Quality control metaproteomics

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```
##libraries
library(tidyverse)
```

```
-- Attaching packages ------------------------------------- tidyverse 1.3.2 --
v ggplot2 3.4.0      v purrr   1.0.1
v tibble  3.1.8      v dplyr   1.0.10
v tidyr   1.2.1      v stringr 1.5.0
v readr   2.1.3      v forcats 0.5.2
-- Conflicts ---------------------------------------- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```

```
library(here)
```

```
here() starts at /Users/sebastiansaenz/Documents/github/MicroTutorials
```

```
## input data
df_qc <- read.table(here::here("rawdata/summary.txt"),
                    header = TRUE,
                    sep="\t",
                    check.names = FALSE)

colnames(df_qc)
```

```
 [1] "Raw file"
 [2] "Experiment"
 [3] "Fraction"
 [4] "Enzyme"
 [5] "Enzyme mode"
 [6] "Enzyme first search"
 [7] "Enzyme mode first search"
 [8] "Use enzyme first search"
 [9] "Variable modifications"
[10] "Fixed modifications"
[11] "Multi modifications"
[12] "Variable modifications first search"
[13] "Use variable modifications first search"
[14] "Requantify"
[15] "Multiplicity"
[16] "Max. missed cleavages"
[17] "Labels0"
[18] "LC-MS run type"
[19] "Time-dependent recalibration"
[20] "MS"
[21] "MS/MS"
[22] "MS3"
[23] "MS/MS Submitted"
[24] "MS/MS Submitted (SIL)"
[25] "MS/MS Submitted (ISO)"
[26] "MS/MS Submitted (PEAK)"
[27] "MS/MS Identified"
[28] "MS/MS Identified (SIL)"
[29] "MS/MS Identified (ISO)"
[30] "MS/MS Identified (PEAK)"
[31] "MS/MS Identified [%]"
[32] "MS/MS Identified (SIL) [%]"
[33] "MS/MS Identified (ISO) [%]"
[34] "MS/MS Identified (PEAK) [%]"
[35] "Peptide Sequences Identified"
[36] "Peaks"
[37] "Peaks Sequenced"
[38] "Peaks Sequenced [%]"
[39] "Peaks Repeatedly Sequenced"
[40] "Peaks Repeatedly Sequenced [%]"
[41] "Isotope Patterns"
[42] "Isotope Patterns Sequenced"
[43] "Isotope Patterns Sequenced (z>1)"
```

```
[44] "Isotope Patterns Sequenced [%]"
[45] "Isotope Patterns Sequenced (z>1) [%]"
[46] "Isotope Patterns Repeatedly Sequenced"
[47] "Isotope Patterns Repeatedly Sequenced [%]"
[48] "Recalibrated"
[49] "Av. Absolute Mass Deviation [ppm]"
[50] "Mass Standard Deviation [ppm]"
[51] "Av. Absolute Mass Deviation [mDa]"
[52] "Mass Standard Deviation [mDa]"
[53] "Label free norm param"
```