Figure 4b _data

```r
library(readr)
library(pathview)
```

```
##
## ##############################################################################
## Pathview is an open source software package distributed under GNU General
## Public License version 3 (GPLv3). Details of GPLv3 is available at
## http://www.gnu.org/licenses/gpl-3.0.html. Particullary, users are required to
## formally cite the original Pathview paper (not just mention it) in publications
## or products. For details, do citation("pathview") within R.
##
## The pathview downloads and uses KEGG data. Non-academic uses may require a KEGG
## license agreement (details at http://www.kegg.jp/kegg/legal.html).
## ##############################################################################
```

```r
library(data.table)
```

```r
#pathview.csv from KNIME folder "Figure4_RNA_seq"
ko_test <- read.csv("pathview.csv", sep = ",",header = TRUE, row.names = 1)
as.matrix(ko_test) -> ko_mat
```

```r
# run with ko numbers centred values--------------------
#"04150" = mTOR signaling
# 04630 Jak-STAT signaling pathway (23)
# 04064 NF-kappa B signaling pathway (28)
# 04668 TNF signaling pathway (35)
# 04350 TGF-beta signaling pathway (38)
# 04010 MAPK signaling pathway (110)
# 04620 Toll-like receptor signaling pathway (23)
# 00480 Glutathion pathway
# 04610 Complement and coagulation cascades
# 04621 NOD-like receptor
# 04625 C-type lectin receptor signaling pathway
# 05145    Toxoplasmosis

my_pathways <- c("04064", "04620")
```

```r
pv_ko.out <-   pathview(gene.data = ko_mat[, c(2,3,4)],
                        pathway.id = my_pathways,  #pathways of interest
                        species = "ko", # ko
                        out.suffix = "Centered_Sym_Apo_Mg",
                        limit = list(gene = 7, cpd = 1),
                        gene.idtype = "kegg",
                        kegg.native = TRUE,
                        low = list(gene = "firebrick3", cpd = "firebrick3"), #set colors
                        mid = list(gene = "gray", cpd = "gray"),   # set colors
                        high = list(gene = "dodgerblue3", cpd = "dodgerblue3")) # set colors
```

```
## Note: Only KEGG ortholog gene ID is supported, make sure it looks like "K01488"!

## Note: Mapping via KEGG gene ID (not Entrez) is supported for this species,
## it looks like "K01488"!

## Info: Working in directory /Users/sebastian/Documents/Arbeit/GuseLab/R!/Figure4b_data

## Info: Writing image file ko04064.Centered_Sym_Apo_Mg.multi.png

## Info: Working in directory /Users/sebastian/Documents/Arbeit/GuseLab/R!/Figure4b_data

## Info: Writing image file ko04620.Centered_Sym_Apo_Mg.multi.png
```

```r
pv_ko.out <- pathview(gene.data = ko_mat[, c(6,7,10)],
                      pathway.id = my_pathways,  #pathways of interest
                      species = "ko",
                      out.suffix = "Significant_Sym-vs-Apo_Sym-vs-Sym-Apo_Sym-vs-Mg", # ko
                      limit = list(gene = 7, cpd = 1),
                      gene.idtype = "kegg",
                      kegg.native = TRUE,
                      low = list(gene = "firebrick3", cpd = "firebrick3"), #set colors
                      mid = list(gene = "gray", cpd = "gray"),   # set colors
                      high = list(gene = "dodgerblue3", cpd = "dodgerblue3")) # set colors
```

```
## Note: Only KEGG ortholog gene ID is supported, make sure it looks like "K01488"!

## Note: Mapping via KEGG gene ID (not Entrez) is supported for this species,
## it looks like "K01488"!

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## Info: Working in directory /Users/sebastian/Documents/Arbeit/GuseLab/R!/Figure4b_data

## Info: Writing image file ko04620.Significant_Sym-vs-Apo_Sym-vs-Sym-Apo_Sym-vs-Mg.multi.png
```