

# Figure S12 Reporter-ChIP-nexus expression quantification

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## Enviroment setup

```
library(GenomicRanges, warn.conflicts=F)
library(magrittr)
library(Rmisc)
library(reshape2)

setwd("/data/analysis_code")
options(knitr.figure_dir =
  "FigureS12_expression_quantification")

source("shared_code/knitr_common.r")
source("shared_code/ggplot_common.r")
source("shared_code/granges_common.r")
source("shared_code/metapeak_common.r")
```

## Analysis

```
expression <- read.csv("expression_quantification.csv")

prepare_expression_df <- function(genes){
  downstream_exp <- subset(expression, gene %in% genes) %>%
    melt(., id.vars = "gene", na.rm = T)
  summary <- summarySE(downstream_exp, measurevar="value", groupvars="gene")
  summary$gene <- factor(summary$gene, levels = genes)
  summary
}

downstream <- c("pepck", "act5c", "pepck-pk", "pepck-dve", "act5c-pk")
tata <- c("pk", "comm2", "dve",
  "act5c_up_pk", "act5c_up_comm2", "act5c_up_dve",
  "tata_pk", "tata_comm2", "tata_dve")
inr <- c("dve", "act5c_up_dve", "act5c_dve_down", "dve_act5c_inr")
inr_2 <- c("dve", "pk", "scp", "dve-inr-T", "dve-inr-A", "pk-inr-T", "scp-inr-T")
```

```

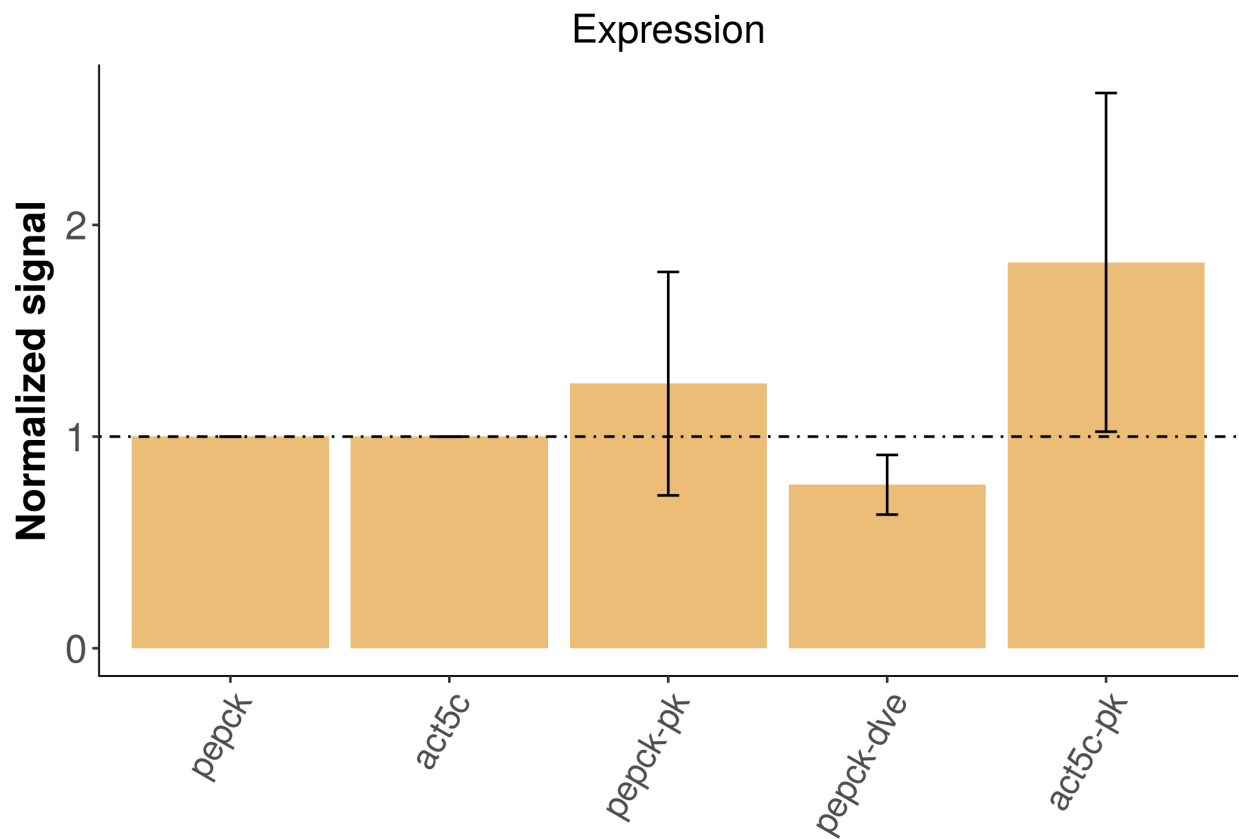
sample_list <- list(downstream = downstream,tata=tata, inr= inr, inr2= inr_2)

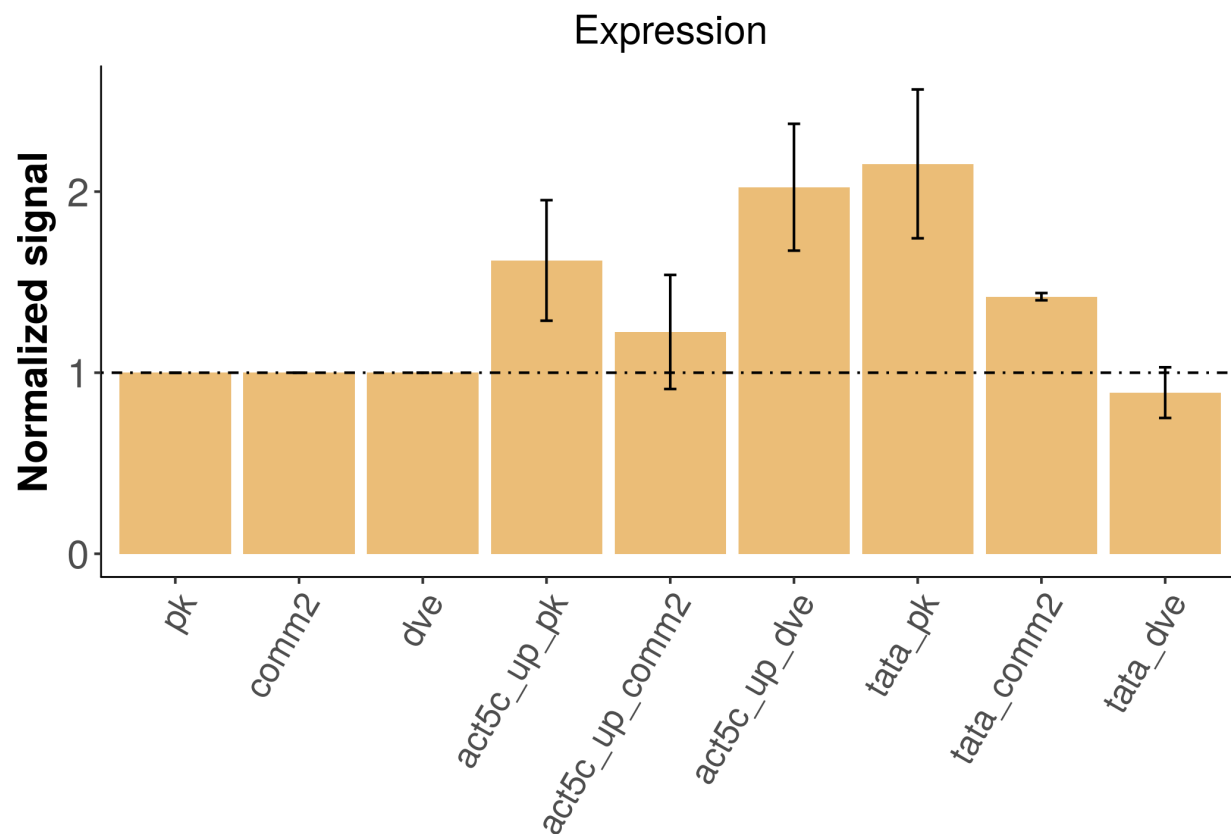
expression_df <- lapply(sample_list, prepare_expression_df)

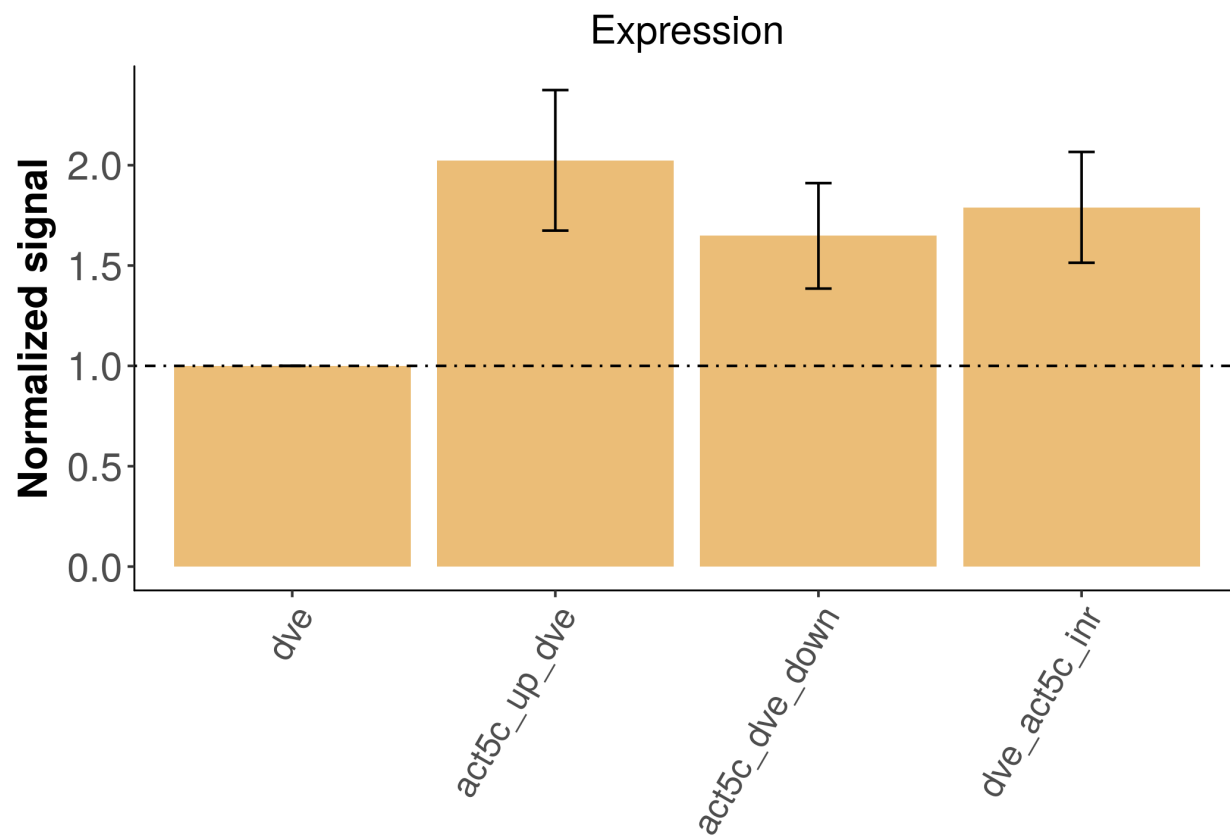
plotting_expression <- function(exp_df){
  x <- ggplot(exp_df, aes(x=gene, y=value)) +
    geom_bar(stat= "identity", position = "dodge",
            fill = "#EBBD77") +
    geom_errorbar(aes(ymin=value-se, ymax=value+se),
                 width=.1, position=position_dodge(.9)) +
    ylab("Normalized signal") +
    xlab("")+
    ggtitle("Expression")+
    geom_hline(yintercept = 1, lty = 4) +
    theme(axis.text.x = element_text(size=14, angle = 60, hjust = 1))
  print(x)
}

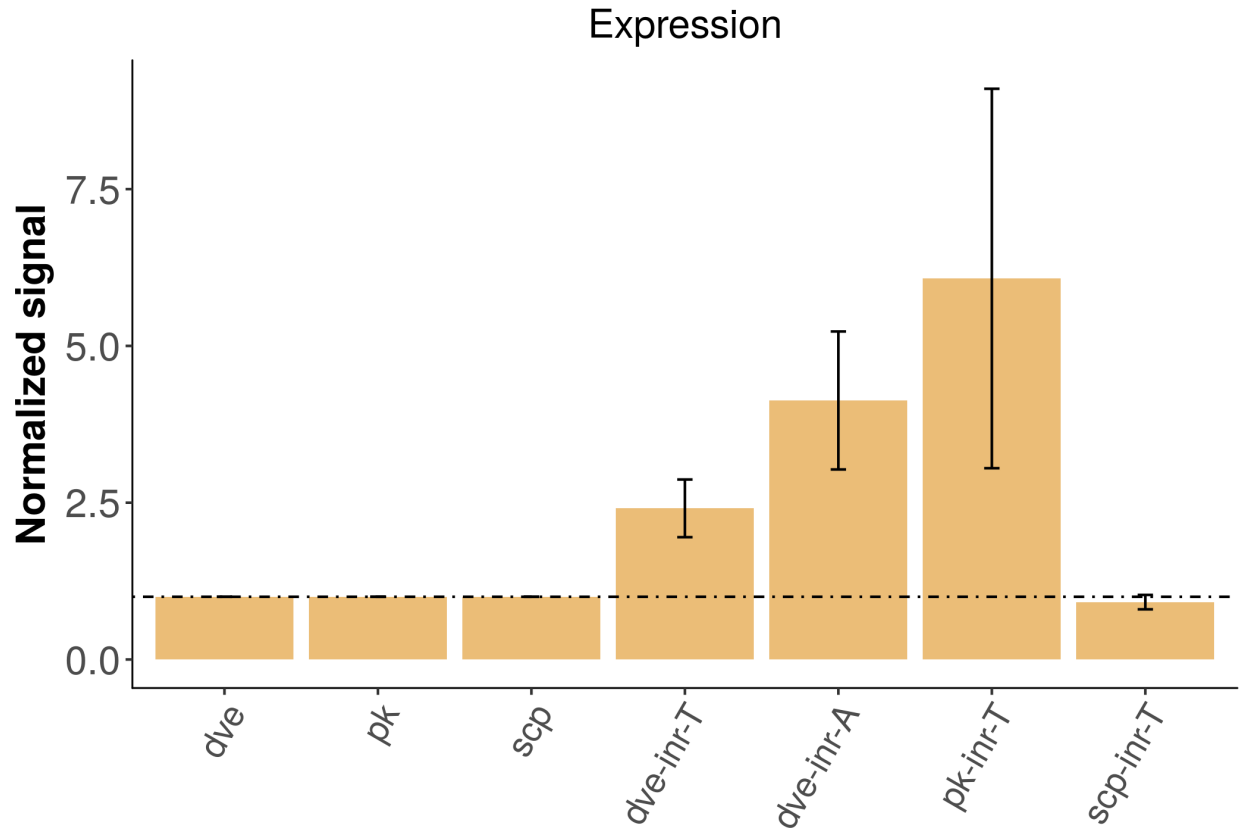
nothing <- lapply(expression_df, plotting_expression)

```









## Session Info

This analysis was performed with the following R/Bioconductor session:

```
sessionInfo()
```

```
## R version 3.4.4 (2018-03-15)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.4 LTS
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats4      stats      graphics  grDevices  utils      datasets
```

```
## [8] methods    base
##
## other attached packages:
## [1] rtracklayer_1.38.3    ggplot2_2.2.1        pander_0.6.1
## [4] reshape2_1.4.3        Rmisc_1.5            plyr_1.8.4
## [7] lattice_0.20-35       magrittr_1.5         GenomicRanges_1.30.3
## [10] GenomeInfoDb_1.14.0   IRanges_2.12.0       S4Vectors_0.16.0
## [13] BiocGenerics_0.24.0
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.17          compiler_3.4.4
## [3] pillar_1.2.3          XVector_0.18.0
## [5] bitops_1.0-6          tools_3.4.4
## [7] zlibbioc_1.24.0       digest_0.6.15
## [9] evaluate_0.10.1       tibble_1.4.2
## [11] gtable_0.2.0          rlang_0.2.1
## [13] Matrix_1.2-14         DelayedArray_0.4.1
## [15] yaml_2.1.19           GenomeInfoDbData_1.0.0
## [17] stringr_1.3.1         knitr_1.20
## [19] Biostrings_2.46.0     rprojroot_1.3-2
## [21] grid_3.4.4            Biobase_2.38.0
## [23] BiocParallel_1.12.0   XML_3.98-1.11
## [25] rmarkdown_1.10        matrixStats_0.53.1
## [27] GenomicAlignments_1.14.2 backports_1.1.2
## [29] scales_0.5.0          Rsamtools_1.30.0
## [31] htmltools_0.3.6       SummarizedExperiment_1.8.1
## [33] colorspace_1.3-2      labeling_0.3
## [35] stringi_1.2.3         RCurl_1.95-4.10
## [37] lazyeval_0.2.1        munsell_0.5.0
```