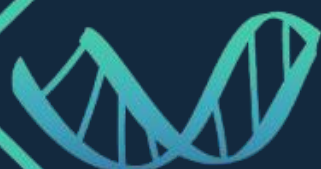
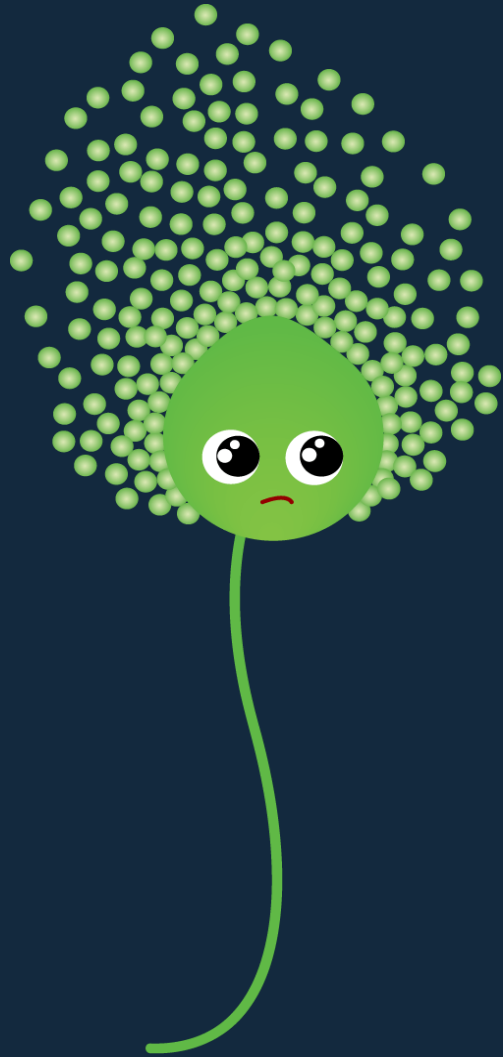


Library of Engineered *Aspergillus* Promoters



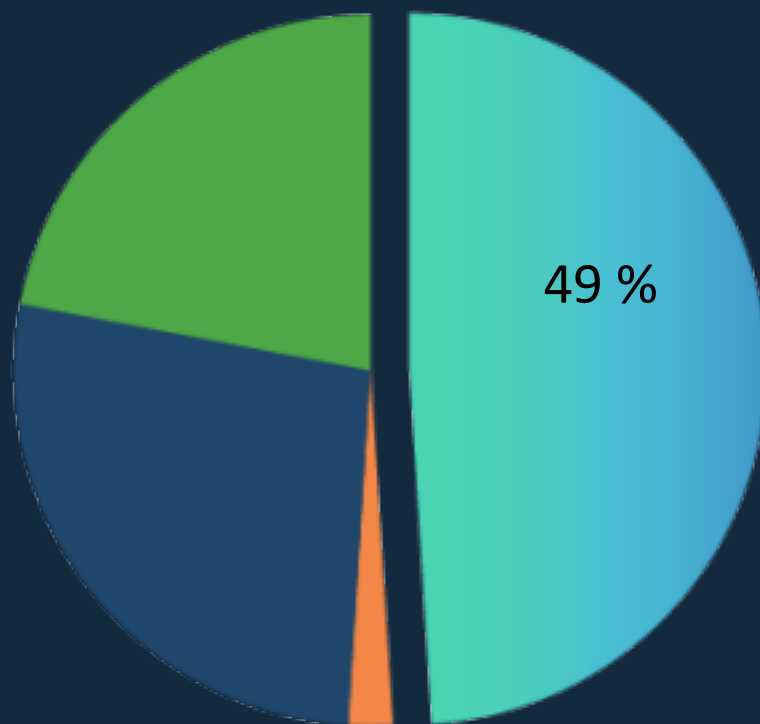
LEAP





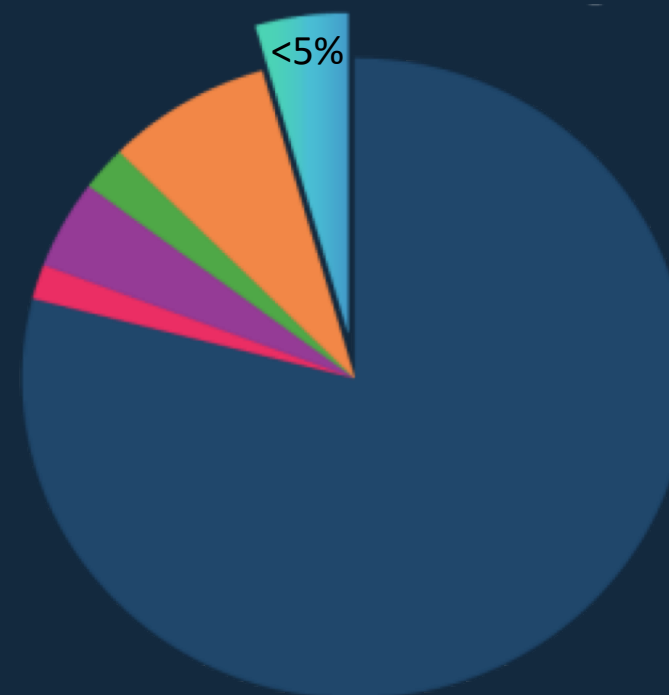
"No one wants to work with me"  
- *Aspergillus niger*

Fraction of industrial enzyme production



Filamentous fungi Yeast Misc. bacteria Others

Promoters in the iGEM registry



*E. coli* *B. subtilis* Bacteriophages  
Misc. prokaryotes Yeast Misc. eukaryotes

# Aims and objectives

proHMMoter

Compiling...

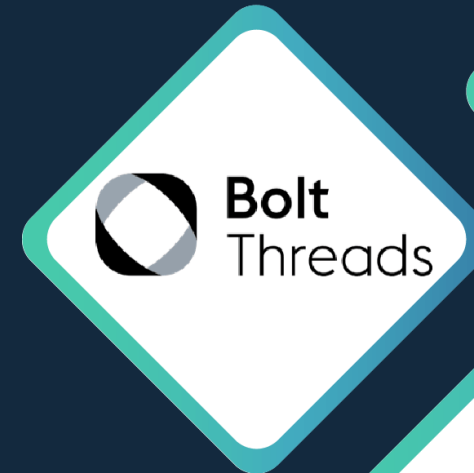
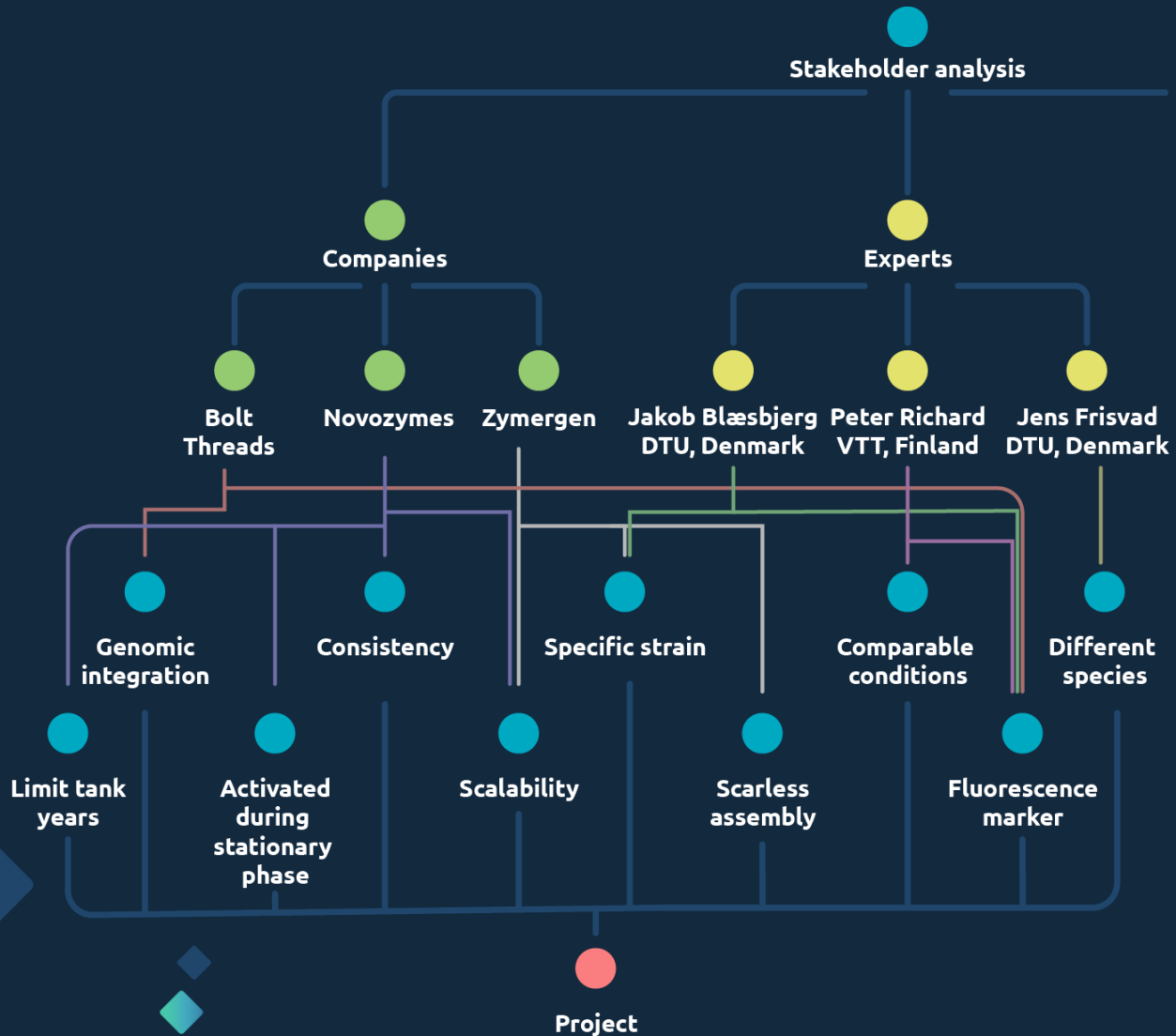
```
#wait for 1 second
time.sleep(1)
print "Start guessing..."
time.sleep(0.5)
#here we see the secret
word = "secret"
#created an variable with
an empty value
guesses = ''
#determine the number of
turns
turns = 10
# Create a while loop
#check if the turns
#more than zero
while turns > 0:
    # Ask the user to
    #enter a character
    char = input("Enter a character: ")
    # Check if the character
    #is in the word
    if char in word:
        # If the character
        #is in the word,
        #show the position
        #of the character
        print "The character", char, "is at position",
        word.index(char)
    else:
        # If the character
        #is not in the word,
        #show an error
        print "The character", char, "is not in the word."
    # Remove the character
    #from the word
    word = word.replace(char, '')
    # Print the word
    print "The word is: ", word
    # Print the number of
    #turns left
    print "You have", turns, "turns left."
    # Decrease the number
    #of turns
    turns = turns - 1
    # If the number of
    #turns is zero,
    #show the word
    if turns == 0:
        print "The word is: ", word
        # End the game
        break
```



# Integrated human practices

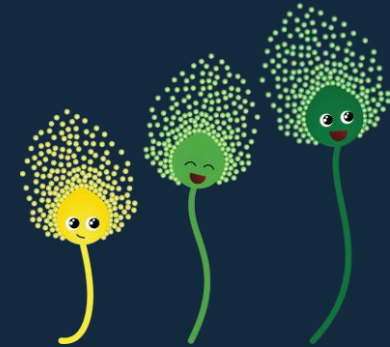


# Integrated human practices



# Objective: Create promoters

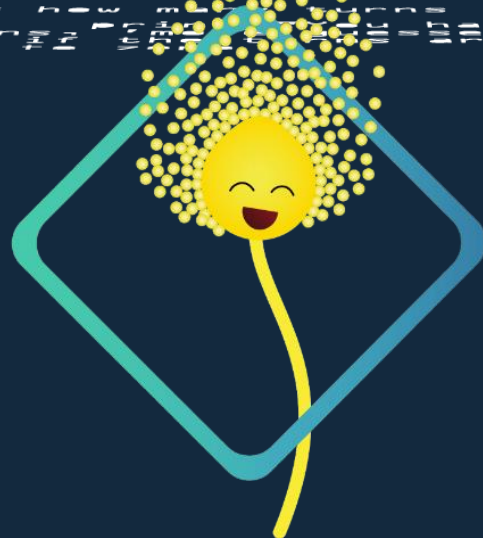
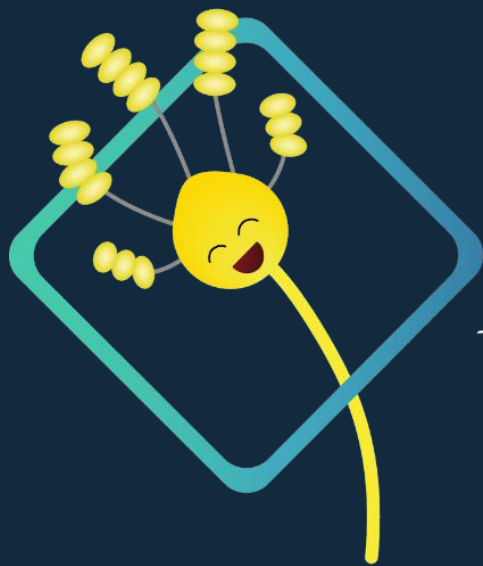
- Scalable
  - Lab → industry
- Be active in different growth stages
- Create a ladder of promoters with different strengths



# New aim

# proHMMoter

# Compiling...

[illegible]



A cluster of several blue and teal diamond shapes of varying sizes and opacities in the top right corner.

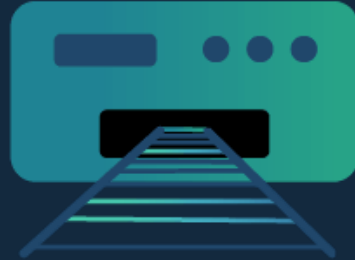
proHMMoter

A few small blue and teal diamond shapes in the bottom left corner.

# Software and Model



Shorter sequences



Easily synthesized



Domestication



Weaker promoters

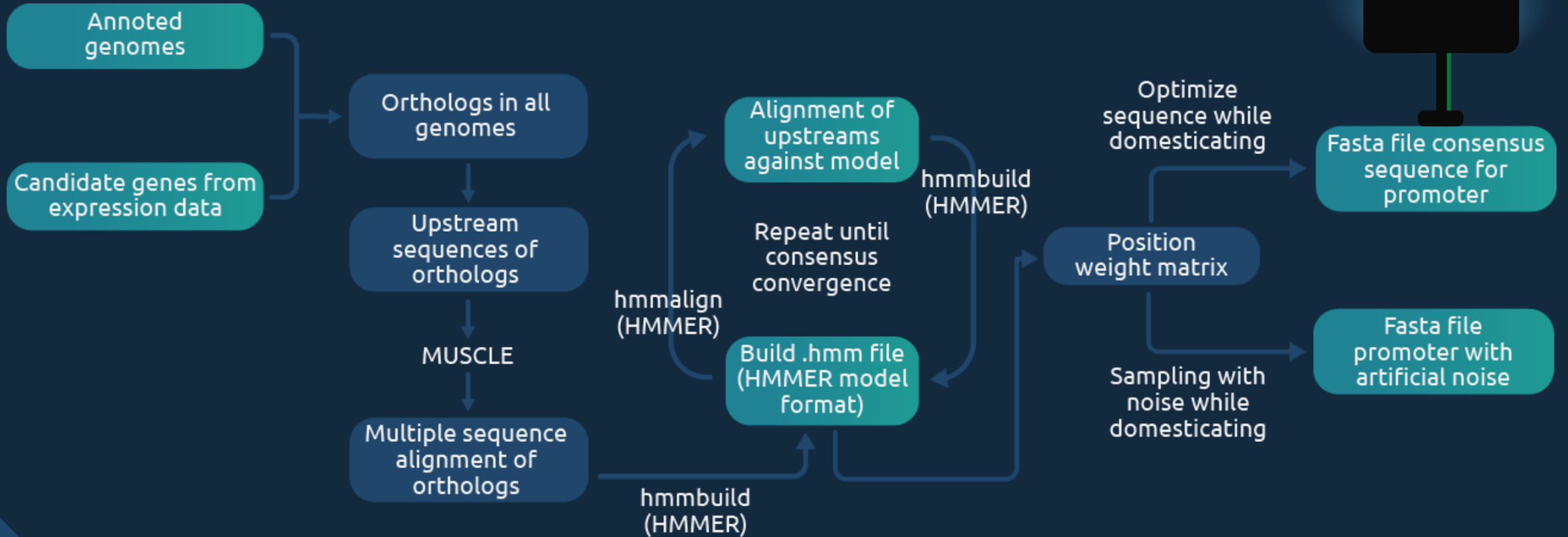


Non homology

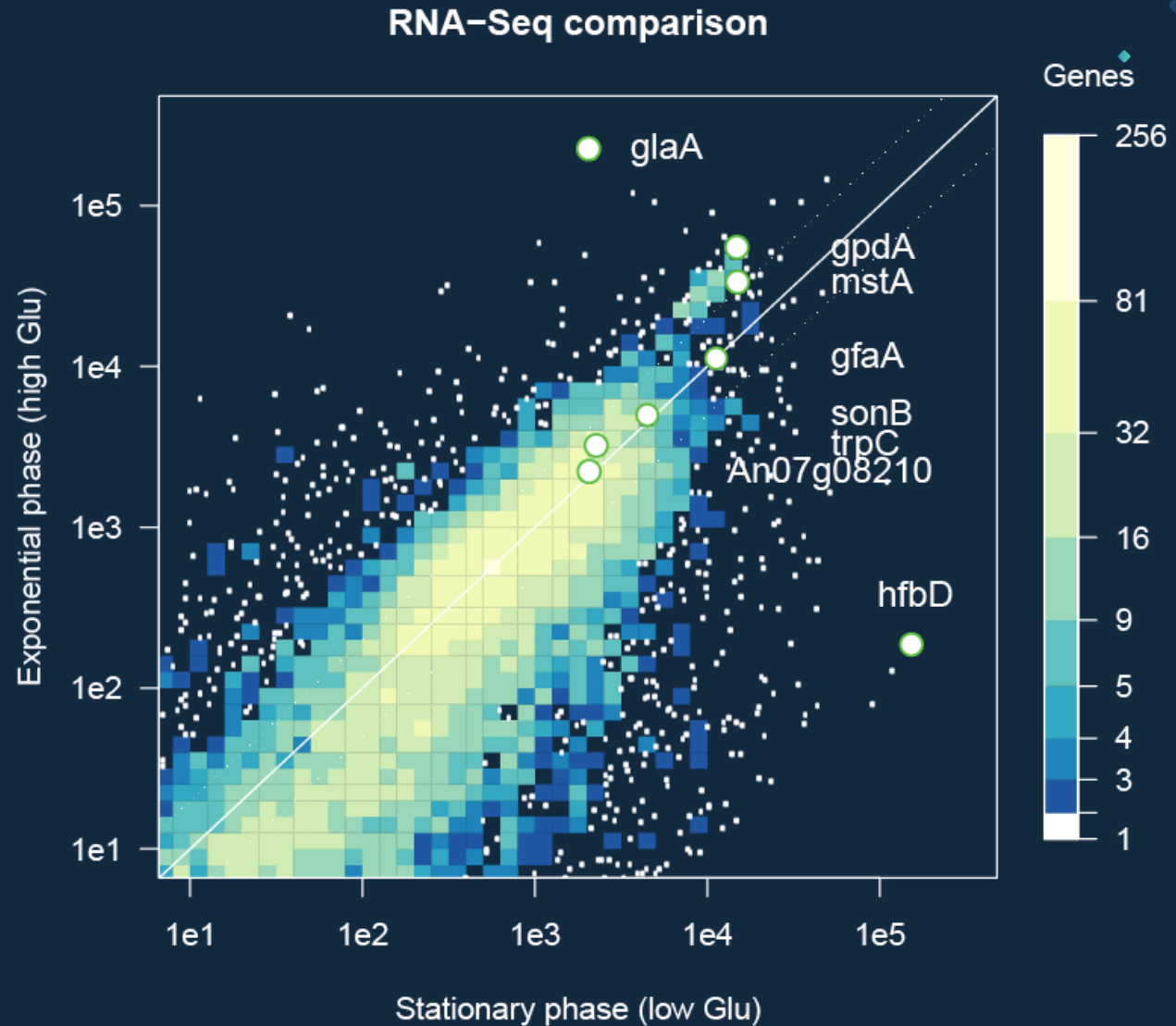


Host versatility

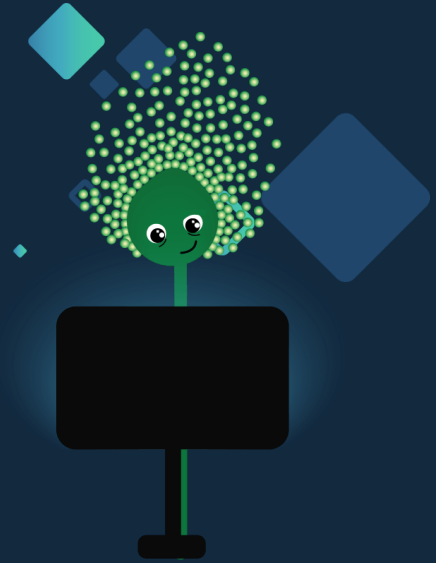
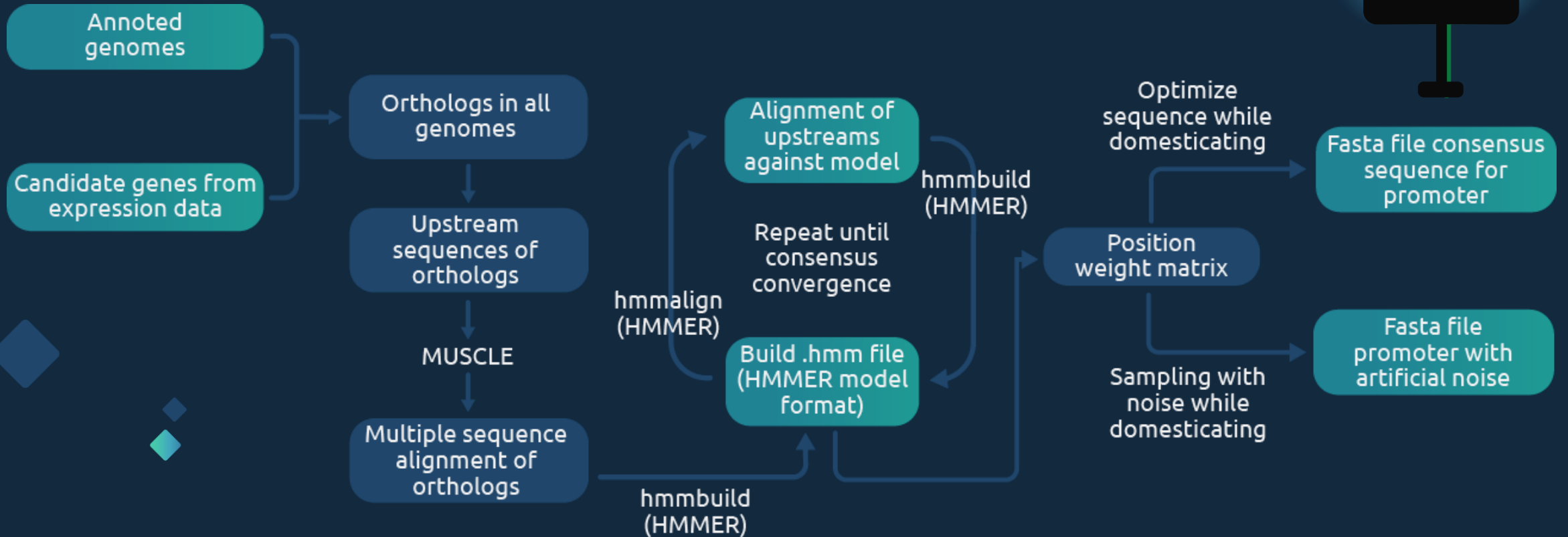
# Software and Model



# Software and Model

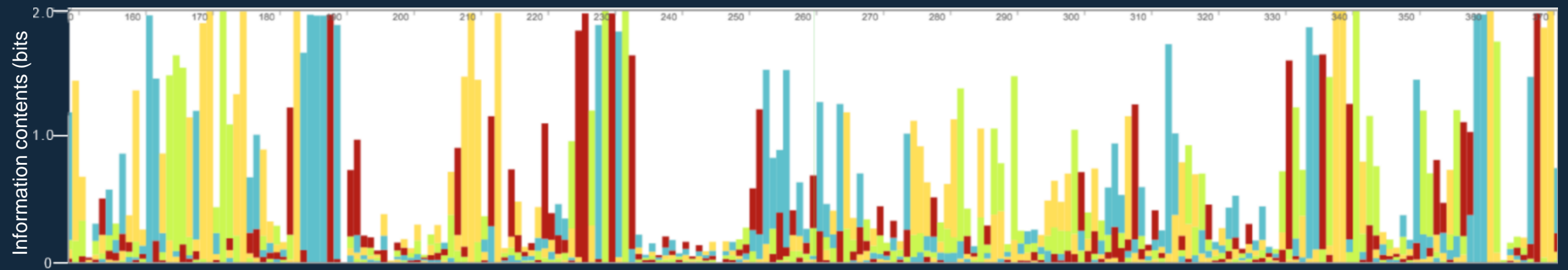


# Software and Model





# Software and Model



# Dry-lab achievements

- 101 *Aspergillus* genomes
- 15 candidate genes
- 46 synthetic promoters

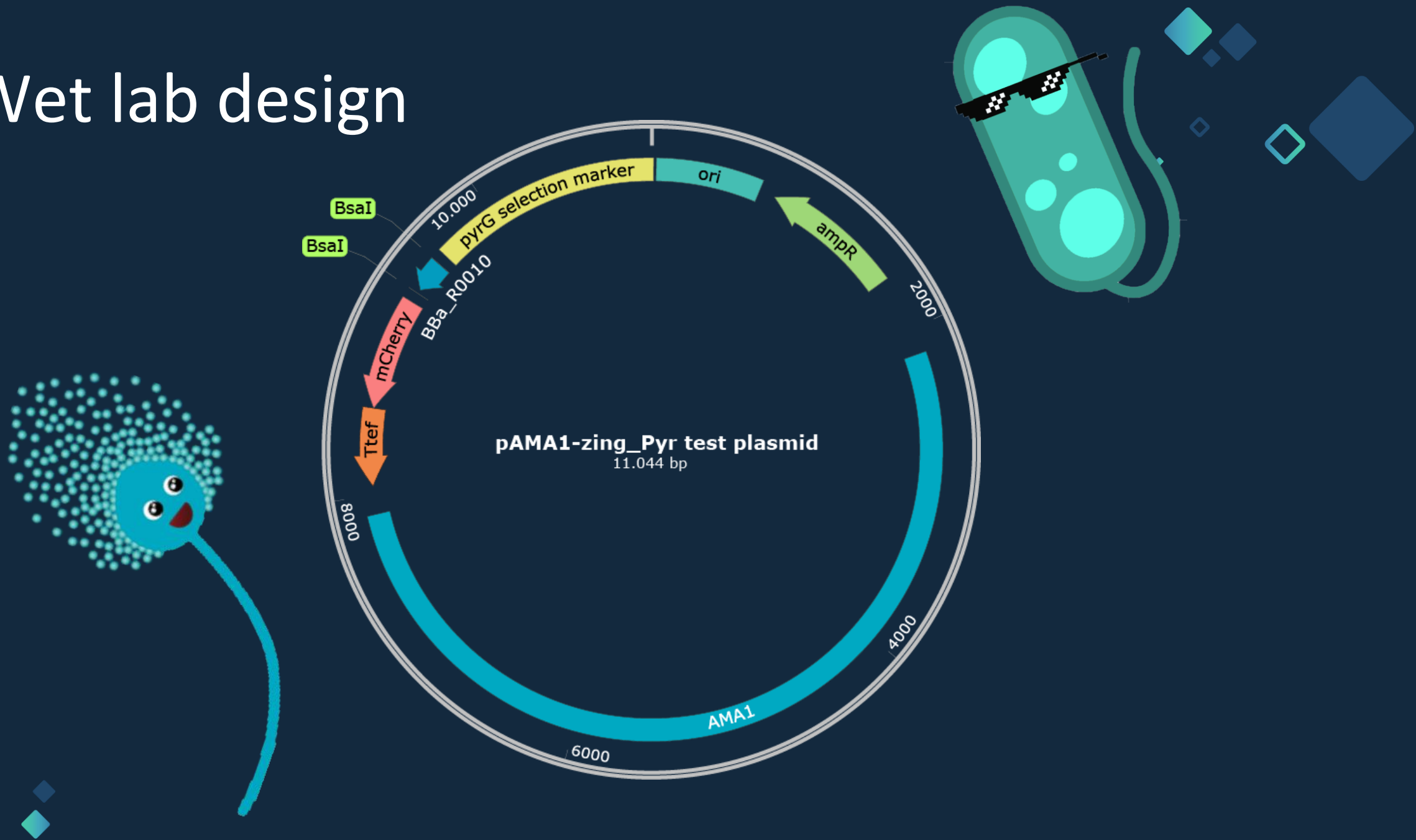




# Promoter parts

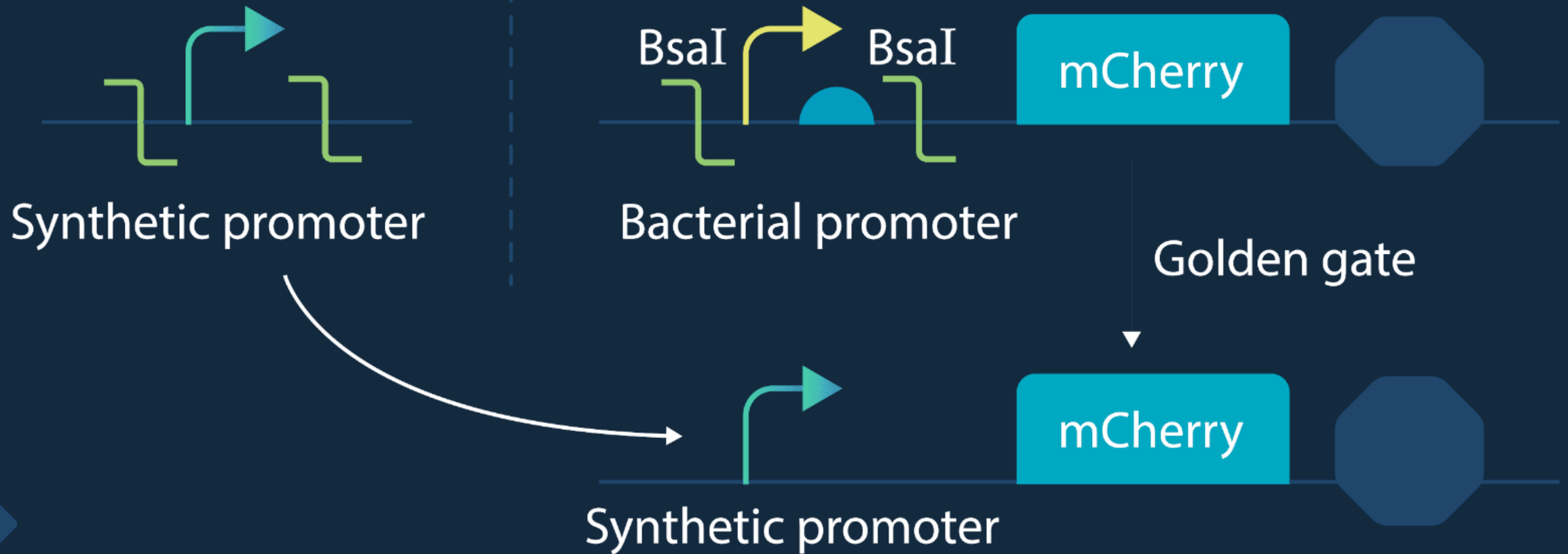
Biobrick number:	Gene annotation:	Gene name:
BBa_K3046001	glaA	Glucoamylase
BBa_K3046003 BBa_K3046004	gpdA	Glyceraldehyde-3-phosphate dehydrogenase
BBa_K3046005	mstA	Monosaccharide transporter
BBa_K3046007	gfaA	Glutamine:fructose-6-phosphate amidotransferase
BBa_K3046002	sonB	Nuclear pore complex protein
BBa_K3046006	An07g08210	Actin filament binding
BBa_K3046008	hfbD	Hydrophobin

# Wet lab design

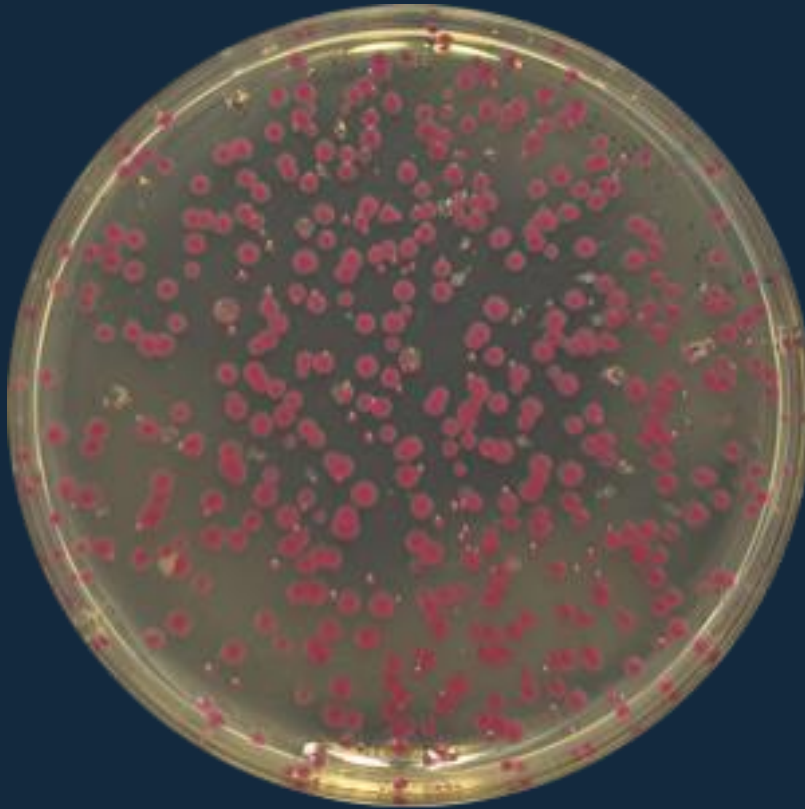


# Fungal promoter test device

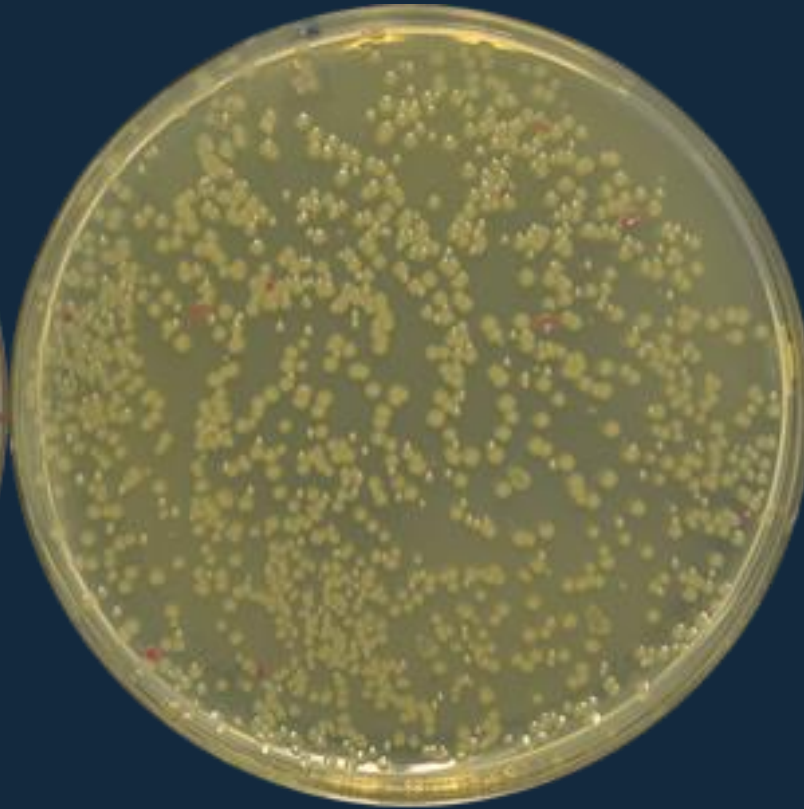
(BBa\_K3046009)



# Wet lab design

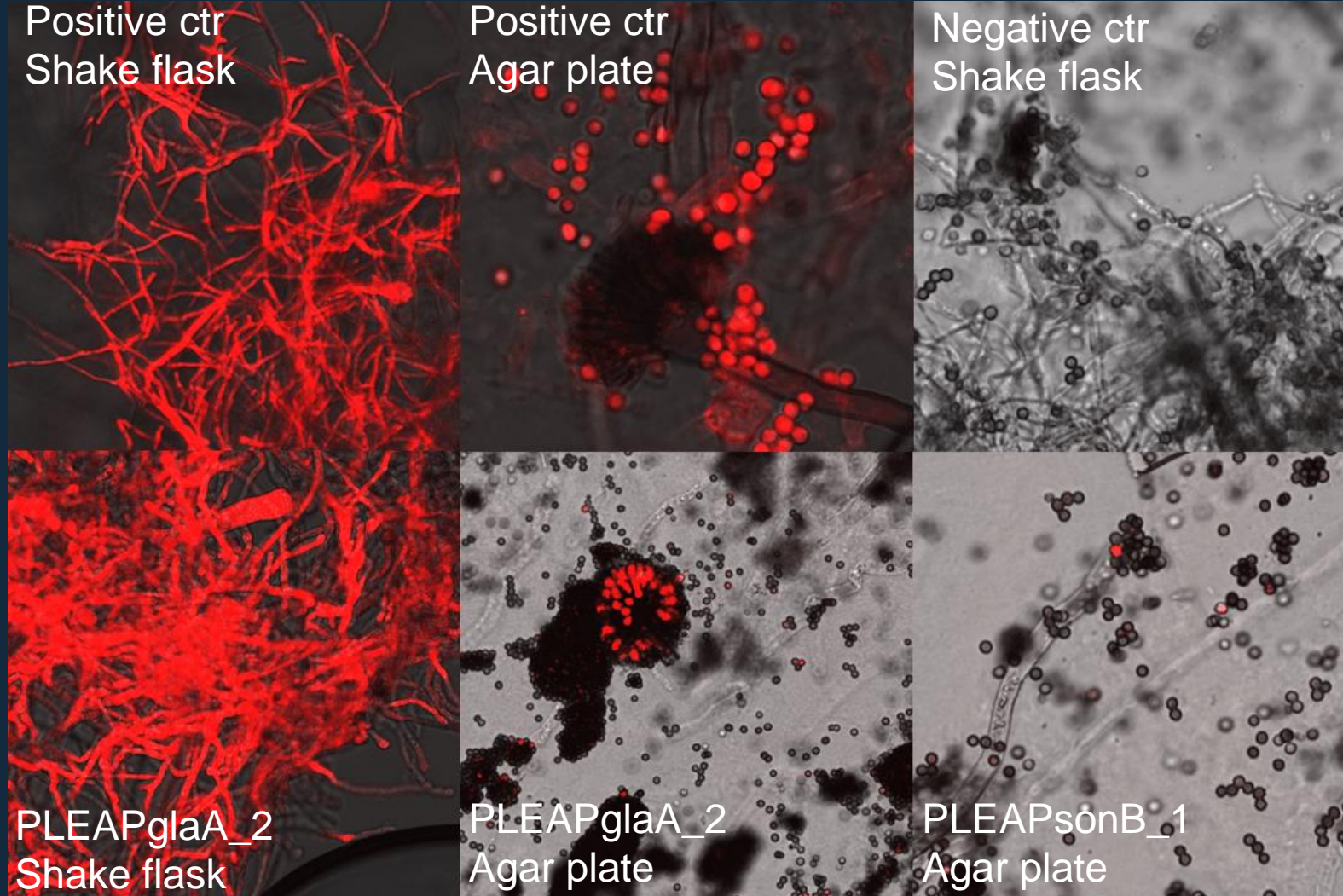


*E. coli*  
with prokaryote promoter



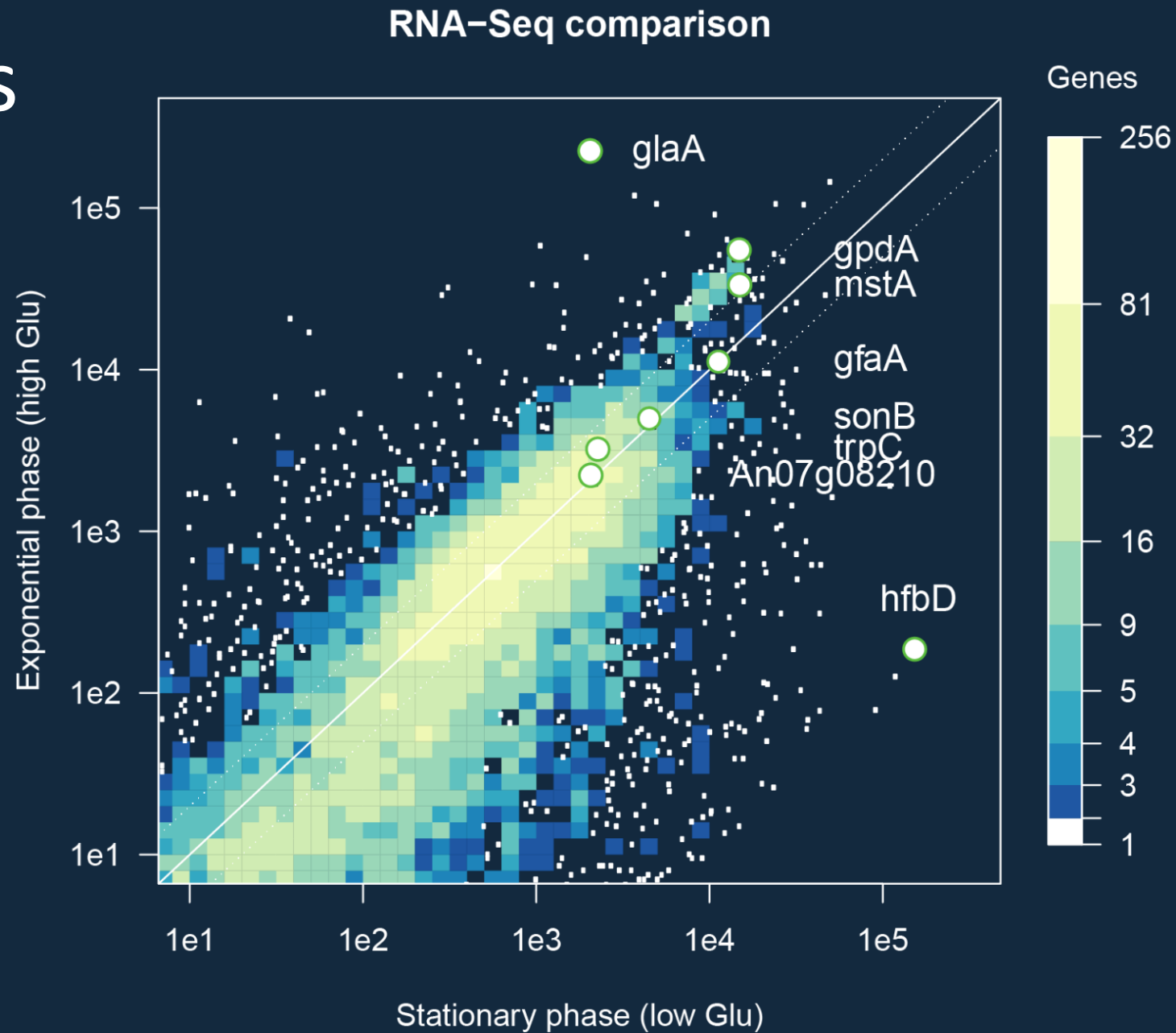
*E. coli*  
with synthetic eukaryote promoter

# Confocal microscopy: *A. niger*



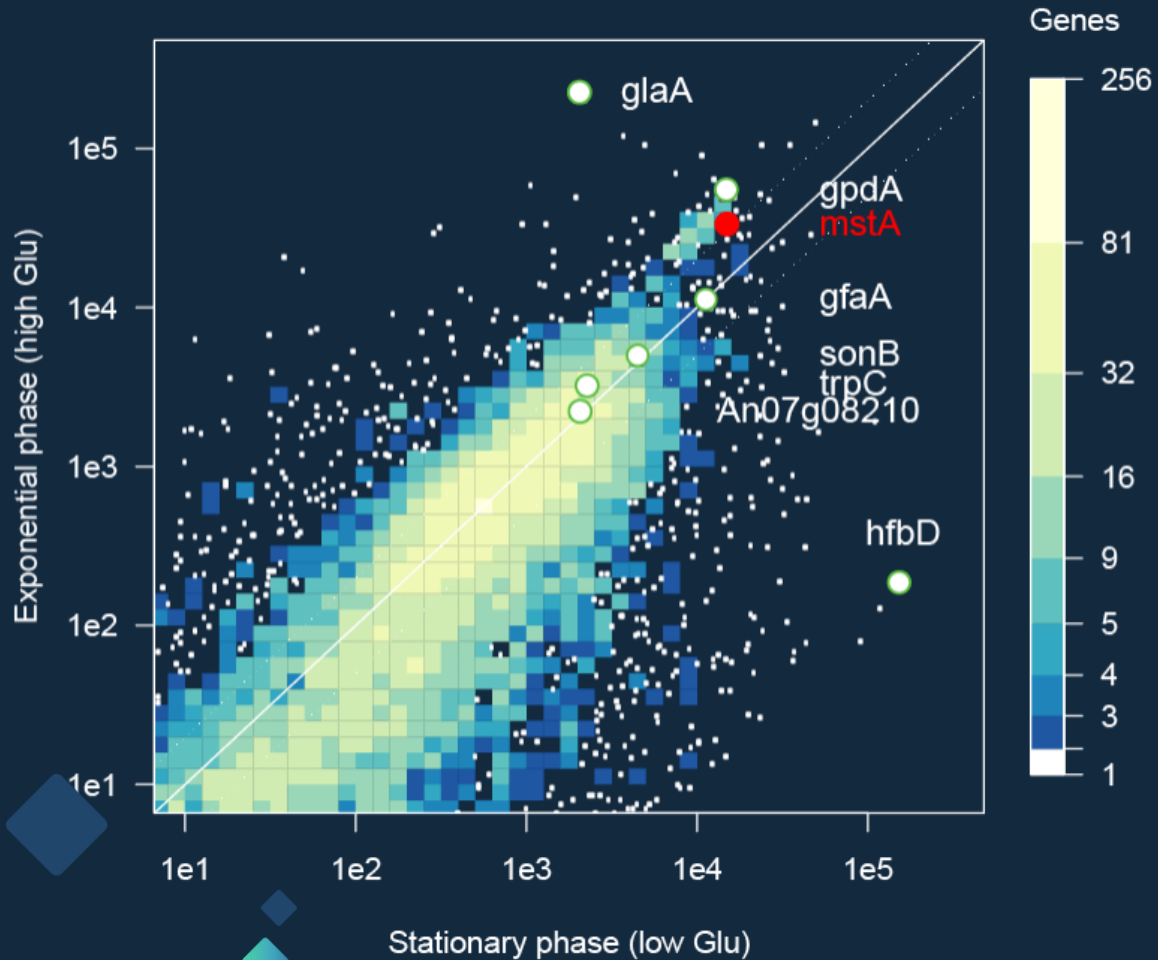


# Results

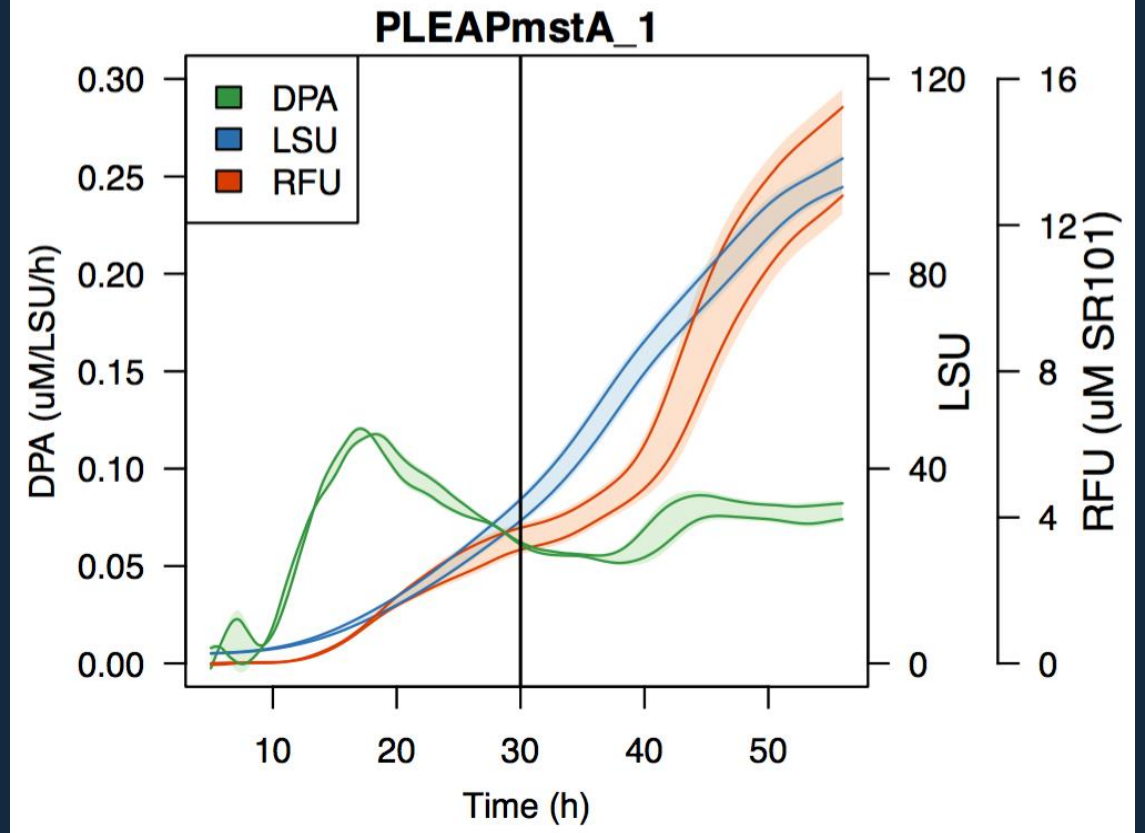


# Results

RNA-Seq comparison

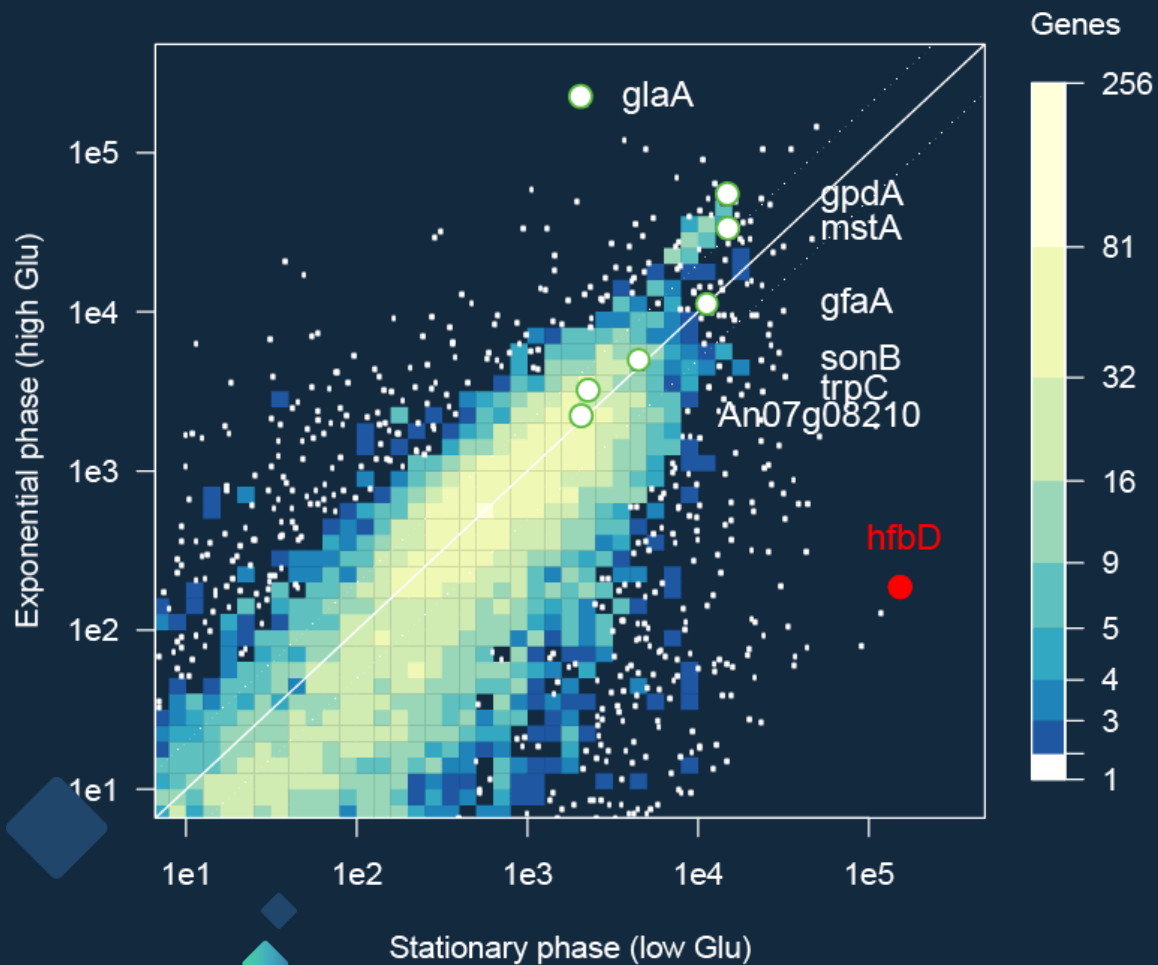


Constitutive

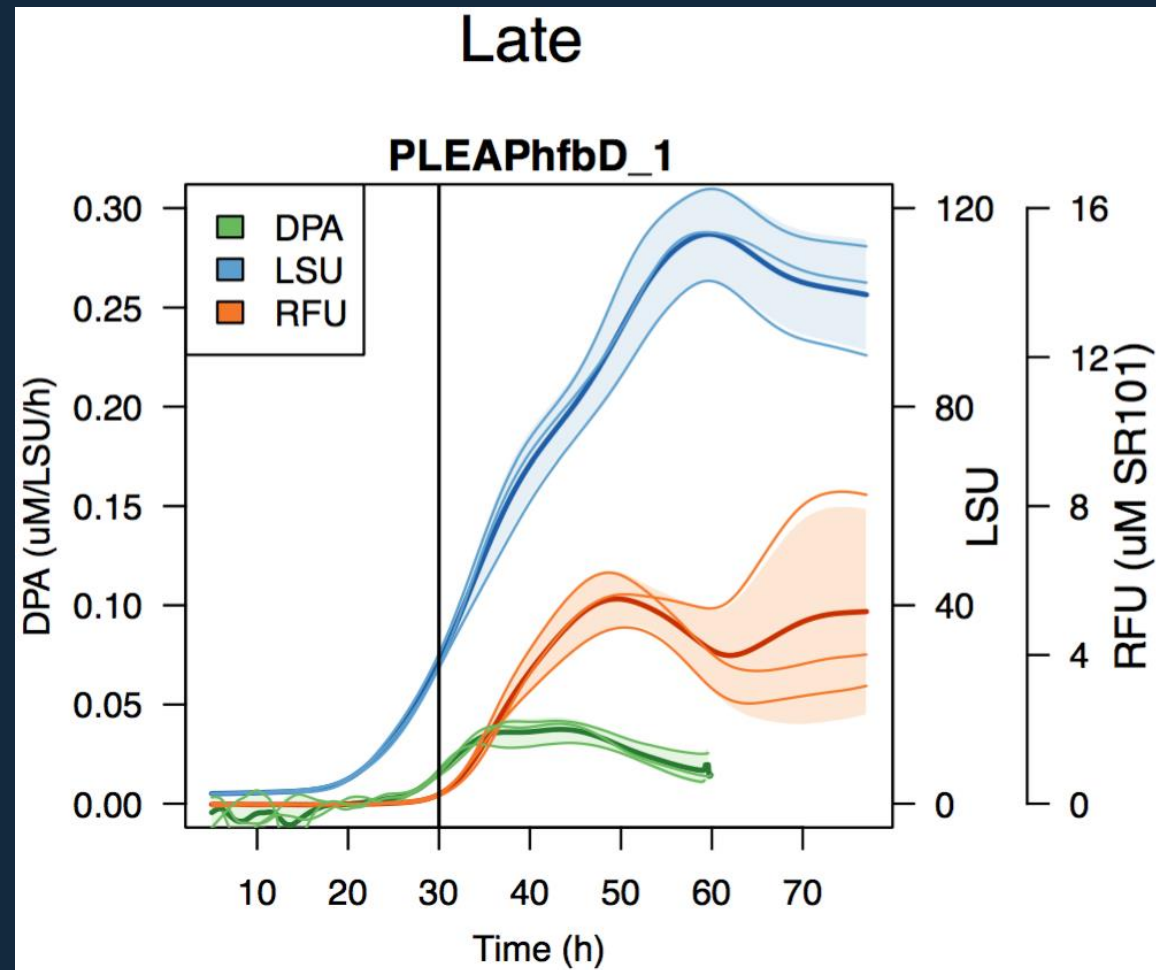


# Results

RNA-Seq comparison



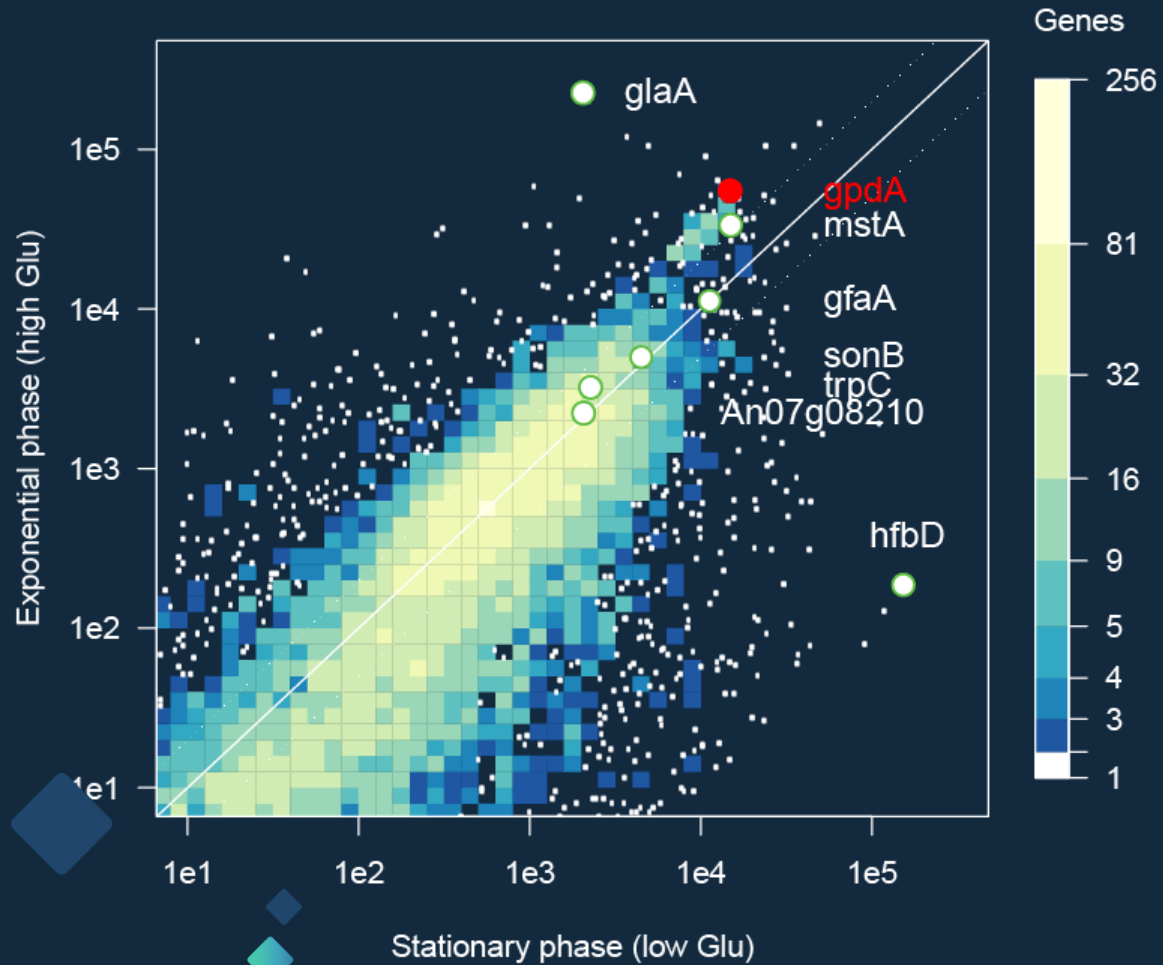
Late



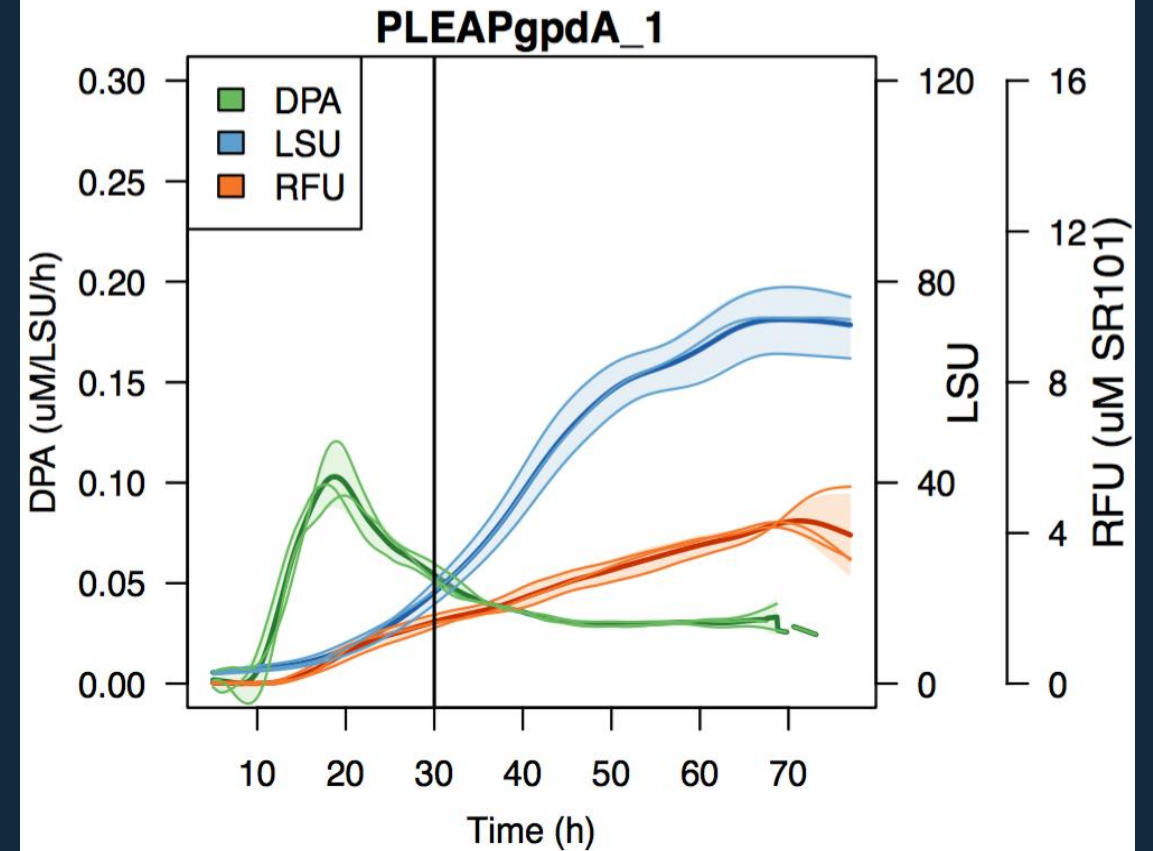


# Results

RNA-Seq comparison

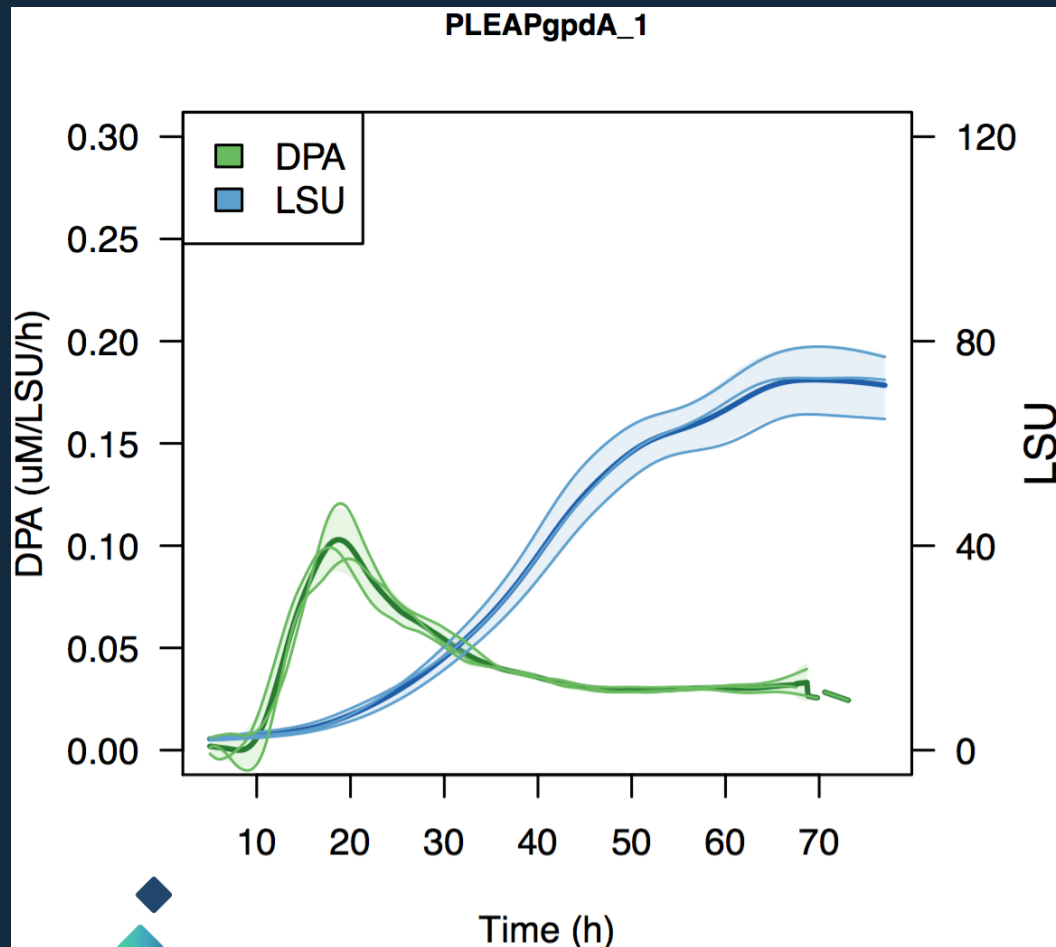


Early

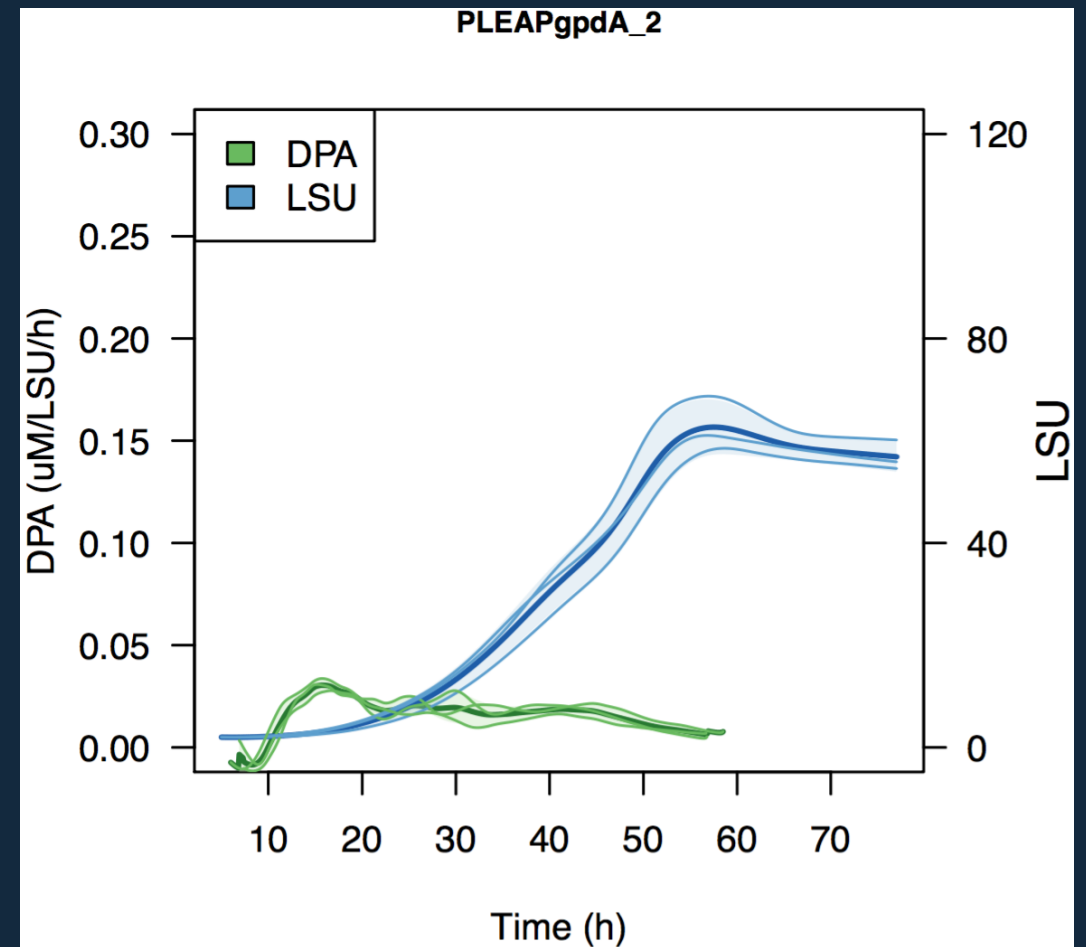


# Results: Biolector (1.5 mL)

Without noise



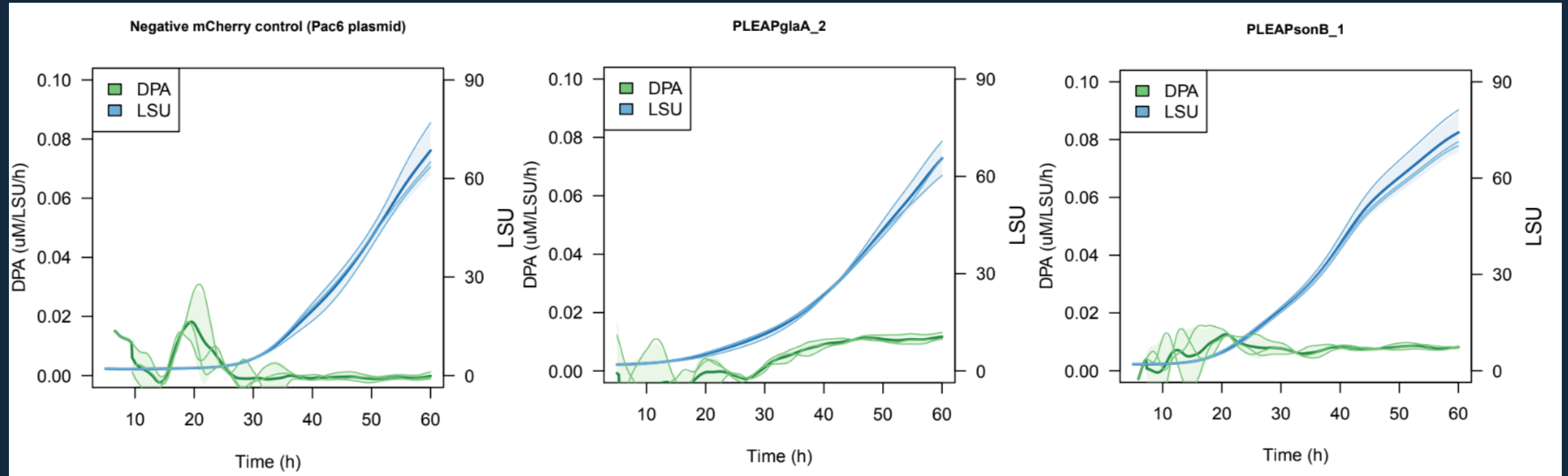
With noise



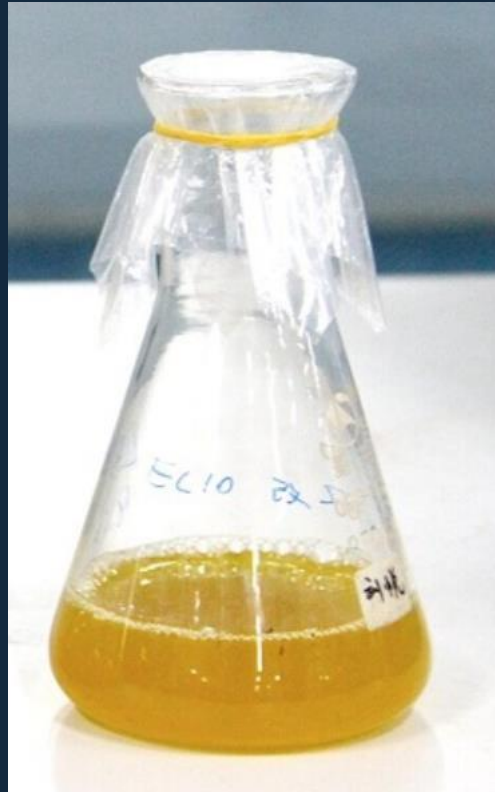
# Results



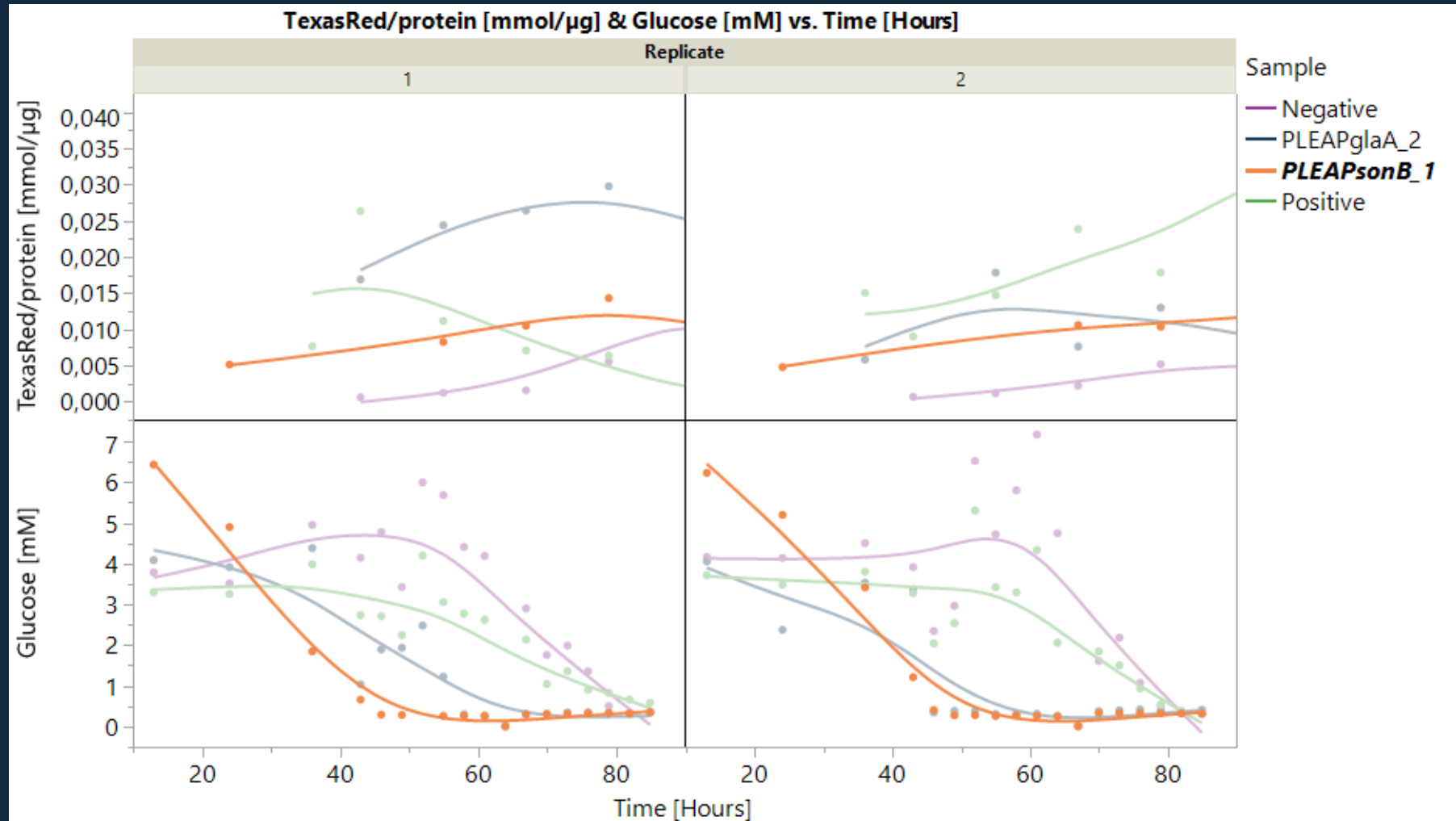
# Results: Biolector (1.5 mL)



# Results: Shake-flasks (200 mL)

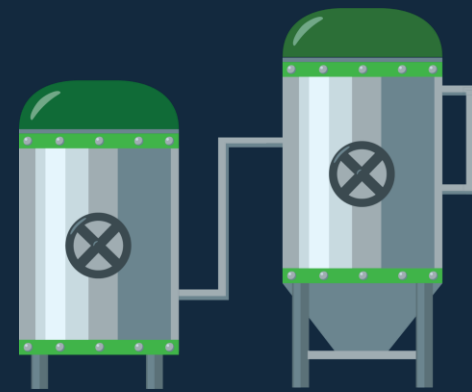
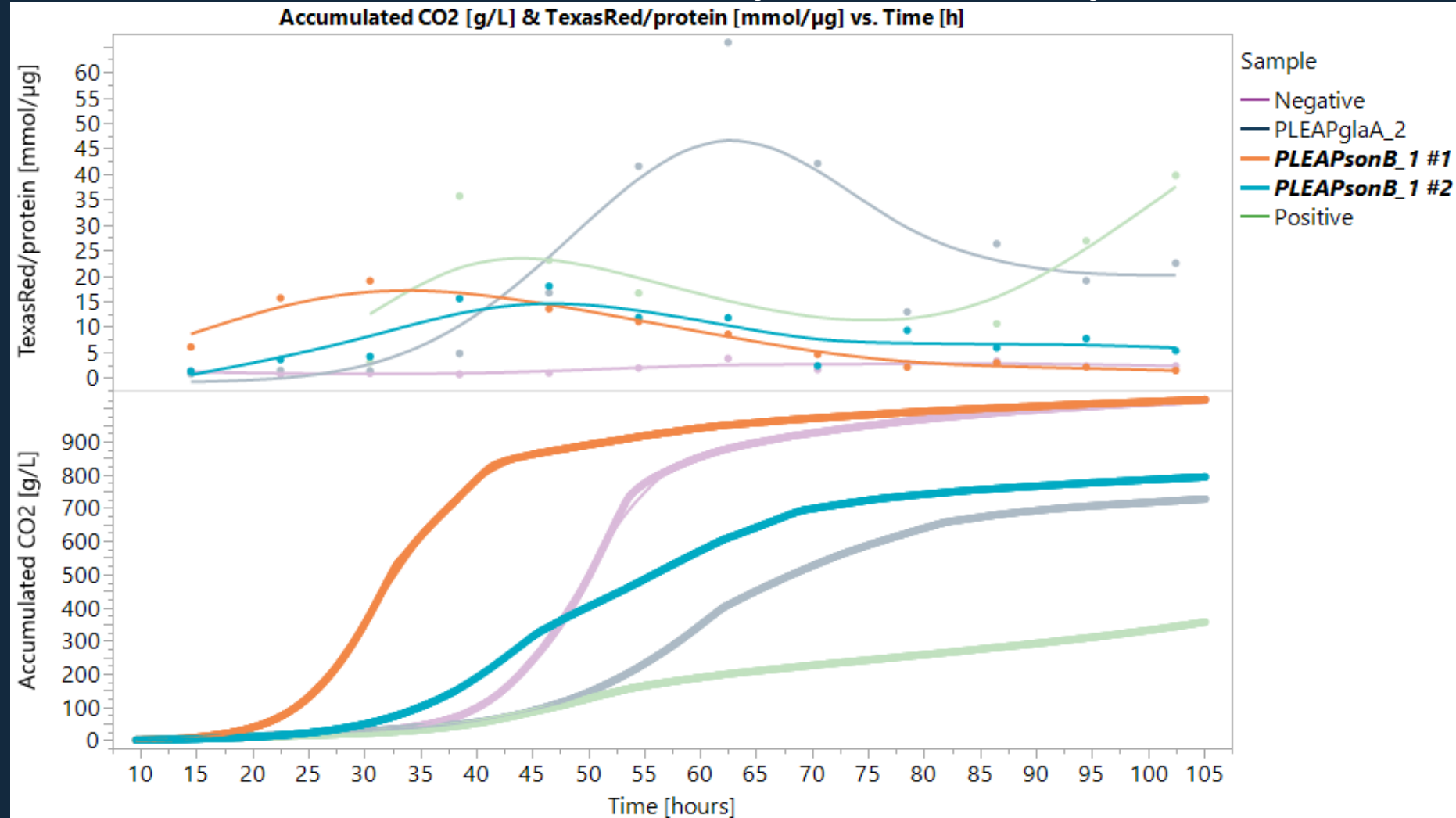


# Results: Shake-flasks (200 mL)

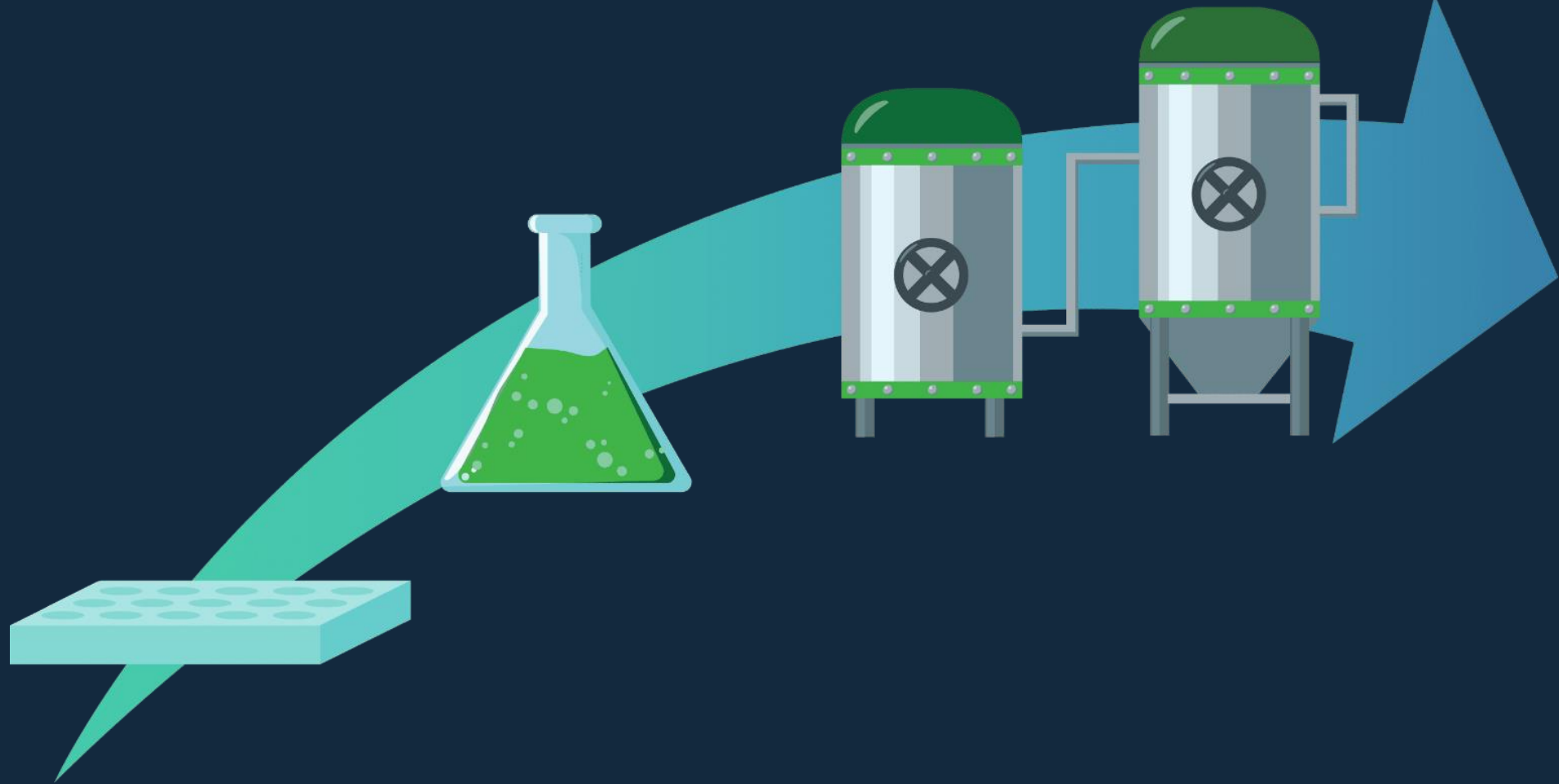




# Results: Bioreactor (1000 mL)



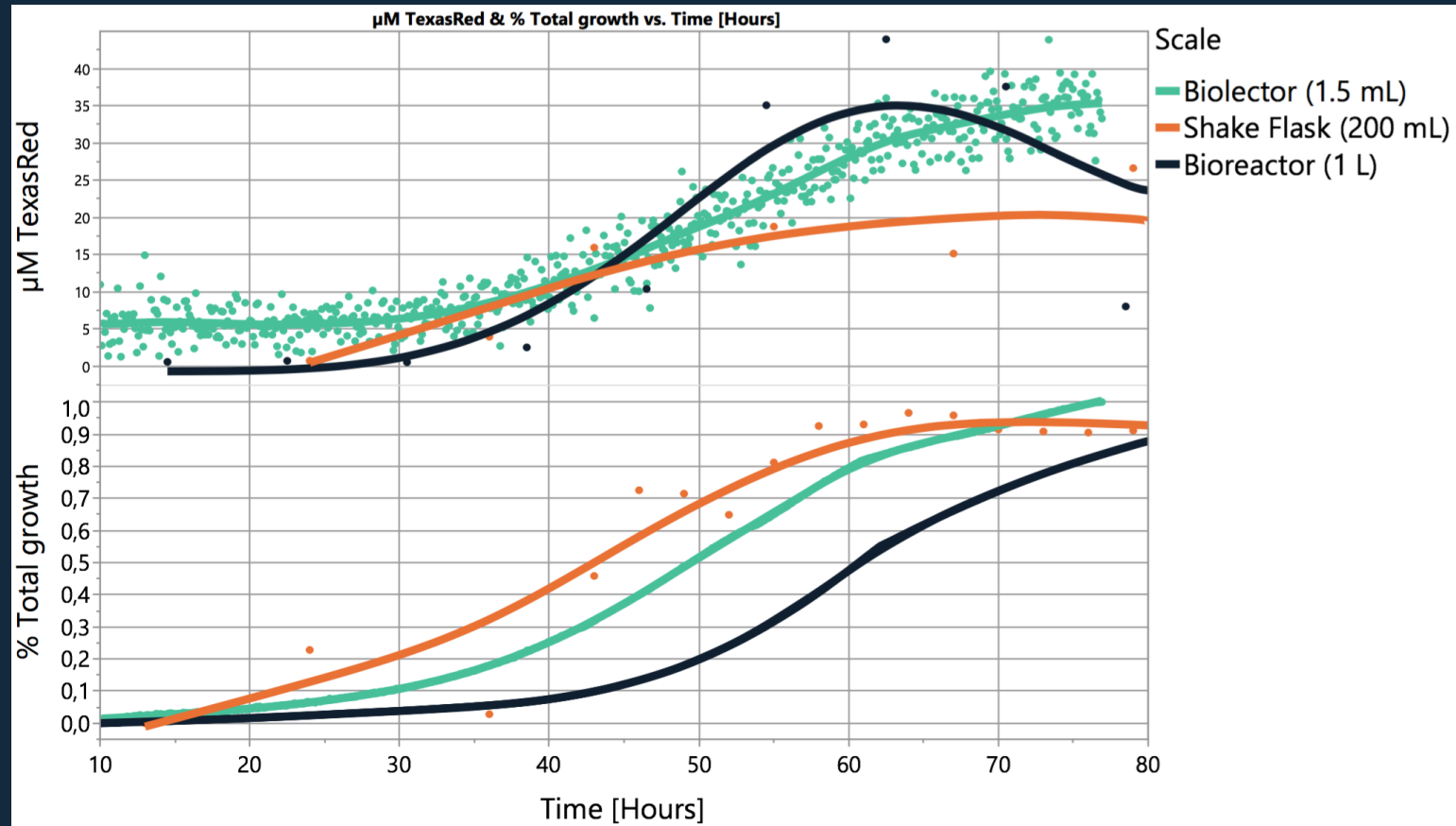
# Demonstrate





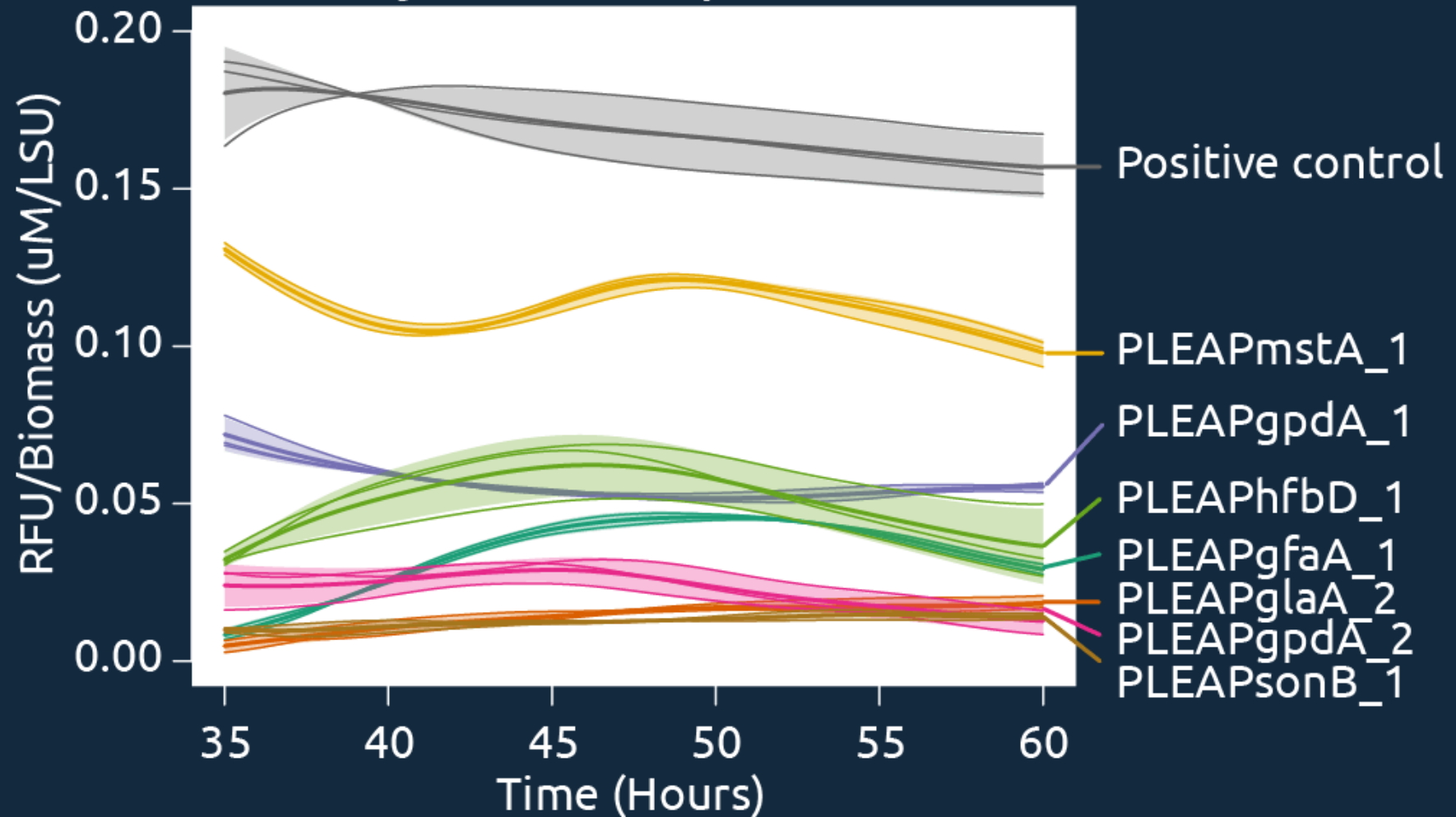
# Demonstrate: Scalability

PLEAPglaA\_2

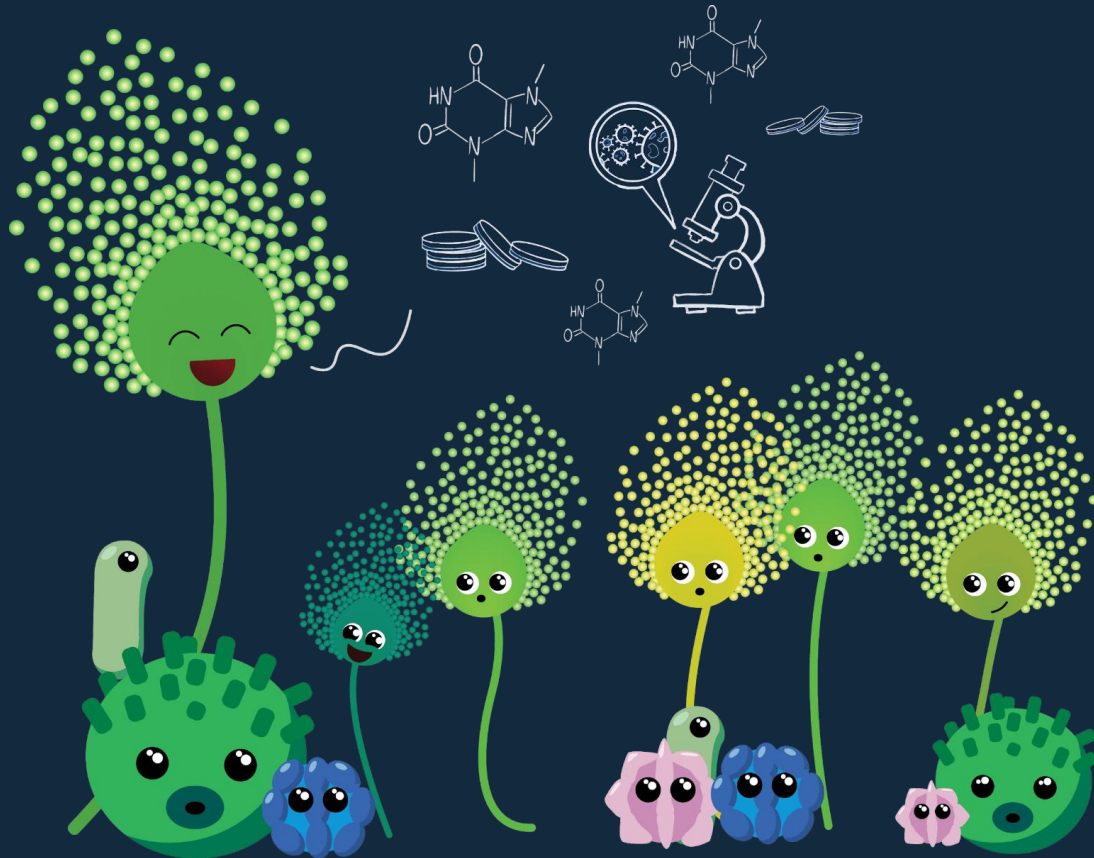


# Demonstrate: Ladder (1.5 mL)

Adjusted RFU/Biomass



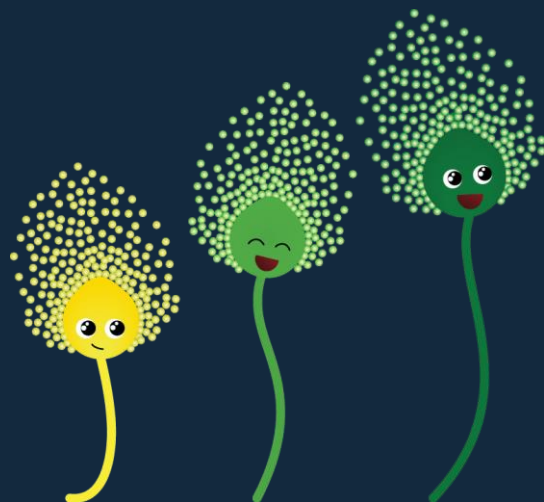
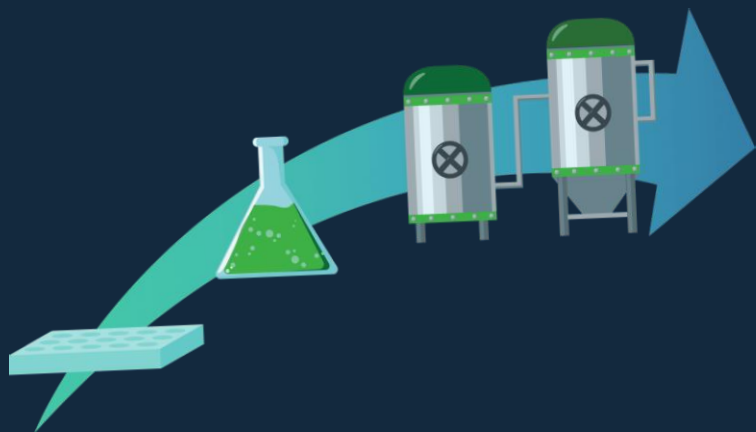
# Education



# Summary



# Summary





# You can do this too!

The image is a composite of three main elements:

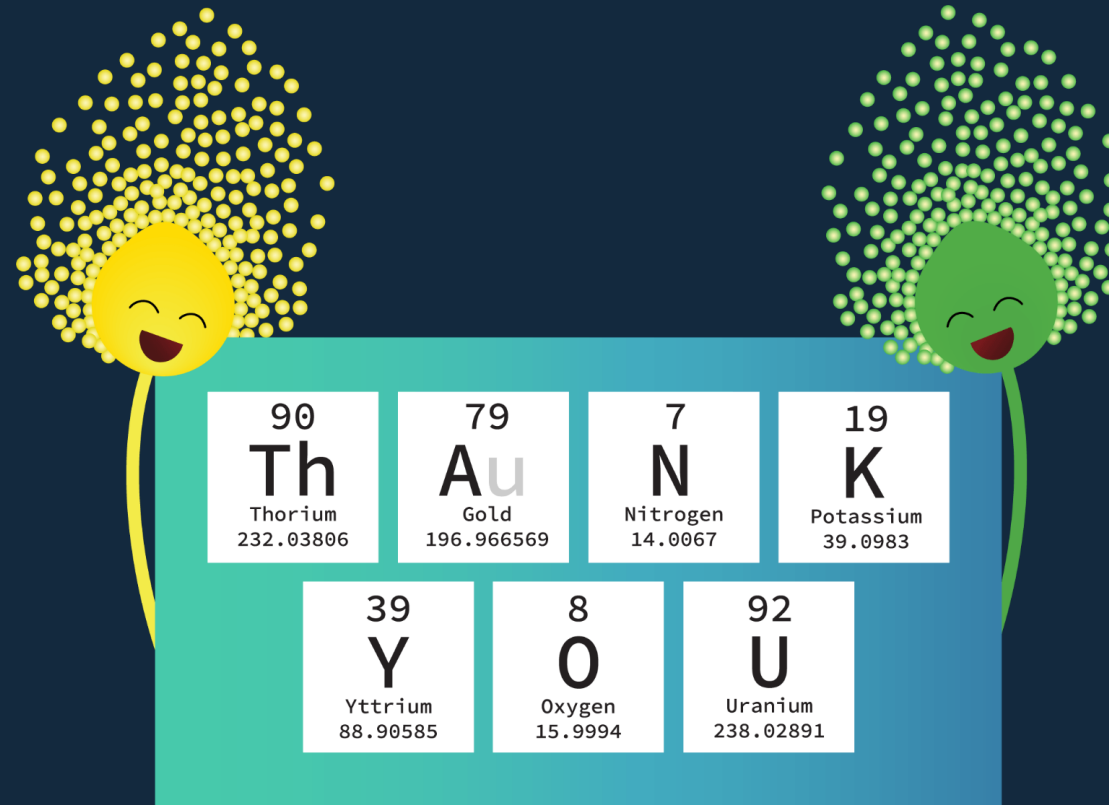
- MycoCosm Web Interface:** A screenshot of the MycoCosm website (mycosm.jgi.doe.gov) showing a hierarchical tree of fungal groups. The tree starts with 'Fungi' at the base, branching into 'Mucoromycota', 'Zoopagomycota', 'Chytridiomycota', 'Dikarya', 'Basidiomycota', and 'Ascomycota'. Each of these further branches into more specific orders and families, such as 'Agaricomycotina', 'Pezizomycotina', 'Eurotiomycetes', etc.
- Python Script:** A screenshot of a terminal window showing a Python script. The script takes command-line arguments for a template genome file, a locus ORF id, and the number of noisy samples. It uses the `sys` module for arguments and `os` for file operations. It checks if the template genome exists and creates a directory for the output if it doesn't.
- BioBuilders Logo:** A purple circular logo with the text 'DTU BioBuilders' and a DNA double helix icon.

# Thank you



*A small step for man, a giant LEAP for iGEM*

# Thank you



*A small step for man, a giant LEAP for iGEM*