Questions from the dataset:

- It would be nice if you could add a README file where you describe how all the columns values (numerical values) were generated and what they mean, so we know how to interpret this data.

- Intensities :

Additional questions:

- Are they proportionally correlated to the expression level of the gene of interest?

- Are the merged intensities an average over the replicates intensities?

- What is the error/standard deviation of the intensity values?

- ratios

- Significance

- 10lgP

- coverage,

- #peptides,

- #unique,

- PTM,

- avg. mass

- Regarding the heatmap:

- Could you provide the script you used to generate it. If that is not possible , could you explain which values did you use and which scaling method did you apply to the data?

- Can you also send us the raw data? How did you calculate the intensity based on the raw data?