

# Data Workshop 4

BABS4 (661) – Gene expression and biochemical interactions strand

Remember the key questions of this module:

- 1) Is there a **functional gam homologue** in *Haemophilus influenzae* (HiGam), and, if so,
- 2) Is HiGam part of a **non-canonical** competence response?



In these data practicals (data workshops 3 and 4) you will ask:

- a) How does gene expression change during **canonical** competence in Hi?
- b) What is the role (if any) of HiGam in this response?

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

The data is from this publication:



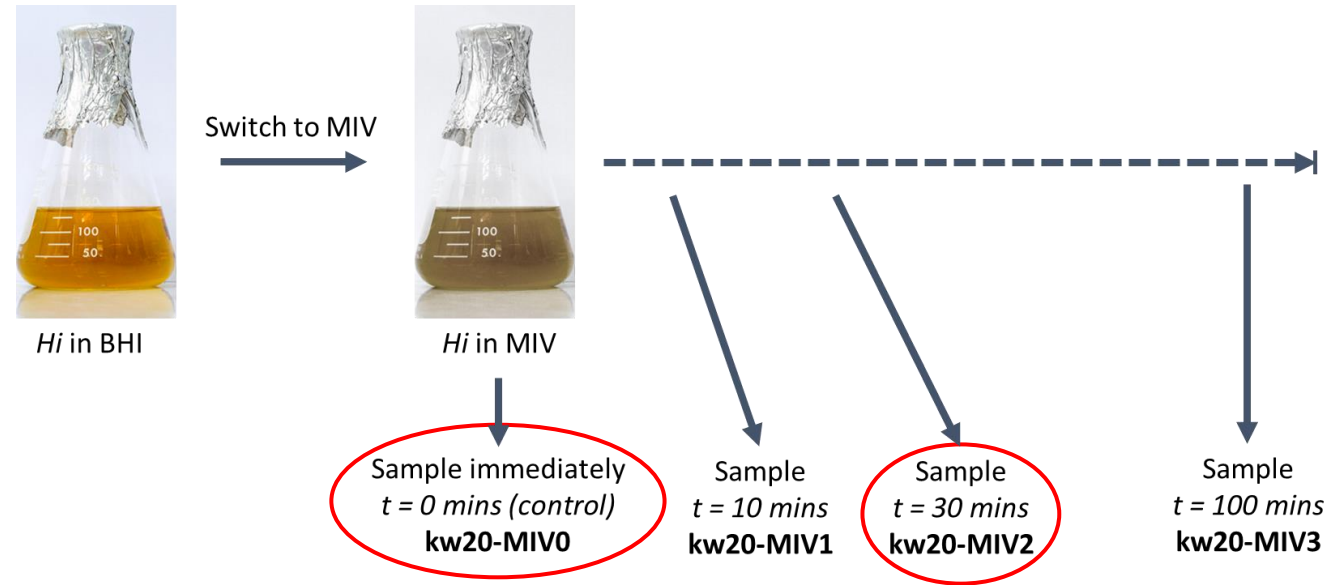
RESEARCH ARTICLE

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

Hailey Findlay Black<sup>1na</sup>, Scott Mastromatteo<sup>1nb</sup>, Sunita Sinha<sup>2</sup>, Rachel L. Ehrlich<sup>3</sup>, Corey Nislow<sup>4</sup>, Joshua Chang Mell<sup>3</sup>, Rosemary J. Redfield<sup>1\*</sup>



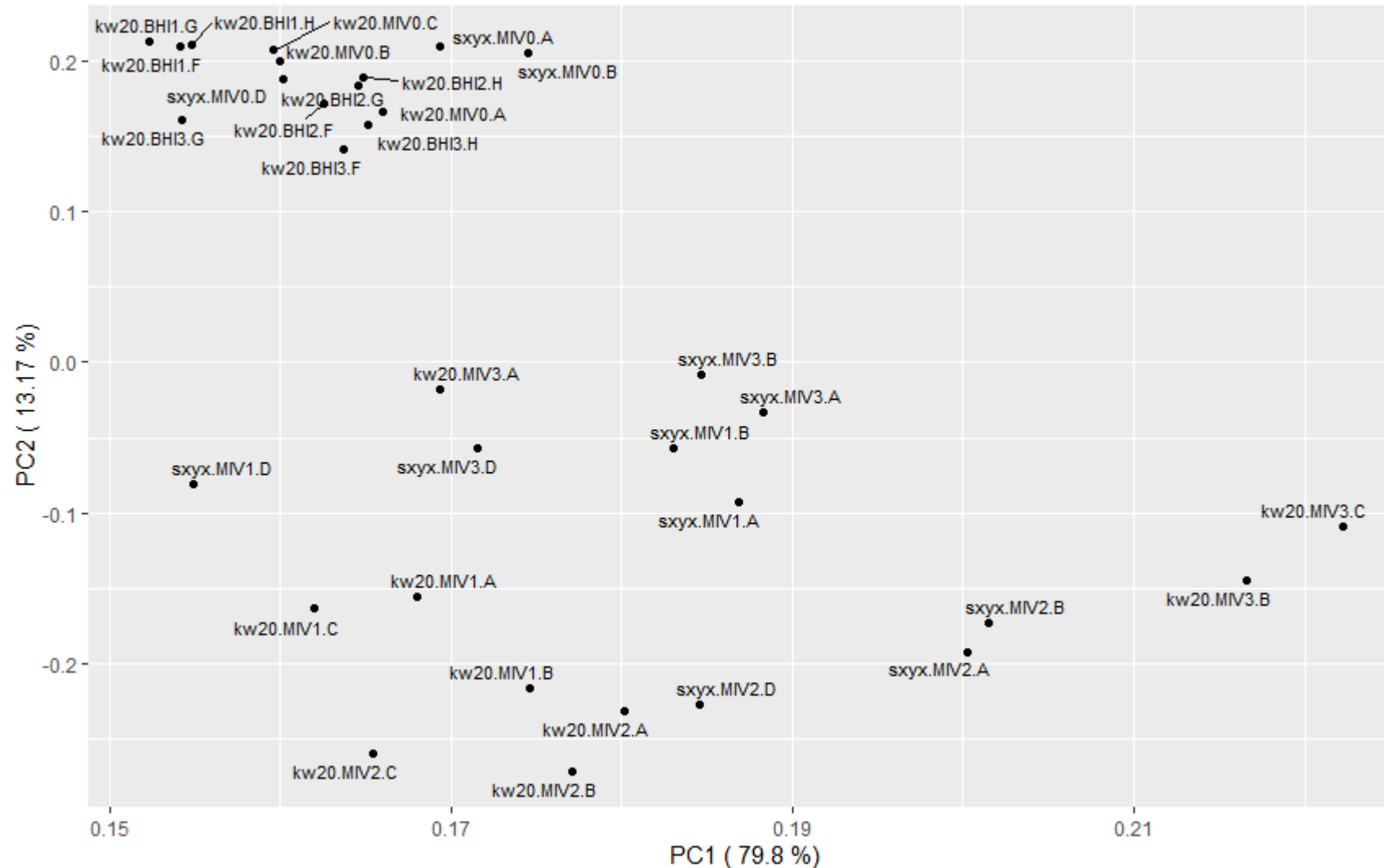
**Citation:** Findlay Black H, Mastromatteo S, Sinha S, Ehrlich RL, Nislow C, Chang Mell J, et al. (2020) A competence-regulated toxin-antitoxin system in *Haemophilus influenzae*. PLoS ONE 15(1): e0217255. <https://doi.org/10.1371/journal.pone.0217255>



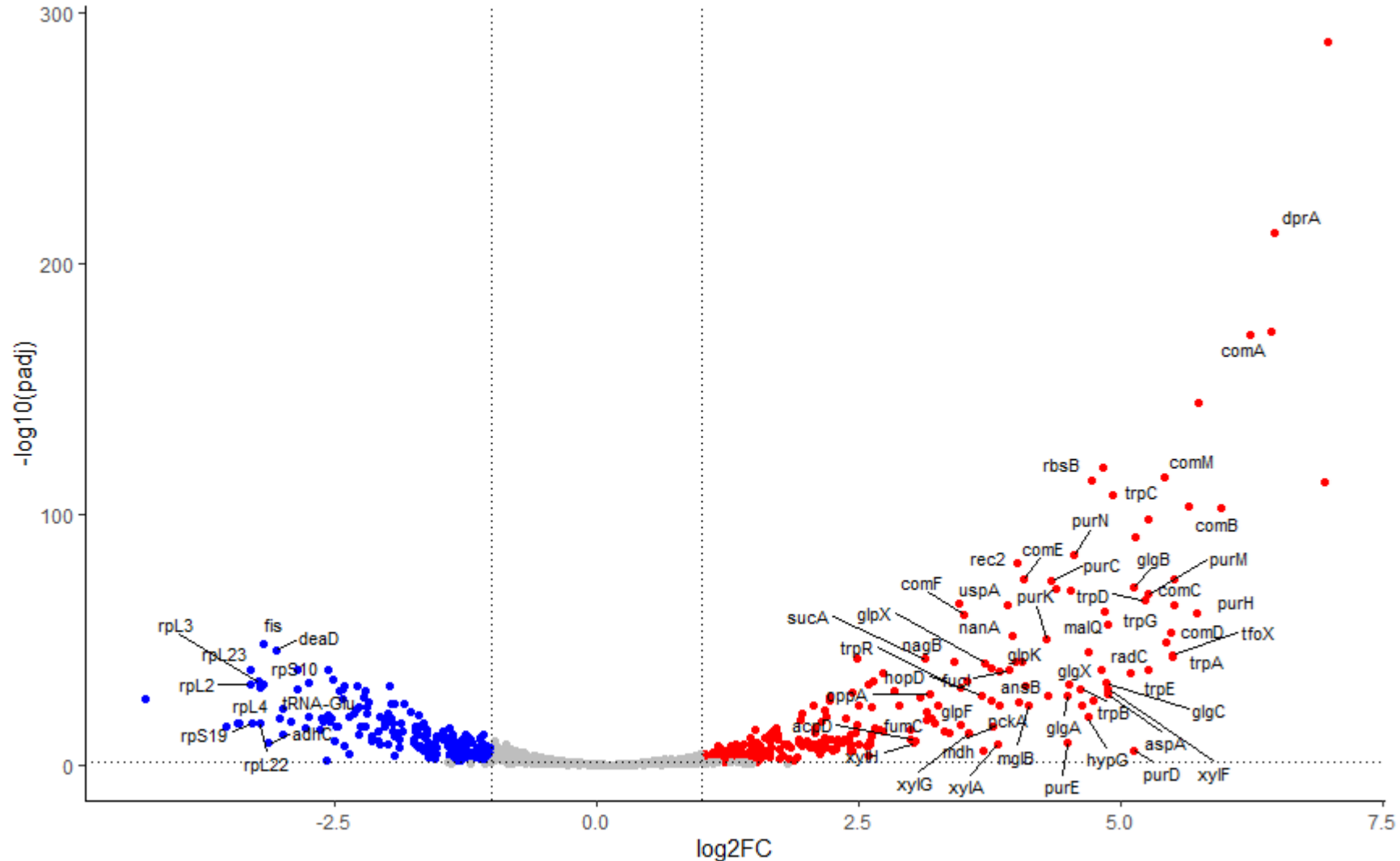
In workshop 3, you:

- 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

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



## Volcano plot – quantified changes in the transcriptome



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

Run a separate DEA and compare with last week's

Work on visualization with a circus plot

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

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