

Dynamics of disease resistance polymorphism at the *Rpm 1* 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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Journal of Experimental Botany, Vol. 67, No. 7 pp. 2093–2105, 2016
doi:10.1093/jxb/erv530
This paper is available online free of all access charges (see http://jxb.oxfordjournals.org/open_access.html for further details)



RESEARCH PAPER

Modulation of *R*-gene expression across environments

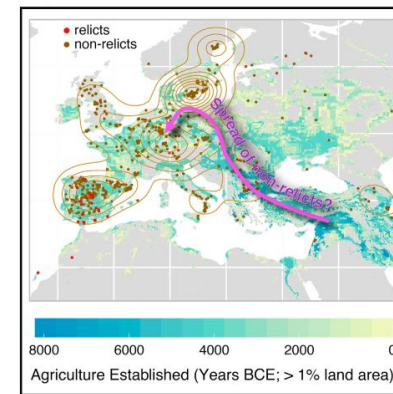
Alice MacQueen and Joy Bergelson*

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

Cell

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

Graphical Abstract



Authors

The 1001 Genomes Consortium

Correspondence

magnus.nordborg@gmi.oeaw.ac.at (Magnus Nordborg),
weigel@weigelworld.org (Detlef Weigel)

In Brief

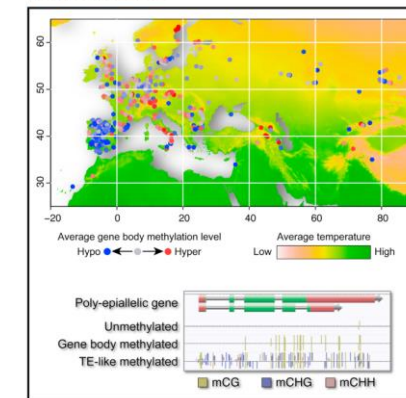
Genomic sequencing analysis of over 1,000 natural inbred lines of *Arabidopsis thaliana* reveals its global population structure, migration patterns, and evolutionary history and provides a rich genetic resource for studying phenotypic variation and adaptation.

Resource

Cell

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

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In Brief

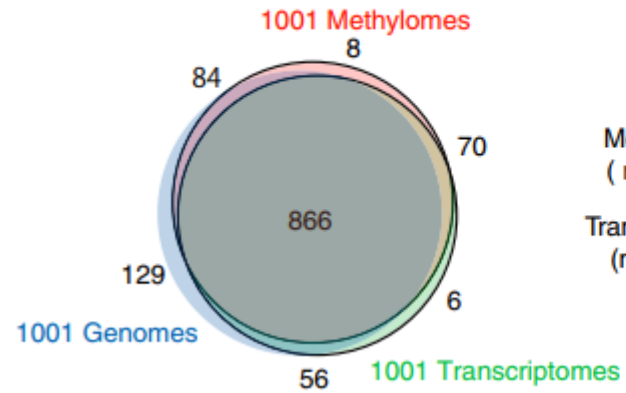
Methylomes and transcriptomes from >1,000 *Arabidopsis thaliana* accessions provide insights on how the epigenome is shaped by natural genomic variation and by the environment.

Resource

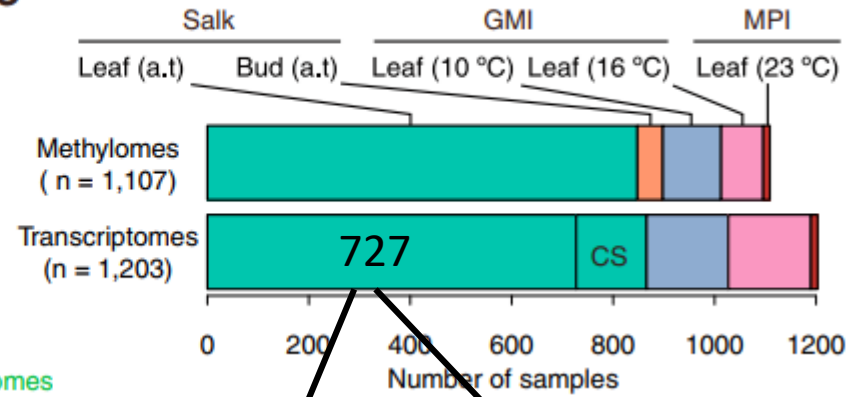
In 2016, I had the following question:

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

A



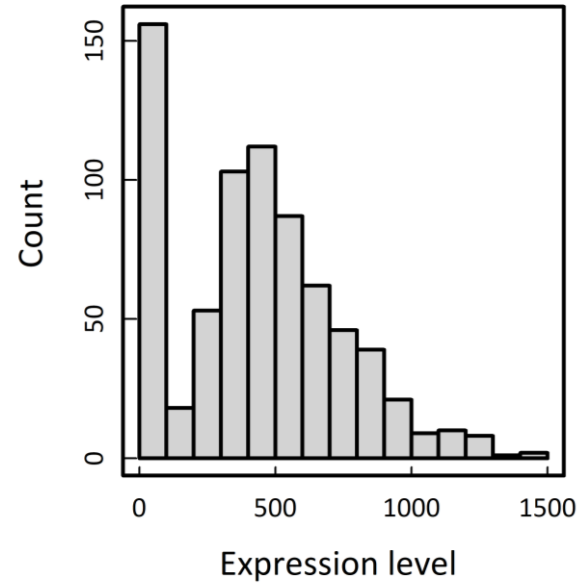
C



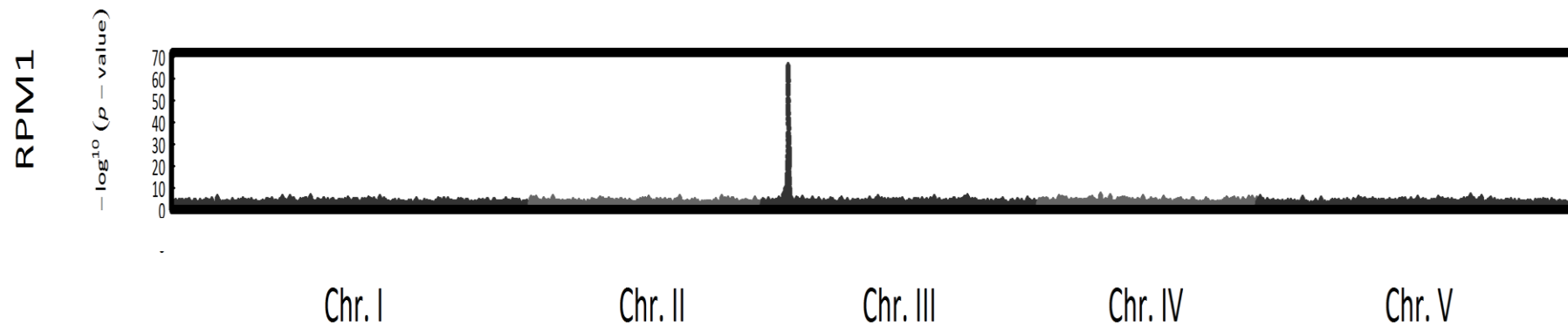
Expression level (normalized count)
for 24,030 genes

Genome sequences for 665 accessions

Variation among accessions in *RPM1* expression



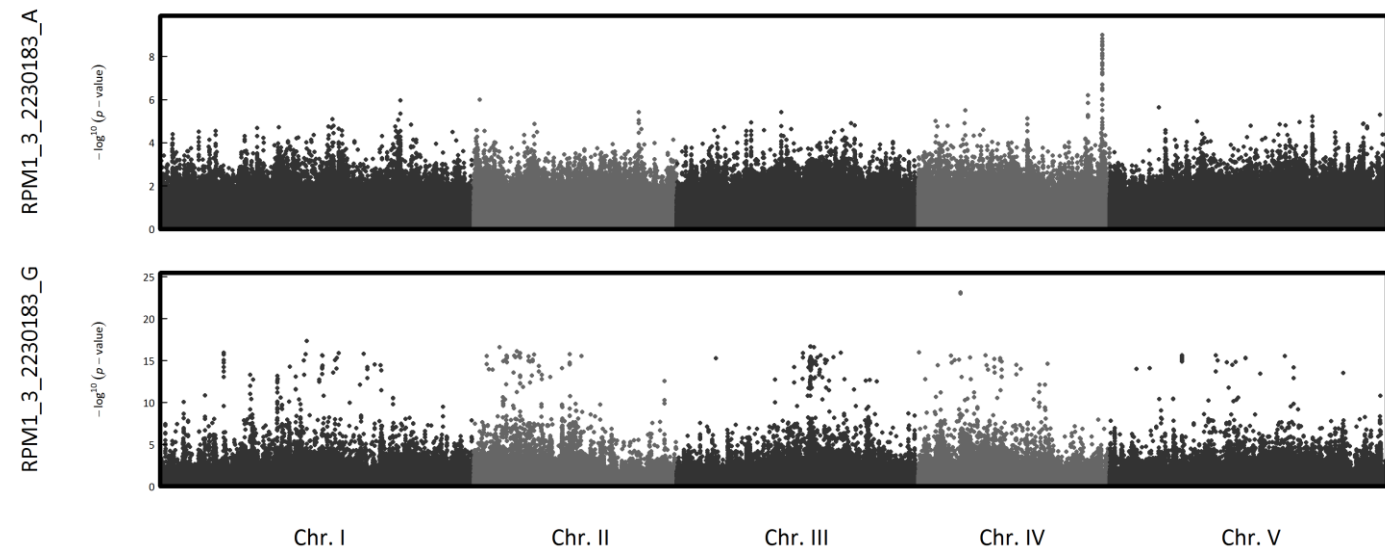
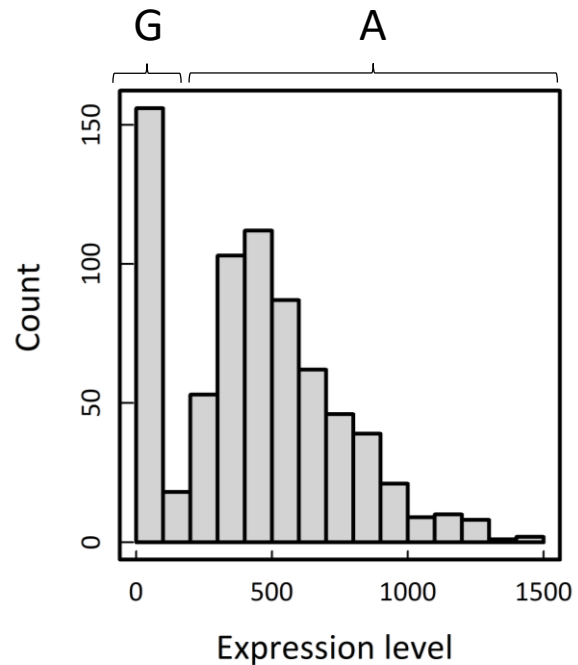
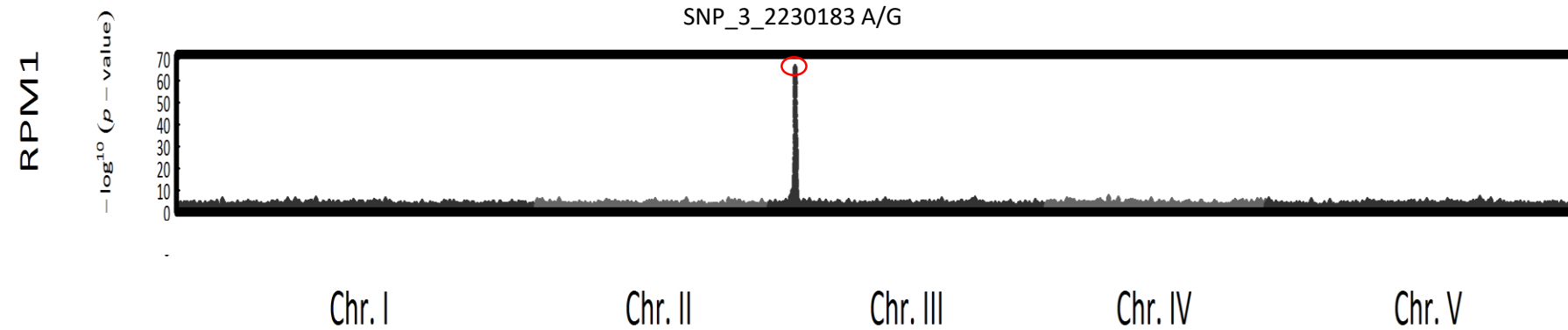
GWA mapping (EMMAX: linear mixed model)



Next step: nested GWA mapping

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

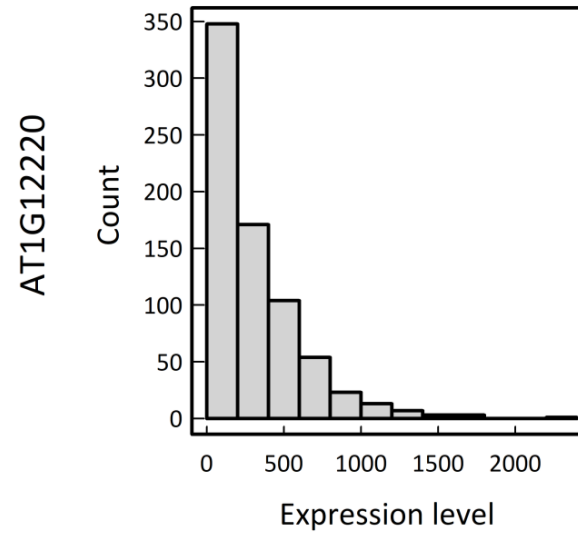
Carine Huard-Chauveau^{1,2}, Laure Perchepped^{1,2}, Marilyne Debieu^{1,2,3}, Susana Rivas^{1,2}, Thomas Kroj^{1,2}, Ilona Kars^{1,2}, Joy Bergelson⁴, Fabrice Roux³, Dominique Roby^{1,2*}



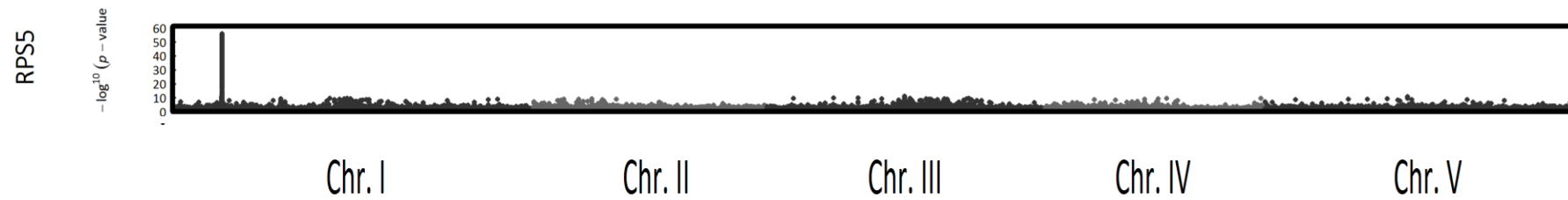
N = 516 acc

N = 138 acc

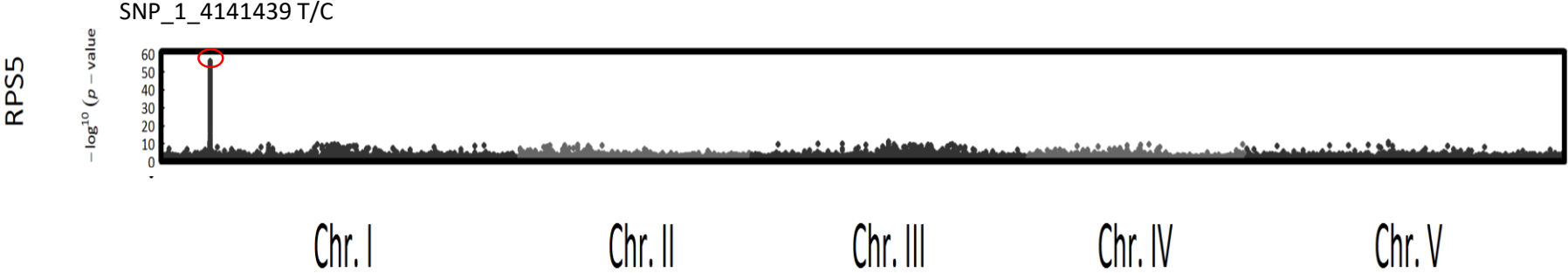
Variation among accessions in *RPS5* expression



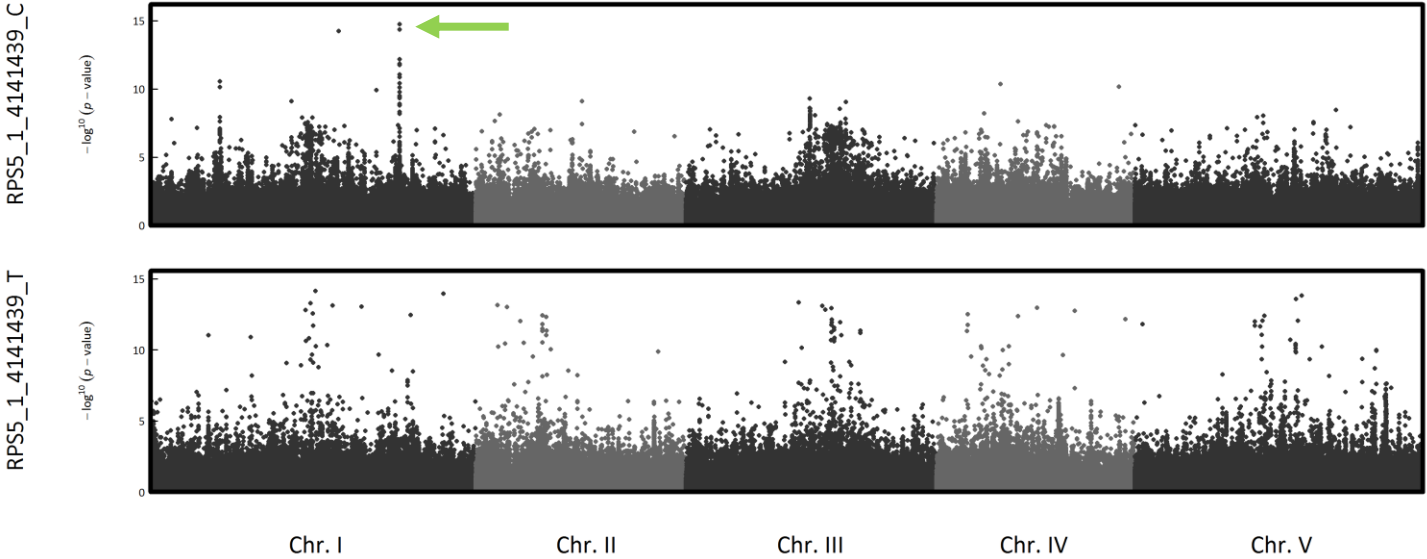
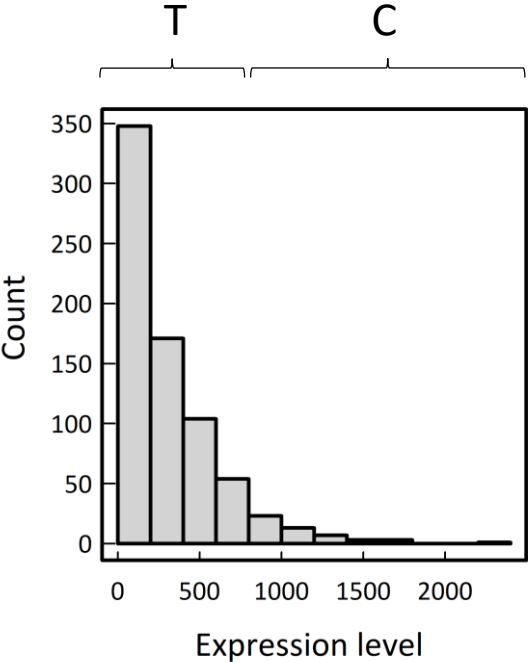
GWA mapping (EMMAX: linear mixed model)



Nested GWA mapping



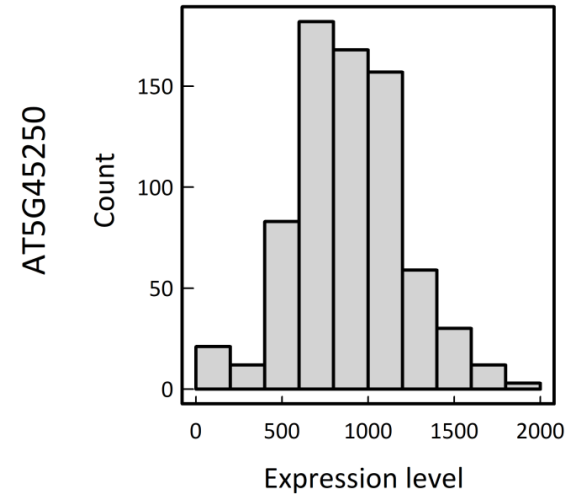
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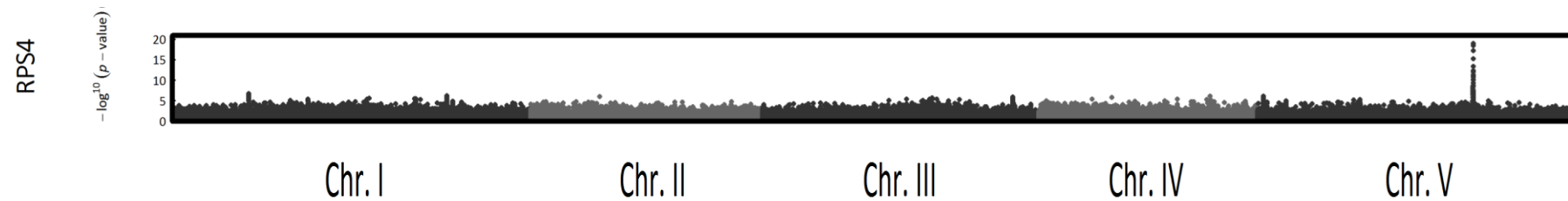
N = 358 acc

N = 261 acc

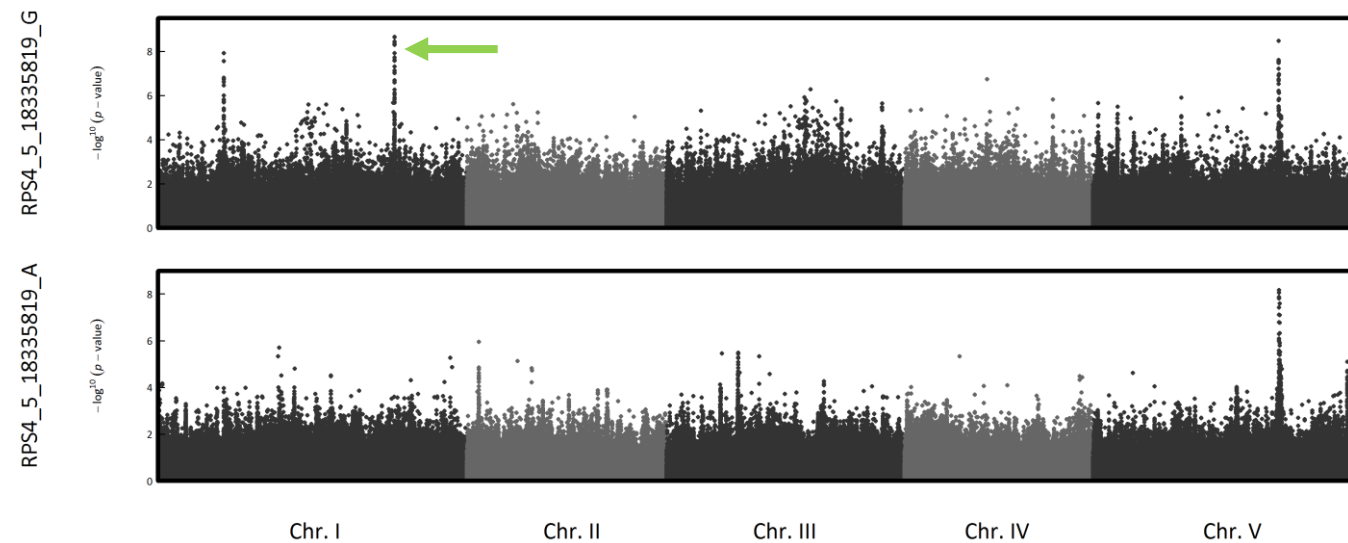
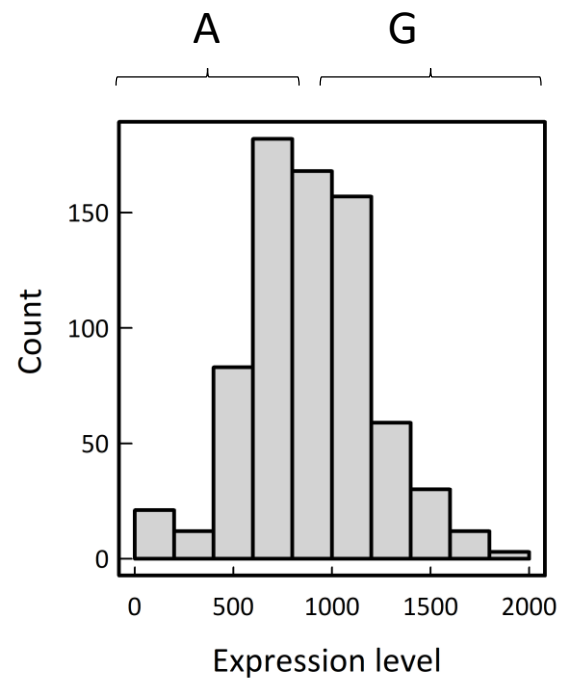
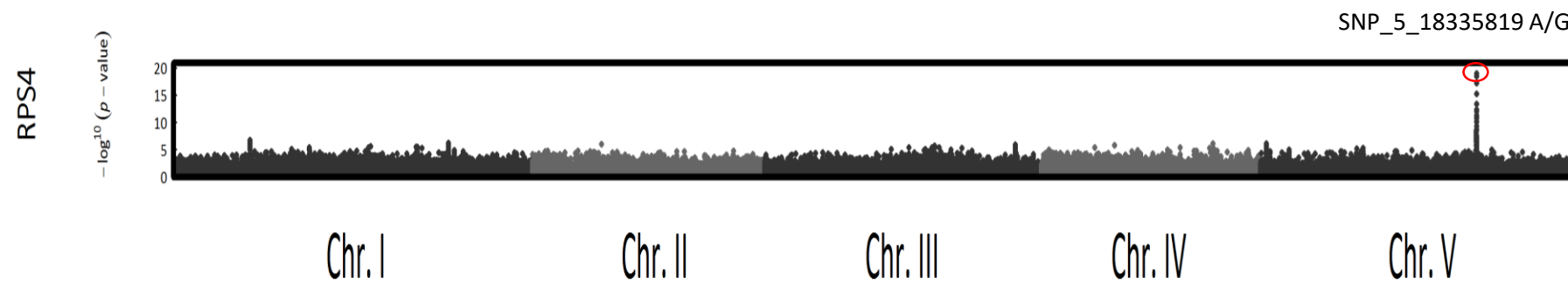
Variation among accessions in *RPS4* expression



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)



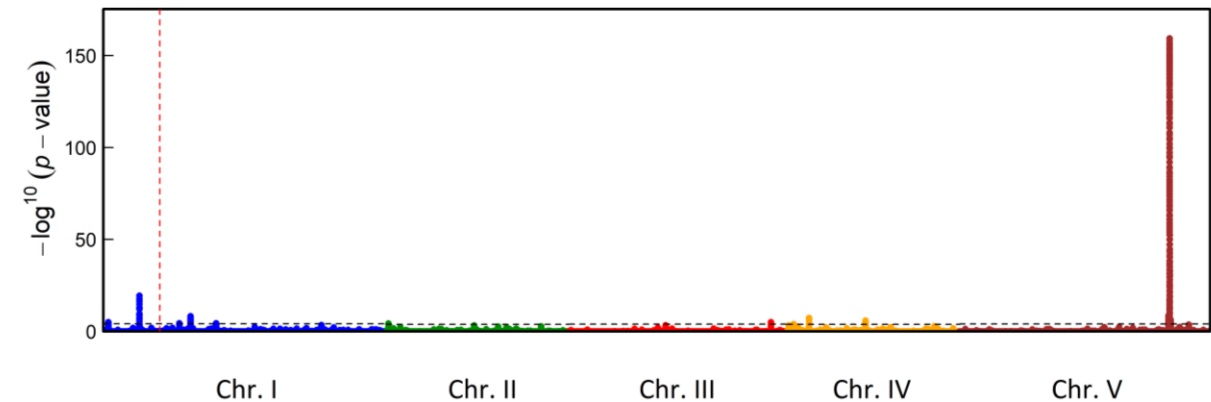
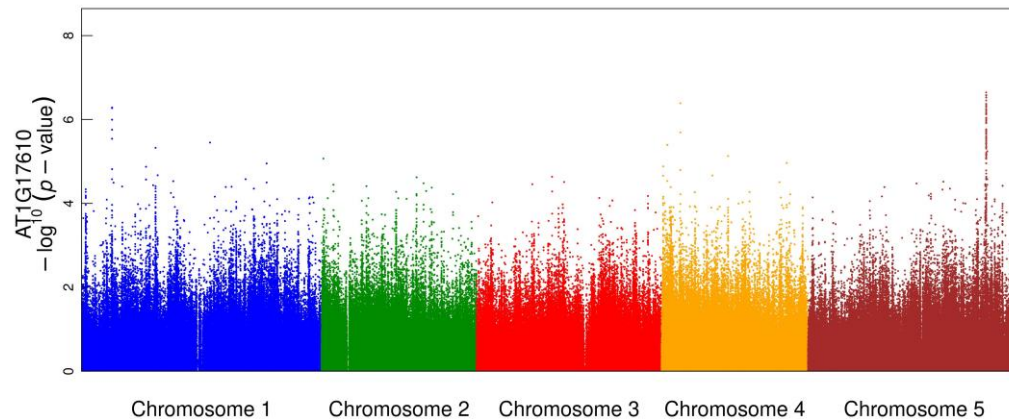
GWA mapping: EMMAX + local score approach

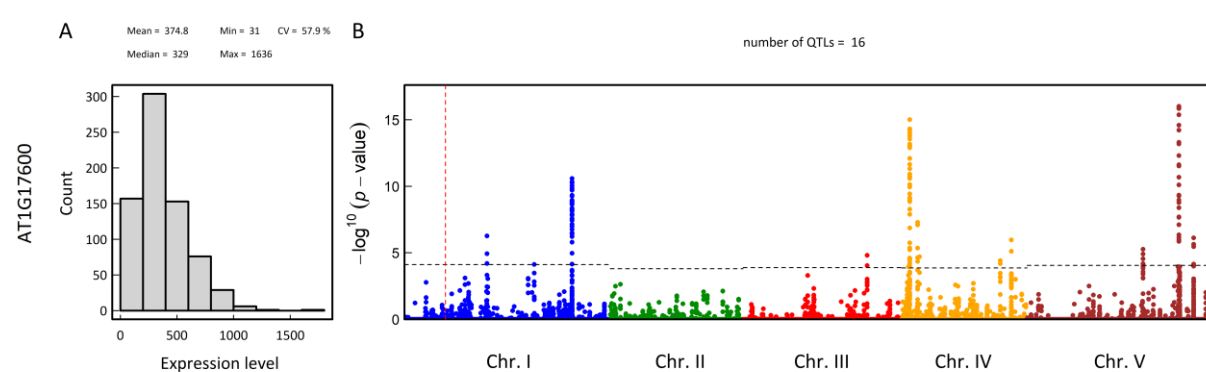
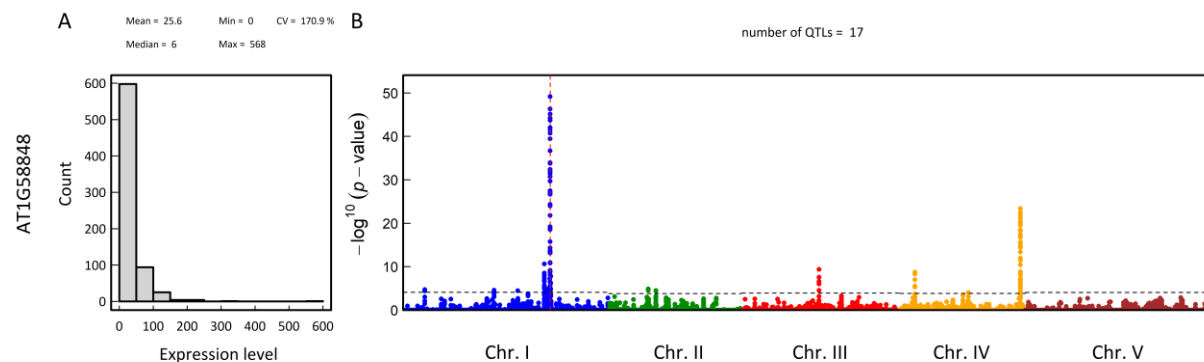
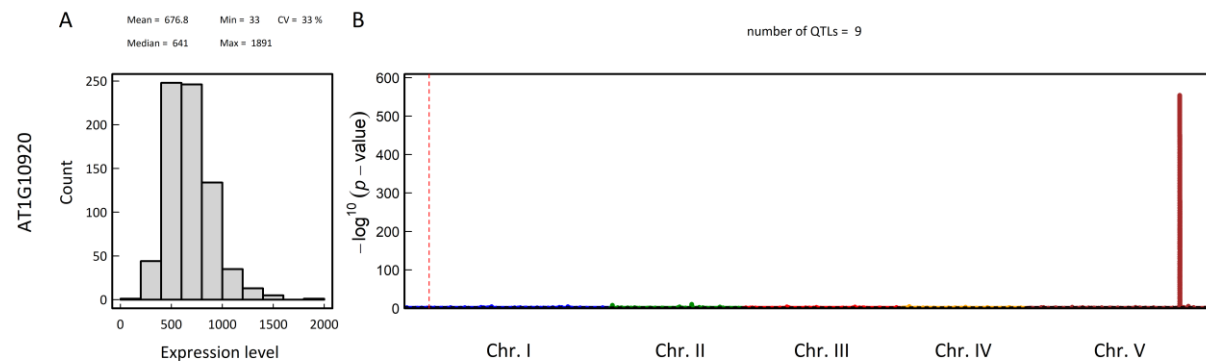
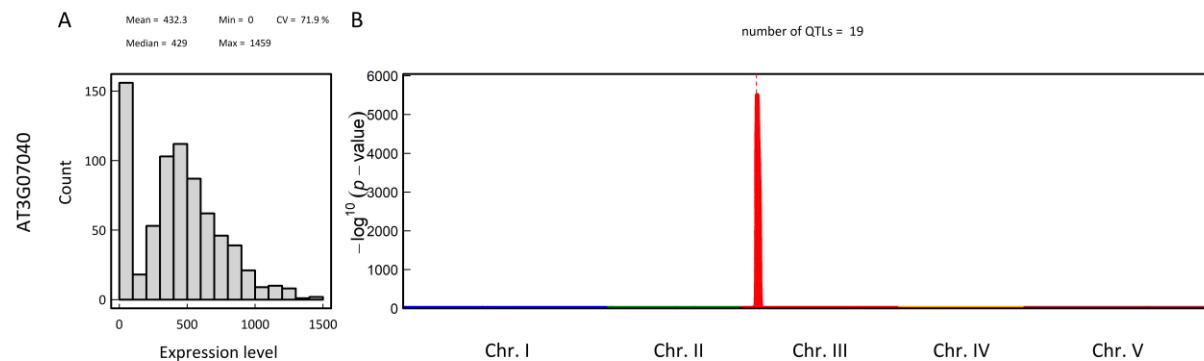
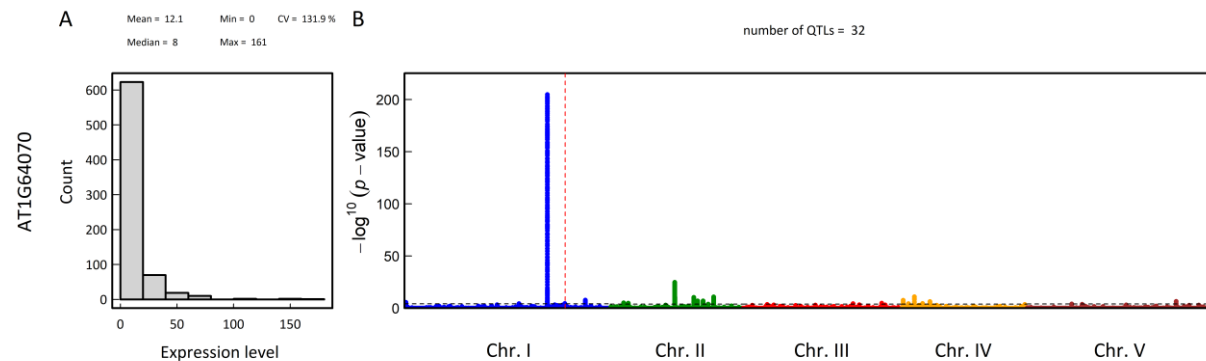
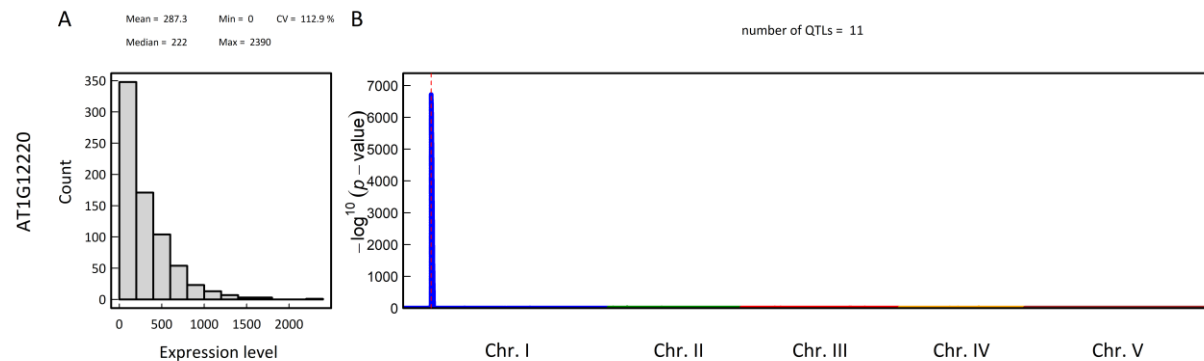
ORIGINAL ARTICLE

WILEY **MOLECULAR ECOLOGY**

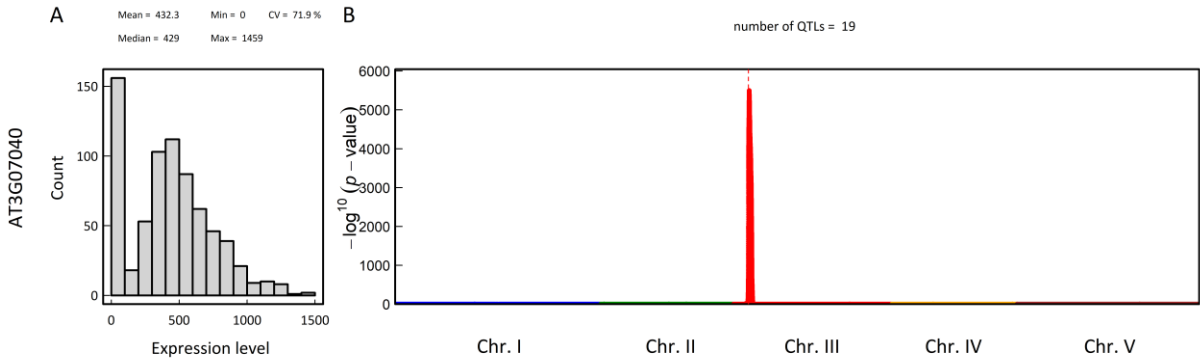
Accounting for linkage disequilibrium in genome scans for selection without individual genotypes: The local score approach

María Inés Fariello^{1,2,3} | Simon Boitard¹ | Sabine Mercier^{4,5} | David Robelin¹ |
Thomas Faraut¹ | Cécile Arnould⁶ | Julien Recoquillay^{7,8} | Olivier Bouchez^{1,9} |
Gérald Salin^{1,9} | Patrice Dehais¹⁰ | David Gourichon¹¹ | Sophie Leroux¹ |
Frédérique Pitel¹ | Christine Leterrier⁶ | Magali SanCristobal^{1,5,12,13}



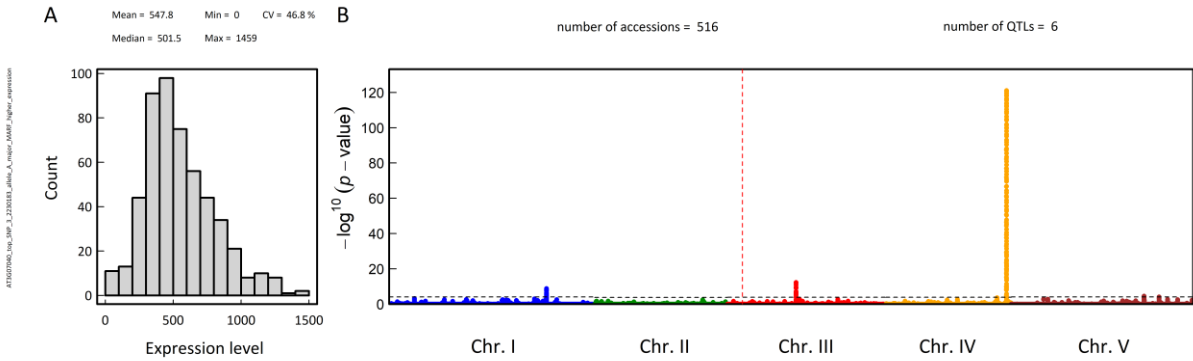
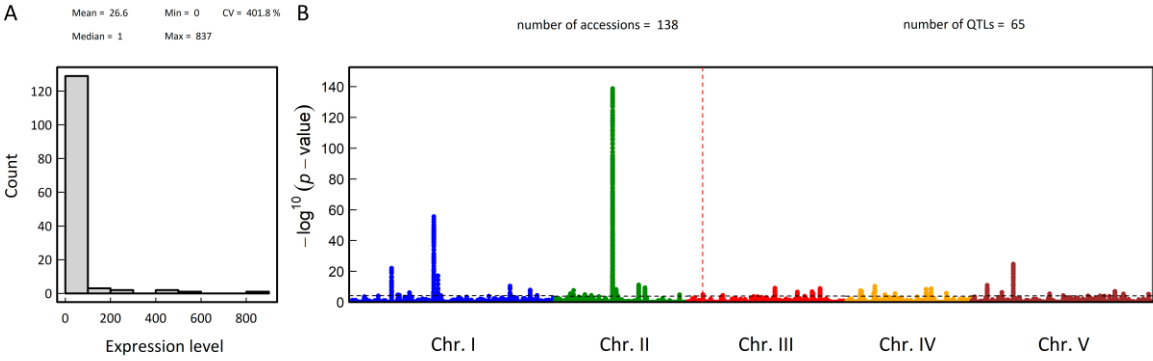


Variation among accessions in *RPM1* expression

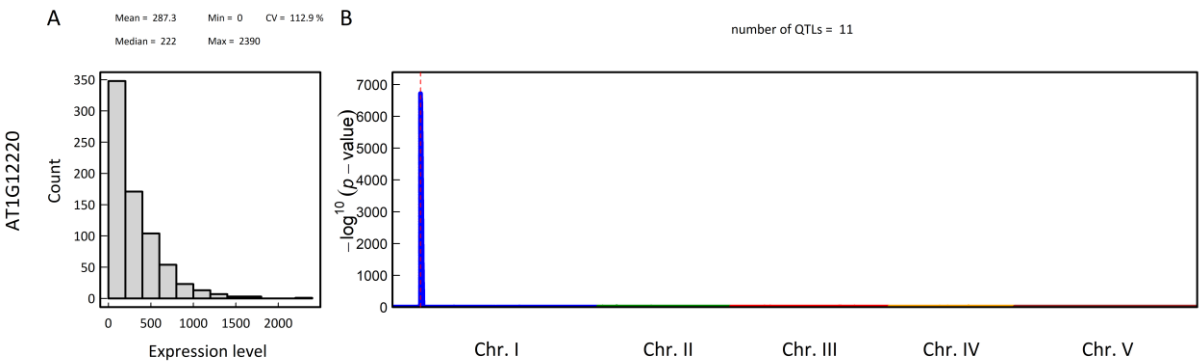


lower expression

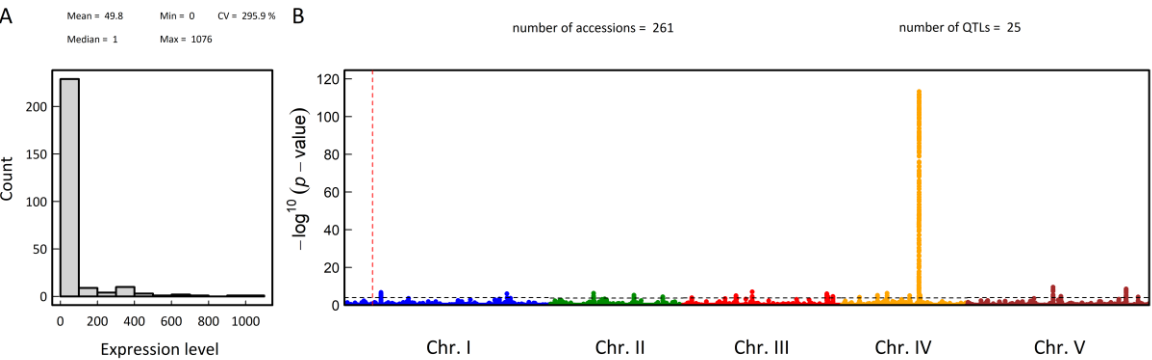
higher expression



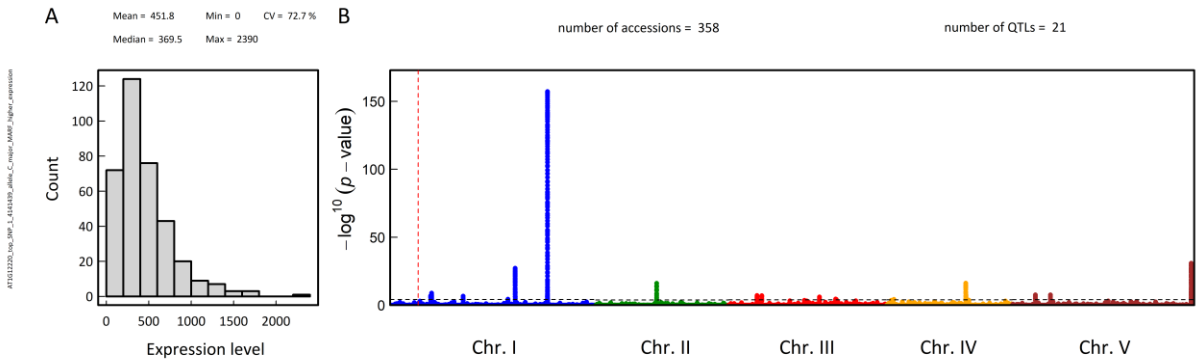
Variation among accessions in *RPS5* expression



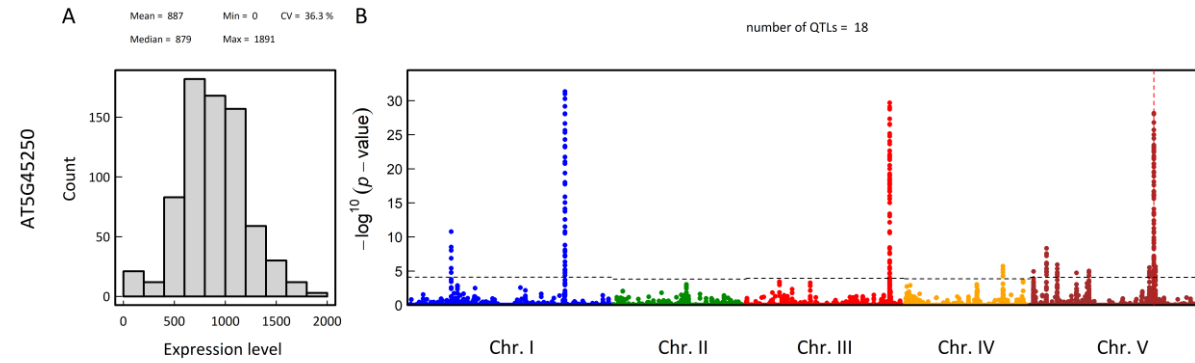
lower expression



higher expression

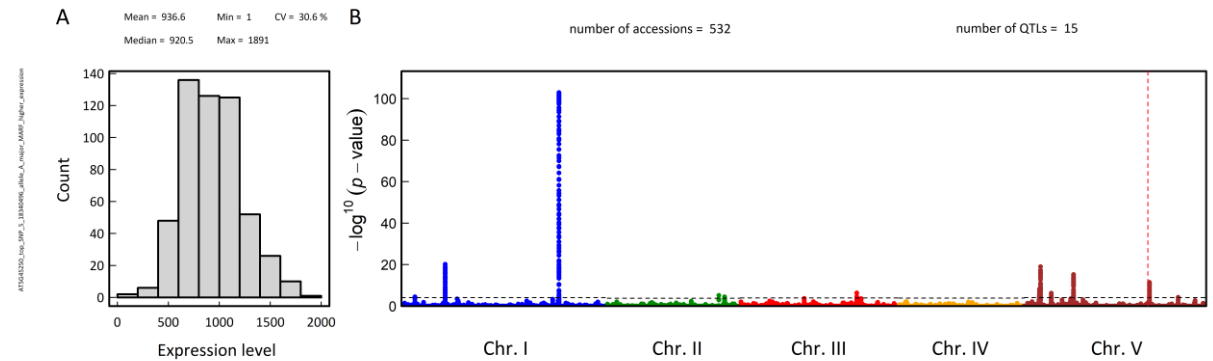
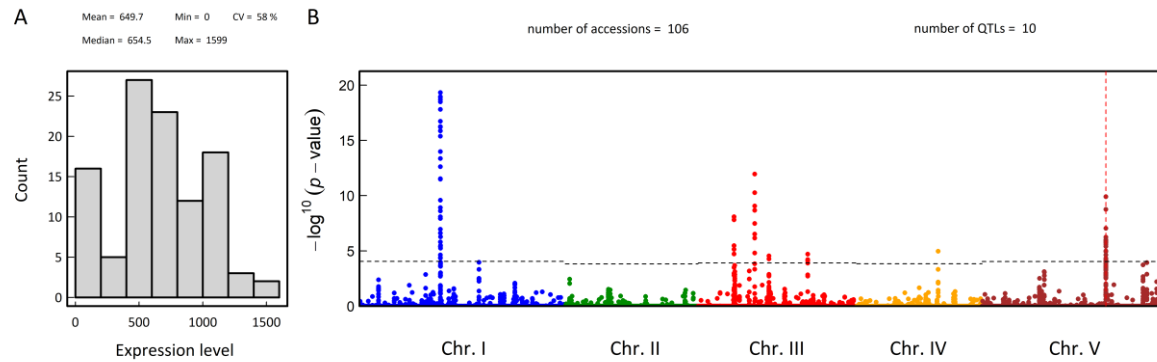


Variation among accessions in *RPS4* expression



lower expression

higher expression



Ecology – expression relationships

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

Ángel Ferrero-Serrano¹ and Sarah M. Assmann¹

471 abiotic factors

