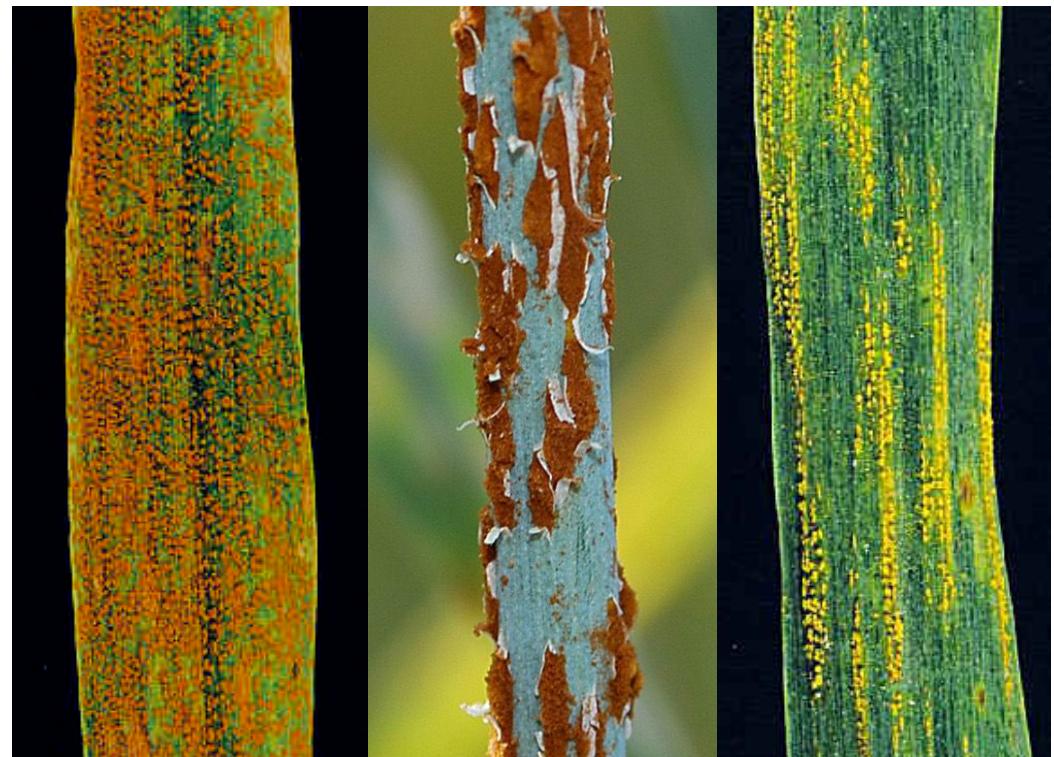


Map-based cloning in complex uncharacterized plant genomes

10 August 2017

Dr. Matthew Moscou
The Sainsbury Laboratory

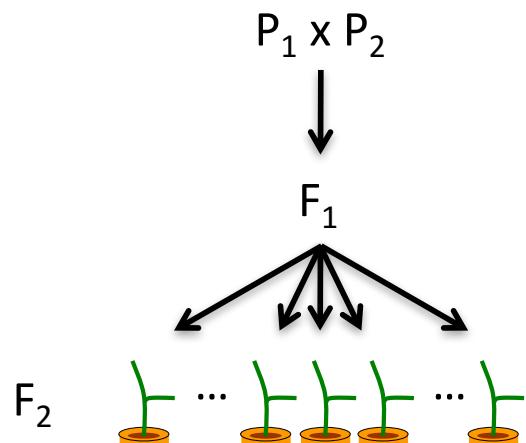
matthew.moscou@tsl.ac.uk



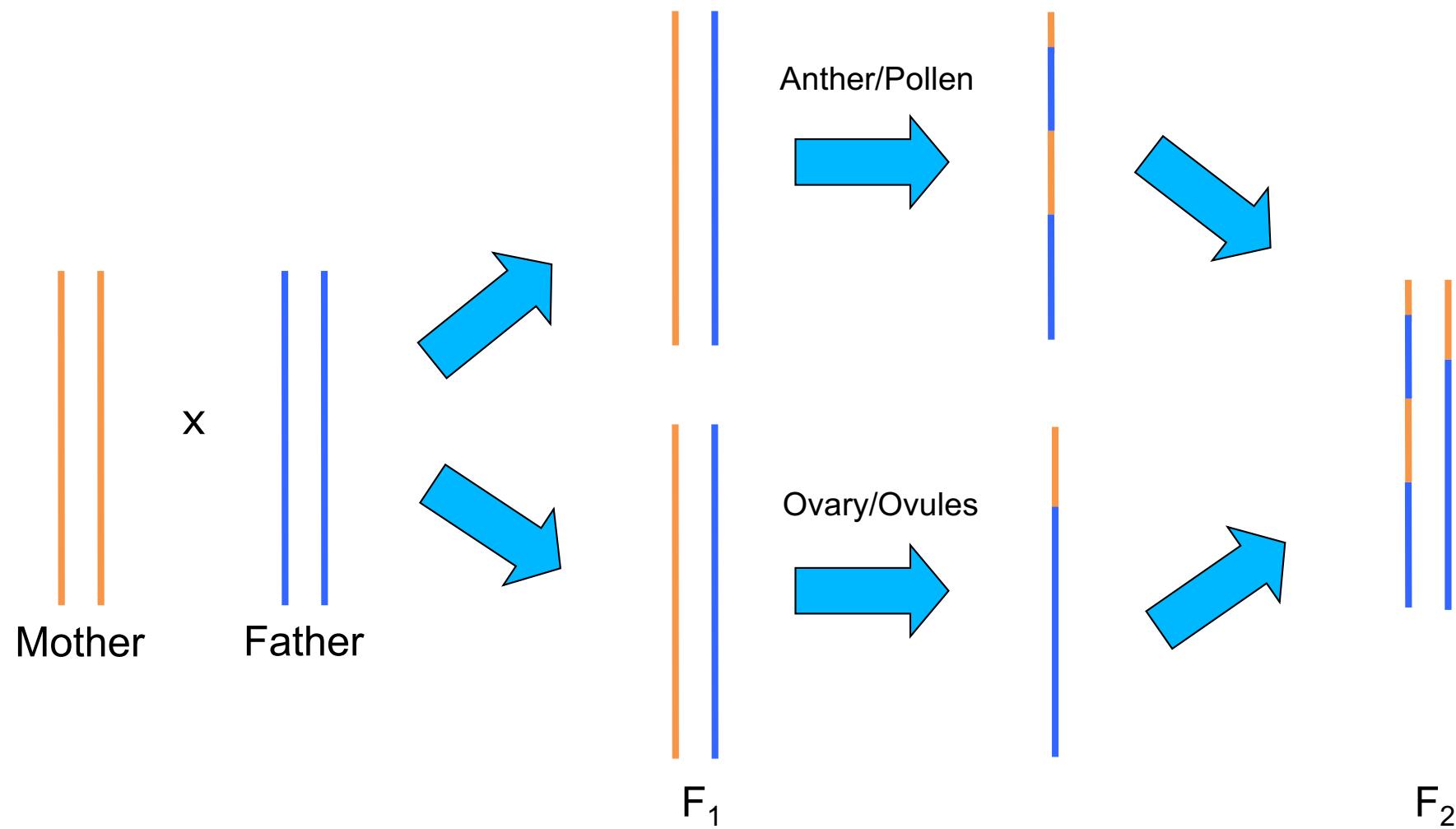
Mendelian genetics

Mendel's First Law - the law of segregation

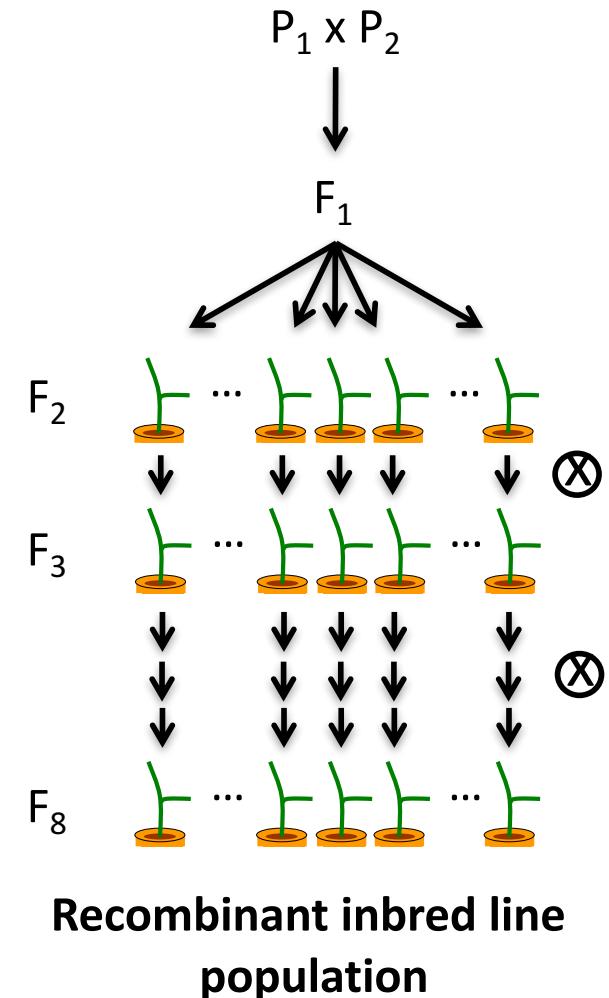
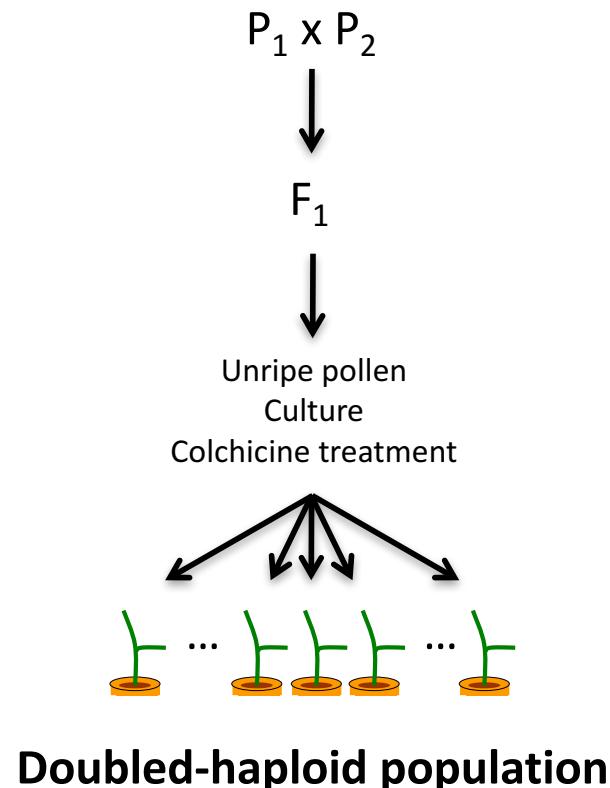
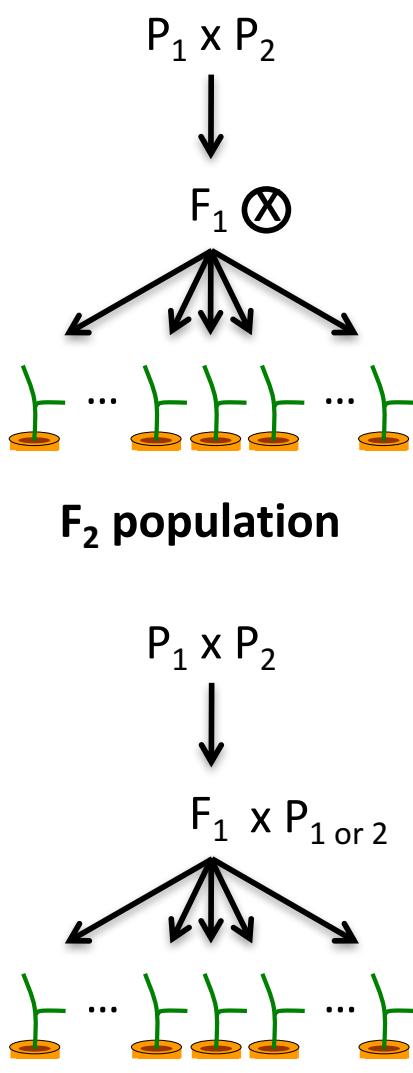
Mendel's Second Law - the law of independent assortment



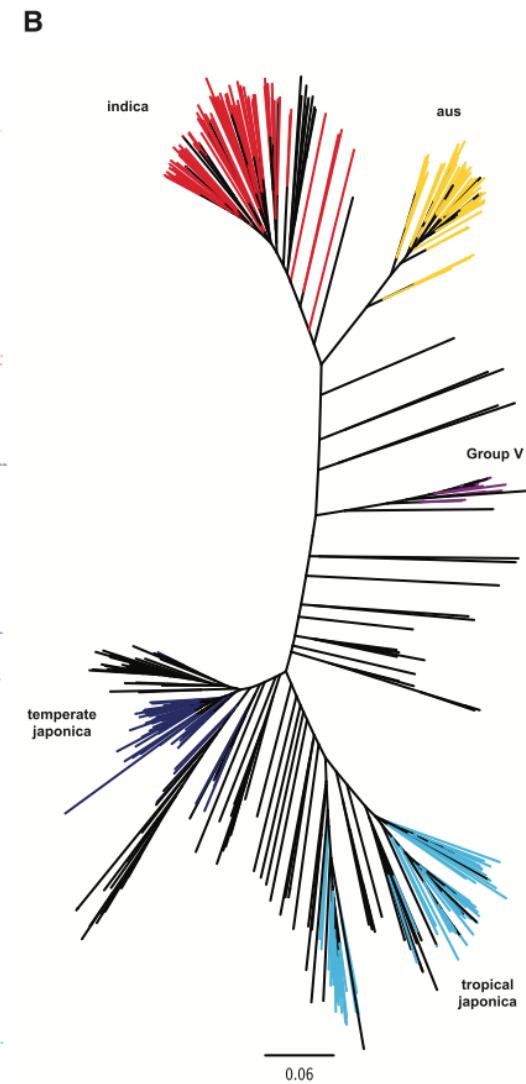
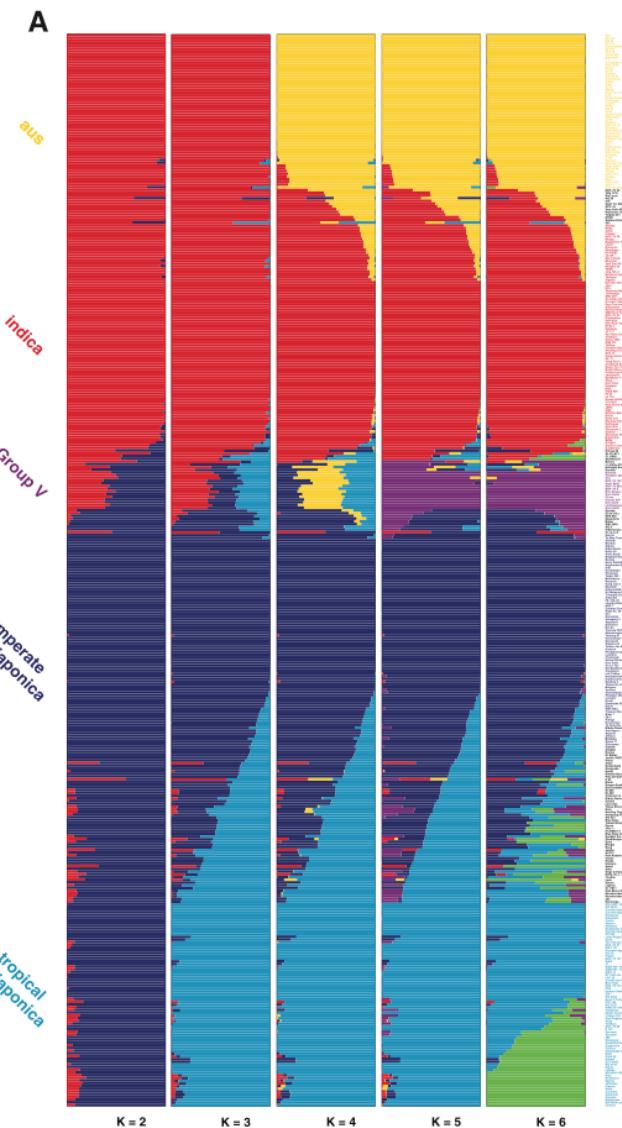
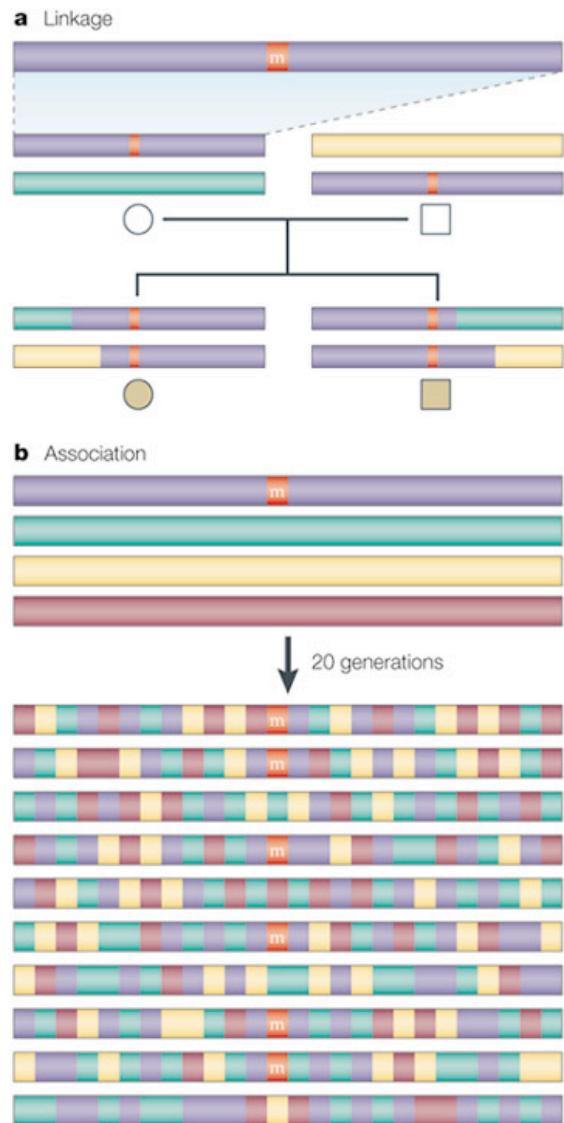
Recombination



Linkage-based mapping



Association mapping



Introgression-based mapping

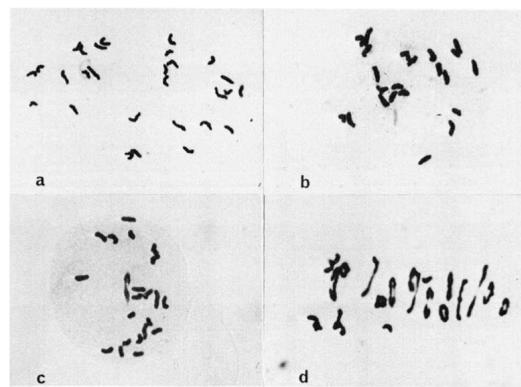


FIG. 1.—Chromosome configurations at metaphase I in pmcs of some wheat×barley F₁ hybrids. a, 28-chromosome normal hybrid (28 I), ×700; b, 22-chromosome hybrid (22 I), ×820; c, 23-chromosome hybrid (21 I+1 II), ×720; d, 35-chromosome hybrid (15 II+5 I), ×970.

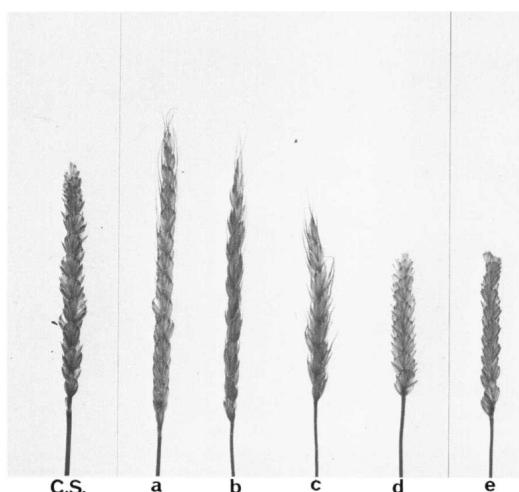


FIG. 2.—Spike morphology of the wheat parent and some wheat×barley F₁ hybrids, ×0.57. C.S., Chinese Spring parent; a, 28-chromosome normal hybrid; b, 31-chromosome hybrid; c, 27-chromosome hybrid; d, 23-chromosome hybrid; e, 21-chromosome "hybrid" (haploid wheat).

TABLE 2

Disomic wheat-barley addition lines and their morphological, physiological and biochemical characteristics

Initial designation	Addition line		Morphological, physiological differences from Chinese Spring	Biochemical* characters of barley
	Barley chromosome present (Islam, 1980)			
4H	A	4	Thick culms and apically awnleted spikes often having supernumerary spikelets	ADH; ACPH; β-Am
5H	B	7	Thick culms and long lax spikes with larger florets and longer anthers	—
6H	C	6	Tapered spikes, with outwardly-curved beaks on lemmas	GOT; AMP
7H	D	1	Bushy at juvenile stage, many tillered with prolonged flowering habit and poor fertility	EST-1.-2; EP
2H	E	2	Prostrate habit at juvenile stage, slender culms with narrow leaves and narrow, elongated florets with awnlets	G6PD
3H	F	3	Similar to Chinese Spring but the spikes are usually smaller and more dense	EST-3, -4
1H	G	5	Not obtained because of sterility	Hordeins; PGI; MDH

* ADH = Alcohol Dehydrogenase; GOT = Glutamic Oxaloacetic Transaminase; AMP = Aminopeptidase; EP = Endopeptidase; EST = Esterase; ACPH = Acid Phosphatase; PGI = Phosphoglucose Isomerase; MDH = Malate Dehydrogenase; G6PD = Glucose-6-phosphate Dehydrogenase; β-Am = β-amylase. From Hart *et al.* (1980) and Powling *et al.* (1981).

Genetic-based approach

Practical considerations

Genome size

Ploidy

Length of genetic map

Degree of genetic variation

Seed generated per plant

Number of researchers working on the organism

Marker development

Phenotypic markers

First-generation markers

Restriction fragment length polymorphism

Second-generation markers

CAP, RAPD, AFLP, S-SAP, SSR, ISSR, VNTR, STS, SCAR, SAMPL

Third-generation markers

Single nucleotide resolution (SNPs, InDels)

Other marker assays

Microarray (DArT, TDM)

Marker assays: Single nucleotide polymorphism

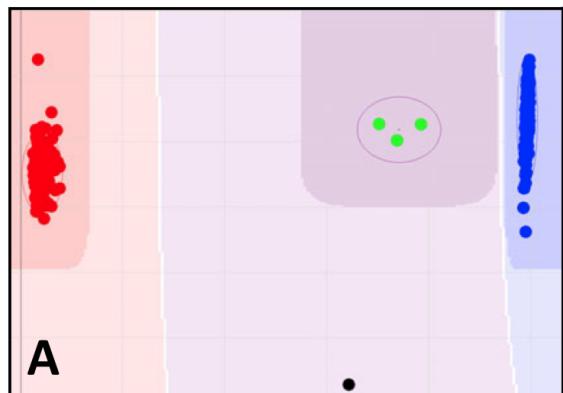
PCR-based

Sequenom

KASP

Fluidigm

GoldenGate OPA

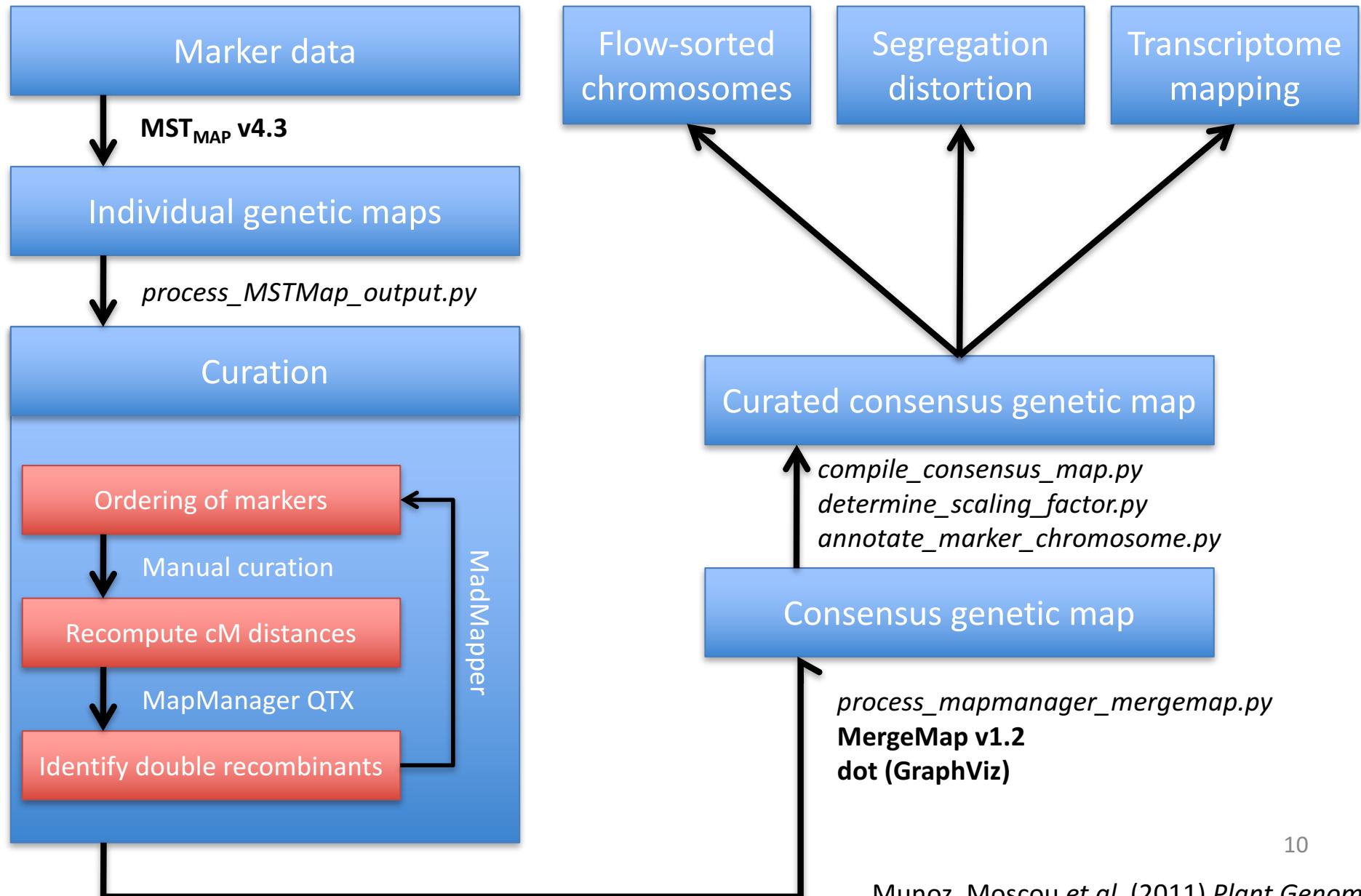


Sequencing-based

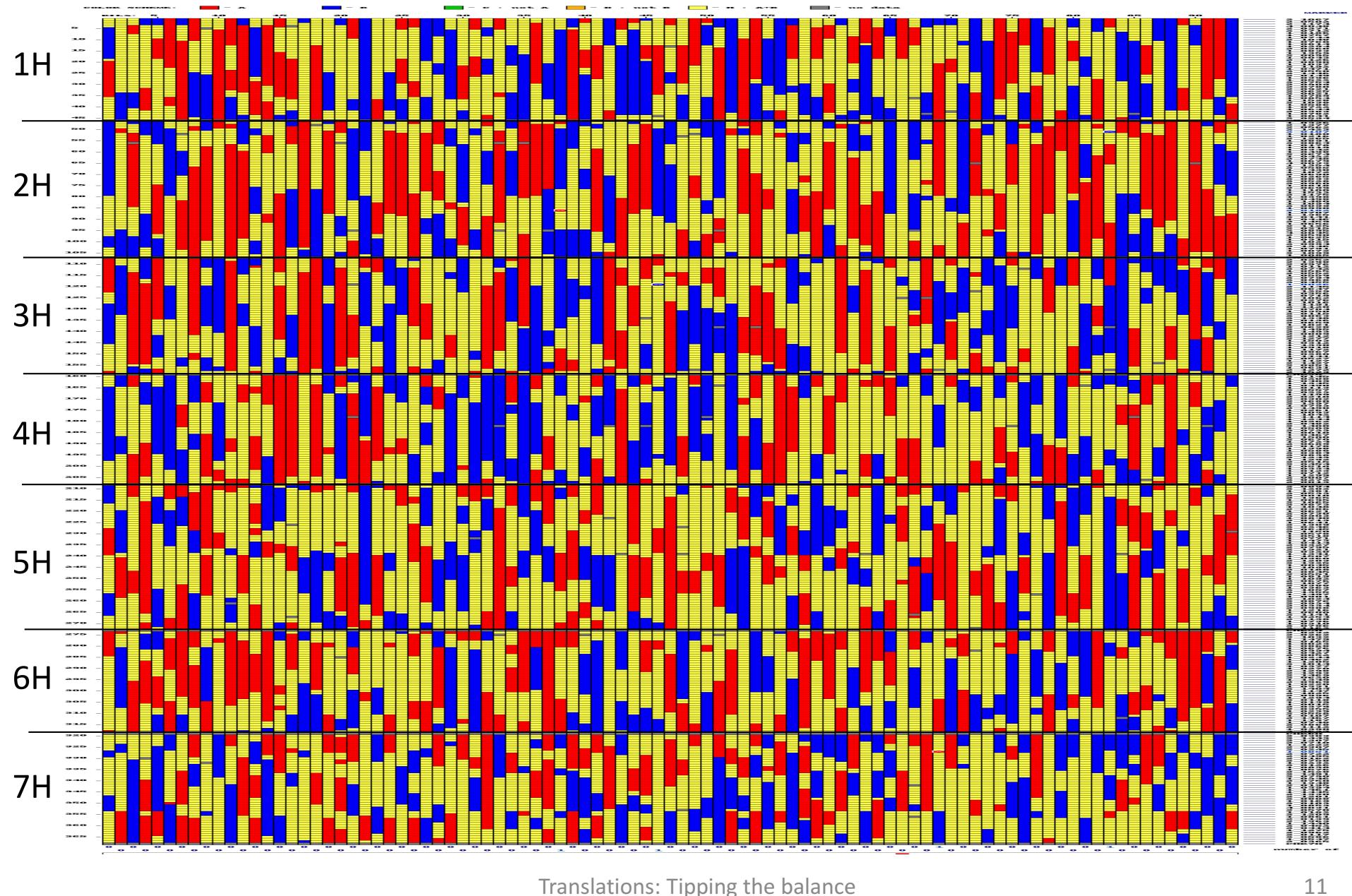
Full genome sequencing

Complexity reduction
Restriction enzyme
Multiplexed PCR
Sequence capture
RNAseq

Genetic map construction: SNP markers



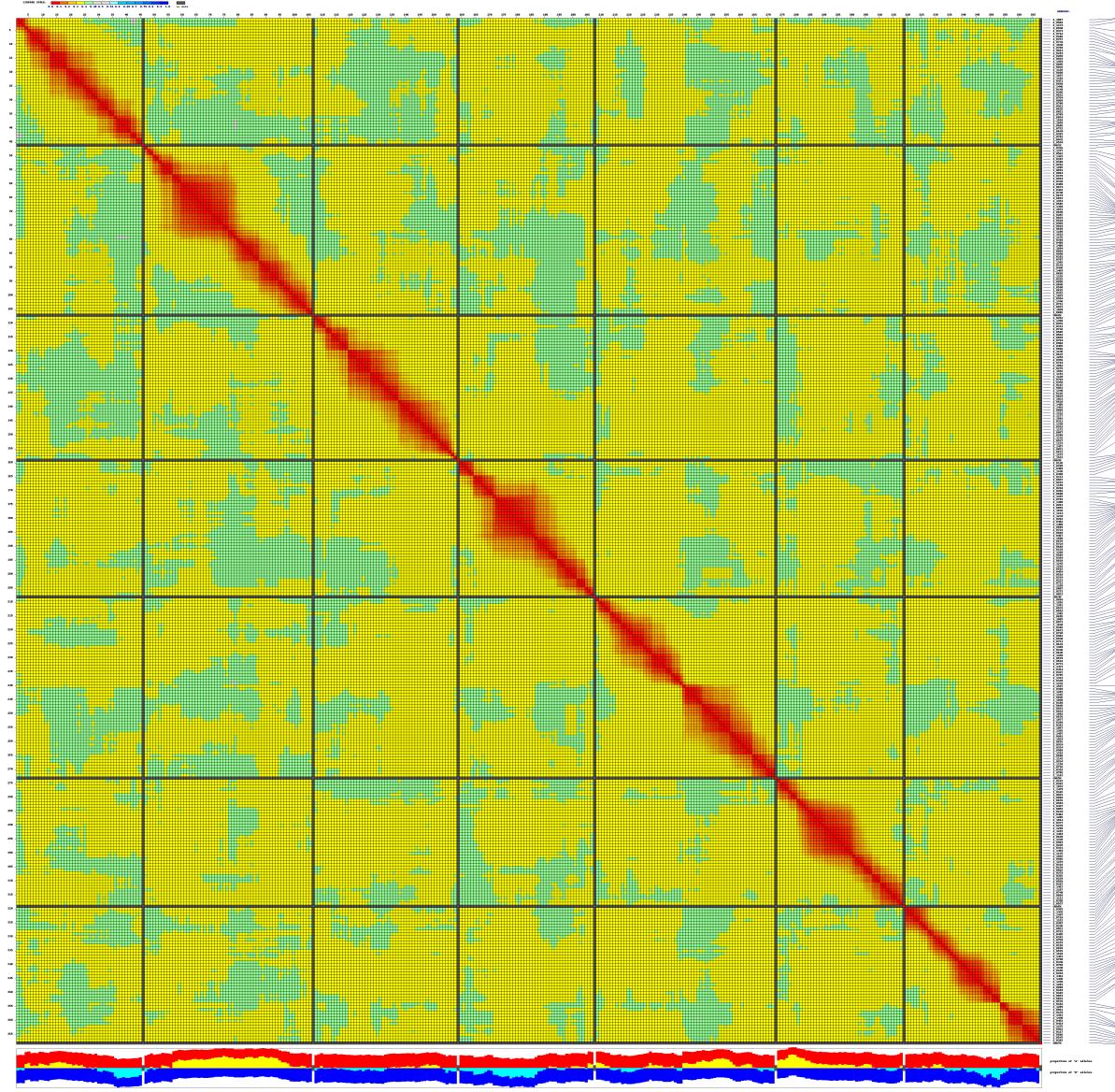
Genetic map construction: F2 population



Translations: Tipping the balance

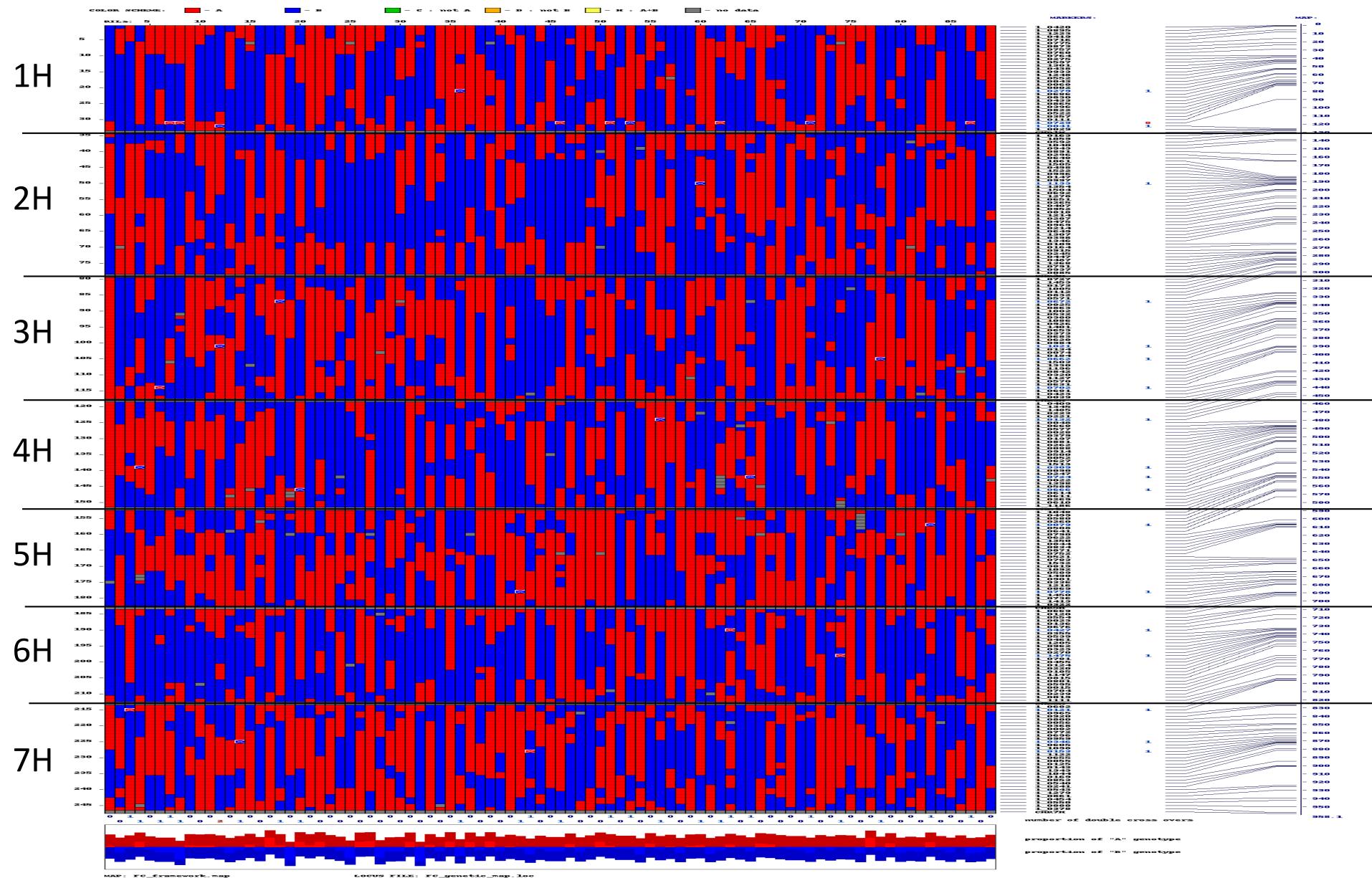
11

Genetic map construction: F2 population



Translations: Tipping the balance

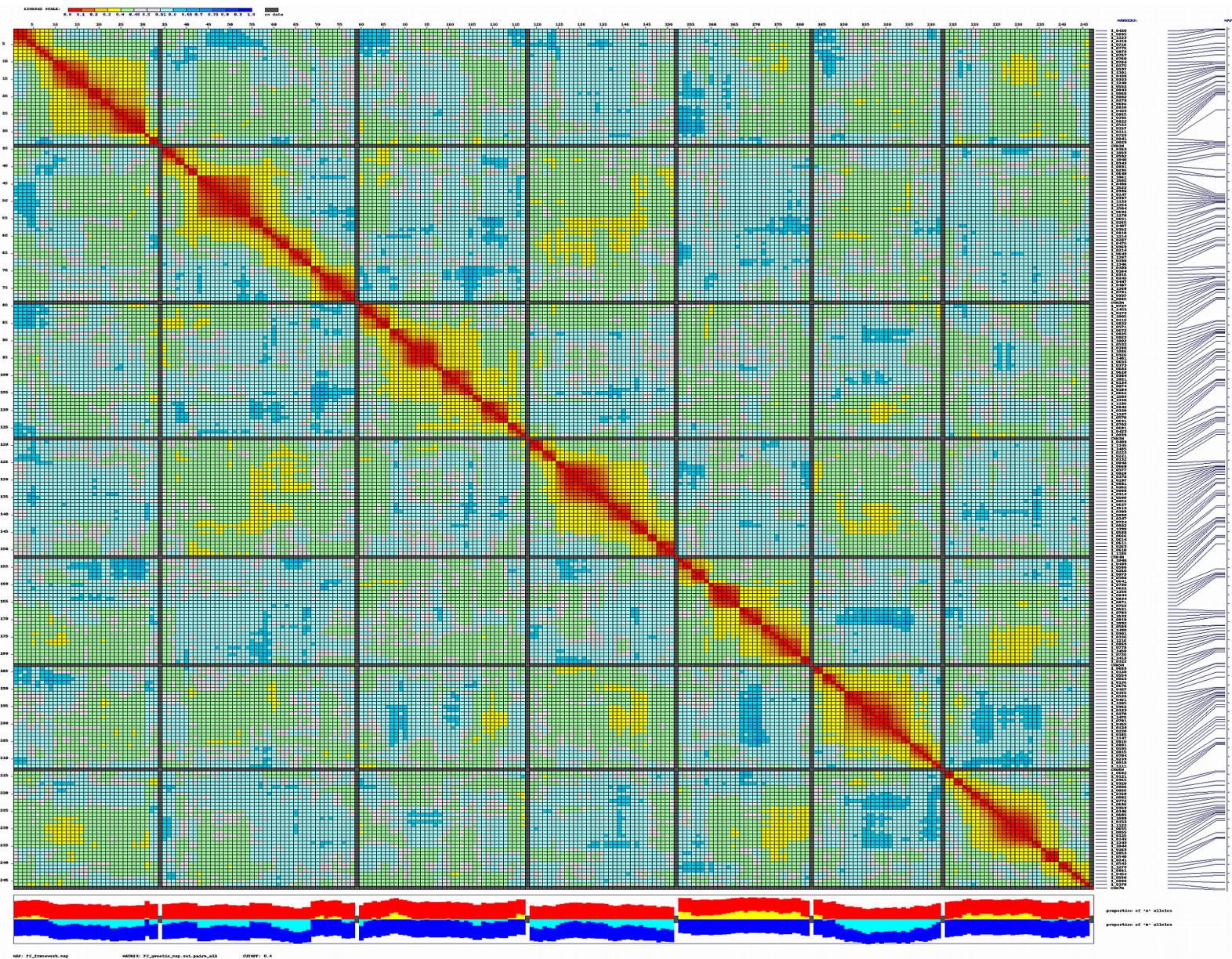
Genetic map construction: DH/RIL population



Translations: Tipping the balance

13

Genetic map construction: DH/RIL population



Genetic map construction: Software

MapMaker

MapManager QTX

JoinMap

Expensive, but it deals with difficult marker data (dominant markers) and population type (heterozygous diploid parents)

MSTMap

Very quick map construction (only F2, DH, or RIL)

MadMapper

THREaDMapper, Carthagene, Record, MultiPoint

I don't use them, but I know people like them.

Phenotypes

Mendelian Genetics

Monogenic Traits

Bimodal Distribution



Quantitative Genetics

Polygenic Traits

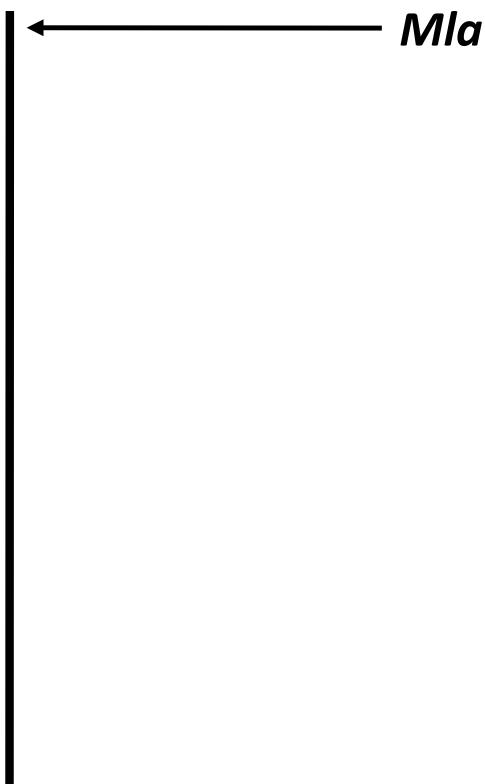
Normal Distribution

Phenotypes

Mendelian Genetics

Monogenic Traits

Bimodal Distribution

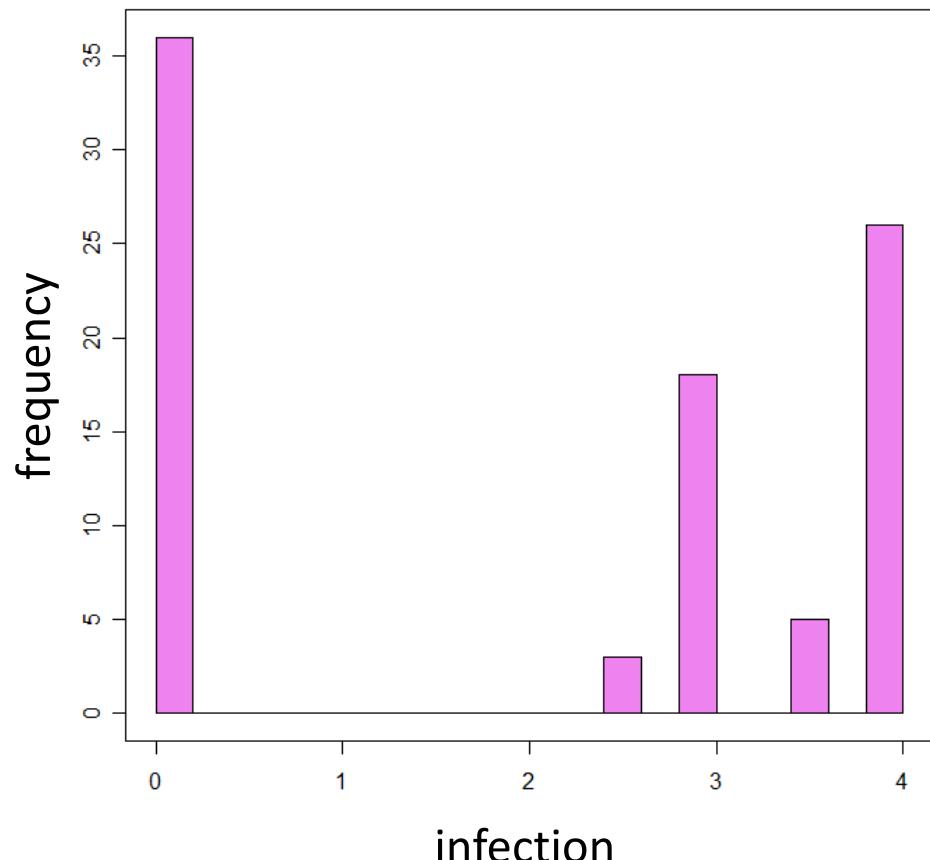


Quantitative Genetics

Polygenic Traits

Normal Distribution

OWB Dom x Rec

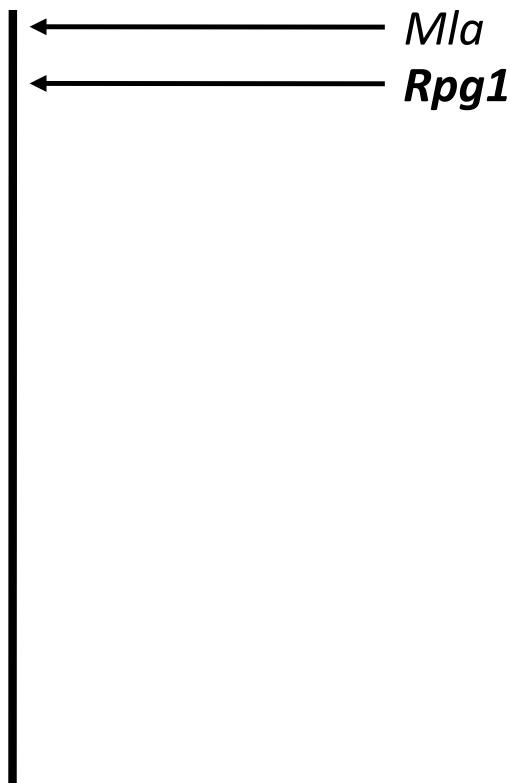


Phenotypes

Mendelian Genetics

Monogenic Traits

Bimodal Distribution

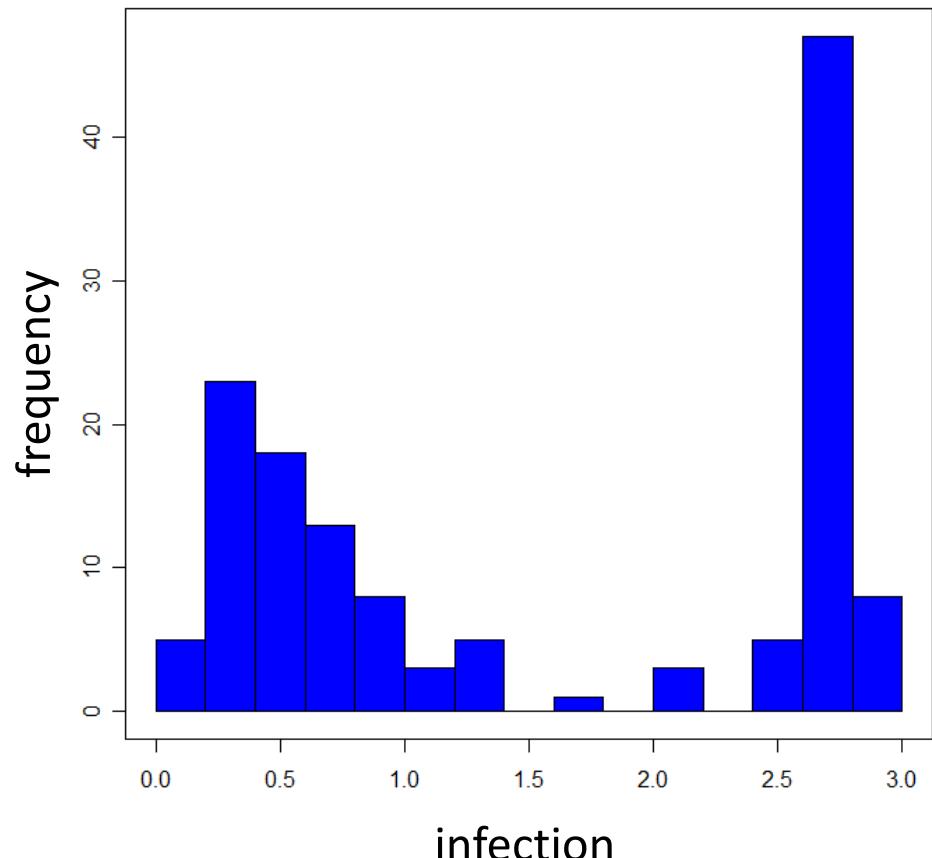


Quantitative Genetics

Polygenic Traits

Normal Distribution

Steptoe x Morex



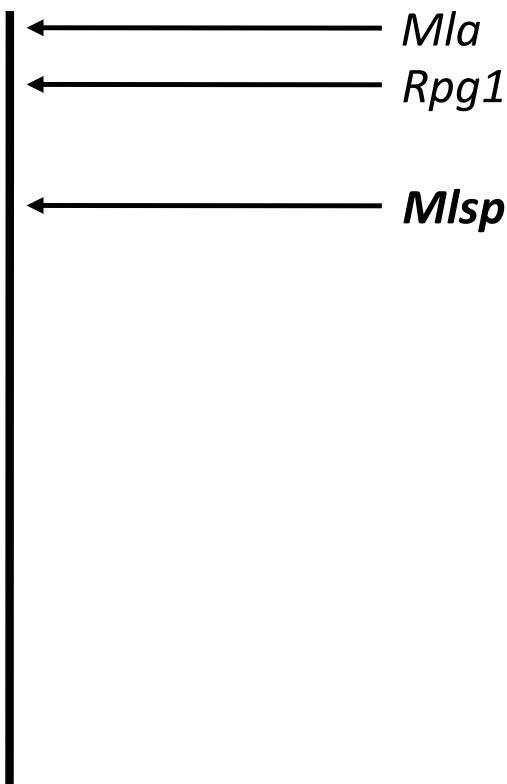
Druka *et al* (2008)

Phenotypes

Mendelian Genetics

Monogenic Traits

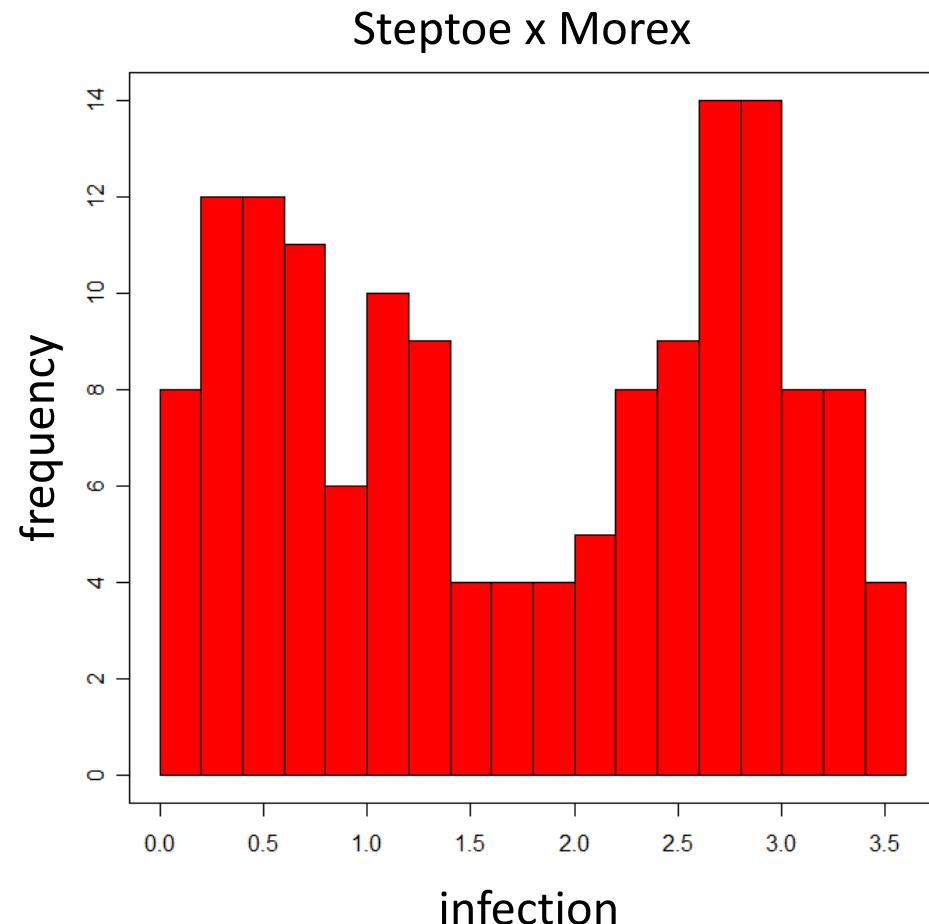
Bimodal Distribution



Quantitative Genetics

Polygenic Traits

Normal Distribution

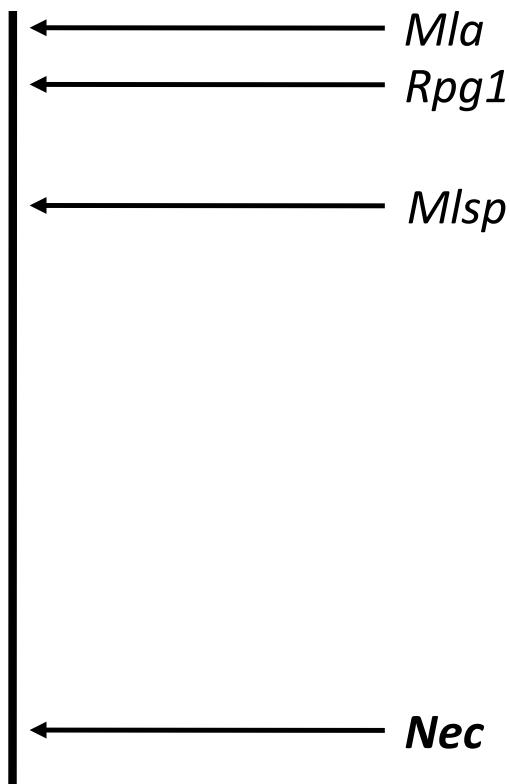


Phenotypes

Mendelian Genetics

Monogenic Traits

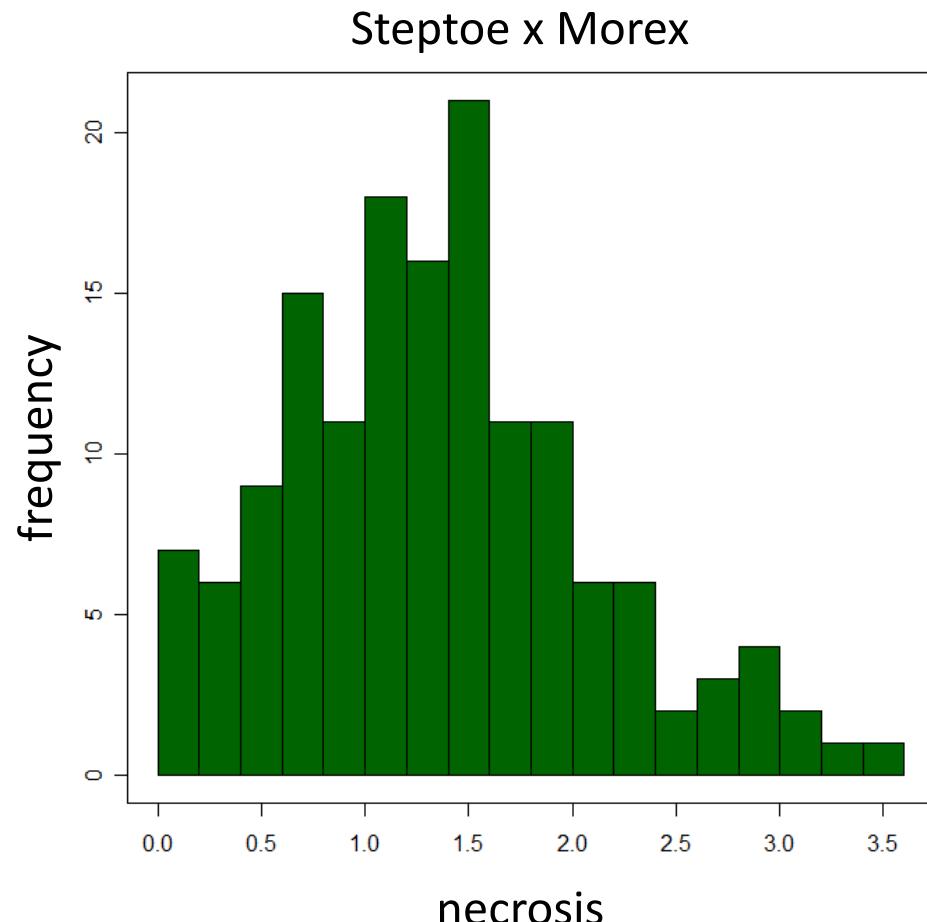
Bimodal Distribution



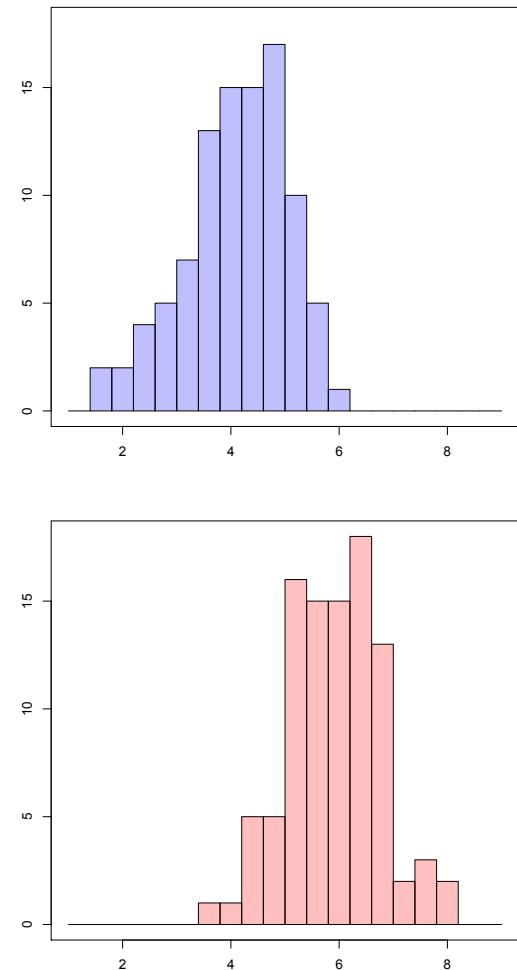
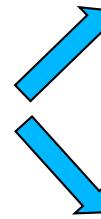
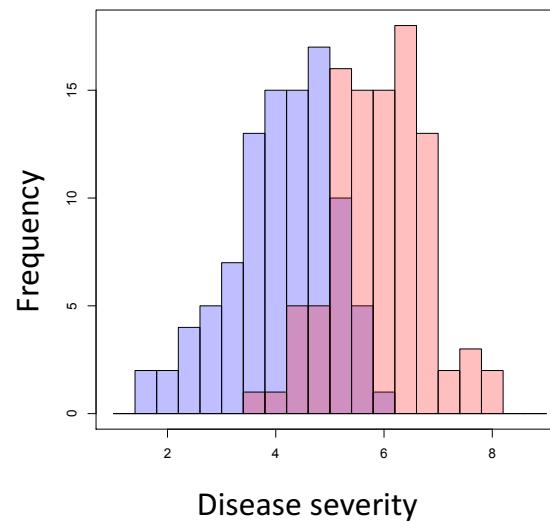
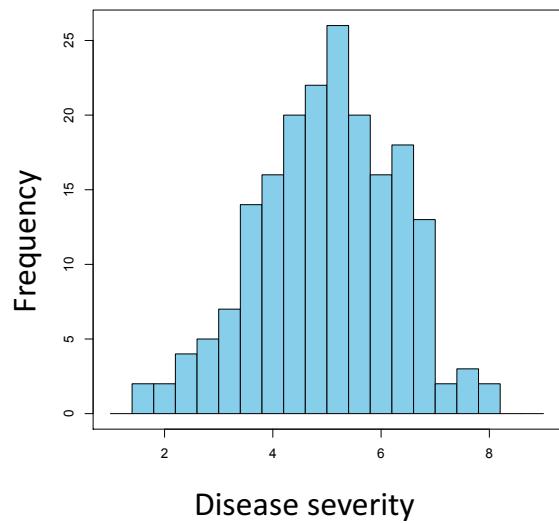
Quantitative Genetics

Polygenic Traits

Normal Distribution

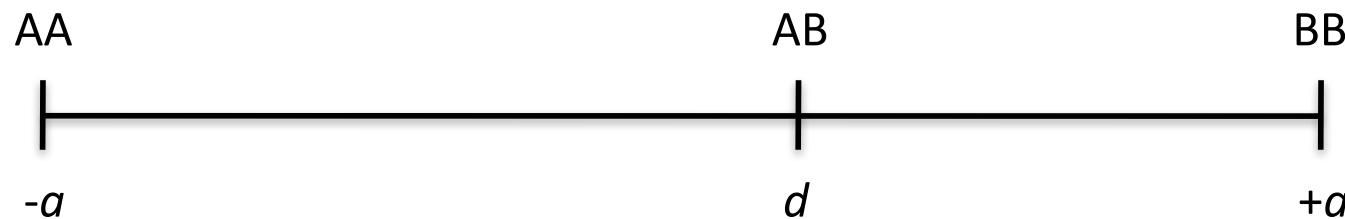


Phenotypes: Quantitative

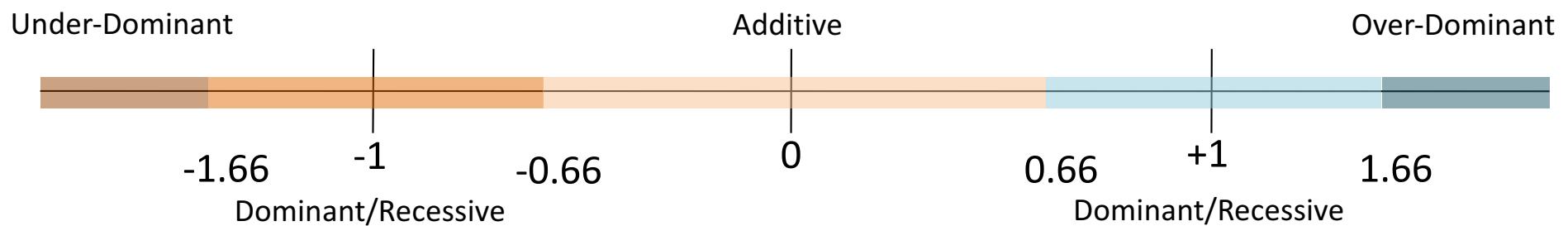


A short course on quantitative genetics

Genotype and Genotypic Values

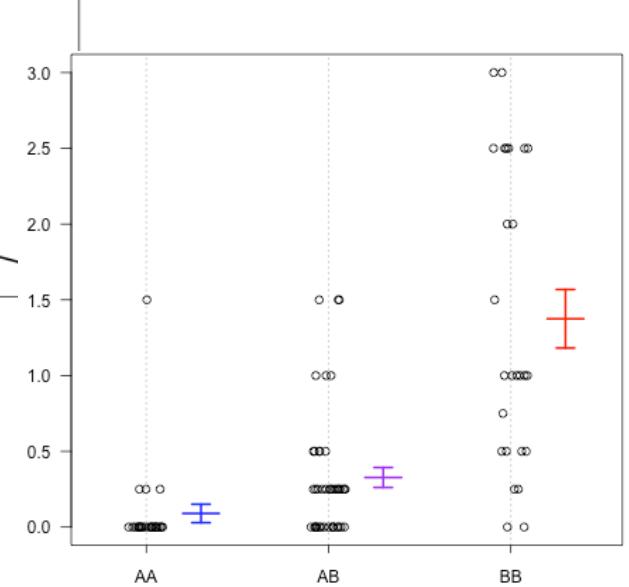
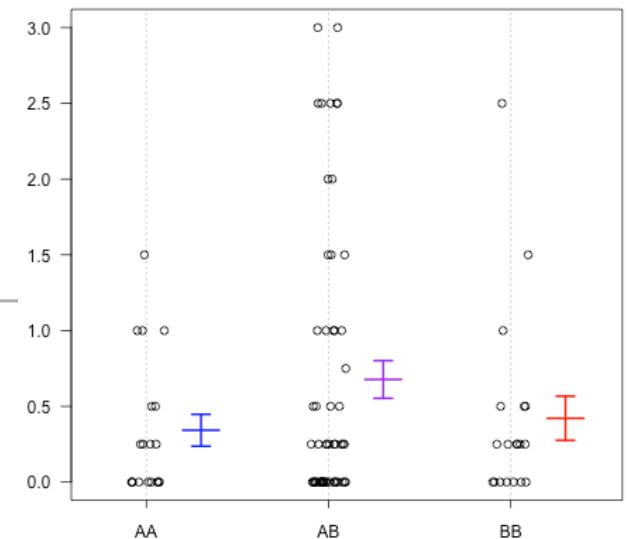
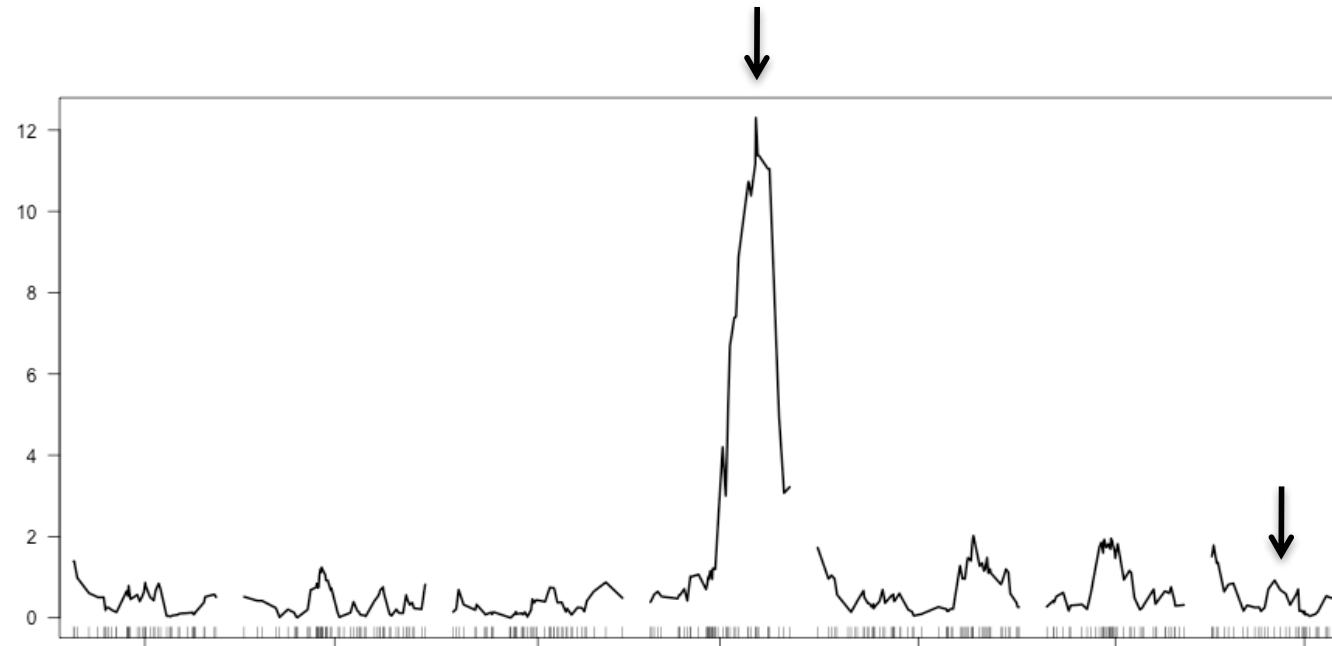


Dominance:Additivity Ratio



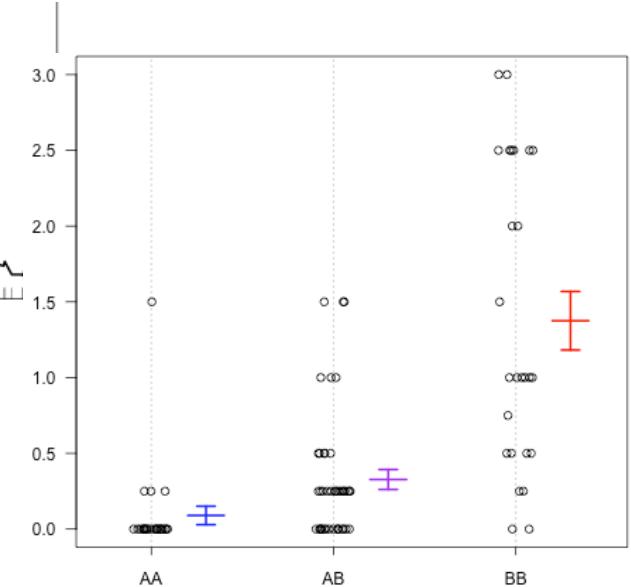
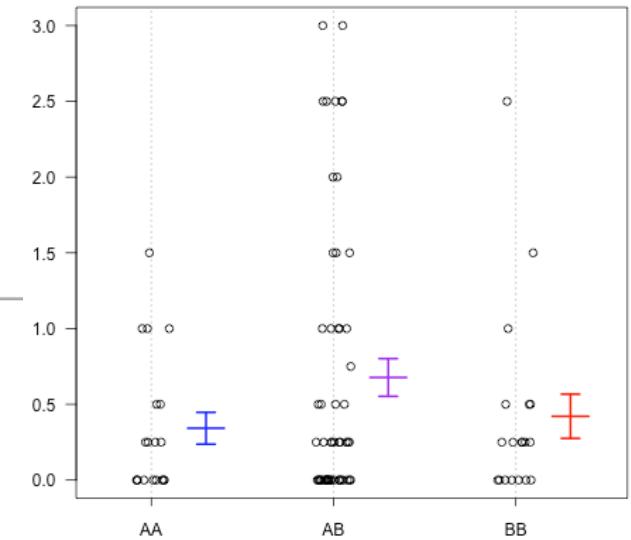
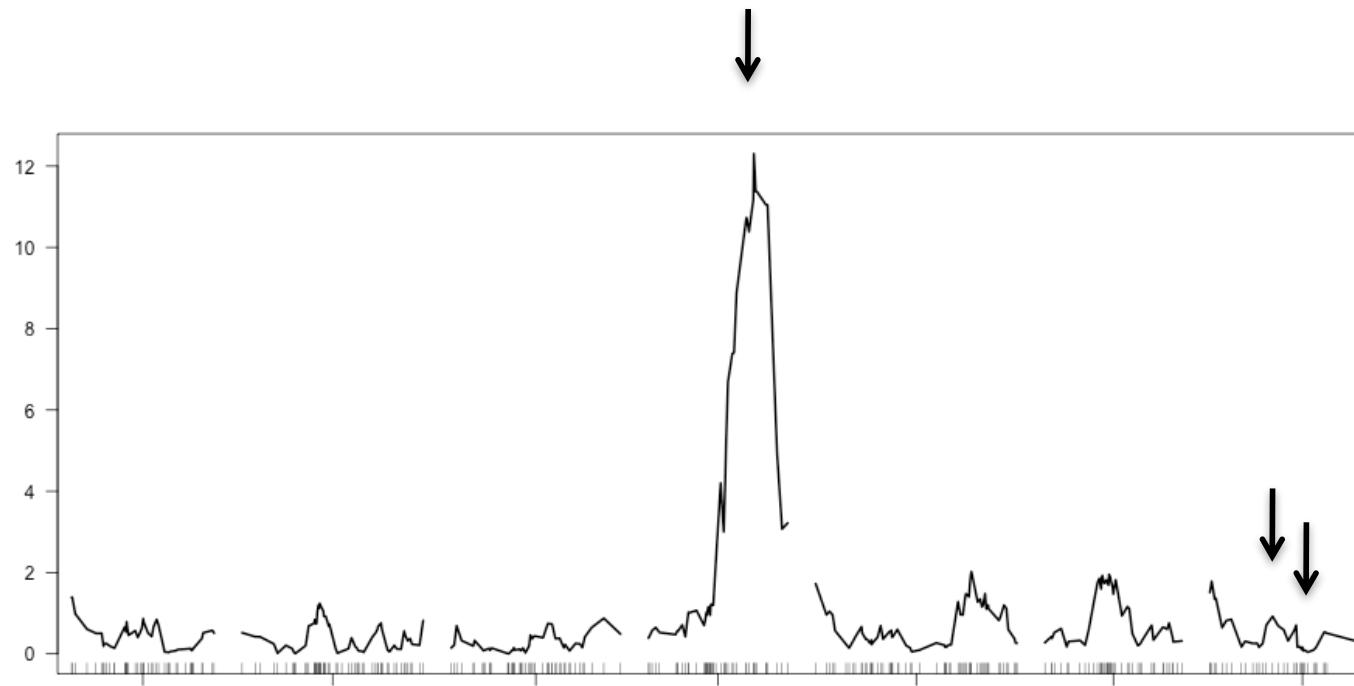
Linear regression

Test for linkage at every marker



Interval mapping

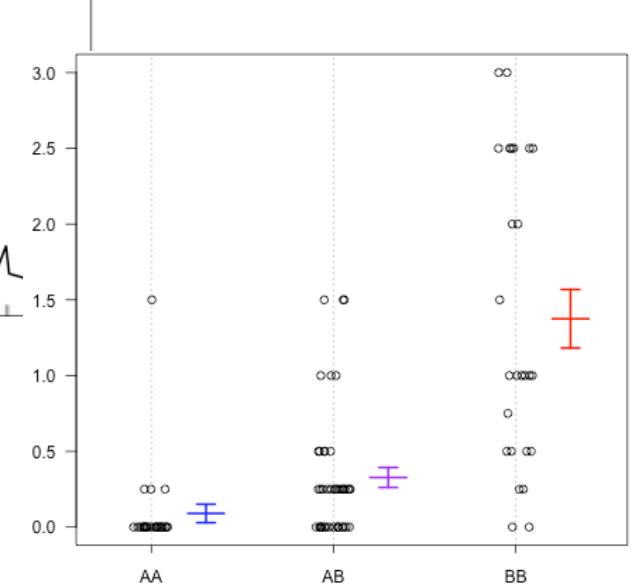
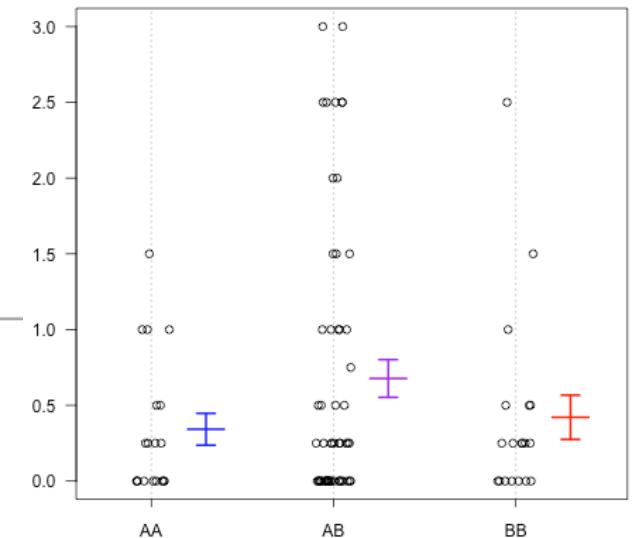
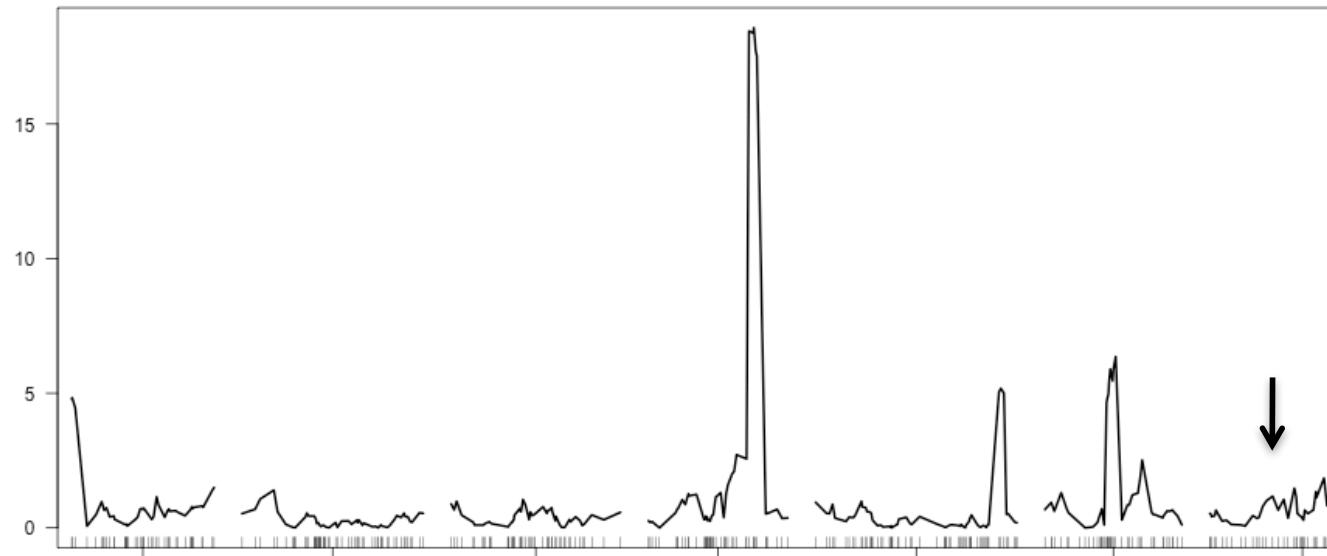
Test for linkage between markers (and including markers)



Composite Interval mapping

Test for linkage between markers (and including markers)

Condition on loci potentially contributing to the phenotype



QTL Analysis: Software

QTL Cartographer

Robust and extremely powerful, open source

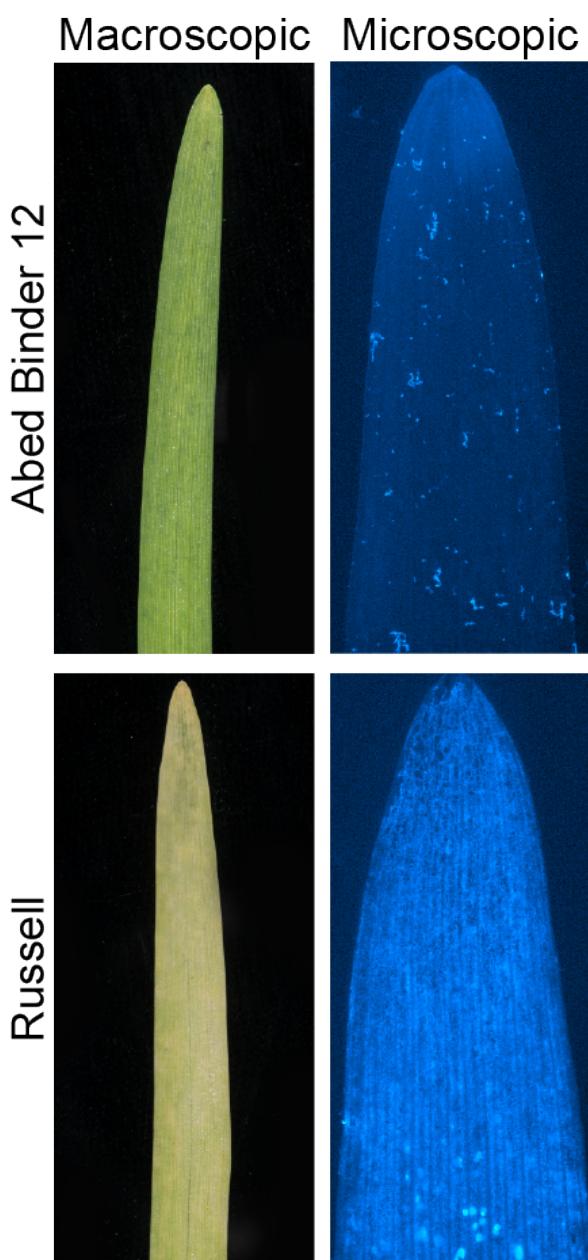
R/qtl

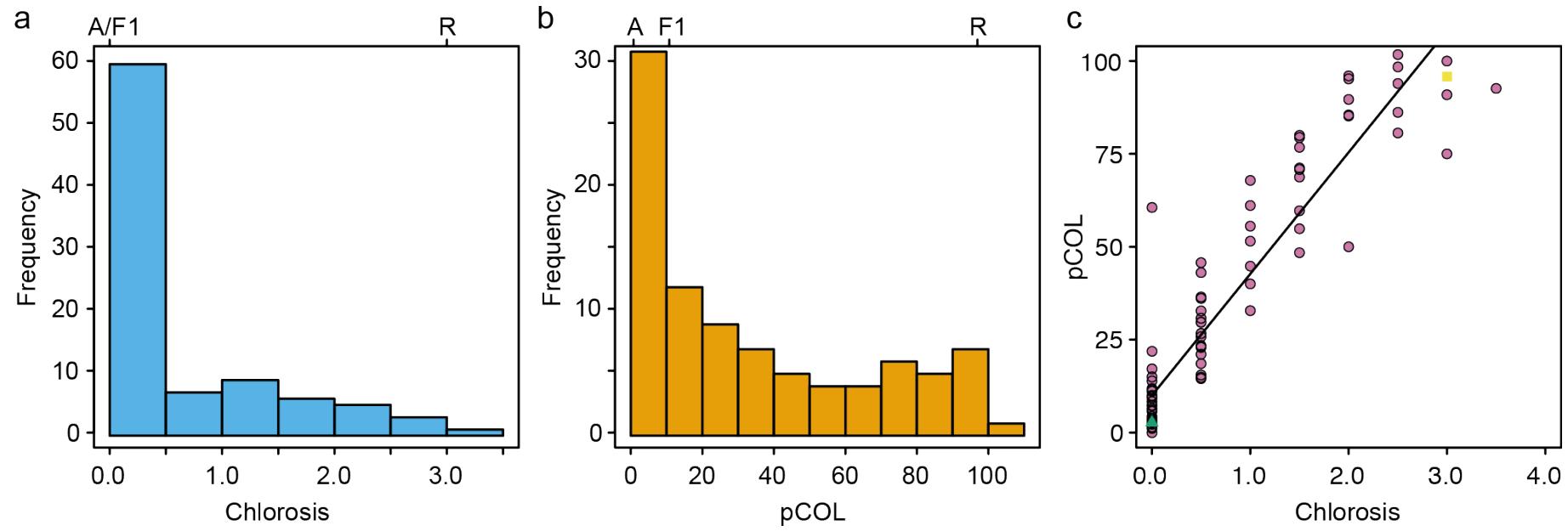
Awesome visualization, generally useful, open source

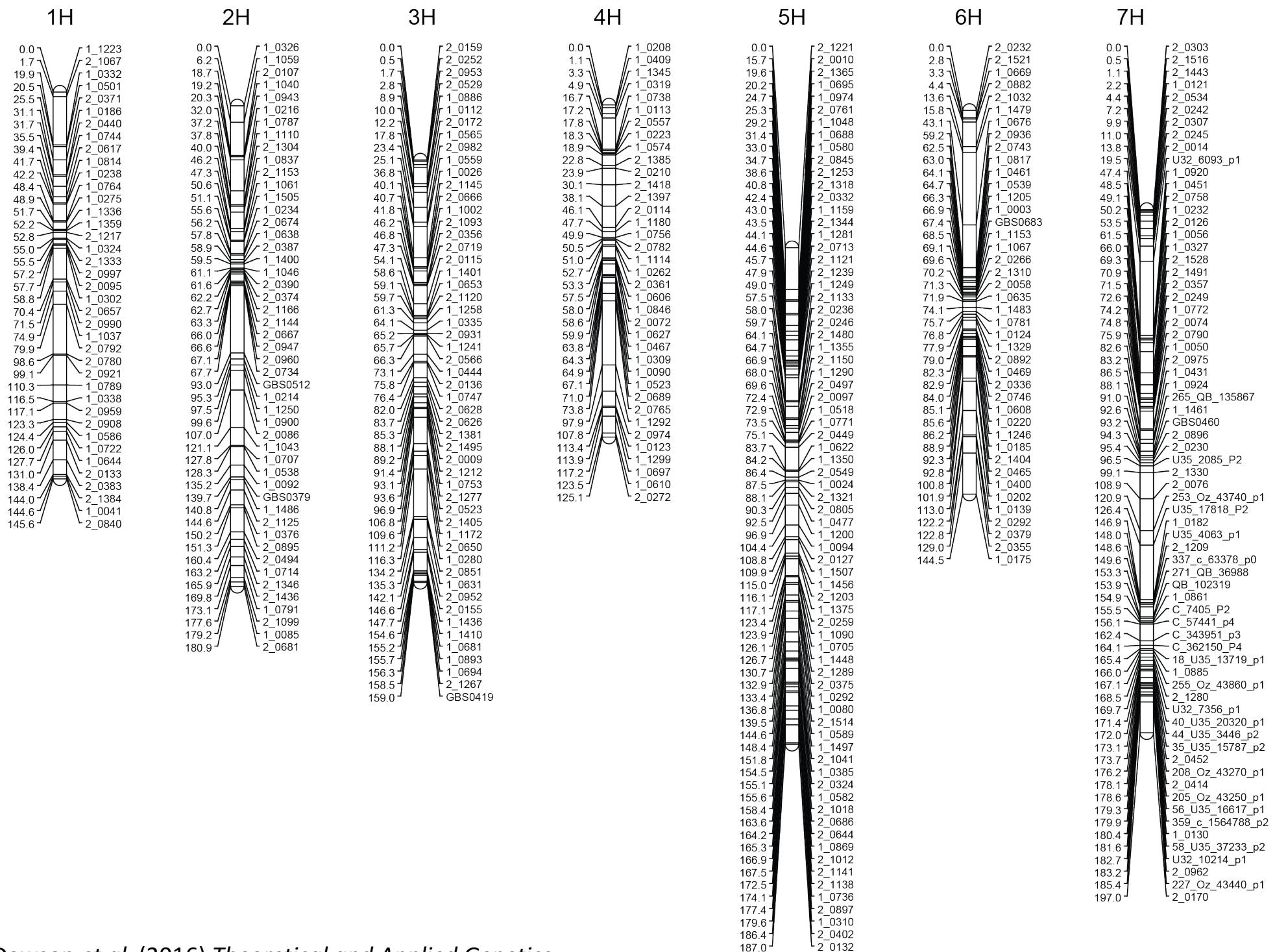
MapQTL

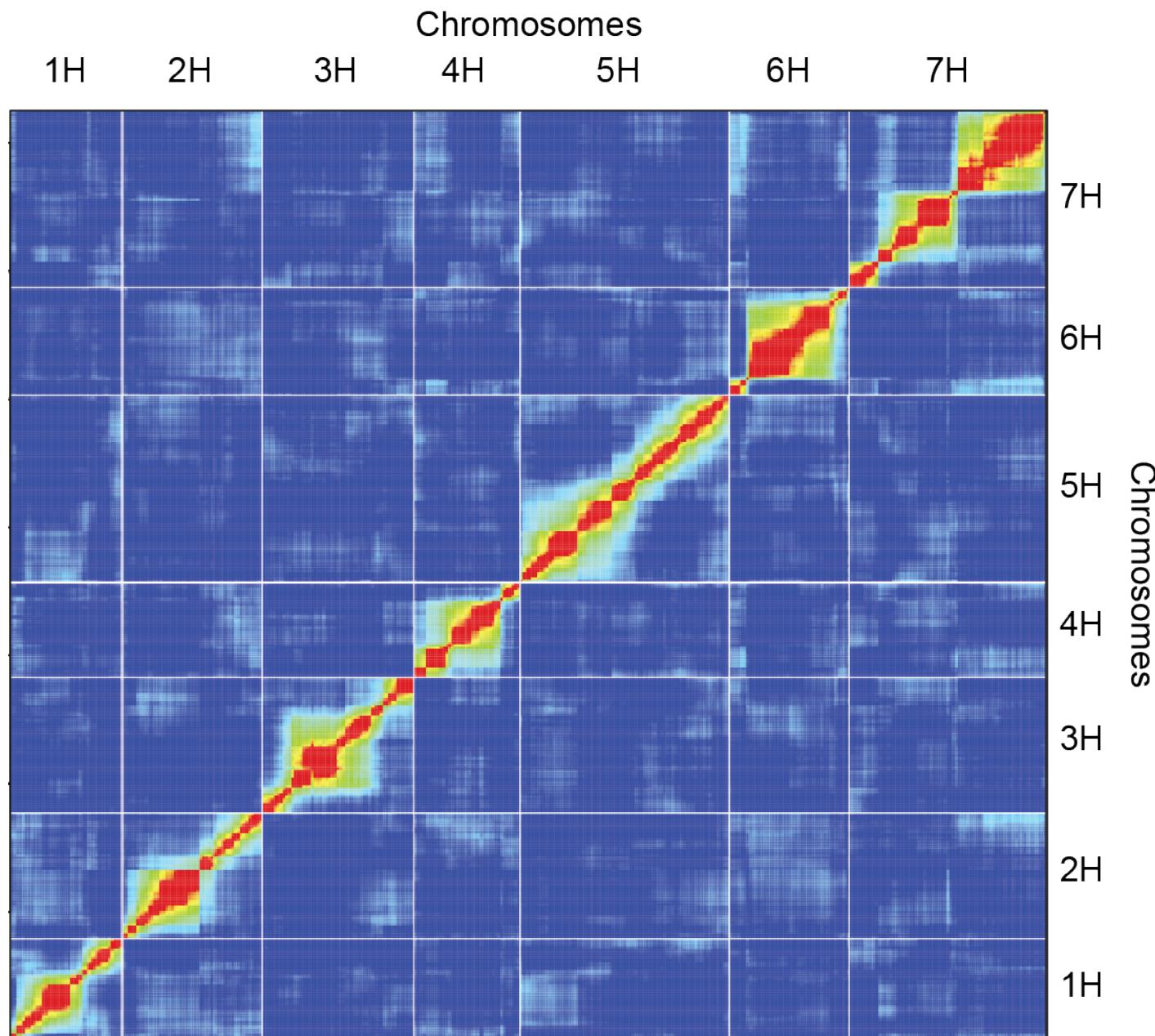
MultiQTL

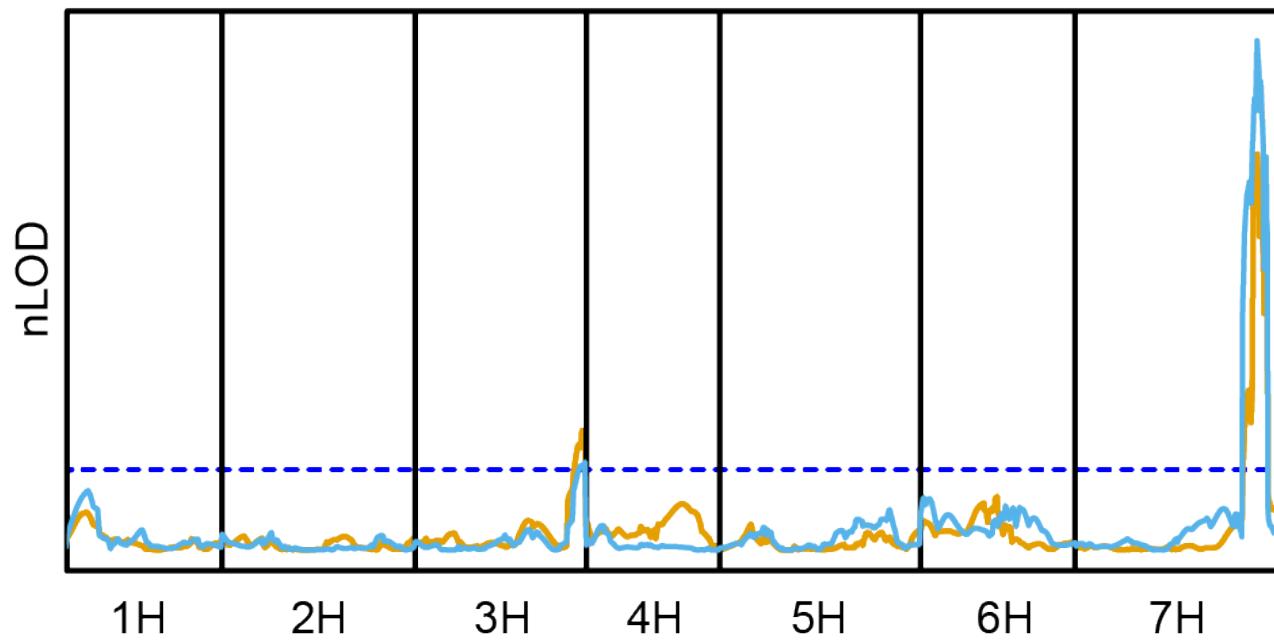
This list could be much longer...

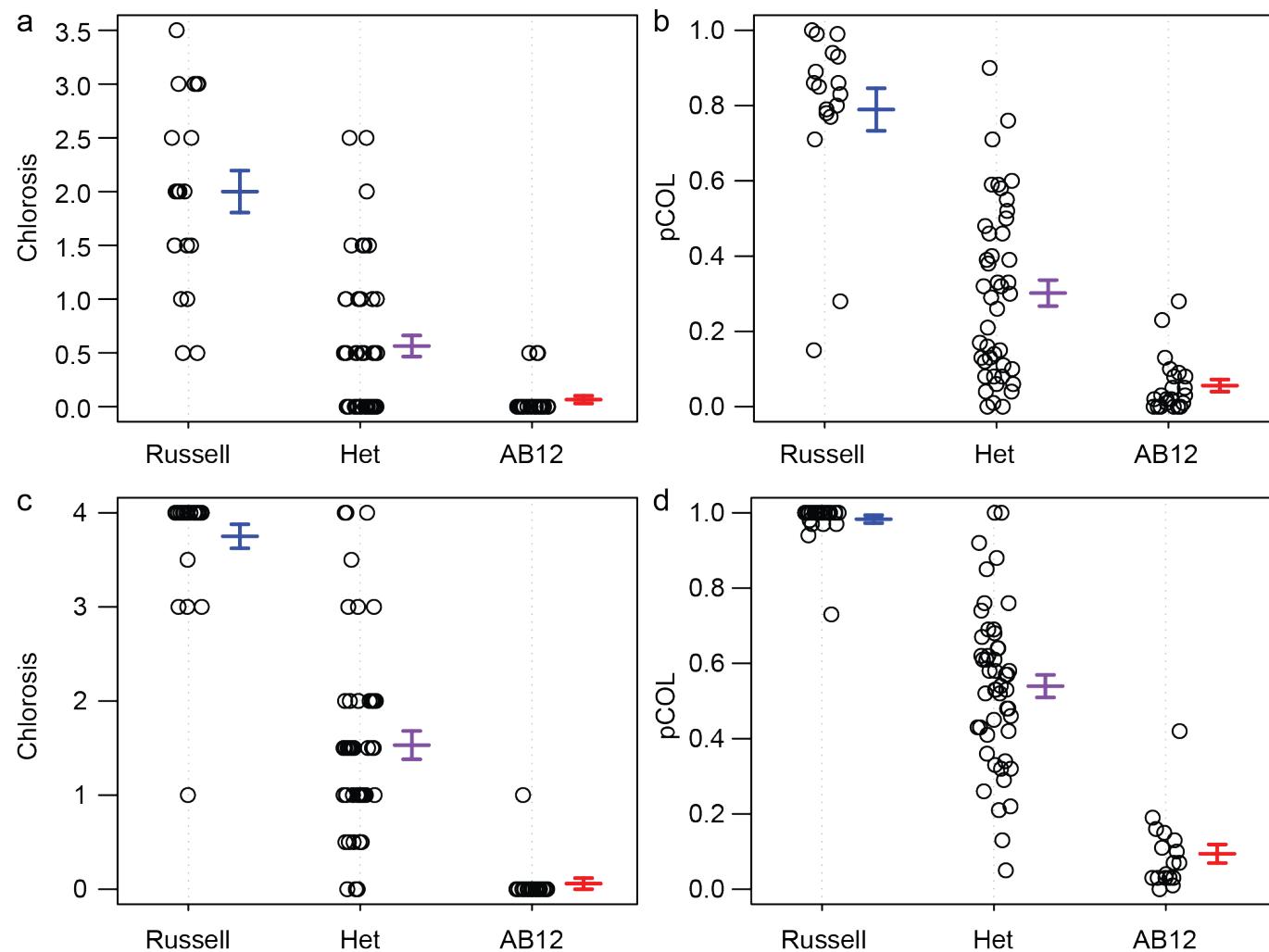


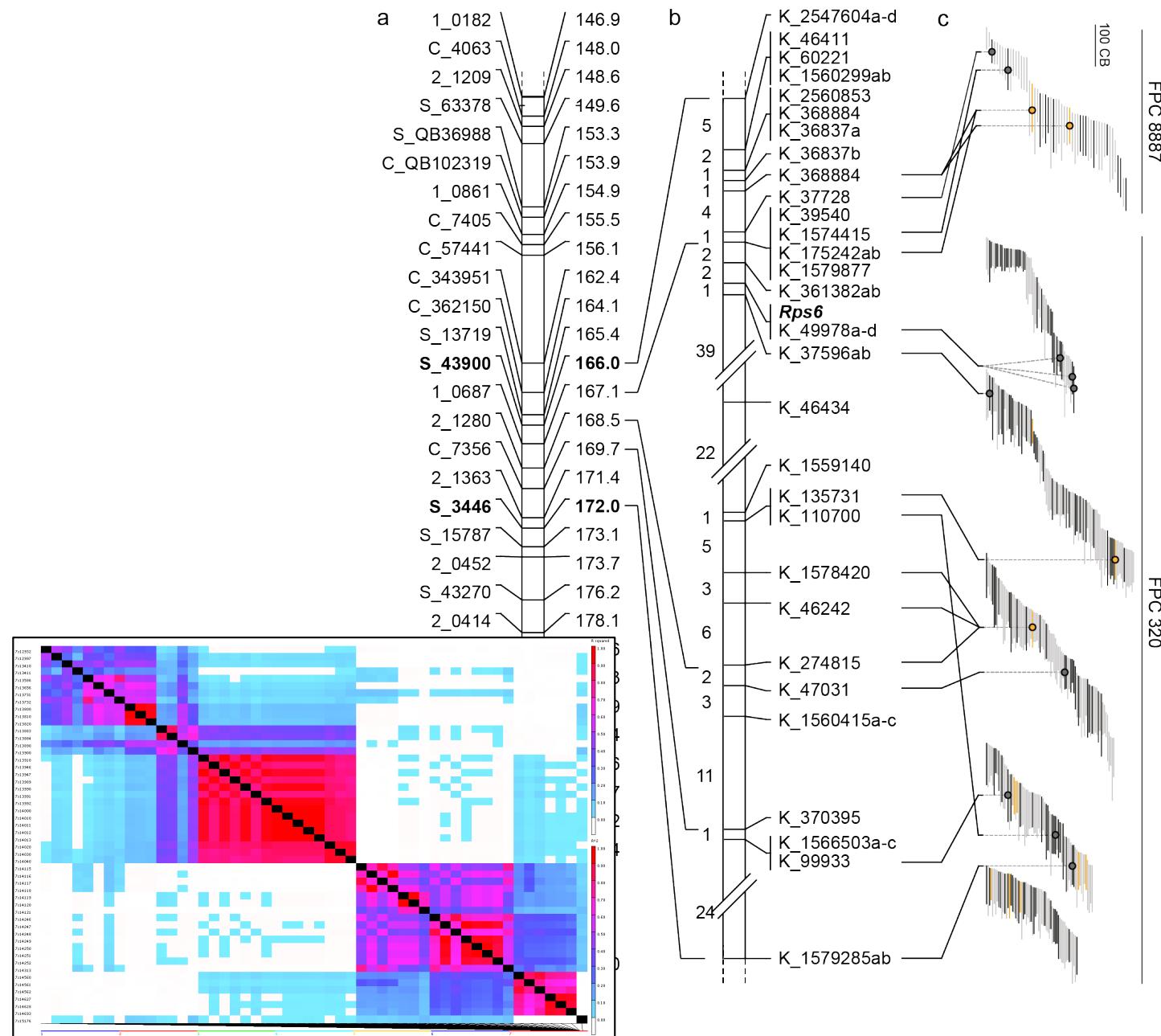








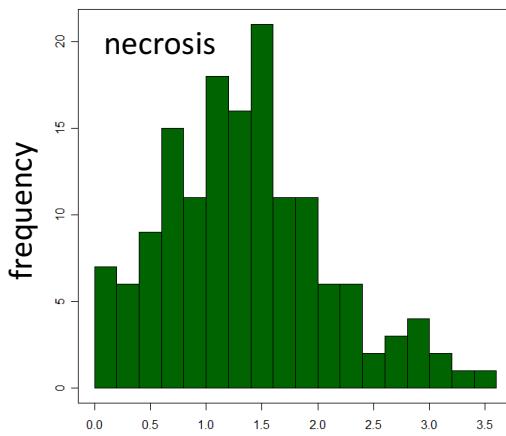
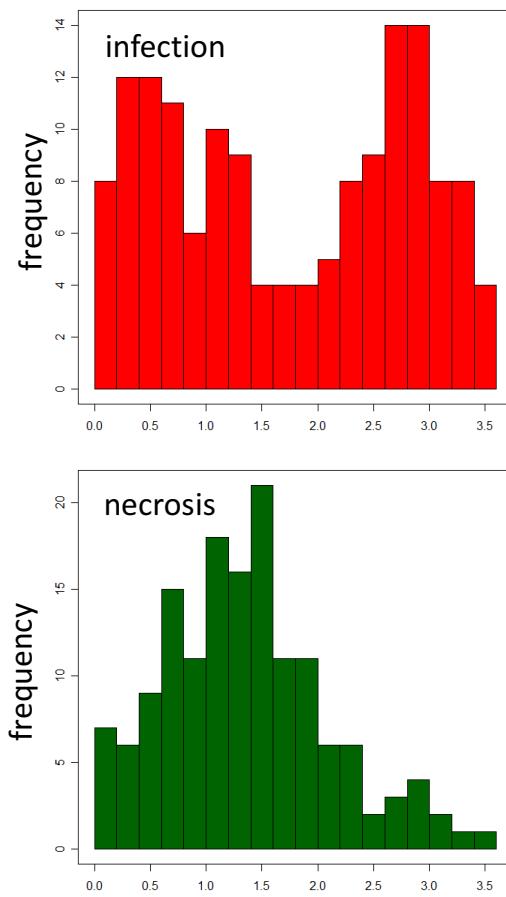




Practical: Using R/qtL



X



X

