# Cancer

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## 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(
  table = peptidesFile,
  fnames = 1,
  ecol = ecols,
  name = "peptideRaw", sep="\t")
```

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))
```

2. Remove reverse sequences (decoys) and contaminants

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

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

3. Drop peptides that were only identified in one sample

We keep peptides that were observed at last twice.

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

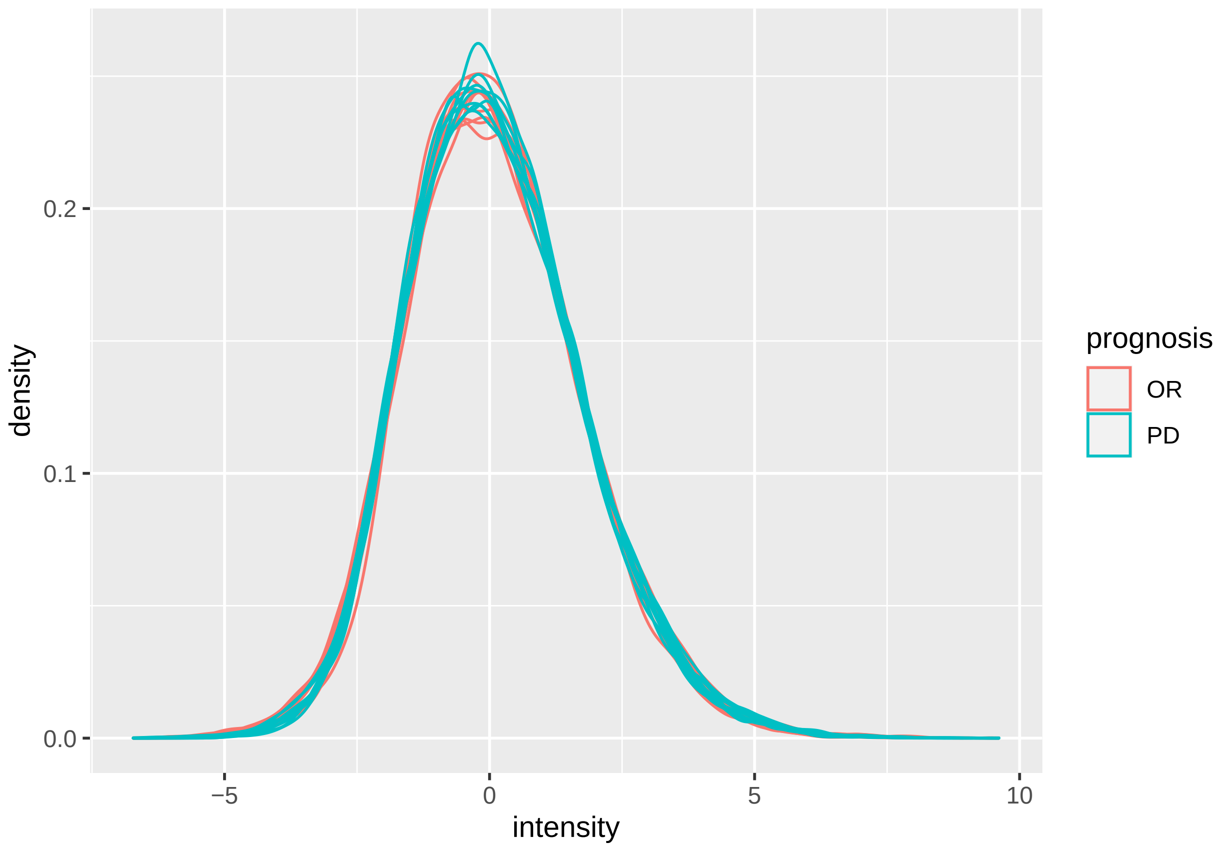
```
pe <- normalize(pe,
                i = "peptideLog",
                name = "peptideNorm",
                method = "center.median")
```

## 3.4 Explore normalized data

Upon the normalisation the density curves are nicely registered

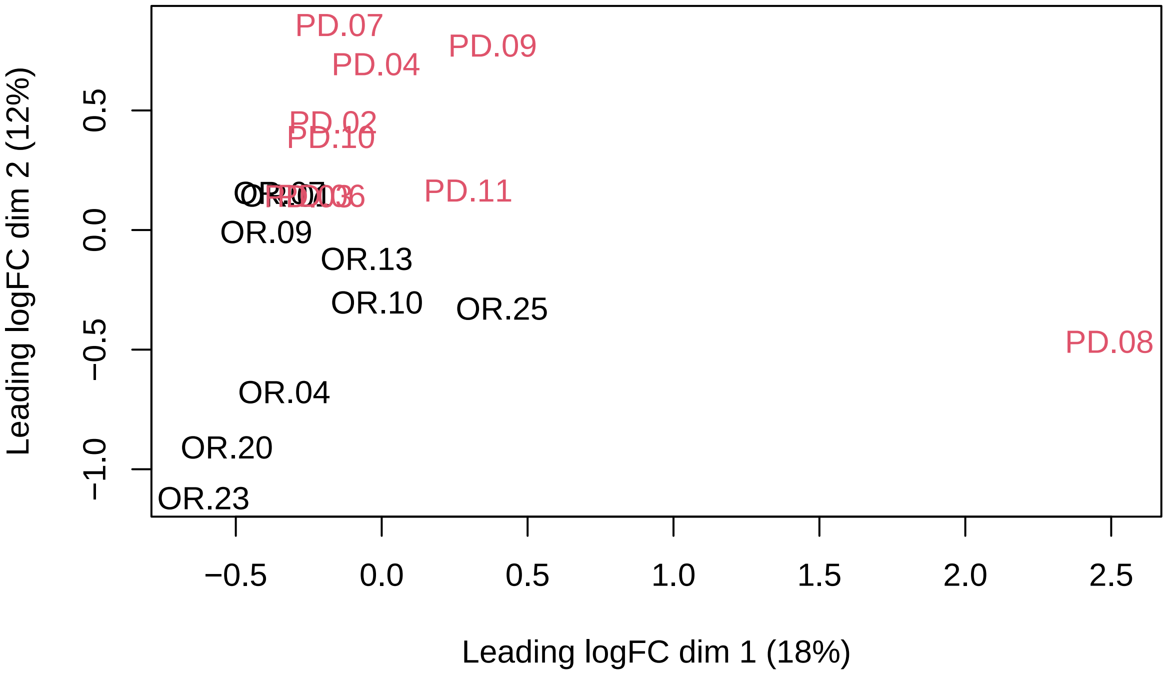
```
pe[["peptideNorm"]] %>%
  assay %>%
  as.data.frame() %>%
  gather(sample, intensity) %>%
  mutate(prognosis = colData(pe)[sample,"prognosis"]) %>%
  ggplot(aes(x = intensity,group = sample,color = prognosis)) +
    geom_density()
```

```
## Warning: Removed 188395 rows containing non-finite values (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.

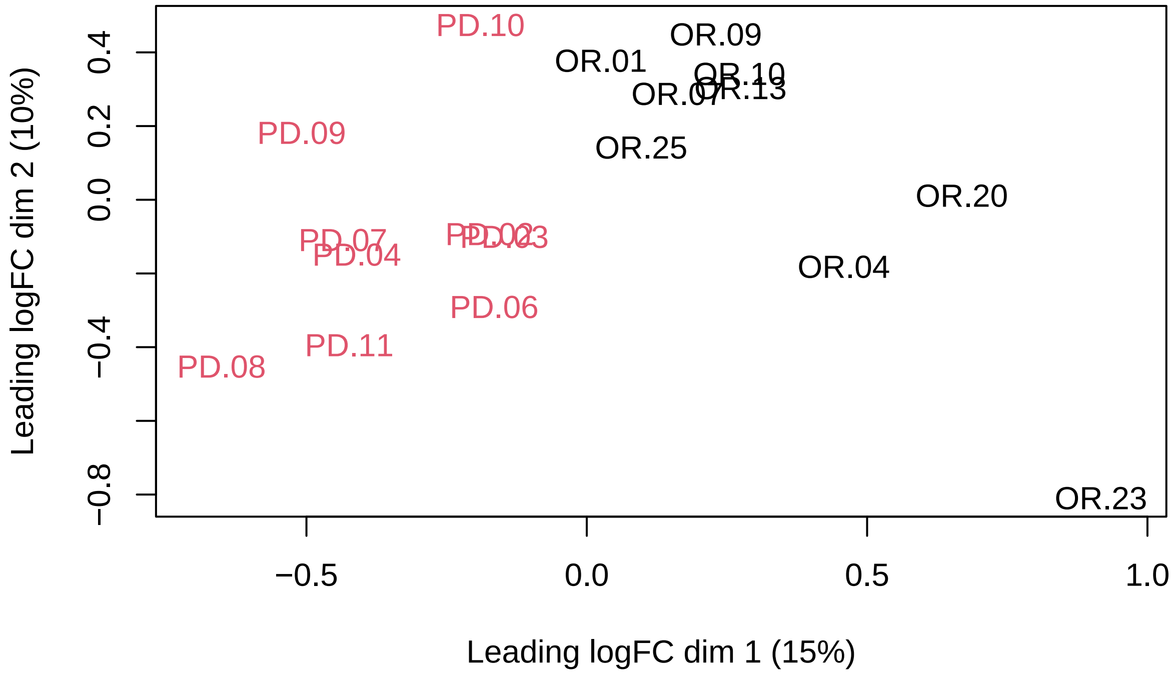
### 3.5 Summarization to protein level

- 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.

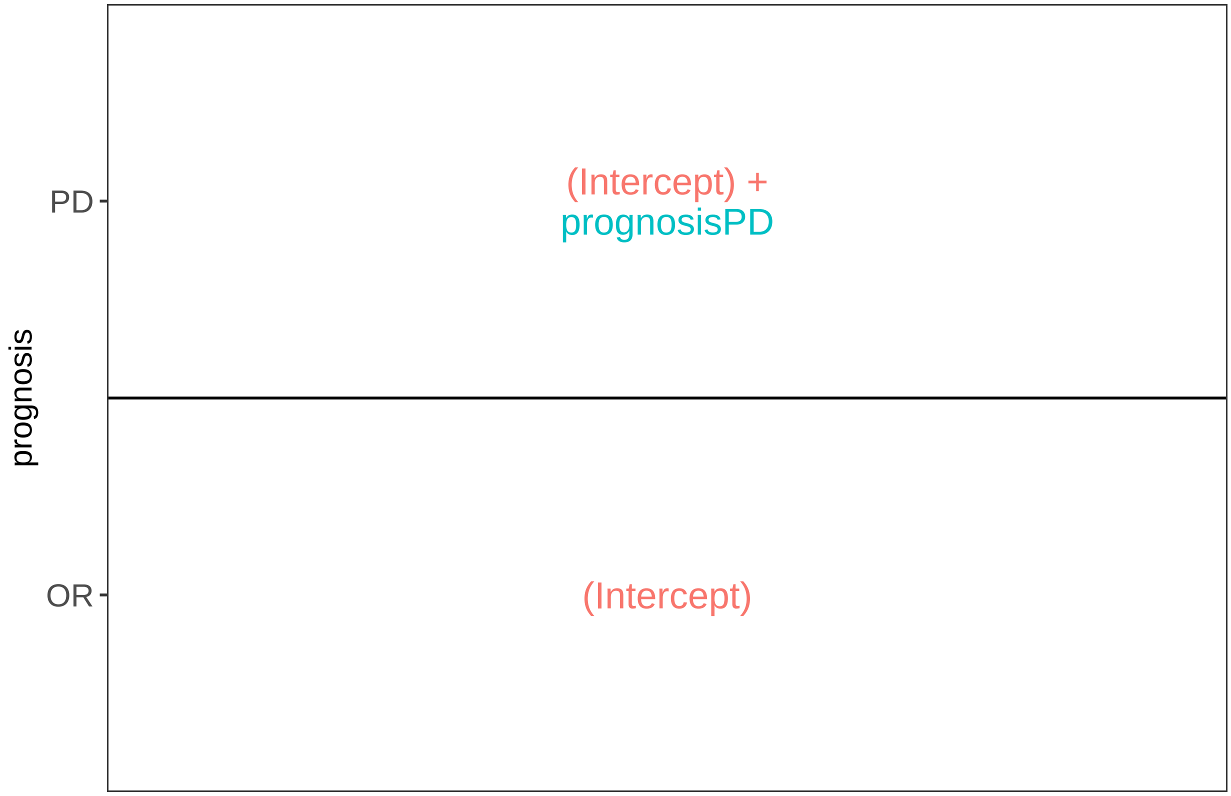
```
getCoef(rowData(pe[["protein"]])$msqrobModels[[1]])
```

```
## (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]]
```



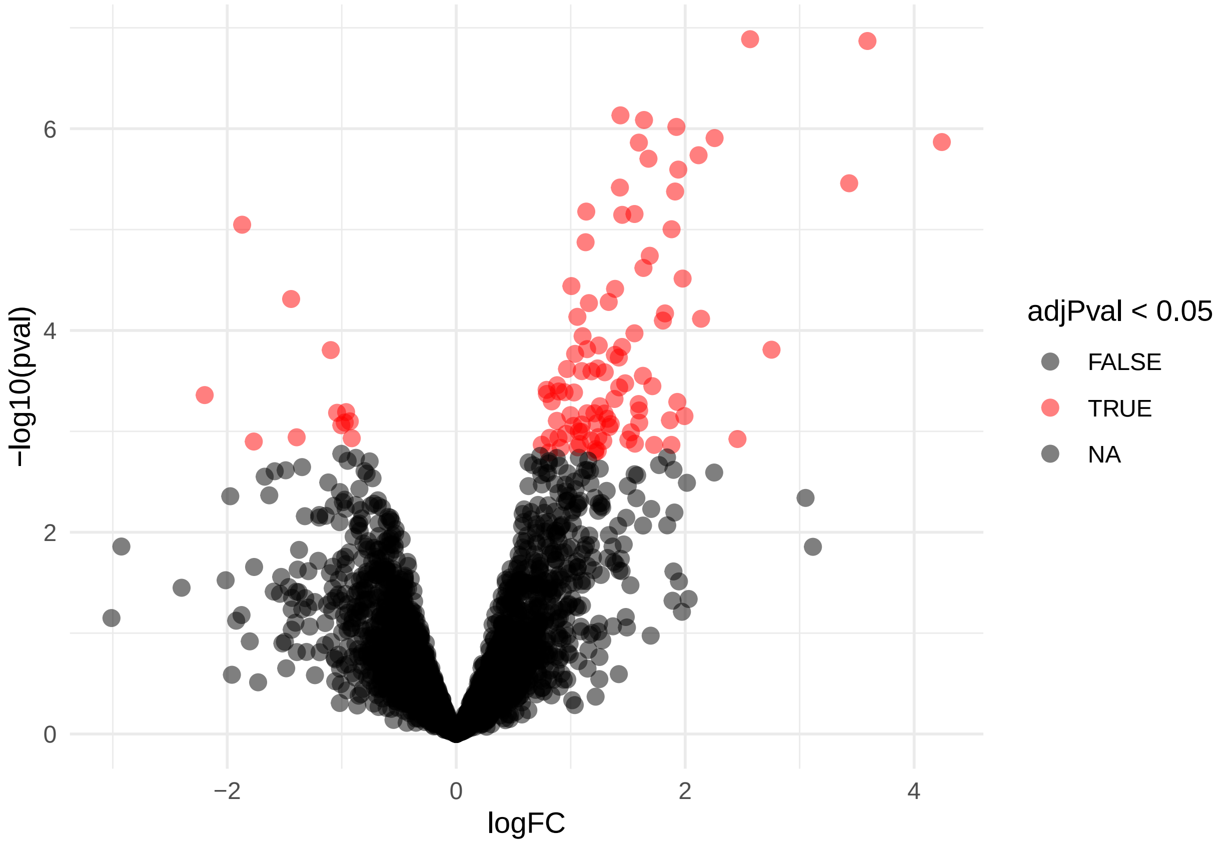
Spike-in condition A is the reference class. So the mean log2 expression for samples from good prognosis (OR) is '(Intercept). The mean log2 expression for samples from poor prognosis (PD) is'(Intercept)+prognosisPD'. Hence, the average log2 fold change between prognosis PD and prognosis OR is modelled 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
```

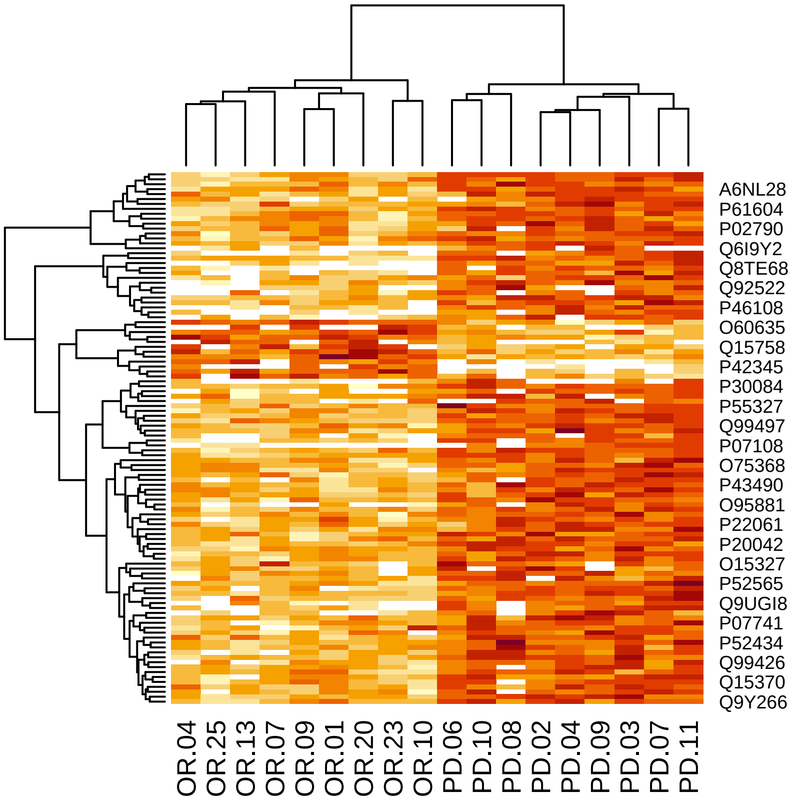


Note, that 108 proteins are found to be differentially abundant.

### 4.3.2 Heatmap

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

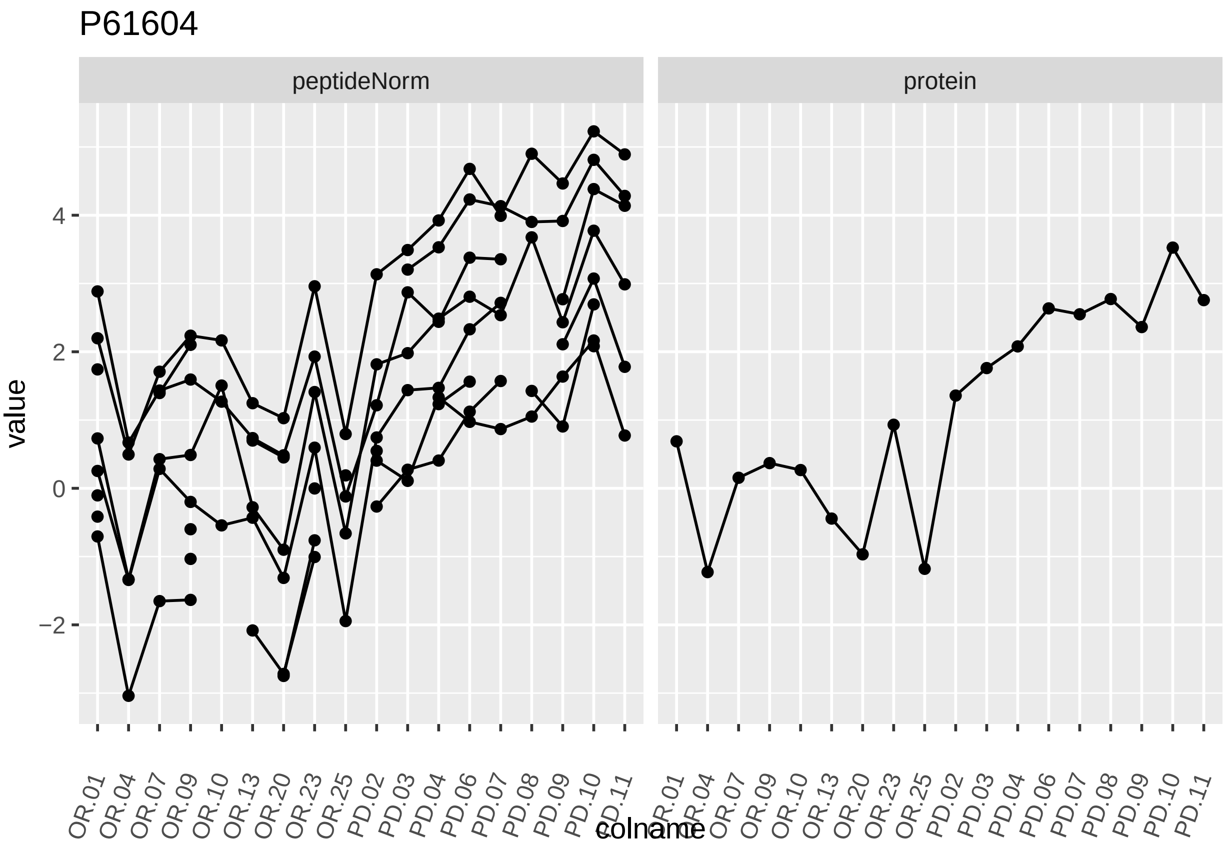
```
sigNames <- rowData(pe[["protein"]])$prognosisPD %>%
  rownames_to_column("protein") %>%
  arrange(pval) %>%
  filter(adjPval<0.05) %>%
  pull(protein)
heatmap(assay(pe[["protein"]])[sigNames, ])
```

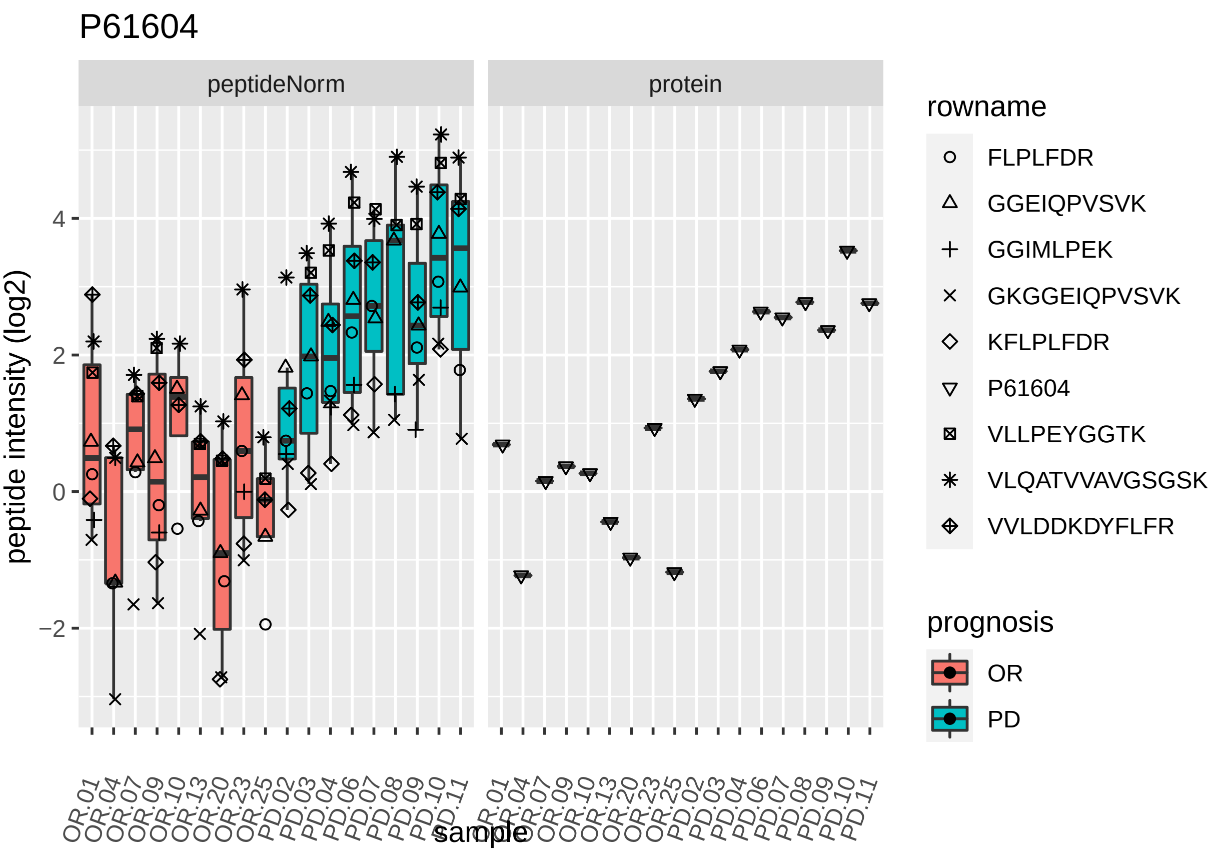


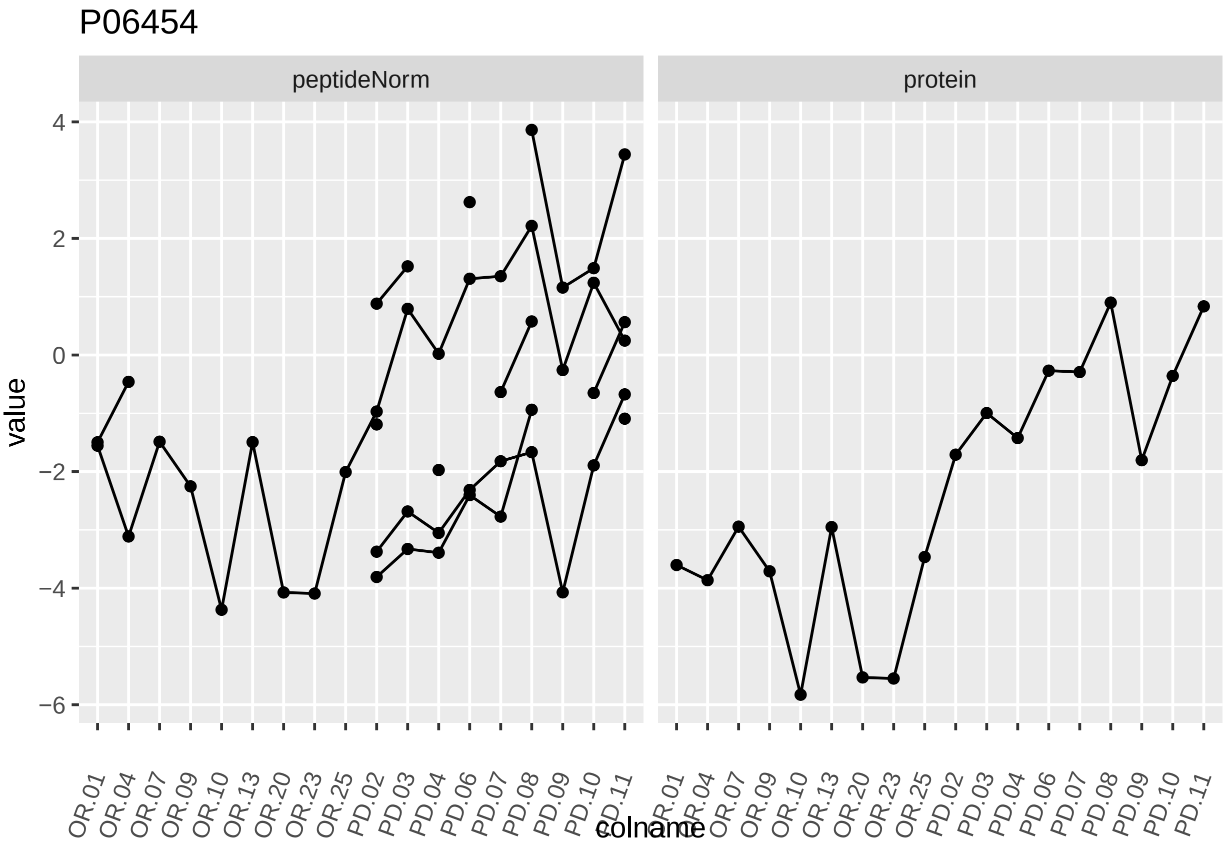
### 4.3.3 Detail plots

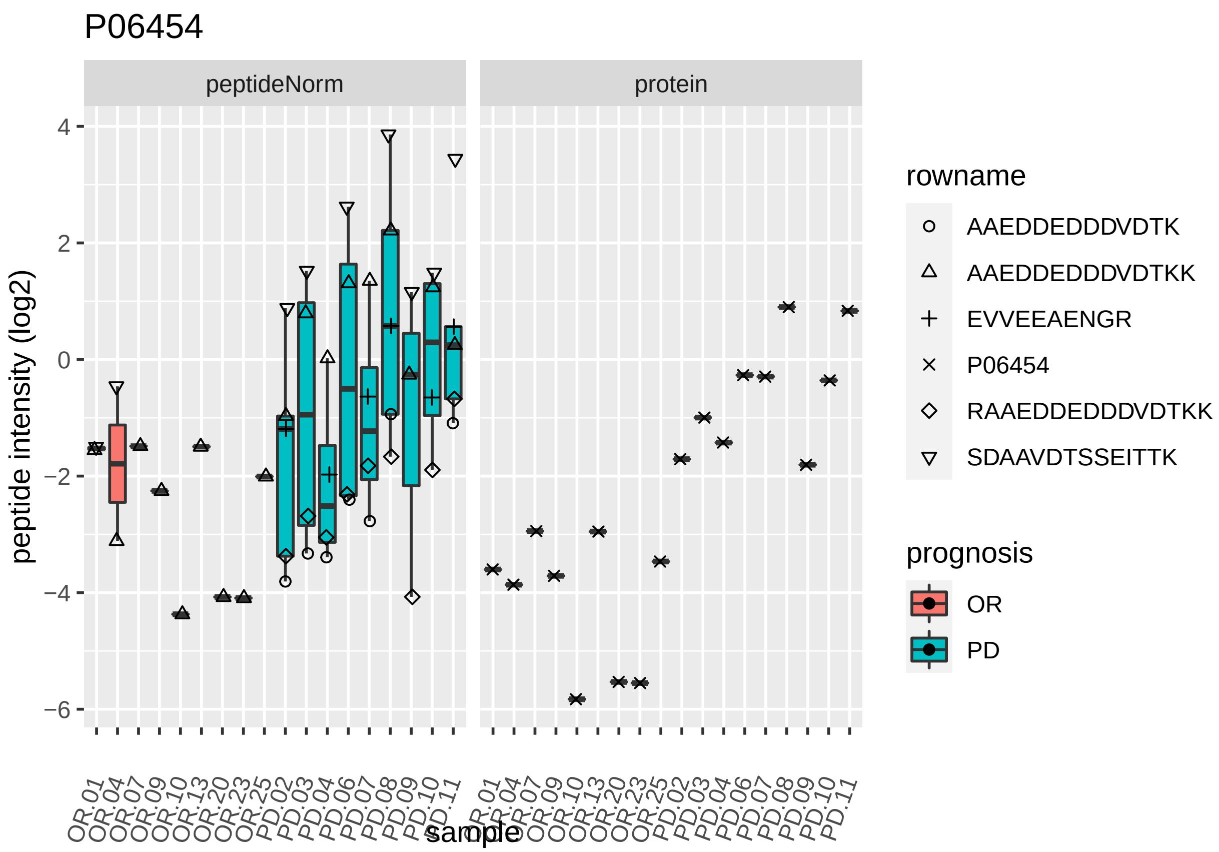
We make detail plots for the top 10 proteins to restrict the number of detail plots.

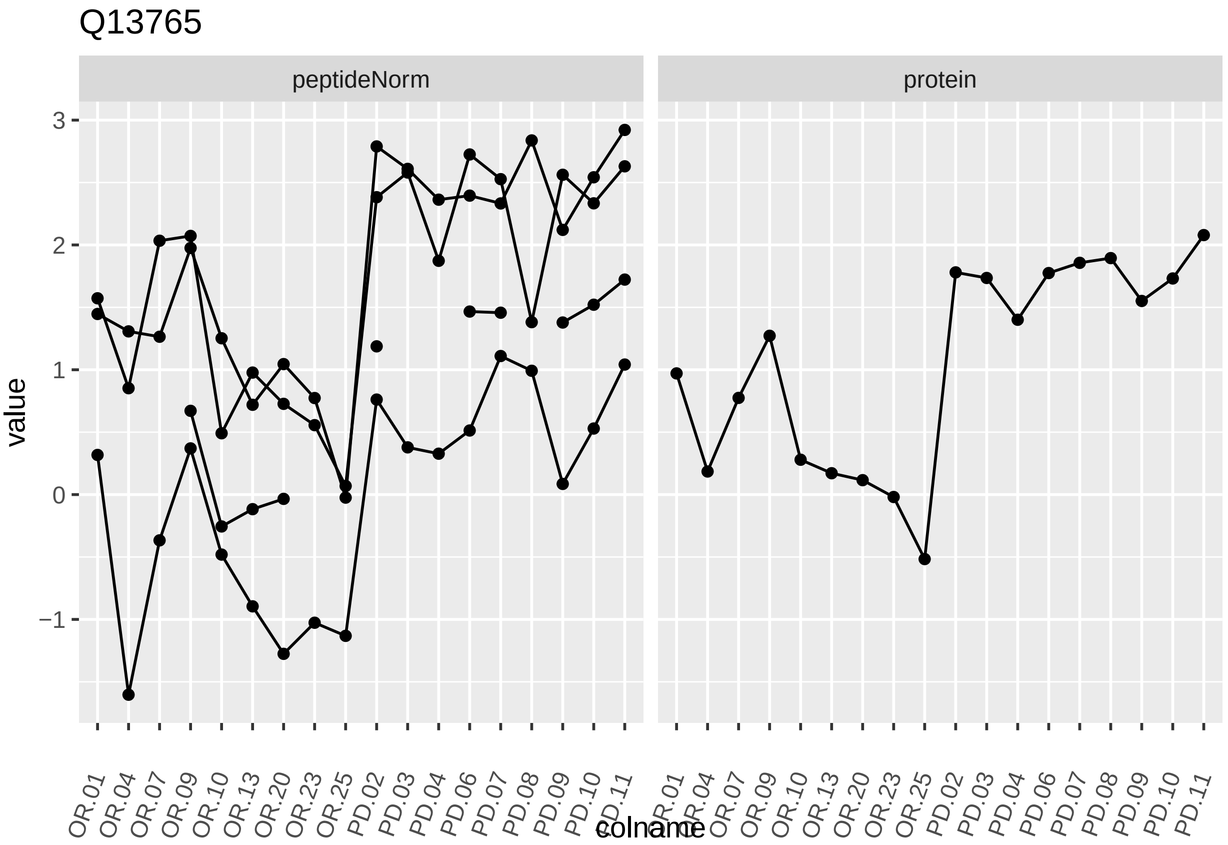
```
for (protName in sigNames)
#for (protName in orderProt[1:10])
{
pePlot <- pe[protName, , c("peptideNorm","protein")]
pePlotDf <- data.frame(longFormat(pePlot))
pePlotDf$assay <- factor(pePlotDf$assay,
                         levels = c("peptideNorm", "protein"))
pePlotDf$prognosis <- as.factor(colData(pePlot)[pePlotDf$colname,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

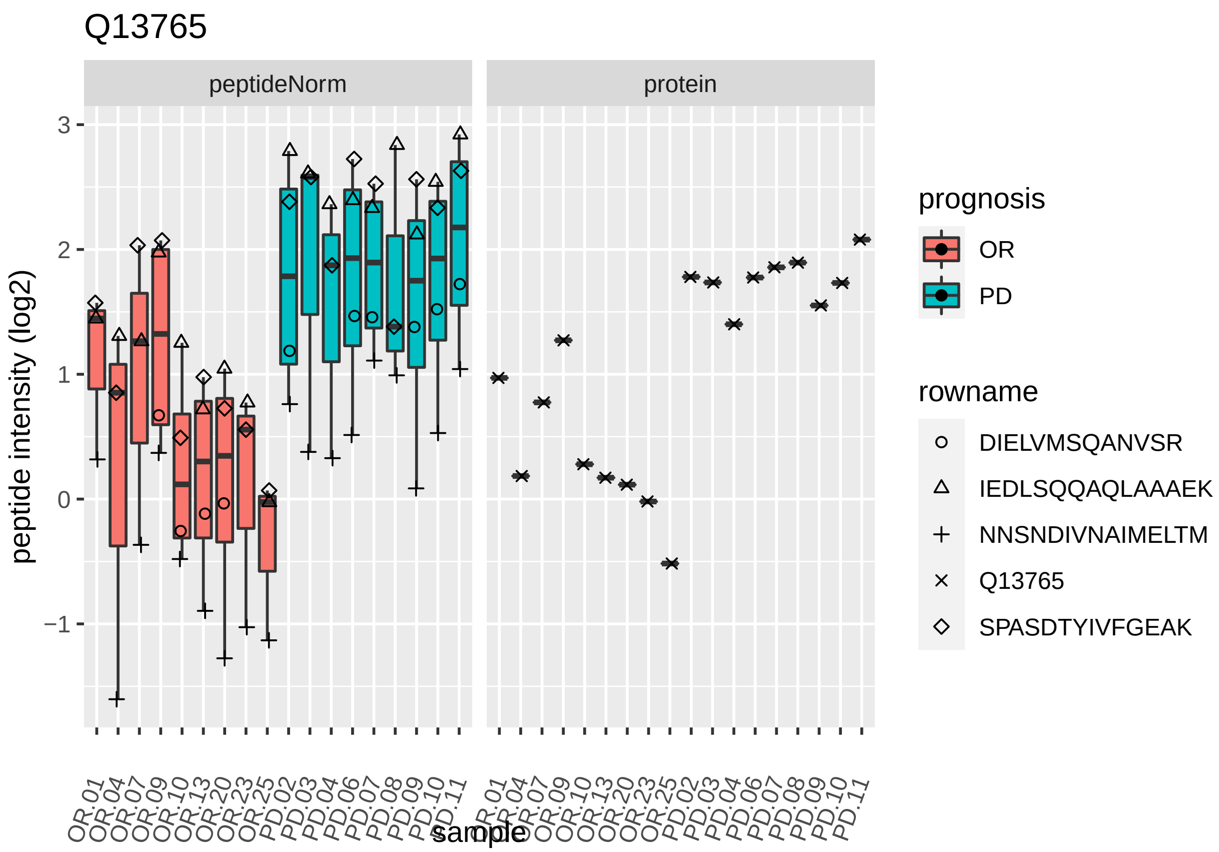


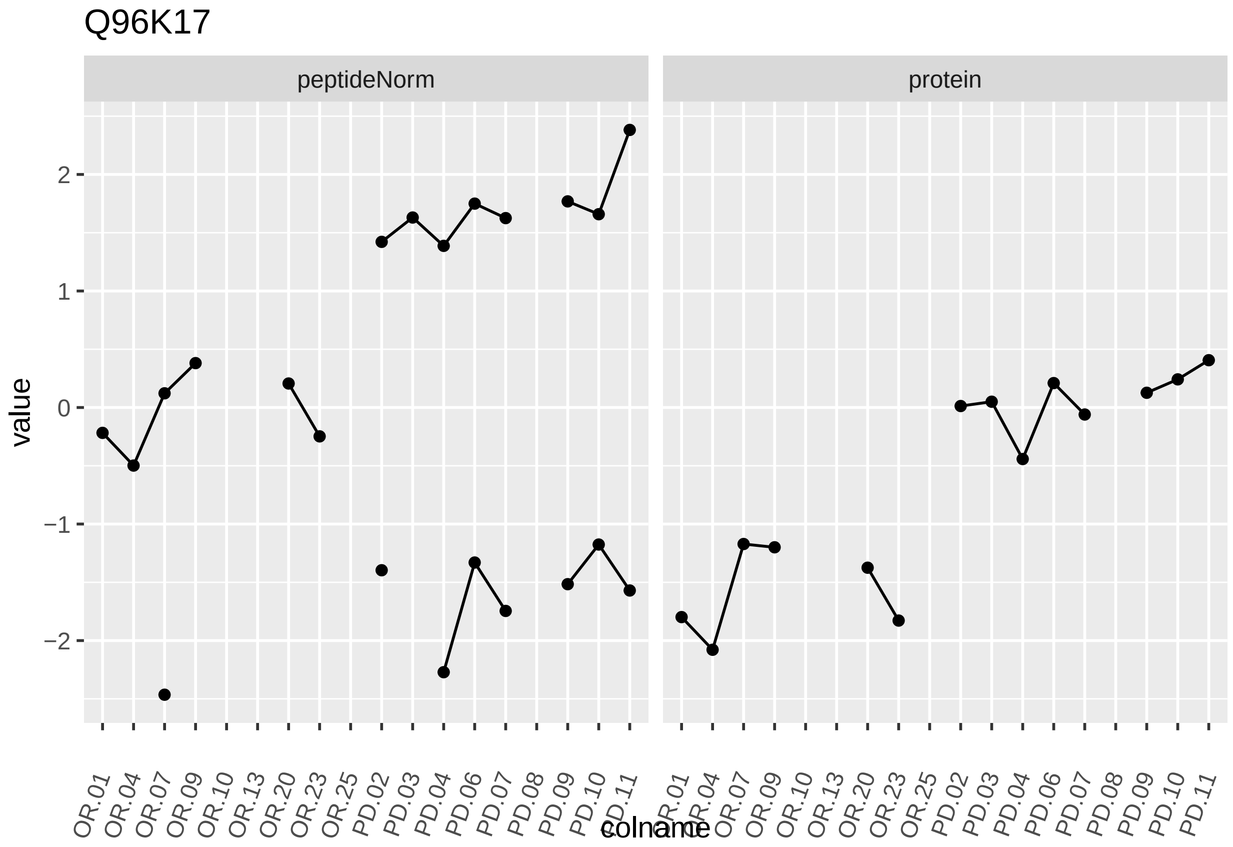

P61604
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
FLPLFDR
GGEIQPVSVK
GGIMLPEK
GKGGEIQPVSVK
KFLPLFDR
P61604
VLLPEYGGTK
VLQATVVAVGSGSK
VVLDDKDYFLFR
prognosis
OR
PD

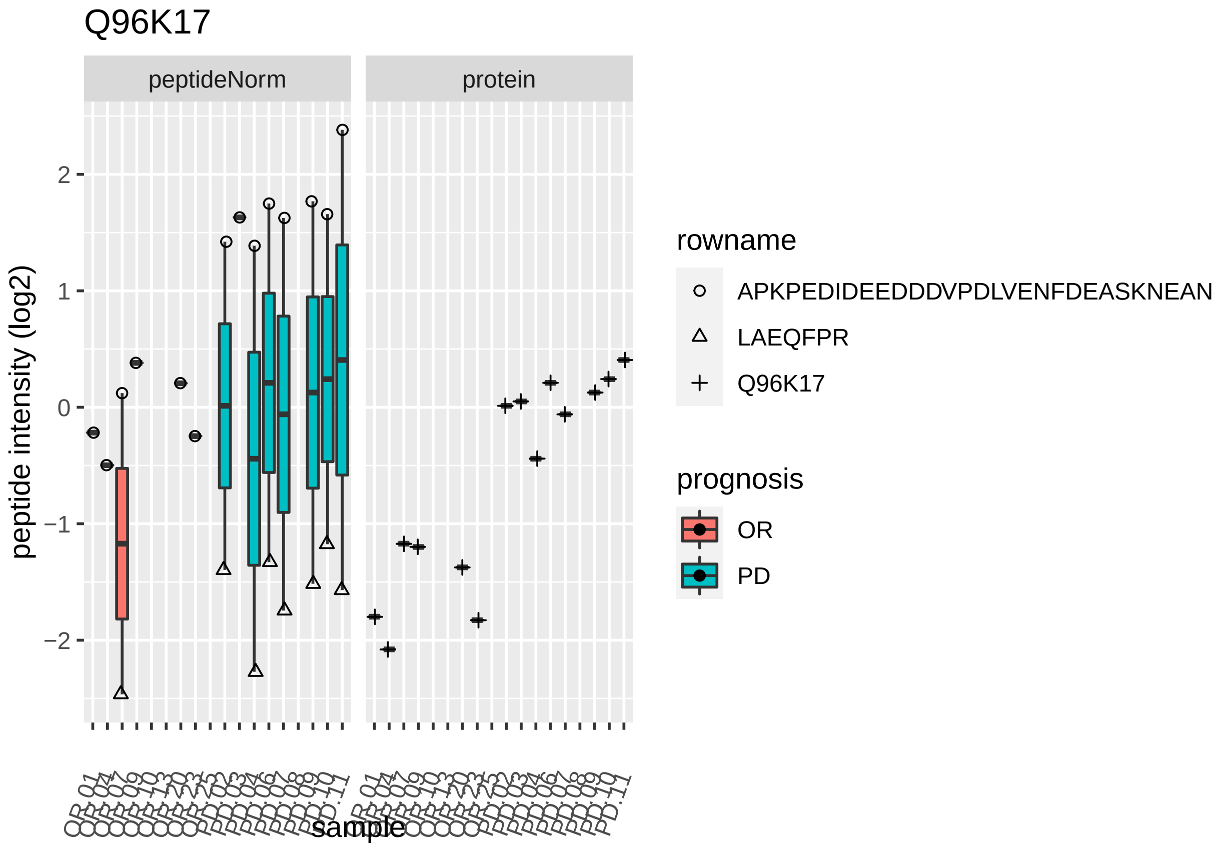

P06454
peptideNorm
protein
value
4
2
0
−2
−4
−6
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

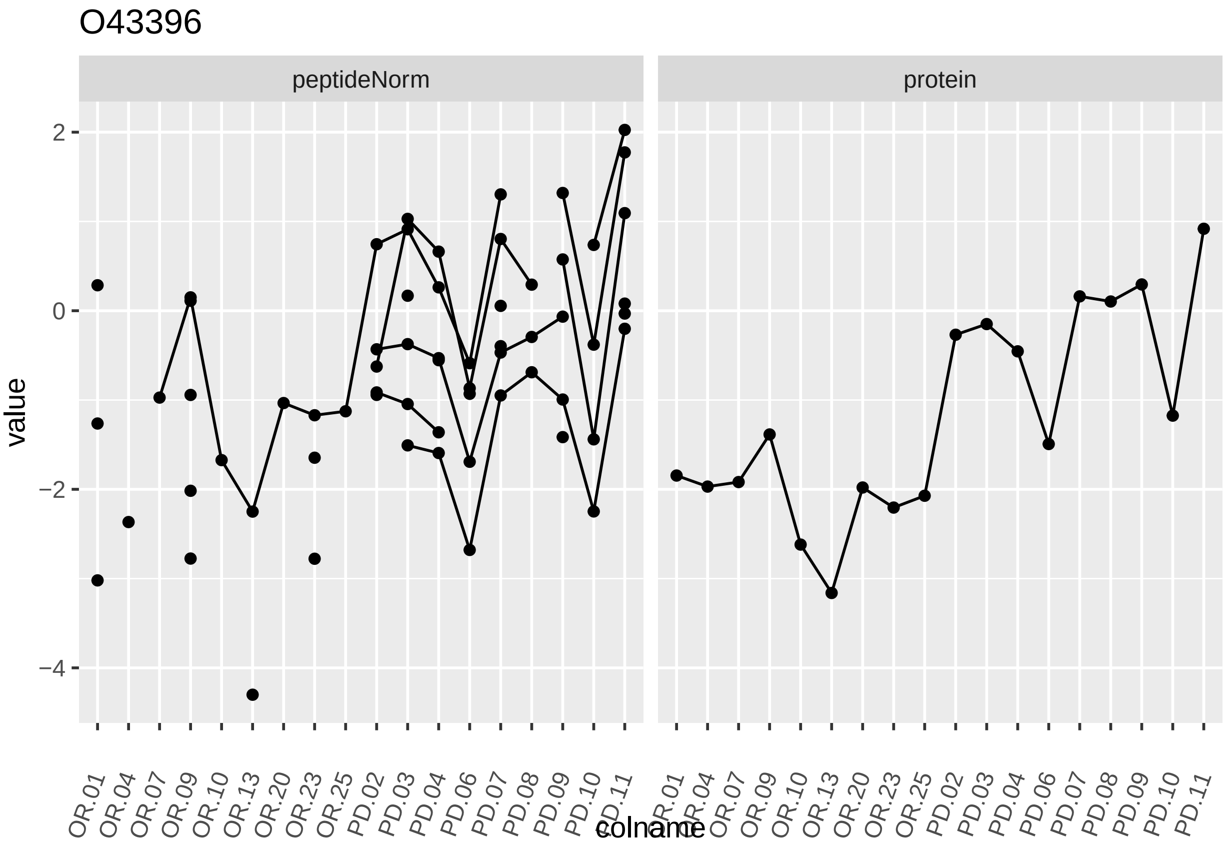

P06454
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
−6
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ AAEDDEDDDVDTK
△ AAEDDEDDDVDTKK
+ EVVEEAENGR
× P06454
◇ RAAEDDEDDDVDTKK
▽ SDAAVDTSSEITTK
prognosis
🟥 OR
🟦 PD

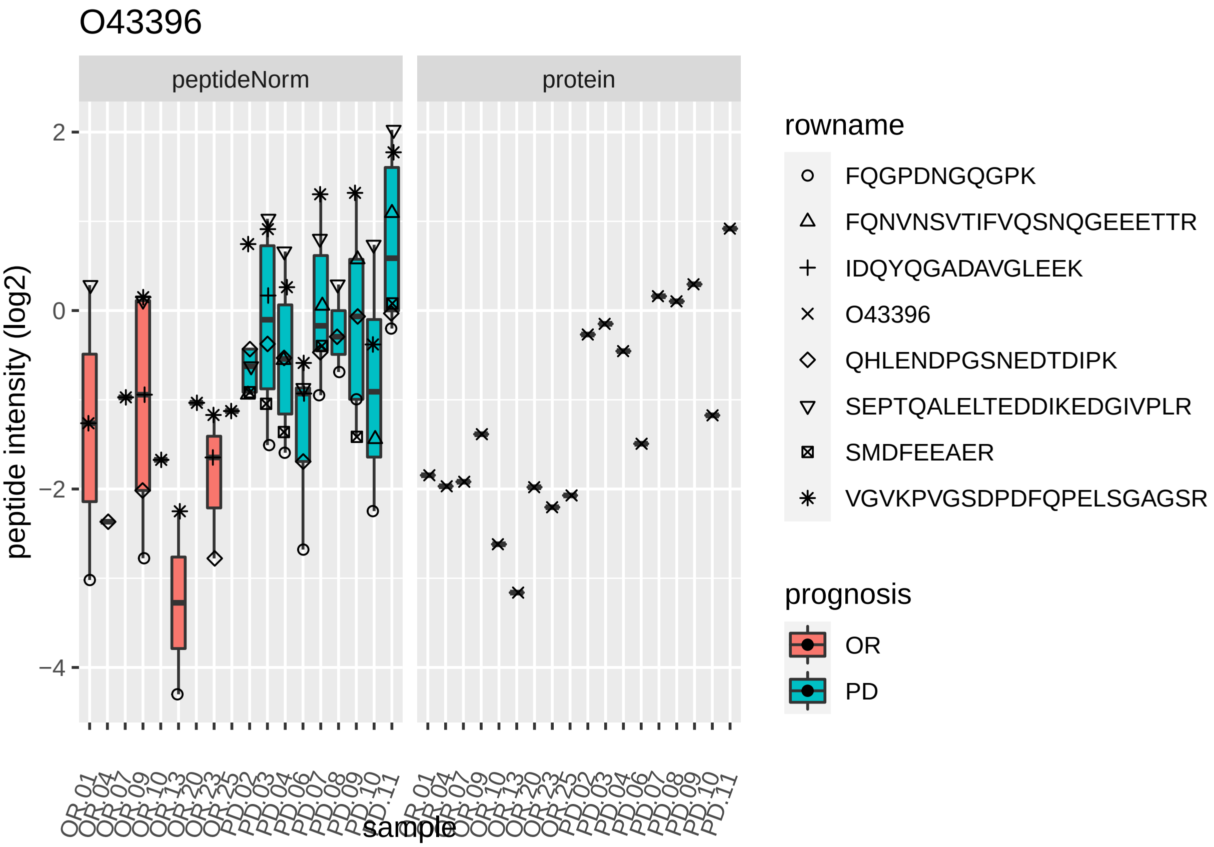

Q13765
peptideNorm
protein
value
3
2
1
0
−1
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

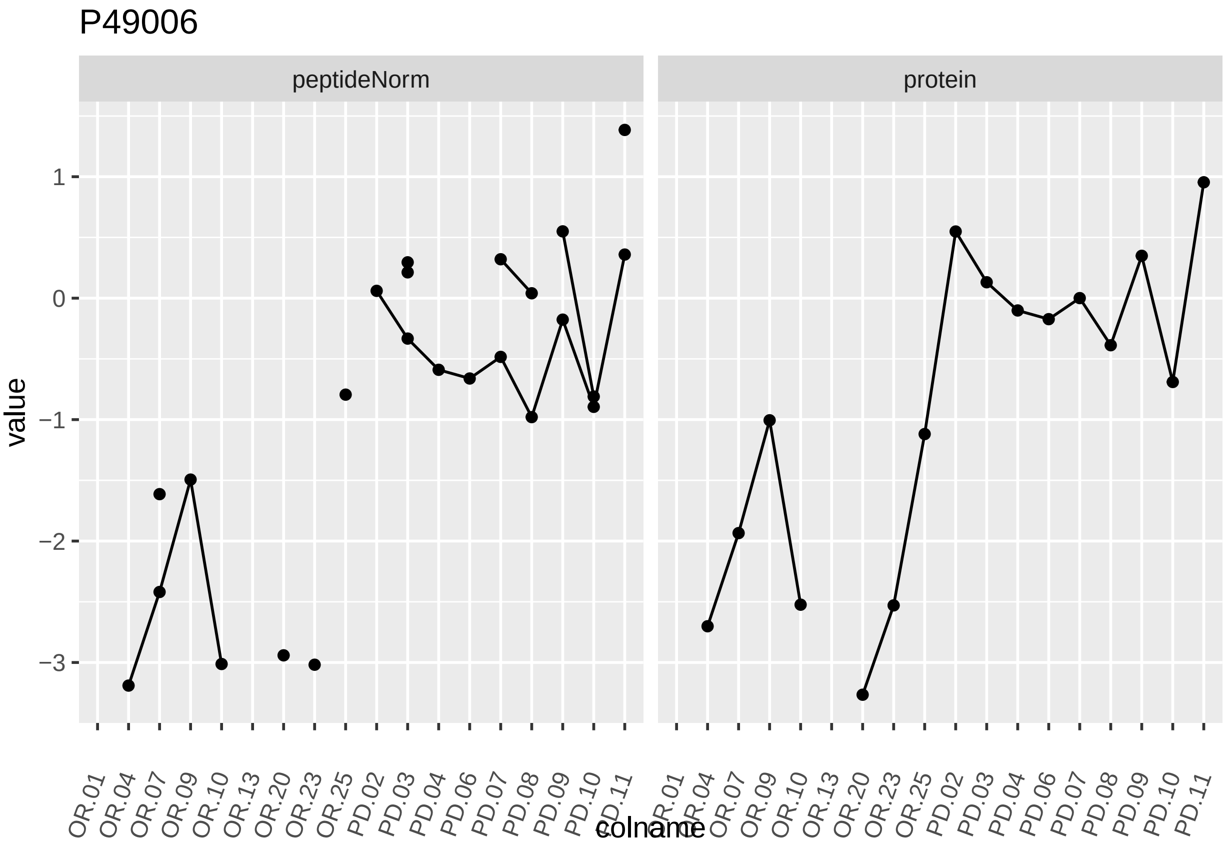

Q13765
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
DIELVMSQANVSR
IEDLSQQAQLAAAEK
NNSNDIVNAIMELTM
Q13765
SPASDTYIVFGEAK

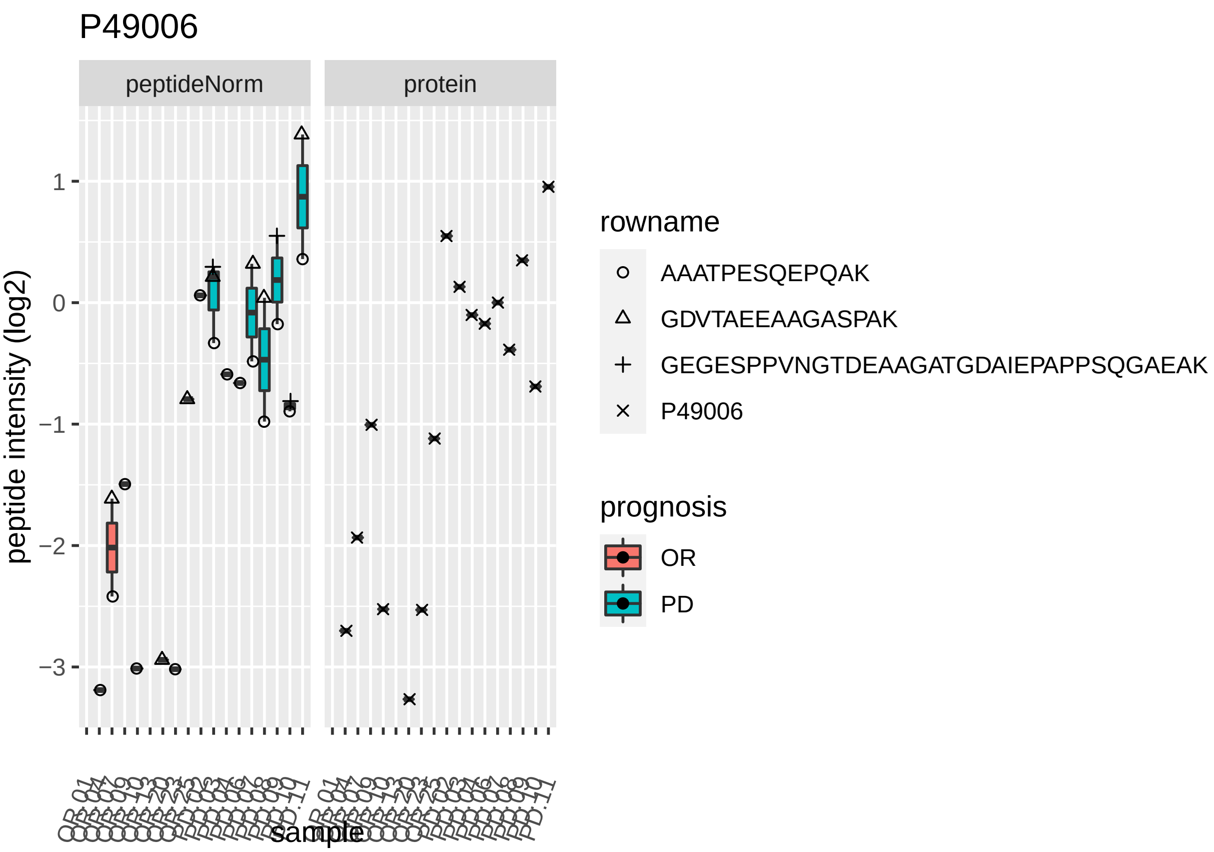

Q96K17
peptideNorm
protein
value
2
1
0
−1
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q96K17
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.21
OR.23
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.21
OR.23
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
APKPEDIDEEDDDVPDLVENFDEASKNEAN
LAEQFPR
Q96K17
prognosis
OR
PD

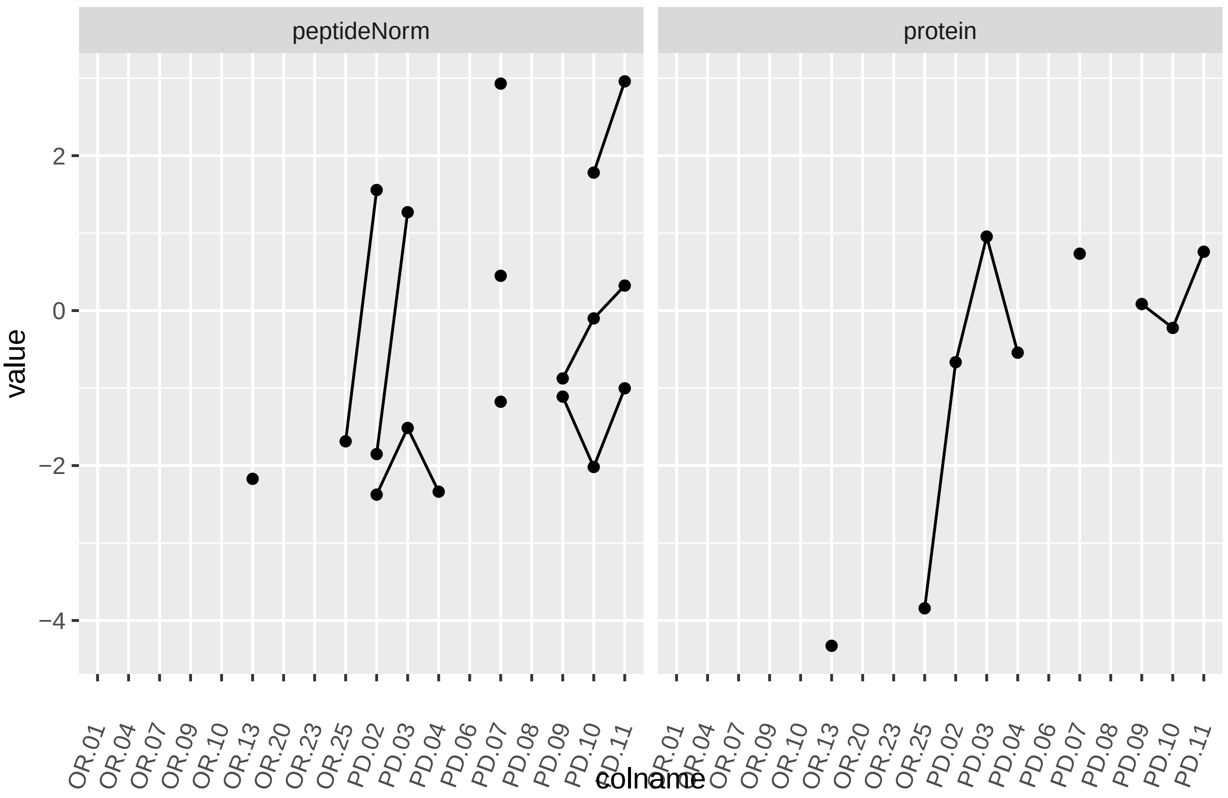

O43396
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

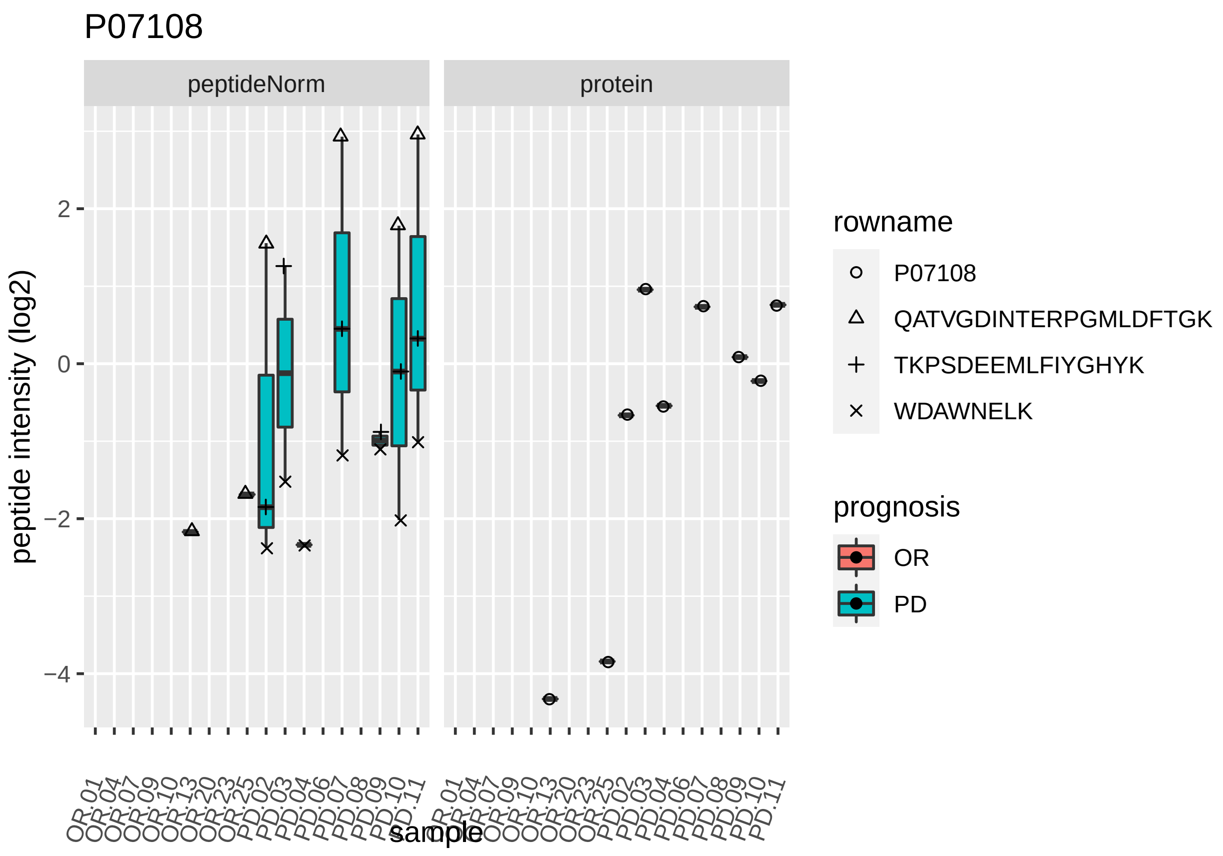

O43396
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ FQGPDNGQGPK
△ FQNVNSVTIFVQSNQGEEETTR
+ IDQYQGADAVGLEEK
× O43396
◇ QHLENDPGSNEDTDIPK
▽ SEPTQALELTEDDIKEDGIVPLR
⊠ SMDFEEAER
✳ VGVKPVGSDPDFQPELSGAGSR
prognosis
🟥 OR
🟦 PD

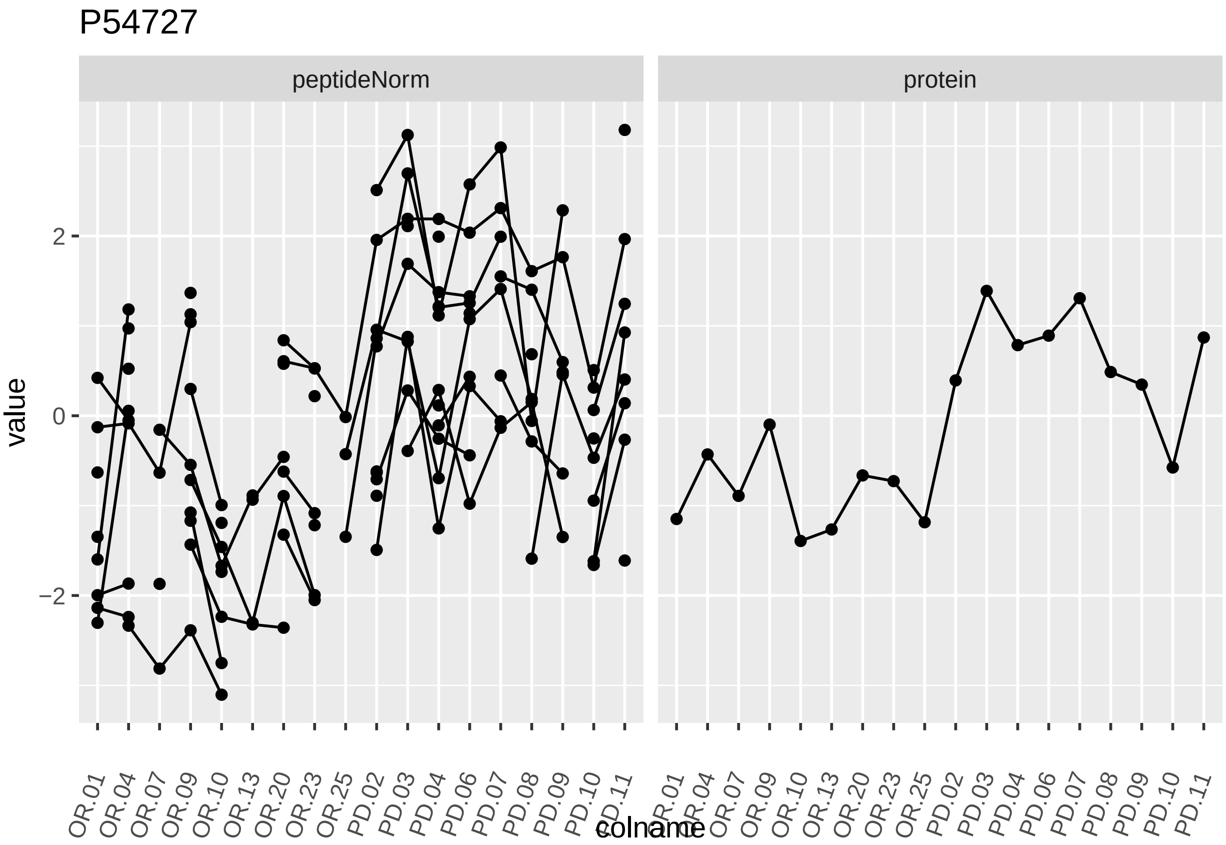

P49006
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

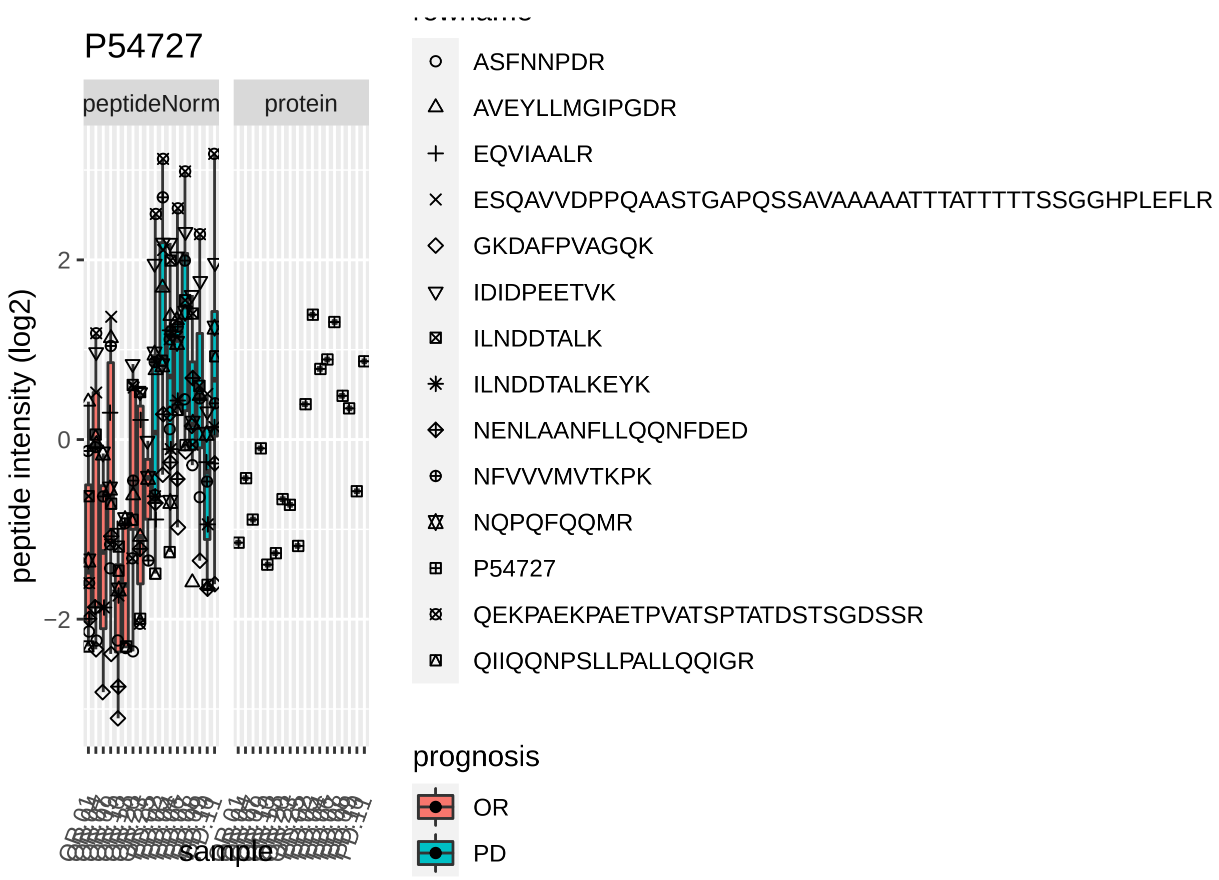

P49006
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
rowname
○ AAATPESQEPQAK
△ GDVTAEEAAGASPAK
+ GEGESPPVNGTDEAAGATGDAIEPAPPSQGAEAK
× P49006
prognosis
OR
PD

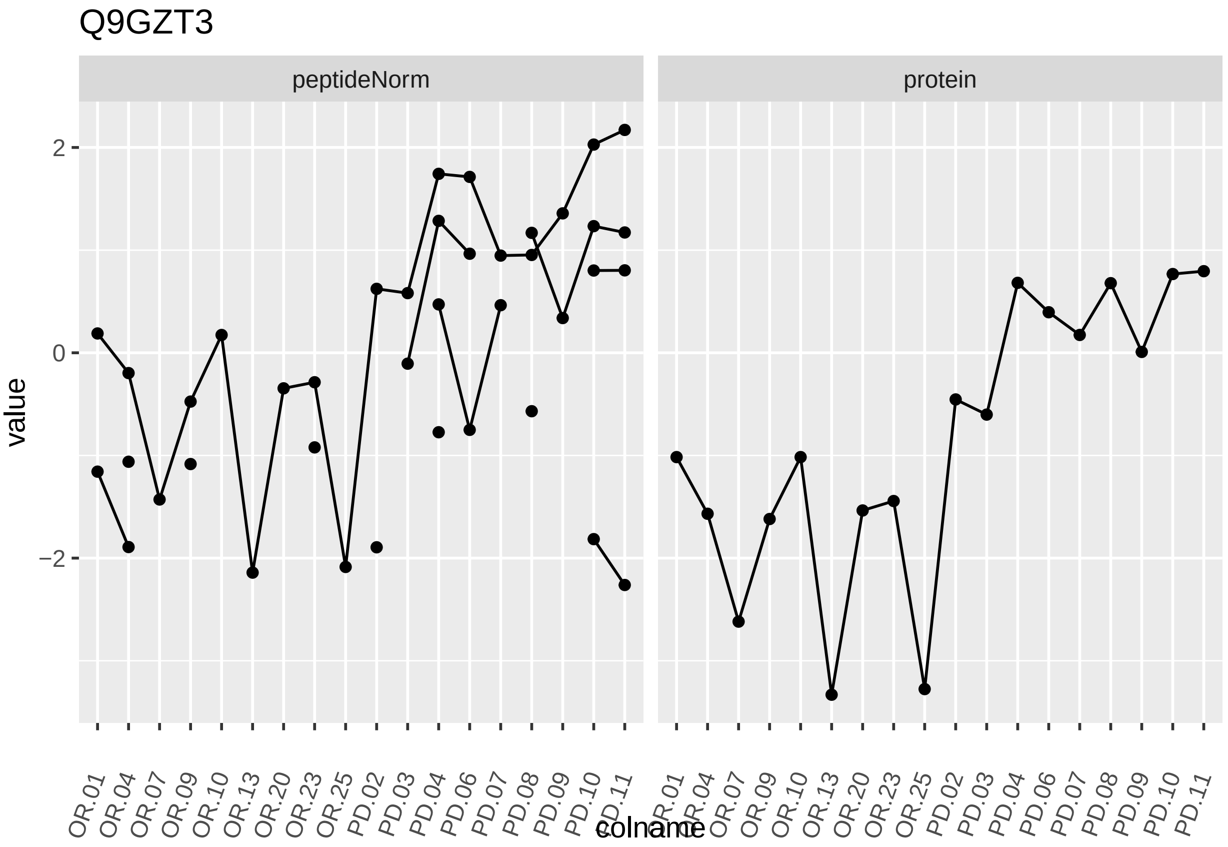
P07108

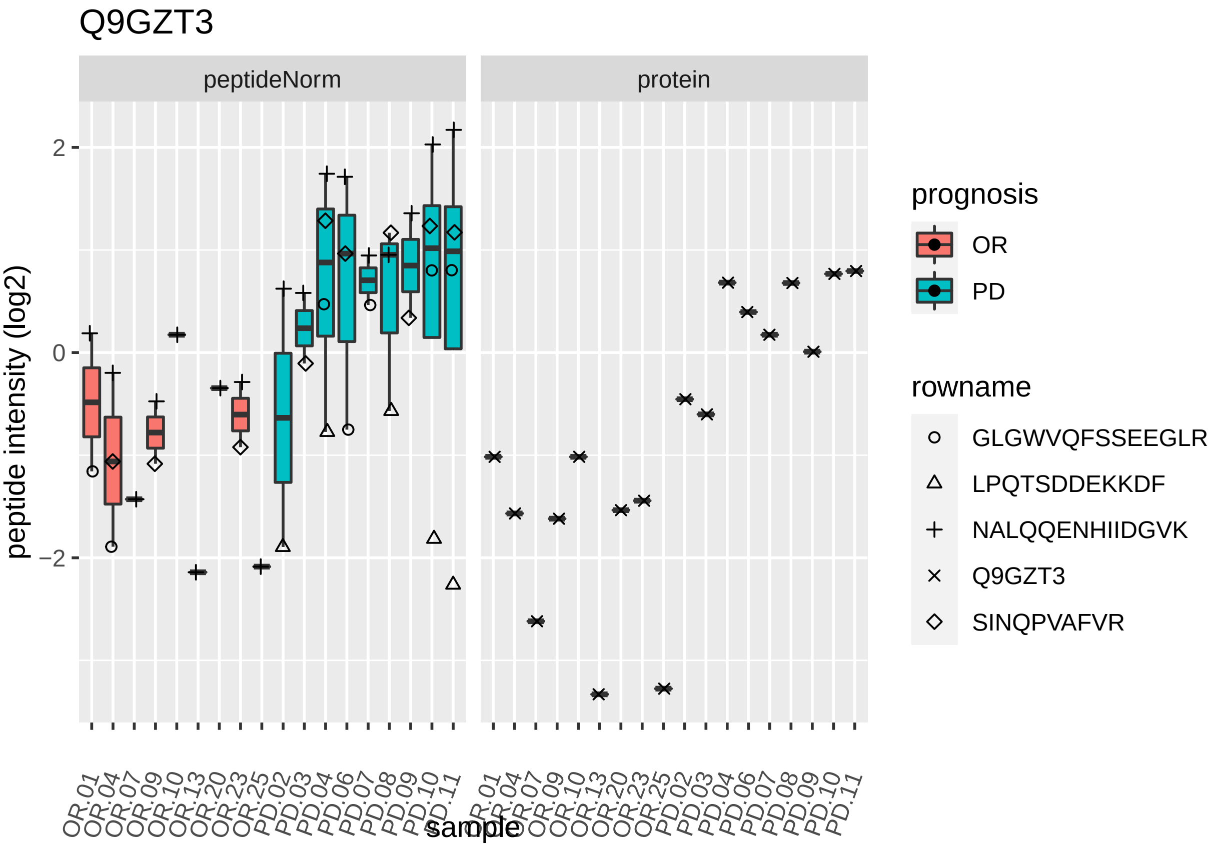

peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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

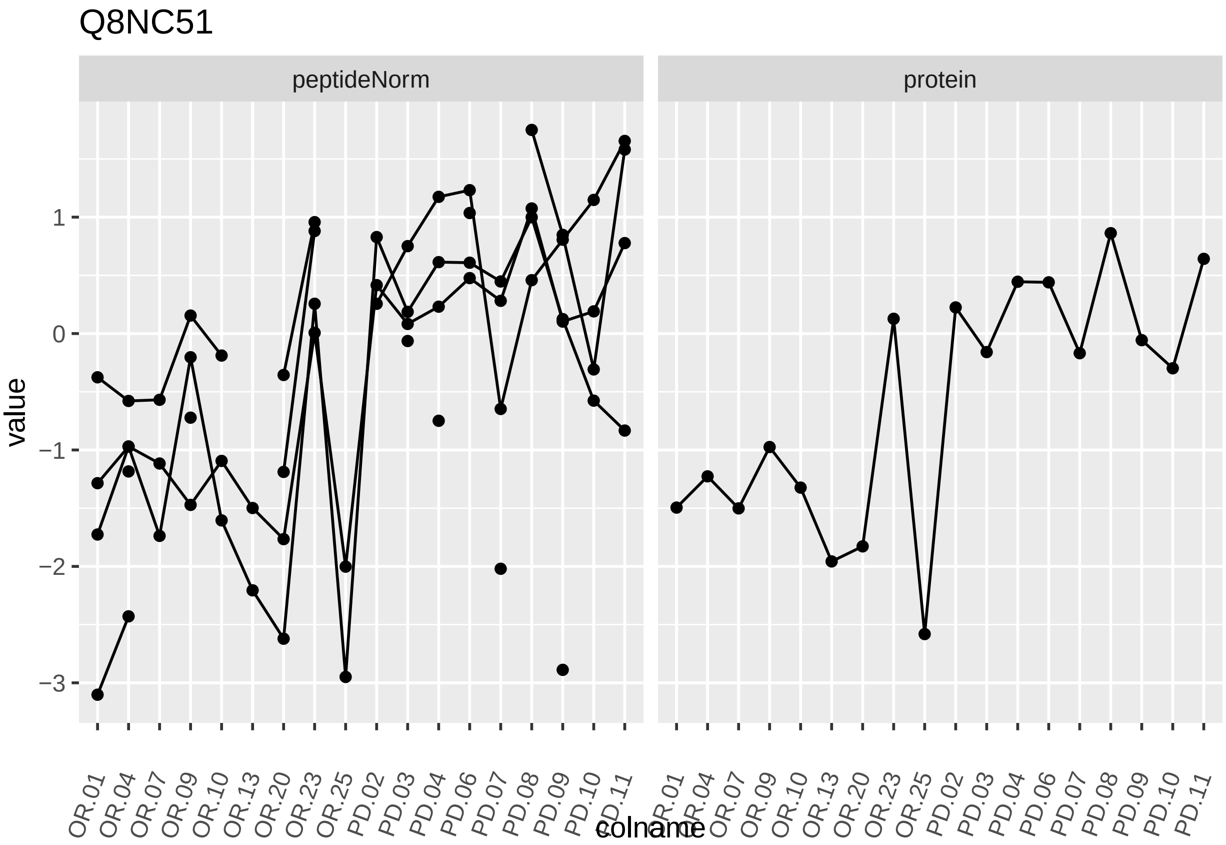

P54727
peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

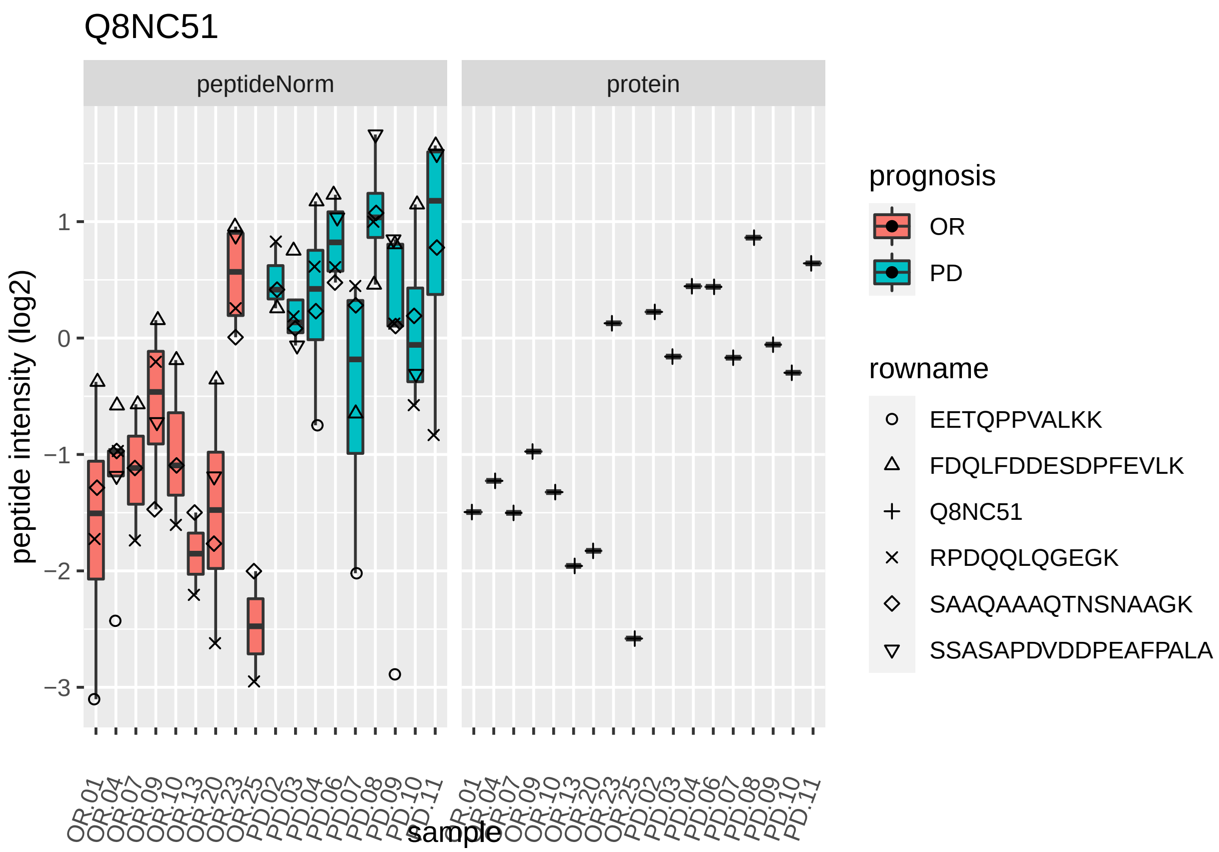

P54727
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
rowname
ASFNNPDR
AVEYLLMGIPGDR
EQVIAALR
ESQAVVDPPQAASTGAPQSSAVAAAAATTTATTTTTSSGGHPLEFLR
GKDAFPVAGQK
IDIDPEETVK
ILNDDTALK
ILNDDTALKEYK
NENLAANFLLQQNFDED
NFVVVMVTKPK
NQPQFQQMR
P54727
QEKPAEKPAETPVATSPTATDSTSGDSSR
QIIQQNPSLLPALLQQIGR
prognosis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

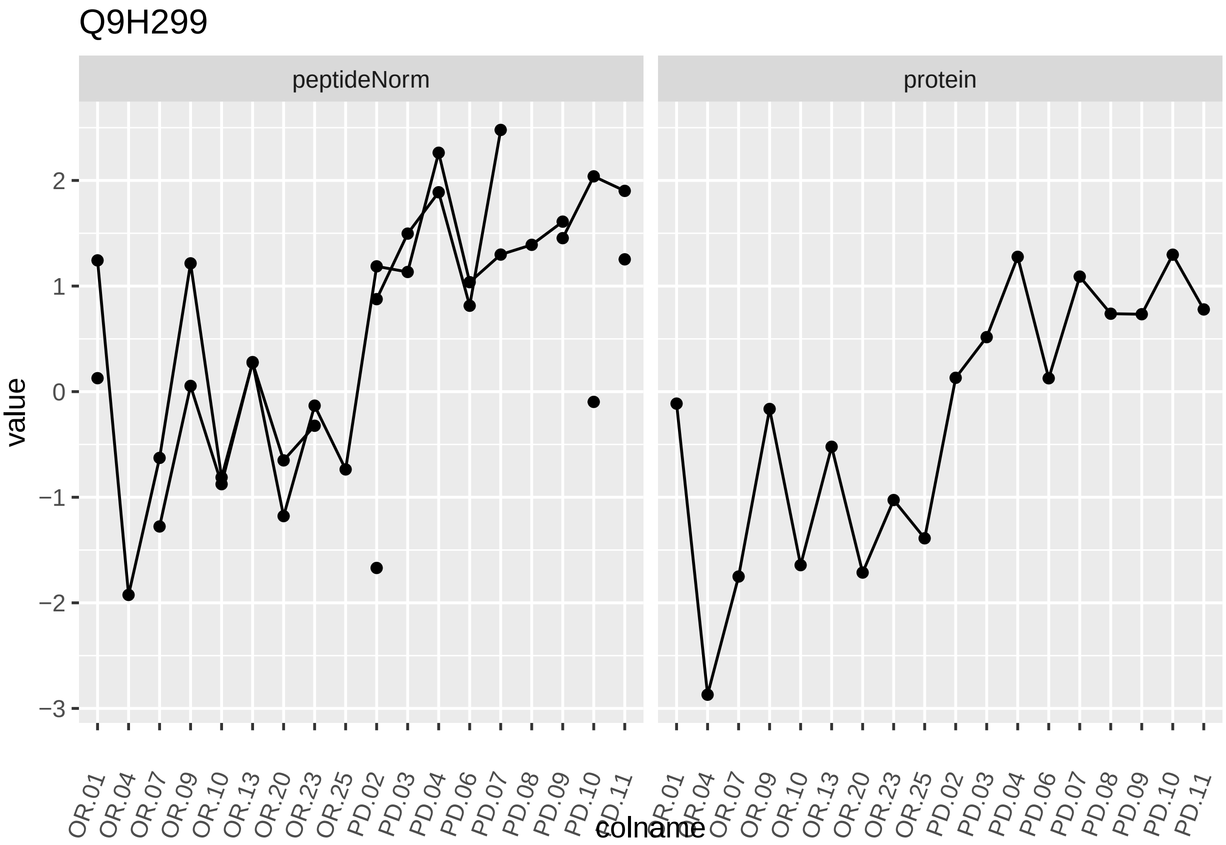

Q9GZT3
peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

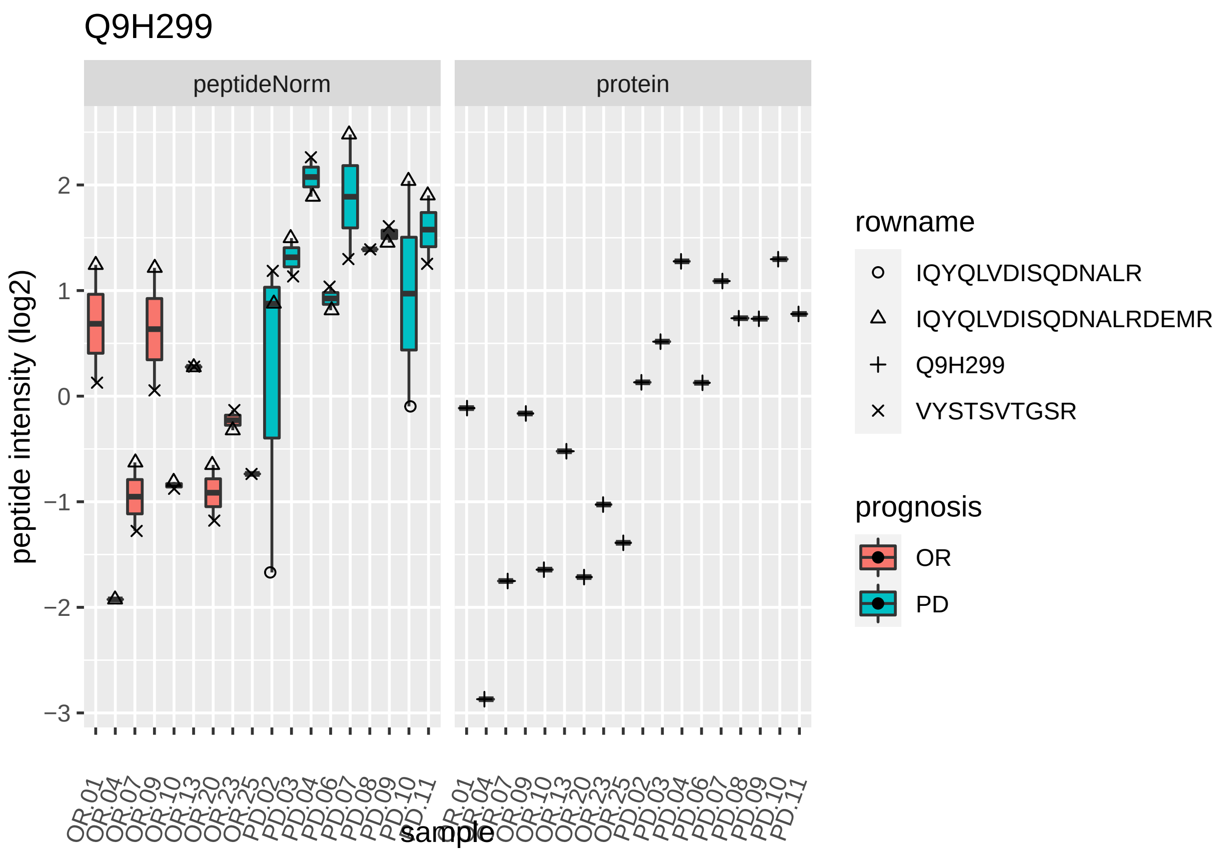


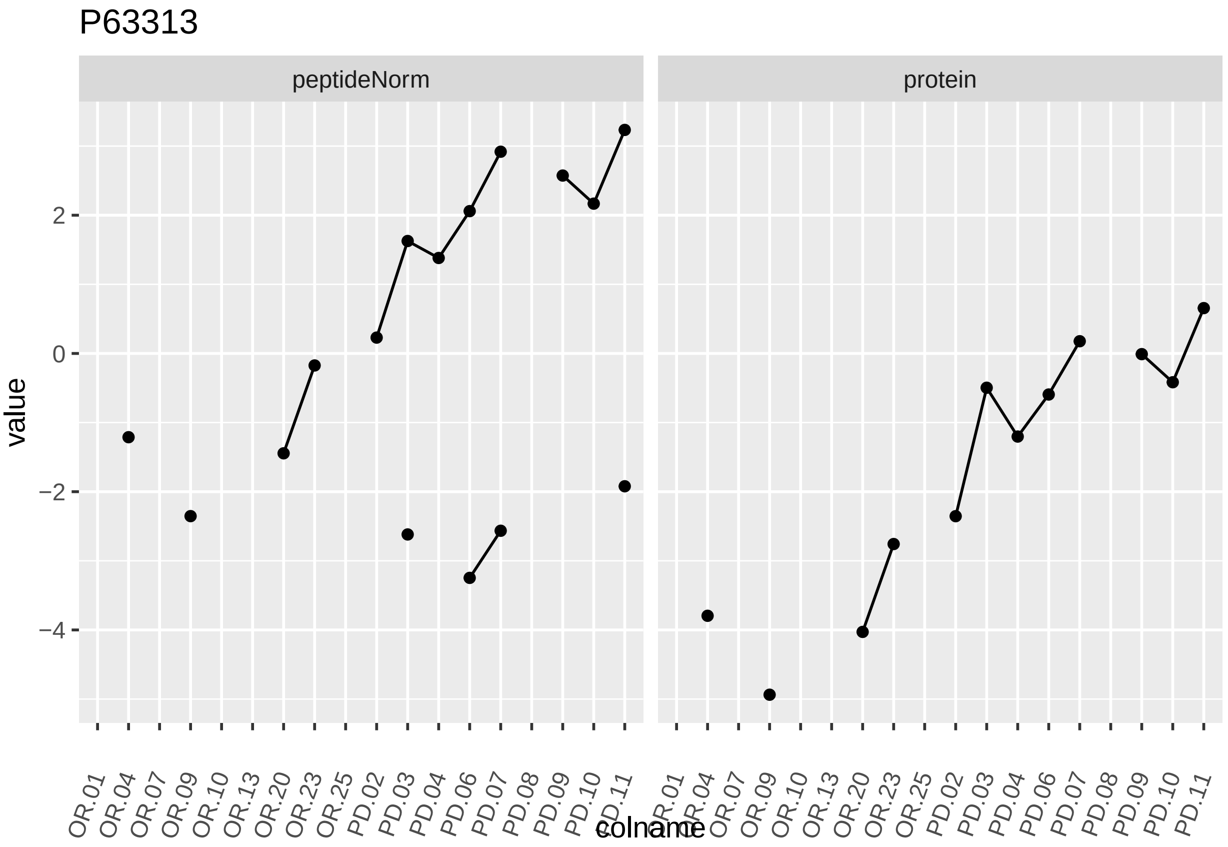
Q9GZT3
peptideNorm
protein
peptide intensity (log2)
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
GLGWVQFSSEEGLR
LPQTSDDEKKDF
NALQQENHIIDGVK
Q9GZT3
SINQPVAFVR

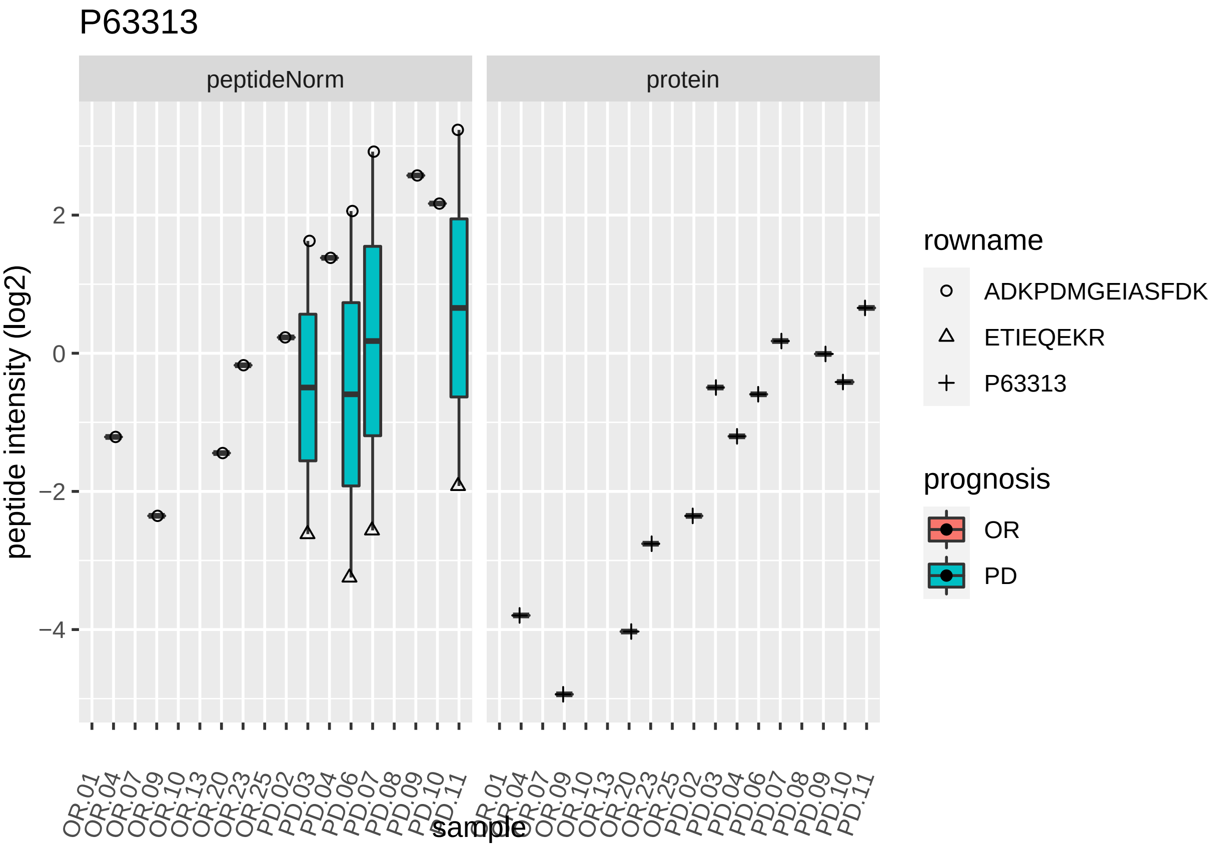

Q8NC51
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

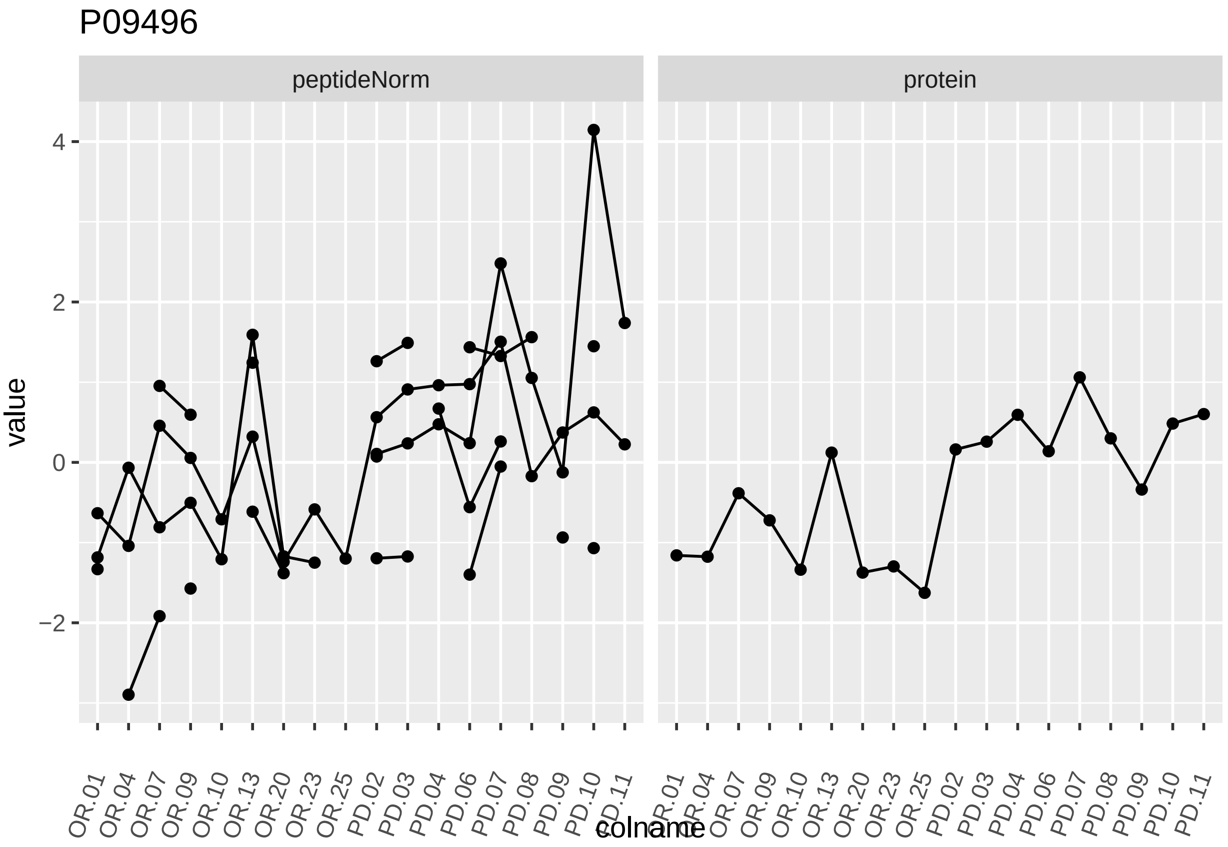

Q8NC51
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
EETQPPVALKK
FDQLFDDESDPFEVLK
Q8NC51
RPDQQLQGEGK
SAAQAAAQTNSNAAGK
SSASAPDVDDPEAFPALA

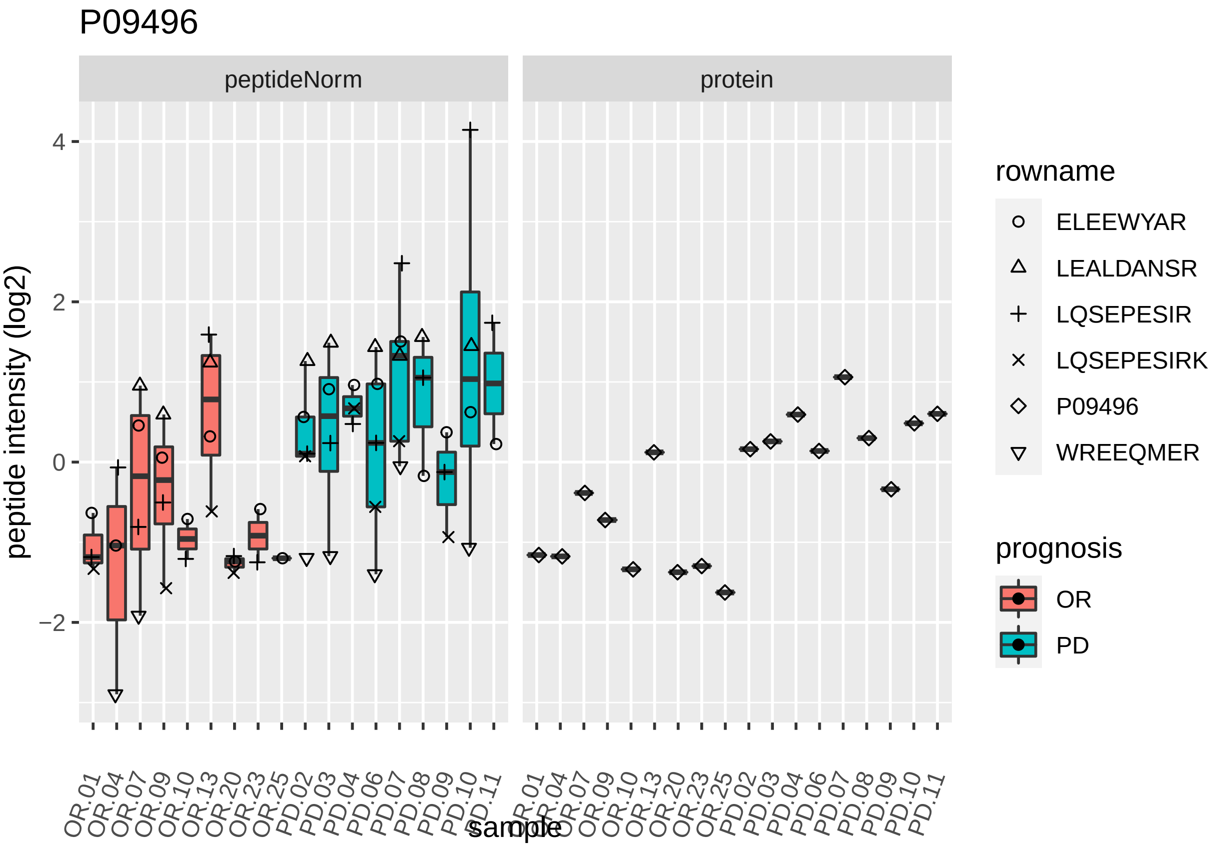

Q9H299
peptideNorm
protein
value
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

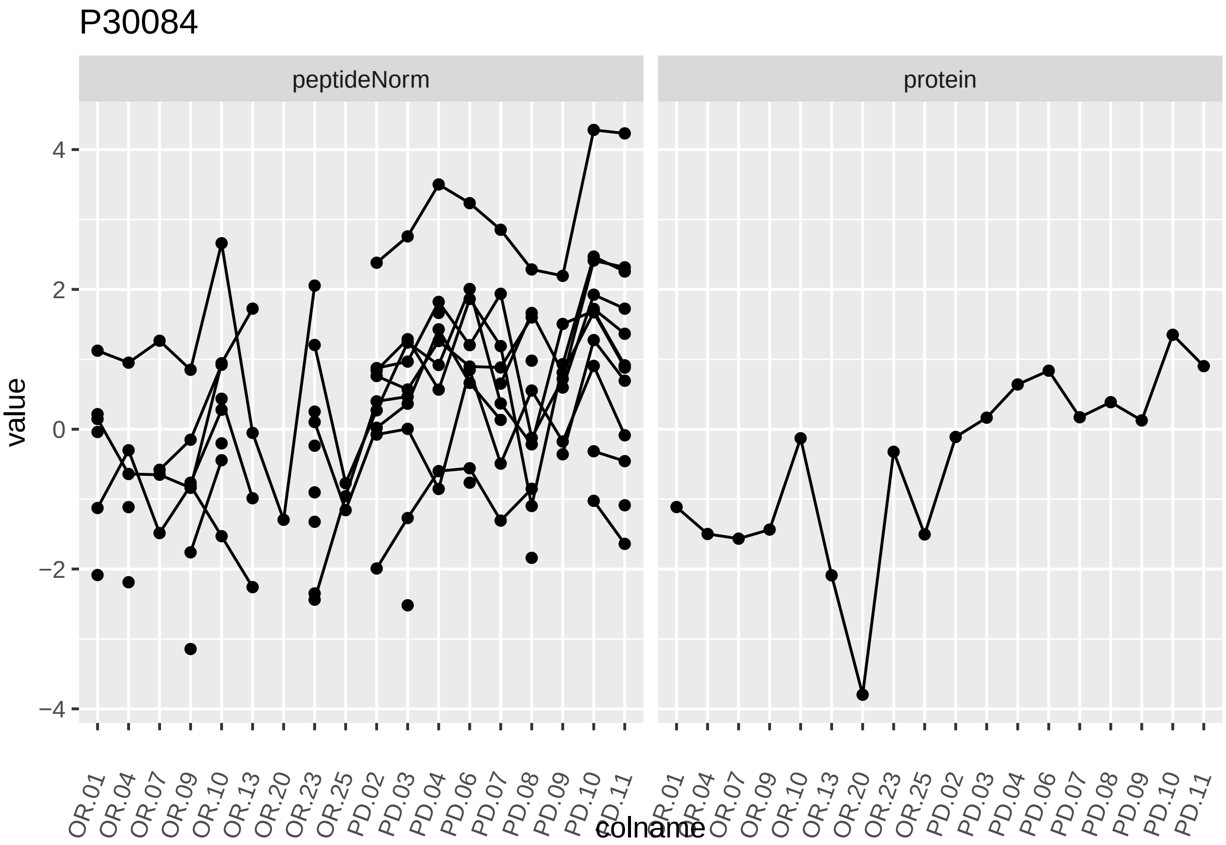

Q9H299
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ IQYQLVDISQDNALR
△ IQYQLVDISQDNALRDEMR
+ Q9H299
× VYSTSVTGSR
prognosis
OR
PD

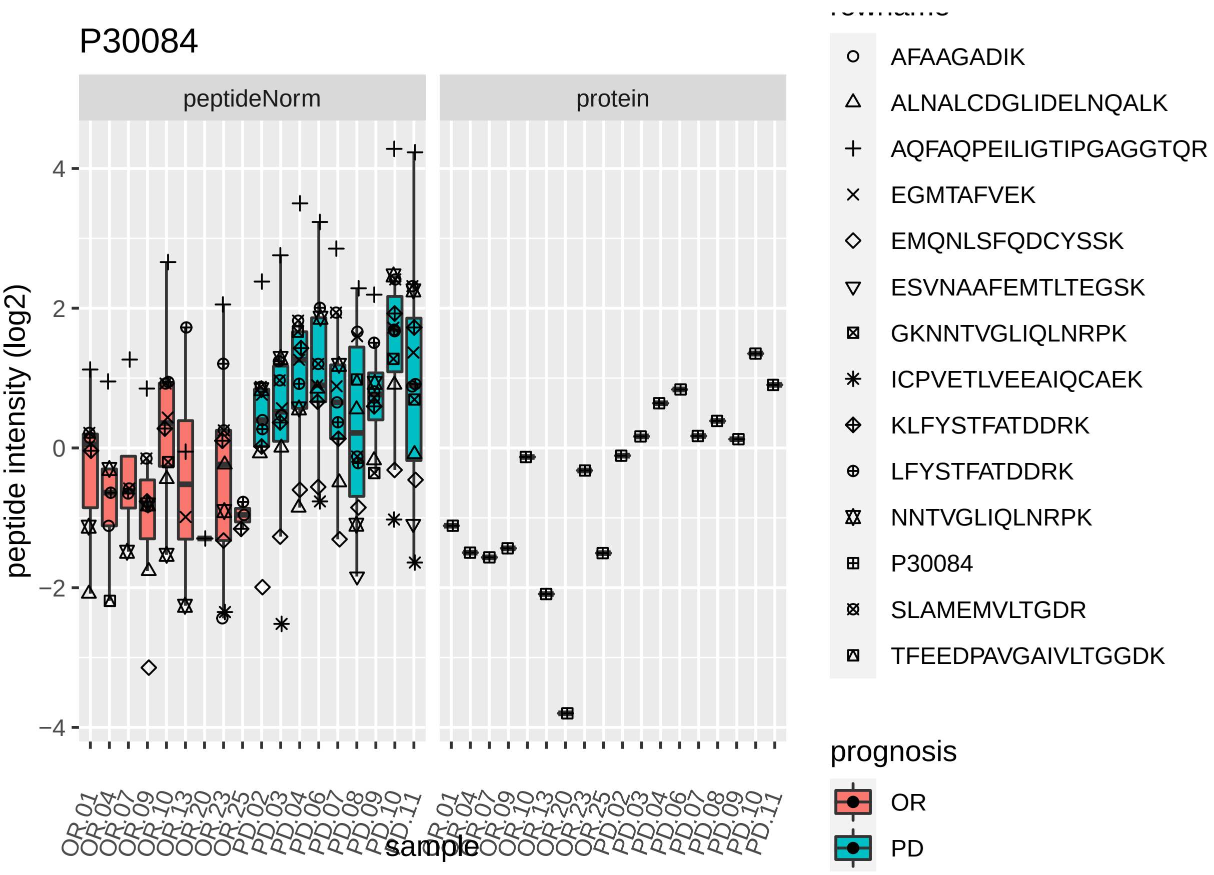

P63313
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

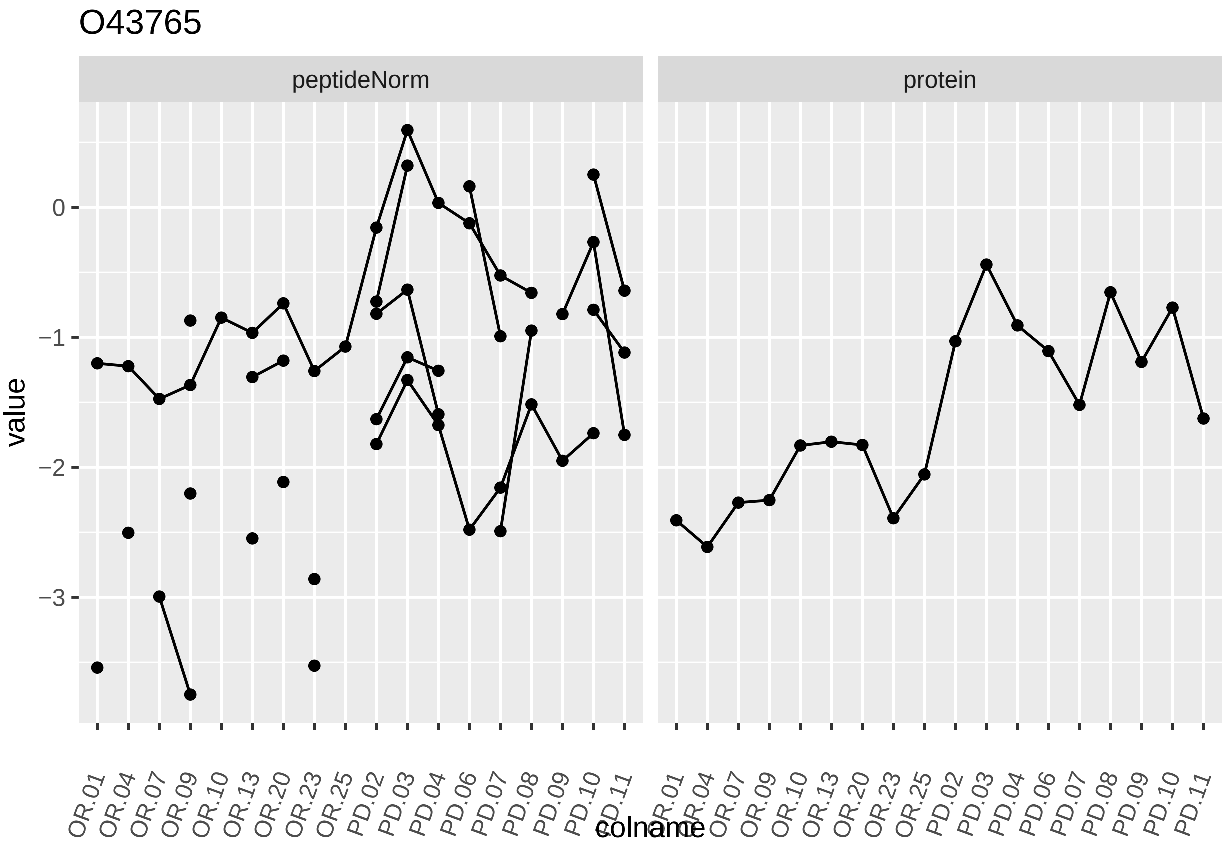

P63313
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ADKPDMGEIASFDK
ETIEQEKR
P63313
prognosis
OR
PD

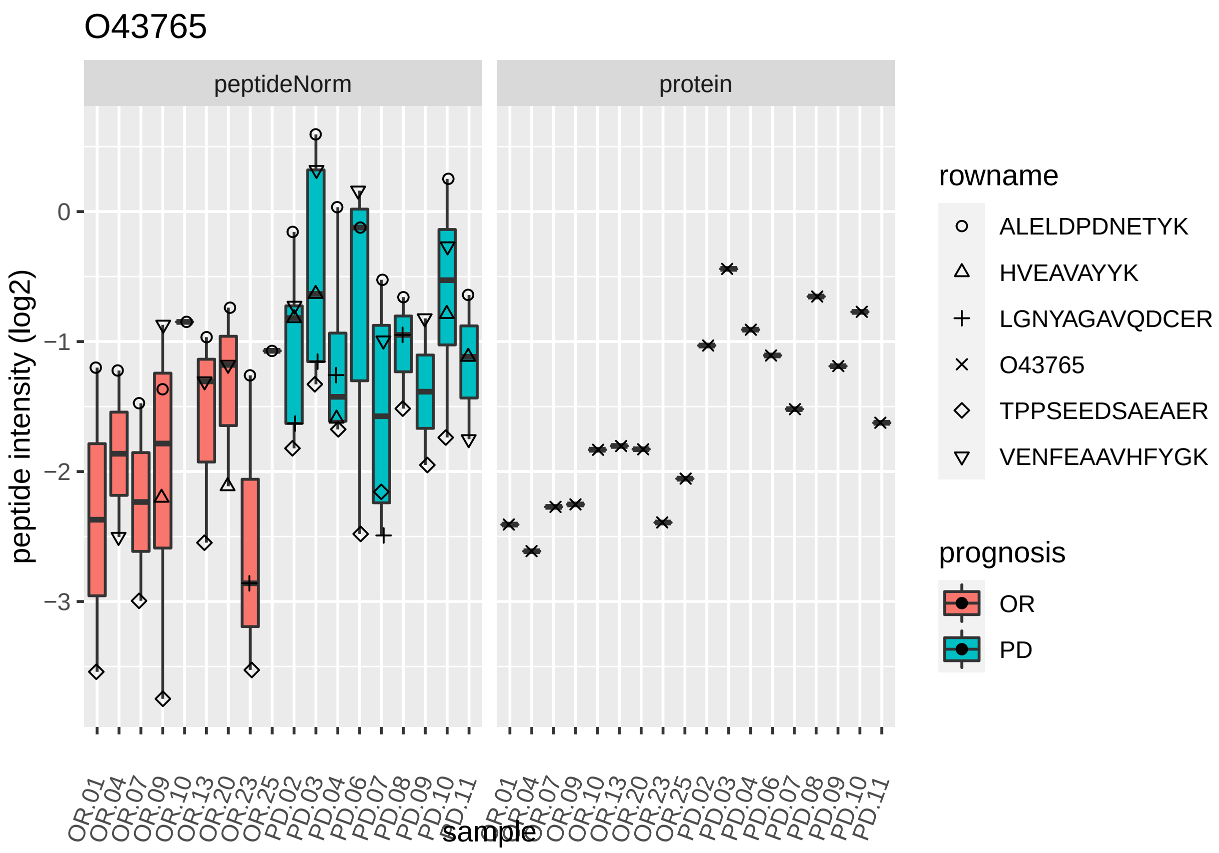

P09496
peptideNorm
protein
value
4
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

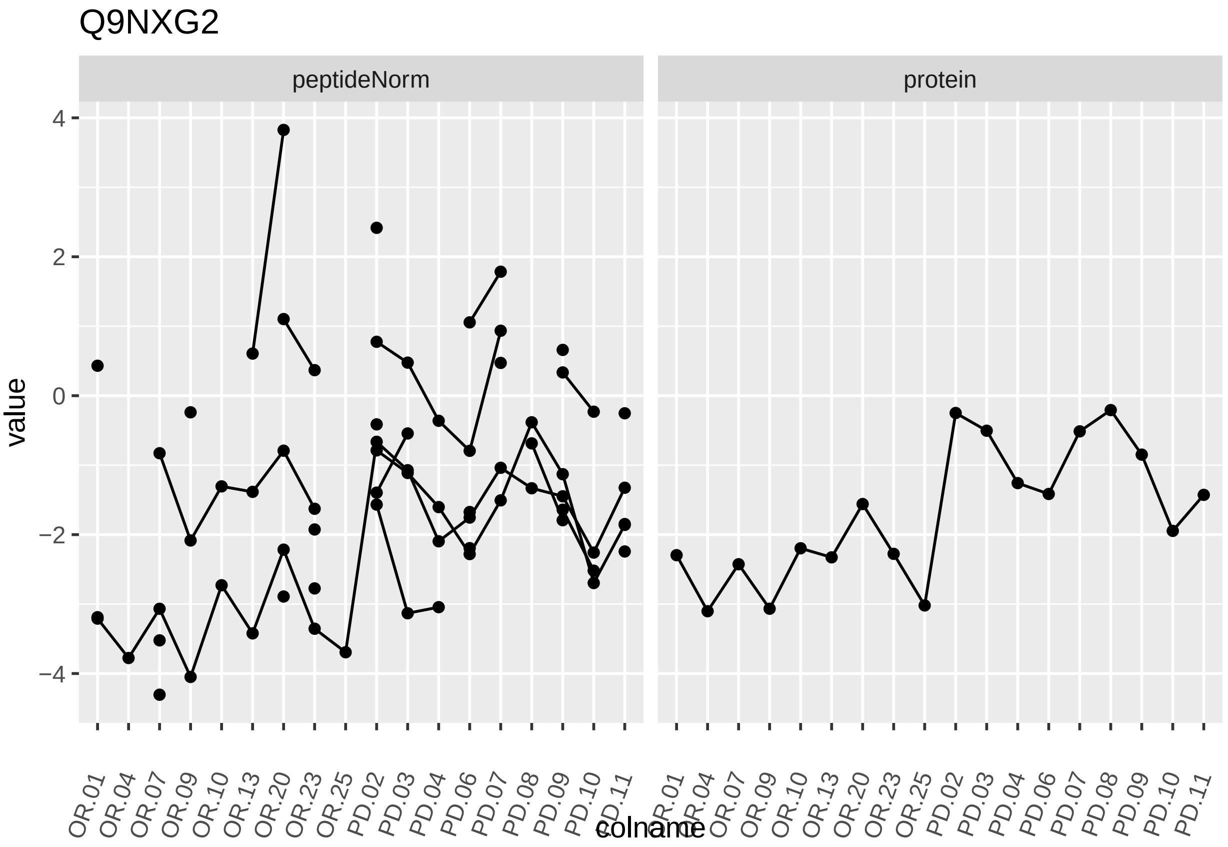

P09496
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ ELEEWYAR
△ LEALDANSR
+ LQSEPESIR
× LQSEPESIRK
◇ P09496
▽ WREEQMER
prognosis
OR
PD

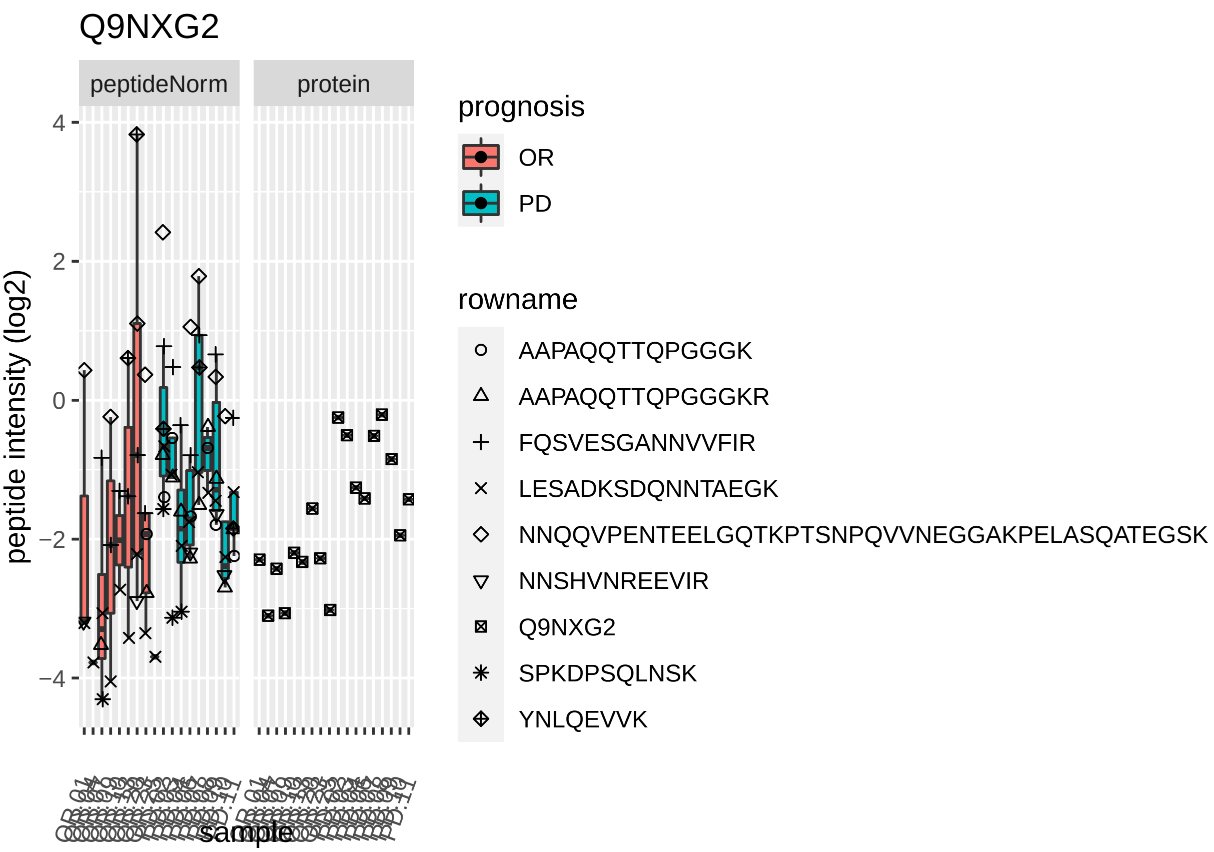

P30084
peptideNorm
protein
value
4
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

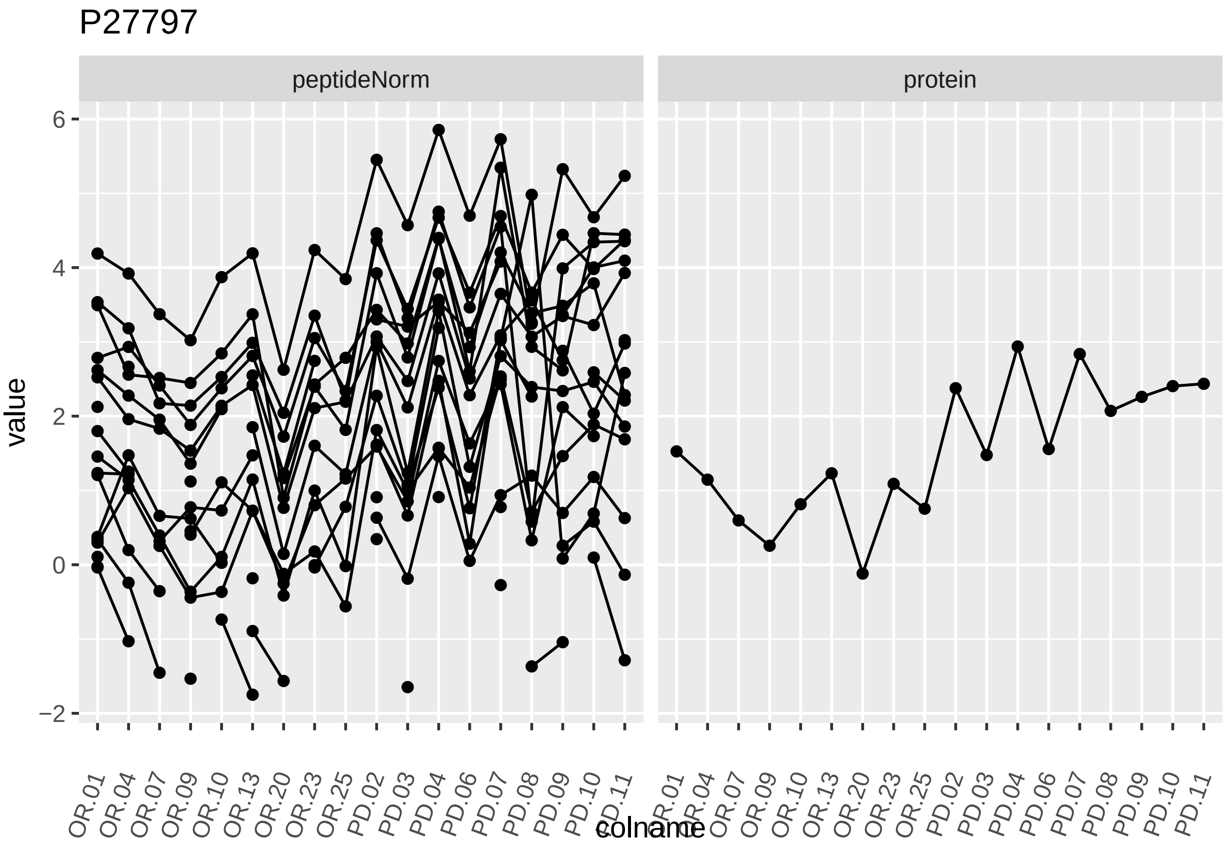

P30084
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AFAAGADIK
ALNALCDGLIDELNQALK
AQFAQPEILIGTIPGAGGTQR
EGMTAFVEK
EMQNLSFQDCYSSK
ESVNAAFEMTLTEGSK
GKNNTVGLIQLNRPK
ICPVETLVEEAIQCAEK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

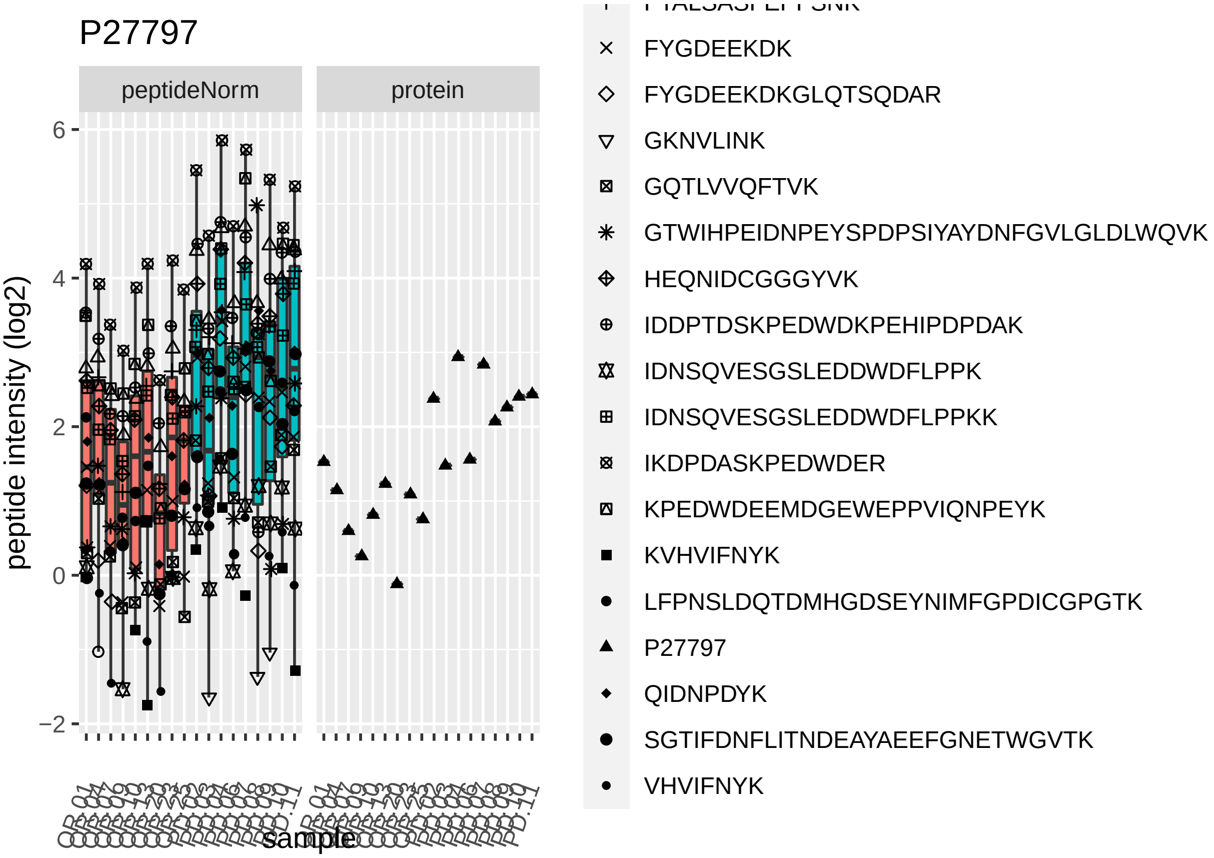

O43765
peptideNorm
protein
value
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

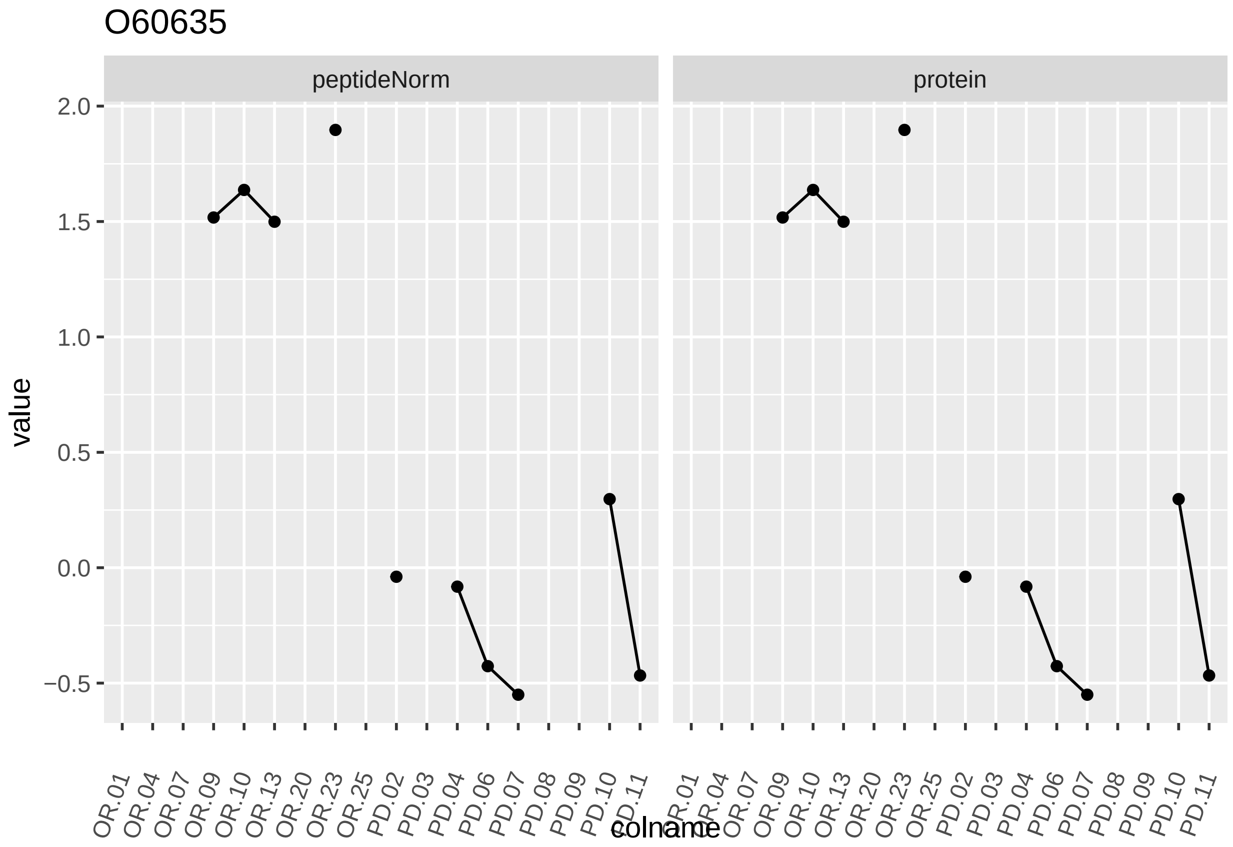

O43765
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ ALELDPDNETYK
△ HVEAVAYYK
+ LGNYAGAVQDCER
× O43765
◇ TPPSEEDSAEAER
▽ VENFEAAVHFYGK
prognosis
OR
PD

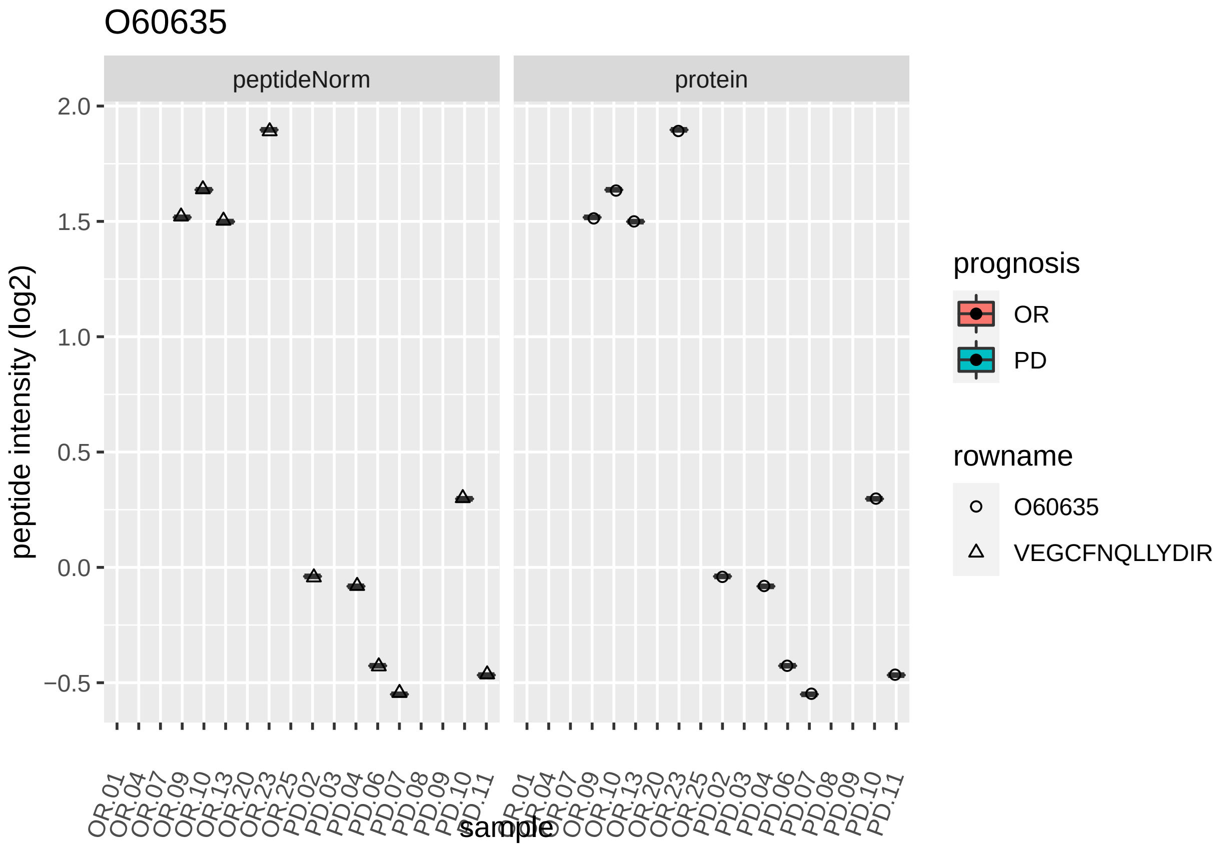

Q9NXG2
peptideNorm
protein
value
4
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

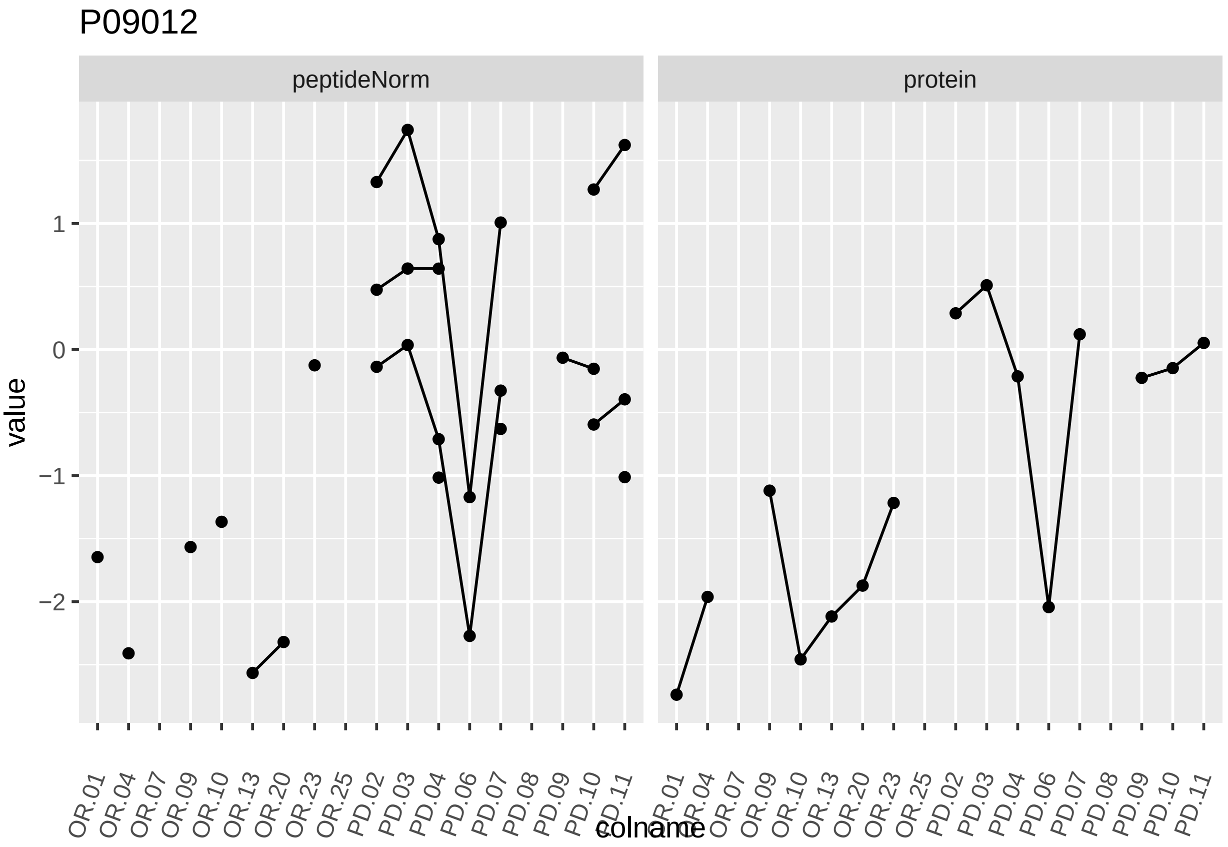

Q9NXG2
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
sample
prognosis
OR
PD
rowname
AAPAQQTTQPGGGK
AAPAQQTTQPGGGKR
FQSVESGANNVVFIR
LESADKSDQNNTAEGK
NNQQVPENTEELGQTKPTSNPQVVNEGGAKPELASQATEGSK
NNSHVNREEVIR
Q9NXG2
SPKDPSQLNSK
YNLQEVVK

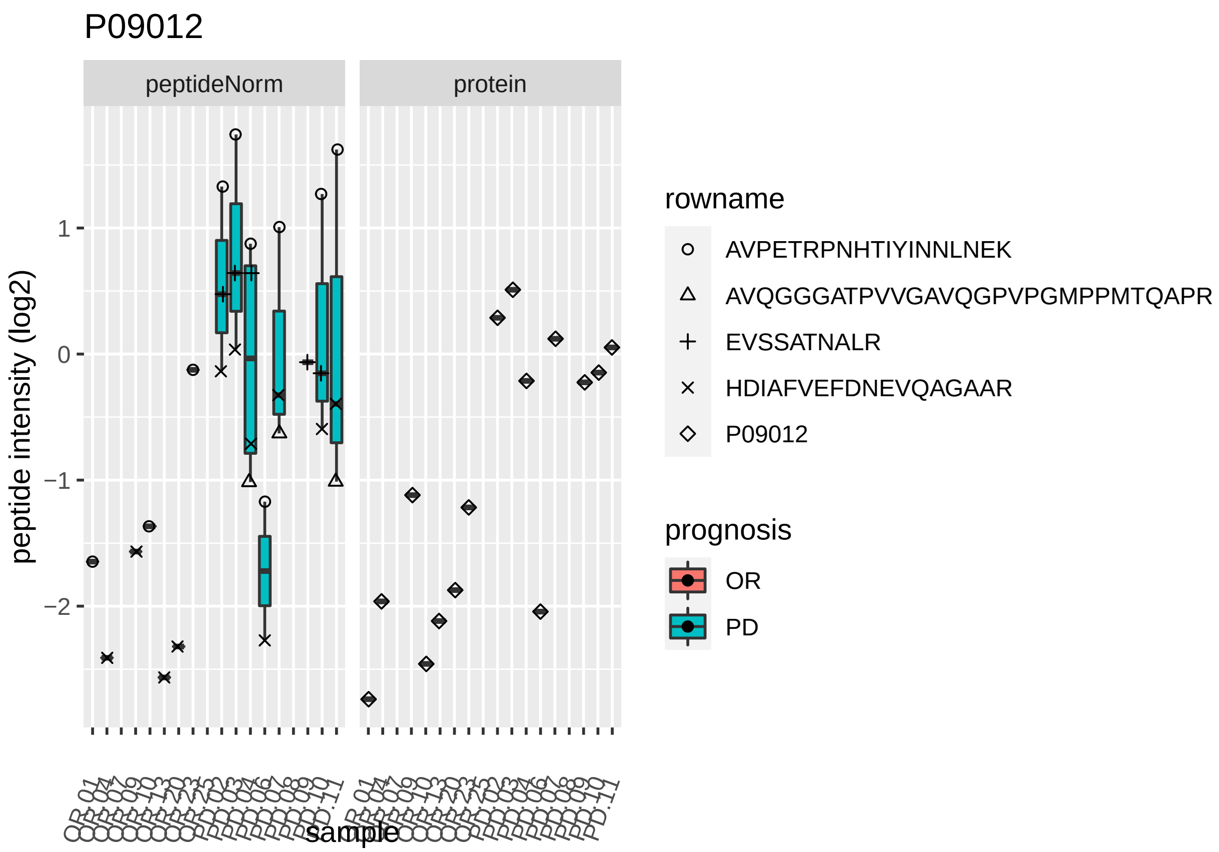

P27797
peptideNorm
protein
value
colname
6
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

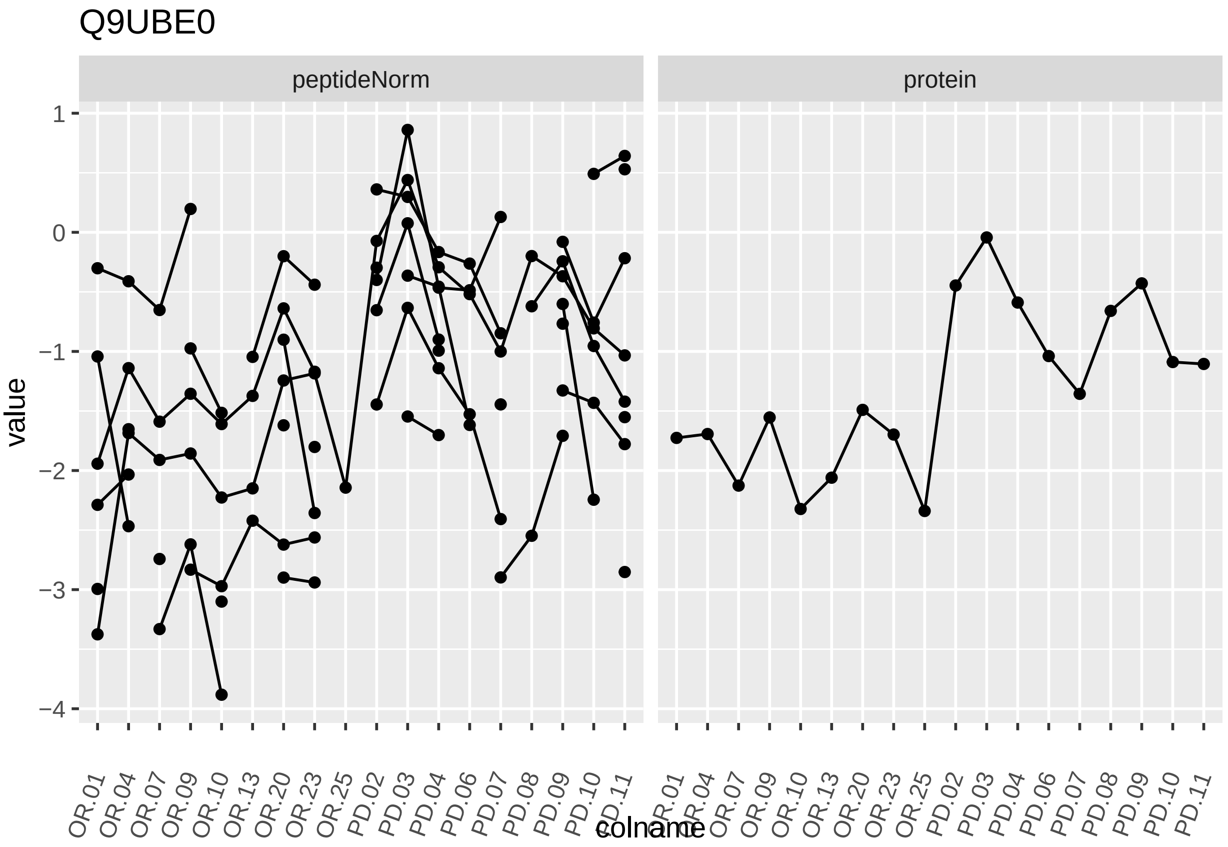

P27797
peptideNorm
protein
peptide intensity (log2)
6
4
2
0
−2
sample
× FYGDEEKDK
◇ FYGDEEKDKGLQTSQDAR
▽ GKNVLINK
⊠ GQTLVVQFTVK
✳ GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK
◈ HEQNIDCGGGYVK
⊕ IDDPTDSKPEDWDKPEHIPDPDAK
✡ IDNSQVESGSLEDDWDFLPPK
⊞ IDNSQVESGSLEDDWDFLPPKK
⊠ IKDPDASKPEDWDER
⊠ KPEDWDEEMDGEWEPPVIQNPEYK
■ KVHVIFNYK
● LFPNSLDQTDMHGDSEYNIMFGPDICGPGTK
▲ P27797
◆ QIDNPDYK
● SGTIFDNFLITNDEAYAEEFGNETWGVTK
• VHIFNYK

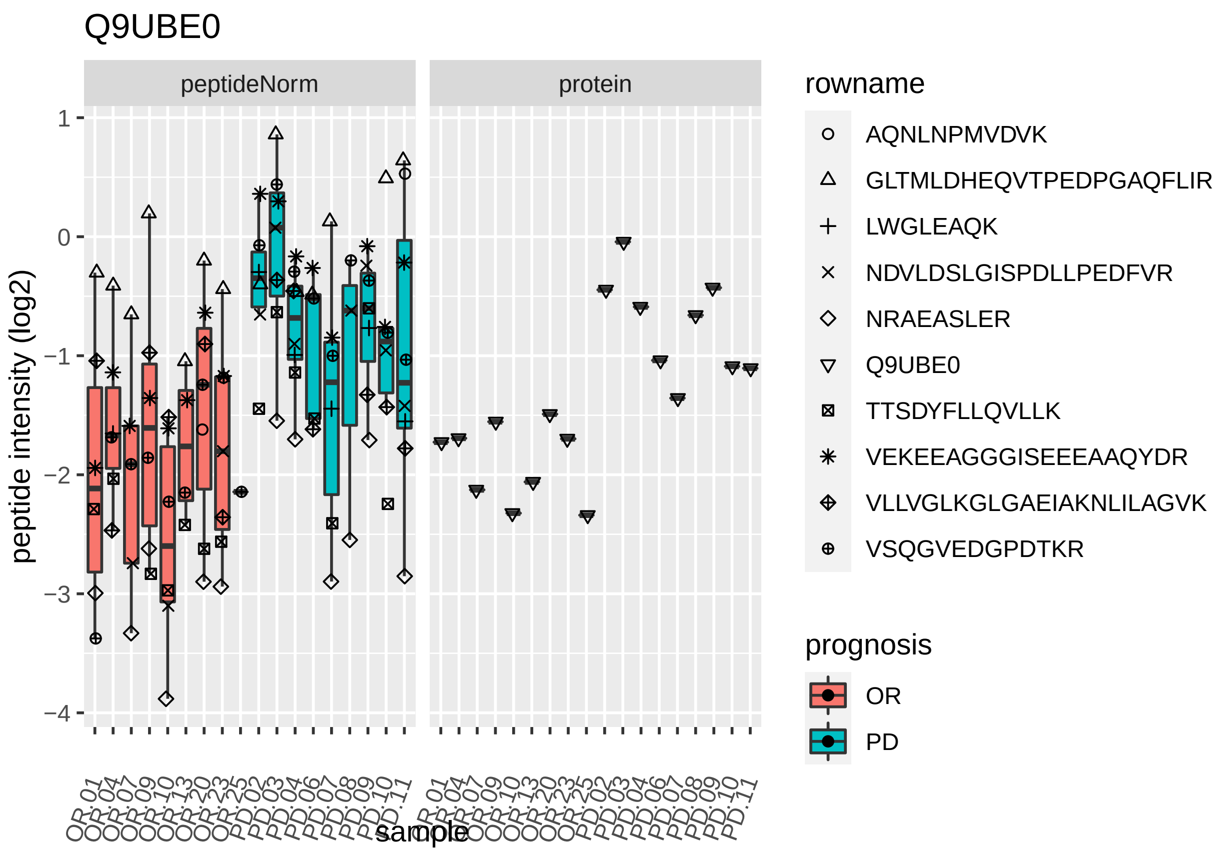

O60635
peptideNorm
protein
value
colname
2.0
1.5
1.0
0.5
0.0
−0.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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

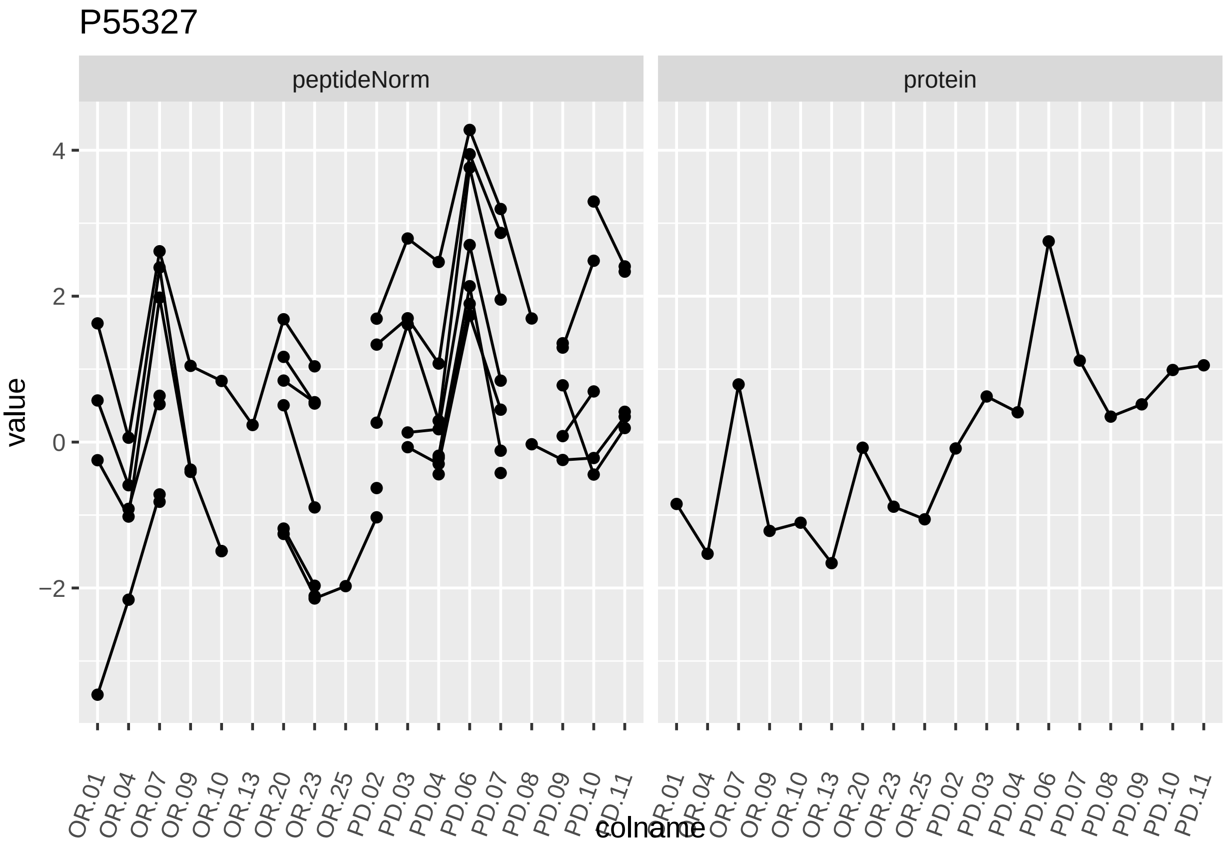

P09012
peptideNorm
protein
value
1
0
−1
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

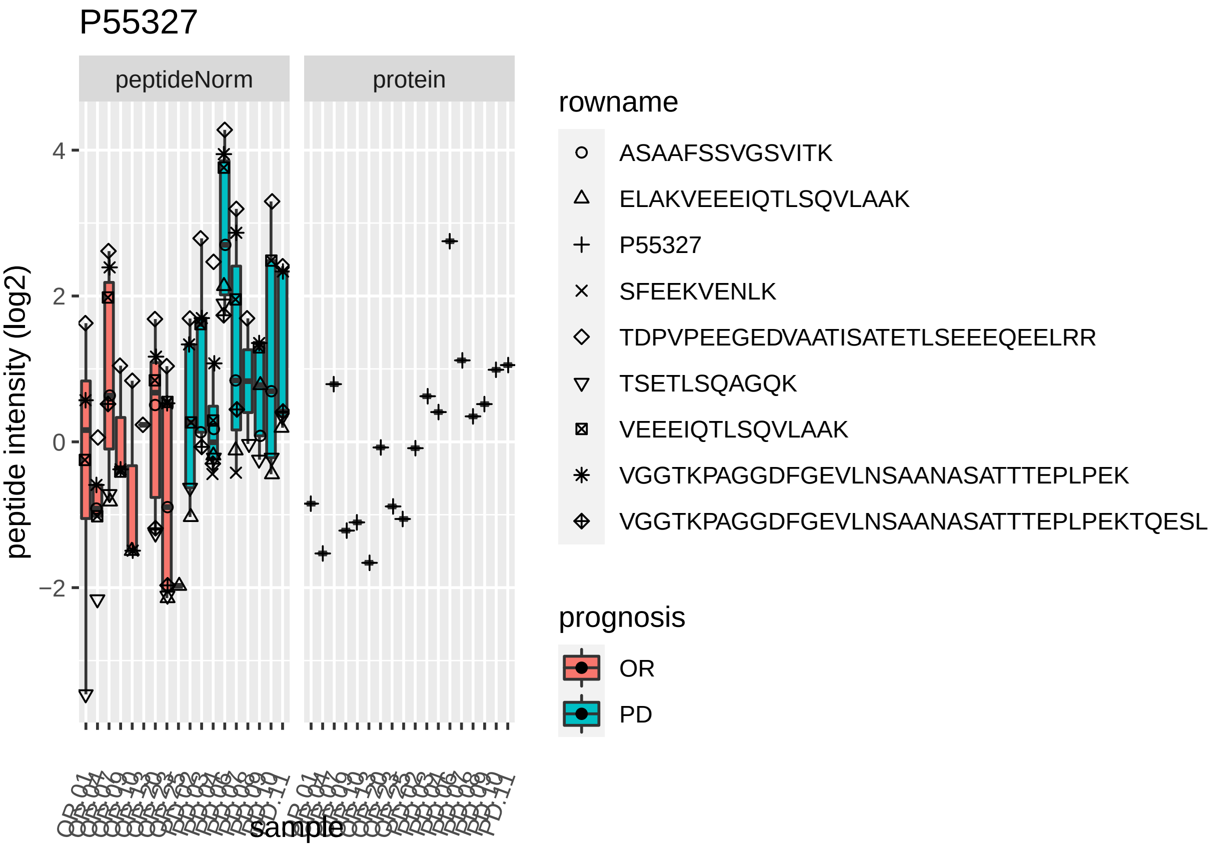

P09012
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.21
OR.23
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ AVPETRPNHTIYINNLNEK
△ AVQGGGATPVVGAVQGPVPGMPPMTQAPR
+ EVSSATNALR
× HDIAFVEFDNEVQAGAAR
◇ P09012
prognosis
OR
PD

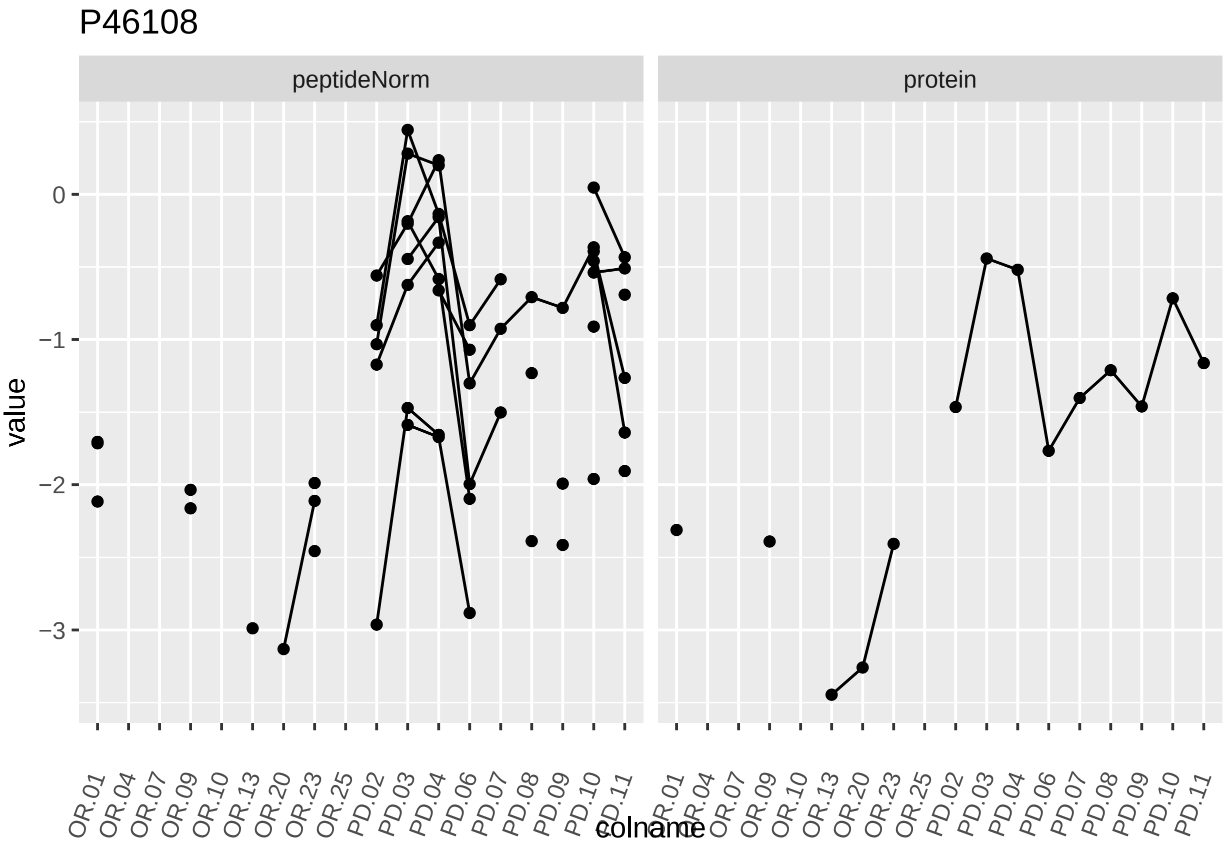

Q9UBE0
peptideNorm
protein
value
1
0
−1
−2
−3
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

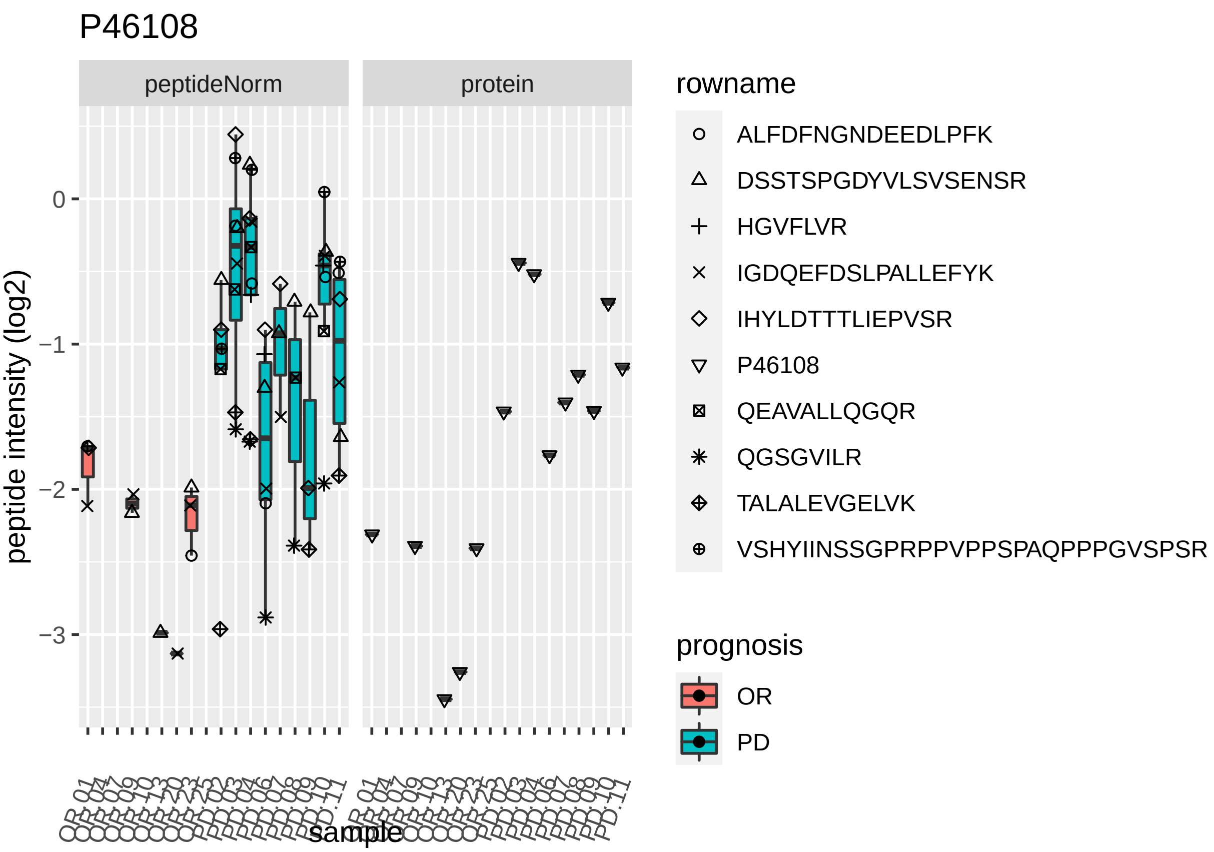


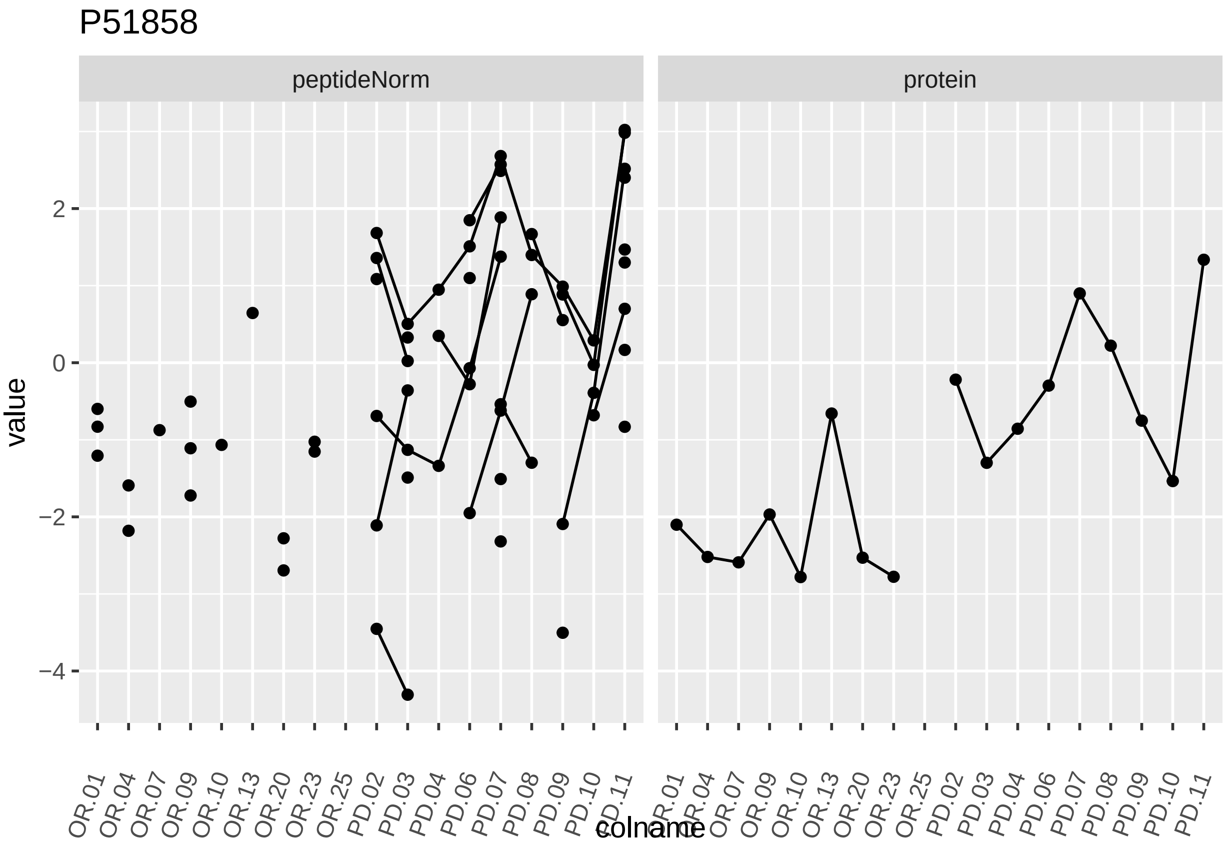
Q9UBE0
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AQNLNPMVDVK
GLTMLDHEQVTPEDPGAQFLIR
LWGLEAQK
NDVLDSLGISPDLLPEDFVR
NRAEASLER
Q9UBE0
TTSDYFLLQVLLK
VEKEEAGGGISEEEAAQYDR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

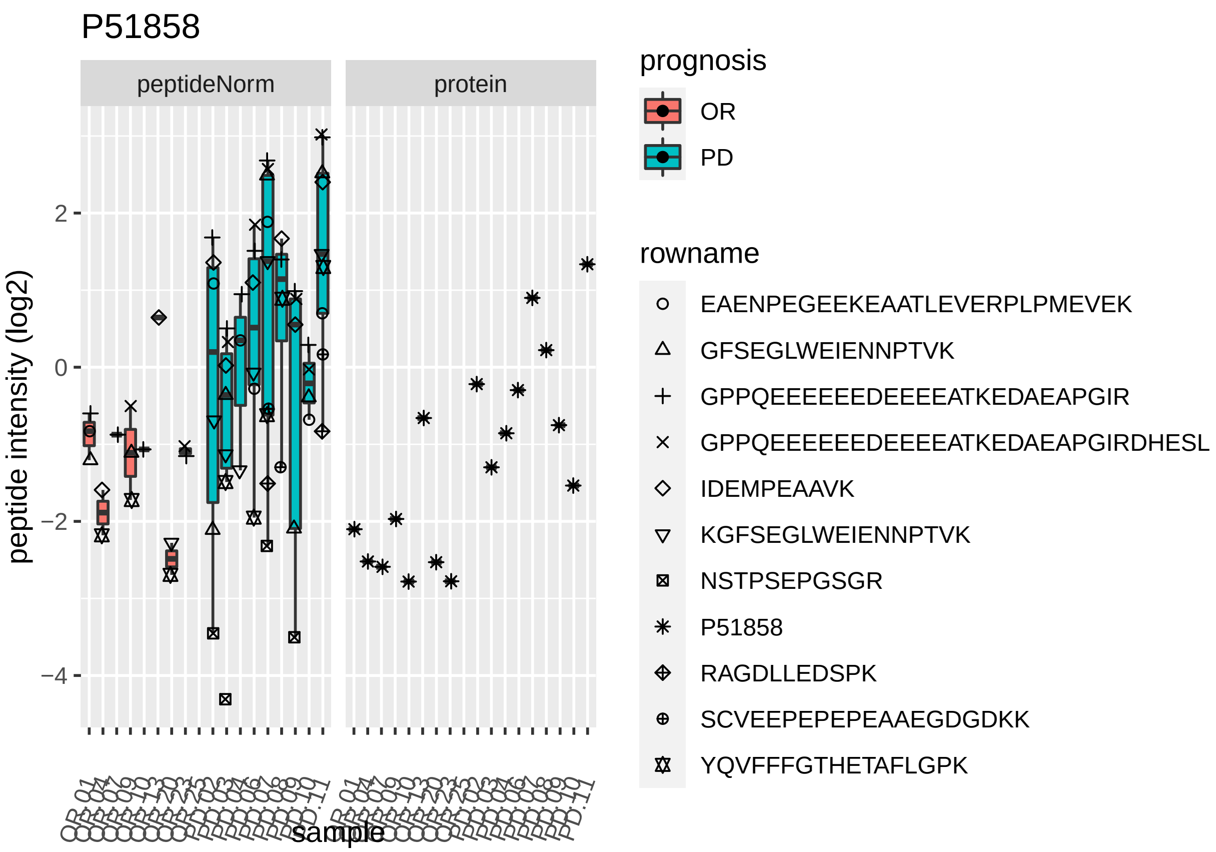

P55327
peptideNorm
protein
value
4
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

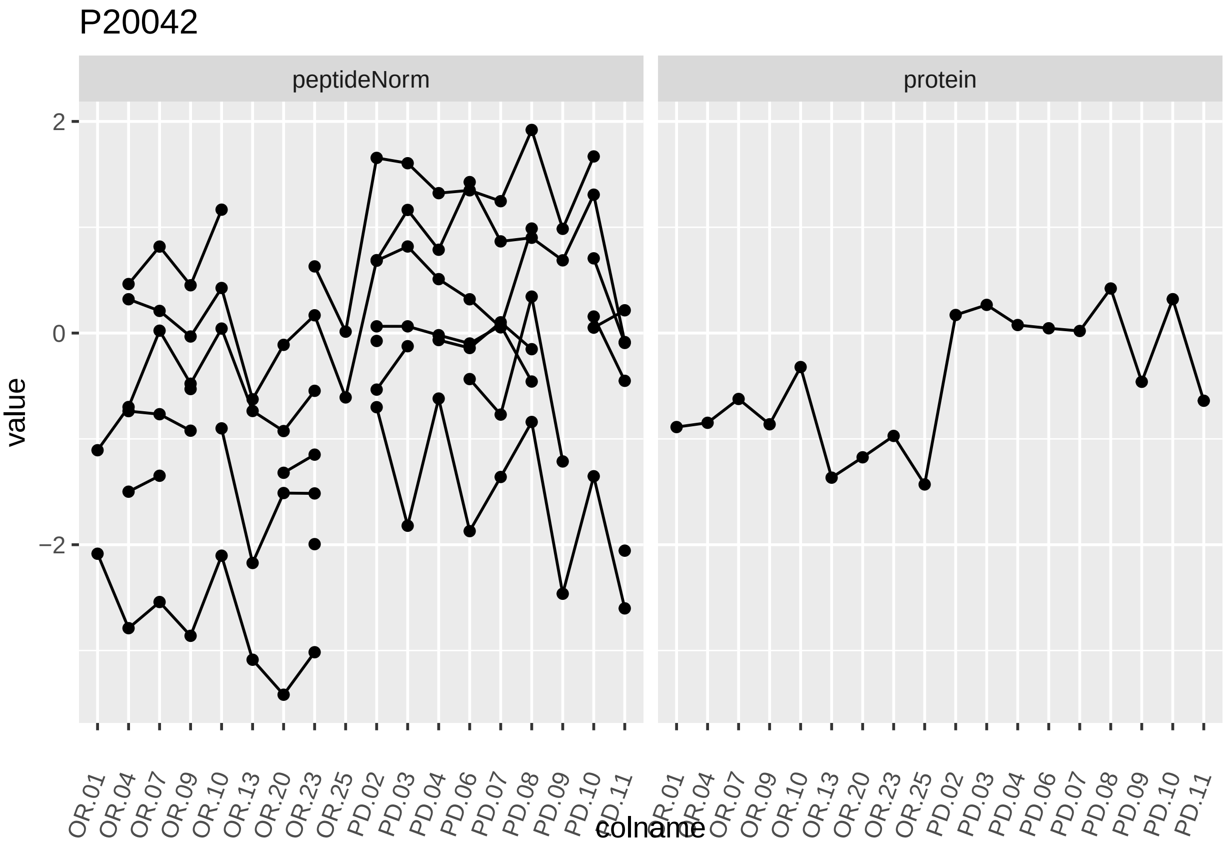

P55327
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
sample
rowname
○ ASAAFSSVGSVITK
△ ELAKVEEEIQTLSQVLAAK
+ P55327
× SFEEKVENLK
◇ TDPVPEEGEDVAATISATETLSEEEQEELRR
▽ TSETLSQAGQK
⊠ VEEEIQTLSQVLAAK
✳ VGGTKPAGGDFGEVLNSAANASATTTEPLPEK
⊕ VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL
prognosis
🟥 OR
🟦 PD


P46108
peptideNorm
protein
value
0
−1
−2
−3
colname
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


P46108
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
ALFDFNGNDEEDLPFK
DSSTSPGDYVLSVSENSR
HGVFLVR
IGDQEFDSLPALLEFYK
IHYLDTTTLIEPVSR
P46108
QEAVALLQGQR
QGSGVILR
TALALEVGELVK
VSHYIINSSGPRPPVPPSPAQPPPGVSPSR
prognosis
OR
PD


P51858
peptideNorm
protein
value
2
0
−2
−4
colname
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


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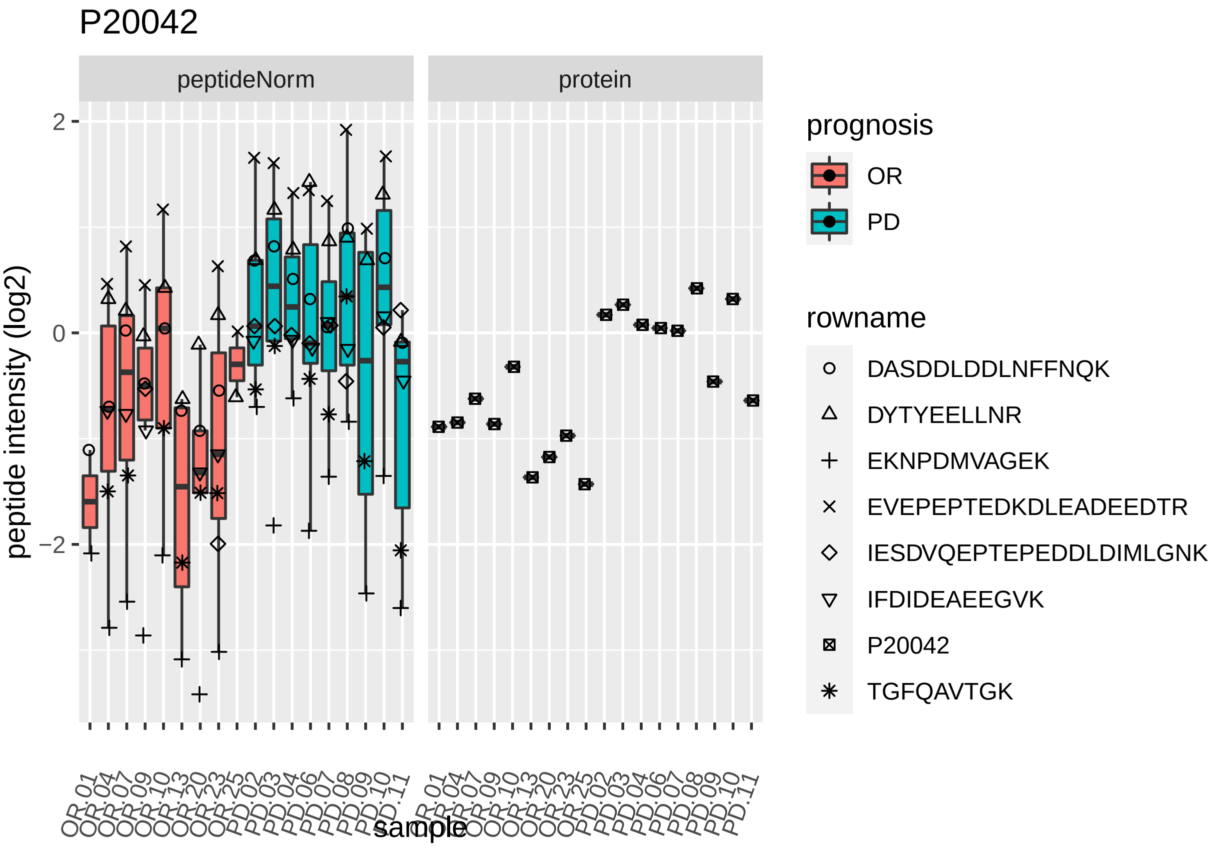
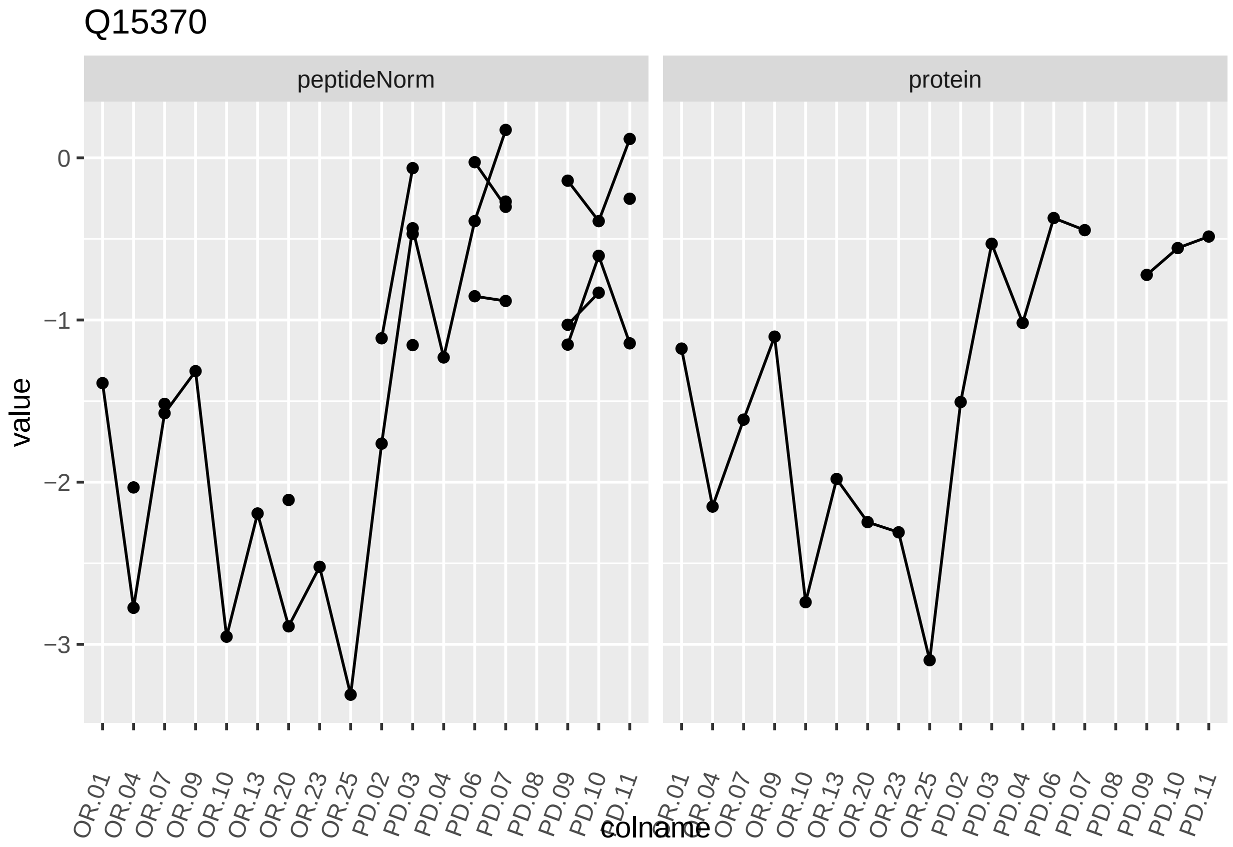
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P20042
peptideNorm
protein
2
0
−2
peptide intensity (log2)
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
prognosis
OR
PD
rowname
DASDDLDDLNFFNQK
DYTYEELLNR
EKNPDMVAGEK
EVEPEPTEDKDLEADEEDTR
IESDVQEPTEPEDDLDIMLGNK
IFDIDEAEEGVK
P20042
TGFQAVTGK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peptideNorm
protein
value
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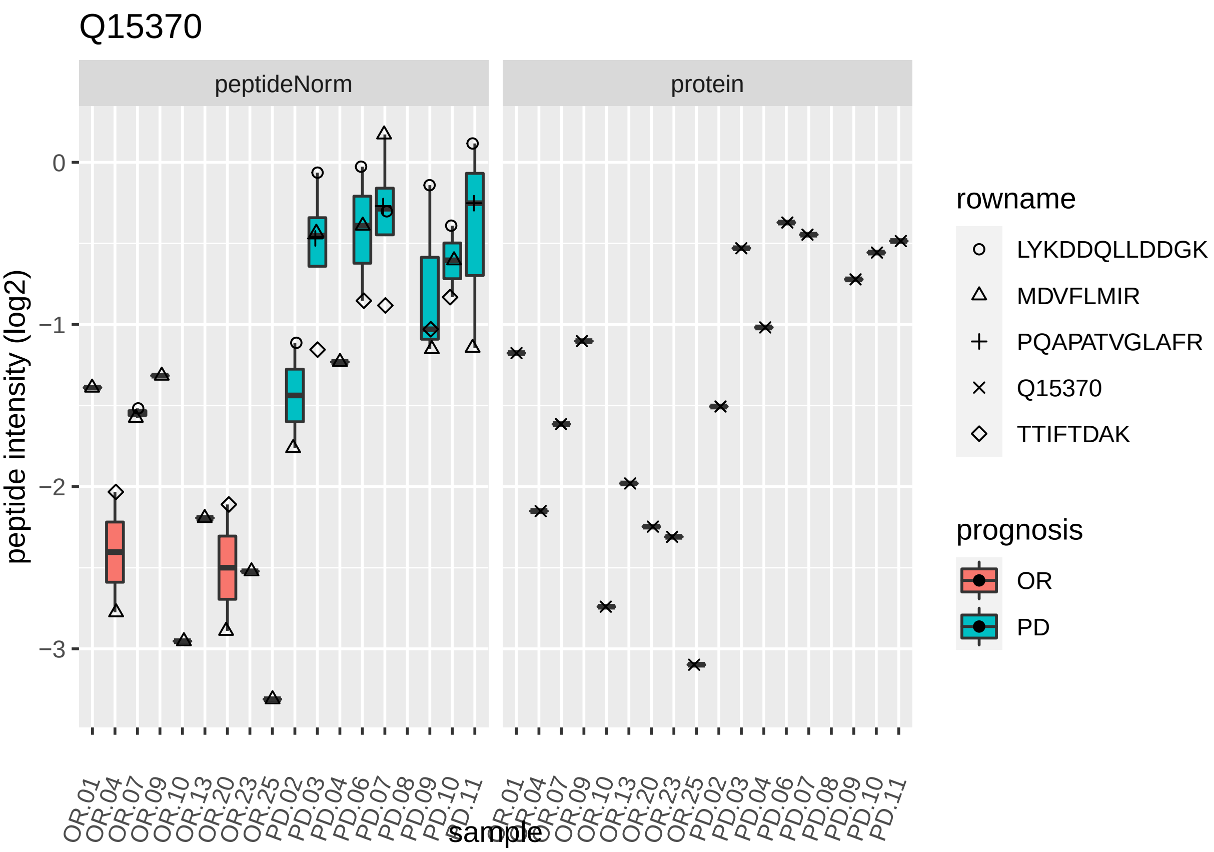
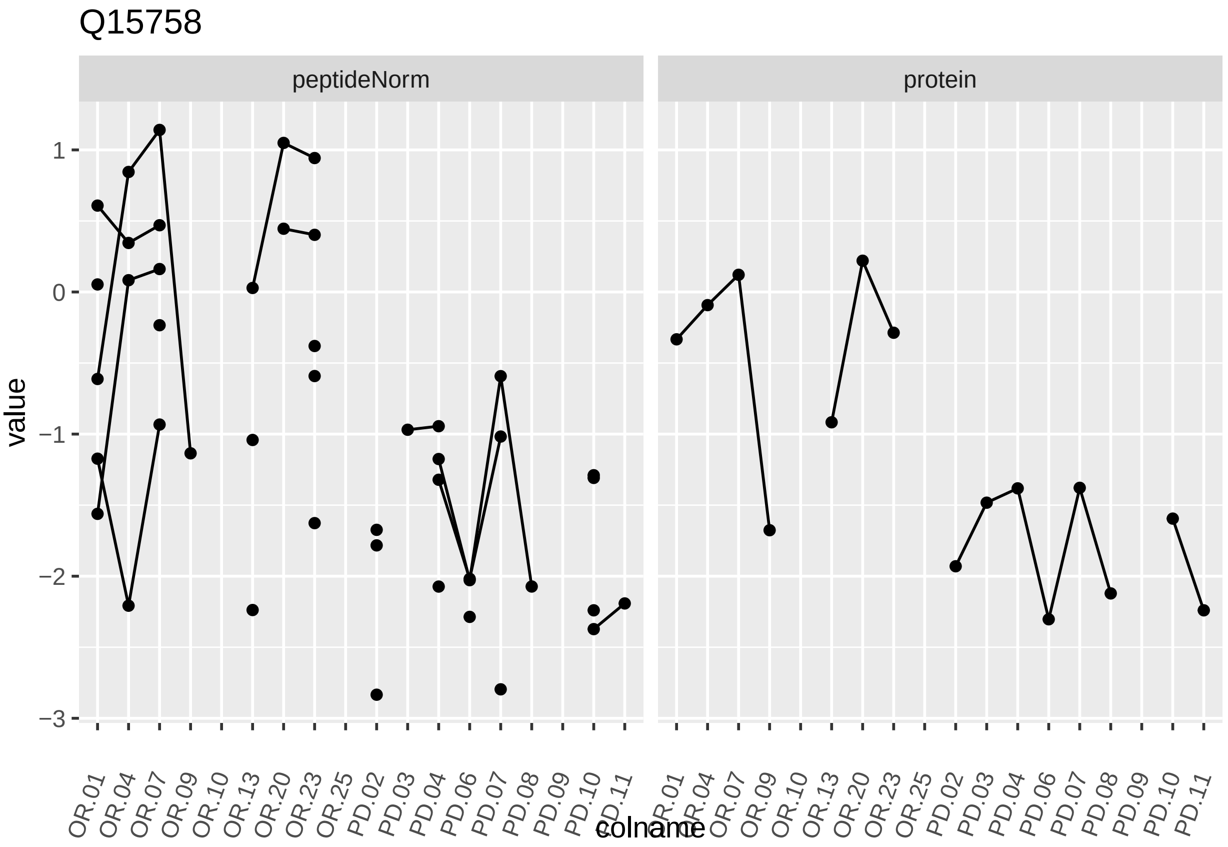
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q15370
peptideNorm
protein
0
−1
−2
−3
peptide intensity (log2)
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
○ LYKDDQLLDDGK
△ MDVFLMIR
+ PQAPATVGLAFR
× Q15370
◇ TTIFTDAK
prognosis
OR
PD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protein
value
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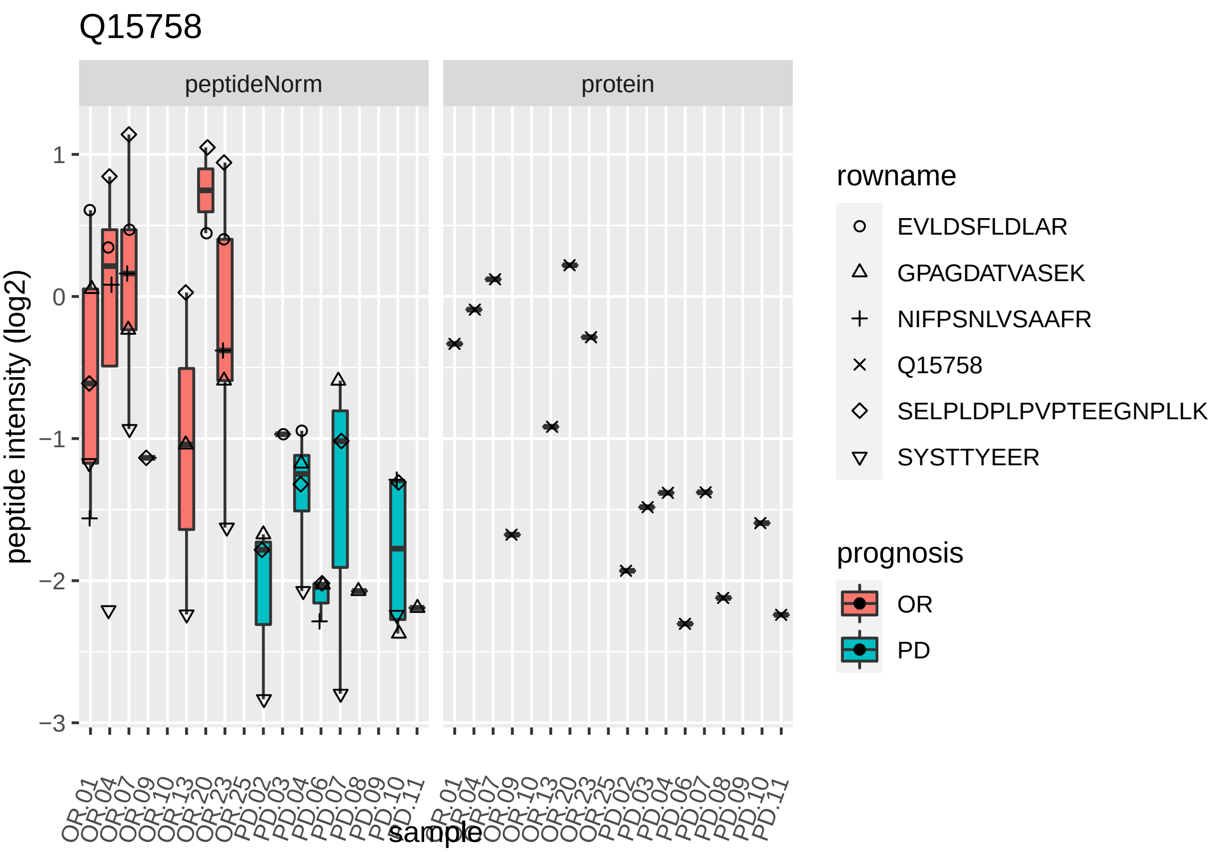
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q15758
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
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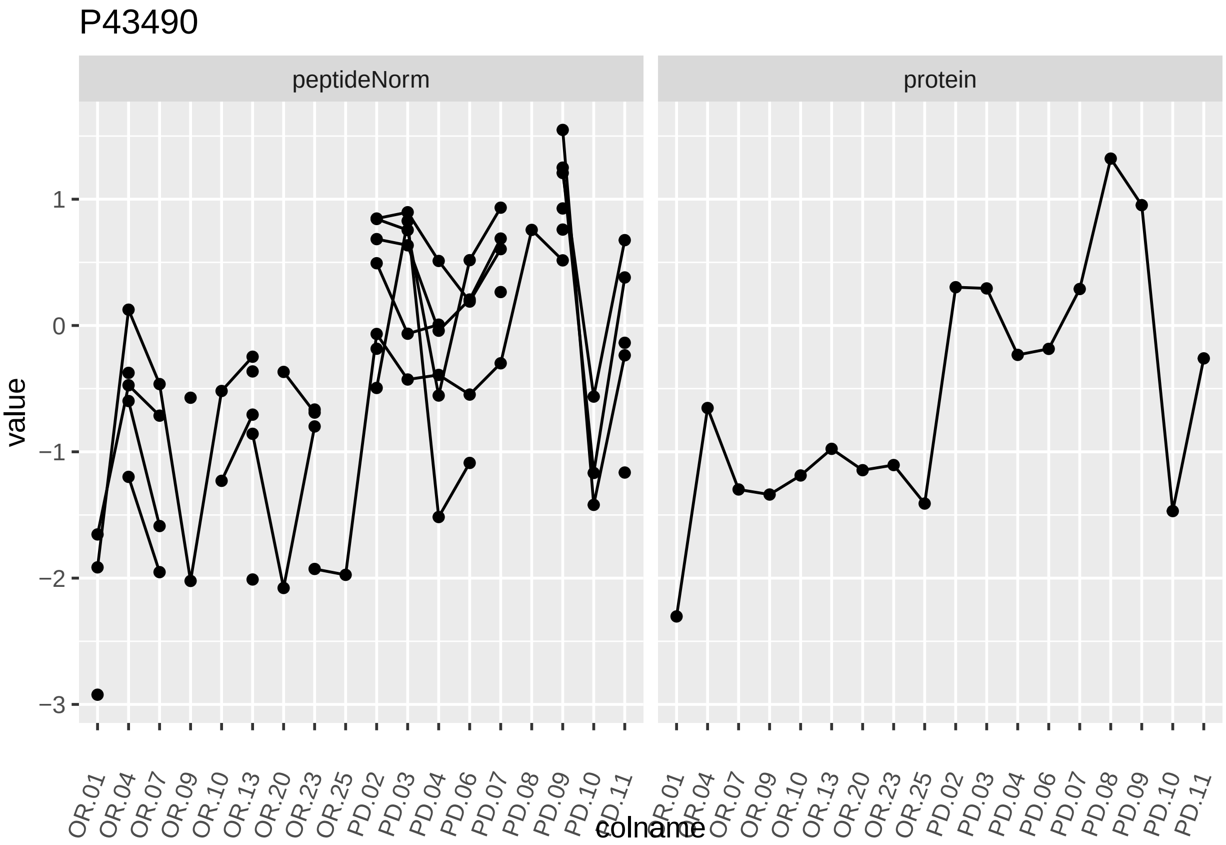
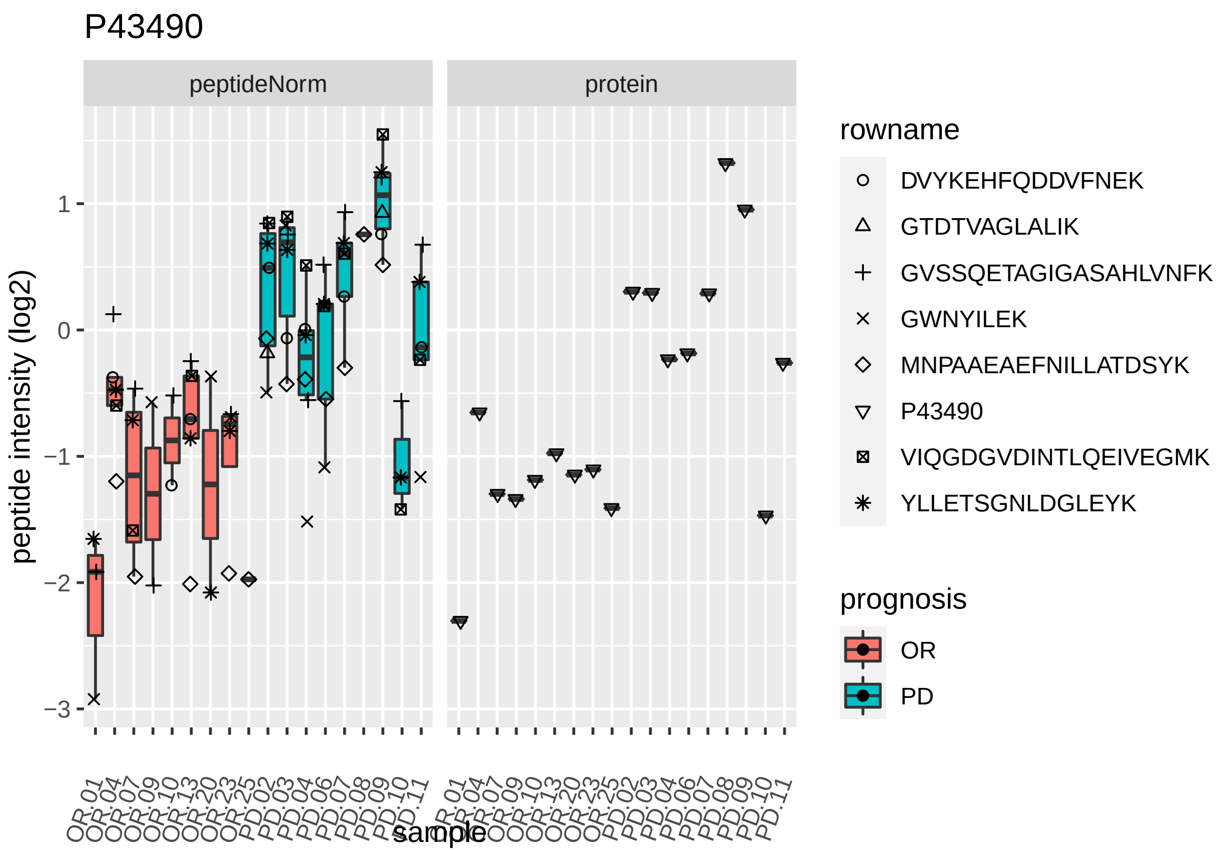
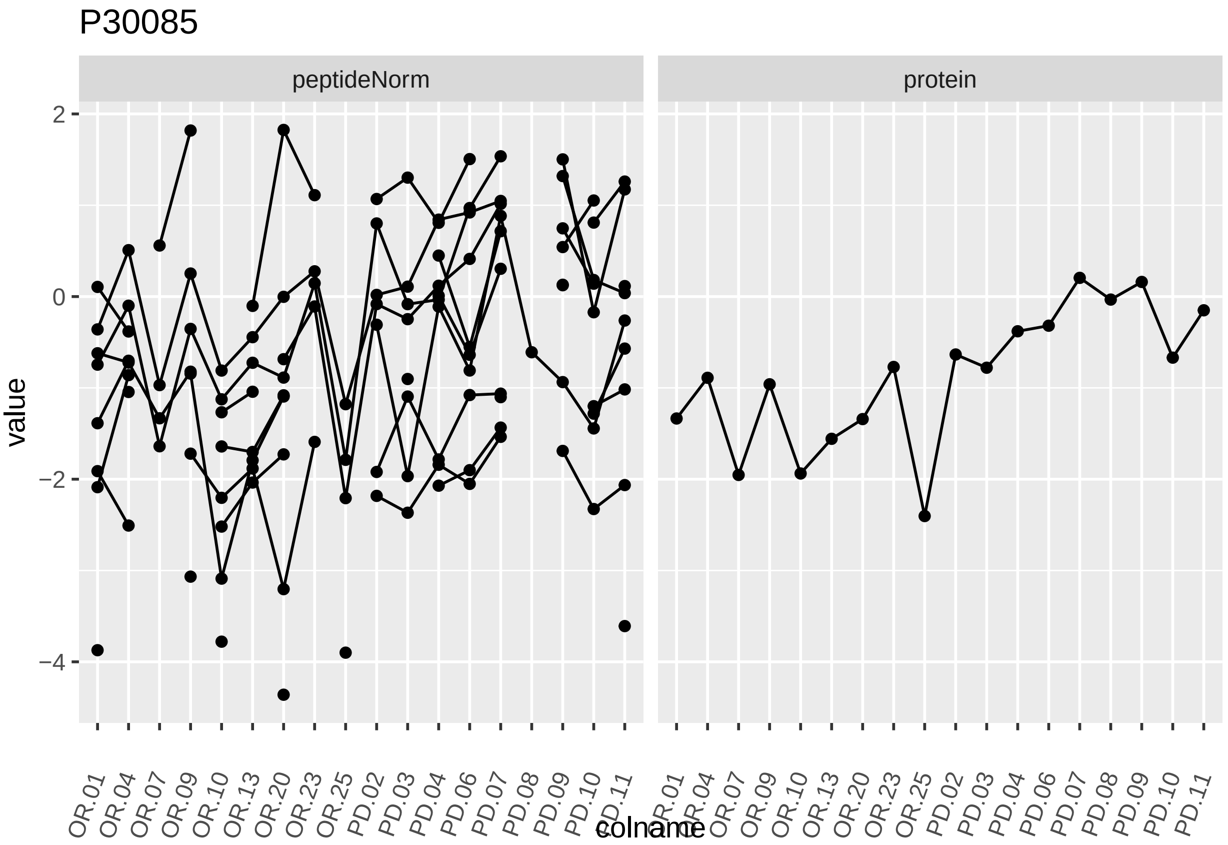
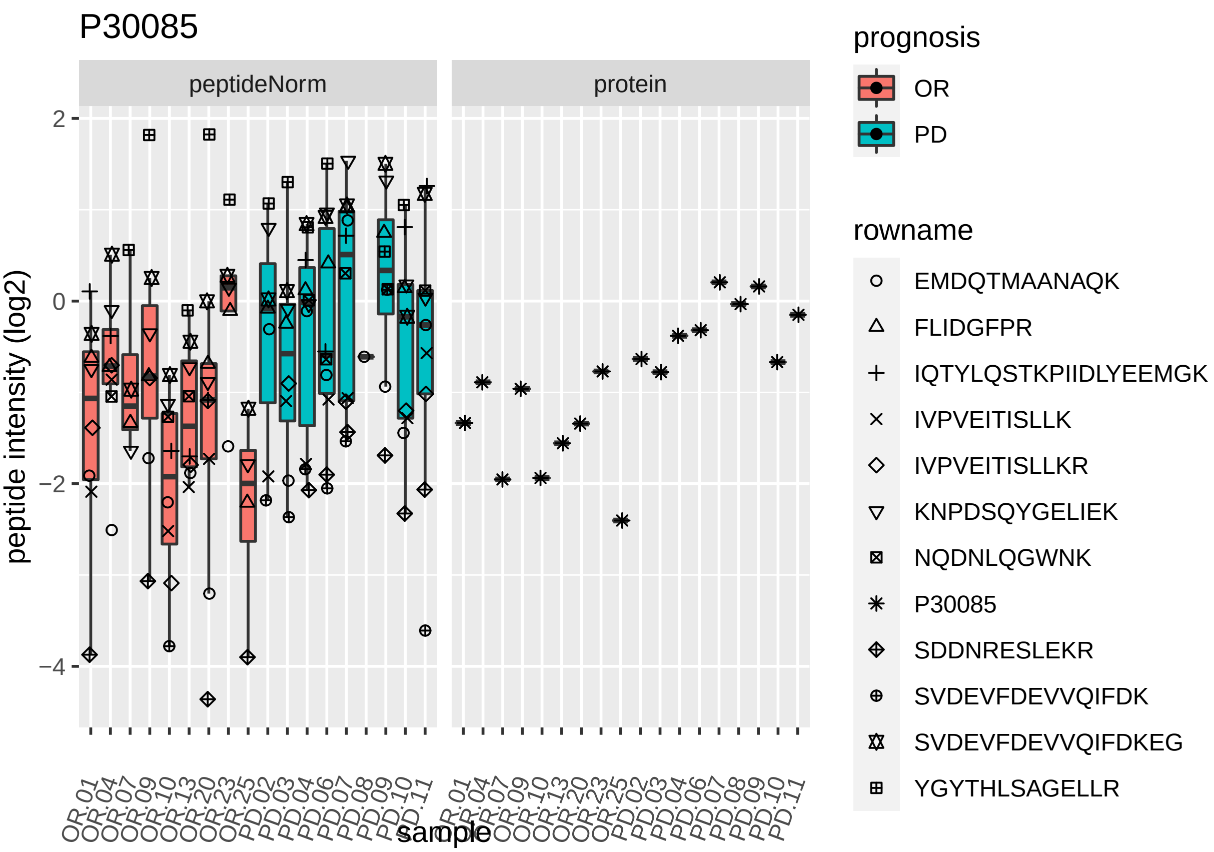
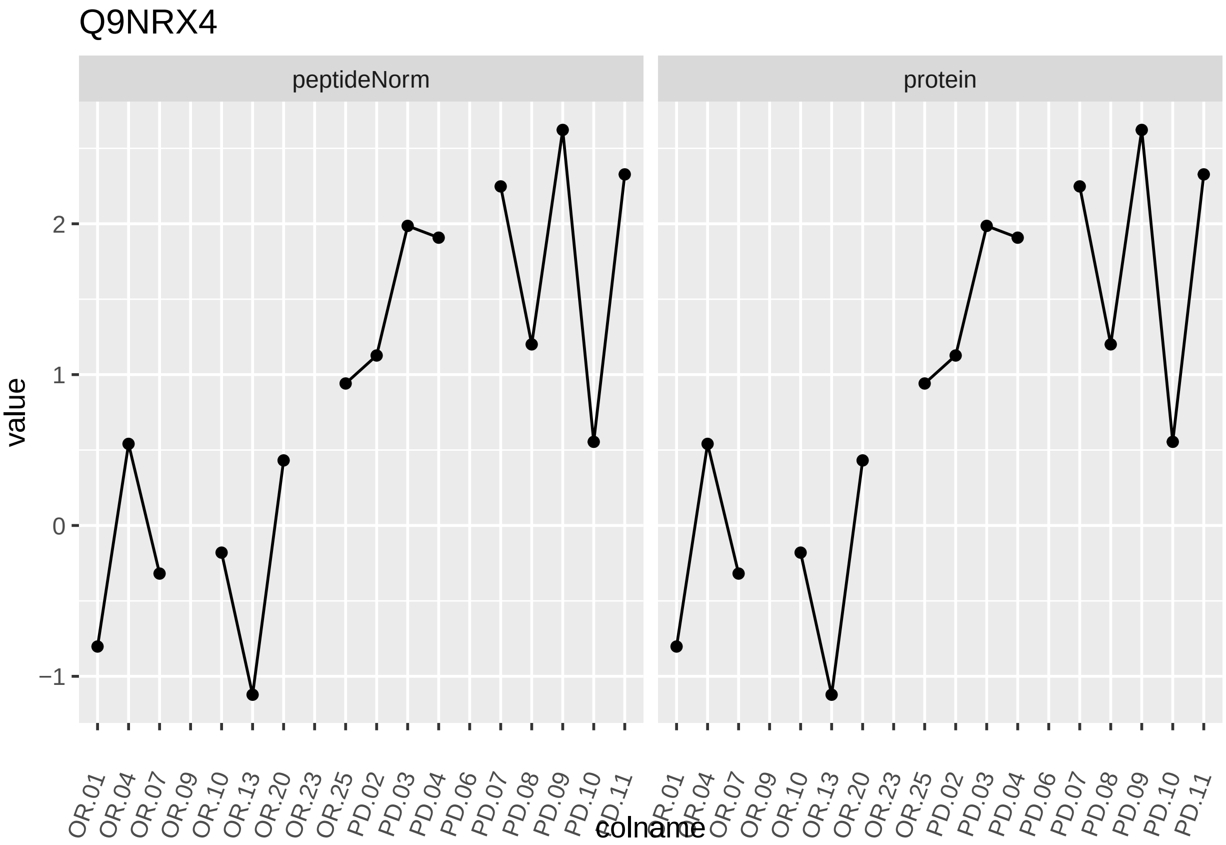
GPAGDATVASEK
NIFPSNLVSAAFR
Q15758
SELPLDPLPVPTEEGNPLLK
SYSTTYEER
prognosis
OR
PD

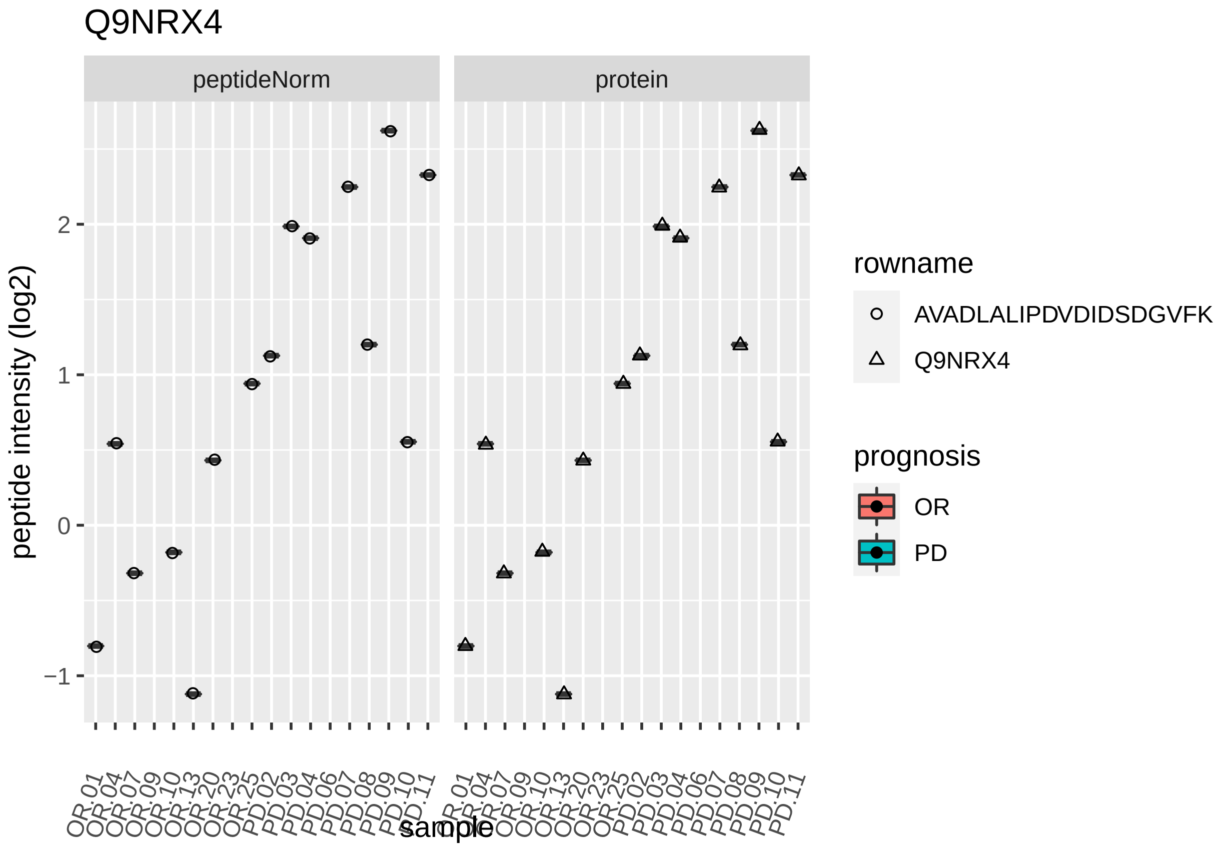

P43490
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

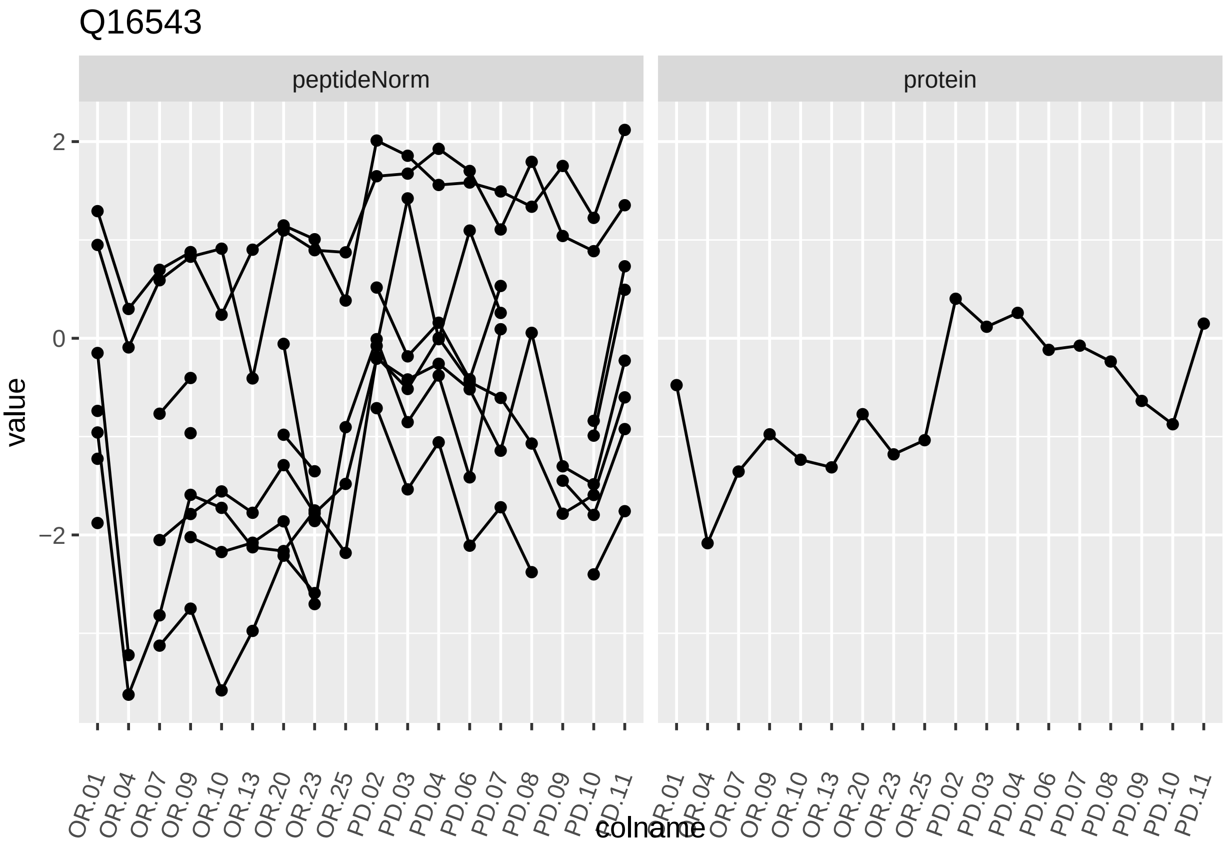

P43490
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
DVYKEHFQDDVFNEK
GTDTVAGLALIK
GVSSQETAGIGASAHLVNFK
GWNYILEK
MNPAAEAEFNILLATDSYK
P43490
VIQGDGVDINTLQEIVEGMK
YLLETSGNLDGLEYK
prognosis
OR
PD


P30085
peptideNorm
protein
value
2
0
−2
−4
colname
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


P30085
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
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
prognosis
OR
PD
rowname
EMDQTMAANAQK
FLIDGFPR
IQTYLQSTKPIIDLYEEMGK
IVPVEITISLLK
IVPVEITISLLKR
KNPDSQYGELIEK
NQDNLQGWNK
P30085
SDDNRESLEKR
SVDEVFDEVVQIFDK
SVDEVFDEVVQIFDKEG
YGYTHLSAGELLR


Q9NRX4
peptideNorm
protein
value
2
1
0
−1
colname
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


Q9NRX4
peptideNorm
protein
peptide intensity (log2)
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
○ AVADLALIPDVDIDSDGVFK
△ Q9NRX4
prognosis
OR
PD


Q16543
peptideNorm
protein
value
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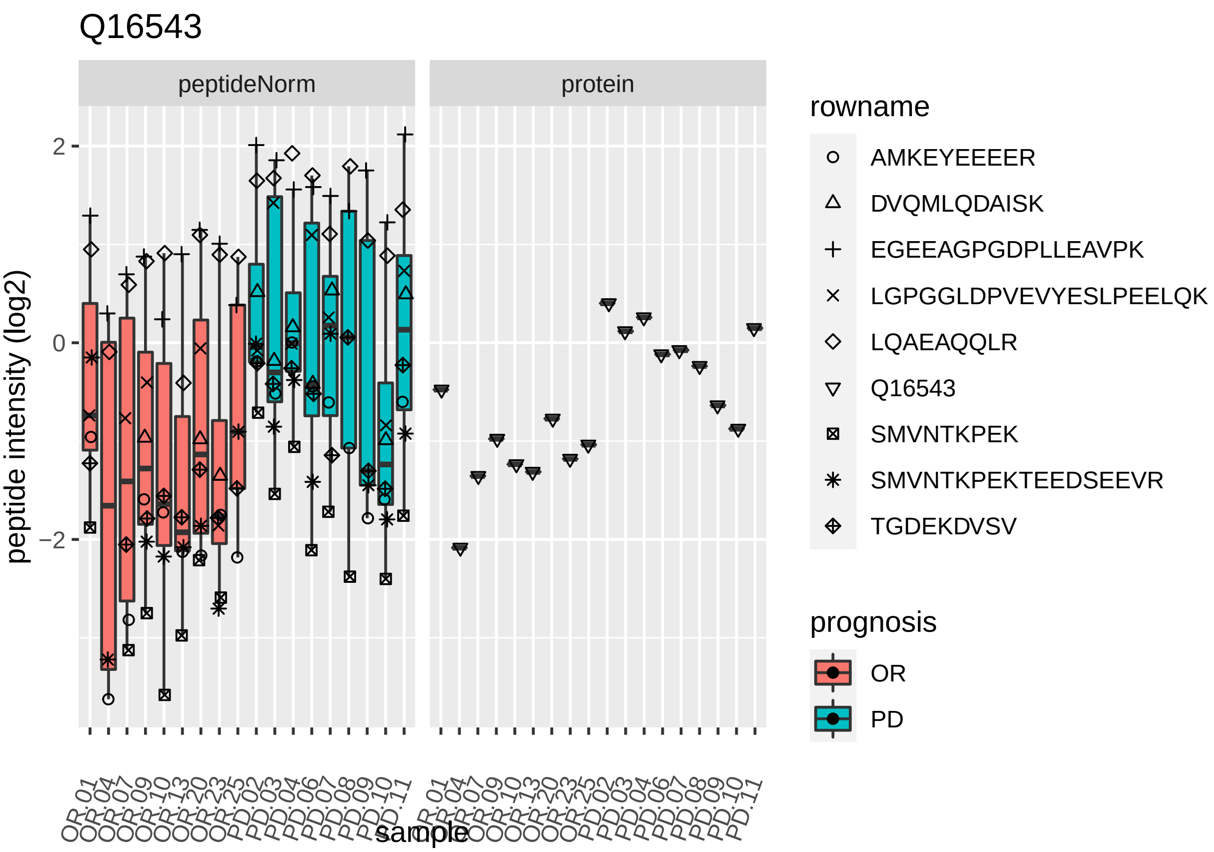
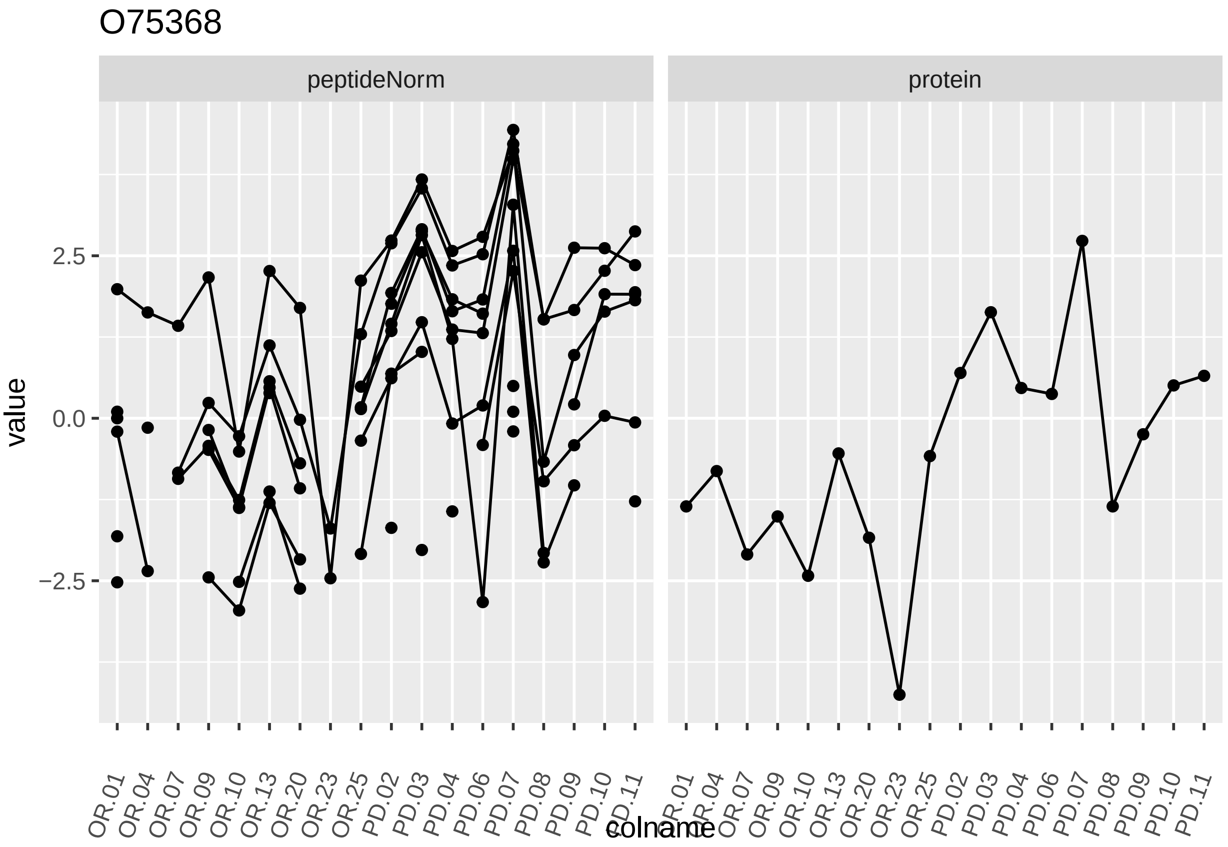
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q16543
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
AMKEYEEEER
DVQMLQDAISK
EGEEAGPGDPLLEAVPK
LGPGGLDPVEVYESLPEELQK
LQAEAQQLR
Q16543
SMVNTKPEK
SMVNTKPEKTEEDSEEVR
TGDEKDVSV
prognosis
OR
PD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peptideNorm
protein
value
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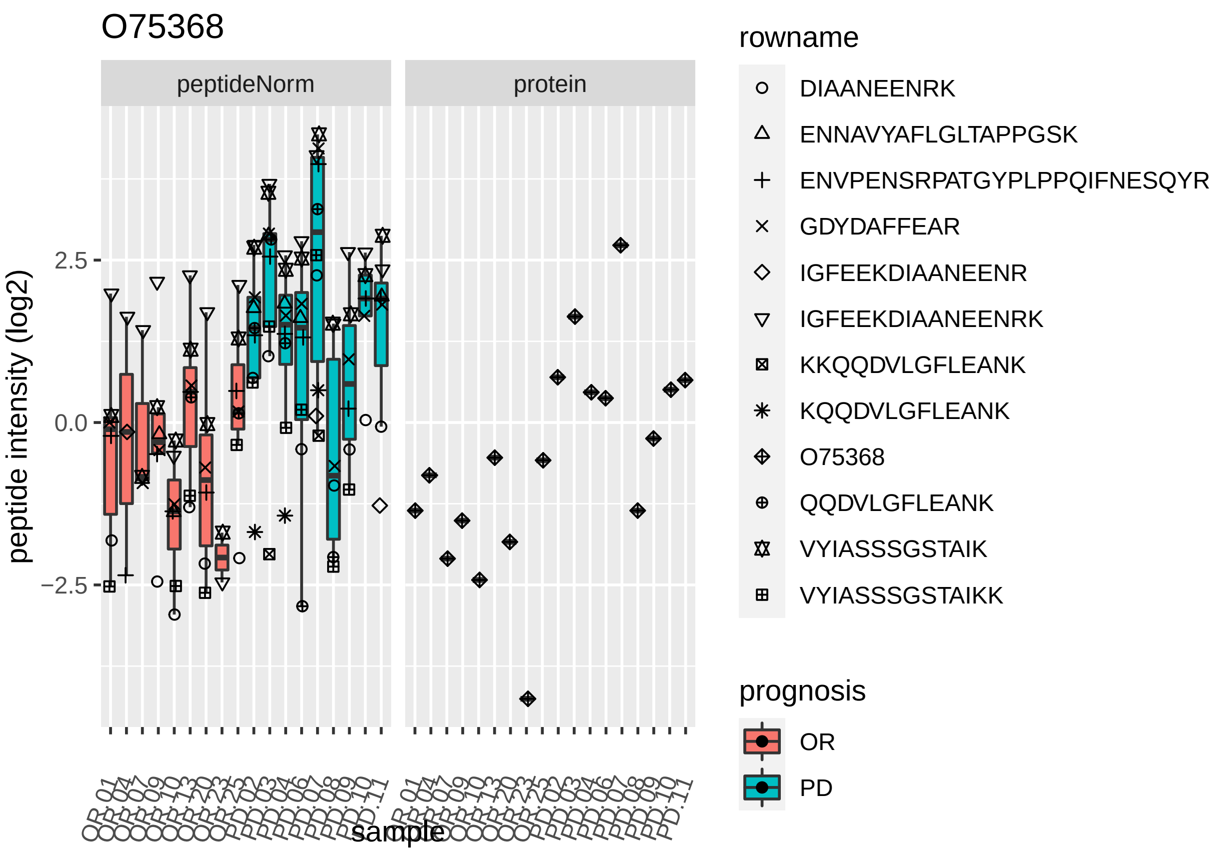
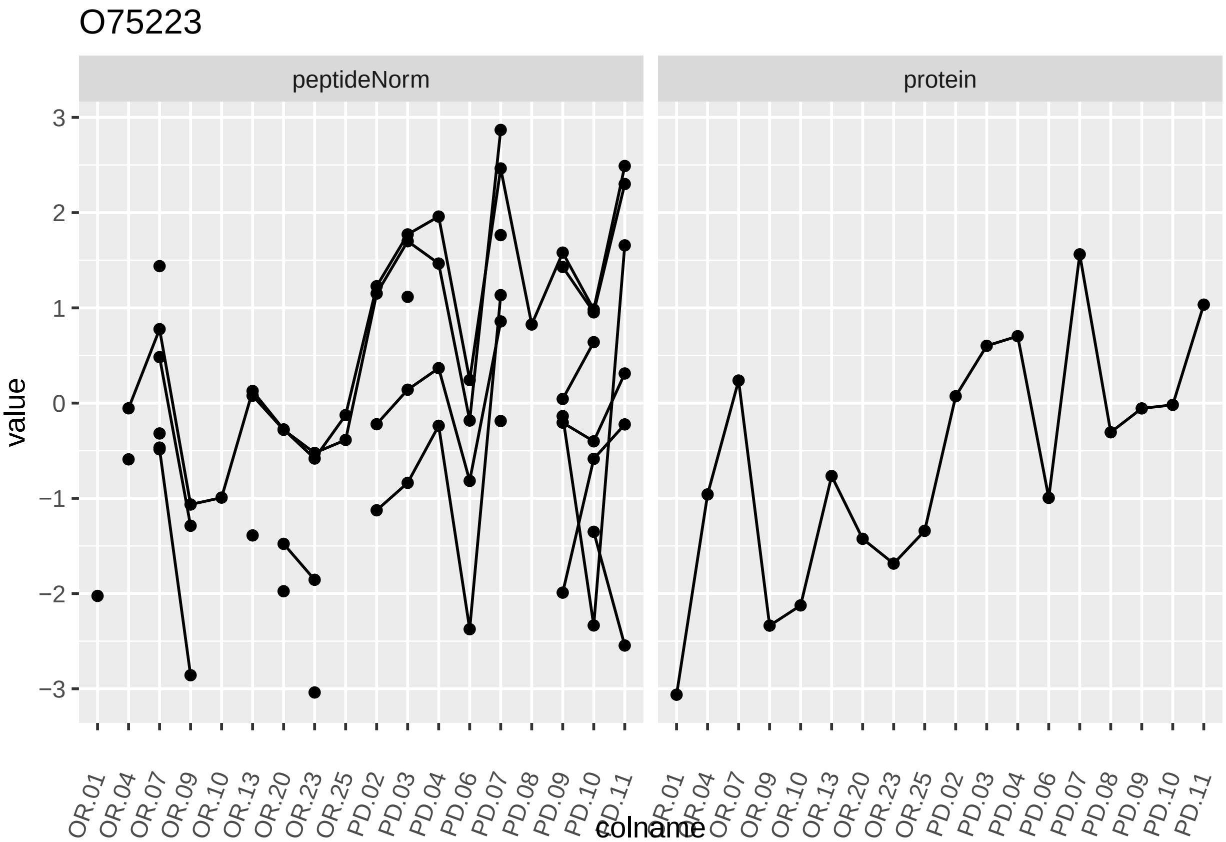
0.0
−2.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


O75368
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
DIAANEENRK
ENNAVYAFLGLTAPPGSK
ENVPENSRPATGYPLPPQIFNESQYR
GDYDAFFEAR
IGFEEKDIAANEENR
IGFEEKDIAANEENRK
KKQQDVLGFLEANK
KQQDVLGFLEANK
O75368
QQDVLGFLEANK
VYIASSSGSTAIK
VYIASSSGSTAIKK
prognosis
OR
PD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peptideNorm
protein
value
3
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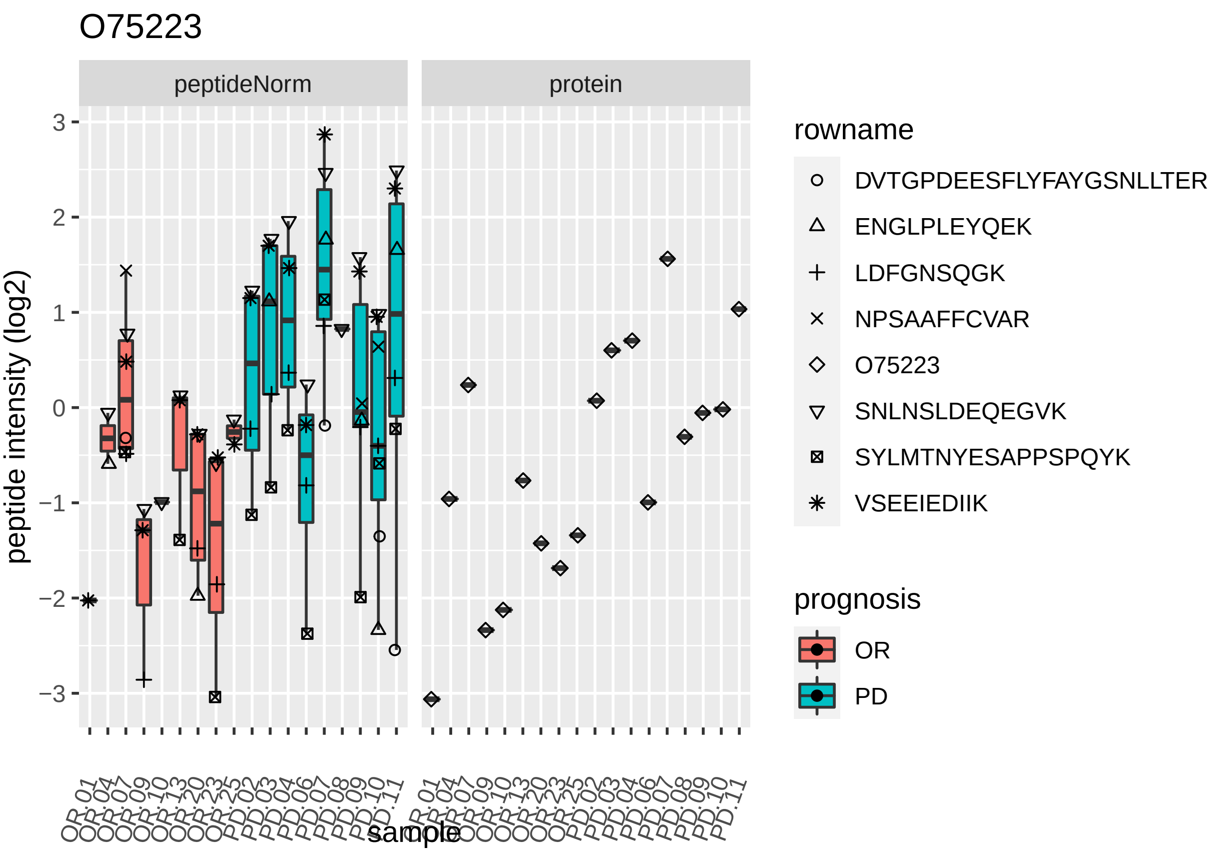
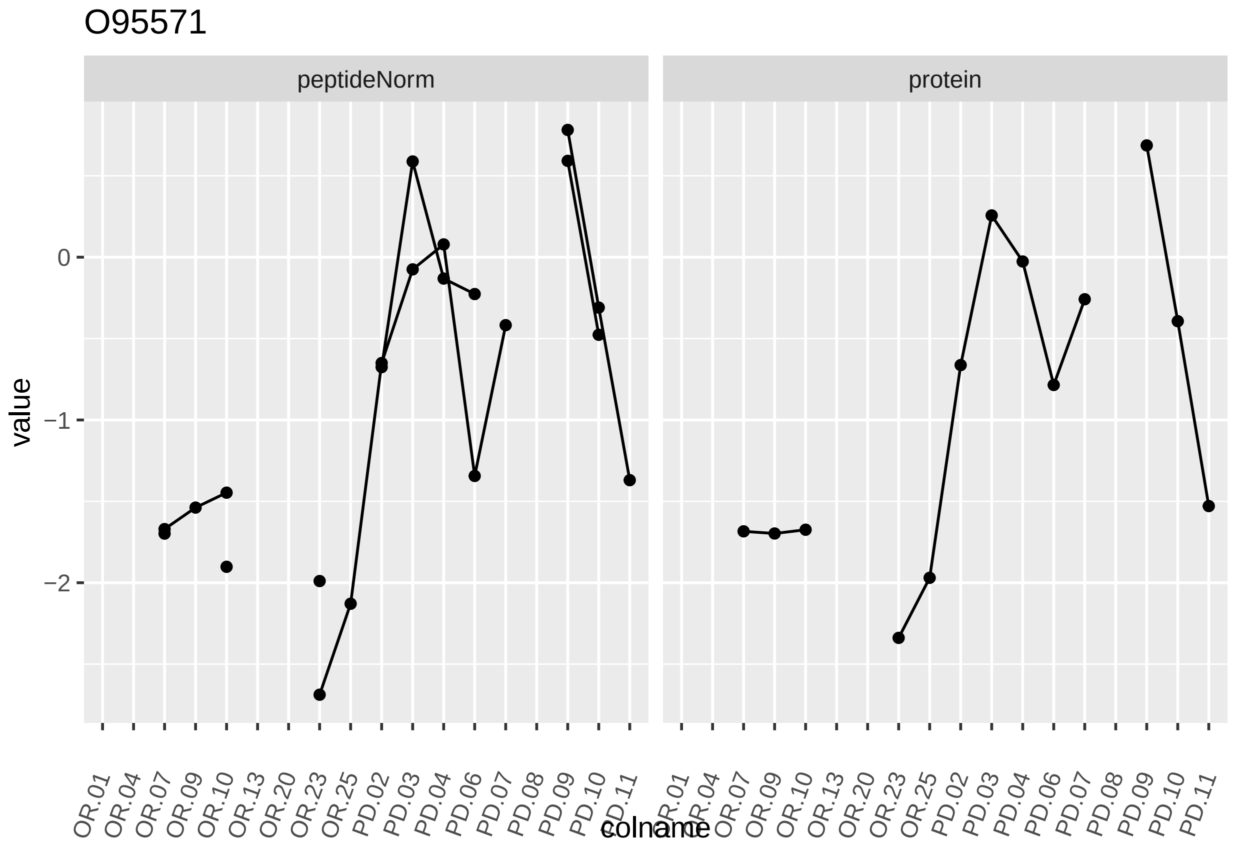
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


O75223
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
−3
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
○ DVTGPDEESFLYFAYGSNLLTER
△ ENGLPLEYQEK
+ LDFGNSQGK
× NPSAAFFCVAR
◇ O75223
▽ SNLNSLDEQEGVK
⊠ SYLMTNYESAPPSPQYK
✳ VSEEIEDIIK
prognosis
OR
PD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peptideNorm
protein
value
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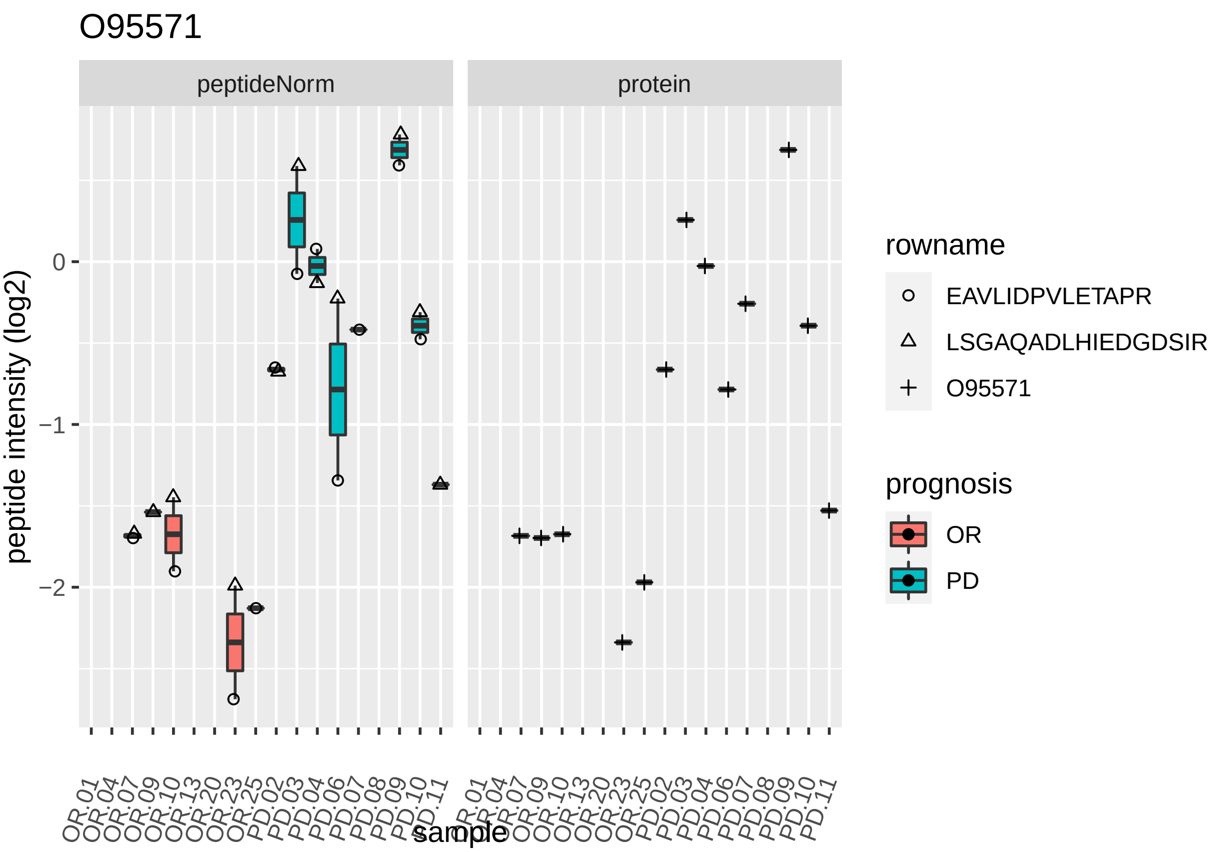
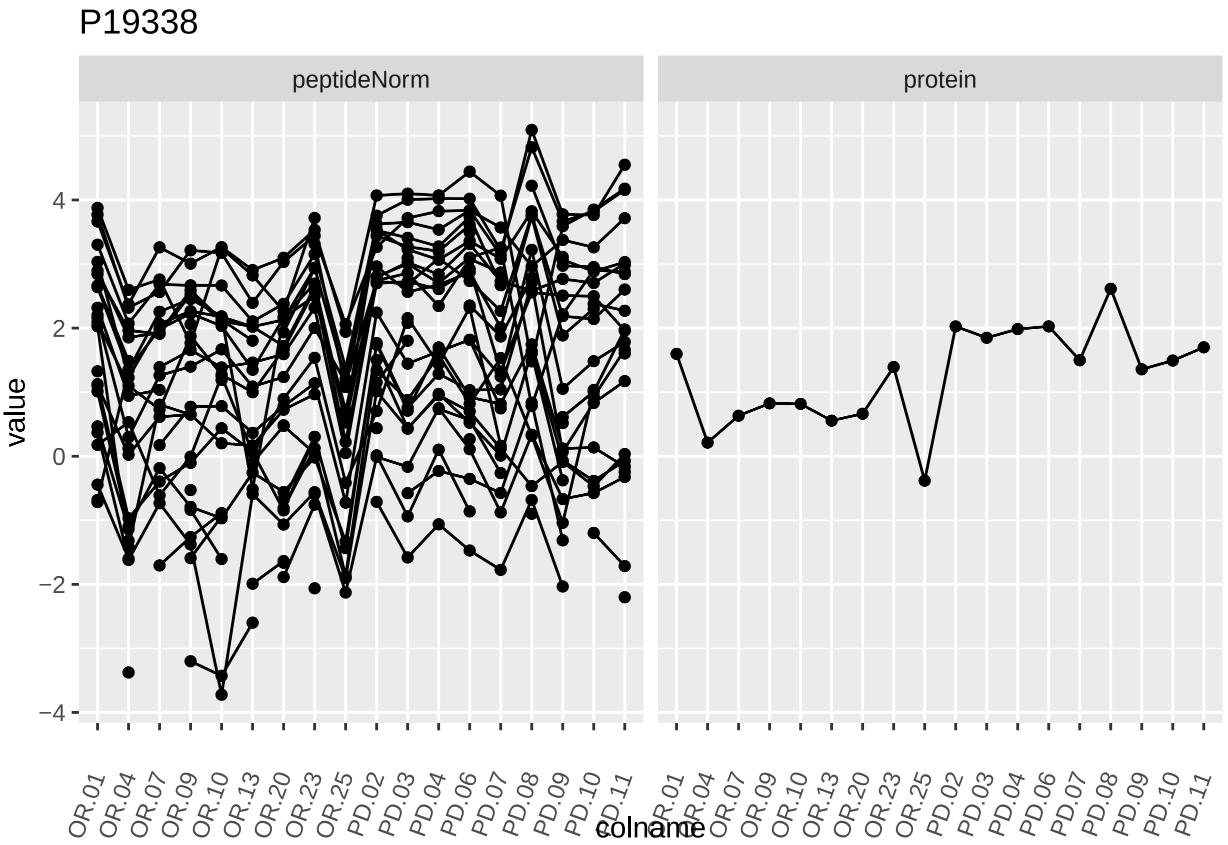
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


O95571
peptideNorm
protein
peptide intensity (log2)
0
−1
−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
○ EAVLIDPVLETAPR
△ LSGAQADLHIEDGDSIR
+ O95571
prognosis
OR
PD


P19338
peptideNorm
protein
value
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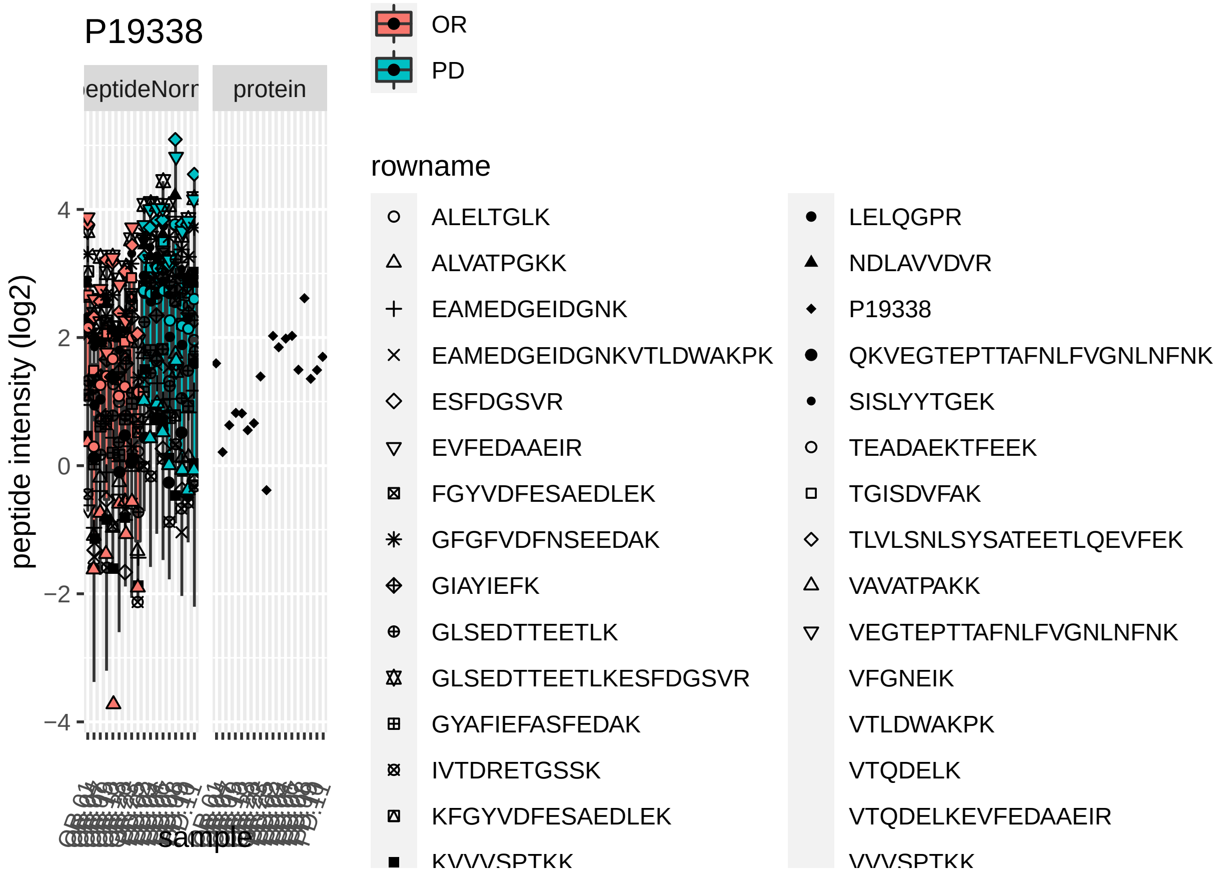
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P19338
eptideNorr
protein
peptide intensity (log2)
4
2
0
−2
−4
sample
OR
PD
rowname
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ALVATPGKK
EAMEDGEIDGNK
EAMEDGEIDGNKVTLDWAKPK
ESFDGSVR
EVFEDAAEIR
FGYVDFESAEDLEK
GFGFVDFNSEEDAK
GIAYIEFK
GLSEDTTEETLK
GLSEDTTEETLKESFDGSVR
GYAFIEFASFEDAK
IVTDRETGSSK
KFGYVDFESAEDLEK
KVVVSPTKK
LELQGPR
NDLAVVDVR
P19338
QKVEGTEPTTAFNLFVGNLNFNK
SISLYYTGEK
TEADAEKTFEEK
TGISDVFAK
TLVLSNLSYSATEETLQEVFEK
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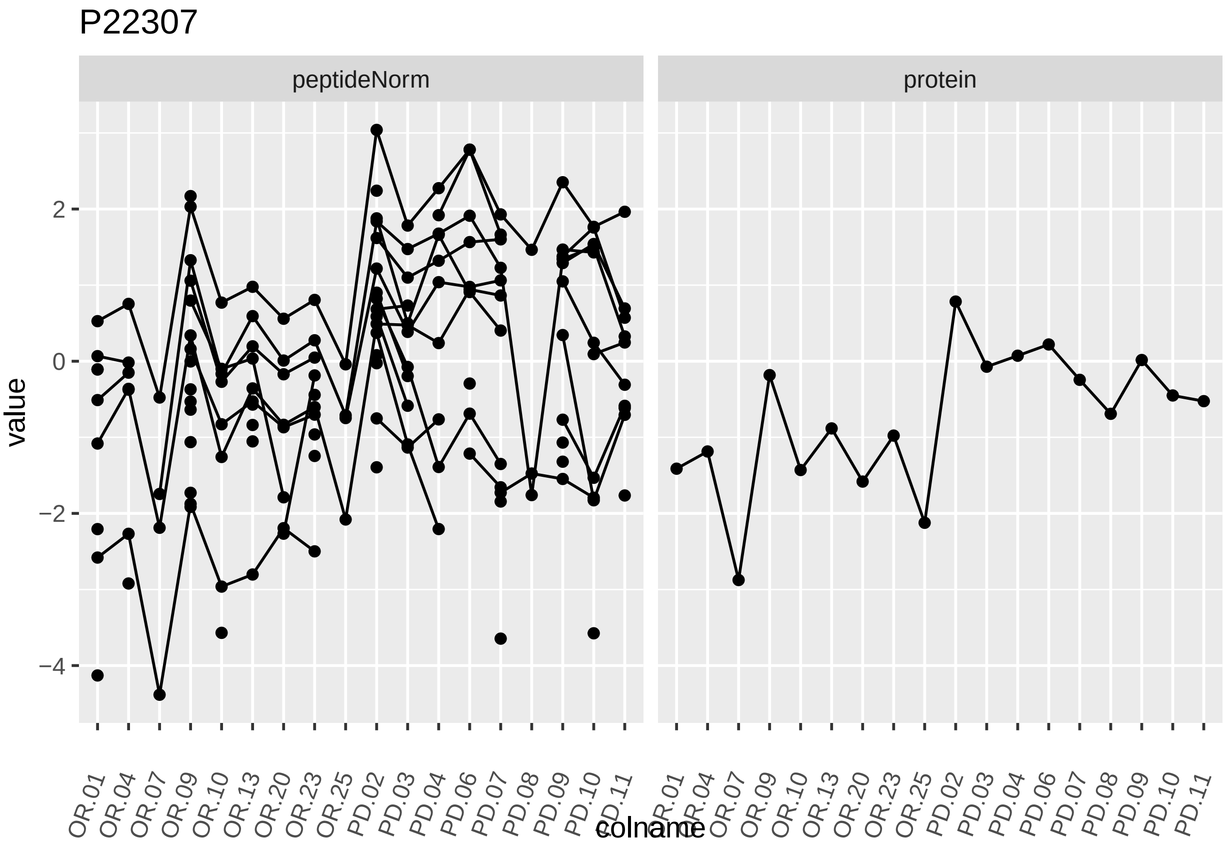
VVVSPTKK


P22307
peptideNorm
protein
value
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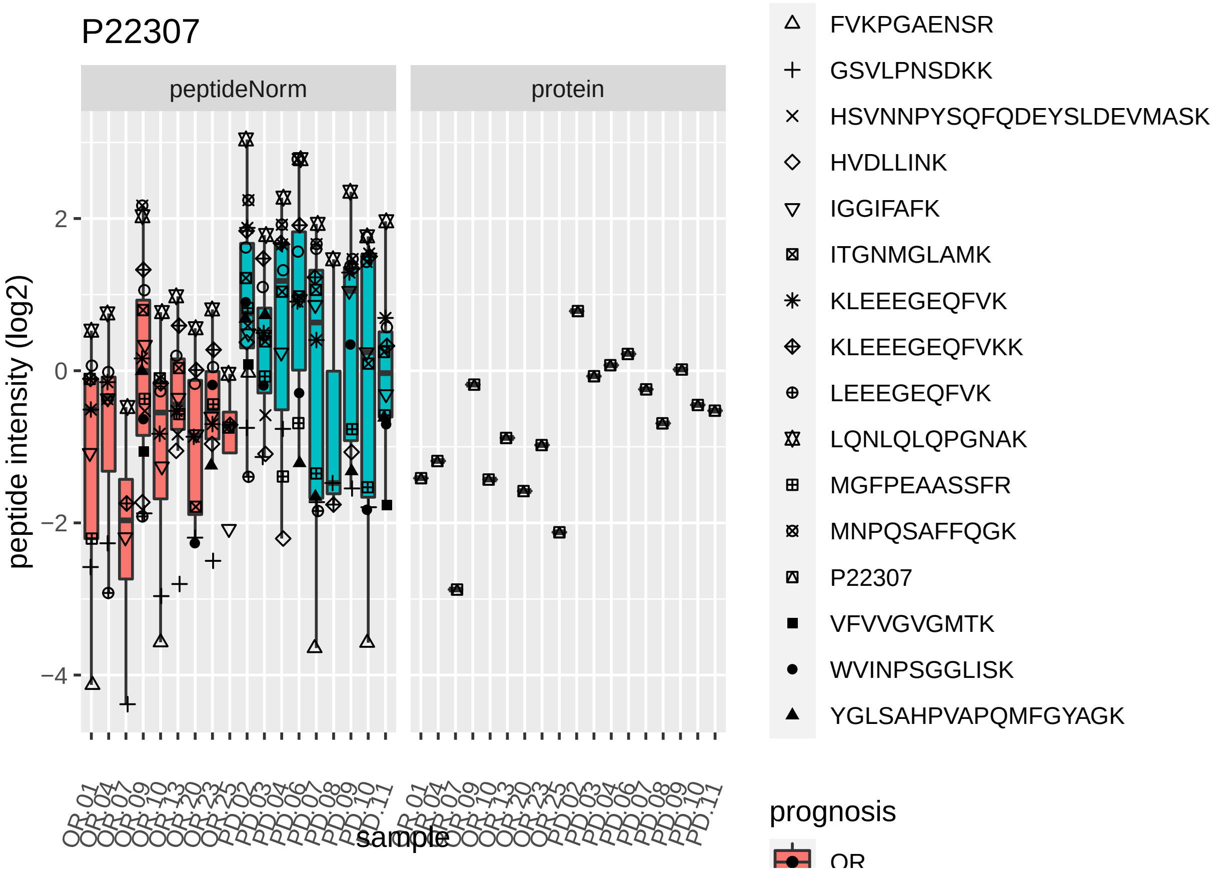
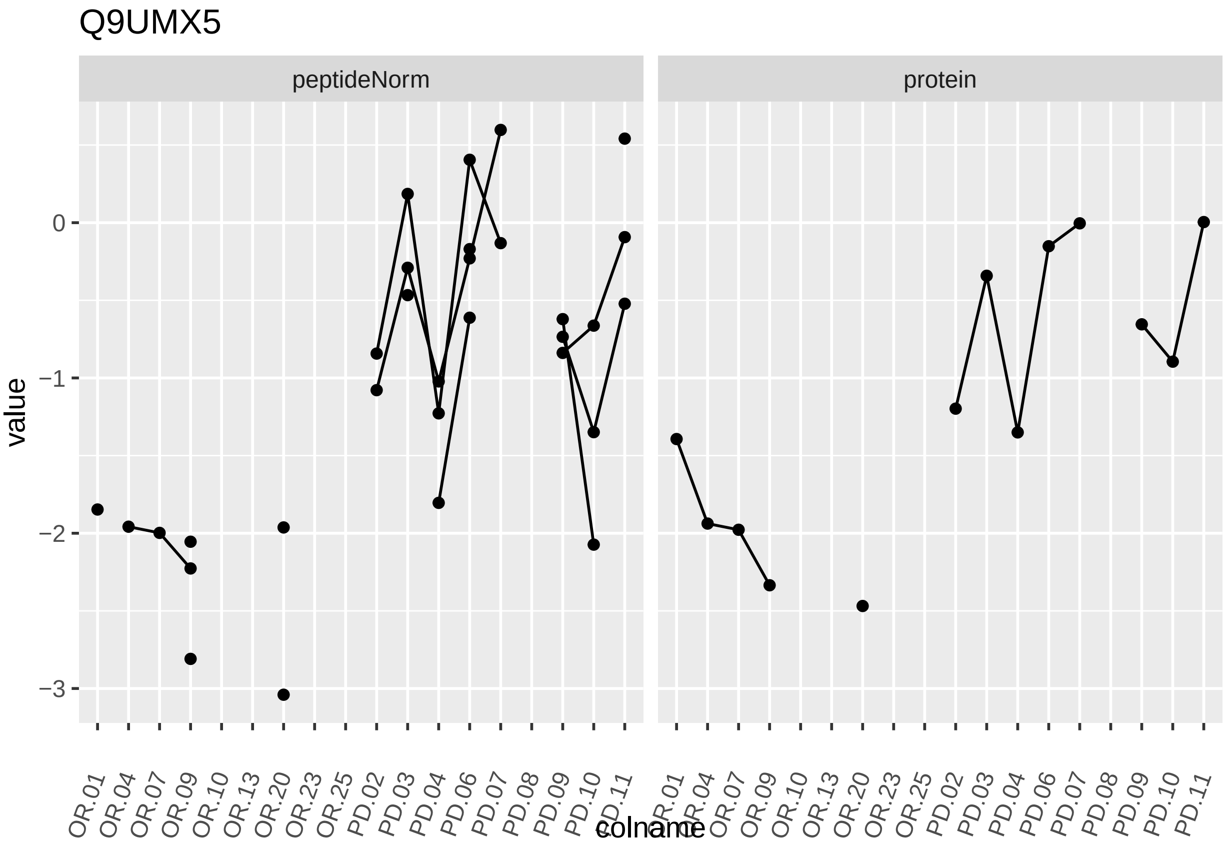
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P22307
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
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
FVKPGAENSR
GSVLPNSDKK
HSVNNPYSQFQDEYSLDEVMASK
HVDLLINK
IGGIFAFK
ITGNMGLAMK
KLEEEGEQFVK
KLEEEGEQFVKK
LEEEGEQFVK
LQNLQLQPGNAK
MGFPEAASSFR
MNPQSAFFQGK
P22307
VFVVGVGMTK
WVINPSGGLISK
YGLSAHPVAPQMFGYAGK
prognosis
OR


Q9UMX5
peptideNorm
protein
value
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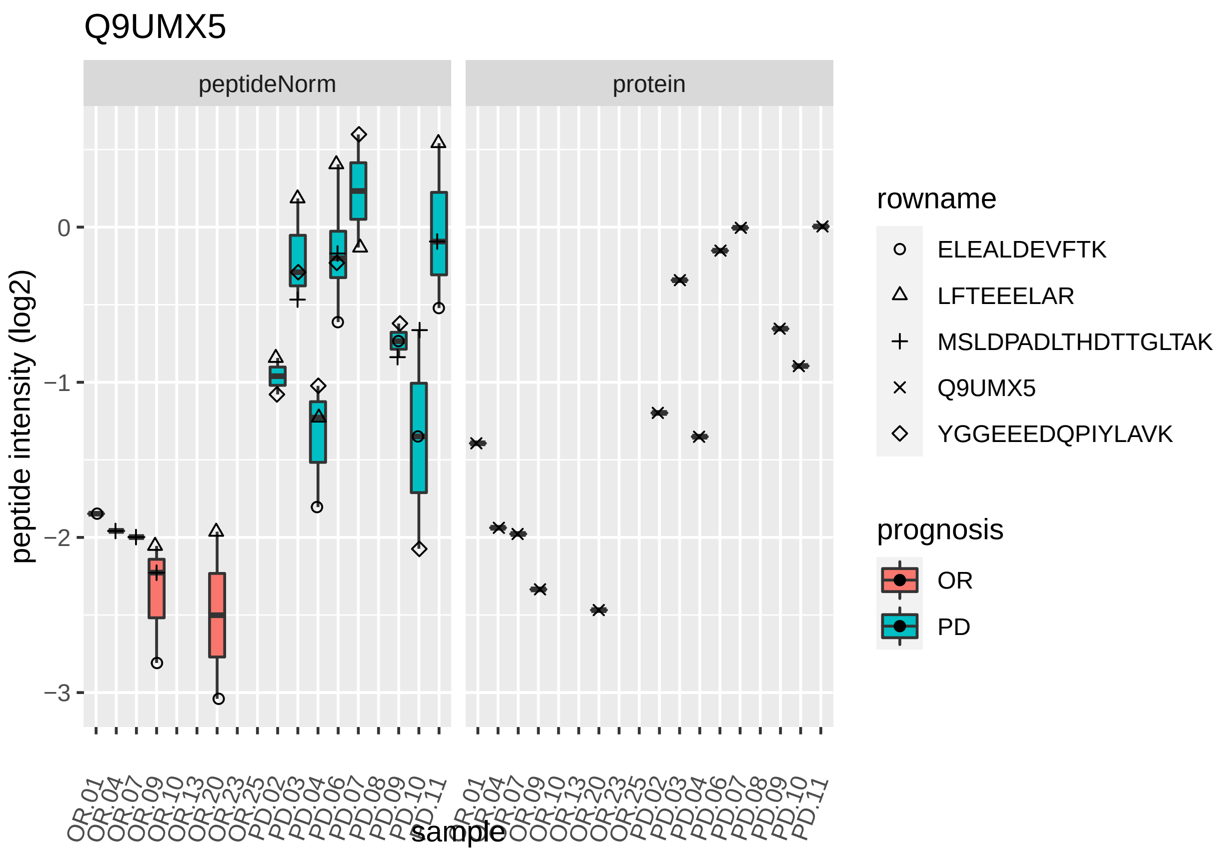
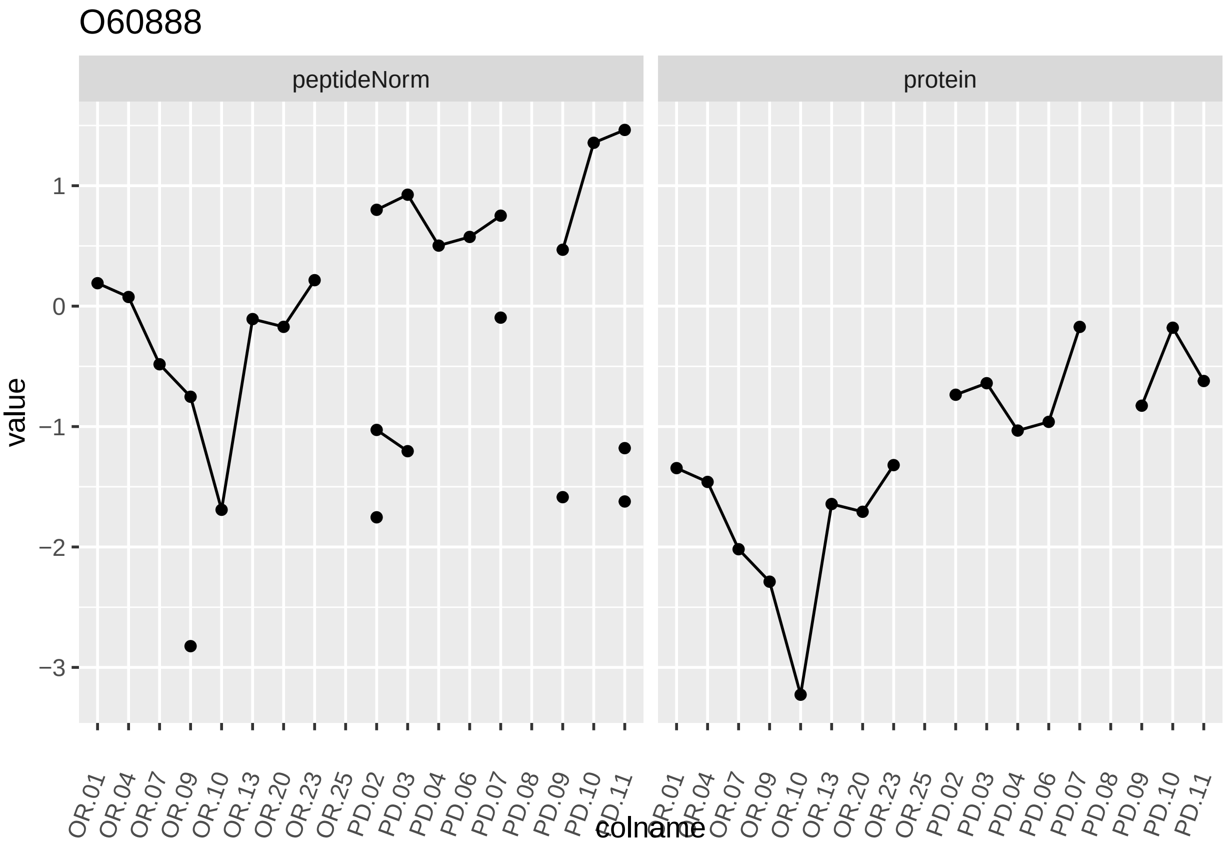
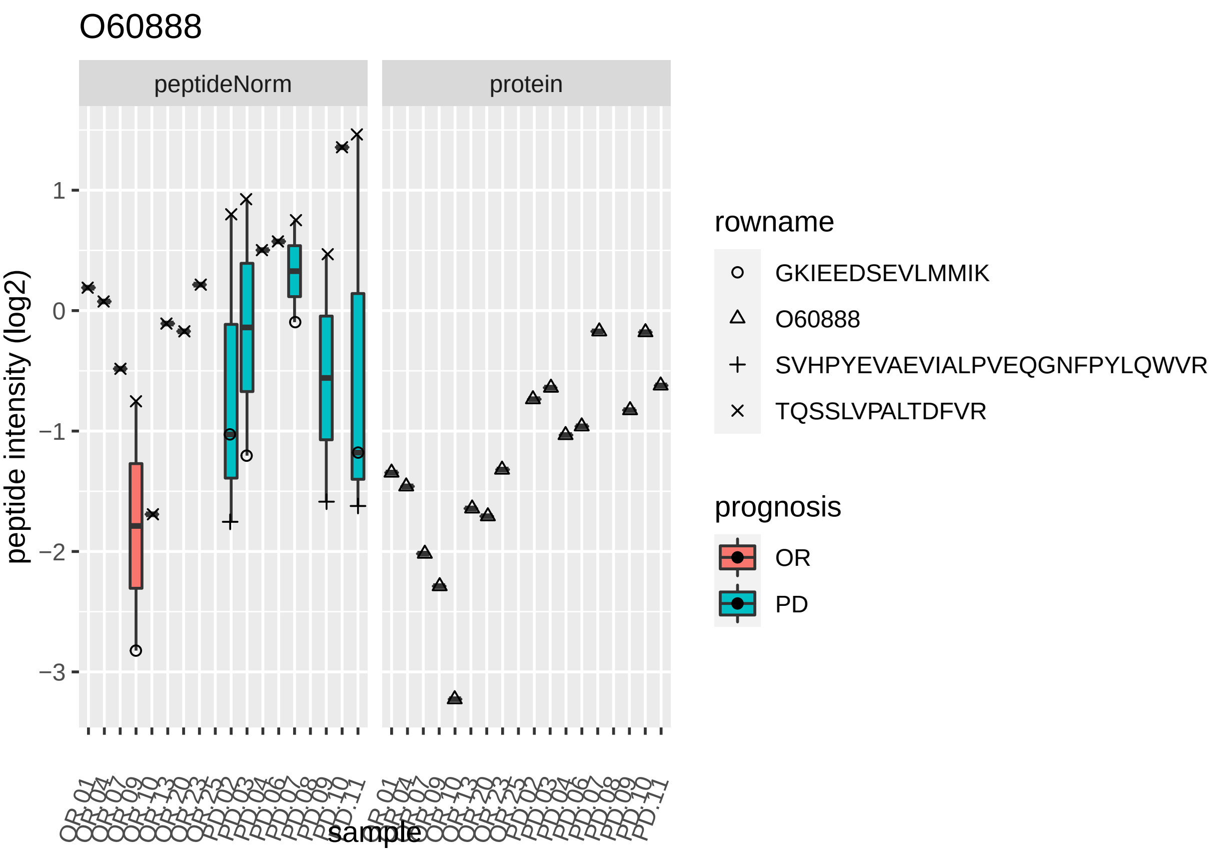
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q9UMX5
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
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
○ ELEALDEVFTK
△ LFTEEELAR
+ MSLDPADLTHDTTGLTAK
× Q9UMX5
◇ YGGEEEDQPIYLAVK
prognosis
OR
PD


O60888
peptideNorm
protein
value
1
0
−1
−2
−3
colname
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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protein
peptide intensity (log2)
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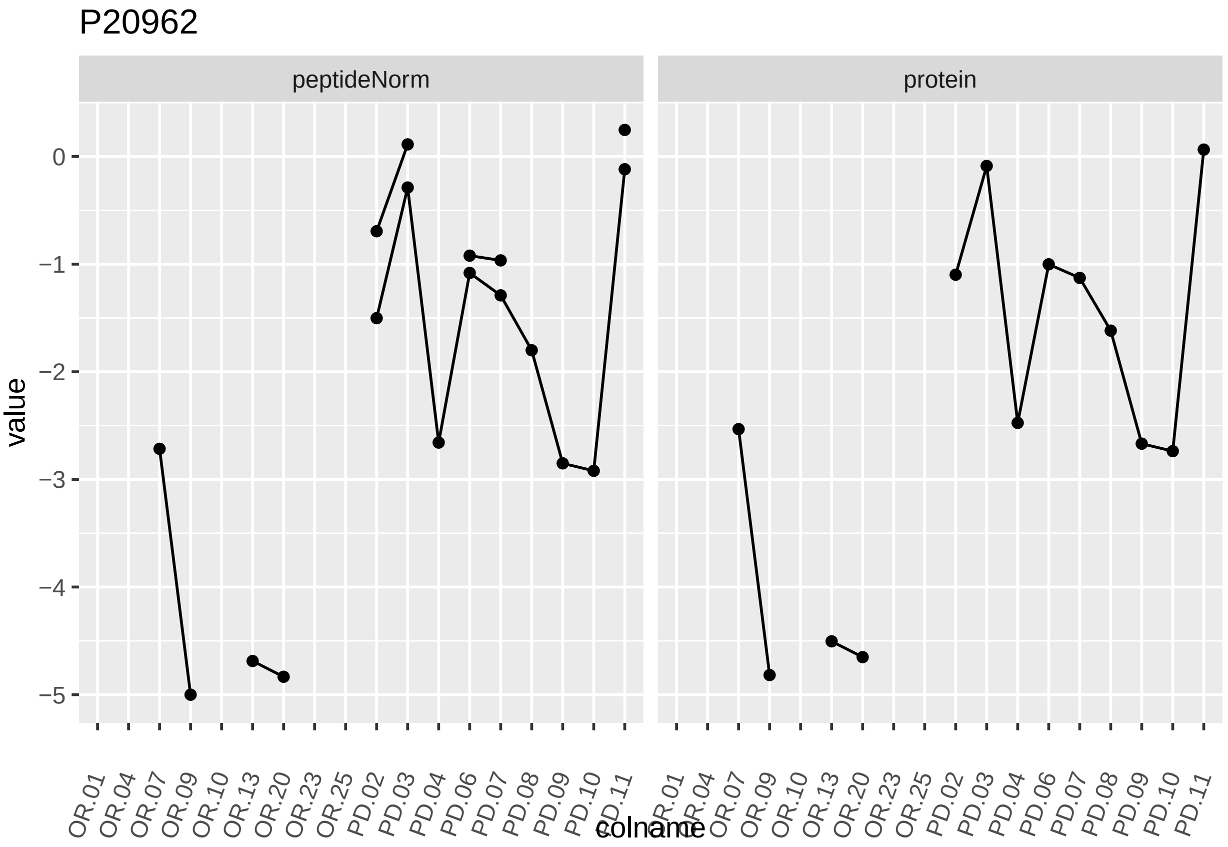
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ GKIEEDSEVLMMIK
△ O60888
+ SVHPYEVAEVIALPVEQGNFPYLQWVR
× TQSSLVPALTDFVR
prognosis
OR
PD


P20962
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protein
value
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−2
−3
−4
−5
colname
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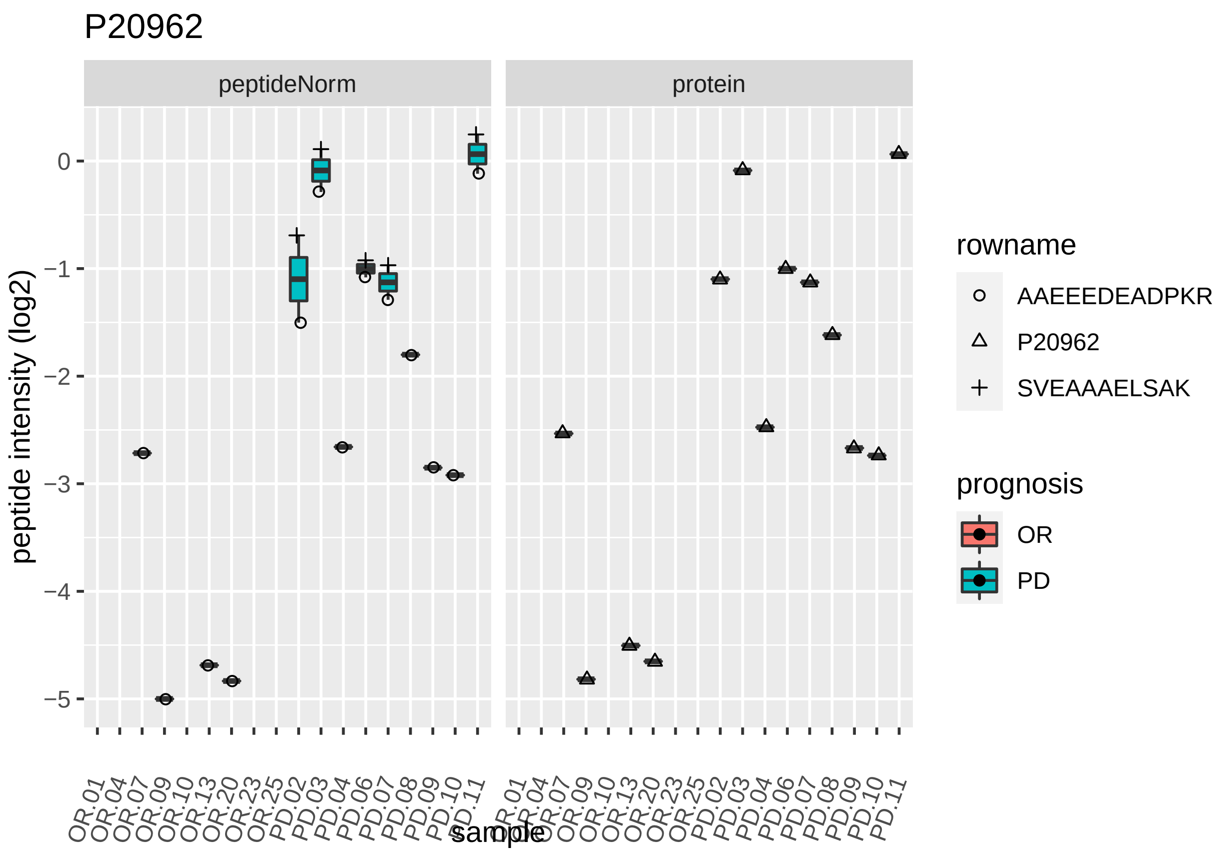
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P20962
peptideNorm
protein
peptide intensity (log2)
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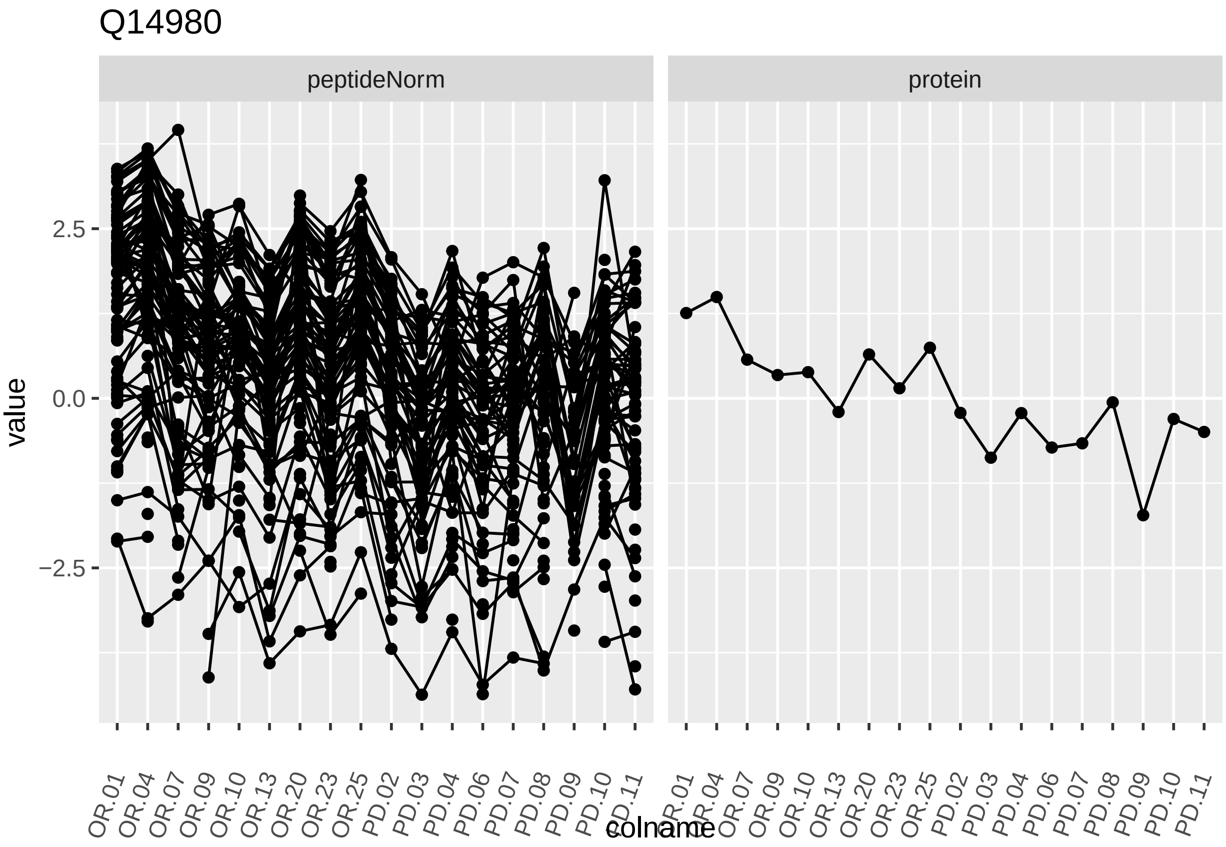
−1
−2
−3
−4
−5
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ AAEEEDEADPKR
△ P20962
+ SVEAAAELSAK
prognosis
OR
PD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protein
value
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0.0
−2.5
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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

| | | | | | | |
|---|---|---|---|---|---|---|
| R | % | HLTAQVR | 7 | LGSPDYGNSALLSLPGYRPTTR | I | QELTSQ |
| | & | HQVEQLSSSLK | 8 | LLQAETASNSAR | J | QEQHEA |
| | ' | HREELEQSK | 9 | LPPKVESLESLYFTPIPAR | K | QFCSTQ |
| AR | ( | IATTTASAATAAAIGATPR | : | LQAQLNELQAQLSQK | L | QFLEVE |
| | ) | IHGTEEGQQILK | ; | LQNALNEQR | M | QLEALE |
| AAGR | * | INQLSEENGDLSFK | < | LQQLGEAHQAETEVLR | N | QPEWLE |
| SEAAGR | + | IQAELAVILK | = | LQQLGEAHQAETEVLRR | O | QQEQAD |
| QQEQASQGLR | , | KHPSSPECLVSAQK | > | LSQLEEHLSQLQDNPPQEK | P | QQLSSL |
| ESECEQLVK | − | KINQLSEENGDLSFK | ? | LTAQVASLTSELTTLNATIQQQDQELAGLK | Q | QQNELA |
| TMR | ▪ | KLDVEEPDSANSSFYSTR | @ | LTAQVEQLEVFQR | R | QQNQEL |
| | / | KNSLISSLEEEVSILNR | A | LVMAESEK | S | RSQAGV |
| | 0 | KQQNQELQEQLR | B | MTMLLLYHSTMSSK | T | SAPASQ |
| | 1 | KVEELQACVETAR | C | NSLISSLEEEVSILNR | U | SLEAQV |
| STQALVSELLPAK | 2 | LADDLSTLQEK | D | PSLSLGTITDEEMK | V | SLVEQH |
| | 3 | LALLNEK | E | Q14980 | W | SNRDEL |
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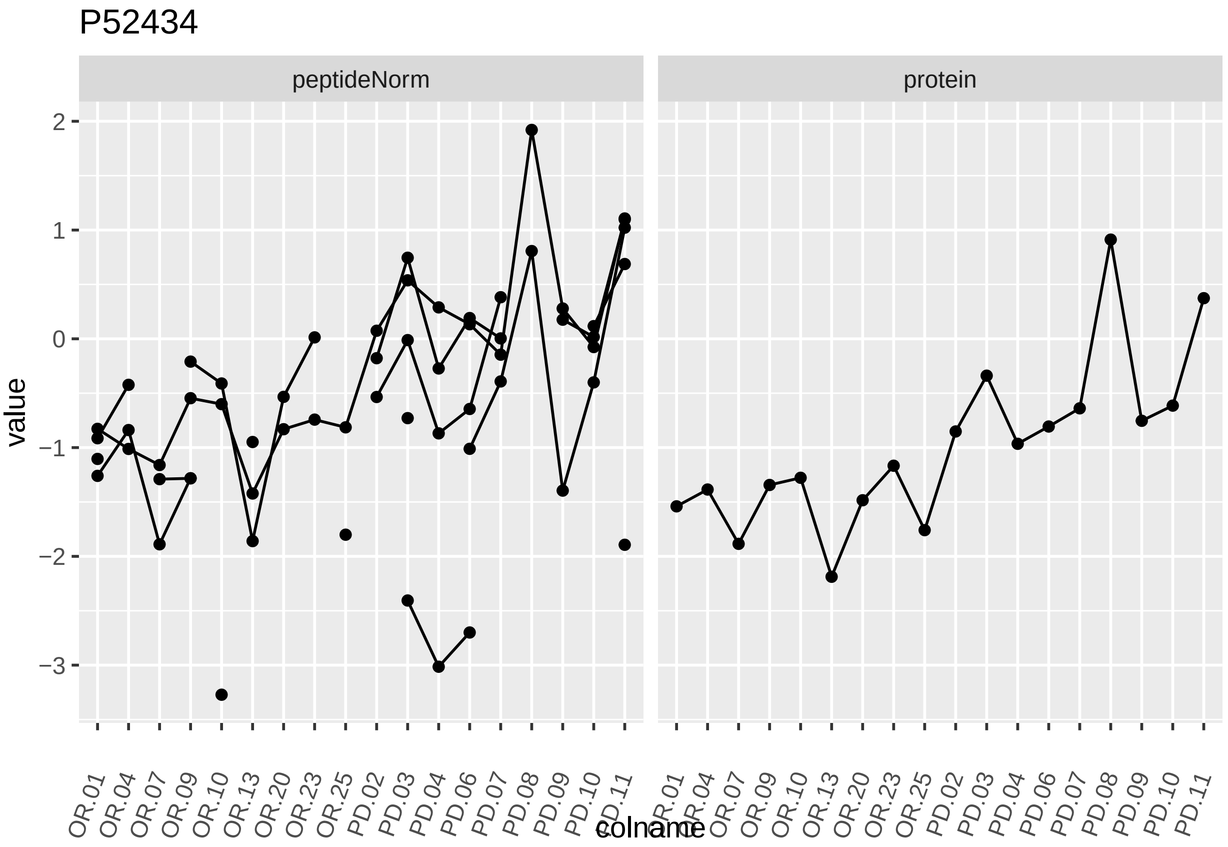
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peptideNorm
protein
value
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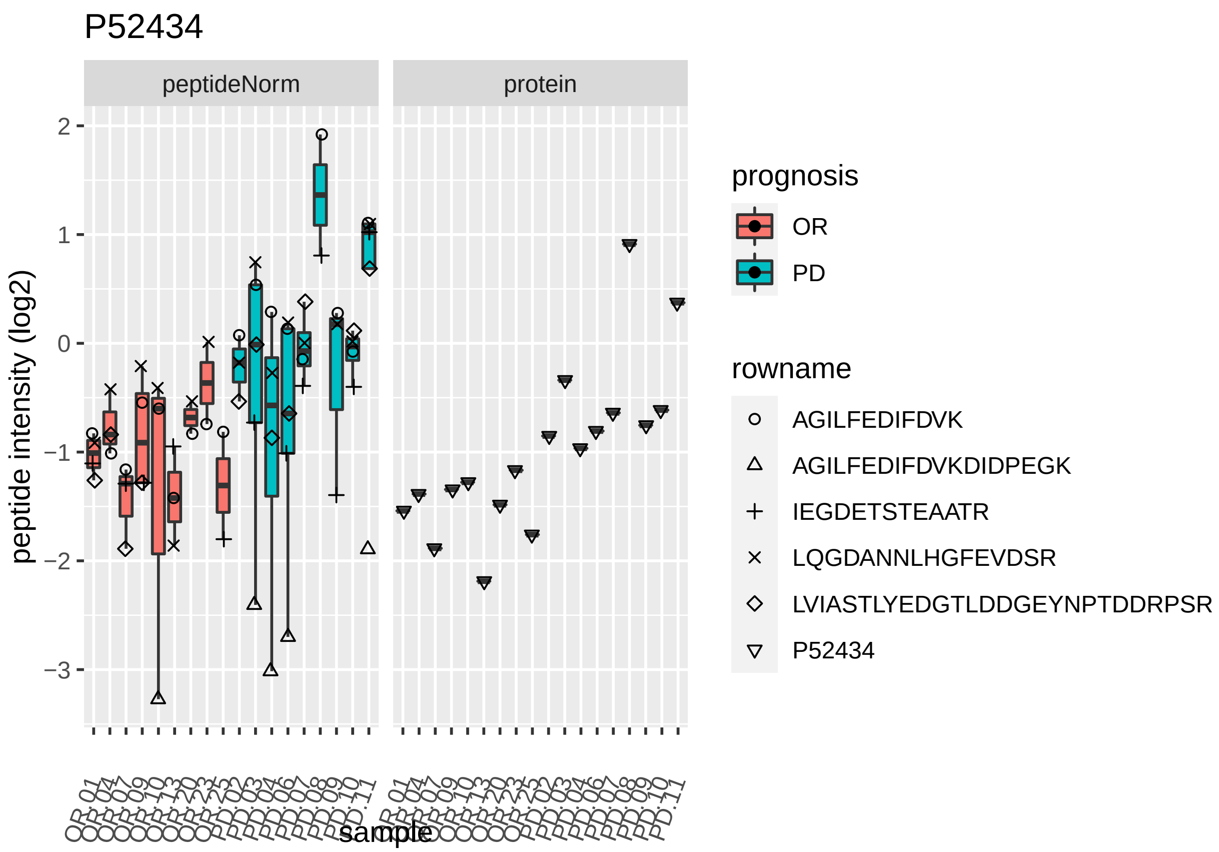
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11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protein
peptide intensity (log2)
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1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
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
prognosis
OR
PD
rowname
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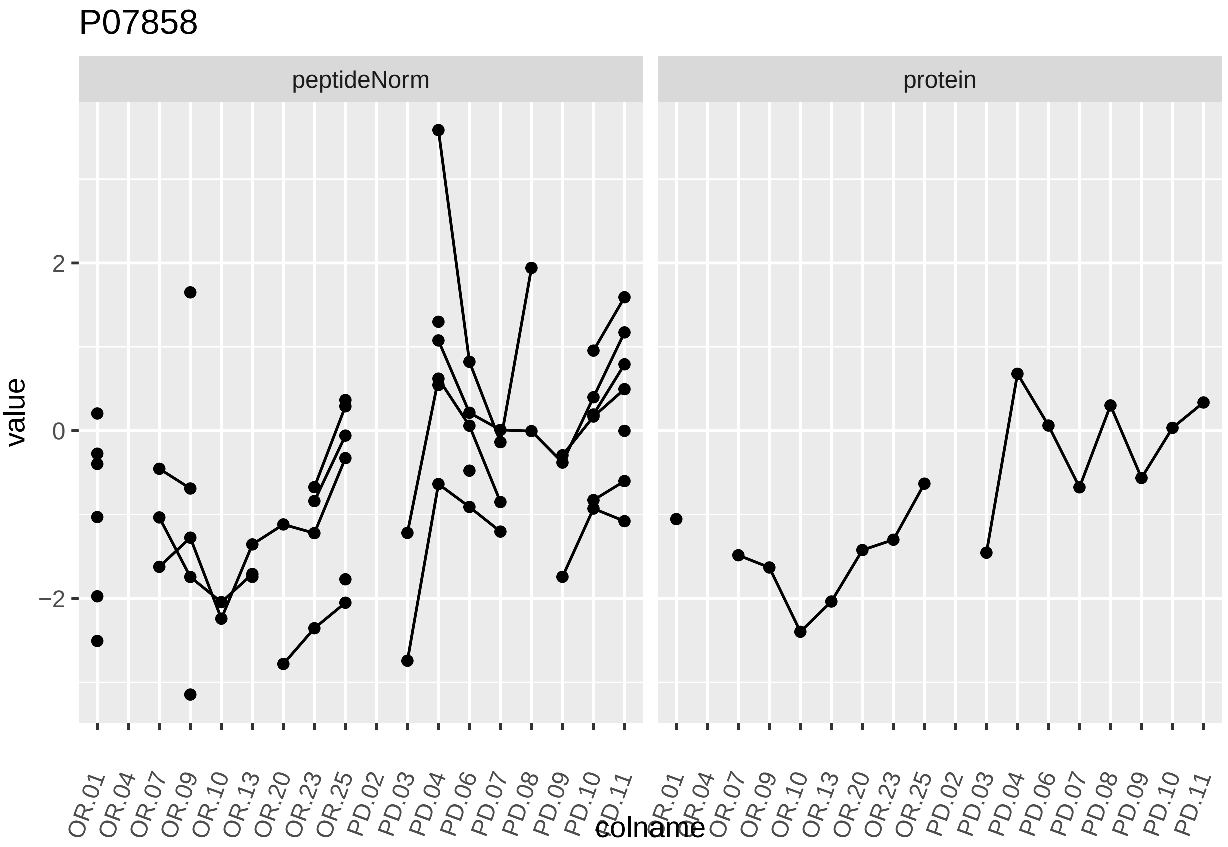
P52434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peptideNorm
protein
value
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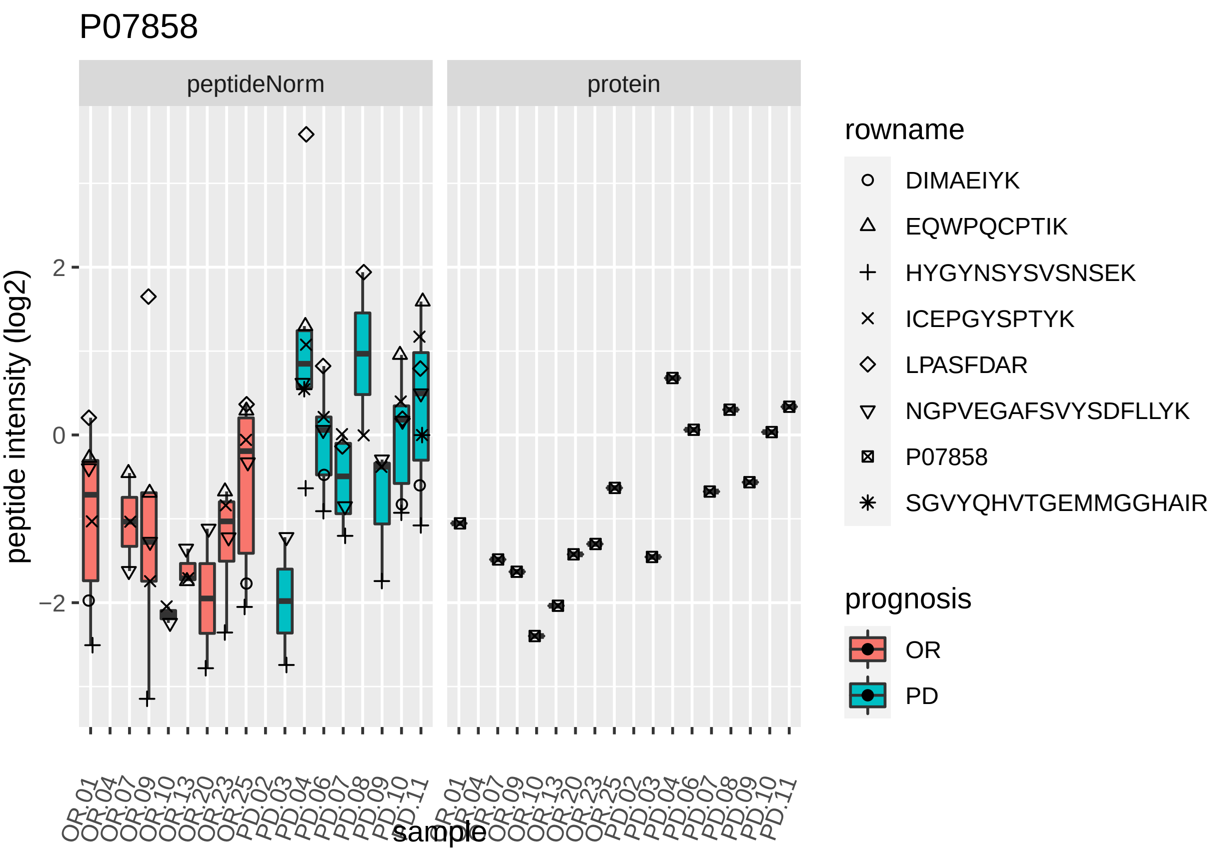
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11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protein
peptide intensity (log2)
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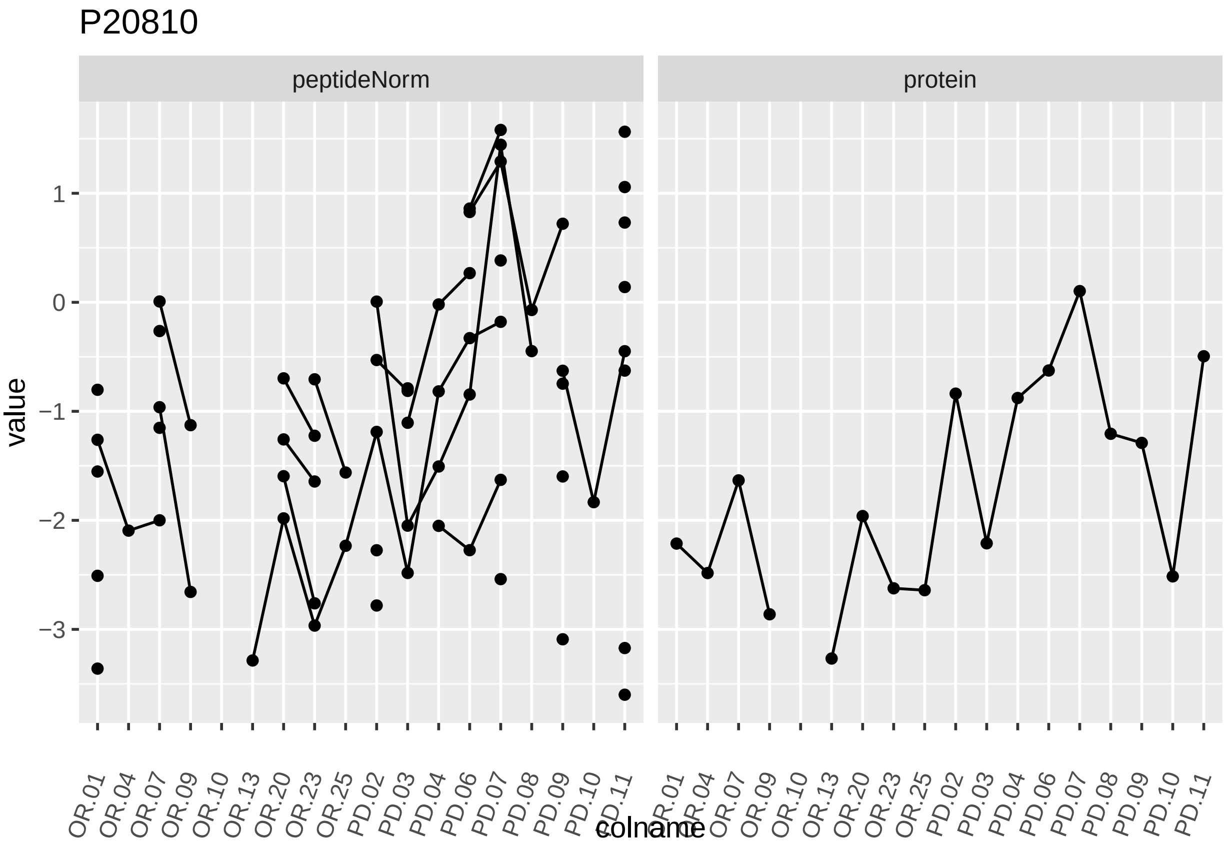
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
DIMAEIYK
EQWPQCPTIK
HYGYNSYSVSNSEK
ICEPGYSPTYK
LPASFDAR
NGPVEGAFSVYSDFLLYK
P07858
SGVYQHVTGEMMGGHAIR
prognosis
OR
PD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protein
value
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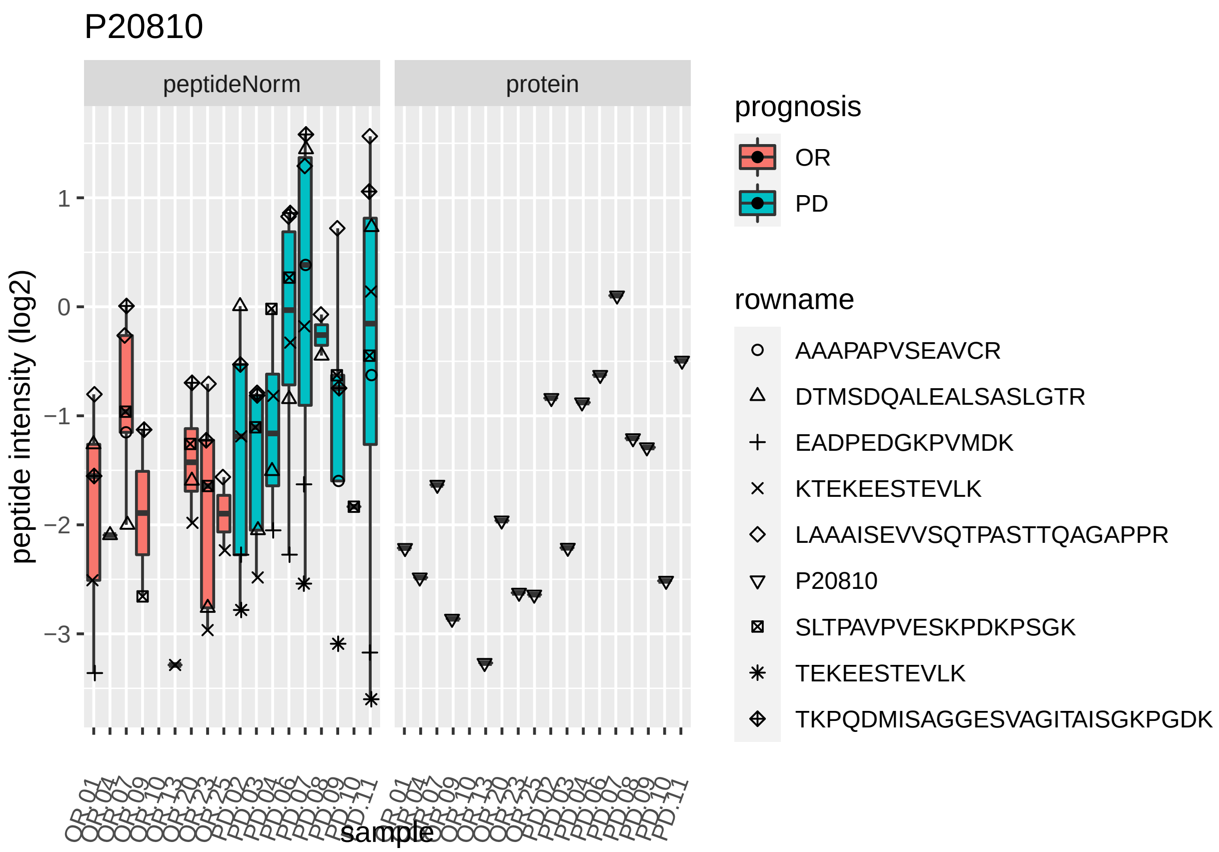
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P20810
peptideNorm
protein
peptide intensity (log2)
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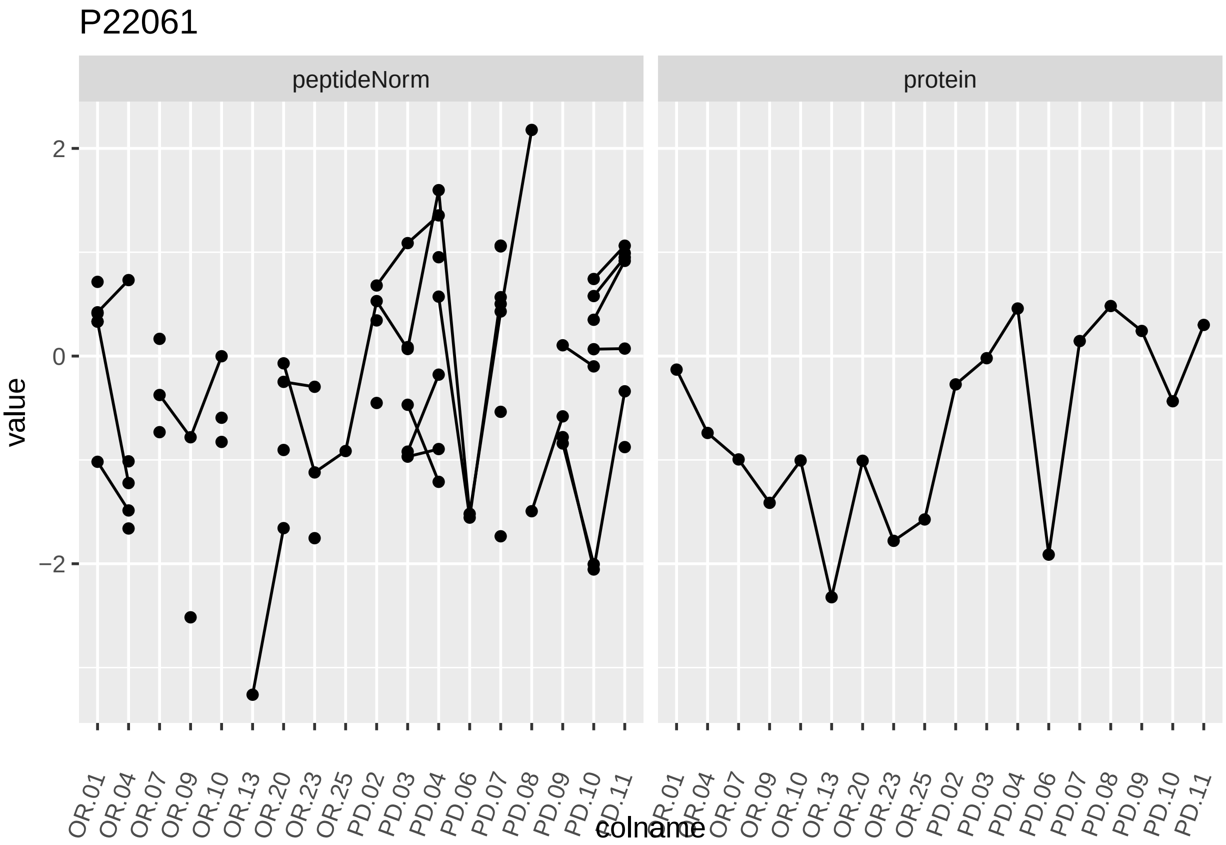
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
AAAPAPVSEAVCR
DTMSDQALEALSASLGTR
EADPEDGKPVMDK
KTEKEESTEVLK
LAAAISEVVSQTPASTTQAGAPPR
P20810
SLTPAVPVESKPDKPSGK
TEKEESTEVLK
TKPQDMISAGGESVAGITAISGKPGDK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peptideNorm
protein
value
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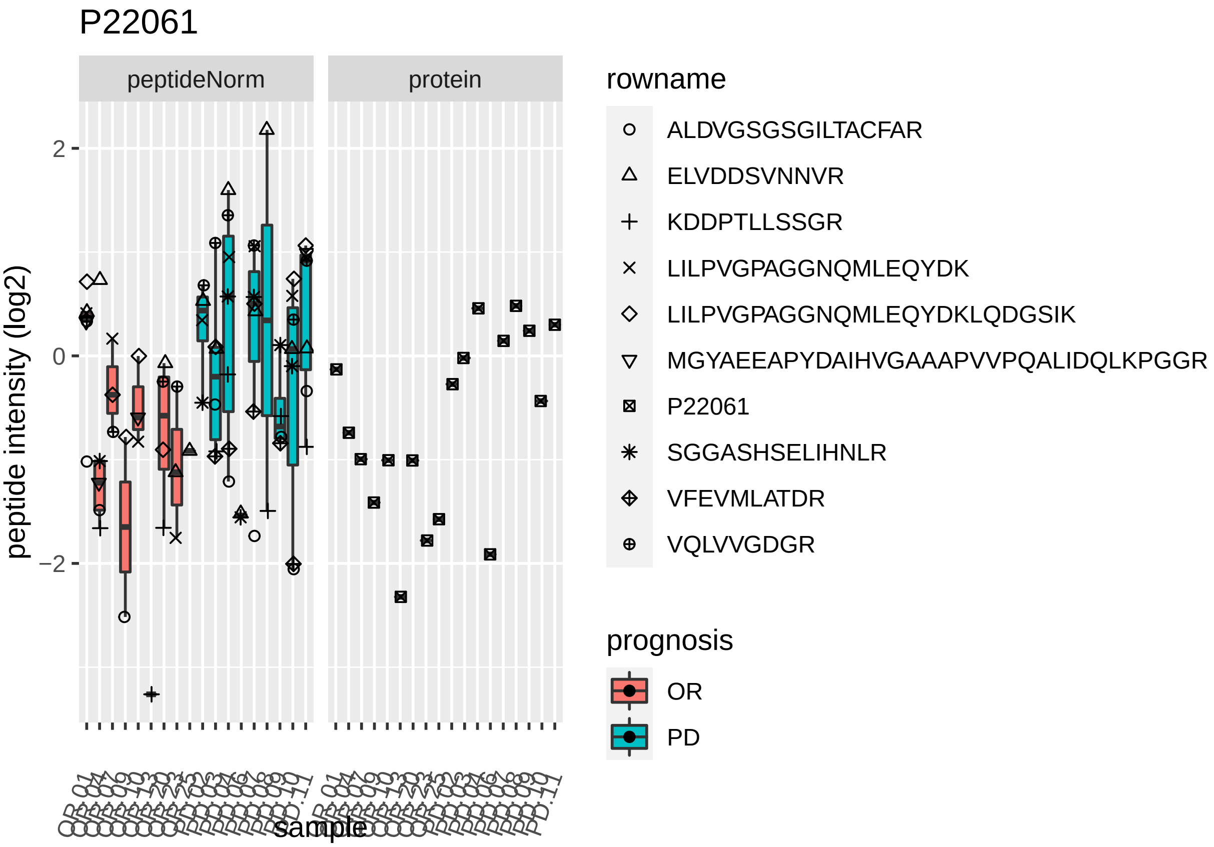
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P22061
peptideNorm
protein
peptide intensity (log2)
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0
−2
sample
rowname
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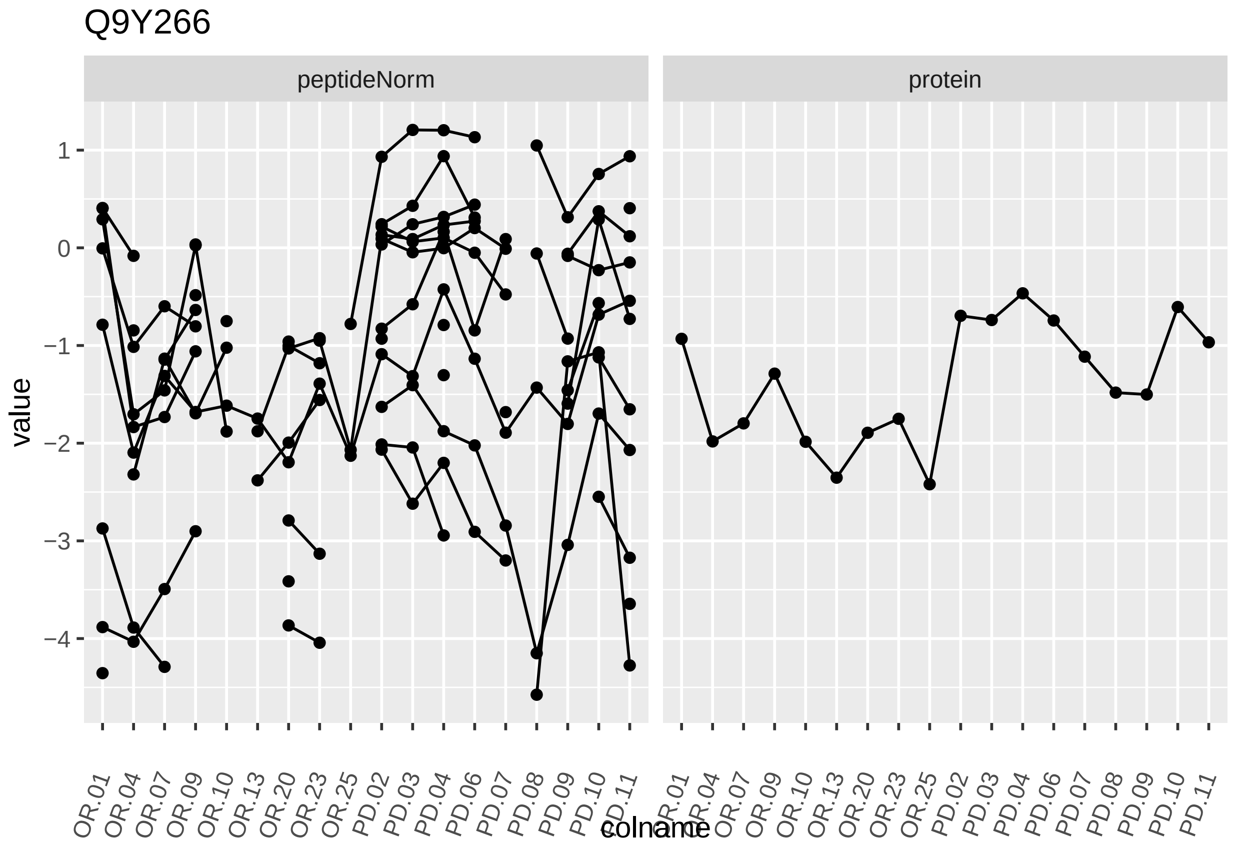
ELVDDSVNNVR
KDDPTLLSSGR
LILPVGPAGGNQMLEQYDK
LILPVGPAGGNQMLEQYDKLQDGSIK
MGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR
P22061
SGGASHSELIHNLR
VFEVMLATDR
VQLVVGDGR
prognosis
OR
PD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protein
value
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−1
−2
−3
−4
colname
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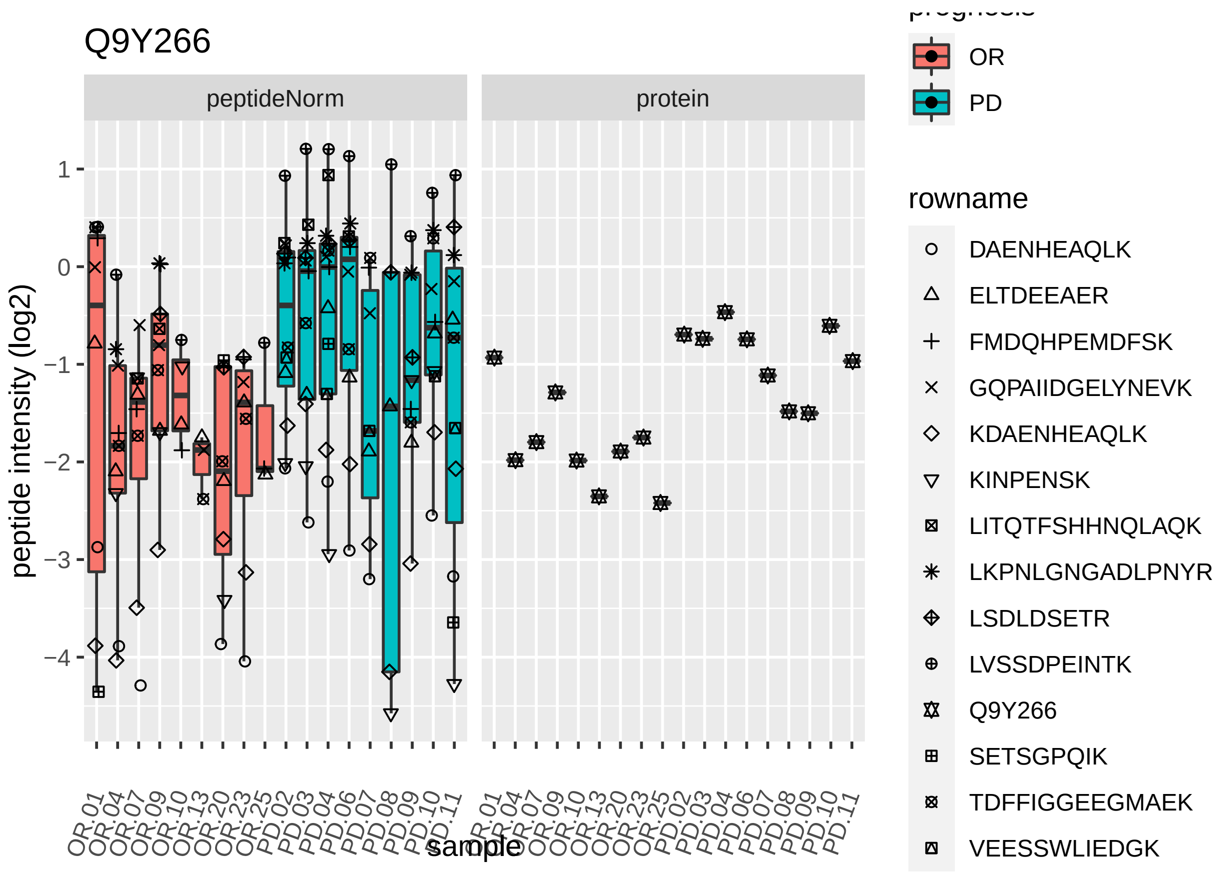
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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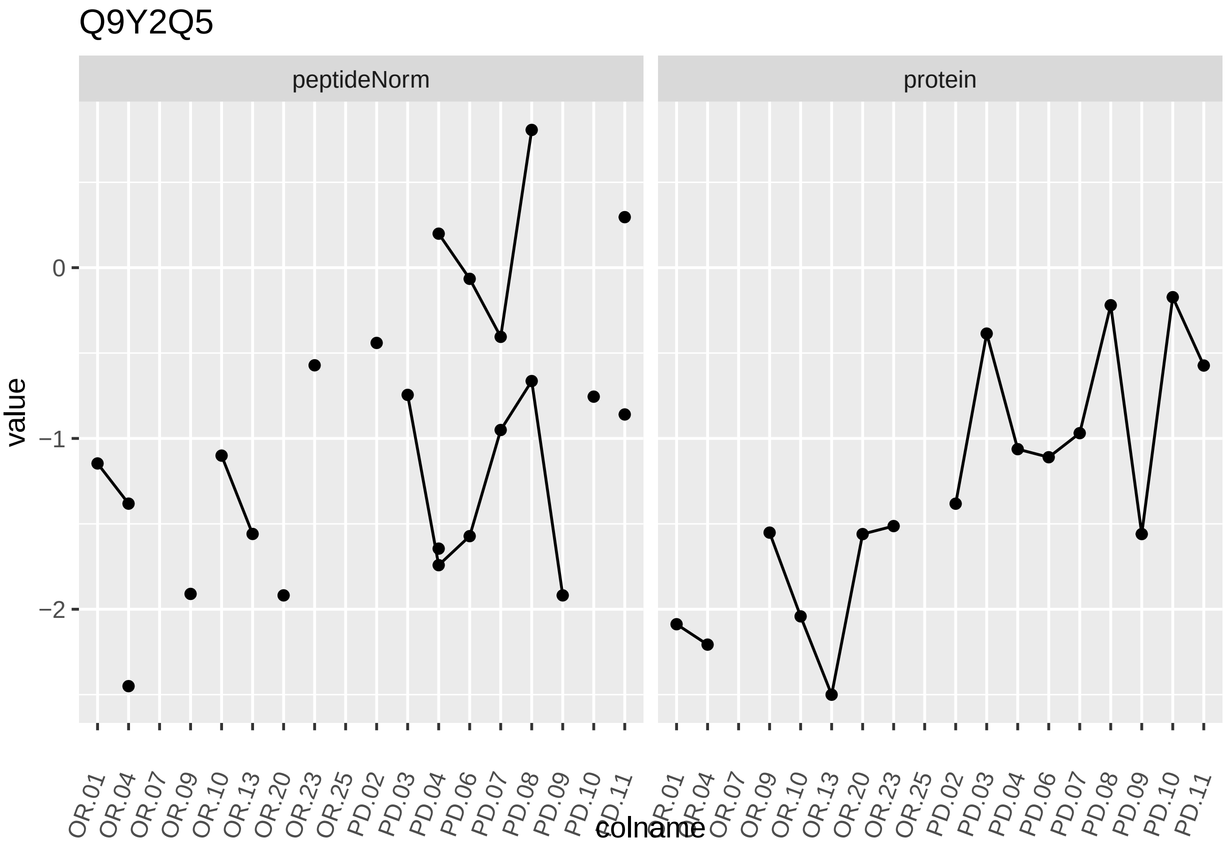
0
−1
−2
−3
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
DAENHEAQLK
ELTDEEAER
FMDQHPEMDFSK
GQPAIIDGELYNEVK
KDAENHEAQLK
KINPENSK
LITQTFSHHNQLAQK
LKPNLGNGADLPNYR
LSDLDSETR
LVSSDPEINTK
Q9Y266
SETSGPQIK
TDFFIGGEEGMAEK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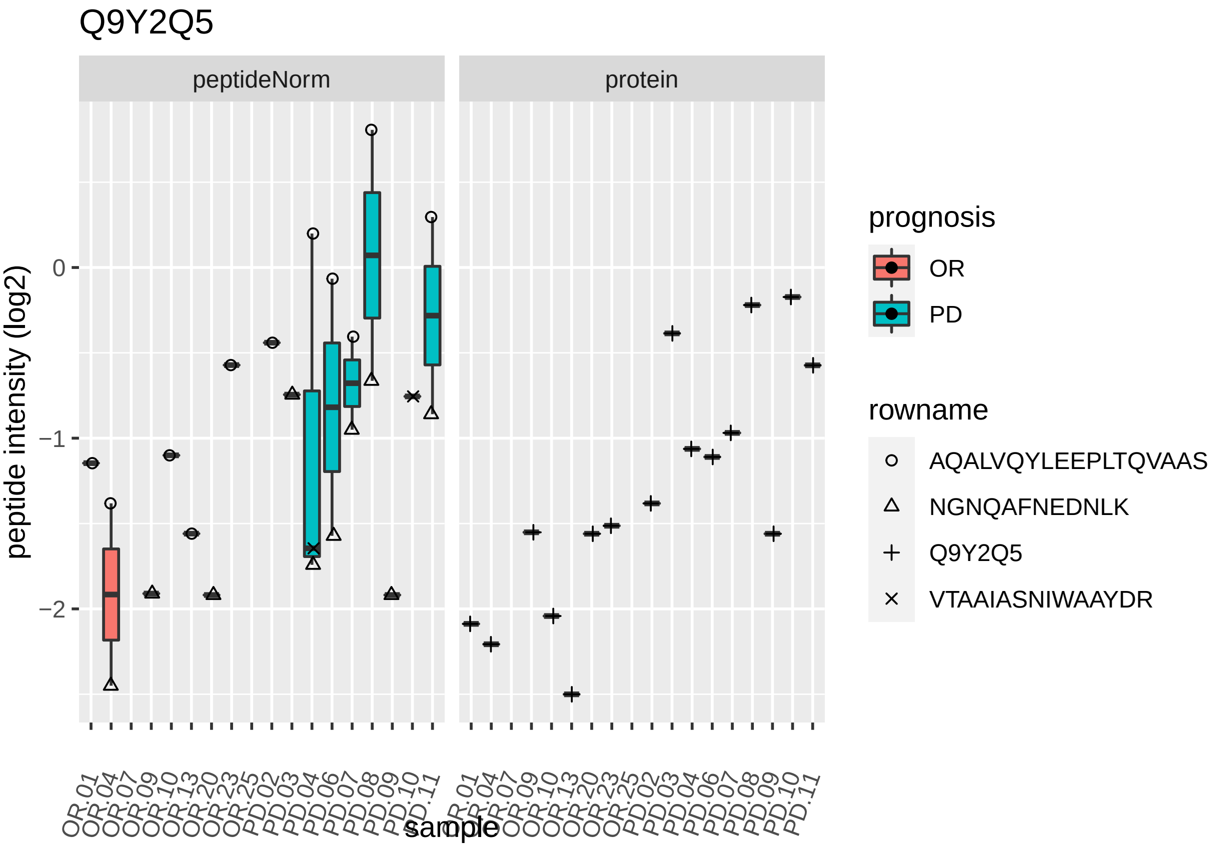
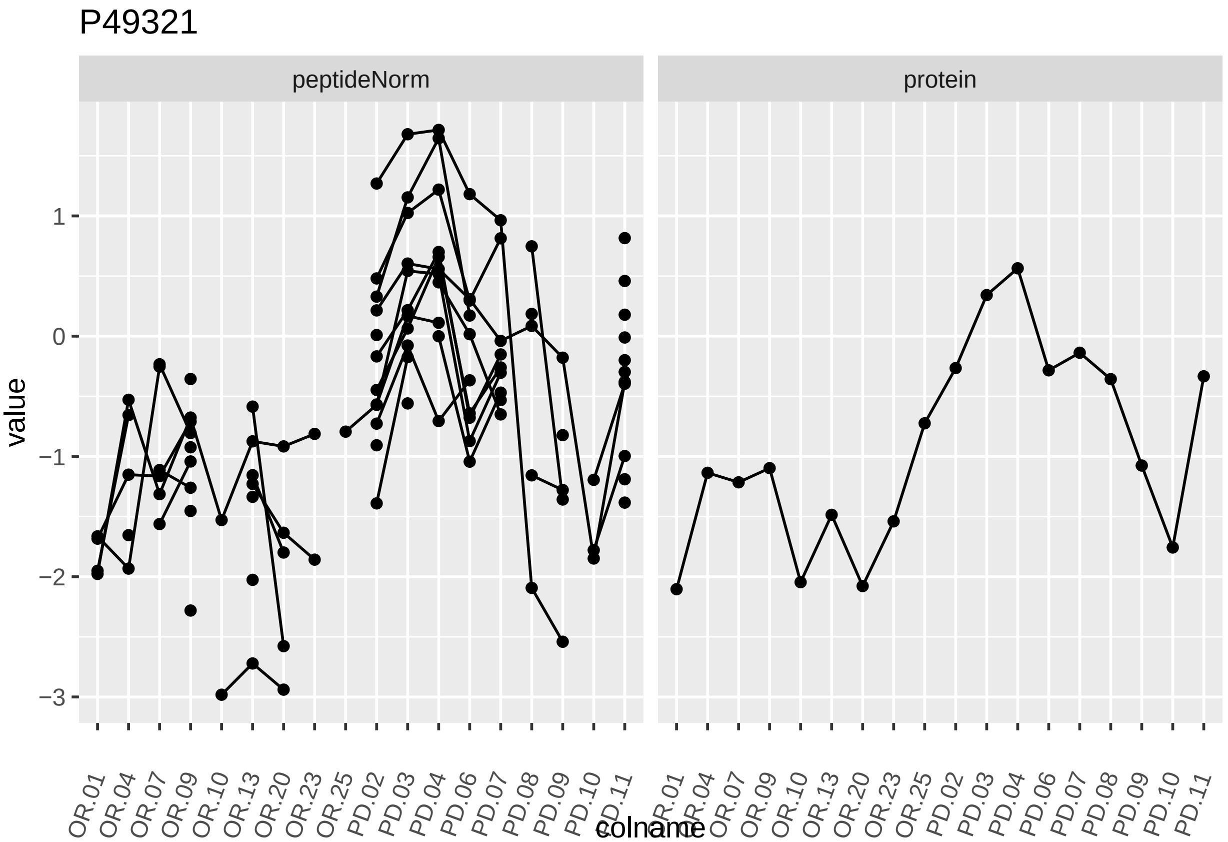
−1
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q9Y2Q5
peptideNorm
protein
peptide intensity (log2)
0
−1
−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
prognosis
OR
PD
rowname
○ AQALVQYLEEPLTQVAAS
△ NGNQAFNEDNLK
+ Q9Y2Q5
× VTAAIASNIWAAYDR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peptideNorm
protein
value
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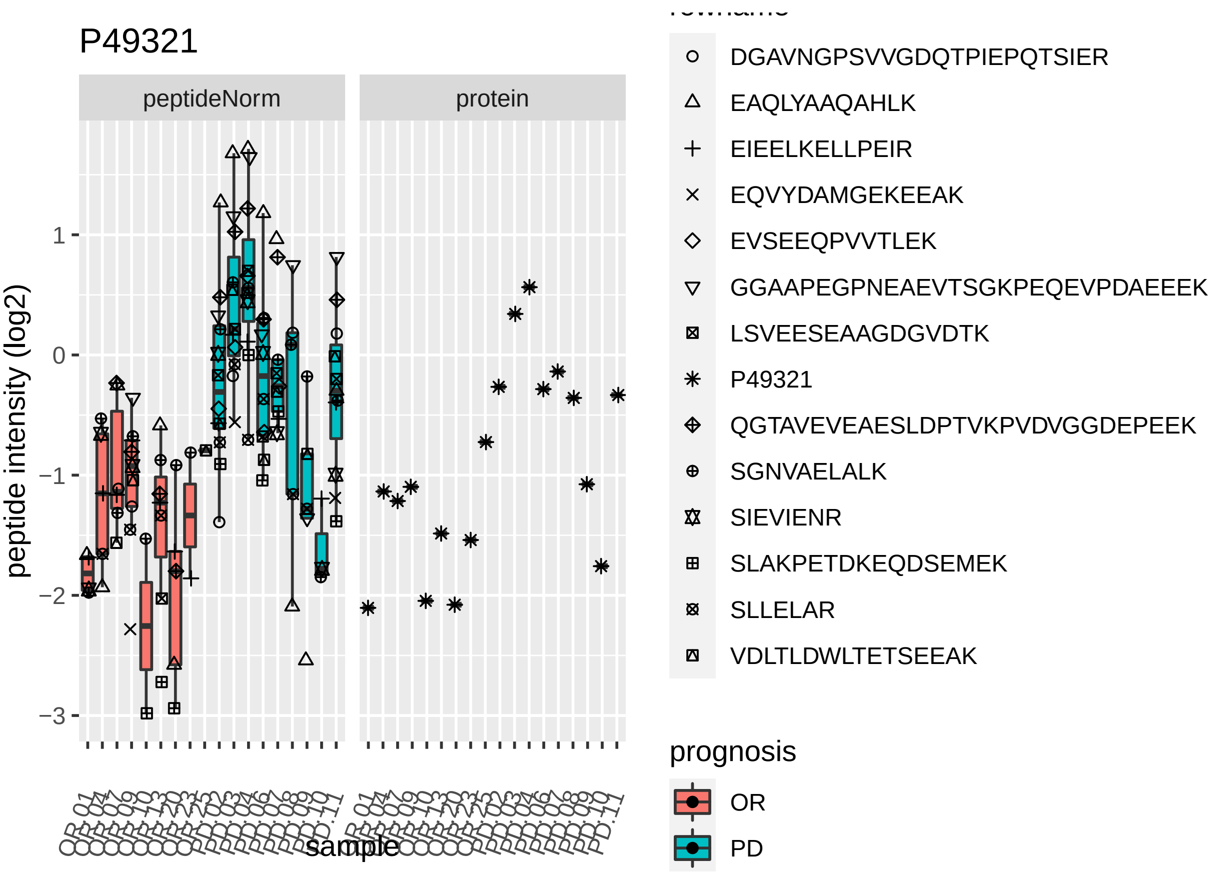
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11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peptideNorm
protein
peptide intensity (log2)
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−1
−2
−3
sample
OR.01
PD.11
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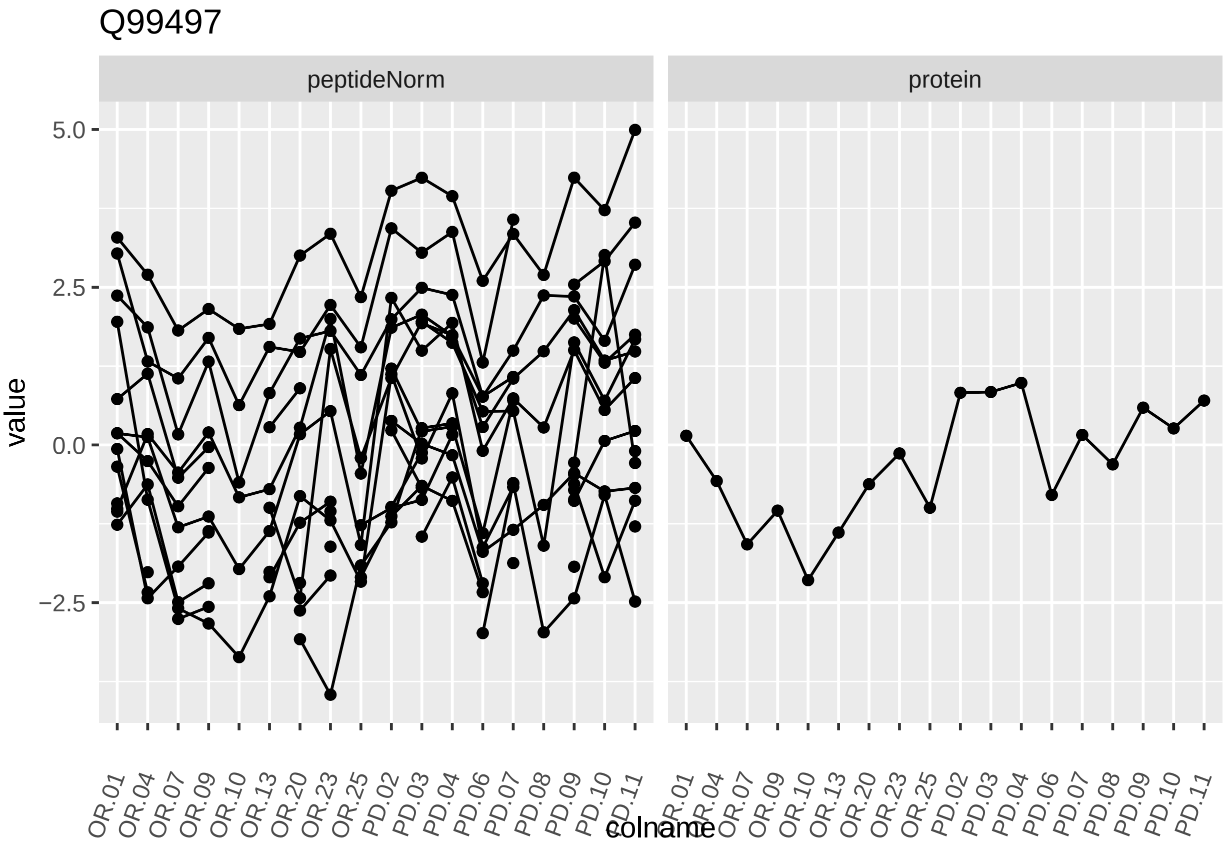
EIEELKELLPEIR
EQVYDAMGEKEEAK
EVSEEQPVVTLEK
GGAAPEGPNEAEVTSGKPEQEVPDAEEEK
LSVEESEAAGDGVDTK
P49321
QGTAVEVEAESLDPTVKPVDVGGDEPEEK
SGNVAELALK
SIEVIENR
SLAKPETDKEQDSEMEK
SLLELAR
VDLTLDWLTETSEEAK
prognosis
OR
PD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protein
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0.0
−2.5
colname
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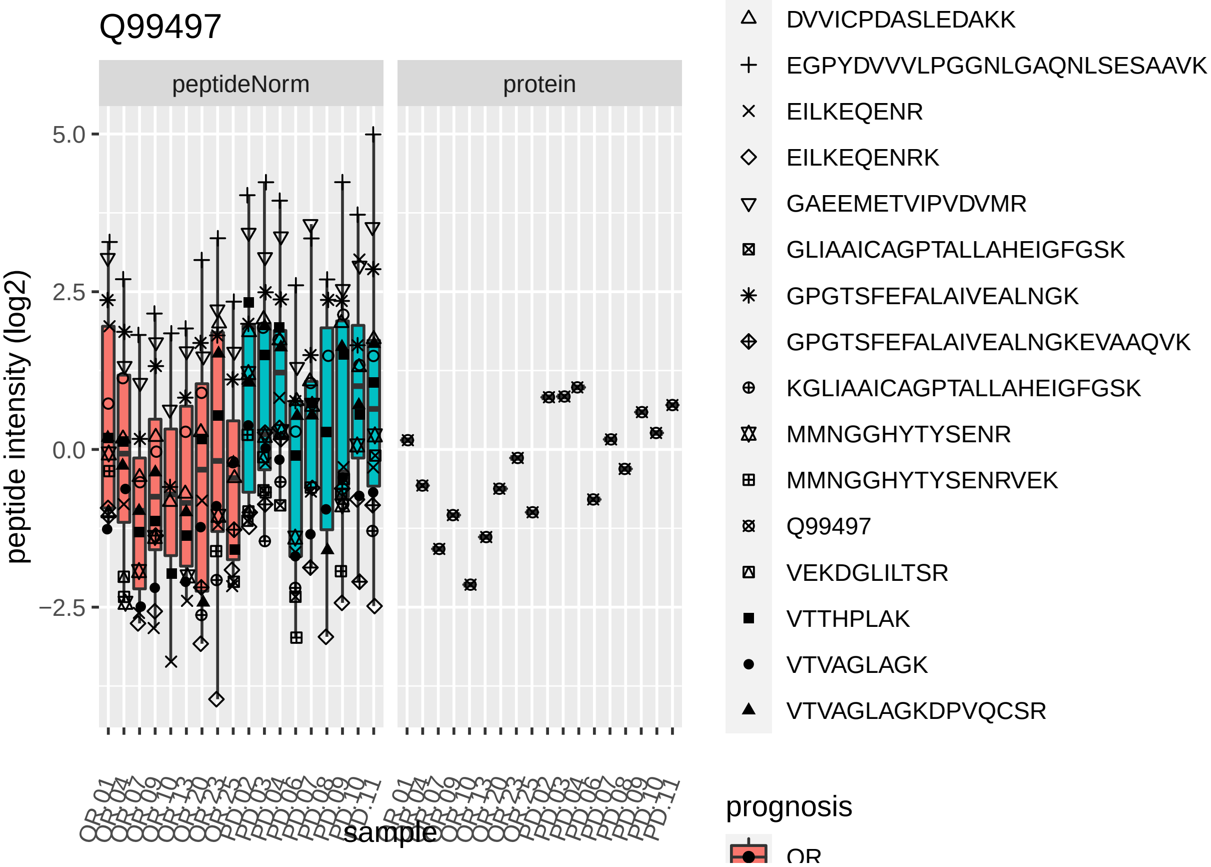
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11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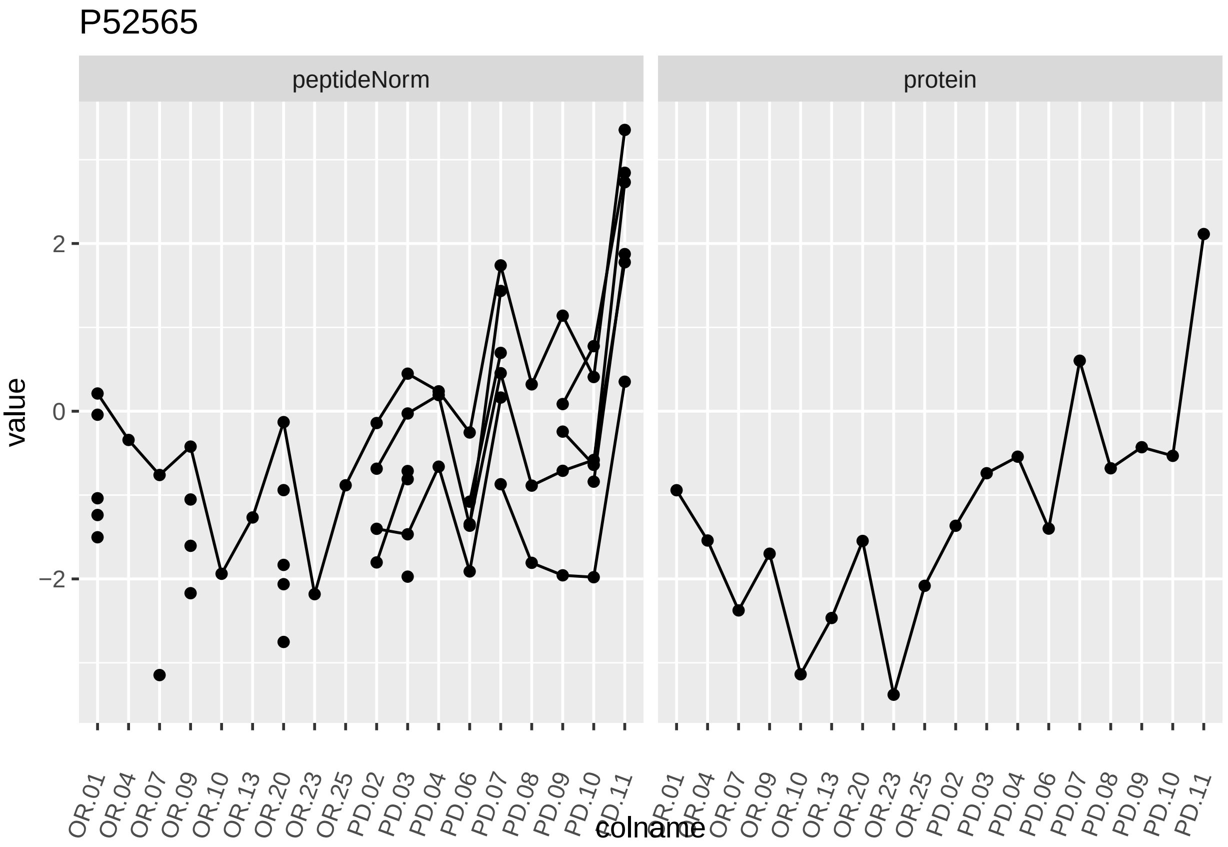
peptideNorm
protein
peptide intensity (log2)
5.0
2.5
0.0
−2.5
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
△ DVVICPDASLEDAKK
+ EGPYDVVVLPGGNLGAQNLSESAAVK
× EILKEQENR
◇ EILKEQENRK
▽ GAEEMETVIPVDVMR
⊠ GLIAAICAGPTALLAHEIGFGSK
✳ GPGTSFEFALAIVEALNGK
◈ GPGTSFEFALAIVEALNGKEVAAQVK
⊕ KGLIAAICAGPTALLAHEIGFGSK
✡ MMNGGHYTYSENR
⊞ MMNGGHYTYSENRVEK
⊗ Q99497
◪ VEKDGLILTSR
■ VTTHPLAK
● VTVAGLAGK
▲ VTVAGLAGKDPVQCSR
prognosis
OR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−2
colname
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OR.07
OR.09
OR.10
OR.13
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OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
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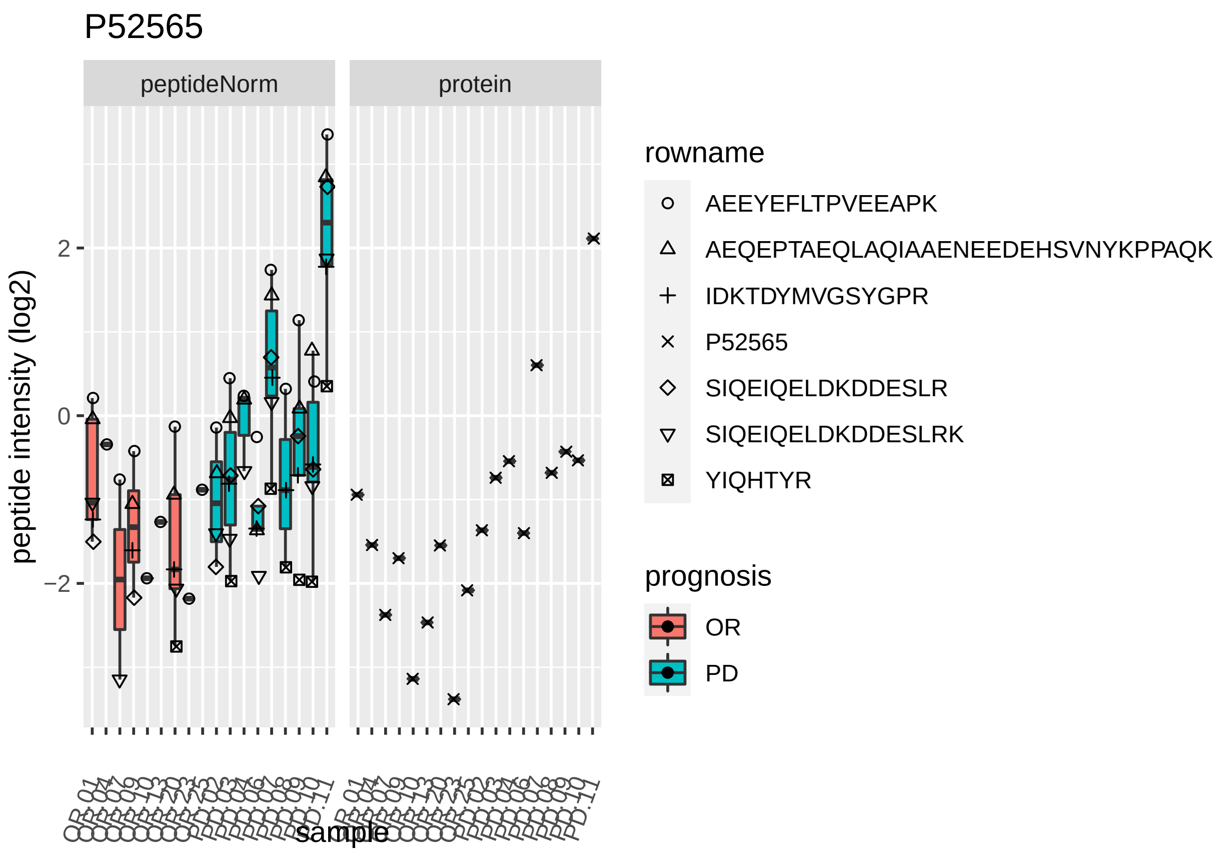
PD.10
PD.11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peptideNorm
protein
peptide intensity (log2)
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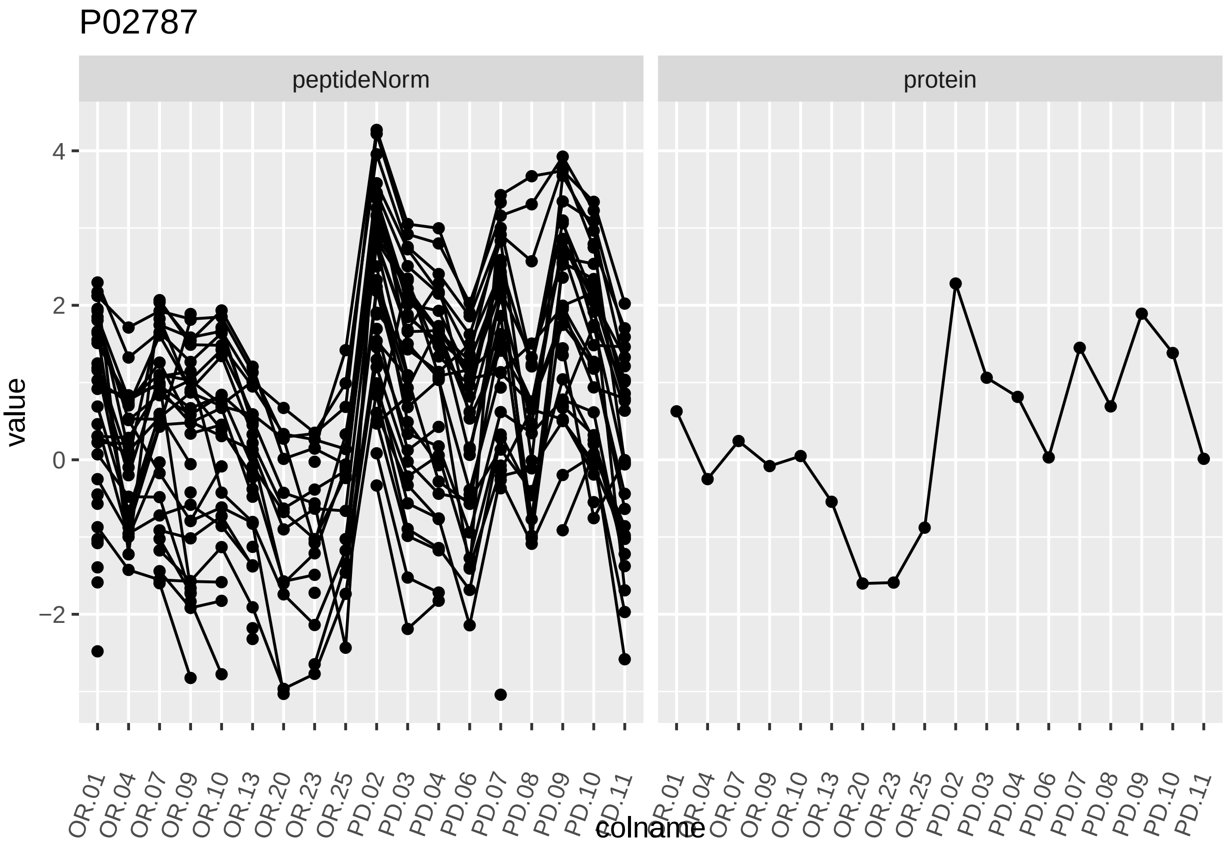
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.21
OR.23
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ AEEYEFLTPVEEAPK
△ AEQEPTAEQLAQIAAENEEDEHSVNYKPPAQK
+ IDKTDYMVGSYGPR
× P52565
◇ SIQEIQELDKDDESLR
▽ SIQEIQELDKDDESLRK
⊠ YIQHTYR
prognosis
🟥 OR
🟦 PD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colname
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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

P02787
peptide intensity (log2)
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2
0
−2
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CDEWSVNSVGK
CSTSSLLEACTFR
DCHLAQVPSHTVVAR
DDTVCLAK
DGAGDVAFVK
DLLFRDDTVCLAK
DQYELLCLDNTR
DSAHGFLK
DSGFQMNQLR
DYELLCLDGTR
EDPQTFYYAVAVVK
EFQLFSSPHGK
EGTCPEAPTDECKPVK
EGYYGYTGAFR
FDEFFSEGCAPGSK
HQTVPQNTGGK
IMNGEADAMSLDGGFVHAGK
KASYLDCIR
KPVDEYKDCHLAQVPSHTVVAR
KPVEEYANCHLAR
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LKCDEWSVNSVGK
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P02787
SAGWNIPIGLLYCDLPEPR
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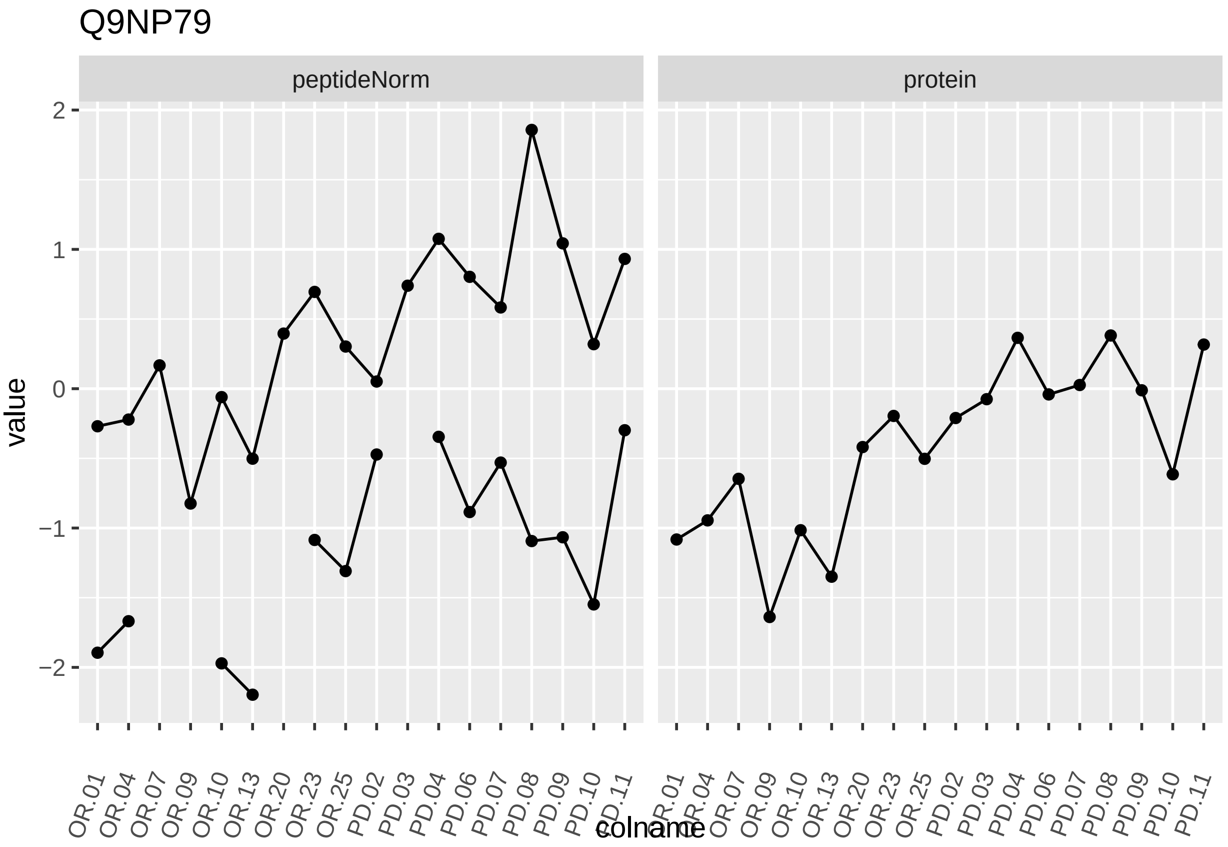
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protein
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−2
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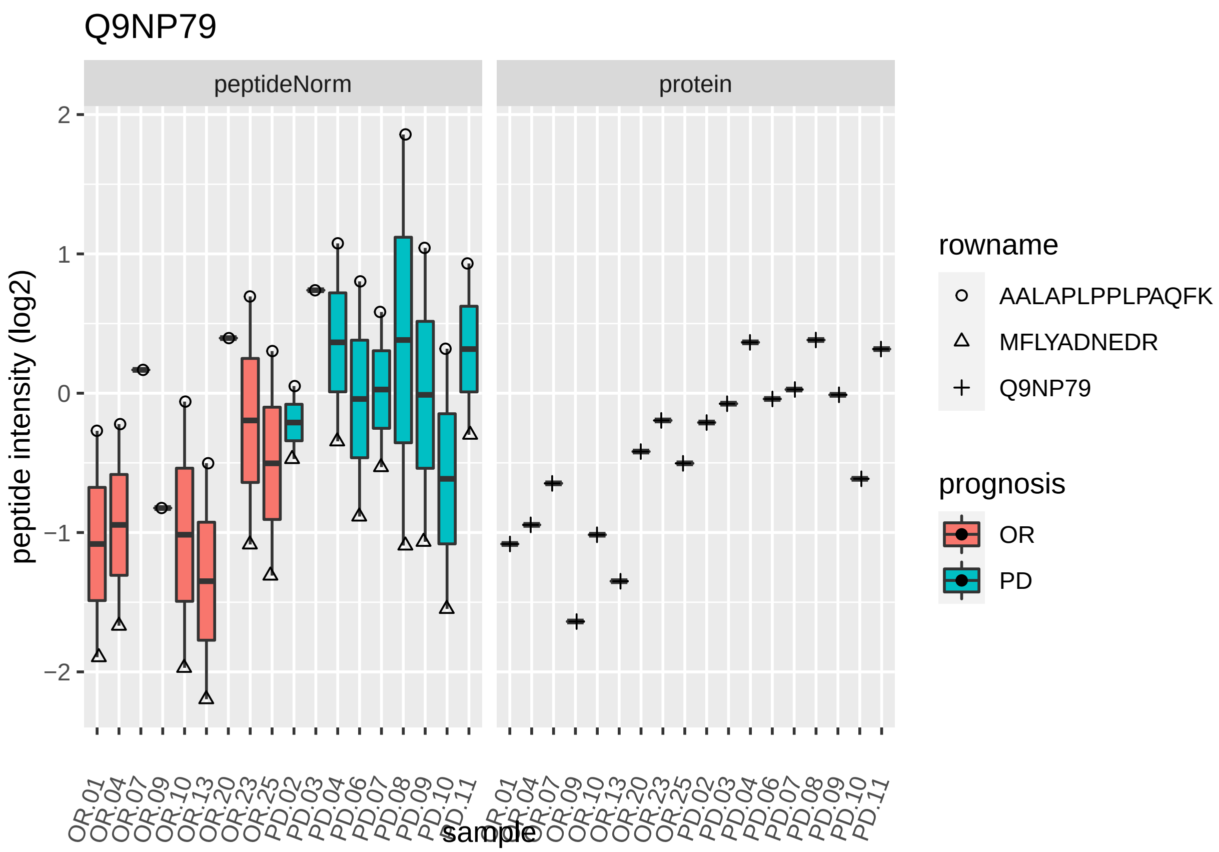
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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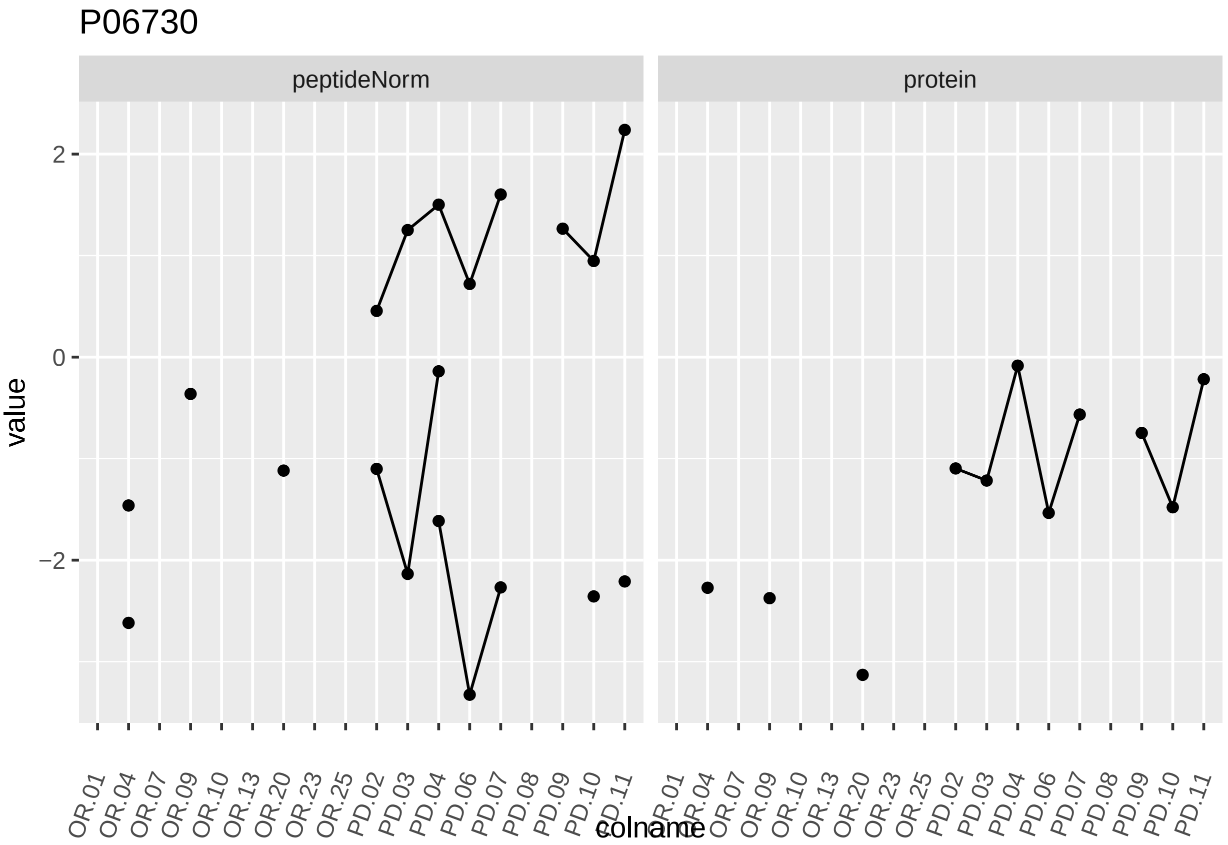
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ AALAPLPPLPAQFK
△ MFLYADNEDR
+ Q9NP79
prognosis
OR
PD


P06730
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protein
value
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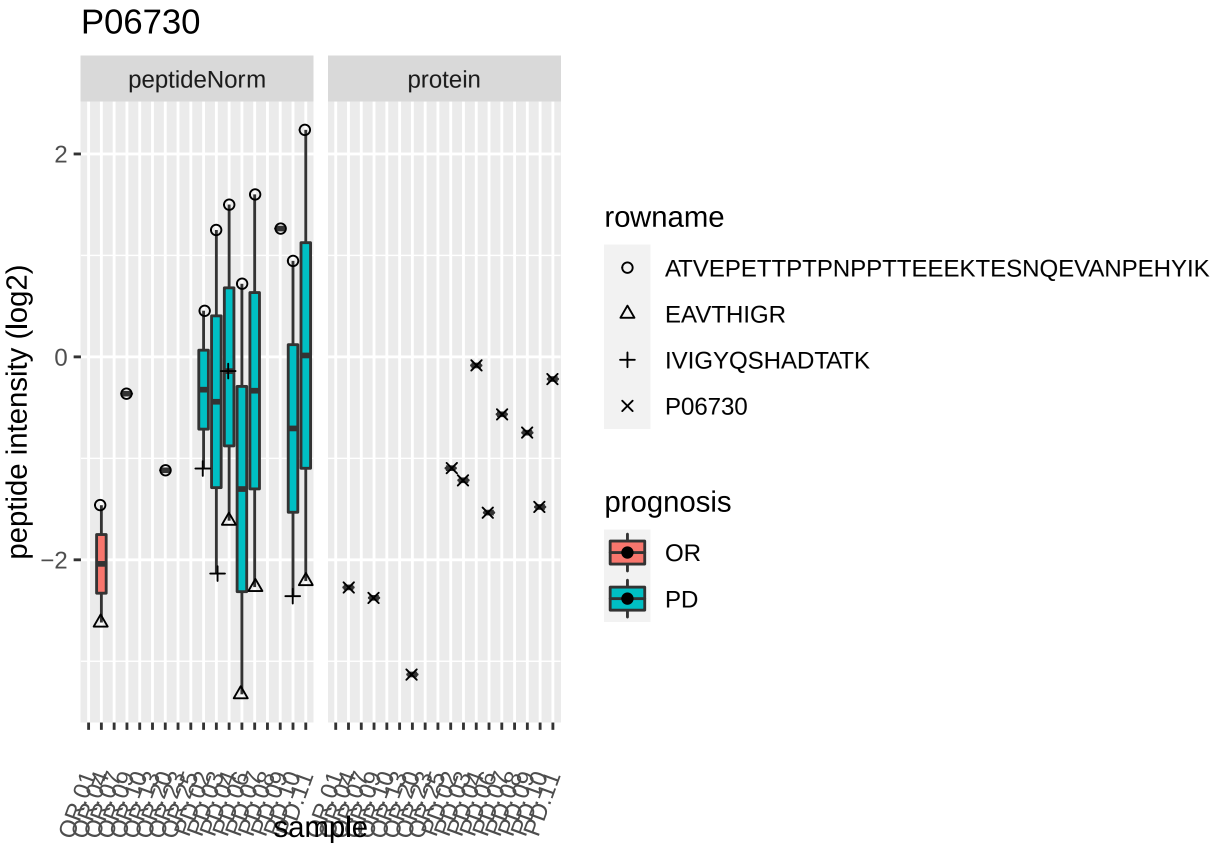
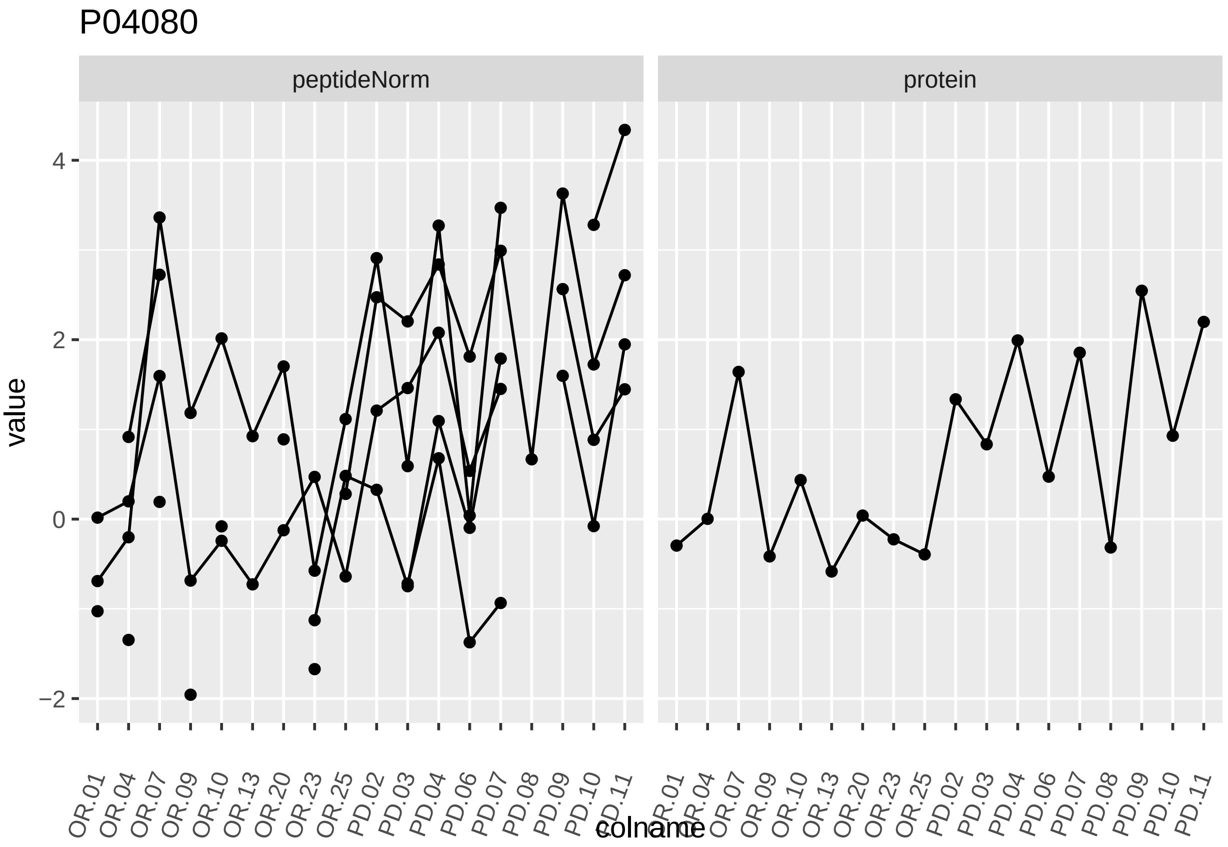
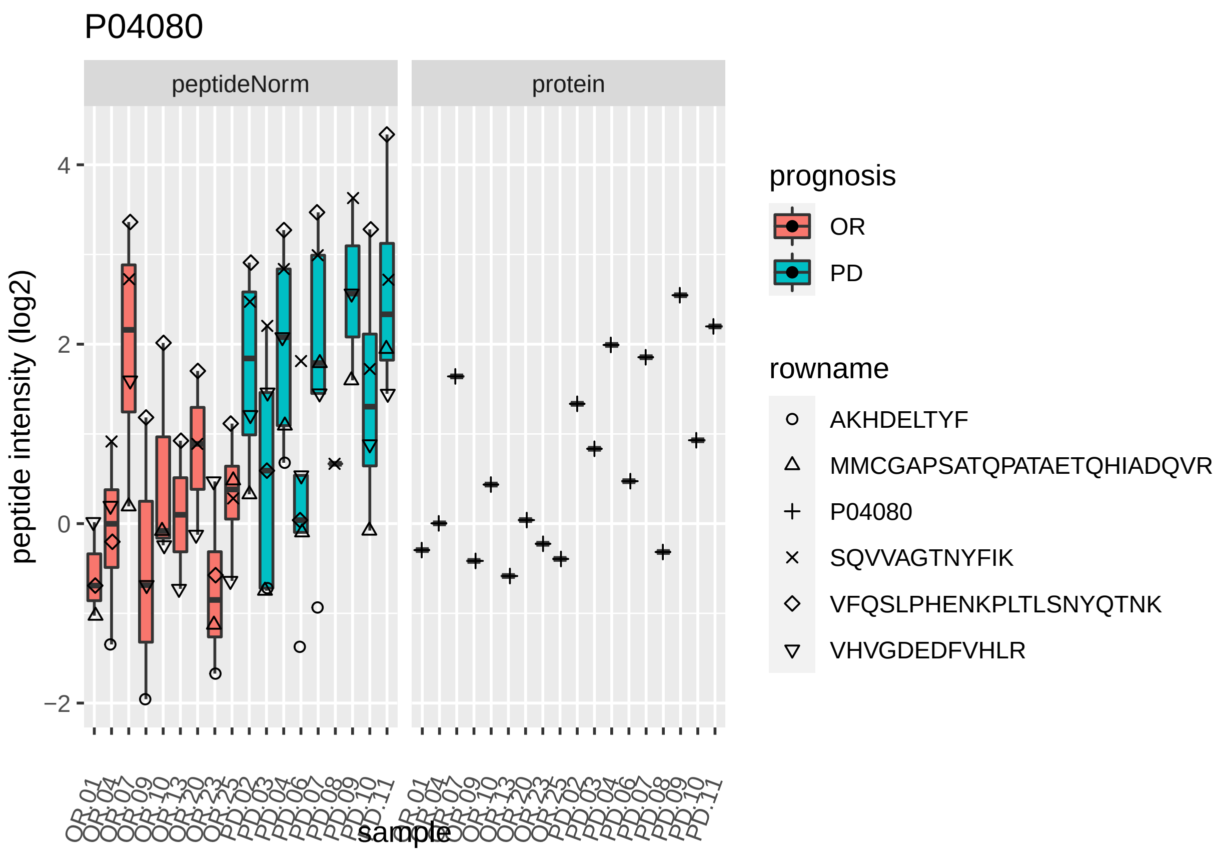
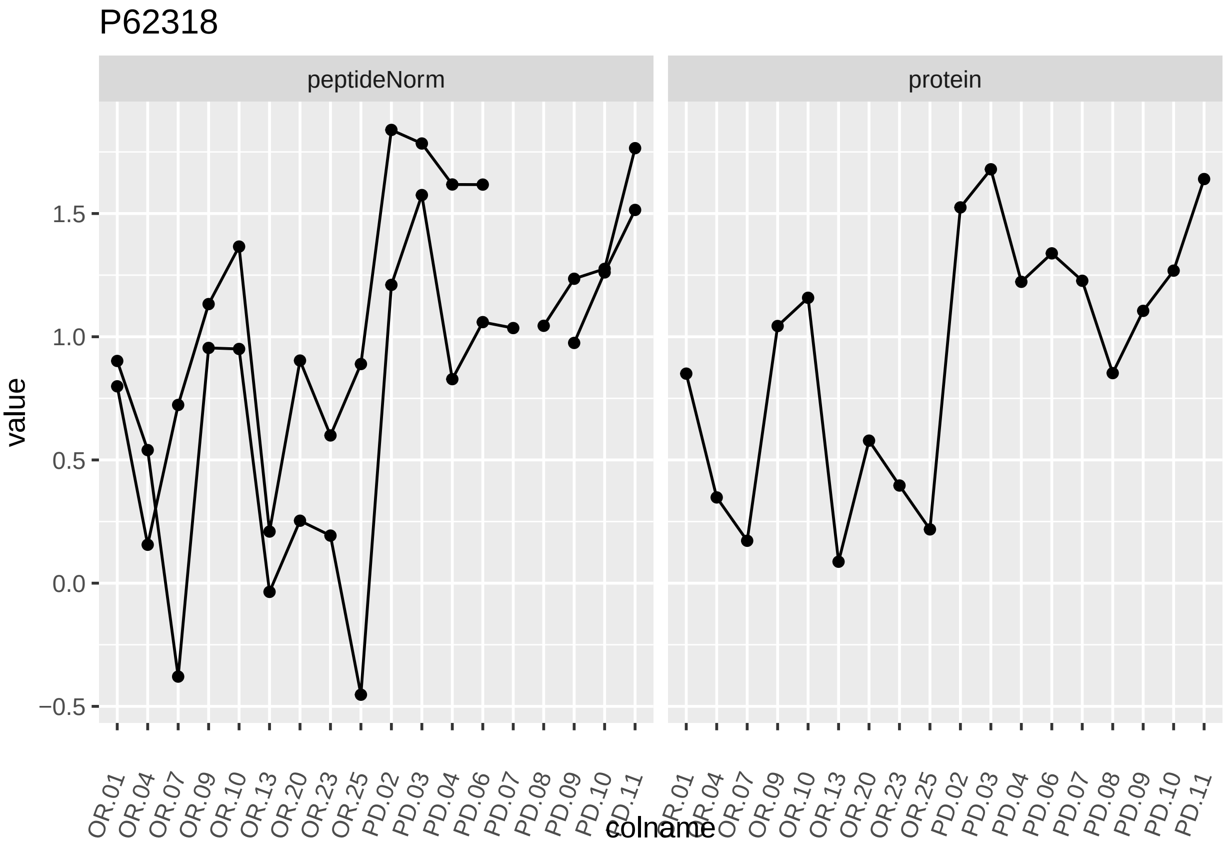
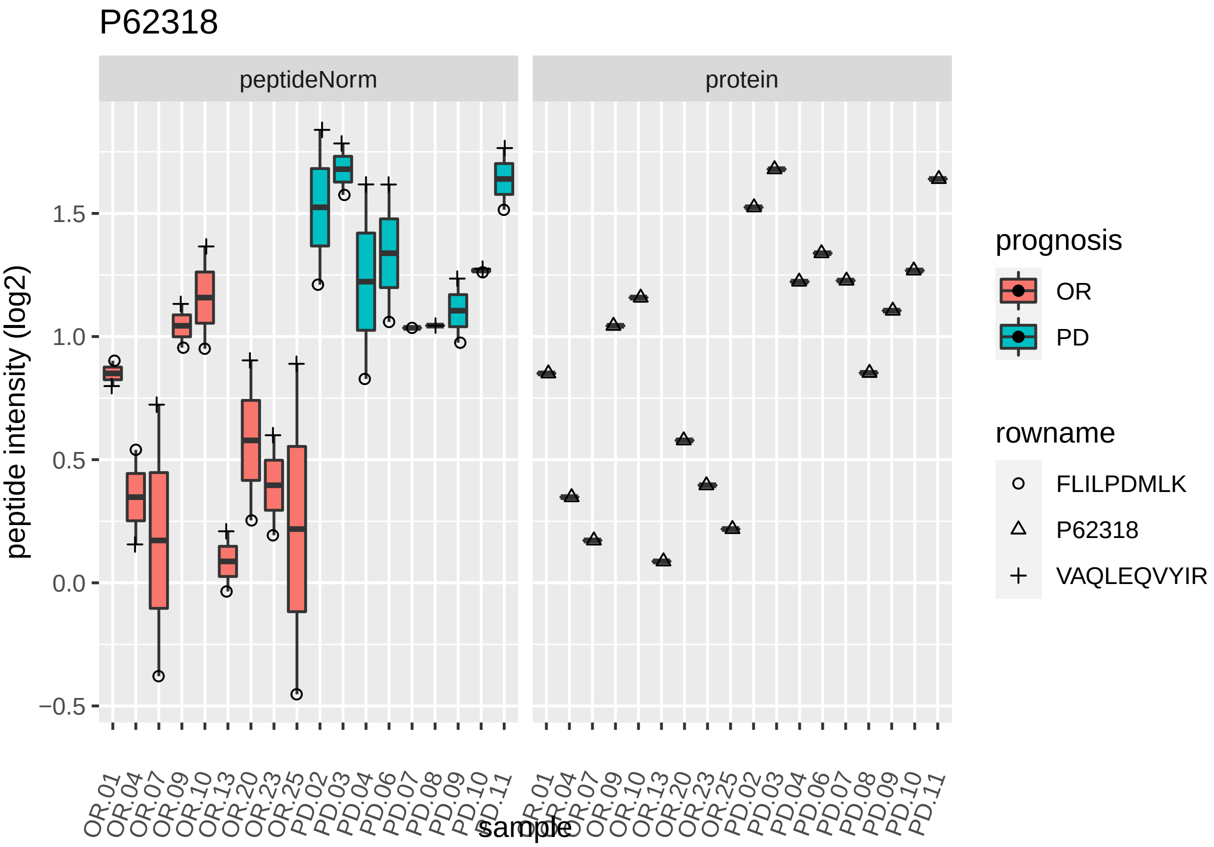
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

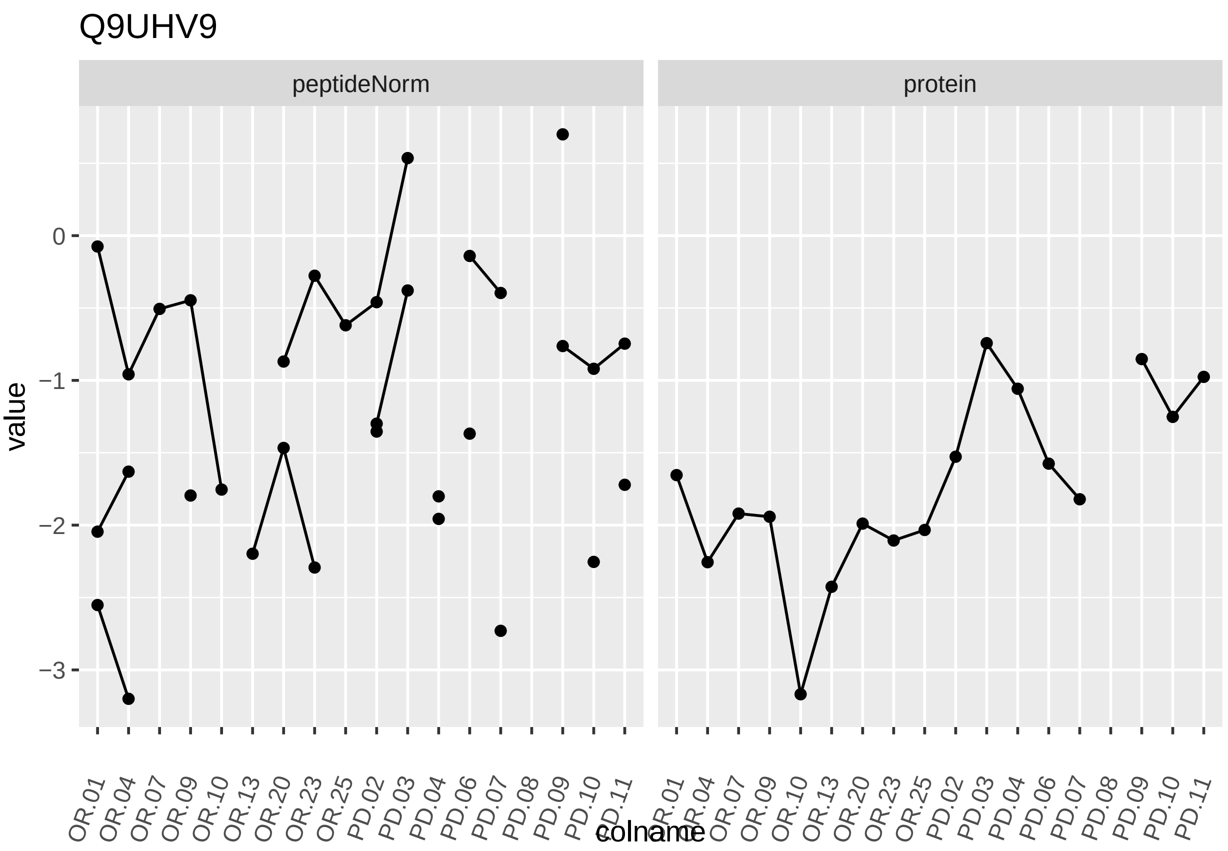

P06730
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
PD.11
rowname
○ ATVEPETTPTPNPPTTEEEKTESNQEVANPEHYIK
△ EAVTHIGR
+ IVIGYQSHADTATK
× P06730
prognosis
OR
PD

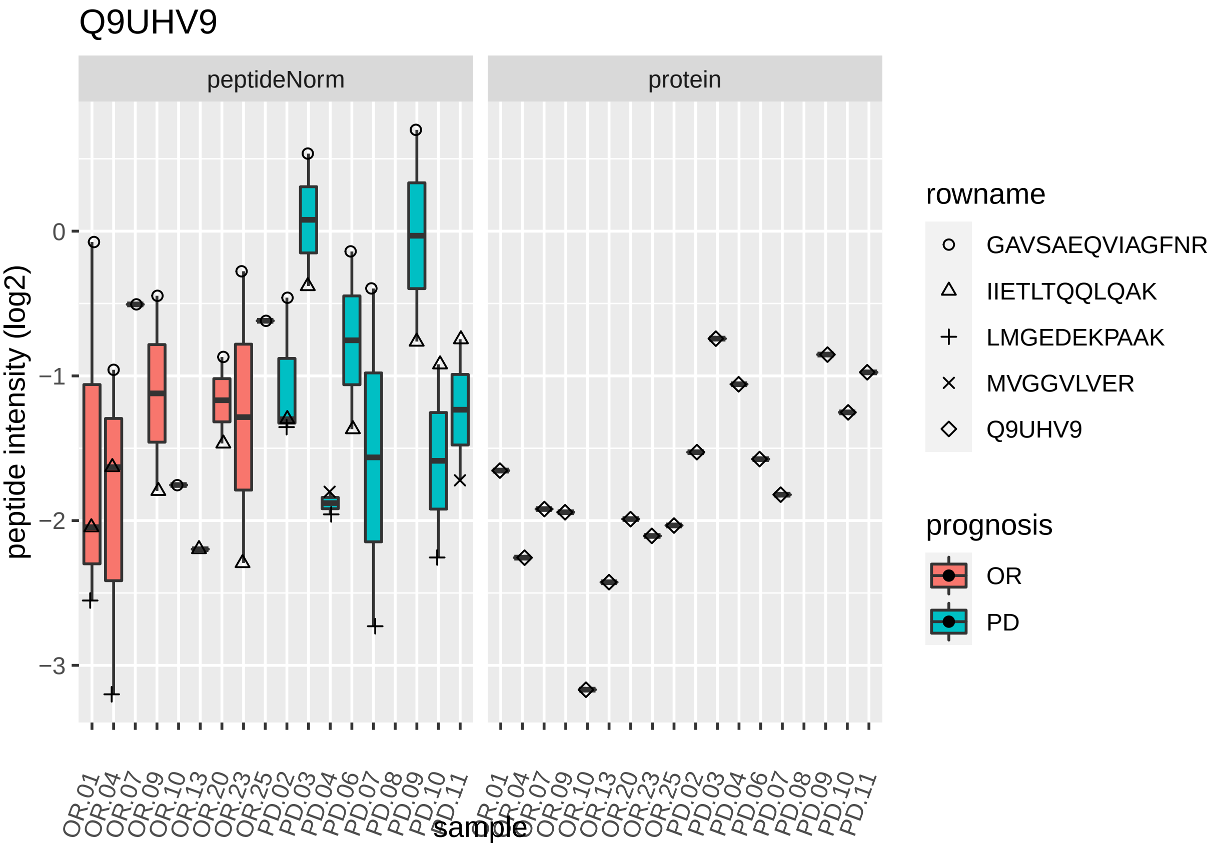

P04080
peptideNorm
protein
value
4
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

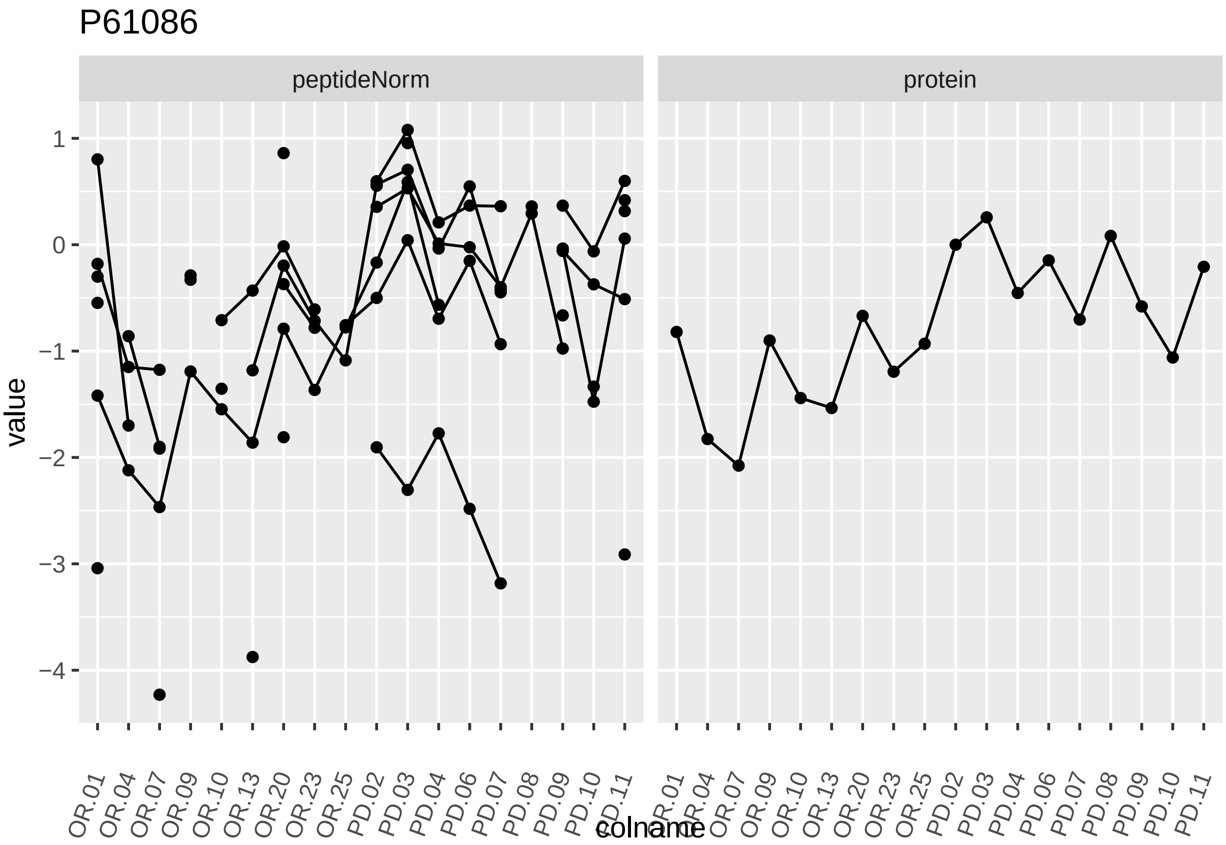

P04080
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname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

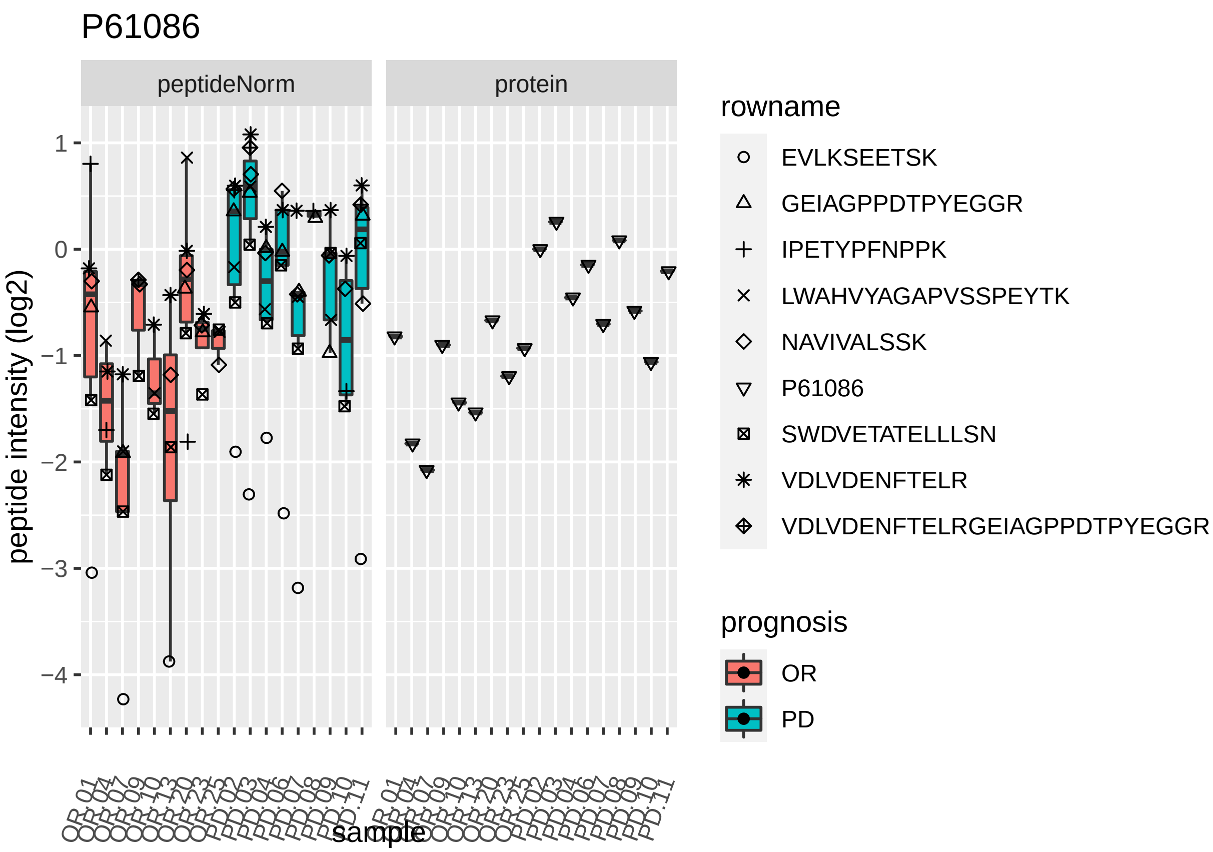

P62318
peptideNorm
protein
value
1.5
1.0
0.5
0.0
−0.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

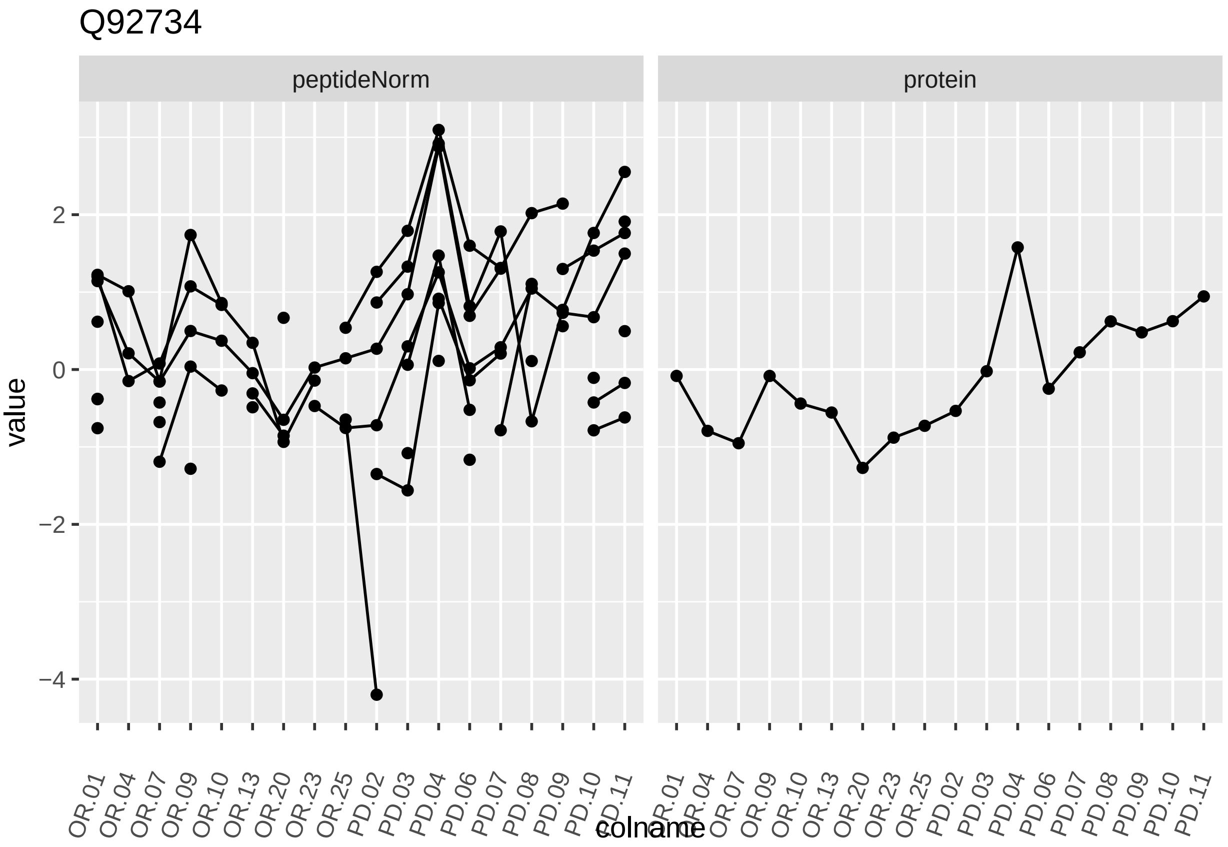

P62318
peptideNorm
protein
peptide intensity (log2)
1.5
1.0
0.5
0.0
−0.5
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
FLILPDMLK
P62318
VAQLEQVYIR

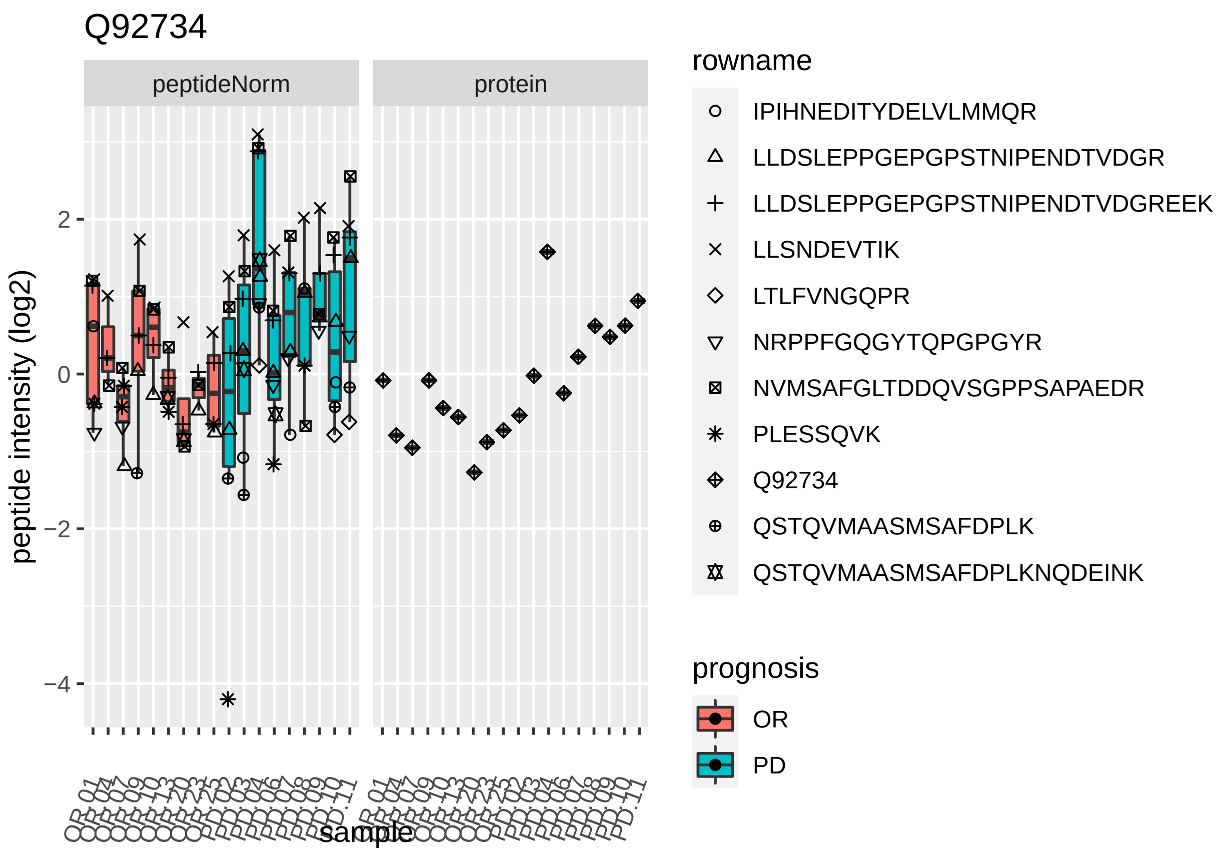

Q9UHV9
peptideNorm
protein
value
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

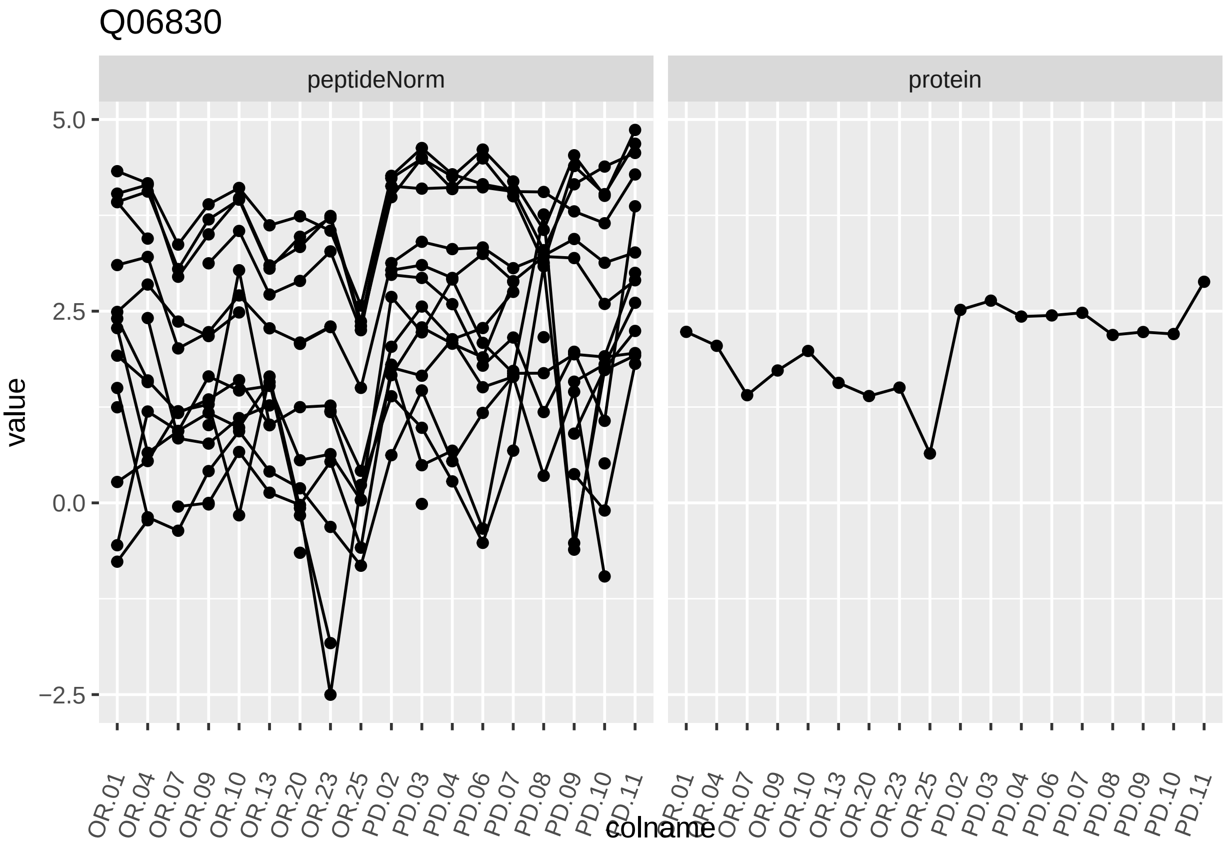

Q9UHV9
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ GAVSAEQVIAGFNR
△ IIETLTQQLQAK
+ LMGEDEKPAAK
× MVGGVLVER
◇ Q9UHV9
prognosis
OR
PD


P61086
peptideNorm
protein
value
1
0
−1
−2
−3
−4
colname
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

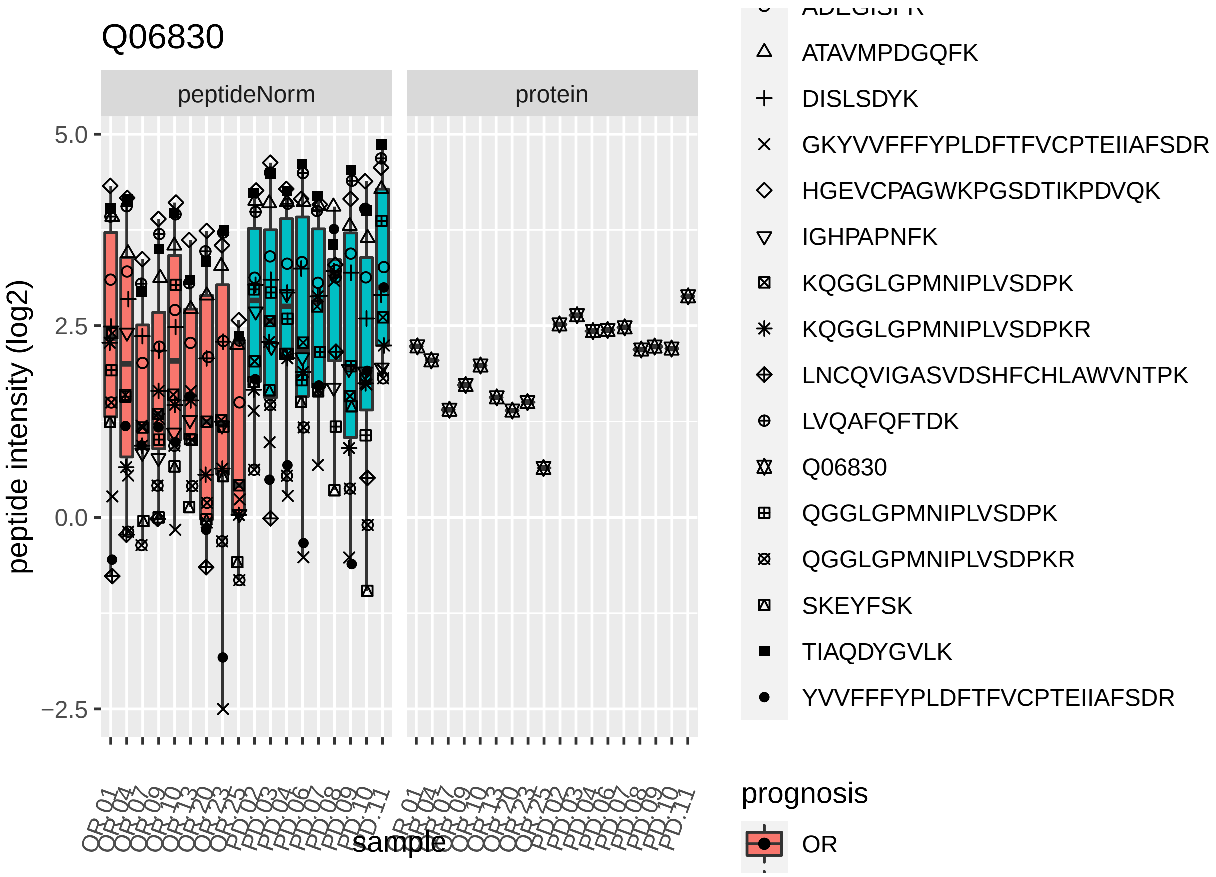

P61086
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ EVLKSEETSK
△ GEIAGPPDTPYEGGR
+ IPETYPFNPPK
× LWAHVYAGAPVSSPEYTK
◇ NAVIVALSSK
▽ P61086
⊠ SWDVETATELLLSN
✳ VDLVDENFTELR
⊕ VDLVDENFTELRGEIAGPPDTPYEGGR
prognosis
🟥 OR
🟦 PD

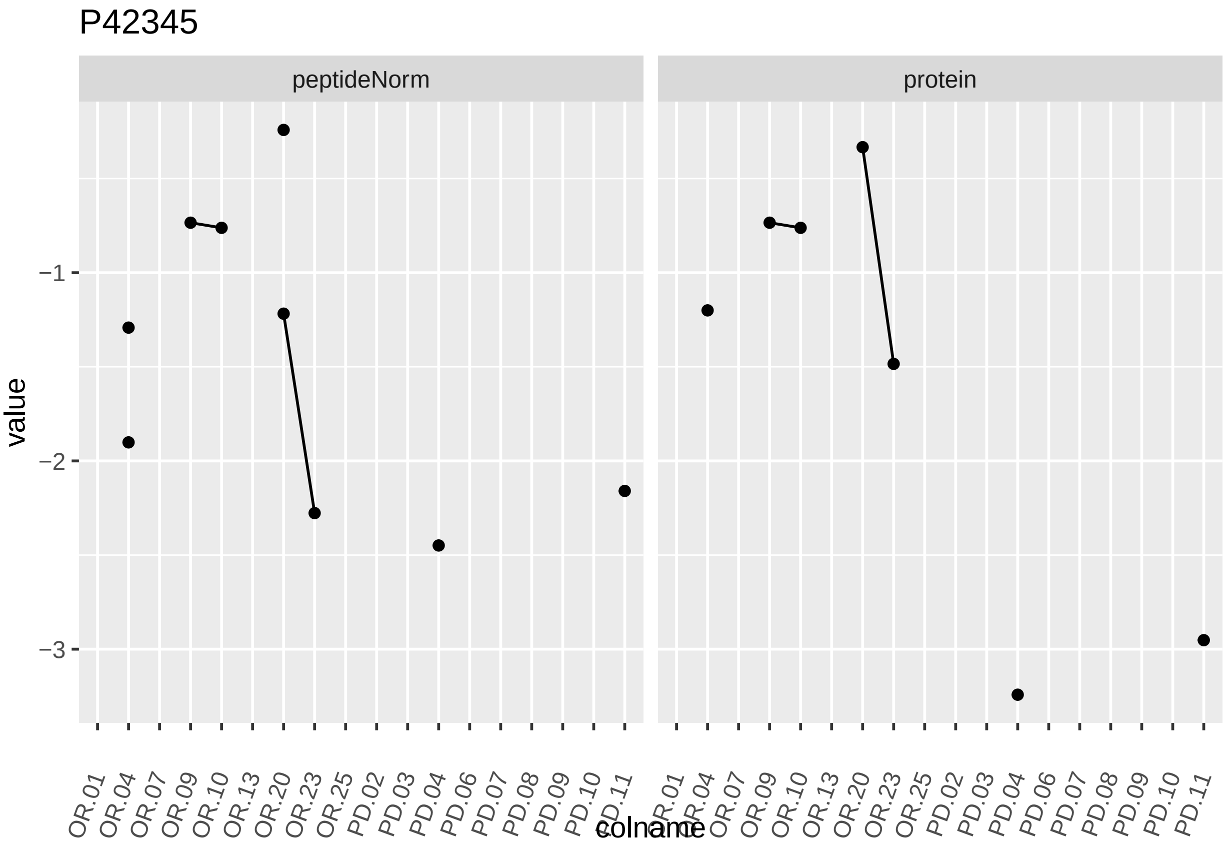

Q92734
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

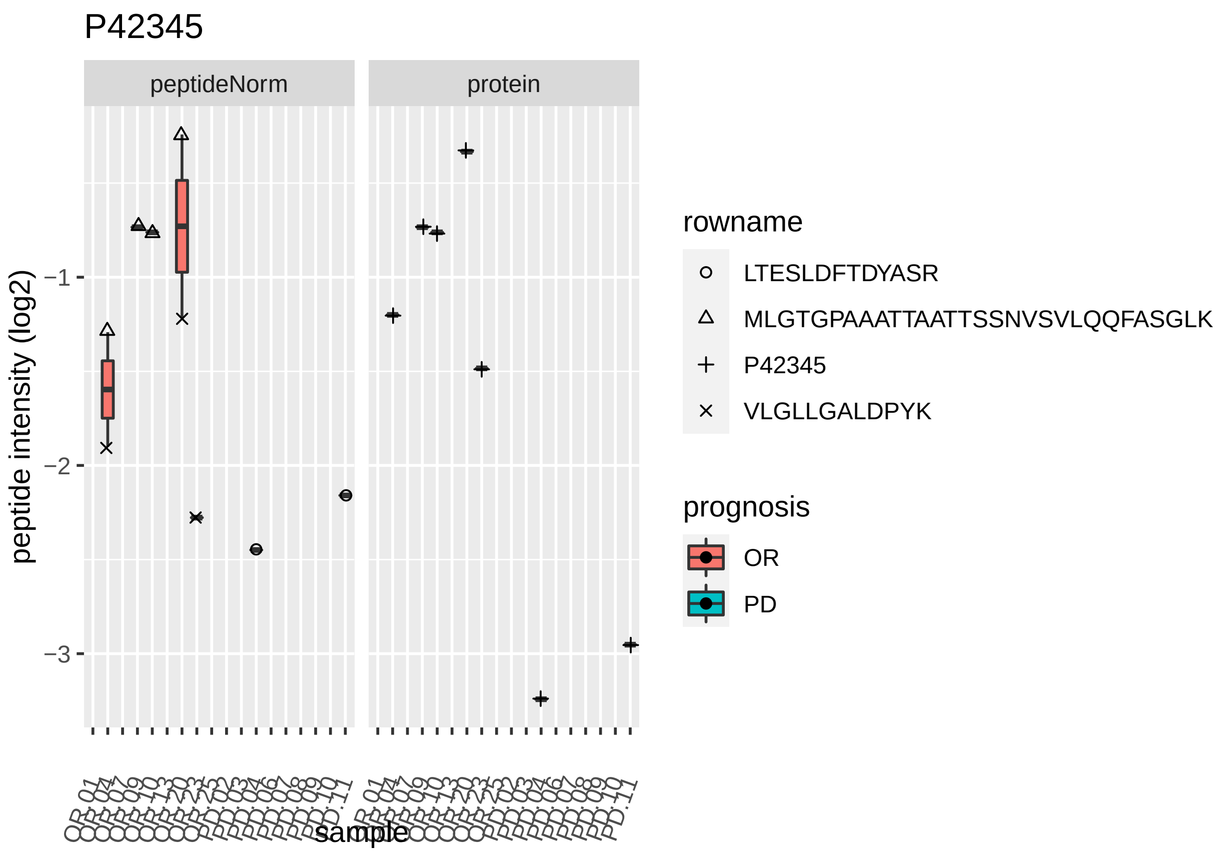

Q92734
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
rowname
○ IPIHNEDITYDELVLMMQR
△ LLDSLEPPGEPGPSTNIPENDTVDGR
+ LLDSLEPPGEPGPSTNIPENDTVDGREEK
× LLSNDEVTIK
◇ LTLFVNGQPR
▽ NRPPFGQGYTQPGPGYR
⊠ NVMSAFGLTDDQVSGPPSAPAEDR
✳ PLESSQVK
◈ Q92734
⊕ QSTQVMAASMSAFDPLK
✡ QSTQVMAASMSAFDPLKNQDEINK
prognosis
🟥 OR
🟦 PD

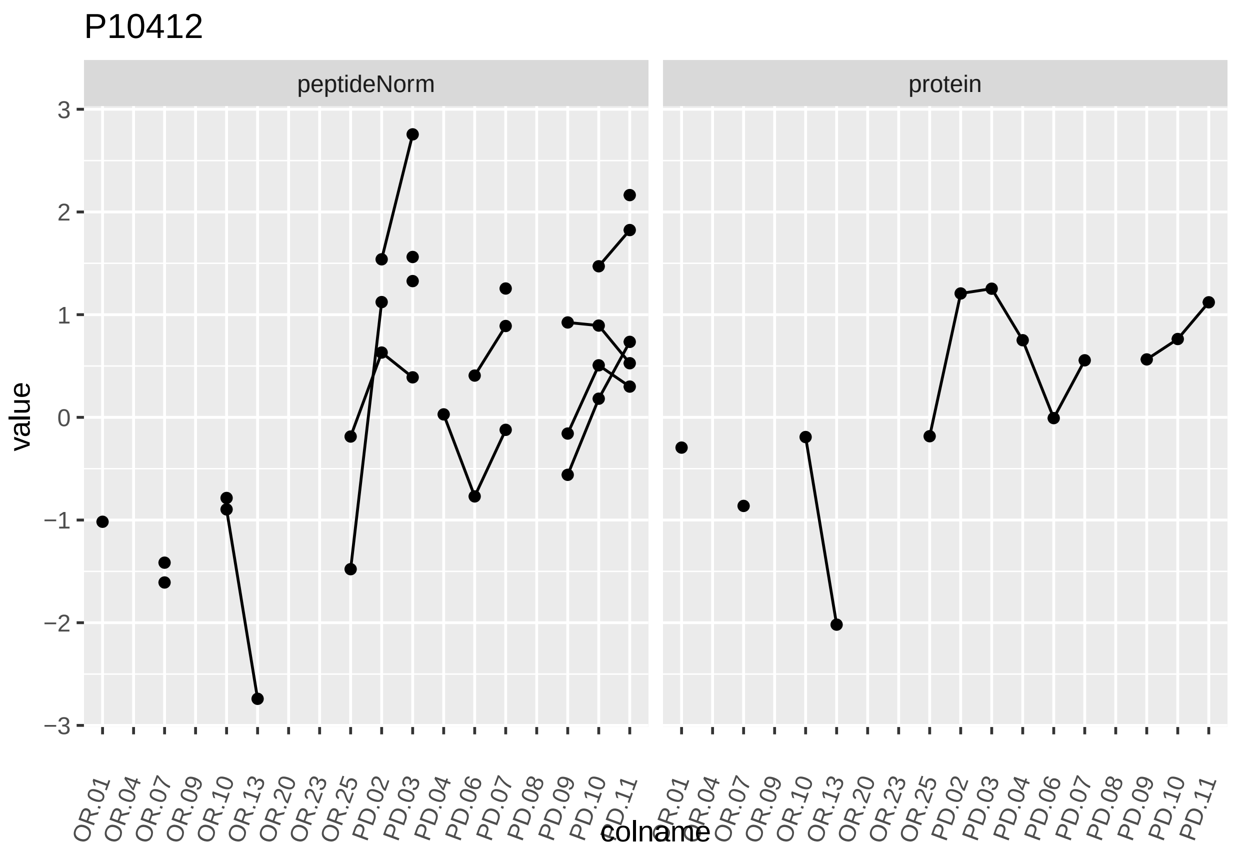


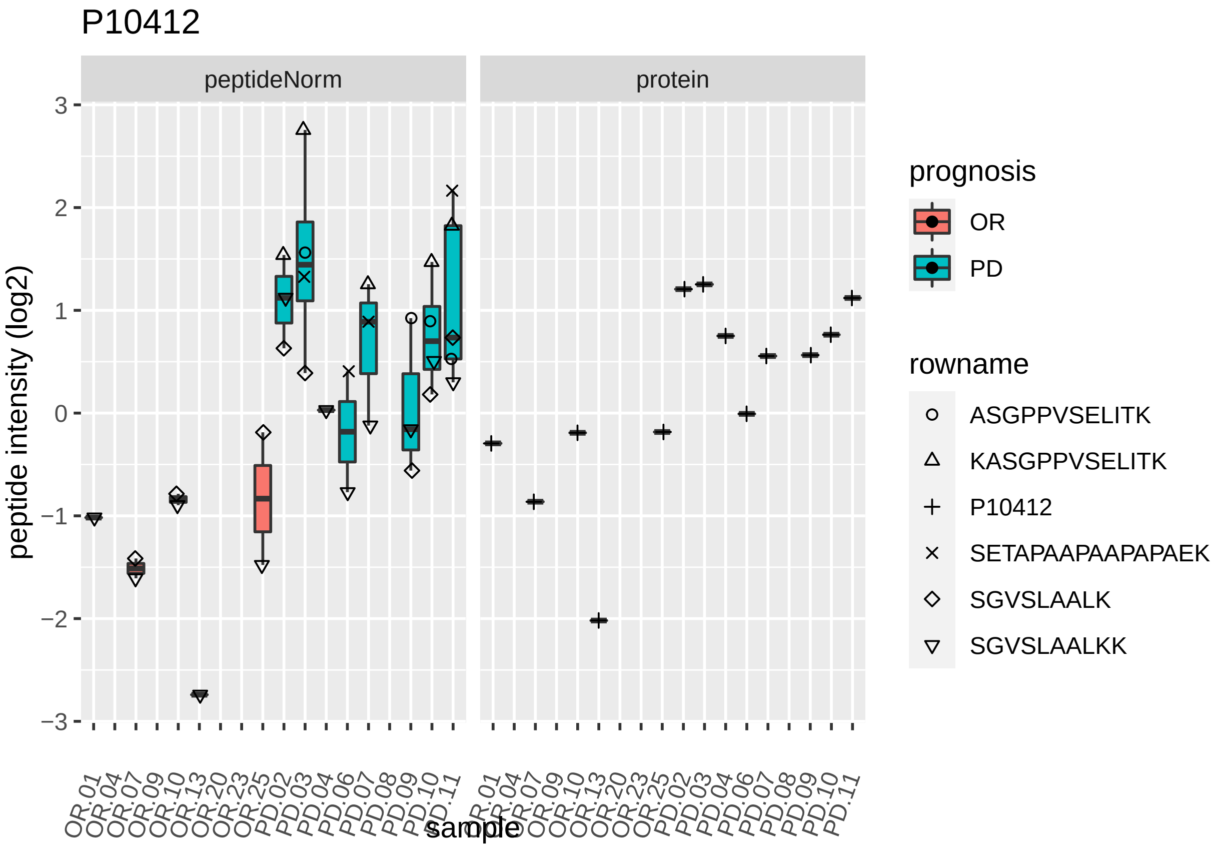
Q06830
peptideNorm
protein
value
5.0
2.5
0.0
−2.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

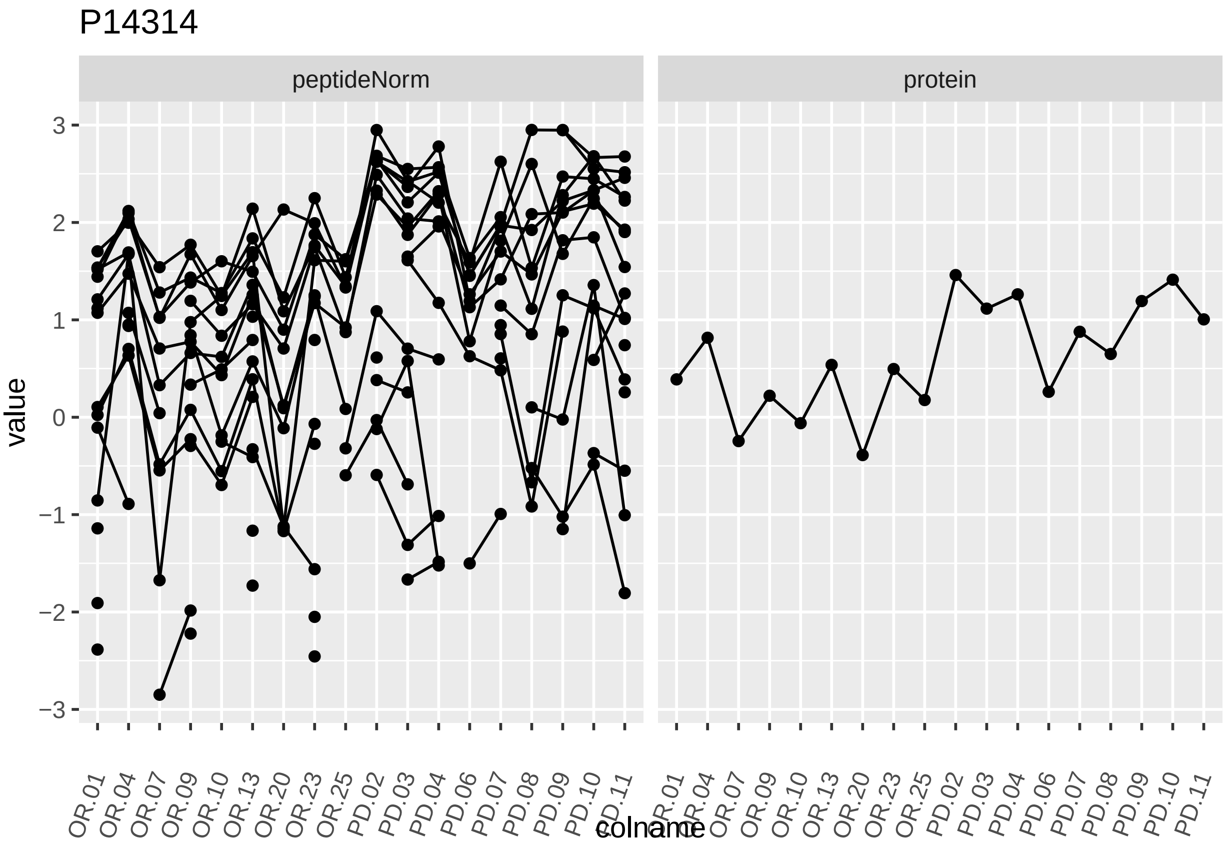

Q06830
peptideNorm
protein
peptide intensity (log2)
5.0
2.5
0.0
−2.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
ADLGISFK
△ ATAVMPDGQFK
+ DISLSDYK
× GKYVVFFFYPLDFTFVCPTEIIAFSDR
◇ HGEVCPAGWKPGSDTIKPDVQK
▽ IGHPAPNFK
⊠ KQGGLGPMNIPLVSDPK
✳ KQGGLGPMNIPLVSDPKR
◈ LNCQVIGASVDSHFCHLAWVNTPK
⊕ LVQAFQFTDK
✡ Q06830
⊞ QGGLGPMNIPLVSDPK
⊠ QGGLGPMNIPLVSDPKR
◪ SKEYFSK
■ TIAQDYGVLK
● YVVFFFYPLDFTFVCPTEIIAFSDR
prognosis
OR

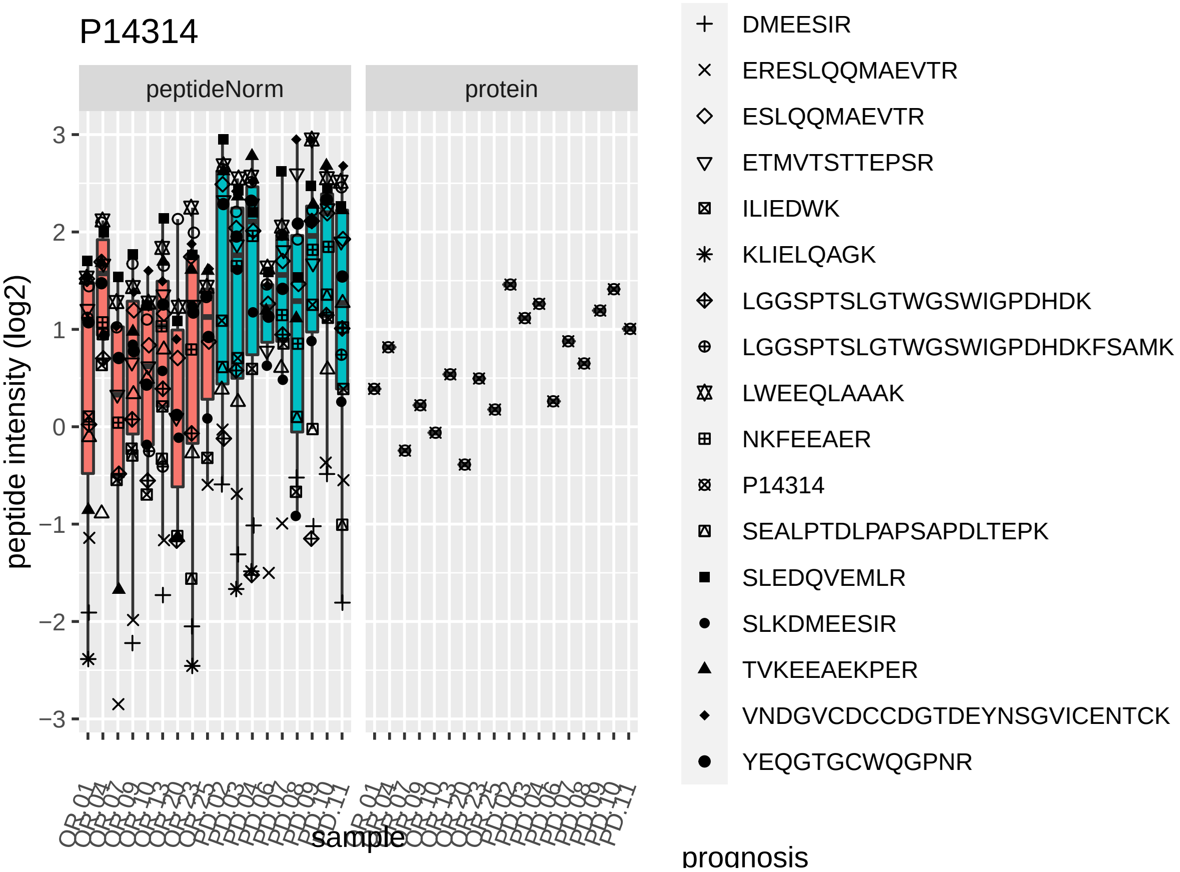

P42345
peptideNorm
protein
value
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

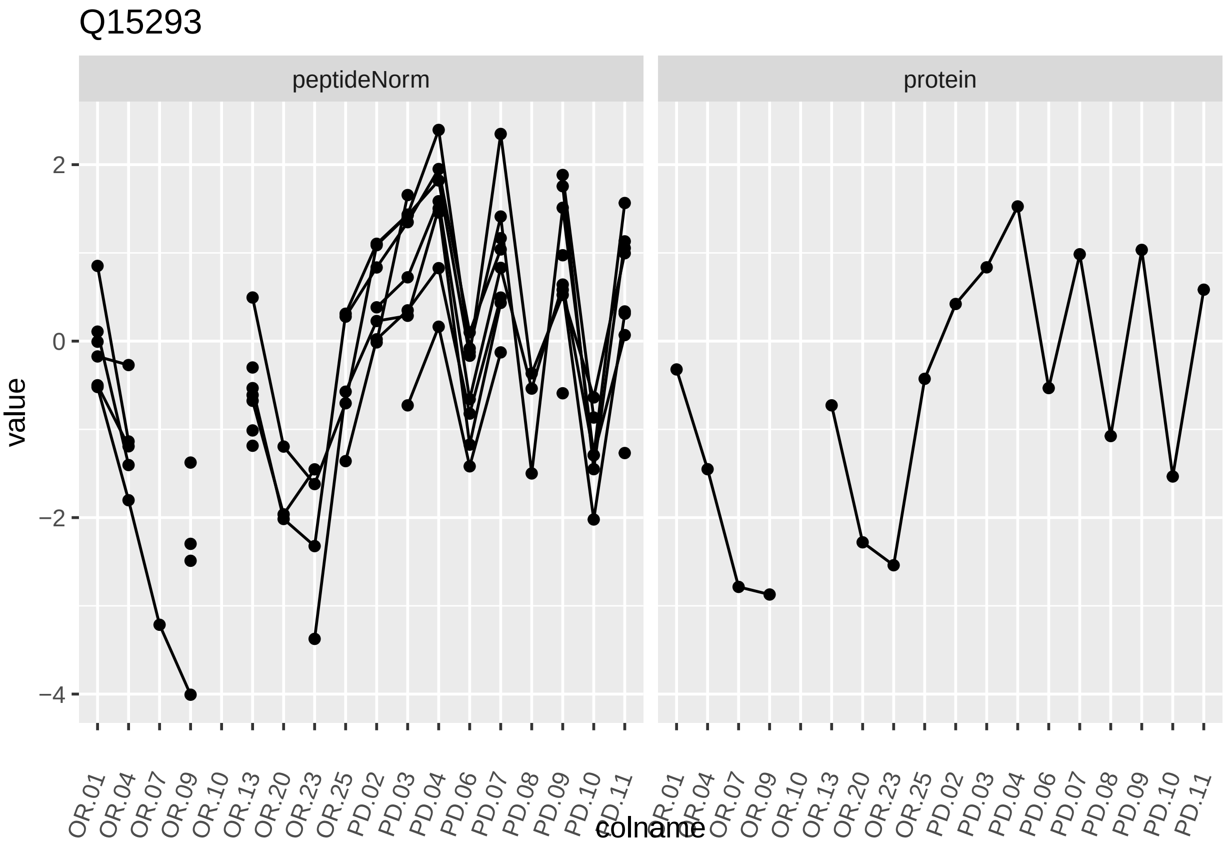

P42345
peptideNorm
protein
peptide intensity (log2)
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ LTESLDFTDYASR
△ MLGTGPAAATTAATTSSNVSVLQQFASGLK
+ P42345
× VLGLLGALDPYK
prognosis
OR
PD

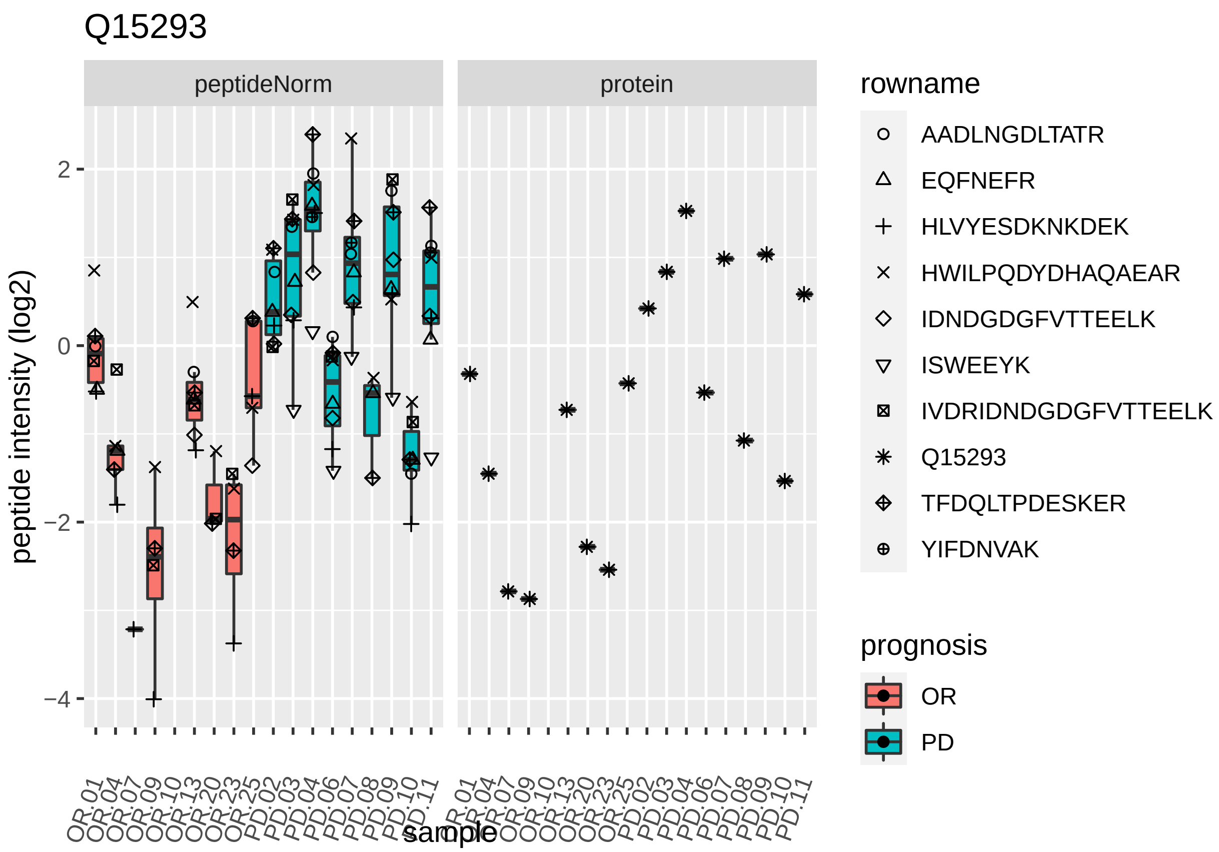

P10412
peptideNorm
protein
value
3
2
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

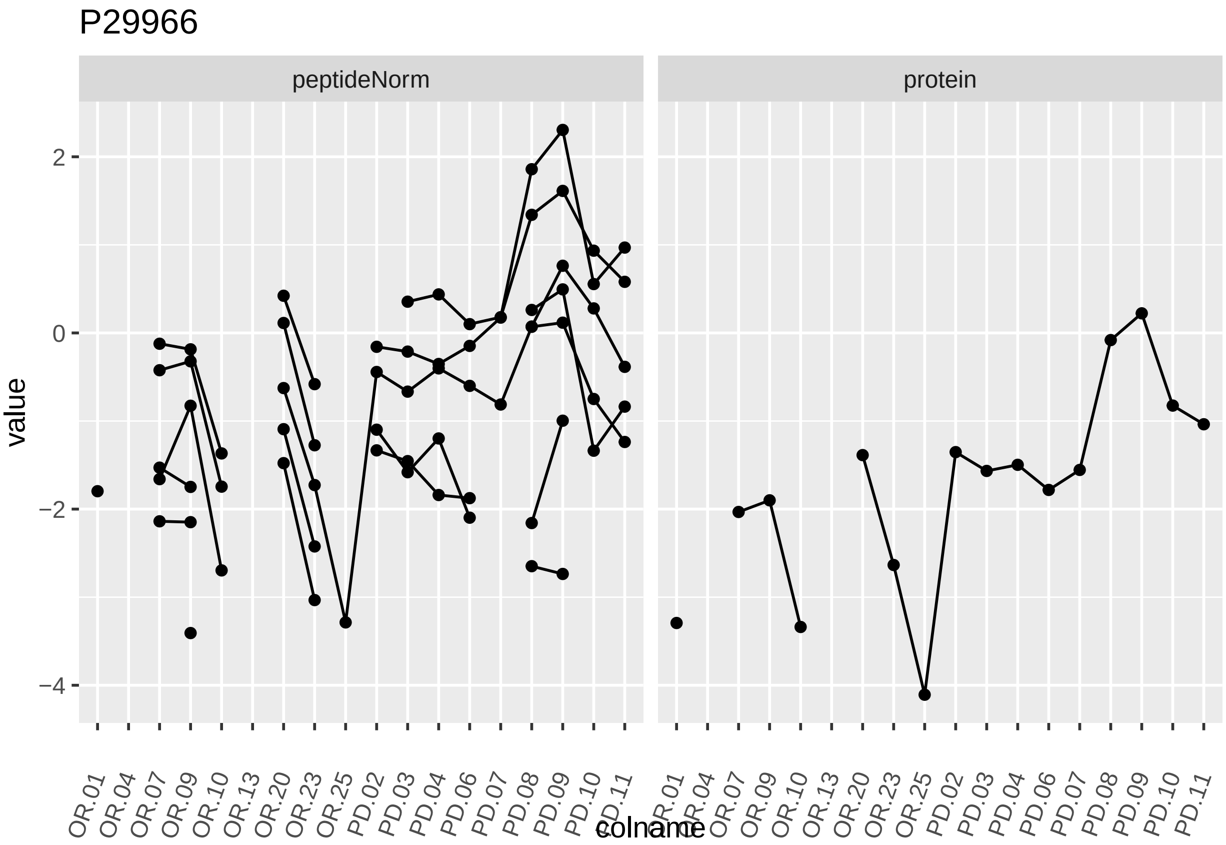

P10412
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
ASGPPVSELITK
KASGPPVSELITK
P10412
SETAPAAPAAPAPAEK
SGVSLAALK
SGVSLAALKK

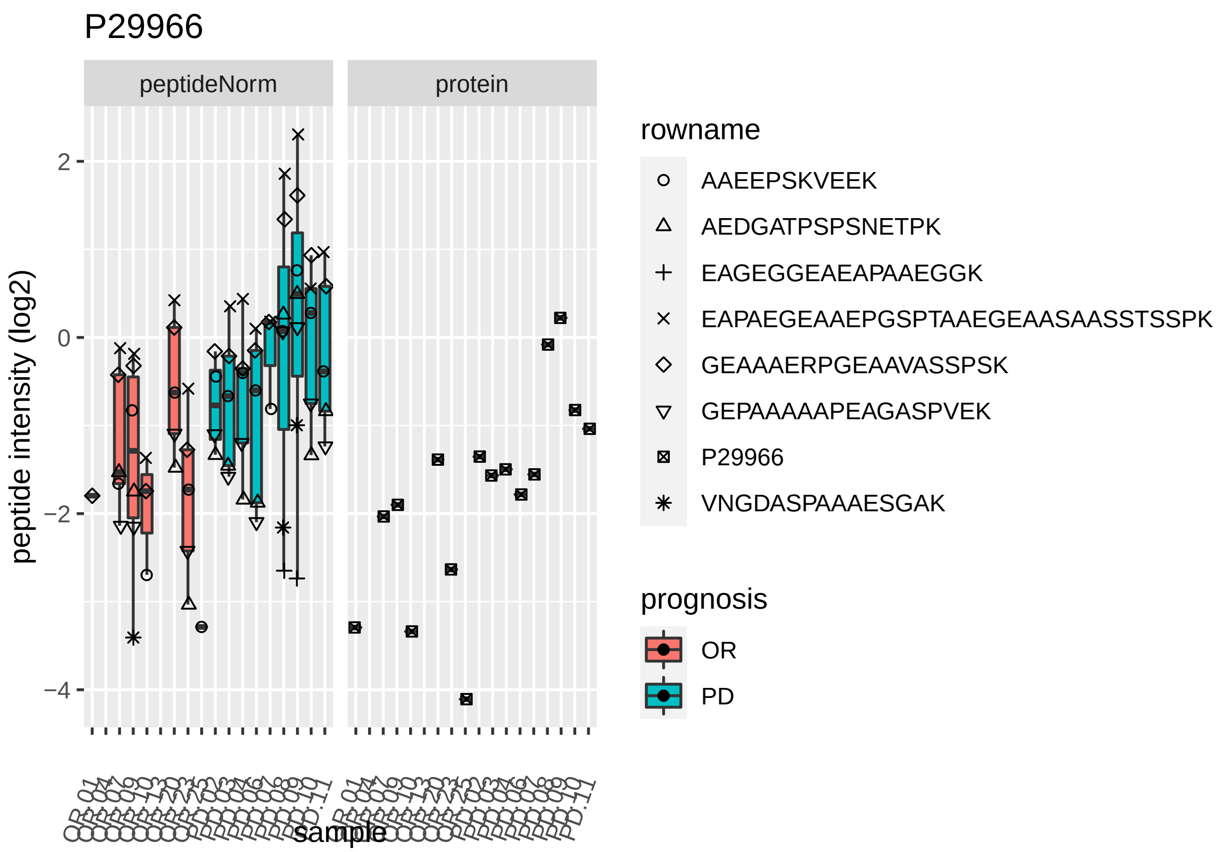

P14314
peptideNorm
protein
value
3
2
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

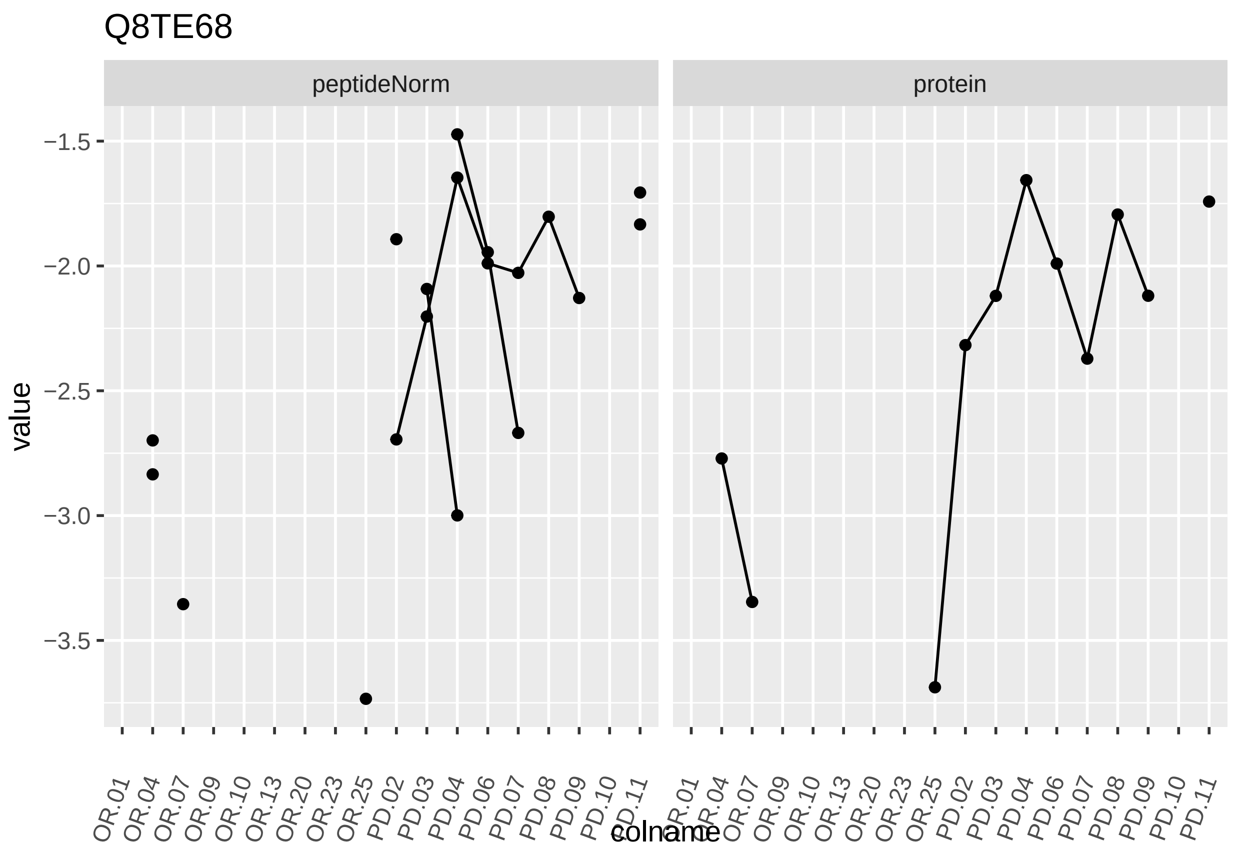

P14314
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
+ DMEESIR
× ERESLQQMAEVTR
◇ ESLQQMAEVTR
▽ ETMVTSTTEPSR
⊠ ILIEDWK
✳ KLIELQAGK
◈ LGGSPTSLGTWGSWIGPDHDK
⊕ LGGSPTSLGTWGSWIGPDHDKFSAMK
✡ LWEEQLAAAK
⊞ NKFEEAER
⊗ P14314
◩ SEALPTDLPAPSAPDLTEPK
■ SLEDQVEMLR
● SLKDMEESIR
▲ TVKEEAEKPER
◆ VNDGVCDCCDGTDEYNSGVICENTCK
● YEQGTGCWQGPNR
prognosis

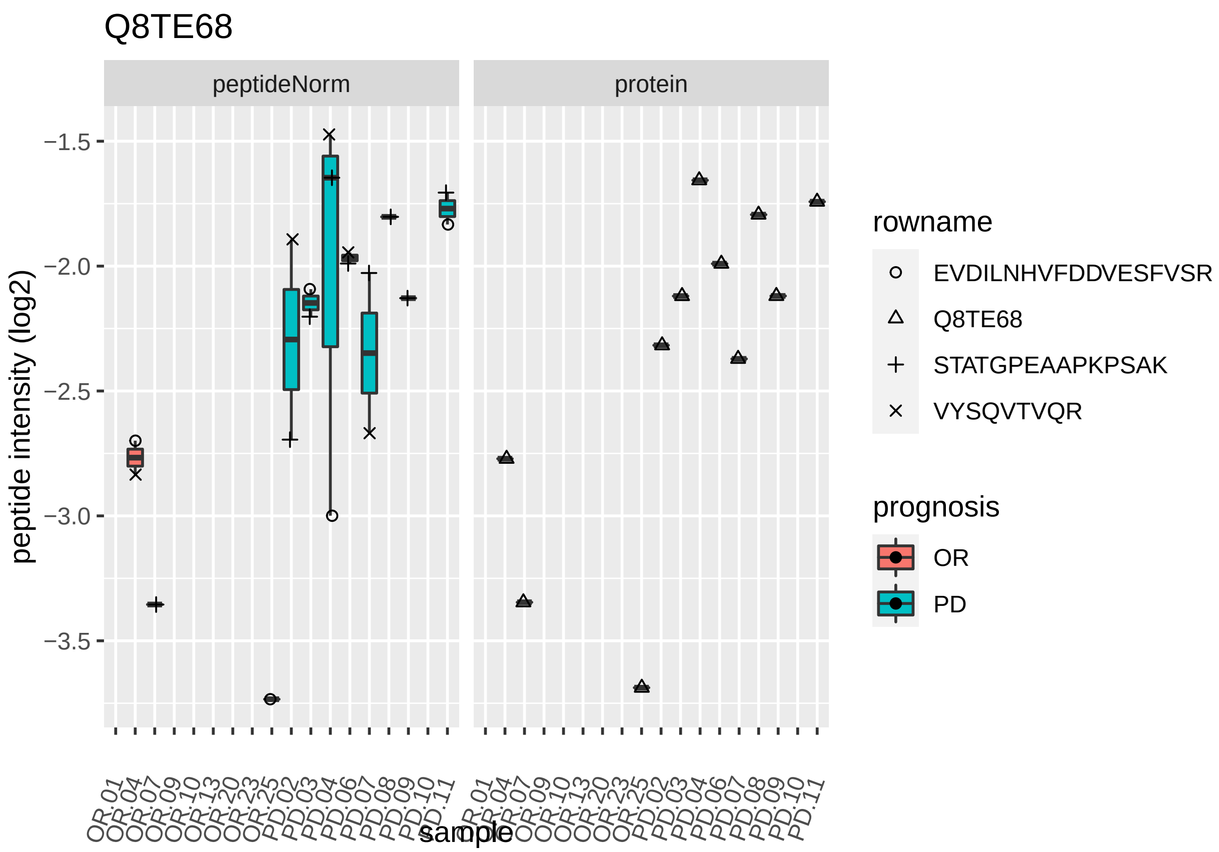

Q15293
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

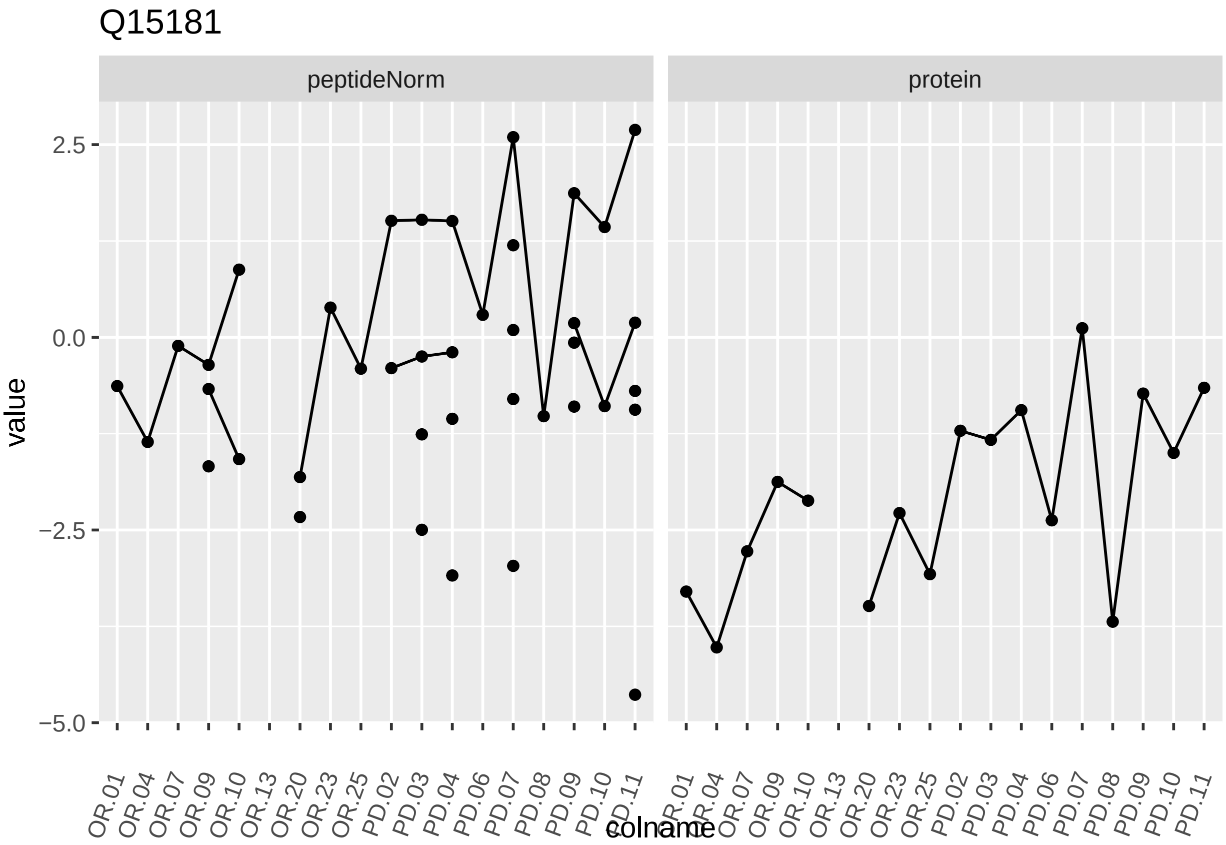

Q15293
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AADLNGDLTATR
EQFNEFR
HLVYESDKNKDEK
HWILPQDYDHAQAEAR
IDNDGDGFVTTEELK
ISWEEYK
IVDRIDNDGDGFVTTEELK
Q15293
TFDQLTPDESKER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

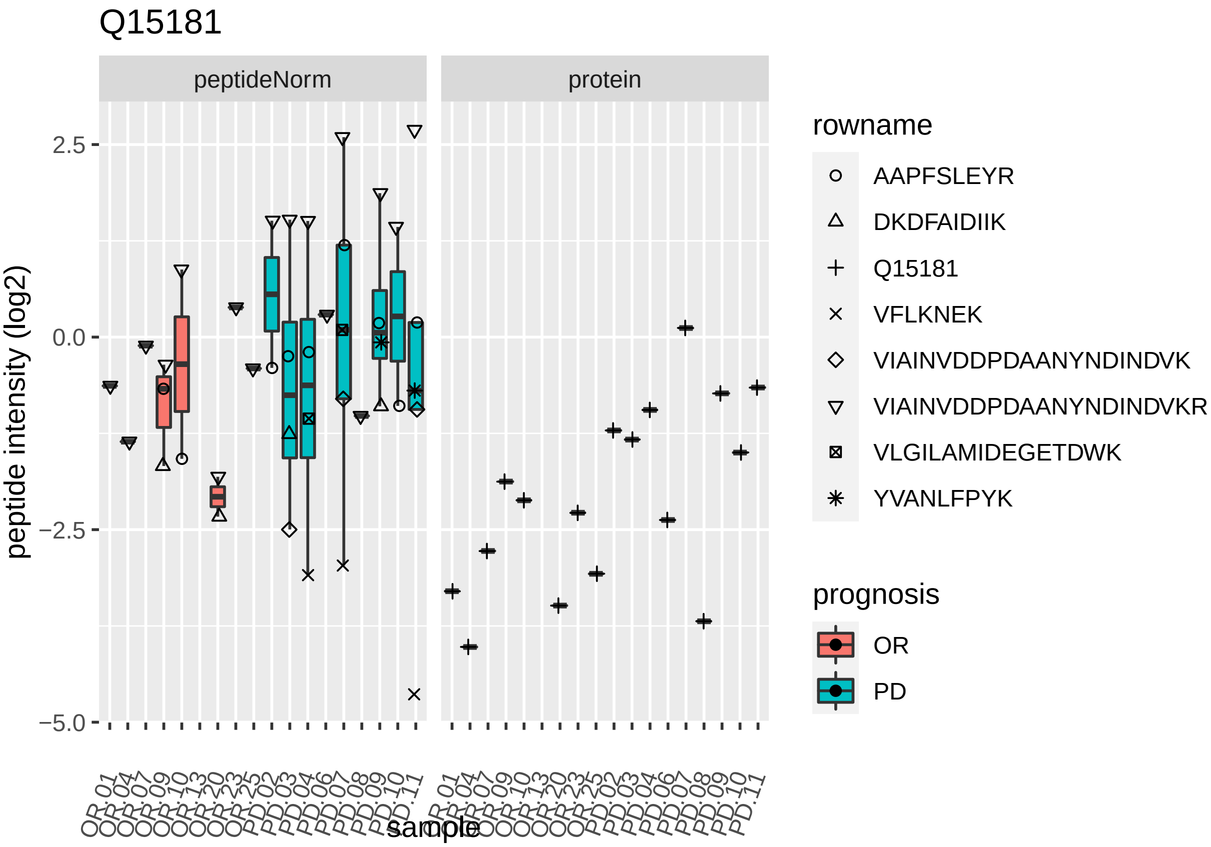

P29966
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

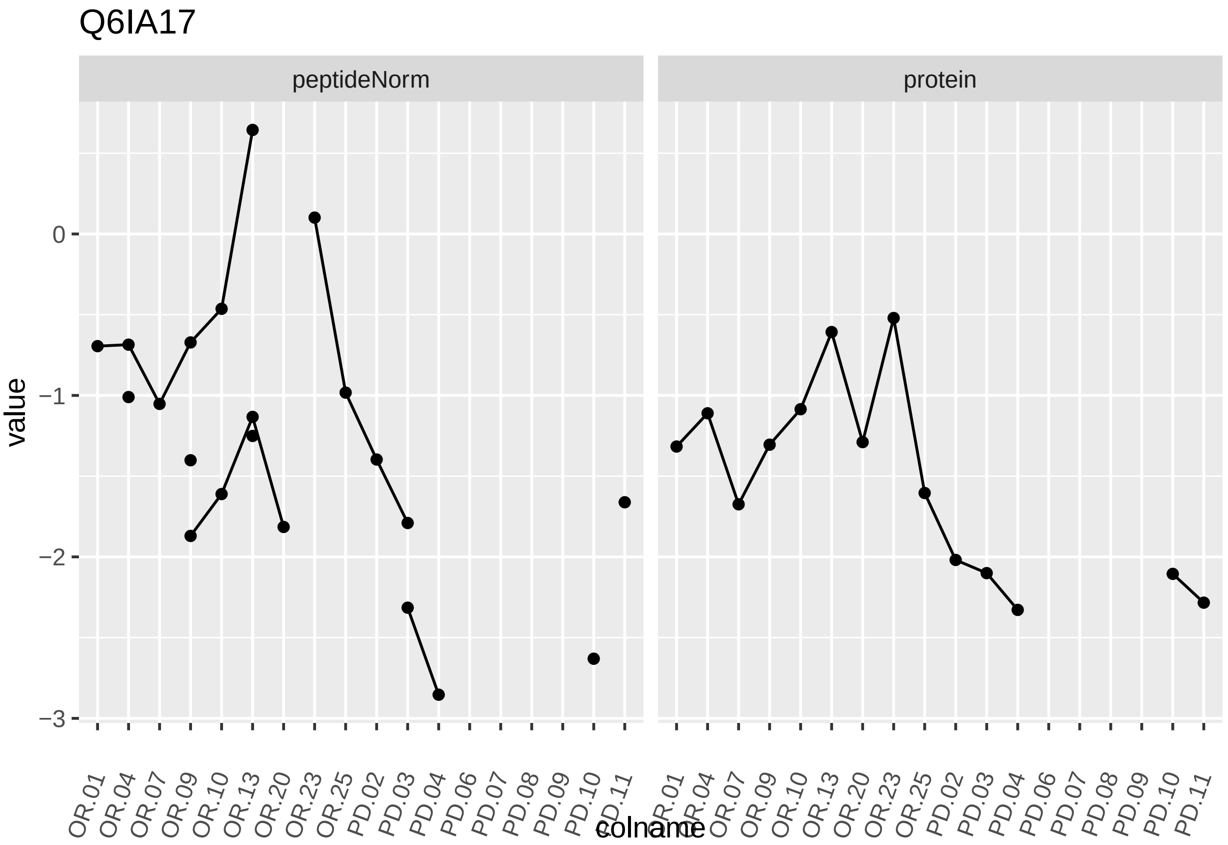

P29966
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
PD.11
sample
rowname
○ AAEEPSKVEEK
△ AEDGATPSPSNETPK
+ EAGEGGEAEAPAAEGGK
× EAPAEGEAAEPGSPTAAEGEAASAASSTSSPK
◇ GEAAAERPGEAAVASSPSK
▽ GEPAAAAAPEAGASPVEK
⊠ P29966
✳ VNGDASPAAAESGAK
prognosis
🟥 OR
🟦 PD

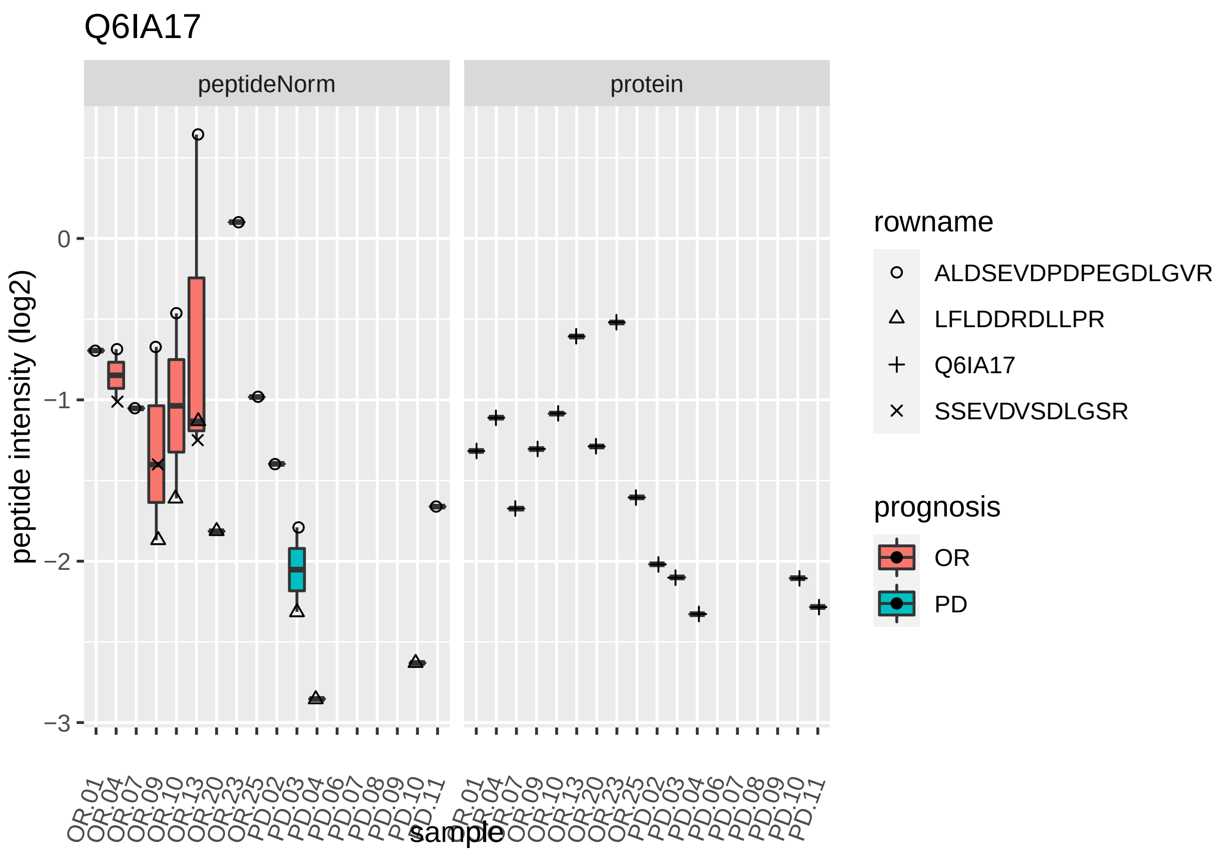

Q8TE68
peptideNorm
protein
value
−1.5
−2.0
−2.5
−3.0
−3.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

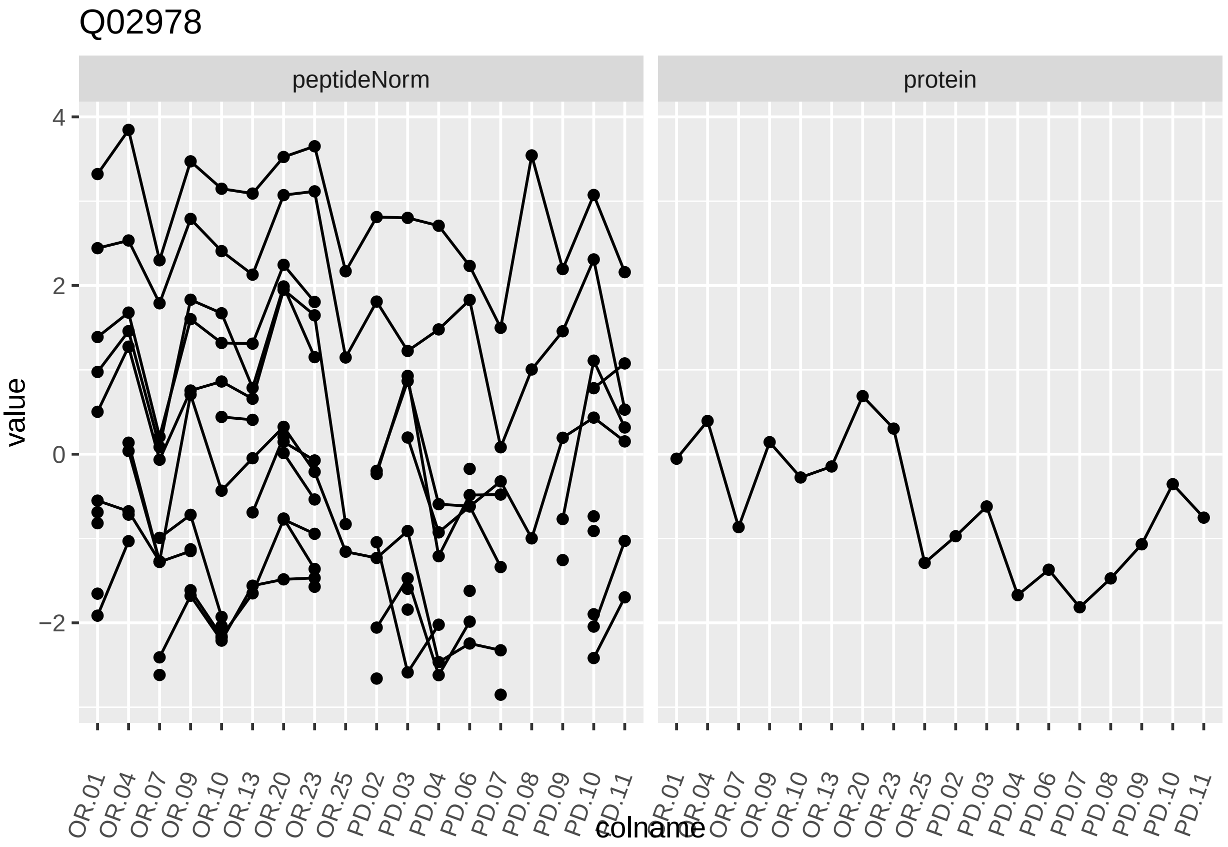

Q8TE68
peptideNorm
protein
peptide intensity (log2)
−1.5
−2.0
−2.5
−3.0
−3.5
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ EVDILNHVFDDVESFVSR
△ Q8TE68
+ STATGPEAAPKPSAK
× VYSQVTVQR
prognosis
🟥 OR
🟦 PD

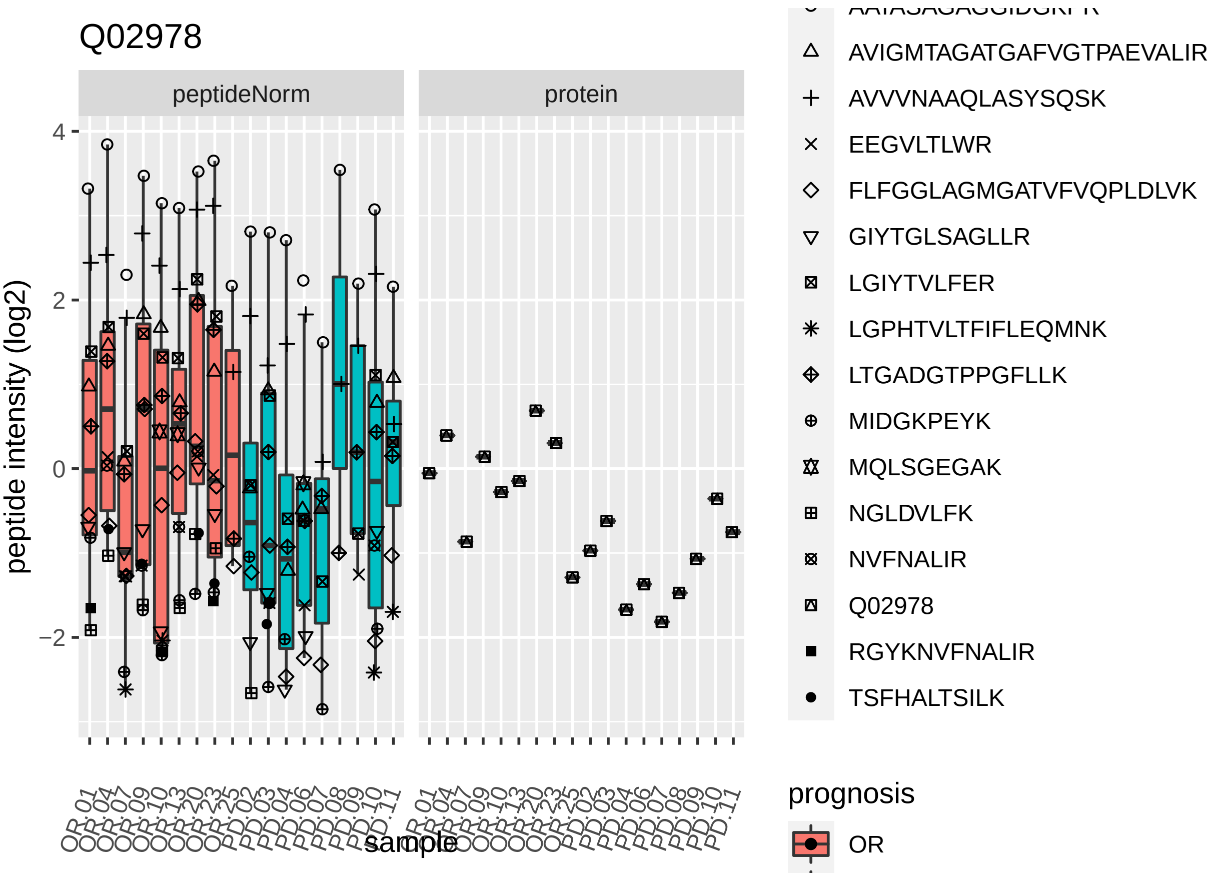

Q15181
peptideNorm
protein
value
2.5
0.0
−2.5
−5.0
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

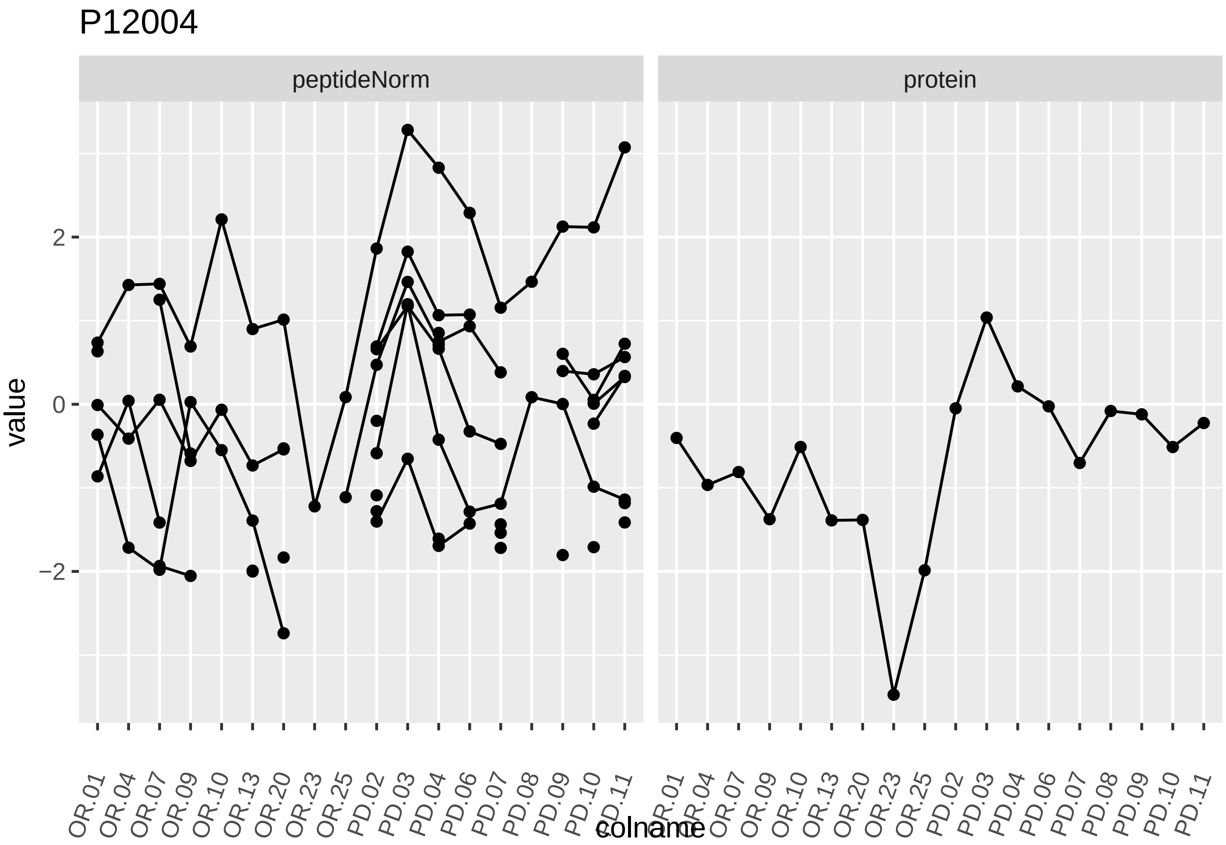

Q15181
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
−5.0
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ AAPFSLEYR
△ DKDFAIDIIK
+ Q15181
× VFLKNEK
◇ VIAINVDDPDAANYNDINDVK
▽ VIAINVDDPDAANYNDINDVKR
⊠ VLGILAMIDEGETDWK
✳ YVANLFPYK
prognosis
🟥 OR
🟦 PD

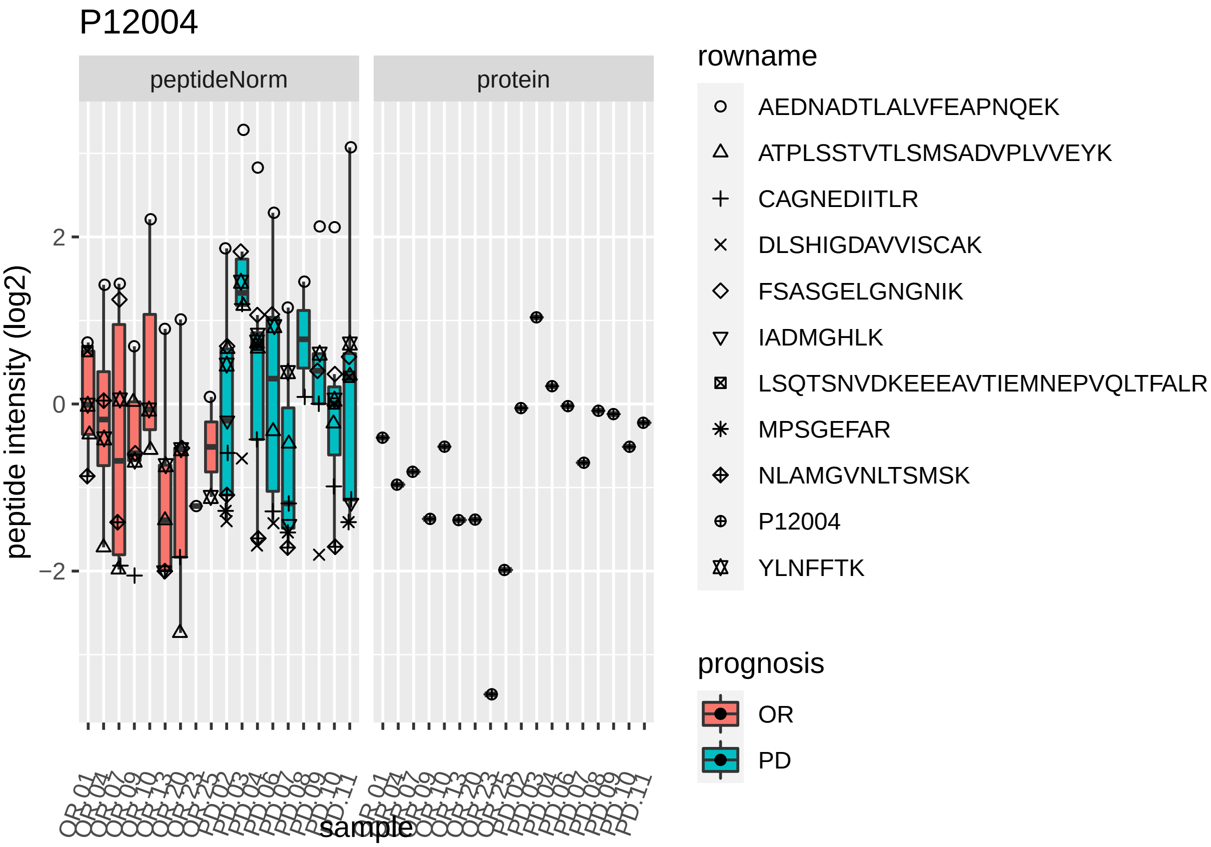

Q6IA17
peptideNorm
protein
value
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

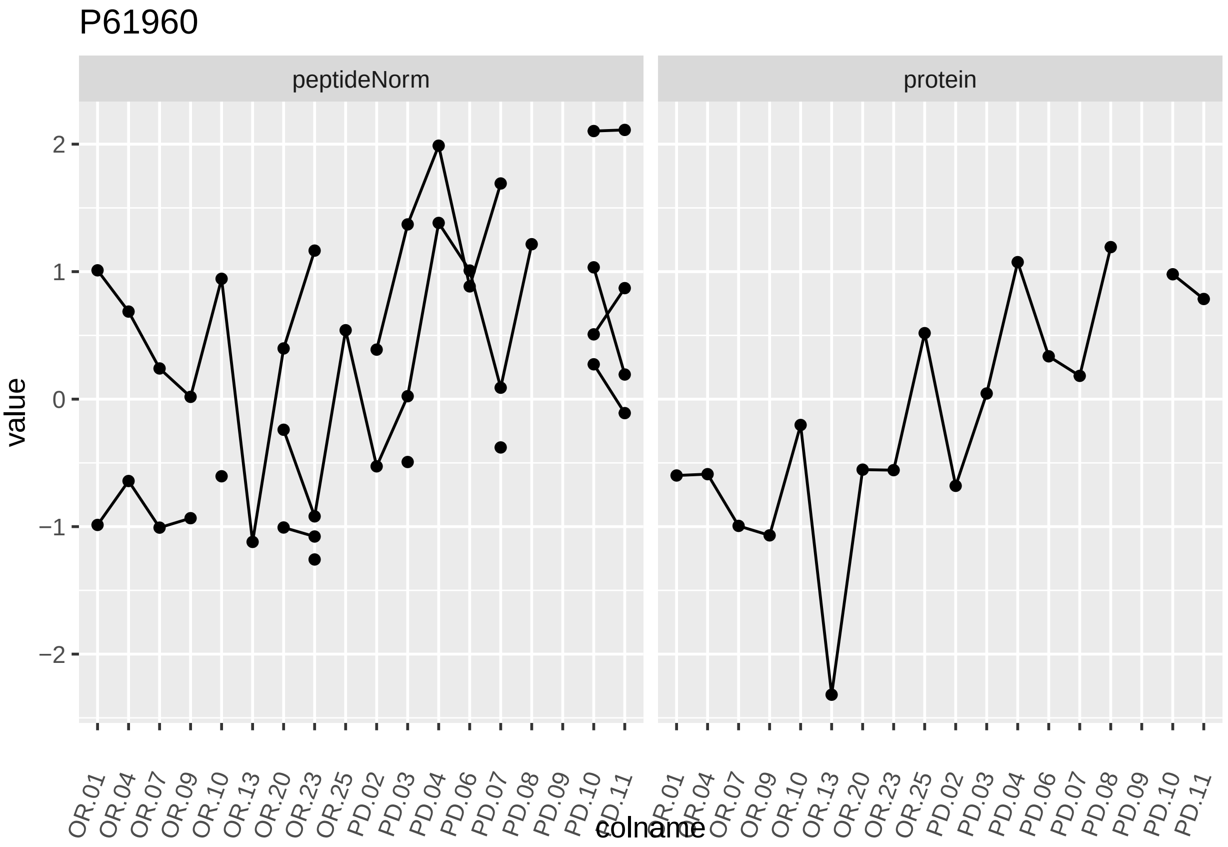

Q6IA17
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ ALDSEVDPDPEGDLGVR
△ LFLDDRDLLPR
+ Q6IA17
× SSEVDVSDLGSR
prognosis
OR
PD

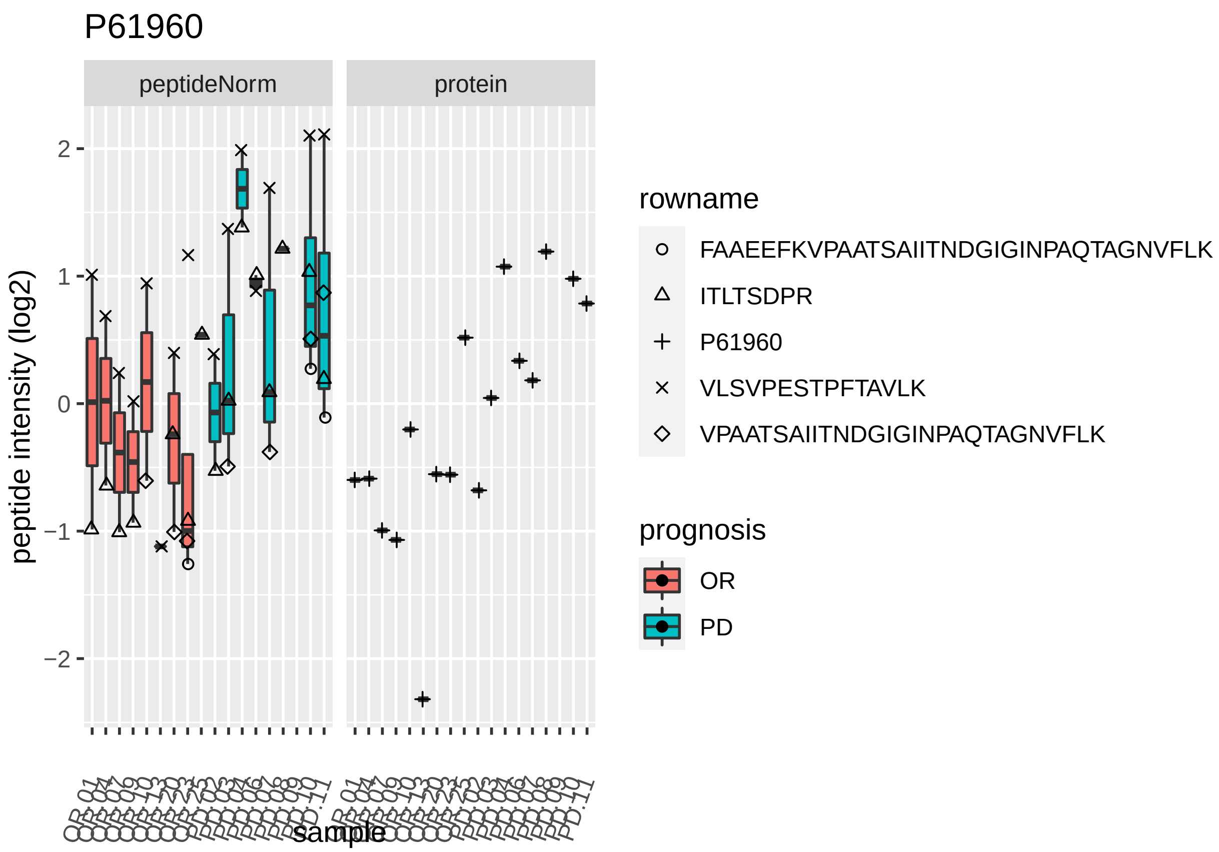

Q02978
peptideNorm
protein
value
4
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

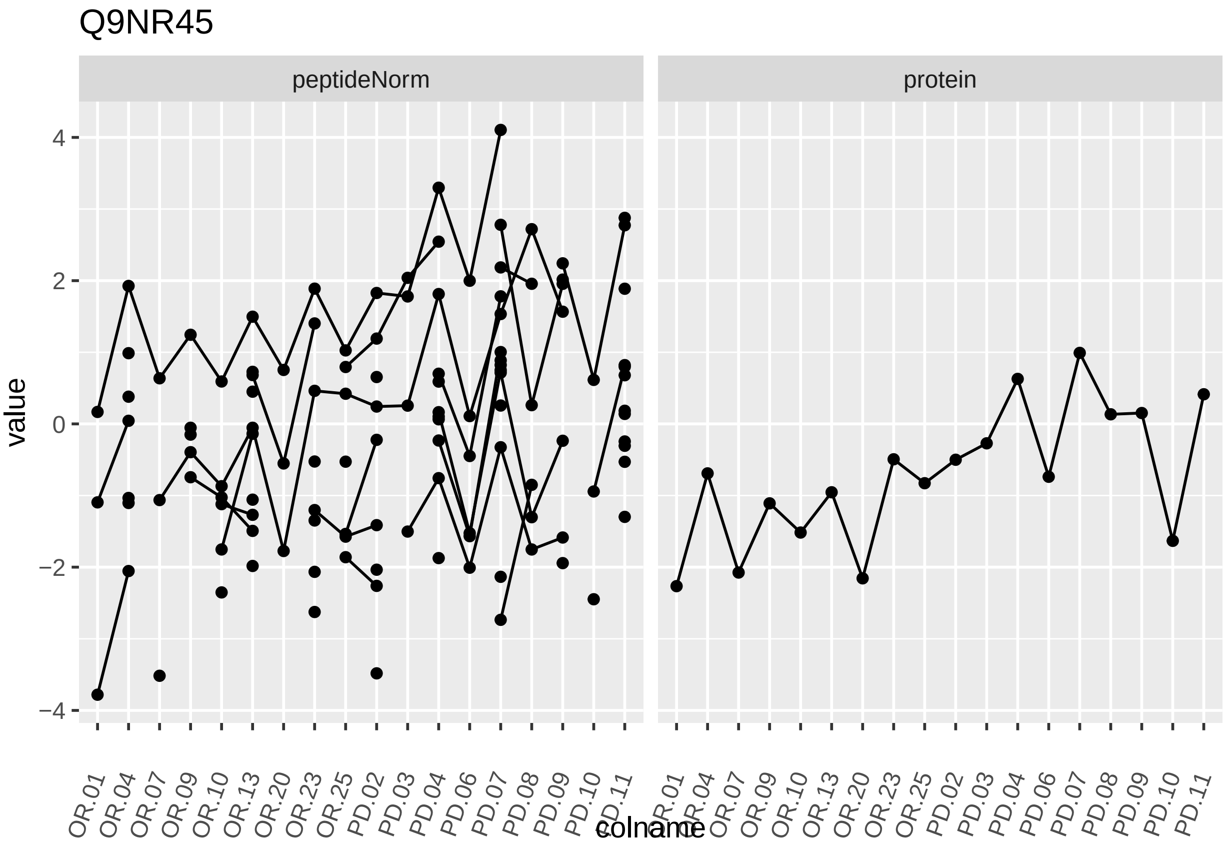

Q02978
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
△ AVIGMTAGATGAFVGTPAEVALIR
+ AVVVNAAQLASYSQSK
× EEGVLTLWR
◇ FLFGGLAGMGATVFVQPLDLVK
▽ GIYTGLSAGLLR
⊠ LGIYTVLFER
✳ LGPHTVLTFIFLEQMNK
◈ LTGADGTPPGFLLK
⊕ MIDGKPEYK
✡ MQLSGEGAK
⊞ NGLDVLFK
⊠ NVFNALIR
◪ Q02978
■ RGYKNVFNALIR
● TSFHALTSILK
prognosis
🟥 OR

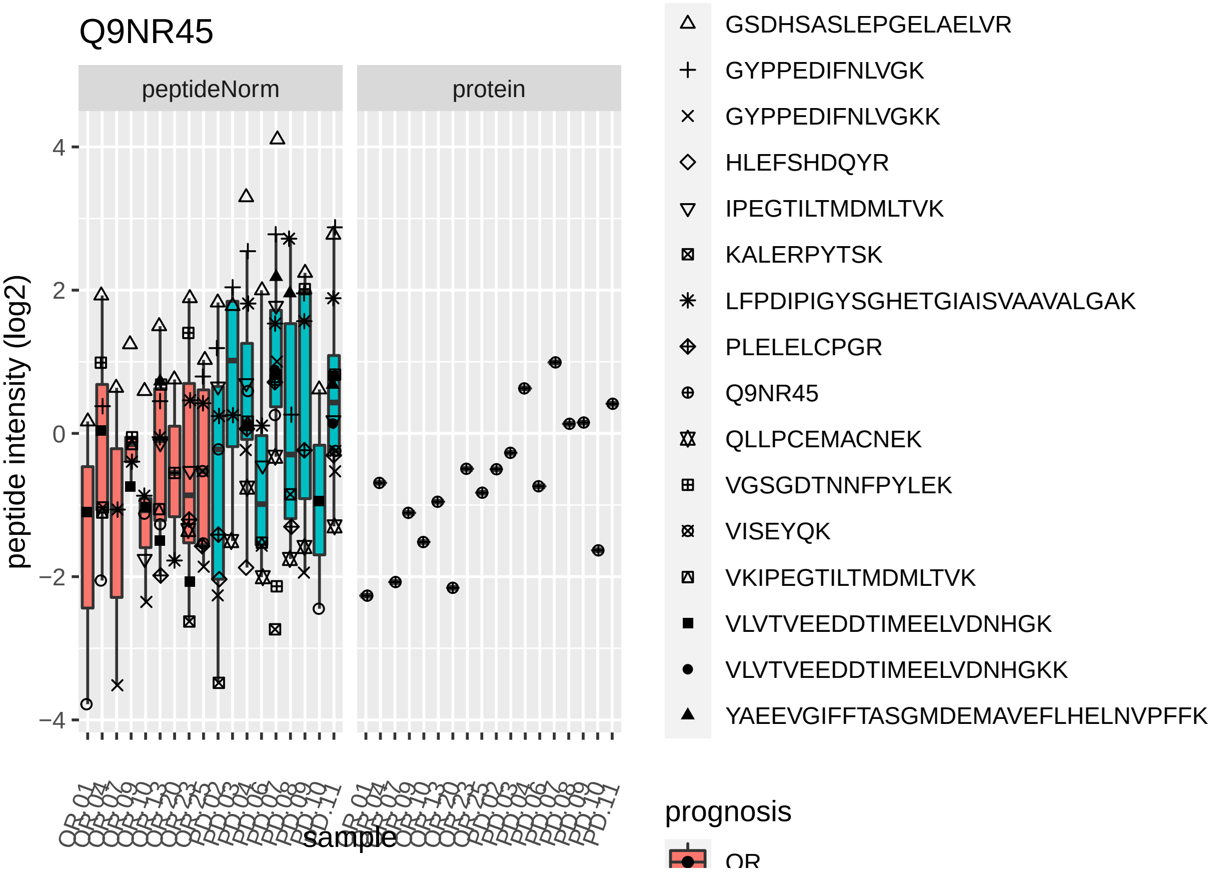

P12004
peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

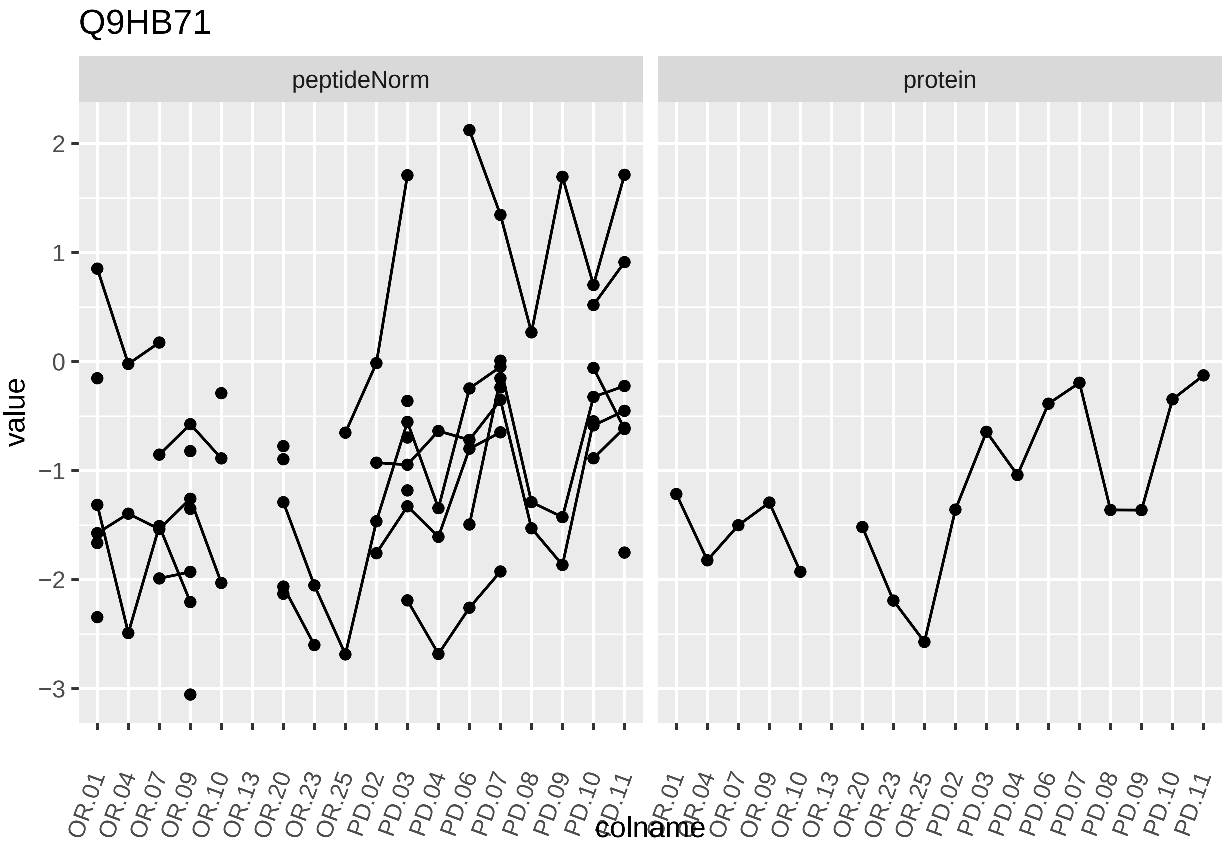

P12004
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AEDNADTLALVFEAPNQEK
ATPLSSTVTLSMSADVPLVVEYK
CAGNEDIITLR
DLSHIGDAVVISCAK
FSASGELGNGNIK
IADMGHLK
LSQTSNVDKEEEAVTIEMNEPVQLTFALR
MPSGEFAR
NLAMGVNLTSMSK
P12004
YLNFFTK
prognosis
OR
PD

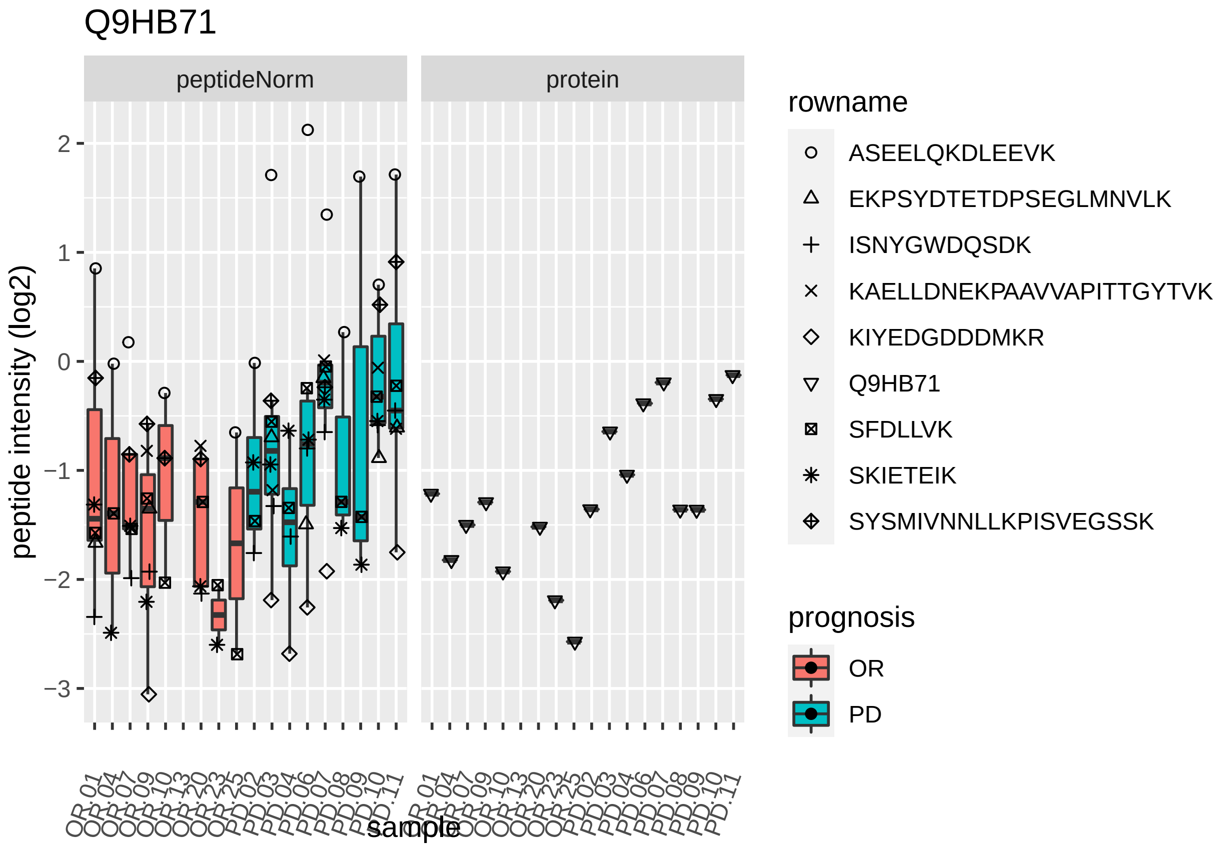

P61960
peptideNorm
protein
value
colname
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

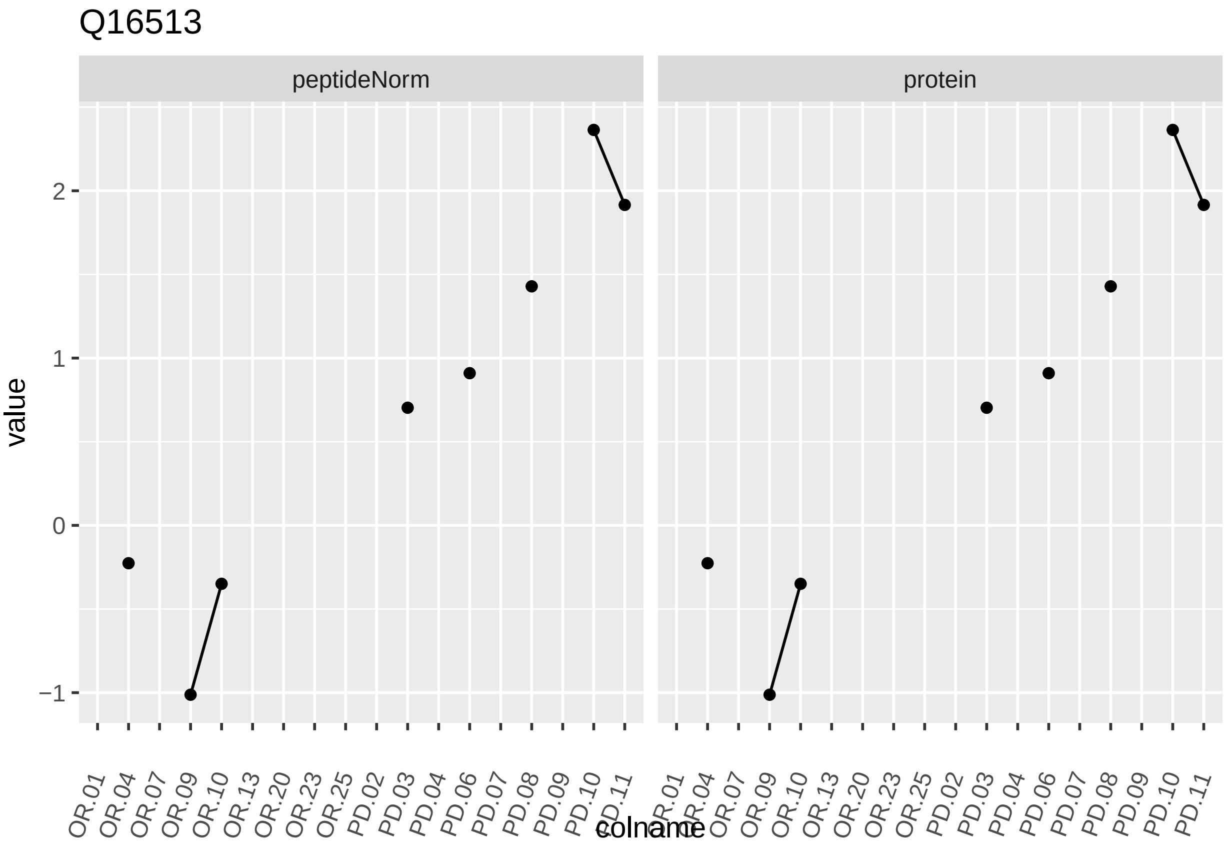

P61960
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
OR.01
PD.11
sample
rowname
○ FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK
△ ITLTSDPR
+ P61960
× VLSVPESTPFTAVLK
◇ VPAATSAIITNDGIGINPAQTAGNVFLK
prognosis
OR
PD

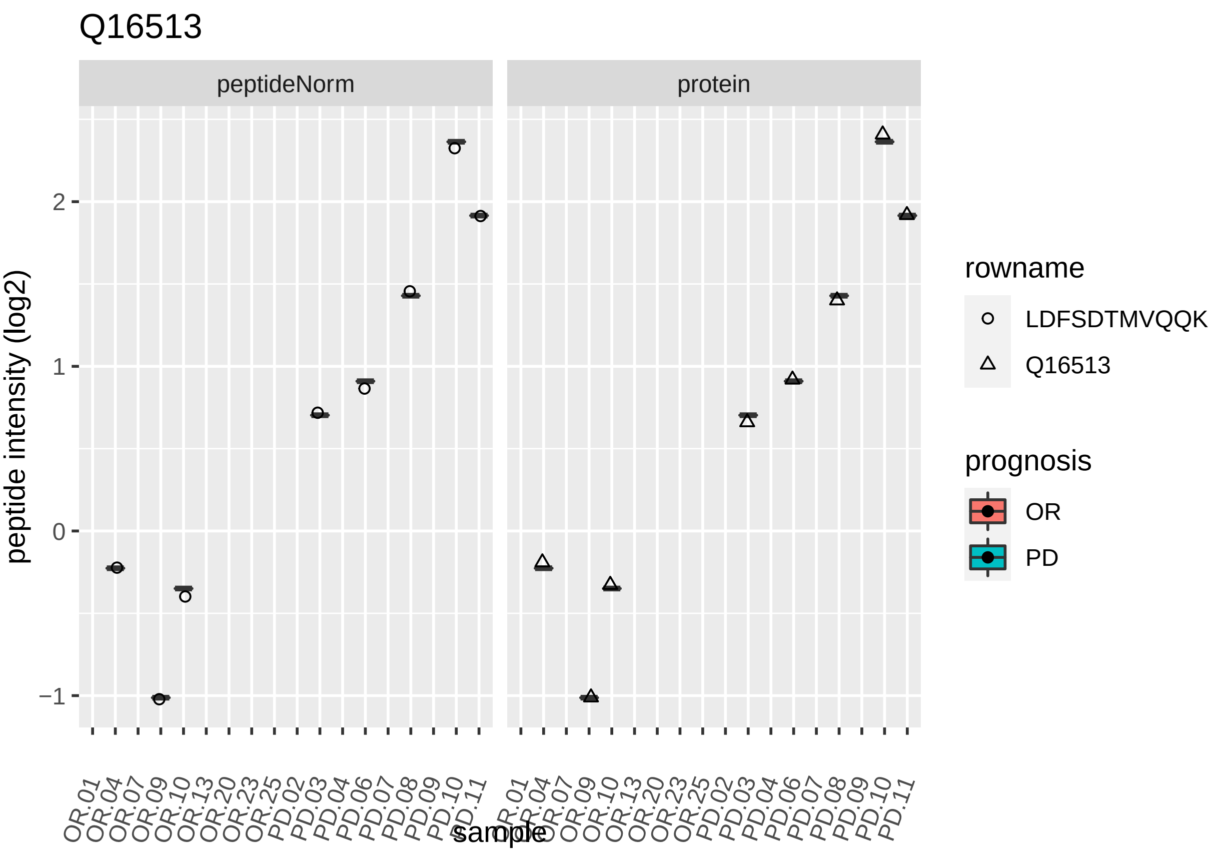

Q9NR45
peptideNorm
protein
value
4
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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

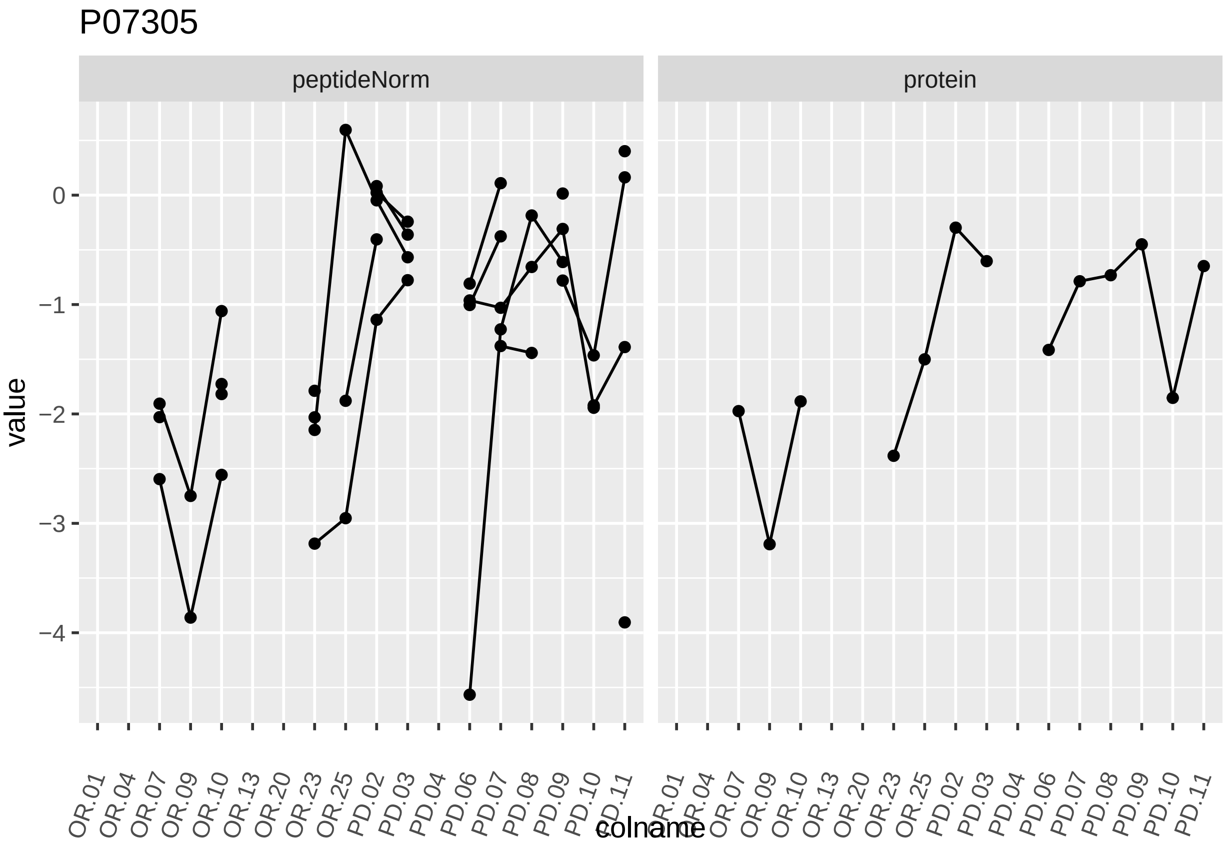

Q9HB71
peptideNorm
protein
value
2
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

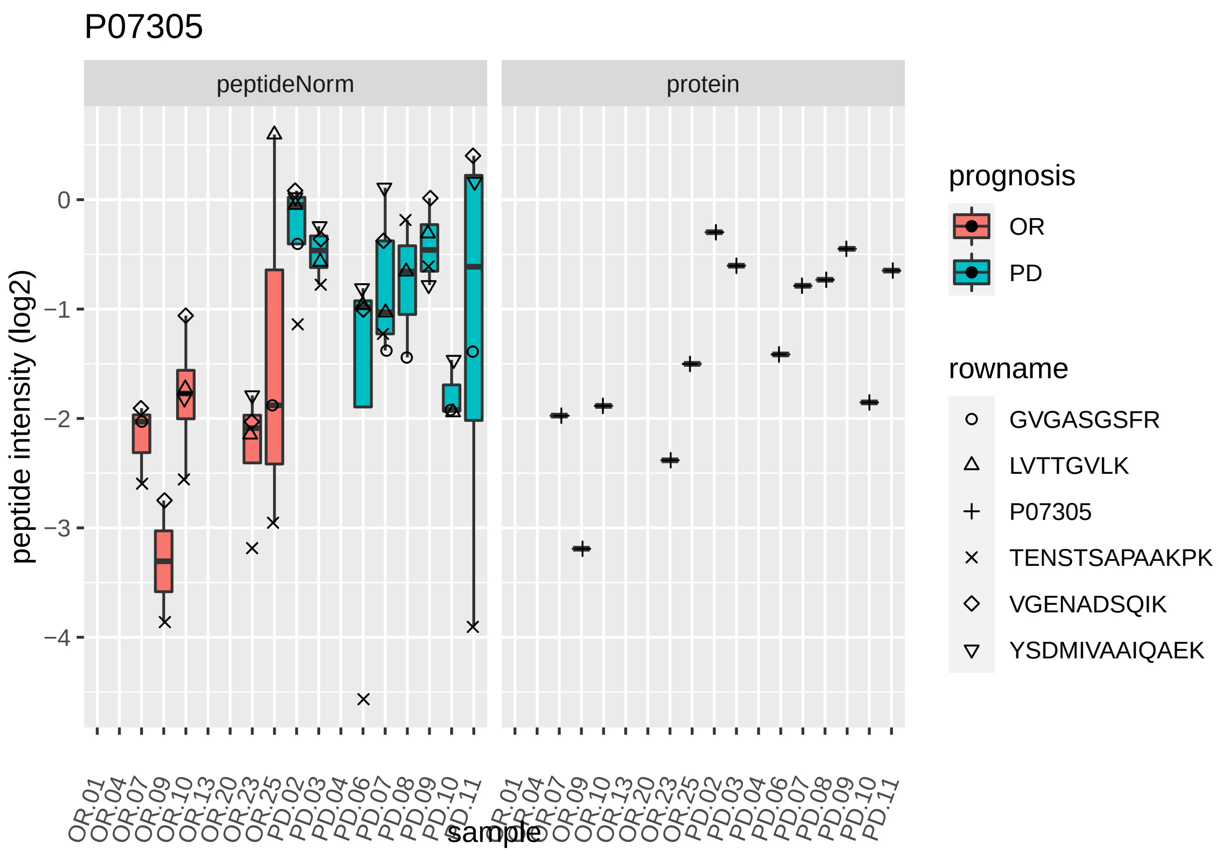

Q9HB71
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
ASEELQKDLEEVK
EKPSYDTETDPSEGLMNVLK
ISNYGWDQSDK
KAELLDNEKPAAVVAPITTGYTVK
KIYEDGDDDMKR
Q9HB71
SFDLLVK
SKIETEIK
SYSMIVNNLLKPISVEGSSK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

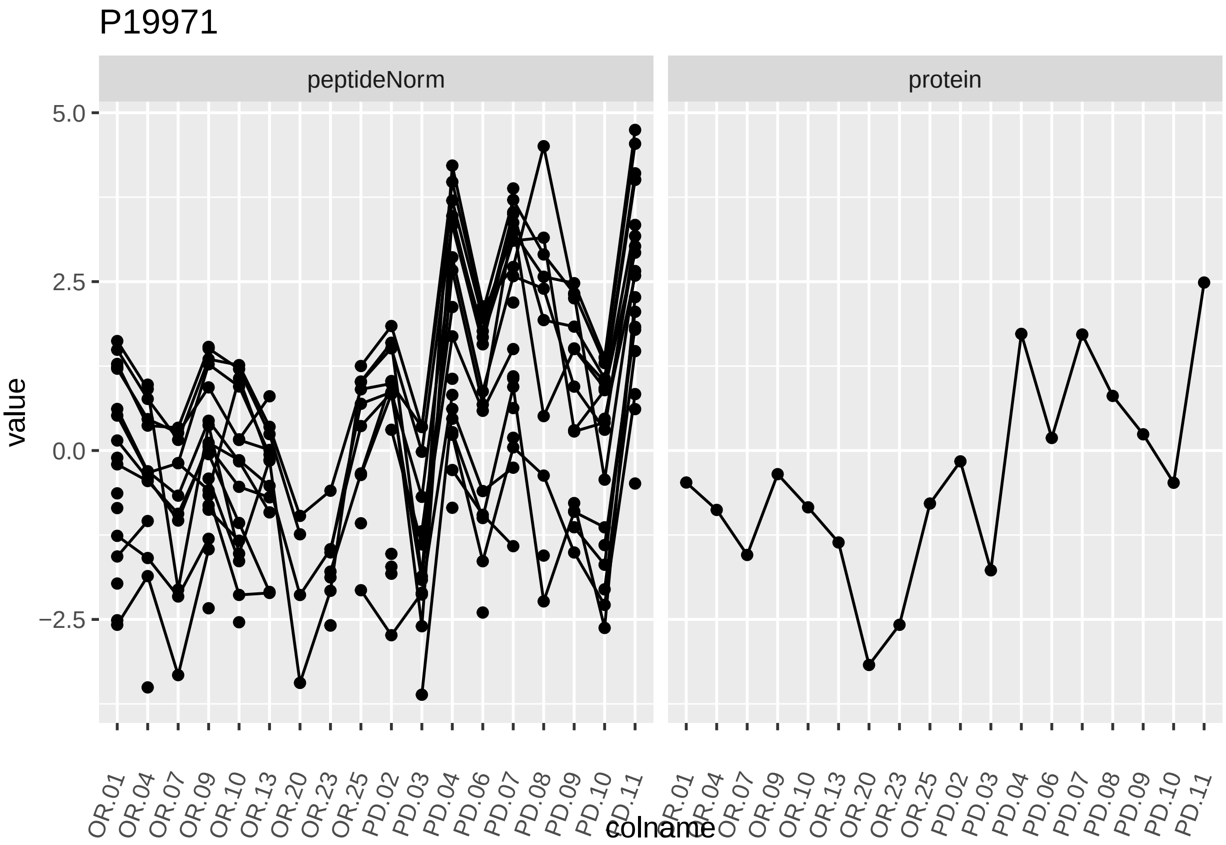

Q16513
peptideNorm
protein
value
2
1
0
−1
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

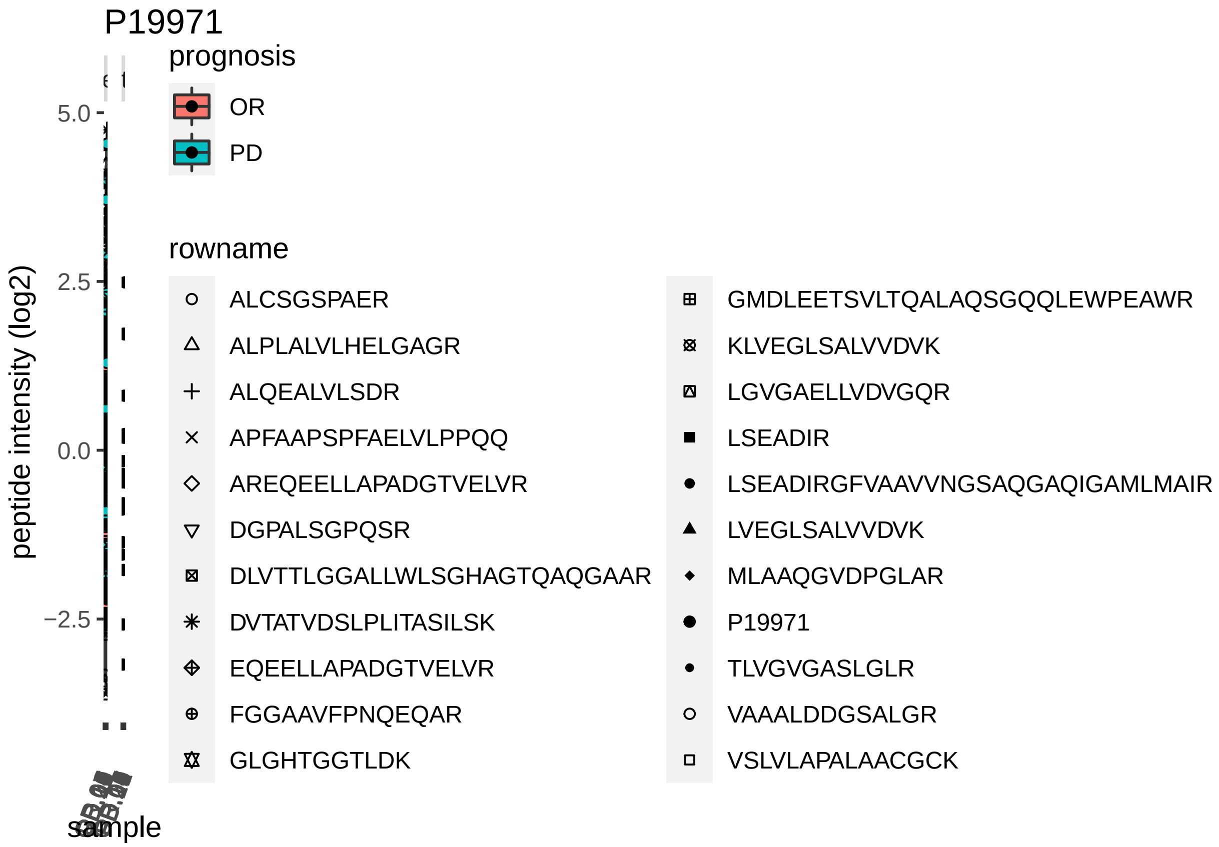


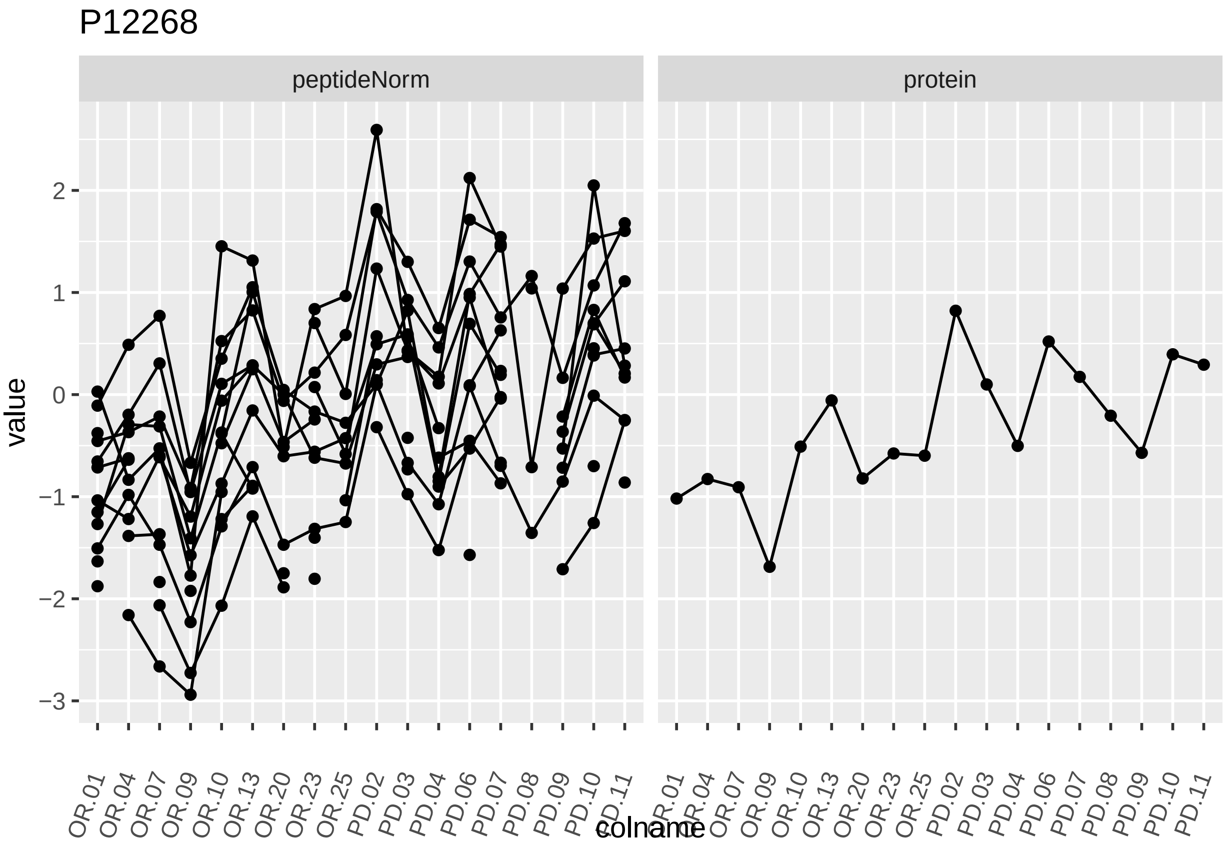
Q16513
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LDFSDTMVQQK
Q16513
prognosis
OR
PD

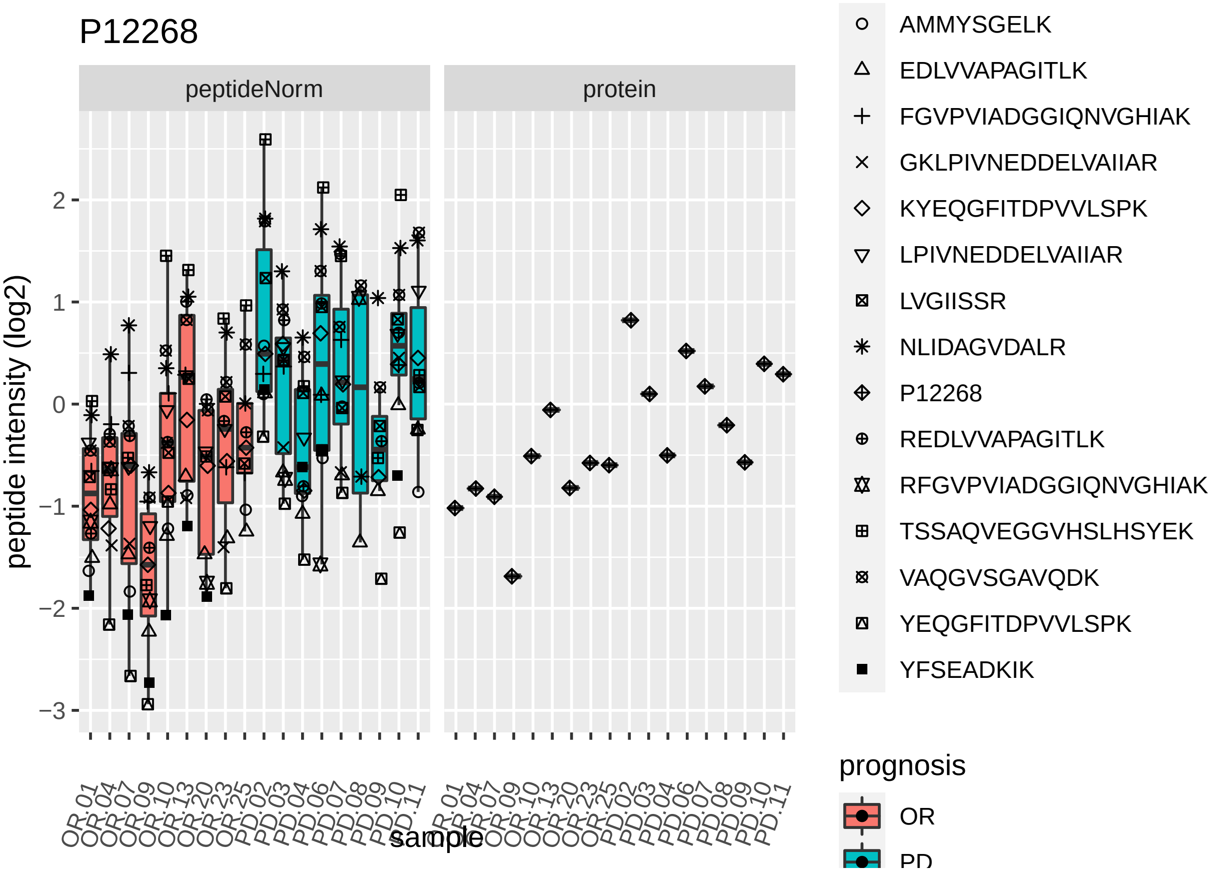

P07305
peptideNorm
protein
value
0
−1
−2
−3
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

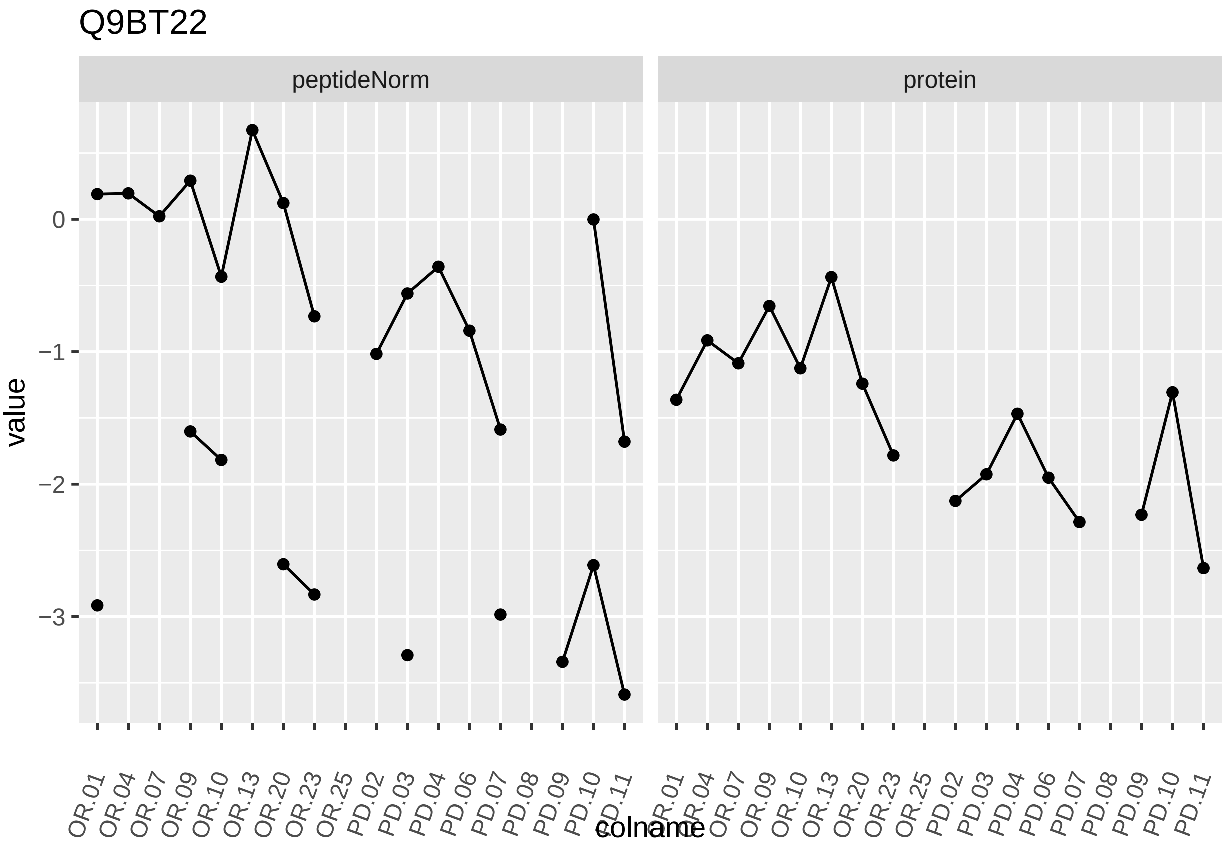

P07305
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
GVGASGSFR
LVTTGVLK
P07305
TENSTSAPAAKPK
VGENADSQIK
YSDMIVAAIQAEK

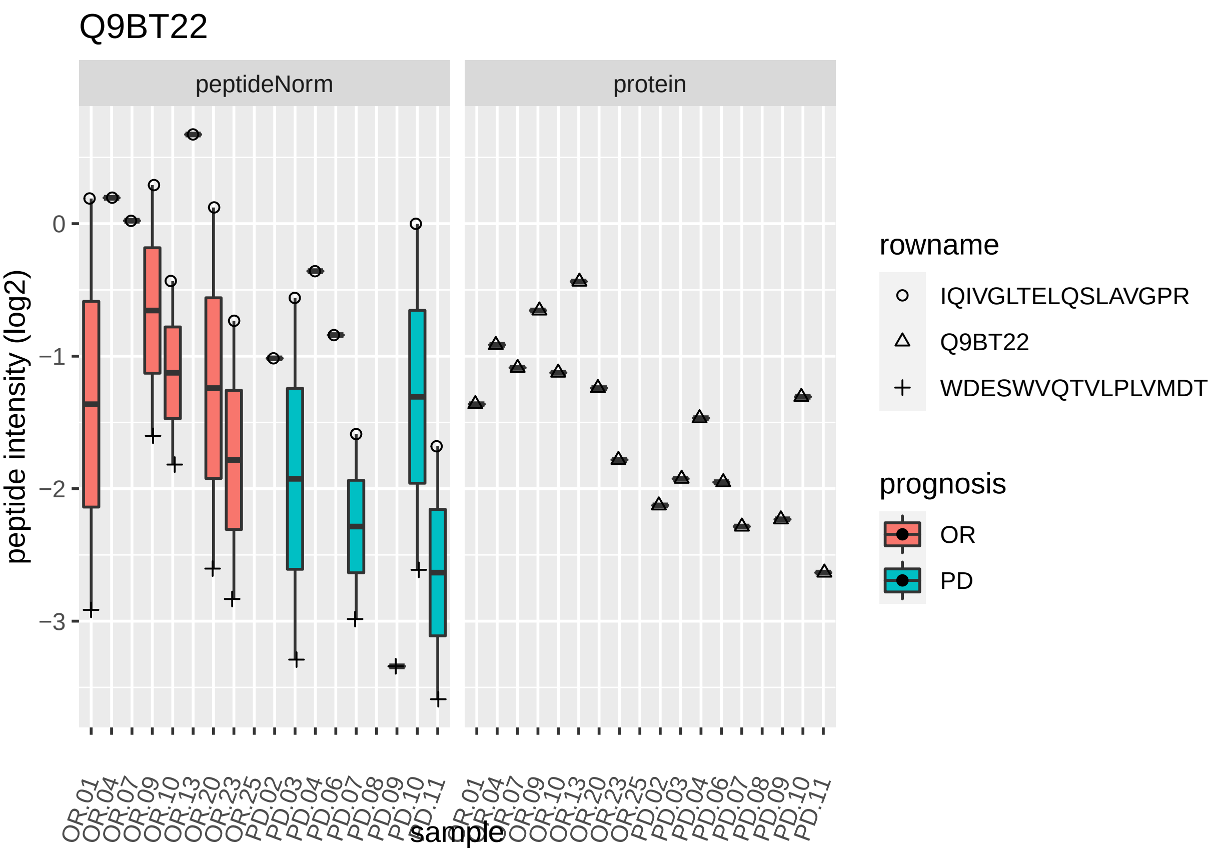

P19971
peptideNorm
protein
value
5.0
2.5
0.0
−2.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

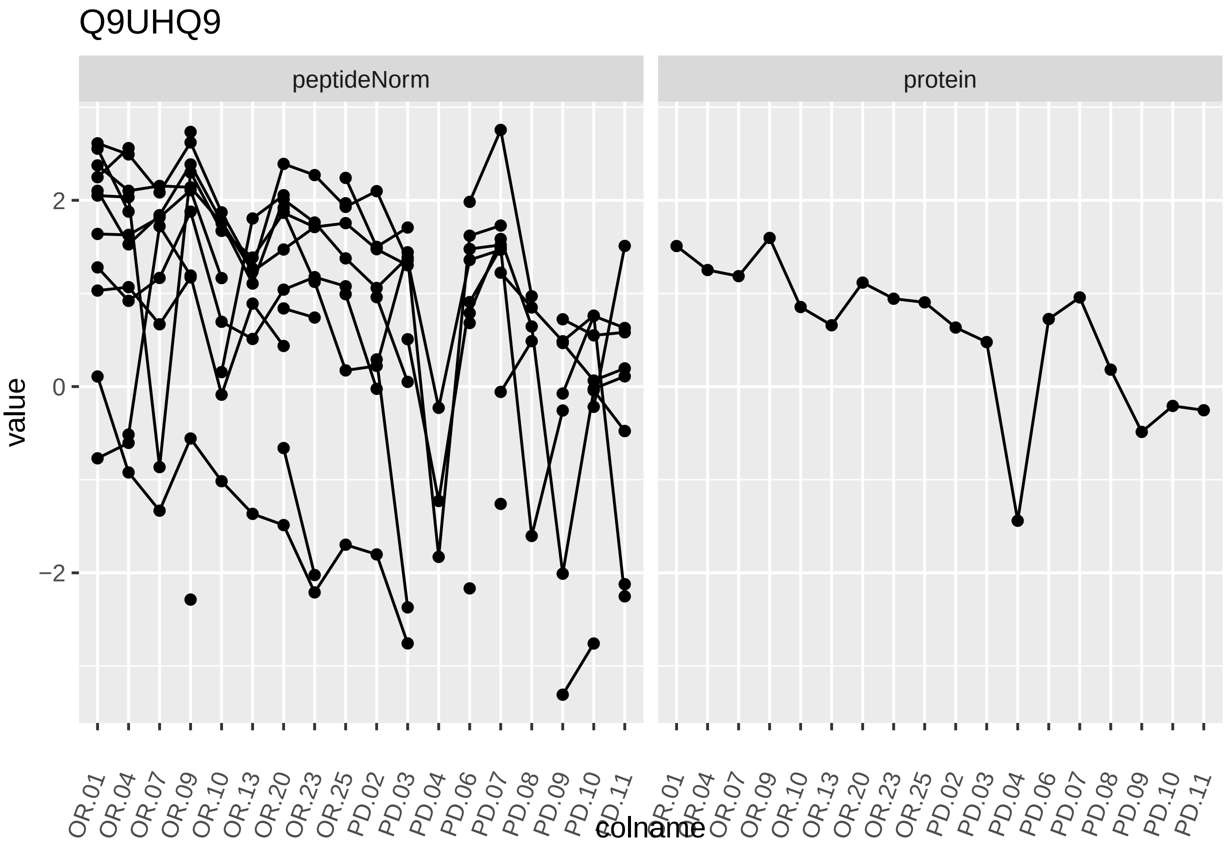

P19971
peptide intensity (log2)
5.0
2.5
0.0
−2.5
sample
prognosis
OR
PD
rowname
ALCSGSPAER
ALPLALVLHELGAGR
ALQEALVLSDR
APFAAPSPFAELVLPPQQ
AREQEELLAPADGTVELVR
DGPALSGPQSR
DLVTTLGGALLWLSGHAGTQAQGAAR
DVTATVDSLPLITASILSK
EQEELLAPADGTVELVR
FGGAAVFPNQEQAR
GLGHTGGTLDK
GMDLEETSVLTQALAQSGQQLEWPEAWR
KLVEGLSALVVDVK
LGVGAELLVDVGQR
LSEADIR
LSEADIRGFVAAVVNGSAQGAQIGAMLMAIR
LVEGLSALVVDVK
MLAAQGVDPGLAR
P19971
TLVGVGASLGLR
VAAALDDGSALGR
VSLVLAPALAACGCK

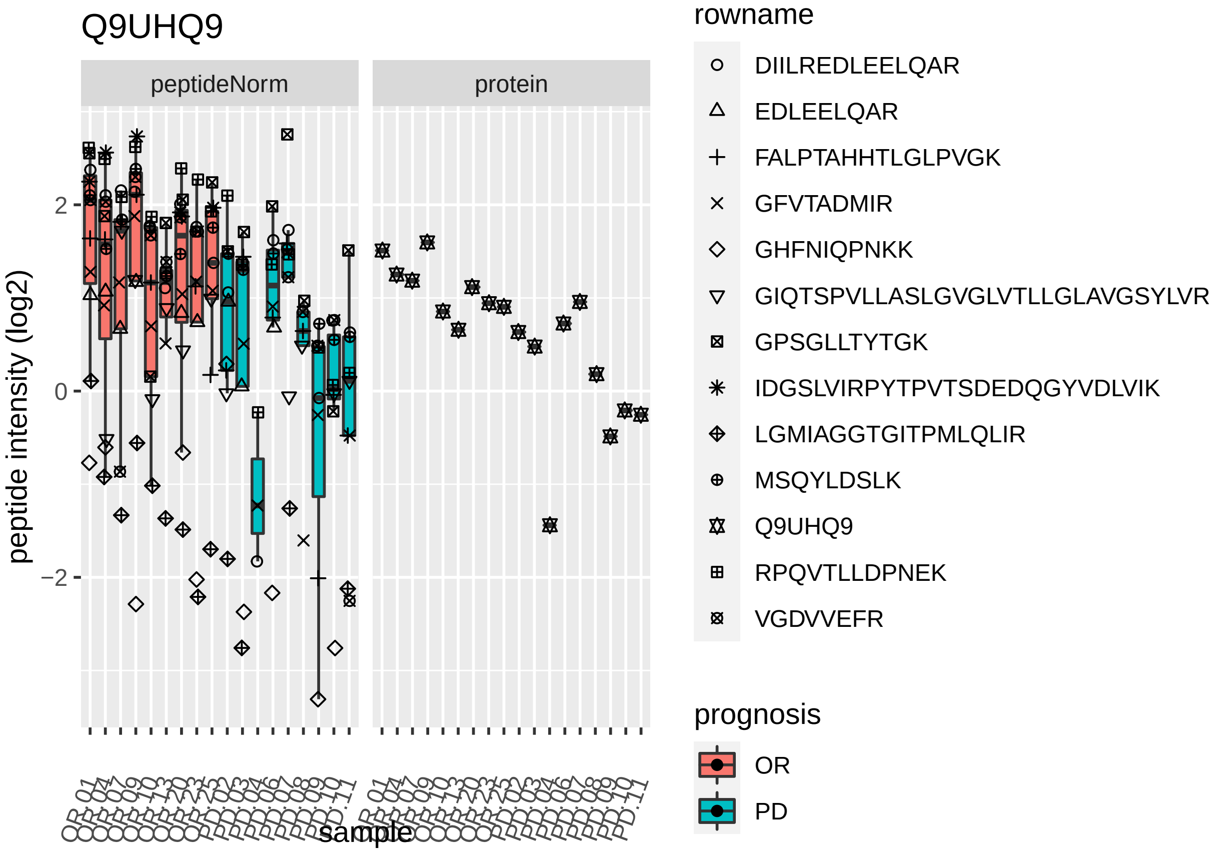

P12268
peptideNorm
protein
value
2
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

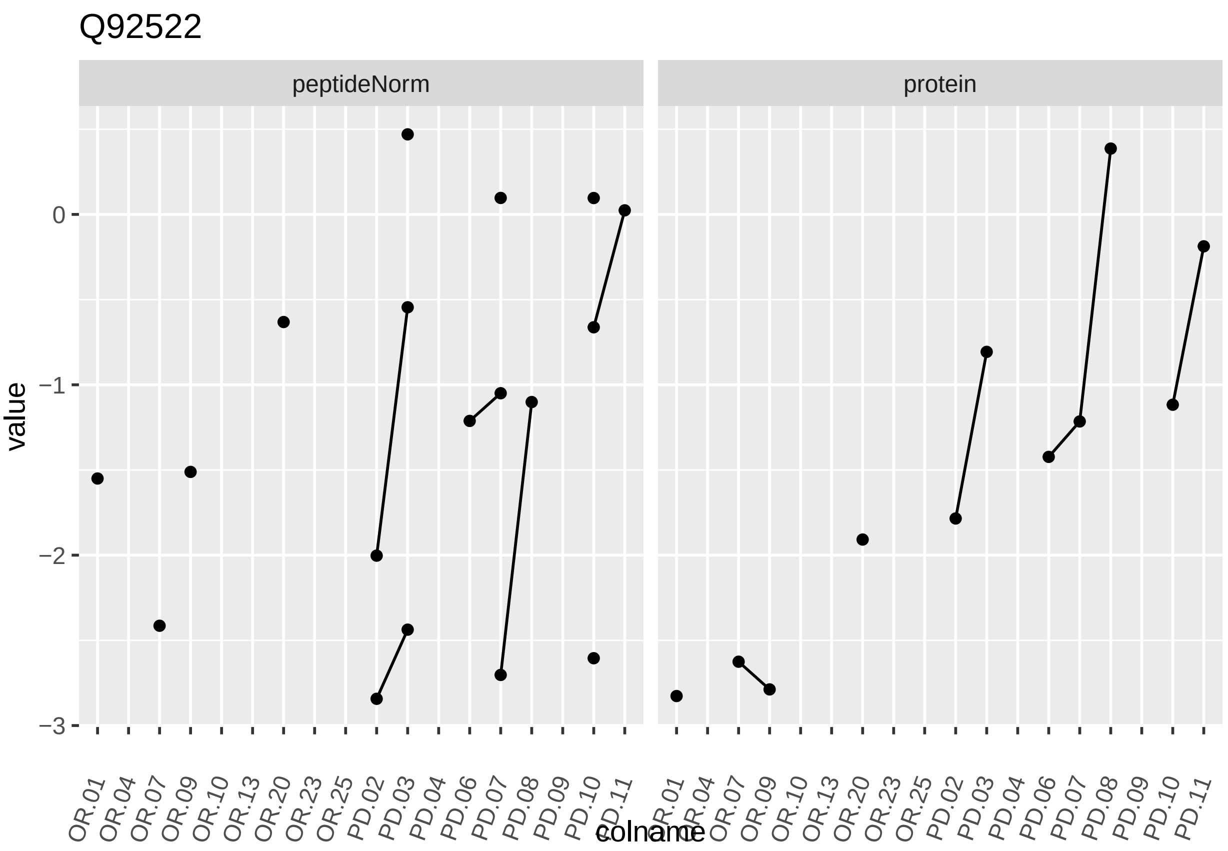

P12268
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
AMMYSGELK
EDLVVAPAGITLK
FGVPVIADGGIQNVGHIAK
GKLPIVNEDDELVAIIAR
KYEQGFITDPVVLSPK
LPIVNEDDELVAIIAR
LVGIISSR
NLIDAGVDALR
P12268
REDLVVAPAGITLK
RFGVPVIADGGIQNVGHIAK
TSSAQVEGGVHSLHSYEK
VAQGVSGAVQDK
YEQGFITDPVVLSPK
YFSEADKIK
prognosis
OR
PD

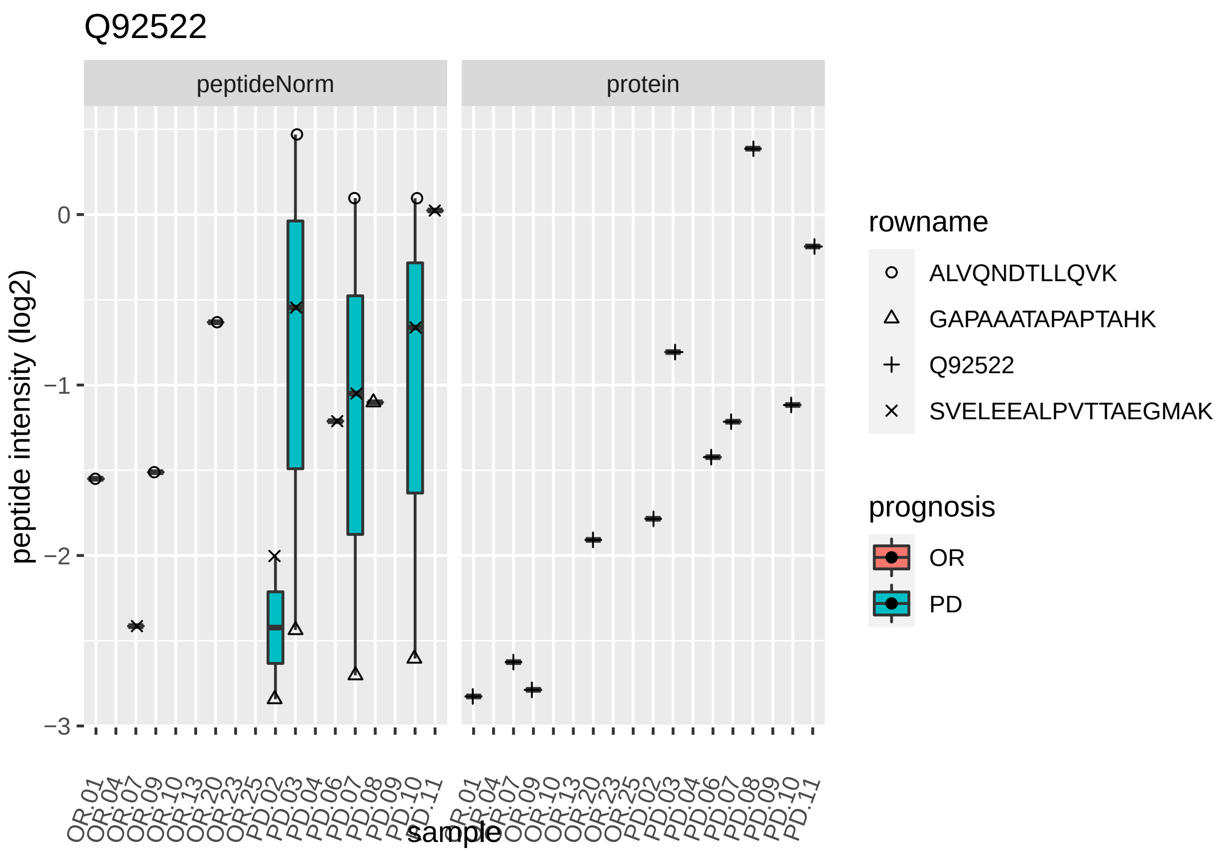

Q9BT22
peptideNorm
protein
value
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

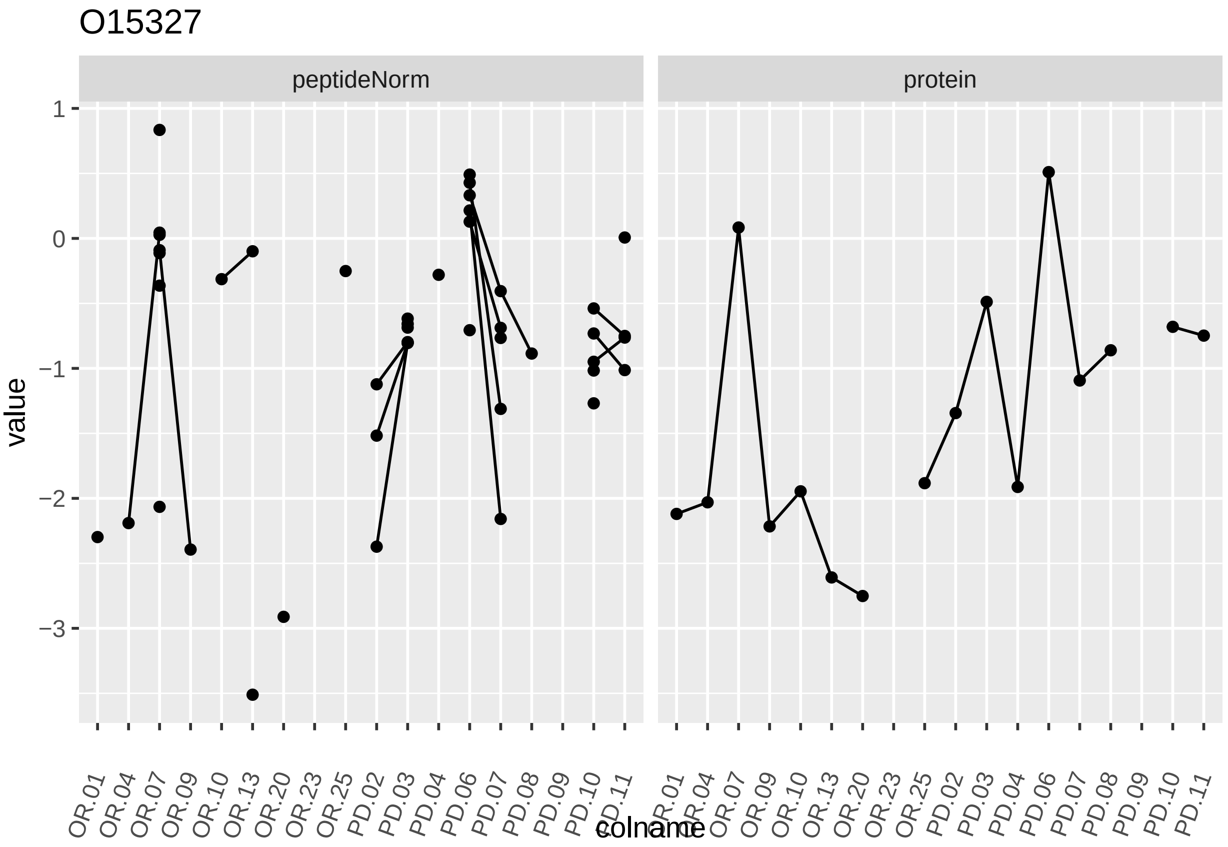

Q9BT22
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ IQIVGLTELQSLAVGPR
△ Q9BT22
+ WDESWVQTVLPLVMDT
prognosis
OR
PD

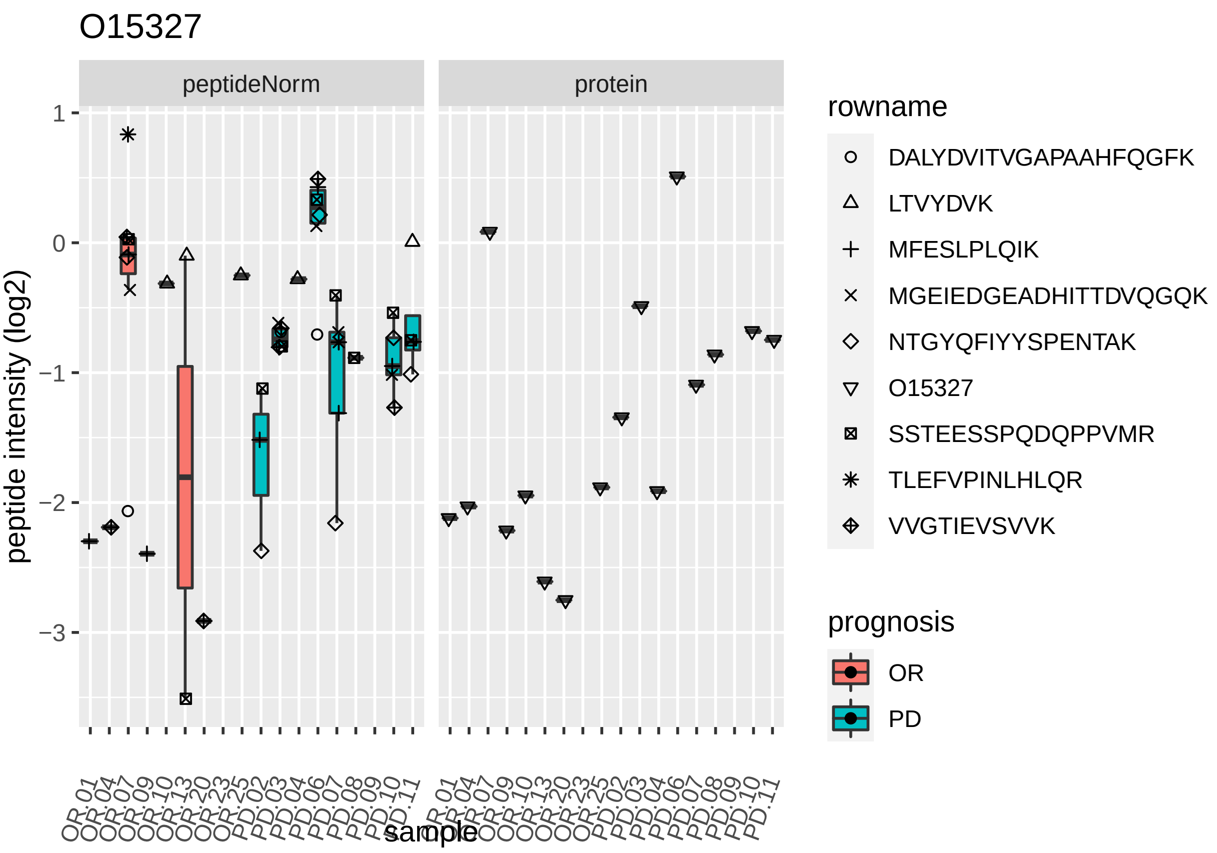

Q9UHQ9
peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

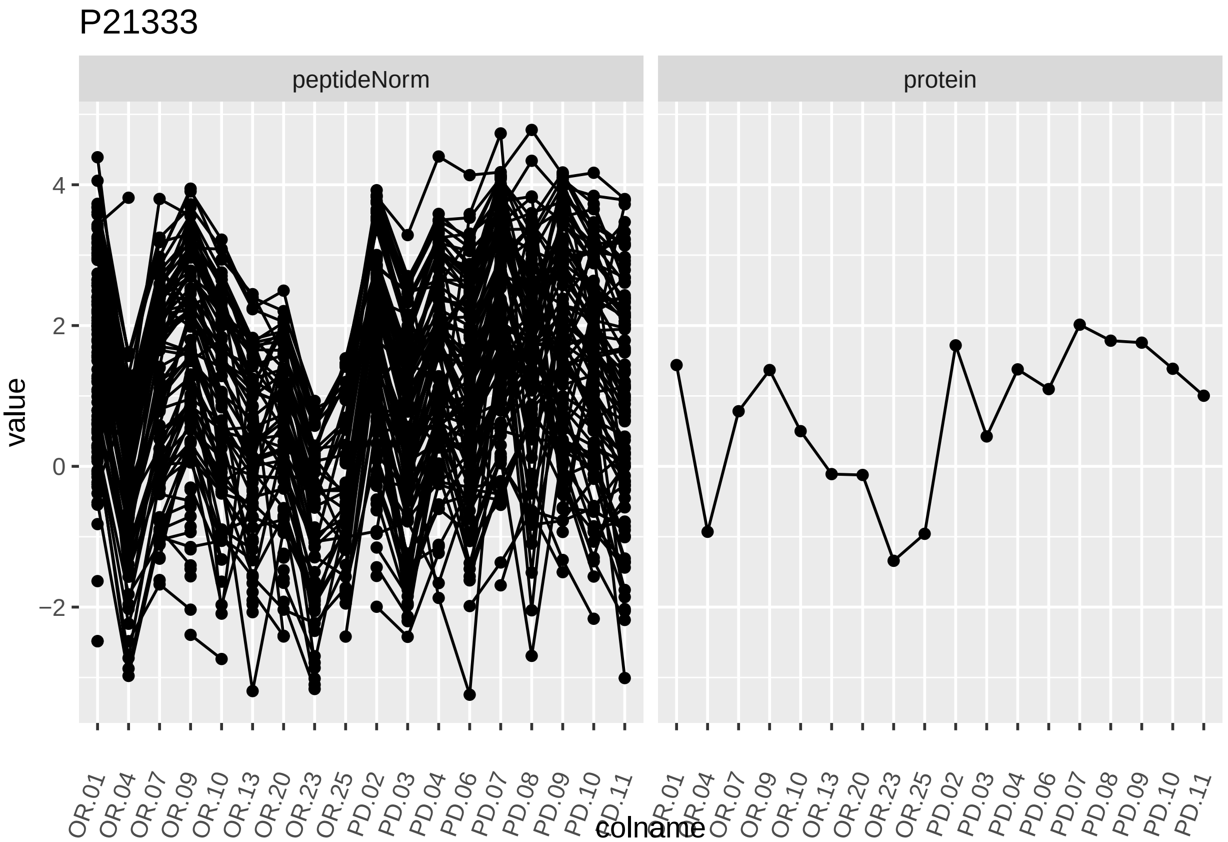

Q9UHQ9
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ DIILREDLEELQAR
△ EDLEELQAR
+ FALPTAHHTLGLPVGK
× GFVTADMIR
◇ GHFNIQPNKK
▽ GIQTSPVLLASLGVGLVTLLGLAVGSYLVR
⊠ GPSGLLTYTGK
✳ IDGSLVIRPYTPVTSDEDQGYVDLVIK
◇ LGMIAGGTGITPMLQLIR
⊕ MSQYLDSLK
✡ Q9UHQ9
⊞ RPQVTLLDPNEK
⊠ VGDVVEFR
prognosis
🟥 OR
🟦 PD


Q92522
peptideNorm
protein
value
0
−1
−2
−3
colname
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


Q92522
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
○ ALVQNDTLLQVK
△ GAPAAATAPAPTAHK
+ Q92522
× SVELEEALPVTTAEGMAK
prognosis
OR
PD


O15327
peptideNorm
protein
value
1
0
−1
−2
−3
colname
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


O15327
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
○ DALYDVITVGAPAAHFQGFK
△ LTVYDVK
+ MFESLPLQIK
× MGEIEDGEADHITTDVQGQK
◇ NTGYQFIYYSPENTAK
▽ O15327
⊠ SSTEESSPQDQPPVMR
✳ TLEFVPINLHLQR
⊕ VVGTIEVSVVK
prognosis
🟥 OR
🟦 PD


P21333
peptideNorm
protein
value
4
2
0
−2
colname
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

| | | | | |
|---|---|---|---|---|
| | ) | GAGSYTIMVLFADQATPTSPIR | < | LVSNHSLHETSSVFVDSLTK |
| VK | * | GAGTGGLGLAVEGPSEAK | = | LYSVSYLLK |
| TYGGHQVPGSPFK | + | GKLDVQFSGLTK | > | MDCQECPEGYR |
| | , | GLVEPVDVVDNADGTQTVNYVPSR | ? | NDNDTFTVK |
| IVTITWGGQNIGR | − | GQHVPGSPFQFTVGPLGEGGAHK | @ | NGHVGISFVPK |
| | · | GTVEPQLEAR | A | NGQHVASSPIPVVISQSEIGDAS |
| | / | HTAMVSWGGVSIPNSPFR | B | P21333 |
| | 0 | IANLQTDLSDGLR | C | PGAPLRPK |
| IVDPNVDEHSVMTYLSQFPK | 1 | IECDDKGDGSCDVR | D | RAEFTVETR |
| | 2 | IPEISIQDMTAQVTSPSGK | E | RAPSVANVGSHCDLSLK |
| FPLEAVAPTKPSK | 3 | IVGPSGAAVPCK | F | RLTVSSLQESGLK |
| | 4 | KGEITGEVR | G | SADFVVEAIGDDVGTLGFSVEG |
| | 5 | KTHIQDNHDGTYTVAYVPDVTGR | H | SAGQGEVLVYVEDPAGHQEEAK |
| | 6 | LDVQFSGLTK | I | SPFEVYVDK |
| | 7 | LIALLEVLSQKK | J | SPFSVAVSPSLDLSK |
| PSVQPPLR | 8 | LLGWIQNKLPQLPITNFSR | K | SPYTVTVGQACNPSACR |
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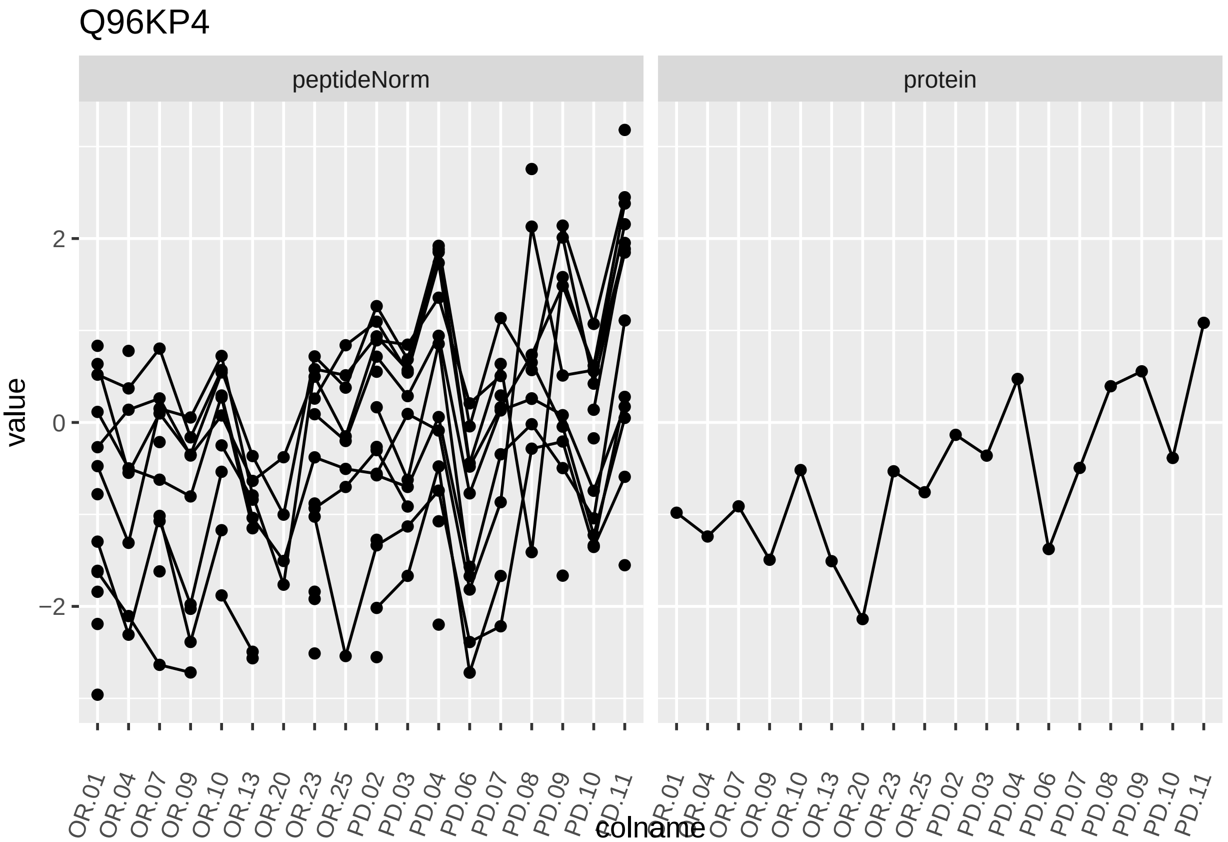
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OR.25
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PD.03
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PD.06
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PD.08
PD.09
PD.10
PD.11
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OR.09
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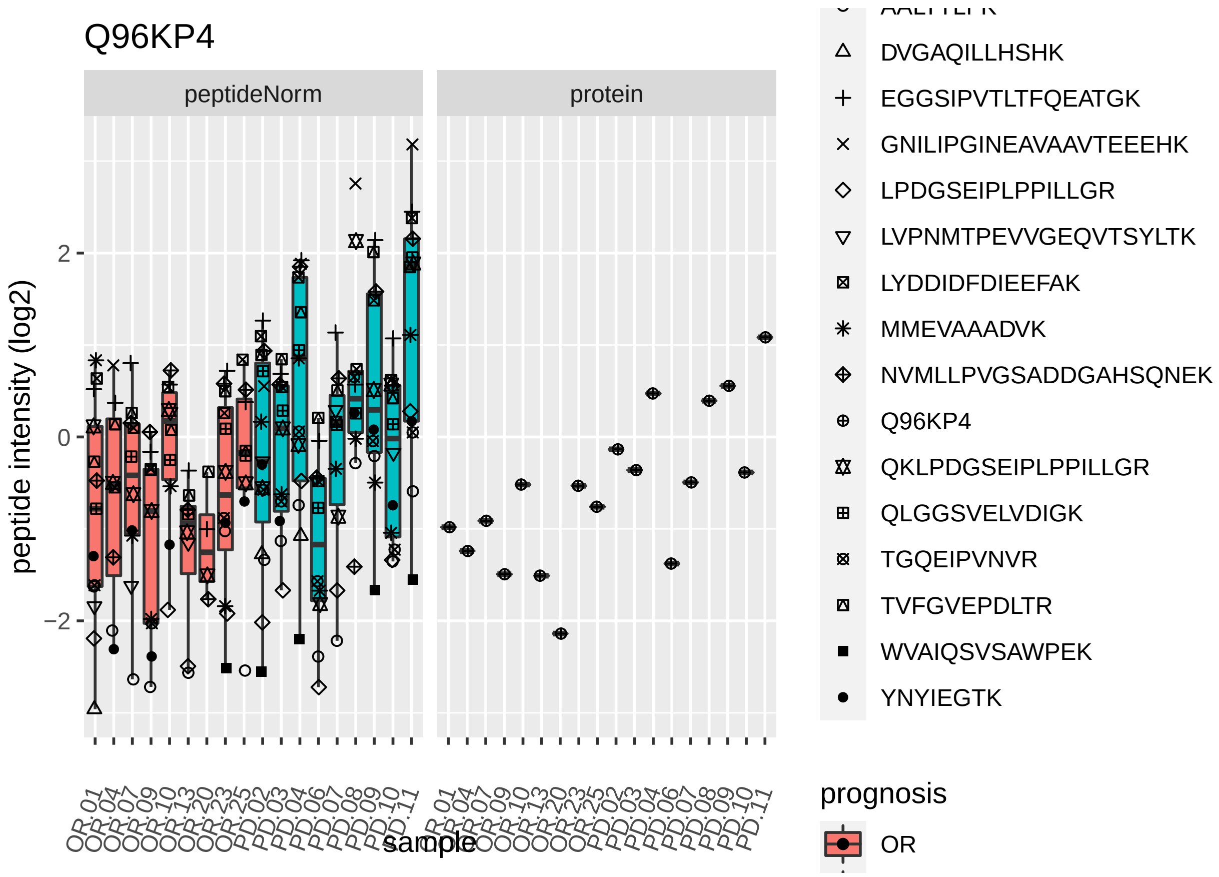
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PD.10
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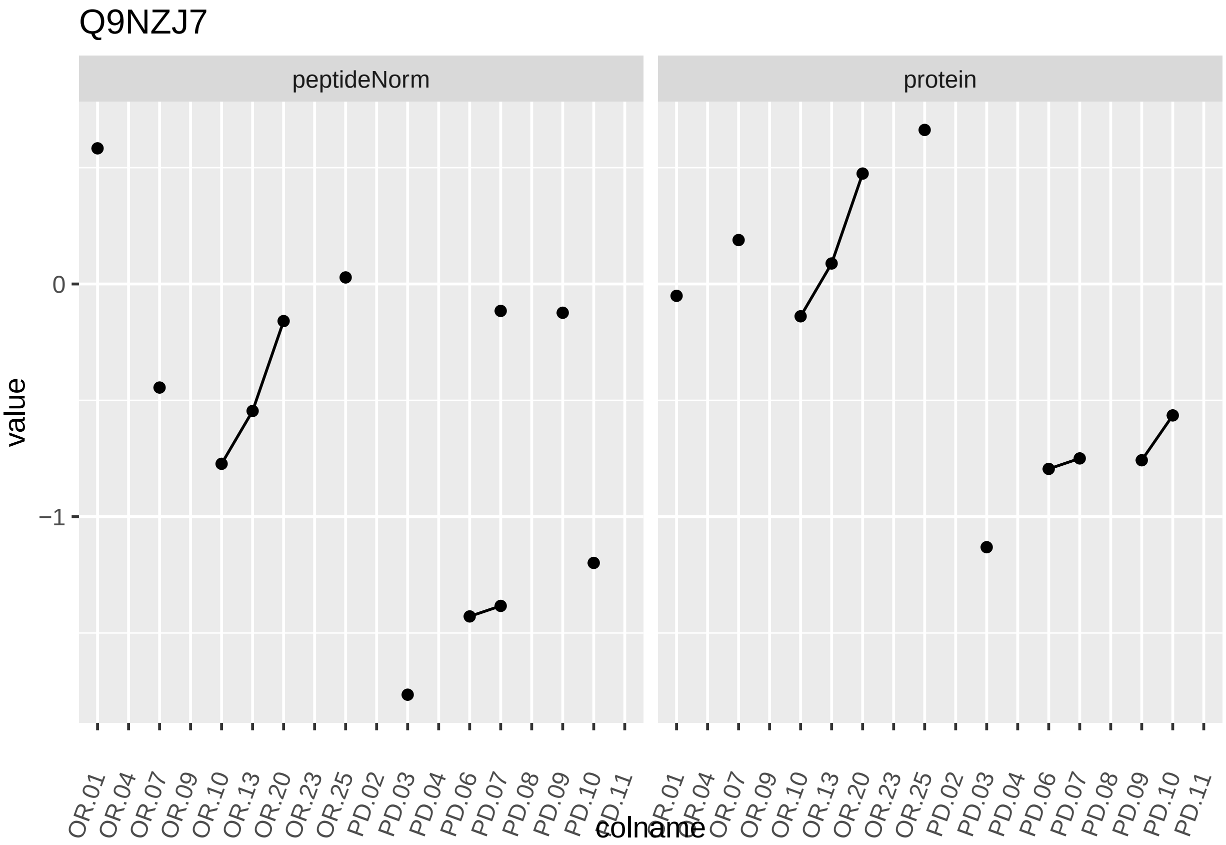
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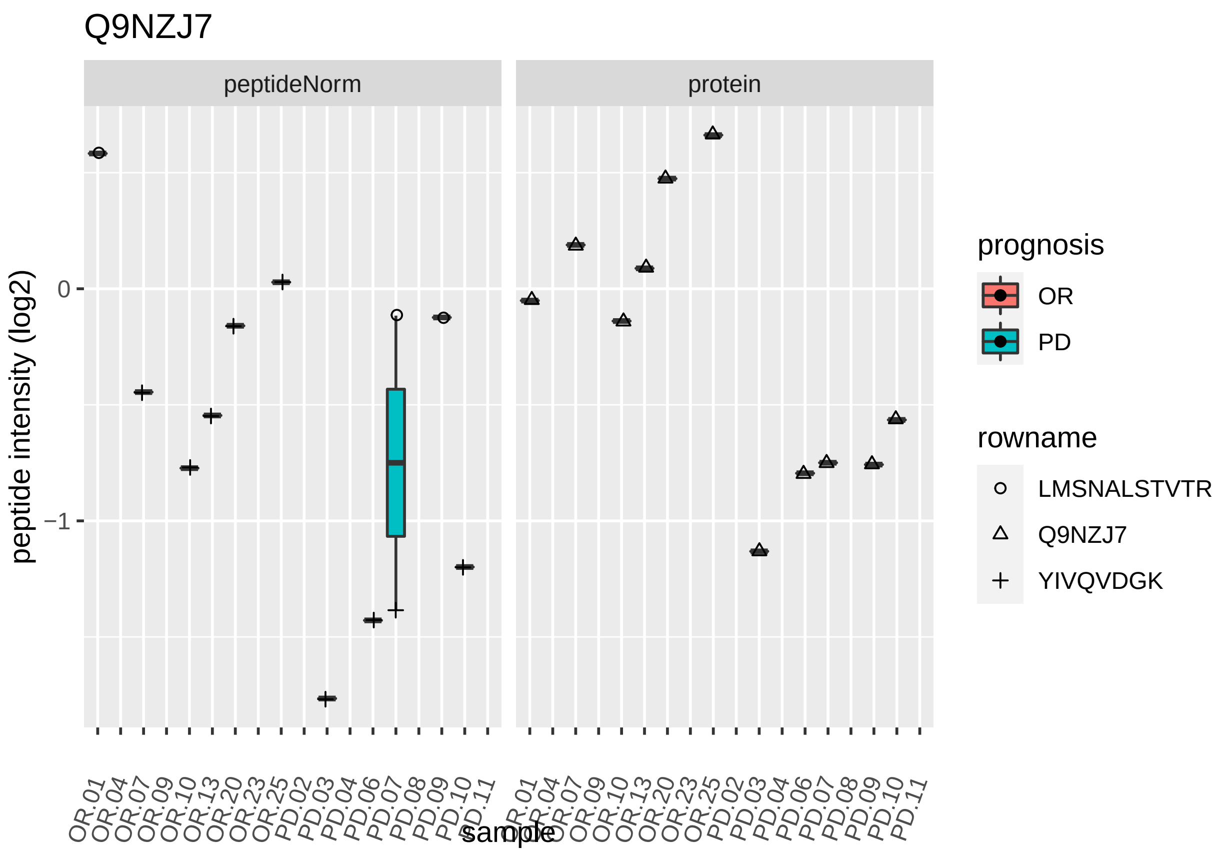
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prognosis
OR
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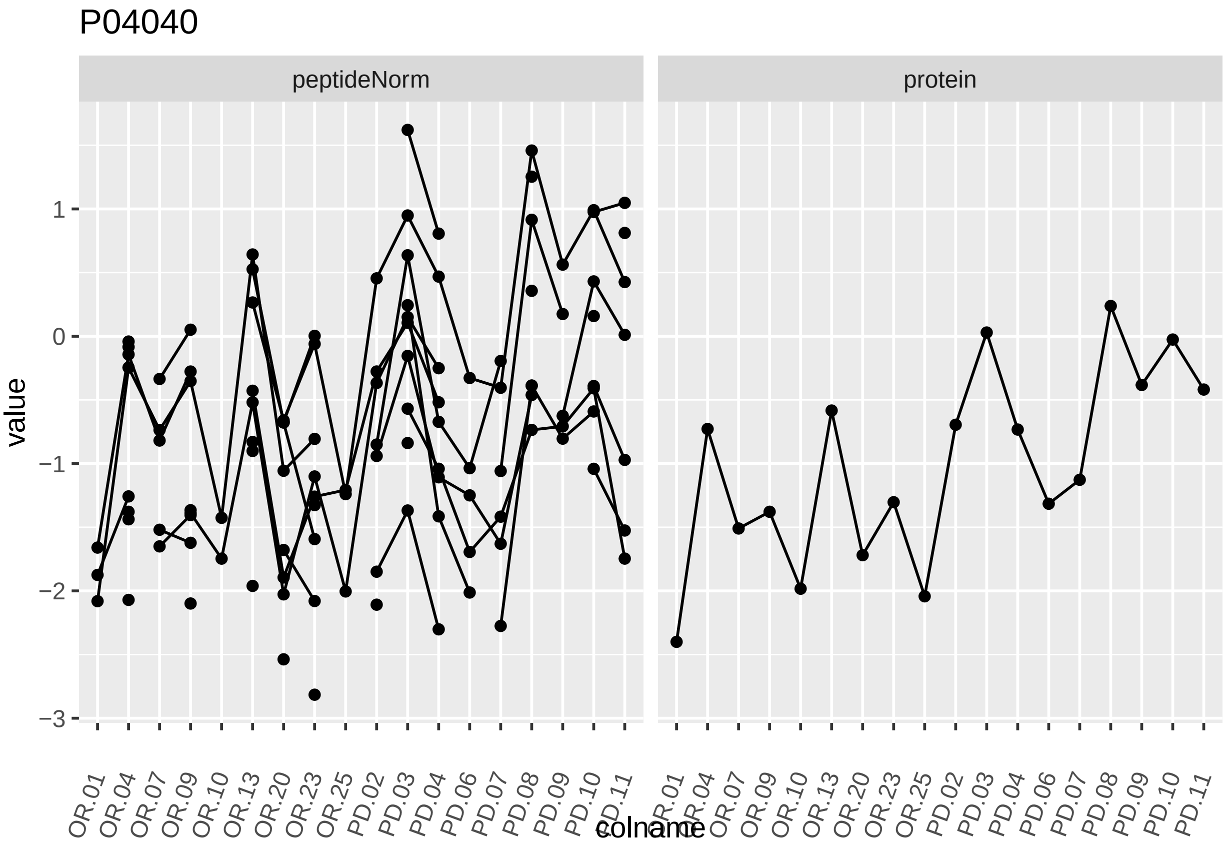

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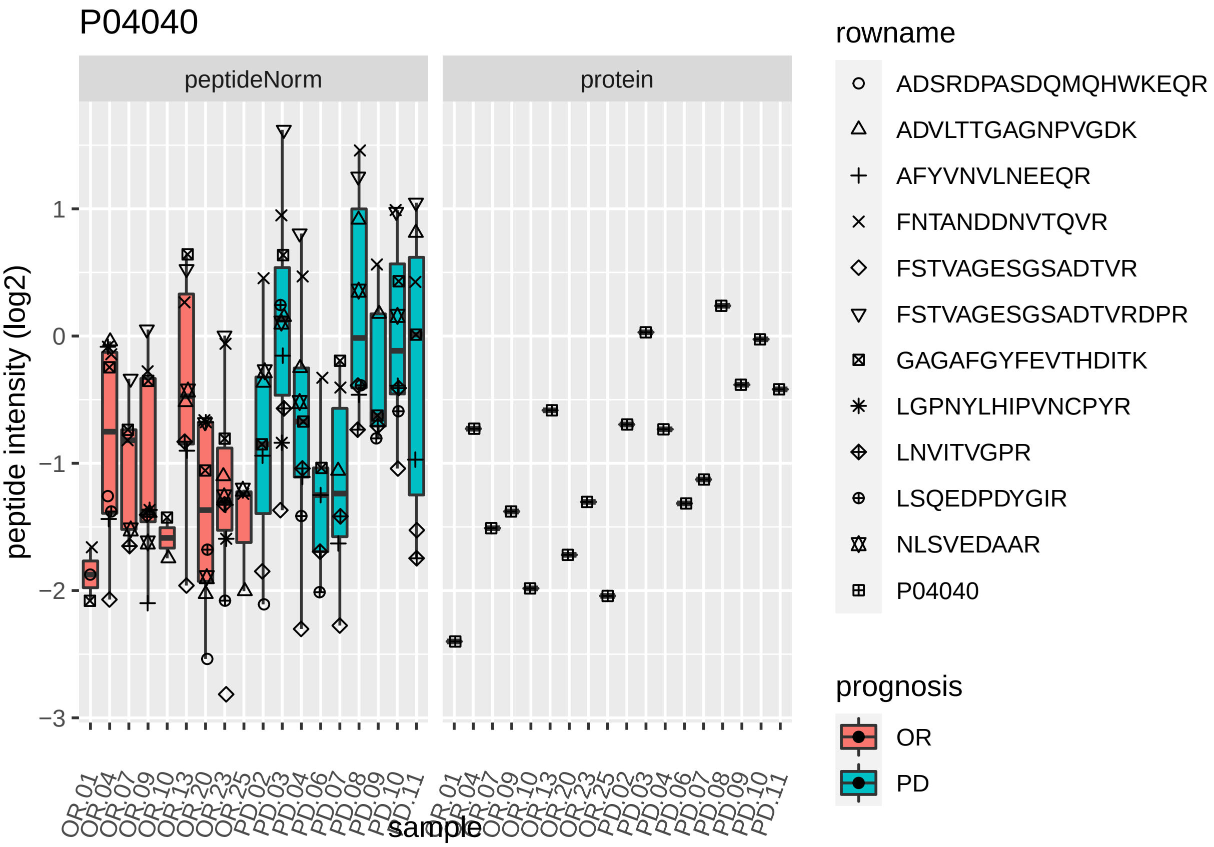
PD.11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OR.20
OR.23
OR.25
PD.02
PD.03
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PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
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prognosis
OR
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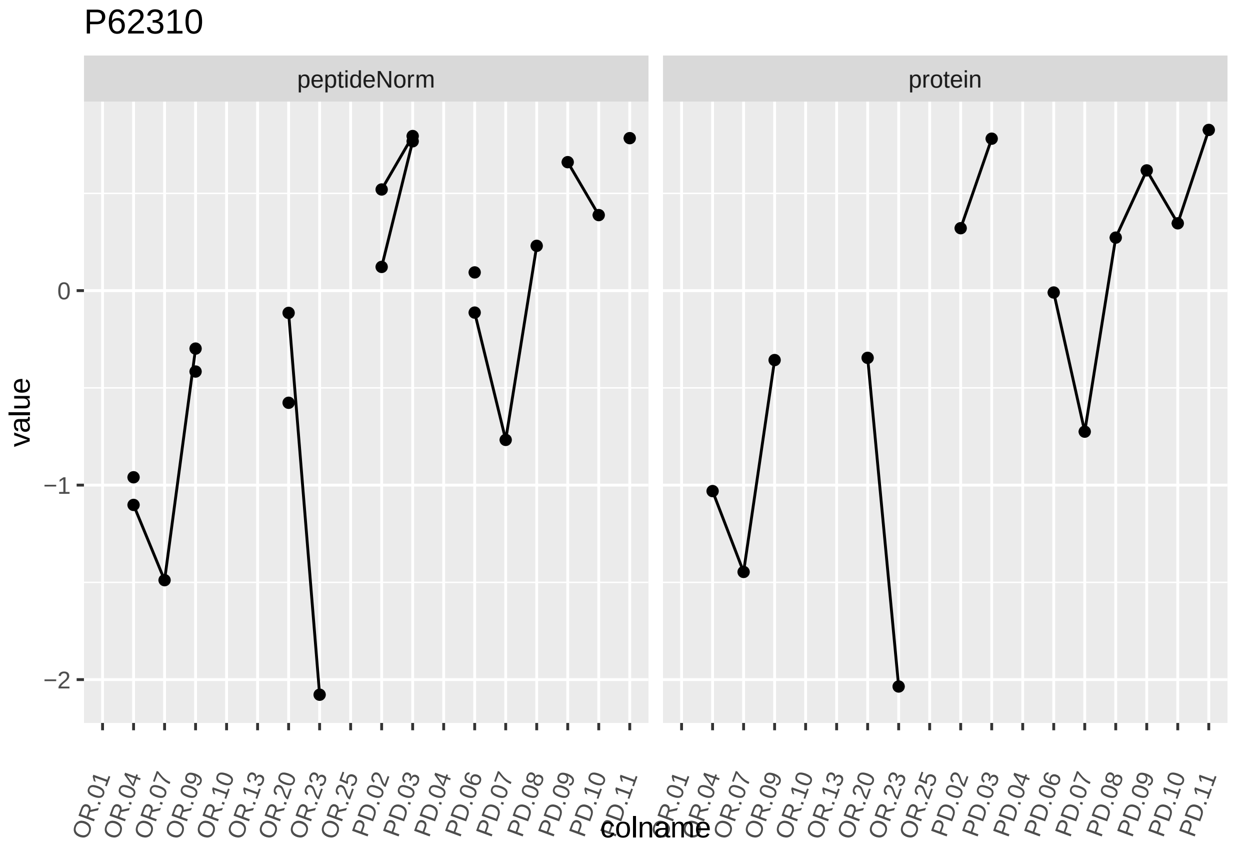
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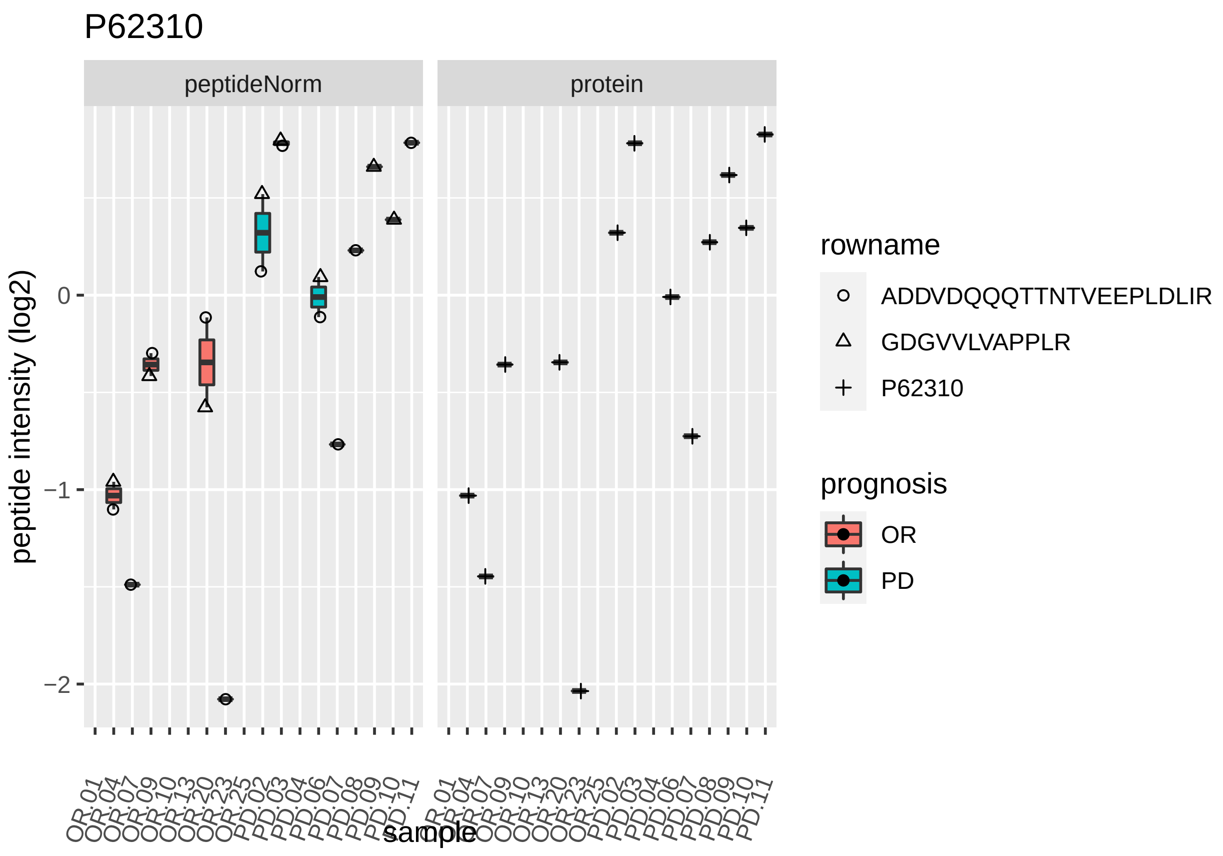
PD.08
PD.09
PD.10
PD.11
colname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OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
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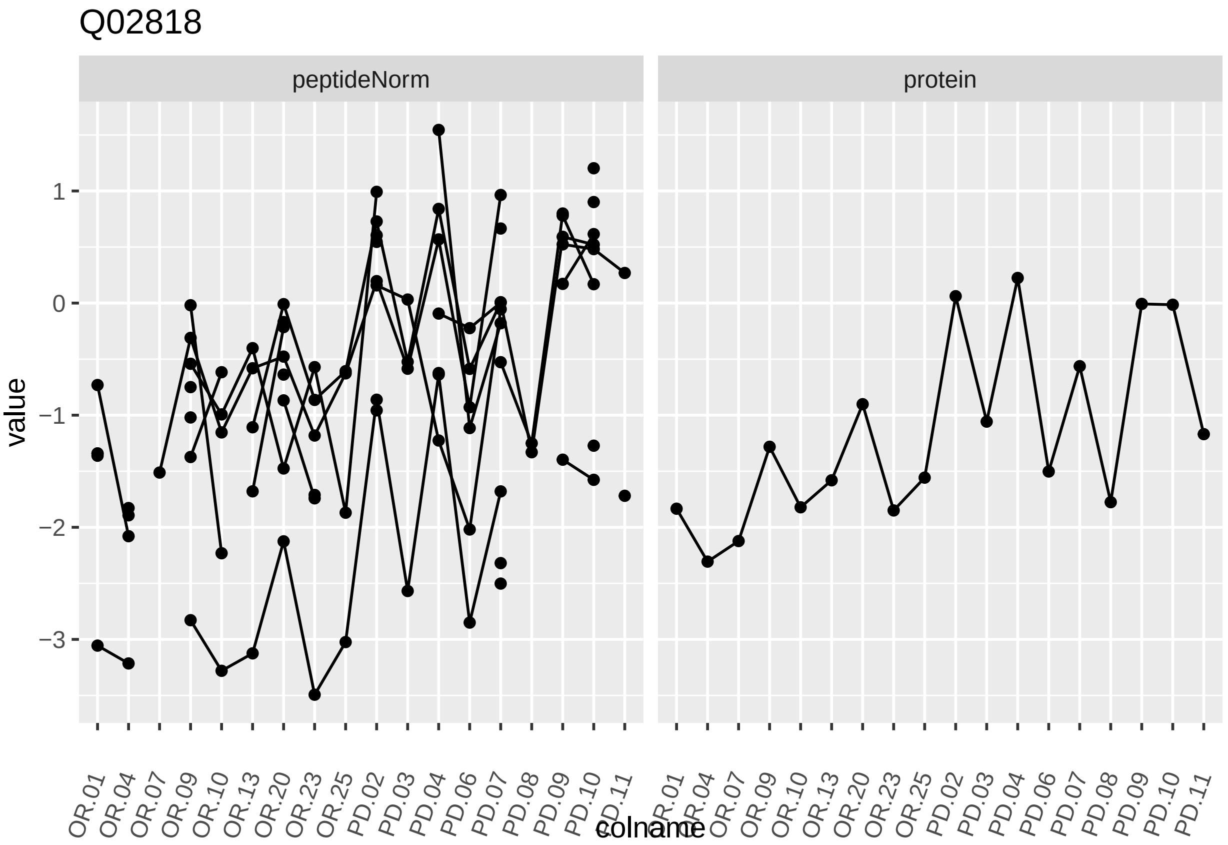
△ GDGVVLVAPPLR
+ P62310
prognosis
🟥 OR
🟦 PD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PD.02
PD.03
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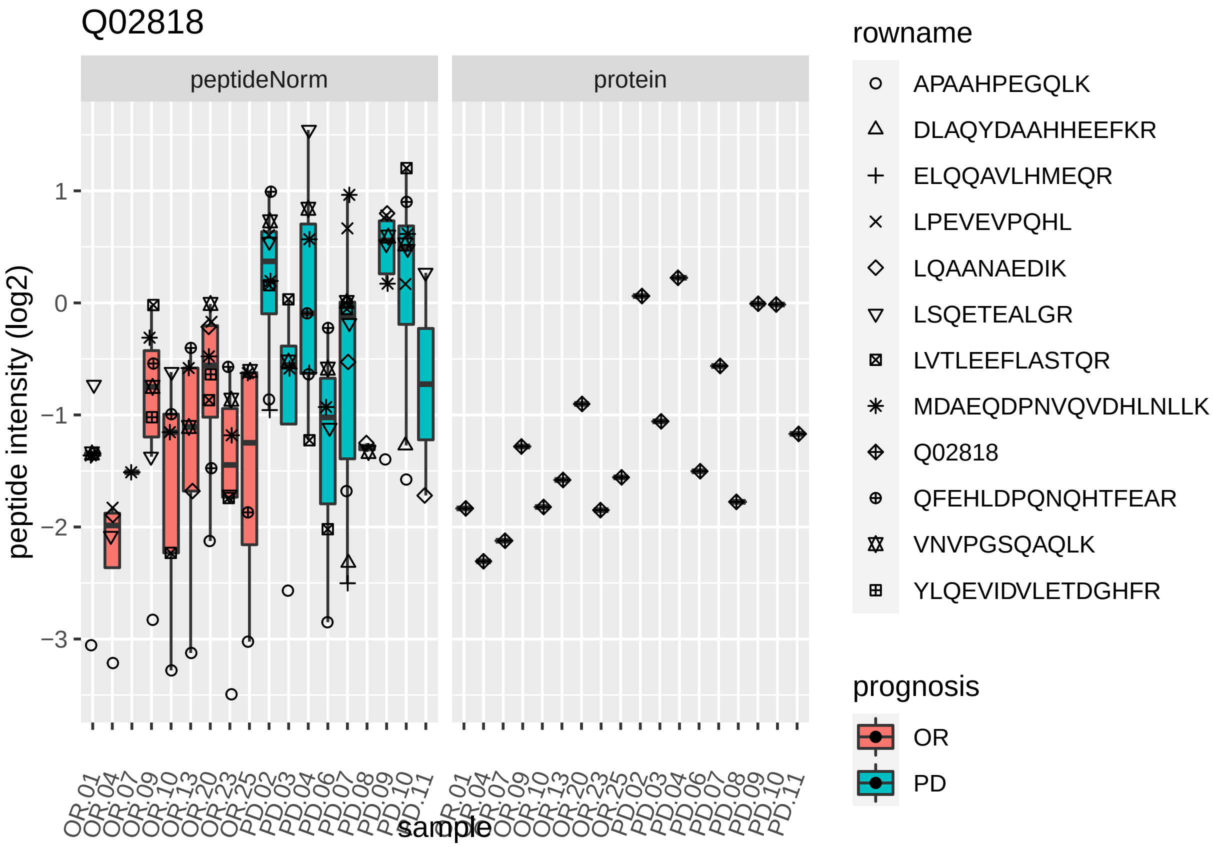
PD.11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peptide intensity (log2)
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−3
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OR.07
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OR.23
OR.25
PD.02
PD.03
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PD.08
PD.09
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PD.11
sample
rowname
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LQAANAEDIK
LSQETEALGR
LVTLEEFLASTQR
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prognosis
OR
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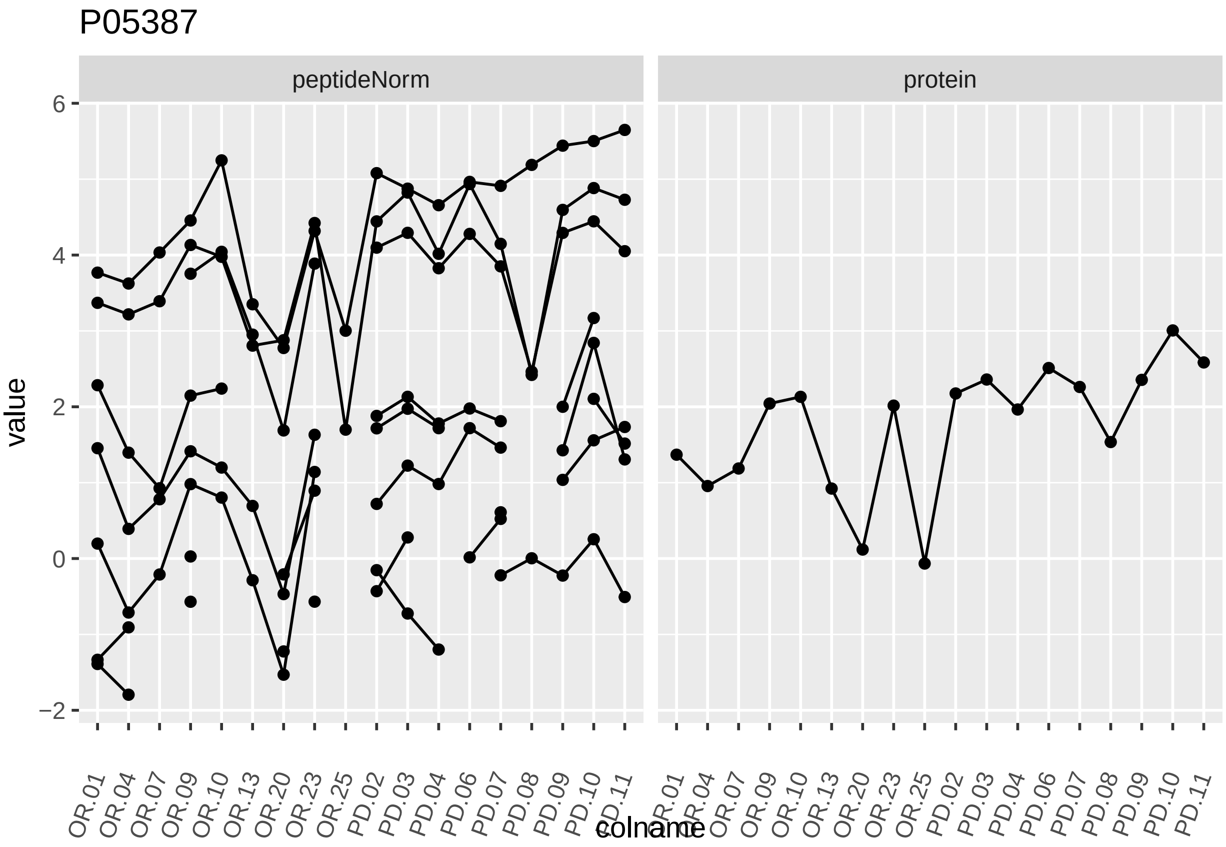
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OR.25
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PD.04
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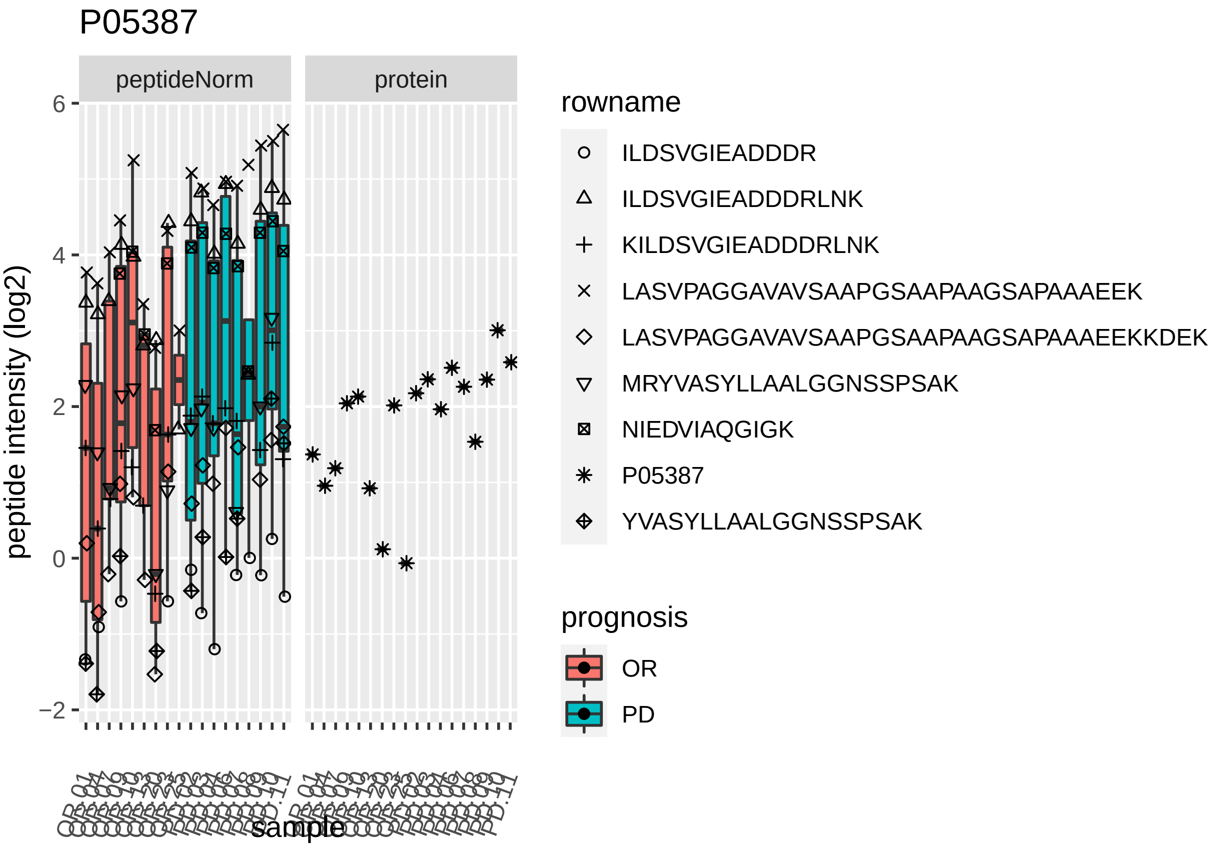
PD.10
PD.11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peptide intensity (log2)
sample
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P05387
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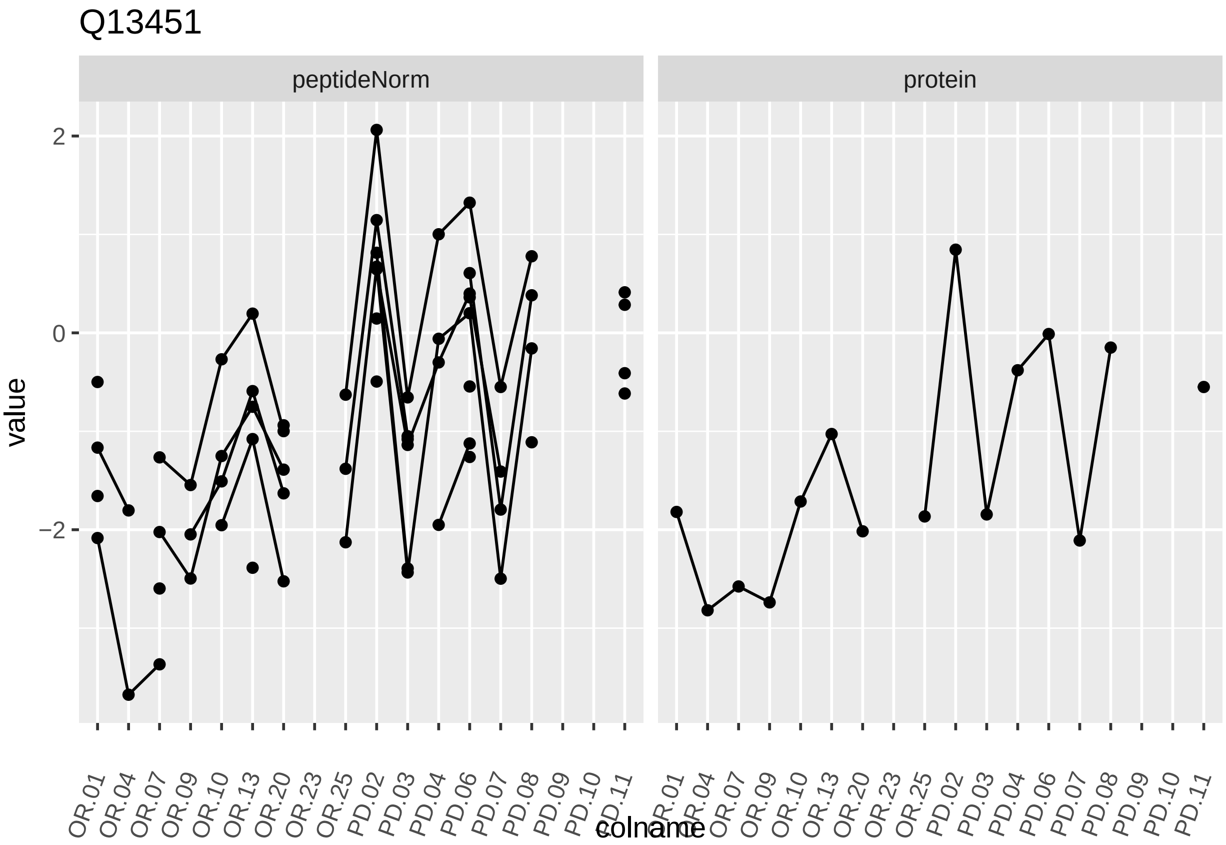
prognosis
OR
PD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OR.25
PD.02
PD.03
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PD.06
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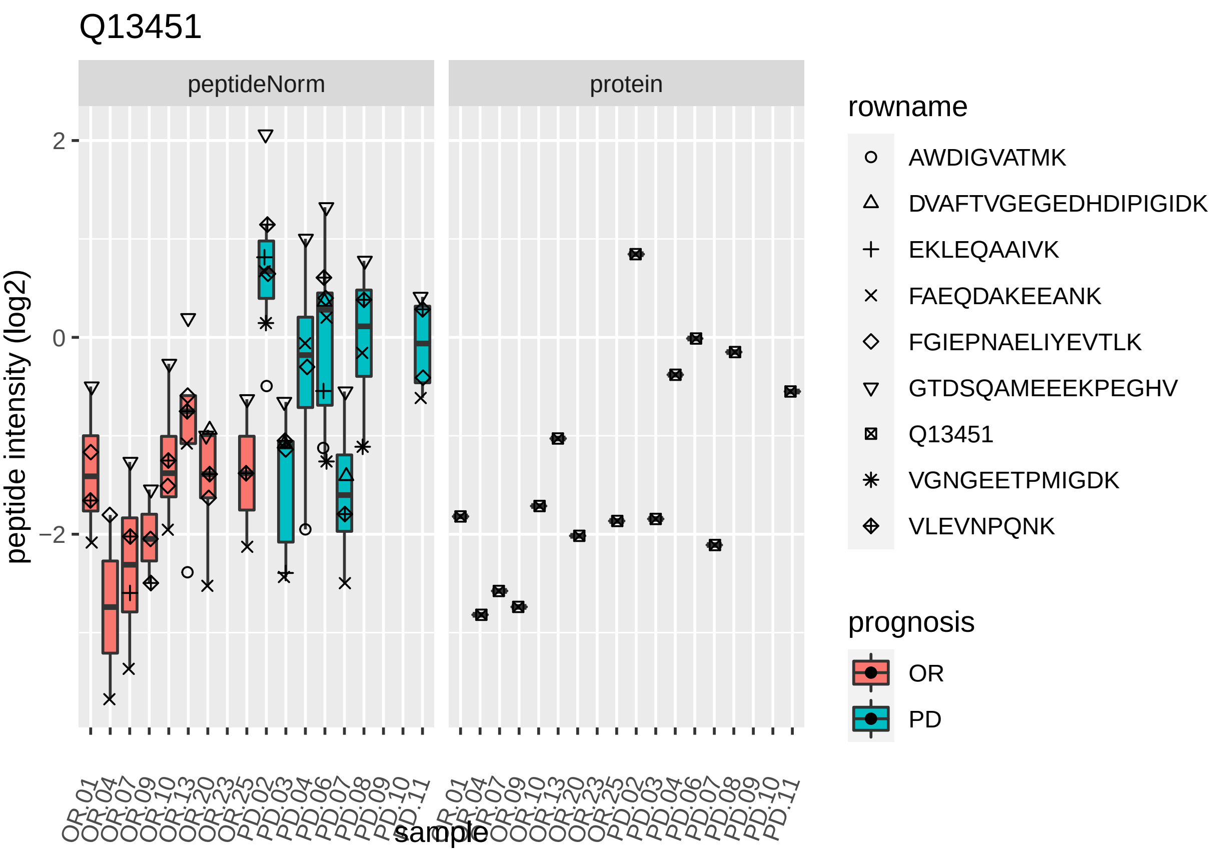
PD.09
PD.10
PD.11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protein
peptide intensity (log2)
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0
−2
sample
OR.01
OR.04
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OR.10
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OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
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△ DVAFTVGEGEDHDIPIGIDK
+ EKLEQAAIVK
× FAEQDAKEEANK
◇ FGIEPNAELIYEVTLK
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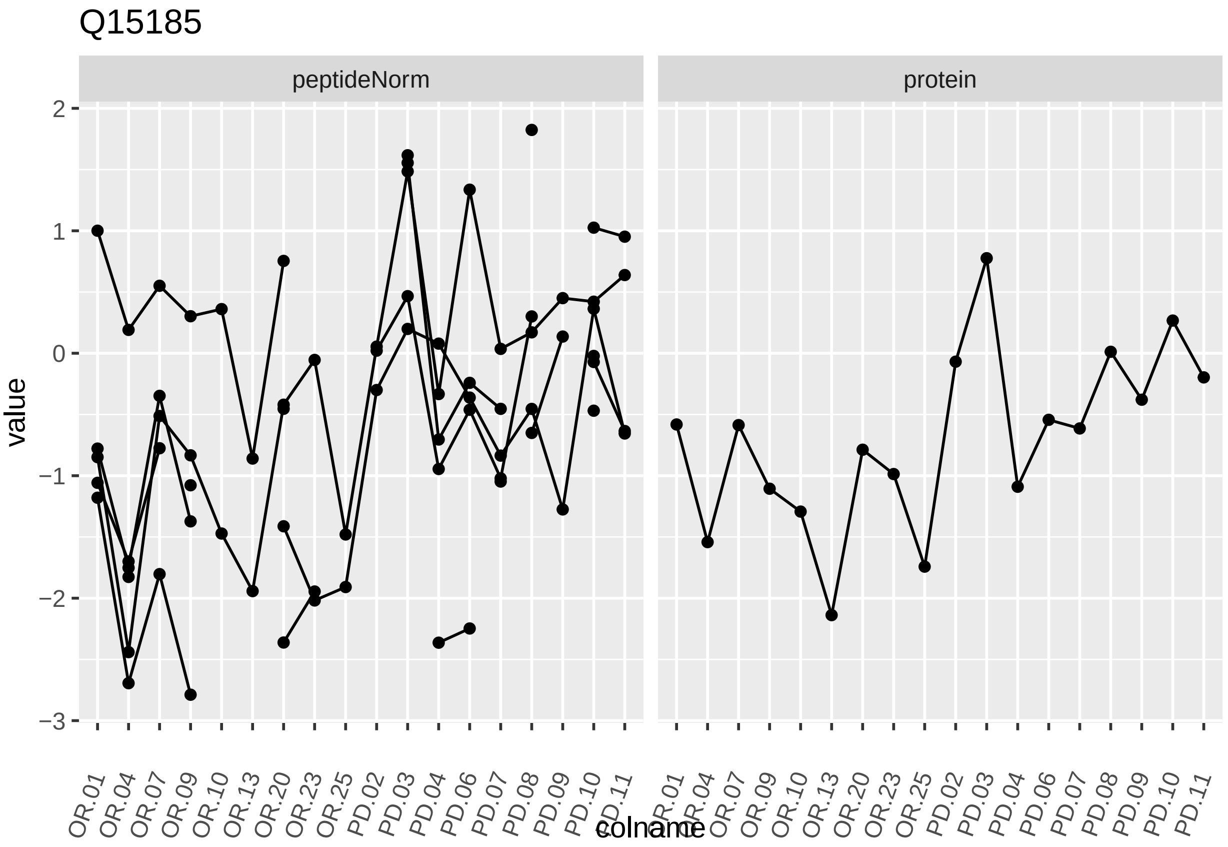
⊠ Q13451
✳ VGNGEETPMIGDK
⊕ VLEVNPQNK
prognosis
OR
PD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OR.25
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PD.06
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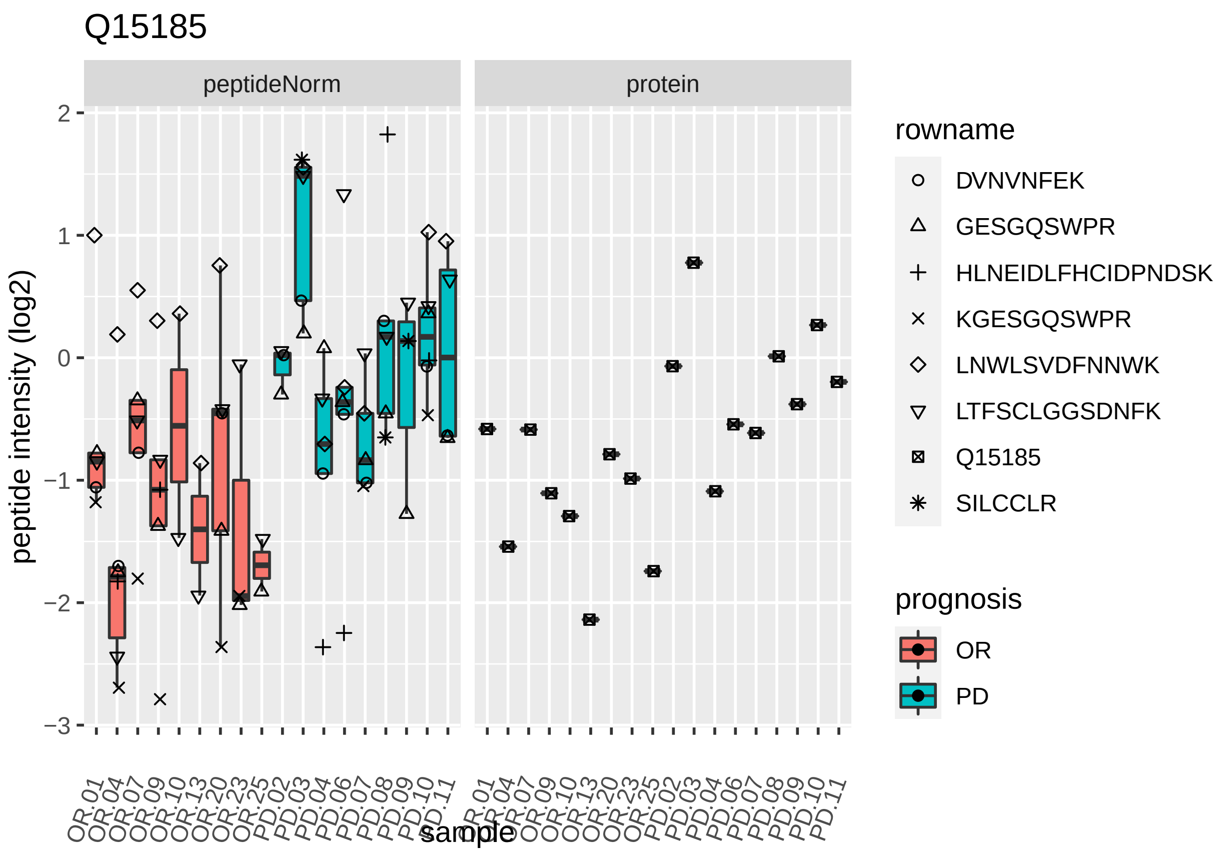
PD.10
PD.11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peptideNorm
protein
peptide intensity (log2)
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0
−1
−2
−3
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OR.04
OR.07
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OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
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PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
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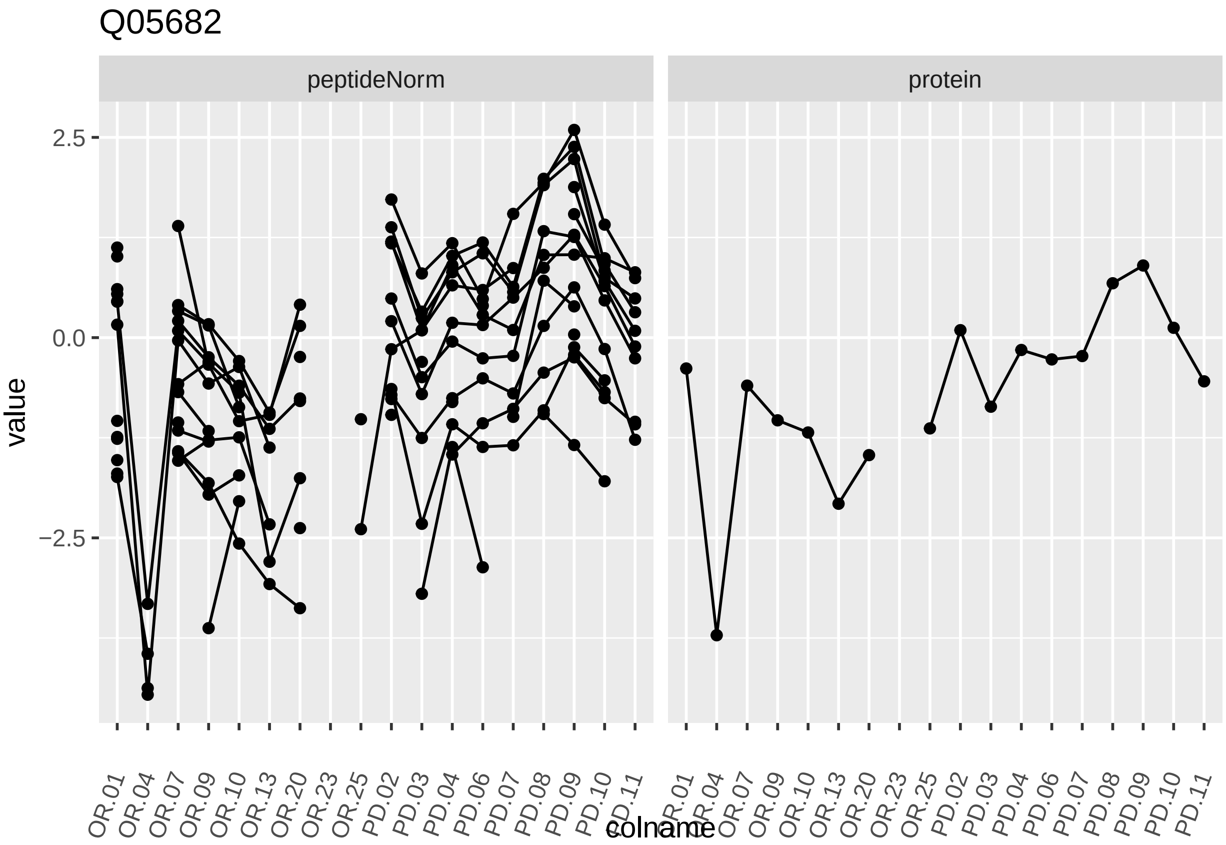
△ GESGQSWPR
+ HLNEIDLFHCIDPNDSK
× KGESGQSWPR
◇ LNWLSVDFNNWK
▽ LTFSCLGGSDNFK
⊠ Q15185
✳ SILCCLR
prognosis
OR
PD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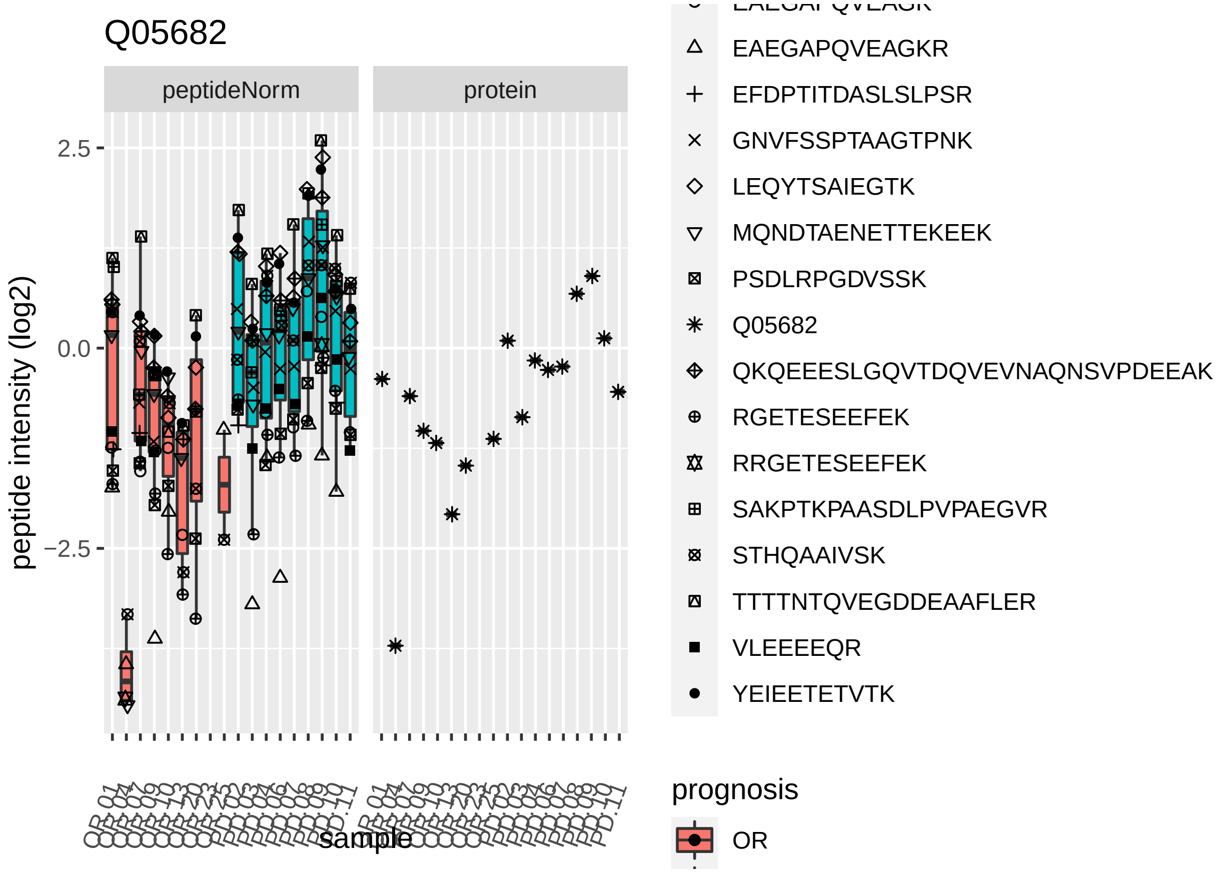
PD.10
PD.11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OR.13
OR.20
OR.23
OR.25
PD.02
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PD.10
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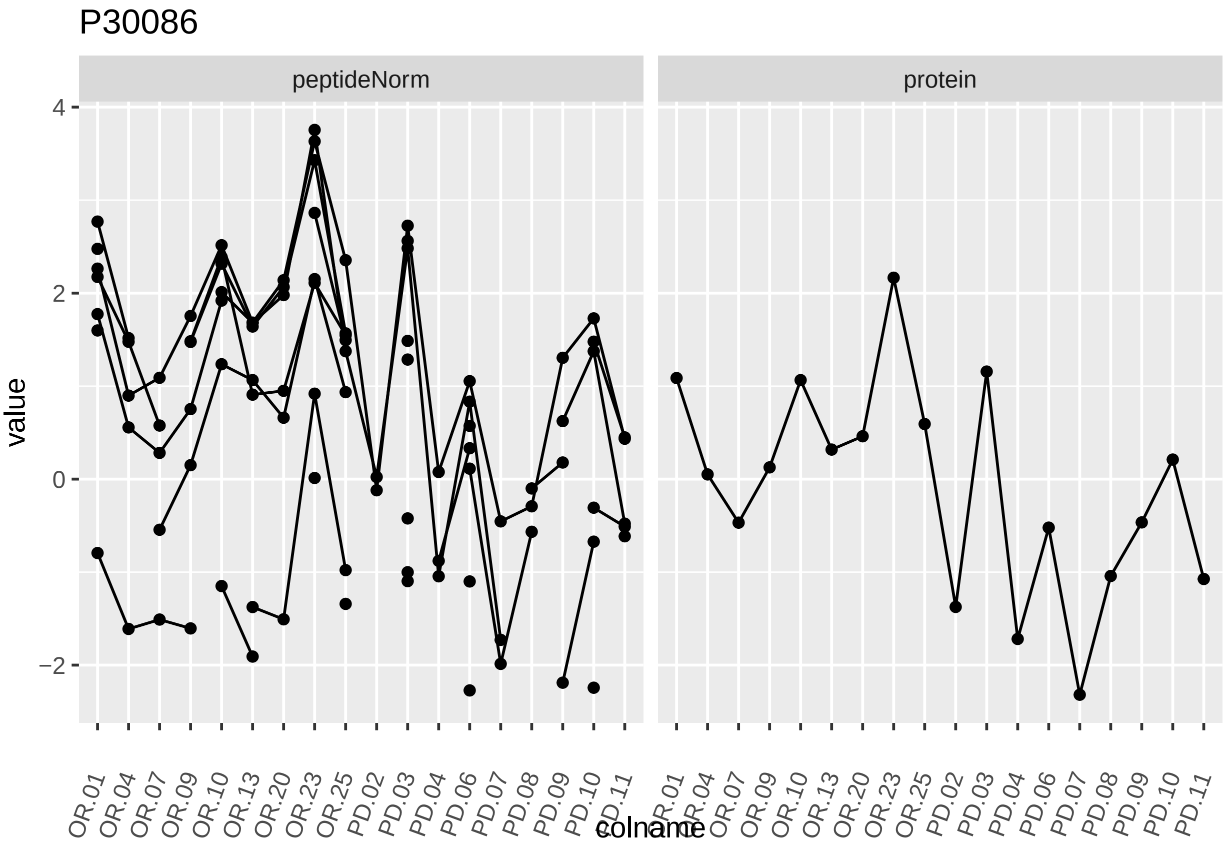
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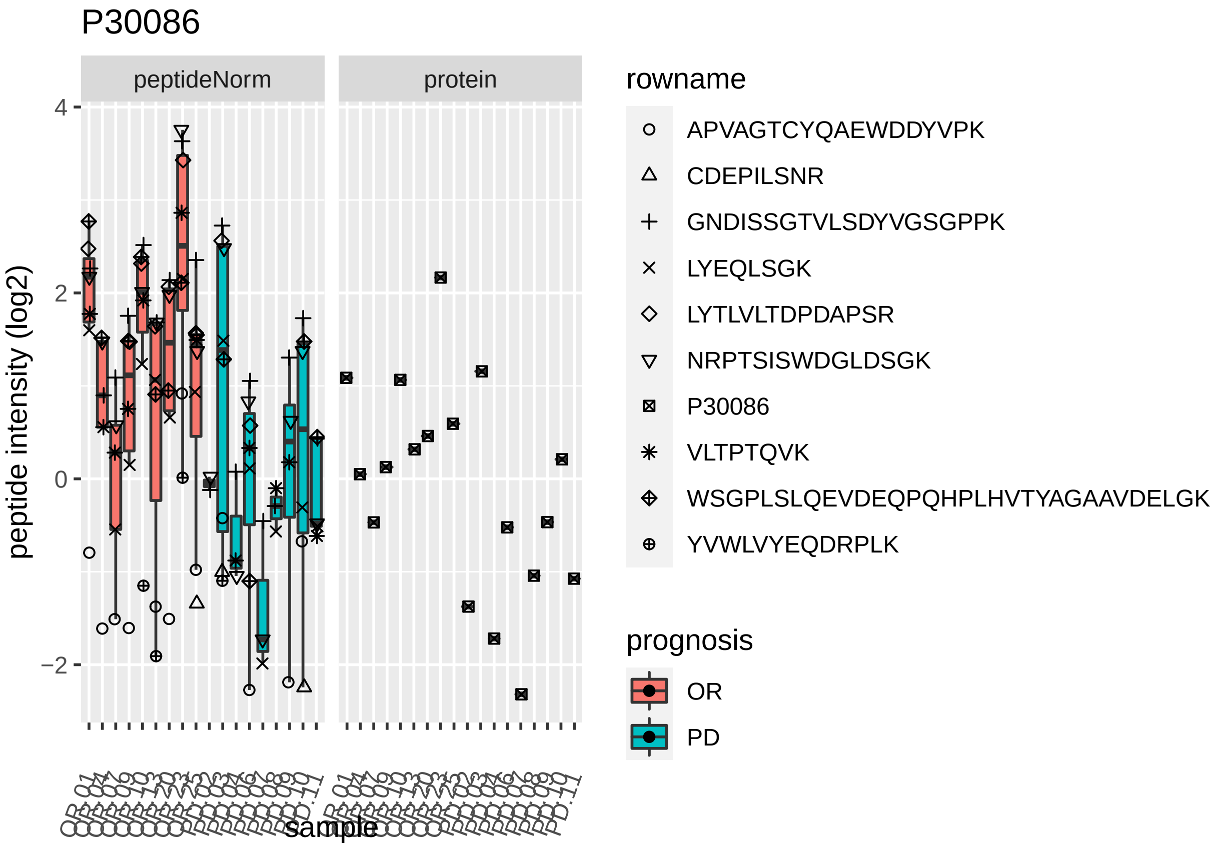
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prognosis
OR
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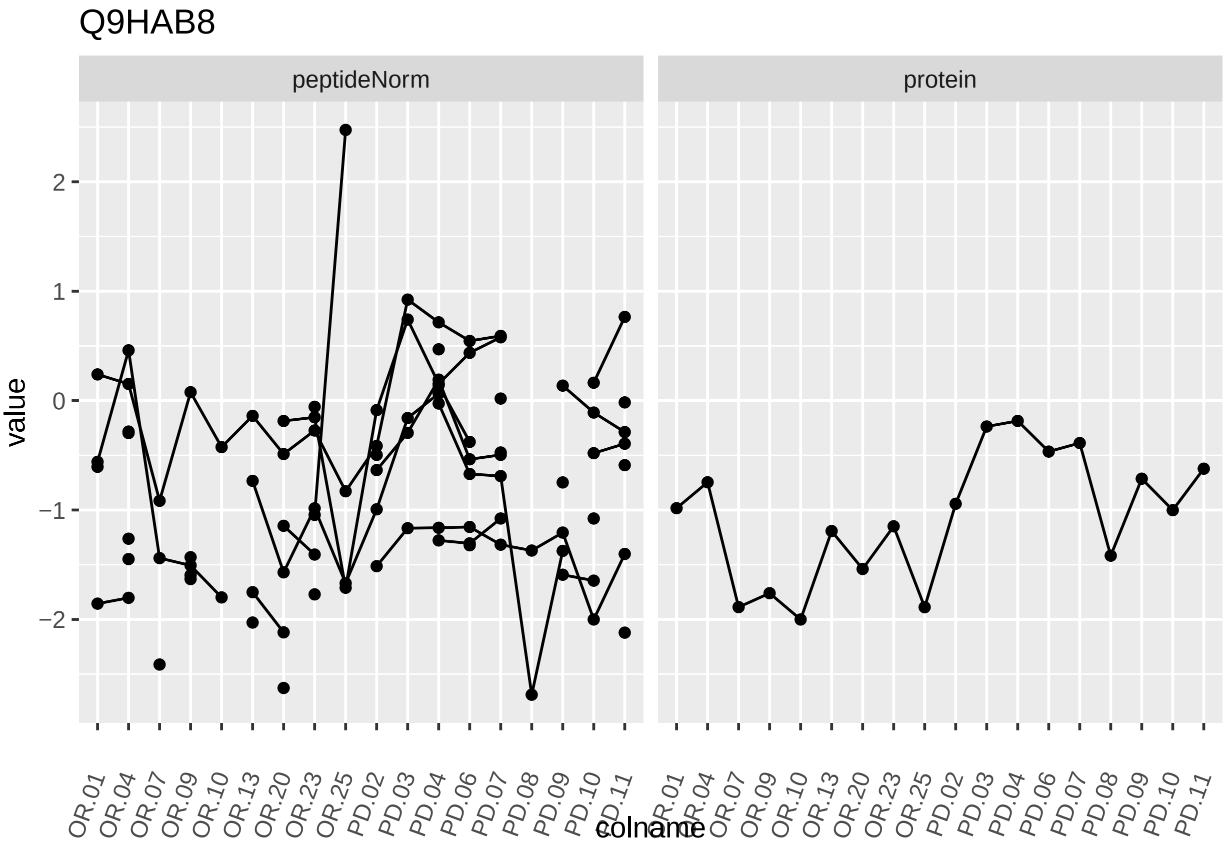
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PD.11
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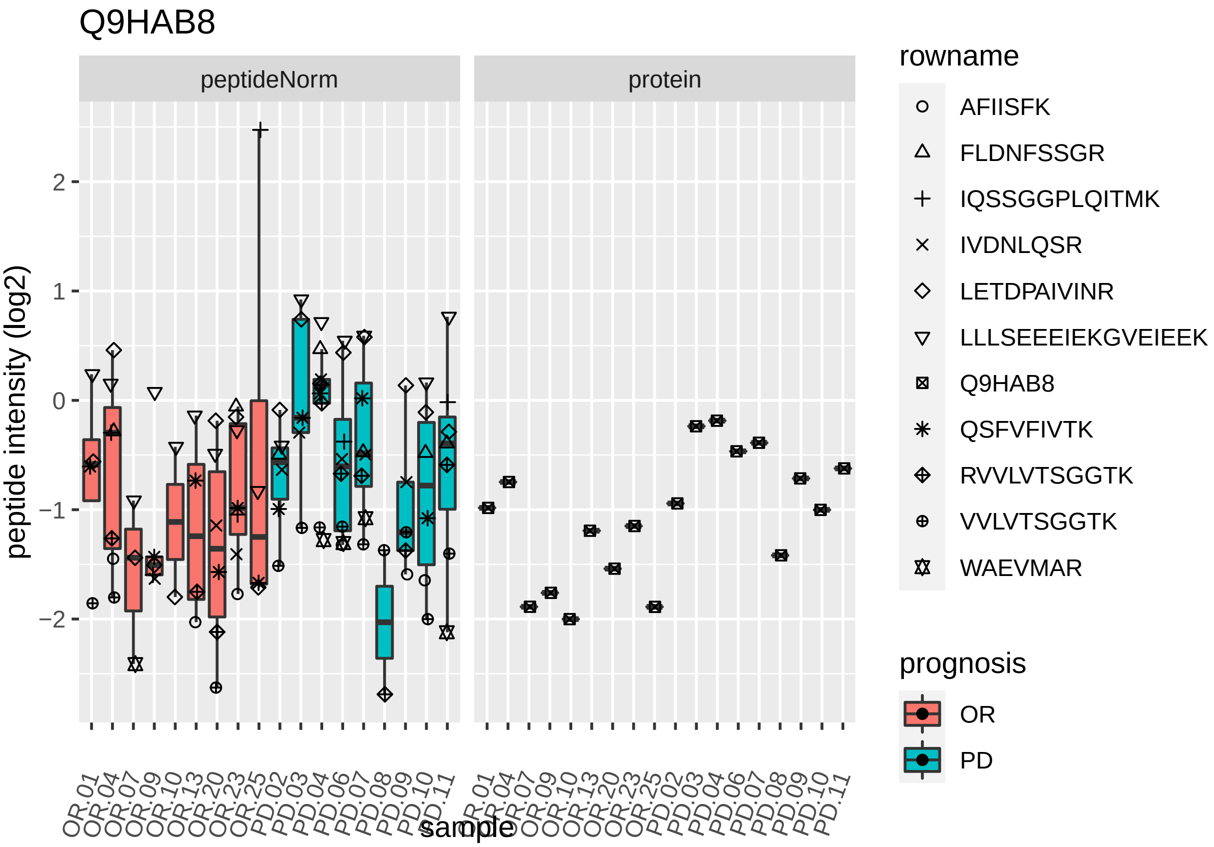
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protein
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PD.11
sample
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prognosis
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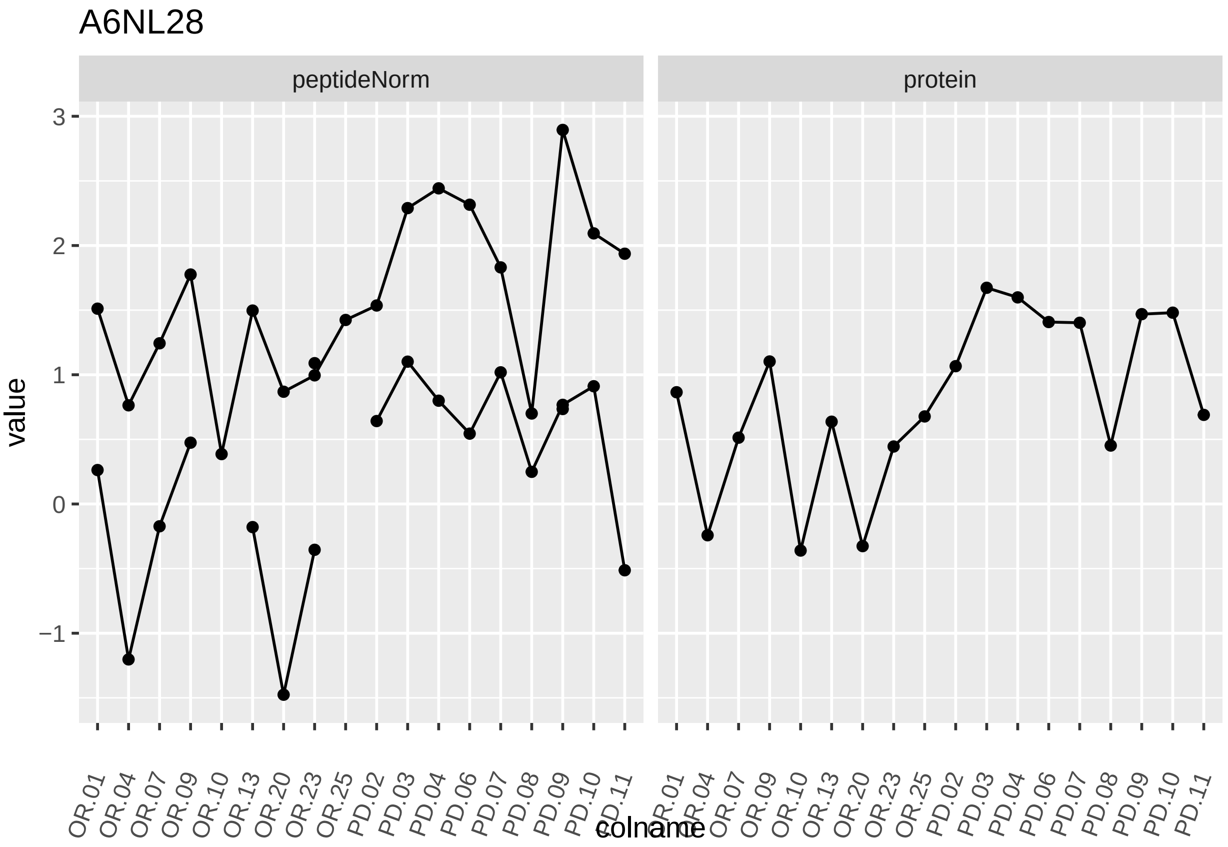
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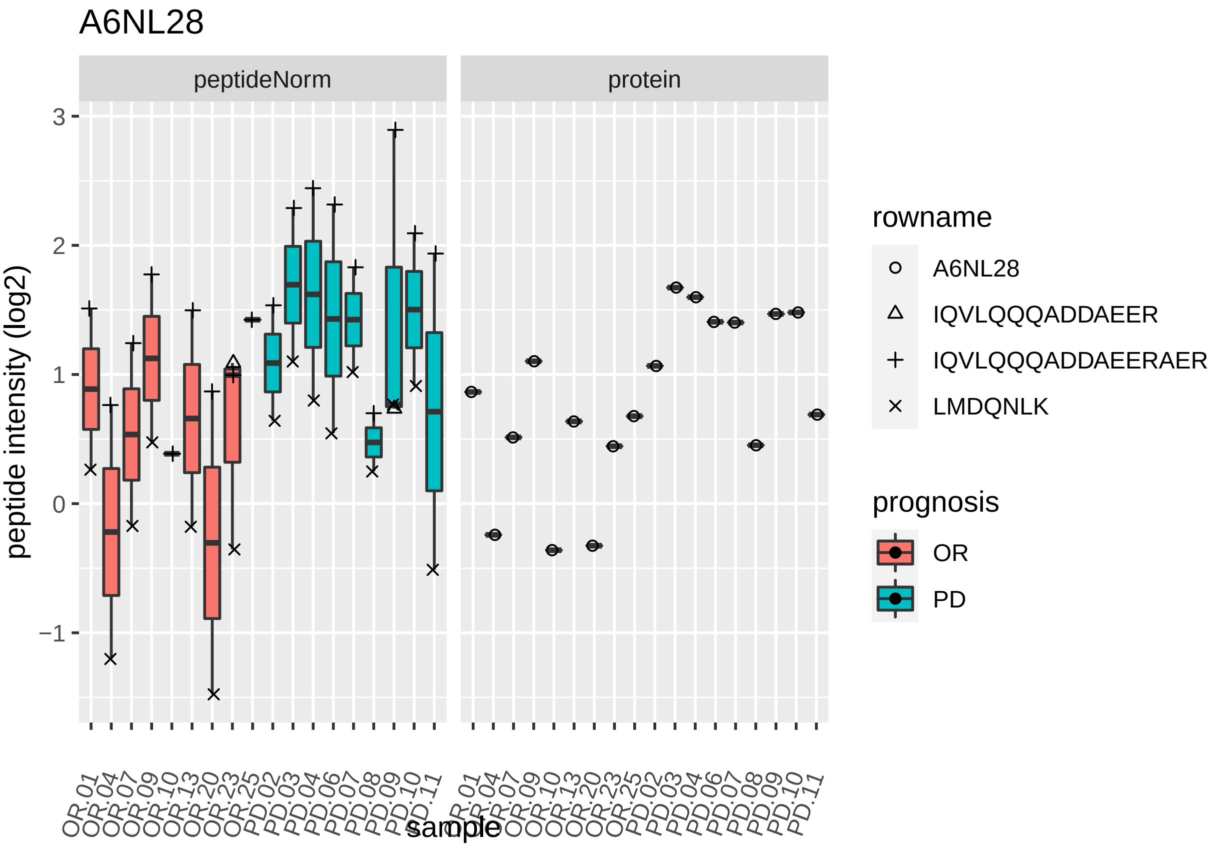
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prognosis
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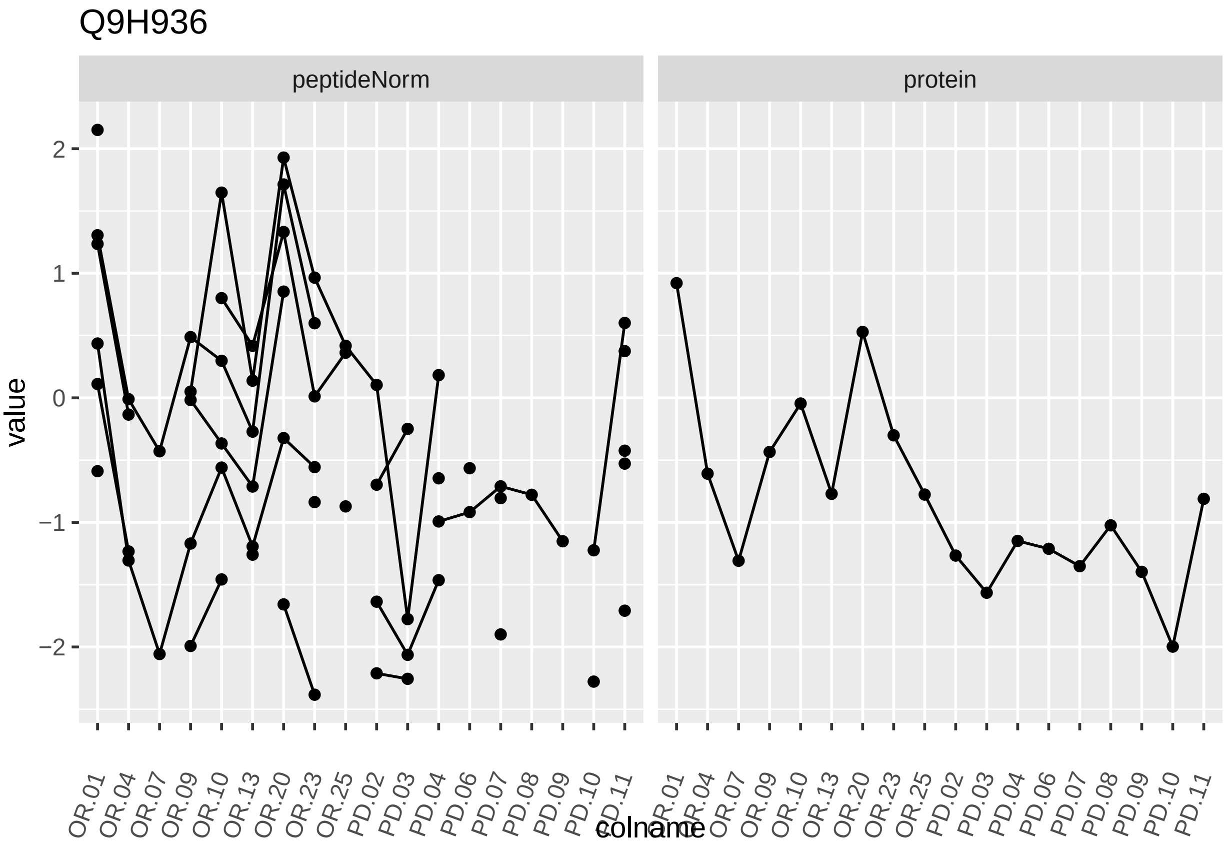
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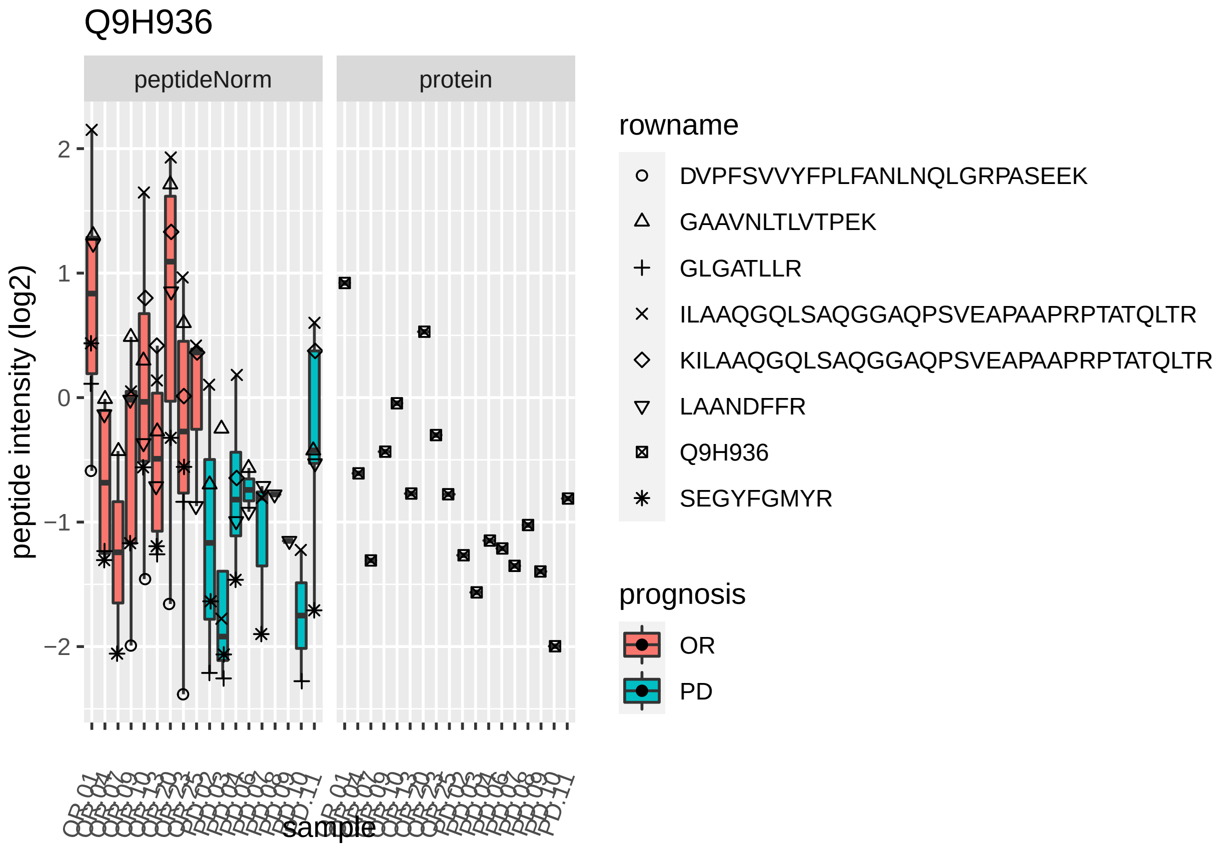
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+ GLGATLLR
× ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
◇ KILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
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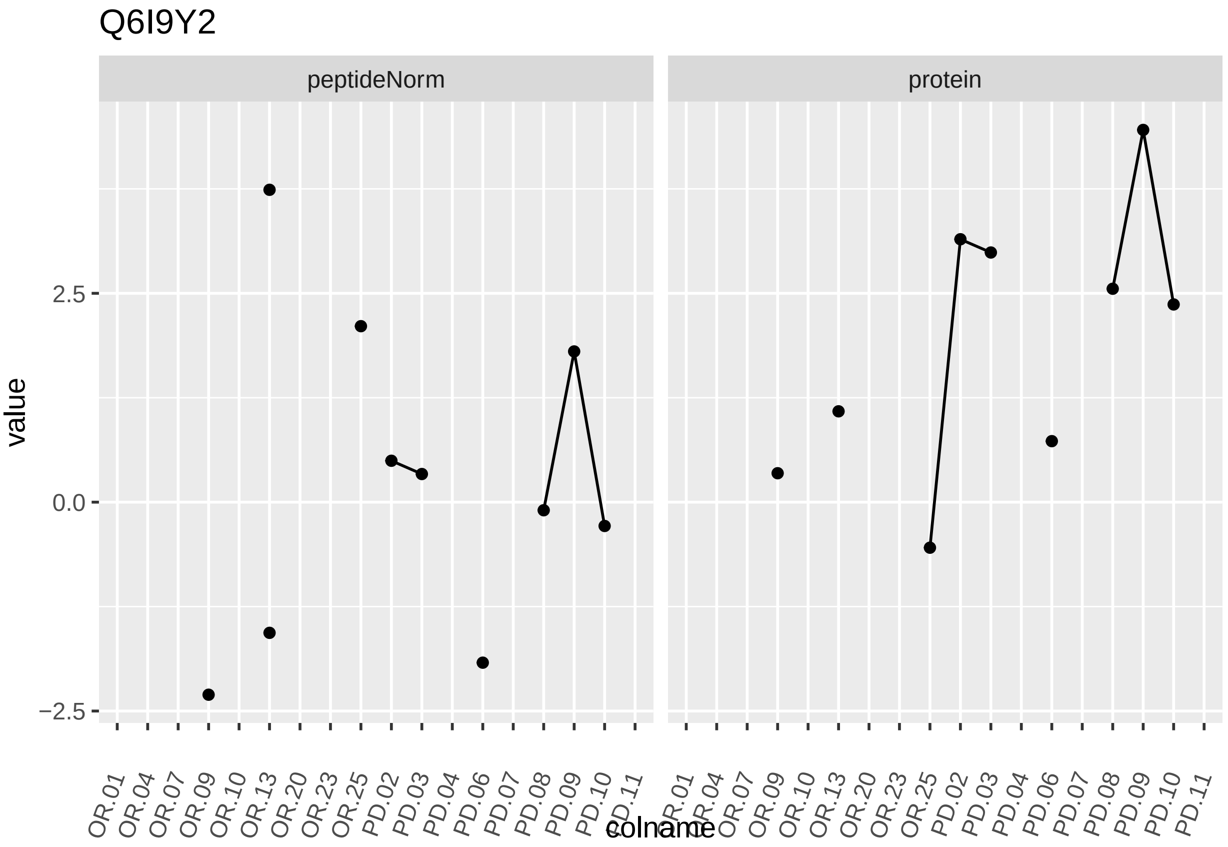
⊠ Q9H936
✳ SEGYFGMYR
prognosis
🟥 OR
🟦 PD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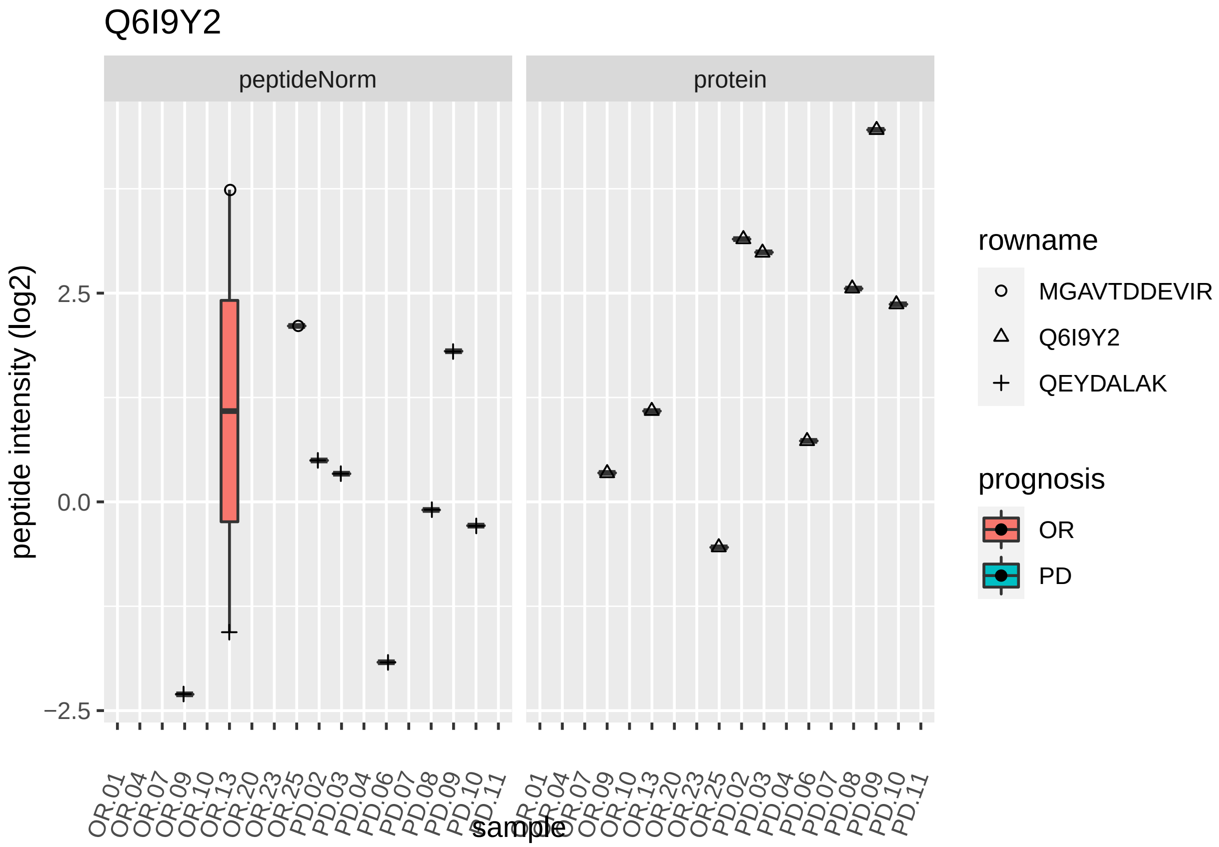
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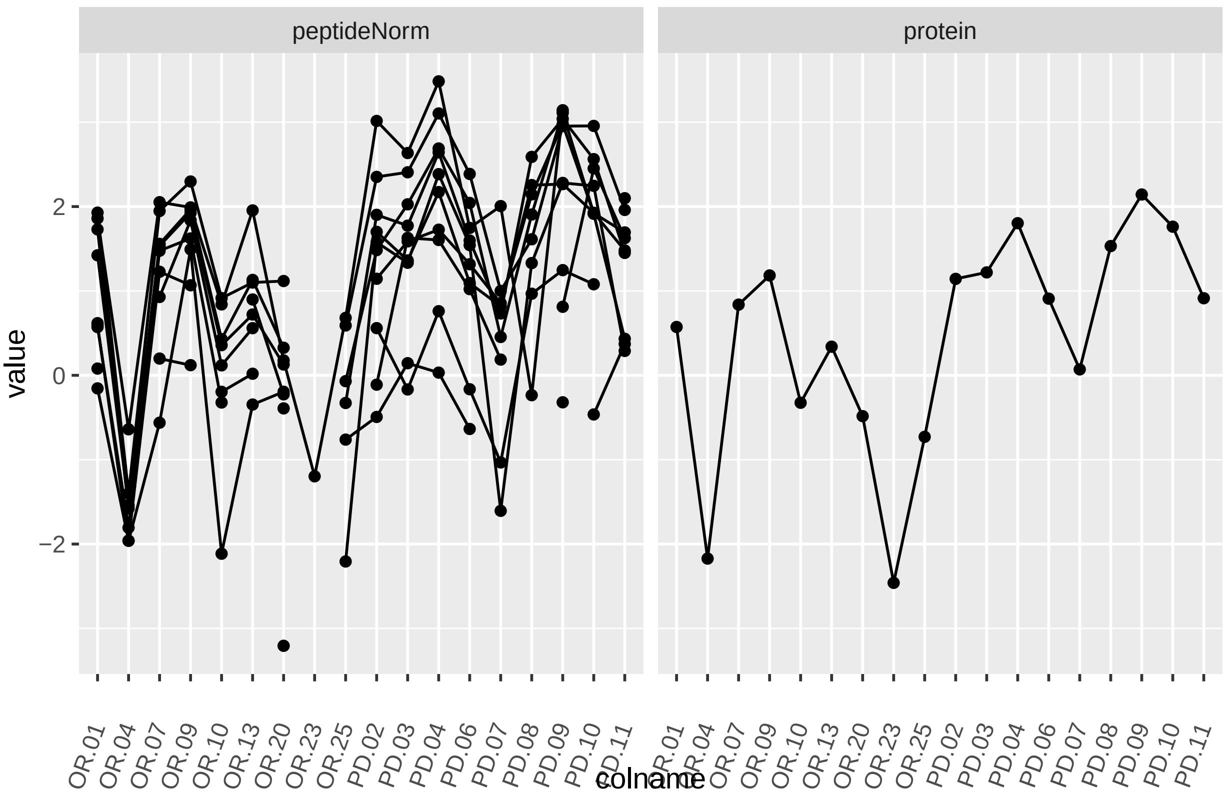
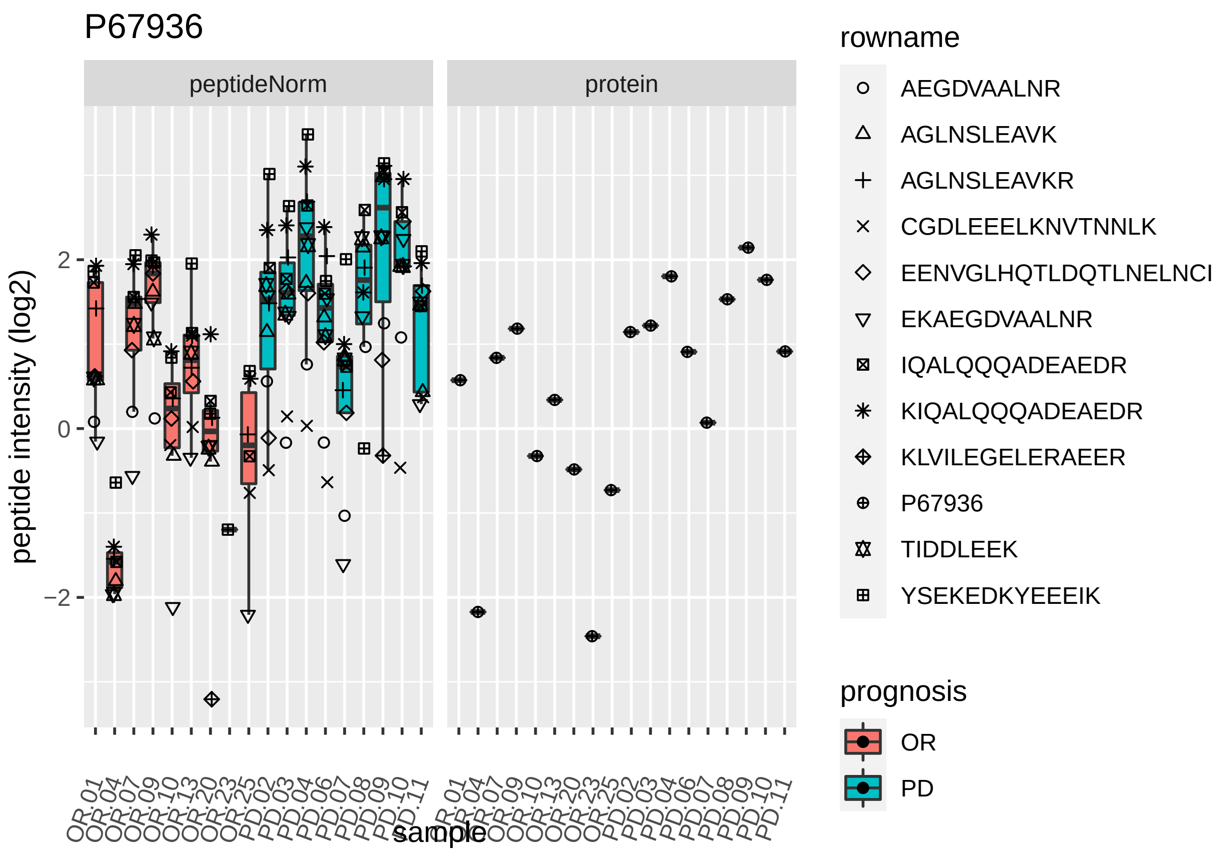
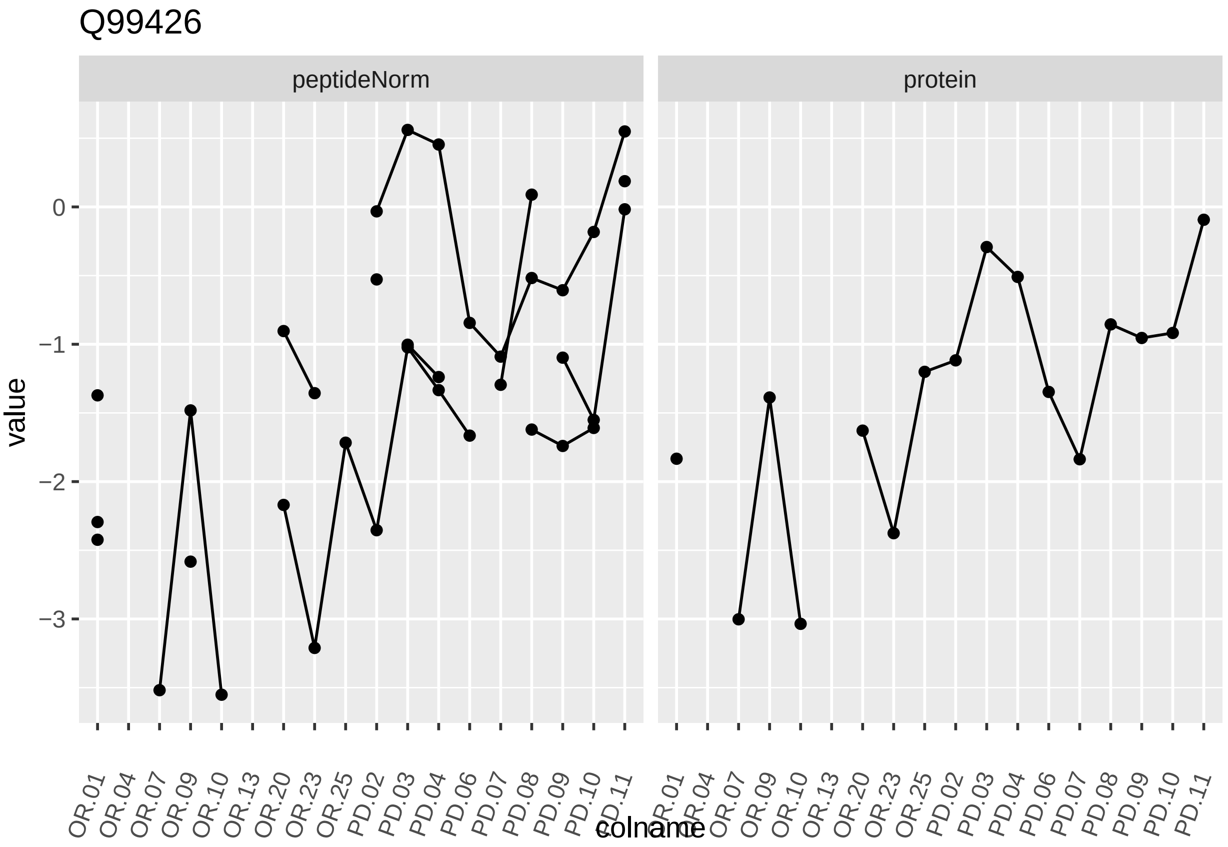
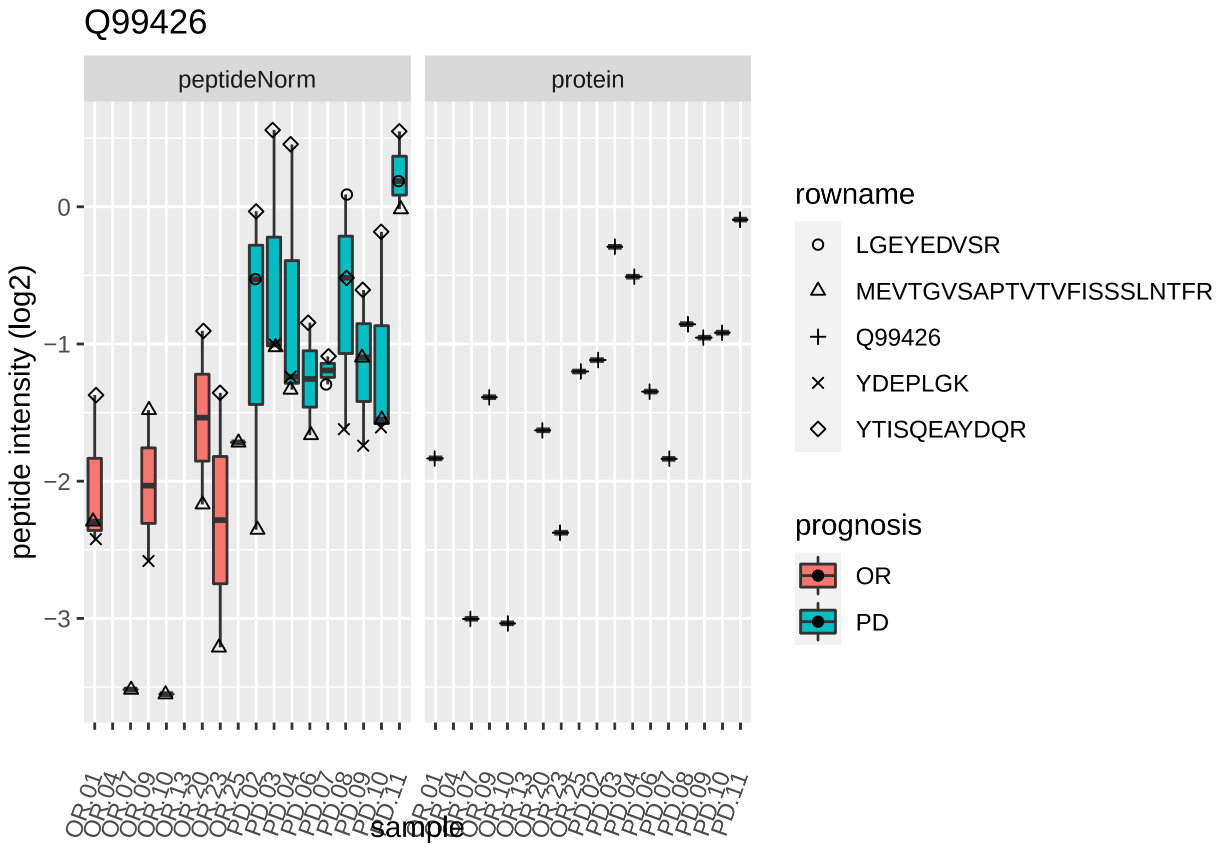
0.0
−2.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
MGAVTDDEVIR
Q6I9Y2
QEYDALAK
prognosis
OR
PD

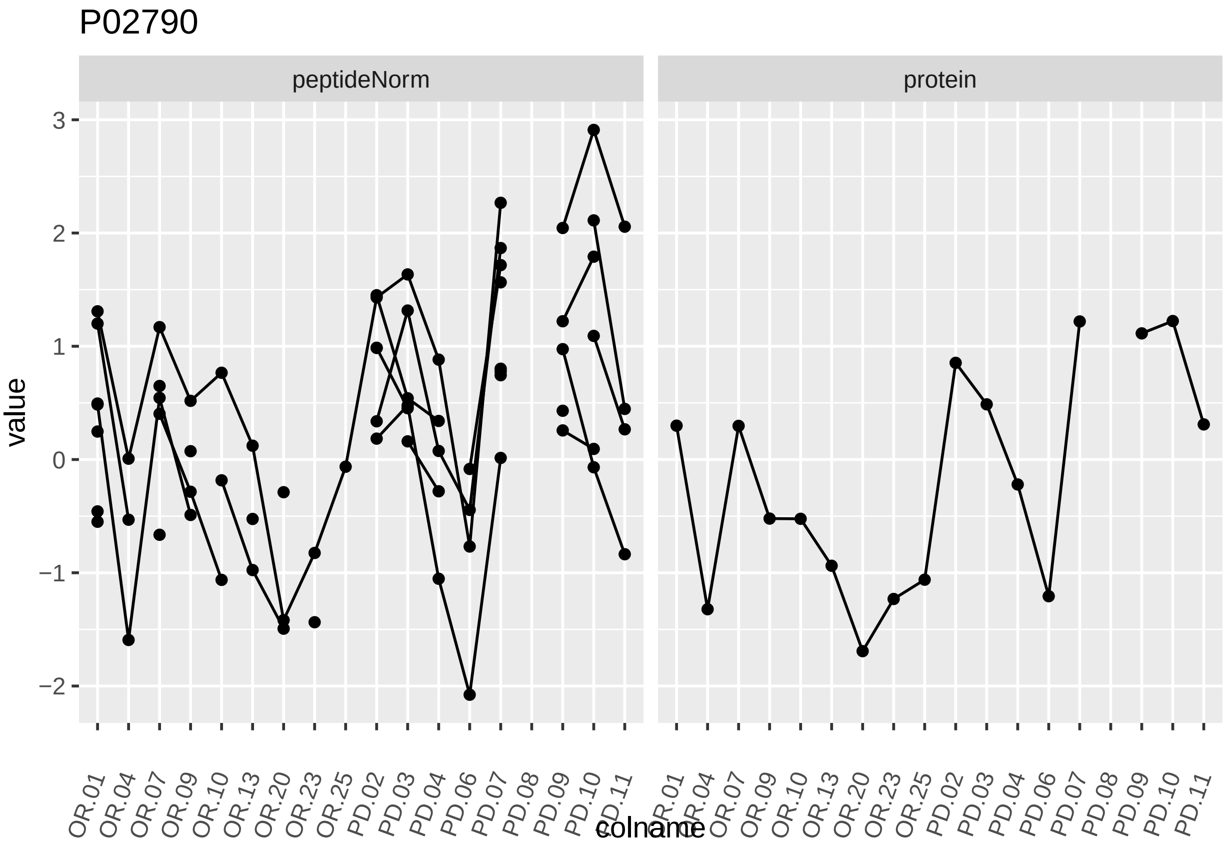
P67936

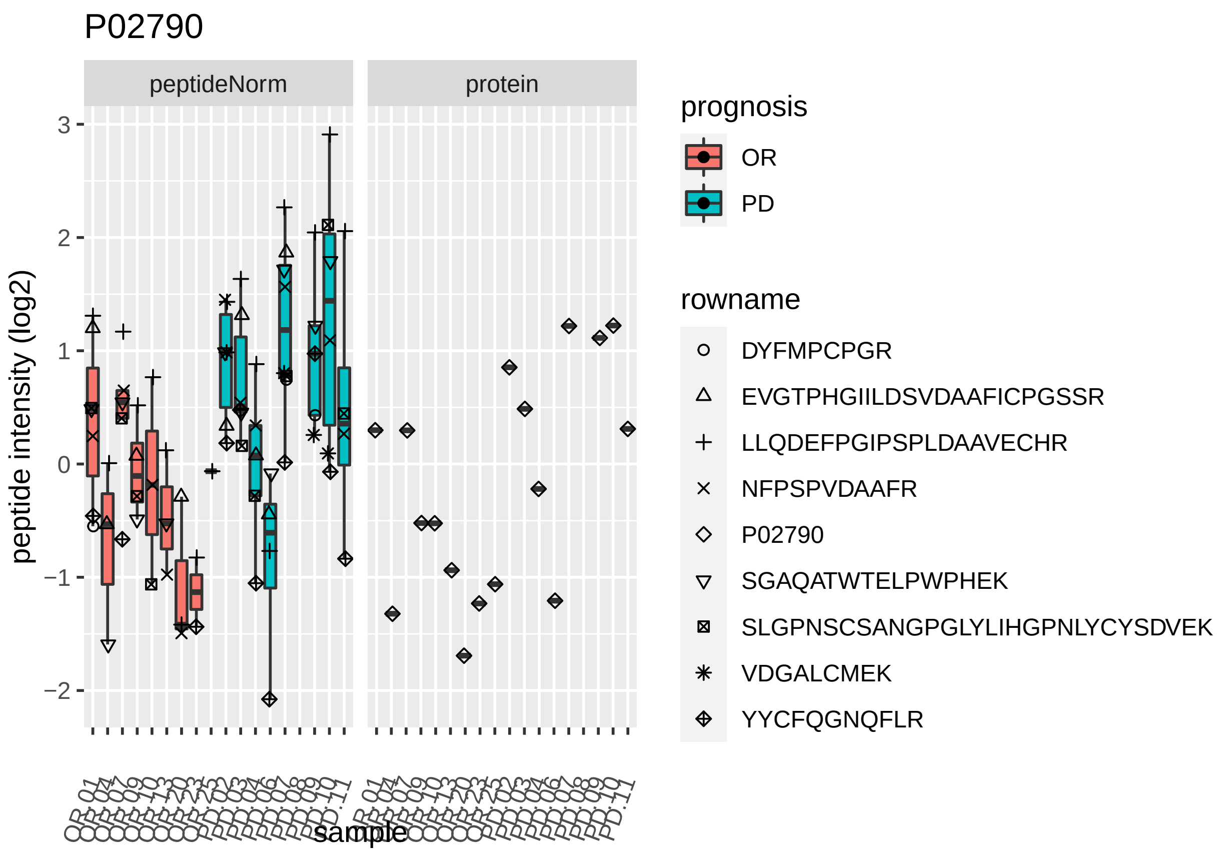

peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

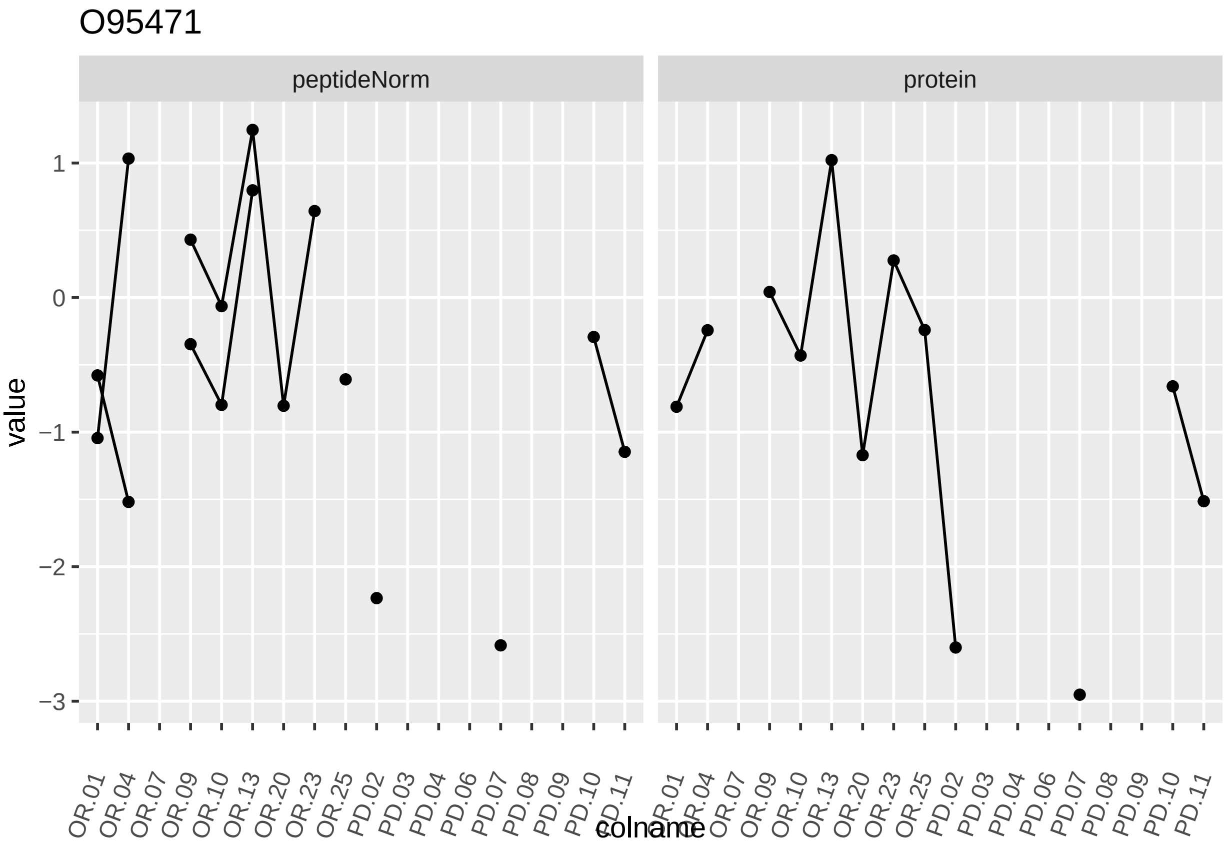

P67936
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AEGDVAALNR
AGLNSLEAVK
AGLNSLEAVKR
CGDLEEELKNVTNNLK
EENVGLHQTLDQTLNELNCI
EKAEGDVAALNR
IQALQQQADEAEDR
KIQALQQQADEAEDR
KLVILEGELERAEER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

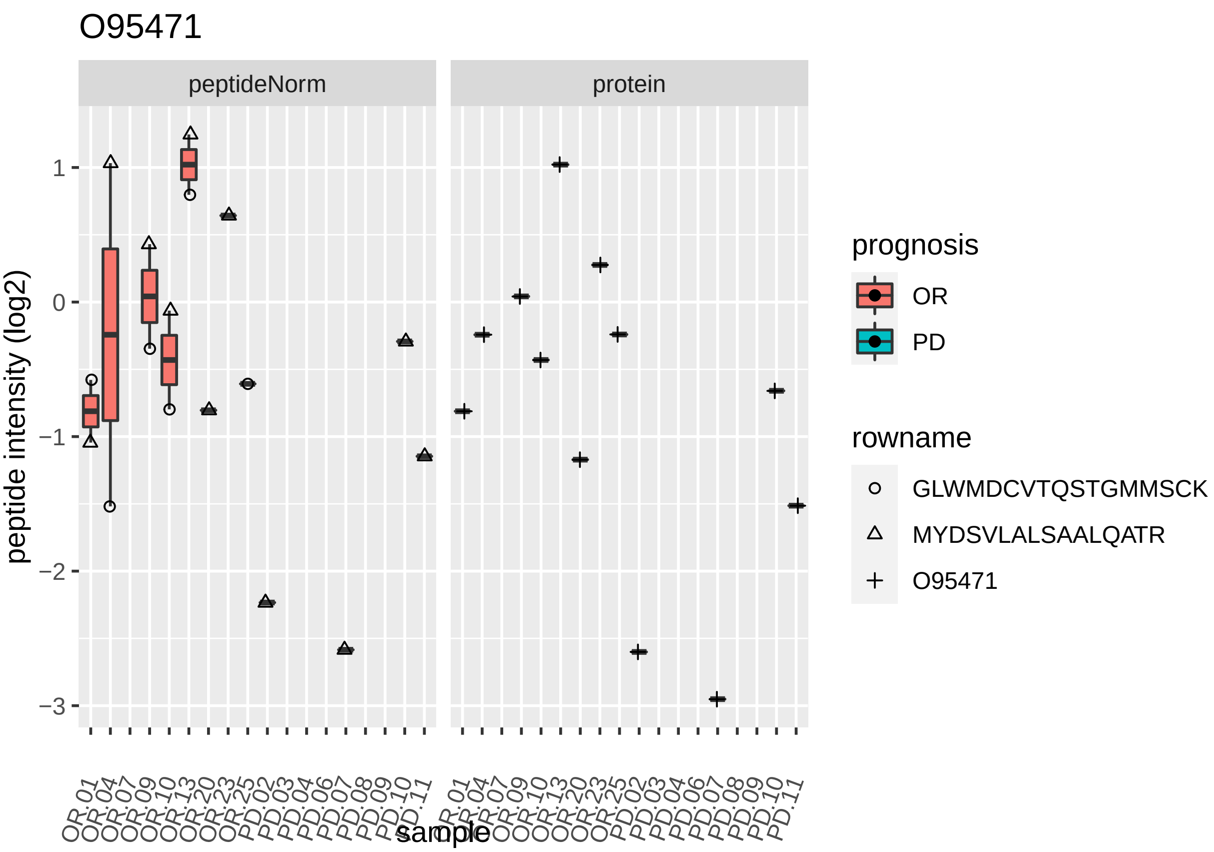

Q99426
peptideNorm
protein
value
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

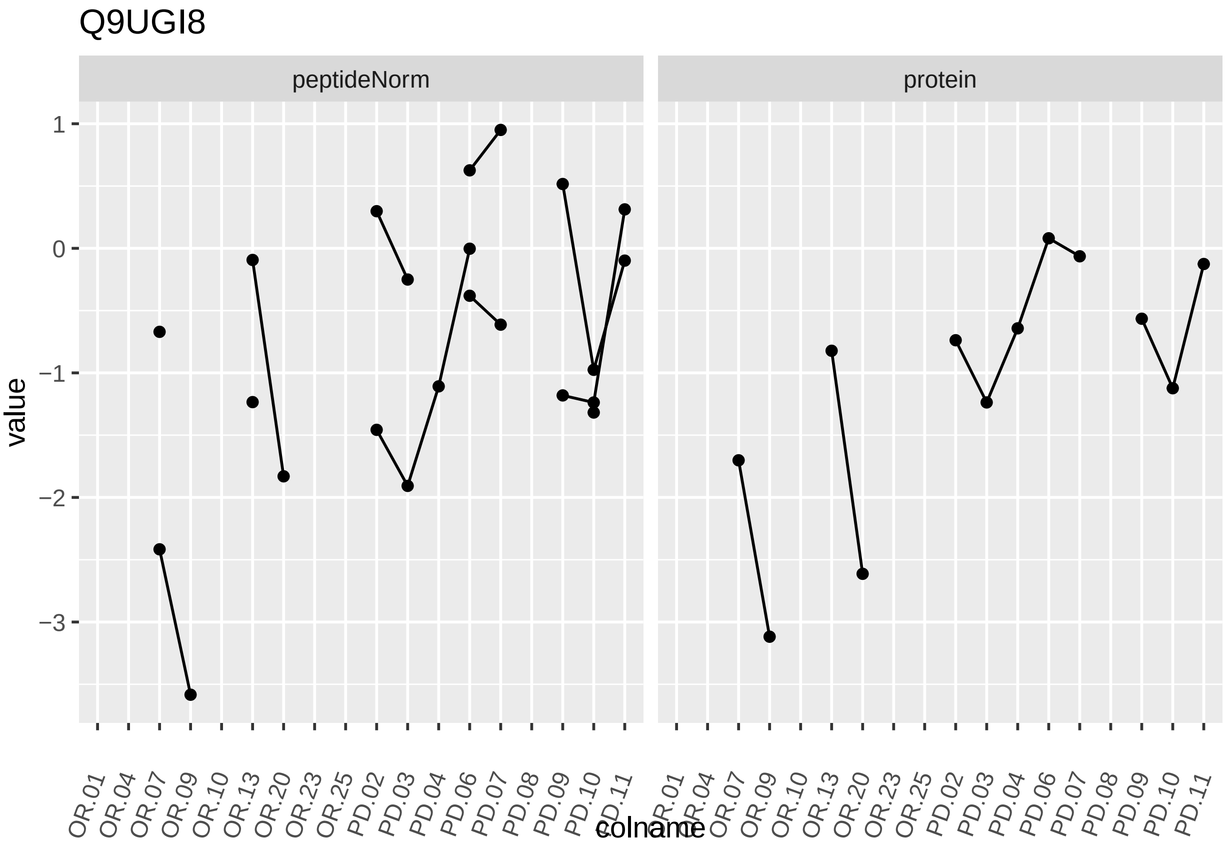
Q99426
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
LGEYEDVSR
MEVTGVSAPTVTVFISSSLNTFR
Q99426
YDEPLGK
YTISQEAYDQR
prognosis
OR
PD

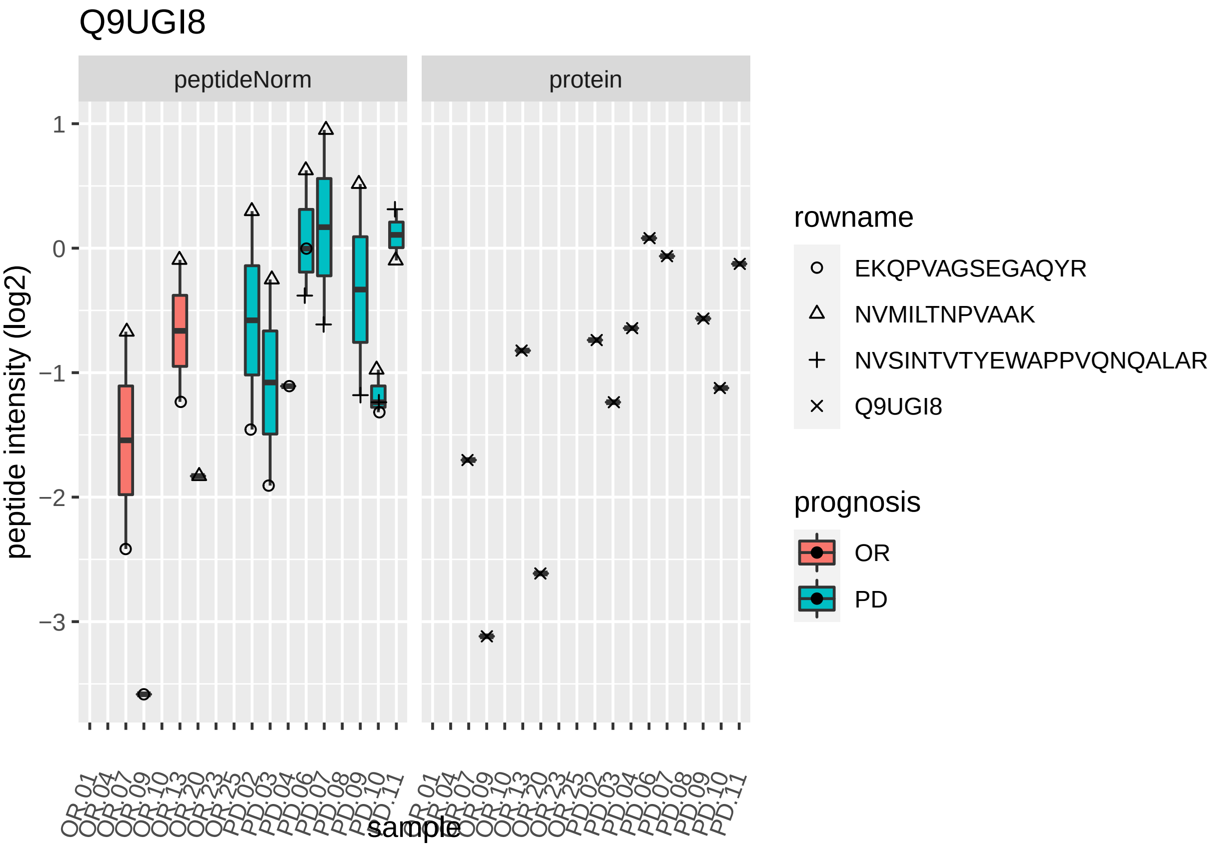

P02790
peptideNorm
protein
value
3
2
1
0
−1
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

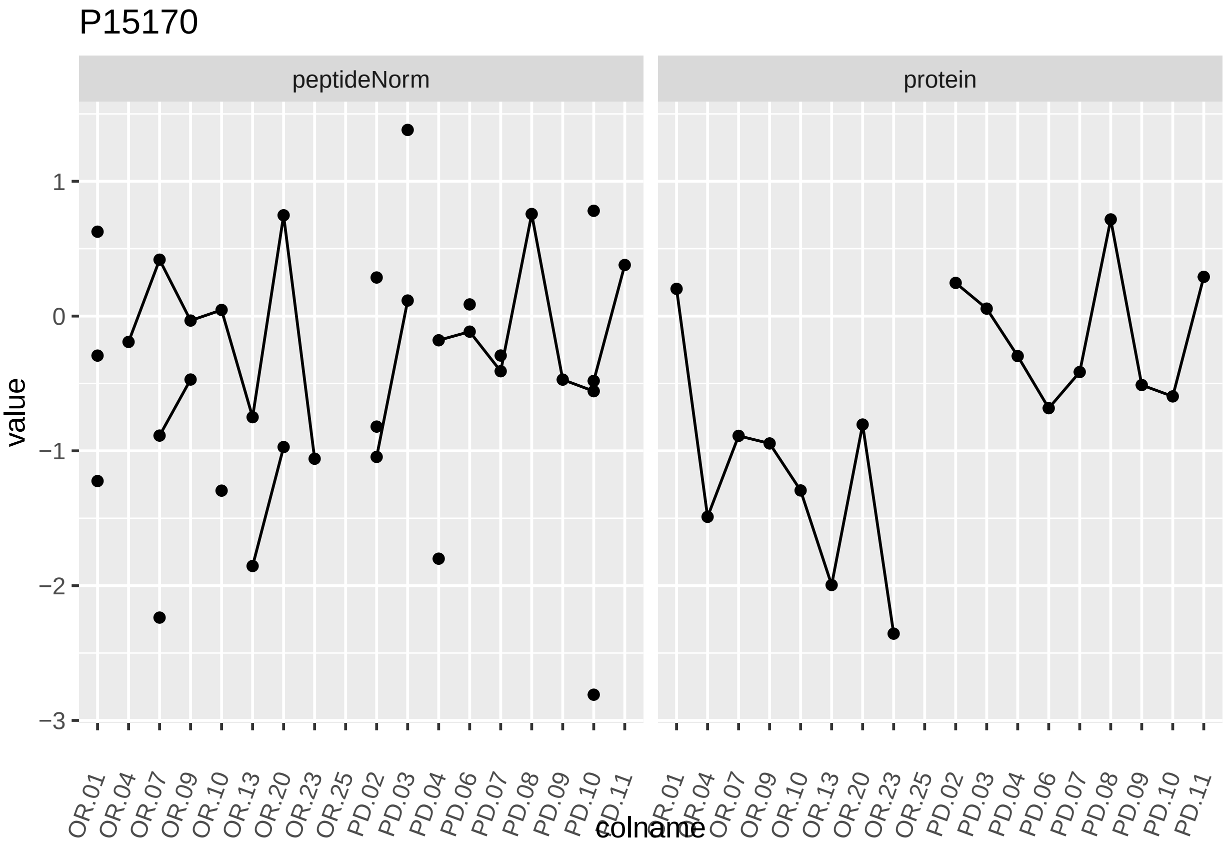

P02790
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
DYFMPCPGR
EVGTPHGIILDSVDAAFICPGSSR
LLQDEFPGIPSPLDAAVECHR
NFPSPVDAAFR
P02790
SGAQATWTELPWPHEK
SLGPNSCSANGPGLYLIHGPNLYCYSDVEK
VDGALCMEK
YYCFQGNQFLR

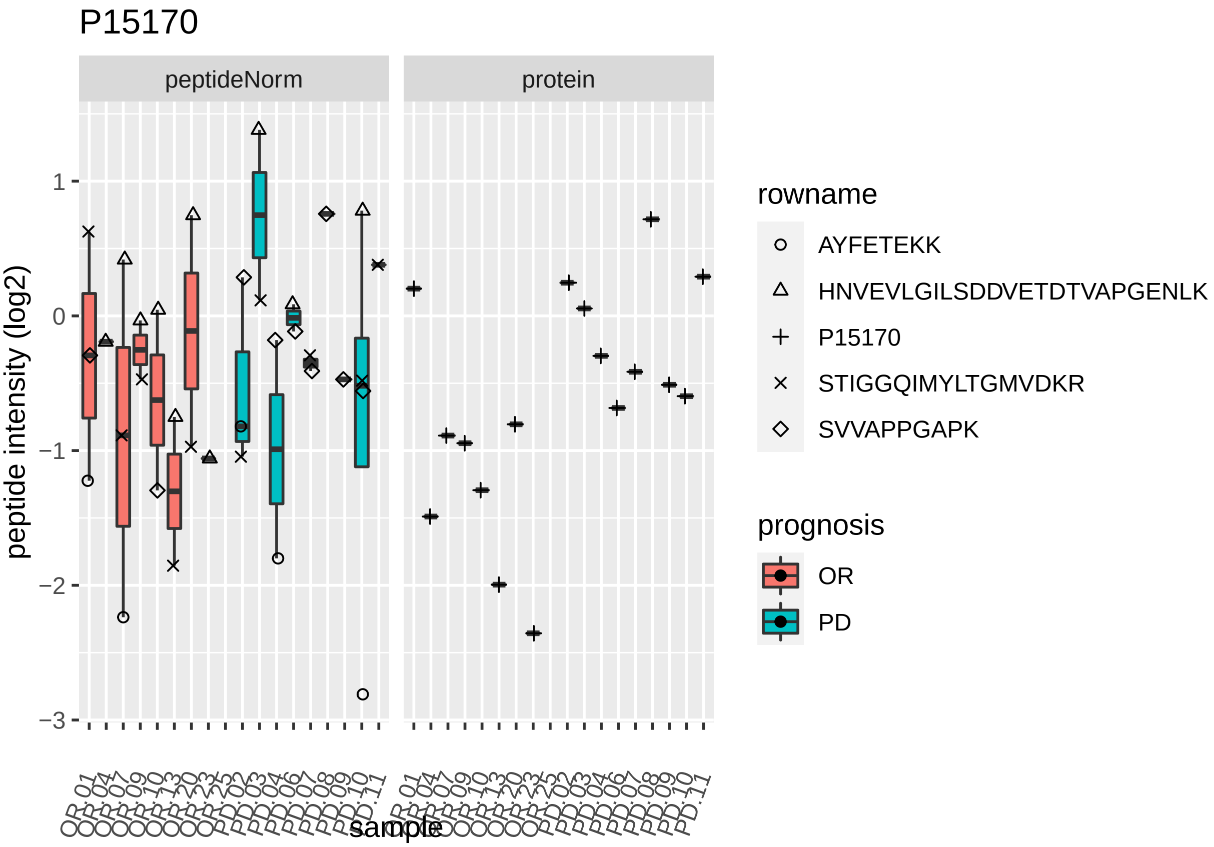

O95471
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

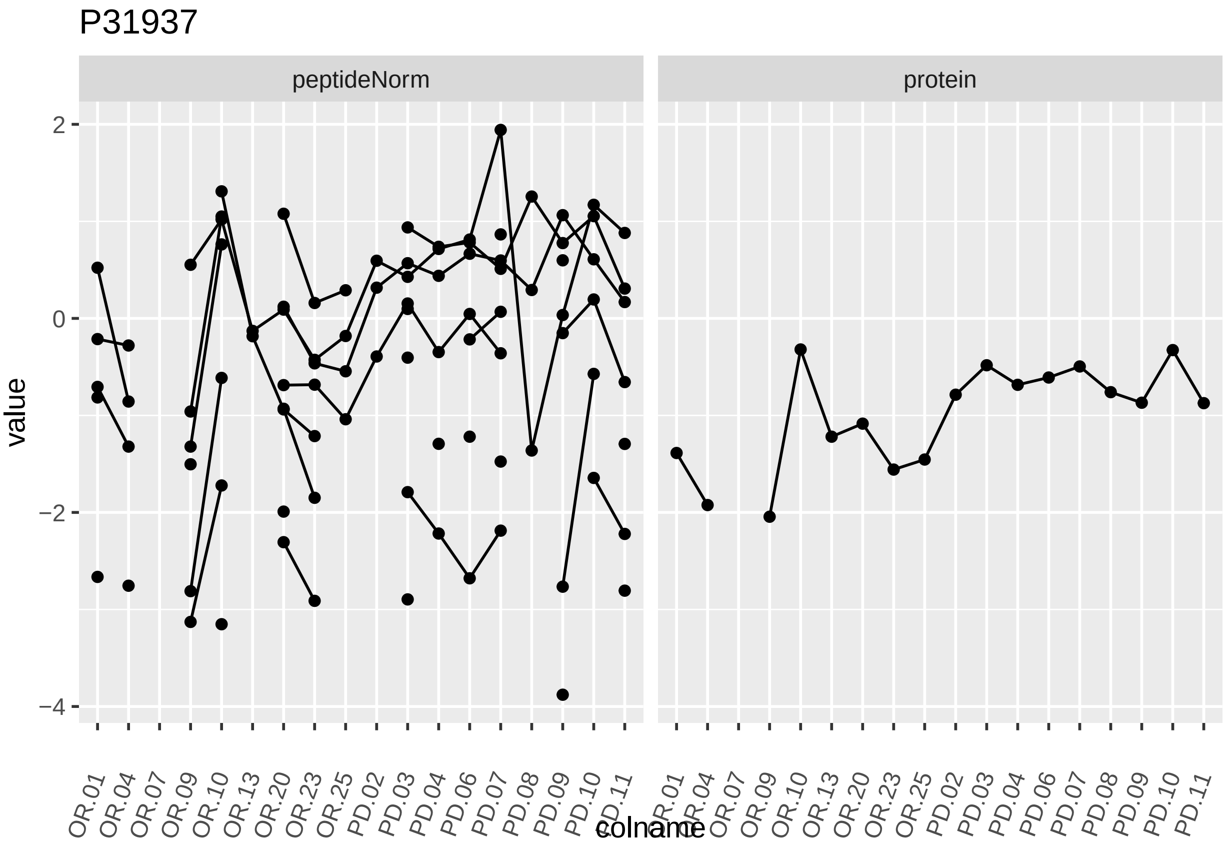

O95471
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
GLWMDCVTQSTGMMSCK
MYDSVLALSAALQATR
O95471

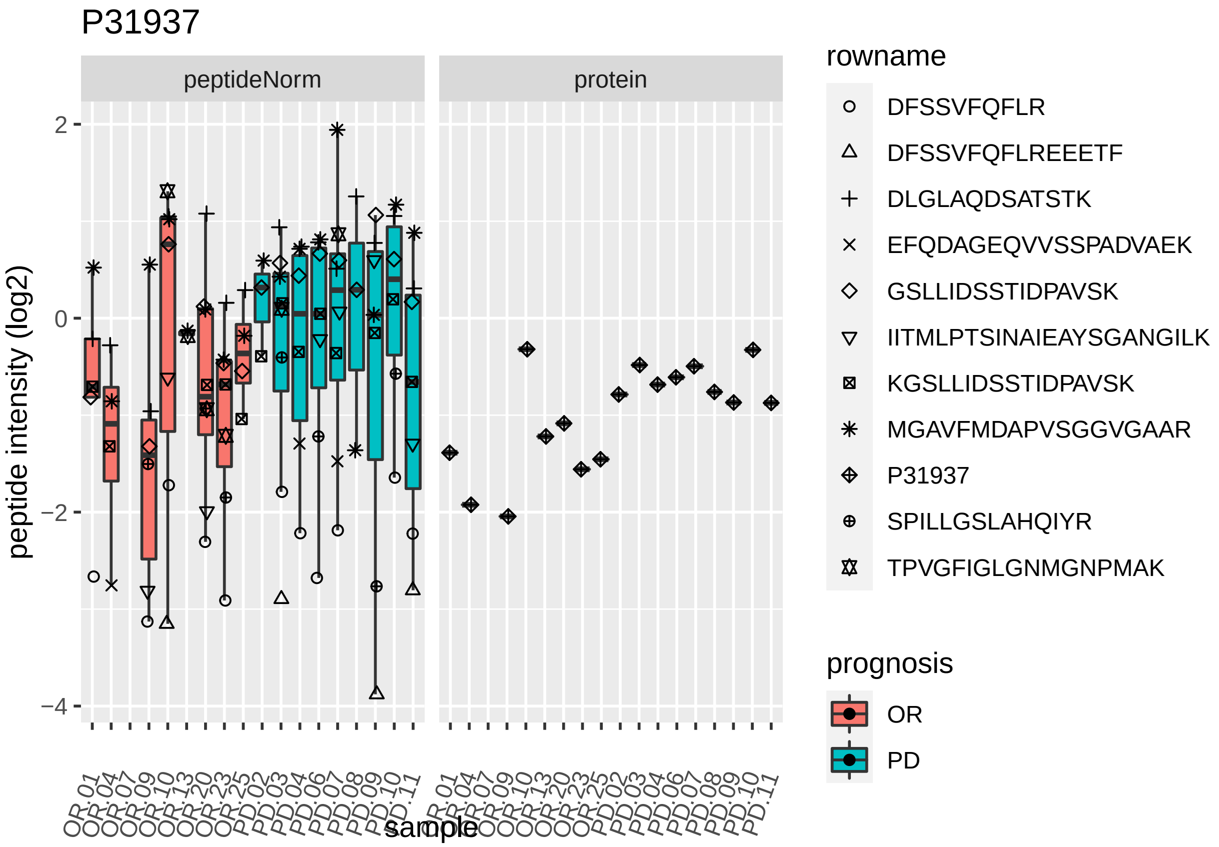

Q9UGI8
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

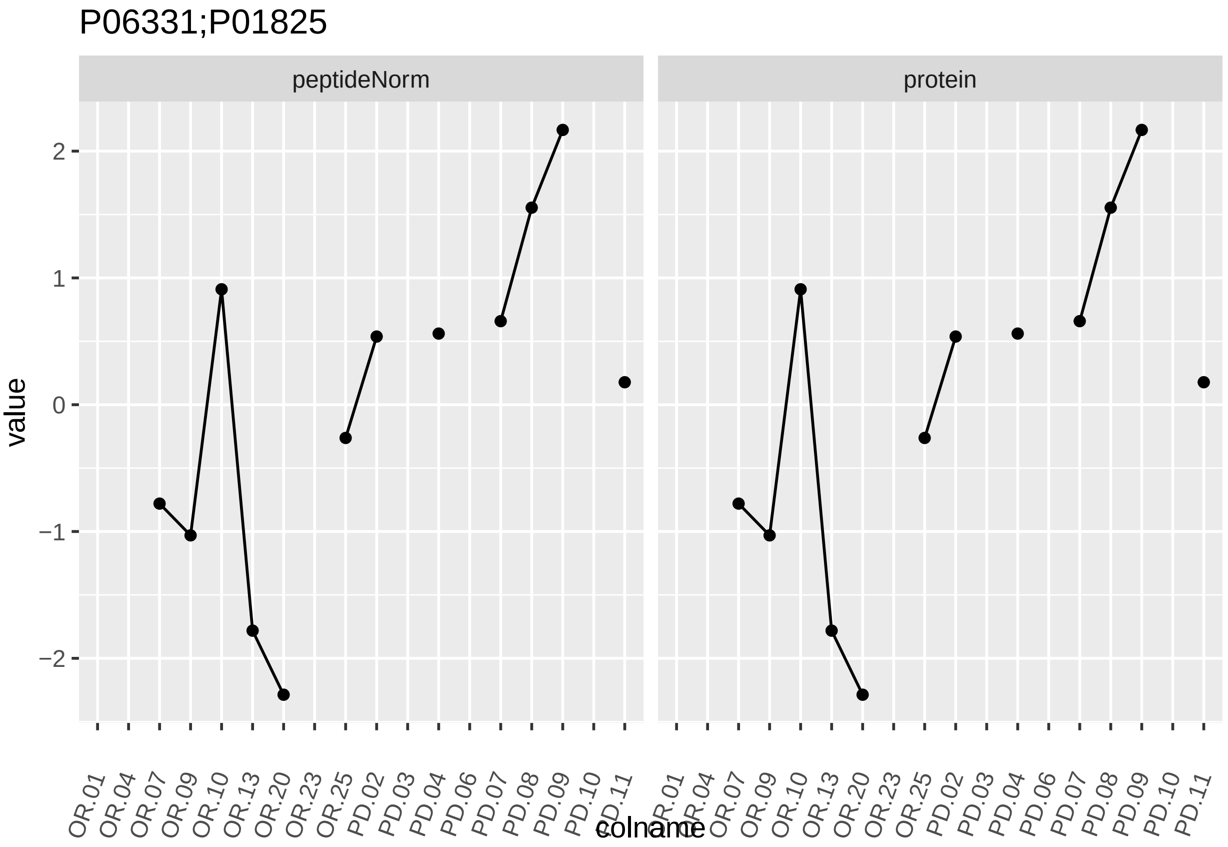

Q9UGI8
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EKQPVAGSEGAQYR
NVMILTNPVAAK
NVSINTVTYEWAPPVQNQALAR
Q9UGI8
prognosis
OR
PD

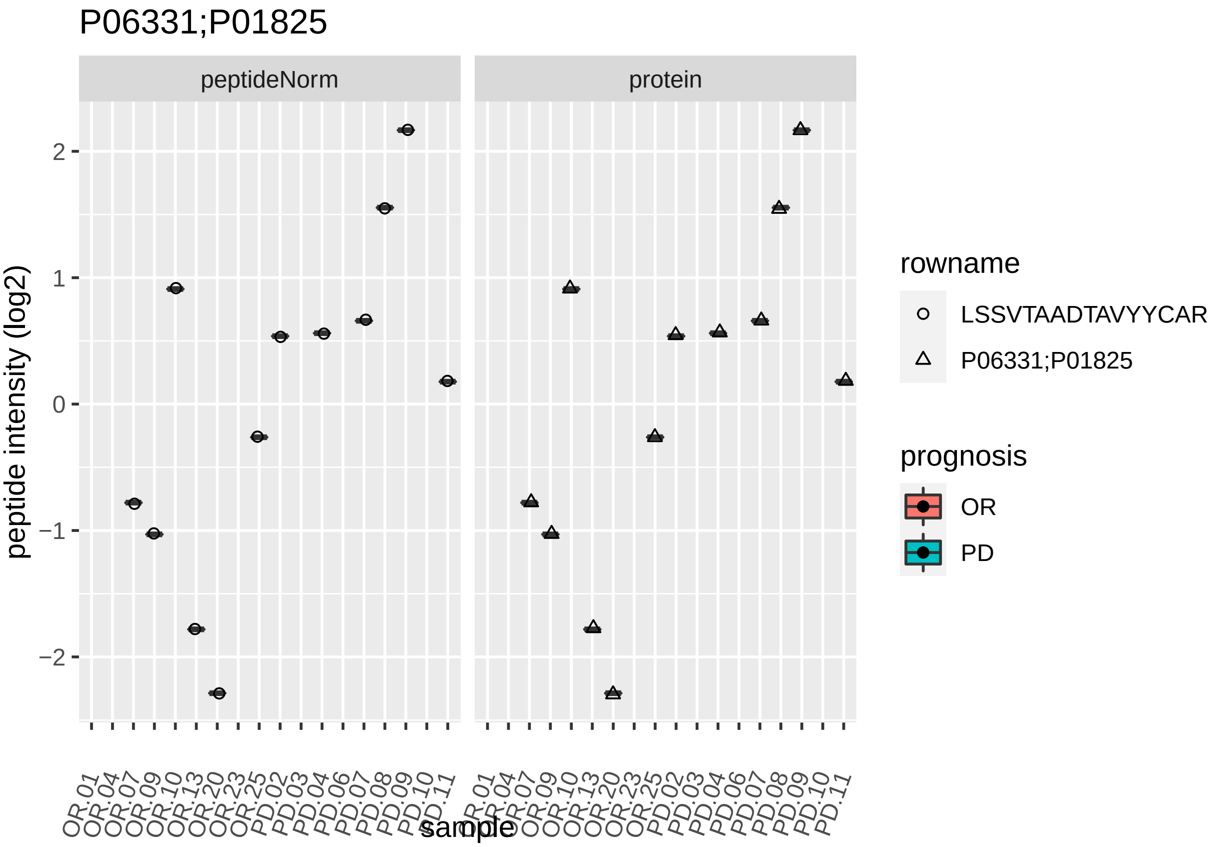

P15170
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

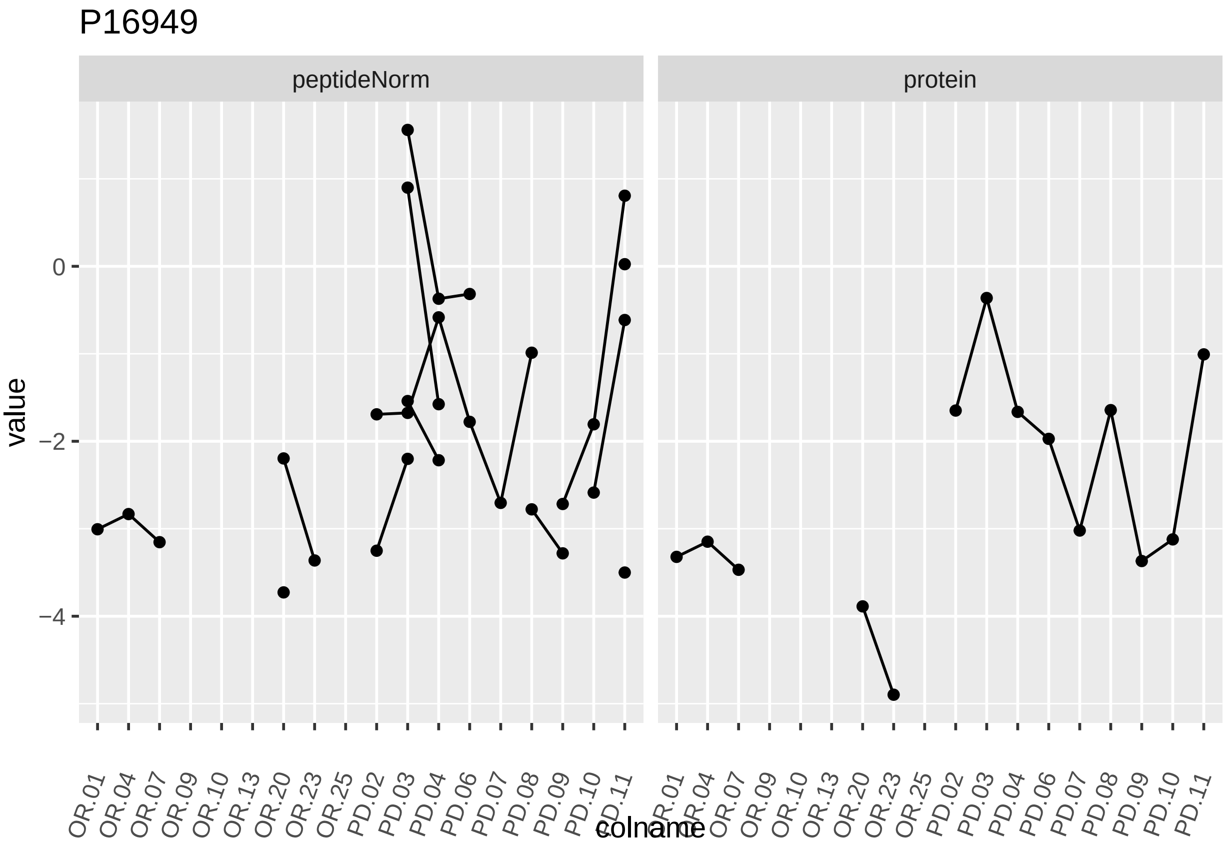

P15170
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ AYFETEKK
△ HNVEVLGILSDDVETDTVAPGENLK
+ P15170
× STIGGQIMYLTGMVDKR
◇ SVVAPPGAPK
prognosis
OR
PD

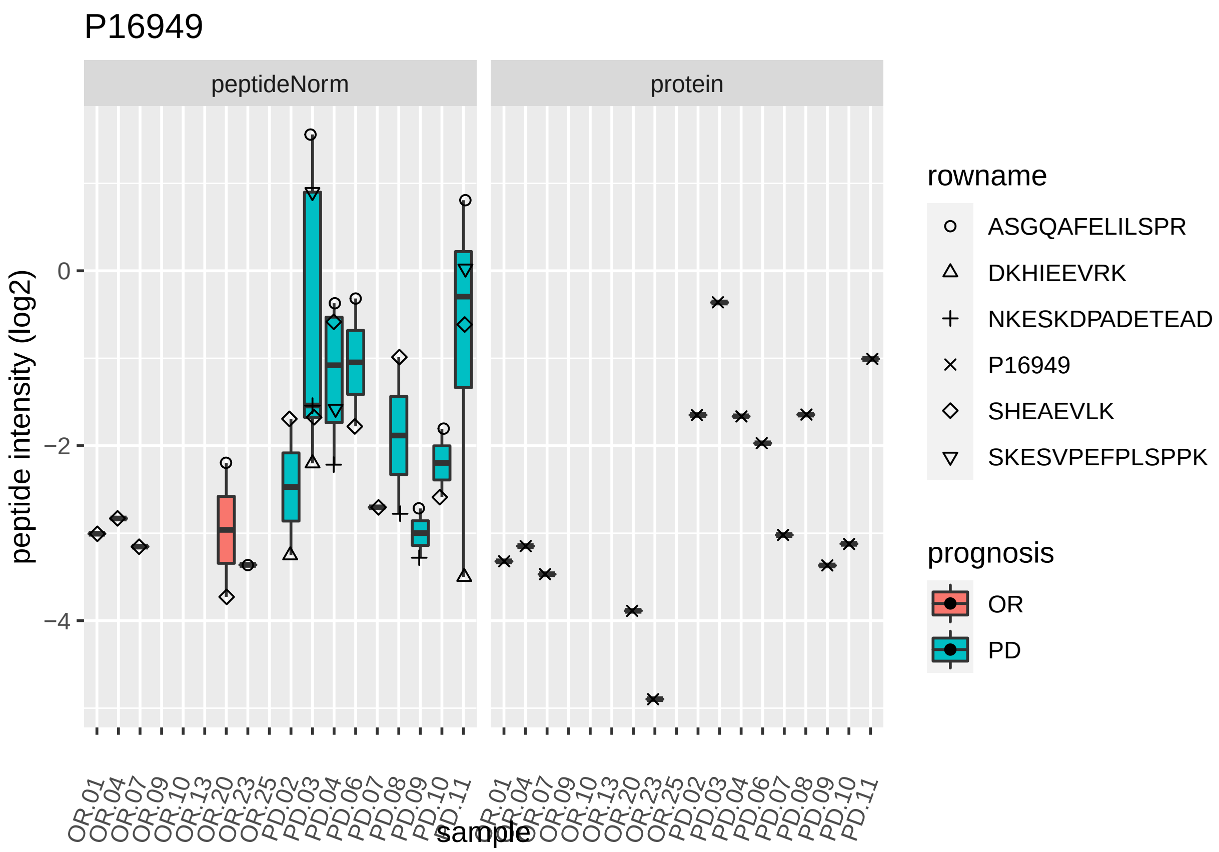

P31937
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

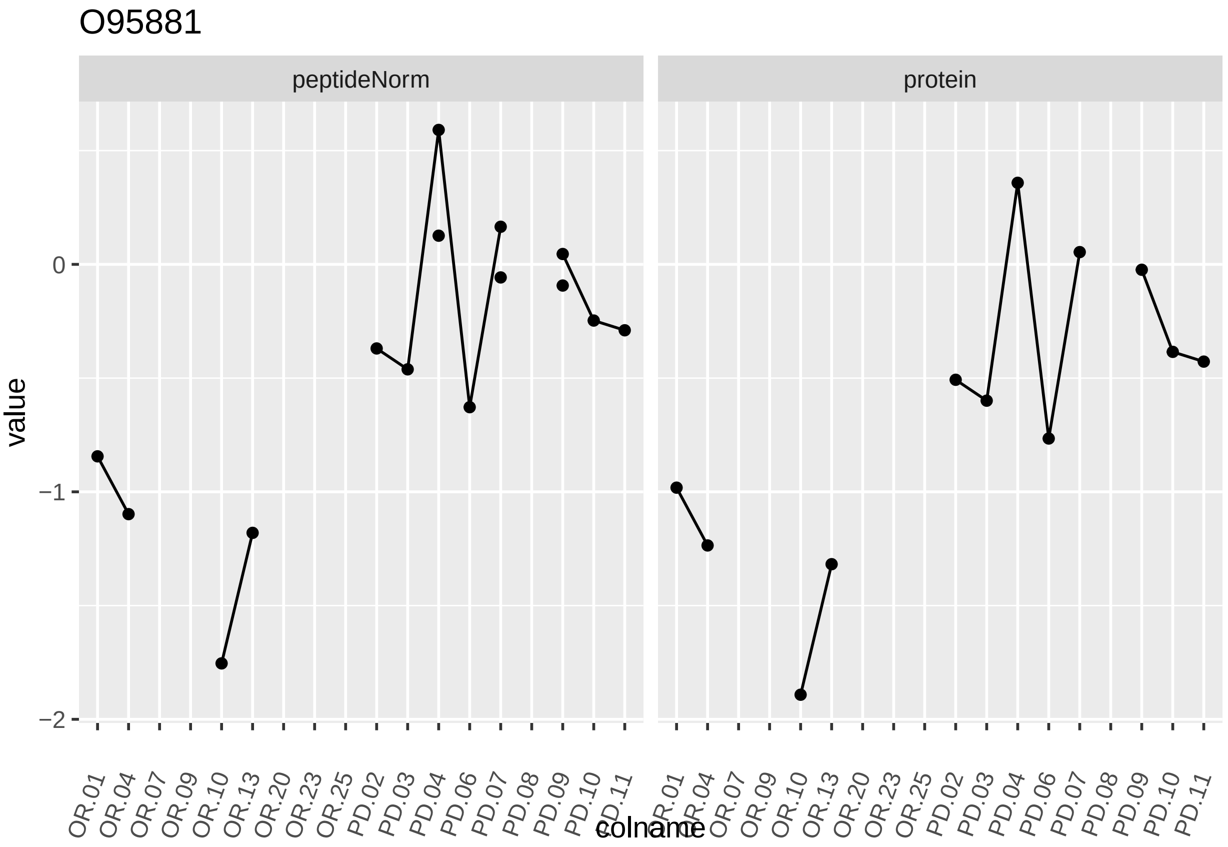

P31937
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
DFSSVFQFLR
DFSSVFQFLREEETF
DLGLAQDSATSTK
EFQDAGEQVVSSPADVAEK
GSLLIDSSTIDPAVSK
IITMLPTSINAIEAYSGANGILK
KGSLLIDSSTIDPAVSK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

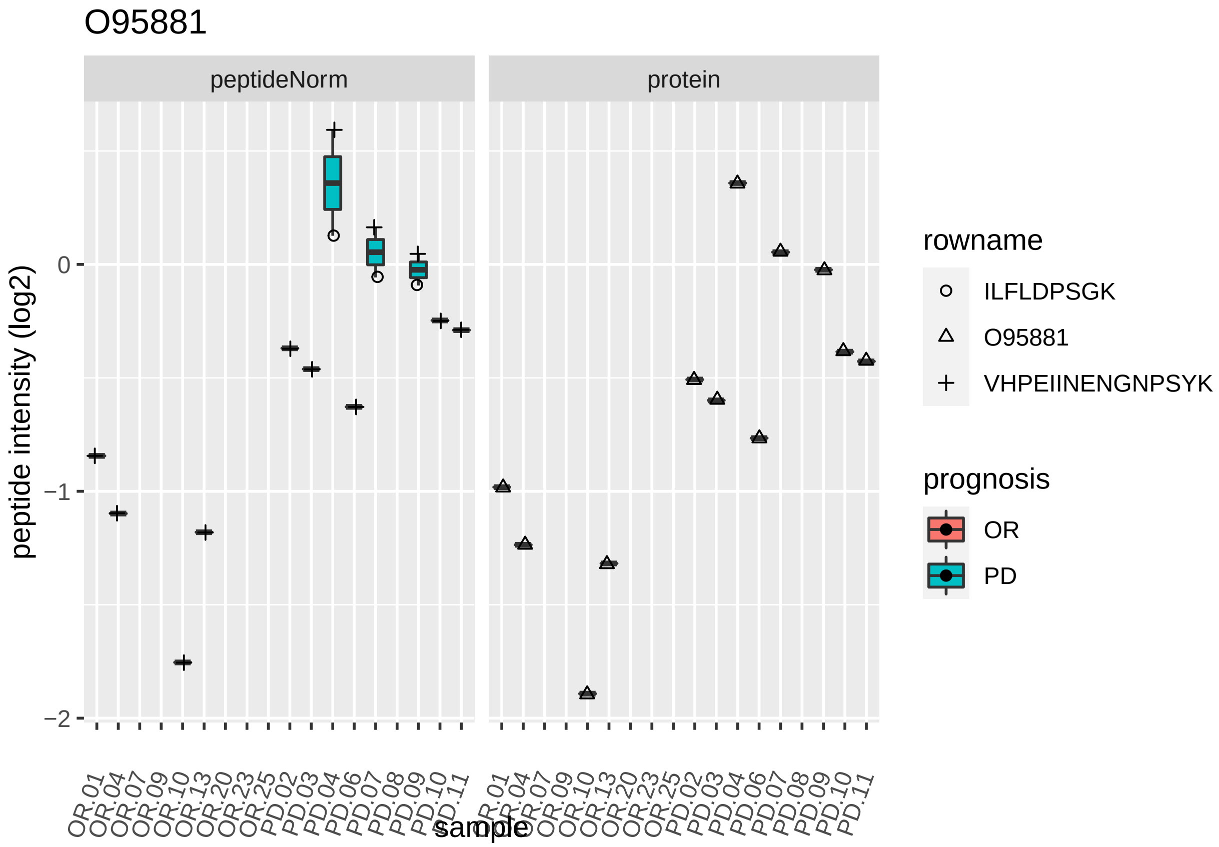

P06331;P01825
peptideNorm
protein
value
2
1
0
−1
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

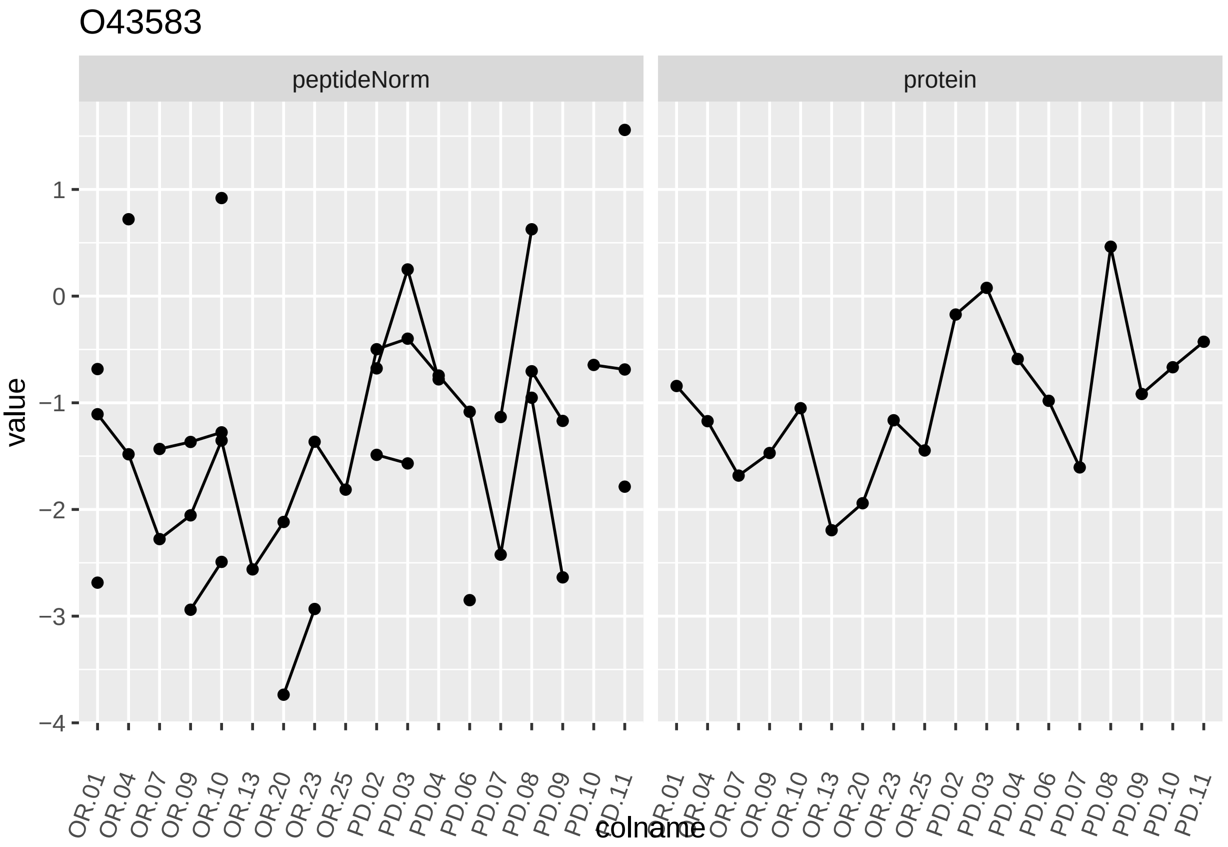

P06331;P01825
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ LSSVTAADTAVYYCAR
△ P06331;P01825
prognosis
OR
PD

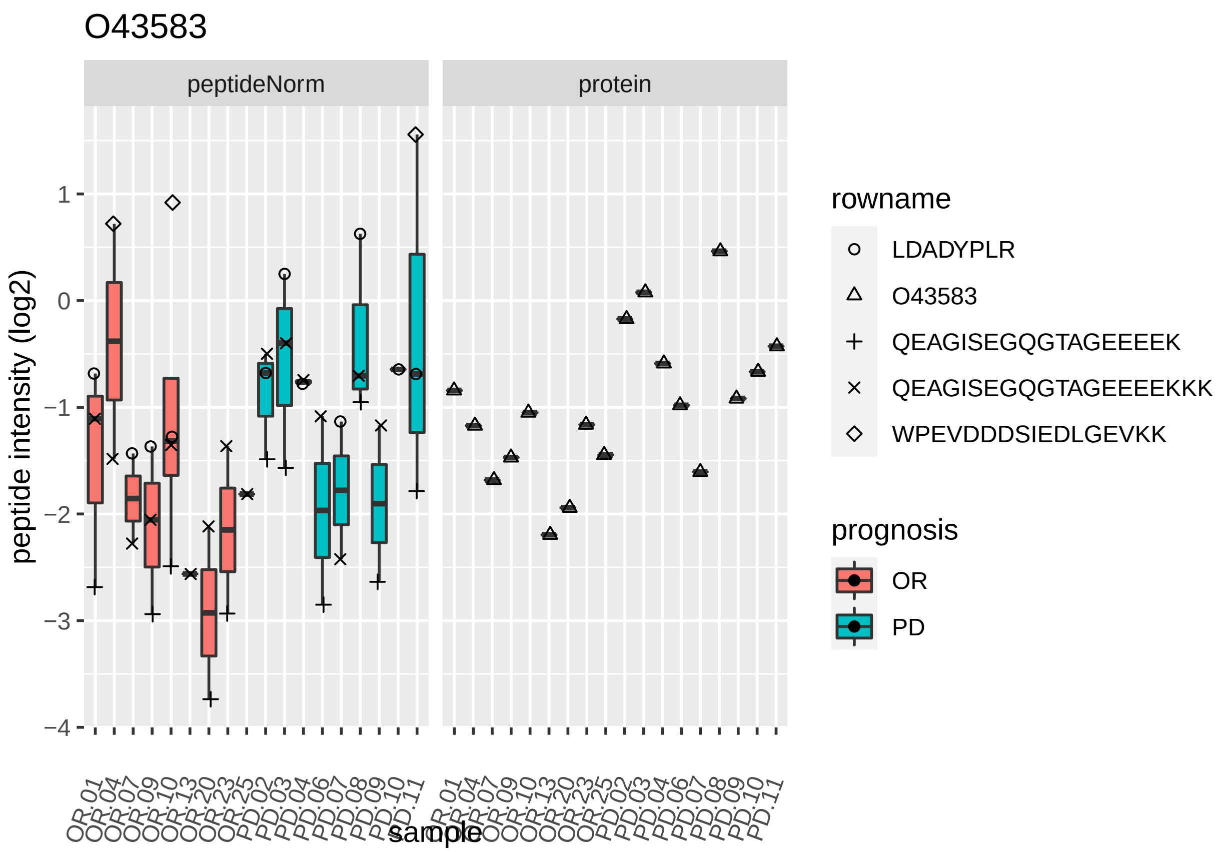

P16949
peptideNorm
protein
value
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

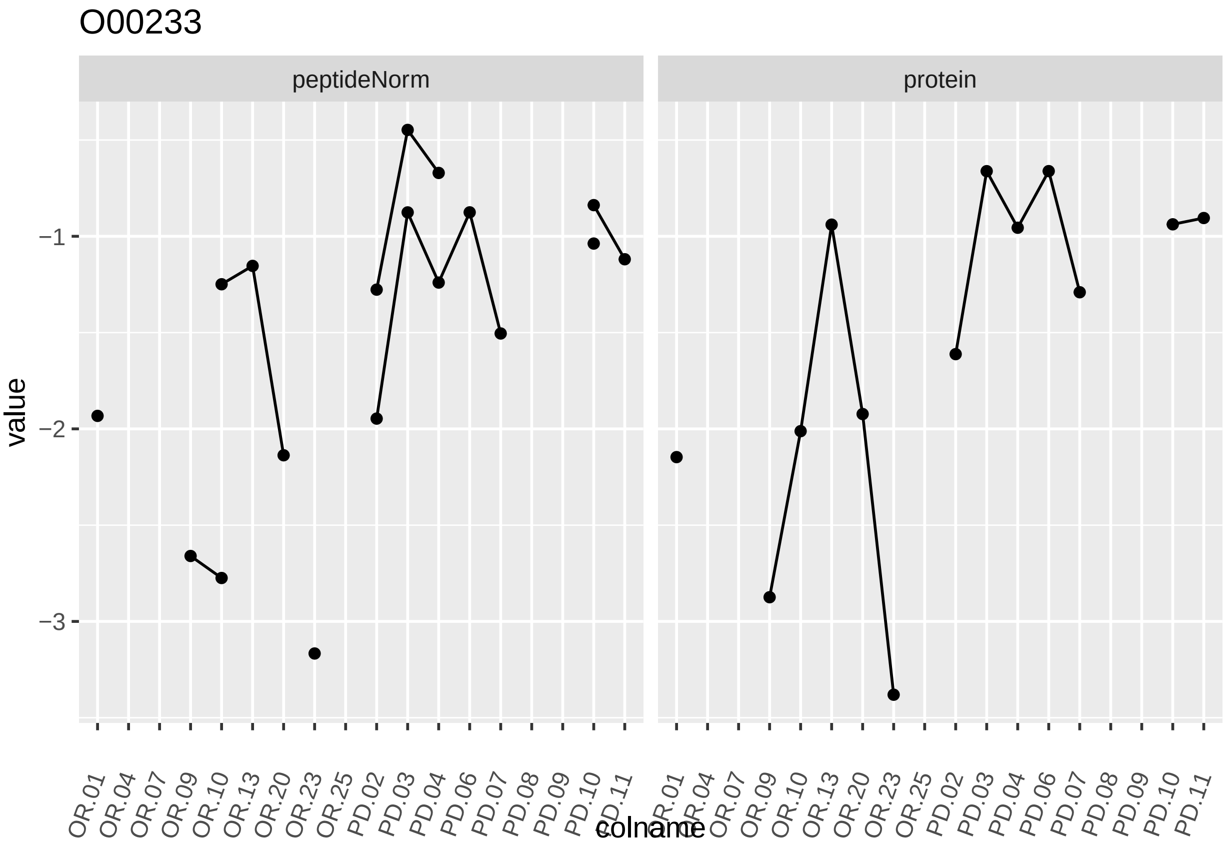

P16949
peptideNorm
protein
peptide intensity (log2)
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
○ ASGQAFELILSPR
△ DKHIEEVRK
+ NKESKDPADETEAD
× P16949
◇ SHEAEVLK
▽ SKESVPEFPLSPPK
prognosis
🟥 OR
🟦 PD

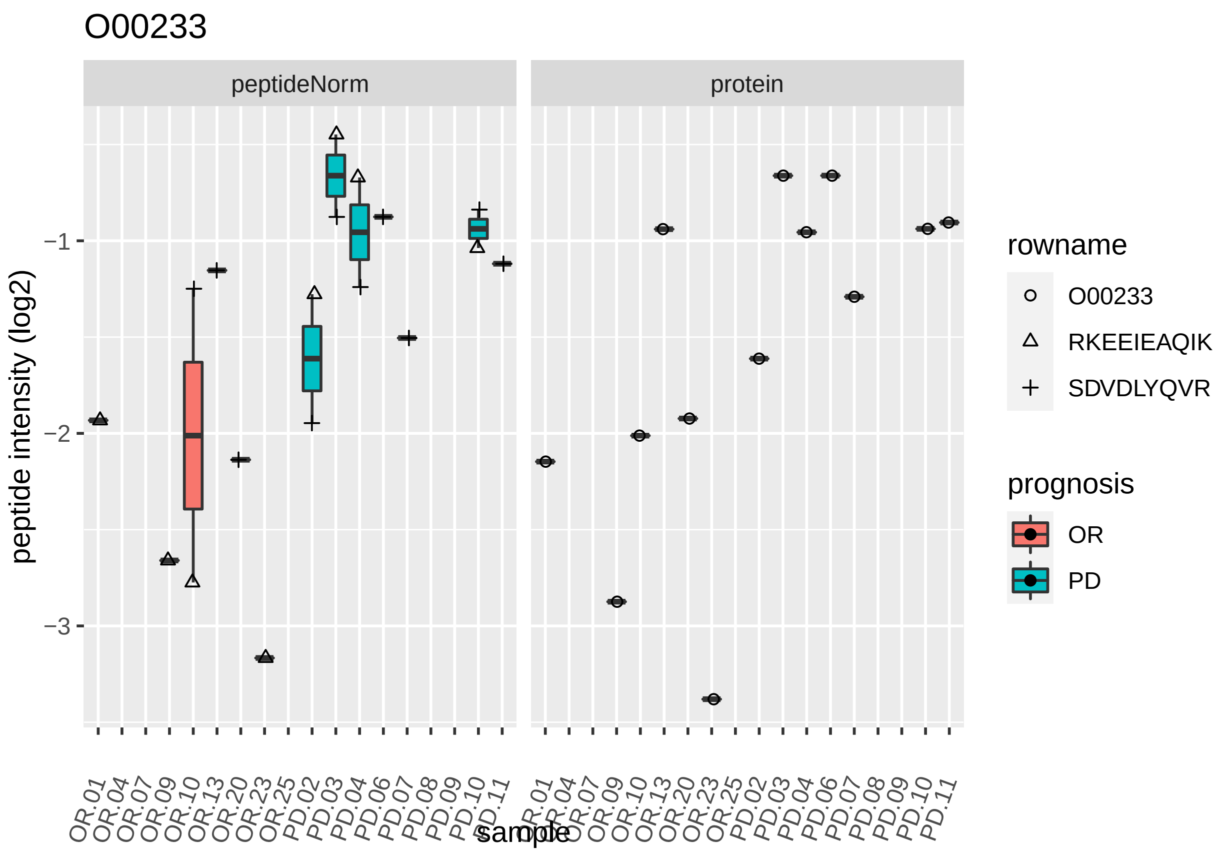

O95881
peptideNorm
protein
value
0
−1
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

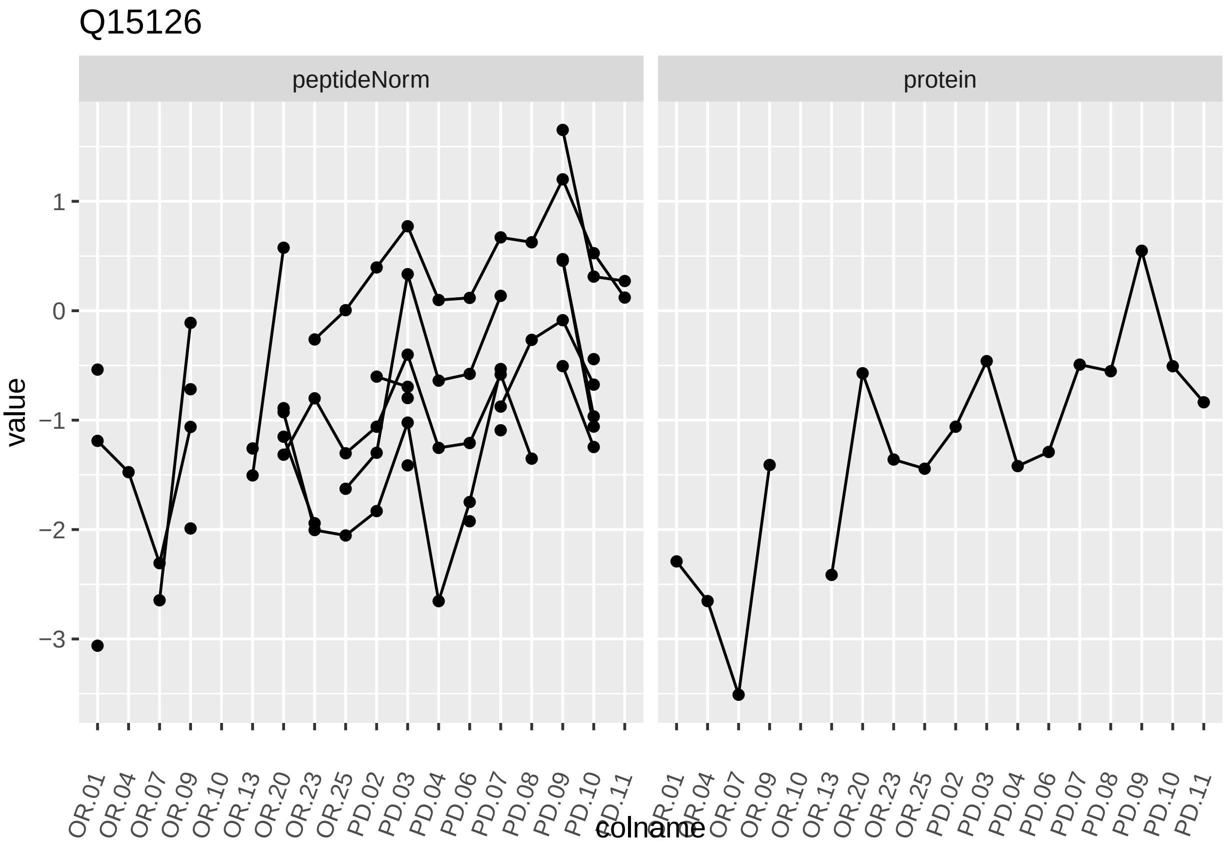

O95881
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ ILFLDPSGK
△ O95881
+ VHPEIINENGNPSYK
prognosis
OR
PD

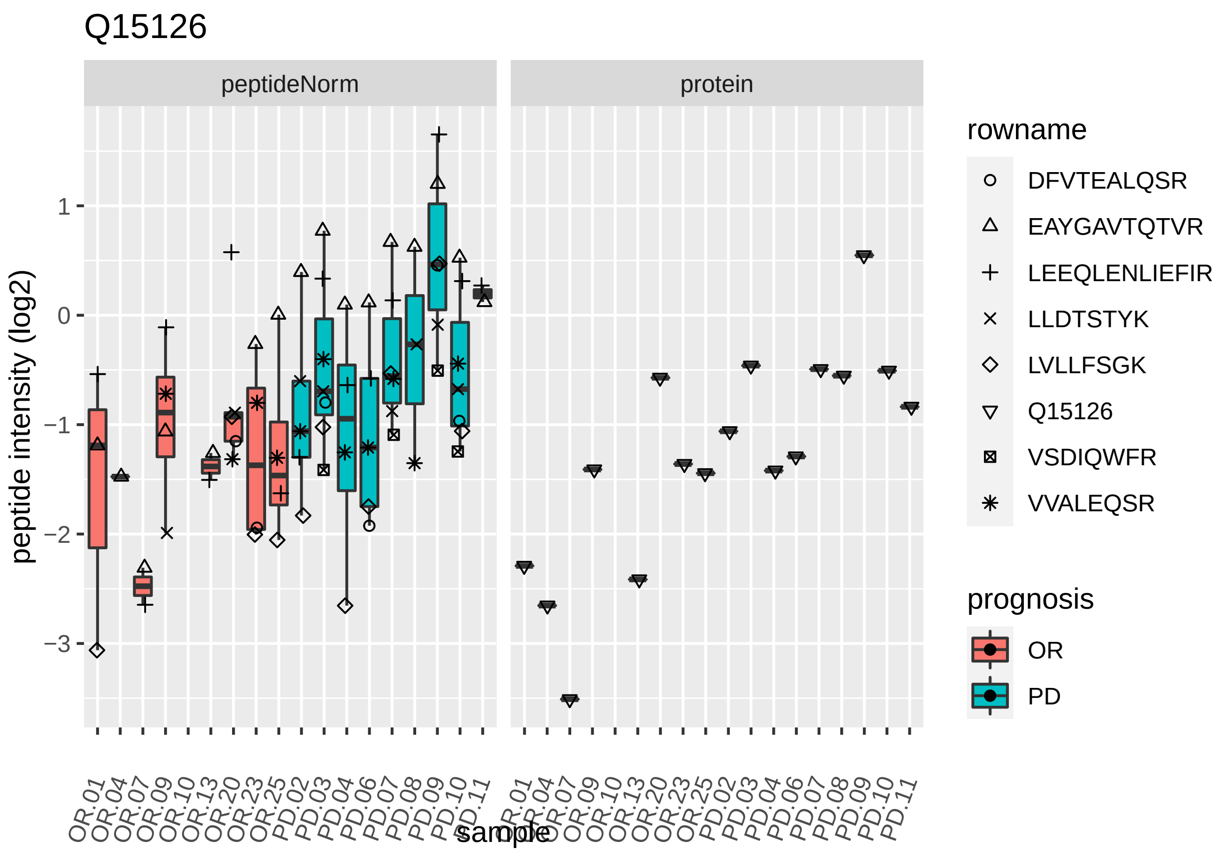

O43583
peptideNorm
protein
value
1
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

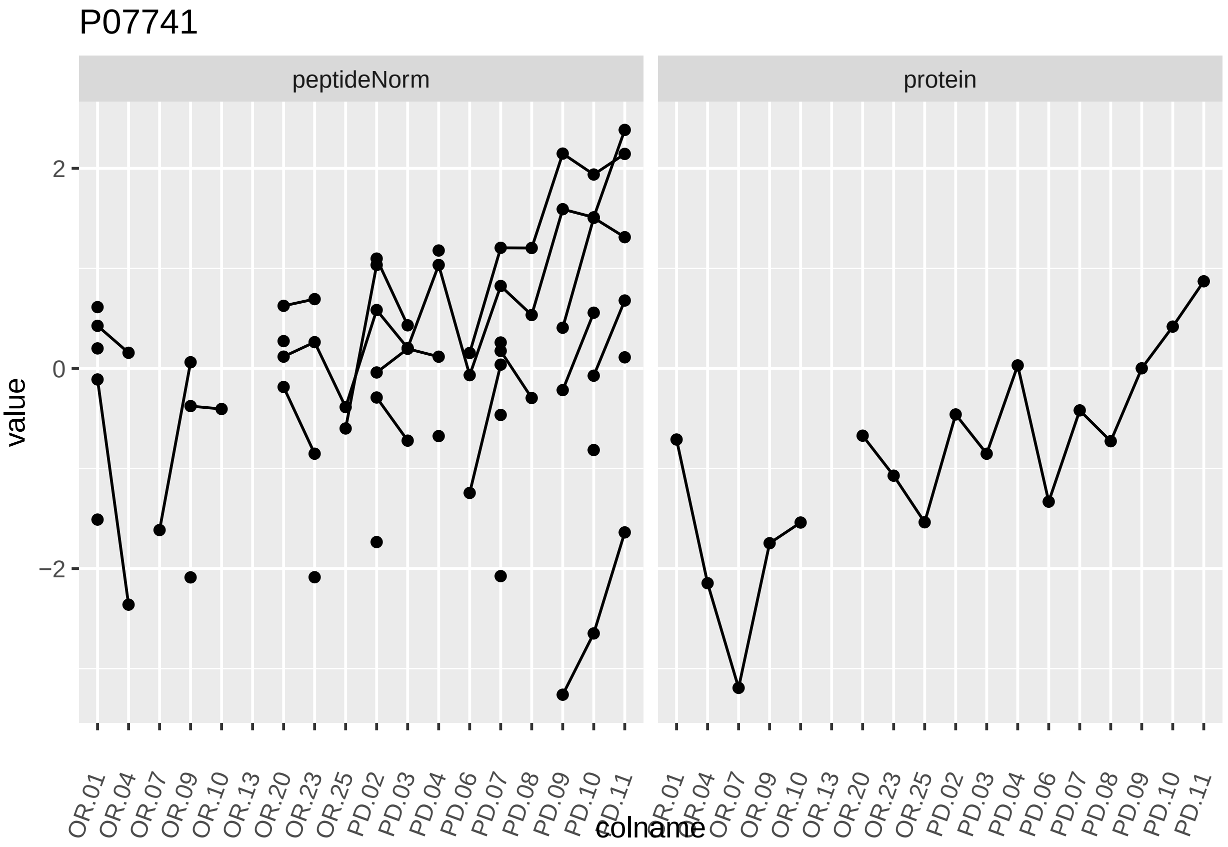

O43583
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LDADYPLR
O43583
QEAGISEGQGTAGEEEEK
QEAGISEGQGTAGEEEEKKK
WPEVDDDSIEDLGEVKK
prognosis
OR
PD


O00233
peptideNorm
protein
value
−1
−2
−3
colname
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

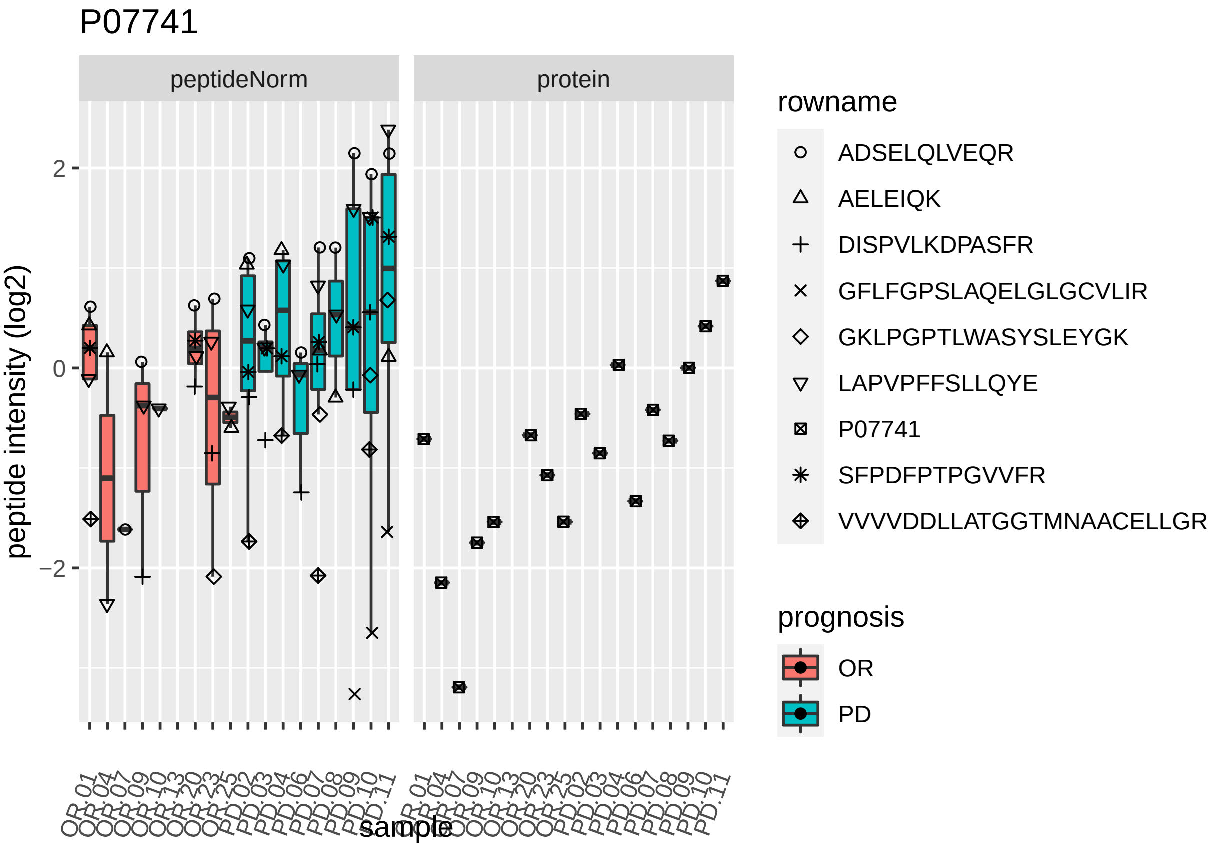

O00233
peptideNorm
protein
peptide intensity (log2)
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
○ O00233
△ RKEEIEAQIK
+ SDVDLYQVR
prognosis
OR
PD

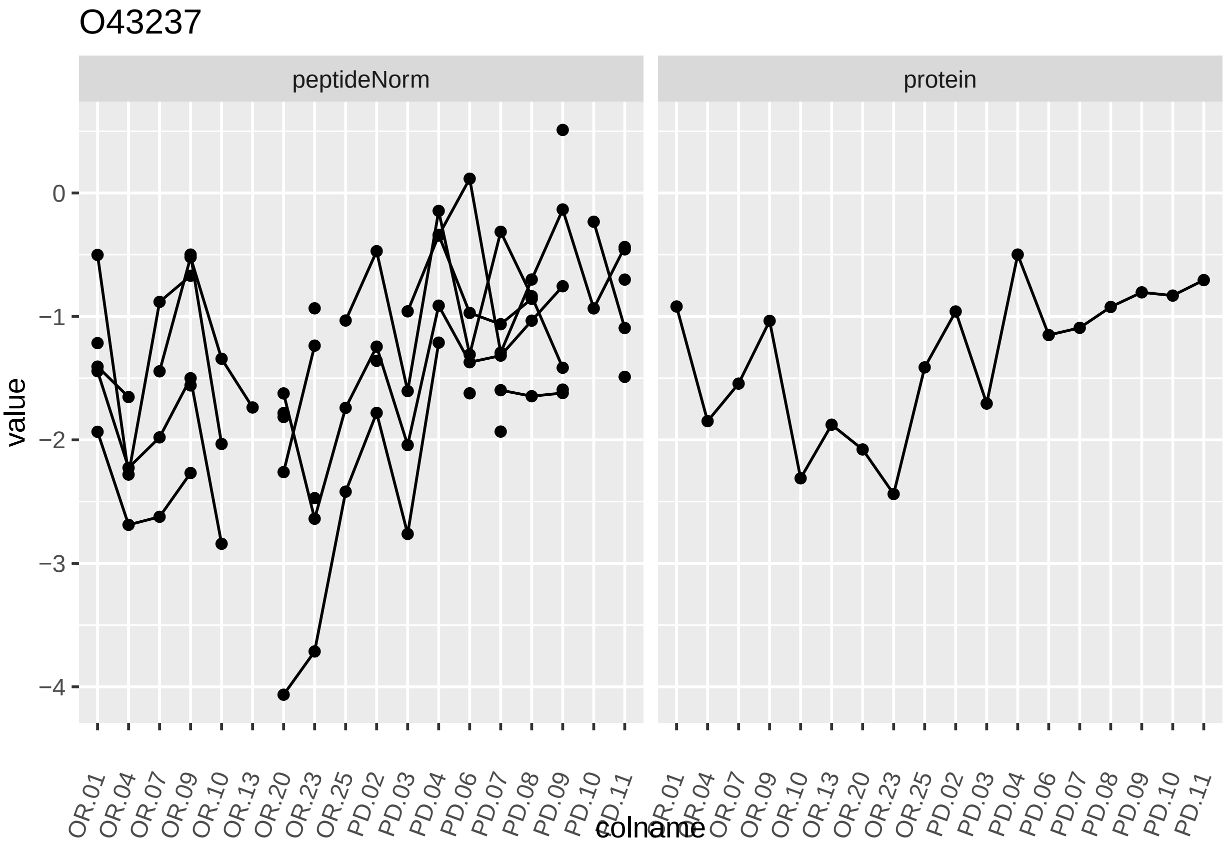

Q15126
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

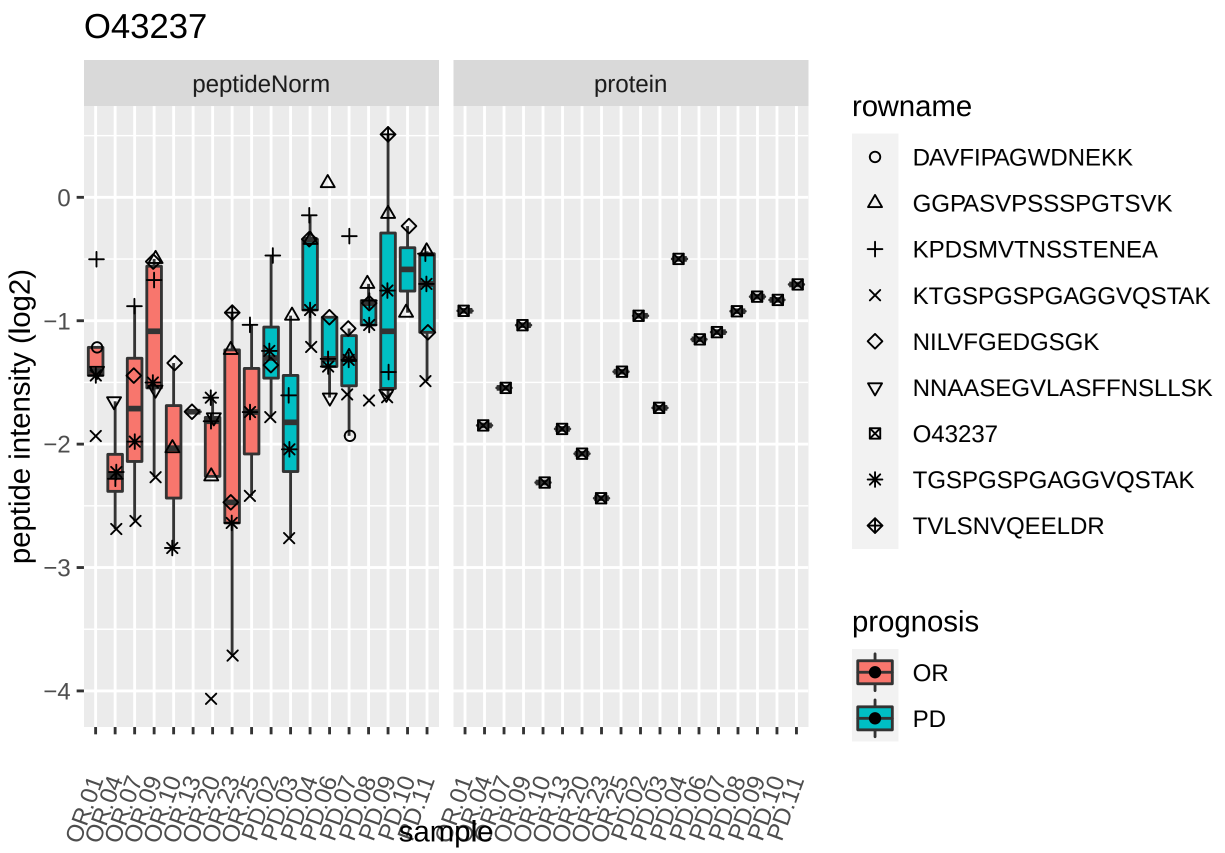

Q15126
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
DFVTEALQSR
EAYGAVTQTVR
LEEQLENLIEFIR
LLDTSTYK
LVLLFSGK
Q15126
VSDIQWFR
VVALEQSR
prognosis
OR
PD



P07741
peptideNorm
protein
value
2
0
−2
colname
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


P07741
peptideNorm
protein
peptide intensity (log2)
2
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
ADSELQLVEQR
AELEIQK
DISPVLKDPASFR
GFLFGPSLAQELGLGCVLIR
GKLPGPTLWASYSLEYGK
LAPVPFFSLLQYE
P07741
SFPDFPTPGVVFR
VVVVDDLLATGGTMNAACELLGR
prognosis
OR
PD


O43237
peptideNorm
protein
value
0
−1
−2
−3
−4
colname
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



## 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 4.2.2 (2022-10-31)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.5 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0
##
## locale:
##  [1] LC_CTYPE=C.UTF-8       LC_NUMERIC=C           LC_TIME=C.UTF-8
##  [4] LC_COLLATE=C.UTF-8     LC_MONETARY=C.UTF-8    LC_MESSAGES=C.UTF-8
##  [7] LC_PAPER=C.UTF-8       LC_NAME=C              LC_ADDRESS=C
## [10] LC_TELEPHONE=C         LC_MEASUREMENT=C.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices datasets  utils     methods
## [8] base
```

```
##
## other attached packages:
##  [1] ExploreModelMatrix_1.8.0    plotly_4.10.0
##  [3] msqrob2_1.4.0               QFeatures_1.6.0
##  [5] MultiAssayExperiment_1.22.0 SummarizedExperiment_1.26.1
##  [7] Biobase_2.56.0              GenomicRanges_1.48.0
##  [9] GenomeInfoDb_1.32.2         IRanges_2.30.0
## [11] S4Vectors_0.34.0            BiocGenerics_0.42.0
## [13] MatrixGenerics_1.8.0        matrixStats_0.62.0
## [15] limma_3.52.1                forcats_0.5.1
## [17] stringr_1.4.1               dplyr_1.0.9
## [19] purrr_0.3.4                 readr_2.1.2
## [21] tidyr_1.2.0                 tibble_3.1.7
## [23] ggplot2_3.3.6               tidyverse_1.3.2
##
## loaded via a namespace (and not attached):
##   [1] googledrive_2.0.0       minqa_1.2.4             colorspace_2.0-3
##   [4] ellipsis_0.3.2          XVector_0.36.0          fs_1.5.2
##   [7] clue_0.3-61             farver_2.1.0            DT_0.23
##  [10] fansi_1.0.3             lubridate_1.8.0         xml2_1.3.3
##  [13] codetools_0.2-18        splines_4.2.2           knitr_1.40.1
##  [16] jsonlite_1.8.0          nloptr_2.0.3            broom_0.8.0
##  [19] cluster_2.1.3           dbplyr_2.1.1            shinydashboard_0.7.2
##  [22] shiny_1.7.1             BiocManager_1.30.18     compiler_4.2.2
##  [25] httr_1.4.3              backports_1.4.1         assertthat_0.2.1
##  [28] Matrix_1.4-1            fastmap_1.1.0           lazyeval_0.2.2
##  [31] gargle_1.2.0            cli_3.3.0               later_1.3.0
##  [34] htmltools_0.5.2         tools_4.2.2             igraph_1.3.2
##  [37] gtable_0.3.0            glue_1.6.2              GenomeInfoDbData_1.2.8
##  [40] Rcpp_1.0.8.3            cellranger_1.1.0        jquerylib_0.1.4
##  [43] vctrs_0.4.1             nlme_3.1-157            rintrojs_0.3.0
##  [46] xfun_0.33               lme4_1.1-29             rvest_1.0.2
##  [49] mime_0.12               lifecycle_1.0.1         renv_0.15.4
##  [52] googlesheets4_1.0.0     zlibbioc_1.42.0         MASS_7.3-57
##  [55] scales_1.2.0            promises_1.2.0.1        hms_1.1.1
##  [58] ProtGenerics_1.28.0     parallel_4.2.2          AnnotationFilter_1.20.0
##  [61] yaml_2.3.5              sass_0.4.1              stringi_1.7.8
##  [64] highr_0.9               boot_1.3-28             BiocParallel_1.30.2
##  [67] rlang_1.0.2             pkgconfig_2.0.3         bitops_1.0-7
##  [70] evaluate_0.16           lattice_0.20-45         htmlwidgets_1.5.4
##  [73] labeling_0.4.2          cowplot_1.1.1           tidyselect_1.1.2
##  [76] magrittr_2.0.3          R6_2.5.1                generics_0.1.2
##  [79] DelayedArray_0.22.0     DBI_1.1.2               pillar_1.7.0
##  [82] haven_2.5.0             withr_2.5.0             MsCoreUtils_1.8.0
##  [85] RCurl_1.98-1.6          modelr_0.1.8            crayon_1.5.1
##  [88] utf8_1.2.2              tzdb_0.3.0              rmarkdown_2.14
##  [91] grid_4.2.2              readxl_1.4.0            data.table_1.14.2
##  [94] reprex_2.0.1            digest_0.6.29           xtable_1.8-4
##  [97] httpuv_1.6.5            munsell_0.5.0           viridisLite_0.4.0
## [100] bslib_0.3.1             shinyjs_2.1.0
```