



***Phytophthora megakarya Stress response
changes in the Theobroma cacao
transcriptomes analyzed using RNAseq.***

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Phytophthora pod rot (Black pod) = Worldspread disease

- 4 species:
- *P. palmivora* (less aggressive),
- *P. megakarya* (most aggressive)
- *P. capsici*, *P. citrophthora*.



Estimating losses due to *Phytophthora* sp.

P. palmivora (15%),

P. megakarya (80%),



Control of the disease

- Chemical
- **Genetic**
- Integrative




Partial resistance to *Phytophthora* in the germplasm collection

Objective

Analyze changes expressed genes:

- **Genes early expressed**
- **Constantly expressed**
- **Genes of known fonctions**


Plant material



UPA 409	3.22	a
GS 29	3.17	a
ICS 89	3.07	a
R15 POS	3.01	a b
NA 32	2.87	a b c
IFC 5	2.85	a b c
IMC 78	2.82	a b c
UF 676	2.81	a b c d
IFC 304	2.79	a b c d
UPA 134	2.76	a b c d
IFC 303	2.71	a b c d
SNK12	2.64	a b c d e f
IMC 6	2.58	a b c d e f
ICS 6	2.58	a b c d e f

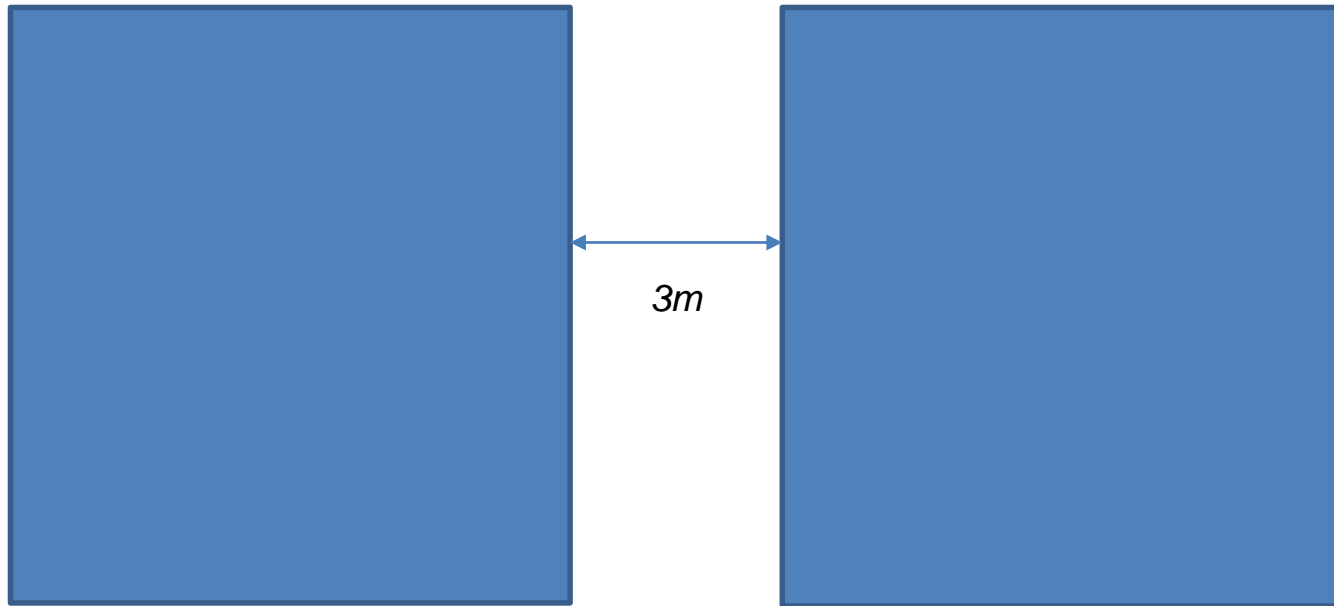
susceptible

ICS 95	1.82	g h i j k l
IFC 371	1.82	h i j k l
T 60/887	1.76	h i j k l
ICS 84	1.75	i j k l
PA 150	1.73	j k l
P 7	1.72	k l
T 79/501	1.70	k l
MO 98	1.70	k l
P 19 A	1.64	k l
IMC 57	1.62	k l
SCA 6	1.19	l



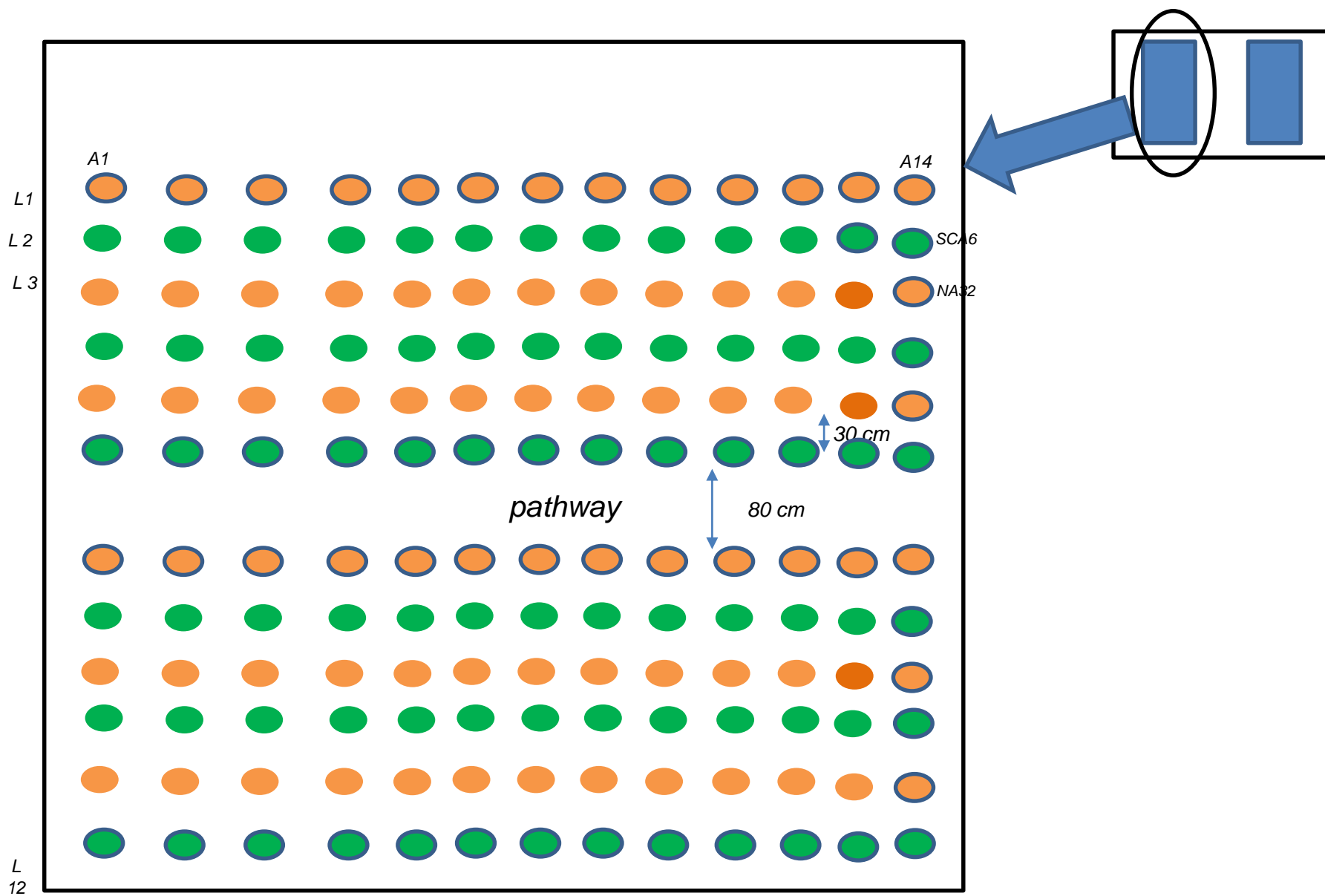
Resistants

***Experimental design in
shade-net house***



Control

Treatment

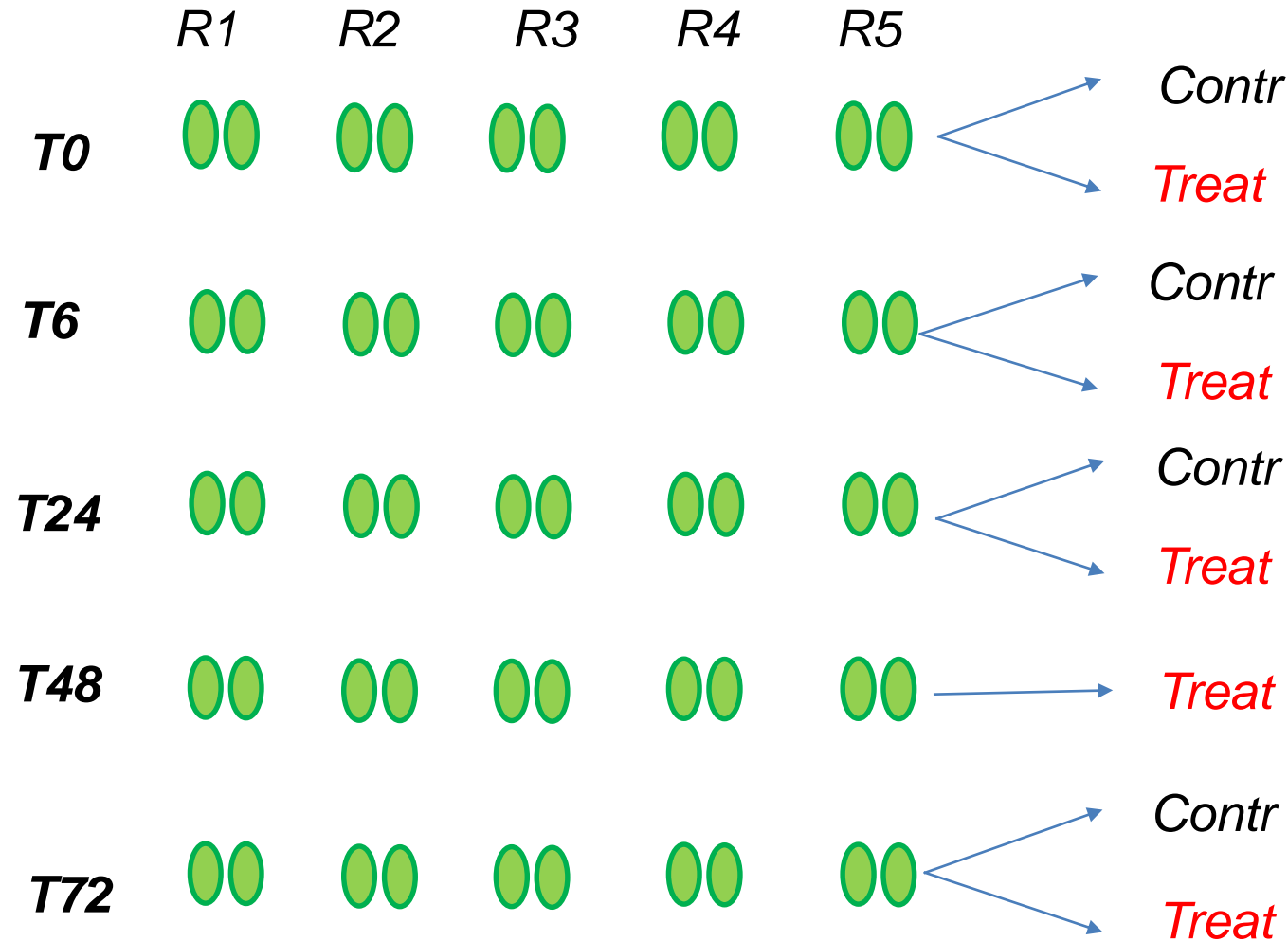


Design of a single bloc: 30 x 30 cm

Treatments



Sampling



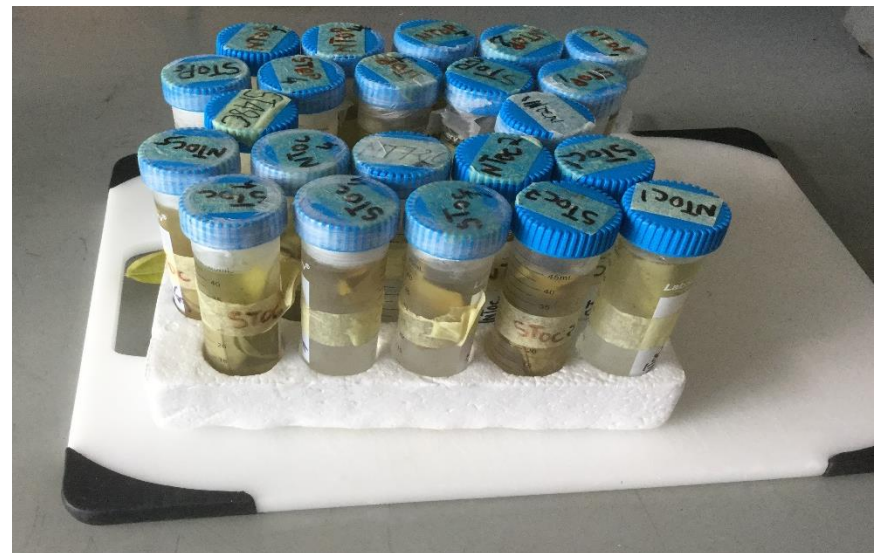
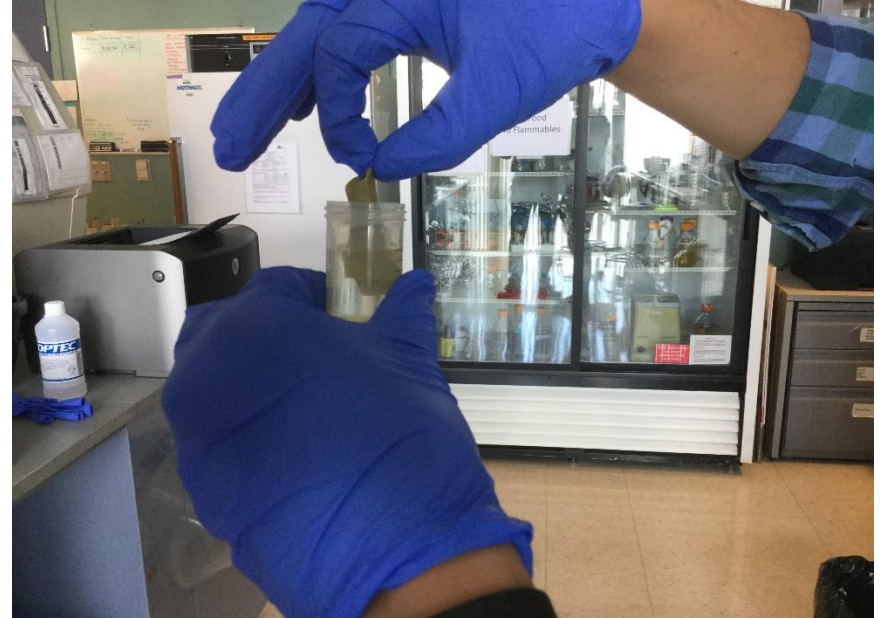
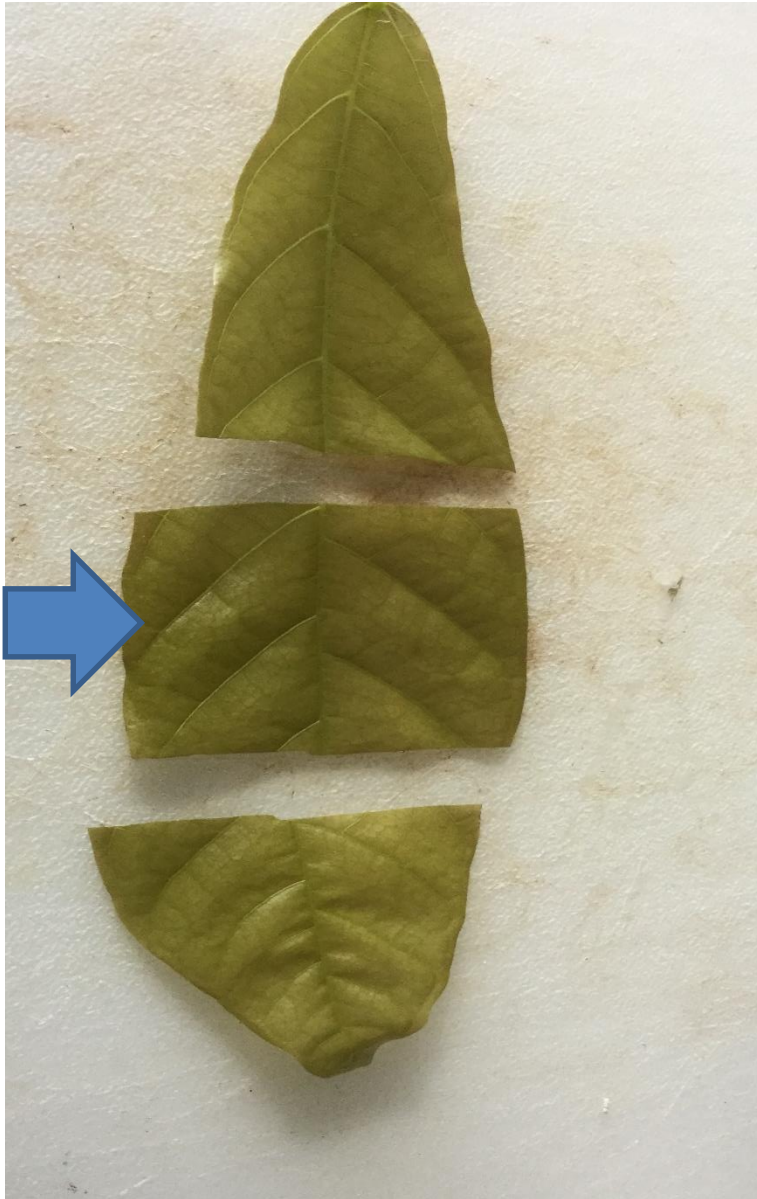
SCA6 / NA 32

Contr = dH₂O

Treat = zoospores

3×10^5 spores / ml

Sample packaging



Symptoms checking (120 Hrs)

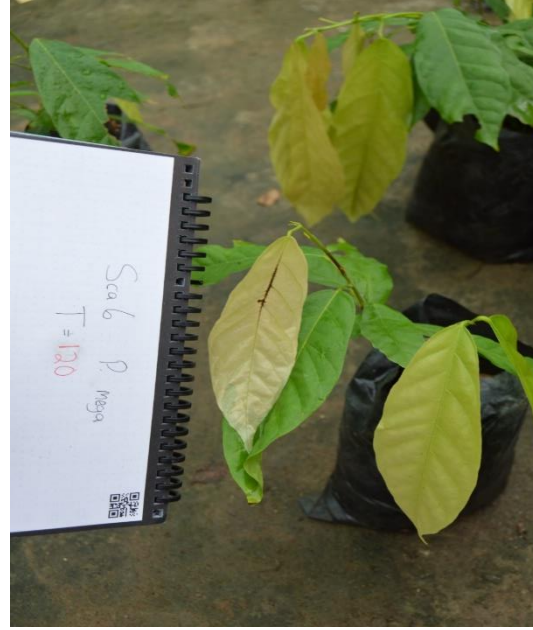
Control NA32



Control SCA6



Infected NA32



Infected SCA6

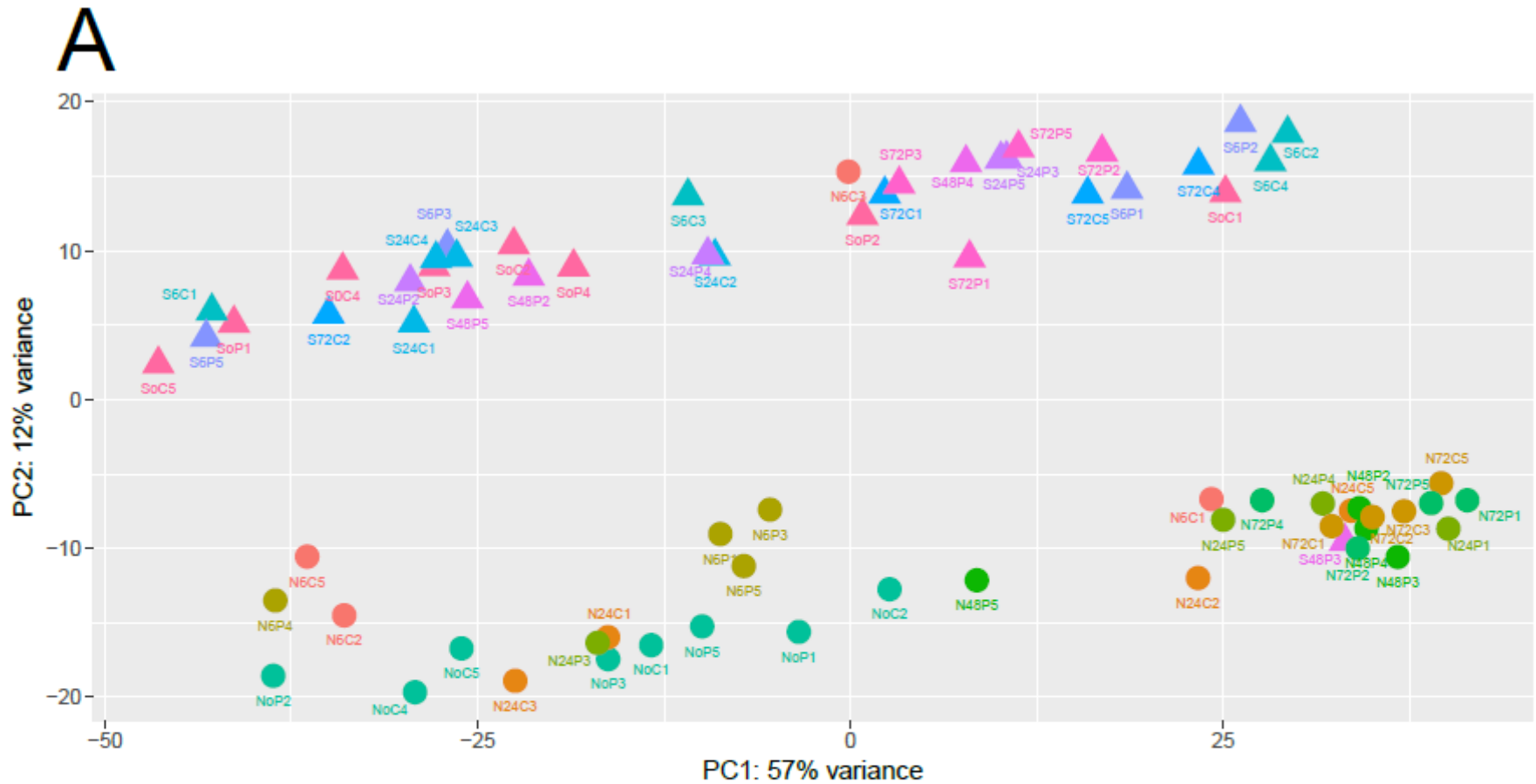
Sequencing

**1. Sequencing by Illumina
Hiseq 2500 (rapid run
mode of 100 nt / single
read)**

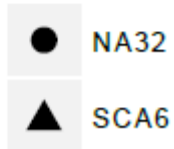
**3. Five(5) technical
replicates of Four (4)
millions reads each**



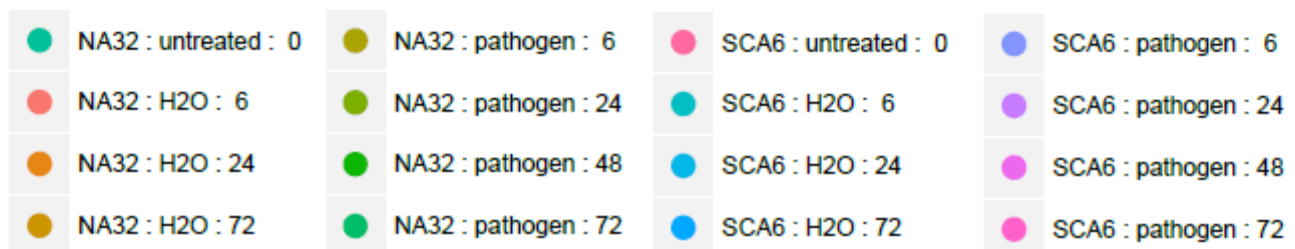
Principal Component Analysis (PCA)



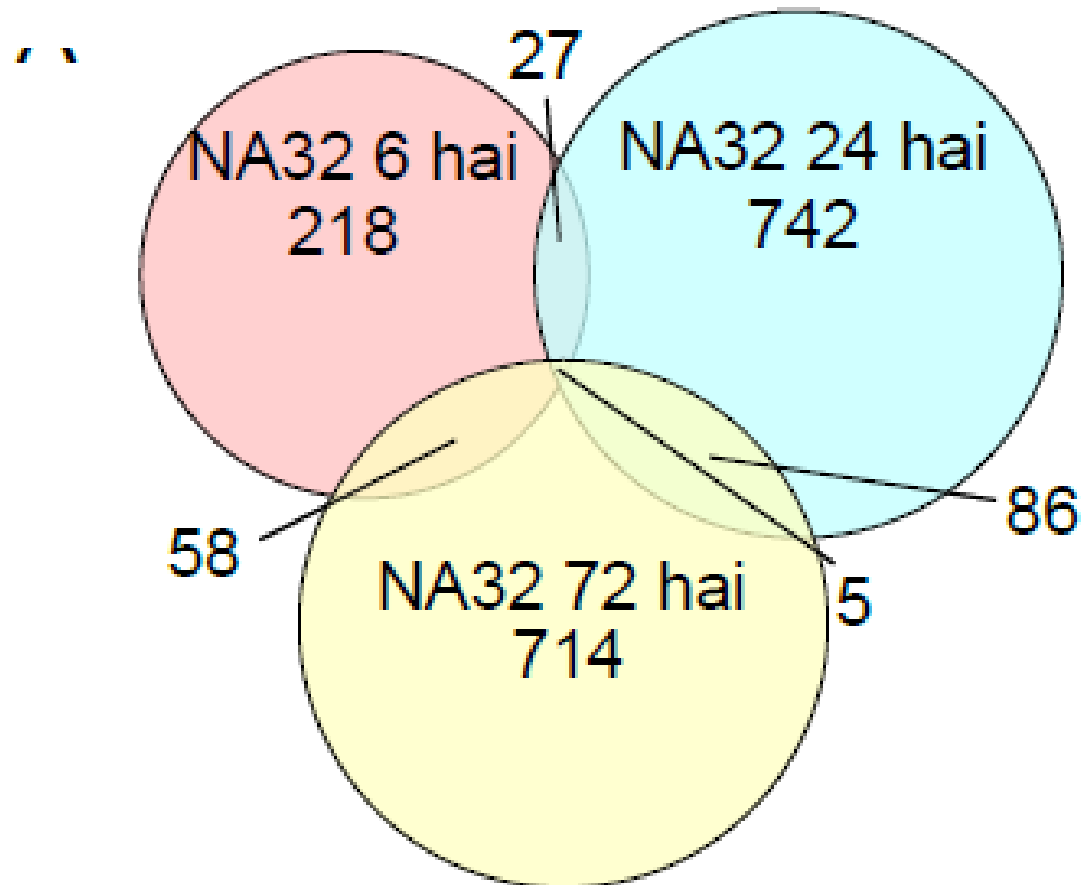
genotype



group

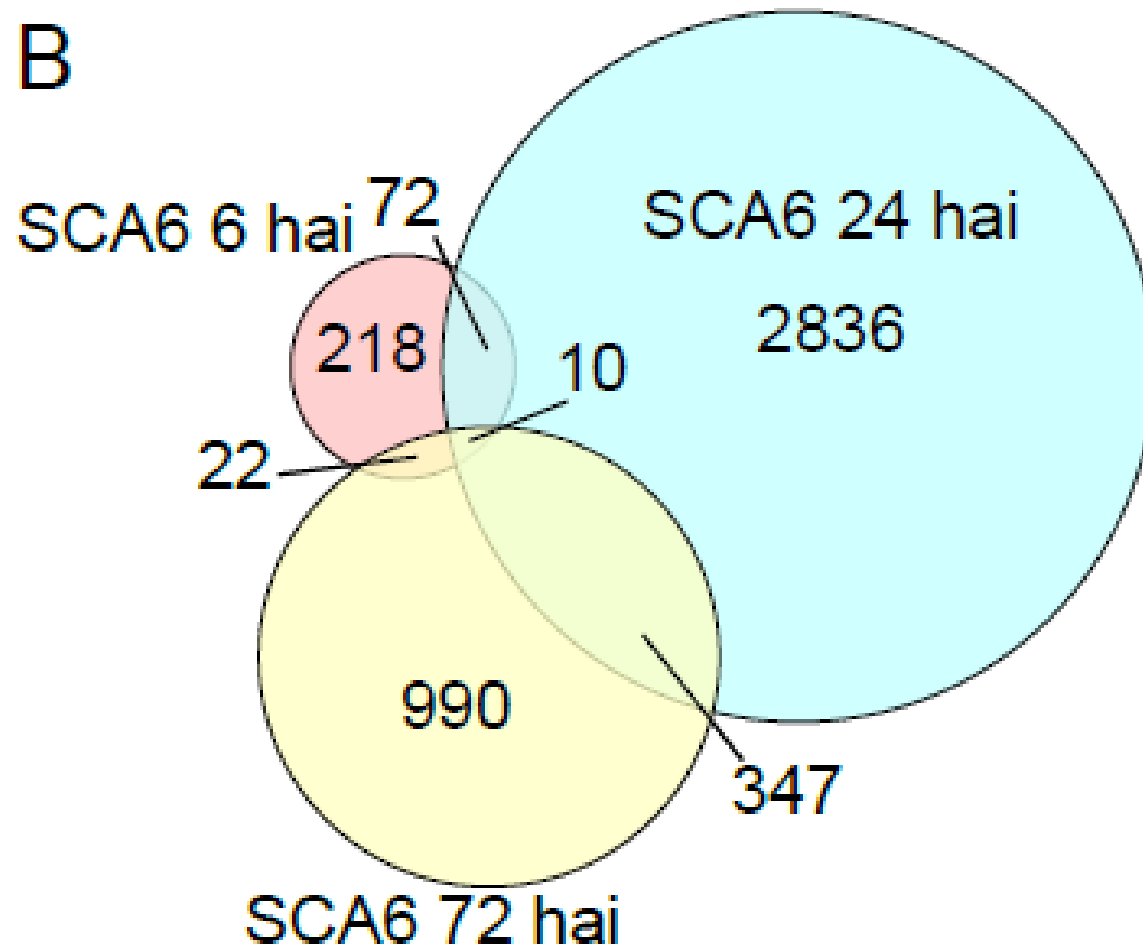


Differentially expressed genes in time points: NA32

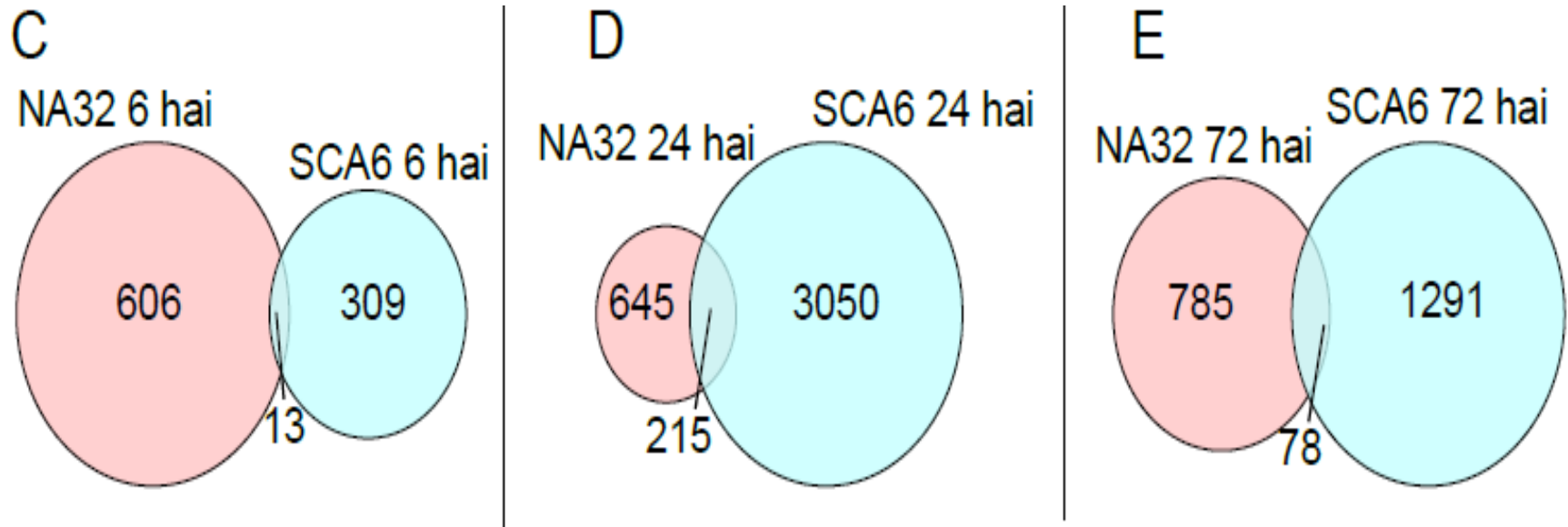


Differentially expressed genes in time points: SCA 6

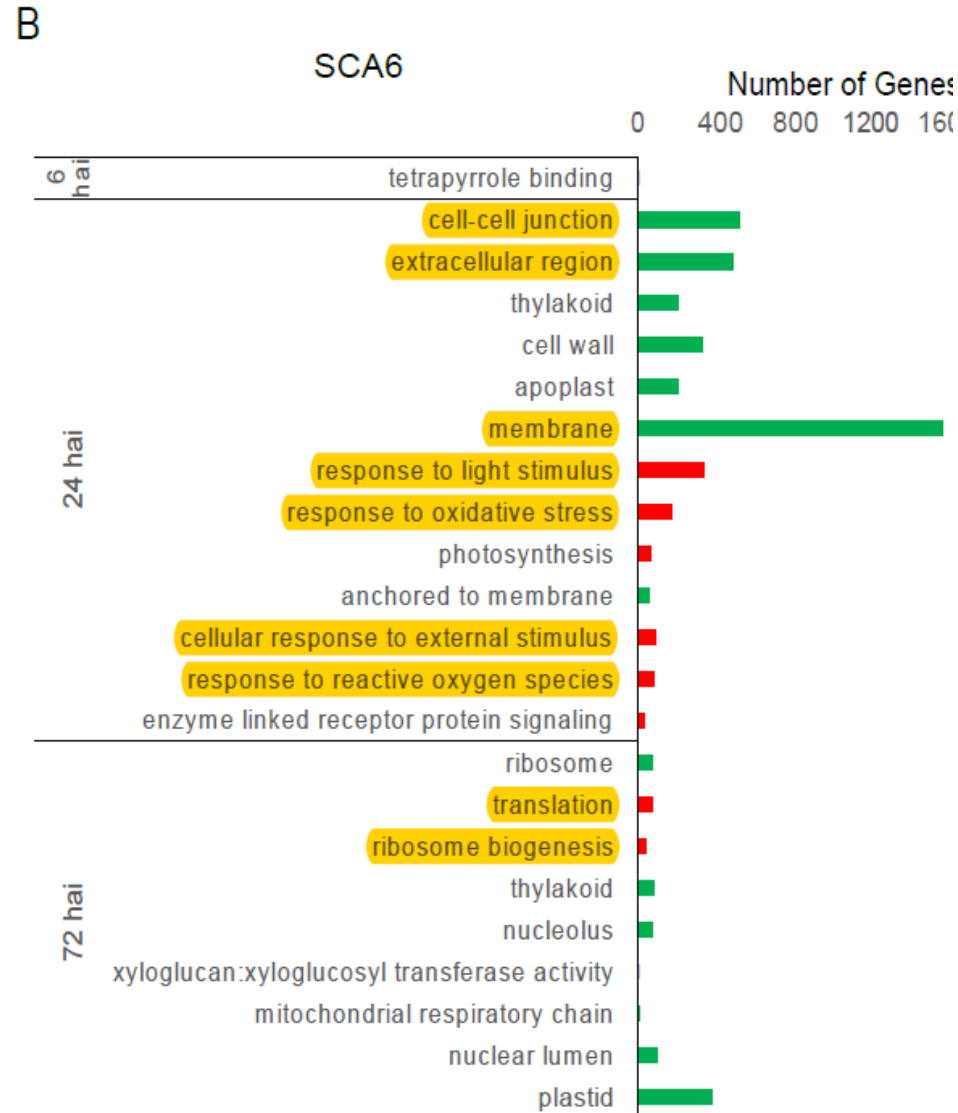
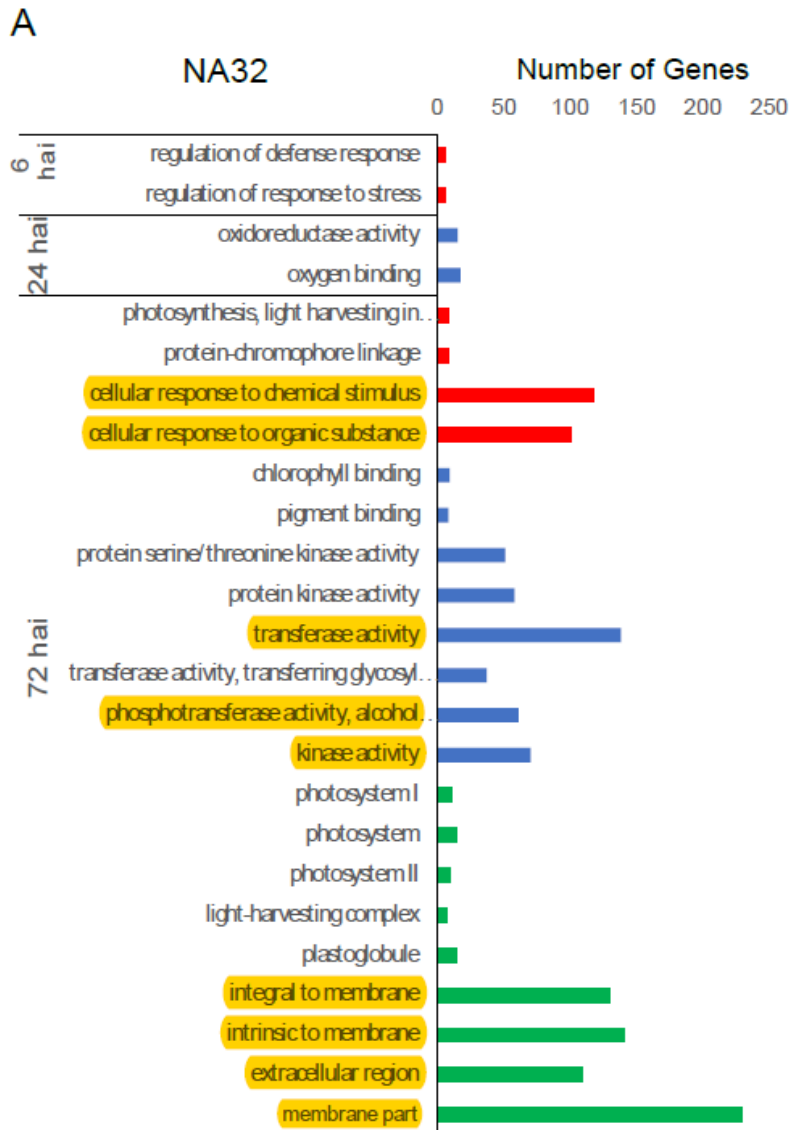
B



Differentially expressed genes between genotypes



GO analysis



Next Steps

- 1. Focus on genes differentially expressed in the principal component 2.*
- 2. Identify common genes across time points*
- 3. Locate these genes on the chromosome*
- 4. validate by qPCR genes inside QTLs*

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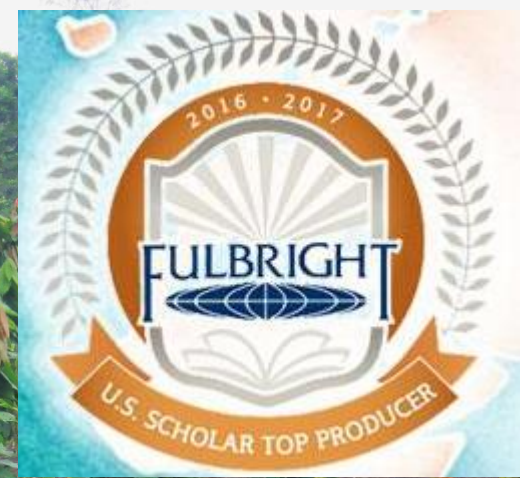
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Thank you