



Mechanisms of resistance to indaziflam in *Poa annua*

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INTRODUCTION

Poa annua (annual bluegrass)

- Grassy weed
- Difficult to control
- Cosmopolitan
- Tetraploid



Image 1: *Poa annua*

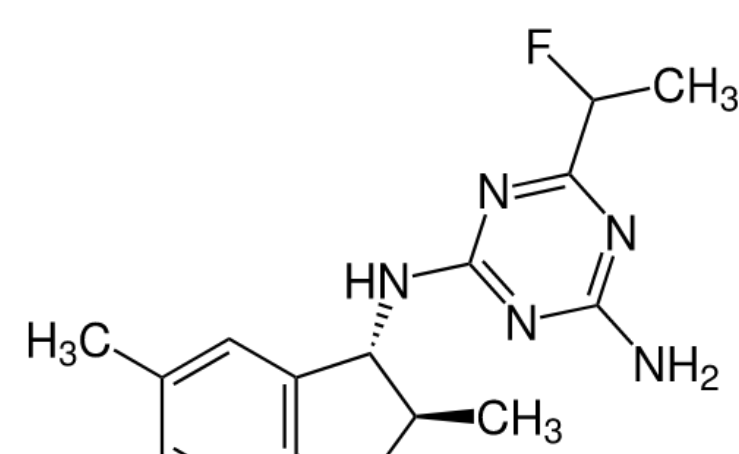


Image 2: The chemical structure of indaziflam

Indaziflam

- Broad-spectrum, pre-emergence herbicide
- Classified as a cellulose biosynthesis inhibitor

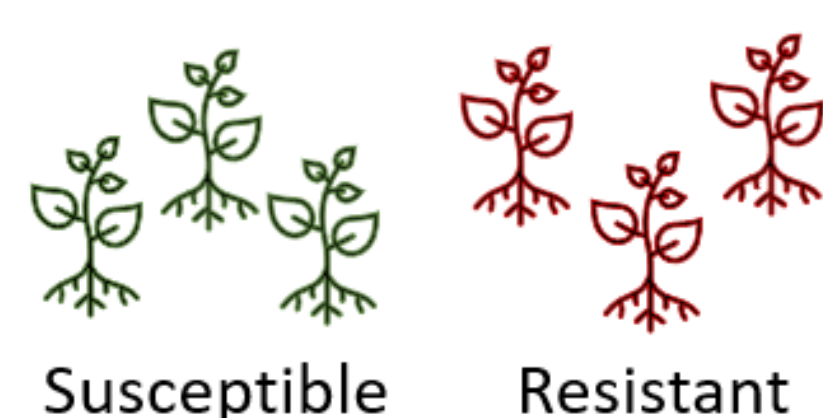
Some populations of *P. annua* have developed resistance to indaziflam

OBJECTIVES

- Identify genes that may be involved in the resistance to indaziflam in *P. annua*
 - Hypothesis: Genes responsible for resistance will be expressed differently in resistant than susceptible populations
- Identify possible target proteins of indaziflam to better understand its mechanism of action
 - Hypothesis: The protein that indaziflam binds to most favorably is likely its target site

METHODS

RNA-Seq Analysis



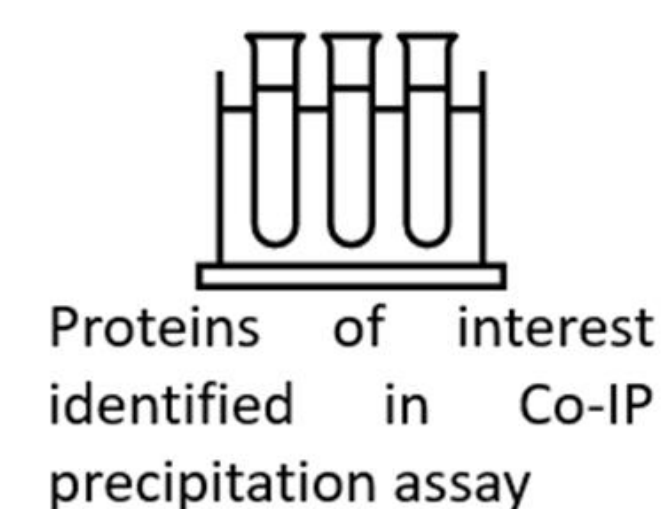
Illumina Sequencing

Align to transcriptome from genome assembly

Count # of reads per gene
Analyze differential expression

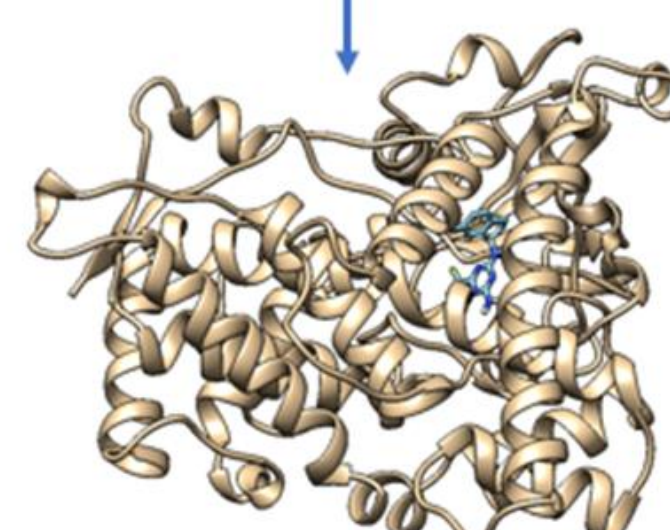
Assign gene functions based on genome annotation

Molecular Docking



Arabidopsis thaliana protein sequence

Protein refolding



QVina-W Molecular Docking

RESULTS

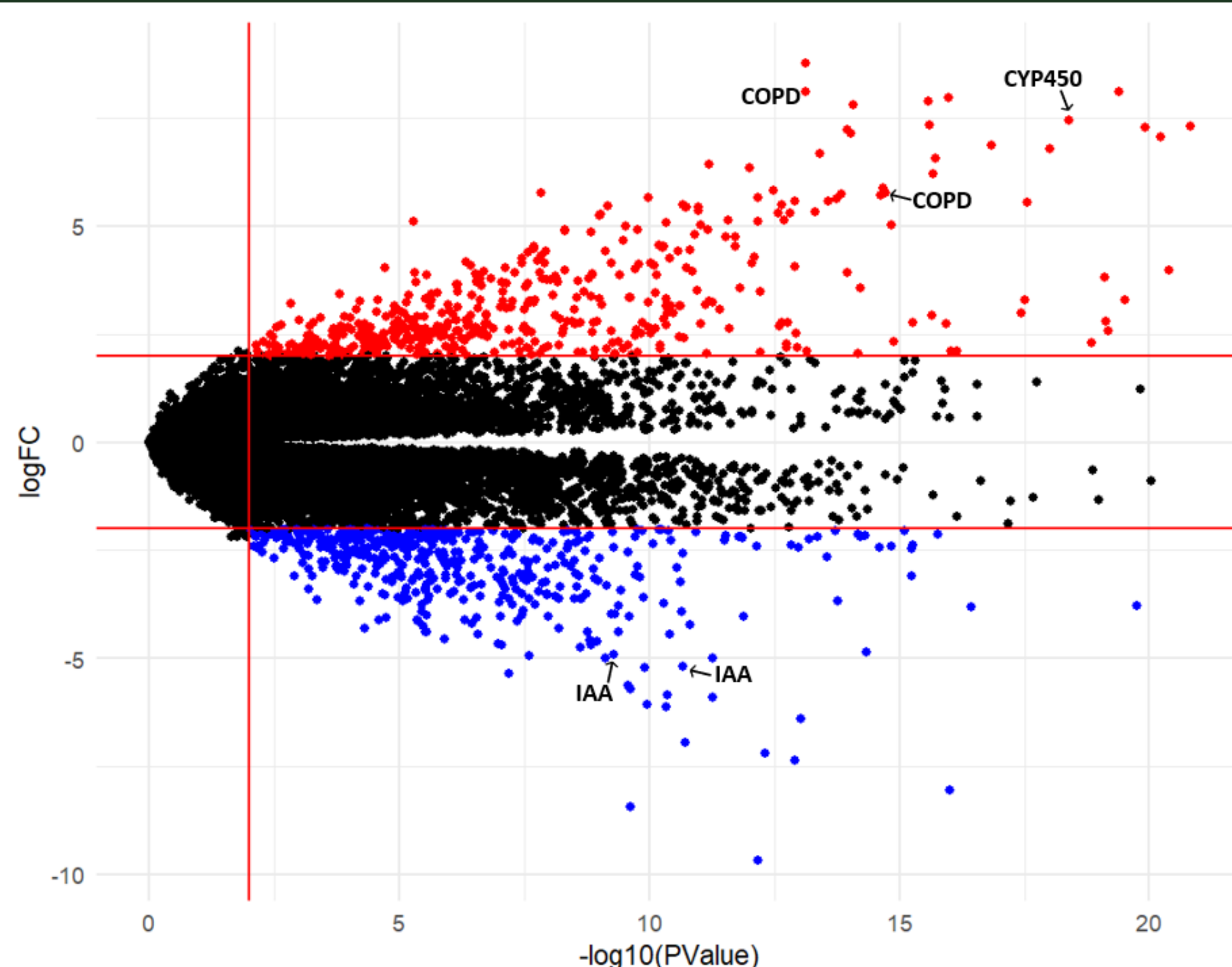


Figure 1: Volcano plot of differentially expressed genes in resistant and susceptible populations

Predicted Function	Expression
Coatomer subunit delta (COPD)	Over
Protein kinase	Under
Cytochrome P450 (CYP450)	Over
F-box-like domain superfamily	Under
Ammonium transmembrane transporter	Over
Zinc finger CCHC-type	Under
Protein FAR1-related sequence 5-like	Over
UDP-glycosyltransferase	Over
Auxin-responsive protein IAA9-like (IAA)	Under
Acetyltransferase	Over
Xyloglucan endotransglucosylase/hydrolase	Over

Table 1: Predicted function and expression of differentially expressed genes

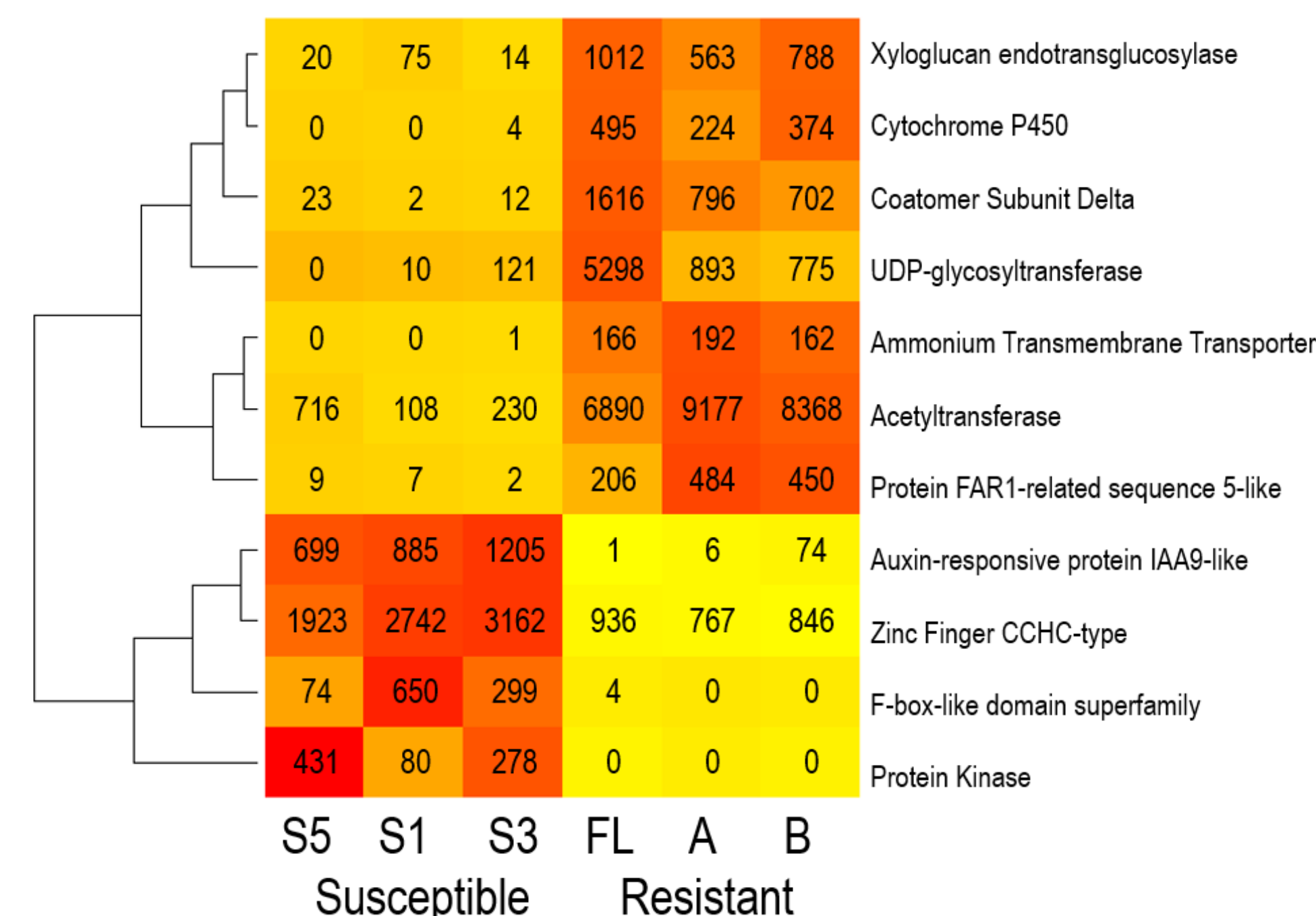


Figure 2: Heat map of differentially expressed genes between resistant and susceptible populations with raw data counts

RESULTS

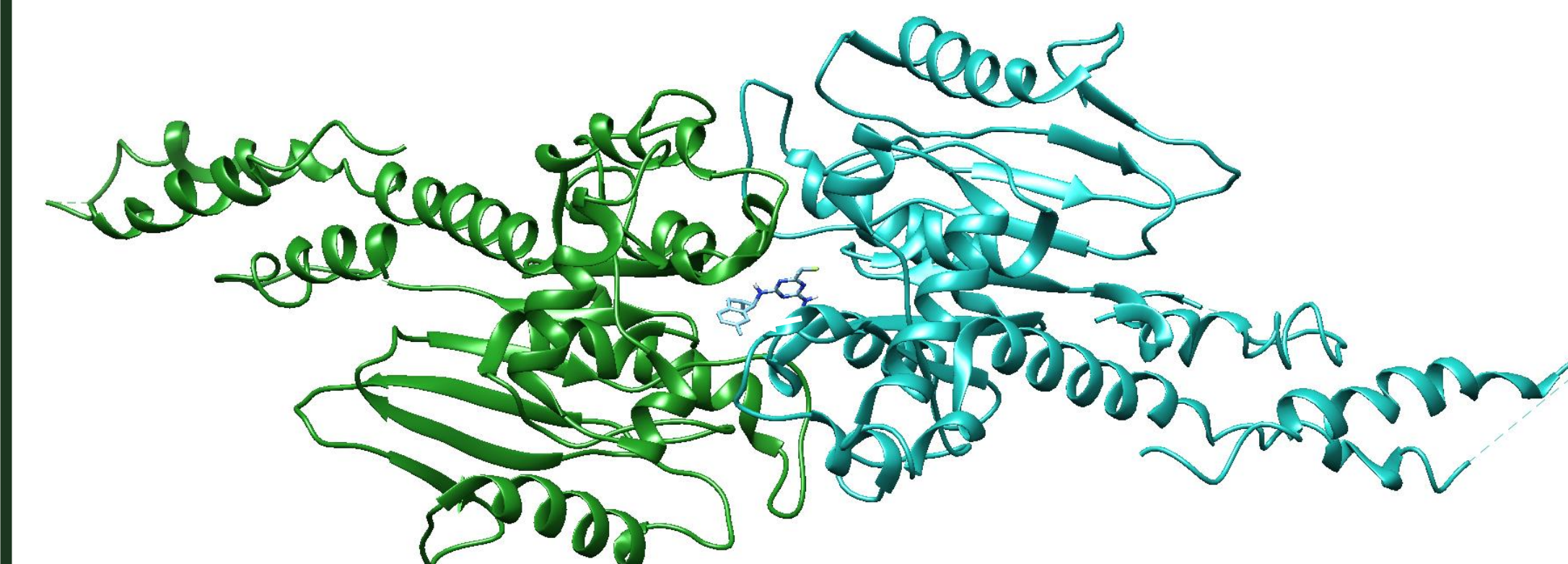


Figure 3: Indaziflam bound to dynamin related protein

Receptor	Indaziflam Binding Free Energy (kcal/mol)
Dynamin related protein	-9.4
Coatomer subunit gamma	-9.1
Cytochrome P450	-8.9
Coatomer subunit alpha	-8.3
Clathrin heavy chain 1	-7.9
Zinc finger	-7.6
Coatomer subunit beta	-7.4
Exocyst complex component 5	-7.3
Root hair defective 3	-7.2
Coatomer subunit delta	-6.5

Table 2: Qvina-W binding free energies of ten possible protein targets of indaziflam

CONCLUSIONS

- Coatomer subunit delta and cytochrome P450, among other genes, are potential sources of resistance to indaziflam in *P. annua*
- Dynamin related protein, coatomer subunit gamma, and cytochrome P450 are potential targets of indaziflam

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INTERNATIONAL WEED GENOMICS CONSORTIUM