



# An atlas of the genomes of *Phytophthora infestans*

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## Introduction

The causative agent of the Irish Potato Famine, *Phytophthora infestans*, continues to cost billions of dollars in mitigation and crop loss, annually. Late blight of potato and tomato, therefore, play an important role in world food security. To date, 26 genomes of this pathogen have been sequenced. Lineages US-8 and US-22 have been characterized as having resistance to the commonly used fungicide metalaxyl. The mode of action for metalaxyl has been reported to include transcription, such that RNA polymerases, and their associated proteins, have been promoted as candidate loci. We present a genome-wide survey of markers which bioinformatically differentiate these fungicide resistant lineages from susceptible lineages and characterize whether these candidate loci contain polymorphisms which segregate in a manner which may confer resistance.

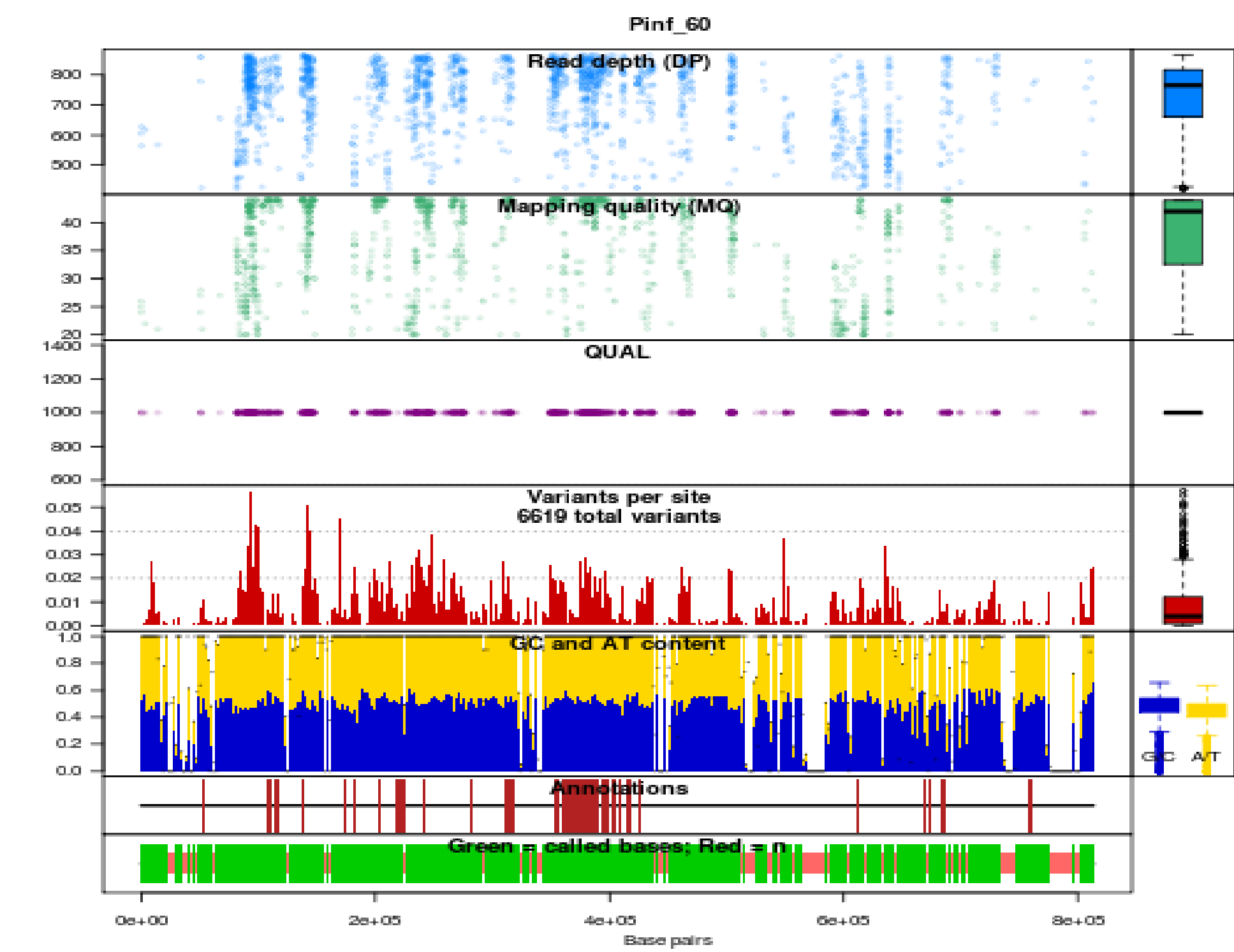
## Bioinformatic methods

- ▶ Sequence reads were acquired through publicly available archives as well as novel sequencing
- ▶ Reads were mapped to the T30-4 reference with bowtie2
- ▶ Variants were called using SAMtools
- ▶ Varients were post-processed with custom code

## Genome summaries

Missing  
Figure Barplot of RR, RA, AA.

## Visualization of Supercontig 60

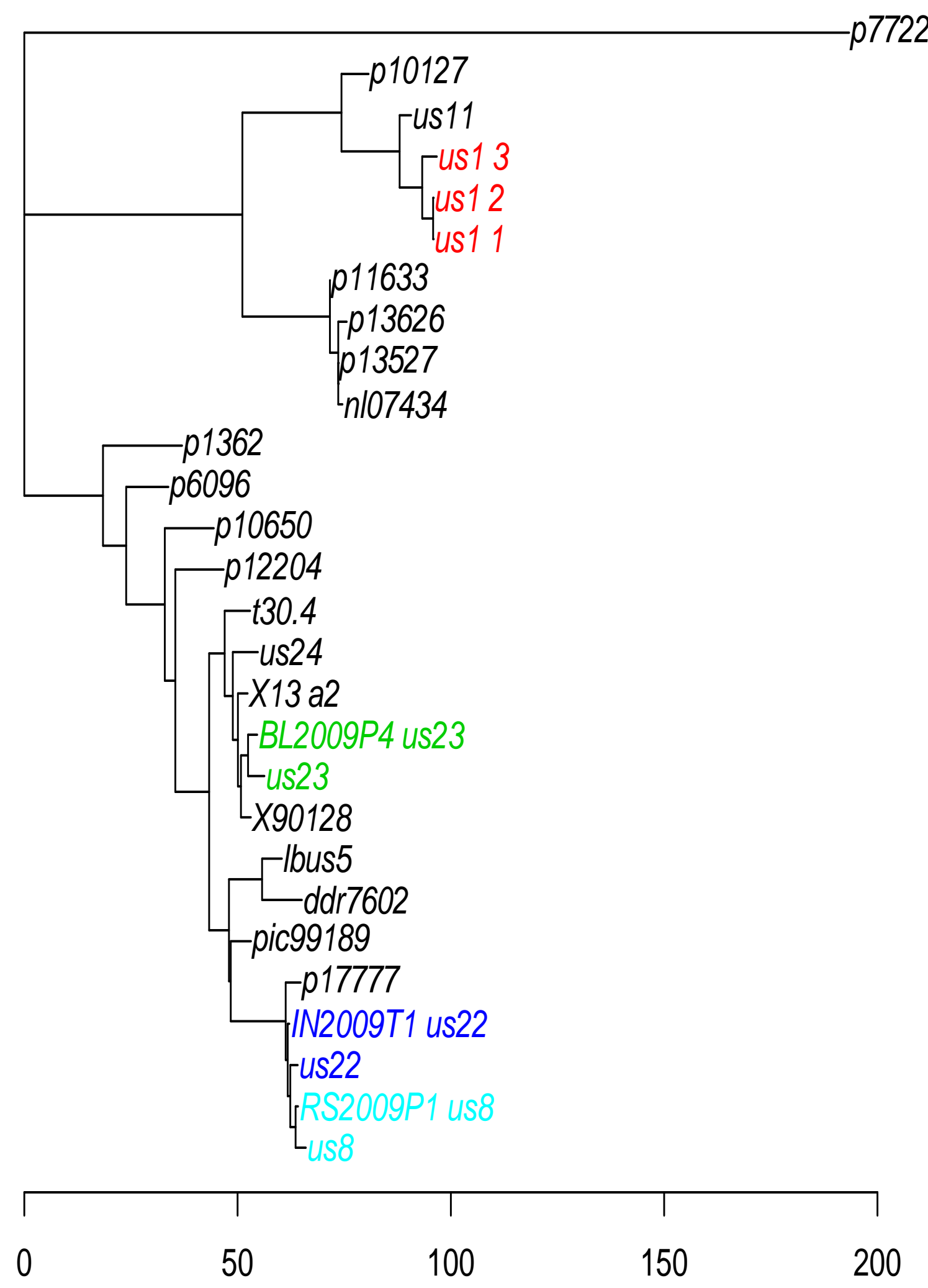


Describe the plot.

- ▶ Filtered on read depth
- ▶ Filtered on quality (QUAL)

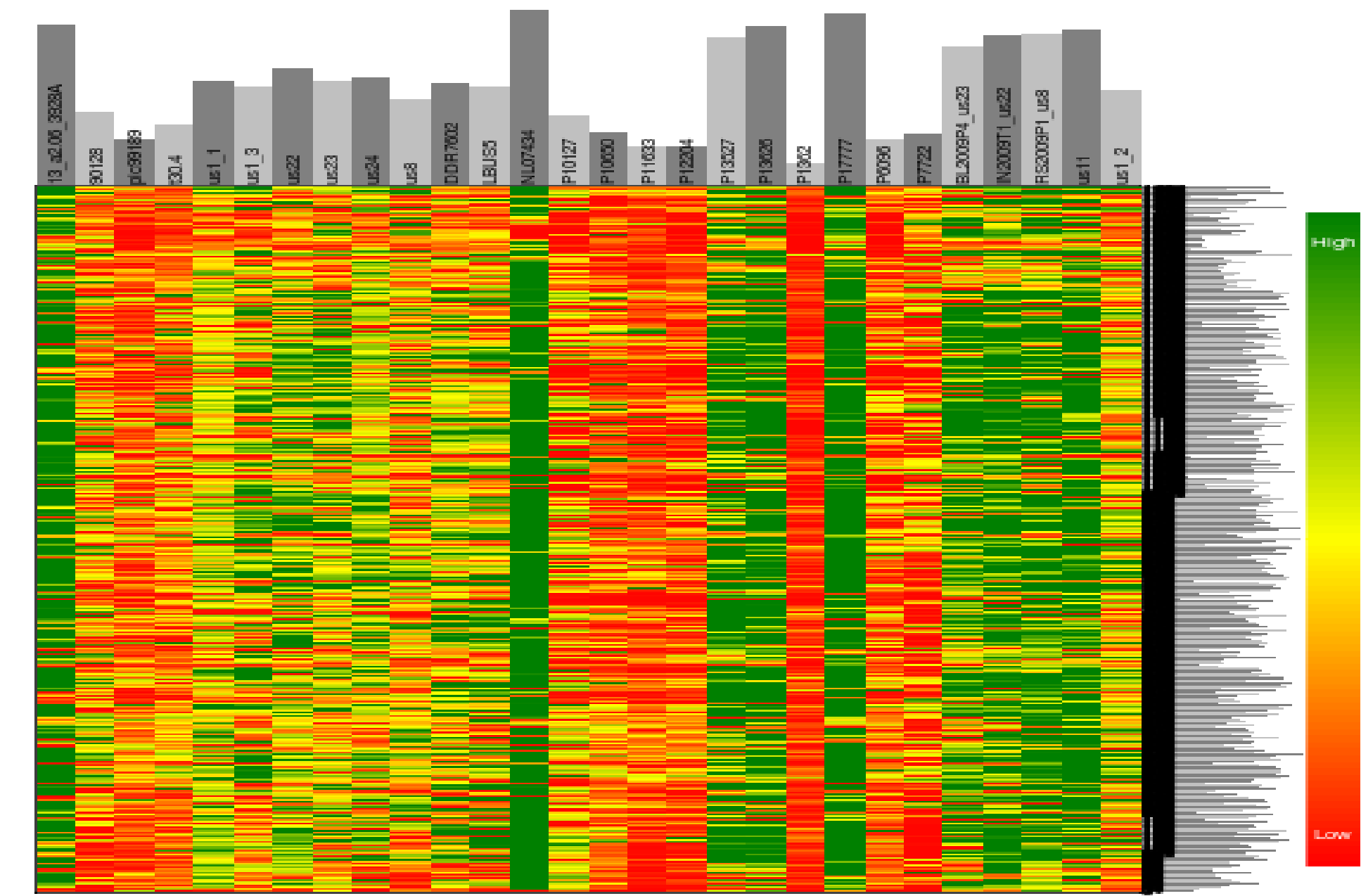
## Mitochondrial phylogeny of *Phytophthora infestans*

Neighbor-joining tree based on Euclidian distances to describe relationships within *Phytophthora infestans*.



- ▶ *P. mirabilis* (p7722) is the outgroup
- ▶ Lineage US-1 forms an independant clade (samples us1 1, us1 2 and us1 3 are the same lineage)
- ▶ Lineages US-8, US-22 and sample p17777 form a clade (assumedly all fungicide resistant)

## Genotypic quality for Supercontig 60



Summary of genotype qualities

- ▶ Most genotypes are of intermediate quality
- ▶ Only genotypes of  $\geq 100X$  coverage are of high quality (green)
- ▶ Most genotypes are of moderate quality

## Variants identifying fungicide resistant lineages (US-8 & US-22)

Supercontig	Position
Supercontig_1.NN	nnn
Supercontig_1.NN	nnn

## Discussion

Blah, blah and blah.

## Conclusions

- ▶ Lineages characterized as having fungicide resistance (US-8 and US-22) form a clade
- ▶ #N variants define this fungicide resistant clade
- ▶ Conclusion 3

## Acknowledgements

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