

Overview of the Genotyping-By-Sequencing Technology and Its Applications

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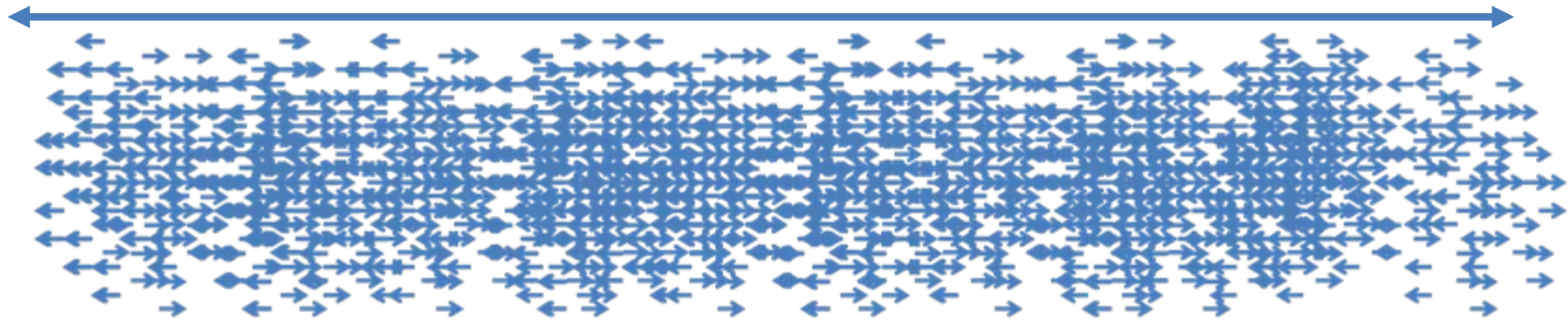
Cornell University

Whole Genome Shotgun (WGS)

De novo Assembly

Coverage: 100x, (multiple libraries with different insertion size)

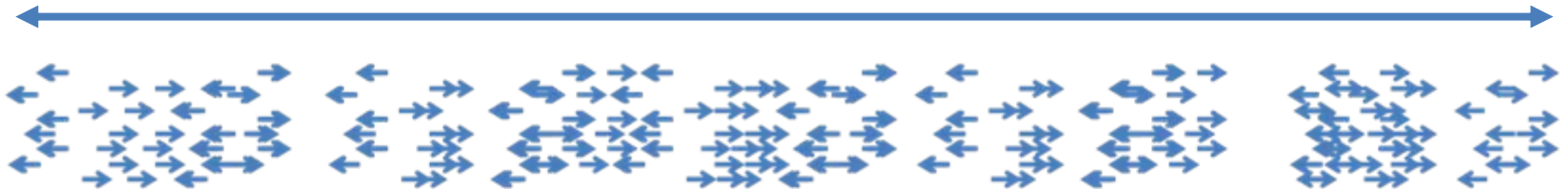
Cost: ~\$25,000



SNP/INDEL detection through alignment to reference genome

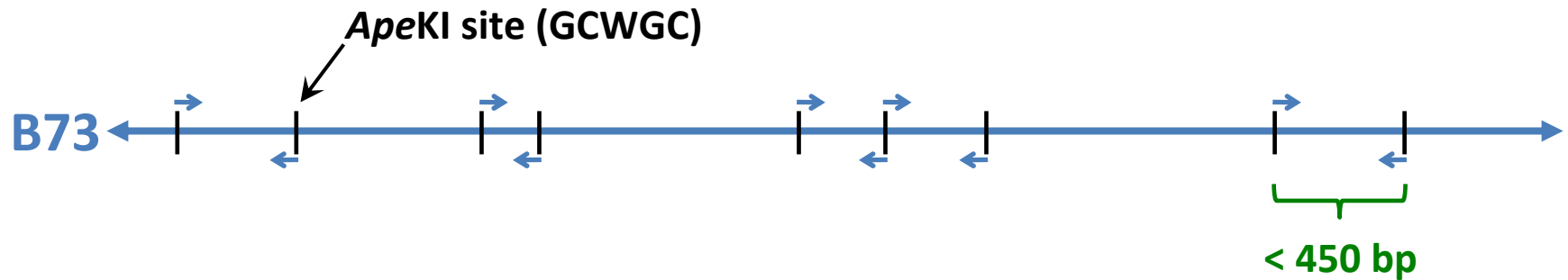
Coverage: 1 to 10x

Cost: \$250 to \$25,00



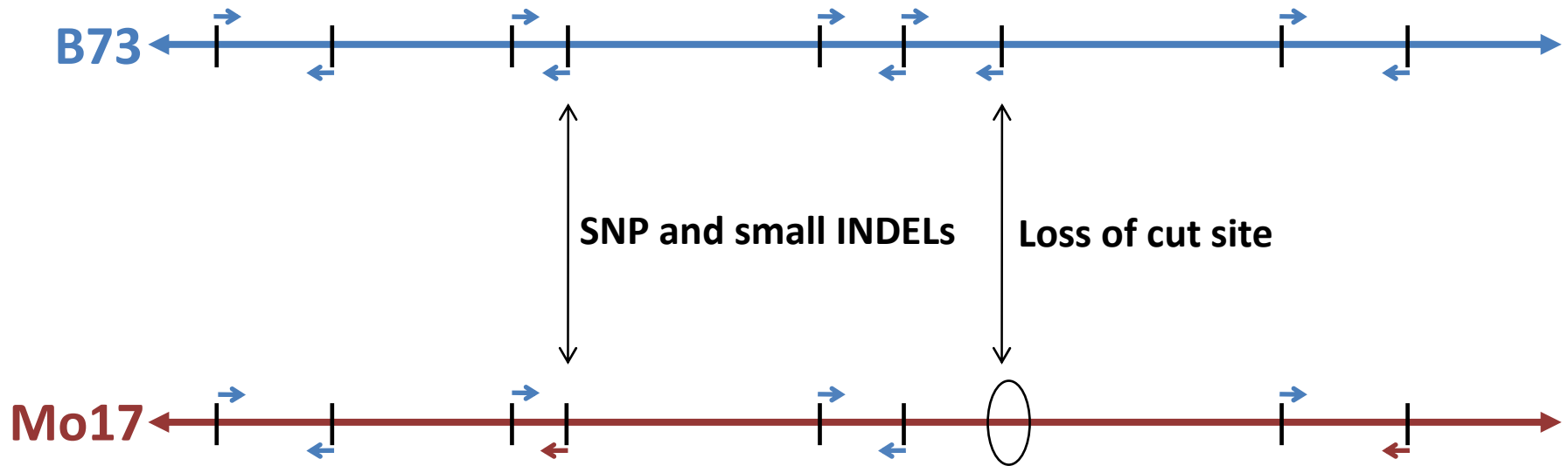
Genotyping by Sequencing (GBS)

(→) 64-base sequence tag

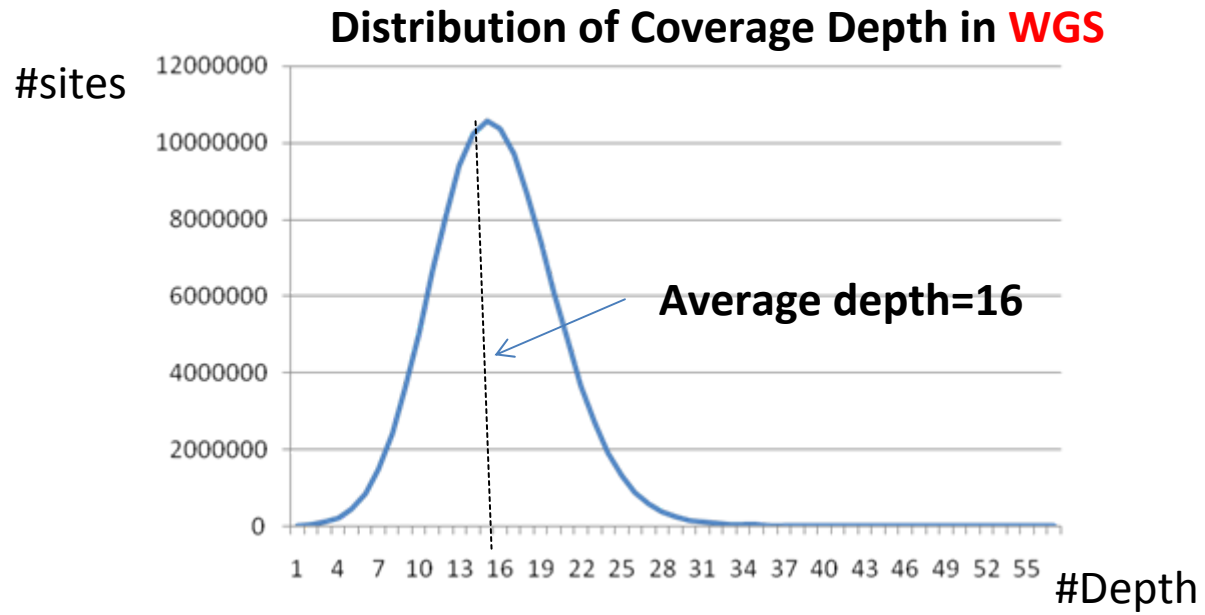
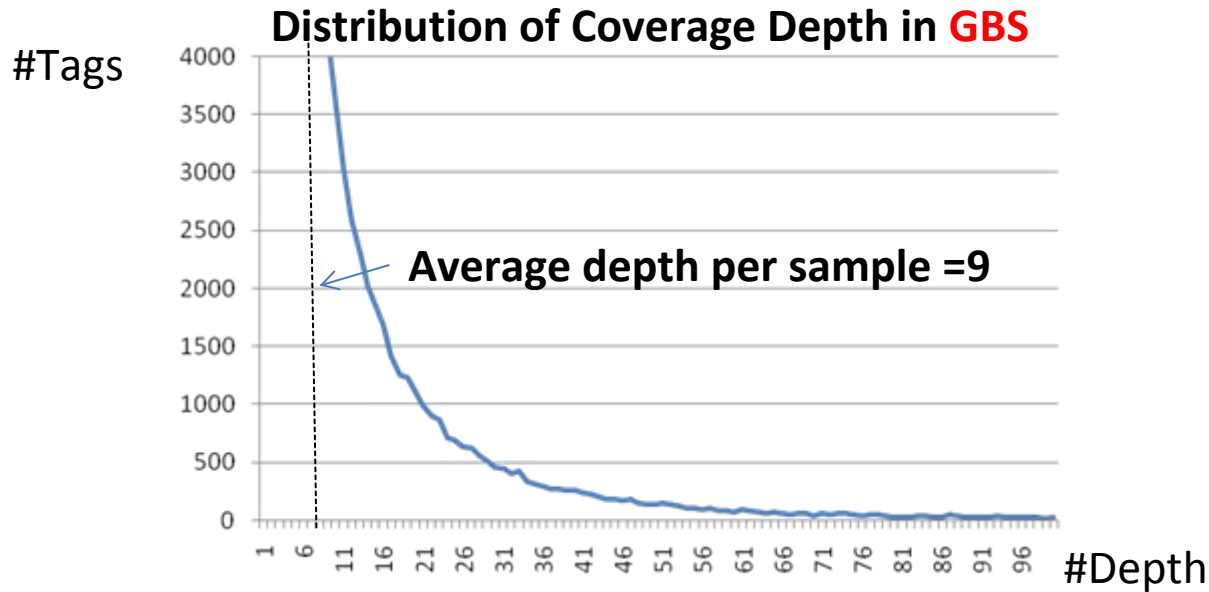


- **Reduced genome representation;**
- **Reads can be aligned without reference genome;**
- **Low coverage per individual, coverage achieved by combining the reads from a population.**

Identification of markers with/without the reference genome



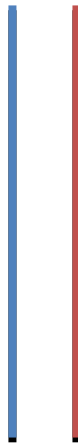
Difference of Coverage depth between GBS and Whole Genome Sequencing data



GBS on Grape F1 population

chardonnay

rupestrisB38



X



86 F1 population

GBS of the F1 population

160 million reads

0.7 million tags

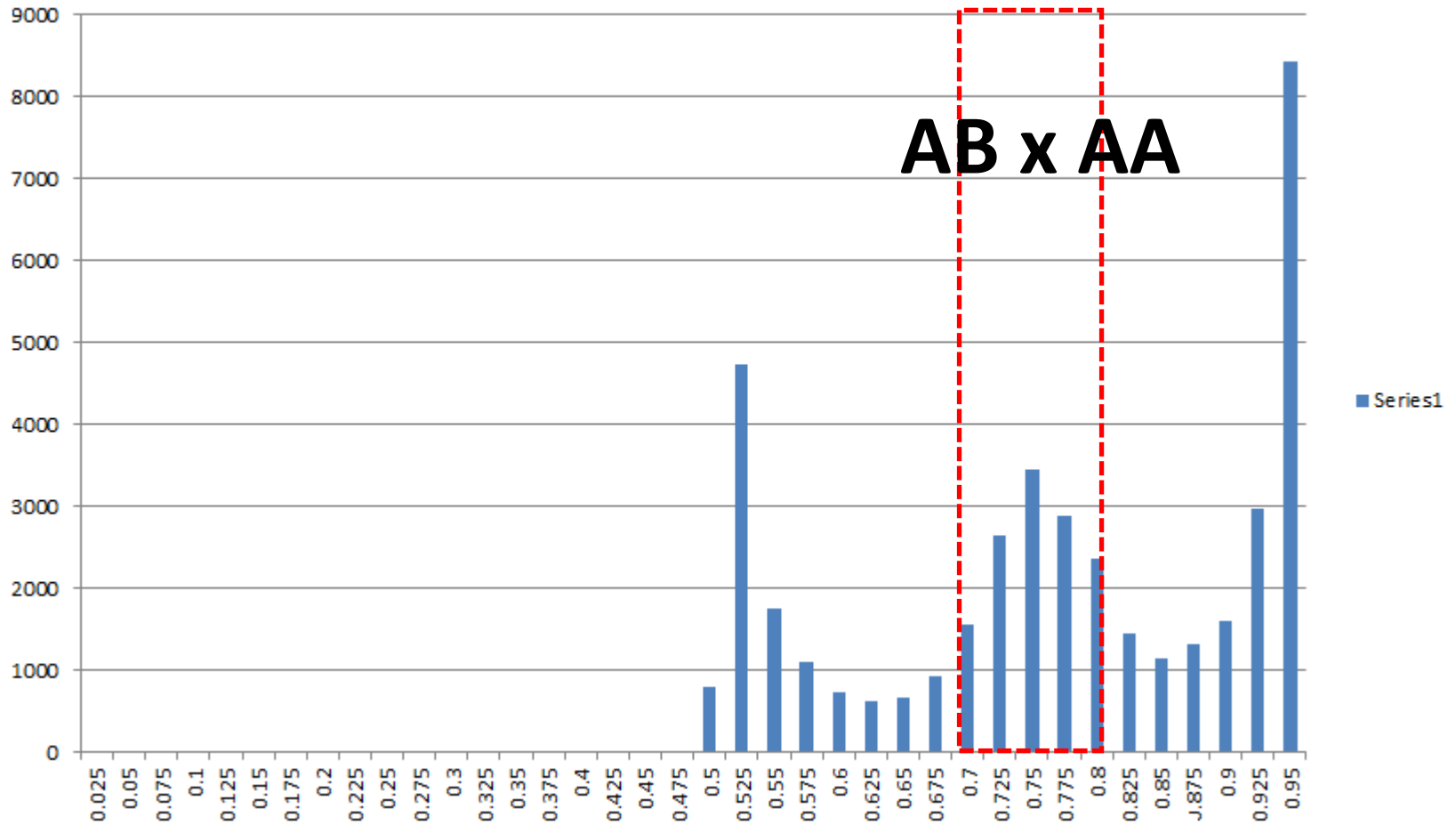
10k biallelic markers

i.80% coverage

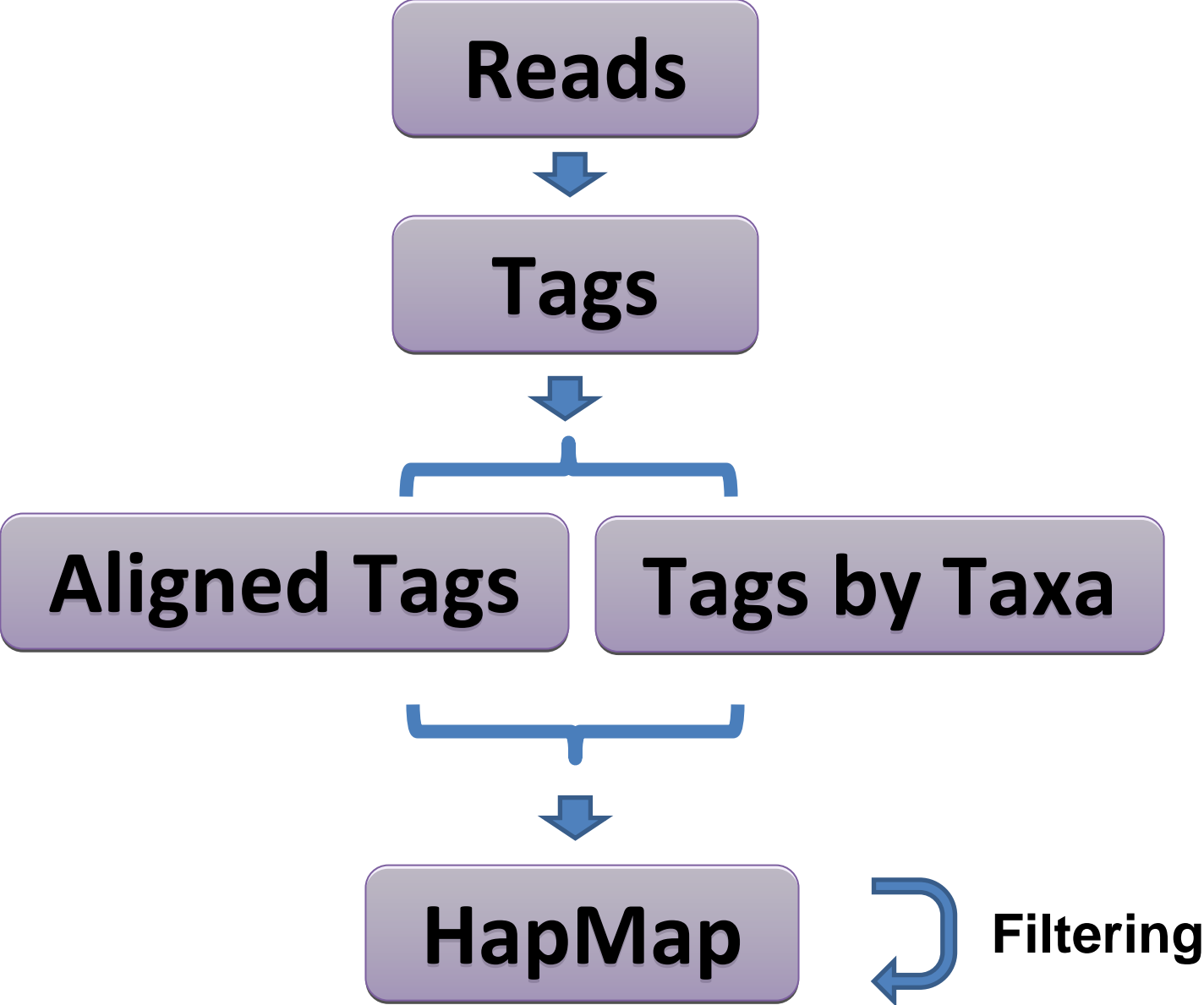
ii.MAF 25%

iii.physical map match genetic map)

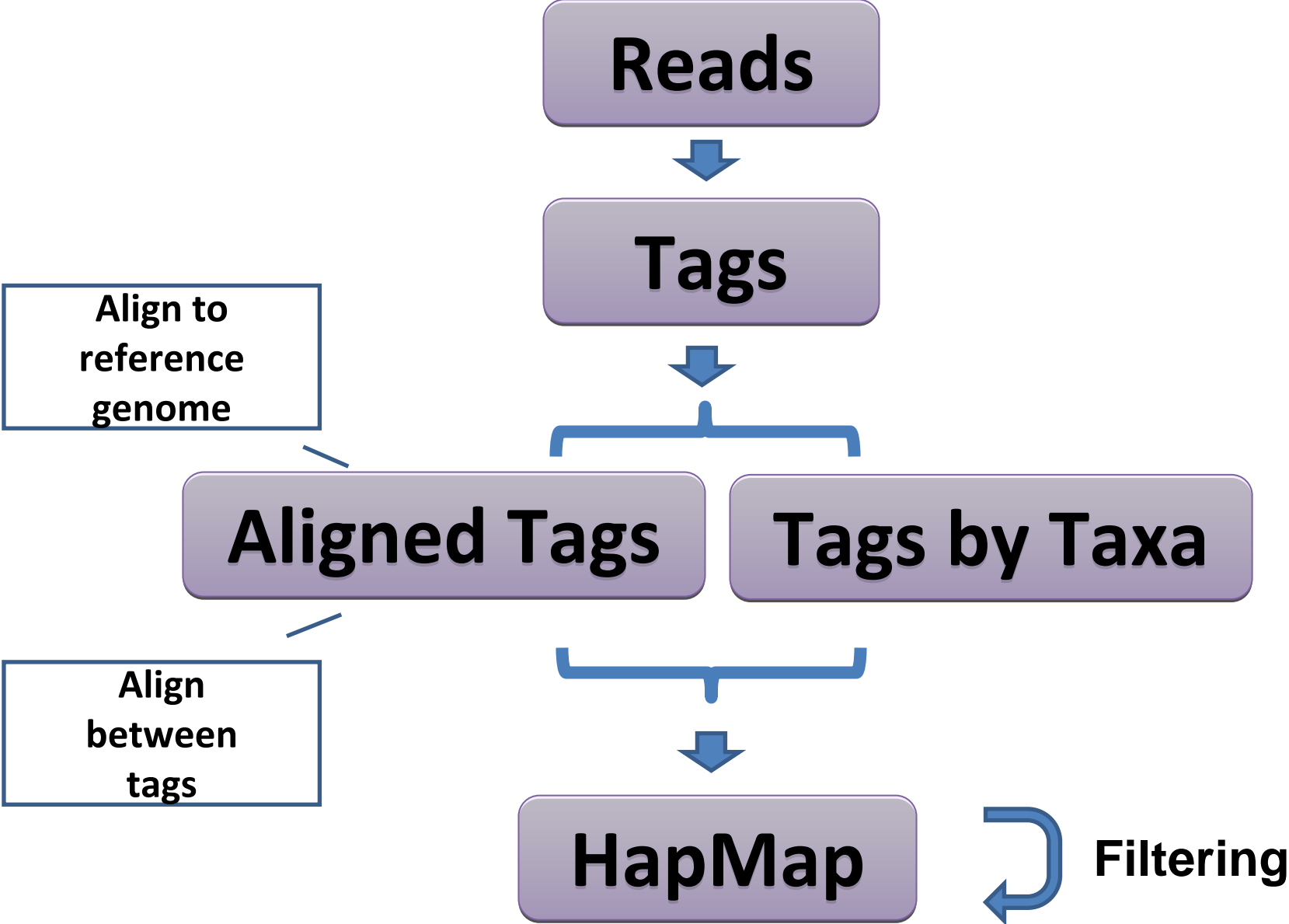
Strategy for Map Construction



GBS Data Analysis Pipeline



GBS Data Analysis Pipeline



Applications of the GBS markers

Goal of year 1:

1.Marker discovery

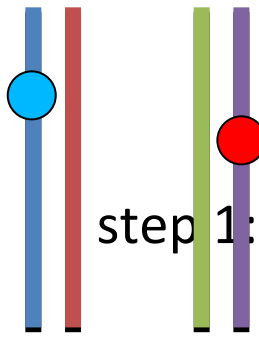
2.Linkage map construction.

3.QTL mapping.

Goal of year 2 -3:

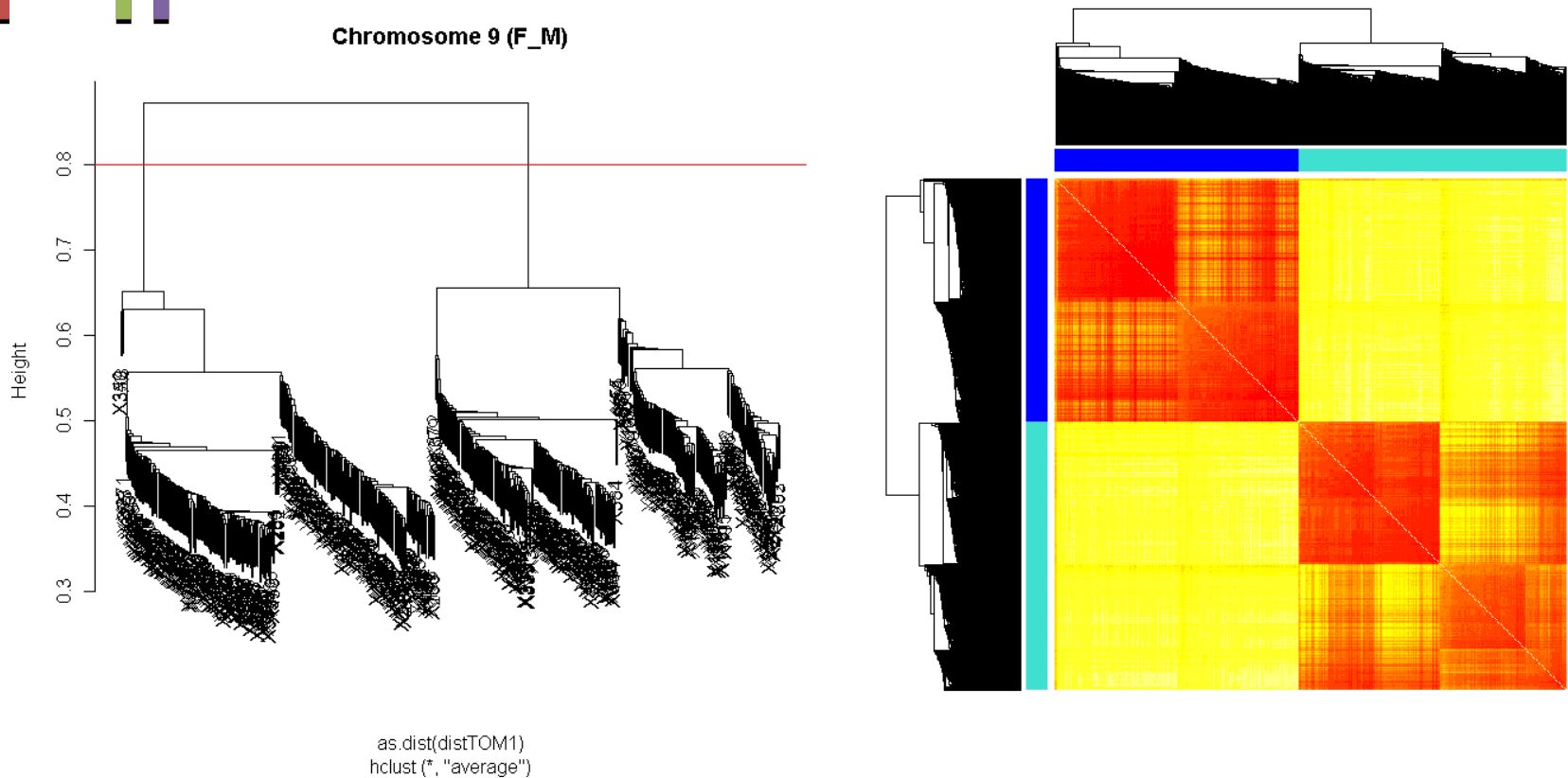
1.HapMap construction. Integration of GBS maps with genome sequences.

2.Genomic selection.

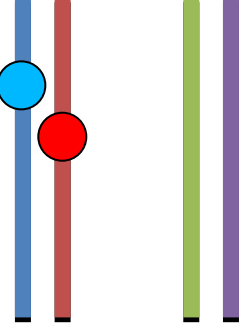


Strategy for Map Construction

step 1: For each marker, assign the minor alleles to one of the parents



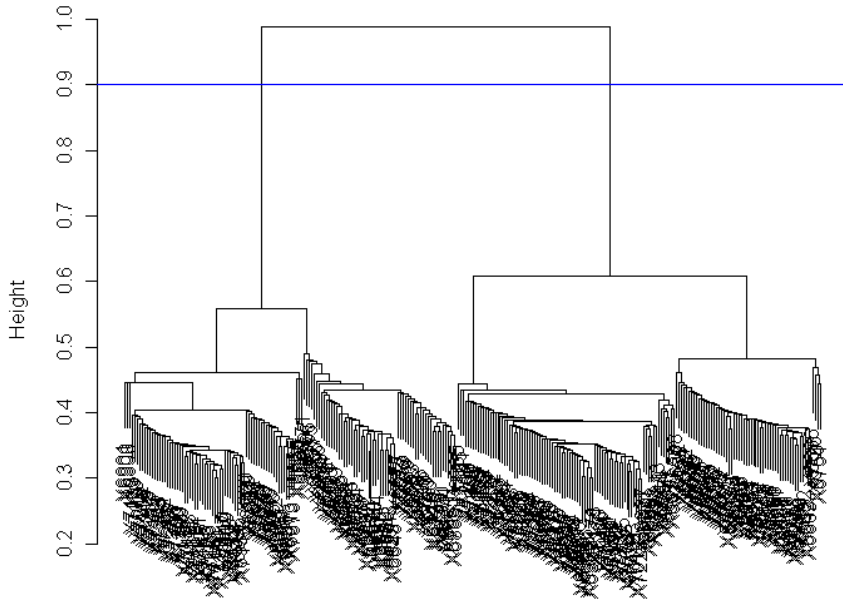
Chromosomal assignments of 10% to 50% of the markers are inconsistent with the released genome assembly (Pinot Noir)



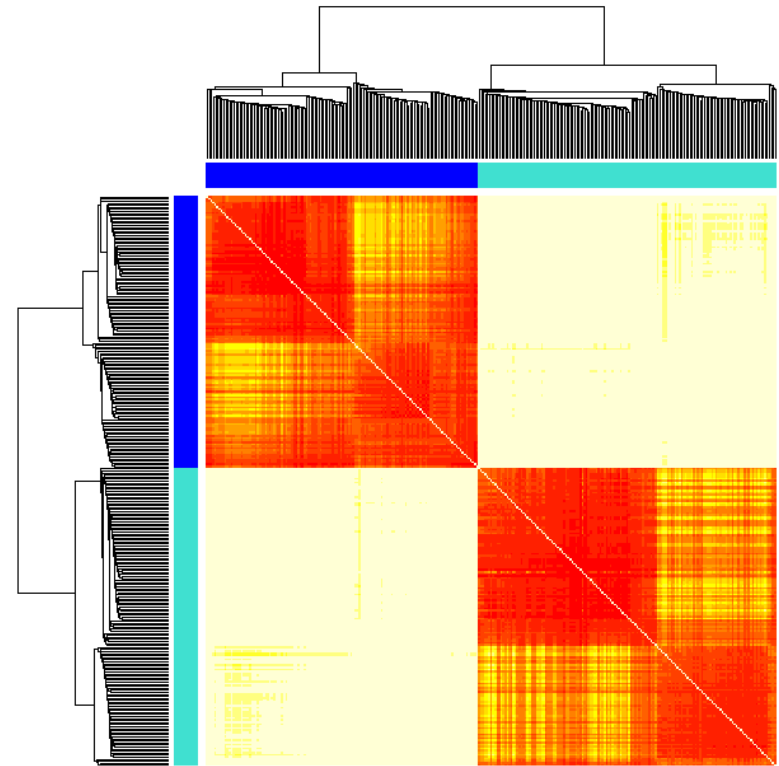
Strategy for Map Construction

step 2: phasing of the heterozygous markers

chromosome 9 (F)



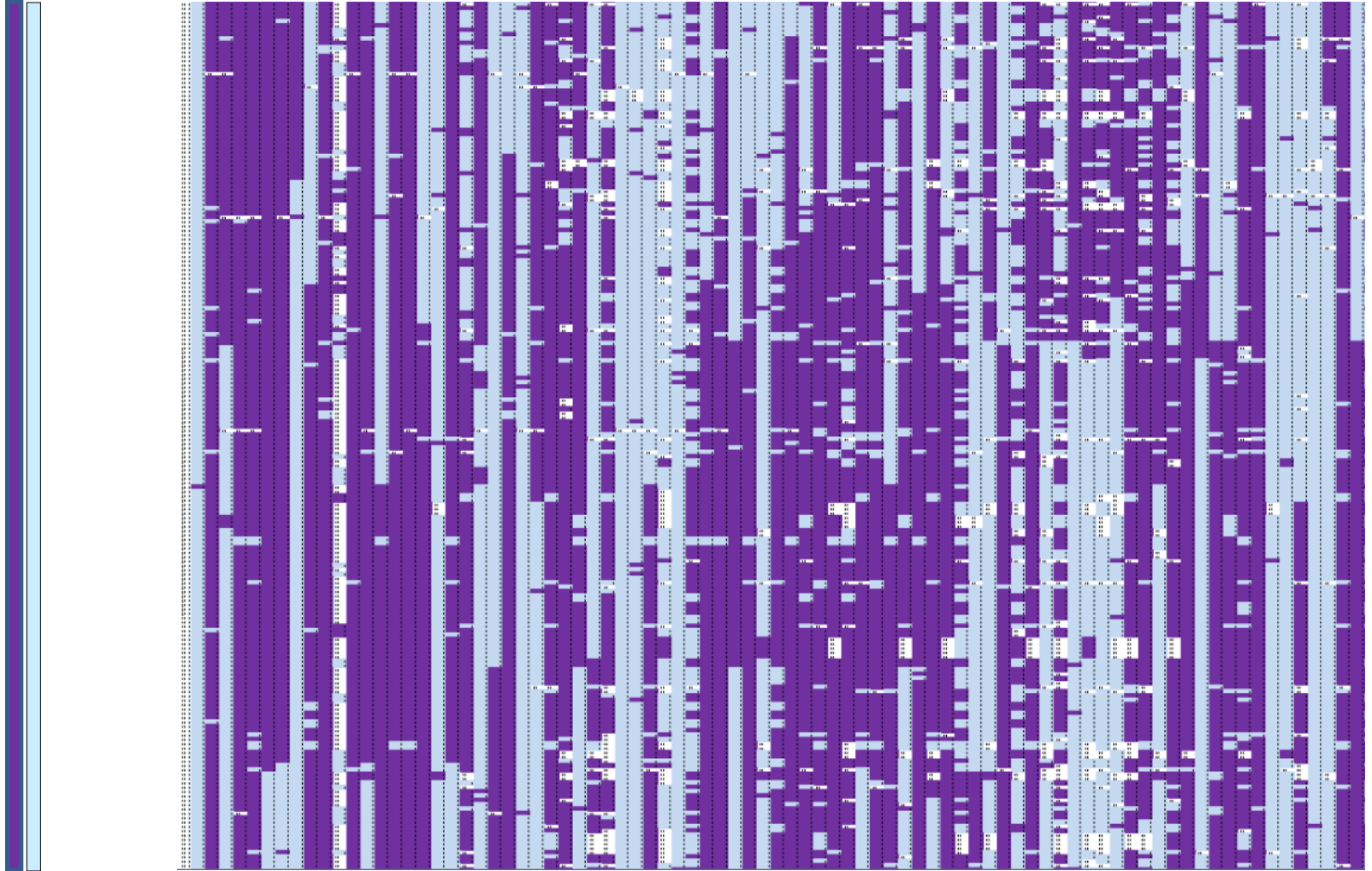
```
as.dist(distTOM1)  
hclust("average")
```



Step 3. Error correction, ordering and imputation (work in progress)

Parent 1

86 F1 progenies



Map before imputation


10 K biallelic markers can be genetically mapped

12386	Markers with 20% or less missing data
8259	Genetically and physically mapped to the same chromosome
2495	Genetically and physically mapped to different chromosomes
1632	not mapable

GBS Workshop

Ithaca, NY Feb.16-17, 2012

Buckler lab - IGD - CBSU



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Genotyping-by-Sequencing (GBS)

February 16-17 2012

[Click here to register for this workshop](#)

Cornell's Institute for Genomic Diversity and Computational Biology Service Unit are jointly offering a two-day workshop on genotyping-by-sequencing (GBS), a new method for generating large numbers of single nucleotide polymorphisms (SNPs) for use in genetic analyses. The workshop will be held at 655 Rhodes Hall, Cornell University, Ithaca, New York.


The first day of the workshop will comprise a series of lectures with emphasis on data analysis with current pipelines. On the second day, a computer lab will be available for analyzing raw GBS sequence data from several species. Participation in the computer lab is limited to 40 individuals.

Workshop Outline

[Session 1](#) 2/16/2012 9:30:00 AM 655 Rhodes Hall
Lectures

[Session 2](#) 2/17/2012 9:30:00 AM 655 Rhodes Hall
Computer Lab

For people coming to the workshop from outside Cornell, we have reserved a block of hotel rooms at the Best Western near campus. Call 607-272-6100 and request the GBS workshop rate (\$99) to reserve a room. Email Theresa.tf12@cornell.edu if problems or other logistical questions.

 [login](#) [BioHPC @ CBSU](#)

Google: GBS workshop

Acknowledgement

GBS Platform

Ed Buckler
Jeff Glaubitz
James Harriman
Robert Elshire
Sharon Mitchell

VitisGen

Bruce Reisch
Lance Cadle-Davidson
Paola Barba

Computational Biology Service Unit

Jarek Pillardy
Robert Bukowski
Minghui Wang

