

Volcano and Heatmap

```
In [1]: library("tidyverse")
```

Warning message:

"package 'tidyverse' was built under R version 4.1.2"

-- Attaching packages

----- tidyverse 1.3.1 --

```
v ggplot2 3.3.5      v purrr  0.3.4
v tibble  3.1.4      v dplyr  1.0.7
v tidyr   1.1.4      v stringr 1.4.0
v readr   2.0.2      v forcats 0.5.1
```

Warning message:

"package 'ggplot2' was built under R version 4.1.2"

-- Conflicts

----- tidyverse_conflicts() --

x dplyr::filter() masks stats::filter()

x dplyr::lag() masks stats::lag()

```
In [2]: library(dplyr)
library(tidyr)
```

```
In [3]: FoldChange <- read.table("./FoldChange.csv", sep=',', header = T, row.names
```

```
In [4]: head(FoldChange)
```

A data.frame: 6 × 3

	pvalue	log2FC	Gene
	<dbl>	<dbl>	<chr>
Q09666	0.002141511	1.25644317	AHNAK
Q15149-3	0.340135415	0.08117139	PLEC
Q15149	0.000319444	0.91329164	PLEC
Q15149-8	0.006280590	-0.37684673	PLEC
Q15149-4	0.000223258	1.38131662	PLEC
P21333-2	0.146827666	-0.11675658	FLNA

```
In [5]: FoldChange$difference <- "NO"

head(FoldChange)
```

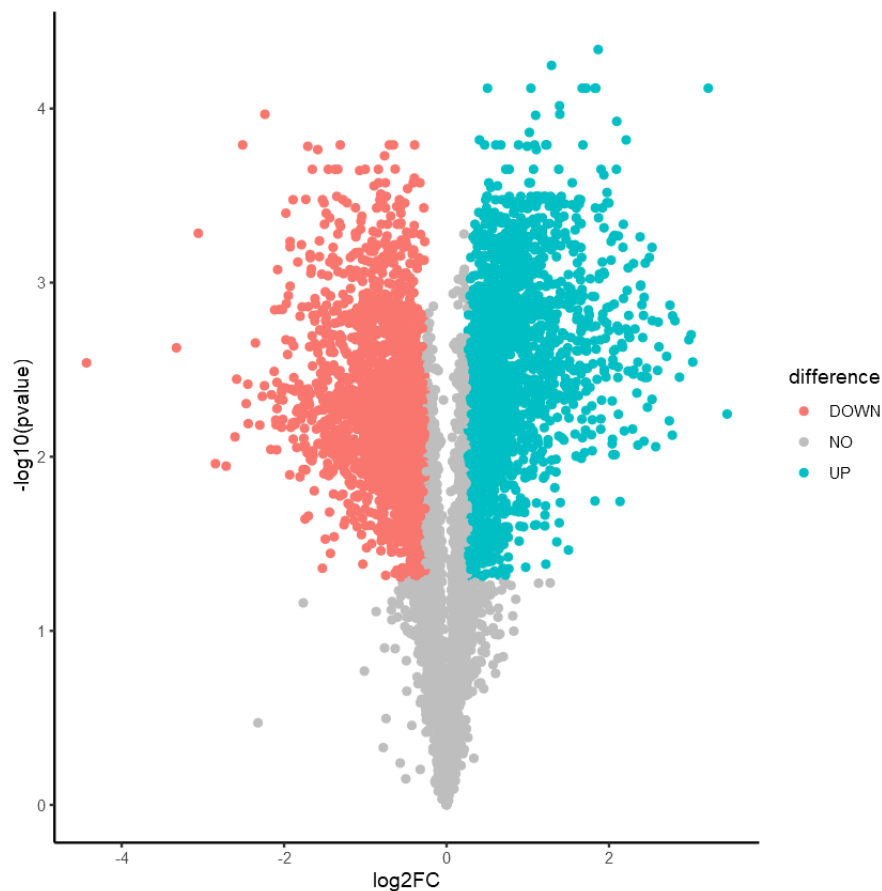
A data.frame: 6 × 4

	pvalue	log2FC	Gene	difference
	<dbl>	<dbl>	<chr>	<chr>
Q09666	0.002141511	1.25644317	AHNAK	NO
Q15149-3	0.340135415	0.08117139	PLEC	NO
Q15149	0.000319444	0.91329164	PLEC	NO
Q15149-8	0.006280590	-0.37684673	PLEC	NO
Q15149-4	0.000223258	1.38131662	PLEC	NO
P21333-2	0.146827666	-0.11675658	FLNA	NO

```
In [6]: FoldChange$difference[ FoldChange$log2FC > log(1.2,2) & FoldChange$pvalue
FoldChange$difference[ FoldChange$log2FC < -log(1.2,2) & FoldChange$pvalue
```

```
In [7]: p1 <- ggplot(data=FoldChange, aes(x=log2FC, y=-log10(pvalue), col=difference)
geom_point() +theme_classic() +
scale_color_manual(values = c("#F8766D", "gray", "#00BFC4"))

p1
```



ggplot dot labeling

```
In [8]: library(ggrepel)
```

```
In [9]: head(FoldChange)
```

A data.frame: 6 × 4

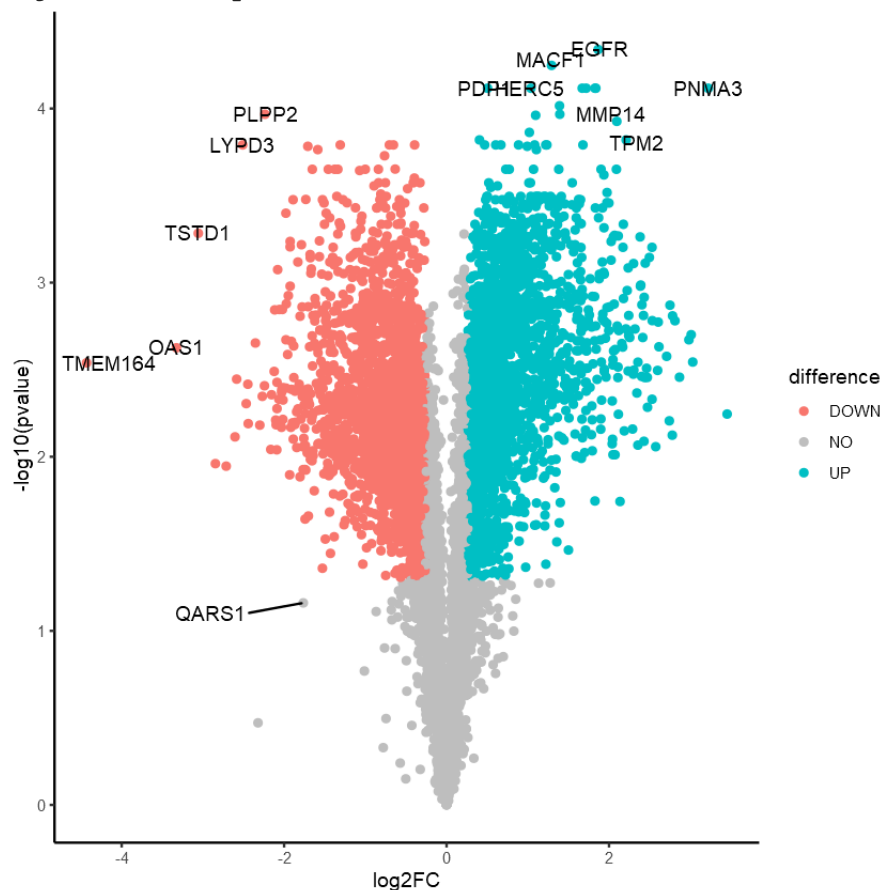
	pvalue	log2FC	Gene	difference
	<dbl>	<dbl>	<chr>	<chr>
Q09666	0.002141511	1.25644317	AHNAK	UP
Q15149-3	0.340135415	0.08117139	PLEC	NO
Q15149	0.000319444	0.91329164	PLEC	UP
Q15149-8	0.006280590	-0.37684673	PLEC	DOWN
Q15149-4	0.000223258	1.38131662	PLEC	UP
P21333-2	0.146827666	-0.11675658	FLNA	NO

```
In [10]: p2 <- ggplot(data=FoldChange, aes(x=log2FC, y=-log10(pvalue), col=difference)) +
  geom_point() + theme_classic() +
  scale_color_manual(values = c("#F8766D", "gray", "#00BFC4")) +
  geom_text_repel(color="black")

p2
```

Warning message:

"ggrepel: 7719 unlabeled data points (too many overlaps). Consider increasing max.overlaps"



In []:

In [11]: `FoldChange.label <- read.table("../FoldChange_label.csv", sep=',', header = TRUE)`

In [12]: `head(FoldChange.label)`

A data.frame: 6 × 5

	Accession	pvalue	log2FC	Gene	Label
	<chr>	<dbl>	<dbl>	<chr>	<chr>
1	A0A024QZ33	0.009851432	0.2470688	NSRP1	NO
2	A0A024QZW4	0.003714018	-0.6503038	SLC35B3	NO
3	A0A024R4E5	0.001340196	0.1430792	HDLBP	NO
4	A0A024R571	0.001533934	0.9758036	EHD1	YES
5	A0A024RAC6	0.000161727	-0.7039957	ELOA	NO
6	A0A024RCR6	0.052040553	0.1463875	BAG6	NO

```
In [13]: FoldChange.label$difference <- "NO"

FoldChange.label$difference[ FoldChange.label$log2FC > log(1.2,2) & FoldC

FoldChange.label$difference[ FoldChange.label$log2FC < -log(1.2,2) & FoldC
```

```
In [14]: FoldChange.label$Label[ FoldChange.label$Label == "YES" ] <- FoldChange.l
FoldChange.label$Label[ FoldChange.label$Label == "NO" ] <- NA
```

```
In [15]: head(FoldChange.label)
```

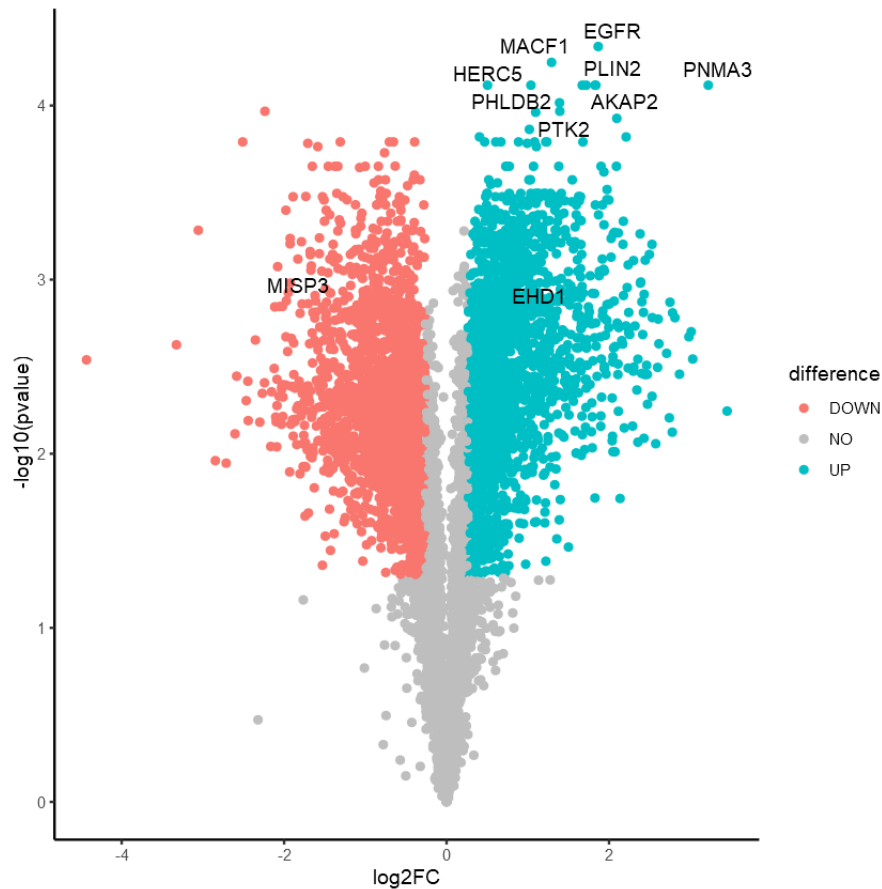
A data.frame: 6 × 6

	Accession	pvalue	log2FC	Gene	Label	difference
	<chr>	<dbl>	<dbl>	<chr>	<chr>	<chr>
1	A0A024QZ33	0.009851432	0.2470688	NSRP1	NA	NO
2	A0A024QZW4	0.003714018	-0.6503038	SLC35B3	NA	DOWN
3	A0A024R4E5	0.001340196	0.1430792	HDLBP	NA	NO
4	A0A024R571	0.001533934	0.9758036	EHD1	EHD1	UP
5	A0A024RAC6	0.000161727	-0.7039957	ELOA	NA	DOWN
6	A0A024RCR6	0.052040553	0.1463875	BAG6	NA	NO

```
In [16]: p3 <- ggplot(data=FoldChange.label, aes(x=log2FC, y=-log10(pvalue), col=difference)) +
  geom_point() + theme_classic() +
  scale_color_manual(values = c("#F8766D", "gray", "#00BFC4")) +
  geom_text_repel(color="black")

p3
```

Warning message:
 "Removed 7743 rows containing missing values (geom_text_repel)."
 Warning message:
 "ggrepel: 4 unlabeled data points (too many overlaps). Consider increasing max.overlaps"



Heatmap data

```
In [17]: library(pheatmap)
```

Warning message:
 "package 'pheatmap' was built under R version 4.1.2"

```
In [18]: selet_DEPs <- read.table("./Select_Proteins_Normalized_abundance.txt",
  sep='\t', header = T, row.names = 1)
```

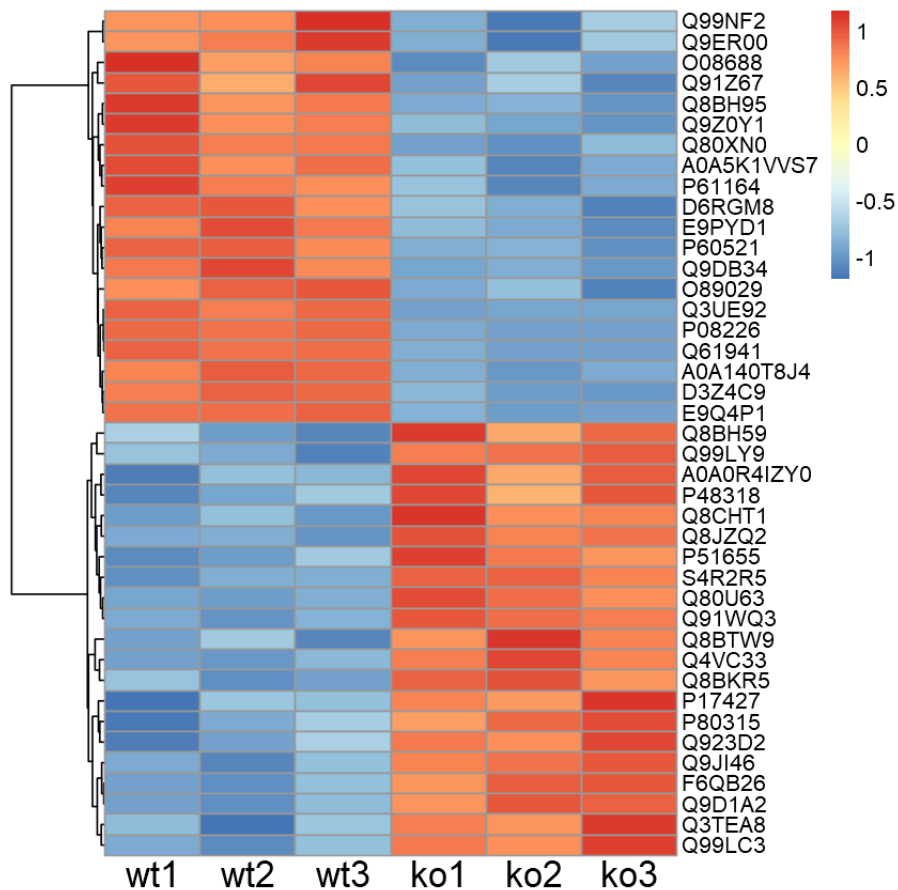
```
In [19]: head(selet_DEPs)
```

A data.frame: 6 × 6

	wt1	wt2	wt3	ko1	ko2	ko3
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
AOA0R4IZY0	8.600989	8.630331	8.627368	8.788076	8.751789	8.779232
AOA140T8J4	7.438014	7.531732	7.505277	6.570411	6.506607	6.557987
AOA5K1VVS7	4.033107	4.010788	4.021532	3.897513	3.874956	3.888540
D3Z4C9	5.720125	5.734133	5.730803	5.549447	5.533970	5.530733
D6RGM8	2.155996	2.163340	2.125520	1.866826	1.848495	1.806531
E9PYD1	2.874815	2.911906	2.880786	2.618299	2.606916	2.579025

In [20]:

```
pheatmap(selet_DEPs, scale="row", cluster_cols=FALSE, cluster_row=TRUE,
  angle_col = c("0"), fontsize=12, fontsize_col = 20, legend = TRUE,
  show_rownames=TRUE)
```



heatmap with label

In [21]:

```
selet_DEPs_label <- read.table("./Select_Proteins_Normalized_abundance_with_
  sep='\t', header = T, row.names = 1)
```

```
In [22]: head(selet_DEPs_label)
```

A data.frame: 6 × 7

	wt1	wt2	wt3	ko1	ko2	ko3	labs
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>
A0A0R4IZY0	8.600989	8.630331	8.627368	8.788076	8.751789	8.779232	A0A0R4IZY0
A0A140T8J4	7.438014	7.531732	7.505277	6.570411	6.506607	6.557987	
A0A5K1VVS7	4.033107	4.010788	4.021532	3.897513	3.874956	3.888540	
D3Z4C9	5.720125	5.734133	5.730803	5.549447	5.533970	5.530733	
D6RGM8	2.155996	2.163340	2.125520	1.866826	1.848495	1.806531	D6RGM8
E9PYD1	2.874815	2.911906	2.880786	2.618299	2.606916	2.579025	

```
In [23]: heatmap.label <- selet_DEPs_label$labs
selet_DEPs <- selet_DEPs_label[, 1:6]
```

```
In [24]: head(heatmap.label)
head(selet_DEPs)
```

'A0A0R4IZY0' . " . " . " . 'D6RGM8' . "

A data.frame: 6 × 6

	wt1	wt2	wt3	ko1	ko2	ko3
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
A0A0R4IZY0	8.600989	8.630331	8.627368	8.788076	8.751789	8.779232
A0A140T8J4	7.438014	7.531732	7.505277	6.570411	6.506607	6.557987
A0A5K1VVS7	4.033107	4.010788	4.021532	3.897513	3.874956	3.888540
D3Z4C9	5.720125	5.734133	5.730803	5.549447	5.533970	5.530733
D6RGM8	2.155996	2.163340	2.125520	1.866826	1.848495	1.806531
E9PYD1	2.874815	2.911906	2.880786	2.618299	2.606916	2.579025

```
In [25]: pheatmap(selet_DEPs, scale="row", cluster_cols=FALSE, cluster_row=TRUE,
  angle_col = c("0"), fontsize=12, fontsize_col = 20, legend = TRUE,
  show_rownames=TRUE, labels_row=heatmap.label)
```