# Regeneration *Drosophila melanogaster* new RNAseq samples sequenced at the CRG

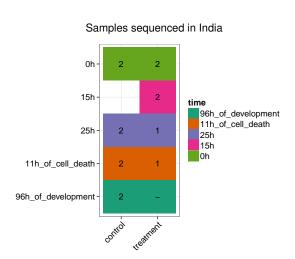
## Outline

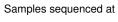
Overview of RNA-seq samples

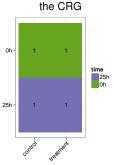
Mapping statistics

Correlation between replicates

# RNAseq samples







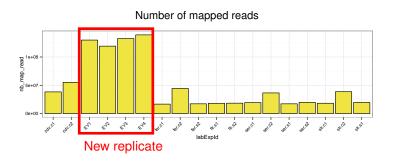
## Outline

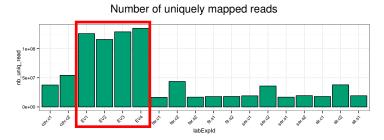
Overview of RNA-seq samples

Mapping statistics

Correlation between replicates

# Mapping statistiques



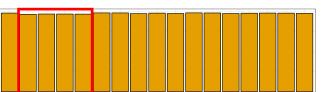


# Mapping statistiques

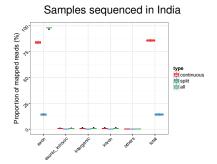
7: Todord Lead



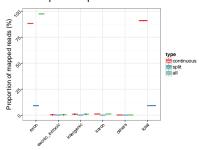
Proportion of mapped reads over mapped reads



# Genomic regions

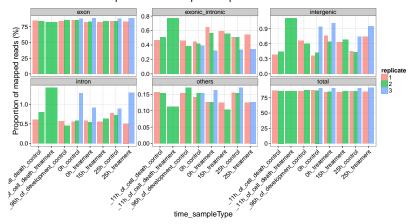






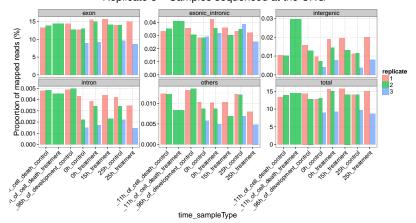
## Genomic regions - conitnuous mapping

Replicates 1 and 2 = Samples sequenced in India Replicate 3 = Samples sequenced at the CRG



## Genomic regions - split mapping

Replicates 1 and 2 = Samples sequenced in India Replicate 3 = Samples sequenced at the CRG



## Outline

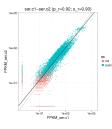
Overview of RNA-seq samples

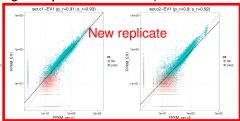
Mapping statistics

Correlation between replicates

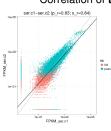
### Oh control

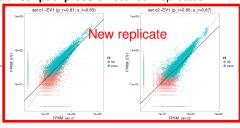






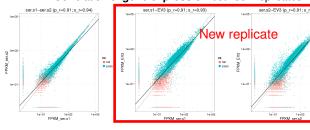
#### Correlation of transcript expression between replicates





#### Oh treatment

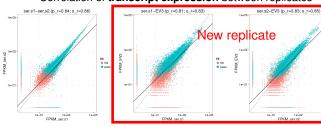




#### Correlation of transcript expression between replicates

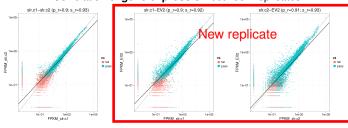
V4 • fall • pass

10+02



### 25h control

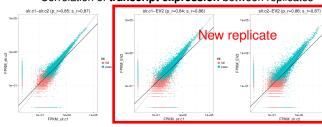




#### Correlation of transcript expression between replicates

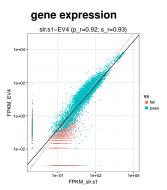
V4 • fall • pass

10+05



# 25h treatment - Only one replicate from India and one from the CRG

#### Correlation between replicates



#### transcript expression

