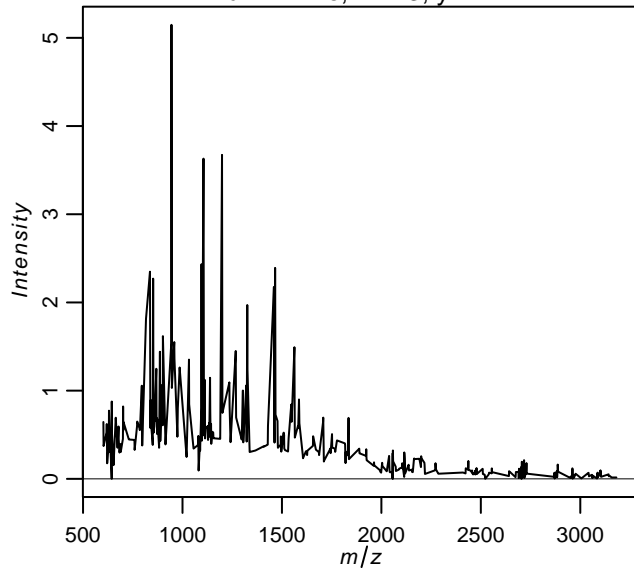


Quality control during preprocessing

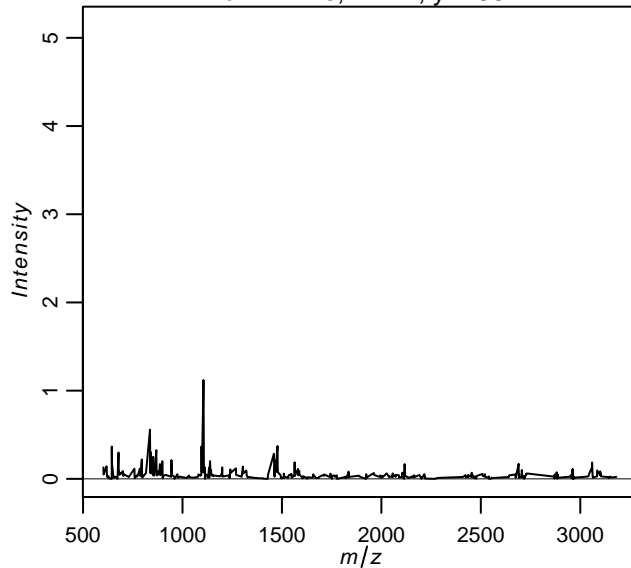
Filename: files_

Input spectra

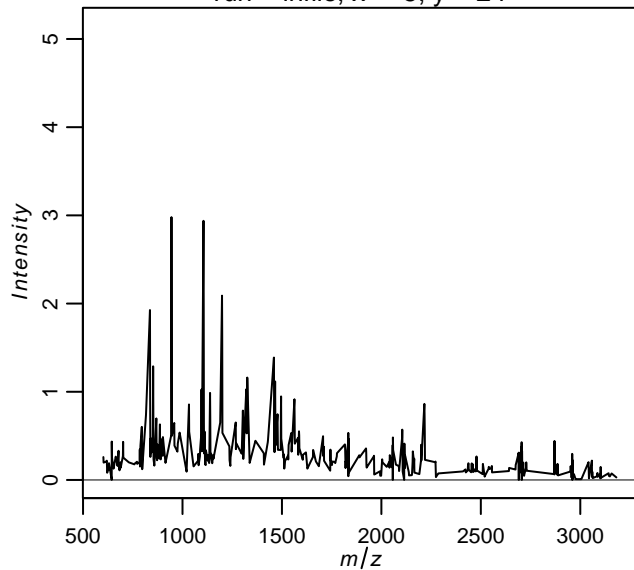
run = infile, x = 3, y = 4



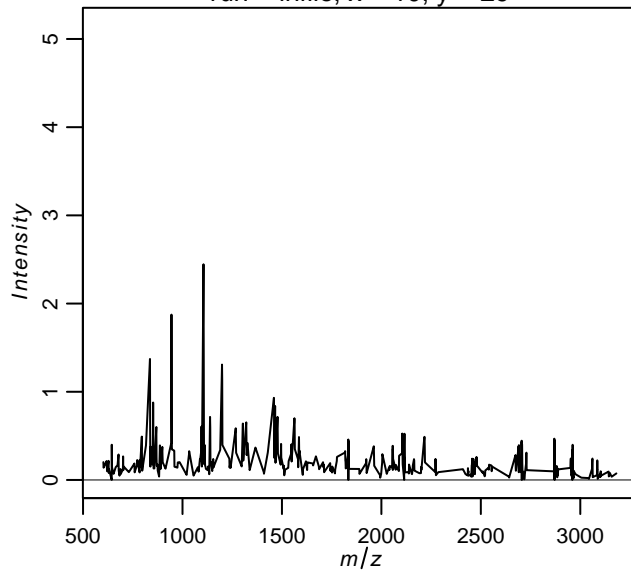
run = infile, x = 7, y = 53



run = infile, x = 5, y = 24

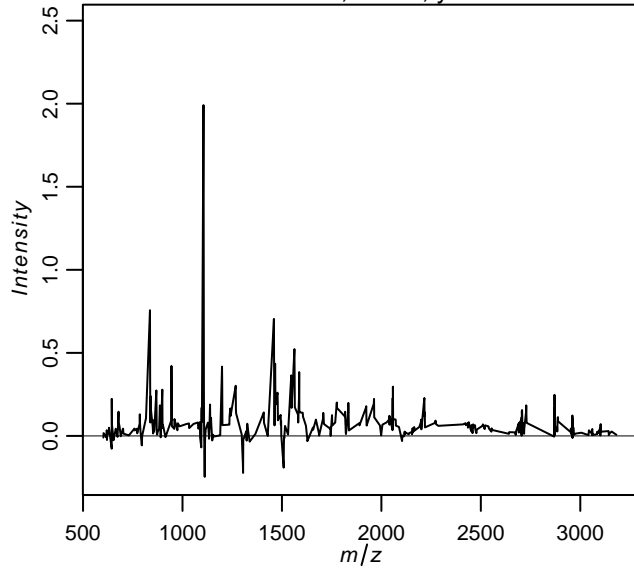


run = infile, x = 10, y = 29

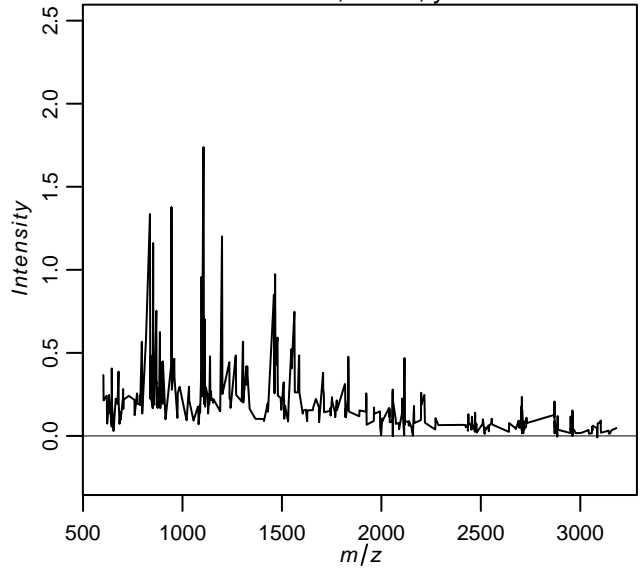


Spectra after ComBat batch correction

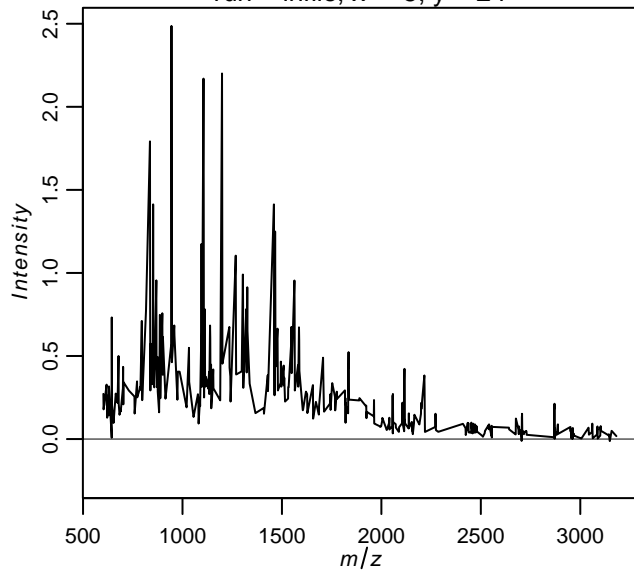
run = infile, x = 3, y = 4



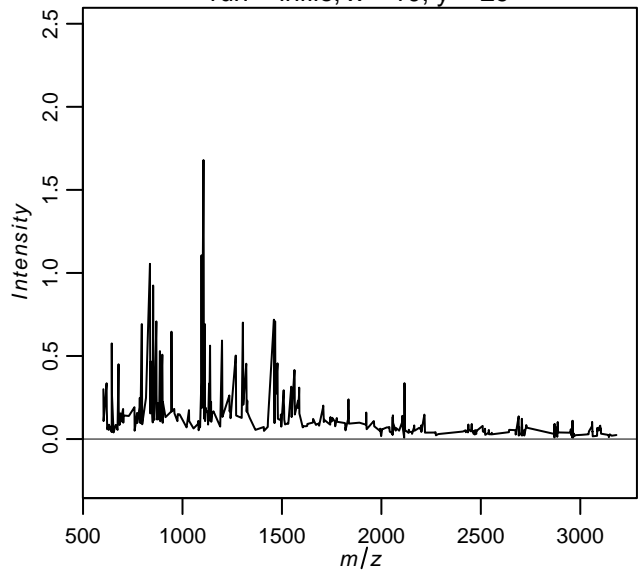
run = infile, x = 7, y = 53



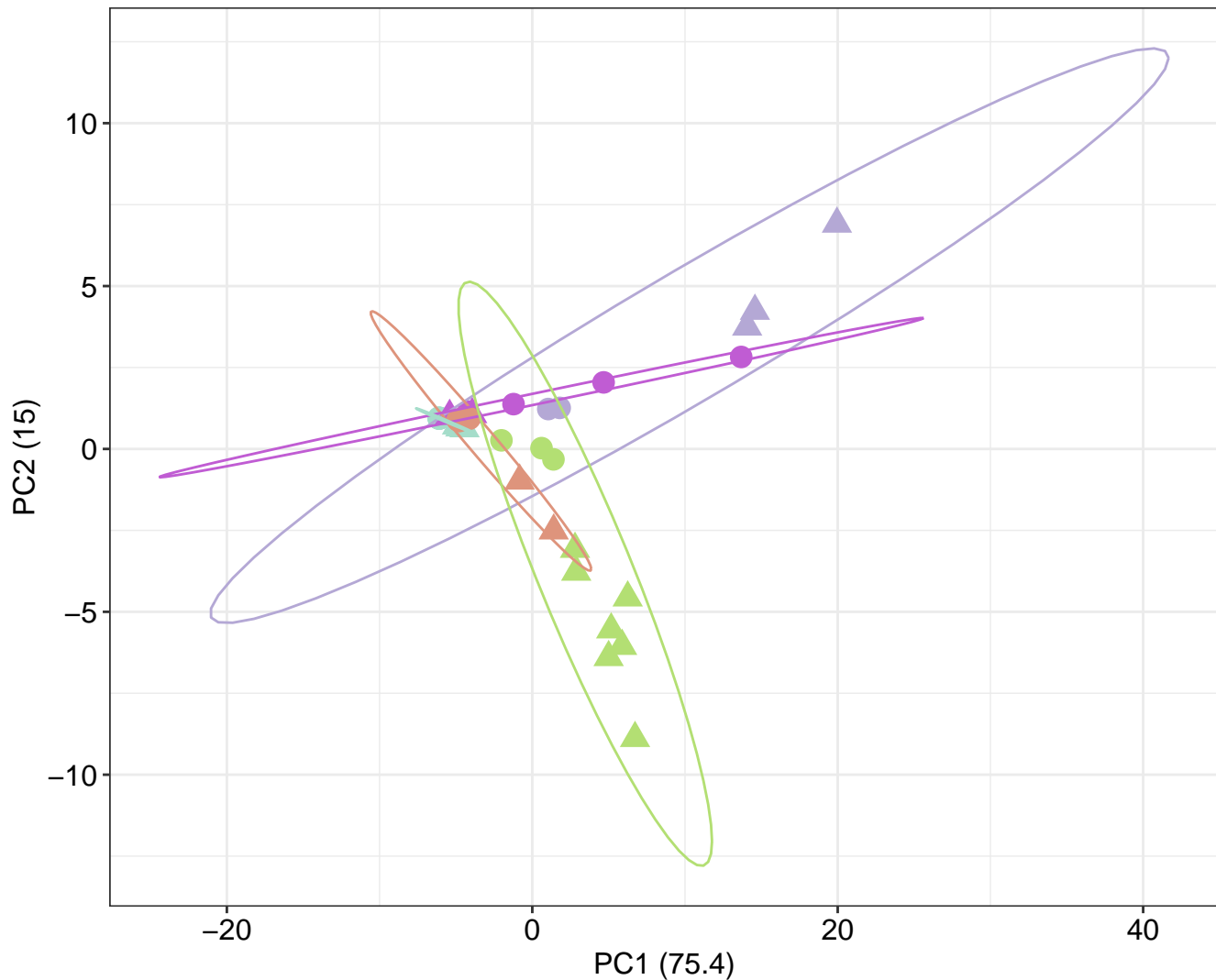
run = infile, x = 5, y = 24



run = infile, x = 10, y = 29



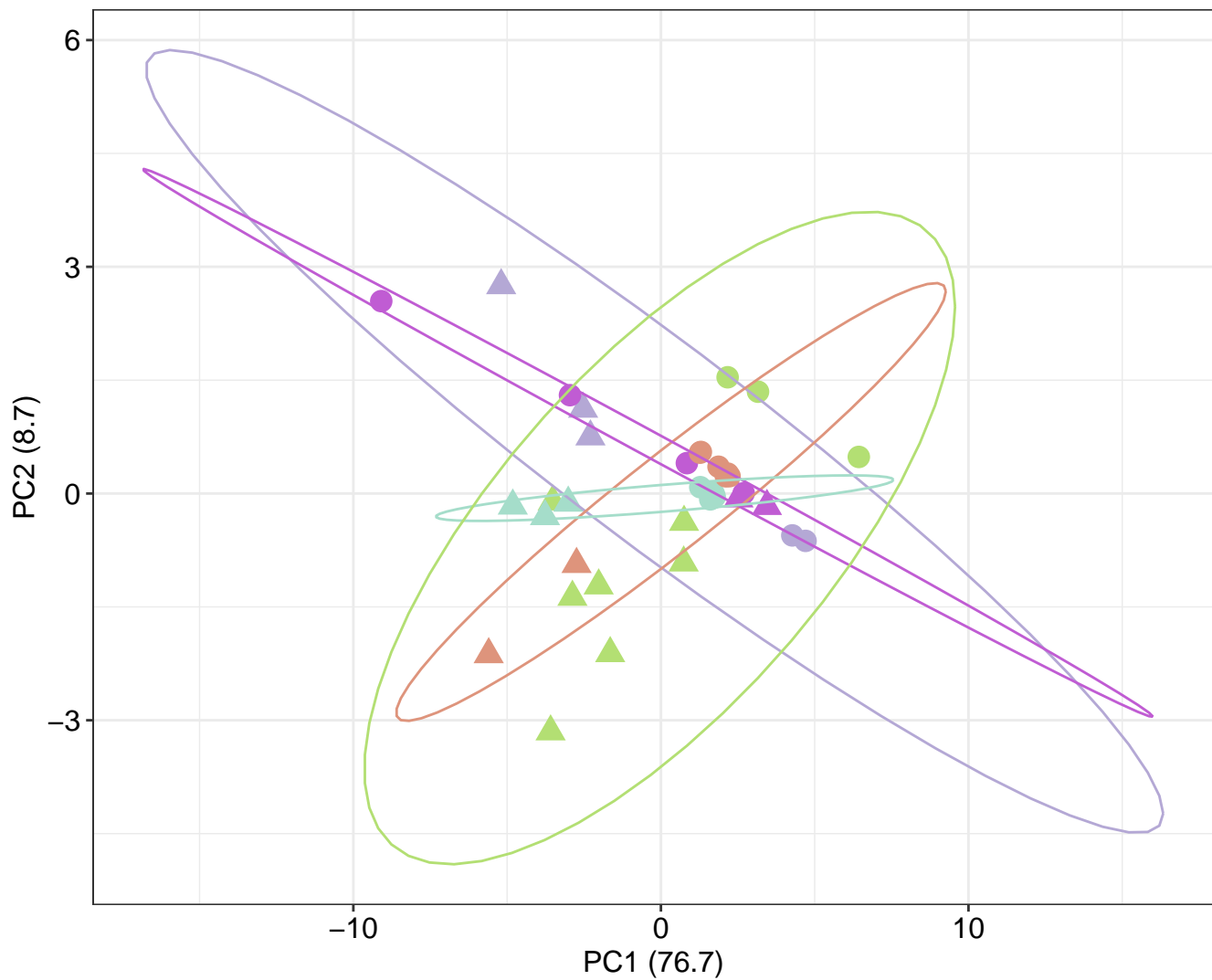
input data



Conditions ● Stroma ▲ Tumor

Batches ● TMA_394 ● TMA_397 ● TMA_398 ● TMA_400 ● TMA_402

batch corrected



Conditions ● Stroma ▲ Tumor

Batches ● TMA_394 ● TMA_397 ● TMA_398 ● TMA_400 ● TMA_402

	min m/z	max mz	# features	# spectra
<i>inputdata</i>	602.32	3181.63	388	40
<i>batch_corrected</i>	602.32	3181.63	388	40