Cancer

Lieven Clement

statOmics, Ghent University (https://statomics.github.io)

Contents

This is part of the online course Proteomics Data Analysis (PDA)

1 Background

Eighteen Estrogen Receptor Positive Breast cancer tissues from from patients treated with tamoxifen upon recurrence have been assessed in a proteomics study. Nine patients had a good outcome (OR) and the other nine had a poor outcome (PD). The proteomes have been assessed using an LTQ-Orbitrap and the thermo output .RAW files were searched with MaxQuant (version 1.4.1.2) against the human proteome database (FASTA version 2012-09, human canonical proteome).

2 Data

We first import the data from peptide.txt file. This is the file containing your peptide-level intensities. For a MaxQuant search [6], this peptide.txt file can be found by default in the "path_to_raw_files/combined/txt/" folder from the MaxQuant output, with "path_to_raw_files" the folder where the raw files were saved.

We generate the object peptideFile with the path to the peptide.txt file. Using the `grepEcols` function, we find the columns that contain the expression data of the peptide in the peptide.txt file.

```
library(tidyverse)
library(limma)
library(QFeatures)
```

```
library(msqrob2)
library(plotly)

peptidesFile <- "https://raw.githubusercontent.com/statOmics/PDA22GTPB/data/quantification/cancer/peptic

ecols <- grep(
  "Intensity\\.",
  names(read.delim(peptidesFile))
  )
```

Next, we read the data and store it in QFeatures object

```
pe <- readQFeatures(
  assayData = read.delim(peptidesFile),
  fnames = 1,
  quantCols = ecols,
  name = "peptideRaw")
```

```
## Checking arguments.

## Loading data as a 'SummarizedExperiment' object.

## Formatting sample annotations (colData).

## Formatting data as a 'QFeatures' object.
```

The QFeatures object pe currently contains a single assay, named peptideRaw.

We extract the column names from the peptideRaw assay and see that this contains information about the prognosis.

```
colnames(pe[["peptideRaw"]])
```

```
##  [1] "Intensity.OR.01" "Intensity.OR.04" "Intensity.OR.07" "Intensity.OR.09"
##  [5] "Intensity.OR.10" "Intensity.OR.13" "Intensity.OR.20" "Intensity.OR.23"
##  [9] "Intensity.OR.25" "Intensity.PD.02" "Intensity.PD.03" "Intensity.PD.04"
## [13] "Intensity.PD.06" "Intensity.PD.07" "Intensity.PD.08" "Intensity.PD.09"
## [17] "Intensity.PD.10" "Intensity.PD.11"
```

We rename the colnames by dropping the "Intensity." from the name.

```
(newNames <-  sub(
  pattern = "Intensity\\.",
  replacement = "",
  colnames(pe[["peptideRaw"]]))
 )
```

```
##  [1] "OR.01" "OR.04" "OR.07" "OR.09" "OR.10" "OR.13" "OR.20" "OR.23" "OR.25"
## [10] "PD.02" "PD.03" "PD.04" "PD.06" "PD.07" "PD.08" "PD.09" "PD.10" "PD.11"
```

```
pe <- renameColname(pe,
                    i = "peptideRaw",
                    newNames)
pe <- renamePrimary(pe, newNames)
colnames(pe[["peptideRaw"]])
```

```
##  [1] "OR.01" "OR.04" "OR.07" "OR.09" "OR.10" "OR.13" "OR.20" "OR.23" "OR.25"
## [10] "PD.02" "PD.03" "PD.04" "PD.06" "PD.07" "PD.08" "PD.09" "PD.10" "PD.11"
```

In the following code chunk, we add the prognosis of the patients that we can read in the raw file name to the colData.

```
colData(pe)$prognosis <-
  colnames(pe[["peptideRaw"]]) %>%
  substr(start = 1, stop = 2) %>%
  as.factor
colData(pe)$prognosis
```

```
##  [1] OR OR OR OR OR OR OR OR OR PD PD PD PD PD PD PD PD PD
## Levels: OR PD
```

We calculate how many non zero intensities we have per peptide and this will be useful for filtering.

```
rowData(pe[["peptideRaw"]])$nNonZero <- rowSums(assay(pe[["peptideRaw"]]) > 0)
```

Peptides with zero intensities are missing peptides and should be represent with a `NA` value rather than `0`.

```
pe <- zeroIsNA(pe, "peptideRaw") # convert 0 to NA
```

Look at the column names of the data to know the variables that you can use for filtering.

```
pe[["peptideRaw"]] %>% rowData %>% names
```

```
##  [1] "Sequence"               "Proteins"               "Leading.razor.protein"
##  [4] "Gene.names"             "Protein.names"          "Unique..Groups."
##  [7] "Unique..Proteins."      "Charges"                "PEP"
## [10] "Score"                  "Slice.Average"          "Slice.Std..Dev."
## [13] "Slice.1"                "Unique.Slice.Average"   "Unique.Slice.Std..Dev."
## [16] "Unique.Slice.1"         "Experiment.OR.01"       "Experiment.OR.04"
## [19] "Experiment.OR.07"       "Experiment.OR.09"       "Experiment.OR.10"
## [22] "Experiment.OR.13"       "Experiment.OR.20"       "Experiment.OR.23"
## [25] "Experiment.OR.25"       "Experiment.PD.02"       "Experiment.PD.03"
## [28] "Experiment.PD.04"       "Experiment.PD.06"       "Experiment.PD.07"
## [31] "Experiment.PD.08"       "Experiment.PD.09"       "Experiment.PD.10"
## [34] "Experiment.PD.11"       "Intensity"              "Reverse"
## [37] "Contaminant"            "id"                     "Protein.group.IDs"
## [40] "Mod..peptide.IDs"       "Evidence.IDs"           "MS.MS.IDs"
## [43] "Best.MS.MS"             "Oxidation..M..site.IDs" "nNonZero"
```

So we will filter on the "Reverse", "Contaminant" and "nNonZero" column.

2.1 Data exploration

47% of all peptide intensities are missing and for some peptides we do not even measure a signal in any sample.

3 Preprocessing

This section preforms preprocessing for the peptide data. This include

- log transformation,
- filtering and
- summarisation of the data.

3.1 Log transform the data

```
pe <- logTransform(pe, base = 2, i = "peptideRaw", name = "peptideLog")
```

3.2 Filtering

1. Handling overlapping protein groups

In our approach a peptide can map to multiple proteins, as long as there is none of these proteins present in a smaller subgroup.

```
pe <- filterFeatures(pe, ~ Proteins %in% smallestUniqueGroups(rowData(pe[["peptideLog"]])$Proteins))
```

```
## 'Proteins' found in 2 out of 2 assay(s)
```

2. Remove reverse sequences (decoys) and contaminants

We now remove the contaminants and peptides that map to decoy sequences.

```
pe <- filterFeatures(pe,~Reverse != "+")
```

```
## 'Reverse' found in 2 out of 2 assay(s)
```

```
pe <- filterFeatures(pe,~ Contaminant != "+")
```

```
## 'Contaminant' found in 2 out of 2 assay(s)
```

3. Drop peptides that were only identified in one sample

We keep peptides that were observed at last twice.

```
pe <- filterFeatures(pe,~ nNonZero >=2)
```

```
## 'nNonZero' found in 2 out of 2 assay(s)
```

```
nrow(pe[["peptideLog"]])
```

```
## [1] 26696
```

We keep 26696 peptides upon filtering.

3.3 Normalize the data using median centering

We normalize the data by substracting the sample median from every intensity for peptide p in a sample i:

$$y_{ip}^{\text{norm}} = y_{ip} - \hat{\mu}_i$$

with $\hat{\mu}_i$ the median intensity over all observed peptides in sample i.

```
pe <- normalize(pe,
                i = "peptideLog",
                name = "peptideNorm",
                method = "center.median")
```

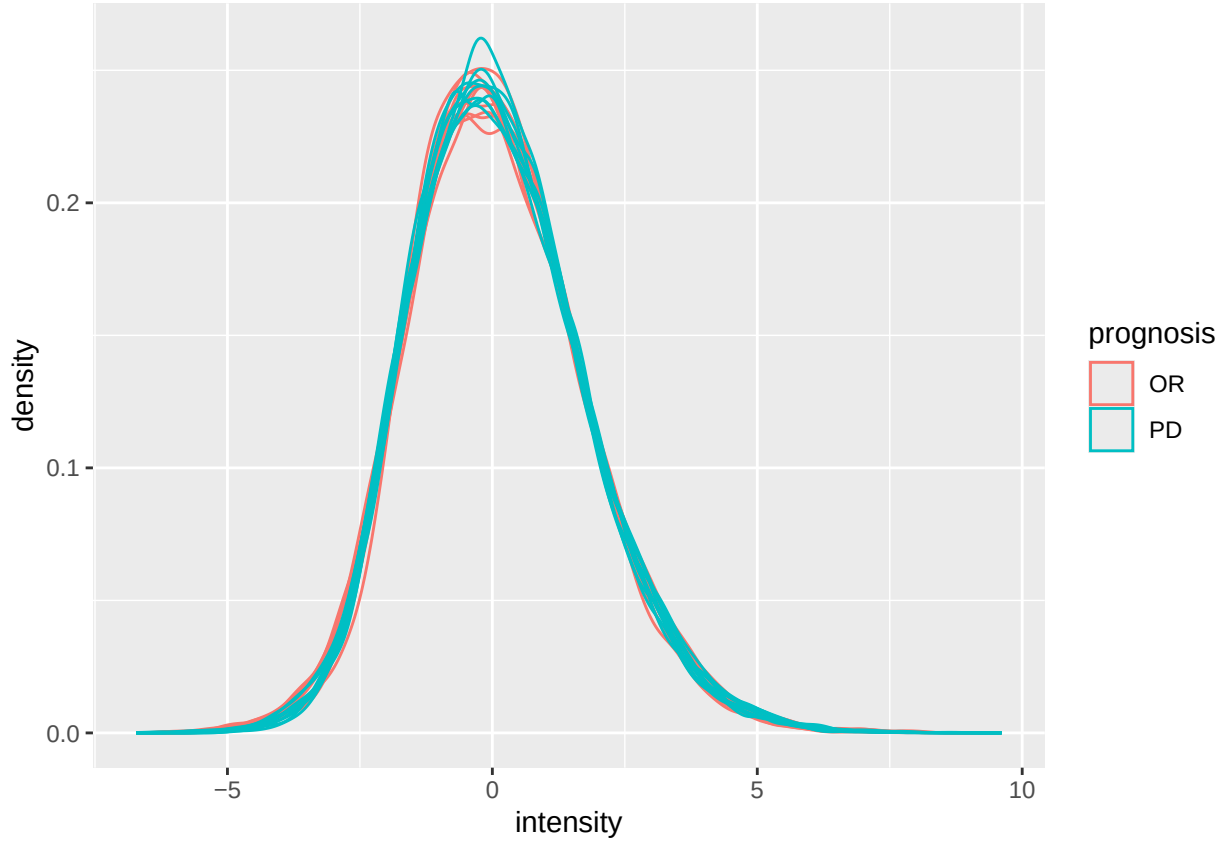
3.4 Explore normalized data

Upon the normalisation the density curves are nicely registered

```
pe[["peptideNorm"]] %>%
  assay %>%
  as.data.frame() %>%
```

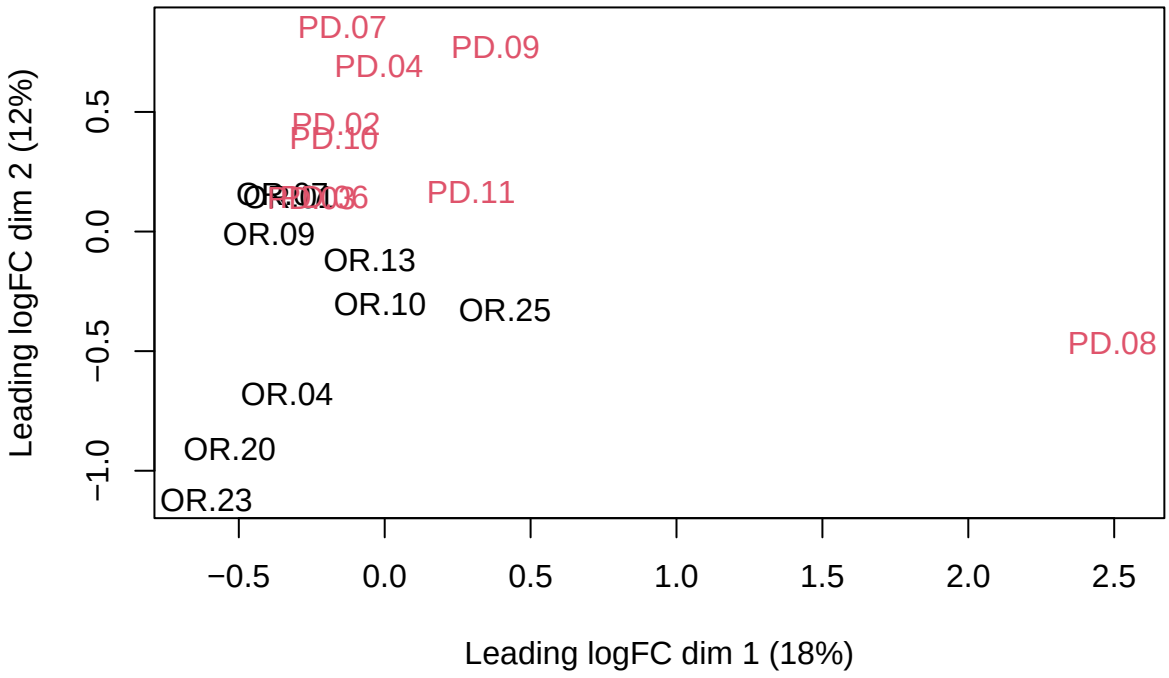
```
  gather(sample, intensity) %>%
  mutate(prognosis = colData(pe)[sample,"prognosis"]) %>%
  ggplot(aes(x = intensity,group = sample,color = prognosis)) +
    geom_density()
```

```
## Warning: Removed 188395 rows containing non-finite outside the scale range
## (`stat_density()`).
```



We can visualize our data using a Multi Dimensional Scaling plot, eg. as provided by the `limma` package.

```
pe[["peptideNorm"]] %>%
  assay %>%
  limma::plotMDS(col = as.numeric(colData(pe)$prognosis))
```



The first axis in the plot is showing the leading log fold changes (differences on the log scale) between the samples. We observe one outlying sample. In the second dimension we observe a separation according to prognosis.

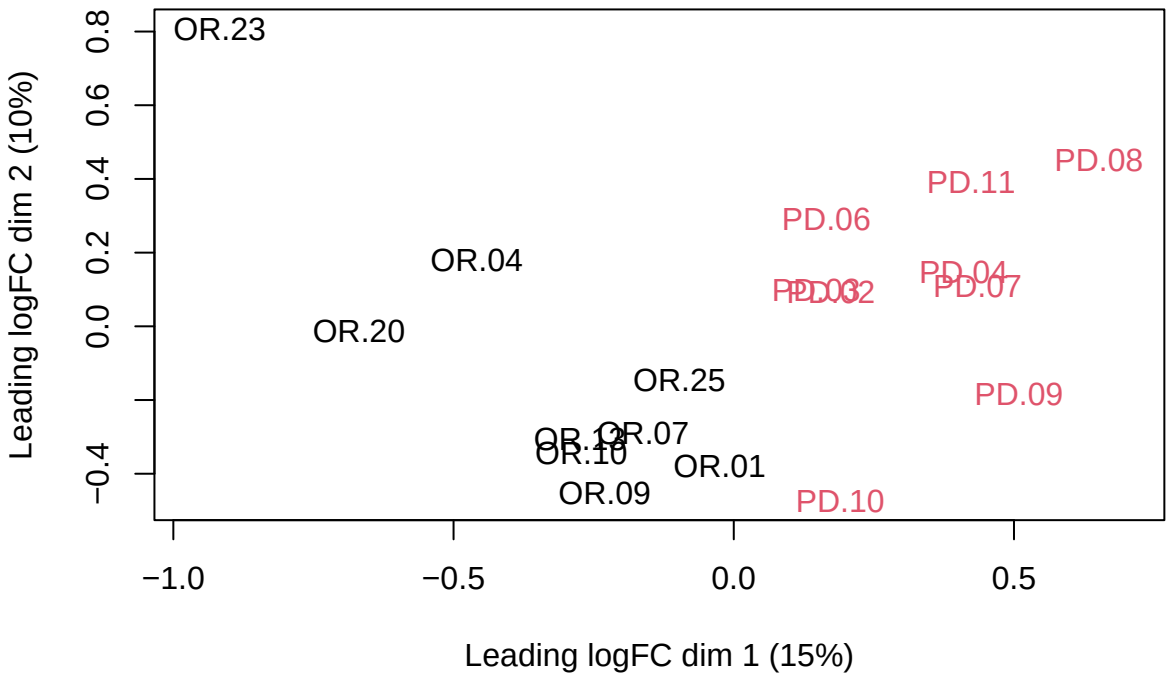
3.5 Summarization to protein level

- By default robust summarization is used: `fun = MsCoreUtils::robustSummary()`

```
pe <- aggregateFeatures(pe,
  i = "peptideNorm",
  fcol = "Proteins",
  na.rm = TRUE,
  name = "protein")
```

```
## Your quantitative and row data contain missing values. Please read the
## relevant section(s) in the aggregateFeatures manual page regarding the
## effects of missing values on data aggregation.
```

```
plotMDS(assay(pe[["protein"]]), col = as.numeric(colData(pe)$prognosis))
```



Note that the samples upon robust summarisation show a separation according to the prognosis.

4 Data Analysis

4.1 Estimation

We model the protein level expression values using `msqrob`. By default `msqrob2` estimates the model parameters using robust regression.

We will model the data with a different group mean. The group is incoded in the variable `prognosis` of the colData. We can specify this model by using a formula with the factor condition as its predictor: `formula = ~prognosis`.

Note, that a formula always starts with a symbol '~'.

```
pe <- msqrob(object = pe, i = "protein", formula = ~prognosis)
```

4.2 Inference

First, we extract the parameter names of the model by looking at the first model. The models are stored in the row data of the assay under the default name msqrobModels.

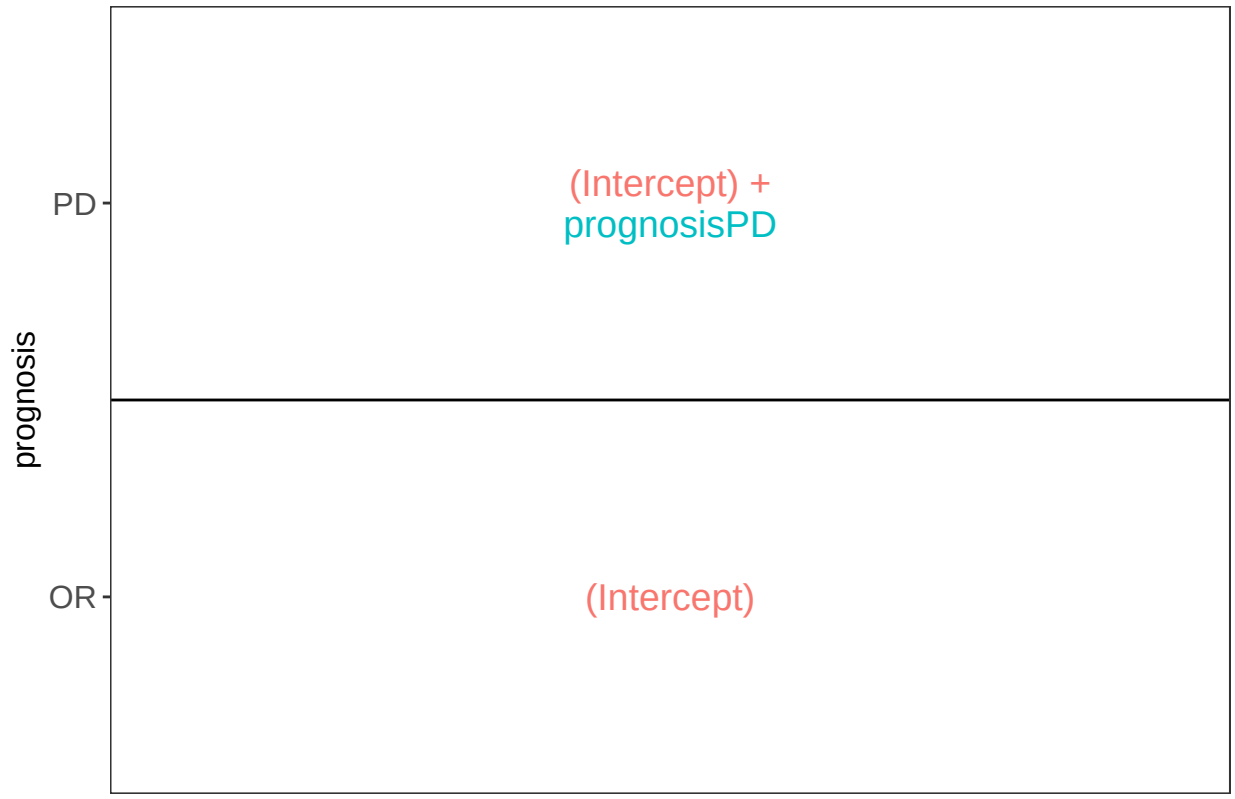
```
getCoef(rowData(pe[["protein"]])$msqrobModels[[1]])
```

```
## (Intercept) prognosisPD
##  -1.1185468   0.4007461
```

We can also explore the design of the model that we specified using the the package `ExploreModelMatrix`

```
library(ExploreModelMatrix)
VisualizeDesign(colData(pe),~prognosis)$plotlist
```

```
## [[1]]
```



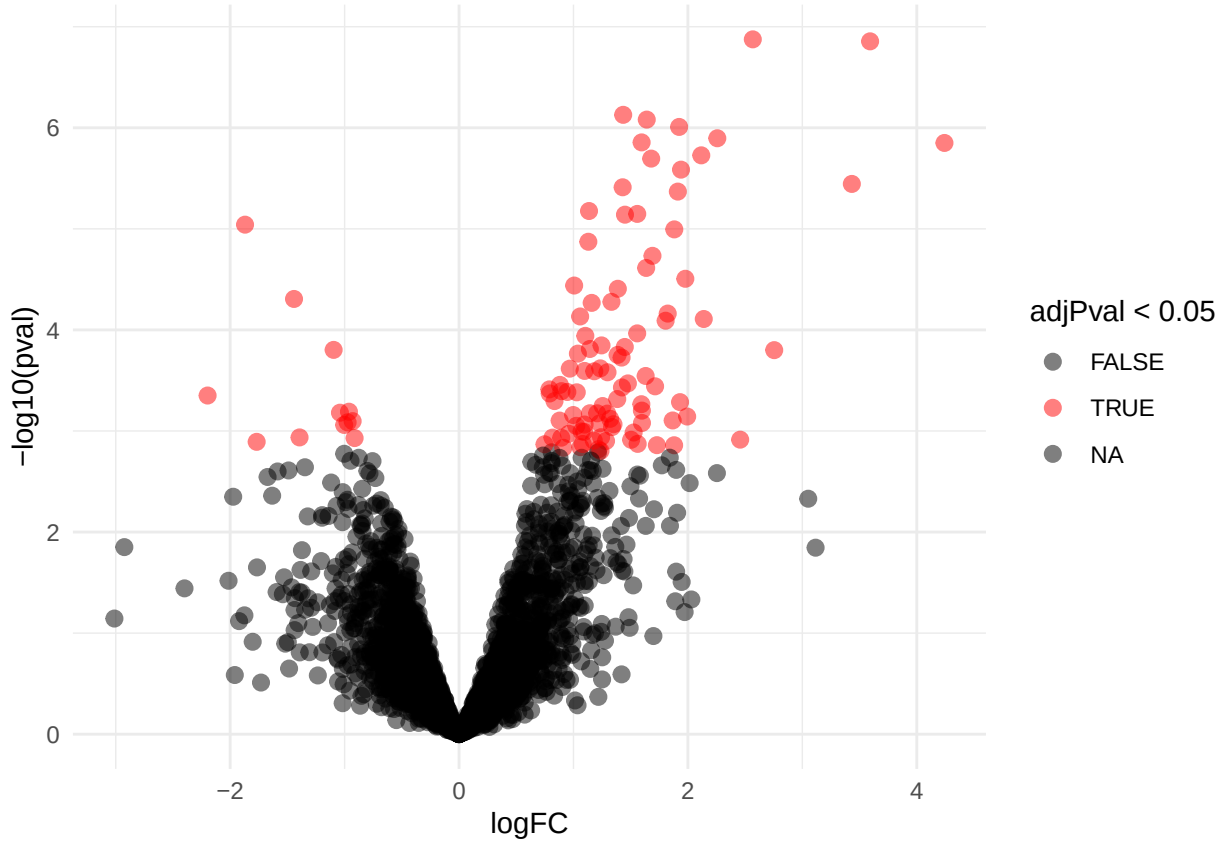
Spike-in condition `A` is the reference class. So the mean log2 expression for samples from good prognosis (OR) is '(Intercept). The mean log2 expression for samples from poor prognosis (PD) is'(Intercept)+prognosisPD'. Hence, the average log2 fold change between prognosis PD and prognosis OR is modelled using the parameter 'conditionPD'. Thus, we assess the contrast 'conditionPD = 0' with our statistical test.

```
L <- makeContrast("prognosisPD=0", parameterNames = c("prognosisPD"))
pe <- hypothesisTest(object = pe, i = "protein", contrast = L)
```

4.3 Plots

4.3.1 Volcano-plot

```
volcano <- ggplot(rowData(pe[["protein"]])$prognosisPD,
                  aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)) +
  geom_point(cex = 2.5) +
  scale_color_manual(values = alpha(c("black", "red"), 0.5)) + theme_minimal()
volcano
```

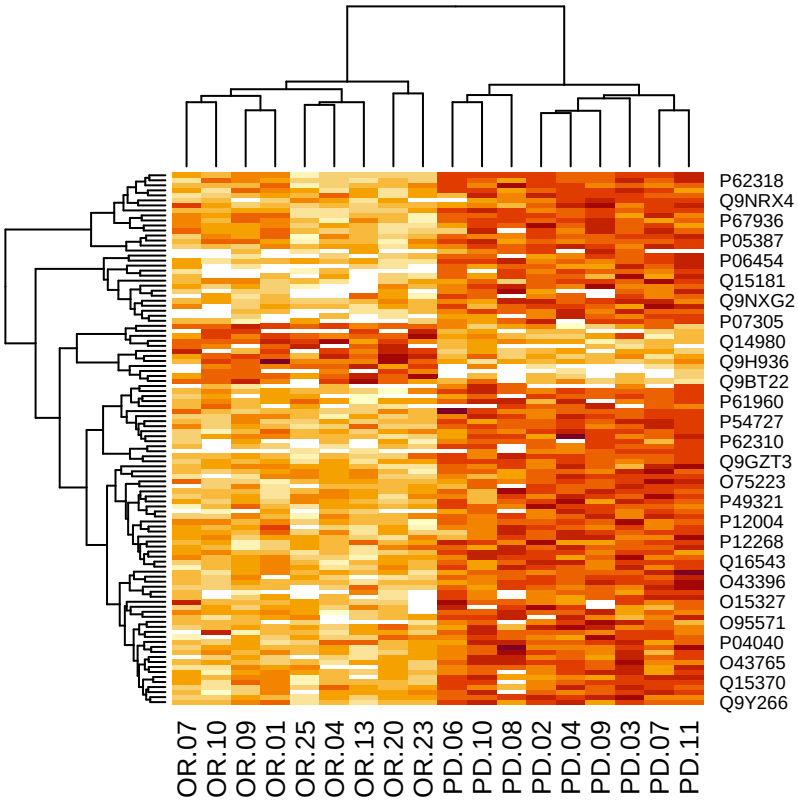


Note, that 106 proteins are found to be differentially abundant.

4.3.2 Heatmap

Note, that we also order the sigNames according to statistical significance.

```
sigNames <- rowData(pe[["protein"]])$prognosisPD %>%
  rownames_to_column("protein") %>%
  arrange(pval) %>%
  filter(adjPval<0.05) %>%
  pull(protein)
heatmap(assay(pe[["protein"]])[sigNames, ])
```

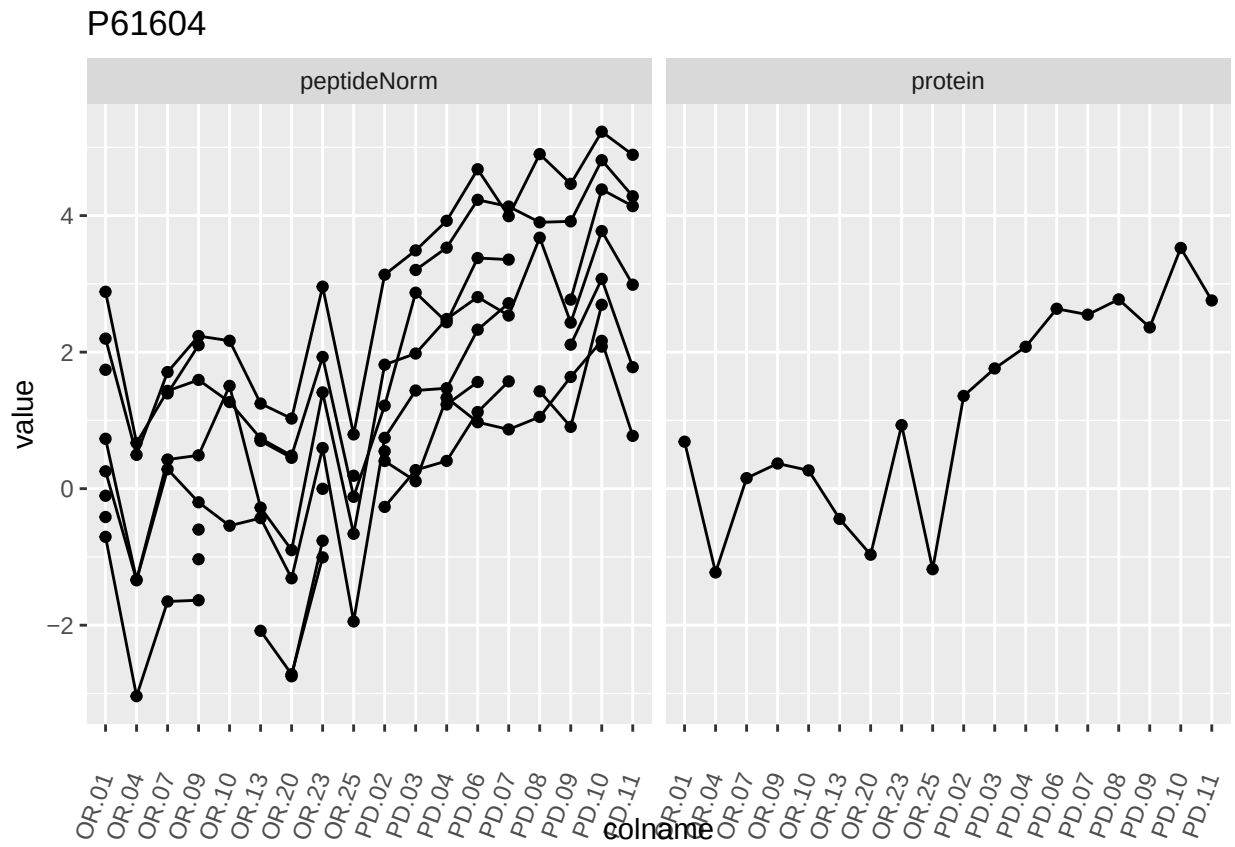


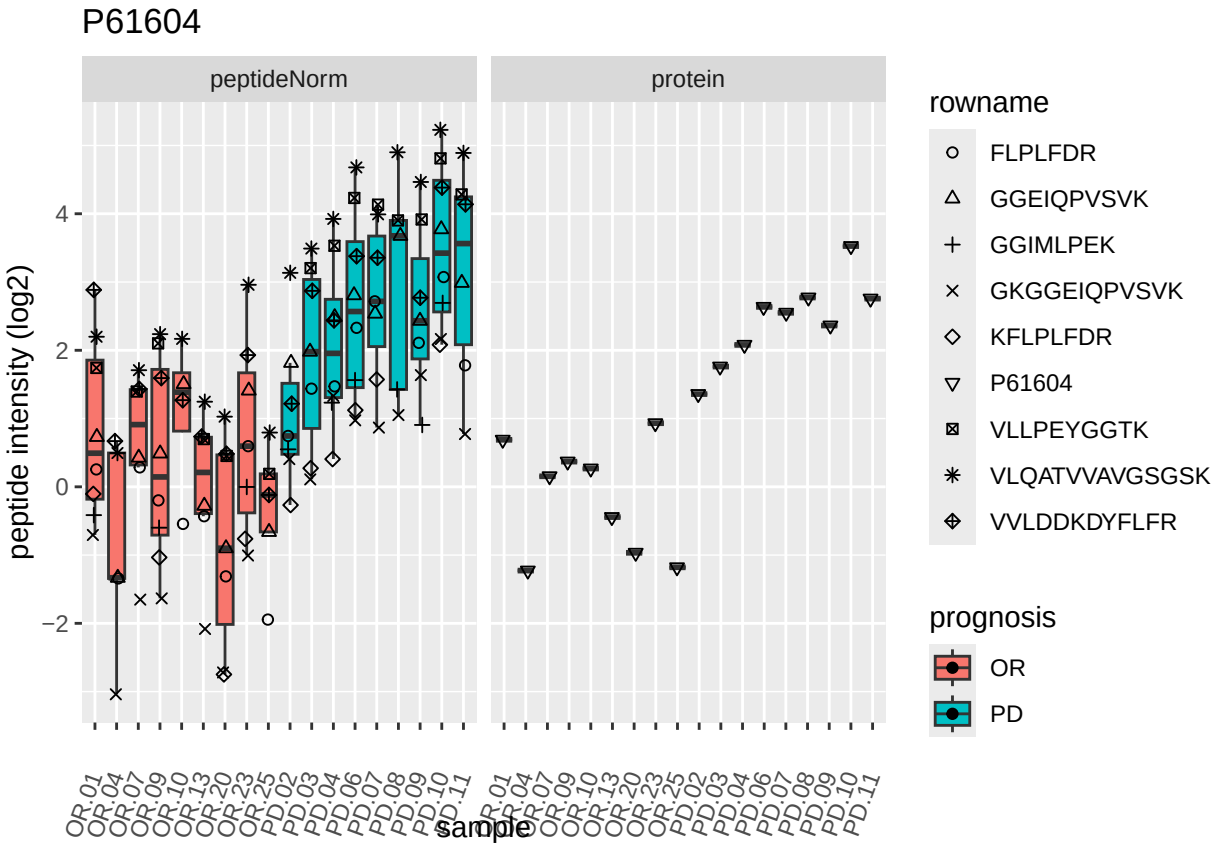
4.3.3 Detail plots

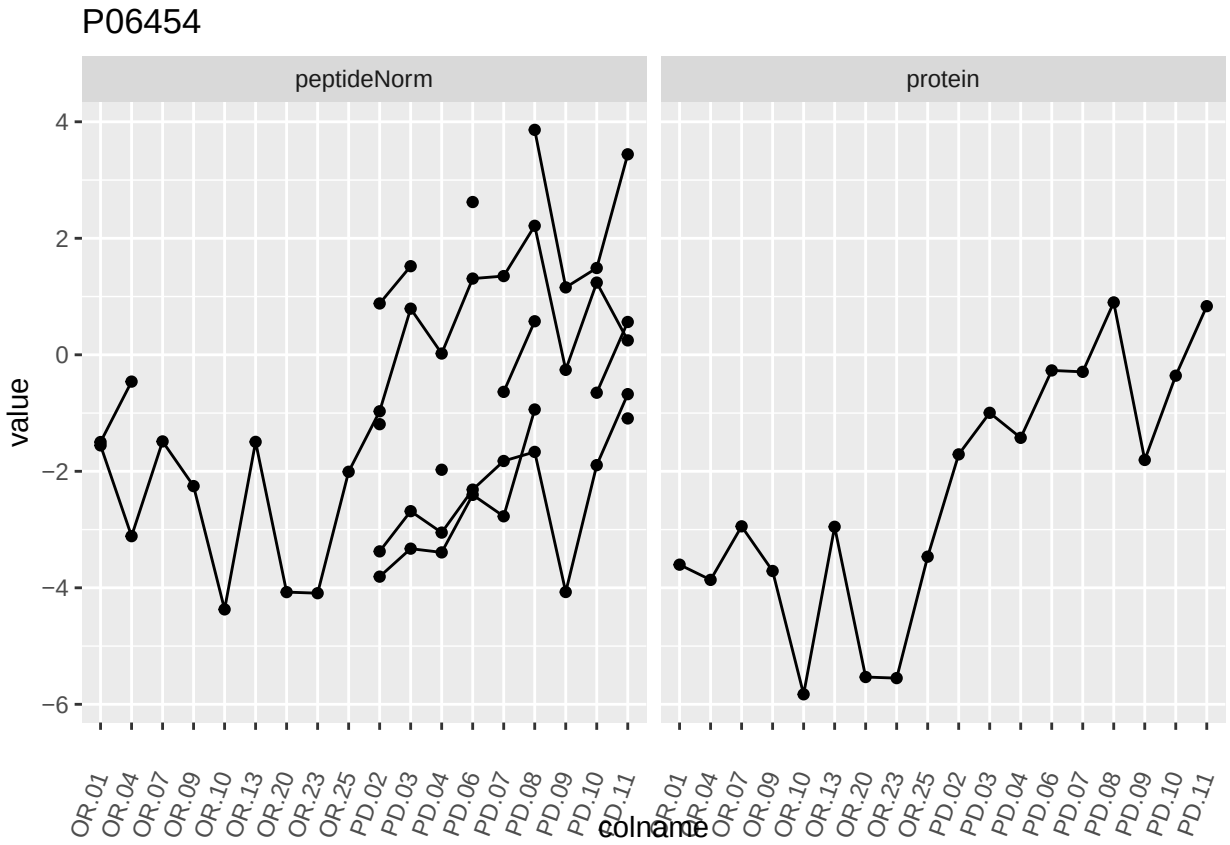
We make detail plots for the top 10 proteins to restrict the number of detail plots.

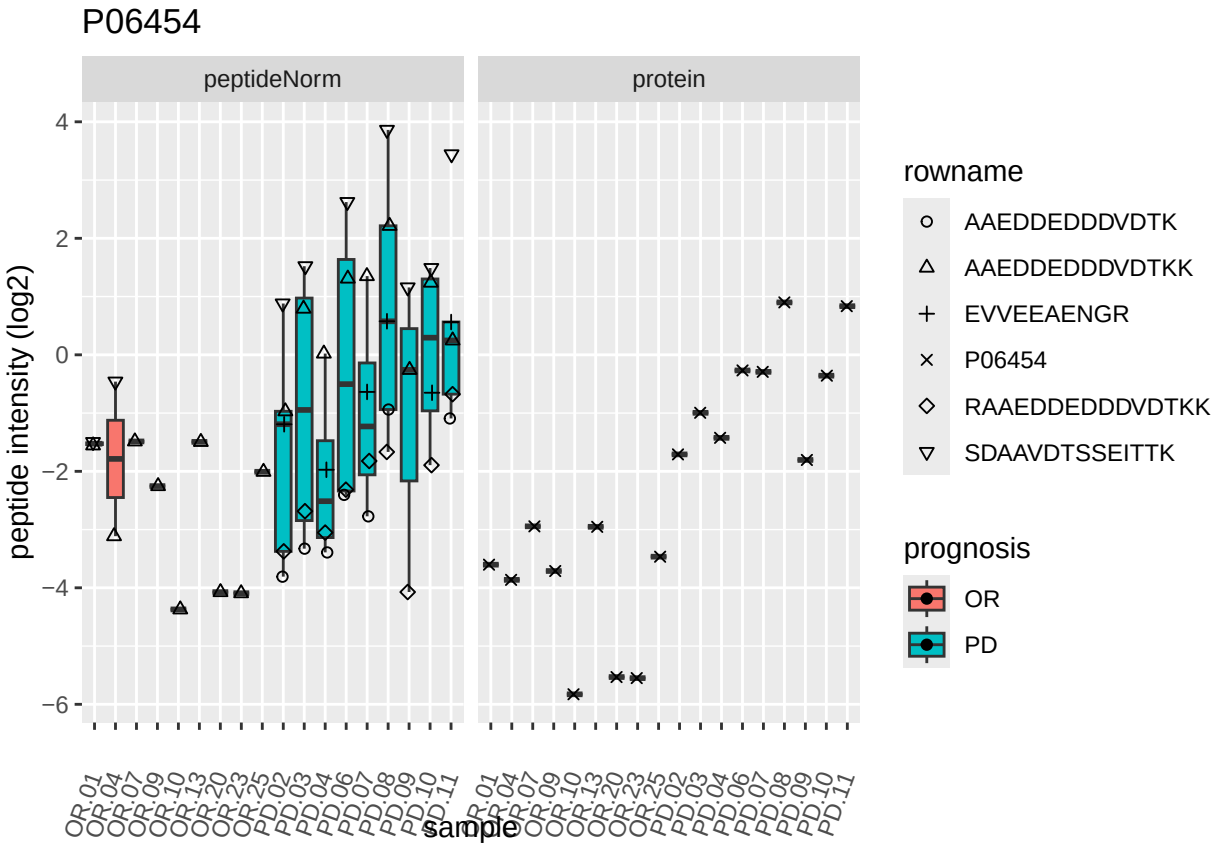
```
for (protName in sigNames)
#for (protName in orderProt[1:10])
{
pePlot <- pe[protName, , c("peptideNorm","protein")]
pePlotDf <- data.frame(longFormat(pePlot))
pePlotDf$assay <- factor(pePlotDf$assay,
                         levels = c("peptideNorm", "protein"))
pePlotDf$prognosis <- as.factor(colData(pePlot)[pePlotDf$colname, "prognosis"])

# plotting
p1 <- ggplot(data = pePlotDf,
       aes(x = colname, y = value, group = rowname)) +
    geom_line() +
    geom_point() +
    theme(axis.text.x = element_text(angle = 70, hjust = 1, vjust = 0.5)) +
    facet_grid(~assay) +
    ggtitle(protName)
print(p1)

# plotting 2
p2 <- ggplot(pePlotDf, aes(x = colname, y = value, fill = prognosis)) +
  geom_boxplot(outlier.shape = NA) +
```

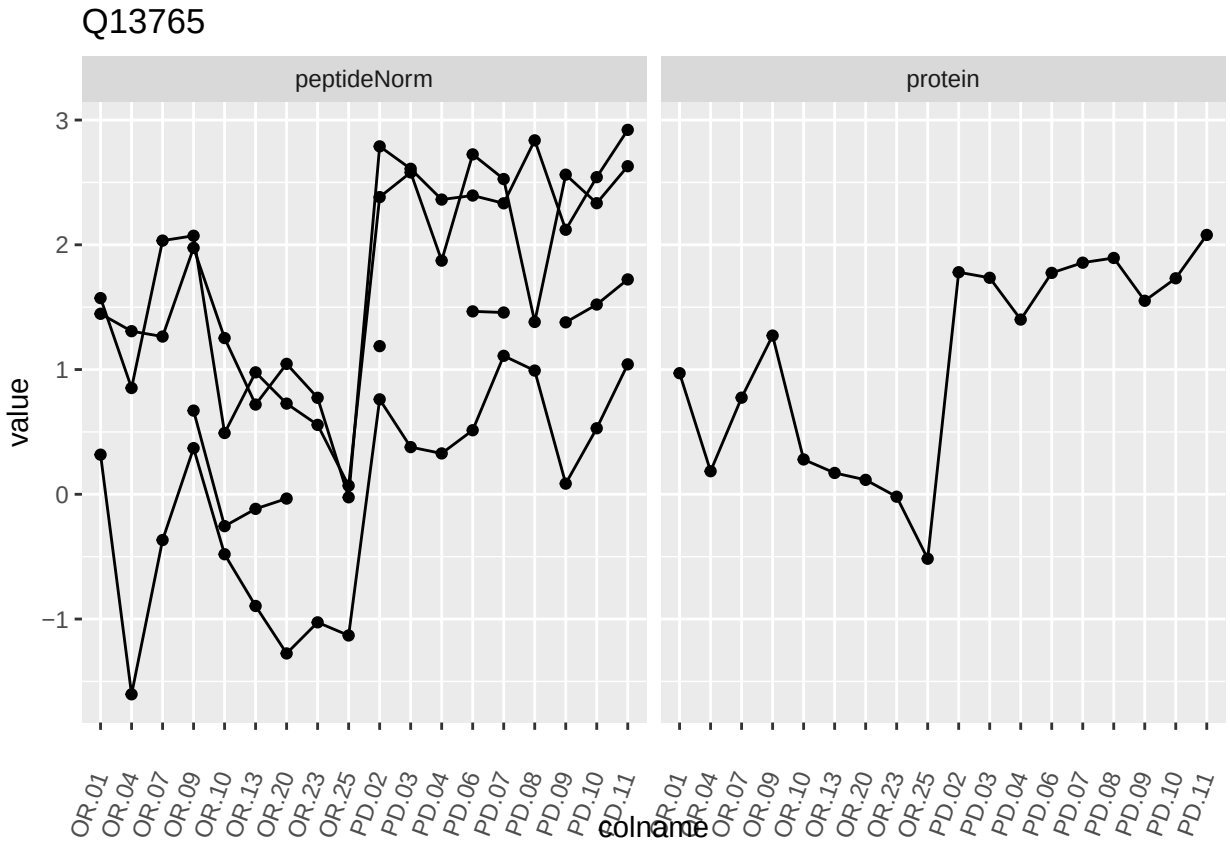
```
  geom_point(
    position = position_jitter(width = .1),
    aes(shape = rowname)) +
  scale_shape_manual(values = 1:nrow(pePlotDf)) +
  labs(title = protName, x = "sample", y = "peptide intensity (log2)") +
  theme(axis.text.x = element_text(angle = 70, hjust = 1, vjust = 0.5)) +
  facet_grid(~assay)
print(p2)
}
```

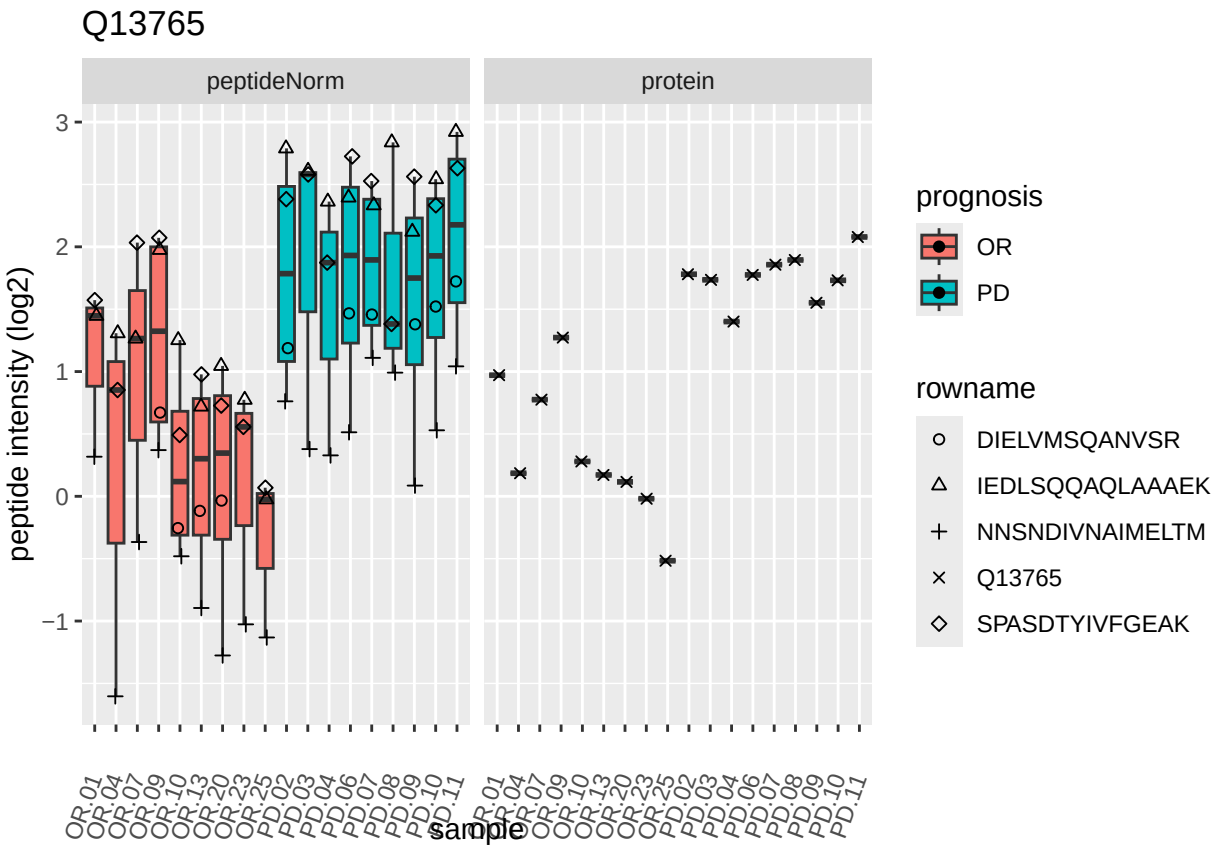


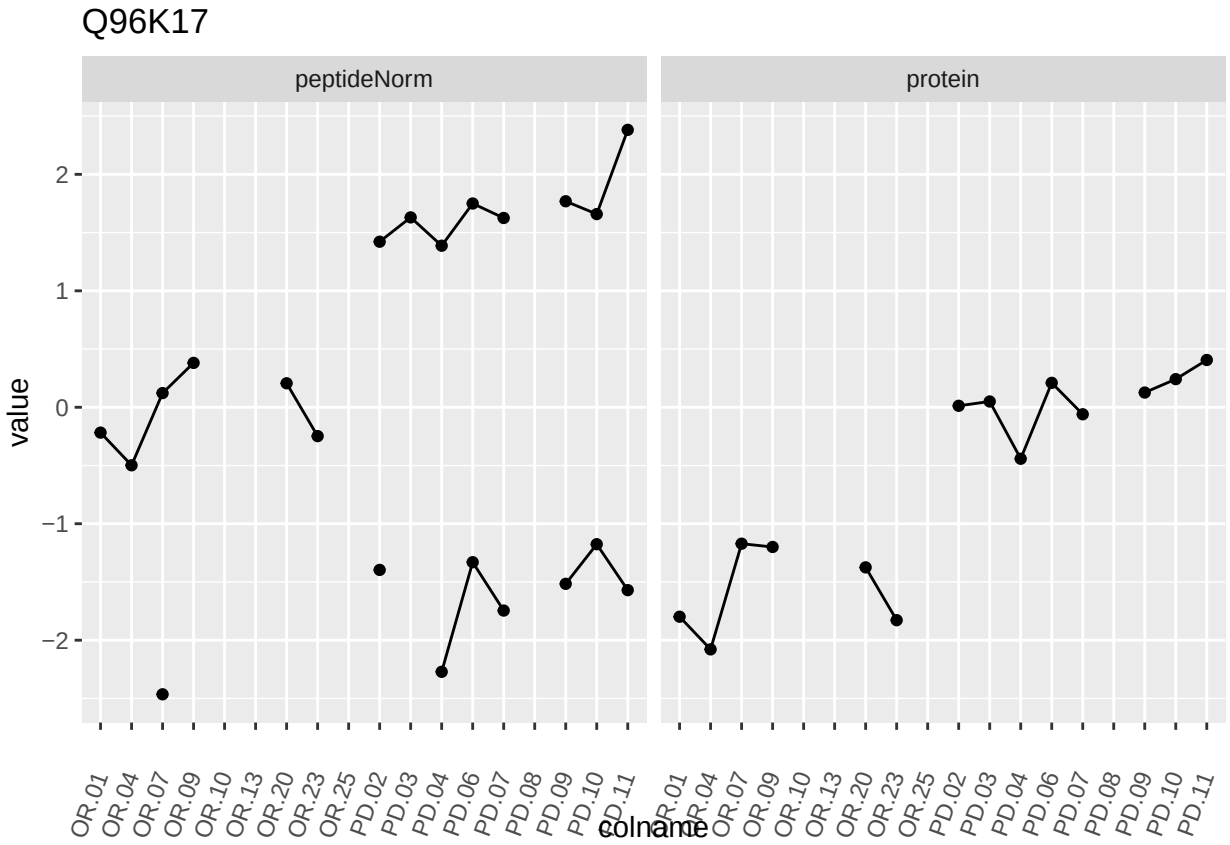

P61604
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
FLPLFDR
GGEIQPVSVK
GGIMLPEK
GKGGEIQPVSVK
KFLPLFDR
P61604
VLLPEYGGTK
VLQATVVAVGSGSK
VVLDDKDYFLFR
prognosis
OR
PD

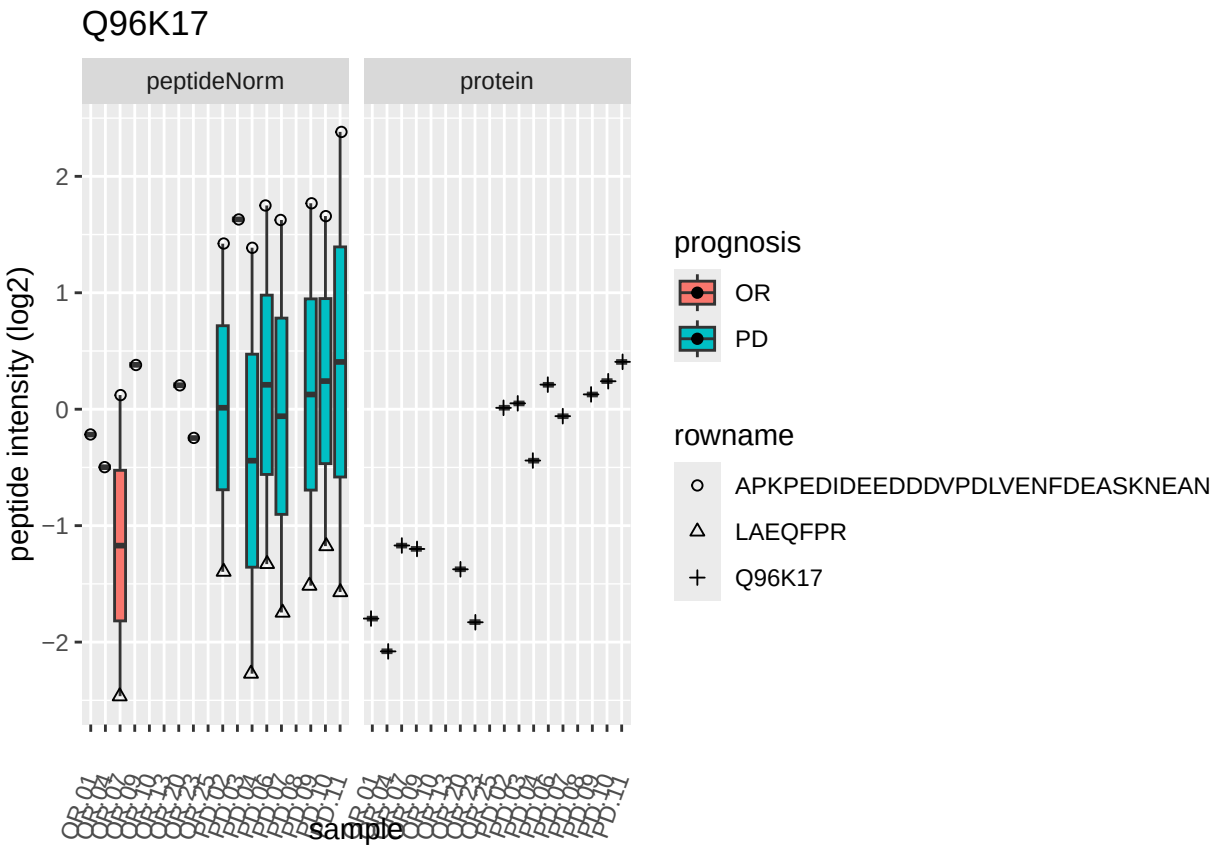

P06454
peptideNorm
protein
value
4
2
0
−2
−4
−6
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

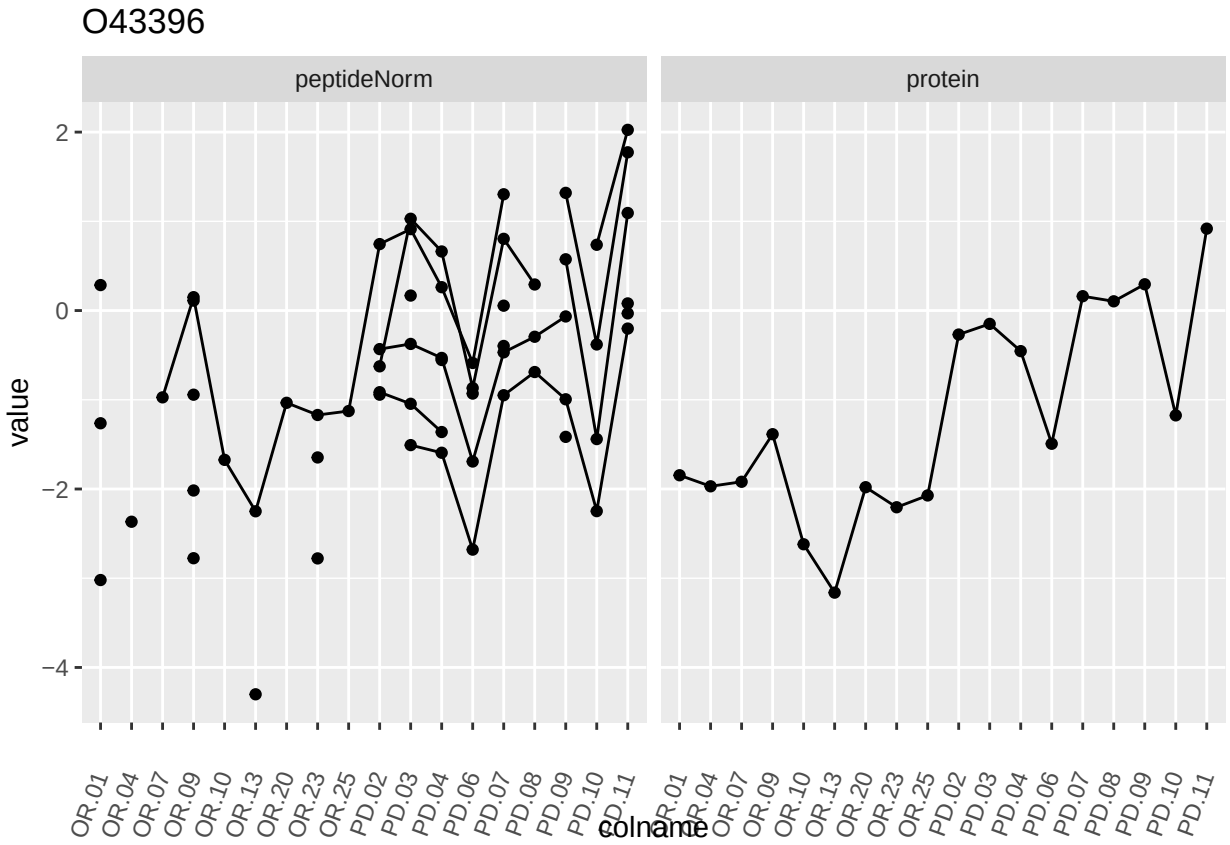

P06454
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
−6
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AAEDDEDDDVDTK
AAEDDEDDDVDTKK
EVVEEAENGR
P06454
RAAEDDEDDDVDTKK
SDAAVDTSSEITTK
prognosis
OR
PD

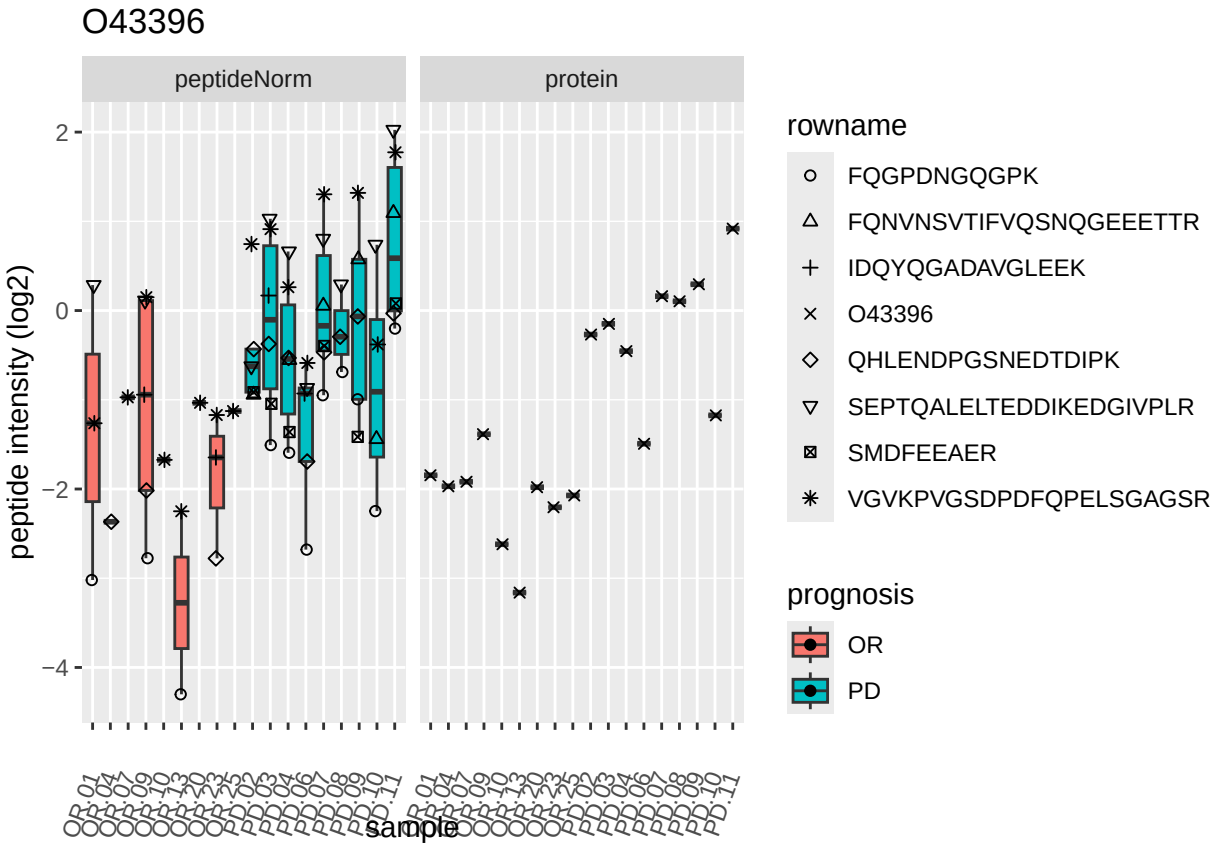

Q13765
peptideNorm
protein
value
3
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

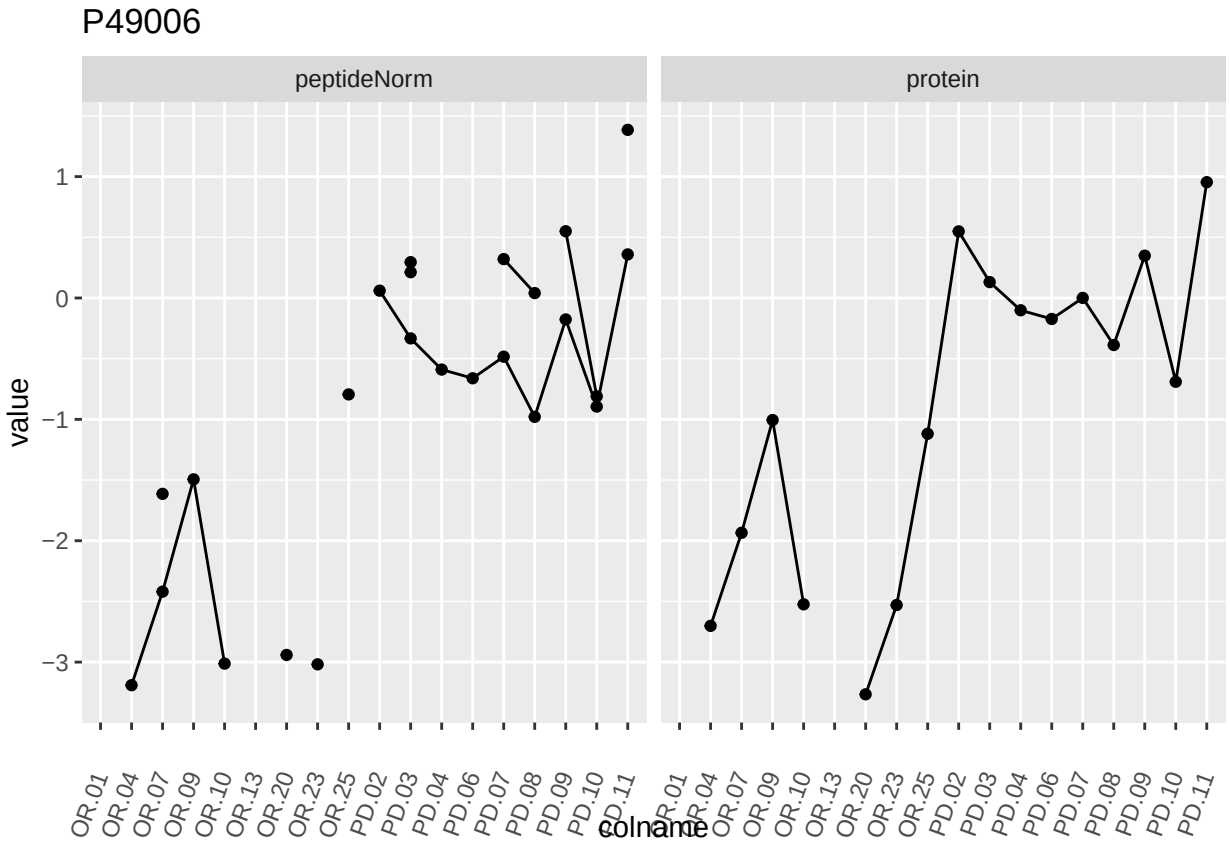

Q13765
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
DIELVMSQANVSR
IEDLSQQAQLAAAEK
NNSNDIVNAIMELTM
Q13765
SPASDTYIVFGEAK

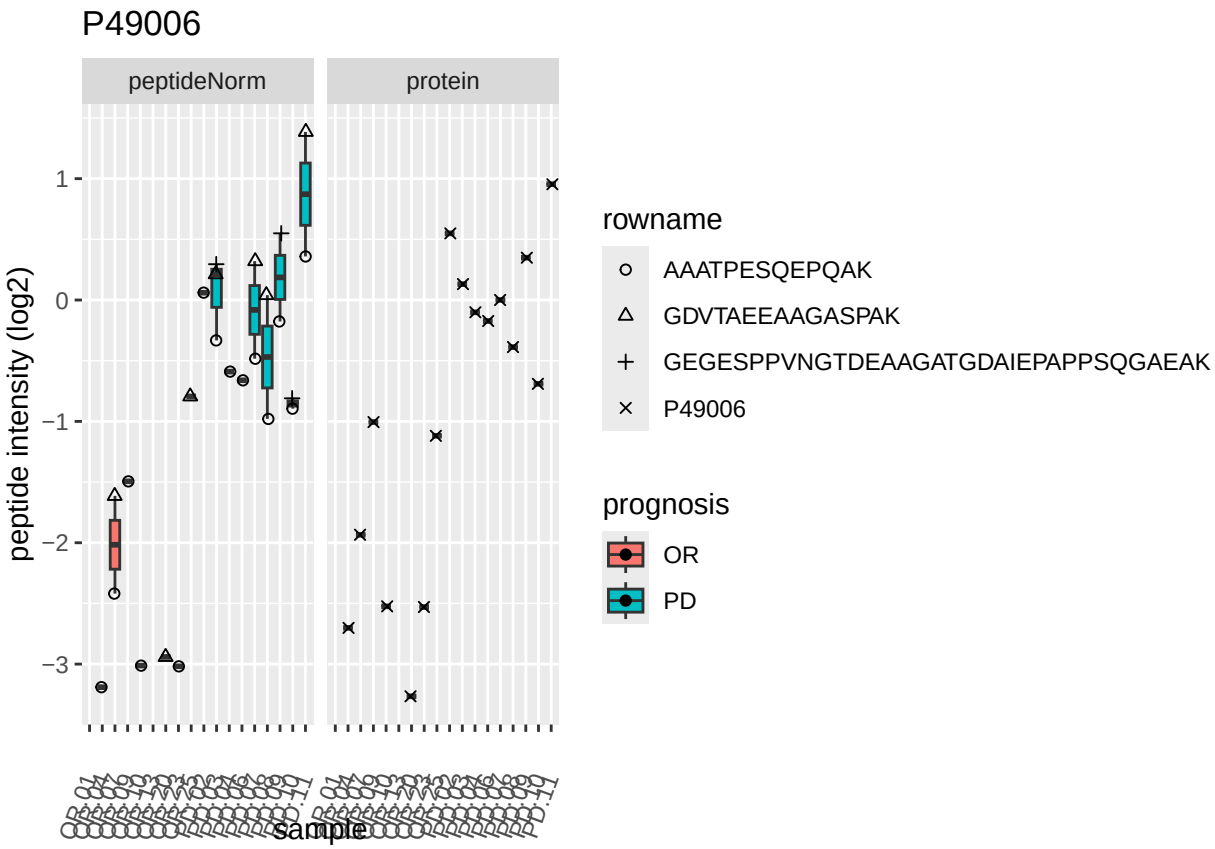

Q96K17
peptideNorm
protein
value
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q96K17
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
sample
prognosis
OR
PD
rowname
APKPEDIDEEDDDVPDLVENFDEASKNEAN
LAEQFPR
Q96K17


O43396
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O43396
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR:01
OR:04
OR:07
OR:09
OR:10
OR:13
OR:20
OR:23
OR:25
PD:02
PD:03
PD:04
PD:06
PD:07
PD:08
PD:09
PD:10
PD:11
sample
rowname
FQGPDNGQGPK
FQNVNSVTIFVQSNQGEEETTR
IDQYQGADAVGLEEK
O43396
QHLENDPGSNEDTDIPK
SEPTQALELTEDDIKEDGIVPLR
SMDFEEAER
VGVKPVGSDPDFQPELSGAGSR
prognosis
OR
PD


P49006
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P49006
peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
sample
rowname
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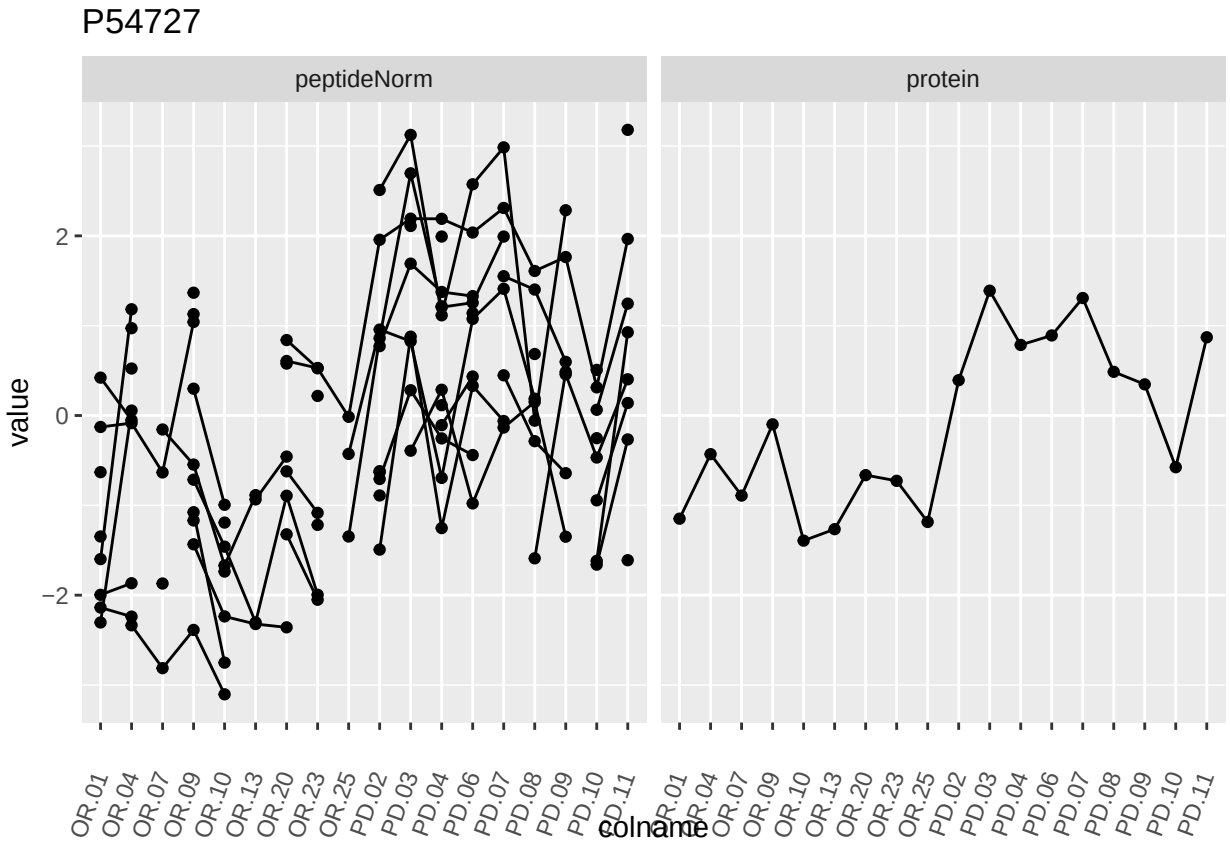
GDVTAEEAAGASPAK
GEGESPPVNGTDEAAGATGDAIEPAPPSQGAEAK
P49006
prognosis
OR
PD


P54727
peptideNorm
protein
value
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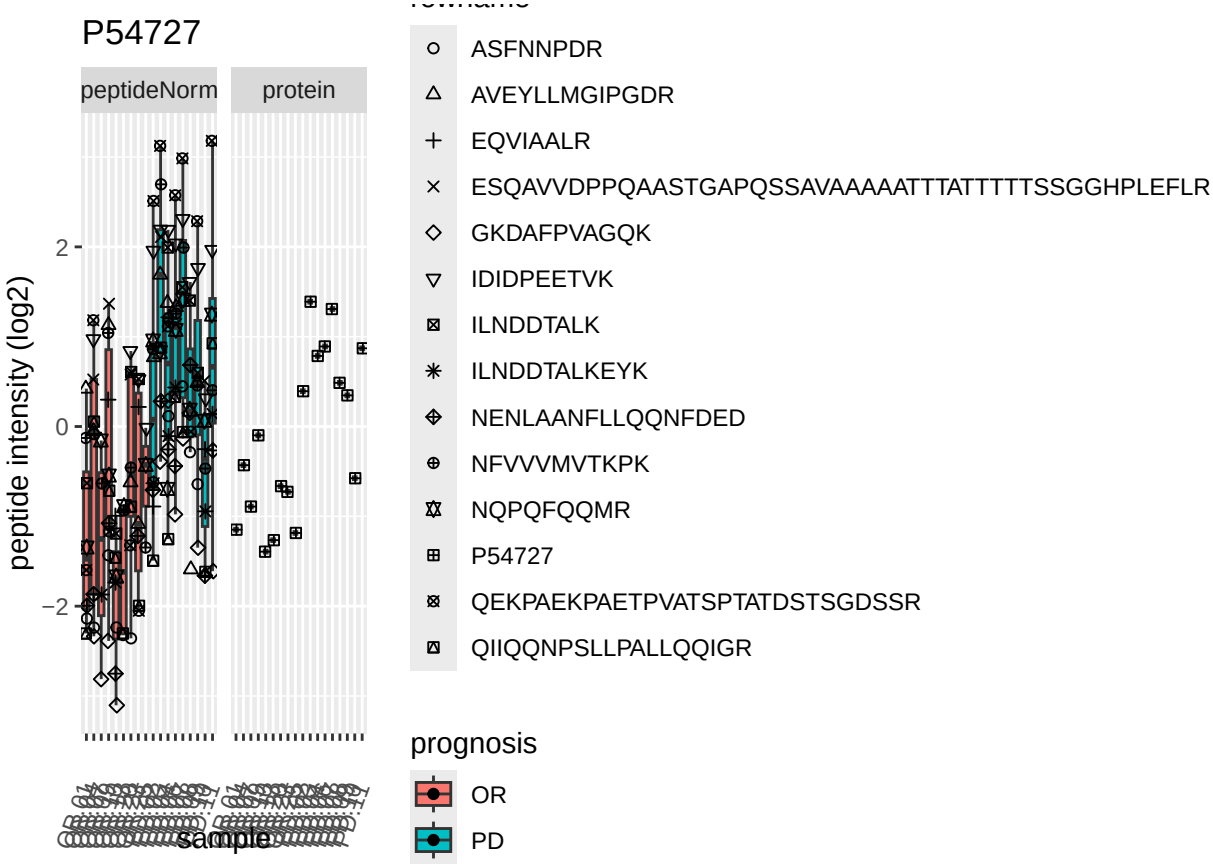
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P54727
peptideNorm
protein
peptide intensity (log2)
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0
−2
sample
rowname
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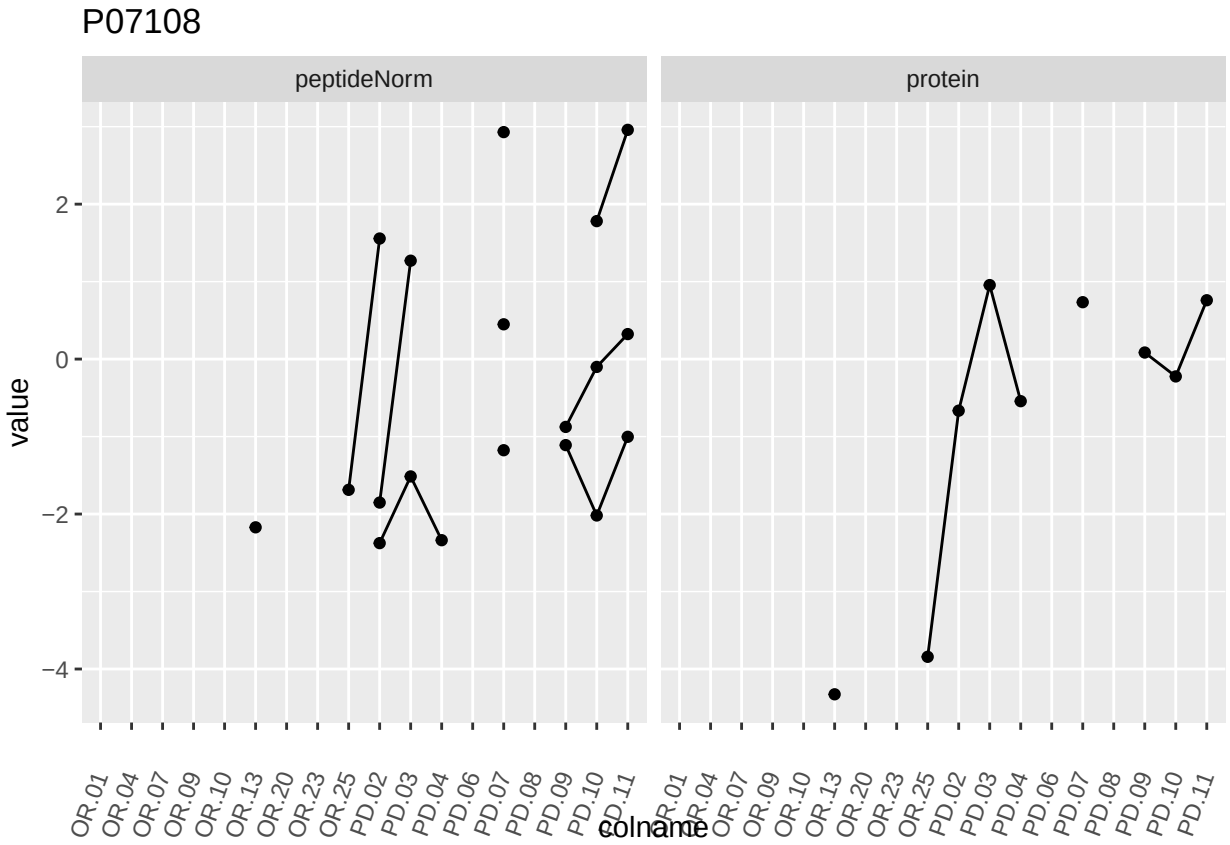
AVEYLLMGIPGDR
EQVIAALR
ESQAVVDPPQAASTGAPQSSAVAAAAATTTATTTTTSSGGHPLEFLR
GKDAFPVAGQK
IDIDPEETVK
ILNDDTALK
ILNDDTALKEYK
NENLAANFLLQQNFDED
NFVVVMVTKPK
NQPQFQQMR
P54727
QEKPAEKPAETPVATSPTATDSTSGDSSR
QIIQQNPSLLPALLQQIGR
prognosis
OR
PD


P07108
peptideNorm
protein
value
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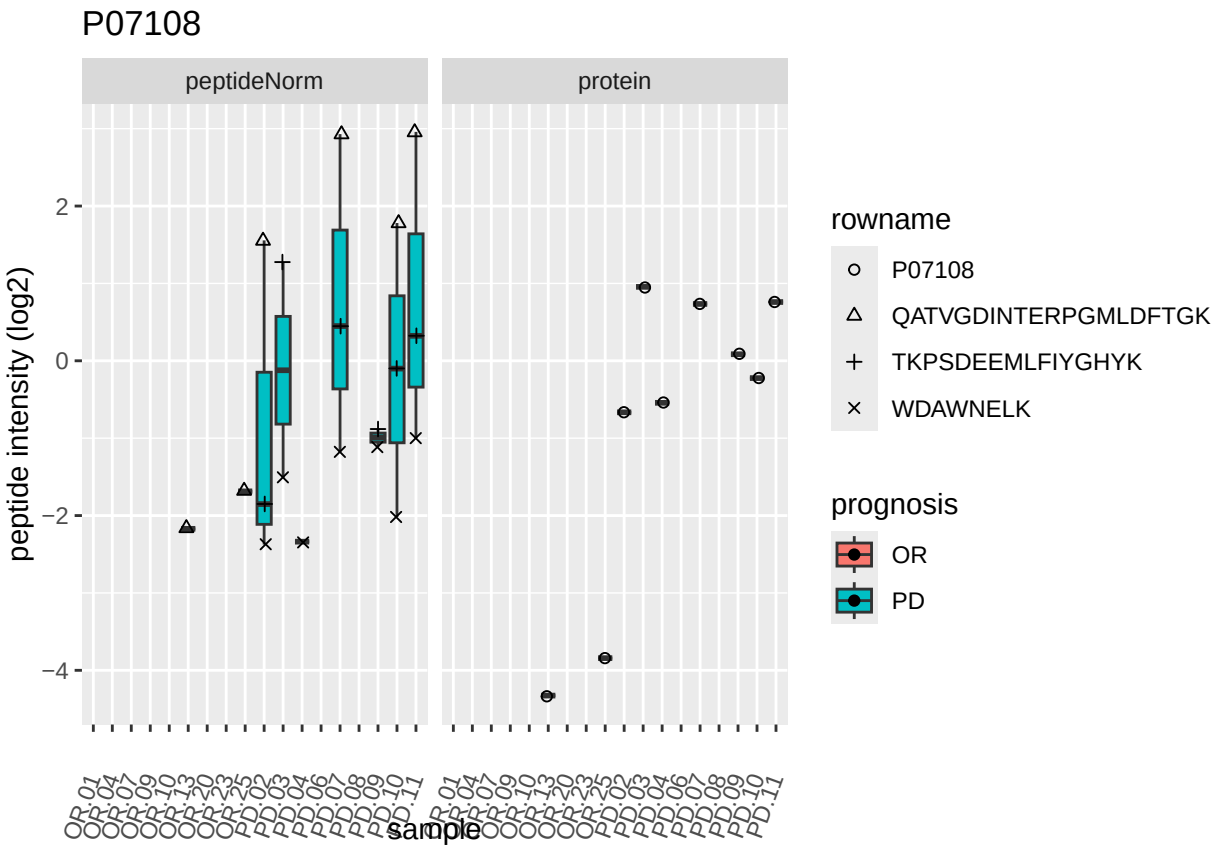
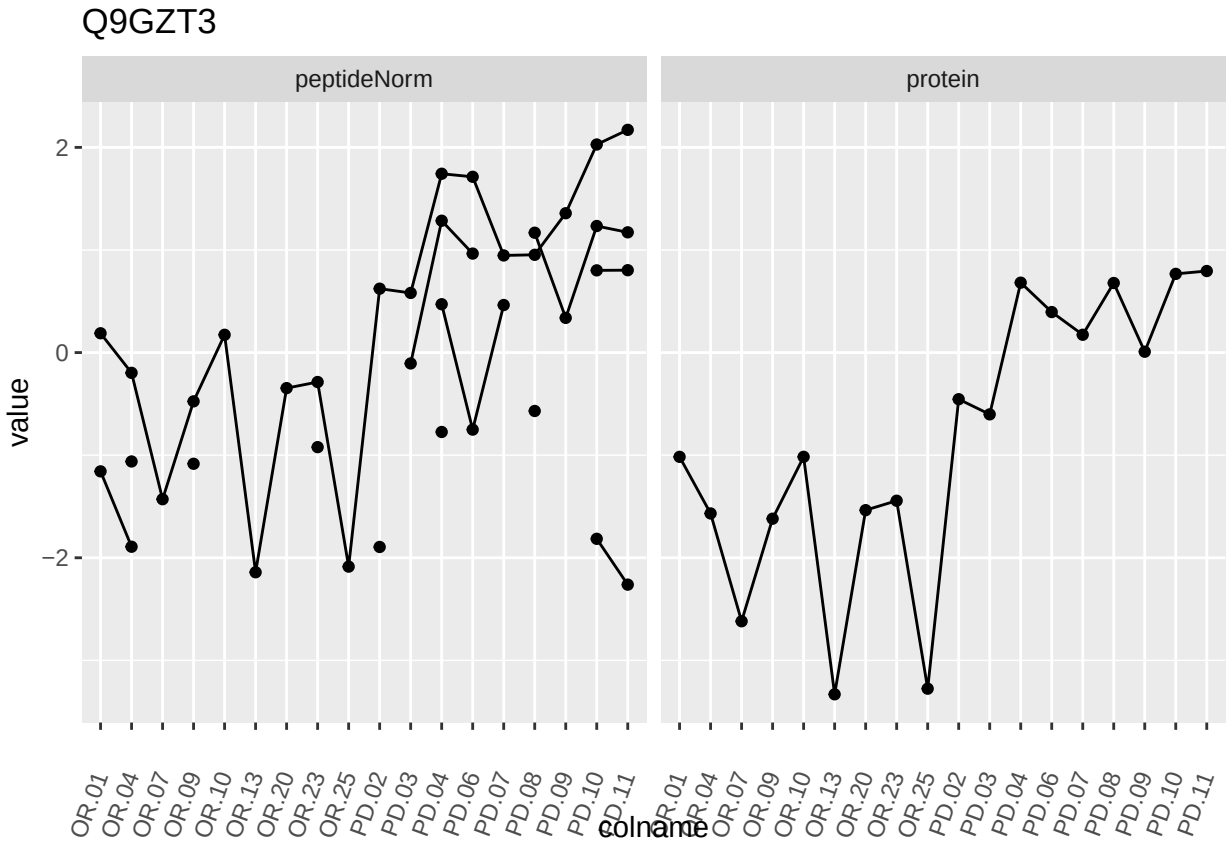
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P07108
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
P07108
QATVGDINTERPGMLDFTGK
TKPSDEEMLFIYGHYK
WDAWNELK
prognosis
OR
PD


Q9GZT3
peptideNorm
protein
value
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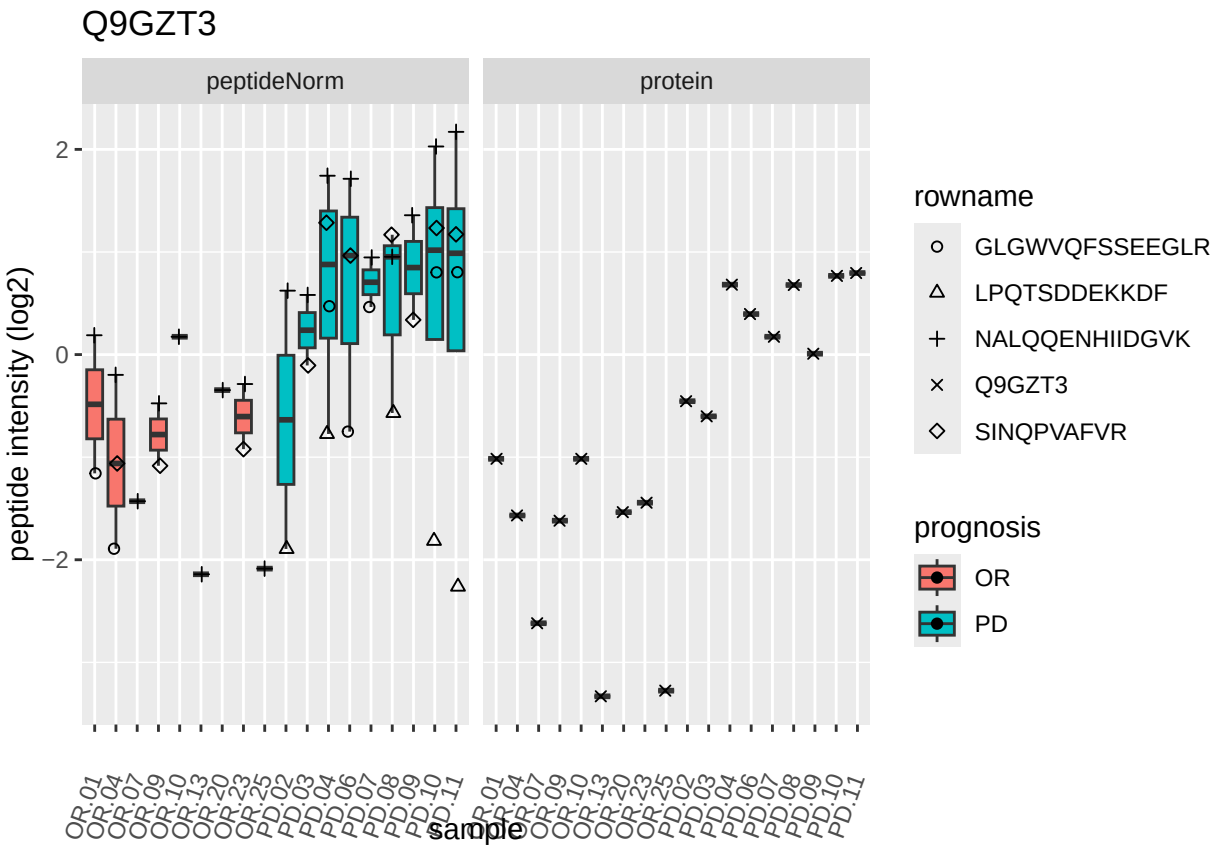
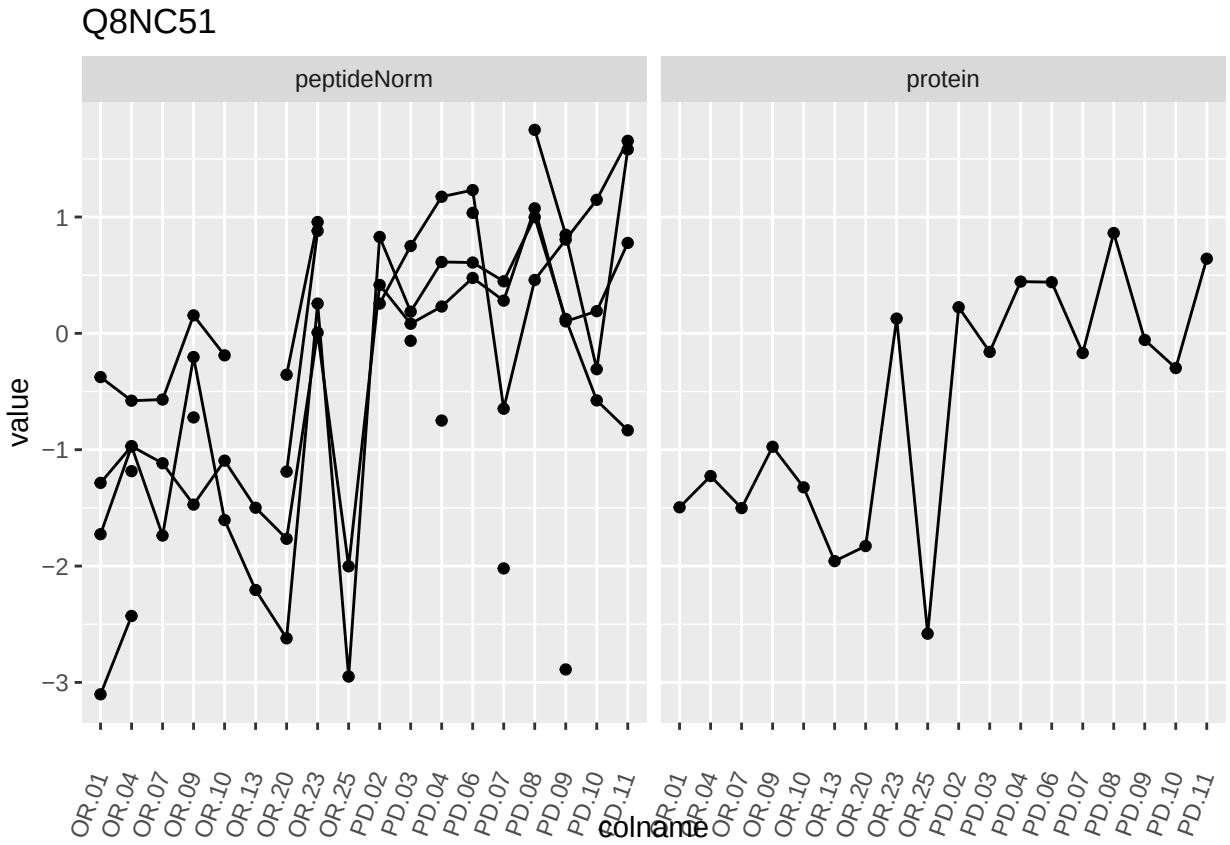
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9GZT3
peptideNorm
protein
peptide intensity (log2)
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
GLGWVQFSSEEGLR
LPQTSDDEKKDF
NALQQENHIIDGVK
Q9GZT3
SINQPVAFVR
prognosis
OR
PD


Q8NC51
peptideNorm
protein
value
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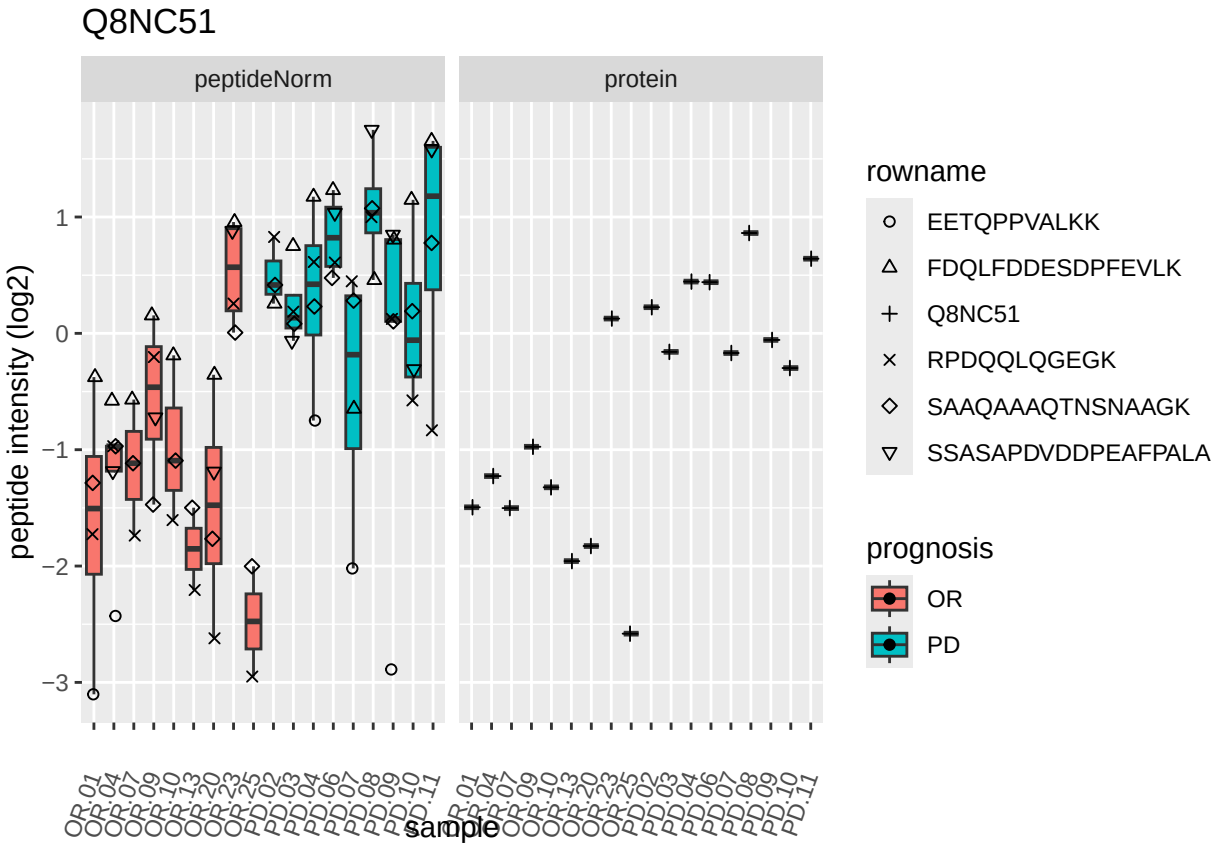
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q8NC51
peptideNorm
protein
peptide intensity (log2)
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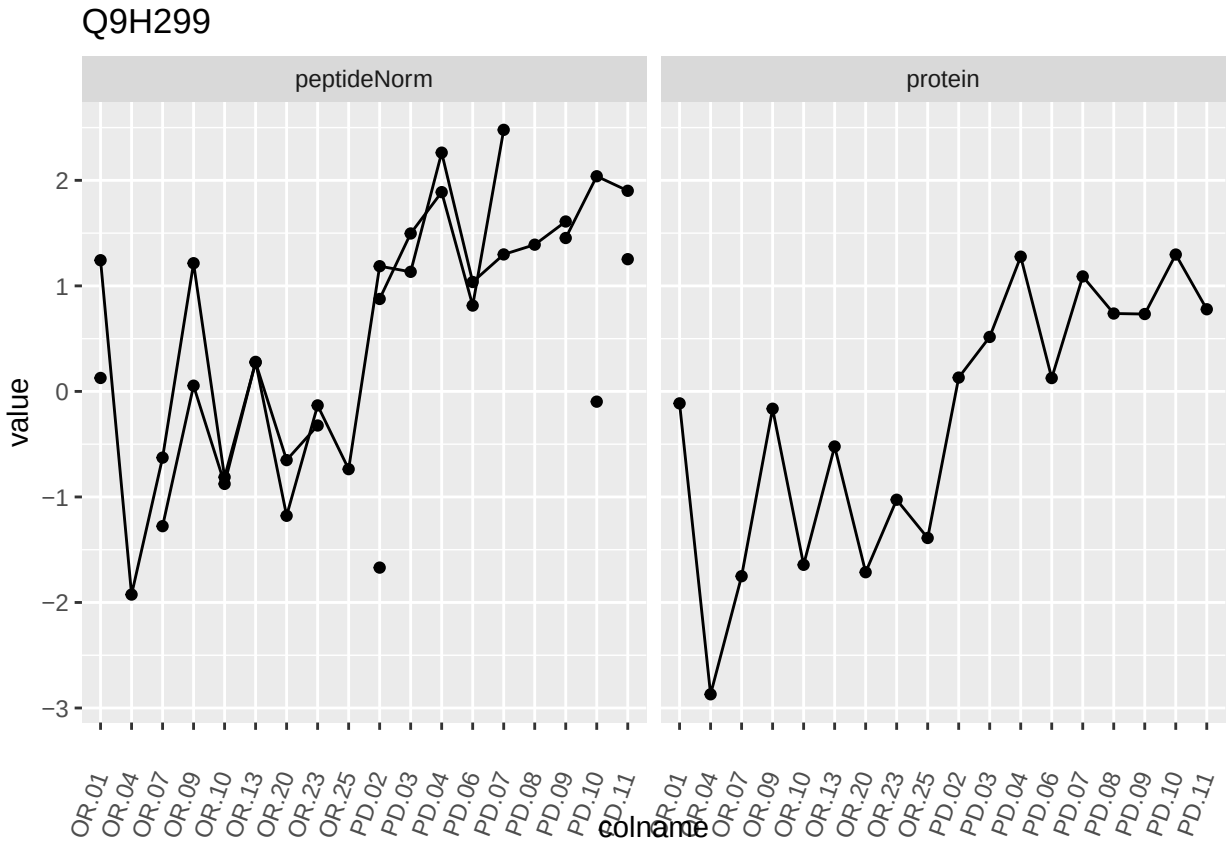
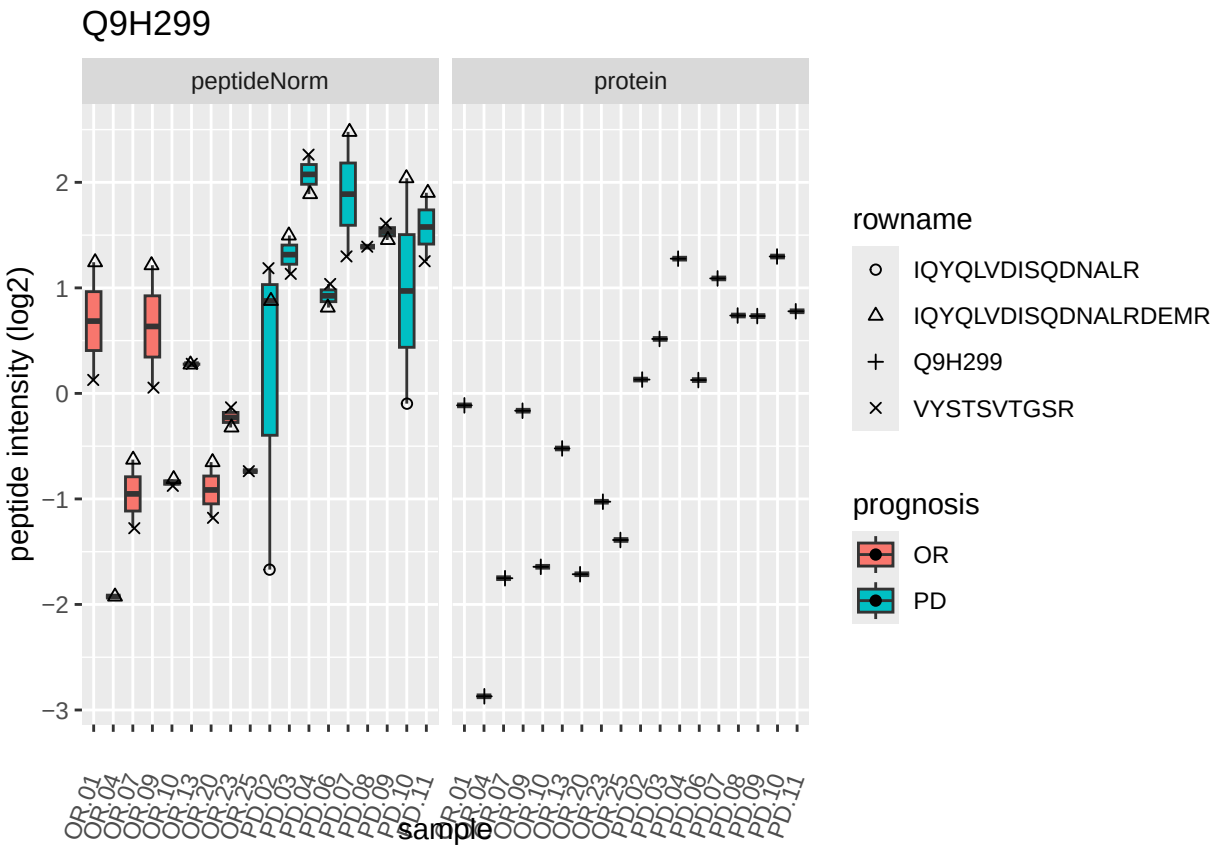
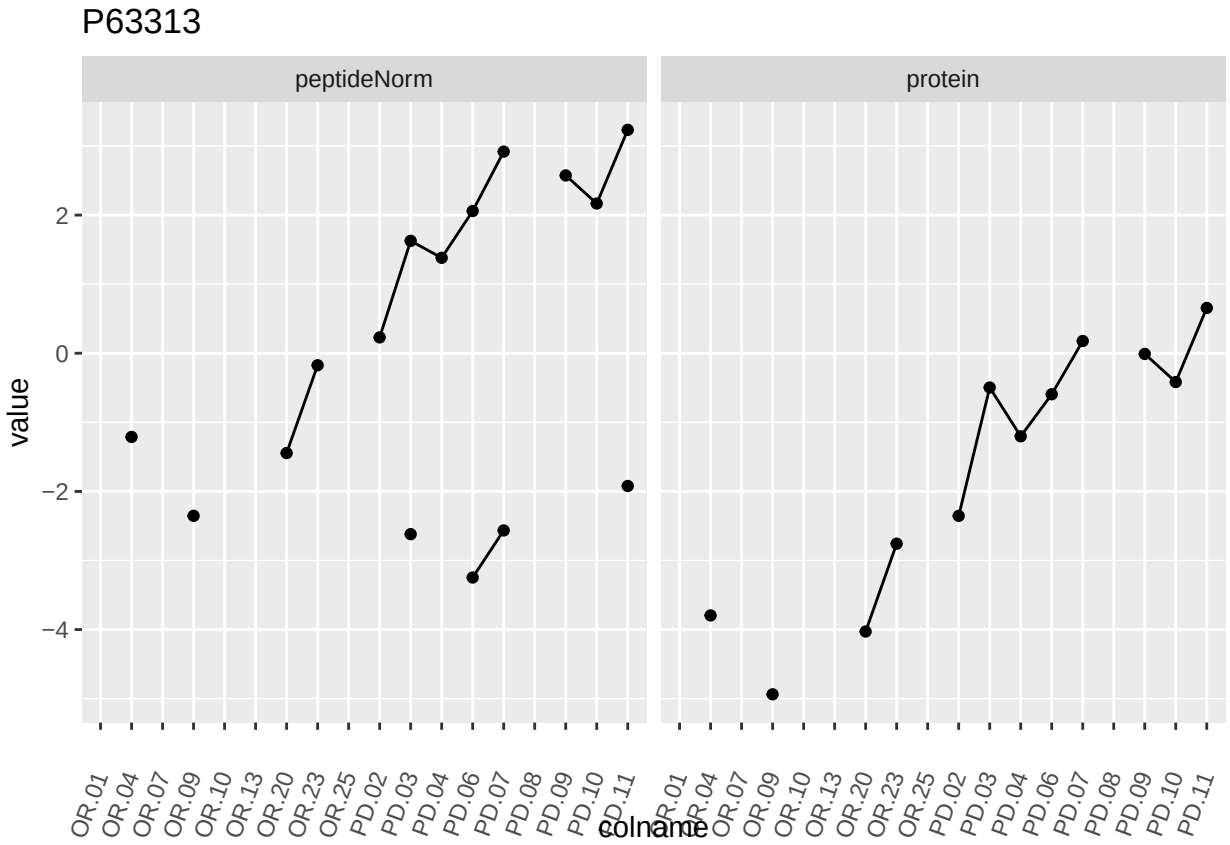
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EETQPPVALKK
FDQLFDDESDPFEVLK
Q8NC51
RPDQQLQGEGK
SAAQAAAQTNSNAAGK
SSASAPDVDDPEAFPALA
prognosis
OR
PD


Q9H299
peptideNorm
protein
value
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9H299
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
IQYQLVDISQDNALR
IQYQLVDISQDNALRDEMR
Q9H299
VYSTSVTGSR
prognosis
OR
PD


P63313
peptideNorm
protein
value
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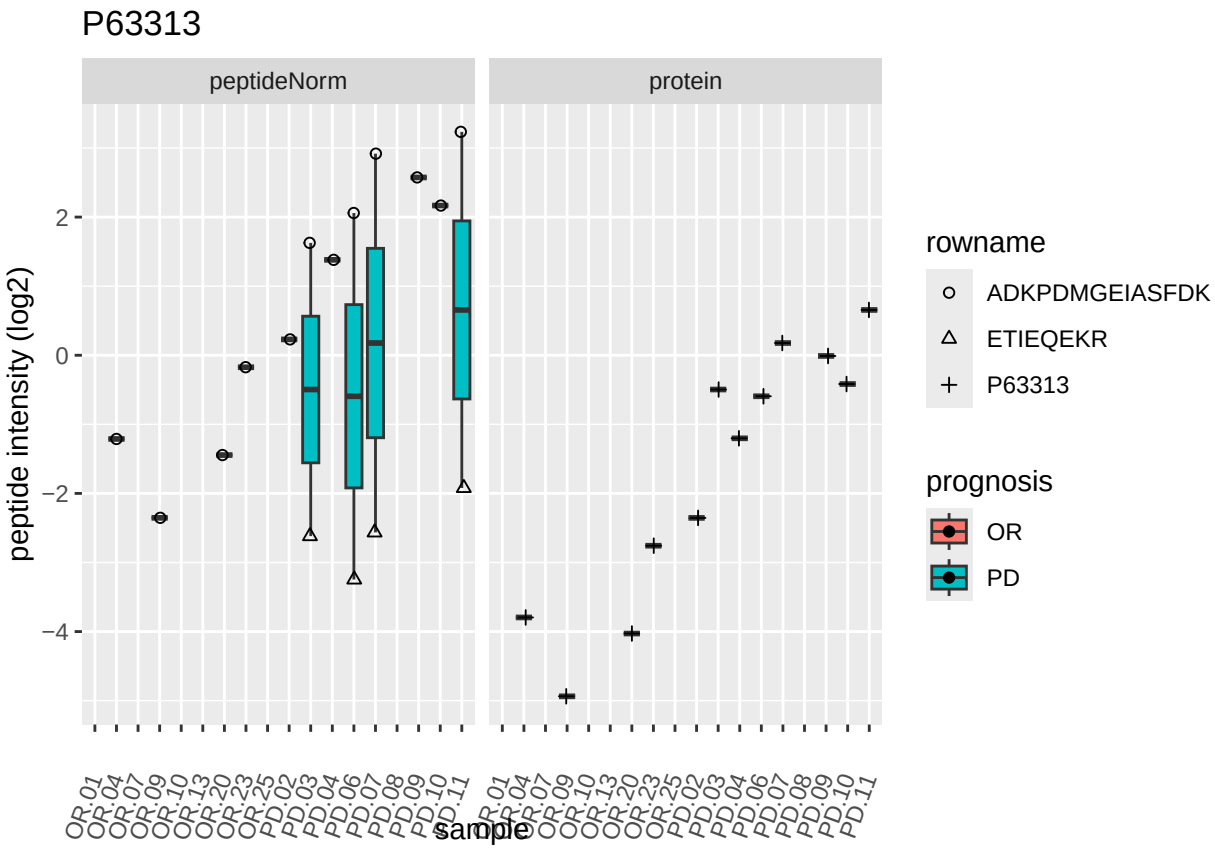
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P63313
peptideNorm
protein
peptide intensity (log2)
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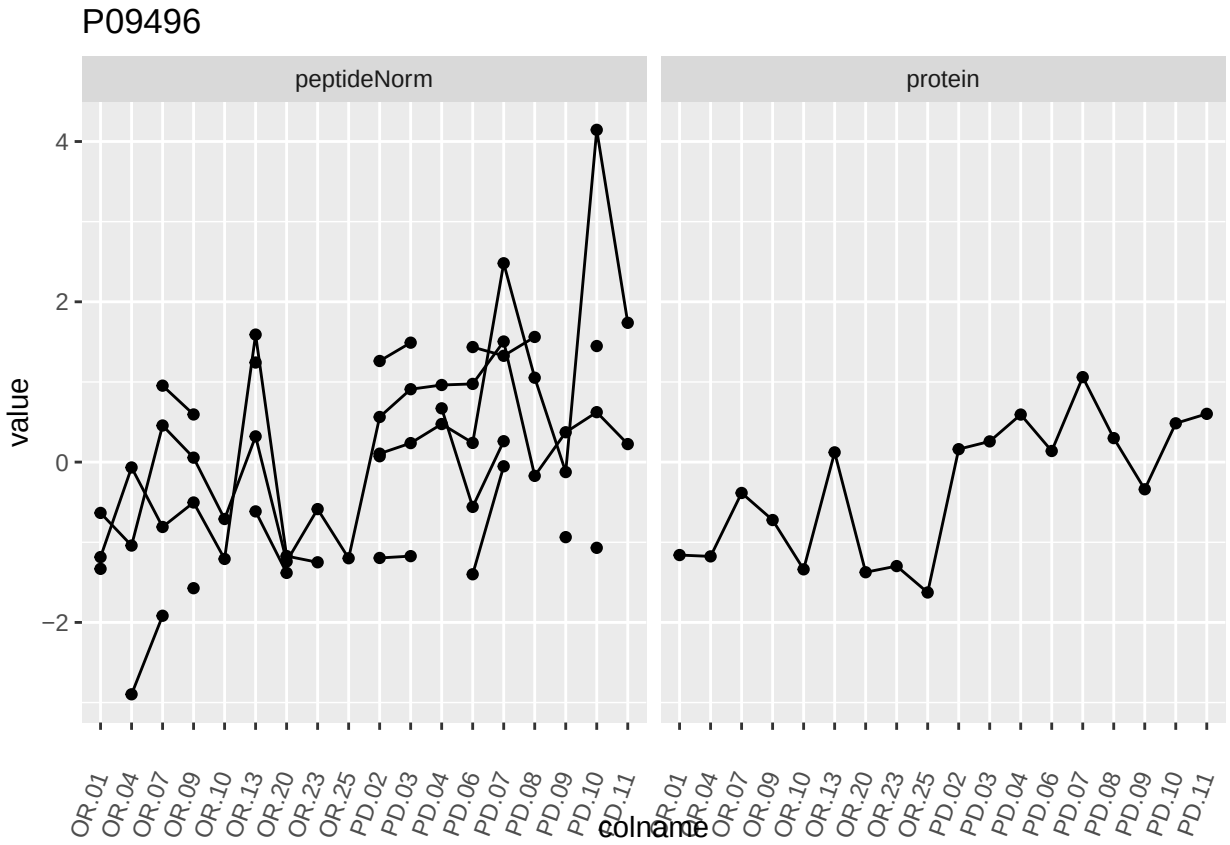
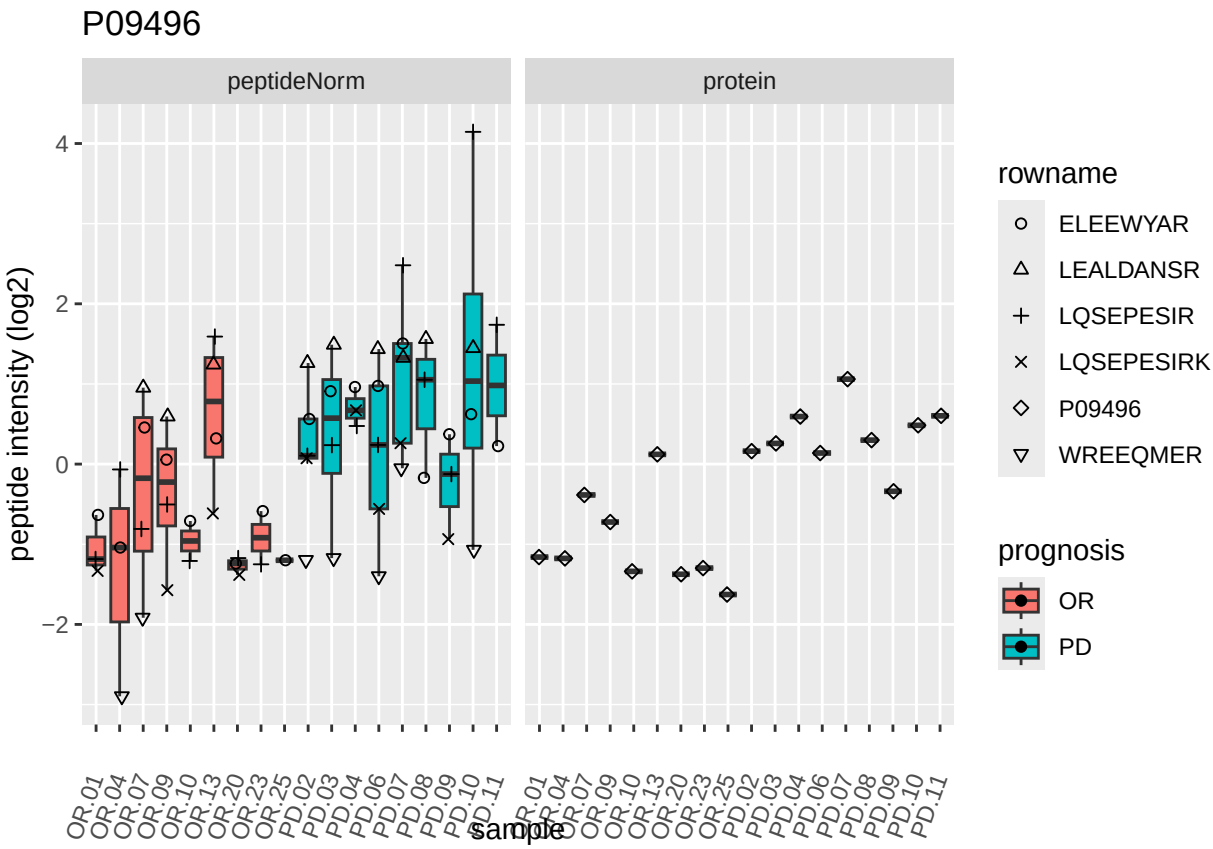
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ADKPDMGEIASFDK
ETIEQEKR
P63313
prognosis
OR
PD


P09496
peptideNorm
protein
value
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P09496
peptideNorm
protein
peptide intensity (log2)
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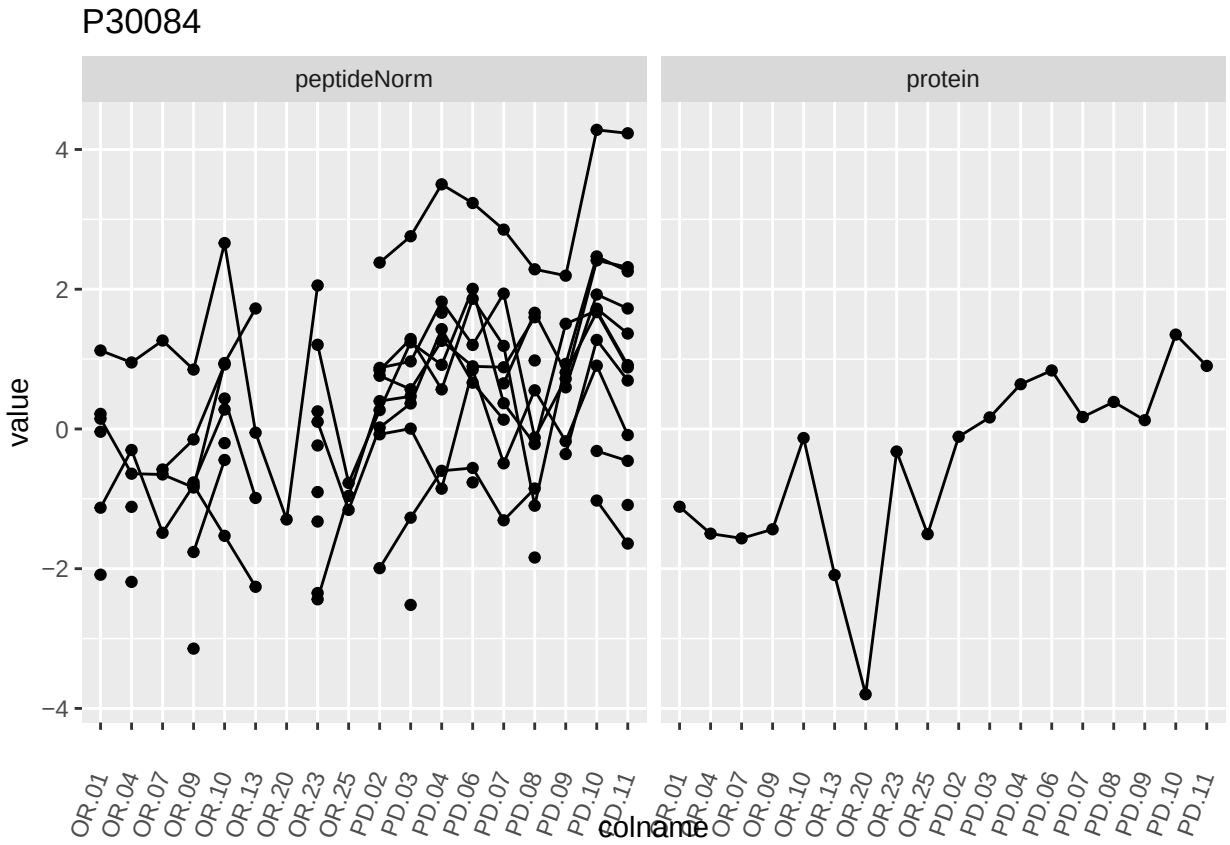
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ELEEWYAR
LEALDANSR
LQSEPESIR
LQSEPESIRK
P09496
WREEQMER
prognosis
OR
PD


P30084
peptideNorm
protein
value
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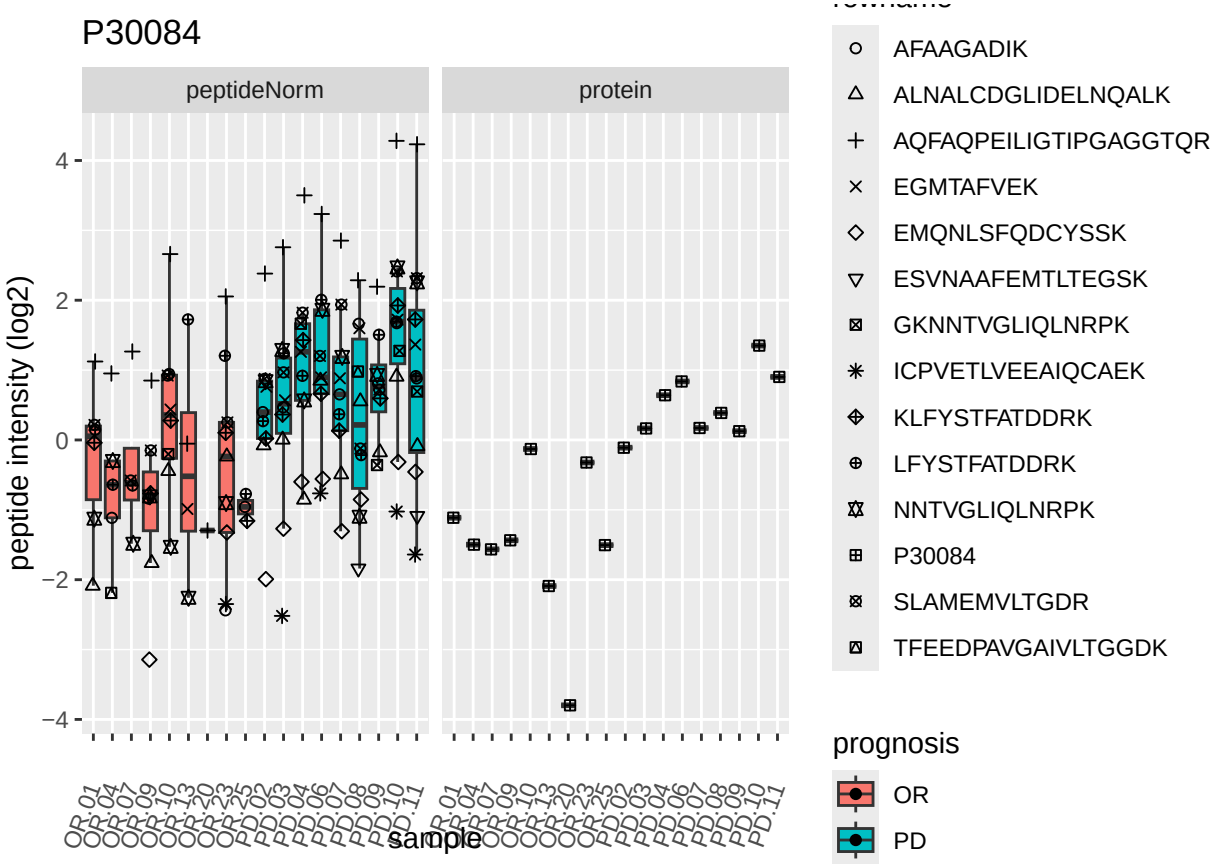
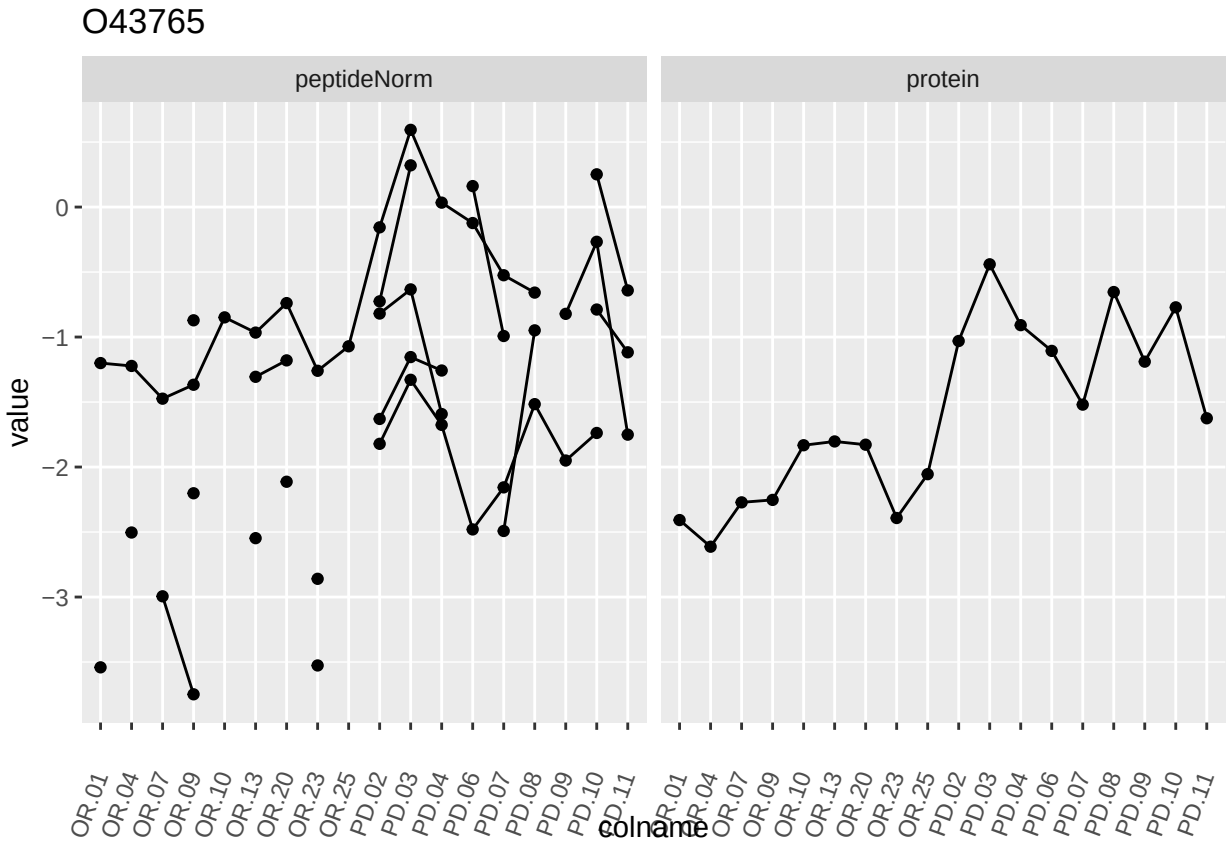
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P30084
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
AFAAGADIK
ALNALCDGLIDELNQALK
AQFAQPEILIGTIPGAGGTQR
EGMTAFVEK
EMQNLSFQDCYSSK
ESVNAAFEMTLTEGSK
GKNNTVGLIQLNRPK
ICPVETLVEEAIQCAEK
KLFYSTFATDDRK
LFYSTFATDDRK
NNTVGLIQLNRPK
P30084
SLAMEMVLTGDR
TFEEDPAVGAIVLTGGDK
prognosis
OR
PD


O43765
peptideNorm
protein
value
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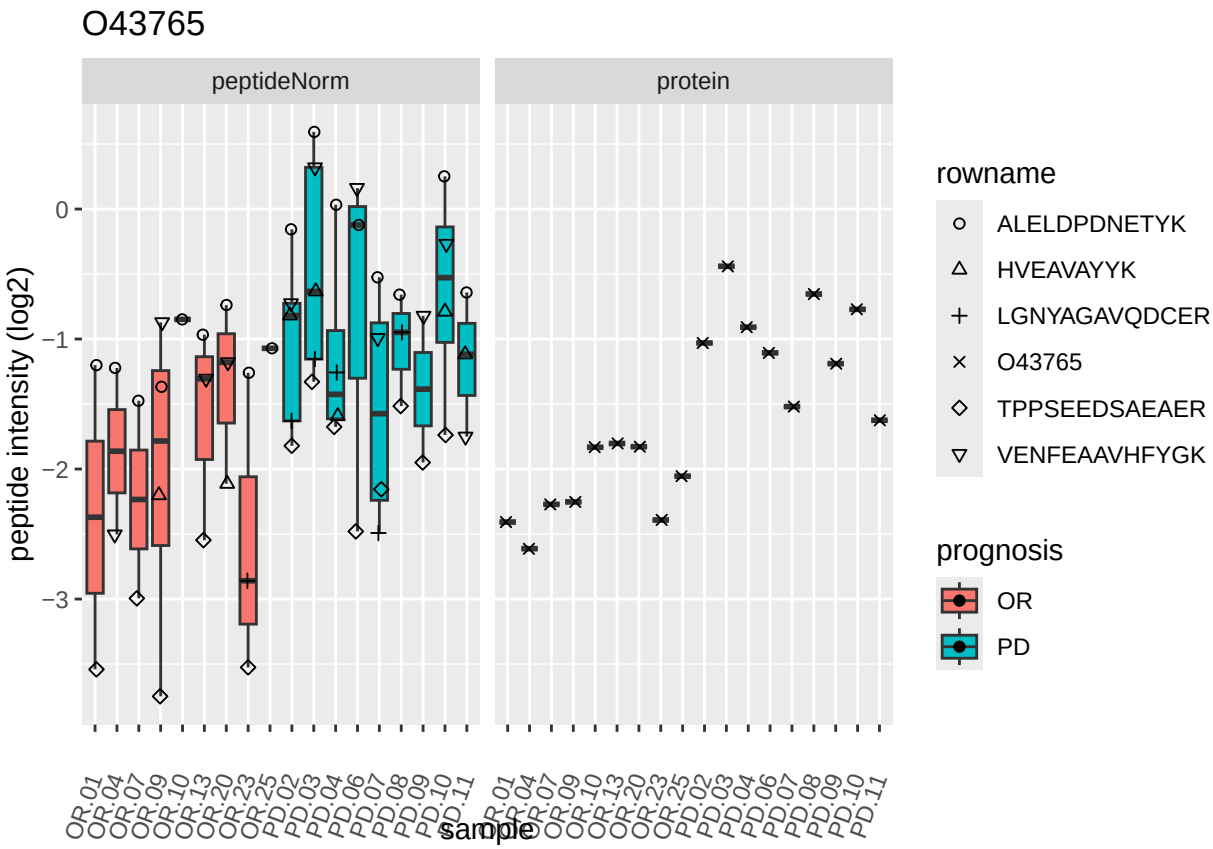
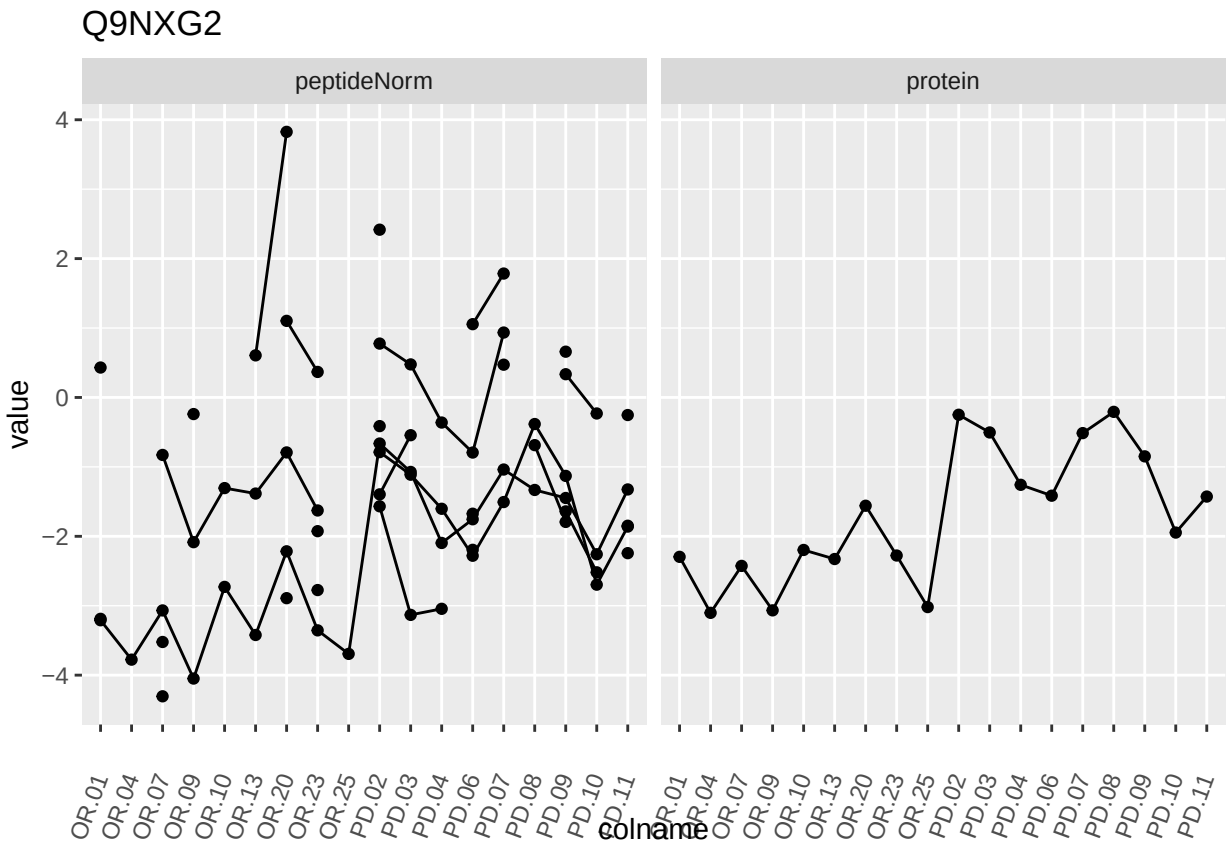
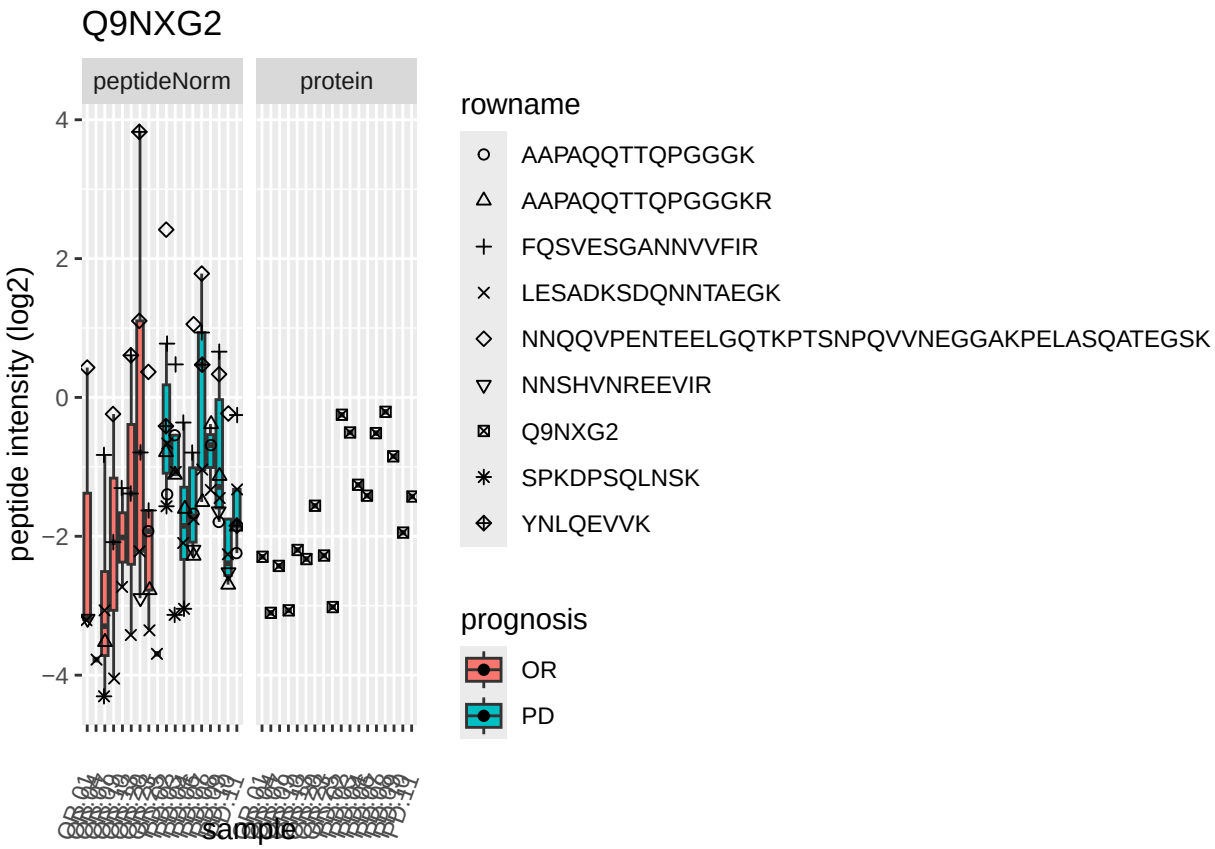
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O43765
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ALELDPDNETYK
HVEAVAYYK
LGNYAGAVQDCER
O43765
TPPSEEDSAEAER
VENFEAAVHFYGK
prognosis
OR
PD


Q9NXG2
peptideNorm
protein
value
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NXG2
peptideNorm
protein
peptide intensity (log2)
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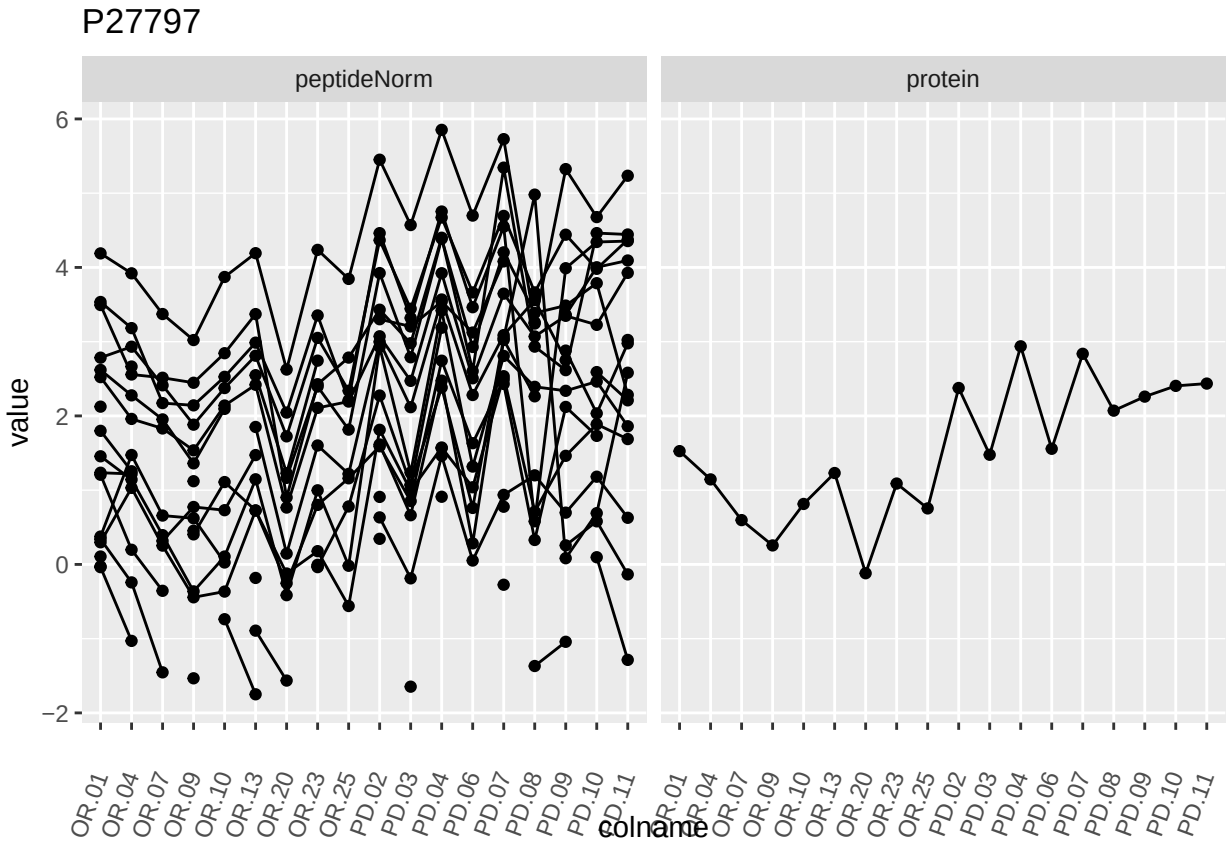
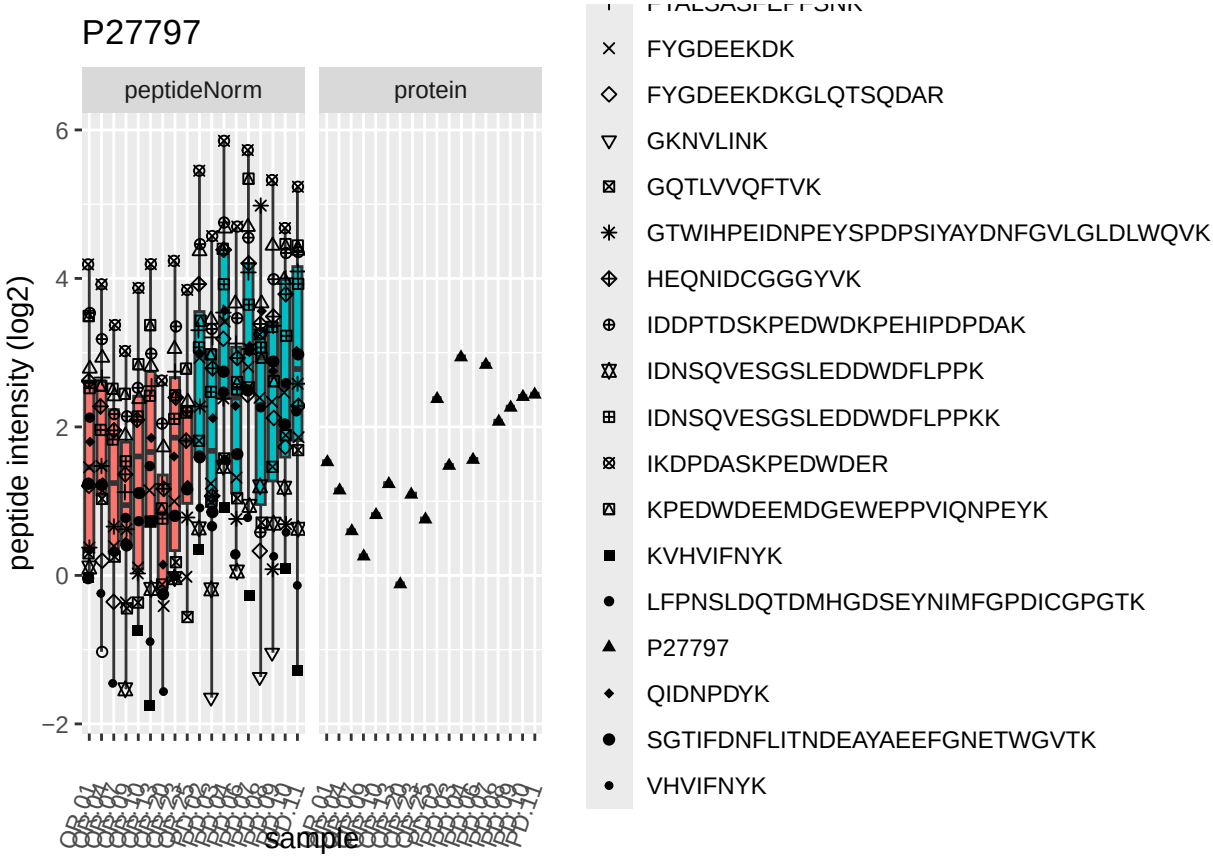
2
0
−2
−4
sample
rowname
AAPAQQTTQPGGGK
AAPAQQTTQPGGGKR
FQSVESGANNVVFIR
LESADKSDQNNTAEGK
NNQQVPENTEELGQTKPTSNPQVVNEGGAKPELASQATEGSK
NNSHVNREEVIR
Q9NXG2
SPKDPSQLNSK
YNLQEVVK
prognosis
OR
PD


P27797
peptideNorm
protein
value
6
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P27797
peptideNorm
protein
peptide intensity (log2)
6
4
2
0
−2
sample
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FYGDEEKDKGLQTSQDAR
GKNVLINK
GQTLVVQFTVK
GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK
HEQNIDCGGGYVK
IDDPTDSKPEDWDKPEHIPDPDAK
IDNSQVESGSLEDDWDFLPPK
IDNSQVESGSLEDDWDFLPPKK
IKDPDASKPEDWDER
KPEDWDEEMDGEWEPPVIQNPEYK
KVHVIFNYK
LFPNSLDQTDMHGDSEYNIMFGPDICGPGTK
P27797
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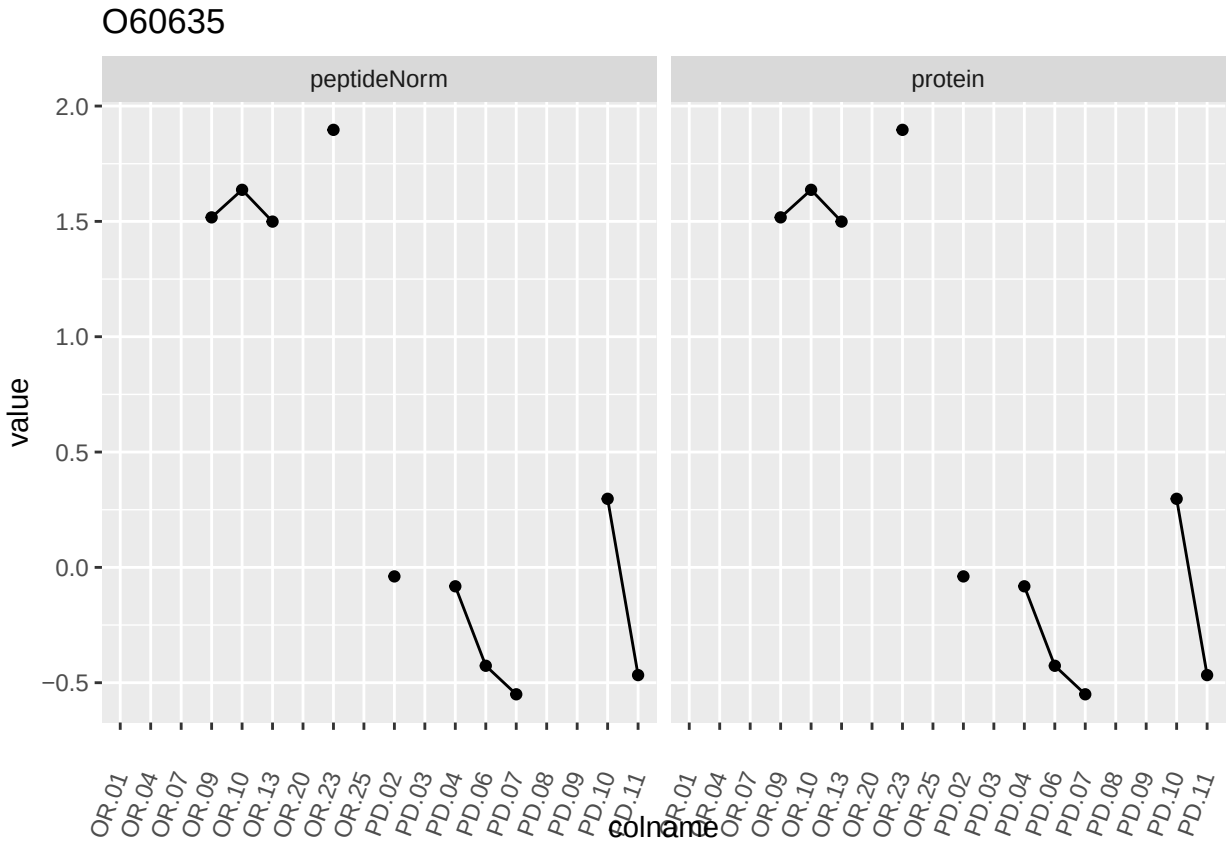
VHVIFNYK


O60635
peptideNorm
protein
value
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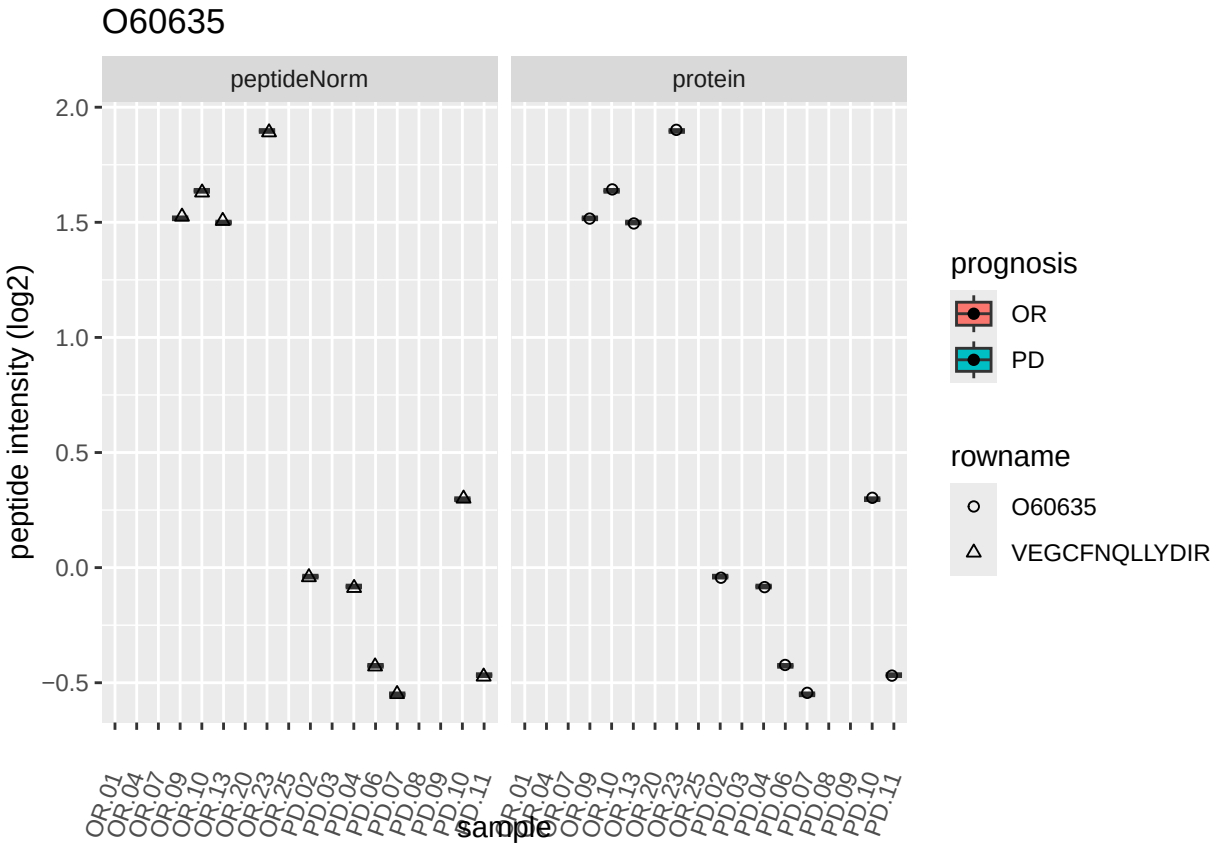
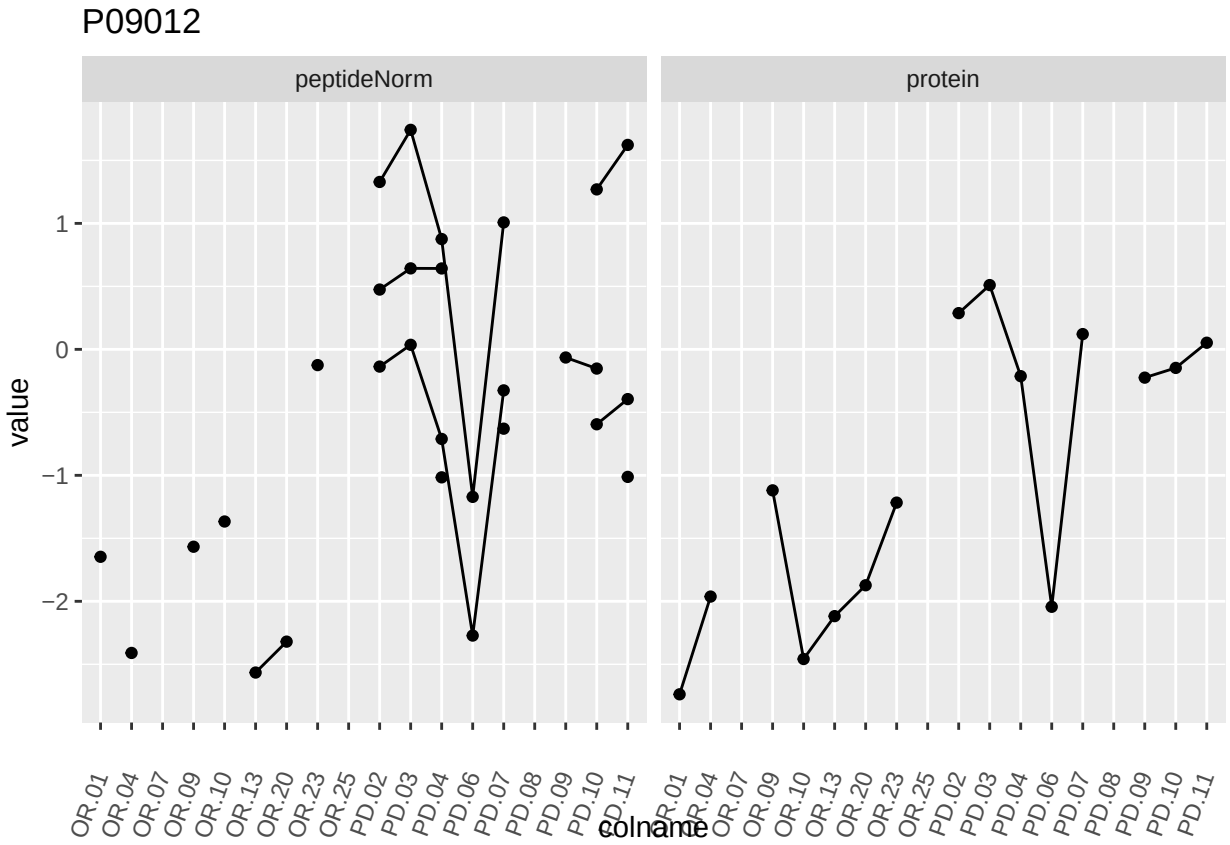
1.5
1.0
0.5
0.0
−0.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O60635
peptideNorm
protein
peptide intensity (log2)
2.0
1.5
1.0
0.5
0.0
−0.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
O60635
VEGCFNQLLYDIR


P09012
peptideNorm
protein
value
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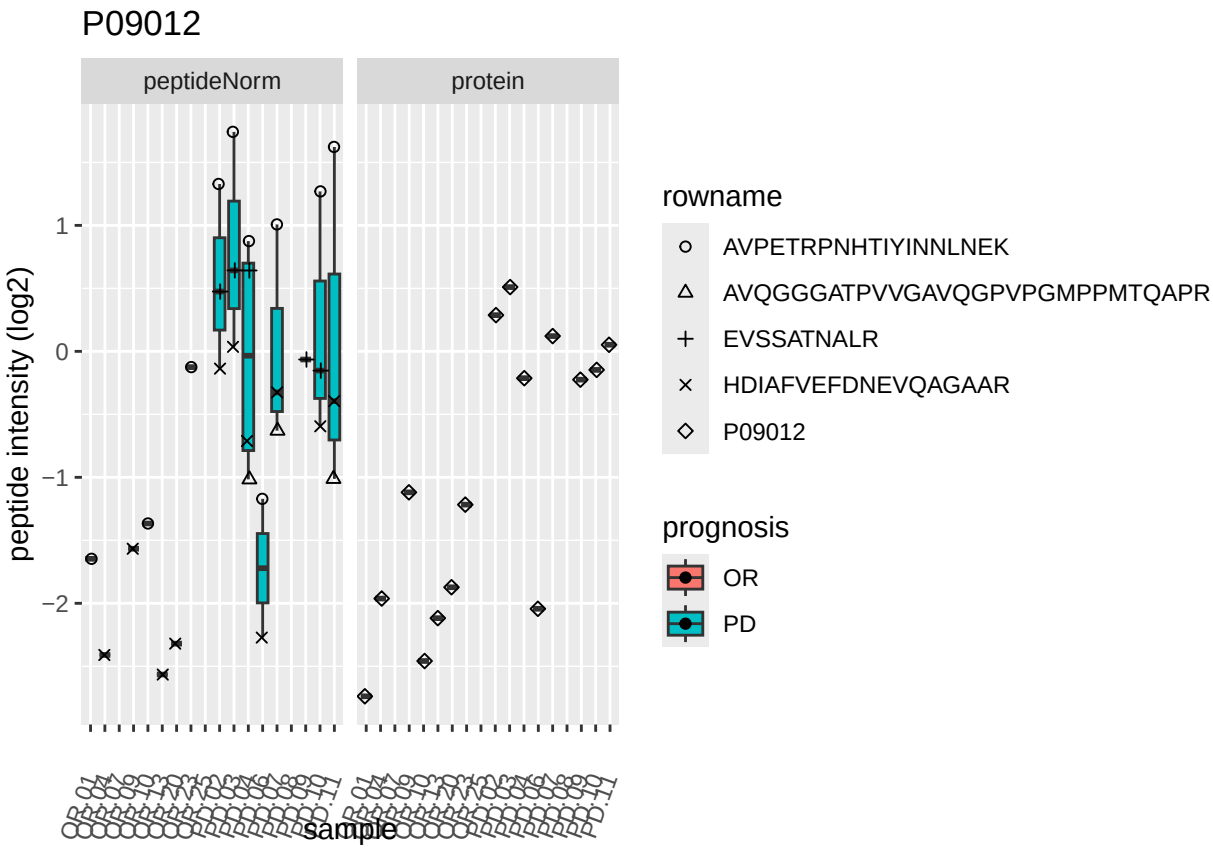
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P09012
peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
sample
rowname
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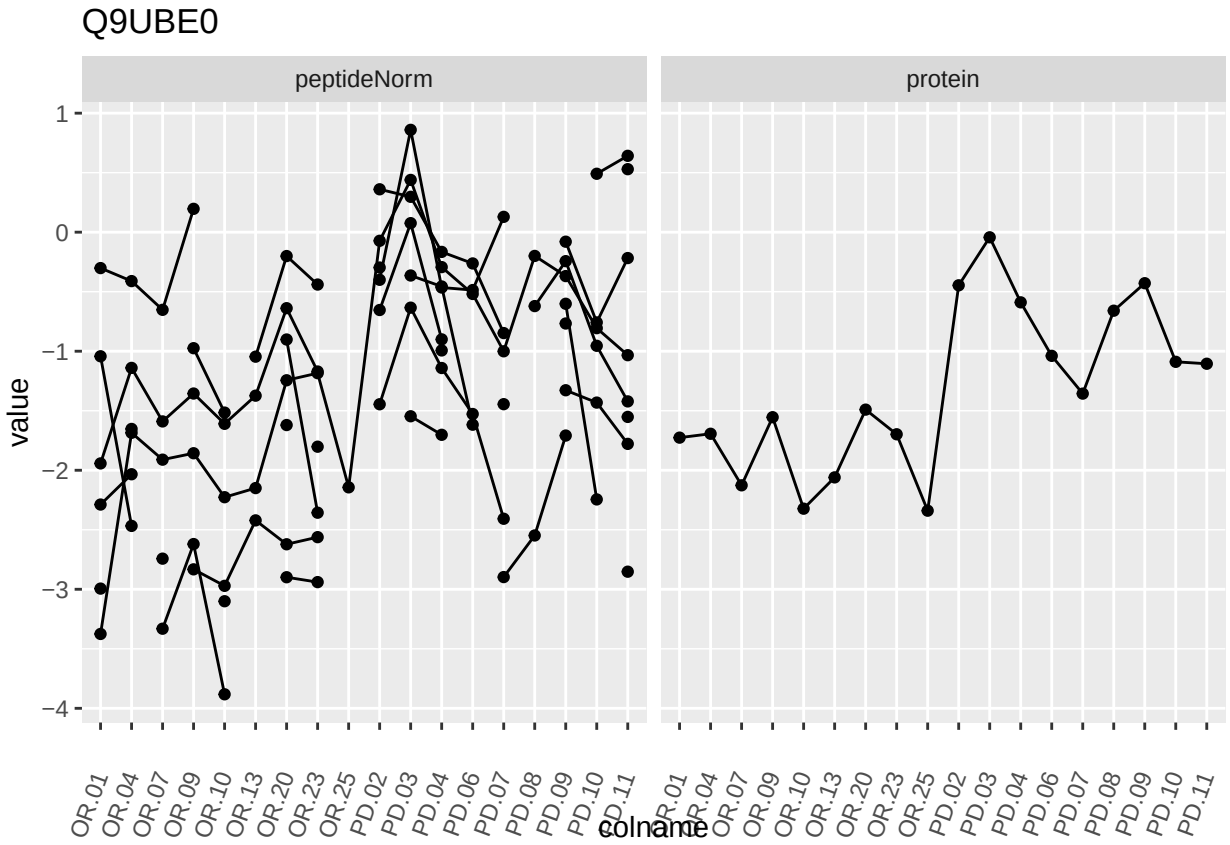
AVQGGGATPVVGAVQGPVPGMPPMTQAPR
EVSSATNALR
HDIAFVEFDNEVQAGAAR
P09012
prognosis
OR
PD


Q9UBE0
peptideNorm
protein
value
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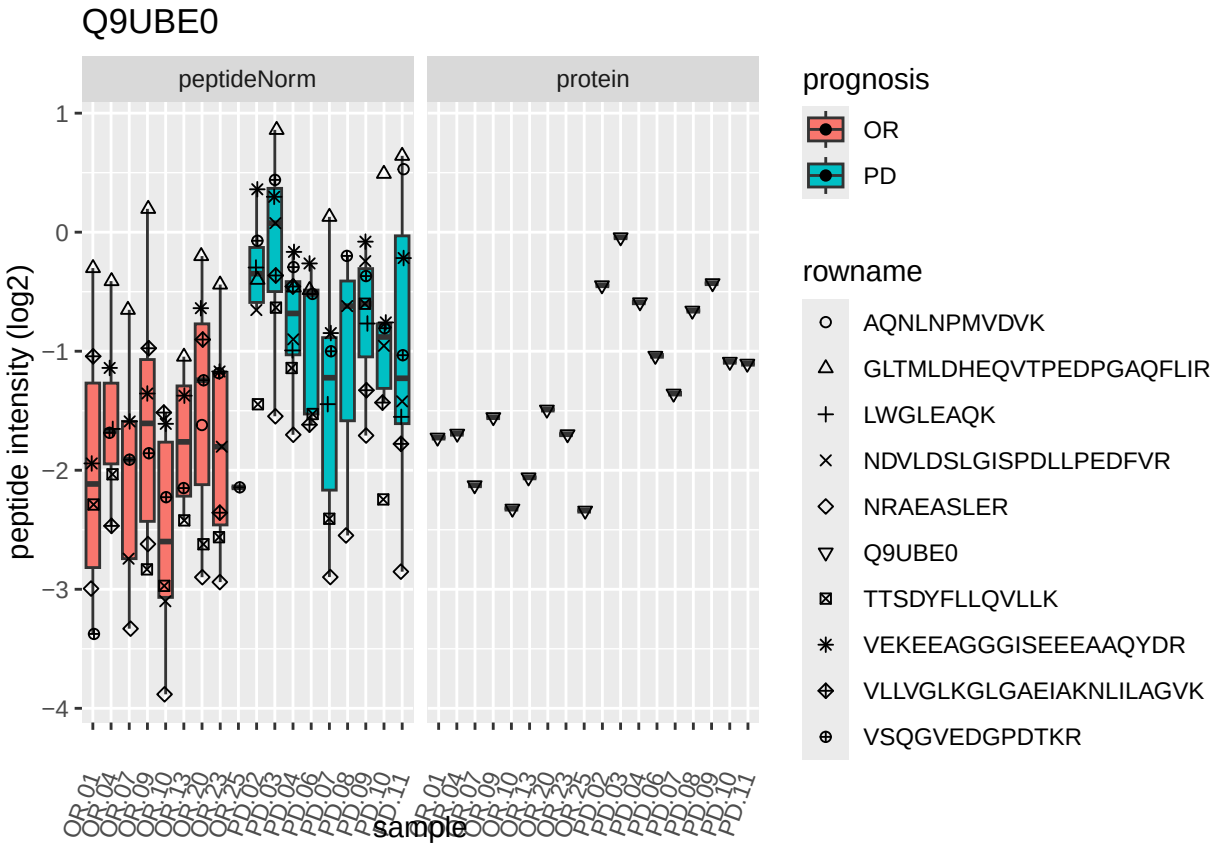
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
AQNLNPMVDVK
GLTMLDHEQVTPEDPGAQFLIR
LWGLEAQK
NDVLDSLGISPDLLPEDFVR
NRAEASLER
Q9UBE0
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VEKEEAGGGISEEEAAQYDR
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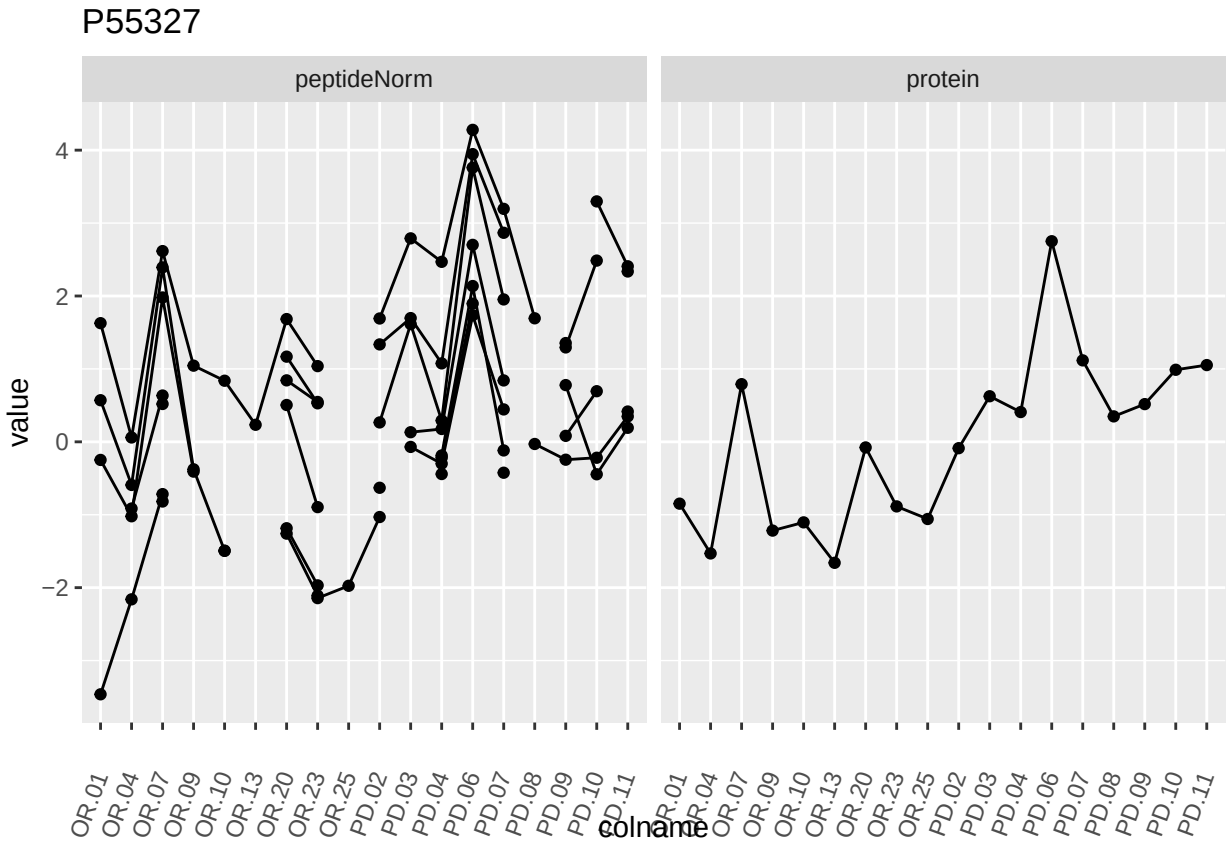
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peptideNorm
protein
value
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2
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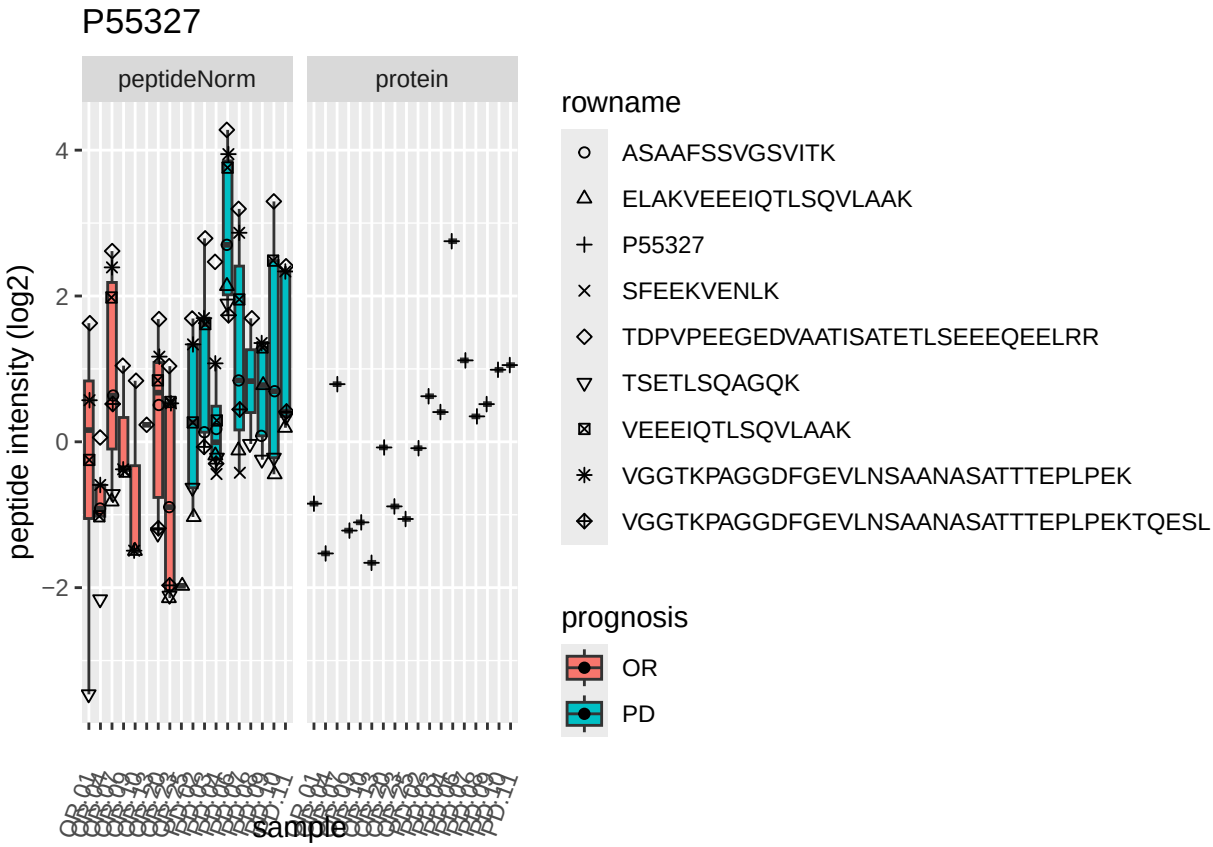
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P55327
peptideNorm
protein
peptide intensity (log2)
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2
0
−2
sample
rowname
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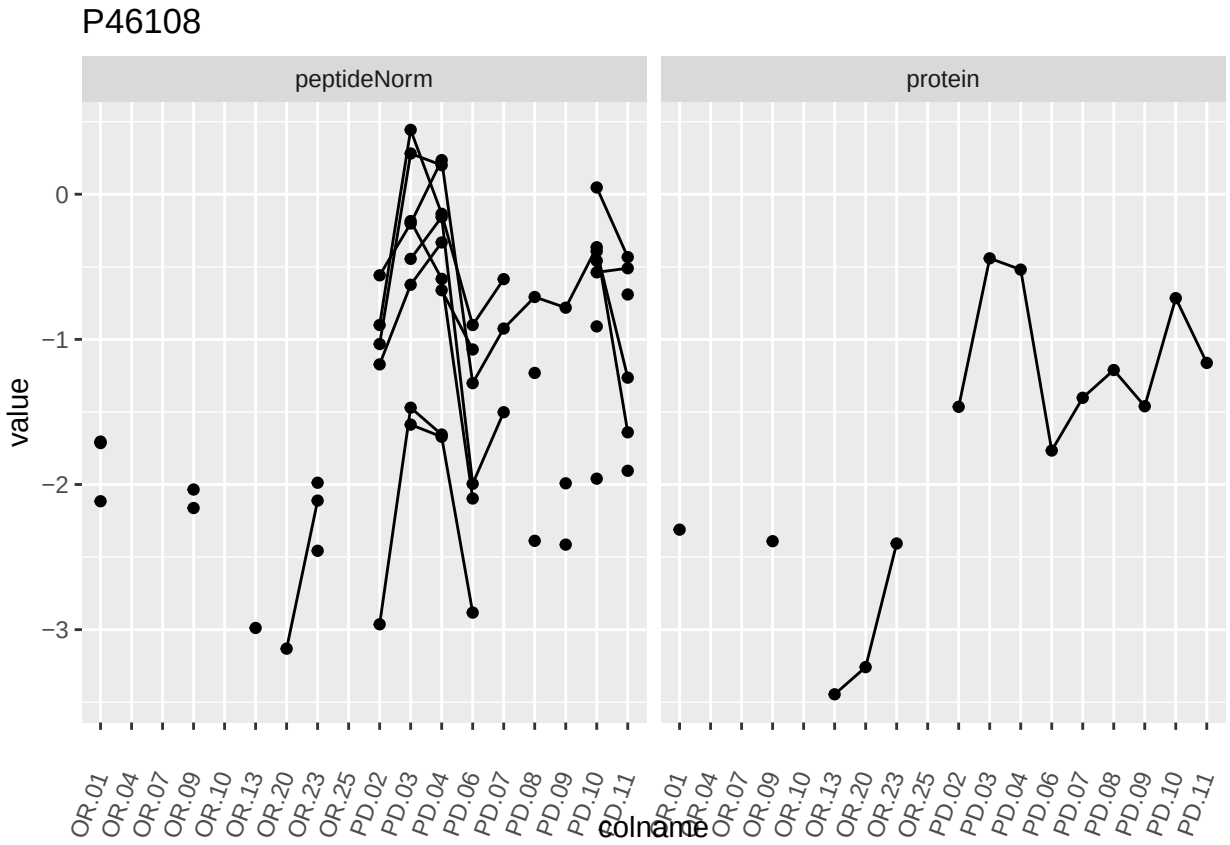
ELAKVEEEIQTLSQVLAAK
P55327
SFEEKVENLK
TDPVPEEGEDVAATISATETLSEEEQEELRR
TSETLSQAGQK
VEEEIQTLSQVLAAK
VGGTKPAGGDFGEVLNSAANASATTTEPLPEK
VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL
prognosis
OR
PD


P46108
peptideNorm
protein
value
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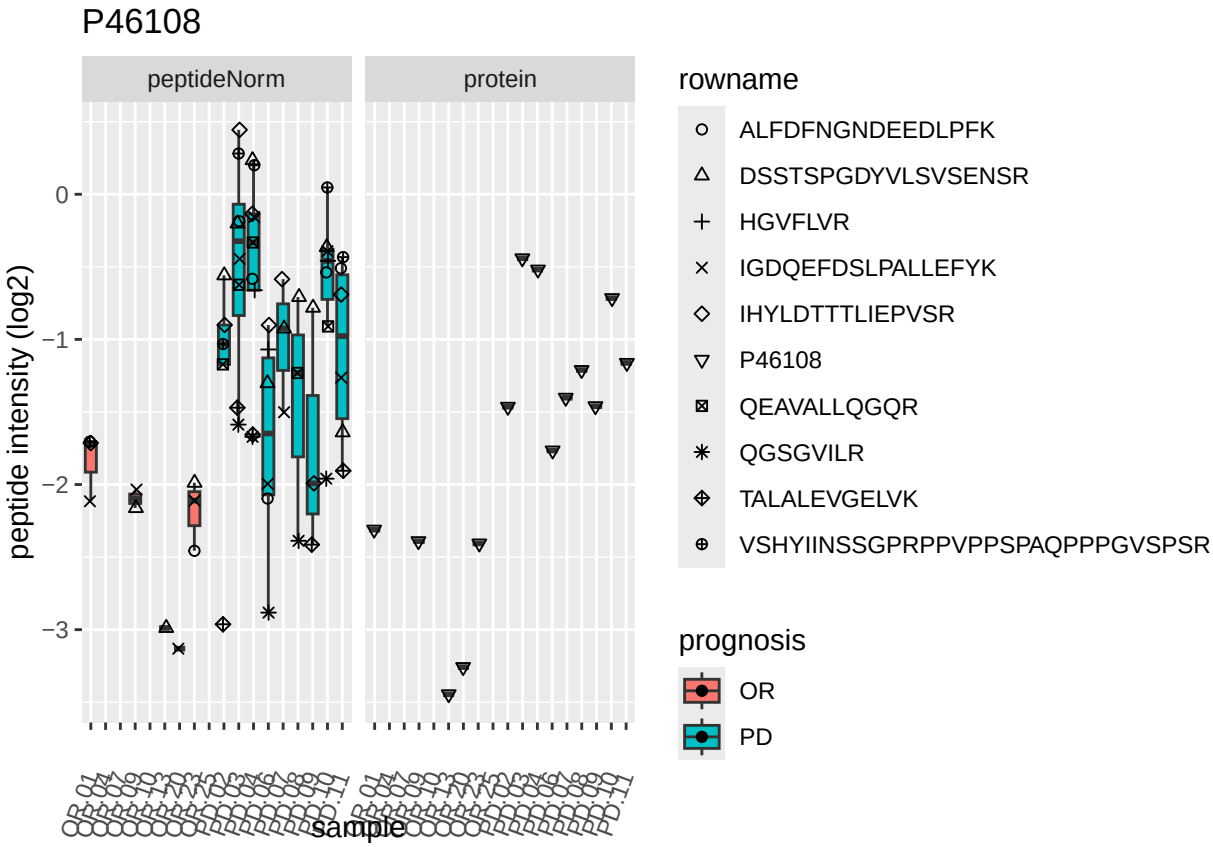
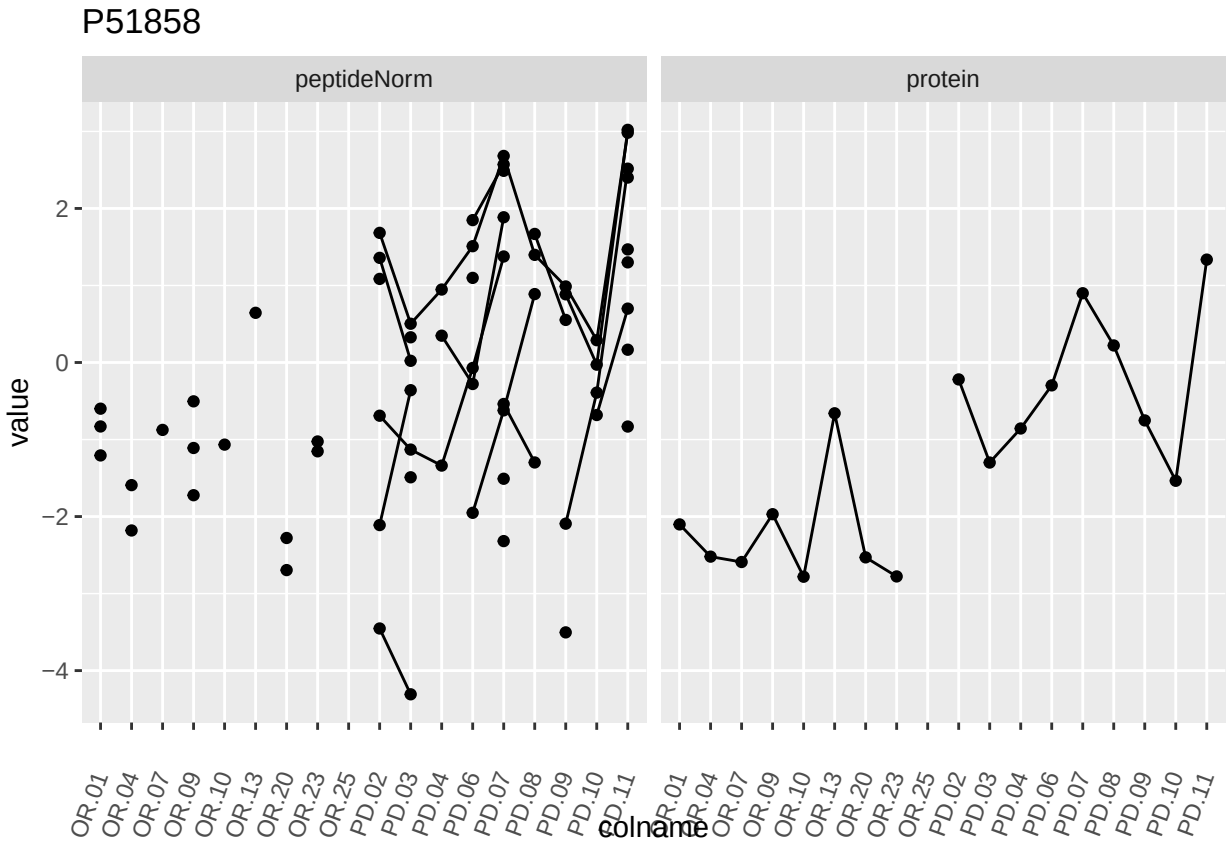
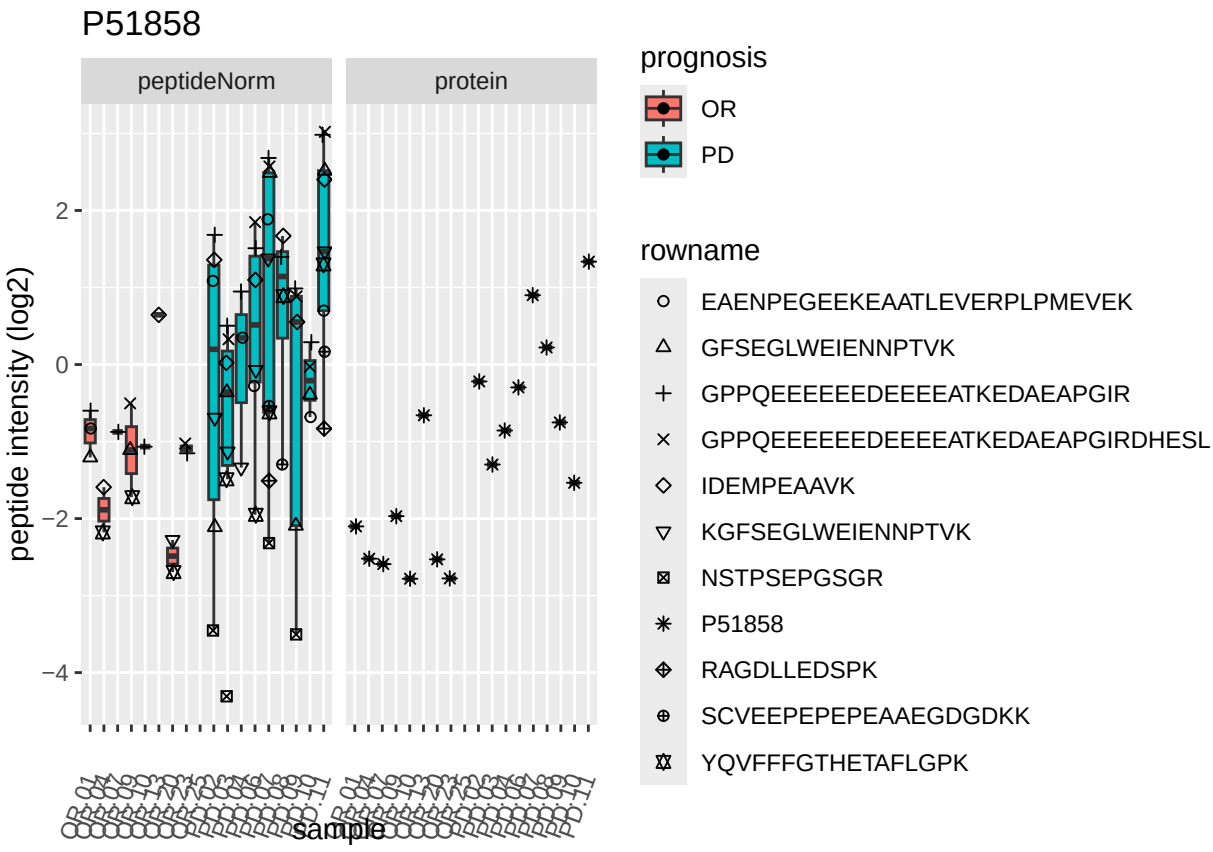
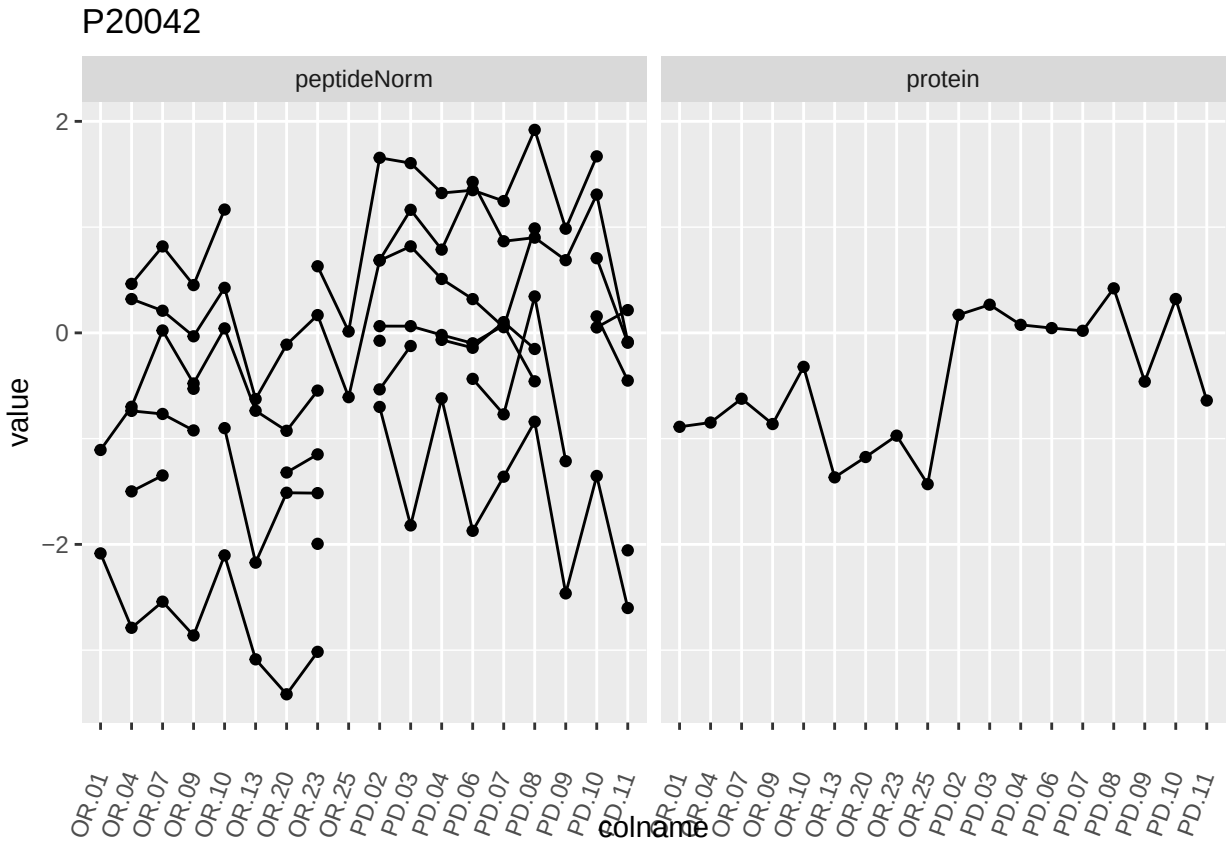
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P46108
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
rowname
ALFDFNGNDEEDLPFK
DSSTSPGDYVLSVSENSR
HGVFLVR
IGDQEFDSLPALLEFYK
IHYLDTTTLIEPVSR
P46108
QEAVALLQGQR
QGSGVILR
TALALEVGELVK
VSHYIINSSGPRPPVPPSPAQPPPGVSPSR
prognosis
OR
PD


P51858
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P51858
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
prognosis
OR
PD
rowname
EAENPEGEEKEAATLEVERPLPMEVEK
GFSEGLWEIENNPTVK
GPPQEEEEEEDEEEEATKEDAEAPGIR
GPPQEEEEEEDEEEEATKEDAEAPGIRDHESL
IDEMPEAAVK
KGFSEGLWEIENNPTVK
NSTPSEPGSGR
P51858
RAGDLLEDSPK
SCVEEPEPEPEAAEGDGDKK
YQVFFFGTHETAFLGPK


P20042
peptideNorm
protein
value
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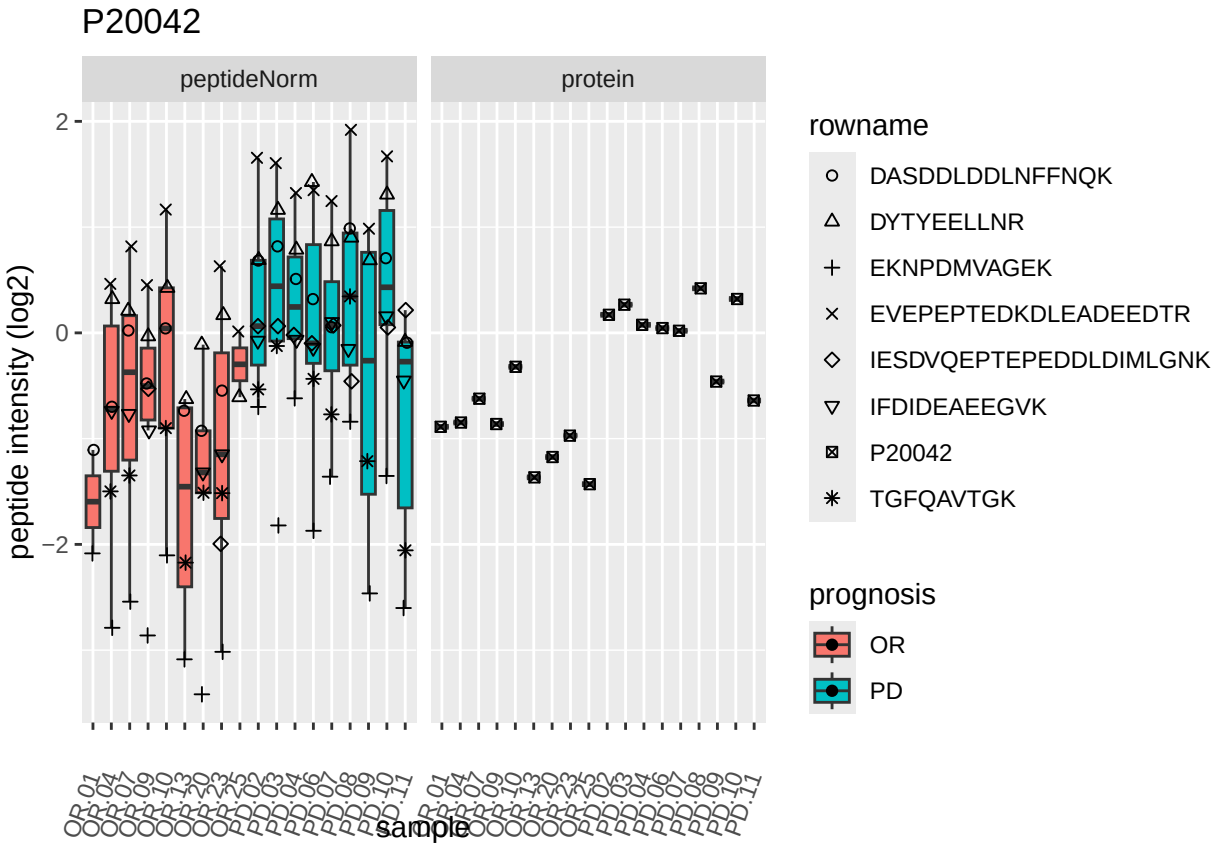
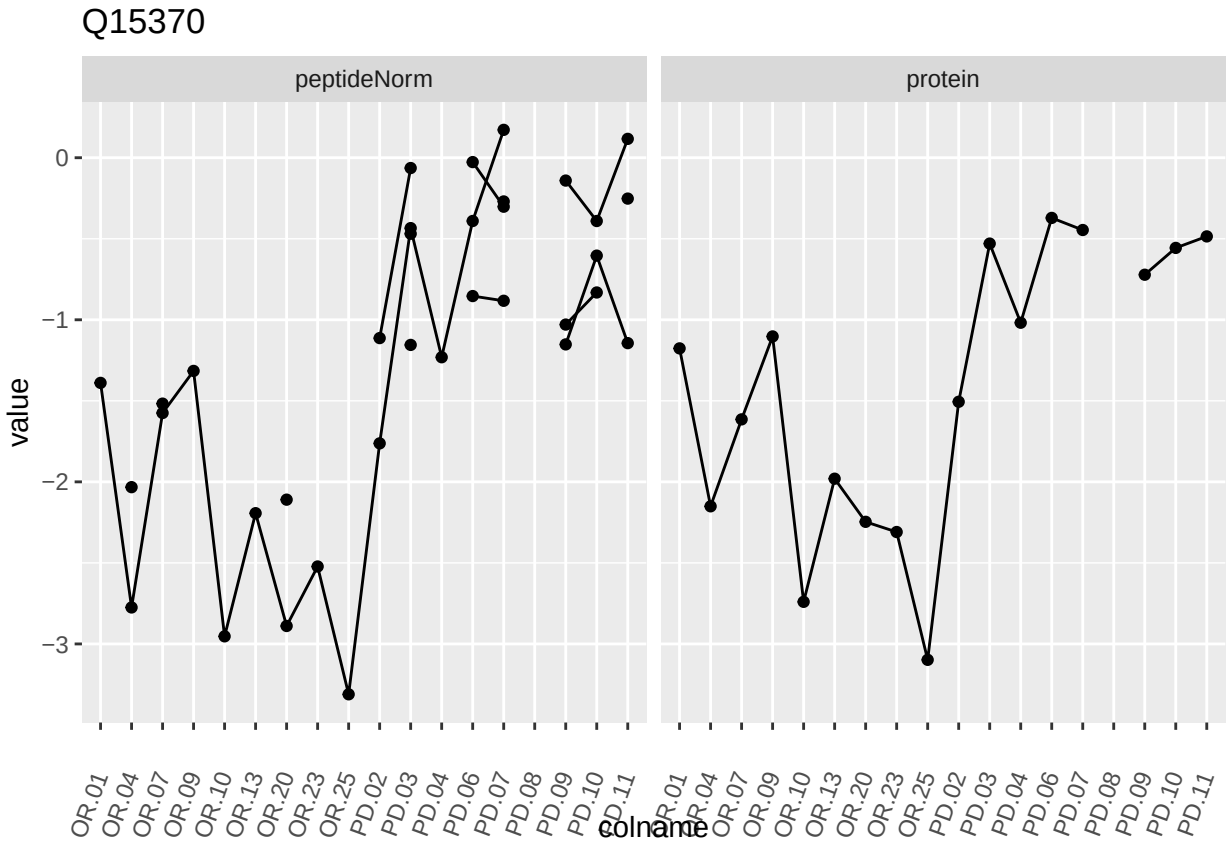
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P20042
peptideNorm
protein
peptide intensity (log2)
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
DASDDLDDLNFFNQK
DYTYEELLNR
EKNPDMVAGEK
EVEPEPTEDKDLEADEEDTR
IESDVQEPTEPEDDLDIMLGNK
IFDIDEAEEGVK
P20042
TGFQAVTGK
prognosis
OR
PD


Q15370
peptideNorm
protein
value
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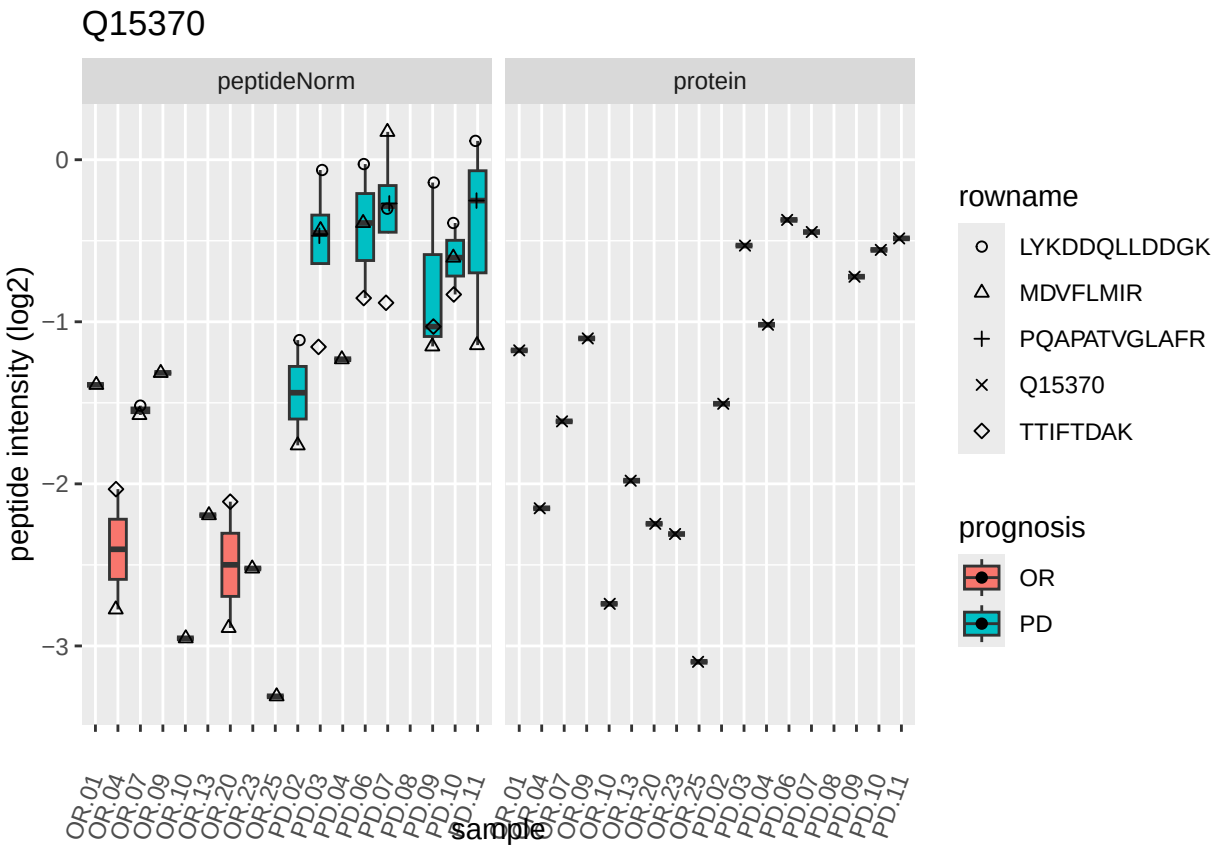
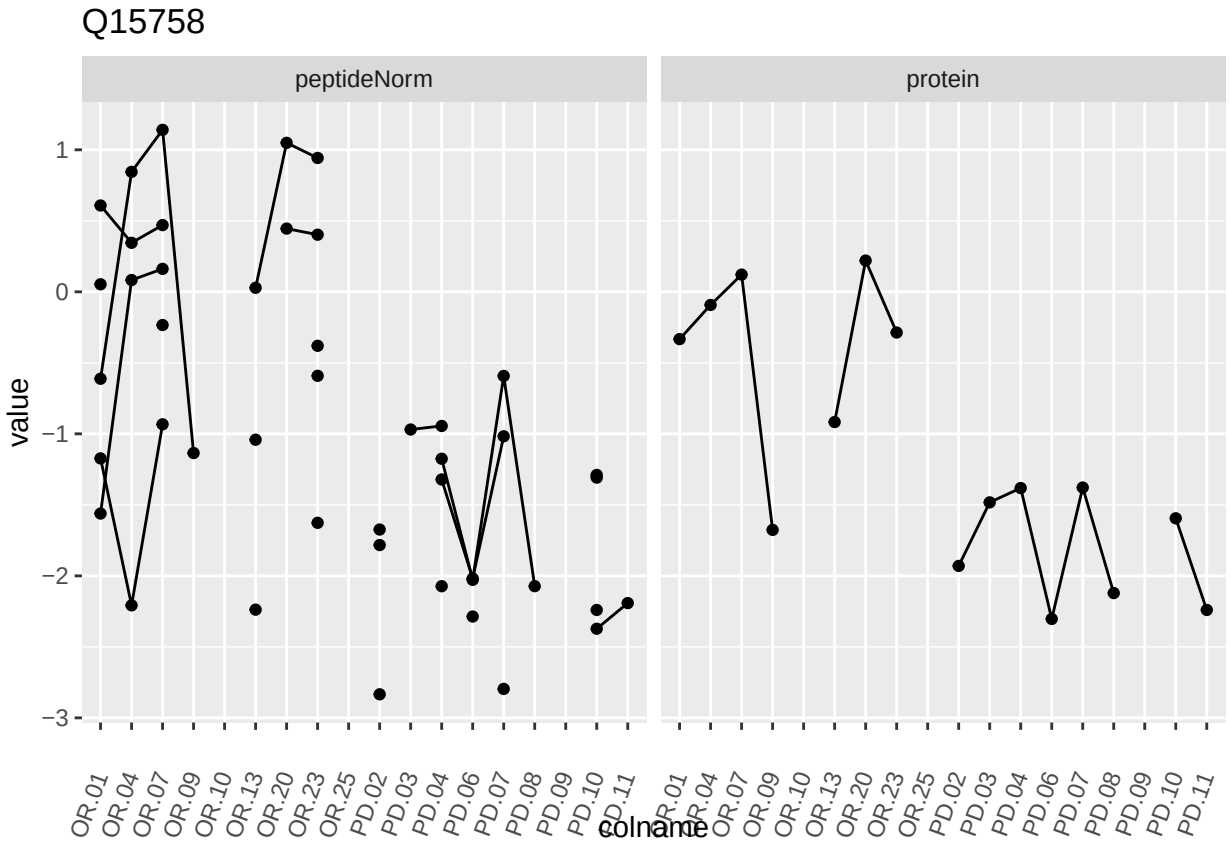
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q15370
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LYKDDQLLDDGK
MDVFLMIR
PQAPATVGLAFR
Q15370
TTIFTDAK
prognosis
OR
PD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peptideNorm
protein
value
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−3
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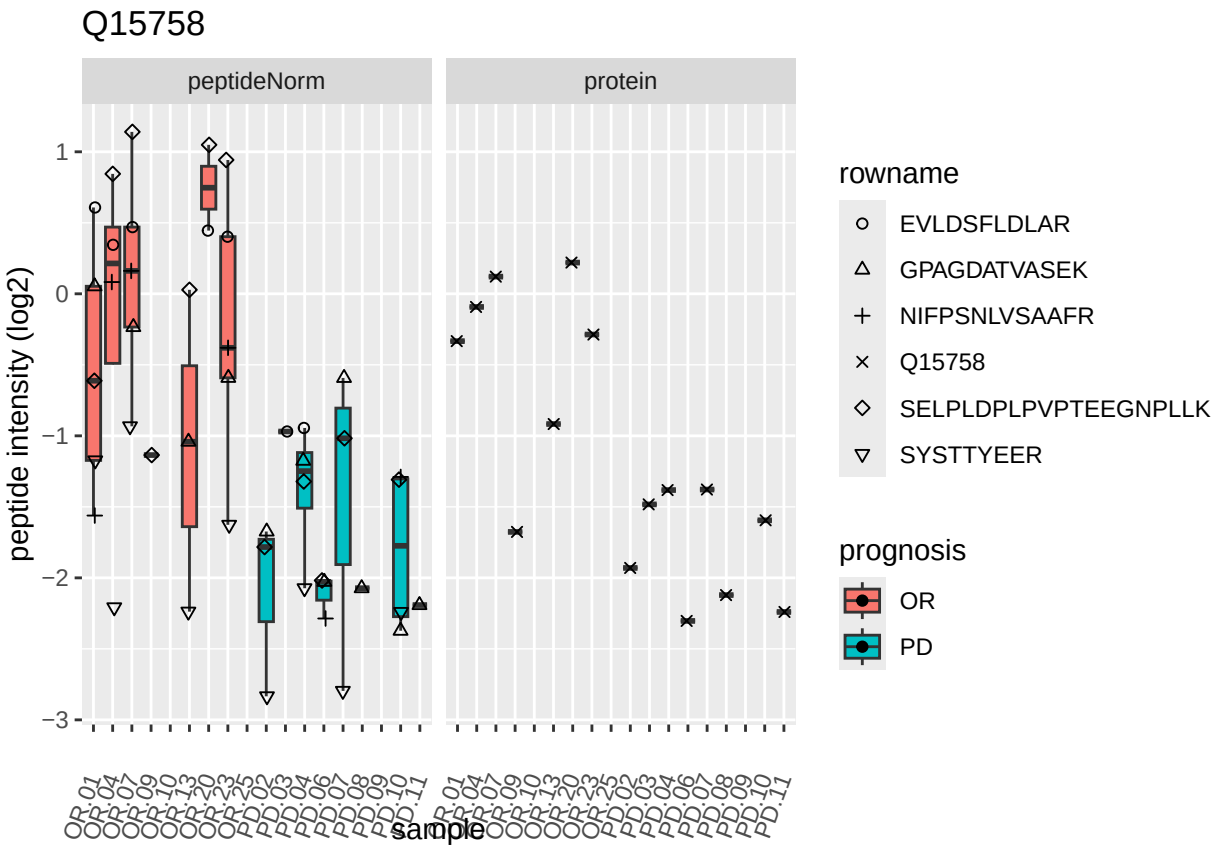
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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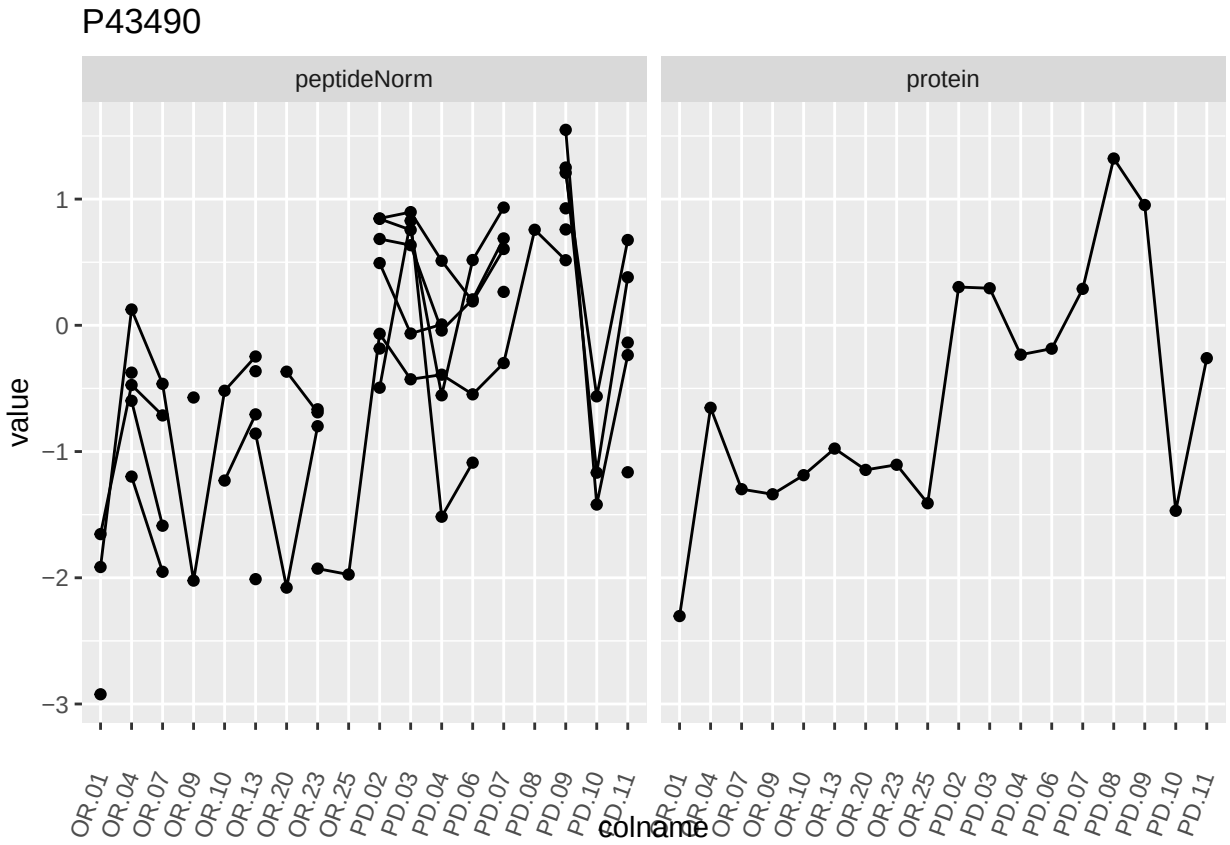
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EVLDSFLDLAR
GPAGDATVASEK
NIFPSNLVSAAFR
Q15758
SELPLDPLPVPTEEGNPLLK
SYSTTYEER
prognosis
OR
PD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peptideNorm
protein
value
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−2
−3
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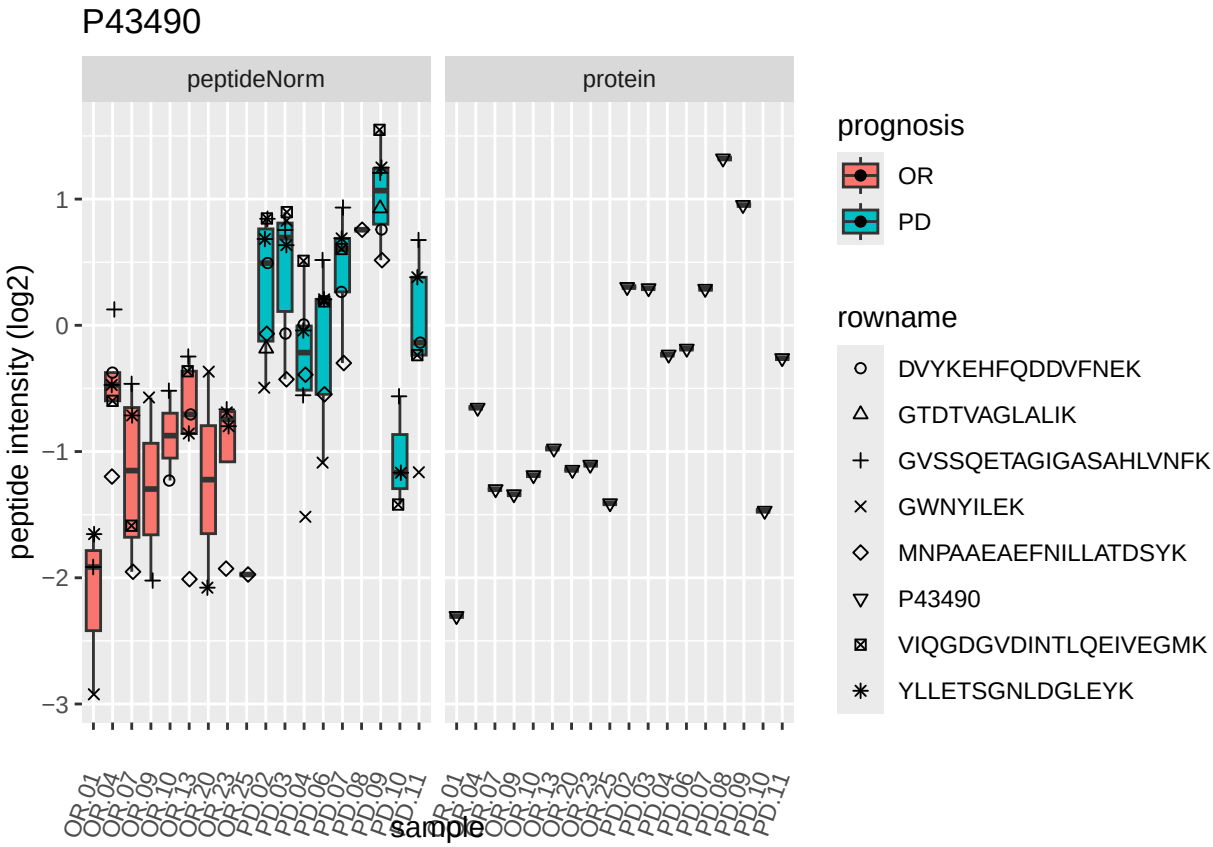
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
DVYKEHFQDDVFNEK
GTDTVAGLALIK
GVSSQETAGIGASAHLVNFK
GWNYILEK
MNPAAEAEFNILLATDSYK
P43490
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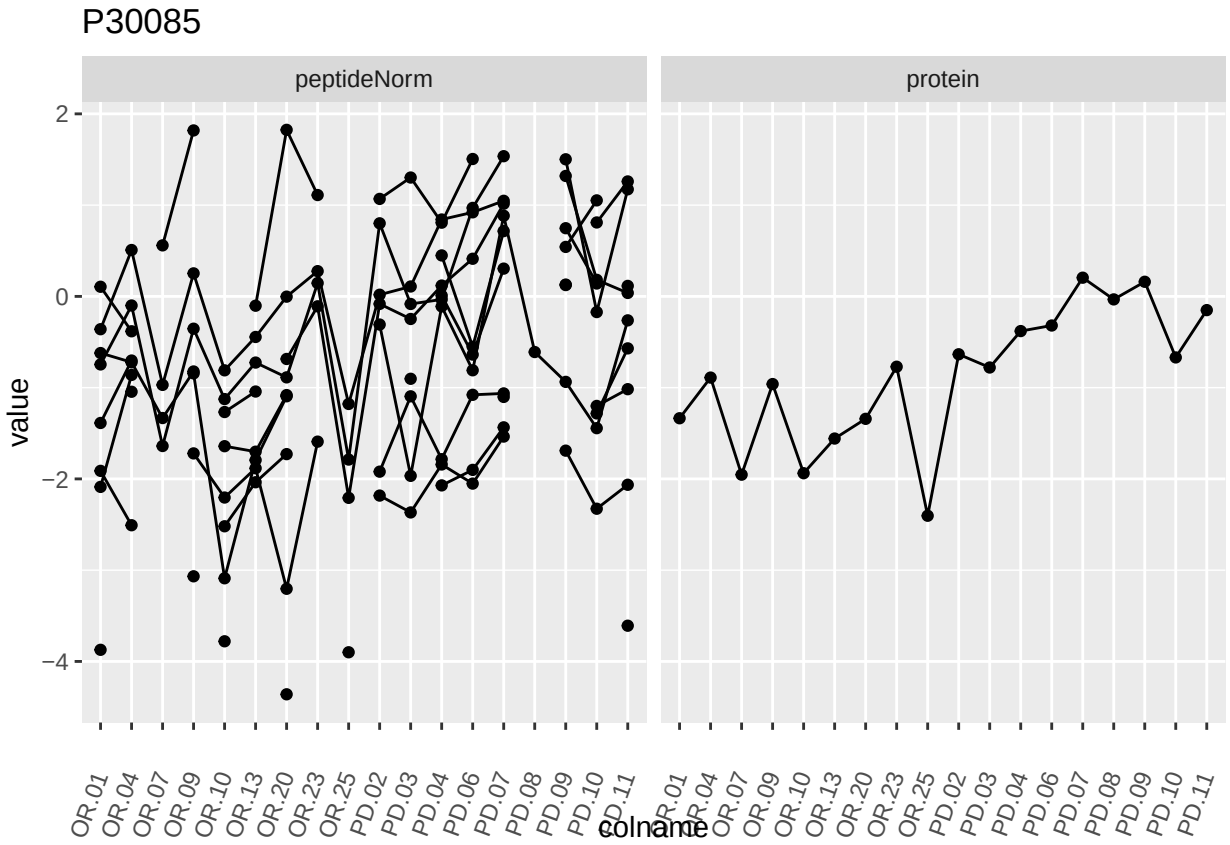
YLLETSGNLDGLEYK


P30085
peptideNorm
protein
value
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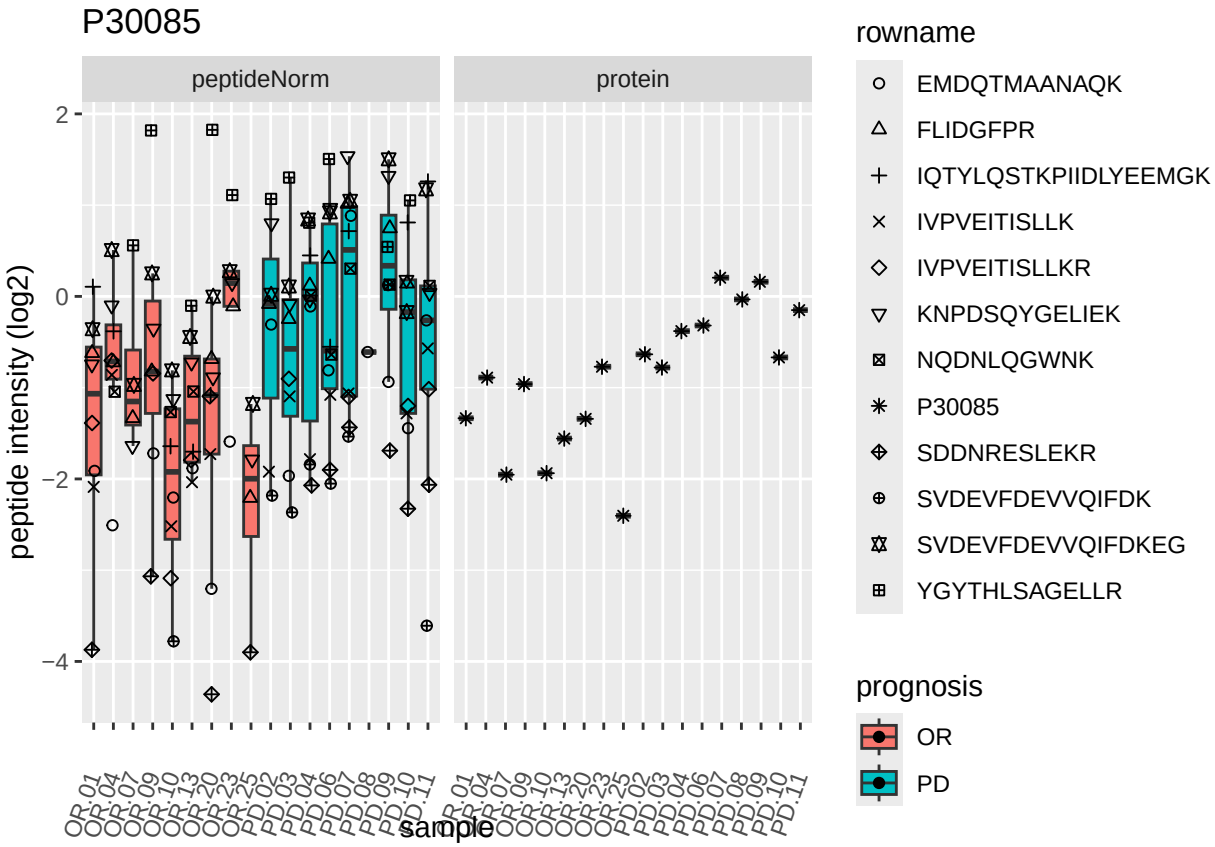
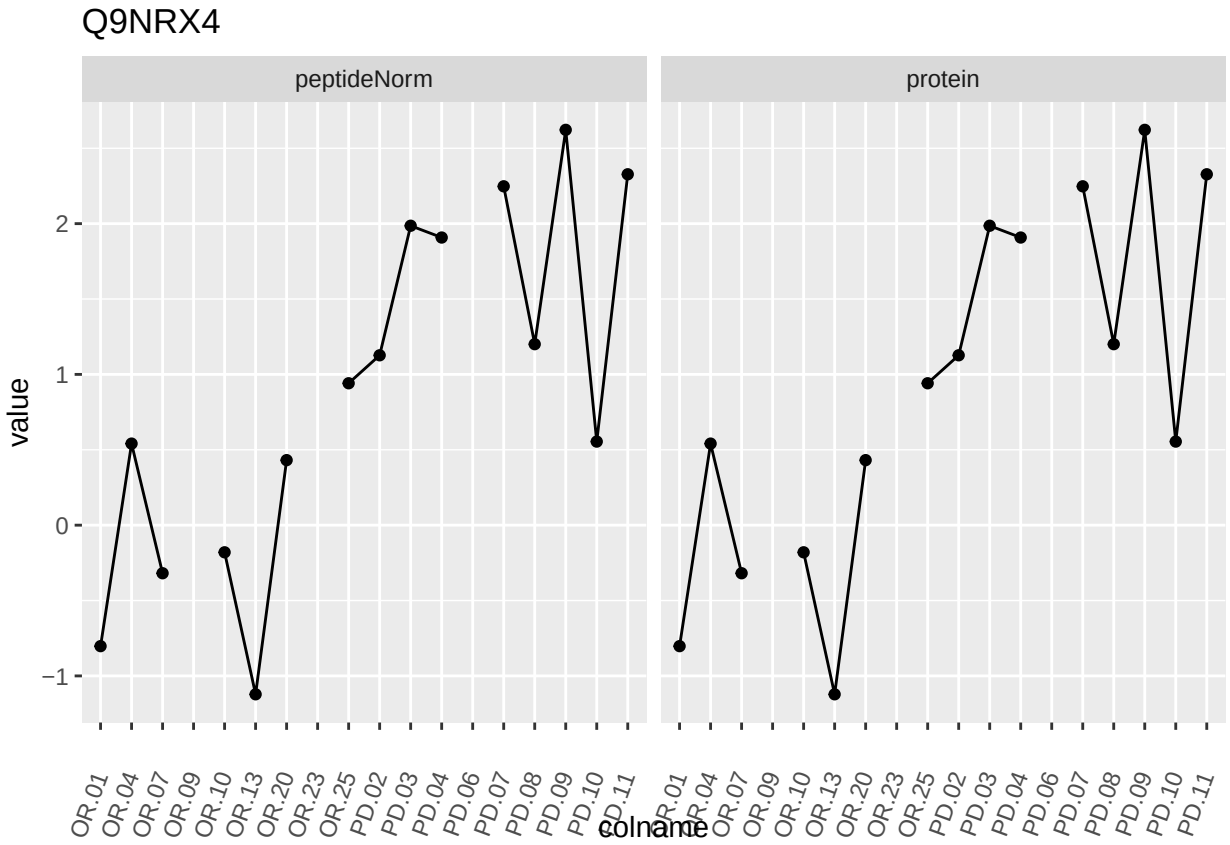
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P30085
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EMDQTMAANAQK
FLIDGFPR
IQTYLQSTKPIIDLYEEMGK
IVPVEITISLLK
IVPVEITISLLKR
KNPDSQYGELIEK
NQDNLQGWNK
P30085
SDDNRESLEKR
SVDEVFDEVVQIFDK
SVDEVFDEVVQIFDKEG
YGYTHLSAGELLR
prognosis
OR
PD


Q9NRX4
peptideNorm
protein
value
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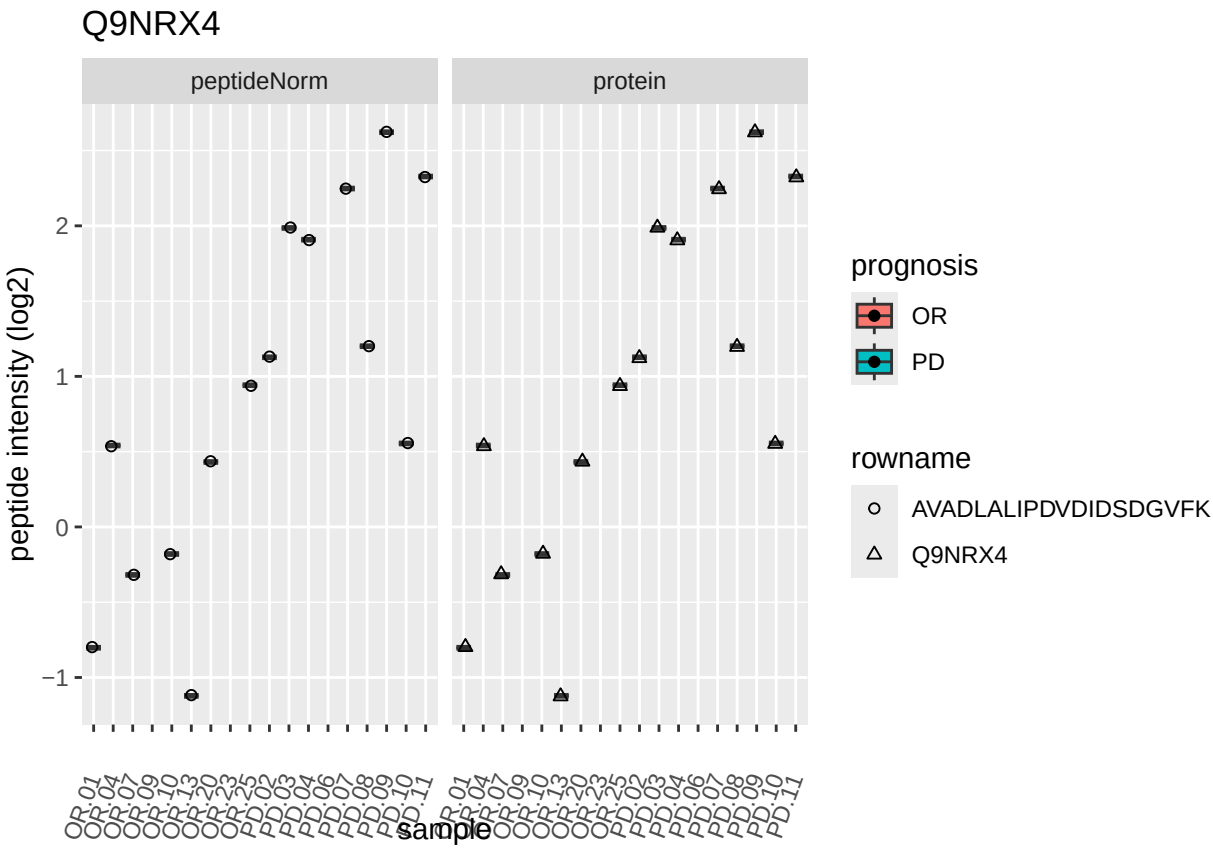
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NRX4
peptideNorm
protein
peptide intensity (log2)
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1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
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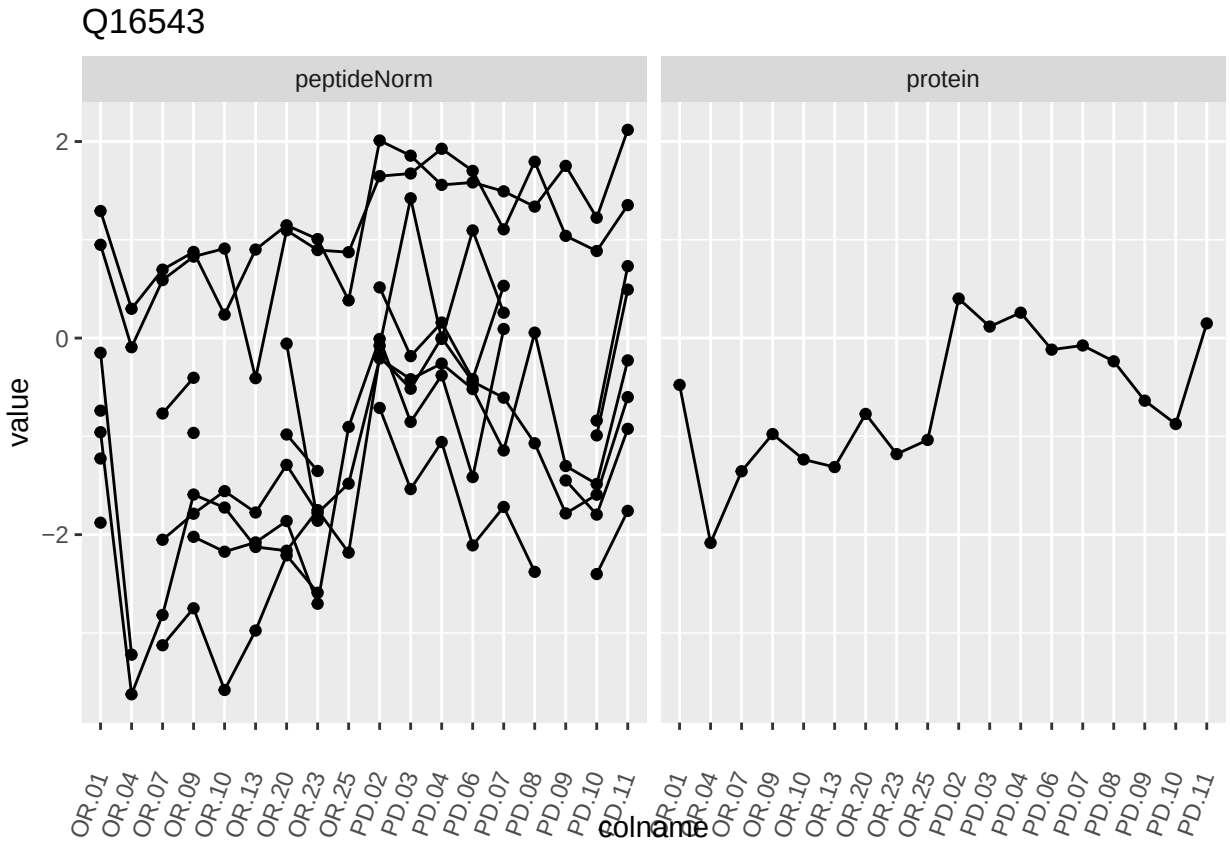
Q9NRX4


Q16543
peptideNorm
protein
value
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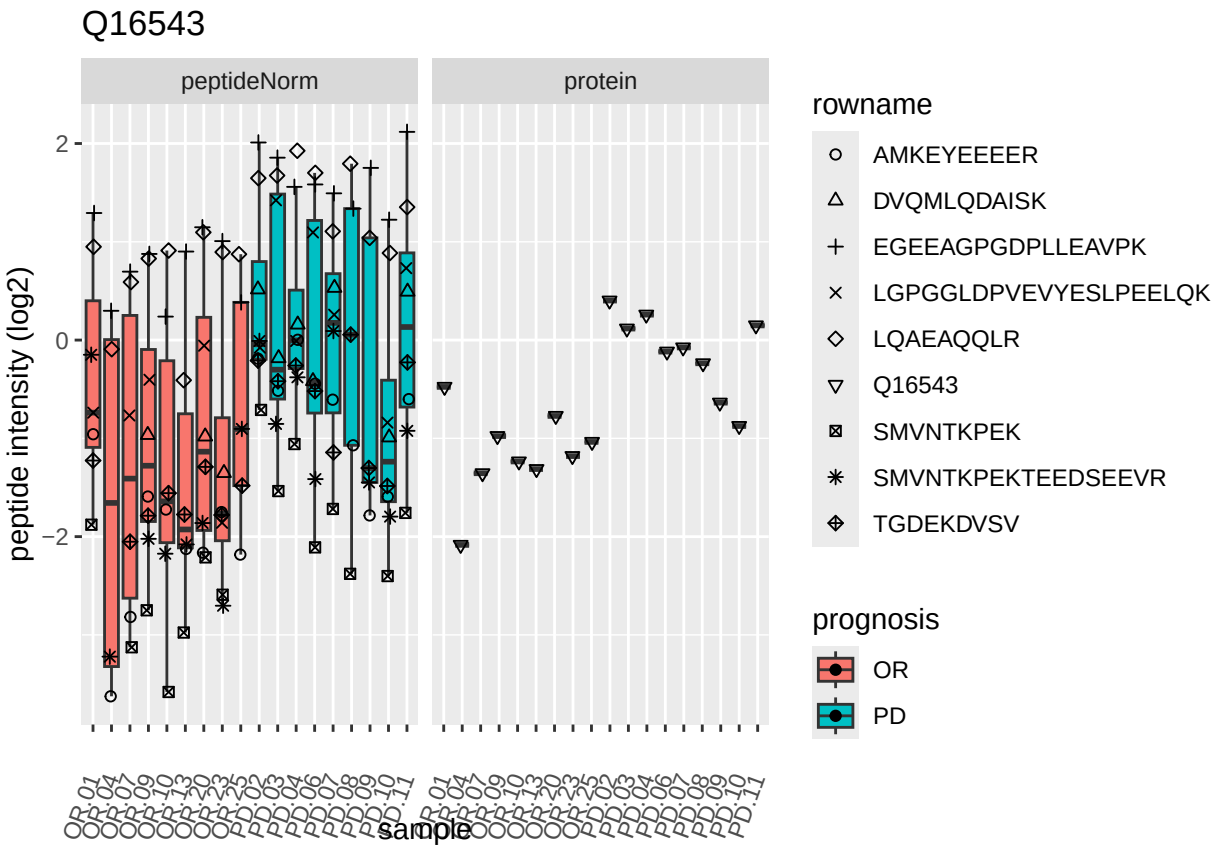
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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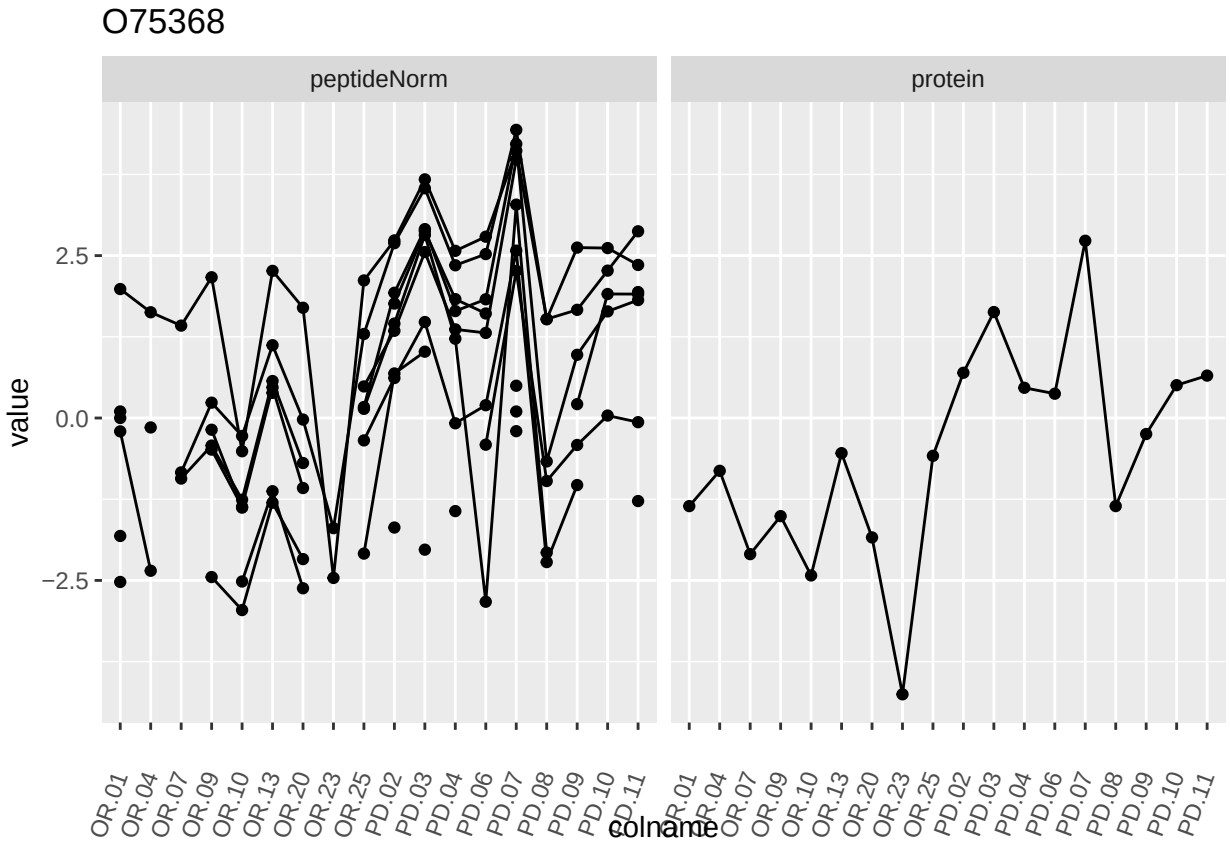
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AMKEYEEEER
DVQMLQDAISK
EGEEAGPGDPLLEAVPK
LGPGGLDPVEVYESLPEELQK
LQAEAQQLR
Q16543
SMVNTKPEK
SMVNTKPEKTEEDSEEVR
TGDEKDVSV
prognosis
OR
PD


O75368
peptideNorm
protein
value
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−2.5
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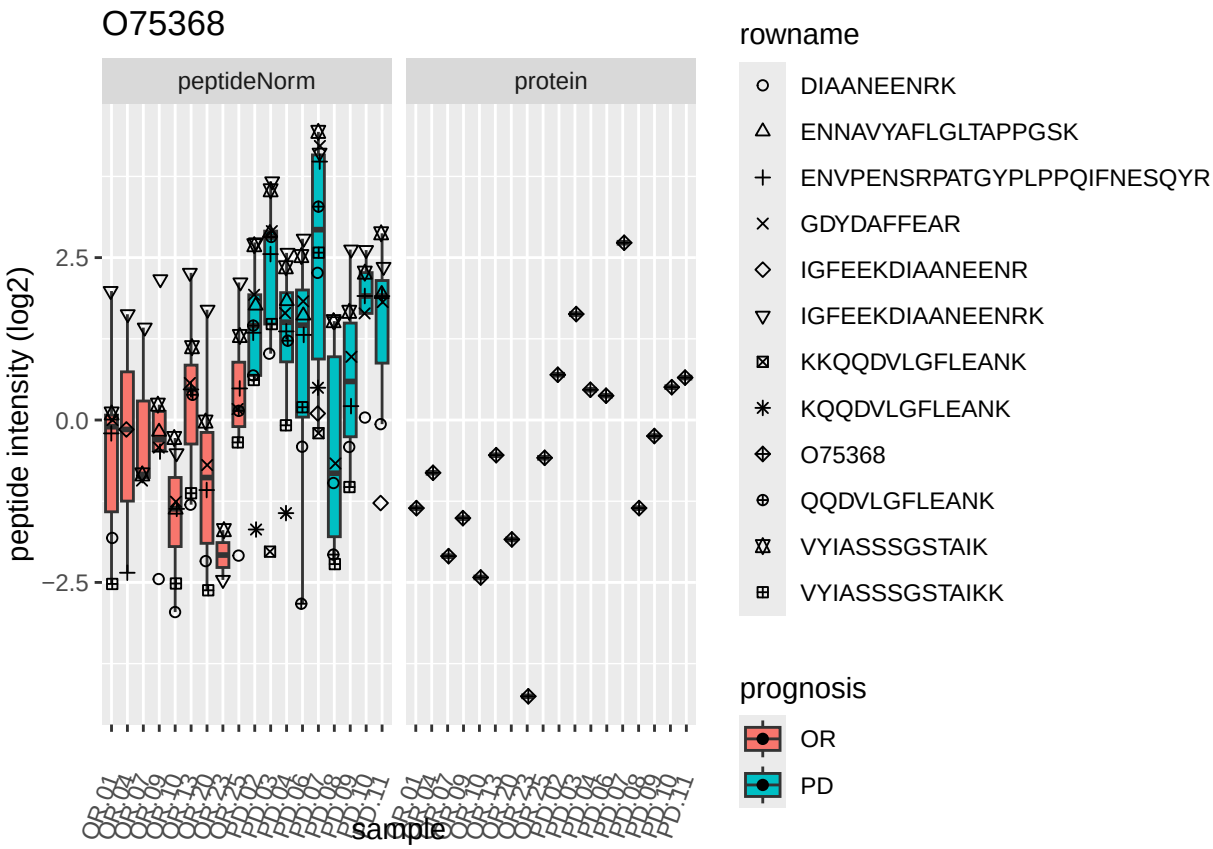
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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0.0
−2.5
sample
rowname
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ENNAVYAFLGLTAPPGSK
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GDYDAFFEAR
IGFEEKDIAANEENR
IGFEEKDIAANEENRK
KKQQDVLGFLEANK
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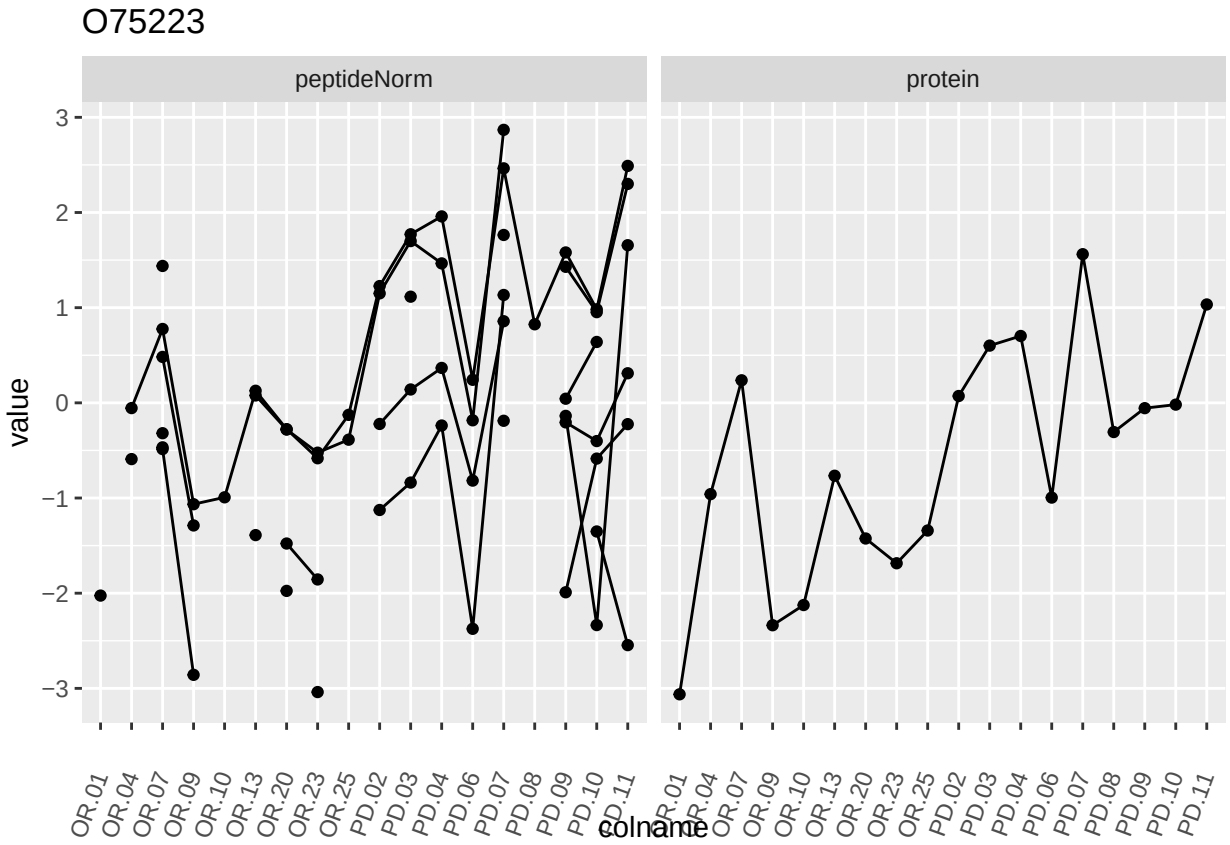
O75368
QQDVLGFLEANK
VYIASSSGSTAIK
VYIASSSGSTAIKK
prognosis
OR
PD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protein
value
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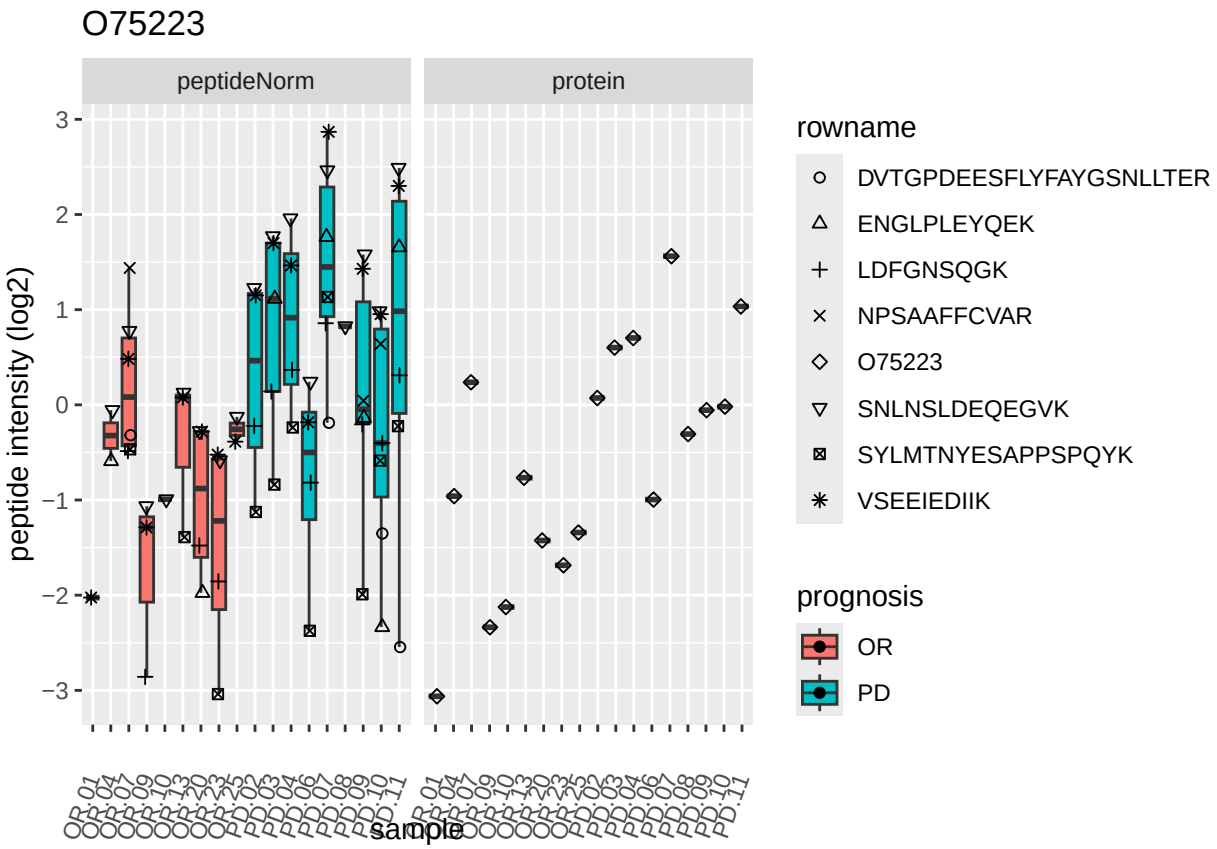
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O75223
peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
OR:01
OR:04
OR:07
OR:09
OR:10
OR:13
OR:20
OR:23
OR:25
PD:02
PD:03
PD:04
PD:06
PD:07
PD:08
PD:09
PD:10
PD:11
sample
rowname
DVTGPDEESFLYFAYGSNLLTER
ENGLPLEYQEK
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O75223
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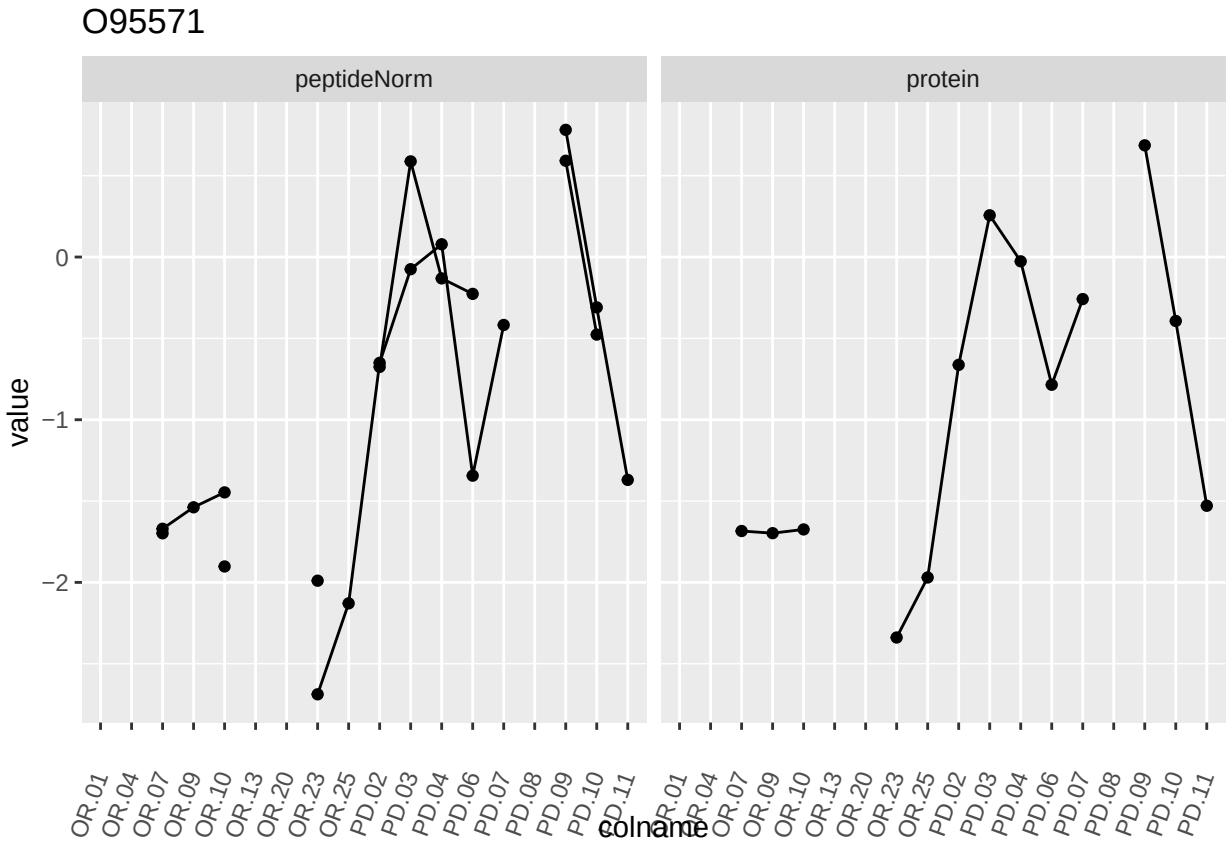
prognosis
OR
PD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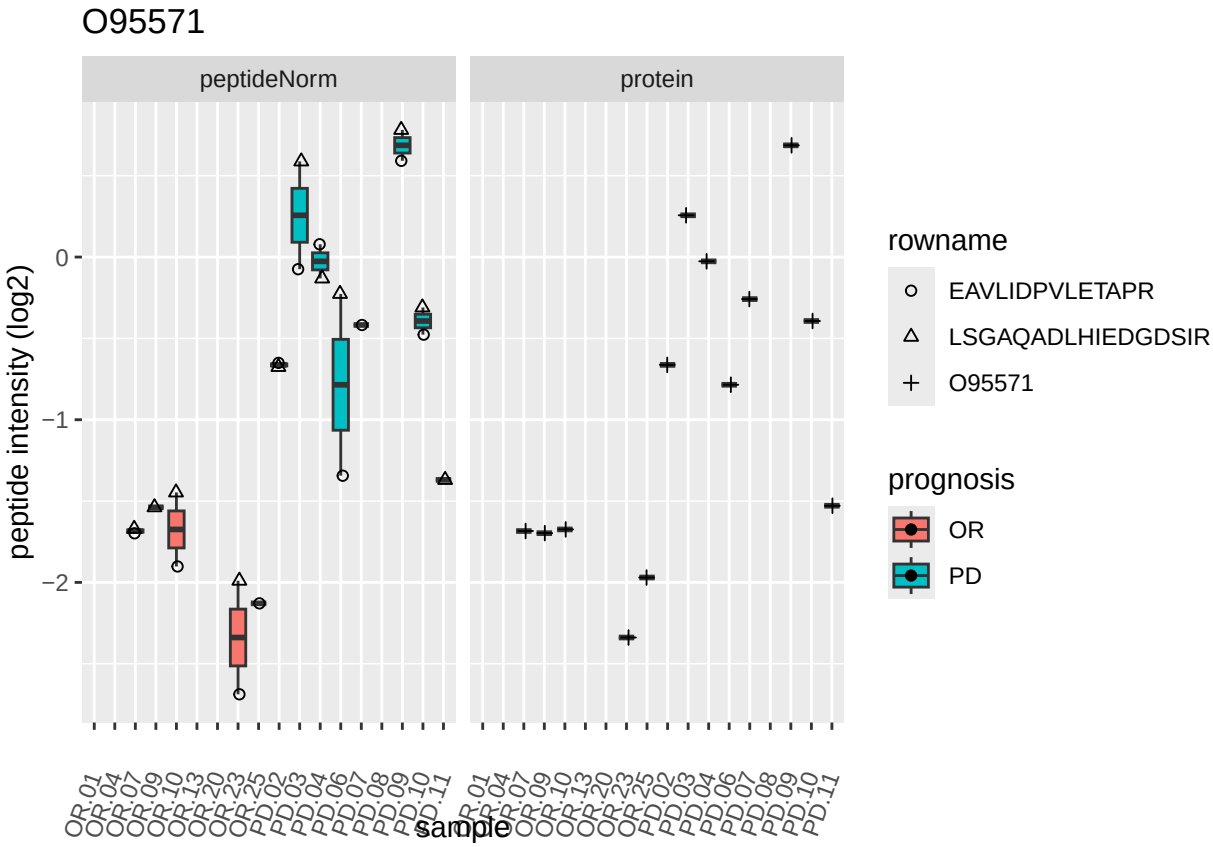
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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−1
−2
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OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EAVLIDPVLETAPR
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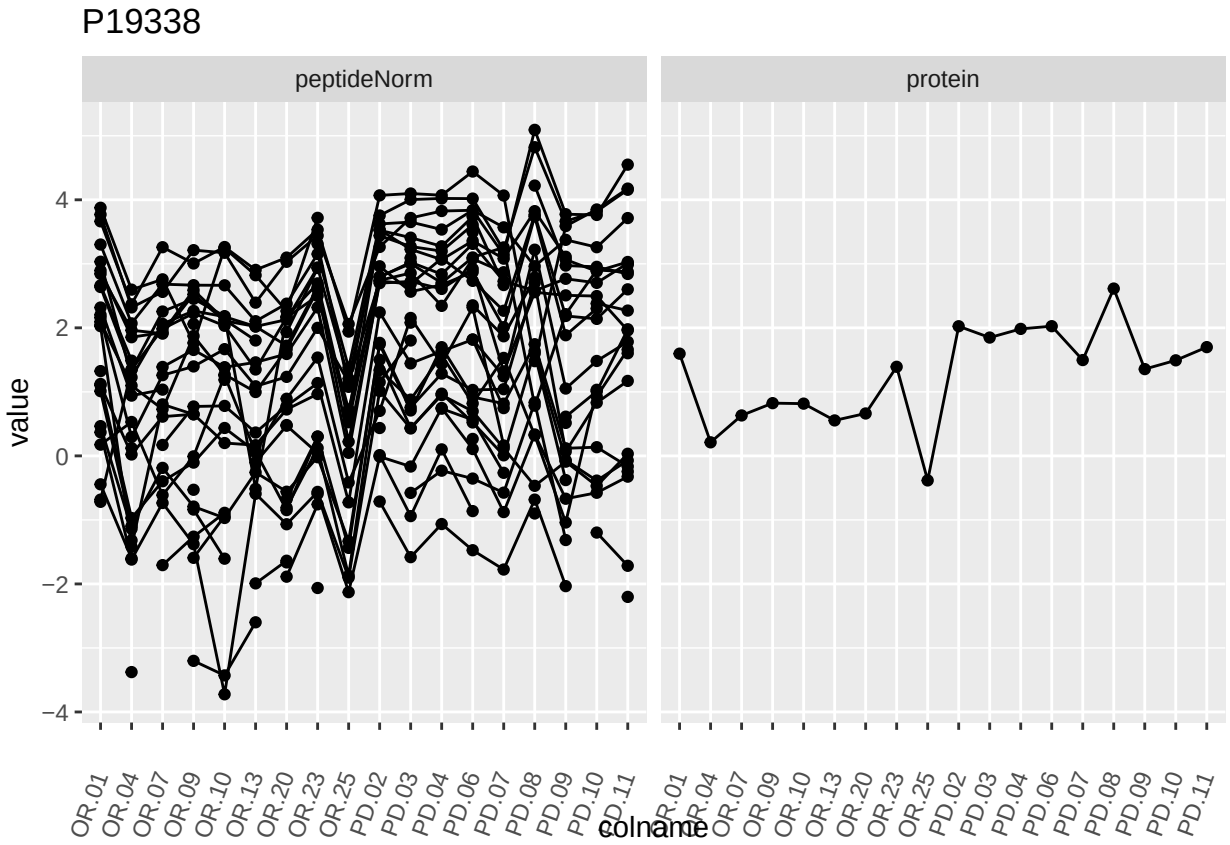
O95571
prognosis
OR
PD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peptideNorm
protein
value
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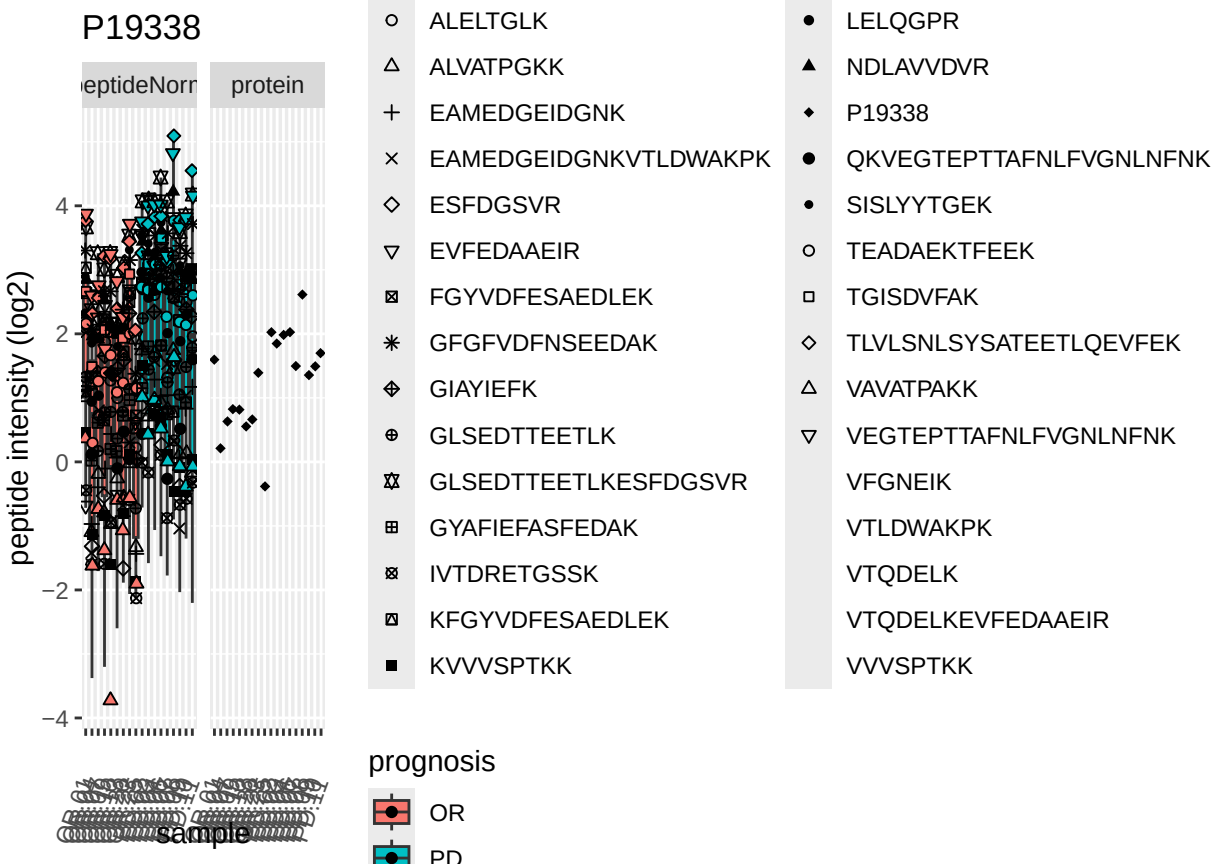
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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eptideNorm
protein
peptide intensity (log2)
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2
0
−2
−4
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EAMEDGEIDGNKVTLDWAKPK
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EVFEDAAEIR
FGYVDFESAEDLEK
GFGFVDFNSEEDAK
GIAYIEFK
GLSEDTTEETLK
GLSEDTTEETLKESFDGSVR
GYAFIEFASFEDAK
IVTDRETGSSK
KFGYVDFESAEDLEK
KVVVSPTKK
LELQGPR
NDLAVVDVR
P19338
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SISLYYTGEK
TEADAEKTFEEK
TGISDVFAK
TLVLSNLSYSATEETLQEVFEK
VAVATPAKK
VEGTEPTTAFNLFVGNLNFNK
VFGNEIK
VTLDWAKPK
VTQDELK
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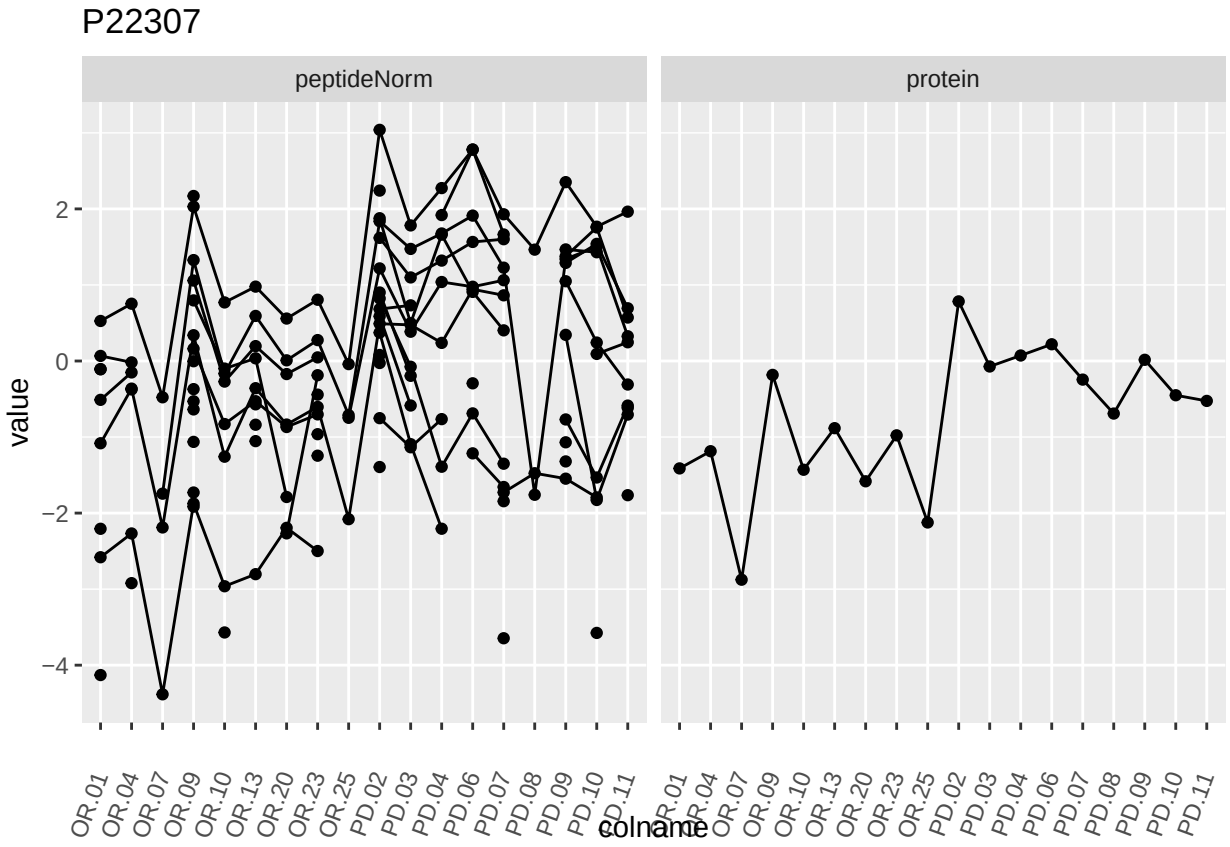
VVVSPTKK
prognosis
OR
PD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peptideNorm
protein
value
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−2
−4
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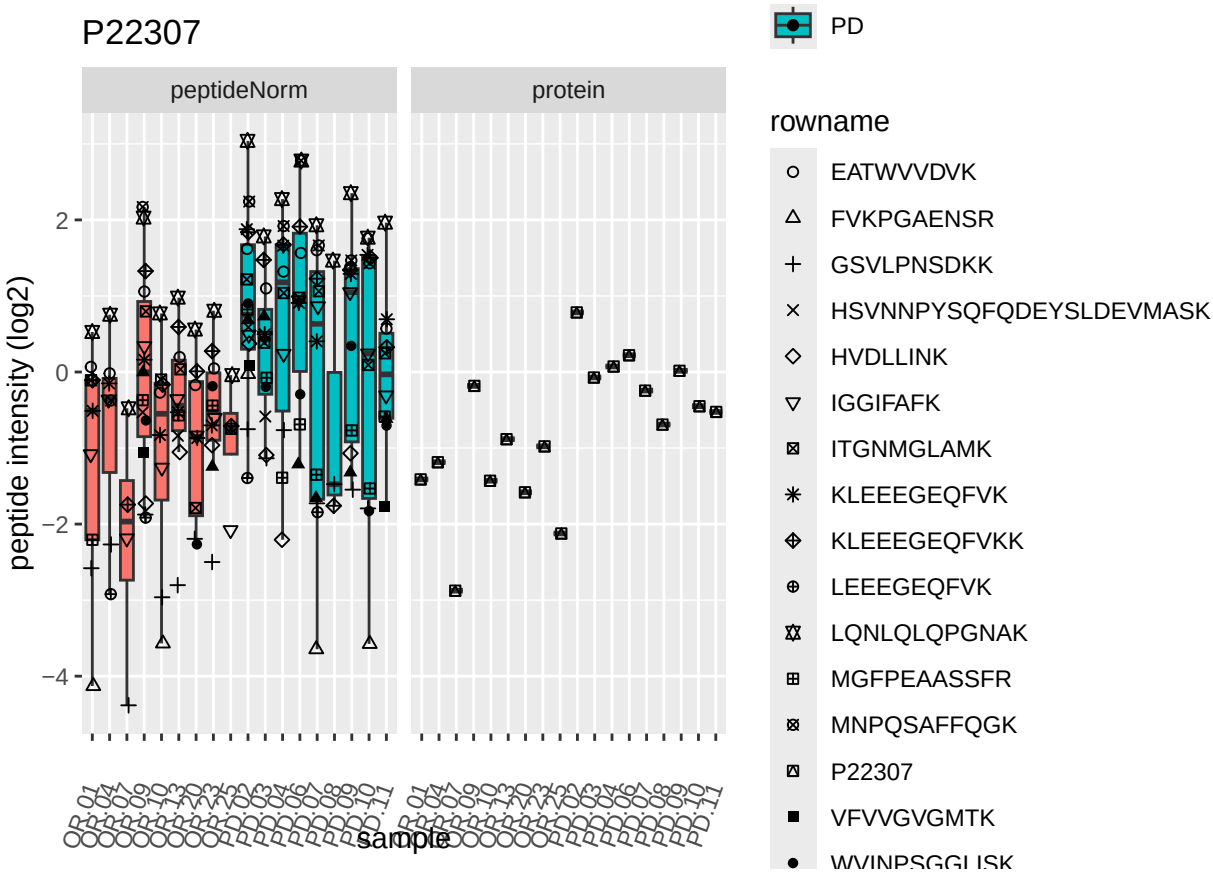
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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0
−2
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
PD
rowname
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FVKPGAENSR
GSVLPNSDKK
HSVNNPYSQFQDEYSLDEVMASK
HVDLLINK
IGGIFAFK
ITGNMGLAMK
KLEEEGEQFVK
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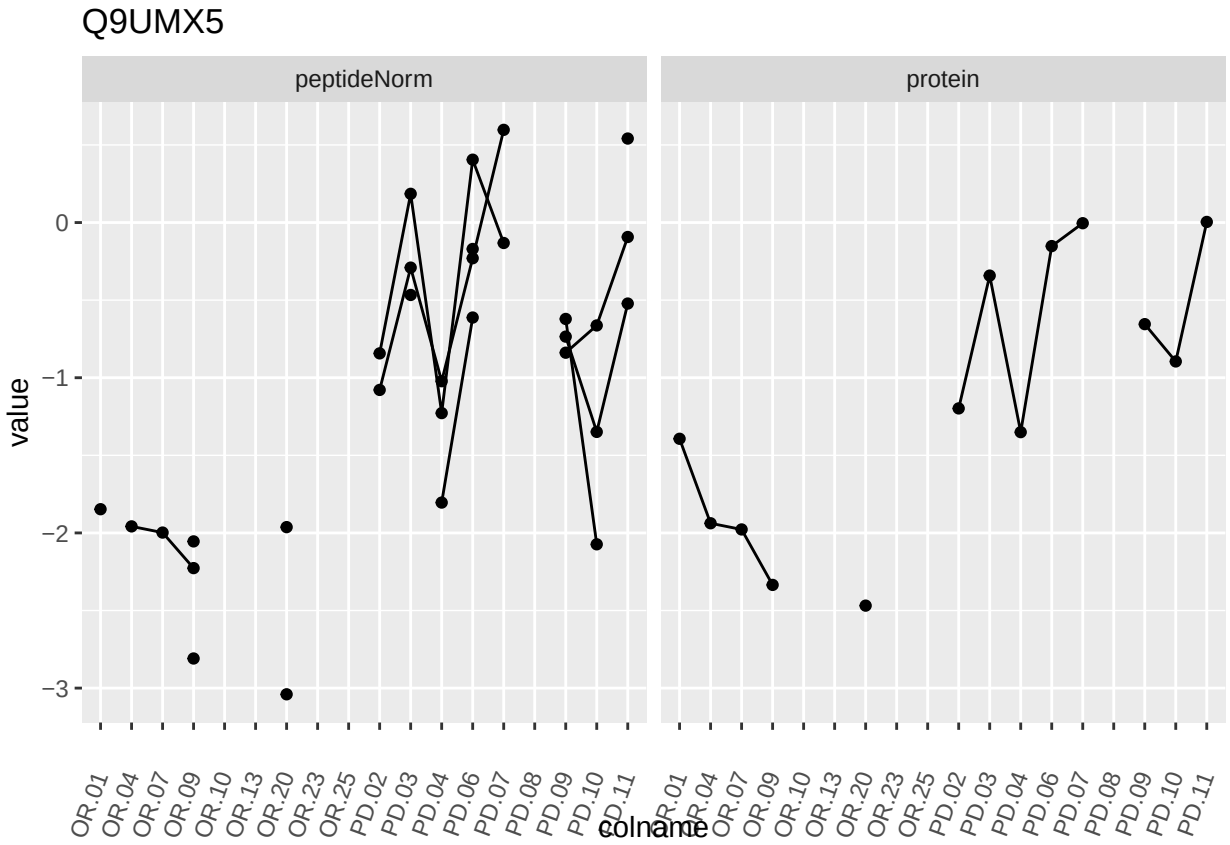
LEEEGEQFVK
LQNLQLQPGNAK
MGFPEAASSFR
MNPQSAFFQGK
P22307
VFVVGVGMTK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protein
value
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−2
−3
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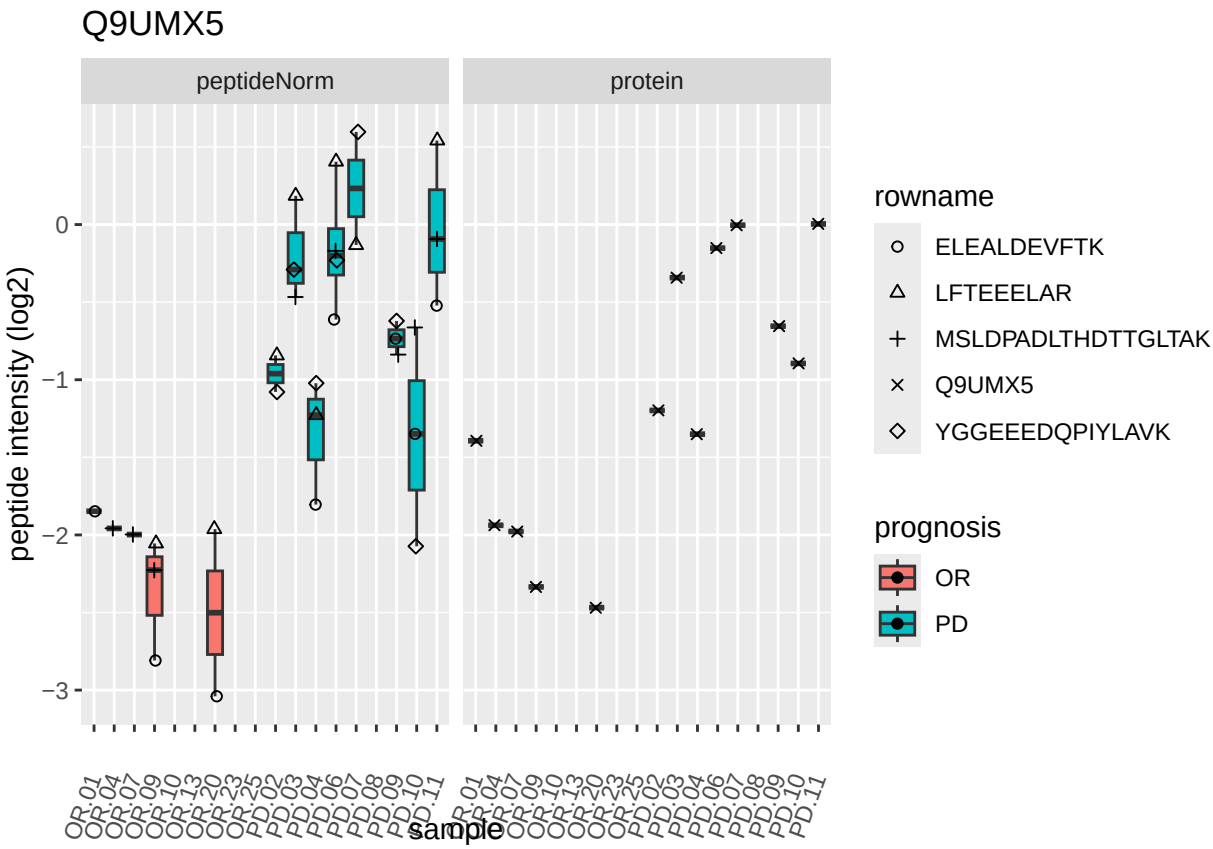
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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−1
−2
−3
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OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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LFTEEELAR
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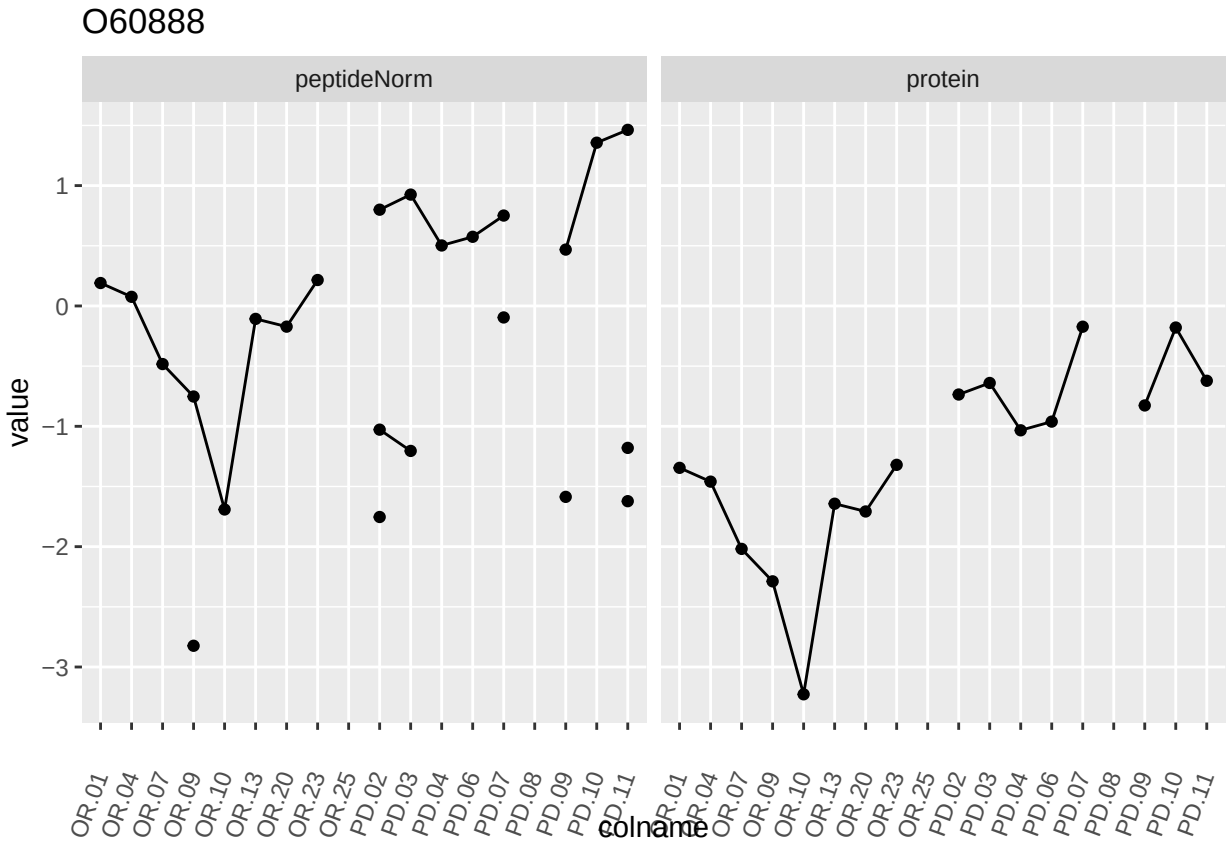
Q9UMX5
YGGEEEDQPIYLAVK
prognosis
OR
PD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−2
−3
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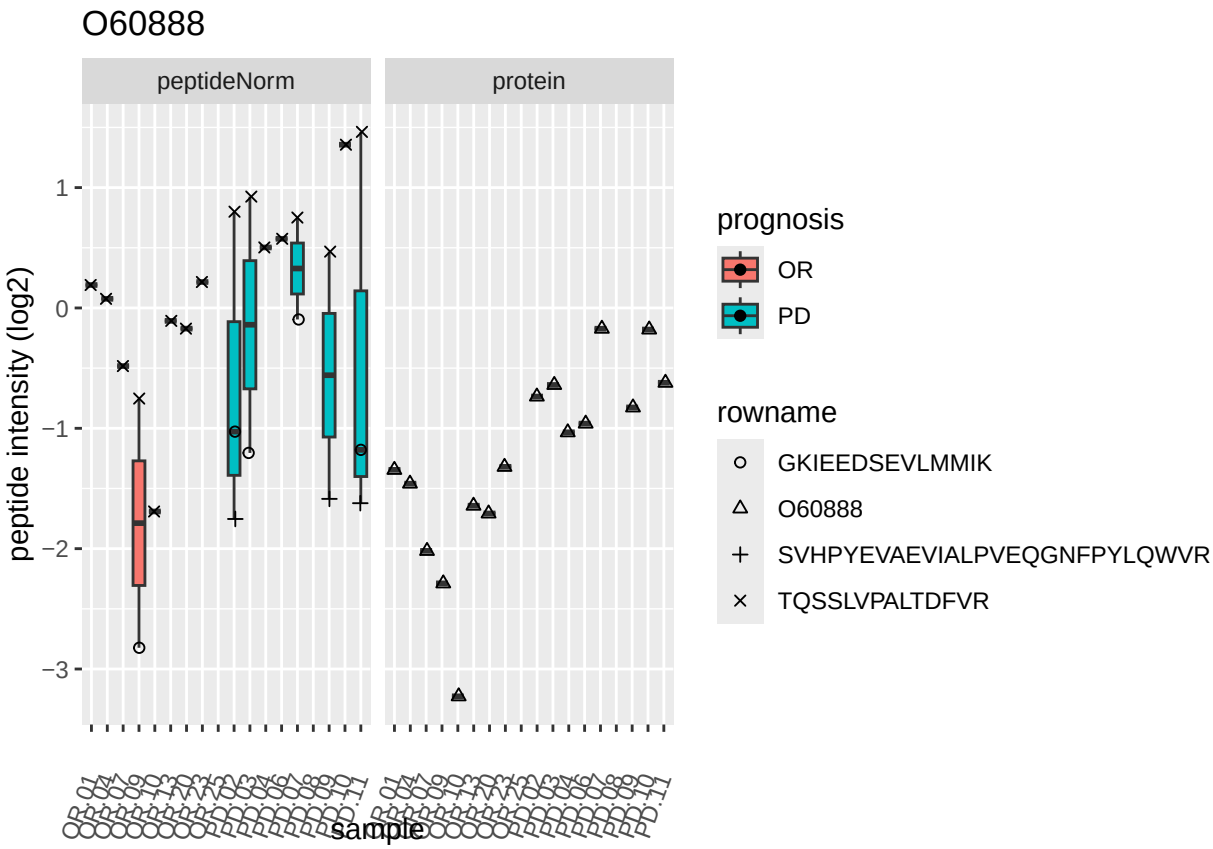
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
sample
prognosis
OR
PD
rowname
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O60888
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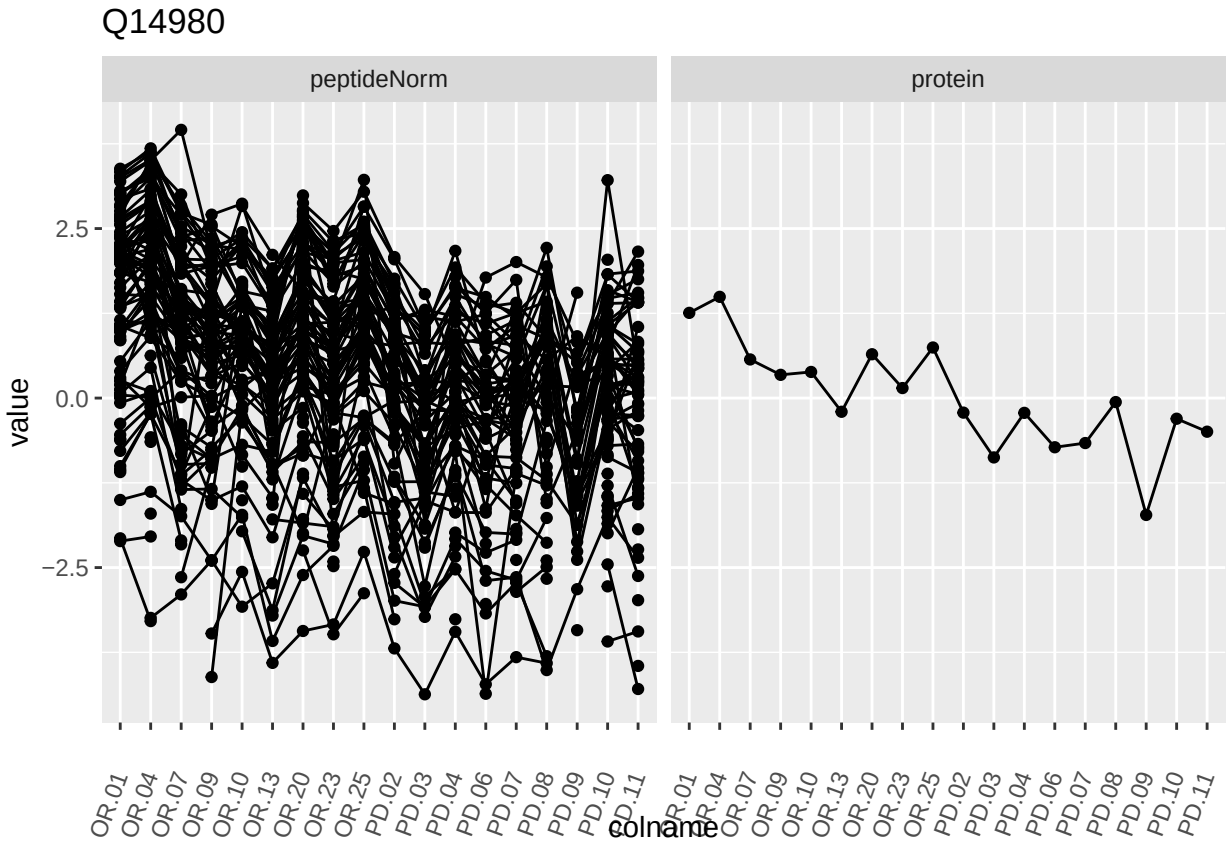
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OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

	&	HQVEQLSSSLR	8	LEQALTASNSAR	I	QEQHEA	
	'	HREELEQSK	9	LPPKVESLESLYFTPIPAR	K	QFCSTQ	
\R	(	IATTTASAATAAAIGATPR	:	LQAQLNELQAQLSQK	L	QFLEVE	
	)	IHGTEEGQQILK	;	LQNALNEQR	M	QLEALE	
\AGR	*	INQLSEENGDLSFK	<	LQQLGEAHQAETEVLR	N	QPEWLE	
SEAAGR	+	IQAELAVILK	=	LQQLGEAHQAETEVLRR	O	QQEQAI	
)QEQASQGLR	,	KHPSSPECLVSAQK	>	LSQLEEHLSQLQDNPPQEK	P	QQLSSL	
ESECEQLVK	-	KINQLSEENGDLSFK	?	LTAQVASLTSELTTLNATIQQQDQELAGLK	Q	QQNELA	
TMR	.	KLDVEEPDSANSSFYSTR	@	LTAQVEQLEVFQR	R	QQNQEI	
	/	KNSLISSLEEEVSILNR	A	LVMAESEK	S	RSQAGV	
	0	KQQNQELQEQLR	B	MTMLLLYHSTMSSK	T	SAPASQ	
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STQALVSELLPAK	2	LADDLSTLQEK	D	PSLSLGTITDEEMK	V	SLVEQH	
	3	LALLNEK	E	Q14980	W	SNRDEL	
EDLENFLQK	4	LDFVCSFLQK	F	QAQLAQTLQQQEQASQGLR	X	SNRDEL	
LK	5	LEILQQQLQVANEAR	G	QDHAQQLATAAEER	Y	SQAPLE	
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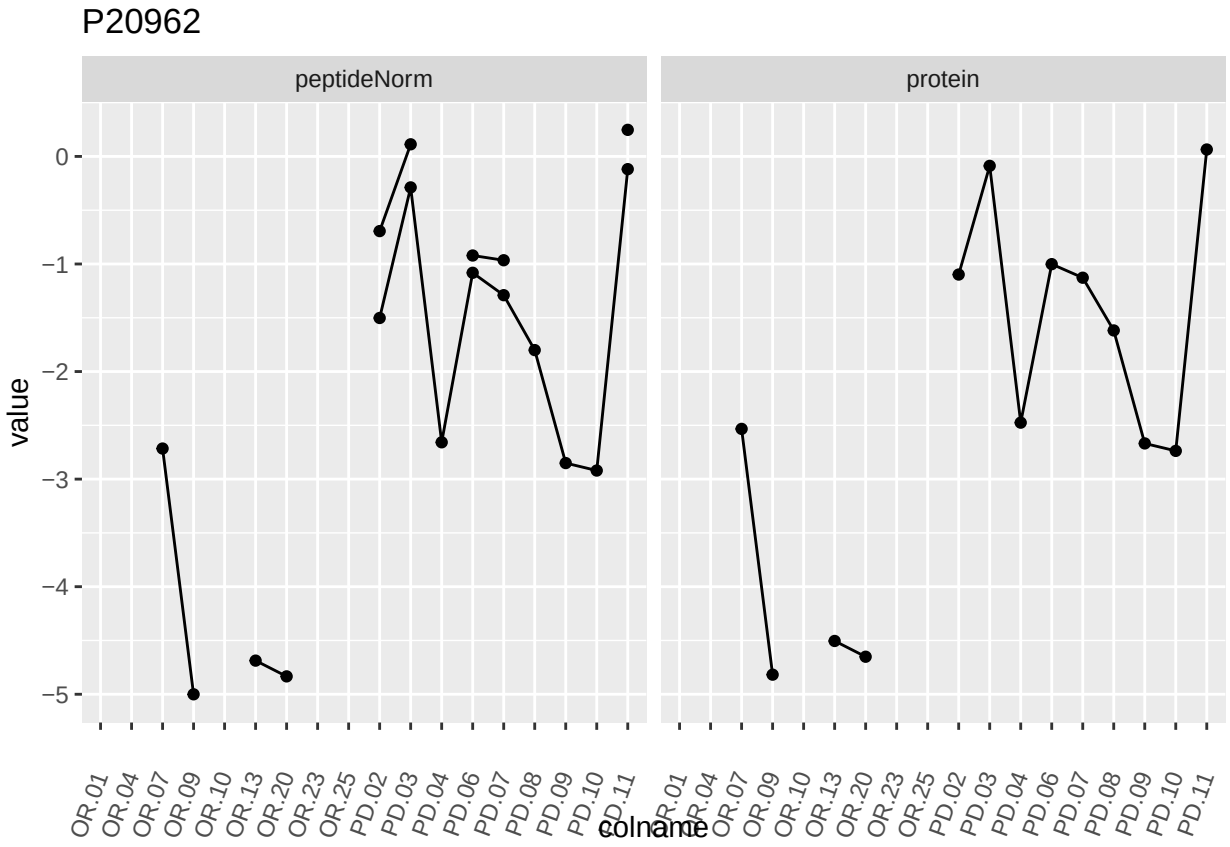
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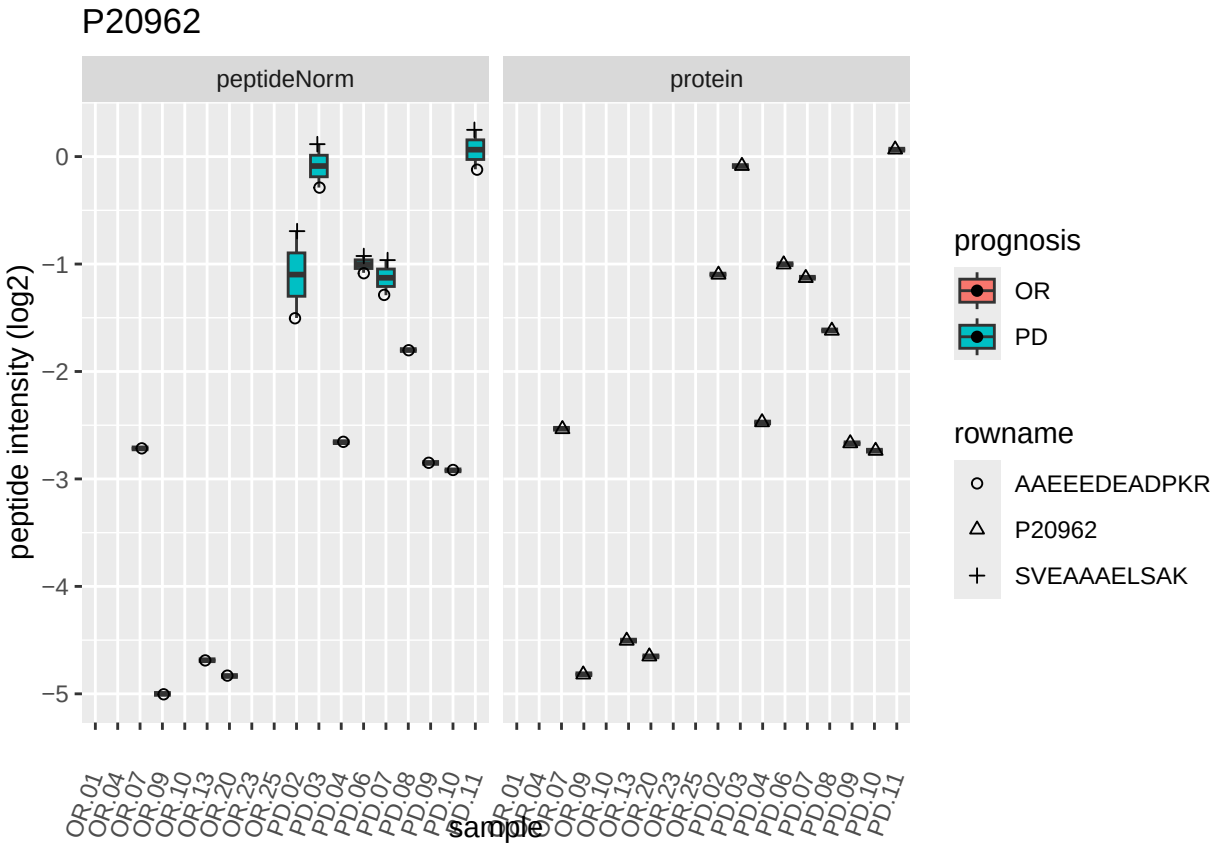
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptide intensity (log2)
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OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
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P20962
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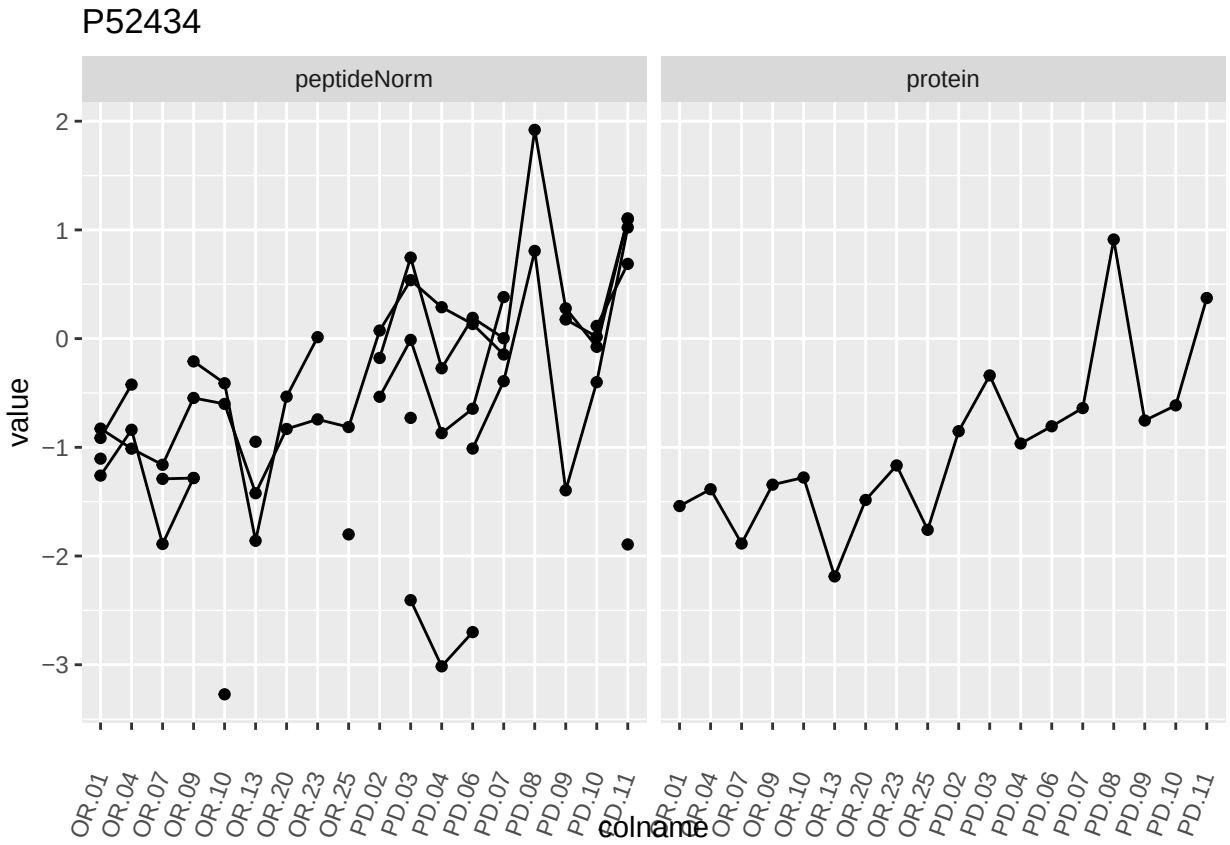
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protein
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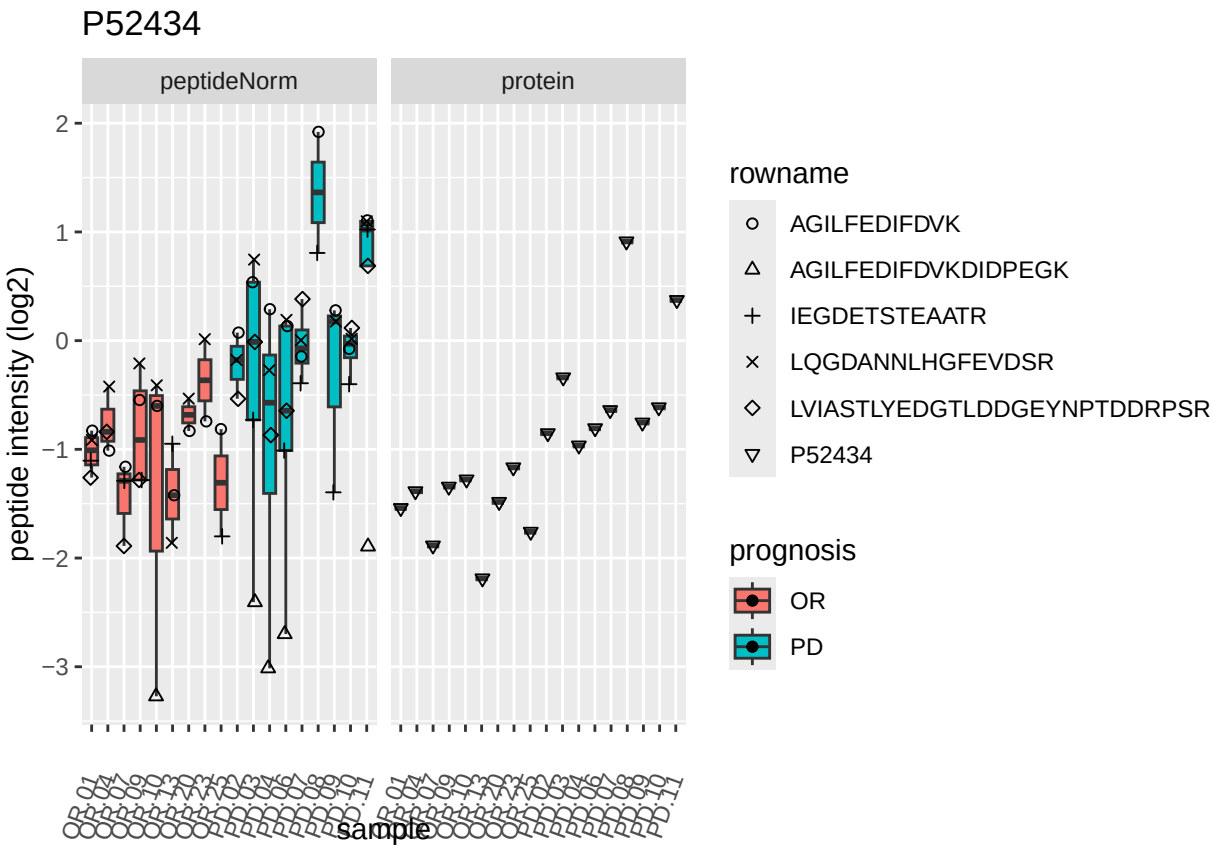
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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protein
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−1
−2
−3
sample
rowname
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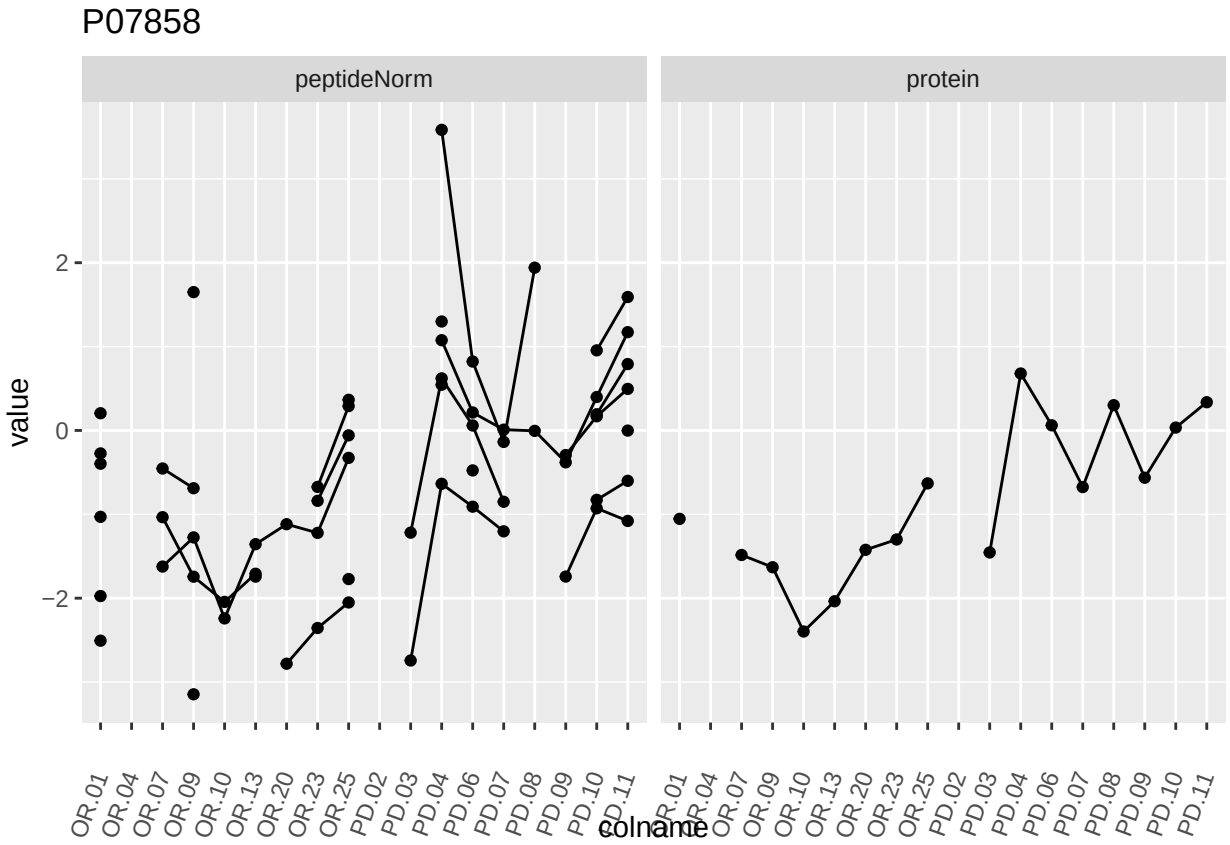
P52434
prognosis
OR
PD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OR.07
OR.09
OR.10
OR.13
OR.20
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OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
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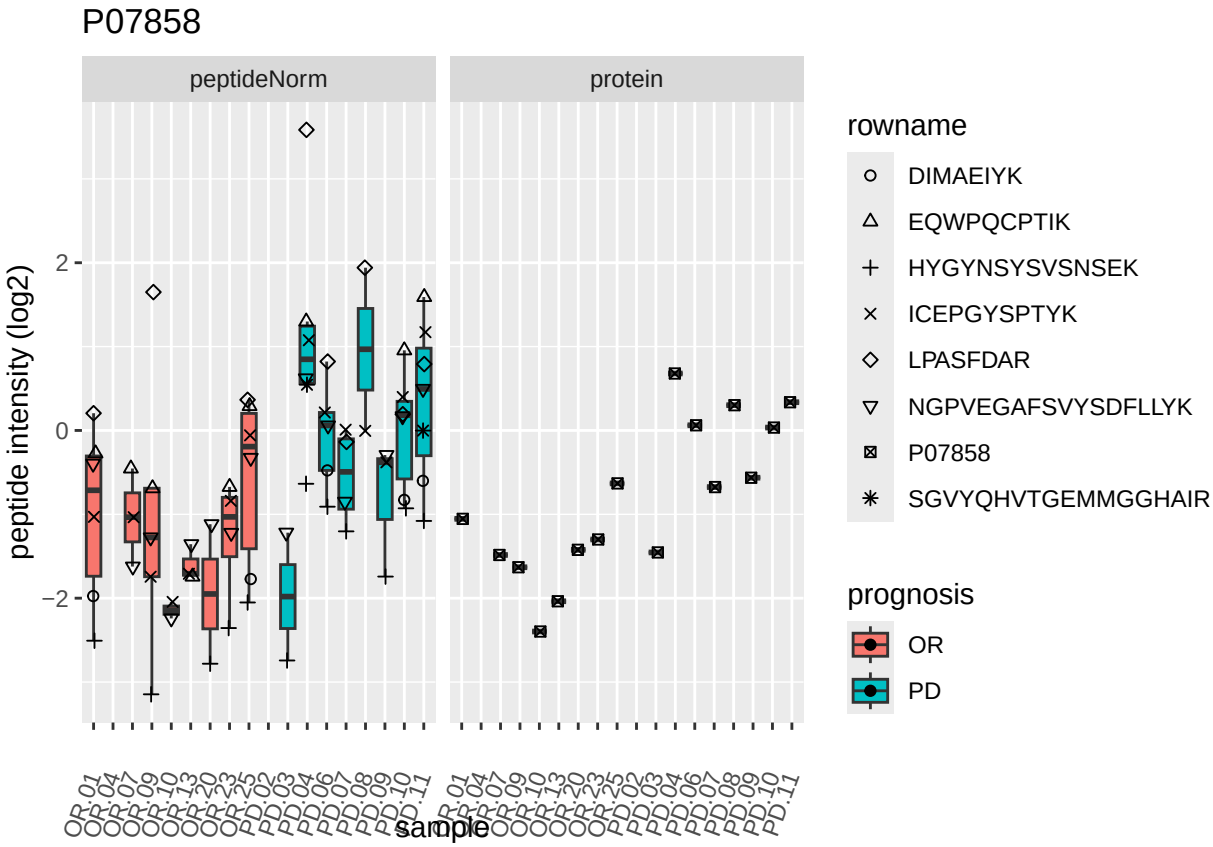
PD.10
PD.11
colname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peptide intensity (log2)
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OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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HYGYNSYSVSNSEK
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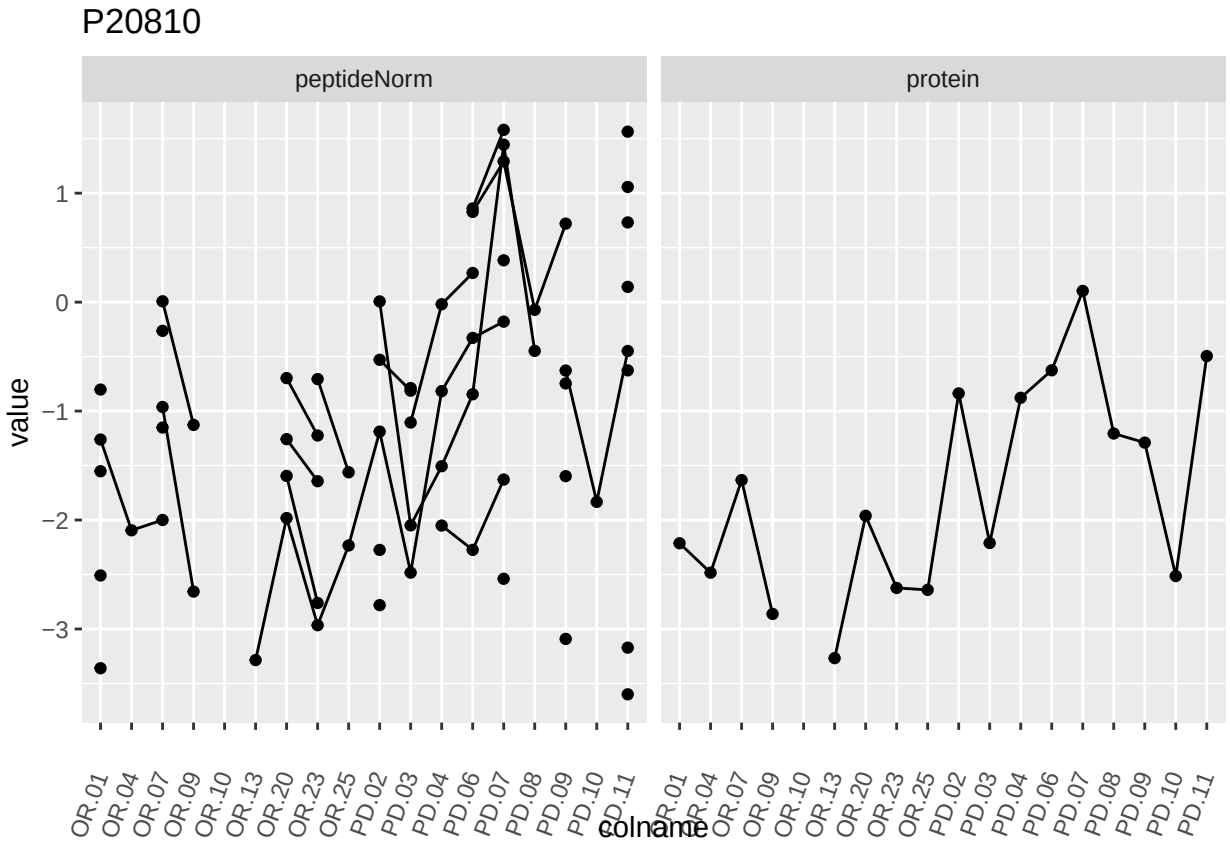
LPASFDAR
NGPVEGAFSVYSDFLLYK
P07858
SGVYQHVTGEMMGGHAIR
prognosis
OR
PD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peptideNorm
protein
value
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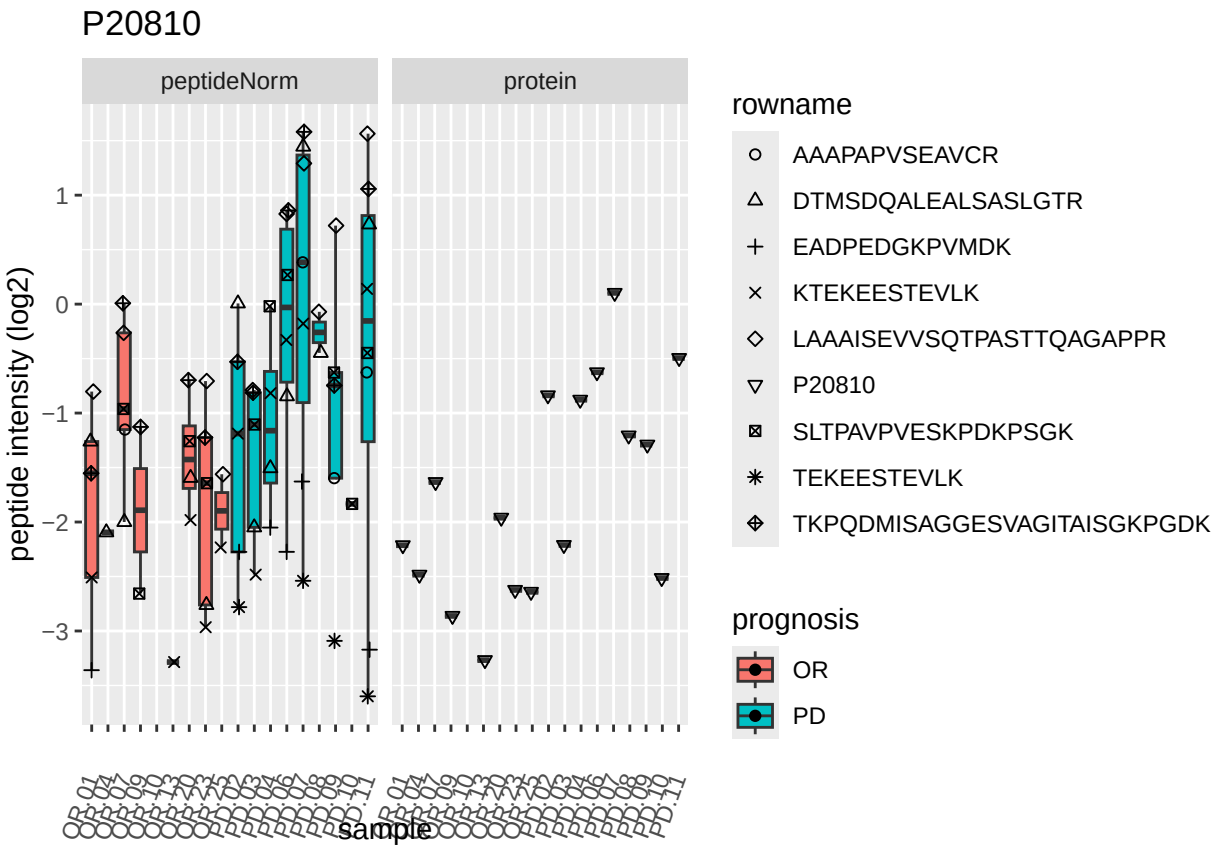
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
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peptide intensity (log2)
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−2
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sample
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P20810
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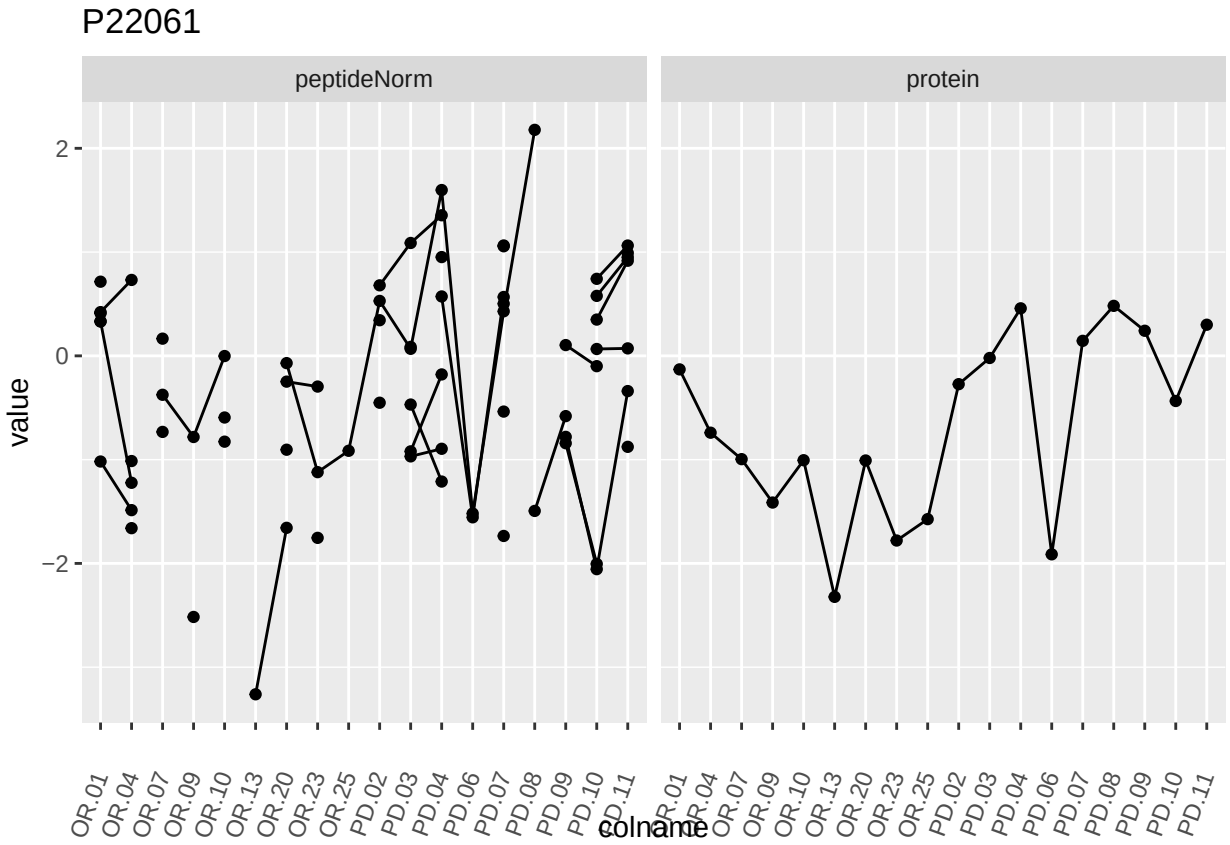
prognosis
OR
PD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protein
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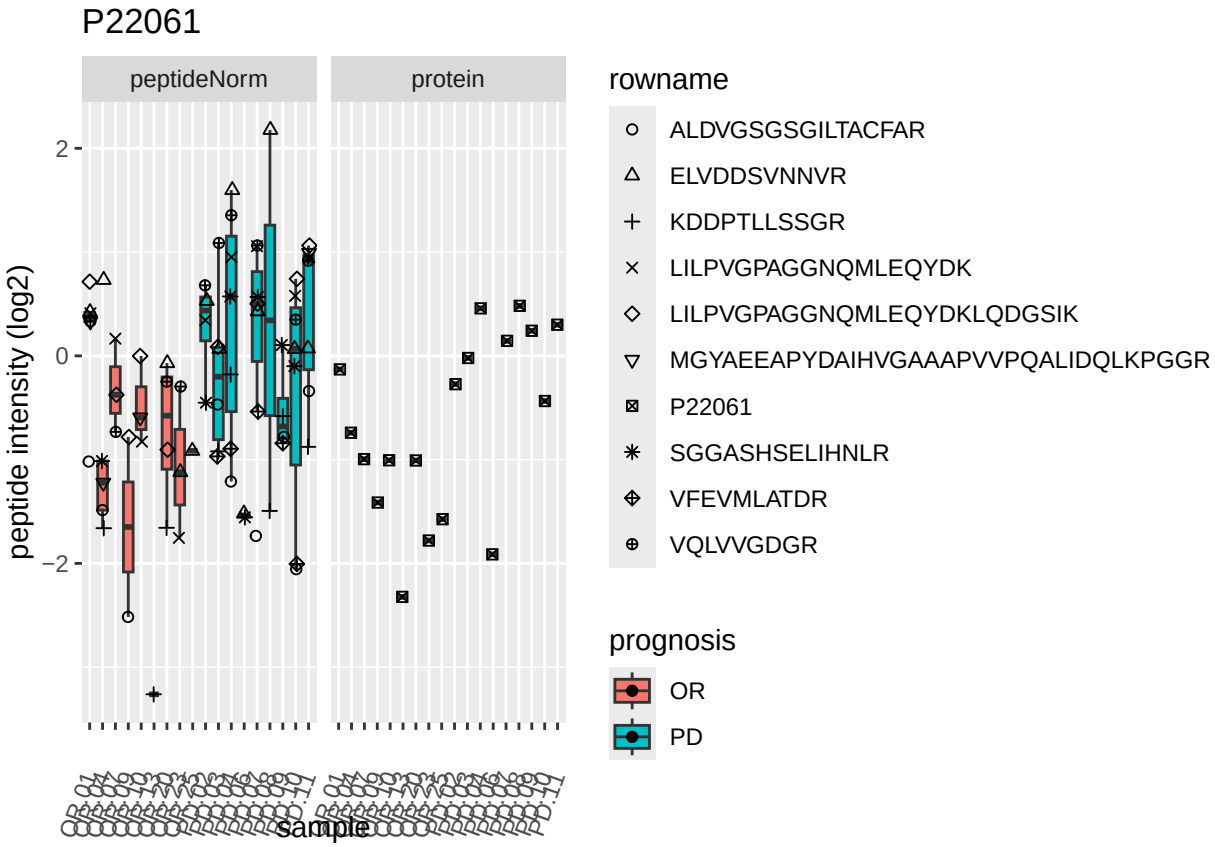
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P22061
peptideNorm
protein
peptide intensity (log2)
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0
−2
sample
rowname
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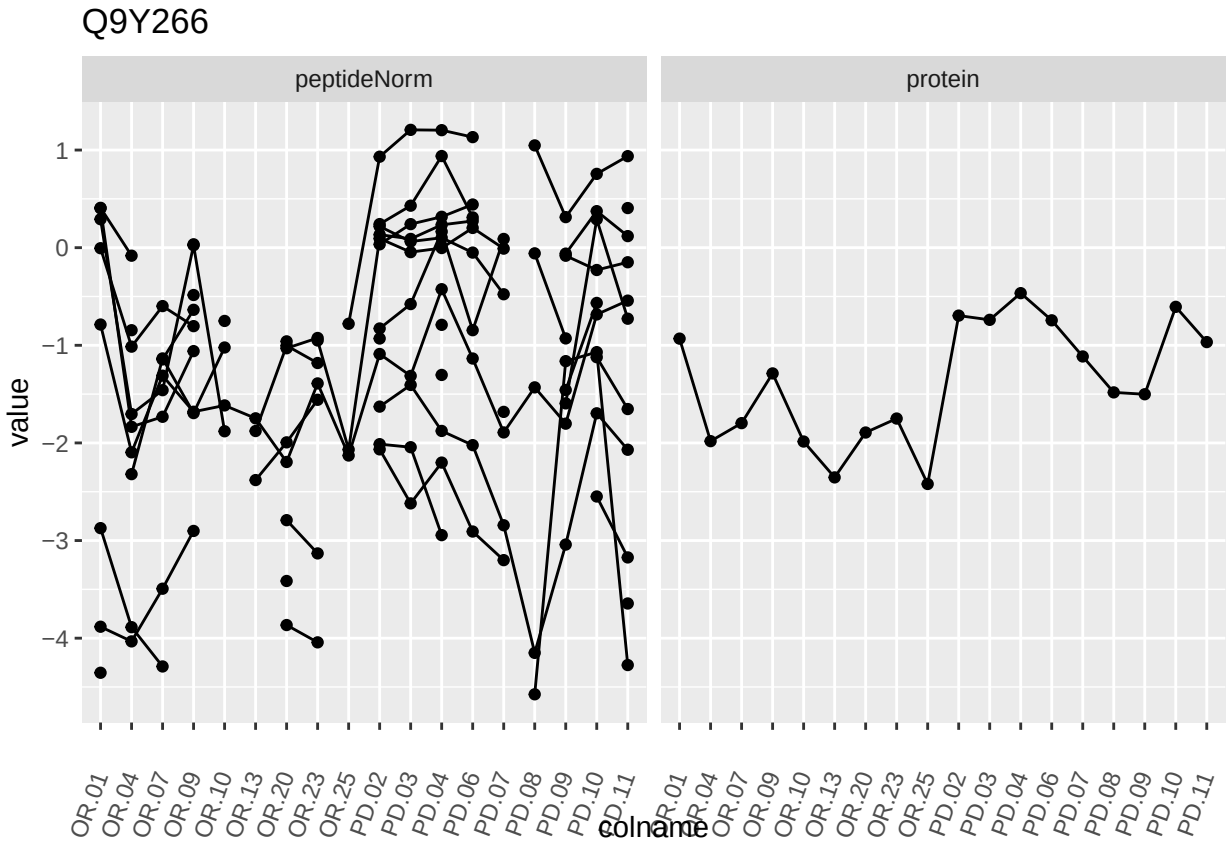
MGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR
P22061
SGGASHSELIHNLR
VFEVMLATDR
VQLVVGDGR
prognosis
OR
PD


Q9Y266
peptideNorm
protein
value
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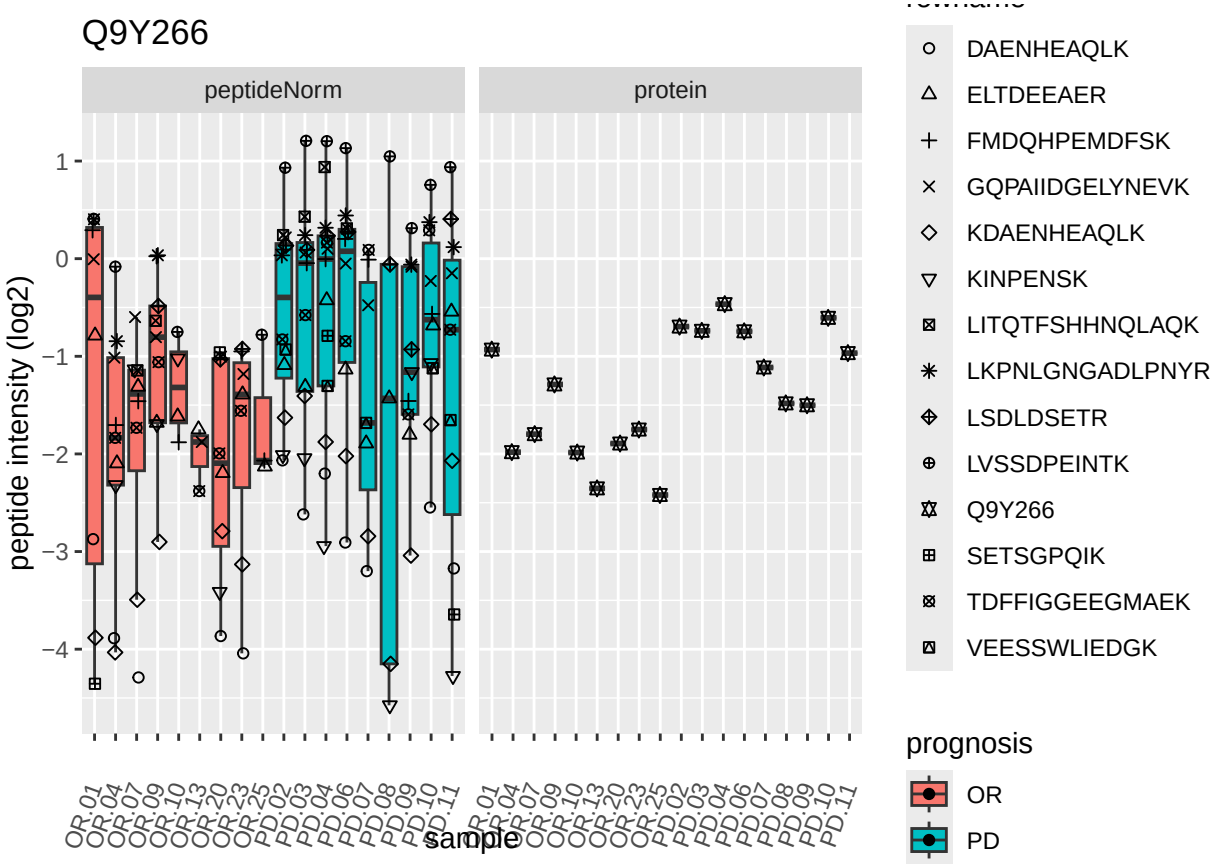
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9Y266
peptideNorm
protein
peptide intensity (log2)
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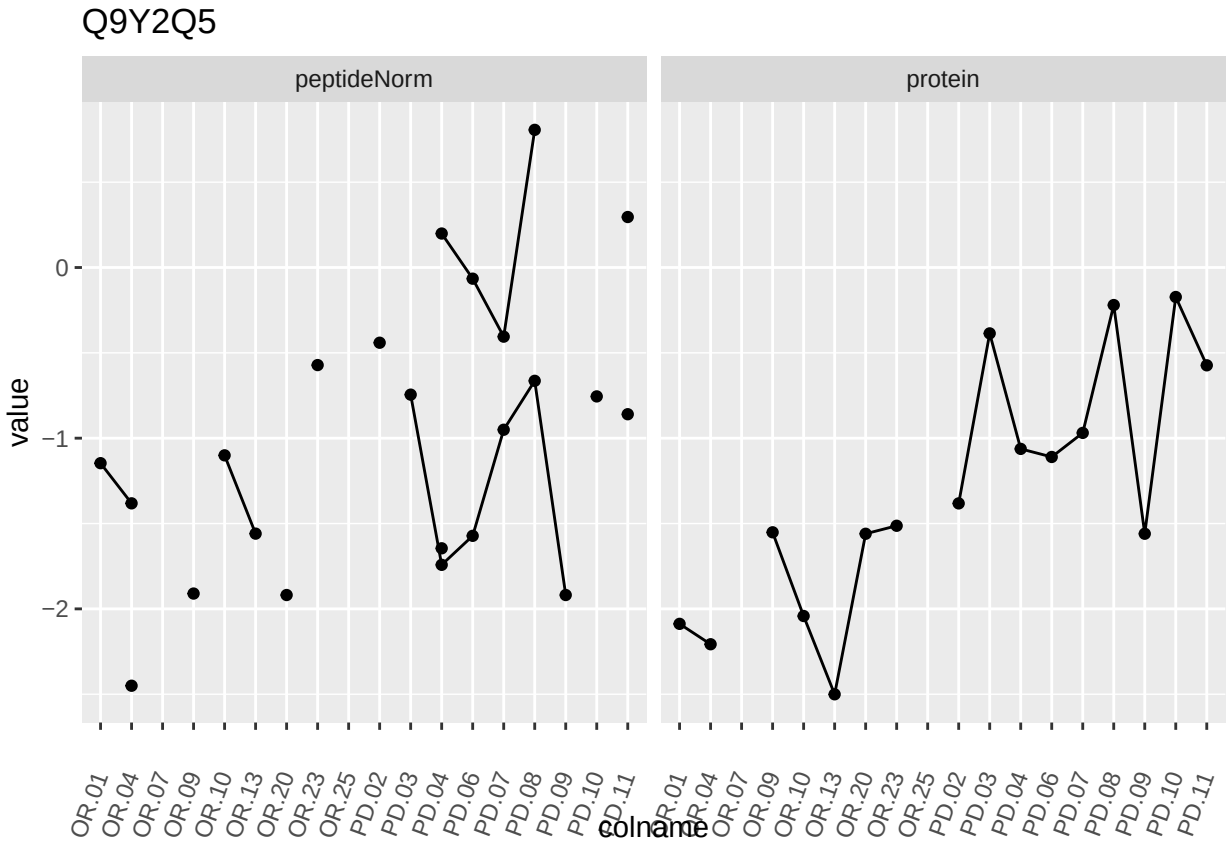
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
DAENHEAQLK
ELTDEEAER
FMDQHPEMDFSK
GQPAIIDGELYNEVK
KDAENHEAQLK
KINPENSK
LITQTFSHHNQLAQK
LKPNLGNGADLPNYR
LSDLDSETR
LVSSDPEINTK
Q9Y266
SETSGPQIK
TDFFIGGEEGMAEK
VEESSWLIEDGK
prognosis
OR
PD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peptideNorm
protein
value
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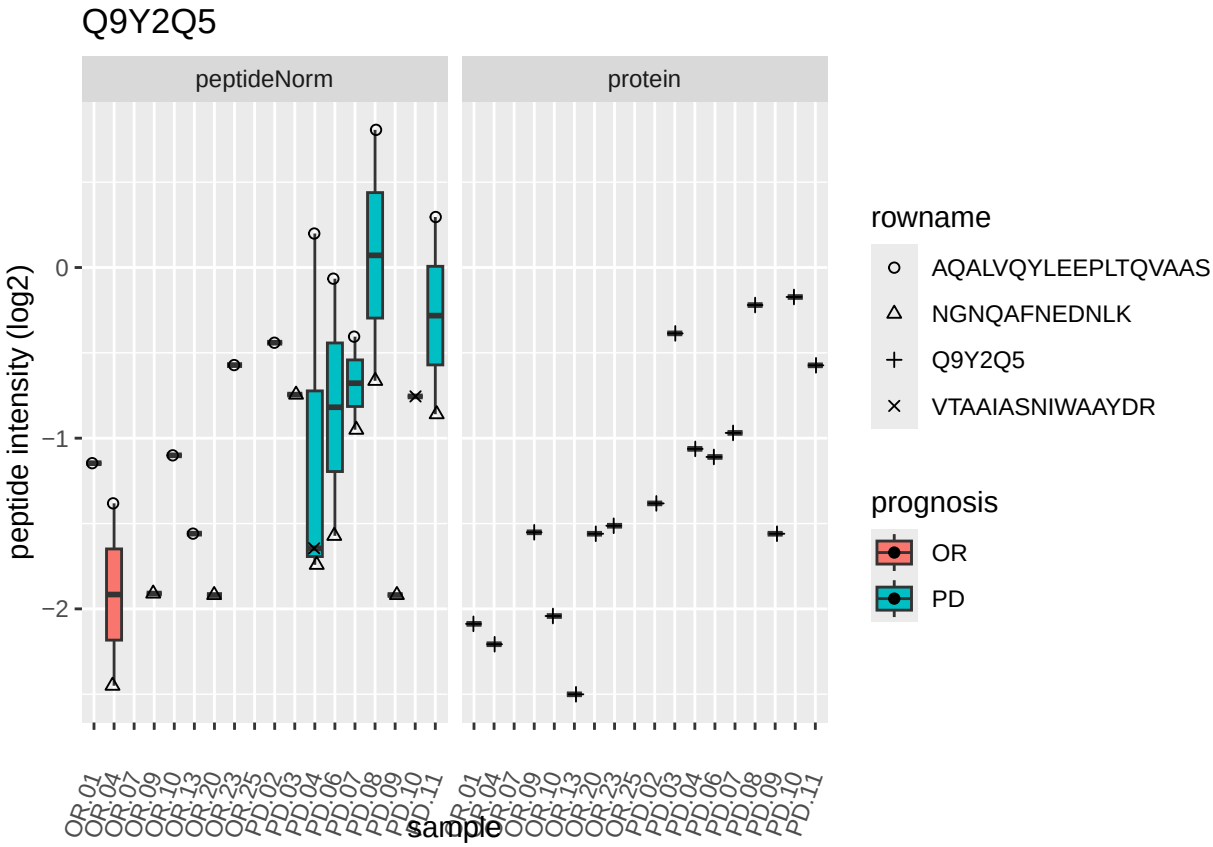
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9Y2Q5
peptideNorm
protein
peptide intensity (log2)
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−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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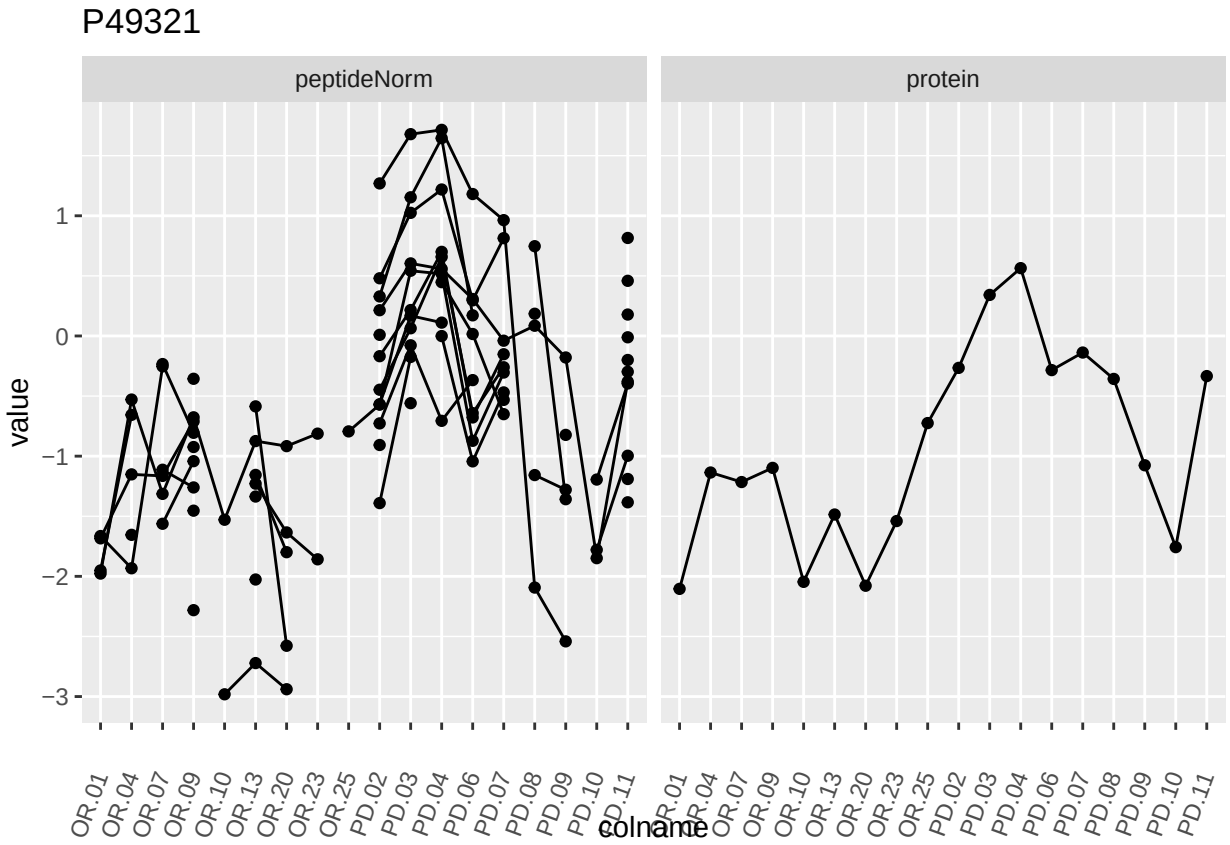
Q9Y2Q5
VTAAIASNIWAAYDR
prognosis
OR
PD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peptideNorm
protein
value
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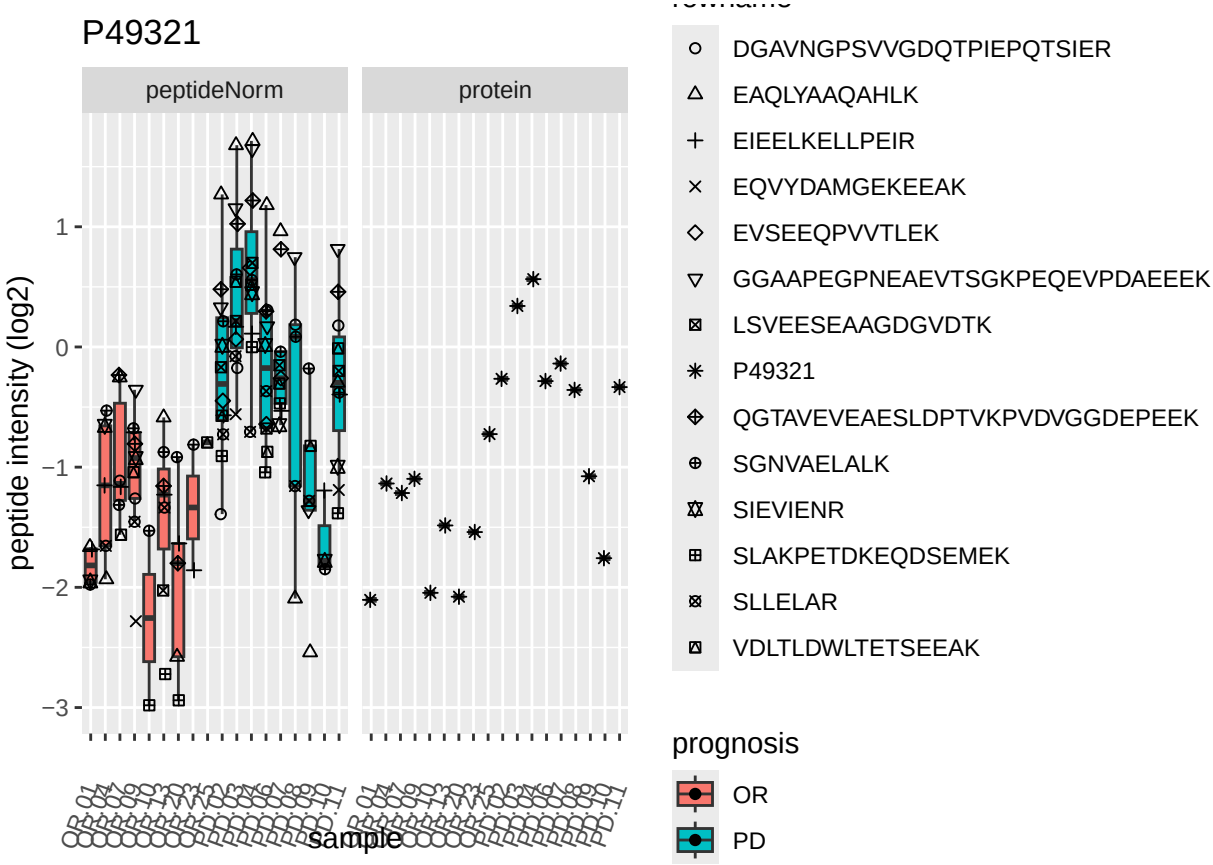
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P49321
peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
sample
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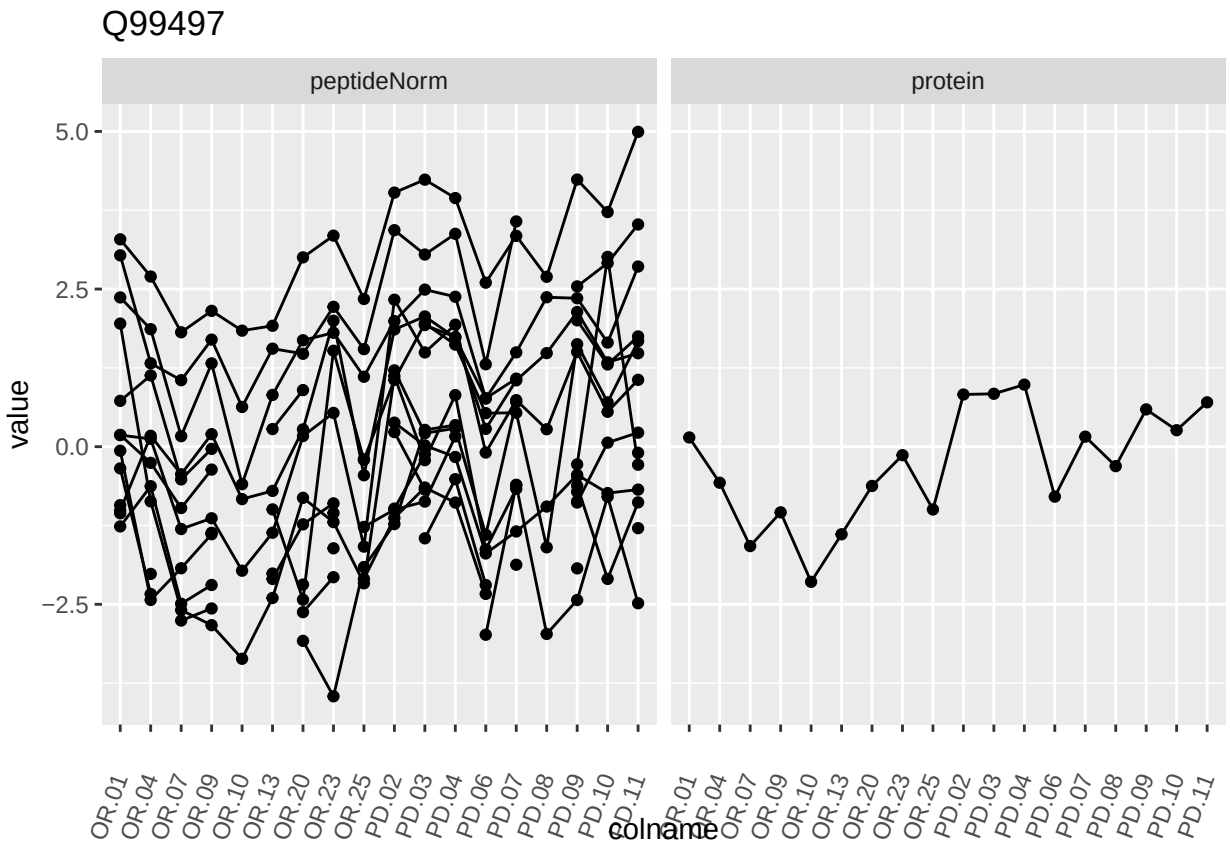
EIEELKELLPEIR
EQVYDAMGEKEEAK
EVSEEQPVVTLEK
GGAAPEGPNEAEVTSGKPEQEVPDAEEEK
LSVEESEAAGDGVDTK
P49321
QGTAVEVEAESLDPTVKPVDVGGDEPEEK
SGNVAELALK
SIEVIENR
SLAKPETDKEQDSEMEK
SLLELAR
VDLTLDWLTETSEEAK
prognosis
OR
PD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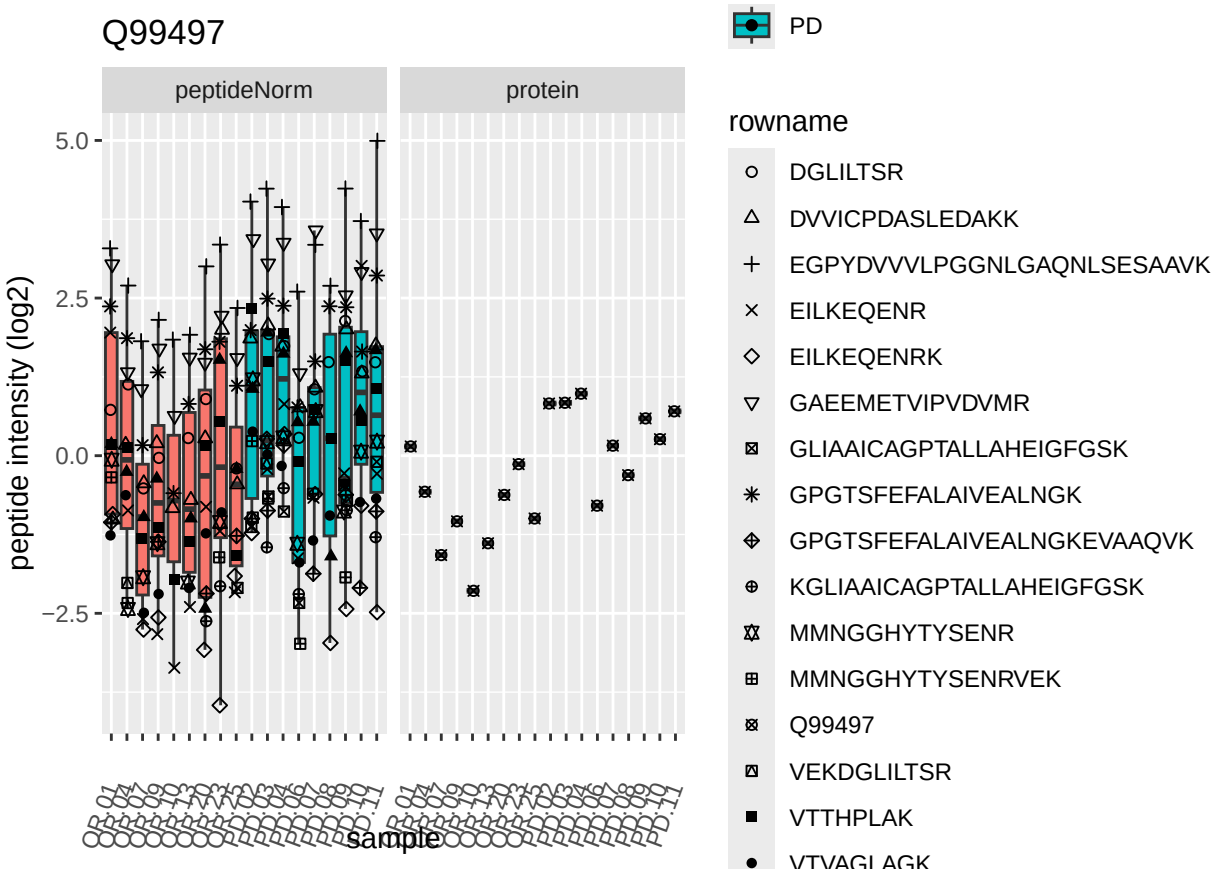
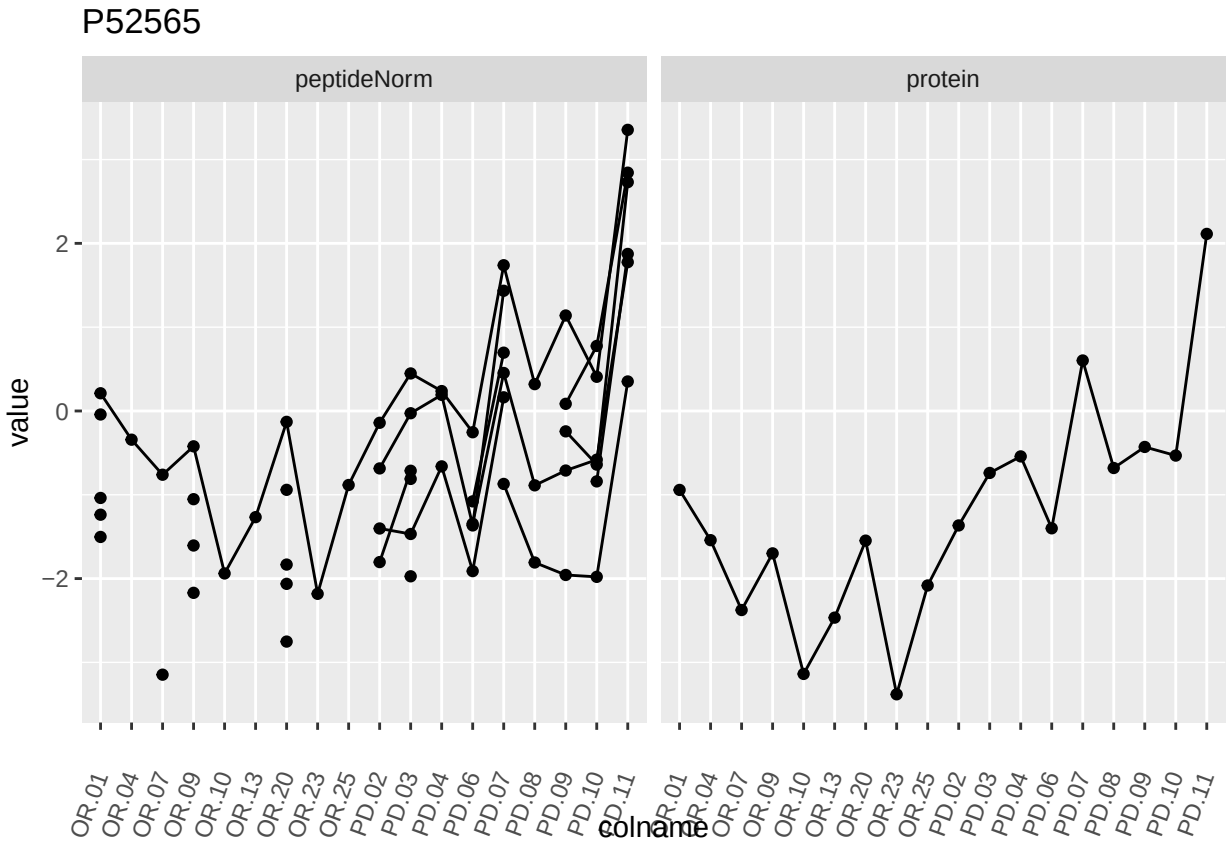
peptideNorm
protein
5.0
2.5
0.0
−2.5
value
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q99497
peptideNorm
protein
peptide intensity (log2)
5.0
2.5
0.0
−2.5
sample
PD
rowname
DGLILTSR
DVVICPDASLEDAKK
EGPYDVVVLPGGNLGAQNLSESAAVK
EILKEQENR
EILKEQENRK
GAEEMETVIPVDVMR
GLIAAICAGPTALLAHEIGFGSK
GPGTSFEFALAIVEALNGK
GPGTSFEFALAIVEALNGKEVAAQVK
KGLIAAICAGPTALLAHEIGFGSK
MMNGGHYTYSENR
MMNGGHYTYSENRVEK
Q99497
VEKDGLILTSR
VTTHPLAK
VTVAGLAGK


P52565
peptideNorm
protein
value
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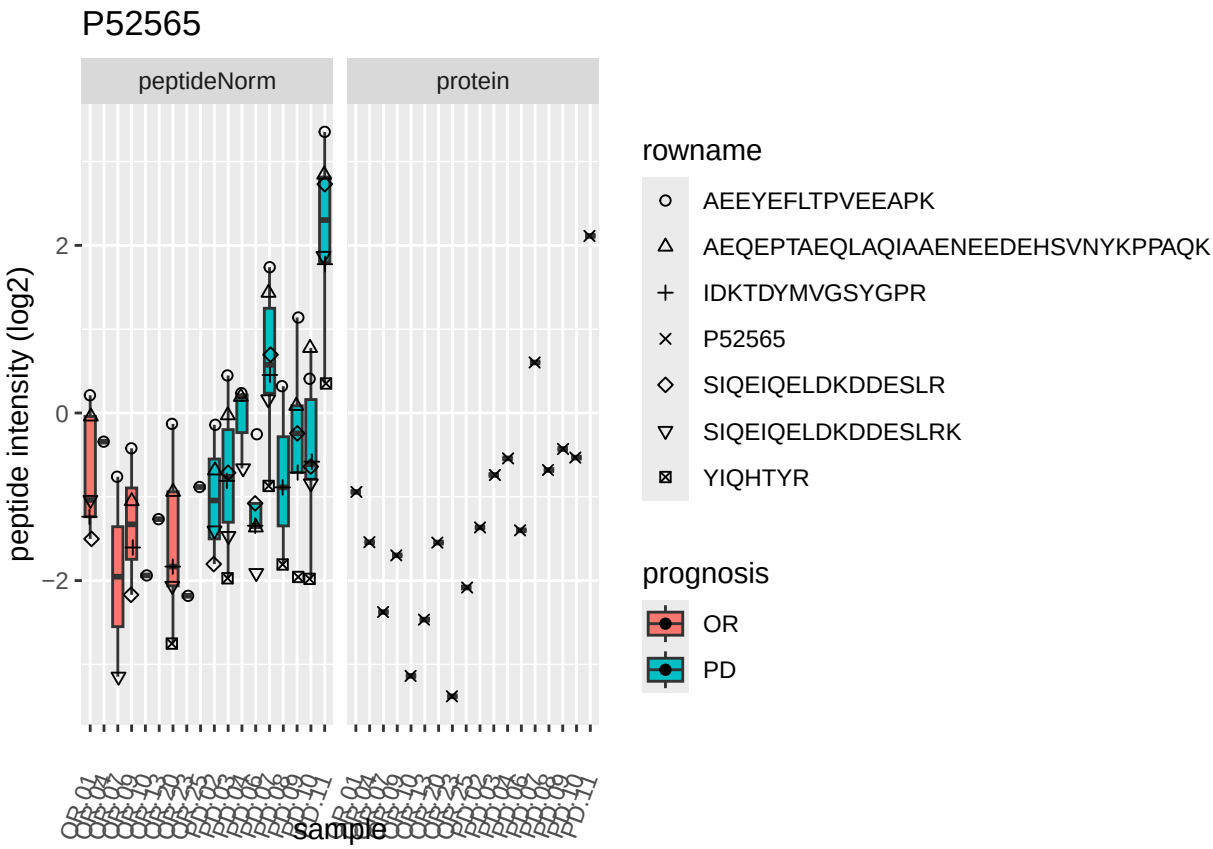
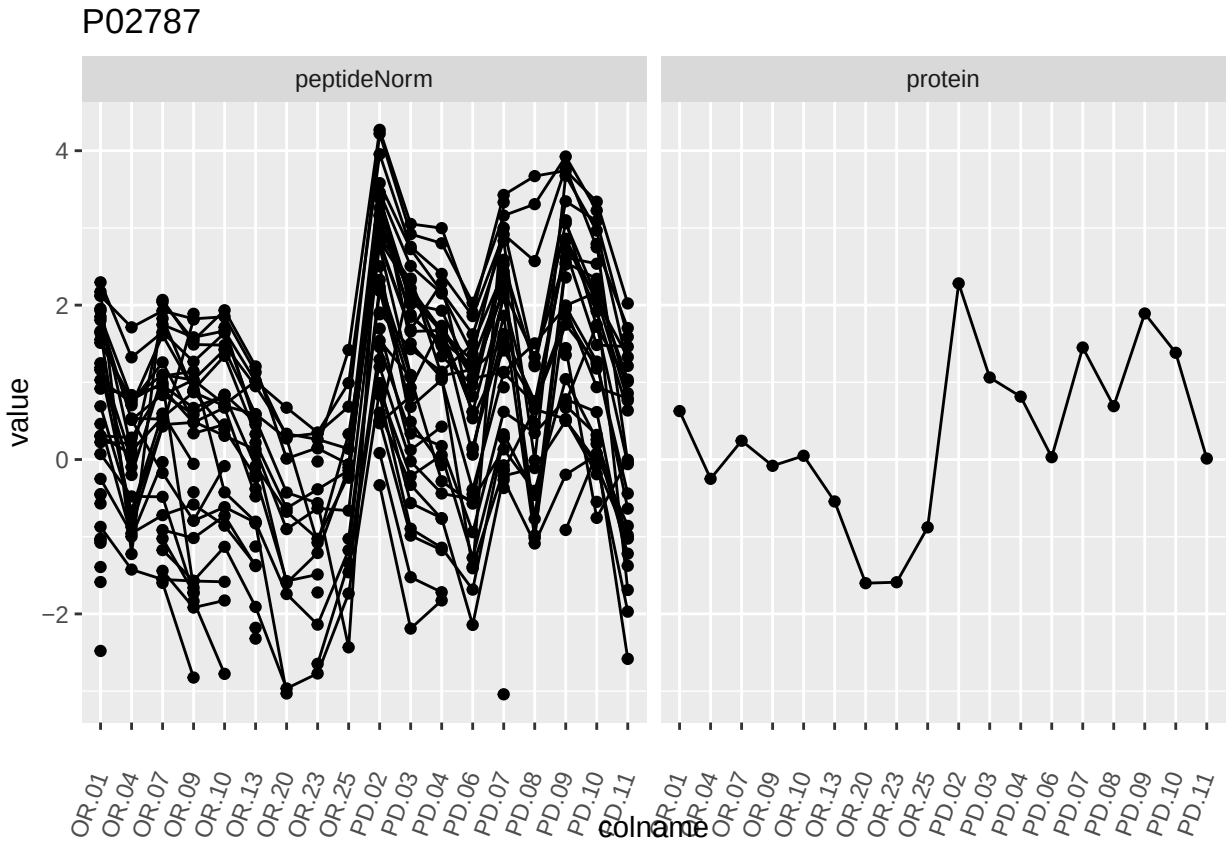
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P52565
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
rowname
AEEYEFLTPVEEAPK
AEQEPTAEQLAQIAAENEEDEHSVNYKPPAQK
IDKTDYMVGSYGPR
P52565
SIQEIQELDKDDESLR
SIQEIQELDKDDESLRK
YIQHTYR
prognosis
OR
PD


P02787
peptideNorm
protein
value
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P02787
peptide intensity (log2)
4
2
0
−2
sample
APNHAVVTR
ASYLDCIR
CDEWSVNSVGK
CSTSSLLEACTFR
DCHLAQVPSHTVVAR
DDTVCLAK
DGAGDVAFVK
DLLFRDDTVCLAK
DQYELLCLDNTR
DSAHGFLK
DSGFQMNQLR
DYELLCLDGTR
EDPQTFYYAVAVVK
EFQLFSSPHGK
EGTCPEAPTDECKPVK
EGYYGYTGAFR
FDEFFSEGCAPGSK
HQTVPQNTGGK
IMNGLADAMSLDGGFVYIAGK
KASYLDCIR
KPVDEYKDCHLAQVPSHTVVAR
KPVEEYANCHLAR
LCMGSGLNLCEPNNK
LKCDEWSVNSVGK
MYLGYEYVTAIR
NLNEKDYELLCLDGTR
NPDPWAK
P02787
SAGWNIPIGLLYCDLPEPR
SASDLTWDNLK
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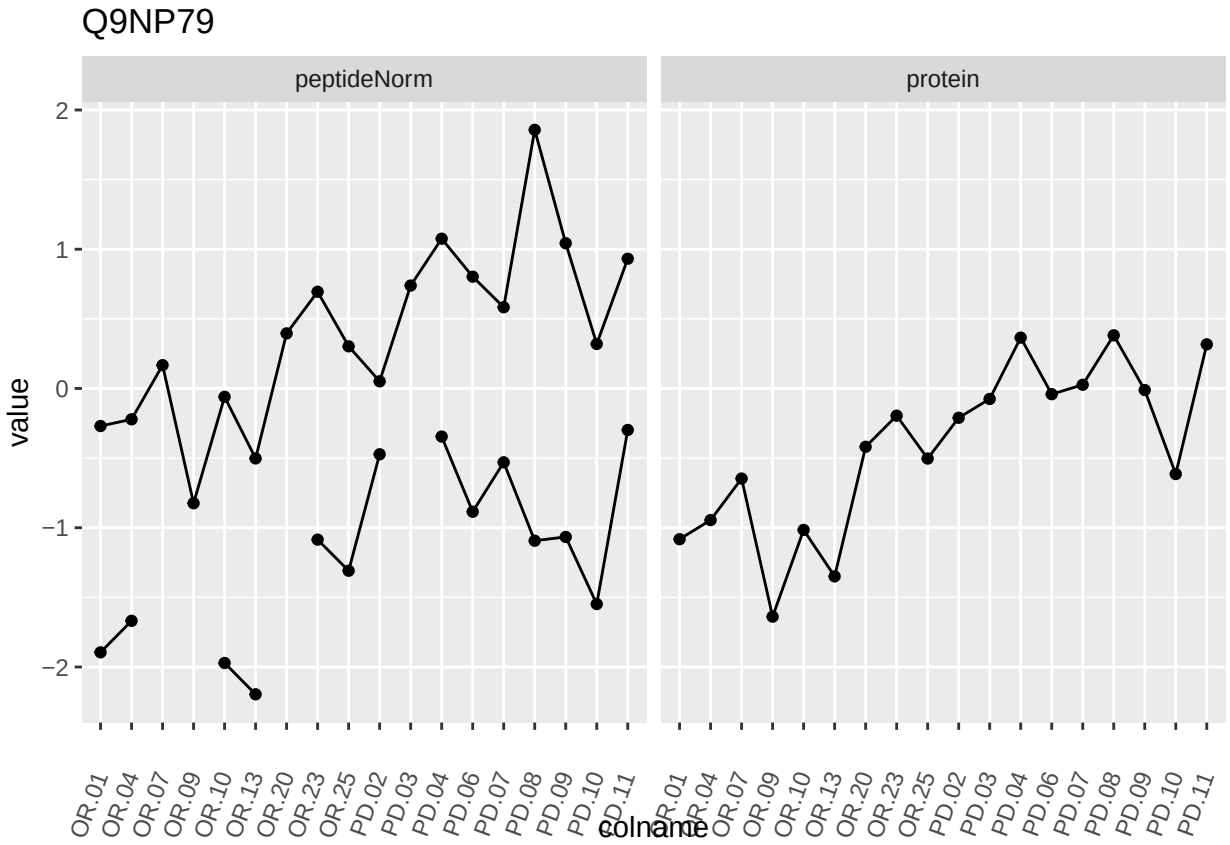
SVIPSDGPSVACVK
TAGWNIPMGLLYNK
WCALSHHER
WCAVSEHEATK
YLGEEYVK


Q9NP79
peptideNorm
protein
value
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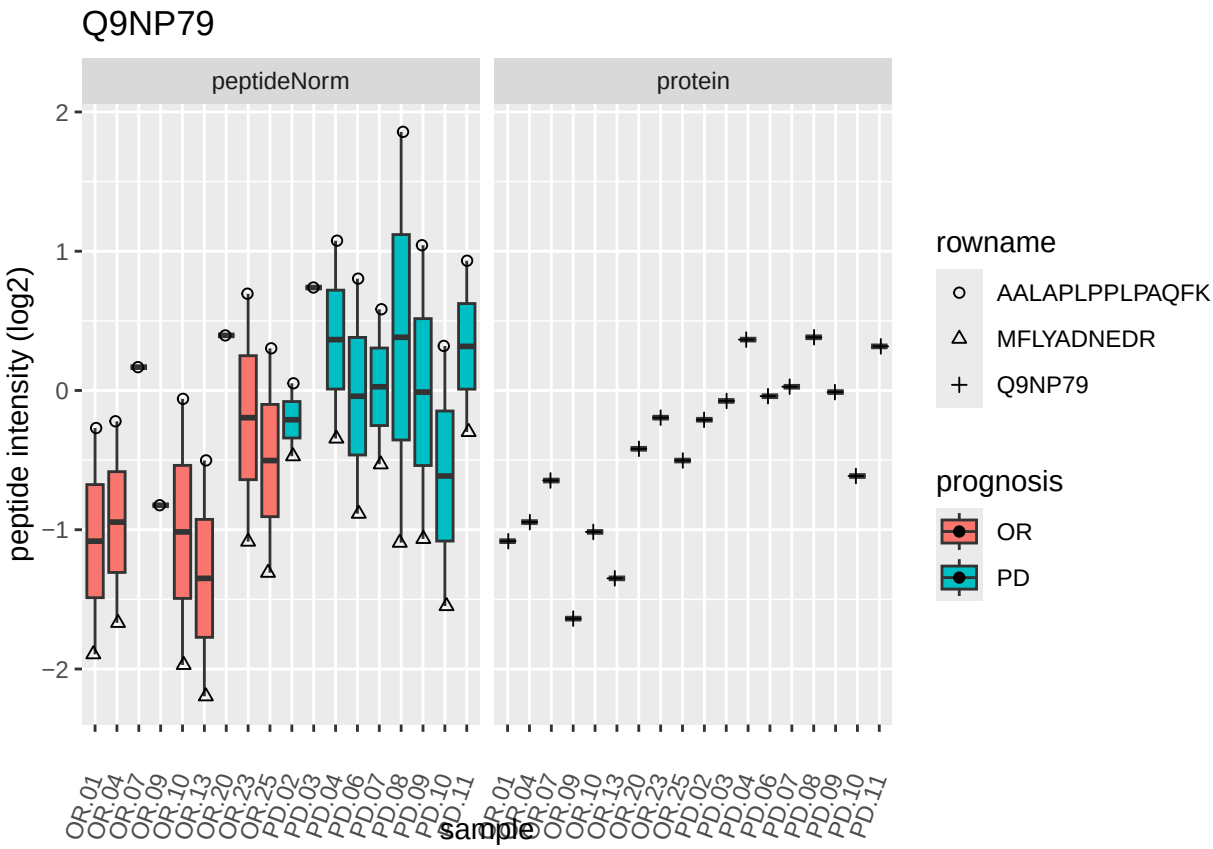
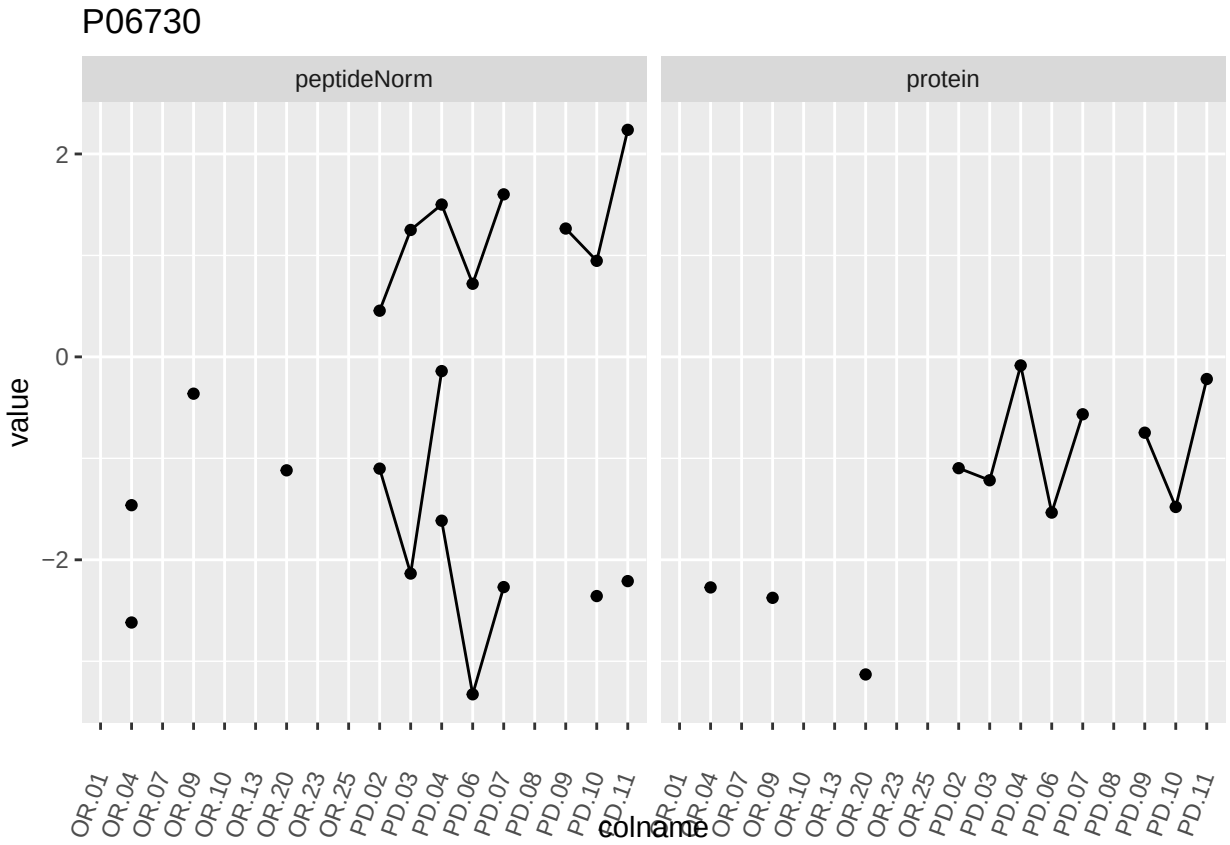
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NP79
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AALAPLPPLPAQFK
MFLYADNEDR
Q9NP79
prognosis
OR
PD


P06730
peptideNorm
protein
value
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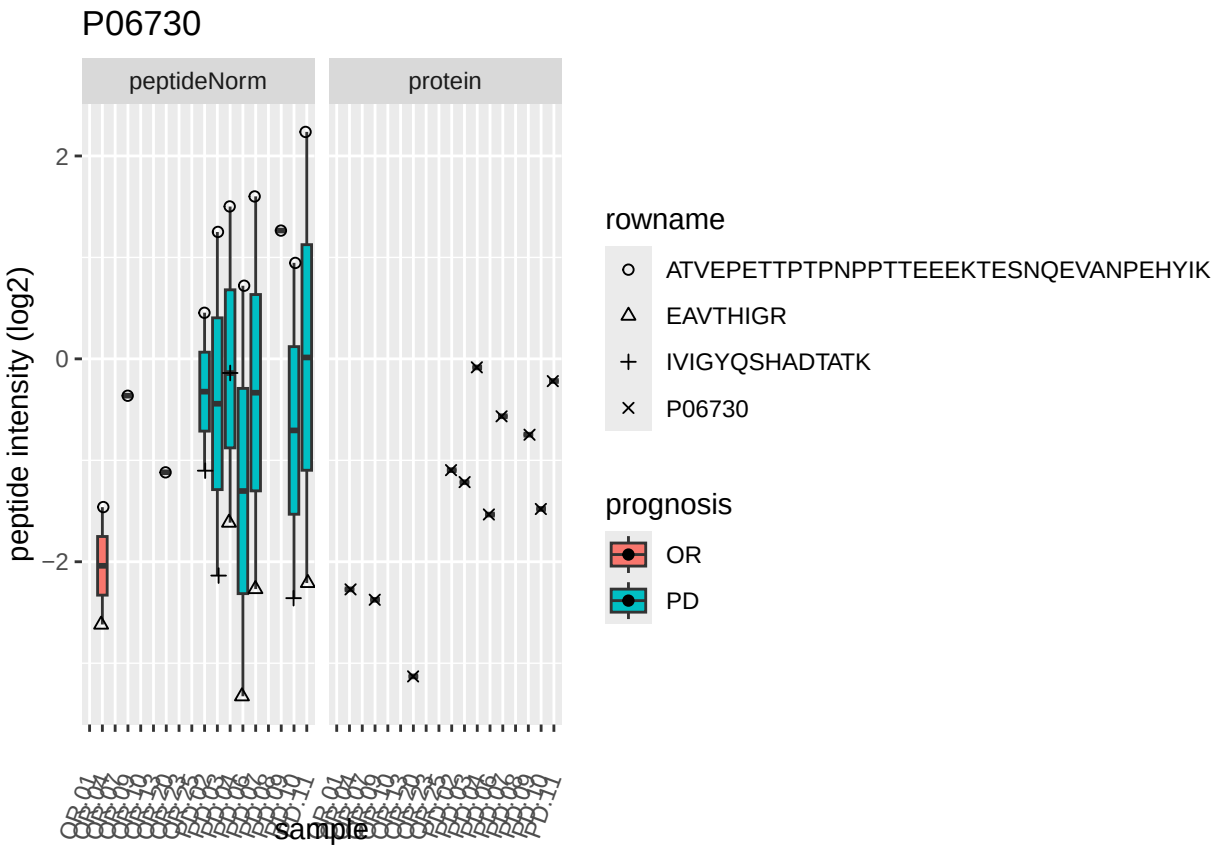
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P06730
peptideNorm
protein
peptide intensity (log2)
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0
−2
sample
rowname
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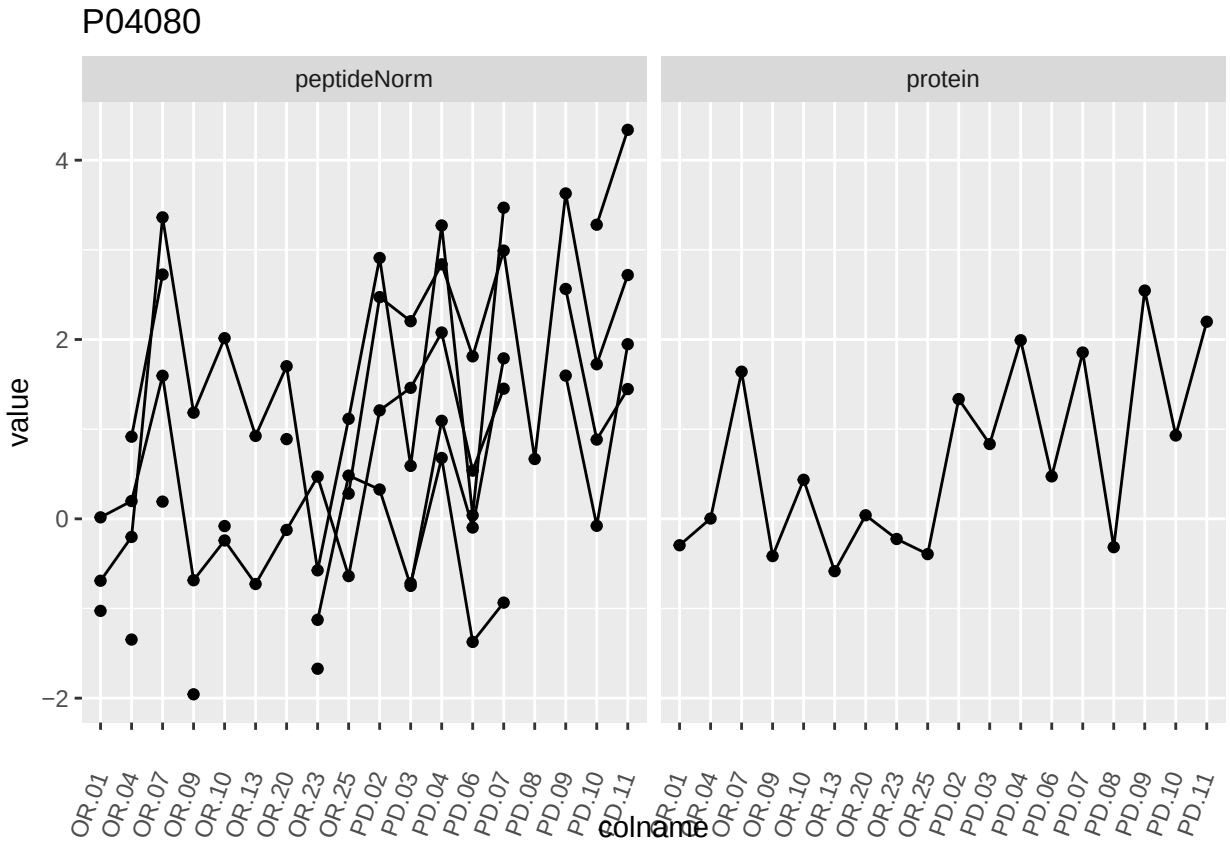
EAVTHIGR
IVIGYQSHADTATK
P06730
prognosis
OR
PD


P04080
peptideNorm
protein
value
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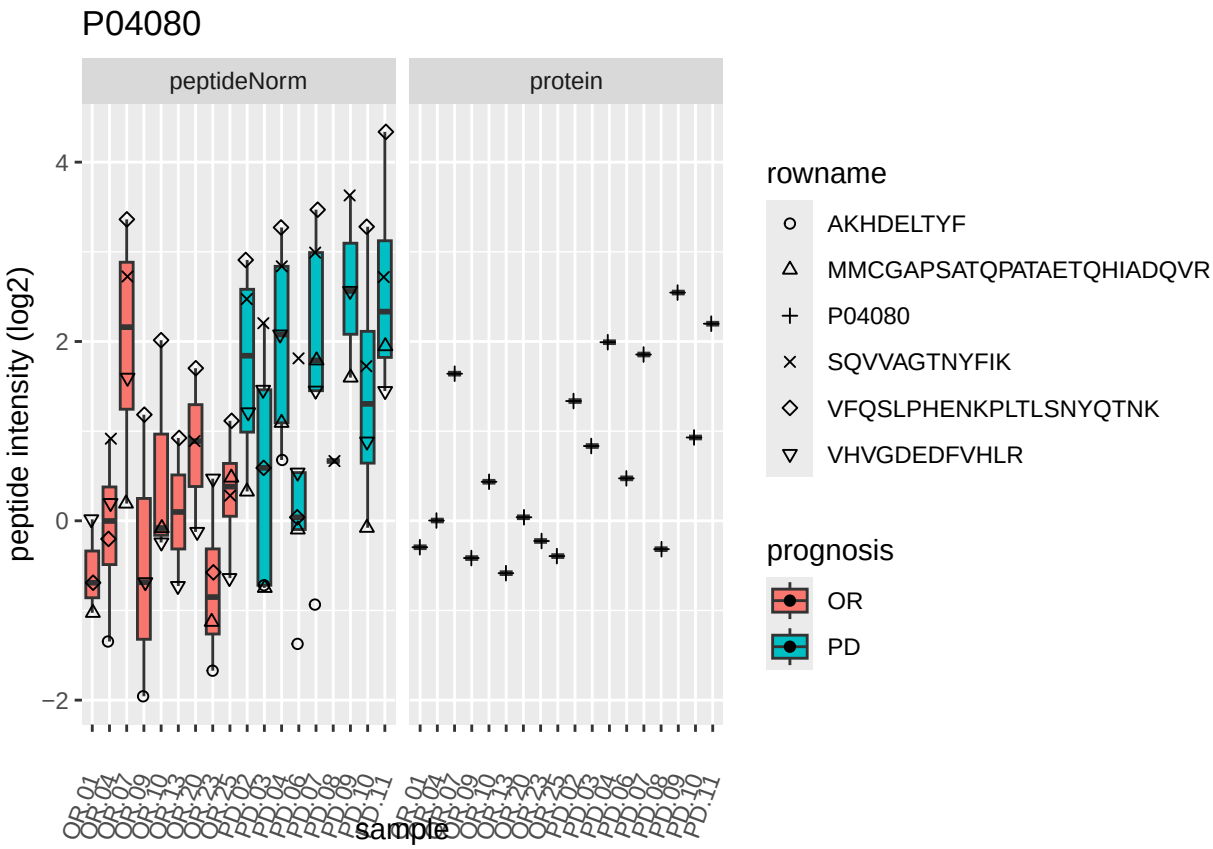
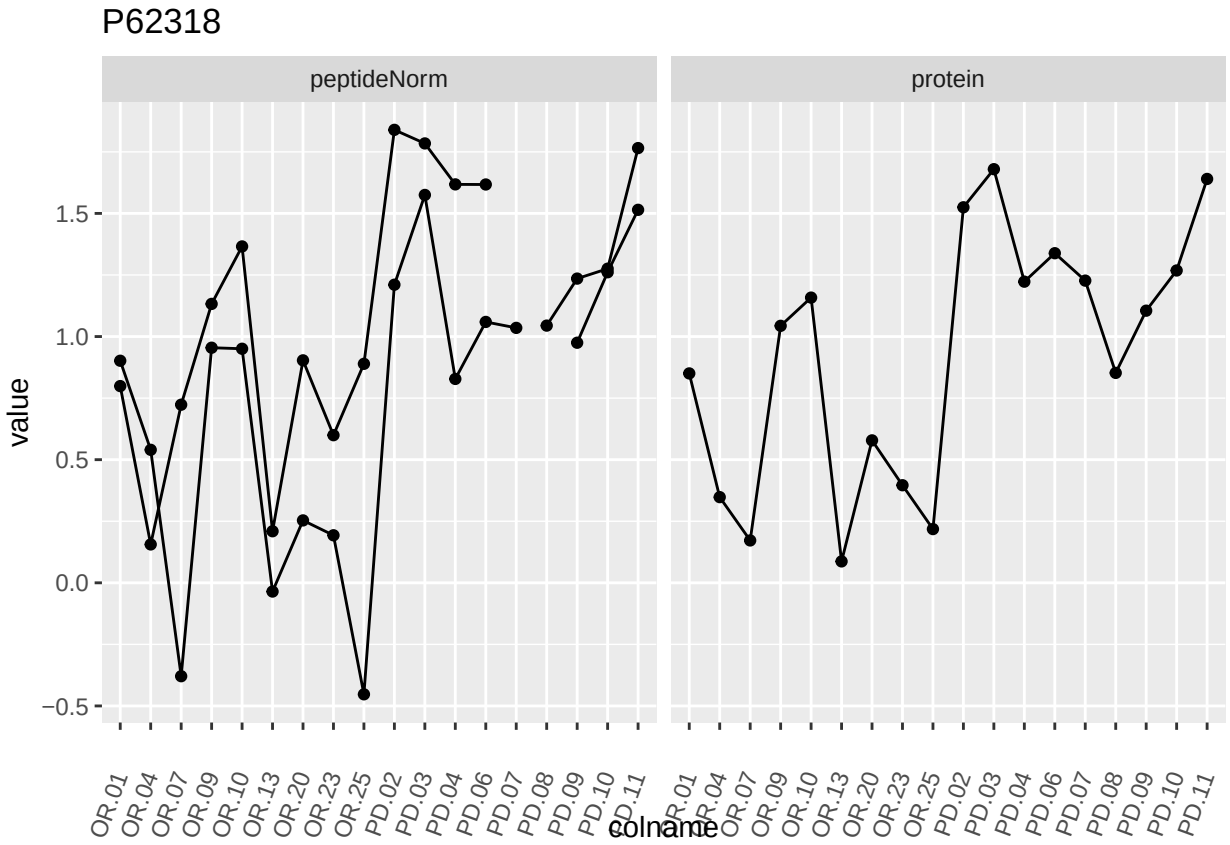
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P04080
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR:01
OR:04
OR:07
OR:09
OR:10
OR:13
OR:20
OR:23
OR:25
PD:02
PD:03
PD:04
PD:06
PD:07
PD:08
PD:09
PD:10
PD:11
sample
rowname
AKHDELTYF
MMCGAPSATQPATAETQHIADQVR
P04080
SQVVAGTNYFIK
VFQSLPHENKPLTLSNYQTNK
VHVGDEDFVHLR
prognosis
OR
PD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peptideNorm
protein
value
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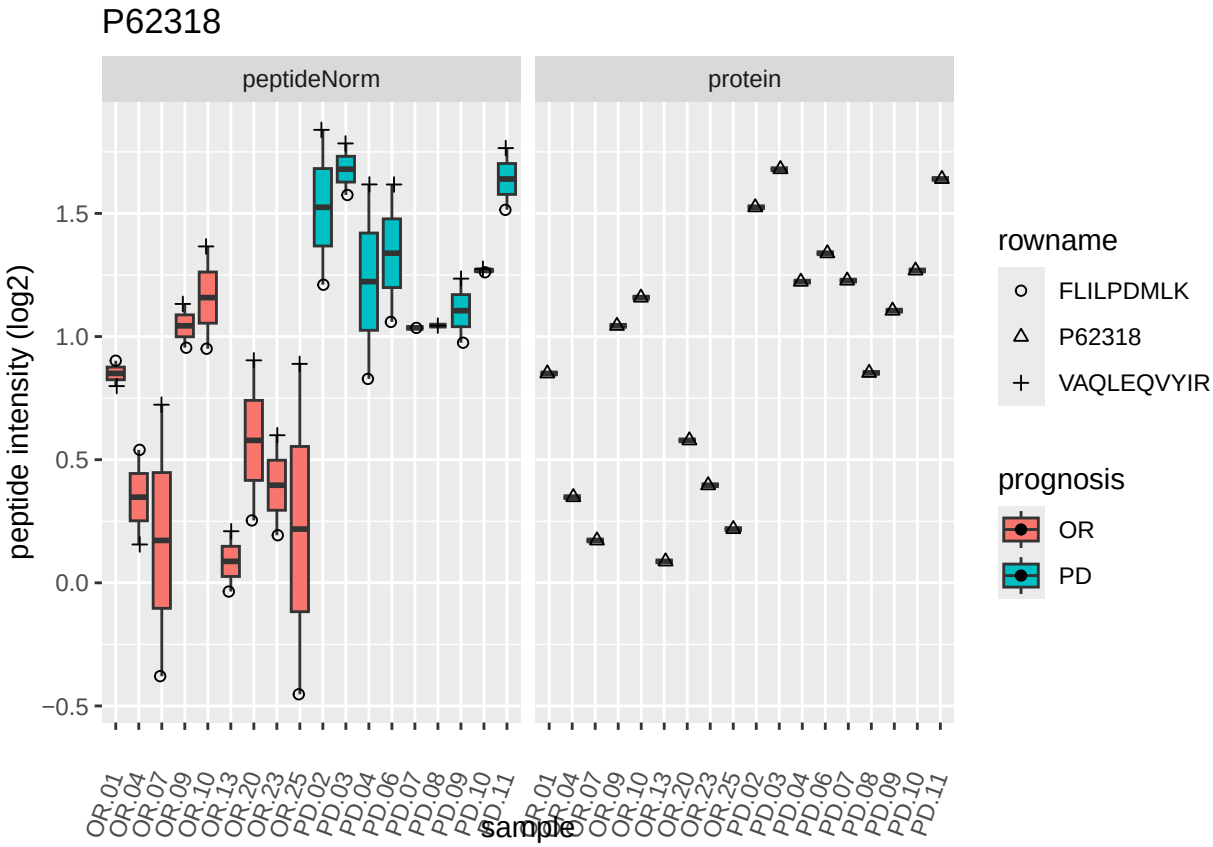
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P62318
peptideNorm
protein
peptide intensity (log2)
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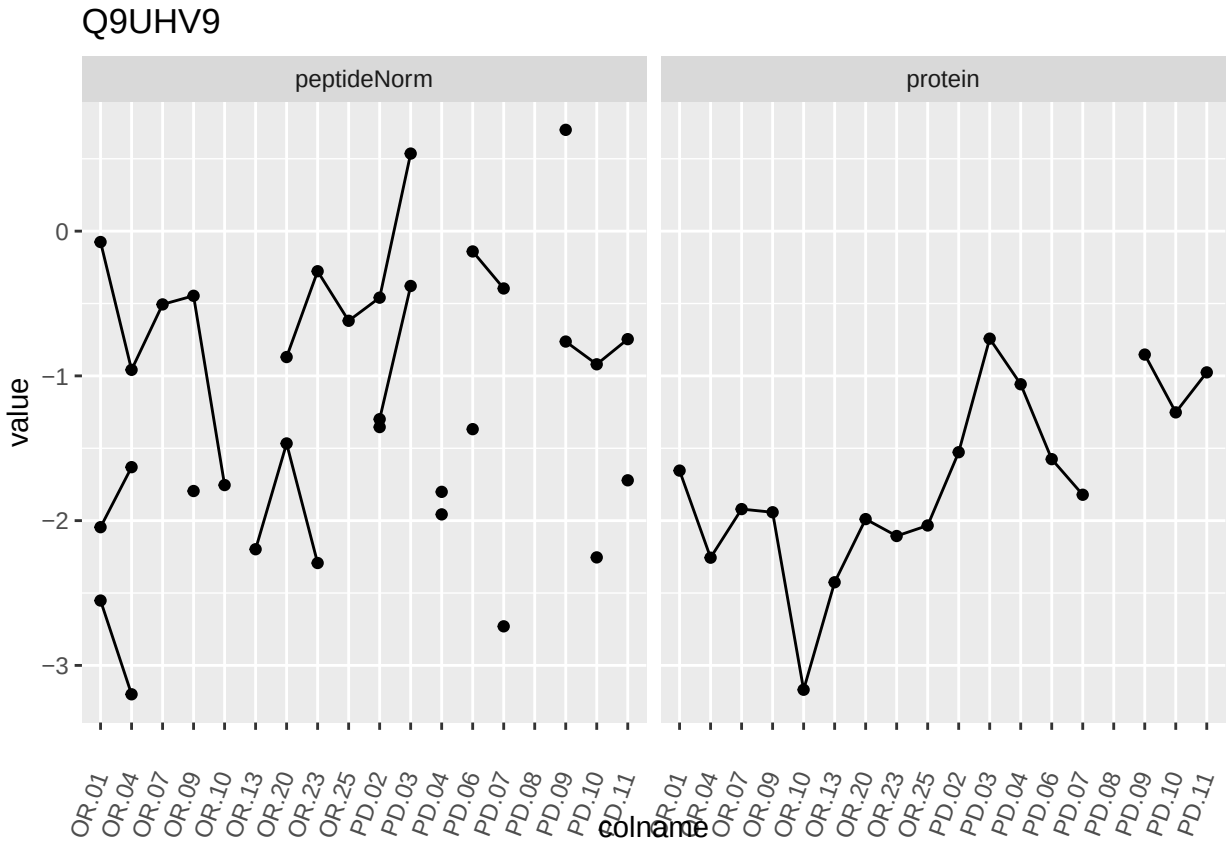
1.0
0.5
0.0
−0.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
FLILPDMLK
P62318
VAQLEQVYIR
prognosis
OR
PD


Q9UHV9
peptideNorm
protein
value
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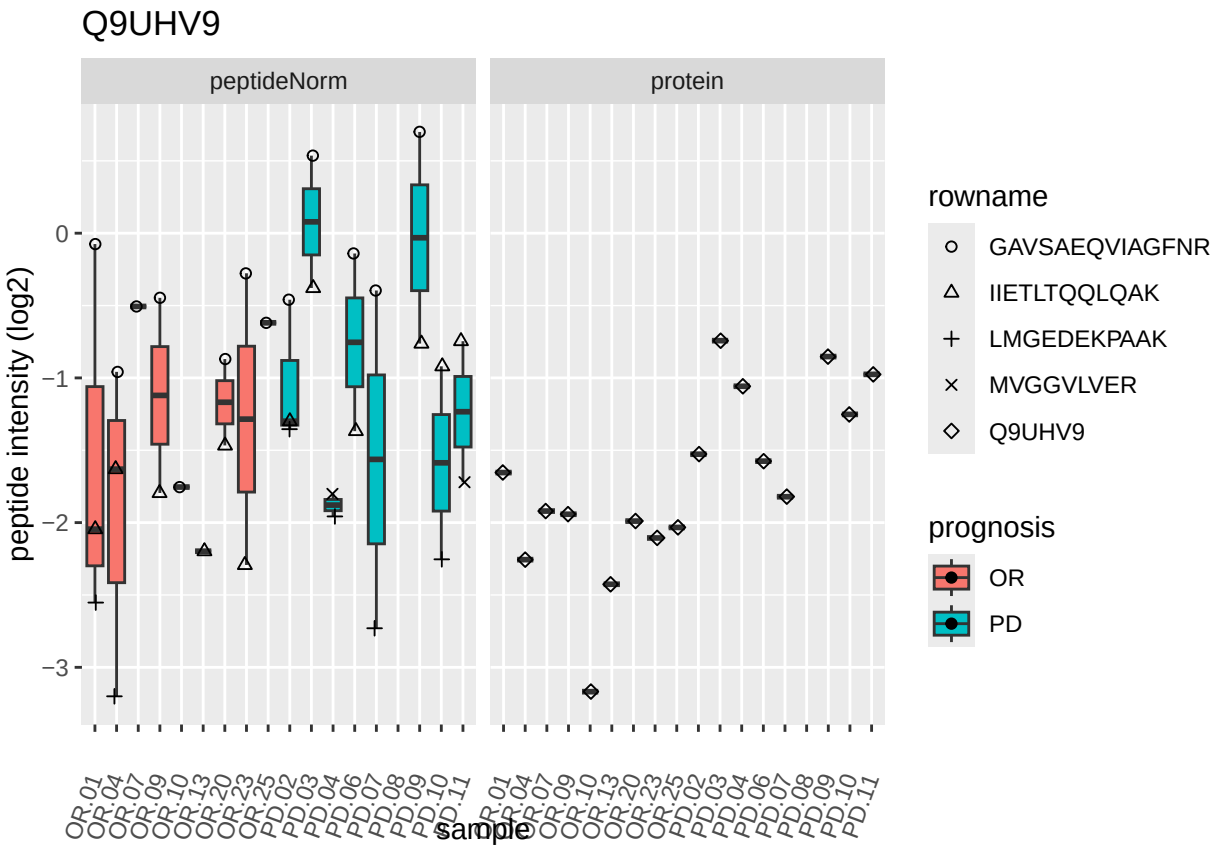
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9UHV9
peptideNorm
protein
peptide intensity (log2)
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−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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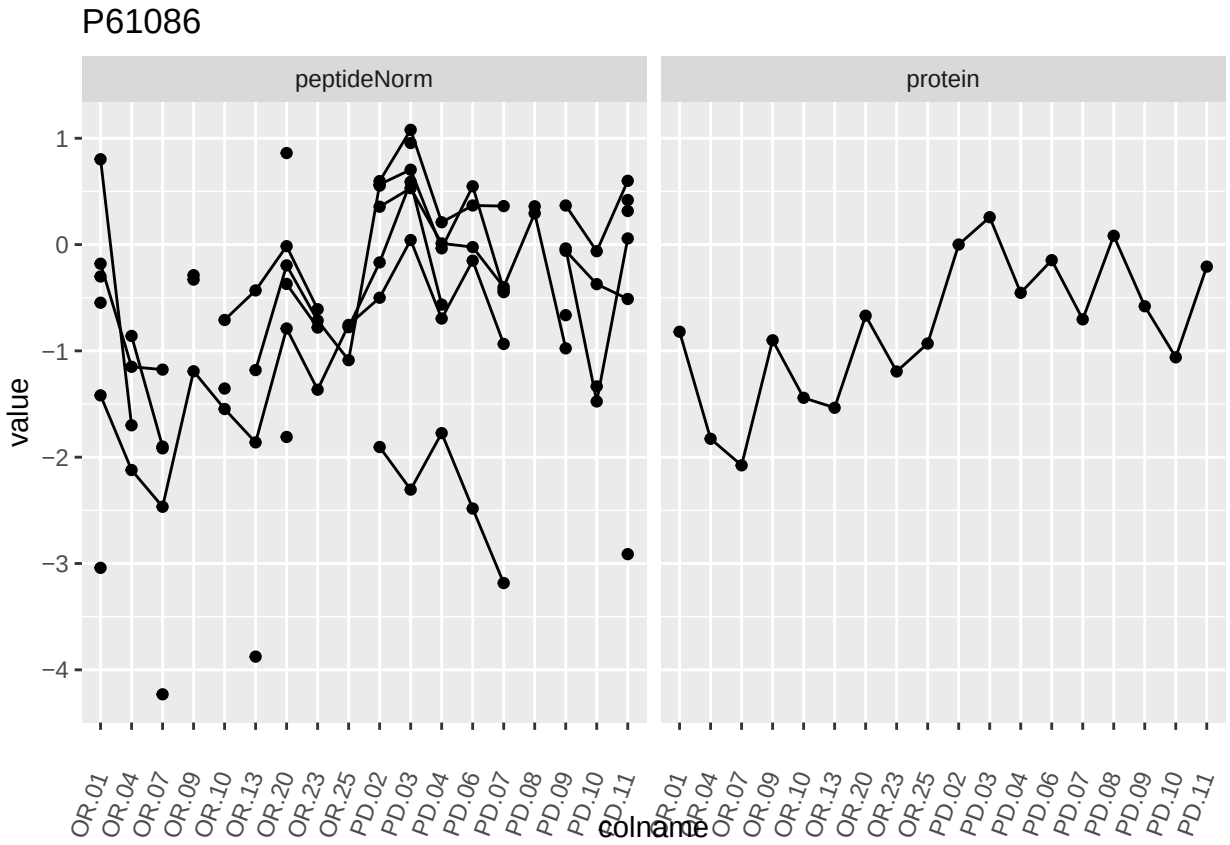
IIETLTQQLQAK
LMGEDEKPAAK
MVGGVLVER
Q9UHV9
prognosis
OR
PD


P61086
peptideNorm
protein
value
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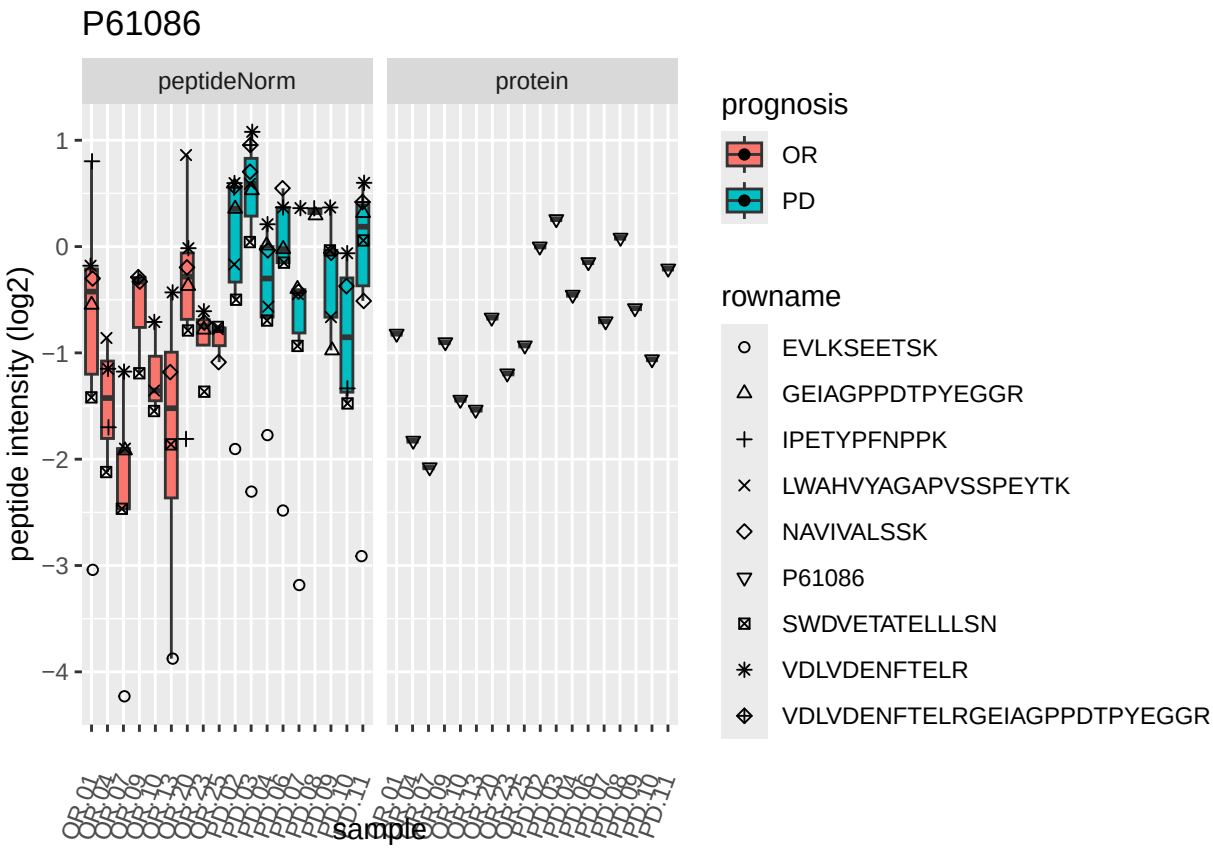
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P61086
peptideNorm
protein
peptide intensity (log2)
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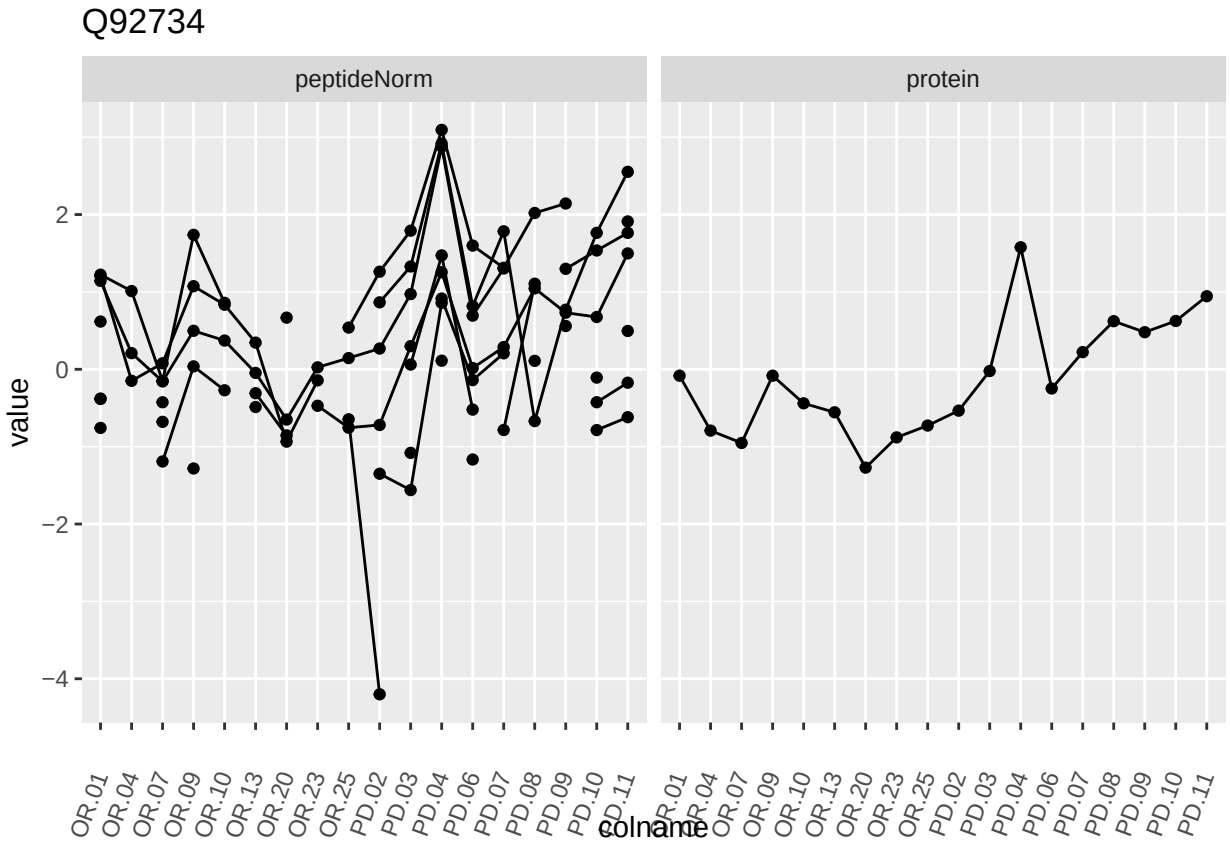
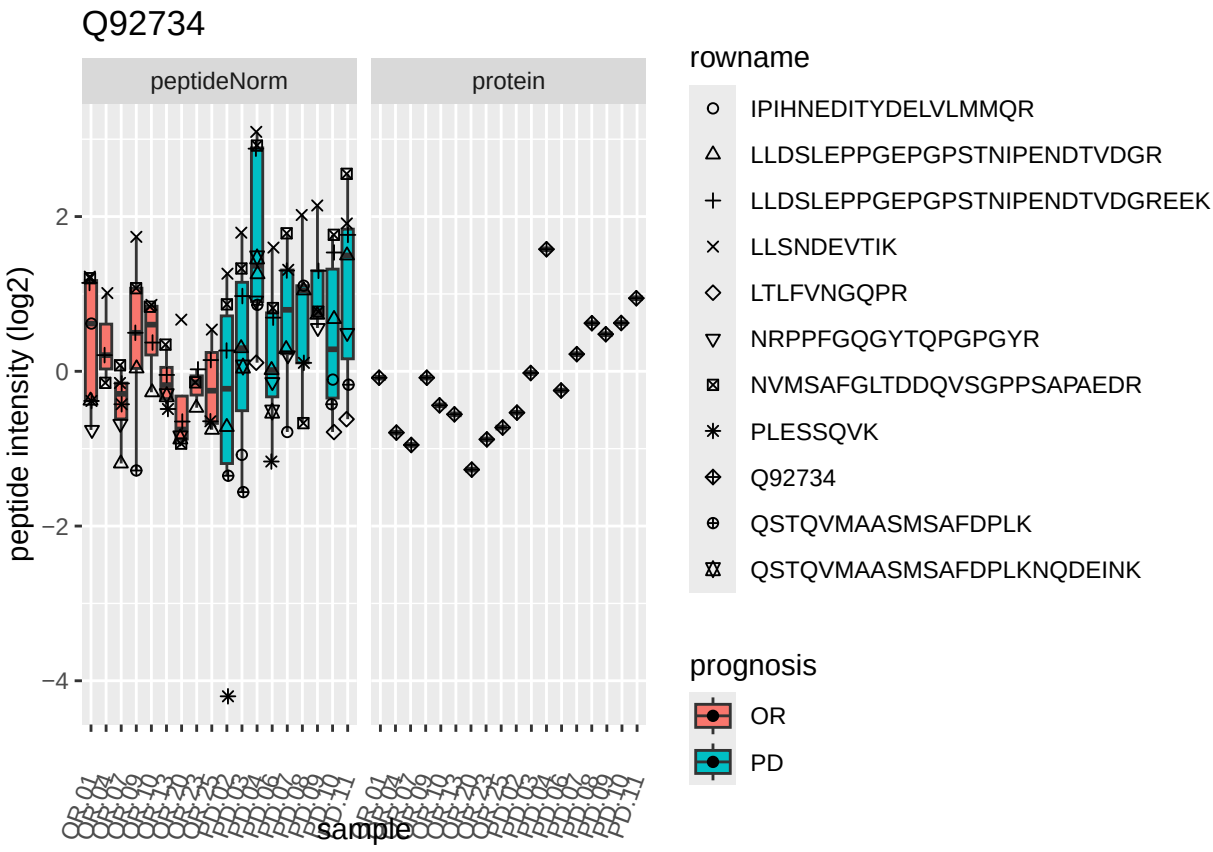
0
−1
−2
−3
−4
sample
prognosis
OR
PD
rowname
EVLKSEETSK
GEIAGPPDTPYEGGR
IPETYPFNPPK
LWAHVYAGAPVSSPEYTK
NAVIVALSSK
P61086
SWDVETATELLLSN
VDLVDENFTELR
VDLVDENFTELRGEIAGPPDTPYEGGR


Q92734
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q92734
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
rowname
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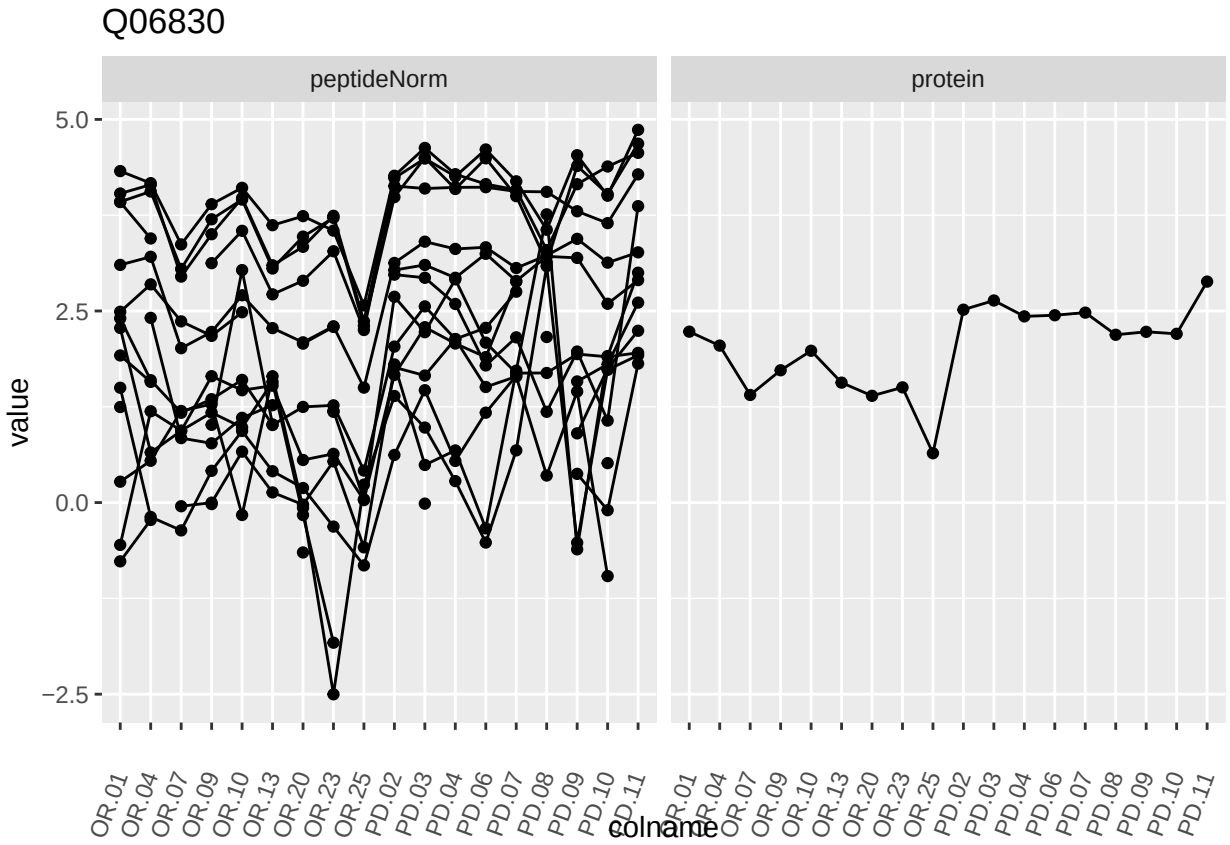
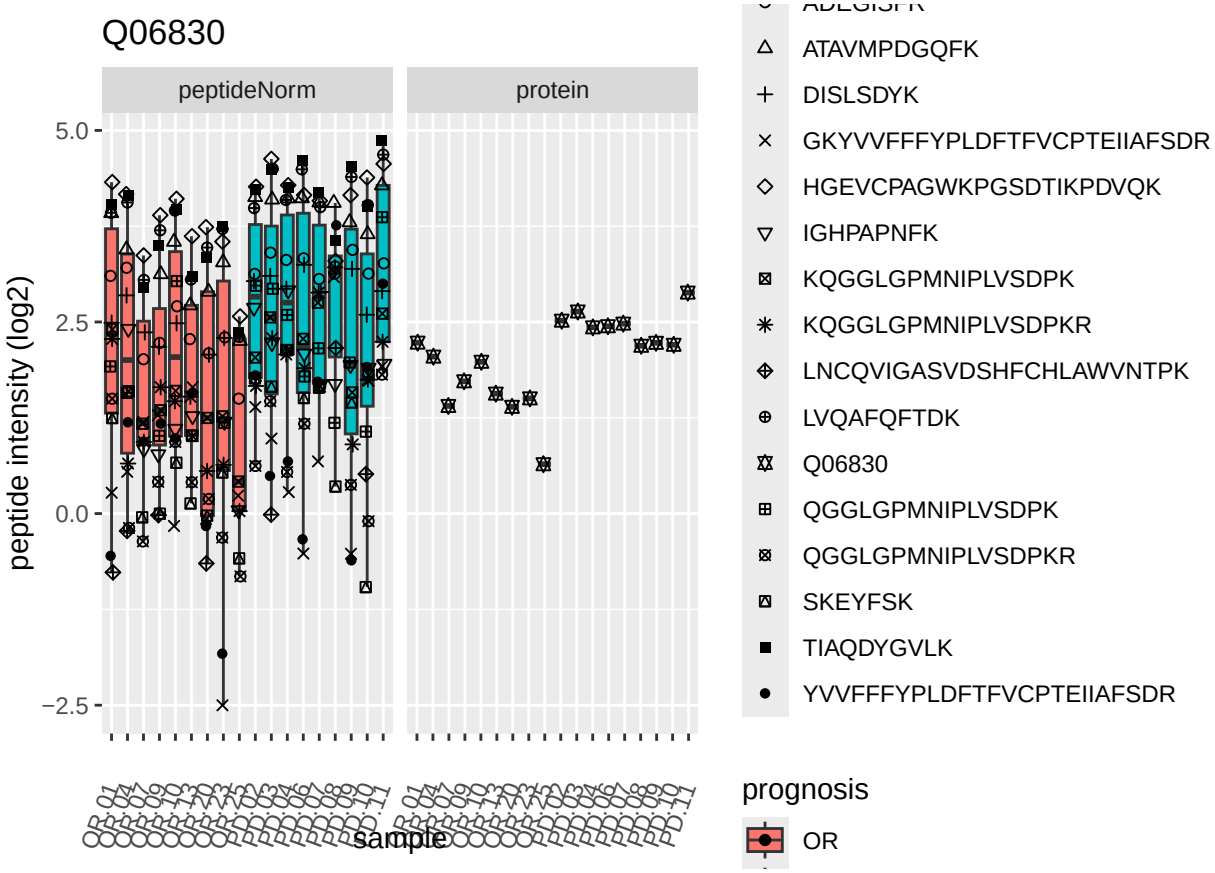
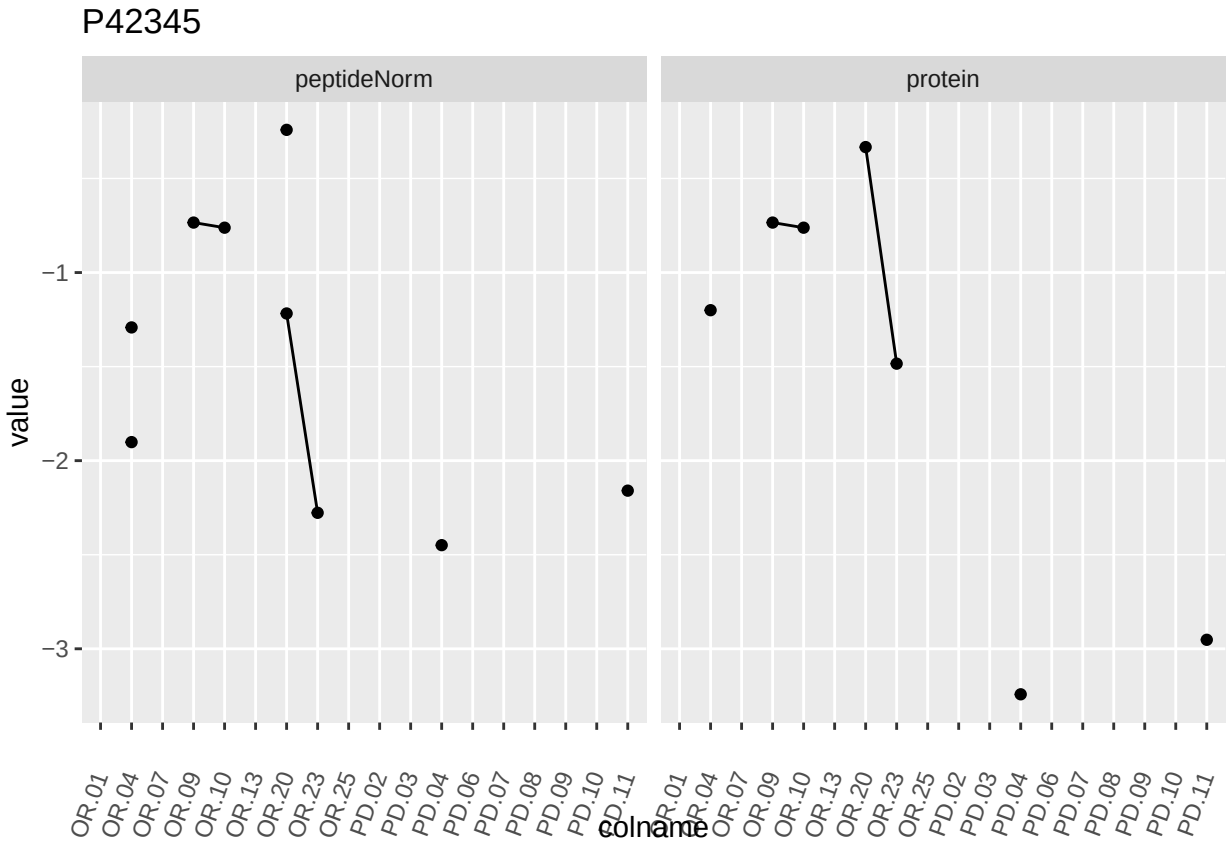
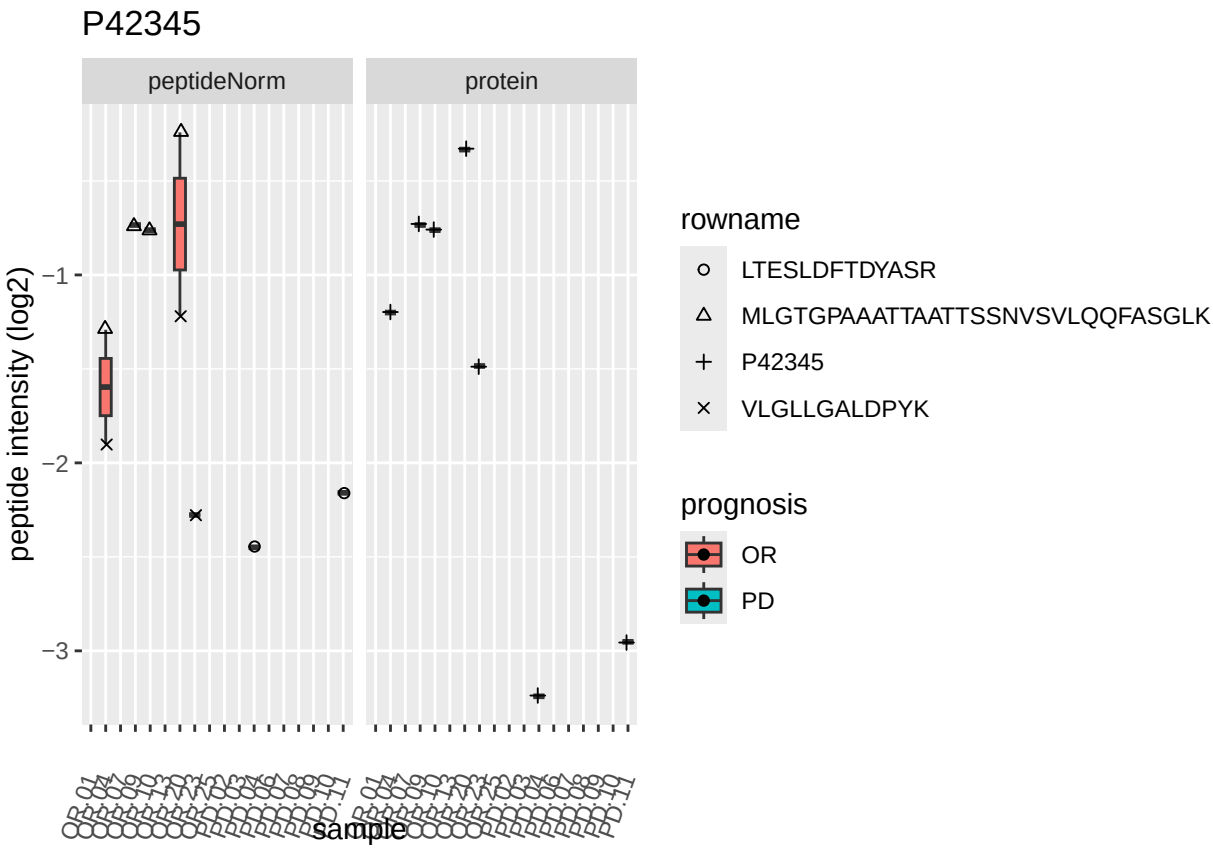
LLDSLEPPGEPGPSTNIPENDTVDGR
LLDSLEPPGEPGPSTNIPENDTVDGREEK
LLSNDEVTIK
LTLFVNGQPR
NRPPFGQGYTQPGPGYR
NVMSAFGLTDDQVSGPPSAPAEDR
PLESSQVK
Q92734
QSTQVMAASMSAFDPLK
QSTQVMAASMSAFDPLKNQDEINK
prognosis
OR
PD


Q06830
peptideNorm
protein
5.0
2.5
0.0
−2.5
value
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q06830
peptideNorm
protein
peptide intensity (log2)
5.0
2.5
0.0
−2.5
sample
ATAVMPDGQFK
DISLSDYK
GKYVVFFFYPLDFTFVCPTEIIAFSDR
HGEVCPAGWKPGSDTIKPDVQK
IGHPAPNFK
KQGGLGPMNIPLVSDPK
KQGGLGPMNIPLVSDPKR
LNCQVIGASVDSHFCHLAWVNTPK
LVQAFQFTDK
Q06830
QGGLGPMNIPLVSDPK
QGGLGPMNIPLVSDPKR
SKEYFSK
TIAQDYGVLK
YVVFFFYPLDFTFVCPTEIIAFSDR
prognosis
OR


P42345
peptideNorm
protein
value
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P42345
peptideNorm
protein
peptide intensity (log2)
−1
−2
−3
sample
rowname
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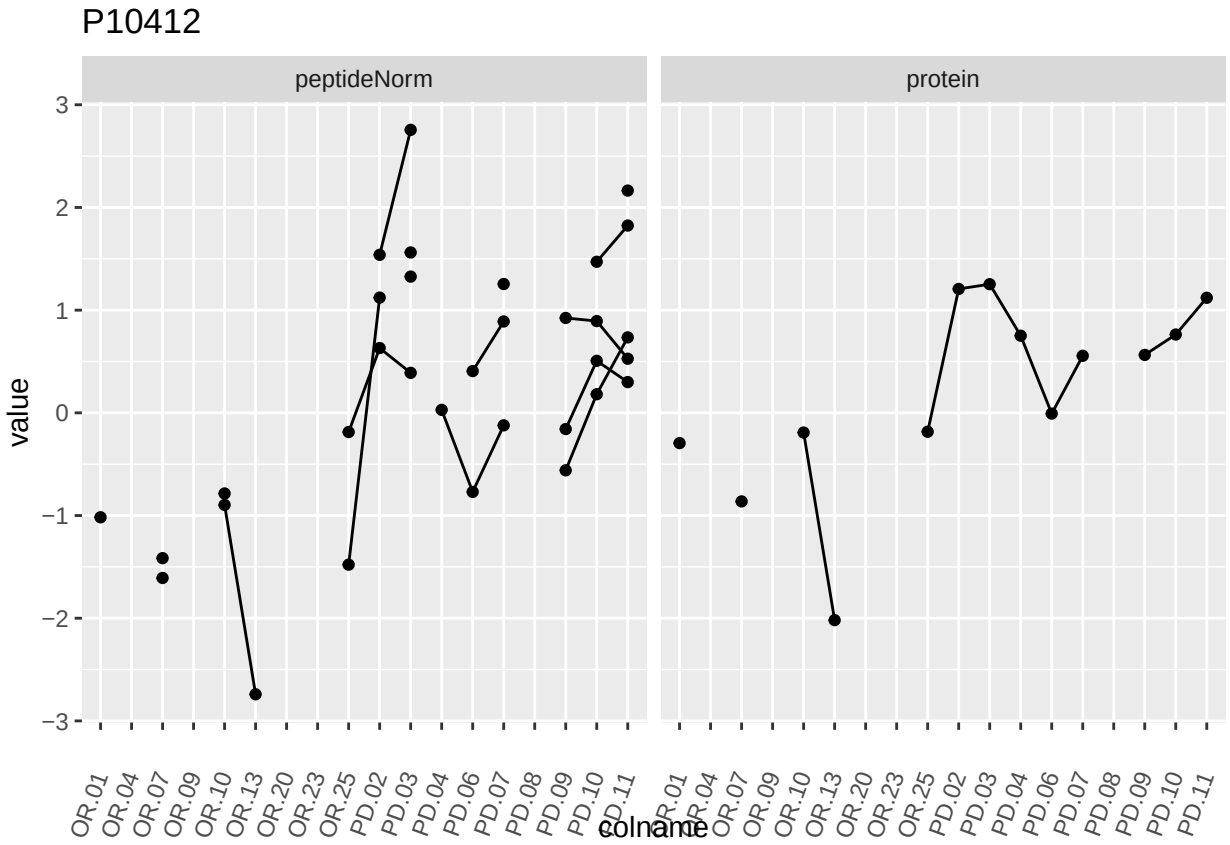
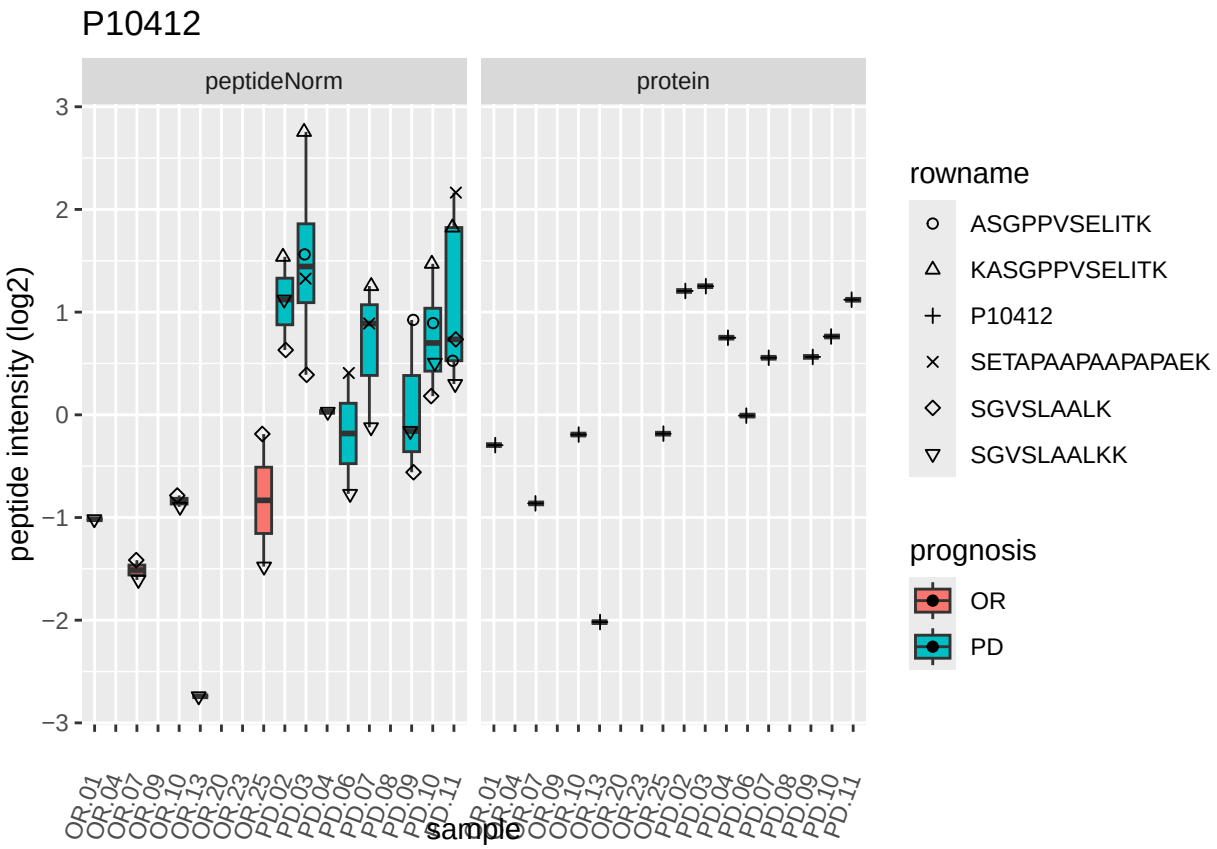
MLGTGPAAATTAATTSSNVSVLQQFASGLK
P42345
VLGLLGALDPYK
prognosis
OR
PD


P10412
peptideNorm
protein
value
3
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P10412
peptideNorm
protein
peptide intensity (log2)
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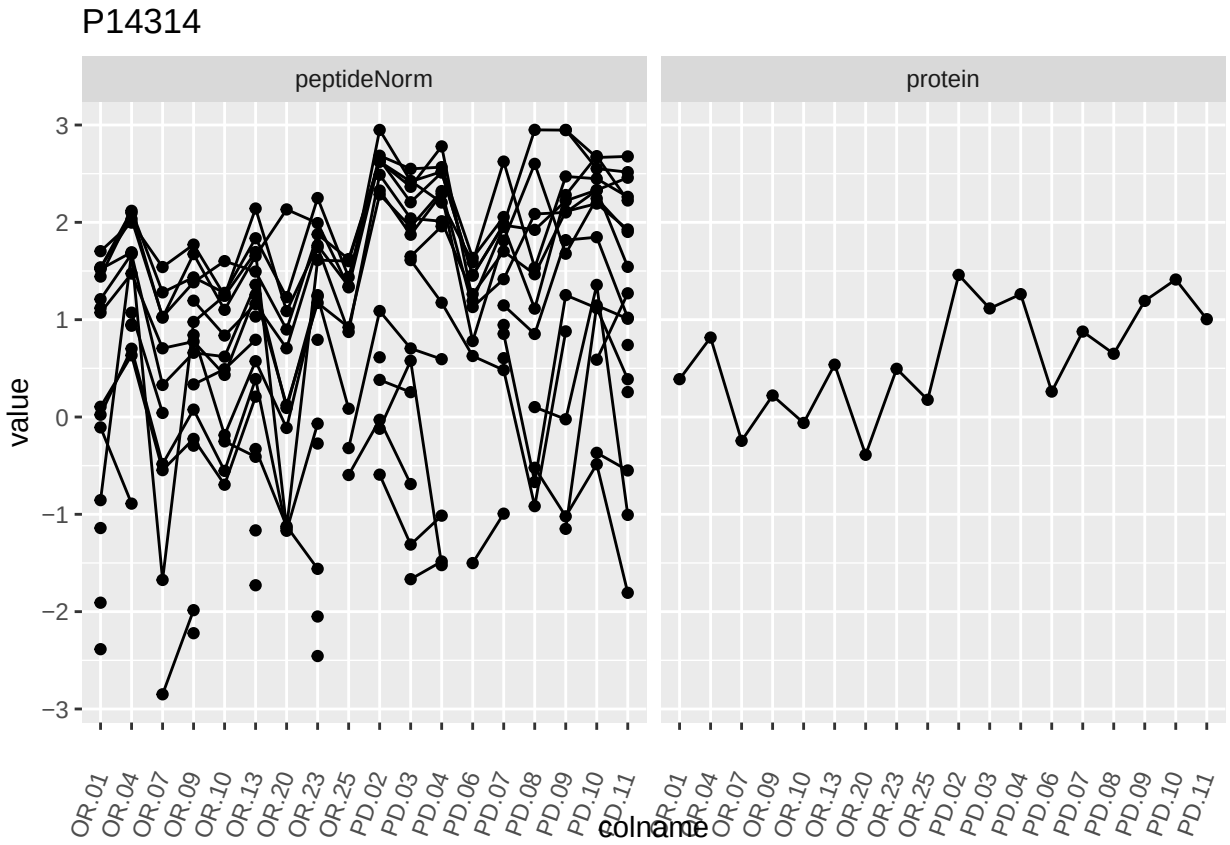
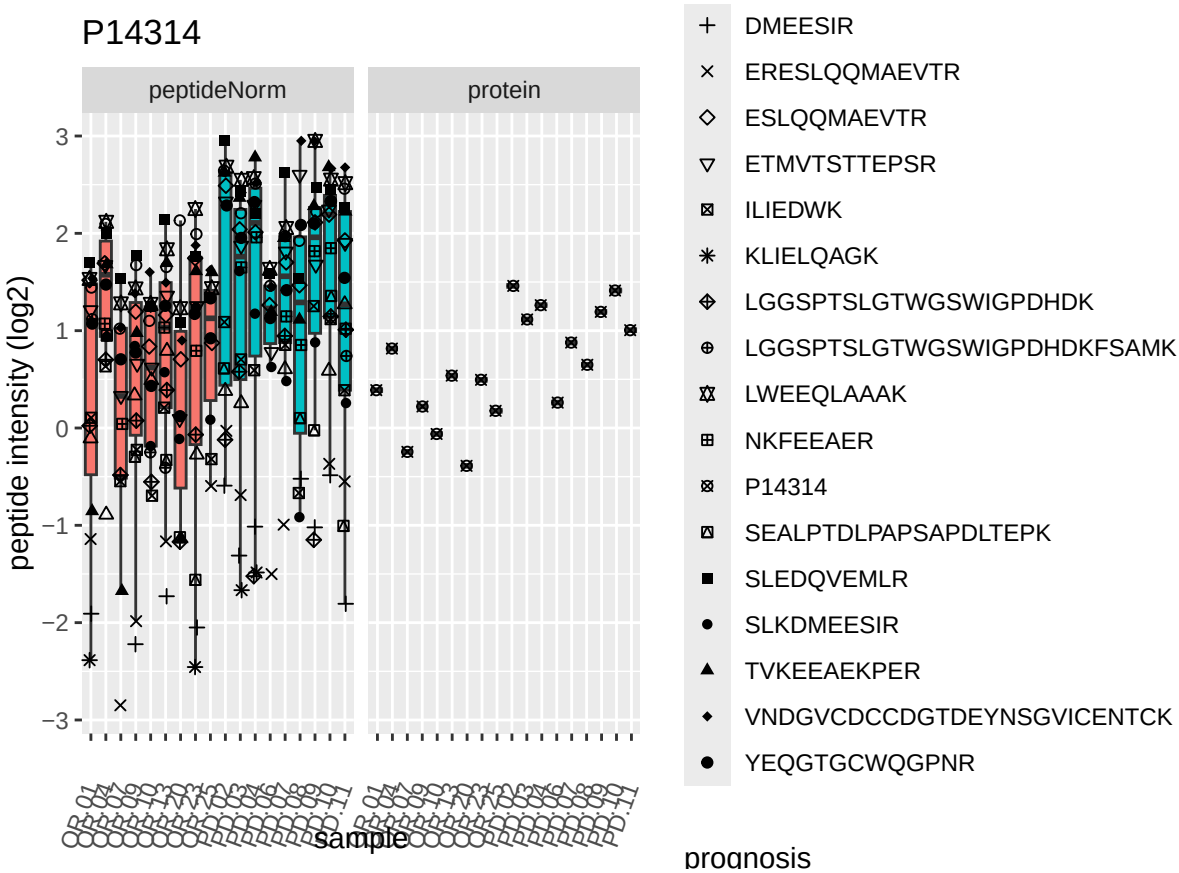
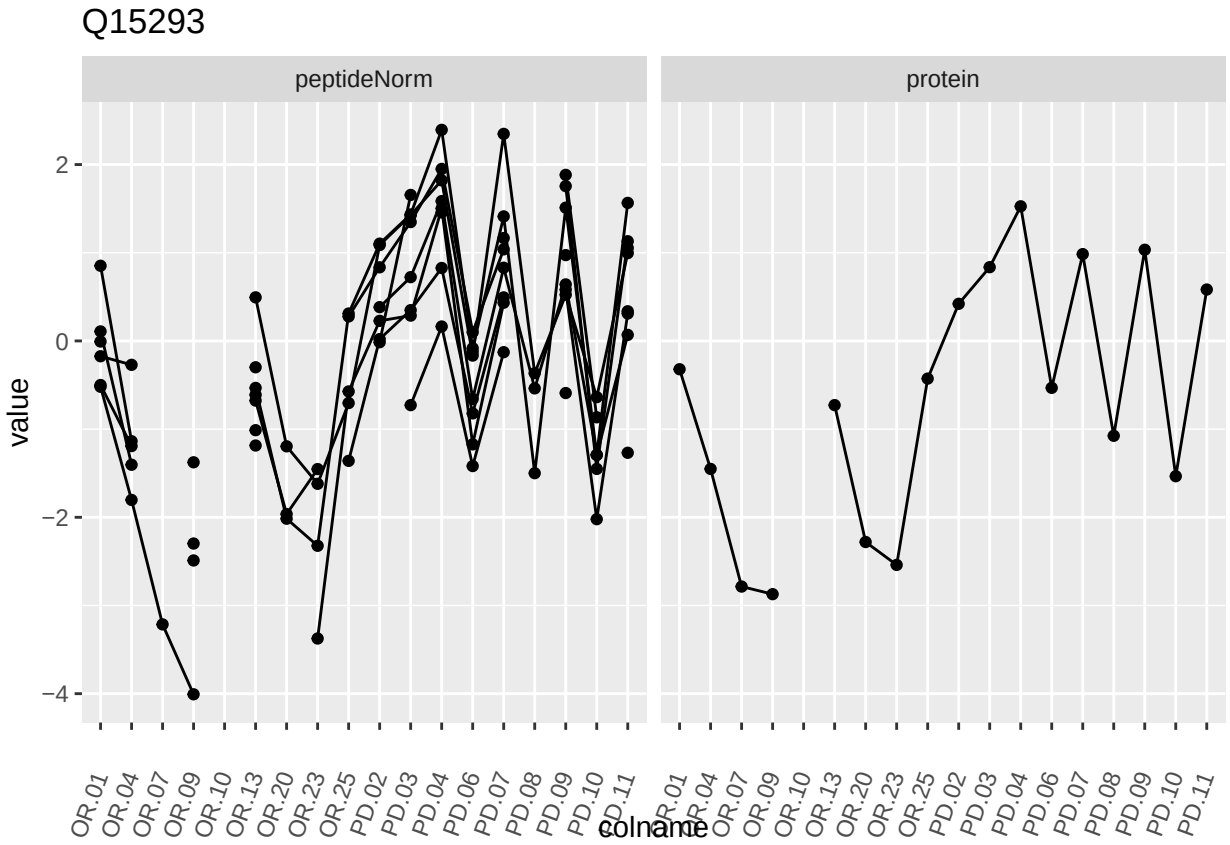
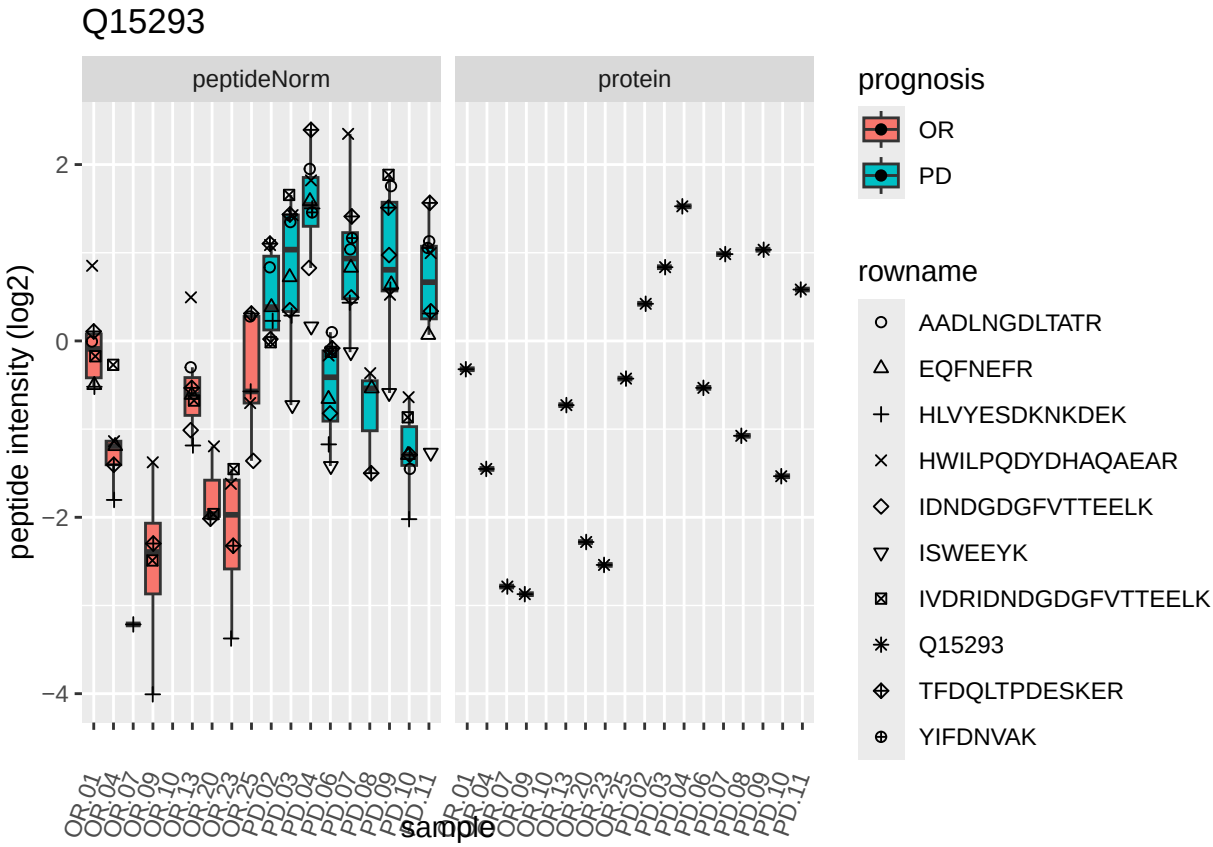
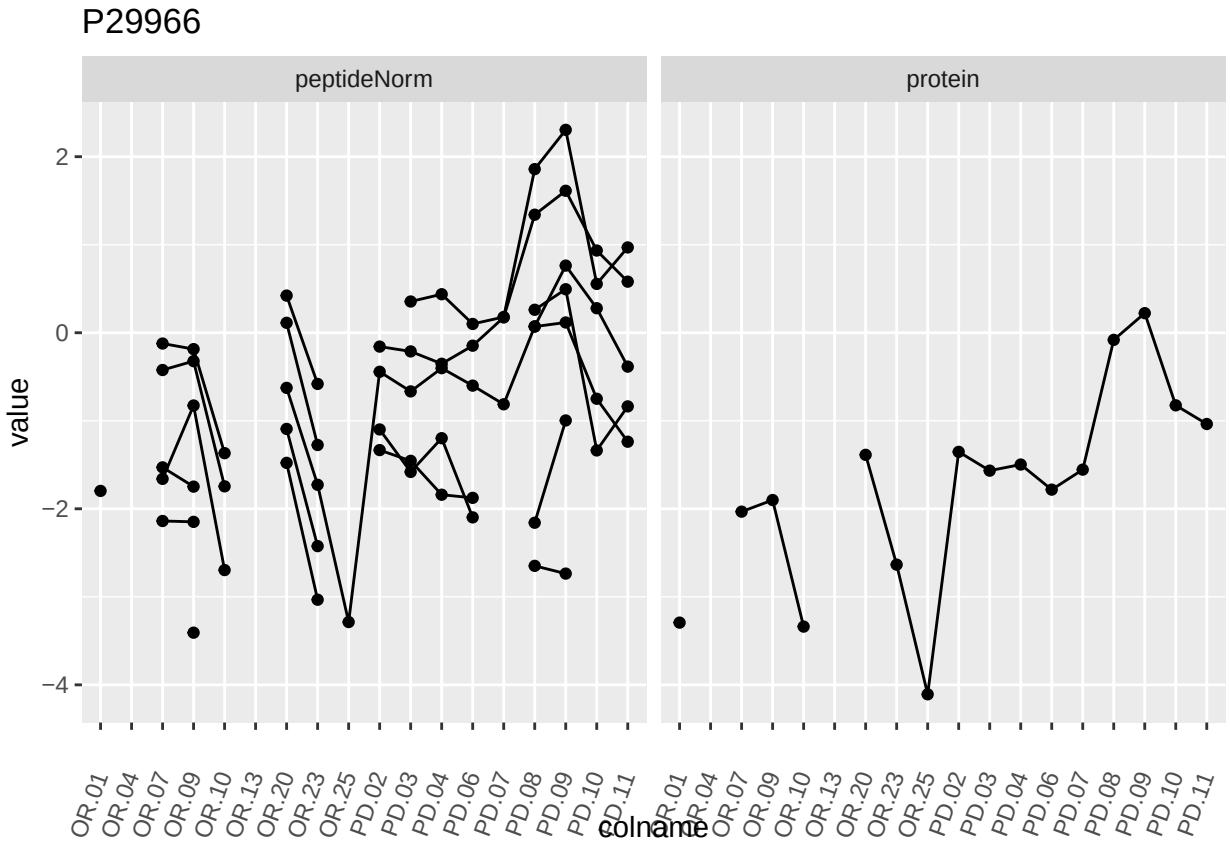
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ASGPPVSELITK
KASGPPVSELITK
P10412
SETAPAAPAAPAPAEK
SGVSLAALK
SGVSLAALKK
prognosis
OR
PD

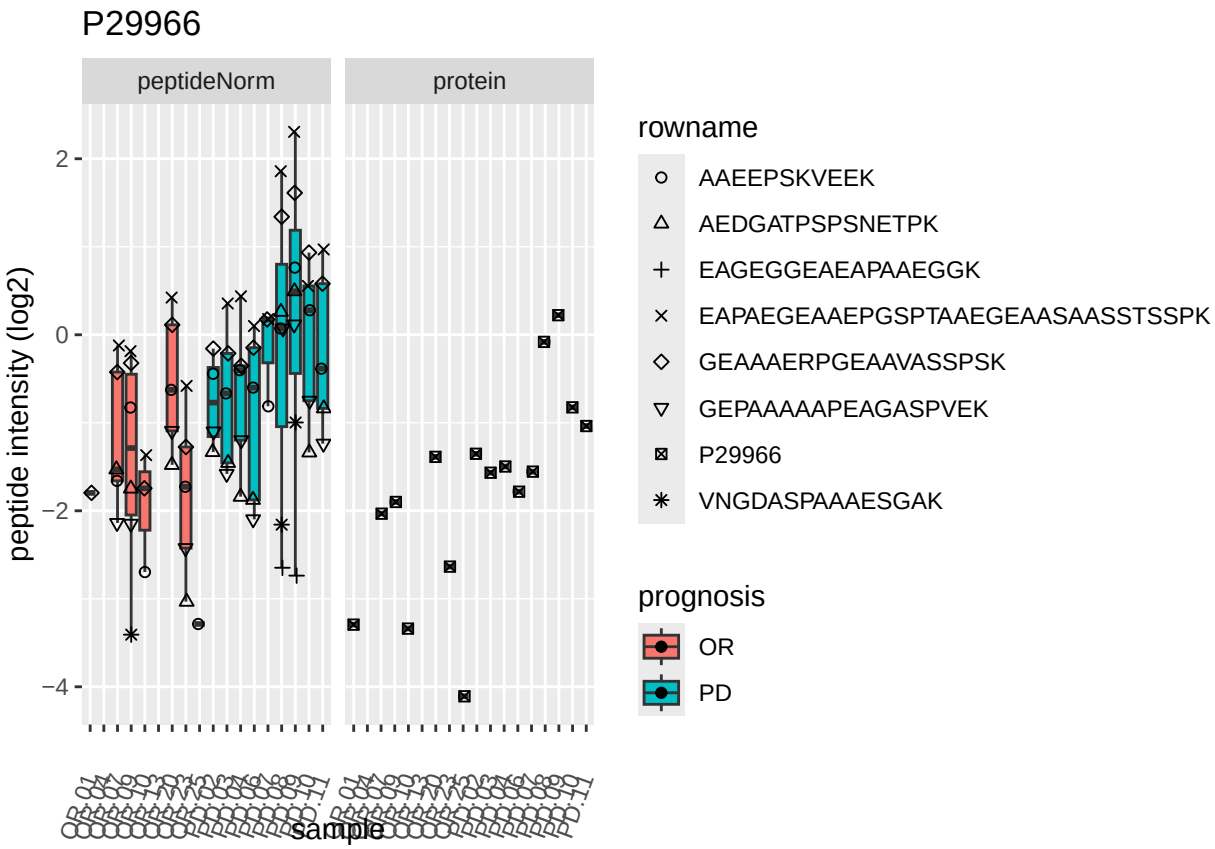

P14314
peptideNorm
protein
value
3
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

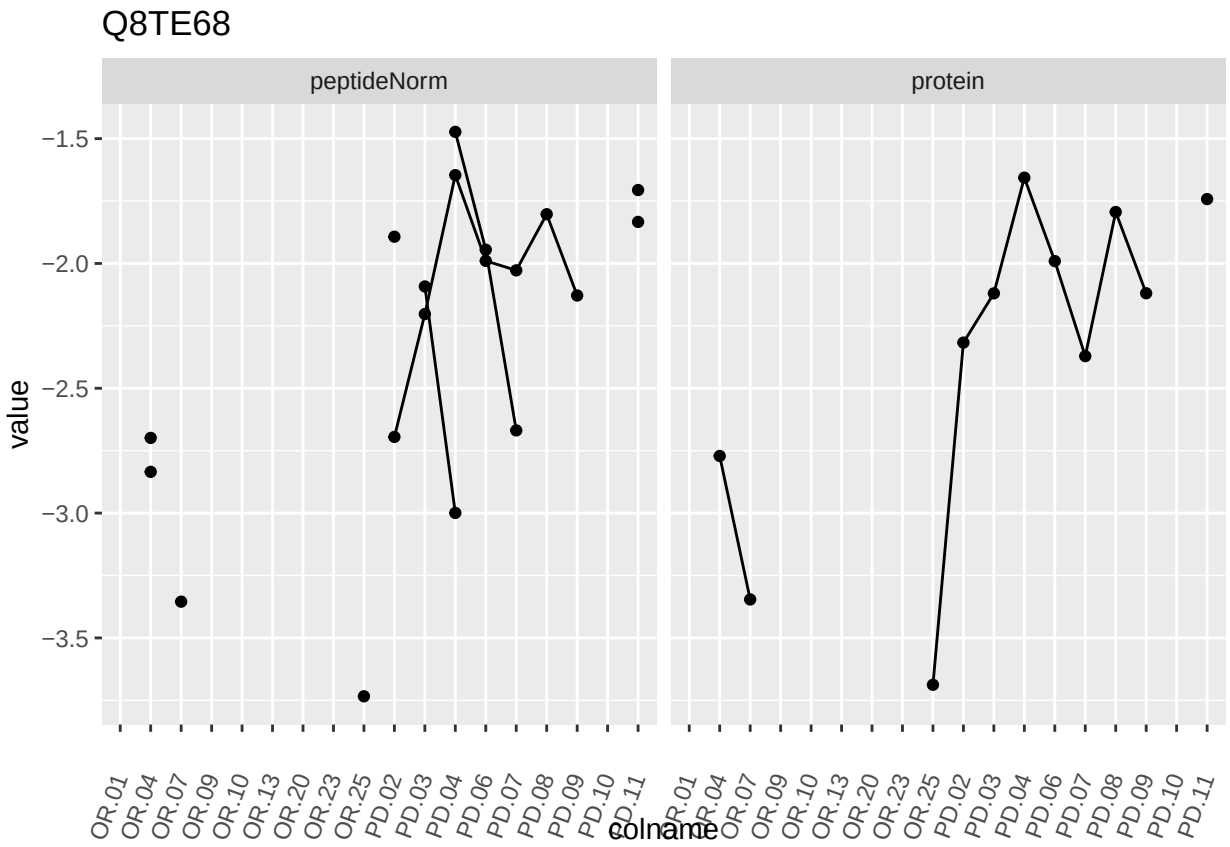

P14314
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
−3
sample
DMEESIR
ERESLQQMAEVTR
ESLQQMAEVTR
ETMVTSTTEPSR
ILIEDWK
KLIELQAGK
LGGSPTSLGTWGSWIGPDHDK
LGGSPTSLGTWGSWIGPDHDKFSAMK
LWEEQLAAAK
NKFEEAER
P14314
SEALPTDLPAPSAPDLTEPK
SLEDQVEMLR
SLKDMEESIR
TVKEEAEKPER
VNDGVCDCCDGTDEYNSGVICENTCK
YEQGTGCWQGPNR
prognosis

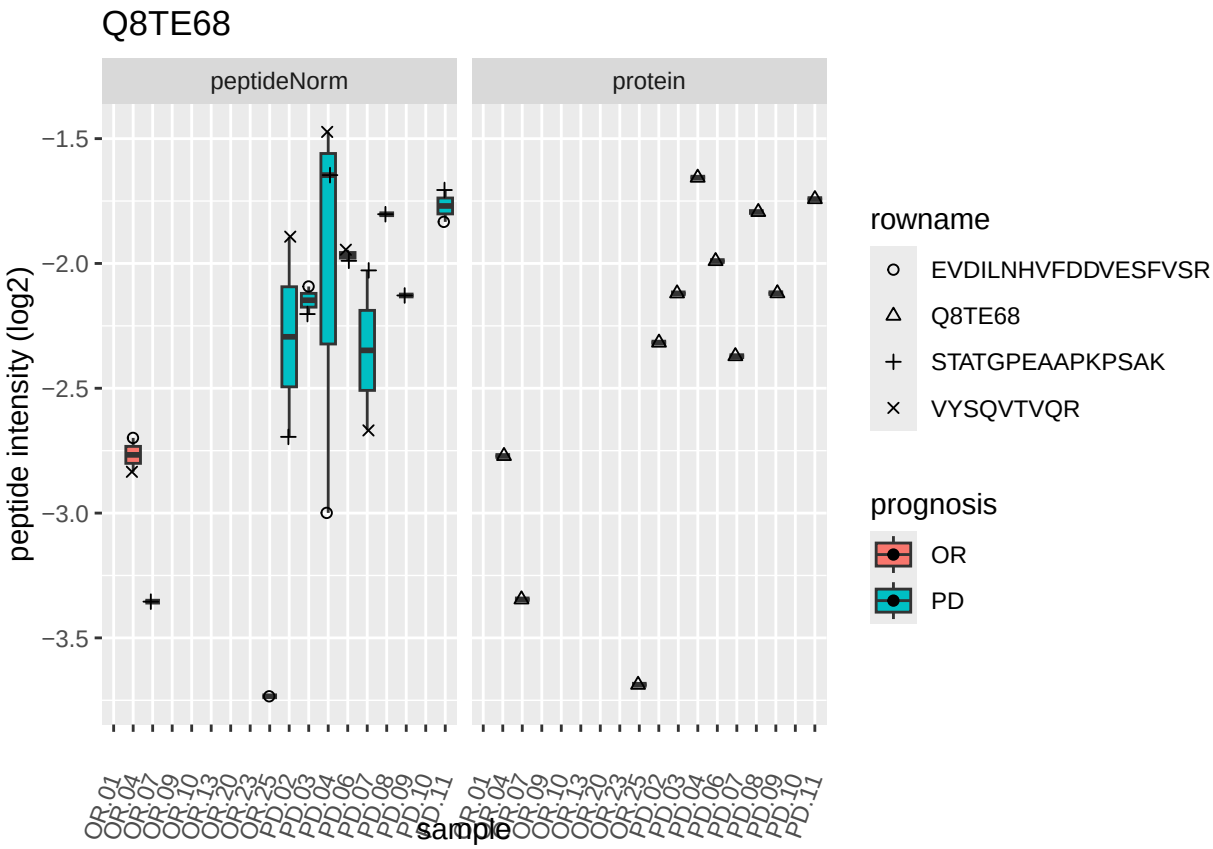

Q15293
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

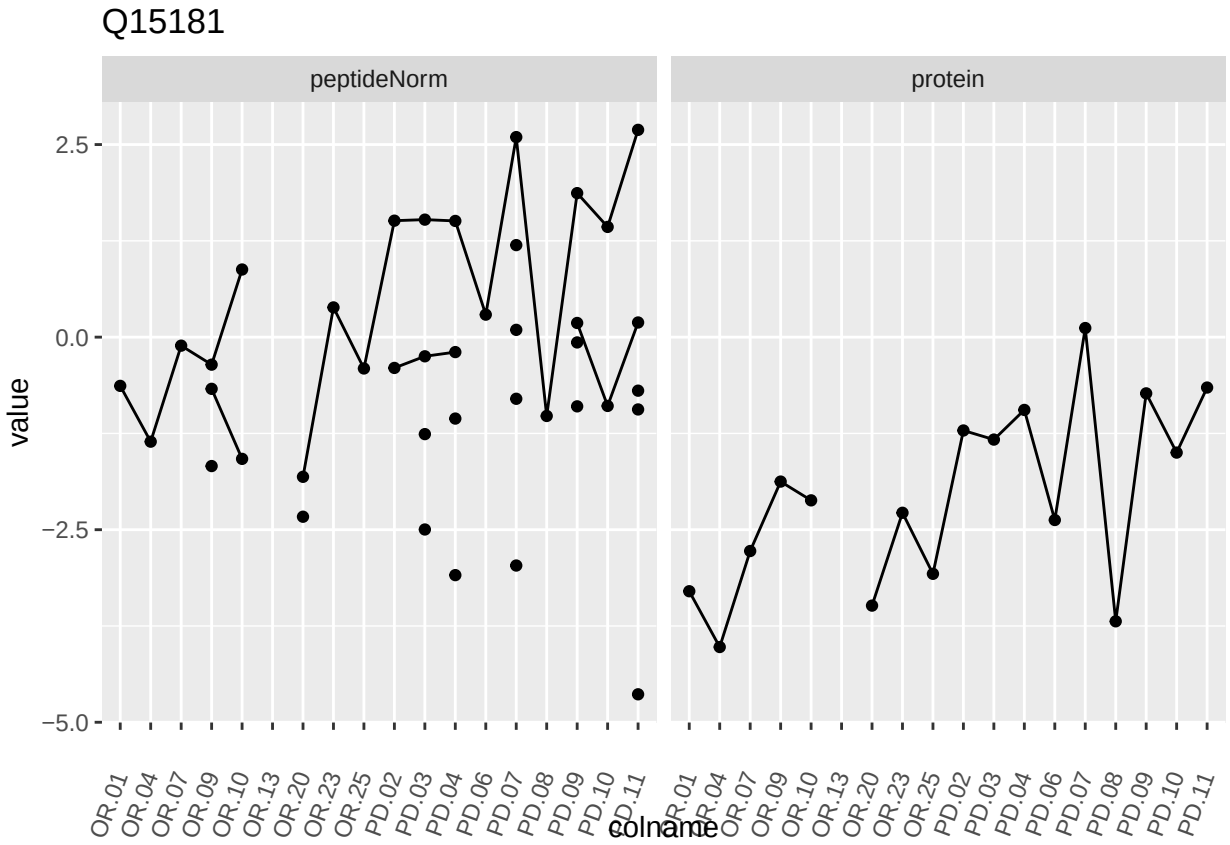

Q15293
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
AADLNGDLTATR
EQFNEFR
HLVYESDKNKDEK
HWILPQDYDHAQAEAR
IDNDGDGFVTTEELK
ISWEEYK
IVDRIDNDGDGFVTTEELK
Q15293
TFDQLTPDESKER
YIFDNVAK

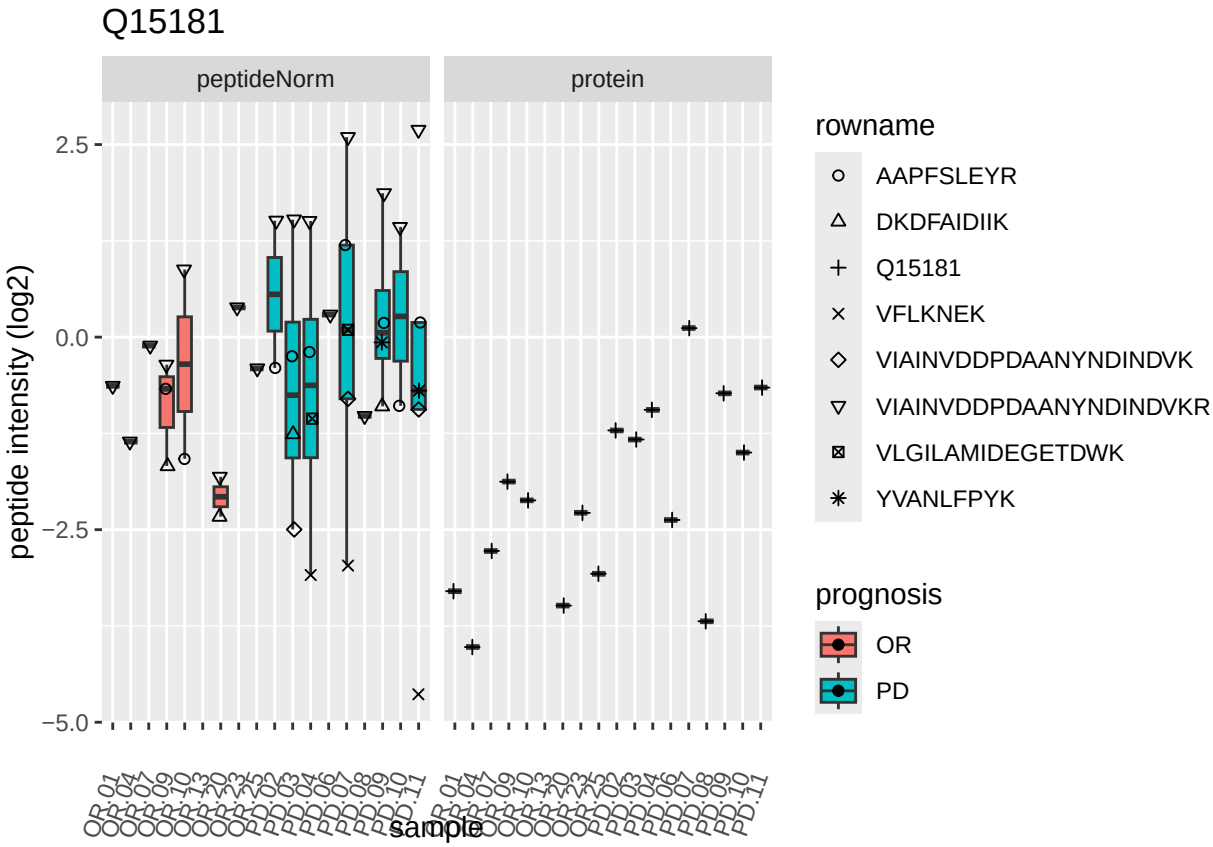

P29966
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P29966
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
rowname
AAEEPSKVEEK
AEDGATPSPSNETPK
EAGEGGEAEAPAAEGGK
EAPAEGEAAEPGSPTAAEGEAASAASSTSSPK
GEAAAERPGEAAVASSPSK
GEPAAAAAPEAGASPVEK
P29966
VNGDASPAAAESGAK
prognosis
OR
PD


Q8TE68
peptideNorm
protein
value
−1.5
−2.0
−2.5
−3.0
−3.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q8TE68
peptideNorm
protein
peptide intensity (log2)
−1.5
−2.0
−2.5
−3.0
−3.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EVDILNHVFDDVESFVSR
Q8TE68
STATGPEAAPKPSAK
VYSQVTVQR
prognosis
OR
PD


Q15181
peptideNorm
protein
value
2.5
0.0
−2.5
−5.0
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q15181
peptideNorm
protein
peptide intensity (log2)
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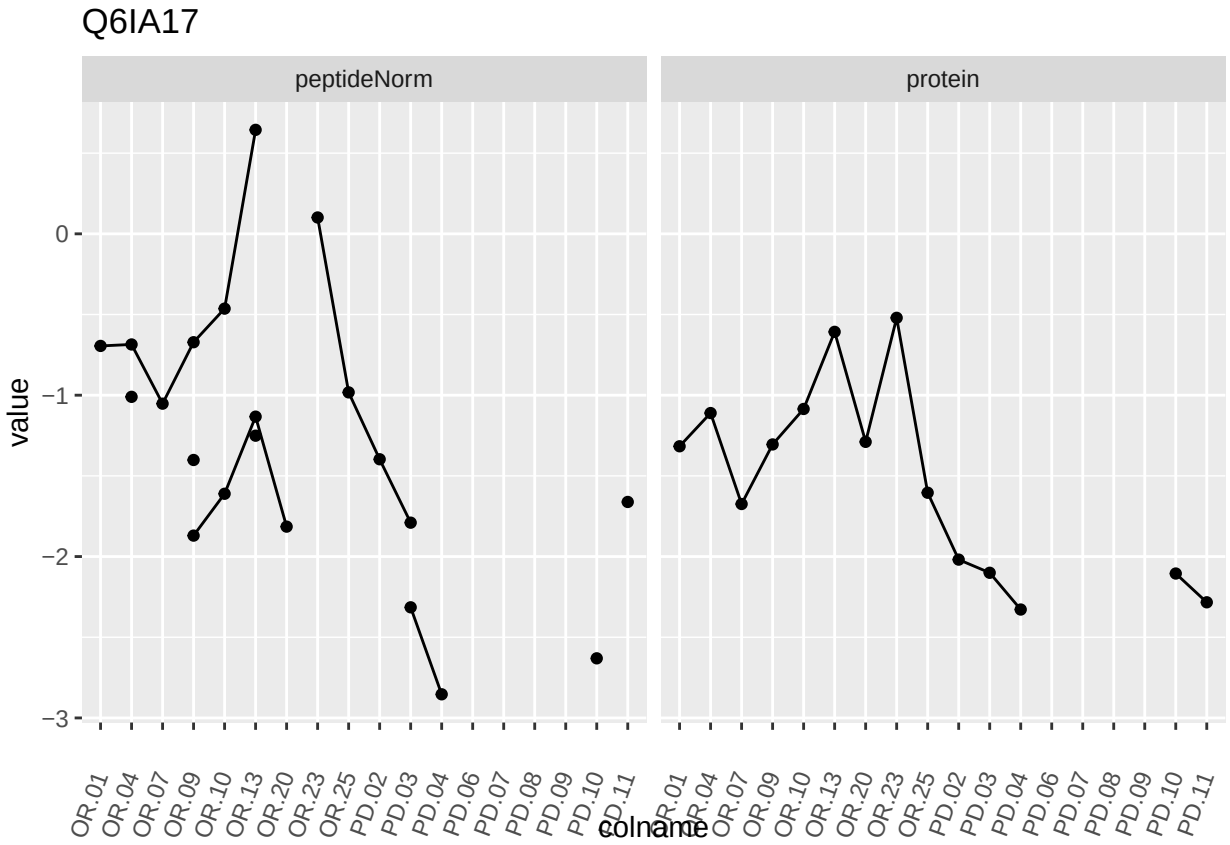
0.0
−2.5
−5.0
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AAPFSLEYR
DKDFAIDIIK
Q15181
VFLKNEK
VIAINVDDPDAANYNDINDVK
VIAINVDDPDAANYNDINDVKR
VLGILAMIDEGETDWK
YVANLFPYK
prognosis
OR
PD


Q6IA17
peptideNorm
protein
value
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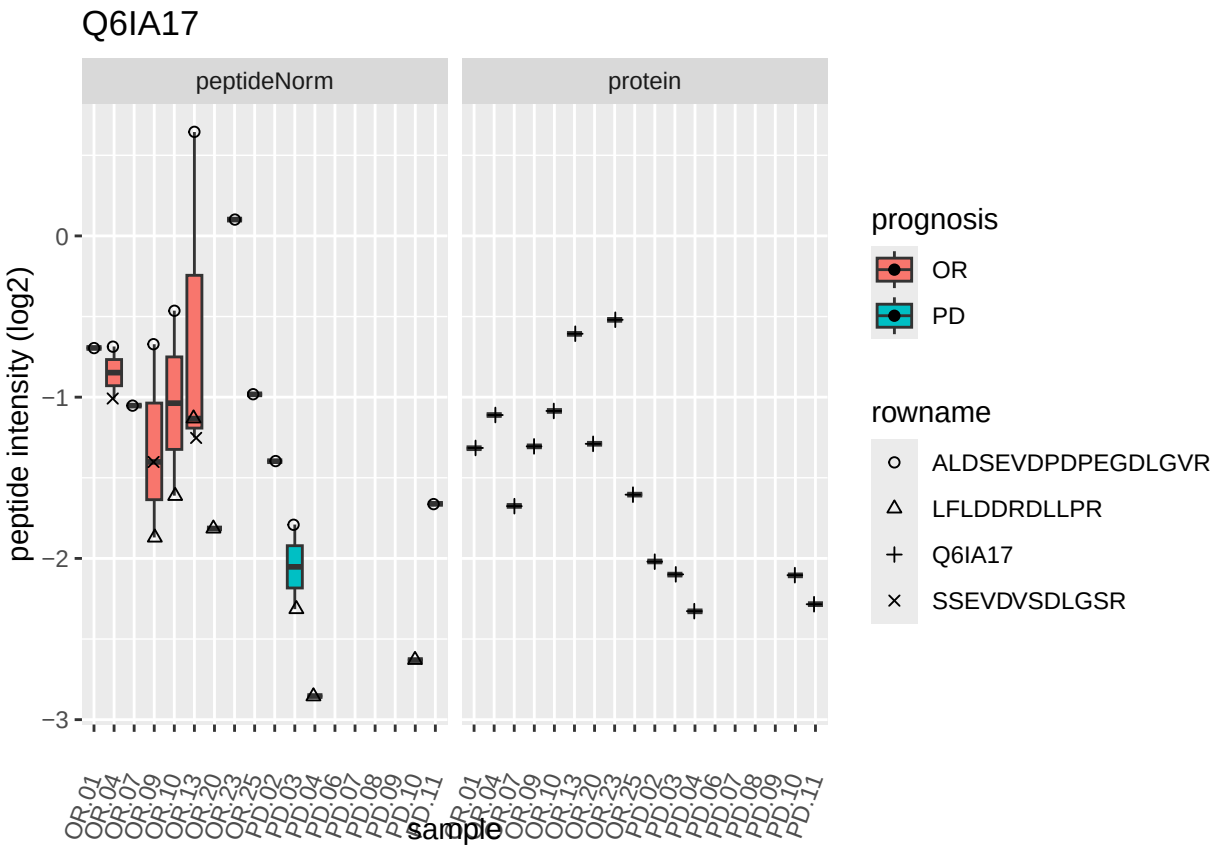
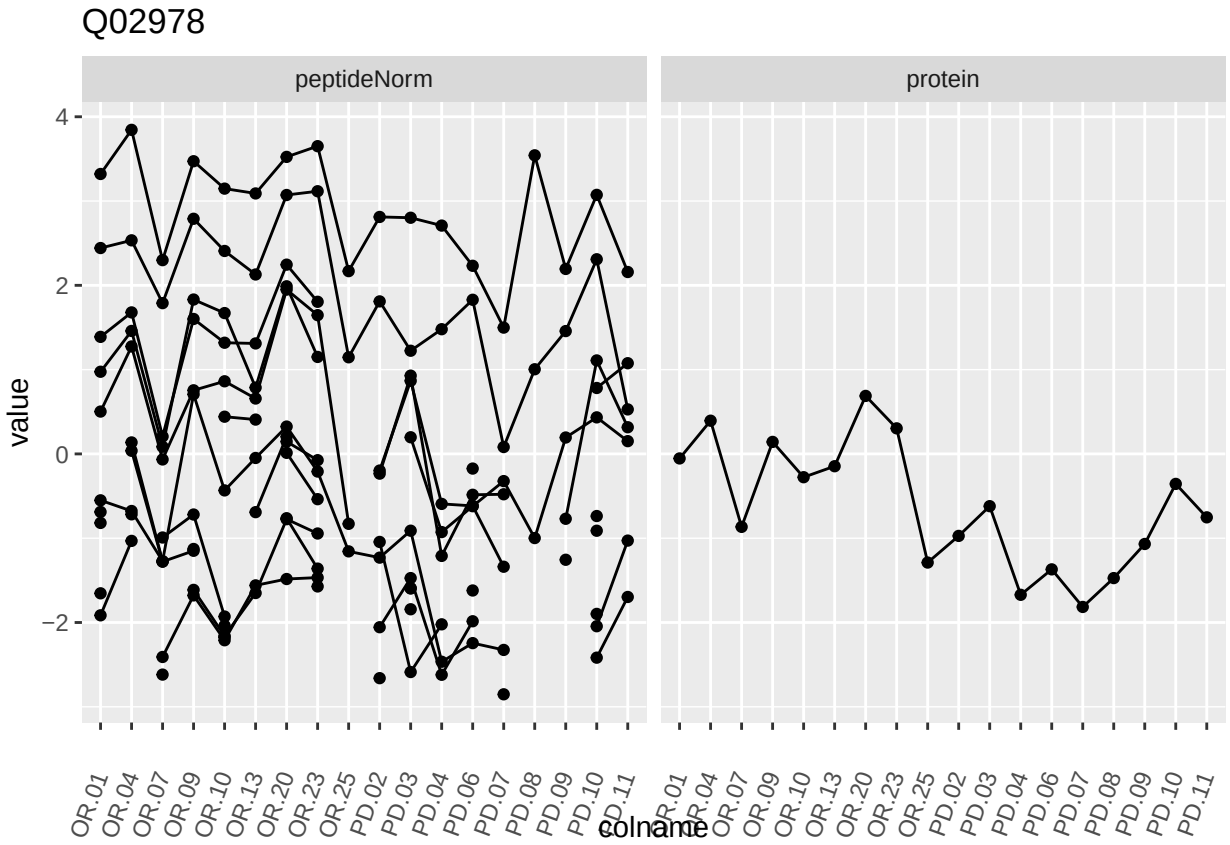
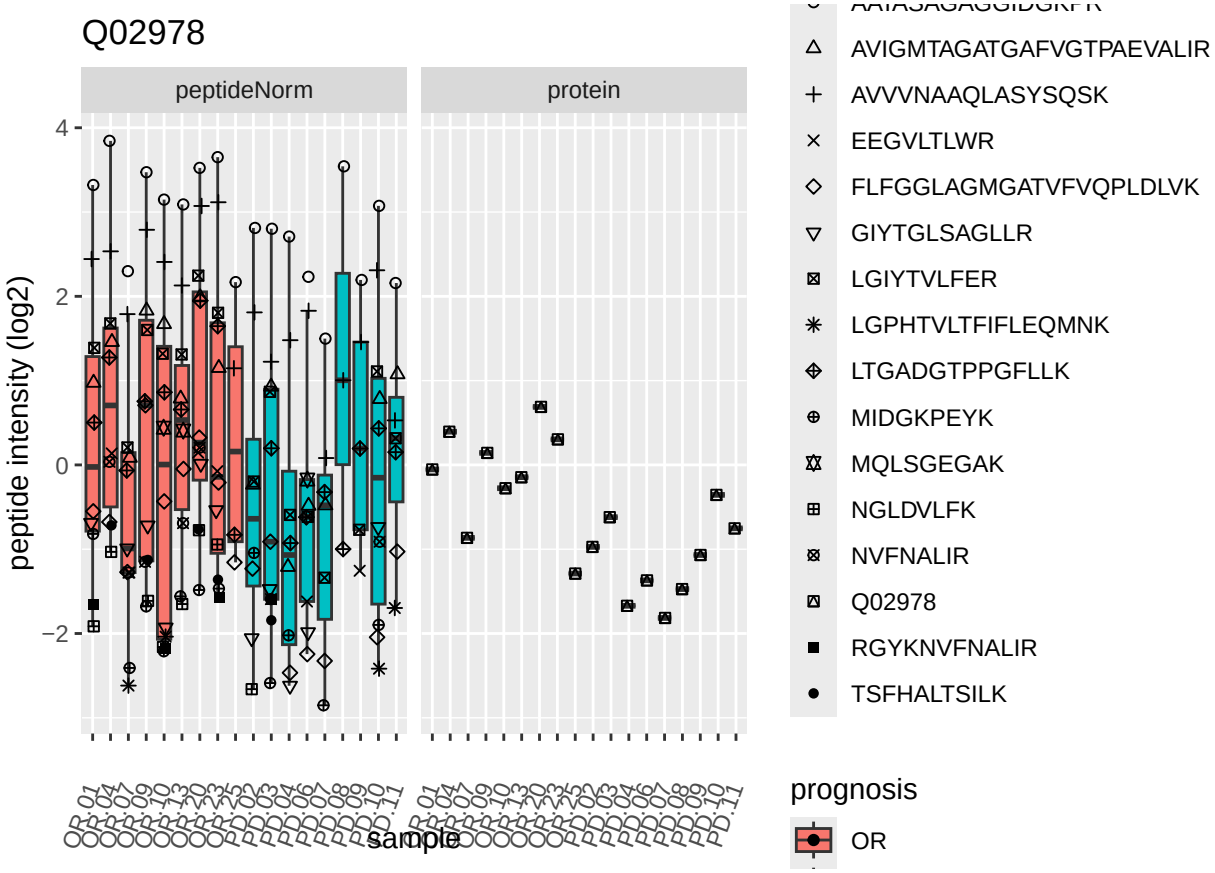
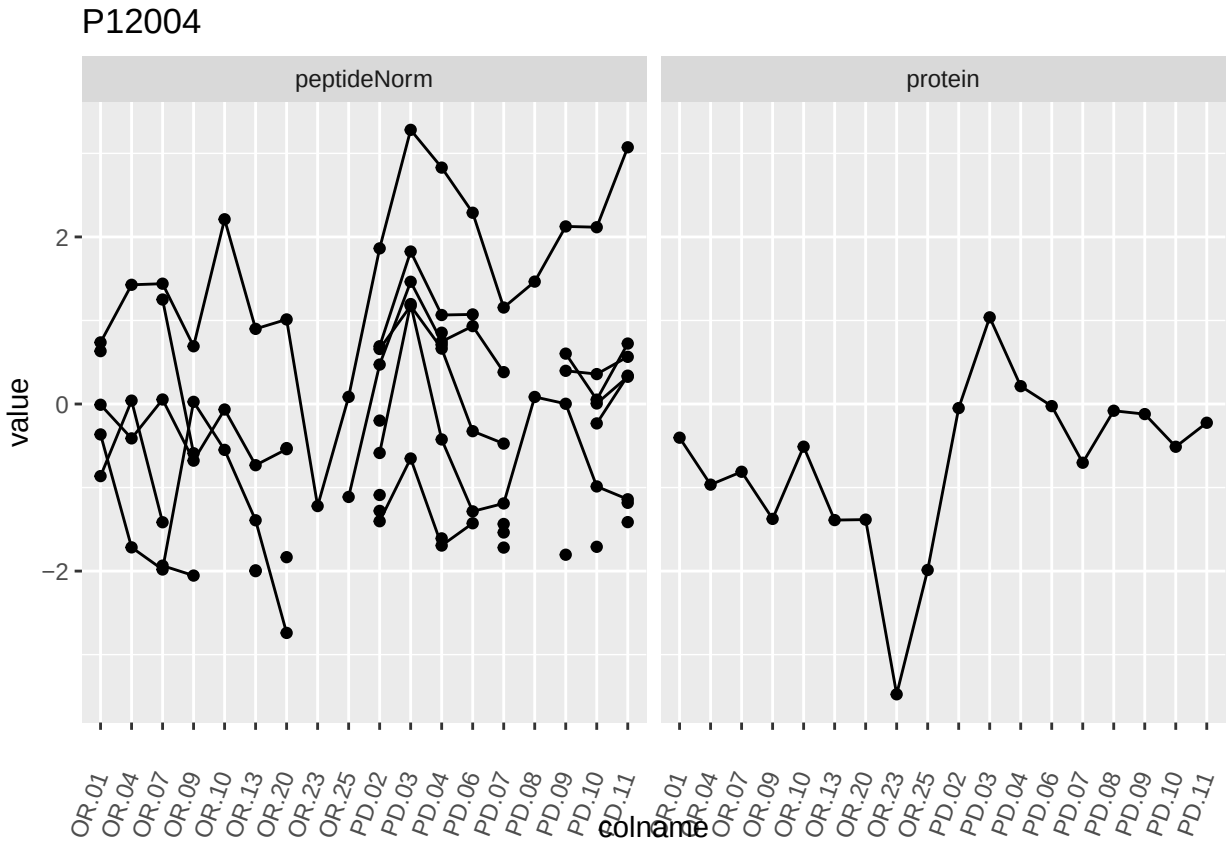
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q6IA17
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
ALDSEVDPDPEGDLGVR
LFLDDRDLLPR
Q6IA17
SSEVDVSDLGSR


Q02978
peptideNorm
protein
value
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q02978
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
AVIGMTAGATGAFVGTPAEVALIR
AVVVNAAQLASYSQSK
EEGVLTLWR
FLFGGLAGMGATVFVQPLDLVK
GIYTGLSAGLLR
LGIYTVLFER
LGPHTVLTFIFLEQMNK
LTGADGTPPGFLLK
MIDGKPEYK
MQLSGEGAK
NGLDVLFK
NVFNALIR
Q02978
RGYKNVFNALIR
TSFHALTSILK
prognosis
OR


P12004
peptideNorm
protein
value
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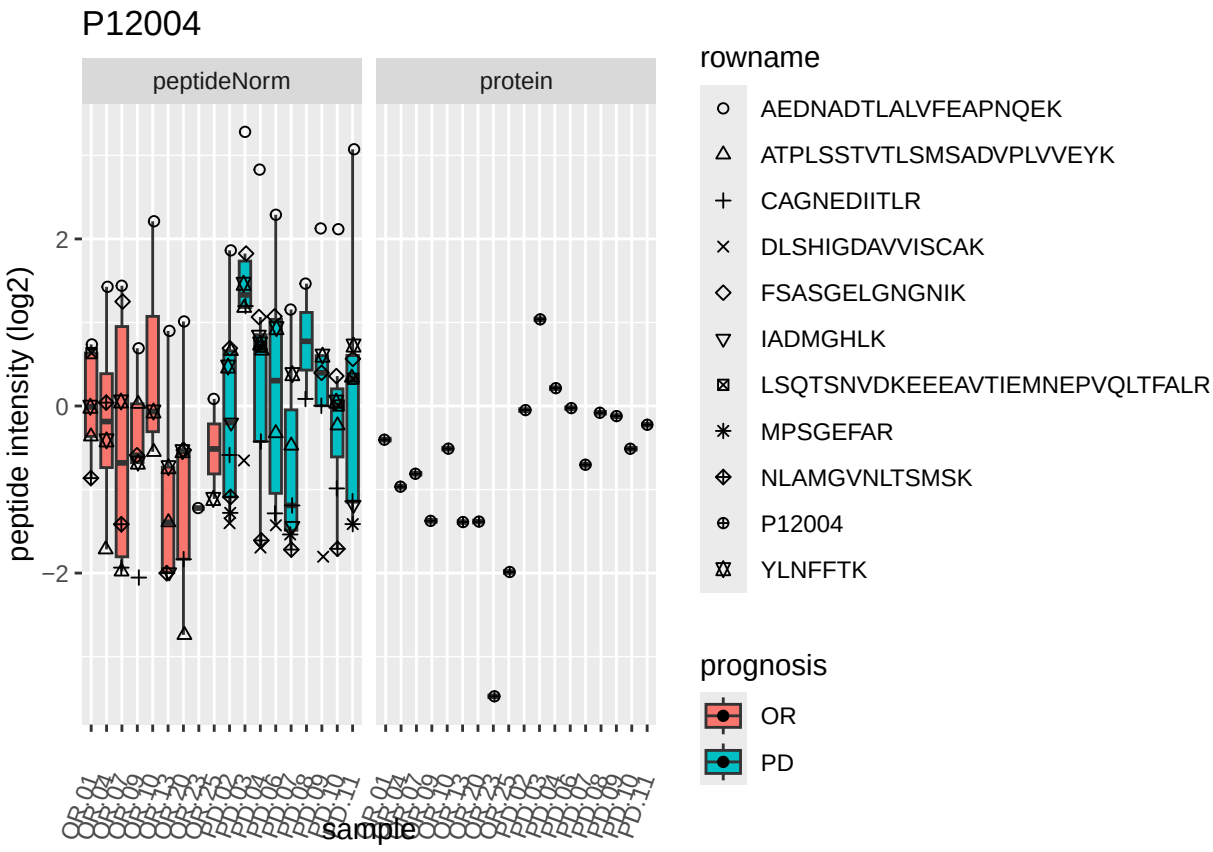
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P12004
peptideNorm
protein
peptide intensity (log2)
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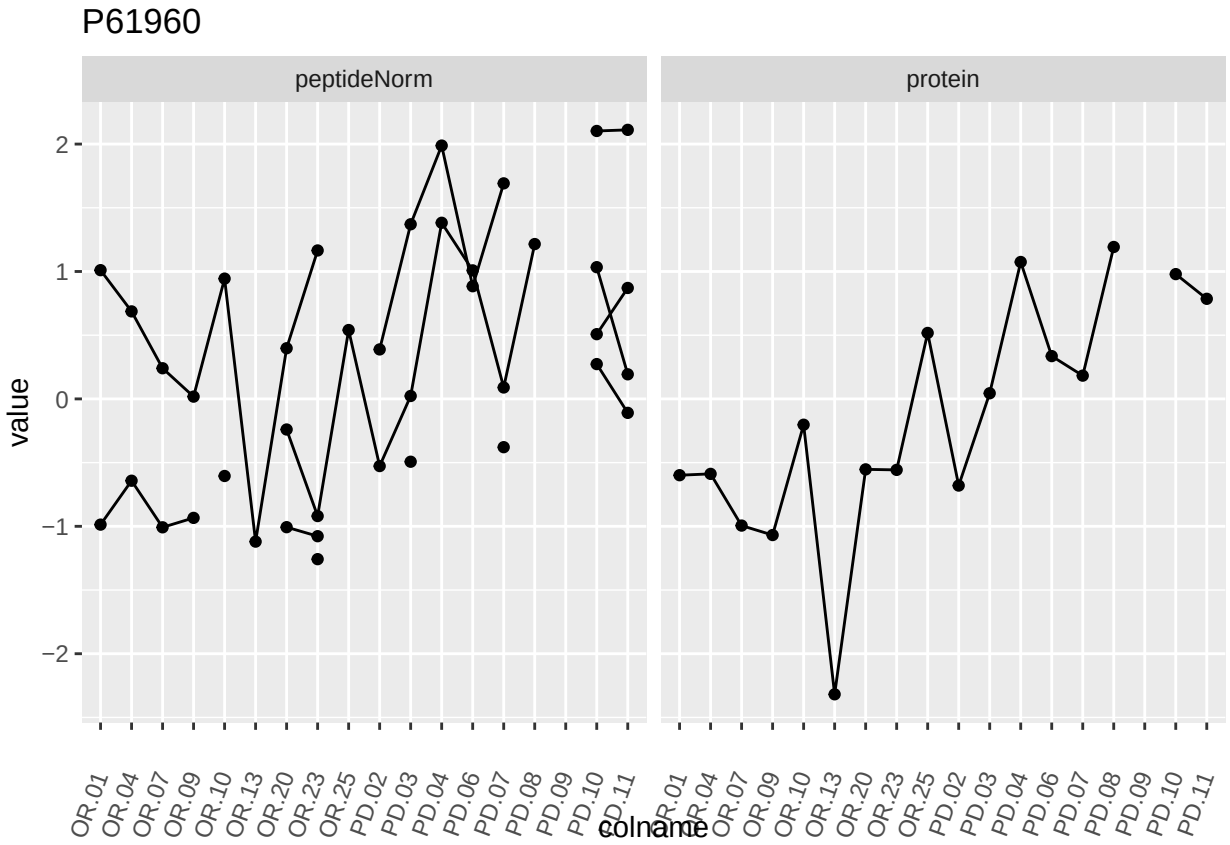
0
−2
sample
rowname
AEDNADTLALVFEAPNQEK
ATPLSSTVTLSMSADVPLVVEYK
CAGNEDIITLR
DLSHIGDAVVISCAK
FSASGELGNGNIK
IADMGHLK
LSQTSNVDKEEEAVTIEMNEPVQLTFALR
MPSGEFAR
NLAMGVNLTSMSK
P12004
YLNFFTK
prognosis
OR
PD


P61960
peptideNorm
protein
value
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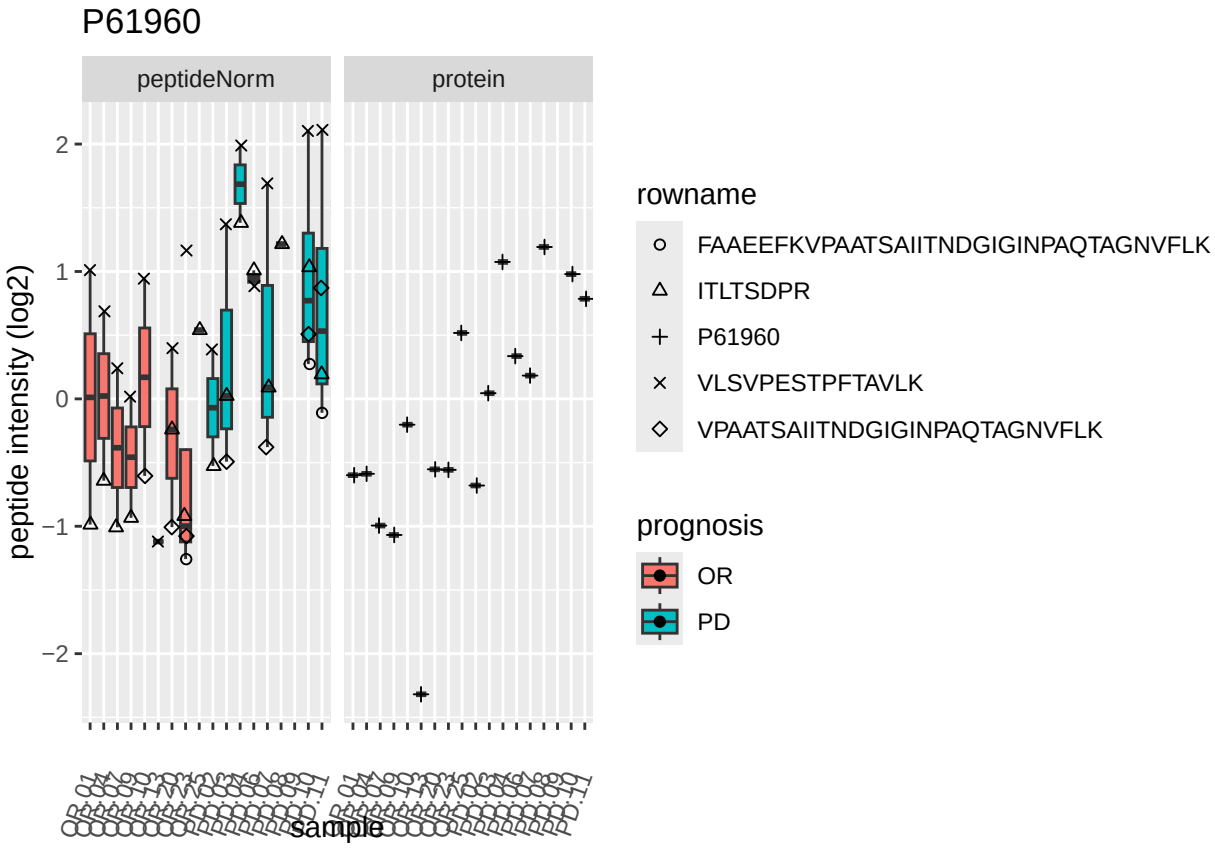
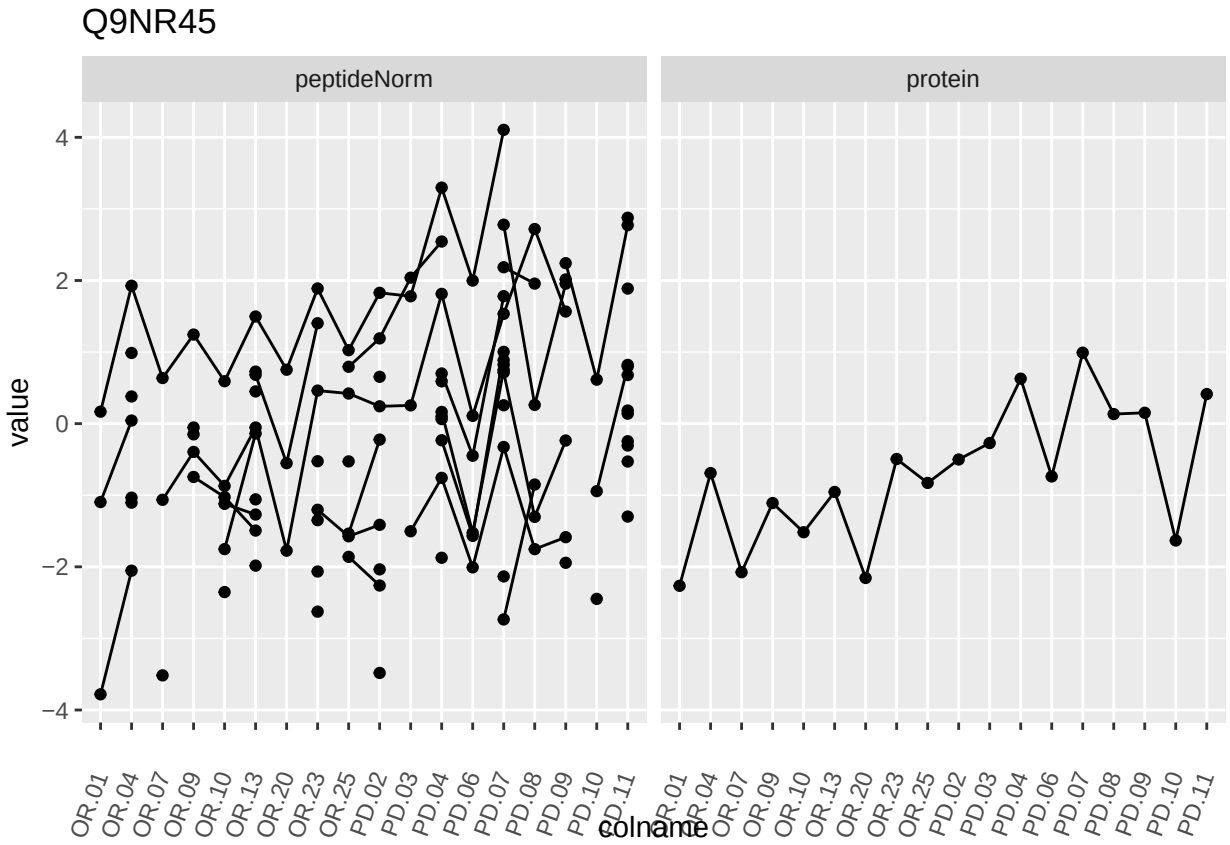
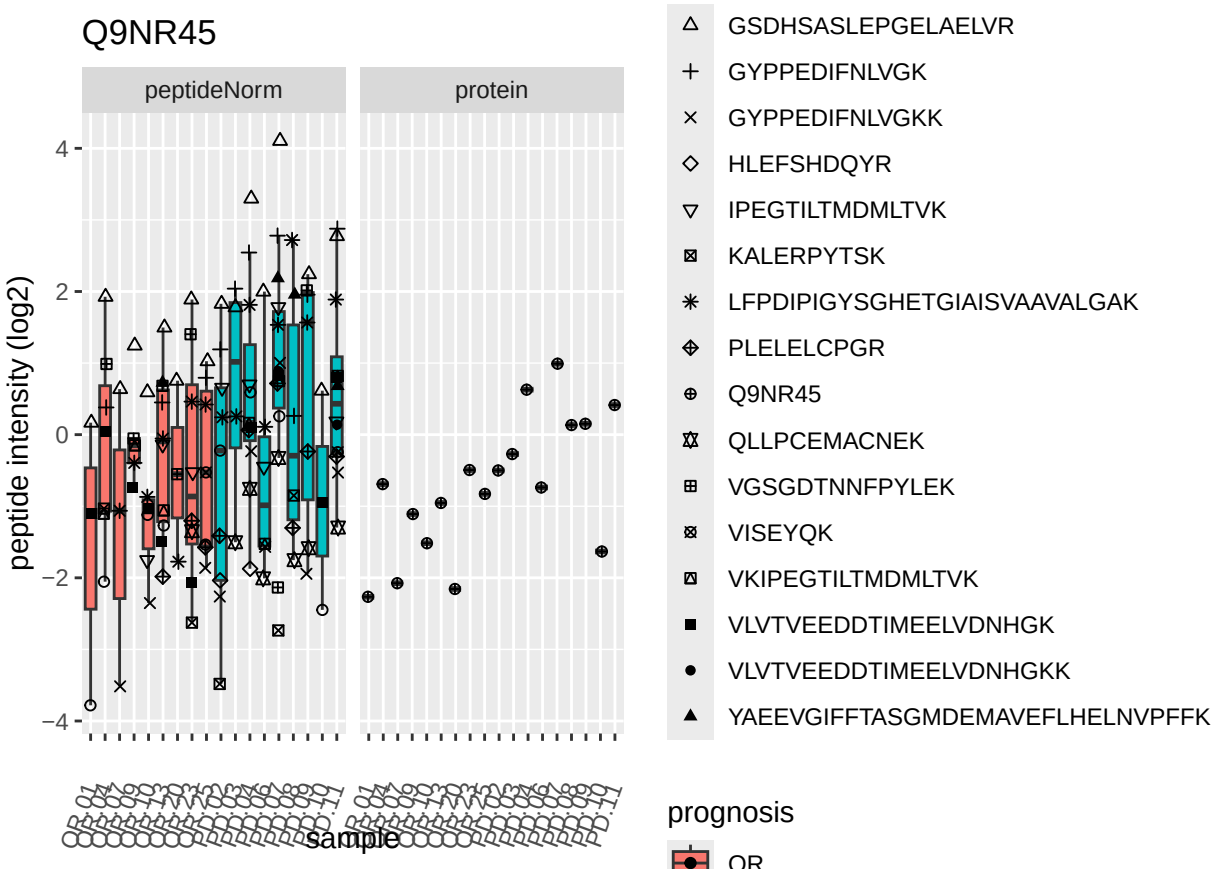
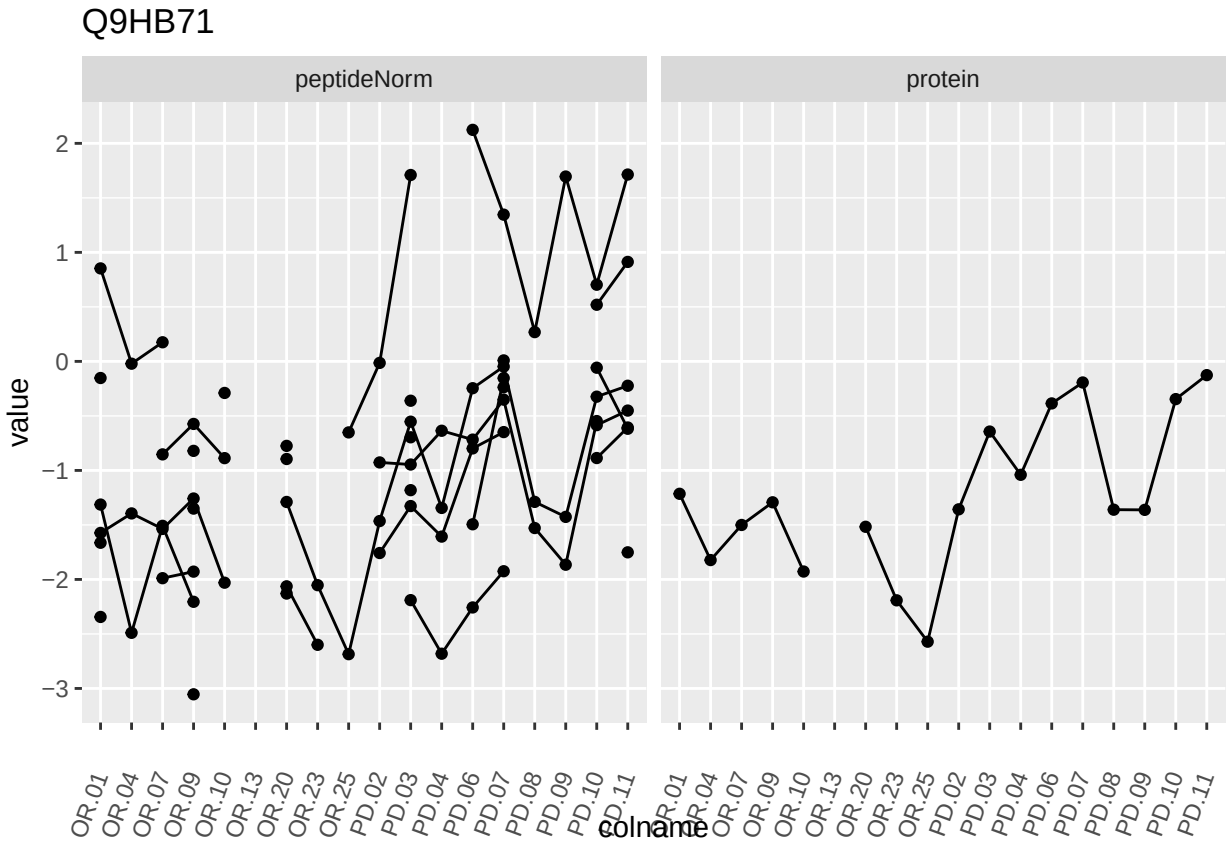
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P61960
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
sample
rowname
FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK
ITLTSDPR
P61960
VLSVPESTPFTAVLK
VPAATSAIITNDGIGINPAQTAGNVFLK
prognosis
OR
PD


Q9NR45
peptideNorm
protein
value
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NR45
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
sample
GSDHSASLEPGELAELVR
GYPPEDIFNLVGK
GYPPEDIFNLVGKK
HLEFSHDQYR
IPEGTILTMDMLTVK
KALERPYTSK
LFPDIPIGYSGHETGIAISVAAVALGAK
PLELELCPGR
Q9NR45
QLLPCEMACNEK
VGSGDTNNFPYLEK
VISEYQK
VKIPEGTILTMDMLTVK
VLVTVEEDDTIMEELVDNHGK
VLVTVEEDDTIMEELVDNHGKK
YAEEVGIFFTASGMDEMAVEFLHELNVPFFK
prognosis
OR


Q9HB71
peptideNorm
protein
value
2
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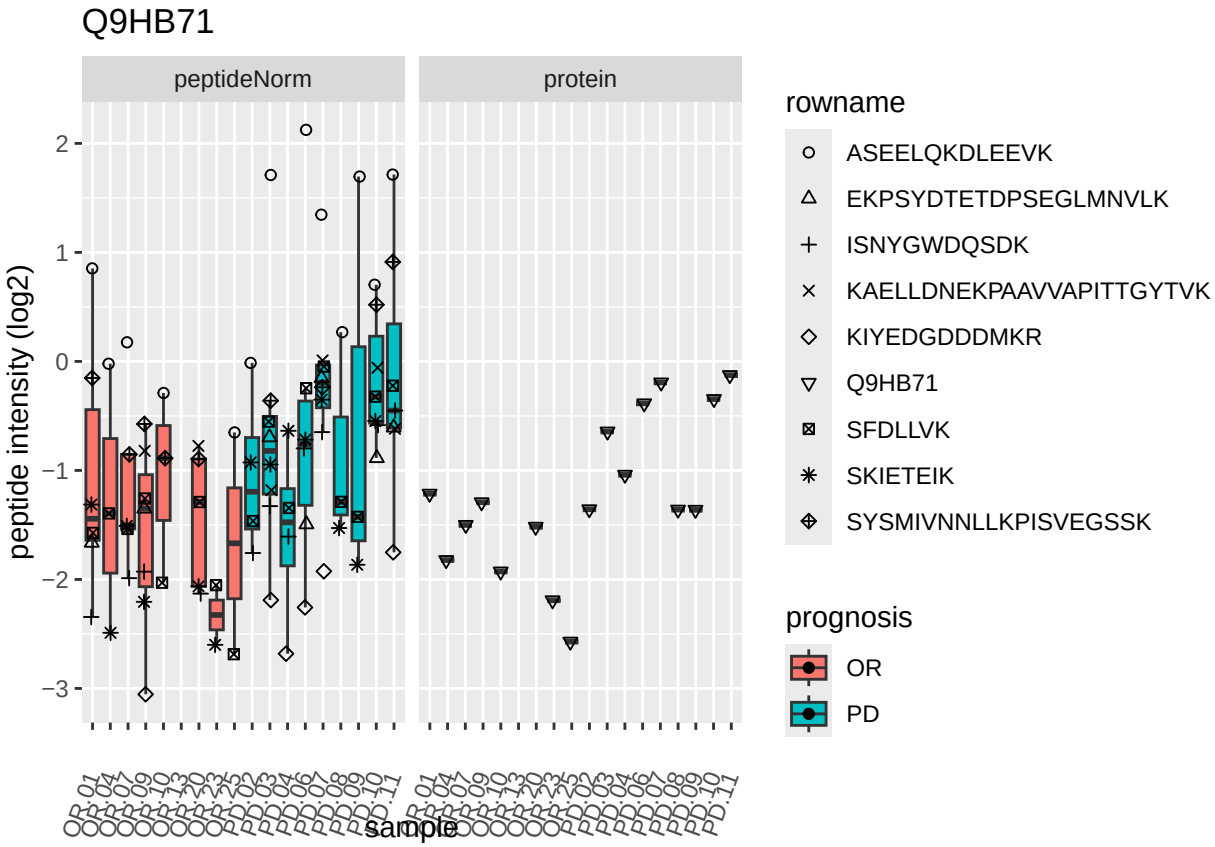
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9HB71
peptideNorm
protein
peptide intensity (log2)
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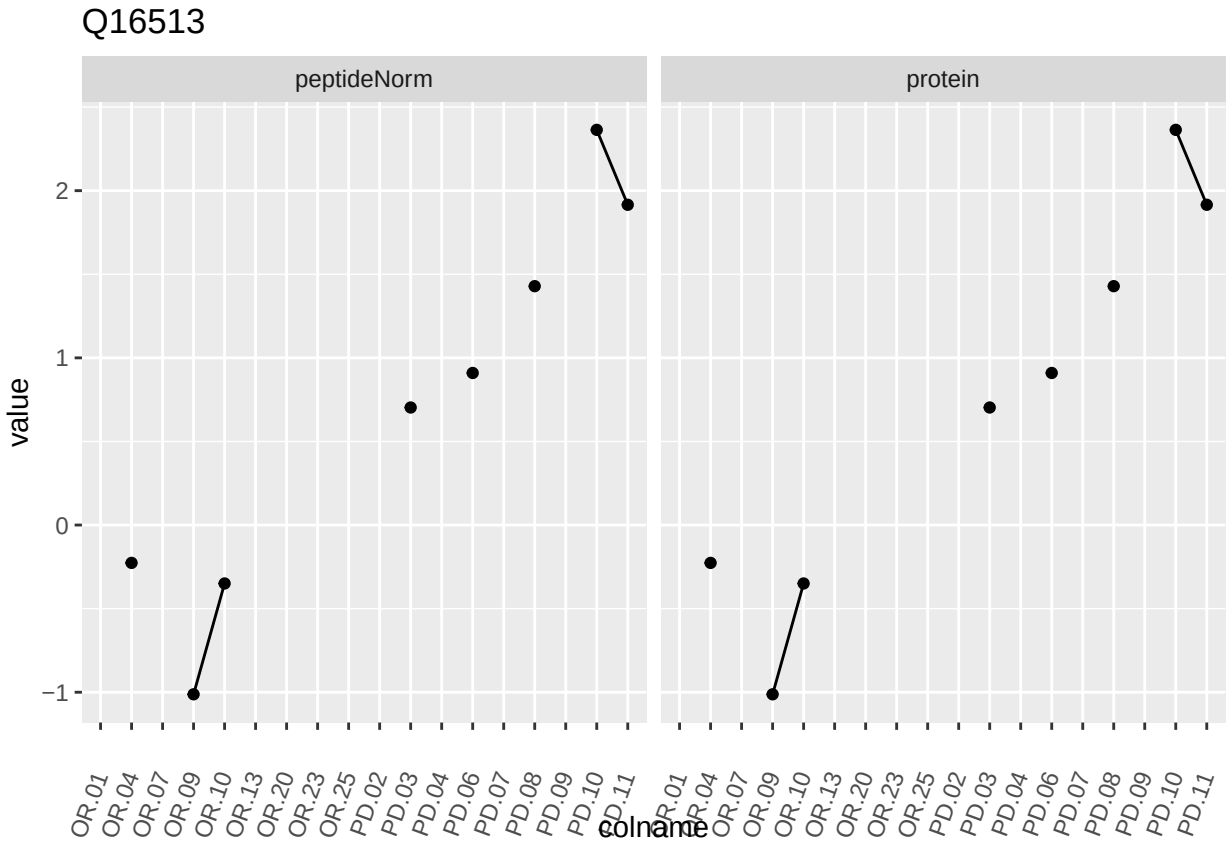
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ASEELQKDLEEVK
EKPSYDTETDPSEGLMNVLK
ISNYGWDQSDK
KAELLDNEKPAAVVAPITTGYTVK
KIYEDGDDDMKR
Q9HB71
SFDLLVK
SKIETEIK
SYSMIVNNLLKPISVEGSSK
prognosis
OR
PD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peptideNorm
protein
value
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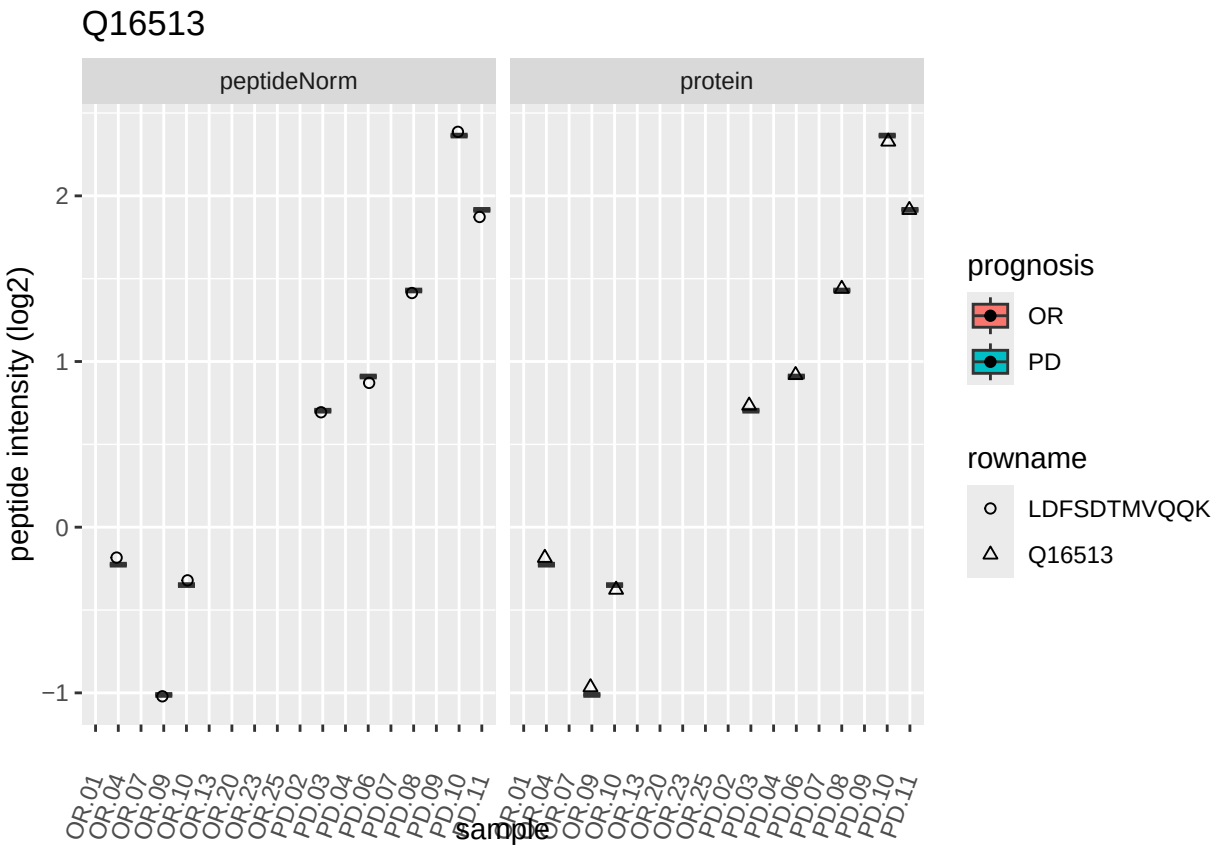
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q16513
peptideNorm
protein
peptide intensity (log2)
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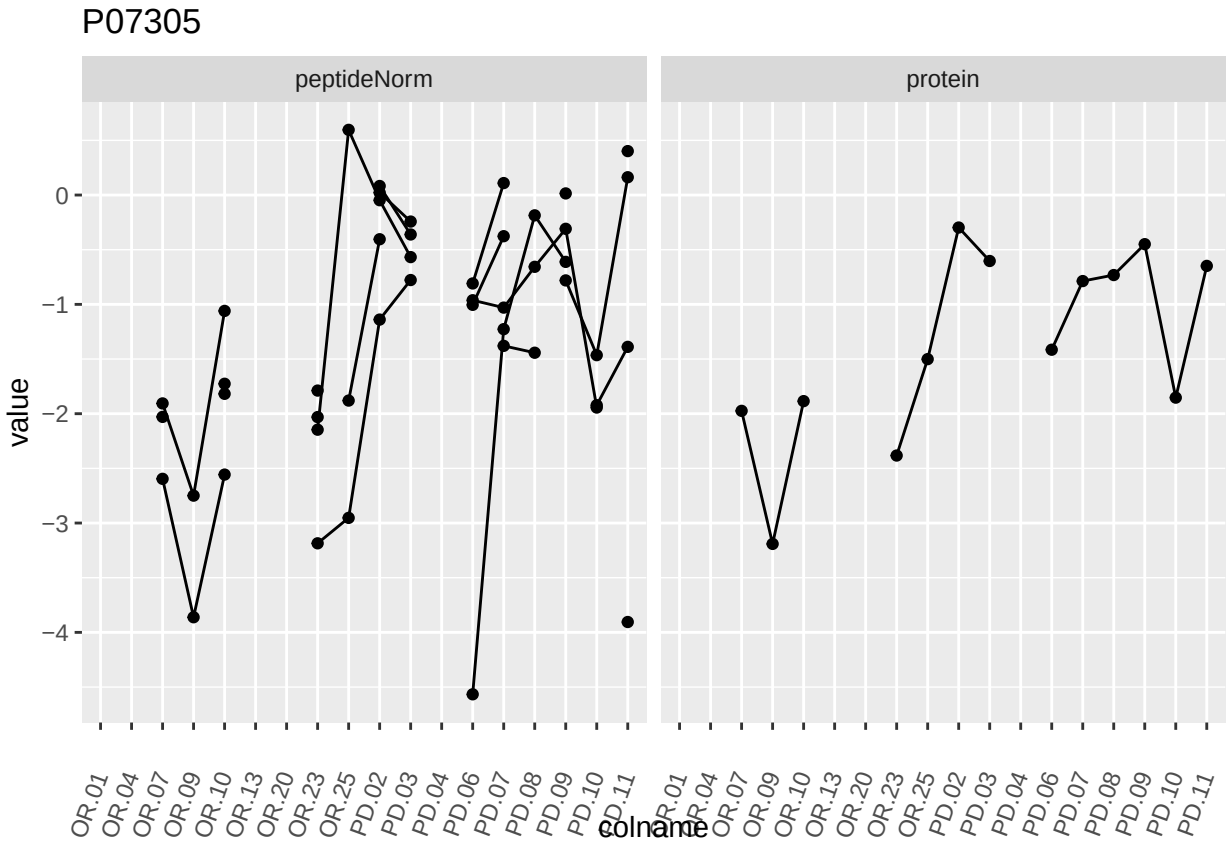
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
LDFSDTMVQQK
Q16513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peptideNorm
protein
value
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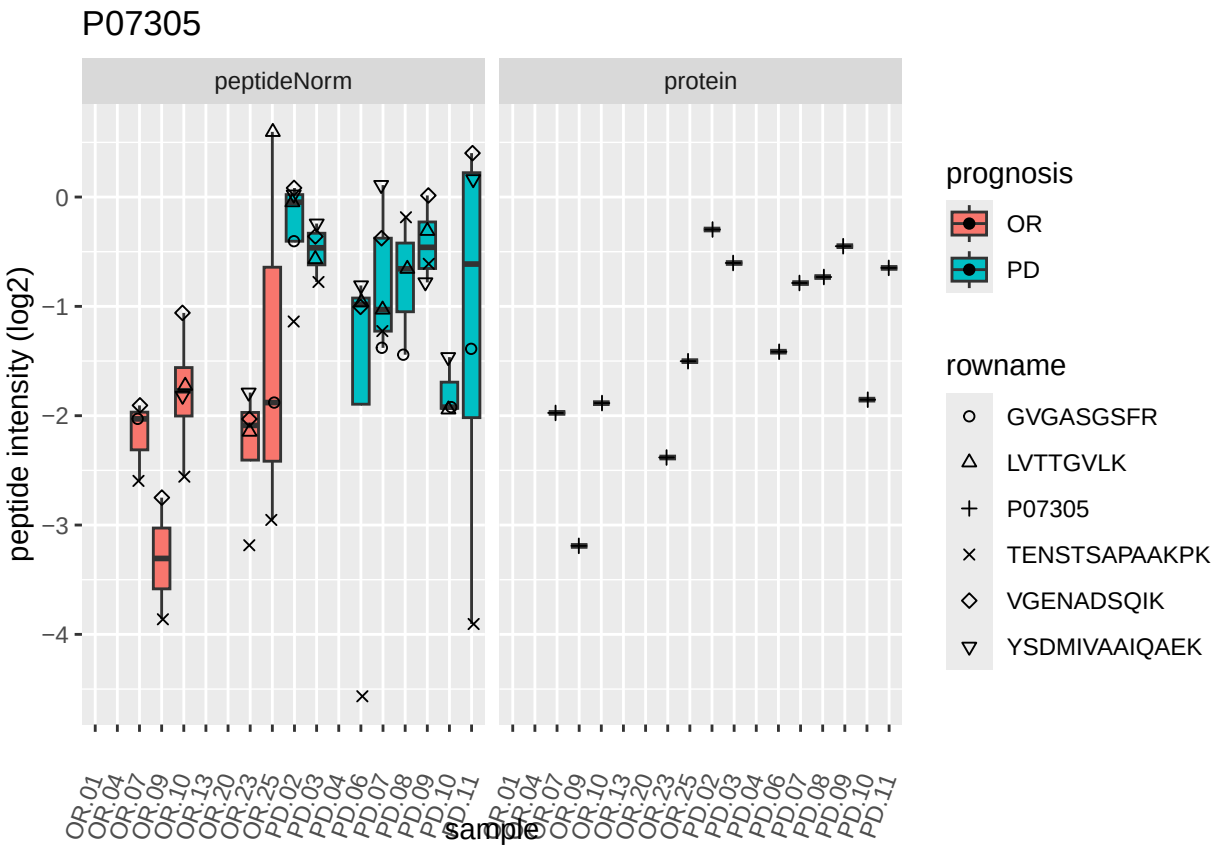
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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−2
−3
−4
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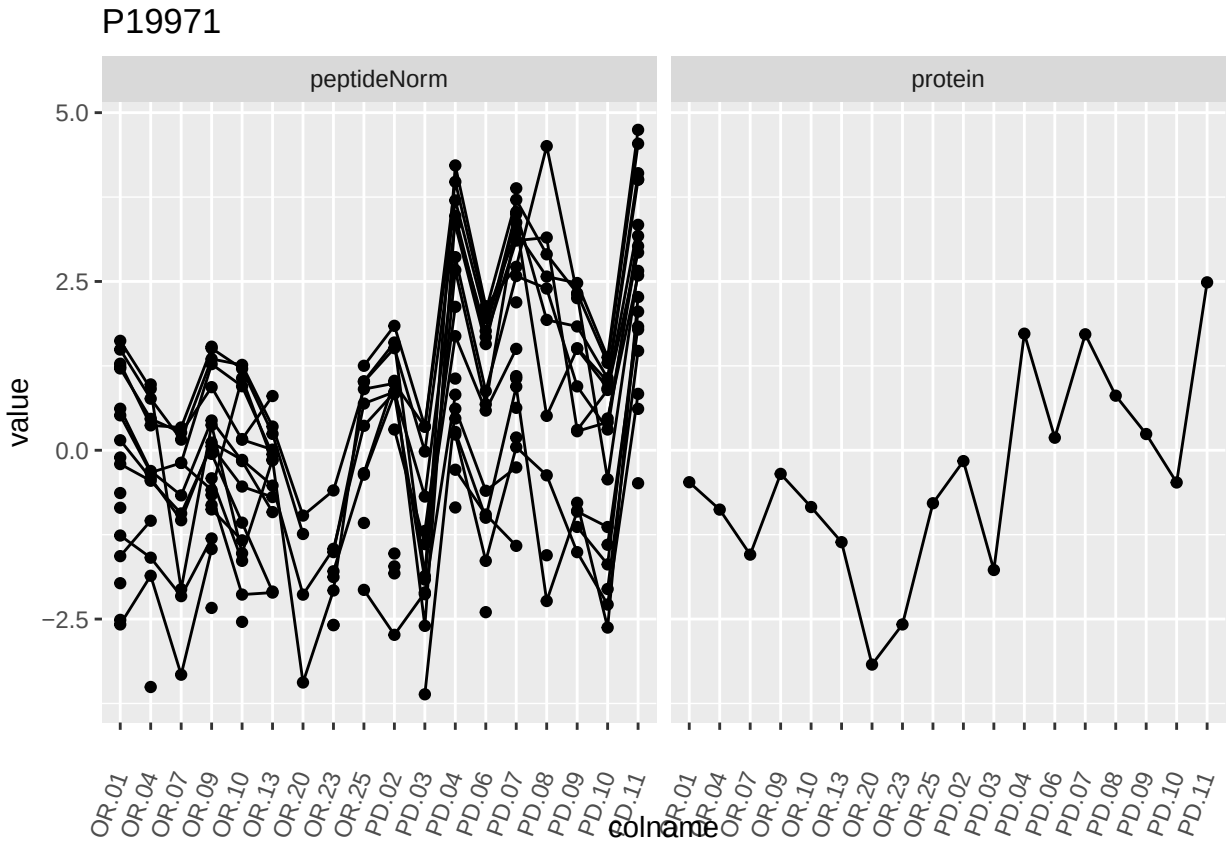
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
GVGASGSFR
LVTTGVLK
P07305
TENSTSAPAAKPK
VGENADSQIK
YSDMIVAAIQAEK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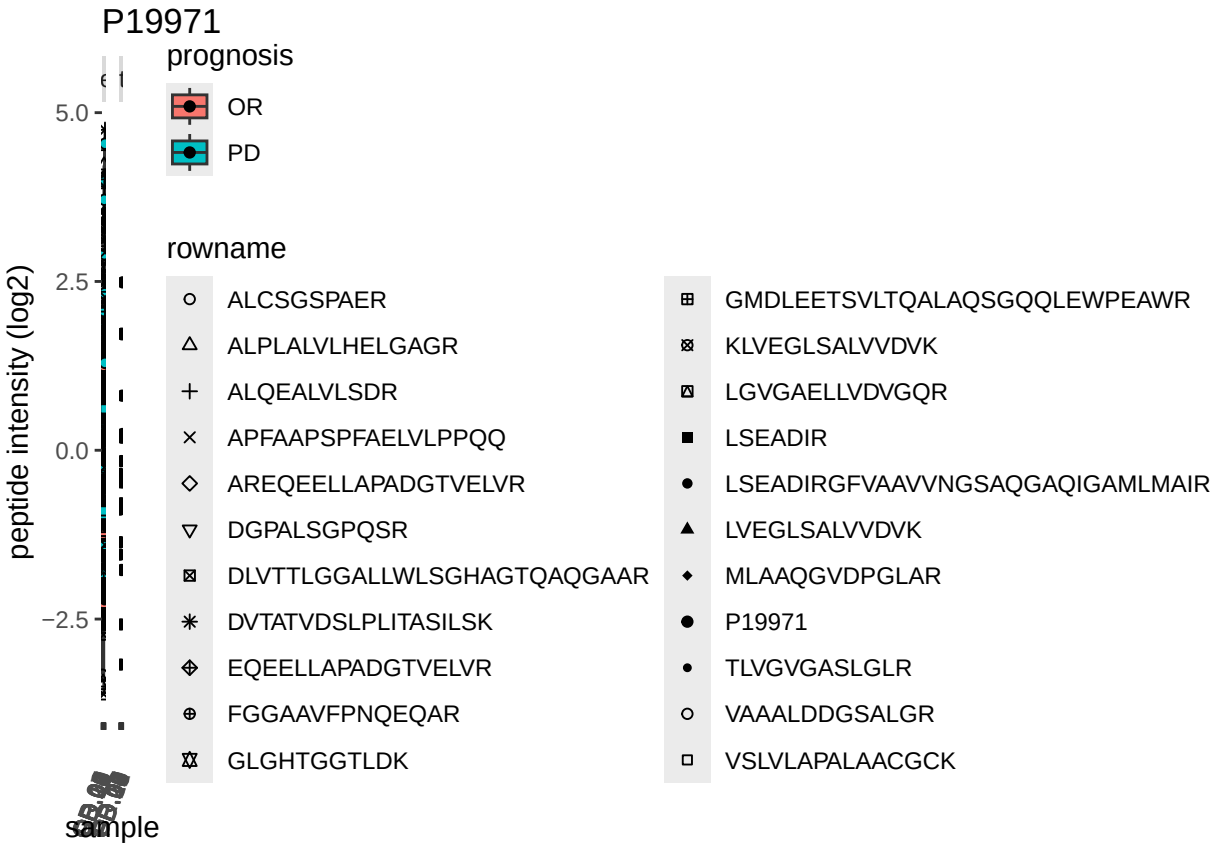
peptideNorm
protein
5.0
2.5
0.0
−2.5
value
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P19971
prognosis
OR
PD
rowname
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ALPLALVLHELGAGR
ALQEALVLSDR
APFAAPSPFAELVLPPQQ
AREQEELLAPADGTVELVR
DGPALSGPQSR
DLVTTLGGALLWLSGHAGTQAQGAAR
DVTATVDSLPLITASILSK
EQEELLAPADGTVELVR
FGGAAVFPNQEQAR
GLGHTGGTLDK
GMDLEETSVLTQALAQSGQQLEWPEAWR
KLVEGLSALVVDVK
LGVGAELLVDVGQR
LSEADIR
LSEADIRGFVAAVVNGSAQGAQIGAMLMAIR
LVEGLSALVVDVK
MLAAQGVDPGLAR
P19971
TLVGVGASLGLR
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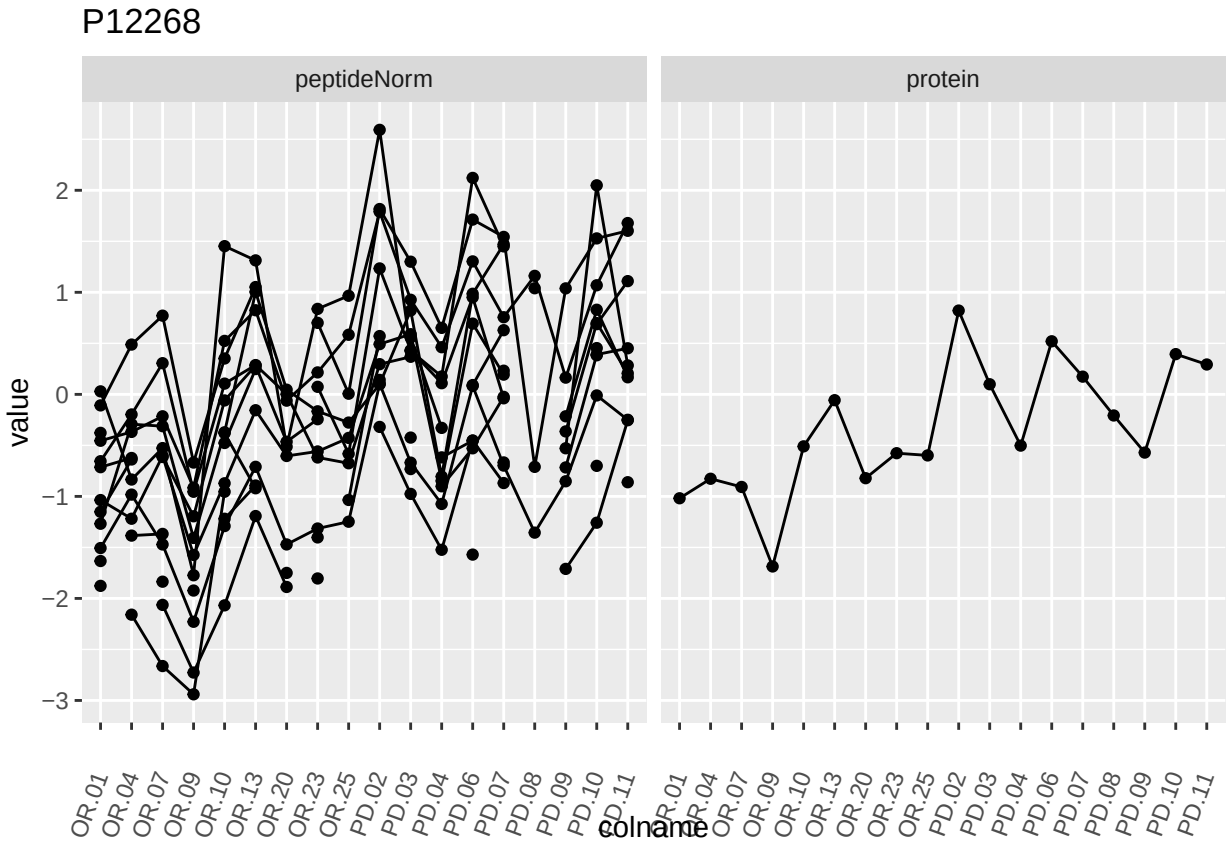
VSLVLAPALAACGCK
peptide intensity (log2)
5.0
2.5
0.0
−2.5
sample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peptideNorm
protein
value
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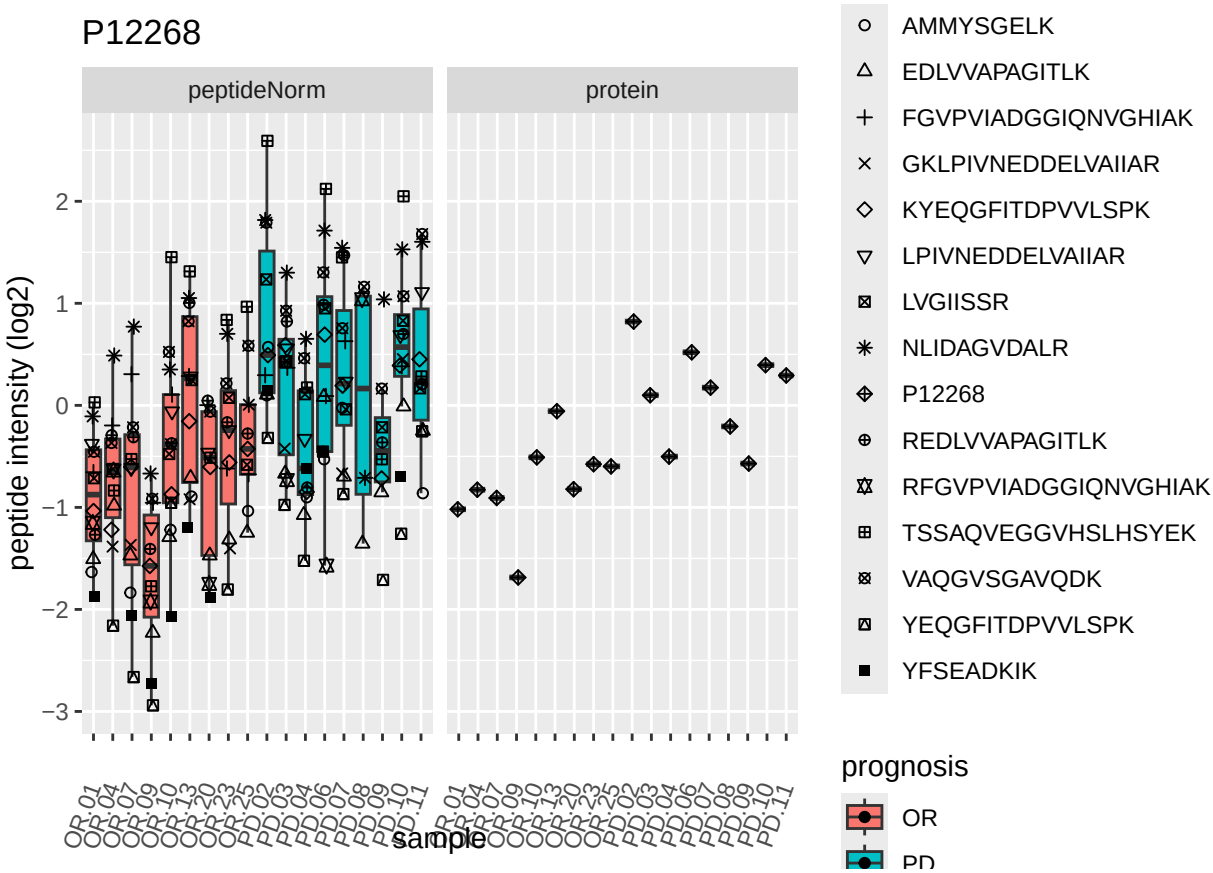
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
AMMYSGELK
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FGVPVIADGGIQNVGHIAK
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KYEQGFITDPVVLSPK
LPIVNEDDELVAIIAR
LVGIISSR
NLIDAGVDALR
P12268
REDLVVAPAGITLK
RFGVPVIADGGIQNVGHIAK
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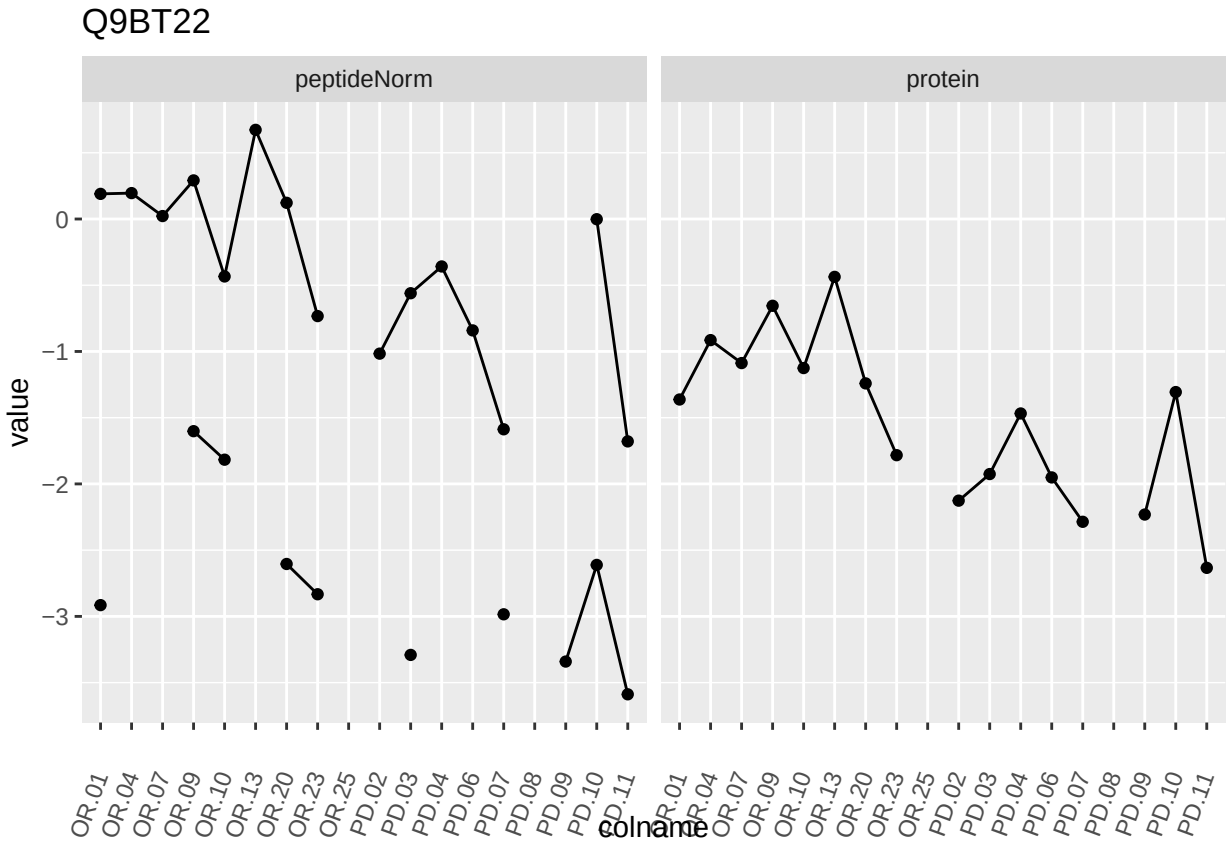
YEQGFITDPVVLSPK
YFSEADKIK
prognosis
OR
PD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protein
value
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−2
−3
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OR.04
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OR.09
OR.10
OR.13
OR.20
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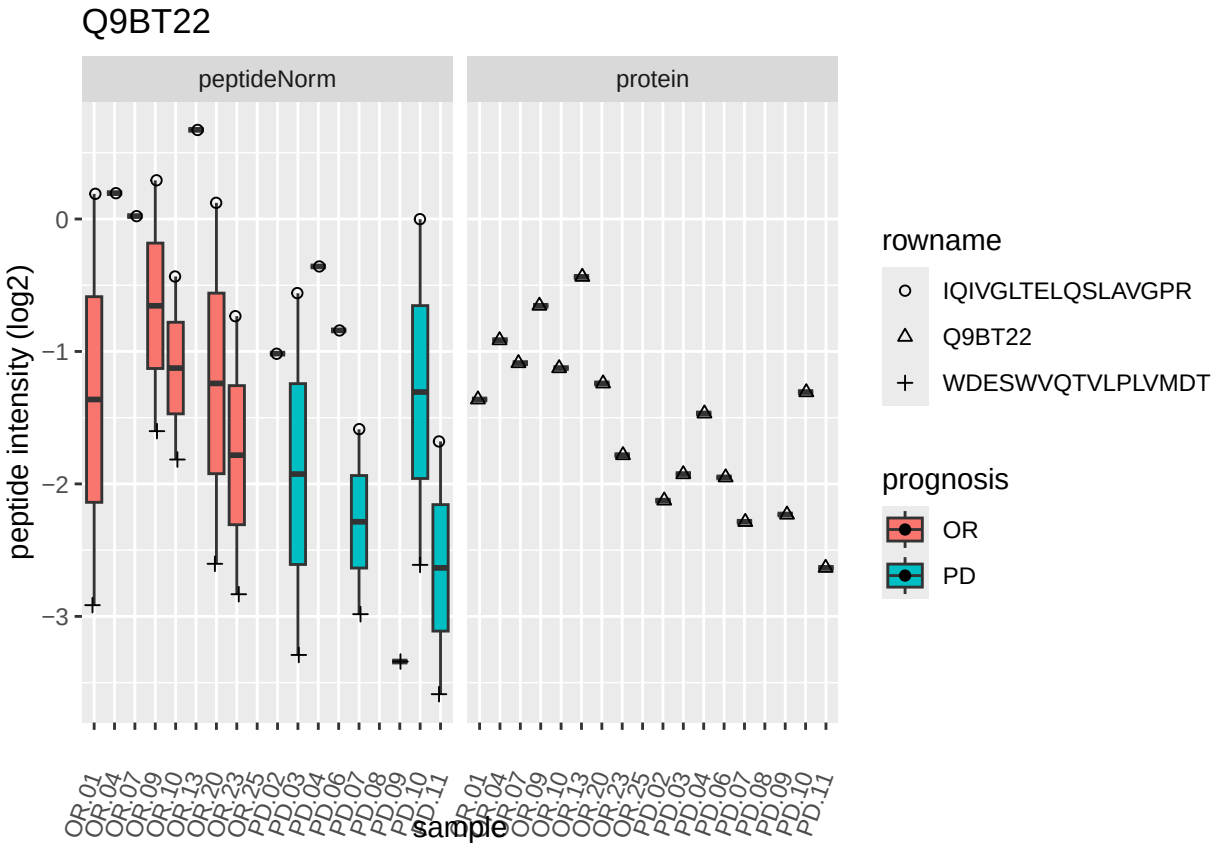
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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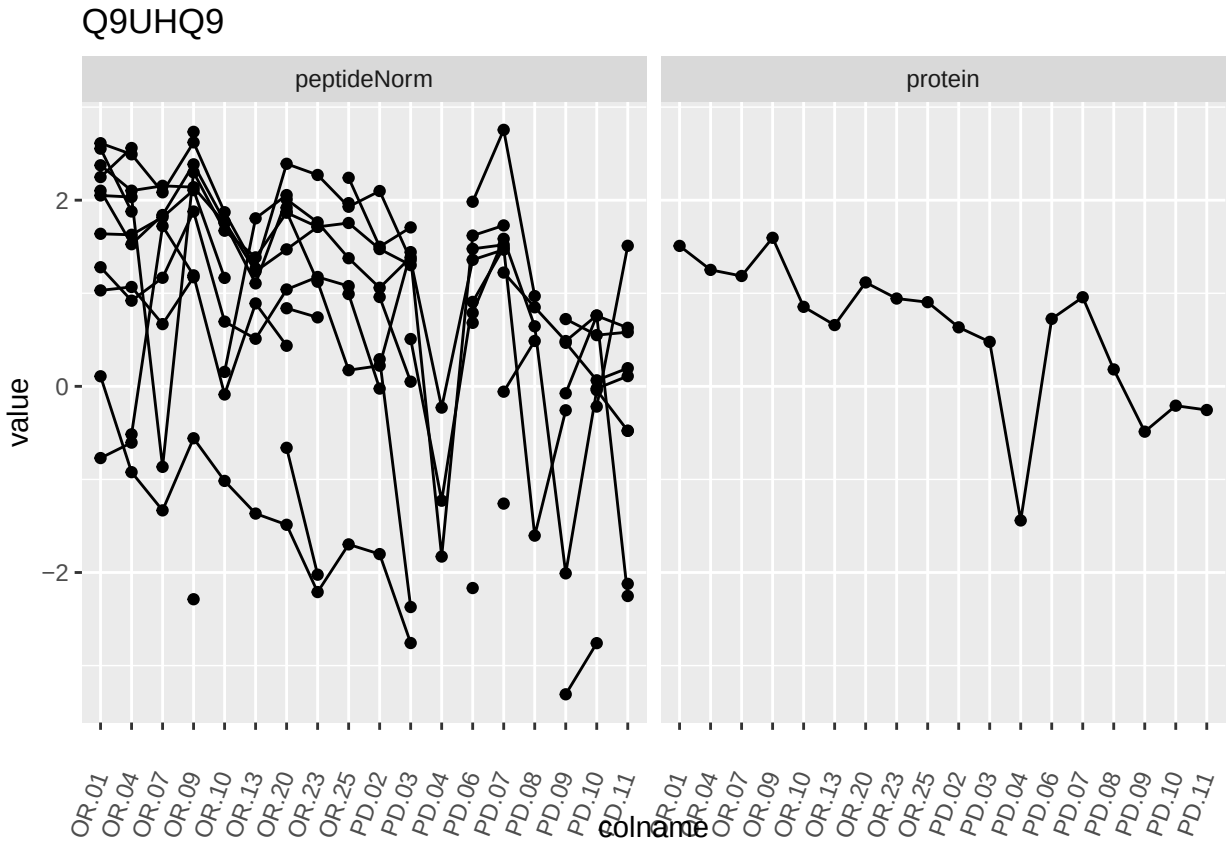
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
IQIVGLTELQSLAVGPR
Q9BT22
WDESWVQTVLPLVMDT
prognosis
OR
PD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protein
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−2
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OR.07
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OR.10
OR.13
OR.20
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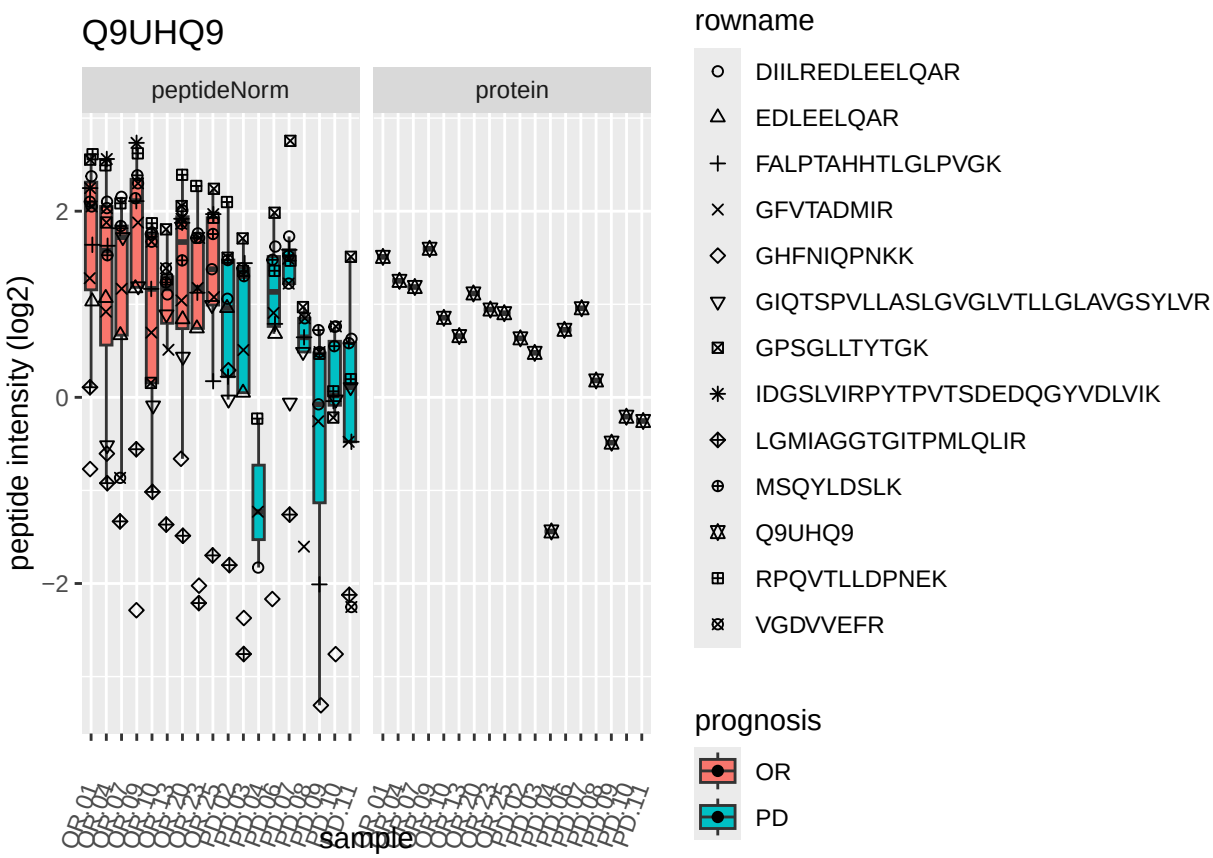
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9UHQ9
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
rowname
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EDLEELQAR
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GHFNIQPNKK
GIQTSPVLLASLGVGLVTLLGLAVGSYLVR
GPSGLLTYTGK
IDGSLVIRPYTPVTSDEDQGYVDLVIK
LGMIAGGTGITPMLQLIR
MSQYLDSLK
Q9UHQ9
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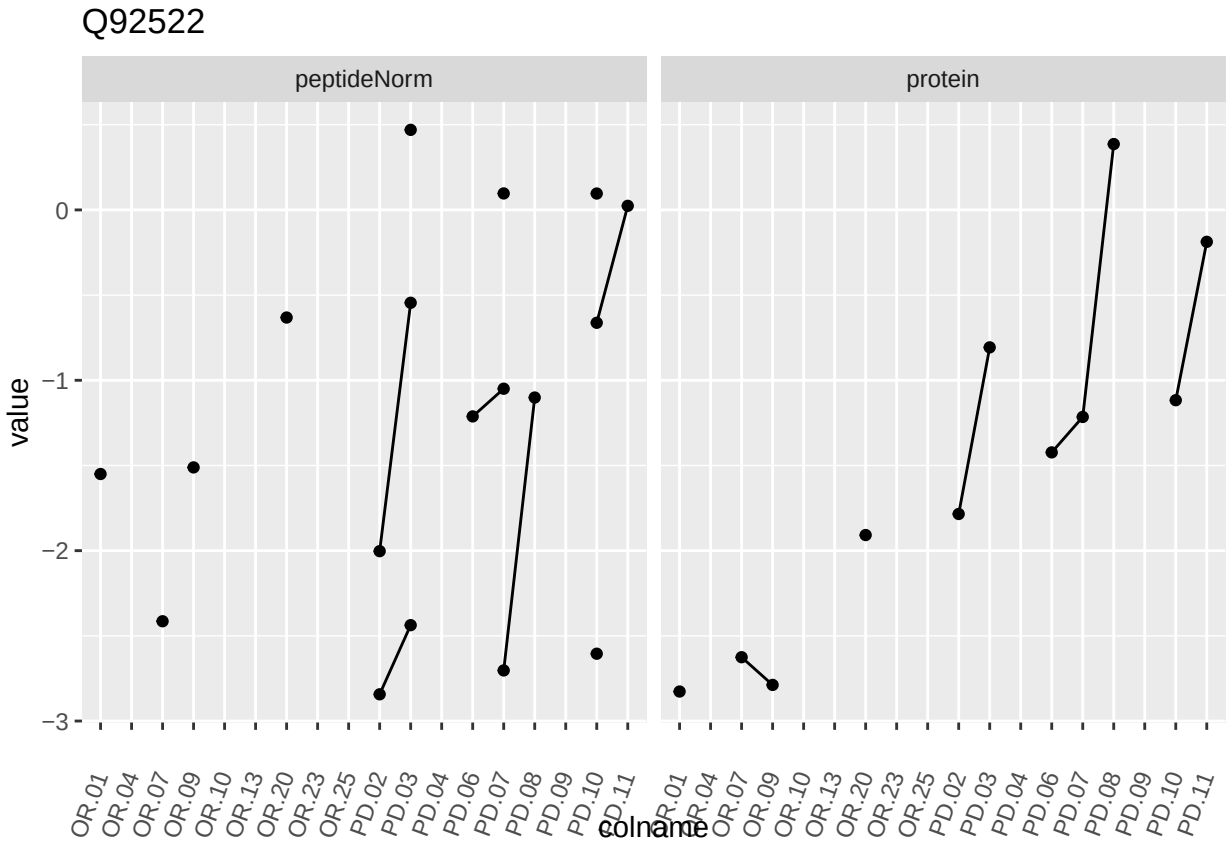
VGDVVEFR
prognosis
OR
PD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peptideNorm
protein
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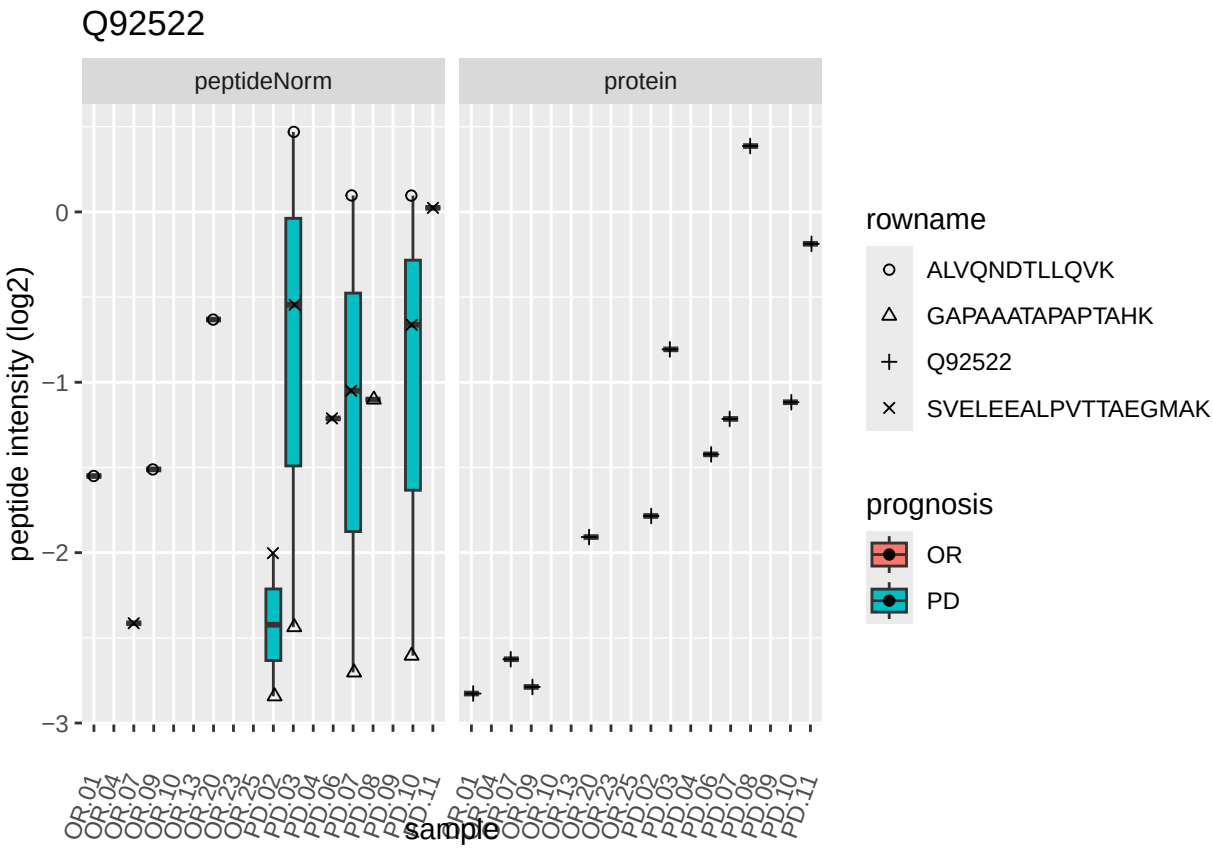
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q92522
peptideNorm
protein
peptide intensity (log2)
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−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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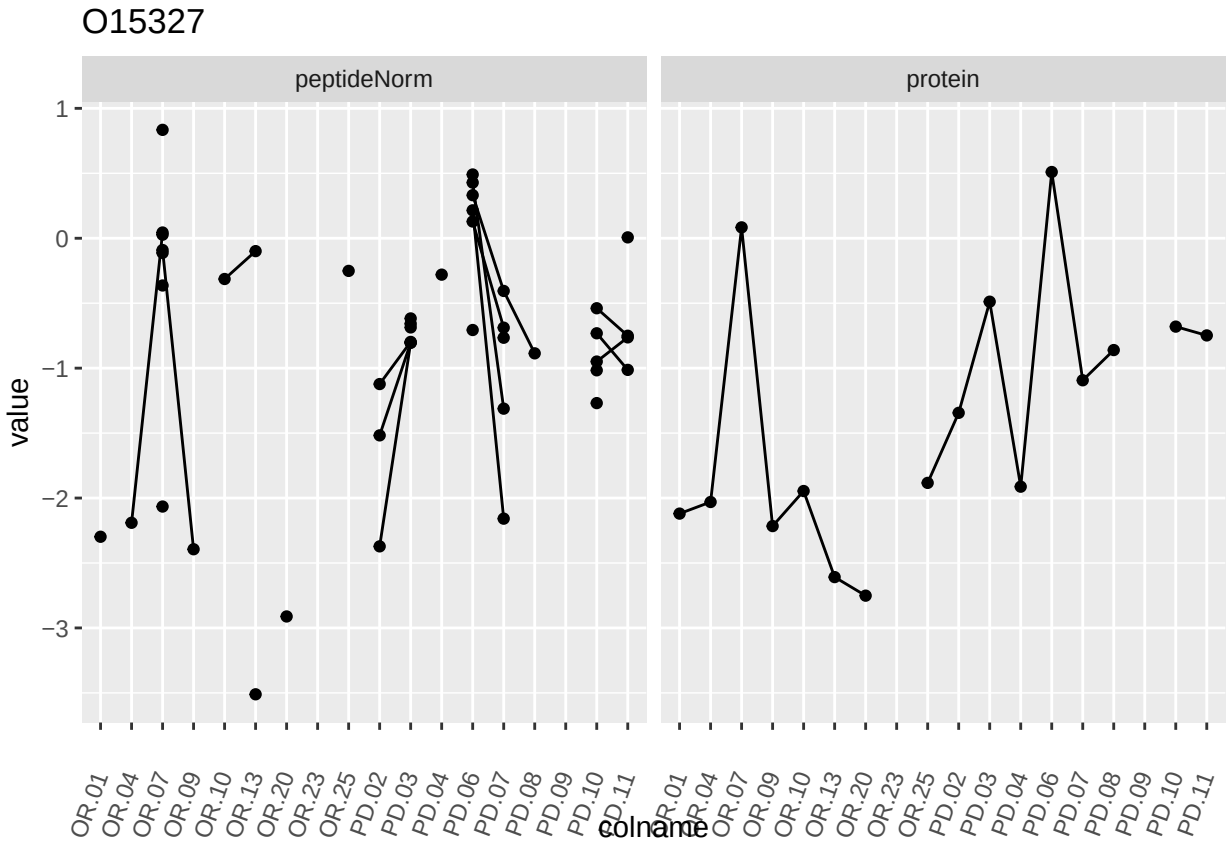
Q92522
SVELEEALPVTTAEGMAK
prognosis
OR
PD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protein
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−2
−3
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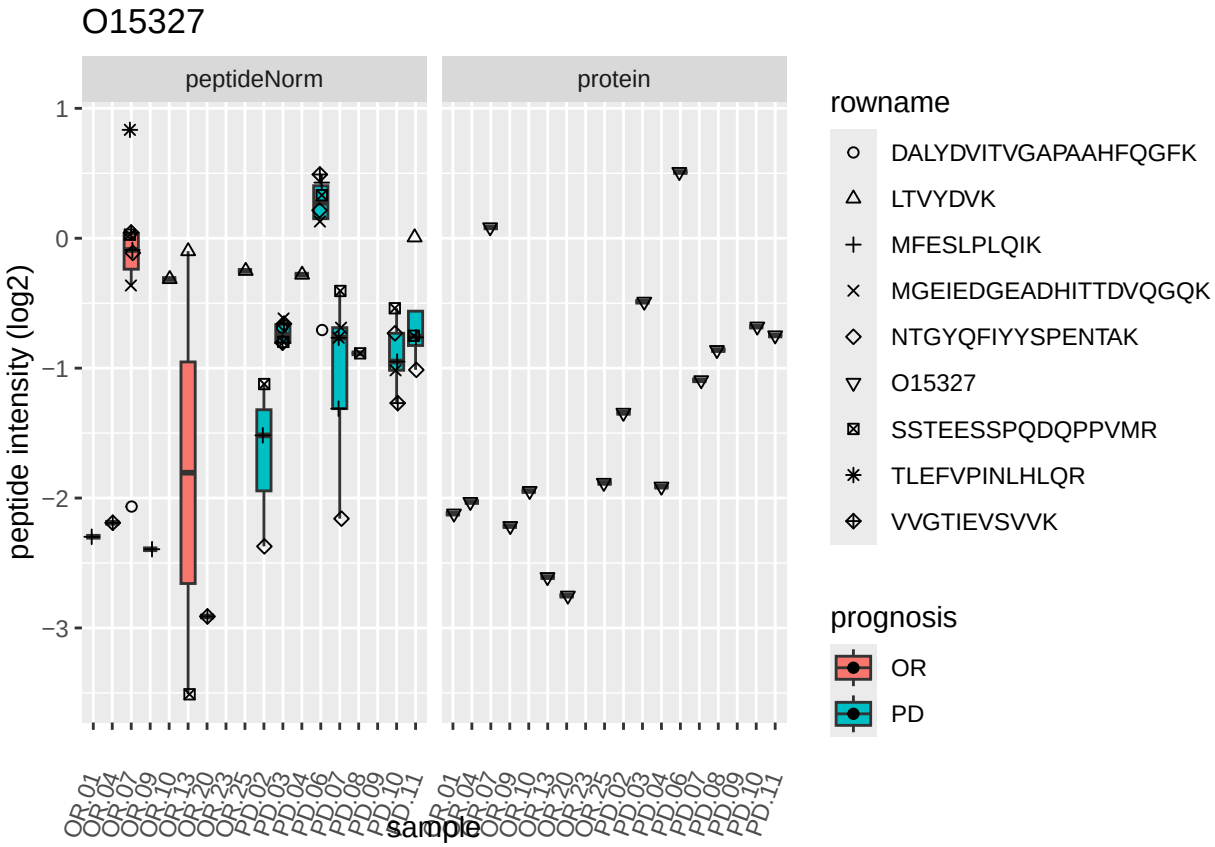
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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−1
−2
−3
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OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
DALYDVITVGAPAAHFQGFK
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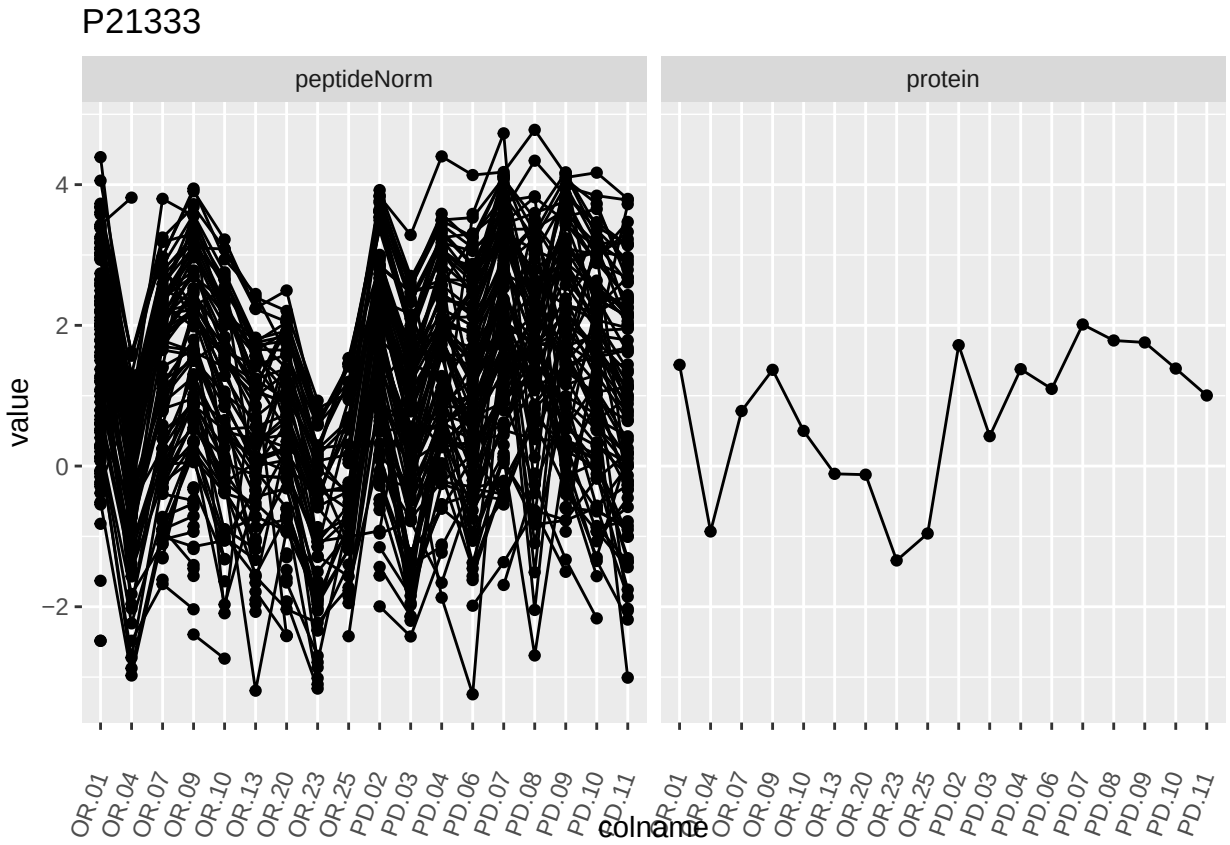
MGEIEDGEADHITTDVQGQK
NTGYQFIYYSPENTAK
O15327
SSTEESSPQDQPPVMR
TLEFVPINLHLQR
VVGTIEVSVVK
prognosis
OR
PD


P21333
peptideNorm
protein
value
4
2
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−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

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VK	*	GAGTGGLGLAVEGPSEAK	=	LYSVSYLLK
TYGGHQVPGSPFK	+	GKLDVQFSGLTK	>	MDCQECPEGYR
	'	GLVEPVDVVDNADGTQTVNYVPSR	?	NDNDTFTVK
IVTITWGGQNIGR	–	GQHVPGSPFQFTVGPLGEGGAHK	@	NGHVGISFVPK
	·	GTVEPQLEAR	A	NGQHVASSPIPVVISQSEIGDASI
	/	HTAMVSWGGVSIPNSPFR	B	P21333
	0	IANLQTDLSDGLR	C	PGAPLRPK
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	2	IPEISIQDMTAQVTSPSGK	E	RAPSVANVGSHCDLSLK
PFPLEAVAPTKPSK	3	IVGPSGAAVPCK	F	RLTVSSLQESGLK
	4	KGEITGEVR	G	SADFVVEAIGDDVGTLGFSVEGI
	5	KTHIQDNHDGTYTVAYVPDVTGR	H	SAGQGEVLVYVEDPAGHQEEAK
	6	LDVQFSGLTK	I	SPFEVYVDK
	7	LIALLEVLSQKK	J	SPFSVAVSPSLDLSK
QPSVQPPLR	8	LLGWIQNKLPQLPITNFSR	K	SPYTVTVGQACNPSACR
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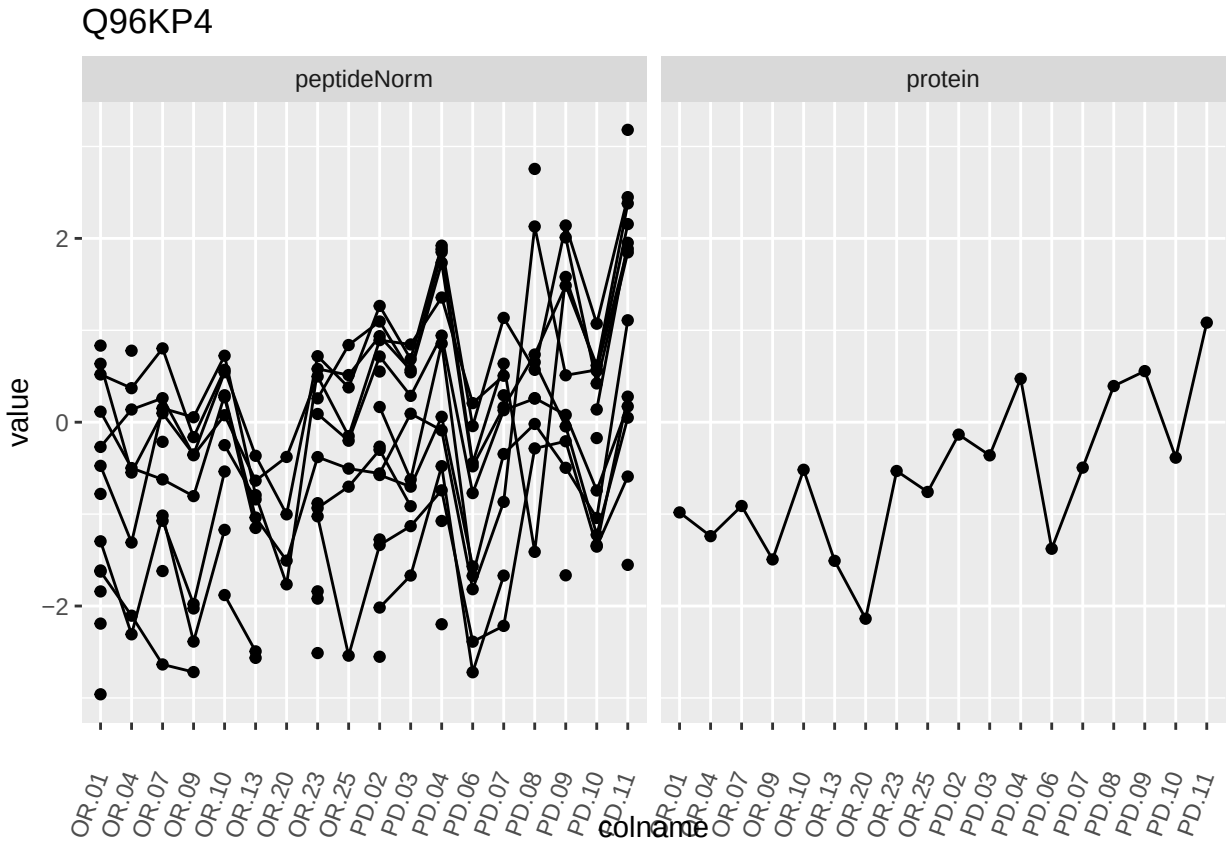
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protein
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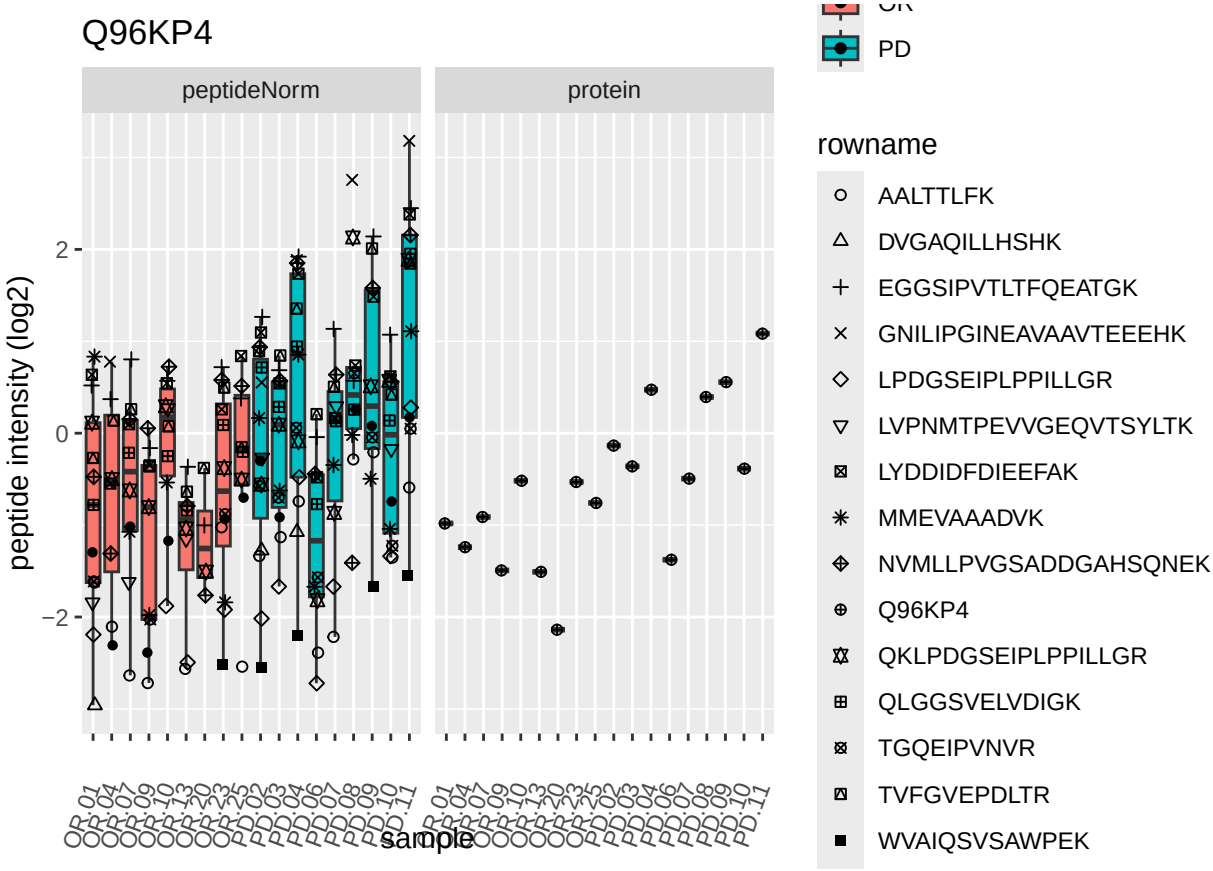
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q96KP4
peptideNorm
protein
peptide intensity (log2)
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−2
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OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
OR
PD
rowname
AALTTLFK
DVGAQILLHSHK
EGGSIPVTLTFQEATGK
GNILIPGINEAVAAVTEEEHK
LPDGSEIPLPPILLGR
LVPNMTPEVVGEQVTSYLTK
LYDDIDFDIEEFAK
MMEVAAADVK
NVMLLPVGSADDGAHSQNEK
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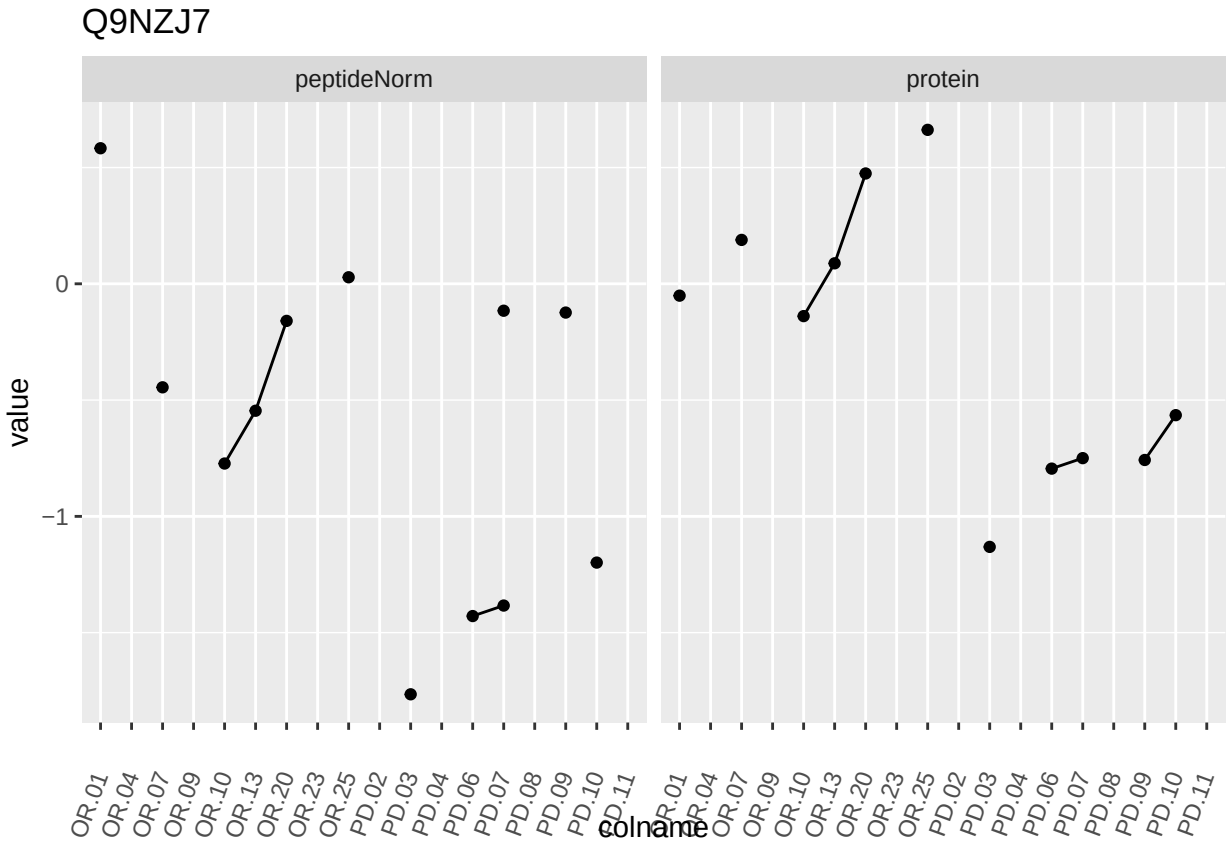
Q9NZJ7
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protein
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OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
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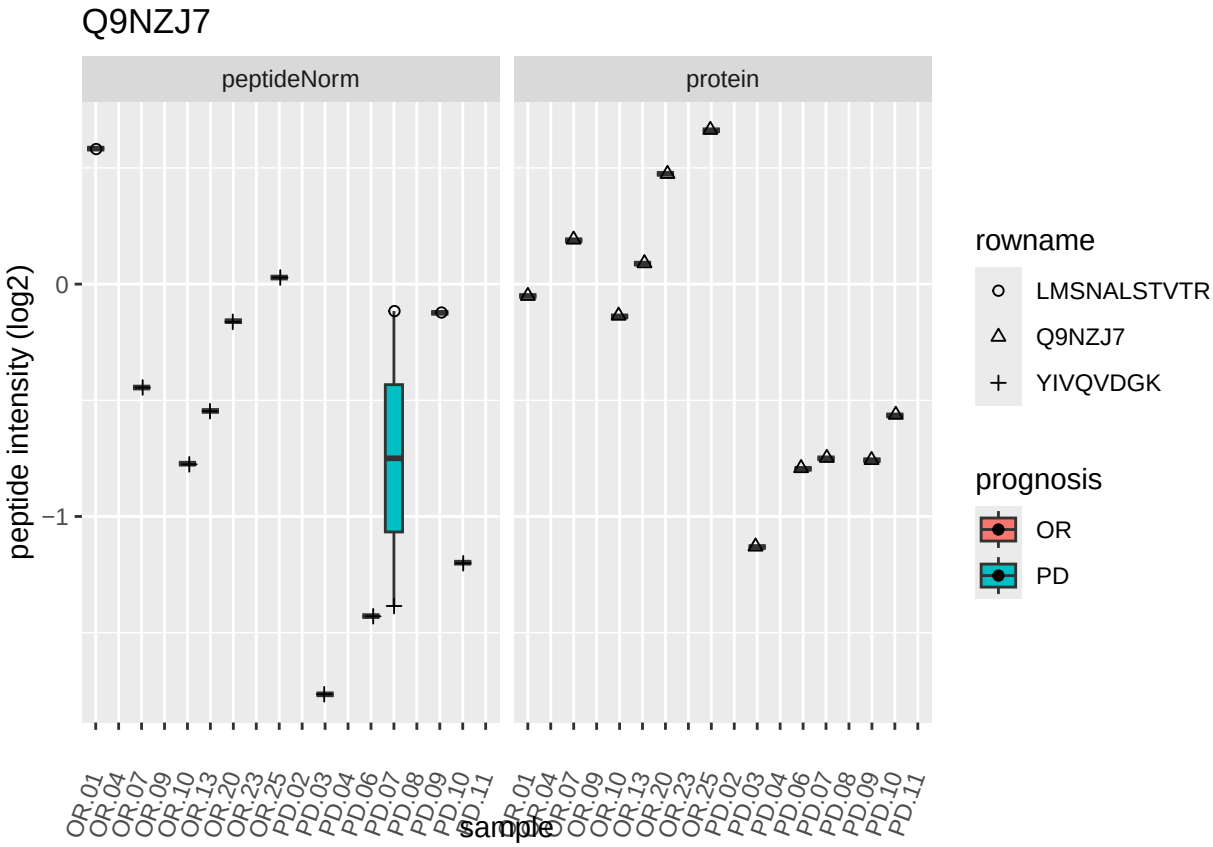
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NZJ7
peptideNorm
protein
peptide intensity (log2)
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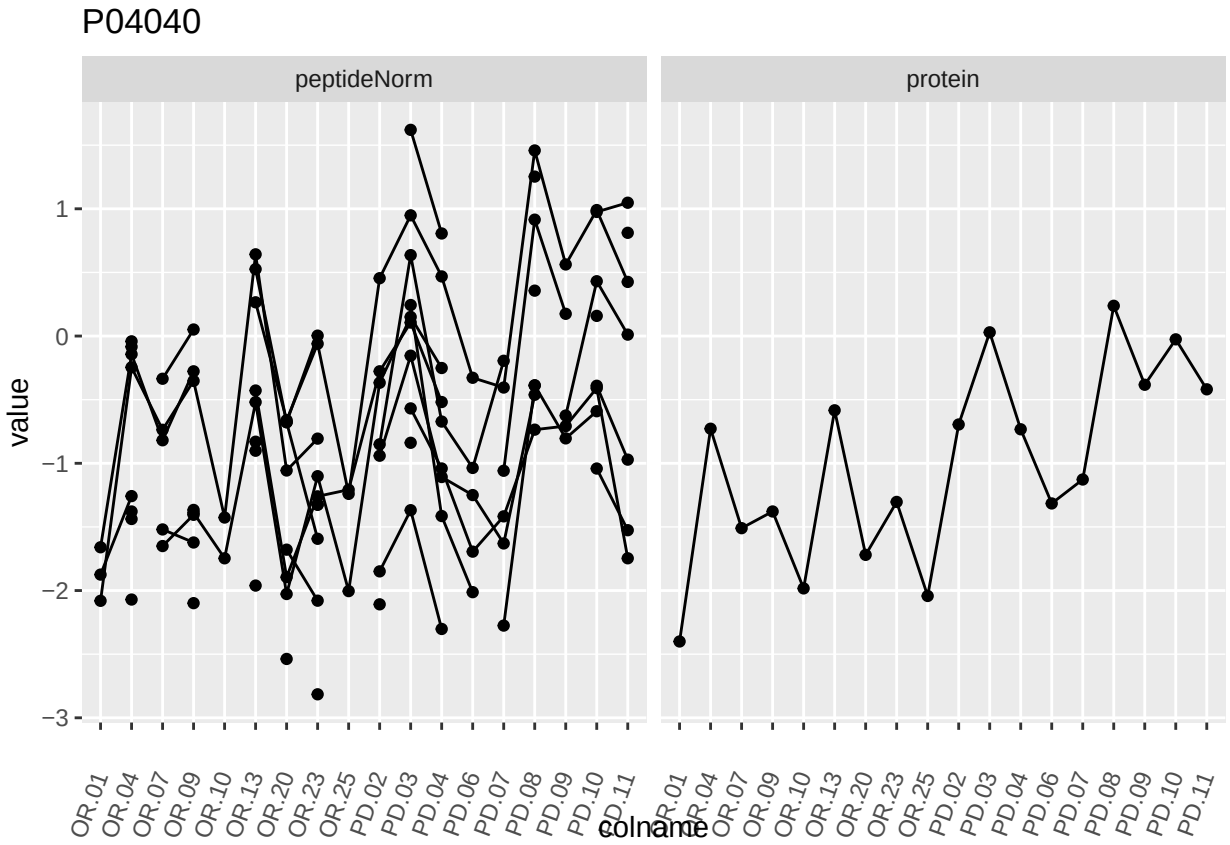
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LMSNALSTVTR
Q9NZJ7
YIVQVDGK
prognosis
OR
PD


P04040
peptideNorm
protein
value
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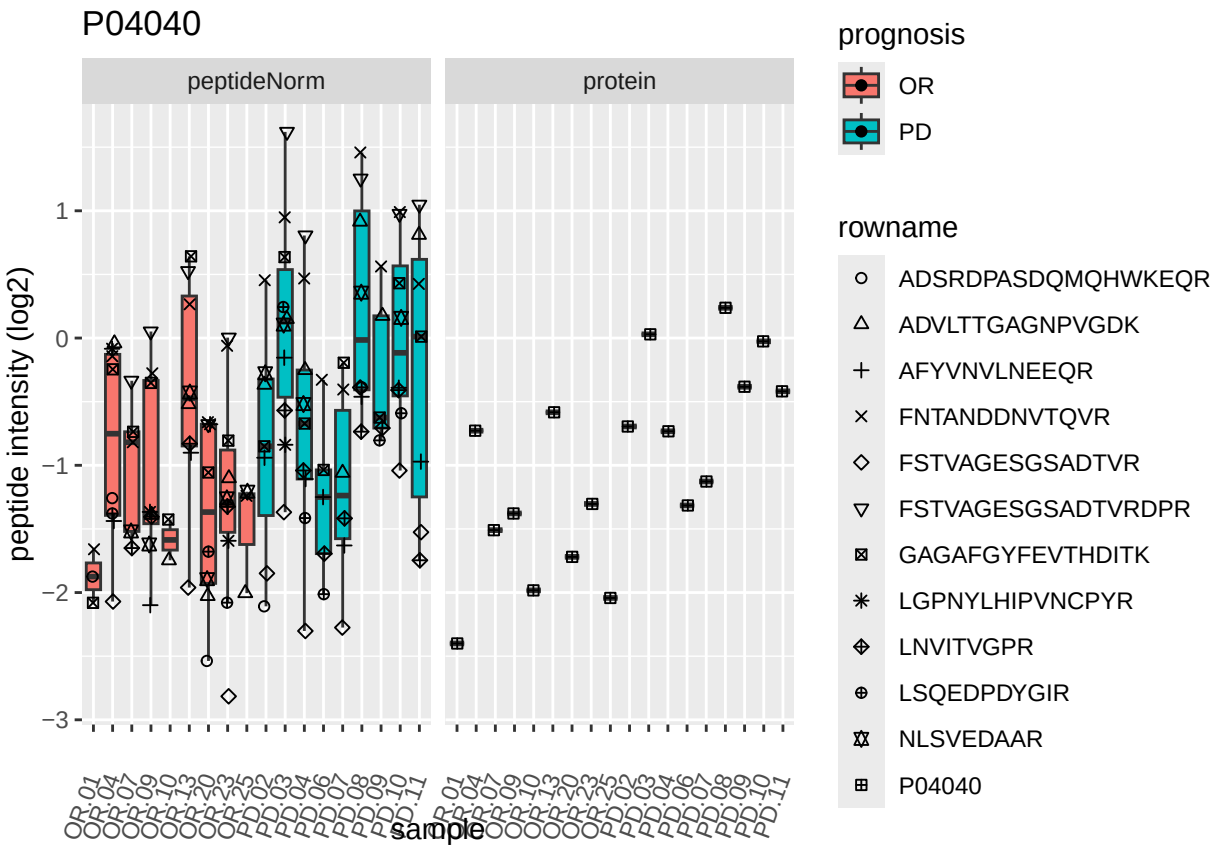
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
ADSRDPASDQMQHWKEQR
ADVLTTGAGNPVGDK
AFYVNVLNEEQR
FNTANDDNVTQVR
FSTVAGESGSADTVR
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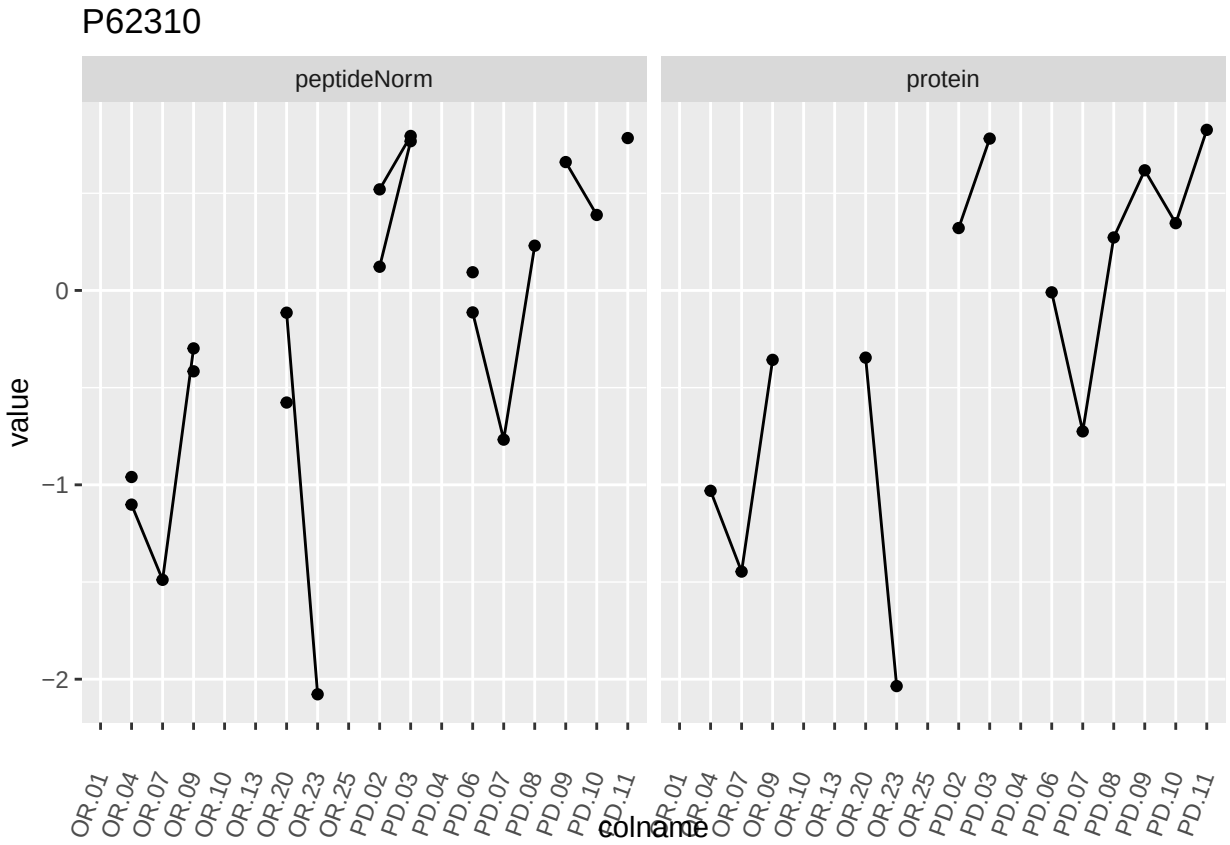
LGPNYLHIPVNCPYR
LNVITVGPR
LSQEDPDYGIR
NLSVEDAAR
P04040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peptideNorm
protein
value
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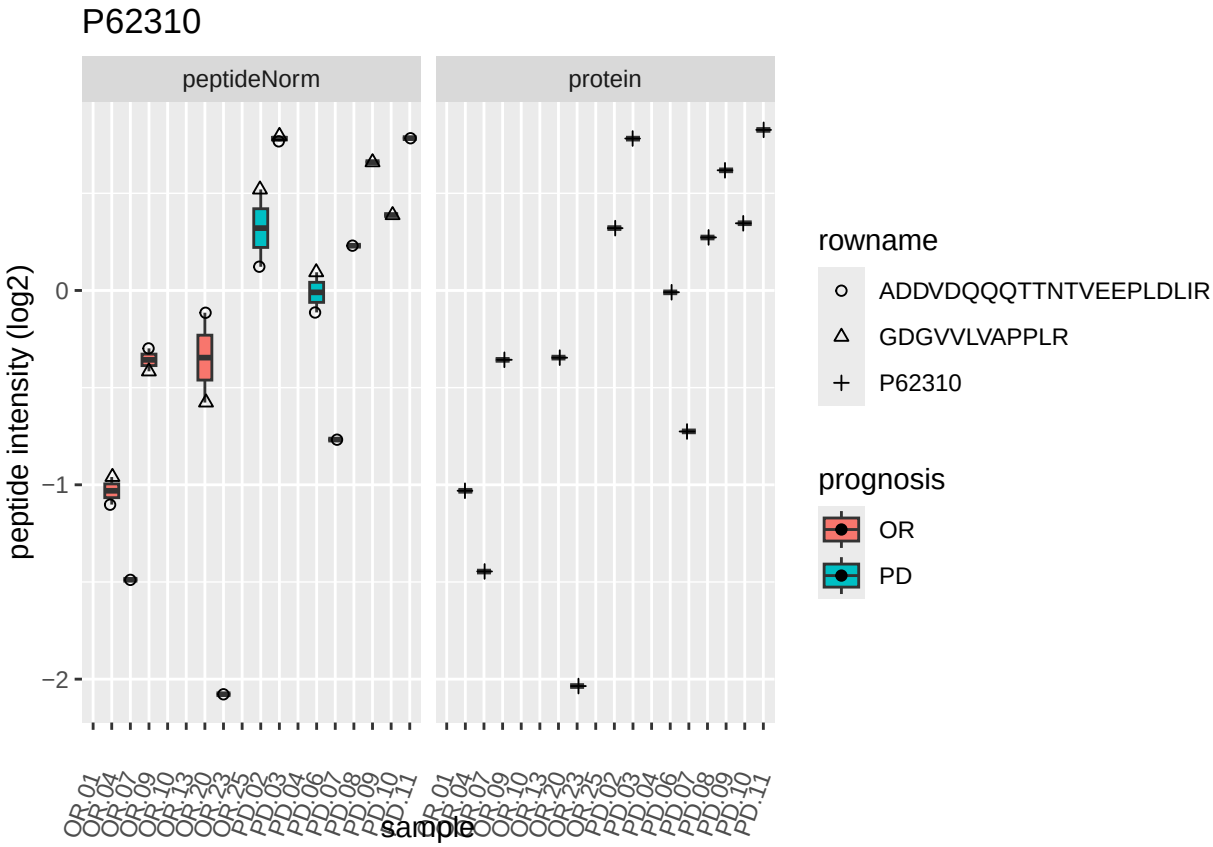
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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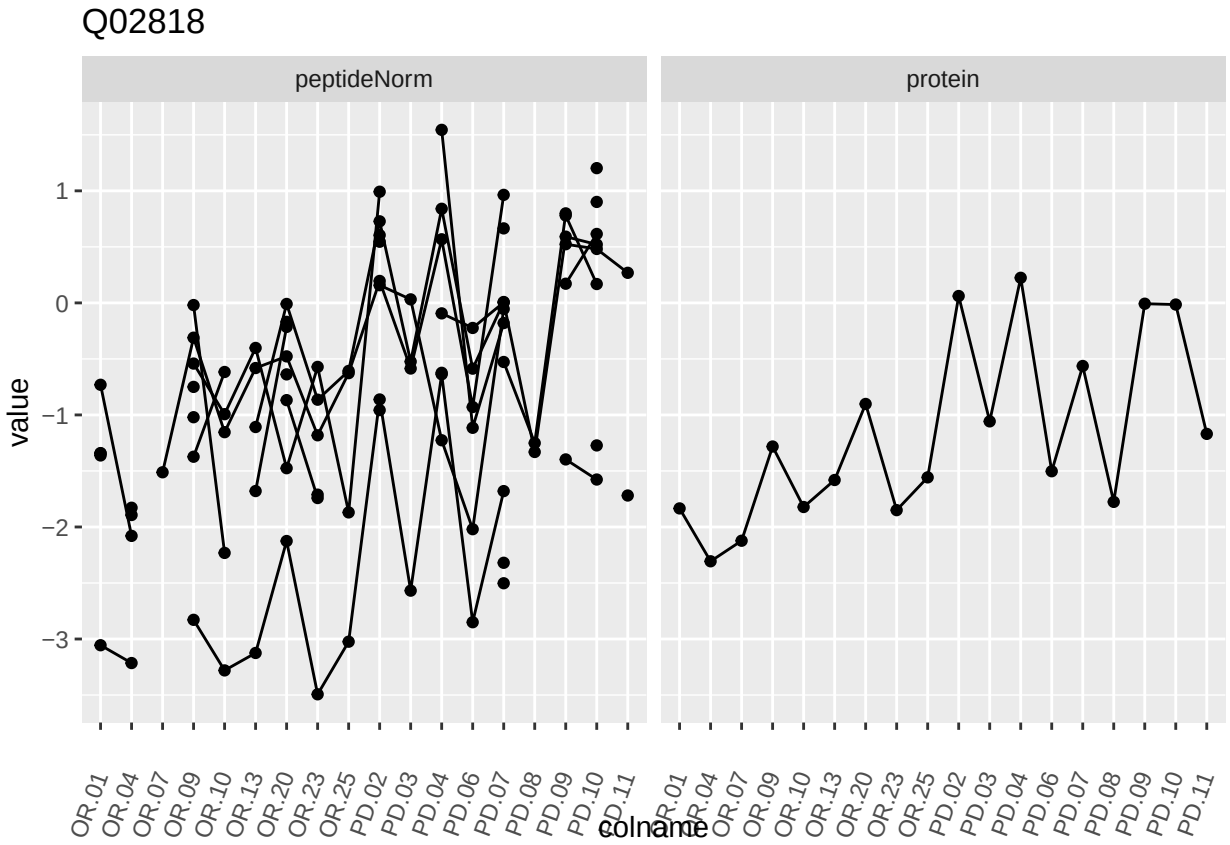
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ADDVDQQQTTNTVEEPLDLIR
GDGVVLVAPPLR
P62310
prognosis
OR
PD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peptideNorm
protein
value
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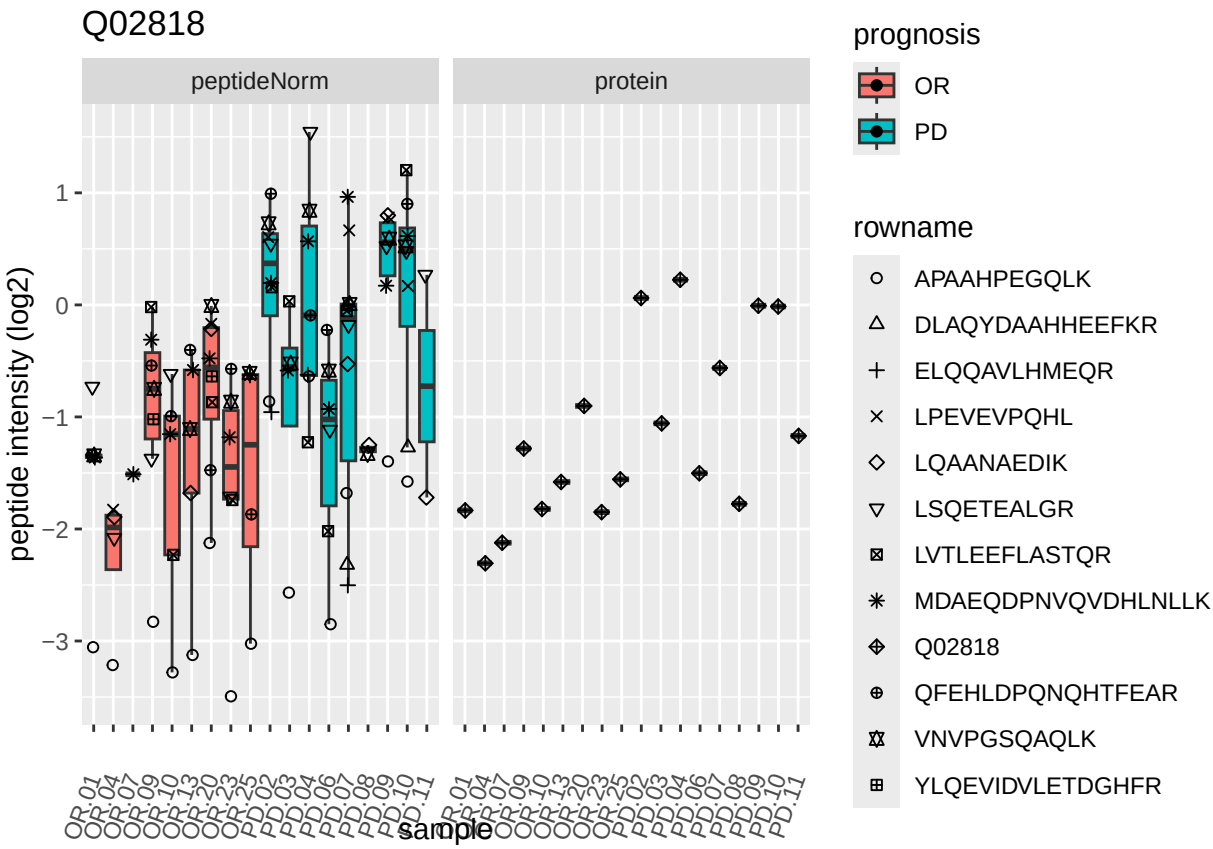
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname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peptideNorm
protein
peptide intensity (log2)
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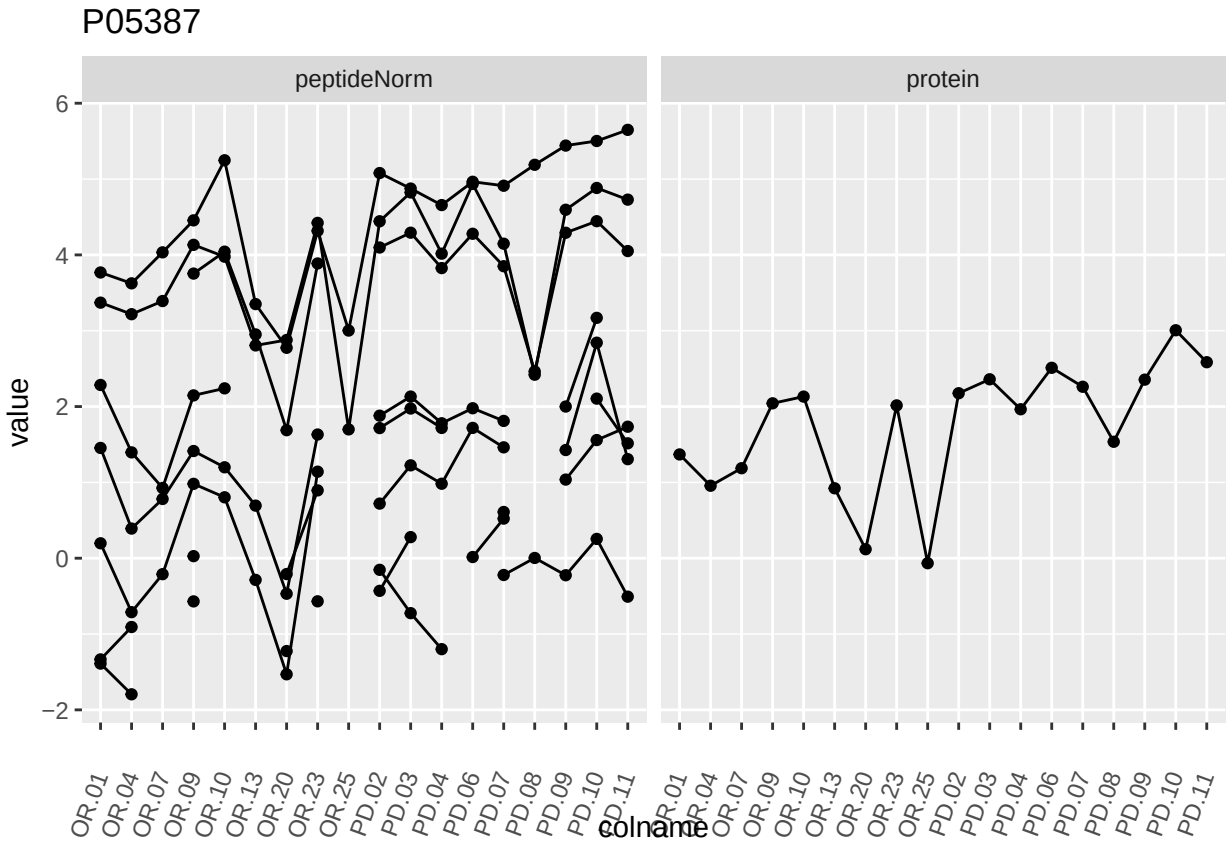
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
APAAHPEGQLK
DLAQYDAAHHEEFKR
ELQQAVLHMEQR
LPEVEVPQHL
LQAANAEDIK
LSQETEALGR
LVTLEEFLASTQR
MDAEQDPNVQVDHLNLLK
Q02818
QFEHLDPQNQHTFEAR
VNVPGSQAQLK
YLQEVIDVLETDGHFR


P05387
peptideNorm
protein
value
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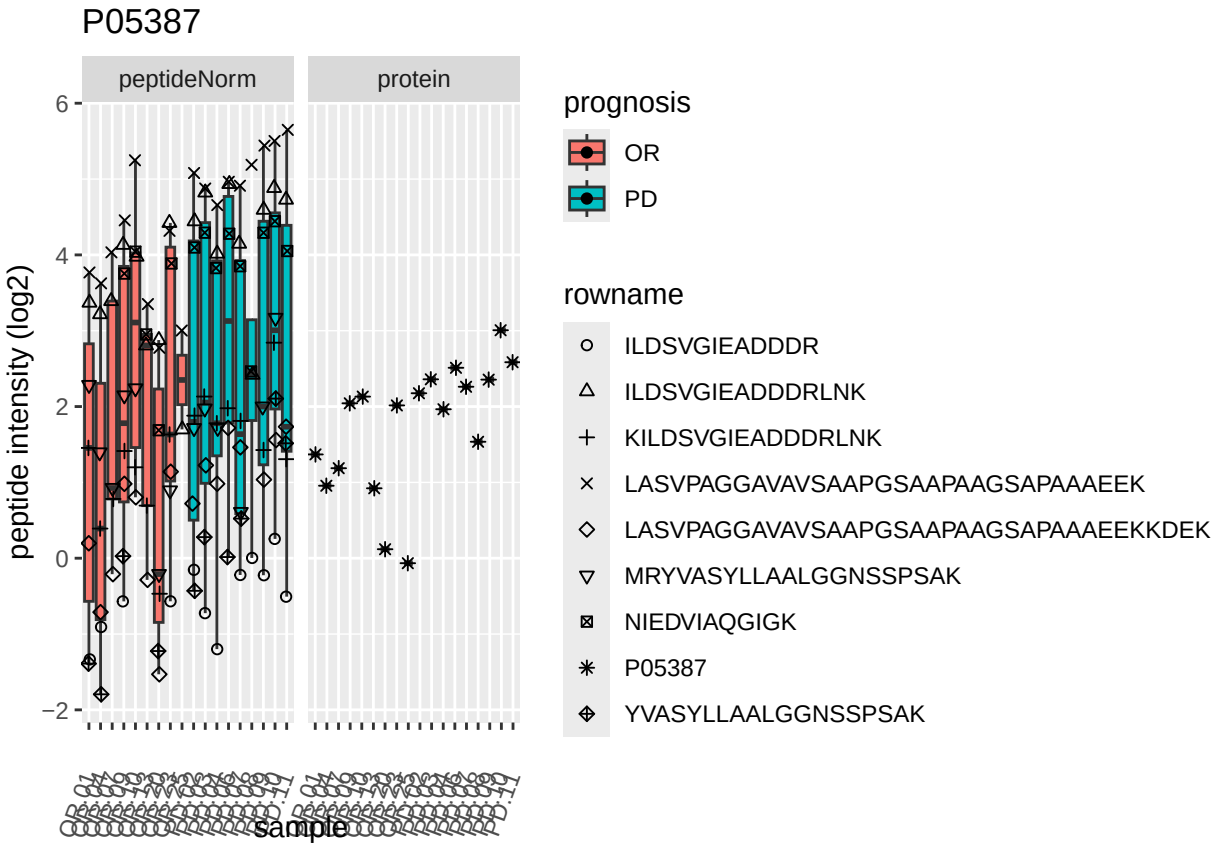
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P05387
peptideNorm
protein
peptide intensity (log2)
6
4
2
0
−2
sample
prognosis
OR
PD
rowname
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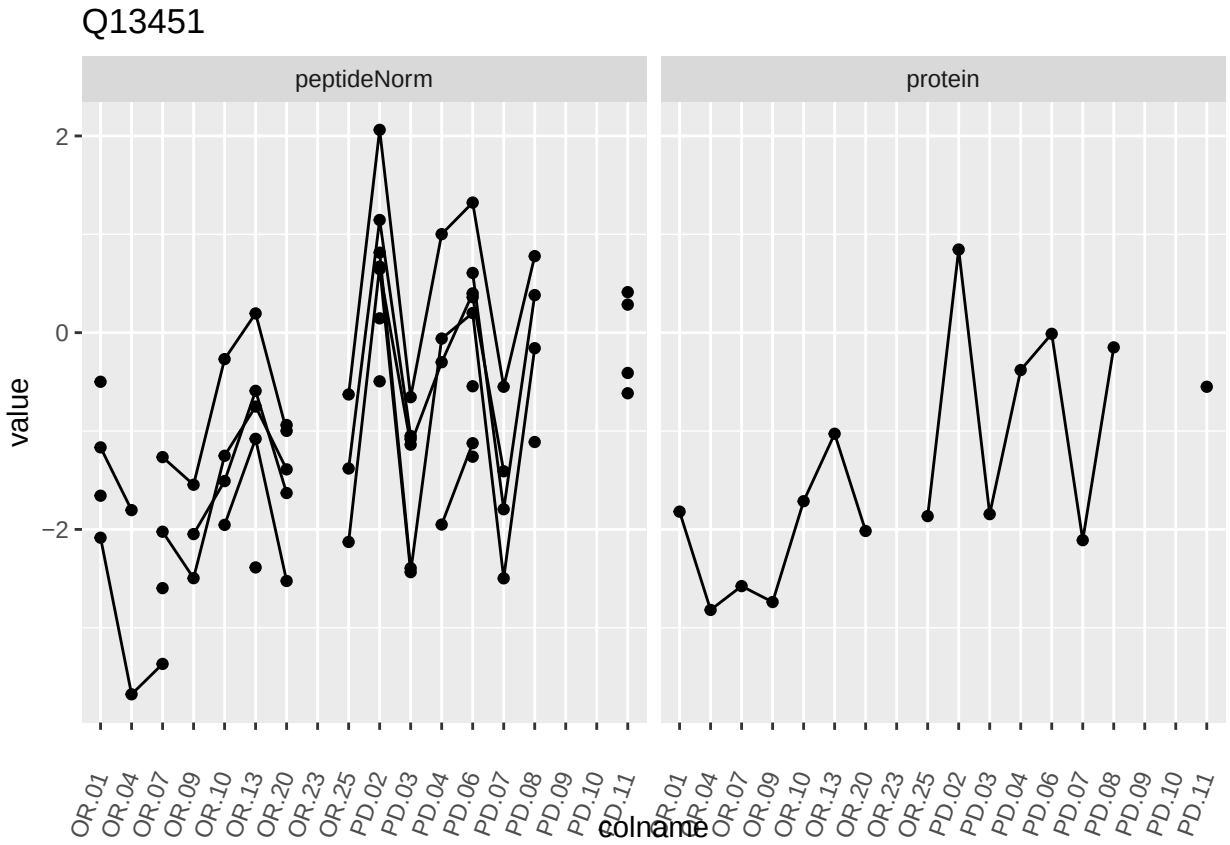
ILDSVGIEADDDRLNK
KILDSVGIEADDDRLNK
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEK
MRYVASYLLAALGGNSSPSAK
NIEDVIAQGIGK
P05387
YVASYLLAALGGNSSPSAK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peptideNorm
protein
value
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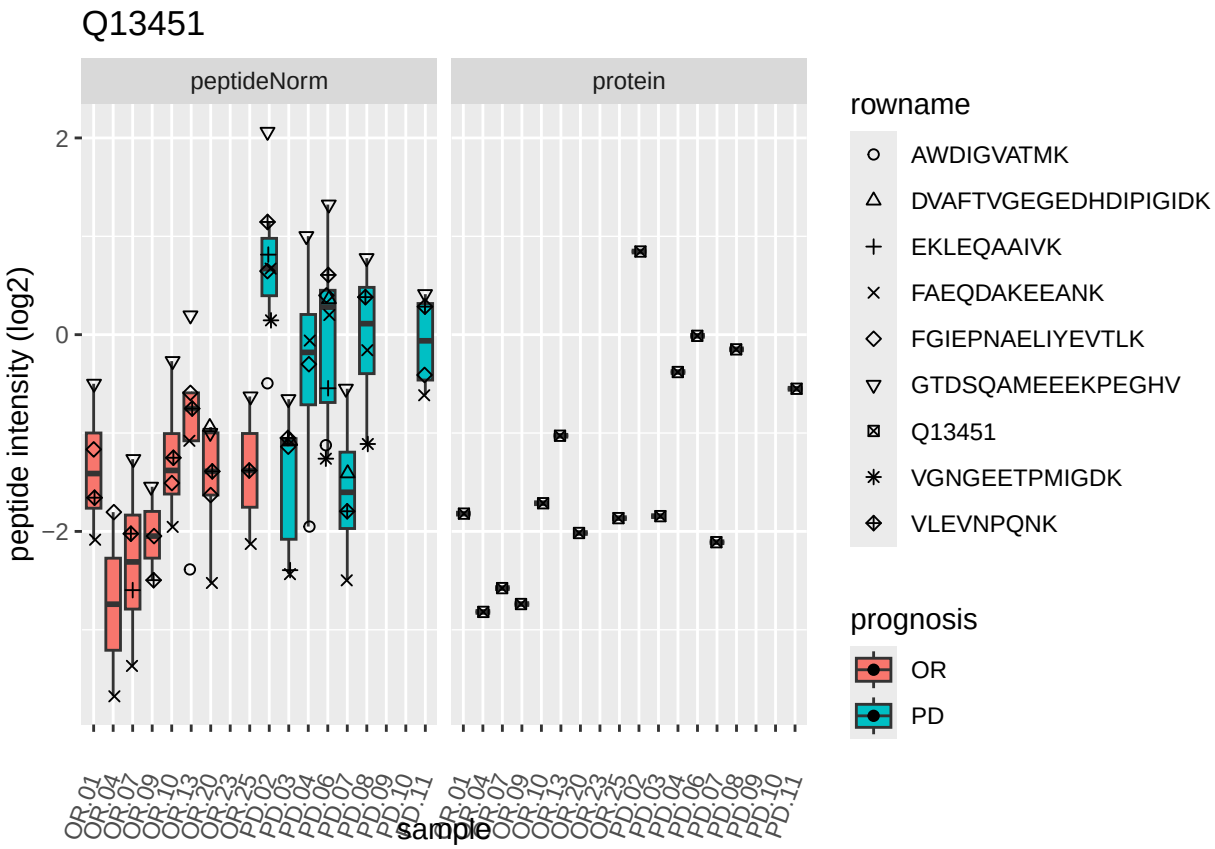
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q13451
peptideNorm
protein
peptide intensity (log2)
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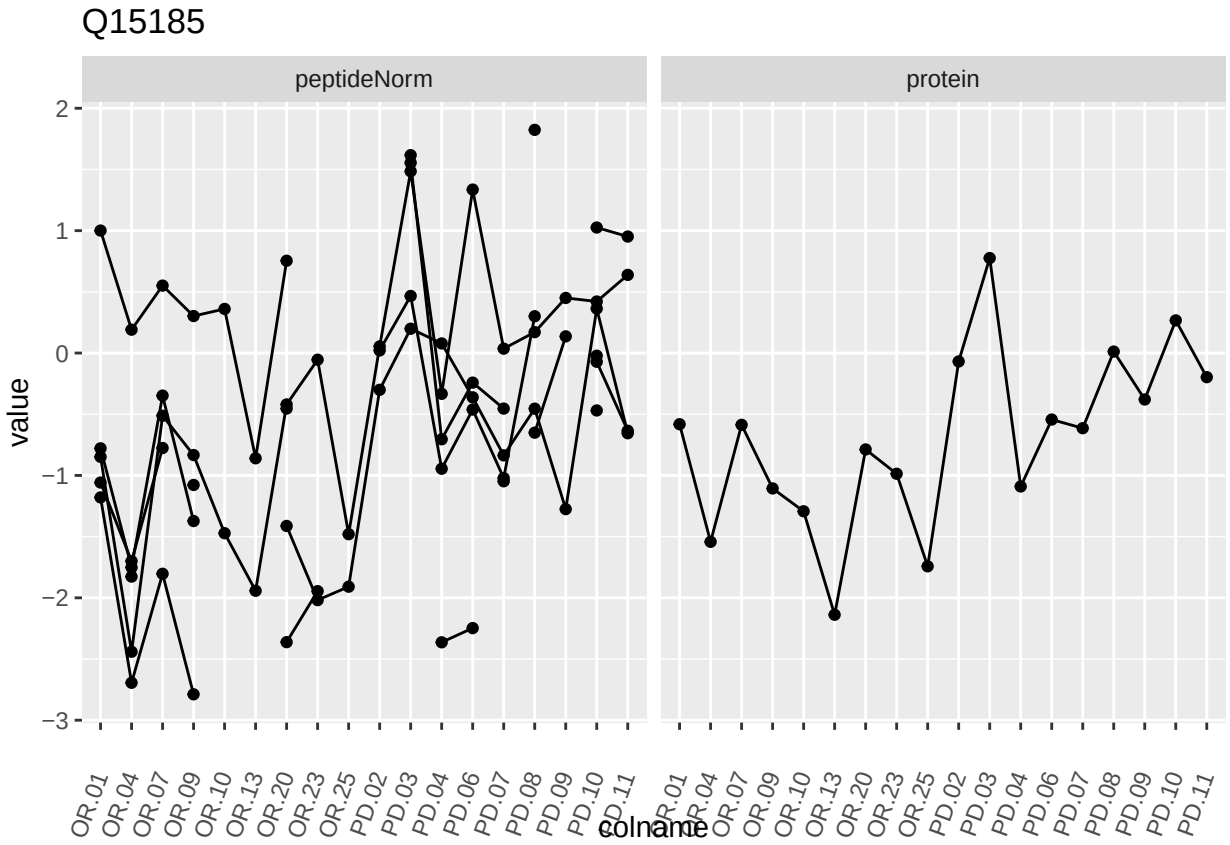
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AWDIGVATMK
DVAFTVGEGEDHDIPIGIDK
EKLEQAAIVK
FAEQDAKEEANK
FGIEPNAELIYEVTLK
GTDSQAMEEEKPEGHV
Q13451
VGNGEETPMIGDK
VLEVNPQNK
prognosis
OR
PD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peptideNorm
protein
value
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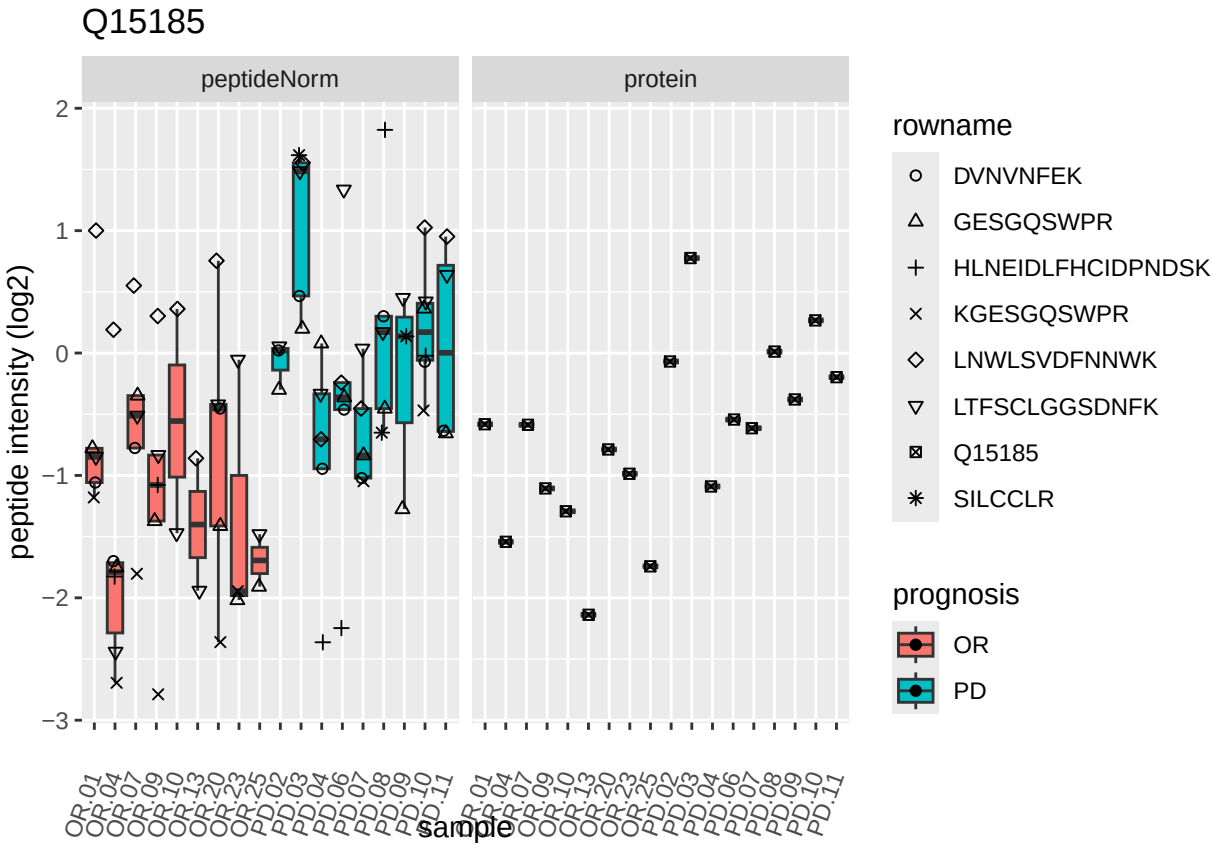
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q15185
peptideNorm
protein
peptide intensity (log2)
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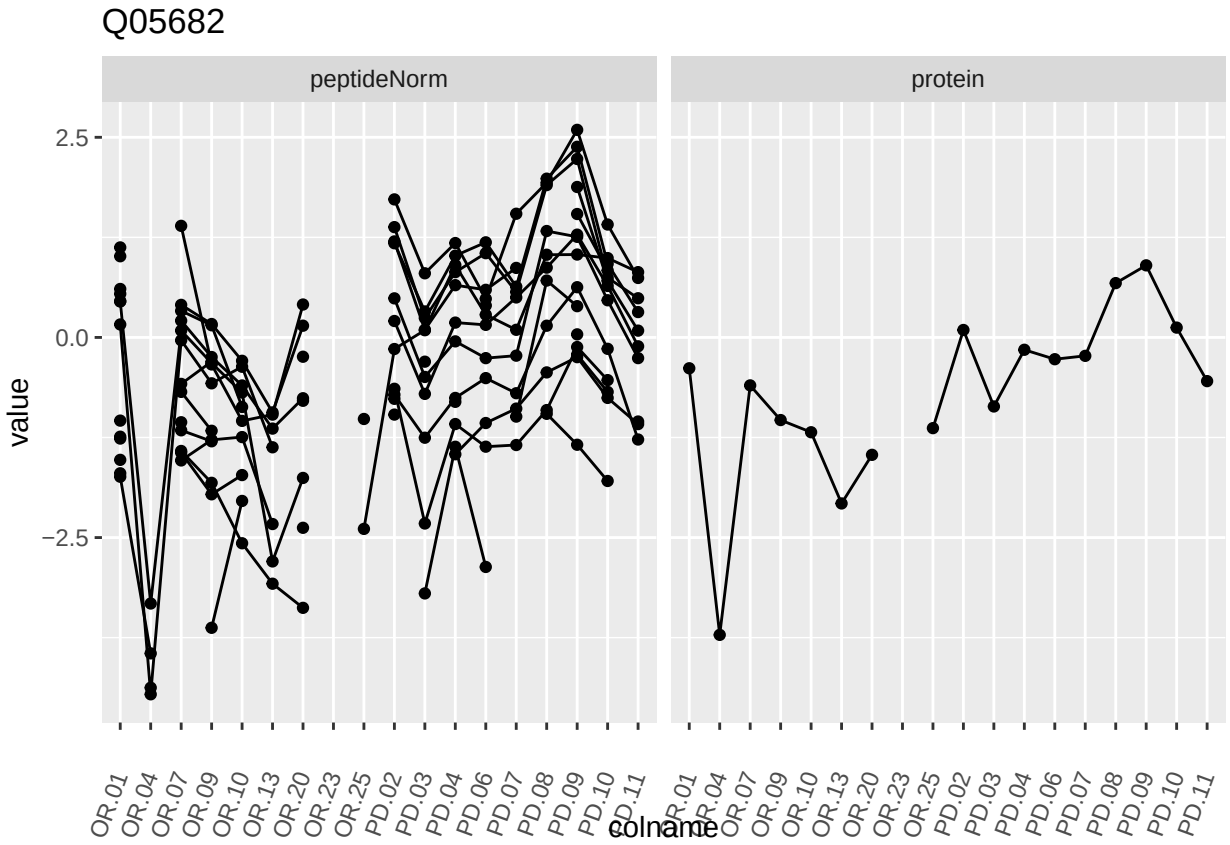
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
DVNVNFEK
GESGQSWPR
HLNEIDLFHCIDPNDSK
KGESGQSWPR
LNWLSVDFNNWK
LTFSCLGGSDNFK
Q15185
SILCCLR
prognosis
OR
PD


Q05682
peptideNorm
protein
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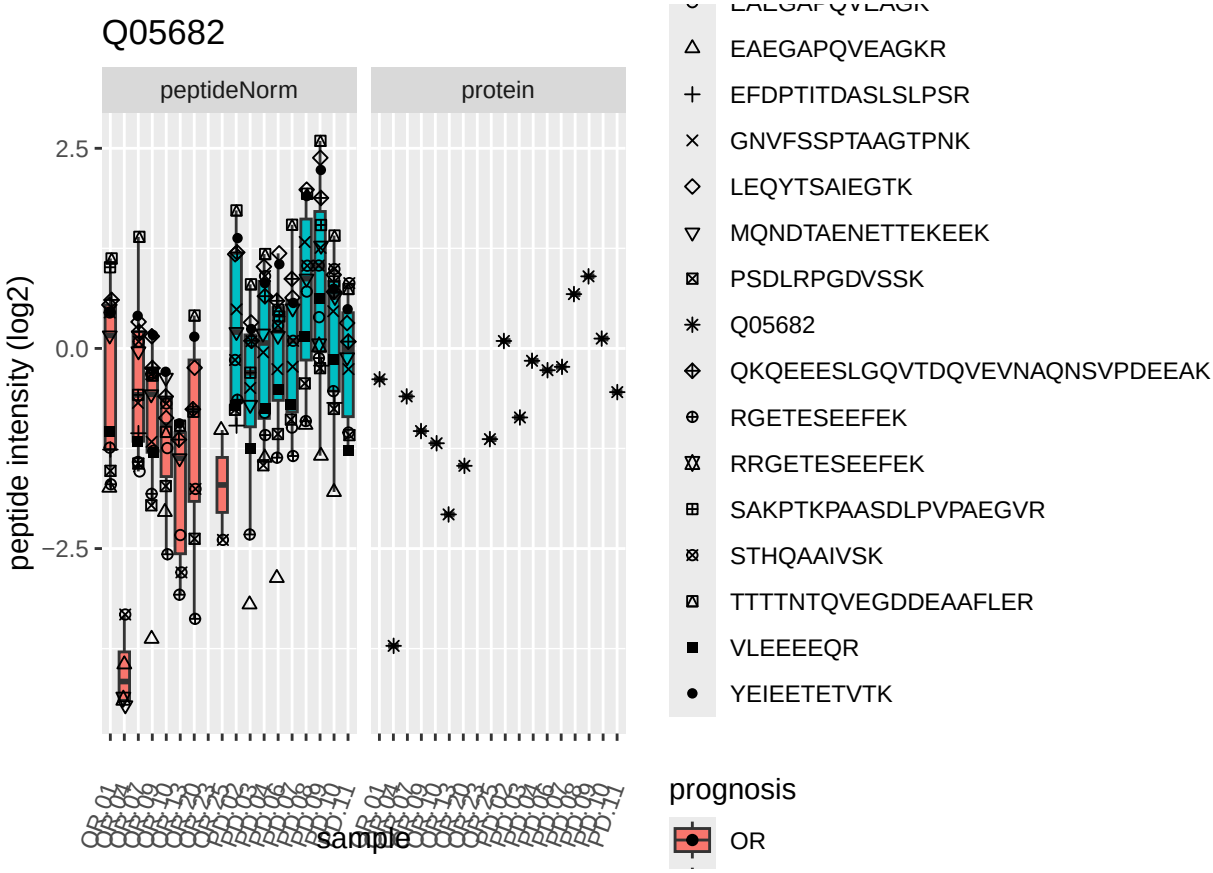
0.0
−2.5
value
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q05682
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
sample
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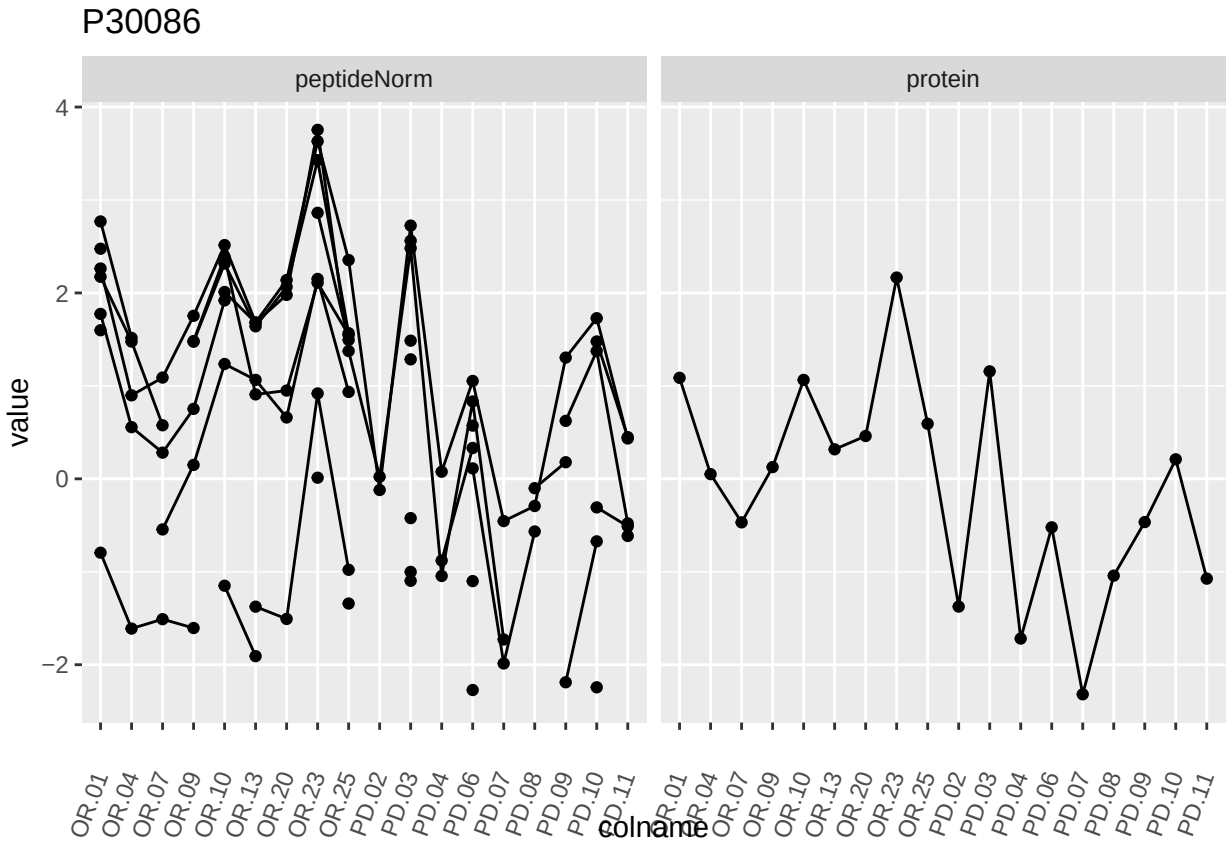
EFDPTITDASLSLPSR
GNVFSSPTAAGTPNK
LEQYTSAIEGTK
MQNDTAENETTEKEEK
PSDLRPGDVSSK
Q05682
QKQEEESLGQVTDQVEVNAQNSVPDEEAK
RGETESEEFEK
RRGETESEEFEK
SAKPTKPAASDLPVPAEGVR
STHQAAIVSK
TTTTNTQVEGDDEAAFLER
VLEEEEQR
YEIEETETVTK
prognosis
OR


P30086
peptideNorm
protein
value
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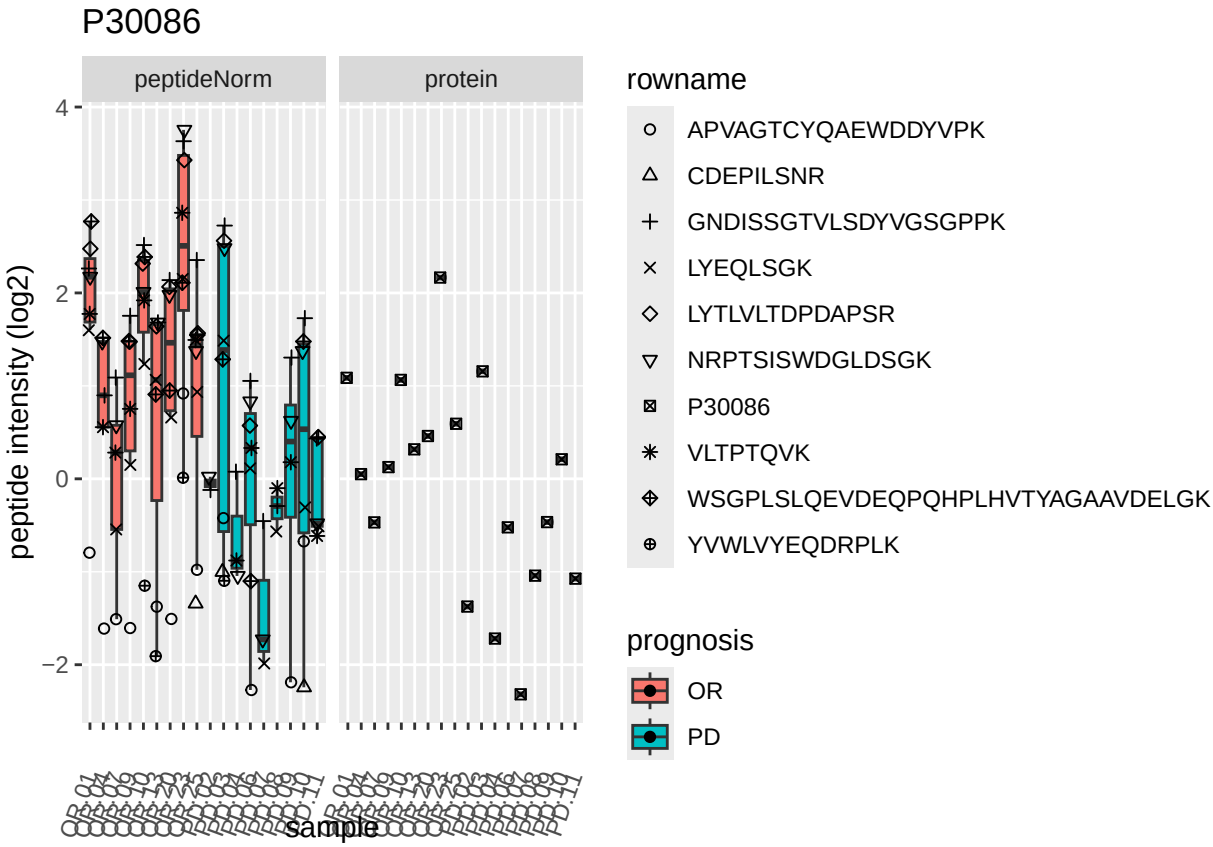
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P30086
peptideNorm
protein
peptide intensity (log2)
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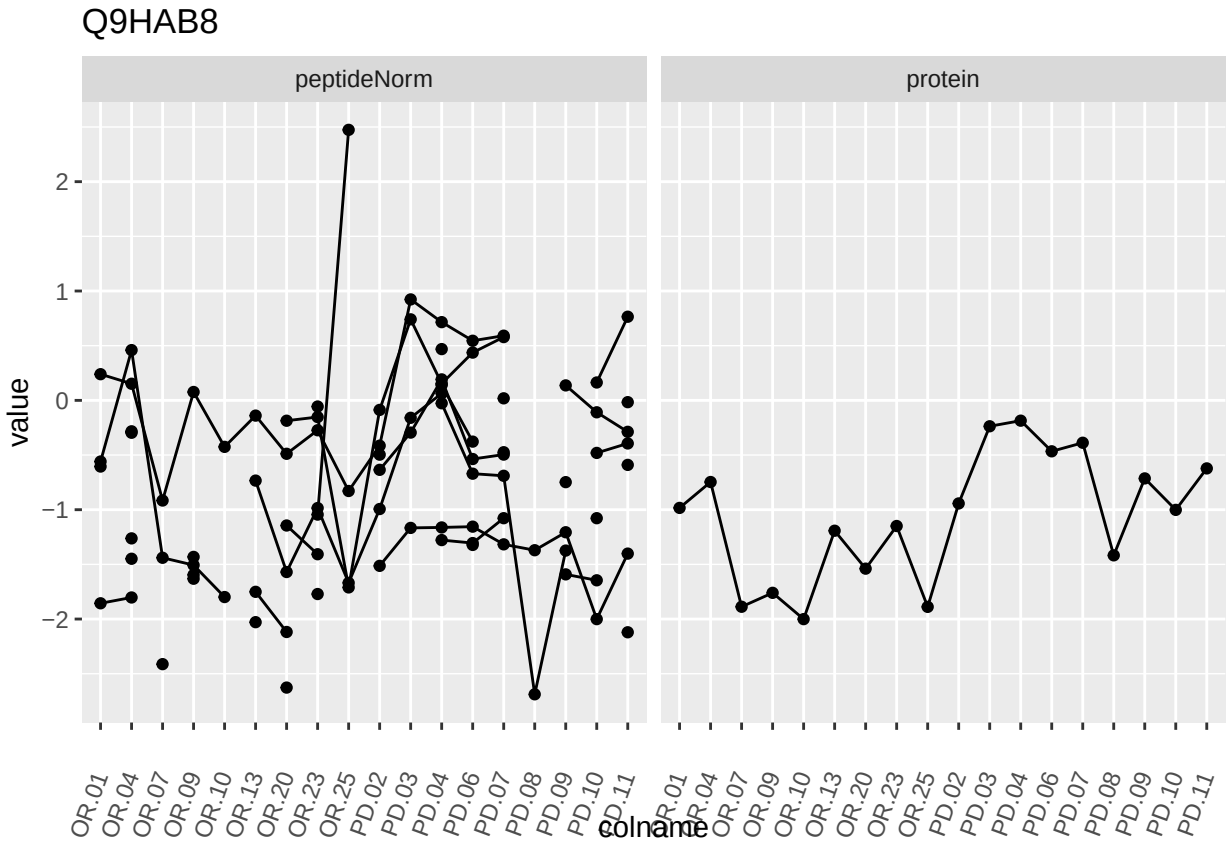
2
0
−2
sample
rowname
APVAGTCYQAEWDDYVPK
CDEPILSNR
GNDISSGTVLSDYVGSGPPK
LYEQLSGK
LYTLVLTDPDAPSR
NRPTSISWDGLDSGK
P30086
VLTPTQVK
WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK
YVWLVYEQDRPLK
prognosis
OR
PD


Q9HAB8
peptideNorm
protein
value
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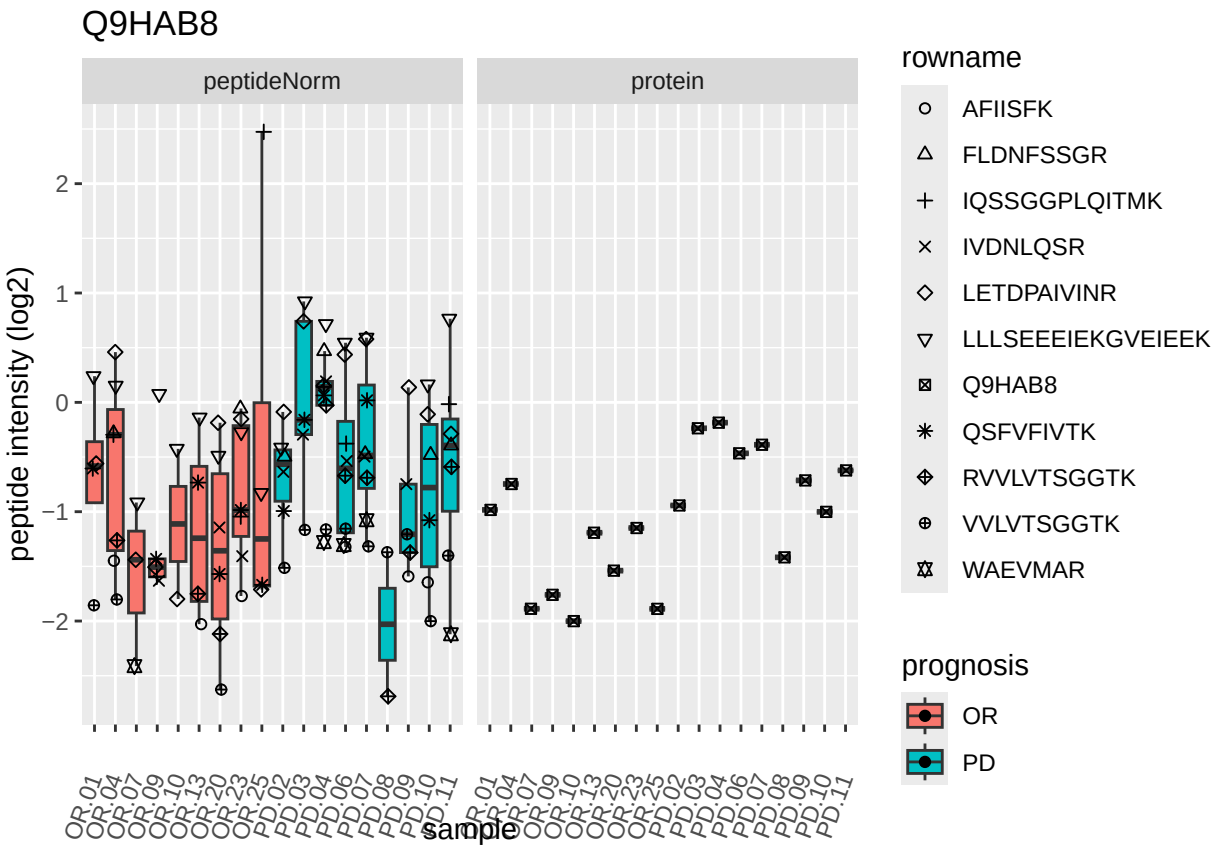
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9HAB8
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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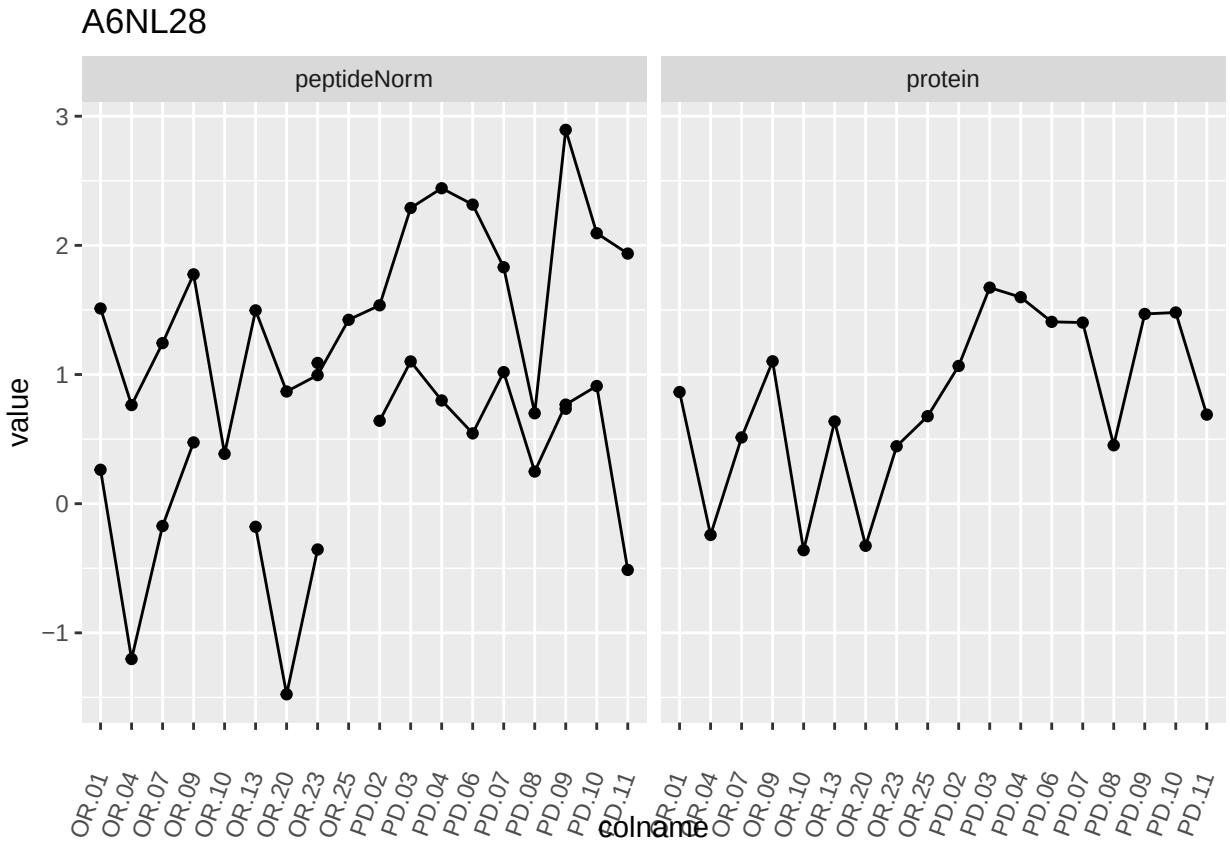
FLDNFSSGR
IQSSGGPLQITMK
IVDNLQSR
LETDPAIVINR
LLLSEEEIEKGVEIEEK
Q9HAB8
QSFVFIVTK
RVVLVTSGGTK
VVLVTSGGTK
WAEVMAR
prognosis
OR
PD


A6NL28
peptideNorm
protein
value
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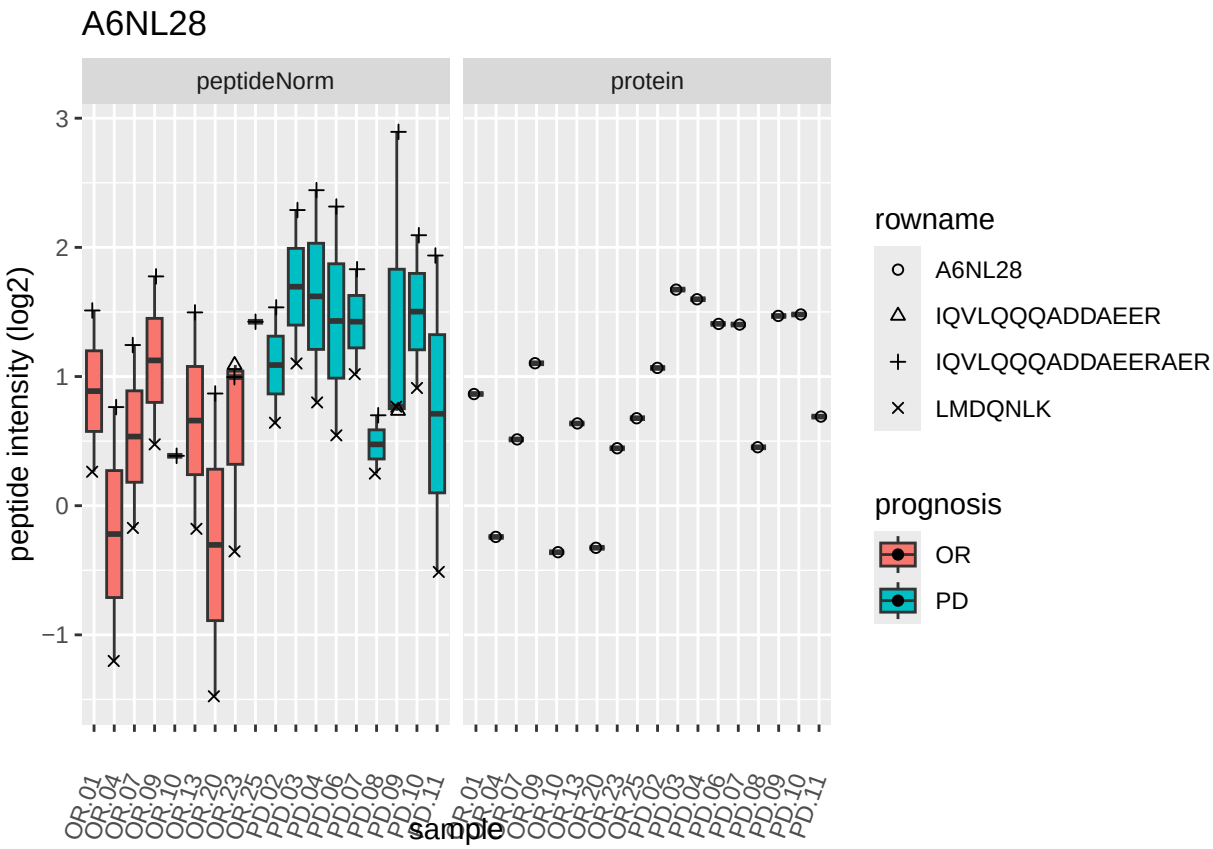
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


A6NL28
peptideNorm
protein
peptide intensity (log2)
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2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
A6NL28
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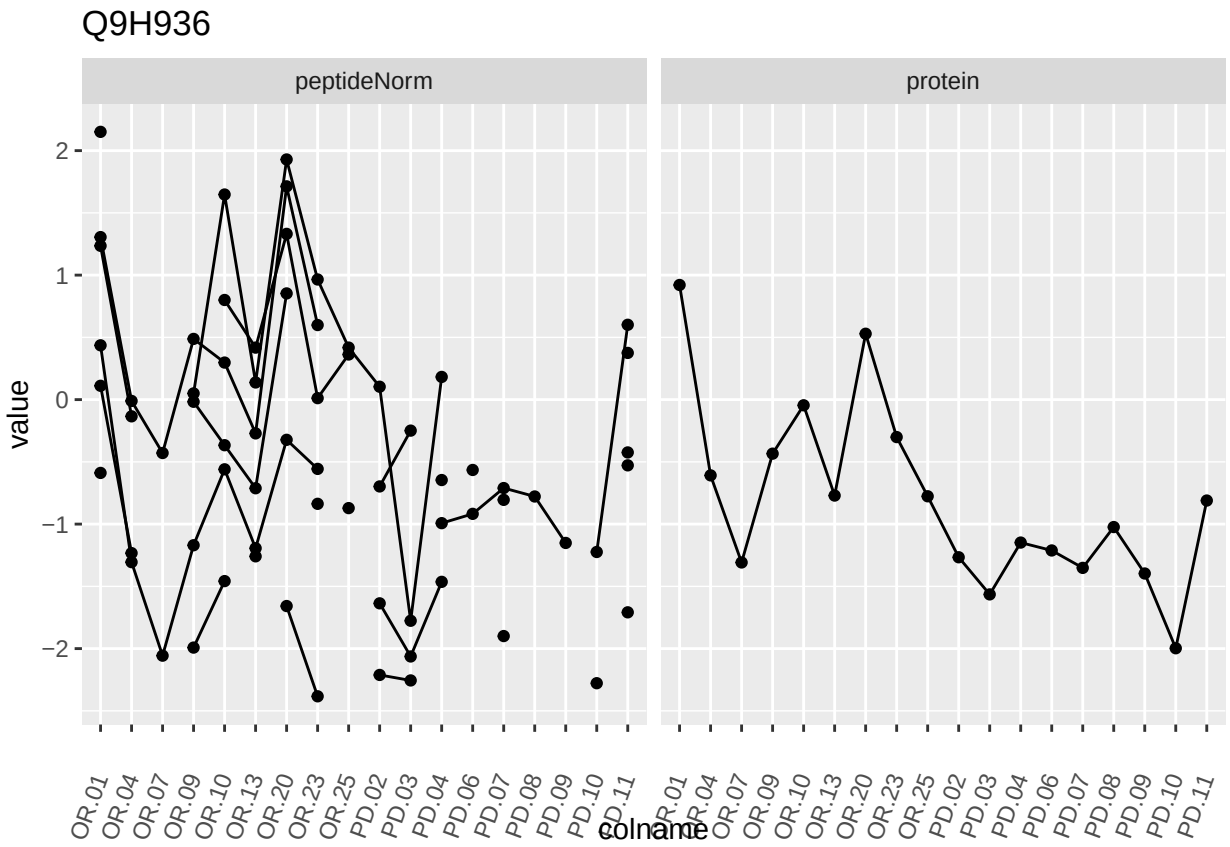
IQVLQQQADDAEERAER
LMDQNLK
prognosis
OR
PD


Q9H936
peptideNorm
protein
value
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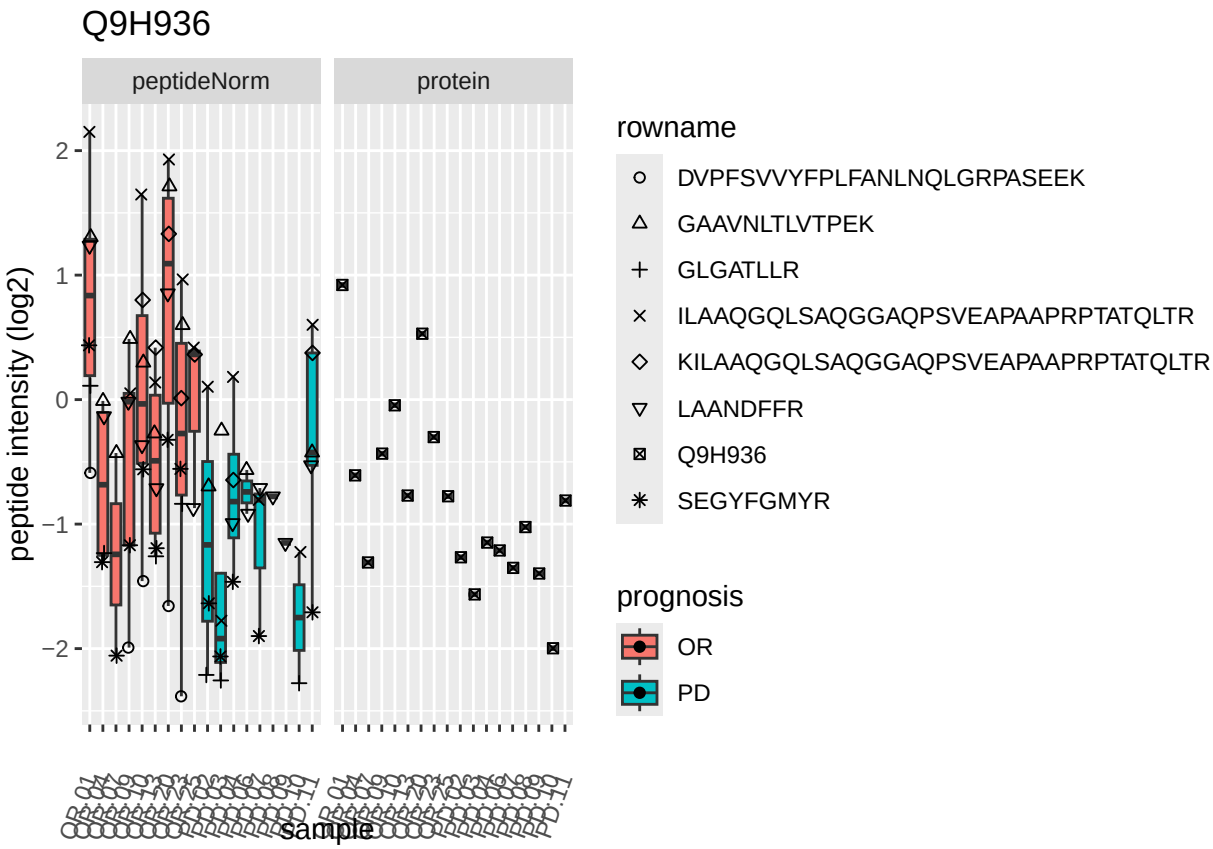
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9H936
peptideNorm
protein
peptide intensity (log2)
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1
0
−1
−2
sample
rowname
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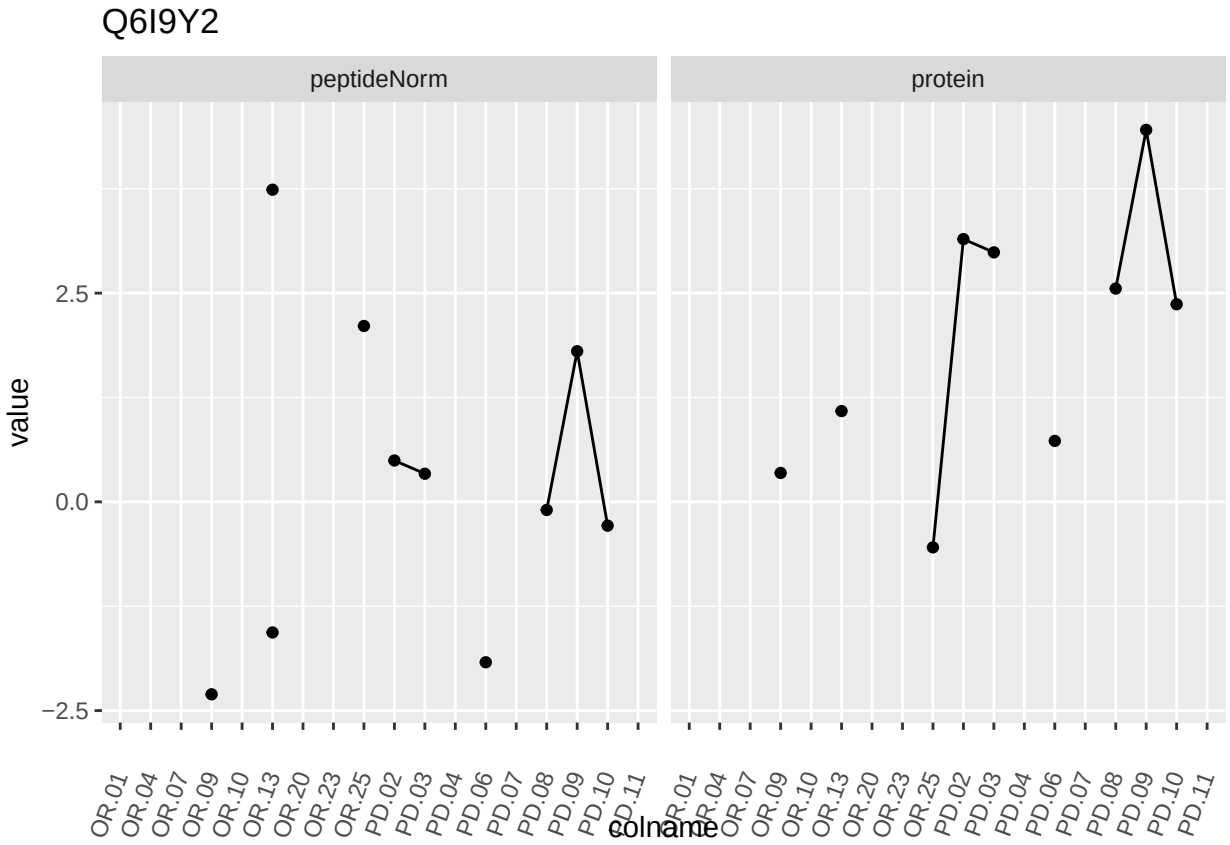
GAAVNLTLVTPEK
GLGATLLR
ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
KILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
LAANDFFR
Q9H936
SEGYFGMYR
prognosis
OR
PD


Q6I9Y2
peptideNorm
protein
value
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−2.5
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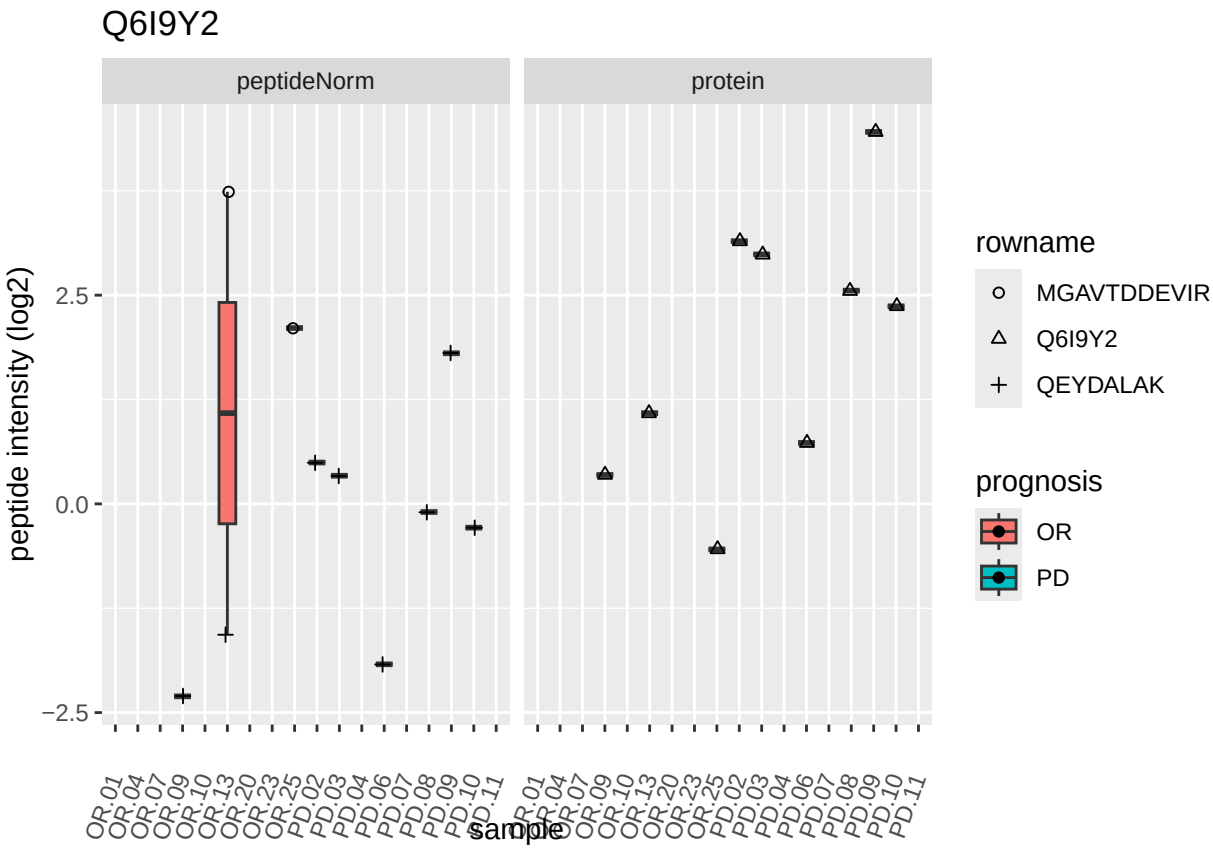
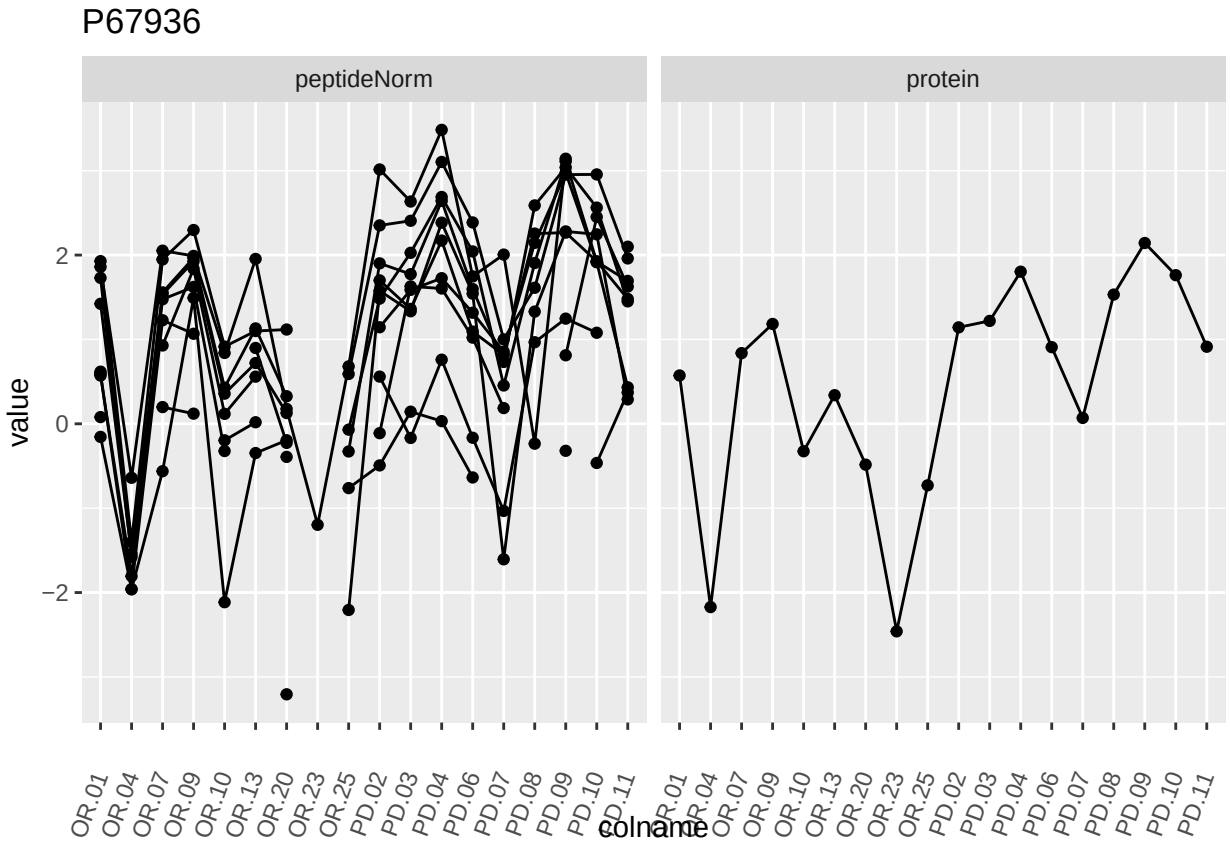
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q6I9Y2
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
MGAVTDDEVIR
Q6I9Y2
QEYDALAK
prognosis
OR
PD


P67936
peptideNorm
protein
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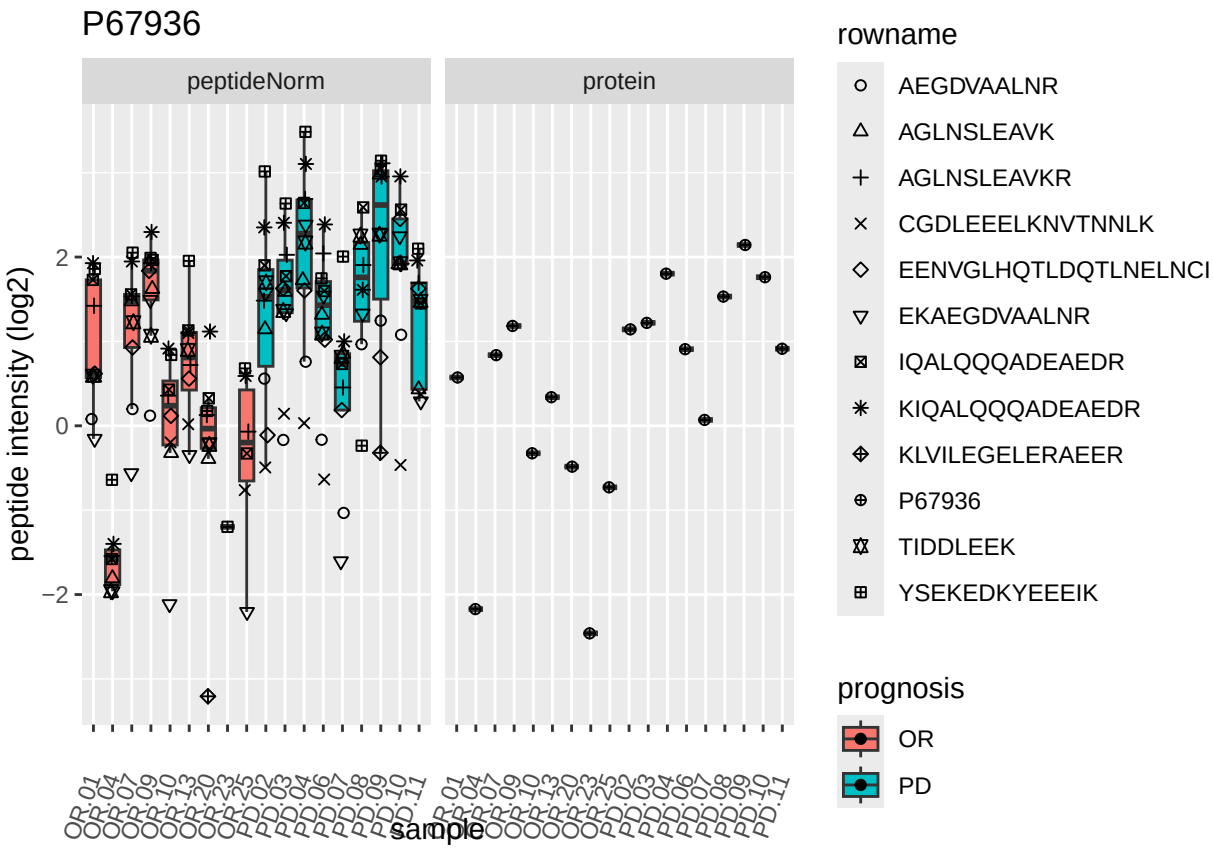
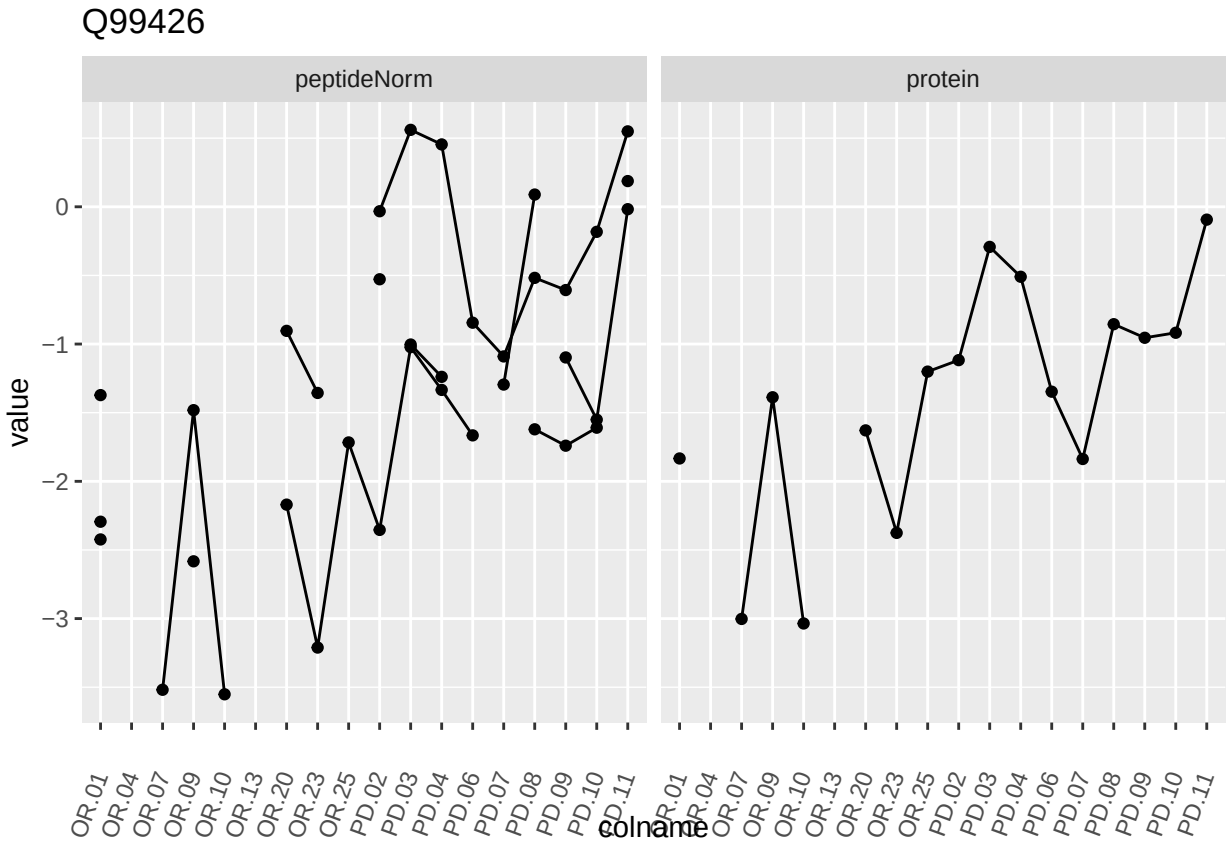
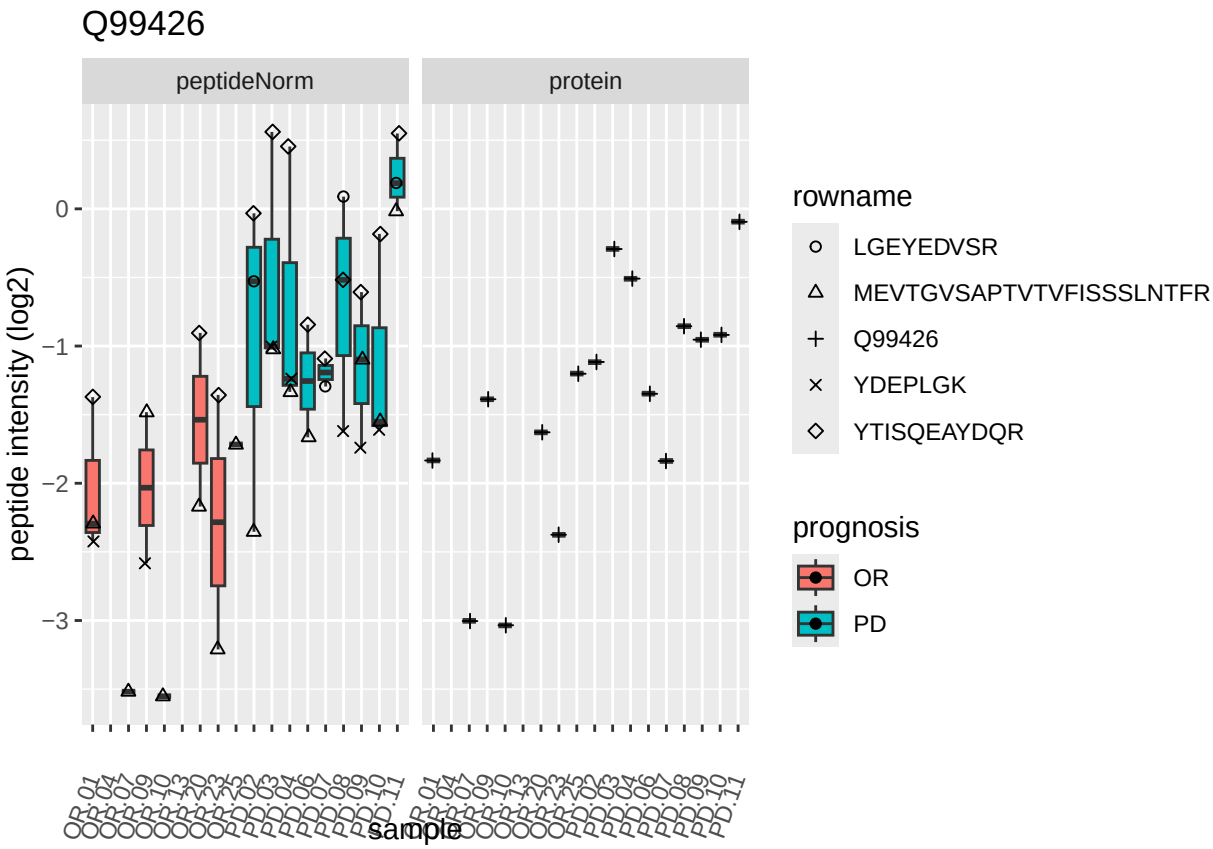
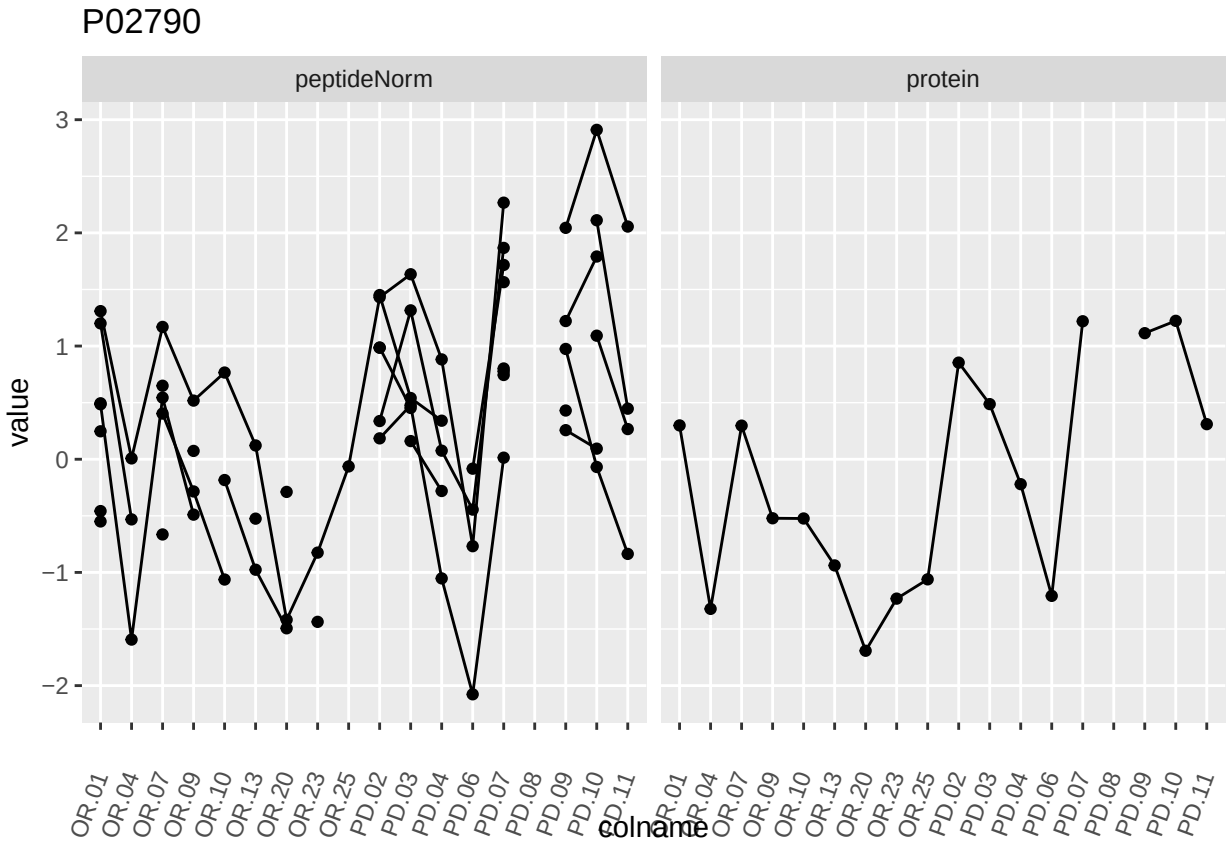
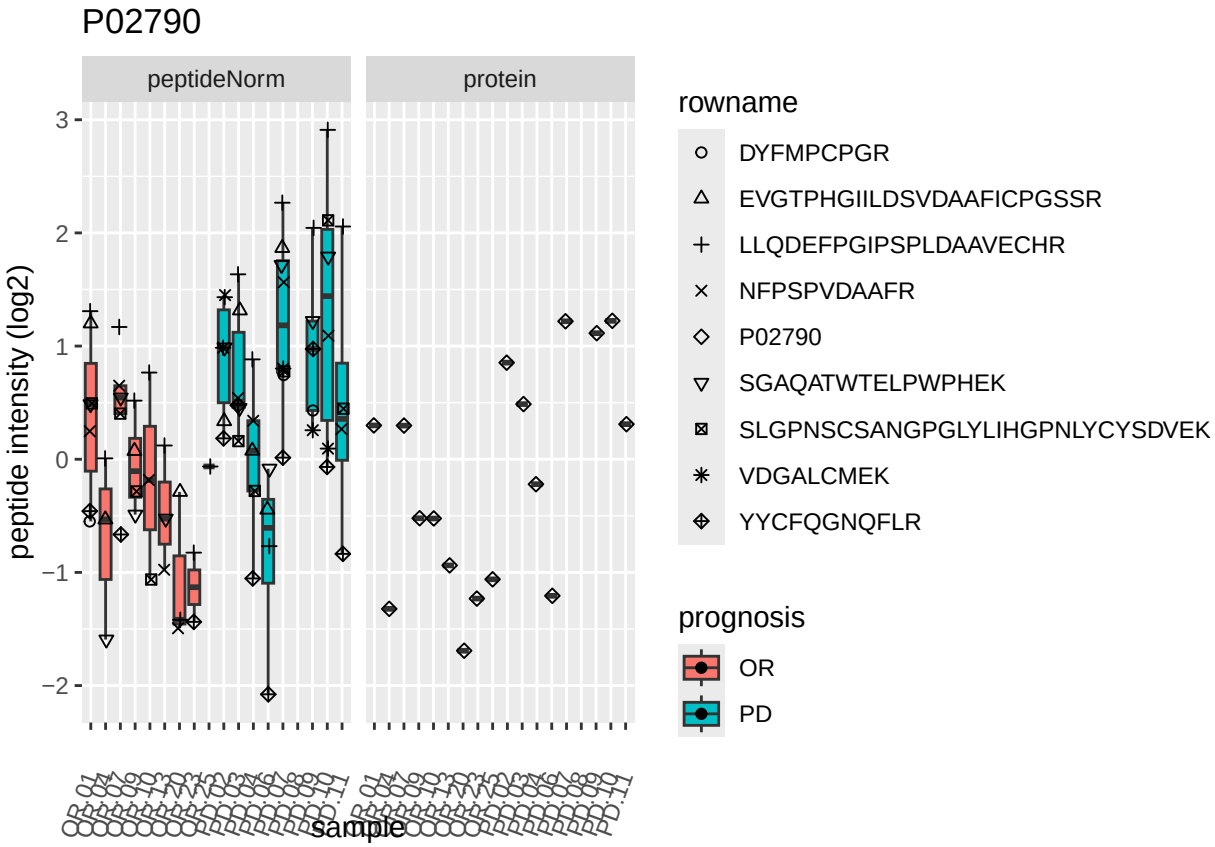
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

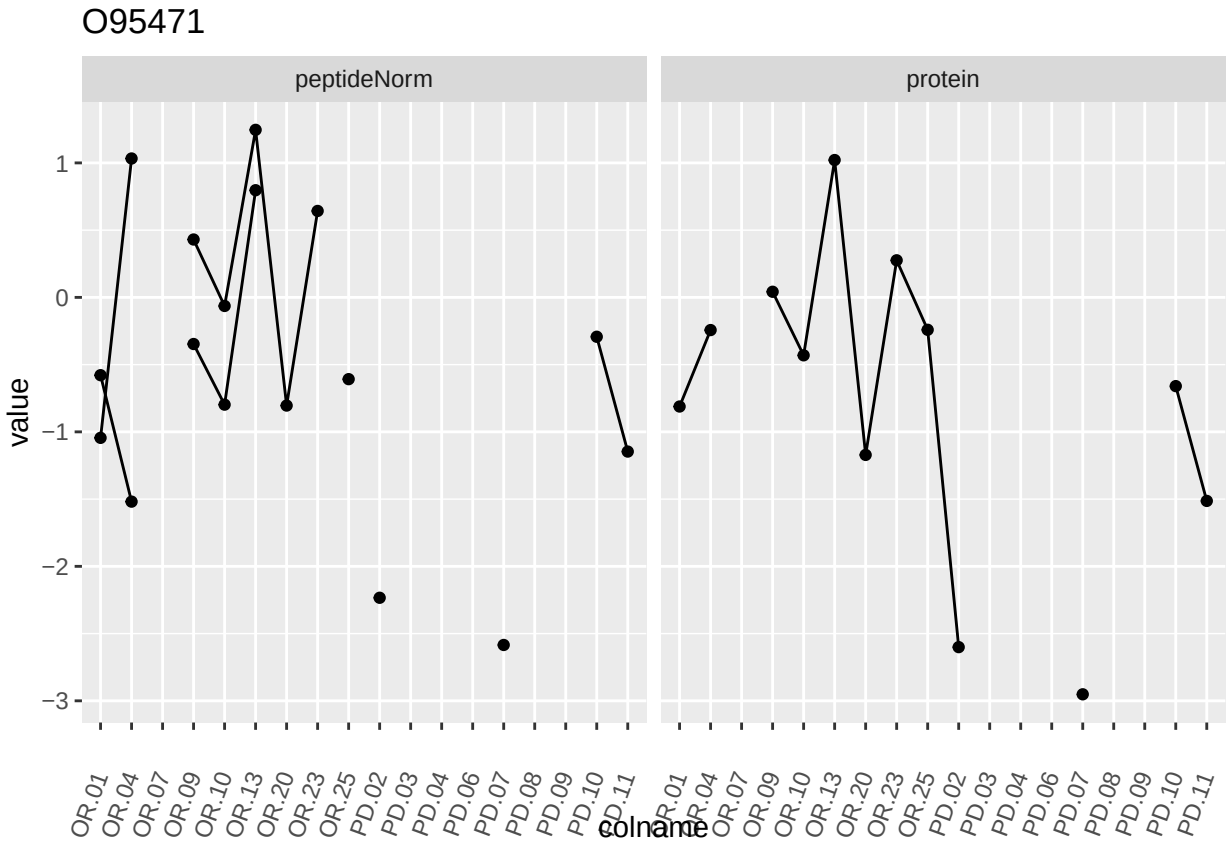

P67936
peptideNorm
protein
peptide intensity (log2)
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AEGDVAALNR
AGLNSLEAVK
AGLNSLEAVKR
CGDLEEELKNVTNNLK
EENVGLHQTLDQTLNELNCI
EKAEGDVAALNR
IQALQQQADEAEDR
KIQALQQQADEAEDR
KLVILEGELERAEER
P67936
TIDDLEEK
YSEKEDKYEEEIK
prognosis
OR
PD

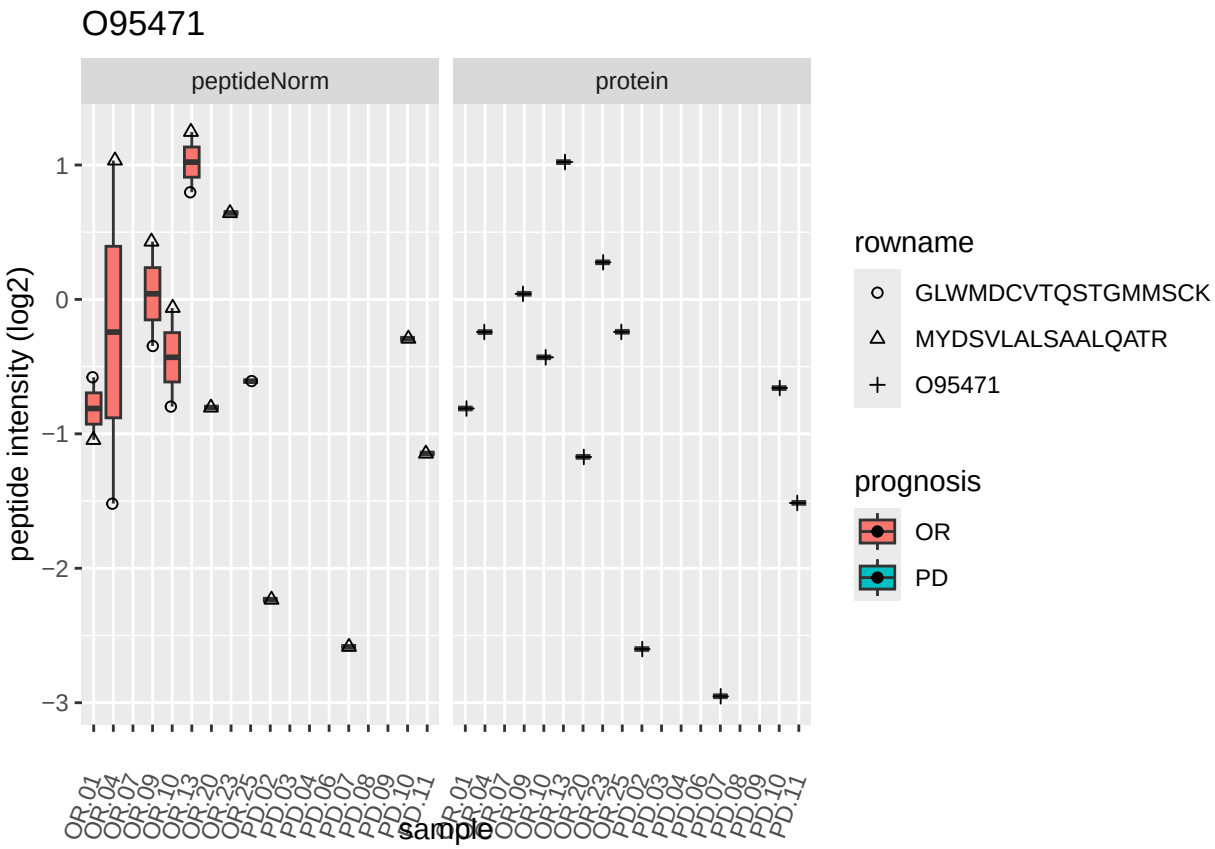

Q99426
peptideNorm
protein
value
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

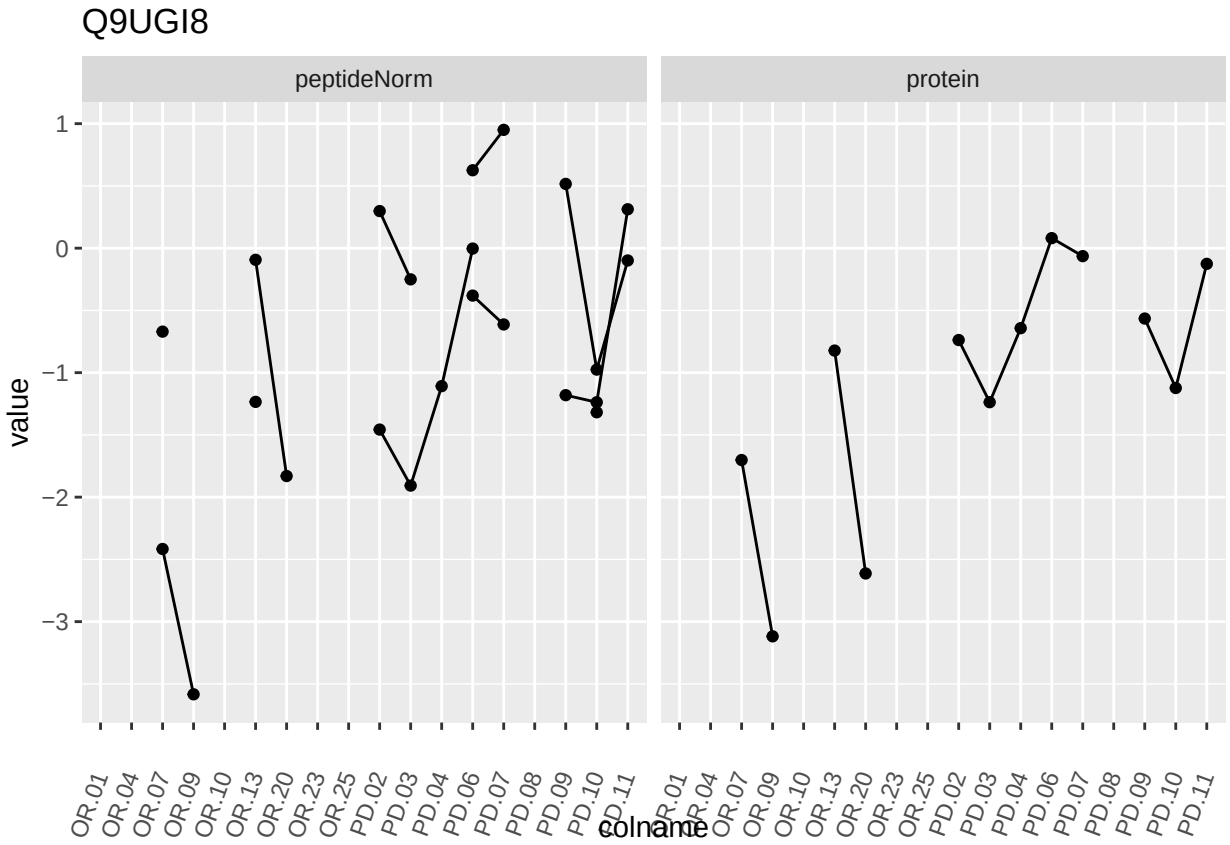

Q99426
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LGEYEDVSR
MEVTGVSAPTVTVFISSSLNTFR
Q99426
YDEPLGK
YTISQEAYDQR
prognosis
OR
PD

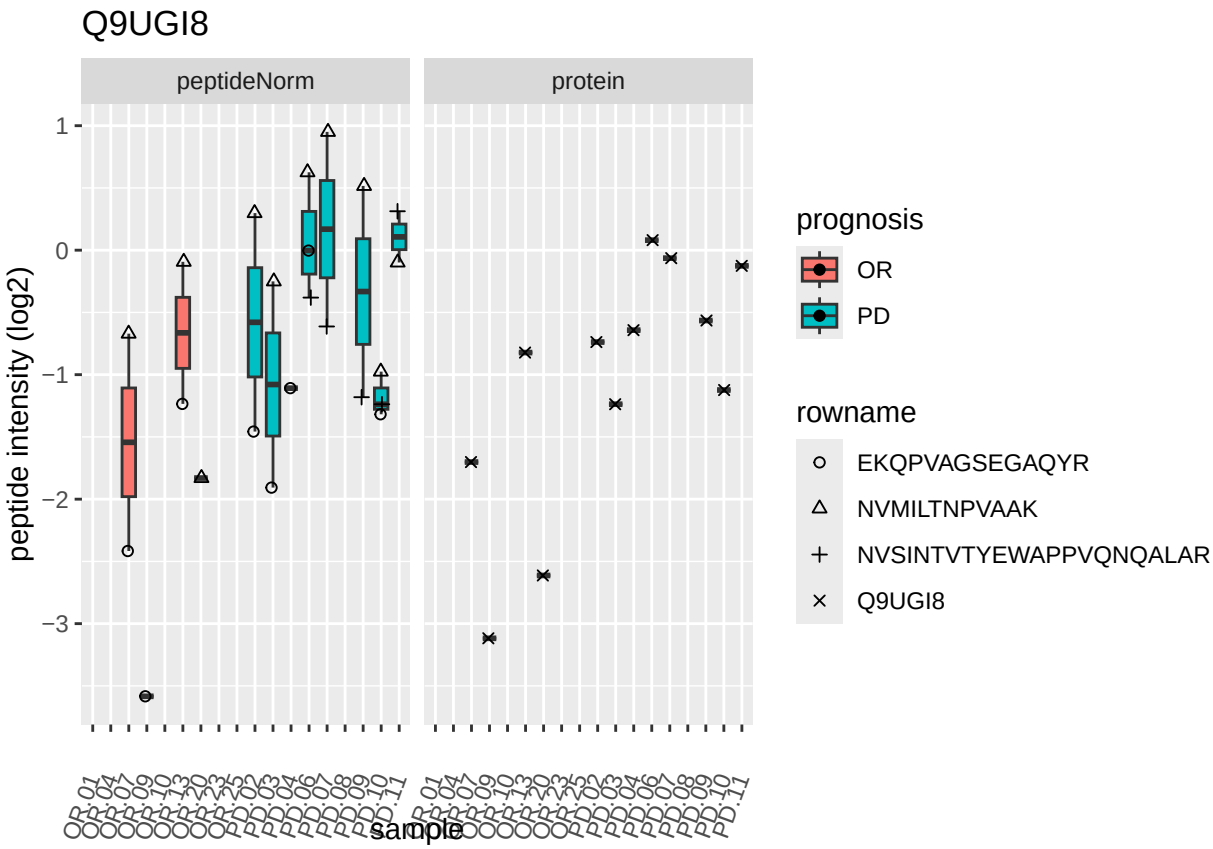

P02790
peptideNorm
protein
value
3
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

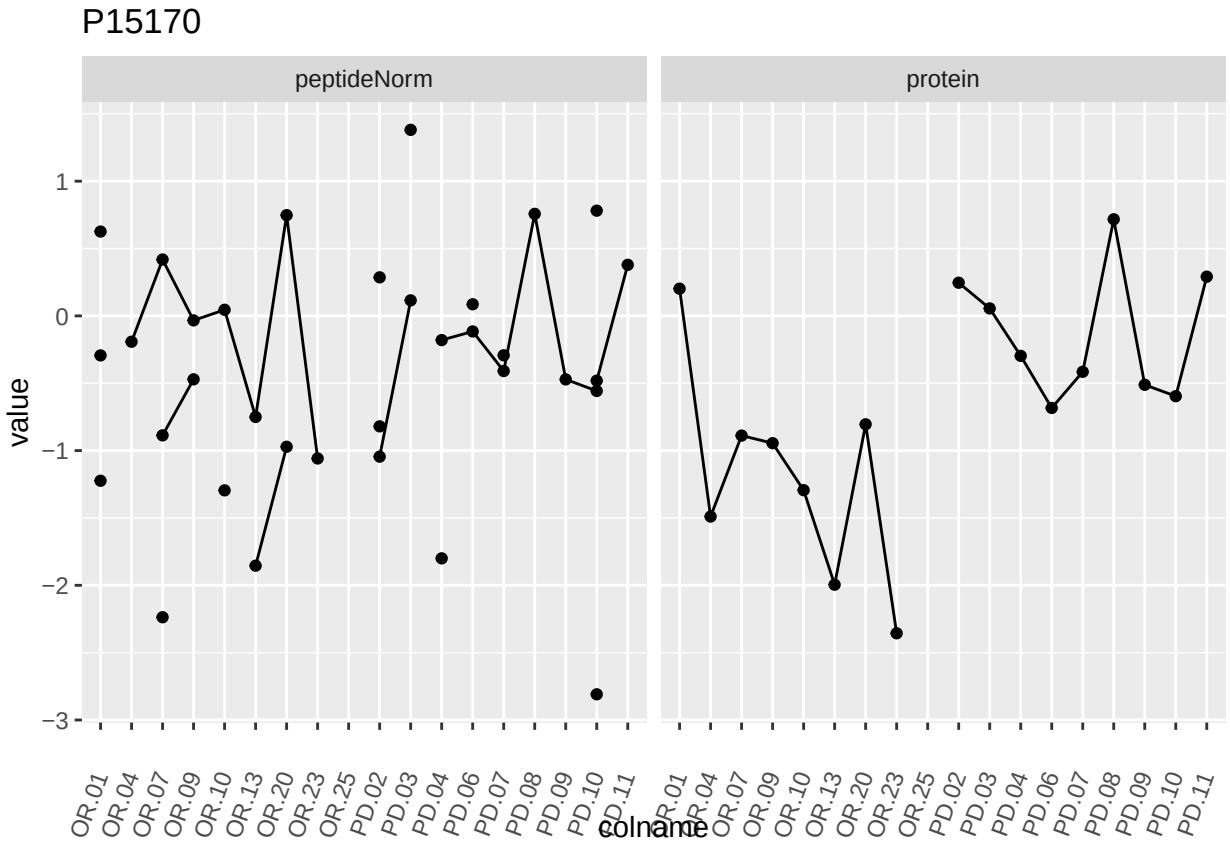

P02790
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
sample
rowname
DYFMPCPGR
EVGTPHGIILDSVDAAFICPGSSR
LLQDEFPGIPSPLDAAVECHR
NFPSPVDAAFR
P02790
SGAQATWTELPWPHEK
SLGPNSCSANGPGLYLIHGPNLYCYSDVEK
VDGALCMEK
YYCFQGNQFLR
prognosis
OR
PD

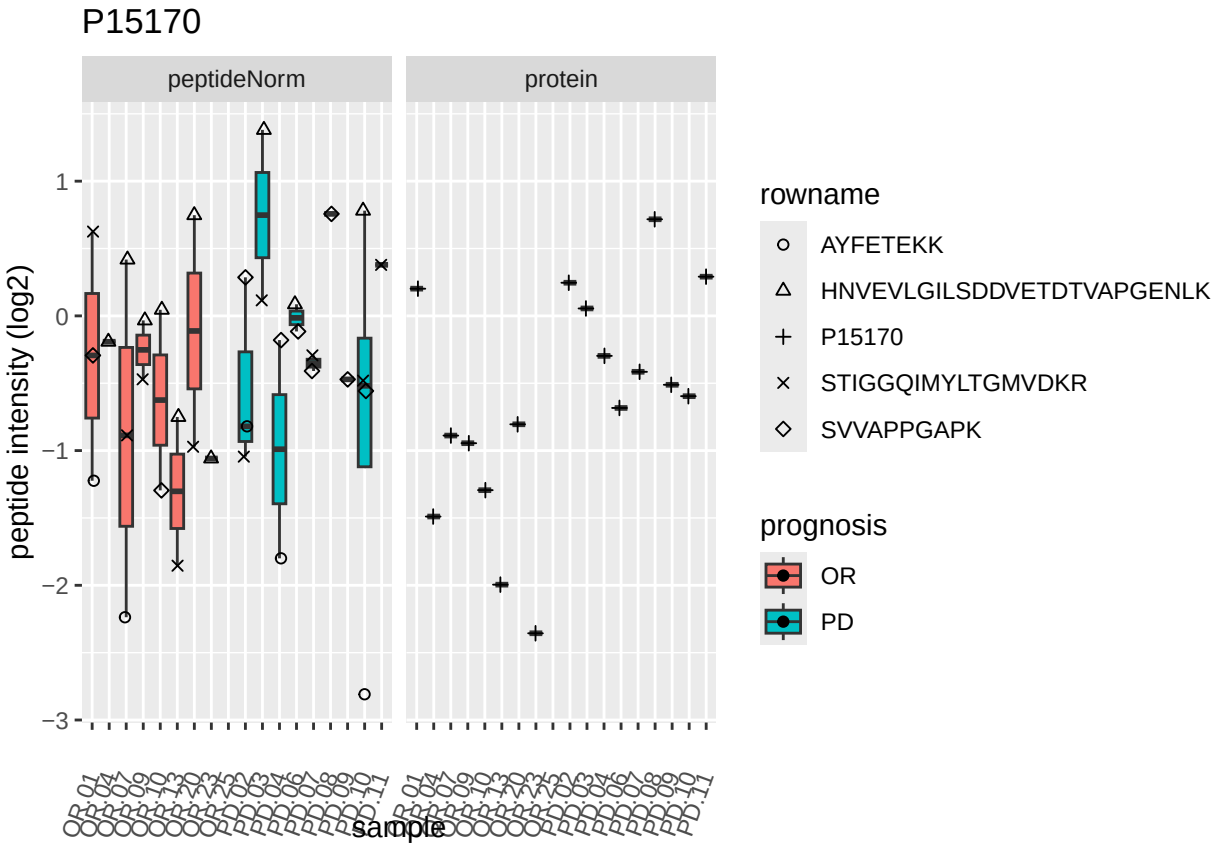

O95471
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

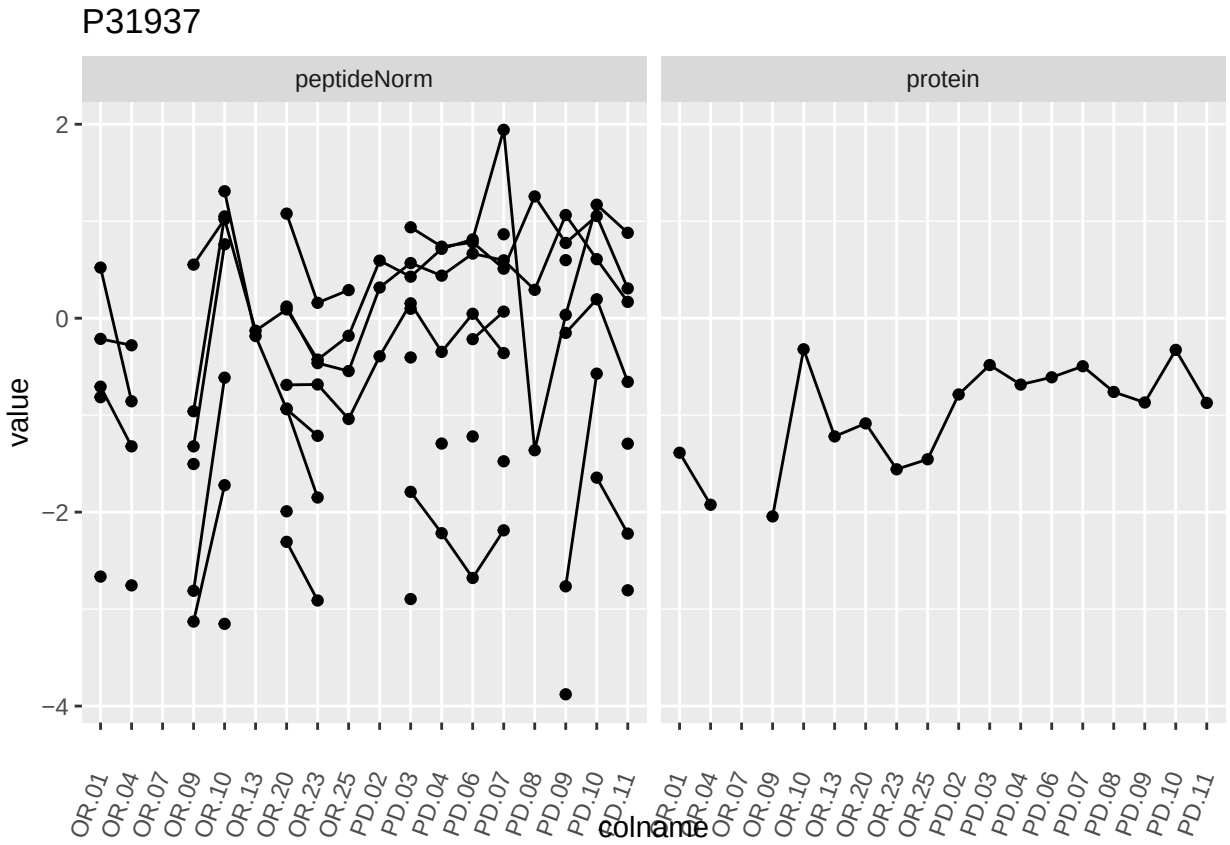

O95471
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
GLWMDCVTQSTGMMSCK
MYDSVLALSAALQATR
O95471
prognosis
OR
PD

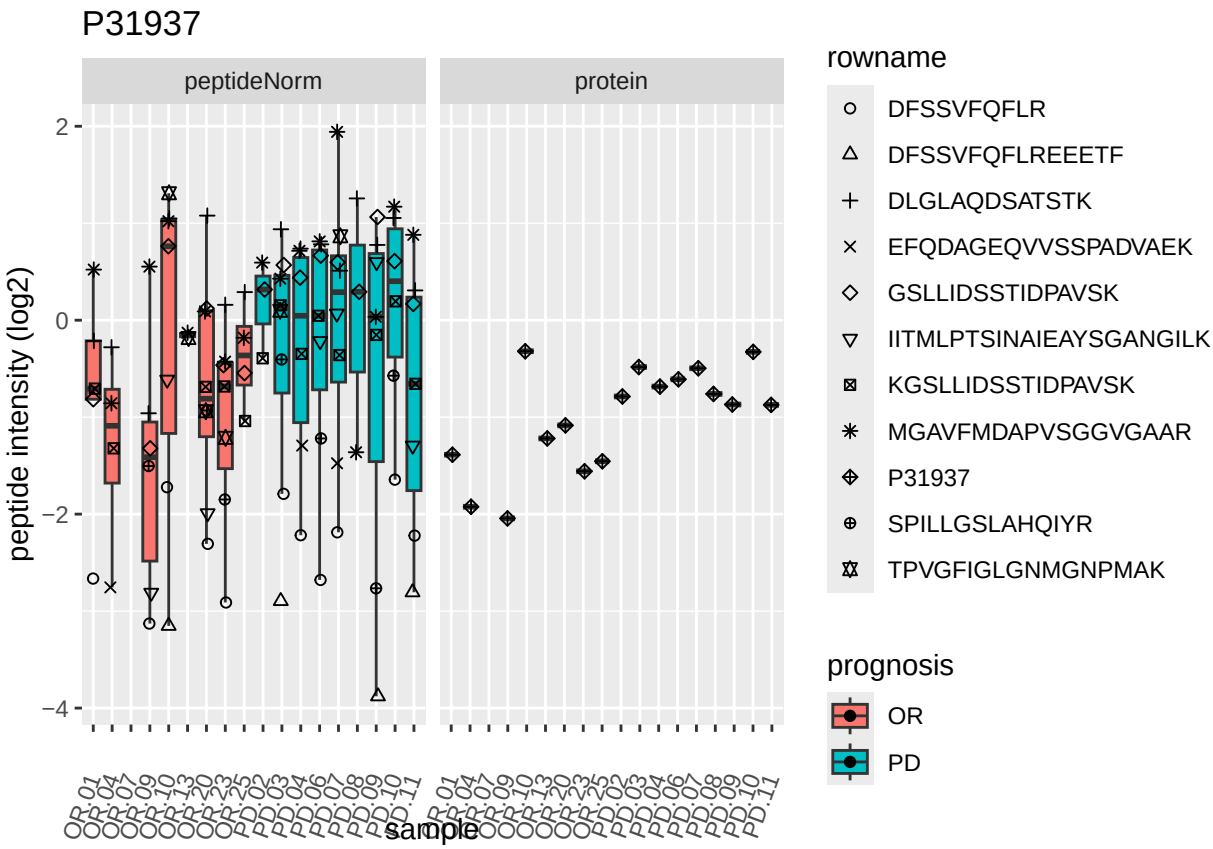

Q9UGI8
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

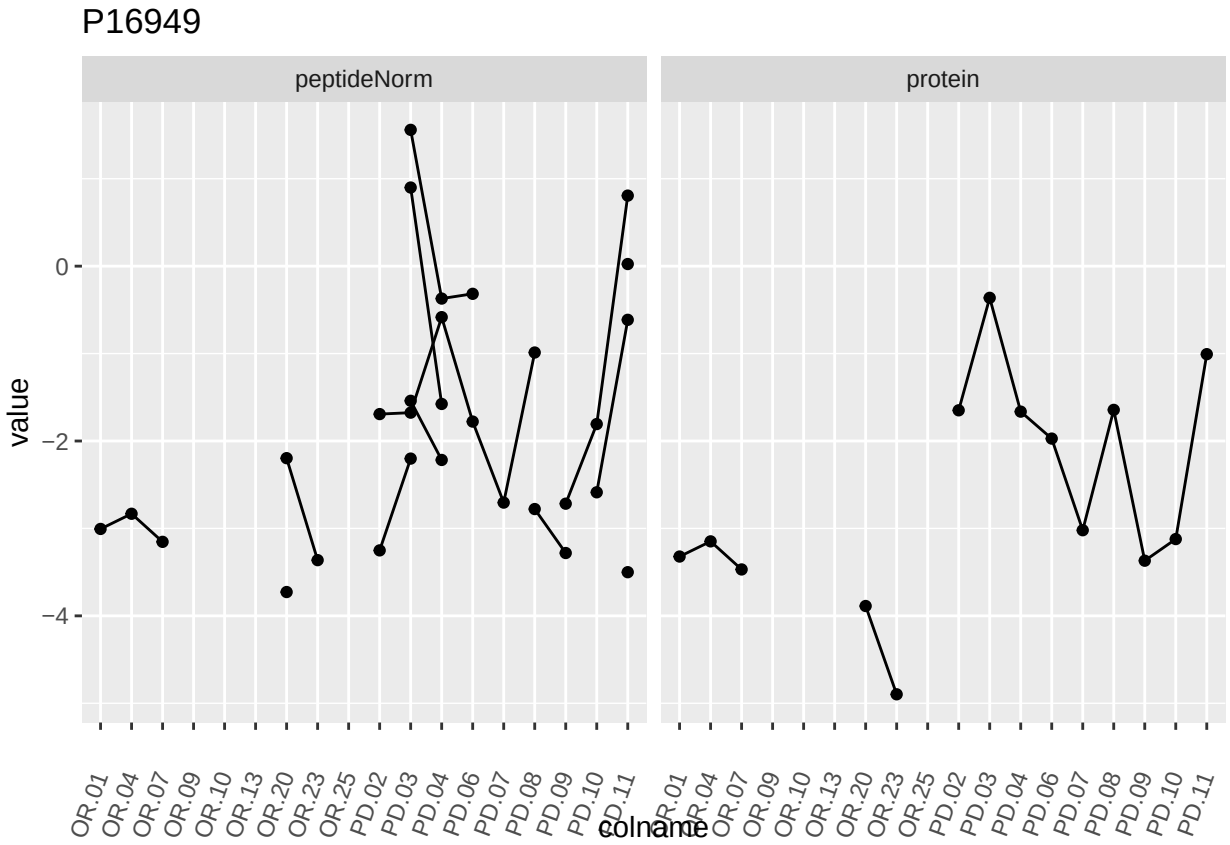

Q9UGI8
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
EKQPVAGSEGAQYR
NVMILTNPVAAK
NVSINTVTYEWAPPVQNQALAR
Q9UGI8

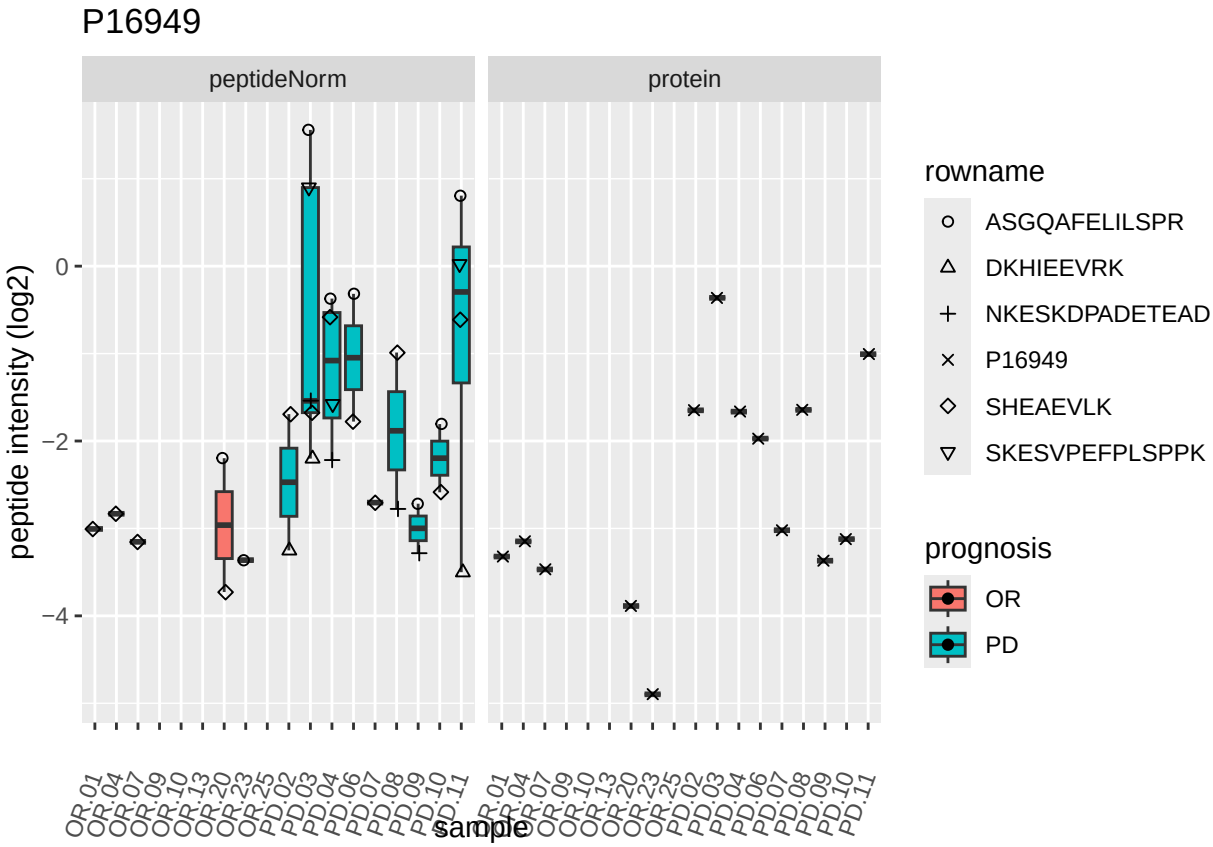

P15170
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

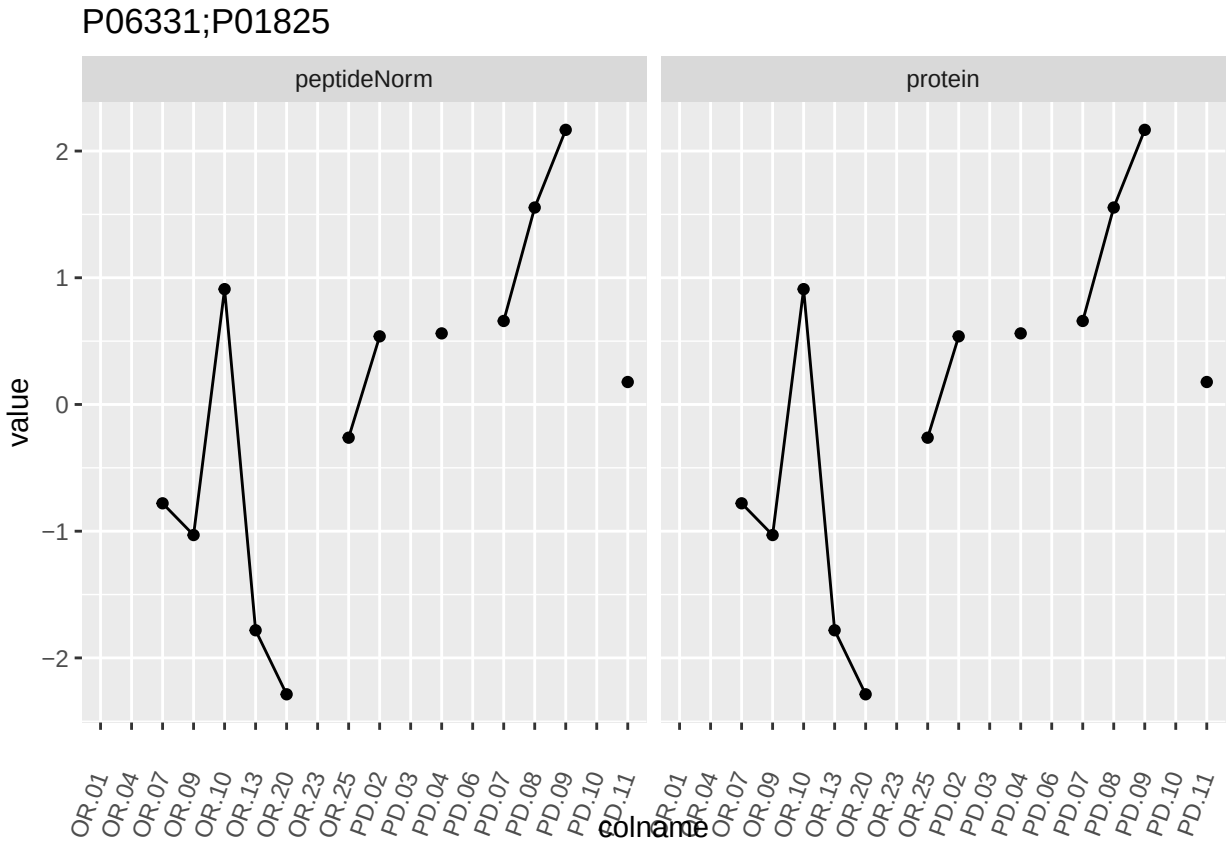

P15170
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR:01
OR:04
OR:07
OR:09
OR:10
OR:13
OR:20
OR:23
OR:25
PD:03
PD:04
PD:06
PD:07
PD:08
PD:09
PD:10
PD:11
sample
rowname
AYFETEKK
HNVEVLGILSDDVETDTVAPGENLK
P15170
STIGGQIMYLTGMVDKR
SVVAPPGAPK
prognosis
OR
PD

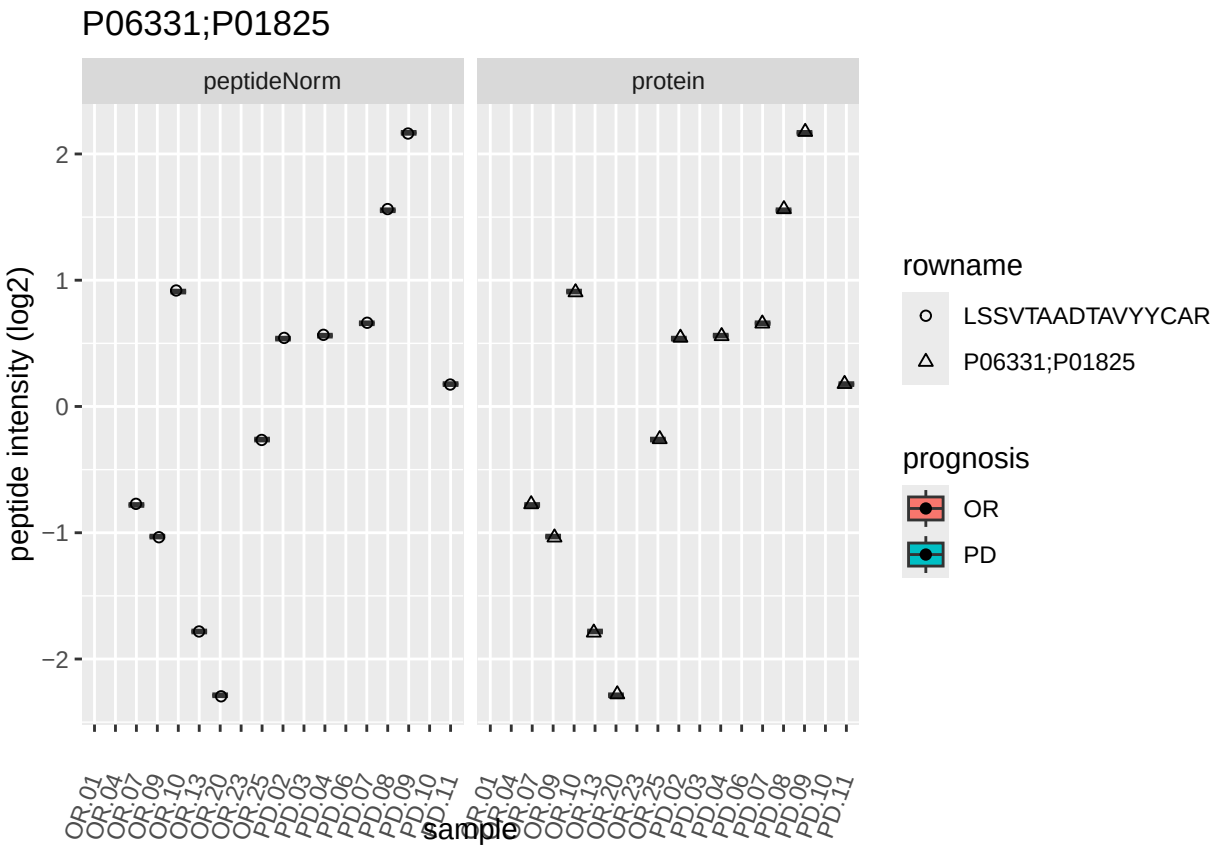

P31937
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

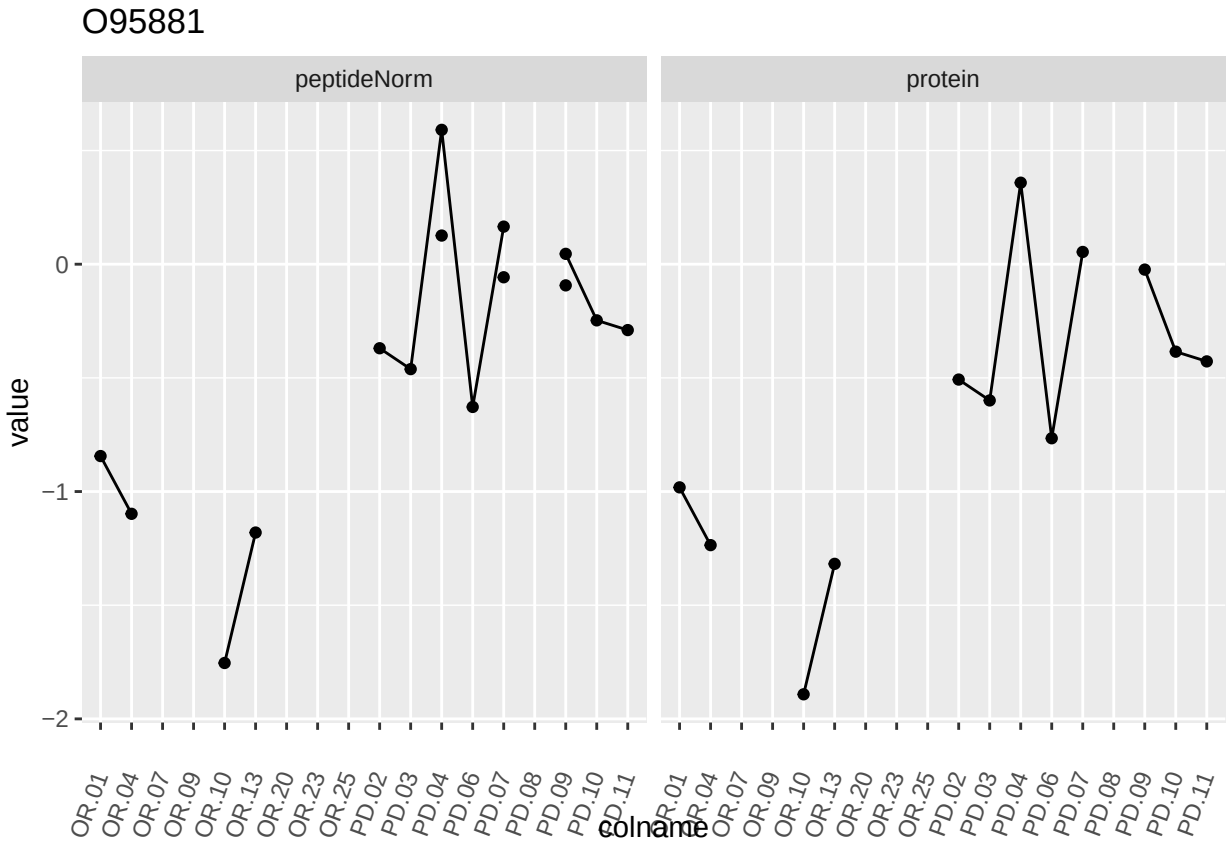

P31937
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
DFSSVFQFLR
DFSSVFQFLREEETF
DLGLAQDSATSTK
EFQDAGEQVVSSPADVAEK
GSLLIDSSTIDPAVSK
IITMLPTSINAIEAYSGANGILK
KGSLLIDSSTIDPAVSK
MGAVFMDAPVSGGVGAAR
P31937
SPILLGSLAHQIYR
TPVGFIGLGNMGNPMAK
prognosis
OR
PD

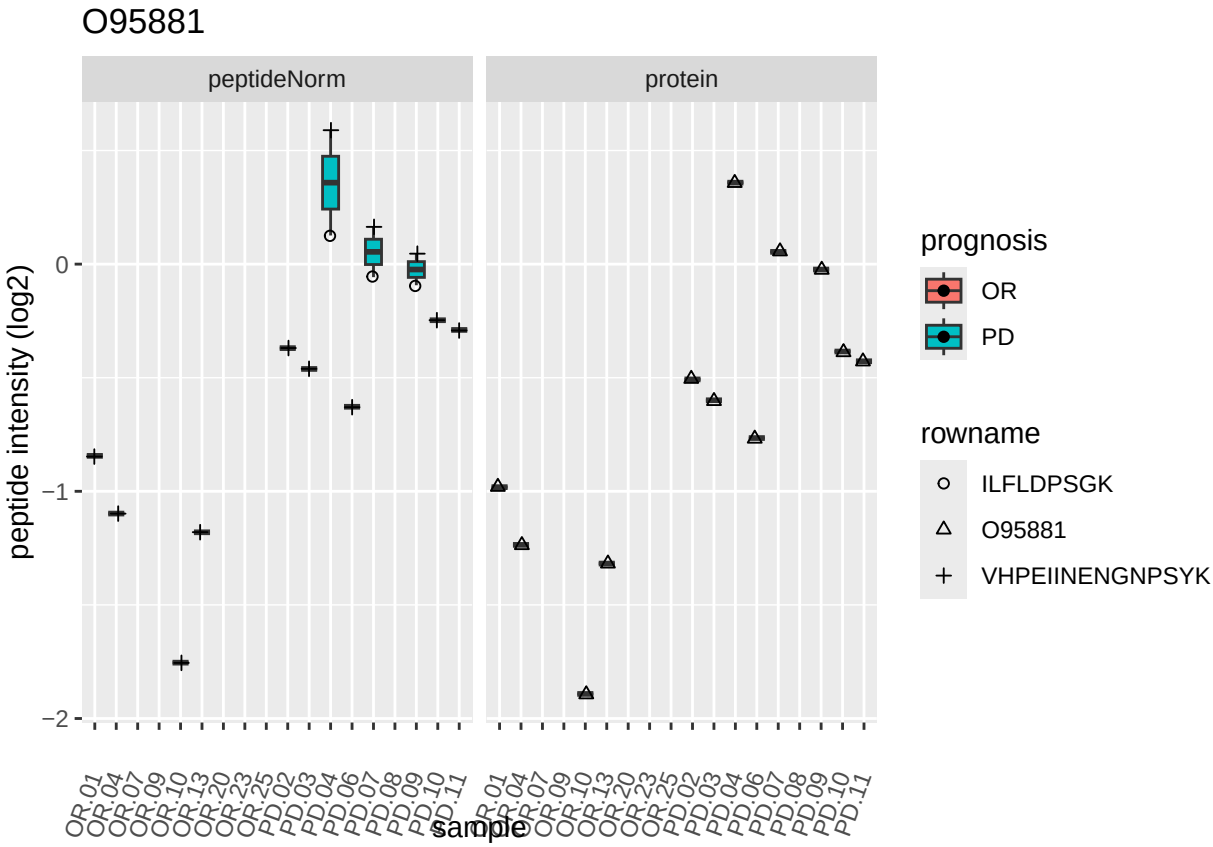

P16949
peptideNorm
protein
value
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

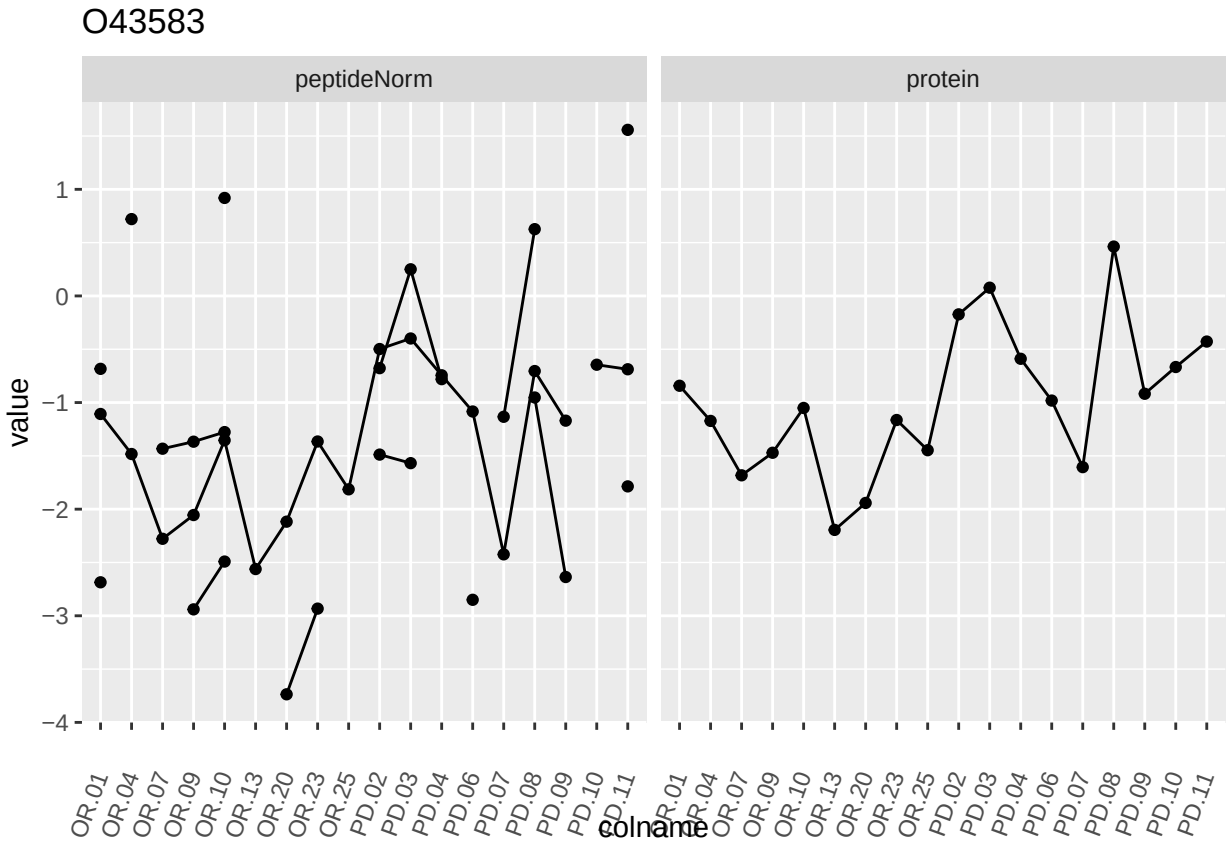

P16949
peptideNorm
protein
peptide intensity (log2)
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ASGQAFELILSPR
DKHIEEVRK
NKESKDPADETEAD
P16949
SHEAEVLK
SKESVPEFPLSPPK
prognosis
OR
PD


P06331;P01825
peptideNorm
protein
value
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P06331;P01825
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LSSVTAADTAVYYCAR
P06331;P01825
prognosis
OR
PD


O95881
peptideNorm
protein
value
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O95881
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
ILFLDPSGK
O95881
VHPEIINENGNPSYK


O43583
peptideNorm
protein
value
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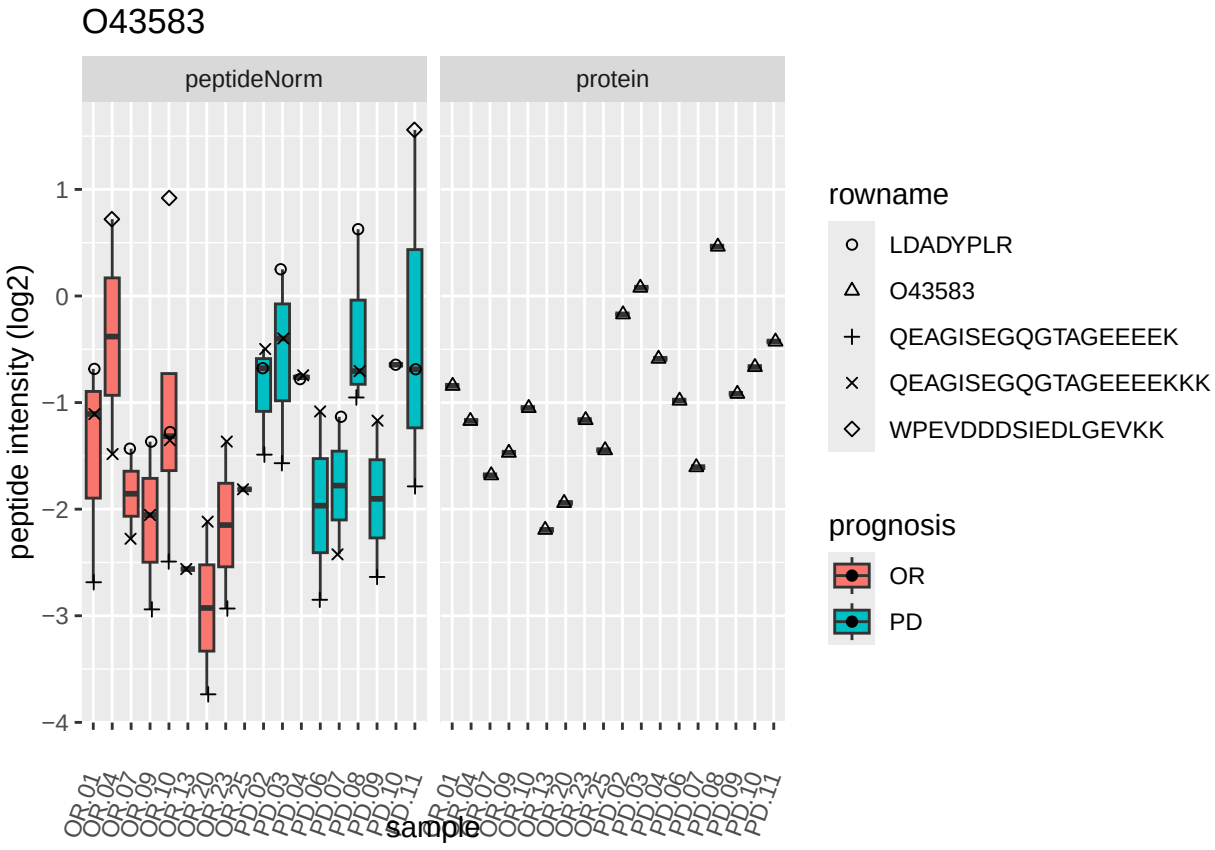
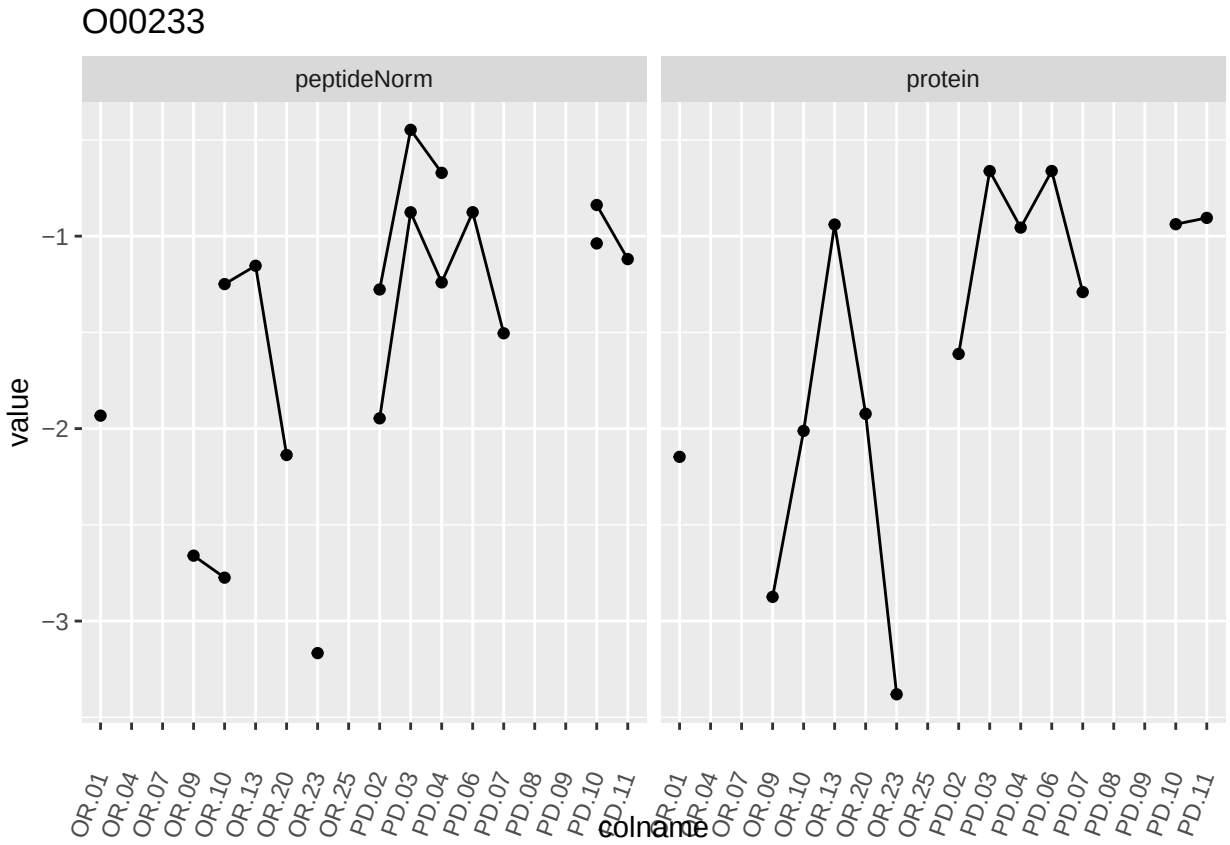
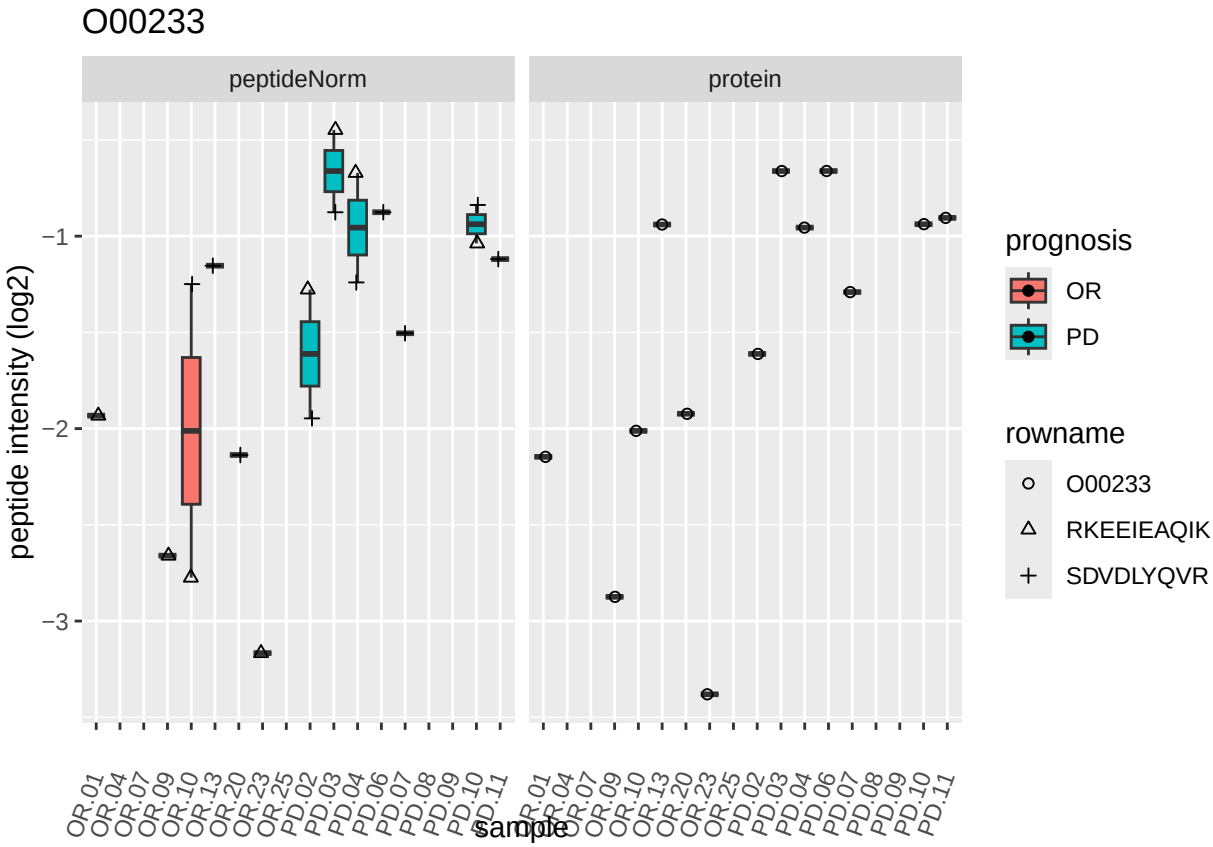
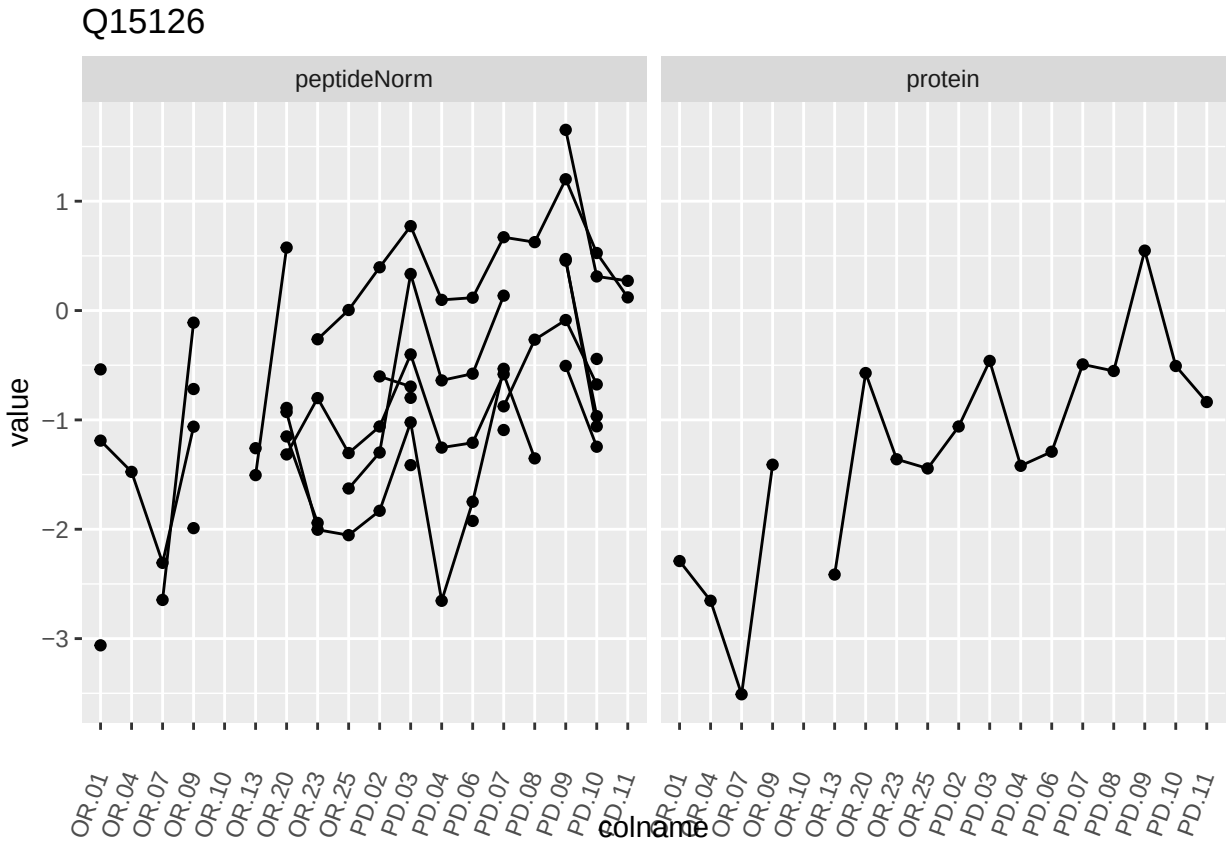
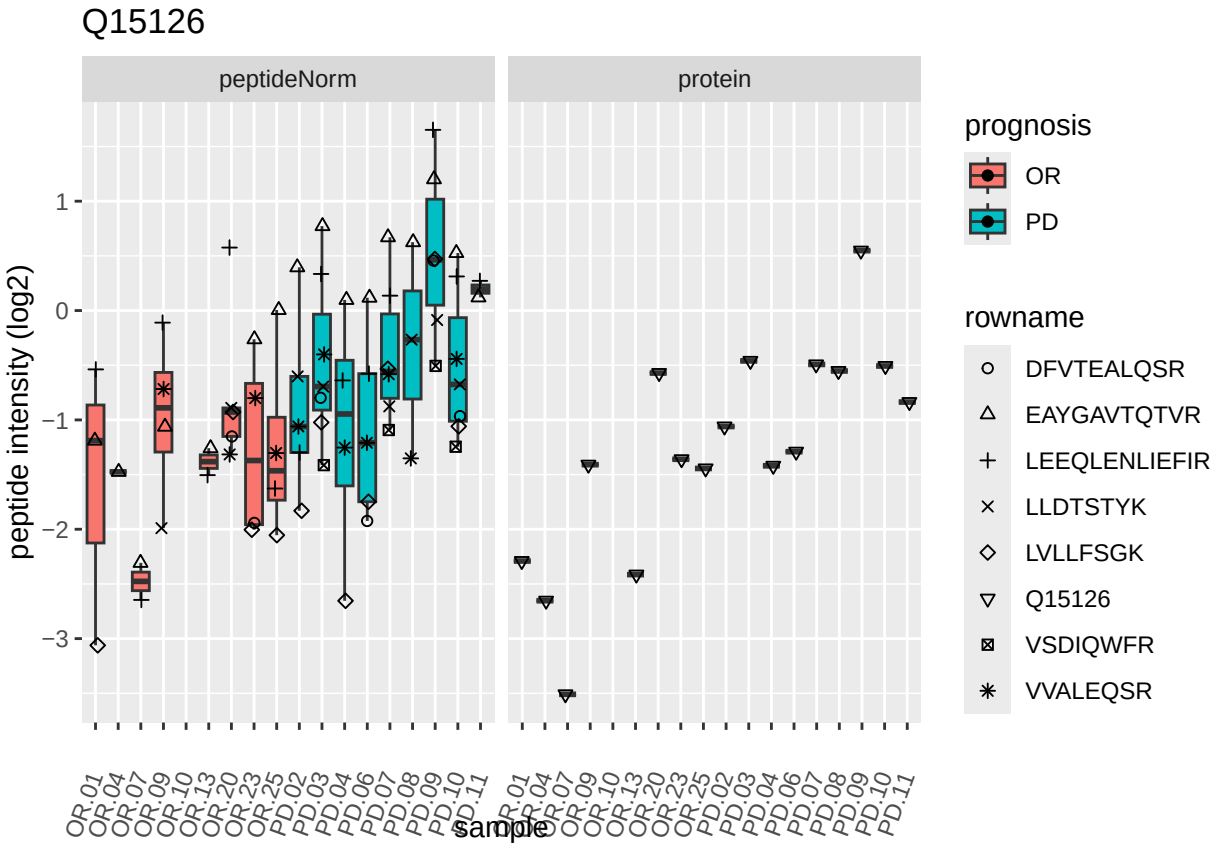
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O43583
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LDADYPLR
O43583
QEAGISEGQGTAGEEEEK
QEAGISEGQGTAGEEEEKKK
WPEVDDDSIEDLGEVKK
prognosis
OR
PD


O00233
peptideNorm
protein
value
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O00233
peptideNorm
protein
peptide intensity (log2)
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
O00233
RKEEIEAQIK
SDVDLYQVR


Q15126
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname



5 Session Info

With respect to reproducibility, it is highly recommended to include a session info in your script so that readers of your output can see your particular setup of R.

```
sessionInfo()
```

```
## R version 4.4.0 RC (2024-04-16 r86468)
## Platform: aarch64-apple-darwin20
## Running under: macOS Big Sur 11.6
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;  LAPACK v
##
## locale:
## [1] C/UTF-8/C/C/C/C
##
## time zone: Europe/Brussels
## tzcode source: internal
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
```

```
##  [1] ExploreModelMatrix_1.16.0   plotly_4.10.4
##  [3] msqrob2_1.12.0              QFeatures_1.14.2
##  [5] MultiAssayExperiment_1.30.3 SummarizedExperiment_1.34.0
##  [7] Biobase_2.64.0              GenomicRanges_1.56.1
##  [9] GenomeInfoDb_1.40.1         IRanges_2.38.1
## [11] S4Vectors_0.42.1            BiocGenerics_0.50.0
## [13] MatrixGenerics_1.16.0       matrixStats_1.4.1
## [15] limma_3.60.6                lubridate_1.9.3
## [17] forcats_1.0.0               stringr_1.5.1
## [19] dplyr_1.1.4                 purrr_1.0.2
## [21] readr_2.1.5                 tidyr_1.3.1
## [23] tibble_3.2.1                ggplot2_3.5.1
## [25] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] rlang_1.1.4             magrittr_2.0.3          shinydashboard_0.7.2
##  [4] clue_0.3-65             compiler_4.4.0          vctrs_0.6.5
##  [7] reshape2_1.4.4          ProtGenerics_1.36.0     pkgconfig_2.0.3
## [10] crayon_1.5.3            fastmap_1.2.0           XVector_0.44.0
## [13] fontawesome_0.5.2       labeling_0.4.3          utf8_1.2.4
## [16] promises_1.3.0          rmarkdown_2.28          tzdb_0.4.0
## [19] UCSC.utils_1.0.0        nloptr_2.1.1            xfun_0.47
## [22] zlibbioc_1.50.0         cachem_1.1.0            jsonlite_1.8.9
## [25] later_1.3.2             highr_0.11              DelayedArray_0.30.1
## [28] BiocParallel_1.38.0     parallel_4.4.0          cluster_2.1.6
## [31] R6_2.5.1                bslib_0.8.0             stringi_1.8.4
## [34] boot_1.3-31             jquerylib_0.1.4         Rcpp_1.0.13
## [37] knitr_1.48              BiocBaseUtils_1.6.0     httpuv_1.6.15
## [40] Matrix_1.7-0            splines_4.4.0           igraph_2.0.3
## [43] timechange_0.3.0        tidyselect_1.2.1        abind_1.4-8
## [46] yaml_2.3.10             codetools_0.2-20        lattice_0.22-6
## [49] plyr_1.8.9              shiny_1.9.1             withr_3.0.1
## [52] evaluate_1.0.0          pillar_1.9.0            DT_0.33
## [55] shinyjs_2.1.0           generics_0.1.3          hms_1.1.3
## [58] munsell_0.5.1           scales_1.3.0            minqa_1.2.8
## [61] xtable_1.8-4            glue_1.8.0              lazyeval_0.2.2
## [64] tools_4.4.0             data.table_1.16.0       lme4_1.1-35.5
## [67] cowplot_1.1.3           grid_4.4.0              MsCoreUtils_1.16.1
## [70] colorspace_2.1-1        nlme_3.1-166            GenomeInfoDbData_1.2.12
## [73] cli_3.6.3               fansi_1.0.6             S4Arrays_1.4.1
## [76] viridisLite_0.4.2       AnnotationFilter_1.28.0 gtable_0.3.5
## [79] rintrojs_0.3.4          sass_0.4.9              digest_0.6.37
## [82] SparseArray_1.4.8       htmlwidgets_1.6.4       farver_2.1.2
## [85] htmltools_0.5.8.1       lifecycle_1.0.4         httr_1.4.7
## [88] mime_0.12               statmod_1.5.0           MASS_7.3-61
```