

# Dynamics of disease resistance polymorphism at the *Rpm1* locus of *Arabidopsis*

1999

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DOI: 10.1534/genetics.109.112383

## Impact of Initial Pathogen Density on Resistance and Tolerance in a Polymorphic Disease Resistance Gene System in *Arabidopsis thaliana*

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Department of Ecology and Evolution, University of Chicago, Chicago, Illinois 60637

Journal of Experimental Botany, Vol. 67, No. 7 pp. 2093–2105, 2016  
doi:10.1093/jxb/erv530  
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RESEARCH PAPER

## Modulation of *R*-gene expression across environments

Alice MacQueen and Joy Bergelson\*

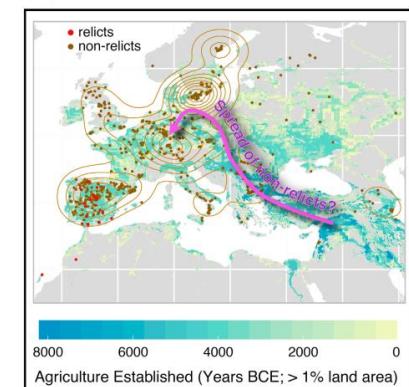
Department of Ecology and Evolution, University of Chicago, 1101 East 57th Street, Chicago, IL 60637, USA.

## Cell

Resource

### 1,135 Genomes Reveal the Global Pattern of Polymorphism in *Arabidopsis thaliana*

#### Graphical Abstract



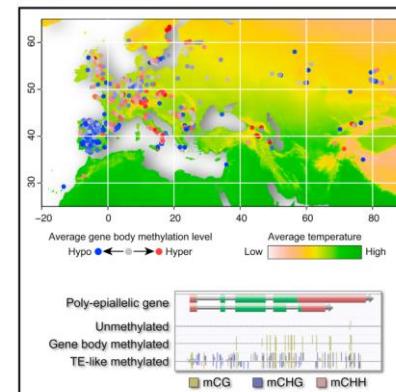
**Authors**  
The 1001 Genomes Consortium  
**Correspondence**  
[magnus.nordborg@gmi.oew.ac.at](mailto:magnus.nordborg@gmi.oew.ac.at) (Magnus Nordborg),  
[weigel@weigelworld.org](mailto:weigel@weigelworld.org) (Detlef Weigel)  
**In Brief**  
Genomic sequencing analysis of over 1,000 natural inbred lines of *Arabidopsis thaliana* reveals its global population structure, migration patterns, and evolutionary history and provides a rich genetic resource for studying phenotypic variation and adaptation.

## Cell

Resource

### Epigenomic Diversity in a Global Collection of *Arabidopsis thaliana* Accessions

#### Graphical Abstract



**Authors**  
Taiji Kawakatsu, Shao-shan Carol Huang, Florian Jupe, ..., Detlef Weigel, Magnus Nordborg, Joseph R. Ecker

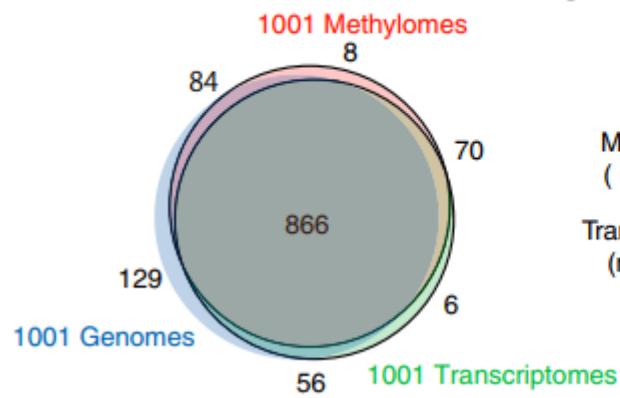
**Correspondence**  
[ecker@salk.edu](mailto:ecker@salk.edu)

**In Brief**  
Methylomes and transcriptomes from >1,000 *Arabidopsis thaliana* accessions provide insights on how the epigenome is shaped by natural genomic variation and by the environment.

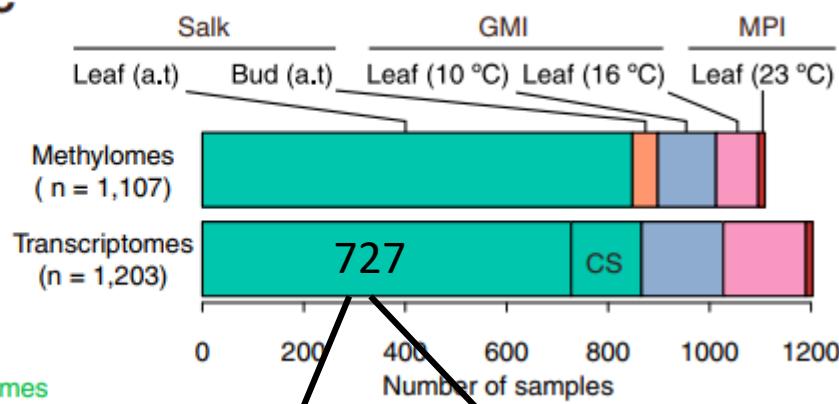
In 2016, I had the following question:

What is the genetic architecture of *RPM1* expression level ?

A



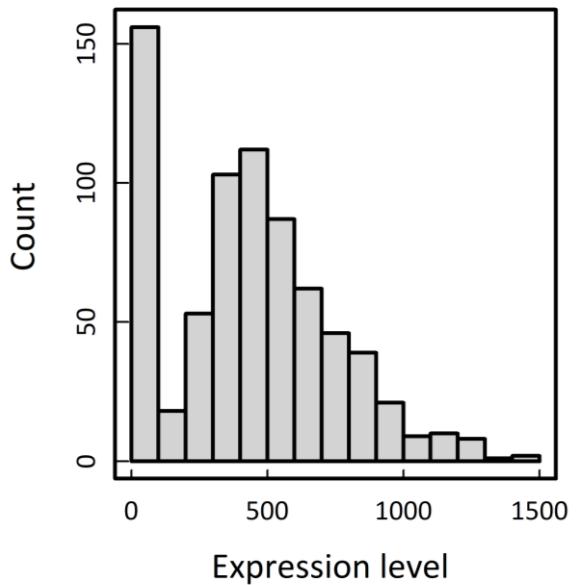
C



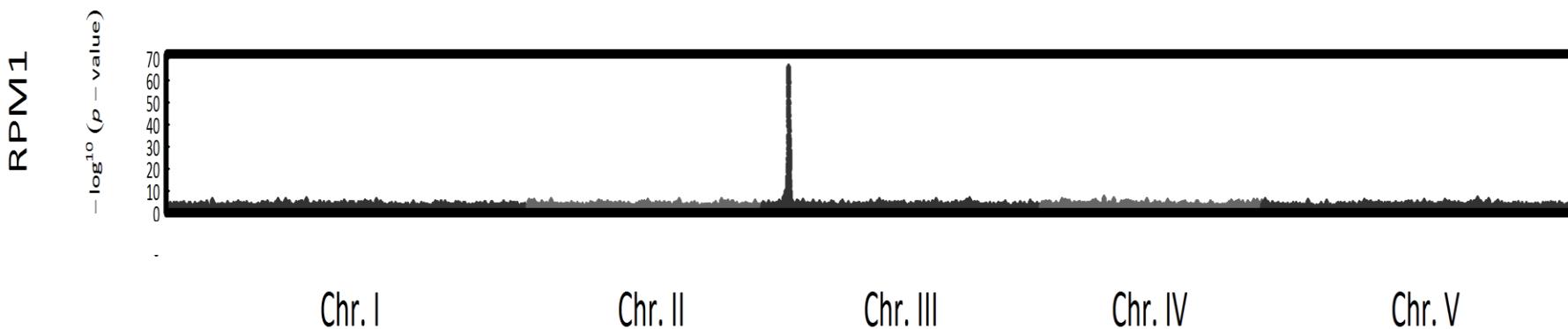
Expression level (normalized count)  
for 24,030 genes

Genome sequences for 665 accessions

## Variation among accessions in *RPM1* expression



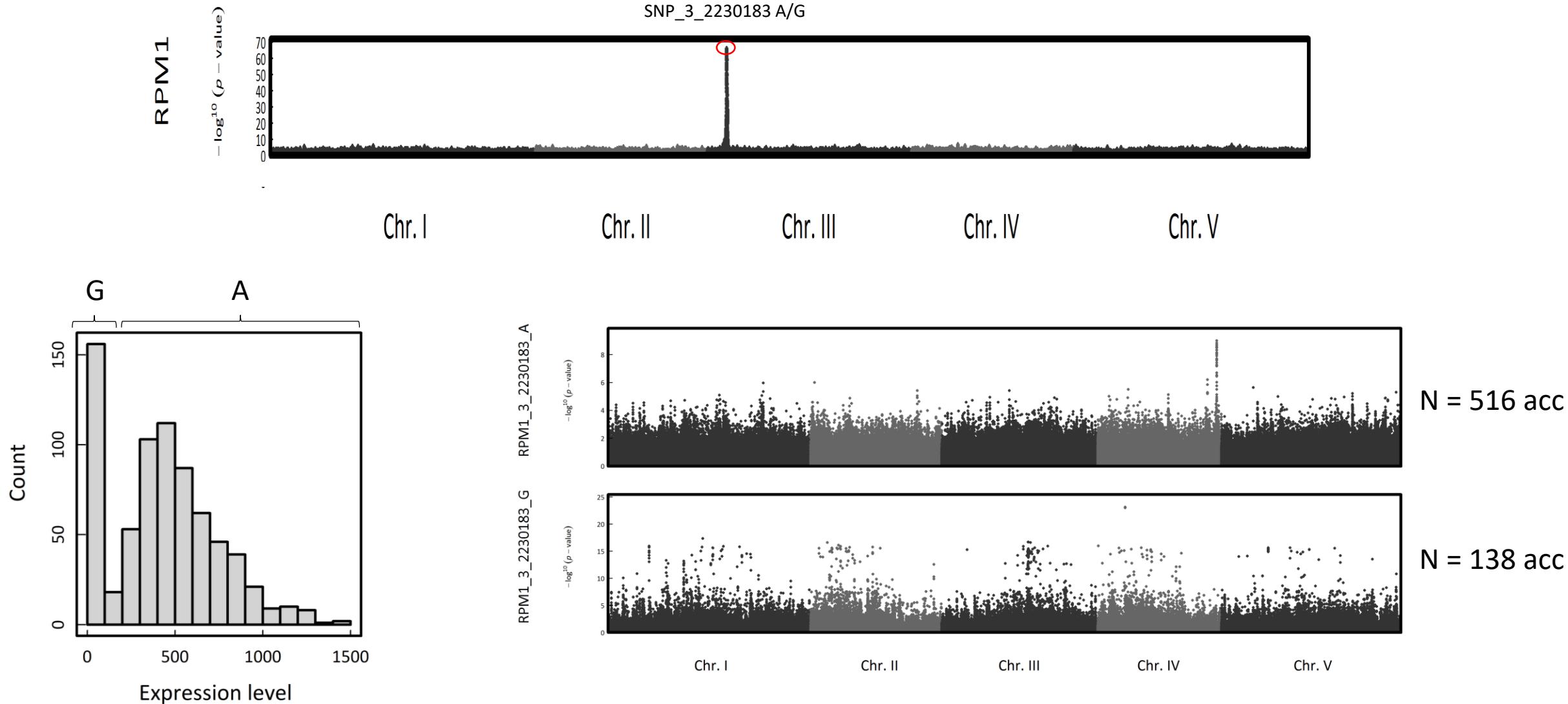
## GWA mapping (EMMAX: linear mixed model)



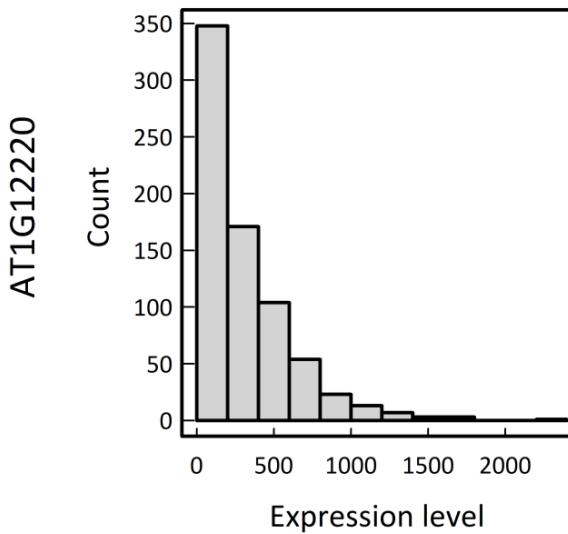
## Next step: nested GWA mapping

# An Atypical Kinase under Balancing Selection Confers Broad-Spectrum Disease Resistance in Arabidopsis

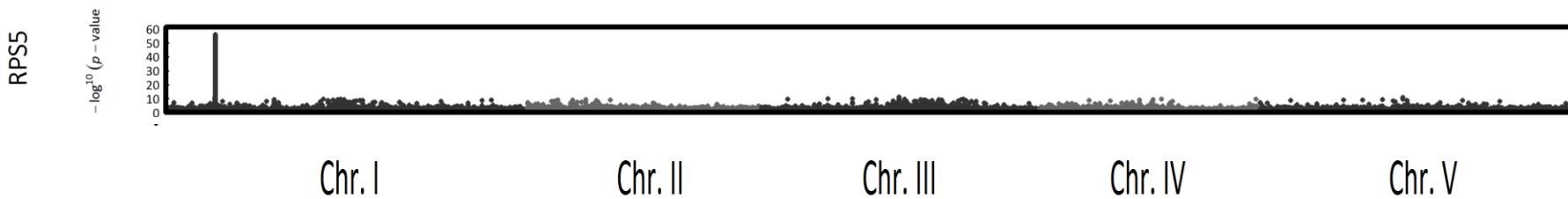
Carine Huard-Chauveau<sup>1,2</sup>, Laure Perche pied<sup>1,2</sup>, Marilyne Debieu<sup>1,2,3</sup>, Susana Rivas<sup>1,2</sup>, Thomas Kroj<sup>1,2</sup>, Ilona Kars<sup>1,2</sup>, Joy Bergelson<sup>4</sup>, Fabrice Roux<sup>3</sup>, Dominique Roby<sup>1,2\*</sup>



## Variation among accessions in *RPS5* expression

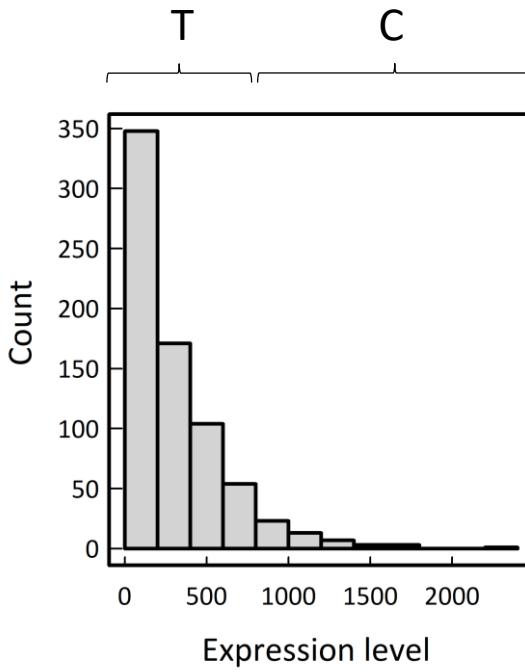


## GWA mapping (EMMAX: linear mixed model)

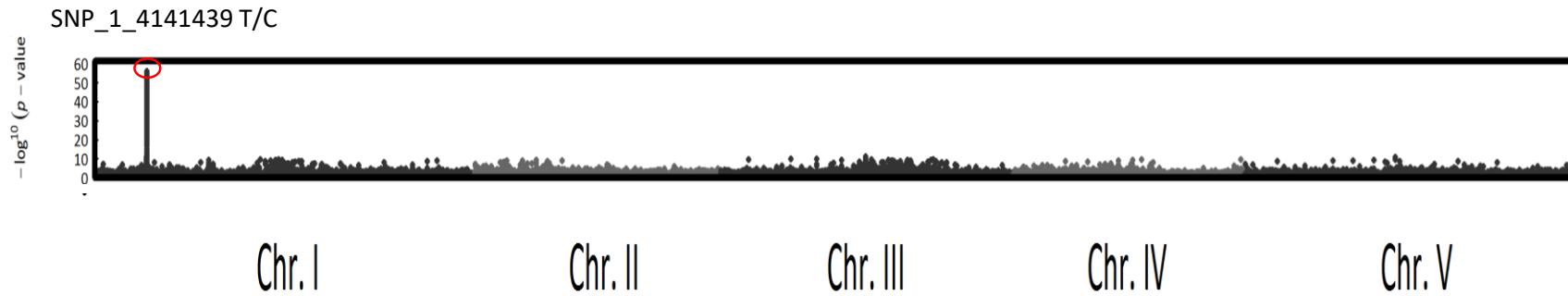


## Nested GWA mapping

AT1G12220



RPS5



Chr. I

Chr. II

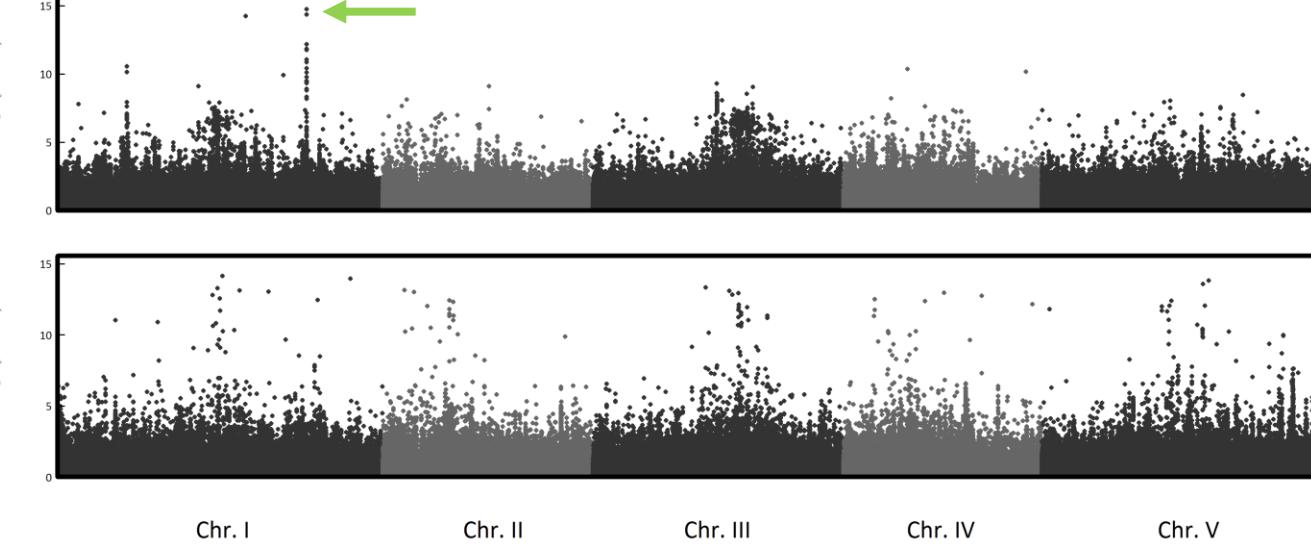
Chr. III

Chr. IV

Chr. V

RPS5\_1\_4141439\_T

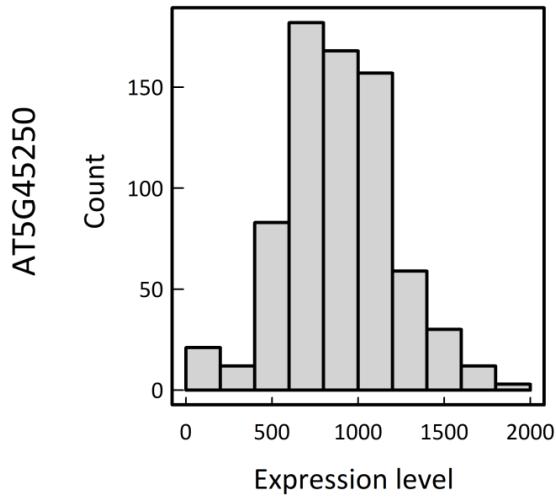
RPS5\_1\_4141439\_C



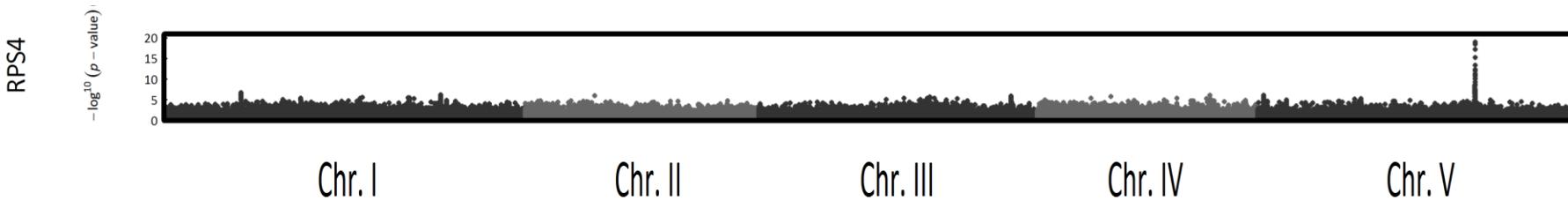
N = 358 acc

N = 261 acc

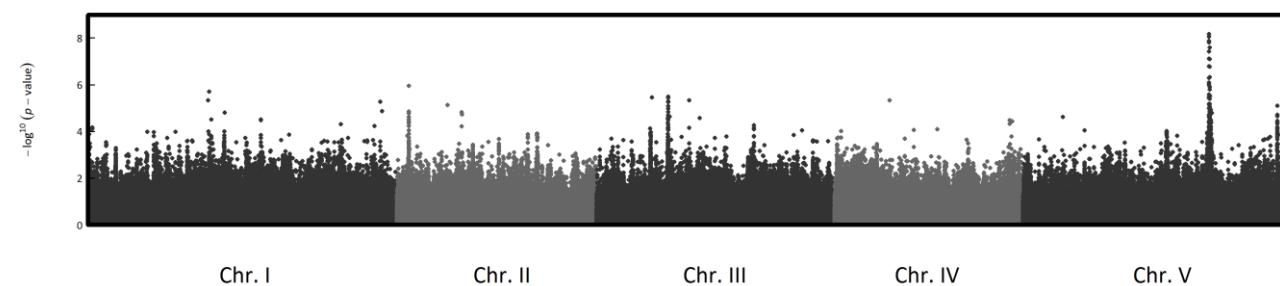
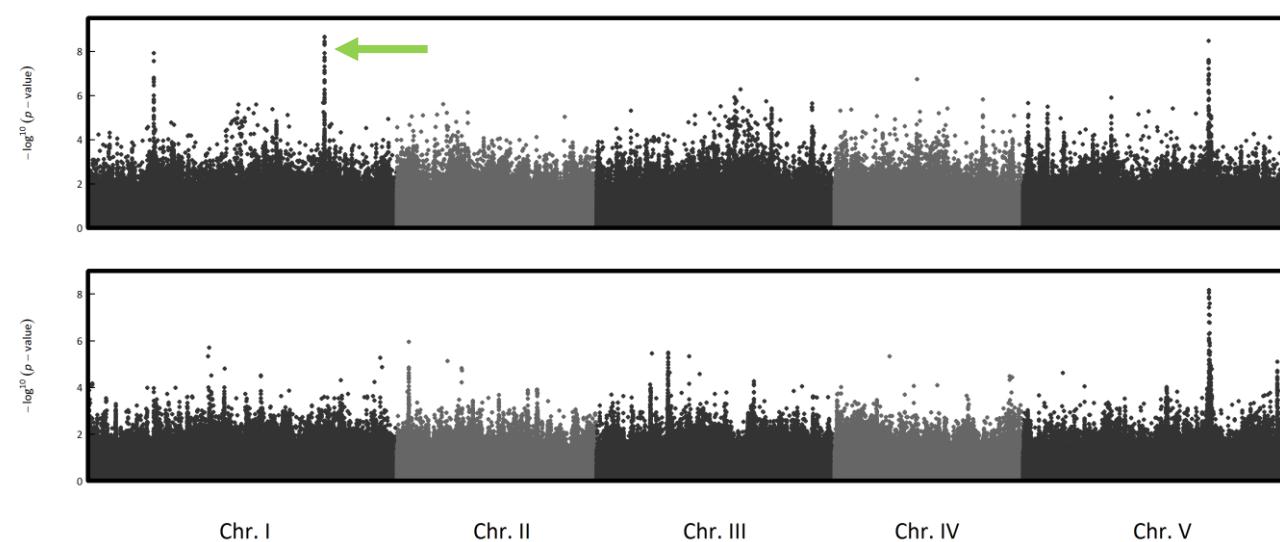
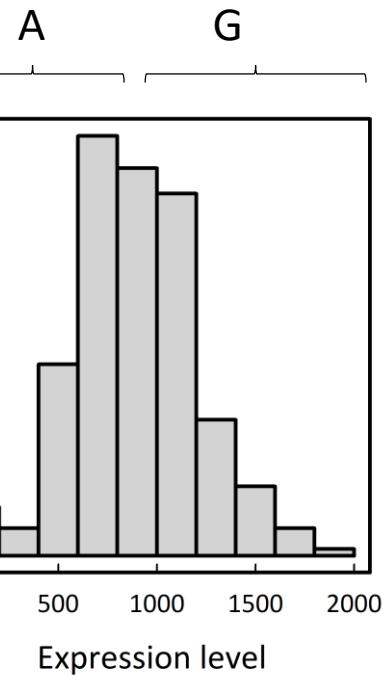
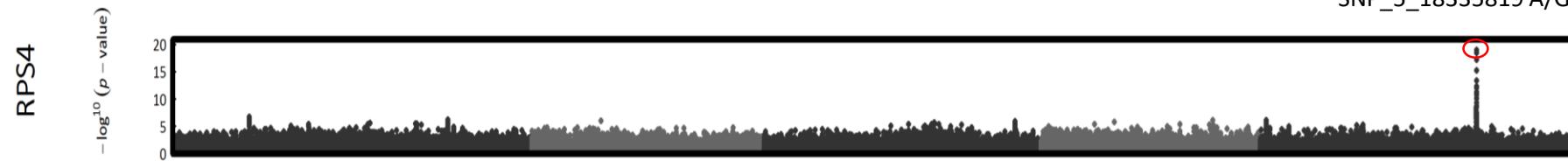
## Variation among accessions in *RPS4* expression



## GWA mapping (EMMAX: linear mixed model)



## Nested GWA mapping



TEN YEARS LATER

Hanna from Joy's group sent me a list of 211 *NLR* genes



195 have transcriptomic data for 727 accessions (including 665 with genome sequences)



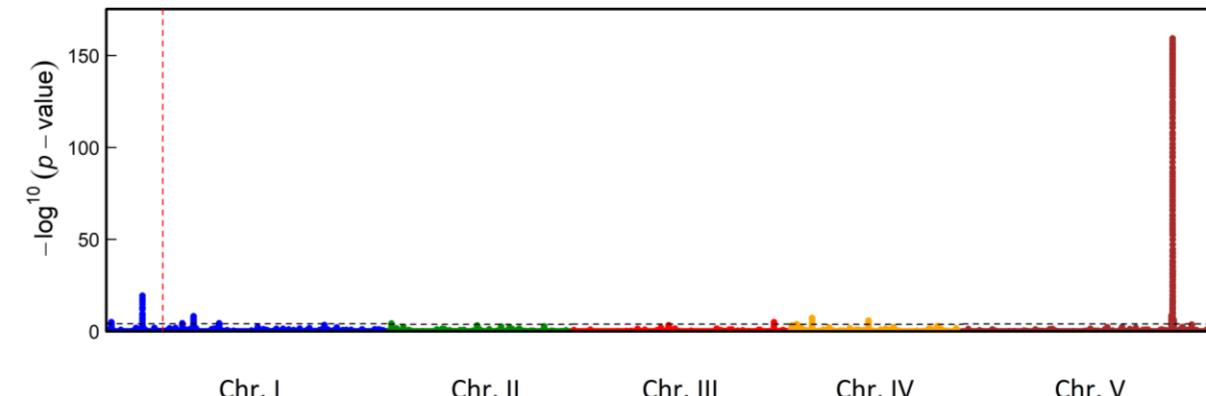
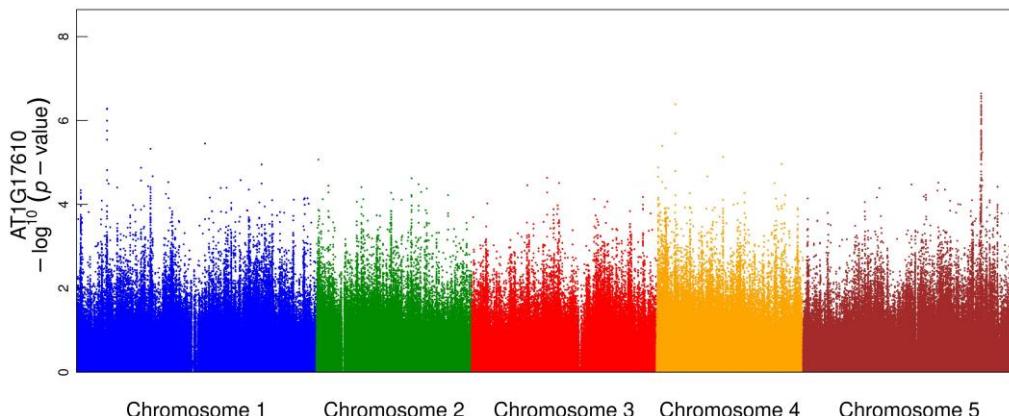
ORIGINAL ARTICLE

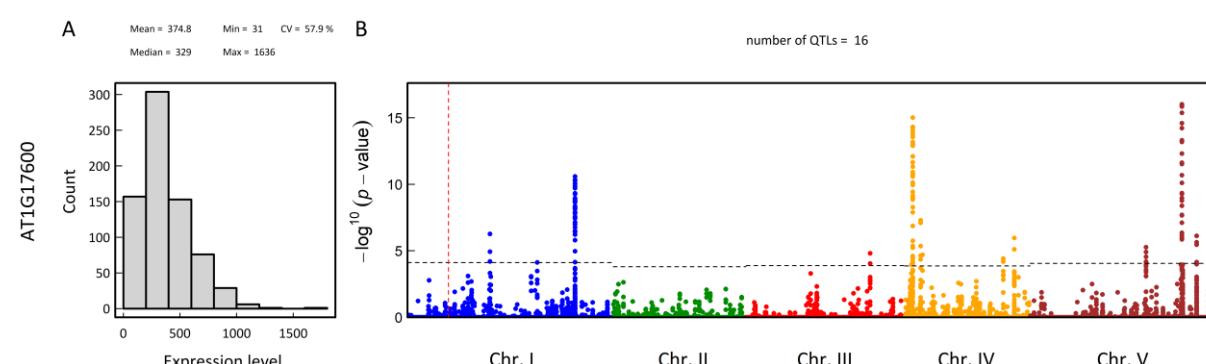
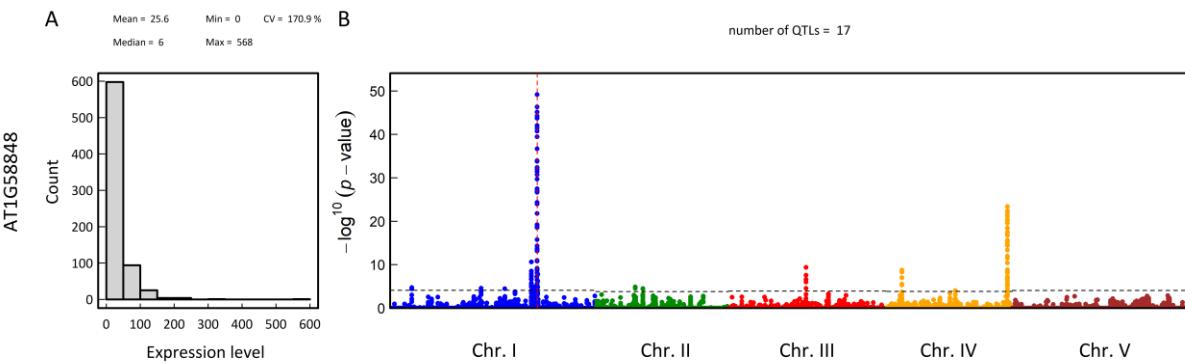
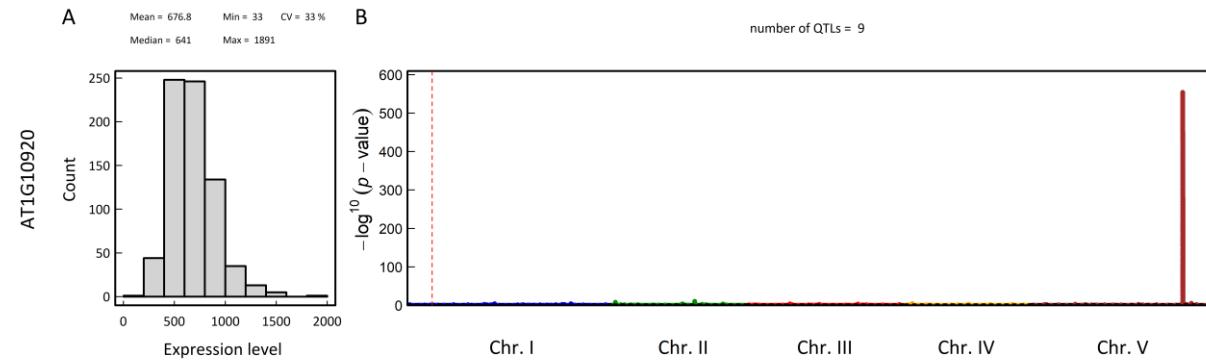
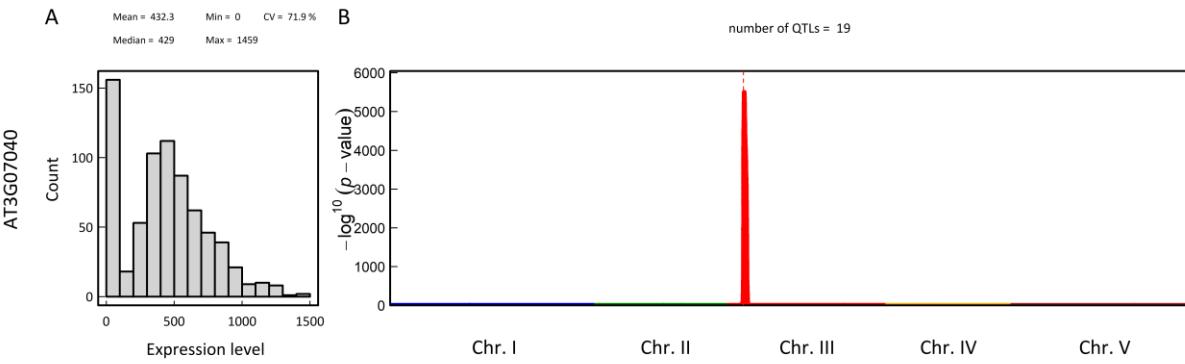
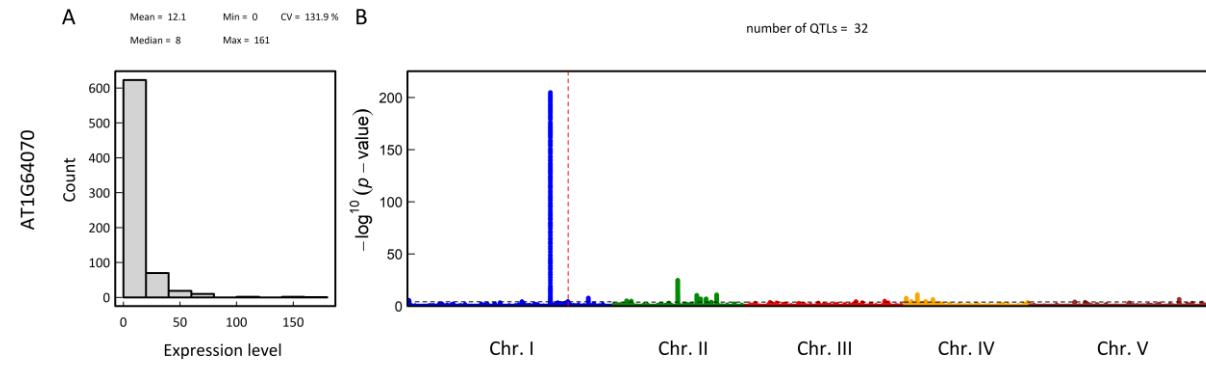
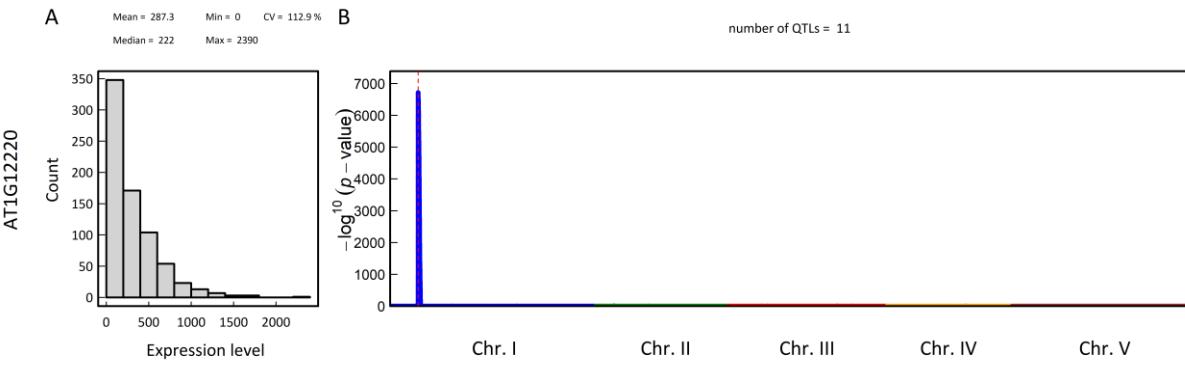
WILEY MOLECULAR ECOLOGY

GWA mapping: EMMAx + local score approach

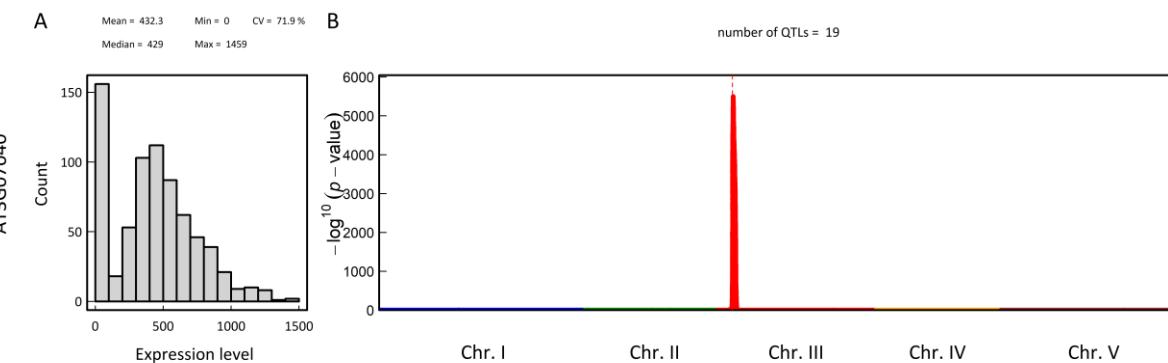
## Accounting for linkage disequilibrium in genome scans for selection without individual genotypes: The local score approach

Maria Inés Fariello<sup>1,2,3</sup> | Simon Boitard<sup>1</sup> | Sabine Mercier<sup>4,5</sup> | David Robelin<sup>1</sup> | Thomas Faraut<sup>1</sup> | Cécile Arnould<sup>6</sup> | Julien Recoquillay<sup>7,8</sup> | Olivier Bouchez<sup>1,9</sup> | Gérald Salin<sup>1,9</sup> | Patrice Dehais<sup>10</sup> | David Gourichon<sup>11</sup> | Sophie Leroux<sup>1</sup> | Frédérique Pitel<sup>1</sup> | Christine Leterrier<sup>6</sup> | Magali SanCristobal<sup>1,5,12,13</sup>

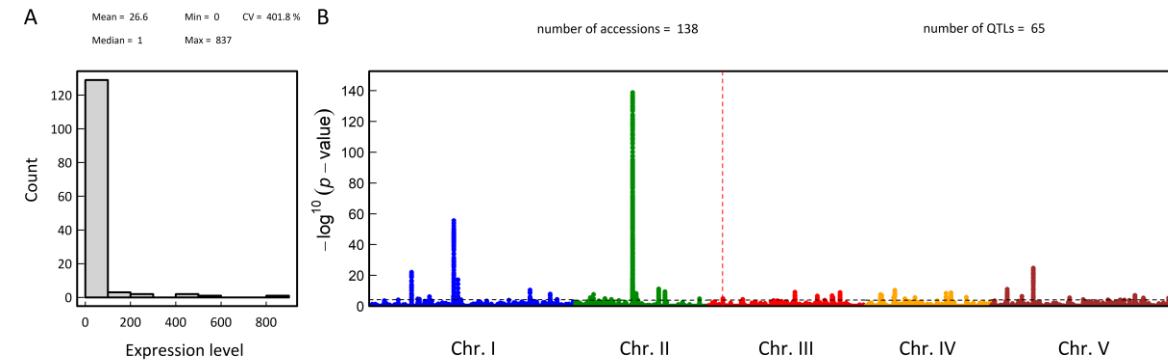




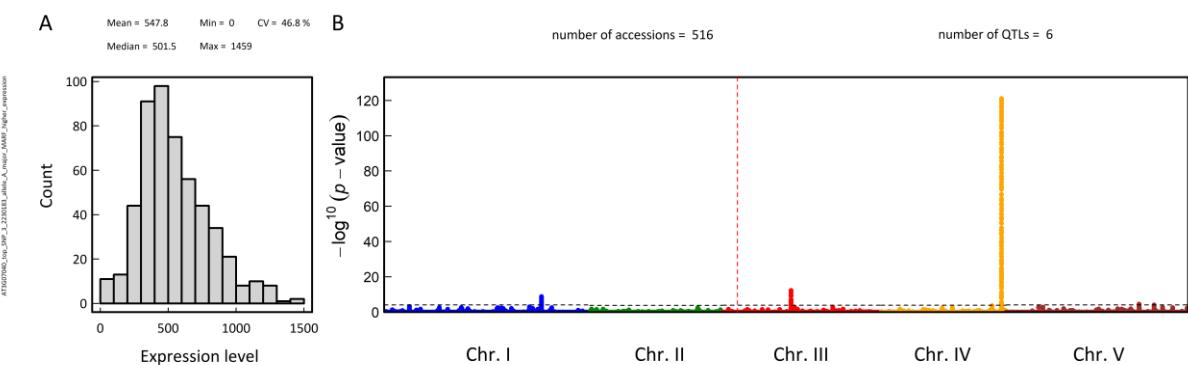
# Variation among accessions in *RPM1* expression



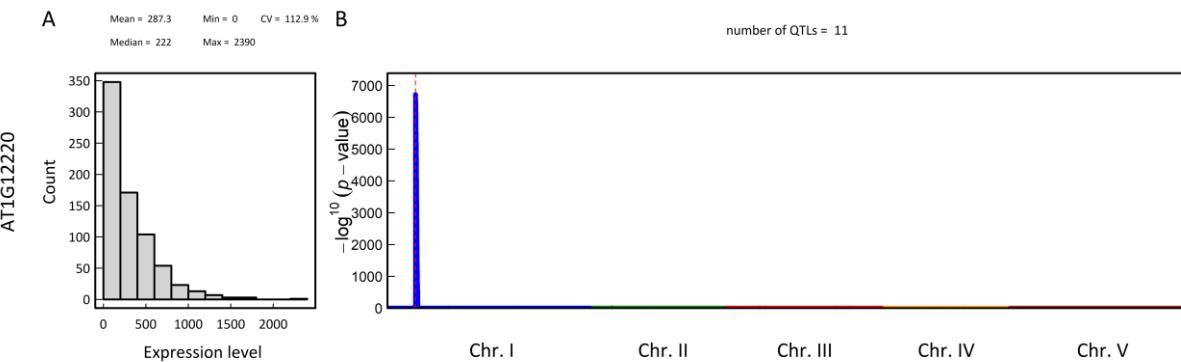
lower expression



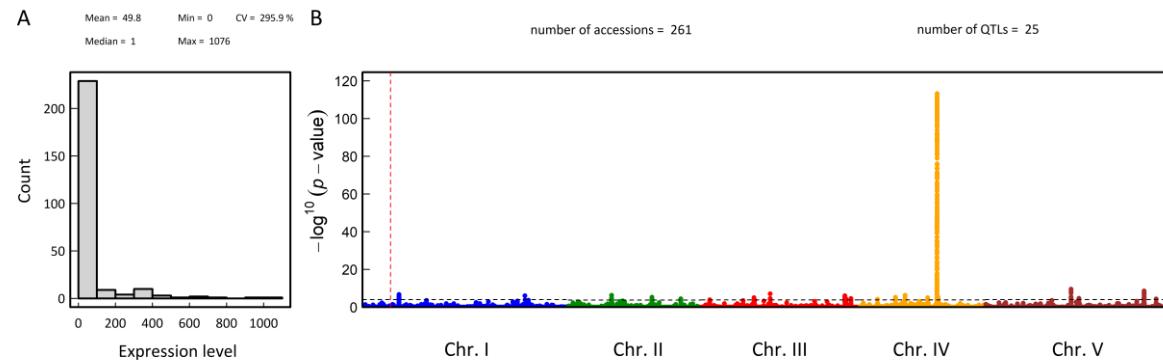
higher expression



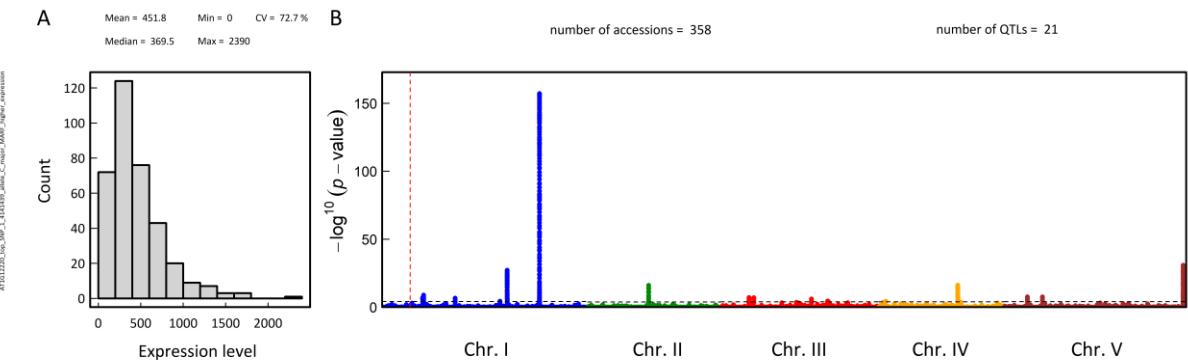
# Variation among accessions in *RPS5* expression



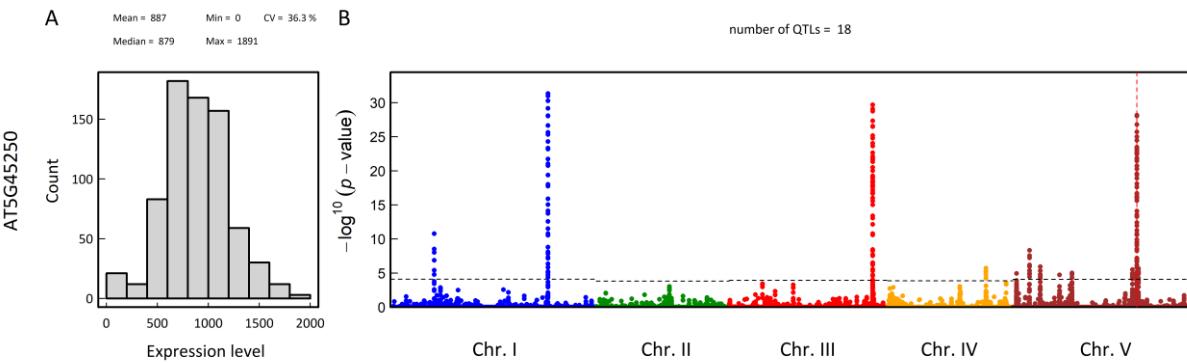
lower expression



higher expression

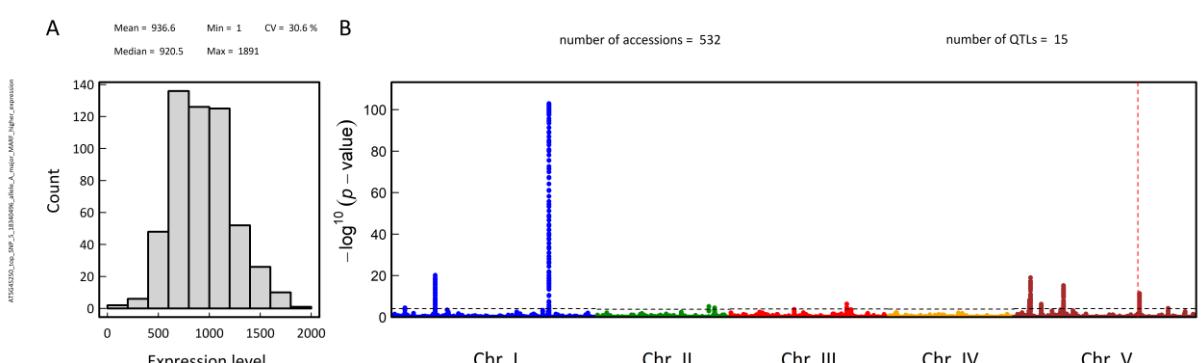
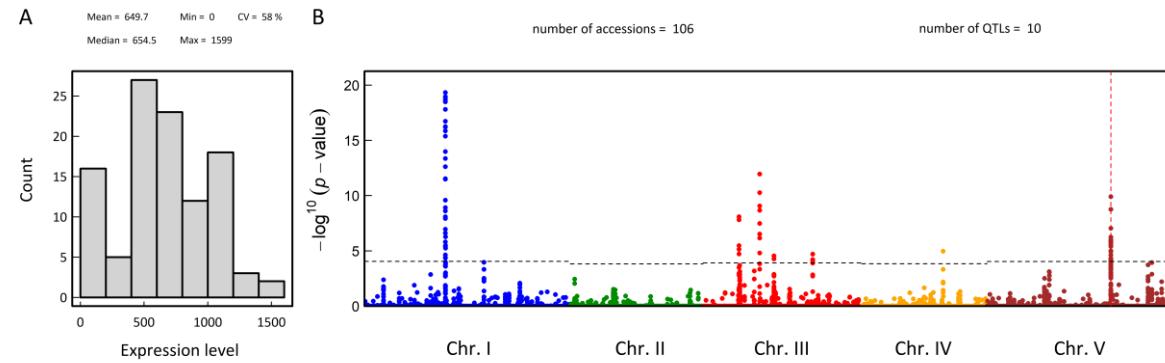


## Variation among accessions in *RPS4* expression



## lower expression

## higher expression



# Ecology – expression relationships

ARTICLES

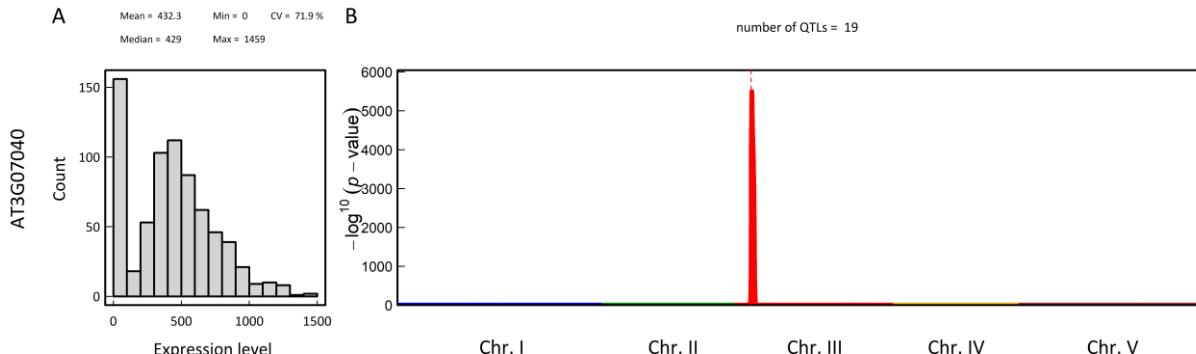
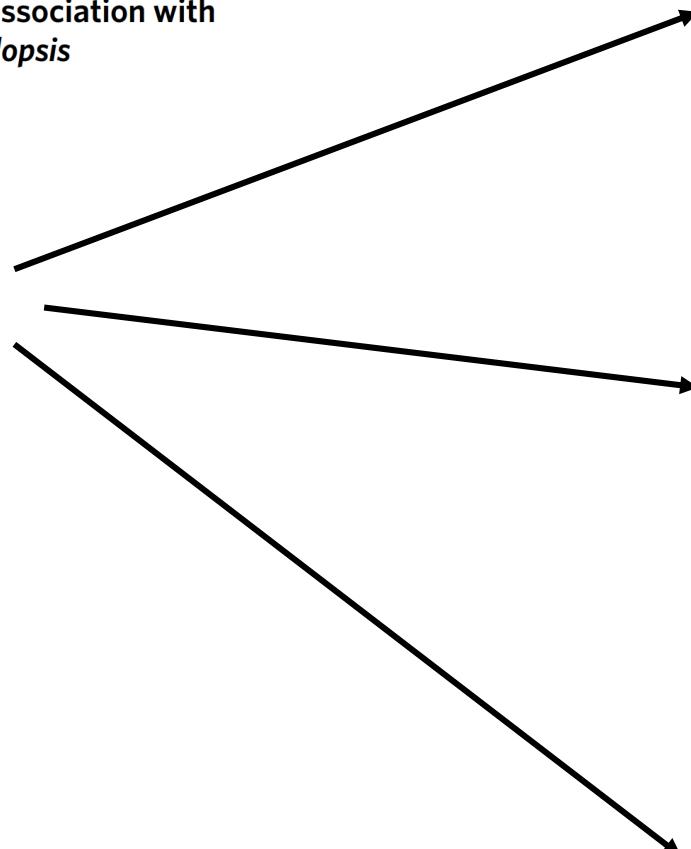
<https://doi.org/10.1038/s41559-018-0754-5>

nature  
ecology & evolution

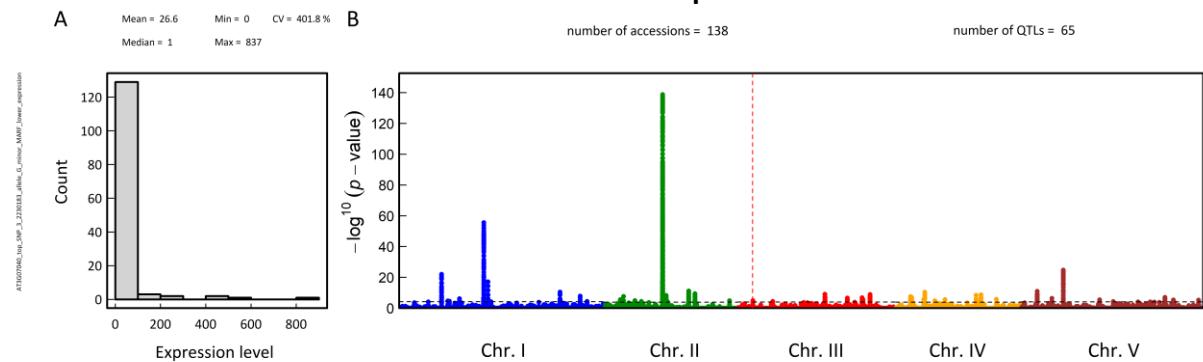
## Phenotypic and genome-wide association with the local environment of *Arabidopsis*

Ángel Ferrero-Serrano \* and Sarah M. Assmann \*

471 abiotic factors



lower expression



higher expression

