

# A foundation for reliable spatial proteomics experiments data analysis: organelle markers

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May 6, 2014

## Contents

<b>1</b>	<b>Introduction</b>	<b>2</b>
<b>2</b>	<b>Overview of the markers</b>	<b>3</b>
<b>3</b>	<b>Arabidopsis markers</b>	<b>5</b>
<b>4</b>	<b>Gallus markers</b>	<b>6</b>
<b>5</b>	<b>Yeast markers</b>	<b>7</b>
<b>6</b>	<b>Fly markers</b>	<b>8</b>
<b>7</b>	<b>Human markers</b>	<b>9</b>
<b>8</b>	<b>Mouse markers</b>	<b>10</b>

# 1 Introduction

This document describes the marker proteins distributed with the pRoloc package. We provide the exact code used to generate the respective outputs and figures.

The first code chunk provides loads the package and prepares the data for the following sections.

```
library("pRoloc")

atha <- pRolocmarkers("atha")
dmel <- pRolocmarkers("dmel")
ggal <- pRolocmarkers("ggal")
hsap <- pRolocmarkers("hsap")
scer <- pRolocmarkers("scer")
mmus <- pRolocmarkers("mmus")

m1 <- list(atha = atha,
          dmel = dmel,
          ggal = ggal,
          hsap = hsap,
          mmus = mmus,
          scer = scer)

describe <- function(m) {
  n <- length(m)
  m <- length(unique(m))
  x <- MSnbase::getVariableName(match.call(), "m")
  c(n, m)
}
```

## 2 Overview of the markers

The `pRolocmarkers` function describes the available marker lists. When run with a species identifier (for example `pRolocmarkers("hsap")`, see below for more examples), the appropriate markers are returned as a `vector`.

```
pRolocmarkers()
```

```
6 marker lists available:
```

```
Arabidopsis thaliana [atha]:
```

```
  Ids: TAIR, 543 markers
```

```
Drosophila melanogaster [dmel]:
```

```
  Ids: Annotation symbol, 144 markers
```

```
Gallus gallus [ggal]:
```

```
  Ids: IPI, 102 markers
```

```
Homo sapiens [hsap]:
```

```
  Ids: Uniprot, 205 markers
```

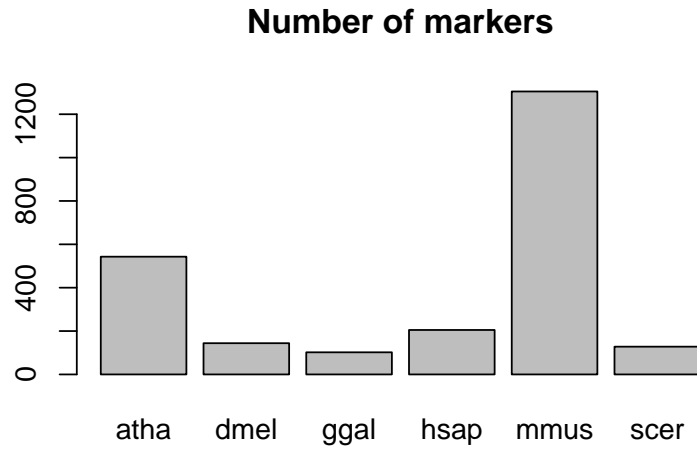
```
Mus musculus [mmus]:
```

```
  Ids: Uniprot, 1305 markers
```

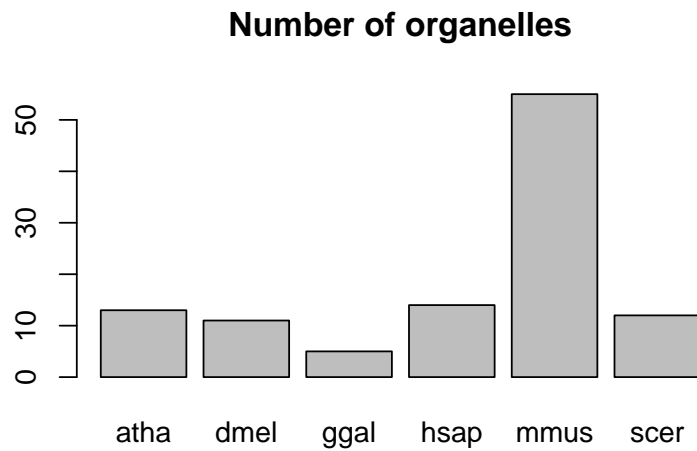
```
Saccharomyces cerevisiae [scer]:
```

```
  Ids: SGD, 128 markers
```

```
barplot(sapply(ml, length), main = "Number of markers")
```

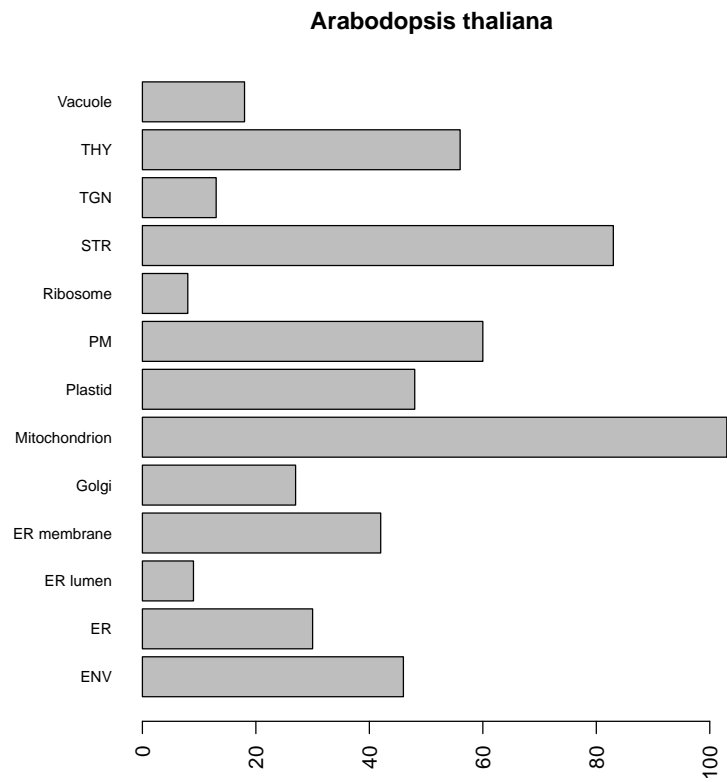


```
barplot(sapply(ml, function(x) length(unique(x))),  
main = "Number of organelles")
```



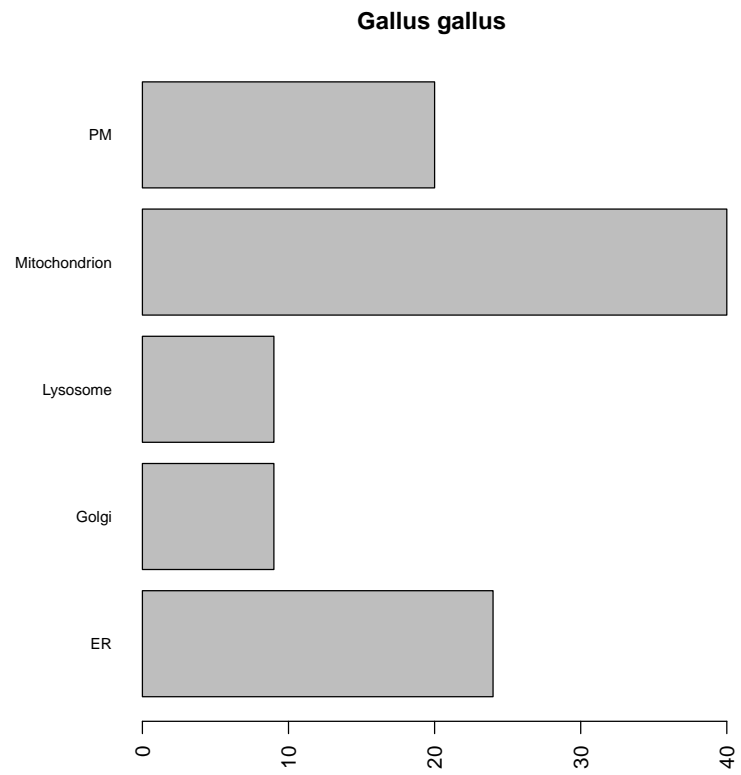
### 3 Arabidopsis markers

```
par(mar = c(5, 10, 3, 1))  
barplot(table(atha), horiz = TRUE, las = 2, cex.names = .75,  
main = "Arabodopsis thaliana")
```



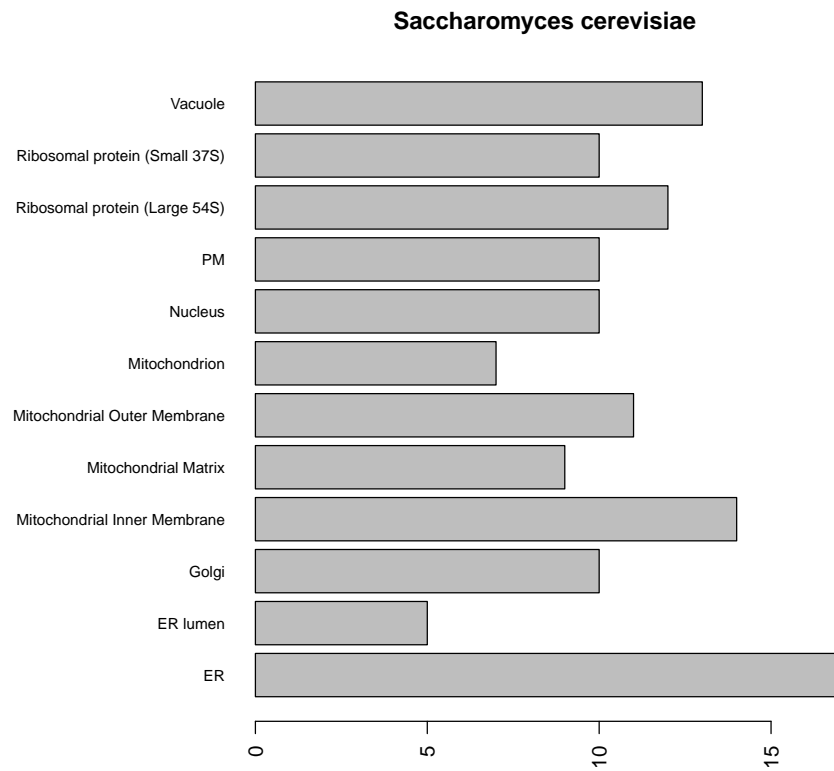
## 4 Gallus markers

```
par(mar = c(5, 10, 3, 1))  
barplot(table(ggal), horiz = TRUE, las = 2, cex.names = .75,  
main = "Gallus gallus")
```



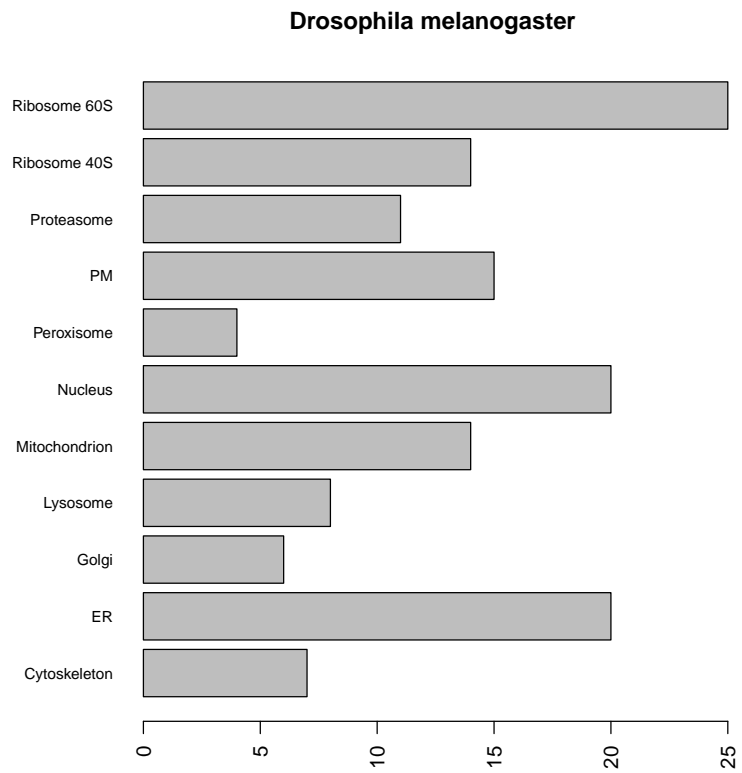
## 5 Yeast markers

```
par(mar = c(5, 10, 3, 1))  
barplot(table(scer), horiz = TRUE, las = 2, cex.names = .75,  
main = "Saccharomyces cerevisiae")
```



## 6 Fly markers

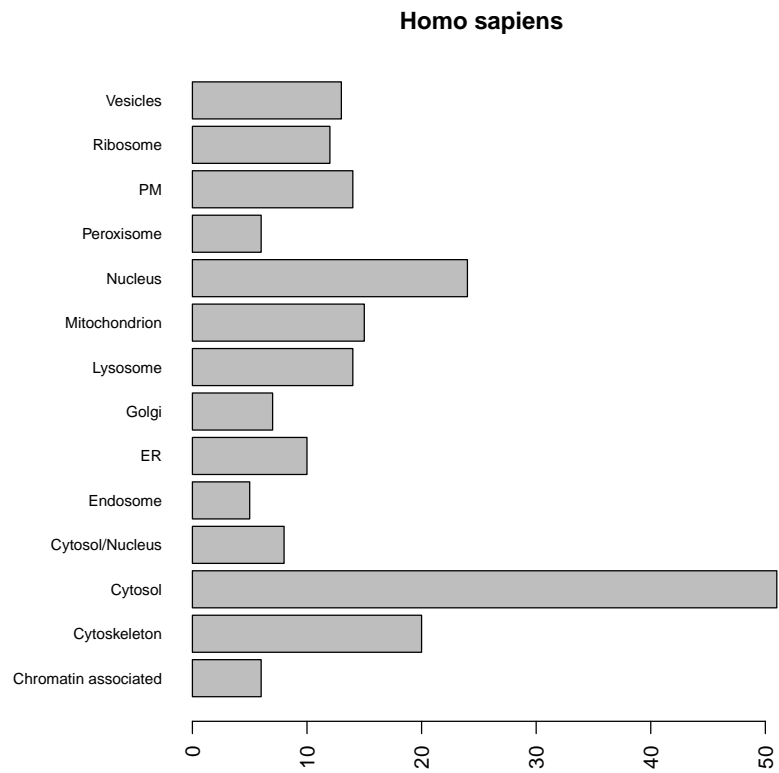
```
par(mar = c(5, 10, 3, 1))  
barplot(table(dmel), horiz = TRUE, las = 2, cex.names = .75,  
main = "Drosophila melanogaster")
```





## 7 Human markers

```
par(mar = c(5, 10, 3, 1))  
barplot(table(hsap), horiz = TRUE, las = 2, cex.names = .75,  
main = "Homo sapiens")
```



## 8 Mouse markers

```
par(mar = c(5, 10, 3, 1))
barplot(table(mmus), horiz = TRUE, las = 2, cex.names = .75,
main = "Mus musculus")
```

