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Data Workshop 4

22/03/2024

BABS4 (66I) – Gene expression and biochemical interactions strand



QR code for the material
(direct link on VLE W6)

Haemophilus influenzae (Hi) gene expression analysis

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You will analyse RNAseq counts data which will support your lab practicals

The data is from this publication:



RESEARCH ARTICLE

A competence-regulated toxin-antitoxin system in *Haemophilus influenzae*

Hailey Findlay Black^{1na}, Scott Mastromatteo^{1nb}, Sunita Sinha², Rachel L. Ehrlich³, Corey Nislow⁴, Joshua Chang Mell³, Rosemary J. Redfield^{1*}



Citation: Findlay Black H, Mastromatteo S, Sinha S, Ehrlich RL, Nislow C, Chang Mell J, et al. (2020) A competence-regulated toxin-antitoxin system in *Haemophilus influenzae*. PLoS ONE 15(1): e0217255. <https://doi.org/10.1371/journal.pone.0217255>

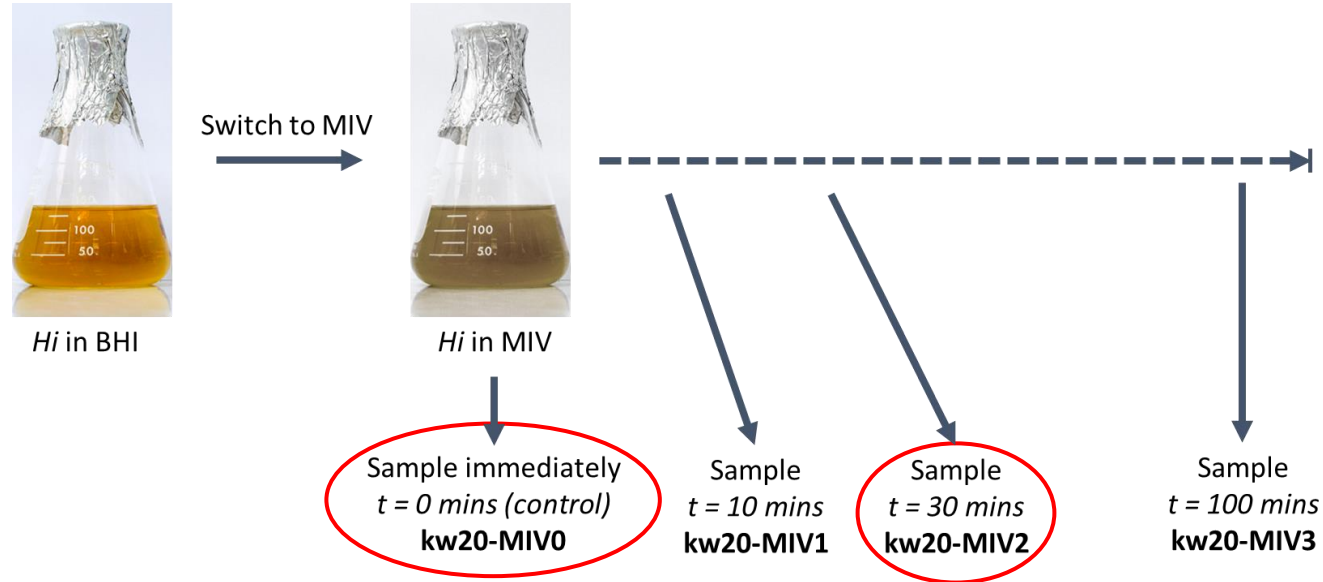
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RESEARCH QUESTION

What is the competence-induced transcriptomic response of Hi?



In workshop 3, you:

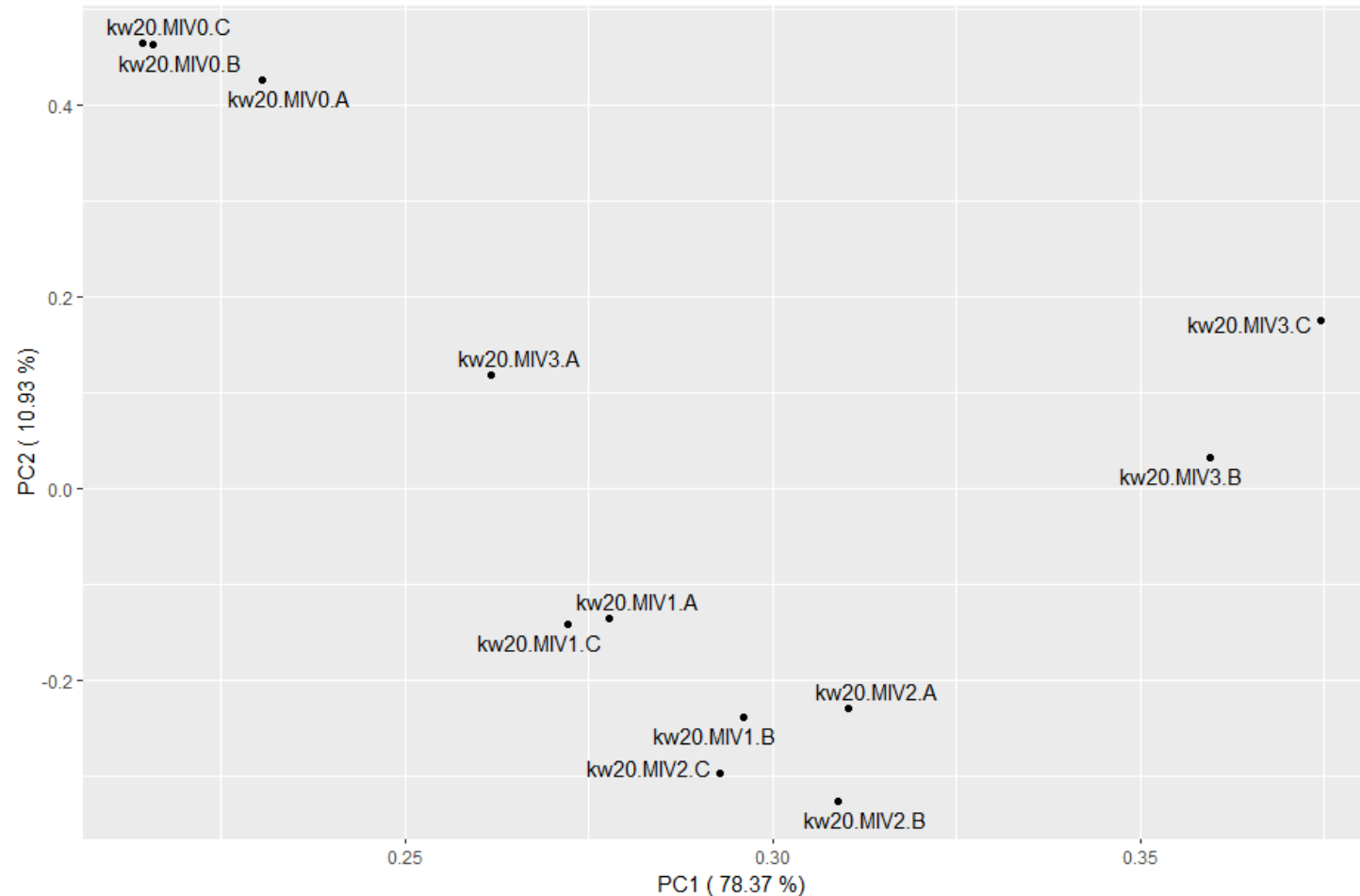
- Set up your RStudio Project
- Downloaded raw data and installed required libraries
- Inspected data and performed normalization (TPMs)
- Looked for sample variability with PCA
- Performed differential expression analysis

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PCA – plots high dimension data giving a high-level sample summary

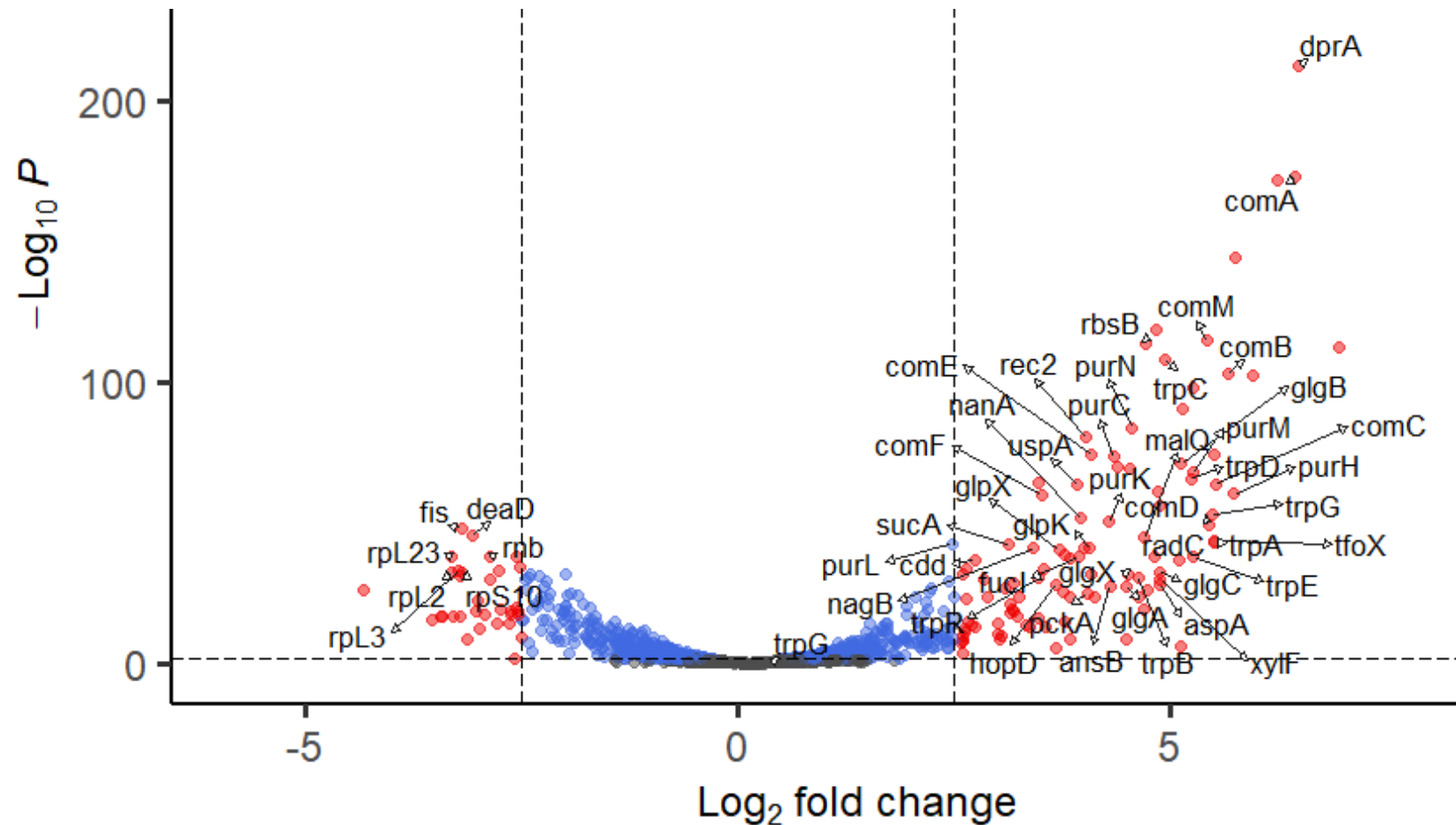


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Volcano plot – quantified changes in the transcriptome



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NB. I have provided some ggplot() code in case your EnhancedVolcano() is not working properly

What does it all mean and why should I care?

It should help you understand competence response and get some context for gam, but let's show you how.

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In this workshop – focus on the biology

6

Set up your RStudio Project *(remember that this is also assessed, not just the report)*

- *you may want a fresh one for the workshop, but it needs to be one project on submission*

Load your libraries *(with any installations)*

Refresh your memory from last week

Perform gene set enrichment analysis (GSEA)

Run a separate DEA and compare with last week's

Ask whether this data can be used to assess *gam* co-expression

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