



An atlas for the genomes of *Phytophthora infestans*

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Abstract

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, plays 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.

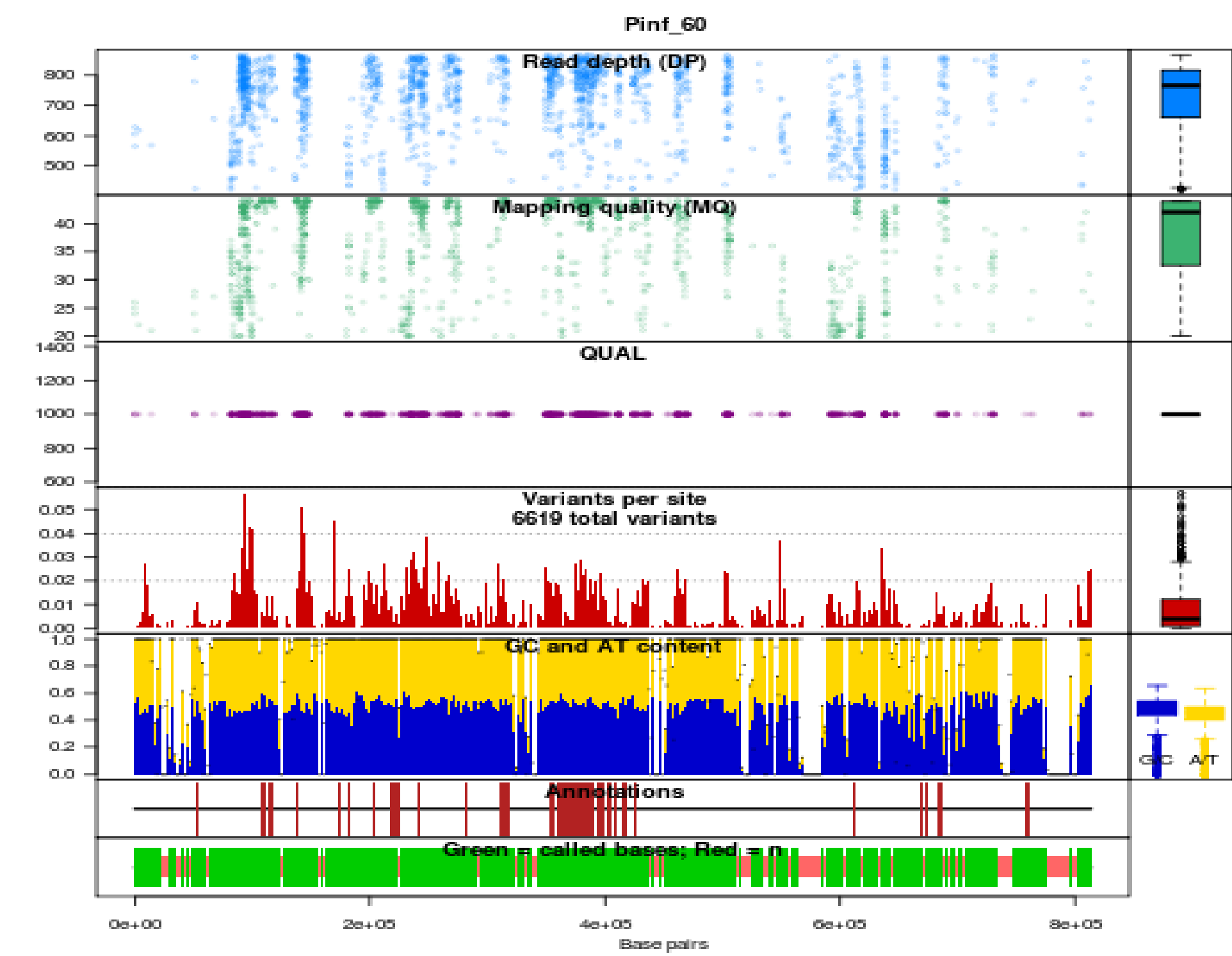
Bioinformatic methods

- ▶ Sequence reads (Illumina of various lengths and Roche 454) 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
- ▶ Variants were post-processed for quality and coverage with custom code

Genome summaries

Missing figure Barplot of RR, RA, AA.

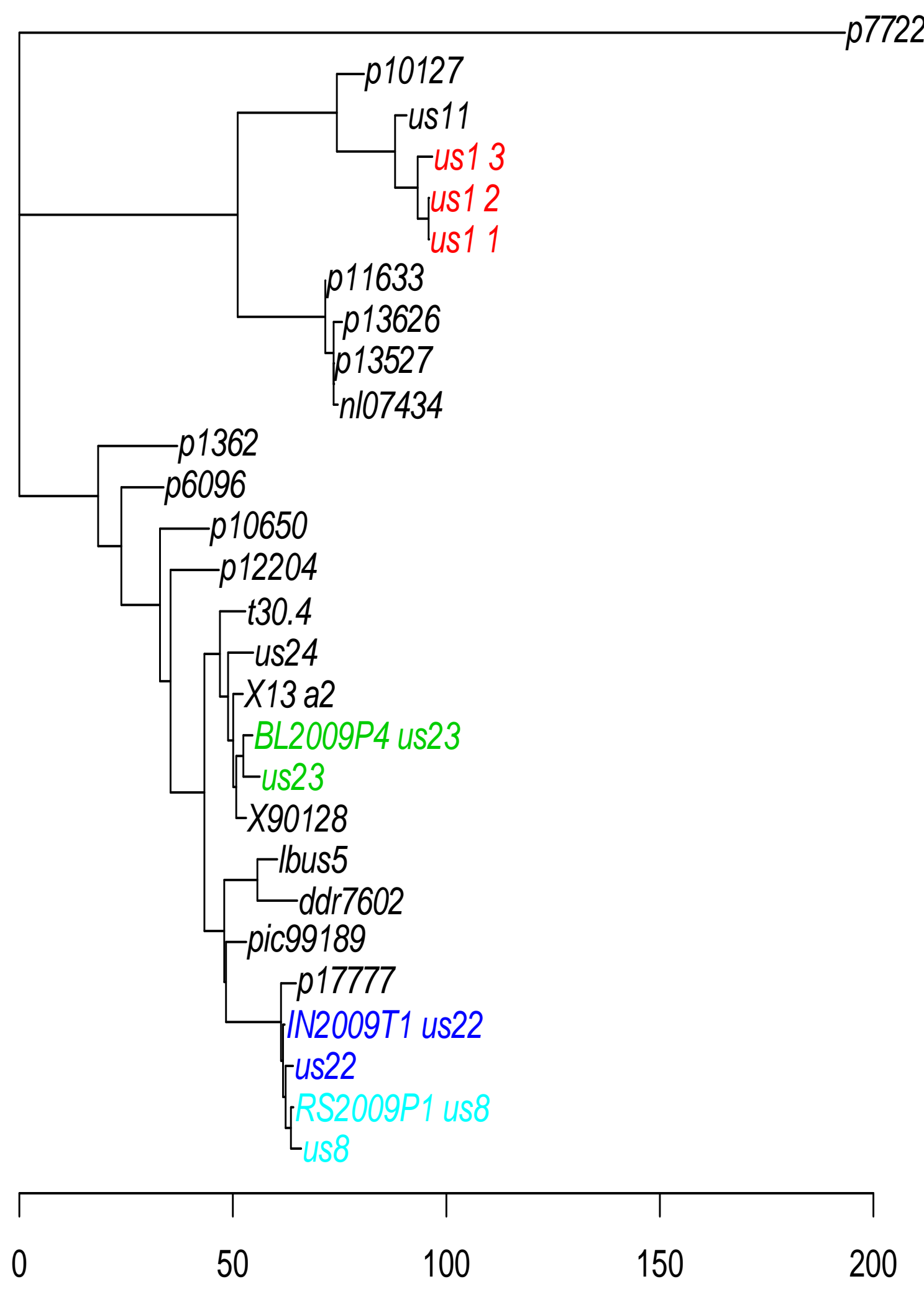
Visualization of Supercontig 60



- Describe the plot.
- ▶ Filtered on read depth
 - ▶ Filtered on quality (QUAL)

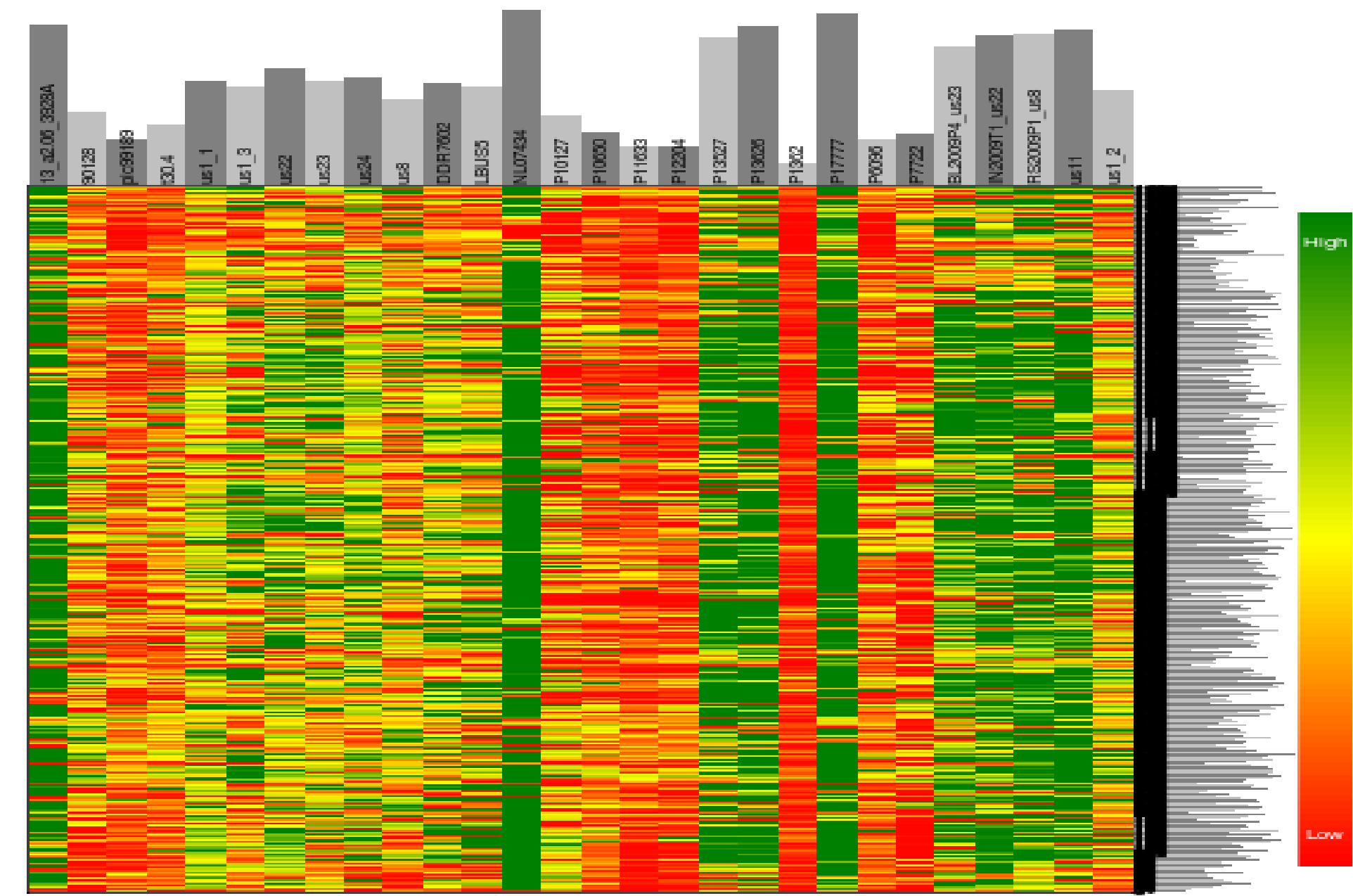
Mitochondrial phylogeny of *Phytophthora infestans*

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



- ▶ *P. mirabilis* (p7722) is the outgroup
- ▶ The *Phytophthora* mitochondrion consists of 40,NNN nucleotides
- ▶ 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 uniquely define this fungicide resistant clade (homozygote for versus homozygote against)
- ▶ Functional genomics will attempt to validate these candidates for fungicide resistance

Acknowledgements

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