

# Adaptation to partial resistance in grapevine downy mildew



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# Who did the work?

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## The grapevine downy mildew



*Plasmopara viticola*



# Recent use of partially resistant cultivars

Important yield loss for traditional cultivars

Controlled using fungicides



→ Recent breeding and use (15-10 years ago) of partially resistant grapevine cultivars

Resistance QTLs from wild North-American and Asian grapevine species

Represent a low percentage of cultivated grapevines

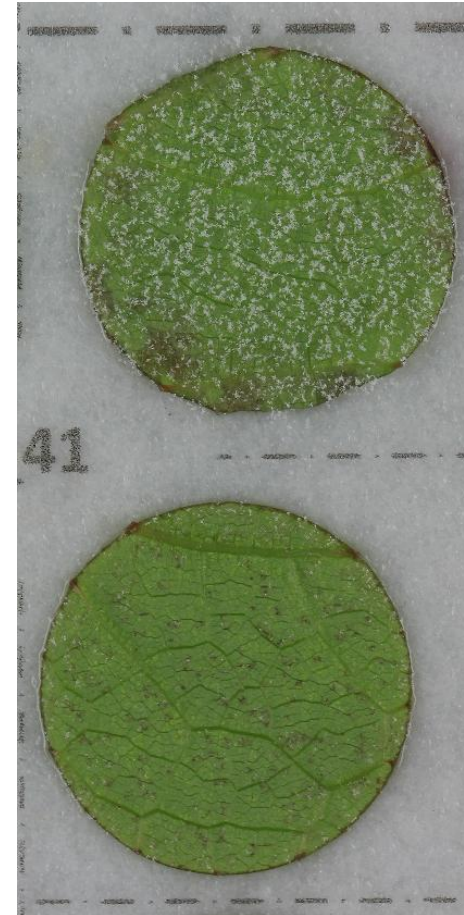
# Adaptation of *P. viticola* to grapevine partial resistance

Fast erosion of plant resistance  
→ Increase of pathogen aggressiveness

Delmas et al. 2016, *Evolutionary Applications*  
Delmotte et al. 2014, *Infection, Genetics and Evolution*

Dynamics of adaptation

What genes are involved?  
→ Population genetics approach with genome scans



Isolate from  
resistant cultivar

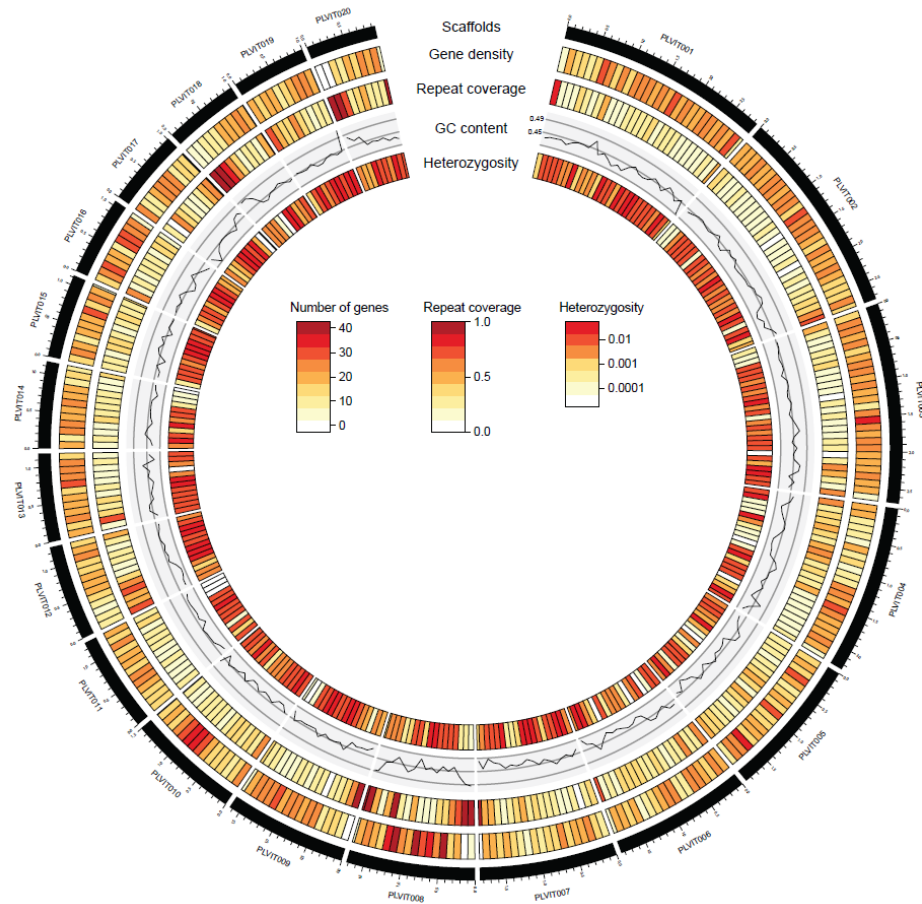
Isolate from  
susceptible cultivar

# A new high-quality reference genome

Obtaining a better genome reference with PacBio sequencing at deep coverage (185x)

	PV221 v1 (Dussert <i>et al.</i> 2016)	<b>PV221 PacBio (Dussert <i>et al.</i> 2018)</b>
Assembly size (Mb)	74.8	<b>93.0</b>
Scaffold number	1886	<b>359</b>
Max. scaffold length (Mb)	0.76	<b>2.85</b>
N <sub>50</sub> (kb / nb. scaffolds)	180.6 / 130	<b>706.5 / 38</b>
Completeness (BUSCO)	92.8% (4.7% duplicated)	<b>95.7% (1.7% duplicated)</b>

# A new high-quality reference genome

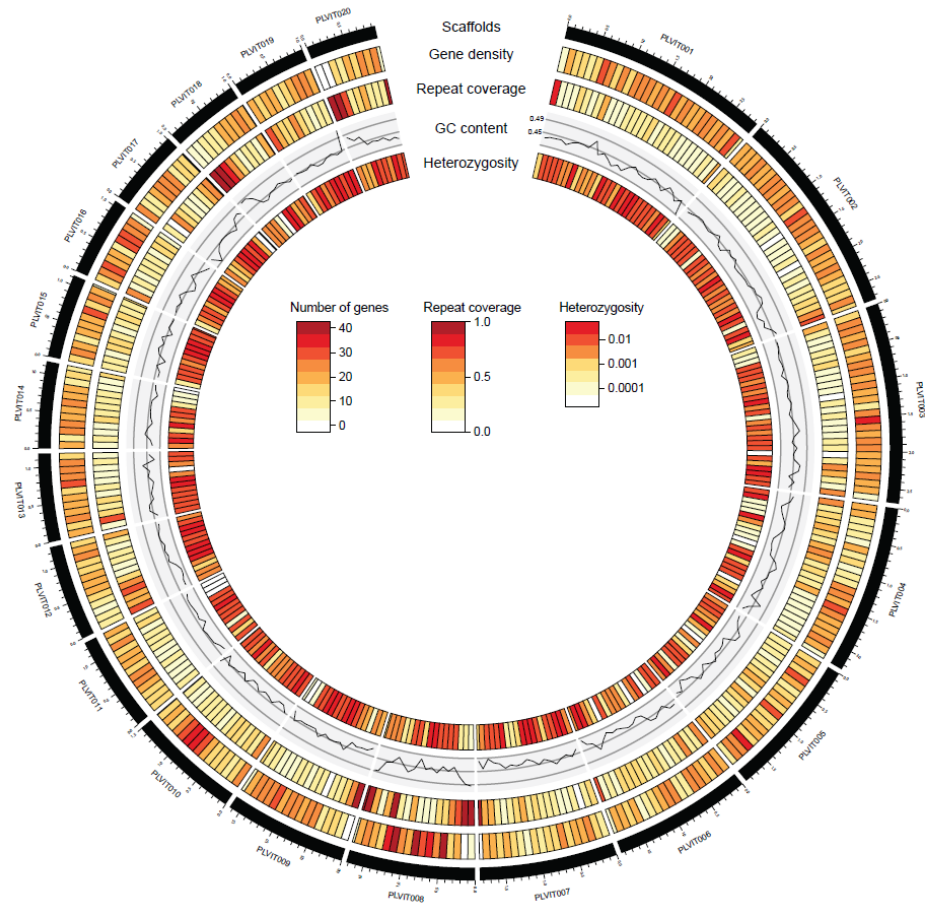


+ assembly of *Plasmopara muralis*, infecting wild grapevines (*Parthenocissus* sp.)




Repertoire of pathogenicity genes

Genes under positive selection = adaptation to the grapevine host

# A new high-quality reference genome



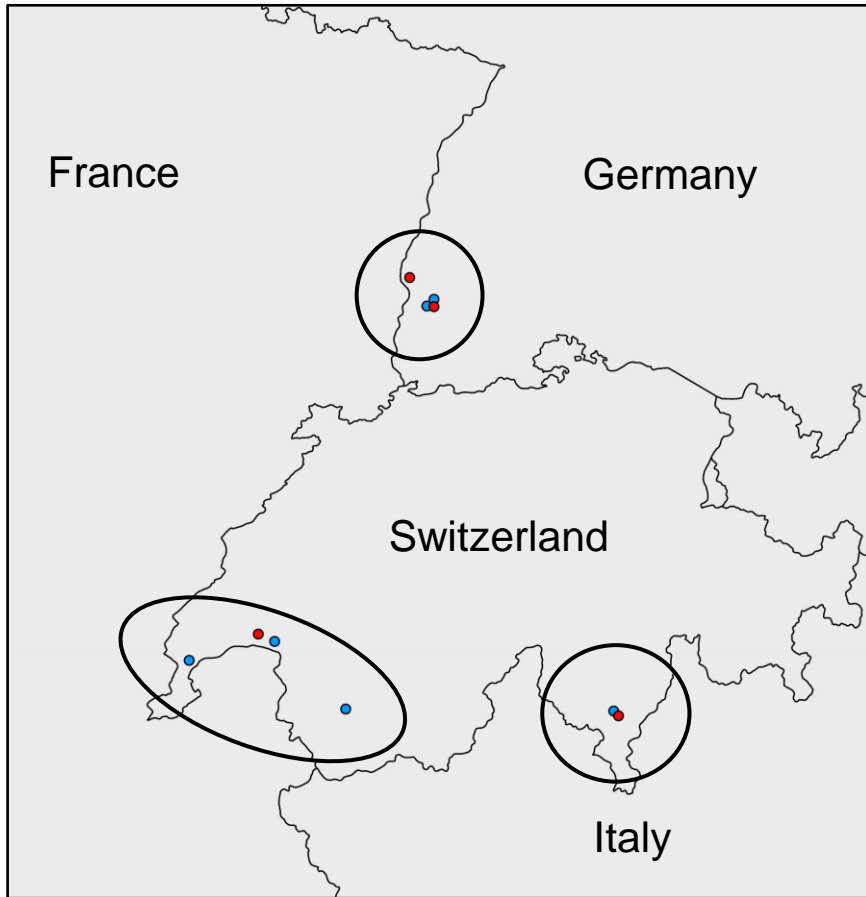
## A high-quality grapevine downy mildew genome assembly reveals rapidly evolving and lineage-specific putative host adaptation genes

 Yann Dussert, Isabelle D. Mazet, Carole Couture,  Jerome Gouzy, Marie-Christine Piron, Claire Kuchly, Olivier Bouchez, Claude Rispe,  Pere Mestre, Francois Delmotte

doi: <https://doi.org/10.1101/350041>



# Adaptation to partially resistant grapevine



42 isolates (mean coverage: 30 to 110x)

3 wine-producing regions

Collected on:

Susceptible grapevine

Partially resistant grapevine (RPV3 QTL)

1.8 million SNPs (around 990,000 with  
MAF < 0.1)

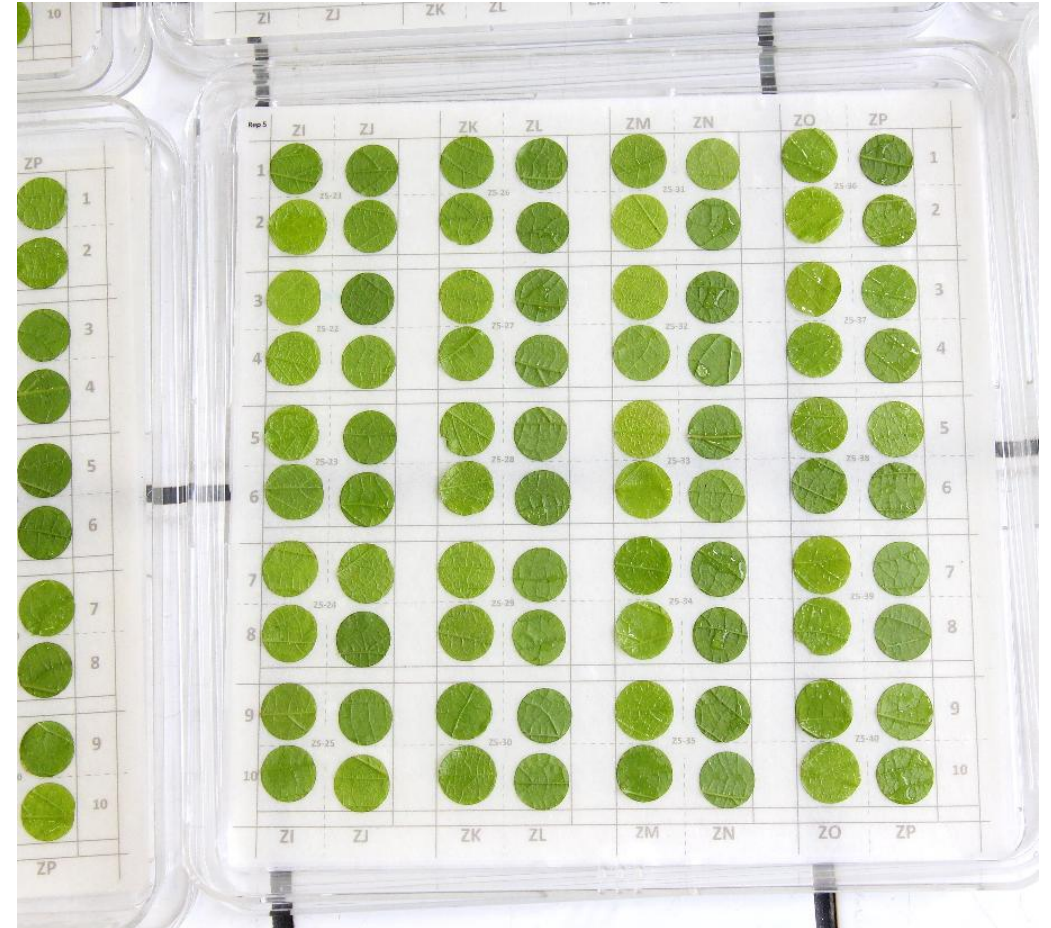
# Phenotyping: aggressiveness of isolates on partially resistant cultivar

Measured traits for the 42 isolates:

- Sporangium production
- Sporangium size
- Latency period

On two hosts: susceptible host (Cabernet Sauvignon) and partially resistant host (RPV3 cultivar)

8 replicates



# Phenotyping: aggressiveness of isolates

Sporangium production on  
a partially resistant plant

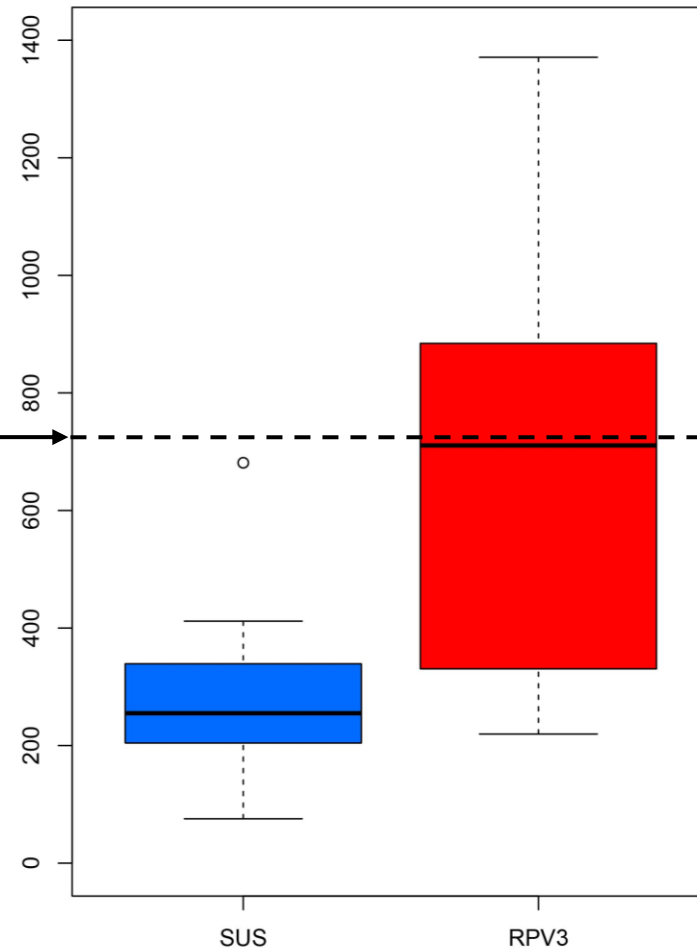
Isolates collected on  
susceptible vines

VS

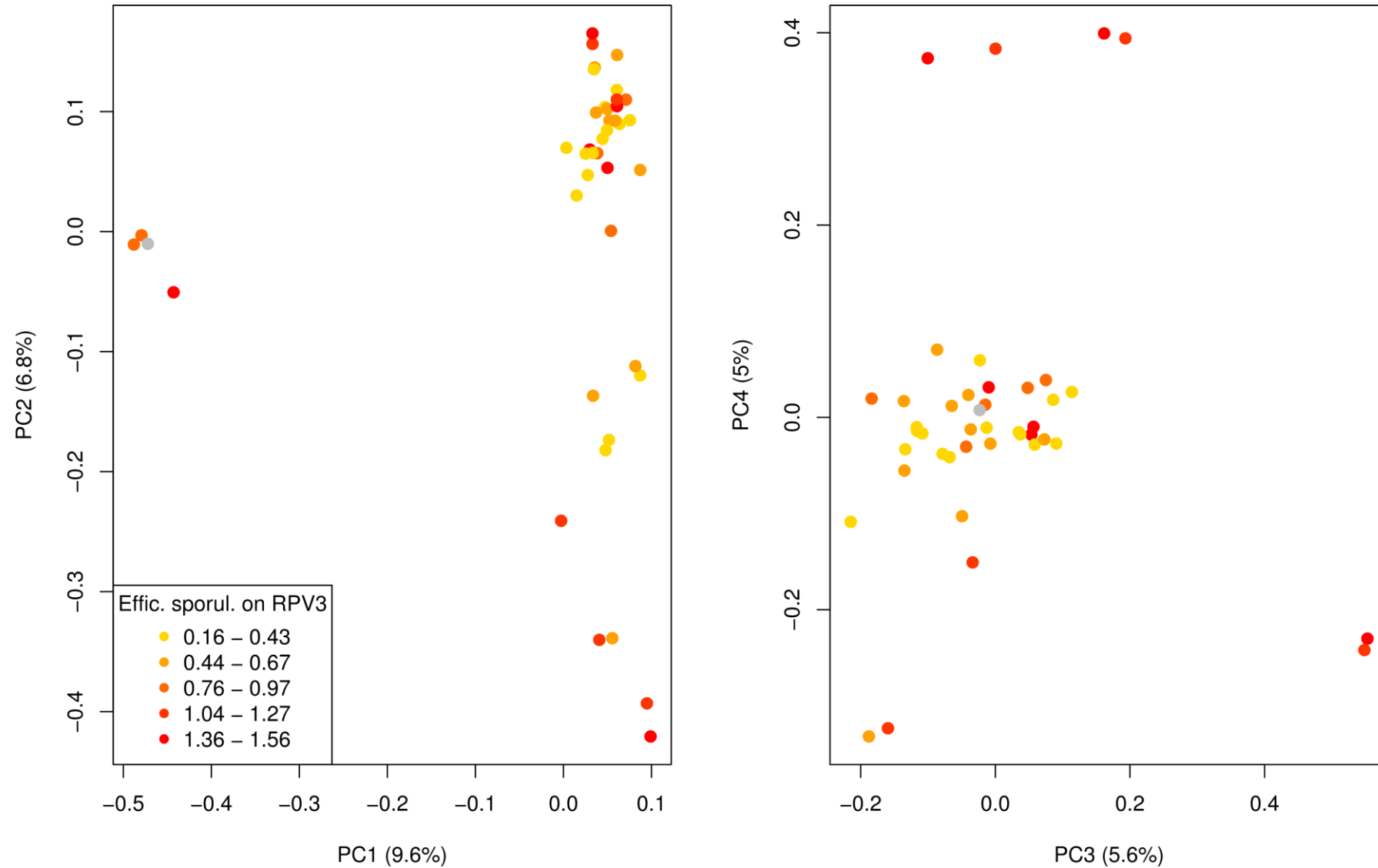
Isolates collected on  
resistant vines

Sporulation on  
sensible cultivar

Number of  
sporangia /  
mm<sup>2</sup>

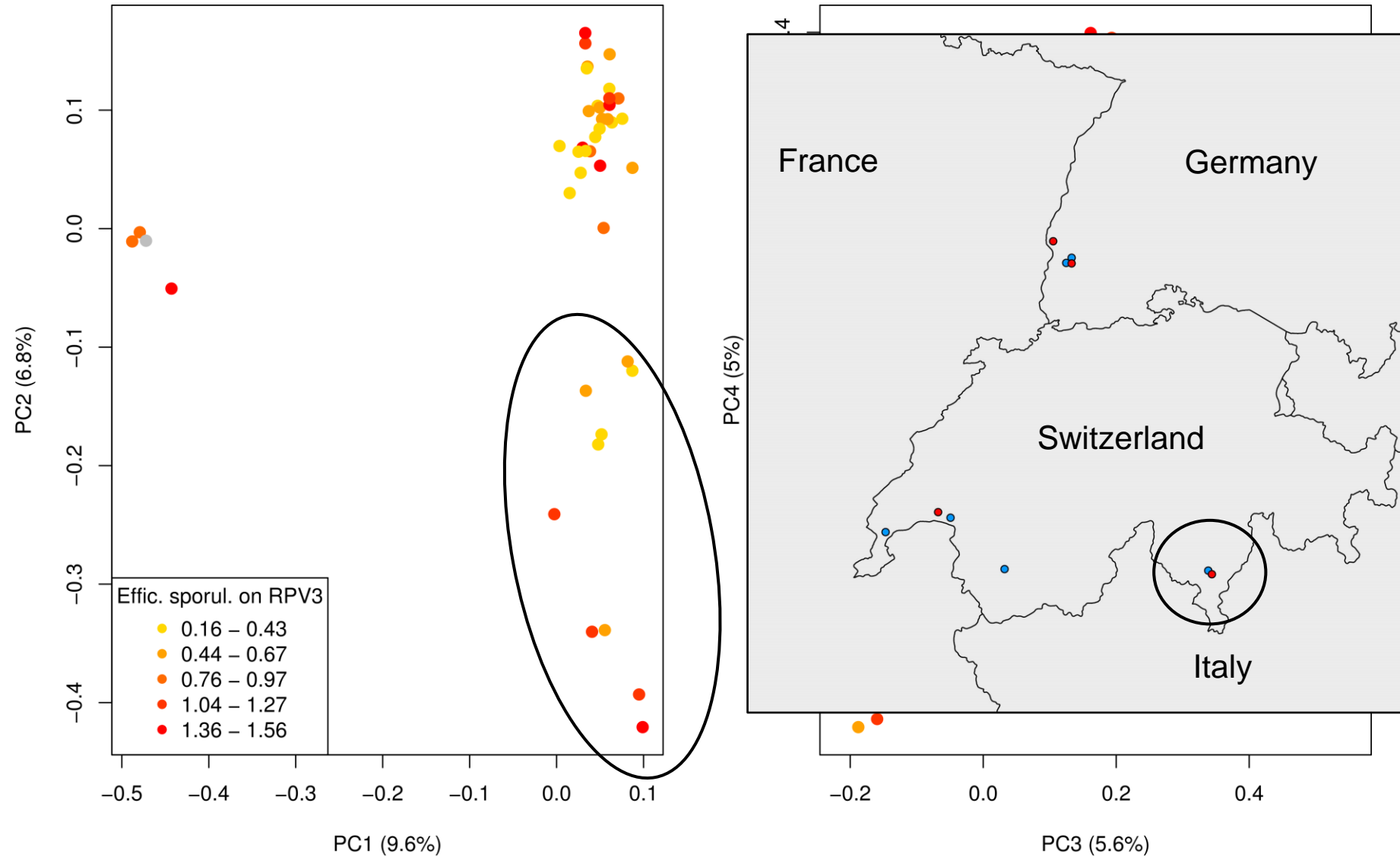


# Genetic structure & aggressiveness

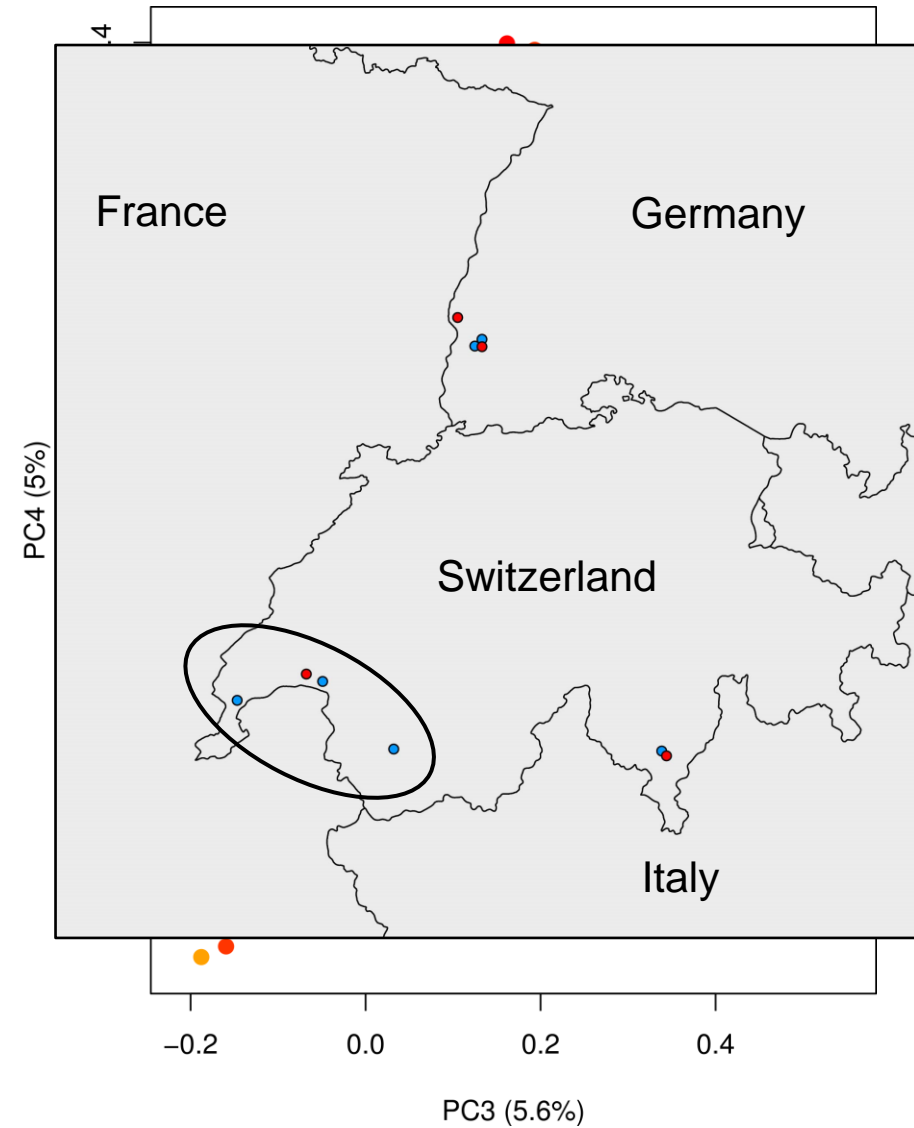
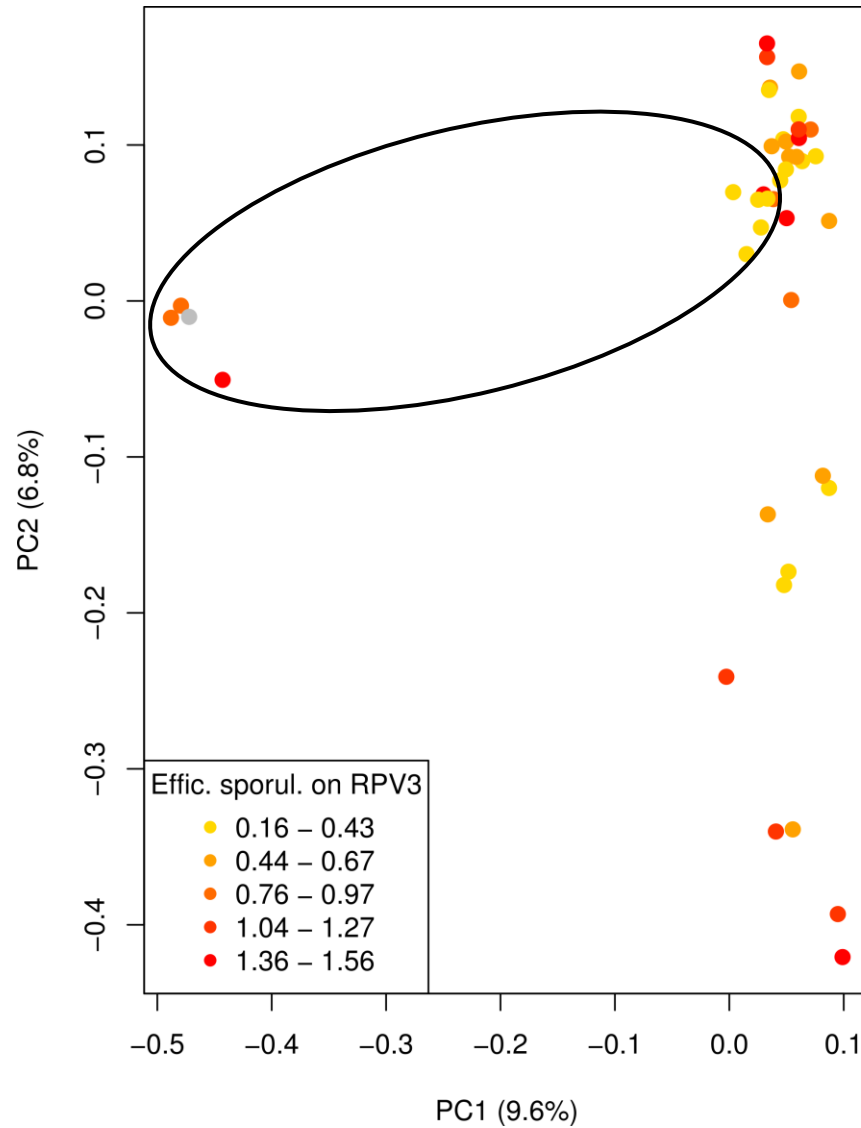




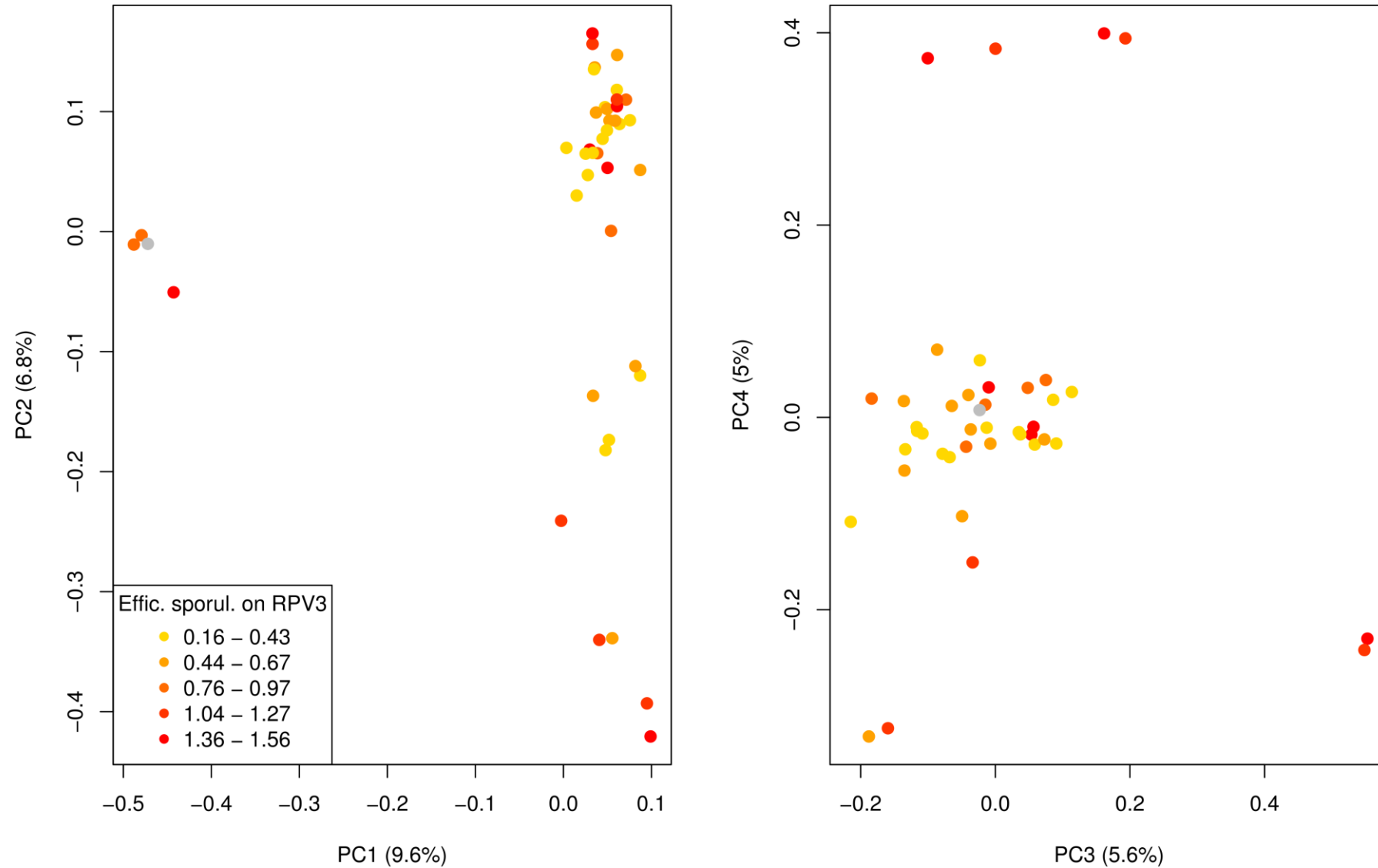
# Genetic structure & aggressiveness



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# Genetic structure & aggressiveness



# Detection of genomic regions involved in adaptation to partial resistance

Which genes are under selection?

Multiple methods:

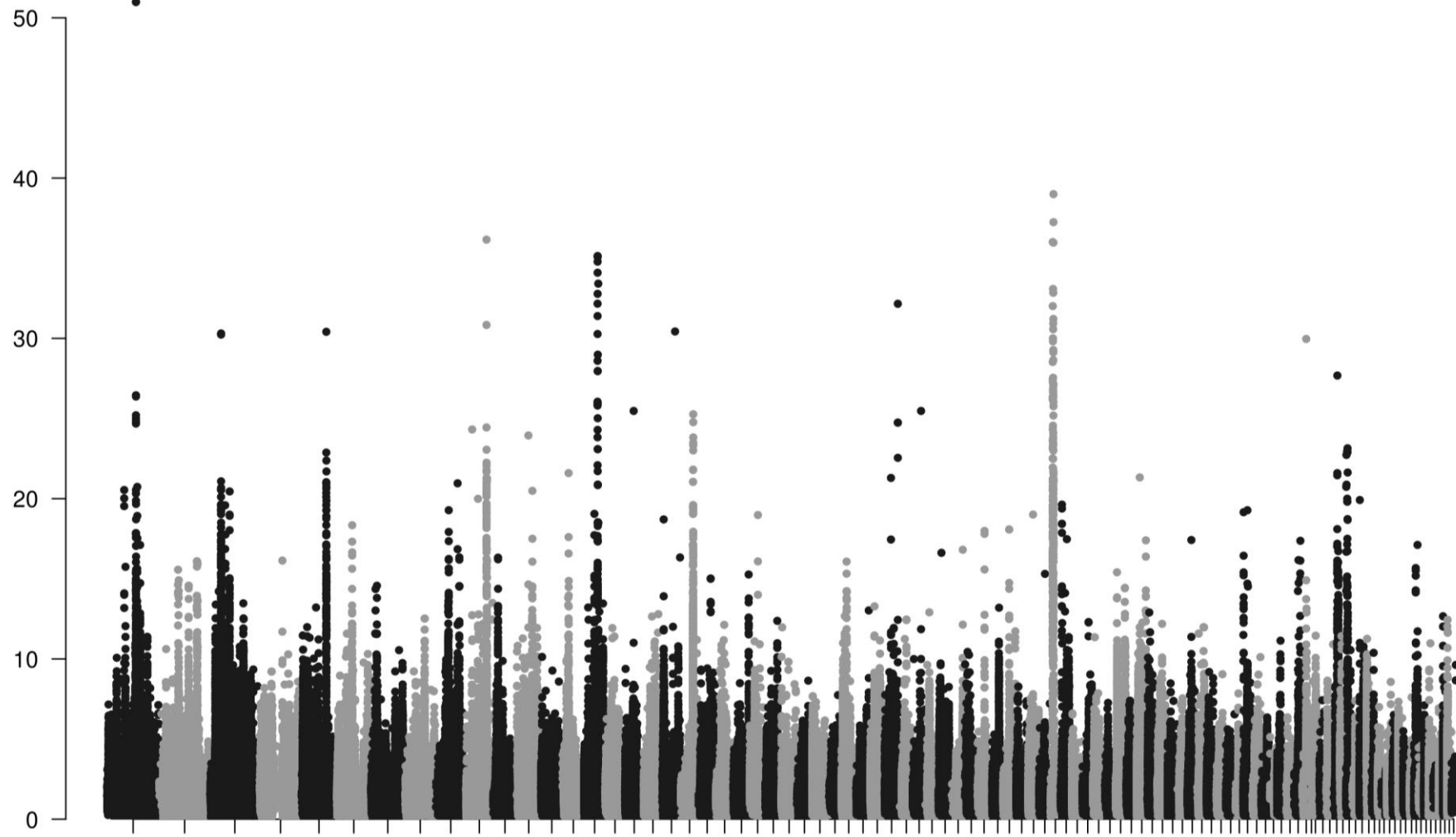
- Regression of SNPs by principal components of PCA (PCAdapt, Luu *et al.* 2017)
- $F_{ST}$  computed from allelic frequencies inferred with clustering (sNMF, Frichot *et al.* 2014)
- $X^tX$  statistic (BayPass, Gautier 2015)

Combined using approach of Verity *et al.* (2016): Mahalanobis distance on stats (Minotaur R package)



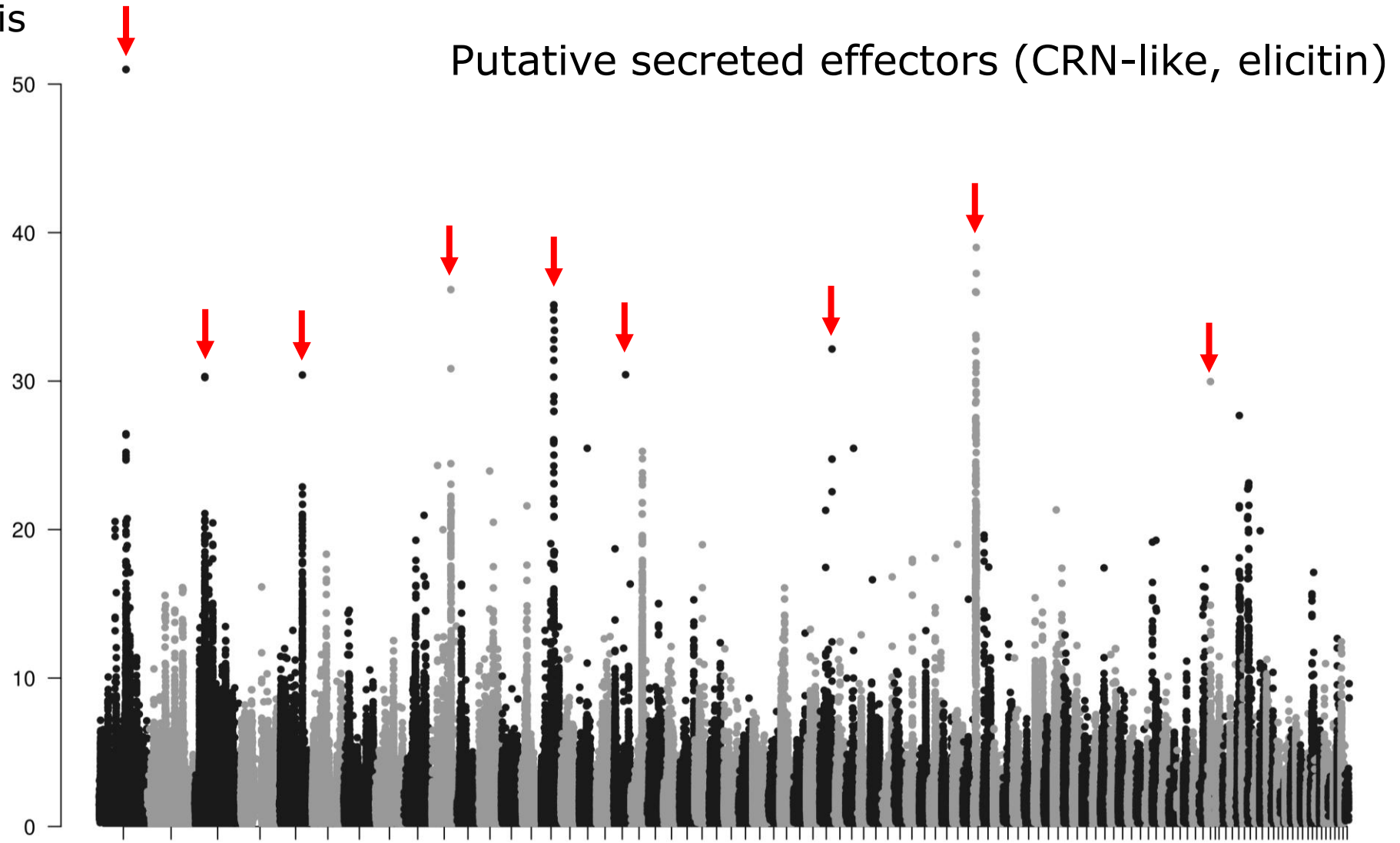
# Outlier regions in combined selection tests

Mahalanobis  
distance



# Outlier regions in combined selection tests

Mahalanobis  
distance



# On-going analyses

More detailed analysis of outlier regions:

- Genetic diversity, frequency spectrum
- Effect of SNPs? (synonymous/non-synonymous/intergenic)
- Linkage disequilibrium, haplotype structure

Selection of the same genes for all aggressive isolates?

## In summary

New reference sequence of high quality for *Plasmopara viticola*



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New reference sequence of high quality for *Plasmopara viticola*

Adaptation to partial plant resistance

- Isolates with high aggressiveness on resistant plants are genetically differentiated, but not in one single group: independent adaptations
- Detection of selected genomic regions: combination of multiple methods to find outliers (some interesting candidates)