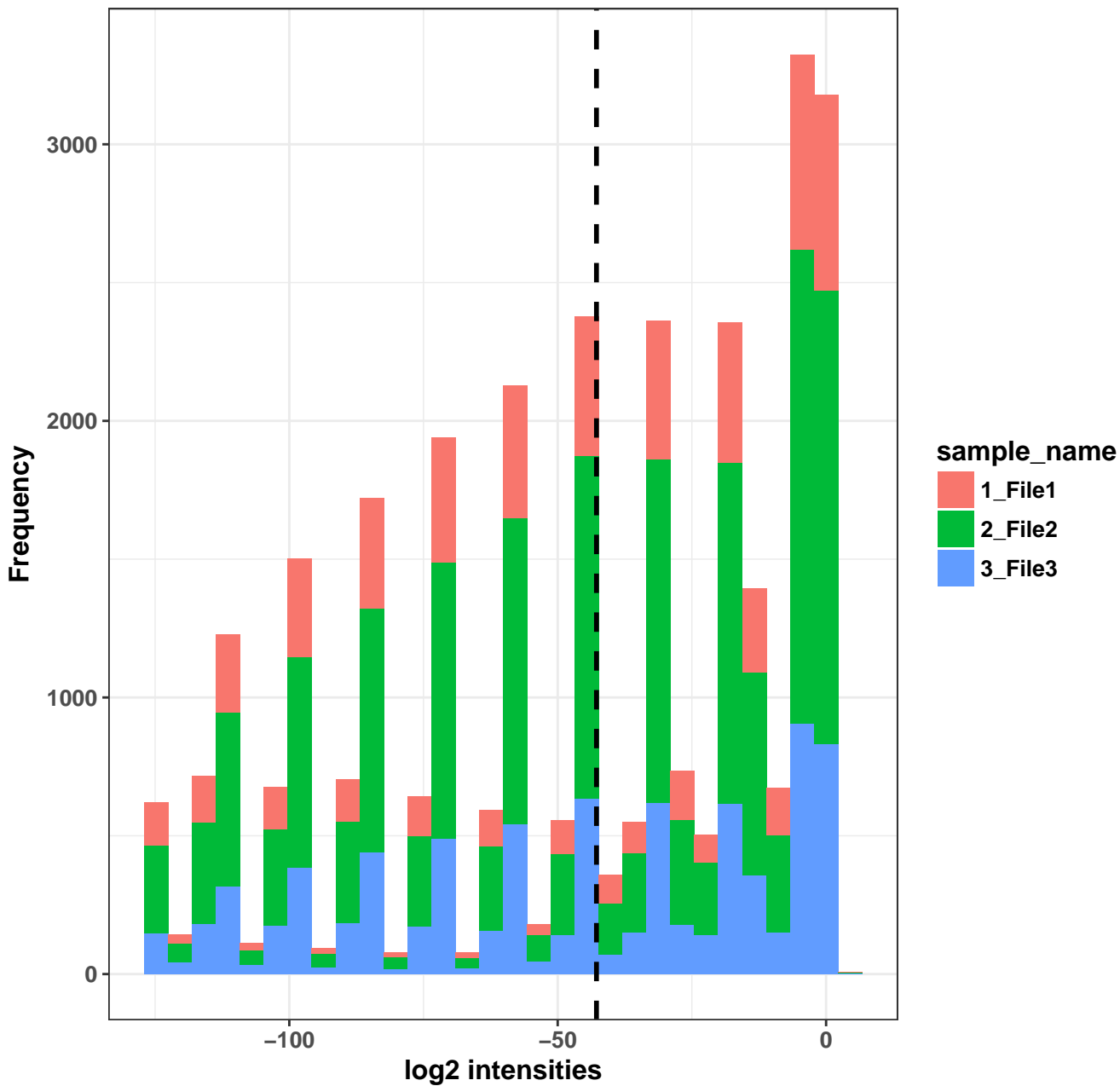
Median intensity per spectrum



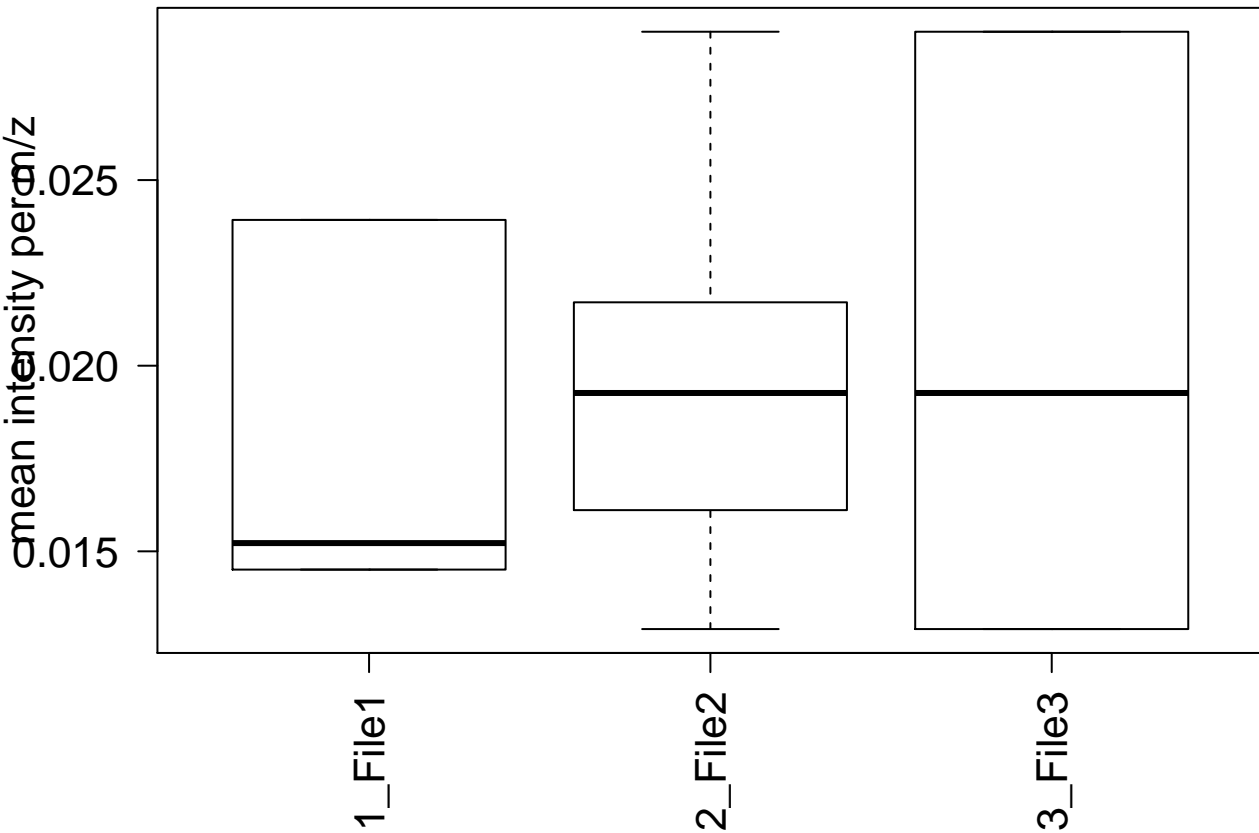
Log2-transformed intensities



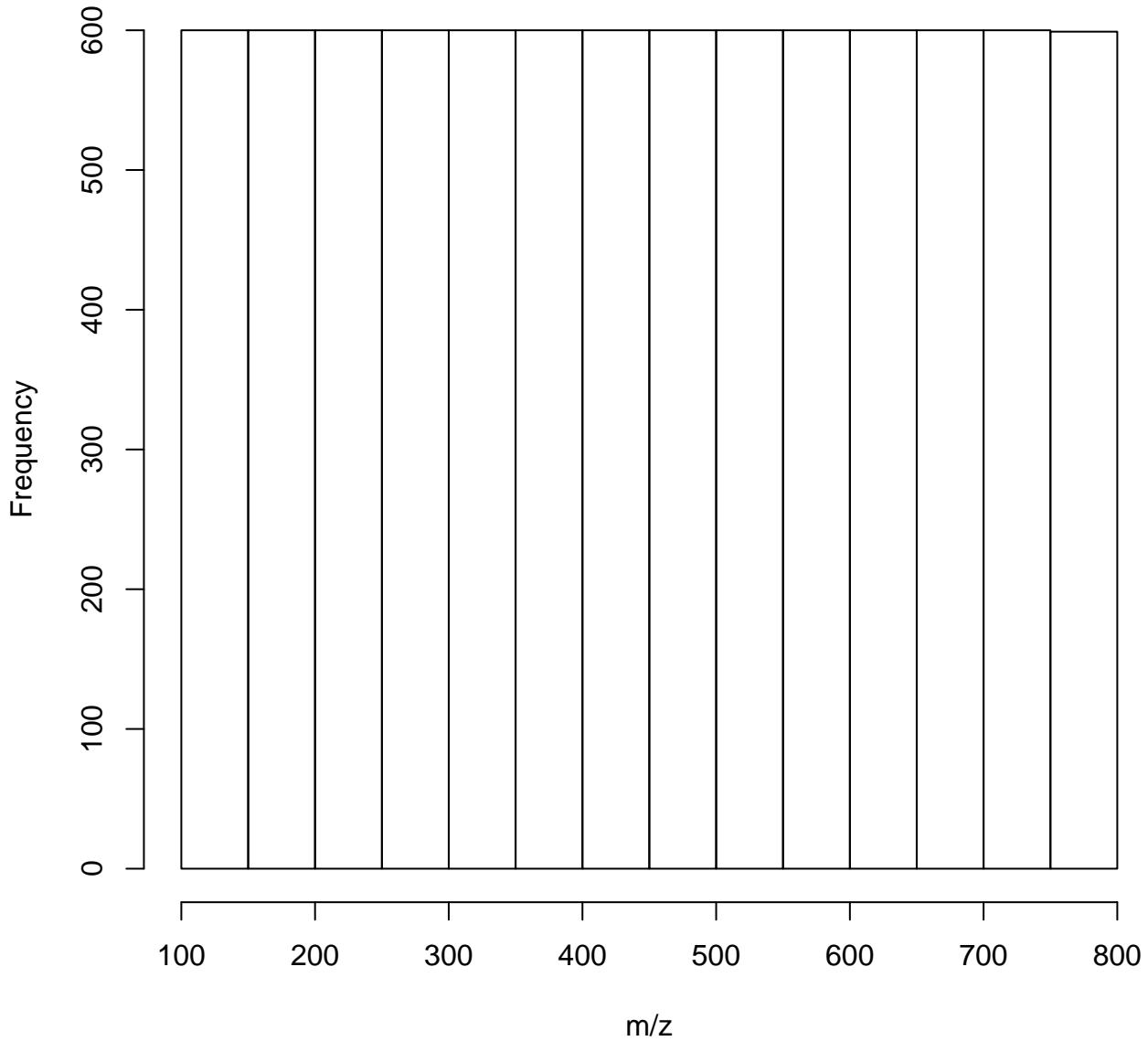
Log2-transformed intensities per sample



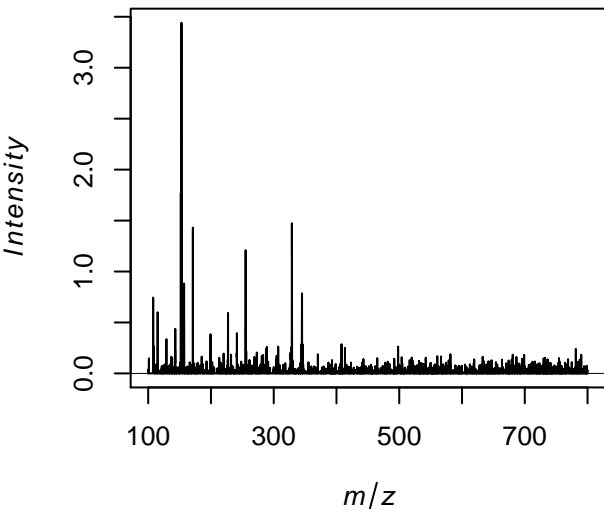
Mean intensities per m/z and sample



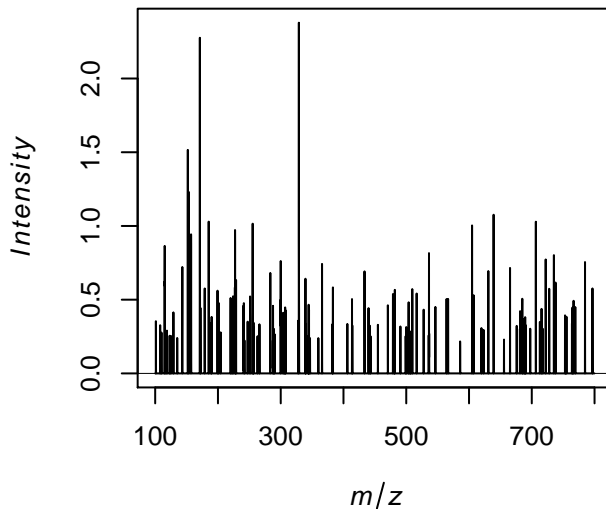
Histogram of m/z values



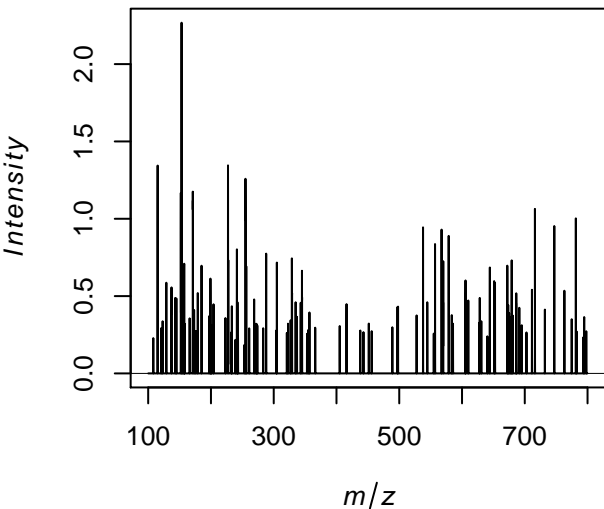
Average spectrum



Spectrum at x = 3, y = 2



Spectrum at x = 1, y = 3



Spectrum at x = 4, y = 3

