Cancer

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

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

```
pe <- readQFeatures(
  table = peptidesFile,
  fnames = 1,
  ecol = ecols,
  name = "peptideRaw", sep="\t")</pre>
```

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"
```

```
## [1] "OR.O1" "OR.O4" "OR.O7" "OR.O9" "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"
    [4] "Gene.names"
                                  "Protein.names"
                                                            "Unique..Groups."
##
                                                            "PEP"
                                  "Charges"
##
  [7] "Unique..Proteins."
                                                            "Slice.Std..Dev."
## [10] "Score"
                                  "Slice.Average"
## [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")</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>
```

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 != "+")</pre>
```

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.

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 1imma 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.

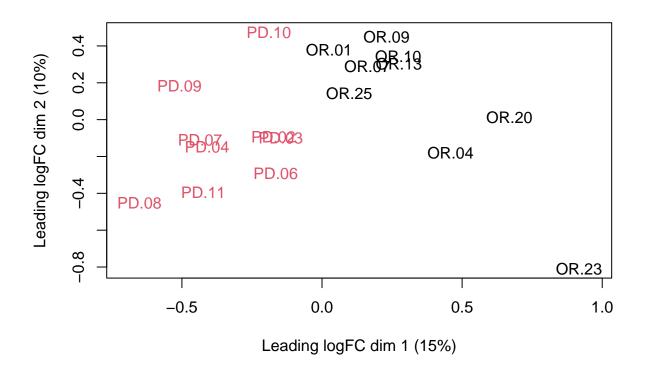
3.5 Summarization to protein level

• 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]]
```

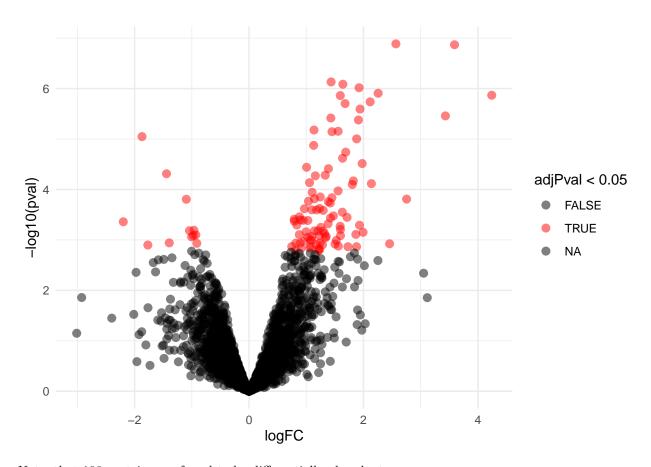


Spike-in condition A is the reference class. So the mean $\log 2$ expression for samples from good prognosis (OR) is '(Intercept). The mean $\log 2$ expression for samples from poor prognosis (PD) is '(Intercept)+prognosisPD'. Hence, the average $\log 2$ fold change between prognosis PD and prognosis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



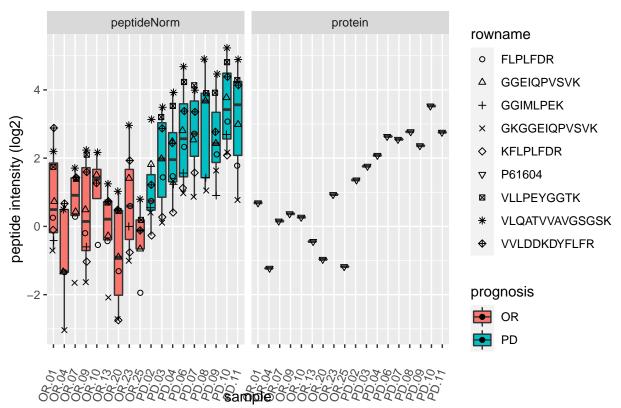
4.3.3 Detail plots

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

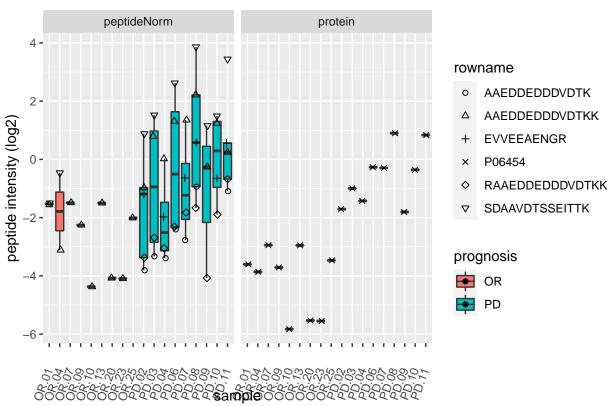
```
for (protName in sigNames)
#for (protName in orderProt[1:10])
pePlot <- pe[protName, , c("peptideNorm", "protein")]</pre>
pePlotDf <- data.frame(longFormat(pePlot))</pre>
pePlotDf$assay <- factor(pePlotDf$assay,</pre>
                          levels = c("peptideNorm", "protein"))
pePlotDf$prognosis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





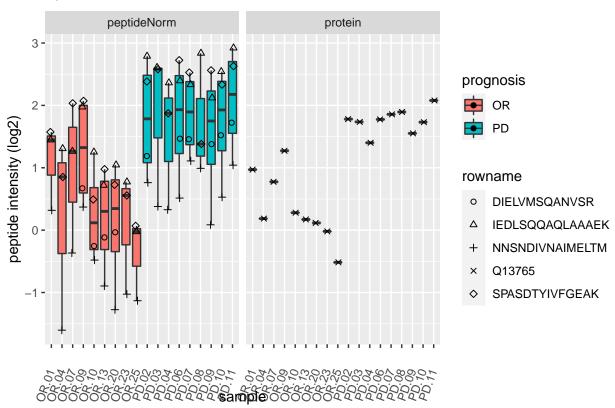




Q13765



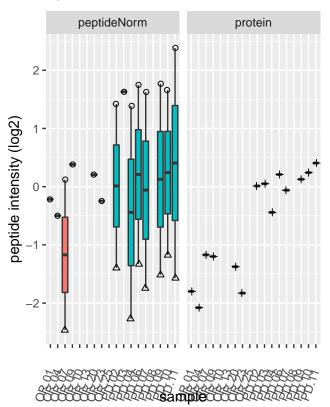
Q13765



Q96K17



Q96K17



rowname

- APKPEDIDEEDDDVPDLVENFDEASKNEAN
- △ LAEQFPR
- + Q96K17

prognosis



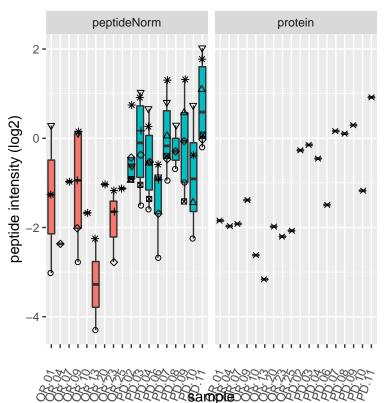
OR



O43396



O43396



rowname

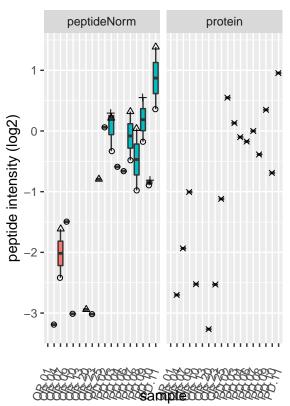
- FQGPDNGQGPK
- FQNVNSVTIFVQSNQGEEETTR
- IDQYQGADAVGLEEK
- O43396
- QHLENDPGSNEDTDIPK
- SEPTQALELTEDDIKEDGIVPLR
- SMDFEEAER
- VGVKPVGSDPDFQPELSGAGSR

prognosis









rowname

- AAATPESQEPQAK
- △ GDVTAEEAAGASPAK
- + GEGESPPVNGTDEAAGATGDAIEPAPPSQGAEAK
- × P49006

prognosis

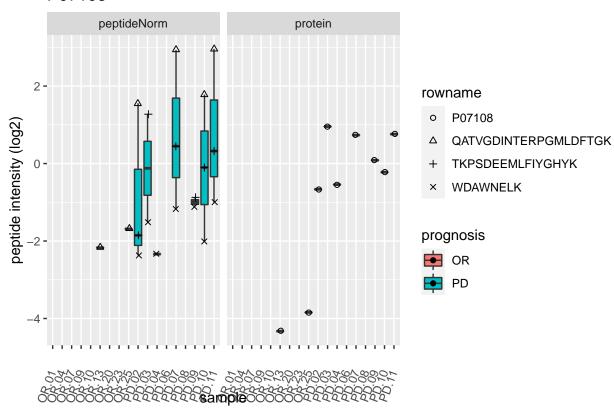


OR

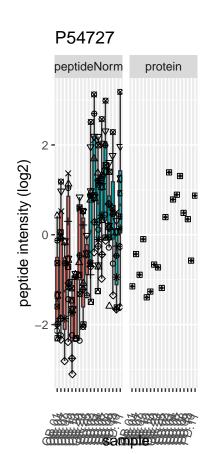


PD









- **ASFNNPDR**
- AVEYLLMGIPGDR Δ
- + EQVIAALR
- ESQAVVDPPQAASTGAPQSSAVAAAAATTTATTTTTSSGGHPLEFLR
- GKDAFPVAGQK \Diamond
- **IDIDPEETVK** ∇
- ILNDDTALK
- ILNDDTALKEYK
- NENLAANFLLQQNFDED
- NFVVVMVTKPK
- □ NQPQFQQMR
- P54727 ⊞
- QEKPAEKPAETPVATSPTATDSTSGDSSR
- QIIQQNPSLLPALLQQIGR

prognosis

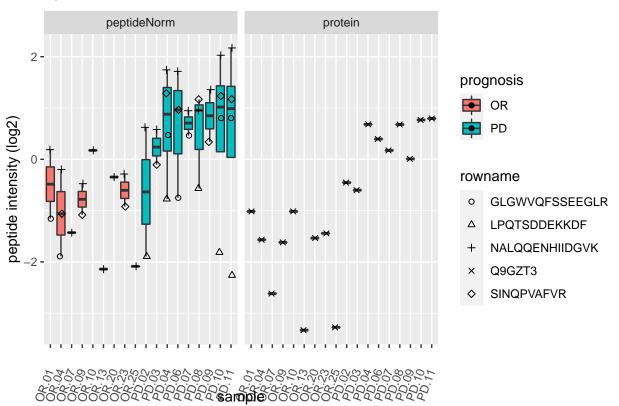




Q9GZT3



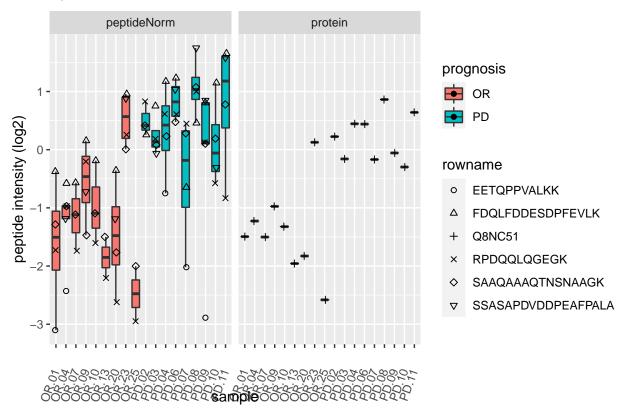
Q9GZT3



Q8NC51



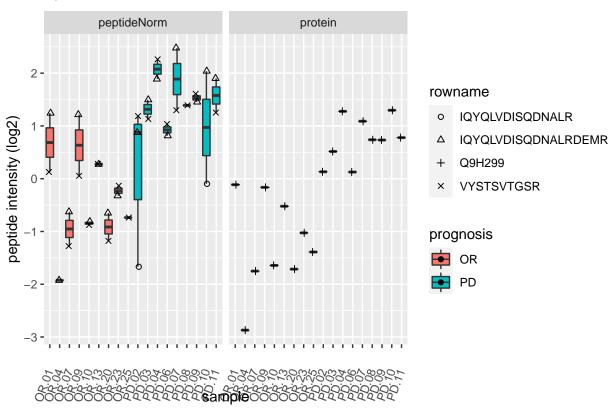
Q8NC51



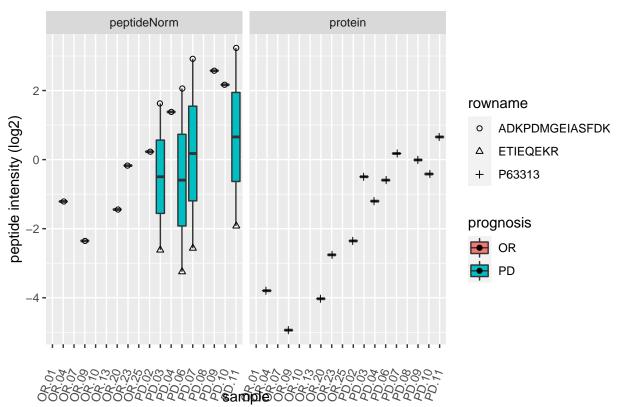
Q9H299



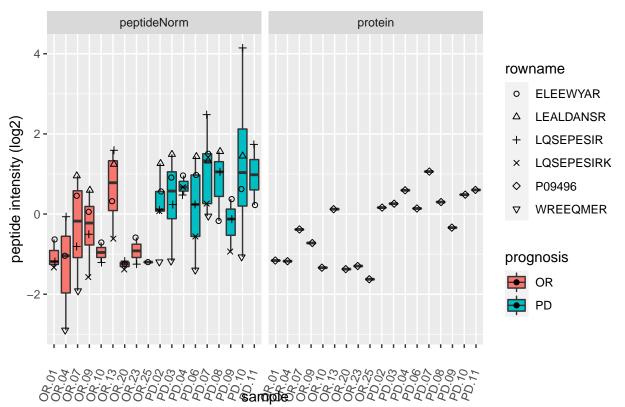
Q9H299



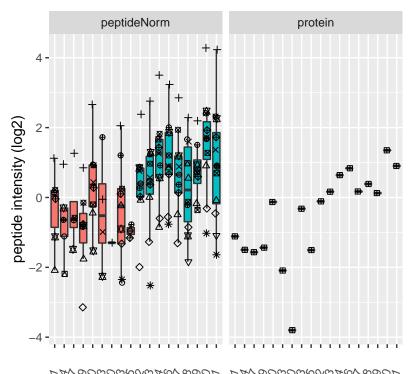












- AFAAGADIK
- ALNALCDGLIDELNQALK
- AQFAQPEILIGTIPGAGGTQR
- **EGMTAFVEK**
- **EMQNLSFQDCYSSK**
- **ESVNAAFEMTLTEGSK**
- GKNNTVGLIQLNRPK
- ICPVETLVEEAIQCAEK
- KLFYSTFATDDRK
- LFYSTFATDDRK
- NNTVGLIQLNRPK 苁
- P30084 Ш
- SLAMEMVLTGDR
- TFEEDPAVGAIVLTGGDK

prognosis

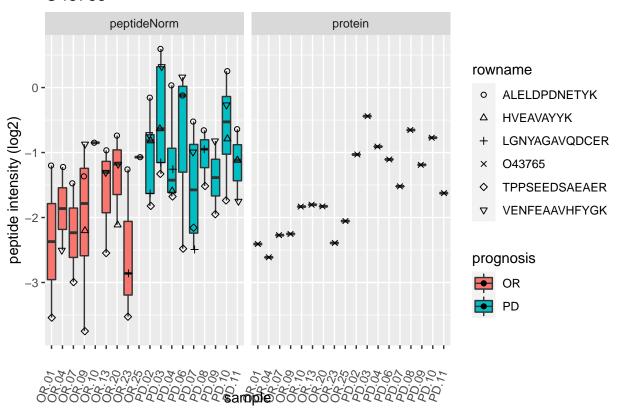




O43765



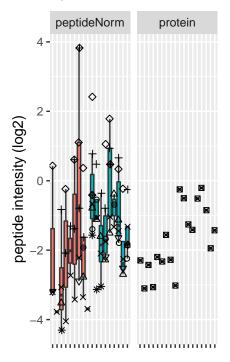
O43765



Q9NXG2



Q9NXG2



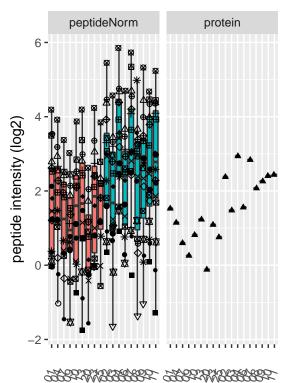
prognosis



rowname

- AAPAQQTTQPGGGK
- △ AAPAQQTTQPGGGKR
- + FQSVESGANNVVFIR
- × LESADKSDQNNTAEGK
- ♦ NNQQVPENTEELGQTKPTSNPQVVNEGGAKPELASQATEGSK
- ∇ NNSHVNREEVIR
- Q9NXG2
- * SPKDPSQLNSK
- ♦ YNLQEVVK



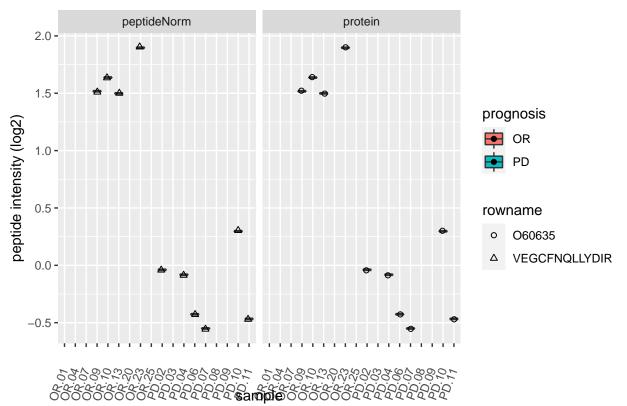


- I IALUAUI LI I UNIN
- × FYGDEEKDK
- ♦ FYGDEEKDKGLQTSQDAR
- ∇ GKNVLINK
- GQTLVVQFTVK
- * GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK
- ♦ HEQNIDCGGGYVK
- IDDPTDSKPEDWDKPEHIPDPDAK
- ☆ IDNSQVESGSLEDDWDFLPPK
- IDNSQVESGSLEDDWDFLPPKK
- KPEDWDEEMDGEWEPPVIQNPEYK
- KVHVIFNYK
- LFPNSLDQTDMHGDSEYNIMFGPDICGPGTK
- ▲ P27797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

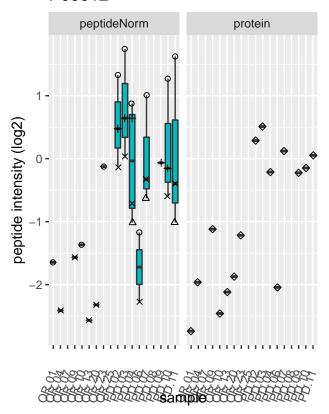
O60635



O60635







rowname

- AVPETRPNHTIYINNLNEK
- △ AVQGGGATPVVGAVQGPVPGMPPMTQAPR
- + EVSSATNALR
- × HDIAFVEFDNEVQAGAAR
- ♦ P09012

prognosis

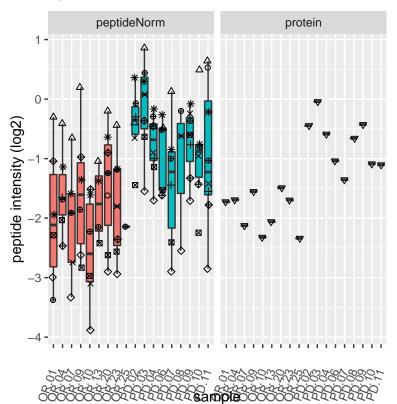


OR

Q9UBE0



Q9UBE0



rowname

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

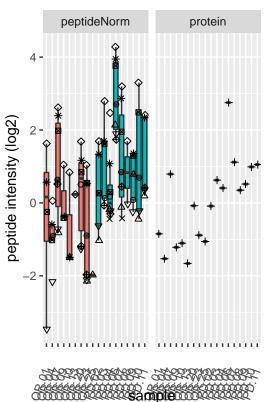
prognosis



OR







rowname

- ASAAFSSVGSVITK
- △ ELAKVEEEIQTLSQVLAAK
- + P55327
- × SFEEKVENLK
- ♦ TDPVPEEGEDVAATISATETLSEEEQEELRR
- ▼ TSETLSQAGQK
- VEEEIQTLSQVLAAK
- * VGGTKPAGGDFGEVLNSAANASATTTEPLPEK
- ♦ VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL

prognosis

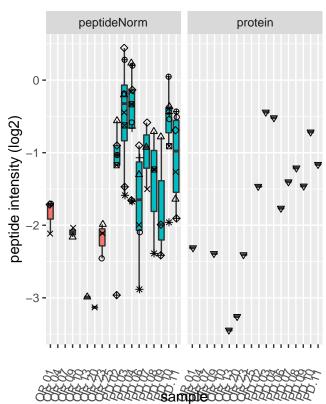


OR



PD





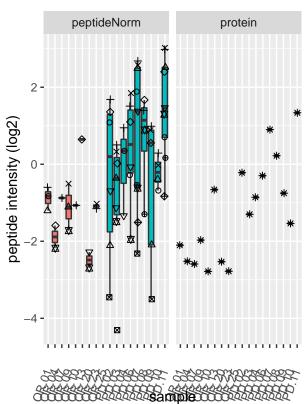
rowname

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

prognosis







prognosis



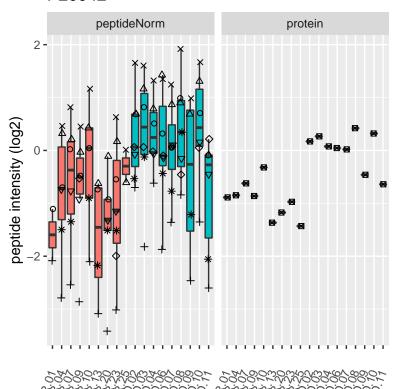
OR



rowname

- EAENPEGEEKEAATLEVERPLPMEVEK
- △ GFSEGLWEIENNPTVK
- + GPPQEEEEEEDEEEEATKEDAEAPGIR
- × GPPQEEEEEEDEEEEATKEDAEAPGIRDHESL
- ♦ IDEMPEAAVK
- ▼ KGFSEGLWEIENNPTVK
- NSTPSEPGSGR
- * P51858
- ♦ RAGDLLEDSPK
- SCVEEPEPEPEAAEGDGDKK
- ▼ YQVFFFGTHETAFLGPK





prognosis

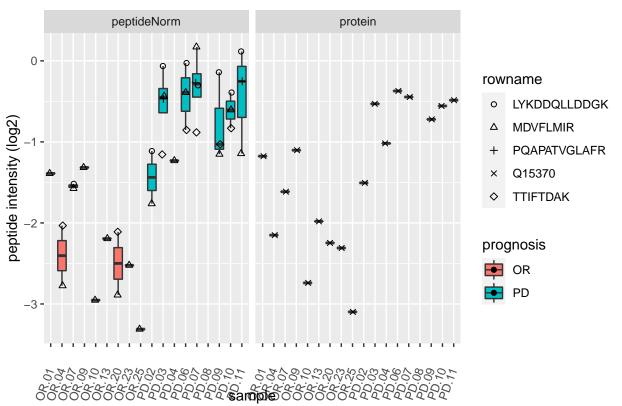




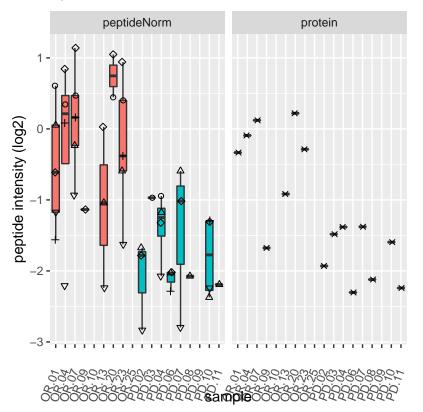
rowname

- DASDDLDDLNFFNQK
- DYTYEELLNR
- EKNPDMVAGEK
- EVEPEPTEDKDLEADEEDTR
- IESDVQEPTEPEDDLDIMLGNK
- **IFDIDEAEEGVK**
- P20042 ×
- TGFQAVTGK









rowname

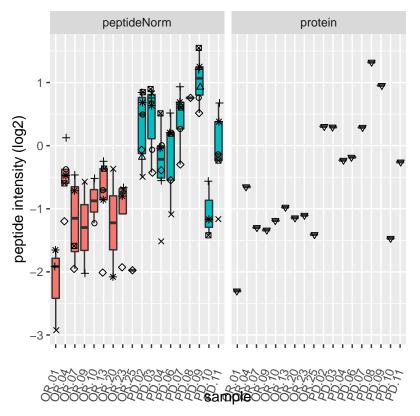
- EVLDSFLDLAR
- △ GPAGDATVASEK
- + NIFPSNLVSAAFR
- × Q15758
- ♦ SELPLDPLPVPTEEGNPLLK
- ∇ SYSTTYEER

prognosis



₱ PD





rowname

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

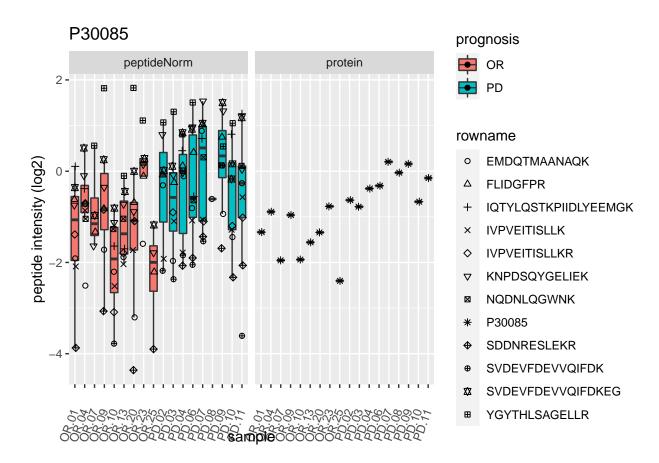
prognosis



OR



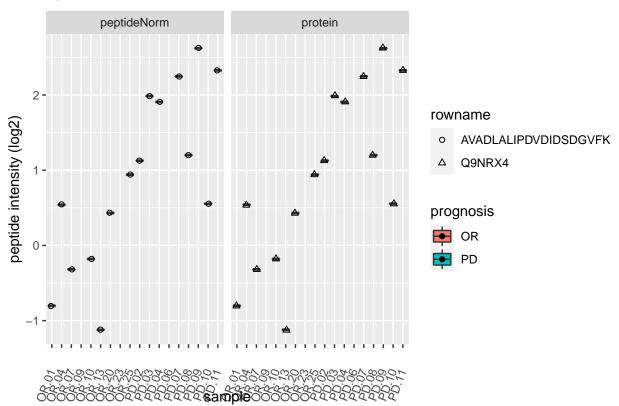




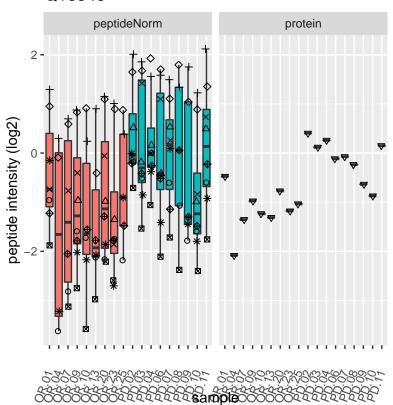
Q9NRX4



Q9NRX4







rowname

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

prognosis

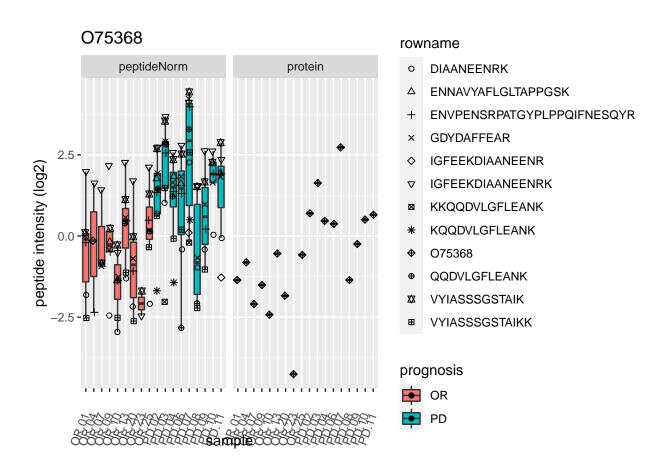


OR



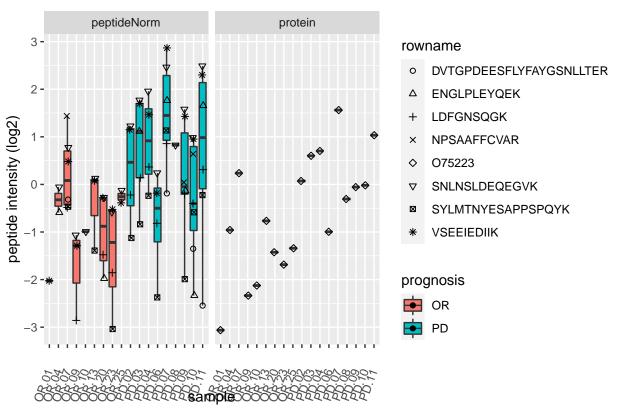
O75368





O75223

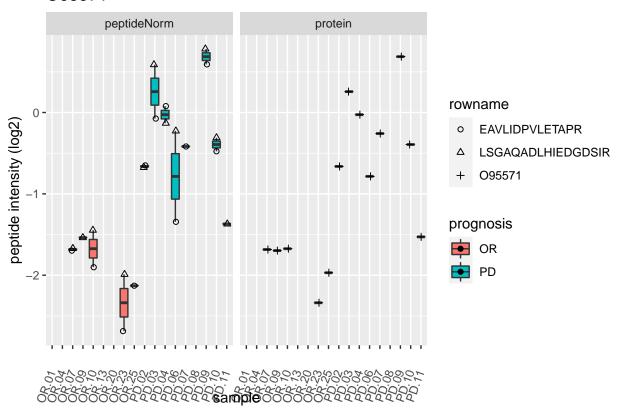




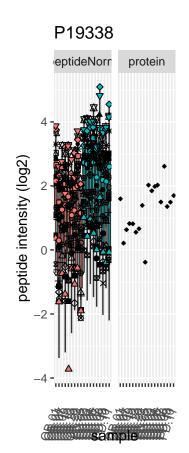
O95571



O95571









rowname

- ALELTGLK
- △ ALVATPGKK
- + EAMEDGEIDGNK
- × EAMEDGEIDGNKVTLDWAKPK
- ♦ ESFDGSVR
- ▽ EVFEDAAEIR
- FGYVDFESAEDLEK
- * GFGFVDFNSEEDAK
- ♦ GIAYIEFK
- GLSEDTTEETLK
- ☆ GLSEDTTEETLKESFDGSVR
- GYAFIEFASFEDAK
- IVTDRETGSSK
- ☑ KFGYVDFESAEDLEK
- K\/\/\SPTKK

- LELQGPR
- ▲ NDLAVVDVR
- P19338
- QKVEGTEPTTAFNLFVGNLNFNK
- SISLYYTGEK
- TEADAEKTFEEK
- TGISDVFAK
- ♦ TLVLSNLSYSATEETLQEVFEK
- △ VAVATPAKK
- ▽ VEGTEPTTAFNLFVGNLNFNK

VFGNEIK

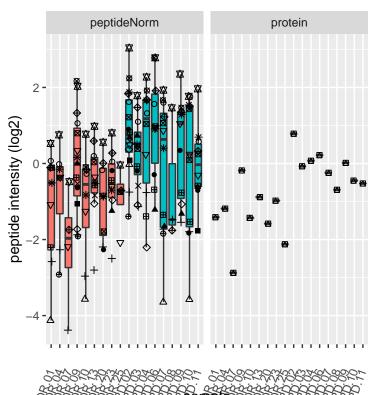
VTLDWAKPK

VTQDELK

VTQDELKEVFEDAAEIR

VVVSPTKK





- △ FVKPGAENSR
- + GSVLPNSDKK
- × HSVNNPYSQFQDEYSLDEVMASK
- ♦ HVDLLINK
- □ IGGIFAFK
- ☑ ITGNMGLAMK
- * KLEEEGEQFVK
- ♦ KLEEEGEQFVKK
- LEEEGEQFVK
- MGFPEAASSFR
- MNPQSAFFQGK
- □ P22307
- VFVVGVGMTK
- WVINPSGGLISK
- ▲ YGLSAHPVAPQMFGYAGK

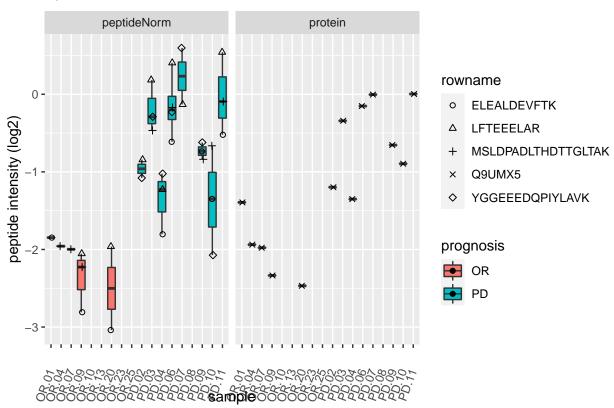
prognosis

OR

Q9UMX5



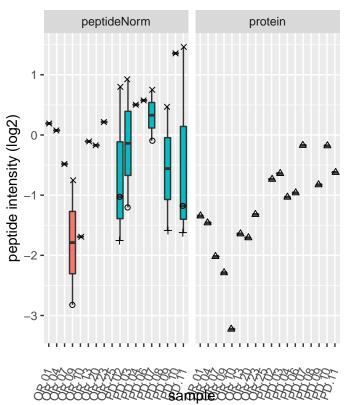
Q9UMX5



O60888



O60888



rowname

- GKIEEDSEVLMMIK
- O60888
- SVHPYEVAEVIALPVEQGNFPYLQWVR
- TQSSLVPALTDFVR

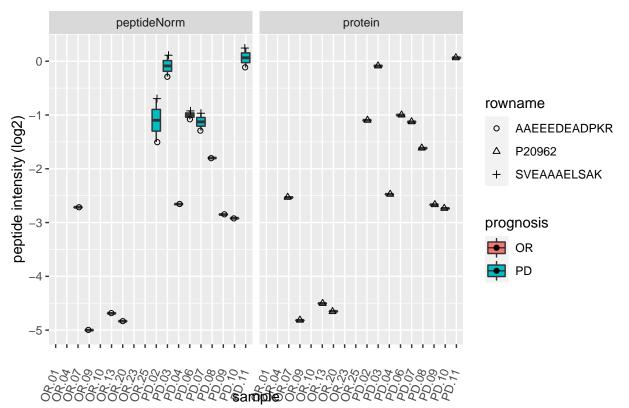
prognosis





PD



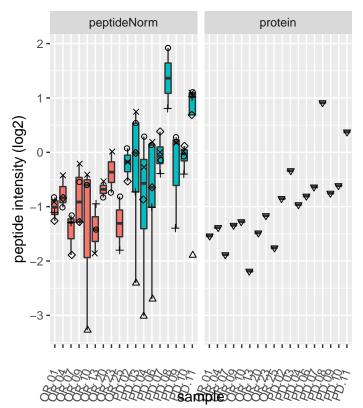


Q14980



 	%	HLTAQVR	7	LGSPDYGNSALLSLPGYRPTTR	ı	QELTSQ
	&	HQVEQLSSSLK	8	LLQAETASNSAR	J	QEQHE/
		HREELEQSK	9	LPPKVESLESLYFTPIPAR	К	QFCSTC
١R	(IATTTASAATAAAIGATPR	:	LQAQLNELQAQLSQK	L	QFLEVE
)	IHGTEEGQQILK	;	LQNALNEQR	М	QLEALE
AAGR	٠	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	Е	Q14980	W	SNRDEL
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prognosis



OR

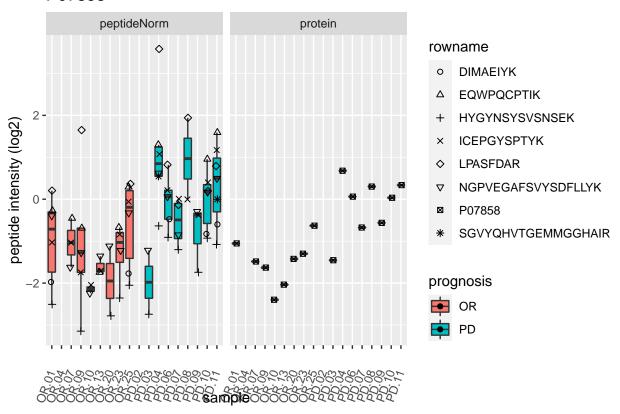


PD

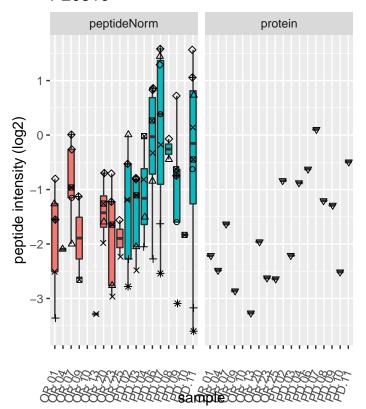
rowname

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









prognosis





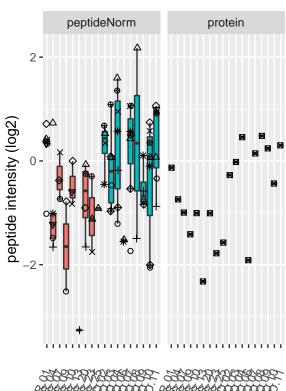


PD

rowname

- AAAPAPVSEAVCR
- DTMSDQALEALSASLGTR
- EADPEDGKPVMDK
- KTEKEESTEVLK
- LAAAISEVVSQTPASTTQAGAPPR
- P20810
- SLTPAVPVESKPDKPSGK
- TEKEESTEVLK
- TKPQDMISAGGESVAGITAISGKPGDK





rowname

- ALDVGSGSGILTACFAR
- △ ELVDDSVNNVR
- + KDDPTLLSSGR
- × LILPVGPAGGNQMLEQYDK
- ♦ LILPVGPAGGNQMLEQYDKLQDGSIK
- ▼ MGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR
- P22061
- * SGGASHSELIHNLR
- ♦ VFEVMLATDR
- ⊕ VQLVVGDGR

prognosis

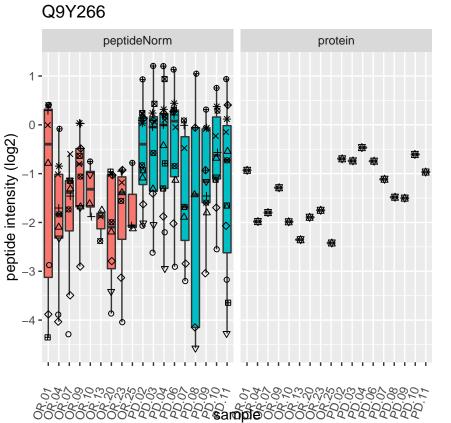


OR



Q9Y266







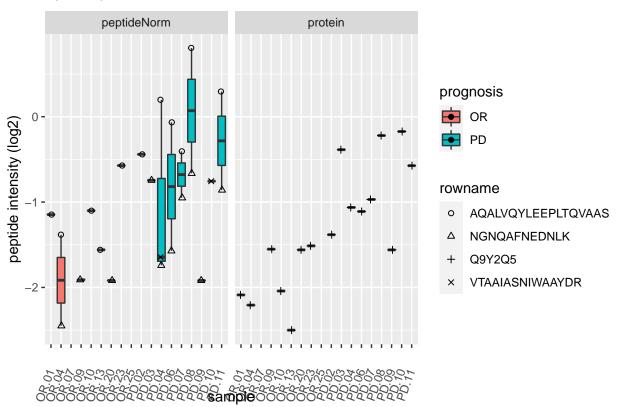
rowname

- DAENHEAQLK
- △ ELTDEEAER
- + FMDQHPEMDFSK
- × GQPAIIDGELYNEVK
- ♦ KDAENHEAQLK
- ∇ KINPENSK
- LITQTFSHHNQLAQK
- * LKPNLGNGADLPNYR
- ♦ LSDLDSETR
- ⊕ LVSSDPEINTK
- **☎** Q9Y266
- SETSGPQIK
- TDFFIGGEEGMAEK
- ▼ VEESSWLIEDGK

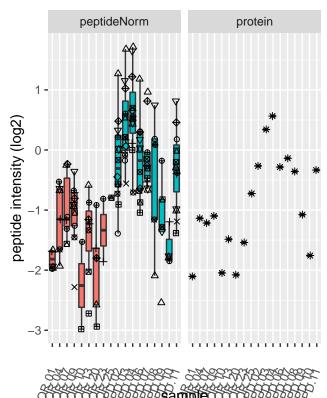
Q9Y2Q5



Q9Y2Q5







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

prognosis

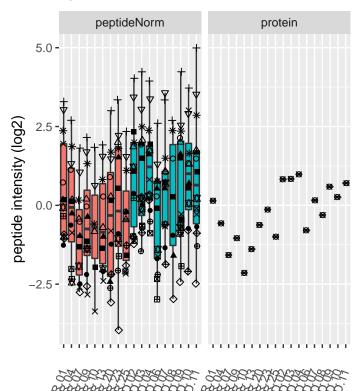




Q99497



Q99497

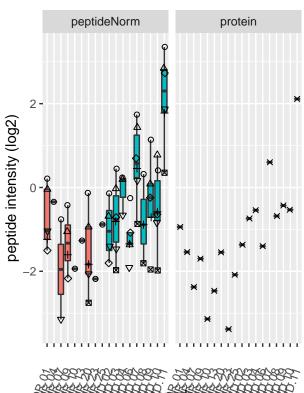


- DVVICPDASLEDAKK
- **EGPYDVVVLPGGNLGAQNLSESAAVK**
- × **EILKEQENR**
- **EILKEQENRK**
- GAEEMETVIPVDVMR
- GLIAAICAGPTALLAHEIGFGSK
- **GPGTSFEFALAIVEALNGK**
- **GPGTSFEFALAIVEALNGKEVAAQVK**
- KGLIAAICAGPTALLAHEIGFGSK
- MMNGGHYTYSENR
- ⊞ MMNGGHYTYSENRVEK
- Q99497
- VEKDGLILTSR
- VTTHPLAK
- VTVAGLAGK
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prognosis







rowname

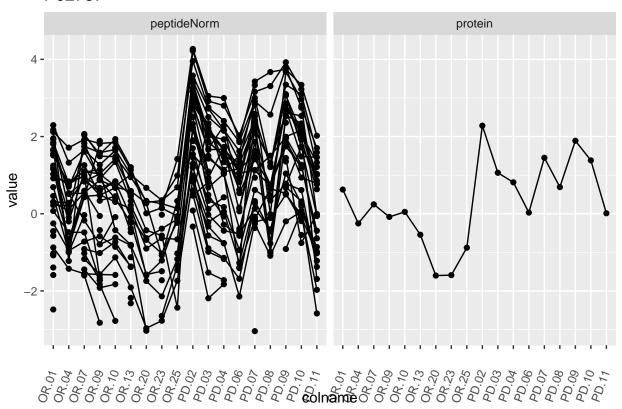
- AEEYEFLTPVEEAPK
- △ AEQEPTAEQLAQIAAENEEDEHSVNYKPPAQK
- + IDKTDYMVGSYGPR
- × P52565
- ♦ SIQEIQELDKDDESLR
- ∇ SIQEIQELDKDDESLRK
- ☑ YIQHTYR

prognosis



OR







- A KASYLDCIR

 ▼ KPVDEYKDCHLAQVPSHTVVAR

 KPVEEYANCHLAR

 LCMGSGLNLCEPNNK

 LKCDEWSVNSVGK

 MYLGYEYVTAIR

 NLNEKDYELLCLDGTR

 NPDPWAK
 - SASDLTWDNLK* SKEFQLFSSPHGK

SAGWNIPIGLLYCDLPEPR

\$ SVIPSDGPSVACVK* TAGWNIPMGLLYNK& WCALSHHER

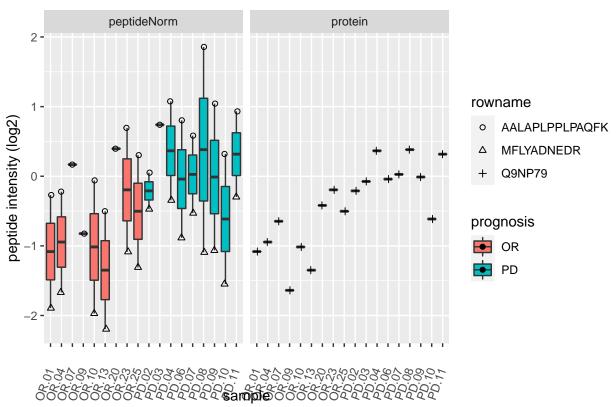
WCAVSEHEATK

YLGEEYVK

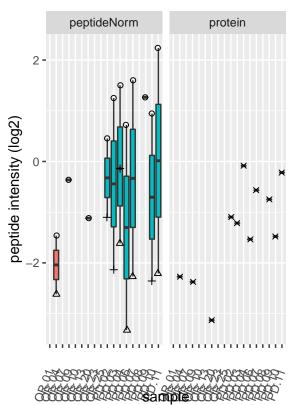
Q9NP79



Q9NP79







rowname

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

prognosis

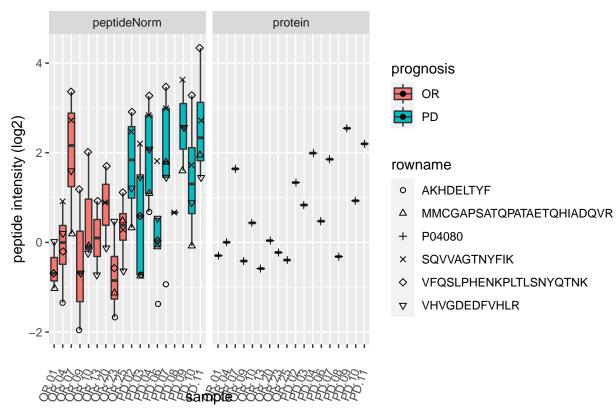


OR



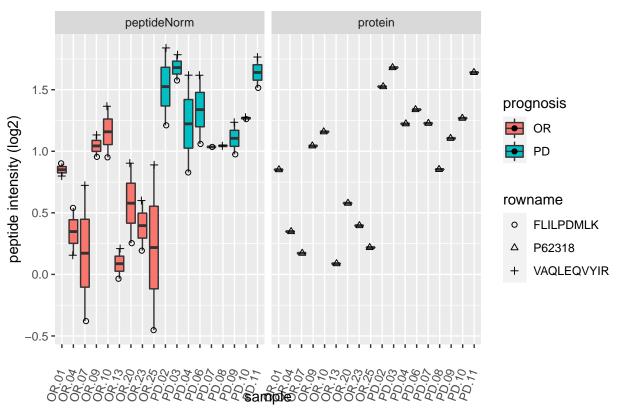
PD







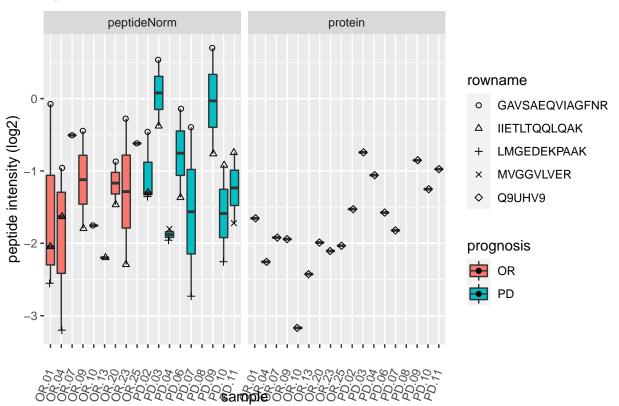




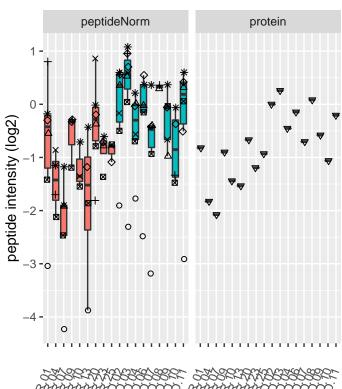
Q9UHV9



Q9UHV9







rowname

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

prognosis

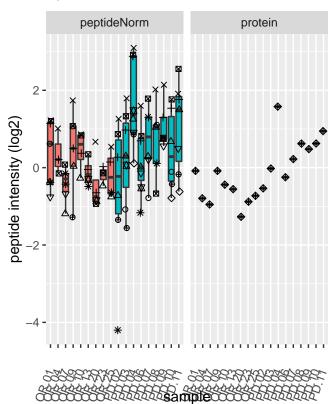


OR



PD





rowname

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

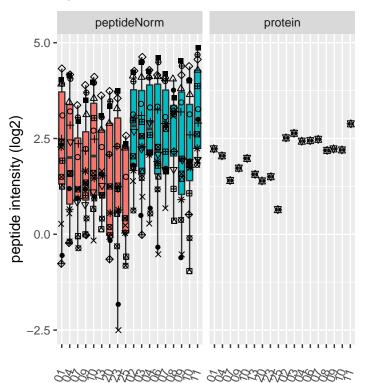
prognosis



OR







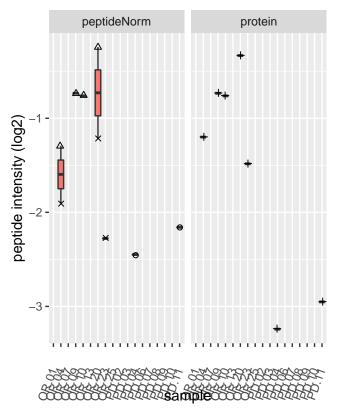
- ~ VDF0101 IV
- △ ATAVMPDGQFK
- + DISLSDYK
- × GKYVVFFFYPLDFTFVCPTEIIAFSDR
- ♦ HGEVCPAGWKPGSDTIKPDVQK
- ∇ IGHPAPNFK
- KQGGLGPMNIPLVSDPK
- * KQGGLGPMNIPLVSDPKR
- ◆ LNCQVIGASVDSHFCHLAWVNTPK
- ⊕ LVQAFQFTDK
- **☎** Q06830
- QGGLGPMNIPLVSDPK
- QGGLGPMNIPLVSDPKR
- SKEYFSK
- TIAQDYGVLK
- YVVFFFYPLDFTFVCPTEIIAFSDR

prognosis



OR





rowname

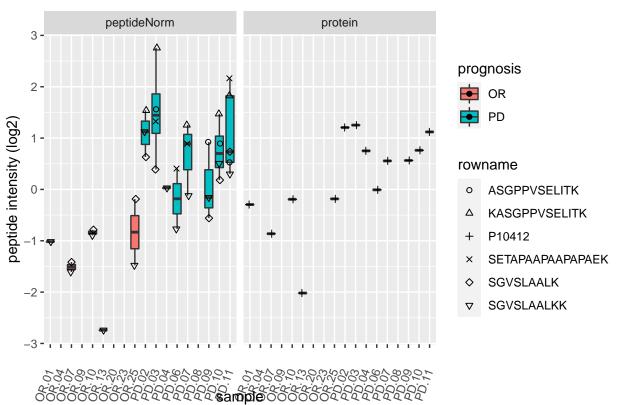
- LTESLDFTDYASR
- △ MLGTGPAAATTAATTSSNVSVLQQFASGLK
- + P42345
- × VLGLLGALDPYK

prognosis



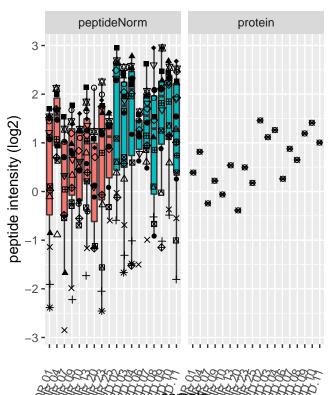
PD PD





P14314

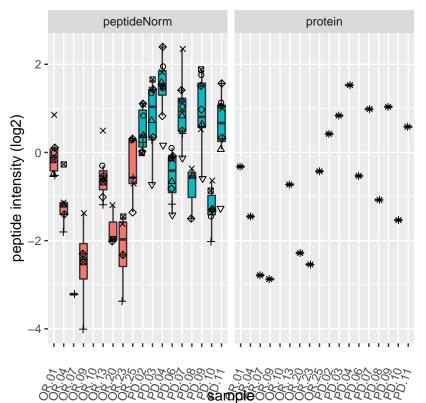




- + DMEESIR
- × ERESLQQMAEVTR
- ♦ ESLQQMAEVTR
- ▽ ETMVTSTTEPSR
- ILIEDWK
- * KLIELQAGK
- ♦ LGGSPTSLGTWGSWIGPDHDK
- LGGSPTSLGTWGSWIGPDHDKFSAMK
- NKFEEAER
- ₿ P14314
- SEALPTDLPAPSAPDLTEPK
- SLEDQVEMLR
- SLKDMEESIR
- ▲ TVKEEAEKPER
- VNDGVCDCCDGTDEYNSGVICENTCK
- YEQGTGCWQGPNR

prognosis





rowname

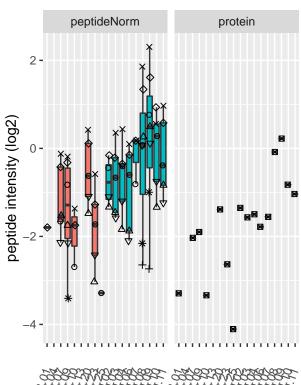
- AADLNGDLTATR
- EQFNEFR
- HLVYESDKNKDEK
- HWILPQDYDHAQAEAR
- IDNDGDGFVTTEELK
- **ISWEEYK**
- IVDRIDNDGDGFVTTEELK
- Q15293
- TFDQLTPDESKER
- YIFDNVAK

prognosis









rowname

- AAEEPSKVEEK
- △ AEDGATPSPSNETPK
- + EAGEGGEAEAPAAEGGK
- × EAPAEGEAAEPGSPTAAEGEAASAASSTSSPK
- ♦ GEAAAERPGEAAVASSPSK
- ▼ GEPAAAAAPEAGASPVEK
- P29966
- * VNGDASPAAAESGAK

prognosis



OR DD

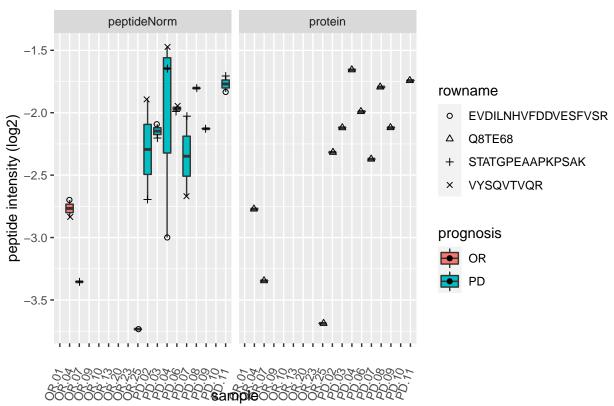


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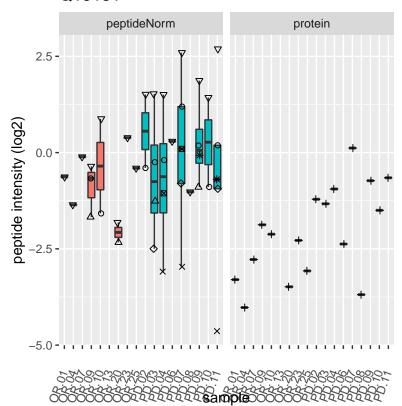
Q8TE68



Q8TE68







rowname

- **AAPFSLEYR**
- DKDFAIDIIK
- Q15181
- VFLKNEK
- VIAINVDDPDAANYNDINDVK
- VIAINVDDPDAANYNDINDVKR
- VLGILAMIDEGETDWK
- YVANLFPYK

prognosis

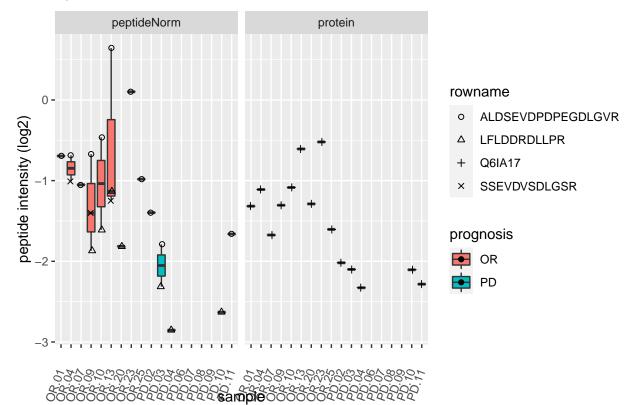


OR PD

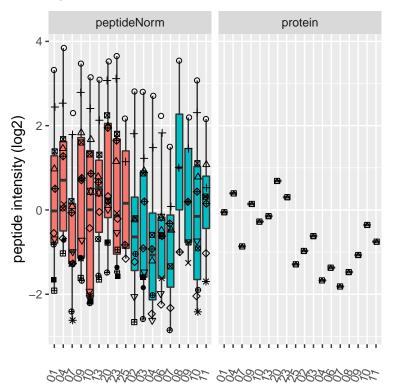
Q6IA17



Q6IA17







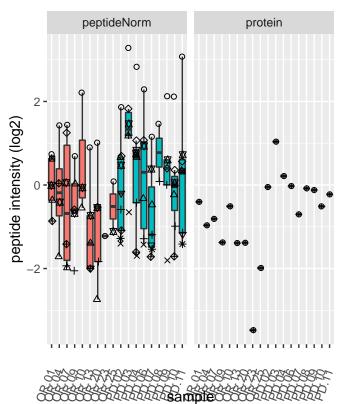
- ANIAOAGAGGIDGINI IX
- △ AVIGMTAGATGAFVGTPAEVALIR
- + AVVVNAAQLASYSQSK
- × EEGVLTLWR
- ♦ FLFGGLAGMGATVFVQPLDLVK
- ∇ GIYTGLSAGLLR
- LGIYTVLFER
- * LGPHTVLTFIFLEQMNK
- ◆ LTGADGTPPGFLLK
- ⊕ MIDGKPEYK
- NGLDVLFK
- NVFNALIR
- **■** Q02978
- RGYKNVFNALIR
- TSFHALTSILK

prognosis



OR





rowname

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

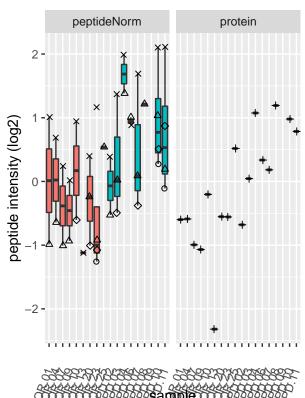
prognosis



OR







rowname

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

prognosis



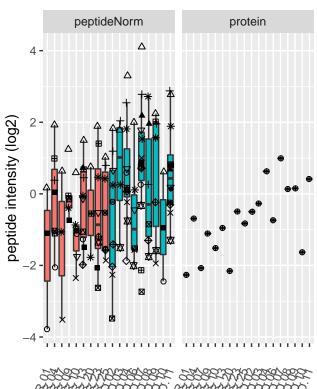
OR



Q9NR45



Q9NR45



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

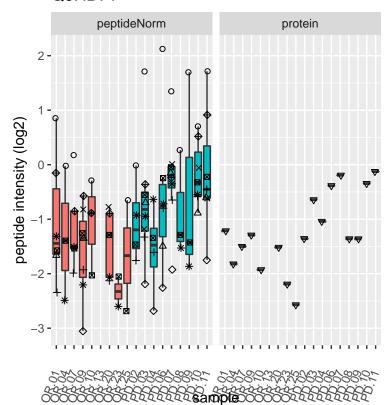
prognosis



Q9HB71



Q9HB71



rowname

- ASEELQKDLEEVK
- △ EKPSYDTETDPSEGLMNVLK
- + ISNYGWDQSDK
- × KAELLDNEKPAAVVAPITTGYTVK
- ♦ KIYEDGDDDMKR
- ∇ Q9HB71
- SFDLLVK
- * SKIETEIK
- ♦ SYSMIVNNLLKPISVEGSSK

prognosis

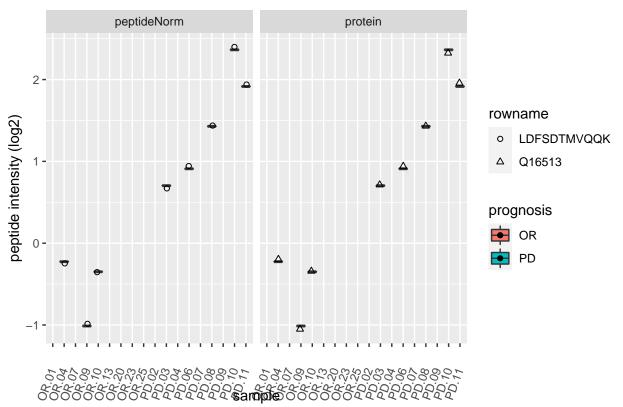


PD

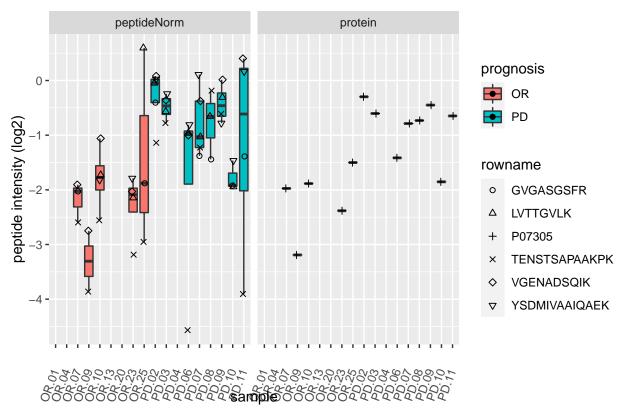
Q16513



Q16513



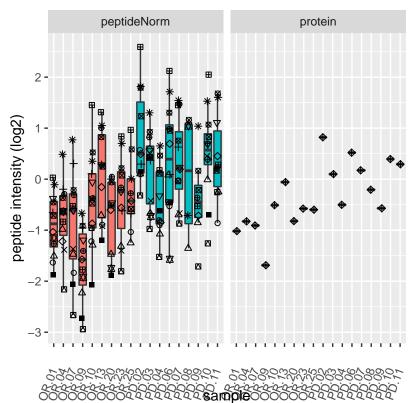












- AMMYSGELK
- △ EDLVVAPAGITLK
- + FGVPVIADGGIQNVGHIAK
- × GKLPIVNEDDELVAIIAR
- ♦ KYEQGFITDPVVLSPK
- □ LPIVNEDDELVAIIAR
- LVGIISSR
- * NLIDAGVDALR
- ♦ P12268
- ⊕ REDLVVAPAGITLK
- ☆ RFGVPVIADGGIQNVGHIAK
- TSSAQVEGGVHSLHSYEK
- VAQGVSGAVQDK
- YEQGFITDPVVLSPK
- YFSEADKIK

prognosis

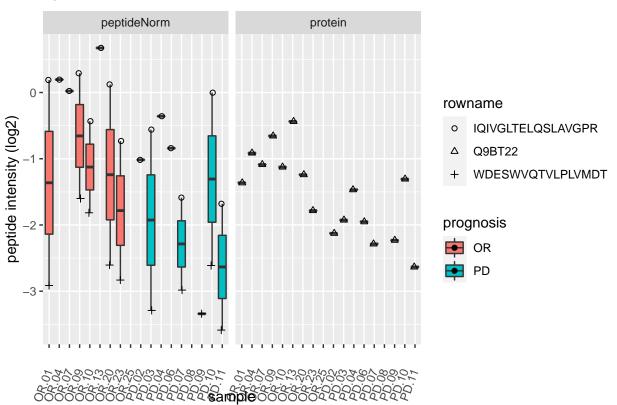


PD

Q9BT22



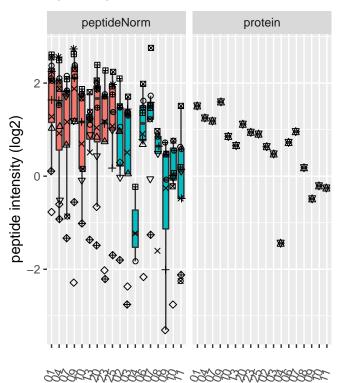
Q9BT22



Q9UHQ9



Q9UHQ9



rowname

- DIILREDLEELQAR
- **EDLEELQAR**
- FALPTAHHTLGLPVGK
- **GFVTADMIR**
- **GHFNIQPNKK**
- GIQTSPVLLASLGVGLVTLLGLAVGSYLVR
- **GPSGLLTYTGK**
- IDGSLVIRPYTPVTSDEDQGYVDLVIK
- LGMIAGGTGITPMLQLIR
- MSQYLDSLK
- Q9UHQ9
- **RPQVTLLDPNEK**
- VGDVVEFR

prognosis

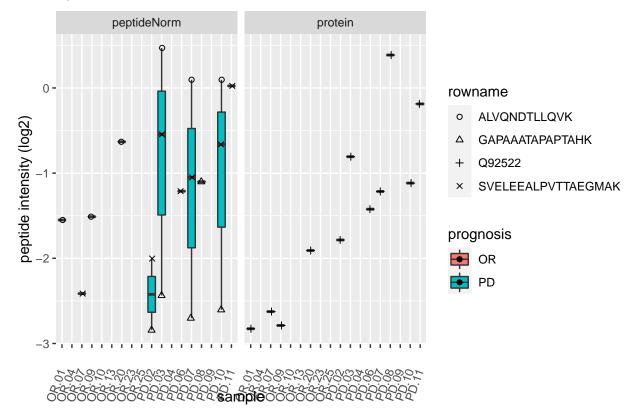




Q92522



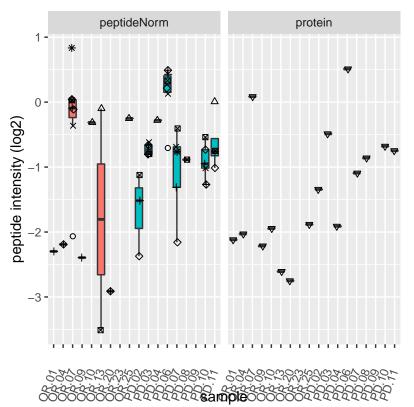
Q92522



O15327



O15327



rowname

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

prognosis



OR



PD

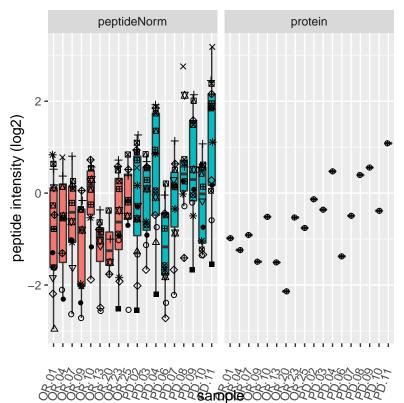


)	GAGSYTIMVLFADQATPTSPIR	<	LVSNHSLHETSSVFVDSLTK
/K	*	GAGTGGLGLAVEGPSEAK	=	LYSVSYLLK
TYGGHQVPGSPFK	+	GKLDVQFSGLTK	>	MDCQECPEGYR
	,	GLVEPVDVVDNADGTQTVNYVPSR	?	NDNDTFTVK
IVTITWGGQNIGR	-	GQHVPGSPFQFTVGPLGEGGAHK	@	NGHVGISFVPK
	•	GTVEPQLEAR	Α	NGQHVASSPIPVVISQSEIGDASI
	/	HTAMVSWGGVSIPNSPFR	В	P21333
	0	IANLQTDLSDGLR	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
QPSVQPPLR	8	LLGWIQNKLPQLPITNFSR	К	SPYTVTVGQACNPSACR
DAR	9	LQVEPAVDTSGVQCYGPGIEGQGVFR	L	TFSVWYVPEVTGTHK

Q96KP4



Q96KP4



- ~ ~~LIILIN
- △ DVGAQILLHSHK
- + EGGSIPVTLTFQEATGK
- × GNILIPGINEAVAAVTEEEHK
- ♦ LPDGSEIPLPPILLGR
- □ LVPNMTPEVVGEQVTSYLTK
- LYDDIDFDIEEFAK
- * MMEVAAADVK
- ♦ NVMLLPVGSADDGAHSQNEK
- ₱ Q96KP4
- □ QKLPDGSEIPLPPILLGR
- QLGGSVELVDIGK
- ▼ TGQEIPVNVR
- ▼ TVFGVEPDLTR
- WVAIQSVSAWPEK
- YNYIEGTK

prognosis

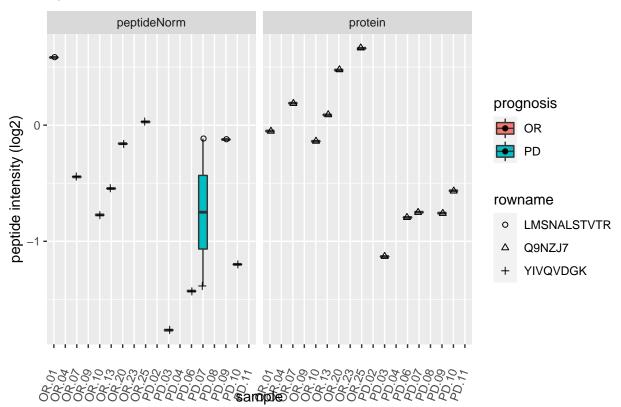


OR

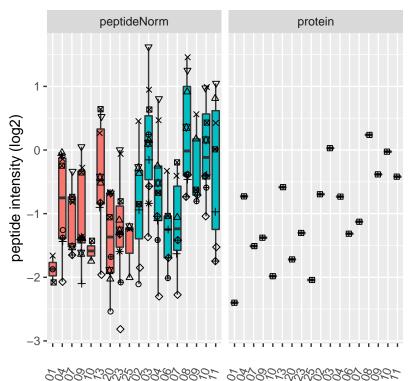
Q9NZJ7



Q9NZJ7







rowname

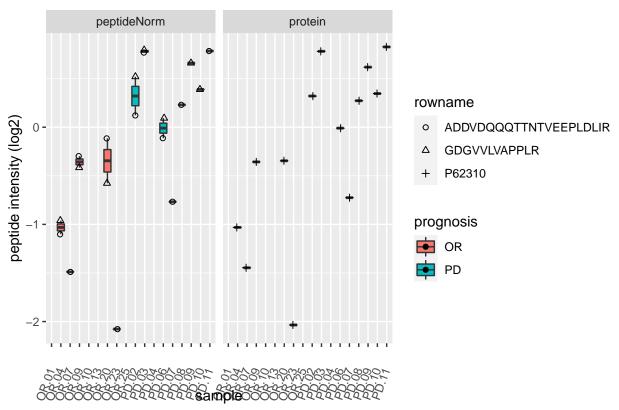
- ADSRDPASDQMQHWKEQR
- △ ADVLTTGAGNPVGDK
- + AFYVNVLNEEQR
- × FNTANDDNVTQVR
- ♦ FSTVAGESGSADTVR
- ▼ FSTVAGESGSADTVRDPR
- GAGAFGYFEVTHDITK
- * LGPNYLHIPVNCPYR
- ◆ LNVITVGPR
- ⊕ LSQEDPDYGIR
- ₩ NLSVEDAAR
- **■** P04040

prognosis



pD

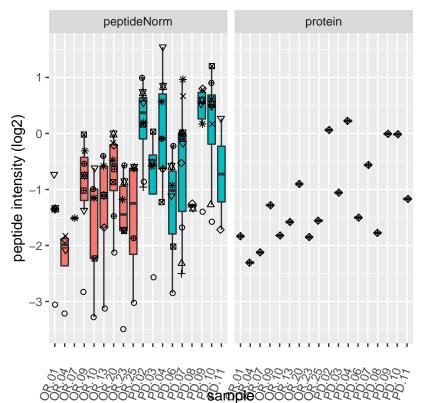




Q02818



Q02818



rowname

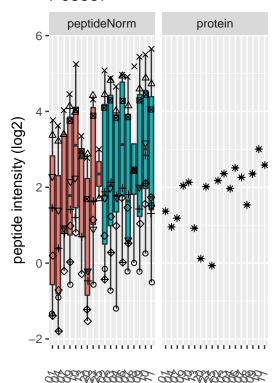
- APAAHPEGQLK
- △ DLAQYDAAHHEEFKR
- + ELQQAVLHMEQR
- × LPEVEVPQHL
- ♦ LQAANAEDIK
- LVTLEEFLASTQR
- * MDAEQDPNVQVDHLNLLK
- ♦ Q02818
- QFEHLDPQNQHTFEAR
- ▼ VNVPGSQAQLK
- YLQEVIDVLETDGHFR

prognosis



PD





rowname

- ILDSVGIEADDDR
- △ ILDSVGIEADDDRLNK
- + KILDSVGIEADDDRLNK
- × LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK
- ♦ LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEK
- NIEDVIAQGIGK
- * P05387
- ♦ YVASYLLAALGGNSSPSAK

prognosis

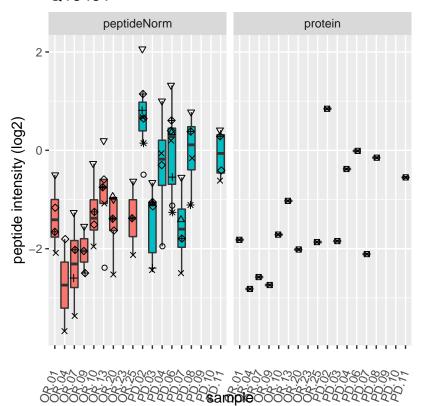


OR



PD





rowname

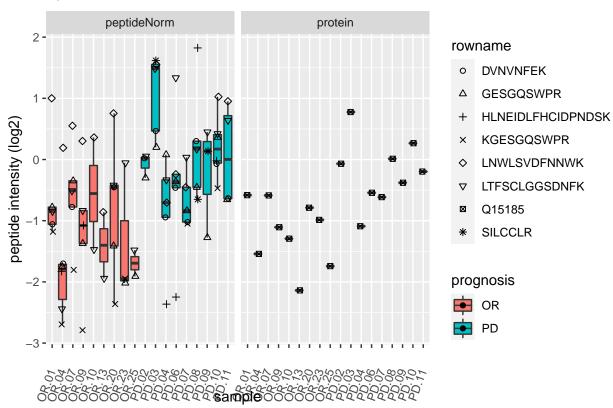
- AWDIGVATMK
- △ DVAFTVGEGEDHDIPIGIDK
- + EKLEQAAIVK
- × FAEQDAKEEANK
- ♦ FGIEPNAELIYEVTLK
- □ GTDSQAMEEEKPEGHV
- ☑ Q13451
- * VGNGEETPMIGDK
- ♦ VLEVNPQNK

prognosis

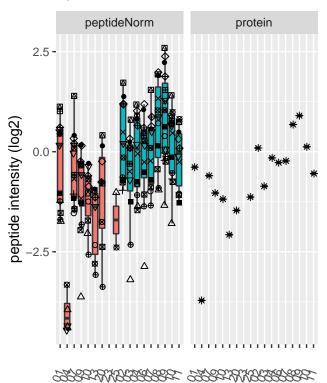


喜 PD









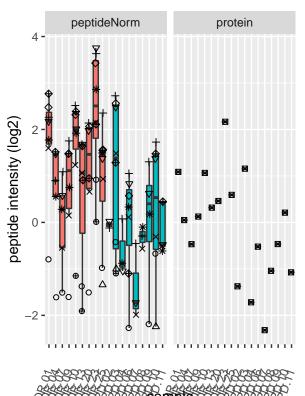
- LALUAI QVLAUN
- △ EAEGAPQVEAGKR
- + EFDPTITDASLSLPSR
- × GNVFSSPTAAGTPNK
- ♦ LEQYTSAIEGTK
- PSDLRPGDVSSK
- * Q05682
- ♦ QKQEEESLGQVTDQVEVNAQNSVPDEEAK
- ⊕ RGETESEEFEK
- **☎** RRGETESEEFEK
- SAKPTKPAASDLPVPAEGVR
- STHQAAIVSK
- TTTTNTQVEGDDEAAFLER
- VLEEEEQR
- YEIEETETVTK

prognosis



OR





rowname

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

prognosis

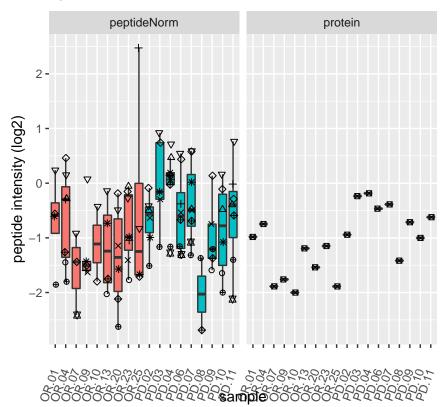


PD

Q9HAB8



Q9HAB8



rowname

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

prognosis

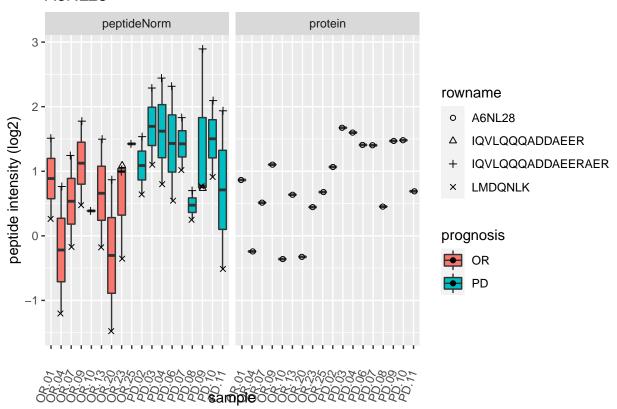


掉 PD

A6NL28



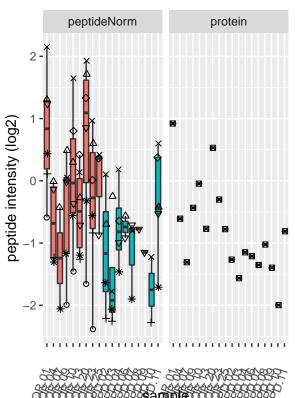
A6NL28



Q9H936



Q9H936



rowname

- DVPFSVVYFPLFANLNQLGRPASEEK
- GAAVNLTLVTPEK
- GLGATLLR
- ILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
- KILAAQGQLSAQGGAQPSVEAPAAPRPTATQLTR
- LAANDFFR
- Q9H936
- SEGYFGMYR

prognosis

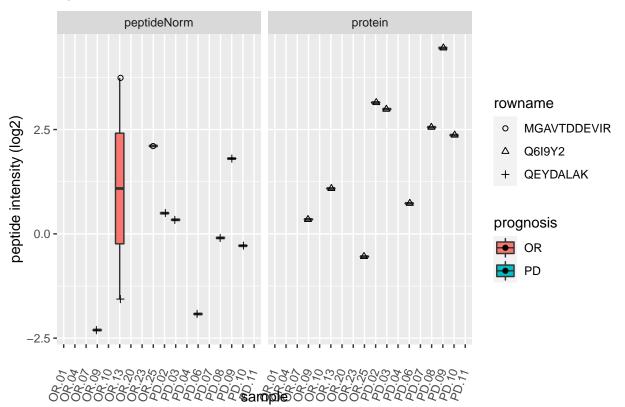




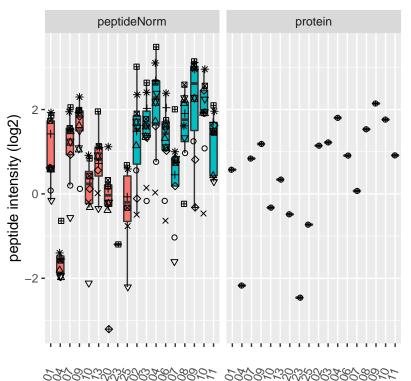
Q6I9Y2



Q6I9Y2







rowname

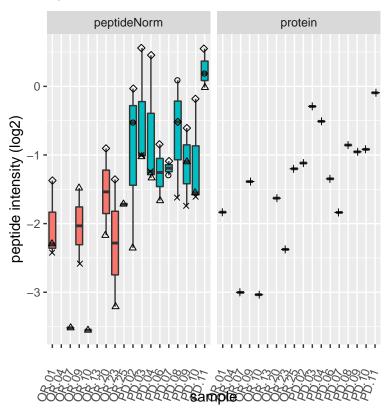
- AEGDVAALNR
- △ AGLNSLEAVK
- + AGLNSLEAVKR
- × CGDLEEELKNVTNNLK
- ♦ EENVGLHQTLDQTLNELNCI
- ▼ EKAEGDVAALNR
- IQALQQQADEAEDR
- * KIQALQQQADEAEDR
- ♦ KLVILEGELERAEER
- ⊕ P67936
- **☆** TIDDLEEK
- YSEKEDKYEEEIK

prognosis



PD





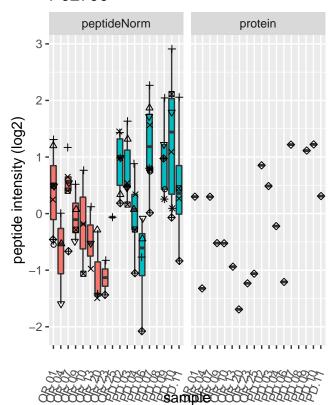
rowname

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

prognosis







prognosis





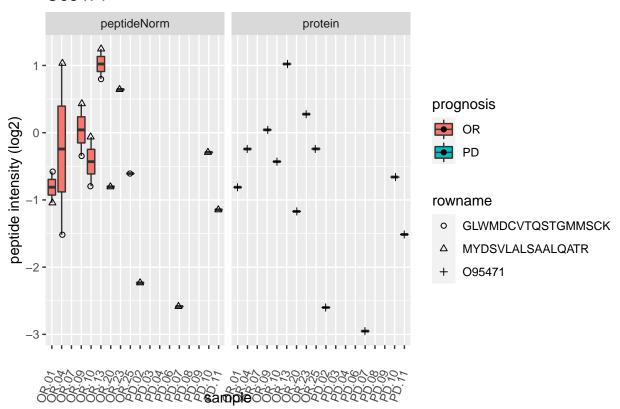
rowname

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

O95471



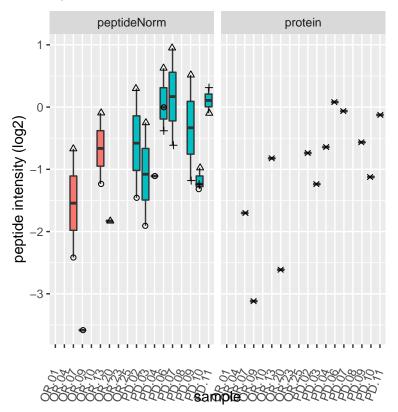
O95471



Q9UGI8



Q9UGI8



rowname

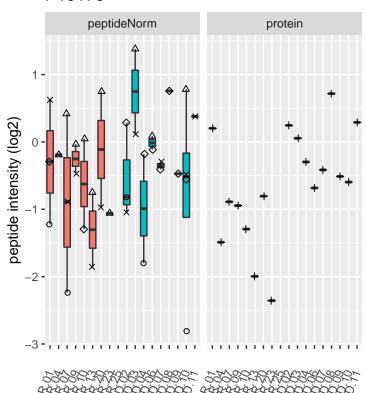
- EKQPVAGSEGAQYR
- △ NVMILTNPVAAK
- + NVSINTVTYEWAPPVQNQALAR
- × Q9UGI8

prognosis









rowname

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

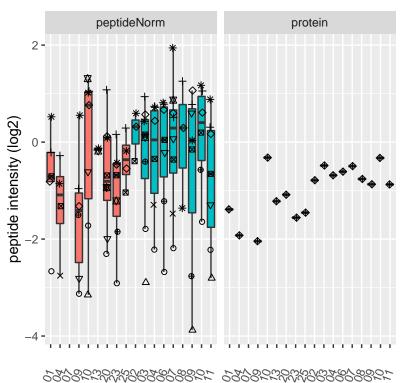
prognosis

OR









rowname

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

prognosis



OR

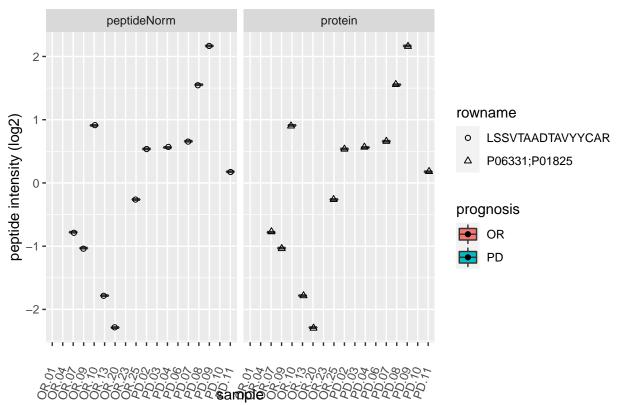


亩 PD

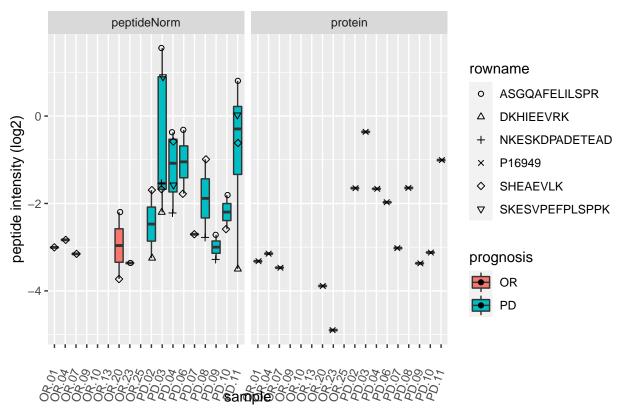
P06331;P01825



P06331;P01825

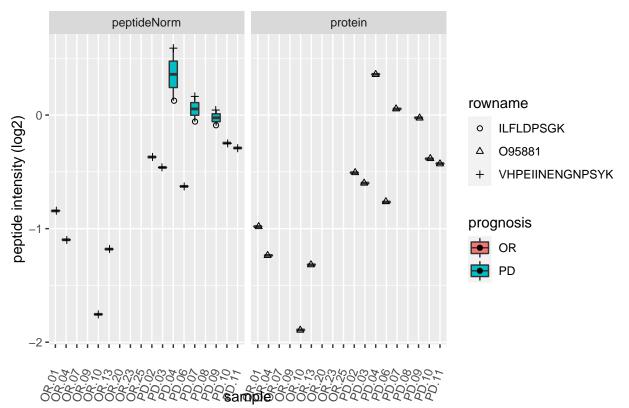




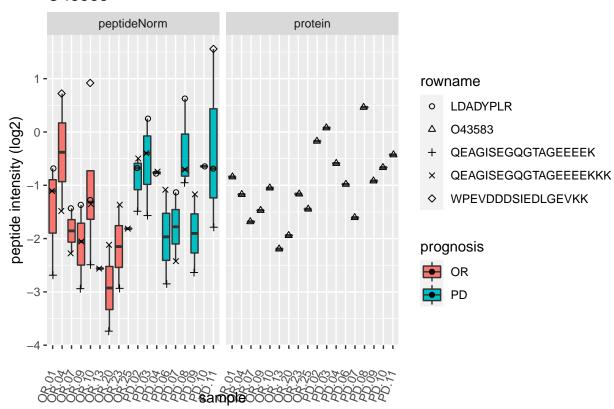


O95881

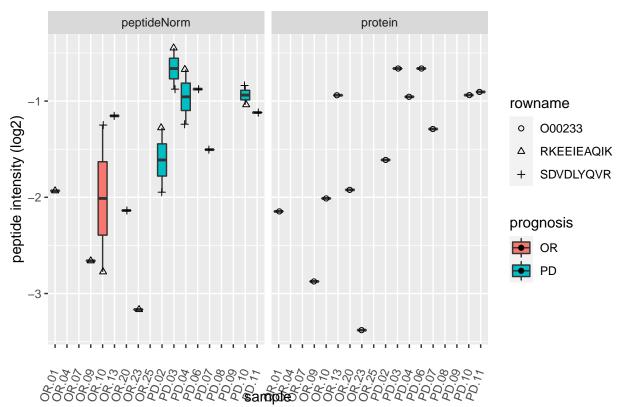








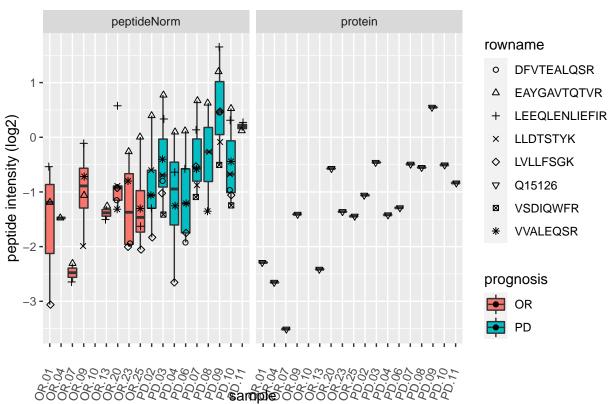




Q15126



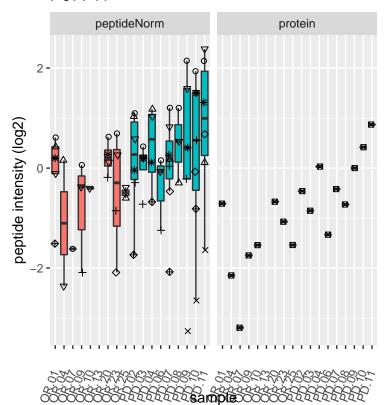
Q15126



P07741



P07741



rowname

- ADSELQLVEQR
- △ AELEIQK
- + DISPVLKDPASFR
- × GFLFGPSLAQELGLGCVLIR
- ♦ GKLPGPTLWASYSLEYGK
- ∇ LAPVPFFSLLQYE
- P07741
- * SFPDFPTPGVVFR
- ◆ VVVVDDLLATGGTMNAACELLGR

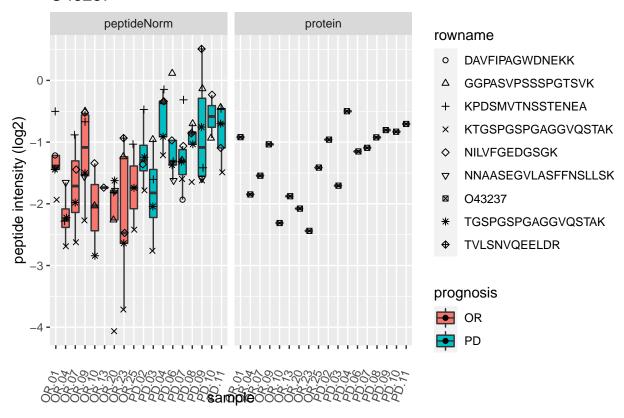
prognosis



OR PD







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
           /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
                           graphics grDevices datasets utils
                 stats
                                                                    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
                                     tidyverse_1.3.2
## [23] ggplot2_3.3.6
##
## loaded via a namespace (and not attached):
##
     [1] googledrive_2.0.0
                                                          colorspace_2.0-3
                                  minqa_1.2.4
##
     [4] ellipsis_0.3.2
                                  XVector 0.36.0
                                                          fs 1.5.2
                                  farver_2.1.0
                                                          DT_0.23
##
     [7] clue_0.3-61
##
    [10] fansi_1.0.3
                                  lubridate_1.8.0
                                                          xm12 1.3.3
##
   [13] codetools_0.2-18
                                  splines_4.2.2
                                                          knitr_1.40.1
                                                          broom_0.8.0
  [16] jsonlite_1.8.0
                                  nloptr_2.0.3
##
  [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
                                                          later_1.3.0
                                  cli_3.3.0
##
   [34] htmltools_0.5.2
                                  tools_4.2.2
                                                          igraph_1.3.2
##
  [37] gtable_0.3.0
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                                                          GenomeInfoDbData_1.2.8
##
  [40] Rcpp_1.0.8.3
                                                          jquerylib_0.1.4
                                  cellranger_1.1.0
##
   [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
                                                          MASS_7.3-57
                                  zlibbioc_1.42.0
                                  promises_1.2.0.1
##
    [55] scales 1.2.0
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##
   [58] ProtGenerics_1.28.0
                                  parallel_4.2.2
                                                          AnnotationFilter_1.20.0
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                                  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
```