## RNA-seq = big datasets, numerous tools with numerous parameters = many different interpretations from the same dataset

« RNA-seq detects all RNAs »: Is my gene not expressed?

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Starting material:

- Which tissue?

Laser microdissection vs whole plant

- Which extraction protocol?

Small RNAs, ImmunoPrecipitation

- Which library synthesis protocol?
  polyA selection/ribosomal depletion/size selection
- Sequencing technology?

Illumina, PacBio, nanopore, IonTorrent...

- Sequencing depth?

« RNA-seq detects all RNAs »: Is my gene not expressed?

detected

Starting material:

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Laser microdissection vs whole plant

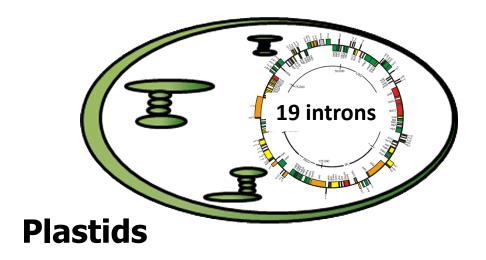
- Which extraction protocol?

Small RNAs, ImmunoPrecipitation

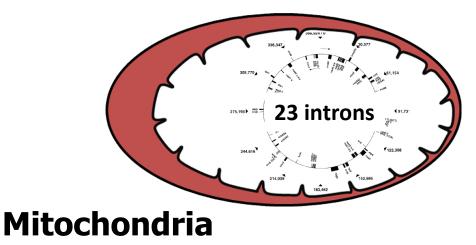
- Which library synthesis protocol?
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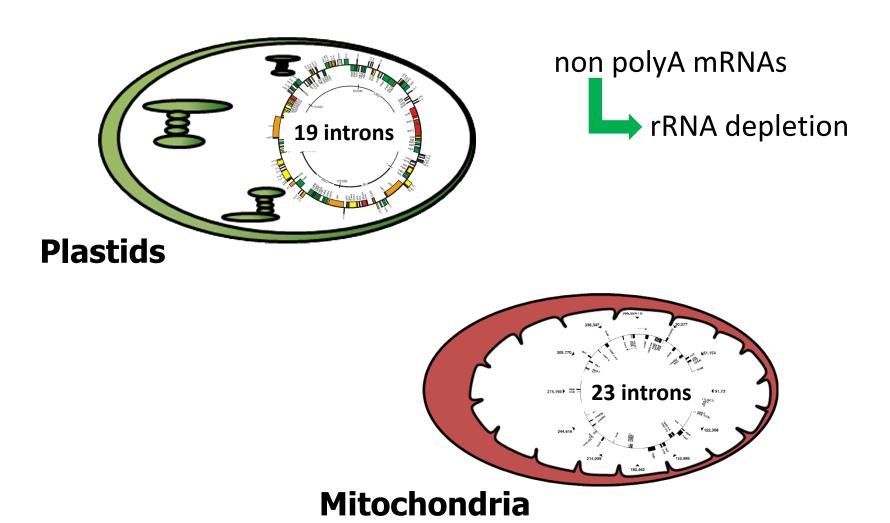
Illumina, PacBio, nanopore, IonTorrent...

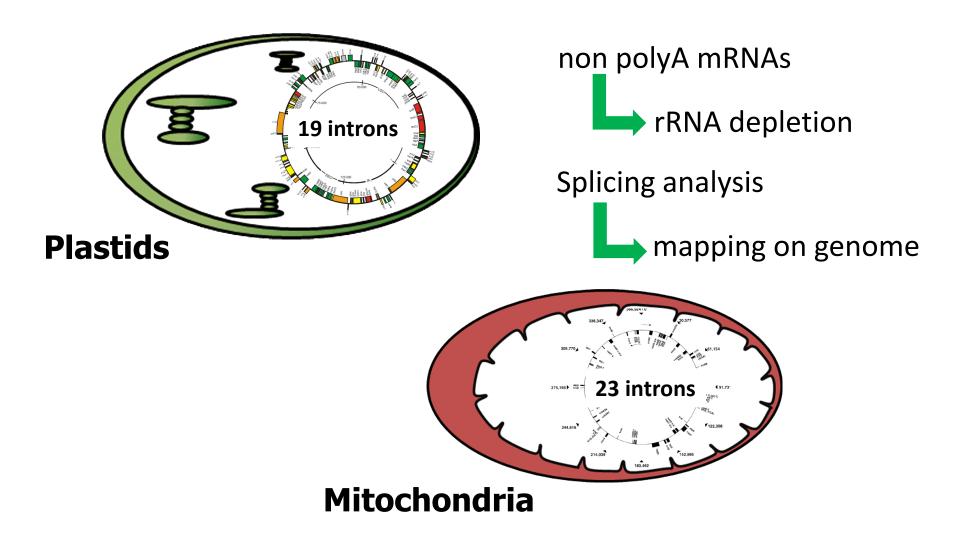
- Sequencing depth?

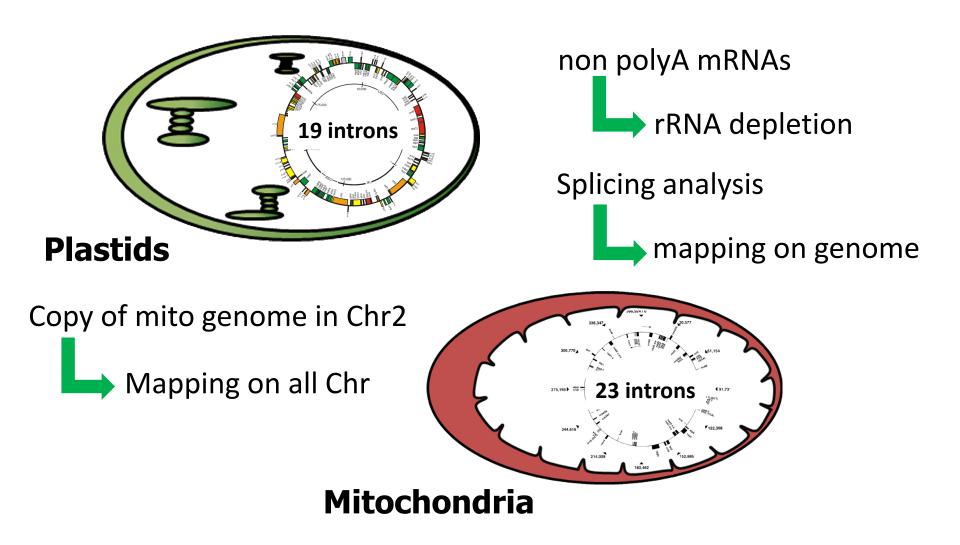


Organelles contain small genomes encoding key proteins and RNA necessary for their biology









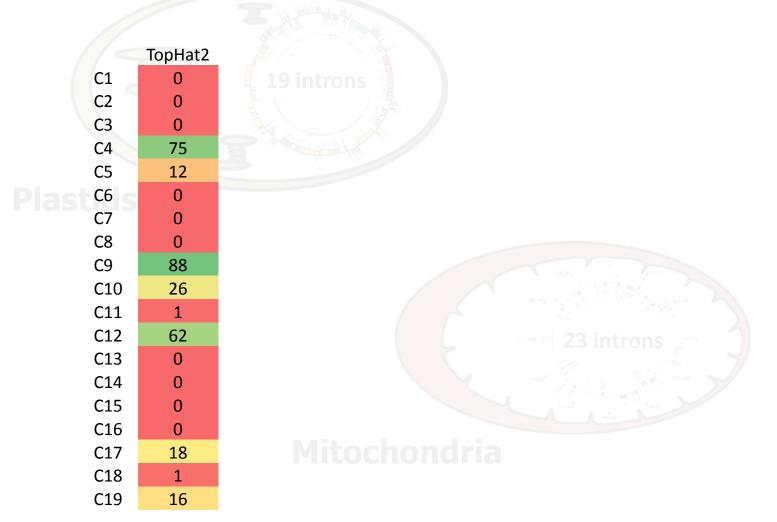
> TopHat2 or STAR? Genome annotation or not?

Plastids

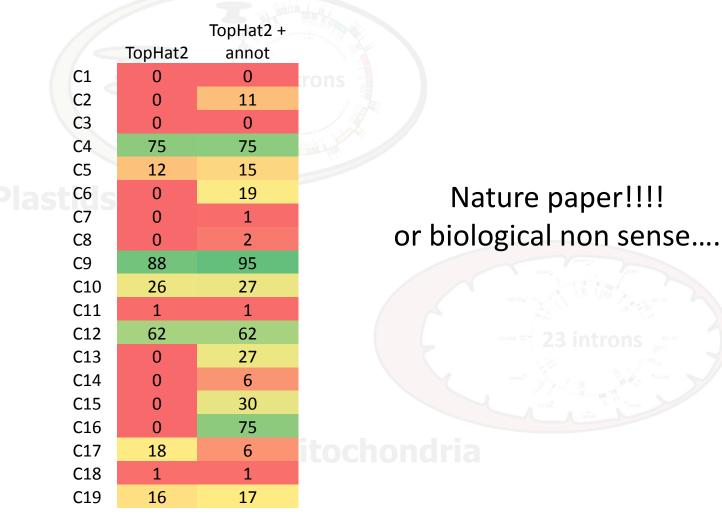


#### Mitochondria

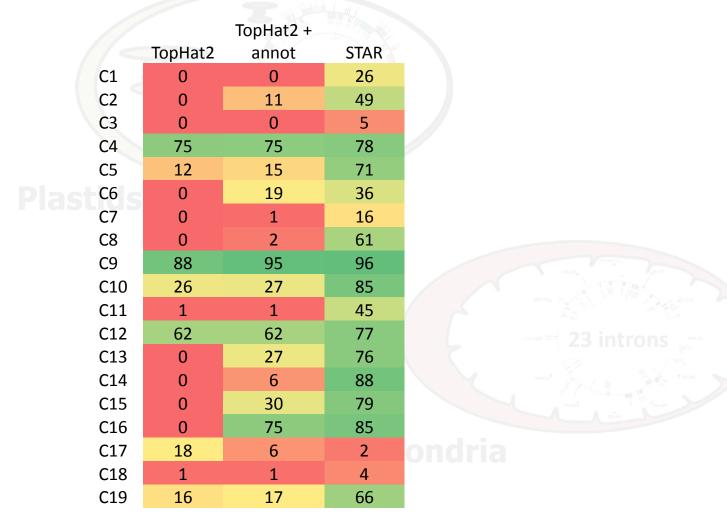
TopHat2 or STAR? Genome annotation or not?



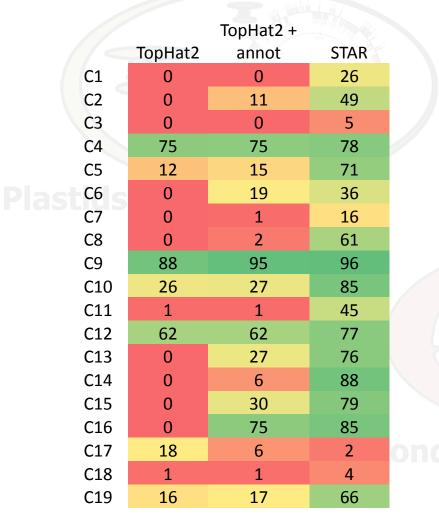
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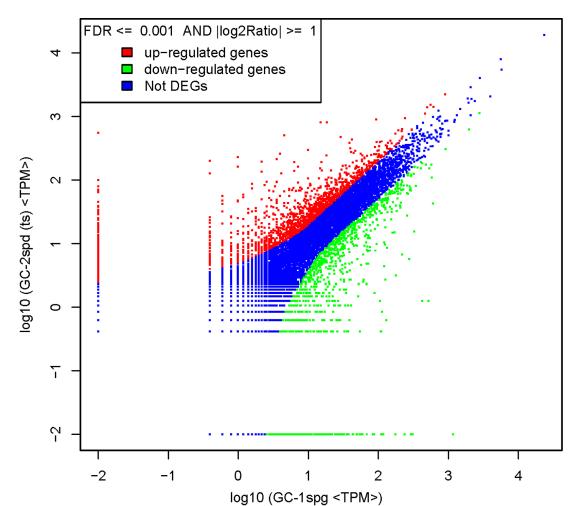


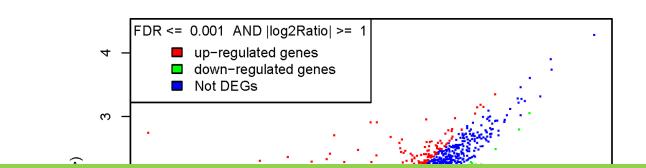
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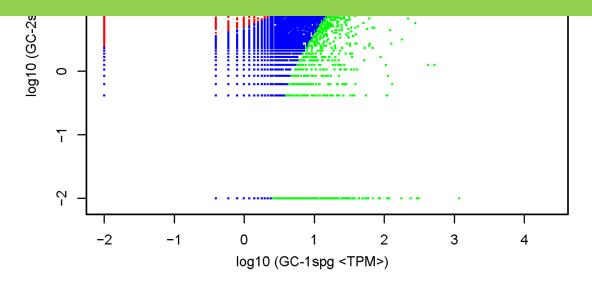
Use your biological expertise or borrow it from someone else!!!

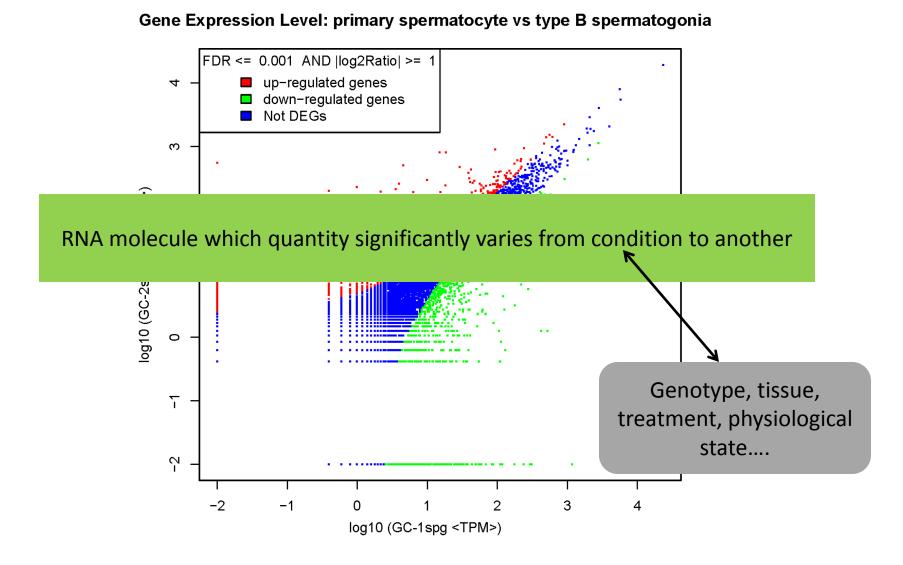
# Material and methods analysis

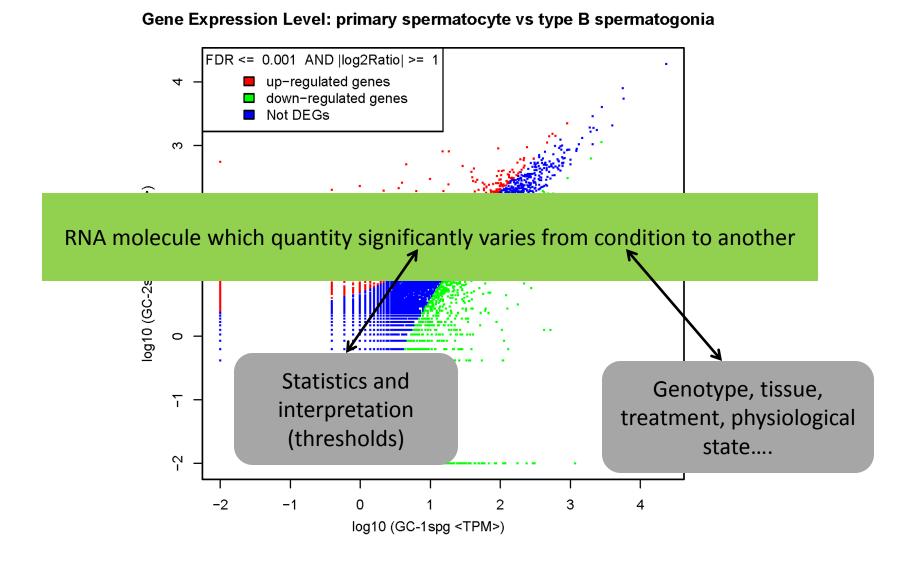


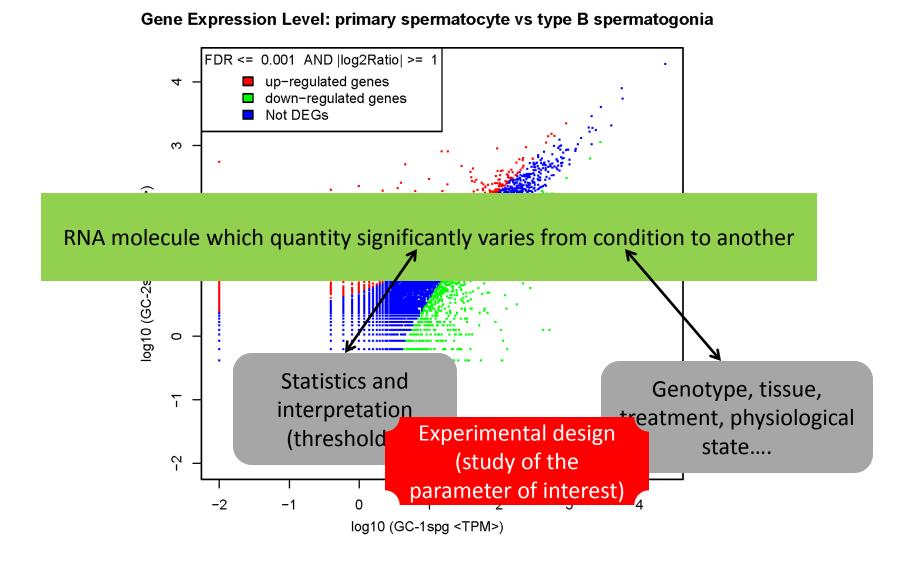


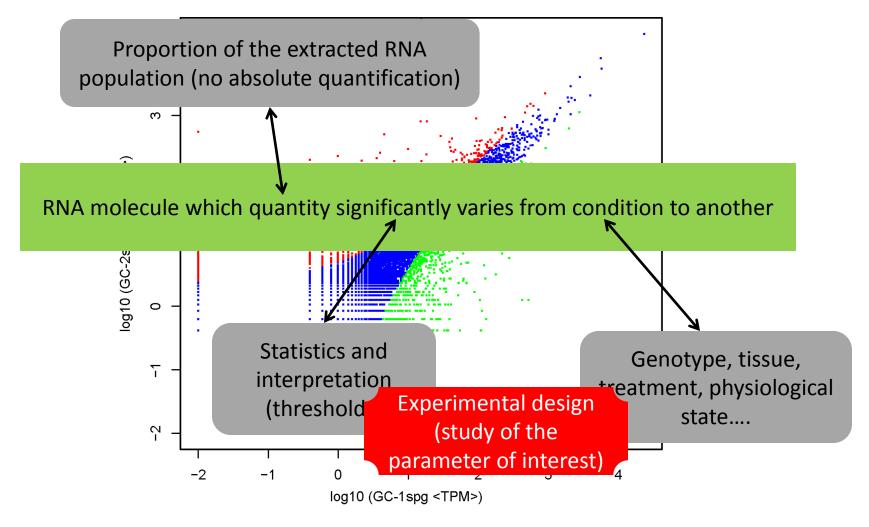
Gene Expression Level: primary spermatocyte vs type B spermatogonia

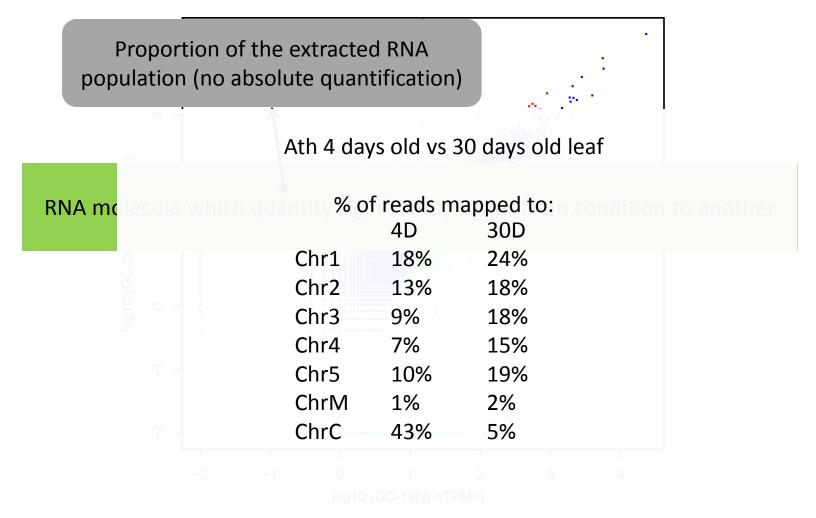


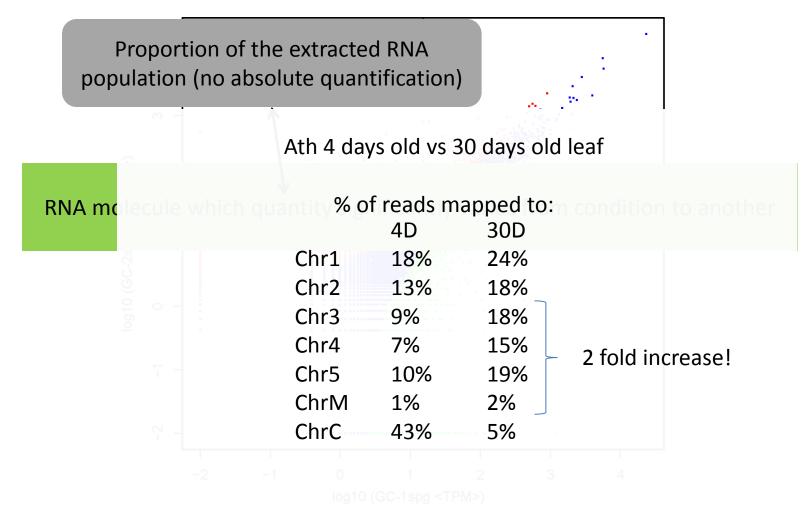


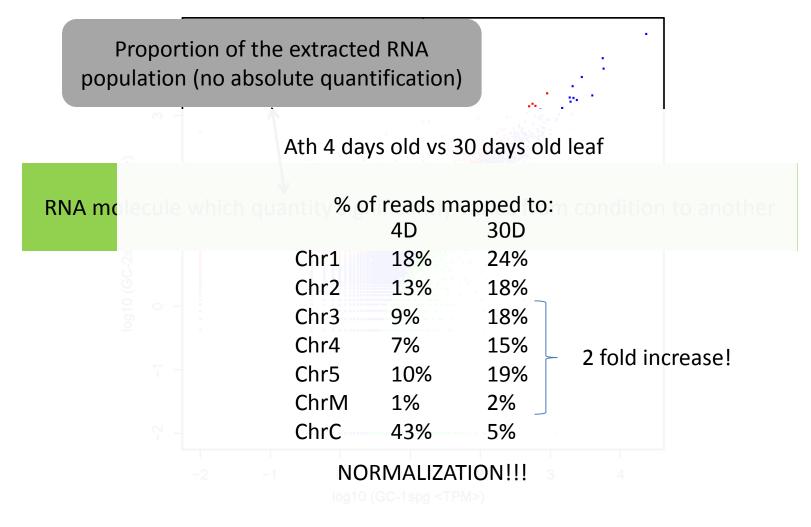












RNA molecule which quantity significantly varies from condition to another

How?

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How?

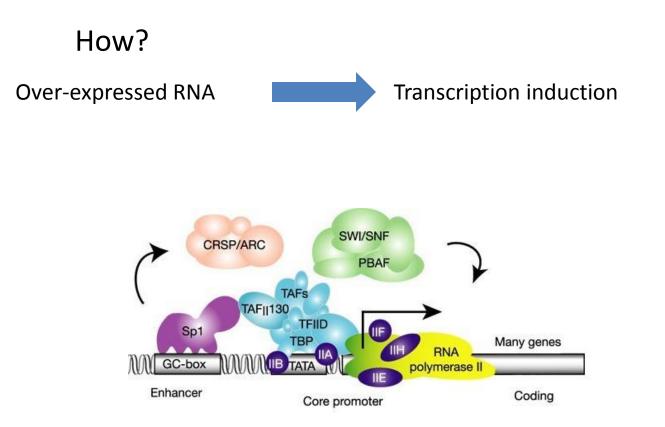
**Over-expressed RNA** 

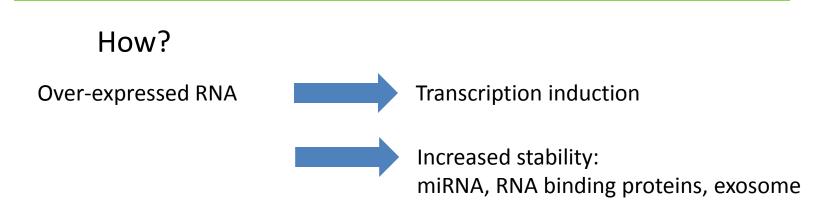
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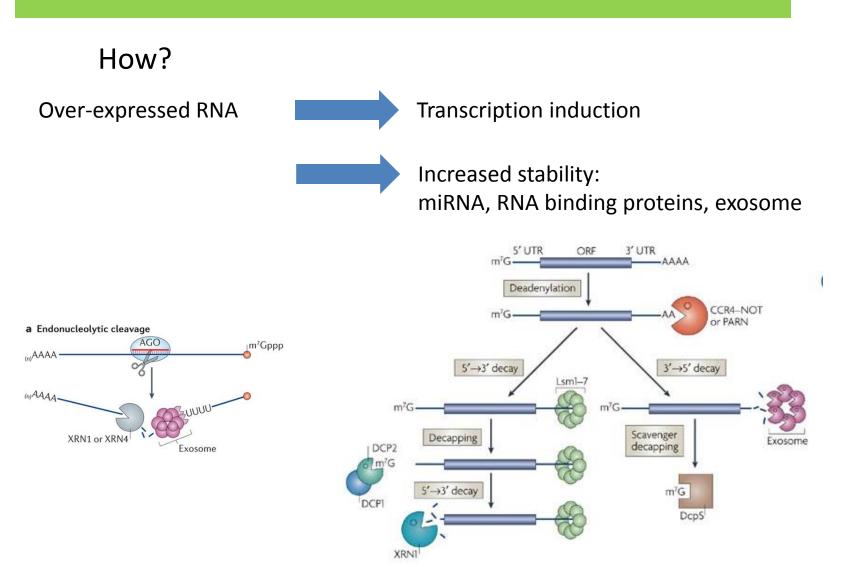
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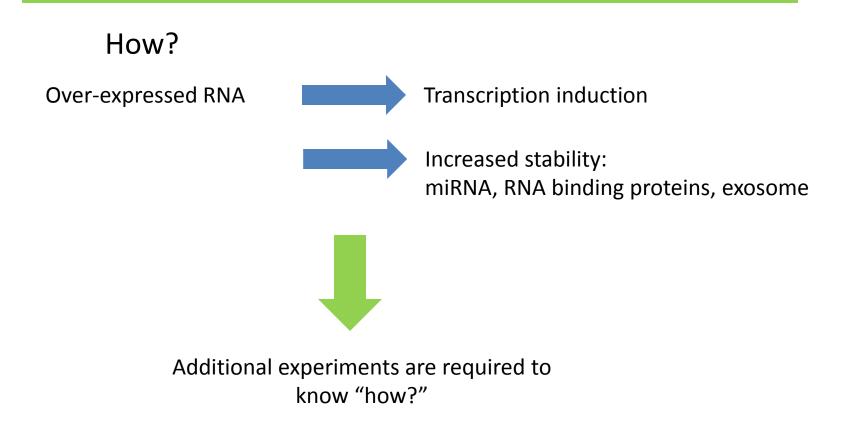
**Over-expressed RNA** 

Transcription induction









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What for?

RNA molecule which quantity significantly varies from condition to another

What for?

Differentially expressed RNA = Response to changes of the cellular context

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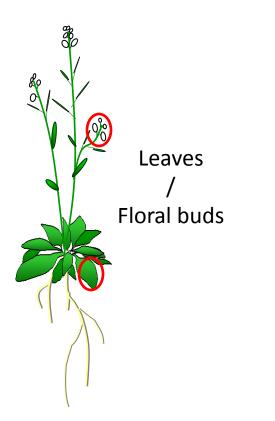
Differentially expressed RNA = Response to changes of the cellular context

Experimental design (study of the parameter of interest)

RNA molecule which quantity significantly varies from condition to another

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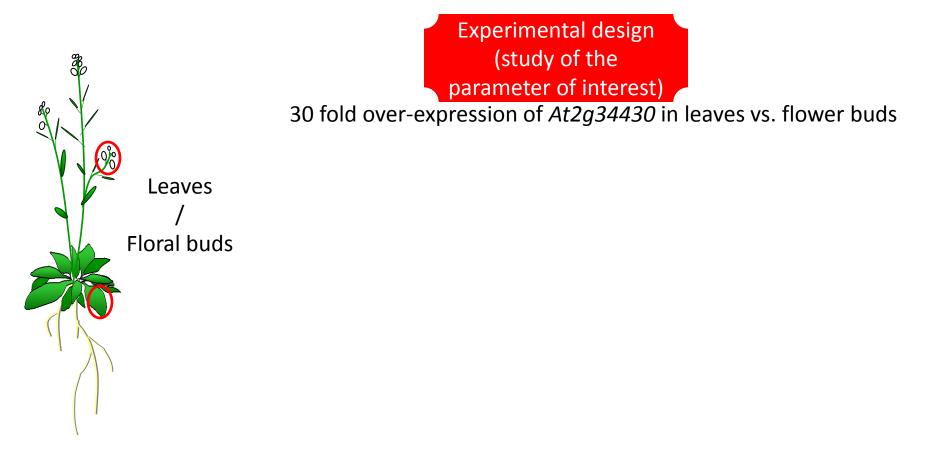
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Experimental design (study of the parameter of interest)

30 fold over-expression of At2g34430 in leaves vs. flower buds

Leaves

At2g34430 = LHCB1.4 :

"Light-harvesting chlorophyll-protein complex II subunit B1"

Floral buds

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30 fold over-expression of At2g34430 in leaves vs. flower buds

Leaves

Floral buds

At2g34430 = LHCB1.4 : "Light-harvesting chlorophyll-protein complex II subunit B1"

In leaves, there is more photosynthesis than in floral buds so More LHCB1.4 is required to capture light

RNA molecule which quantity significantly varies from condition to another

What for?

Differentially expressed RNA = Response to changes of the cellular context

Experimental design (study of the parameter of interest)

30 fold over-expression of At2g34430 in leaves vs. flower buds

Leaves /

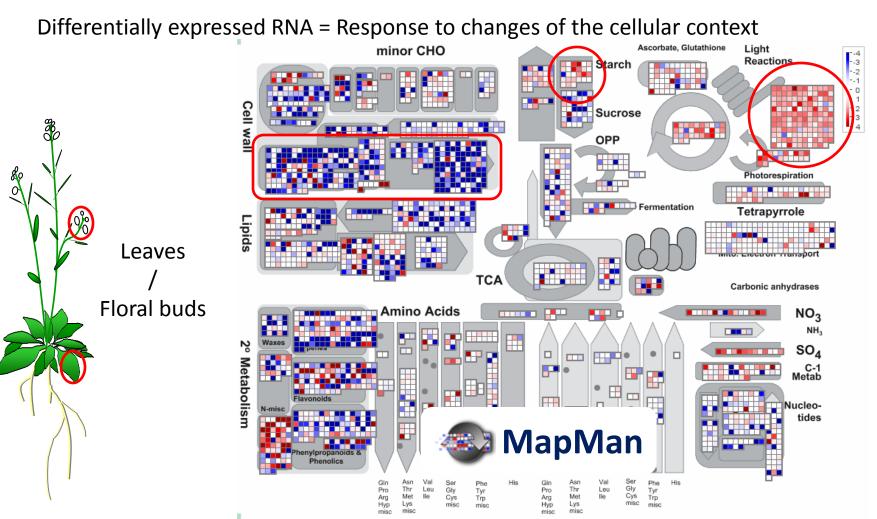
Floral buds

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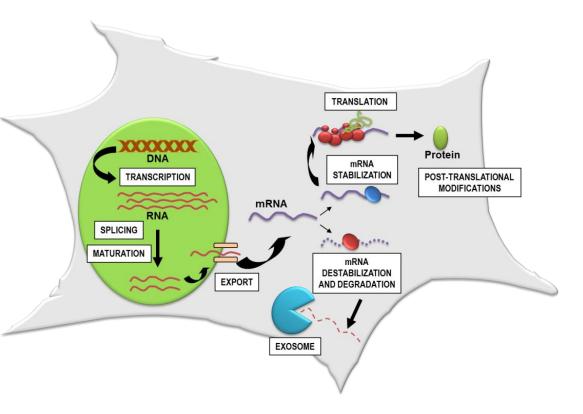
RNA molecule which quantity significantly varies from condition to another

### What for?



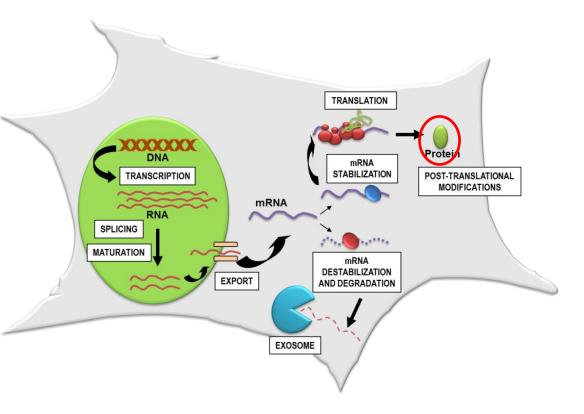
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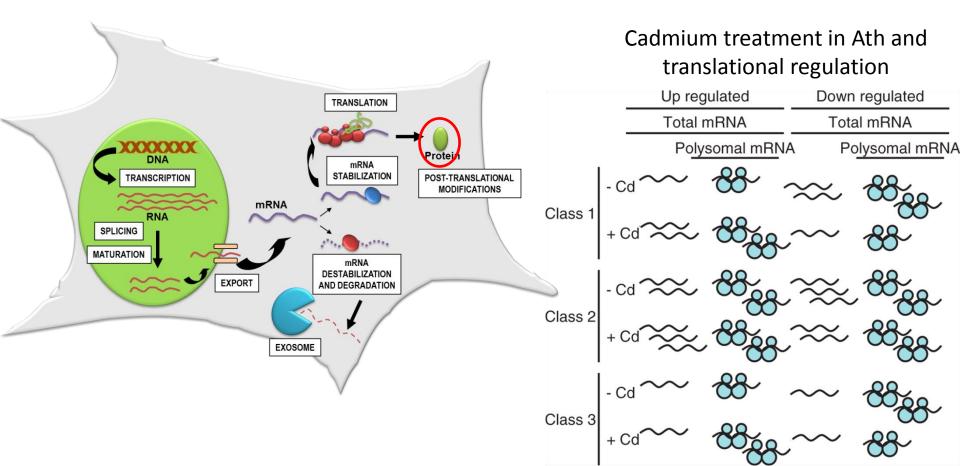
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What for?



RNA molecule which quantity significantly varies from condition to another

Biomarker?

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Biomarker?

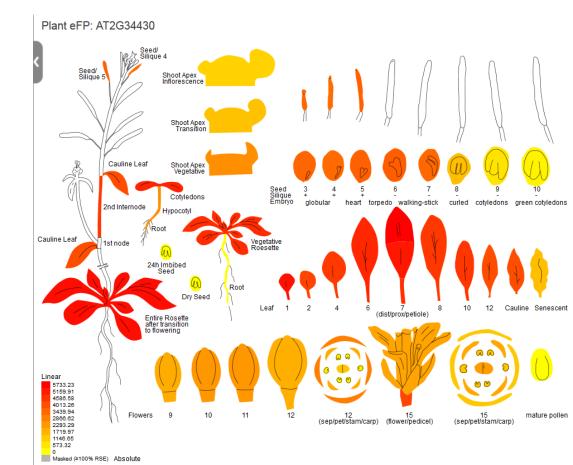
Differentially expressed RNA = Specific (?) response to this change of the cellular context

RNA molecule which quantity significantly varies from condition to another

**Biomarker?** 

Differentially expressed RNA = Specific (?) response to this change of the cellular context

**Expression profile** 



RNA molecule which quantity significantly varies from condition to another

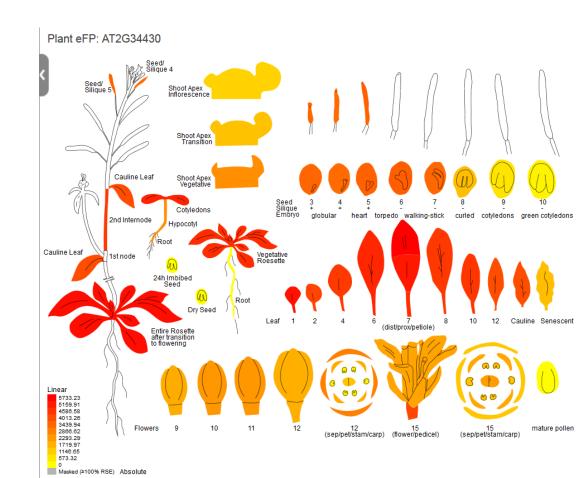
**Biomarker?** 

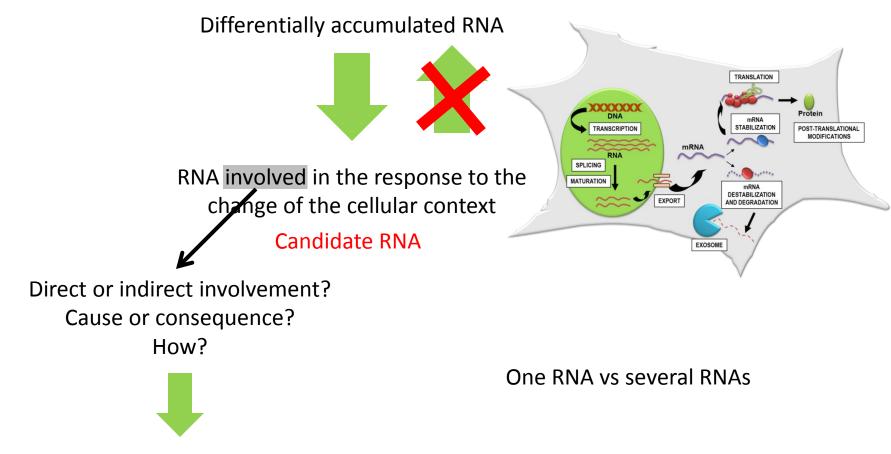
Differentially expressed RNA = Specific (?) response to this change of the cellular context

**Expression profile** 

A single RNA is never specific

Combination of transcripts (multivariate analysis)

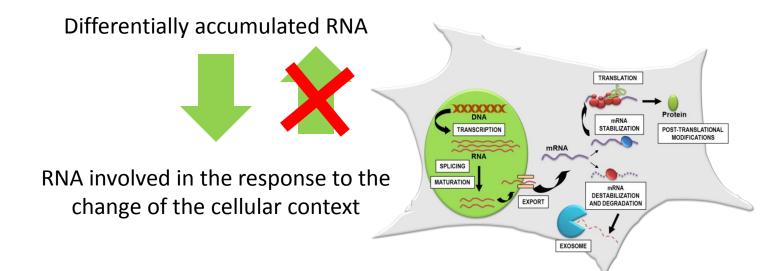


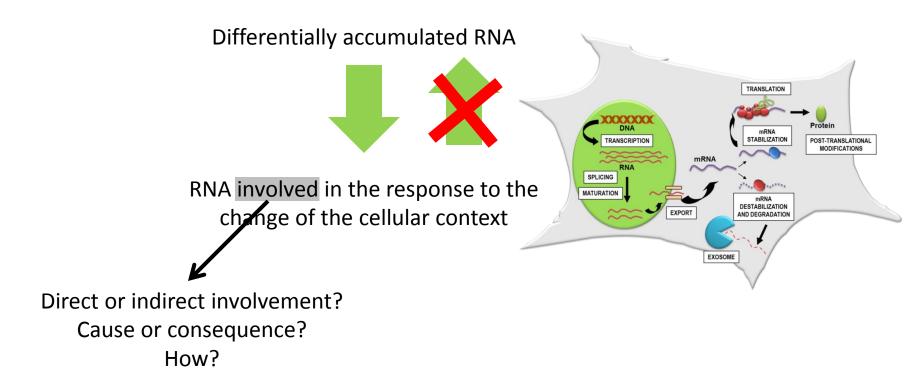


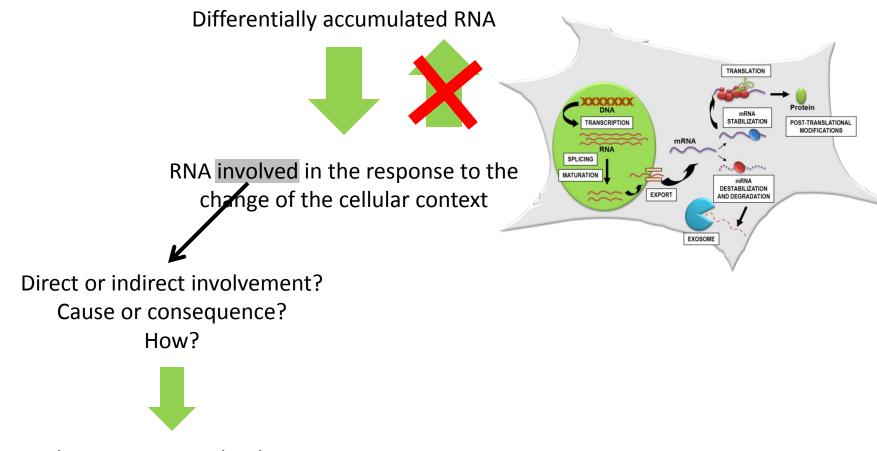
Differentially accumulated RNA

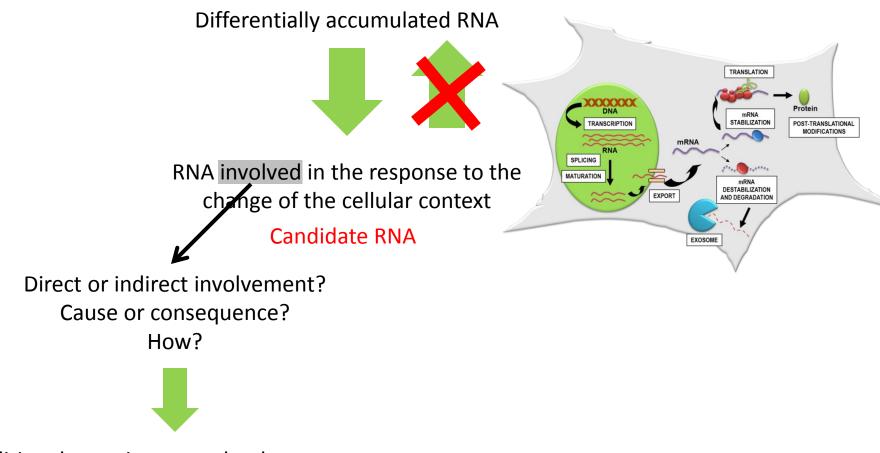
Differentially accumulated RNA

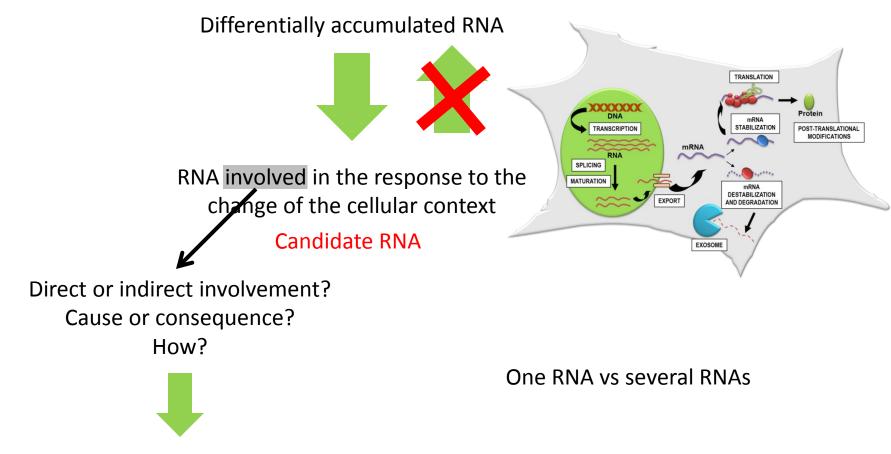
RNA involved in the response to the change of the cellular context

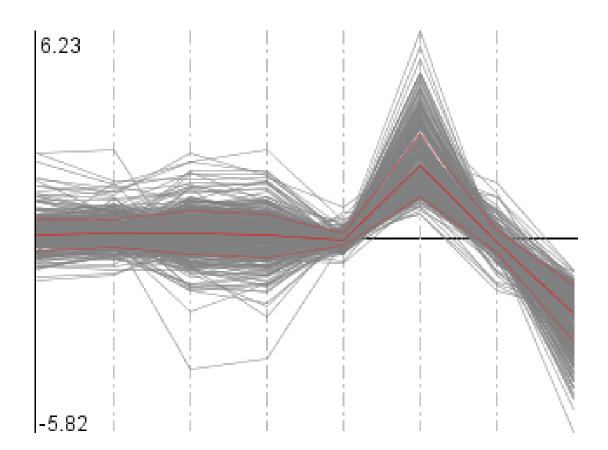


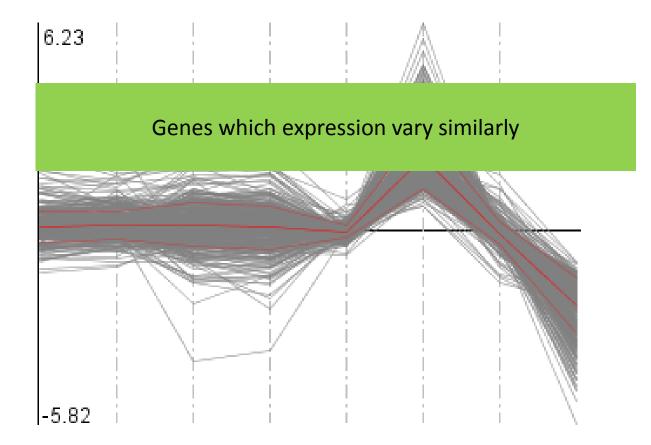


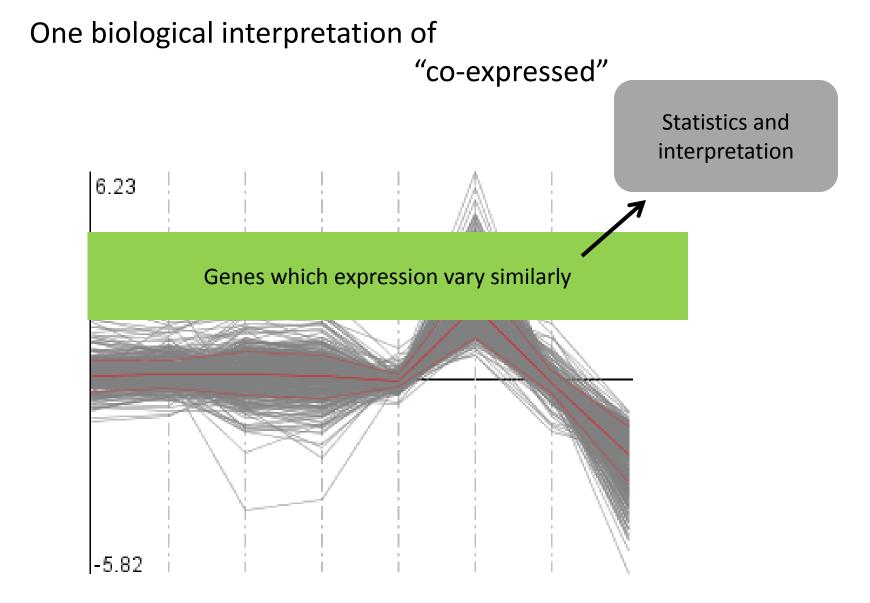


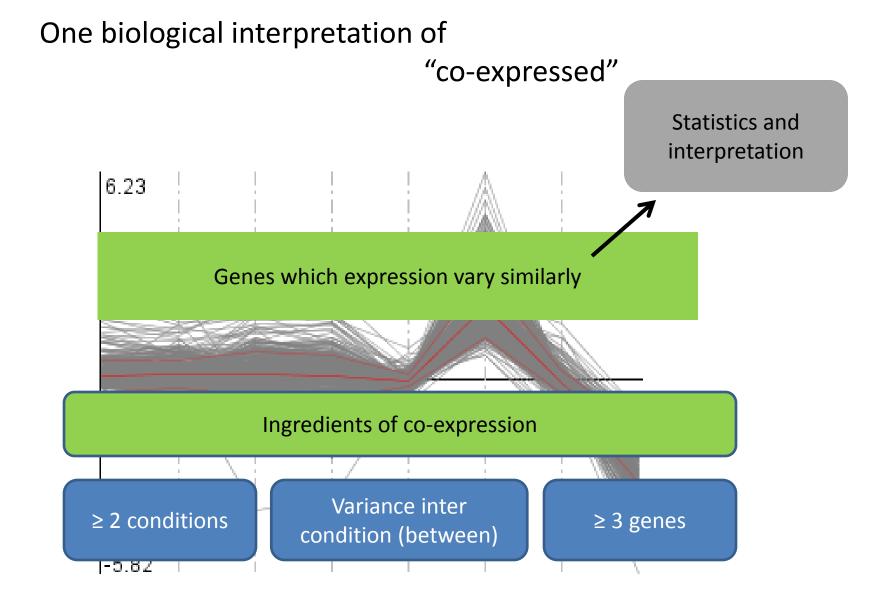


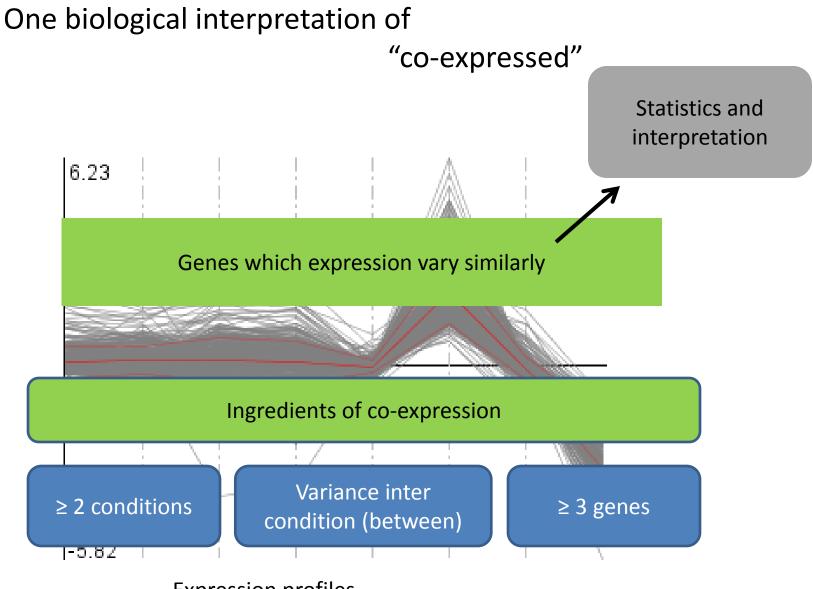




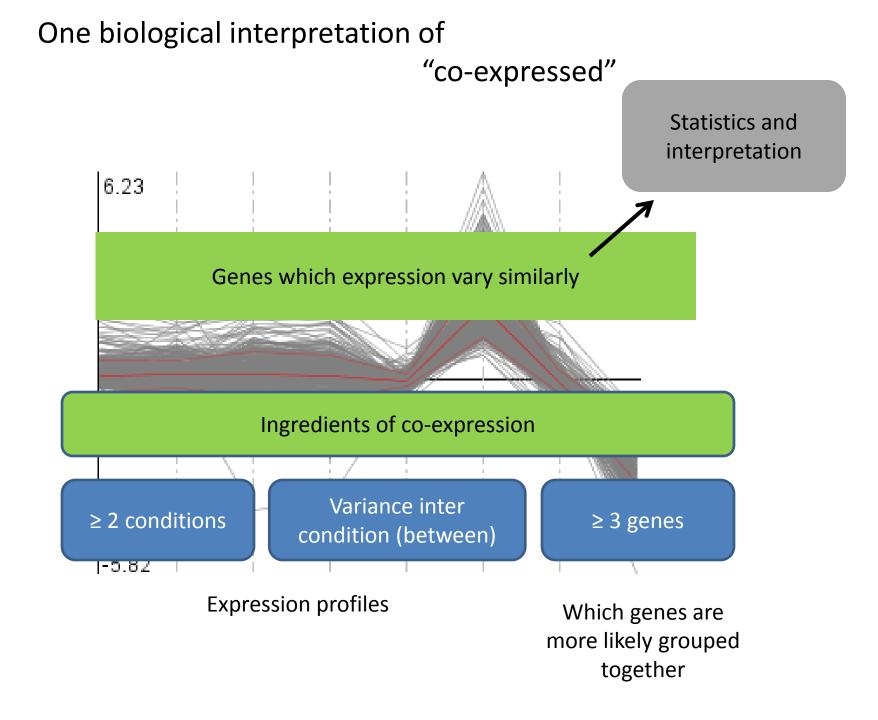








Expression profiles



### "co-expressed"

Genes which expression vary similarly

What for?

Co-expressed genes= genes involved in the same responses to the same changes of the cellular context?

= genes involved in the same biological processes?

### "co-expressed"

Genes which expression vary similarly

What for?

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Genes which expression vary similarly

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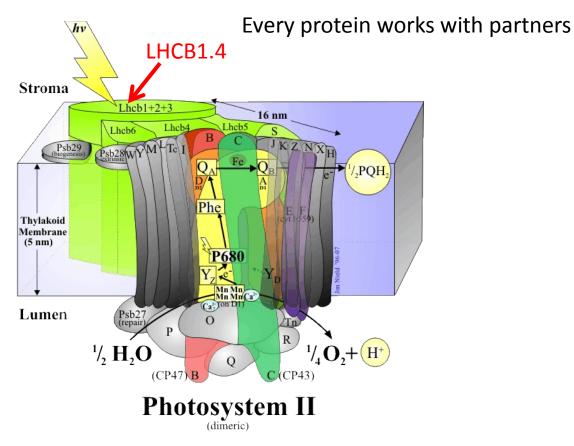
>Co-expressed genes  $\rightarrow$  functional partners?

Every protein works with partners

#### "co-expressed"

Genes which expression vary similarly

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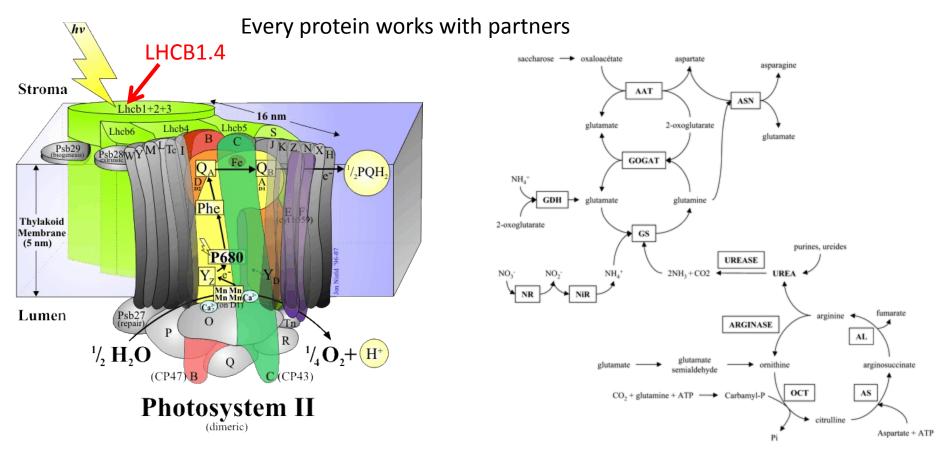


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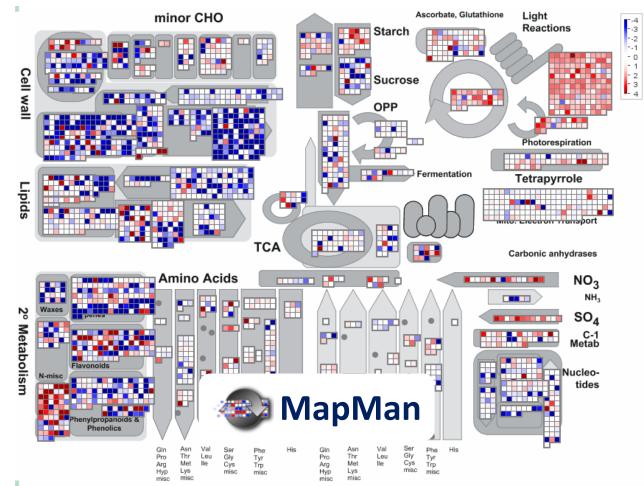


Nitrate assimilation pathway

### "co-expressed"

Genes which expression vary similarly

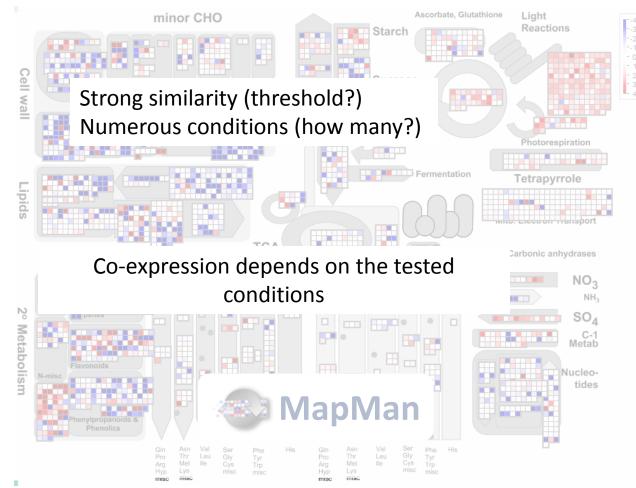
### What for?



### "co-expressed"

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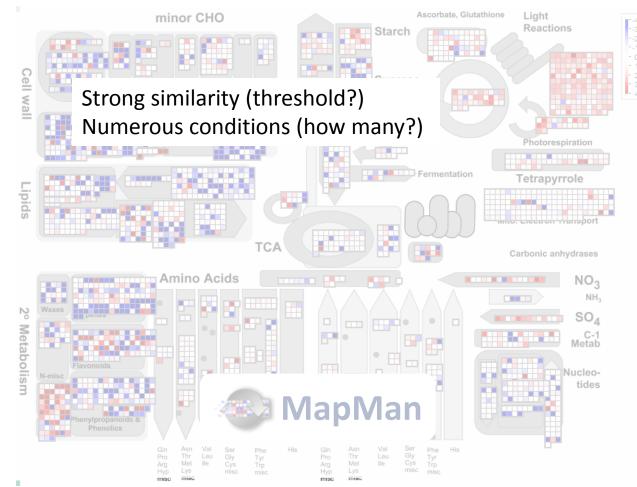
# What for?



### "co-expressed"

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# What for?



### "co-expressed"

Genes which expression vary similarly

How?

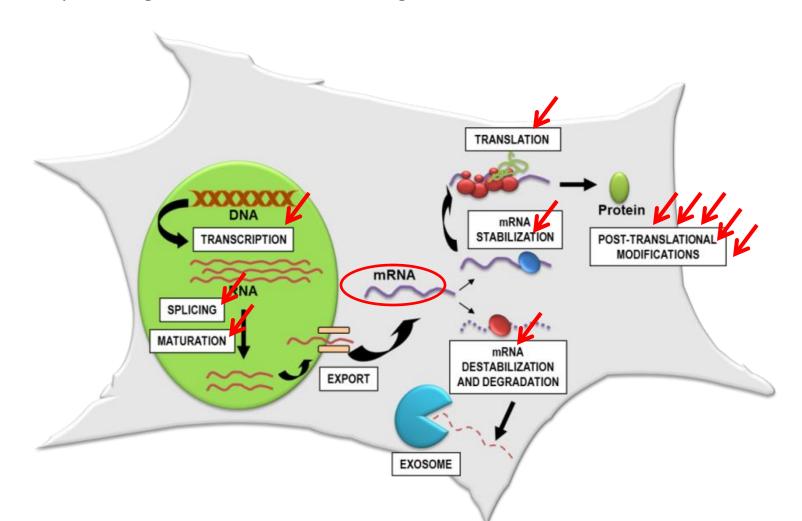
Co-expressed genes= under the same regulations ?

### "co-expressed"

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Co-expressed genes=-under the same regulations?

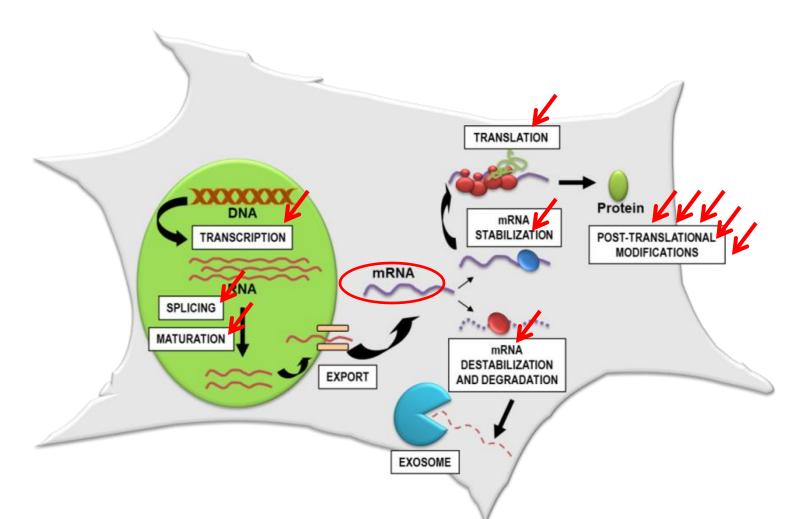


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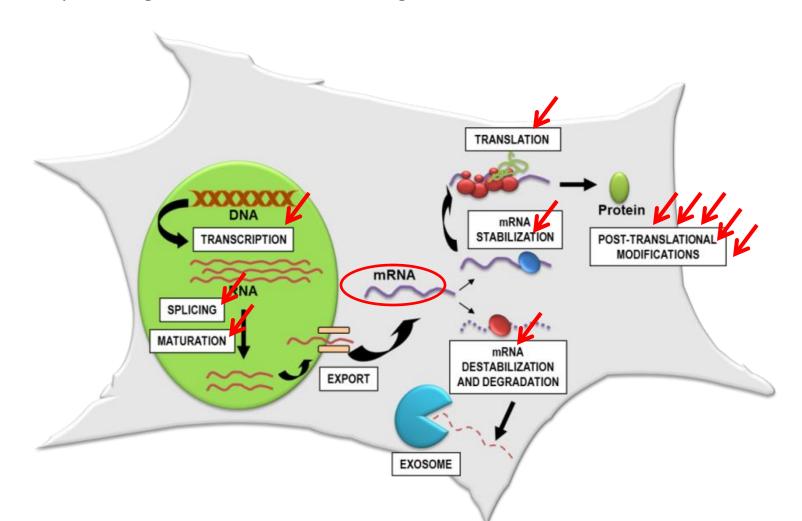


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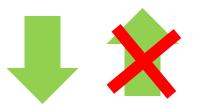
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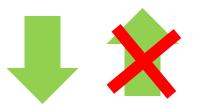


Co-expressed genes



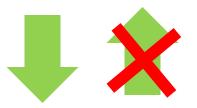
Genes potentially involved in the same biological processes given the studied context

Co-expressed genes



Genes potentially involved in the same biological processes given the studied context

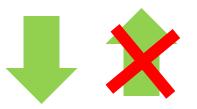
Co-expressed genes



Genes potentially involved in the same biological processes given the studied context

Putative functional annotation

Co-expressed genes



Genes potentially involved in the same biological processes given the studied context

Putative functional annotation