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R Markdown

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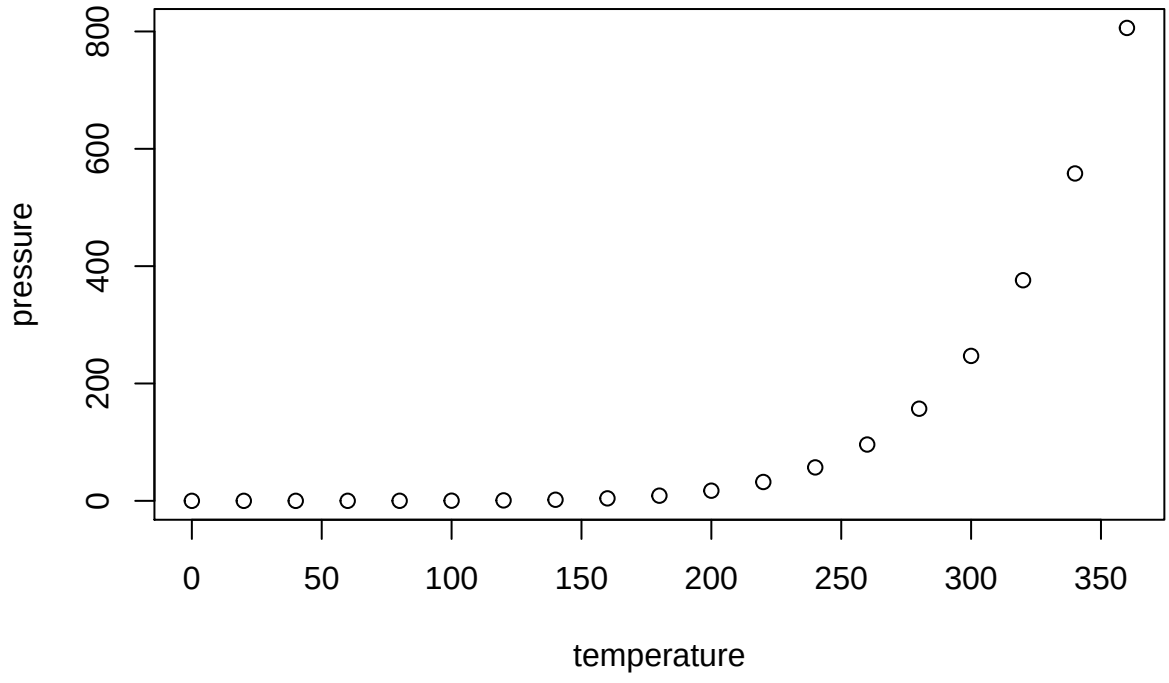
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed           dist       
##  Min.   : 4.0   Min.   :  2.00  
##  1st Qu.:12.0   1st Qu.: 26.00  
##  Median :15.0   Median : 36.00  
##  Mean   :15.4   Mean   : 42.98  
##  3rd Qu.:19.0   3rd Qu.: 56.00  
##  Max.   :25.0   Max.   :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

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http://www.bacandrology.com/content/23/1/7

BASIC AND CLINICAL ANDROLOGY

RESEARCH ARTICLE Open Access

Comparative testicular transcriptome of wild type and globozoospermic *Dpy19l2* knock out mice

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Abstract

Background: Globozoospermia is a male infertility phenotype characterized by the presence in the ejaculate of near 100% acrosomeless round-headed spermatozoa with normal chromosomal content. Following intracytoplasmic sperm injection (ICSI) these spermatozoa give a poor fertilization rate and embryonic development. We showed previously that most patients have a 200 kb homozygous deletion, which includes *DPY19L2* whole coding sequence. Furthermore we showed that the DPY19L2 protein is located in the inner nuclear membrane of spermatids during spermiogenesis and that it is necessary to anchor the acrosome to the nucleus thus performing a function similar to that realized by Sun proteins within the *LINC-complex* (Linker of Nucleoskeleton and Cytoskeleton). SUN1 was described to be necessary for gametogenesis and was shown to interact with the telomeres. It is therefore possible that Dpy19l2 could also interact, directly or indirectly, with the DNA and modulate gene expression during spermatogenesis.
In this study, we compared the transcriptome of testes from *Dpy19l2* knock out and wild type mice in order to identify a potential deregulation of transcripts that could explain the poor fertilization potential of *Dpy19l2* mutated spermatozoa.

Methods: RNA was extracted from testes from *DPY19L2* knock out and wild type mice. The transcriptome was carried out using GeneChip® Mouse Exon 1.0 ST Arrays. The biological processes and molecular functions of the differentially regulated genes were analyzed with the PANTHER software.

Results: A total of 76 genes were deregulated, 70 were up-regulated and 6 (including *Dpy19l2*) were down-regulated. These genes were found to be involved in DNA/RNA binding, structural organization, transport and catalytic activity.

Conclusions: We describe that an important number of genes are differentially expressed in *Dpy19l2* mice. This work could help improving our understanding of *Dpy19l2* functions and lead to a better comprehension of the molecular mechanism involved in spermatogenesis.

Keywords: Male infertility, Globozoospermia, Spermatogenesis, Dpy19l2, Transcriptome

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