

## Supplementary Data 23. R script used to map mouse to human RNA seq data set

```
# read in the human and mouse data
human.data <- read.table('humman.genes.txt')
mouse.data <- read.table('mouse.genes.txt')

# merge the human data and mouse data by mapping mouse gene symbols to
human gene symbols
mouse.data$mouse.geneID <- toupper(mouse.data$mouse.geneID)

mapped.data <- merge(human.data, mouse.data, by.x='human.geneID',
by.y='mouse.geneID')

write.table(mapped.data, file='merged.data.txt')
```