

Proteomics data analysis: heart

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Contents

1	Background	2
2	Data	2
2.1	Data import	3
2.2	Data exploration	4
3	Preprocessing	4
3.1	Log transform the data	4
3.2	Filtering	5
3.3	Normalize the data	7
3.4	Explore normalized data	7
3.5	Summarization to protein level	9
4	Data Analysis	10
4.1	Estimation	10
4.2	Inference	10
4.3	Evaluate results contrast $\log_2 FC_{V-A}^L$	12
4.4	Evaluate results contrast $\log_2 FC_{V-A}^R$	22
4.5	Evaluate results average contrast $\log_2 FC_{V-A}$	27
4.6	Interaction	46
5	Large difference in number of proteins that are returned	48
5.1	Reason	49
5.2	Msqrob	50

1 Background

Researchers have assessed the proteome in different regions of the heart for 3 patients (identifiers 3, 4, and 8). For each patient they sampled the left atrium (LA), right atrium (RA), left ventricle (LV) and the right ventricle (RV). The data are a small subset of the public dataset PXD006675 on PRIDE.

Suppose that researchers are mainly interested in comparing the ventricular to the atrial proteome. Particularly, they would like to compare the left atrium to the left ventricle, the right atrium to the right ventricle, the average ventricular vs atrial proteome and if ventricular vs atrial proteome shifts differ between left and right heart region.

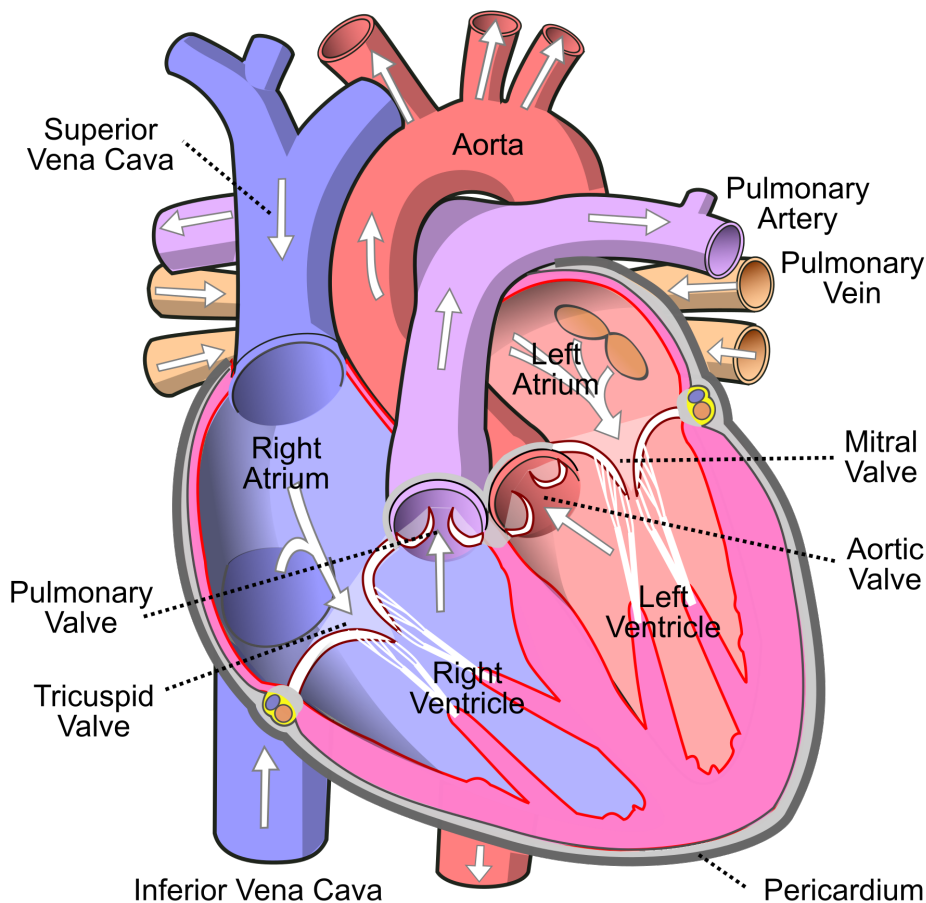


Figure 1: Representation of the heart

2 Data

We first import the peptides.txt file. This is the file that contains your peptide-level intensities. For a MaxQuant search [6], this peptides.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 raw files were saved. In this tutorial, we will use a MaxQuant peptides file from MaxQuant that can be found in the data tree of the SGA2020 github repository <https://github.com/statOmics/SGA2020/tree/data/quantification/heart>.

2.1 Data import

Click to see background and code

To import the data we use the `QFeatures` package.

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

```
library(tidyverse)
library(limma)
library(QFeatures)
library(msqrob2)
library(plotly)

peptidesFile <- "https://raw.githubusercontent.com/statOmics/PDA21/data/quantification/heart/peptides.txt"

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

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

pe
```

```
## An instance of class QFeatures containing 1 assays:
## [1] peptideRaw: SummarizedExperiment with 31319 rows and 12 columns
```

```
pe[["peptideRaw"]]
```

```
## class: SummarizedExperiment
## dim: 31319 12
## metadata(0):
## assays(1): ''
## rownames(31319): AAAAAAAAAAK AAAAAAAAEQQSSNGPVK ... YYTPVPCESATAK
## YYTYLIMNK
## rowData names(91): Sequence N.term.cleavage.window ...
## Oxidation..M..site.IDs MS.MS.Count
## colnames(12): Intensity.LA3 Intensity.LA4 ... Intensity.RV4
## Intensity.RV8
## colData names(0):
```

We will make use from data wrangling functionalities from the `tidyverse` package. The `%>%` operator allows us to pipe the output of one function to the next function.

```
colData(pe)$location <- substr(
  colnames(pe[["peptideRaw"]]),
  11,
  11) %>%
  unlist %>%
```

```

as.factor

colData(pe)$tissue <- substr(
  colnames(pe[["peptideRaw"]]),
  12,
  12) %>%
  unlist %>%
  as.factor

colData(pe)$patient <- substr(
  colnames(pe[["peptideRaw"]]),
  13,
  13) %>%
  unlist %>%
  as.factor

```

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

```

2.2 Data exploration

[Click to see background and code](#)

63% of all peptide intensities are missing and for some peptides we do not even measure a signal in any sample. The missingness is similar across samples.

3 Preprocessing

[Click to see background and code](#)

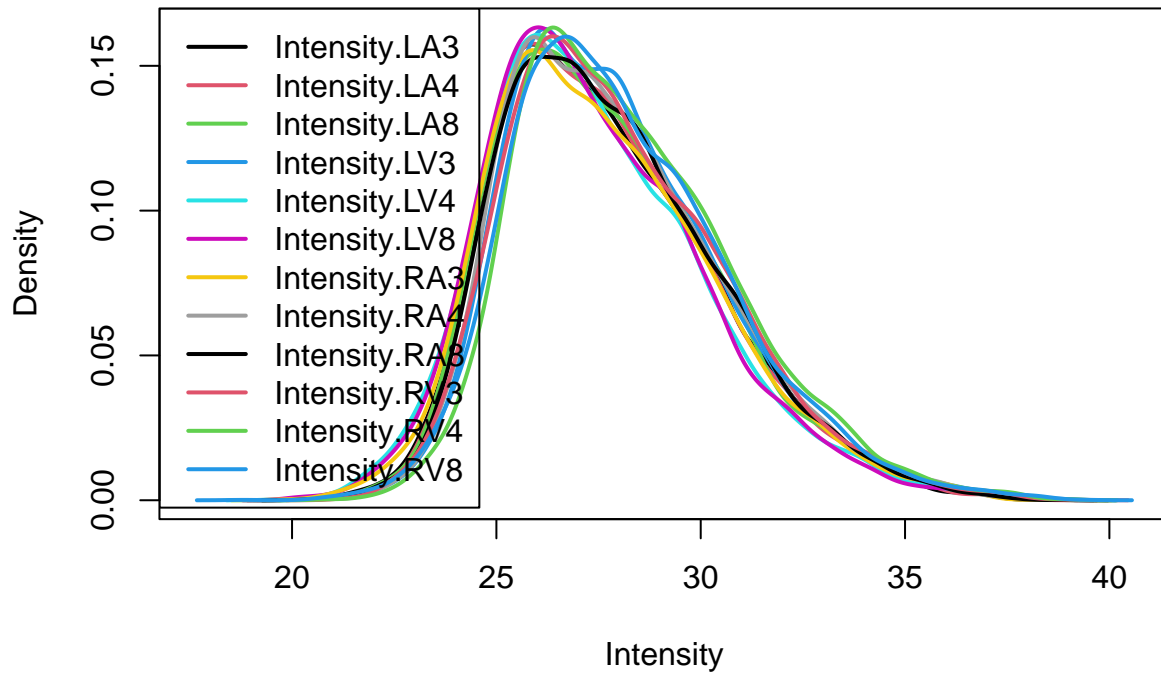
This section performs standard preprocessing for the peptide data. This includes log transformation, filtering and summarisation of the data.

3.1 Log transform the data

```

pe <- logTransform(pe, base = 2, i = "peptideRaw", name = "peptideLog")
limma::plotDensities(assay(pe[["peptideLog"]]))

```



3.2 Filtering

[Click to see background and code](#)

3.2.1 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))
```

3.2.2 Remove reverse sequences (decoys) and contaminants

We now remove the contaminants, peptides that map to decoy sequences, and proteins which were only identified by peptides with modifications.

First look to the names of the variables for the peptide features

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

```
## [1] "Sequence" "N.term.cleavage.window"
```

```
## [3] "C.term.cleavage.window" "Amino.acid.before"
## [5] "First.amino.acid"      "Second.amino.acid"
## [7] "Second.last.amino.acid" "Last.amino.acid"
## [9] "Amino.acid.after"      "A.Count"
## [11] "R.Count"               "N.Count"
## [13] "D.Count"               "C.Count"
## [15] "Q.Count"               "E.Count"
## [17] "G.Count"               "H.Count"
## [19] "I.Count"               "L.Count"
## [21] "K.Count"               "M.Count"
## [23] "F.Count"               "P.Count"
## [25] "S.Count"               "T.Count"
## [27] "W.Count"               "Y.Count"
## [29] "V.Count"               "U.Count"
## [31] "O.Count"               "Length"
## [33] "Missed.cleavages"      "Mass"
## [35] "Proteins"              "Leading.razor.protein"
## [37] "Start.position"         "End.position"
## [39] "Gene.names"             "Protein.names"
## [41] "Unique..Groups."        "Unique..Proteins."
## [43] "Charges"                "PEP"
## [45] "Score"                  "Identification.type.LA3"
## [47] "Identification.type.LA4" "Identification.type.LA8"
## [49] "Identification.type.LV3" "Identification.type.LV4"
## [51] "Identification.type.LV8" "Identification.type.RA3"
## [53] "Identification.type.RA4" "Identification.type.RA8"
## [55] "Identification.type.RV3" "Identification.type.RV4"
## [57] "Identification.type.RV8" "Fraction.Average"
## [59] "Fraction.Std..Dev."      "Fraction.1"
## [61] "Fraction.2"              "Fraction.3"
## [63] "Fraction.4"              "Fraction.5"
## [65] "Fraction.6"              "Fraction.7"
## [67] "Fraction.8"              "Fraction.100"
## [69] "Experiment.LA3"          "Experiment.LA4"
## [71] "Experiment.LA8"          "Experiment.LV3"
## [73] "Experiment.LV4"          "Experiment.LV8"
## [75] "Experiment.RA3"          "Experiment.RA4"
## [77] "Experiment.RA8"          "Experiment.RV3"
## [79] "Experiment.RV4"          "Experiment.RV8"
## [81] "Intensity"               "Reverse"
## [83] "Potential.contaminant"   "id"
## [85] "Protein.group.IDs"       "Mod..peptide.IDs"
## [87] "Evidence.IDs"            "MS.MS.IDs"
## [89] "Best.MS.MS"              "Oxidation..M..site.IDs"
## [91] "MS.MS.Count"             "nNonZero"
```

No information on decoys.

```
pe <- filterFeatures(pe, ~ Potential.contaminant != "+")
```

3.2.3 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] 17432
```

We keep 17432 peptides after filtering.

3.3 Normalize the data

[Click to see background and code](#)

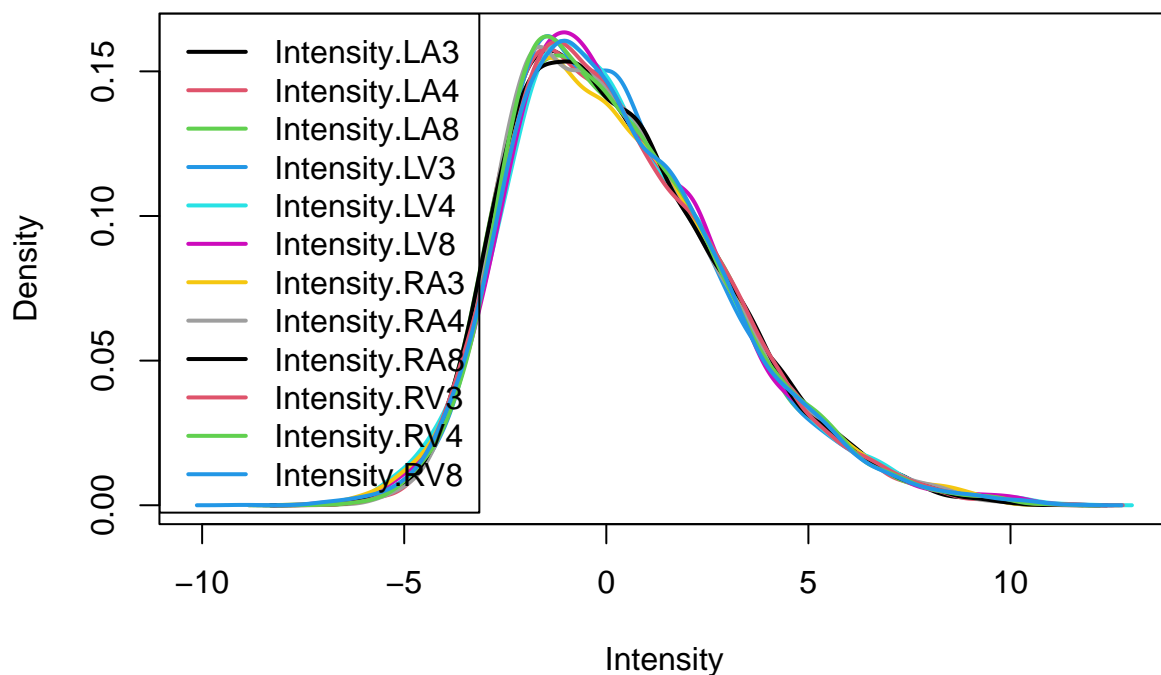
```
pe <- normalize(pe,
               i = "peptideLog",
               name = "peptideNorm",
               method = "center.median")
```

3.4 Explore normalized data

[Click to see background and code](#)

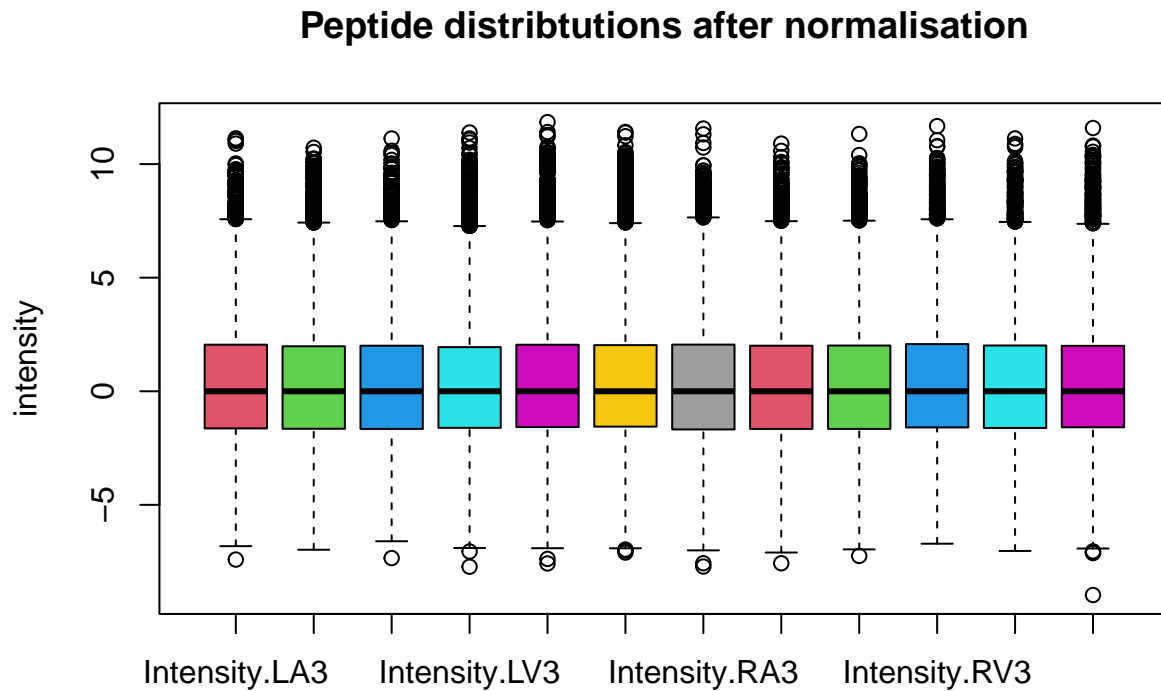
After normalisation the density curves for all samples are comparable.

```
limma::plotDensities(assay(pe[["peptideNorm"]]))
```



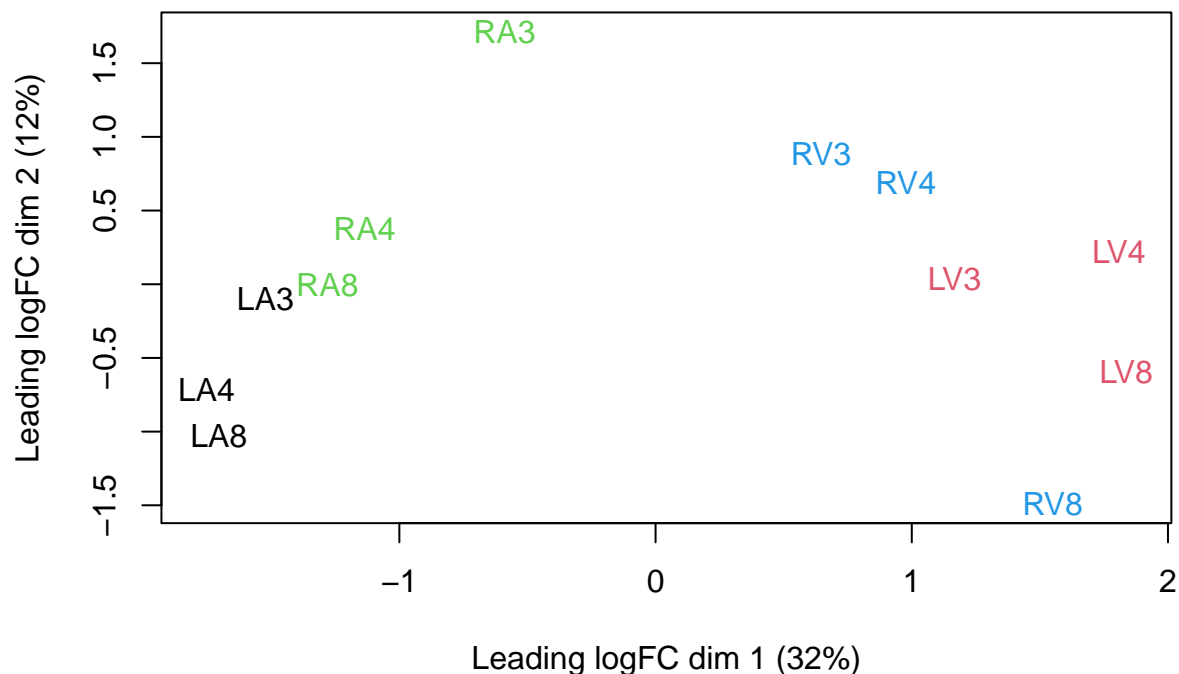
This is more clearly seen in a boxplot.

```
boxplot(assay(pe[["peptideNorm"]]), col = palette()[-1],
        main = "Peptide distributions after normalisation", ylab = "intensity")
```



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

```
limma::plotMDS(assay(pe[["peptideNorm"]]),
               col = colData(pe)$location:colData(pe)$tissue %>%
                 as.numeric,
               labels = colData(pe) %>%
                 rownames %>%
                 substr(start = 11, stop = 13)
               )
```

The first axis in the plot is showing the leading log fold changes (differences on the log scale) between the samples.

3.5 Summarization to protein level

[Click to see background and code](#)

We use robust summarization in `aggregateFeatures`. This is the default workflow of `aggregateFeatures` so you do not have to specify the argument `fun`. However, because we compare methods we have included the `fun` argument to show the summarization method explicitly.

```
pe <- aggregateFeatures(pe,
  i = "peptideNorm",
  fcol = "Proteins",
  na.rm = TRUE,
  name = "proteinRobust",
  fun = MsCoreUtils::robustSummary)
```

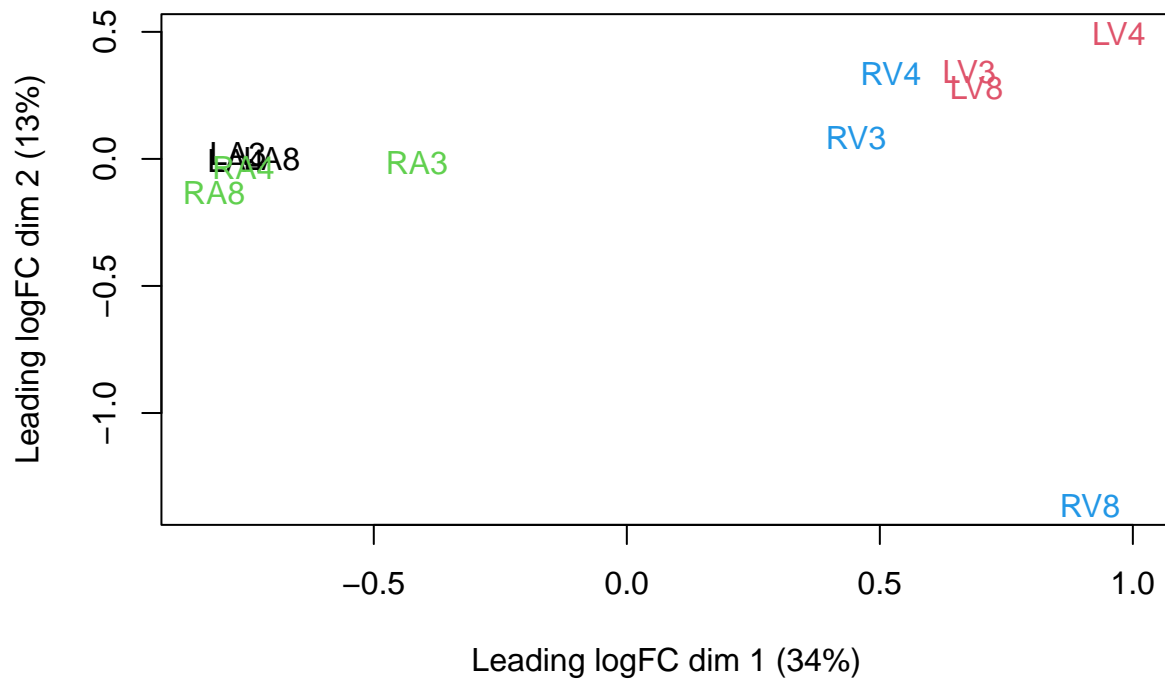
```
## Your quantitative and row data contain missing values. Please read the
## relevant section(s) in the aggregateFeatures manual page regarding the
## effects of missing values on data aggregation.
```

```
plotMDS(assay(pe[["proteinRobust"]]),
  col = colData(pe)$location:colData(pe)$tissue %>%
    as.numeric,
```

```

labels = colData(pe) %>%
  rownames %>%
  substr(start = 11, stop = 13)
)

```



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.

```

pe <- msqrob(
  object = pe,
  i = "proteinRobust",
  formula = ~ location*tissue + patient)

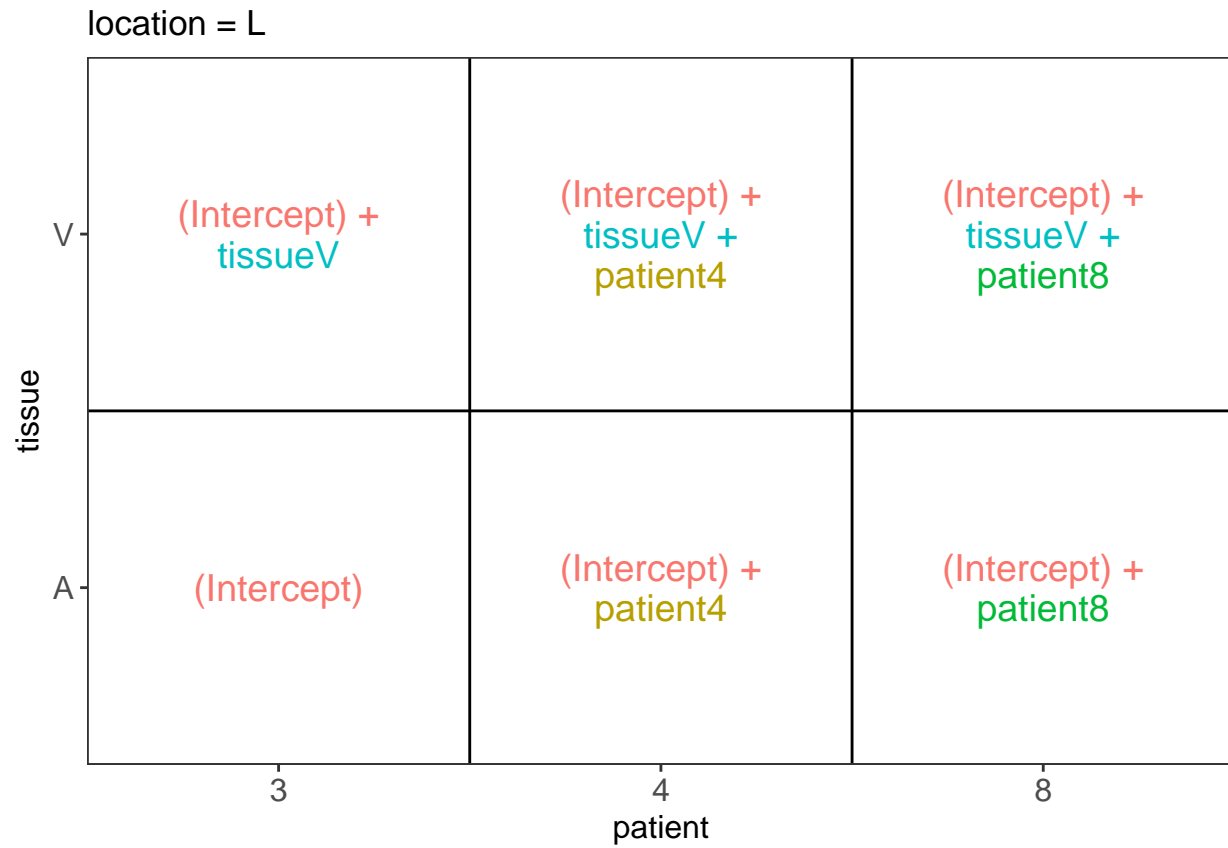
```

4.2 Inference

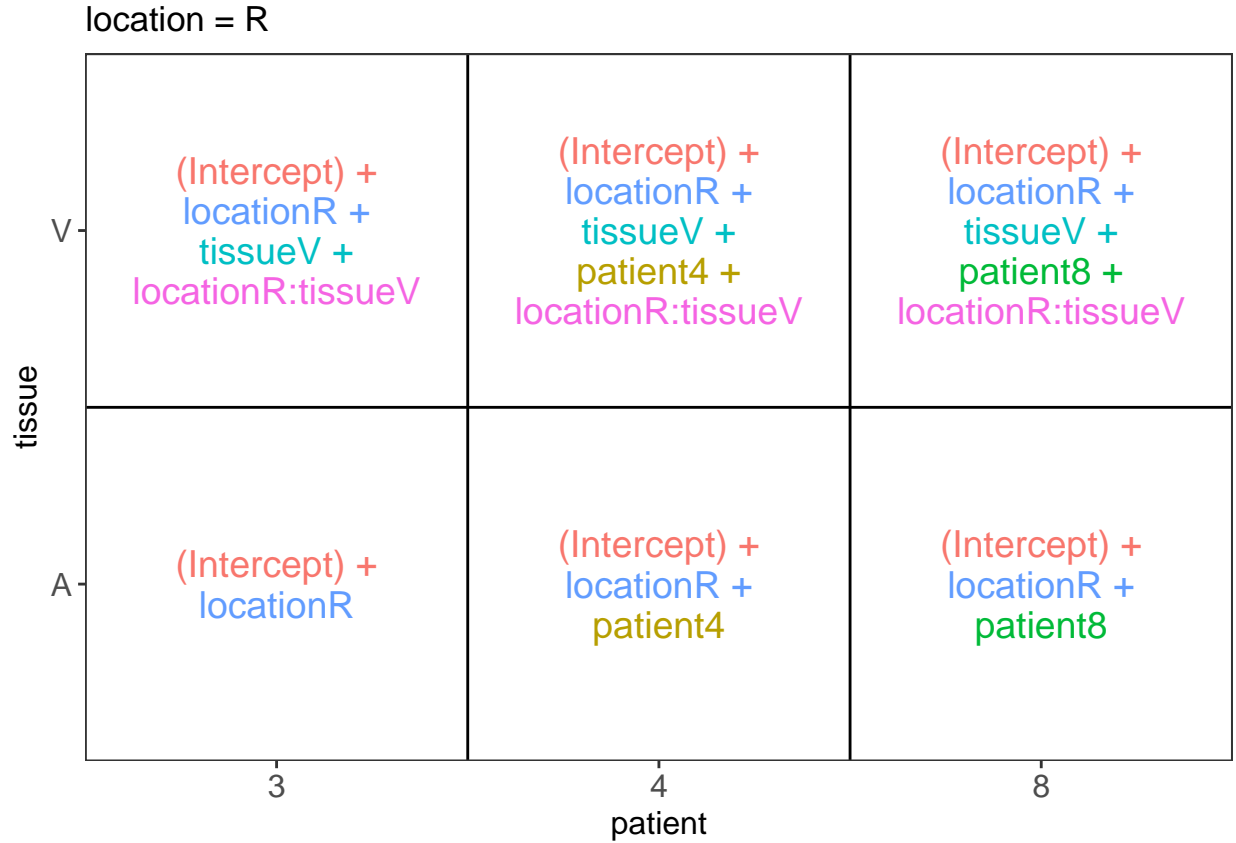
Explore Design

```
library(ExploreModelMatrix)
VisualizeDesign(colData(pe), ~ location*tissue + patient)$plotlist
```

```
## $'location = L'
```



```
##
## $'location = R'
```



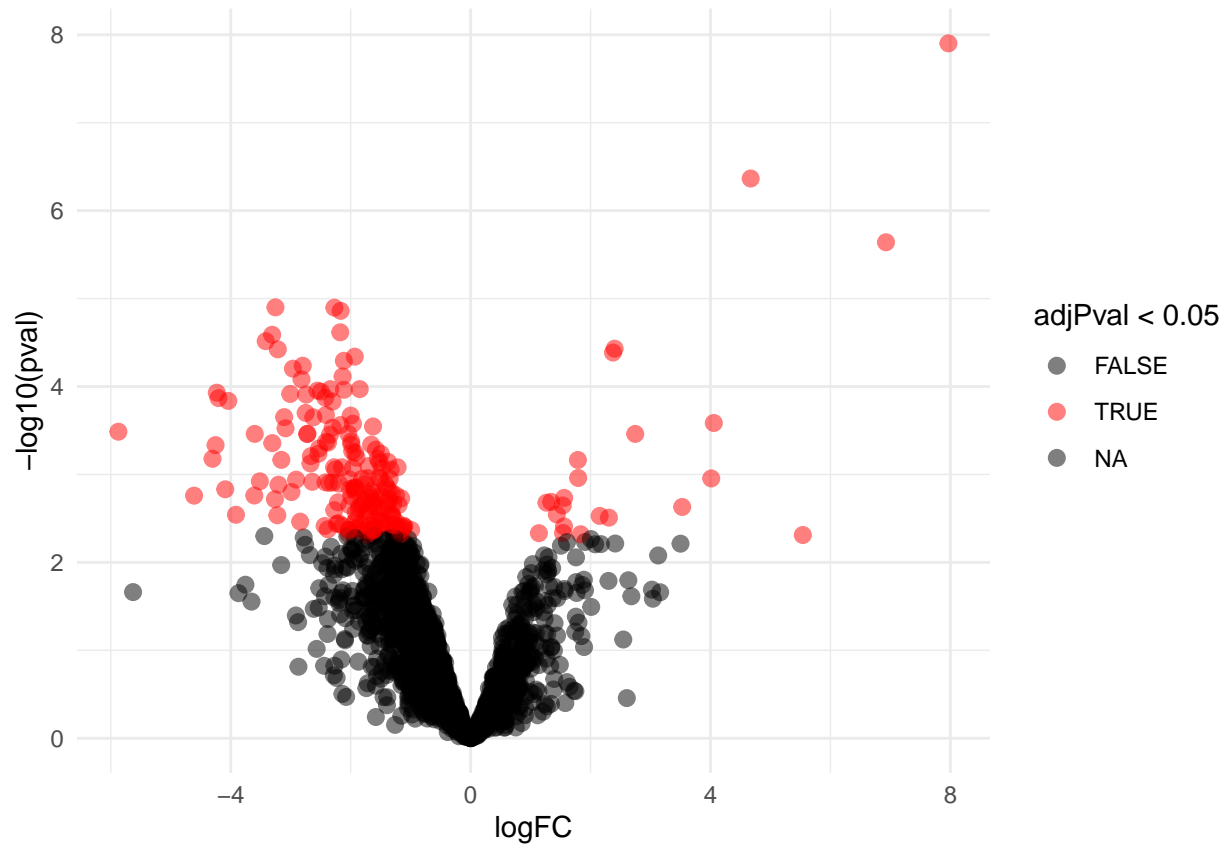
```
design <- model.matrix(~location*tissue + patient, data = colData(pe))
L <- makeContrast(
  c(
    "tissueV = 0",
    "tissueV + locationR:tissueV = 0",
    "tissueV + 0.5*locationR:tissueV = 0", "locationR:tissueV = 0"),
  parameterNames = colnames(design)
)

pe <- hypothesisTest(object = pe, i = "proteinRobust", contrast = L, overwrite=TRUE)
```

4.3 Evaluate results contrast $\log_2 FC_{V-A}^L$

4.3.1 Volcano-plot

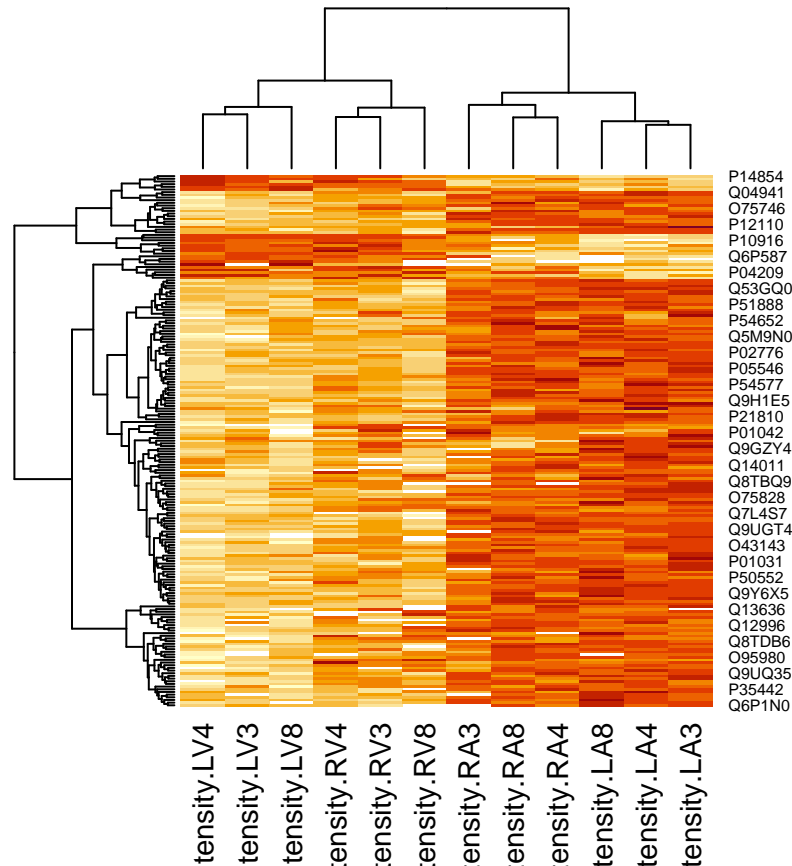
```
volcanoLeft <- ggplot(rowData(pe[["proteinRobust"]])$"tissueV",
  aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)) +
  geom_point(cex = 2.5) +
  scale_color_manual(values = alpha(c("black", "red"), 0.5)) + theme_minimal()
volcanoLeft
```



4.3.2 Heatmap

We first select the names of the proteins that were declared significant.

```
sigNamesLeft <- rowData(pe[["proteinRobust"]])$tissueV %>%
  rownames_to_column("proteinRobust") %>%
  filter(adjPval<0.05) %>%
  pull(proteinRobust)
heatmap(assay(pe[["proteinRobust"]])[sigNamesLeft, ])
```



There are 199 proteins significantly differentially expressed at the 5% FDR level.

```
rowData(pe[["proteinRobust"]])$tissueV %>%
  cbind(.,rowData(pe[["proteinRobust"]])$Protein.names) %>%
  na.exclude %>%
  filter(adjPval<0.05) %>%
  arrange(pval) %>%
  knitr::kable(.)
```

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
P08590	0.670541	0.129487	1147	2.129870	0.00000254	0.00000254	immunoglobulin light chain 3
P12843	0.698827	0.162811	1147	2.564868	0.00000479	0.00000479	immunoglobulin heavy chain 7
P10946	0.260082	0.143671	1147	0.926000	0.023506	0.023506	immunoglobulin regulatory light chain 2, ventricular/cardiac muscle isoform
Q6UWY5	0.382889	0.13260	0.00000260	0.00000260	0.00000260	0.00000260	ectomedin-like protein 1
	3.2536428			8.497596			
O75368	0.271928	0.12260	0.00000260	0.00000260	0.00000260	0.00000260	domain-binding glutamic acid-rich-like protein
	2.2715945			8.365932			
P46821	0.263267	0.12147	0.00000260	0.00000260	0.00000260	0.00000260	microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1
	2.1668803			8.230871			
O95865	0.282367	0.12147	0.00000260	0.00000260	0.00000260	0.00000260	phosphatidylethanolamine N,N-dimethylarginine dimethylaminohydrolase 2
	2.1732192			7.689536			
Q8N474	0.380749	0.12481	0.00000260	0.00000260	0.00000260	0.00000260	secreted frizzled-related protein 1
	3.3090235			8.697787			
Q9ULL5	0.399876	0.12127	0.00000260	0.00000260	0.00000260	0.00000260	serine-rich protein 12
3	3.4165405			8.543546			

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P14834	0.1013	0.5783	317	0.1765	0.0000	0.0000	cytochrome c oxidase subunit 6B1
P21810	0.4218	0.7355	796	0.0000	0.0000	0.0000	Glycan
	3.2145	4.20		7.6231	94		
O94873	0.4000	0.0861	100	0.4523	0.0000	0.0000	in and SH3 domain-containing protein 2
	10						
P05546	0.2699	0.271	1661	0.0000	0.0000	0.0000	Heparin cofactor 2
	1.9318	824		7.1556	98		
P29622	0.3013	0.4357	147	0.0000	0.0000	0.0000	statin
	2.1134	4793		7.0135	27		
Q16647	0.3962	0.428	244	0.0000	0.0000	0.0000	stacyclin synthase
	2.7991	521		7.0642	17		
P02452	0.3999	0.292	268	0.0000	0.0000	0.0000	agen alpha-1(I) chain
	2.9630	153		7.4091	10		
P51884	0.3160	0.757	371	0.0000	0.0000	0.0000	ican
	2.1343	314		6.7525	66		
Q8TBQ9	0.4068	0.642	892	0.0000	0.0000	0.0000	ein kish-A
	2.8189	960		6.9422	32		
P07451	0.2890	0.267	147	0.0000	0.0000	0.0000	onic anhydrase 3
	1.8489	373		6.3838	89		
P36955	0.3358	0.493	555	0.0000	0.0000	0.0000	ient epithelium-derived factor
	2.3377	901		6.9649	84		
P00325	0.3238	0.287	4001	0.0000	0.0000	0.0000	hol dehydrogenase 1B
	2.1119	462		6.5259	31		
Q9UBG0	0.3974	0.702	396	0.0000	0.0000	0.0000	pe mannose receptor 2
	2.5547	510		6.4275	31		
P24844	0.3930	0.351	1934	0.0000	0.0000	0.0000	sin regulatory light polypeptide 9
	2.4962	161		6.3514	47		
P23083	0.5732	0.240	147	0.0000	0.0000	0.0000	avy chain V-I region V35
	4.2325	442		7.3837	42		
P51888	0.4007	0.449	338	0.0000	0.0000	0.0000	argin
	3.0081	810		7.5113	53		
Q15113	0.4328	0.165	821	0.0000	0.0000	0.0000	ollagen C-endopeptidase enhancer 1
	2.7424	988		6.3365	51		
Q53GQ0	0.3900	0.257	570	0.0000	0.0000	0.0000	-long-chain 3-oxoacyl-CoA reductase
	2.4232	423		6.2035	61		
Q06828	0.6622	0.309	004	0.0000	0.0000	0.0000	omodulin
	4.2030	186		6.3465	69		
P13533	0.6482	0.098	373	0.0000	0.0000	0.0000	sin-6
	4.0404	076		6.2328	76		
P35442	0.3528	0.307	147	0.0000	0.0000	0.0000	mbospondin-2
	2.3010	500		6.5350	12		
P08294	0.4255	0.161	1617	0.0000	0.0000	0.0000	acellular superoxide dismutase [Cu-Zn]
	2.7503	241		6.4635	43		
Q96LL9	0.3982	0.707	147	0.0000	0.0000	0.0000	homolog subfamily C member 30
	2.4127	080		6.0588	55		
P18428	0.3385	0.835	859	0.0000	0.0000	0.0000	polysaccharide-binding protein
	1.9996	058		5.9058	30		
P36021	0.5038	0.067	147	0.0000	0.0000	0.0000	ocarboxylate transporter 8
	3.1085	951		6.1702	18		
Q9UL18	0.4093	0.670	316	0.0000	0.0000	0.0000	ein argonaute-1
	2.6225	313		6.4062	96		
Q92508	0.5503	0.357	1367	0.0000	0.0000	0.0000	-type mechanosensitive ion channel component 1

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P46060	0.3259357	1.9620904	6.019876	0.0002018	0.0002018	0.0002018	R405GTPase-activating protein 1
P02743	0.3848307	2.1700557	5.639288	0.0002018	0.0002018	0.0002018	156755 amyloid P-component;Serum amyloid P-component(1-203)
Q14764	0.2898357	1.6267934	5.611689	0.0002018	0.0002018	0.0002018	11244 vault protein
Q9UGT4	0.4078631	2.3006162	5.640659	0.0002018	0.0002018	0.0002018	11244 domain-containing protein 2
P05997	0.5406267	3.0856148	5.707478	0.0002018	0.0002018	0.0002018	11244 collagen alpha-2(V) chain
Q8WWA0	0.9875030	5.8725166	5.946832	0.0002018	0.0002018	0.0002018	11244 lectin-1
Q9P2B2	0.3730337	2.0393915	5.467480	0.0003418	0.0003418	0.0003418	P4266 taglandin F2 receptor negative regulator
O43677	0.4718080	2.7199107	5.769748	0.0003418	0.0003418	0.0003418	N420H dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial
O60760	0.6218377	3.5990151	5.791158	0.0003418	0.0003418	0.0003418	H420 atopoietic prostaglandin D synthase
Q9UBB1	0.5073963	2.7450739	5.480034	0.0003418	0.0003418	0.0003418	11244 N420 N-methyl-CpG-binding domain protein 2
Q9BW30	0.4898299	2.7245919	5.571480	0.0003418	0.0003418	0.0003418	11244 T420 lin polymerization-promoting protein family member 3
P40261	0.4269420	2.3445730	5.491570	0.0003510	0.0003510	0.0003510	N420 tinamide N-methyltransferase
P00748	0.3699783	1.9914680	5.389946	0.0004207	0.0004207	0.0004207	C497 regulation factor XII;Coagulation factor XIIa heavy chain;Beta-factor XIIa part 1;Coagulation factor XIIa light chain
Q9NZ01	0.4362063	2.4109216	5.527049	0.0004254	0.0004254	0.0004254	V497 7-long-chain enoyl-CoA reductase
O14967	0.4289852	2.3785961	5.544702	0.0004317	0.0004317	0.0004317	C497 negin
Q92736	0.6048683	3.3064395	5.473615	0.0004417	0.0004417	0.0004417	R497 odine receptor 2
P12110	0.3538969	1.9881397	5.630590	0.0004508	0.0004508	0.0004508	C497 collagen alpha-2(VI) chain
Q07954	0.3159407	1.6573532	5.258970	0.0004573	0.0004573	0.0004573	P495 low-density lipoprotein receptor-related protein 1;Low-density lipoprotein receptor-related protein 1 85 kDa subunit;Low-density lipoprotein receptor-related protein 1 515 kDa subunit;Low-density lipoprotein receptor-related protein 1 intracellular domain
O00180	0.7668367	4.2526703	5.545857	0.0004617	0.0004617	0.0004617	P497 ssium channel subfamily K member 1
O95980	0.4558786	2.5277905	5.550964	0.0005008	0.0005008	0.0005008	R950 version-inducing cysteine-rich protein with Kazal motifs
P31994	0.3019879	1.5795166	5.239074	0.0005228	0.0005228	0.0005228	E576 affinity immunoglobulin gamma Fc region receptor II-b
O00264	0.3784405	1.9731043	5.213653	0.0005402	0.0005402	0.0005402	N997 membrane-associated progesterone receptor component 1
Q8TBP6	0.3698907	1.9233155	5.200951	0.0005670	0.0005670	0.0005670	S921 te carrier family 25 member 40
Q14195	0.4959220	2.5380012	5.117743	0.0005811	0.0005811	0.0005811	B921 dropyrimidinase-related protein 3
Q8WZA9	0.2916078	1.4960398	5.130437	0.0005821	0.0005821	0.0005821	B921 unity-related GTPase family Q protein

	logFC	se	df	t	pval	adjPval	rowData(pe[[“proteinRobust”]])\$Protein.names
Q9BXN1	0.5179959	1.110	0.0006187	0.275	0.0006187	0.275	perin
	2.6634064			5.141743			
O43464	0.3759944	1.486	0.0006409	0.558	0.0006409	0.558	the protease HTRA2, mitochondrial
	1.9028432			5.071620			
P01699	0.6886928	1.678	0.0006627	0.537	0.0006627	0.537	lambda chain V-I region VOR
	4.3035389			6.251575			
P41240	0.3048927	1.098	0.0006620	0.537	0.0006620	0.537	sine-protein kinase CSK
	1.5466953			5.079582			
Q9GZY4	0.5785702	1.273	0.0006827	0.601	0.0006827	0.601	chrome c oxidase assembly factor 1 homolog
	3.1557642			5.454783			
P06818	0.7890928	1.449	0.0006957	0.561	0.0006957	0.561	protein lipase
Q8NAT1	0.2789207	1.624	0.0007021	0.544	0.0007021	0.544	tein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2
	1.3792038			4.948303			
P04083	0.3089367	1.147	0.0007281	0.548	0.0007281	0.548	exin A1
	1.5201990			4.924495			
P02747	0.4696997	1.471	0.0007501	0.699	0.0007501	0.699	plement C1q subcomponent subunit C
	2.6697776			5.684373			
Q92621	0.3509462	1.182	0.0008022	0.580	0.0008022	0.580	ear pore complex protein Nup205
	1.7036447			4.857201			
Q9NY15	0.4439390	1.476	0.0008282	0.586	0.0008282	0.586	ilin-1
	2.1436460			4.837723			
A6NMZ7	0.4709367	1.147	0.0008292	0.589	0.0008292	0.589	agen alpha-6(VI) chain
	2.2762344			4.833535			
O14980	0.2518307	1.147	0.0008302	0.589	0.0008302	0.589	ortin-1
	1.2169774			4.832729			
P02775	0.4079367	1.147	0.0008402	0.580	0.0008402	0.580	slet basic protein;Connective tissue-activating peptide
	1.9622566			4.819887			III;TC-2;Connective tissue-activating peptide
							III(1-81);Beta-thromboglobulin;Neutrophil-activating peptide
							2(74);Neutrophil-activating peptide 2(73);Neutrophil-activating peptide
							2;TC-1;Neutrophil-activating peptide 2(1-66);Neutrophil-activating
							peptide 2(1-63)
Q96C86	0.3026409	1.986	0.0008402	0.580	0.0008402	0.580	pppX diphosphatase
	1.4762676			4.877936			
Q92604	0.4678639	1.173	0.0008702	0.607	0.0008702	0.607	-CoA:lysophosphatidylglycerol acyltransferase 1
	2.2504519			4.810036			
P48681	0.2789309	1.182	0.0008702	0.607	0.0008702	0.607	in
	1.3334013			4.793288			
P50552	0.3238683	1.622	0.0010786	0.614	0.0010786	0.614	ilator-stimulated phosphoprotein
	1.5288544			4.730872			
P24311	0.7930866	1.374	0.0010926	0.614	0.0010926	0.614	chrome c oxidase subunit 7B, mitochondrial
Q7L4S7	0.3243409	1.840	0.0010926	0.614	0.0010926	0.614	tein ARMCX6
	1.7124303			5.279615			
Q9UN11	0.2038595	1.889	0.0011026	0.614	0.0011026	0.614	NA-binding protein Nova-2
P49207	0.3206974	1.215	0.0011026	0.614	0.0011026	0.614	ribosomal protein L34
	1.5105253			4.711493			
Q8WY22	0.3738387	1.147	0.0011026	0.614	0.0011026	0.614	NA-binding protein
	1.8091979			4.849894			
P46063	0.2888429	1.952	0.0011026	0.614	0.0011026	0.614	D-dependent DNA helicase Q1
	1.3496984			4.672705			
P56539	0.4208375	1.584	0.0011026	0.614	0.0011026	0.614	olin-3
	2.0161968			4.790916			

	logFC	se	df	t	pval	adjPval	rowData(pe[[“proteinRobust”]])\$Protein.names
Q53GG5-2	0.6018556	0.356632	0.0010428	1.026702	0.0010428	0.0010428	and LIM domain protein 3
Q5M9N0	0.7318332	0.32430	0.0010925	1.025743	0.0010925	0.0010925	coiled-coil domain-containing protein 158
Q6SZW1	0.5186367	0.3147	0.0010275	1.025743	0.0010275	0.0010275	le alpha and TIR motif-containing protein 1
Q9HAV4	0.4846303	0.317284	0.0010275	1.025743	0.0010275	0.0010275	artin-5
Q5NDL2	0.4878362	0.32509	0.0010275	1.025743	0.0010275	0.0010275	domain-specific O-linked N-acetylglucosamine transferase
Q9BXR6	0.5178361	0.3182	0.0010275	1.025743	0.0010275	0.0010275	plement factor H-related protein 5
Q92681	0.4497379	0.3124	0.0010275	1.025743	0.0010275	0.0010275	ulatory solute carrier protein family 1 member 1
O15239	0.3048386	0.336	0.0010275	1.025743	0.0010275	0.0010275	min subunit alpha-5
Q8TDB6	0.3837043	0.3834	0.0010275	1.025743	0.0010275	0.0010275	ubiquitin-protein ligase DTX3L
Q96H79	0.5756912	0.3172	0.0010275	1.025743	0.0010275	0.0010275	finger CCCH-type antiviral protein 1-like
P14550	0.3048386	0.336	0.0010275	1.025743	0.0010275	0.0010275	alcohol dehydrogenase [NADP(+)]
Q15274	0.4007362	0.3286	0.0010275	1.025743	0.0010275	0.0010275	adipate-nucleotide pyrophosphorylase [carboxylating]
Q9BUF5	0.4272927	0.31853	0.0010275	1.025743	0.0010275	0.0010275	ulin beta-6 chain
O15111	0.3816383	0.3146	0.0010275	1.025743	0.0010275	0.0010275	inhibitor of nuclear factor kappa-B kinase subunit alpha
Q12996	0.3792340	0.329	0.0010275	1.025743	0.0010275	0.0010275	avage stimulation factor subunit 3
Q9Y5U8	0.9189286	0.368	0.0010275	1.025743	0.0010275	0.0010275	chondrial pyruvate carrier 1
P06727	0.3018578	0.31743	0.0010275	1.025743	0.0010275	0.0010275	lipoprotein A-IV
P04196	0.3967553	0.3131	0.0010275	1.025743	0.0010275	0.0010275	dine-rich glycoprotein
O75828	0.3759307	0.3147	0.0010275	1.025743	0.0010275	0.0010275	onyl reductase [NADPH] 3
Q9UBI9	0.6065037	0.38007	0.0010275	1.025743	0.0010275	0.0010275	case protein homolog
P01031	0.2898439	0.31718	0.0010275	1.025743	0.0010275	0.0010275	plement C5; Complement C5 beta chain; Complement C5 alpha chain; C5a anaphylatoxin; Complement C5 alpha chain
Q9ULC3	0.3628906	0.31470	0.0010275	1.025743	0.0010275	0.0010275	related protein Rab-23
Q6ZSY5	0.3854332	0.32684	0.0010275	1.025743	0.0010275	0.0010275	tein phosphatase 1 regulatory subunit 3F
P45877	0.2872367	0.3147	0.0010275	1.025743	0.0010275	0.0010275	idyl-prolyl cis-trans isomerase C
P02461	0.7978373	0.3561	0.0010275	1.025743	0.0010275	0.0010275	gen alpha-1(III) chain
P04003	0.3412369	0.3835	0.0010275	1.025743	0.0010275	0.0010275	binding protein alpha chain

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P14555	0.93001760	0.3351	0.001031	1.430	0.1439	0.1439	pholipase A2, membrane associated
	4.6109150			4.955432			
Q8N5M1	0.4550069	0.2735	0.001070	1.701	0.1764	0.1764	synthase mitochondrial F1 complex assembly factor 2
	1.9899041			4.367233			
P08582	0.3932327	0.606	0.001823	2.2686	0.2326	0.2326	notransferrin
	1.6911943			4.300091			
Q6YNF6	0.6005313	0.2674	0.001843	2.2958	0.2295	0.2295	oxysteroid dehydrogenase-like protein 2
P34932	0.2699338	0.541	0.001868	2.2344	0.2344	0.2344	shock 70 kDa protein 4
	1.1578310			4.302077			
Q9UQ35	0.3179207	0.7887	0.001022	1.3614	0.1361	0.1361	ne/arginine repetitive matrix protein 2
	1.3570787			4.268609			
O75746	0.3585999	0.528	0.001032	1.414	0.1370	0.1370	dium-binding mitochondrial carrier protein Aralar1
	1.5795706			4.402415			
Q13636	0.6324030	0.434	0.001032	1.414	0.1370	0.1370	related protein Rab-31
	3.2633858			5.160293			
Q5VIR6-	0.4128026	0.4008	0.002033	1.492	0.2033	0.2033	olar protein sorting-associated protein 53 homolog
4	1.7638024			4.272750			
P02776	0.3927875	0.973	0.002039	1.492	0.2039	0.2039	let factor 4;Platelet factor 4, short form
	1.7615098			4.491540			
P04004	0.3758737	0.887	0.002043	1.492	0.2039	0.2039	nectin;Vitronectin V65 subunit;Vitronectin V10
	1.6269790			4.331499			subunit;Somatomedin-B
Q9H1E5	0.3289327	0.147	0.002043	1.492	0.2039	0.2039	redoxin-related transmembrane protein 4
	1.3852786			4.221707			
P04203	0.4301206	0.7374	0.002053	1.492	0.2039	0.2039	mbda chain V-II region NIG-84
P01042	0.4729753	0.167	0.002073	1.492	0.2039	0.2039	ogen-1;Kininogen-1 heavy
	2.2103015			4.673166			chain;T-kinin;Bradykinin;Lysyl-bradykinin;Kininogen-1 light chain;Low
							molecular weight growth-promoting factor
Q8WWQ0	0.3850367	0.147	0.002083	1.492	0.2039	0.2039	interacting protein
	1.6224614			4.208358			
P15926	0.4880037	0.3052	0.002093	1.492	0.2039	0.2039	hoplakin
Q2TAA5	0.3067961	0.244	0.002103	1.492	0.2039	0.2039	P-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase
	1.2916274			4.210046			
Q9BTV4	0.4319358	0.605	0.002225	1.492	0.2039	0.2039	smembrane protein 43
	1.8099873			4.198158			
P05455	0.2850126	0.952	0.002230	1.492	0.2039	0.2039	plus La protein
	1.2004499			4.204543			
Q08945	0.4658367	0.147	0.002232	1.492	0.2039	0.2039	IT complex subunit SSRP1
	2.0204841			4.338444			
Q04725	0.5358466	0.9003	0.002257	1.492	0.2039	0.2039	rogenic locus notch homolog protein 2;Notch 2 extracellular
							truncation;Notch 2 intracellular domain
Q53T59	0.4183082	0.426	0.002258	1.492	0.2039	0.2039	LS1-binding protein 3
	1.8461756			4.412822			
Q9Y6X5	0.3248451	0.882	0.002272	1.492	0.2039	0.2039	(5-adenosyl)-triphosphatase ENPP4
	1.3875045			4.271291			
P09619	0.3850563	0.401	0.002287	1.492	0.2039	0.2039	let-derived growth factor receptor beta
	1.6085799			4.177519			
Q5JPH2	0.2803055	0.7307	0.002303	1.492	0.2039	0.2039	able glutamate-tRNA ligase, mitochondrial
O60262	0.3669827	0.805	0.002363	1.492	0.2039	0.2039	nine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-7
	1.5577722			4.244810			
O75348	0.4529307	0.147	0.002429	1.492	0.2039	0.2039	pe proton ATPase subunit G 1
	1.8591253			4.108278			

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
O00303	0.3498357	0.0024035	1146	14.397975	0.0000000	0.0000000	Eukaryotic translation initiation factor 3 subunit F
	1.4561773			4.162459			
P01034	0.4078285	0.0025353	108	15.921	0.0000000	0.0000000	Stat-C
	1.6978634			4.168290			
P49458	0.5037808	0.0025036	5108	19.8623	0.0000000	0.0000000	Signal recognition particle 9 kDa protein
	2.2735269			4.518307			
P25940	0.4259202	0.0026203	7035	16.407	0.0000000	0.0000000	Fibrogen alpha-3(V) chain
	1.7454125			4.097911			
P62760	0.4698586	0.0027038	594	16.554	0.0000000	0.0000000	Actin-like protein 1
	1.9146688			4.074988			
P08311	0.3218727	0.0028103	5116	11.9026	0.0000000	0.0000000	Chapsin G
	1.3139510			4.092302			
Q9UK96	0.7028531	0.0028608	3028	24.539	0.0000000	0.0000000	Protein kinase C and casein kinase substrate in neurons protein 3
Q14019	0.8342307	0.0028739	6710	29.07147	0.0000000	0.0000000	Adenosin-like protein
	3.9129083			4.690111			
P36551	0.3266525	0.0029083	6710	11.556	0.0000000	0.0000000	Cytochrome c-dependent coproporphyrinogen-III oxidase, mitochondrial
	1.3202398			4.041659			
O15116	0.6508251	0.0029129	6710	22.34148	0.0000000	0.0000000	mRNA-associated Sm-like protein LSm1
	3.2231772			4.952445			
P30405	0.3806387	0.0029289	6710	12.87147	0.0000000	0.0000000	1,4-bisphosphatidyl-prolyl cis-trans isomerase F, mitochondrial
	1.5177122			3.986967			
Q9UKX3	0.5537293	0.0029480	2963	18.9795	0.0000000	0.0000000	Skp1-13
Q9Y2Z0	0.4387267	0.0030100	1923	14.4147	0.0000000	0.0000000	Suppressor of G2 allele of SKP1 homolog
	1.7414076			3.969206			
P54577	0.3238603	0.0030560	1819	10.467819	0.0000000	0.0000000	Tyrosine-tRNA ligase, cytoplasmic; Tyrosine-tRNA ligase, cytoplasmic, N-terminally processed
	1.3002728			4.017281			
P19429	0.6065968	0.0030794	3882	30.0409229	0.0000000	0.0000000	Myosin I, cardiac muscle
P54652	0.4019278	0.0030841	17419	12.8544	0.0000000	0.0000000	Shock-related 70 kDa protein 2
	1.5932853			3.973066			
O75475	0.4838339	0.0032622	2956	14.78788	0.0000000	0.0000000	SRF and SFRS1-interacting protein
	1.9038879			3.934575			
P25311	0.3738903	0.0033063	7841	11.303030	0.0000000	0.0000000	alpha-2-glycoprotein
	1.5051007			4.030810			
P60468	0.3608422	0.0034073	7568	10.2346	0.0000000	0.0000000	Protein transport protein Sec61 subunit beta
	1.4647431			4.064796			
Q9BS26	0.3209307	0.0034373	7568	9.37620	0.0000000	0.0000000	Cytoplasmic reticulum resident protein 44
	1.2463986			3.892639			
Q7LBR1	0.7318267	0.0034454	7568	21.267147	0.0000000	0.0000000	Large multivesicular body protein 1b
	2.8413335			3.882531			
Q04941	0.4959868	0.0035184	1965	13.974	0.0000000	0.0000000	Scavenger lipid protein 2
	1.9356392			3.908925			
P03950	0.5449282	0.0035784	1536	15.1933	0.0000000	0.0000000	Prothymosin
	2.2030636			4.042851			
Q1KMD3	0.3778422	0.0035980	1536	10.2210	0.0000000	0.0000000	Heterogeneous nuclear ribonucleoprotein U-like protein 2
	1.4744120			3.902186			
Q13641	0.5229058	0.0036607	7218	14.5658	0.0000000	0.0000000	Prothoblast glycoprotein
	2.2297004			4.263335			
P26447	0.4678885	0.0036725	2218	12.5342	0.0000000	0.0000000	Protein S100-A4
	1.8372154			3.933335			
Q96PK6	0.3379465	0.0037054	1536	9.474	0.0000000	0.0000000	Protein-binding protein 14
	1.3089284			3.875547			

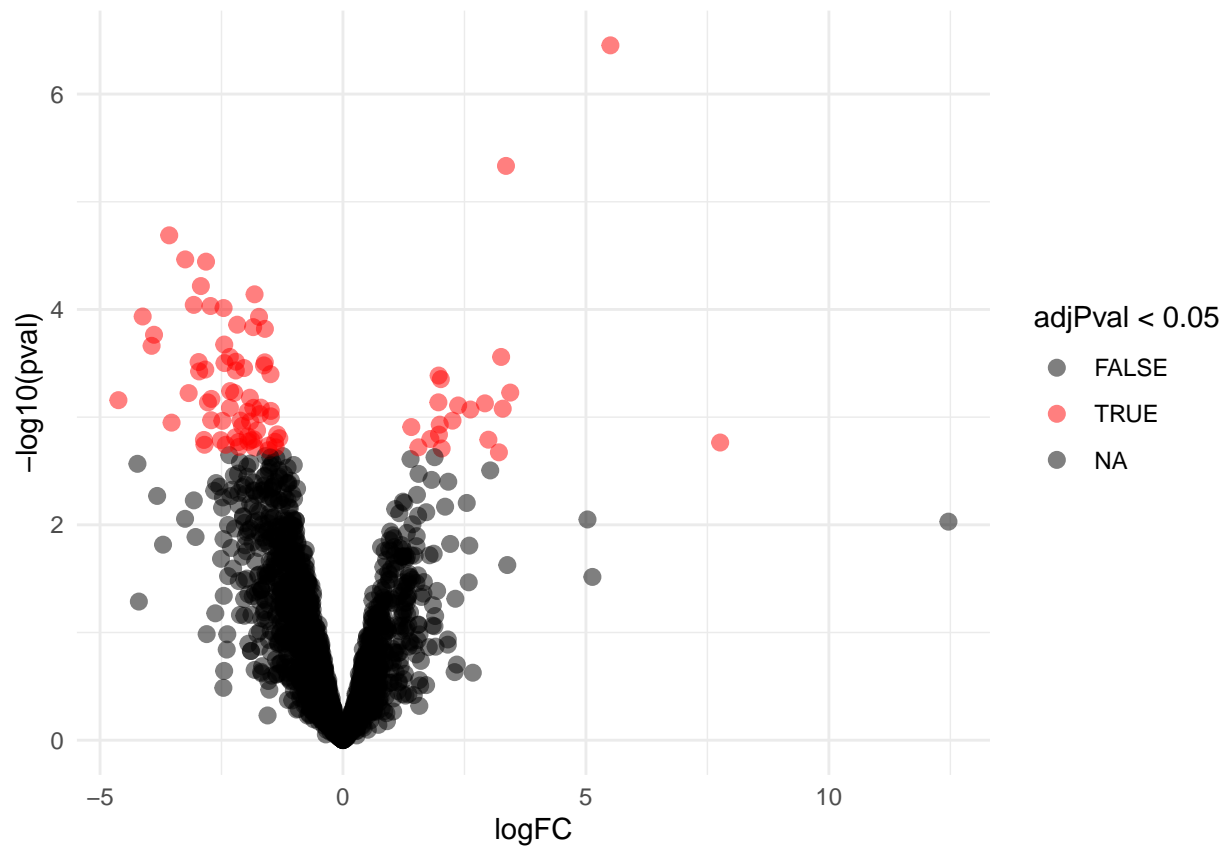
	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
Q9Y3B4	0.3260615	0.015209	0.0038043	5581	0.0038043	5581	Acting factor 3B subunit 6
	1.2603707			3.865414			
Q9HB40	0.4806708	0.048	0.0038043	5581	0.0038043	5581	Stimulin-inducible serine carboxypeptidase
	2.1393191			4.451581			
P01024	0.2906403	0.01573	0.0038043	5581	0.0038043	5581	Complement C3;Complement C3 beta chain;C3-beta-c;Complement C3
	1.1180307			3.846785			alpha chain;C3a anaphylatoxin;Acylation stimulating
							protein;Complement C3b alpha chain;Complement C3c alpha chain
							fragment 1;Complement C3dg fragment;Complement C3g
							fragment;Complement C3d fragment;Complement C3f
							fragment;Complement C3c alpha chain fragment 2
O00567	0.6370892	0.0457	0.0038043	5581	0.0038043	5581	Leolar protein 56
	2.4335450			3.819803			
P12814	0.4228155	0.0643	0.0038043	5581	0.0038043	5581	Tha-actinin-1
	1.6827515			3.985531			
Q13478	0.4168997	0.04897	0.0038043	5581	0.0038043	5581	Interleukin-18 receptor 1
	1.6083281			3.859681			
Q86MU5	0.5806100	0.07140	0.0038043	5581	0.0038043	5581	Chol O-methyltransferase domain-containing protein 1
P07384	0.2899123	0.0204	0.0038043	5581	0.0038043	5581	Tha-1 catalytic subunit
	1.1052065			3.818222			
P01008	0.4138323	0.0357	0.0040057	1199	0.0040057	1199	Thrombin-III
	1.5692162			3.791914			
P14543	0.3769290	0.0089	0.0040057	1199	0.0040057	1199	Tha-1
	1.4365423			3.819276			
O94919	0.2959130	0.0892	0.0040057	1199	0.0040057	1199	Tha-1 nuclease domain-containing 1 protein
	1.1247209			3.810121			
Q9UK22	0.4296385	0.0956	0.0040057	1199	0.0040057	1199	Tha-1 only protein 2
	1.8807802			4.376569			
P07357	0.3019128	0.0682	0.0040057	1199	0.0040057	1199	Complement component C8 alpha chain
	1.1425305			3.789753			
Q7Z3T8	0.4198582	0.0932	0.0040057	1199	0.0040057	1199	Tha-1 finger FYVE domain-containing protein 16
	1.6269924			3.876021			
O95486	0.4479102	0.0990	0.0040057	1199	0.0040057	1199	Tha-1 transport protein Sec24A
	1.7001274			3.802477			
Q9BXY0	0.4360027	0.0155	0.0040057	1199	0.0040057	1199	Tha-1 MAK16 homolog
	1.9170100			4.396722			
Q14011	0.6088033	0.0933	0.0040057	1199	0.0040057	1199	Tha-1 inducible RNA-binding protein
	2.3803571			3.914650			
Q9Y2D4	0.5288489	0.0332	0.0040057	1199	0.0040057	1199	Tha-1 cyst complex component 6B
	2.0300937			3.839431			
Q96ST3	0.4240553	0.0453	0.0040057	1199	0.0040057	1199	Tha-1 amphipathic helix protein Sin3a
	1.6077298			3.785937			
O43143	0.2649267	0.0147	0.0040057	1199	0.0040057	1199	Tha-1 mRNA-splicing factor ATP-dependent RNA helicase DHX15
	0.9916403			3.745907			
P56199	0.3308060	0.0476	0.0040057	1199	0.0040057	1199	Tha-1 grin alpha-1
	1.2716373			3.844058			
Q6IC98	0.3048102	0.0633	0.0040057	1199	0.0040057	1199	Tha-1 domain-containing protein 4
	1.1710653			3.841831			
P09467	0.4940220	0.0615	0.0040057	1199	0.0040057	1199	Tha-1,6-bisphosphatase 1
	2.0219103			4.092623			
P51665	0.3459391	0.0310	0.0040057	1199	0.0040057	1199	Tha-1 proteasome non-ATPase regulatory subunit 7
	1.2958979			3.751475			

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
Q9BVC6	0.4379467	1.467147	0.0043506	3.7711	0.0003771	0.0003771	transmembrane protein 109
	1.6329609			3.732978			
P50991	0.4658151	1.032	0.0043216	3.959	0.0003959	0.0003959	complex protein 1 subunit delta
	1.7929240			3.850651			
Q96FI1	0.4088506	1.492078	0.0043268	3.969	0.0003969	0.0003969	protein light chain 2, cytoplasmic
P23434	0.4390936	1.507167	0.0043265	4.3796	0.0004379	0.0004379	proline cleavage system H protein, mitochondrial
Q8NBF2	0.3146082	1.232	0.0043181	4.151	0.0004151	0.0004151	repeat-containing protein 2
	1.1613746			3.691495			
P04843	0.5398883	1.3743	0.0043674	4.011	0.0004011	0.0004011	chyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1
	2.0344244			3.771026			
Q53FA5	0.5348855	1.998071	0.0043804	4.8940	0.0004894	0.0004894	flavine oxidoreductase PIG3
Q6P1N0	0.4246929	1.225	0.0048244	4.840	0.0004840	0.0004840	coiled-coil and C2 domain-containing protein 1A
	1.7290768			4.075037			
Q6P585	0.5391432	1.572233	0.0048861	4.818	0.0004818	0.0004818	pyruvate FAHD1, mitochondrial

4.4 Evaluate results contrast $\log_2 FC_{V-A}^R$

4.4.1 Volcano-plot

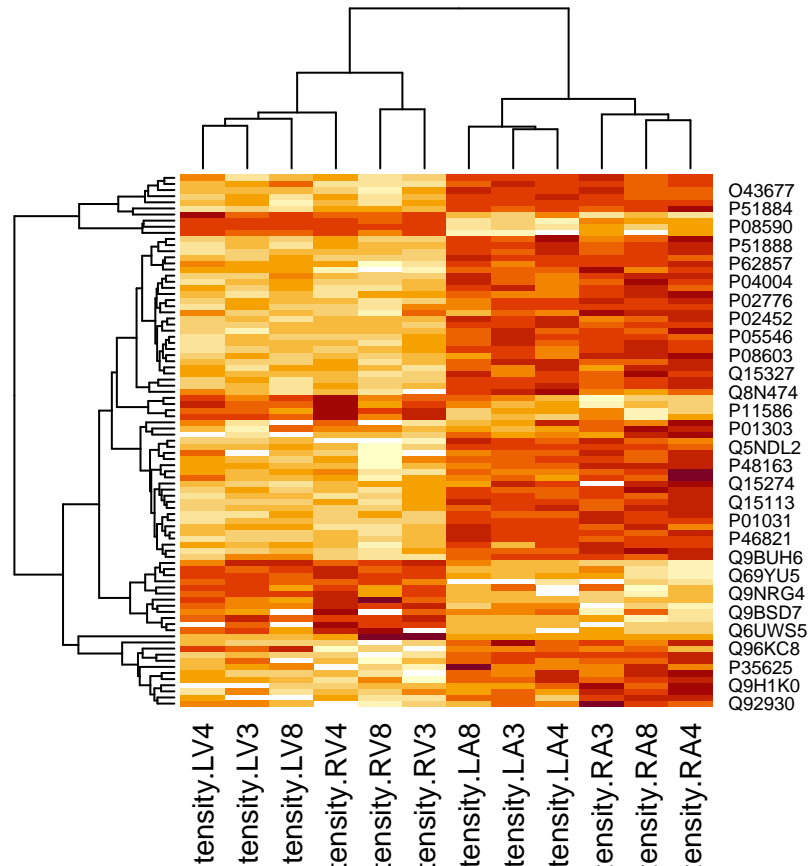
```
volcanoRight <- ggplot(rowData(pe[["proteinRobust"]])$"tissueV + locationR:tissueV",
  aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)) +
  geom_point(cex = 2.5) +
  scale_color_manual(values = alpha(c("black", "red"), 0.5)) + theme_minimal()
volcanoRight
```



4.4.2 Heatmap

We first select the names of the proteins that were declared significant.

```
sigNamesRight <- rowData(pe[["proteinRobust"]])$"tissueV + locationR:tissueV" %>%
  rownames_to_column("proteinRobust") %>%
  filter(adjPval<0.05) %>%
  pull(proteinRobust)
heatmap(assay(pe[["proteinRobust"]])[sigNamesRight, ])
```



There are 87 proteins significantly differentially expressed at the 5% FDR level.

```
rowData(pe[["proteinRobust"]])$"tissueV + locationR:tissueV" %>%
  cbind(.,rowData(pe[["proteinRobust"]])$Protein.names) %>%
  na.exclude %>%
  filter(adjPval<0.05) %>%
  arrange(pval) %>%
  knitr::kable(.)
```

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
P08590	3.383	0.371	127	9.127	0.0000000167	0.0000000167	Insulin light chain 3
P06855	4.463	0.492	147	9.064	0.00000001205	0.00000001205	Protein lipase
Q9ULD0	0.373	0.227	147	1.647	0.00000001038	0.00000001038	Glutarate dehydrogenase-like, mitochondrial
	3.575	0.906		3.935			
P35442	0.406	0.828	147	0.491	0.00000001265	0.00000001265	Endomorphin-2
	3.246	0.460		7.054			
P02776	0.342	0.157	147	2.179	0.00000001265	0.00000001265	Platelet factor 4; Platelet factor 4, short form
	2.818	0.363		7.738			
P21810	0.408	0.156	147	2.618	0.00000001265	0.00000001265	Myosin
	2.924	0.783		3.735			
O75368	0.269	0.123	147	2.189	0.00000001265	0.00000001265	Glutamic acid-binding protein
	1.819	0.326		5.579			
A6NMZ70	0.470	0.267	147	1.761	0.00000001265	0.00000001265	Collagen alpha-6(VI) chain
	3.070	0.848		3.620			

	logFC	se	df	t	pval	adjPval	rowData(pe[[“proteinRobust”]])\$Protein.names
P54652	0.4117048	1.544	0.0000000	0.267128	0.97128	0.97128	shock-related 70 kDa protein 2
	2.726681			6.622904			
Q6UWY5	0.3739352	1.260	0.0000000	0.2970128	0.970128	0.970128	ectomedin-like protein 1
	2.456874			6.570320			
Q06828	0.6368199	1.004	0.0000000	0.628286	0.286	0.286	comodulin
	4.122091			6.477083			
P05546	0.2722278	1.661	0.0000000	0.1719828	0.86	0.86	parin cofactor 2
	1.727800			6.346960			
P28066	0.3385629	1.782	0.0000000	0.1855246	0.85	0.85	asome subunit alpha type-5
	2.176824			6.429476			
P29622	0.3019437	1.147	0.0000000	0.265216	0.8216	0.8216	istatin
	1.847919			6.132273			
P46824	0.2632327	1.147	0.0000000	0.2255216	0.85	0.85	otubule-associated protein 1B;MAP1B heavy chain;MAP1 light
	1.606539			6.102419			chain LC1
P13533	0.6376498	1.373	0.0000000	0.4818208	0.8	0.8	sin-6
	3.888317			6.097975			
Q9UGT4	0.4143431	1.824	0.0000000	0.2215753	0.85	0.85	Bi domain-containing protein 2
	2.443145			5.896430			
P35625	0.6167886	1.282	0.0000000	0.4745753	0.8	0.8	aloproteinase inhibitor 3
	3.938312			6.392443			
Q6PCB0	0.4038938	1.041	0.0000000	0.363652	0.7652	0.7652	Villebrand factor A domain-containing protein 1
	2.328852			5.773148			
Q69YU5	0.5473558	1.395	0.0000000	0.363652	0.7652	0.7652	characterized protein C12orf73
Q15327	0.3936278	1.415	0.0000000	0.273652	0.85	0.85	yrin repeat domain-containing protein 1
	2.203003			5.596523			
O43677	0.5068222	1.596	0.0000000	0.3273652	0.85	0.85	DH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial
	2.969964			5.865758			
Q14764	0.2898937	1.147	0.0000000	0.223652	0.85	0.85	or vault protein
	1.608232			5.547661			
P60468	0.4118822	1.346	0.0000000	0.303652	0.85	0.85	ein transport protein Sec61 subunit beta
	2.438022			5.929209			
P01031	0.2818191	1.718	0.0000000	0.303652	0.85	0.85	plement C5;Complement C5 beta chain;Complement C5 alpha
	1.626524			5.781772			chain;C5a anaphylatoxin;Complement C5 alpha chain
Q9P2B2	0.3739352	1.147	0.0000000	0.303652	0.85	0.85	taglandin F2 receptor negative regulator
	2.035226			5.456312			
Q92930	0.4667028	1.745	0.0000000	0.303652	0.85	0.85	related protein Rab-8B
	2.833666			6.079489			
P02775	0.4079137	1.147	0.0000000	0.303652	0.85	0.85	let basic protein;Connective tissue-activating peptide
	2.205543			5.417470			III;TC-2;Connective tissue-activating peptide
							III(1-81);Beta-thromboglobulin;Neutrophil-activating peptide
							2(74);Neutrophil-activating peptide 2(73);Neutrophil-activating peptide
							2;TC-1;Neutrophil-activating peptide 2(1-66);Neutrophil-activating
							peptide 2(1-63)
P48163	0.4887269	1.840	0.0000000	0.263652	0.85	0.85	P-dependent malic enzyme
	2.959729			6.059718			
P48681	0.2782408	1.182	0.0000000	0.223652	0.85	0.85	in
	1.491288			5.359530			
P128969	0.0659483	1.687	0.0000000	0.0269164	0.85	0.85	sin-7
P115861	0.3351849	1.622	0.0000000	0.2080859	0.85	0.85	C-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate
							dehydrogenase;Methenyltetrahydrofolate
							cyclohydrolase;Formyltetrahydrofolate synthetase;C-1-tetrahydrofolate
							synthase, cytoplasmic, N-terminally processed

	logFC	se	df	t	pval	adjPval	Data(pe[["proteinRobust"]])\$Protein.names
P30711	0.4483332	0.0005723	365	7.7367409	0.0005723	0.0005723	Gamma-Glutamyltransferase theta-1
2.321740				5.178408			
Q9B7H4	0.4280511	0.0005903	370	7.2637360	0.0005903	0.0005903	Repeat-containing protein 11
Q9H1K0	0.3906302	0.0005953	147	6.54409	0.0005953	0.0005953	Enosyn-5
2.237374				5.726736			
Q9UHG2	0.6108871	0.0005973	100	10.337409	0.0005973	0.0005973	SAAS;KEP;Big SAAS;Little SAAS;Big PEN-LEN;PEN;Little
3.175806				5.198401			LEN;Big LEN
P00748	0.3787283	0.0006035	103	6.259772	0.0006035	0.0006035	Regulation factor XII;Coagulation factor XIIa heavy chain;Beta-factor
1.915326				5.057248			XIIa part 1;Coagulation factor XIIa light chain
Q5NDL2	0.5255004	0.0006735	1509	7.75772	0.0006735	0.0006735	Domain-specific O-linked N-acetylglucosamine transferase
2.708130				5.153345			
O00180	0.8854407	0.0006955	147	12.69772	0.0006955	0.0006955	Sodium channel subfamily K member 1
4.621308				5.219183			
Q00C26	0.4023591	0.0007100	595	5.74710	0.0007100	0.0007100	Tipin-5
P23142	0.5087785	0.0007335	834	6.91772	0.0007335	0.0007335	Lin-1
2.779235				5.469018			
P10921	0.5297467	0.0007485	100	7.085772	0.0007485	0.0007485	Sin regulatory light chain 2, ventricular/cardiac muscle isoform
Q09237	0.3707386	0.0007795	113	4.759772	0.0007795	0.0007795	Hear cap-binding protein subunit 1
P18428	0.3459282	0.0008133	659	4.250772	0.0008133	0.0008133	Polysaccharide-binding protein
1.690875				4.895012			
Q9BW30	0.4728199	0.0008133	217	5.7772	0.0008133	0.0008133	Actin polymerization-promoting protein family member 3
2.326597				4.924870			
P30405	0.3806587	0.0008203	147	4.59772	0.0008203	0.0008203	Adipyl-prolyl cis-trans isomerase F, mitochondrial
1.842938				4.841321			
Q5JBH8	0.7518476	0.0008355	371	9.059772	0.0008355	0.0008355	Probable glutamate-tRNA ligase, mitochondrial
Q9NR62	0.2495188	0.0008495	106	2.959772	0.0008495	0.0008495	Sine methyltransferase SMYD2
Q9BUH6	0.3063402	0.0008756	2080	3.4859	0.0008756	0.0008756	Pein PAXX
1.485484				4.844388			
P35052	0.3779177	0.0008926	1113	4.2859	0.0008926	0.0008926	Glypican-1;Secreted glypican-1
1.965366				5.200513			
O15061	0.3609377	0.0009385	147	4.3929	0.0009385	0.0009385	Annin
1.710970				4.747319			
P08603	0.3148067	0.0009833	147	3.2259	0.0009833	0.0009833	Complement factor H
1.484314				4.715011			
Q96FN9	0.5552567	0.0010689	147	5.131	0.0010689	0.0010689	Probable D-tyrosyl-tRNA(Tyr) deacylase 2
2.712489				4.885119			
Q8N474	0.4207397	0.0010739	1481	3.9421	0.0010739	0.0010739	Secreted frizzled-related protein 1
2.108536				5.012244			
Q04262	0.4328708	0.0010789	2098	4.021	0.0010789	0.0010789	Acylglutathione lyase
Q96KC8	0.5055255	0.0010829	1005	4.6121	0.0010829	0.0010829	U homologue subfamily C member 1
2.480944				4.905335			
P04004	0.3998531	0.0010999	1887	3.5121	0.0010999	0.0010999	Conectin;Vitronectin V65 subunit;Vitronectin V10
1.908509				4.773059			subunit;Somatomedin-B
Q99983	0.6606206	0.0011249	6719	5.879	0.0011249	0.0011249	Comodulin
3.527403				5.343578			
P24298	0.1391882	0.0011737	107	1.174238	0.0011737	0.0011737	Sine aminotransferase 1
P62857	0.4153740	0.0012067	192	3.4054	0.0012067	0.0012067	Ribosomal protein S28
2.074531				4.994359			
P23434	0.6043685	0.0012361	3007	4.9719	0.0012361	0.0012361	Sine cleavage system H protein, mitochondrial
P24844	0.3919688	0.0013303	1934	2.9096	0.0013303	0.0013303	Sin regulatory light polypeptide 9
1.767461				4.518410			

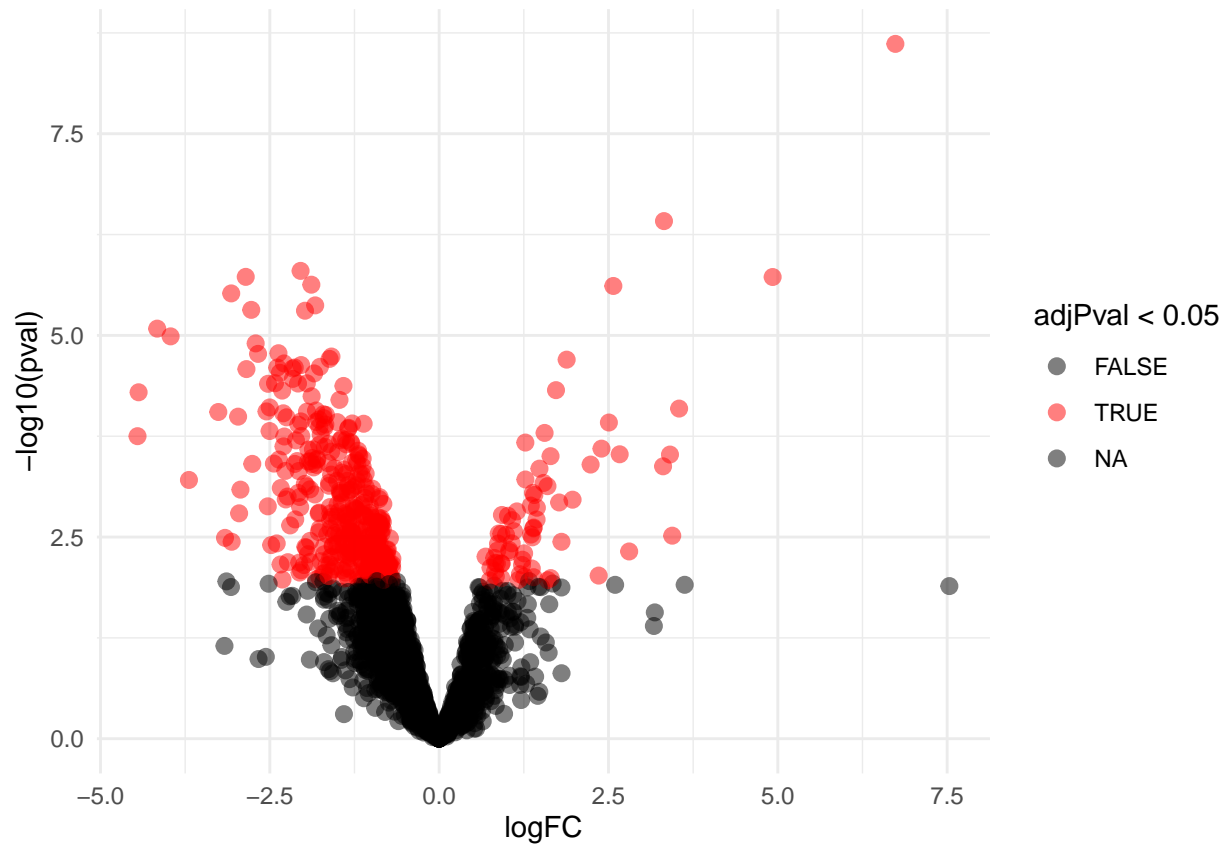
	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
P04275	0.2988133	0.001445	141	20806	0.001445	0.001445	Willebrand factor; von Willebrand antigen 2
	1.352764			4.532424			
Q6P178	0.75693	0.000973	962	7710	0.000973	0.000973	Transmembrane protein 65
Q15113	0.439933	0.001610	51	2821	0.001610	0.001610	collagen C-endopeptidase enhancer 1
	1.959899			4.454929			
P01611	0.501936	0.001640	35	1614	0.001640	0.001640	kappa chain V-I region Wes
	2.213481			4.409491			
Q86WV6	0.296923	0.001608	53	1627	0.001608	0.001608	Regulator of interferon genes protein
	1.310297			4.422592			
Q6UM79	0.583672	0.000882	983	300	0.000882	0.000882	Protein PET117 homolog, mitochondrial
P51888	0.373690	0.001605	51	1838	0.001605	0.001605	Argin
	1.838614			4.920156			
Q9B2D9	0.321090	0.001237	22	4390	0.001237	0.001237	Chaperone-related nucleoside-triphosphatase
P04350	0.573699	0.001628	51	2826	0.001628	0.001628	Thrombin beta-4A chain
	2.861432			4.987600			
Q7L4S7	0.510640	0.001636	51	2840	0.001636	0.001636	Protein ARM CX6
	2.514619			4.924387			
P08294	0.404740	0.001640	51	1617	0.001640	0.001640	Extracellular superoxide dismutase [Cu-Zn]
	1.884866			4.661544			
P82663	0.446937	0.001693	52	2390	0.001693	0.001693	Ribosomal protein S25, mitochondrial
	1.944516			4.354262			
P50453	0.316892	0.001694	53	1440	0.001694	0.001694	Protein B9
	1.398216			4.420644			
P01303	0.486830	0.001702	51	2212	0.001702	0.001702	Neuropeptide Y; Neuropeptide Y; C-flanking peptide of NPY
	2.151374			4.418962			
Q9UL72	0.630750	0.001746	35	700	0.001746	0.001746	Protein related protein Rab-22A
Q9HCB6	0.543890	0.001805	52	1682	0.001805	0.001805	Spindlin-1
	2.412515			4.435619			
Q8TDB4	0.548613	0.001805	53	1626	0.001805	0.001805	Protein MGARP
	2.849906			5.193780			
Q9Y6X5	0.346862	0.001837	63	1682	0.001837	0.001837	(5'-adenosyl)-triphosphatase ENPP4
	1.531154			4.420673			
Q15274	0.468706	0.001889	63	1626	0.001889	0.001889	Glutamate-nucleotide pyrophosphorylase [carboxylating]
	2.142900			4.577796			
Q6YN15	0.303639	0.001924	27	1426	0.001924	0.001924	Proxysteroid dehydrogenase-like protein 2
P51884	0.322990	0.001907	63	1626	0.001907	0.001907	Protein Bican
	1.386041			4.301927			
P02452	0.406899	0.001946	63	1626	0.001946	0.001946	Collagen alpha-1(I) chain
	1.816507			4.466489			
P61926	0.310436	0.001952	24	1025	0.001952	0.001952	Protein kinase inhibitor alpha
P07360	0.353570	0.002028	57	1608	0.002028	0.002028	Complement component C8 gamma chain
	1.535545			4.340638			
Q96N12	0.093462	0.002084	132	380	0.002084	0.002084	Heat shock 70 kDa protein 12B

4.5 Evaluate results average contrast $\log_2 FC_{V-A}$

4.5.1 Volcano-plot

```
volcanoAvg <- ggplot(rowData(pe[["proteinRobust"]])$tissueV + 0.5 * locationR:tissueV",
  aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)) +
```

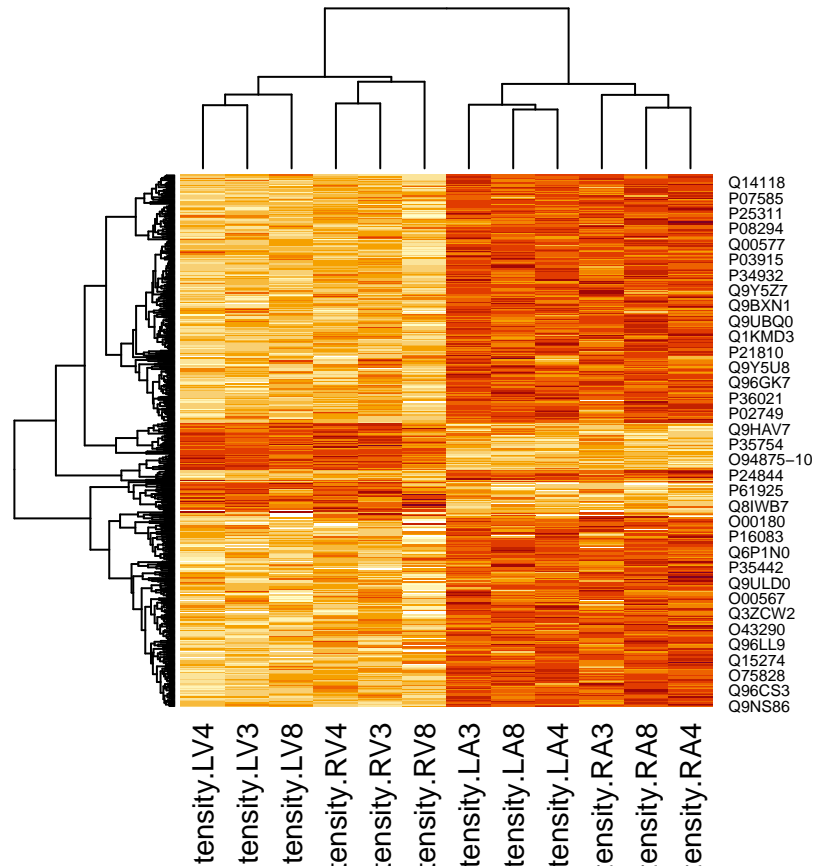
```
geom_point(cex = 2.5) +
scale_color_manual(values = alpha(c("black", "red"), 0.5)) + theme_minimal()
volcanoAvg
```



4.5.2 Heatmap

We first select the names of the proteins that were declared significant.

```
sigNamesAvg <- rowData(pe[["proteinRobust"]])$"tissueV + 0.5 * locationR:tissueV" %>%
rownames_to_column("proteinRobust") %>%
filter(adjPval<0.05) %>%
pull(proteinRobust)
heatmap(assay(pe[["proteinRobust"]])[sigNamesAvg, ])
```



There are 449 proteins significantly differentially expressed at the 5% FDR level.

```
rowData(pe[["proteinRobust"]])$"tissueV + 0.5 * locationR:tissueV" %>%
  cbind(.,rowData(pe[["proteinRobust"]])$Protein.names) %>%
  na.exclude %>%
  filter(adjPval<0.05) %>%
  arrange(pval) %>%
  knitr::kable(.)
```

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
P08590	0.35893	0.03367	117	10.32900	0.00000	0.00000	sin light chain 3
P12883	0.19026	0.03181	112	5.36345	0.00000	0.00000	sin-7
O75368	0.19135	0.02892	260	6.60000	0.00000	0.00000	domain-binding glutamic acid-rich-like protein
	2.0454601			10.689106			
Q6UWY5	0.26799	0.03260		8.20000	0.00000	0.00000	otomedin-like protein 1
	2.8552584			10.670003			
P10946	0.23043	0.03671	137	6.14834	0.00000	0.00000	sin regulatory light chain 2, ventricular/cardiac muscle isoform
P46821	0.18693	0.03671	147	5.06000	0.00000	0.00000	otubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1
P06835	0.17193	0.03194	126	5.20819	0.00000	0.00000	protein lipase
P21810	0.29387	0.05679	6	5.176796	0.00000	0.00000	can
	3.0696624			10.472314			
P05546	0.19162	0.02716	61	6.9545370	0.00000	0.00000	arin cofactor 2
	1.8298412						

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P35442	0.2689	2.367	147	0.0000	0.0001	0.0001	Tbambospondin-2
	2.7737551			10.314070			
P29622	0.2130	3.867	147	0.0000	0.0001	0.0001	U3H141statin
	1.9806994			9.295484			
Q06828	0.4592	2.363	147	0.0000	0.0001	0.0001	EBI65comodulin
	4.1625547			9.064061			
P13533	0.4545	2.798	147	0.0000	0.0001	0.0001	PLN72sin-6
	3.9643622			8.721124			
Q8N474	0.2827	1.827	147	0.0000	0.0001	0.0001	Secreted frizzled-related protein 1
	2.7087798			9.599391			
Q9UGT4	0.2907	1.028	147	0.0000	0.0001	0.0001	SH domain-containing protein 2
	2.3718806			8.159126			
A6NMZ7	0.3329	2.367	147	0.0000	0.0001	0.0001	Collagen alpha-6(VI) chain
	2.6735410			8.028783			
O95865	0.1998	3.427	147	0.0000	0.0001	0.0001	ECN(5),N(G)-dimethylarginine dimethylaminohydrolase 2
	1.5898713			7.955611			
Q14764	0.2049	3.367	147	0.0000	0.0001	0.0001	Br vault protein
	1.6175126			7.890852			
O94873	0.2826	2.385	147	0.0000	0.0001	0.0001	SH3 domain-containing protein 2
	10						
P02776	0.2602	2.275	147	0.0000	0.0001	0.0001	Platelet factor 4;Platelet factor 4, short form
	2.2899367			8.799713			
Q9P2B2	0.2637	3.367	147	0.0000	0.0001	0.0001	Prostaglandin F2 receptor negative regulator
	2.0373086			7.724288			
P51884	0.2256	2.727	147	0.0000	0.0001	0.0001	Calican
	1.7601864			7.799750			
P24844	0.2772	2.311	147	0.0000	0.0001	0.0001	SH3 domain-containing protein 1
	2.1318385			7.689181			
P02452	0.2858	2.222	147	0.0000	0.0001	0.0001	Collagen alpha-1(I) chain
	2.3897612			8.384480			
Q16647	0.2760	1.828	147	0.0000	0.0001	0.0001	Macrolactam synthase
	2.1622988			7.833887			
O43677	0.3458	2.357	147	0.0000	0.0001	0.0001	MDH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial
	2.8449373			8.228647			
Q15113	0.3085	2.725	147	0.0000	0.0001	0.0001	Collagen C-endopeptidase enhancer 1
	2.3511987			7.619599			
P18428	0.2418	2.438	147	0.0000	0.0001	0.0001	Polysaccharide-binding protein
	1.8452405			7.629891			
P54652	0.2873	2.778	147	0.0000	0.0001	0.0001	SH3 domain-containing protein 2
	2.1599833			7.516383			
P51888	0.2713	2.755	147	0.0000	0.0001	0.0001	Argin
	2.4233975			8.930701			
P00748	0.2645	2.710	147	0.0000	0.0001	0.0001	Regulation factor XII;Coagulation factor XIIa heavy chain;Beta-factor
	1.9533971			7.383809			XIIa part 1;Coagulation factor XIIa light chain
P02775	0.2878	2.367	147	0.0000	0.0001	0.0001	Platelet basic protein;Connective tissue-activating peptide
	2.0838997			7.238905			III;TC-2;Connective tissue-activating peptide
							III(1-81);Beta-thromboglobulin;Neutrophil-activating peptide
							2(74);Neutrophil-activating peptide 2(73);Neutrophil-activating peptide
							2;TC-1;Neutrophil-activating peptide 2(1-66);Neutrophil-activating
							peptide 2(1-63)
Q9BW30	0.3399	2.729	147	0.0000	0.0001	0.0001	SH3 domain-containing protein family member 3
	2.5255943			7.428830			

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P48681	0.1967281	1.4123446	7.179175	0.0000425	0.0000425	0.0000425	in
P14854	0.2250827	1.4123446	7.179175	0.0000425	0.0000425	0.0000425	chrome c oxidase subunit 6B1
P08294	0.2927451	2.3175953	7.916749	0.0000402	0.0000402	0.0000402	acellular superoxide dismutase [Cu-Zn]
O00189	0.5858377	4.4369891	7.575947	0.0000502	0.0000502	0.0000502	ssium channel subfamily K member 1
P02743	0.2729307	1.8823835	6.917936	0.0000563	0.0000563	0.0000563	m amyloid P-component;Serum amyloid P-component(1-203)
P01031	0.2028638	1.4711401	7.280573	0.0000603	0.0000603	0.0000603	plement C5;Complement C5 beta chain;Complement C5 alpha chain;C5a anaphylatoxin;Complement C5 alpha chain
Q5NDE2	0.3585102	2.5014769	6.977247	0.0000782	0.0000782	0.0000782	domain-specific O-linked N-acetylglucosamine transferase
Q92595	0.4308786	3.543087	6.77147	0.0000808	0.0000808	0.0000808	type mechanosensitive ion channel component 1
Q53GQ0	0.2763257	1.8169289	6.575413	0.0000854	0.0000854	0.0000854	long-chain 3-oxoacyl-CoA reductase
P05997	0.3783581	2.5486728	6.736140	0.0000874	0.0000874	0.0000874	agen alpha-2(V) chain
P60468	0.2743822	1.9513827	7.111933	0.0000884	0.0000884	0.0000884	tein transport protein Sec61 subunit beta
P23083	0.4233367	3.2601200	7.700684	0.0000894	0.0000894	0.0000894	avy chain V-I region V35
Q9ULL5-	0.3157296	2.3006667	7.300700	0.0000925	0.0000925	0.0000925	ne-rich protein 12
3	2.3006667	2.3006667	7.300700	0.0000925	0.0000925	0.0000925	
Q8TBP6	0.2569337	1.7084465	6.648854	0.0000945	0.0000945	0.0000945	te carrier family 25 member 40
P28066	0.2478829	1.6712466	6.747351	0.0000964	0.0000964	0.0000964	asome subunit alpha type-5
P35625	0.4157946	2.9679404	7.139594	0.0001081	0.0001081	0.0001081	alloproteinase inhibitor 3
Q14195-	0.3489630	2.2534620	6.464943	0.0001087	0.0001087	0.0001087	dropyrimidinase-related protein 3
2	2.2534620	2.2534620	6.464943	0.0001087	0.0001087	0.0001087	
P46060	0.2489377	1.7047689	6.848188	0.0001062	0.0001062	0.0001062	GTPase-activating protein 1
Q15327	0.2767246	1.7740861	6.410333	0.0001103	0.0001103	0.0001103	ryn repeat domain-containing protein 1
Q9ULD0	0.2767246	2.0406330	7.393273	0.0001062	0.0001062	0.0001062	oglutarate dehydrogenase-like, mitochondrial
Q6PCB0	0.2808661	1.8163629	6.478527	0.0001084	0.0001084	0.0001084	Villebrand factor A domain-containing protein 1
P00325	0.2338958	1.5034066	6.450965	0.0001084	0.0001084	0.0001084	hol dehydrogenase 1B
Q69YU5	0.5050638	1.7956123	6.290600	0.0001203	0.0001203	0.0001203	characterized protein C12orf73
P07451	0.2047936	1.2833190	6.266322	0.0001204	0.0001204	0.0001204	onic anhydrase 3
O14989	0.1789637	1.1146843	6.260035	0.0001204	0.0001204	0.0001204	ortin-1
P30405	0.2699737	1.6803249	6.242542	0.0001274	0.0001274	0.0001274	idyl-prolyl cis-trans isomerase F, mitochondrial
Q92604	0.3317299	2.0782169	6.263469	0.0001284	0.0001284	0.0001284	-CoA:lysophosphatidylglycerol acyltransferase 1

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P04004	0.2743072	1.7677440	3071	1.887	0.0001304	0.0011	nectin;Vitronectin V65 subunit;Vitronectin V10 subunit;Somatomedin-B
P36955	0.2522803	1.6933164	3043	1.555	0.0001304	0.0011	ment epithelium-derived factor
P41240	0.2115097	1.3344948	3097	1.098	0.0001304	0.0011	sine-protein kinase CSK
P04083	0.2182307	1.3421955	3047	1.147	0.0001304	0.0011	exin A1
P36021	0.3847886	2.5034435	3867	1.147	0.0001304	0.0011	lodicarboxylate transporter 8
Q6YN15	0.5601257	1.5601257	3307	1.471	0.0001304	0.0011	oxysteroid dehydrogenase-like protein 2
Q8TBQ9	0.2778052	1.7482778	3022	1.592	0.0001304	0.0011	ein kish-A
Q15274	0.3067886	2.0357040	3862	1.286	0.0001304	0.0011	inate-nucleotide pyrophosphorylase [carboxylating]
Q8WWA0	0.6849310	4.4529908	3928	1.594	0.0001304	0.0011	ectin-1
Q9BXN1	0.3737852	2.2858485	3852	1.110	0.0001304	0.0011	orin
P04003	0.2367969	1.4359842	3069	1.835	0.0001304	0.0011	binding protein alpha chain
O15230	0.2231436	1.3744676	3036	1.336	0.0001304	0.0011	linin subunit alpha-5
Q9Y6X5	0.2378292	1.4593292	3091	1.882	0.0001304	0.0011	(5-adenosyl)-triphosphatase ENPP4
Q7L4S7	0.3027739	2.1135247	3998	1.540	0.0001304	0.0011	ein ARM CX6
P14550	0.2159802	1.3048277	3042	1.749	0.0001304	0.0011	hol dehydrogenase [NADP(+)]
P23434	0.2720831	1.4272083	3049	1.867	0.0001304	0.0011	sine cleavage system H protein, mitochondrial
Q07954	0.2228437	1.2959588	3071	1.147	0.0001304	0.0011	low-density lipoprotein receptor-related protein 1;Low-density lipoprotein receptor-related protein 1 85 kDa subunit;Low-density lipoprotein receptor-related protein 1 515 kDa subunit;Low-density lipoprotein receptor-related protein 1 intracellular domain
Q9UBG0	0.2780047	1.6345146	3072	1.2396	0.0001304	0.0011	ype mannose receptor 2
P49207	0.2318971	1.3710319	3071	1.215	0.0001304	0.0011	ribosomal protein L34
Q9BUF5	0.3039727	1.7682813	3277	1.583	0.0001304	0.0011	ulin beta-6 chain
P23142	0.3519937	2.2973847	3583	1.584	0.0001304	0.0011	lin-1
P04196	0.2571653	1.6877176	3053	1.131	0.0001304	0.0011	dine-rich glycoprotein
Q9N134	0.3970489	1.3970489	3651	1.057	0.0001304	0.0011	sine methyltransferase SMYD2
Q9NZ01	0.3148732	1.8635396	3827	1.777	0.0001304	0.0011	-long-chain enoyl-CoA reductase
O95980	0.3148732	1.9294212	3827	1.596	0.0001304	0.0011	ersion-inducing cysteine-rich protein with Kazal motifs
P04275	0.2068942	1.1968998	3042	1.2806	0.0001304	0.0011	Willebrand factor;von Willebrand antigen 2

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P12110	0.262816	0.0020	0.00027064602				Aggen alpha-2(VI) chain
	1.5935296		6.065519				
O75828	0.265237	0.00028054760					Conoyl reductase [NADPH] 3
	1.4912698		5.623030				
P07357	0.211718	0.00029067011					Complement component C8 alpha chain
	1.1909118		5.624991				
Q9B2H6	0.504978	0.0003936981002906					WD repeat-containing protein 11
Q5JPH0	0.705442	0.00030067011					Probable glutamate-tRNA ligase, mitochondrial
Q86WV6	0.210852	0.00030067011					Indulator of interferon genes protein
	1.1787564		5.590434				
P24296	0.440487	0.00030067011					Aspartate aminotransferase 1
P62760	0.336362	0.00030067011					Actin-like protein 1
	1.8748180		5.573799				
P01024	0.203014	0.00030067011					Complement C3; Complement C3 beta chain; C3-beta-c; Complement C3
	1.1291448		5.561340				alpha chain; C3a anaphylatoxin; Acylation stimulating
							protein; Complement C3b alpha chain; Complement C3c alpha chain
							fragment 1; Complement C3dg fragment; Complement C3g
							fragment; Complement C3d fragment; Complement C3f
							fragment; Complement C3c alpha chain fragment 2
P30711	0.322923	0.00030067011					Cathionine S-transferase theta-1
	1.7974916		5.580063				
Q9UHG2	0.420884	0.00030067011					SAAS; KEP; Big SAAS; Little SAAS; Big PEN-LEN; PEN; Little
	2.3658698		5.621492				LEN; Big LEN
Q92681	0.301587	0.00030067011					Regulatory solute carrier protein family 1 member 1
	1.8052155		5.985708				
Q9UQ35	0.224632	0.00030067011					Re/arginine repetitive matrix protein 2
	1.2247564		5.452518				
Q9HCB6	0.370857	0.00030067011					Actin-1
	2.0954145		5.656290				
P12814	0.326815	0.00030067011					Actin-1
	1.9016090		5.830451				
P48163	0.318097	0.00030067011					ATP-dependent malic enzyme
	1.9351889		6.083652				
Q9Y3B4	0.234222	0.00030067011					Acting factor 3B subunit 6
	1.2875533		5.497136				
P25940	0.300973	0.00030067011					Aggen alpha-3(V) chain
	1.6429098		5.462664				
P50453	0.219890	0.00030067011					Actin B9
	1.2078225		5.507626				
Q53GG5-	0.428235	0.00030067011					Actin and LIM domain protein 3
2	2.4399434		5.697097				
Q5M9N0	0.483933	0.00030067011					Coiled-coil domain-containing protein 158
	2.7584485		5.699667				
P07585	0.393720	0.00030067011					Actin
	2.1323372		5.415987				
P49458	0.302383	0.00030067011					Actin recognition particle 9 kDa protein
	1.8786710		6.212876				
P19429	0.366859	0.00030067011					Actin I, cardiac muscle
Q53T59	0.311298	0.00030067011					Actin-binding protein 3
	1.8080103		5.809627				
Q9UNF0	0.306032	0.00030067011					Actin-binding protein Nova-2

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
O94919	0.2100643	0.000145	892	0.000145	0.000145	0.000145	nuclease domain-containing 1 protein
	1.1297756			5.378231			
P02747	0.2972492	0.000138	471	0.000138	0.000138	0.000138	plement C1q subcomponent subunit C
	1.8530999			6.234226			
P01008	0.2920823	0.000140	357	0.000140	0.000140	0.000140	thrombin-III
	1.5453986			5.290988			
Q00Q26	0.2681035	0.000135	508	0.000135	0.000135	0.000135	ipin-5
O00264	0.2635374	0.000150	1168	0.000150	0.000150	0.000150	brane-associated progesterone receptor component 1
	1.4077482			5.341736			
O60769	0.4118337	0.000178	1147	0.000178	0.000178	0.000178	matopoietic prostaglandin D synthase
	2.2693850			5.520786			
Q6SZW1	0.3497357	0.000180	1147	0.000180	0.000180	0.000180	le alpha and TIR motif-containing protein 1
	2.0732831			5.928664			
Q9ULC3	0.2659107	0.000500	1470	0.000500	0.000500	0.000500	related protein Rab-23
	1.4313739			5.382908			
Q9BS26	0.2270401	0.000500	1620	0.000500	0.000500	0.000500	oplasmic reticulum resident protein 44
	1.1794250			5.194575			
Q8WZA9	0.2079793	0.000508	1039	0.000508	0.000508	0.000508	unity-related GTPase family Q protein
	1.0848657			5.216213			
P14543	0.2626950	0.000520	1089	0.000520	0.000520	0.000520	gen-1
	1.3732462			5.227532			
P08603	0.2226337	0.000526	1147	0.000526	0.000526	0.000526	plement factor H
	1.1479994			5.157195			
Q9BTV4	0.3065143	0.000532	1605	0.000532	0.000532	0.000532	smembrane protein 43
	1.5944595			5.201232			
Q2TAA5	0.2187821	0.000607	1244	0.000607	0.000607	0.000607	-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase
	1.1153927			5.098178			
P11586	0.2730423	0.000617	1956	0.000617	0.000617	0.000617	tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methenyltetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase;C-1-tetrahydrofolate synthase, cytoplasmic, N-terminally processed
	1.1586734			5.098178			
Q9UKR5	0.7006734	0.000610	1780	0.000610	0.000610	0.000610	able ergosterol biosynthetic protein 28
	3.6937409			5.271700			
Q9UJC5	0.2412327	0.000632	1075	0.000632	0.000632	0.000632	domain-binding glutamic acid-rich-like protein 2
	1.2143605			5.034295			
Q8WY22	0.2849337	0.000635	1147	0.000635	0.000635	0.000635	-binding protein
	1.5074312			5.290848			
P13671	0.2703327	0.000635	1147	0.000635	0.000635	0.000635	plement component C6
	1.3576211			5.020926			
O14967	0.3128357	0.000671	1297	0.000671	0.000671	0.000671	egin
	1.6233066			5.197312			
Q6PII7	0.4206234	0.000675	1889	0.000675	0.000675	0.000675	smembrane protein 65
P01042	0.3517273	0.000691	1167	0.000691	0.000691	0.000691	ogen-1;Kininogen-1 heavy chain;T-kinin;Bradykinin;Lysyl-bradykinin;Kininogen-1 light chain;Low molecular weight growth-promoting factor
	1.9829048			5.636499			
Q8WWQ0	0.2726367	0.000721	1147	0.000721	0.000721	0.000721	Interacting protein
	1.3446280			4.932367			
Q92621	0.2480457	0.000724	1182	0.000724	0.000724	0.000724	lear pore complex protein Nup205
	1.2226648			4.929192			
Q12996	0.2706240	0.000731	10629	0.000731	0.000731	0.000731	vage stimulation factor subunit 3
	1.6262833			6.015988			
Q9HAT5	0.2992352	0.000740	1809	0.000740	0.000740	0.000740	te O-acetyltransferase
	1.5992352			5.014863			

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P20774	0.3708601	0.0007410	5847	5.277741	0.0007410	0.0007410	Secan
Q9BUH6	0.2190953	0.0007611	53080	4.942437	0.0007611	0.0007611	tein PAXX
Q16082	0.2540456	0.0007669	163	4.971383	0.0007669	0.0007669	shock protein beta-2
Q8TDB4	0.3846732	0.0007801	2826	6.079718	0.0007801	0.0007801	tein MGARP
P45877	0.2030367	0.0007931	147	4.864079	0.0007931	0.0007931	idyl-prolyl cis-trans isomerase C
Q14314	0.3928364	0.0008003	1182	4.850299	0.0008003	0.0008003	leukin
P35052	0.2457794	0.0008040	1113	5.278154	0.0008040	0.0008040	ican-1;Secreted glypican-1
P02461	0.5758373	0.0008070	3561	5.093632	0.0008070	0.0008070	agen alpha-1(III) chain
P02790	0.2719333	0.0008327	3595	4.833533	0.0008327	0.0008327	opexin
P01034	0.2965805	0.0008413	5921	4.949824	0.0008413	0.0008413	atin-C
Q86VP6	0.2705069	0.0008811	9745	4.992852	0.0008811	0.0008811	n-associated NEDD8-dissociated protein 1
P40261	0.2999820	0.0008926	2790	4.813234	0.0008926	0.0008926	tinamide N-methyltransferase
Q86VU3	0.3846289	0.0009070	3374	4.778710	0.0009070	0.0009070	chol O-methyltransferase domain-containing protein 1
P50479	0.4098163	0.0009089	13814	5.084608	0.0009089	0.0009089	and LIM domain protein 4
P28300	0.2816771	0.0009023	1987	5.199244	0.0009023	0.0009023	tein-lysine 6-oxidase
P06727	0.2190587	0.0009128	7743	4.896720	0.0009128	0.0009128	lipoprotein A-IV
Q15126	0.2092367	0.0009211	367147	4.760285	0.0009211	0.0009211	phomevalonate kinase
O95183	0.3056337	0.0009377	367147	4.747910	0.0009377	0.0009377	le-associated membrane protein 5
Q9HAV4	0.3517611	0.0009382	17284	5.219807	0.0009382	0.0009382	ortin-5
Q9NRX4	0.4503916	0.0009522	2482	4.951244	0.0009522	0.0009522	Da phosphohistidine phosphatase
Q96H79	0.3816014	0.0009941	17712	5.866853	0.0009941	0.0009941	finger CCCH-type antiviral protein 1-like
O43175	0.4347016	0.0010082	168272	4.738201	0.0010082	0.0010082	phosphoglycerate dehydrogenase
O43143	0.1879307	0.0010112	367147	4.695622	0.0010112	0.0010112	mRNA-splicing factor ATP-dependent RNA helicase DHX15
P13667	0.2314854	0.0010311	19096	4.731772	0.0010311	0.0010311	tein disulfide-isomerase A4
P34932	0.1892733	0.0010613	3541	4.682936	0.0010613	0.0010613	shock 70 kDa protein 4
Q15582	0.4552424	0.0010811	24872	4.974325	0.0010811	0.0010811	sforming growth factor-beta-induced protein ig-h3
Q09169	0.9700082	0.0011635	160068	10.883006	0.0011635	0.0011635	ear cap-binding protein subunit 1

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
Q9NY15	0.3139370	1.4385610	476	0.00107743455	1.4385610	4.594463	lin-1
Q9UKX7	0.3203780	1.4385610	476	0.00107743455	1.4385610	4.594463	sin-13
P46940	0.2405446	1.1105871	608	0.00109161365	1.1105871	4.616963	GTPase-activating-like protein IQGAP1
P00747	0.1804735	0.8238672	2996	0.00122861719	0.8238672	4.564962	Plasminogen; Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B
P26447	0.3198725	1.4990741	342	0.00124919306	1.4990741	4.686469	ein S100-A4
O60262	0.2675546	1.2559109	5895	0.00125891060	1.2559109	4.694045	nine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-7
Q96CS3	0.2499453	1.1510089	275	0.00126714949	1.1510089	4.605044	associated factor 2
Q6UW35	0.2920667	1.3529266	2388	0.00128891306	1.3529266	4.7382738	tein PET117 homolog, mitochondrial
P01019	0.2239742	1.0239723	2108	0.00130795278	1.0239723	4.575714	Angiotensinogen; Angiotensin-1; Angiotensin-2; Angiotensin-3; Angiotensin-4; Angiotensin 1-9; Angiotensin 1-7; Angiotensin 1-5; Angiotensin 1-4
O95445	0.5528304	2.5298428	48550	0.00131065281	2.5298428	4.576159	lipoprotein M
P27658	0.3584367	1.6133702	147	0.00134724057	1.6133702	4.500743	agen alpha-1(VIII) chain; Vastatin
Q96JB2	0.4358507	2.0512914	307	0.00134954957	2.0512914	4.708473	erved oligomeric Golgi complex subunit 3
Q07507	0.2597875	1.2545210	5411	0.00136195436	1.2545210	4.829391	matopontin
Q9BXM9	0.3051597	1.4930515	2360	0.00136925543	1.4930515	4.829391	characterized protein C14orf142
P09619	0.2746983	1.2391198	3401	0.00139705710	1.2391198	4.510829	let-derived growth factor receptor beta
P02748	0.2688492	1.2229145	492765	0.00141850198	1.2229145	4.562276	plement component C9; Complement component C9a; Complement component C9b
Q96LL9	0.2732567	1.2440322	57117	0.001481125370	1.2440322	4.552625	homolog subfamily C member 30
Q04721	0.4802579	1.4802579	1008474	0.001521068887	1.4802579	4.744993	rogenic locus notch homolog protein 2; Notch 2 extracellular truncation; Notch 2 intracellular domain
Q92930	0.3068236	1.4774889	238745	0.00153028385	1.4774889	4.815434	related protein Rab-8B
Q9UQR1	0.3597180	1.7724910	180587	0.001572672148	1.7724910	4.930831	finger protein 148
P54577	0.2281963	1.0184999	3466	0.00158577148	1.0184999	4.463276	sine-tRNA ligase, cytoplasmic; Tyrosine-tRNA ligase, cytoplasmic, N-terminally processed
O95486	0.3119258	1.3819063	1990	0.00160542148	1.3819063	4.443060	tein transport protein Sec24A
Q99983	0.5887496	2.9528995	496719	0.00160720548	2.9528995	5.015589	omodulin
P83916	0.3062367	1.6056296	147	0.001608702148	1.6056296	5.243487	mobox protein homolog 1
P03950	0.3848951	1.7791248	1933	0.00160962148	1.7791248	4.628425	ogenin
Q9UBV8	0.2558508	1.1380629	1086	0.001631107521	1.1380629	4.455098	in
P15904	0.2665202	1.0272365	2365356	0.00163177027	1.0272365	4.536023	hoplakin

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
Q7Z3T8	0.3051	5.532	932	0.0016	0.017	5.527	finger FYVE domain-containing protein 16
	1.3746	348		4.5048	15		
P00352	0.2488	6.381	138	0.0017	0.017	5.527	mal dehydrogenase 1
	1.1346	512		4.5740	33		
Q9H1E5	0.2320	2.667	147	0.0017	0.017	5.527	redoxin-related transmembrane protein 4
	1.0067	711		4.3388	12		
O75480	0.1608	2.349	387	0.0017	0.017	5.527	ADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial
O15061	0.2548	4.467	147	0.0017	0.017	5.527	min
	1.1041	834		4.3327	37		
P62857	0.2882	2.750	192	0.0017	0.017	5.527	ribosomal protein S28
	1.3551	185		4.7015	59		
P80723	0.3279	2.741	199	0.0017	0.017	5.527	acid soluble protein 1
	1.5107	829		4.6070	79		
Q9NS69	0.2448	3.342	188	0.0017	0.017	5.527	chondrial import receptor subunit TOM22 homolog
	1.0847	694		4.4342	65		
P19447	0.3333	3.667	147	0.0017	0.017	5.527	basal transcription factor complex helicase XPB subunit
	1.5879	548		4.7634	39		
Q96CX2	0.2093	2.288	202	0.0017	0.017	5.527	/POZ domain-containing protein KCTD12
	0.9045	513		4.3199	20		
Q9NS86	0.2292	2.370	255	0.0018	0.018	5.527	C-like protein 2
	0.9960	486		4.3451	26		
P52907	0.1989	3.667	147	0.0018	0.018	5.527	tin-capping protein subunit alpha-1
	0.8523	732		4.2833	62		
Q08945	0.3088	4.467	147	0.0018	0.018	5.527	ACT complex subunit SSRP1
	1.3761	500		4.4674	05		
Q9BYN0	0.2972	2.007	184	0.0019	0.019	5.527	redoxin-1
	1.2801	043		4.3072	06		
O15118	0.4187	2.367	147	0.0019	0.019	5.527	mann-Pick C1 protein
	2.1247	916		5.0743	79		
Q9UBH3	0.3880	2.836	367	0.0019	0.019	5.527	5'-methyl-CpG-binding domain protein 2
P62328	0.2882	2.653	159	0.0019	0.019	5.527	inosin beta-4; Hematopoietic system regulatory peptide
	1.3455	146		4.6676	28		
Q9Y287	0.3774	3.304	184	0.0019	0.019	5.527	integral membrane protein 2B; BRI2, membrane form; BRI2 intracellular
	1.6105	936		4.2672	53		domain; BRI2C, soluble form; Bri23 peptide
Q8N142	0.2768	2.501	226	0.0019	0.019	5.527	phyllosuccinate synthetase isozyme 1
Q14118	0.1948	0.728	528	0.0019	0.019	5.527	roglycan; Alpha-dystroglycan; Beta-dystroglycan
	0.8487	363		4.3568	75		
P82663	0.3163	3.309	796	0.0020	0.020	5.527	ribosomal protein S25, mitochondrial
	1.3399	129		4.2357	14		
P31323	0.2175	1.195	650	0.0020	0.020	5.527	MP-dependent protein kinase type II-beta regulatory subunit
	0.9232	294		4.2446	97		
Q8NAT1	0.1965	0.807	624	0.0020	0.020	5.527	tein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2
	0.8308	927		4.2265	84		
P61009	0.2042	2.742	190	0.0020	0.020	5.527	al peptidase complex subunit 3
	0.8882	212		4.3481	11		
Q07065	0.2218	0.907	519	0.0020	0.020	5.527	skeleton-associated protein 4
	0.9488	623		4.2800	98		
P50991	0.3455	0.711	1032	0.0020	0.020	5.527	plex protein 1 subunit delta
	1.5101	244		4.3699	37		
P07384	0.2057	0.248	294	0.0020	0.020	5.527	ain-1 catalytic subunit
	0.8641	607		4.2000	15		

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
Q6IC98	0.2102800	2.802	633	0.0021820	0.0021820	0.0021820	RAM domain-containing protein 4
	0.9057366			4.307102			
A5D6W6	0.4938725	2.592	7	0.0022620	0.0022620	0.0022620	storage-inducing transmembrane protein 1
	2.1994339			4.453538			
P05455	0.2042684	2.795	2	0.0022620	0.0022620	0.0022620	La protein
	0.8562036			4.191561			
Q96AG4	0.2559796	2.639	0	0.0022020	0.0022020	0.0022020	serine-rich repeat-containing protein 59
	1.0641384			4.157119			
Q12988	0.2428862	2.381	0	0.0023321	0.0023321	0.0023321	heat shock protein beta-3
	1.0103210			4.159643			
Q04763	0.3958981	2.729	8	0.0021021	0.0021021	0.0021021	acylglutathione lyase
P13796	0.2129176	2.454	0	0.0021321	0.0021321	0.0021321	histone H2
	0.8819572			4.151955			
Q8IYI6	0.2270356	2.285	0	0.0021321	0.0021321	0.0021321	ubiquitin-protein ligase complex component 8
	0.9330152			4.108487			
P62277	0.3165727	2.670	0	0.0021521	0.0021521	0.0021521	ribosomal protein S13
	1.3005300			4.108183			
P61923	0.3910131	2.732	4	0.0021621	0.0021621	0.0021621	protein kinase inhibitor alpha
P50238	0.4218467	2.847	0	0.0021821	0.0021821	0.0021821	serine-rich protein 1
	1.7621993			4.182309			
Q9H1K0	0.3566487	2.147	0	0.0021821	0.0021821	0.0021821	ubiquitin-protein ligase complex component 5
	1.6022771			4.492591			
Q96A65	0.2036061	2.182	0	0.0021021	0.0021021	0.0021021	ubiquitin-protein ligase complex component 4
	0.8321129			4.086862			
P05543	0.2627095	2.488	0	0.0021021	0.0021021	0.0021021	toxine-binding globulin
	1.1801143			4.492224			
Q9UK22	0.2914733	2.956	0	0.0021021	0.0021021	0.0021021	only protein 2
	1.3974278			4.794352			
Q9Y490	0.2099433	2.353	0	0.0021021	0.0021021	0.0021021	protein 1
	0.8597753			4.095275			
P62745	0.2868977	2.677	0	0.0021021	0.0021021	0.0021021	related GTP-binding protein RhoB
	1.1929691			4.159700			
P24311	0.5063273	3.964	1	0.0021021	0.0021021	0.0021021	cytochrome c oxidase subunit 7B, mitochondrial
O00625	0.2729387	2.147	0	0.0021021	0.0021021	0.0021021	
	1.1028338			4.040897			
P58546	0.3158695	2.643	0	0.0021021	0.0021021	0.0021021	ubiquitin-protein ligase complex component 8
	1.2963604			4.109419			
O75348	0.3199387	2.147	0	0.0021021	0.0021021	0.0021021	type proton ATPase subunit G 1
	1.2891767			4.028827			
Q96FN9	0.4248367	2.147	0	0.0021021	0.0021021	0.0021021	ubiquitin-protein ligase complex component 2
	1.7766077			4.189288			
P04843	0.3688416	2.713	0	0.0021021	0.0021021	0.0021021	ethyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1
	1.5241453			4.132887			
P63306	0.7905359	7.387	1	0.0021021	0.0021021	0.0021021	ponin C, slow skeletal and cardiac muscles
Q9UL18	0.3093860	2.316	0	0.0021021	0.0021021	0.0021021	arginonaute-1
	1.3184619			4.261436			
Q9HB40	0.3126602	2.048	0	0.0021021	0.0021021	0.0021021	inflammation-inducible serine carboxypeptidase
	1.4736038			4.713116			
Q9Y490	0.2099433	2.353	0	0.0021021	0.0021021	0.0021021	protein 2
Q96C86	0.2113295	2.986	0	0.0021021	0.0021021	0.0021021	pppX diphosphatase
	0.8529077			4.035995			

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
Q8N5M1	0.3177	0.262	735	0.0028	0.0034	0.0034	synthase mitochondrial F1 complex assembly factor 2
	1.2833	584		4.0391	96		
Q96GK7	0.2957	0.357	234	0.0028	0.0035	0.0035	arylacetoacetate hydrolase domain-containing protein 2A
	1.2557	512		4.2554	26		
Q6P1N0	0.3683	0.229	225	0.0029	0.0037	0.0037	ed-coil and C2 domain-containing protein 1A
	1.6508	051		4.4819	80		
Q3ZCW2	0.3096	0.330	294	0.0029	0.0047	0.0047	ctin-related protein
	1.3933	792		4.5085	85		
Q9NQ35	0.5002	0.199	928	0.0078	0.0080	0.0080	R-related lipid transfer protein 7, mitochondrial
Q9UKL9	0.6805	0.061	938	0.0869	0.0900	0.0900	tein kinase C and casein kinase substrate in neurons protein 3
P00492	0.2388	0.339	664	0.0029	0.0038	0.0038	xanthine-guanine phosphoribosyltransferase
	0.9642	312		4.0365	70		
Q15125	0.3853	0.078	077	0.0029	0.0033	0.0033	ta-hydroxysteroid-Delta(8),Delta(7)-isomerase
	1.5522	594		4.0286	44		
Q9NNM4	0.1099	0.193	774	0.0380	0.0380	0.0380	delin
Q00577	0.2545	0.041	1439	0.0030	0.0040	0.0040	criptional activator protein Pur-alpha
	1.0249	972		4.0233	06		
Q53FA7	0.5882	0.272	173	0.0020	0.0030	0.0030	hione oxidoreductase PIG3
P14555	0.7156	0.423	351	0.0032	0.0037	0.0037	pholipase A2, membrane associated
	3.1616	763		4.4185	73		
Q9UHD9	0.2263	0.382	790	0.0032	0.0035	0.0035	quilin-2
	0.8978	150		3.9658	20		
P25311	0.2665	0.328	030	0.0032	0.0037	0.0037	alpha-2-glycoprotein
	1.0782	056		4.0453	01		
O95810	0.1854	0.338	276	0.0032	0.0037	0.0037	m deprivation-response protein
	0.7267	426		3.9190	91		
P09467	0.3327	0.220	615	0.0032	0.0035	0.0035	tose-1,6-bisphosphatase 1
	1.4304	382		4.3071	95		
P50552	0.2329	0.383	622	0.0032	0.0037	0.0037	ilator-stimulated phosphoprotein
	0.9233	883		3.9632	65		
P53618	0.2333	0.377	147	0.0034	0.0036	0.0036	omer subunit beta
	0.9076	351		3.8888	00		
P01303	0.3518	0.063	212	0.0034	0.0036	0.0036	neuropeptide Y;Neuropeptide Y;C-flanking peptide of NPY
	1.3886	725		3.9477	08		
Q7L4E1	0.4899	0.150	716	0.0035	0.0036	0.0036	tein FAM73B
	1.9056	994		3.8958	14		
O15031	0.2322	0.305	474	0.0035	0.0037	0.0037	in-B2
	0.9094	327		3.9151	75		
Q9BVC6	0.3093	0.336	717	0.0035	0.0036	0.0036	ismembrane protein 109
	1.1958	920		3.8662	21		
Q92575	0.2518	0.070	2687	0.0036	0.0036	0.0036	domain-containing protein 4
	0.9922	287		3.9467	01		
P28070	0.2265	0.078	722	0.0036	0.0036	0.0036	asome subunit beta type-4
	0.9263	111		4.0895	35		
Q8IYU8	0.6834	0.367	147	0.0036	0.0036	0.0036	ium uptake protein 2, mitochondrial
	3.0629	900		4.4814	21		
Q96M18	0.6084	0.279	930	0.0350	0.0350	0.0350	shock 70 kDa protein 12B
Q7KZF4	0.2290	0.347	147	0.0036	0.0037	0.0037	hylococcal nuclease domain-containing protein 1
	0.8794	696		3.8398	95		
P21980	0.2358	0.223	692	0.0036	0.0037	0.0037	ein-glutamine gamma-glutamyltransferase 2
	0.9178	411		3.8986	10		

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
Q14258	0.2478858	0.00371027	155	0.00371027	0.9919848	4.008255	ubiquitin/ISG15 ligase TRIM25
A6ND06	0.0610627	0.00371027	155	0.00371027	0.9919848	4.008255	phoglycolate phosphatase
Q8IUX7	0.4995562	0.00371027	155	0.00371027	0.9919848	4.008255	ocyte enhancer-binding protein 1
P43121	0.2729175	0.00371027	155	0.00371027	0.9919848	4.008255	surface glycoprotein MUC18
P14625	0.2529309	0.00371027	155	0.00371027	0.9919848	4.008255	plasmin
P10109	0.0870845	0.00371027	155	0.00371027	0.9919848	4.008255	monodoxin, mitochondrial
Q9Y2D4	0.3883529	0.00371027	155	0.00371027	0.9919848	4.008255	cyst complex component 6B
P27695	0.3919367	0.00371027	155	0.00371027	0.9919848	4.008255	(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, mitochondrial
E5RK69	0.2963337	0.00371027	155	0.00371027	0.9919848	4.008255	exin
Q96PK6	0.2419465	0.00371027	155	0.00371027	0.9919848	4.008255	RNA-binding protein 14
Q9Y5U8	0.6520466	0.00371027	155	0.00371027	0.9919848	4.008255	chondrial pyruvate carrier 1
Q15738	0.2856427	0.00400283	147	0.00400283	1.0818010	3.787259	l-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
Q9BWJ5	0.3118467	0.00400283	147	0.00400283	1.1786521	3.779657	ing factor 3B subunit 5
Q01581	0.3810263	0.00400283	147	0.00400283	1.5736067	4.129965	proxymethylglutaryl-CoA synthase, cytoplasmic
P62312	0.4058757	0.00400283	147	0.00400283	1.5682756	3.863930	mRNA-associated Sm-like protein LSM6
P31949	0.2579399	0.00400283	147	0.00400283	0.9710473	3.775501	ein S100-A11;Protein S100-A11, N-terminally processed
P04207	0.3679020	0.00400283	147	0.00400283	1.4064185	3.822804	appa chain V-III region CLL
P78406	0.3860067	0.00400283	147	0.00400283	1.6990379	4.401581	NA export factor
P49773	0.2498227	0.00400283	147	0.00400283	0.9406572	3.765306	dine triad nucleotide-binding protein 1
P27169	0.2728385	0.00400283	147	0.00400283	1.0408608	3.824822	m paraoxonase/arylesterase 1
Q13636	0.4476750	0.00400283	147	0.00400283	1.9750968	4.412876	related protein Rab-31
Q96EM0	0.3139347	0.00400283	147	0.00400283	1.2281296	3.912034	s-3-hydroxy-L-proline dehydratase
Q2TAY7	0.2740576	0.00400283	147	0.00400283	1.0380001	3.787532	repeat-containing protein SMU1;WD40 repeat-containing protein SMU1, N-terminally processed
Q9BT09	0.3172855	0.00400283	147	0.00400283	1.2017444	3.787537	ein canopy homolog 3
P01699	0.4496208	0.00400283	147	0.00400283	1.9617461	4.367970	mbda chain V-I region VOR
P00488	0.3056227	0.00400283	147	0.00400283	1.1450813	3.745784	gulation factor XIII A chain
Q04941	0.3552268	0.00400283	147	0.00400283	1.3354806	3.759546	leolipid protein 2

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P01611	0.3549367	0.147	0.0041327	0.514	0.3270534	0.3270534	alpha chain V-I region Wes
	1.3210912			3.721864			
P07360	0.2508705	0.608	0.0041929	0.248	0.9290248	0.9290248	complement component C8 gamma chain
	0.9508577			3.797726			
O75165	0.2029463	0.479	0.0045032	0.248	0.5290248	0.5290248	homolog subfamily C member 13
	0.7578962			3.734455			
Q9BXF6	0.2410307	0.147	0.0045229	0.248	0.5290248	0.5290248	1 family-interacting protein 5
	0.8964783			3.709638			
Q02818	0.2686731	0.836	0.0045422	0.248	0.5290248	0.5290248	teobindin-1
	1.1067621			4.119362			
Q9UNN8	0.3238853	0.236	0.0045429	0.248	0.5290248	0.5290248	endothelial protein C receptor
	1.2379487			3.826899			
Q96KP1	0.2563691	0.736	0.0045529	0.248	0.5290248	0.5290248	89S1 complex component 2
	1.0392328			4.053659			
P46063	0.2065123	0.952	0.0045729	0.248	0.5290248	0.5290248	ATP-dependent DNA helicase Q1
	0.7705141			3.730880			
Q9HBI0	0.3602708	0.371	0.0045929	0.248	0.5290248	0.5290248	in-1
P20042	0.2360634	0.030	0.0046029	0.248	0.5290248	0.5290248	eukaryotic translation initiation factor 2 subunit 2
	0.8792944			3.724821			
Q8IVD9	0.2438165	0.517	0.0046537	0.248	0.5290248	0.5290248	TC domain-containing protein 3
	0.9380220			3.858329			
Q13008	0.5804288	0.483	0.0046637	0.248	0.5290248	0.5290248	2a(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
Q5JUC0	0.5016826	0.810	0.0047732	0.248	0.5290248	0.5290248	protein FAM78A
P10643	0.3105456	0.523	0.0047933	0.248	0.5290248	0.5290248	complement component C7
	1.1503065			3.704147			
Q9Y5U9	0.2518567	0.725	0.0048332	0.248	0.5290248	0.5290248	mediate early response 3-interacting protein 1
	0.9688010			3.846636			
P31689	0.3869110	0.049	0.0048430	0.248	0.5290248	0.5290248	homolog subfamily A member 1
	1.4848105			3.837599			
Q53GCG	0.3900798	0.362	0.0048582	0.248	0.5290248	0.5290248	and LIM domain protein 3
Q04837	0.3378507	0.962	0.0048640	0.248	0.5290248	0.5290248	12S-stranded DNA-binding protein, mitochondrial
	1.2706968			3.760378			
Q9BU61	0.3533327	0.147	0.0048837	0.248	0.5290248	0.5290248	ADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor
	1.2937160			3.661782			
Q9BXR6	0.3662489	0.182	0.0048837	0.248	0.5290248	0.5290248	complement factor H-related protein 5
	1.3408193			3.660951			
Q08357	0.3308811	0.243	0.0049038	0.248	0.5290248	0.5290248	12m-dependent phosphate transporter 2
	1.2512681			3.781623			
Q9HCN8	0.2283271	0.872	0.0049130	0.248	0.5290248	0.5290248	renal cell-derived factor 2-like protein 1
	0.8376149			3.668688			
Q8NDY3	0.4836806	0.829	0.0049301	0.248	0.5290248	0.5290248	protein ADP-ribosylarginine] hydrolase-like protein 1
P61020	0.2252816	0.746	0.0050537	0.248	0.5290248	0.5290248	related protein Rab-5B
	0.8349426			3.706218			
P00918	0.2609271	0.179	0.0050571	0.248	0.5290248	0.5290248	carbonic anhydrase 2
	0.9493414			3.649846			
Q8TDB6	0.2672633	0.834	0.0050731	0.248	0.5290248	0.5290248	ubiquitin-protein ligase DTX3L
	0.9819803			3.674197			
P31994	0.2103216	0.055	0.0051038	0.248	0.5290248	0.5290248	2 affinity immunoglobulin gamma Fc region receptor II-b
2	0.7713913			3.667677			
Q8NBF2	0.2239299	0.232	0.0051438	0.248	0.5290248	0.5290248	repeat-containing protein 2
	0.8115466			3.636582			

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
O00299	0.251423	1.421612	0.005055	1.60076			tride intracellular channel protein 1
	0.9153236			3.640298			
Q9UBI9	0.488787	0.80097	0.005063	1.10766			case protein homolog
	1.9350473			3.963798			
O75663	0.461873	0.3339	0.005079	1.70761			1-like protein
	1.6975991			3.674689			
Q9Y5J7	0.397530	0.7147	0.005203	1.1047			chondrial import inner membrane translocase subunit Tim9
	1.4394711			3.620850			
Q8WUM0	0.218382	0.3881	0.005263	1.114			ear pore complex protein Nup133
	0.7928646			3.630508			
O15121	0.377917	0.5551	0.005273	1.9115			ngolipid delta(4)-desaturase DES1
	1.3734454			3.634300			
P00742	0.324676	0.5924	0.005452	1.28701			regulation factor X;Factor X light chain;Factor X heavy
	1.3361965			4.123118			chain;Activated factor Xa heavy chain
P46777	0.288870	0.3996	0.005493	1.30263			ribosomal protein L5
	1.0578875			3.665643			
Q6P1L8	0.505300	0.7435	0.005528	1.3339			ribosomal protein L14, mitochondrial
P49756	0.243826	0.7147	0.005548	1.3314			RNA-binding protein 25
	0.8733625			3.581909			
Q15493	0.437894	0.5242	0.005572	1.33070			calcin
	1.5865116			3.625528			
O00567	0.449048	0.2457	0.005650	1.35702			leolar protein 56
	1.6066654			3.577936			
Q9H4A6	0.276027	0.941	0.005705	1.27090			i phosphoprotein 3
	0.9863755			3.573364			
Q6PCE3	0.338840	0.7566	0.005743	1.33842			ose 1,6-bisphosphate synthase
	1.3068366			3.856780			
P24762	0.146122	0.2025	0.005766	1.31422			yl-CoA acetyltransferase, mitochondrial
O15144	0.283817	0.8089	0.005762	1.34422			n-related protein 2/3 complex subunit 2
	1.0266458			3.622551			
Q9Y646	0.193922	0.1032	0.005848	1.0504			oxypeptidase Q
	0.6906706			3.561953			
Q1KMD3	0.267872	0.2210	0.005923	1.15833			rogeous nuclear ribonucleoprotein U-like protein 2
	0.9588418			3.579466			
P06396	0.316850	0.1875	0.005960	1.67206			olin
	1.1557324			3.651024			
P56199	0.243853	0.3476	0.005990	1.17006			grin alpha-1
	0.8817502			3.623178			
P62330	0.222486	0.563	0.005997	1.1106			-ribosylation factor 6
	0.7931556			3.564969			
Q9HAN9	0.673215	0.2673	0.006038	1.2731			ttinamide/nicotinic acid mononucleotide adenylyltransferase 1
Q96PE7	0.325930	0.7147	0.006043	1.1731			thylmalonyl-CoA epimerase, mitochondrial
	1.1472298			3.528421			
P17050	0.266998	0.2996	0.006092	1.1428			a-N-acetylgalactosaminidase
	0.9454418			3.541005			
Q9UBS4	0.493892	0.1571	0.006303	1.06080			homolog subfamily B member 11
	1.7470606			3.540916			
Q9H9B4	0.217840	0.5504	0.006323	1.03080			roflexin-1
	0.7776690			3.573084			
Q8TCJ2	0.244986	0.7863	0.006347	1.0607			chyl-diphosphooligosaccharide-protein glycosyltransferase subunit
	0.8698436			3.551625			STT3B

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P62191	0.2845	0.2748	632	0.0064	0.0363	0.0363	protease regulatory subunit 4
	1.0000517			3.514782			
Q9Y5Z7	0.4676	0.5253	248	0.0064	0.0363	0.0363	cell factor 2
	1.9019574			4.071384			
P01597	0.6338	0.9297	760	0.0064	0.0363	0.0363	alpha chain V-I region DEE
	2.2333895			3.524349			
P23284	0.2195	0.5229	246	0.0065	0.0365	0.0365	fidyl-prolyl cis-trans isomerase B
	0.7744408			3.527355			
P05062	0.5510	0.3641	182	0.0065	0.0365	0.0365	ribose-bisphosphate aldolase B
	2.0647894			3.747246			
P60903	0.2370	0.6018	479	0.0065	0.0365	0.0365	tein S100-A10
	0.8289441			3.496770			
O43928	0.2968	0.5709	882	0.0065	0.0365	0.0365	DH dehydrogenase [ubiquinone] iron-sulfur protein 5
Q68DH5	0.2738	0.7291	1375	0.0066	0.0368	0.0368	R1 domain-containing protein 2
	0.9839434			3.595361			
P08754	0.2970	0.3677	147	0.0066	0.0368	0.0368	nine nucleotide-binding protein G(k) subunit alpha
	1.0292580			3.465194			
O75643	0.2103	0.3257	147	0.0066	0.0368	0.0368	small nuclear ribonucleoprotein 200 kDa helicase
	0.7286175			3.464284			
Q9HAA8	0.5303	0.3649	611	0.0067	0.0369	0.0369	E protein homolog 1, mitochondrial
P15809	0.2005	0.3588	469	0.0067	0.0369	0.0369	sulfatase B
P30050	0.3250	0.7887	400	0.0067	0.0369	0.0369	ribosomal protein L12
	1.1309945			3.479147			
P17500	0.2104	0.4850	2345	0.0067	0.0369	0.0369	tine kinase S-type, mitochondrial
P27797	0.2533	0.3681	182	0.0067	0.0370	0.0370	eticulin
	0.8755252			3.455605			
O14807	0.2835	0.1521	869	0.0068	0.0370	0.0370	related protein M-Ras
	0.9860449			3.477921			
O43290	0.2153	0.3367	147	0.0068	0.0370	0.0370	U6.U5 tri-snRNP-associated protein 1
	0.7436611			3.452549			
P98160	0.2009	0.8222	685	0.0068	0.0370	0.0370	ment membrane-specific heparan sulfate proteoglycan core
	0.6944147			3.468908			protein;Endorepellin;LG3 peptide
Q9GZY4	0.4429	0.8222	737	0.0068	0.0370	0.0370	chrome c oxidase assembly factor 1 homolog
	1.6172207			3.650753			
Q16204	0.2178	0.8402	720	0.0069	0.0370	0.0370	ed-coil domain-containing protein 6
	0.7607082			3.505328			
Q14019	0.5976	0.8247	147	0.0069	0.0370	0.0370	tosin-like protein
	2.3417241			3.921945			
O75190	0.2230	0.3159	307	0.0070	0.0371	0.0371	homolog subfamily B member 6
3							
Q9Y623	0.5628	0.9336	159	0.0070	0.0371	0.0371	sin-4
	1.9955095			3.547614			
P30101	0.2149	0.3418	665	0.0070	0.0371	0.0371	tein disulfide-isomerase A3
	0.7361350			3.435003			
Q12907	0.4672	0.2220	767	0.0070	0.0371	0.0371	cular integral-membrane protein VIP36
	1.6602075			3.553352			
O75533	0.2189	0.2280	909	0.0070	0.0371	0.0371	ing factor 3B subunit 1
	0.7480960			3.429955			
P21281	0.3926	0.8522	422	0.0070	0.0371	0.0371	type proton ATPase subunit B, brain isoform
	1.3428216			3.419588			
Q6ZVF9	0.3683	0.1457	648	0.0073	0.0386	0.0386	rotein-regulated inducer of neurite outgrowth 3
	1.5316163			4.158478			

	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P41208	0.3218688	0.003594	0.007302	3.0135	0.0035	0.0035	Protein names
	1.1048997			3.432766			
P32119	0.2446873	0.007382	0.007123	3.3875	0.0071	0.0071	Protein names
	0.8759792			3.580284			
P55735	0.2645592	0.007505	0.007505	3.3905	0.0075	0.0075	Protein names
	0.9148870			3.458196			
P56192	0.2978737	0.007363	0.007363	3.9500	0.0073	0.0073	Protein names
	1.0251690			3.446200			
Q5VUF5	0.2974206	0.006995	0.006995	3.9500	0.0069	0.0069	Protein names
Q8NBJ5	0.2928660	0.0070730	0.0070730	3.4144	0.0070	0.0070	Protein names
	1.0090957			3.455259			
O43707	0.3948501	0.0076412	0.0076412	3.3944	0.0076	0.0076	Protein names
	1.3709413			3.471934			
P11021	0.2028563	0.007582	0.007582	3.4144	0.0075	0.0075	Protein names
	0.6930674			3.419941			
P02749	0.2878913	0.0073313	0.0073313	3.3944	0.0073	0.0073	Protein names
	0.9821379			3.420999			
Q92803	0.2762988	0.0051129	0.0051129	3.2461	0.0051	0.0051	Protein names
Q96G03	0.2590367	0.0070147	0.0070147	3.3944	0.0070	0.0070	Protein names
	0.8738839			3.373274			
Q9UK41	0.4608215	0.007373	0.007373	3.3944	0.0073	0.0073	Protein names
	1.5562781			3.377097			
P61026	0.2419533	0.0073968	0.0073968	3.3944	0.0073	0.0073	Protein names
	0.8659400			3.578803			
P43686	0.3872341	0.00801890	0.00801890	3.3944	0.0080	0.0080	Protein names
	1.2985795			3.353104			
Q6Y288	0.3170465	0.0080175	0.0080175	3.3944	0.0080	0.0080	Protein names
	1.0690665			3.365585			
Q9BVG4	0.4270286	0.0080464	0.0080464	3.3944	0.0080	0.0080	Protein names
	1.4282890			3.344717			
Q9UBQ0	0.3287146	0.0080452	0.0080452	3.3944	0.0080	0.0080	Protein names
	1.1043560			3.359625			
Q6ICB0	0.5476511	0.0080201	0.0080201	3.3944	0.0080	0.0080	Protein names
	2.0382992			3.722843			
O60568	0.3190287	0.0080147	0.0080147	3.3944	0.0080	0.0080	Protein names
	1.0635431			3.327439			
Q5T447	0.3038223	0.0080996	0.0080996	3.3944	0.0080	0.0080	Protein names
	1.0258262			3.380520			
P17104	0.2608379	0.0080664	0.0080664	3.3944	0.0080	0.0080	Protein names
Q14011	0.4678233	0.0080933	0.0080933	3.3944	0.0080	0.0080	Protein names
	1.6060873			3.434499			
Q9BSH5	0.2408525	0.0080093	0.0080093	3.3944	0.0080	0.0080	Protein names
	0.8065712			3.355692			
Q9HCJ6	0.2621467	0.0080182	0.0080182	3.3944	0.0080	0.0080	Protein names
	0.8677868			3.310310			
P16455	0.2338298	0.0080415	0.0080415	3.3944	0.0080	0.0080	Protein names
	0.7988054			3.417997			
Q9BX97	0.3968670	0.0080864	0.0080864	3.3944	0.0080	0.0080	Protein names
	1.3847012			3.489081			
Q96LD4	0.5321789	0.0080822	0.0080822	3.3944	0.0080	0.0080	Protein names
	2.0603233			3.871537			

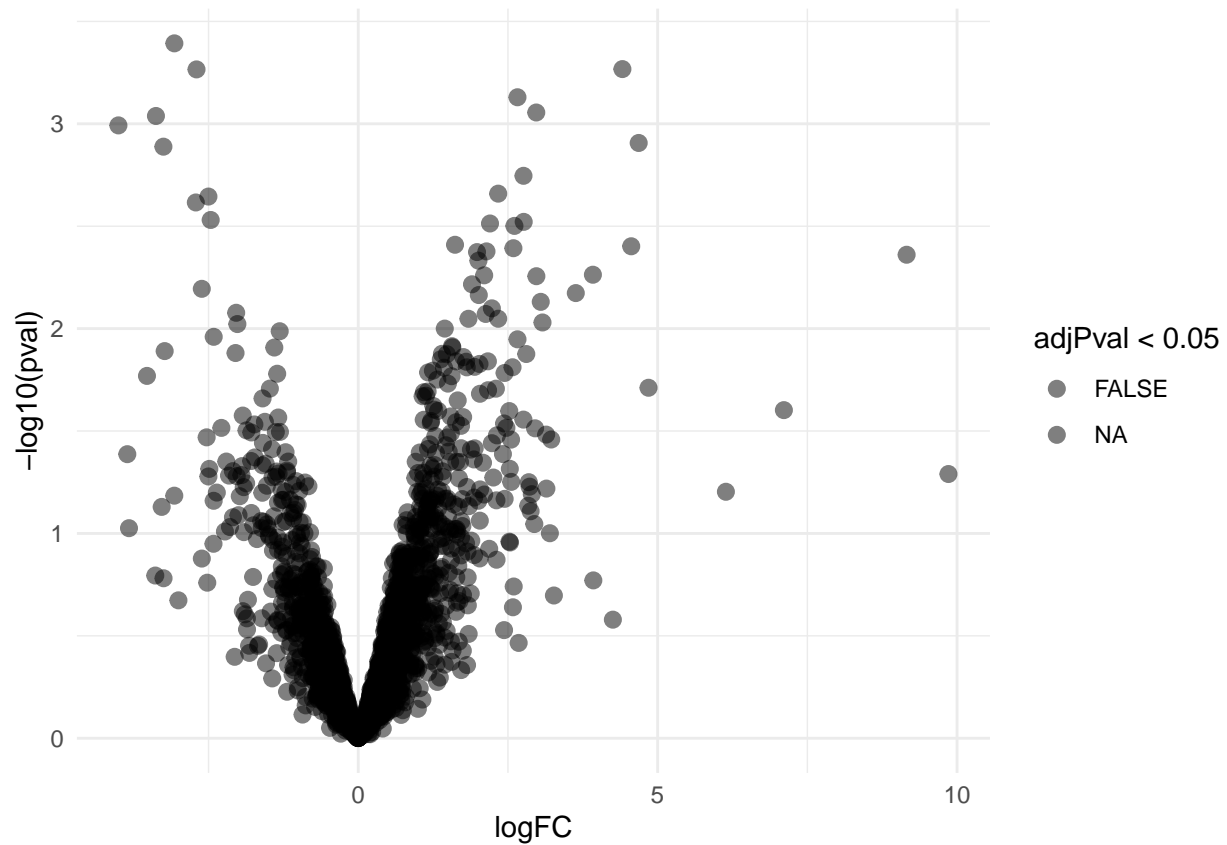
	logFC	se	df	t	pval	adjP	rowData(pe[["proteinRobust"]])\$Protein.names
P29992	0.2945338	0.0087043	33031	3.399222	0.0008295	0.00356	nine nucleotide-binding protein subunit alpha-11
P05387	0.2248668	0.0087774	33344	3.311871	0.0008968	0.00359	acidic ribosomal protein P2
P51692	0.5100496	0.0088295	33817	3.323333	0.0008953	0.00358	sal transducer and activator of transcription 5B
O60927	0.2647212	0.0089547	33336	3.578333	0.0009543	0.00408	tein phosphatase 1 regulatory subunit 11
A4D2B0	0.5058492	0.0089973	33870	3.388464	0.0009073	0.00415	allo-beta-lactamase domain-containing protein 1
P16083	0.2968355	0.0089983	335055	3.383609	0.0009083	0.00415	syldihydronicotinamide dehydrogenase [quinone]
Q13425	0.2319254	0.0090353	33288	3.289806	0.0009353	0.00426	-2-syntrophin
I3L505	0.5192035	0.0091090	33783	3.401449	0.0009461	0.00449	carrier protein
Q9NX08	0.2206251	0.0093475	335229	3.297295	0.0009347	0.00429	MM domain-containing protein 8
Q96CN7	0.3099413	0.0093544	33448	3.278800	0.0009354	0.00429	horismatase domain-containing protein 1
O43592	0.2463027	0.0094702	331135	3.258736	0.0009470	0.00437	ortin-T
Q8N292	0.5099576	0.0095043	33578	3.393677	0.0009504	0.00439	GTPase-activating protein 18
P01621	0.3618797	0.0095152	337835	3.286787	0.0009515	0.00439	kappa chain V-III region NG9
Q9UMR3	0.4717327	0.0096586	337147	3.465748	0.0009658	0.00461	ox transcription factor TBX20
P35704	0.3702377	0.0097456	33232	3.409745	0.0009745	0.00467	aredoxin-1
O60502	0.5703801	0.0098687	33406	3.406563	0.0009868	0.00495	ylate cyclase type 9
Q13823	0.3948092	0.0099387	33671	3.200910	0.0009938	0.00516	ylglutaconyl-CoA hydratase, mitochondrial
O95159	0.5278107	0.0100529	337934	3.350868	0.0010052	0.00519	finger protein-like 1
Q8IWU2	0.2118666	0.0100437	33368	3.333113	0.0010043	0.00536	e/threonine-protein kinase LMTK2
Q6B0K9	0.3997801	0.0100825	331037	3.368015	0.0010082	0.00536	oglobin subunit mu
Q13549	0.5170128	0.0101958	33671	3.405733	0.0010195	0.00536	aryotic translation initiation factor 4E-binding protein 1
Q6UXG3	0.3706179	0.0102279	338044	3.208173	0.0010227	0.00536	F35-like molecule 9
P03915	0.3488364	0.0102186	334164	3.299231	0.0010218	0.00535	H-ubiquinone oxidoreductase chain 5
P14174	0.2608197	0.0103182	331113	3.232881	0.0010318	0.00586	rophage migration inhibitory factor
P34947	0.4397370	0.0103423	338356	3.202173	0.0010342	0.00588	rotein-coupled receptor kinase 5
O75436	0.3058738	0.0105044	338092	3.247407	0.0010504	0.00612	olar protein sorting-associated protein 26A
P19474	0.3407497	0.0105291	337271	3.335584	0.0010529	0.00617	biquitin-protein ligase TRIM21
O14656	0.5548267	0.0105508	337147	3.278015	0.0010550	0.00625	m-1A
Q08AG7	0.3483048	0.0105723	334164	3.440703	0.0010572	0.00612	tic-spindle organizing protein 1

	logFC	se	df	t	pval	adjPval	rowData(pe[["proteinRobust"]])\$Protein.names
P05060	0.67870266	0.00747	0.01063088	839	0.00000000	0.00000000	etogranin-1;PE-11;GAWK peptide;CCB peptide
	2.3136323			3.412414			
Q08211	0.21902851	0.182	0.01063088	839	0.00000000	0.00000000	dependent RNA helicase A
	0.6963521			3.179276			
Q0VAH6	0.30980087	0.05587911	0.01063088	839	0.00000000	0.00000000	modin-3
P51665	0.24558921	0.130	0.01063088	839	0.00000000	0.00000000	proteasome non-ATPase regulatory subunit 7
	0.7816374			3.182703			
Q9H2J4	0.26003591	0.182	0.01063088	839	0.00000000	0.00000000	ducin-like protein 3
	0.8248510			3.171334			
Q8IWB6	0.50998172	0.57331989	0.01063088	839	0.00000000	0.00000000	repeat and FYVE domain-containing protein 1
P51907	0.46092739	0.05411200	0.01063088	839	0.00000000	0.00000000	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
Q15691	0.27782095	0.540	0.01063088	839	0.00000000	0.00000000	otubule-associated protein RP/EB family member 1
	0.9045387			3.261696			

4.6 Interaction

4.6.1 Volcano-plot

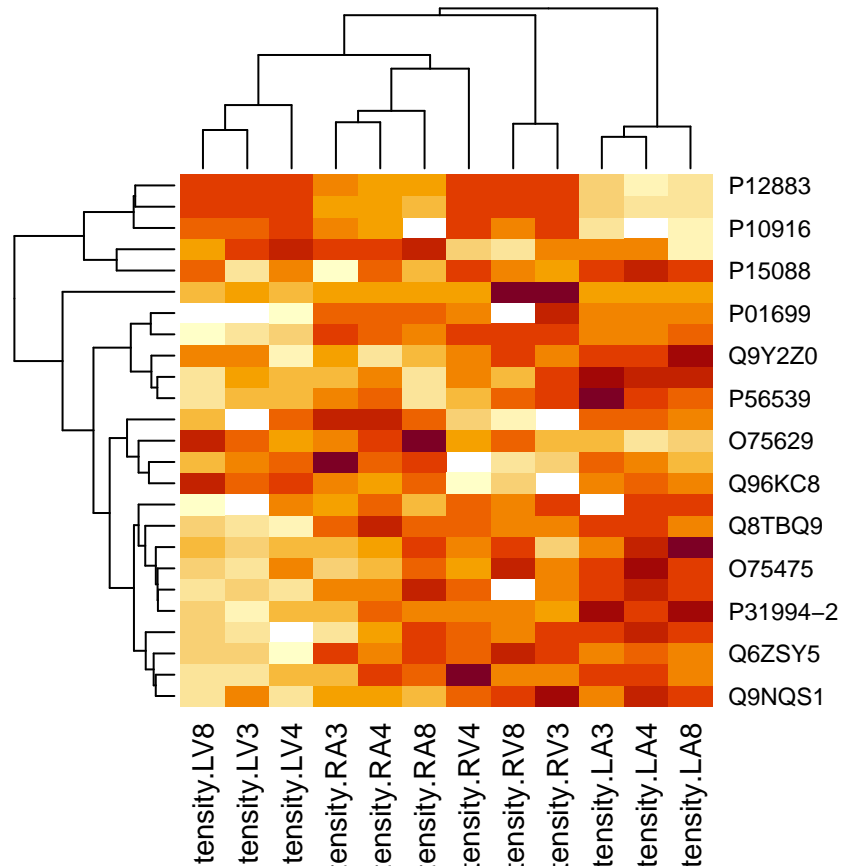
```
volcanoInt <- ggplot(rowData(pe[["proteinRobust"]])$"locationR:tissueV",
  aes(x = logFC, y = -log10(pval), color = adjPval < 0.05)) +
  geom_point(cex = 2.5) +
  scale_color_manual(values = alpha(c("black", "red"), 0.5)) + theme_minimal()
volcanoInt
```



4.6.2 Heatmap

There were no genes significant at the 5% FDR level. We return the top 25 genes.

```
sigNamesInt <- rowData(pe[["proteinRobust"]])$"locationR:tissueV" %>%
  rownames_to_column("proteinRobust") %>%
  filter(adjPval<0.05) %>%
  pull(proteinRobust)
hlp <- order((rowData(pe[["proteinRobust"]])$"locationR:tissueV")[, "adjPval"])[1:25]
heatmap(assay(pe[["proteinRobust"]])[hlp, ])
```



There are 0 proteins significantly differentially expressed at the 5% FDR level.

```
rowData(pe[["proteinRobust"]])$"locationR:tissueV" %>%
  cbind(.,rowData(pe[["proteinRobust"]])$Protein.names) %>%
  na.exclude %>%
  filter(adjPval<0.05) %>%
  arrange(pval)
```

```
## [1] logFC
## [2] se
## [3] df
## [4] t
## [5] pval
## [6] adjPval
## [7] rowData(pe[["proteinRobust"]])$Protein.names
## <0 rows> (or 0-length row.names)
```

5 Large difference in number of proteins that are returned

Note, that much more proteins are returned significant for average contrast ($\log_2 FC_{V-A}$) as compared to contrast for assessing the fold change between ventriculum and atrium left and right. The power for the average contrast is larger than for the contrast left or right because the \log_2 FC can be estimated with higher precision.

For none of the proteins the interaction was significant (change in log2 FC between ventriculum and atrium in the right vs the left heart region). The power for the interaction is typically low.

5.1 Reason

Part of variance covariance matrix of model parameters due to design:

```
X <- model.matrix(~ location*tissue + patient, colData(pe))
covarUnscaled <- solve(t(X) %*% X)
```

Variance of contrasts (diagonal elements) due to design

```
varContrasts <- t(L)%*%covarUnscaled%*%L %>%
  diag
varContrasts
```

```
##                tissueV      tissueV + locationR:tissueV
##                0.6666667      0.6666667
## tissueV + 0.5 * locationR:tissueV      locationR:tissueV
##                0.3333333      1.3333333
```

```
sqrt(varContrasts)
```

```
##                tissueV      tissueV + locationR:tissueV
##                0.8164966      0.8164966
## tissueV + 0.5 * locationR:tissueV      locationR:tissueV
##                0.5773503      1.1547005
```

So it is clear that the standard error of the log2 FC left and right is the same. That of the average contrast is a factor $\sqrt{2}$ smaller! Indeed, we use double the number of samples to estimate it!

```
varContrasts[3]/varContrasts[2]
```

```
## tissueV + 0.5 * locationR:tissueV
##                0.5
```

```
sqrt(varContrasts)[3]/sqrt(varContrasts)[2]
```

```
## tissueV + 0.5 * locationR:tissueV
##                0.7071068
```

```
1/sqrt(2)
```

```
## [1] 0.7071068
```

The standard error of the interaction is a factor $\sqrt{2}$ larger than that of the main effects!

```
varContrasts[4]/varContrasts[2]
```

```
## locationR:tissueV  
## 2
```

```
sqrt(varContrasts)[4]/sqrt(varContrasts)[2]
```

```
## locationR:tissueV  
## 1.414214
```

```
sqrt(2)
```

```
## [1] 1.414214
```

5.2 Msqrob

This is not the case for the standard errors of protein 2???

```
rowData(pe[["proteinRobust"]])$"tissueV"[2,]
```

```
##          logFC          se          df          t          pval      adjPval  
## A0PJW6 0.2355243 0.556499 7.924465 0.423225 0.683383 0.8078152
```

```
rowData(pe[["proteinRobust"]])$"tissueV + locationR:tissueV"[2,]
```

```
##          logFC          se          df          t          pval      adjPval  
## A0PJW6 0.1822338 0.6124218 7.924465 0.2975626 0.7736885 0.8763294
```

```
rowData(pe[["proteinRobust"]])$"tissueV + 0.5 * locationR:tissueV"[2,]
```

```
##          logFC          se          df          t          pval      adjPval  
## A0PJW6 0.2088791 0.4126595 7.924465 0.5061778 0.6265101 0.7376959
```

```
rowData(pe[["proteinRobust"]])$"locationR:tissueV"[2,]
```

```
##          logFC          se          df          t          pval      adjPval  
## A0PJW6 -0.05329048 0.8296697 7.924465 -0.06423095 0.950377 0.9949944
```

Because msqrob is using robust regression to assess DE!

```
pe %>%  
  colData %>%  
  as_tibble %>%  
  mutate(w=getModel(rowData(pe[["proteinRobust"]])$msqrobModels[[2]])$w)
```

```
## # A tibble: 12 x 4
##   location tissue patient      w
##   <fct>      <fct> <fct>   <dbl>
## 1 L          A      3     0.966
## 2 L          A      4      1
## 3 L          A      8     0.667
## 4 L          V      3      1
## 5 L          V      4      1
## 6 L          V      8      1
## 7 R          A      3      1
## 8 R          A      4      1
## 9 R          A      8      1
## 10 R         V      3     0.485
## 11 R         V      4      1
## 12 R         V      8     0.440
```

For protein 2 the samples at the left and right side have different weights!

5.2.1 Part of standard error due to design:

```
covUnscaledRobust <- solve(
  t(X) %*%
  diag(
    getModel(rowData(pe[["proteinRobust"]])$msqrobModels[[2]])$w) %*% X)

varContrastsRobust <- t(L) %*% covUnscaledRobust %*% L %>%
  diag
varContrastsRobust
```

```
##           tissueV      tissueV + locationR:tissueV
##           0.7161526           0.8673176
## tissueV + 0.5 * locationR:tissueV      locationR:tissueV
##           0.3937862           1.5917957
```

```
sqrt(varContrastsRobust)
```

```
##           tissueV      tissueV + locationR:tissueV
##           0.8462580           0.9312989
## tissueV + 0.5 * locationR:tissueV      locationR:tissueV
##           0.6275239           1.2616639
```

5.2.2 Standard errors Contrasts

```
sqrt(varContrastsRobust) * getSigmaPosterior(rowData(pe[["proteinRobust"]])$msqrobModels[[2]])

##           tissueV      tissueV + locationR:tissueV
##           0.5564990           0.6124218
## tissueV + 0.5 * locationR:tissueV      locationR:tissueV
##           0.4126595           0.8296697
```

```
rowData(pe[["proteinRobust"]])$"tissueV"[2,]
```

```
##           logFC           se           df           t           pval      adjPval  
## AOPJW6 0.2355243 0.556499 7.924465 0.423225 0.683383 0.8078152
```

```
rowData(pe[["proteinRobust"]])$"tissueV + locationR:tissueV"[2,]
```

```
##           logFC           se           df           t           pval      adjPval  
## AOPJW6 0.1822338 0.6124218 7.924465 0.2975626 0.7736885 0.8763294
```

```
rowData(pe[["proteinRobust"]])$"tissueV + 0.5 * locationR:tissueV"[2,]
```

```
##           logFC           se           df           t           pval      adjPval  
## AOPJW6 0.2088791 0.4126595 7.924465 0.5061778 0.6265101 0.7376959
```

```
rowData(pe[["proteinRobust"]])$"locationR:tissueV"[2,]
```

```
##           logFC           se           df           t           pval      adjPval  
## AOPJW6 -0.05329048 0.8296697 7.924465 -0.06423095 0.950377 0.9949944
```