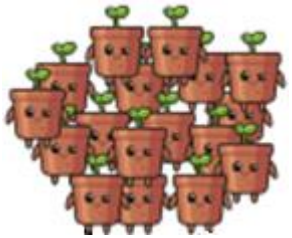

nature plants

Comment | Published: 04 May 2026

On the importance of being powerful to detecting specific regulations in omics studies

Jeremy Ferraro, Virginie Noël, Axel de Zelicourt, Michael Hodges, Elodie Gilbault, Olivier Loudet, José Caïus, Alexandra Launay-Avon, Stéphanie Pateyron, Christine Paysant Le Roux, Marlène Davanture, Marie-Laure Martin ✉, Benoît Castandet ✉, Etienne Delannoy ✉ & Guillem Rigaill ✉

Nature Plants **12**, 900–903 (2026) | Cite this article

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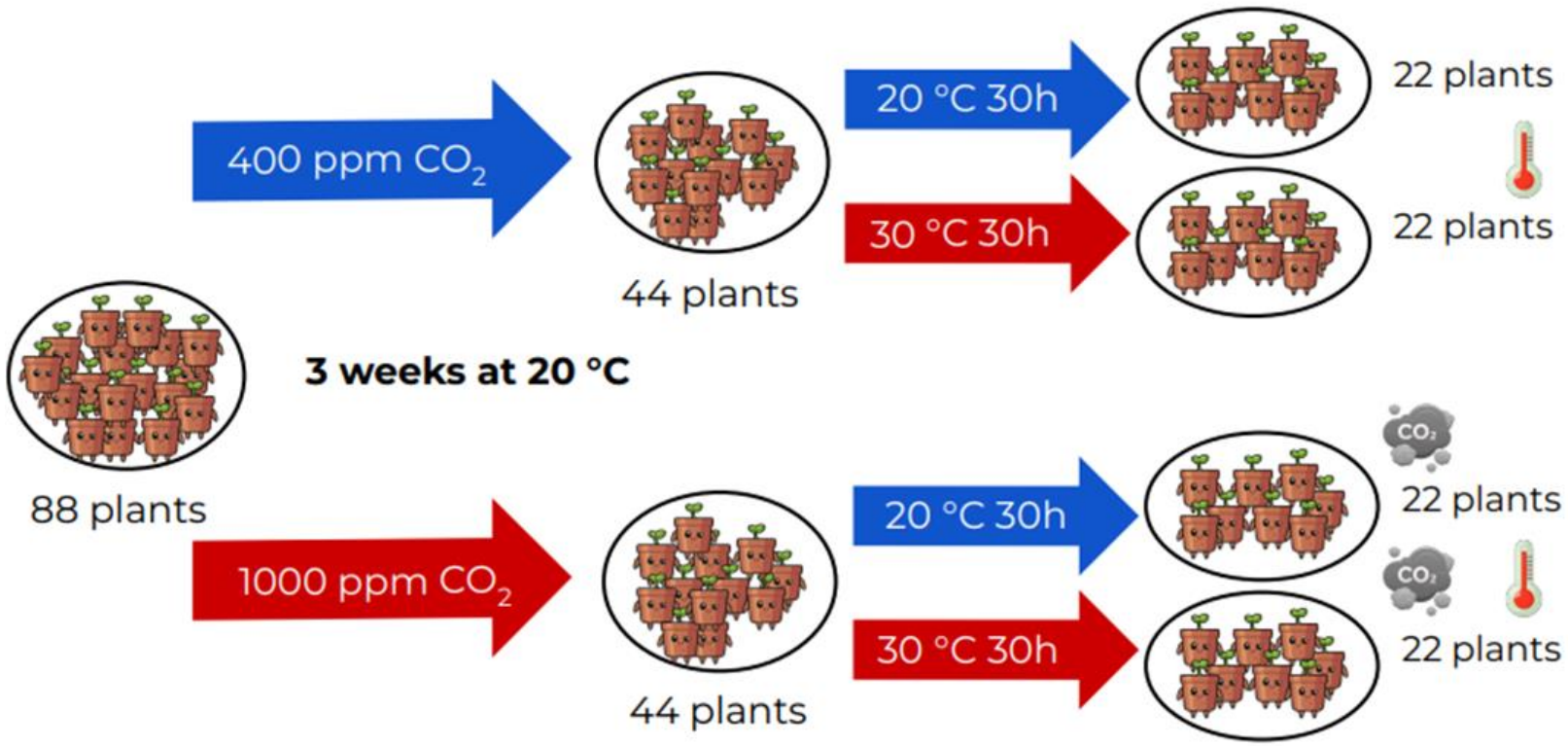
Institute of Plant Sciences
Paris - Saclay

The PEERSIM dataset



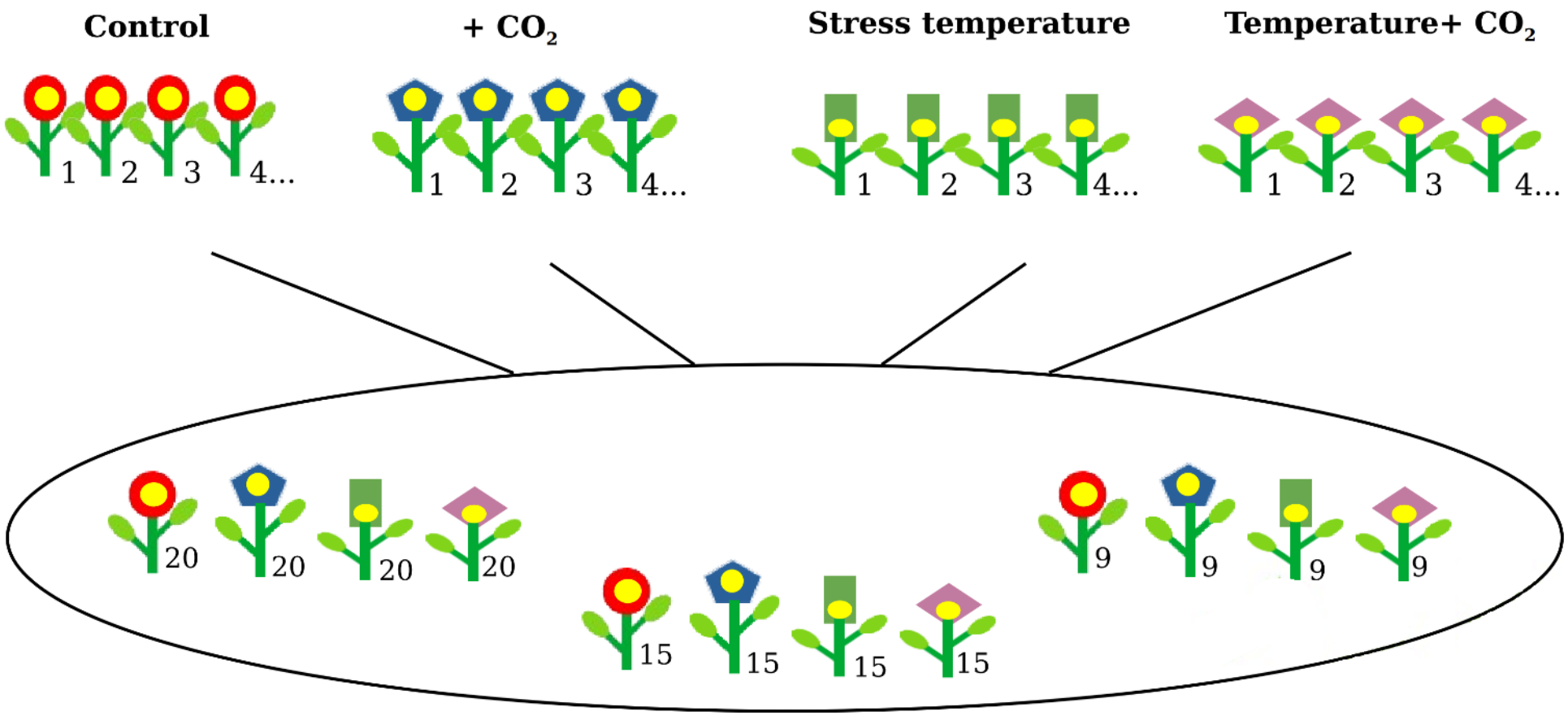
Photosynthetic activity (PAM-fluo)
Transcriptomics
- total RNA-seq
- small RNA-seq

Proteomics
Metabolomics
- GC-MS
- LC-MS

22 independent experiments
to infer regulatory links

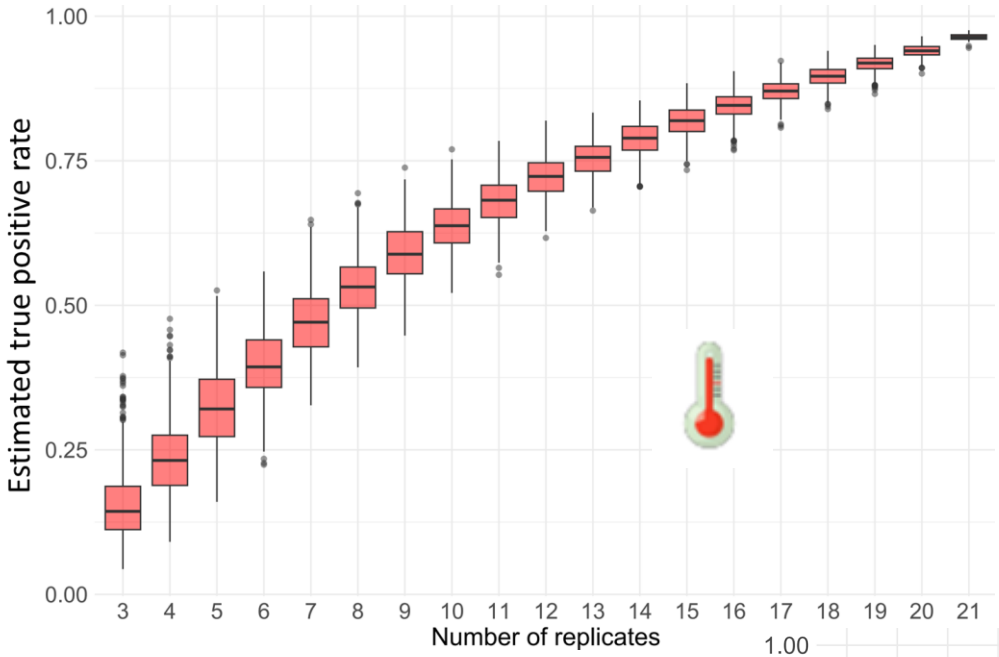
Number of biological replicates: not only a problem of power

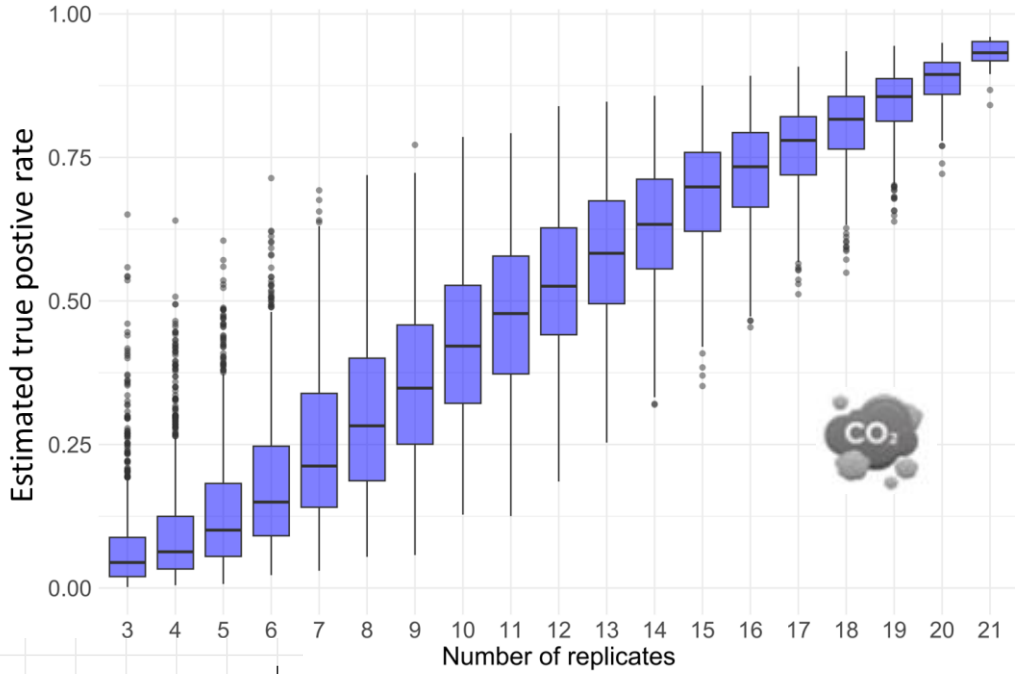
Generating multiple « 3-rep » experiments

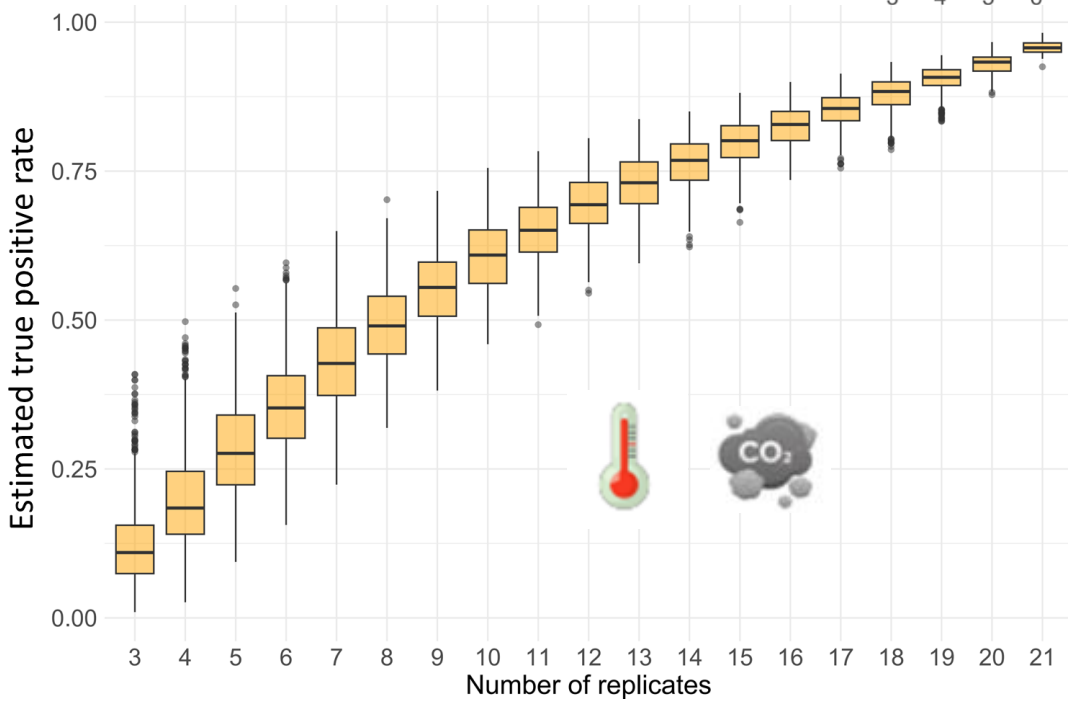


Ferraro *et al.* 2026
Nature plants

Number of biological replicates: not only a problem of power







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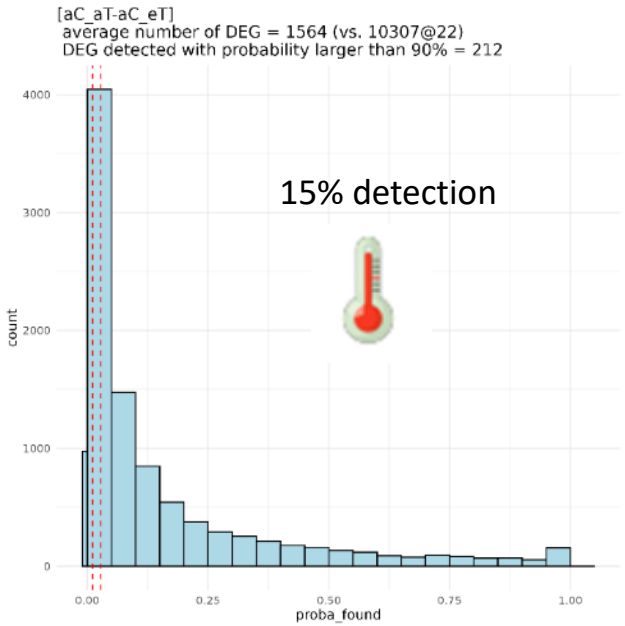
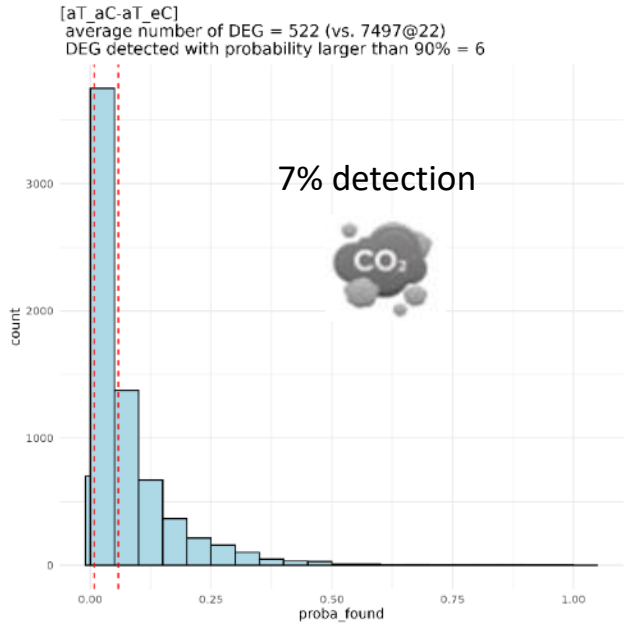
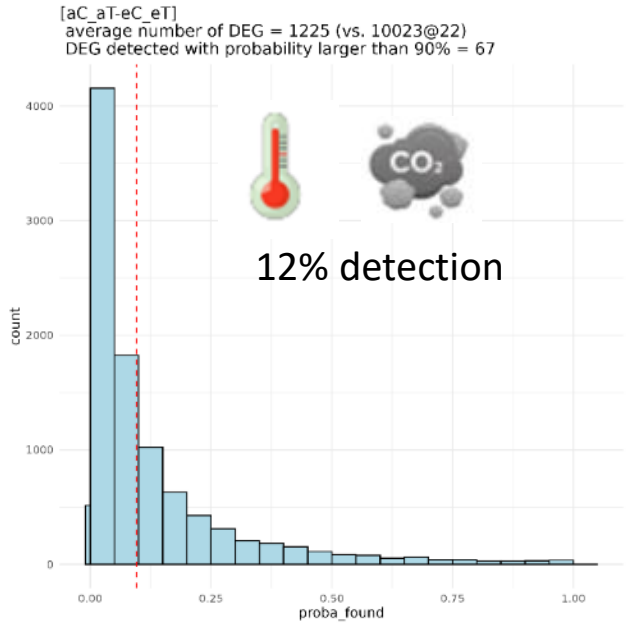


3 reps vs 22 reps



Low power



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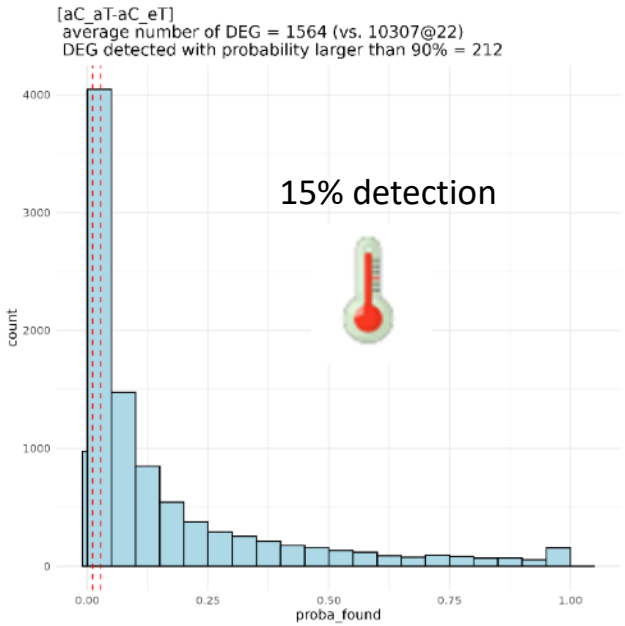
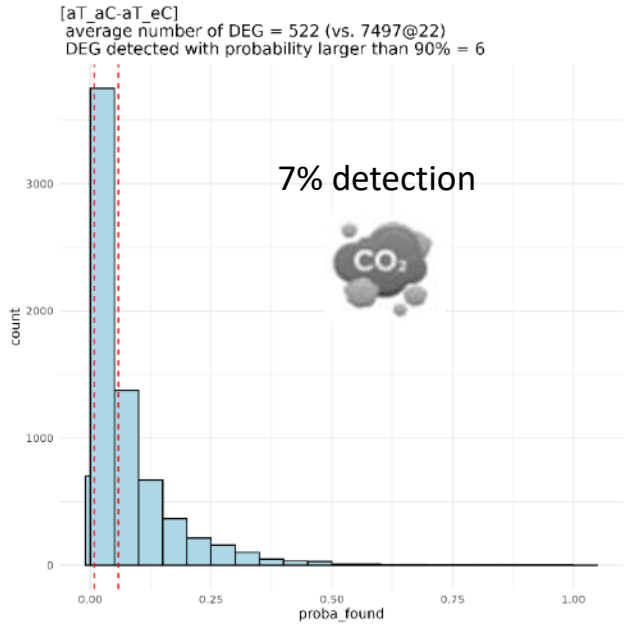


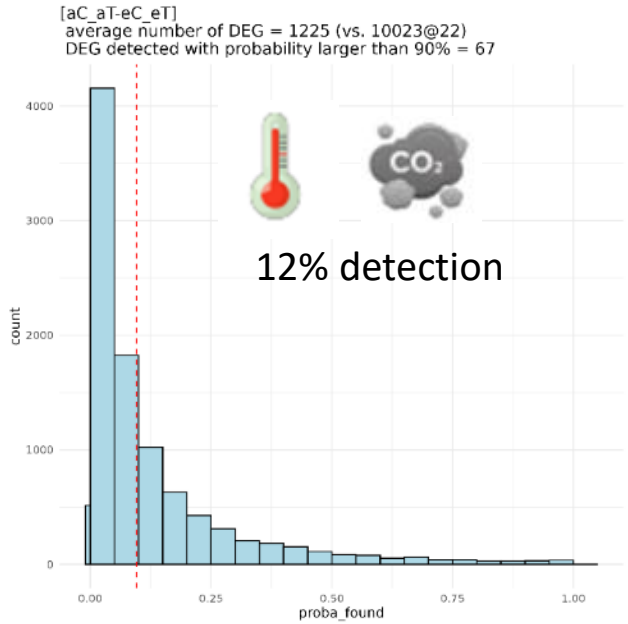
15% detection

3 reps vs 22 reps



7% detection

Low power

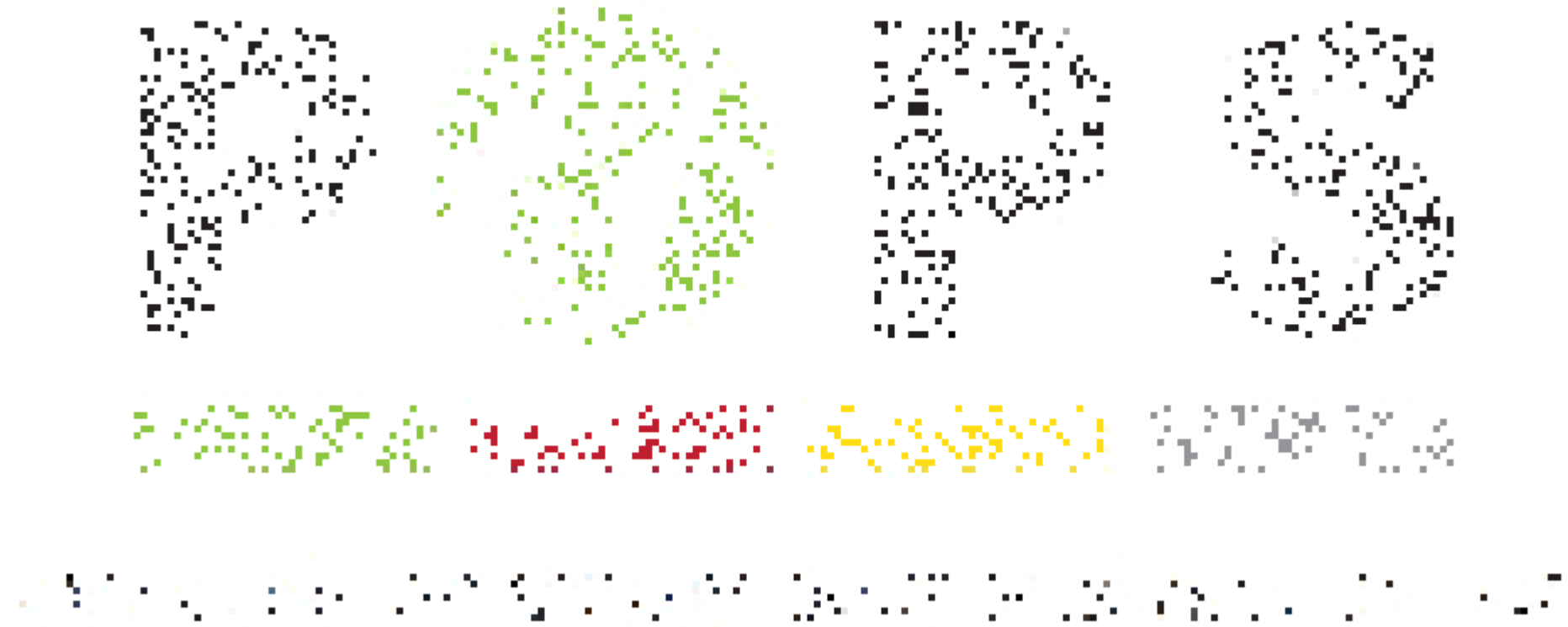


12% detection

No « core » response

Number of biological replicates: not only a problem of power

Some examples of 3-rep omics « analysis » of a picture (15% of TPR)



ASSISTED BY AI

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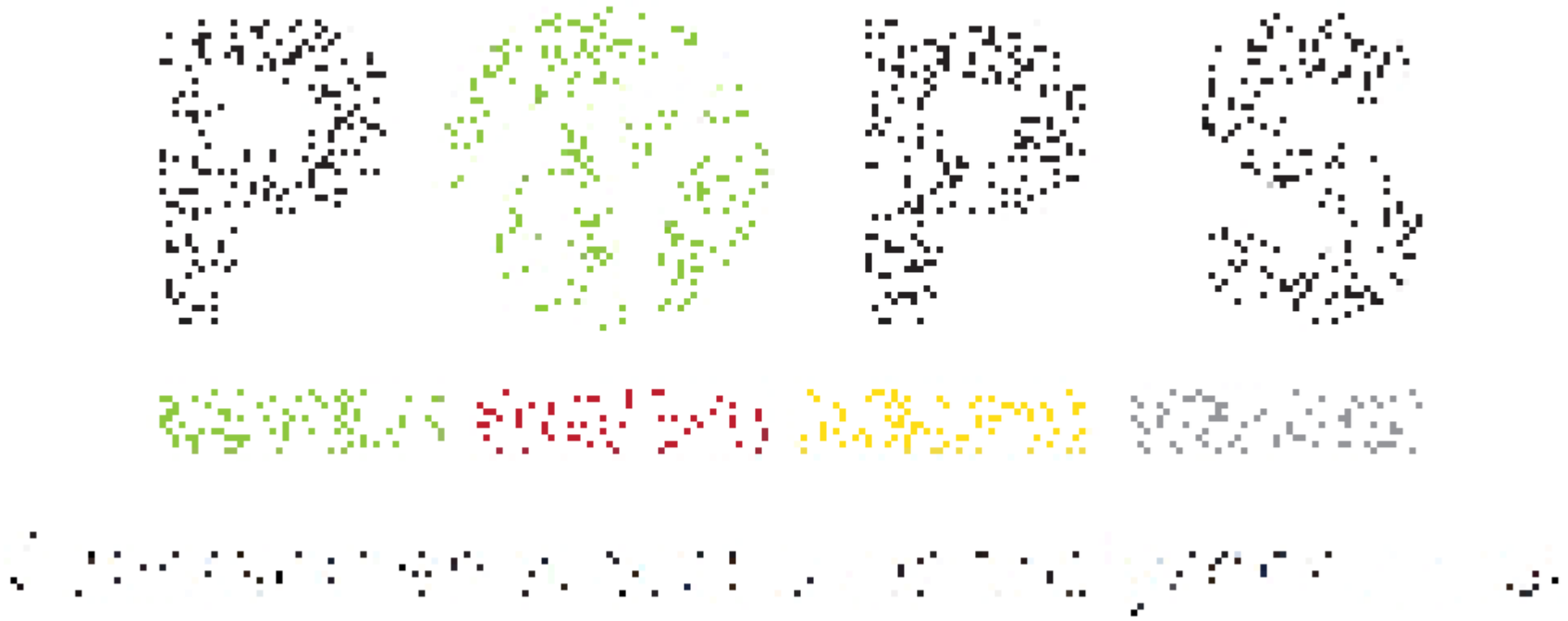

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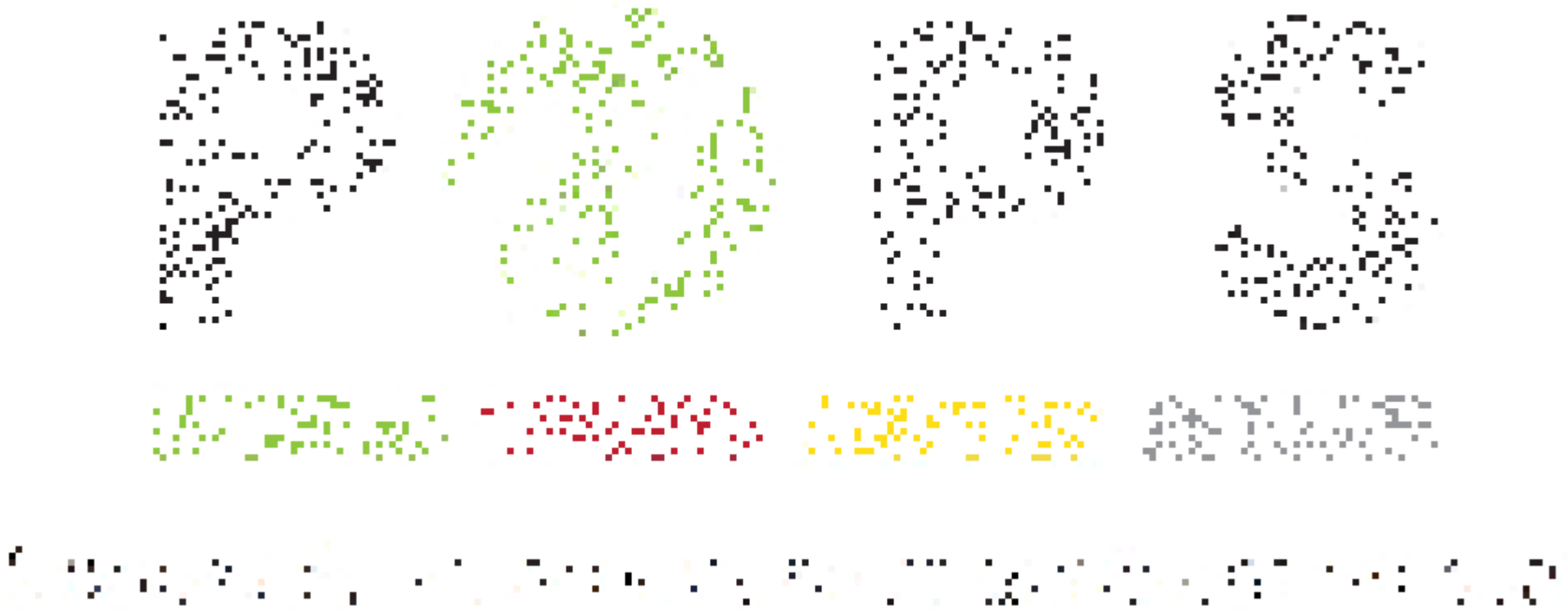

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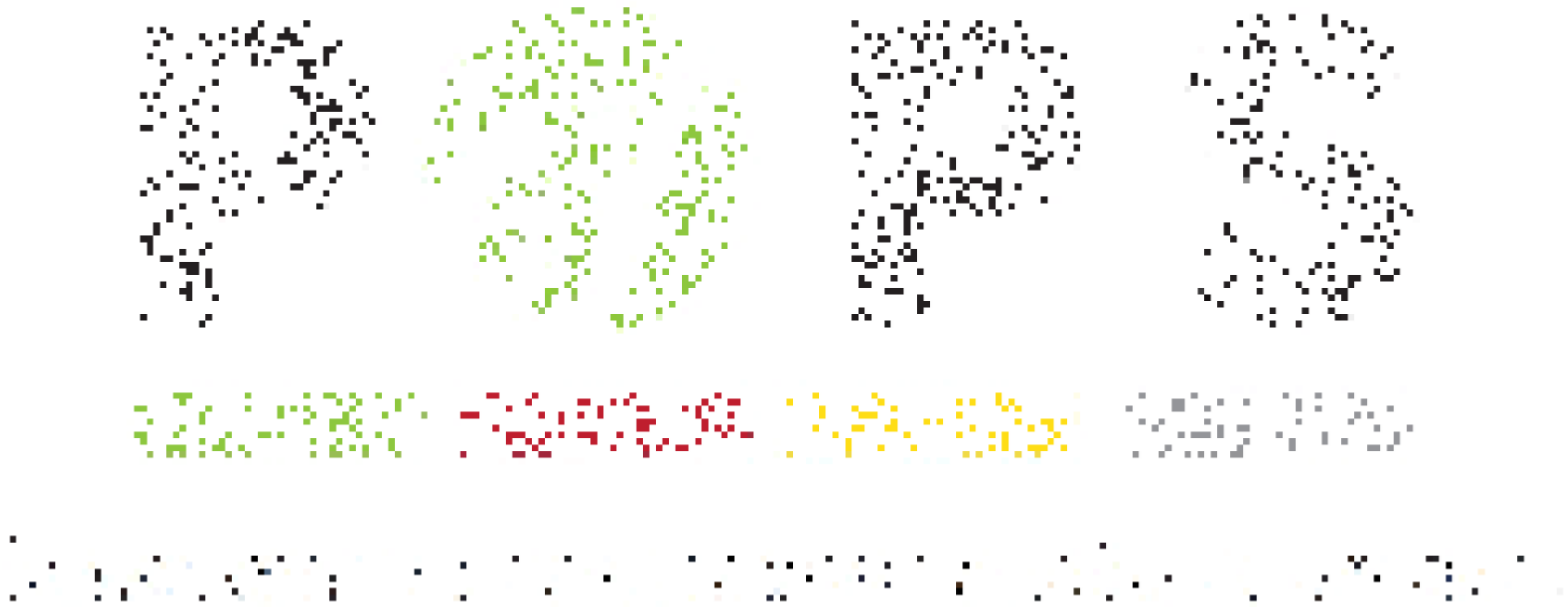

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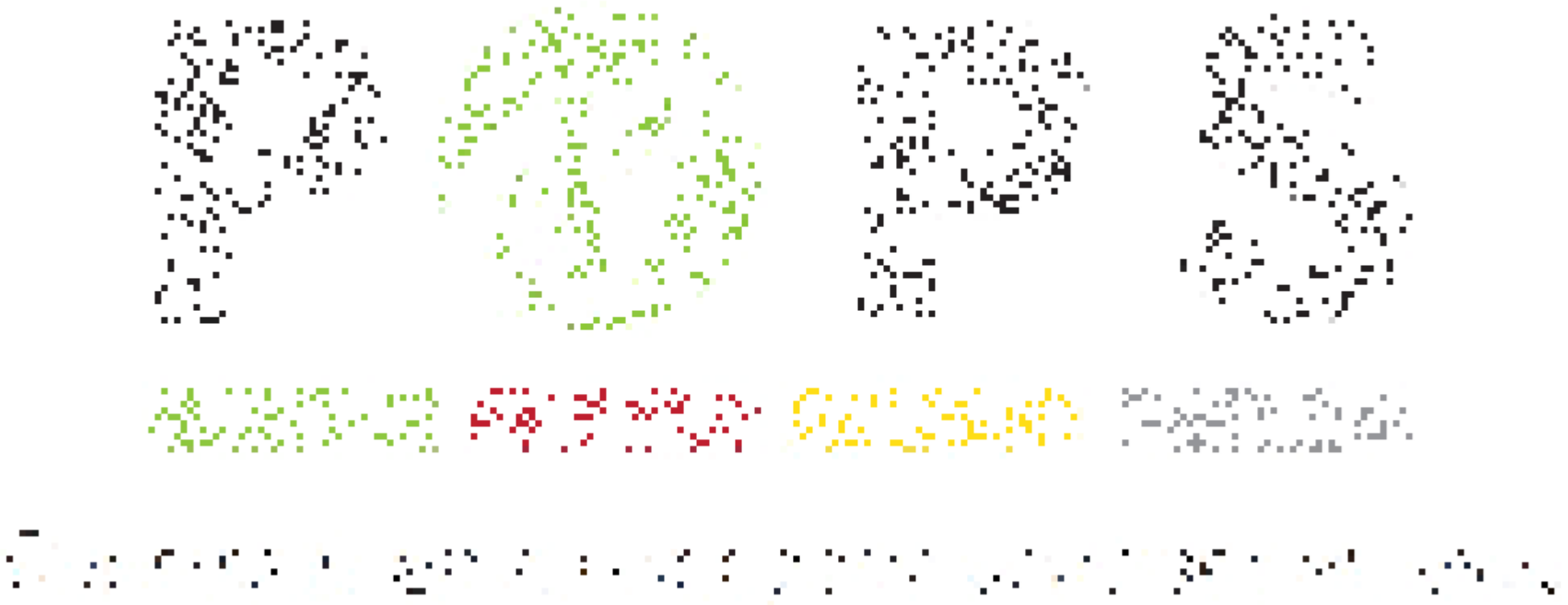

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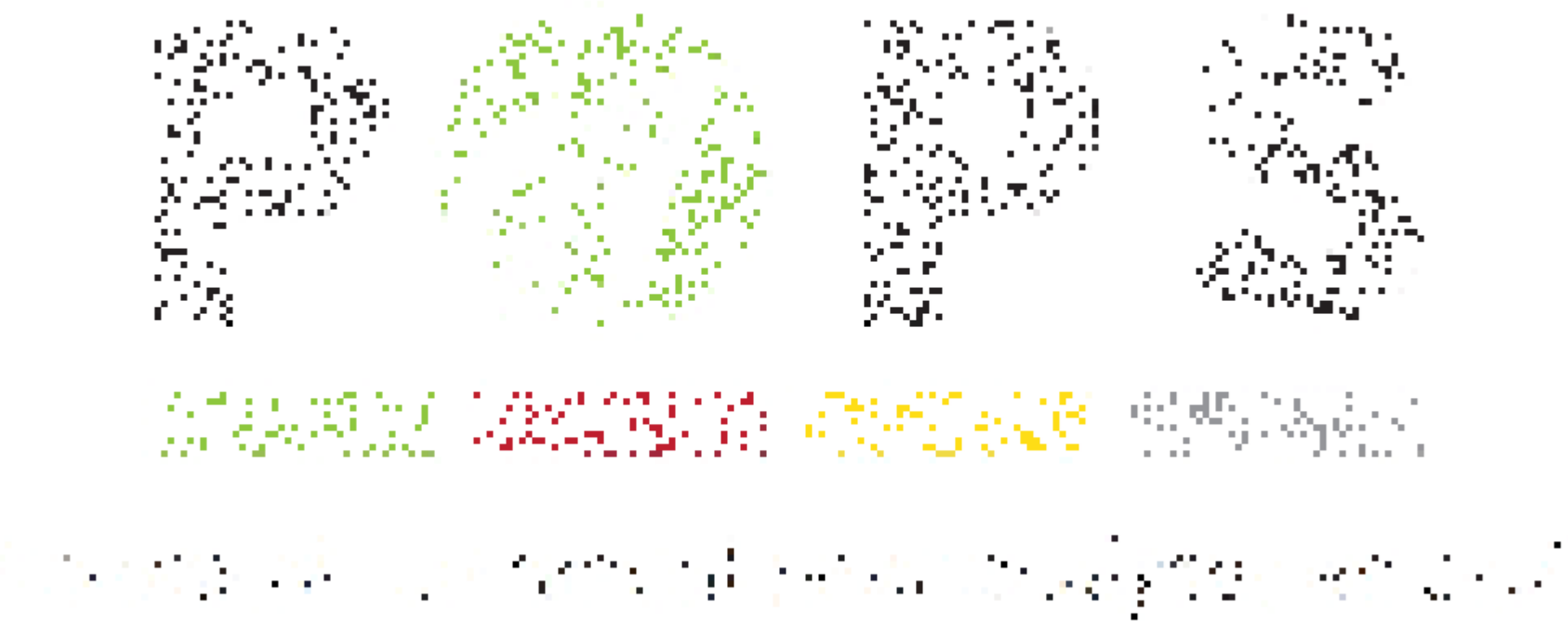

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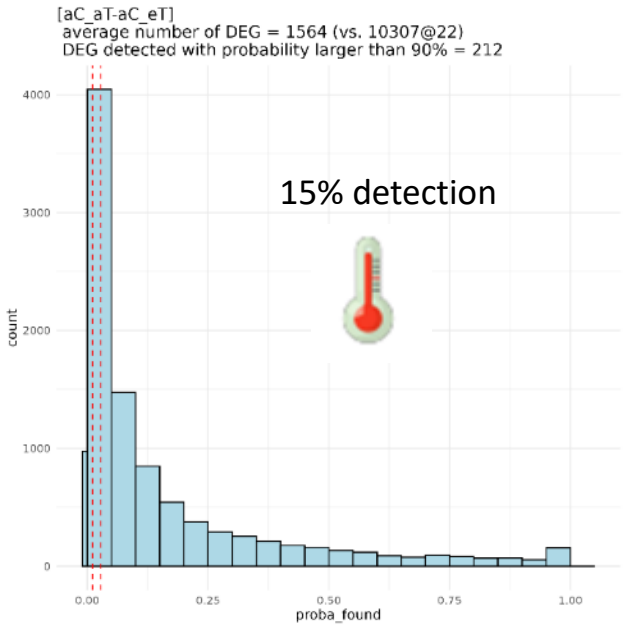
Number of biological replicates: not only a problem of power

The picture…

Concevoir en amont pour analyser en aval

Number of biological replicates: not only a problem of power



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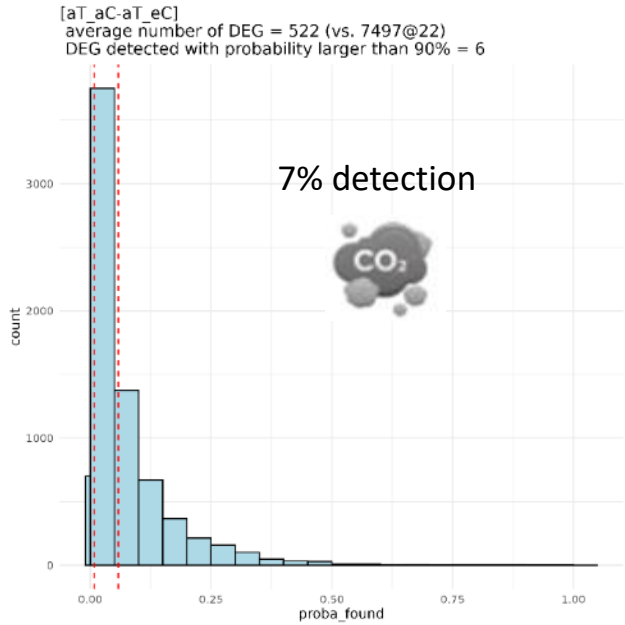
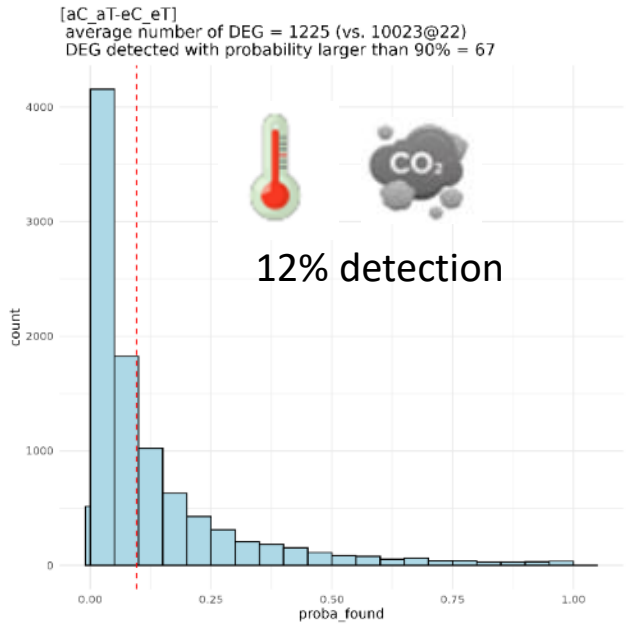


Low power

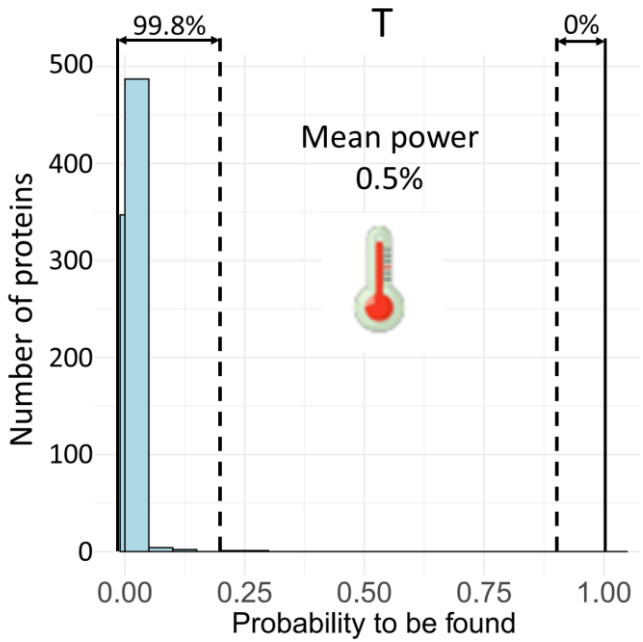


No « core » response

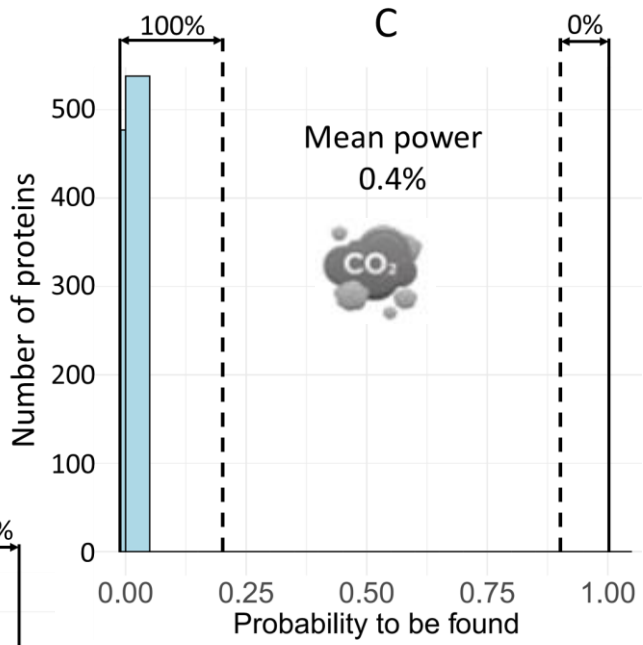
Same results with functional enrichments
Same results with two other datasets

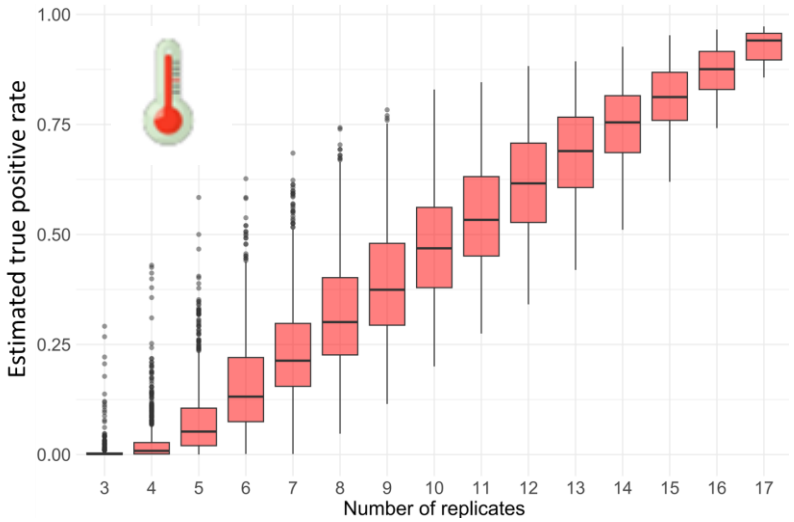
Number of biological replicates: not only a problem of power

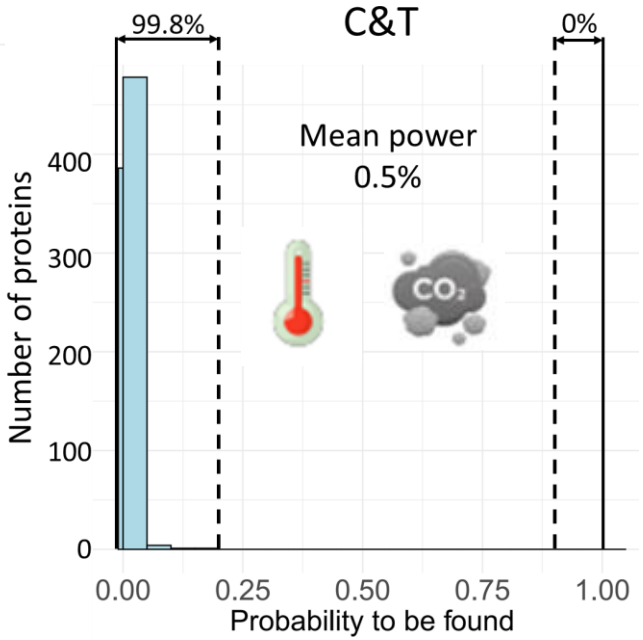
Worse for proteomics…



3 reps vs 18 reps

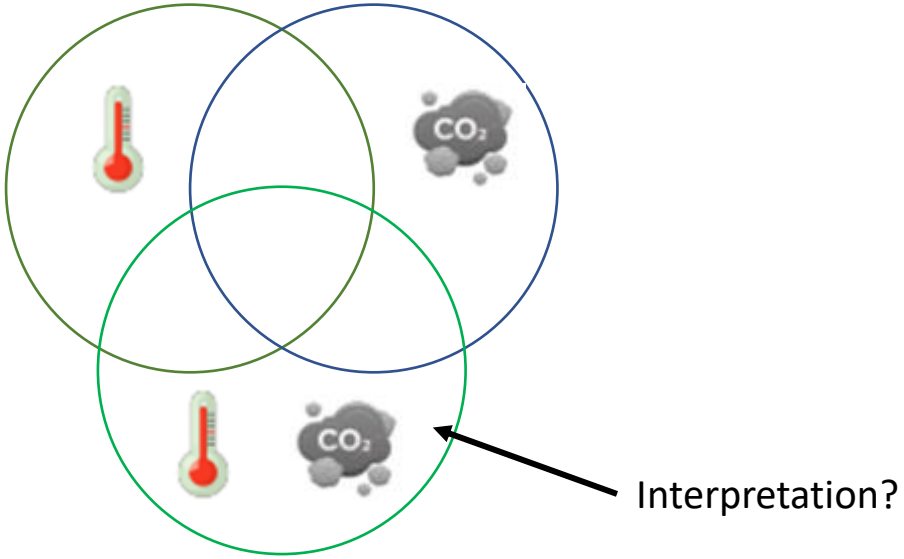






Number of biological replicates: not only a problem of power

Venn diagram of DEG



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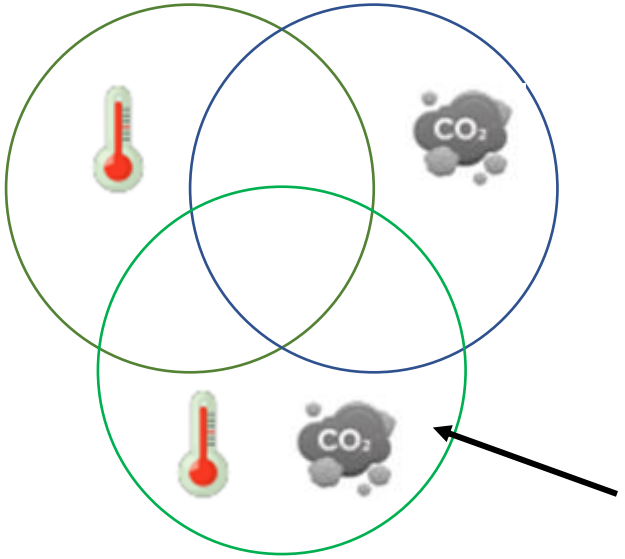
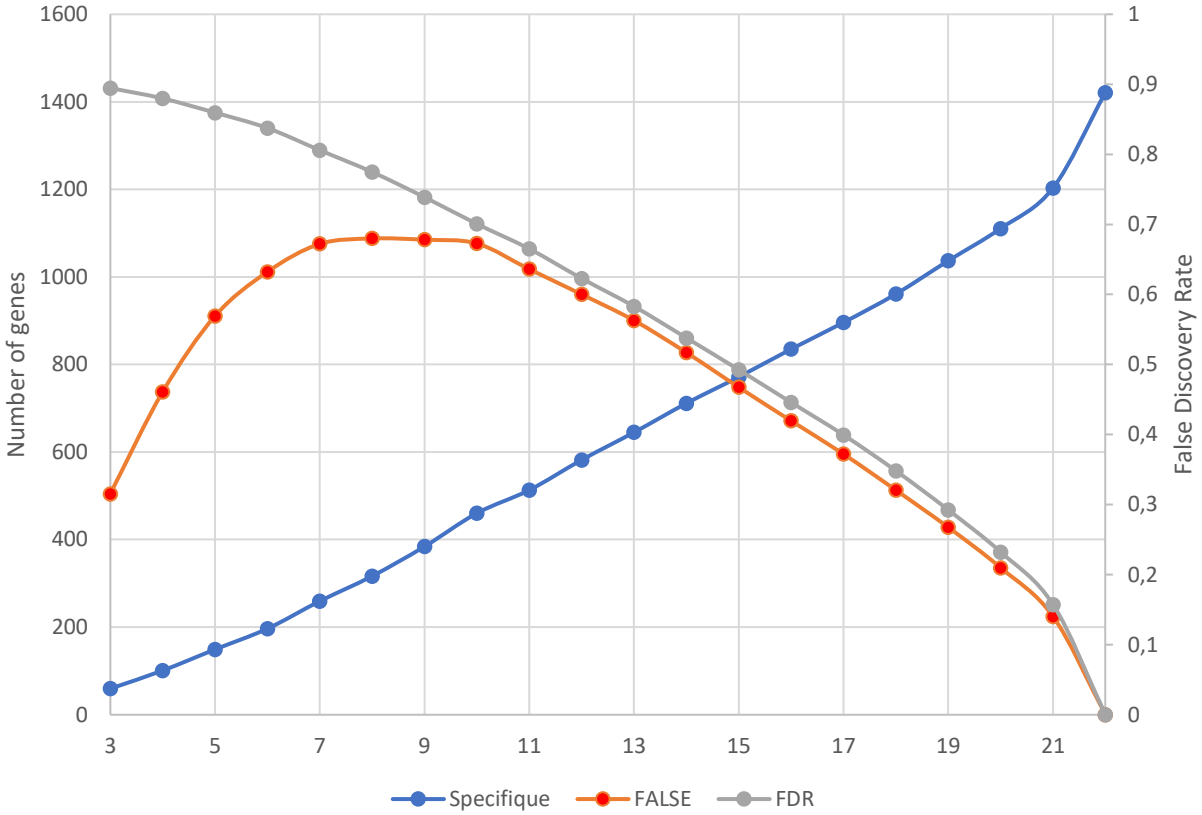
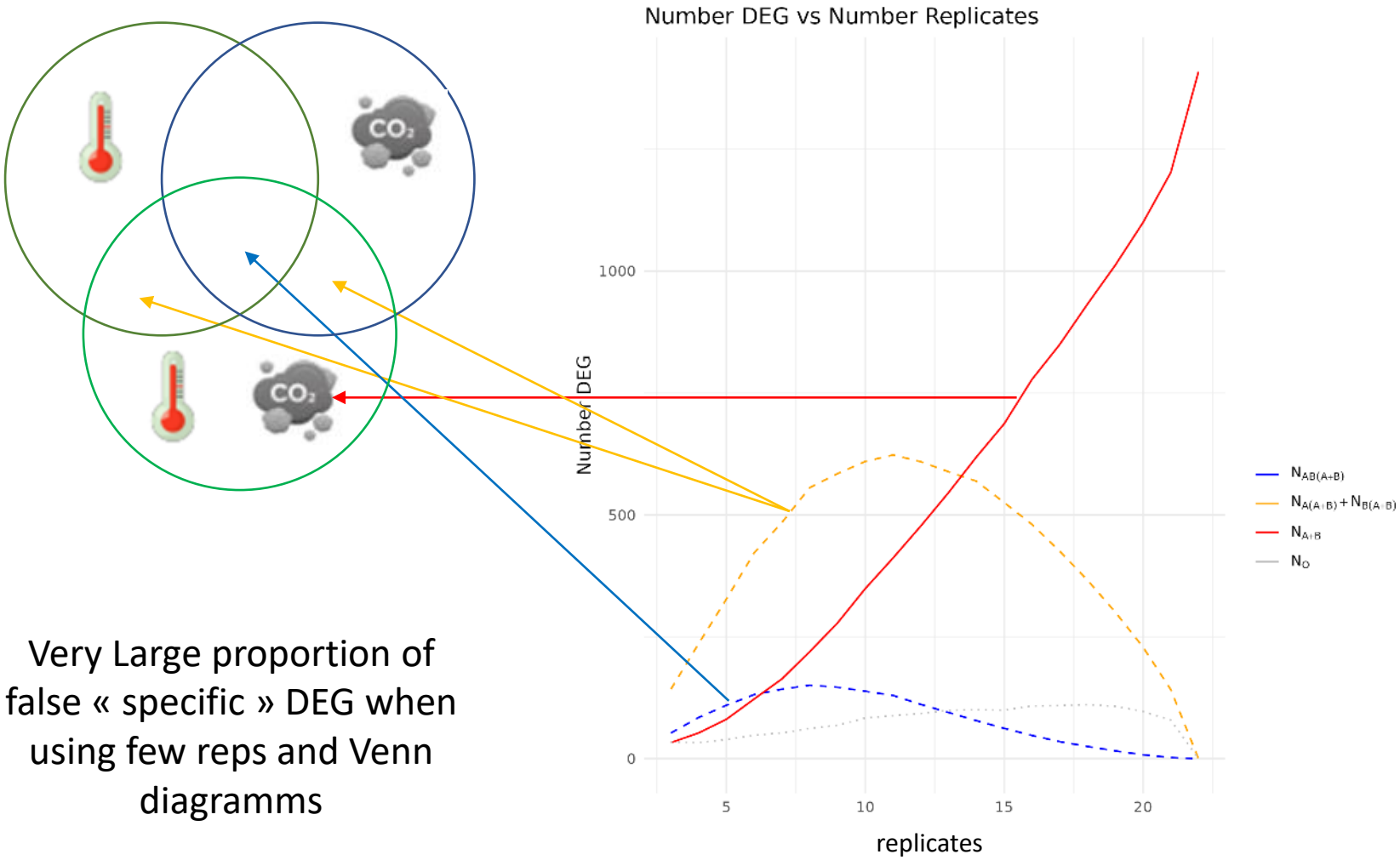


Very Large proportion of false « specific » DEG when using few reps and Venn diagramms



Number of biological replicates: not only a problem of power

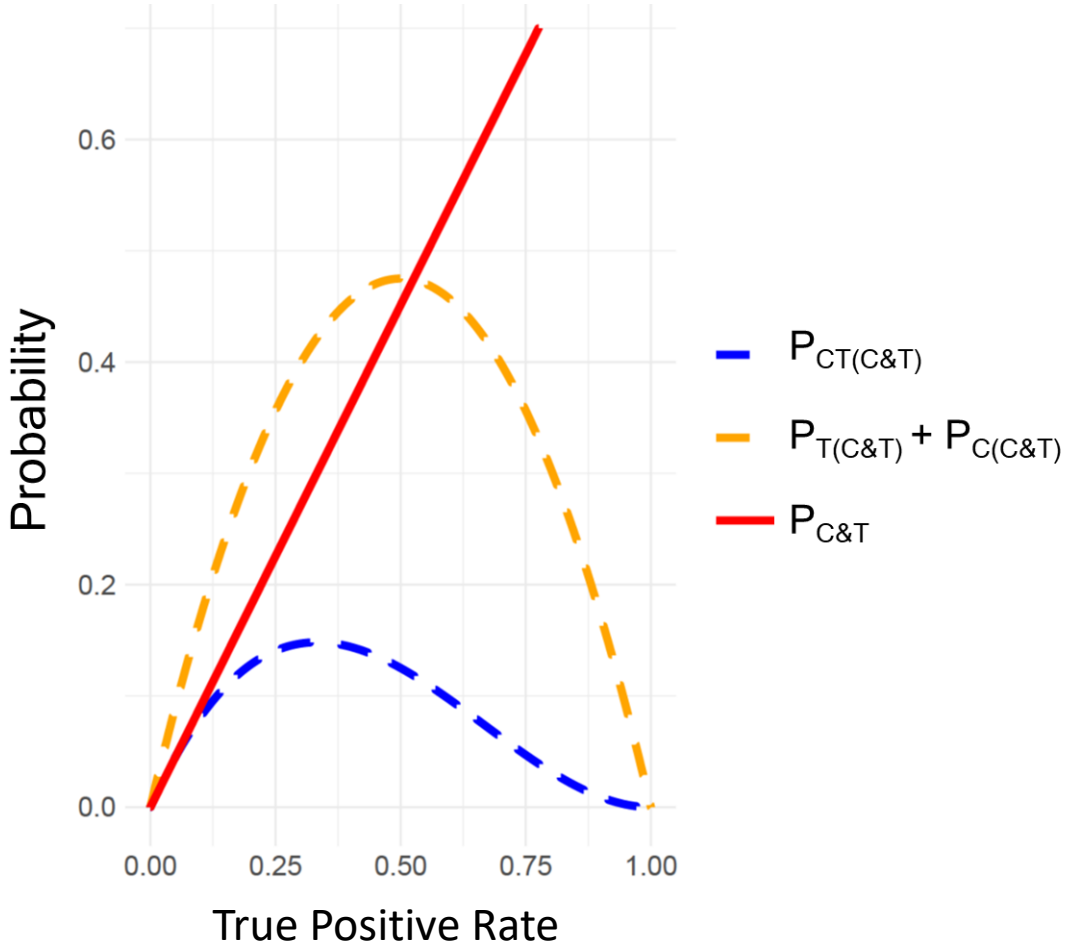
Venn diagram of DEG



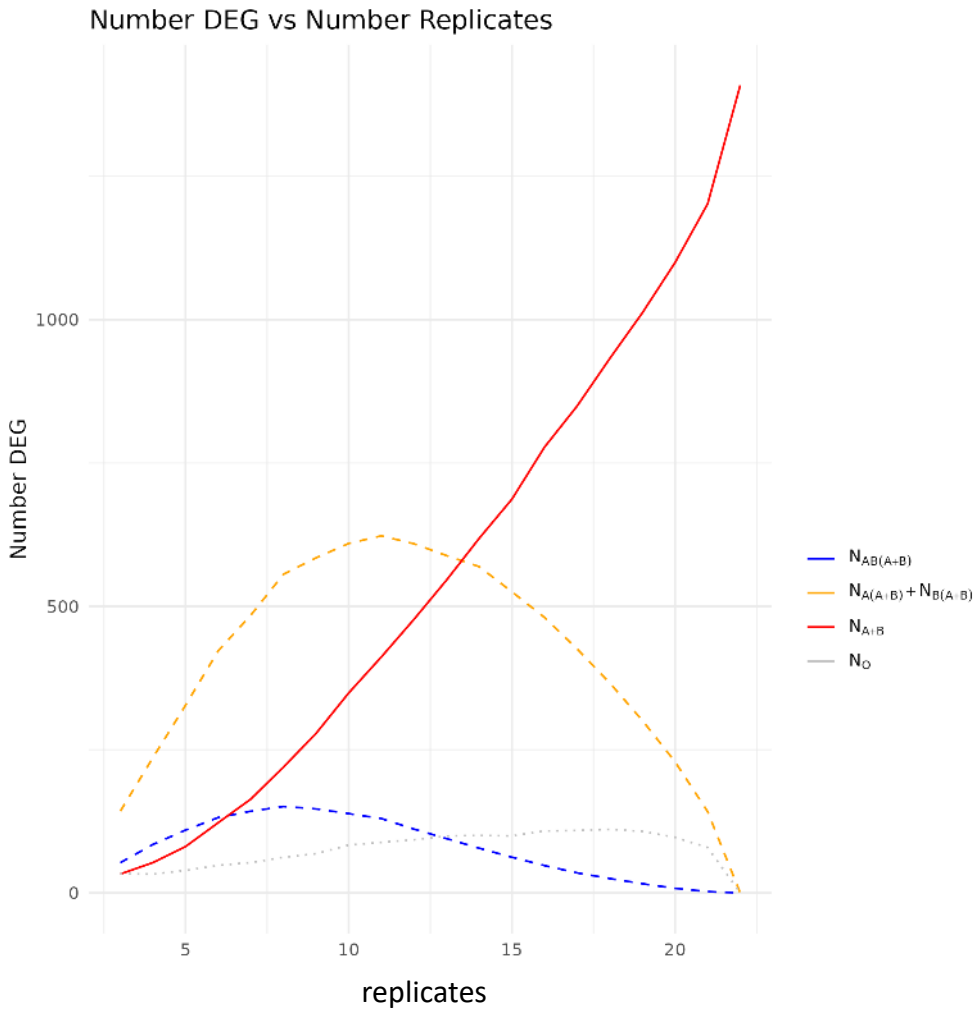
Very Large proportion of false « specific » DEG when using few reps and Venn diagramms

Number of biological replicates: not only a problem of power

Simulation



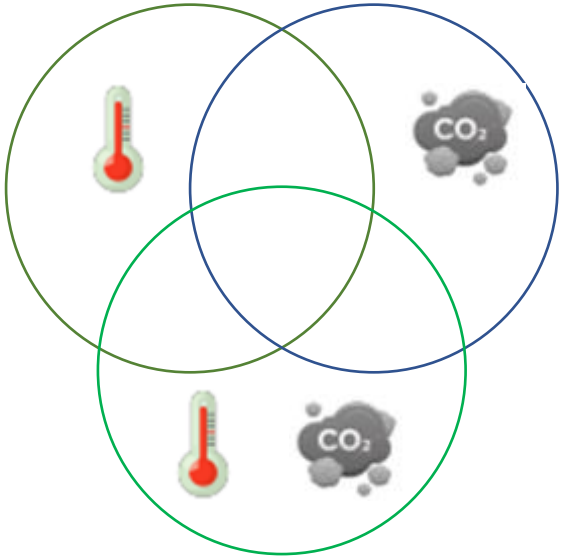
Observation



Mostly explained by the TPR variations

Number of biological replicates: not only a problem of power

Venn diagram of DEG



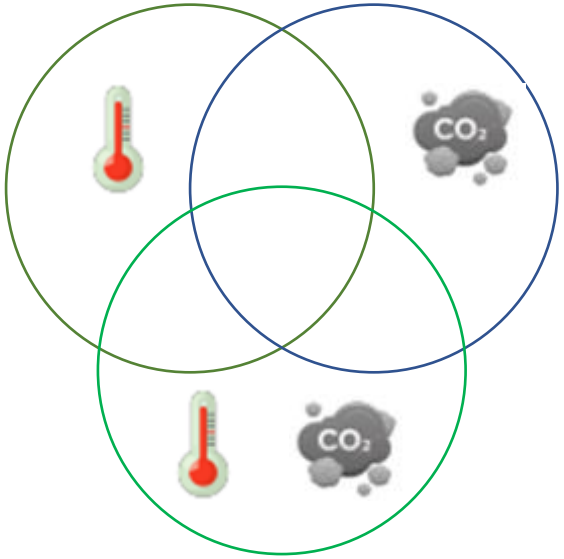
Solutions???

Composite hypothesis testing

Testing for genes that are :
« NOT DE in  » **AND** « NOT DE in  » **AND** « DE in   »

Number of biological replicates: not only a problem of power

Venn diagram of DEG



Solutions???

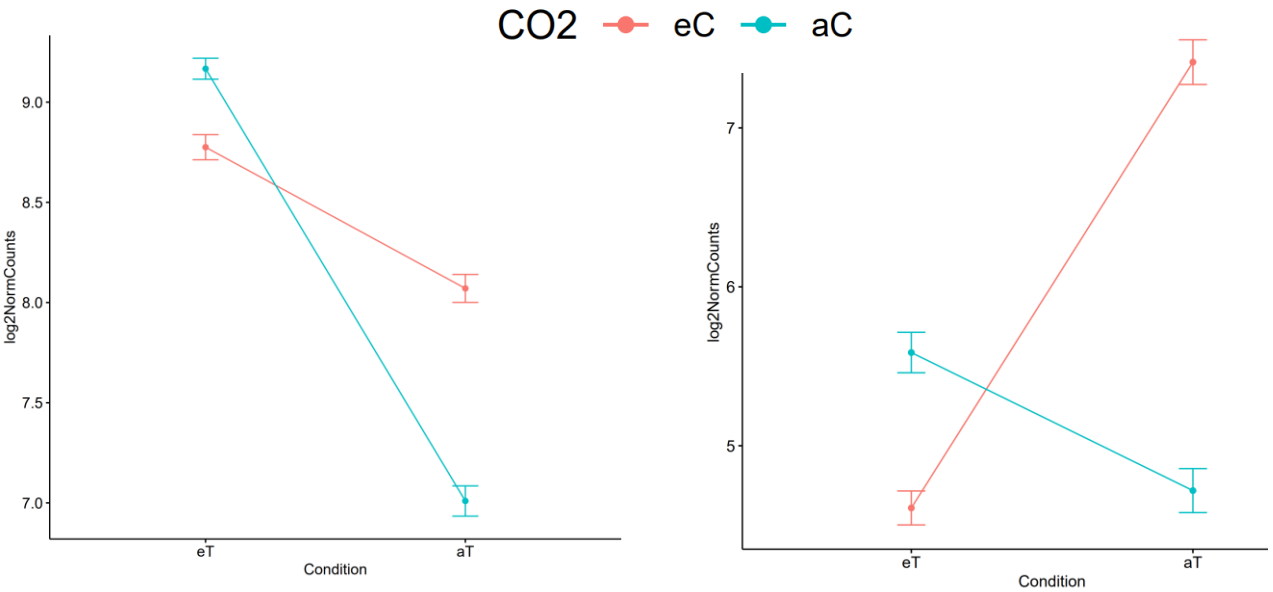
Composite hypothesis testing

Testing for genes that are :
« NOT DE in 🌡 » **AND** « NOT DE in CO₂ » **AND** « DE in 🌡 CO₂ »

➔ not enough power even @22 reps

Number of biological replicates: not only a problem of power

Don’t look for « specific » reponses,
look for responses to one factor that are impacted by another one = statistical interactions



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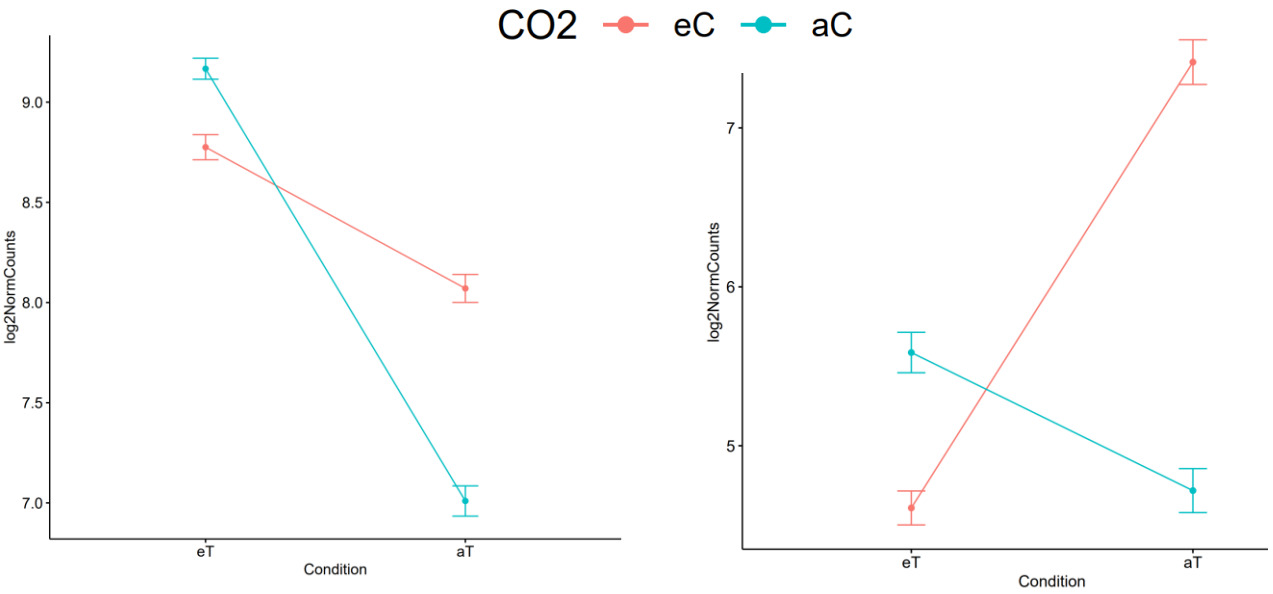
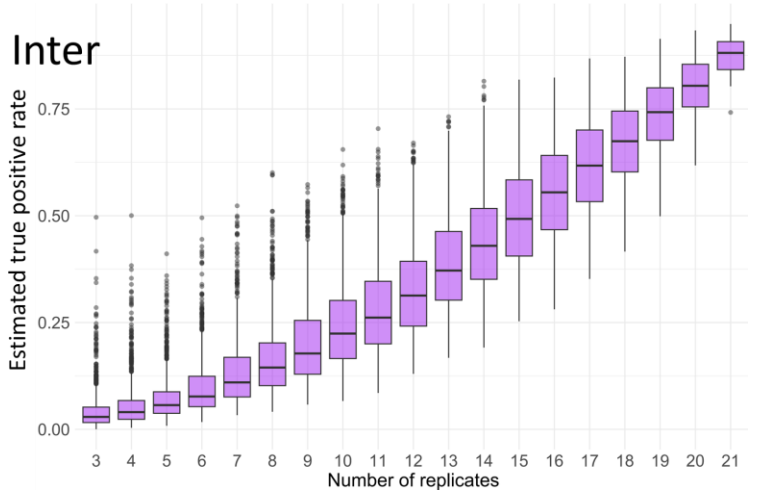
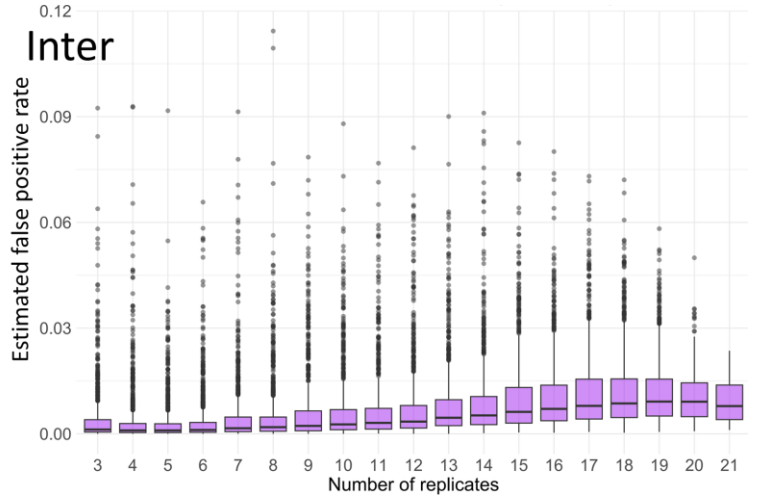




Power not too bad

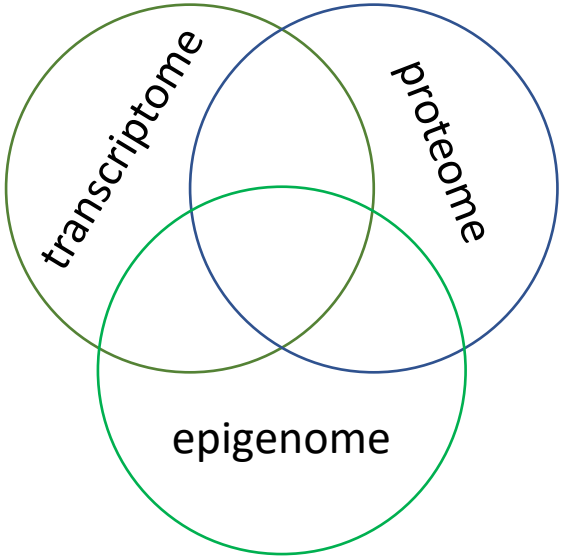


False Positive OK

Number of biological replicates: not only a problem of power

Multi-omics data integration

~~Venn diagram of DEG~~



The same problems apply to the interpretation of multi-omic data « integration »

Number of biological replicates: not only a problem of power

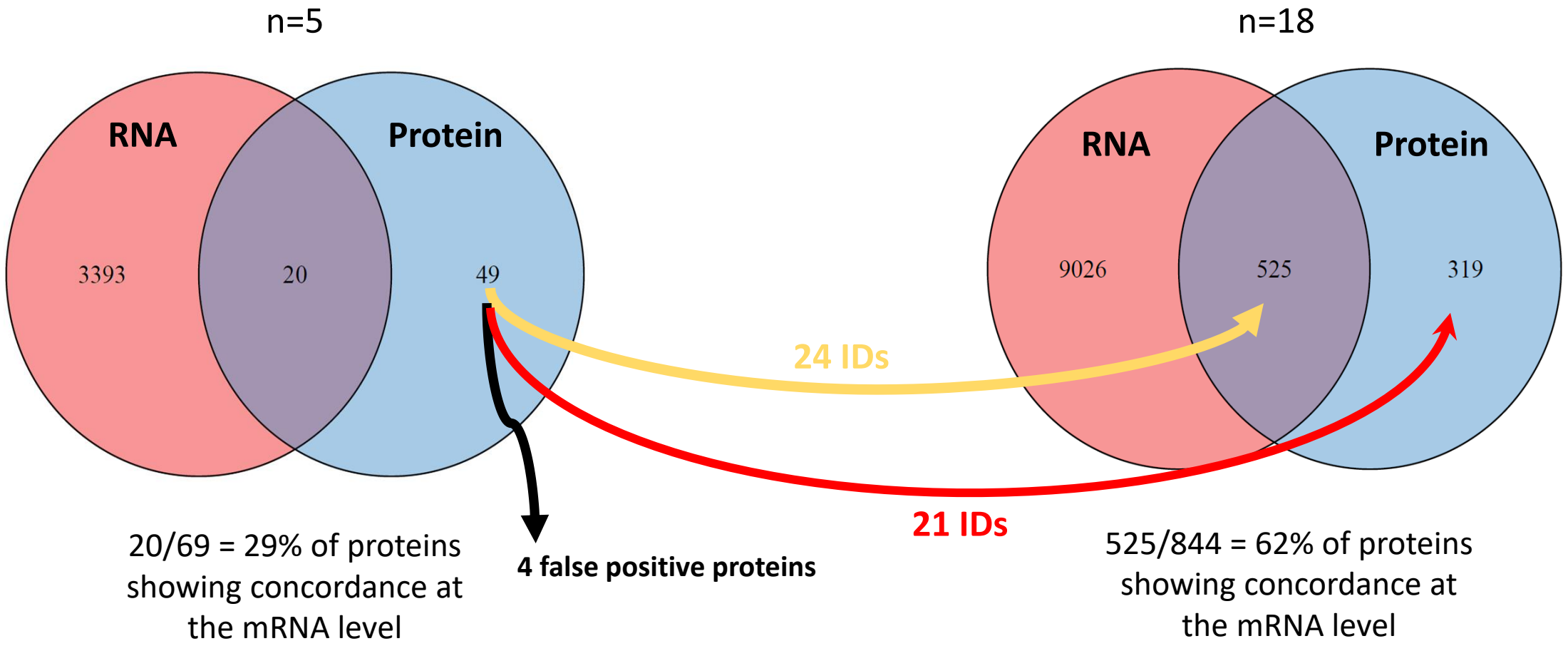
multi-omic data « intersection »

n=5

20/69 = 29% of proteins showing concordance at the mRNA level

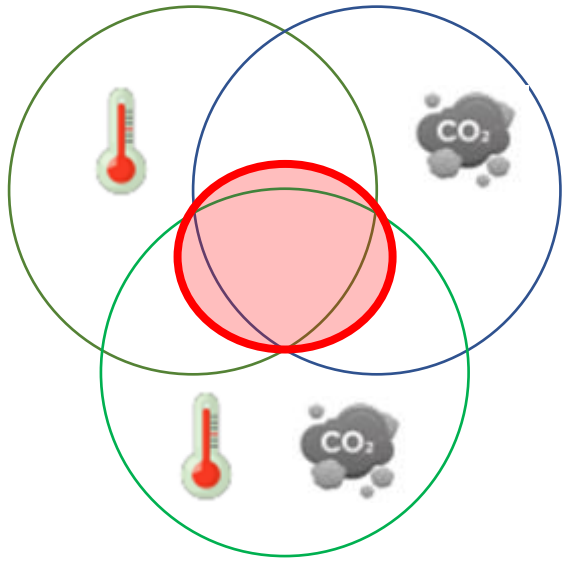
Number of biological replicates: not only a problem of power

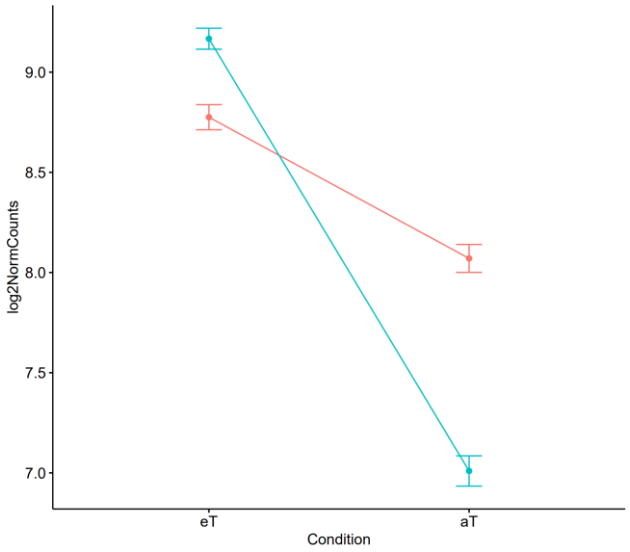
multi-omic data « intersection »



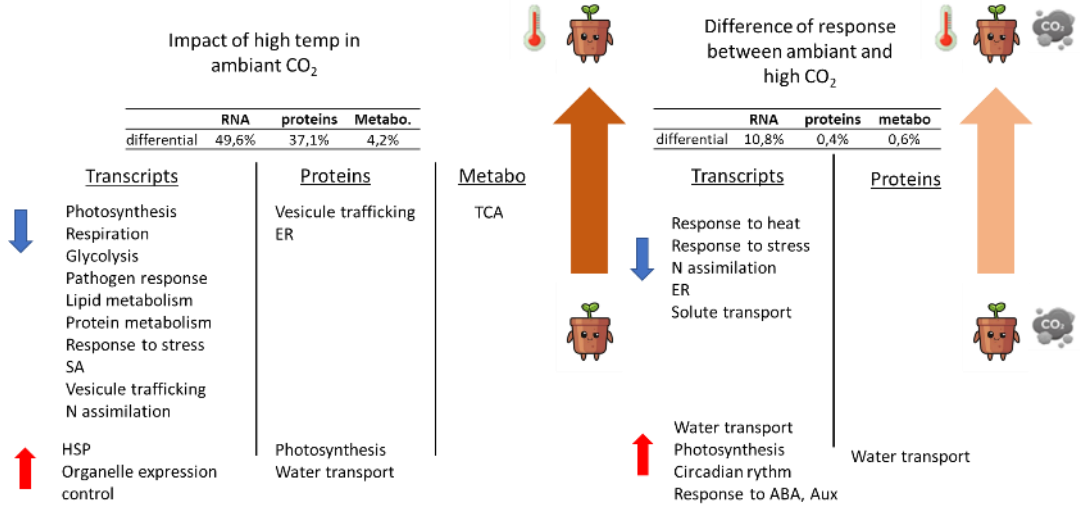
Number of biological replicates: not only a problem of power

Comparison of DEG lists





- When using Venn diagrams, only the intersections are meaningful
- When looking for « condition-specific » responses, use linear models (edgeR, lm) and statistical interactions



Acknowledgments

Omics platforms

Plateforme Métabolisme Métabolome
Isotopic and Metabolomic Solutions

PAPPSO

POPS
Concevoir en amont pour analyser en aval

BORDEAUX METABOLOME

Funding

INRAE
science for people, life & earth
METAPROGRAMME
DIGIT-BIO

GENOPOLE