

Outline

RNAseq samples

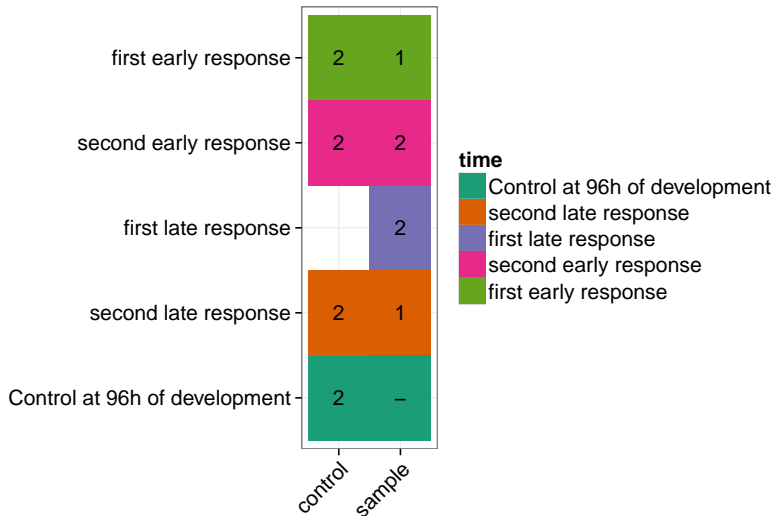
Mapping statistics

Correlation between replicates

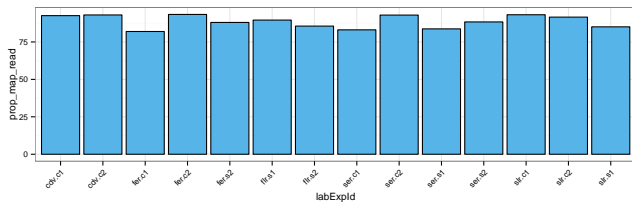
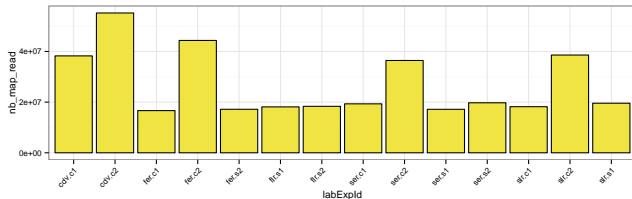
PCA and correlation matrix

Differential gene expression analysis

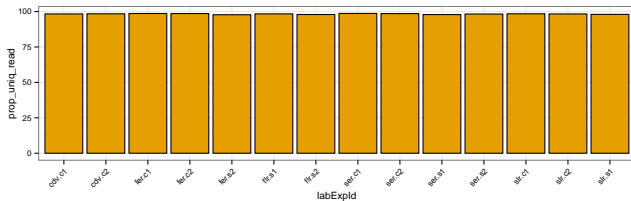
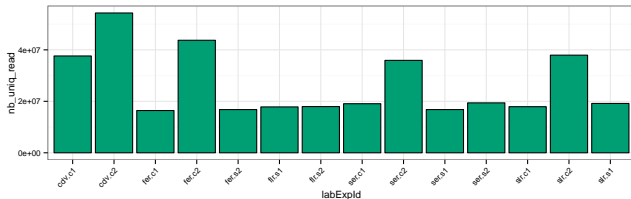
RNAseq samples



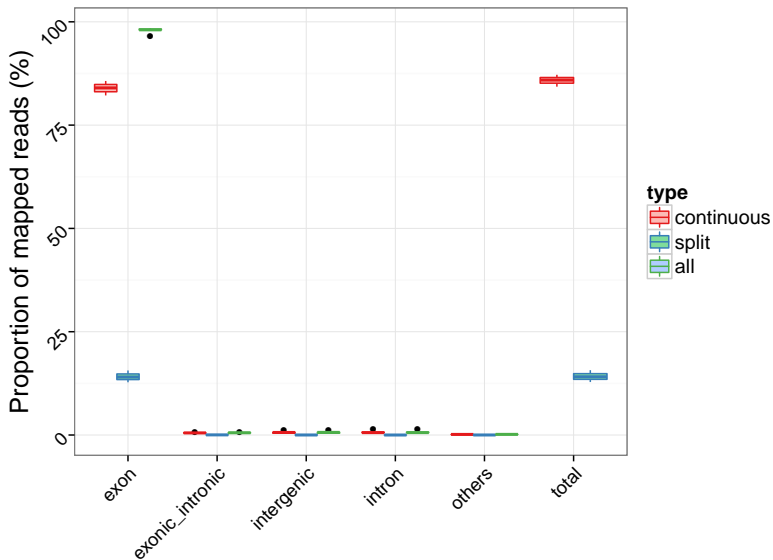
Mapping statistics



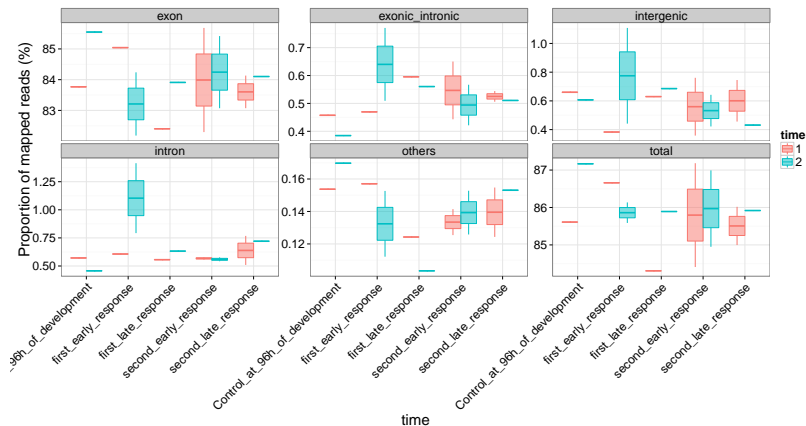
Mapping statistics



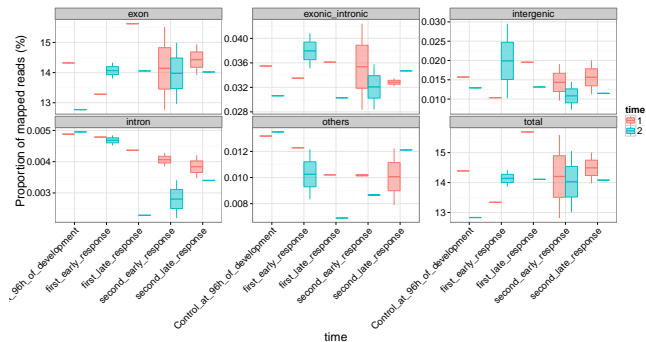
Mapping statistics



Mapping statistics - continuous

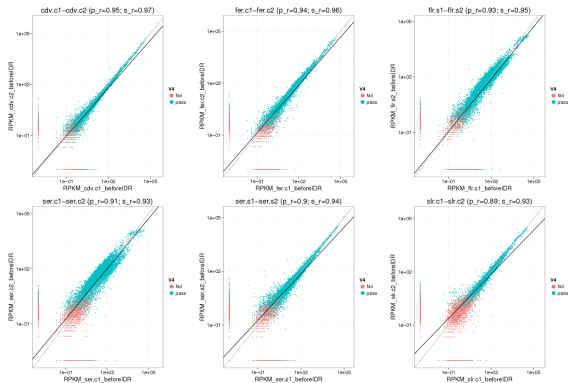


Mapping statistics - split



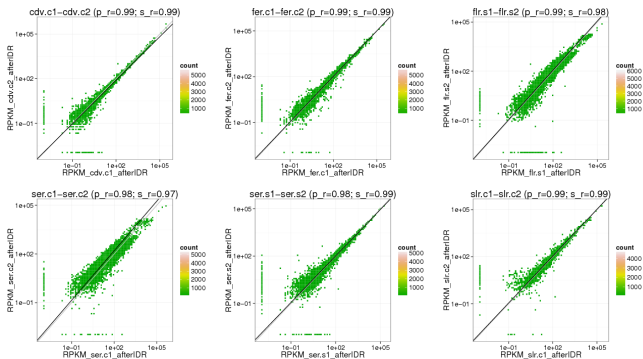
Correlation between replicates - **gene expression** - before filtering by $IDR \leq 0.1$

Pink dots indicate genes that fail IDR due to the difference between replicates.



Replicates	Pass IDR	Fail IDR
cdv.c1-cdv.c2	15071	2087
fer.c1-fer.c2	14775	2383
flr.s1-flr.s2	14742	2416
ser.c1-ser.c2	13728	3430
ser.s1-ser.s2	14001	3157
slr.c1-slr.c2	12484	4674

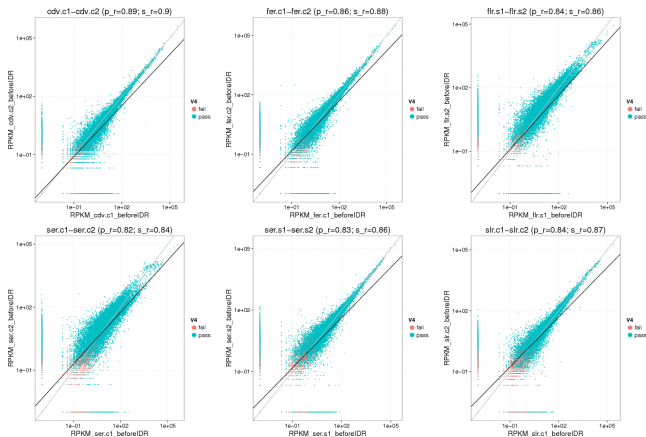
Correlation between replicates - **gene expression** - after filtering by $IDR \leq 0.1$



Correlation between replicates - **transcript expression**

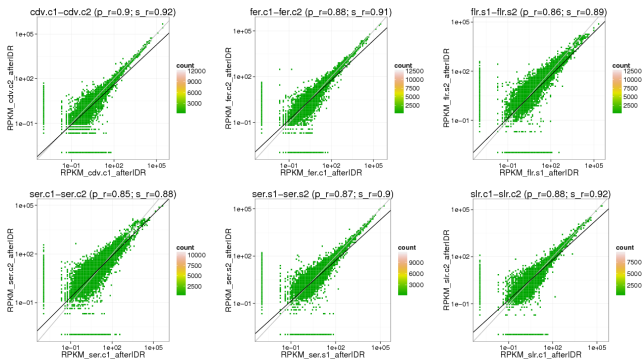
- **before** filtering by $IDR \leq 0.1$

Pink dots indicate transcripts that fail IDR due to the difference between replicates.



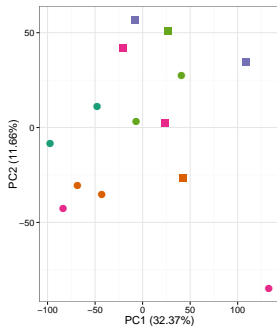
Correlation between replicates - **transcript expression**

- **after filtering by $IDR \leq 0.1$**

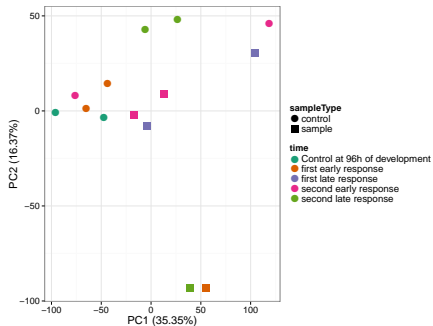


PCA - gene expression

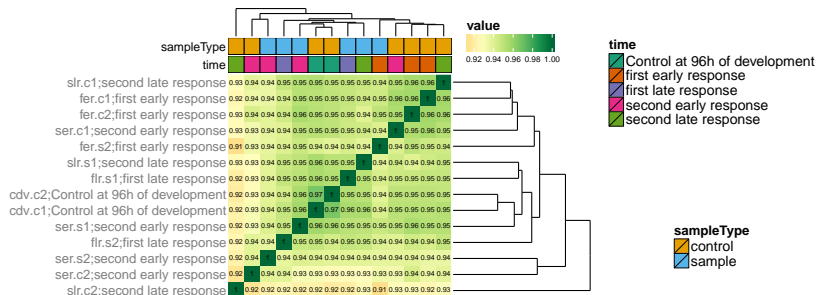
before IDR



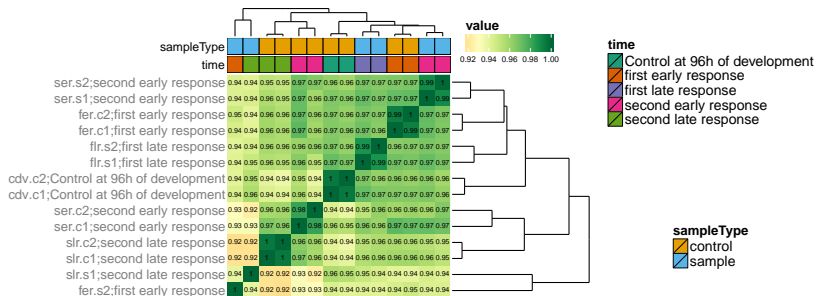
after IDR



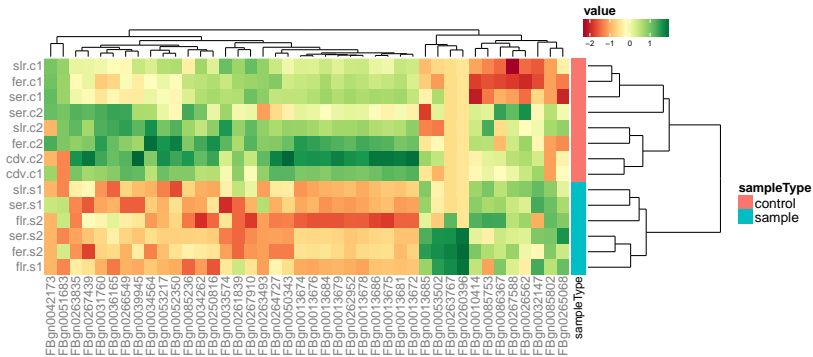
Correlation matrix of gene expression - before IDR (Spearman)



Correlation matrix of gene expression - after IDR (Spearman)



Differential gene expression analysis (EdgeR)



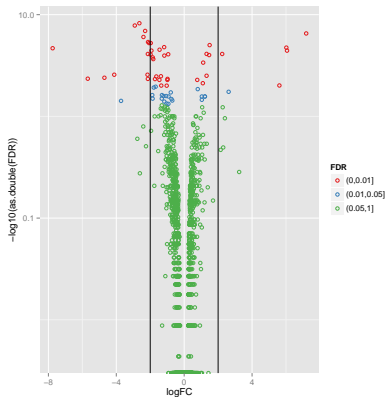
differential expression: control vs sample

FDR < 0.01

threshold for cpm [default=1]

minimum number of samples with cpm > "cpm" [default=2]

Differential gene expression analysis (EdgeR)



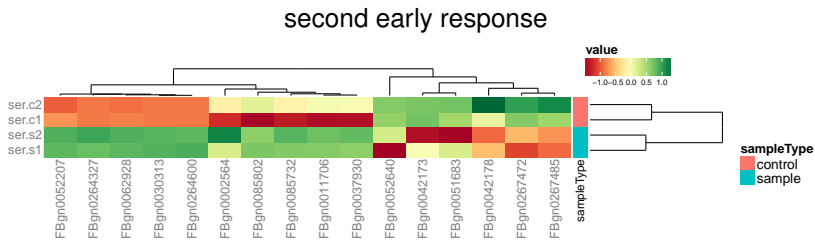
differential expression: control vs sample

$\text{FDR} < 0.01$

threshold for cpm [default=1]

minimum number of samples with cpm $>$ "cpm" [default=2]

Differential gene expression analysis (EdgeR)



differential expression: control vs sample

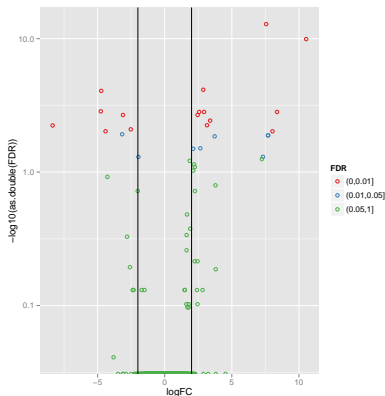
FDR < 0.01

threshold for cpm [default=1]

minimum number of samples with cpm > "cpm" [default=2]

Differential gene expression analysis (EdgeR)

second early response



differential expression: control vs sample

$\text{FDR} < 0.01$

threshold for cpm [default=1]

minimum number of samples with cpm $>$ "cpm" [default=2]