The genome response of *Drosophila suzukii* during its worldwide invasion

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Background

During an invasion: need to adapt to new environments over a short period of time
→ plastic and/or genomic response

The fruit fly *Drosophila suzukii* as a biological model
− native to Asia and recent ongoing invasion (1980 to present time) on a worldwide scale:
Hawai, North/South America, Europe, Reunion Island

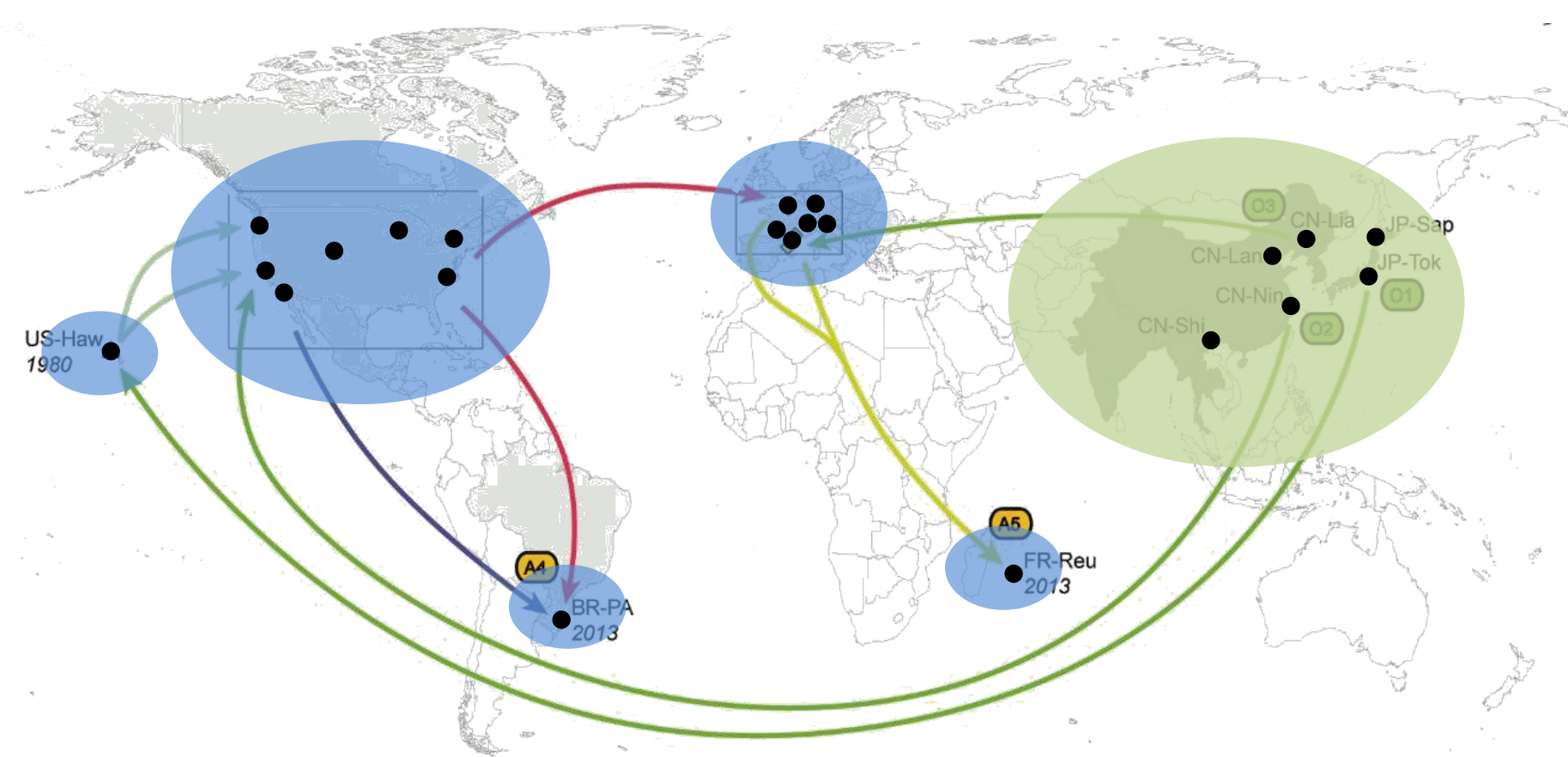− new environment → climatic and other (biotic and abiotic) constraints?

Approach

Genome response to climate variables
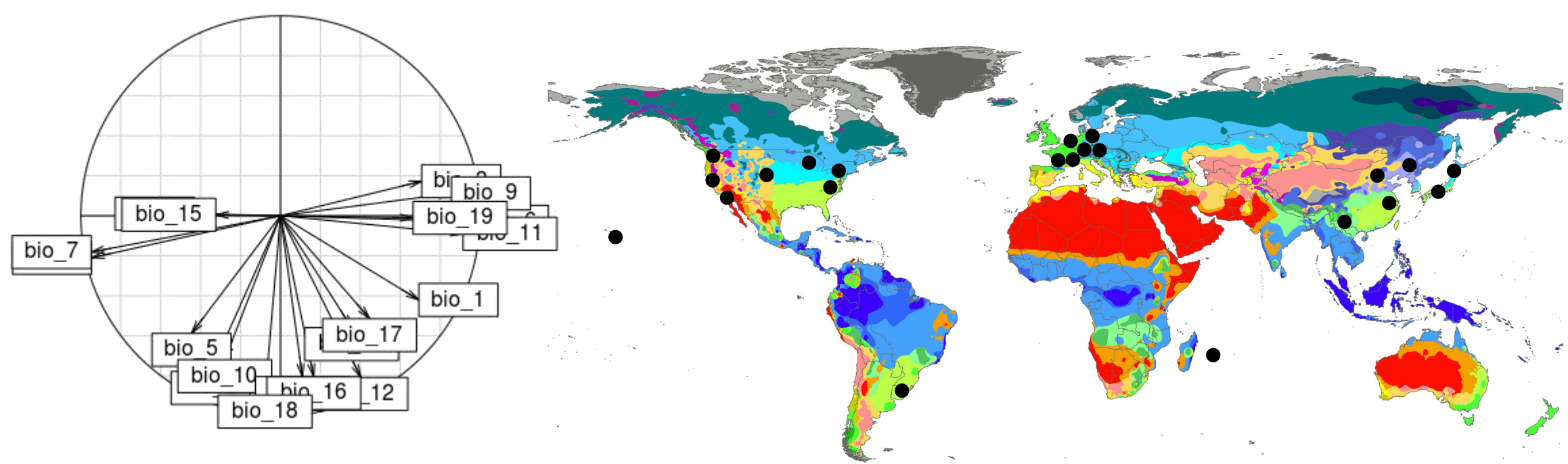
19 bioclimatic variables[1]

Genome response to invasion success


Invaded *vs* **Native** range

Methods

Whole genome pool sequencing
22 populations: 6 native and 16 invasive
60X coverage and n=50 to 100 individuals per pool
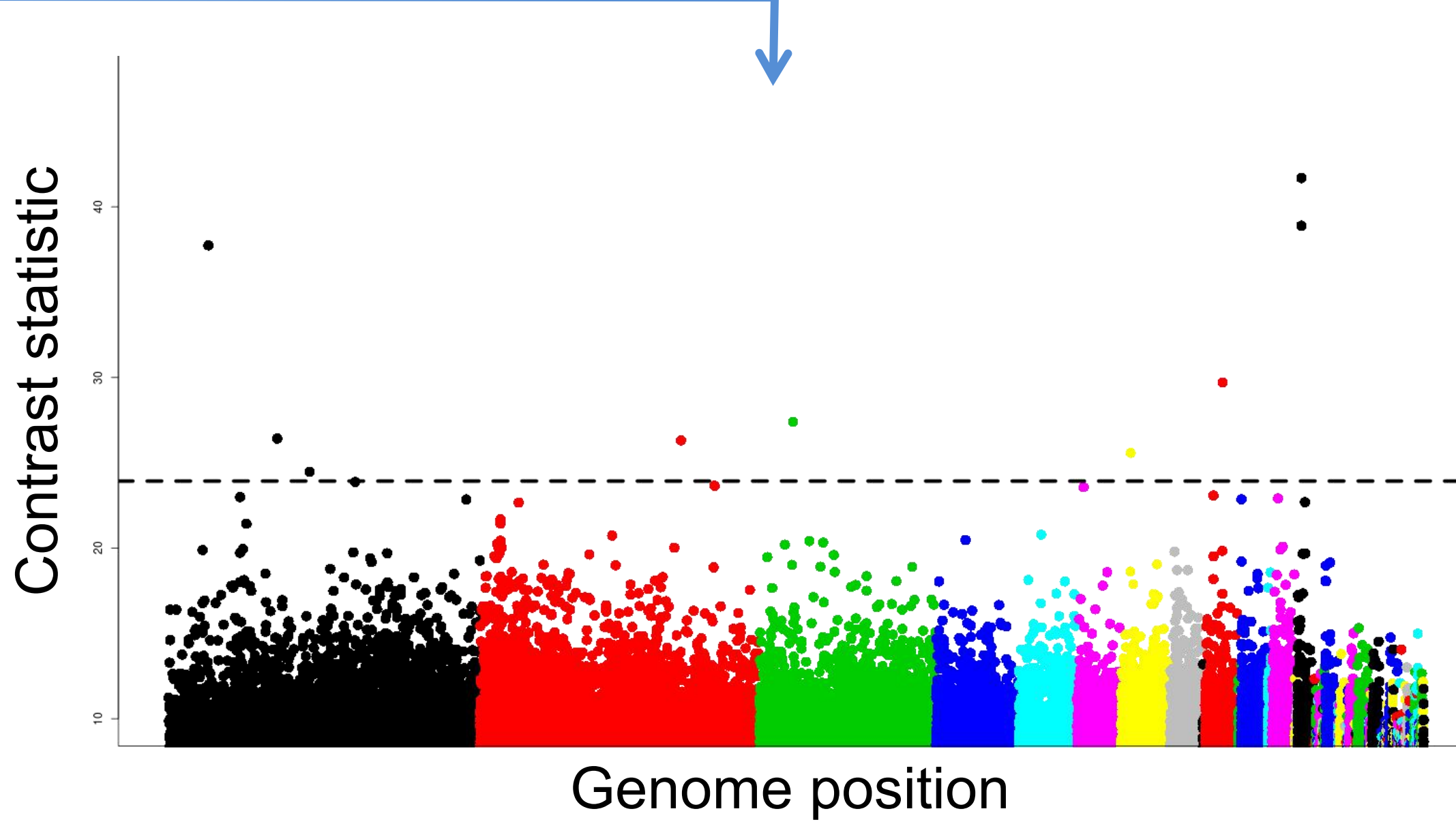
Bioinformatic treatments
Read mapping (*bwa*) on a newly developed high quality assembly[2] (total length=268 Mb, N50=2.6Mb, 546 contigs)
Variant calling (*VarScan*): ~12 x 10⁶ SNP

Results

Association with climate variables
(BAYPASS software[3])
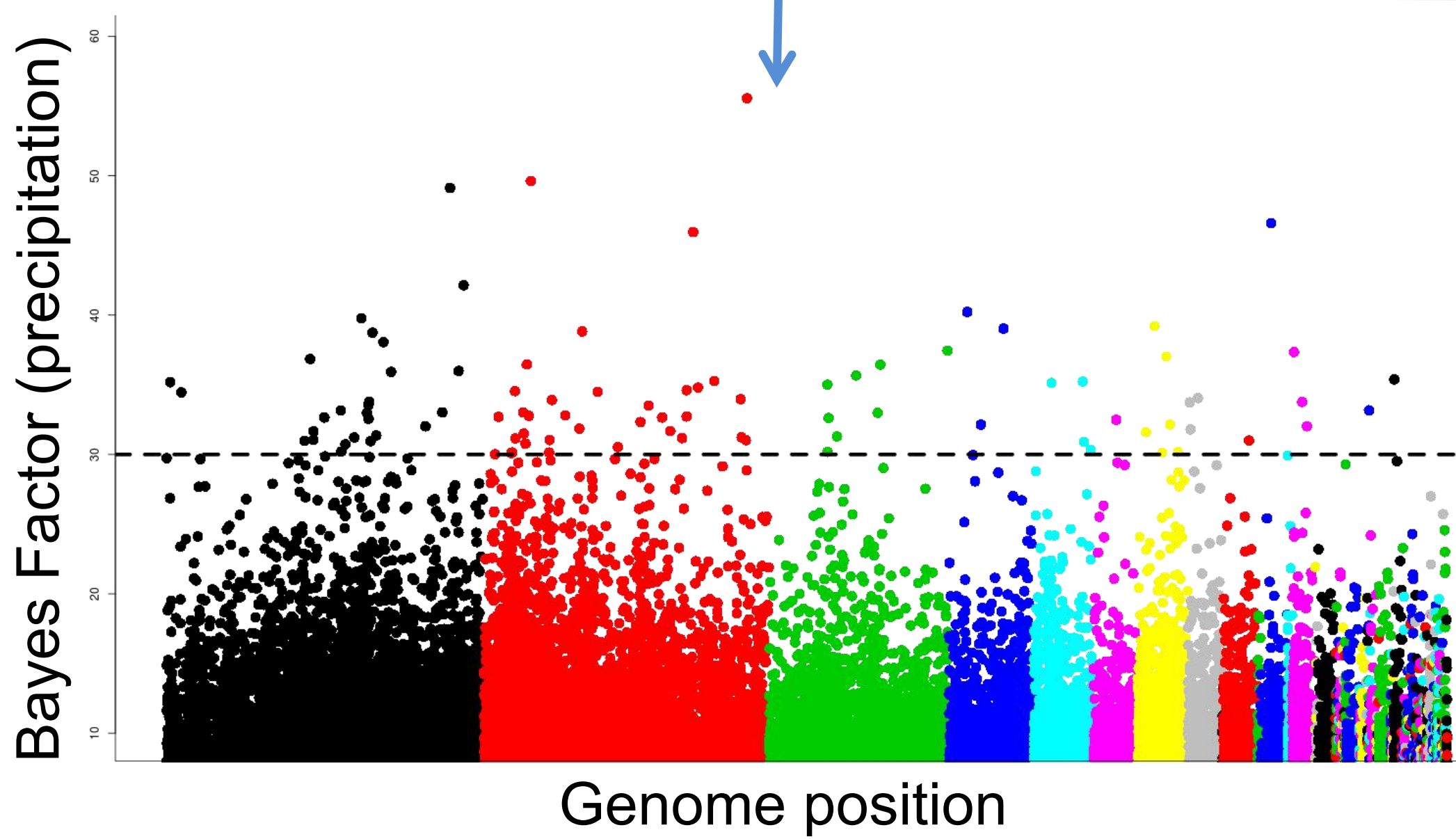
Many highly significant SNPs

Association with invasive *vs* native status
(BAYPASS software: Contrast analysis[4])

Few highly significant SNPs

Perspectives

Global functional analysis to identify
the main physiological pathways involved
in climate adaptation

↓ reverse ecology

Validation using quantitative
genetics approaches

Limited number of genes with
yet unknown functions

↓

Focal exploration and validation
using functional genomic
tools (e.g. RNAi, genome editing)

Take home message

Significant signals indicating a genome response
• many genes associated to climate variables
• only a few genes associated with invasive status
→ **Traits involved in the invasion success?**

References:
1. www.wordclim.org
2. Prud'Homme and Gompel Labs, unpublished
3. Gautier (2015) *Genetics* 201,1555-79
4. Gautier in prep.