

ROSBREED

Enabling marker-assisted breeding in Rosaceae

Infinium SNP genotyping in *Prunus*

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Outline of Presentation

- ❖ Peach SNP array design
- ❖ Peach SNP array evaluation
- ❖ Cherry SNP chip array design
- ❖ Cherry SNP chip evaluation

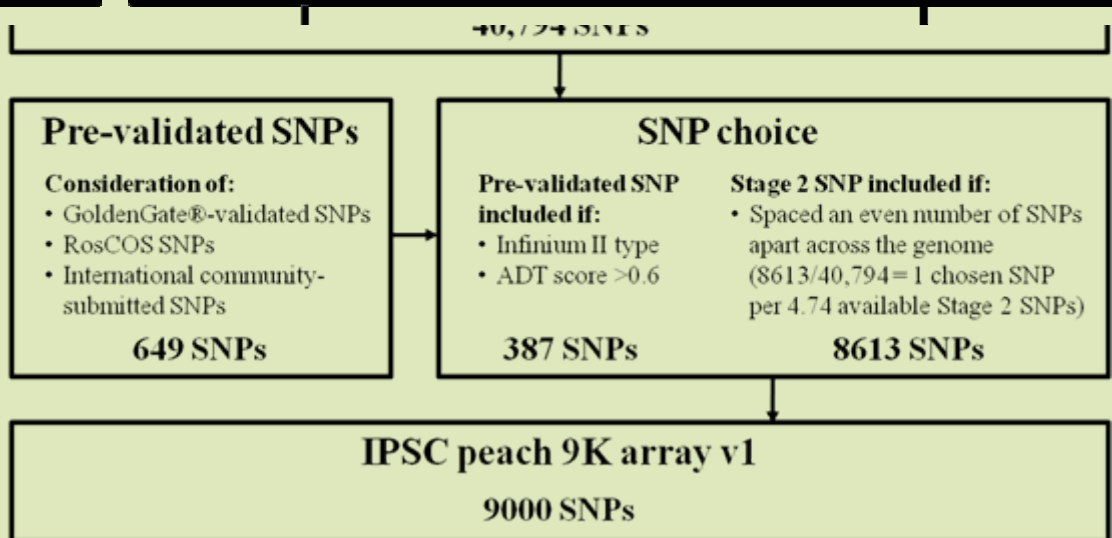
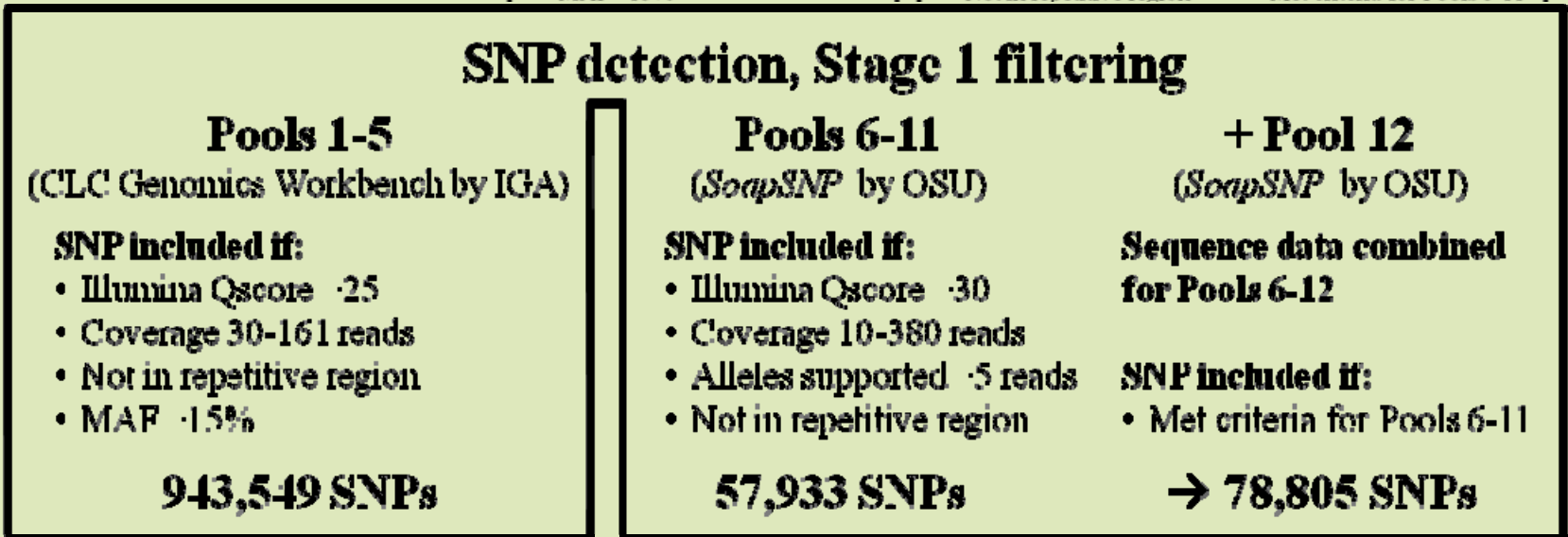
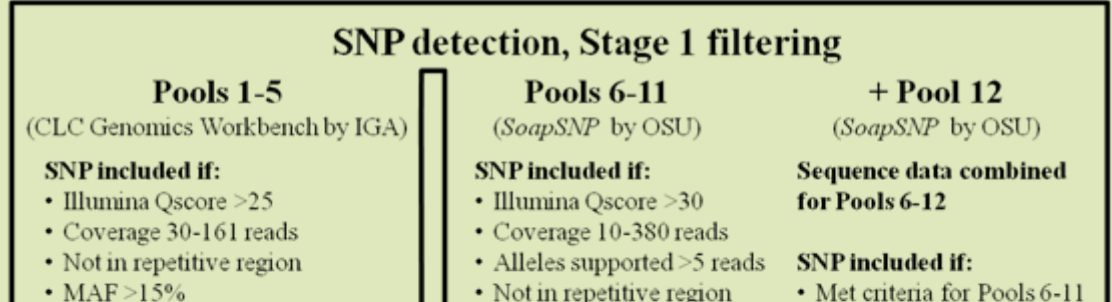


9,000 SNPs

International Peach SNP Consortium
peach 9K SNP array v1



With SNPs that are not found in the reference genome



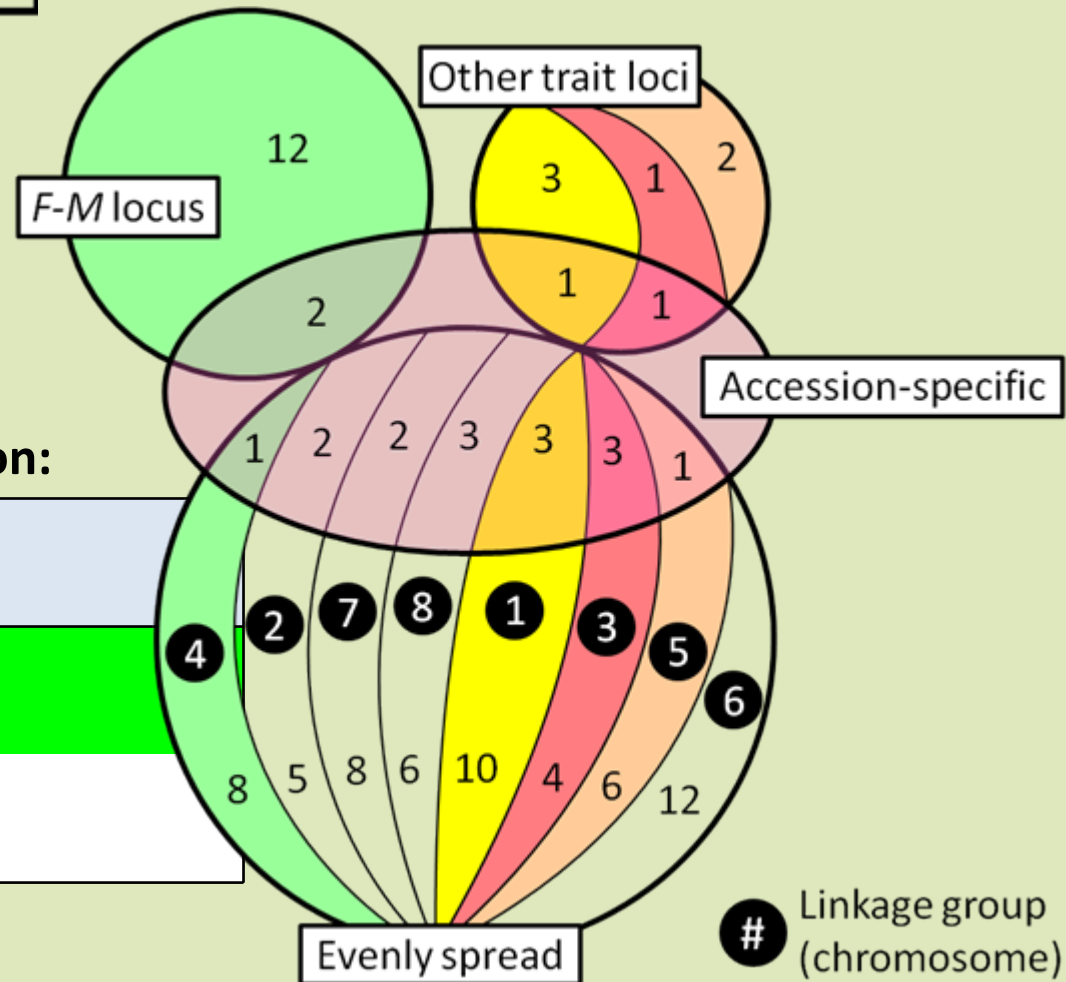
SNP validation

Testing of further potential filtering parameters
with Illumina GoldenGate® assay

96 SNPs screened via
GoldenGate on 160 peach
accessions

Results of the GoldenGate validation:

SNP parameter	Total	Polymorphism proportion
Exonic	30	77%
Intronic	19	74%
UTR	16	50%
Intergenic	31	32%



CHOICE of 9,000 SNPs for final array

1,000,000 SNPs -----> 9,000 SNPs

Stage 2 filtering

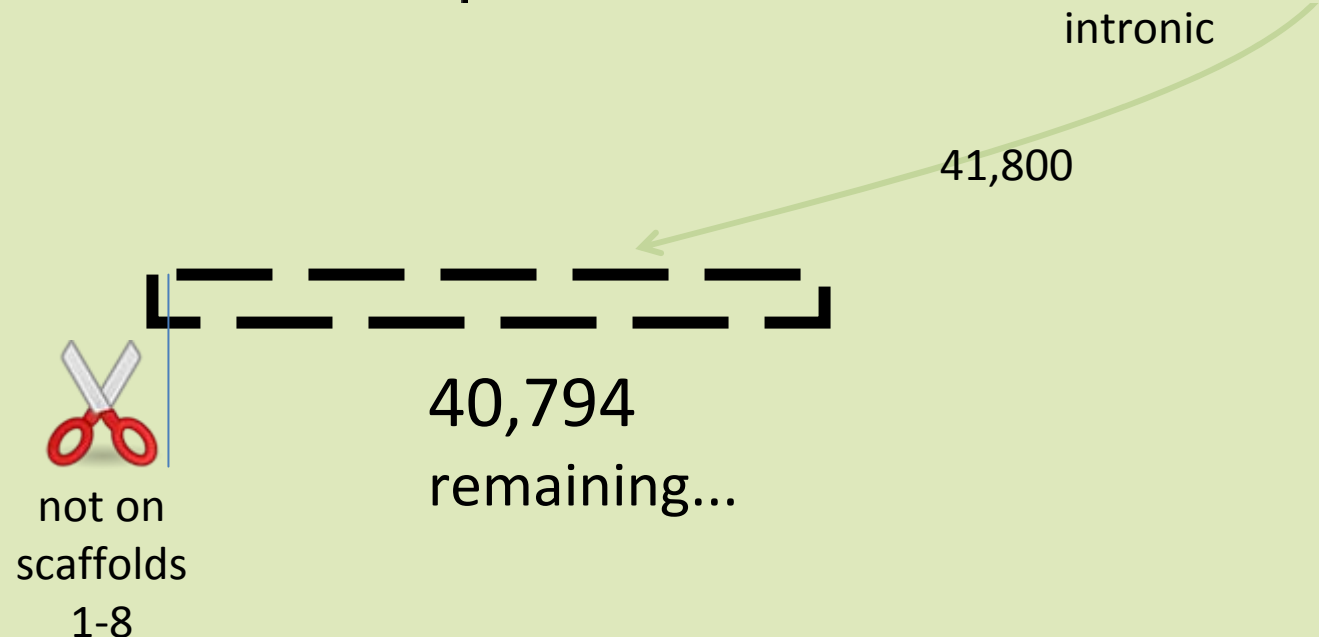
Merged SNPs from Pools 1-12

Removed duplicate SNPs

SNP kept if:

- Supported by ≥4 accessions
- Infinium II type (not A/T or C/G transversion)
- ADT score ≥0.9
- Located in putative exonic region
- Located on pseudomolecules 1-8 only

40,794 SNPs



649 “pre-validated”

- 55 GoldenGate validated
- 453 RosCOS
- 108 Drupomics (Ignazio Verde)
- 33 Chile (Herman Silva)



A/T or C/G,
ADT <0.6

387 included

- 45 GoldenGate validated
- 225 RosCOS
- 87 Drupomics (Ignazio Verde)
- 30 Chile (Herman Silva)

Pre-validated SNPs

Consideration of:

- GoldenGate®-validated SNPs
- RosCOS SNPs
- International community-submitted SNPs

649 SNPs

SNP choice

Pre-validated SNP included if:

- Infinium II type
- ADT score <0.6

387 SNPs

Stage 2 SNP included if:

- Spaced an even number of SNPs apart across the genome (8613/40,794 – 1 chosen SNP per 4.74 available Stage 2 SNPs)

8613 SNPs



Out of 40,794 Stage 2 SNPs 8,613, spaced at one per ~5 SNPs were chosen along 8 pseudomolecules

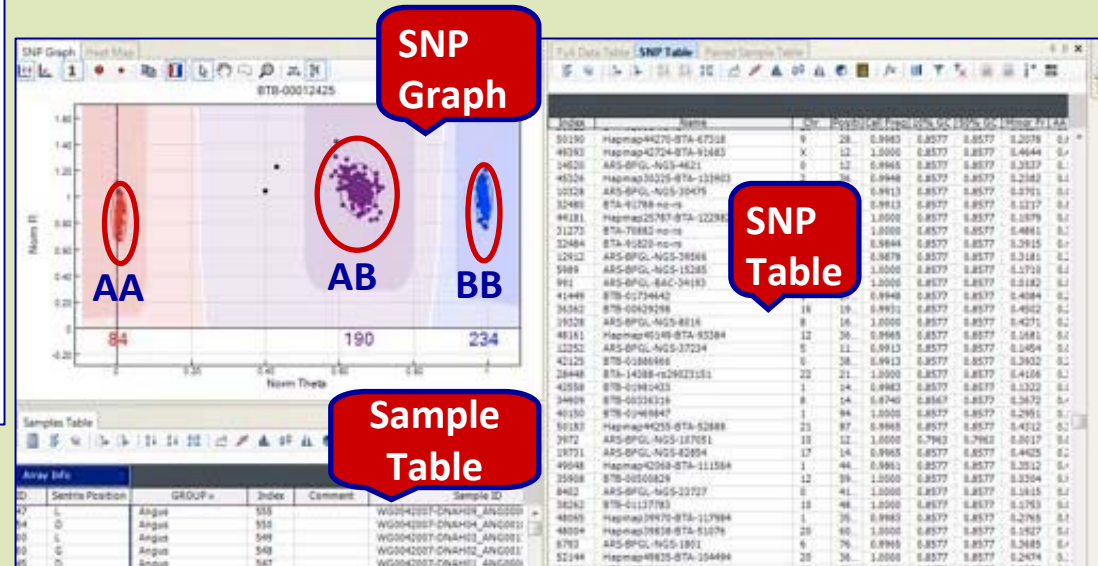
Evaluation

Infinium iSelect® HD Custom Genotyping

- 24 samples per chip



iScan



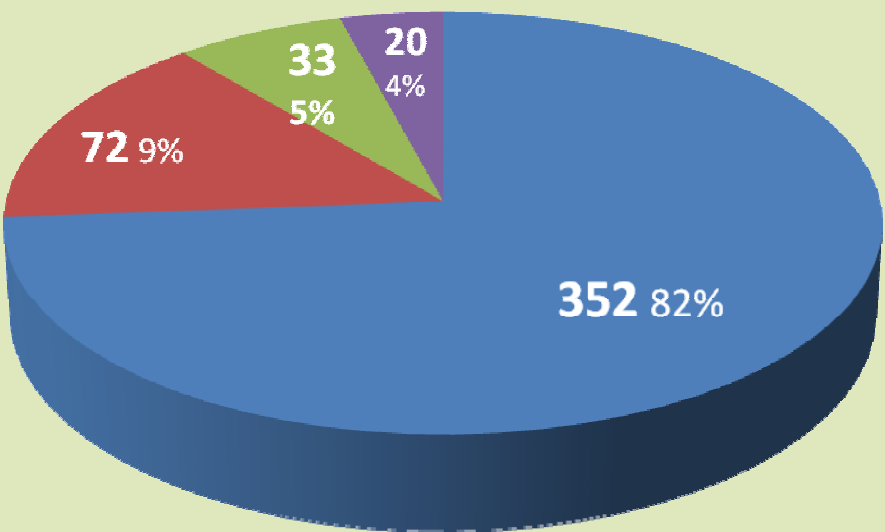
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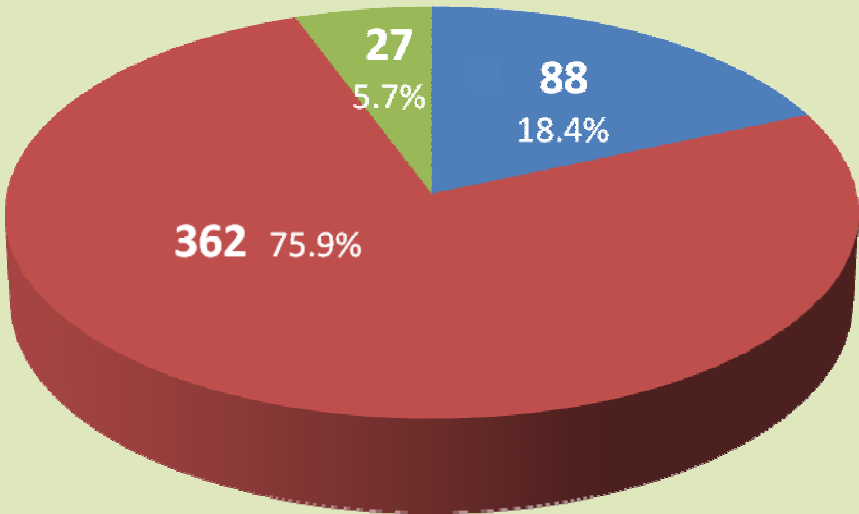
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Material used to evaluate peach 9K Infinium® II array.

Peach related samples include *Prunus davidiana* and *P. mira*; Almond related samples include *P. argentea* and *P. scoparia*



- Peach
- Almond
- Peach related
- Almond related

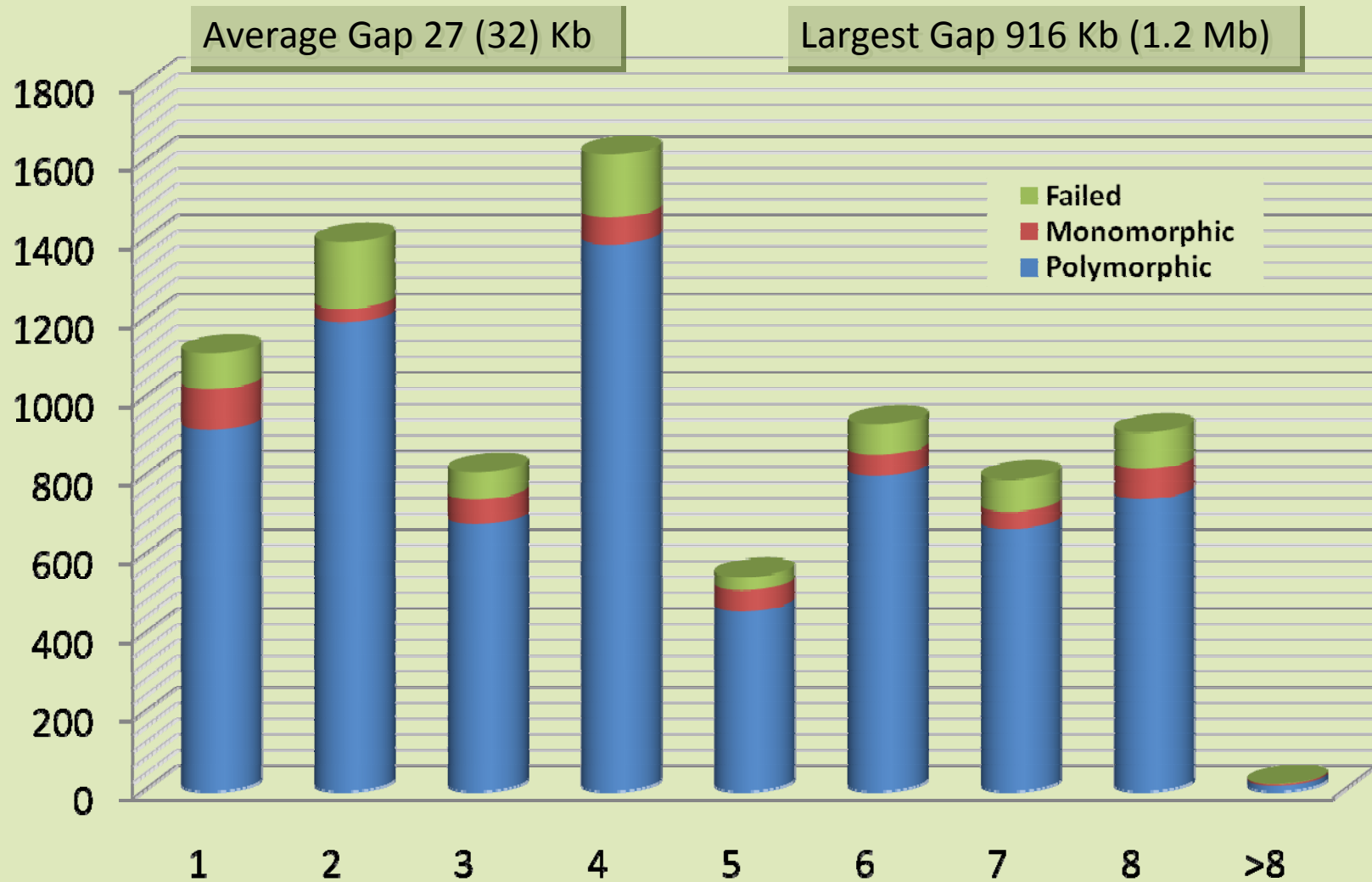


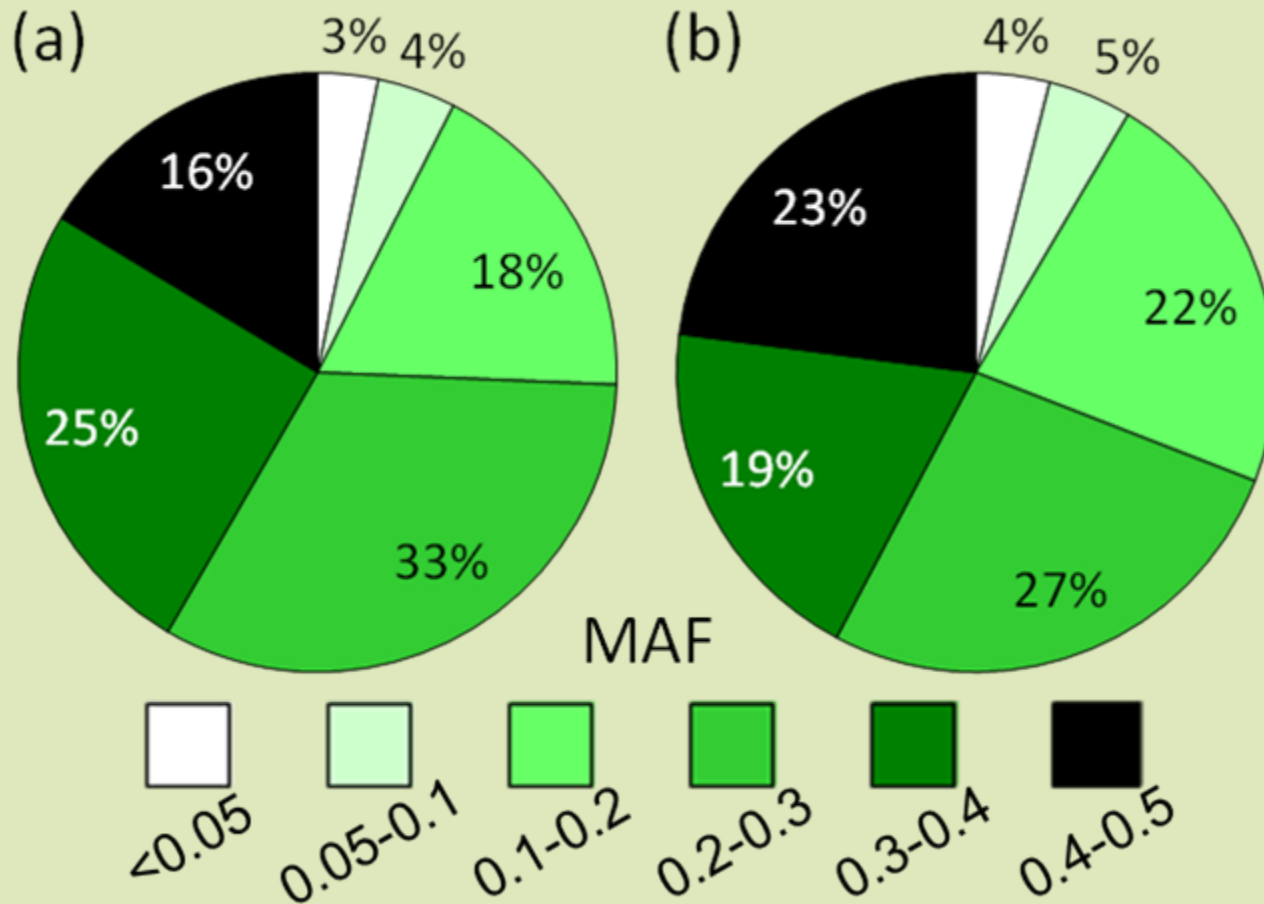
- Cultivars
- Seedlings
- Advanced selections

EU material 99% peach 1% peach related

90% cultivars 10% advanced selections

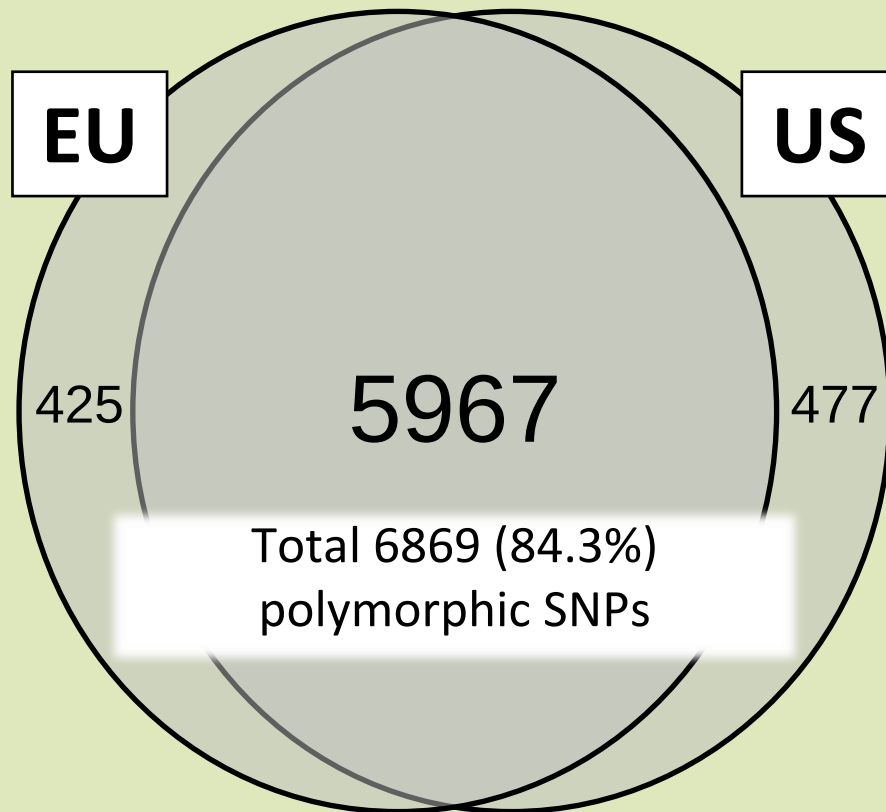
Performance of SNPs on 9K Infinium® II array (n=8144) using both EU and US data sets

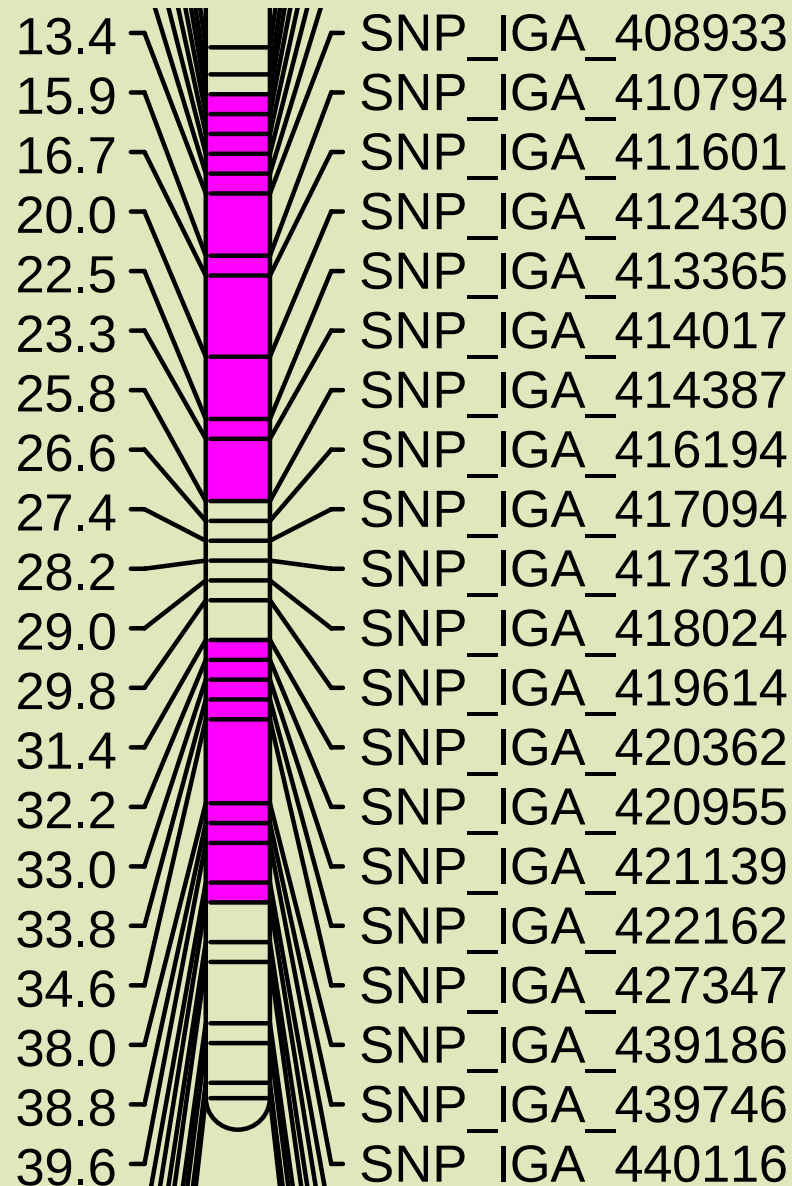
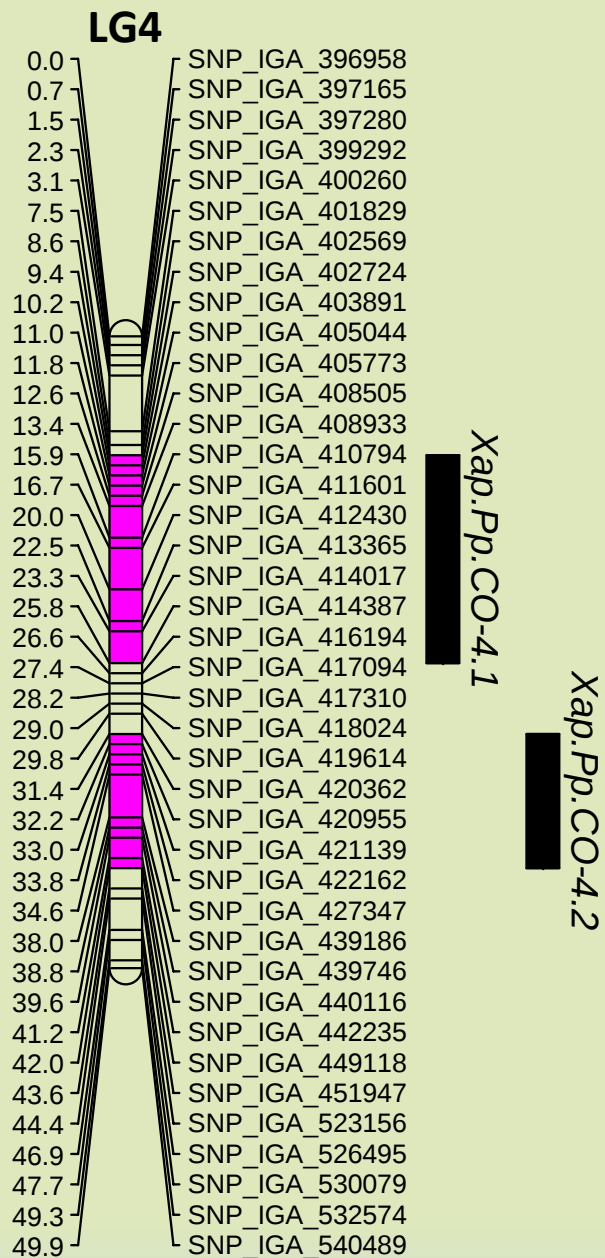




**Polymorphic SNPs Minor Allele Frequency in
EU (a) and US (b) data sets**

Polymorphic SNPs on 9K Infinium® II array (n=8144)





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P0496

P0499

Evaluation of Illumina 6K SNP array for Sweet and Tart cherry

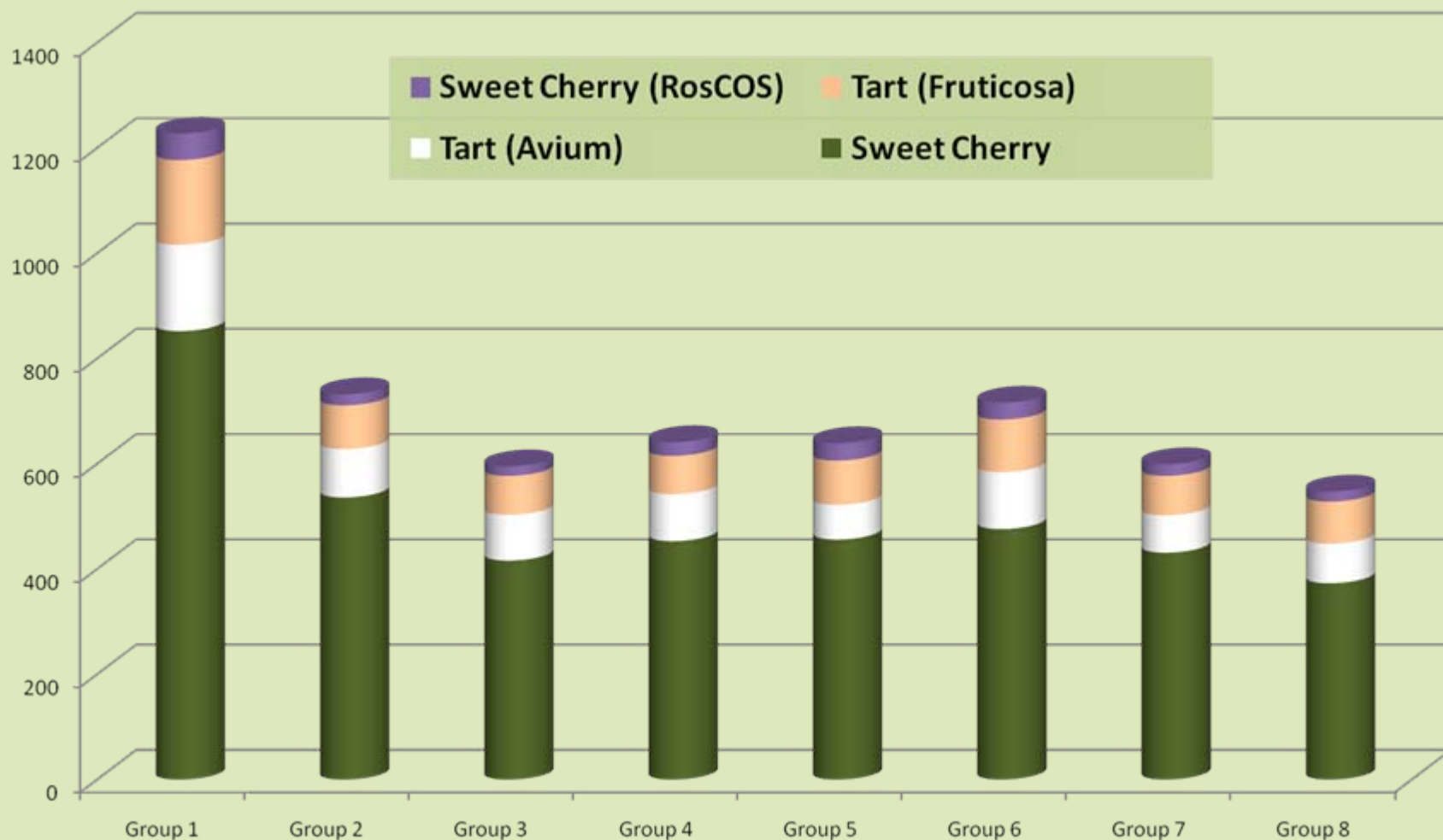


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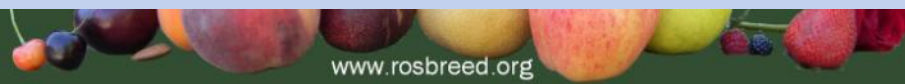
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Total number of markers (n= 5696) grouped by chromosome



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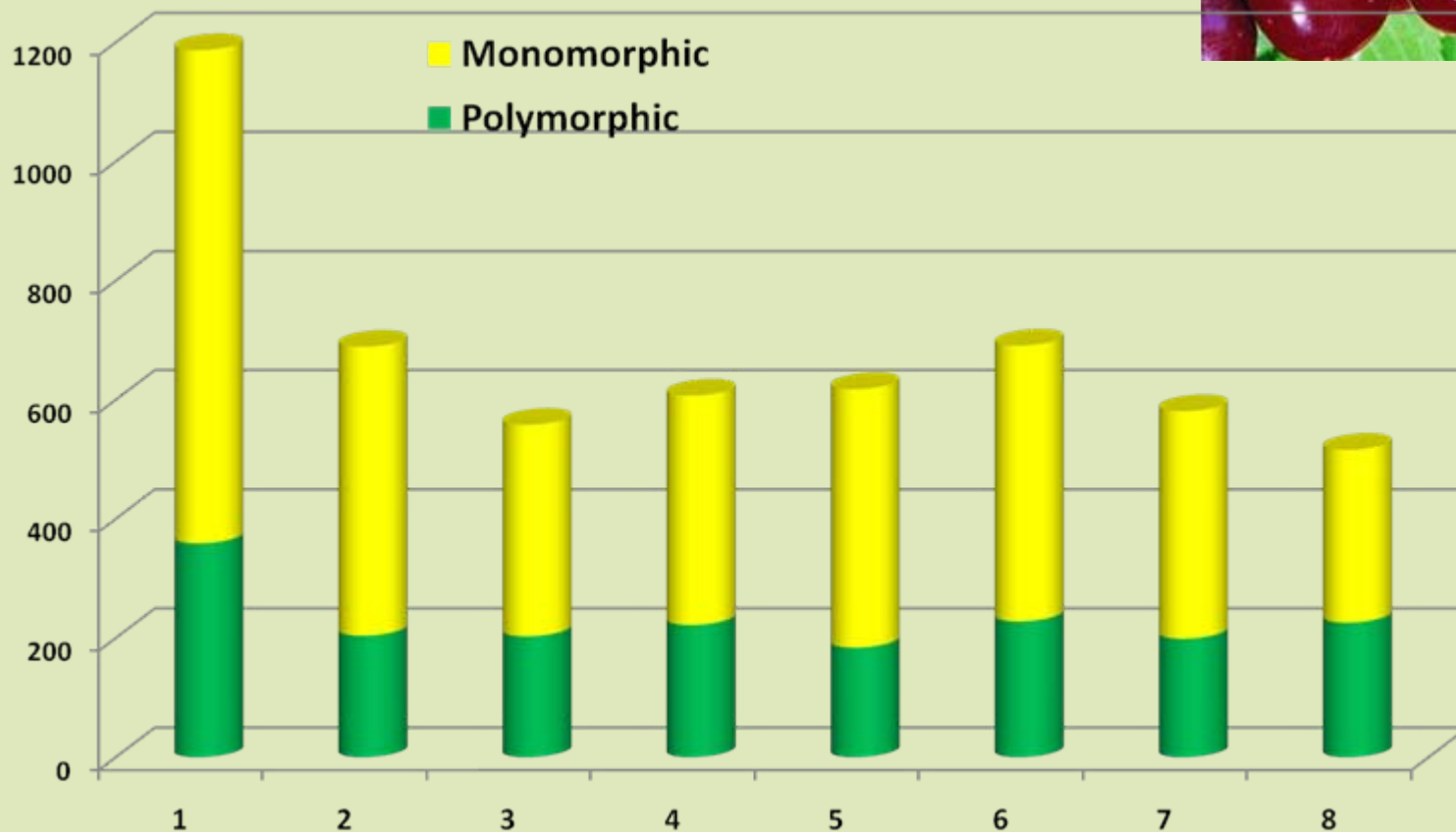
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Sweet cherry

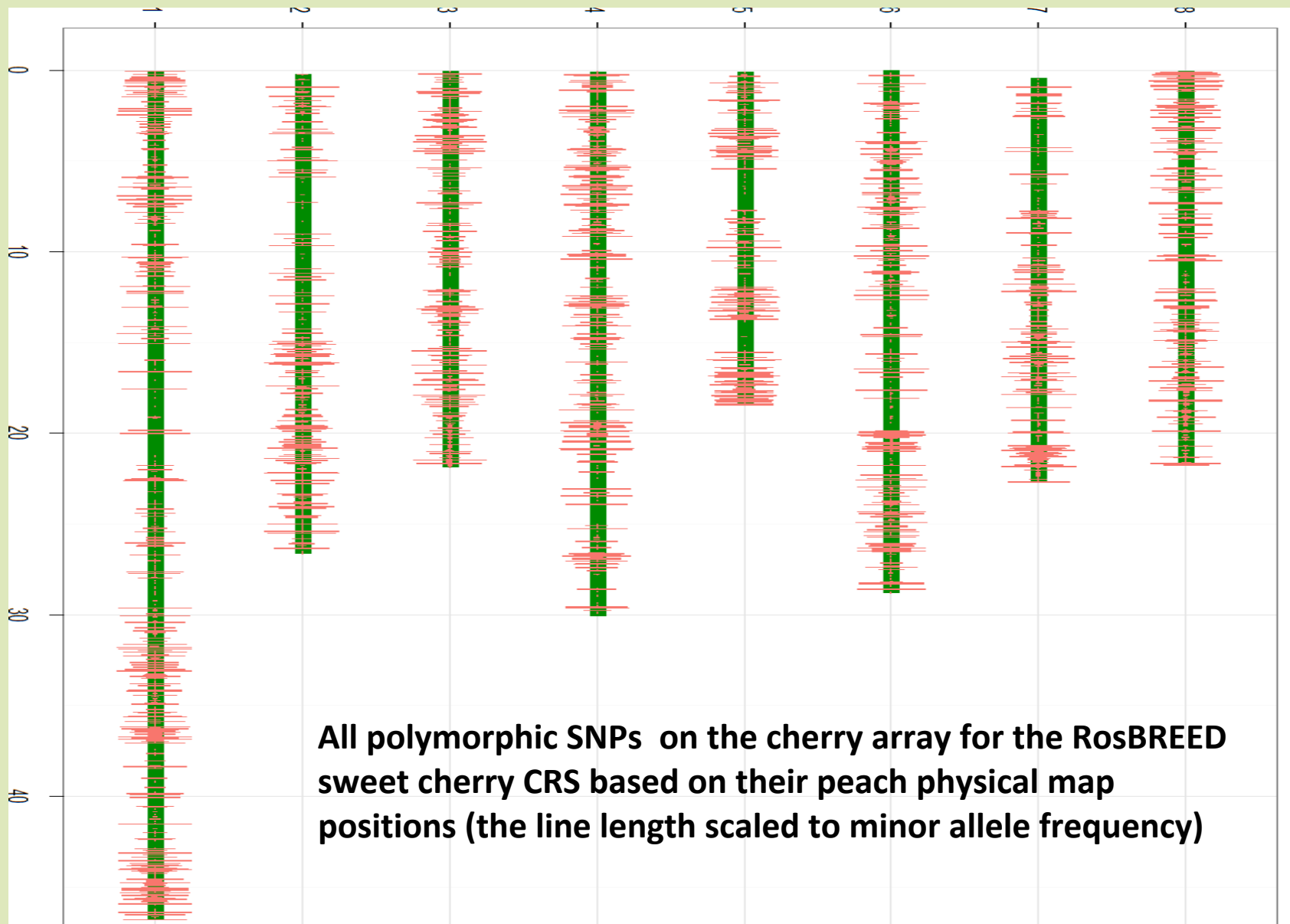
Polymorphic markers by chromosome (for all markers) based on the sweet cherry RosBREED crop reference set (n=270)



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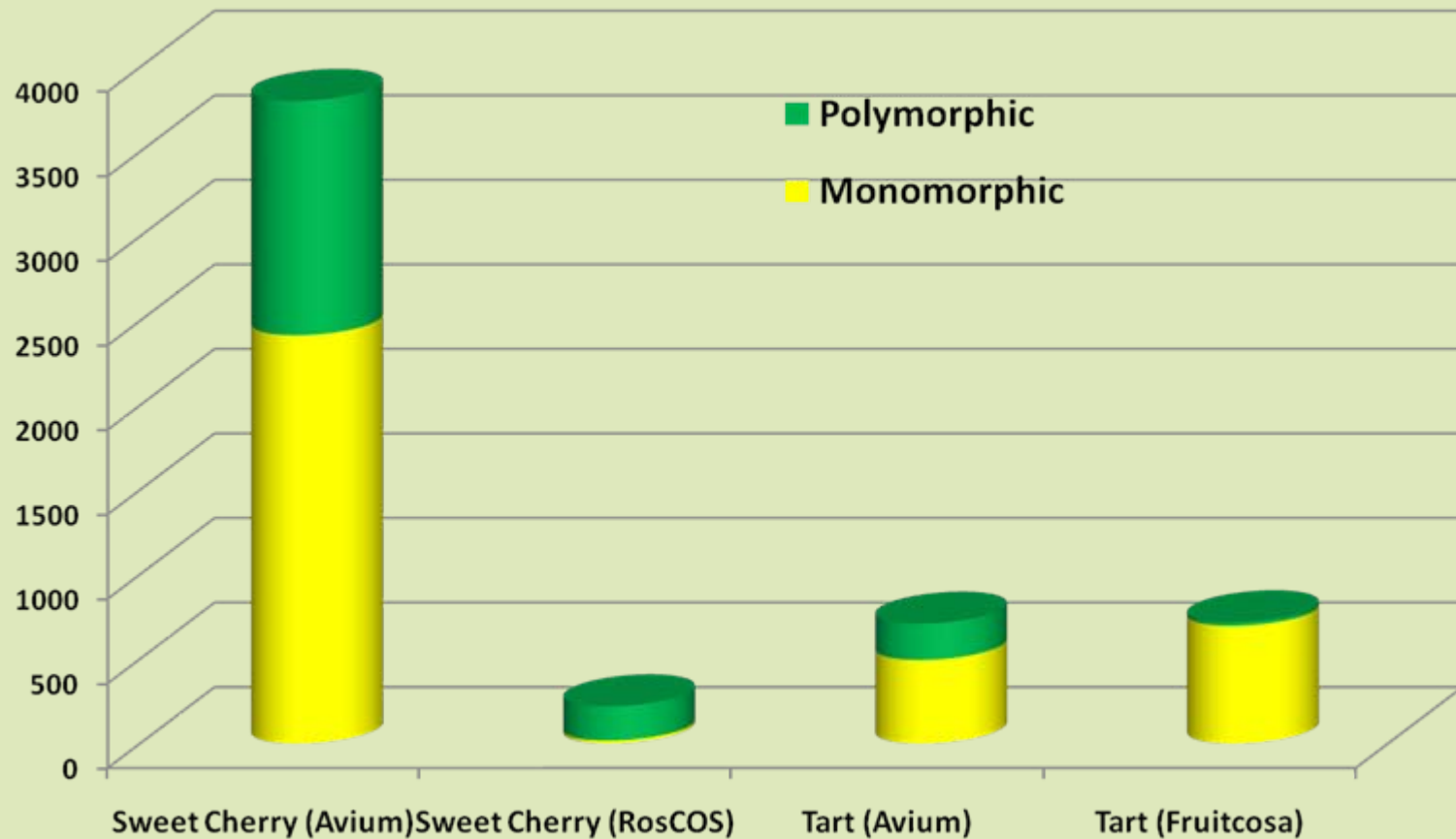
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Polymorphism in Sweet cherry by source of SNP



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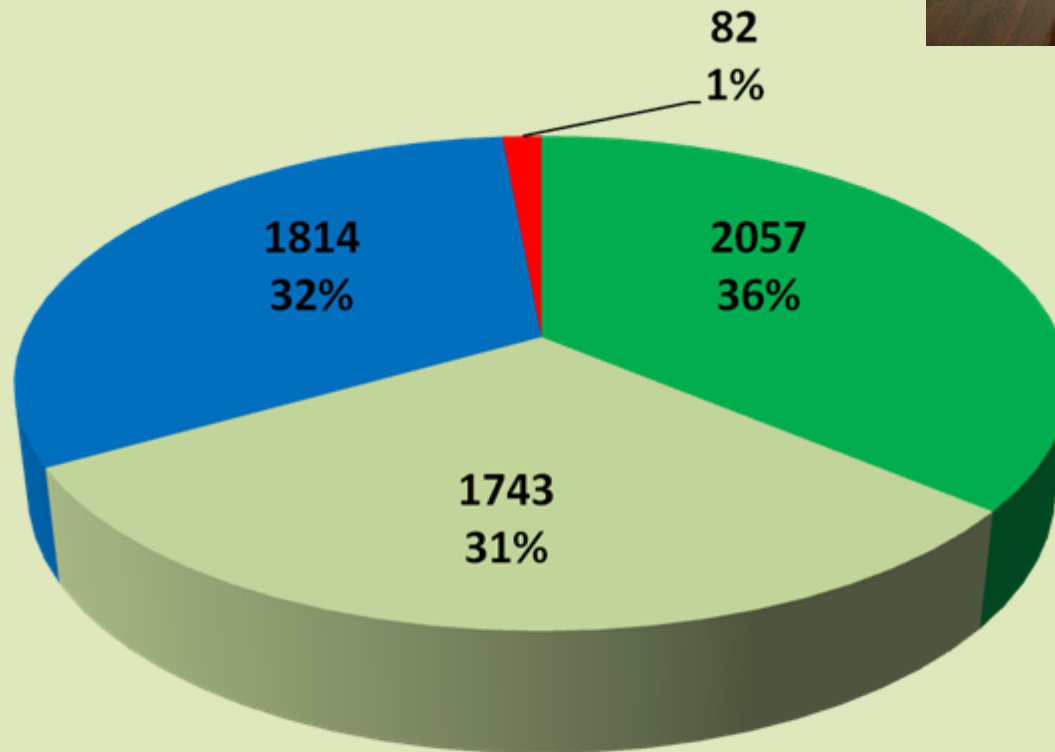
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Tart cherry

Performance of total number of SNPs from analysis of the RosBREED tart cherry crop reference set (n= 330)



■ Polymorphic ■ Unresolved (Polymorphic) ■ Monomorphic ■ Failed

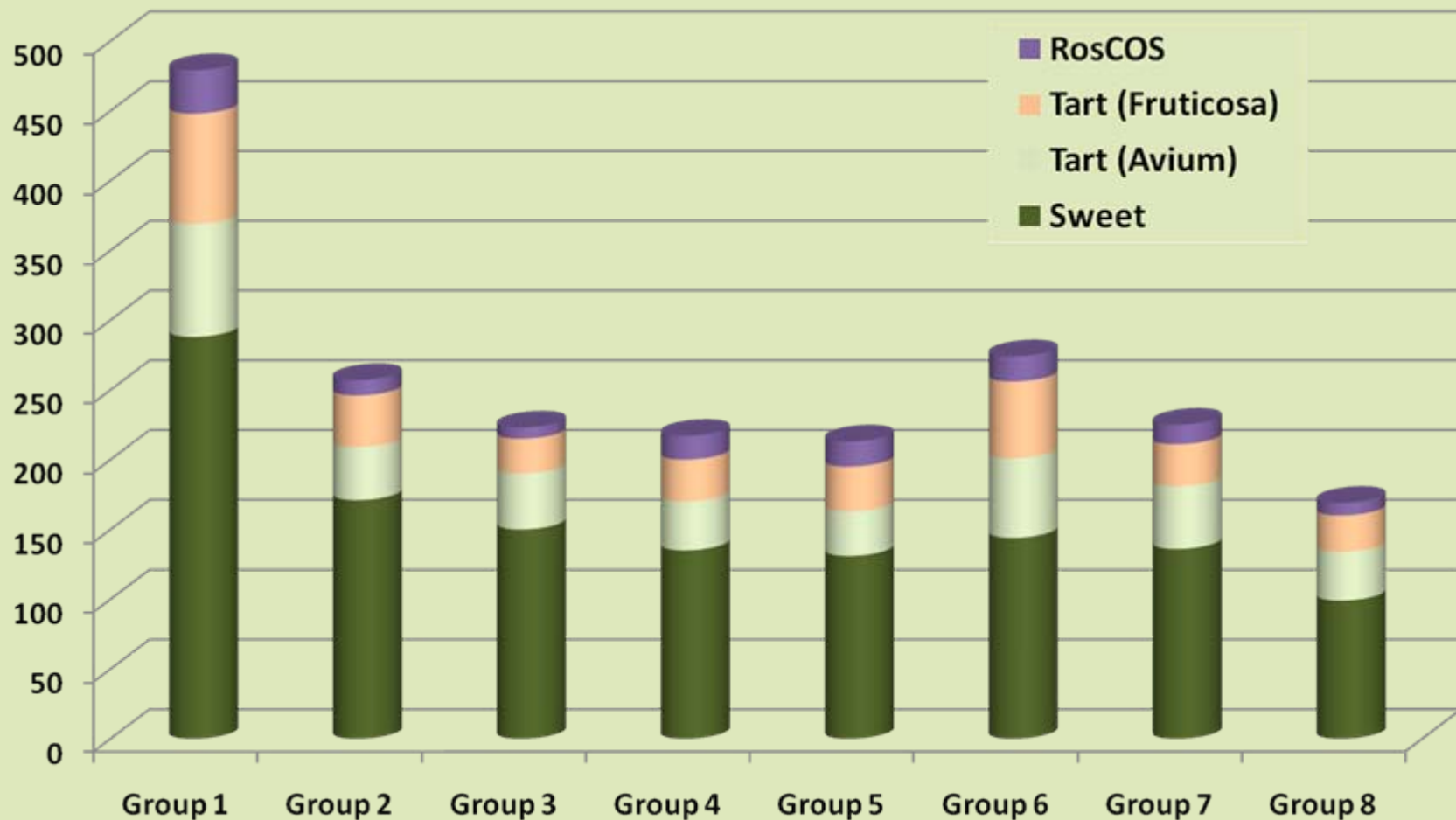
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Number of polymorphic SNPs per chromosome by SNP genome source in the RosBREED Tart cherry crop seference Set (n=330)



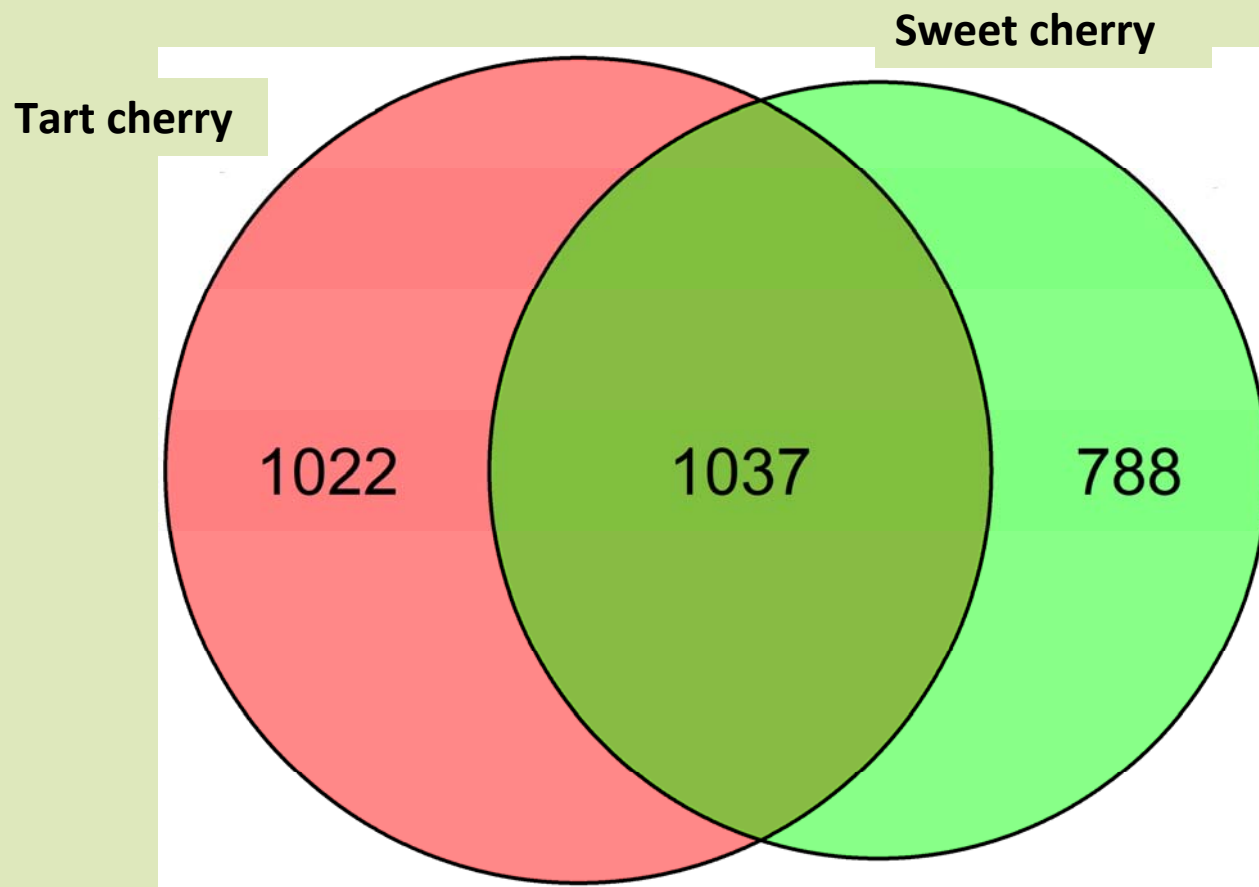
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Number of shared SNP polymorphisms for the tart cherry and sweet cherry CRS



Acknowledgements



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Questions?

