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/pepti

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.

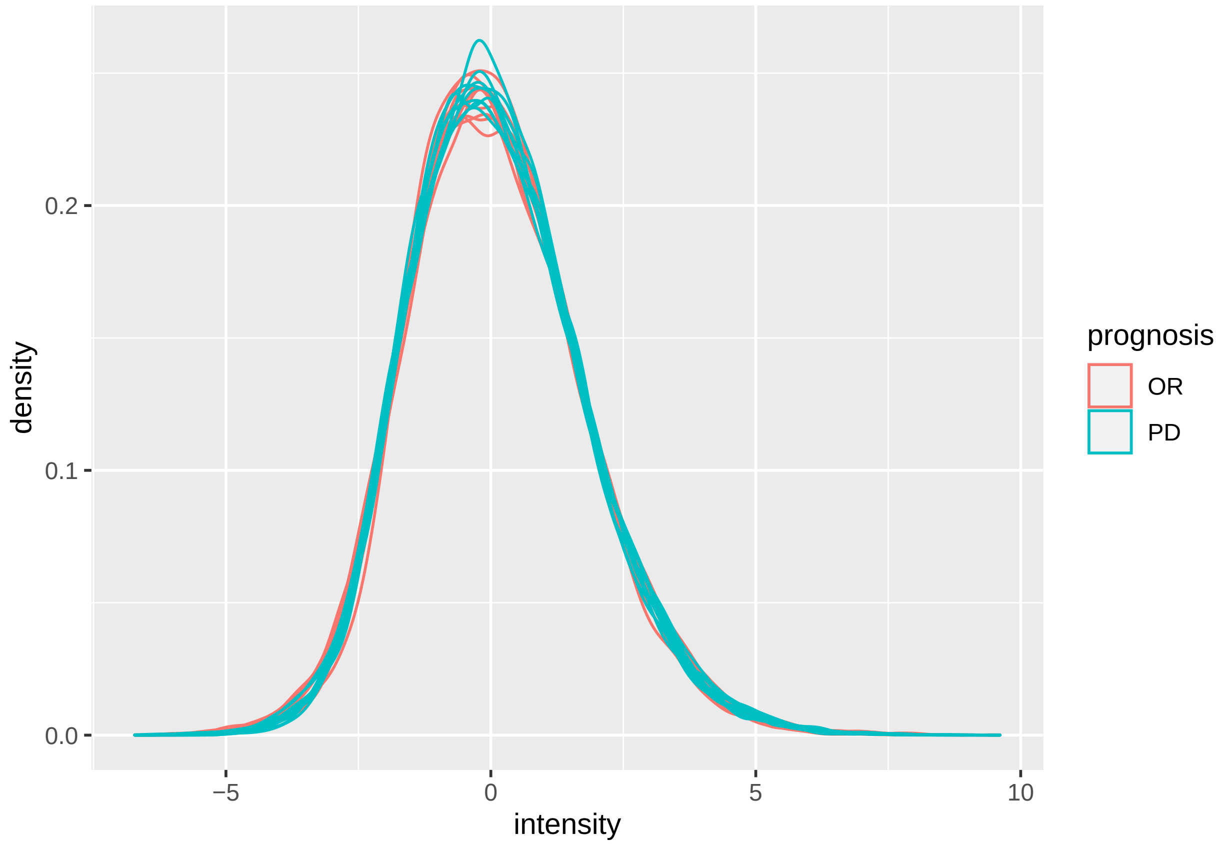
```
pe <- normalize(pe,
                i = "peptideLog",
                name = "peptideNorm",
                method = "center.median")
```

3.4 Explore normalized data

Upon the normalisation the density curves are nicely registered

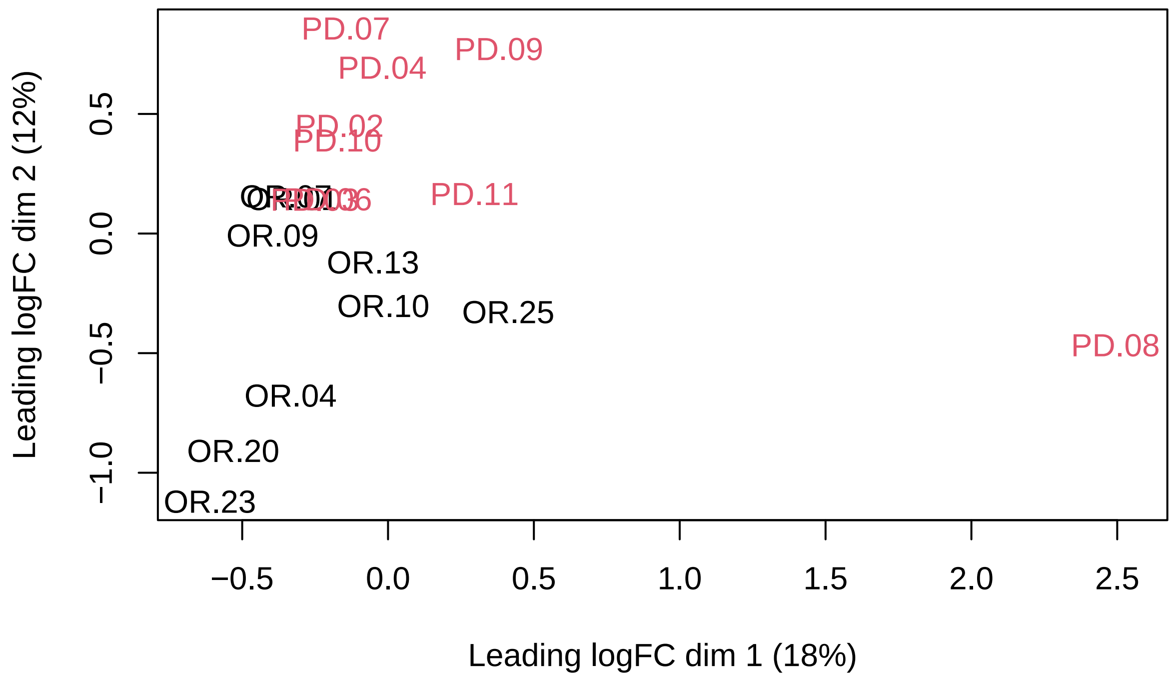
```
pe[["peptideNorm"]] %>%
  assay %>%
  as.data.frame() %>%
  gather(sample, intensity) %>%
  mutate(prognosis = colData(pe)[sample,"prognosis"]) %>%
  ggplot(aes(x = intensity,group = sample,color = prognosis)) +
    geom_density()
```

```
## 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.

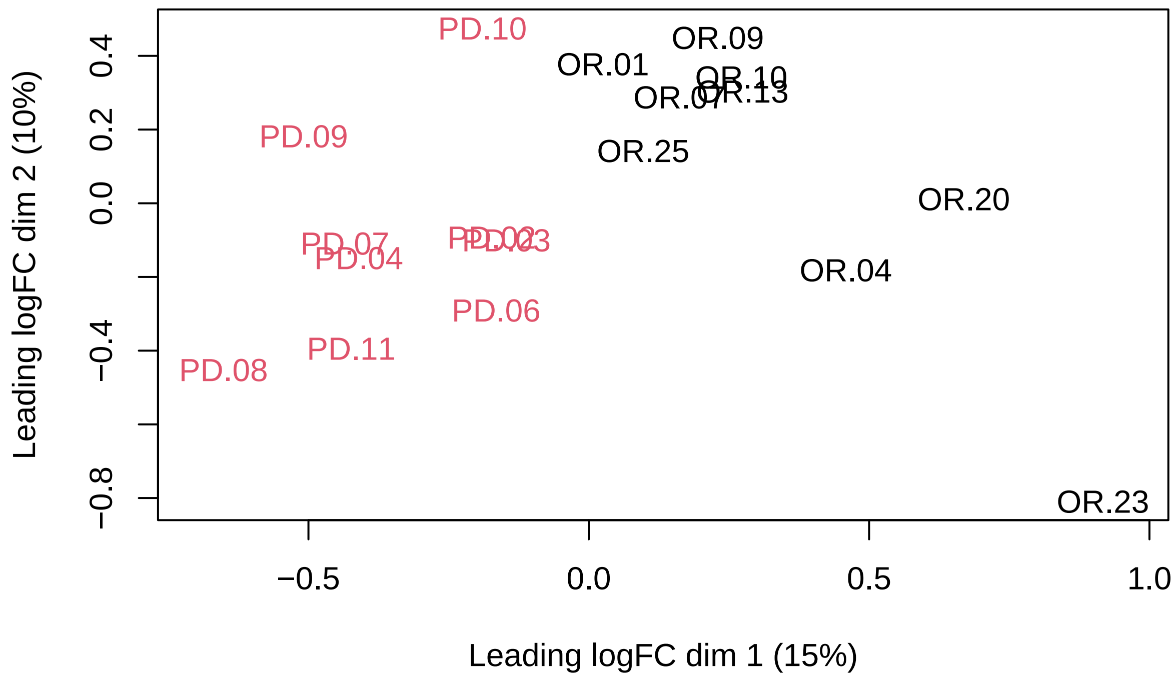
3.5 Summarization to protein level

- 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]]
```

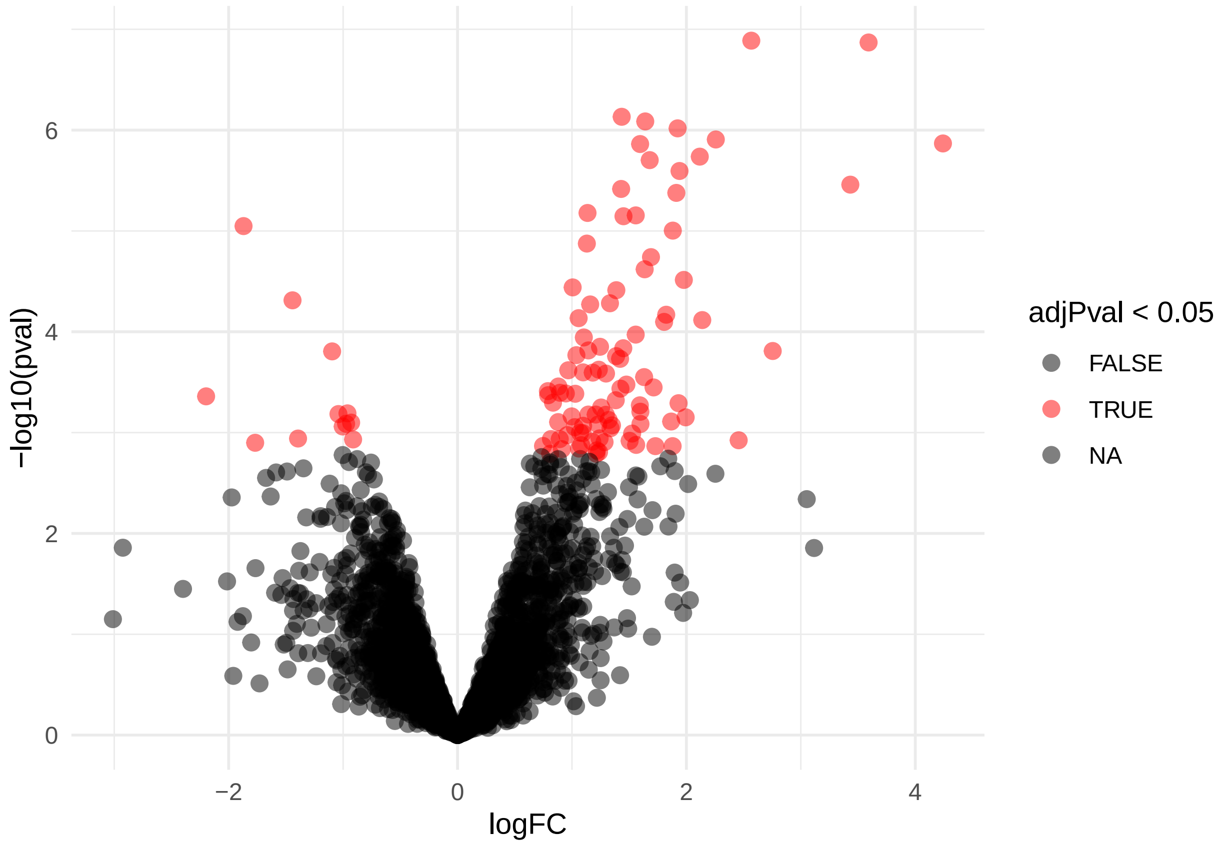
Spike-in condition `A` is the reference class. So the mean log2 expression for samples from good prognosis (OR) is '(Intercept). The mean log2 expression for samples from poor prognosis (PD) is'(Intercept)+prognosisPD'. Hence, the average log2 fold change between prognosis PD and prognosis OR is modelled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

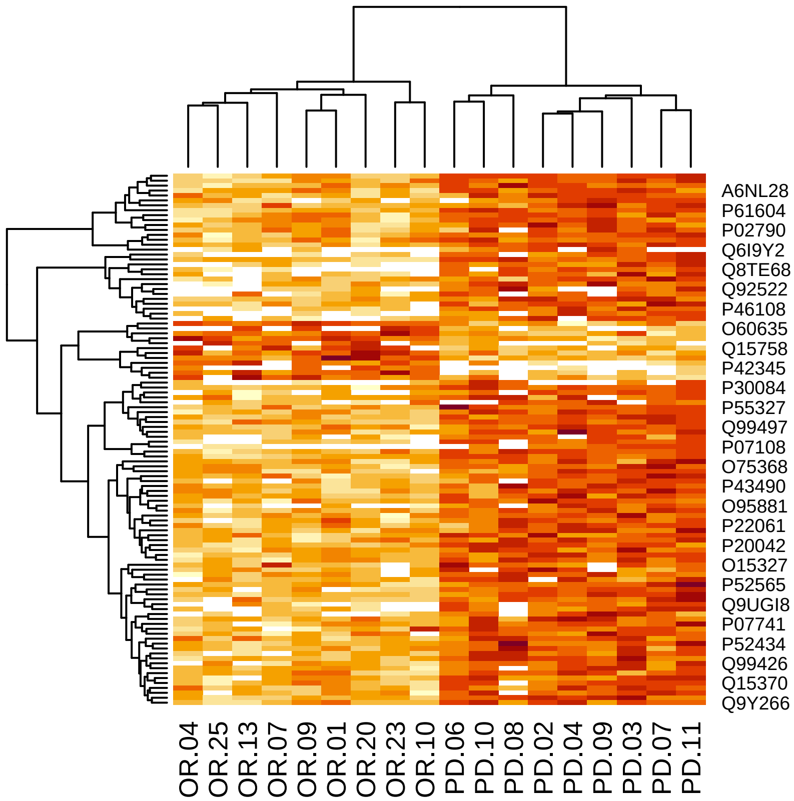


Note, that 108 proteins are found to be differentially abundant.

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, ])
```

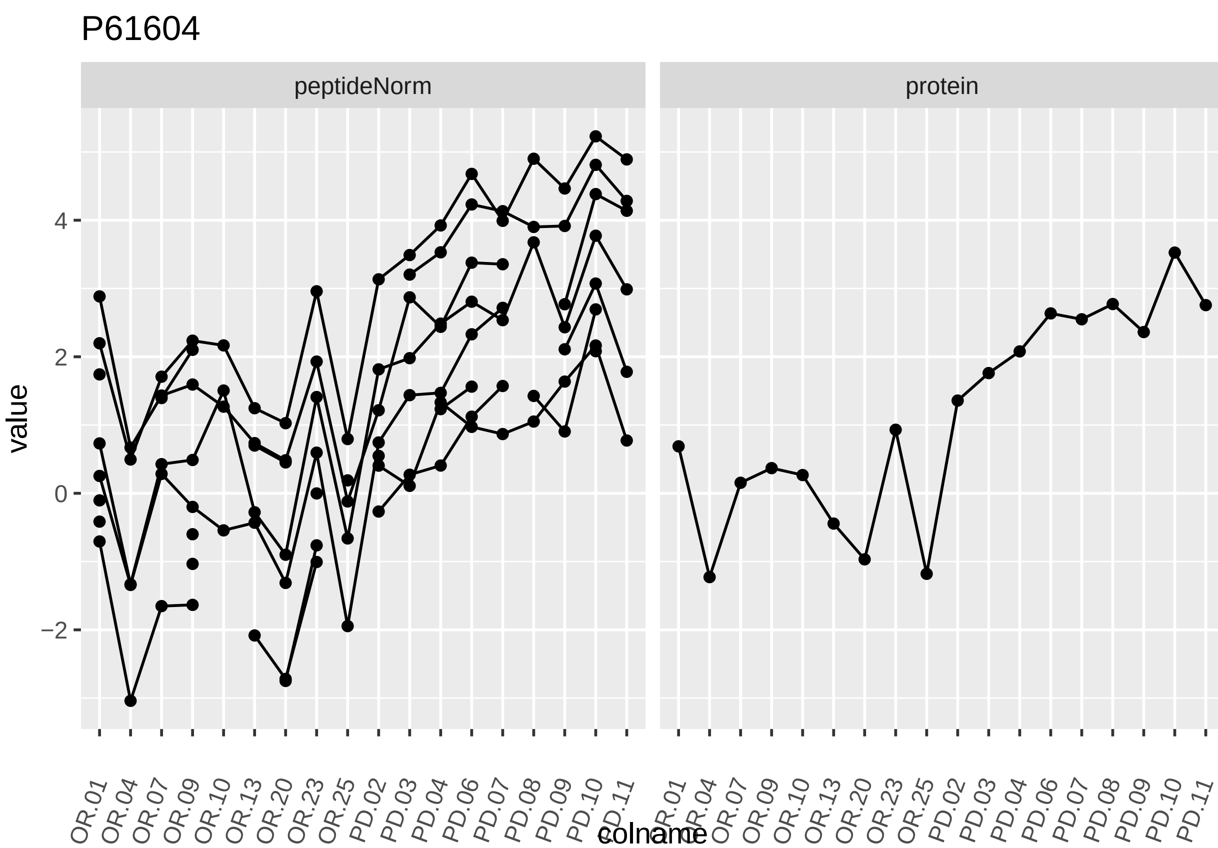


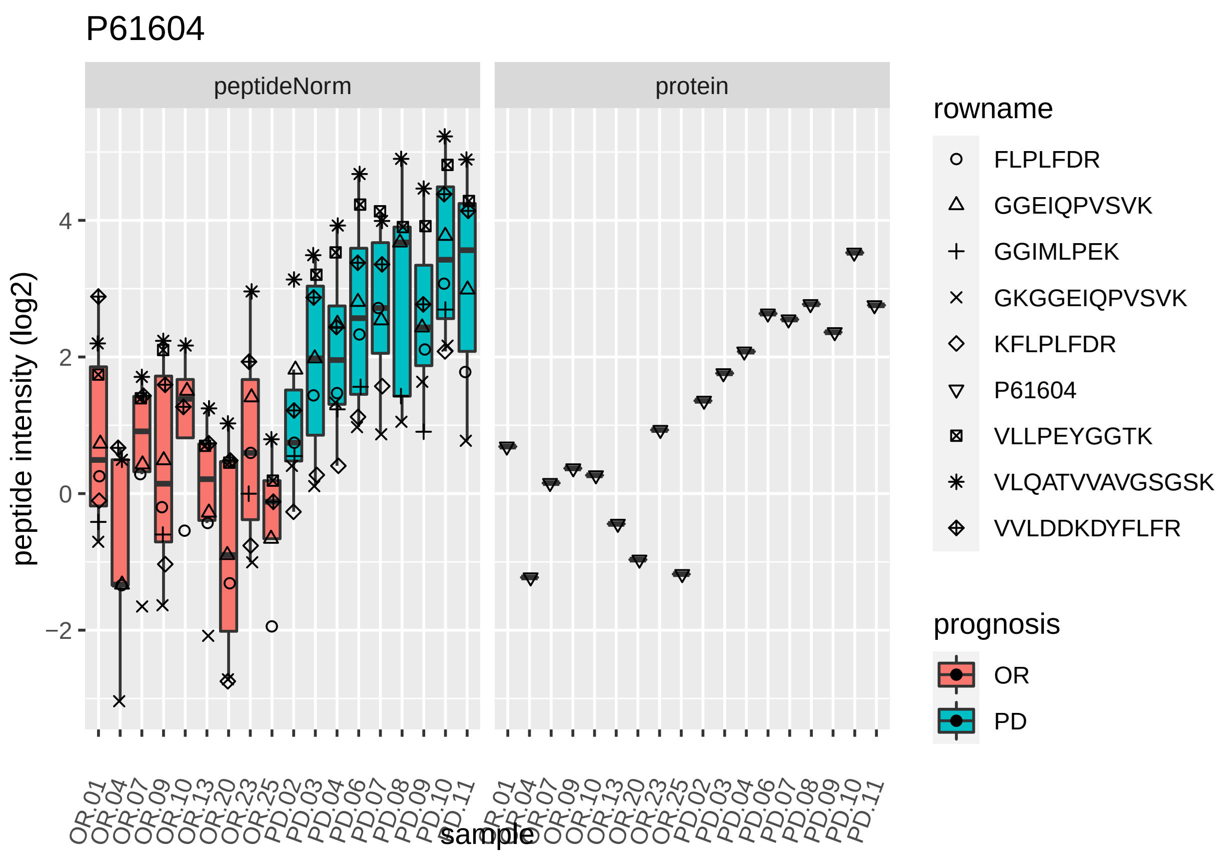
4.3.3 Detail plots

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

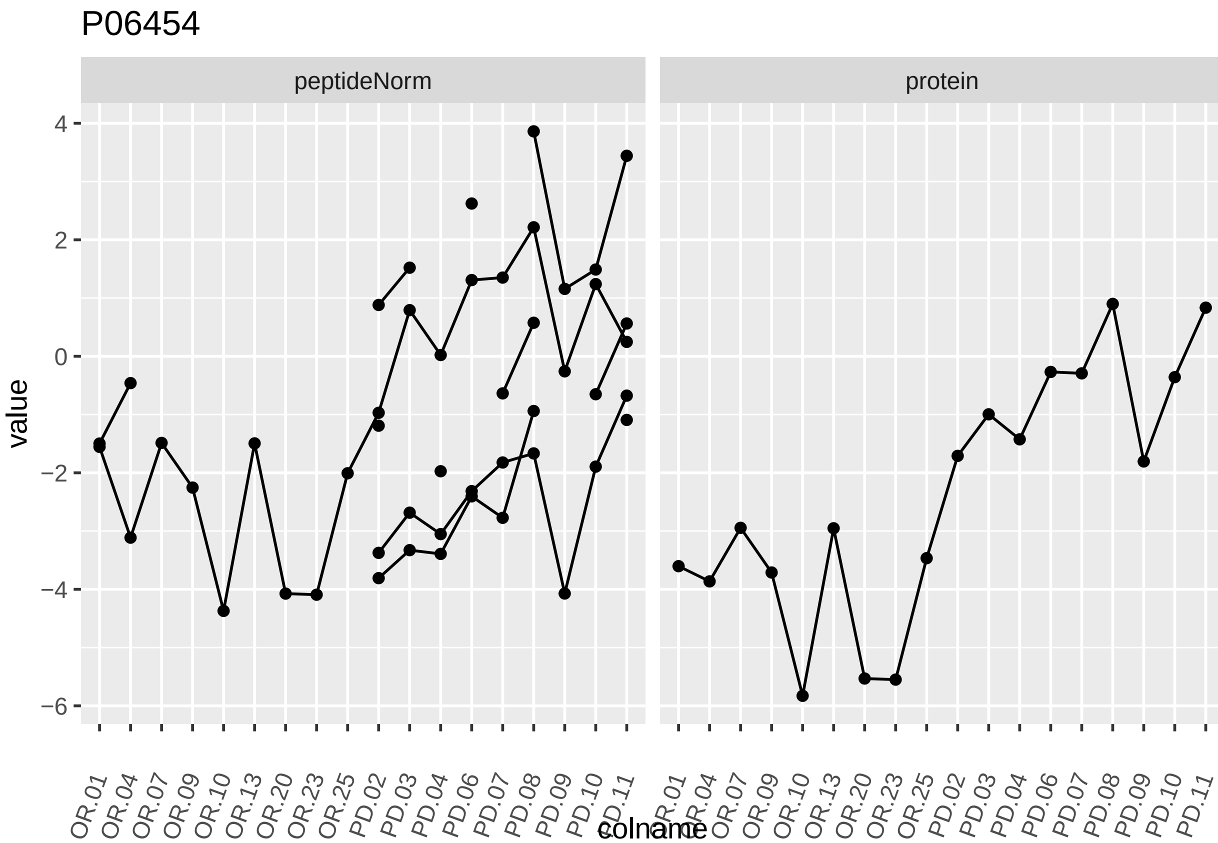
```
for (protName in sigNames)
#for (protName in orderProt[1:10])
{
pePlot <- pe[protName, , c("peptideNorm","protein")]
pePlotDf <- data.frame(longFormat(pePlot))
pePlotDf$assay <- factor(pePlotDf$assay,
                        levels = c("peptideNorm", "protein"))
pePlotDf$prognosis <- as.factor(colData(pePlot)[pePlotDf$colname,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

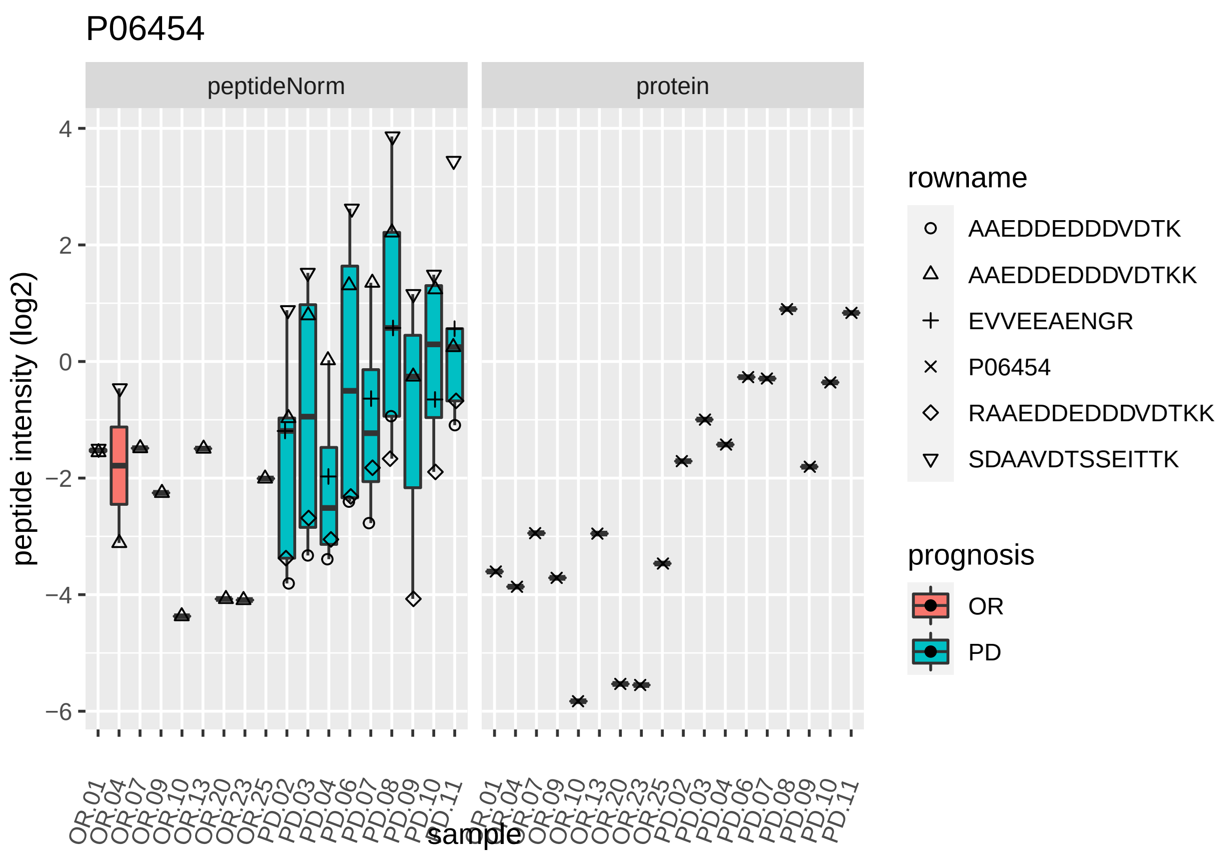




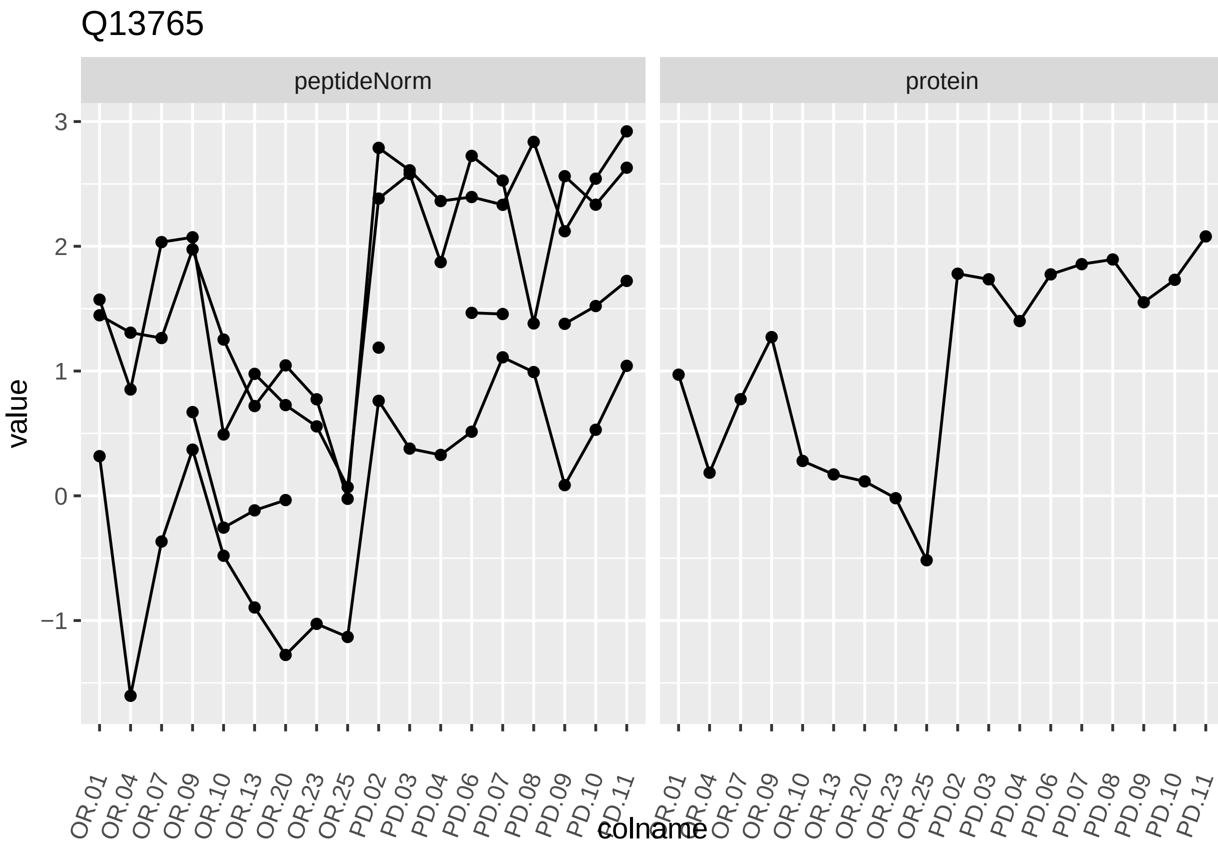
P61604
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
FLPLFDR
GGEIQPVSVK
GGIMLPEK
GKGGEIQPVSVK
KFLPLFDR
P61604
VLLPEYGGTK
VLQATVVAVGSGSK
VVLDDKDYFLFR
prognosis
OR
PD

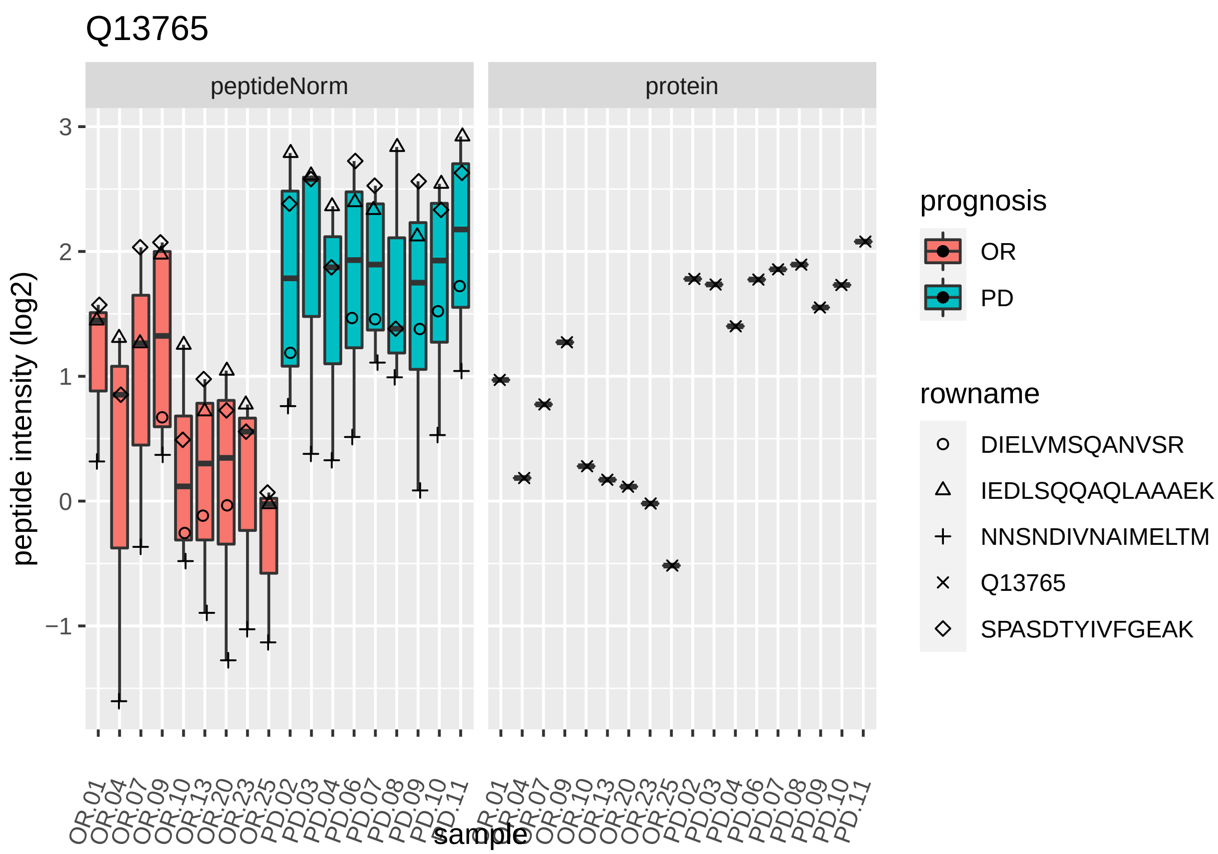


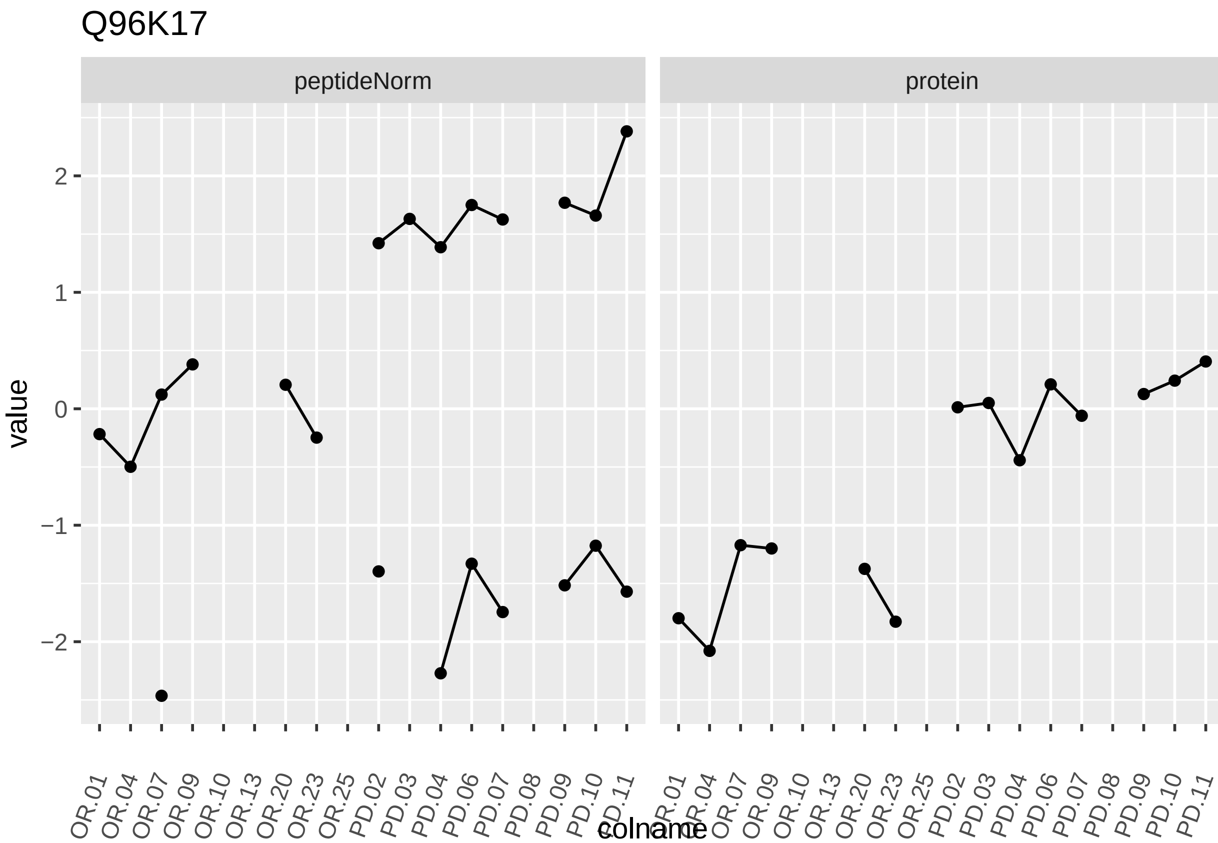
P06454
peptideNorm
protein
value
colname
4
2
0
−2
−4
−6
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

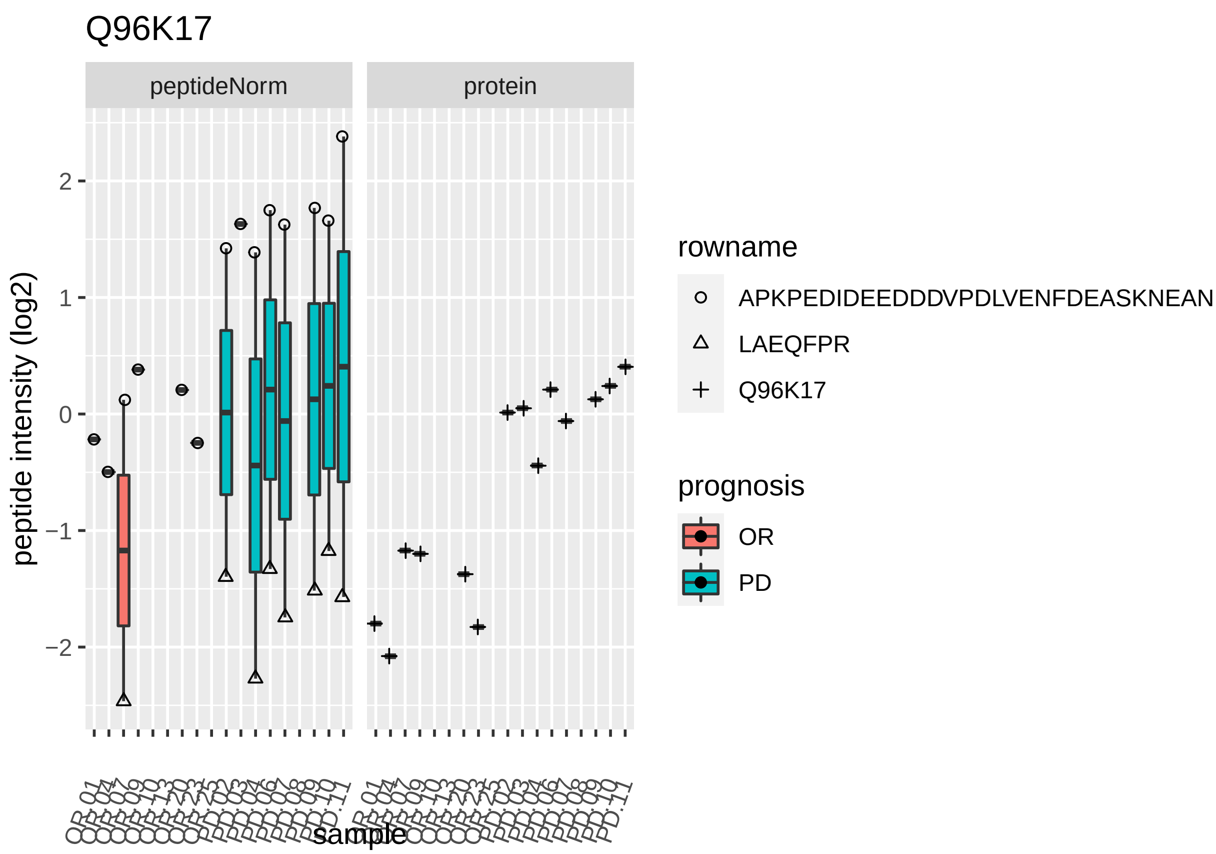


P06454
peptideNorm
protein
peptide intensity (log2)
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AAEDDEDDDVDTK
AAEDDEDDDVDTKK
EVVEEAENGR
P06454
RAAEDDEDDDVDTKK
SDAAVDTSSEITTK
prognosis
OR
PD

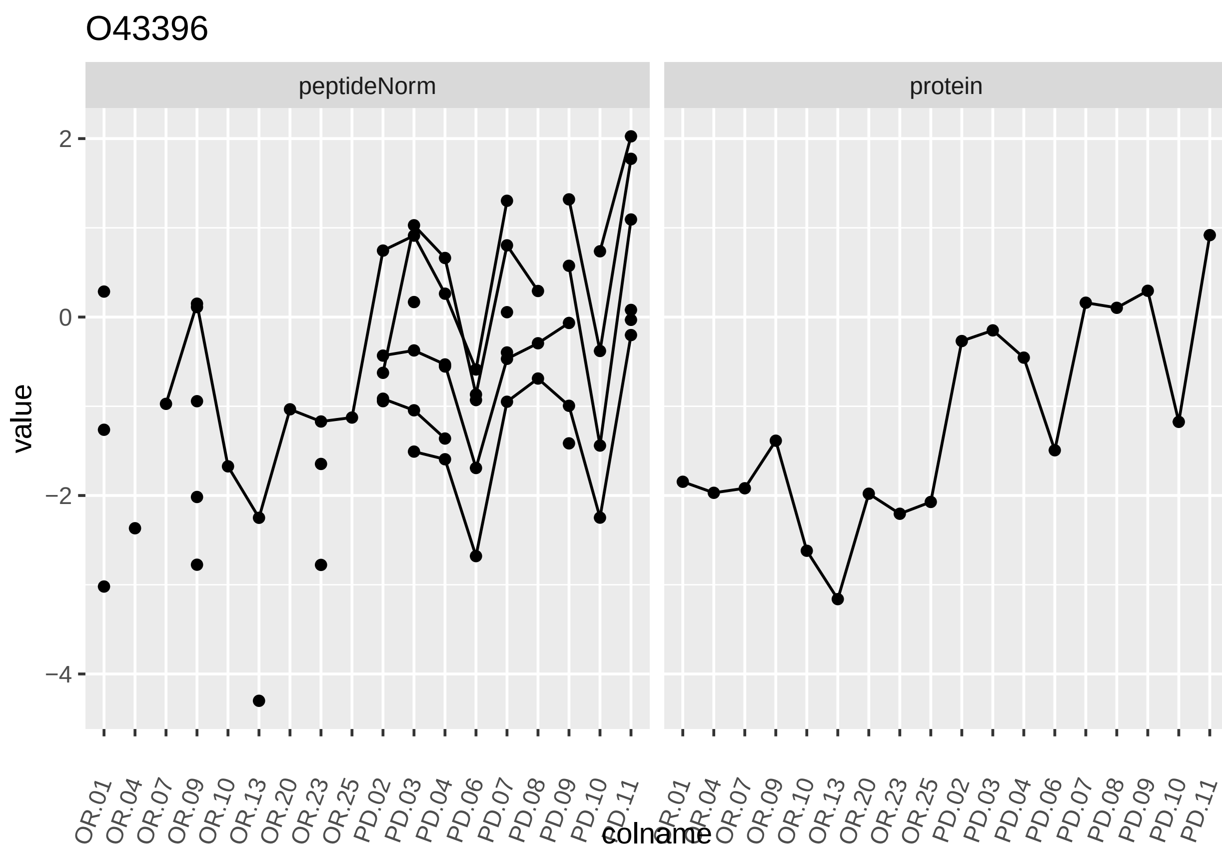

Q13765
peptideNorm
protein
value
3
2
1
0
−1
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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

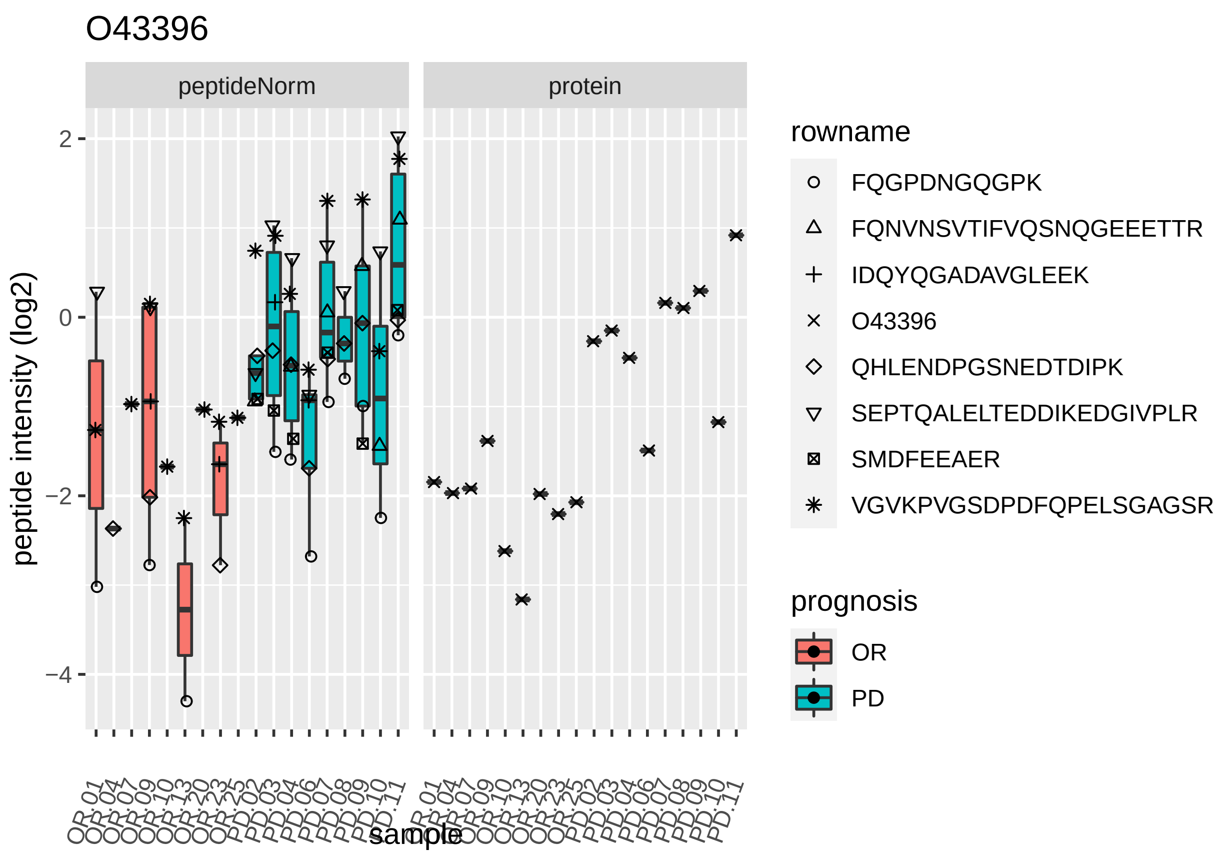

Q96K17
peptideNorm
protein
value
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

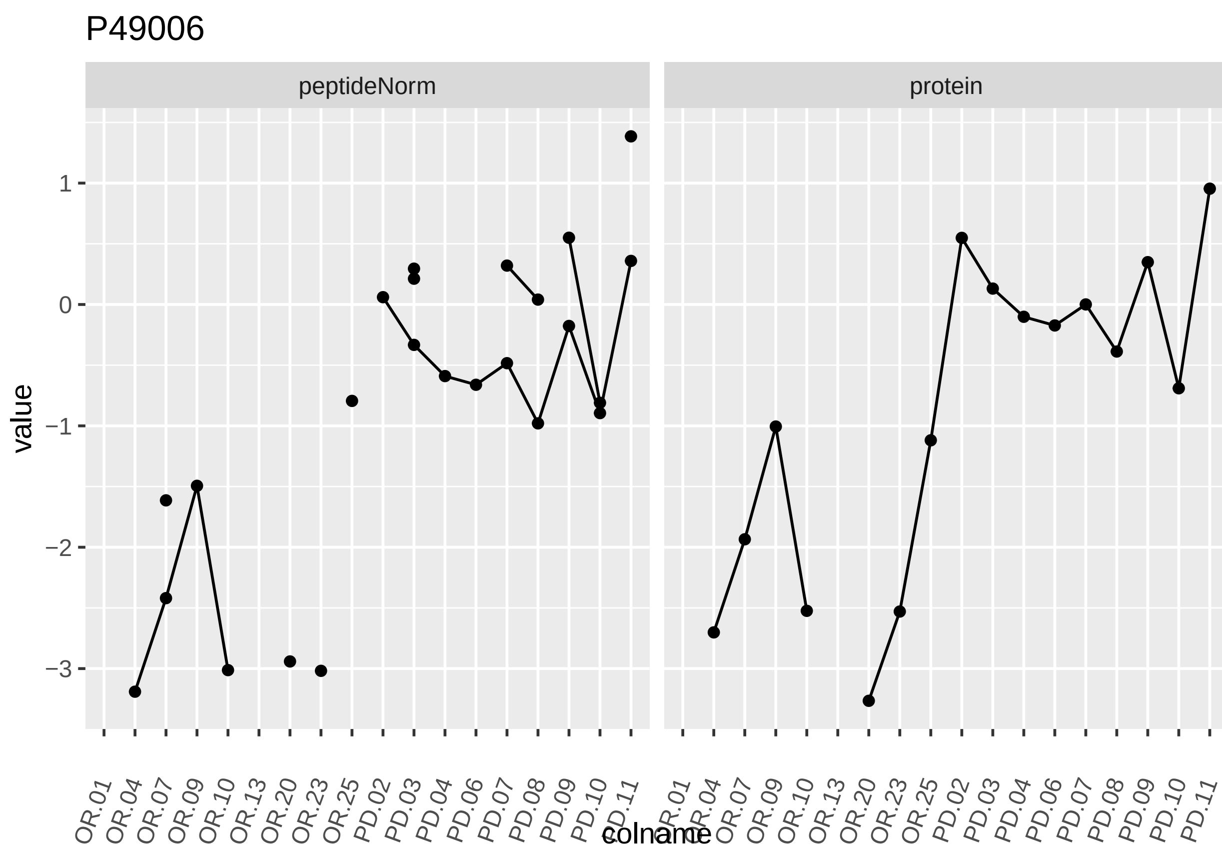


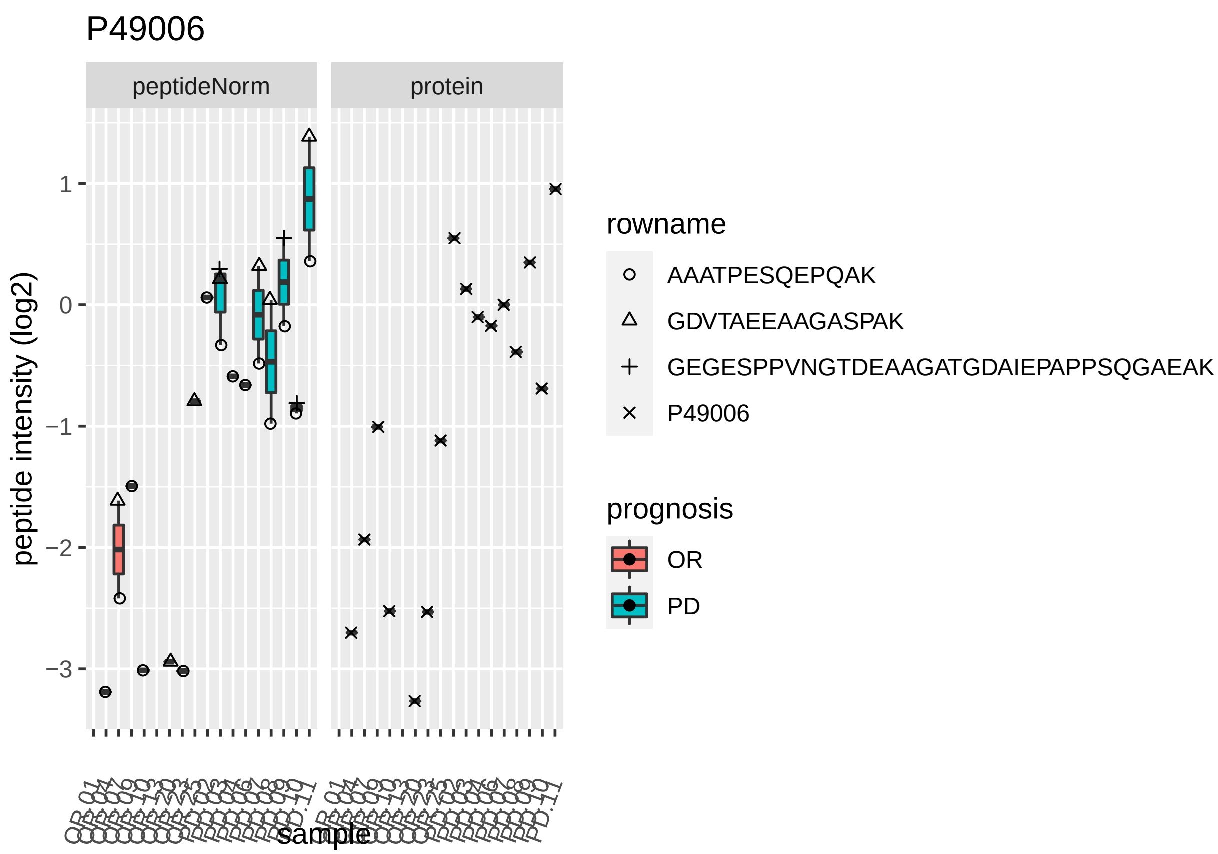
Q96K17
peptideNorm
protein
peptide intensity (log2)
sample
rowname
APKPEDIDEEDDDVPDLVENFDEASKNEAN
LAEQFPR
Q96K17
prognosis
OR
PD

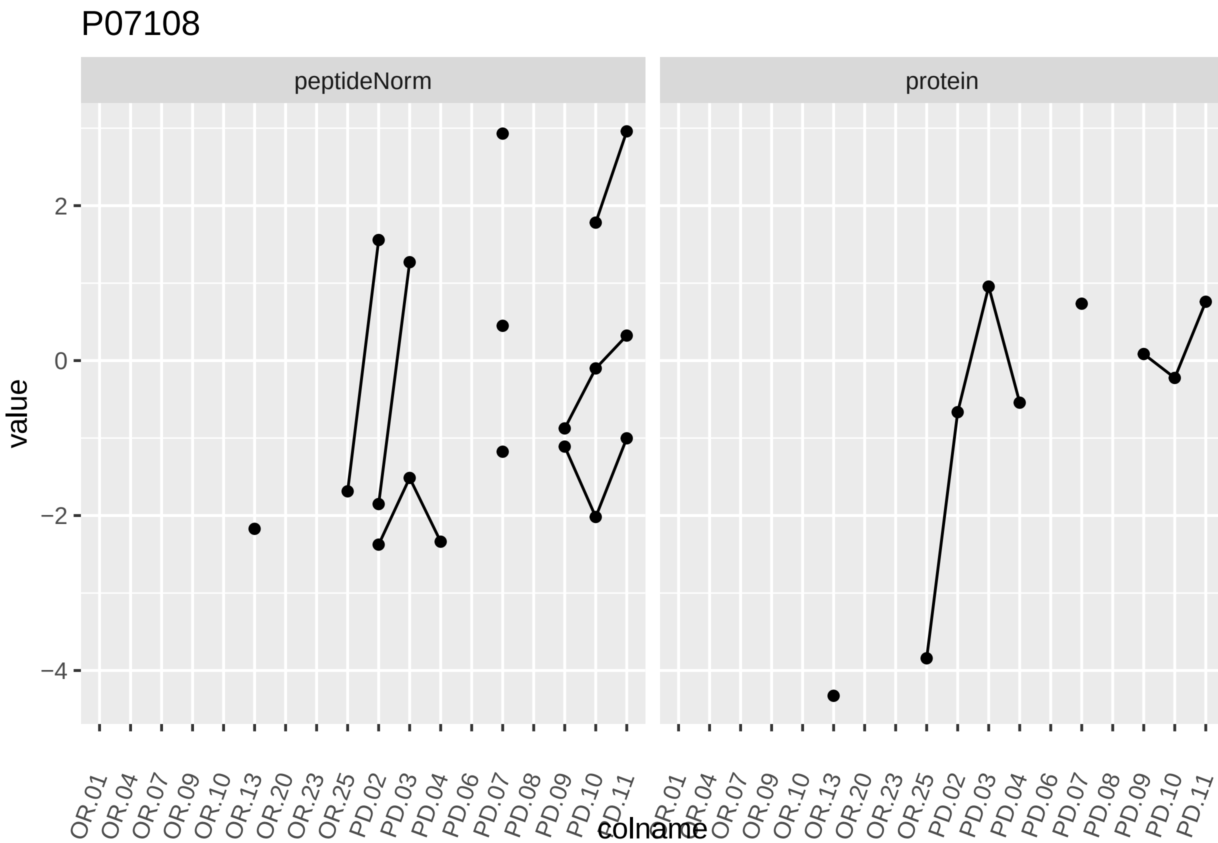


O43396
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

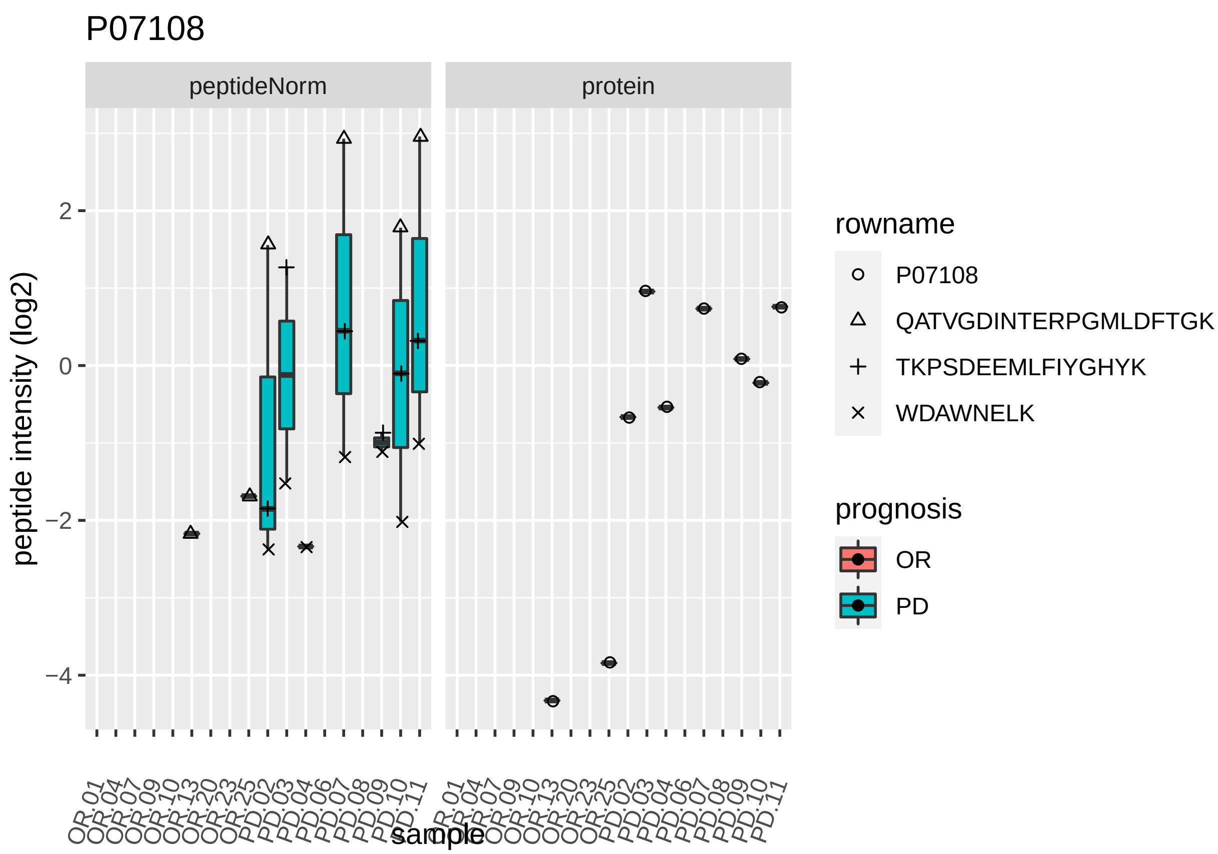

O43396
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
FQGPDNGQGPK
FQNVNSVTIFVQSNQGEEETTR
IDQYQGADAVGLEEK
O43396
QHLENDPGSNEDTDIPK
SEPTQALELTEDDIKEDGIVPLR
SMDFEEAER
VGVKPVGSDPDFQPELSGAGSR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

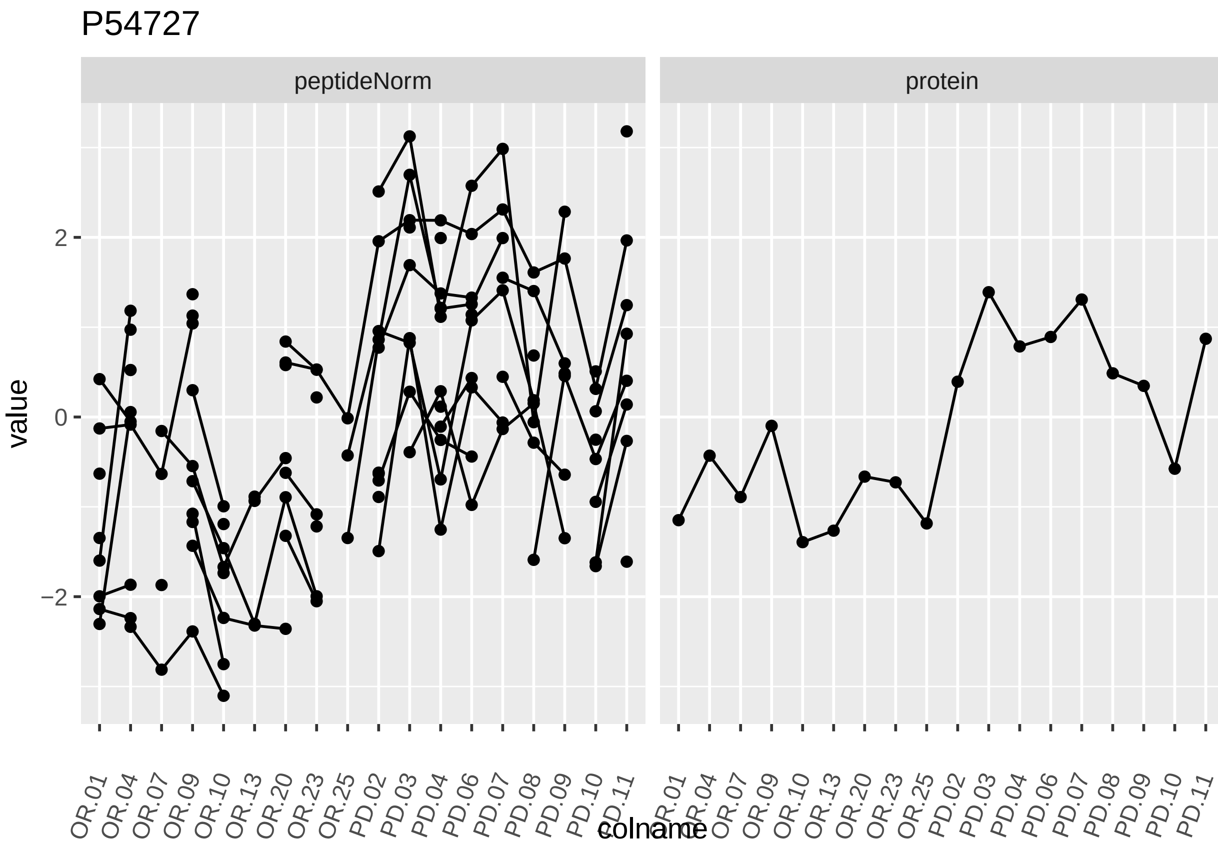

P49006
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

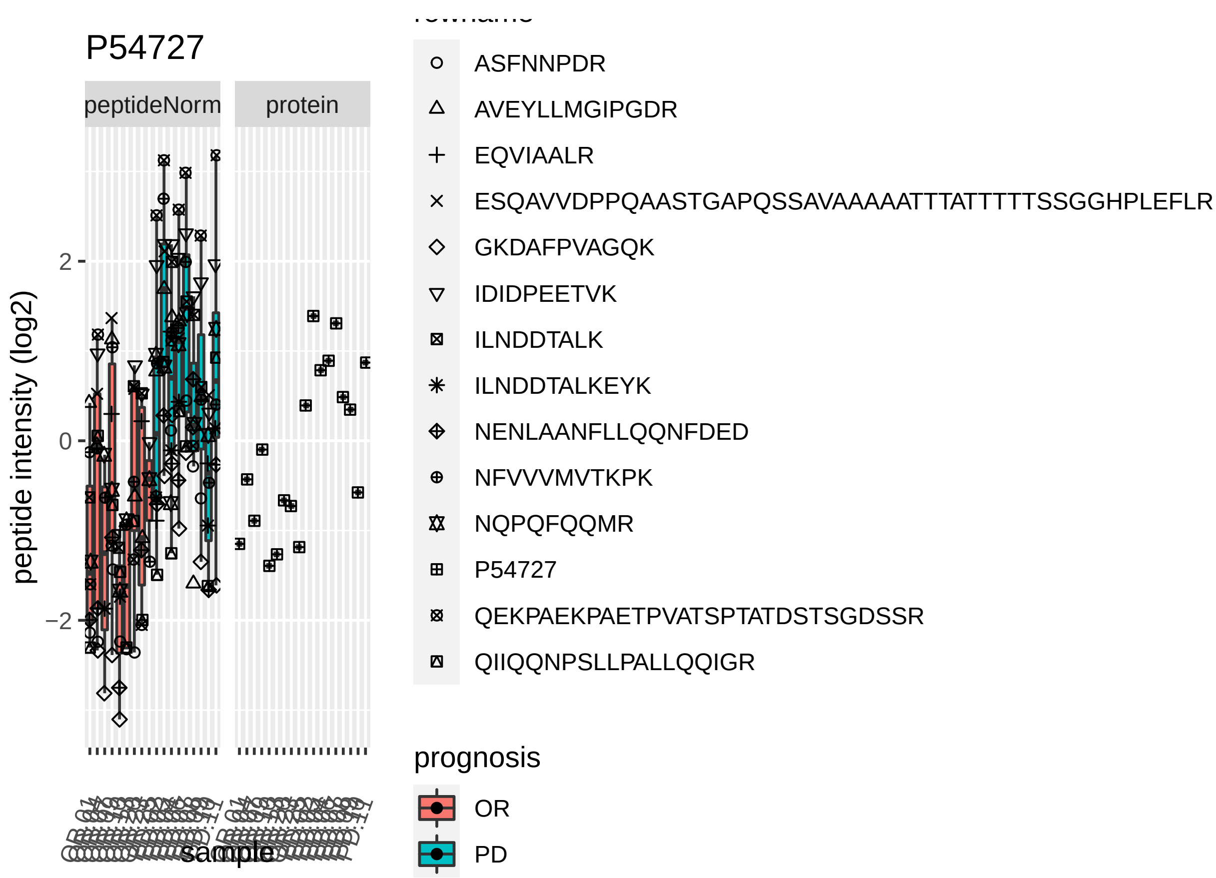

P49006
peptideNorm
protein
peptide intensity (log2)
sample
rowname
AAATPESQEPQAK
GDVTAEEAAGASPAK
GEGESPPVNGTDEAAGATGDAIEPAPPSQGAEAK
P49006
prognosis
OR
PD

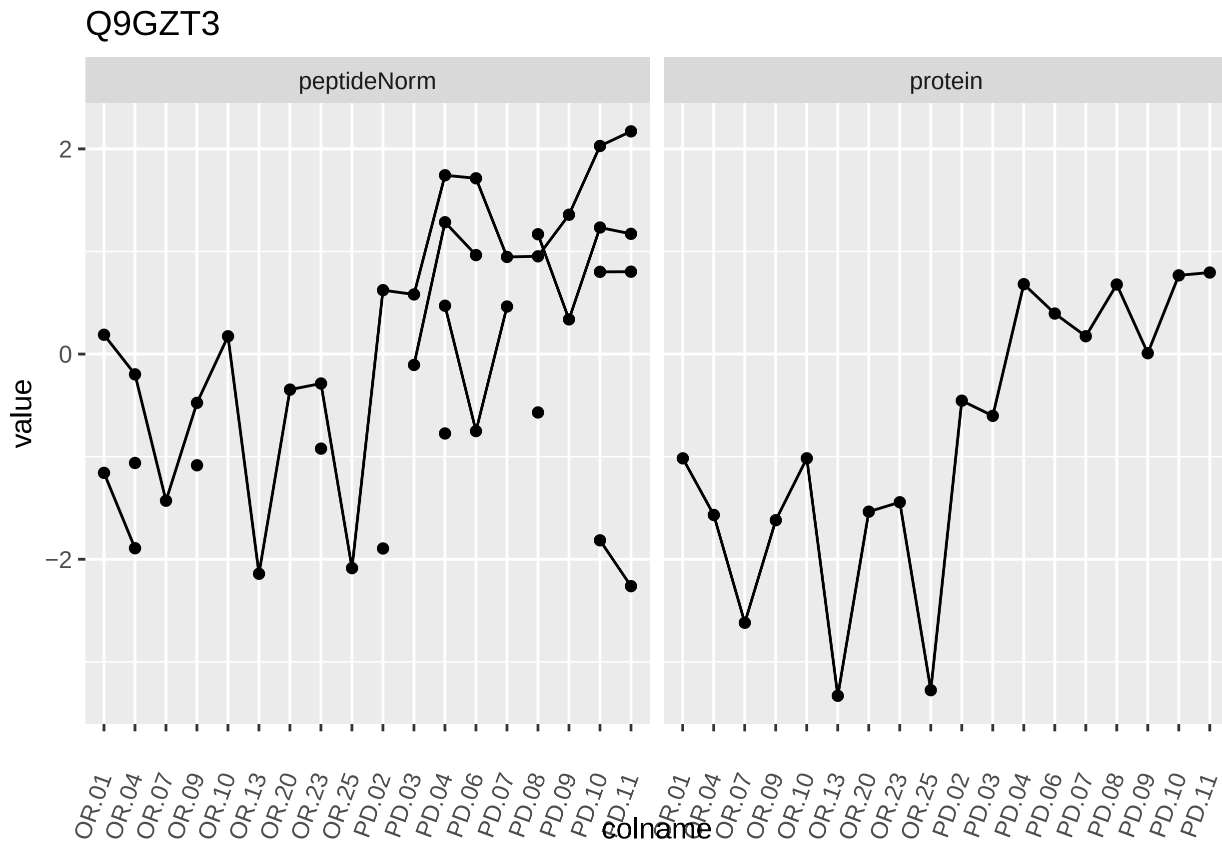


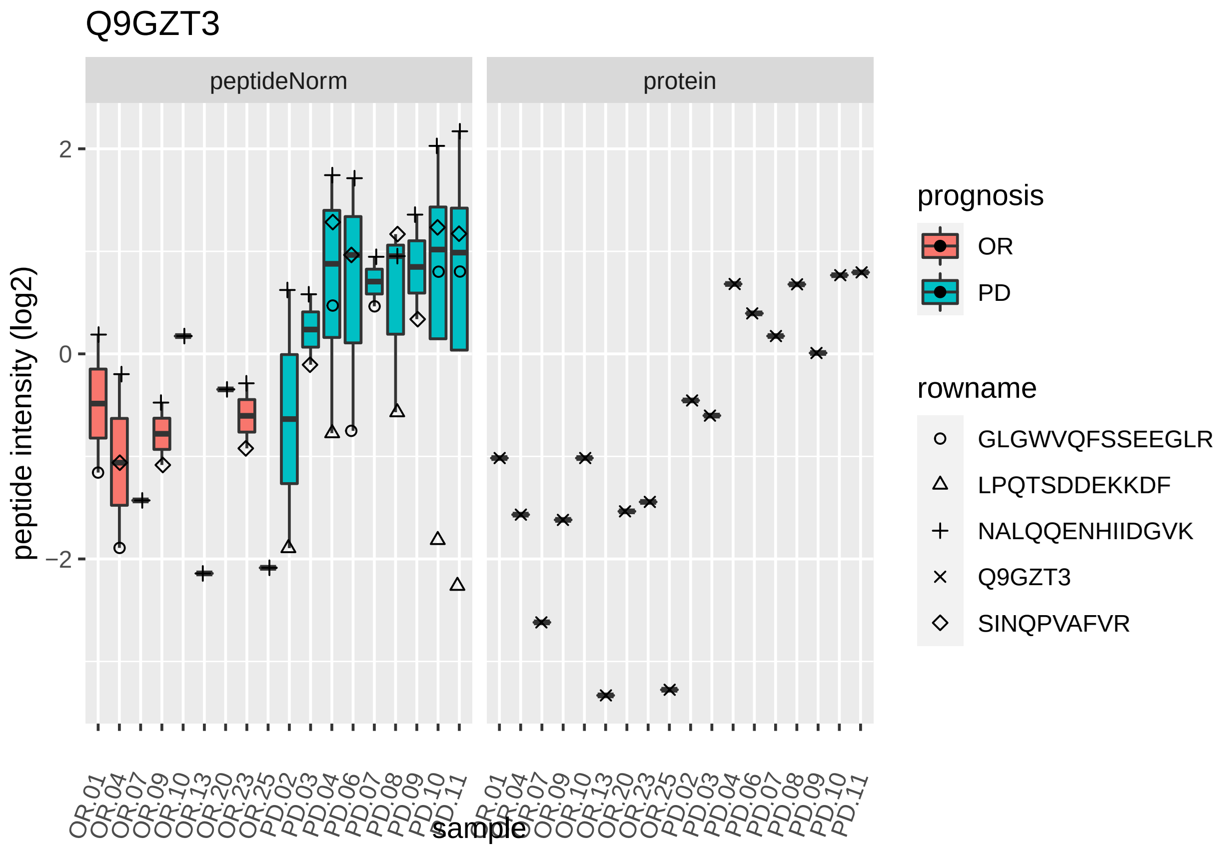
P07108
peptideNorm
protein
value
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


P07108
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
rowname
P07108
QATVGDINTERPGMLDFTGK
TKPSDEEMLFIYGHYK
WDAWNELK
prognosis
OR
PD

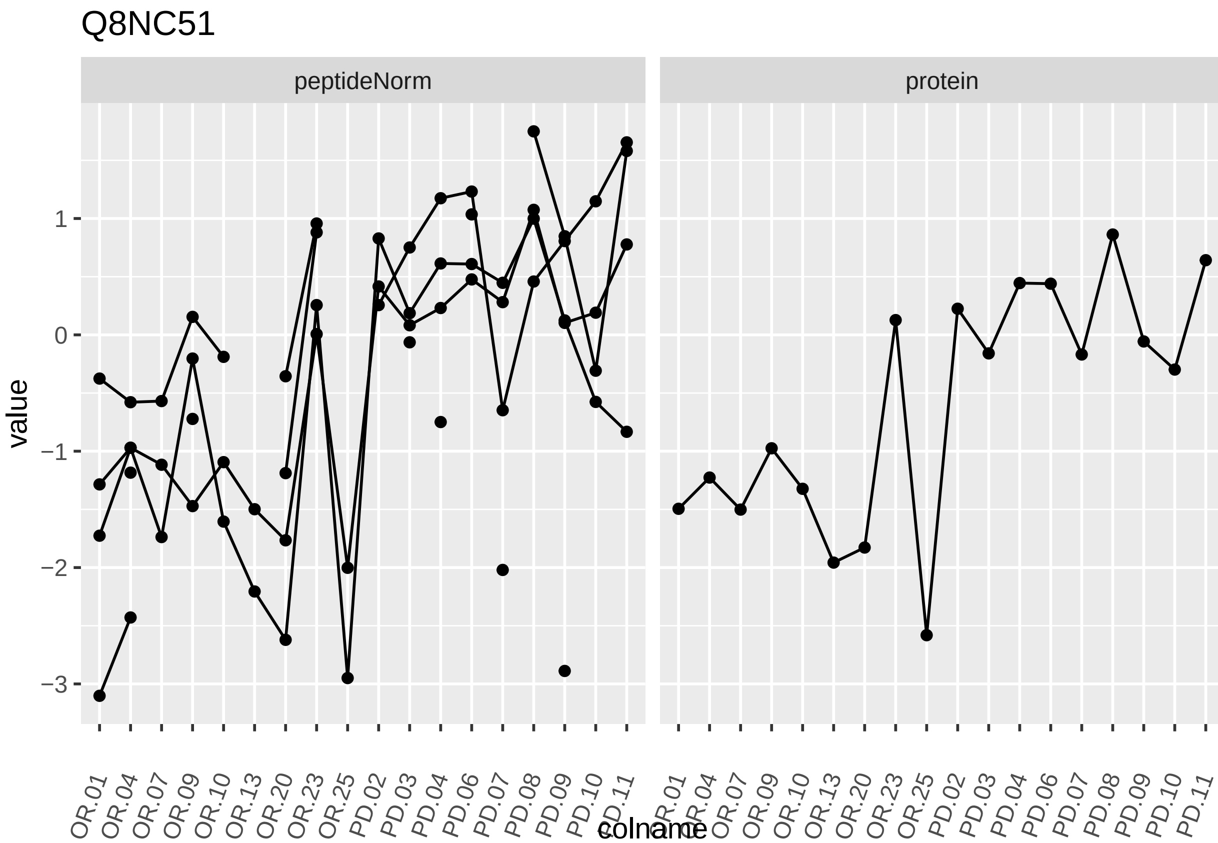

P54727
peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

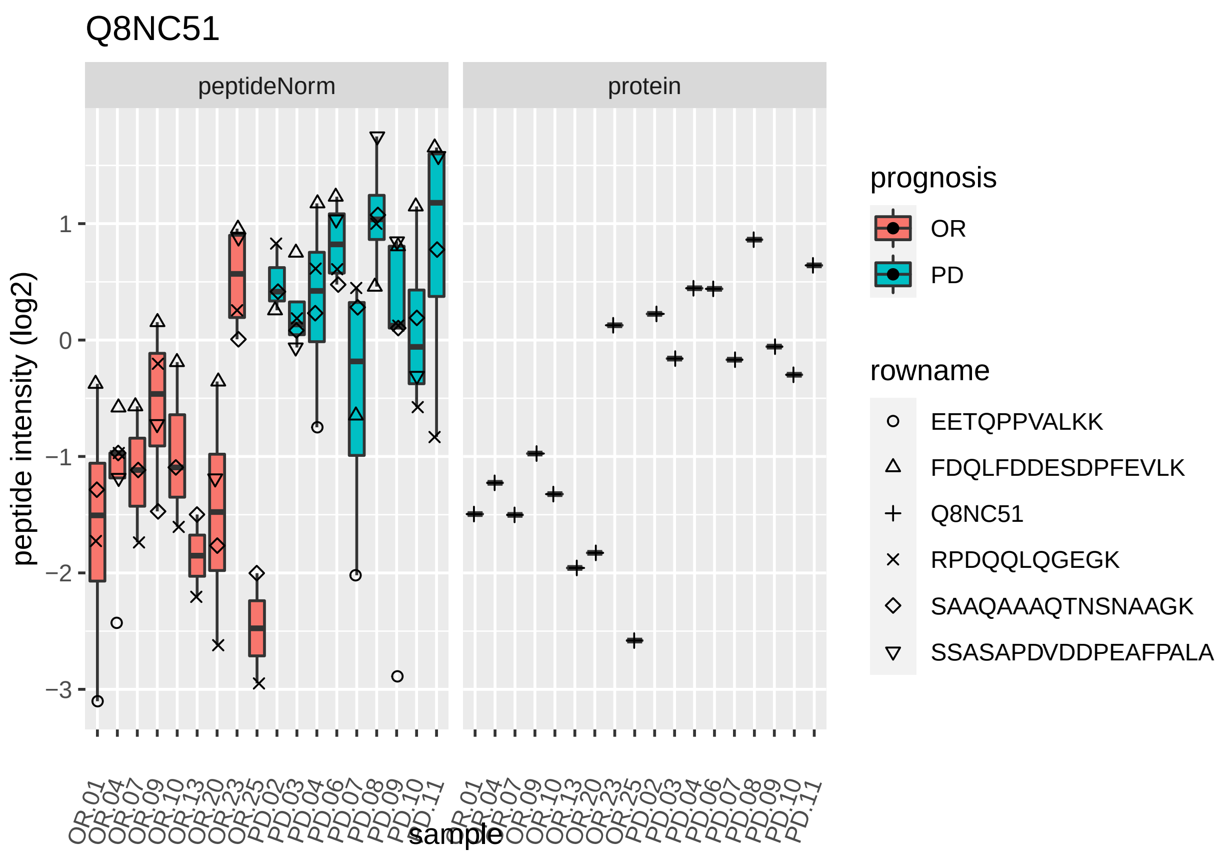

P54727
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
rowname
ASFNNPDR
AVEYLLMGIPGDR
EQVIAALR
ESQAVVDPPQAASTGAPQSSAVAAAAATTTATTTTTSSGGHPLEFLR
GKDAFPVAGQK
IDIDPEETVK
ILNDDTALK
ILNDDTALKEYK
NENLAANFLLQQNFDED
NFVVVMVTKPK
NQPQFQQMR
P54727
QEKPAEKPAETPVATSPTATDSTSGDSSR
QIIQQNPSLLPALLQQIGR
prognosis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

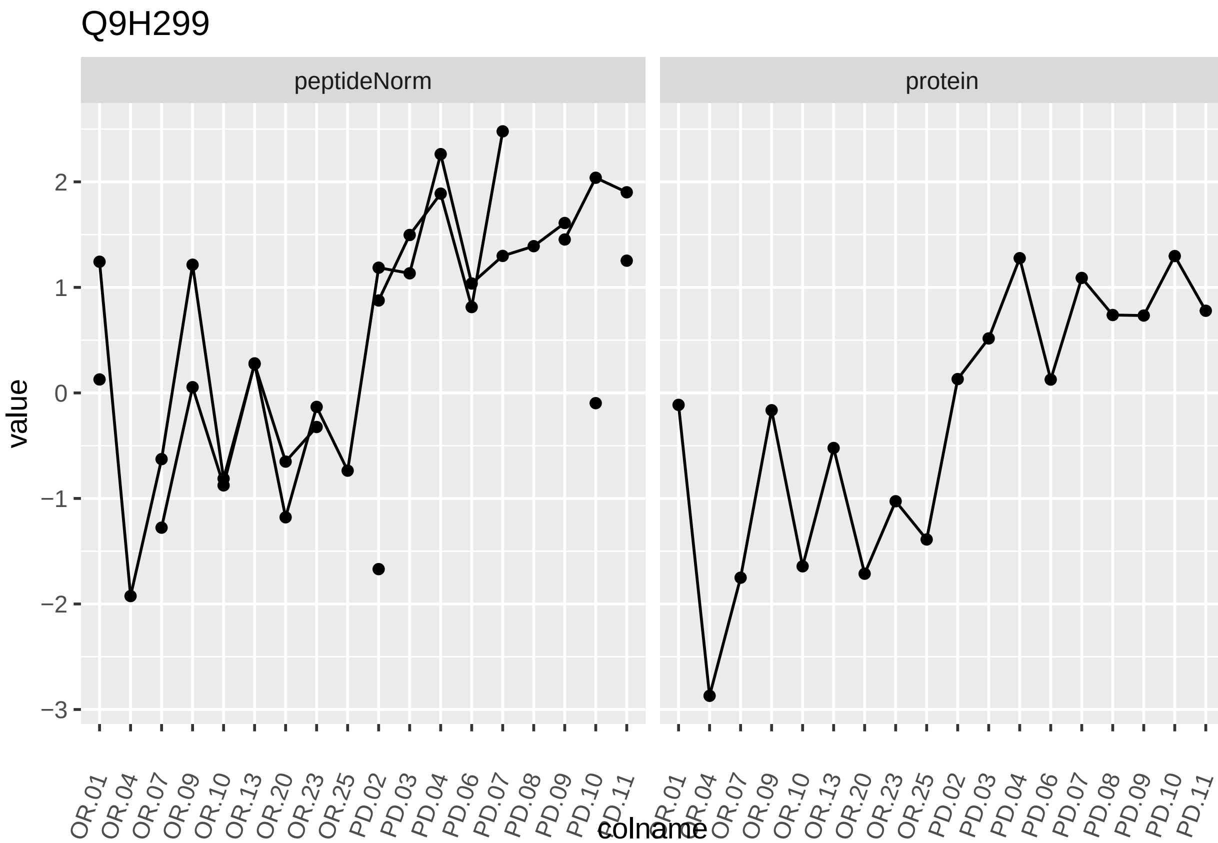


Q9GZT3
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
GLGWVQFSSEEGLR
LPQTSDDEKKDF
NALQQENHIIDGVK
Q9GZT3
SINQPVAFVR

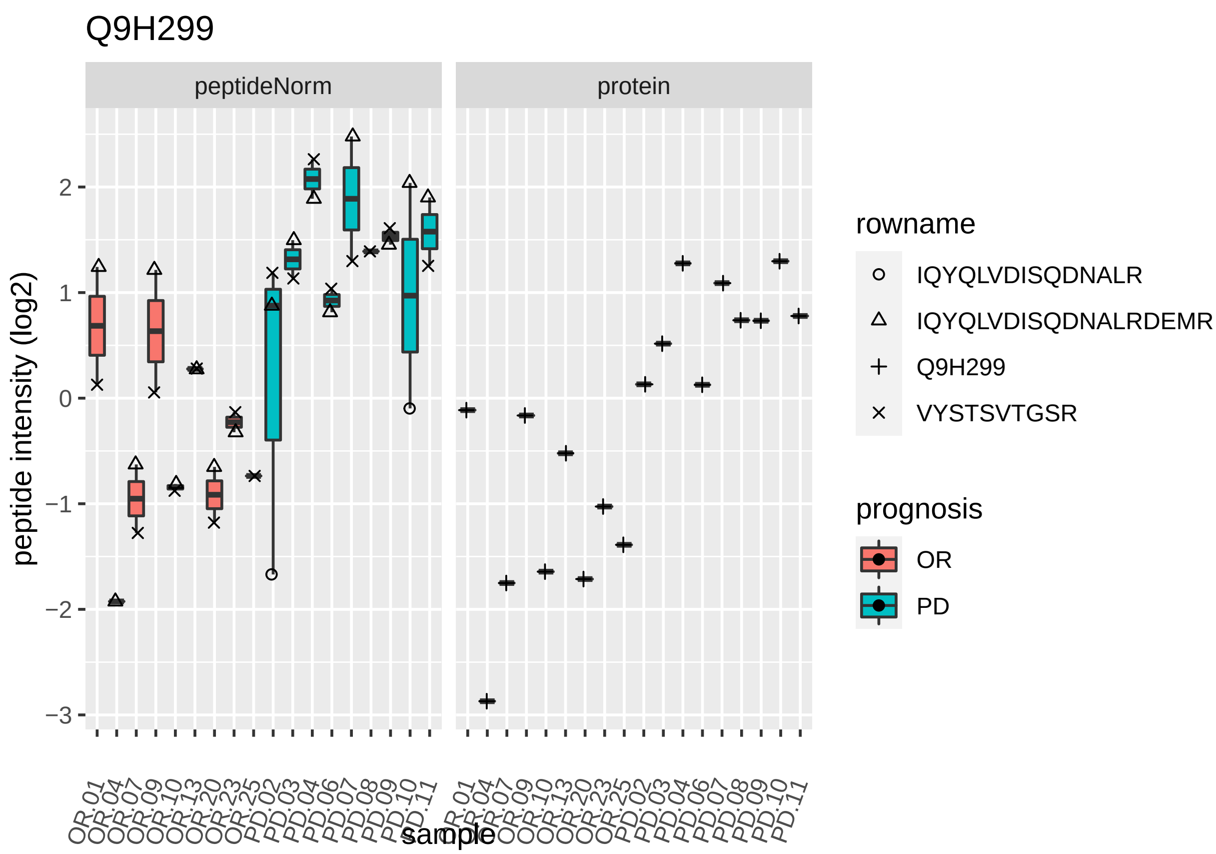

Q8NC51
peptideNorm
protein
value
1
0
−1
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

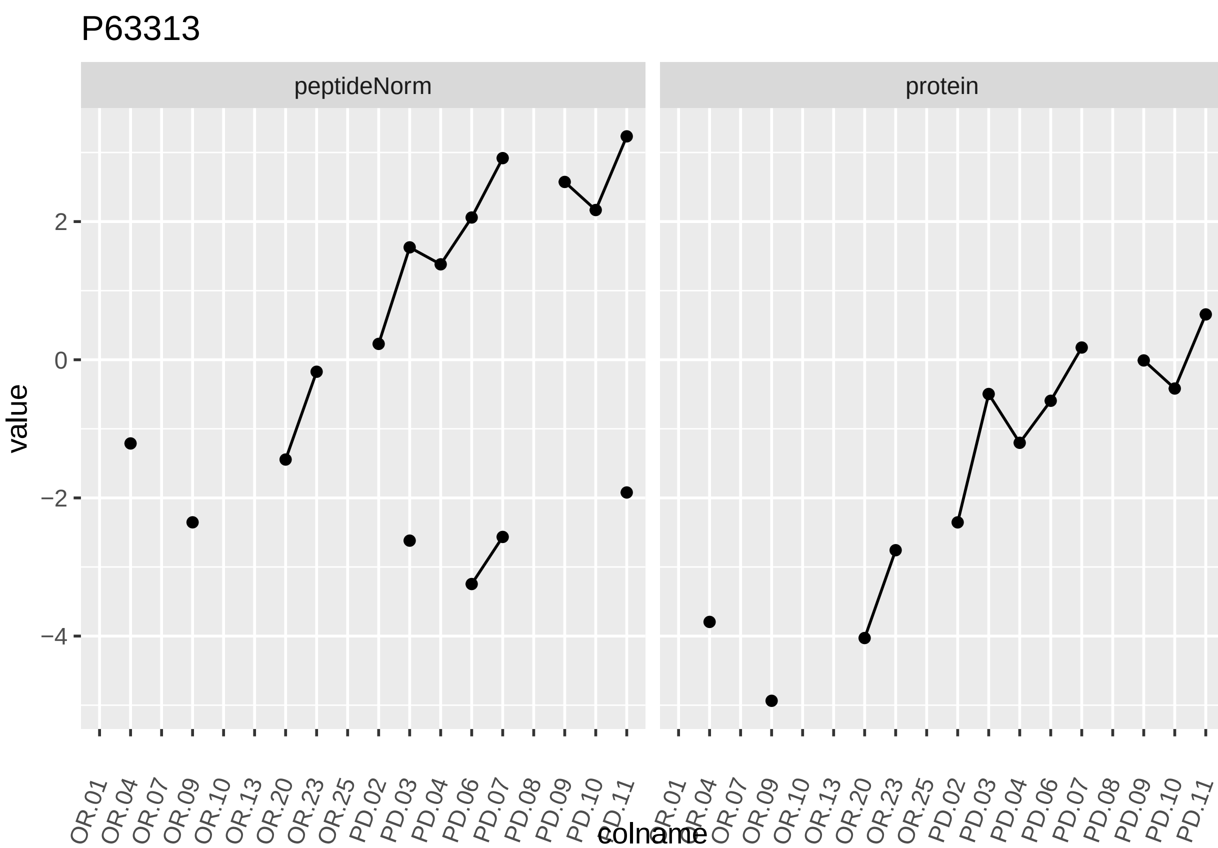


Q8NC51
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
EETQPPVALKK
FDQLFDDESDPFEVLK
Q8NC51
RPDQQLQGEGK
SAAQAAAQTNSNAAGK
SSASAPDVDDPEAFPALA

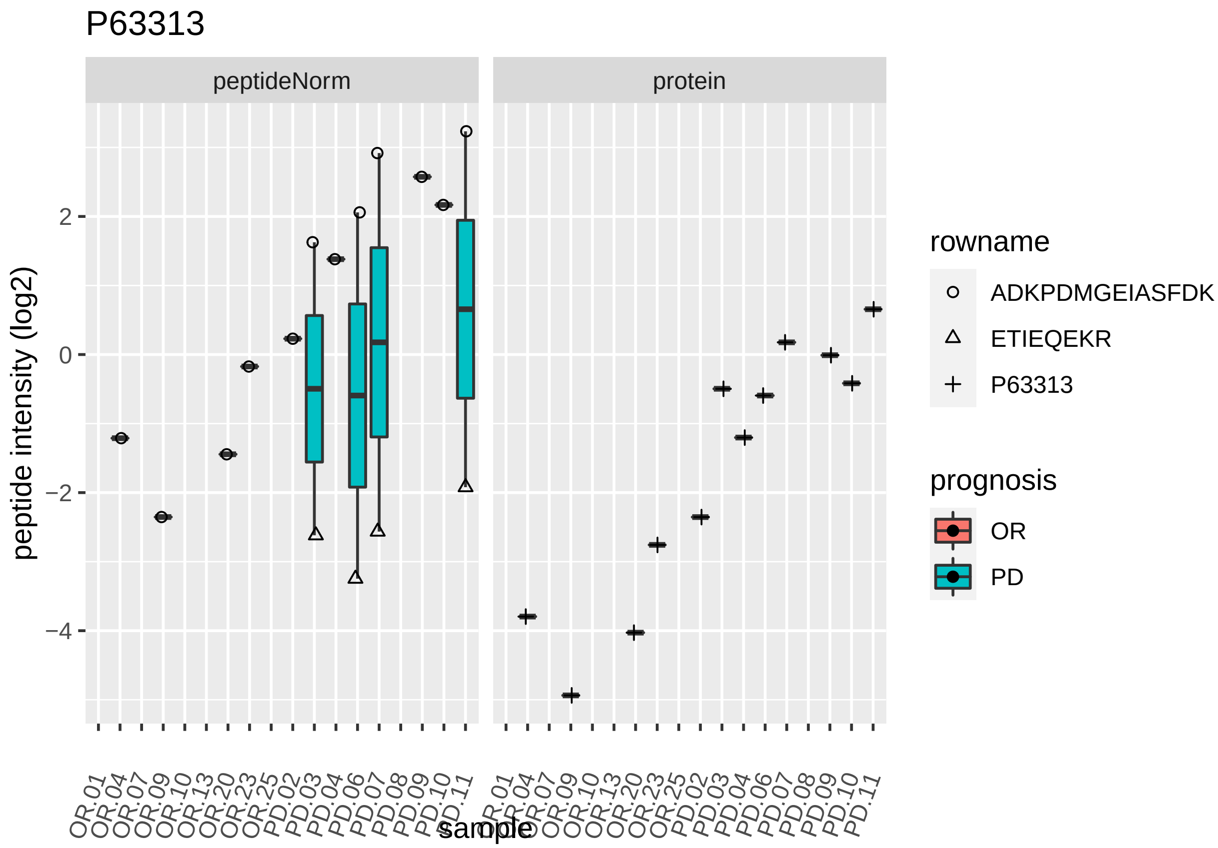


Q9H299
peptideNorm
protein
value
colname
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

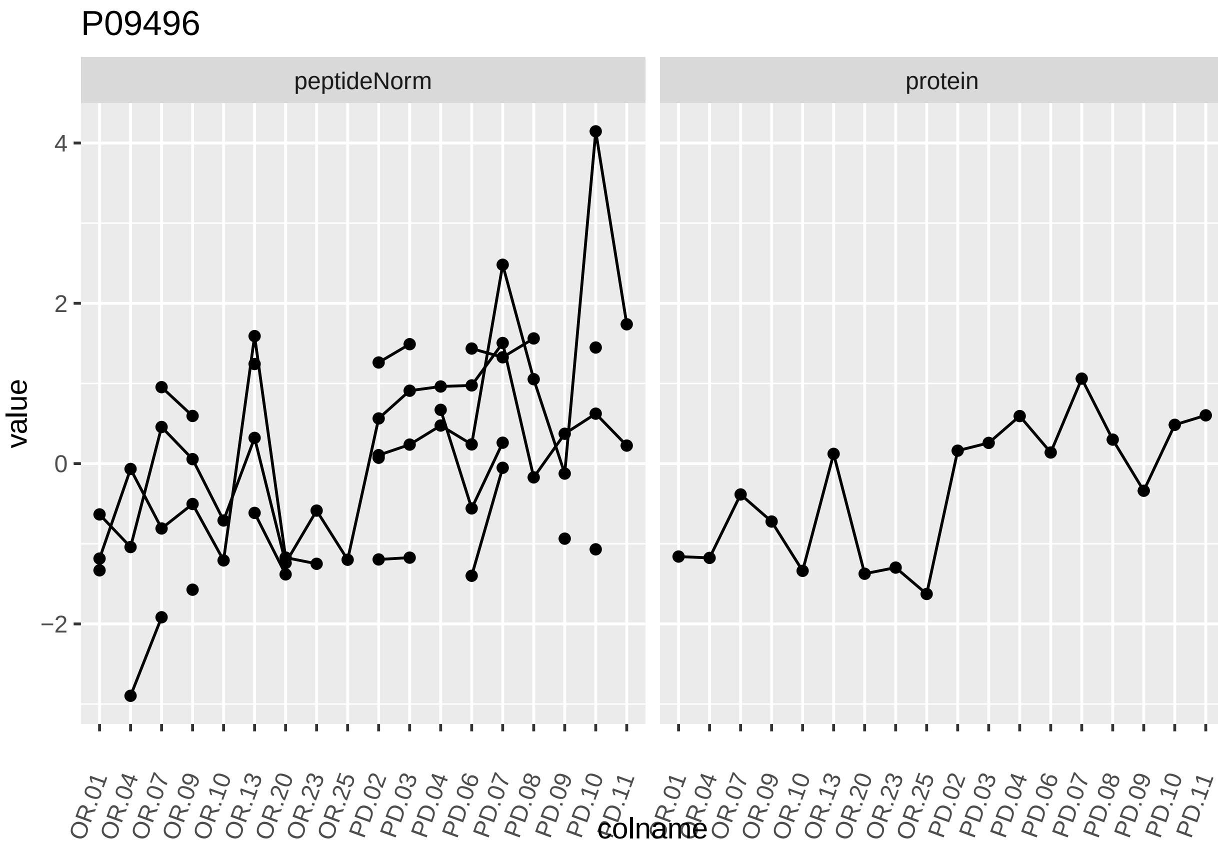

Q9H299
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
IQYQLVDISQDNALR
IQYQLVDISQDNALRDEMR
Q9H299
VYSTSVTGSR
prognosis
OR
PD



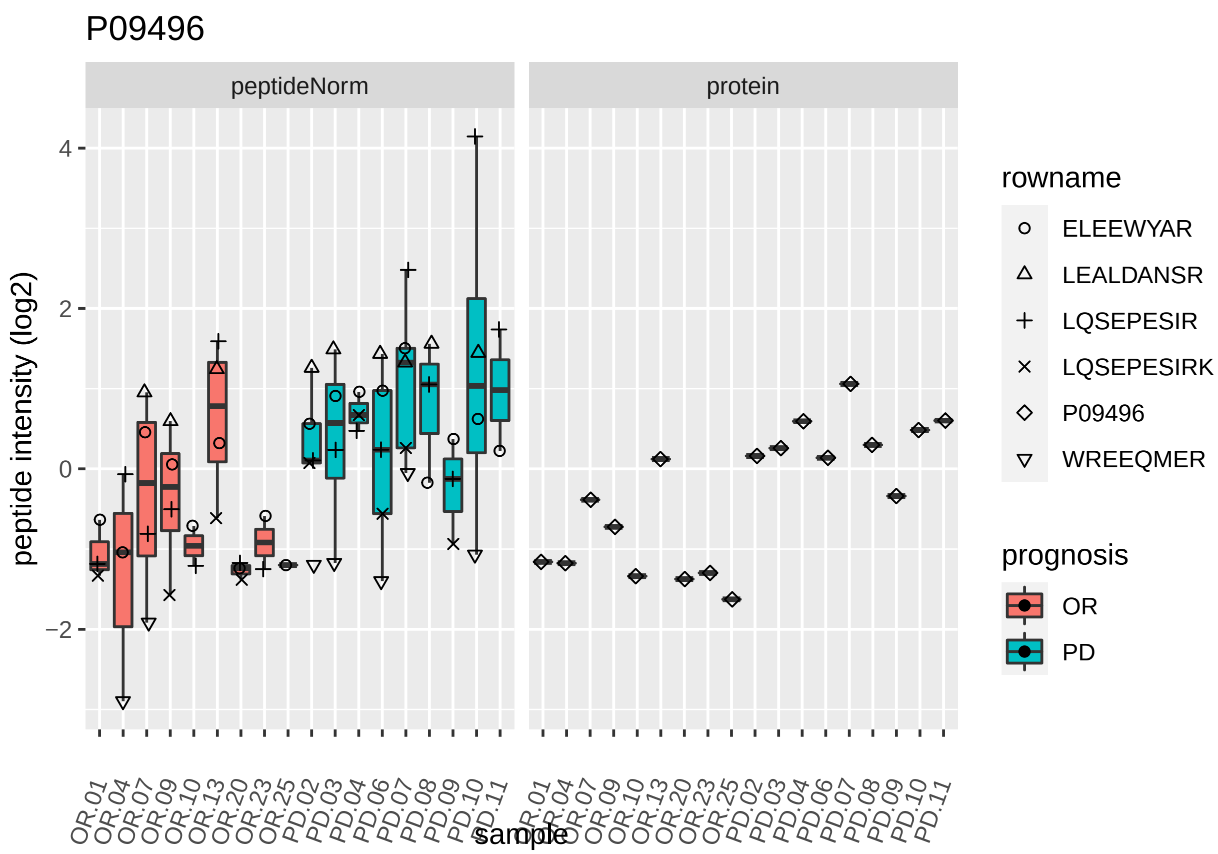
P63313
peptideNorm
protein
value
colname
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



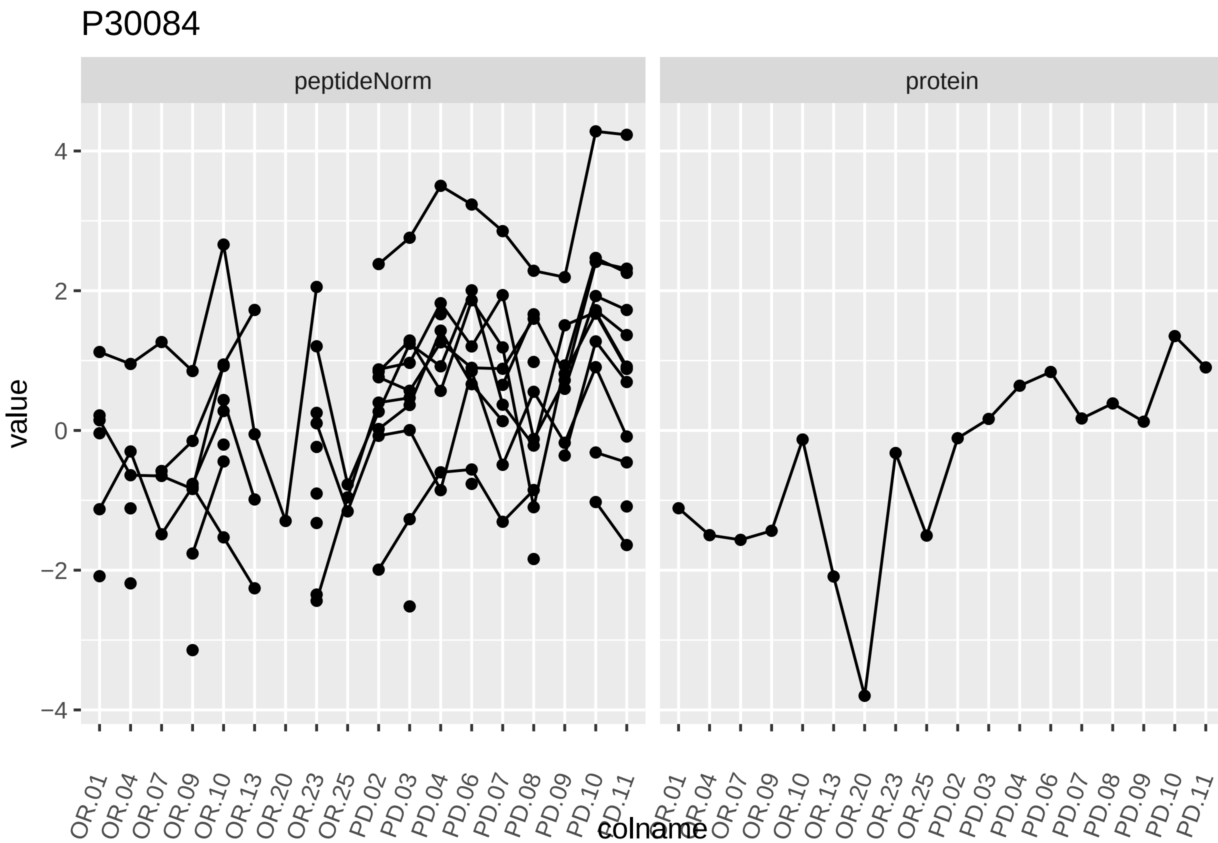
P63313
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ADKPDMGEIASFDK
ETIEQEKR
P63313
prognosis
OR
PD



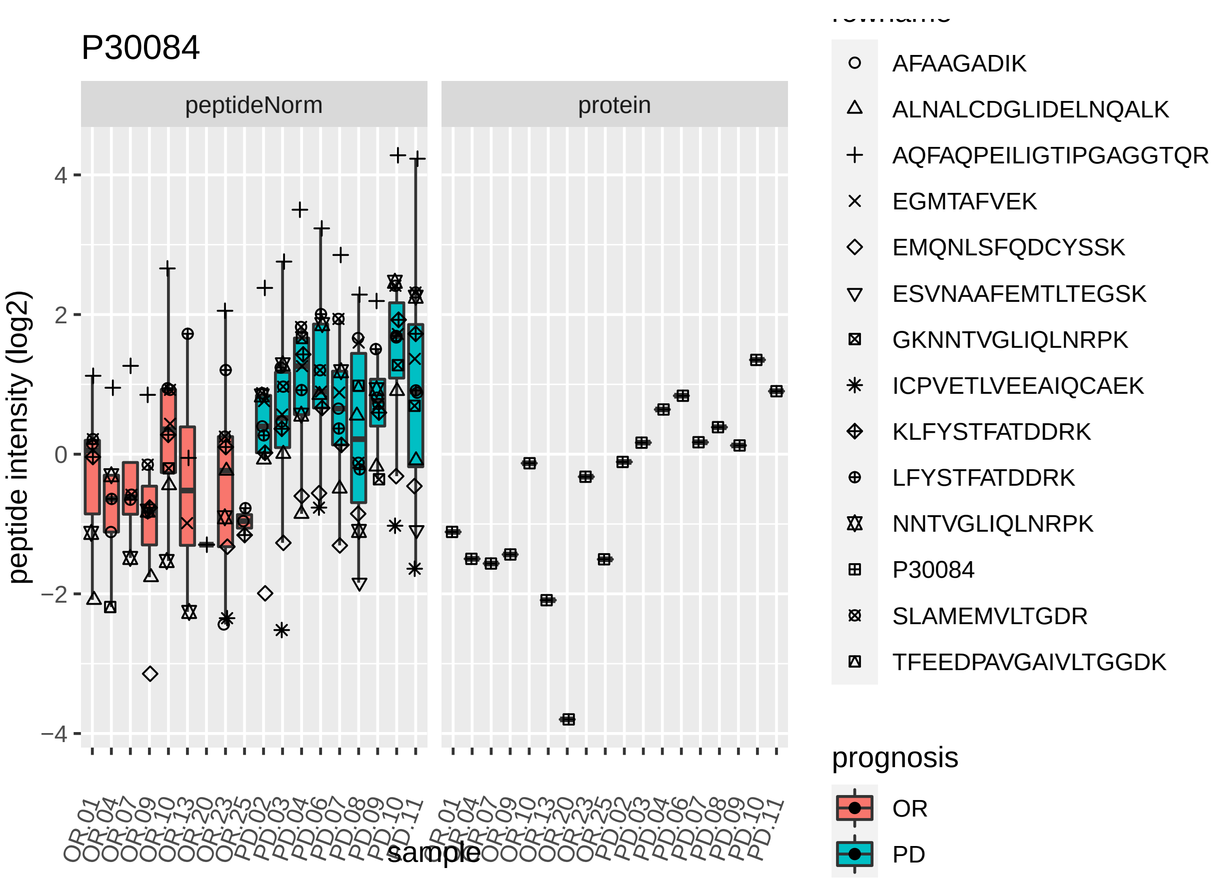
P09496
peptideNorm
protein
value
colname
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



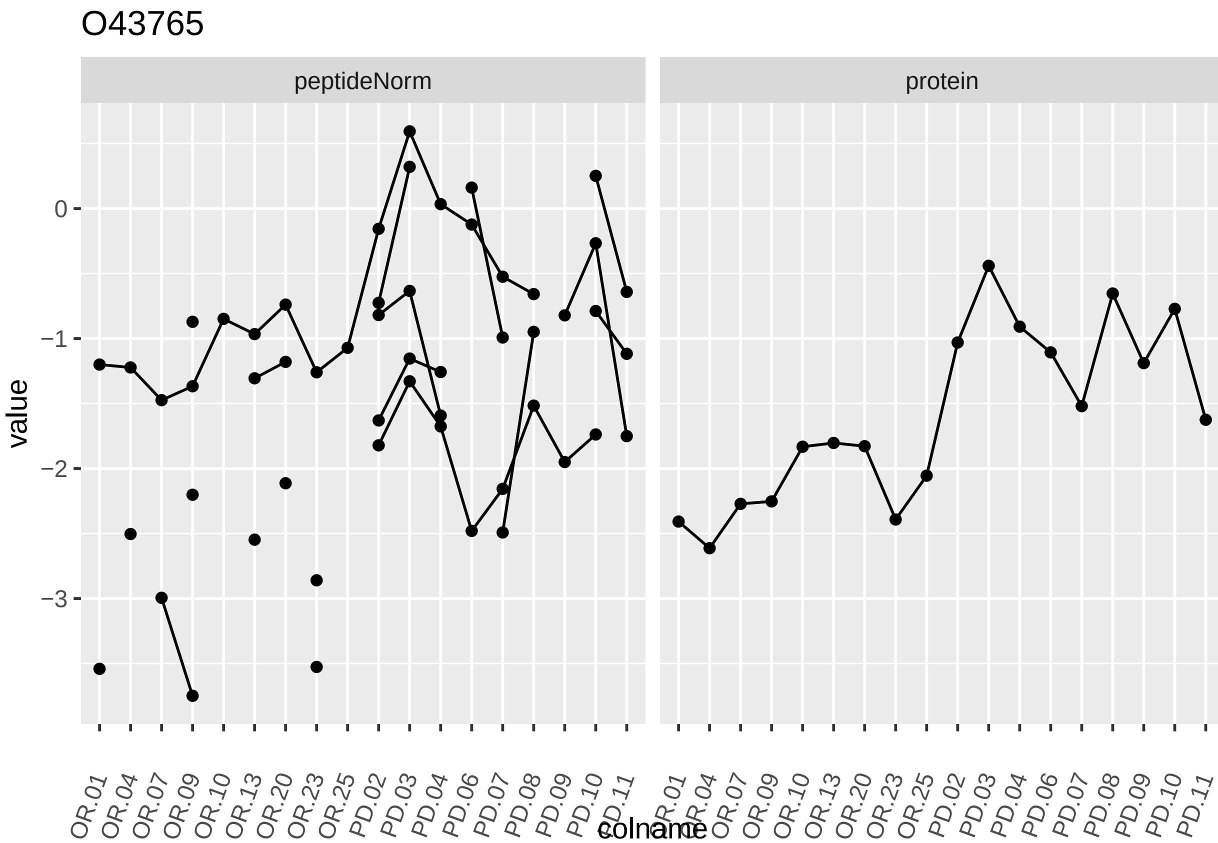
P09496
peptideNorm
protein
peptide intensity (log2)
sample
rowname
ELEEWYAR
LEALDANSR
LQSEPESIR
LQSEPESIRK
P09496
WREEQMER
prognosis
OR
PD



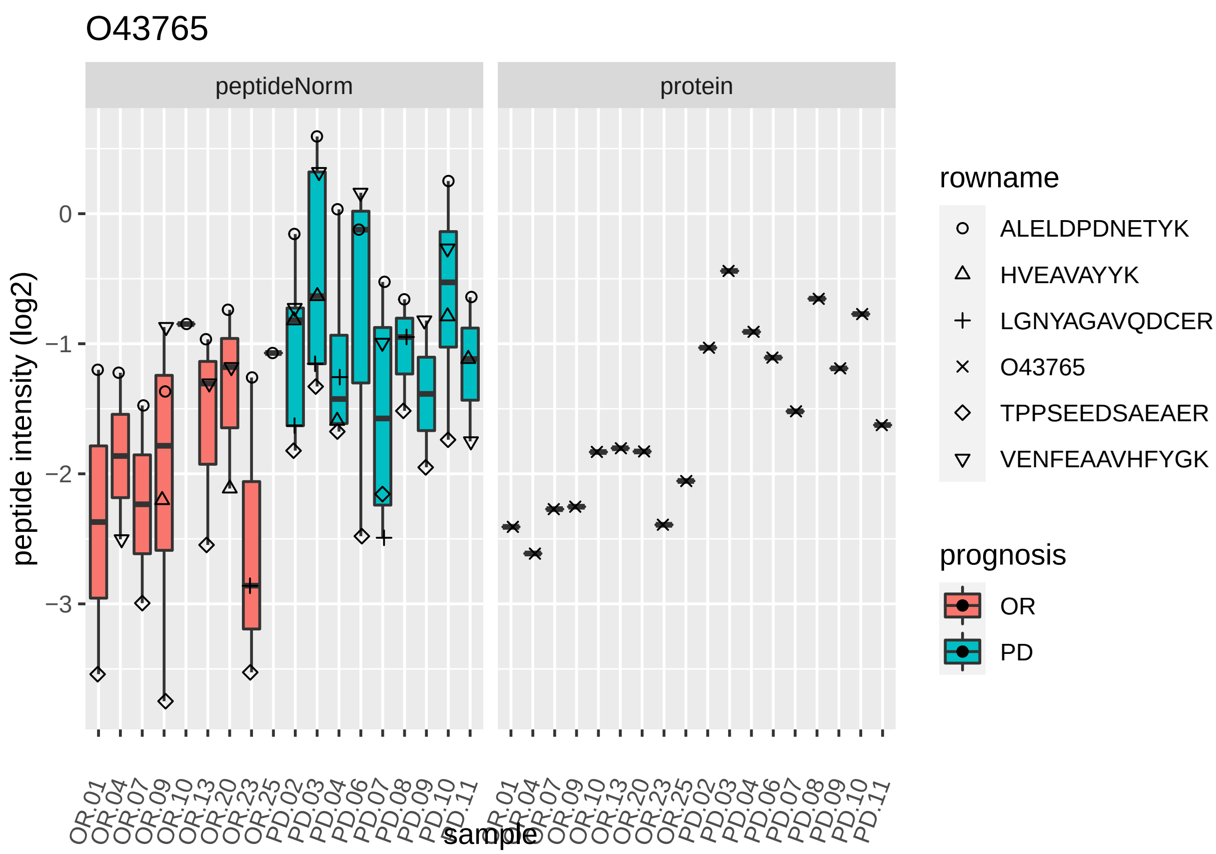
P30084
peptideNorm
protein
value
colname
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



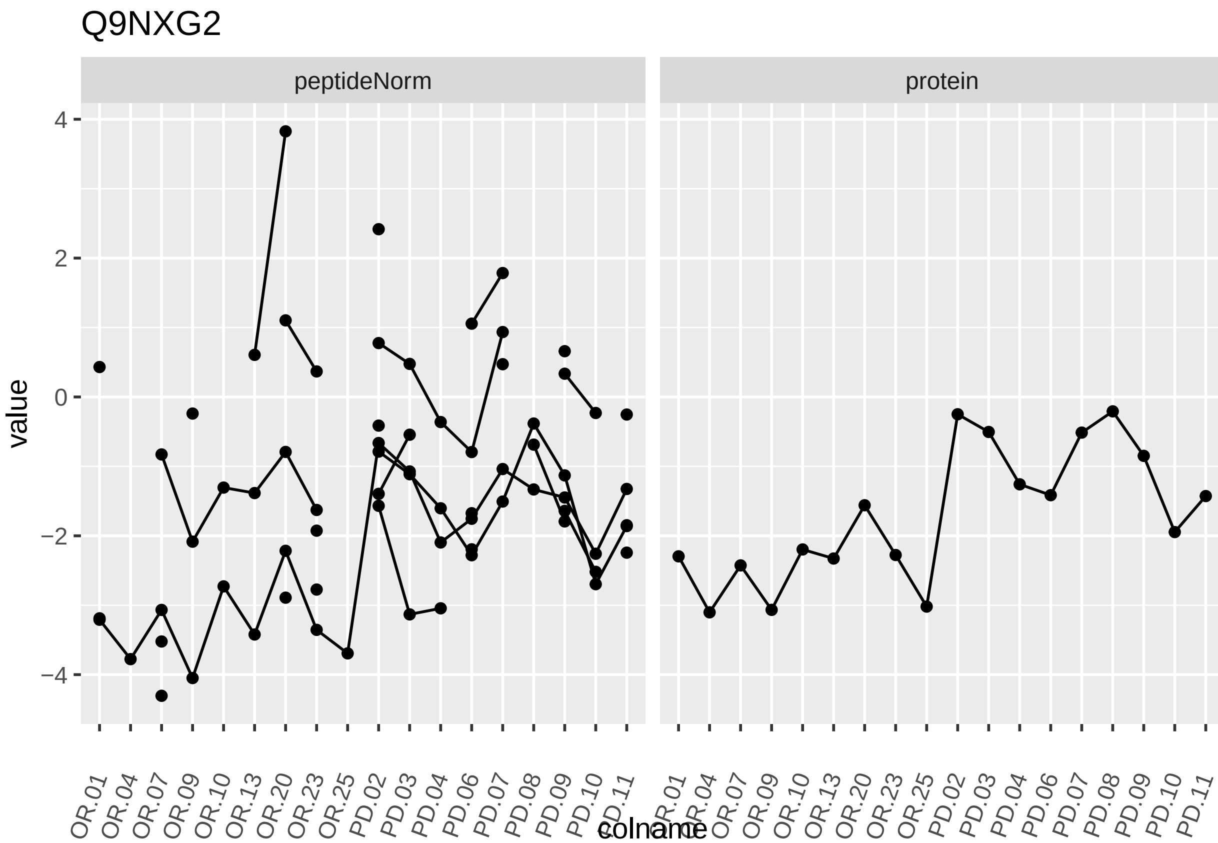
P30084
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
sample
rowname
AFAAGADIK
ALNALCDGLIDELNQALK
AQFAQPEILIGTIPGAGGTQR
EGMTAFVEK
EMQNLSFQDCYSSK
ESVNAAFEMTLTEGSK
GKNNTVGLIQLNRPK
ICPVETLVEEAIQCAEK
KLFYSTFATDDRK
LFYSTFATDDRK
NNTVGLIQLNRPK
P30084
SLAMEMVLTGDR
TFEEDPAVGAIVLTGGDK
prognosis
OR
PD



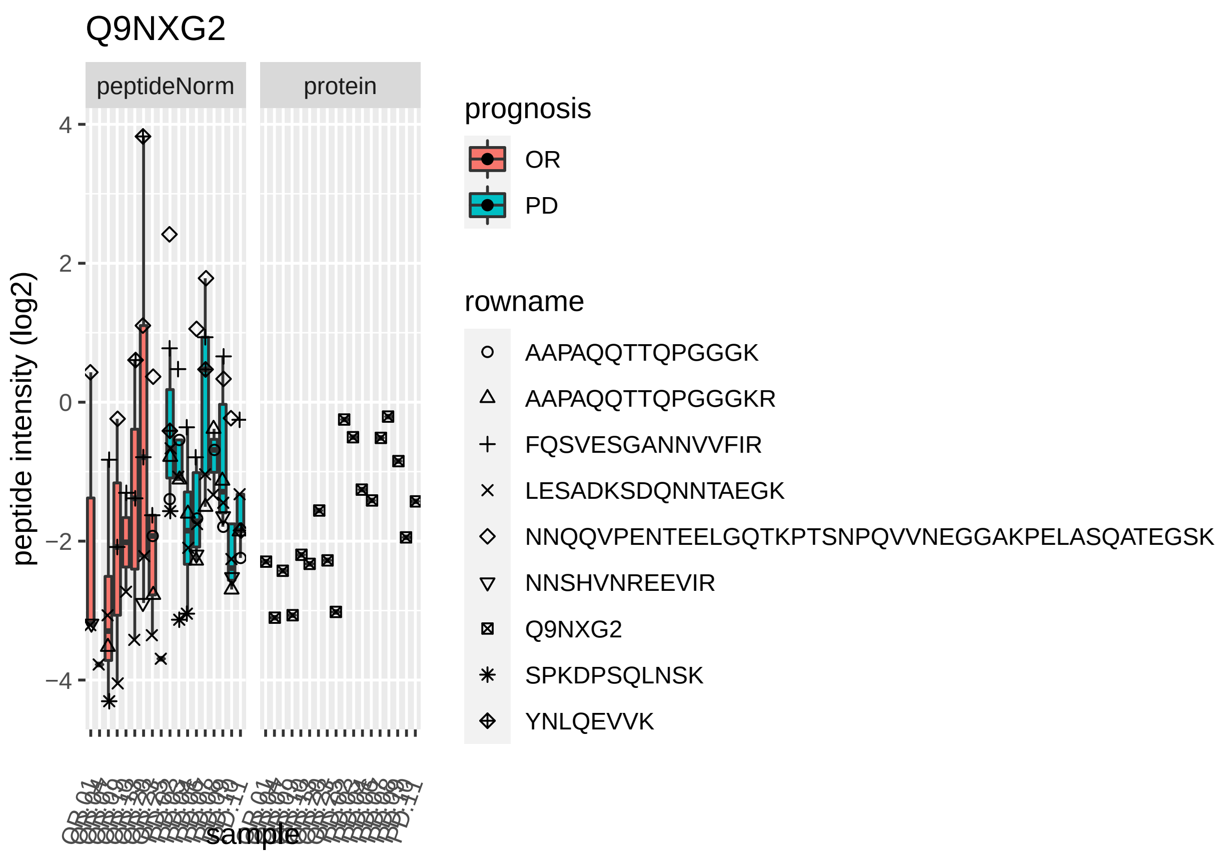
O43765
peptideNorm
protein
value
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname



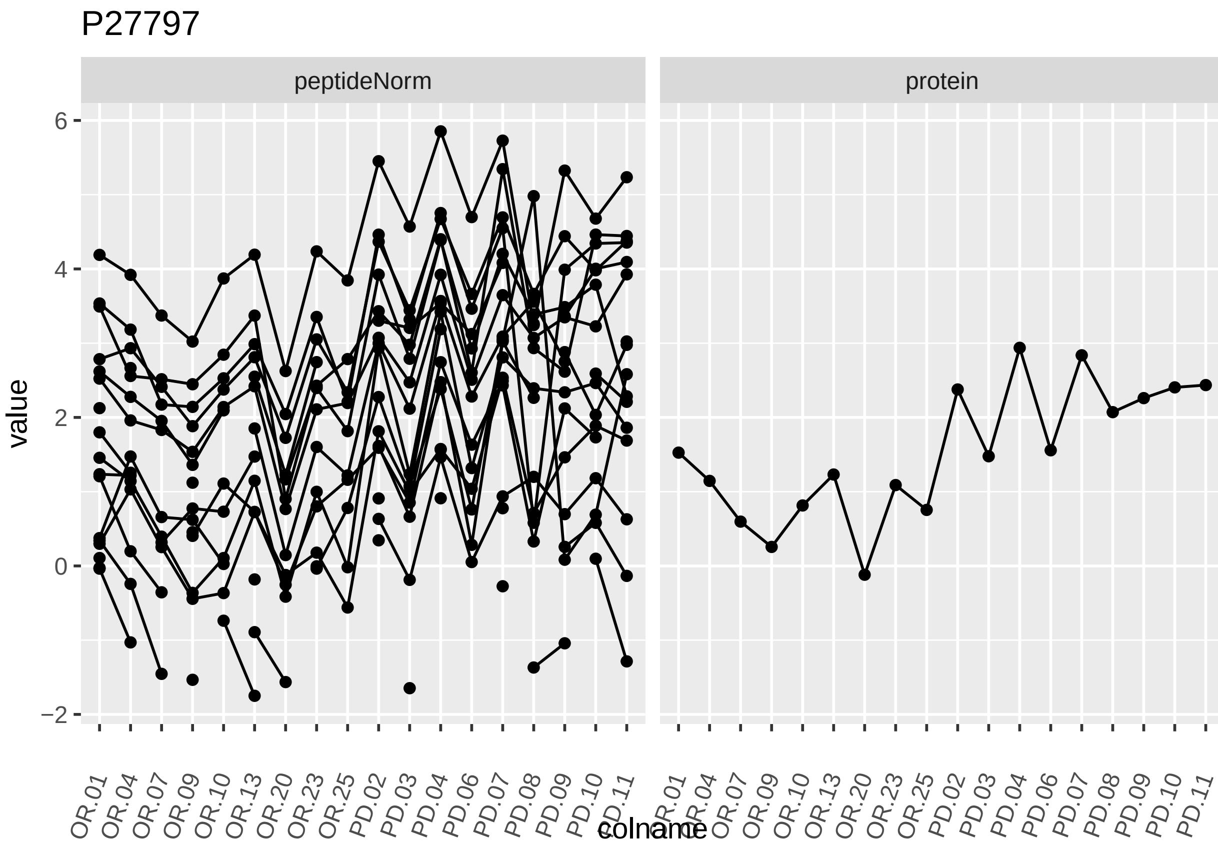
O43765
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ALELDPDNETYK
HVEAVAYYK
LGNYAGAVQDCER
O43765
TPPSEEDSAEAER
VENFEAAVHFYGK
prognosis
OR
PD

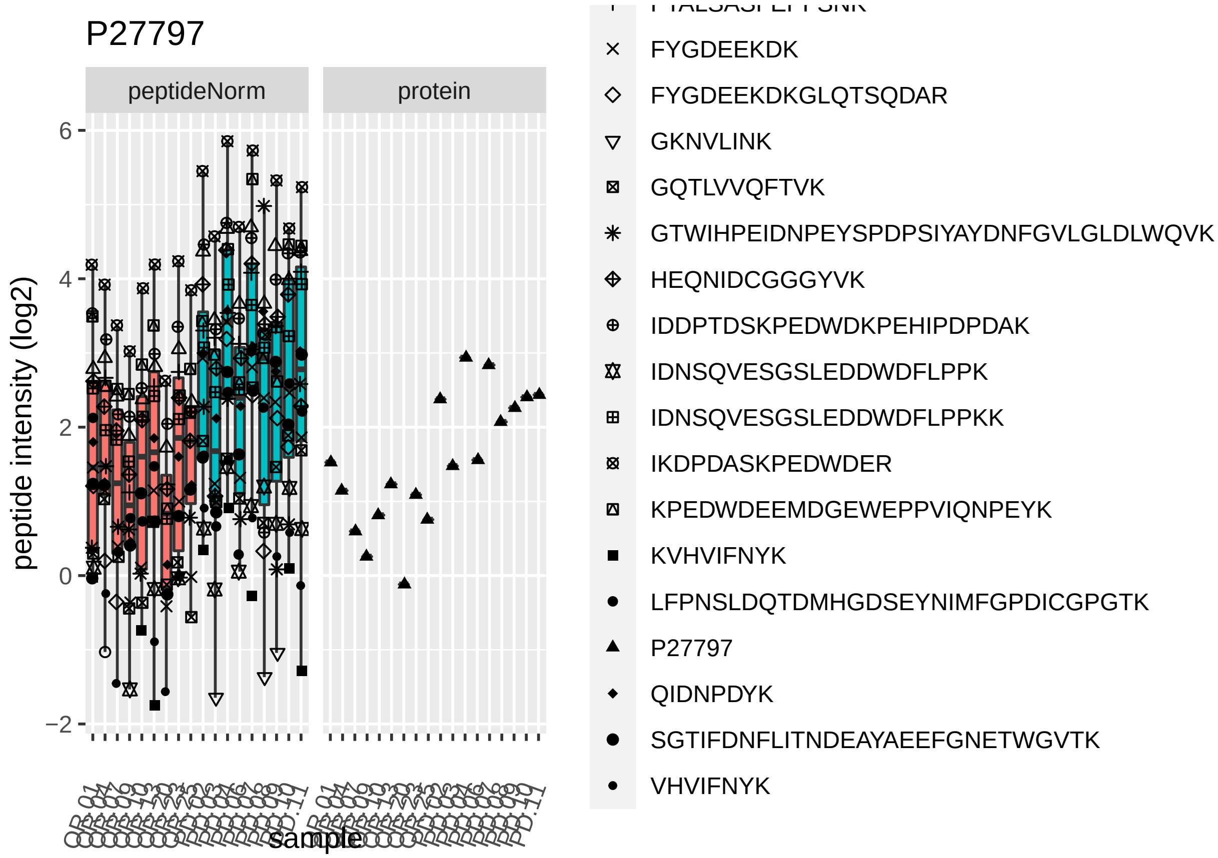


Q9NXG2
peptideNorm
protein
value
colname
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

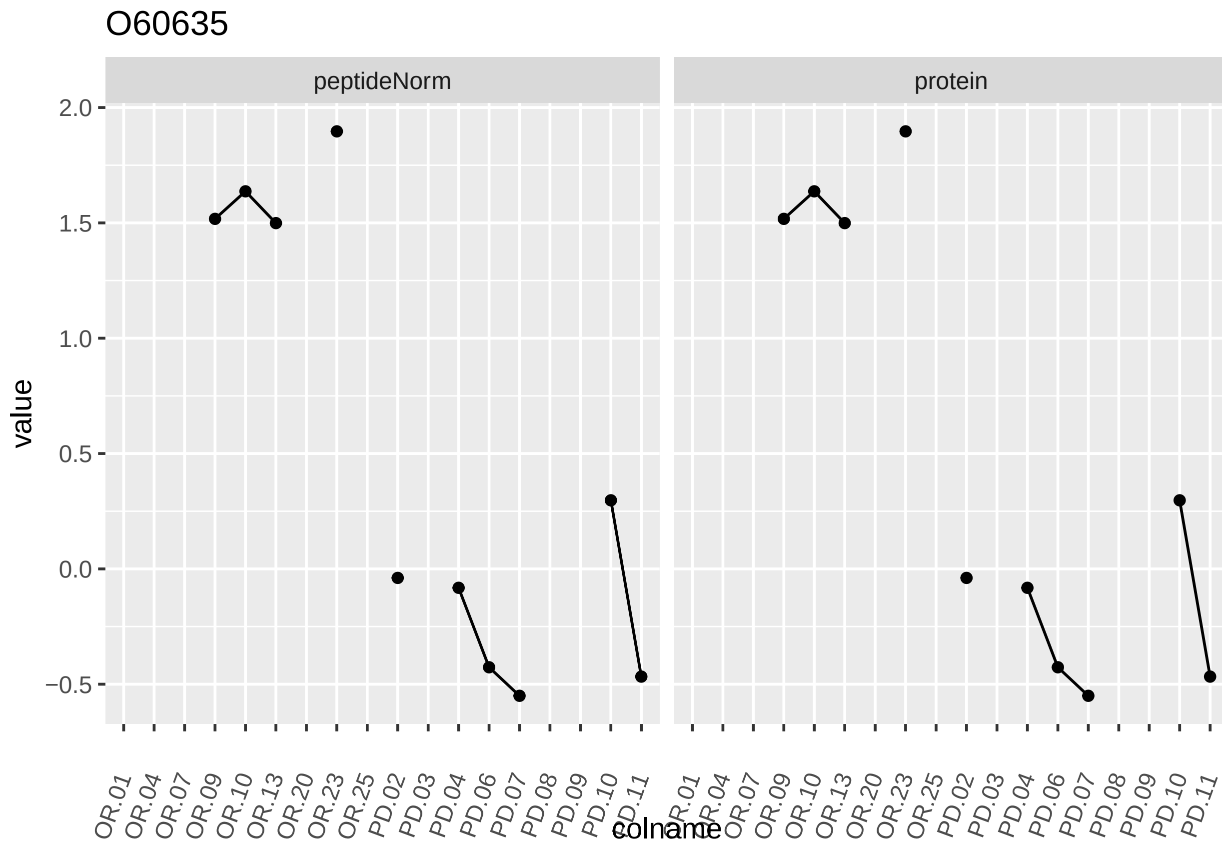


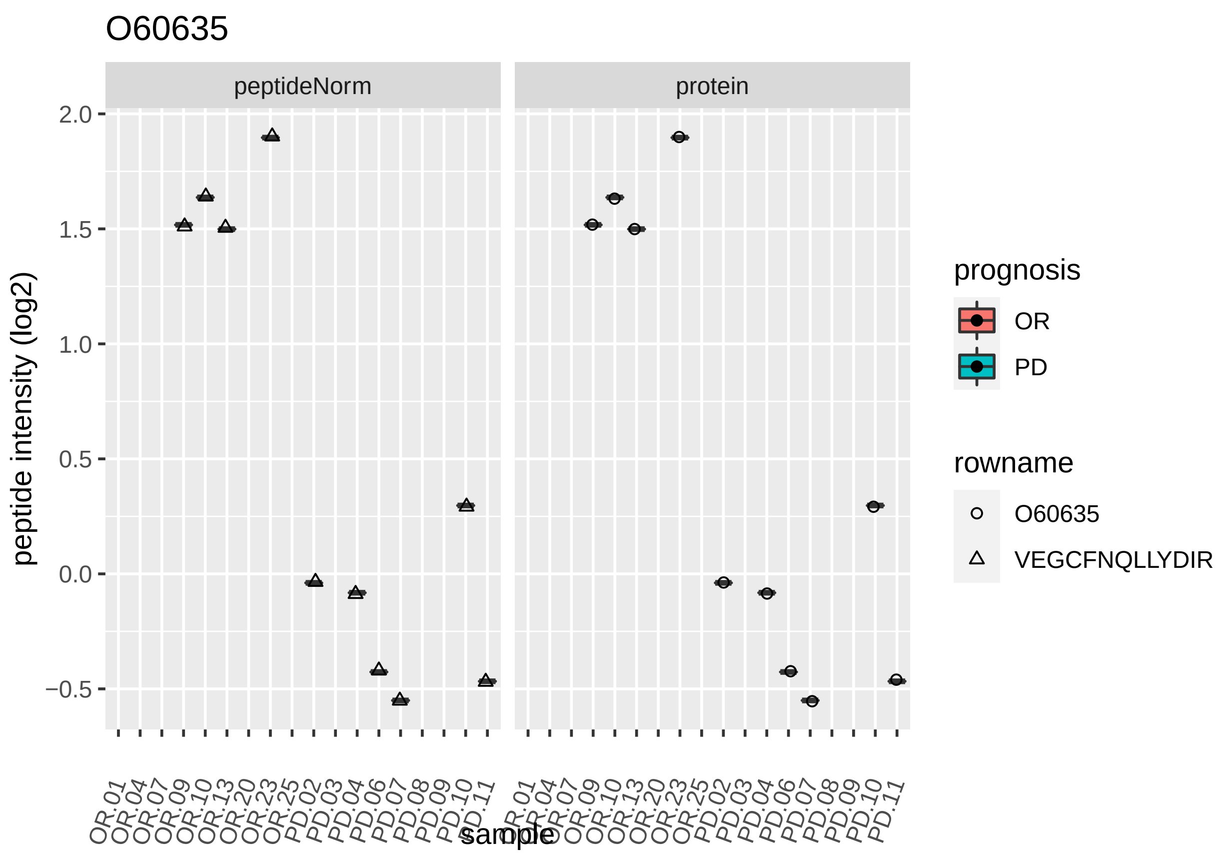
Q9NXG2
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
−4
sample
prognosis
OR
PD
rowname
AAPAQQTTQPGGGK
AAPAQQTTQPGGGKR
FQSVESGANNVVFIR
LESADKSDQNNTAEGK
NNQQVPENTEELGQTKPTSNPQVVNEGGAKPELASQATEGSK
NNSHVNREEVIR
Q9NXG2
SPKDPSQLNSK
YNLQEVVK

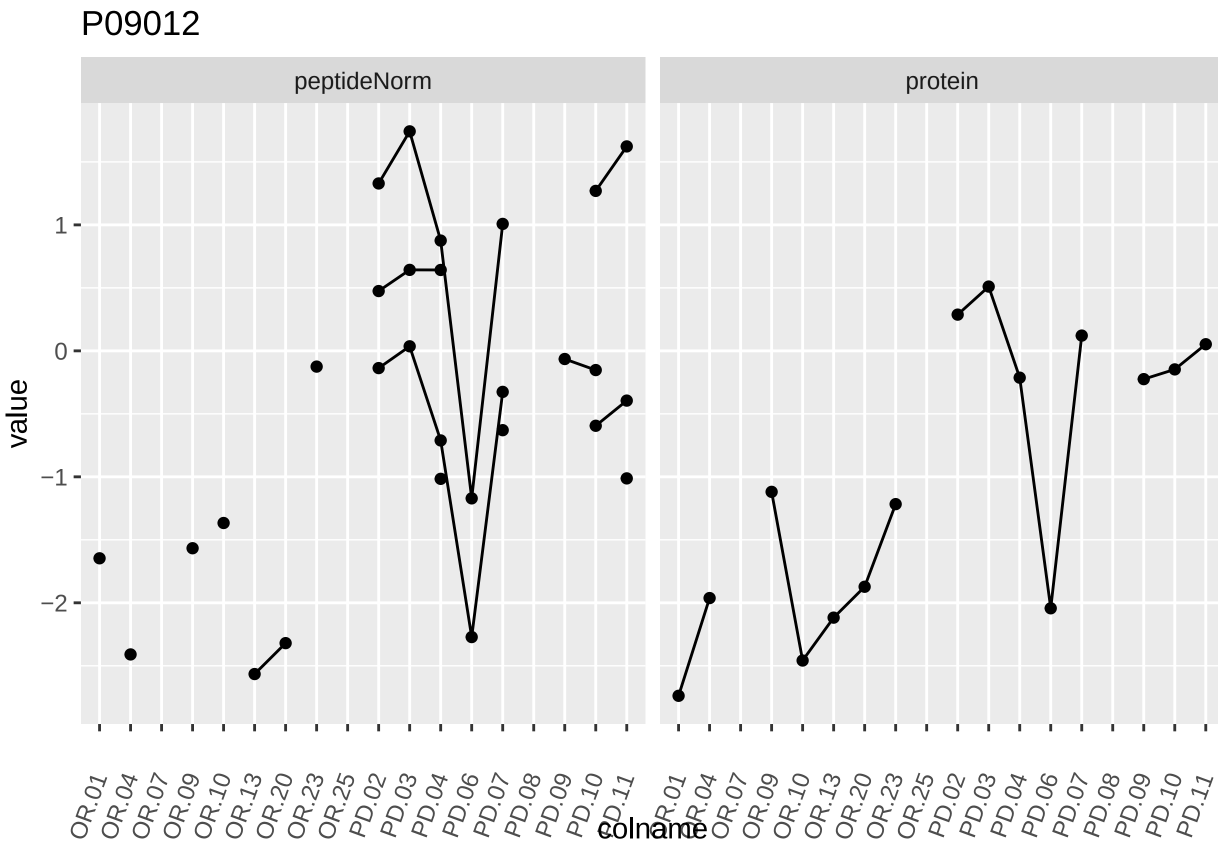

P27797
peptideNorm
protein
value
colname
6
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

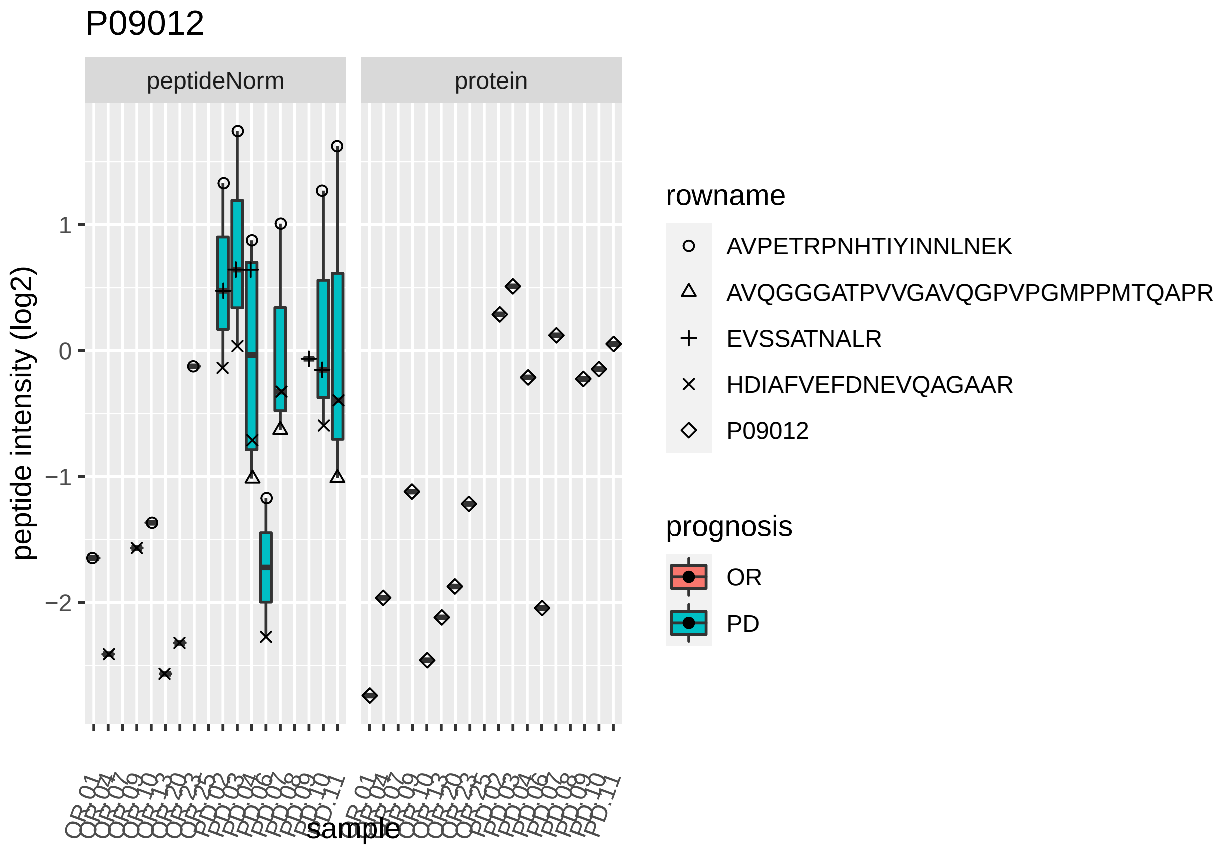


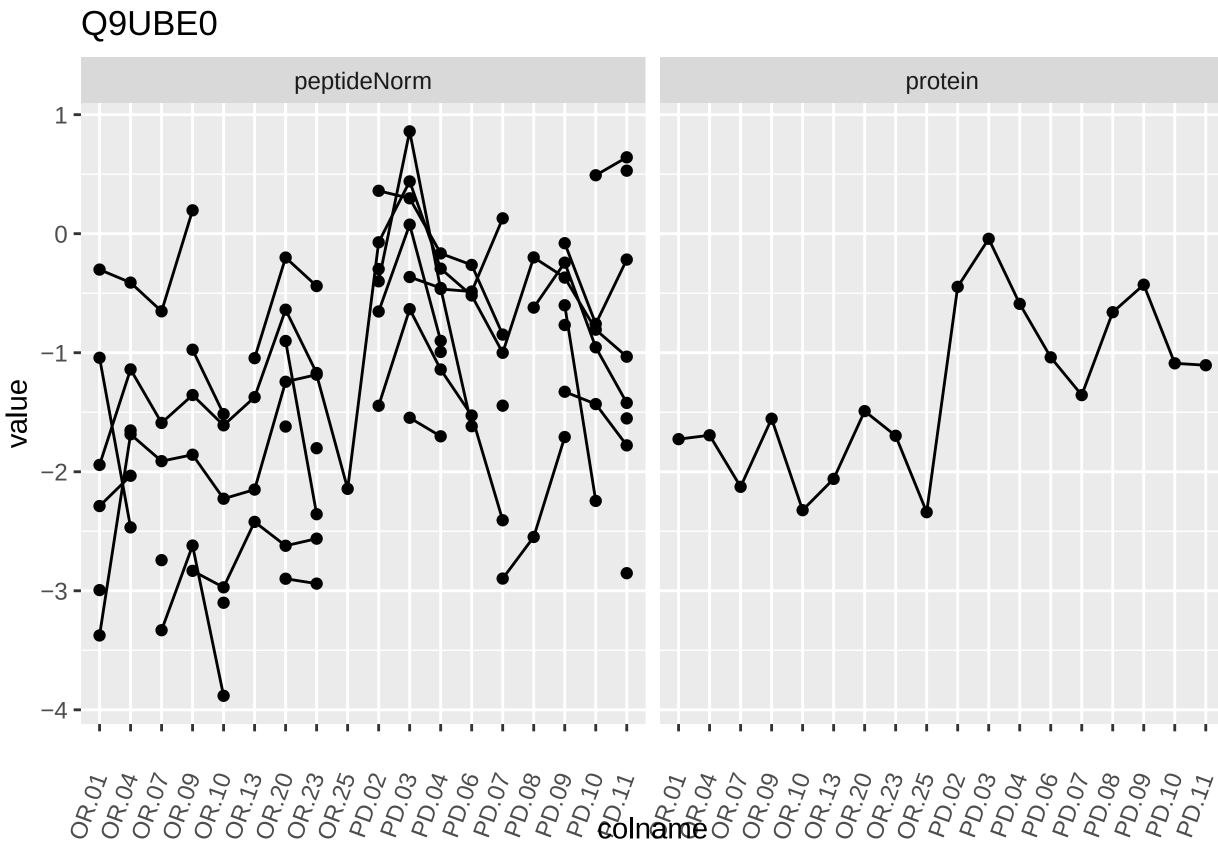
P27797
peptideNorm
protein
peptide intensity (log2)
sample
FYGDEEKDK
FYGDEEKDKGLQTSQDAR
GKNVLINK
GQTLVVQFTVK
GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK
HEQNIDCGGGYVK
IDDPTDSKPEDWDKPEHIPDPDAK
IDNSQVESGSLEDDWDFLPPK
IDNSQVESGSLEDDWDFLPPKK
IKDPDASKPEDWDER
KPEDWDEEMDGEWEPPVIQNPEYK
KVHVIFNYK
LFPNSLDQTDMHGDSEYNIMFGPDICGPGTK
P27797
QIDNPDYK
SGTIFDNFLITNDEAYAEEFGNETWGVTK
VHVIFNYK


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

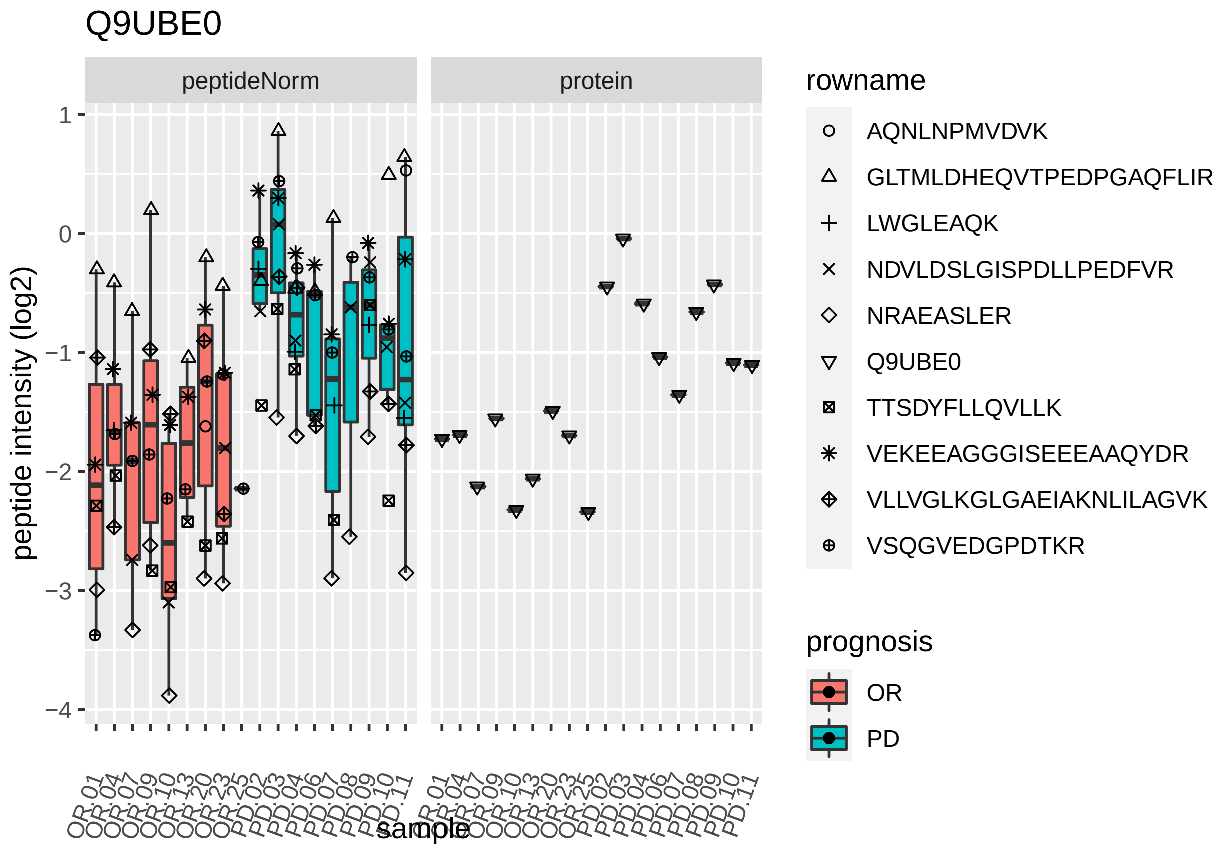

O60635
peptideNorm
protein
peptide intensity (log2)
2.0
1.5
1.0
0.5
0.0
−0.5
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
O60635
VEGCFNQLLYDIR

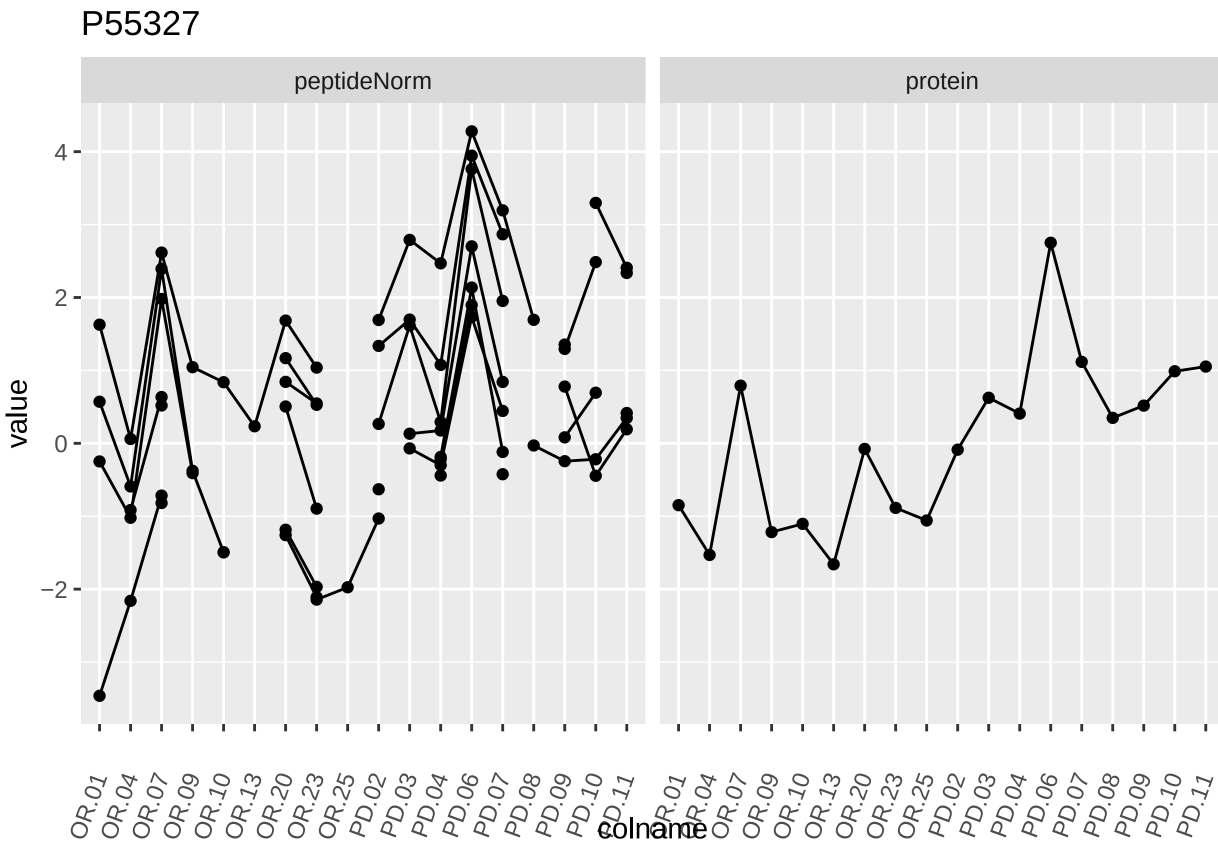

P09012
peptideNorm
protein
value
colname
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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

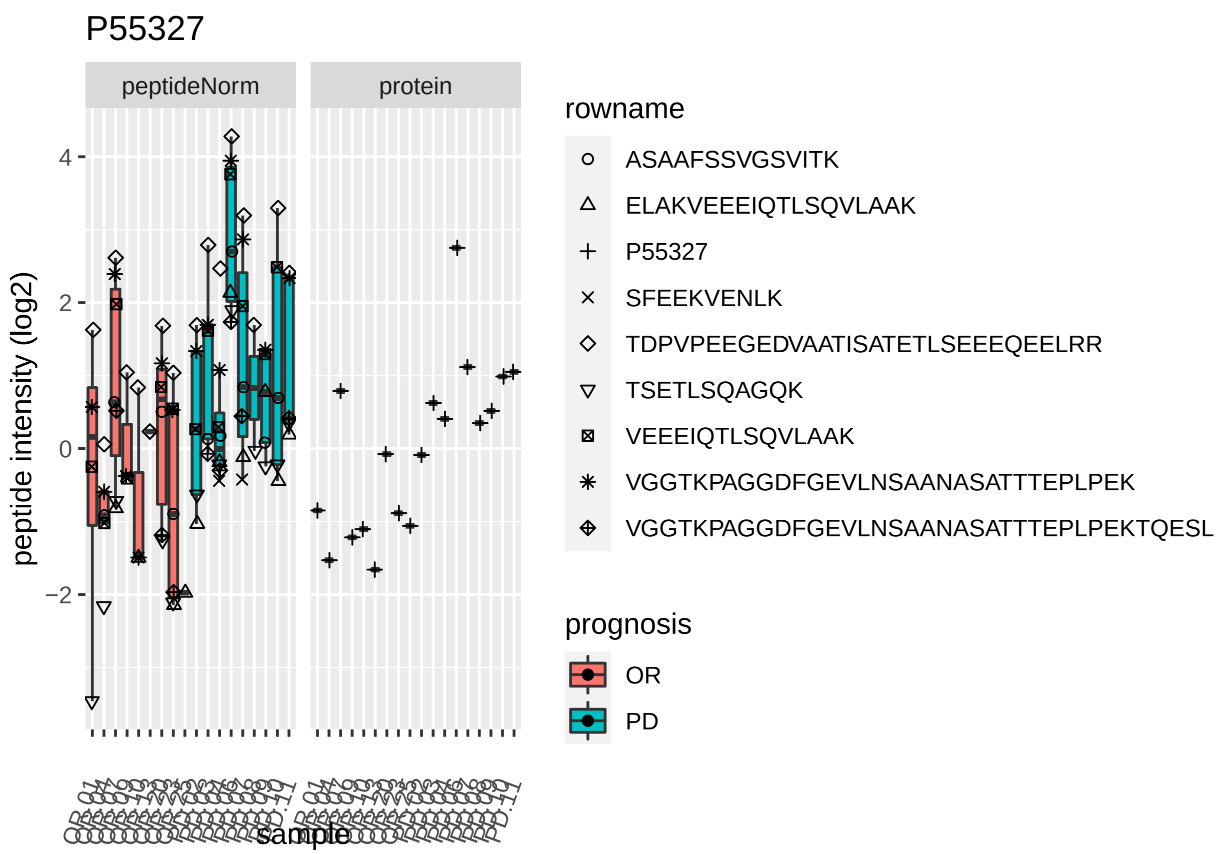


Q9UBE0
peptideNorm
protein
value
colname
1
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

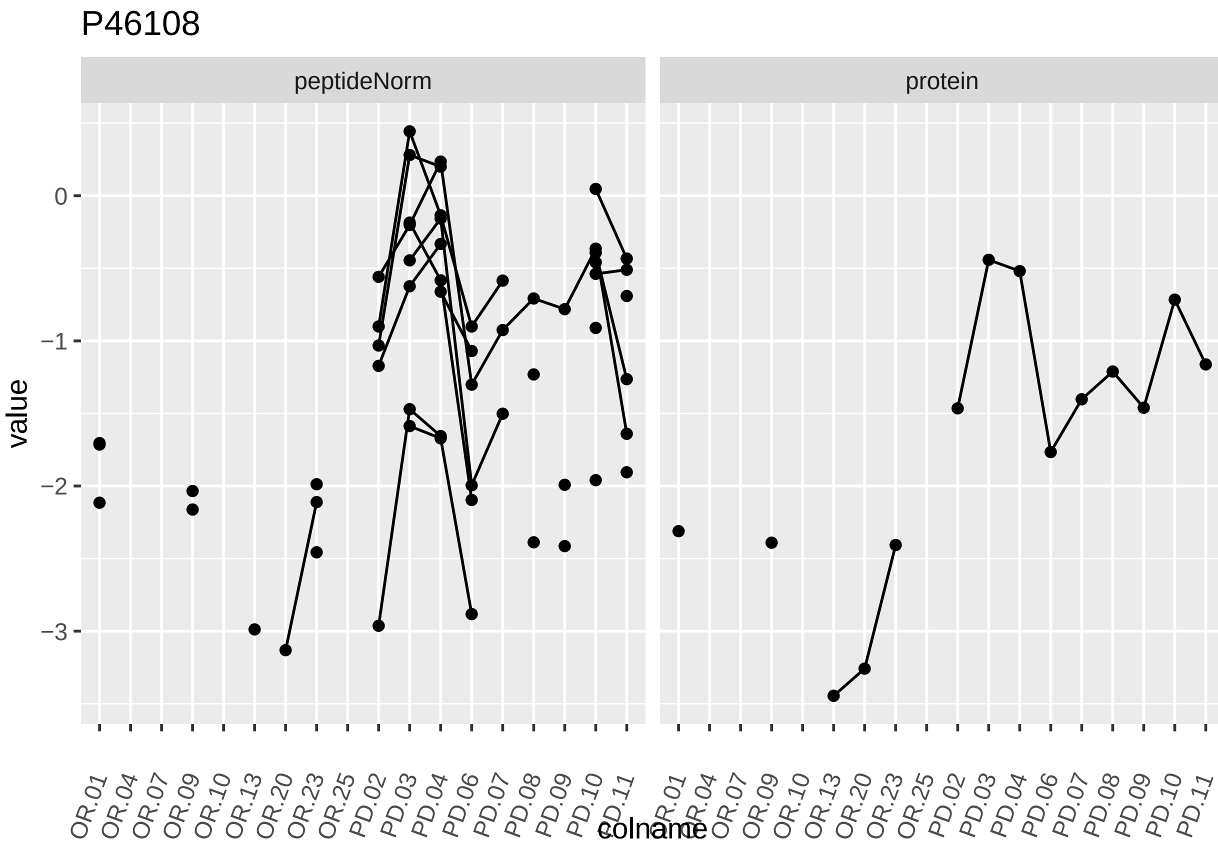

Q9UBE0
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
−4
sample
rowname
AQNLNPMVDVK
GLTMLDHEQVTPEDPGAQFLIR
LWGLEAQK
NDVLDSLGISPDLLPEDFVR
NRAEASLER
Q9UBE0
TTSDYFLLQVLLK
VEKEEAGGGISEEEAAQYDR
VLLVGLKGLGAEIAKNLILAGVK
VSQGVEDGPDTKR
prognosis
OR
PD



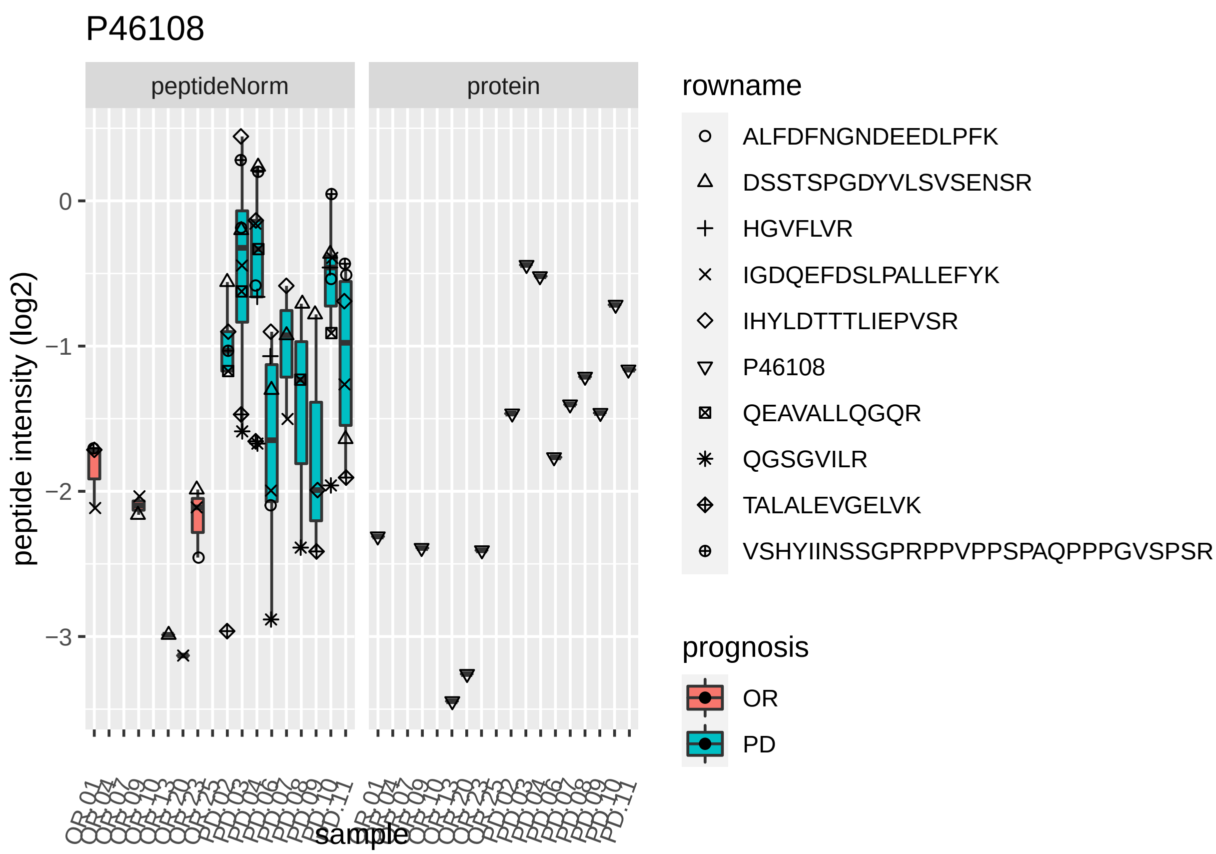
P55327
peptideNorm
protein
value
colname
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

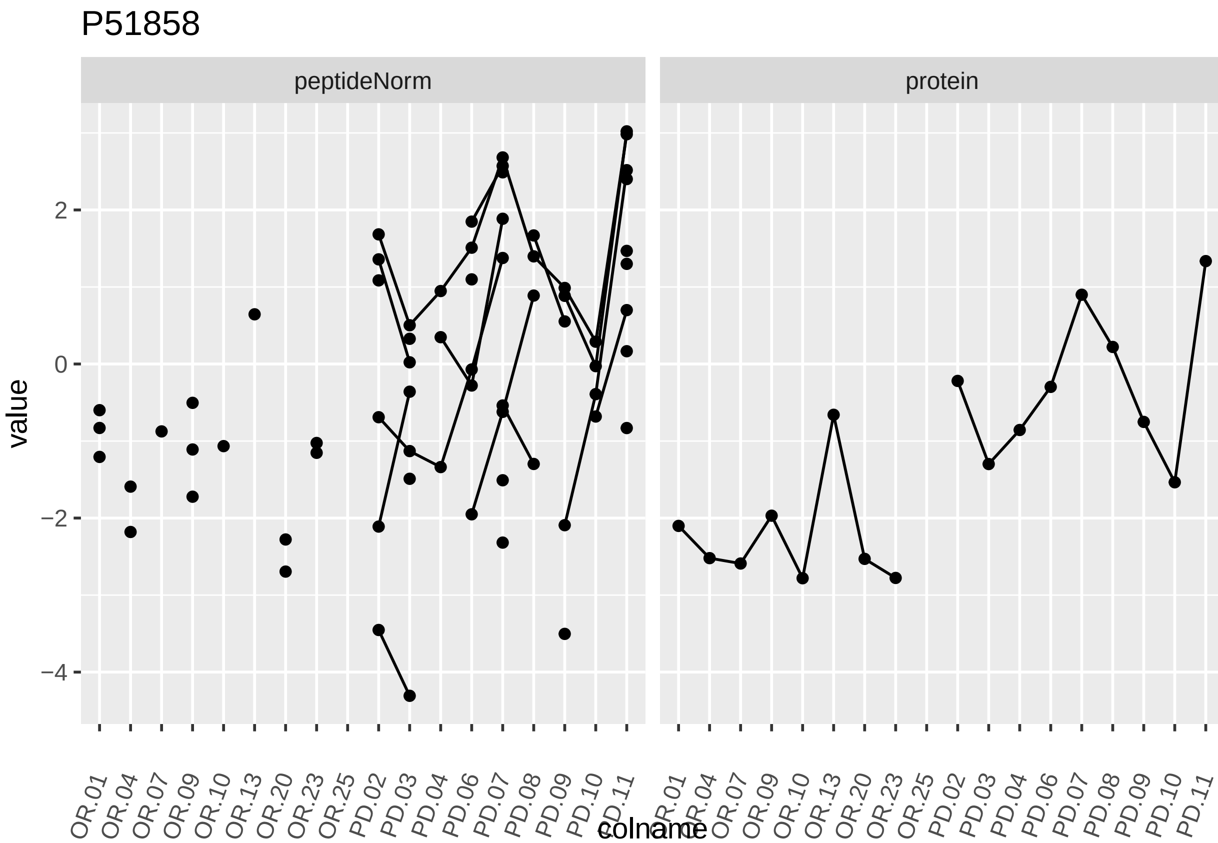


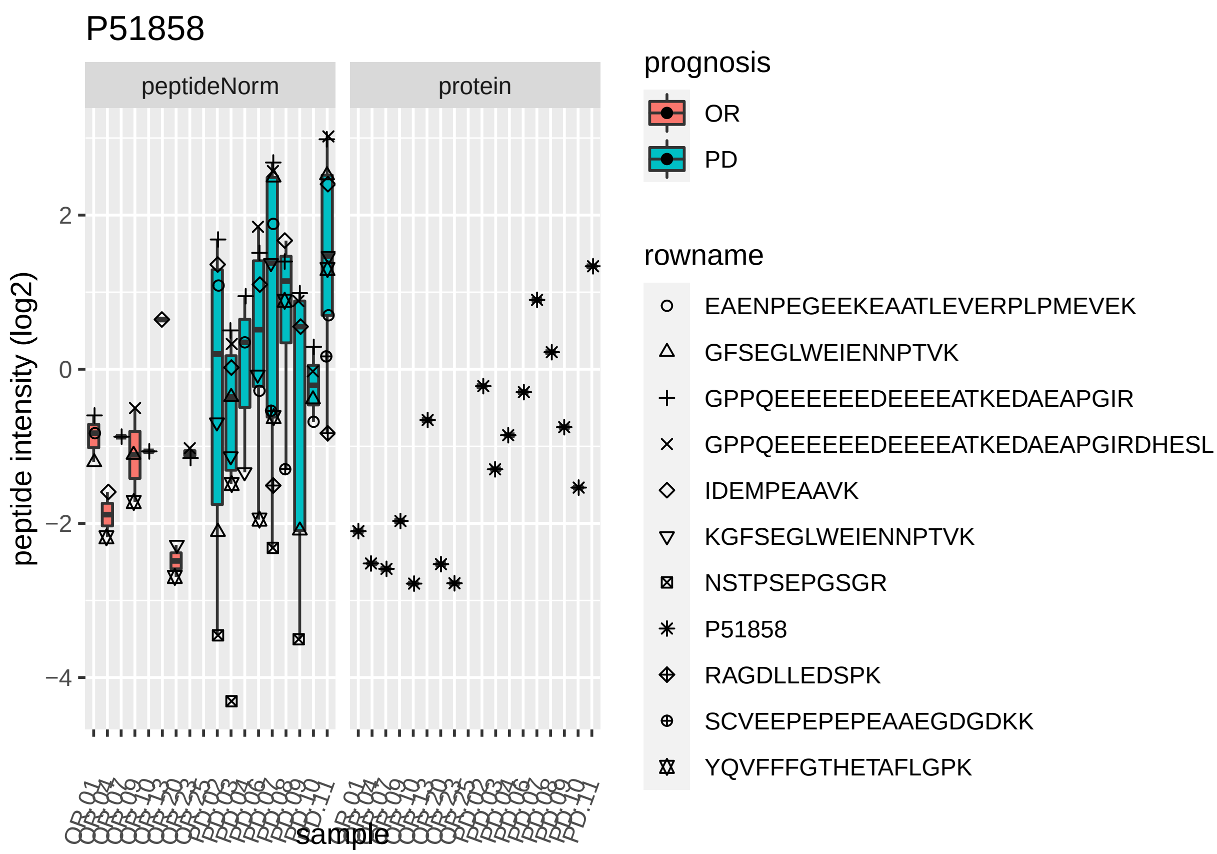
P55327
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
sample
rowname
ASAAFSSVGSVITK
ELAKVEEEIQTLSQVLAAK
P55327
SFEEKVENLK
TDPVPEEGEDVAATISATETLSEEEQEELRR
TSETLSQAGQK
VEEEIQTLSQVLAAK
VGGTKPAGGDFGEVLNSAANASATTTEPLPEK
VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL
prognosis
OR
PD



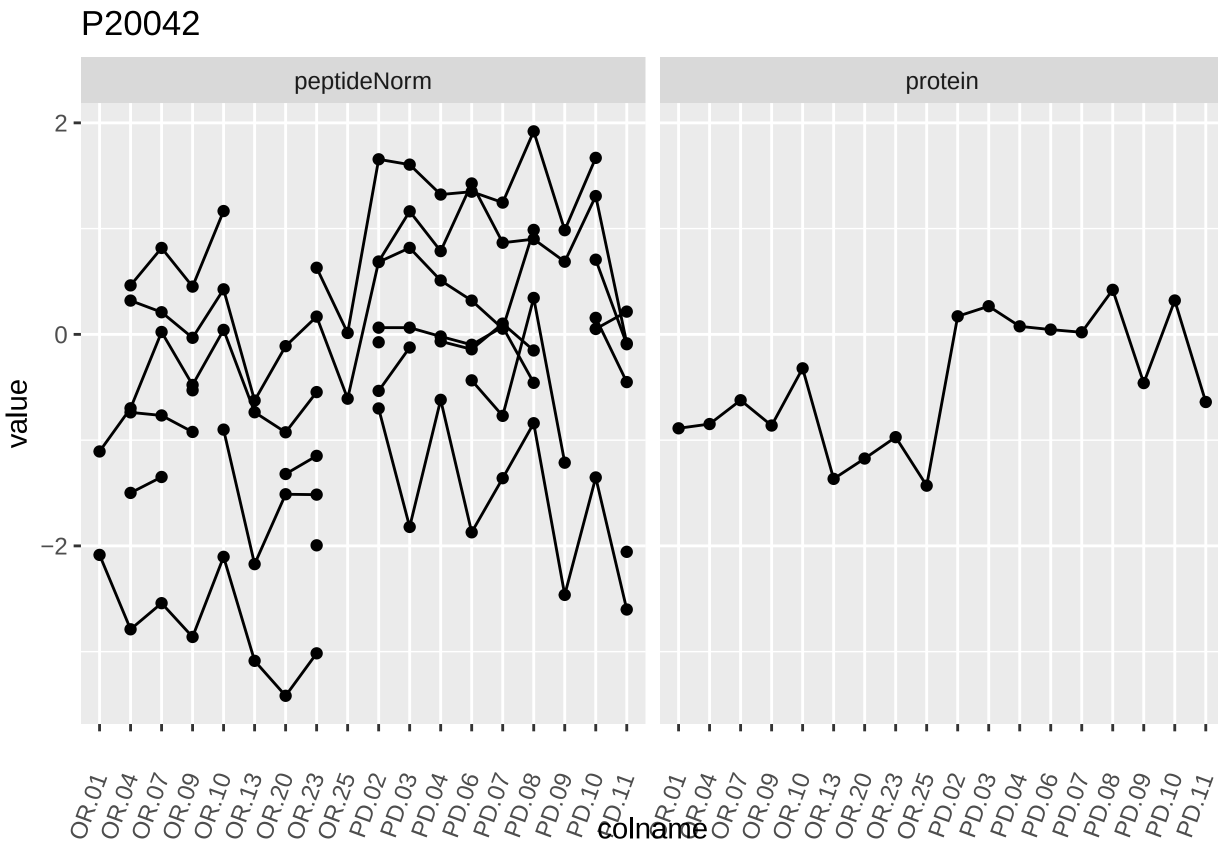
P46108
peptideNorm
protein
value
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

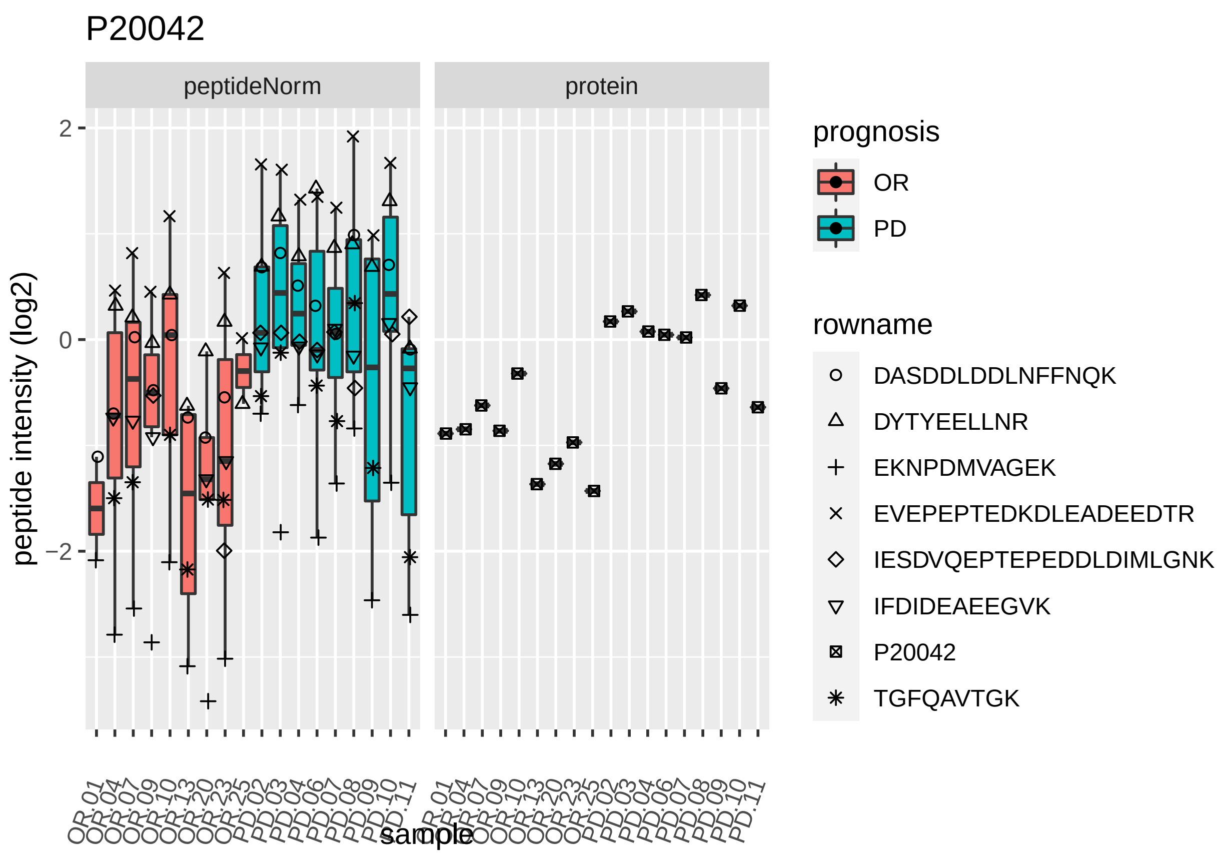

P46108
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
rowname
ALFDFNGNDEEDLPFK
DSSTSPGDYVLSVSENSR
HGVFLVR
IGDQEFDSLPALLEFYK
IHYLDTTTLIEPVSR
P46108
QEAVALLQGQR
QGSGVILR
TALALEVGELVK
VSHYIINSSGPRPPVPPSPAQPPPGVSPSR
prognosis
OR
PD

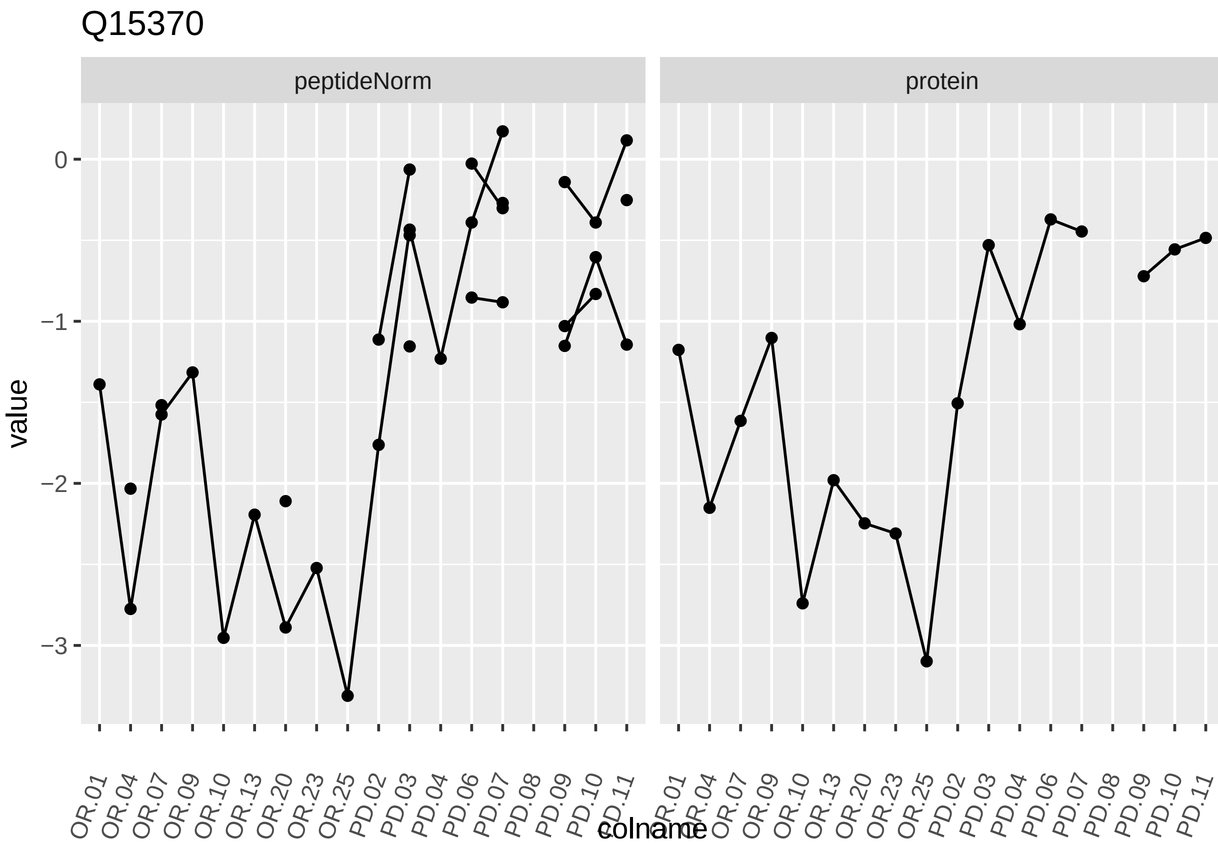

P51858
peptideNorm
protein
value
colname
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

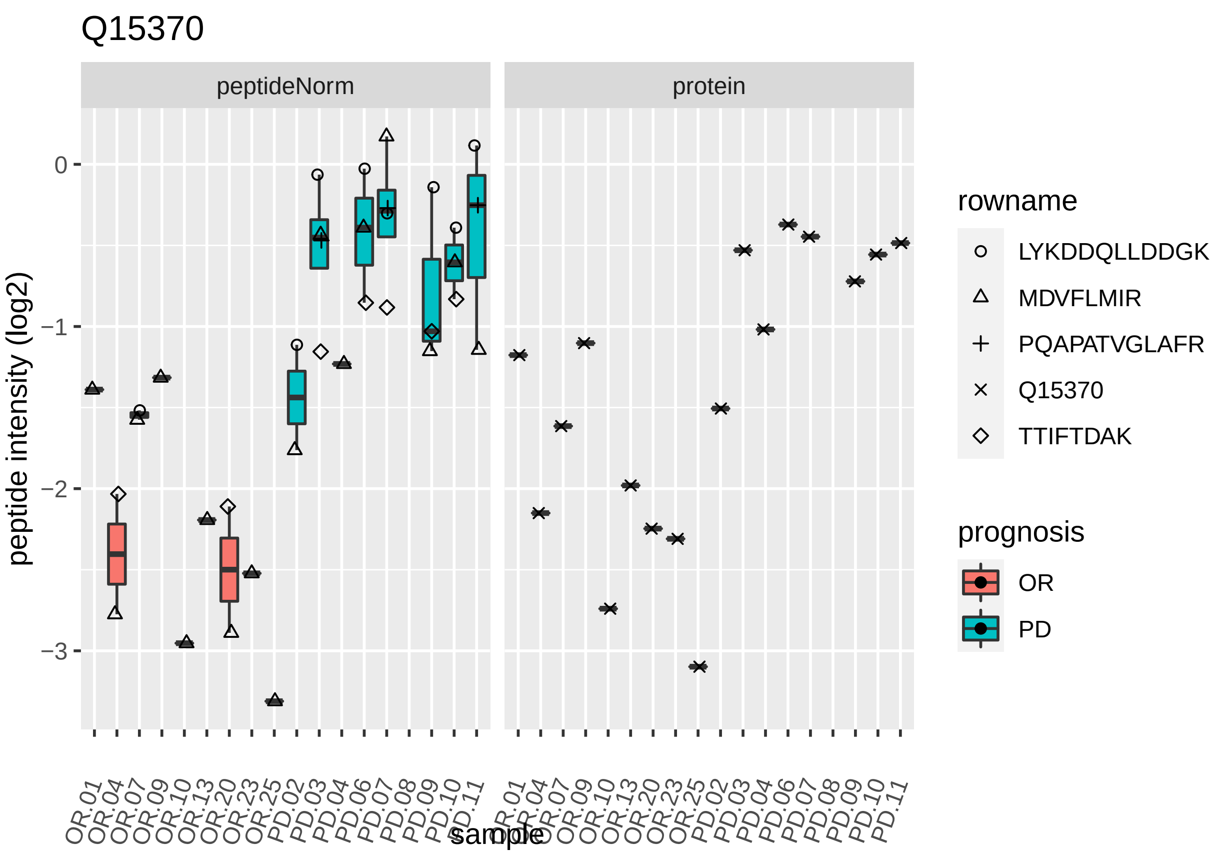


P51858
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
prognosis
OR
PD
rowname
EAENPEGEEKEAATLEVERPLPMEVEK
GFSEGLWEIENNPTVK
GPPQEEEEEEDEEEEATKEDAEAPGIR
GPPQEEEEEEDEEEEATKEDAEAPGIRDHESL
IDEMPEAAVK
KGFSEGLWEIENNPTVK
NSTPSEPGSGR
P51858
RAGDLLEDSPK
SCVEEPEPEPEAAEGDGDKK
YQVFFFGTHETAFLGPK

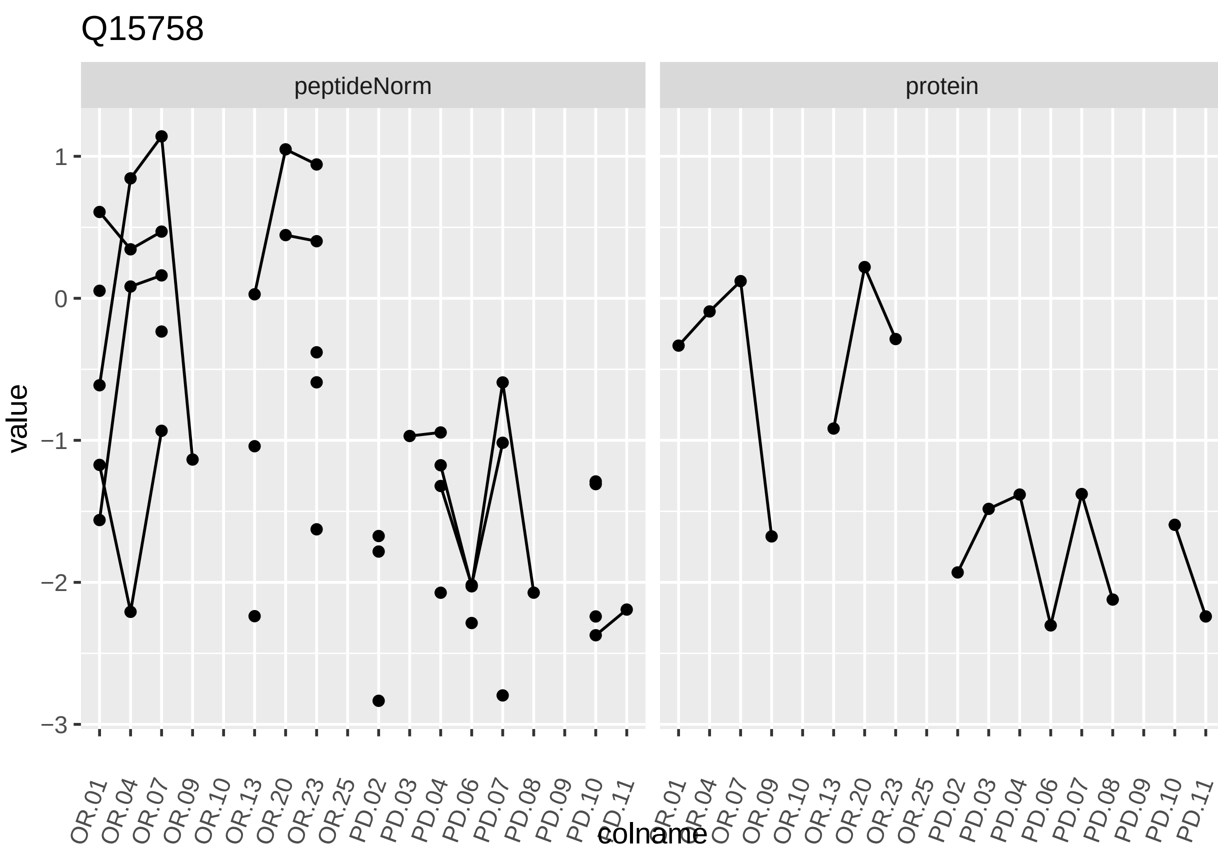

P20042
peptideNorm
protein
2
0
−2
value
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

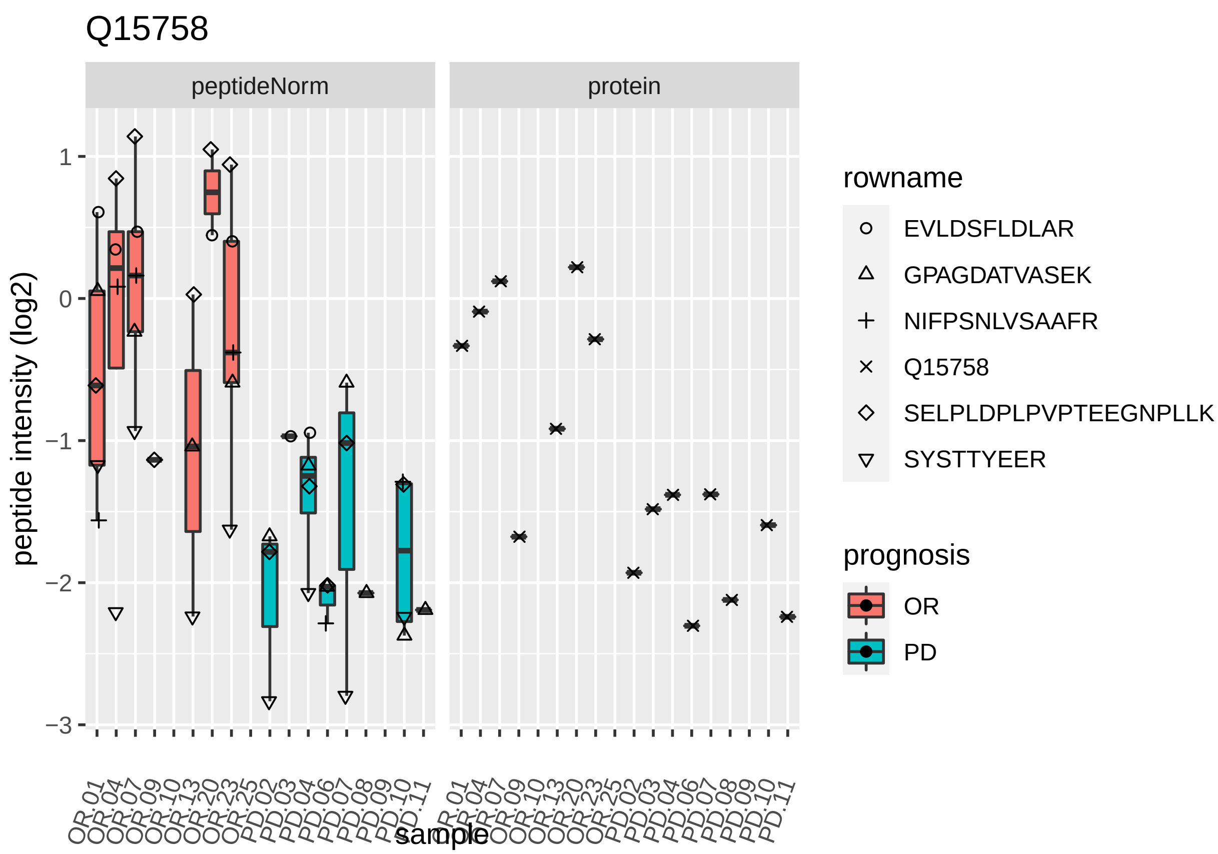

P20042
peptideNorm
protein
peptide intensity (log2)
sample
prognosis
OR
PD
rowname
DASDDLDDLNFFNQK
DYTYEELLNR
EKNPDMVAGEK
EVEPEPTEDKDLEADEEDTR
IESDVQEPTEPEDDLDIMLGNK
IFDIDEAEEGVK
P20042
TGFQAVTGK


Q15370
peptideNorm
protein
value
colname
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

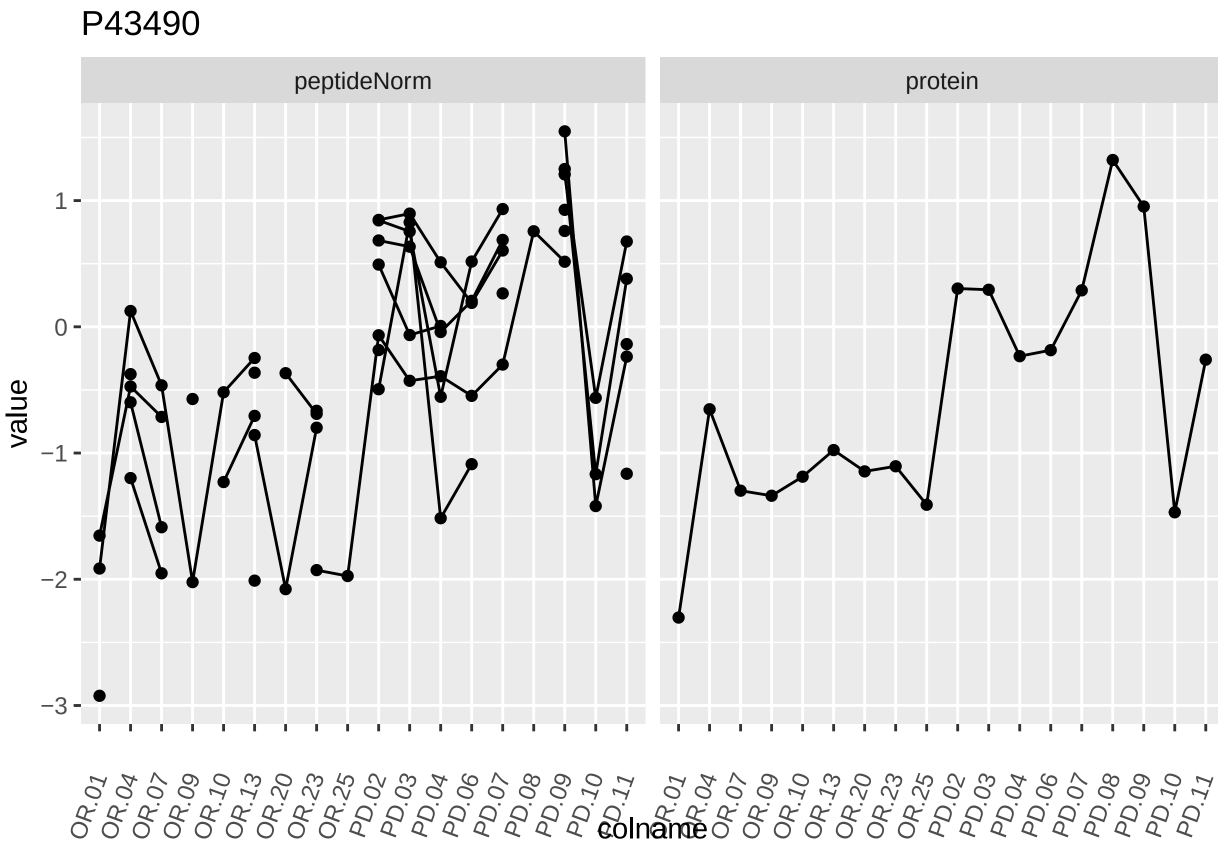


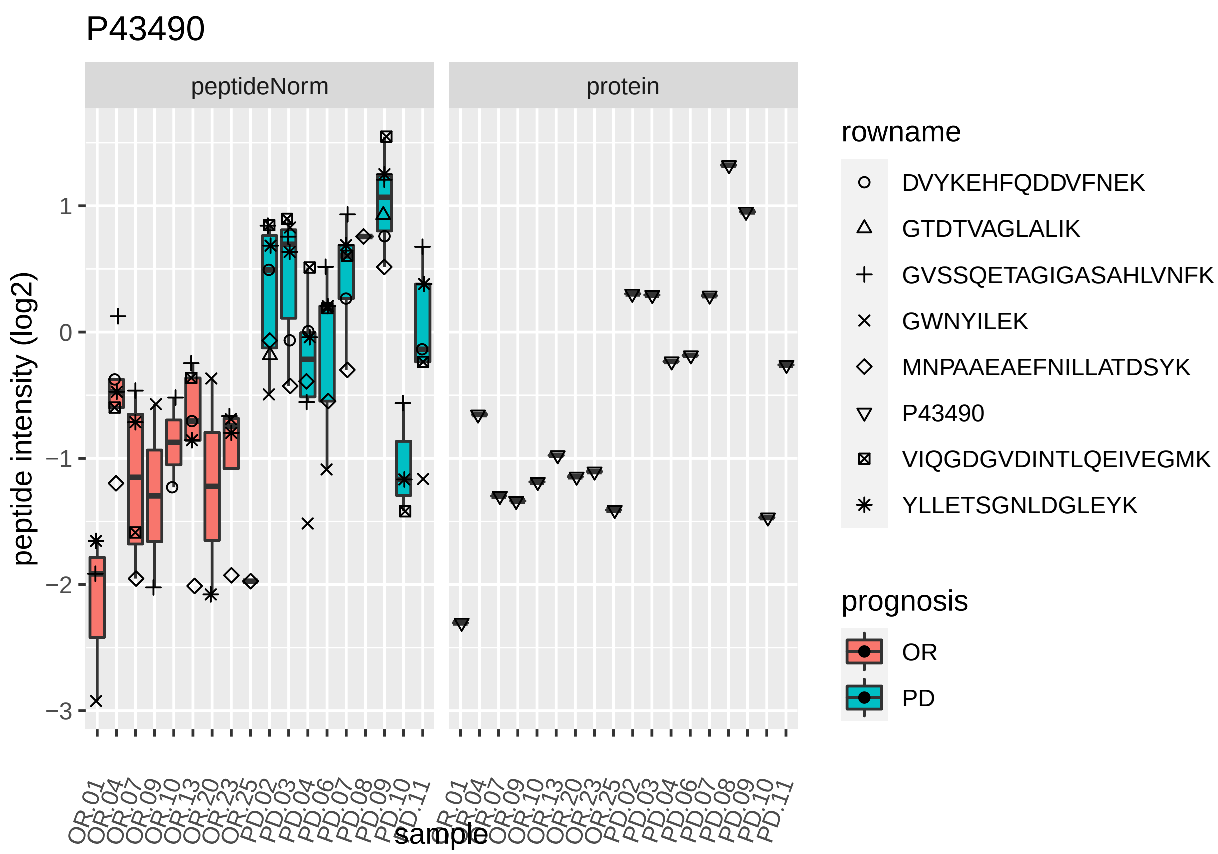
Q15370
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LYKDDQLLDDGK
MDVFLMIR
PQAPATVGLAFR
Q15370
TTIFTDAK
prognosis
OR
PD

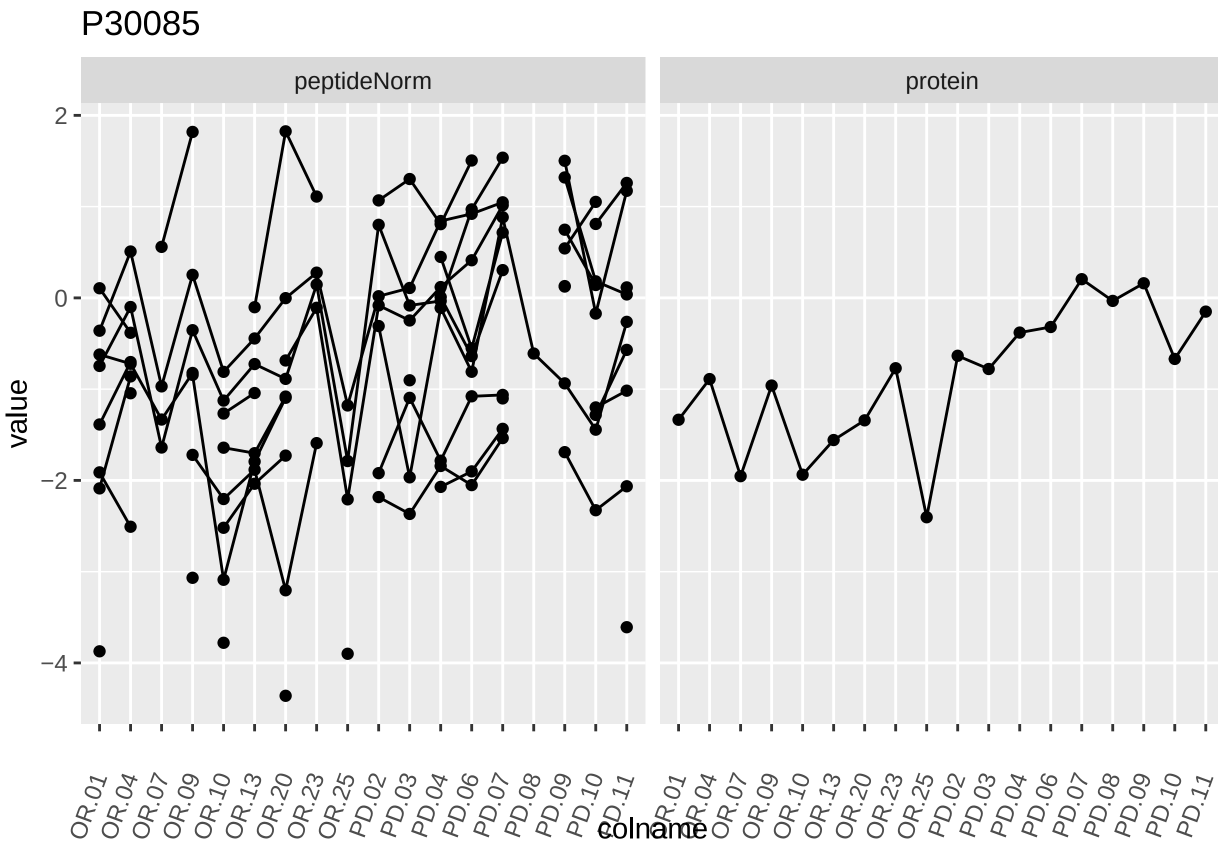

Q15758
peptideNorm
protein
value
colname
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



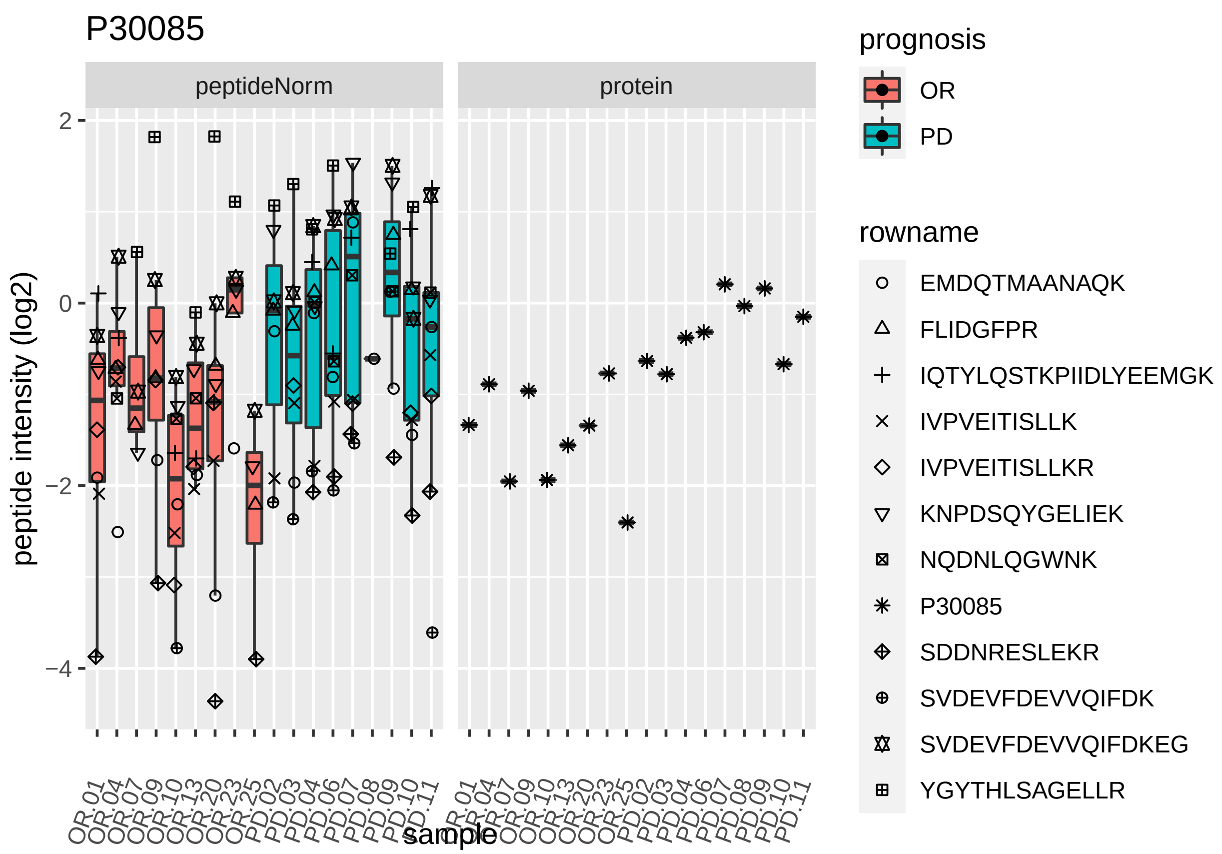
Q15758
peptideNorm
protein
peptide intensity (log2)
sample
rowname
EVLDSFLDLAR
GPAGDATVASEK
NIFPSNLVSAAFR
Q15758
SELPLDPLPVPTEEGNPLLK
SYSTTYEER
prognosis
OR
PD

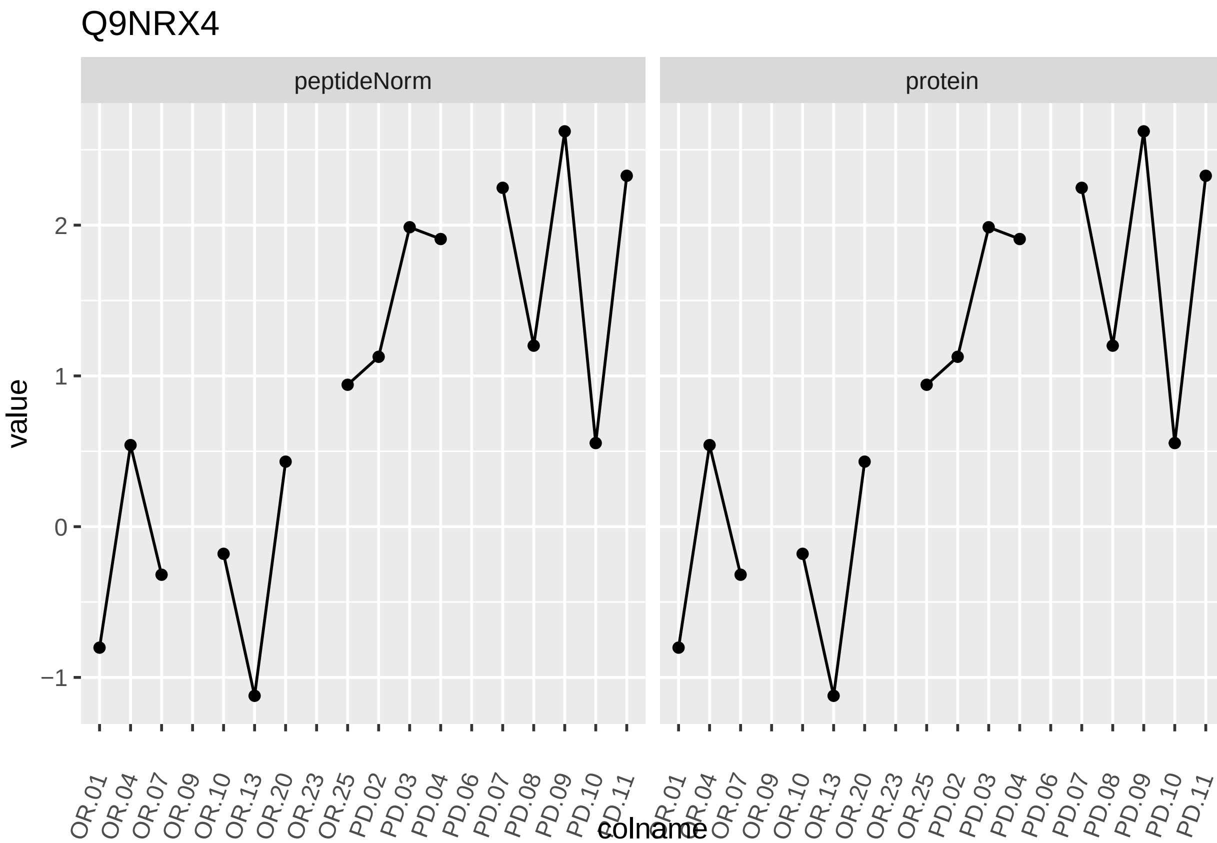

P43490
peptideNorm
protein
value
colname
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P43490
peptideNorm
protein
peptide intensity (log2)
sample
rowname
DVYKEHFQDDVFNEK
GTDTVAGLALIK
GVSSQETAGIGASAHLVNFK
GWNYILEK
MNPAAEAEFNILLATDSYK
P43490
VIQGDGVDINTLQEIVEGMK
YLLETSGNLDGLEYK
prognosis
OR
PD

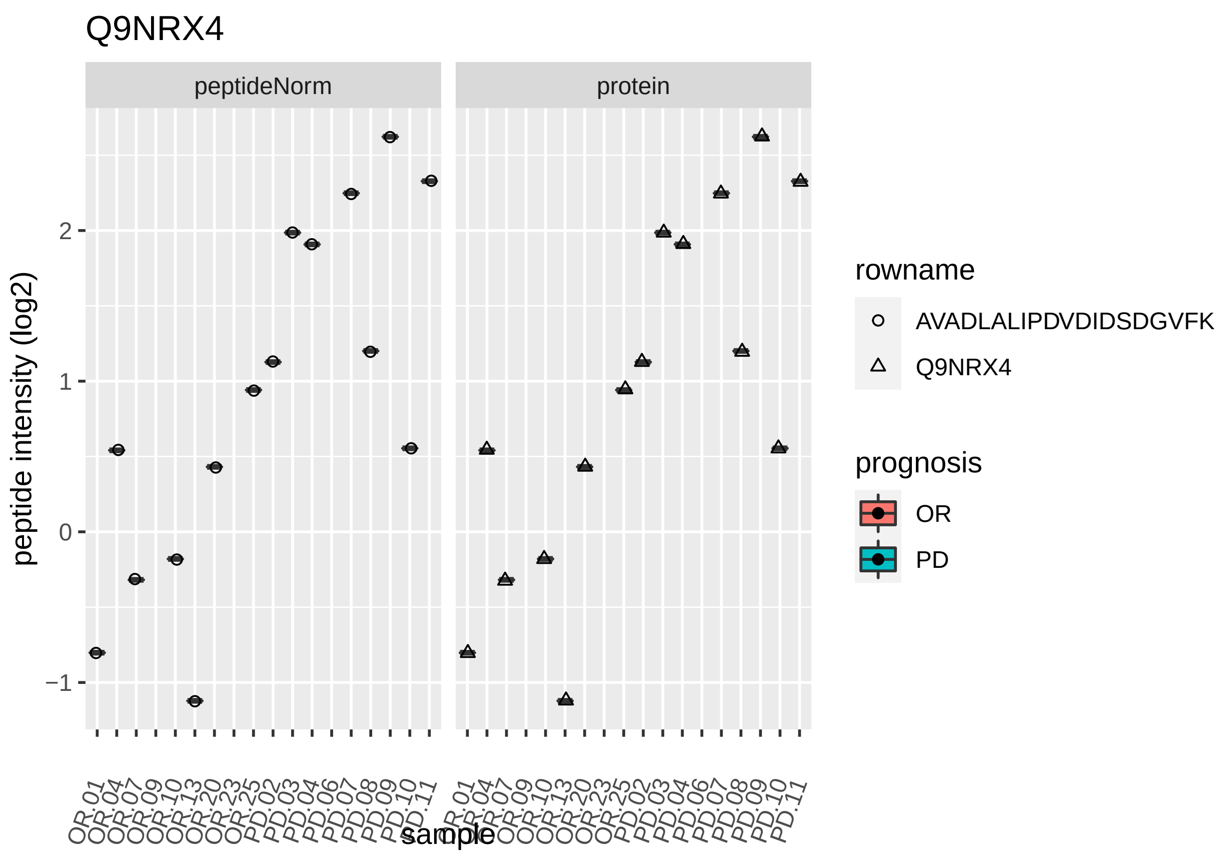


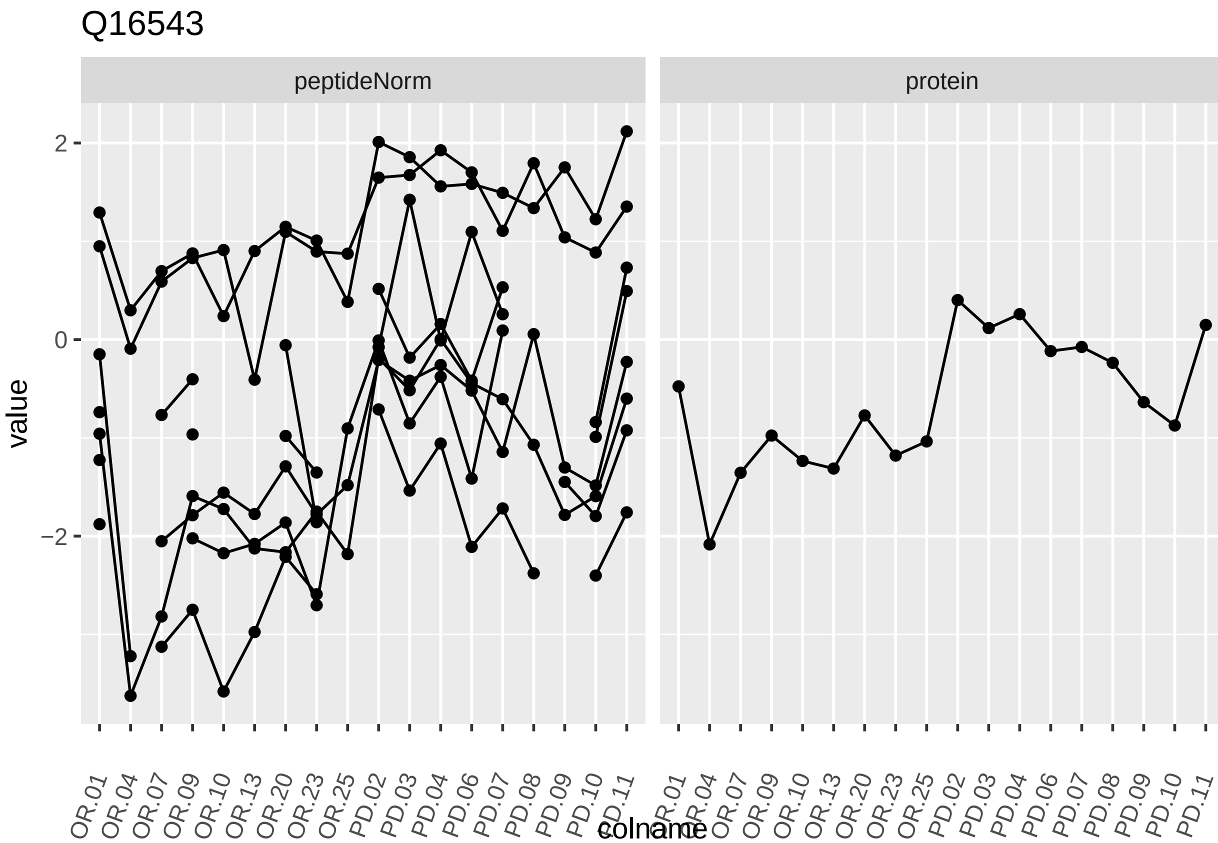
P30085
peptideNorm
protein
value
colname
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


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

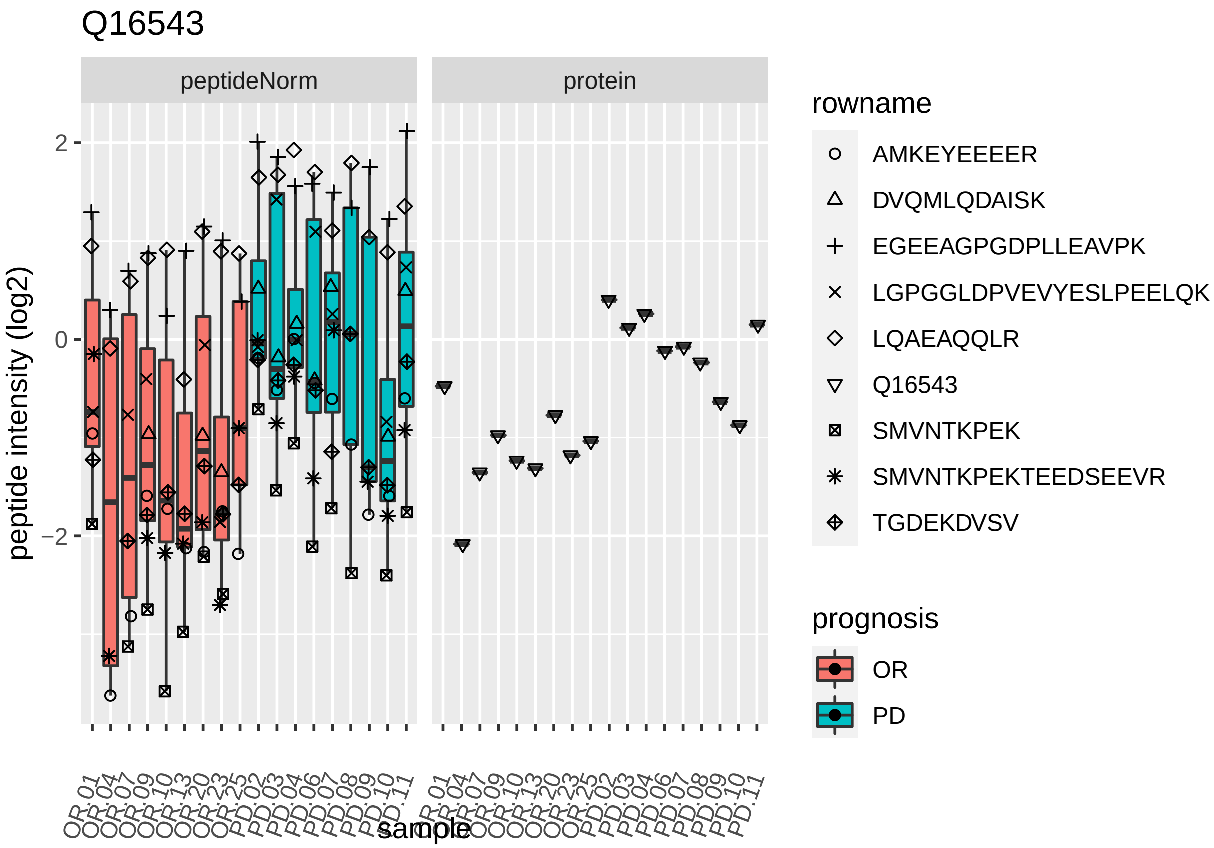


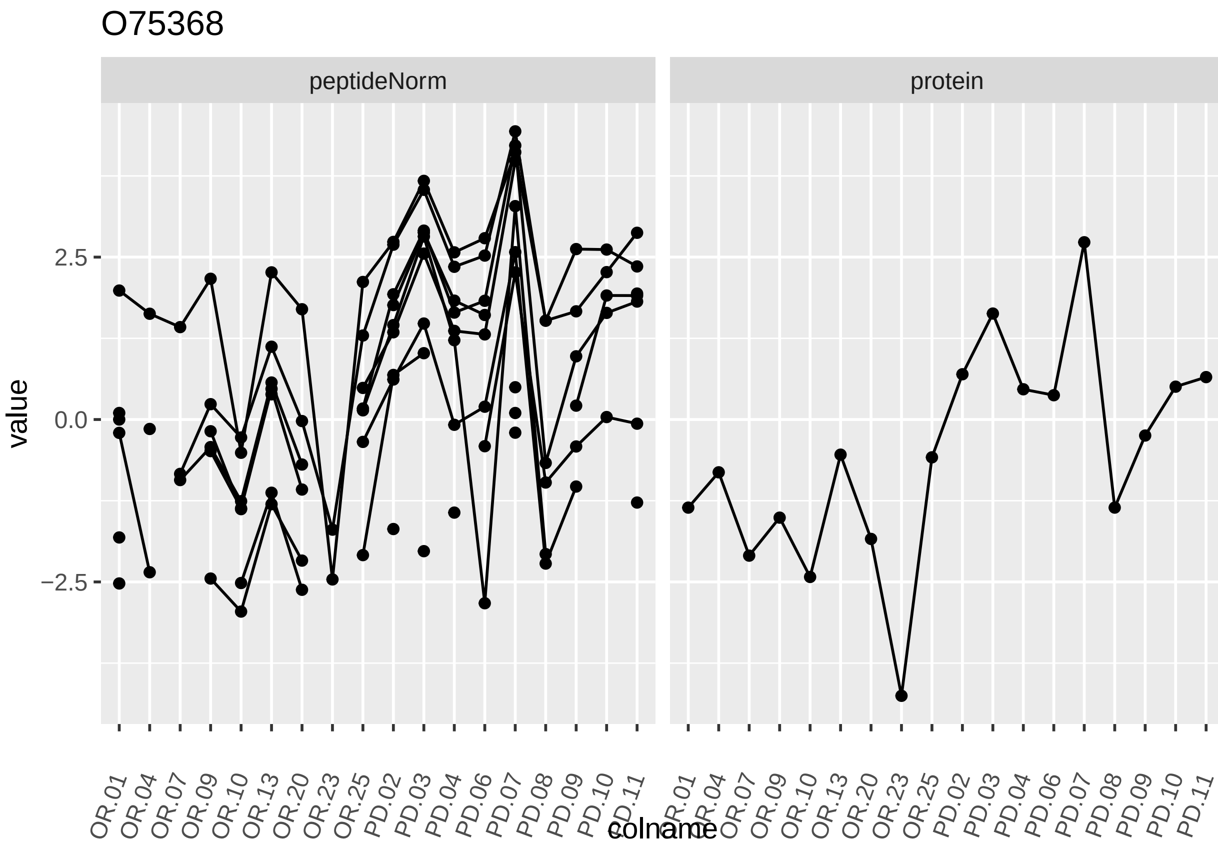
Q9NRX4
peptideNorm
protein
value
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NRX4
peptideNorm
protein
peptide intensity (log2)
sample
rowname
AVADLALIPDVDIDSDGVFK
Q9NRX4
prognosis
OR
PD

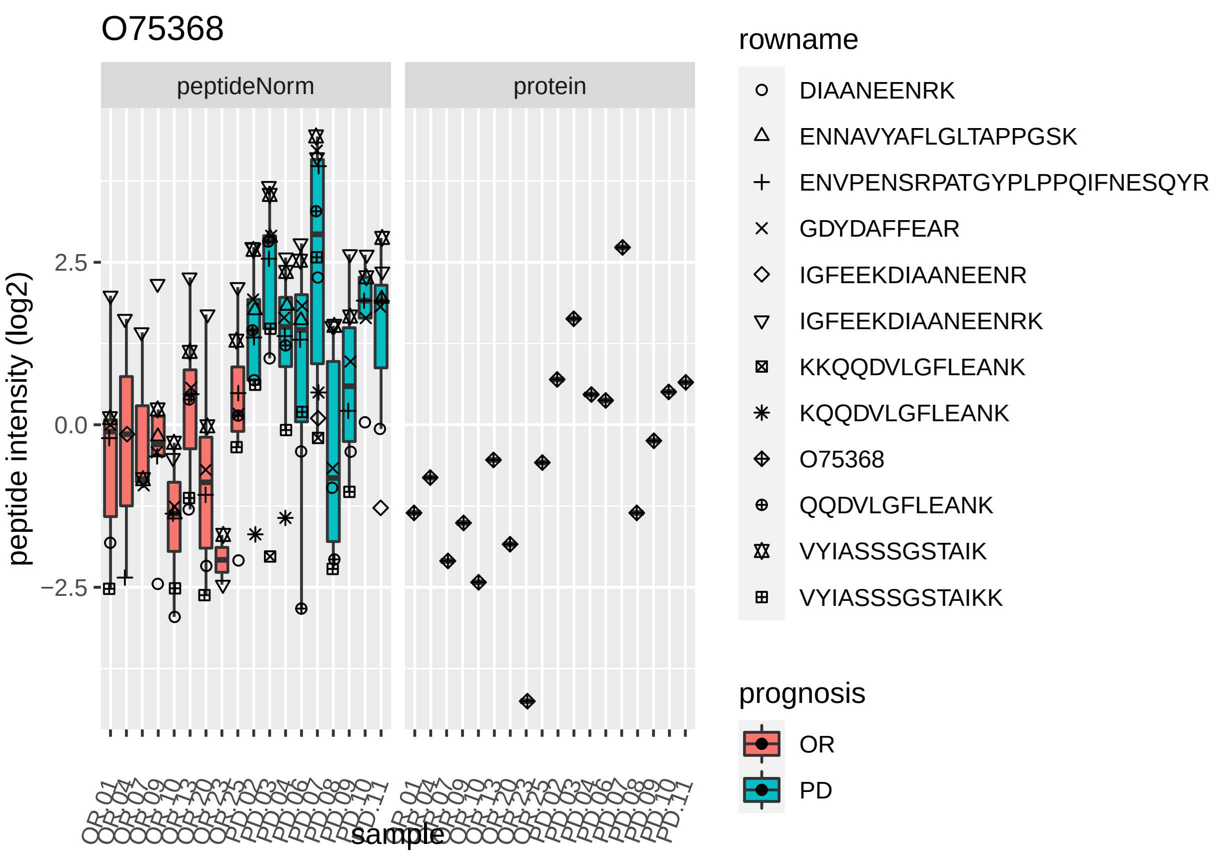


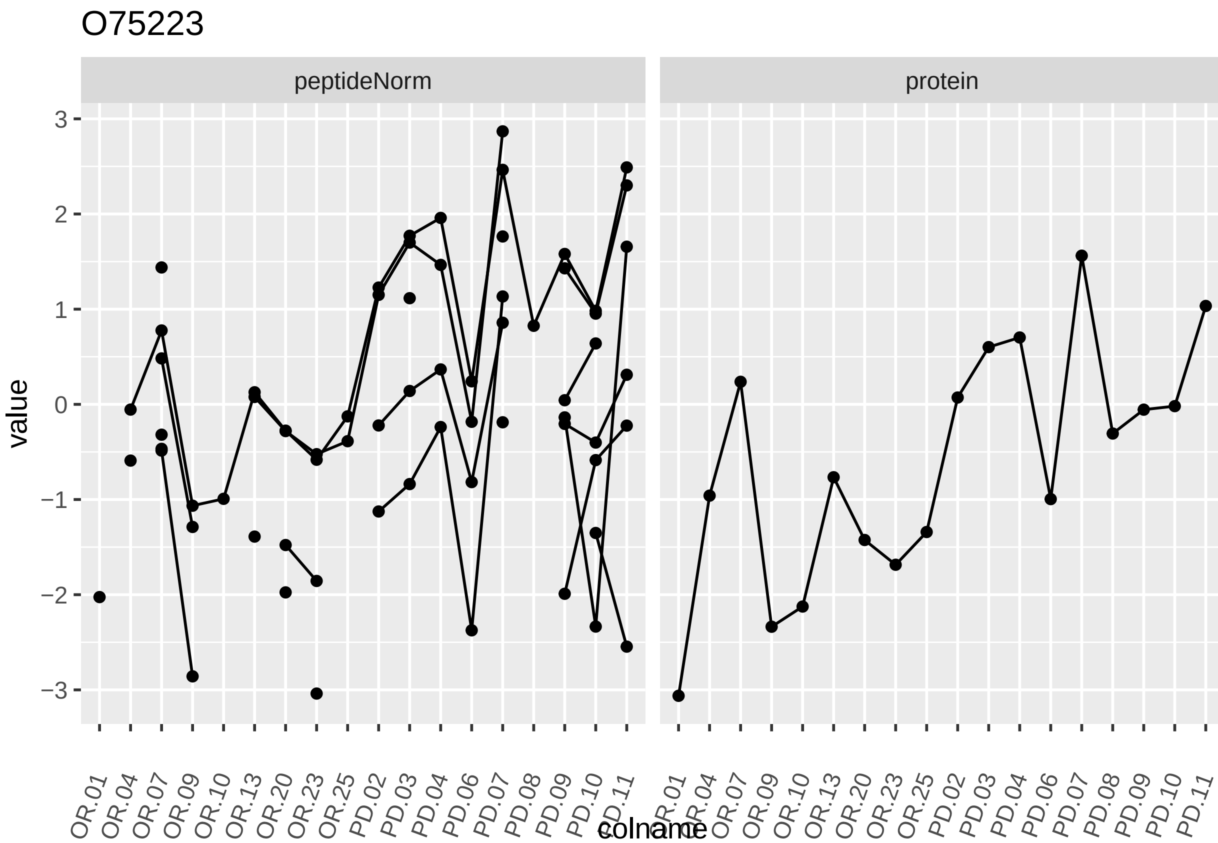
Q16543
peptideNorm
protein
value
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

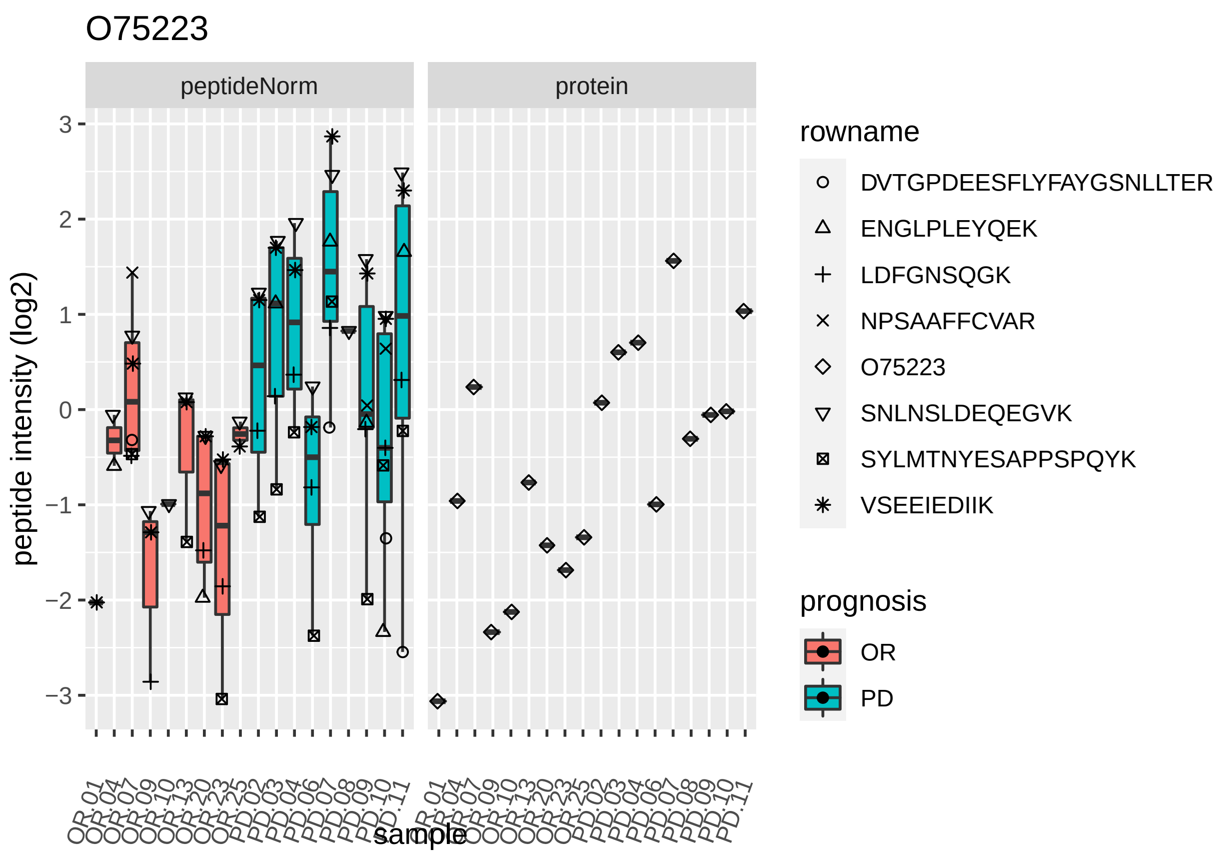

Q16543
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
AMKEYEEEER
DVQMLQDAISK
EGEEAGPGDPLLEAVPK
LGPGGLDPVEVYESLPEELQK
LQAEAQQLR
Q16543
SMVNTKPEK
SMVNTKPEKTEEDSEEVR
TGDEKDVSV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

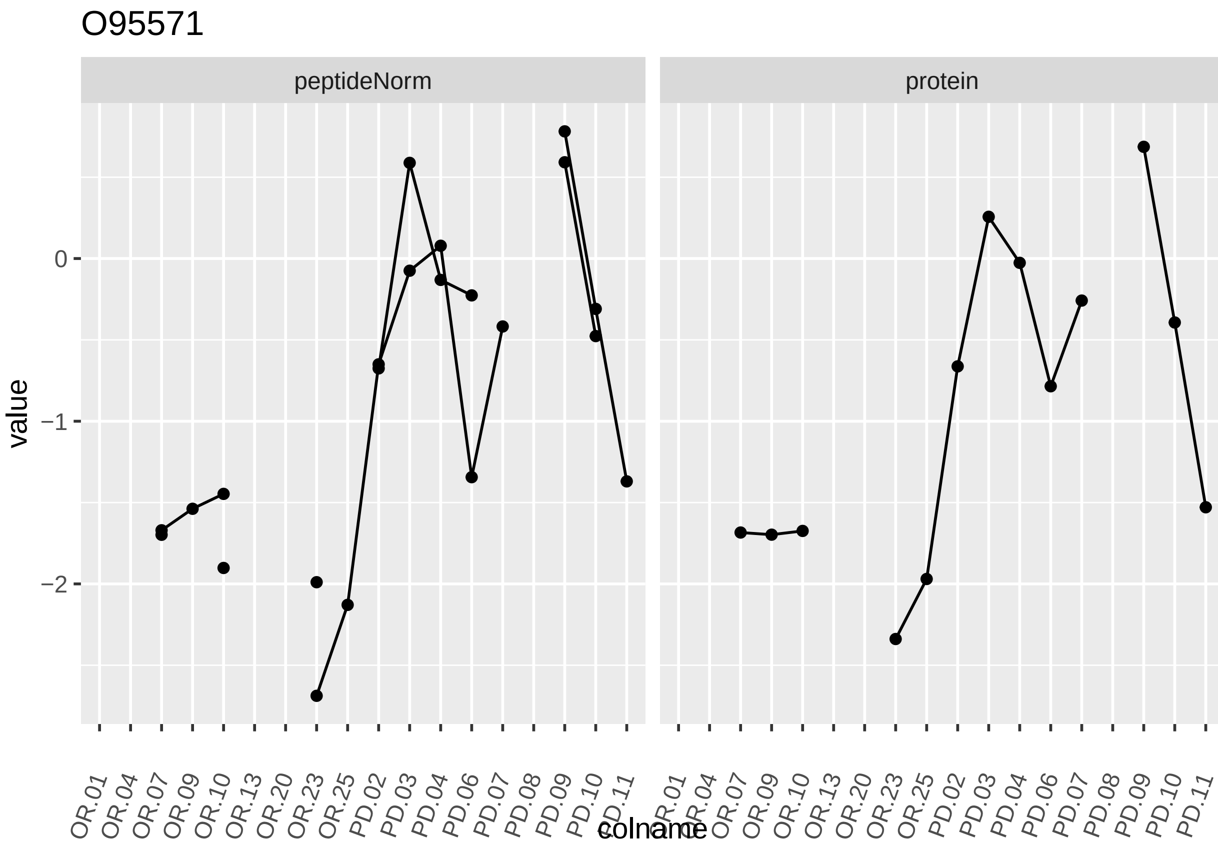


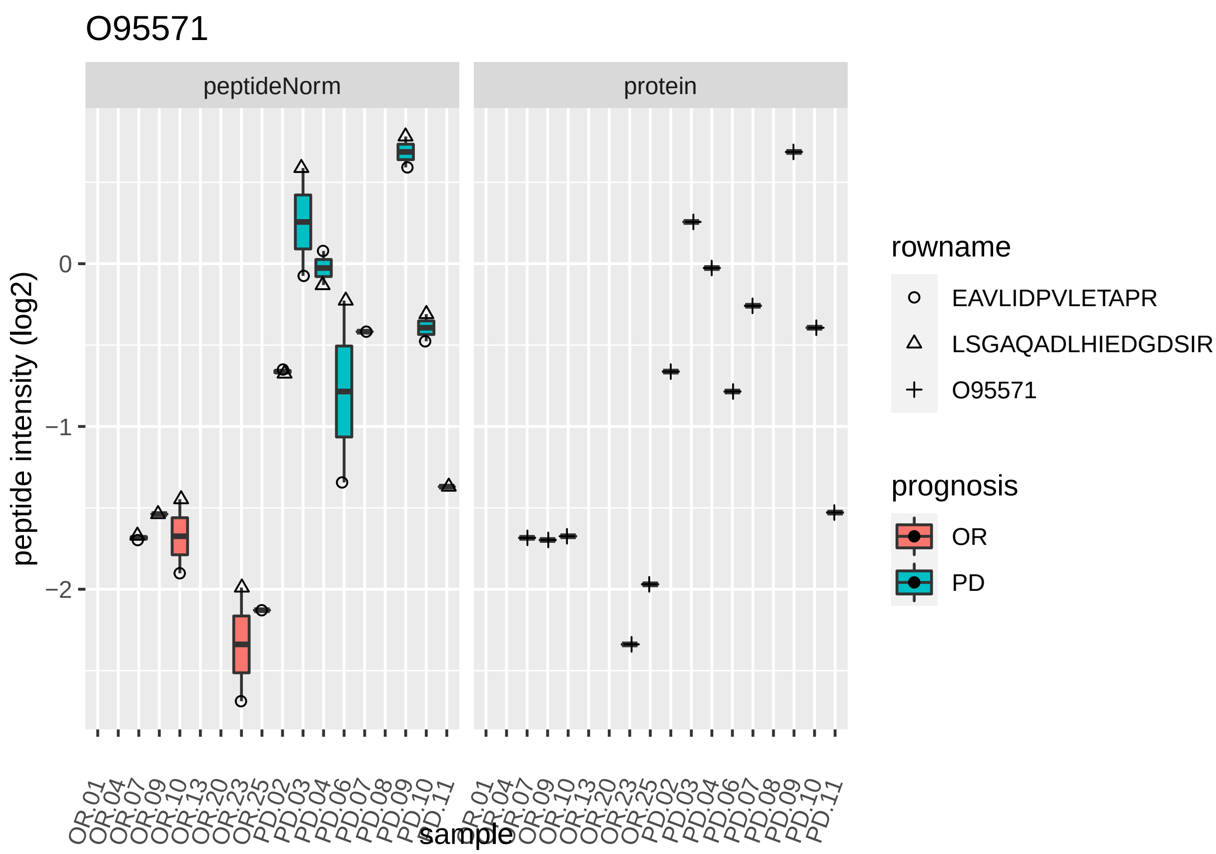
O75368
peptideNorm
protein
value
2.5
0.0
−2.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O75368
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
sample
rowname
DIAANEENRK
ENNAVYAFLGLTAPPGSK
ENVPENSRPATGYPLPPQIFNESQYR
GDYDAFFEAR
IGFEEKDIAANEENR
IGFEEKDIAANEENRK
KKQQDVLGFLEANK
KQQDVLGFLEANK
O75368
QQDVLGFLEANK
VYIASSSGSTAIK
VYIASSSGSTAIKK
prognosis
OR
PD

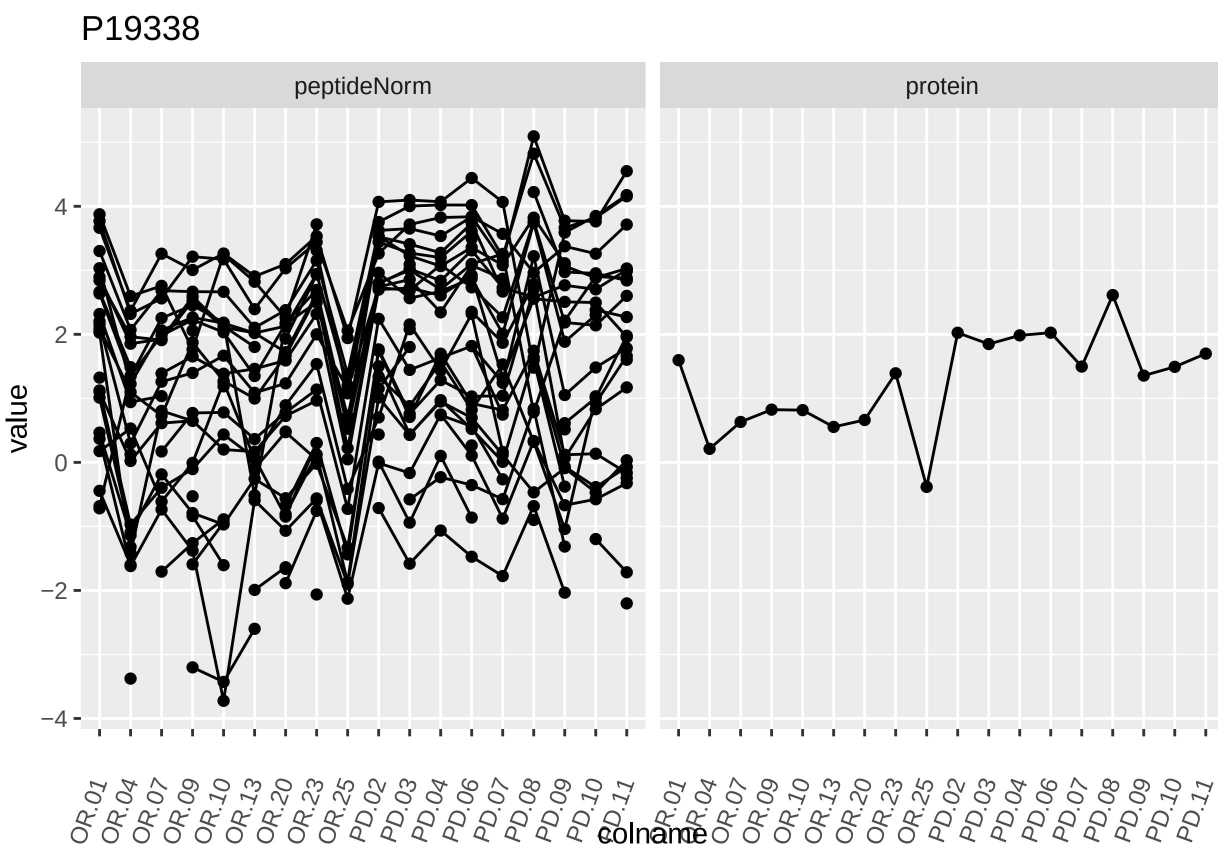

O75223
peptideNorm
protein
value
colname
3
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


O75223
peptideNorm
protein
peptide intensity (log2)
sample
rowname
DVTGPDEESFLYFAYGSNLLTER
ENGLPLEYQEK
LDFGNSQGK
NPSAAFFCVAR
O75223
SNLNSLDEQEGVK
SYLMTNYESAPPSPQYK
VSEEIEDIIK
prognosis
OR
PD

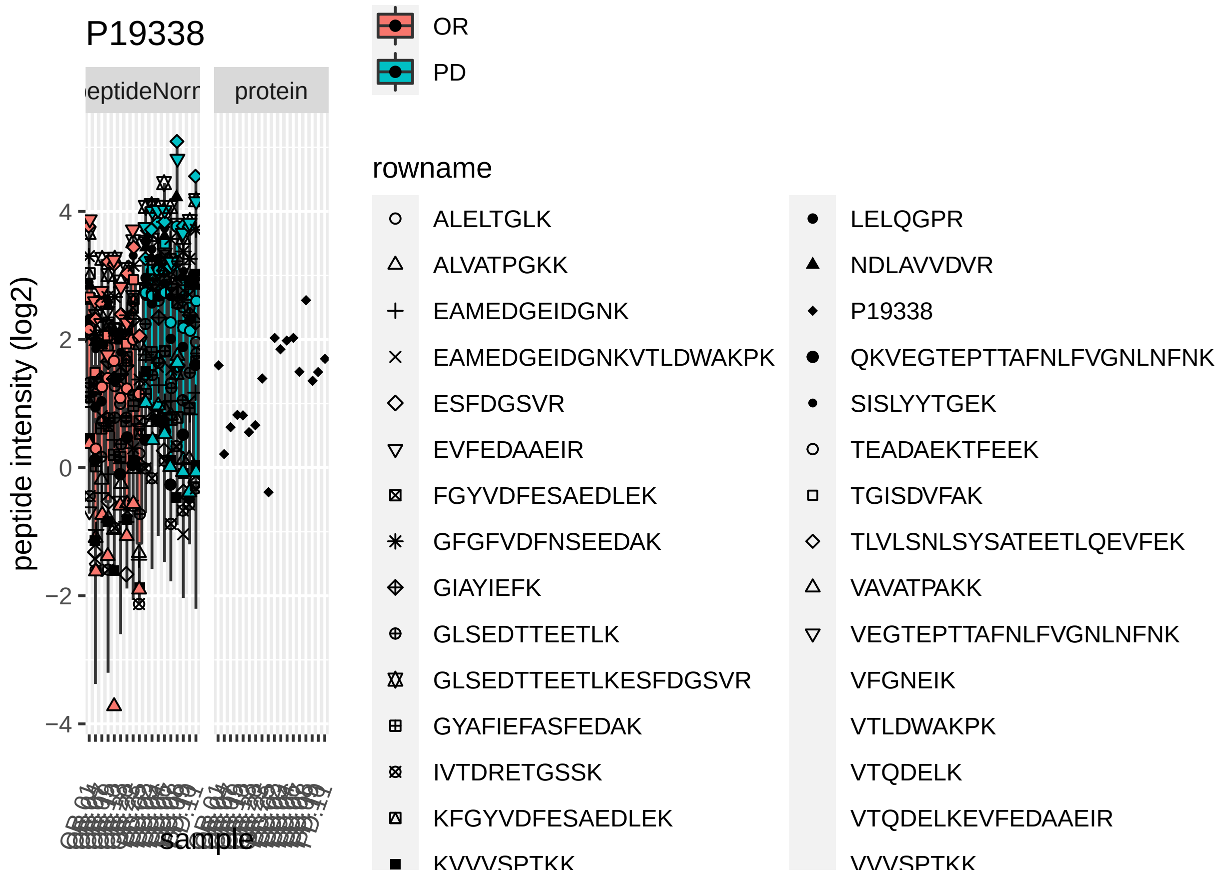

O95571
peptideNorm
protein
value
colname
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

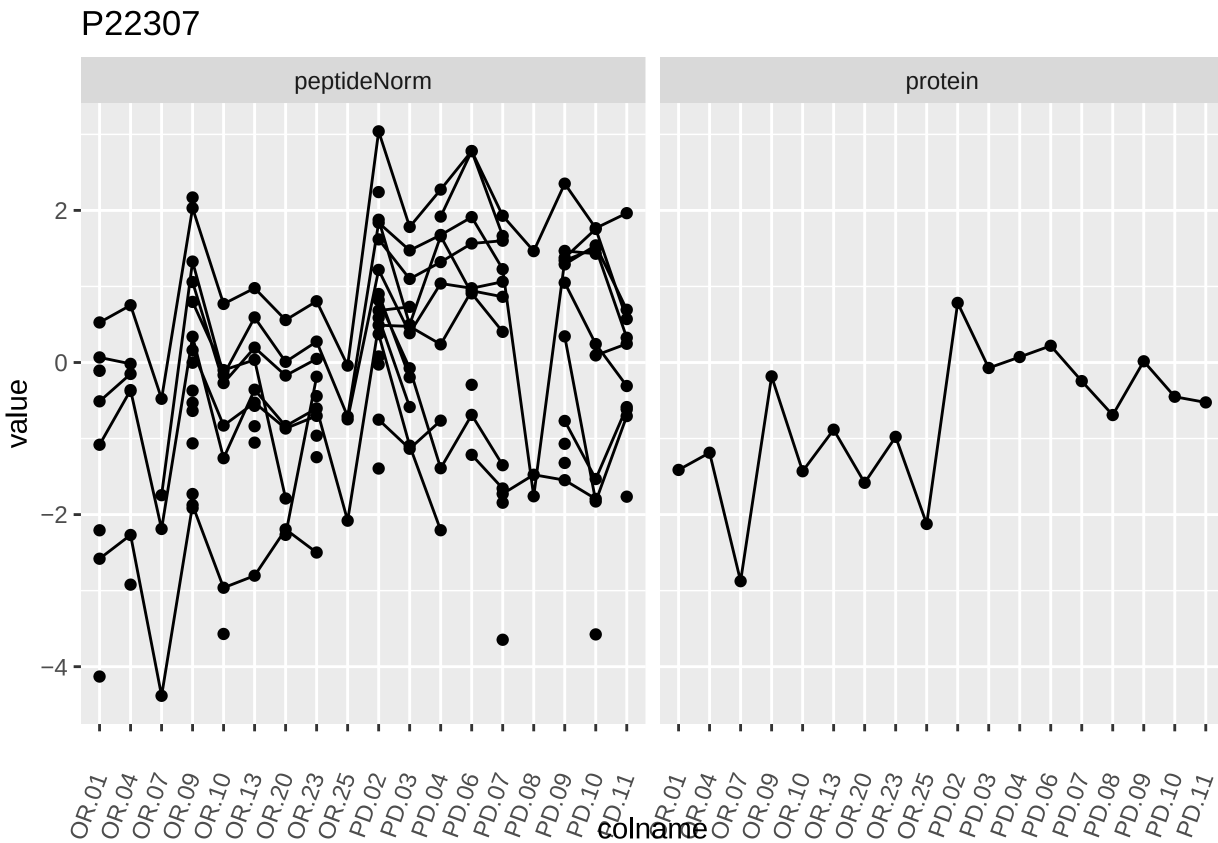


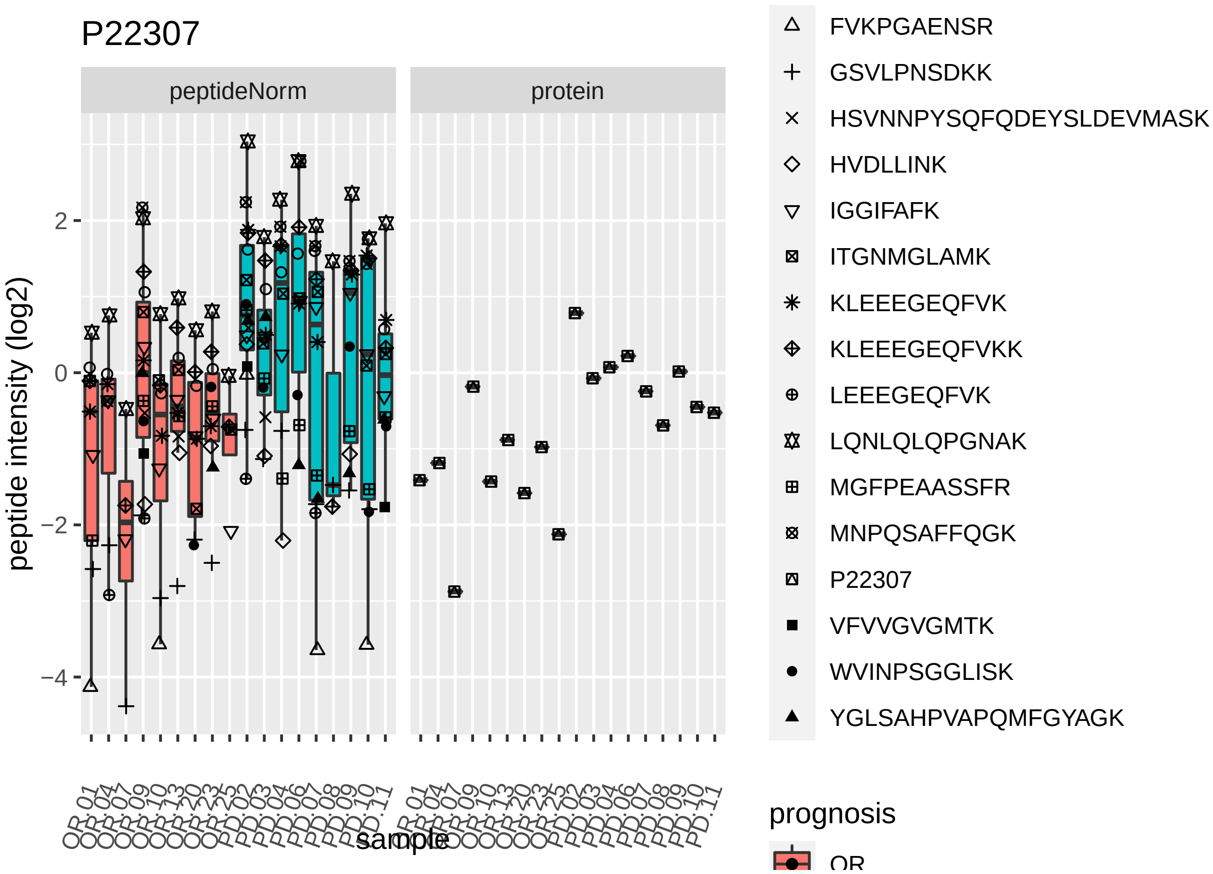
O95571
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
EAVLIDPVLETAPR
LSGAQADLHIEDGDSIR
O95571
prognosis
OR
PD

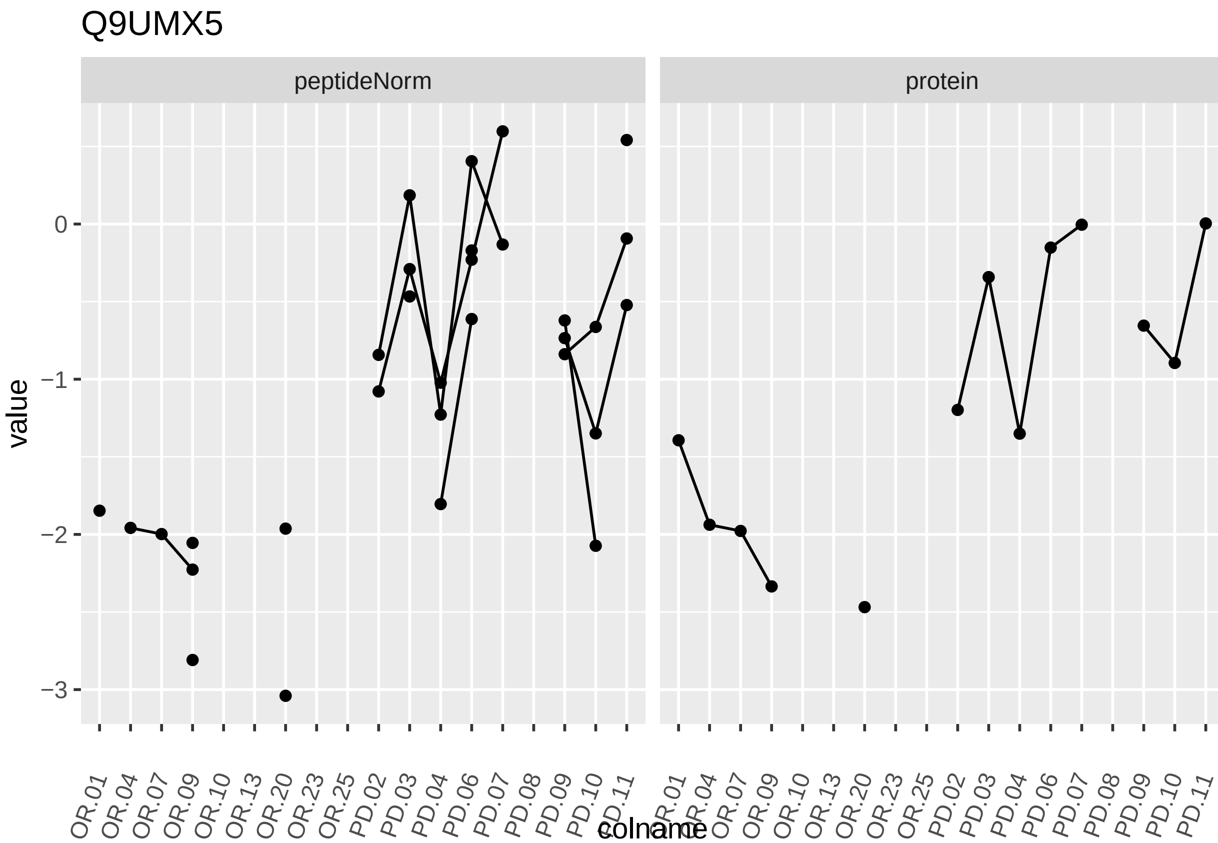


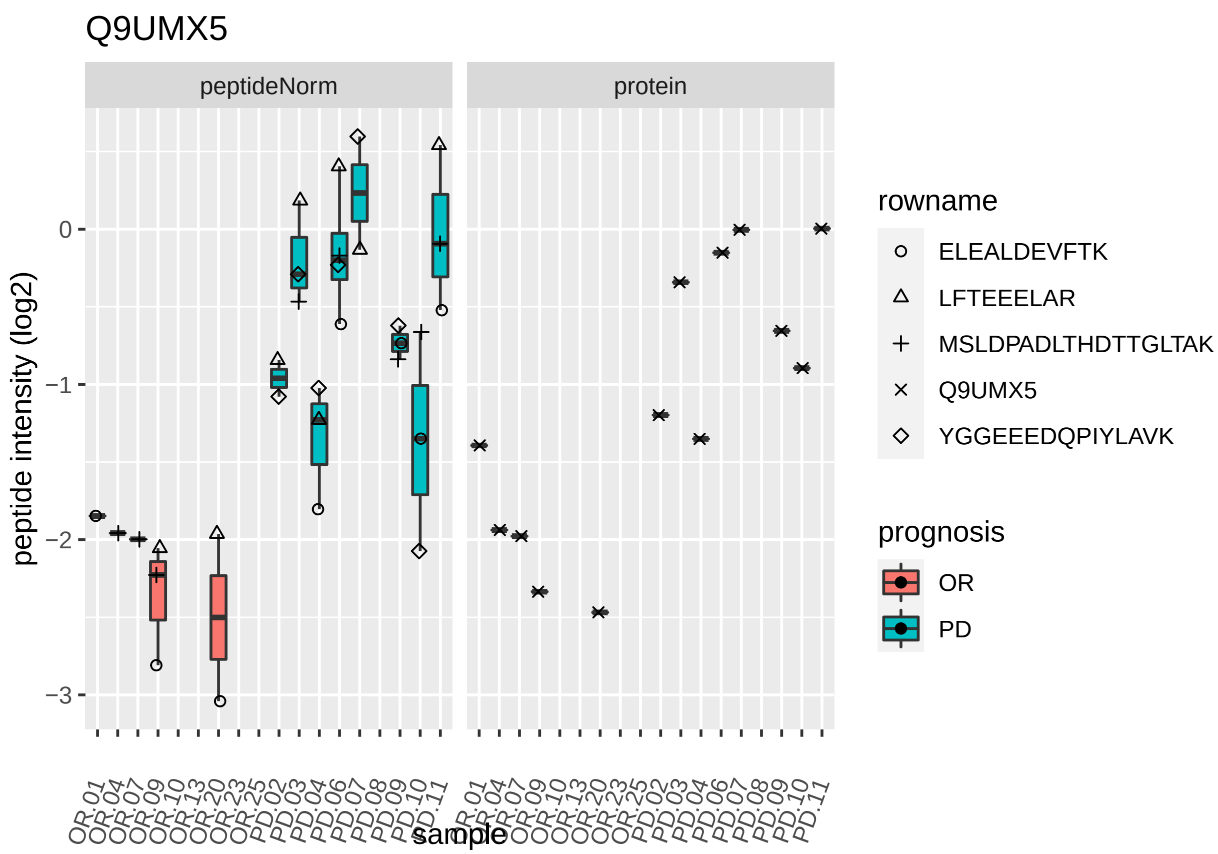
P19338
peptideNorm
protein
value
colname
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

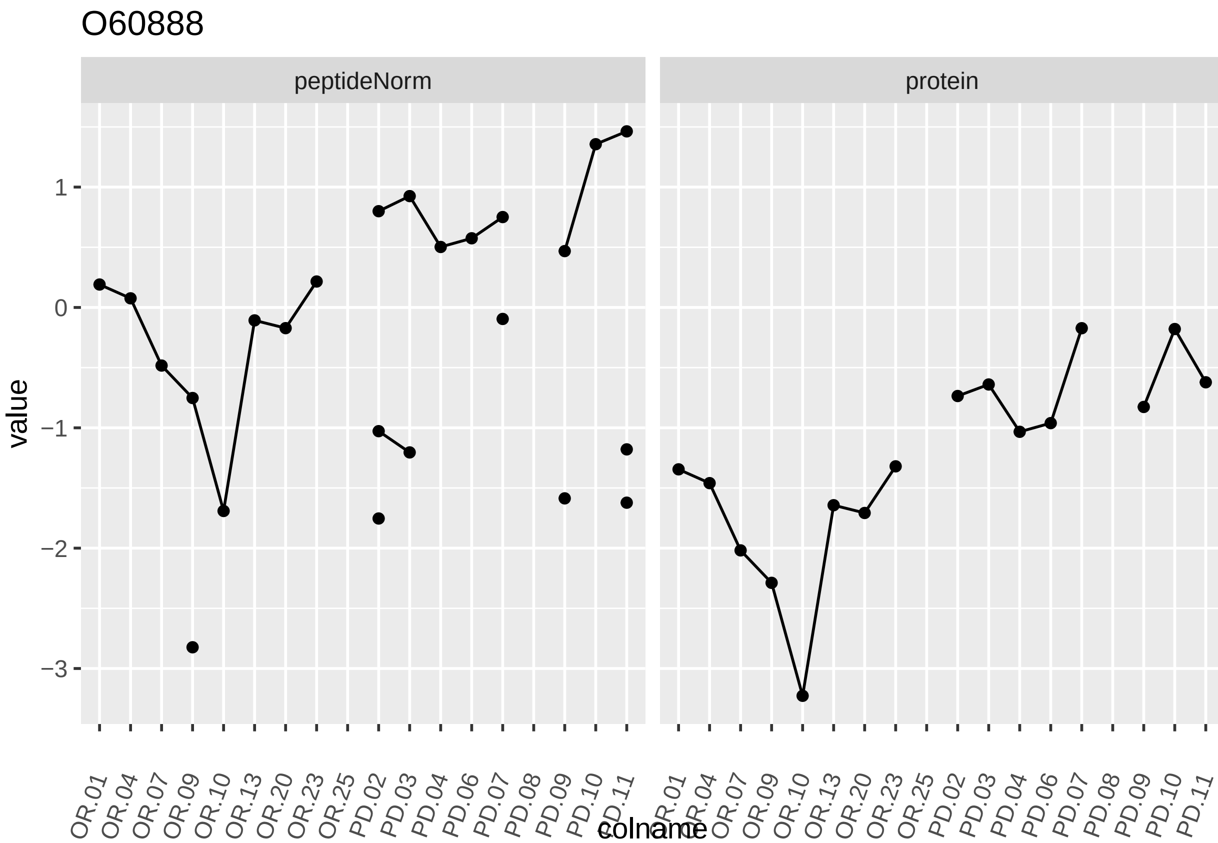

P19338
peptideNorm
protein
peptide intensity (log2)
sample
OR
PD
rowname
ALELTGLK
ALVATPGKK
EAMEDGEIDGNK
EAMEDGEIDGNKVTLDWAKPK
ESFDGSVR
EVFEDAAEIR
FGYVDFESAEDLEK
GFGFVDFNSEEDAK
GIAYIEFK
GLSEDTTEETLK
GLSEDTTEETLKESFDGSVR
GYAFIEFASFEDAK
IVTDRETGSSK
KFGYVDFESAEDLEK
LELQGPR
NDLAVVDVR
P19338
QKVEGTEPTTAFNLFVGNLNFNK
SISLYYTGEK
TEADAEKTFEEK
TGISDVFAK
TLVLSNLSYSATEETLQEVFEK
VAVATPAKK
VEGTEPTTAFNLFVGNLNFNK
VFGNEIK
VTLDWAKPK
VTQDELK
VTQDELKEVFEDAAEIR

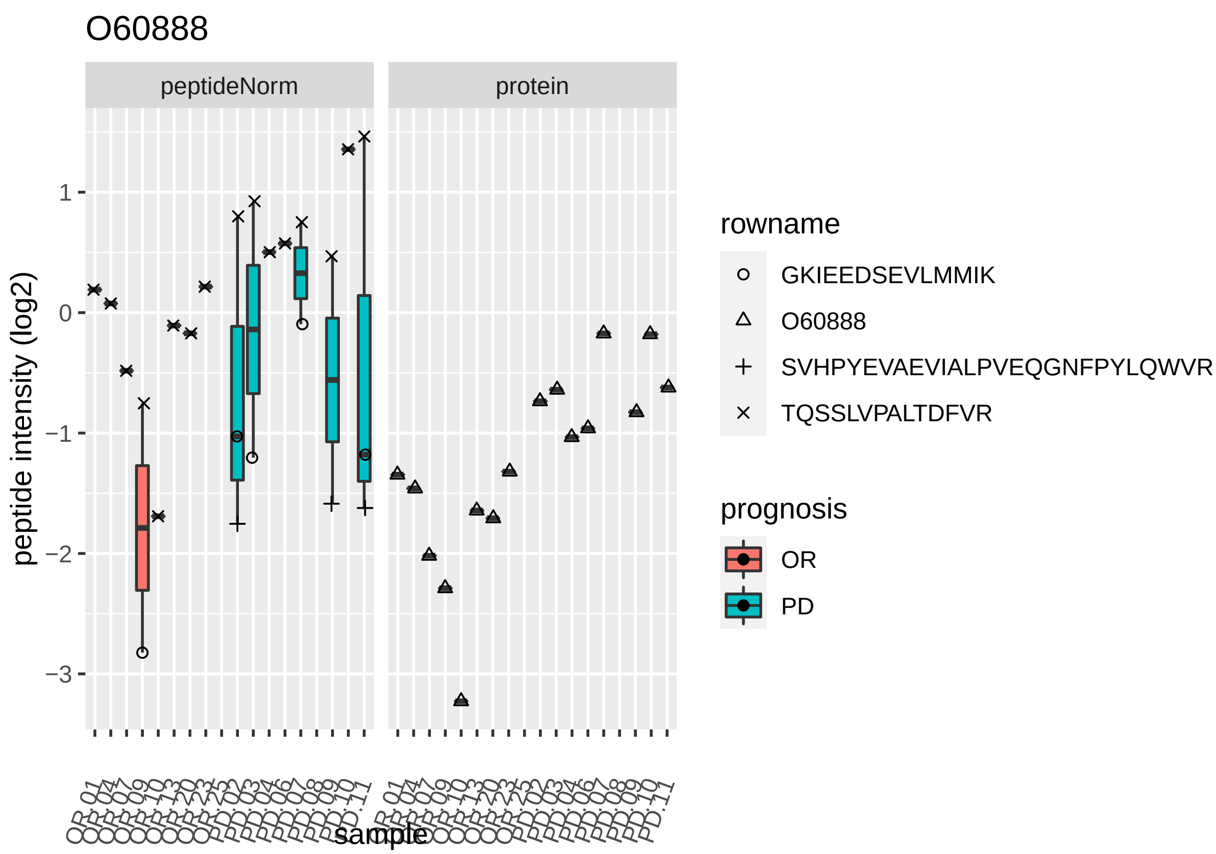

P22307
peptideNorm
protein
value
2
0
−2
−4
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

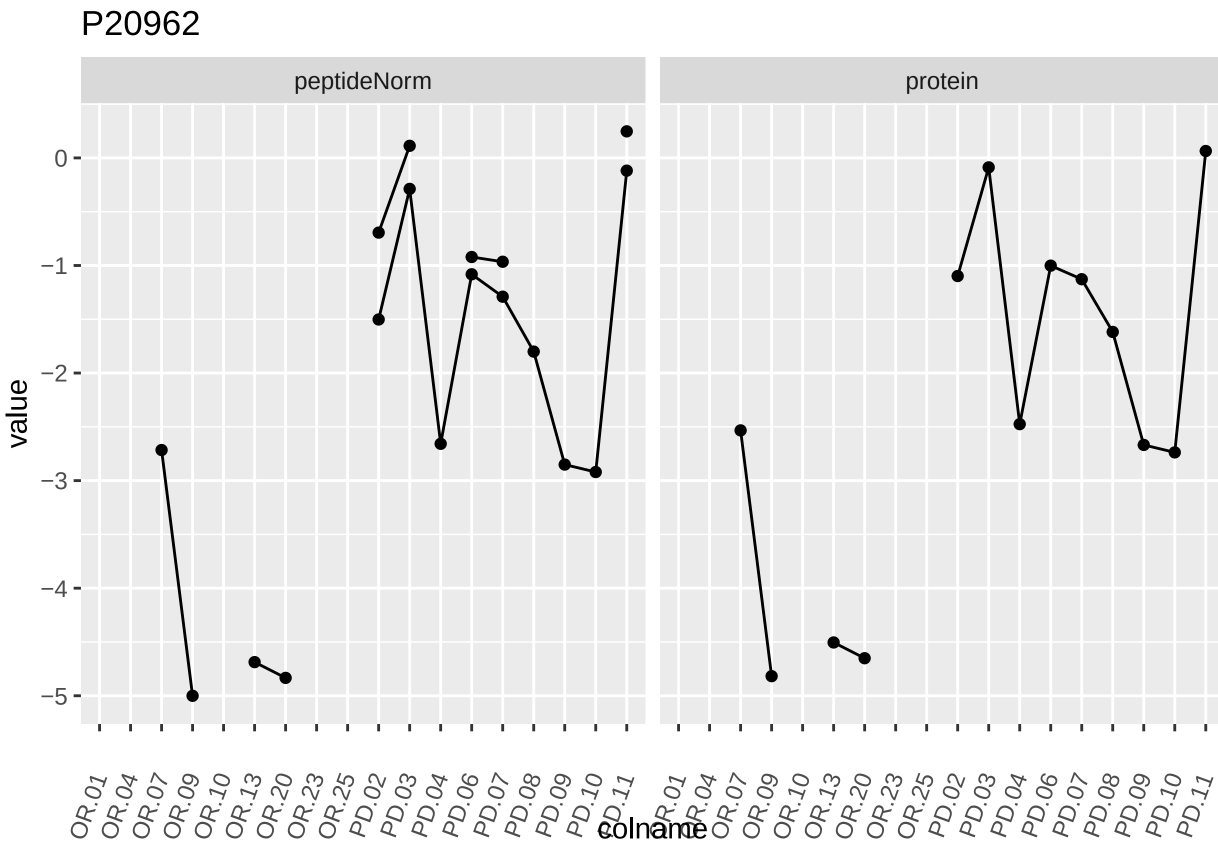

P22307
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
FVKPGAENSR
GSVLPNSDKK
HSVNNPYSQFQDEYSLDEVMASK
HVDLLINK
IGGIFAFK
ITGNMGLAMK
KLEEEGEQFVK
KLEEEGEQFVKK
LEEEGEQFVK
LQNLQLQPGNAK
MGFPEAASSFR
MNPQSAFFQGK
P22307
VFVVGVGMTK
WVINPSGGLISK
YGLSAHPVAPQMFGYAGK
prognosis
OR


Q9UMX5
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

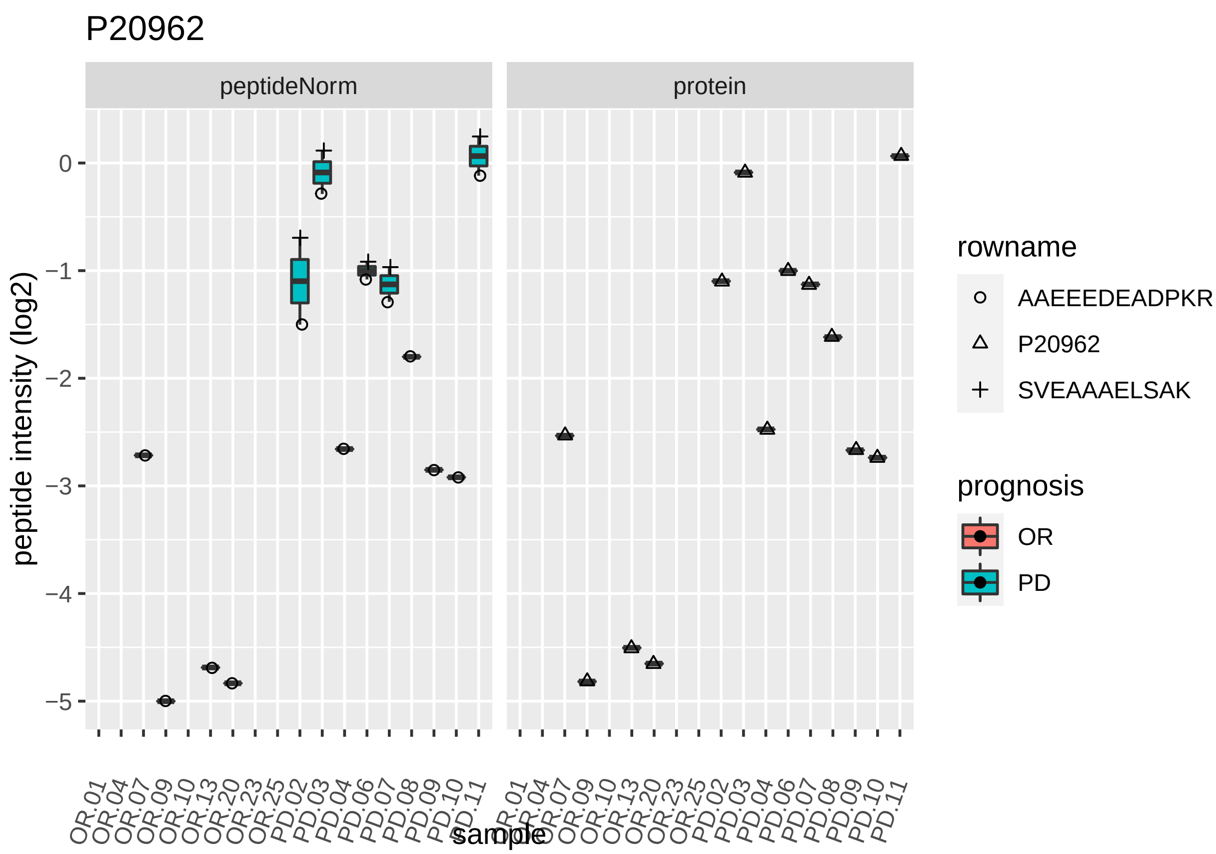

Q9UMX5
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
ELEALDEVFTK
LFTEEELAR
MSLDPADLTHDTTGLTAK
Q9UMX5
YGGEEEDQPIYLAVK
prognosis
OR
PD


O60888
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
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

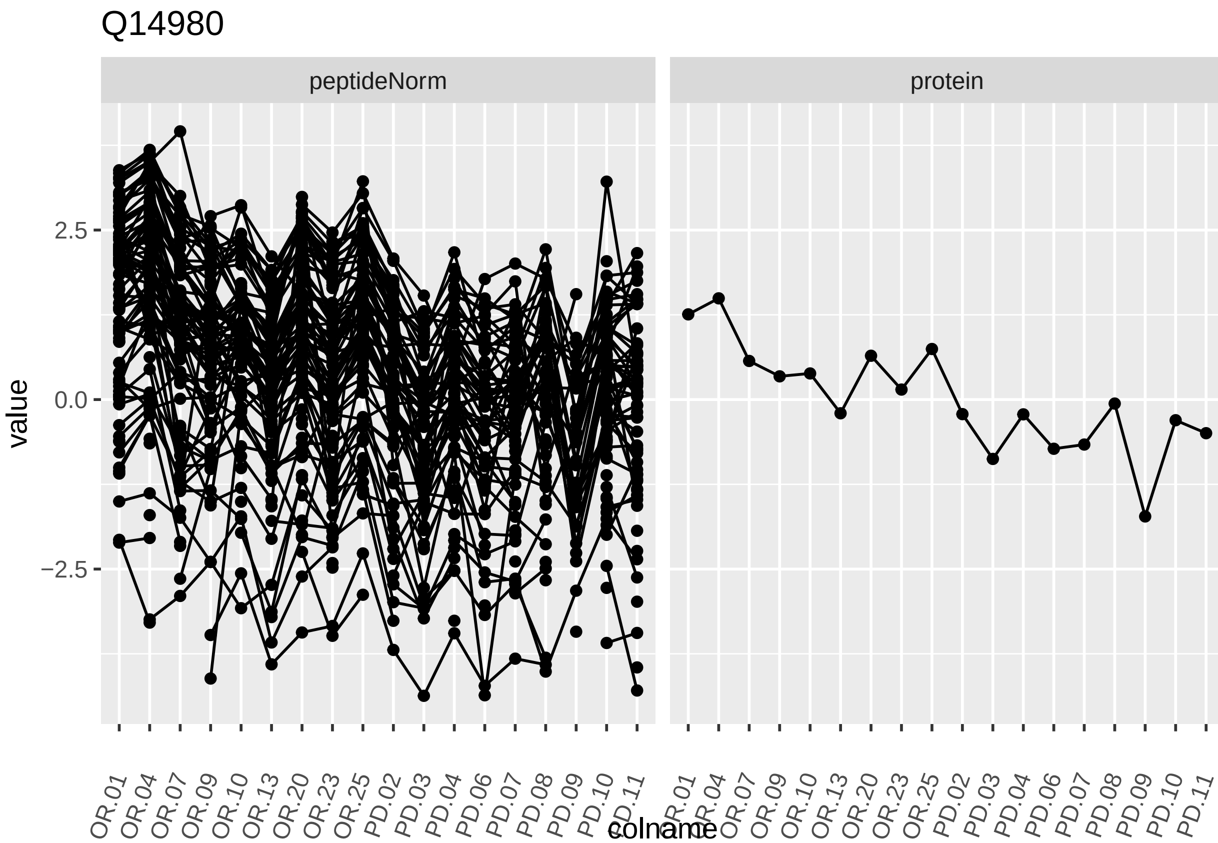

O60888
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
rowname
GKIEEDSEVLMMIK
O60888
SVHPYEVAEVIALPVEQGNFPYLQWVR
TQSSLVPALTDFVR
prognosis
OR
PD



P20962
peptideNorm
protein
value
colname
0
−1
−2
−3
−4
−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

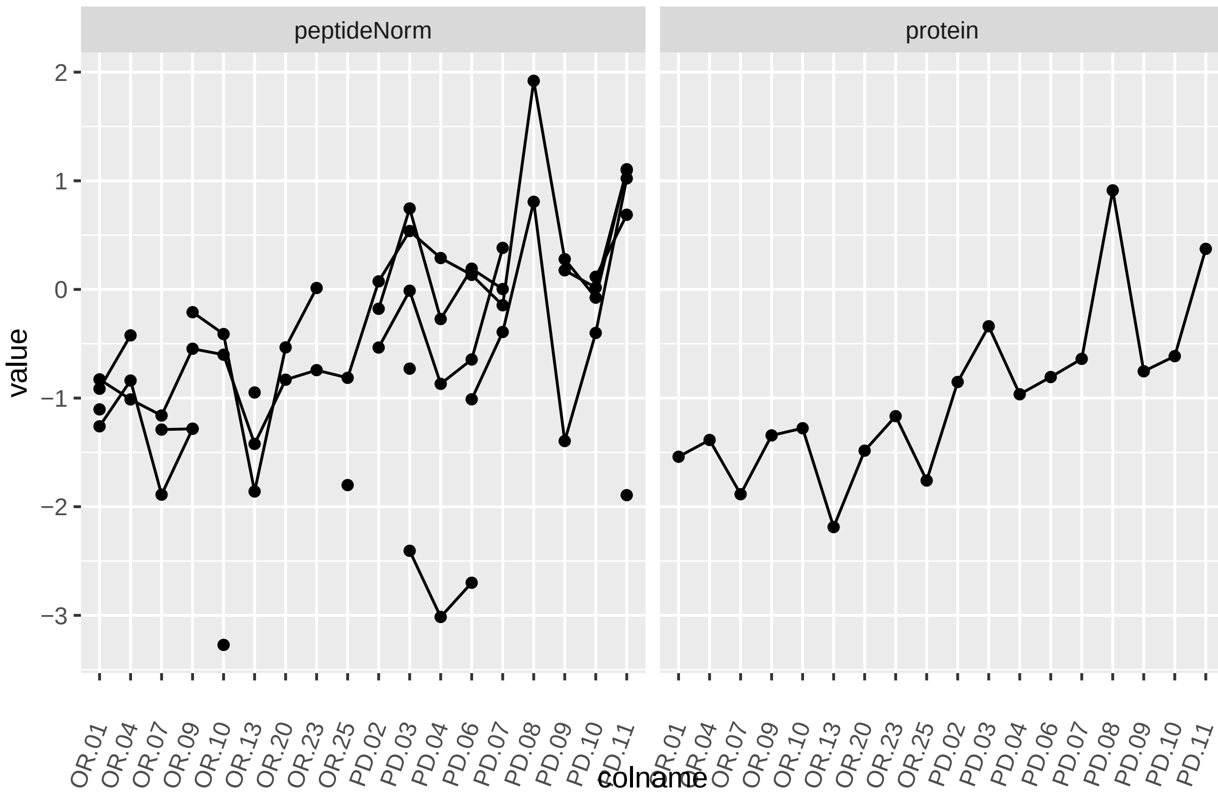


P20962
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
−4
−5
OR.01 OR.04 OR.07 OR.09 OR.10 OR.13 OR.20 OR.23 OR.25 PD.02 PD.03 PD.04 PD.06 PD.07 PD.08 PD.09 PD.10 PD.11
sample
rowname
AAEEEDEADPKR
P20962
SVEAAAELSAK
prognosis
OR
PD

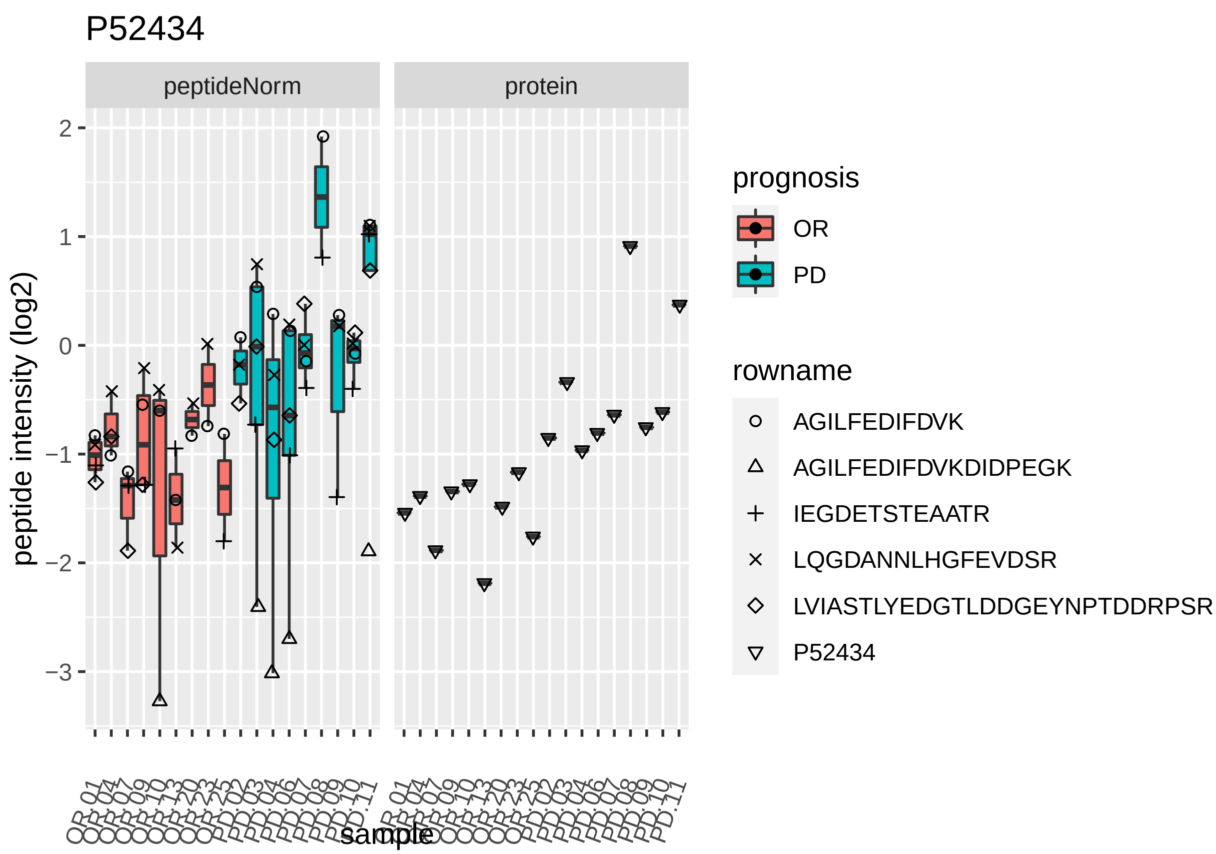

Q14980
peptideNorm
protein
value
2.5
0.0
−2.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

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
EAAGR	+	IQAELAVILK	=	LQQLGEAHQAETEVLRR	O	QQEQAD
QEQASQGLR	,	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
EDLENFLQK	4	LDFVCSFLQK	F	QAQLAQTLQQQEQASQGLR	X	SNRDEL

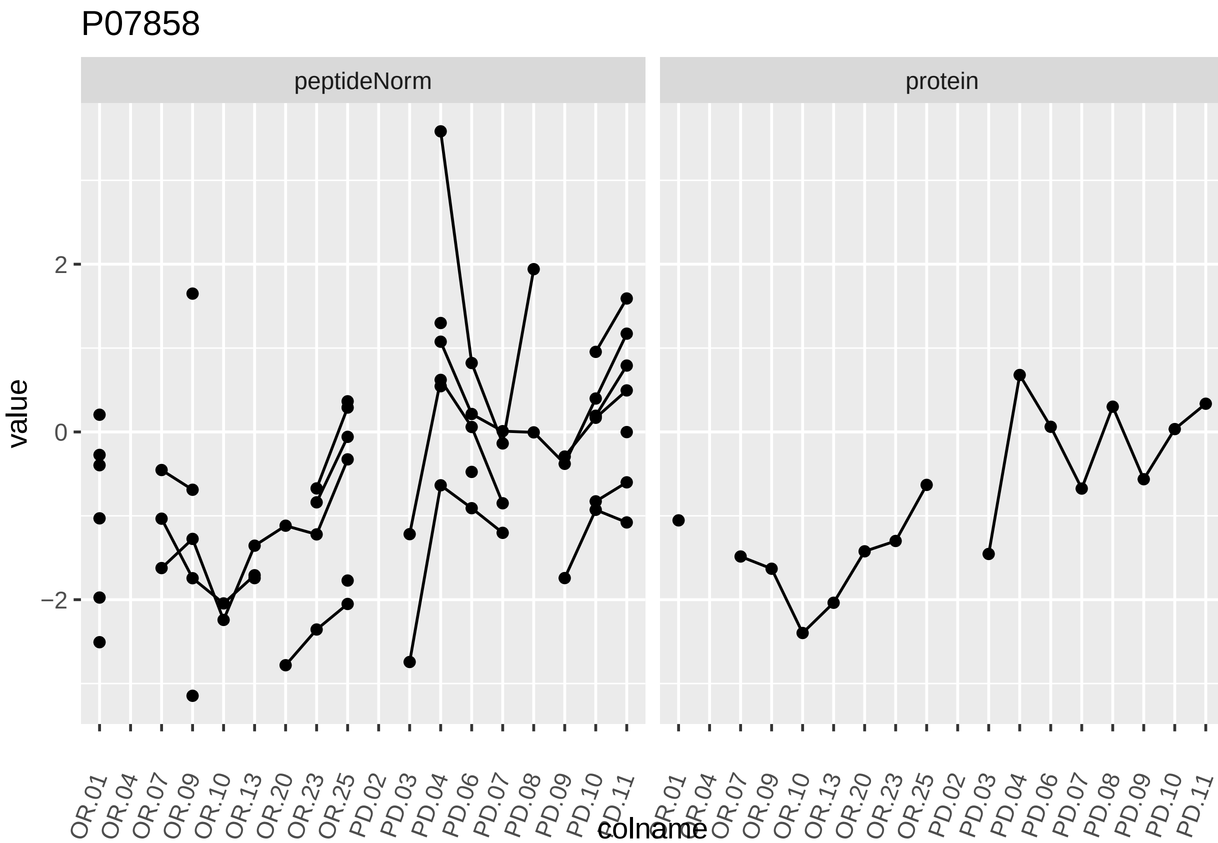
P52434

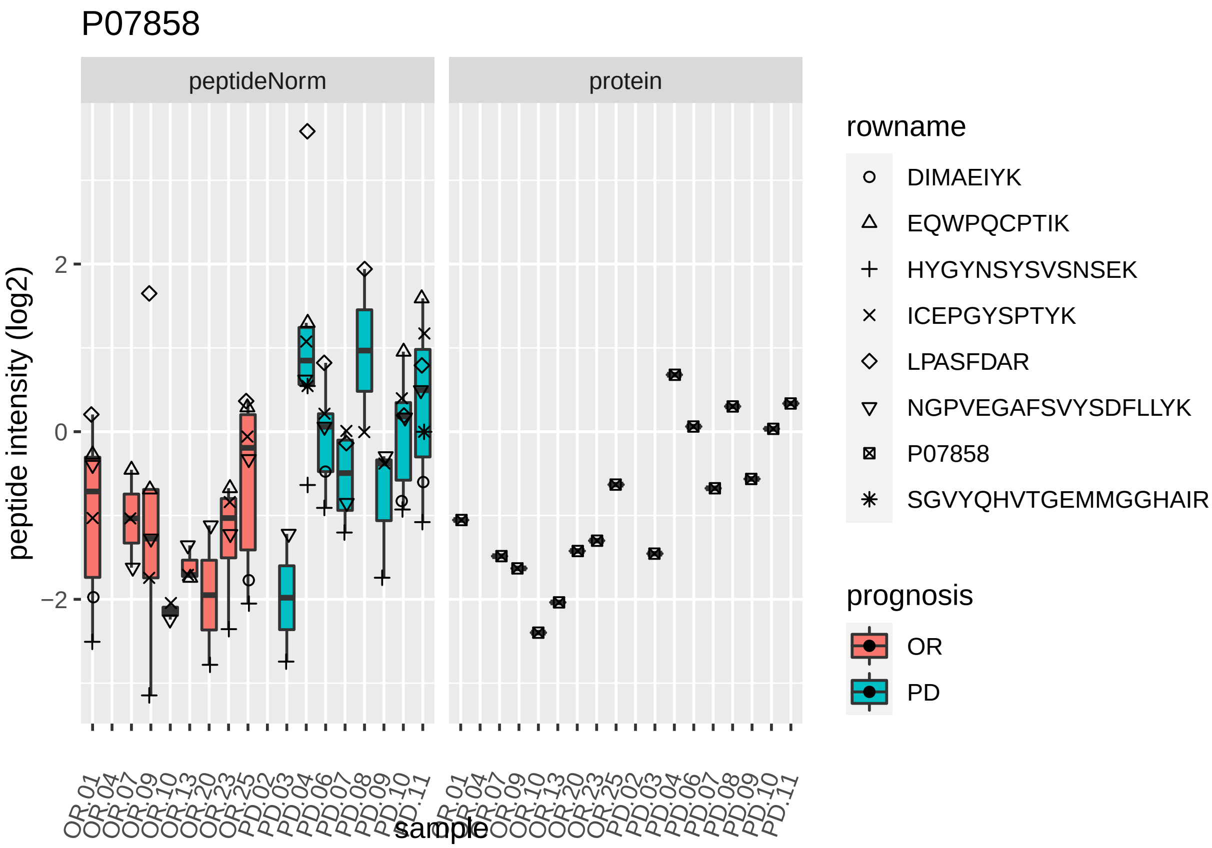


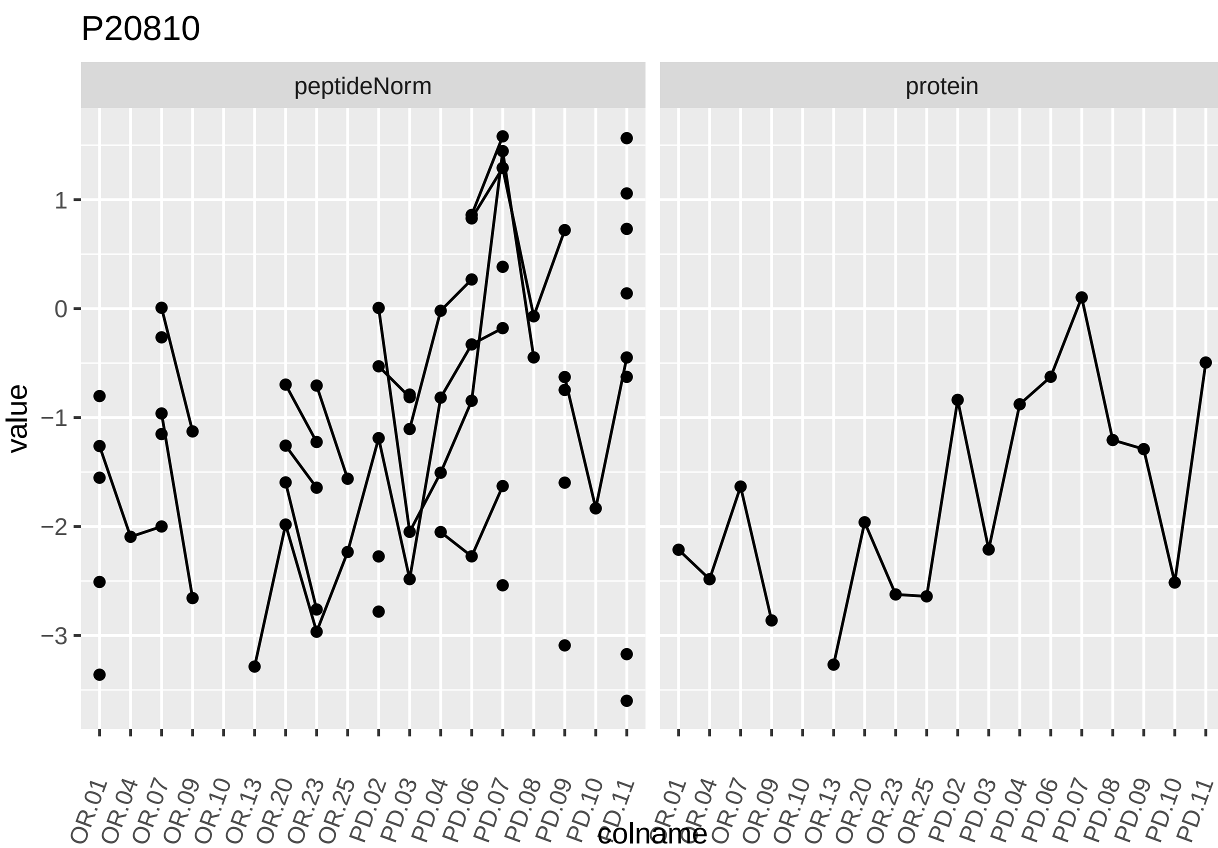
peptideNorm
protein
value
colname
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



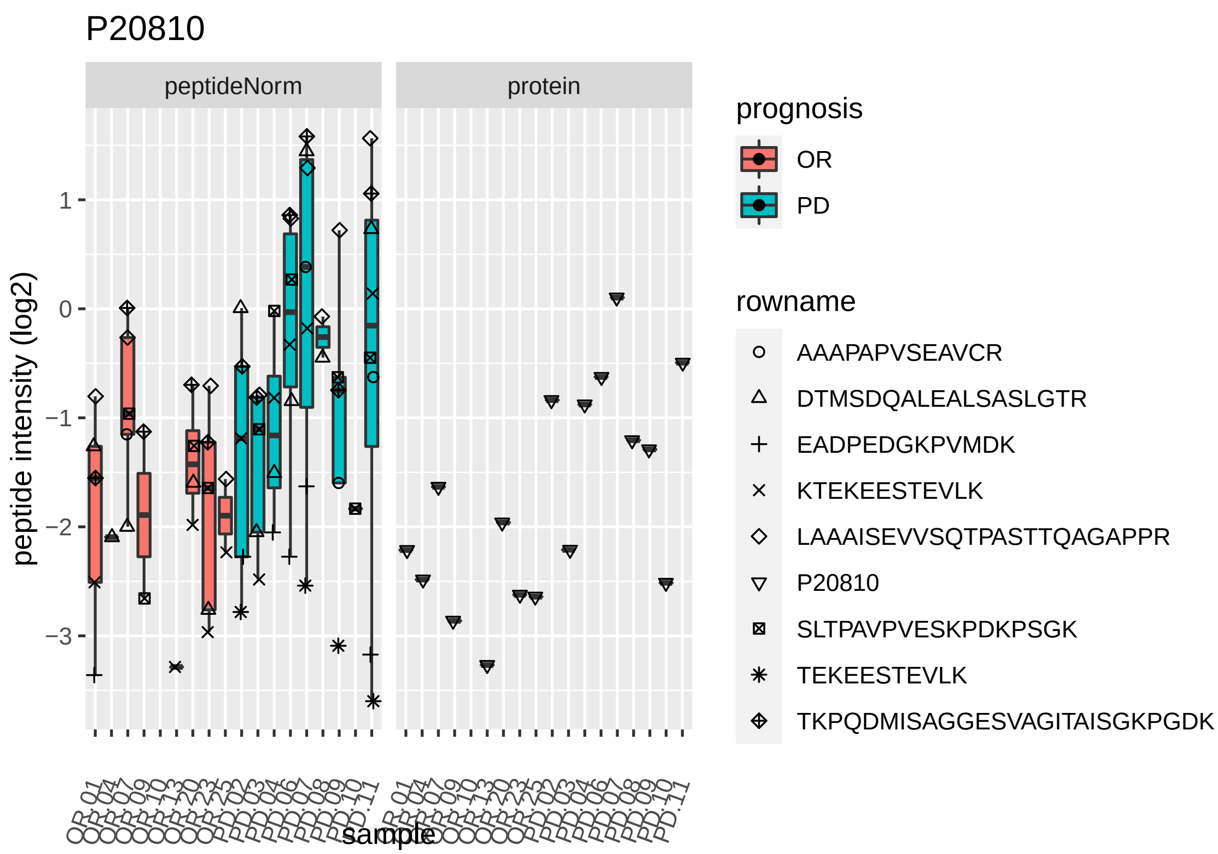
P52434
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
sample
prognosis
OR
PD
rowname
AGILFEDIFDVK
AGILFEDIFDVKDIDPEGK
IEGDETSTEAATR
LQGDANNLHGFEVDSR
LVIASTLYEDGTLDDGEYNPTDDRPSR
P52434


P07858
peptideNorm
protein
value
colname
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

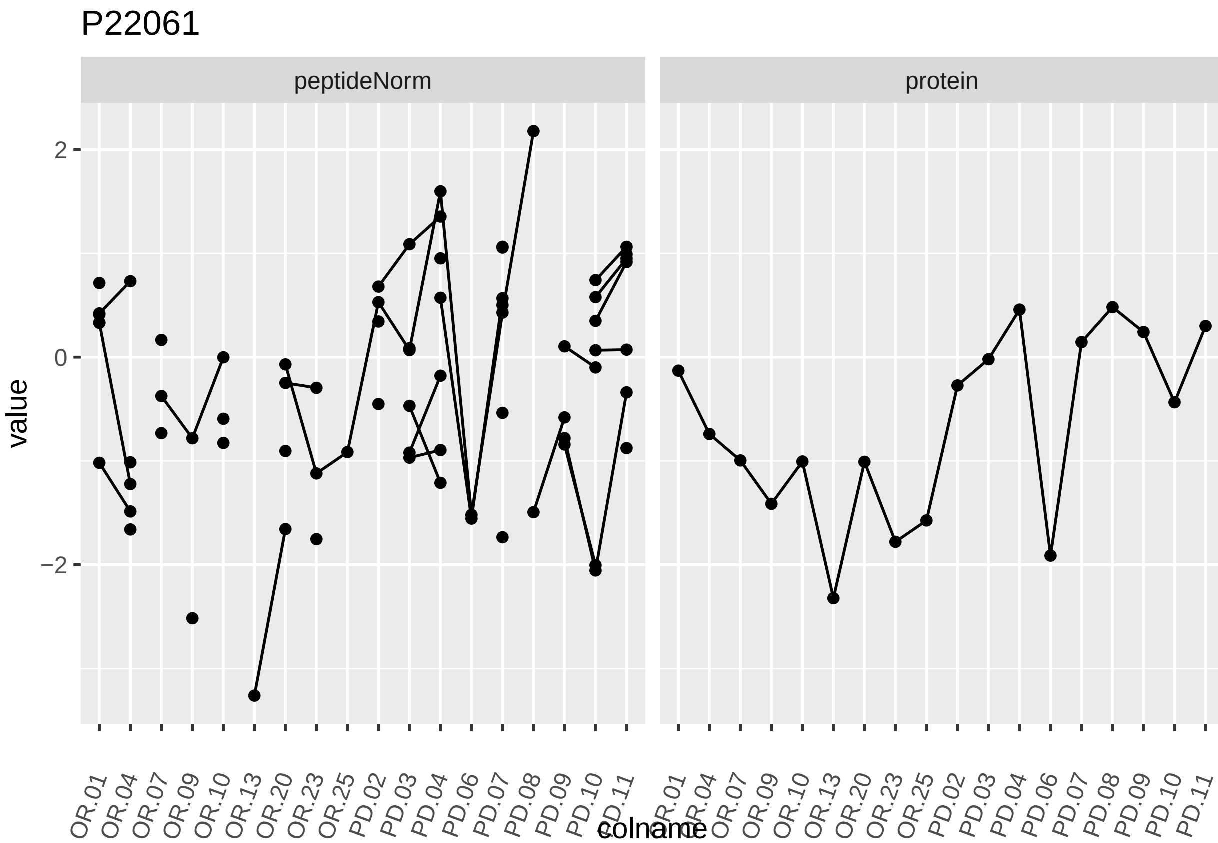

P07858
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
DIMAEIYK
EQWPQCPTIK
HYGYNSYSVSNSEK
ICEPGYSPTYK
LPASFDAR
NGPVEGAFSVYSDFLLYK
P07858
SGVYQHVTGEMMGGHAIR
prognosis
OR
PD



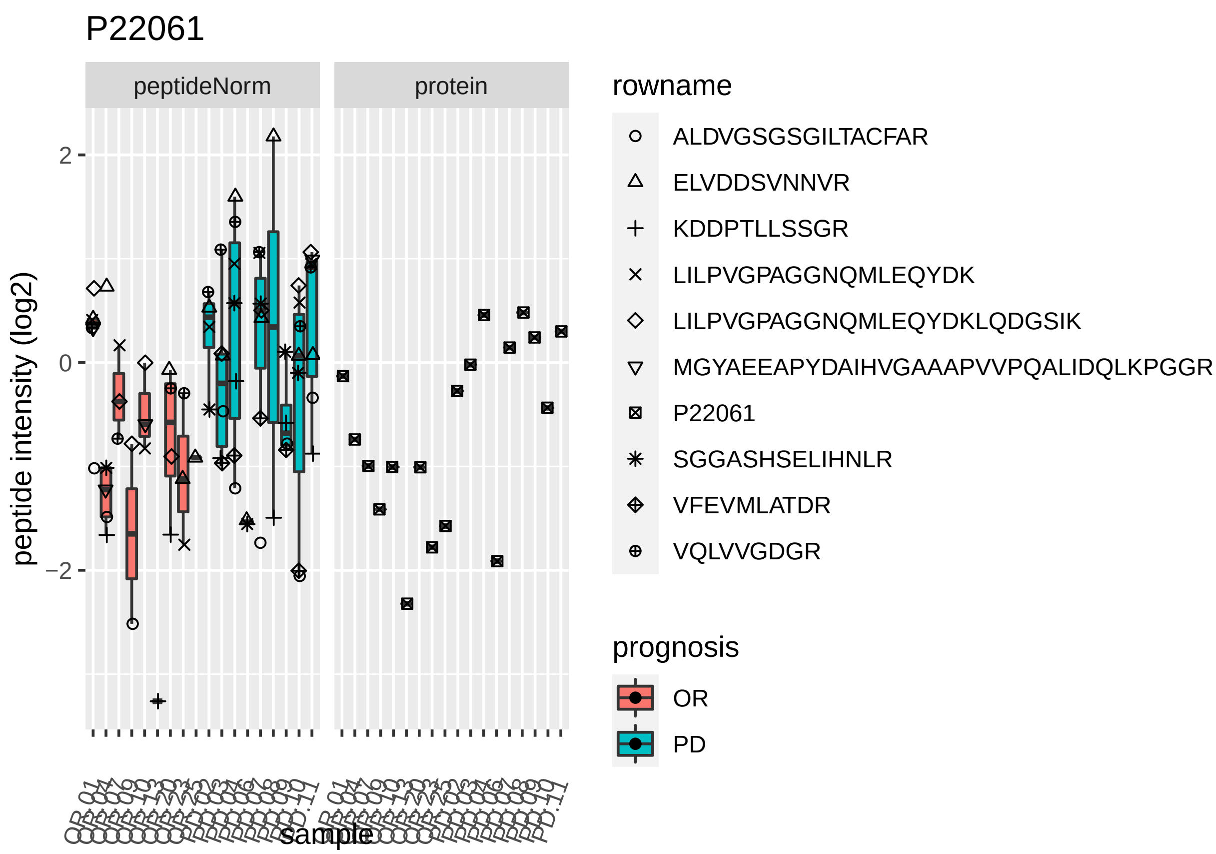
P20810
peptideNorm
protein
value
colname
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



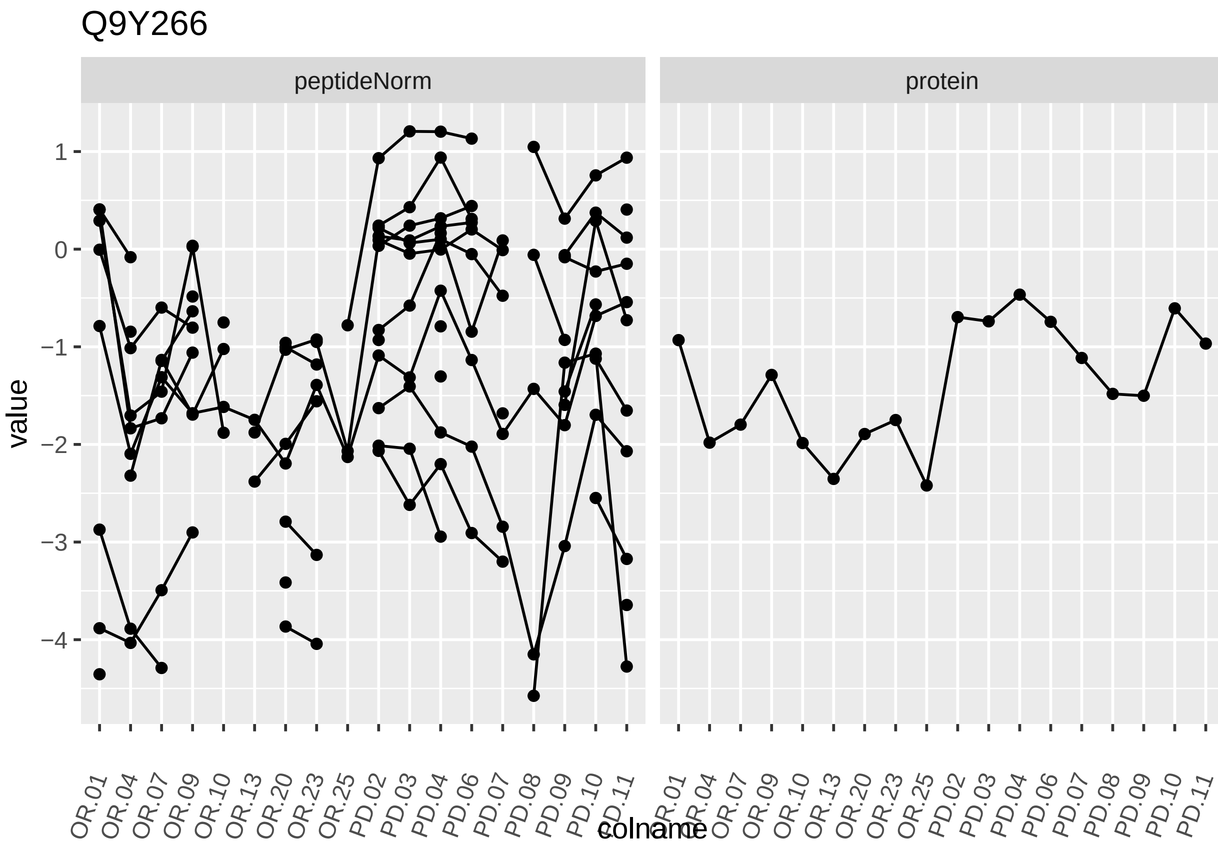
P20810
peptideNorm
protein
peptide intensity (log2)
sample
prognosis
OR
PD
rowname
AAAPAPVSEAVCR
DTMSDQALEALSASLGTR
EADPEDGKPVMDK
KTEKEESTEVLK
LAAAISEVVSQTPASTTQAGAPPR
P20810
SLTPAVPVESKPDKPSGK
TEKEESTEVLK
TKPQDMISAGGESVAGITAISGKPGDK



P22061
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



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



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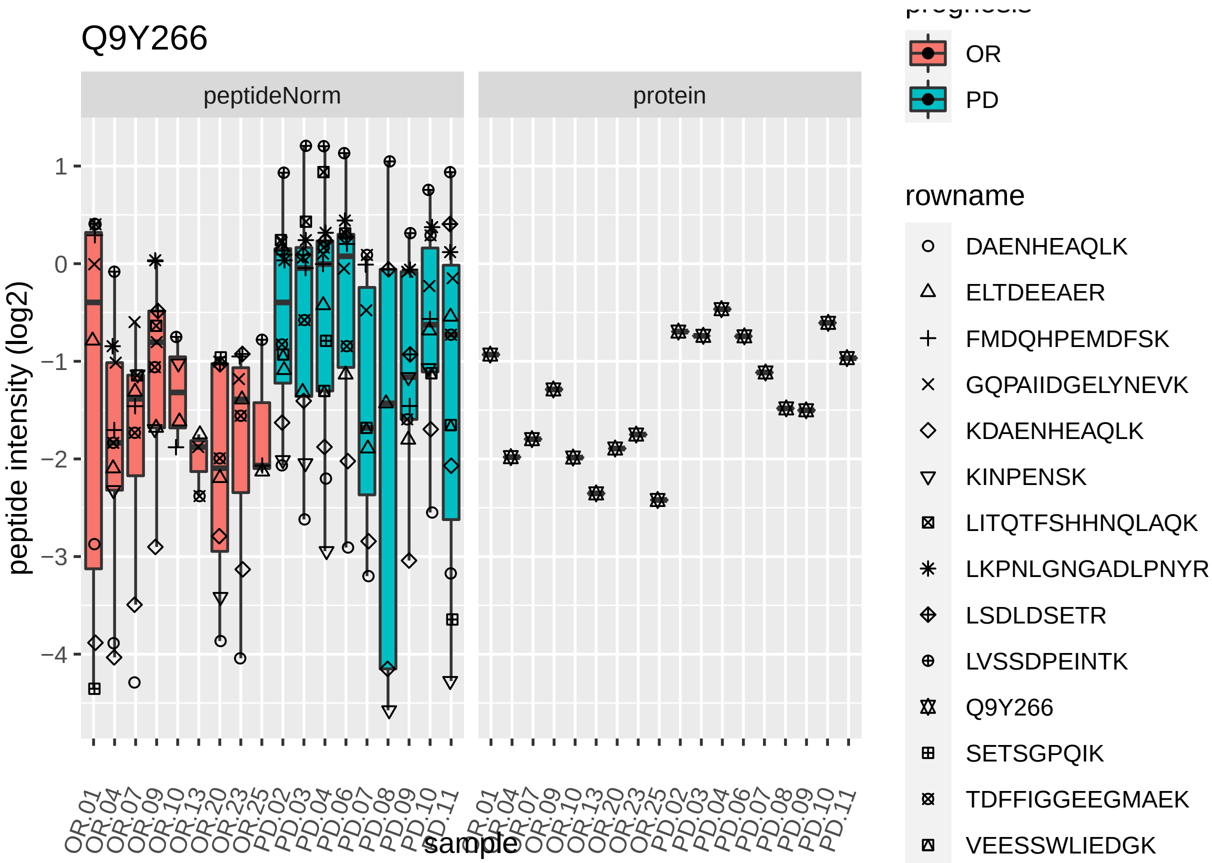
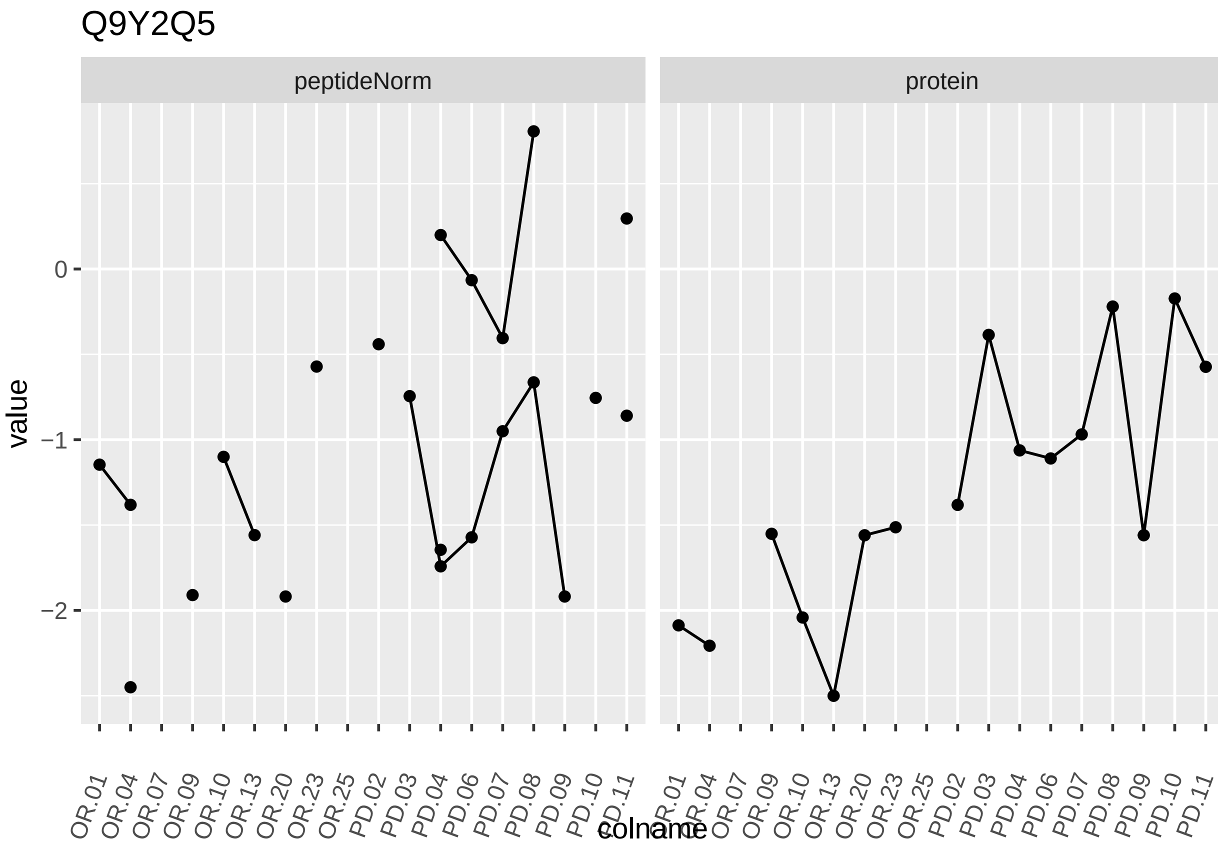
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q9Y266
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
prognosis
OR
PD
rowname
DAENHEAQLK
ELTDEEAER
FMDQHPEMDFSK
GQPAIIDGELYNEVK
KDAENHEAQLK
KINPENSK
LITQTFSHHNQLAQK
LKPNLGNGADLPNYR
LSDLDSETR
LVSSDPEINTK
Q9Y266
SETSGPQIK
TDFFIGGEEGMAEK
VEESSWLIEDGK


Q9Y2Q5
peptideNorm
protein
value
0
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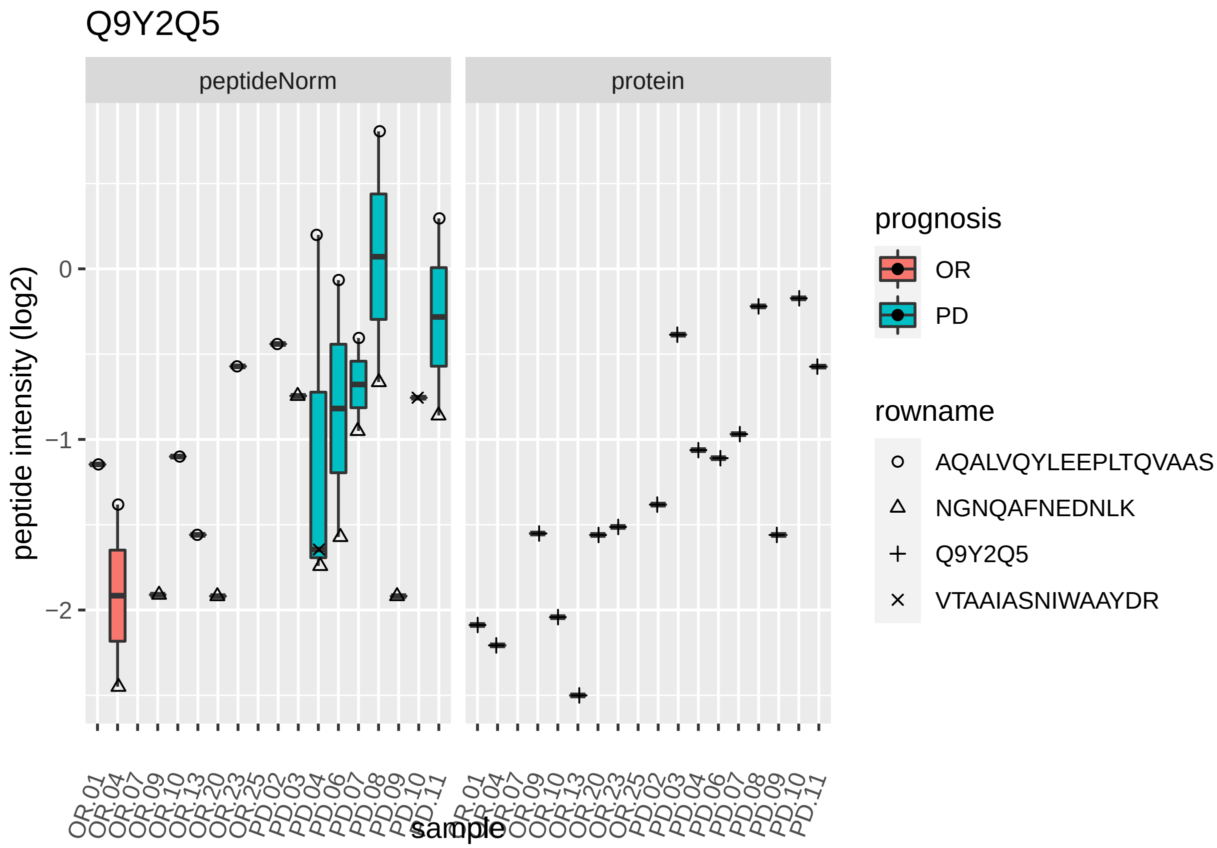
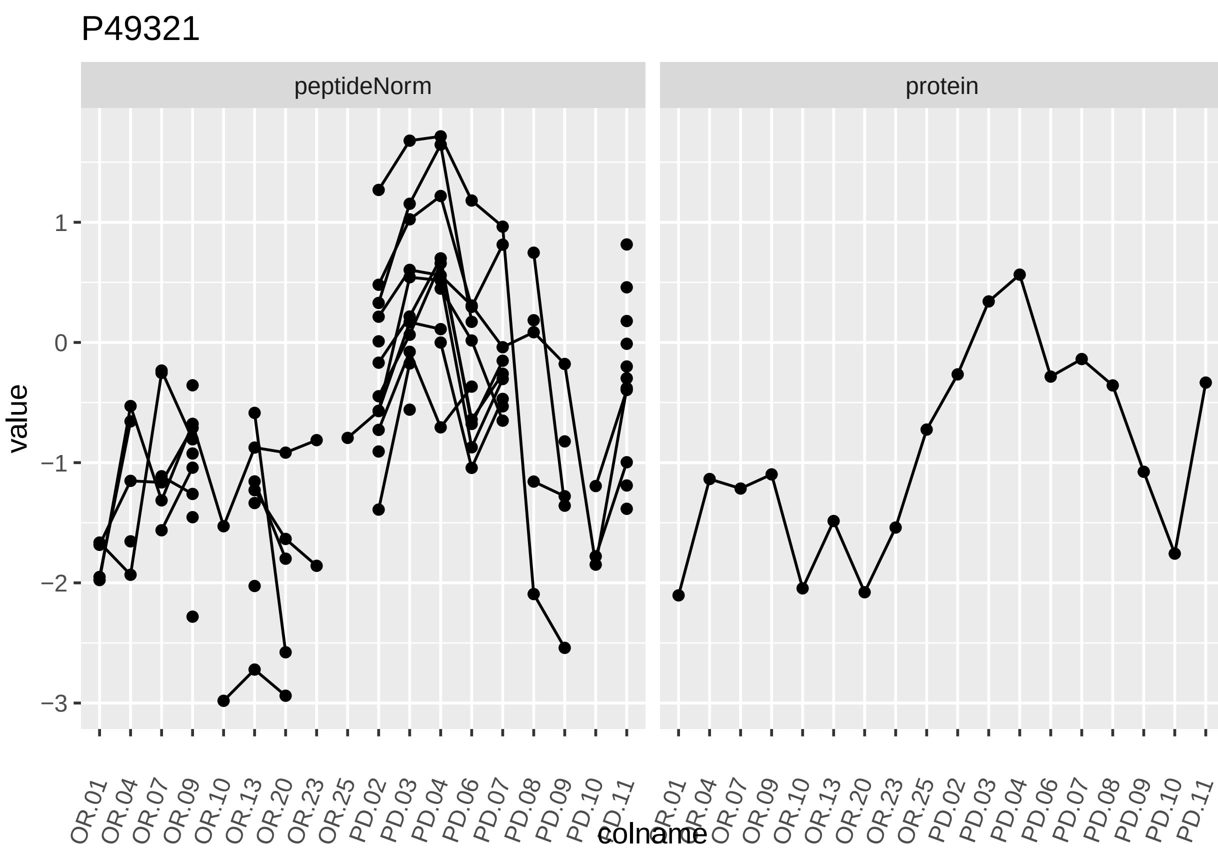
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9Y2Q5
peptideNorm
protein
peptide intensity (log2)
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


P49321
peptideNorm
protein
value
colname
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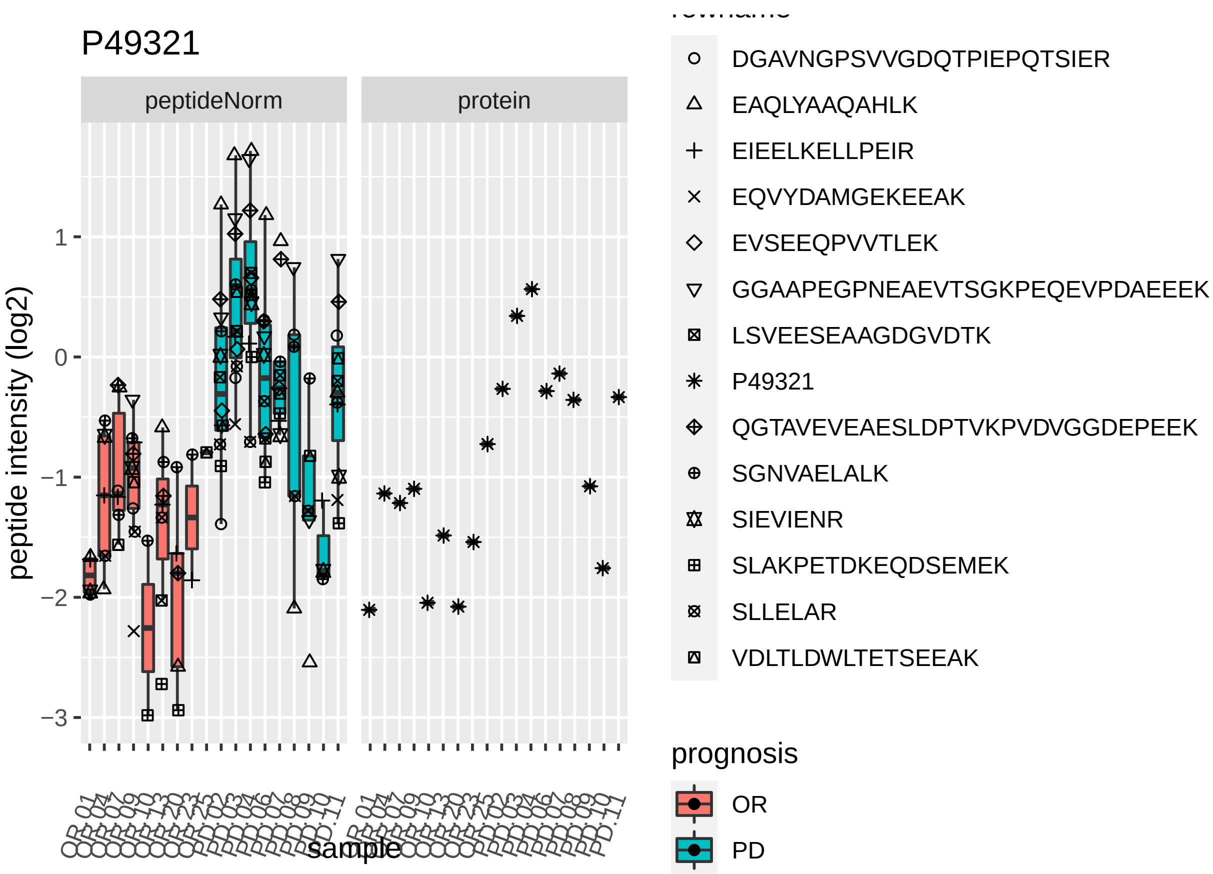
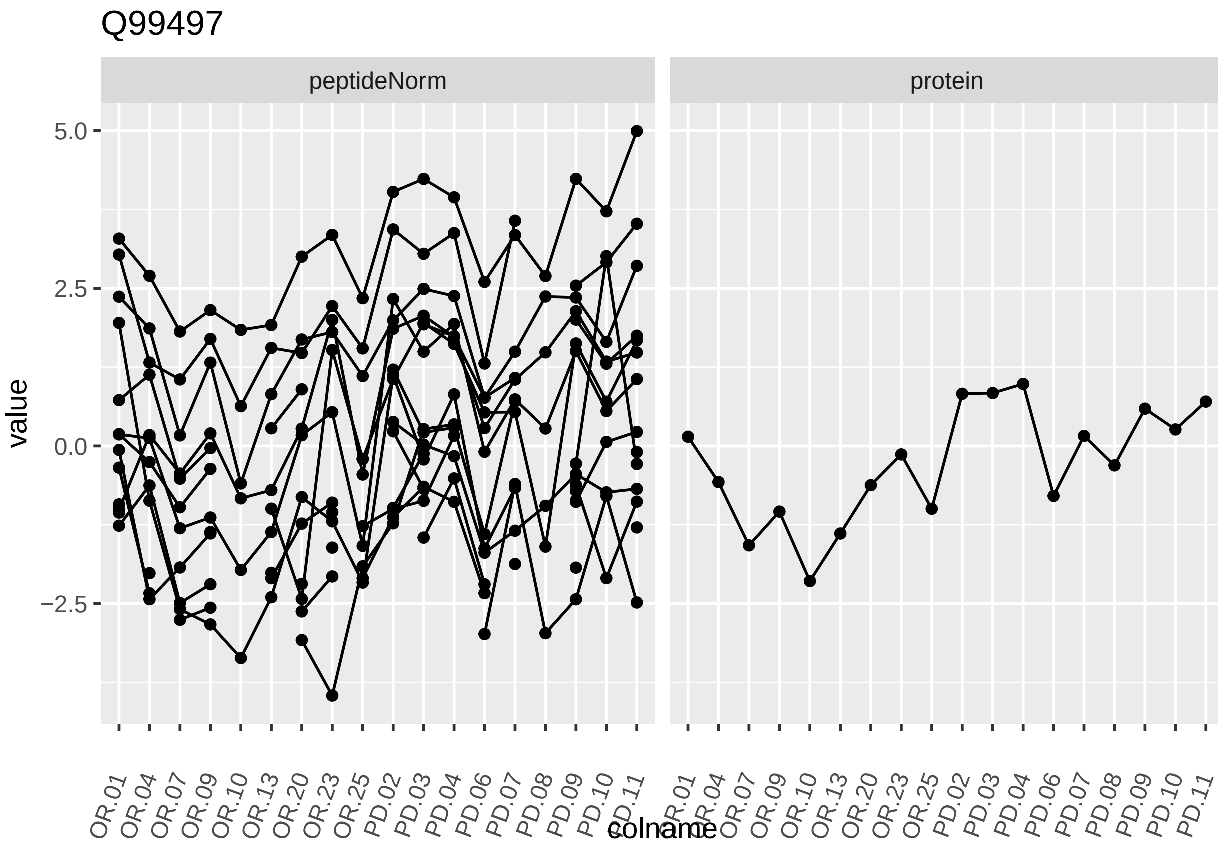
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P49321
peptideNorm
protein
peptide intensity (log2)
sample
rowname
DGAVNGPSVVGDQTPIEPQTSIER
EAQLYAAQAHLK
EIEELKELLPEIR
EQVYDAMGEKEEAK
EVSEEQPVVTLEK
GGAAPEGPNEAEVTSGKPEQEVPDAEEEK
LSVEESEAAGDGVDTK
P49321
QGTAVEVEAESLDPTVKPVDVGGDEPEEK
SGNVAELALK
SIEVIENR
SLAKPETDKEQDSEMEK
SLLELAR
VDLTLDWLTETSEEAK
prognosis
OR
PD



Q99497
peptideNorm
protein
value
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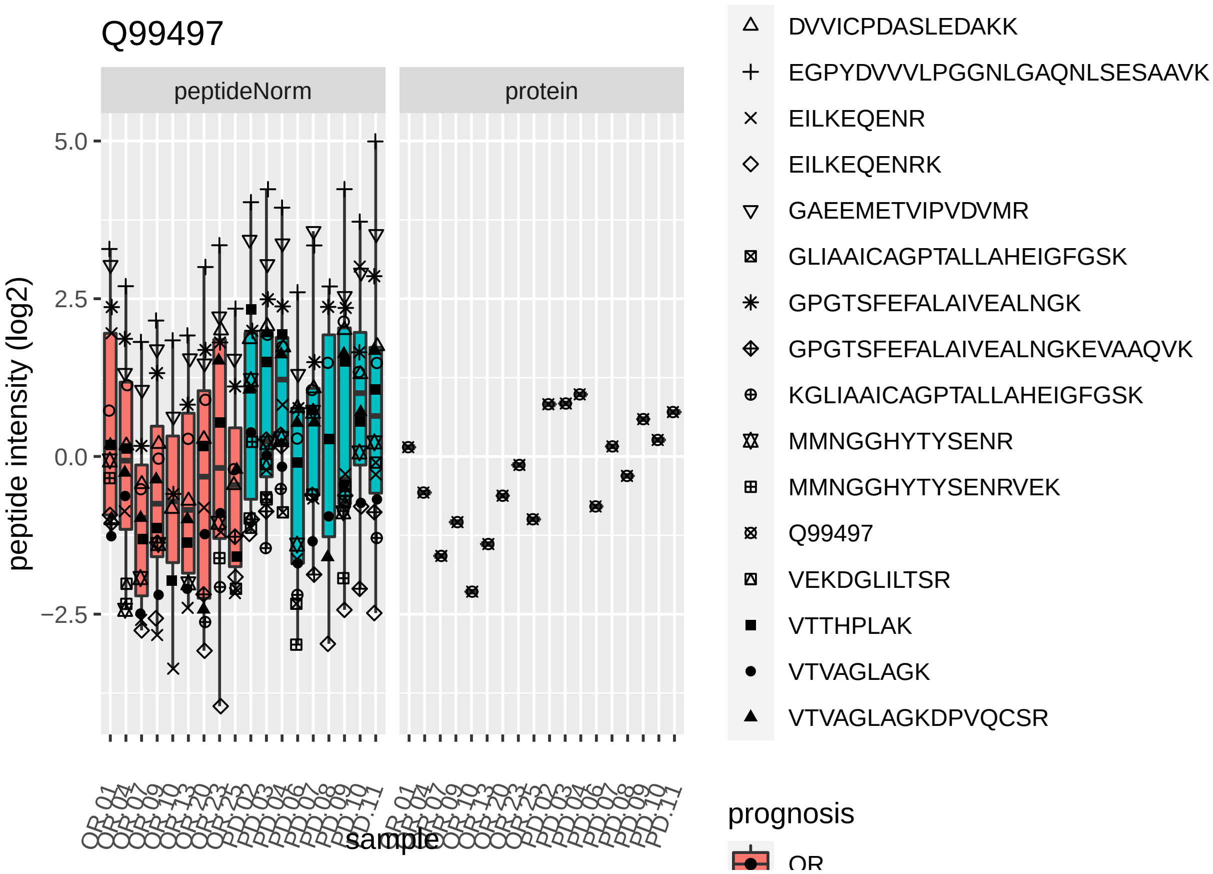
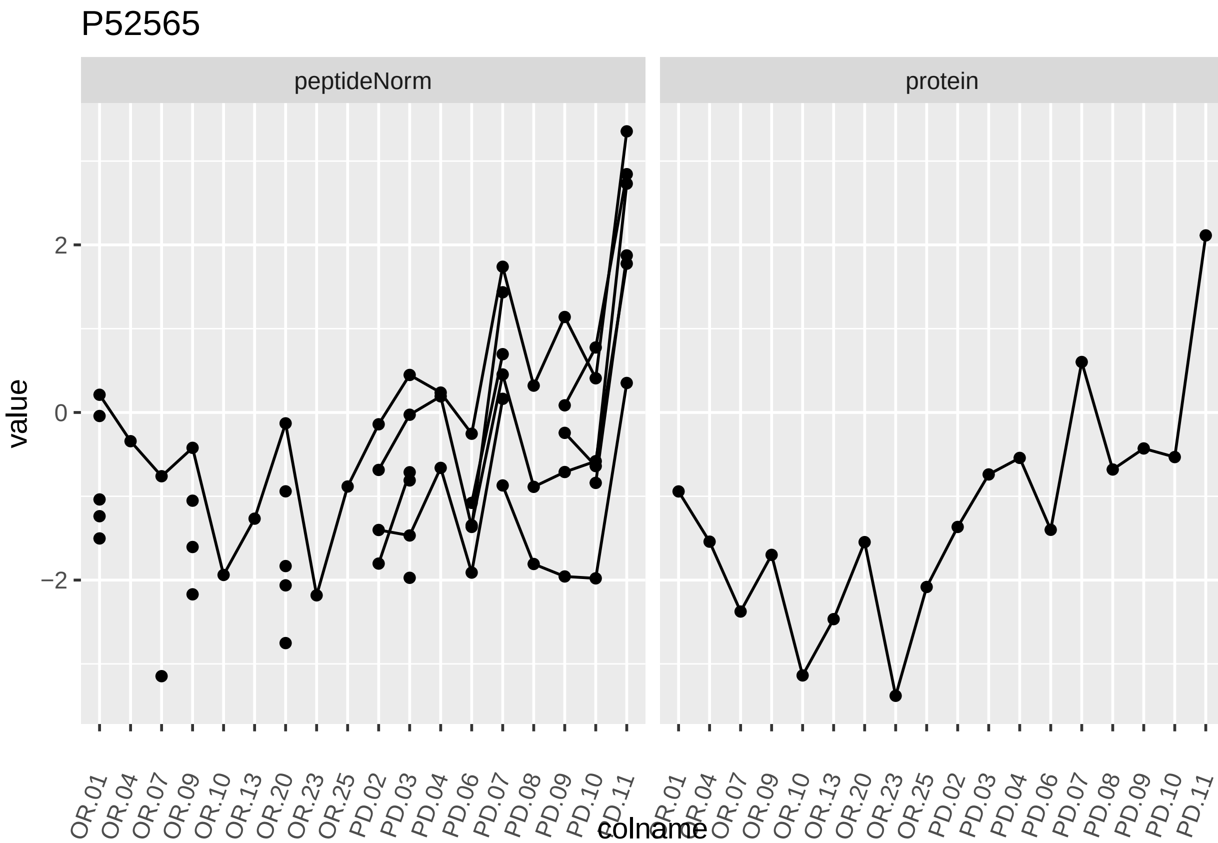
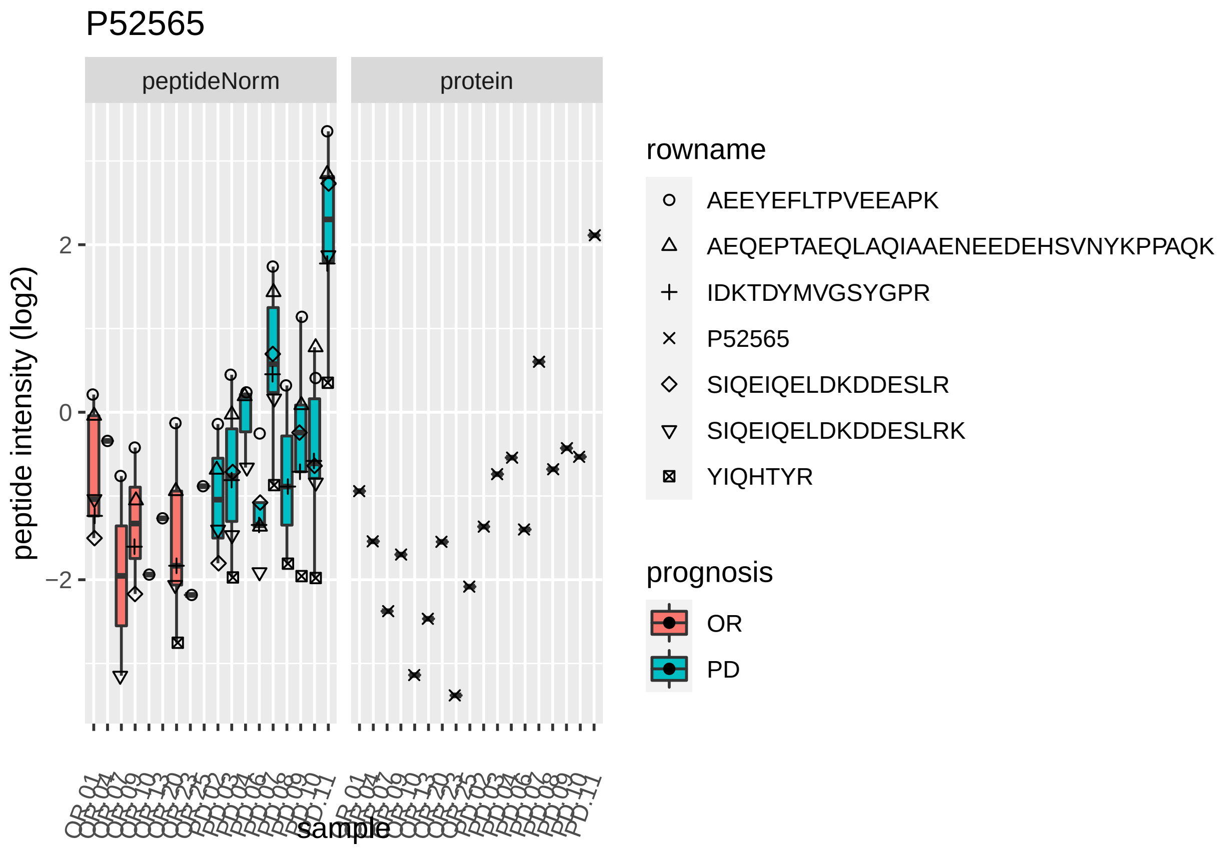
2.5
0.0
−2.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname



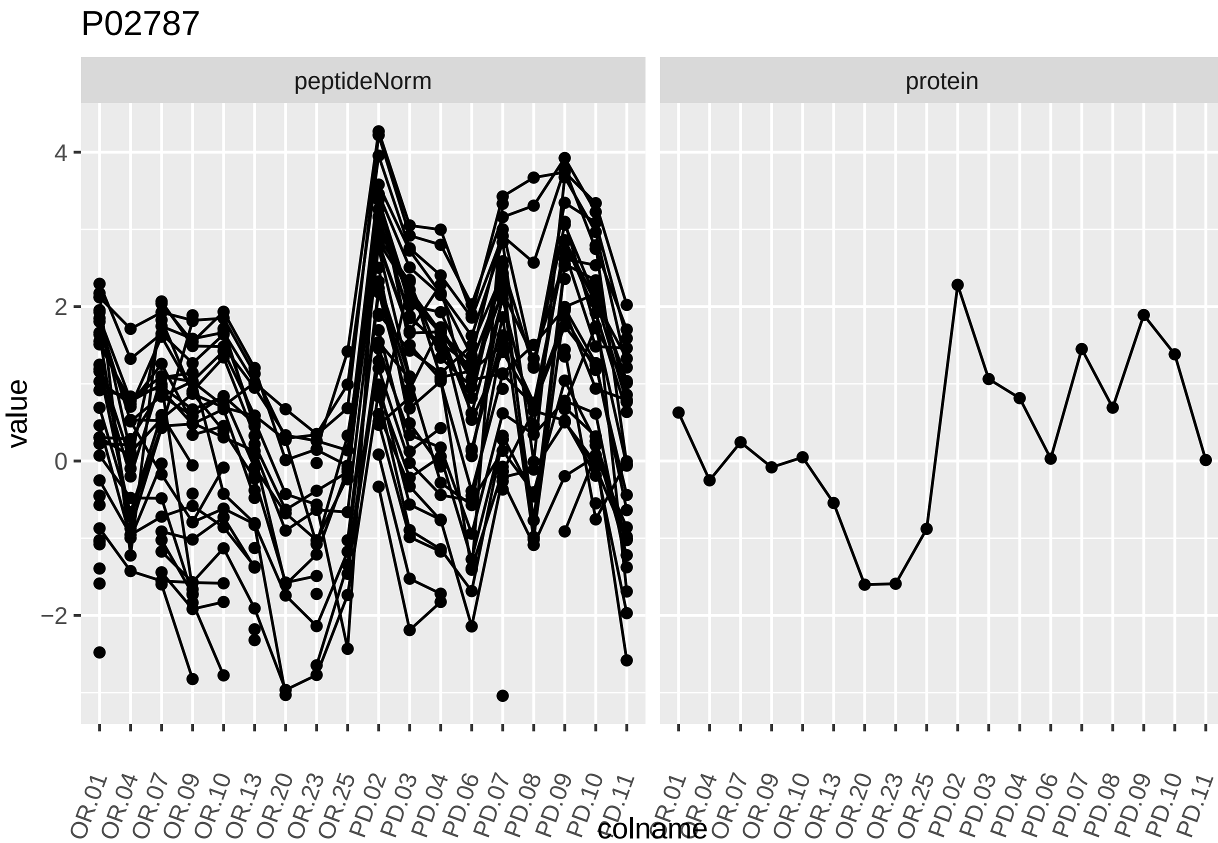
Q99497
peptideNorm
protein
5.0
2.5
0.0
−2.5
peptide intensity (log2)
sample
DVVICPDASLEDAKK
EGPYDVVVLPGGNLGAQNLSESAAVK
EILKEQENR
EILKEQENRK
GAEEMETVIPVDVMR
GLIAAICAGPTALLAHEIGFGSK
GPGTSFEFALAIVEALNGK
GPGTSFEFALAIVEALNGKEVAAQVK
KGLIAAICAGPTALLAHEIGFGSK
MMNGGHYTYSENR
MMNGGHYTYSENRVEK
Q99497
VEKDGLILTSR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



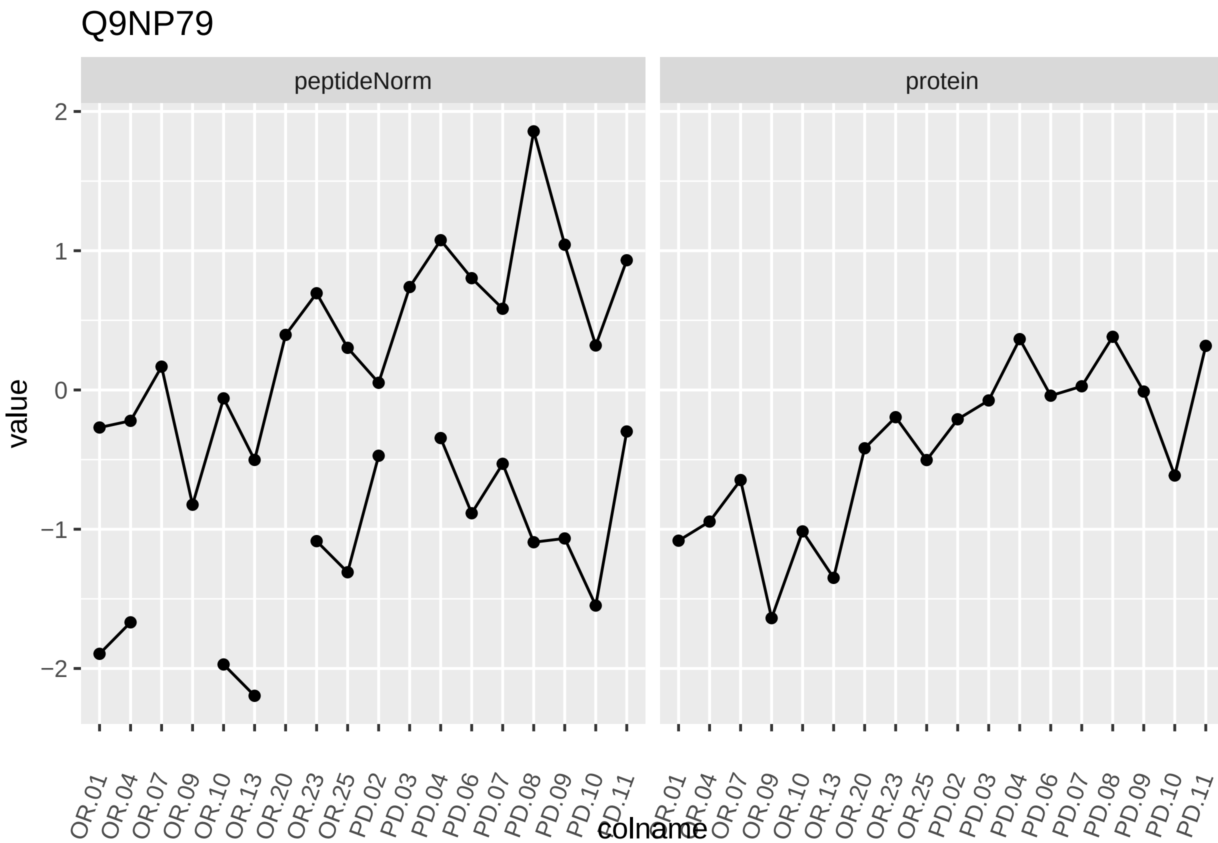
P52565
peptideNorm
protein
value
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

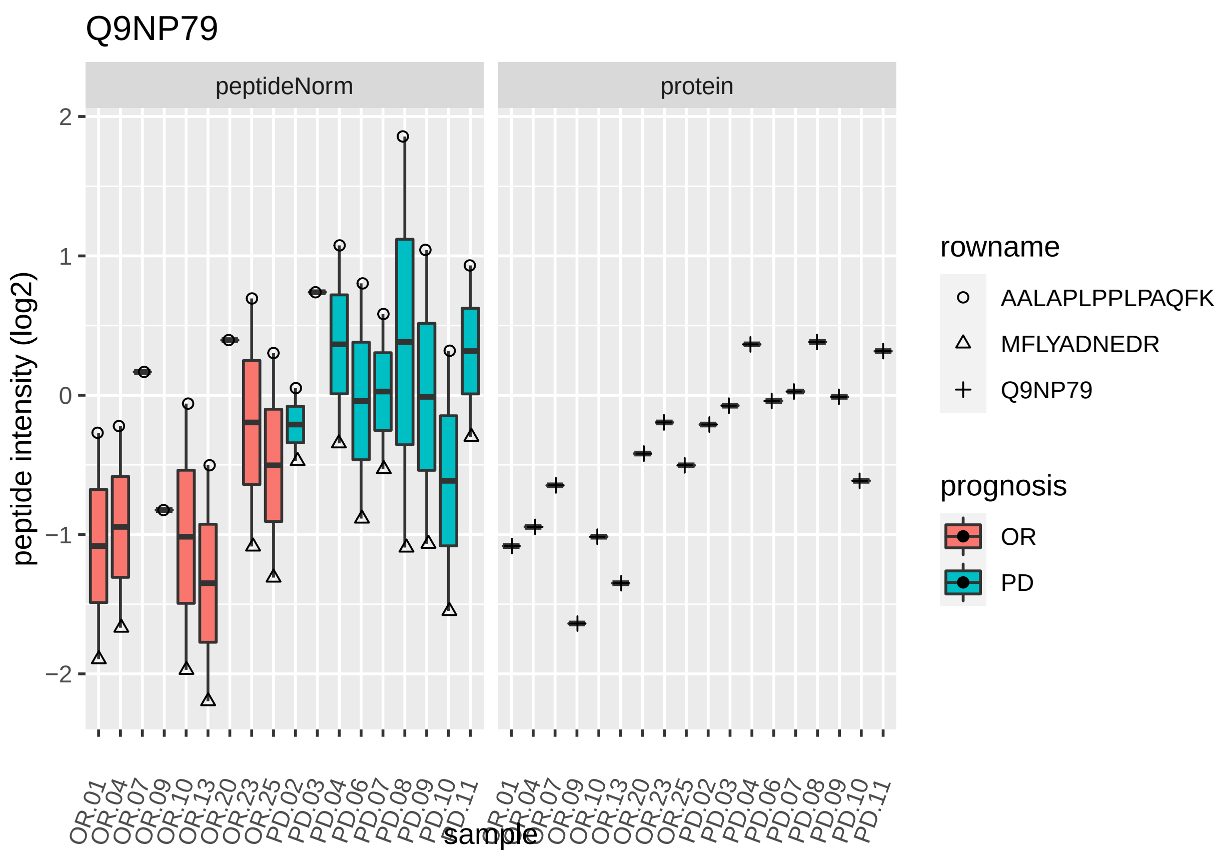


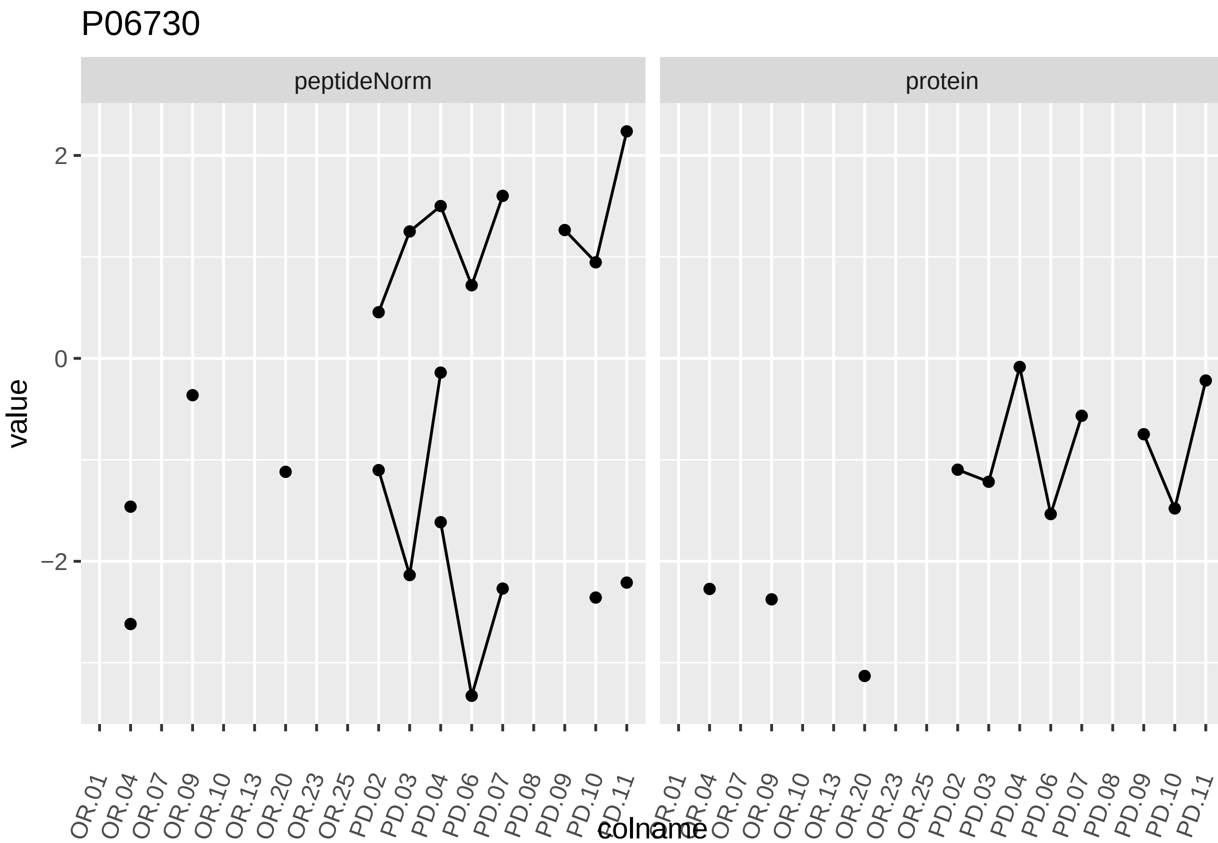
P52565
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
rowname
AEEYEFLTPVEEAPK
AEQEPTAEQLAQIAAENEEDEHSVNYKPPAQK
IDKTDYMVGSYGPR
P52565
SIQEIQELDKDDESLR
SIQEIQELDKDDESLRK
YIQHTYR
prognosis
OR
PD


P02787
peptideNorm
protein
value
colname
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

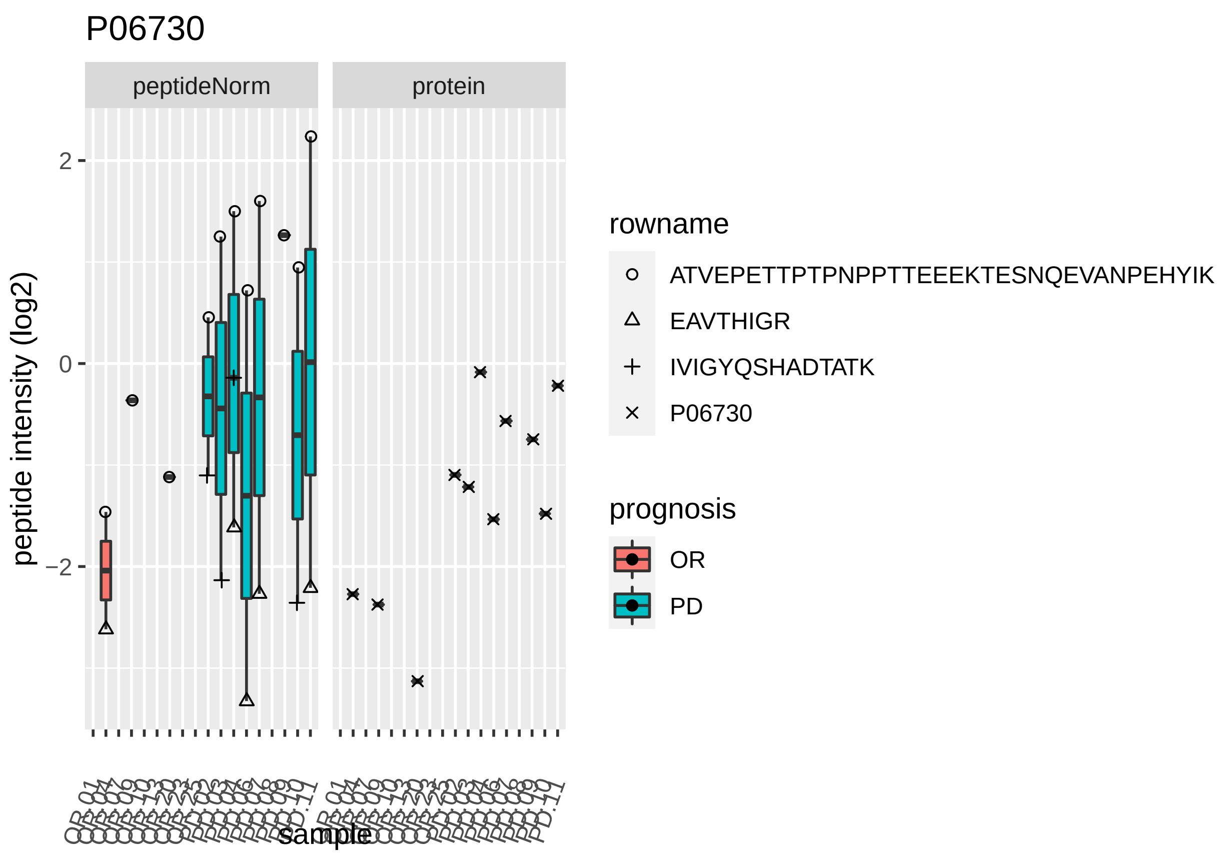

P02787
peptide intensity (log2)
4
2
0
−2
sample
ASYLDCIR
CDEWSVNSVGK
CSTSSLLEACTFR
DCHLAQVPSHTVVAR
DDTVCLAK
DGAGDVAFVK
DLLFRDDTVCLAK
DQYELLCLDNTR
DSAHGFLK
DSGFQMNQLR
DYELLCLDGTR
EDPQTFYYAVAVVK
EFQLFSSPHGK
EGTCPEAPTDECKPVK
EGYYGYTGAFR
FDEFFSEGCAPGSK
HQTVPQNTGGK
KASYLDCIR
KPVDEYKDCHLAQVPSHTVVAR
KPVEEYANCHLAR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

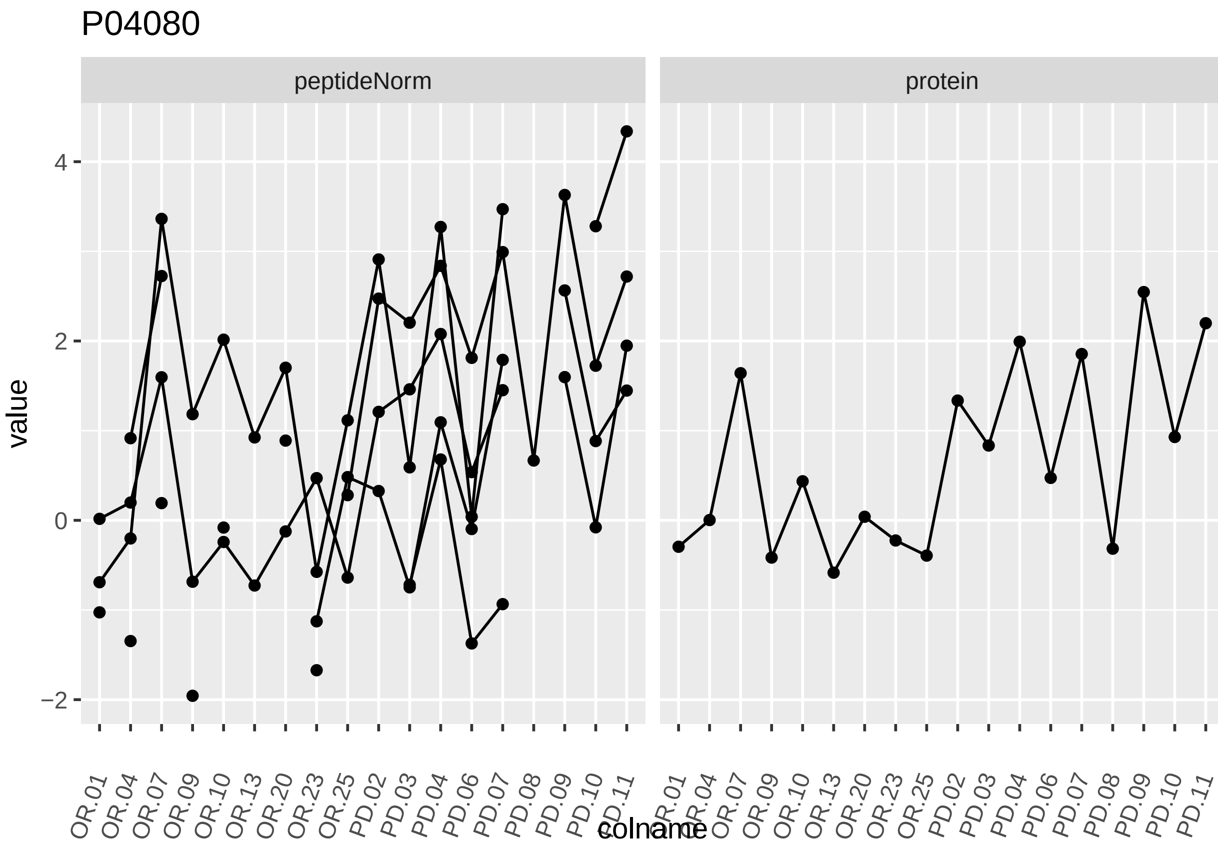

Q9NP79
peptideNorm
protein
value
colname
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

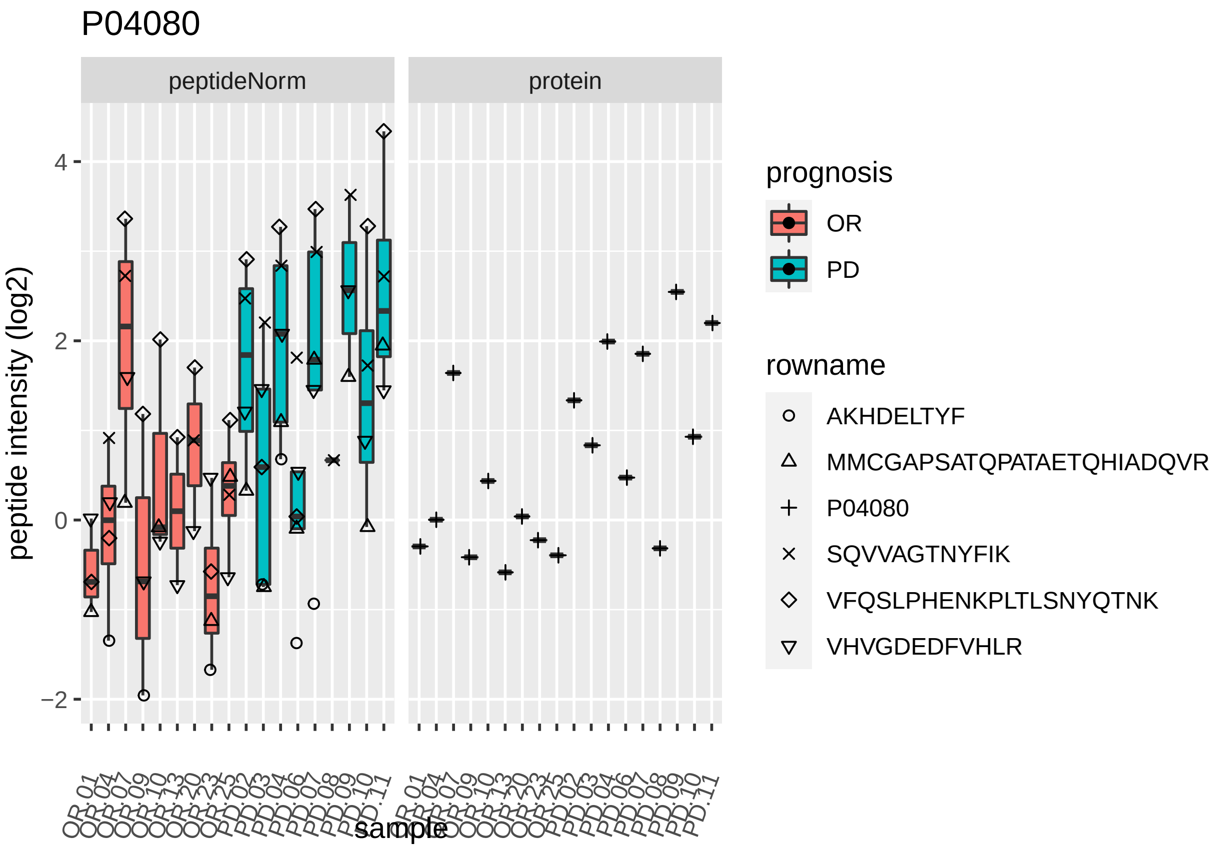

Q9NP79
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AALAPLPPLPAQFK
MFLYADNEDR
Q9NP79
prognosis
OR
PD



P06730
peptideNorm
protein
value
colname
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


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


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



P04080
peptideNorm
protein
peptide intensity (log2)
sample
prognosis
OR
PD
rowname
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P04080
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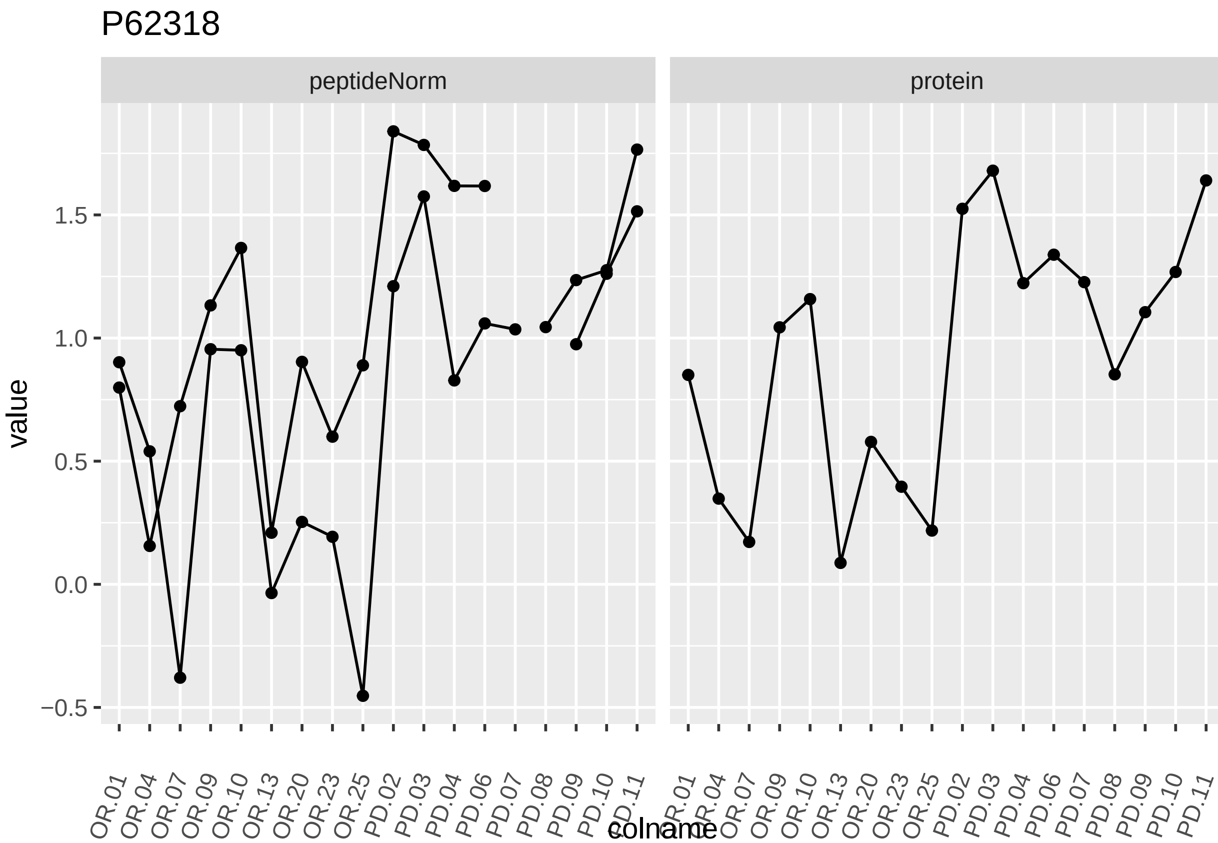
VFQSLPHENKPLTLSNYQTNK
VHVGDEDFVHLR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peptideNorm
protein
value
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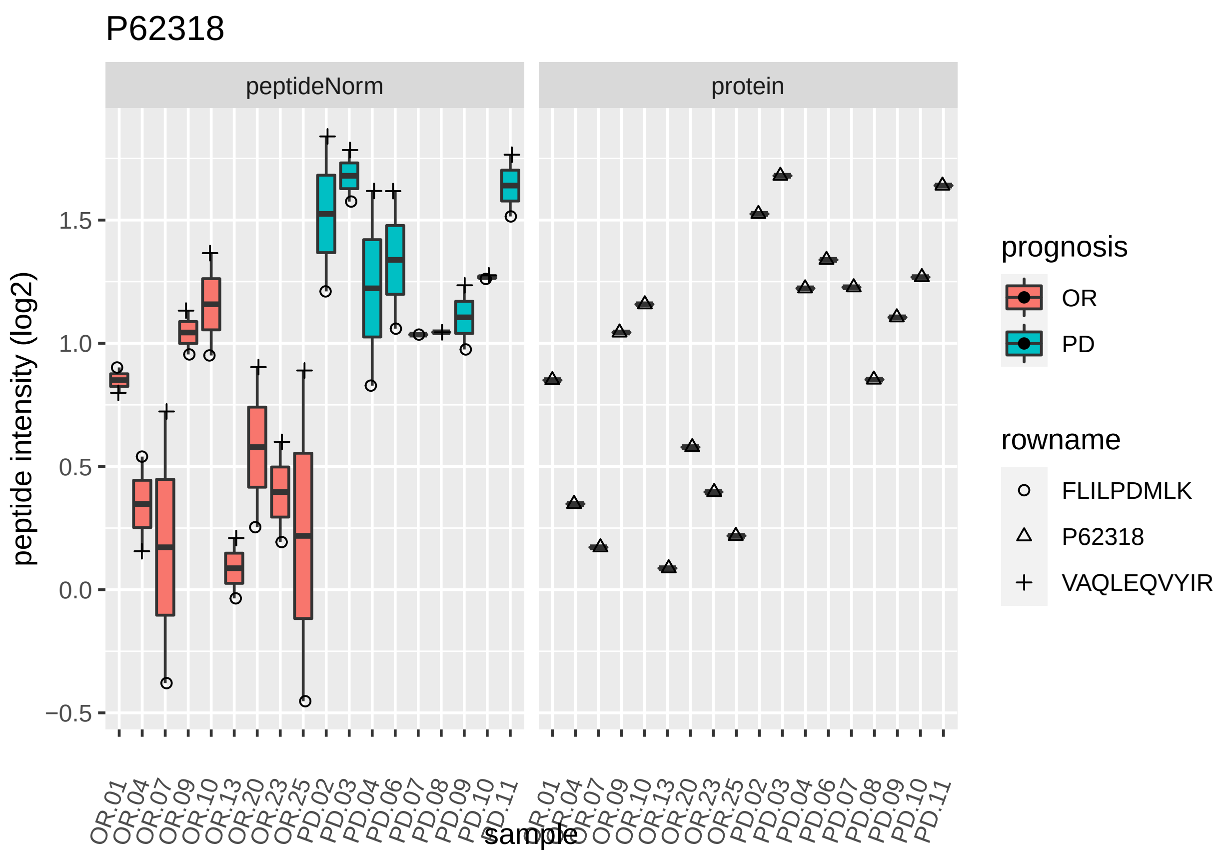
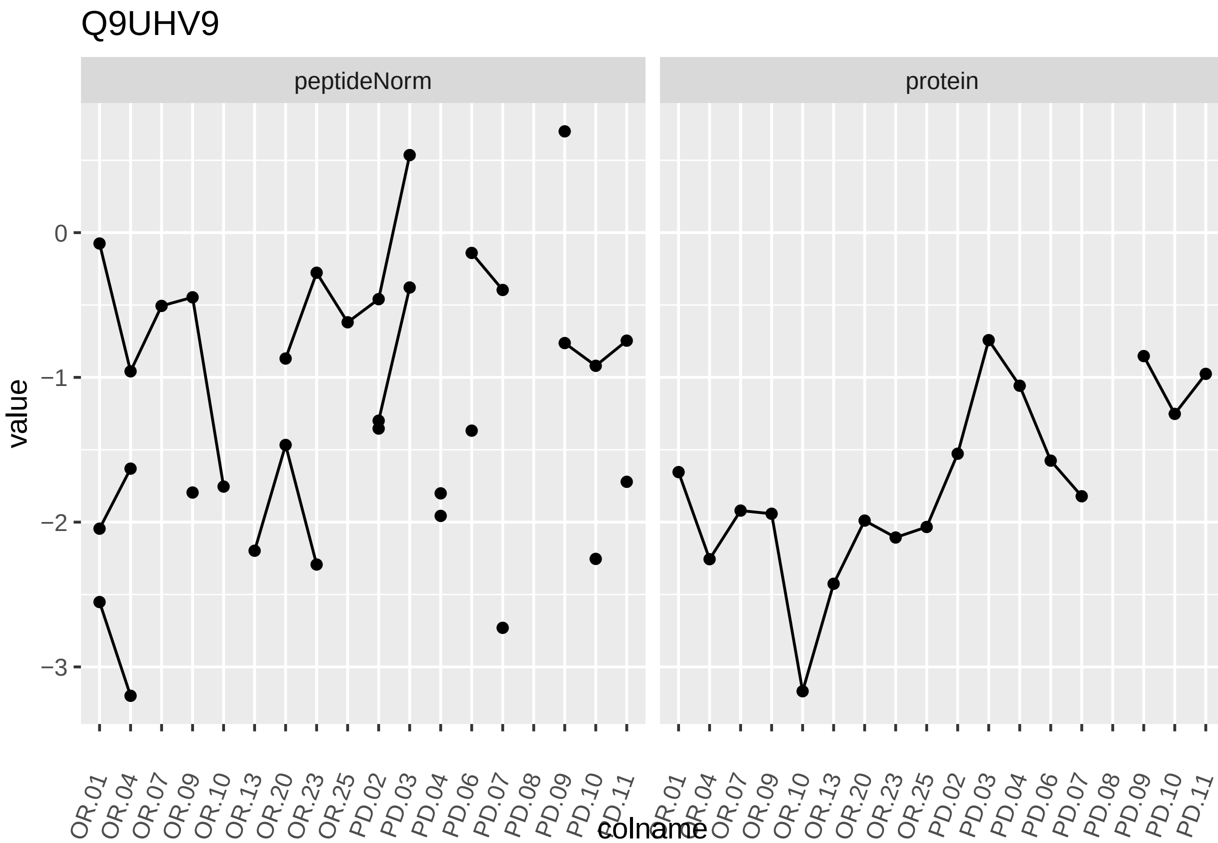
0.5
0.0
−0.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P62318
peptideNorm
protein
peptide intensity (log2)
1.5
1.0
0.5
0.0
−0.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
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
FLILPDMLK
P62318
VAQLEQVYIR



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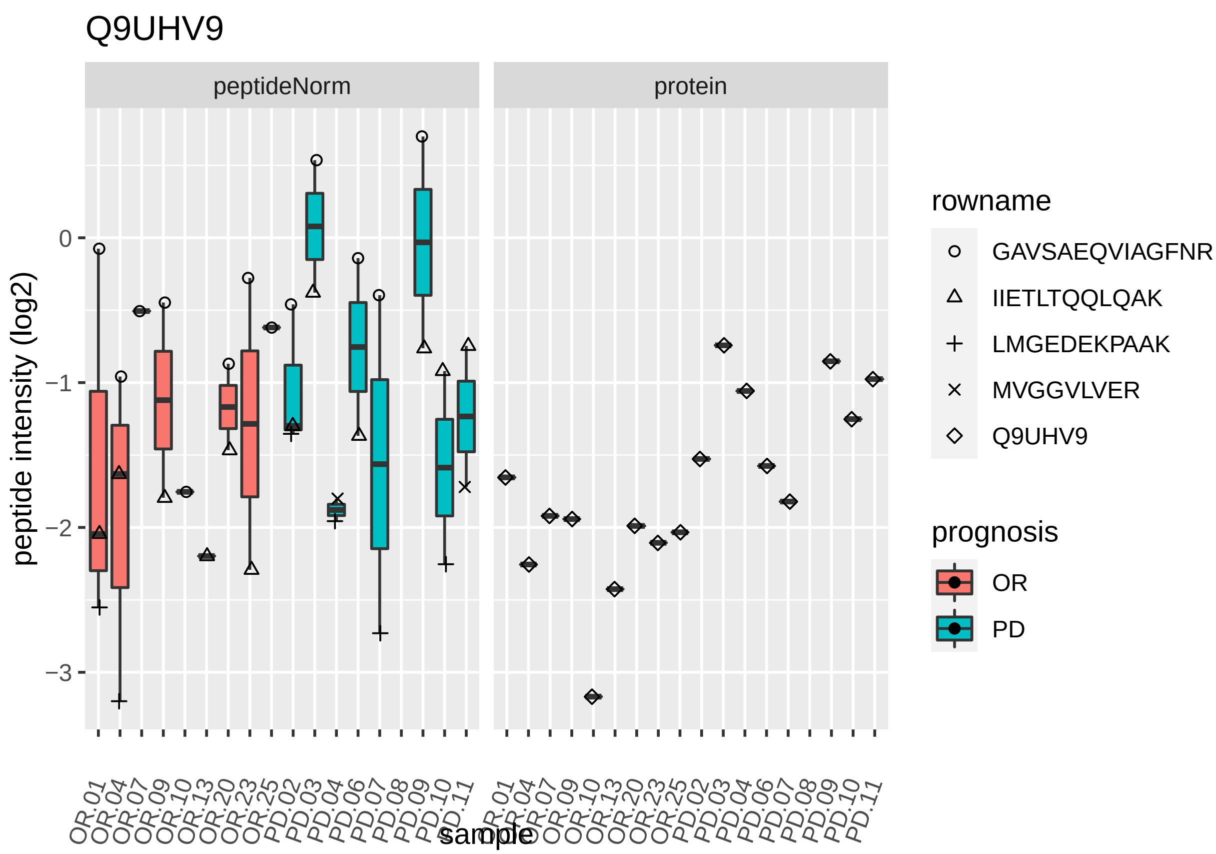
−2
−3
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



Q9UHV9
peptideNorm
protein
peptide intensity (log2)
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−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
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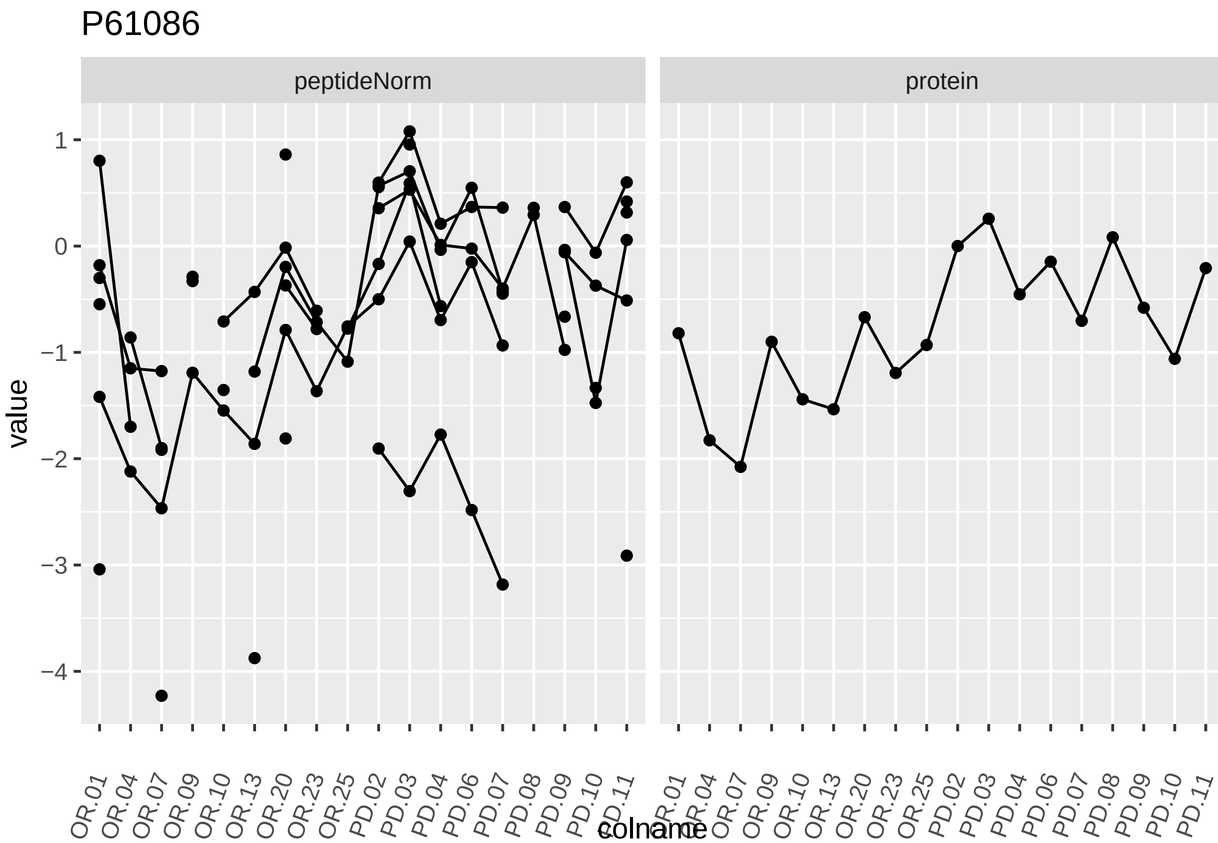
IIETLTQQLQAK
LMGEDEKPAAK
MVGGVLVER
Q9UHV9
prognosis
OR
PD



P61086
peptideNorm
protein
value
colname
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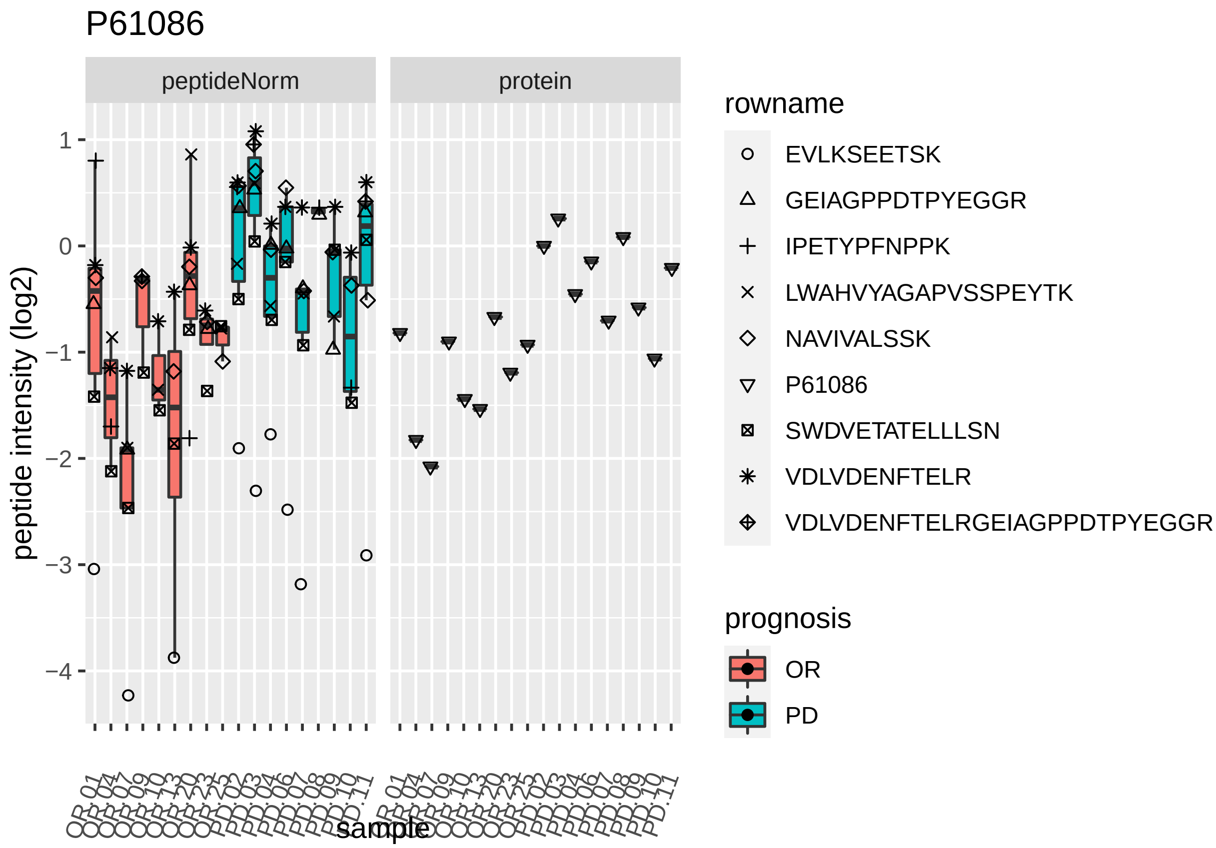
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P61086
peptideNorm
protein
peptide intensity (log2)
sample
rowname
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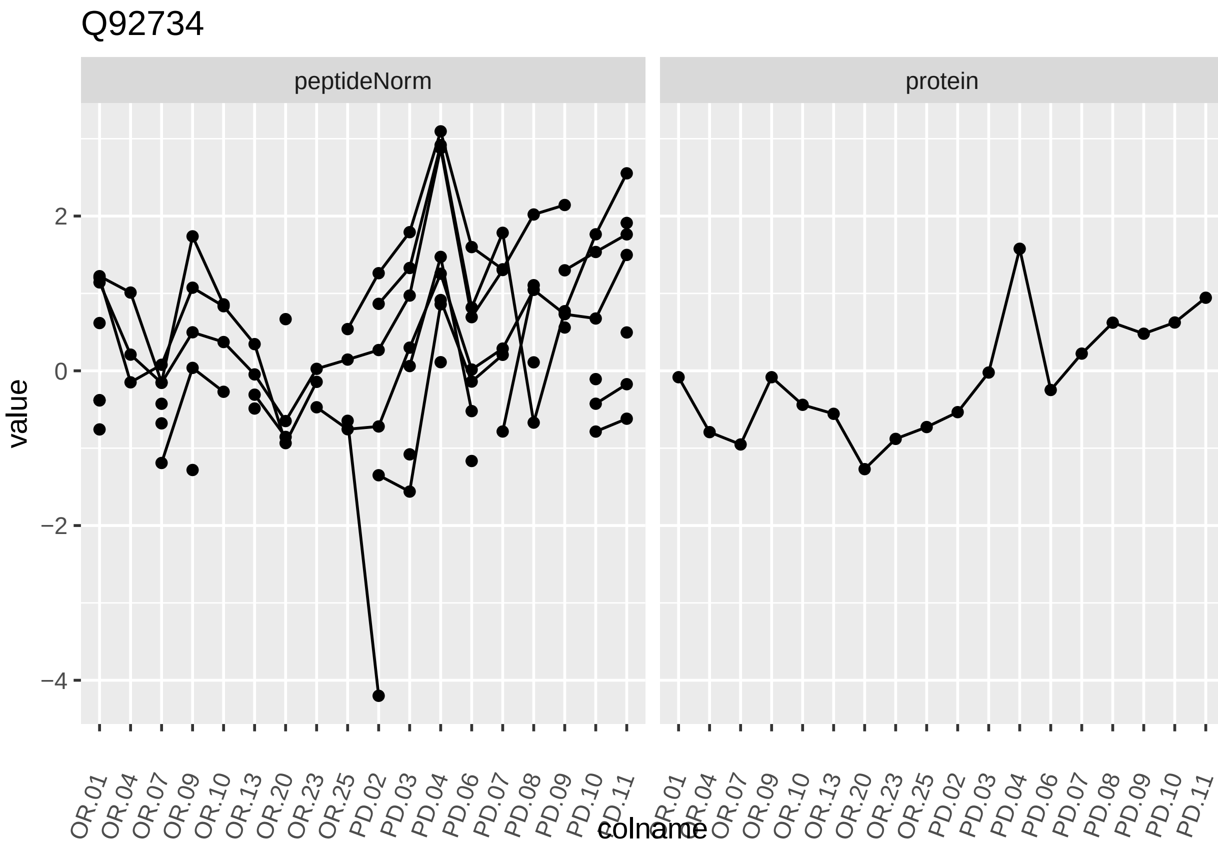
IPETYPFNPPK
LWAHVYAGAPVSSPEYTK
NAVIVALSSK
P61086
SWDVETATELLLSN
VDLVDENFTELR
VDLVDENFTELRGEIAGPPDTPYEGGR
prognosis
OR
PD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peptideNorm
protein
value
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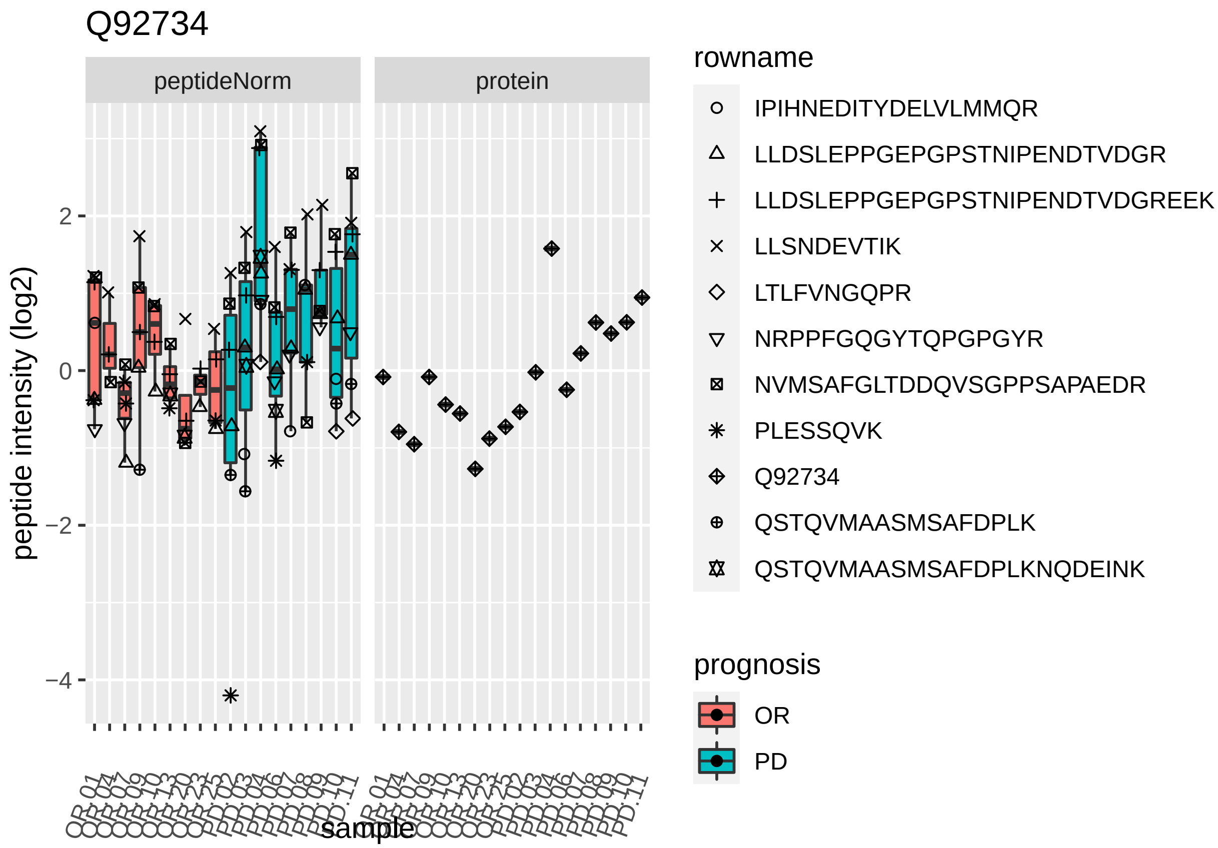
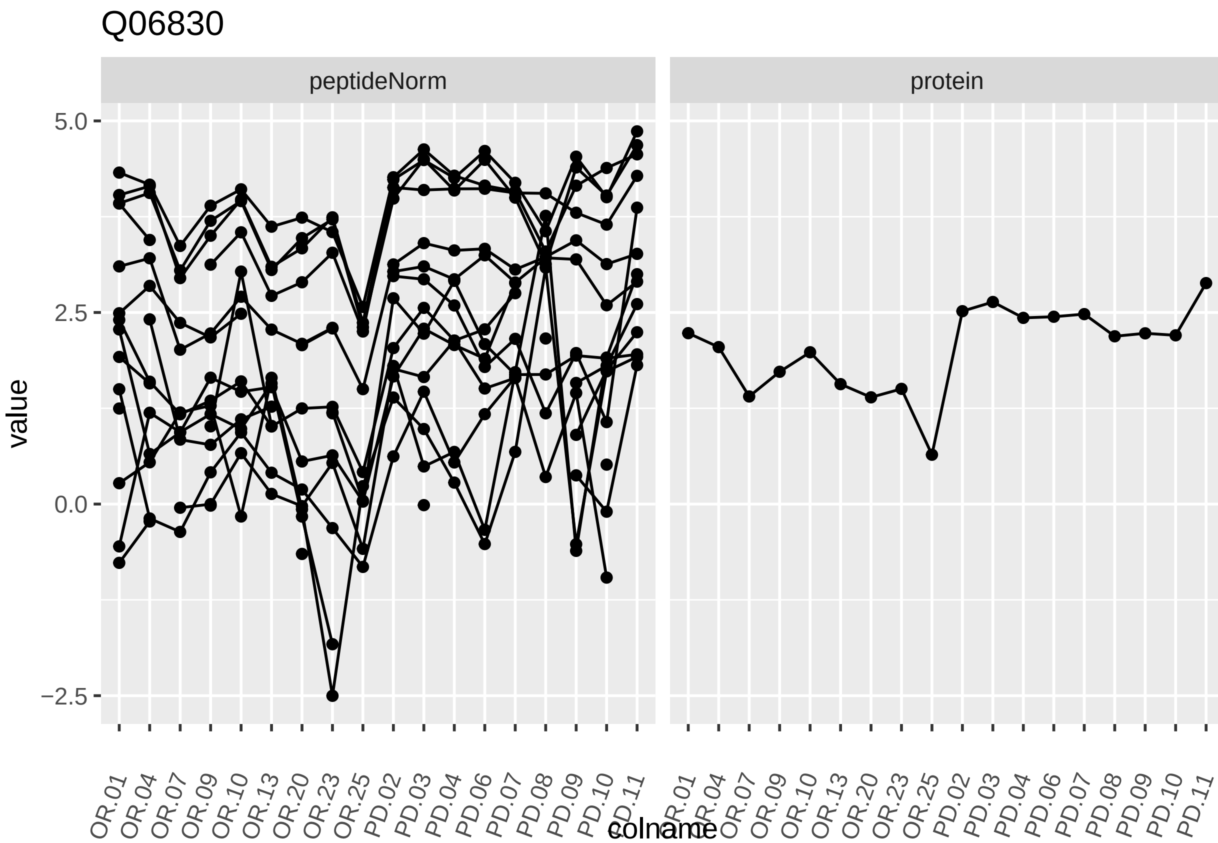
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


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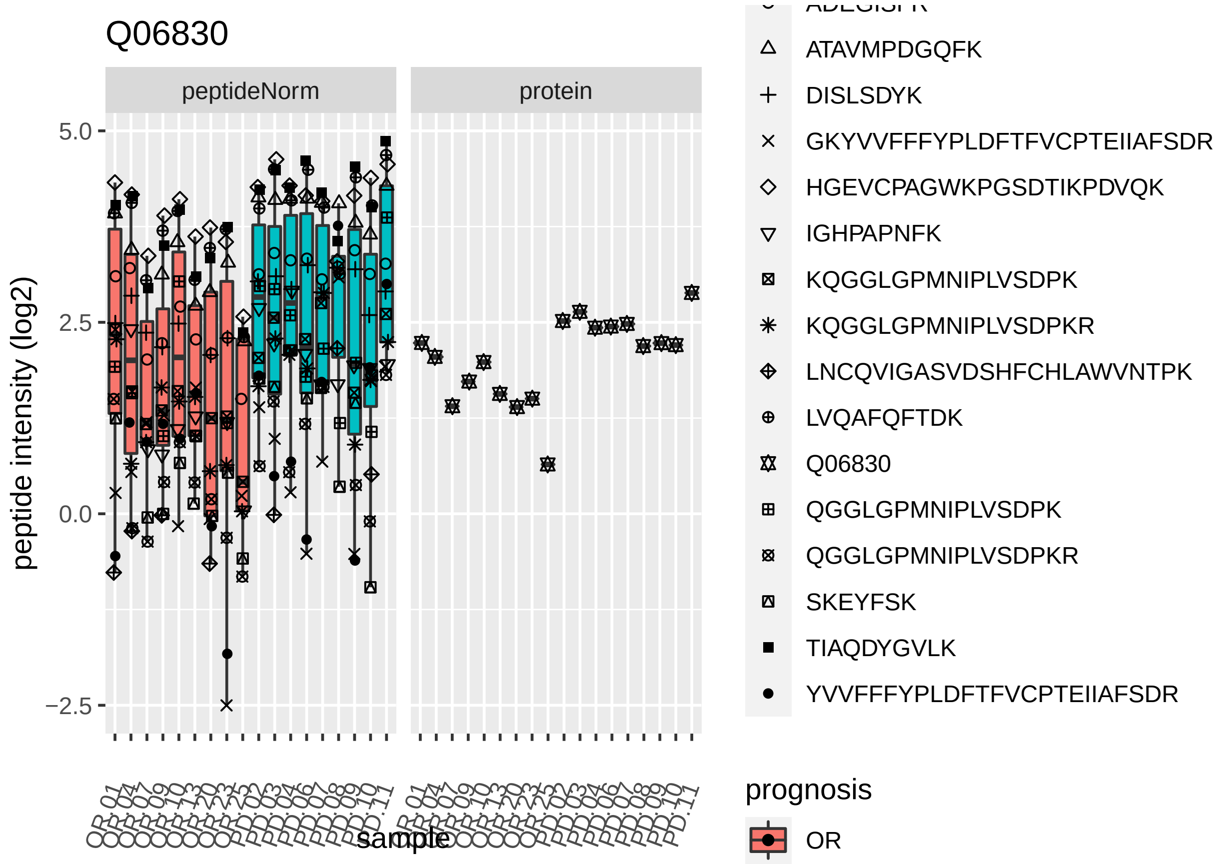
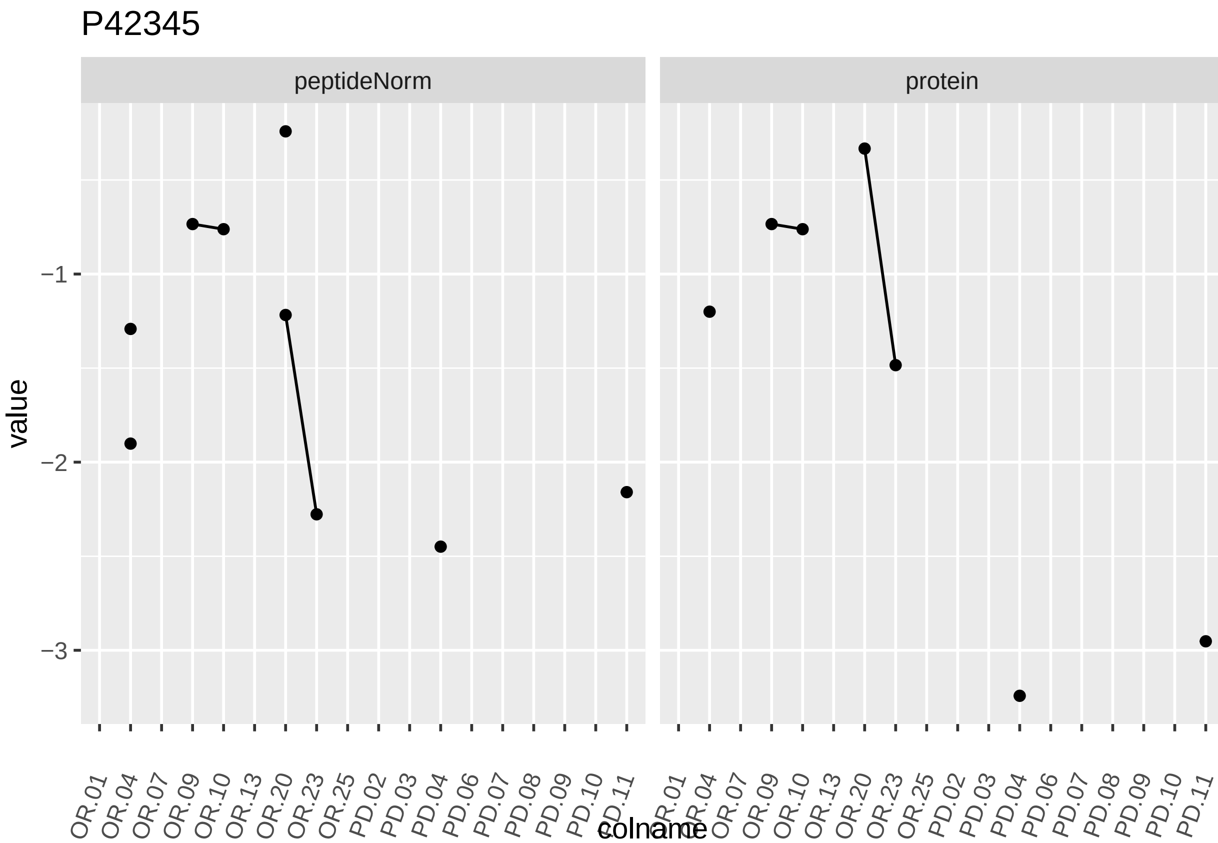
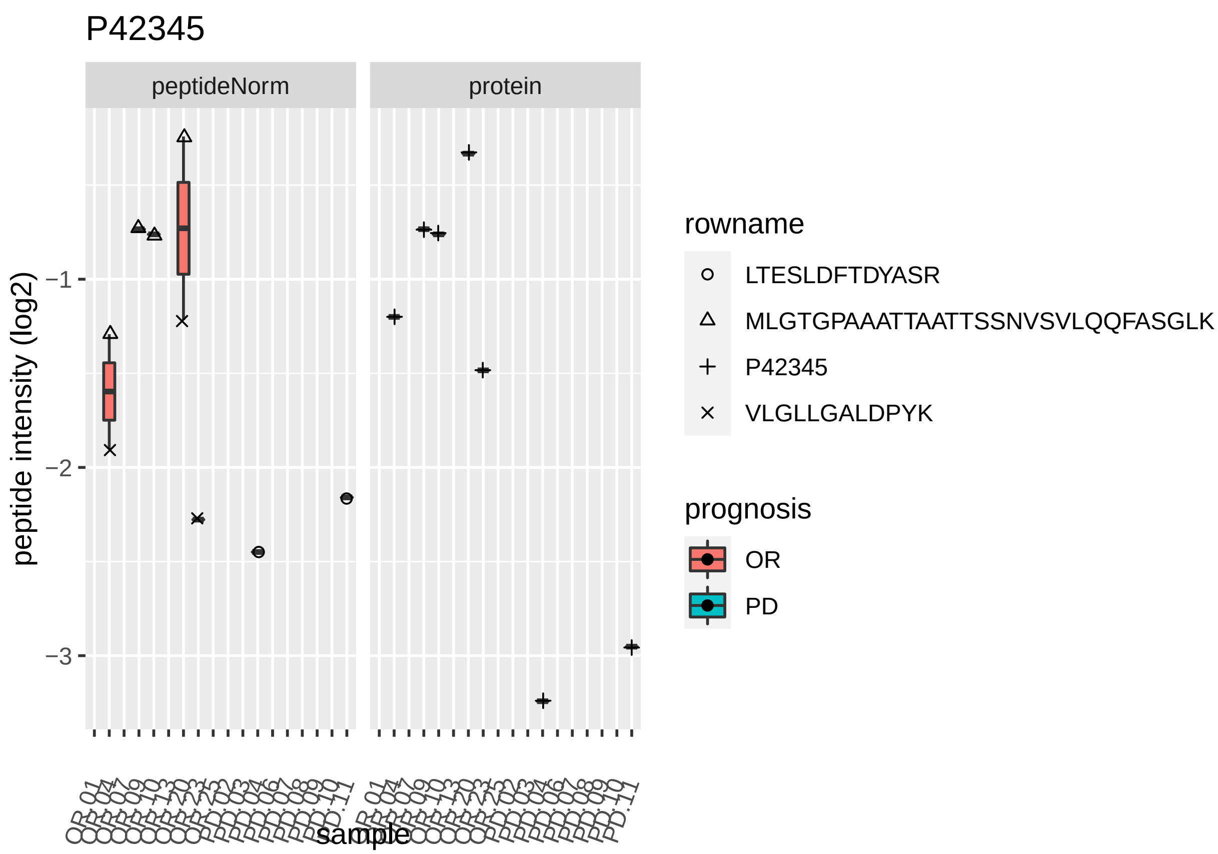
2.5
0.0
−2.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



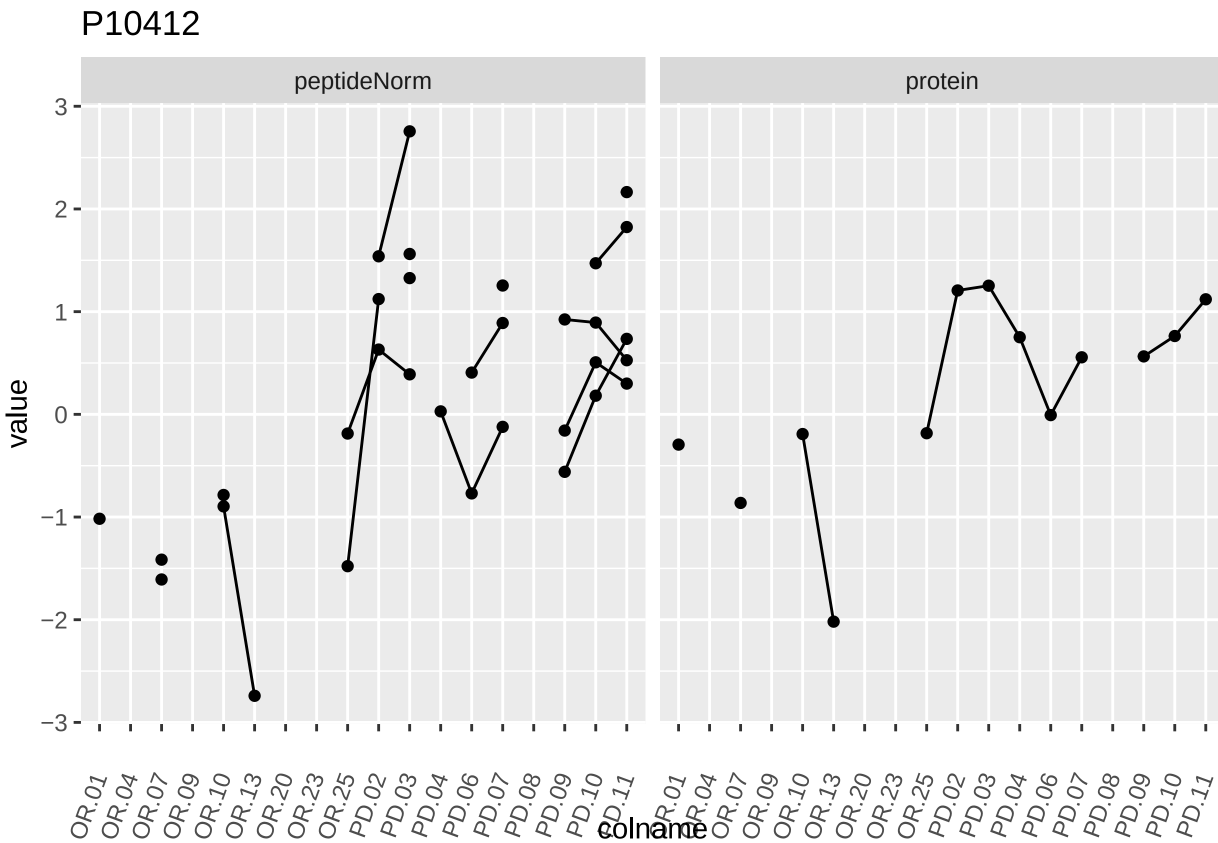
Q06830
peptideNorm
protein
peptide intensity (log2)
5.0
2.5
0.0
−2.5
sample
ATAVMPDGQFK
DISLSDYK
GKYVVFFFYPLDFTFVCPTEIIAFSDR
HGEVCPAGWKPGSDTIKPDVQK
IGHPAPNFK
KQGGLGPMNIPLVSDPK
KQGGLGPMNIPLVSDPKR
LNCQVIGASVDSHFCHLAWVNTPK
LVQAFQFTDK
Q06830
QGGLGPMNIPLVSDPK
QGGLGPMNIPLVSDPKR
SKEYFSK
TIAQDYGVLK
YVVFFFYPLDFTFVCPTEIIAFSDR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



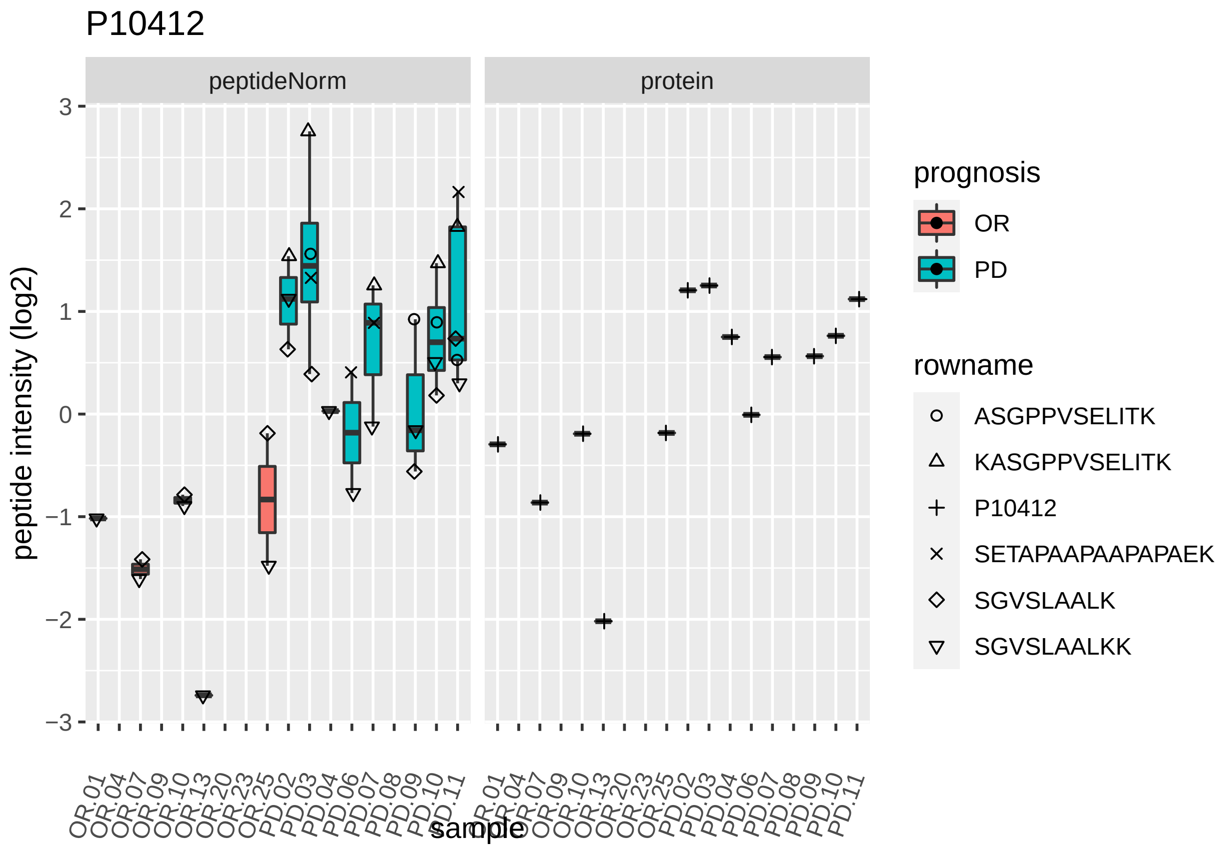
P42345
peptideNorm
protein
value
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname



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

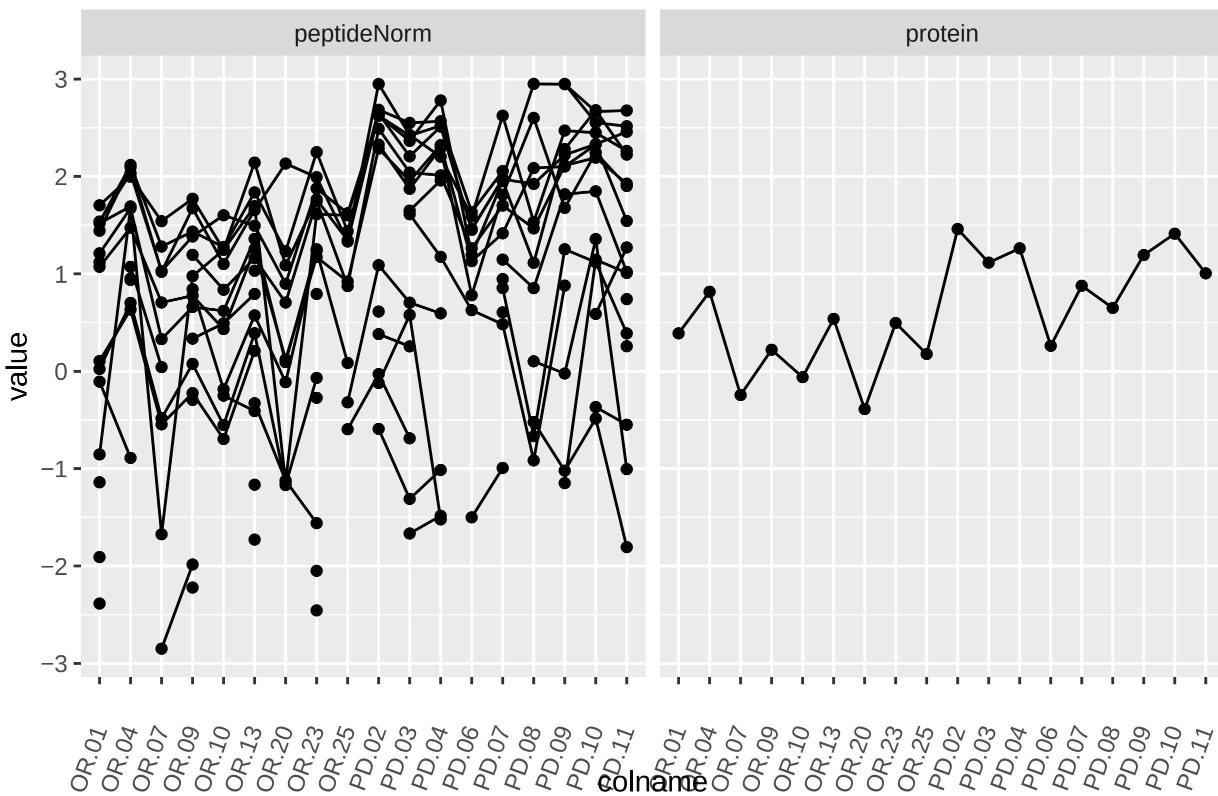


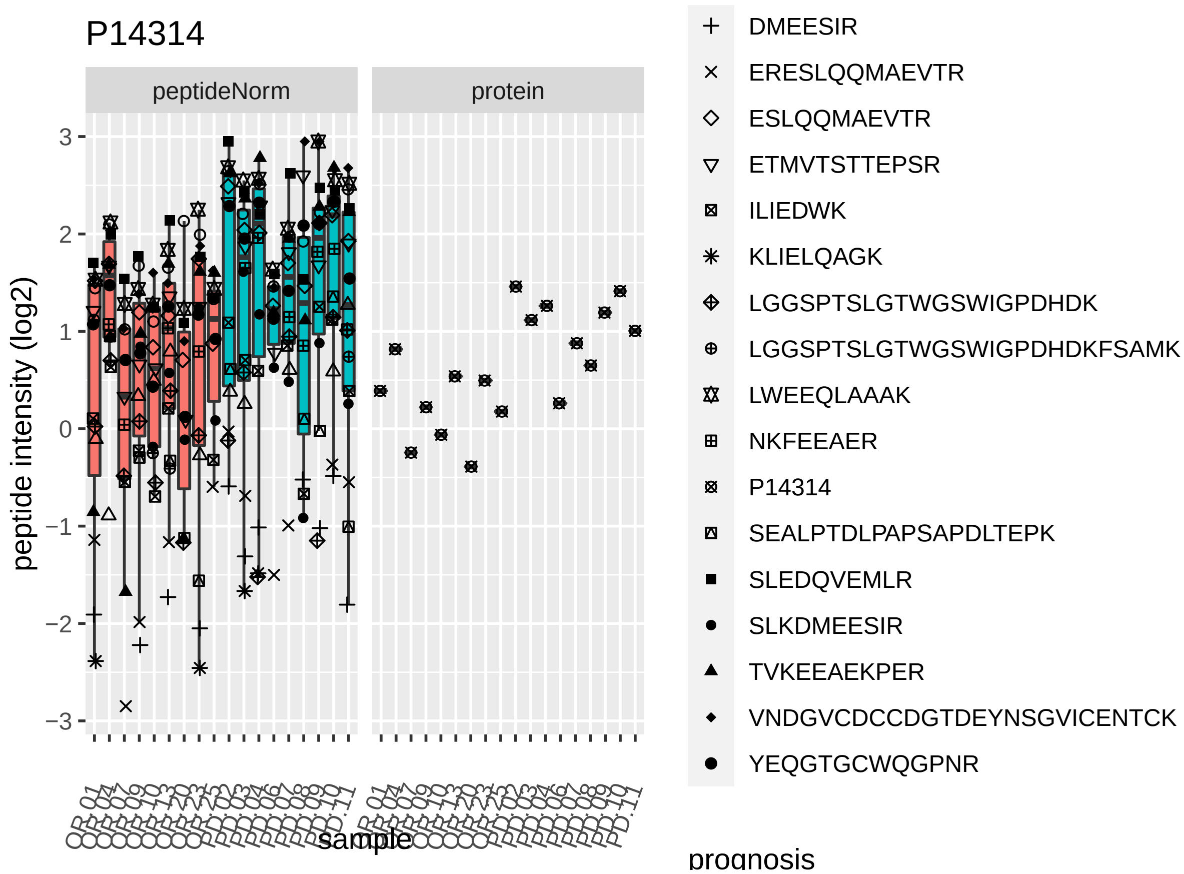
P10412
peptideNorm
protein
value
colname
3
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



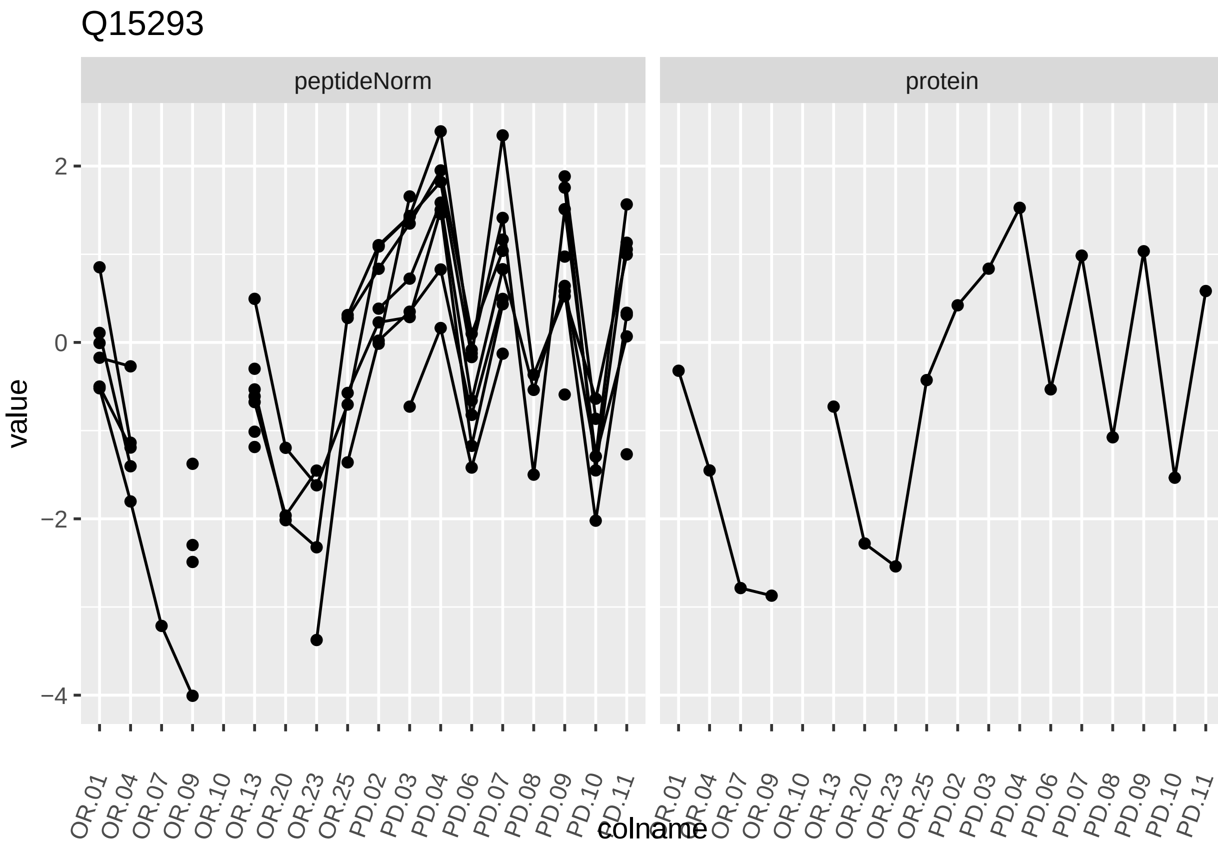
P10412
peptideNorm
protein
peptide intensity (log2)
sample
prognosis
OR
PD
rowname
ASGPPVSELITK
KASGPPVSELITK
P10412
SETAPAAPAAPAPAEK
SGVSLAALK
SGVSLAALKK

P14314

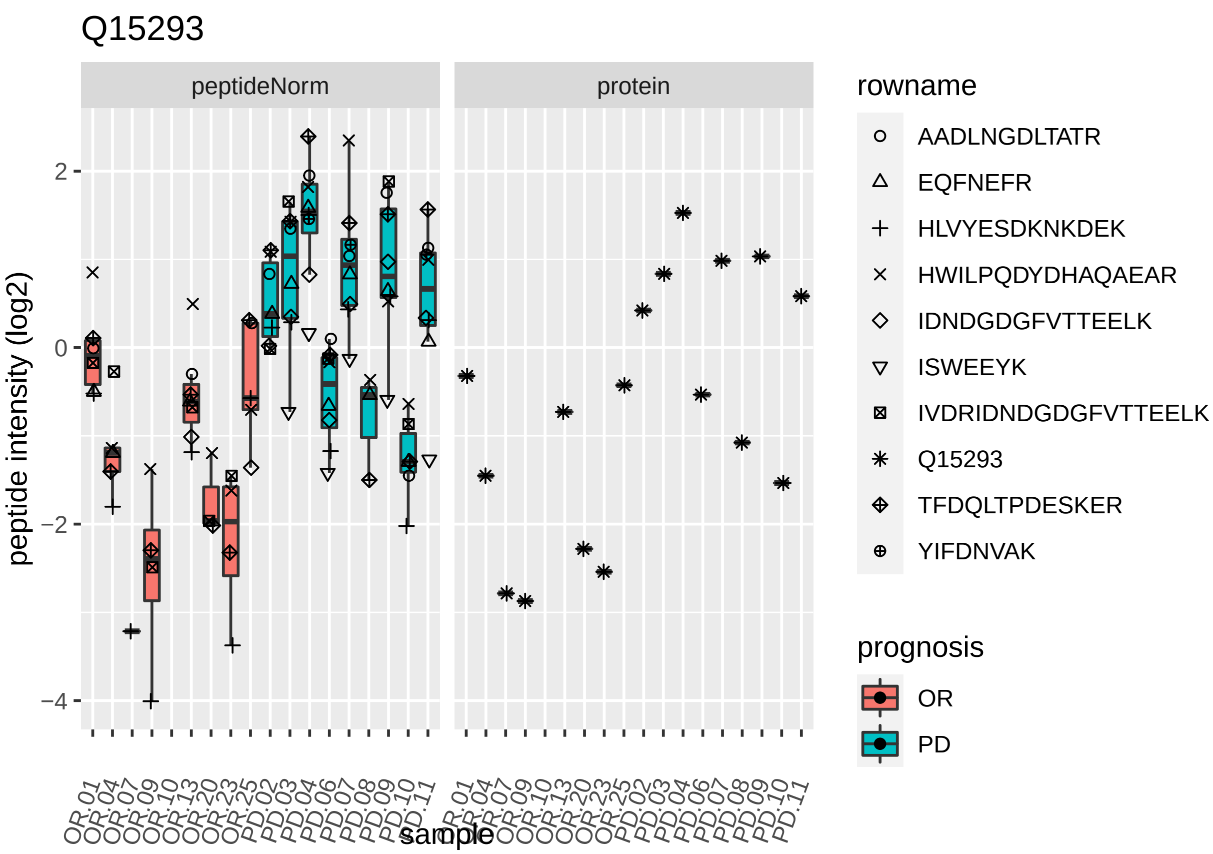

peptideNorm
protein
value
colname
3
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



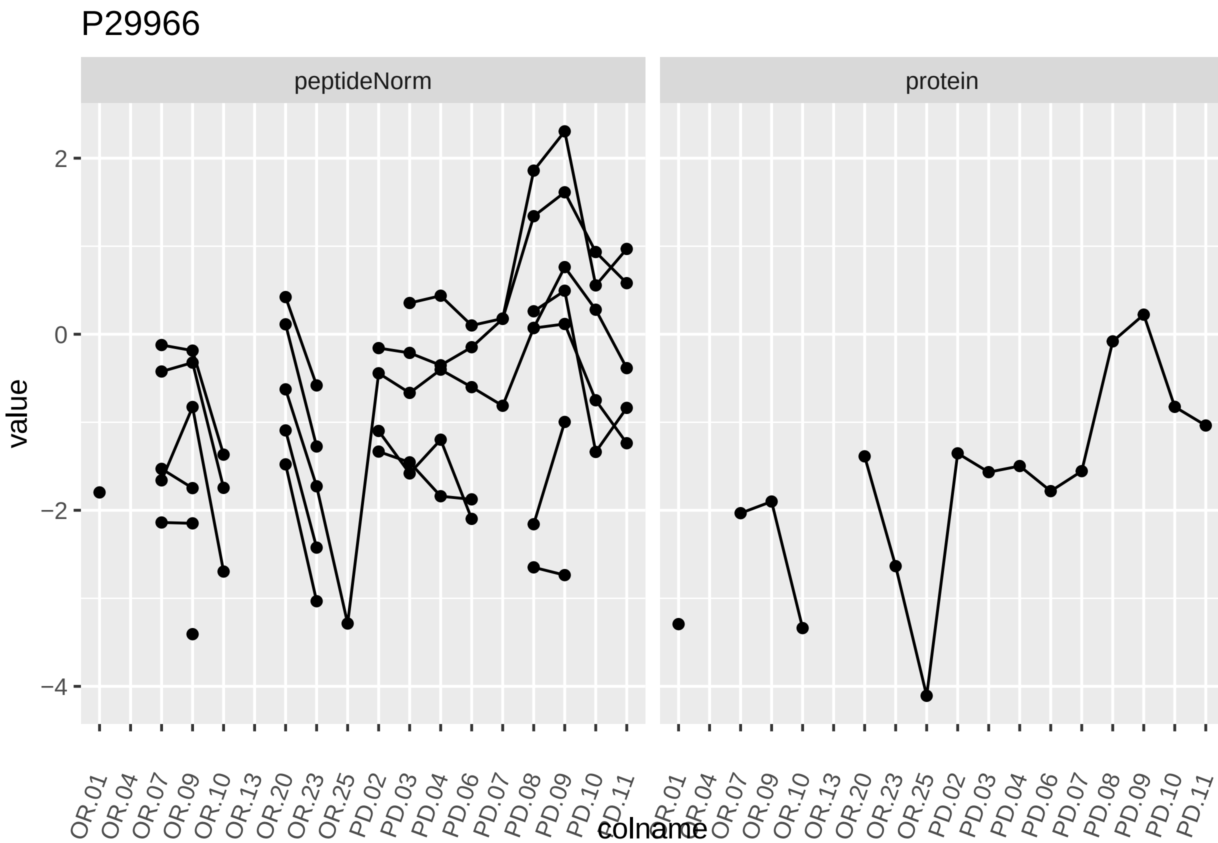
P14314
peptideNorm
protein
peptide intensity (log2)
sample
DMEESIR
ERESLQQMAEVTR
ESLQQMAEVTR
ETMVTSTTEPSR
ILIEDWK
KLIELQAGK
LGGSPTSLGTWGSWIGPDHDK
LGGSPTSLGTWGSWIGPDHDKFSAMK
LWEEQLAAAK
NKFEEAER
P14314
SEALPTDLPAPSAPDLTEPK
SLEDQVEMLR
SLKDMEESIR
TVKEEAEKPER
VNDGVCDCCDGTDEYNSGVICENTCK
YEQGTGCWQGPNR
prognosis



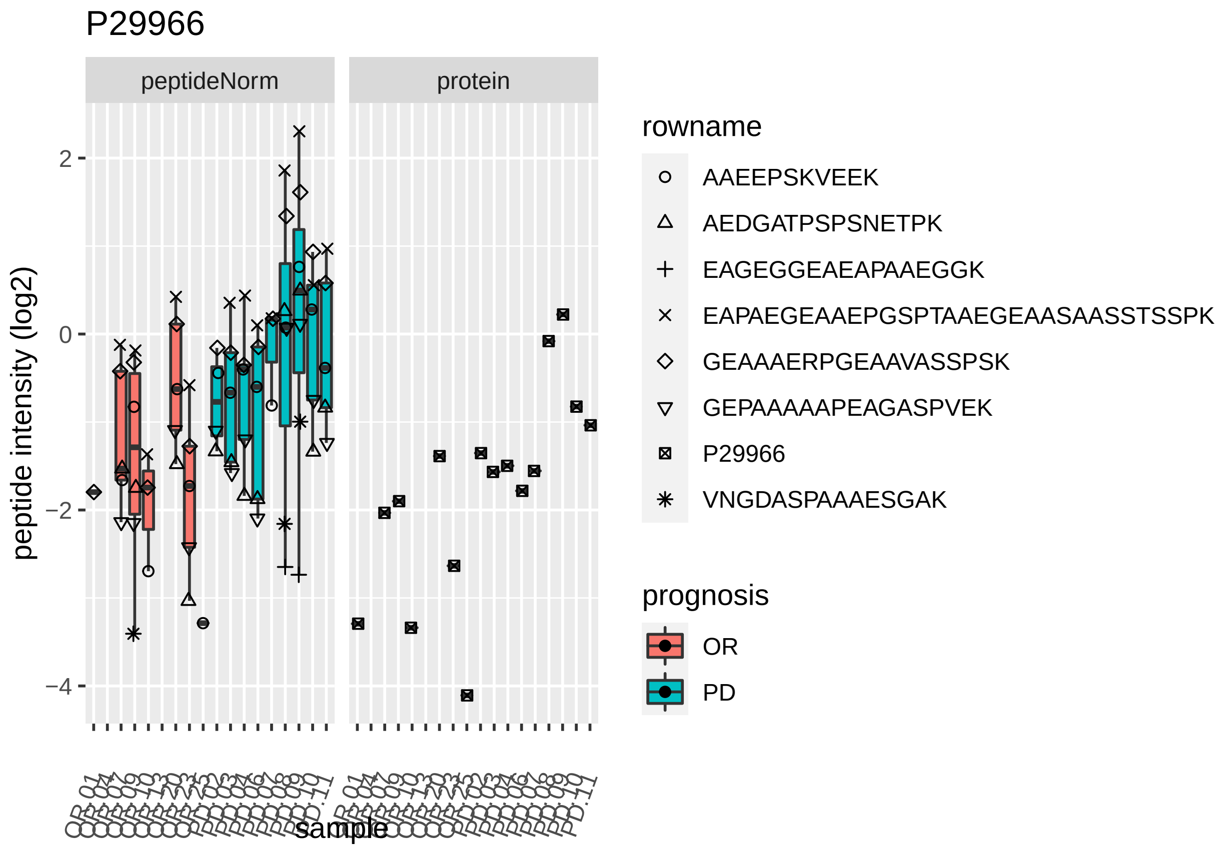
Q15293
peptideNorm
protein
value
colname
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

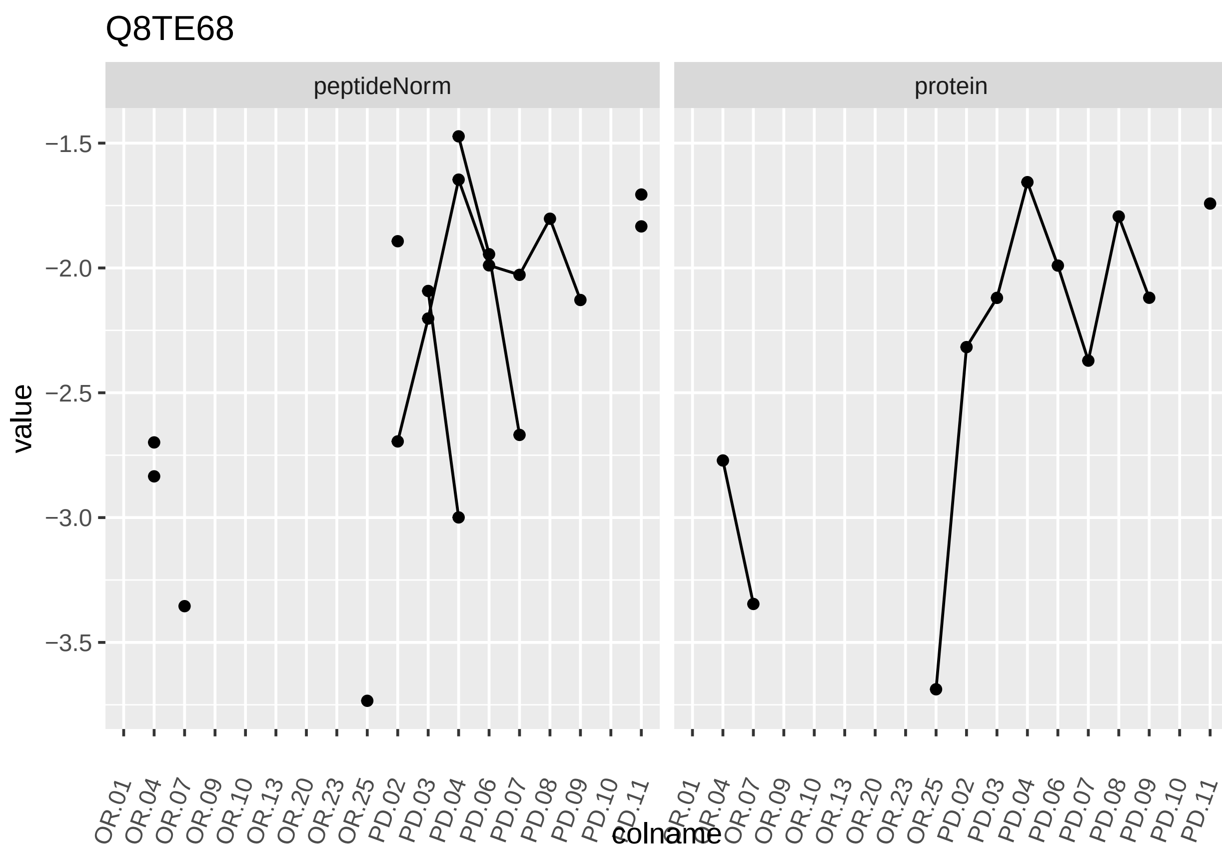


Q15293
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
AADLNGDLTATR
EQFNEFR
HLVYESDKNKDEK
HWILPQDYDHAQAEAR
IDNDGDGFVTTEELK
ISWEEYK
IVDRIDNDGDGFVTTEELK
Q15293
TFDQLTPDESKER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

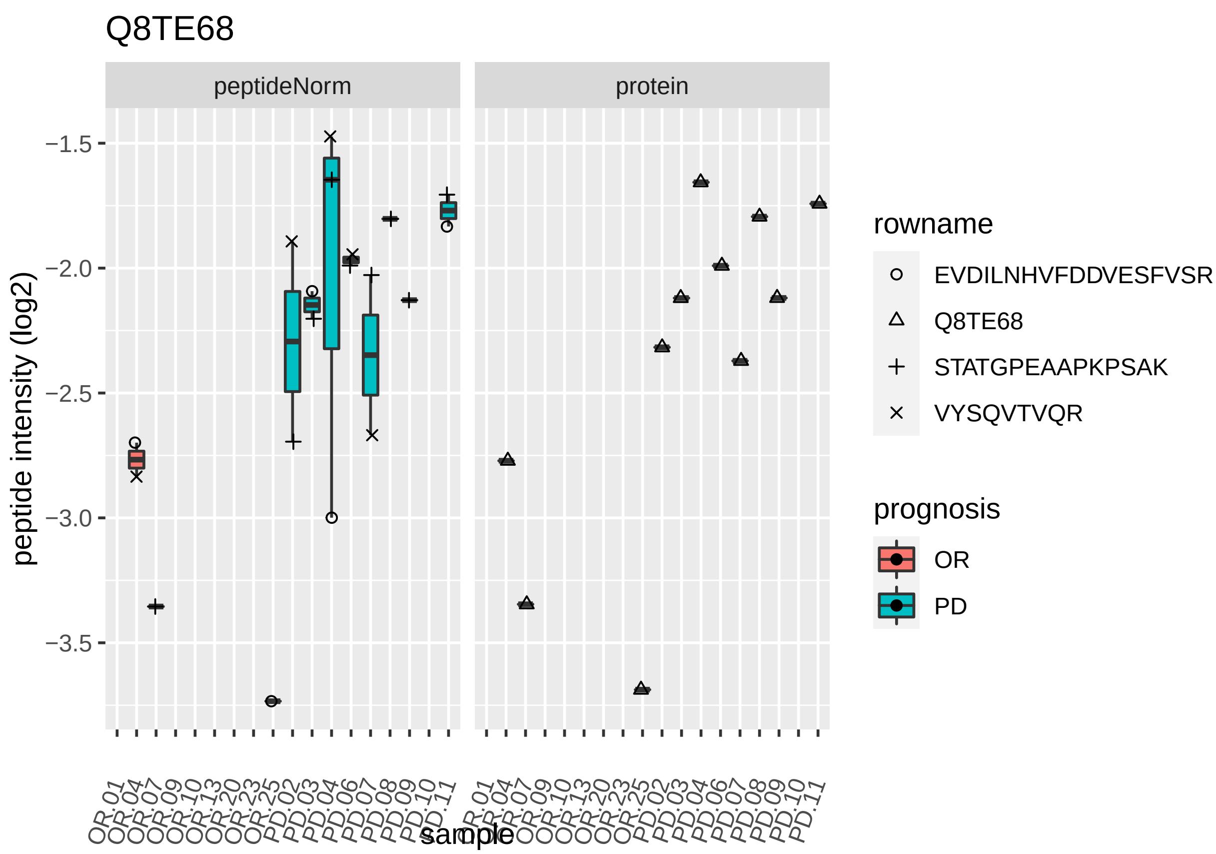


P29966
peptideNorm
protein
value
colname
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

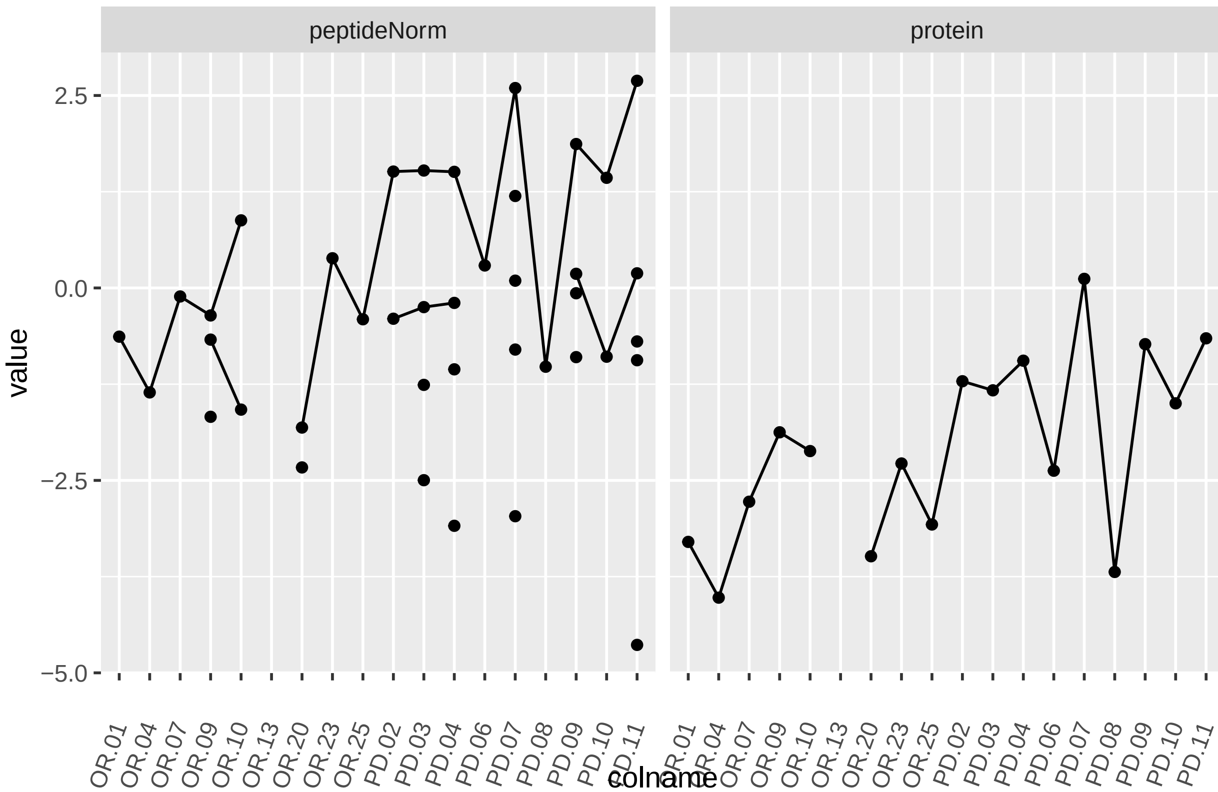

P29966
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
rowname
AAEEPSKVEEK
AEDGATPSPSNETPK
EAGEGGEAEAPAAEGGK
EAPAEGEAAEPGSPTAAEGEAASAASSTSSPK
GEAAAERPGEAAVASSPSK
GEPAAAAAPEAGASPVEK
P29966
VNGDASPAAAESGAK
prognosis
OR
PD



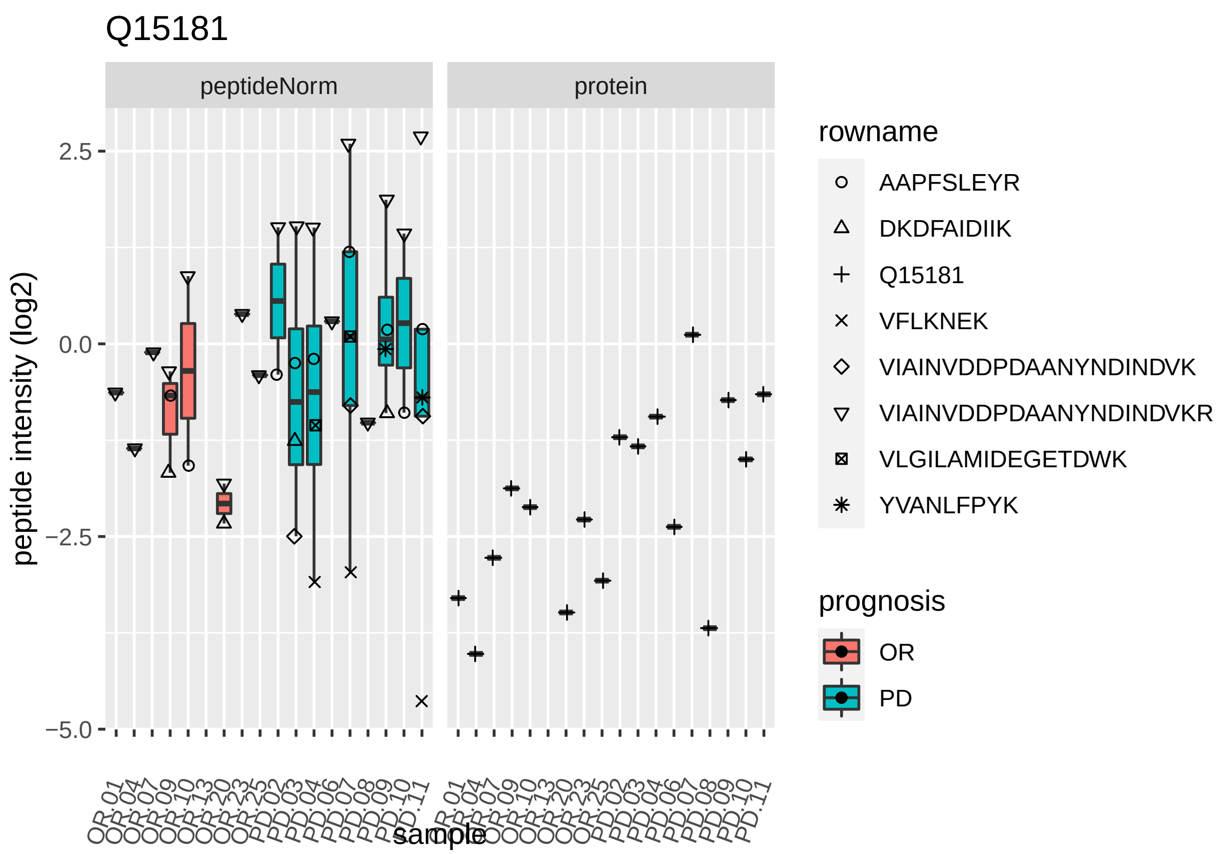
Q8TE68
peptideNorm
protein
value
−1.5
−2.0
−2.5
−3.0
−3.5
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


Q8TE68
peptideNorm
protein
peptide intensity (log2)
−1.5
−2.0
−2.5
−3.0
−3.5
sample
rowname
EVDILNHVFDDVESFVSR
Q8TE68
STATGPEAAPKPSAK
VYSQVTVQR
prognosis
OR
PD

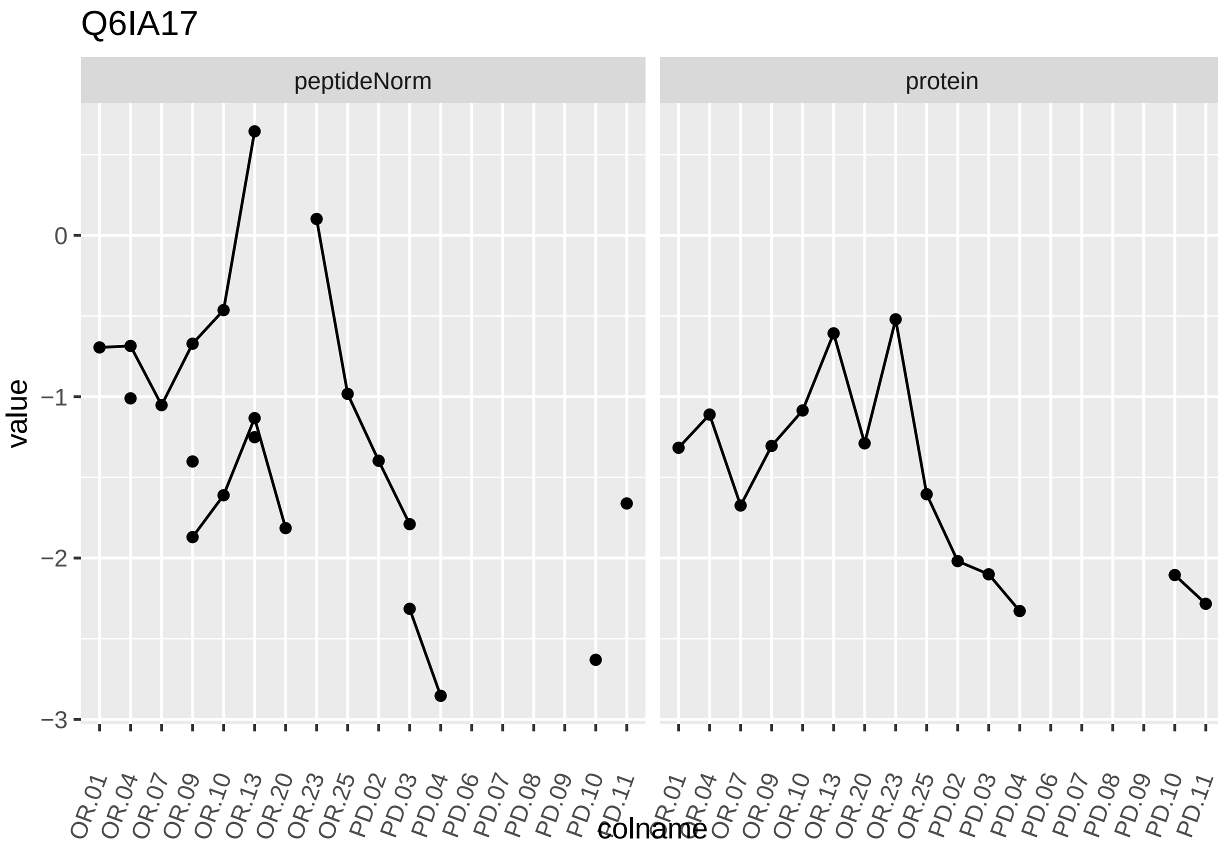
Q15181

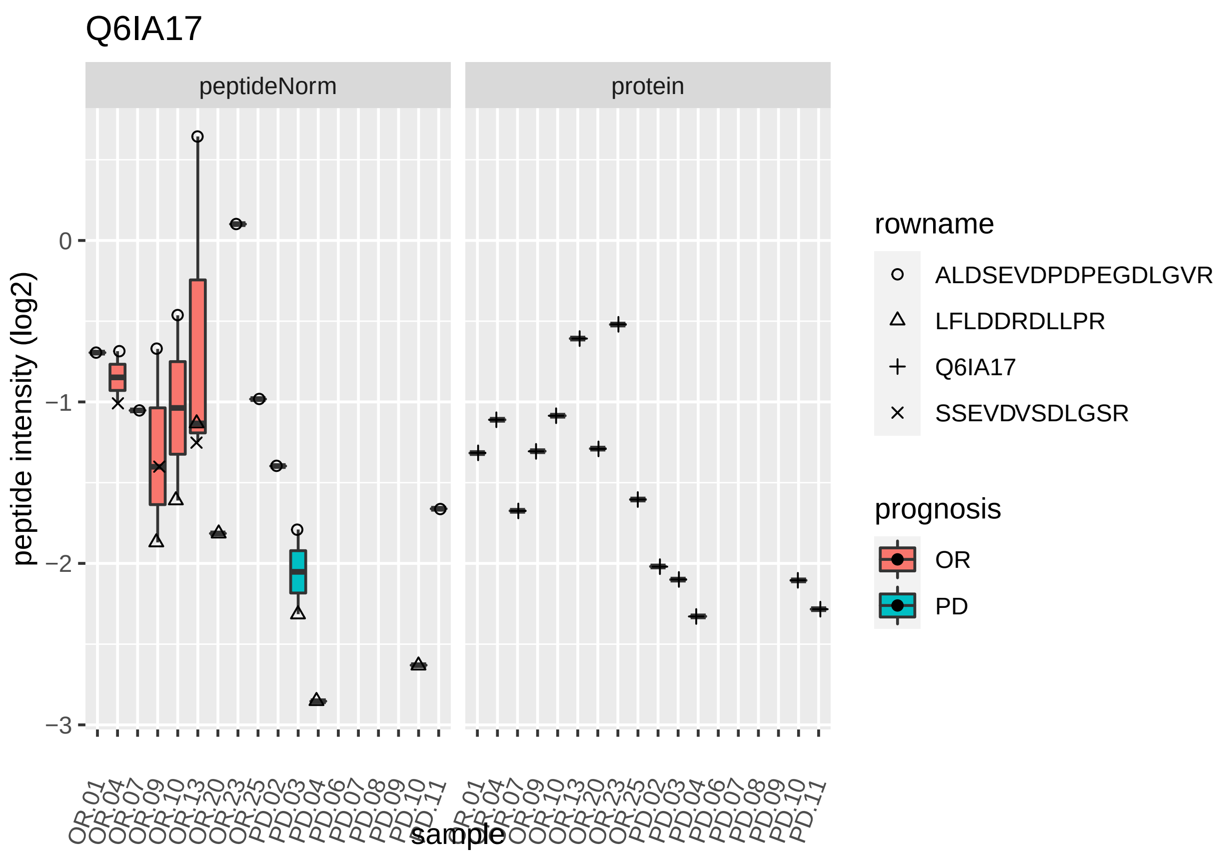


peptideNorm
protein
2.5
0.0
−2.5
−5.0
value
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

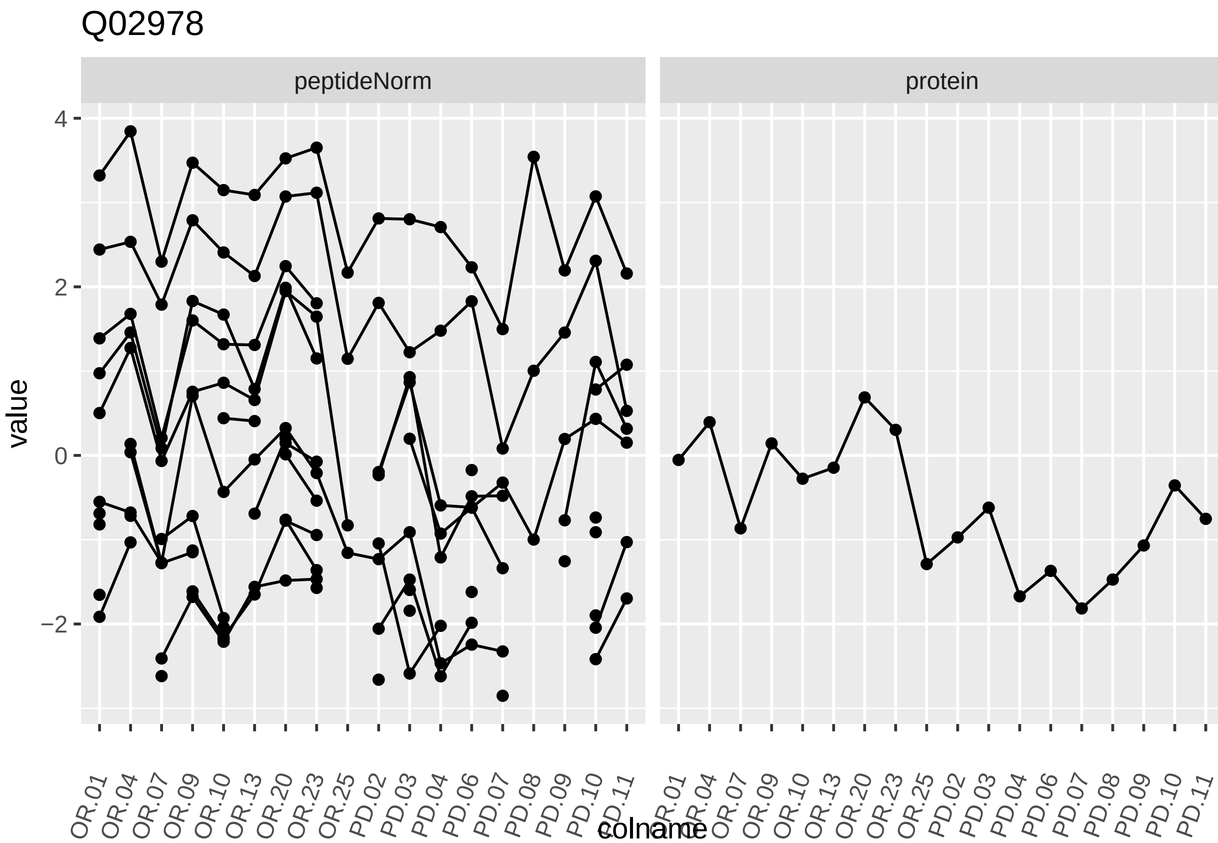


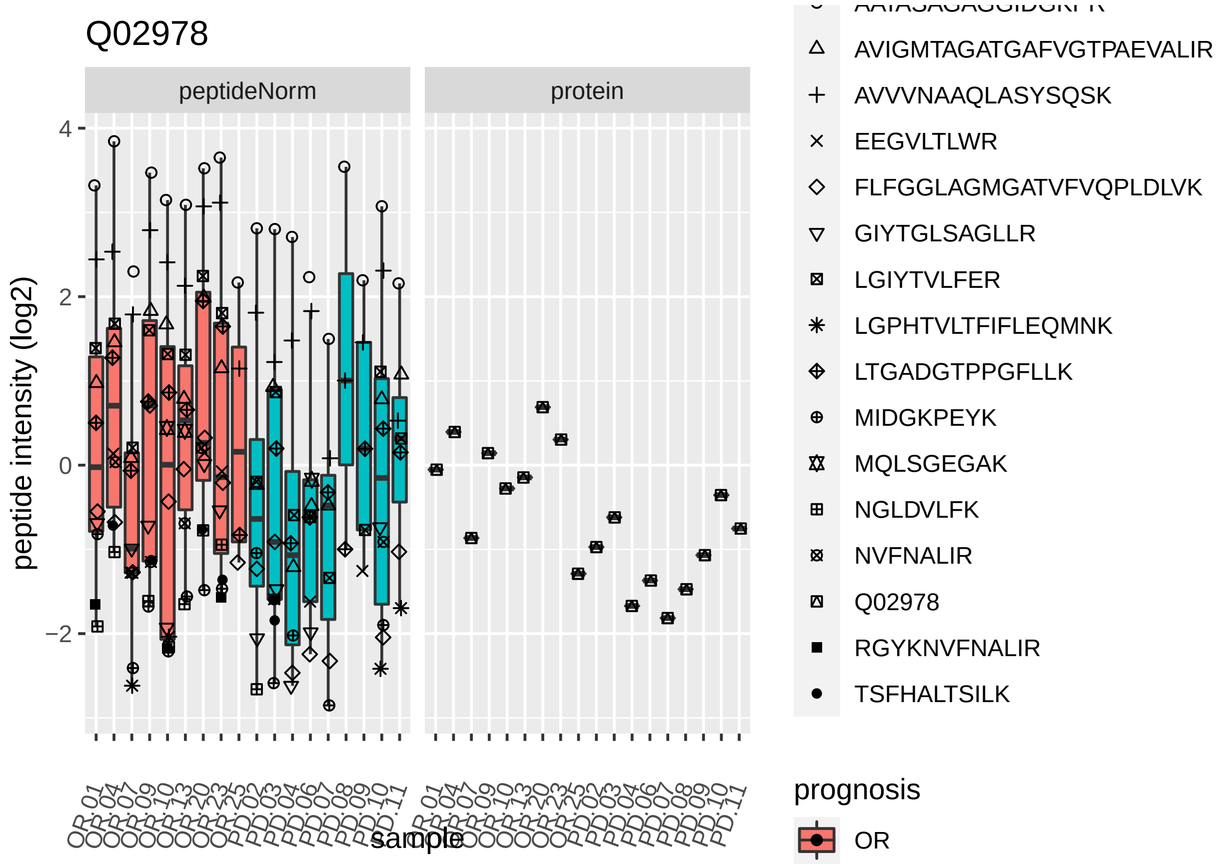
Q15181
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
−5.0
sample
rowname
AAPFSLEYR
DKDFAIDIIK
Q15181
VFLKNEK
VIAINVDDPDAANYNDINDVK
VIAINVDDPDAANYNDINDVKR
VLGILAMIDEGETDWK
YVANLFPYK
prognosis
OR
PD


Q6IA17
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

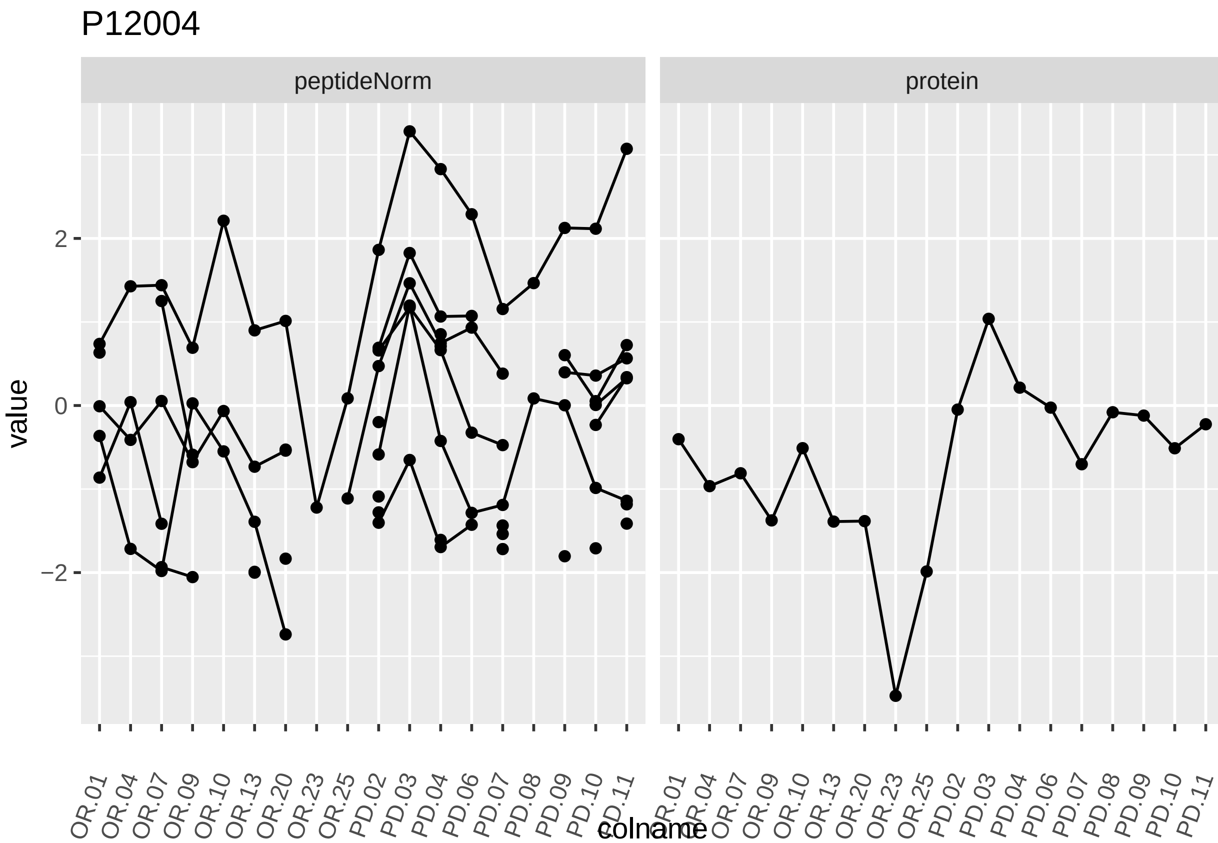


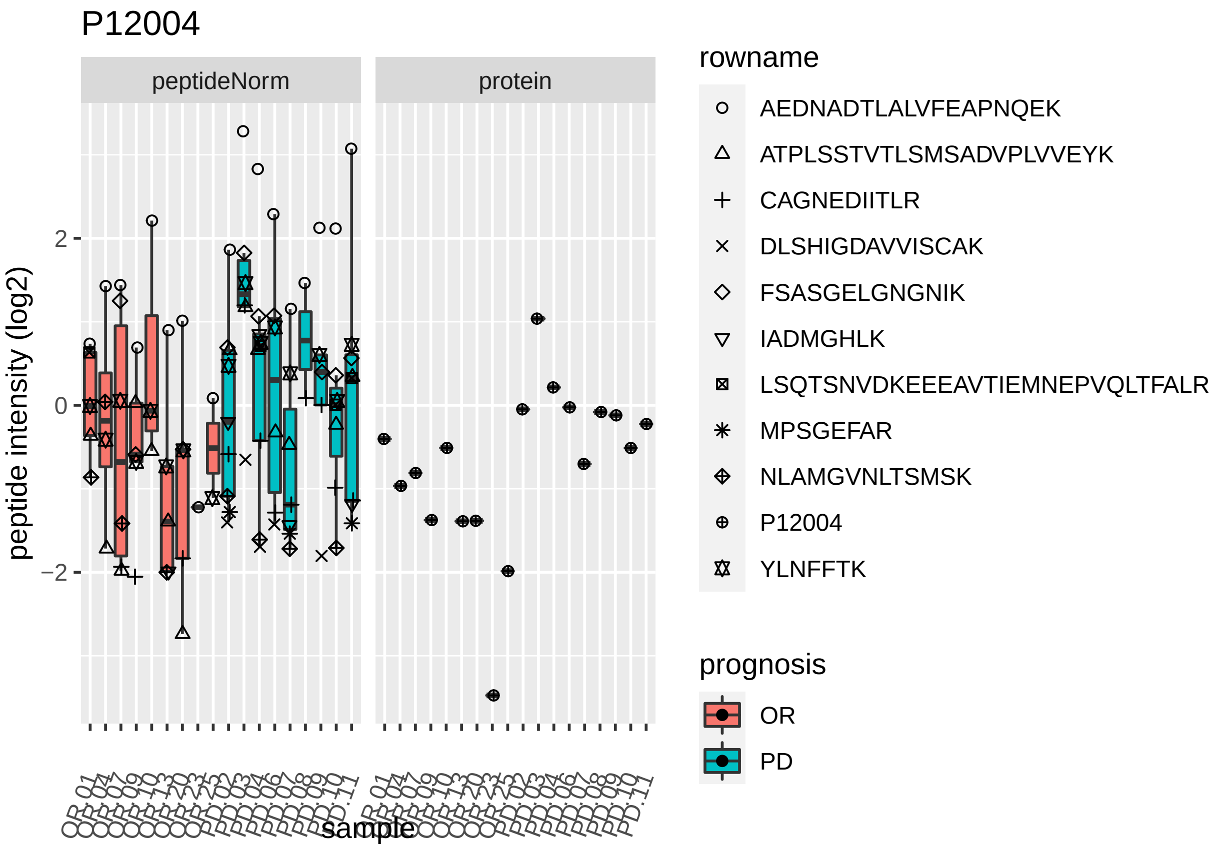
Q6IA17
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ALDSEVDPDPEGDLGVR
LFLDDRDLLPR
Q6IA17
SSEVDVSDLGSR
prognosis
OR
PD

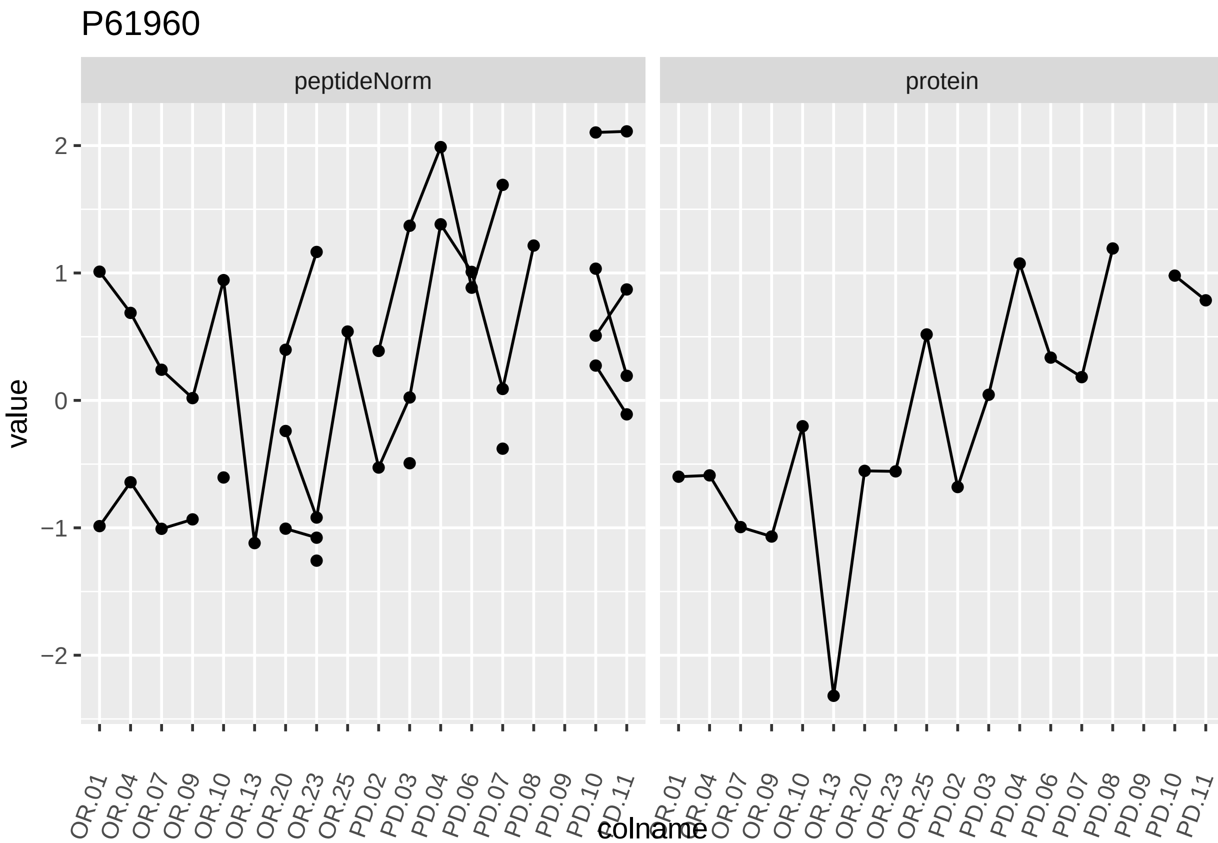

Q02978
peptideNorm
protein
value
colname
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

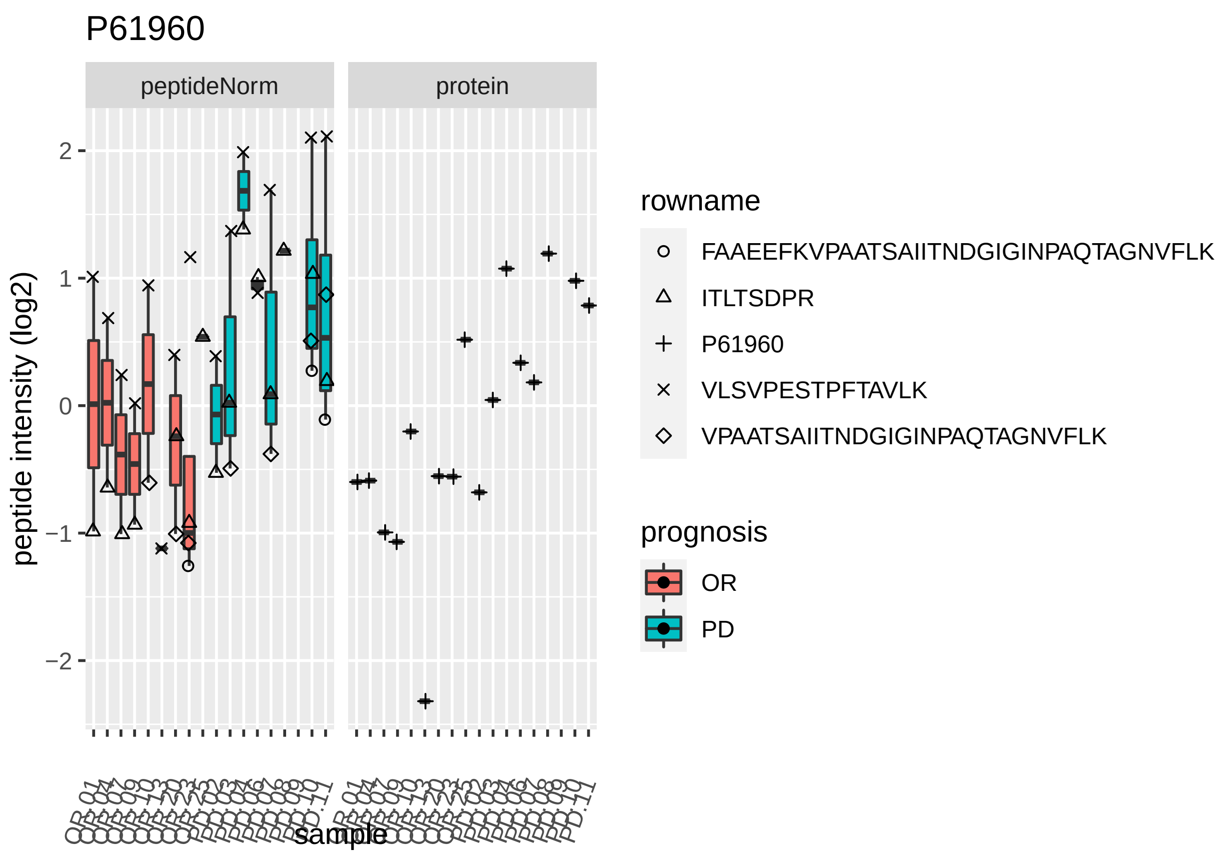


Q02978
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
sample
AVIGMTAGATGAFVGTPAEVALIR
AVVVNAAQLASYSQSK
EEGVLTLWR
FLFGGLAGMGATVFVQPLDLVK
GIYTGLSAGLLR
LGIYTVLFER
LGPHTVLTFIFLEQMNK
LTGADGTPPGFLLK
MIDGKPEYK
MQLSGEGAK
NGLDVLFK
NVFNALIR
Q02978
RGYKNVFNALIR
TSFHALTSILK
prognosis
OR

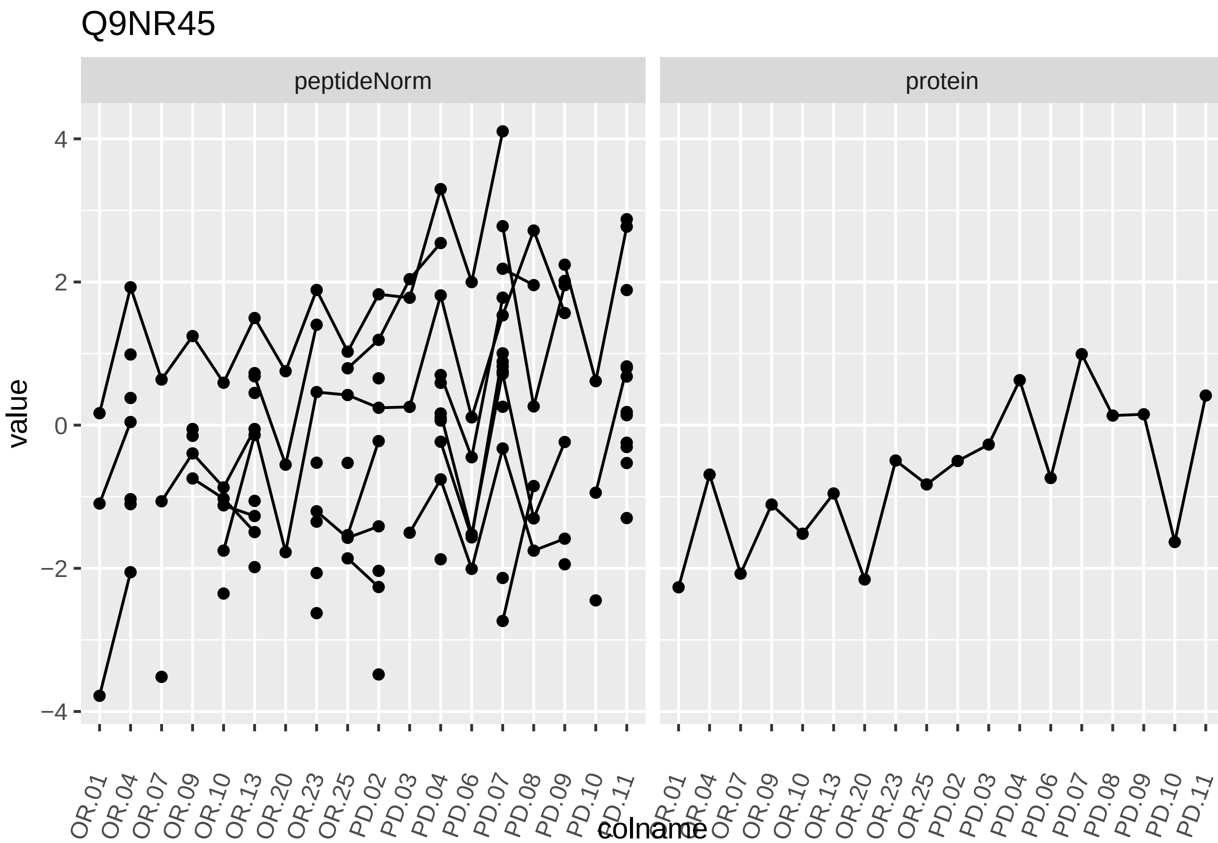

P12004
peptideNorm
protein
value
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


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

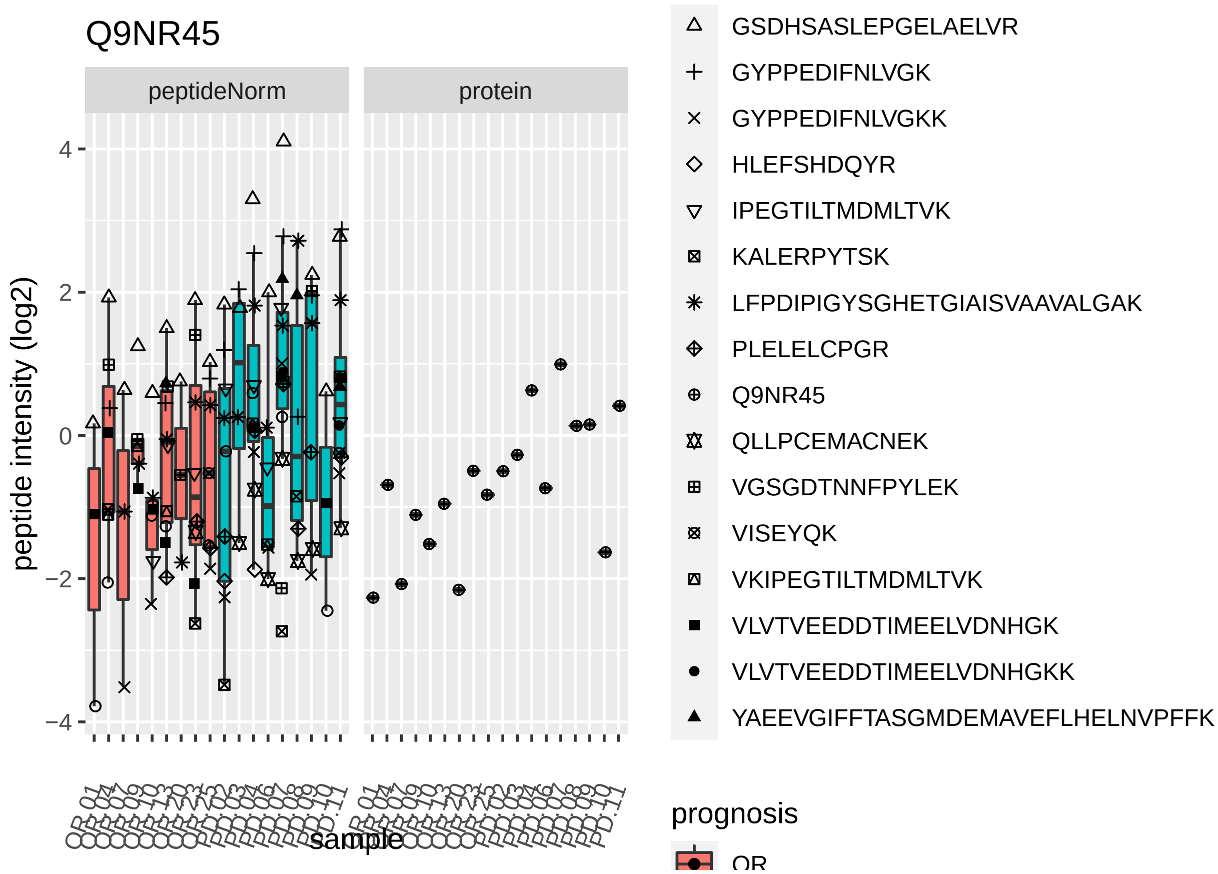

P61960
peptideNorm
protein
value
colname
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

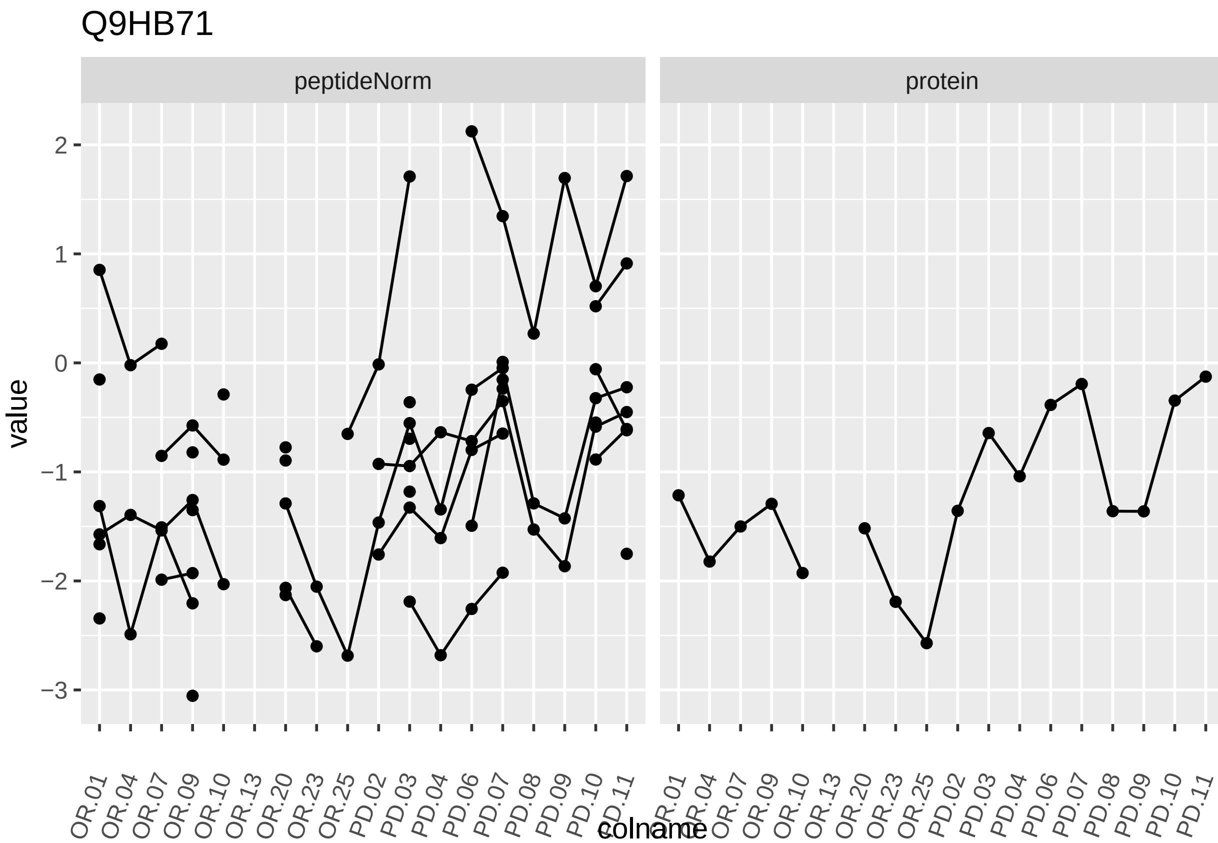


P61960
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
sample
rowname
FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK
ITLTSDPR
P61960
VLSVPESTPFTAVLK
VPAATSAIITNDGIGINPAQTAGNVFLK
prognosis
OR
PD

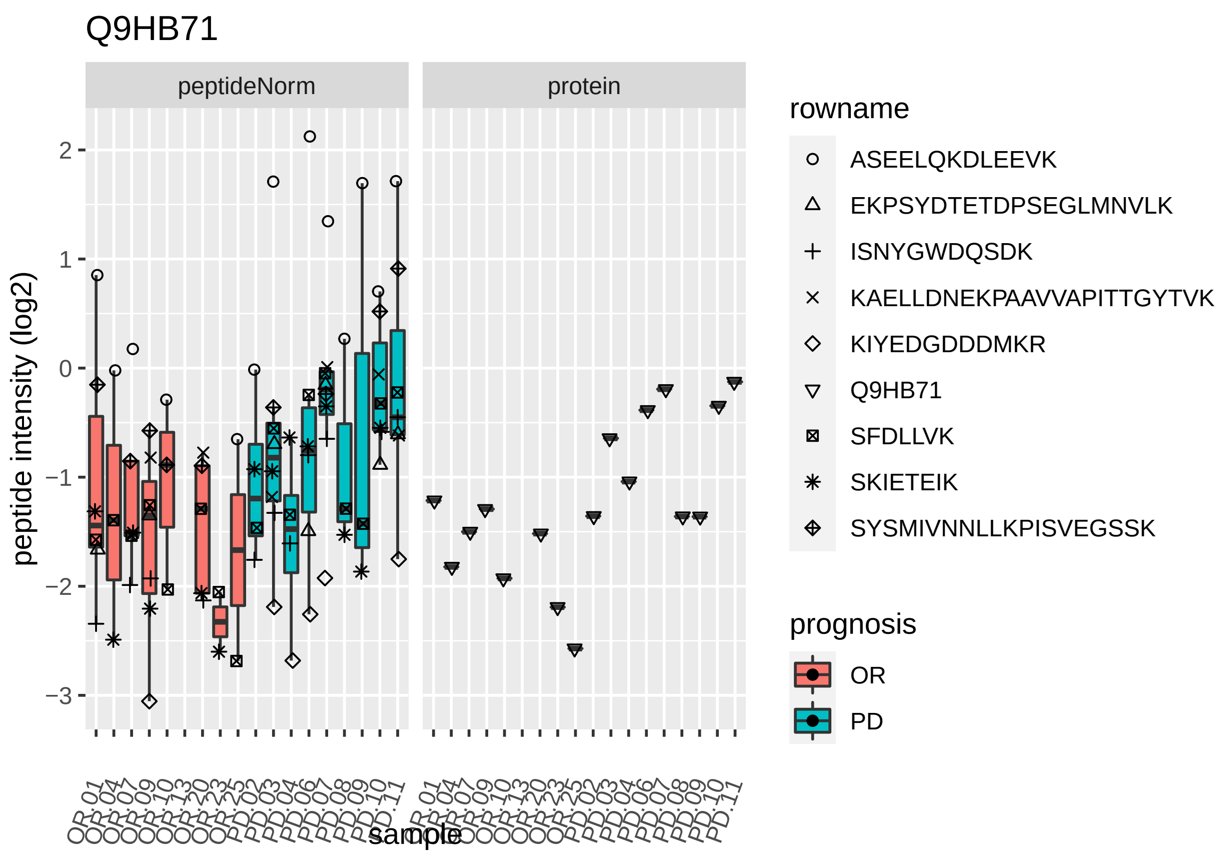


Q9NR45
peptideNorm
protein
value
colname
4
2
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

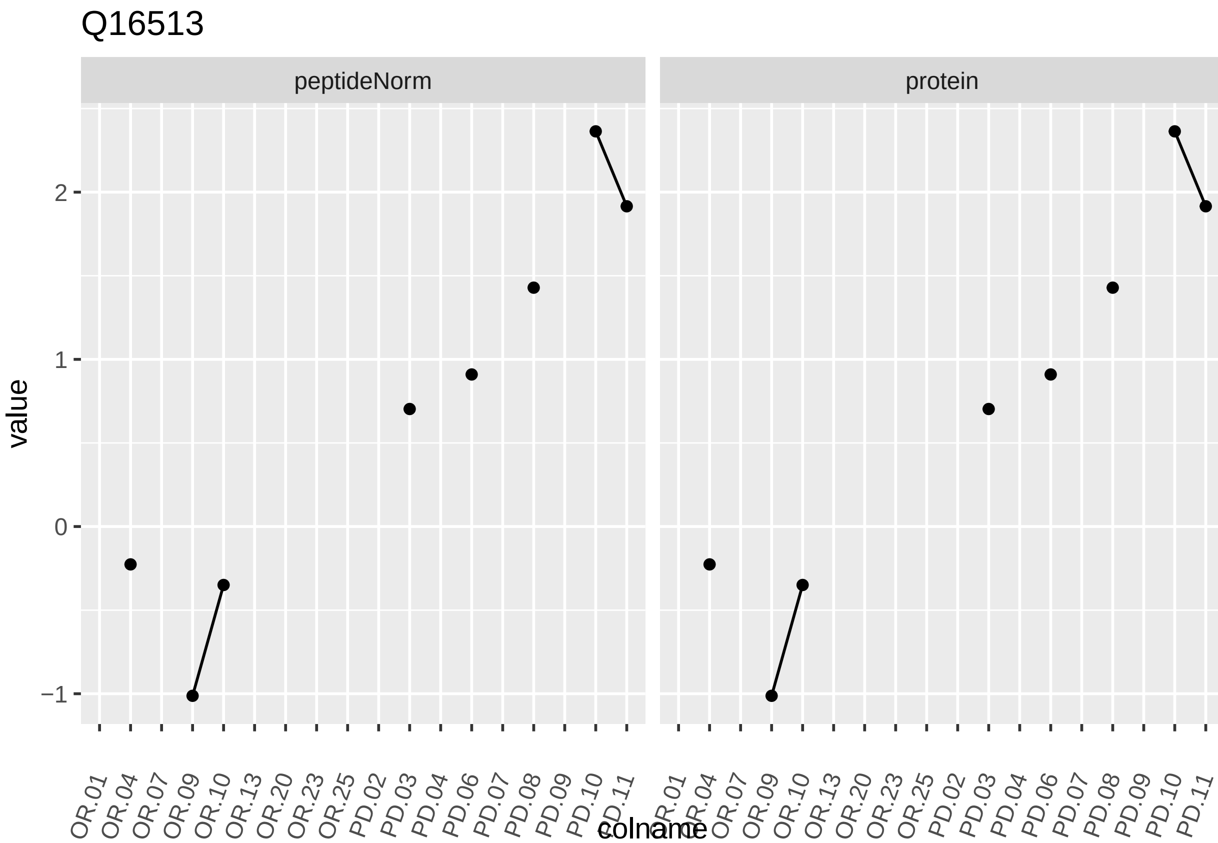

Q9NR45
peptideNorm
protein
peptide intensity (log2)
sample
4
2
0
−2
−4
GSDHSASLEPGELAELVR
GYPPEDIFNLVGK
GYPPEDIFNLVGKK
HLEFSHDQYR
IPEGTILTMDMLTVK
KALERPYTSK
LFPDIPIGYSGHETGIAISVAAVALGAK
PLELELCPGR
Q9NR45
QLLPCEMACNEK
VGSGDTNNFPYLEK
VISEYQK
VKIPEGTILTMDMLTVK
VLVTVEEDDTIMEELVDNHGK
VLVTVEEDDTIMEELVDNHGKK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

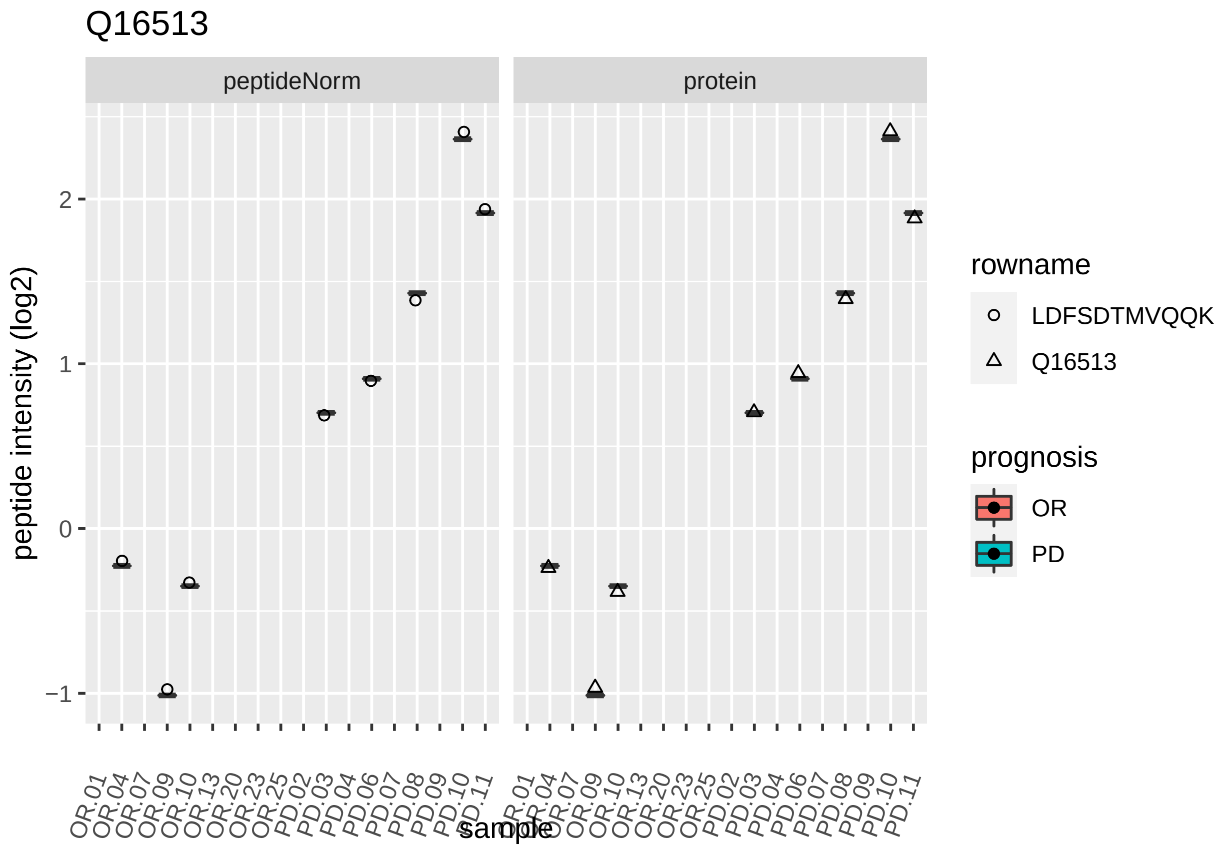


Q9HB71
peptideNorm
protein
value
colname
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

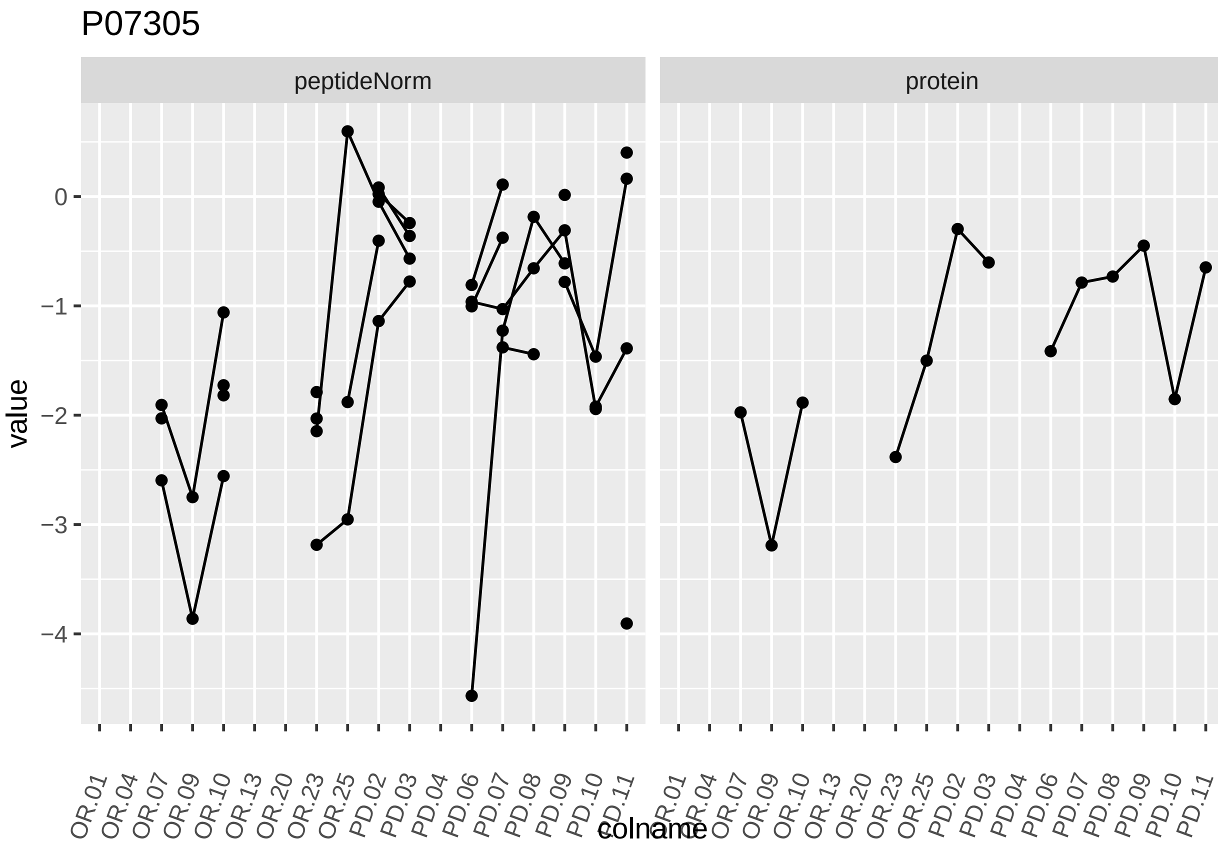


Q9HB71
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
−2
−3
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
ASEELQKDLEEVK
EKPSYDTETDPSEGLMNVLK
ISNYGWDQSDK
KAELLDNEKPAAVVAPITTGYTVK
KIYEDGDDDMKR
Q9HB71
SFDLLVK
SKIETEIK
SYSMIVNNLLKPISVEGSSK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

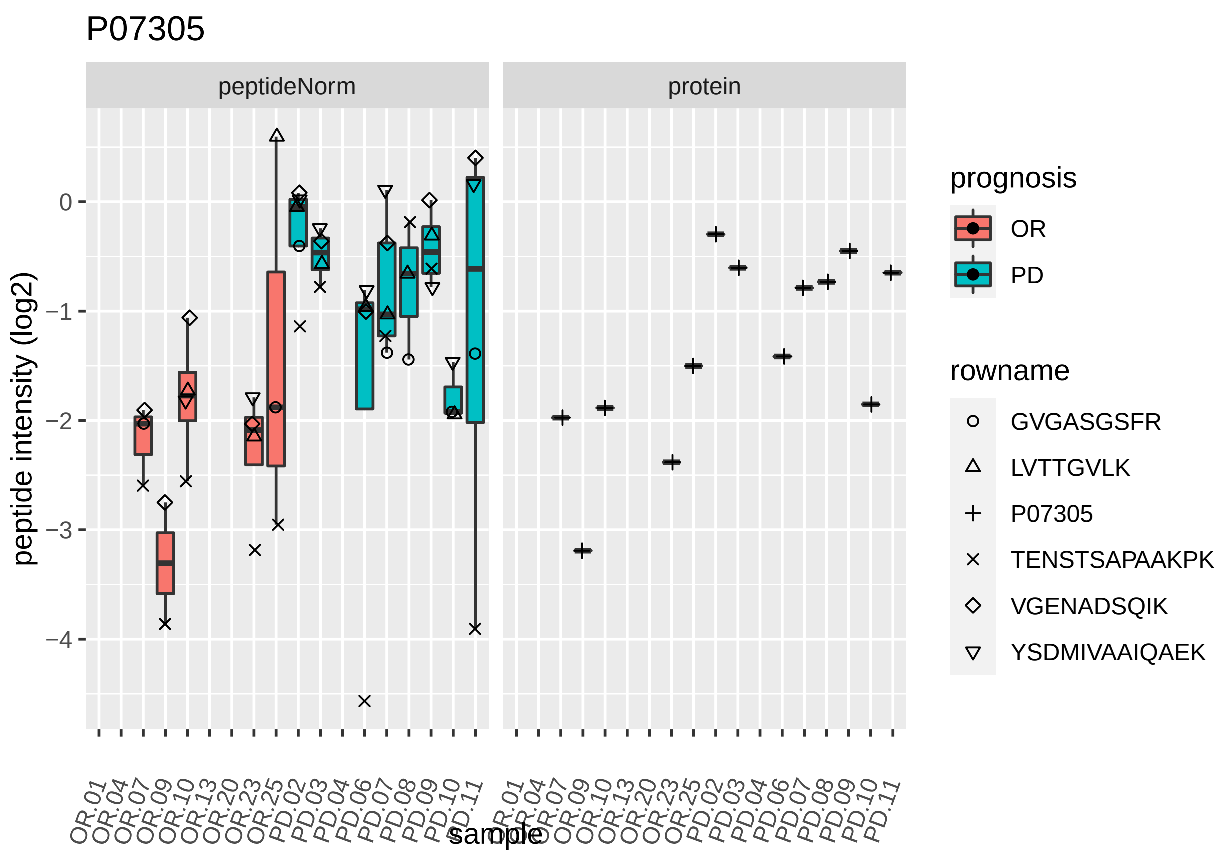

Q16513
peptideNorm
protein
value
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname



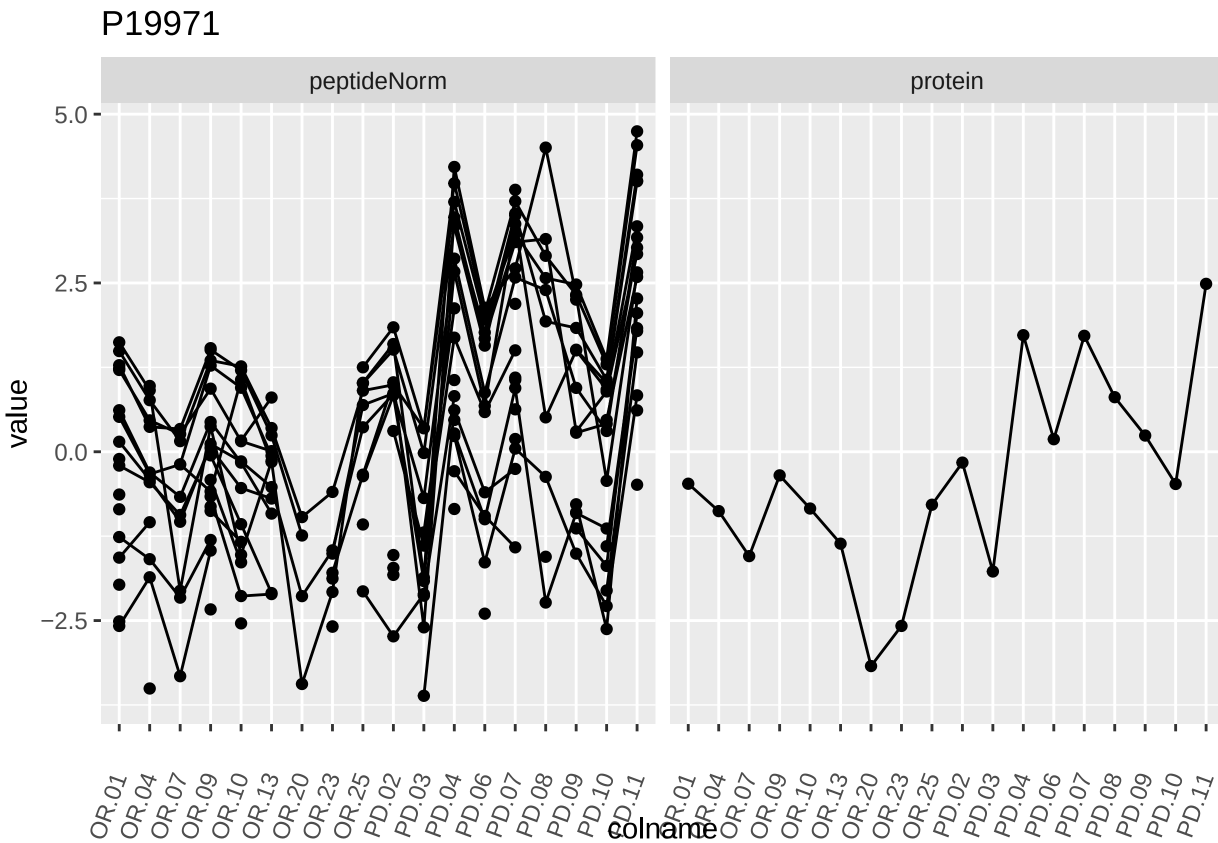
Q16513
peptideNorm
protein
peptide intensity (log2)
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LDFSDTMVQQK
Q16513
prognosis
OR
PD



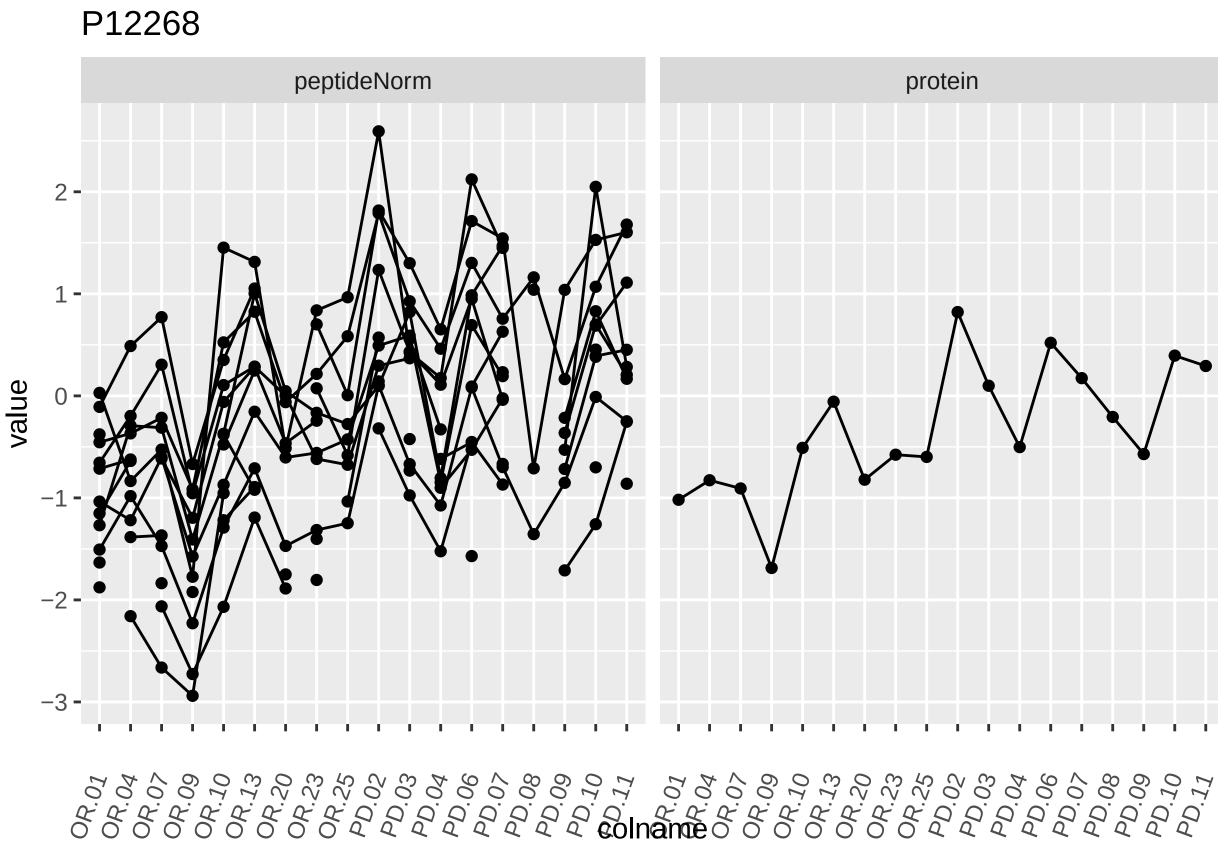
P07305
peptideNorm
protein
value
0
−1
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

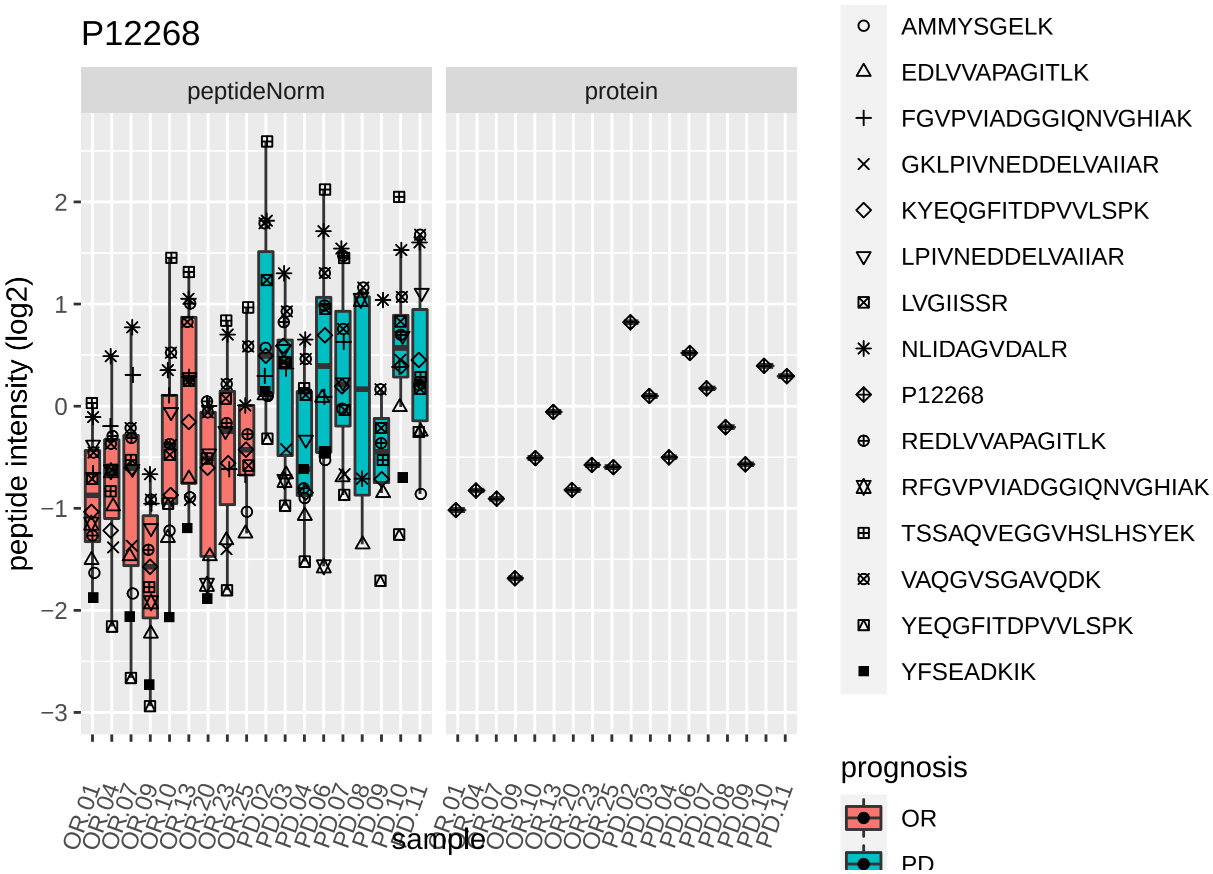


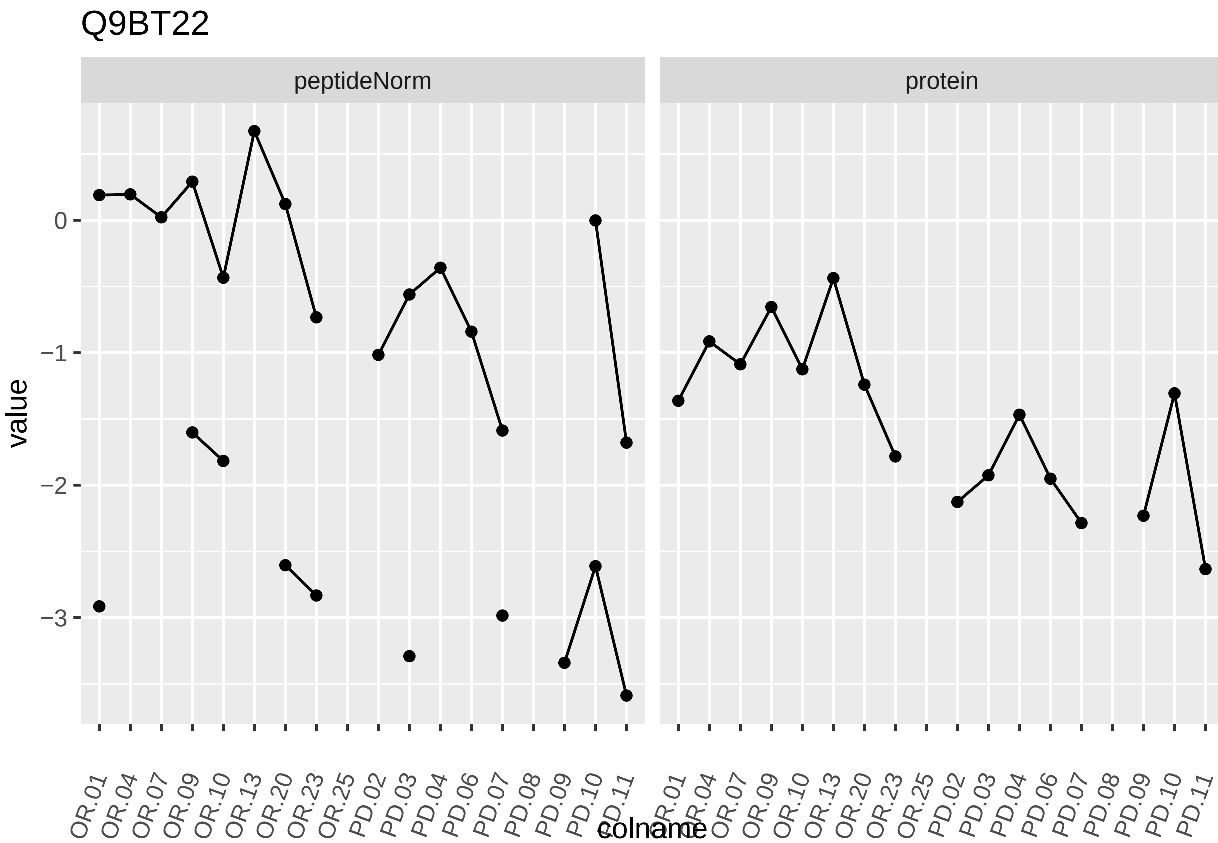
P07305
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
prognosis
OR
PD
rowname
GVGASGSFR
LVTTGVLK
P07305
TENSTSAPAAKPK
VGENADSQIK
YSDMIVAAIQAEK


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

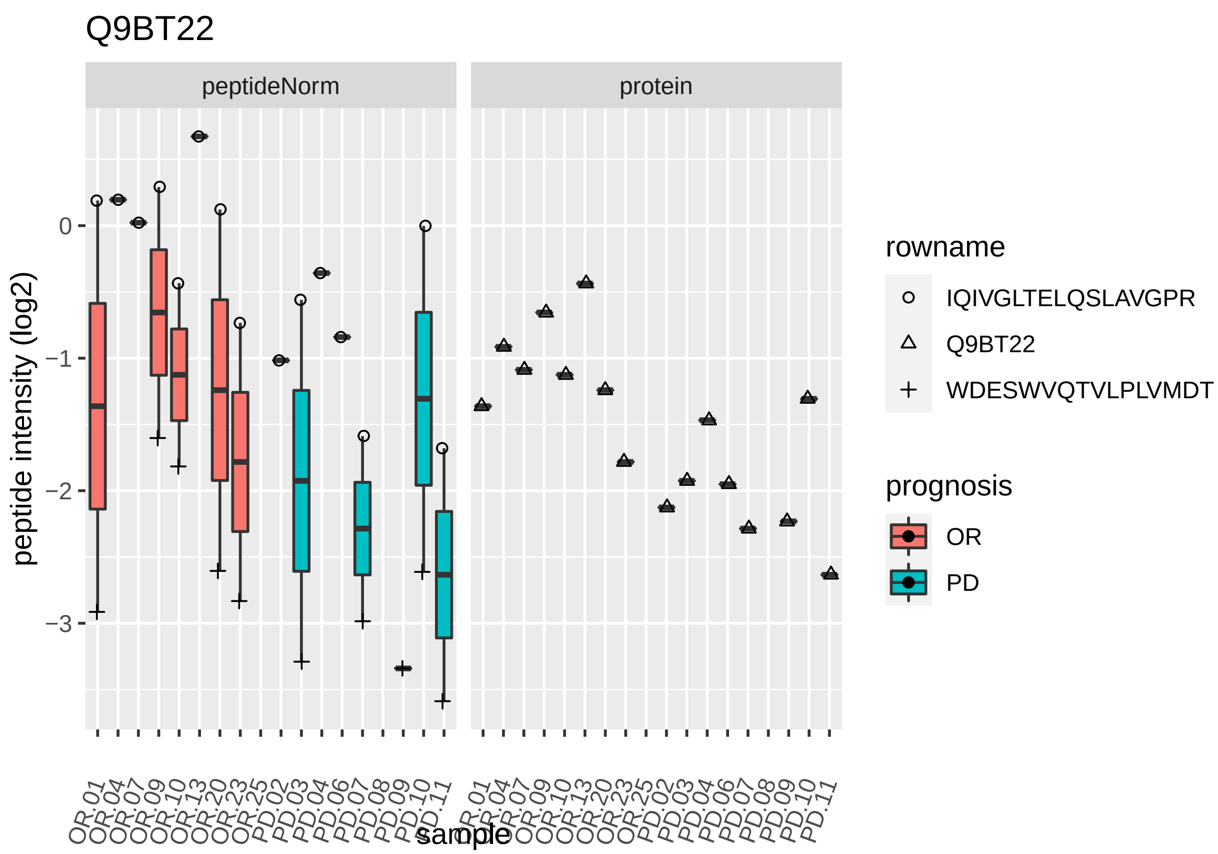

P19971
prognosis
OR
PD
rowname
ALCSGSPAER
ALPLALVLHELGAGR
ALQEALVLSDR
APFAAPSPFAELVLPPQQ
AREQEELLAPADGTVELVR
DGPALSGPQSR
DLVTTLGGALLWLSGHAGTQAQGAAR
DVTATVDSLPLITASILSK
EQEELLAPADGTVELVR
FGGAAVFPNQEQAR
GLGHTGGTLDK
GMDLEETSVLTQALAQSGQQLEWPEAWR
KLVEGLSALVVDVK
LGVGAELLVDVGQR
LSEADIR
LSEADIRGFVAAVVNGSAQGAQIGAMLMAIR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


P12268
peptideNorm
protein
value
colname
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

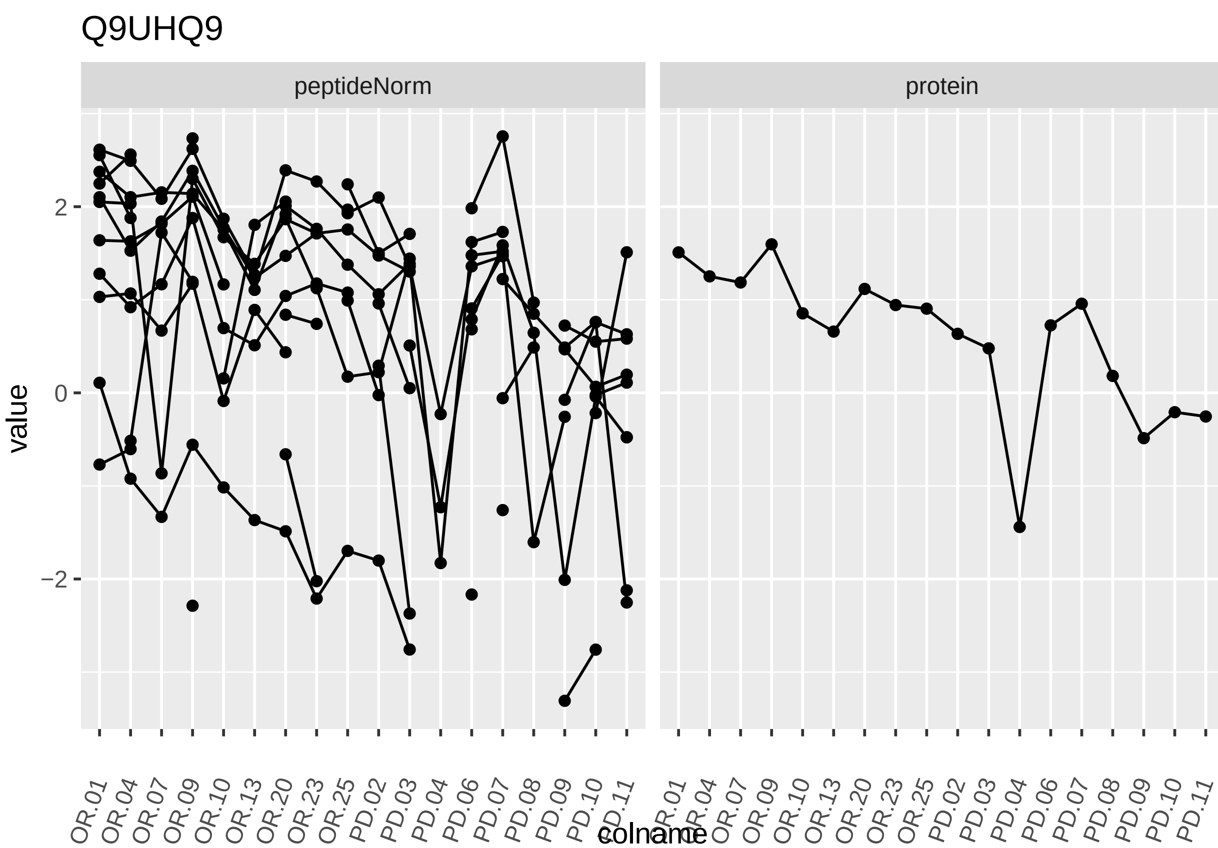

P12268
peptideNorm
protein
peptide intensity (log2)
sample
AMMYSGELK
EDLVVAPAGITLK
FGVPVIADGGIQNVGHIAK
GKLPIVNEDDELVAIIAR
KYEQGFITDPVVLSPK
LPIVNEDDELVAIIAR
LVGIISSR
NLIDAGVDALR
P12268
REDLVVAPAGITLK
RFGVPVIADGGIQNVGHIAK
TSSAQVEGGVHSLHSYEK
VAQGVSGAVQDK
YEQGFITDPVVLSPK
YFSEADKIK
prognosis
OR
PD



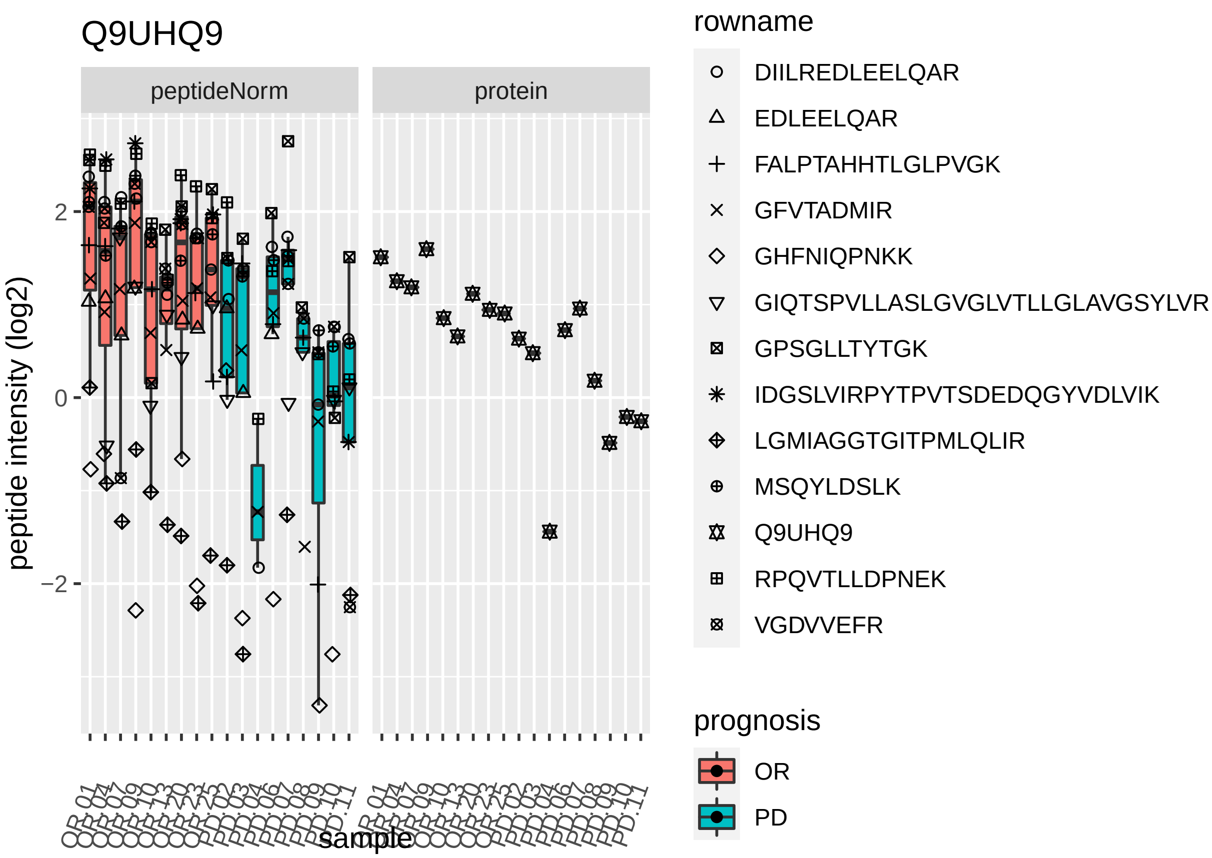
Q9BT22
peptideNorm
protein
value
colname
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



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
rowname
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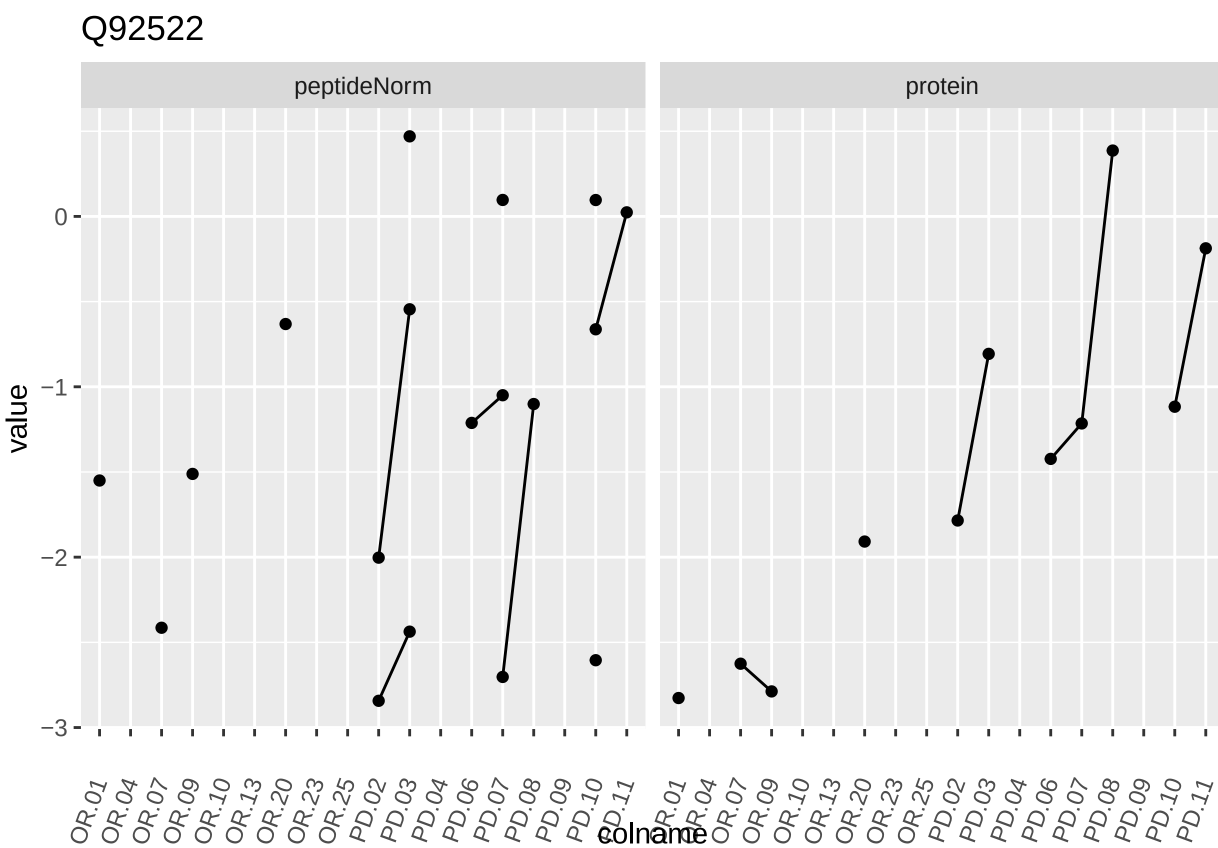
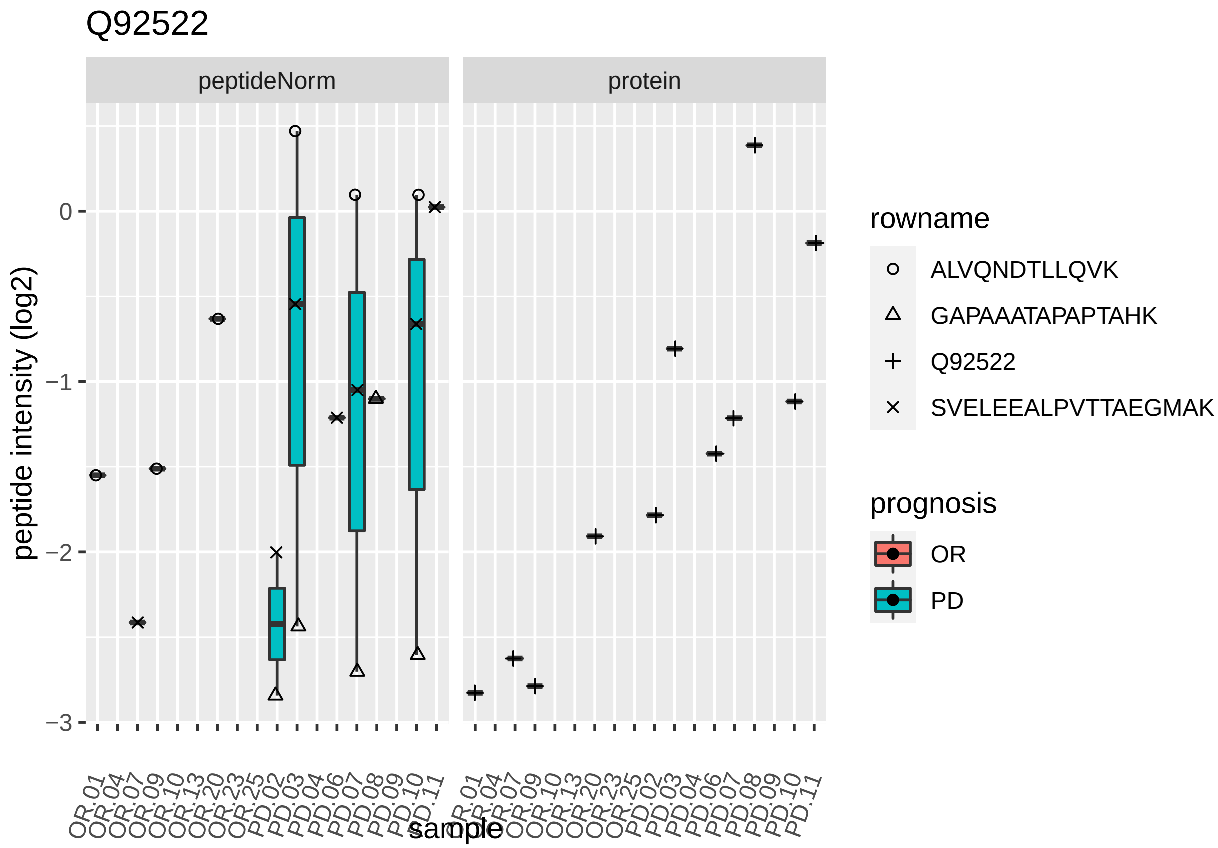
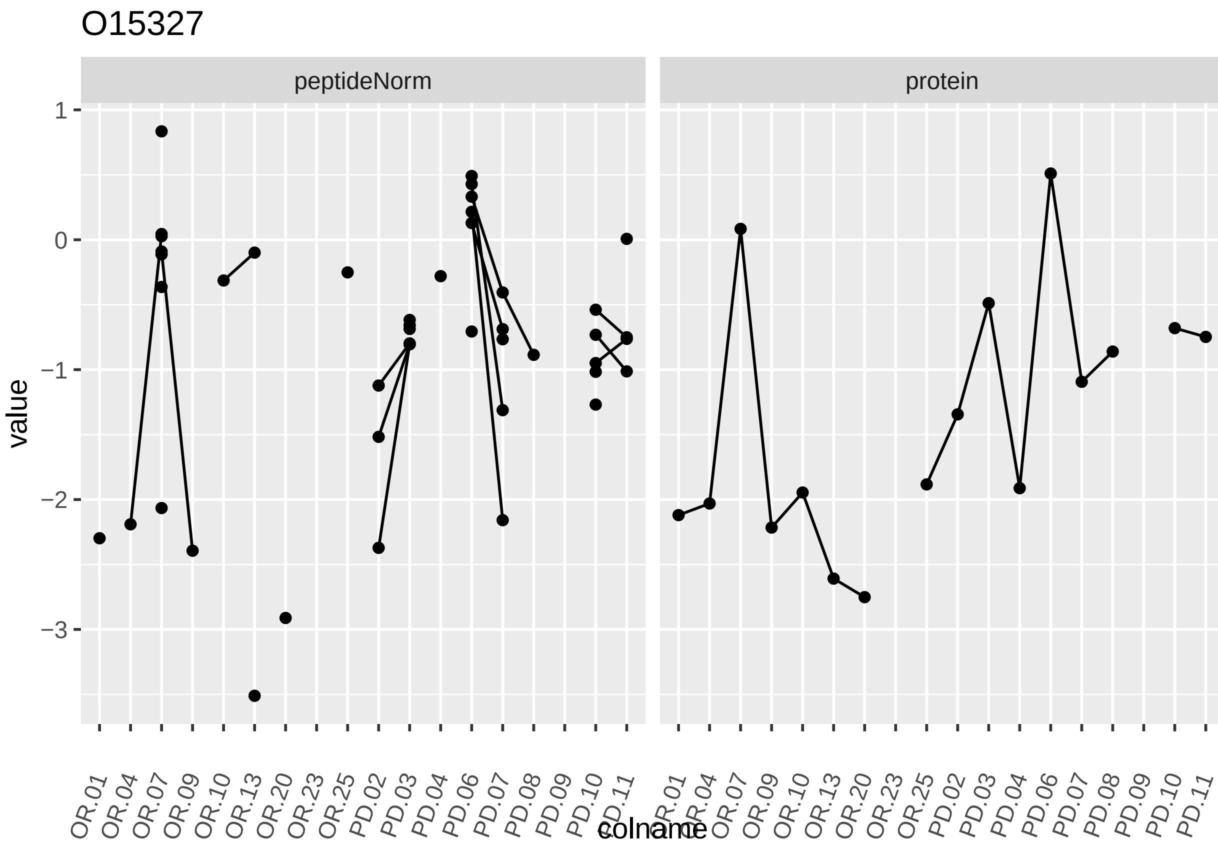
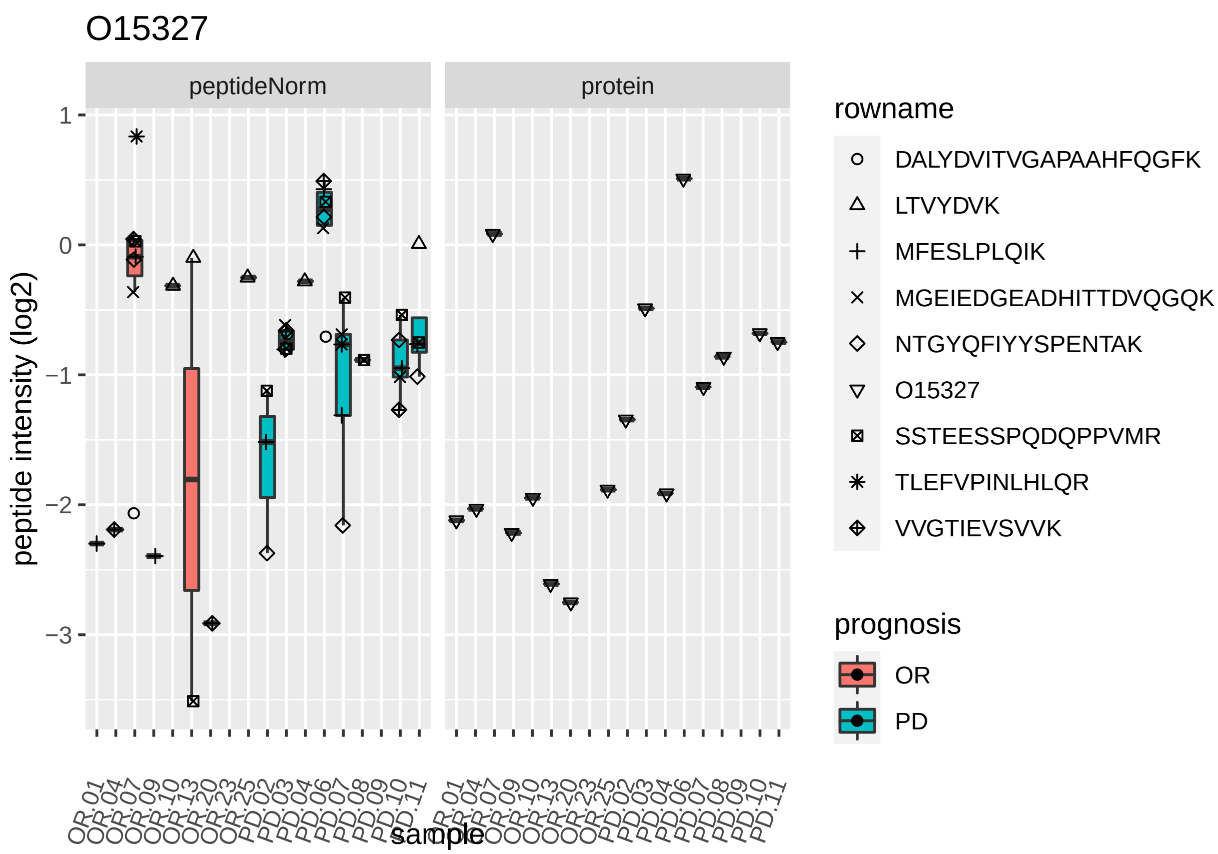
EDLEELQAR
FALPTAHHTLGLPVGK
GFVTADMIR
GHFNIQPNKK
GIQTSPVLLASLGVGLVTLLGLAVGSYLVR
GPSGLLTYTGK
IDGSLVIRPYTPVTSDEDQGYVDLVIK
LGMIAGGTGITPMLQLIR
MSQYLDSLK
Q9UHQ9
RPQVTLLDPNEK
VGDVVEFR
prognosis
OR
PD

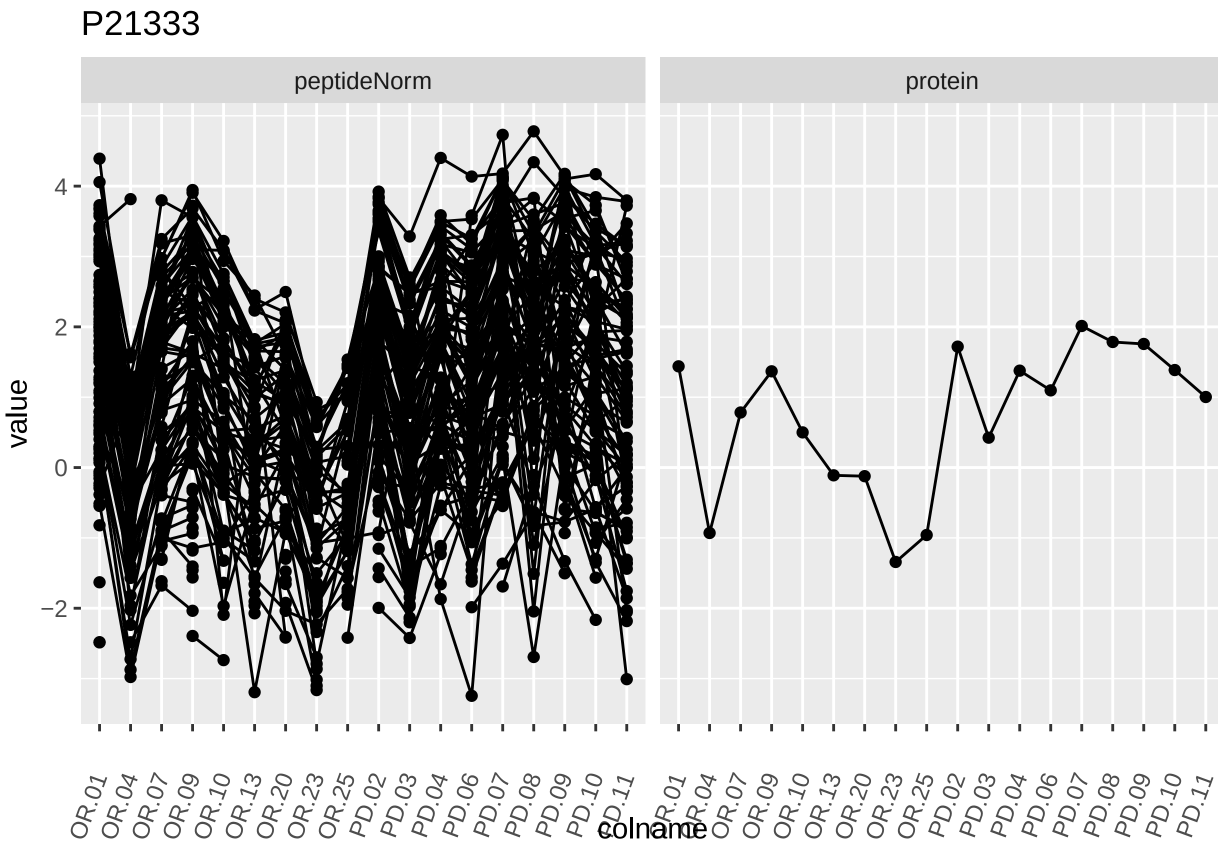

Q92522
peptideNorm
protein
value
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q92522
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
ALVQNDTLLQVK
GAPAAATAPAPTAHK
Q92522
SVELEEALPVTTAEGMAK
prognosis
OR
PD



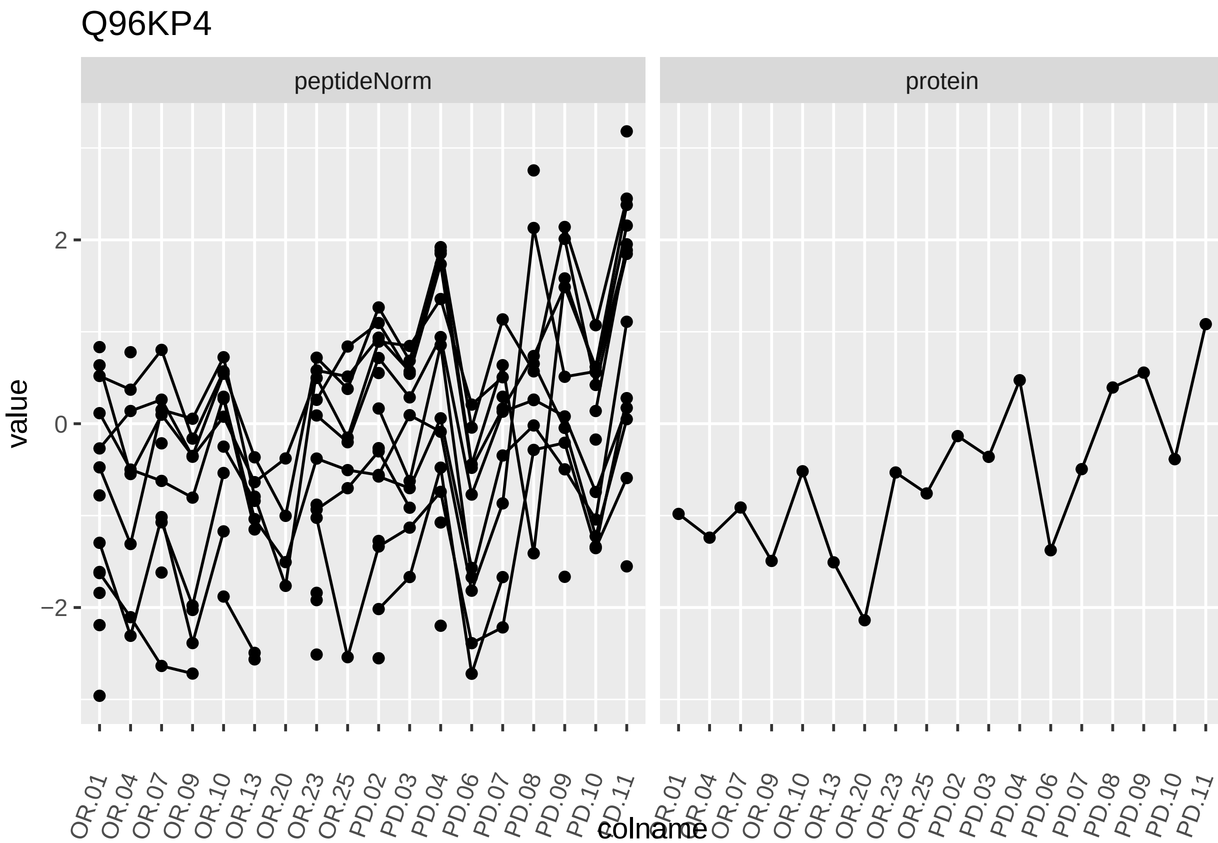
O15327
peptideNorm
protein
value
colname
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

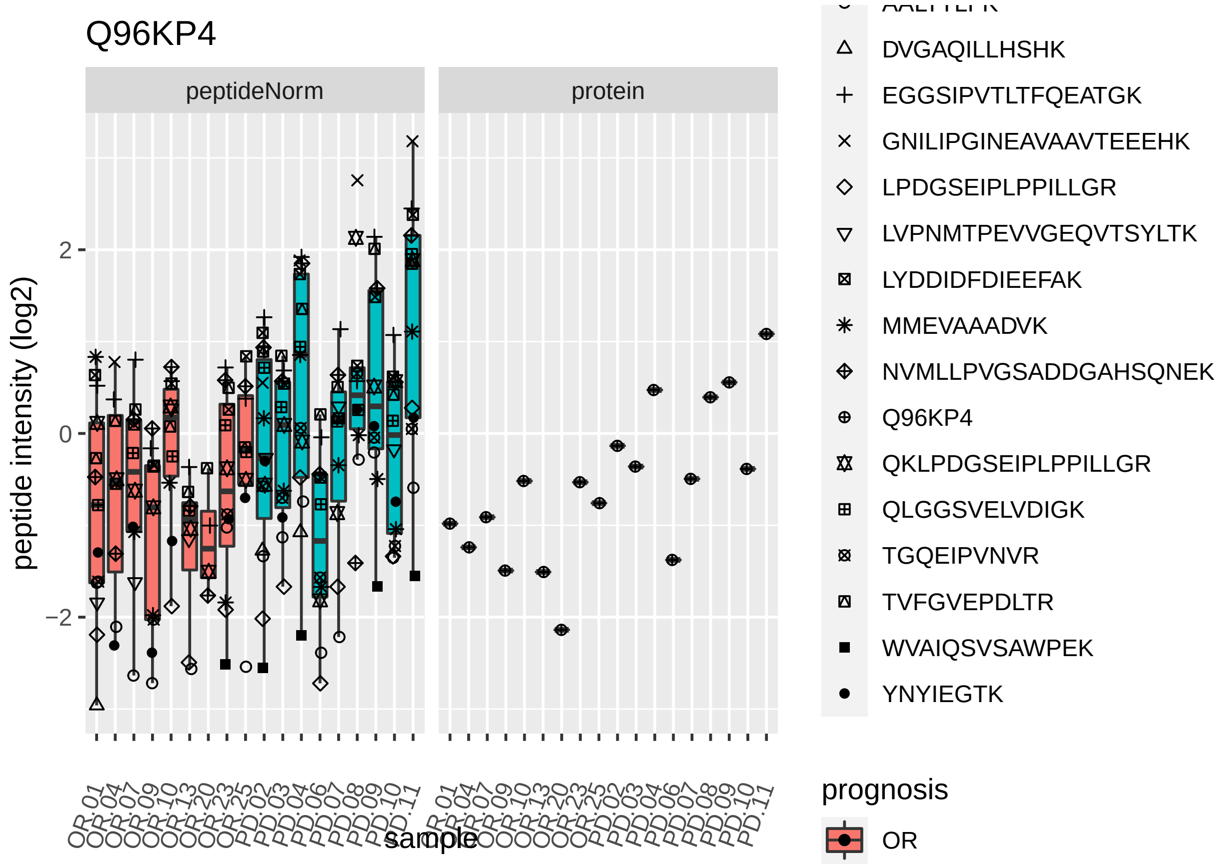

O15327
peptideNorm
protein
peptide intensity (log2)
sample
rowname
DALYDVITVGAPAAHFQGFK
LTVYDVK
MFESLPLQIK
MGEIEDGEADHITTDVQGQK
NTGYQFIYYSPENTAK
O15327
SSTEESSPQDQPPVMR
TLEFVPINLHLQR
VVGTIEVSVVK
prognosis
OR
PD

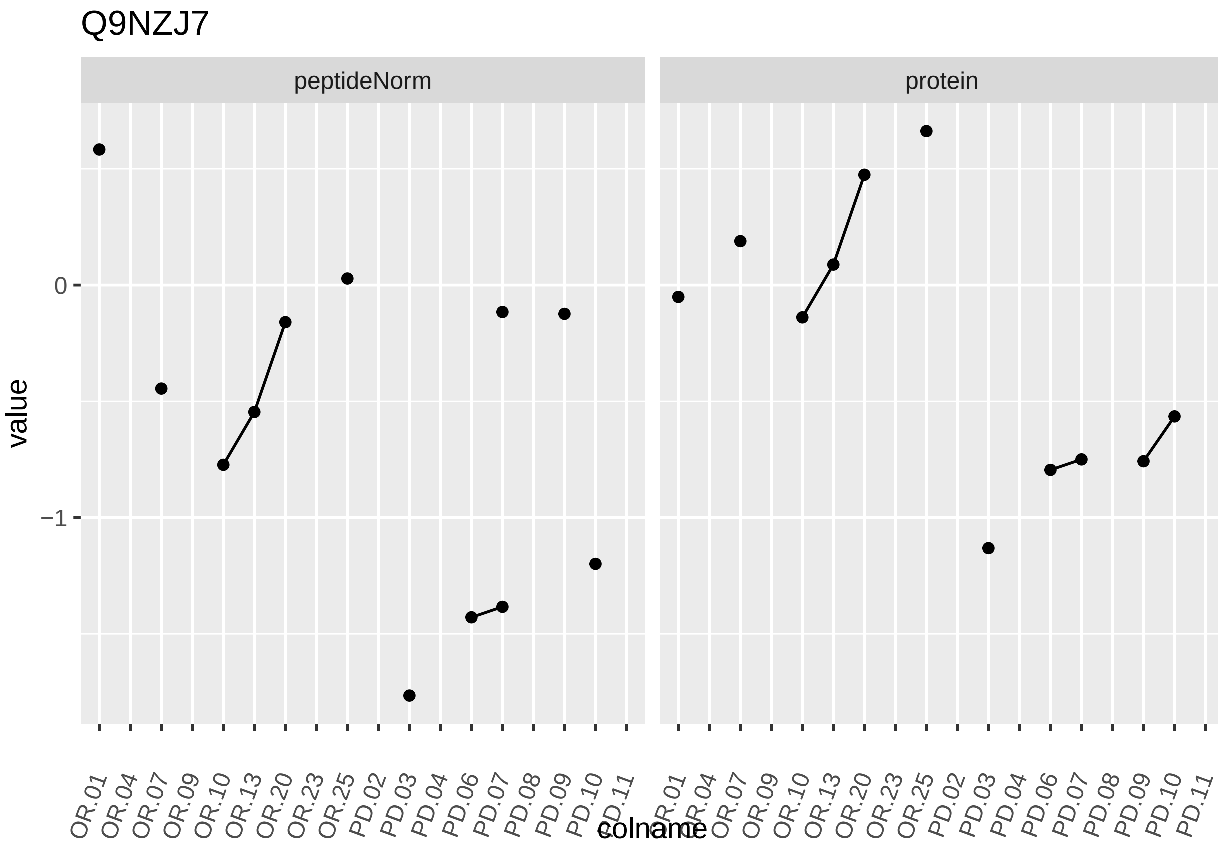


P21333
peptideNorm
protein
value
colname
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

	)	GAGSYTIMVLFADQATPTSPIR	<	LVSNHSLHETSSVFVDSLTK
VK	*	GAGTGGLGLAVEGPSEAK	=	LYSVSYLLK
TYGGHQVPGSPFK	+	GKLDVQFSGLTK	>	MDCQECPEGYR
	,	GLVEPVDVVDNADGTQTVNYVPSR	?	NDNDTFTVK
IVTITWGGQNIGR	-	GQHVPGSPFQFTVGPLGEGGAHK	@	NGHVGISFVPK
	.	GTVEPQLEAR	A	NGQHVASSPIPVVISQSEIGDAS
	/	HTAMVSWGGVSIPNSPFR	B	P21333
	0	IANLQTDLSDGLR	C	PGAPLRPK
EIVDPNVDEHSVMTYLSQFPK	1	IECDDKGDGSCDVR	D	RAEFTVETR
	2	IPEISIQDMTAQVTSPSGK	E	RAPSVANVGSHCDLSLK
PFPLEAVAPTKPSK	3	IVGPSGAAVPCK	F	RLTVSSLQESGLK
	4	KGEITGEVR	G	SADFVVEAIGDDVGTLGFSVEG
	5	KTHIQDNHDGTYTVAYVPDVTGR	H	SAGQGEVLVYVEDPAGHQEEAK
	6	LDVQFSGLTK	I	SPFEVYVDK
	7	LIALLEVLSQKK	J	SPFSVAVSPSLDLSK
QPSVQPPLR	8	LLGWIQNKLPQLPITNFSR	K	SPYTVTVGQACNPSACR
DAR	9	LQVEPAVDTSGVQCYGPGIEGQGVFR	L	TFSVWYVPEVTGTHK


Q96KP4
peptideNorm
protein
value
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q96KP4
peptideNorm
protein
peptide intensity (log2)
sample
DVGAQILLHSHK
EGGSIPVTLTFQEATGK
GNILIPGINEAVAAVTEEEHK
LPDGSEIPLPPILLGR
LVPNMTPEVVGEQVTSYLTK
LYDDIDFDIEEFAK
MMEVAAADVK
NVMLLPVGSADDGAHSQNEK
Q96KP4
QKLPDGSEIPLPPILLGR
QLGGSVELVDIGK
TGQEIPVNVR
TVFGVEPDLTR
WVAIQSVSAWPEK
YNYIEGTK
prognosis
OR



Q9NZJ7
peptideNorm
protein
value
0
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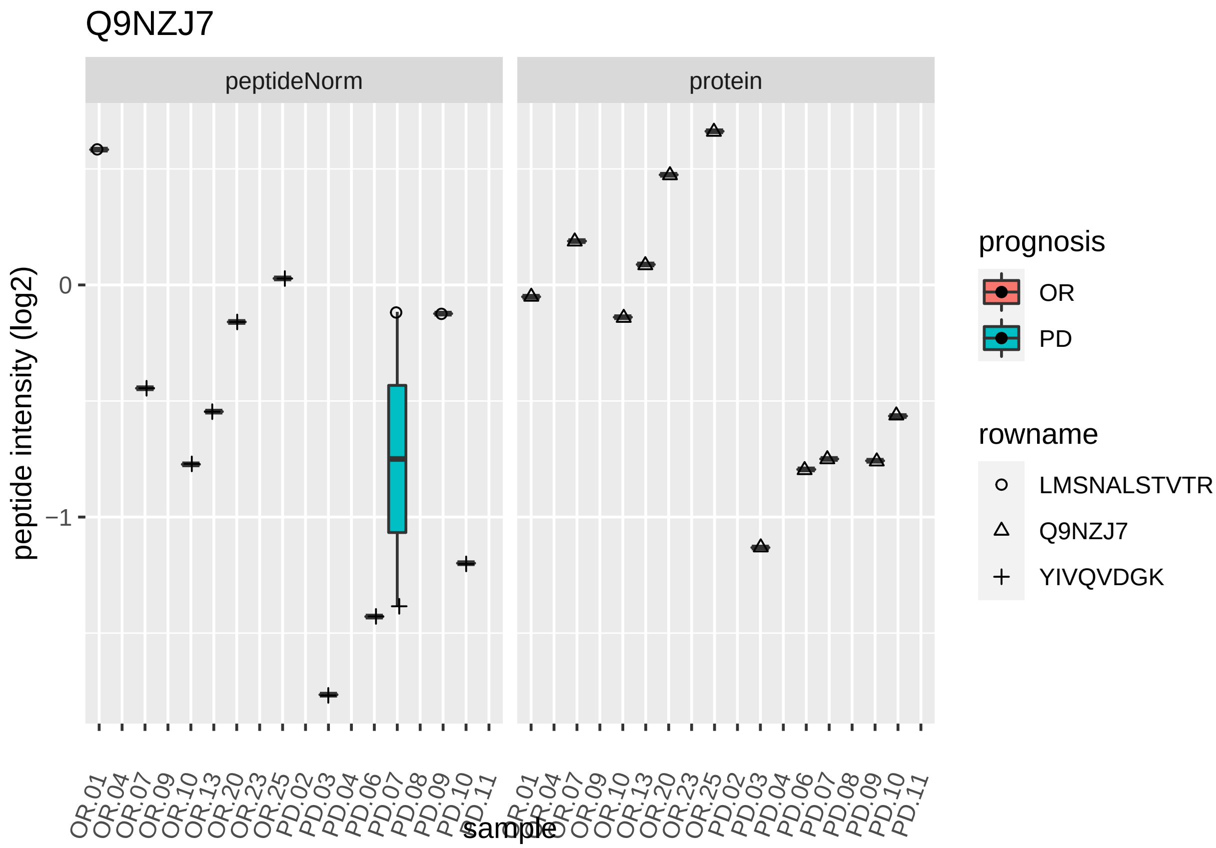
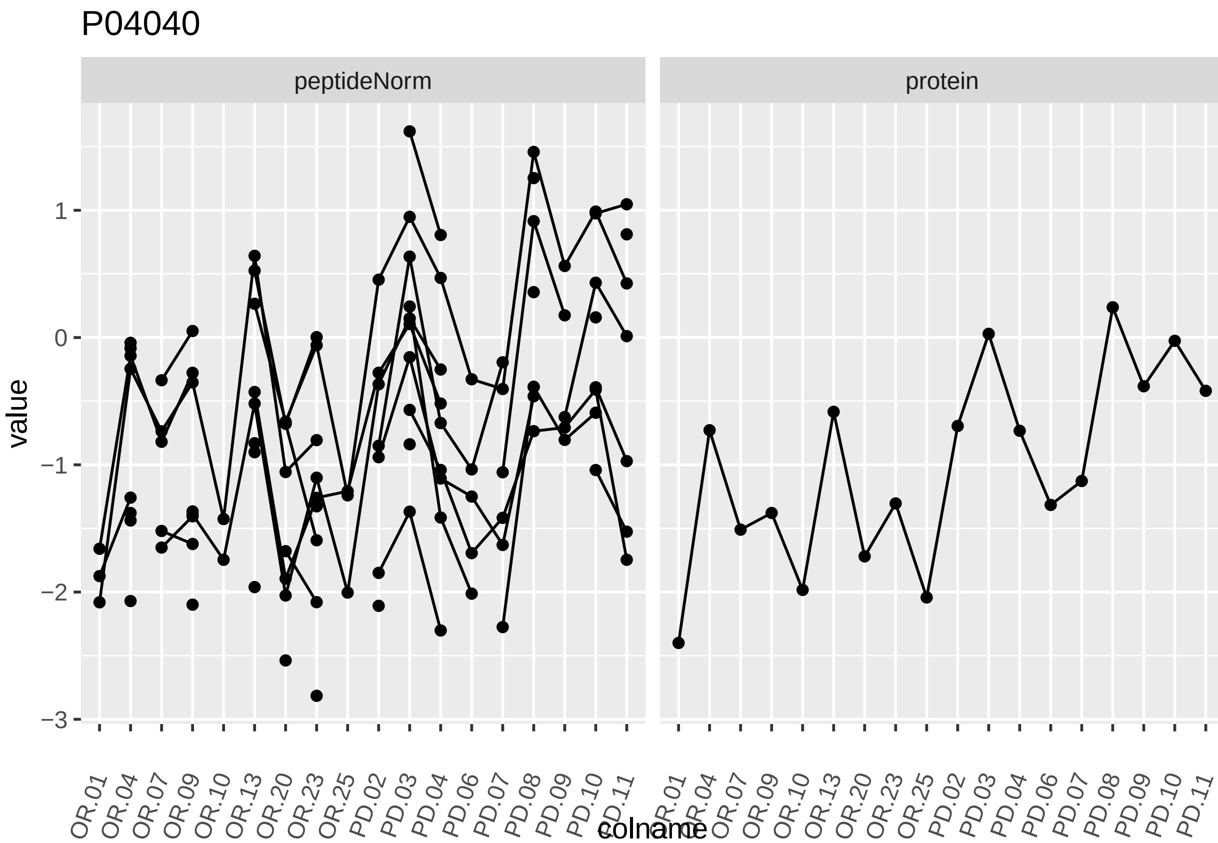
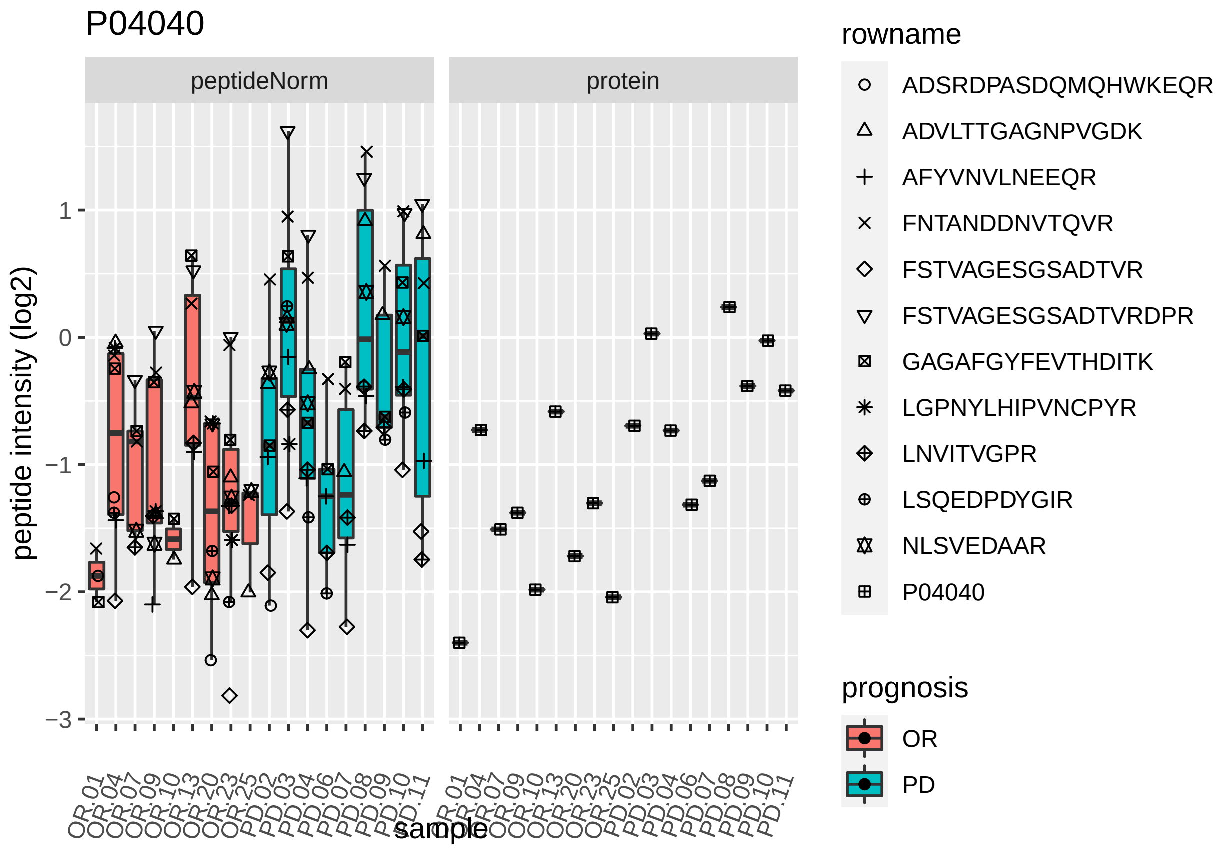
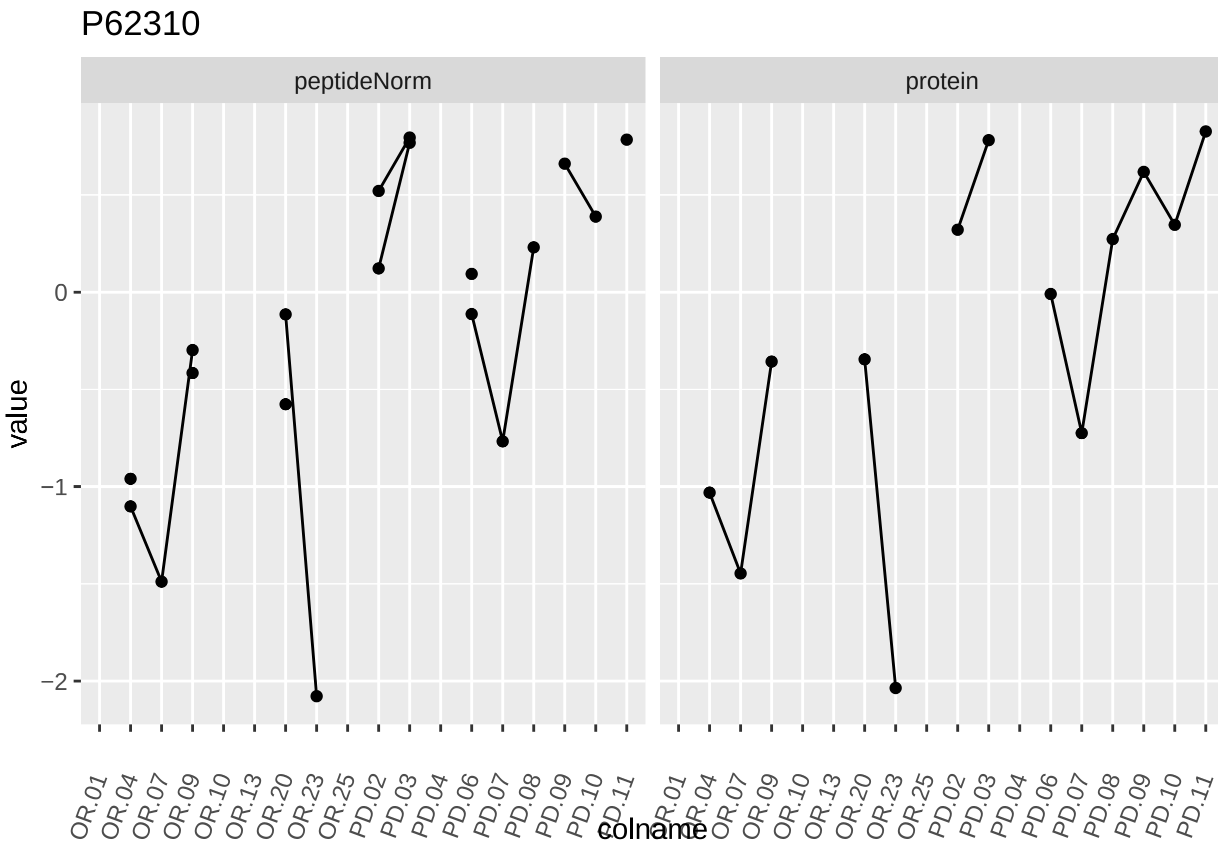
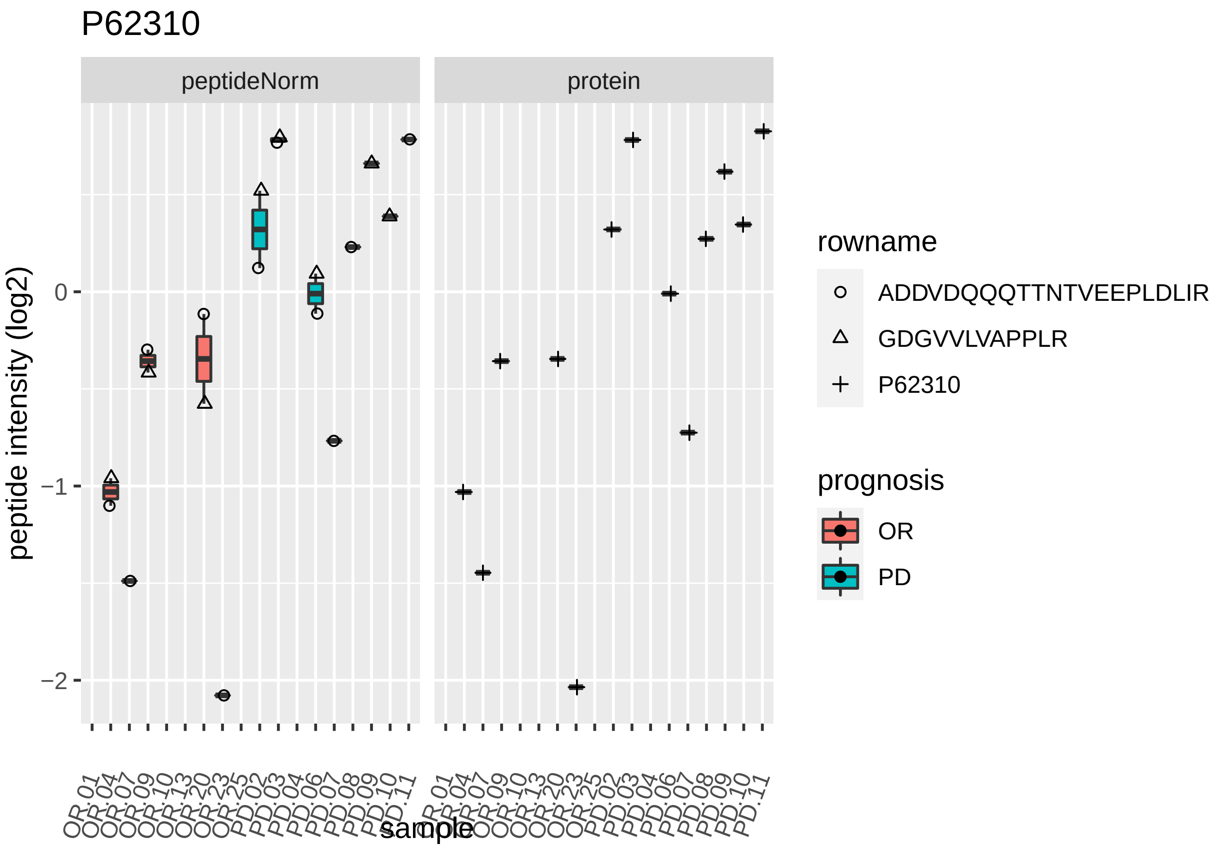
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


Q9NZJ7
peptideNorm
protein
peptide intensity (log2)
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
LMSNALSTVTR
Q9NZJ7
YIVQVDGK

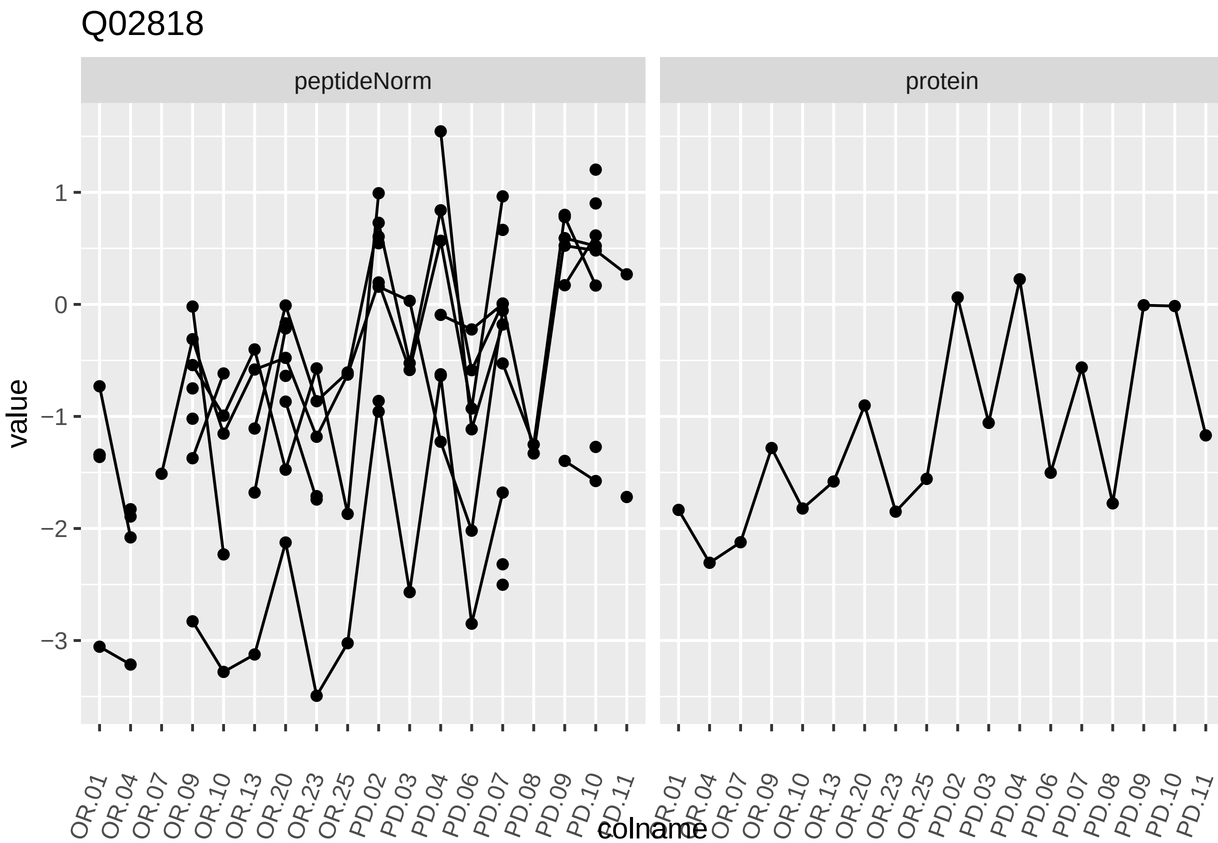

P04040
peptideNorm
protein
value
colname
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P04040
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
ADSRDPASDQMQHWKEQR
ADVLTTGAGNPVGDK
AFYVNVLNEEQR
FNTANDDNVTQVR
FSTVAGESGSADTVR
FSTVAGESGSADTVRDPR
GAGAFGYFEVTHDITK
LGPNYLHIPVNCPYR
LNVITVGPR
LSQEDPDYGIR
NLSVEDAAR
P04040
prognosis
OR
PD

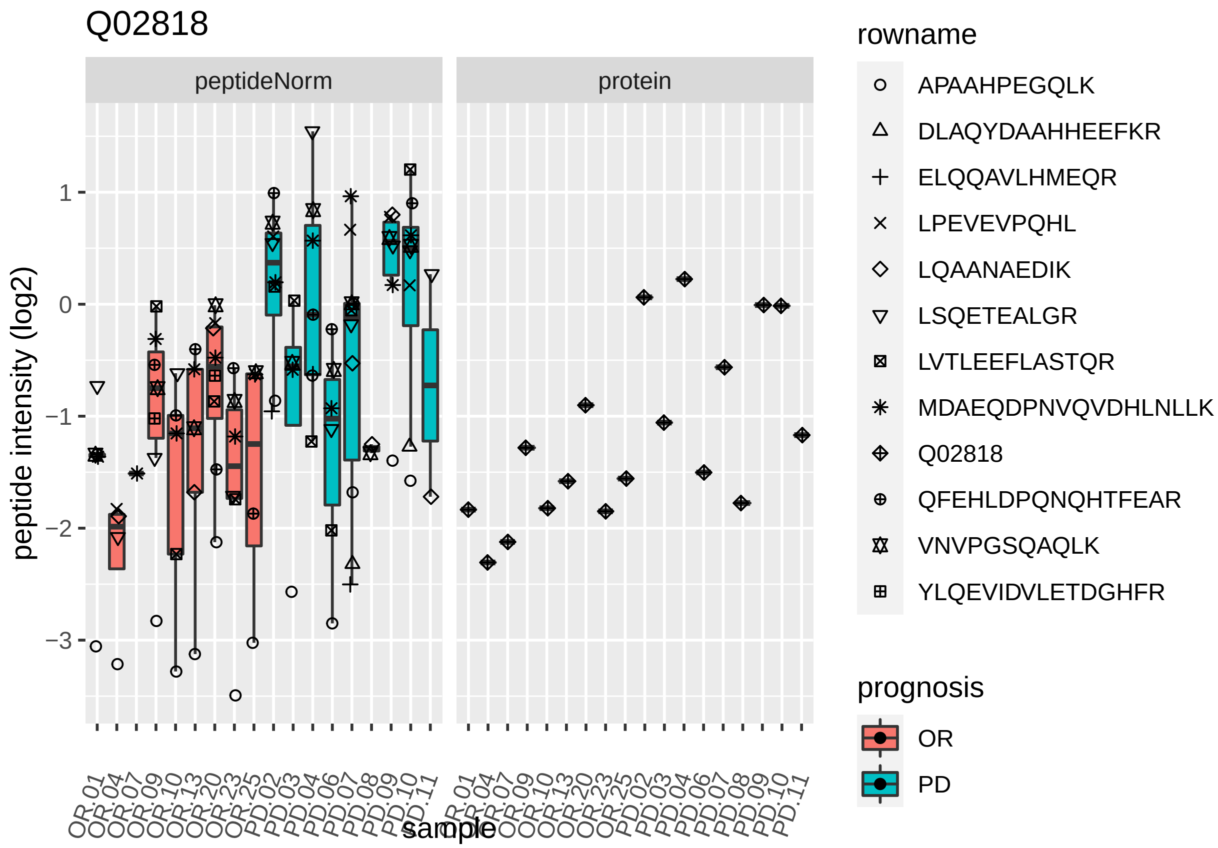

P62310
peptideNorm
protein
value
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname



P62310
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
ADDVDQQQTTNTVEEPLDLIR
GDGVVLVAPPLR
P62310
prognosis
OR
PD

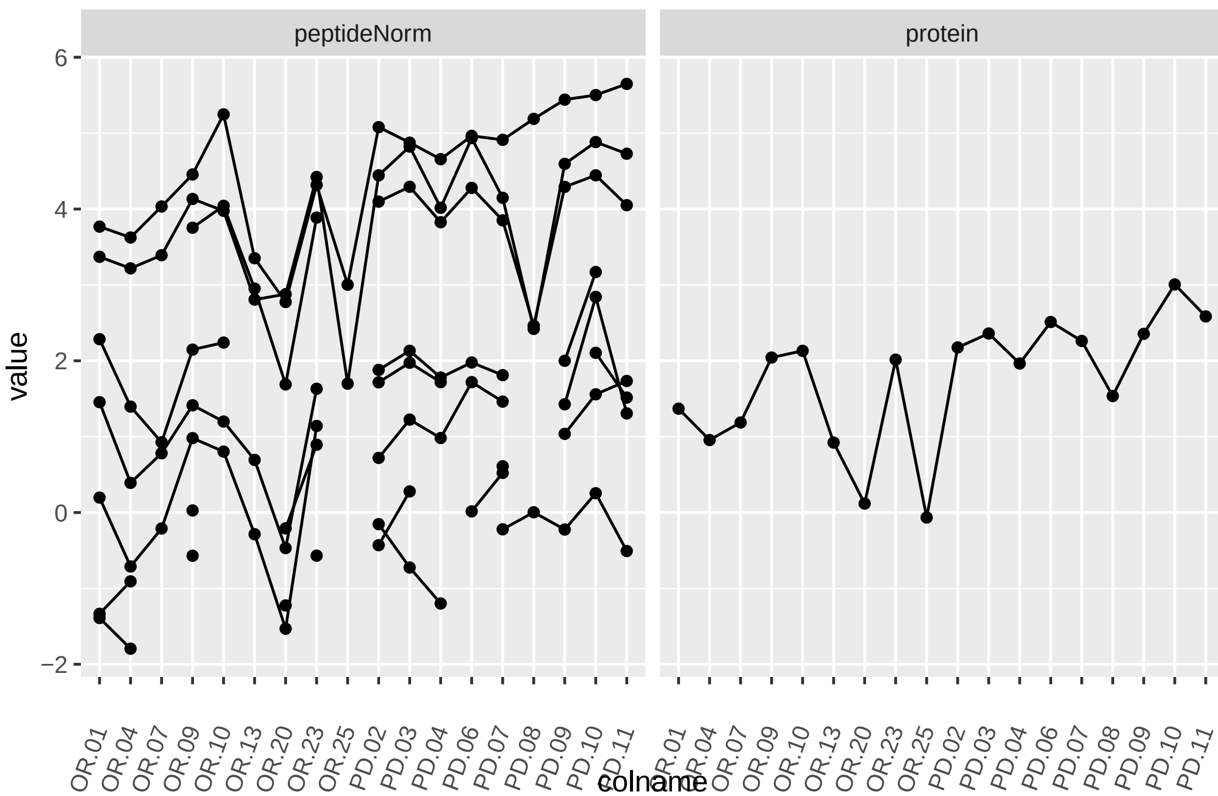


Q02818
peptideNorm
protein
value
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

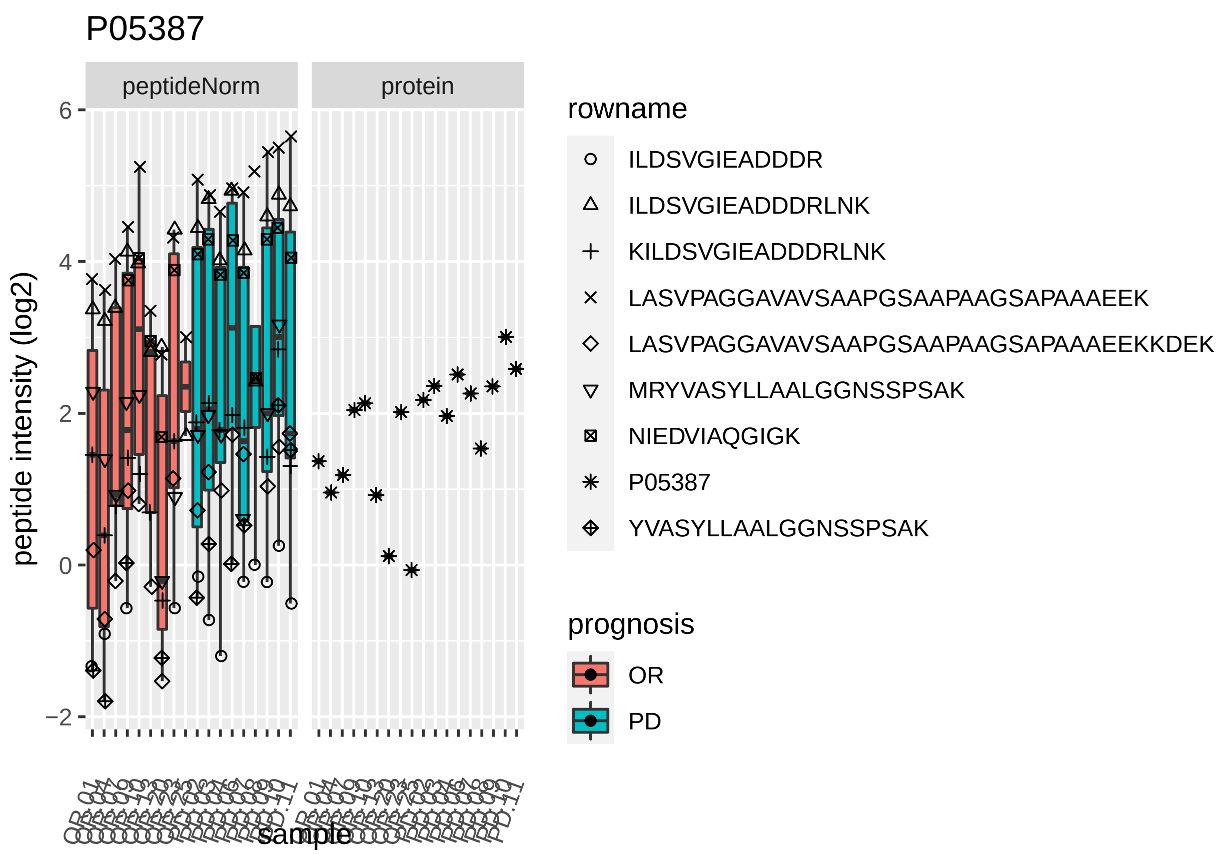


Q02818
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
APAAHPEGQLK
DLAQYDAAHHEEFKR
ELQQAVLHMEQR
LPEVEVPQHL
LQAANAEDIK
LSQETEALGR
LVTLEEFLASTQR
MDAEQDPNVQVDHLNLLK
Q02818
QFEHLDPQNQHTFEAR
VNVPGSQAQLK
YLQEVIDVLETDGHFR
prognosis
OR
PD

P05387

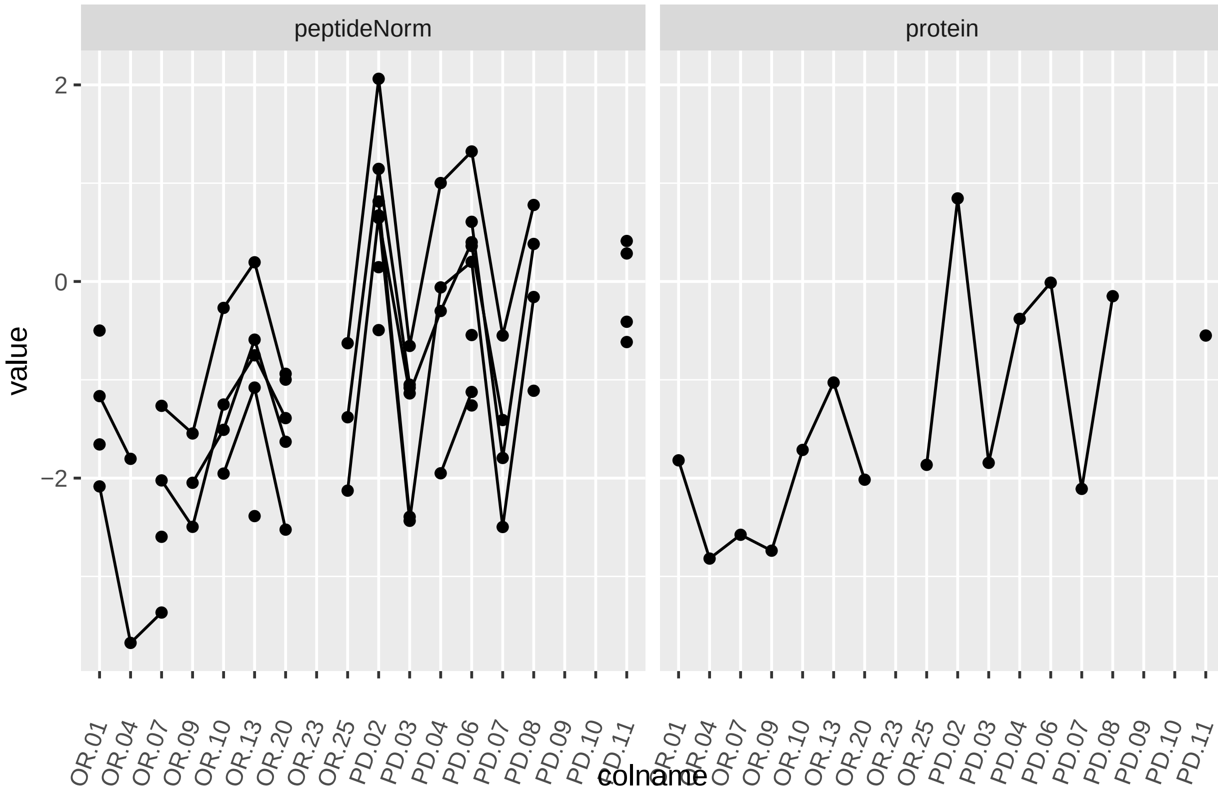


peptideNorm
protein
value
6
4
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

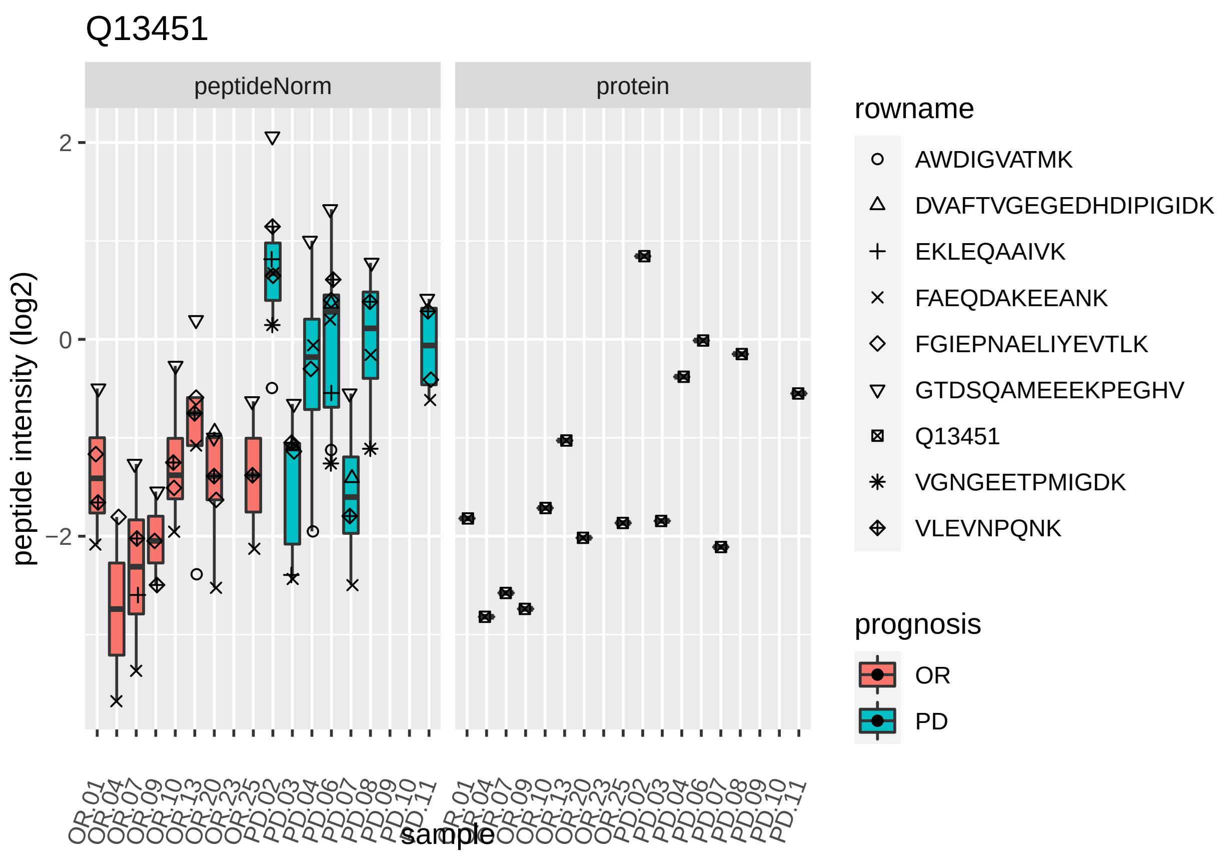


P05387
peptideNorm
protein
peptide intensity (log2)
6
4
2
0
−2
sample
rowname
ILDSVGIEADDDR
ILDSVGIEADDDRLNK
KILDSVGIEADDDRLNK
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEK
MRYVASYLLAALGGNSSPSAK
NIEDVIAQGIGK
P05387
YVASYLLAALGGNSSPSAK
prognosis
OR
PD

Q13451



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



Q13451
peptideNorm
protein
peptide intensity (log2)
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0
−2
sample
rowname
AWDIGVATMK
DVAFTVGEGEDHDIPIGIDK
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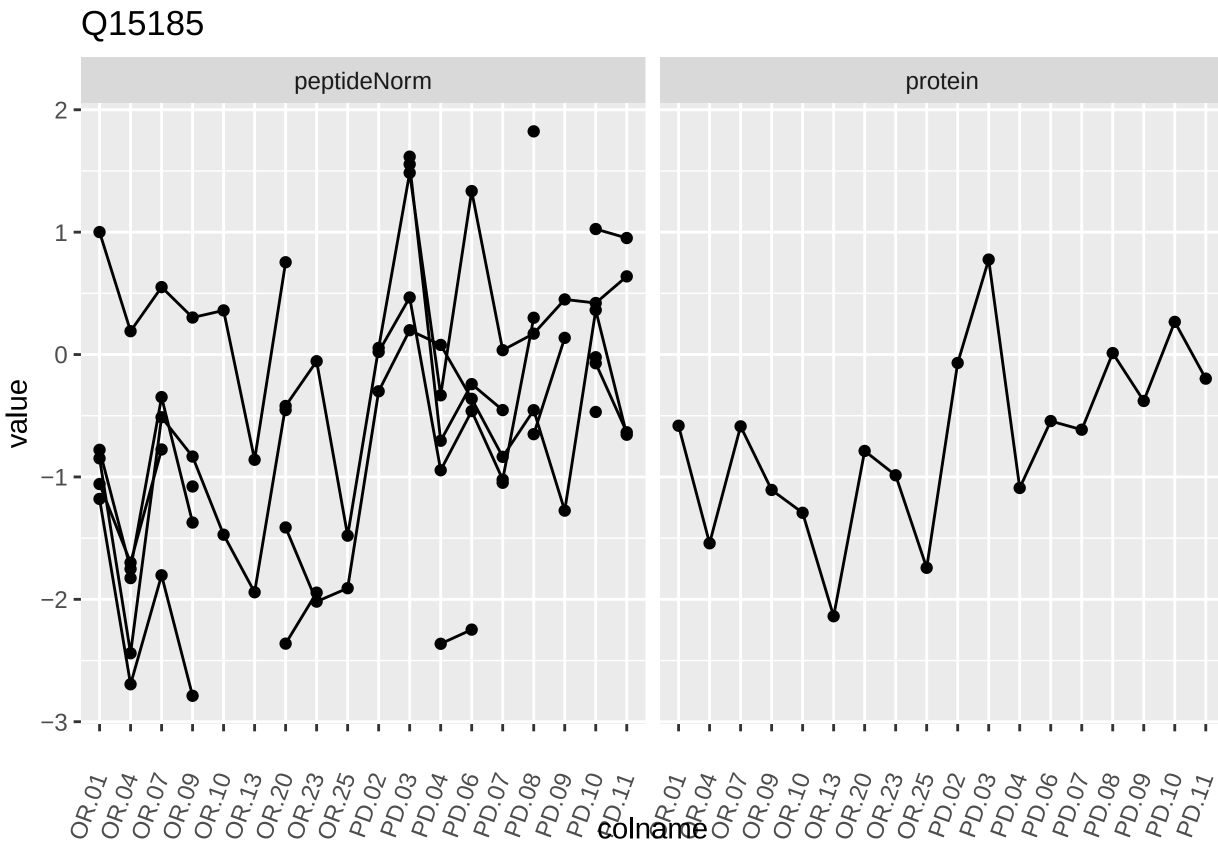
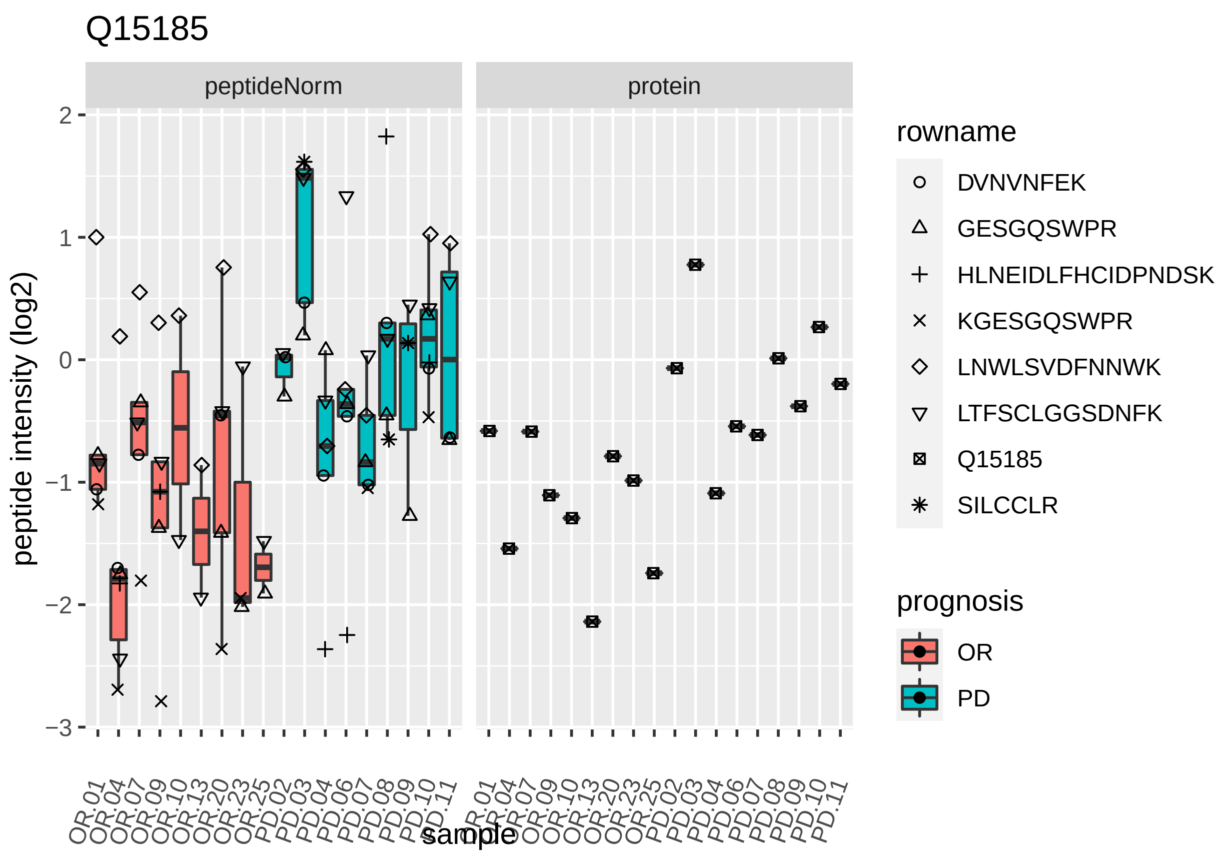
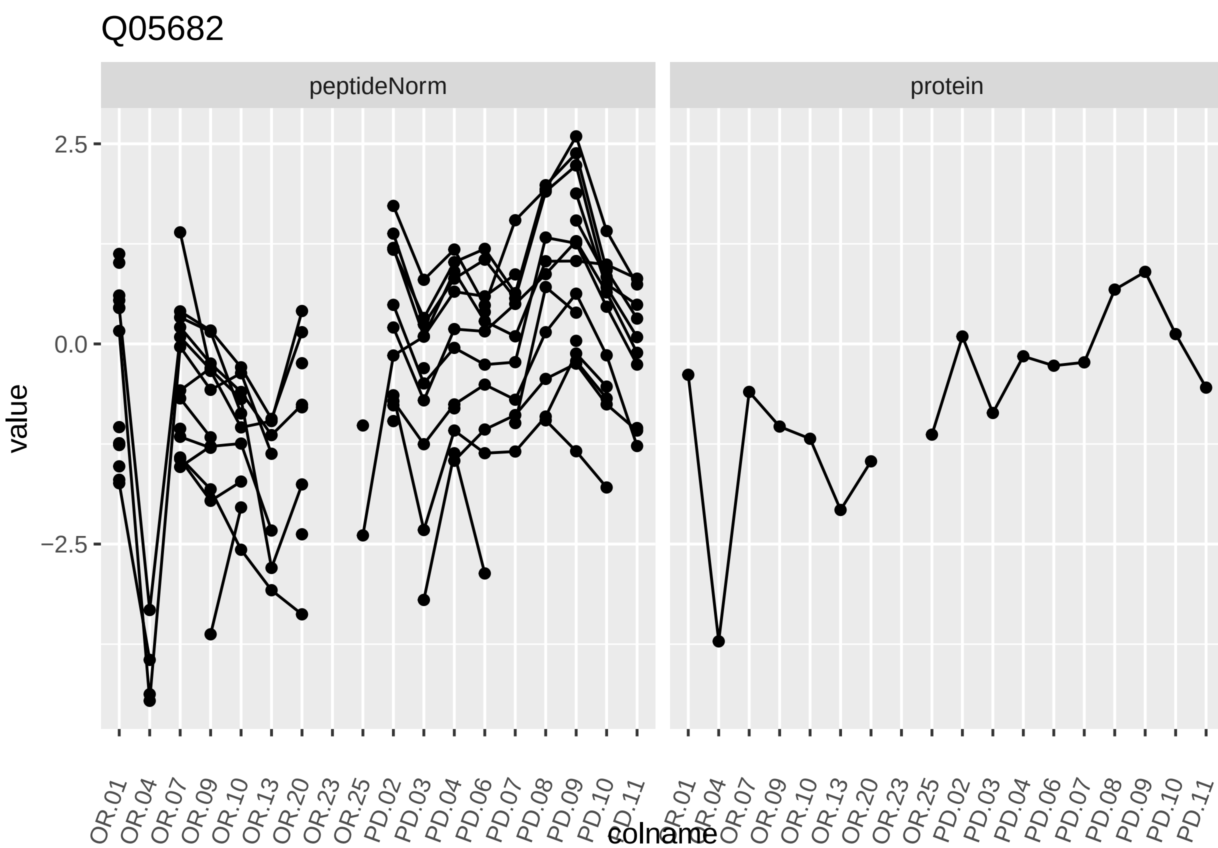
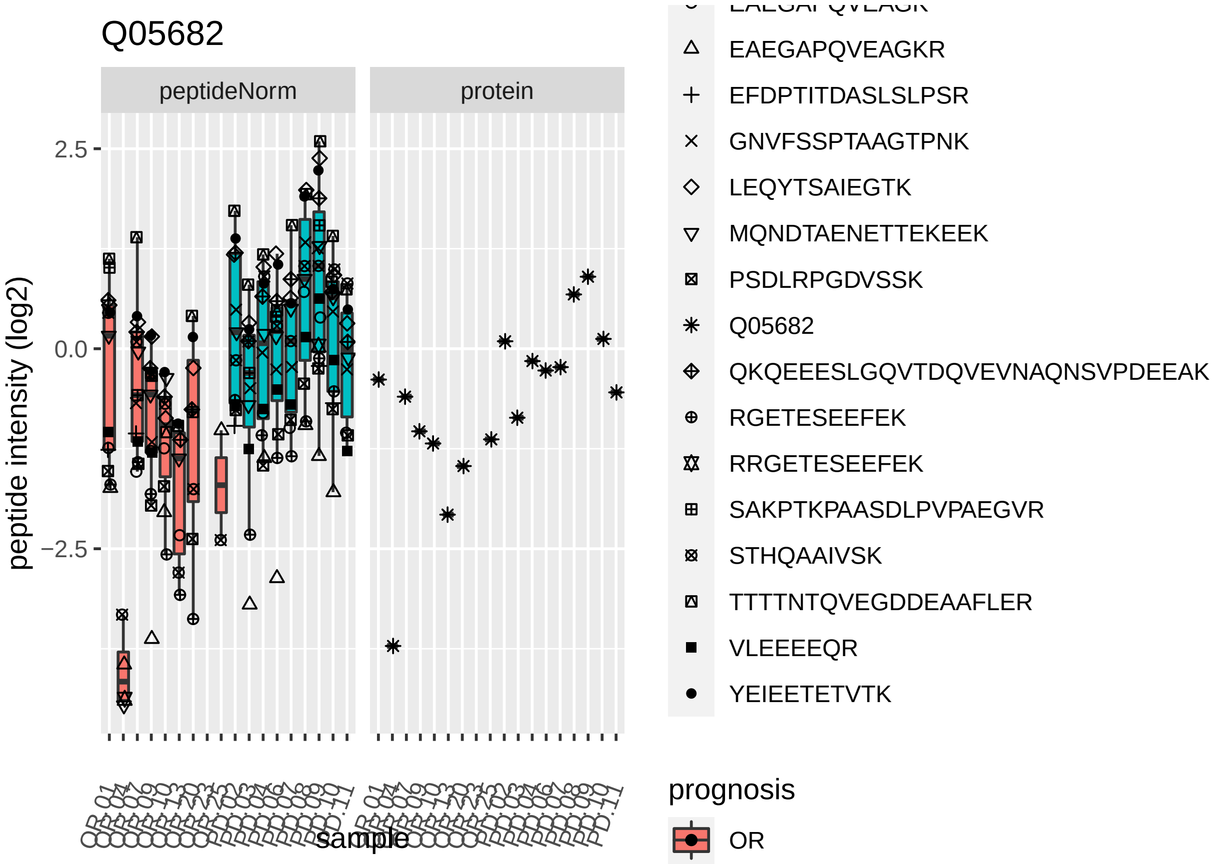
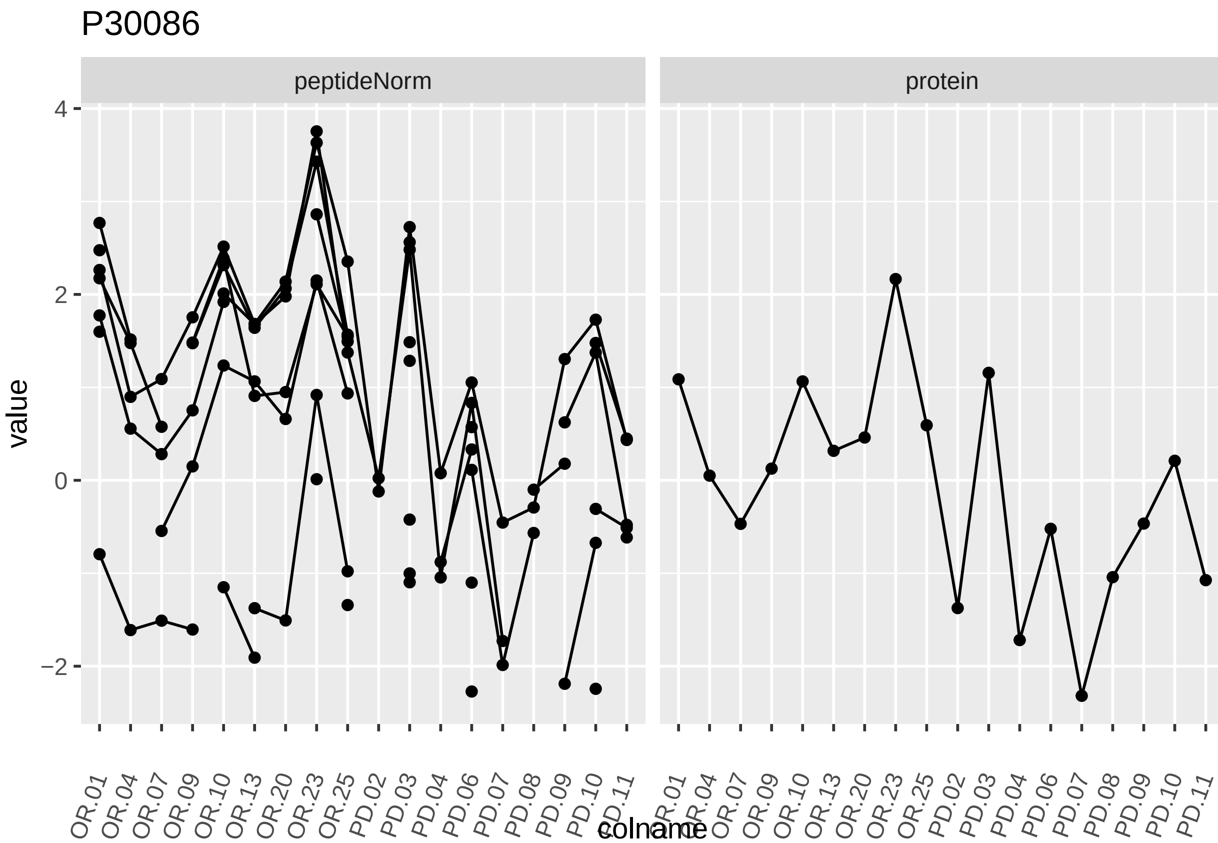
FAEQDAKEEANK
FGIEPNAELIYEVTLK
GTDSQAMEEEKPEGHV
Q13451
VGNGEETPMIGDK
VLEVNPQNK
prognosis
OR
PD

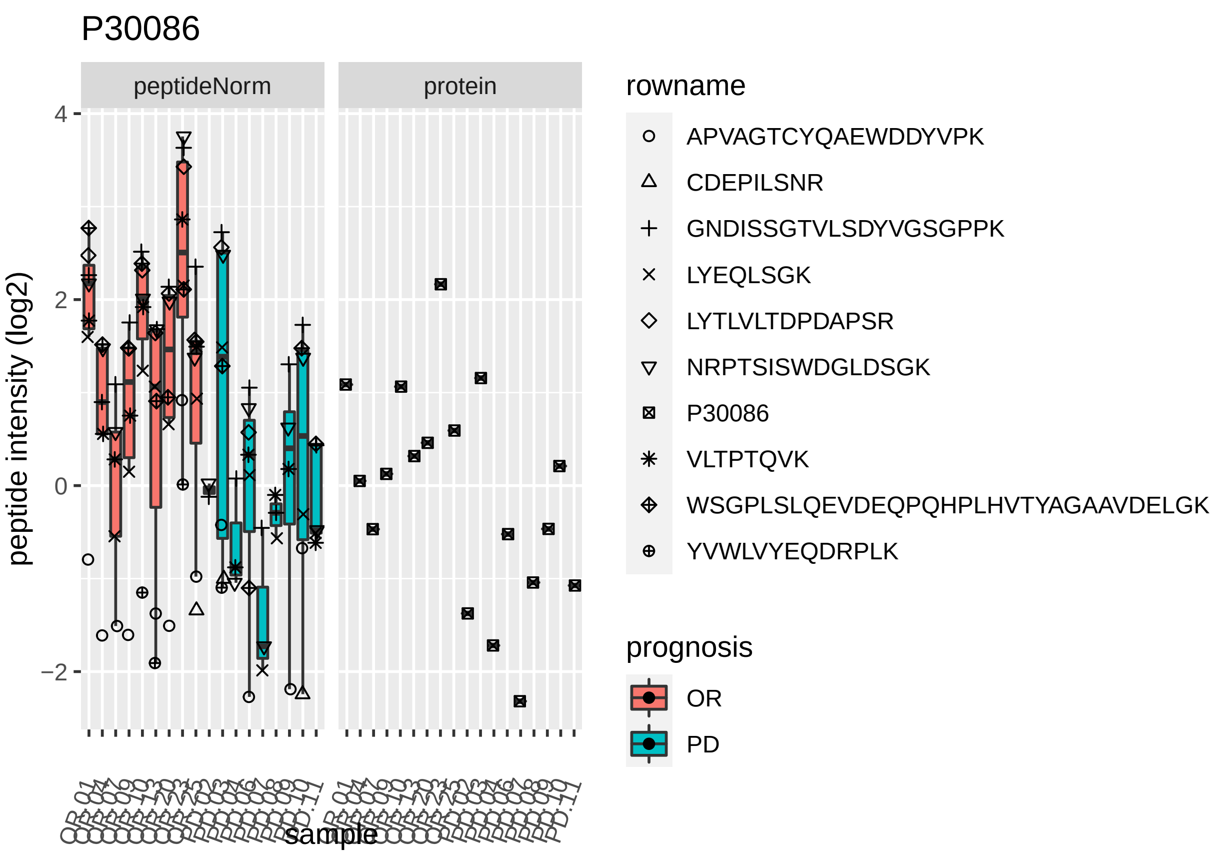

Q15185
peptideNorm
protein
value
colname
2
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

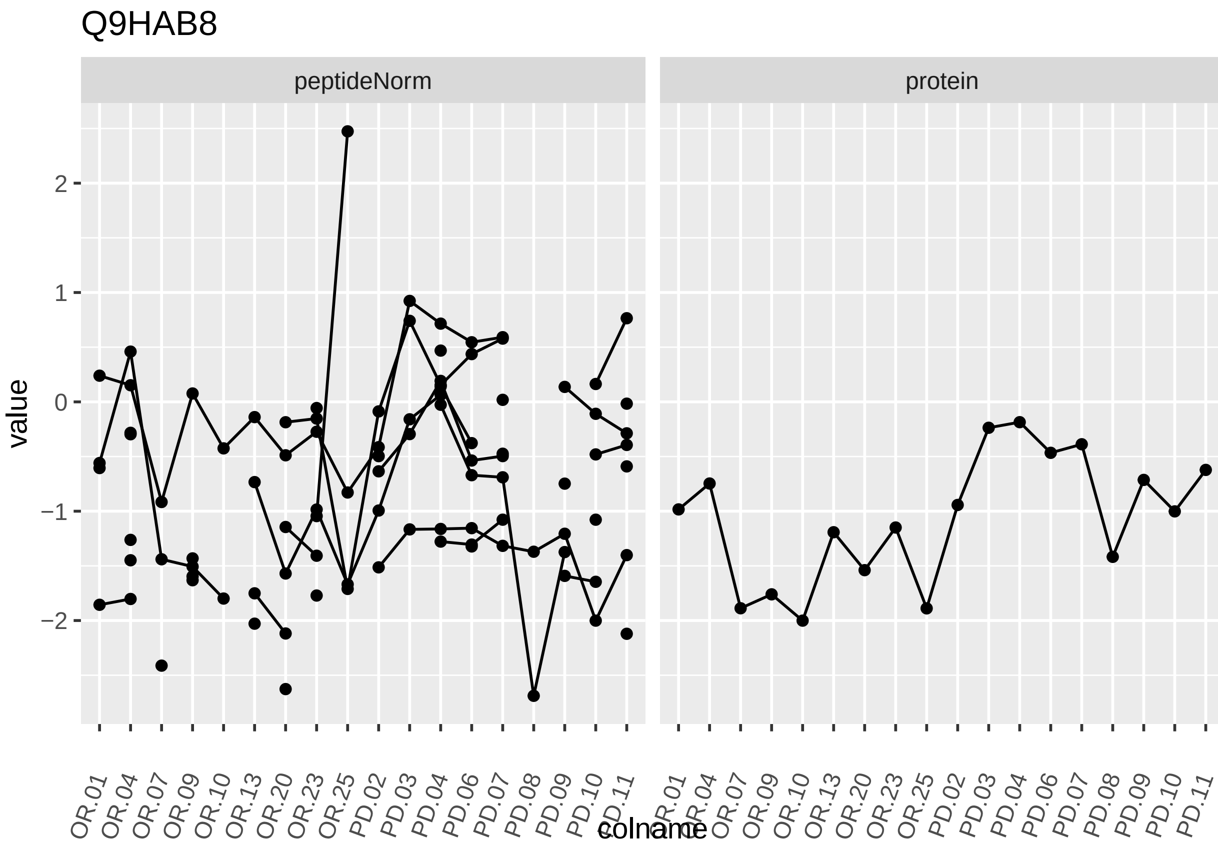

Q15185
peptideNorm
protein
peptide intensity (log2)
sample
rowname
DVNVNFEK
GESGQSWPR
HLNEIDLFHCIDPNDSK
KGESGQSWPR
LNWLSVDFNNWK
LTFSCLGGSDNFK
Q15185
SILCCLR
prognosis
OR
PD


Q05682
peptideNorm
protein
value
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

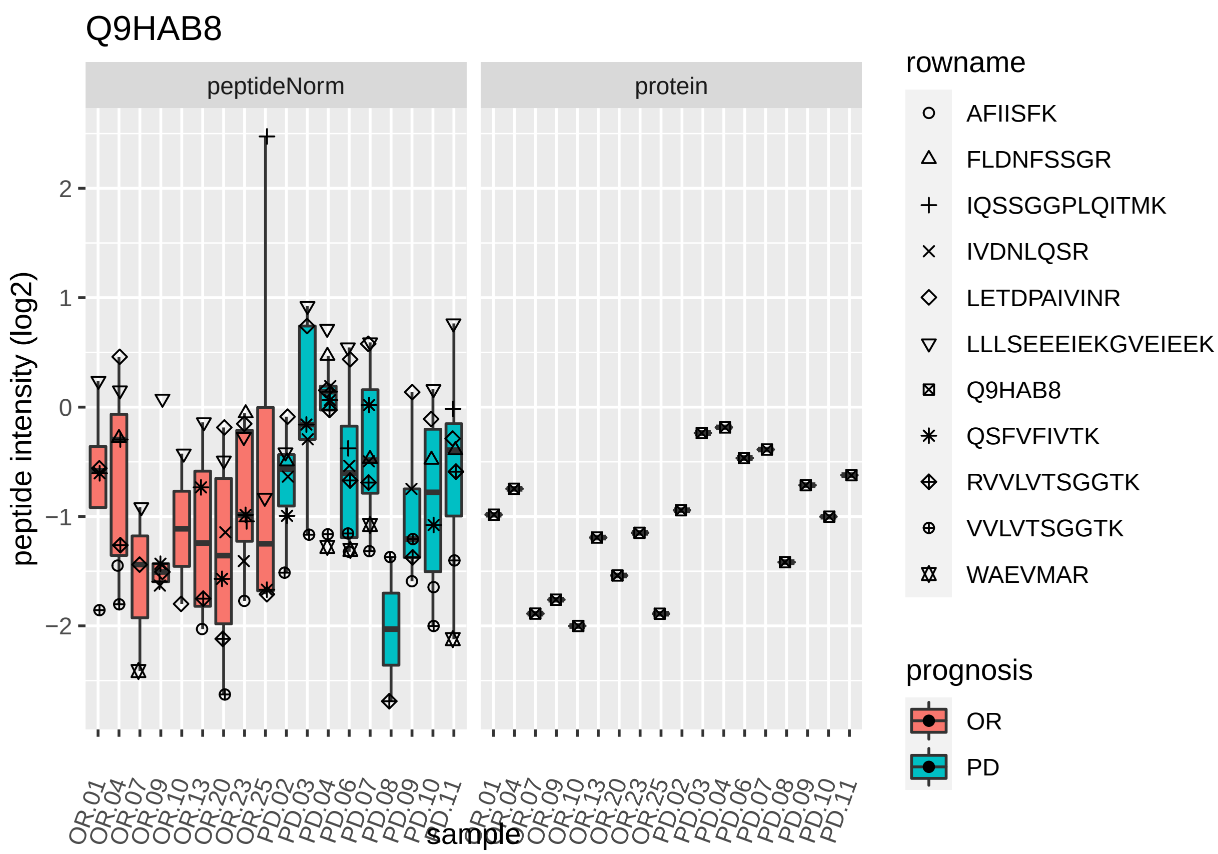

Q05682
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
sample
EAEGAPQVEAGKR
EFDPTITDASLSLPSR
GNVFSSPTAAGTPNK
LEQYTSAIEGTK
MQNDTAENETTEKEEK
PSDLRPGDVSSK
Q05682
QKQEEESLGQVTDQVEVNAQNSVPDEEAK
RGETESEEFEK
RRGETESEEFEK
SAKPTKPAASDLPVPAEGVR
STHQAAIVSK
TTTTNTQVEGDDEAAFLER
VLEEEEQR
YEIEETETVTK
prognosis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


P30086
peptideNorm
protein
value
colname
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

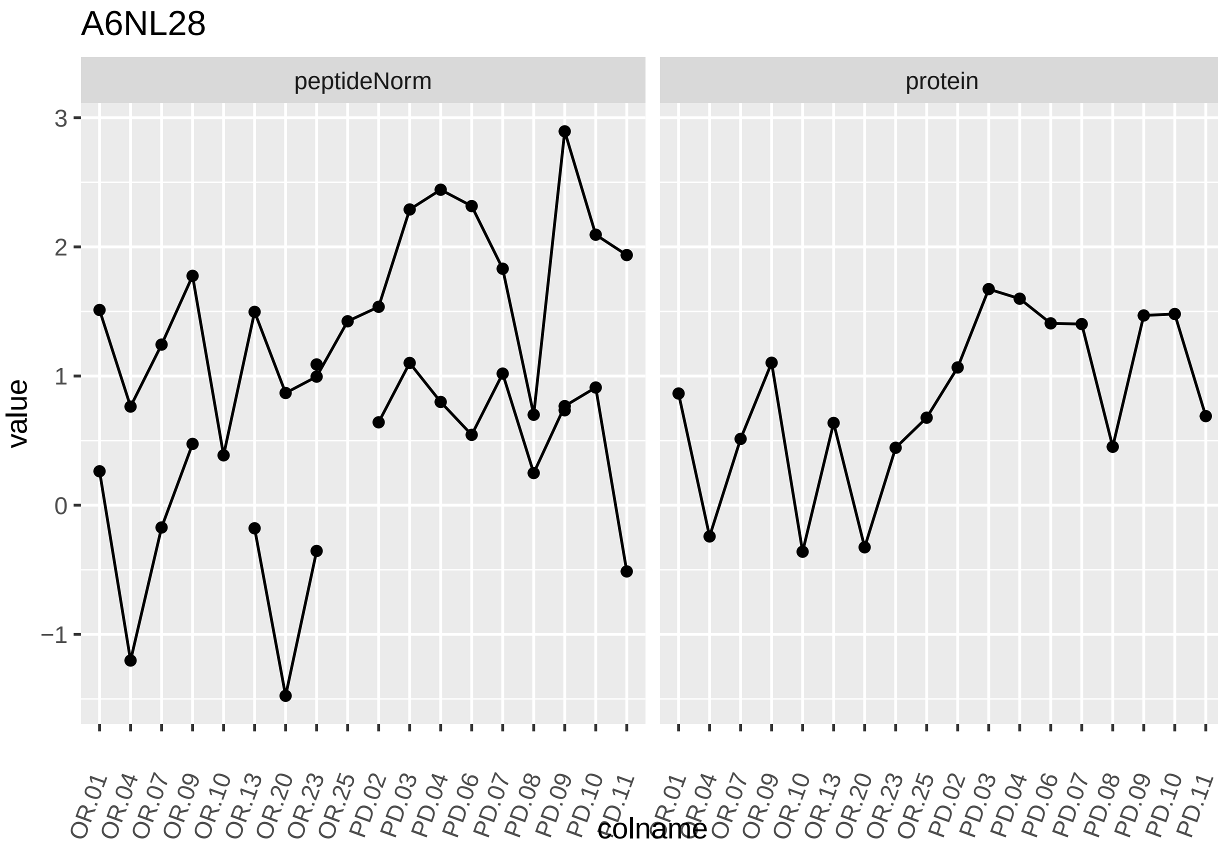

P30086
peptideNorm
protein
peptide intensity (log2)
4
2
0
−2
sample
rowname
APVAGTCYQAEWDDYVPK
CDEPILSNR
GNDISSGTVLSDYVGSGPPK
LYEQLSGK
LYTLVLTDPDAPSR
NRPTSISWDGLDSGK
P30086
VLTPTQVK
WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK
YVWLVYEQDRPLK
prognosis
OR
PD



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



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


A6NL28
peptideNorm
protein
value
colname
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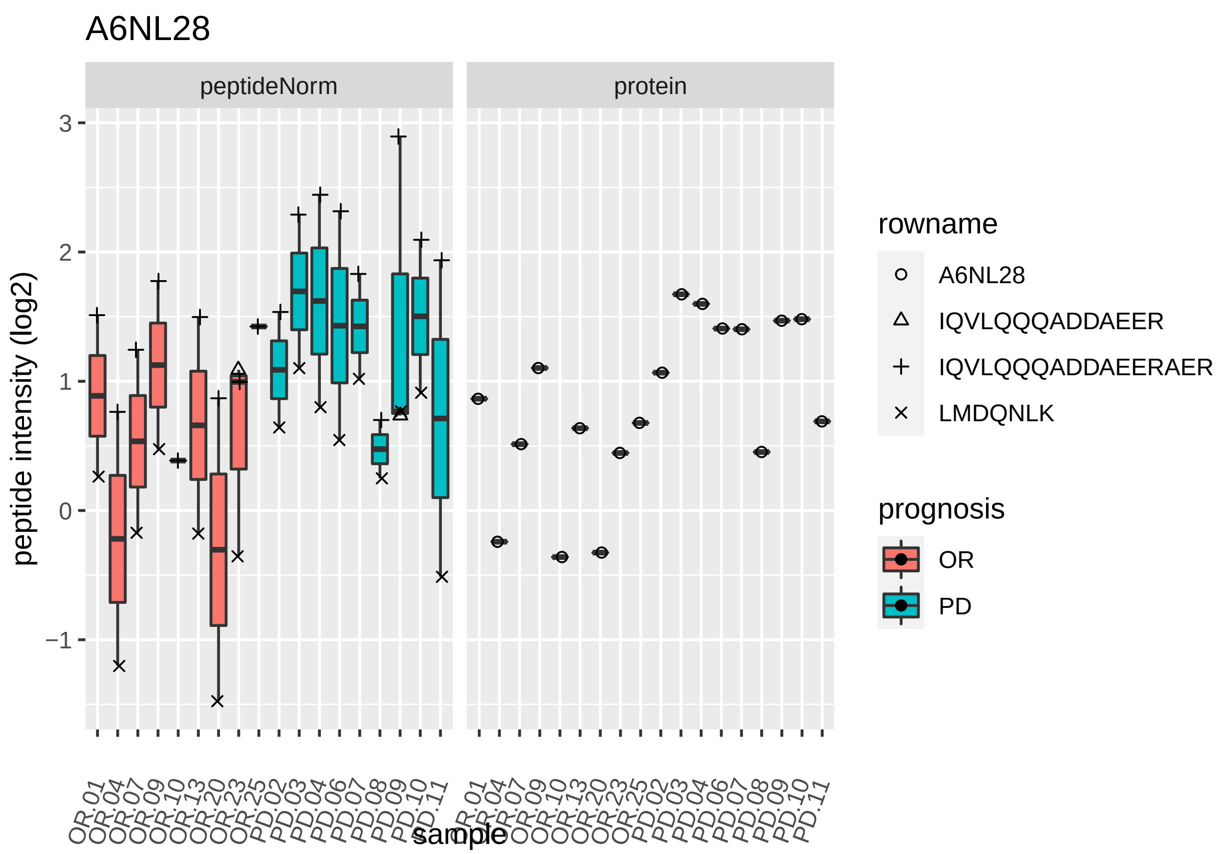
2
1
0
−1
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


A6NL28
peptideNorm
protein
peptide intensity (log2)
sample
rowname
A6NL28
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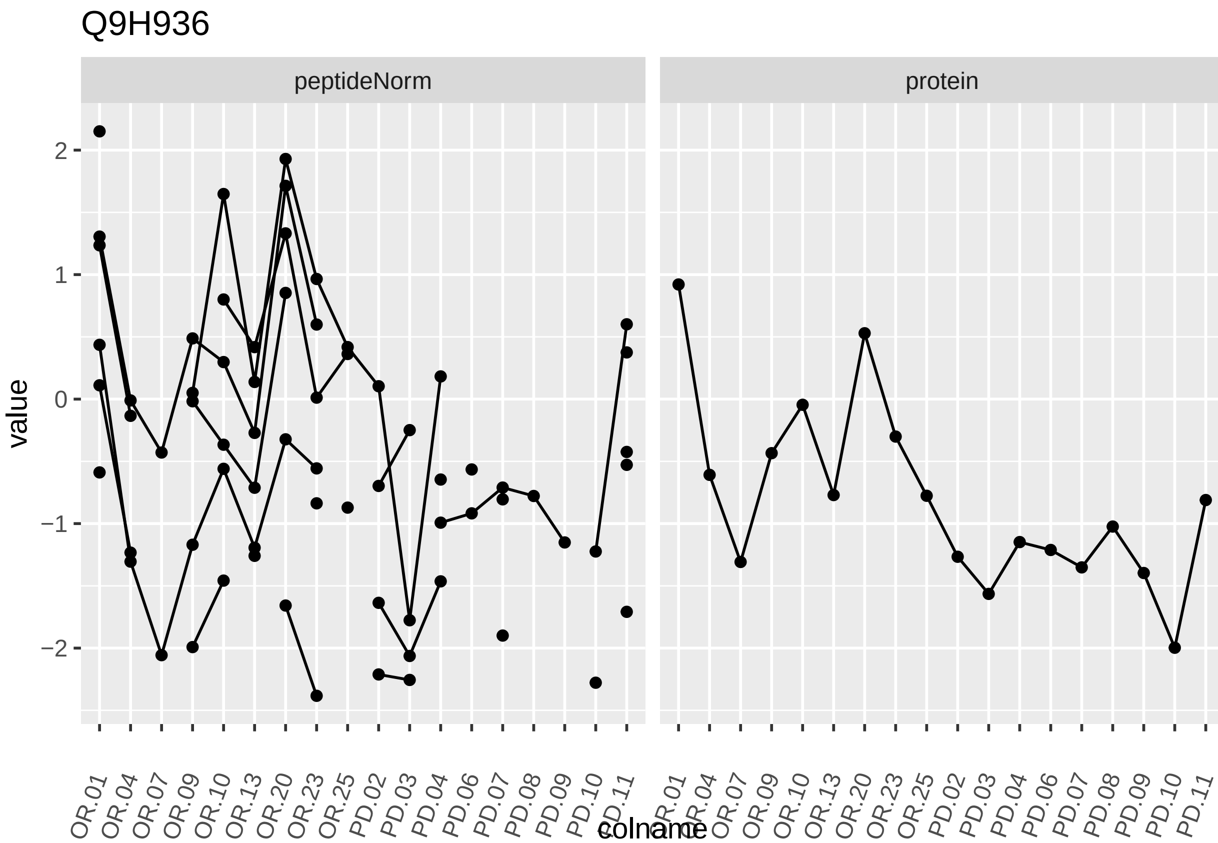
IQVLQQQADDAEERAER
LMDQNLK
prognosis
OR
PD


Q9H936
peptideNorm
protein
value
colname
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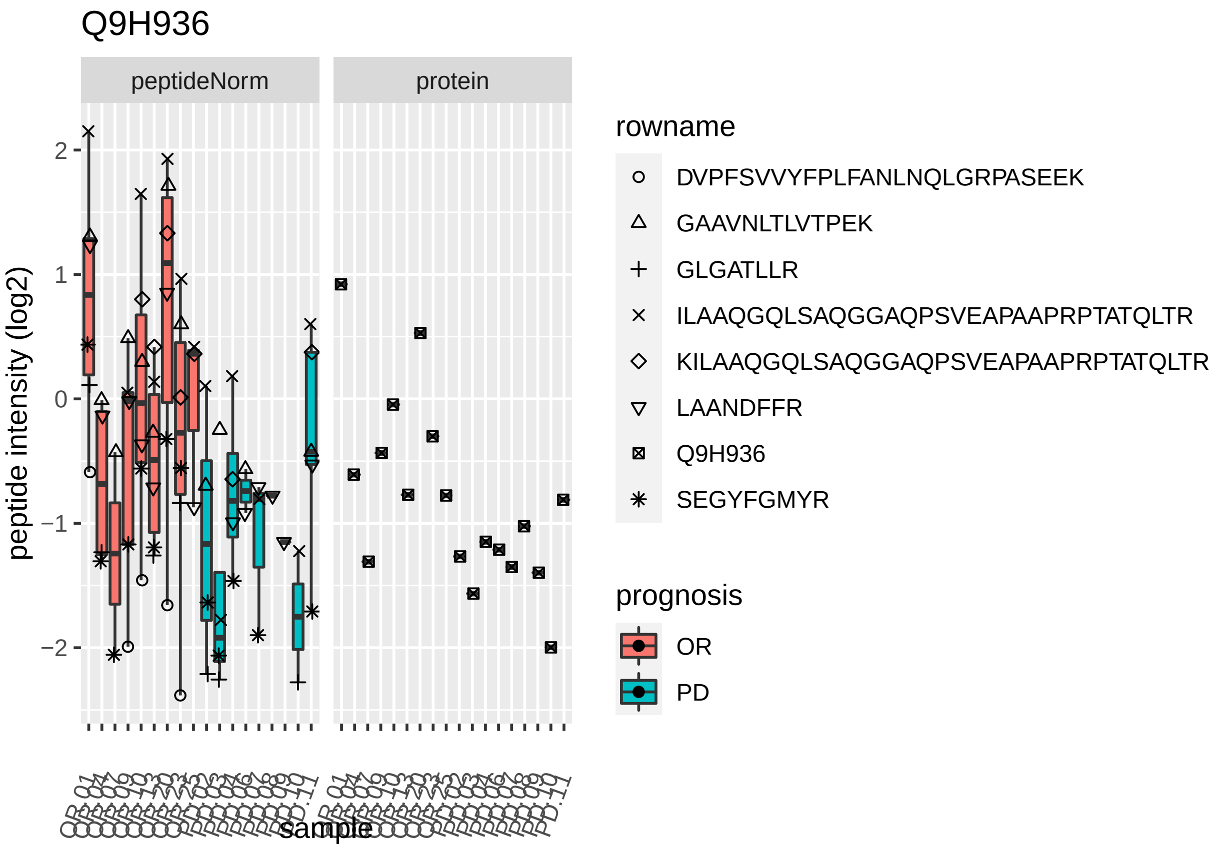
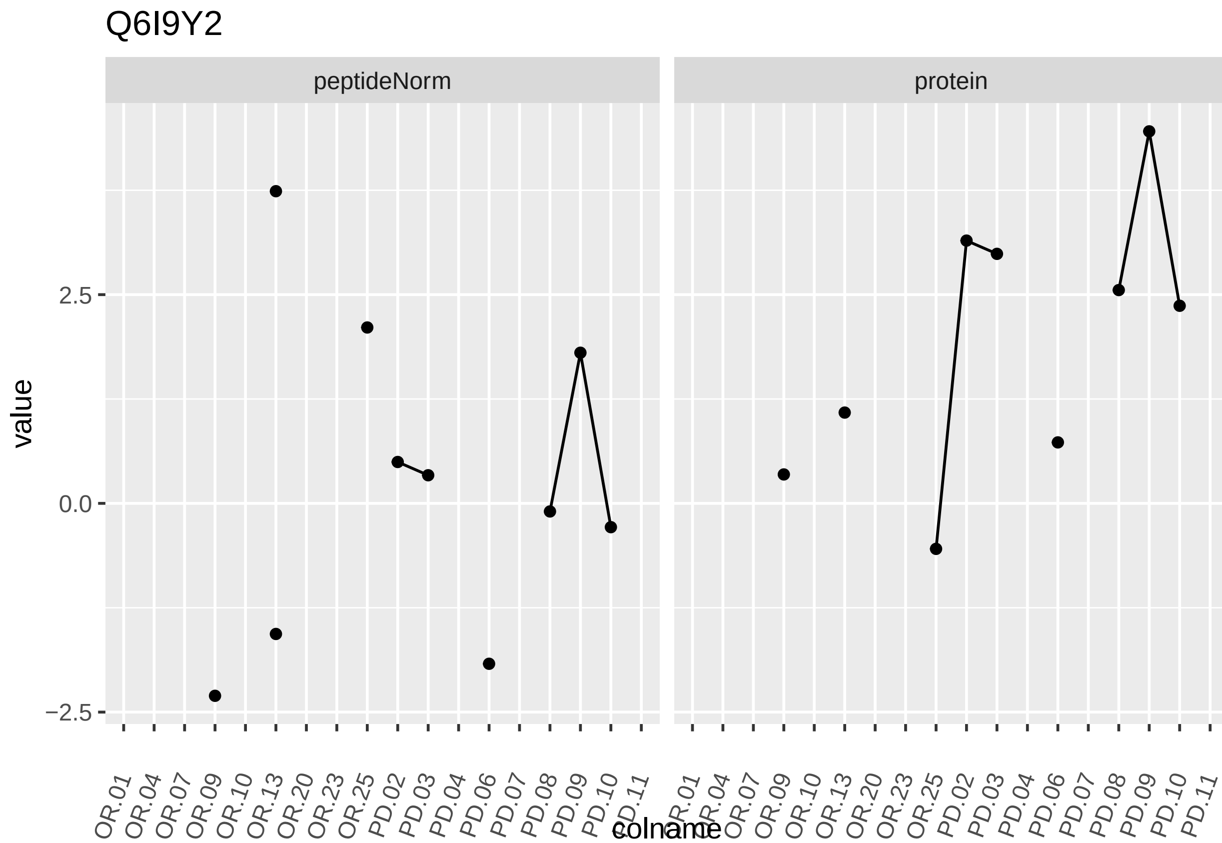
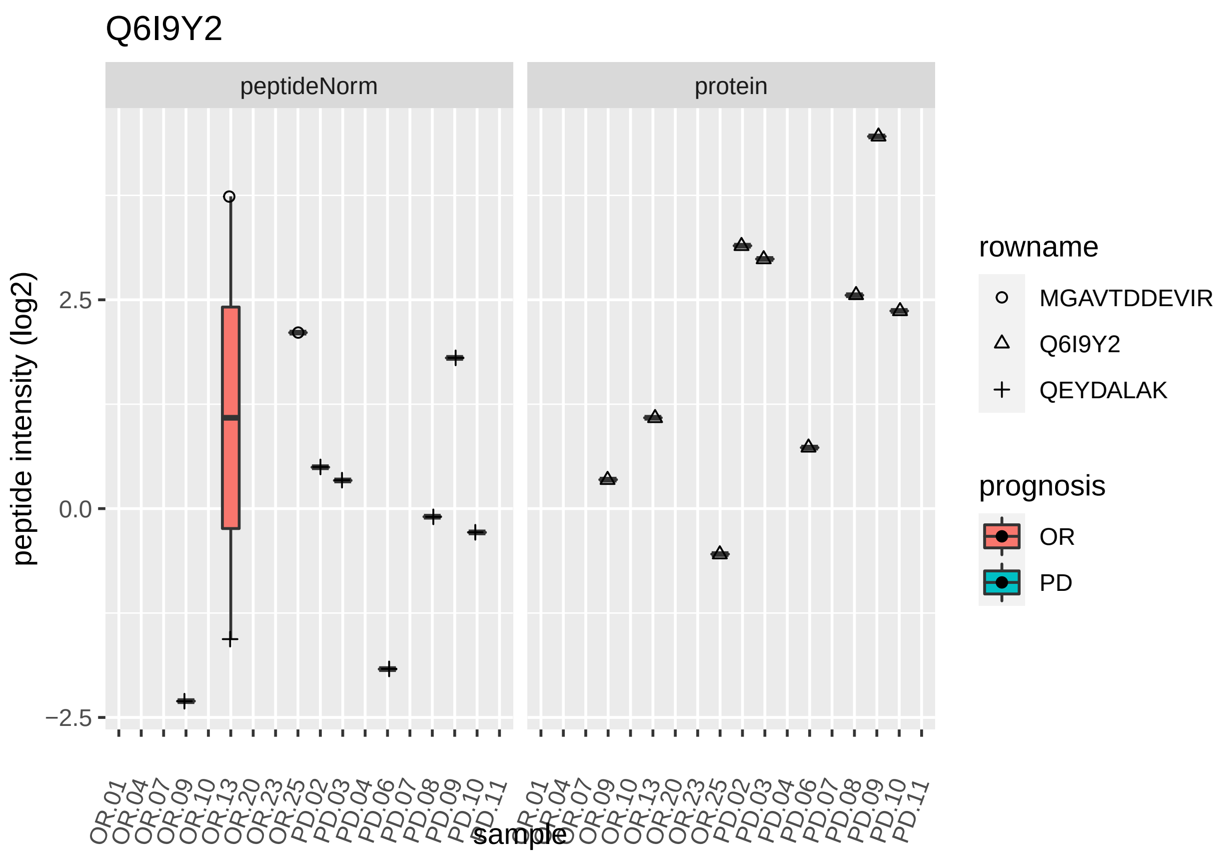
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



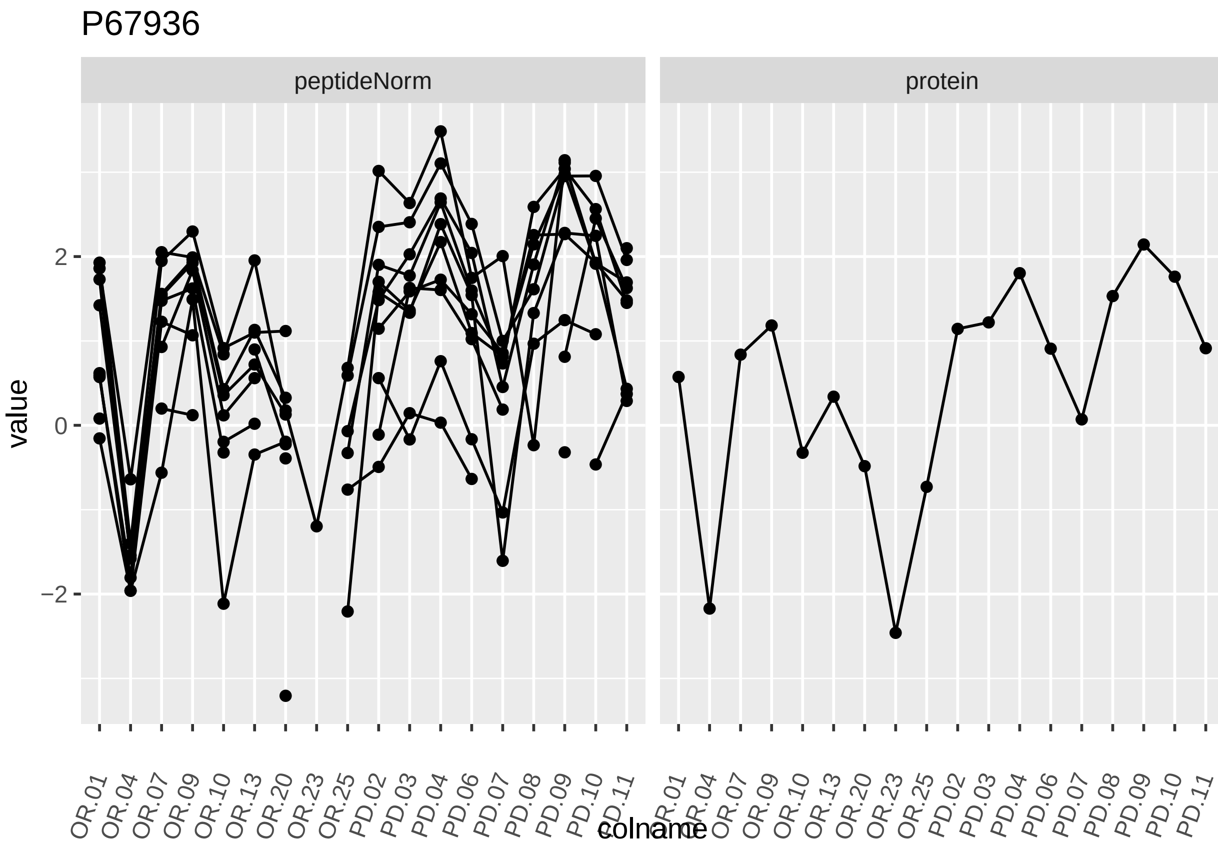
Q9H936
peptideNorm
protein
peptide intensity (log2)
sample
rowname
DVPFSVVYFPLFANLNQLGRPASEEK
GAAVNLTLVTPEK
GLGATLLR
ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
KILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
LAANDFFR
Q9H936
SEGYFGMYR
prognosis
OR
PD



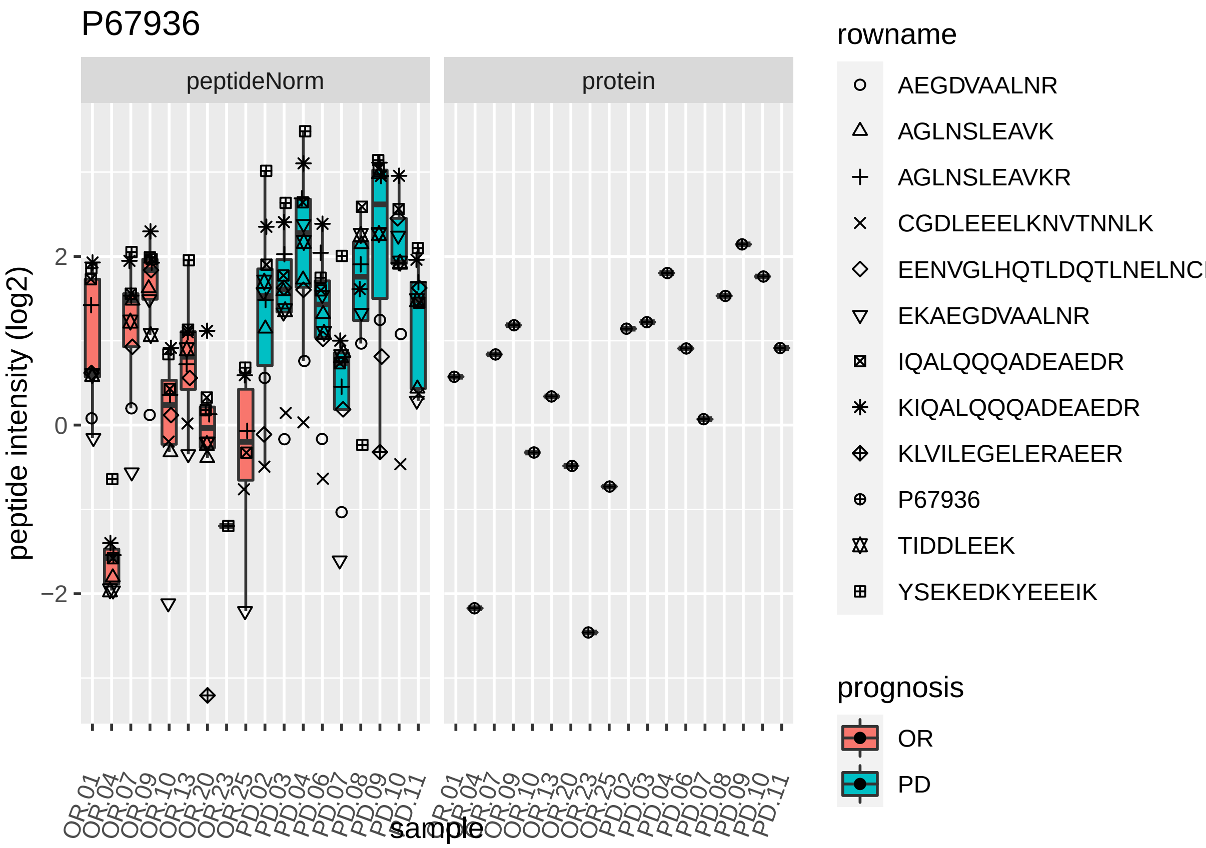
Q6I9Y2
peptideNorm
protein
value
2.5
0.0
−2.5
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

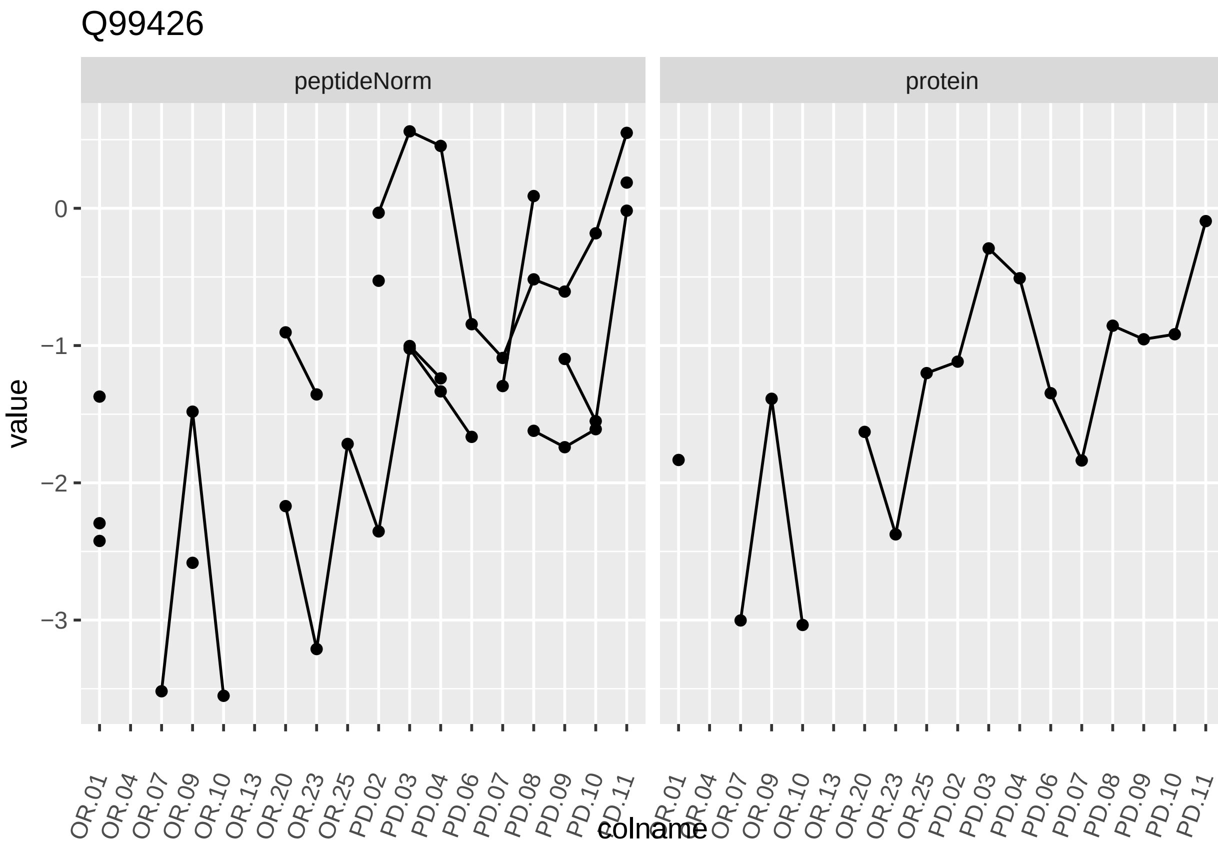


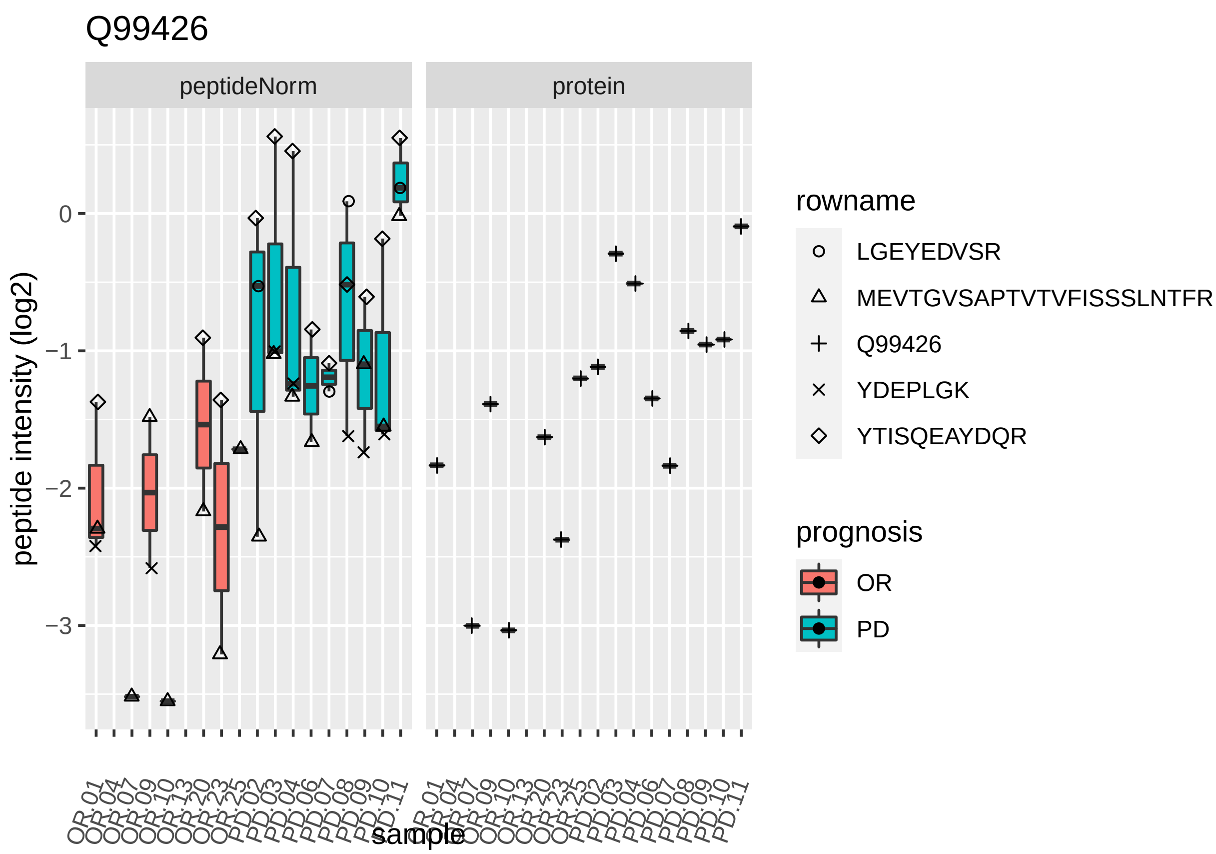
Q6I9Y2
peptideNorm
protein
peptide intensity (log2)
2.5
0.0
−2.5
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
MGAVTDDEVIR
Q6I9Y2
QEYDALAK
prognosis
OR
PD



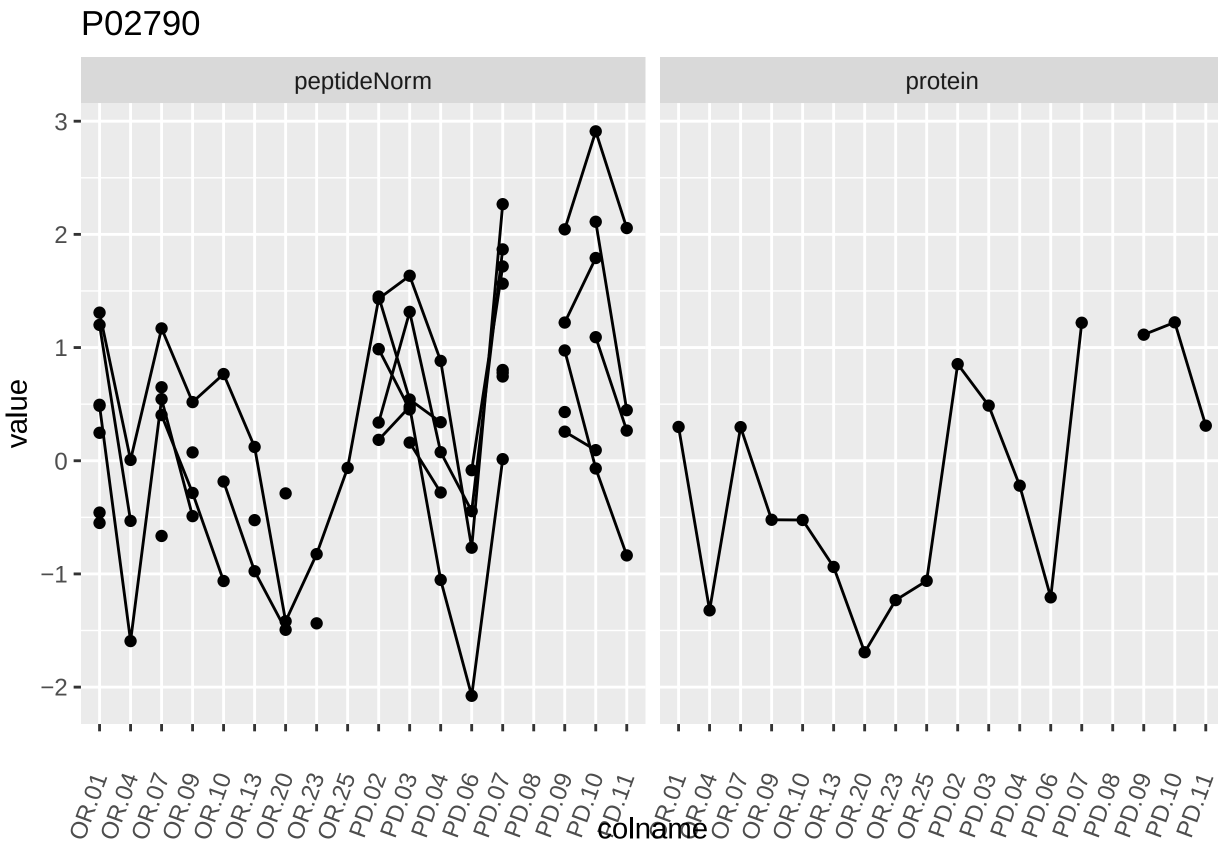
P67936
peptideNorm
protein
value
2
0
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


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

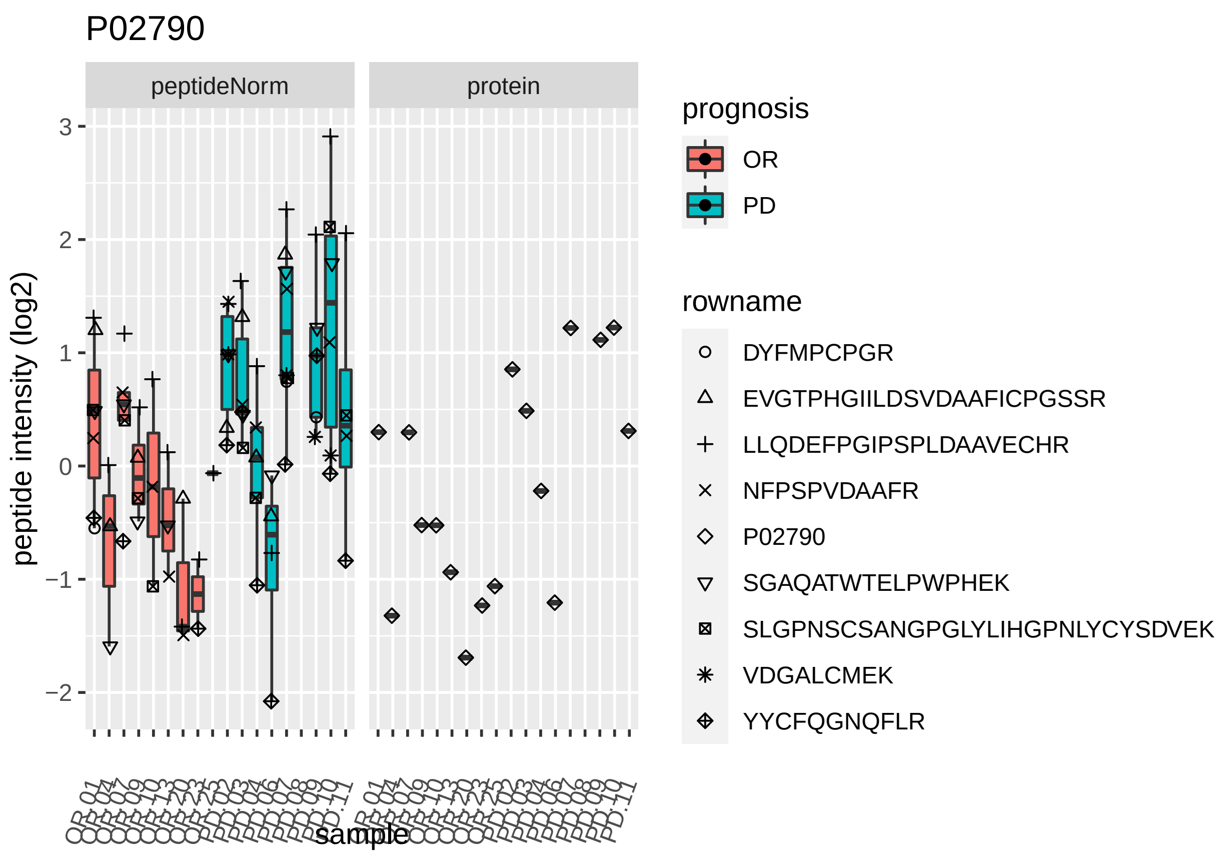

Q99426
peptideNorm
protein
value
colname
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

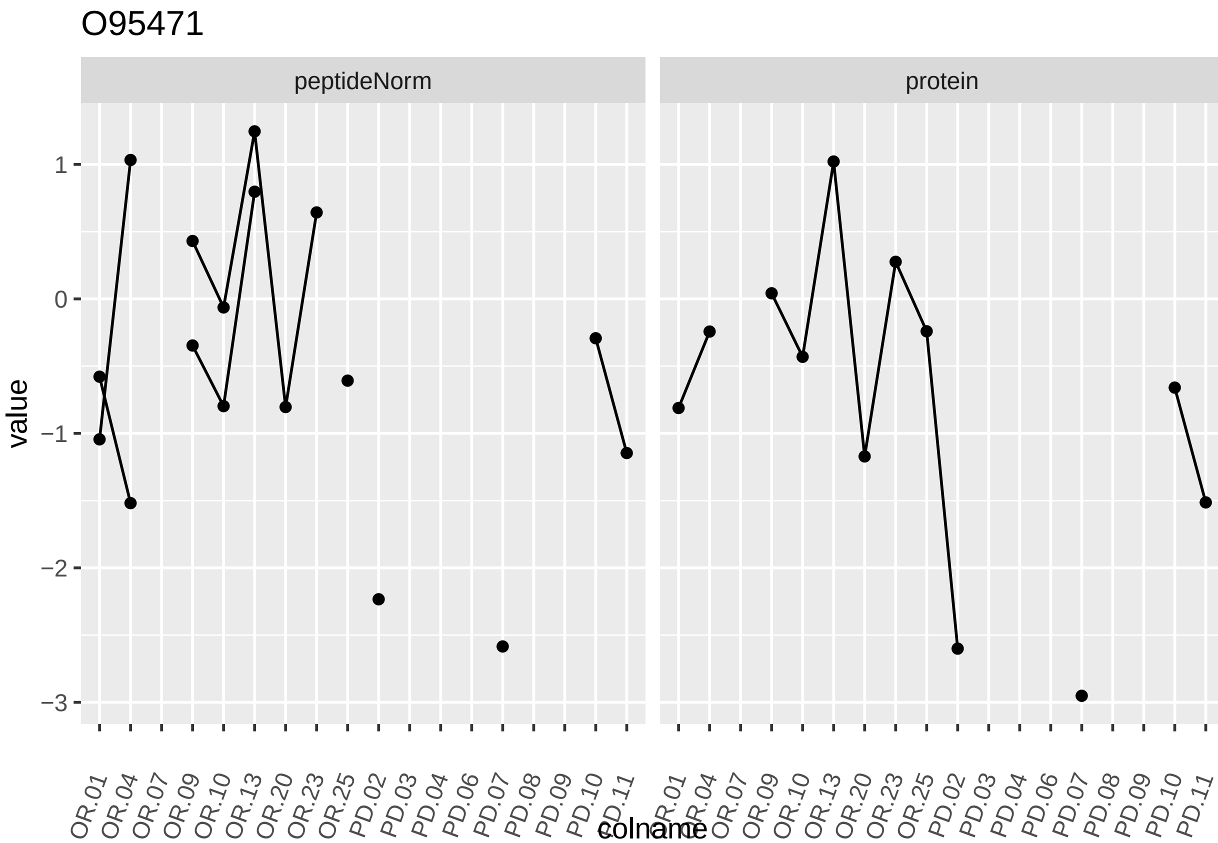


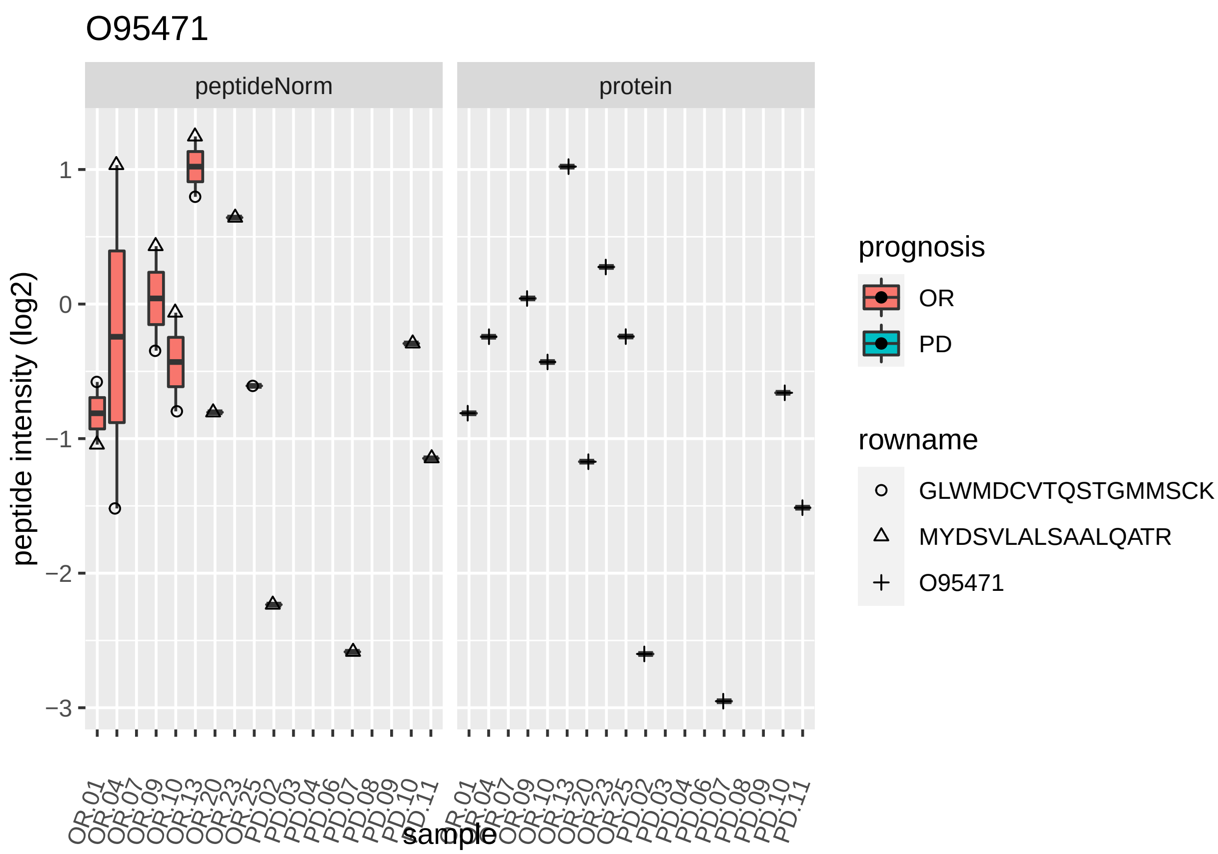
Q99426
peptideNorm
protein
peptide intensity (log2)
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
LGEYEDVSR
MEVTGVSAPTVTVFISSSLNTFR
Q99426
YDEPLGK
YTISQEAYDQR
prognosis
OR
PD



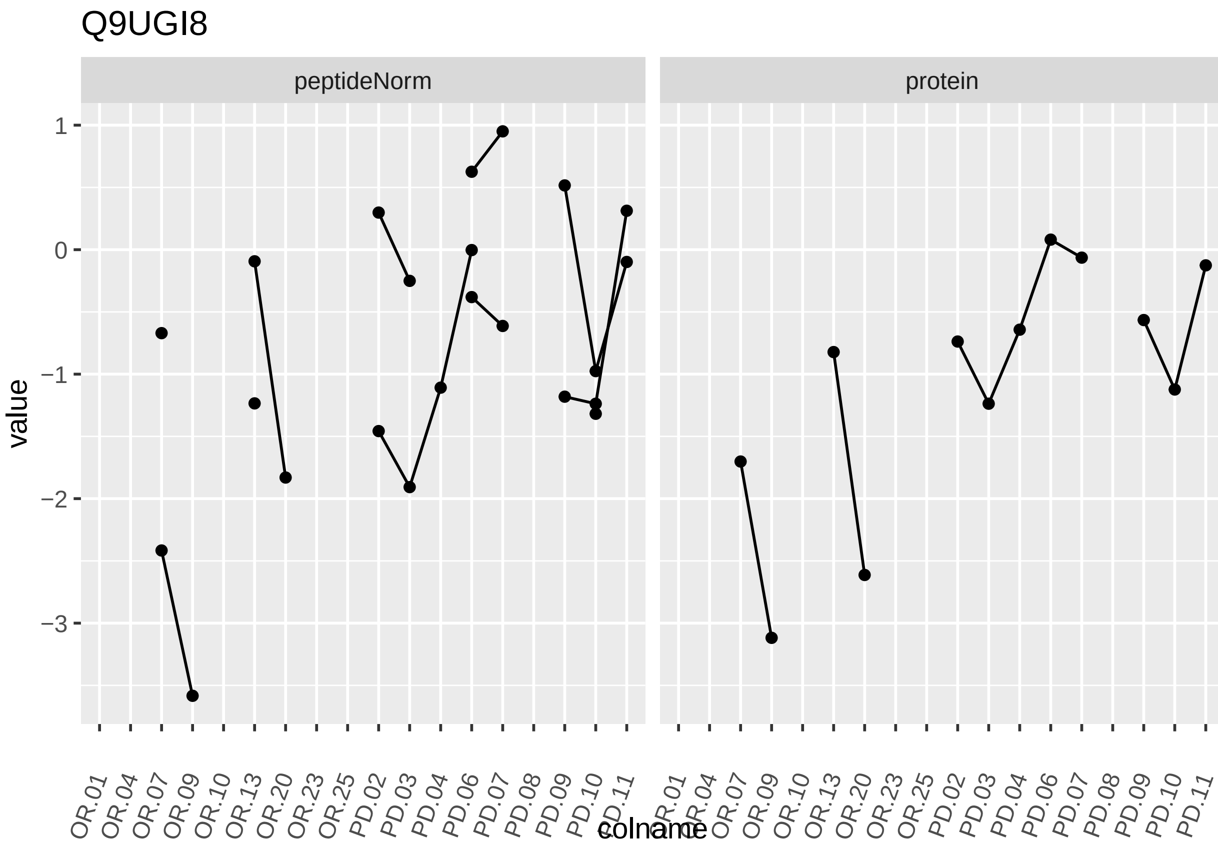
P02790
peptideNorm
protein
value
colname
3
2
1
0
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

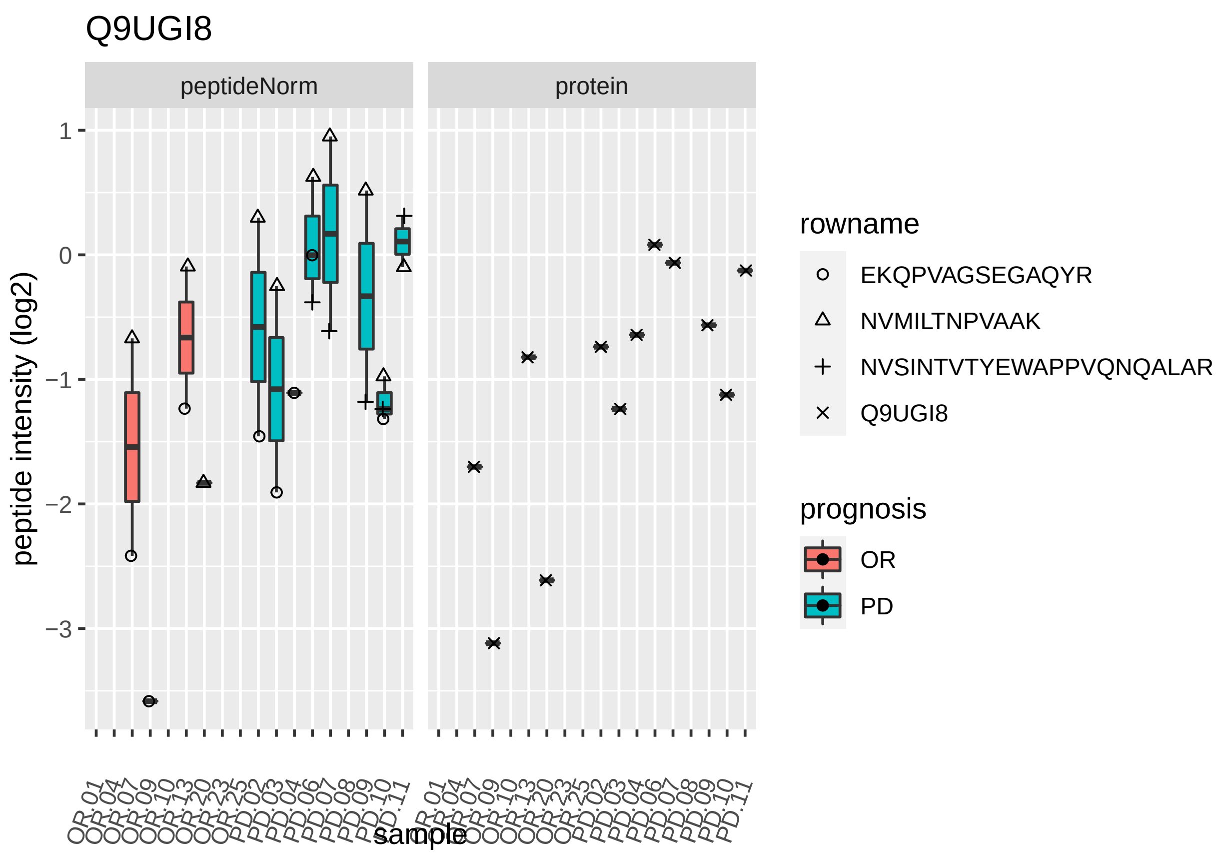

P02790
peptideNorm
protein
peptide intensity (log2)
3
2
1
0
−1
−2
sample
prognosis
OR
PD
rowname
DYFMPCPGR
EVGTPHGIILDSVDAAFICPGSSR
LLQDEFPGIPSPLDAAVECHR
NFPSPVDAAFR
P02790
SGAQATWTELPWPHEK
SLGPNSCSANGPGLYLIHGPNLYCYSDVEK
VDGALCMEK
YYCFQGNQFLR


O95471
peptideNorm
protein
value
colname
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

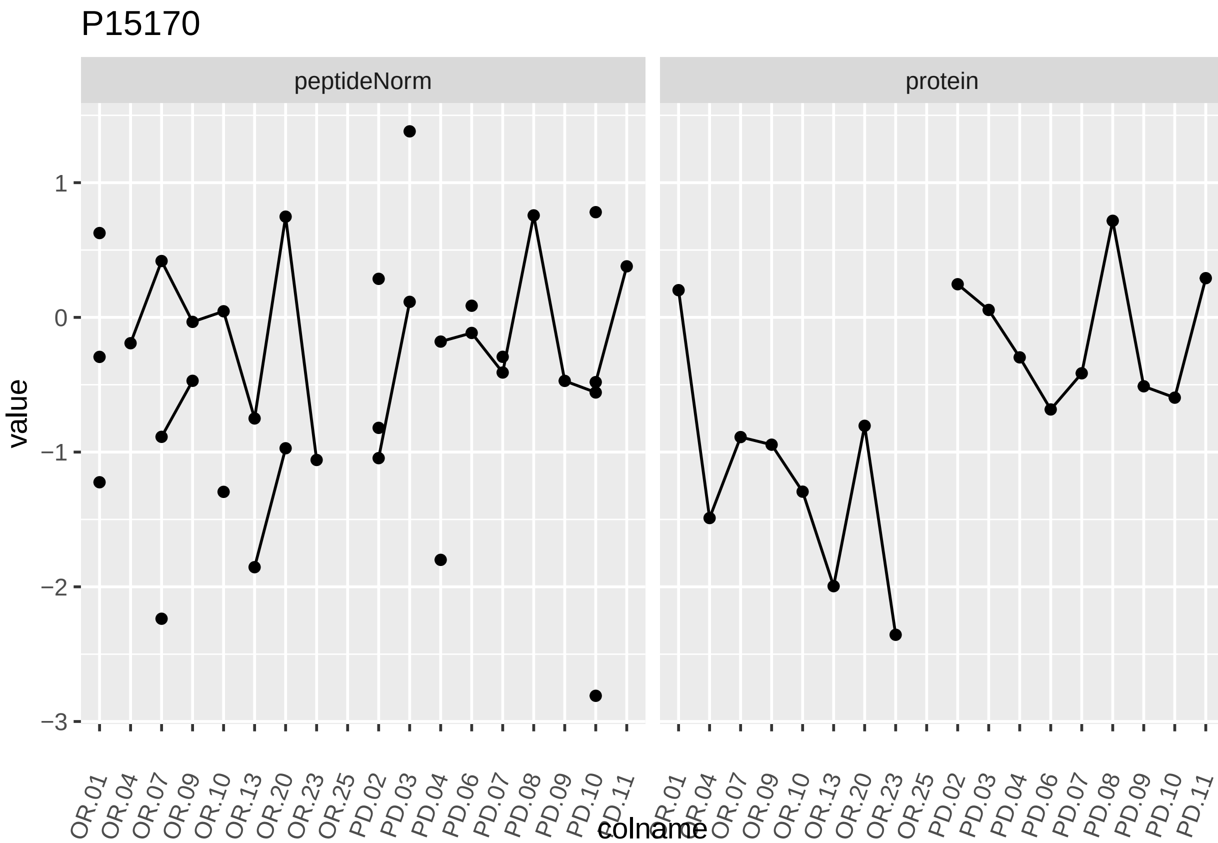


O95471
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
prognosis
OR
PD
rowname
GLWMDCVTQSTGMMSCK
MYDSVLALSAALQATR
O95471


Q9UGI8
peptideNorm
protein
value
colname
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



Q9UGI8
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
EKQPVAGSEGAQYR
NVMILTNPVAAK
NVSINTVTYEWAPPVQNQALAR
Q9UGI8
prognosis
OR
PD


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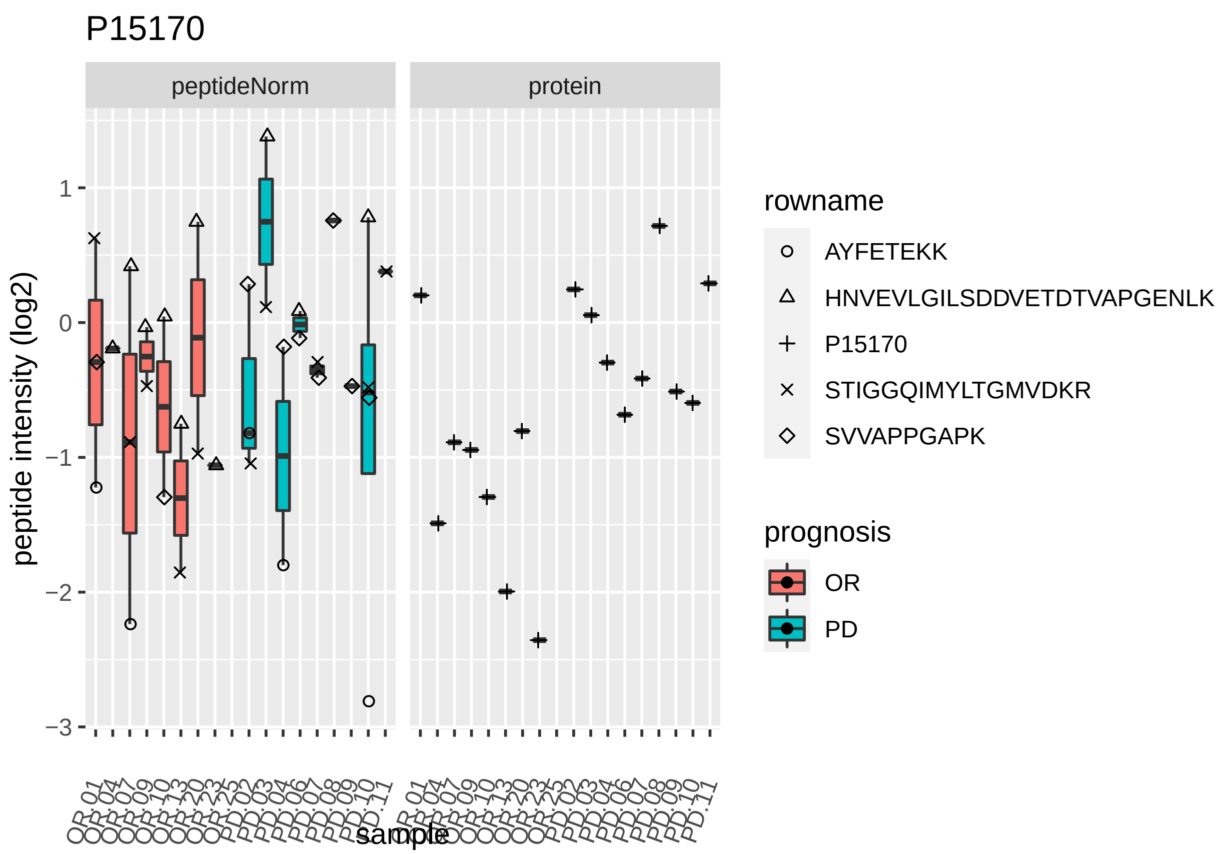
0
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11


P15170
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
sample
rowname
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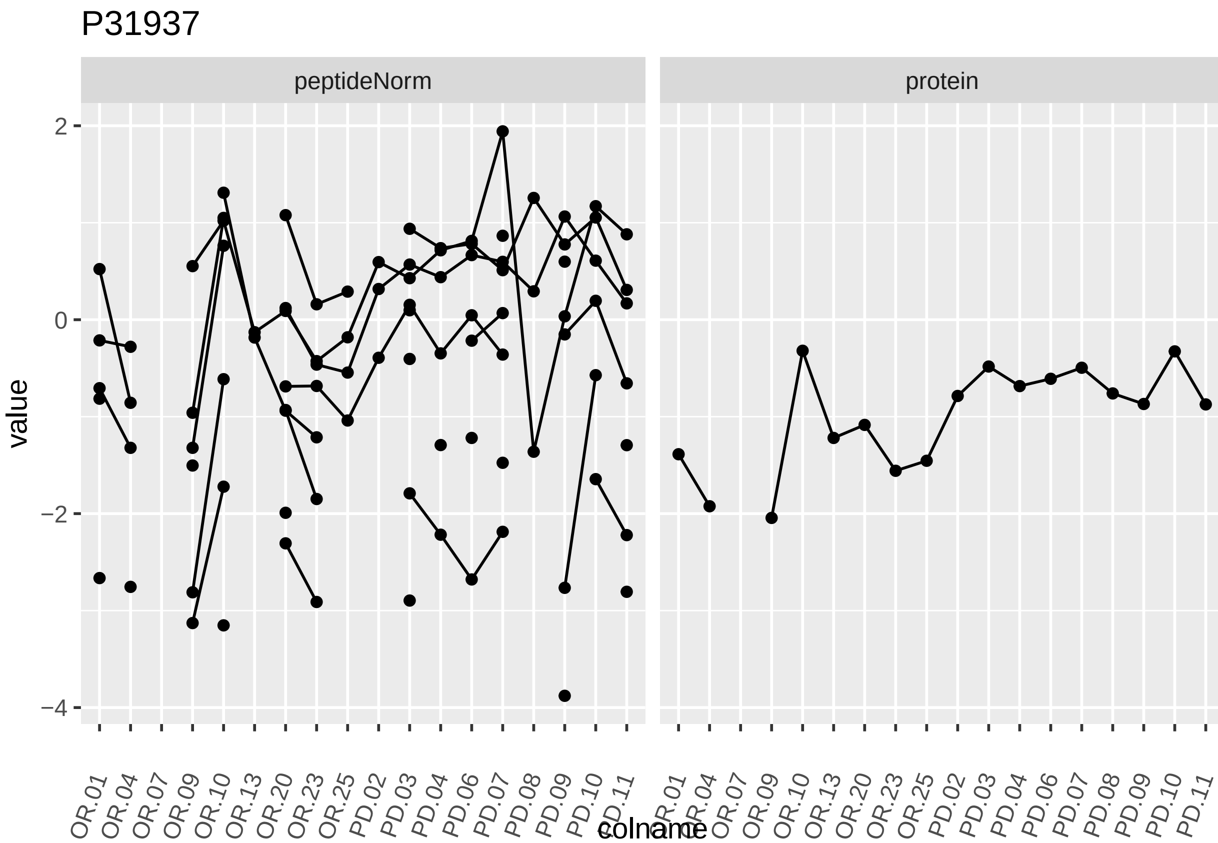
P15170
STIGGQIMYLTGMVDKR
SVVAPPGAPK
prognosis
OR
PD



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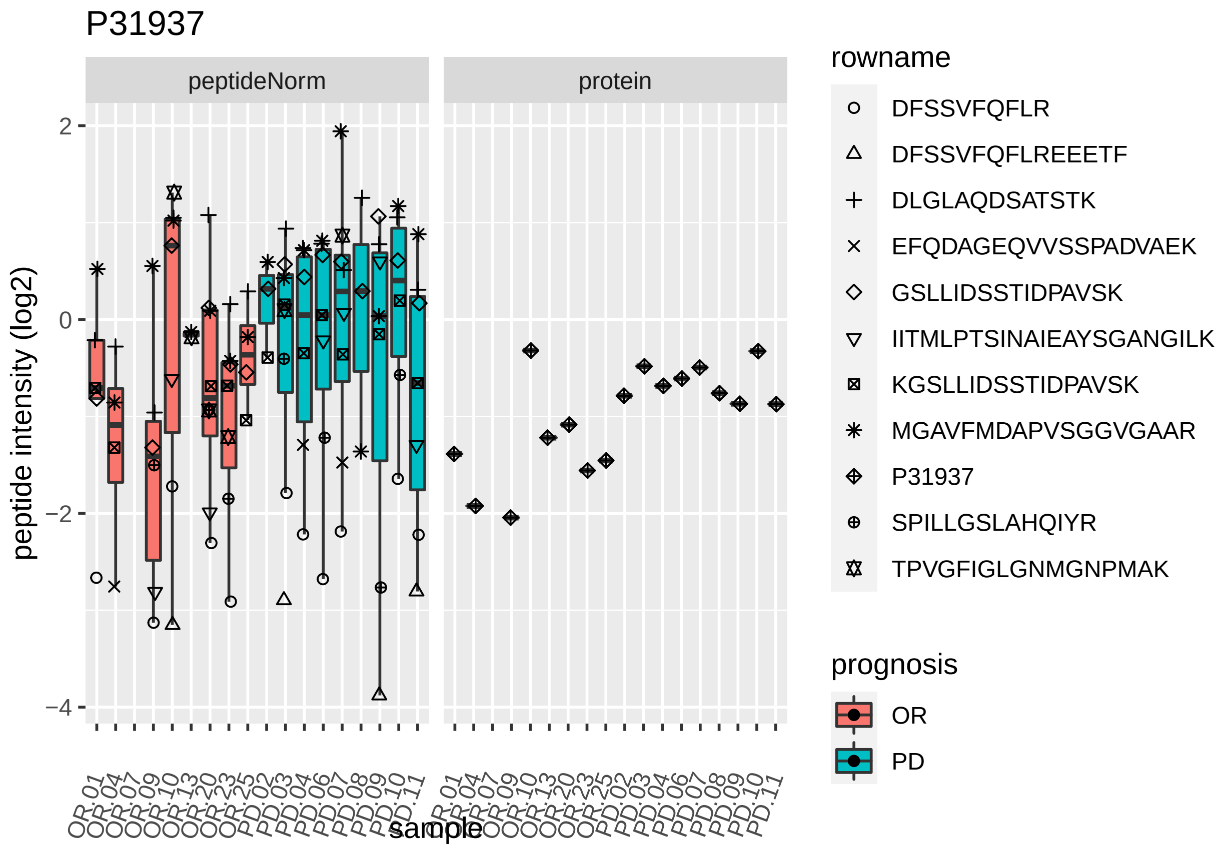
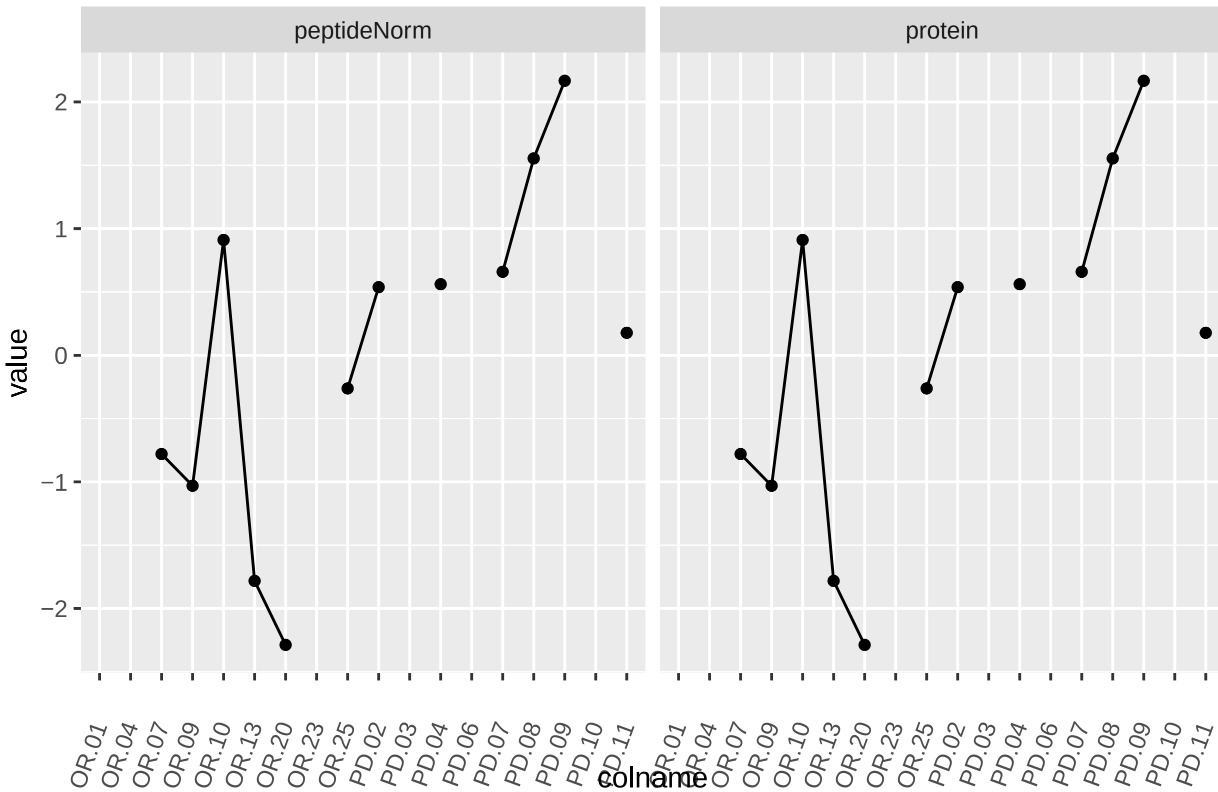
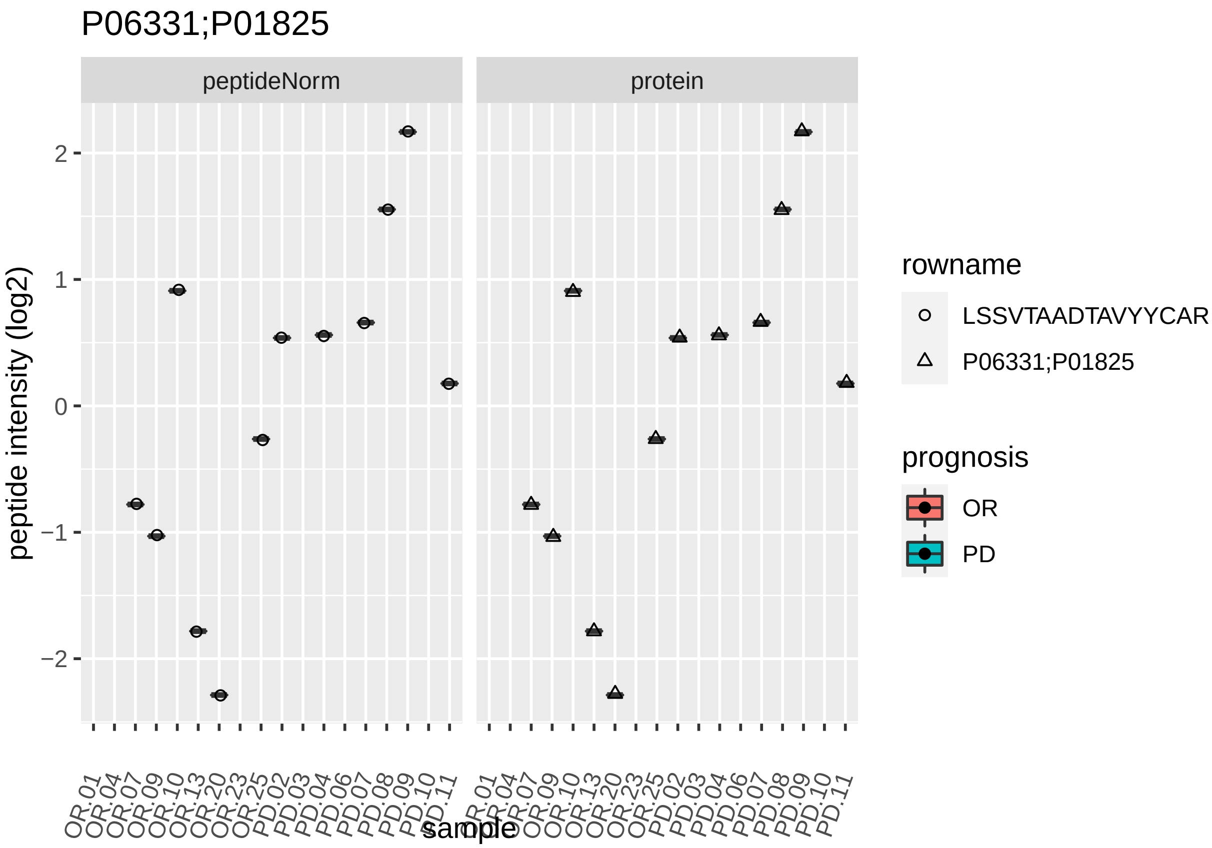
0
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11

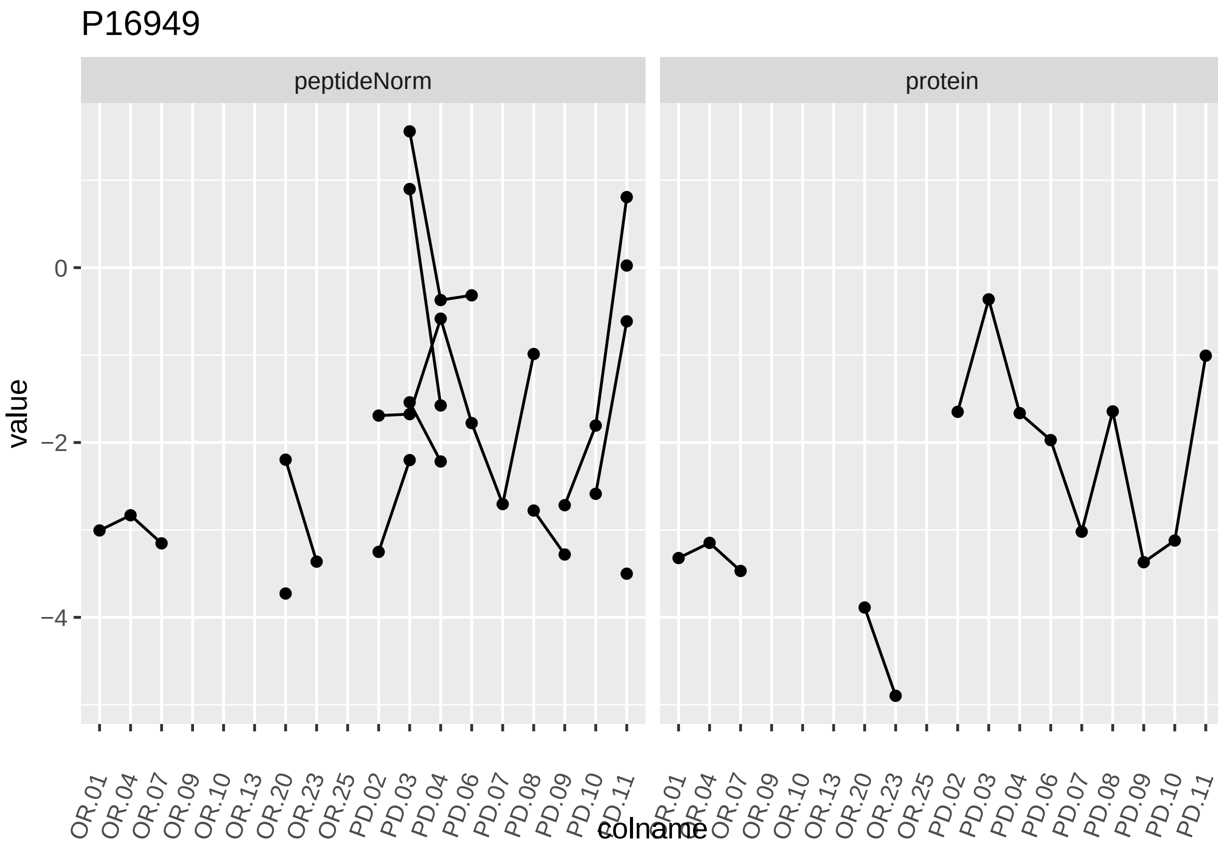

P31937
peptideNorm
protein
peptide intensity (log2)
2
0
−2
−4
sample
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
rowname
DFSSVFQFLR
DFSSVFQFLREEETF
DLGLAQDSATSTK
EFQDAGEQVVSSPADVAEK
GSLLIDSSTIDPAVSK
IITMLPTSINAIEAYSGANGILK
KGSLLIDSSTIDPAVSK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

P06331;P01825





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



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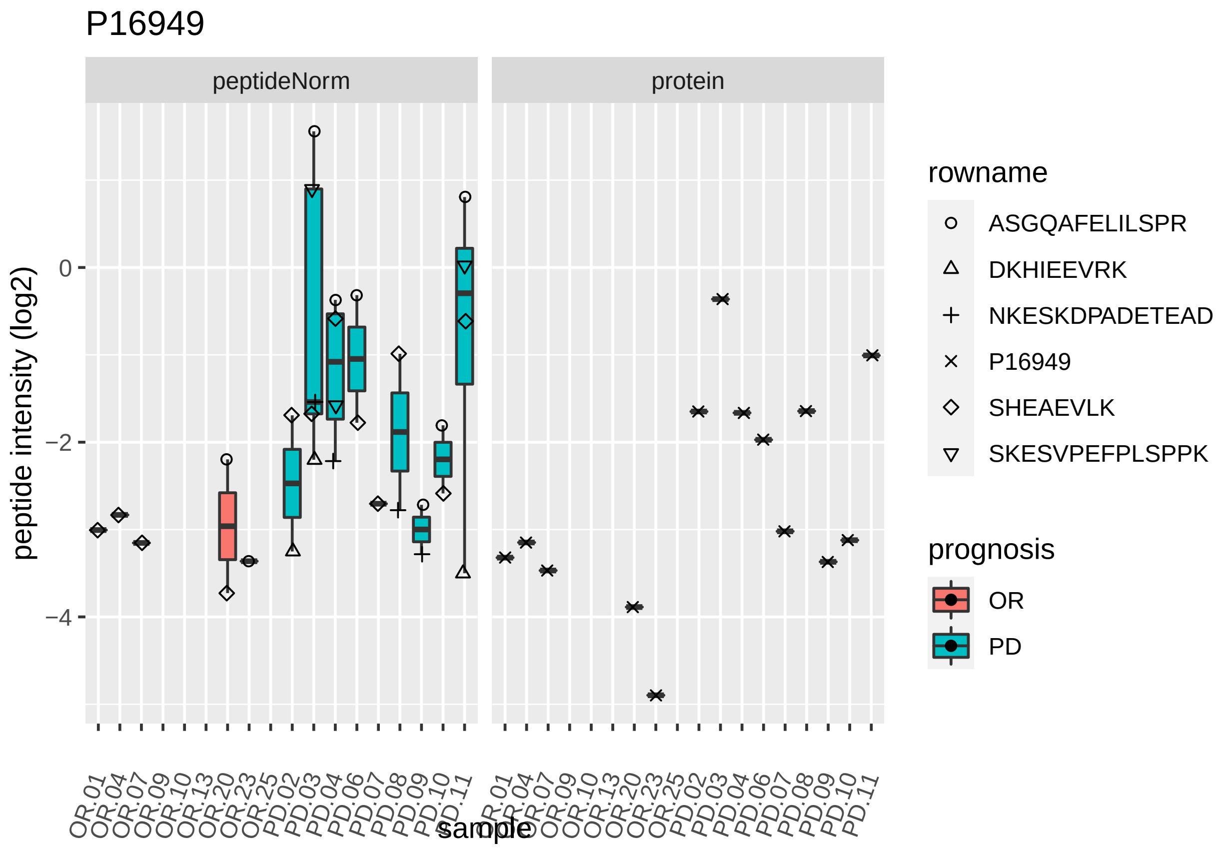
−2
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


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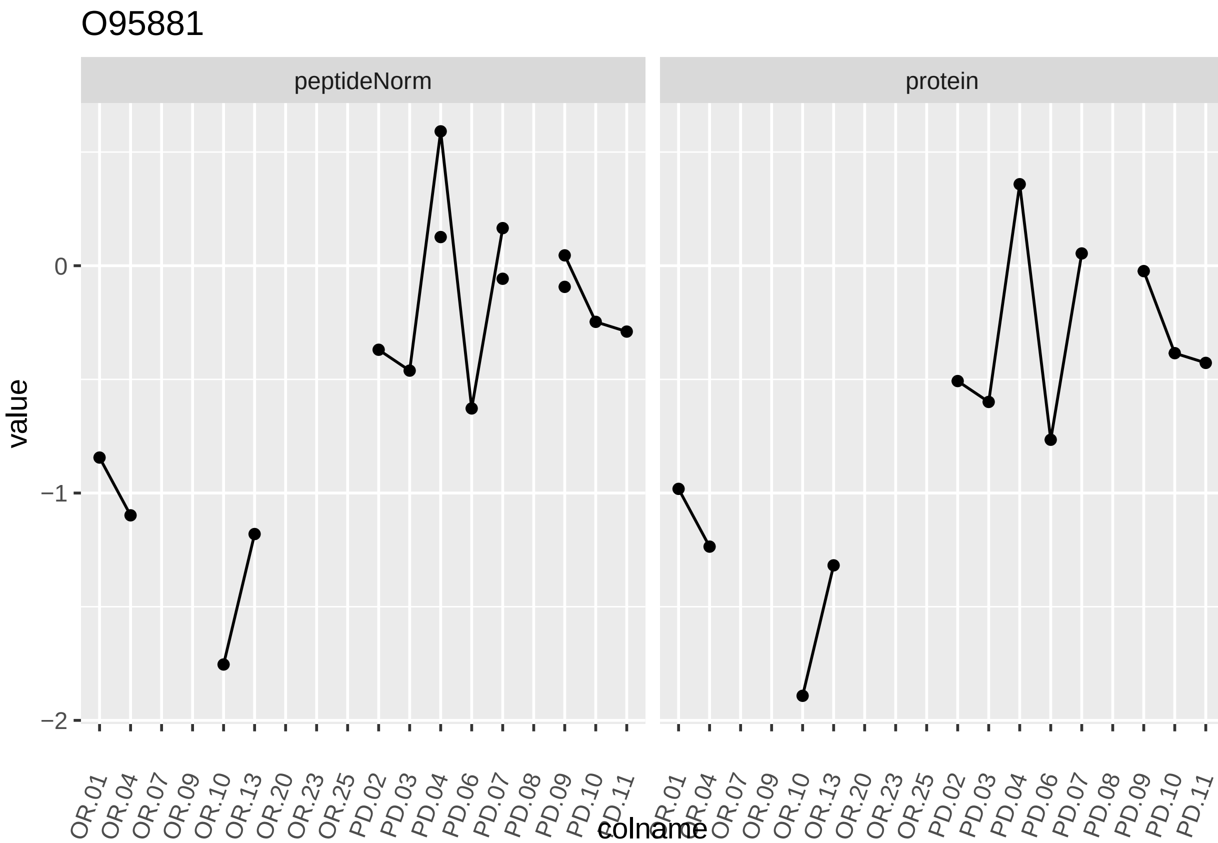
NKESKDPADETEAD
P16949
SHEAEVLK
SKESVPEFPLSPPK
prognosis
OR
PD


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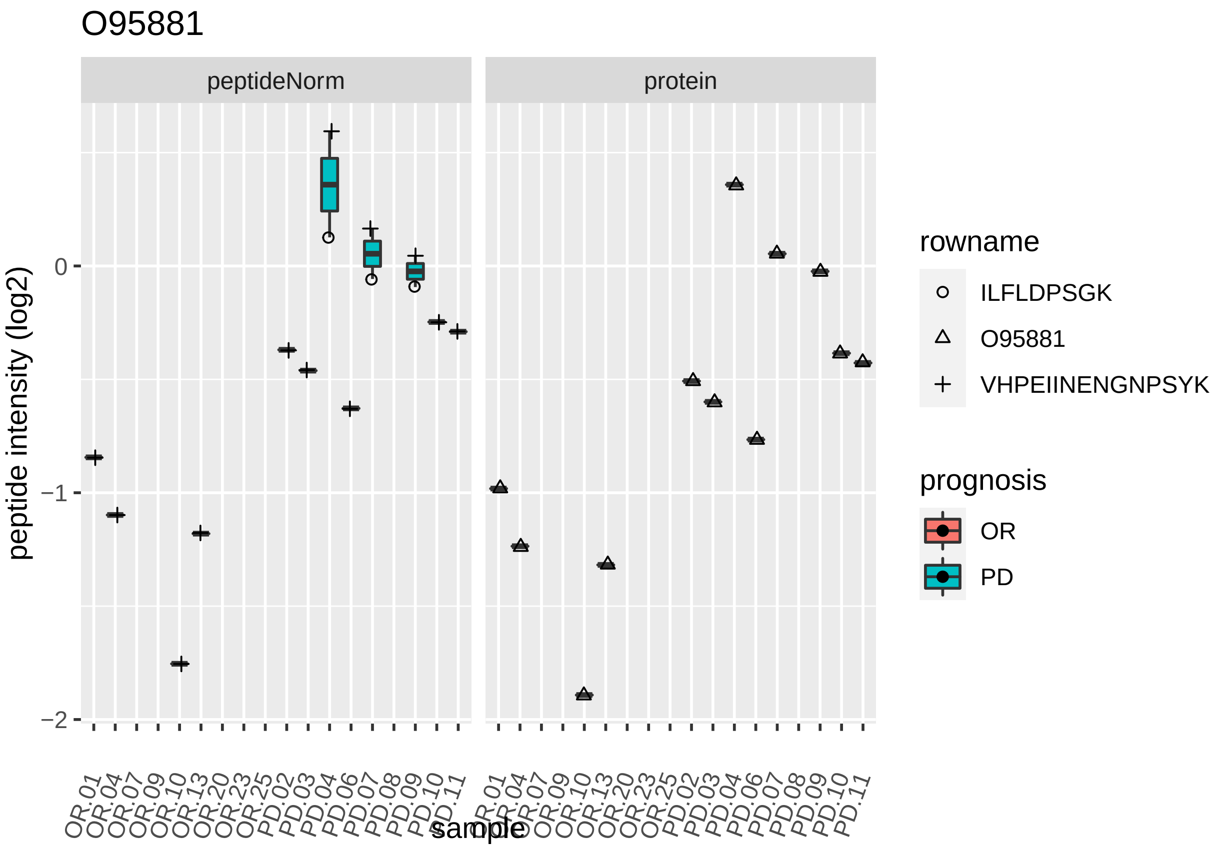
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


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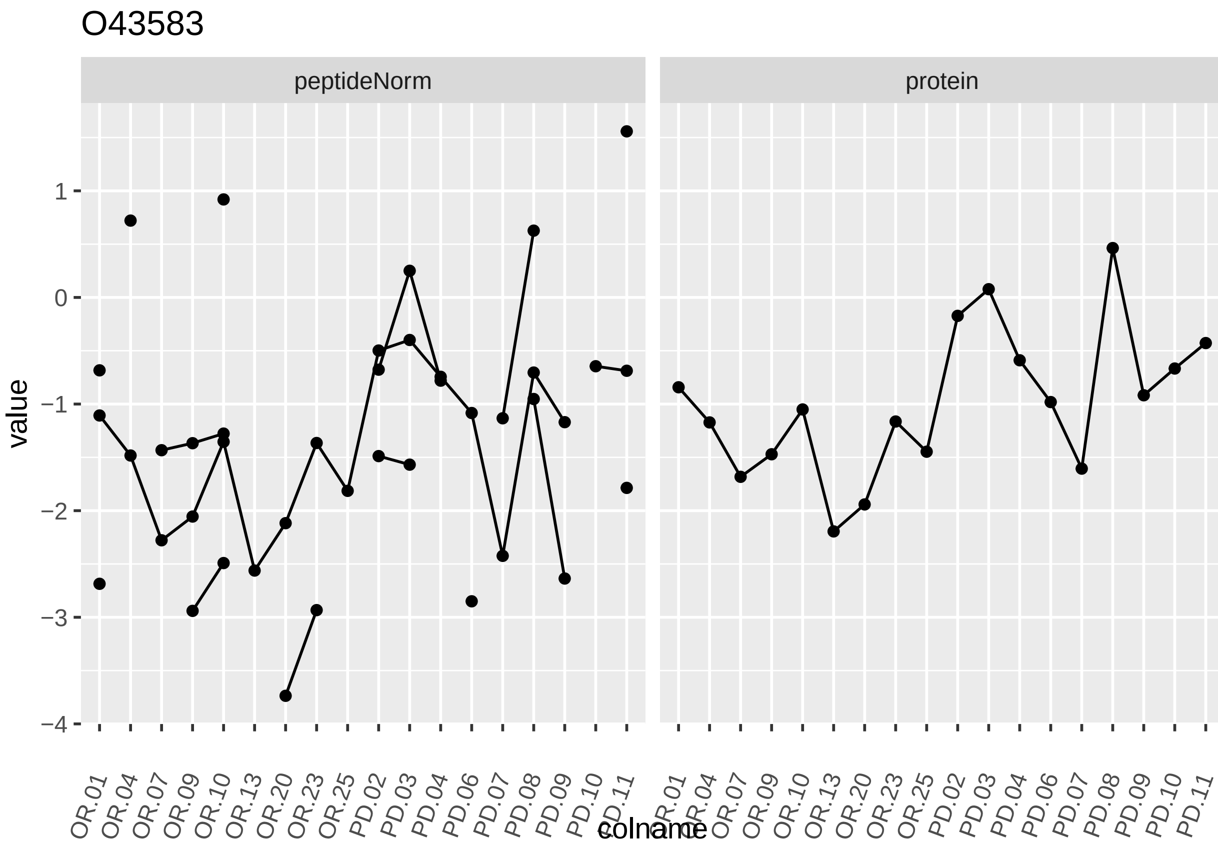
−1
−2
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
ILFLDPSGK
O95881
VHPEIINENGNPSYK
prognosis
OR
PD



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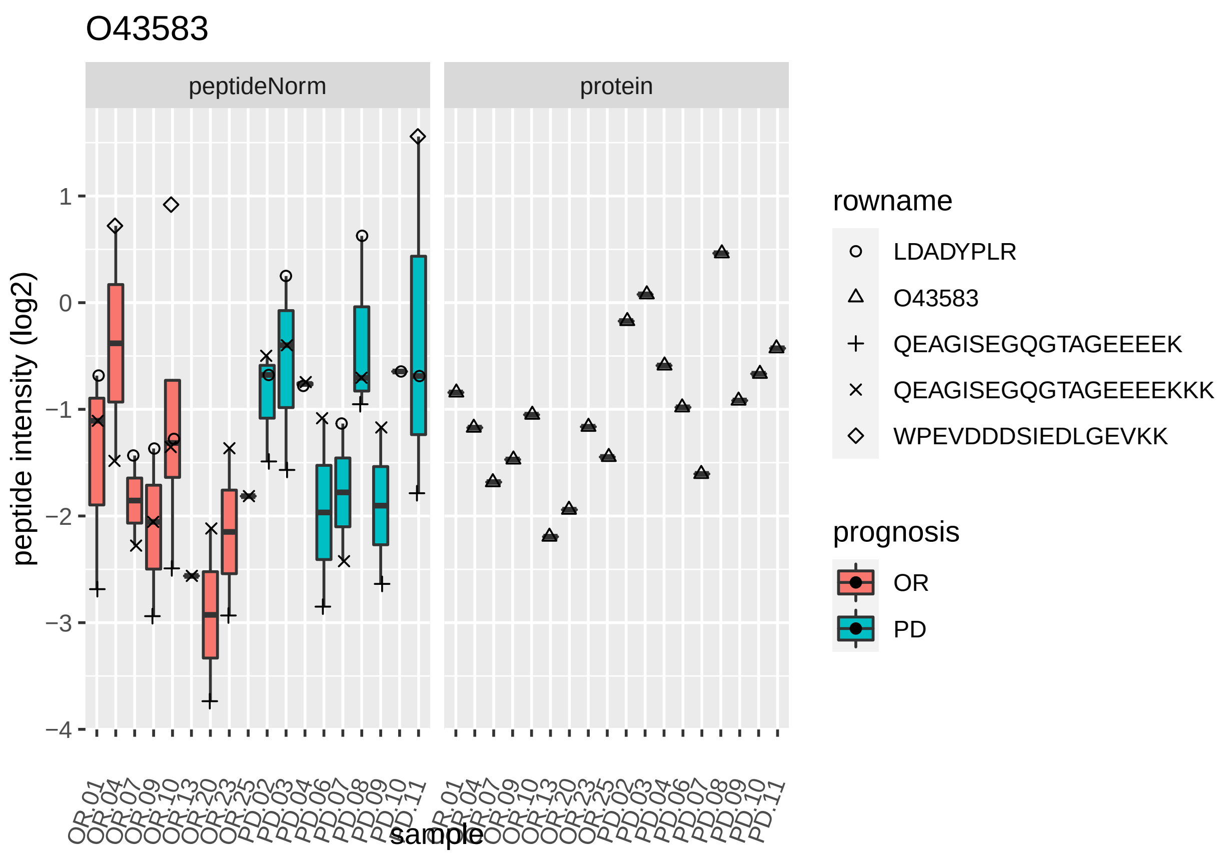
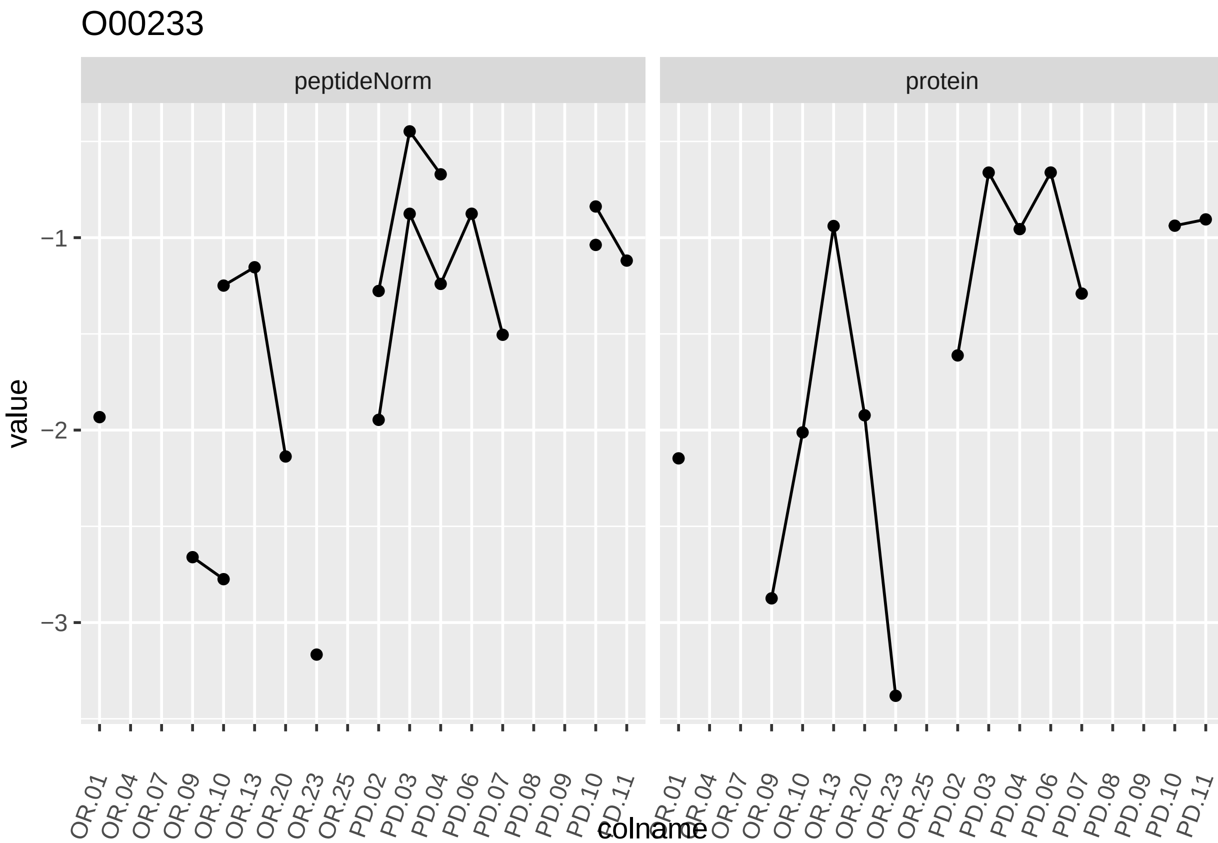
−2
−3
−4
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname


O43583
peptideNorm
protein
peptide intensity (log2)
sample
rowname
LDADYPLR
O43583
QEAGISEGQGTAGEEEEK
QEAGISEGQGTAGEEEEKKK
WPEVDDDSIEDLGEVKK
prognosis
OR
PD


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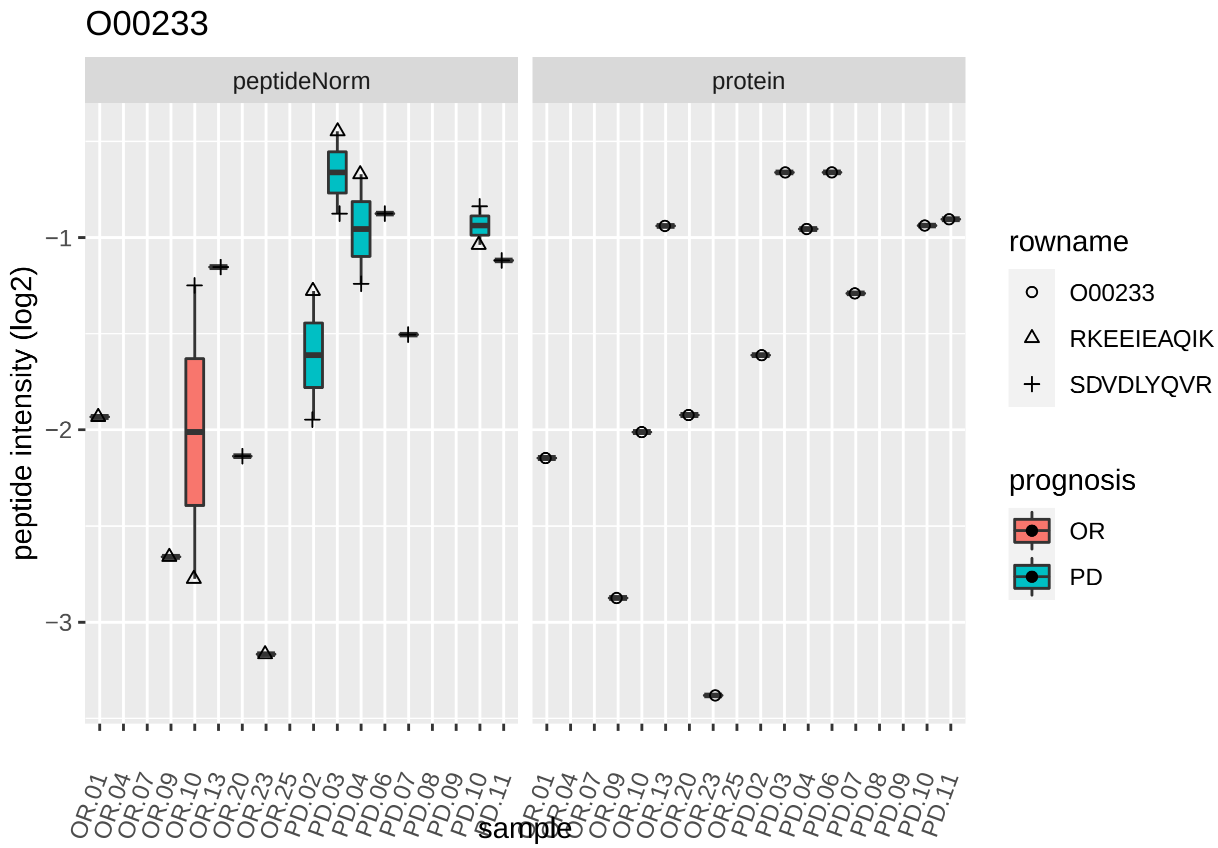
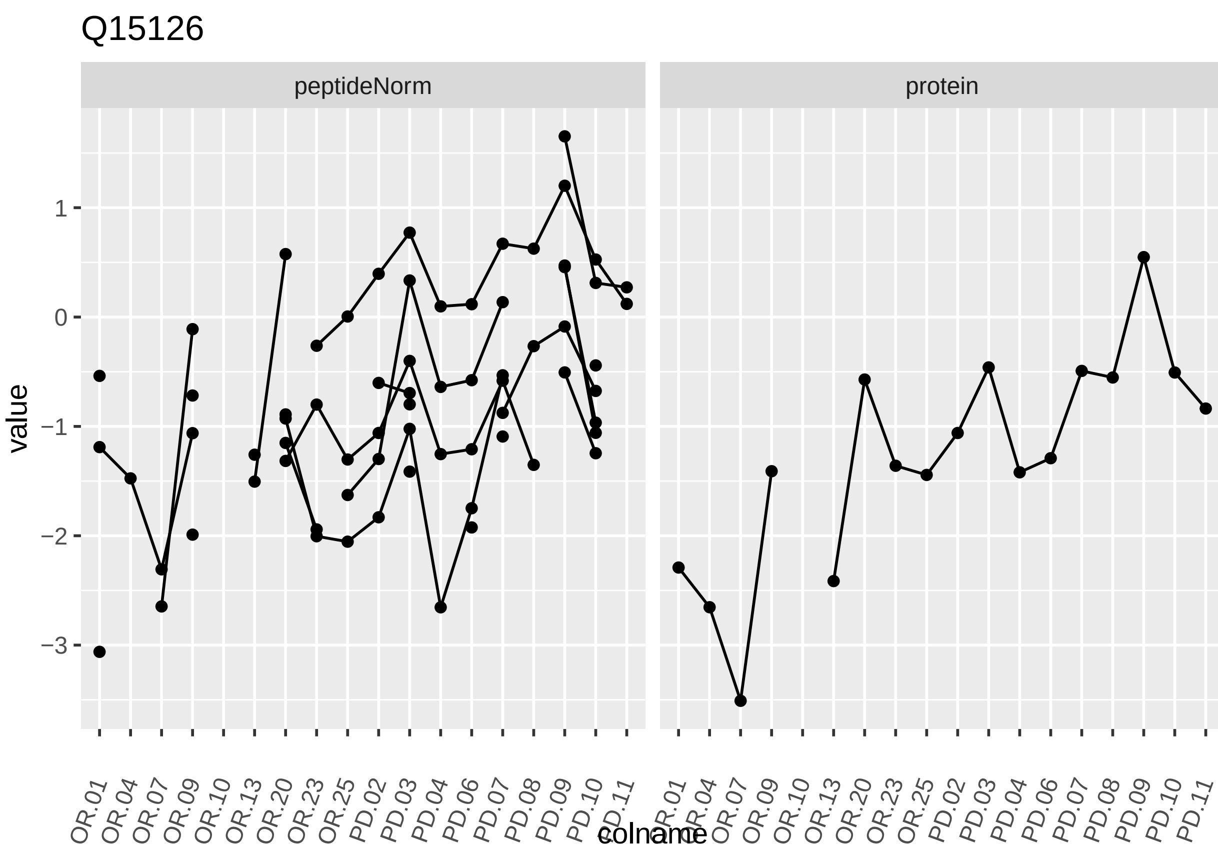
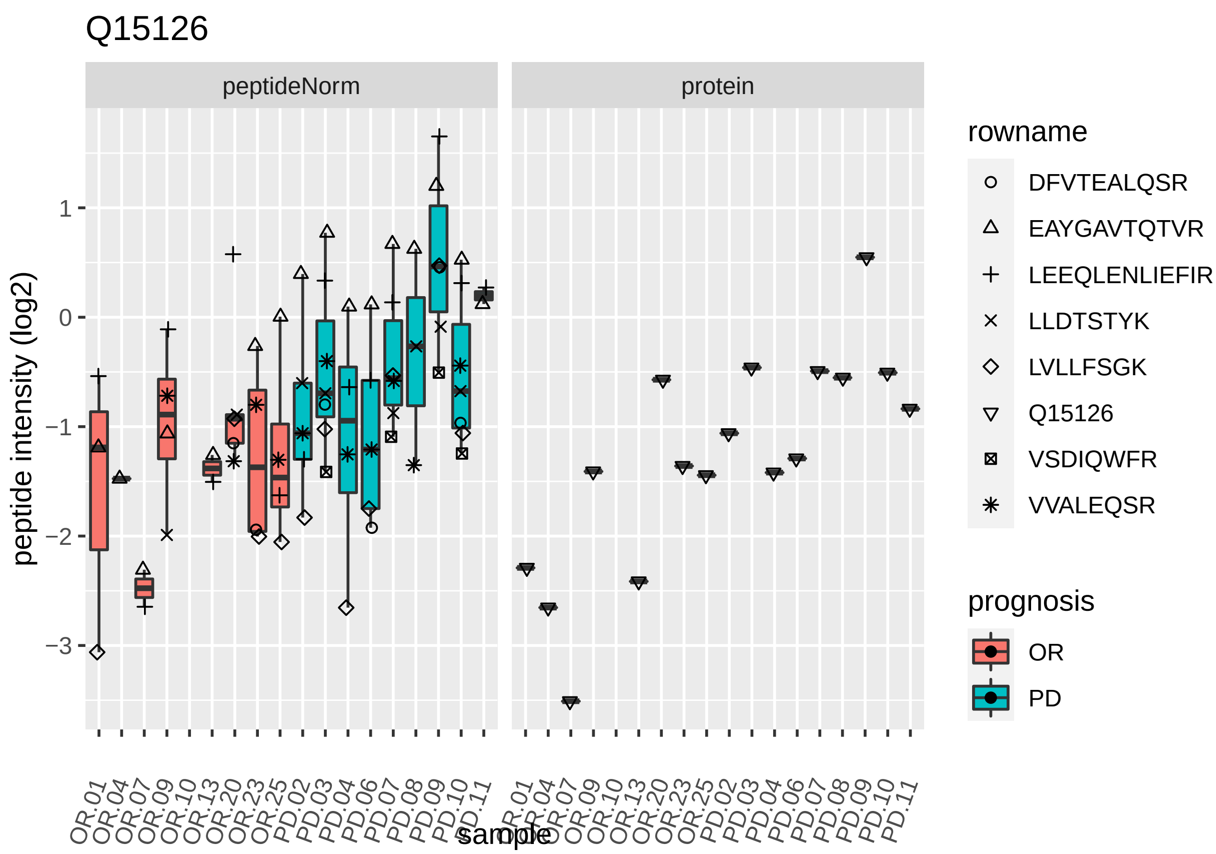
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
colname

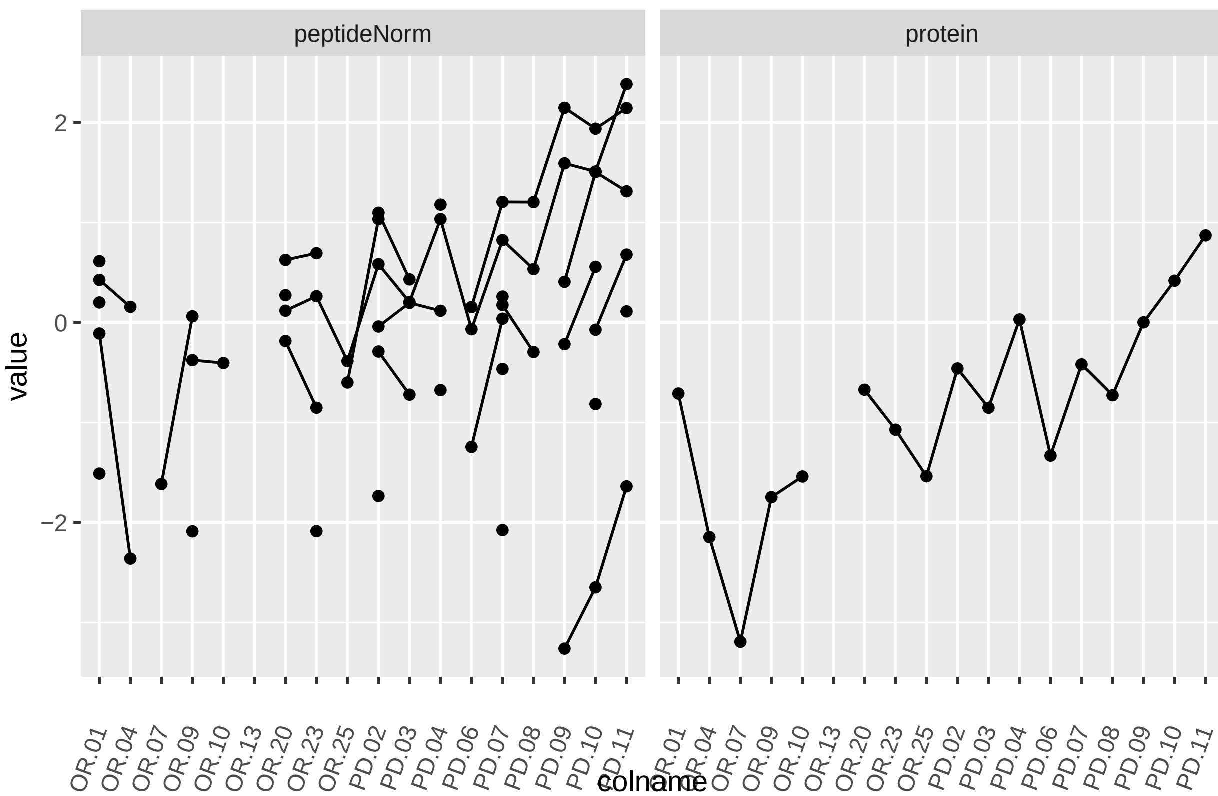

O00233
peptideNorm
protein
peptide intensity (log2)
−1
−2
−3
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11
sample
rowname
O00233
RKEEIEAQIK
SDVDLYQVR
prognosis
OR
PD


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

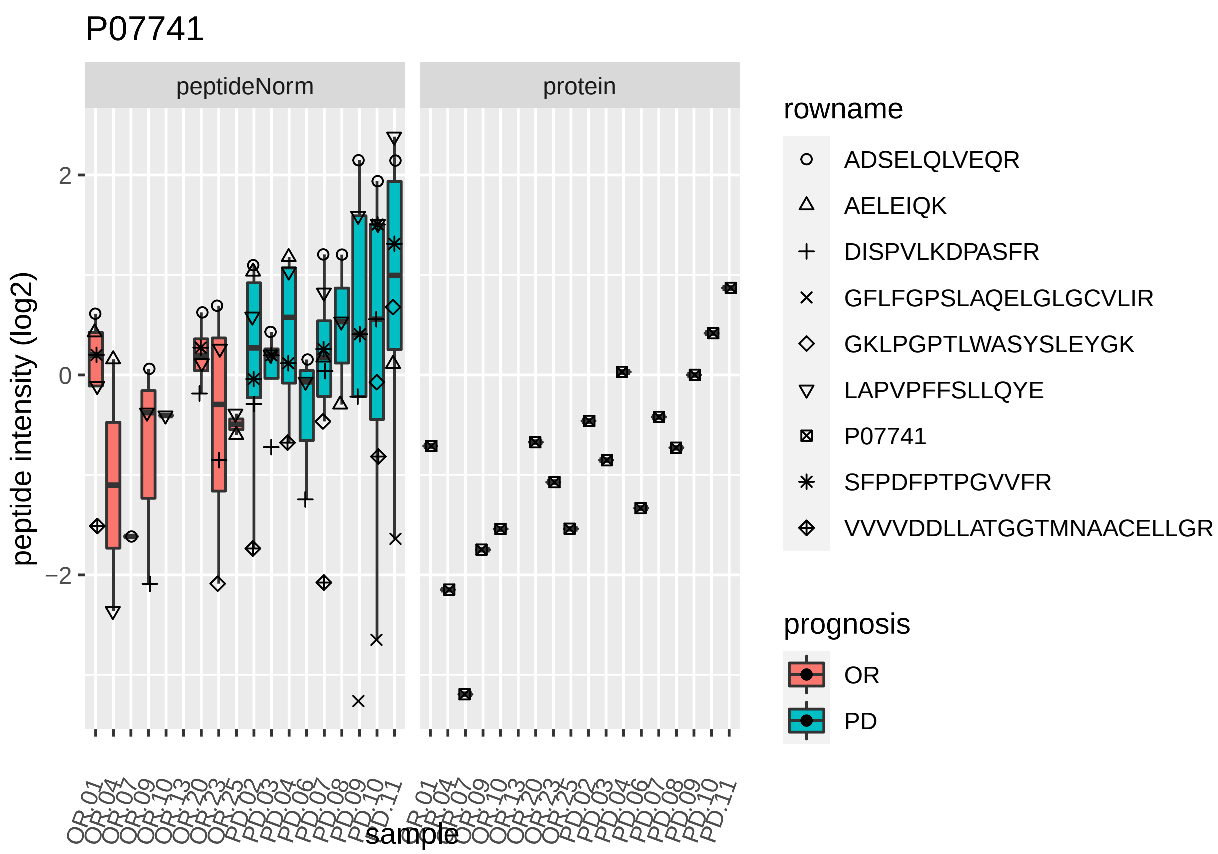


Q15126
peptideNorm
protein
peptide intensity (log2)
1
0
−1
−2
−3
OR.01 OR.04 OR.07 OR.09 OR.10 OR.13 OR.20 OR.23 OR.25 PD.02 PD.03 PD.04 PD.06 PD.07 PD.08 PD.09 PD.10 PD.11
sample
rowname
DFVTEALQSR
EAYGAVTQTVR
LEEQLENLIEFIR
LLDTSTYK
LVLLFSGK
Q15126
VSDIQWFR
VVALEQSR
prognosis
OR
PD

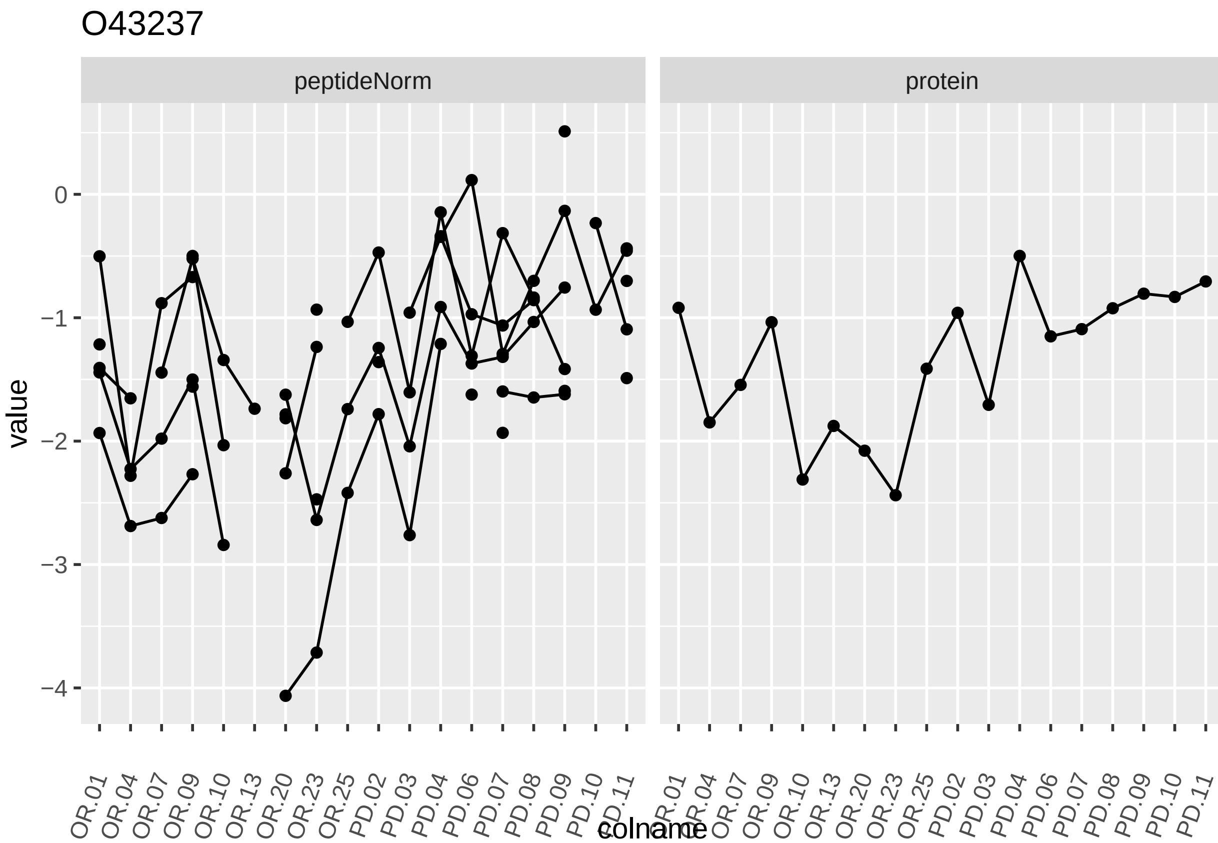
P07741

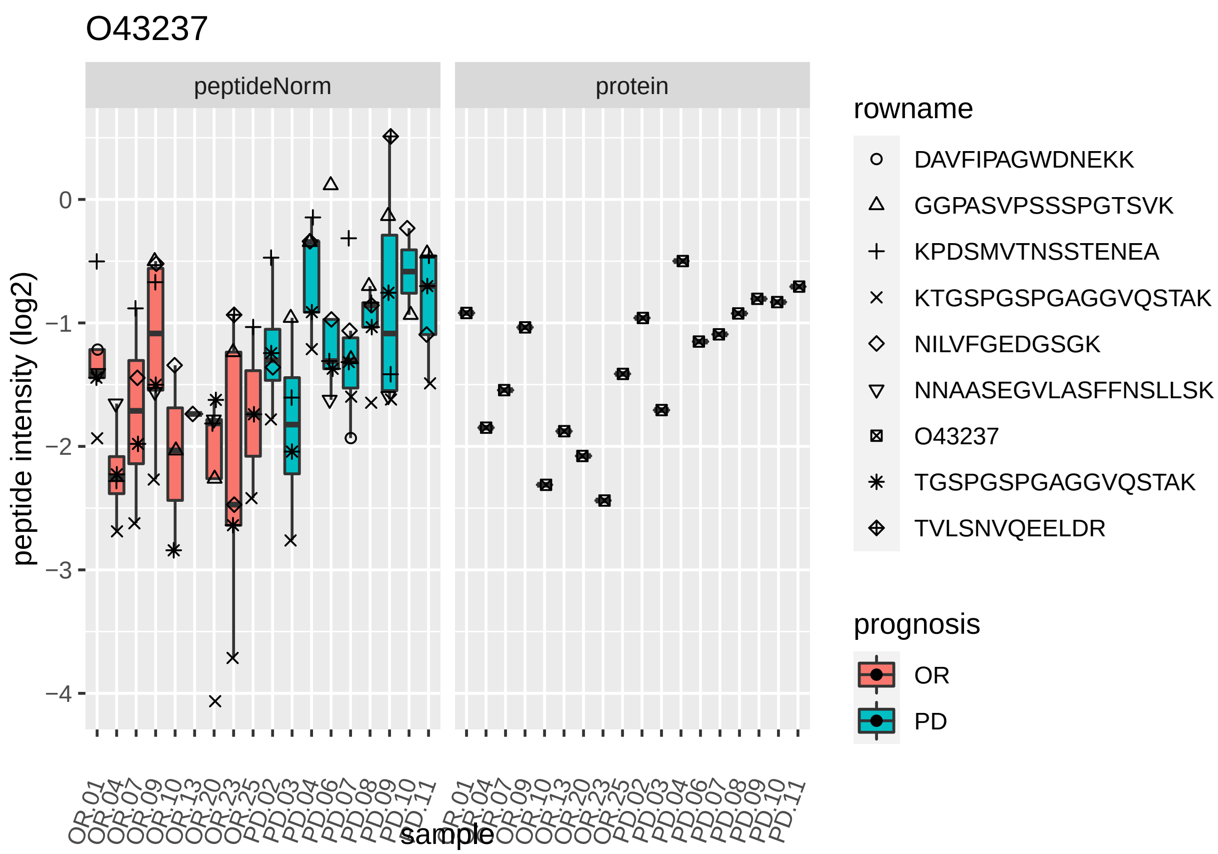


peptideNorm
protein
value
2
0
−2
colname
OR.01
OR.04
OR.07
OR.09
OR.10
OR.13
OR.20
OR.23
OR.25
PD.02
PD.03
PD.04
PD.06
PD.07
PD.08
PD.09
PD.10
PD.11



P07741
peptideNorm
protein
peptide intensity (log2)
2
0
−2
sample
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
```