Cancer

Lieven Clement

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

Contents

1	Background	1
2	Data	1
	2.1 Data exploration	3
3	Preprocessing	5
	3.1 Log transform the data	4
	3.2 Filtering	4
	3.3 Normalize the data using median centering	4
	3.4 Explore normalized data	
	3.5 Summarization to protein level	(
4	Data Analysis	7
	4.1 Estimation	7
	4.2 Inference	7
	4.3 Plots	
5	Session Info	222

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/peptidecols <- grep(
   "Intensity\\.",
   names(read.delim(peptidesFile))
   )</pre>
```

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

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

```
## Checking arguments.
```

- ## Loading data as a 'SummarizedExperiment' object.
- ## Formatting sample annotations (colData).
- ## Formatting data as a 'QFeatures' object.

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

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

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

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

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

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

```
## [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
```

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"
##
                                  "Protein.names"
##
    [4] "Gene.names"
                                                            "Unique..Groups."
   [7] "Unique..Proteins."
                                  "Charges"
                                                            "PEP"
##
                                  "Slice.Average"
## [10] "Score"
                                                            "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"
                                  "Intensity"
                                                            "Reverse"
## [34] "Experiment.PD.11"
                                  "id"
## [37] "Contaminant"
                                                            "Protein.group.IDs"
## [40] "Mod..peptide.IDs"
                                                            "MS.MS.IDs"
                                  "Evidence.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")</pre>
```

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))</pre>
```

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

2. Remove reverse sequences (decoys) and contaminants

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

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

## 'Reverse' found in 2 out of 2 assay(s)
pe <- filterFeatures(pe,~ Contaminant != "+")</pre>
```

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

3. Drop peptides that were only identified in one sample

We keep peptides that were observed at last twice.

```
pe <- filterFeatures(pe,~ nNonZero >=2)
## 'nNonZero' found in 2 out of 2 assay(s)
nrow(pe[["peptideLog"]])
```

[1] 26696

We keep 26696 peptides upon filtering.

3.3 Normalize the data using median centering

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

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

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

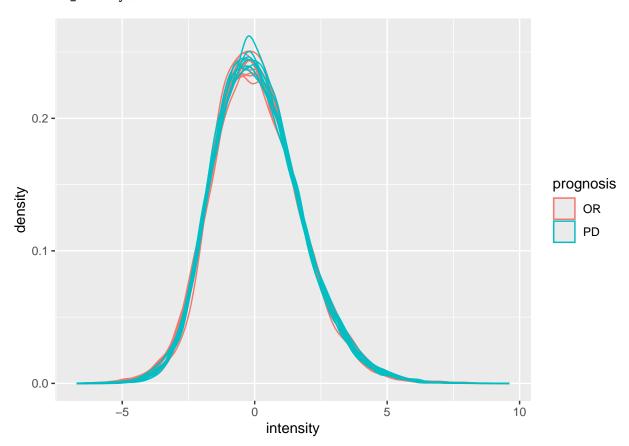
3.4 Explore normalized data

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()
```

 $\mbox{\tt \#\#}$ Warning: Removed 188395 rows containing non-finite outside the scale range $\mbox{\tt \#\#}$ ('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")</pre>
```

```
## 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)</pre>
```

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]]

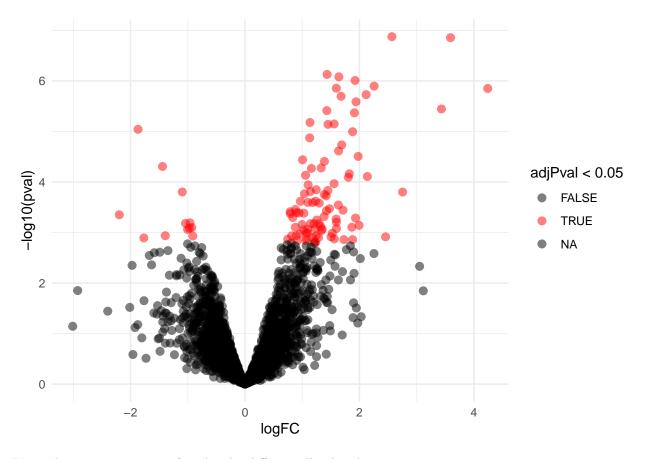


Spike-in condition A is the reference class. So the mean $\log 2$ expression for samples from good prognosis (OR) is '(Intercept). The mean $\log 2$ expression for samples from poor prognosis (PD) is '(Intercept)+prognosisPD'. Hence, the average $\log 2$ fold change between prognosis PD and prognosis 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)</pre>
```

4.3 Plots

4.3.1 Volcano-plot

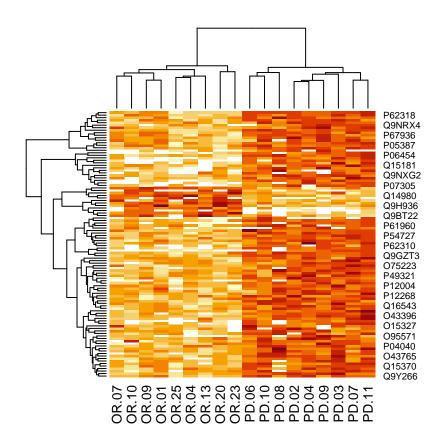


Note, that 106 proteins are found to be differentially abundant.

4.3.2 Heatmap

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

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

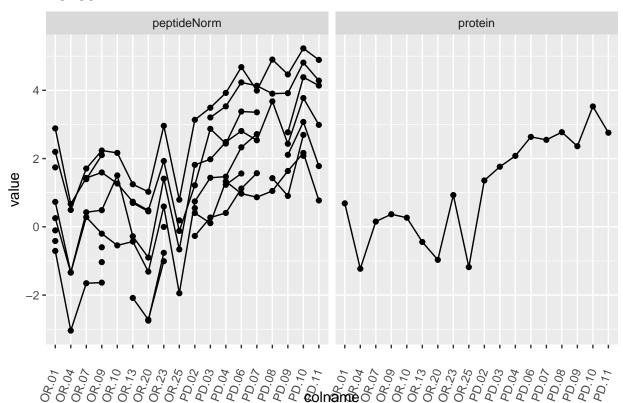


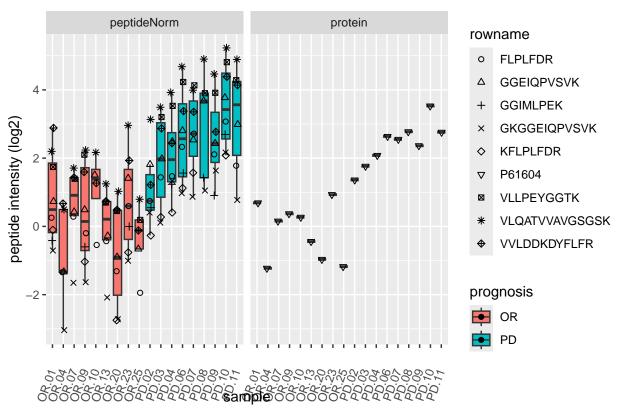
4.3.3 Detail plots

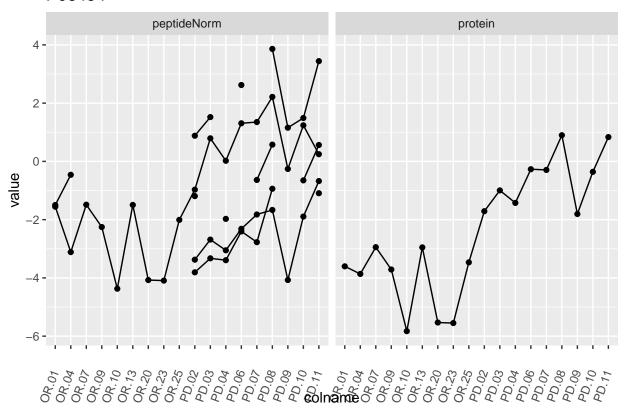
We make detail plots for the top 10 proteins to restrict the number of detail plots.

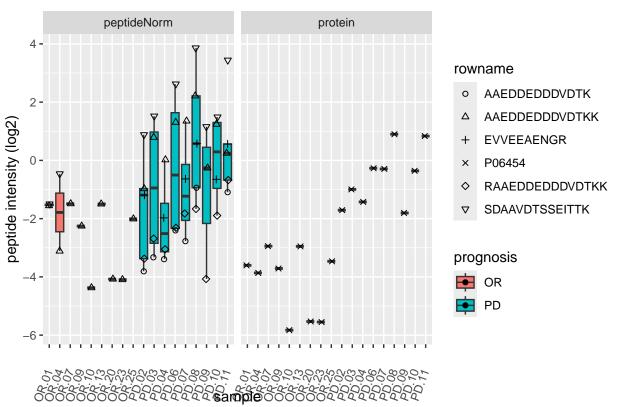
```
for (protName in sigNames)
#for (protName in orderProt[1:10])
pePlot <- pe[protName, , c("peptideNorm", "protein")]</pre>
pePlotDf <- data.frame(longFormat(pePlot))</pre>
pePlotDf$assay <- factor(pePlotDf$assay,</pre>
                         levels = c("peptideNorm", "protein"))
pePlotDf$prognosis <- as.factor(colData(pePlot)[pePlotDf$colname, "prognosis"])</pre>
# plotting
p1 <- ggplot(data = pePlotDf,</pre>
       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)) +</pre>
  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)
}
```





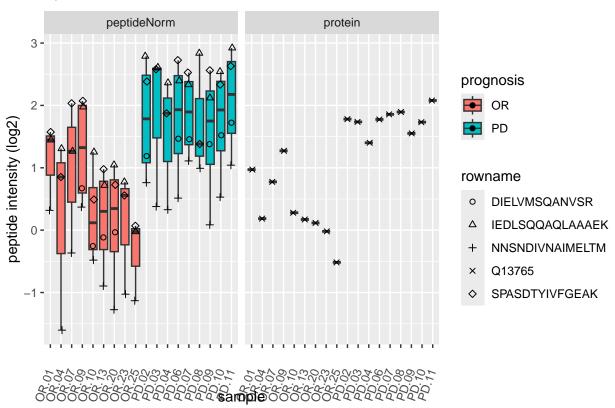




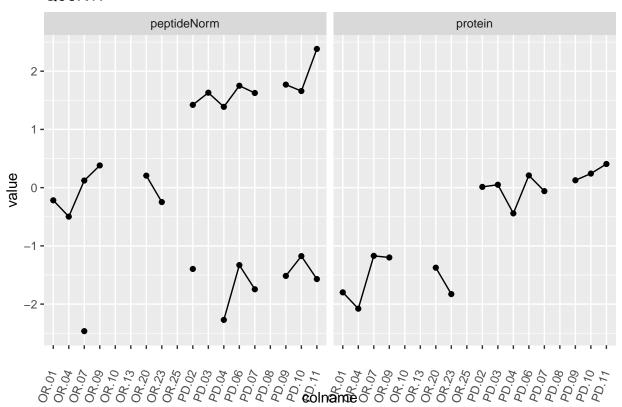
Q13765



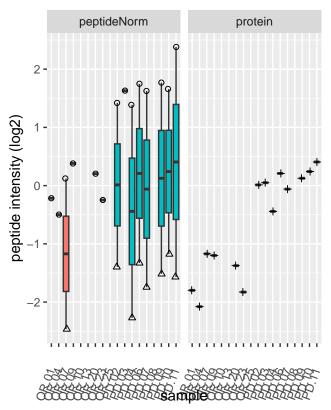
Q13765



Q96K17



Q96K17



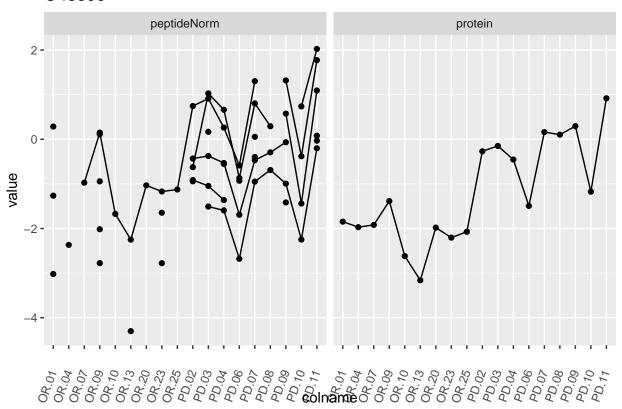
prognosis



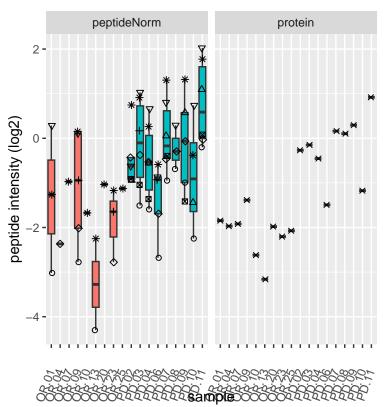
rowname

- APKPEDIDEEDDDVPDLVENFDEASKNEAN
- △ LAEQFPR
- + Q96K17

O43396



O43396



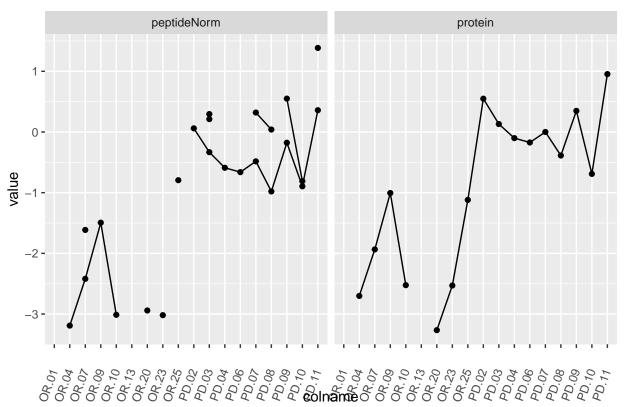
rowname

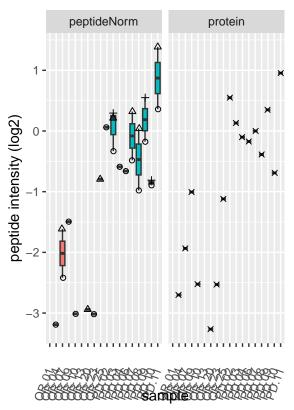
- FQGPDNGQGPK
- FQNVNSVTIFVQSNQGEEETTR Δ
- IDQYQGADAVGLEEK +
- O43396 ×
- QHLENDPGSNEDTDIPK \Diamond
- SEPTQALELTEDDIKEDGIVPLR ∇
- × SMDFEEAER
- VGVKPVGSDPDFQPELSGAGSR

prognosis









rowname

- AAATPESQEPQAK
- GDVTAEEAAGASPAK
- GEGESPPVNGTDEAAGATGDAIEPAPPSQGAEAK
- P49006

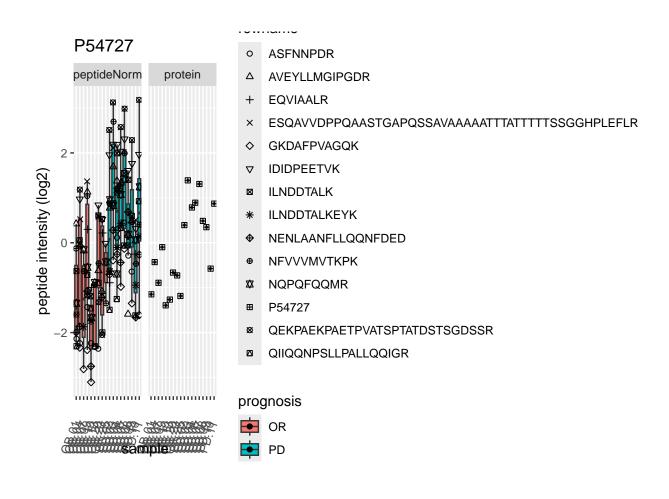
prognosis

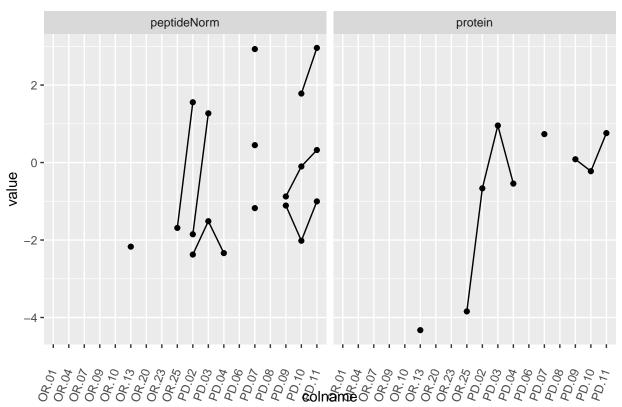


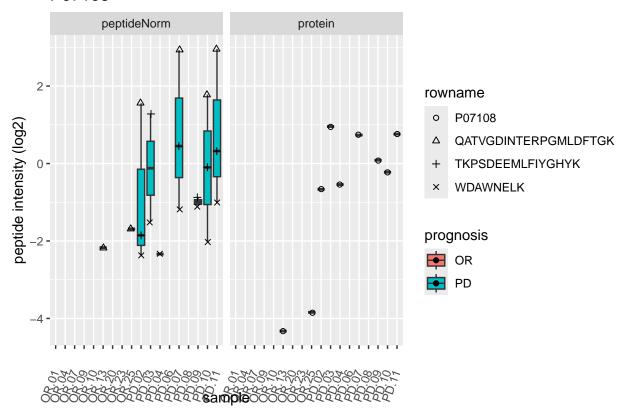


PD

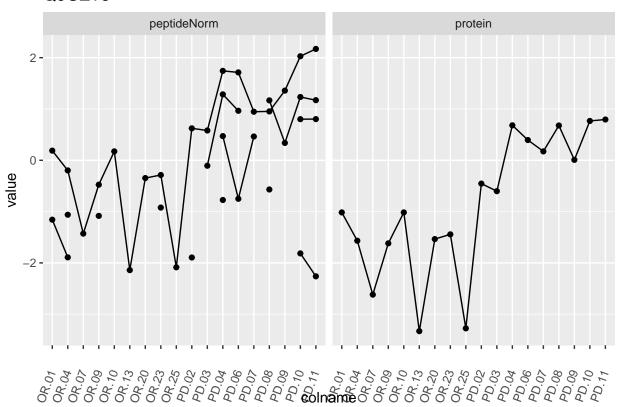




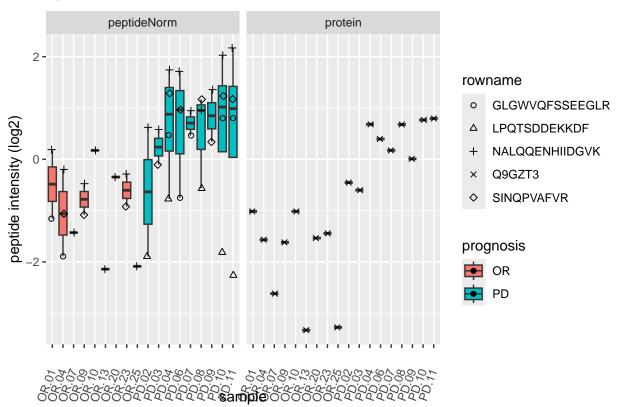




Q9GZT3



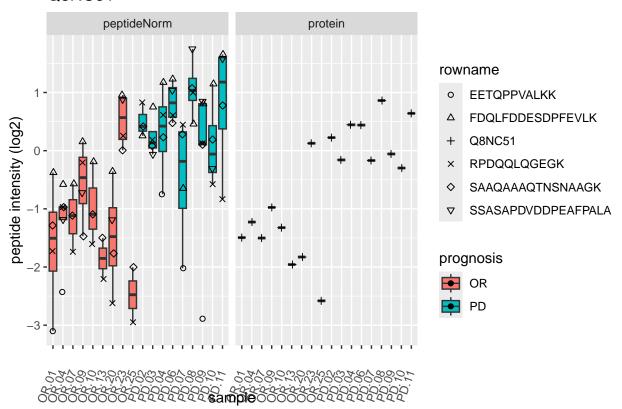
Q9GZT3



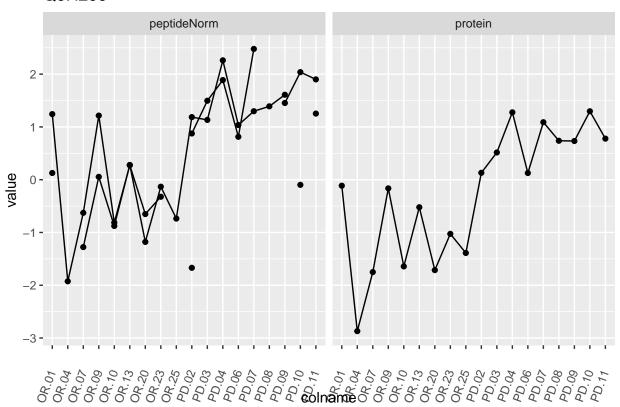
Q8NC51



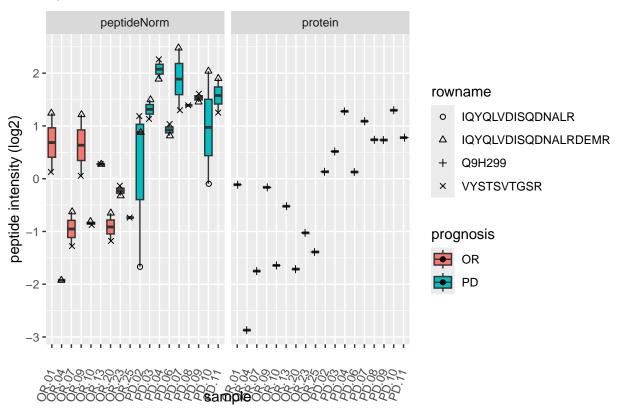
Q8NC51



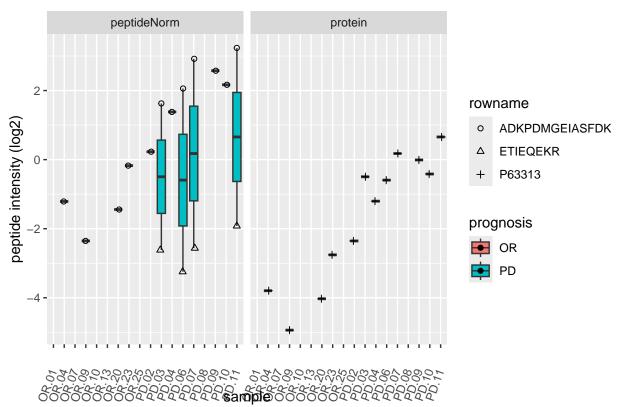
Q9H299



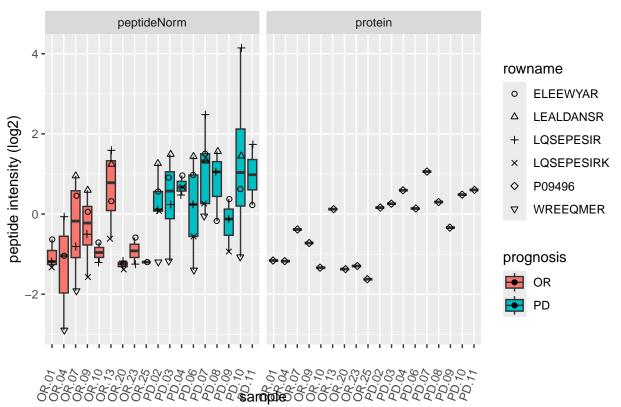
Q9H299

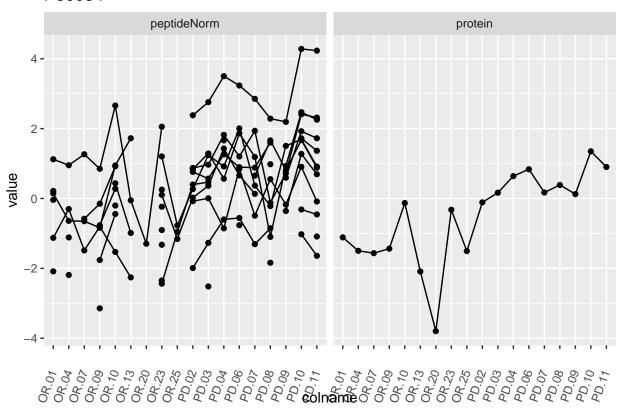


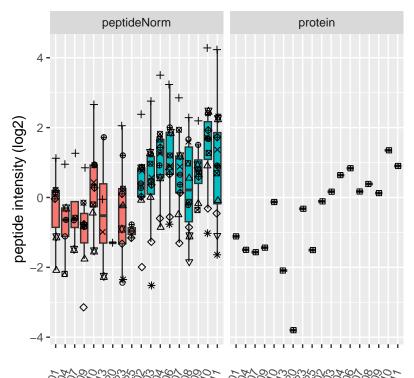












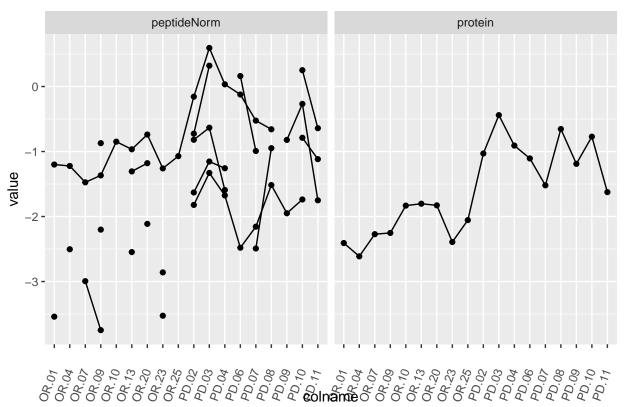
- AFAAGADIK
- ALNALCDGLIDELNQALK
- AQFAQPEILIGTIPGAGGTQR
- **EGMTAFVEK** ×
- **EMQNLSFQDCYSSK**
- **ESVNAAFEMTLTEGSK**
- GKNNTVGLIQLNRPK
- ICPVETLVEEAIQCAEK
- KLFYSTFATDDRK
- LFYSTFATDDRK
- NNTVGLIQLNRPK 苁
- P30084 ⊞
- SLAMEMVLTGDR
- TFEEDPAVGAIVLTGGDK

prognosis

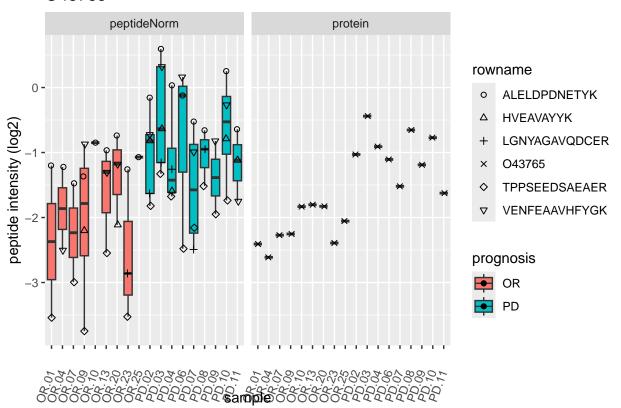




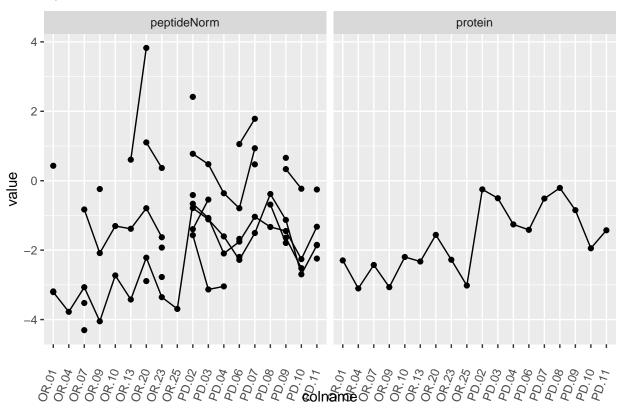
O43765



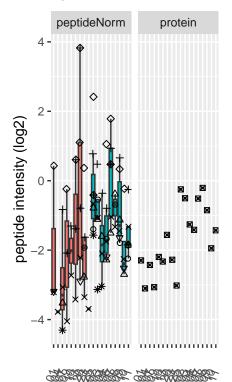
O43765



Q9NXG2



Q9NXG2



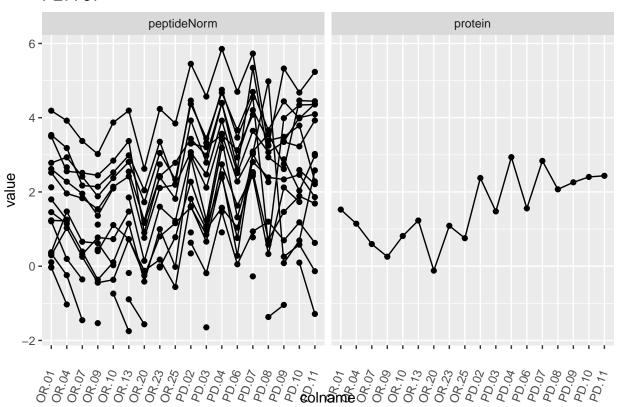
rowname

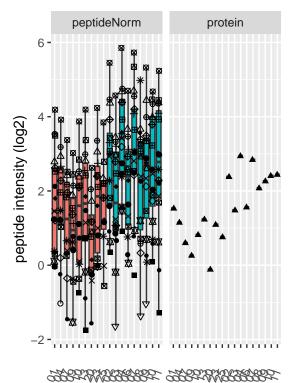
- AAPAQQTTQPGGGK
- AAPAQQTTQPGGGKR Δ
- **FQSVESGANNVVFIR**
- LESADKSDQNNTAEGK
- NNQQVPENTEELGQTKPTSNPQVVNEGGAKPELASQATEGSK
- NNSHVNREEVIR ∇
- Q9NXG2
- SPKDPSQLNSK
- YNLQEVVK

prognosis



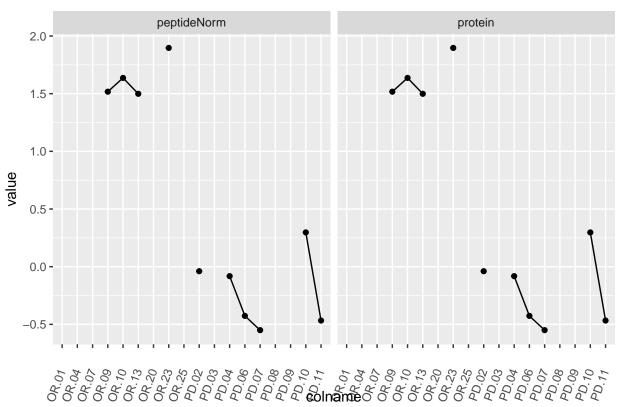




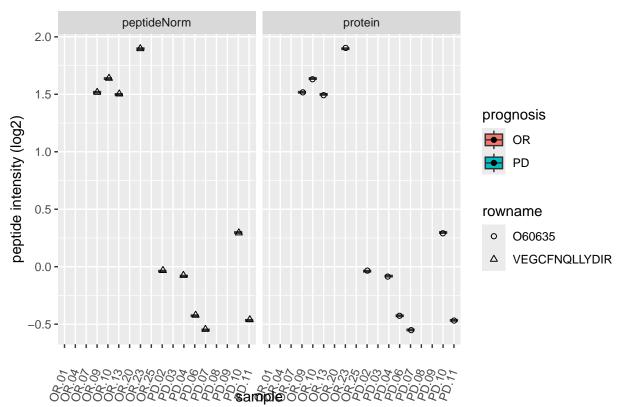


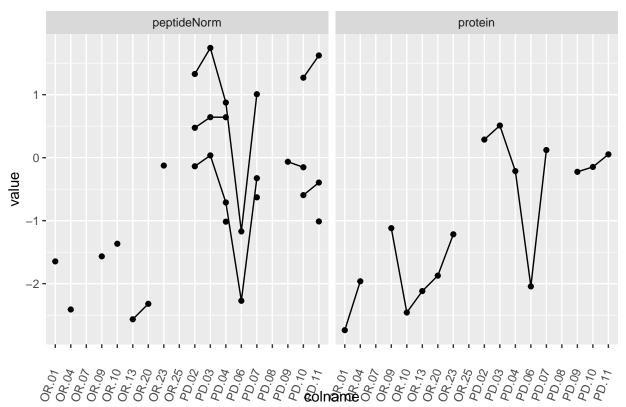
- I IALOAOI LI I ONN
- × FYGDEEKDK
- ♦ FYGDEEKDKGLQTSQDAR
- ∇ GKNVLINK
- GQTLVVQFTVK
- * GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK
- ♦ HEQNIDCGGGYVK
- IDDPTDSKPEDWDKPEHIPDPDAK
- ☆ IDNSQVESGSLEDDWDFLPPK
- IDNSQVESGSLEDDWDFLPPKK
- IKDPDASKPEDWDER
- KPEDWDEEMDGEWEPPVIQNPEYK
- KVHVIFNYK
- LFPNSLDQTDMHGDSEYNIMFGPDICGPGTK
- ▲ P27797
- QIDNPDYK
- SGTIFDNFLITNDEAYAEEFGNETWGVTK
- VHVIFNYK

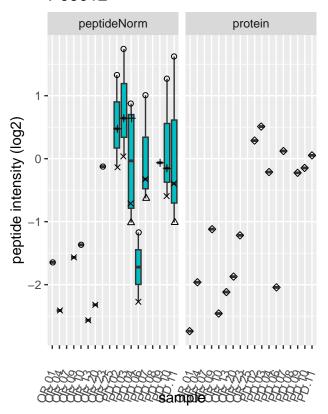
O60635



O60635







rowname

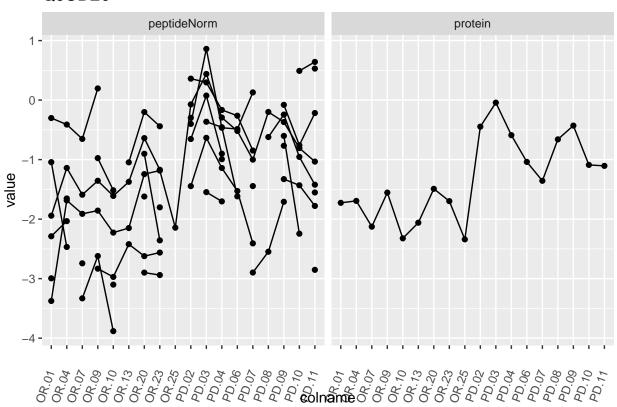
- 0 **AVPETRPNHTIYINNLNEK**
- AVQGGGATPVVGAVQGPVPGMPPMTQAPR Δ
- **EVSSATNALR**
- HDIAFVEFDNEVQAGAAR
- P09012

prognosis

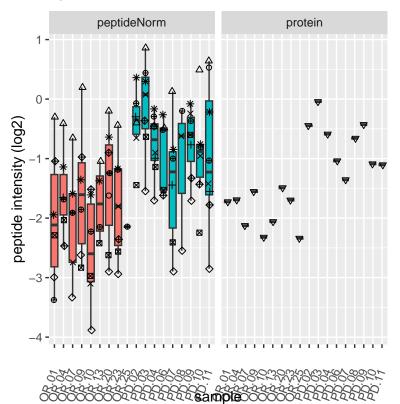


PD

Q9UBE0



Q9UBE0



prognosis

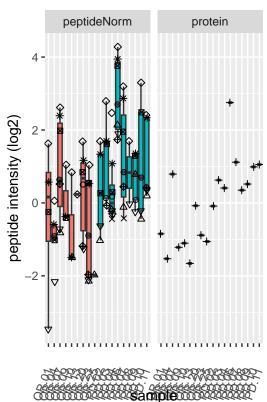




rowname

- AQNLNPMVDVK
- △ GLTMLDHEQVTPEDPGAQFLIR
- + LWGLEAQK
- × NDVLDSLGISPDLLPEDFVR
- ♦ NRAEASLER
- ▽ Q9UBE0
- TTSDYFLLQVLLK
- * VEKEEAGGGISEEEAAQYDR
- ♦ VLLVGLKGLGAEIAKNLILAGVK
- VSQGVEDGPDTKR





rowname

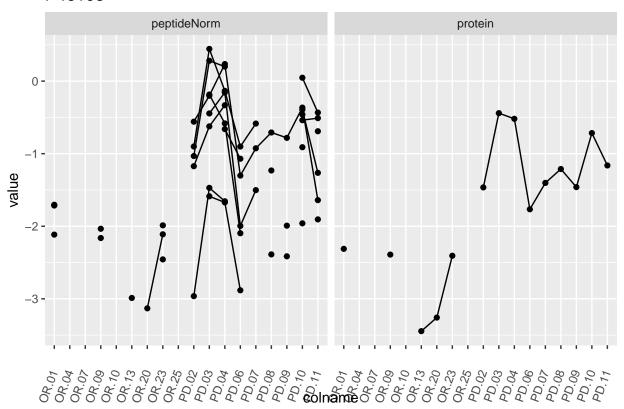
- ASAAFSSVGSVITK
- ELAKVEEEIQTLSQVLAAK Δ
- P55327
- SFEEKVENLK ×
- TDPVPEEGEDVAATISATETLSEEEQEELRR \Diamond
- **TSETLSQAGQK** ∇
- VEEEIQTLSQVLAAK
- VGGTKPAGGDFGEVLNSAANASATTTEPLPEK
- VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL

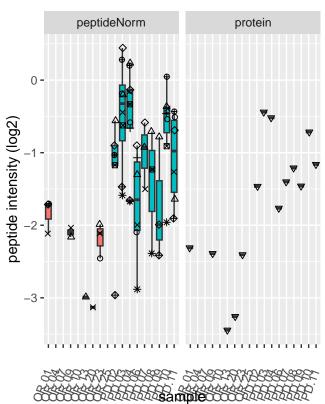
prognosis





PD



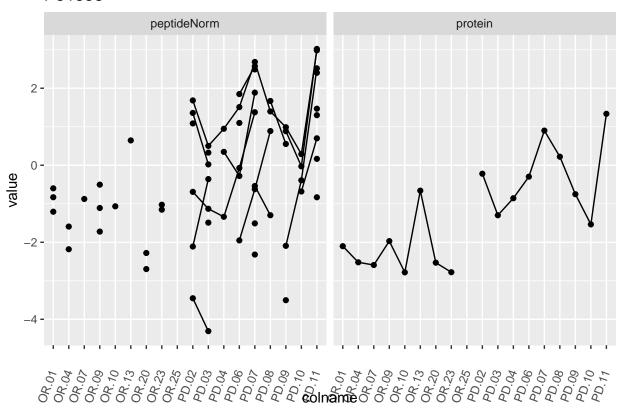


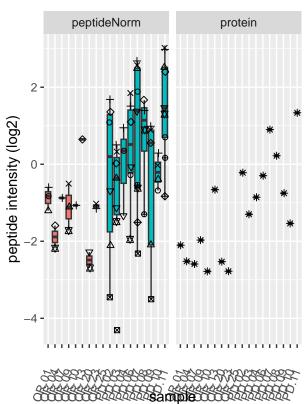
rowname

- ALFDFNGNDEEDLPFK
- △ DSSTSPGDYVLSVSENSR
- + HGVFLVR
- × IGDQEFDSLPALLEFYK
- ♦ IHYLDTTTLIEPVSR
- ▽ P46108
- QEAVALLQGQR
- * QGSGVILR
- ◆ TALALEVGELVK
- VSHYIINSSGPRPPVPPSPAQPPPGVSPSR

prognosis







prognosis

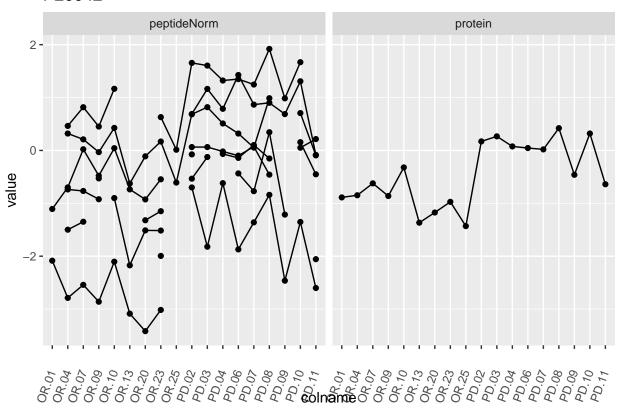


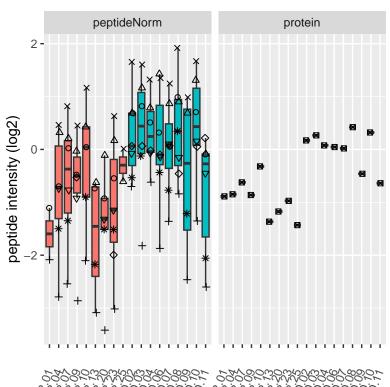
OR

PD

rowname

- EAENPEGEEKEAATLEVERPLPMEVEK
- GFSEGLWEIENNPTVK
- GPPQEEEEEEDEEEEATKEDAEAPGIR
- **GPPQEEEEEEDEEEEATKEDAEAPGIRDHESL**
- IDEMPEAAVK
- KGFSEGLWEIENNPTVK
- NSTPSEPGSGR
- P51858
- RAGDLLEDSPK
- SCVEEPEPEPEAAEGDGDKK
- YQVFFFGTHETAFLGPK





rowname

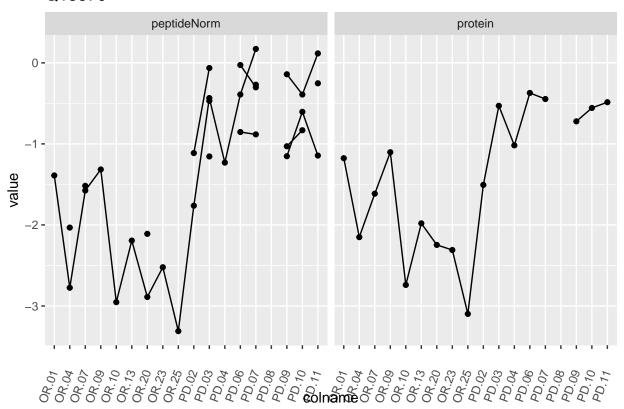
- DASDDLDDLNFFNQK
- Δ DYTYEELLNR
- + EKNPDMVAGEK
- × EVEPEPTEDKDLEADEEDTR
- ♦ IESDVQEPTEPEDDLDIMLGNK
- □ IFDIDEAEEGVK
- P20042
- * TGFQAVTGK

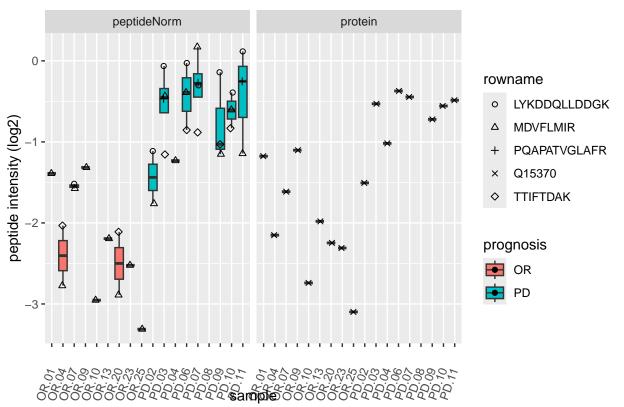
prognosis

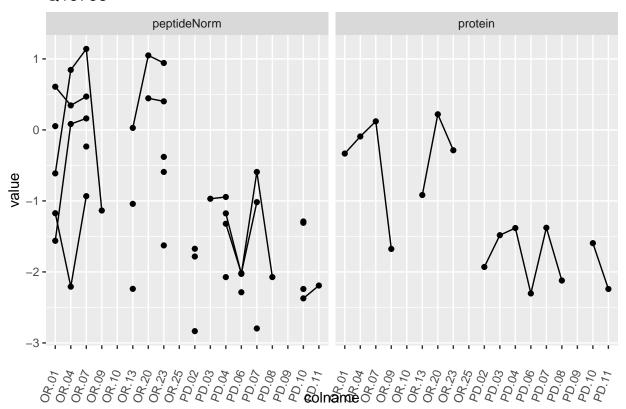


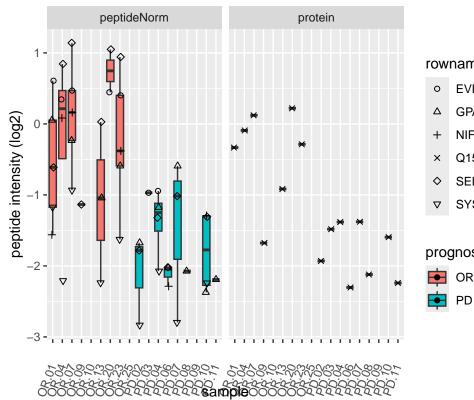
OR









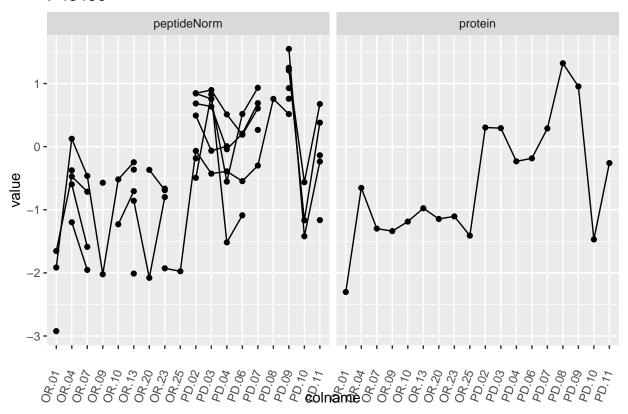


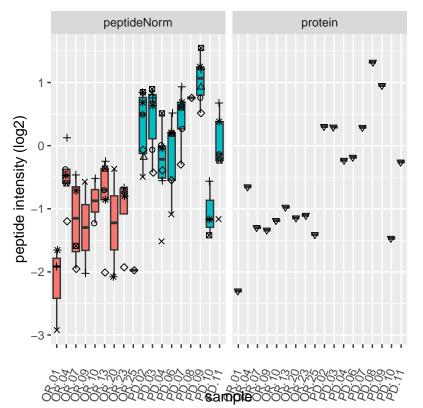
rowname

- **EVLDSFLDLAR**
- GPAGDATVASEK
- NIFPSNLVSAAFR
- Q15758
- SELPLDPLPVPTEEGNPLLK
- SYSTTYEER

prognosis







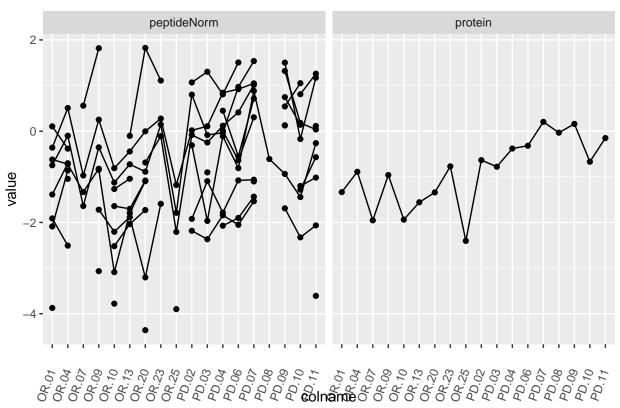
prognosis

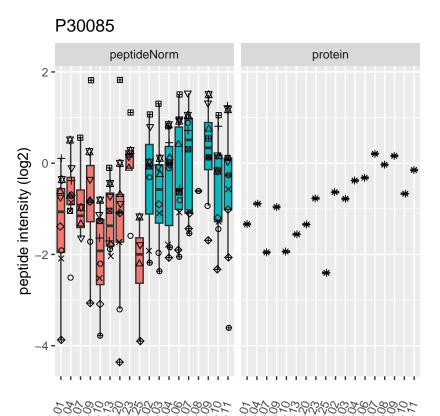




rowname

- DVYKEHFQDDVFNEK
- △ GTDTVAGLALIK
- + GVSSQETAGIGASAHLVNFK
- × GWNYILEK
- ♦ MNPAAEAEFNILLATDSYK
- ▽ P43490
- VIQGDGVDINTLQEIVEGMK
- * YLLETSGNLDGLEYK





rowname

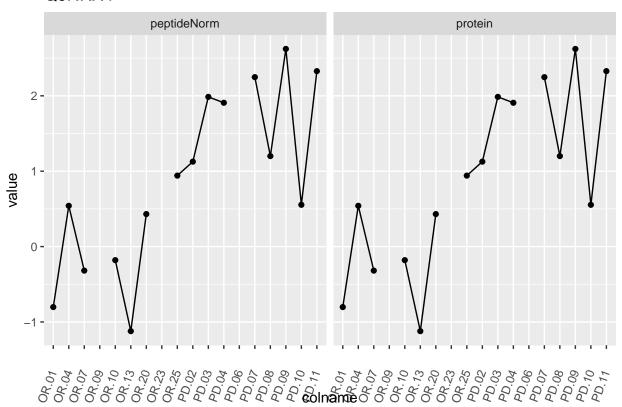
- EMDQTMAANAQK
- Δ FLIDGFPR
- + IQTYLQSTKPIIDLYEEMGK
- × IVPVEITISLLK
- ♦ IVPVEITISLLKR
- ∇ KNPDSQYGELIEK
- NQDNLQGWNK
- * P30085
- ♦ SDDNRESLEKR
- SVDEVFDEVVQIFDK
- YGYTHLSAGELLR

prognosis

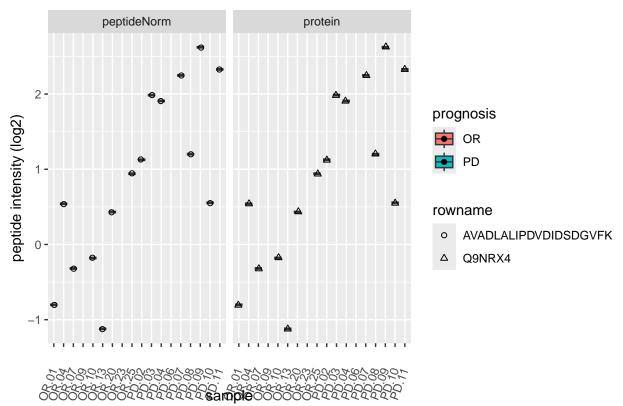


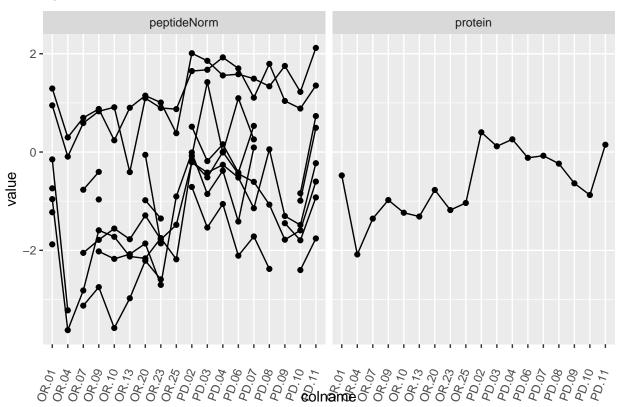


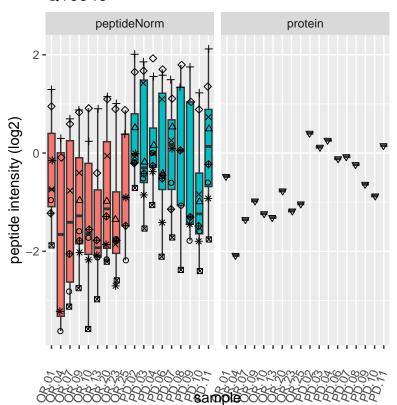
Q9NRX4



Q9NRX4







rowname

- AMKEYEEEER
- △ DVQMLQDAISK
- + EGEEAGPGDPLLEAVPK
- × LGPGGLDPVEVYESLPEELQK
- ♦ LQAEAQQLR
- ▽ Q16543
- SMVNTKPEK
- * SMVNTKPEKTEEDSEEVR
- ◆ TGDEKDVSV

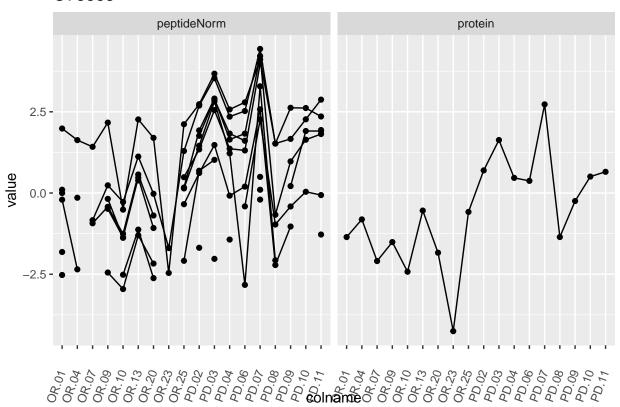
prognosis

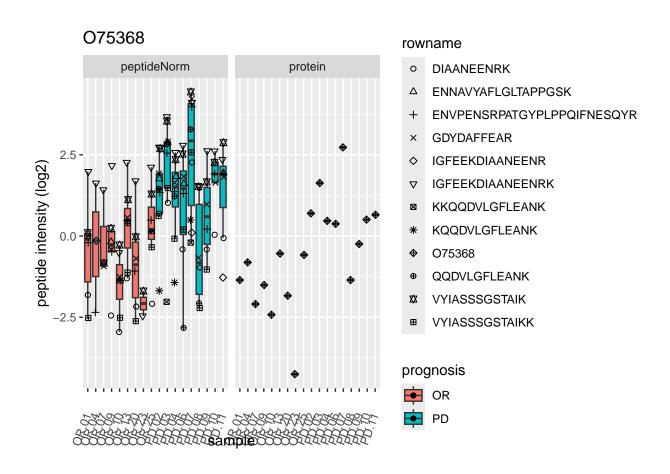


OR

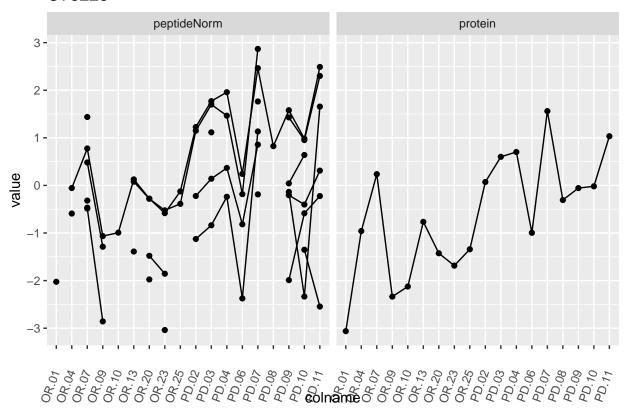


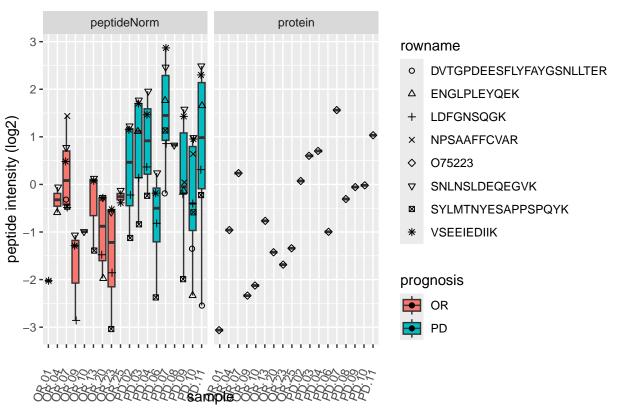
O75368



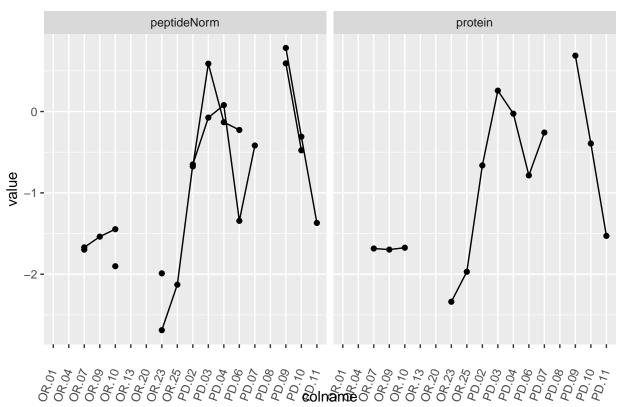


O75223

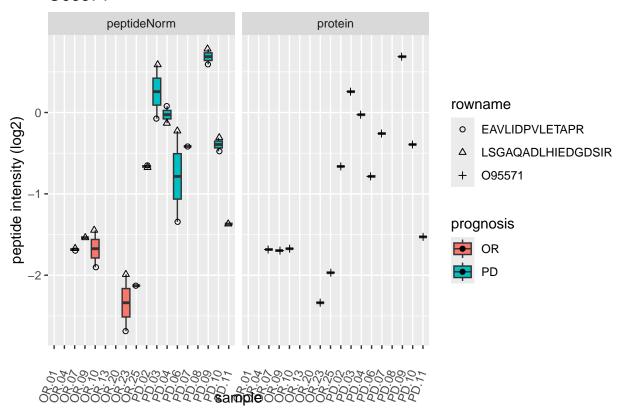




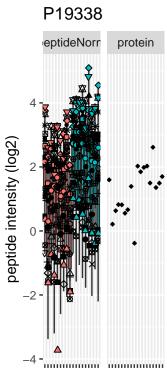
O95571



O95571







- ALELTGLK
- ALVATPGKK Δ
- + **EAMEDGEIDGNK**
- × EAMEDGEIDGNKVTLDWAKPK
- \Diamond **ESFDGSVR**
- **EVFEDAAEIR** ∇
- **FGYVDFESAEDLEK** ×
- **GFGFVDFNSEEDAK**
- GIAYIEFK
- GLSEDTTEETLK
- 邥 GLSEDTTEETLKESFDGSVR
- **GYAFIEFASFEDAK**
- **IVTDRETGSSK**
- KFGYVDFESAEDLEK
- KVVVSPTKK

- **LELQGPR**
- NDLAVVDVR
- P19338
- QKVEGTEPTTAFNLFVGNLNFNK
- SISLYYTGEK
- TEADAEKTFEEK 0
- **TGISDVFAK**
- TLVLSNLSYSATEETLQEVFEK
- VAVATPAKK
- ▼ VEGTEPTTAFNLFVGNLNFNK

VFGNEIK

VTLDWAKPK

VTQDELK

VTQDELKEVFEDAAEIR

VVVSPTKK

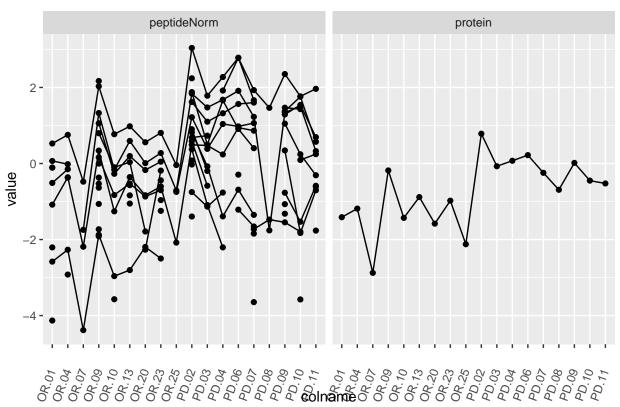


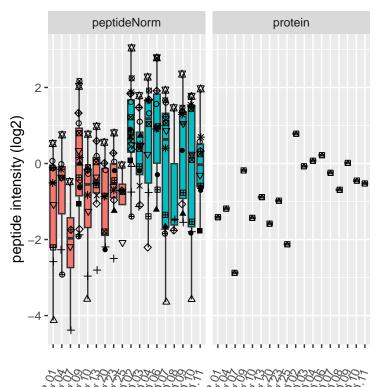




PD





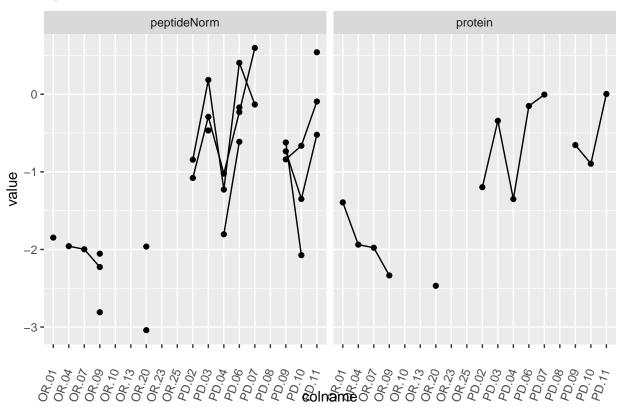




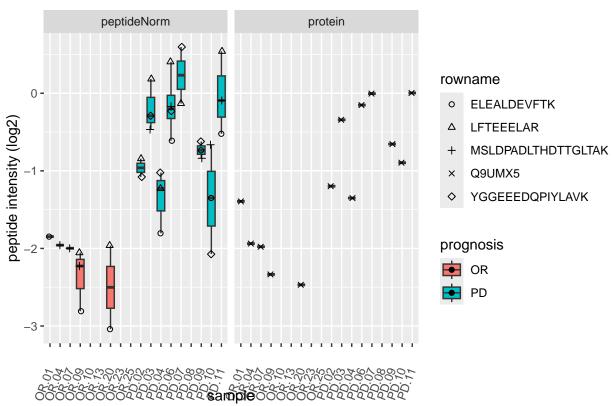
rowname

- o EATWVVDVK
- △ FVKPGAENSR
- + GSVLPNSDKK
- × HSVNNPYSQFQDEYSLDEVMASK
- ♦ HVDLLINK
- □ IGGIFAFK
- ITGNMGLAMK
- * KLEEEGEQFVK
- ♦ KLEEEGEQFVKK
- ⊕ LEEEGEQFVK
- MGFPEAASSFR
- MNPQSAFFQGK
- P22307
- VFVVGVGMTK
- WVINPSGGLISK

Q9UMX5



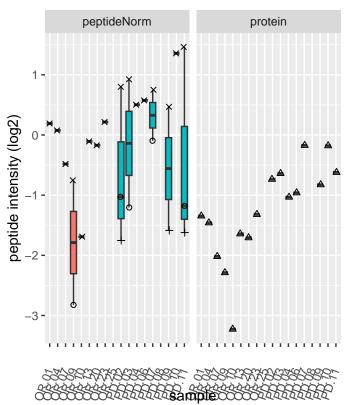
Q9UMX5



O60888



O60888



prognosis

OR

pD PD

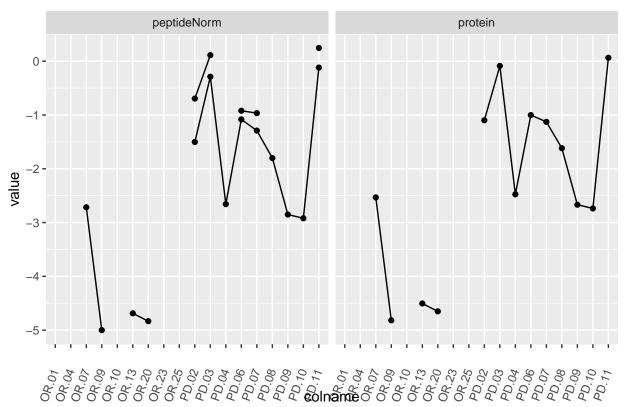
rowname

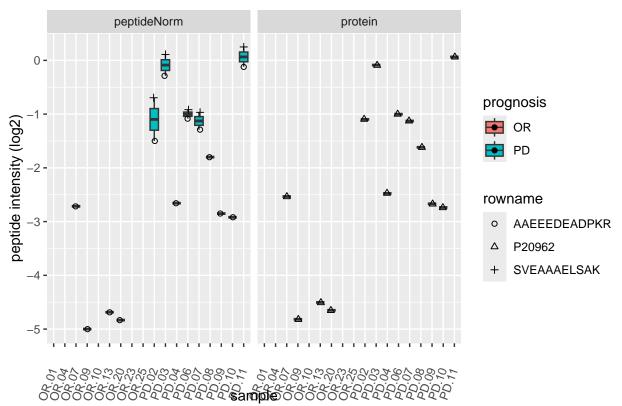
- GKIEEDSEVLMMIK
- Δ O60888
- + SVHPYEVAEVIALPVEQGNFPYLQWVR
- × TQSSLVPALTDFVR

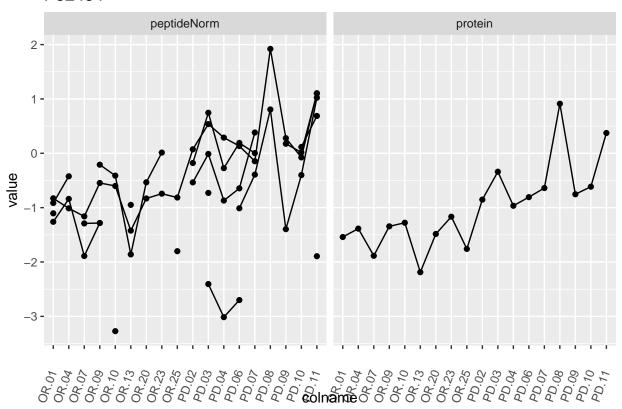
Q14980

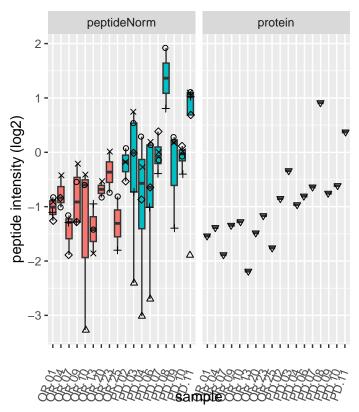


	u	IIQVLQLOOOLN	J	LLWAL IAUNUAN	J	WLWI ILF
		HREELEQSK	9	LPPKVESLESLYFTPIPAR	K	QFCSTC
١R	(IATTTASAATAAAIGATPR	:	LQAQLNELQAQLSQK	L	QFLEVE
)	IHGTEEGQQILK	;	LQNALNEQR	М	QLEALE
AAGR		INQLSEENGDLSFK	<	LQQLGEAHQAETEVLR	N	QPEWLE
3EAAGR	+	IQAELAVILK	=	LQQLGEAHQAETEVLRR	0	QQEQAI
≀QEQASQGLR	,	KHPSSPECLVSAQK	>	LSQLEEHLSQLQDNPPQEK	Р	QQLSSL
ESECEQLVK	-	KINQLSEENGDLSFK	?	LTAQVASLTSELTTLNATIQQQDQELAGLK	Q	QQNELA
ГМР	•	KLDVEEPDSANSSFYSTR	@	LTAQVEQLEVFQR	R	QQNQEI
	/	KNSLISSLEEEVSILNR	Α	LVMAESEK	S	RSQAG\
	0	KQQNQELQEQLR	В	MTMLLLYHSTMSSK	Т	SAPASQ
	1	KVEELQACVETAR	С	NSLISSLEEEVSILNR	U	SLEAQV
STQALVSELLPAK	2	LADDLSTLQEK	D	PSLSLGTITDEEMK	٧	SLVEQH
	3	LALLNEK	E	Q14980	W	SNRDEL
EDLENFLQK	4	LDFVCSFLQK	F	QAQLAQTLQQQEQASQGLR	Х	SNRDEL
LK	5	LEILQQQLQVANEAR	G	QDHAQQLATAAEER	Υ	SQAPLE
\AEKR	6	LGHELQQAGLK	н	QEAATLAANNTQLQAR	Z	SQAPLE









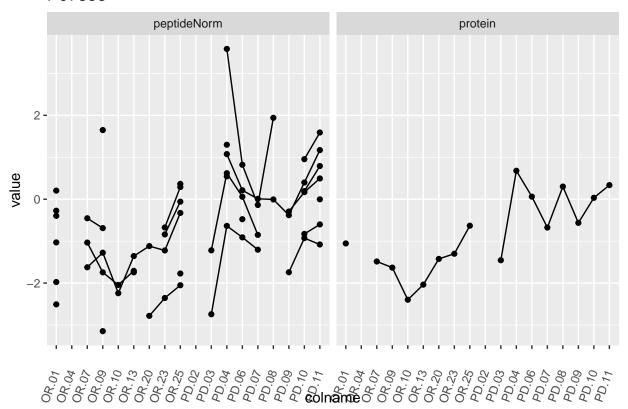
rowname

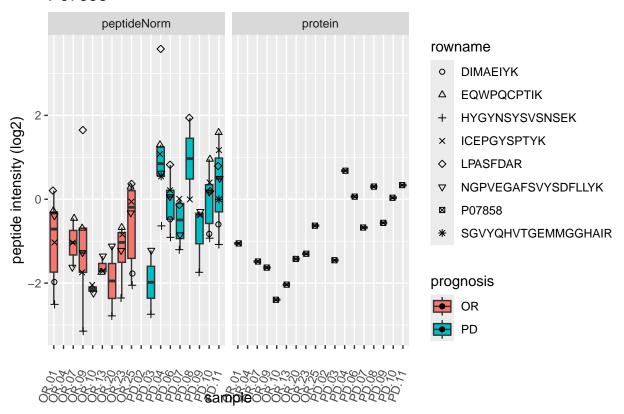
- AGILFEDIFDVK
- △ AGILFEDIFDVKDIDPEGK
- + IEGDETSTEAATR
- × LQGDANNLHGFEVDSR
- ♦ LVIASTLYEDGTLDDGEYNPTDDRPSR
- ▽ P52434

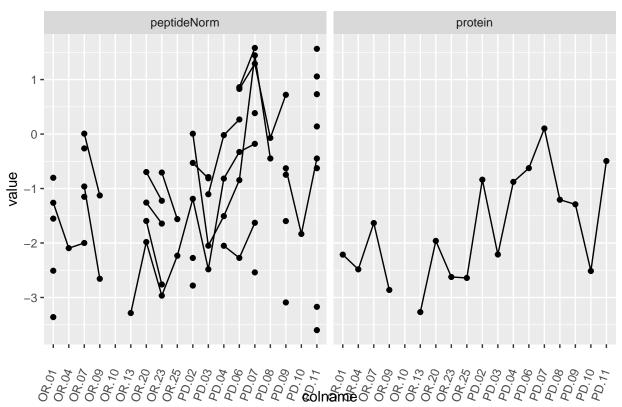
prognosis

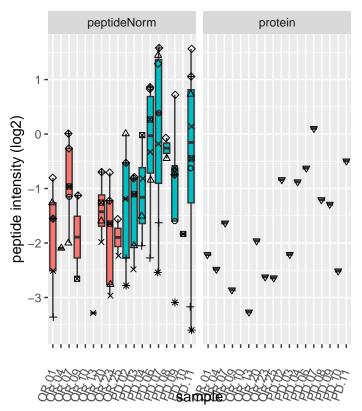












rowname

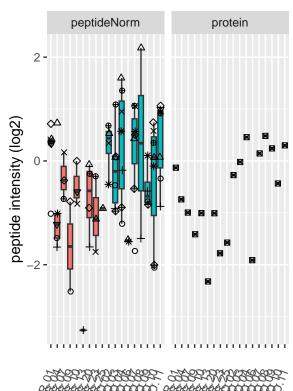
- AAAPAPVSEAVCR
- △ DTMSDQALEALSASLGTR
- + EADPEDGKPVMDK
- × KTEKEESTEVLK
- ♦ LAAAISEVVSQTPASTTQAGAPPR
- ▽ P20810
- SLTPAVPVESKPDKPSGK
- * TEKEESTEVLK
- ◆ TKPQDMISAGGESVAGITAISGKPGDK

prognosis



pD PD





rowname

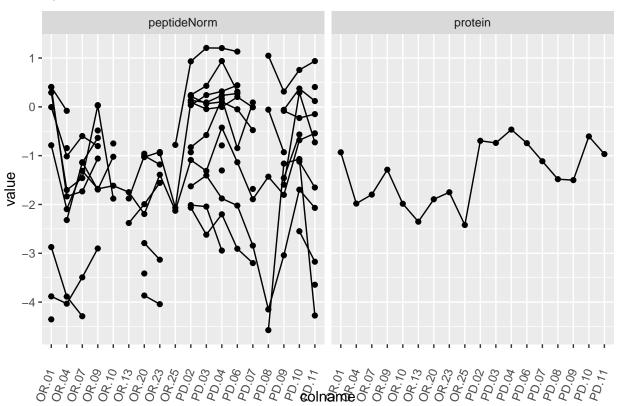
- ALDVGSGSGILTACFAR
- ELVDDSVNNVR
- KDDPTLLSSGR
- LILPVGPAGGNQMLEQYDK
- \Diamond LILPVGPAGGNQMLEQYDKLQDGSIK
- MGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR ∇
- P22061
- SGGASHSELIHNLR
- VFEVMLATDR
- VQLVVGDGR

prognosis





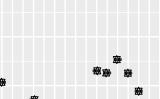
Q9Y266

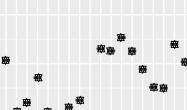


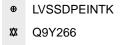
Q9Y266 peptideNorm

peptide intensity (log2)









LSDLDSETR

DAENHEAQLK

FMDQHPEMDFSK

KDAENHEAQLK

KINPENSK

GQPAIIDGELYNEVK

LITQTFSHHNQLAQK LKPNLGNGADLPNYR

ELTDEEAER

+

 \Diamond

 ∇

- SETSGPQIK ⊞ TDFFIGGEEGMAEK
- VEESSWLIEDGK

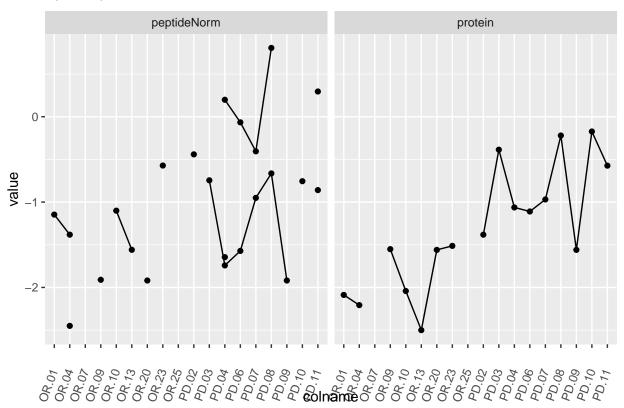
KOKOKOKO ZALAZA ZA Sample KOKOKOKA ZALAZA ZA

prognosis

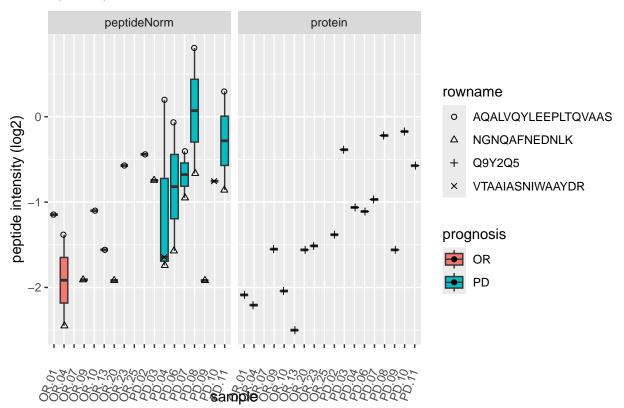


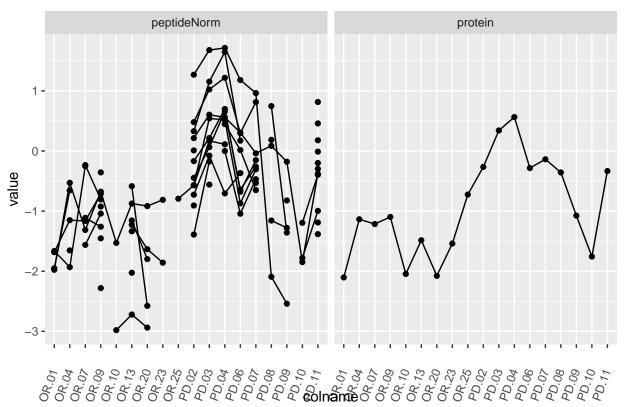


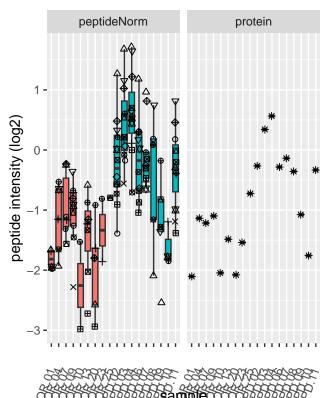
Q9Y2Q5



Q9Y2Q5







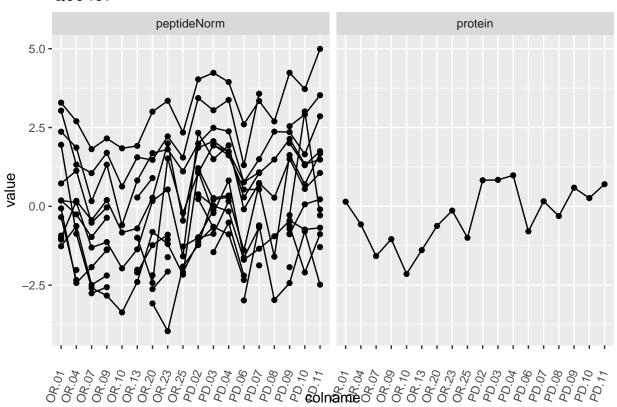
- DGAVNGPSVVGDQTPIEPQTSIER
- Δ **EAQLYAAQAHLK**
- EIEELKELLPEIR
- **EQVYDAMGEKEEAK**
- EVSEEQPVVTLEK ****
- GGAAPEGPNEAEVTSGKPEQEVPDAEEEK
- LSVEESEAAGDGVDTK
- P49321
- QGTAVEVEAESLDPTVKPVDVGGDEPEEK
- **SGNVAELALK**
- **SIEVIENR** 苁
- SLAKPETDKEQDSEMEK
- SLLELAR
- VDLTLDWLTETSEEAK

prognosis

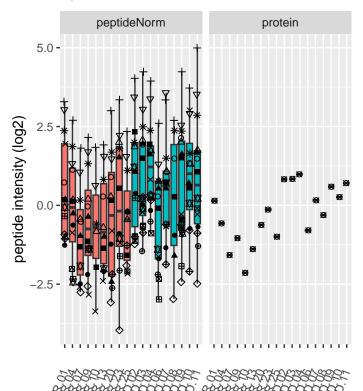




Q99497



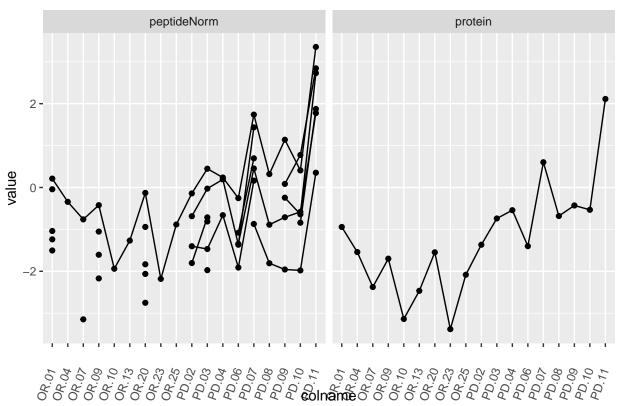
Q99497

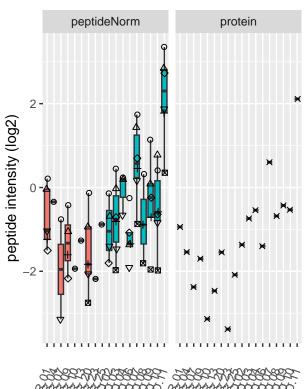




rowname

- o DGLILTSR
- △ DVVICPDASLEDAKK
- + EGPYDVVVLPGGNLGAQNLSESAAVK
- × EILKEQENR
- ♦ EILKEQENRK
- □ GAEEMETVIPVDVMR
- GLIAAICAGPTALLAHEIGFGSK
- * GPGTSFEFALAIVEALNGK
- ◆ GPGTSFEFALAIVEALNGKEVAAQVK
- ⊕ KGLIAAICAGPTALLAHEIGFGSK
- **☎** MMNGGHYTYSENR
- **■** MMNGGHYTYSENRVEK
- ☑ VEKDGLILTSR
- VTTHPLAK
- VTVAGI AGK





rowname

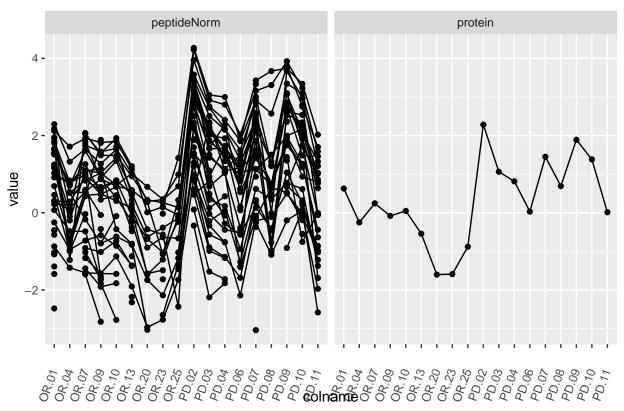
- AEEYEFLTPVEEAPK
- AEQEPTAEQLAQIAAENEEDEHSVNYKPPAQK
- IDKTDYMVGSYGPR
- P52565
- SIQEIQELDKDDESLR
- SIQEIQELDKDDESLRK
- YIQHTYR

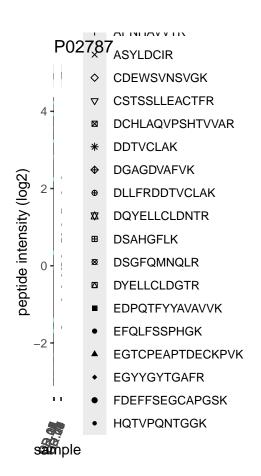
prognosis





PD





- V IIVIINGEADAIVIGEDGGI VITAGIN
- △ KASYLDCIR
- ▼ KPVDEYKDCHLAQVPSHTVVAR

KPVEEYANCHLAR

LCMGSGLNLCEPNNK

LKCDEWSVNSVGK

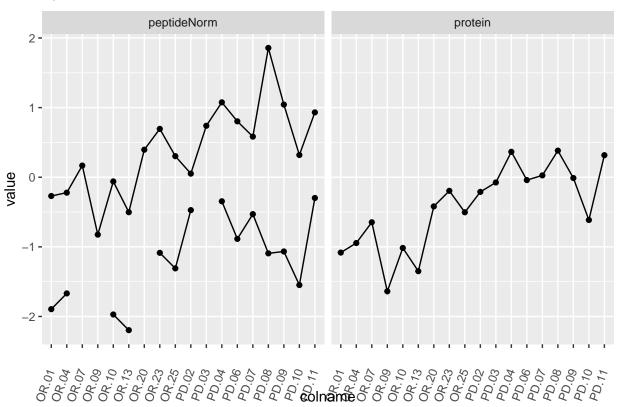
MYLGYEYVTAIR

NLNEKDYELLCLDGTR

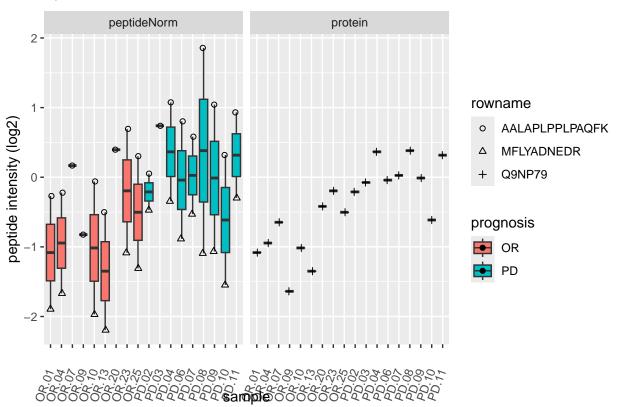
NPDPWAK

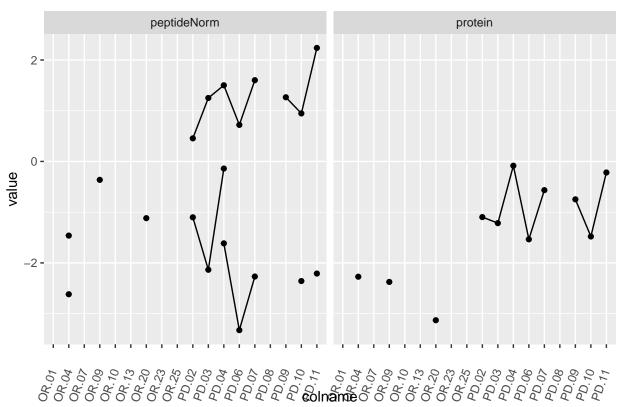
- SAGWNIPIGLLYCDLPEPR
- SASDLTWDNLK
- # SKEFQLFSSPHGK
- SVIPSDGPSVACVK
- * TAGWNIPMGLLYNK
- WCALSHHER
- WCAVSEHEATK
- YLGEEYVK

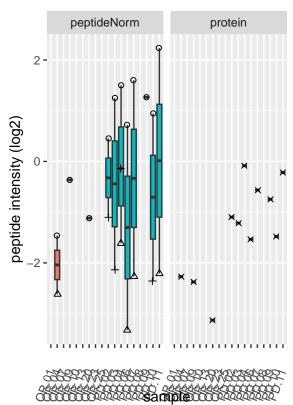
Q9NP79



Q9NP79







rowname

- ATVEPETTPTPNPPTTEEEKTESNQEVANPEHYIK
- **EAVTHIGR**
- IVIGYQSHADTATK
- P06730

prognosis

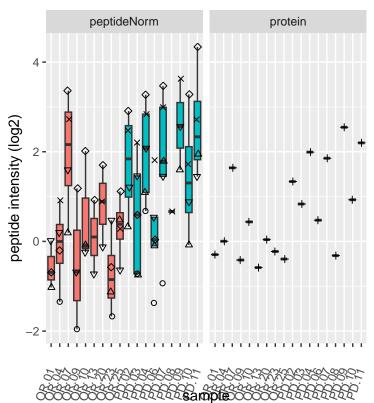


OR



PD





rowname

- AKHDELTYF
- △ MMCGAPSATQPATAETQHIADQVR
- + P04080
- × SQVVAGTNYFIK
- ◇ VFQSLPHENKPLTLSNYQTNK
- ∇ VHVGDEDFVHLR

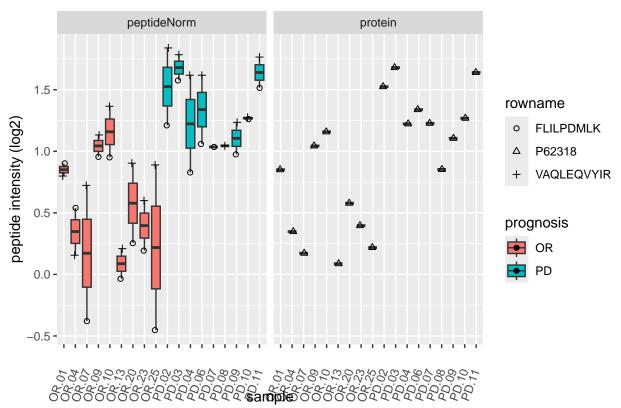
prognosis



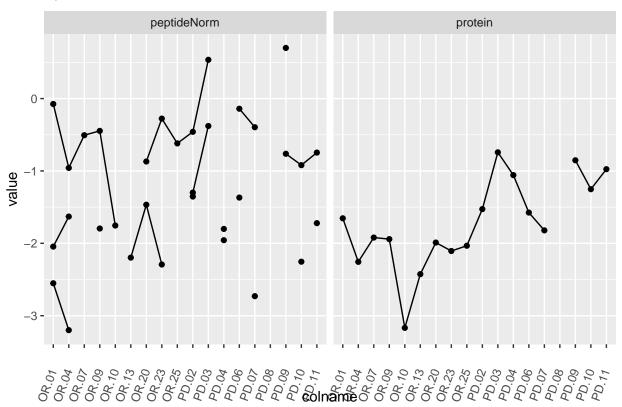
OR



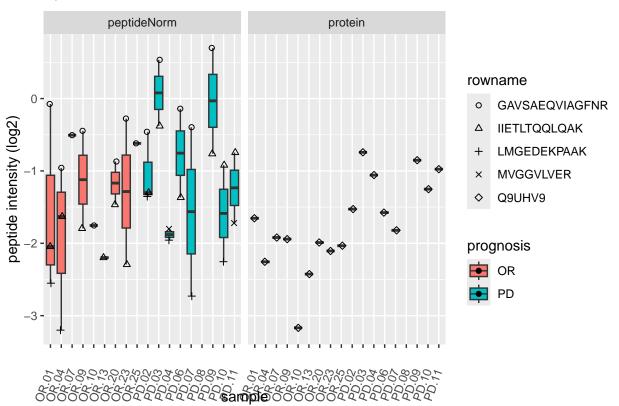


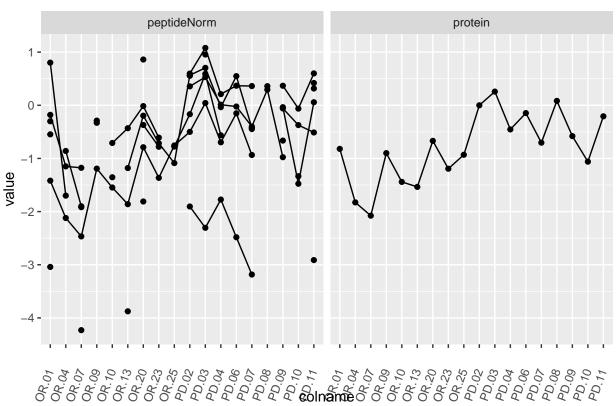


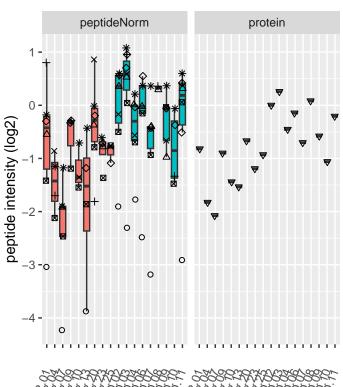
Q9UHV9



Q9UHV9







prognosis

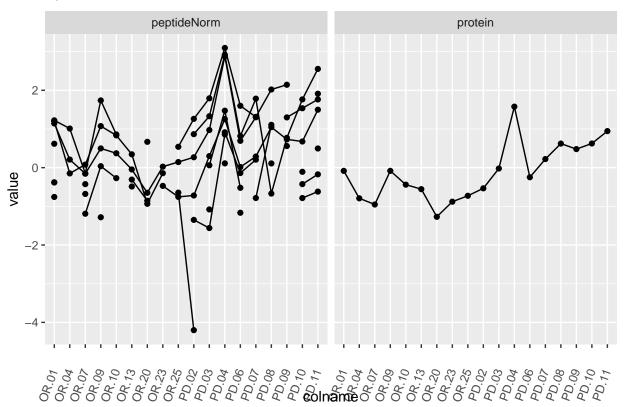


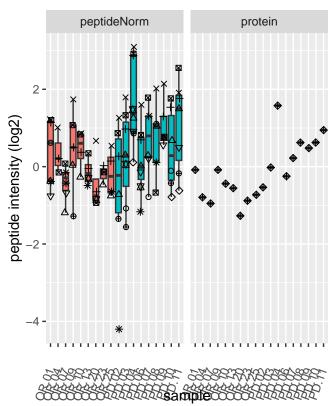
OR PD



rowname

- EVLKSEETSK
- △ GEIAGPPDTPYEGGR
- + IPETYPFNPPK
- × LWAHVYAGAPVSSPEYTK
- ♦ NAVIVALSSK
- ▽ P61086
- SWDVETATELLLSN
- * VDLVDENFTELR
- ♦ VDLVDENFTELRGEIAGPPDTPYEGGR





rowname

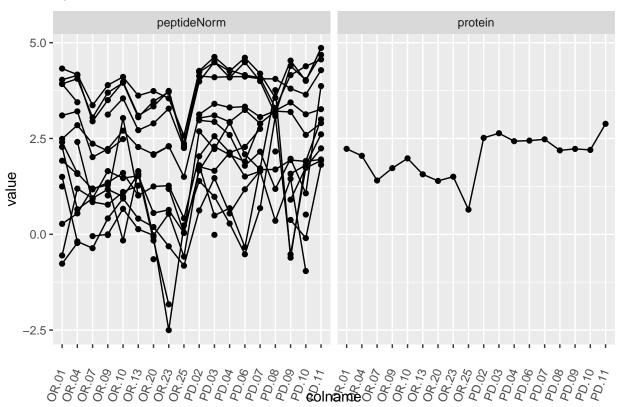
- IPIHNEDITYDELVLMMQR
- △ LLDSLEPPGEPGPSTNIPENDTVDGR
- + LLDSLEPPGEPGPSTNIPENDTVDGREEK
- × LLSNDEVTIK
- ♦ LTLFVNGQPR
- NVMSAFGLTDDQVSGPPSAPAEDR
- * PLESSQVK
- ♦ Q92734
- ⊕ QSTQVMAASMSAFDPLK
- □ QSTQVMAASMSAFDPLKNQDEINK

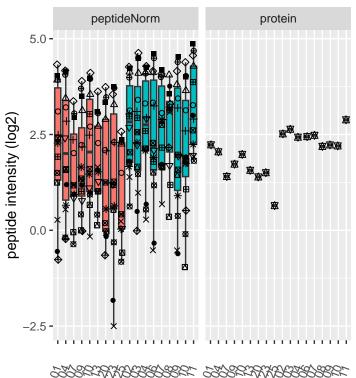
prognosis



OR







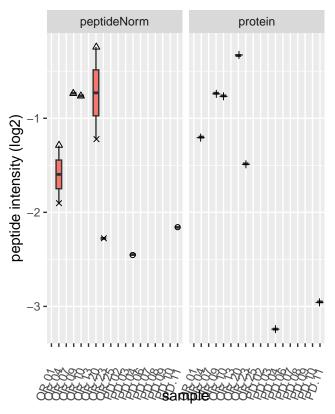
- VDFGIOLIV
- △ ATAVMPDGQFK
- + DISLSDYK
- × GKYVVFFFYPLDFTFVCPTEIIAFSDR
- ♦ HGEVCPAGWKPGSDTIKPDVQK
- ▽ IGHPAPNFK
- KQGGLGPMNIPLVSDPK
- * KQGGLGPMNIPLVSDPKR
- ◆ LNCQVIGASVDSHFCHLAWVNTPK
- ⊕ LVQAFQFTDK
- **☎** Q06830
- QGGLGPMNIPLVSDPK
- QGGLGPMNIPLVSDPKR
- SKEYFSK
- TIAQDYGVLK
- YVVFFFYPLDFTFVCPTEIIAFSDR

prognosis



OR





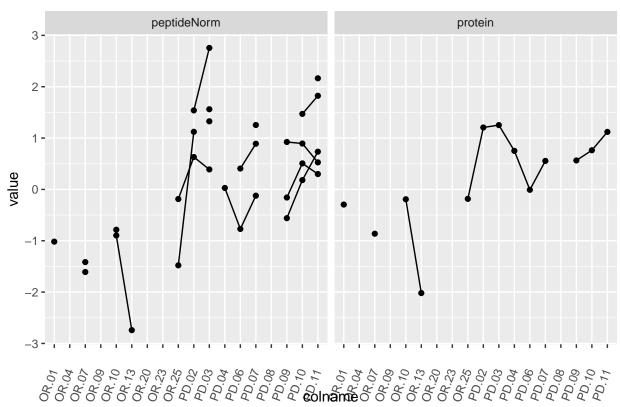
rowname

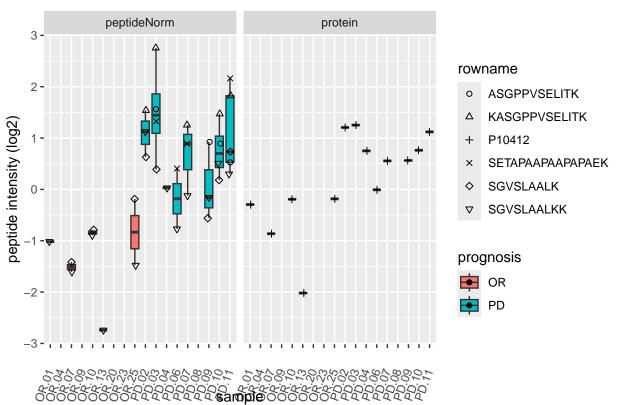
- LTESLDFTDYASR
- △ MLGTGPAAATTAATTSSNVSVLQQFASGLK
- + P42345
- × VLGLLGALDPYK

prognosis

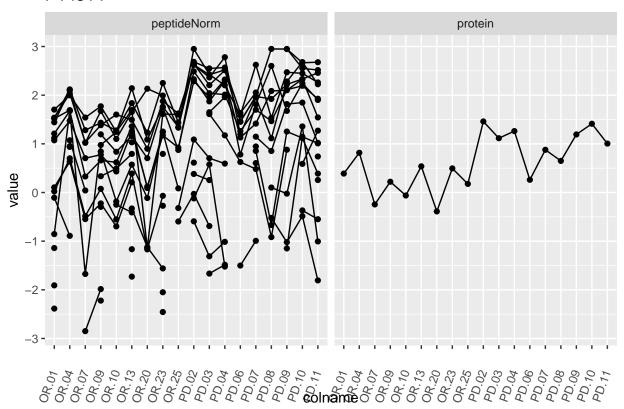


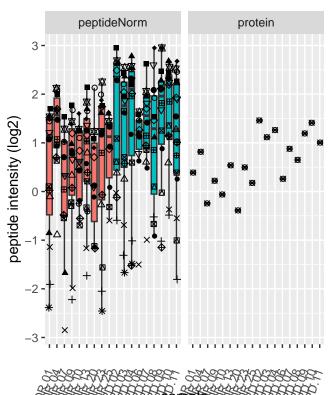






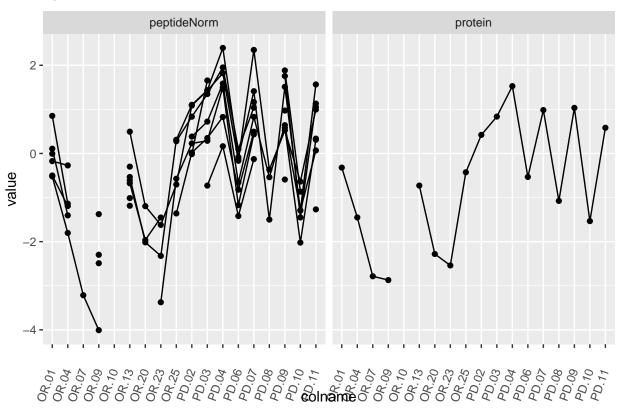
P14314

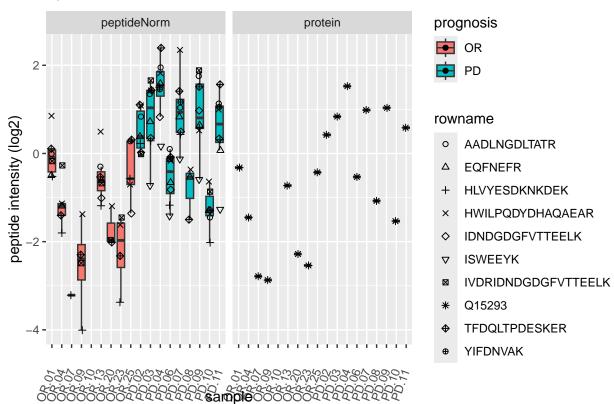




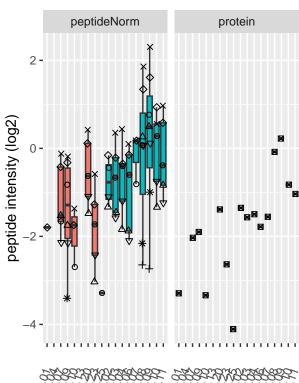
- + DMEESIR
- × ERESLQQMAEVTR
- ♦ ESLQQMAEVTR
- ▽ ETMVTSTTEPSR
- ILIEDWK
- * KLIELQAGK
- ♦ LGGSPTSLGTWGSWIGPDHDK
- LGGSPTSLGTWGSWIGPDHDKFSAMK
- NKFEEAER
- SEALPTDLPAPSAPDLTEPK
- SLEDQVEMLR
- SLKDMEESIR
- ▲ TVKEEAEKPER
- VNDGVCDCCDGTDEYNSGVICENTCK
- YEQGTGCWQGPNR

prognosis









rowname

- AAEEPSKVEEK
- AEDGATPSPSNETPK
- EAGEGGEAEAPAAEGGK
- EAPAEGEAAEPGSPTAAEGEAASAASSTSSPK
- GEAAAERPGEAAVASSPSK
- GEPAAAAAPEAGASPVEK
- P29966
- VNGDASPAAAESGAK

prognosis



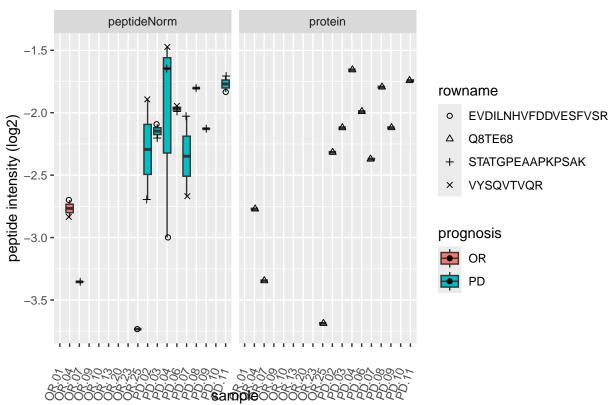




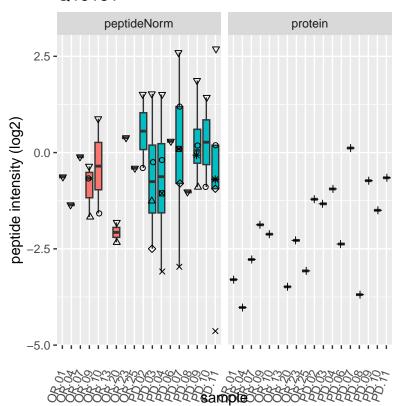
Q8TE68



Q8TE68







rowname

- AAPFSLEYR
- △ DKDFAIDIIK
- + Q15181
- × VFLKNEK
- ♦ VIAINVDDPDAANYNDINDVK
- ▼ VIAINVDDPDAANYNDINDVKR
- VLGILAMIDEGETDWK
- * YVANLFPYK

prognosis



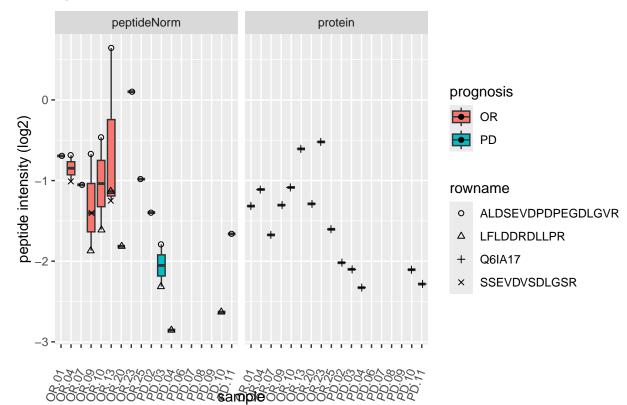
OR

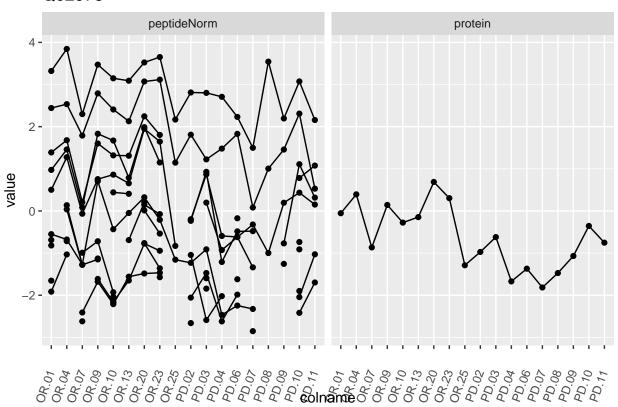


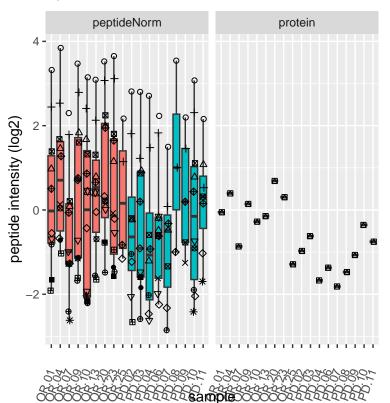
Q6IA17



Q6IA17





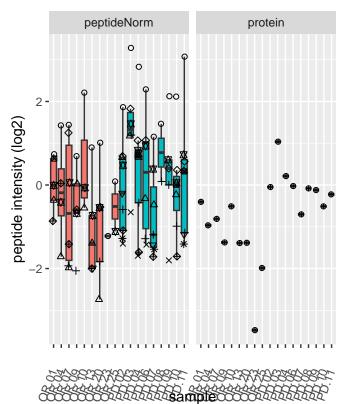


- ANIAGAGAGGIDGINI IX
- AVIGMTAGATGAFVGTPAEVALIR
- AVVVNAAQLASYSQSK
- EEGVLTLWR ×
- FLFGGLAGMGATVFVQPLDLVK \Diamond
- GIYTGLSAGLLR ∇
- LGIYTVLFER \boxtimes
- LGPHTVLTFIFLEQMNK
- LTGADGTPPGFLLK
- MIDGKPEYK
- MQLSGEGAK 苁
- **NGLDVLFK** ⊞
- **NVFNALIR** Ø
- ◩ Q02978
- RGYKNVFNALIR
- **TSFHALTSILK**

prognosis







rowname

- AEDNADTLALVFEAPNQEK
- △ ATPLSSTVTLSMSADVPLVVEYK
- + CAGNEDIITLR
- × DLSHIGDAVVISCAK
- ♦ FSASGELGNGNIK
- □ IADMGHLK
- LSQTSNVDKEEEAVTIEMNEPVQLTFALR
- * MPSGEFAR
- ♦ NLAMGVNLTSMSK
- ⊕ P12004
- ☆ YLNFFTK

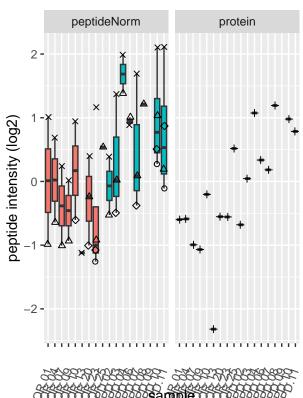
prognosis



OR







rowname

- FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK
- △ ITLTSDPR
- + P61960
- × VLSVPESTPFTAVLK
- ♦ VPAATSAIITNDGIGINPAQTAGNVFLK

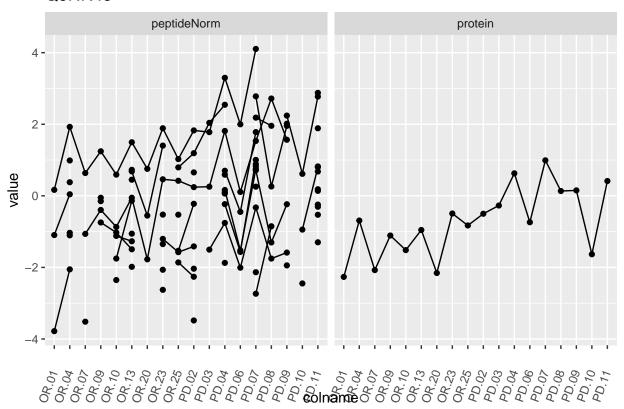
prognosis



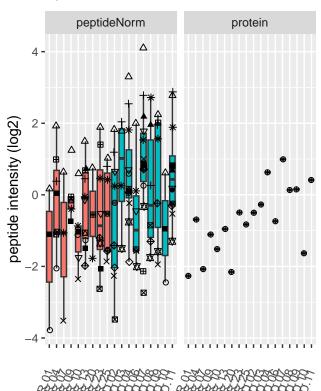
OR



Q9NR45



Q9NR45

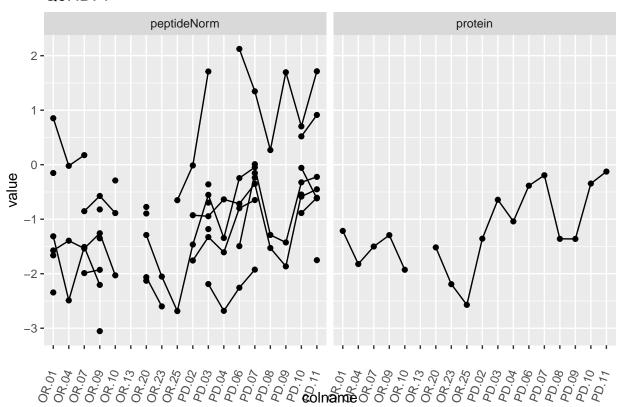


- **GSDHSASLEPGELAELVR**
- GYPPEDIFNLVGK +
- × GYPPEDIFNLVGKK
- \Diamond **HLEFSHDQYR**
- IPEGTILTMDMLTVK ∇
- KALERPYTSK
- LFPDIPIGYSGHETGIAISVAAVALGAK
- PLELELCPGR
- Q9NR45
- QLLPCEMACNEK 苁
- VGSGDTNNFPYLEK ⊞
- VISEYQK
- VKIPEGTILTMDMLTVK
- VLVTVEEDDTIMEELVDNHGK
- VLVTVEEDDTIMEELVDNHGKK
- YAEEVGIFFTASGMDEMAVEFLHELNVPFFK

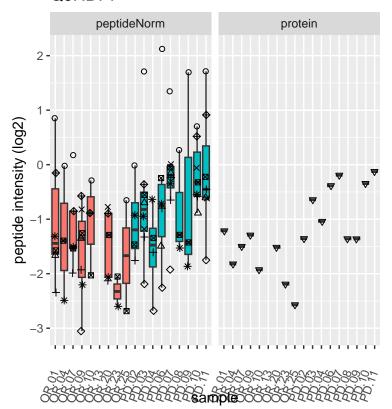
prognosis



Q9HB71



Q9HB71



rowname

- 0 ASEELQKDLEEVK
- EKPSYDTETDPSEGLMNVLK Δ
- ISNYGWDQSDK
- KAELLDNEKPAAVVAPITTGYTVK ×
- KIYEDGDDDMKR ****
- Q9HB71 ∇
- SFDLLVK
- SKIETEIK
- SYSMIVNNLLKPISVEGSSK

prognosis

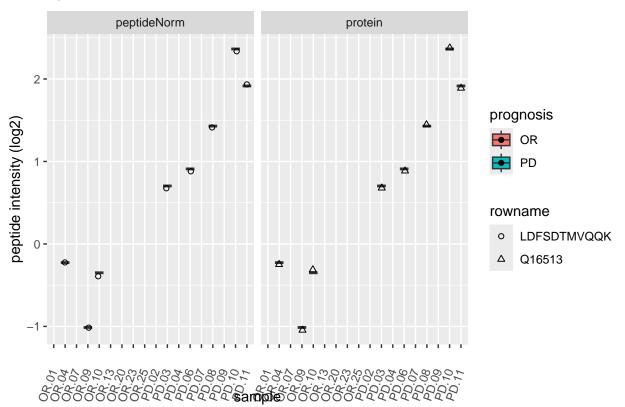


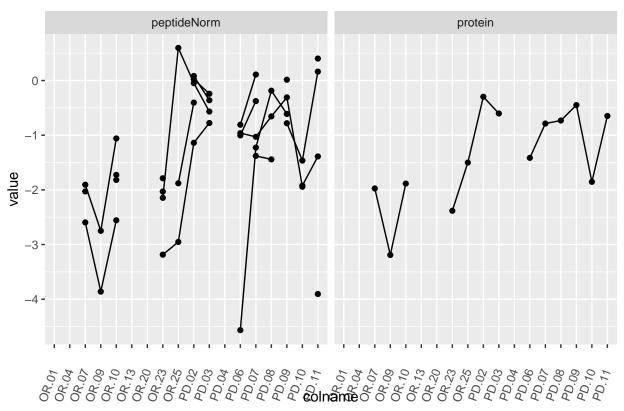


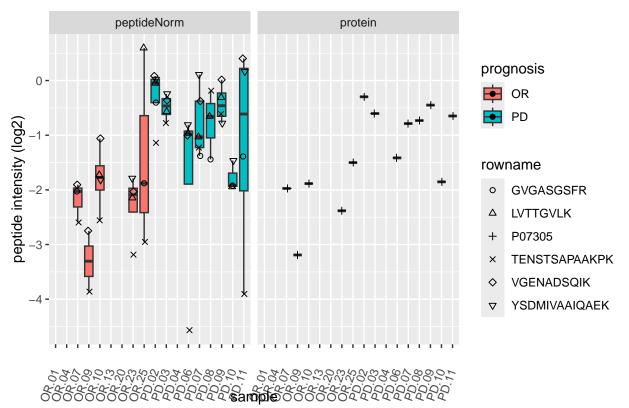
Q16513

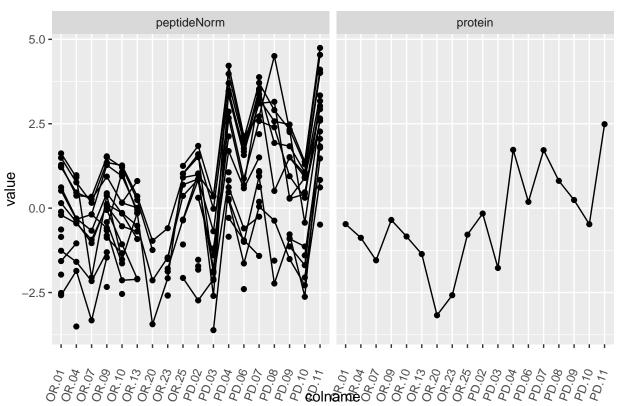


Q16513

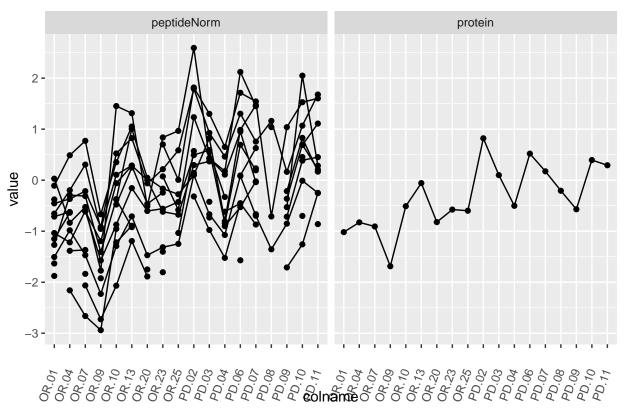


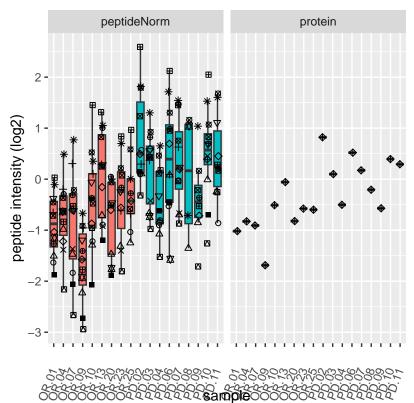












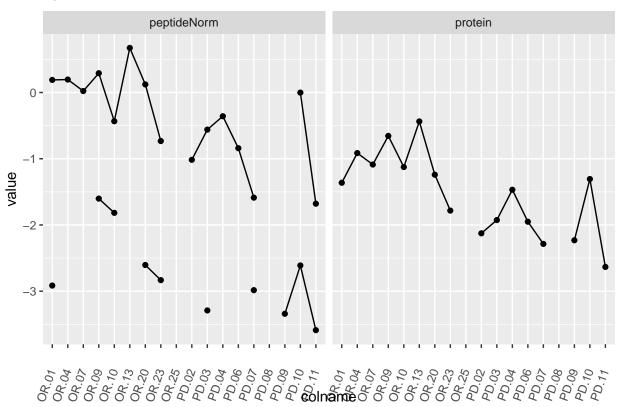
- AMMYSGELK
- △ EDLVVAPAGITLK
- + FGVPVIADGGIQNVGHIAK
- × GKLPIVNEDDELVAIIAR
- ♦ KYEQGFITDPVVLSPK
- □ LPIVNEDDELVAIIAR
- LVGIISSR
- * NLIDAGVDALR
- ♦ P12268
- ⊕ REDLVVAPAGITLK
- ☆ RFGVPVIADGGIQNVGHIAK
- TSSAQVEGGVHSLHSYEK
- VAQGVSGAVQDK
- ☑ YEQGFITDPVVLSPK
- YFSEADKIK

prognosis

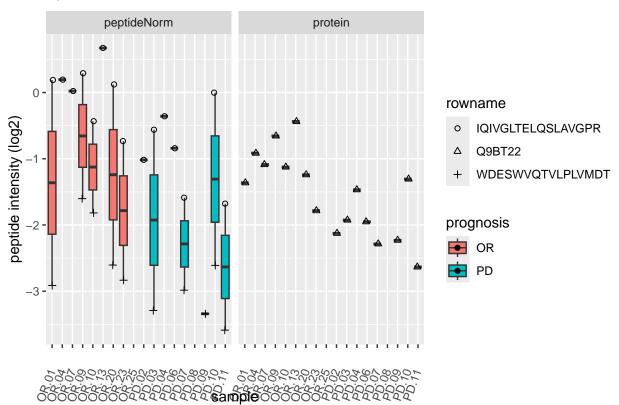


OR PD

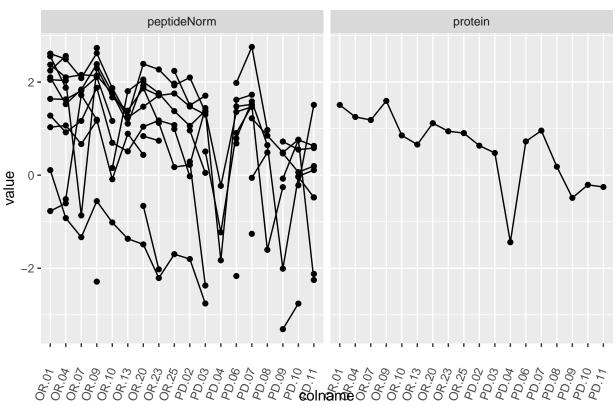
Q9BT22



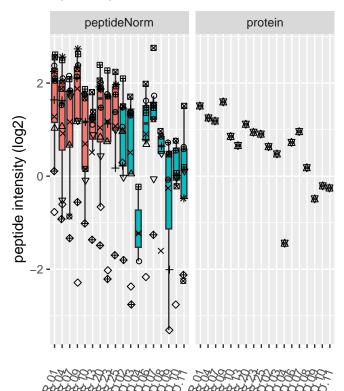
Q9BT22



Q9UHQ9



Q9UHQ9



rowname

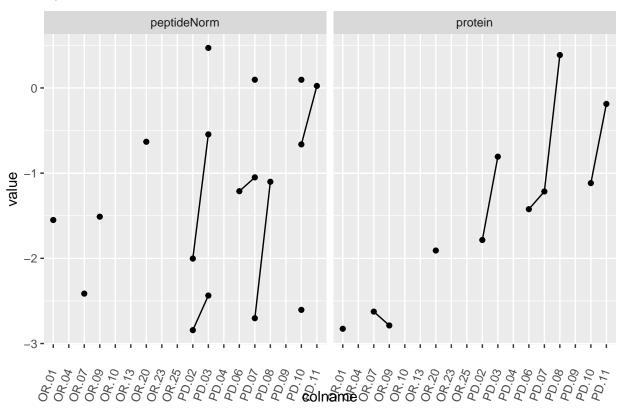
- DIILREDLEELQAR
- **EDLEELQAR**
- FALPTAHHTLGLPVGK
- **GFVTADMIR** ×
- **GHFNIQPNKK** \Diamond
- GIQTSPVLLASLGVGLVTLLGLAVGSYLVR ∇
- **GPSGLLTYTGK**
- IDGSLVIRPYTPVTSDEDQGYVDLVIK
- LGMIAGGTGITPMLQLIR
- MSQYLDSLK
- Q9UHQ9 苁
- RPQVTLLDPNEK
- VGDVVEFR

prognosis

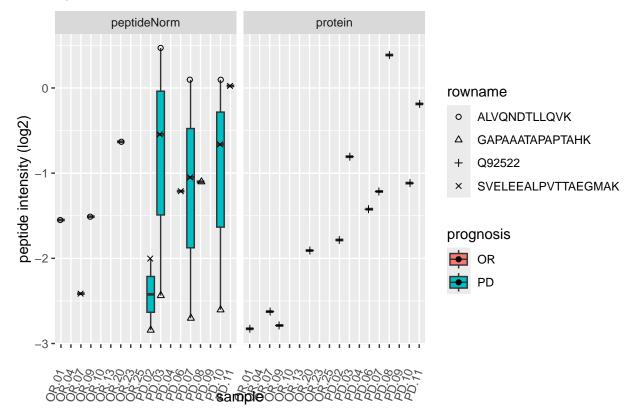




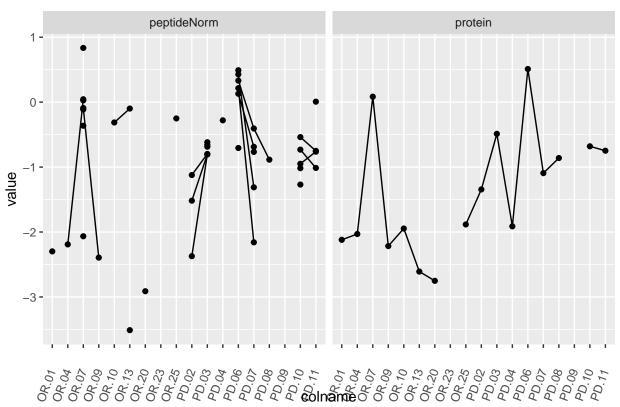
Q92522



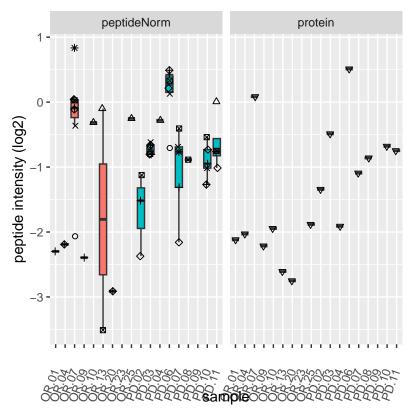
Q92522



O15327



O15327



rowname

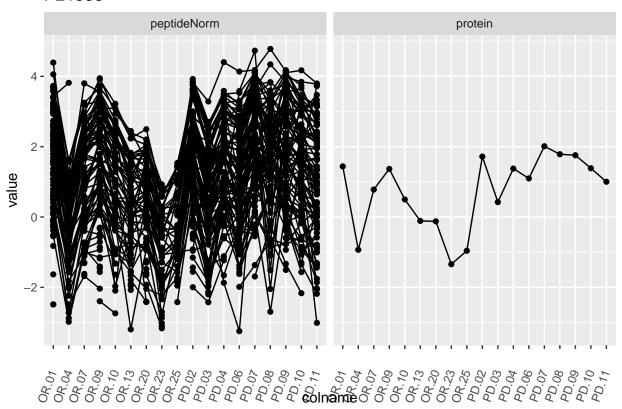
- DALYDVITVGAPAAHFQGFK
- △ LTVYDVK
- + MFESLPLQIK
- × MGEIEDGEADHITTDVQGQK
- ♦ NTGYQFIYYSPENTAK
- ▽ O15327
- SSTEESSPQDQPPVMR
- * TLEFVPINLHLQR
- ♦ VVGTIEVSVVK

prognosis



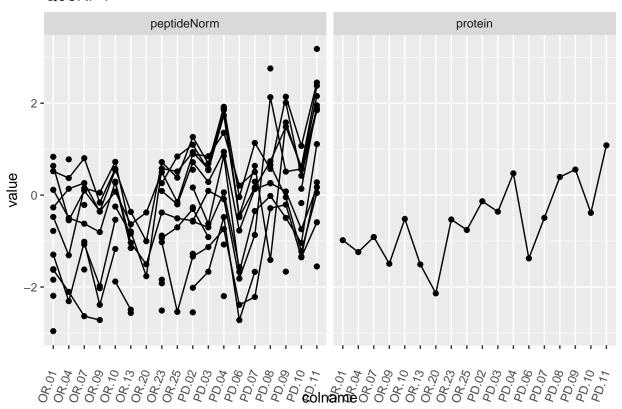
OR



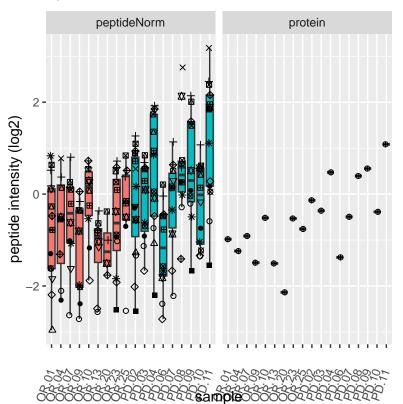


)	GAGSYTIMVLFADQATPTSPIR	<	LVSNHSLHETSSVFVDSLTK
√K	٠	GAGTGGLGLAVEGPSEAK	=	LYSVSYLLK
TYGGHQVPGSPFK	+	GKLDVQFSGLTK	>	MDCQECPEGYR
	,	GLVEPVDVVDNADGTQTVNYVPSR	?	NDNDTFTVK
IVTITWGGQNIGR	-	GQHVPGSPFQFTVGPLGEGGAHK	@	NGHVGISFVPK
	•	GTVEPQLEAR	Α	NGQHVASSPIPVVISQSEIGDAS
	/	HTAMVSWGGVSIPNSPFR	В	P21333
	0	IANLQTDLSDGLR	С	PGAPLRPK
IVDPNVDEHSVMTYLSQFPK	1	IECDDKGDGSCDVR	D	RAEFTVETR
	2	IPEISIQDMTAQVTSPSGK	Е	RAPSVANVGSHCDLSLK
PFPLEAVAPTKPSK	3	IVGPSGAAVPCK	F	RLTVSSLQESGLK
	4	KGEITGEVR	G	SADFVVEAIGDDVGTLGFSVEGF
	5	KTHIQDNHDGTYTVAYVPDVTGR	н	SAGQGEVLVYVEDPAGHQEEAK
	6	LDVQFSGLTK	1	SPFEVYVDK
	7	LIALLEVLSQKK	J	SPFSVAVSPSLDLSK
⊋PSVQPPLR	8	LLGWIQNKLPQLPITNFSR	К	SPYTVTVGQACNPSACR
DAR	9	LQVEPAVDTSGVQCYGPGIEGQGVFR	L	TFSVWYVPEVTGTHK

Q96KP4



Q96KP4





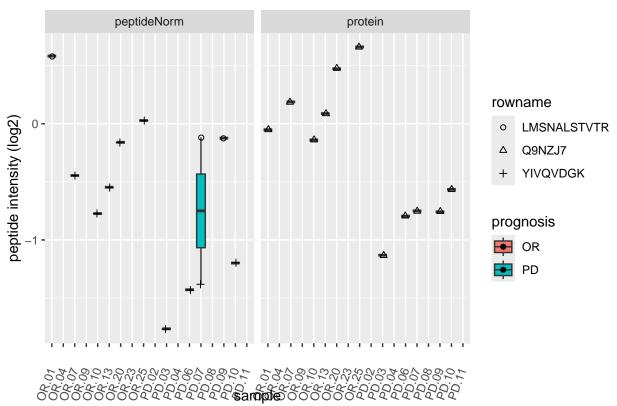
rowname

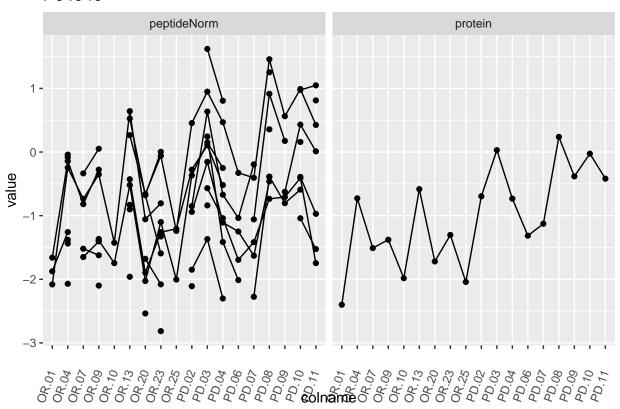
- AALTTLFK
- △ DVGAQILLHSHK
- + EGGSIPVTLTFQEATGK
- × GNILIPGINEAVAAVTEEEHK
- ♦ LPDGSEIPLPPILLGR
- □ LVPNMTPEVVGEQVTSYLTK
- LYDDIDFDIEEFAK
- * MMEVAAADVK
- ♦ NVMLLPVGSADDGAHSQNEK
- ⊕ Q96KP4
- ☆ QKLPDGSEIPLPPILLGR
- QLGGSVELVDIGK
- TGQEIPVNVR
- TVFGVEPDLTR
- WVAIQSVSAWPEK

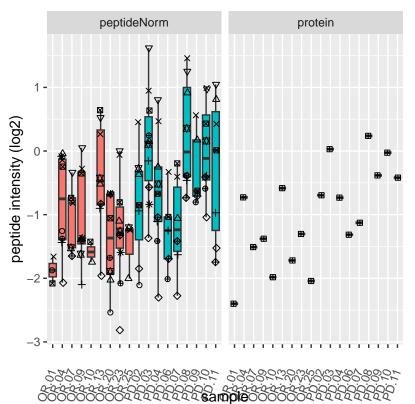
Q9NZJ7



Q9NZJ7







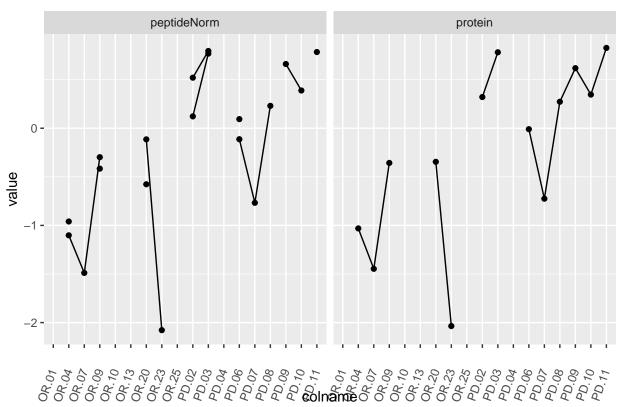
prognosis

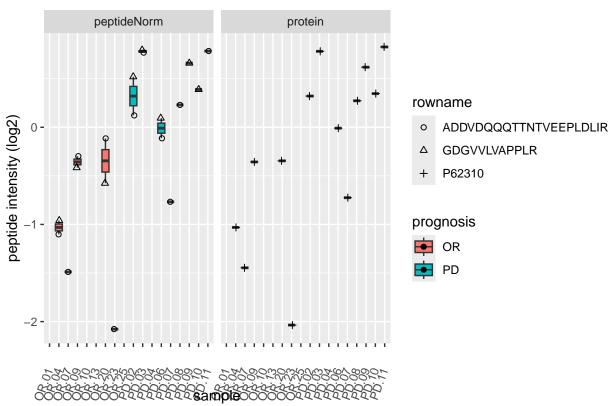




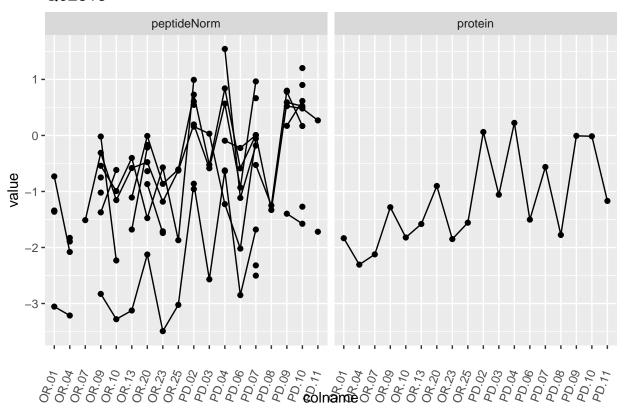
rowname

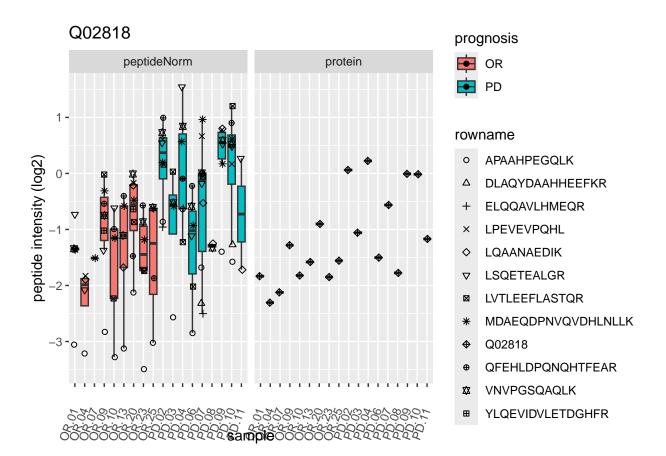
- ADSRDPASDQMQHWKEQR
- △ ADVLTTGAGNPVGDK
- + AFYVNVLNEEQR
- × FNTANDDNVTQVR
- ♦ FSTVAGESGSADTVR
- ▼ FSTVAGESGSADTVRDPR
- GAGAFGYFEVTHDITK
- * LGPNYLHIPVNCPYR
- ♦ LNVITVGPR
- ⊕ LSQEDPDYGIR
- **■** P04040

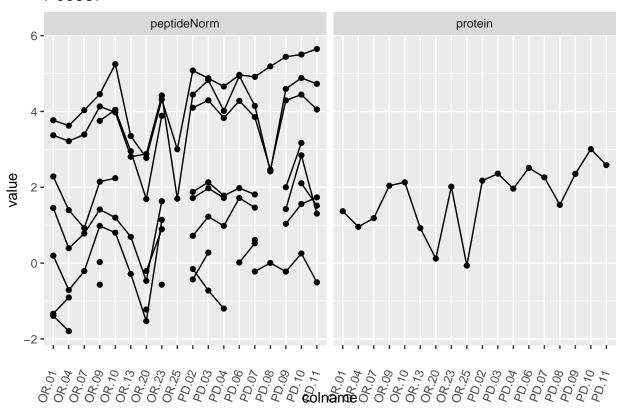


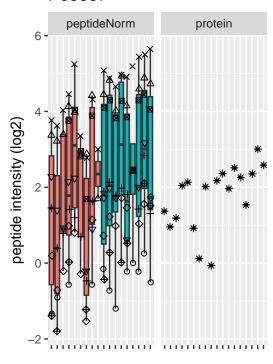


Q02818









prognosis

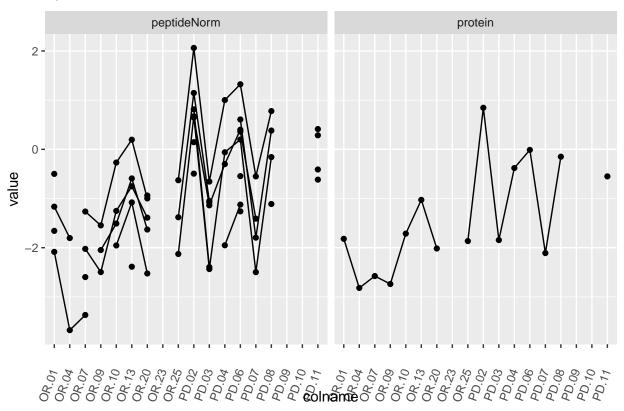


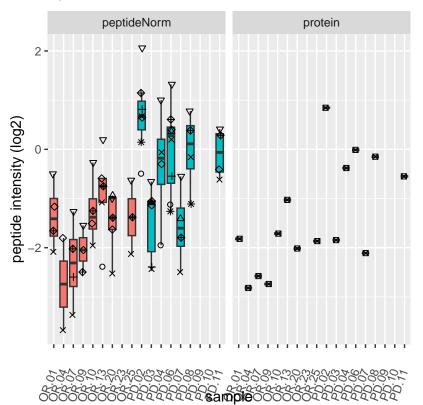
OR



rowname

- ILDSVGIEADDDR
- ILDSVGIEADDDRLNK
- KILDSVGIEADDDRLNK
- LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK
- LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEK \Diamond
- MRYVASYLLAALGGNSSPSAK
- NIEDVIAQGIGK
- P05387
- YVASYLLAALGGNSSPSAK





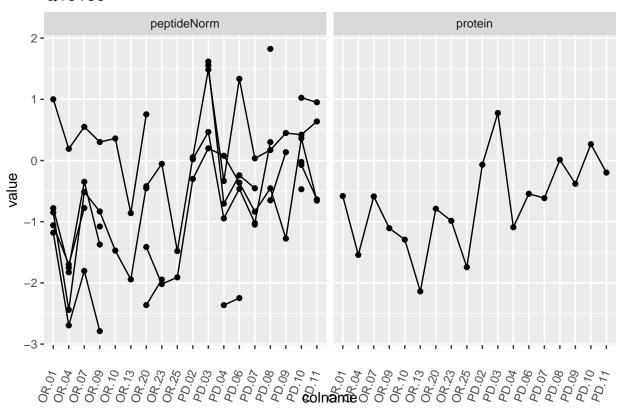
rowname

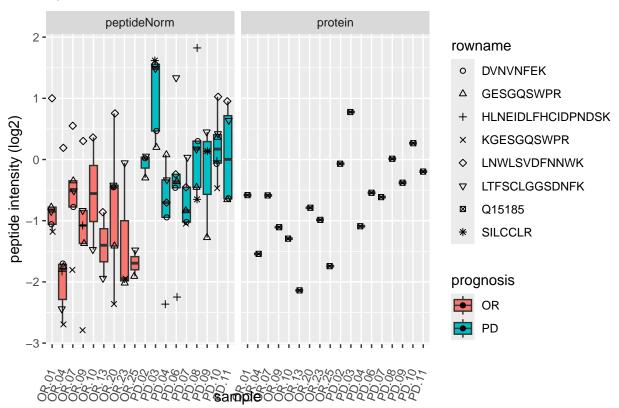
- AWDIGVATMK
- △ DVAFTVGEGEDHDIPIGIDK
- + EKLEQAAIVK
- × FAEQDAKEEANK
- ♦ FGIEPNAELIYEVTLK
- □ GTDSQAMEEEKPEGHV
- Q13451
- * VGNGEETPMIGDK
- ♦ VLEVNPQNK

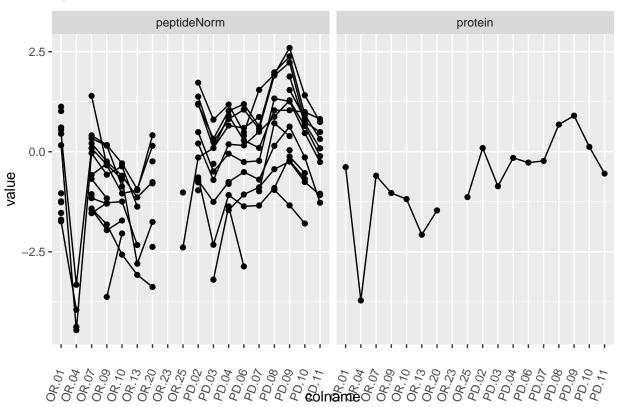
prognosis

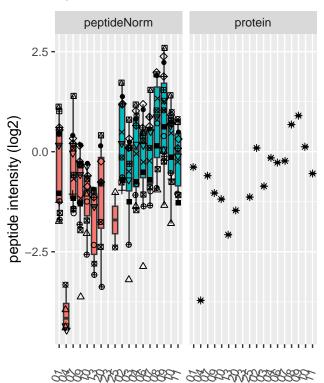


PD







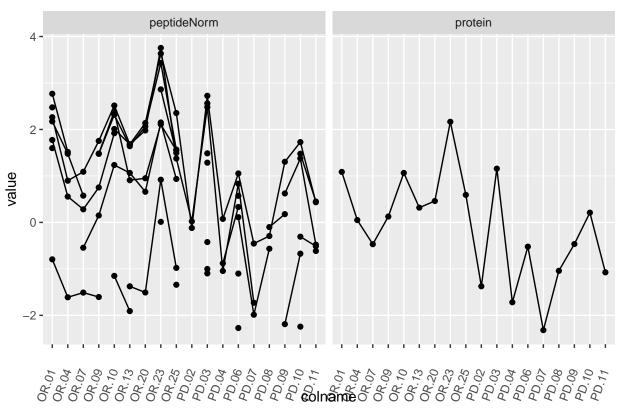


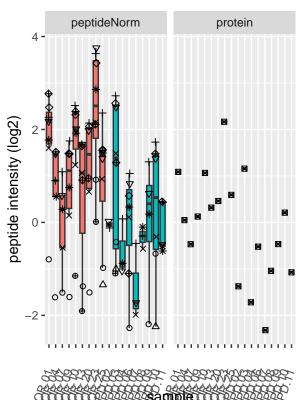
COCCOOL DE LE CONTROL DE LA CO

- LALGAI QVLAGN
- **EAEGAPQVEAGKR** Δ
- EFDPTITDASLSLPSR
- GNVFSSPTAAGTPNK ×
- LEQYTSAIEGTK \Diamond
- MQNDTAENETTEKEEK ∇
- **PSDLRPGDVSSK**
- Q05682
- QKQEEESLGQVTDQVEVNAQNSVPDEEAK
- **RGETESEEFEK** Φ
- 苁 RRGETESEEFEK
- SAKPTKPAASDLPVPAEGVR
- STHQAAIVSK Ø
- TTTTNTQVEGDDEAAFLER
- VLEEEEQR
- YEIEETETVTK

prognosis







rowname

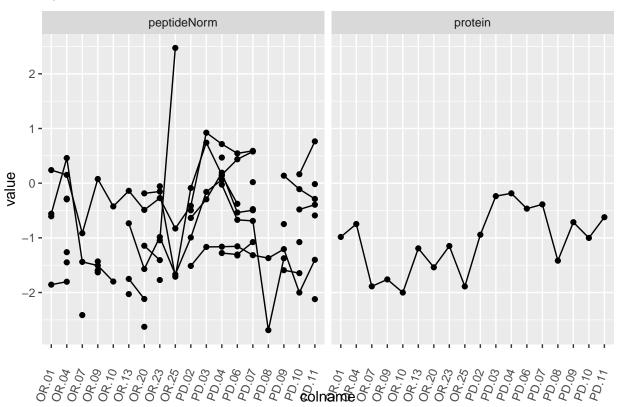
- APVAGTCYQAEWDDYVPK
- △ CDEPILSNR
- + GNDISSGTVLSDYVGSGPPK
- × LYEQLSGK
- ♦ LYTLVLTDPDAPSR
- ▽ NRPTSISWDGLDSGK
- P30086
- * VLTPTQVK
- ♦ WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK
- ⊕ YVWLVYEQDRPLK

prognosis

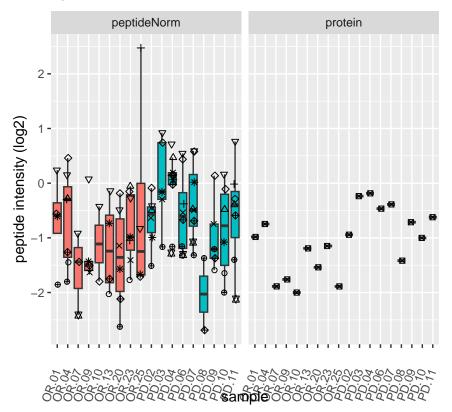


📘 PD

Q9HAB8



Q9HAB8



rowname

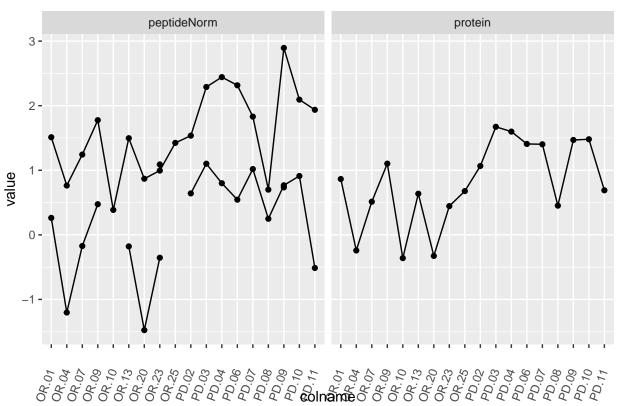
- AFIISFK
- △ FLDNFSSGR
- + IQSSGGPLQITMK
- × IVDNLQSR
- ♦ LETDPAIVINR
- □ LLLSEEEIEKGVEIEEK
- Q9HAB8
- * QSFVFIVTK
- ♦ RVVLVTSGGTK
- ♥ VVLVTSGGTK
- ₩AEVMAR

prognosis

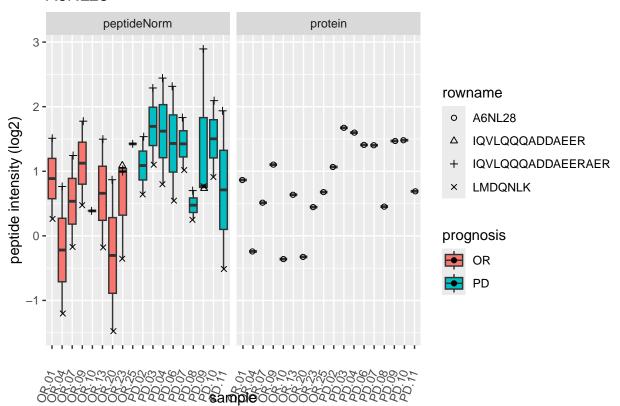


🙀 PD

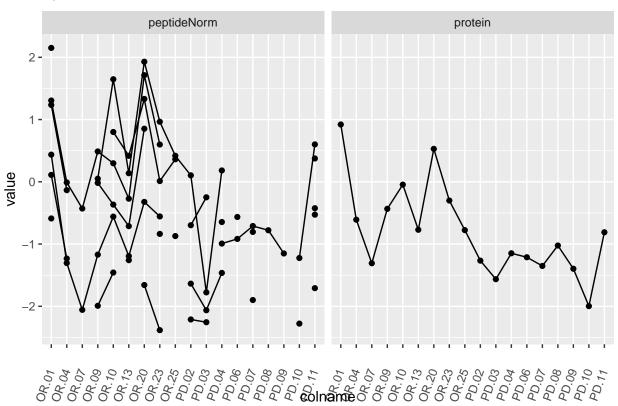
A6NL28



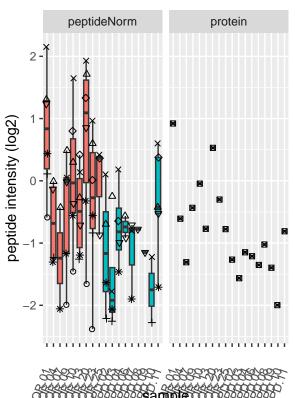
A6NL28



Q9H936



Q9H936



rowname

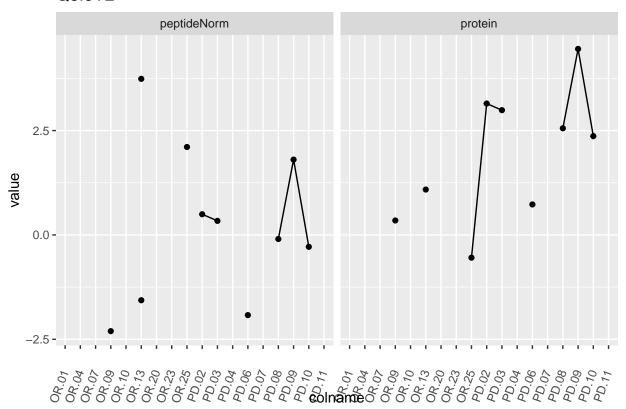
- DVPFSVVYFPLFANLNQLGRPASEEK
- GAAVNLTLVTPEK
- GLGATLLR +
- ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR ×
- KILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR **\rightarrow**
- LAANDFFR ∇
- × Q9H936
- SEGYFGMYR

prognosis

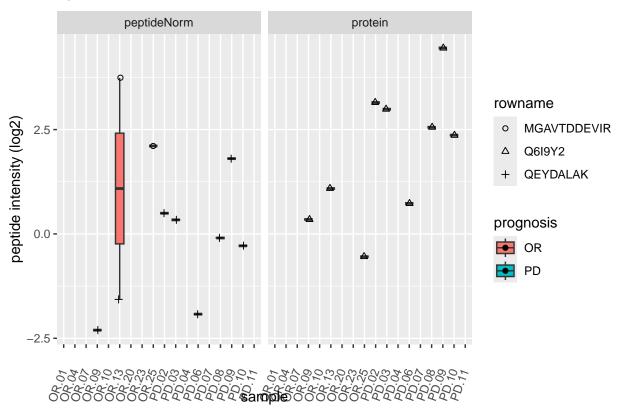




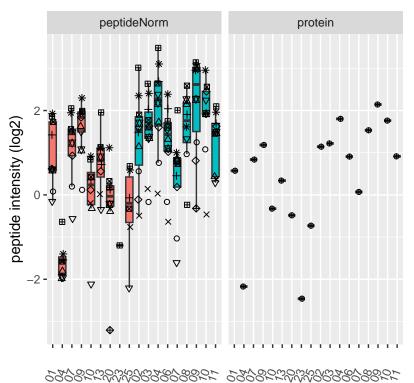
Q6I9Y2



Q6I9Y2







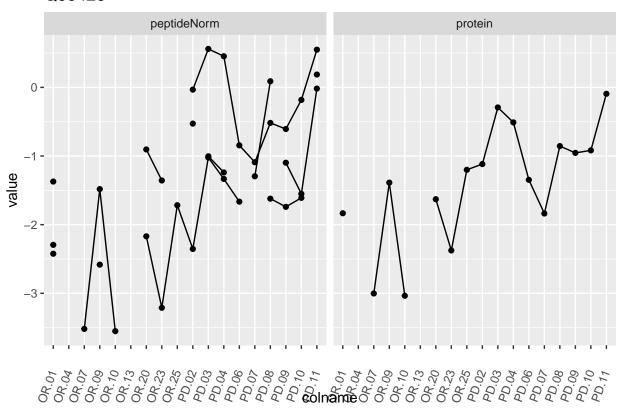
rowname

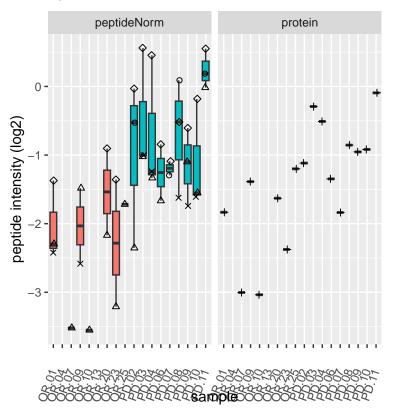
- AEGDVAALNR
- △ AGLNSLEAVK
- + AGLNSLEAVKR
- × CGDLEEELKNVTNNLK
- ♦ EENVGLHQTLDQTLNELNCI
- ▽ EKAEGDVAALNR
- IQALQQQADEAEDR
- * KIQALQQQADEAEDR
- ♦ KLVILEGELERAEER
- ⊕ P67936
- **☆** TIDDLEEK
- YSEKEDKYEEEIK

prognosis



PD PD





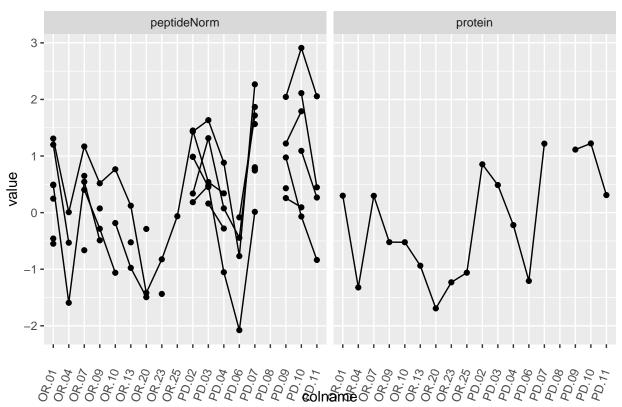
rowname

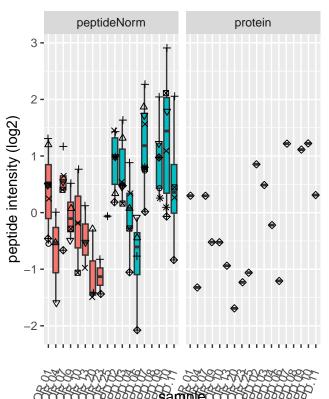
- LGEYEDVSR
- △ MEVTGVSAPTVTVFISSSLNTFR
- + Q99426
- × YDEPLGK
- ♦ YTISQEAYDQR

prognosis



PD





rowname

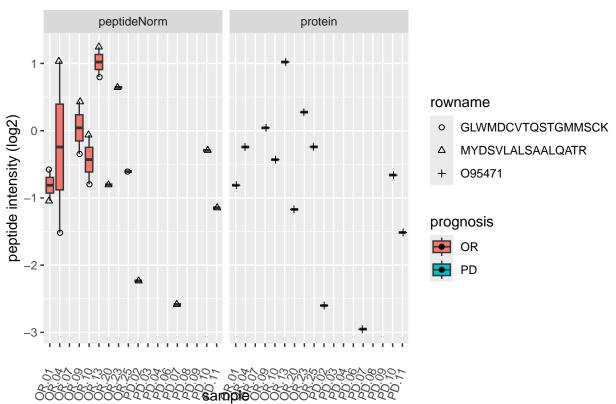
- DYFMPCPGR
- △ EVGTPHGIILDSVDAAFICPGSSR
- + LLQDEFPGIPSPLDAAVECHR
- × NFPSPVDAAFR
- ♦ P02790
- SLGPNSCSANGPGLYLIHGPNLYCYSDVEK
- * VDGALCMEK
- ♦ YYCFQGNQFLR

prognosis

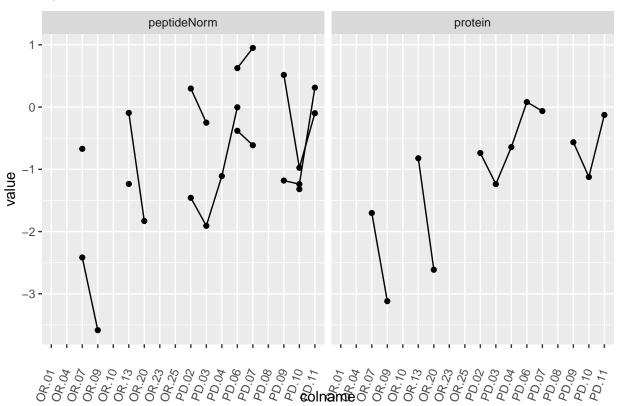


OR PD

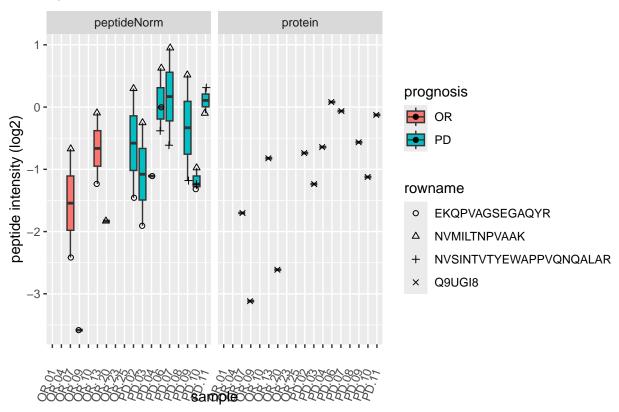


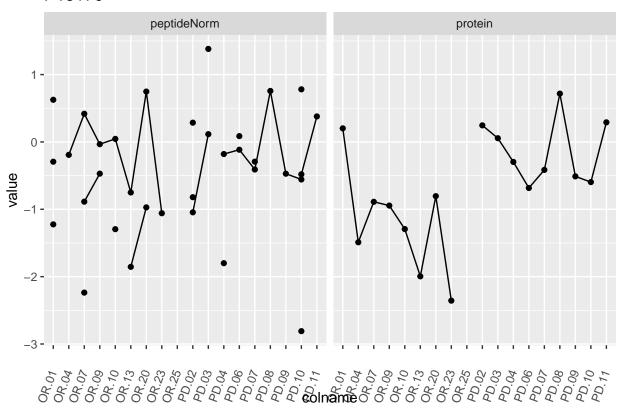


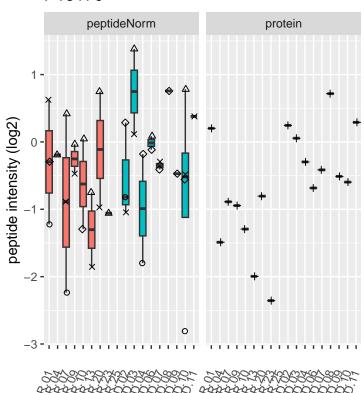
Q9UGI8



Q9UGI8







rowname

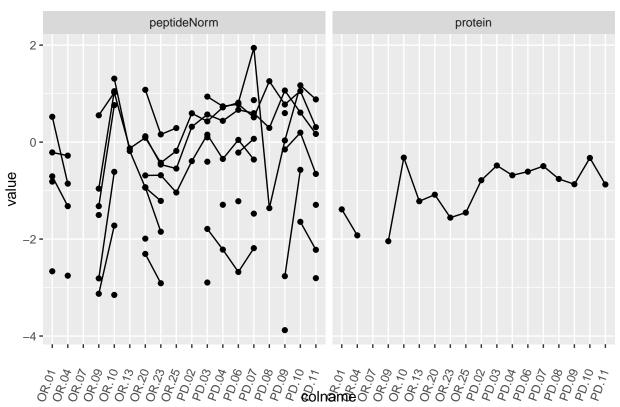
- AYFETEKK
- △ HNVEVLGILSDDVETDTVAPGENLK
- + P15170
- × STIGGQIMYLTGMVDKR
- ♦ SVVAPPGAPK

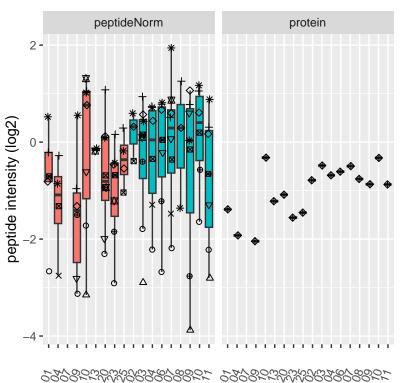
prognosis



OR







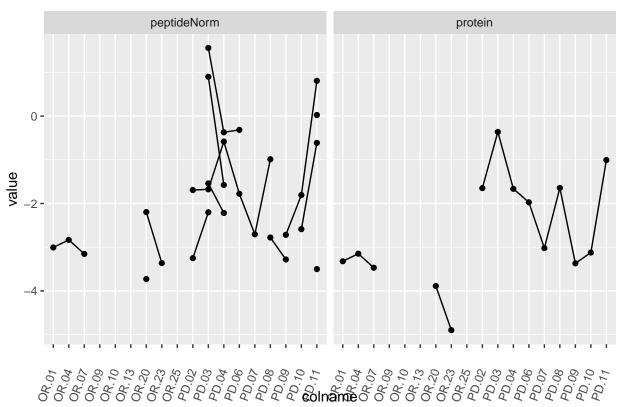
rowname

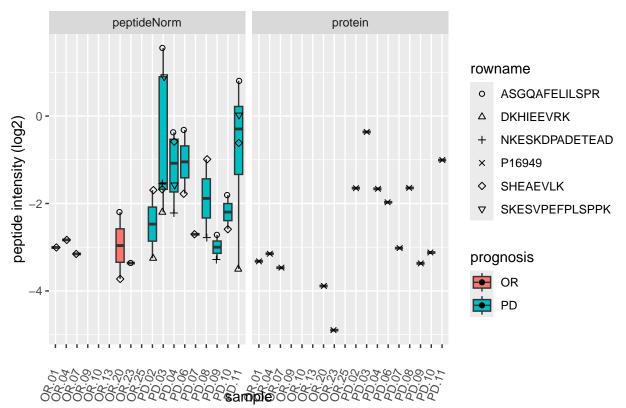
- DFSSVFQFLR
- DFSSVFQFLREEETF
- DLGLAQDSATSTK
- EFQDAGEQVVSSPADVAEK
- GSLLIDSSTIDPAVSK
- IITMLPTSINAIEAYSGANGILK
- × KGSLLIDSSTIDPAVSK
- MGAVFMDAPVSGGVGAAR
- P31937
- SPILLGSLAHQIYR
- TPVGFIGLGNMGNPMAK

prognosis





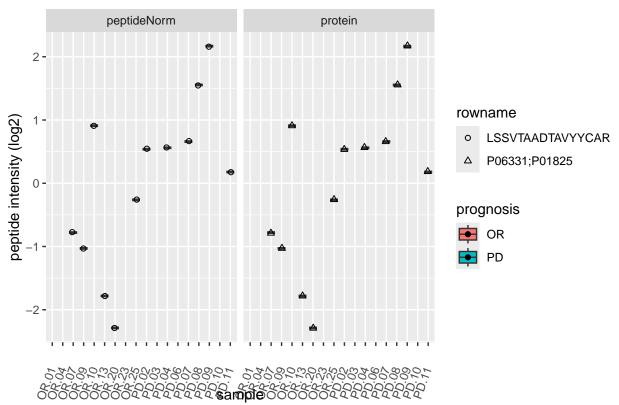




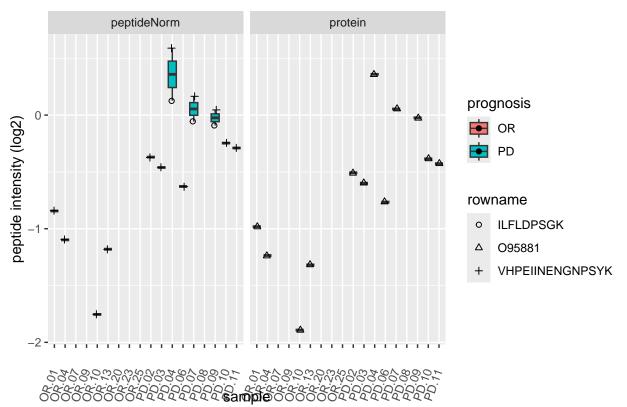
P06331;P01825

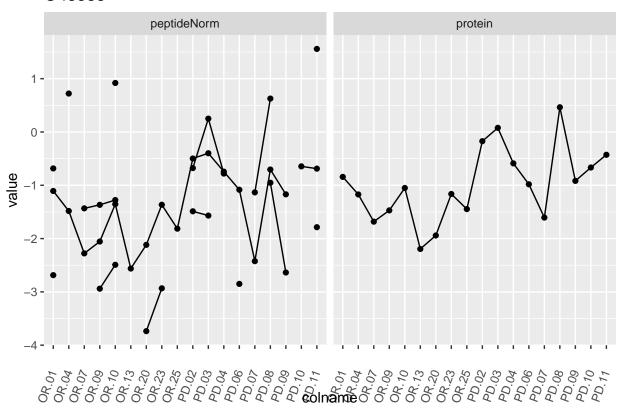


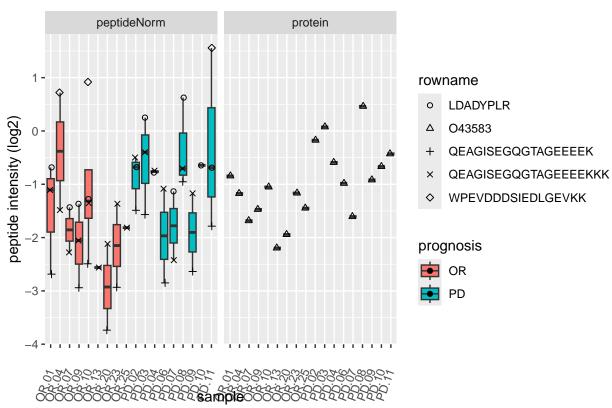
P06331;P01825

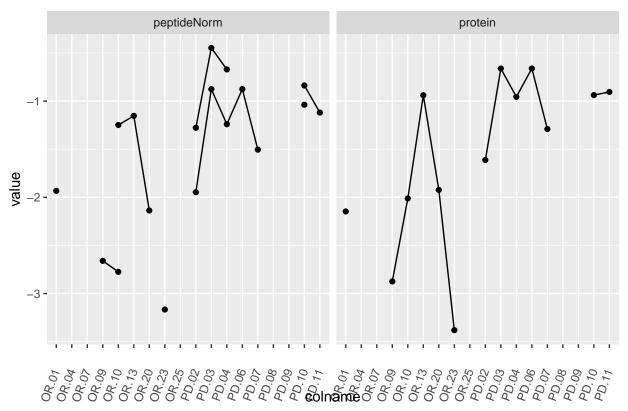


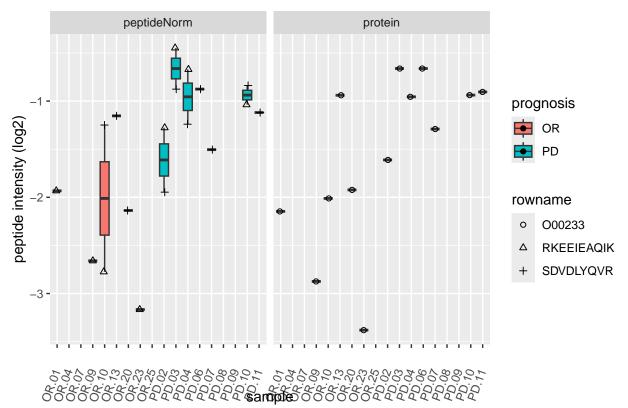


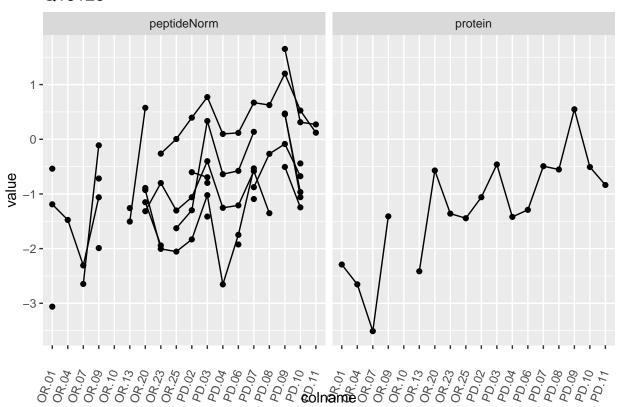


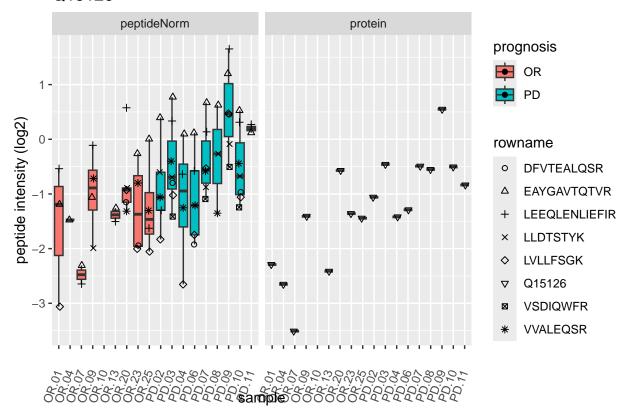












5 Session Info

other attached packages:

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

sessionInfo()

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

```
plotly_4.10.4
    [1] ExploreModelMatrix_1.16.0
##
   [3] msqrob2_1.12.0
                                     QFeatures_1.14.2
  [5] MultiAssayExperiment 1.30.3 SummarizedExperiment 1.34.0
## [7] Biobase_2.64.0
                                     GenomicRanges_1.56.1
##
   [9] GenomeInfoDb 1.40.1
                                     IRanges_2.38.1
## [11] S4Vectors 0.42.1
                                     BiocGenerics 0.50.0
## [13] MatrixGenerics 1.16.0
                                     matrixStats 1.4.1
                                     lubridate_1.9.3
## [15] limma_3.60.6
## [17] forcats 1.0.0
                                     stringr_1.5.1
## [19] dplyr_1.1.4
                                     purrr_1.0.2
## [21] readr_2.1.5
                                     tidyr_1.3.1
## [23] tibble_3.2.1
                                     ggplot2_3.5.1
## [25] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] rlang_1.1.4
                                 magrittr_2.0.3
                                                          shinydashboard_0.7.2
                                                          vctrs_0.6.5
## [4] clue_0.3-65
                                 compiler_4.4.0
## [7] reshape2_1.4.4
                                 ProtGenerics 1.36.0
                                                         pkgconfig_2.0.3
## [10] crayon_1.5.3
                                 fastmap_1.2.0
                                                         XVector_0.44.0
## [13] fontawesome 0.5.2
                                 labeling_0.4.3
                                                         utf8 1.2.4
## [16] promises_1.3.0
                                 rmarkdown_2.28
                                                         tzdb_0.4.0
## [19] UCSC.utils_1.0.0
                                 nloptr_2.1.1
                                                         xfun 0.47
## [22] zlibbioc_1.50.0
                                 cachem 1.1.0
                                                          jsonlite 1.8.9
## [25] later 1.3.2
                                 highr 0.11
                                                         DelayedArray 0.30.1
## [28] BiocParallel 1.38.0
                                 parallel_4.4.0
                                                          cluster 2.1.6
## [31] R6_2.5.1
                                 bslib_0.8.0
                                                          stringi_1.8.4
## [34] boot_1.3-31
                                 jquerylib_0.1.4
                                                         Rcpp_1.0.13-1
## [37] knitr_1.48
                                 BiocBaseUtils_1.6.0
                                                         httpuv_1.6.15
## [40] Matrix_1.7-0
                                 splines_4.4.0
                                                          igraph_2.0.3
## [43] timechange_0.3.0
                                 tidyselect_1.2.1
                                                         rstudioapi_0.16.0
## [46] abind_1.4-8
                                 yaml_2.3.10
                                                          codetools_0.2-20
## [49] lattice_0.22-6
                                 plyr_1.8.9
                                                          shiny_1.9.1
## [52] withr_3.0.1
                                 evaluate_1.0.0
                                                         pillar_1.9.0
## [55] DT_0.33
                                 shinyjs_2.1.0
                                                         generics_0.1.3
## [58] hms 1.1.3
                                                          scales 1.3.0
                                 munsell_0.5.1
## [61] minqa_1.2.8
                                 xtable_1.8-4
                                                         glue_1.8.0
## [64] lazyeval 0.2.2
                                 tools_4.4.0
                                                         data.table 1.16.0
## [67] lme4_1.1-35.5
                                                          grid_4.4.0
                                 cowplot_1.1.3
## [70] MsCoreUtils_1.16.1
                                 colorspace_2.1-1
                                                         nlme_3.1-166
## [73] GenomeInfoDbData_1.2.12 cli_3.6.3
                                                          fansi_1.0.6
## [76] S4Arrays 1.4.1
                                 viridisLite 0.4.2
                                                          AnnotationFilter 1.28.0
## [79] gtable_0.3.5
                                 rintrojs_0.3.4
                                                          sass_0.4.9
## [82] digest_0.6.37
                                 SparseArray_1.4.8
                                                         htmlwidgets_1.6.4
## [85] farver_2.1.2
                                 htmltools_0.5.8.1
                                                         lifecycle_1.0.4
## [88] httr_1.4.7
                                 mime_0.12
                                                         statmod_1.5.0
```

[91] MASS_7.3-61