Colloque EPGV
5-7 octobre 2016
Angers, France

Génotypage haut-débit chez le blé hexaploïde à l'aide de la puce BreedWheat Axiom 420K

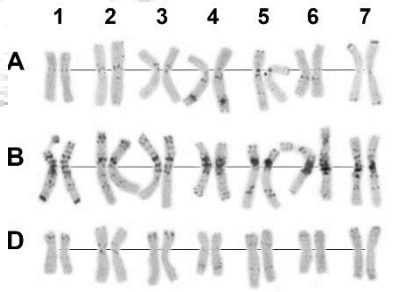
Jonathan Kitt

Structure & Evolution du Génome du Blé
Génétique, Diversité & Ecophysiologie des Céréales
INRA Clermont-Ferrand

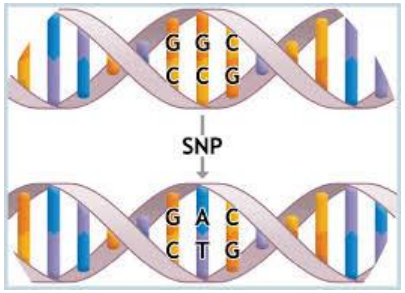
Introduction

- **Blé tendre (*Triticum aestivum*)**

- ✓ Espèce hexaploïde (génomes A,B,D)
- ✓ 17 Gb
- ✓ 80-90% de séquences répétées



- **SNP = Polymorphisme de Nucléotide Unique**
  - ✓ Marqueur moléculaire



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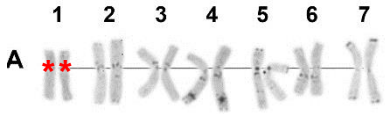
Impact du niveau de ploïdie sur le clustering



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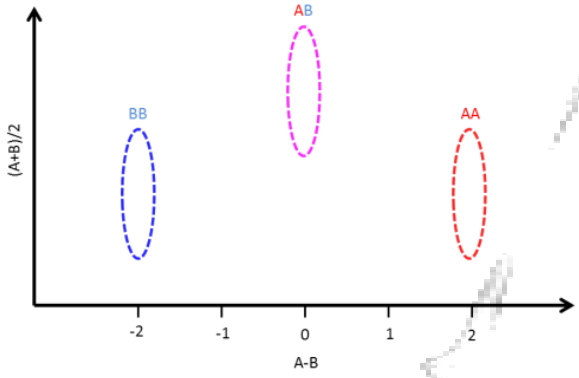
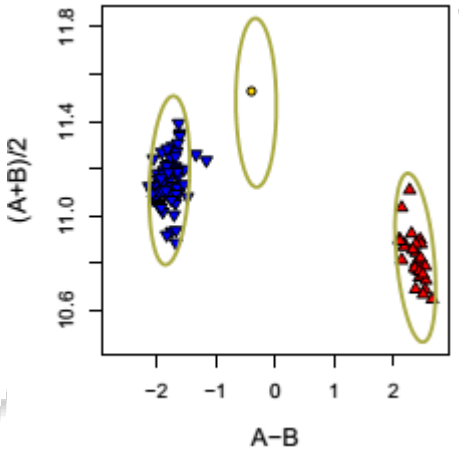
➔ 2 copies





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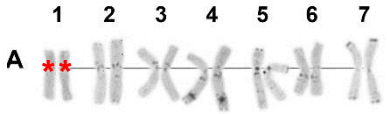

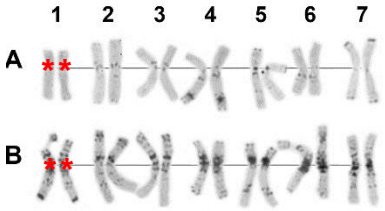

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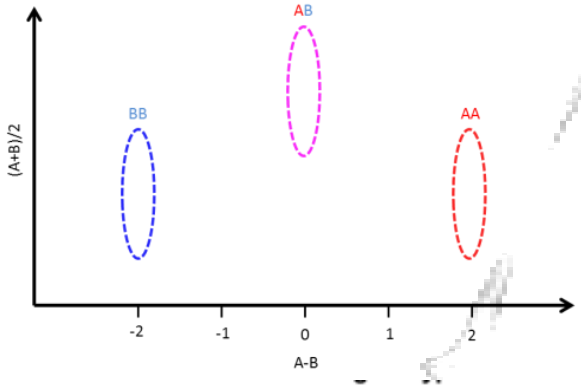

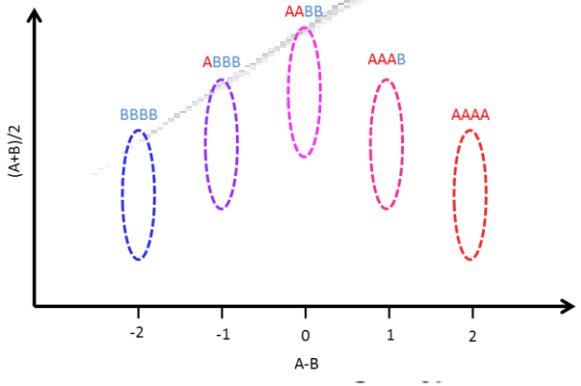

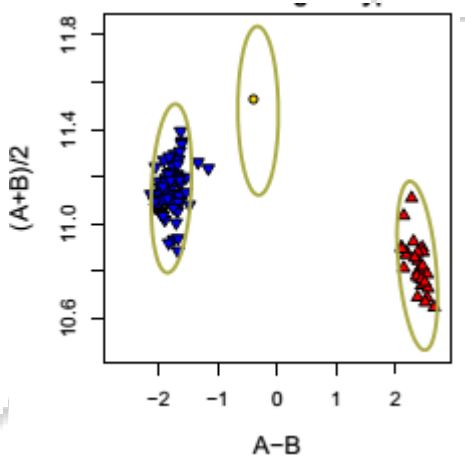

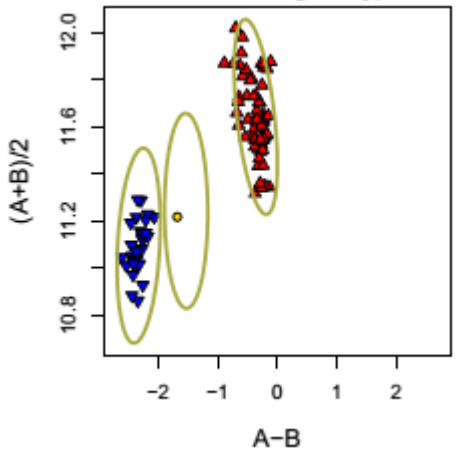

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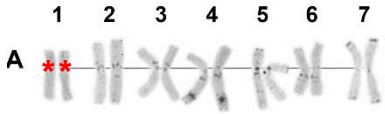

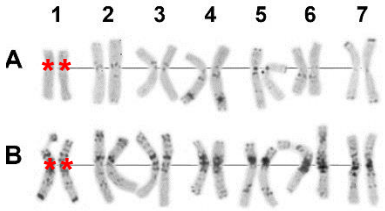

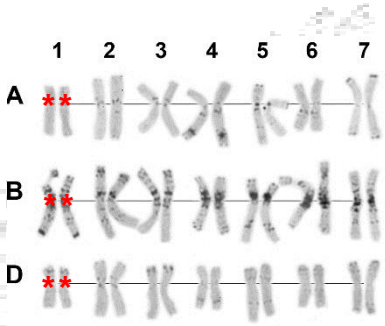

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Hexaploïde
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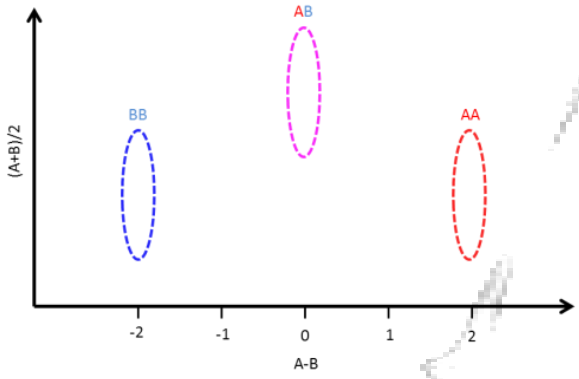
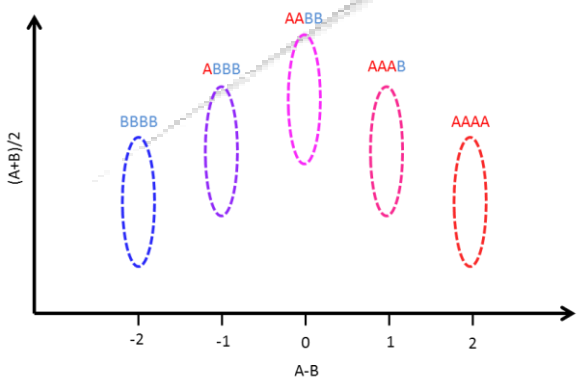
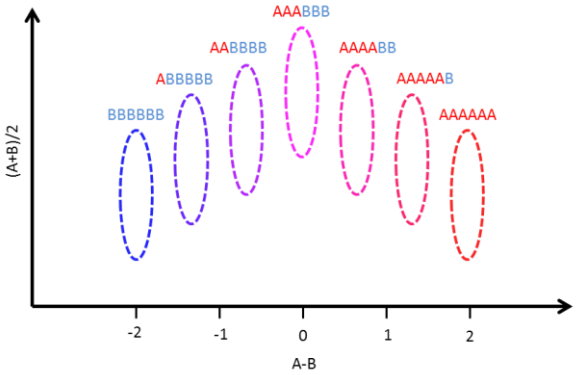
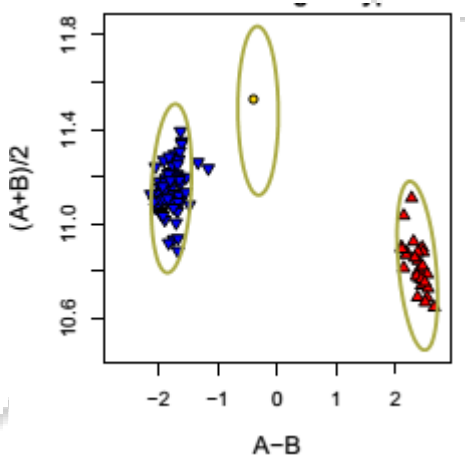
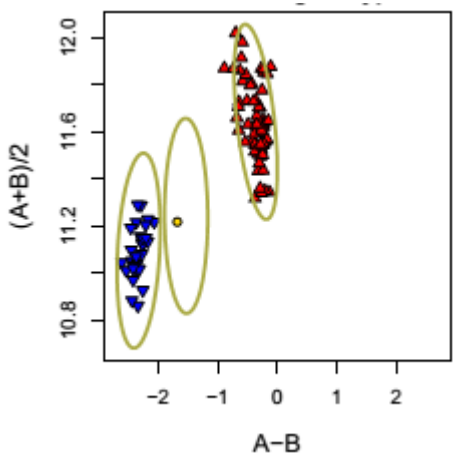
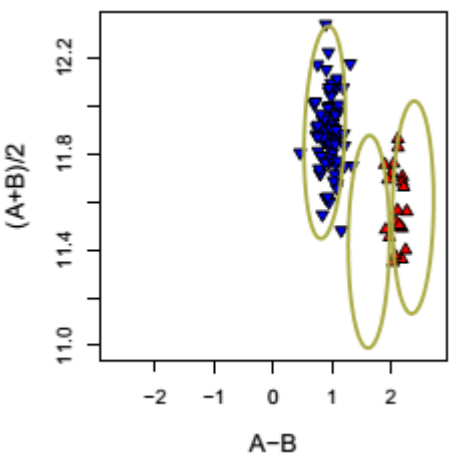




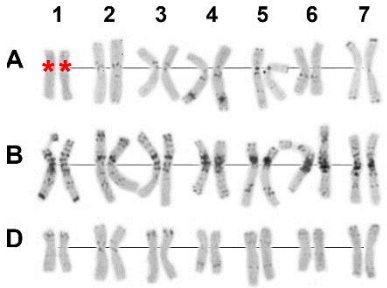




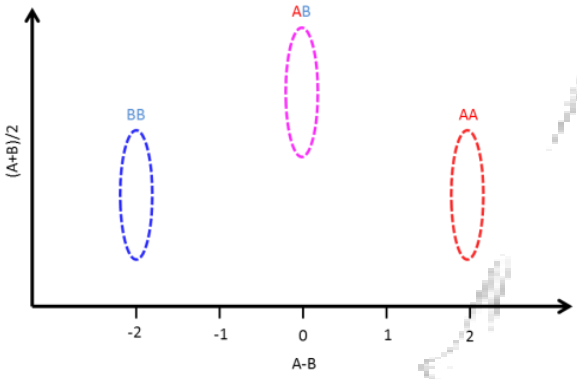


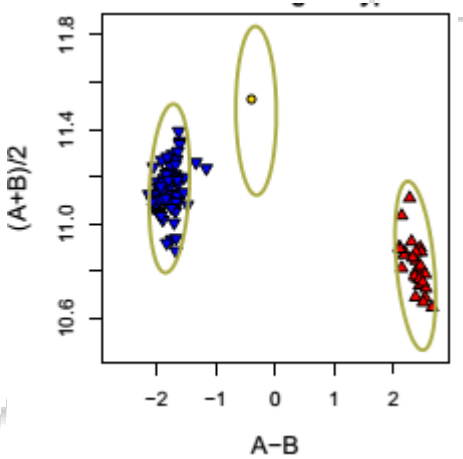


Impact du nombre de copies chez le blé sur le clustering



Comportement diploïde
➔ 2 copies





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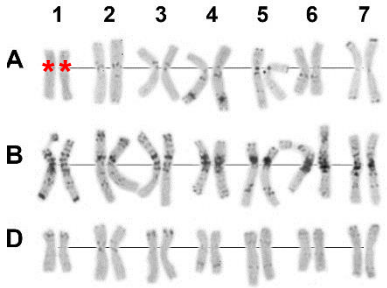

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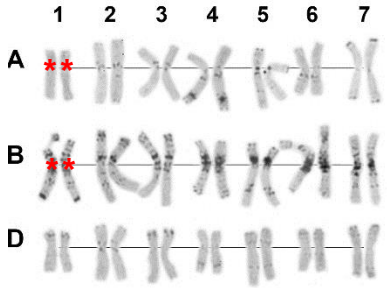

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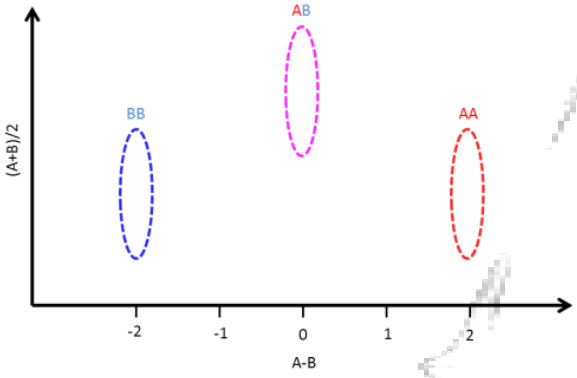

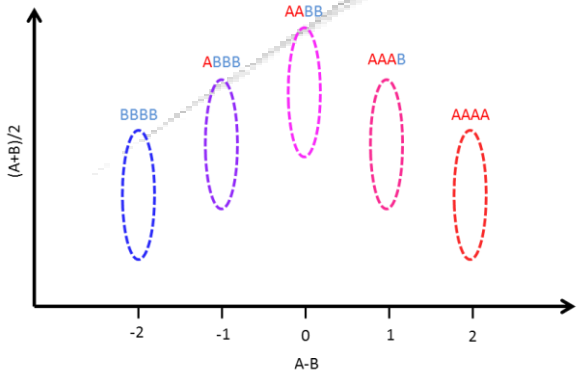

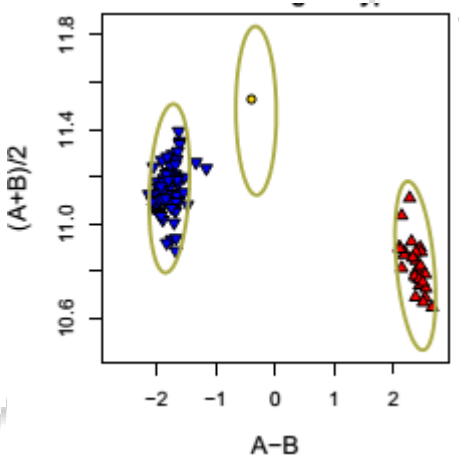

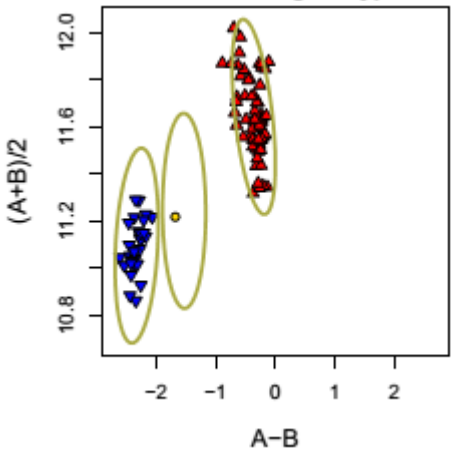

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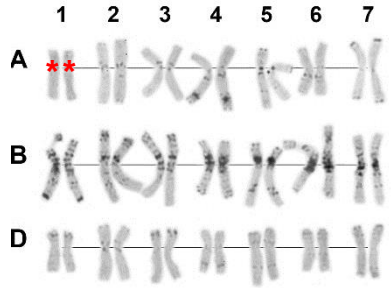

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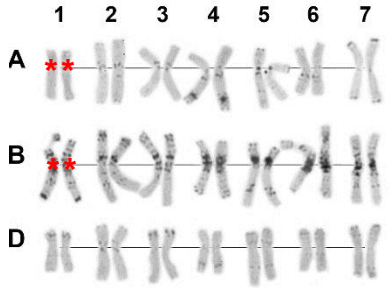

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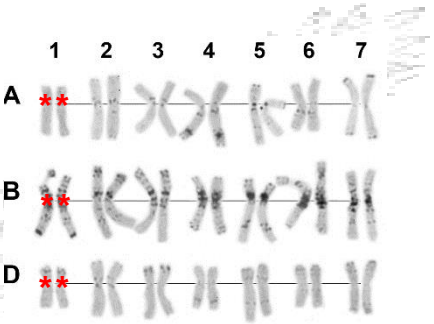

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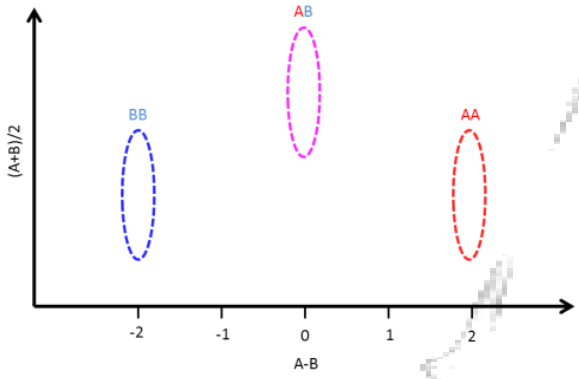

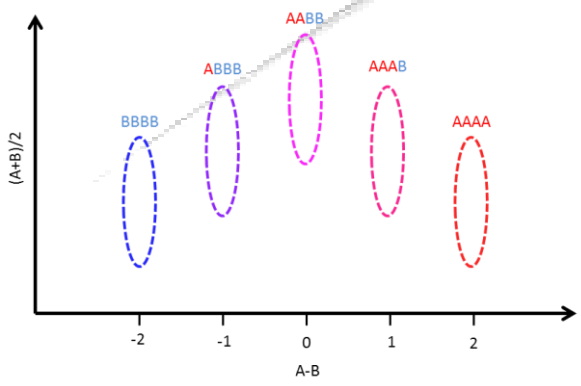

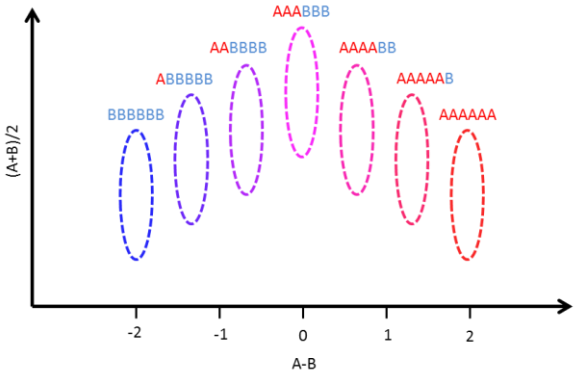

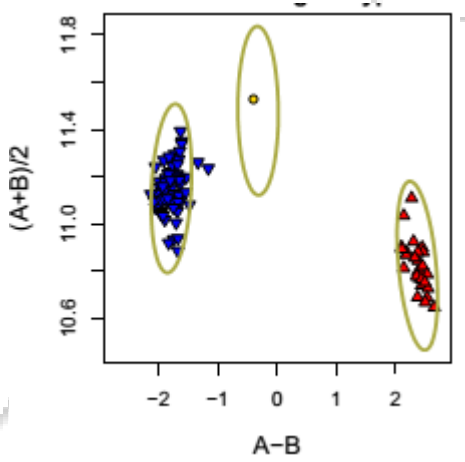

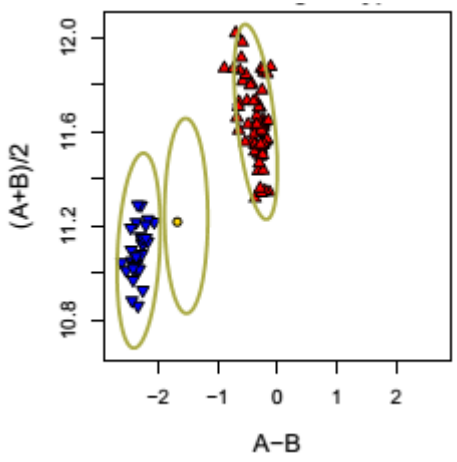

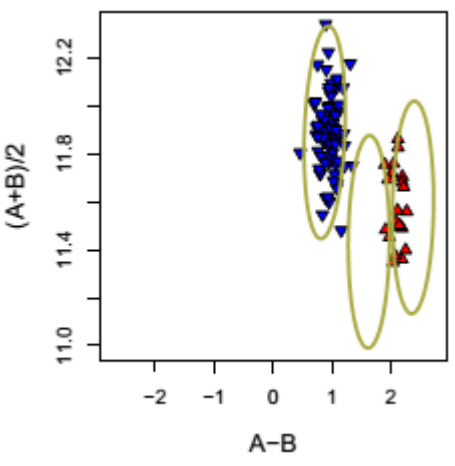

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1. Impact du nombre de copies sur le clustering

2. La puce SNP TaBW420K (Affymetrix Axiom)

3. Comparaison avec la puce iSelect 12K (Illumina Infinium)

4. Exemples d’exploitation de la puce Axiom

La puce SNP TaBW420K BreedWheat

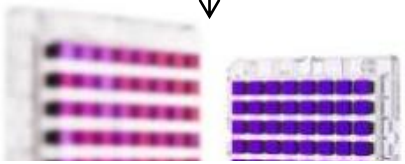
Breed wheat

105,703 SNP issus d'ISBP
9,570 SNP de gènes candidats

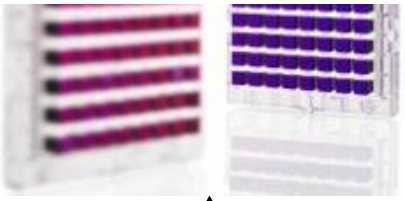
126 SNP de gènes majeurs

Puce Illumina Infinium 90K

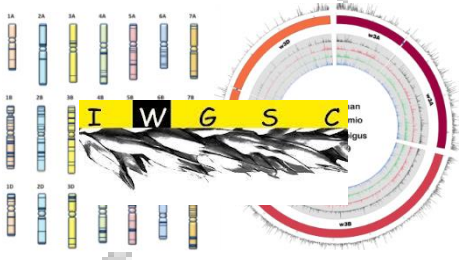
13,670 SNP validés



423,385 SNP



54,280 SNP géniques
225,946 SNP intergéniques



IWGSC chromosome arm sequence survey initiative

4,120 SNP validés

biogemma

4,815 SNP validés sur Axiom

INRA SCIENCE & IMPACT

5,155 SNP validés sur Axiom

University of BRISTOL

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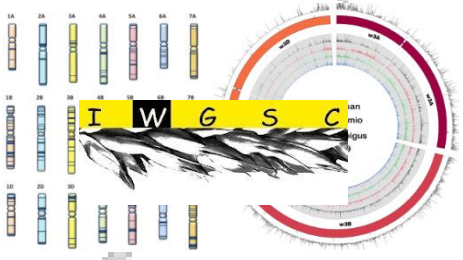

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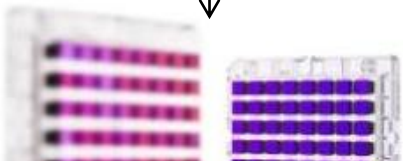

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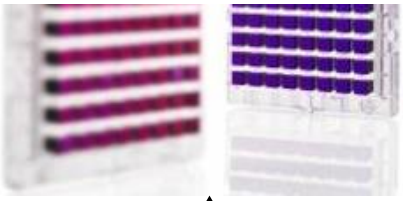

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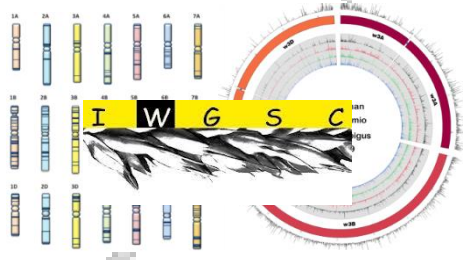

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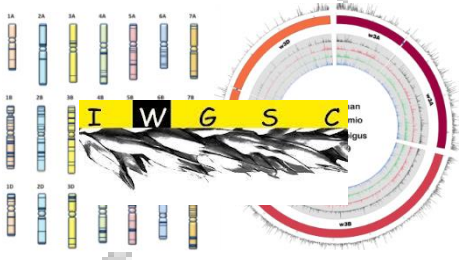

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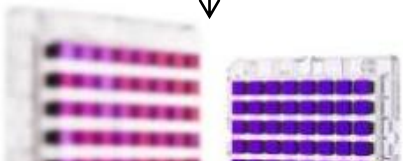

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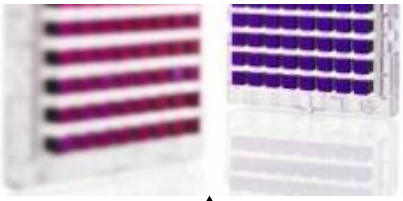

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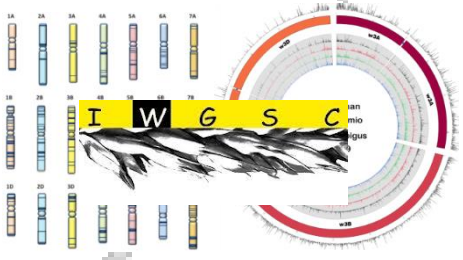

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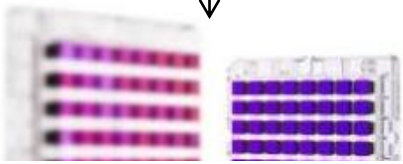

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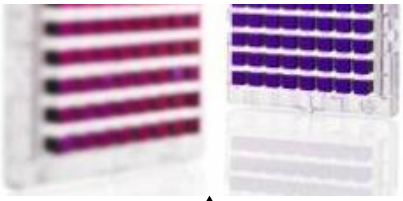

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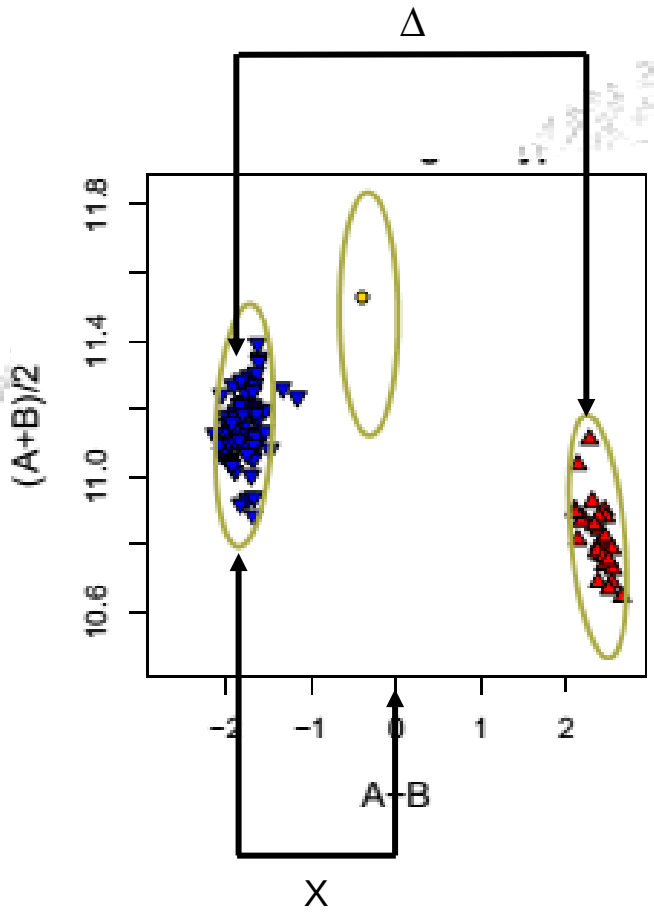
Critères de qualité des SNP



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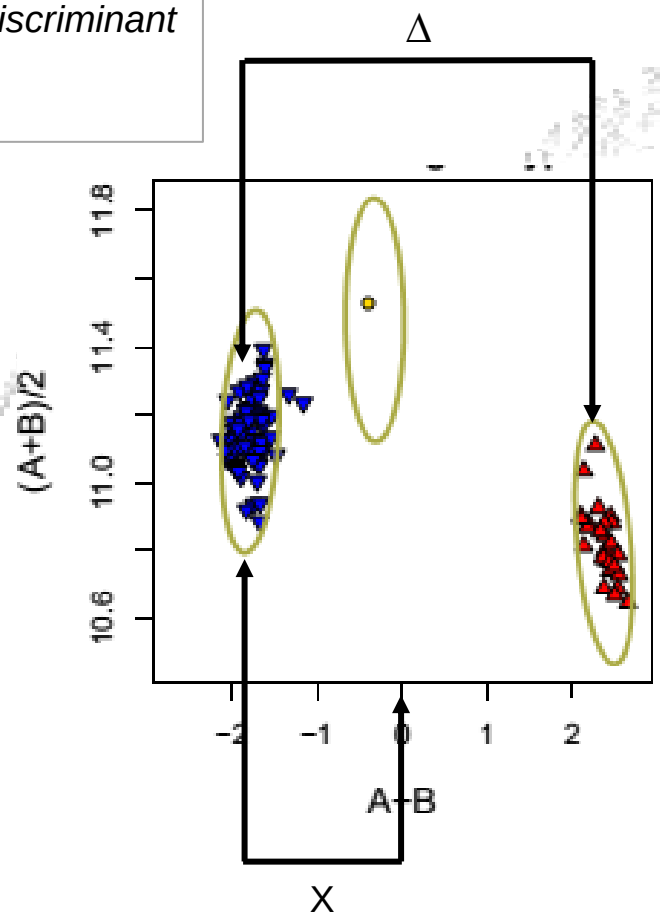
Homozygote Fisher's Linear Discriminant

HomFLD = $f(\Delta/SD)$



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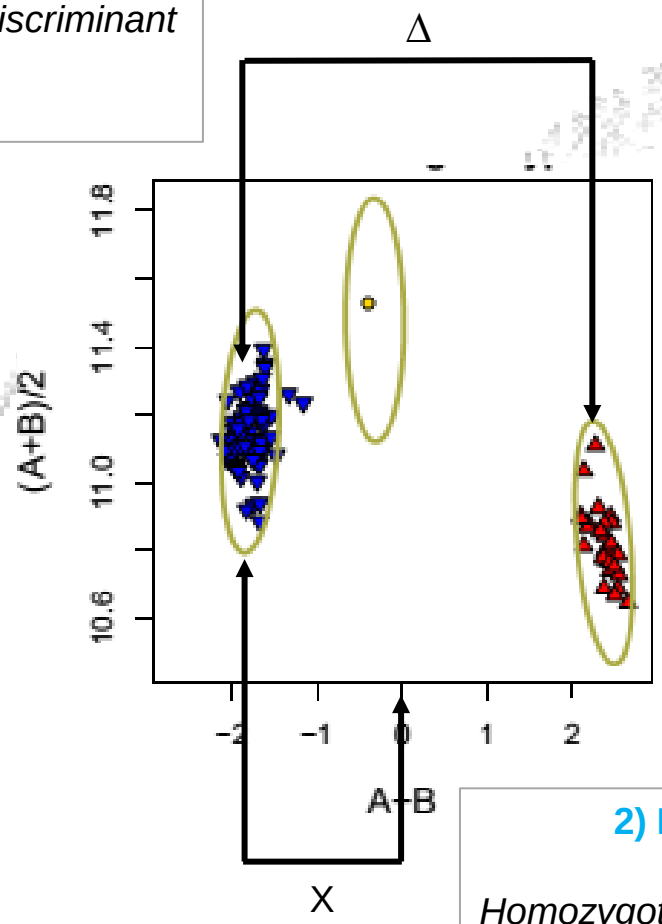
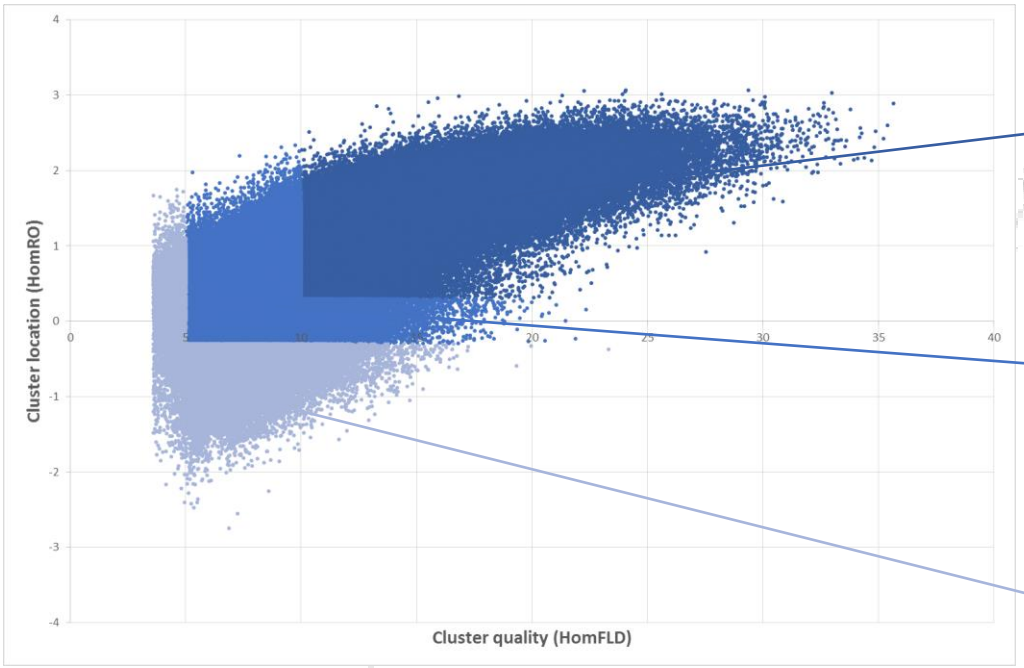


2) Position des clusters

Homozygote Ratio Offset

HomRO = $f(X)$

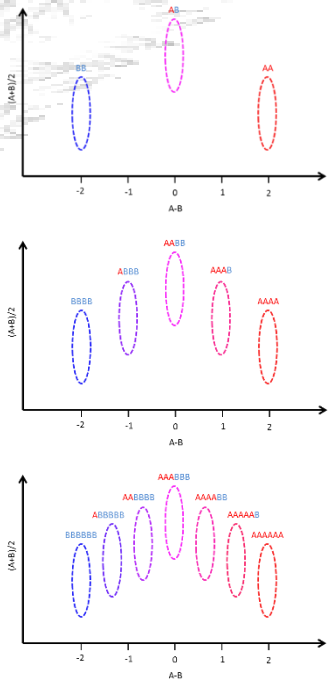
Critères de qualité des SNP



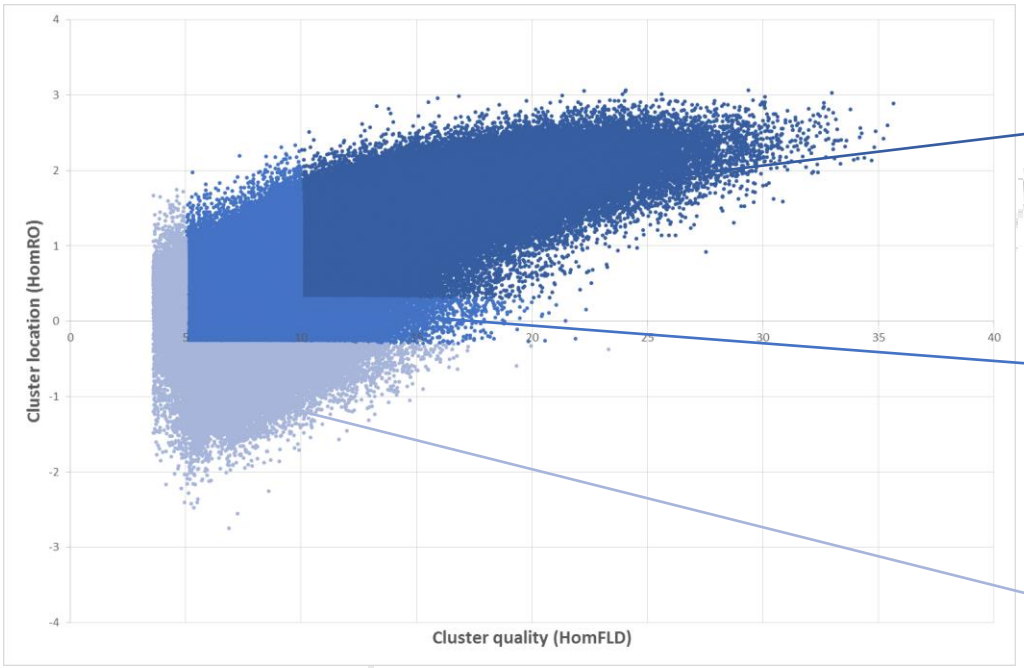
Diploïde

Tetraploïde

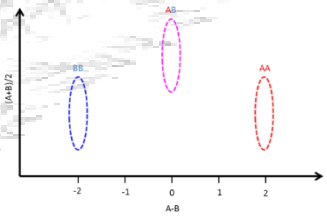
Hexaploïde



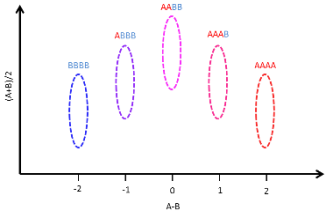
Critères de qualité des SNP



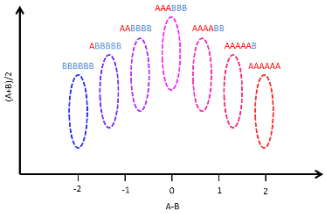
Diploïde



Tetraploïde



Hexaploïde



➔ 49.6% des SNP convertis sont dans un contexte diploïde

Validation de la puce SNP TaBW420K

96 lignées de blé :

- 13 variétés élites européennes
- 83 variétés représentant la diversité mondiale

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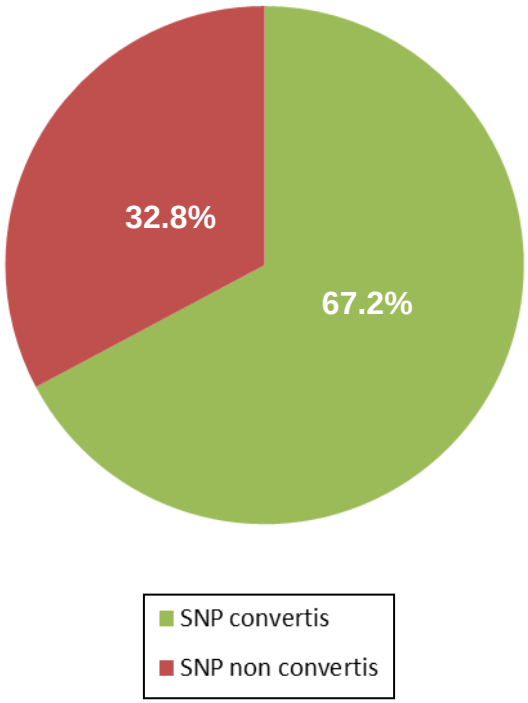

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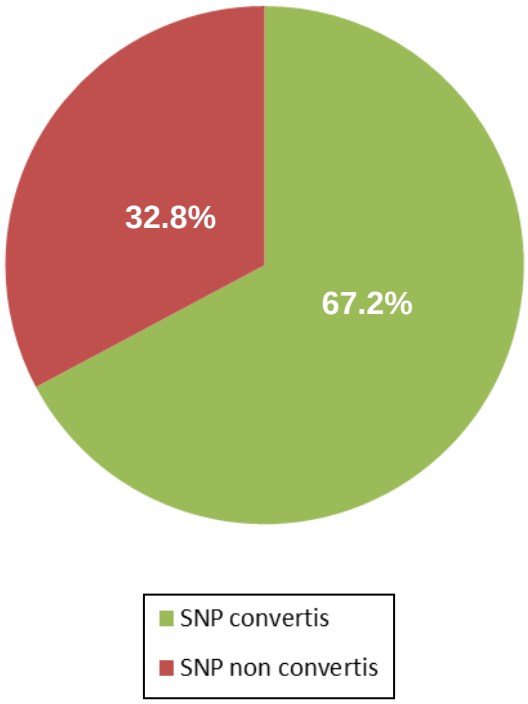
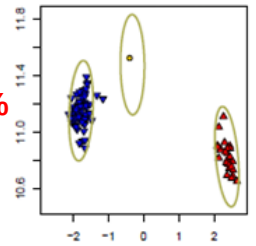


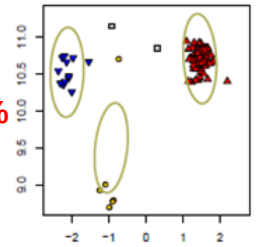
PolyHighResolution

58.3%



OTV

8.9%



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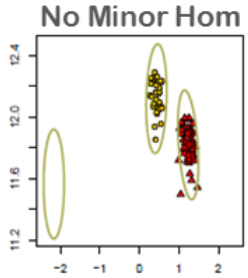
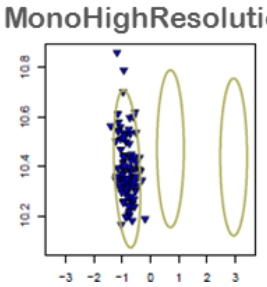
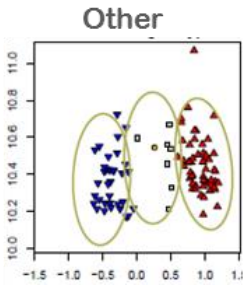


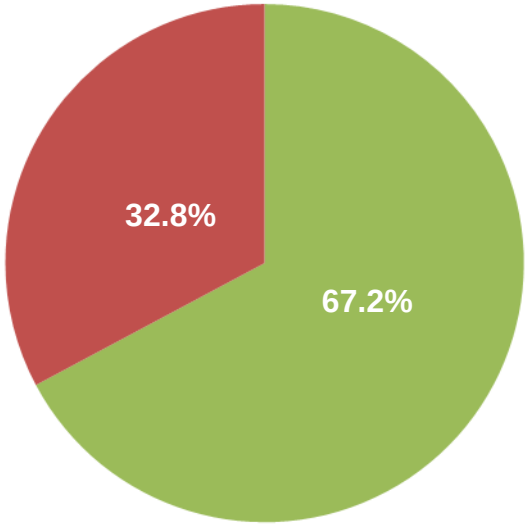
3.6%



19.1%



10%



PolyHighResolution

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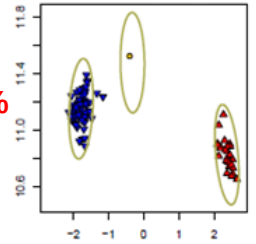

OTV

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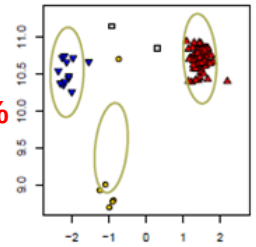
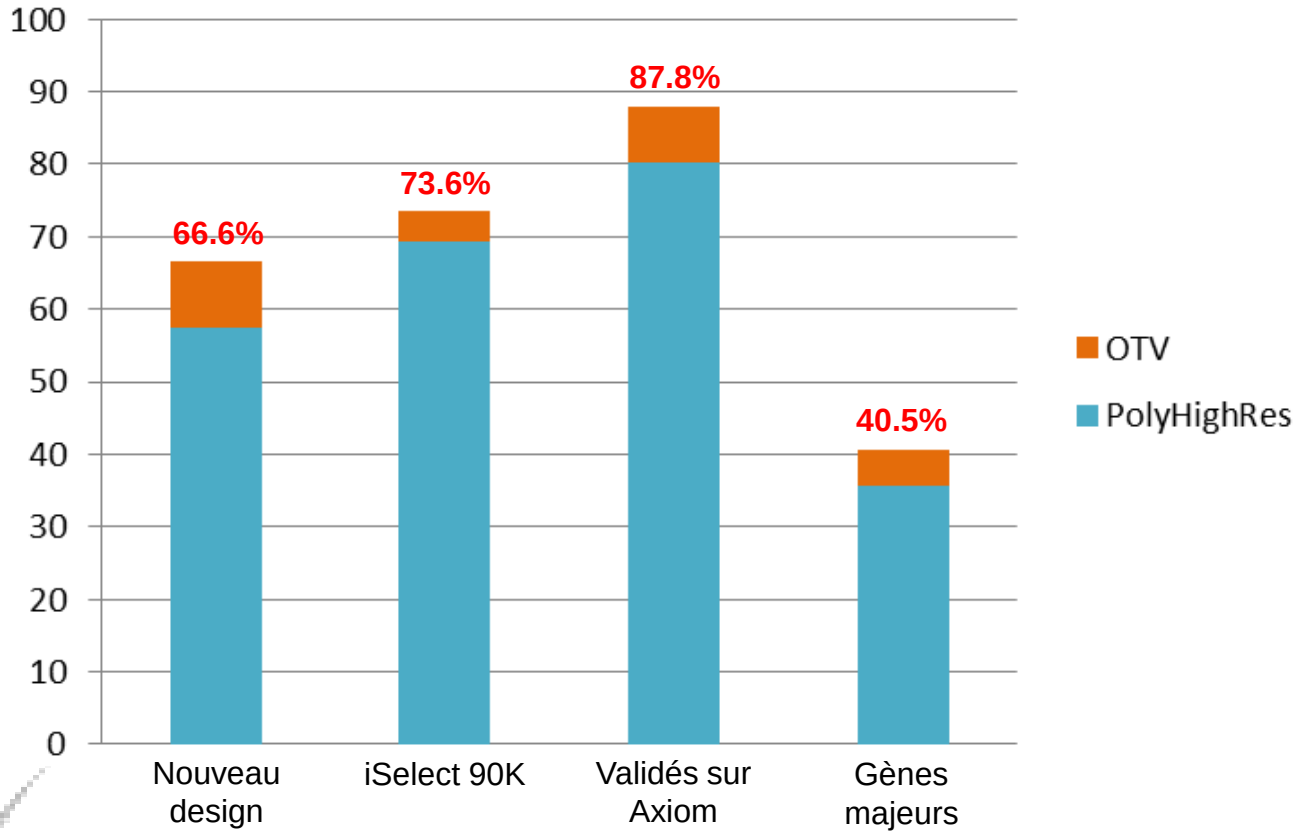


Conversion des SNP en fonction de leur origine



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10,732 SNP
1,152 variétés

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Curation manuelle

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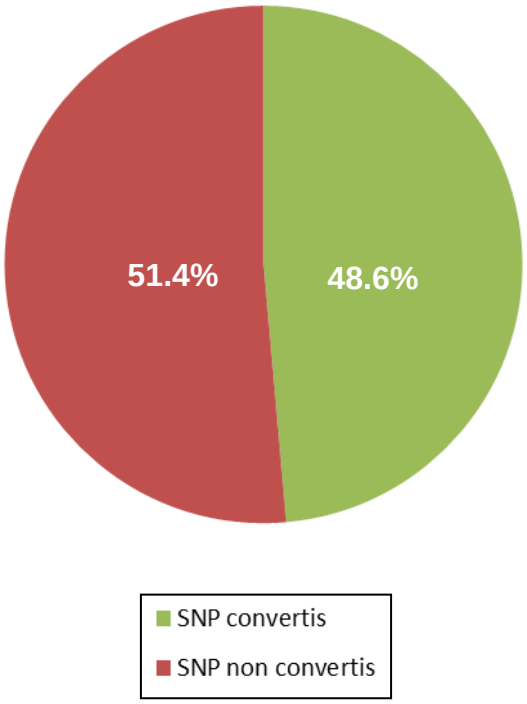

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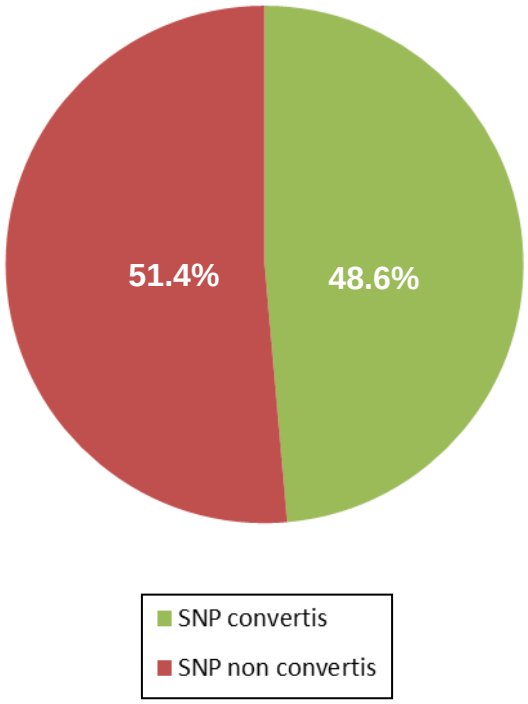
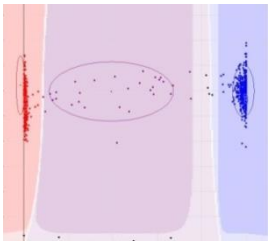


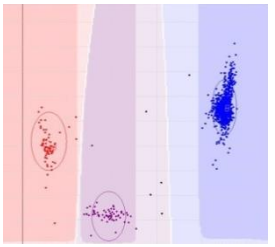
PolyHighResolution

47.1%



OTV

1.5%



Validation de la puce SNP Illumina iSelect 12K

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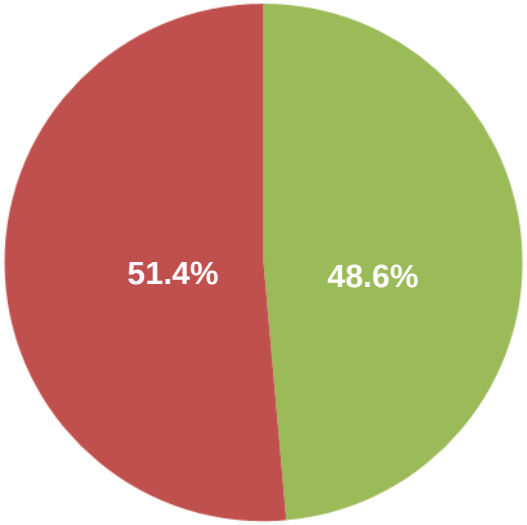
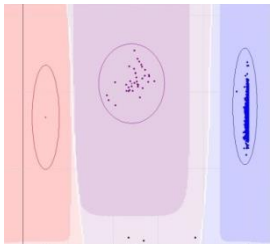
Curation manuelle

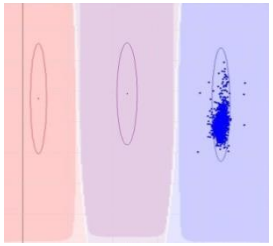


No Minor Hom



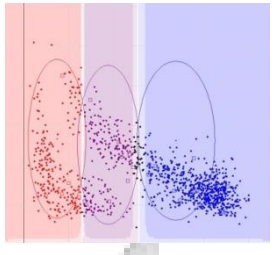
16.8%

MonoHighResolution



25.4%

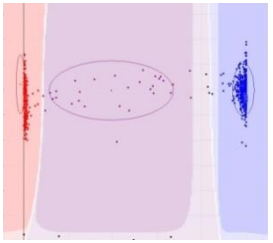
Other



9.2%

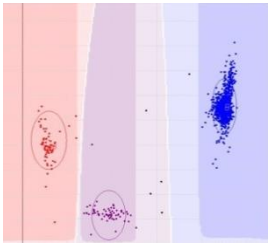
PolyHighResolution

47.1%

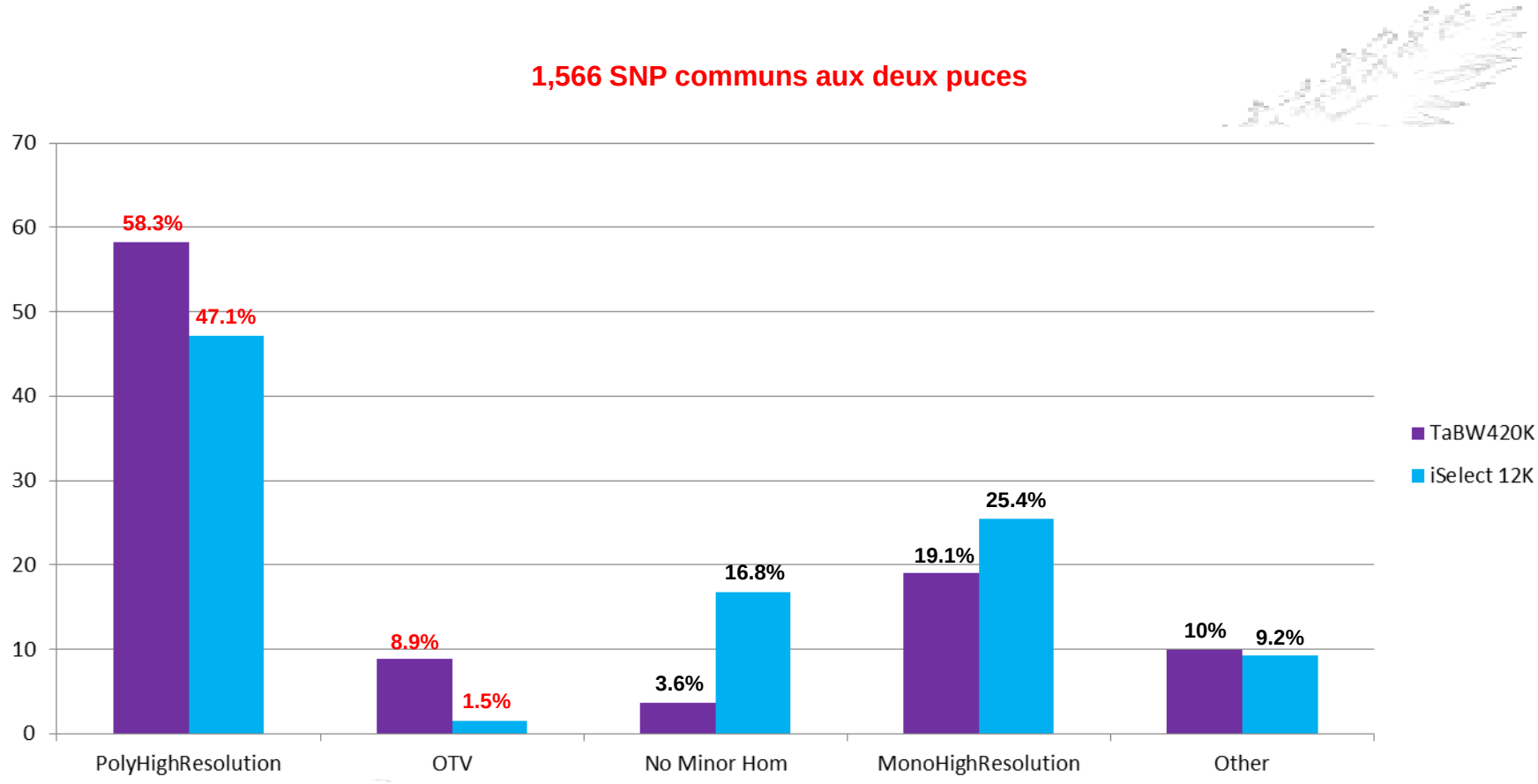


OTV

1.5%



Comparaison TaBW420K / iSelect 12K



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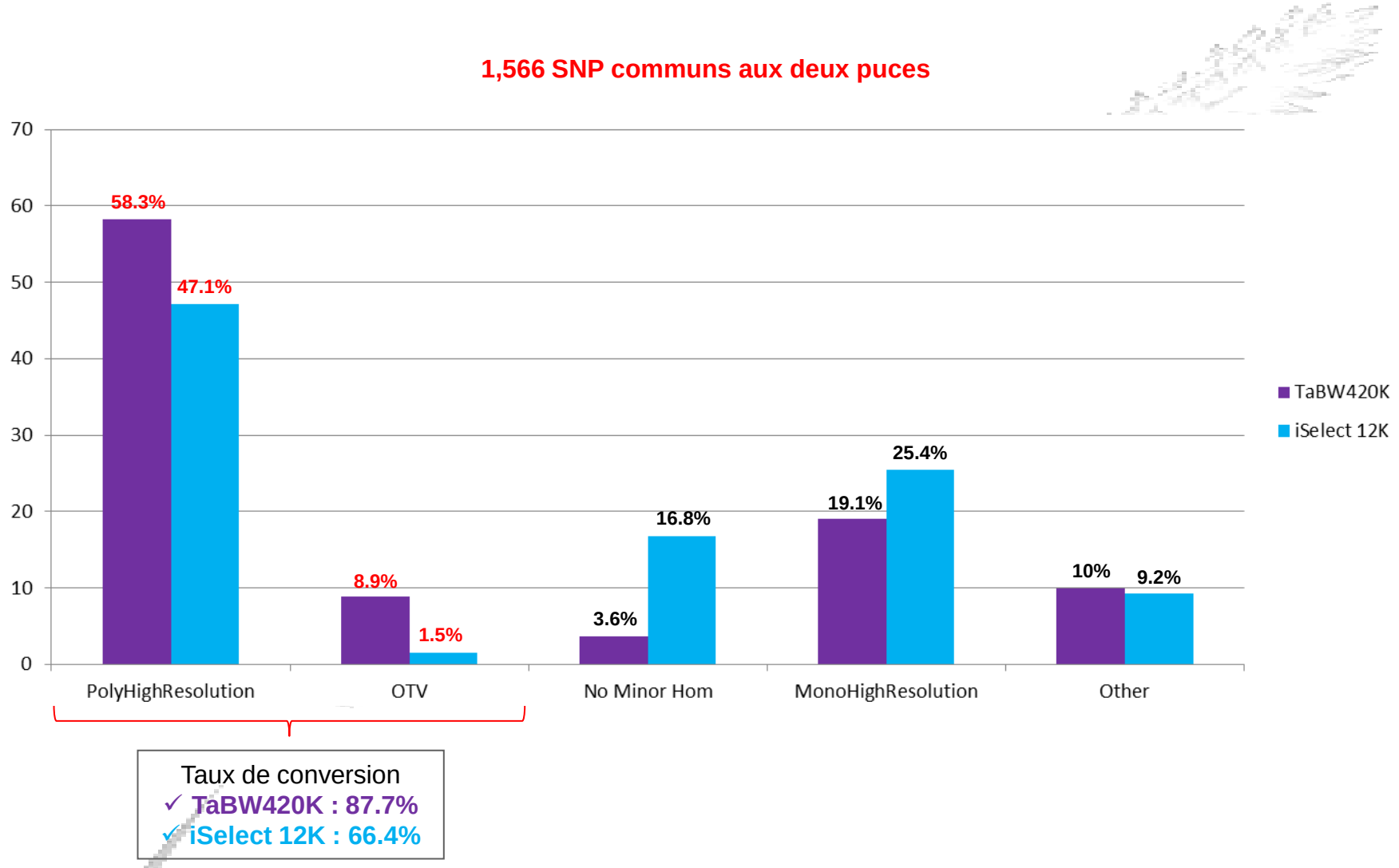
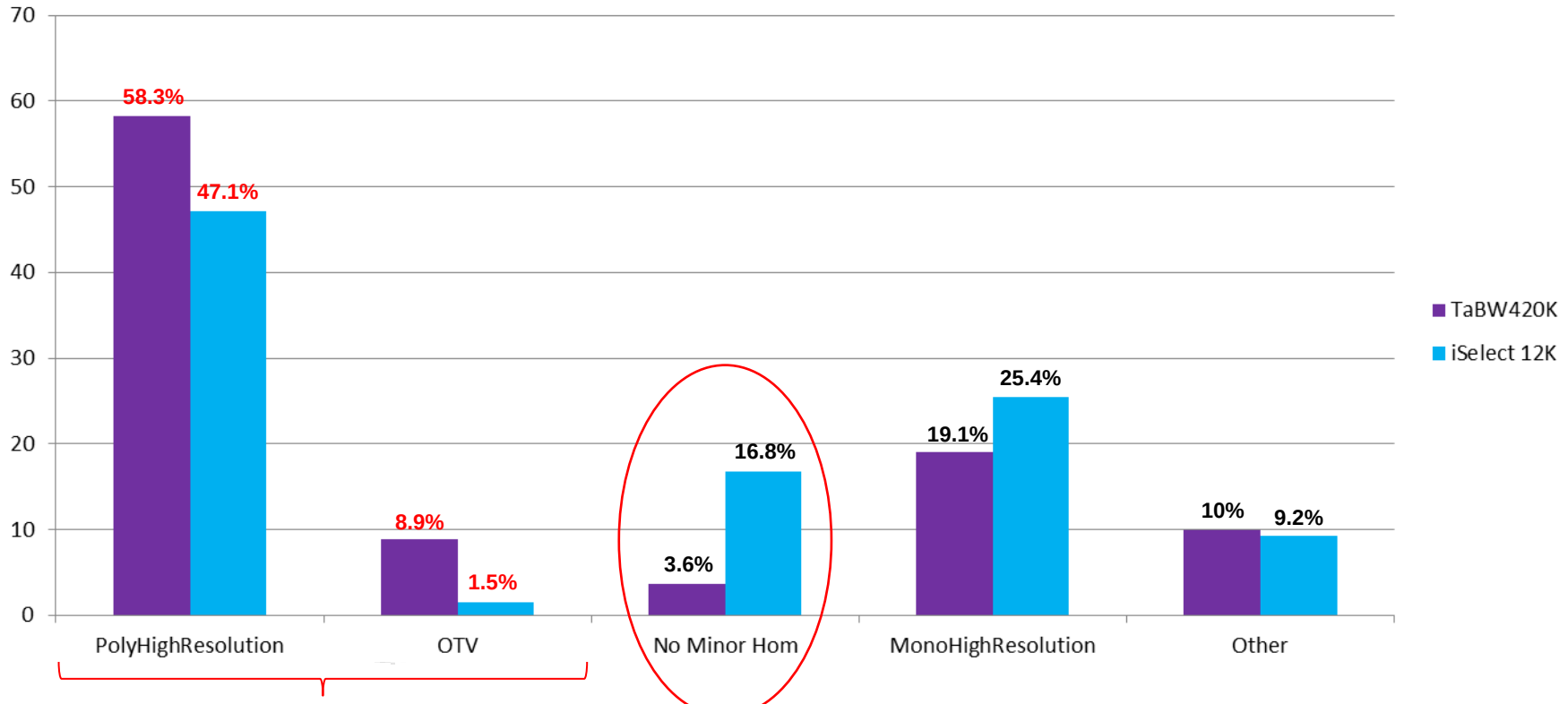


Taux de conversion

- ✓ **TaBW420K : 87.7%**
- ✓ **iSelect 12K : 66.4%**

Comparaison TaBW420K / iSelect 12K

1,566 SNP communs aux deux puces



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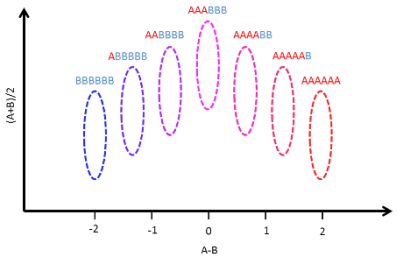

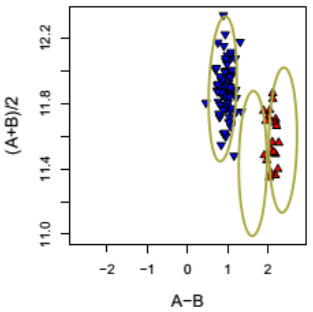

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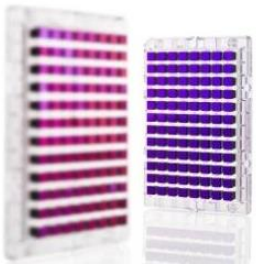
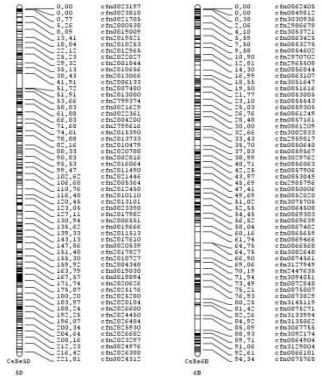
Les panels de génotypage BreedWheat



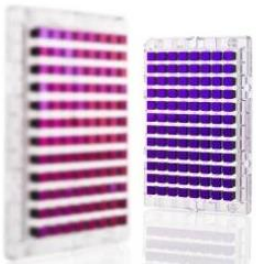
Les panels de génotypage BreedWheat

Cartographie génétique

435 lignées CS x Renan
92 lignées ITMI



~ 300,000 marqueurs



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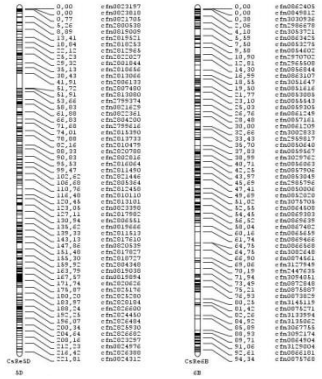

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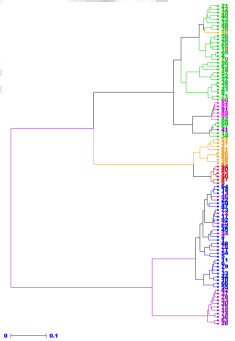
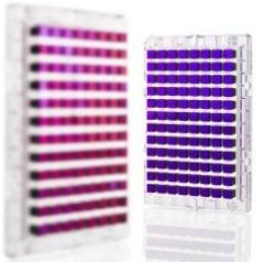
Ressources génétiques

4,506 accessions





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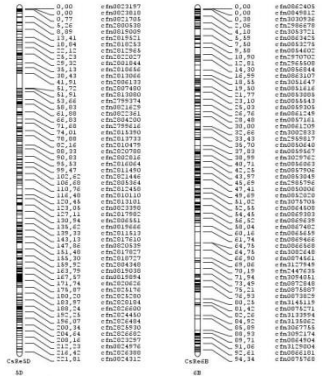

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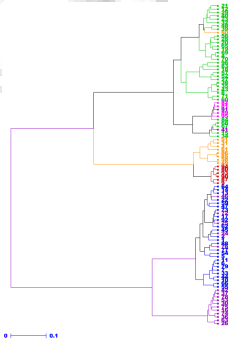
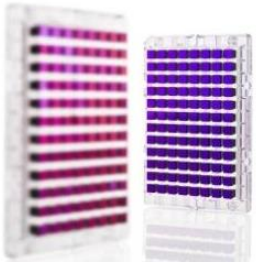
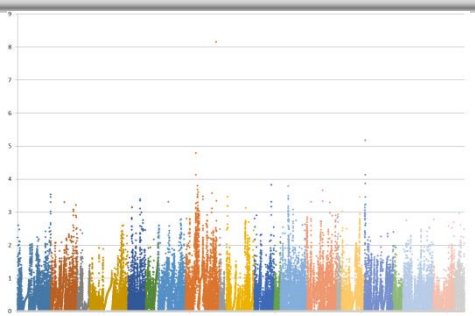




Génétique d'association

515 lignées élites
347 accessions de la Core Collection



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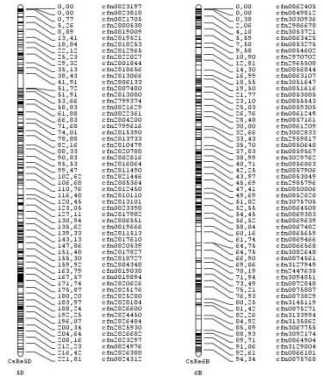

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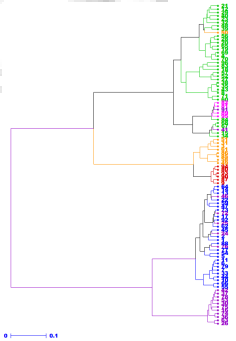
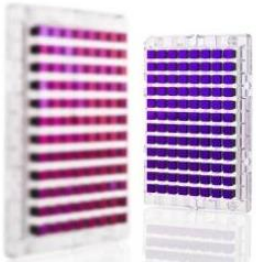
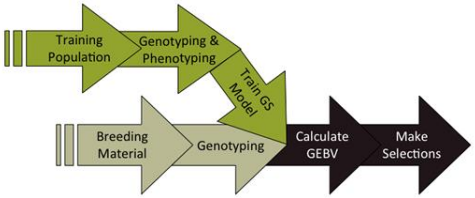




Séléction génomique

2,003 lignées GS
925 lignées MAGIC



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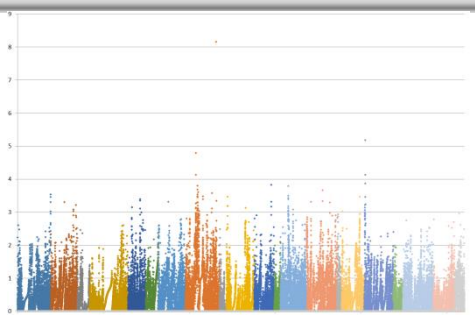

Les panels de génotypage BreedWheat

Cartographie génétique

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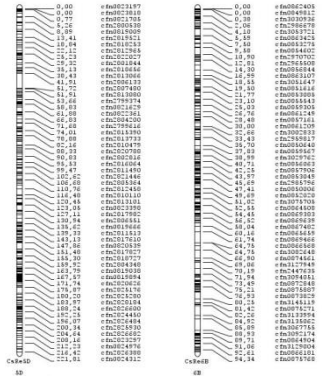
92 lignées ITMI



~ 300,000 marqueurs

Ressources génétiques

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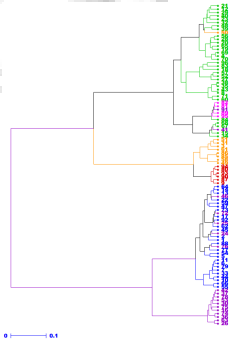

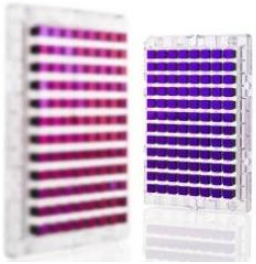

~7,800 lignées

Séléction génomique

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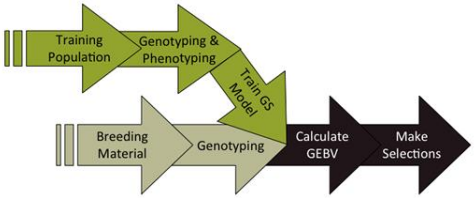
925 lignées MAGIC



Génétique d'association

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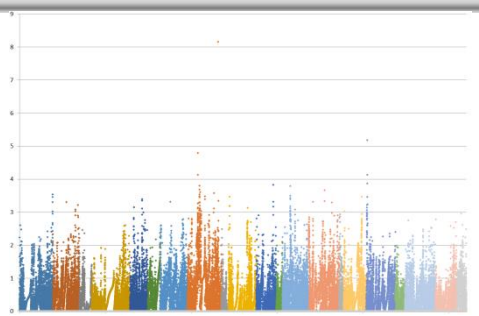

Caractérisation des ressources génétiques

Puce
TaBW420K

X

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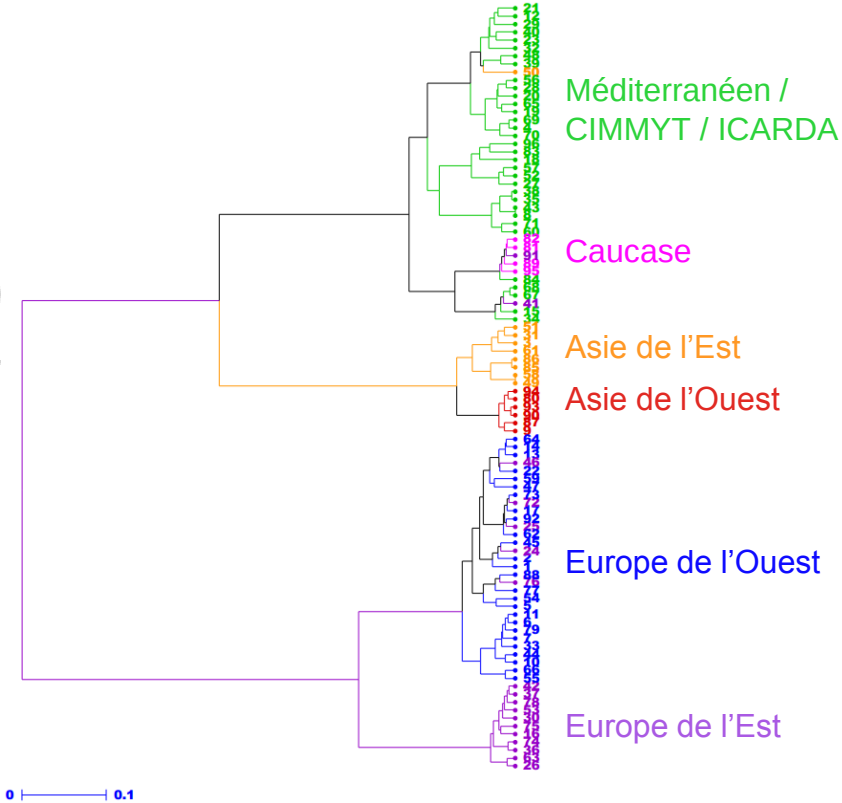
191,900 SNP convertis



Etude d’association pour la germination sur pied

Puce
TaBW420K

X

347 accessions
représentant la
diversité mondiale

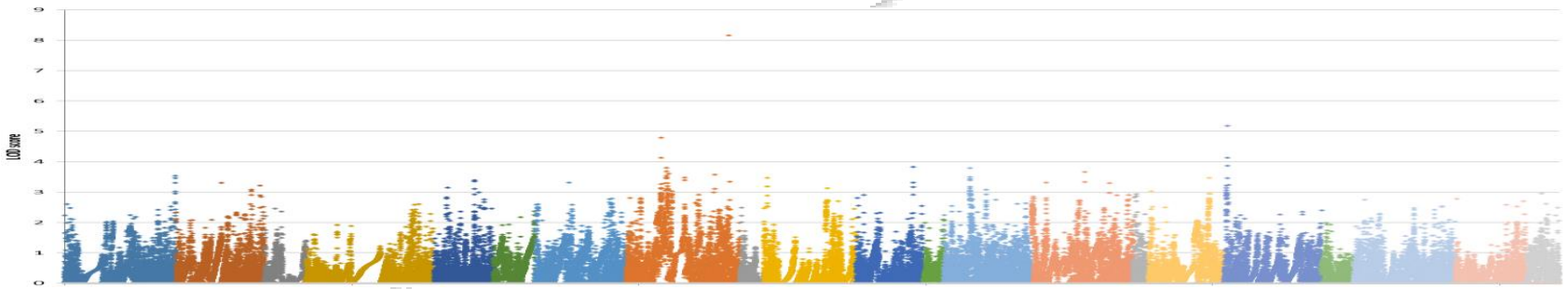
Etude d’association pour la germination sur pied

Puce
TaBW420K

X

347 accessions
représentant la
diversité mondiale

52,074 SNP



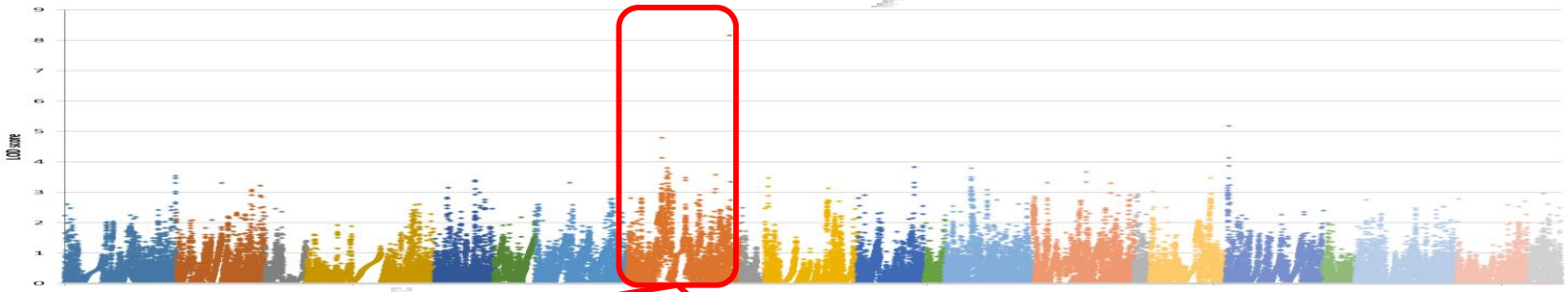
Etude d'association pour la germination sur pied

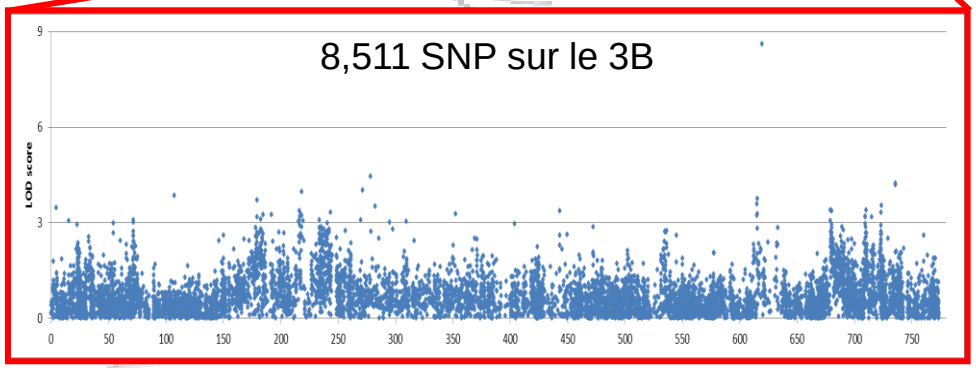
Puce
TaBW420K

X

347 accessions
représentant la
diversité mondiale

52,074 SNP





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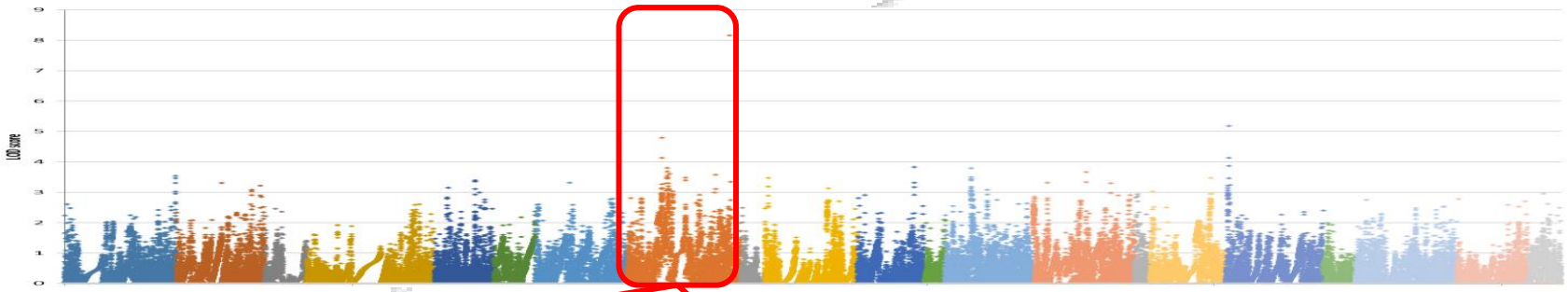
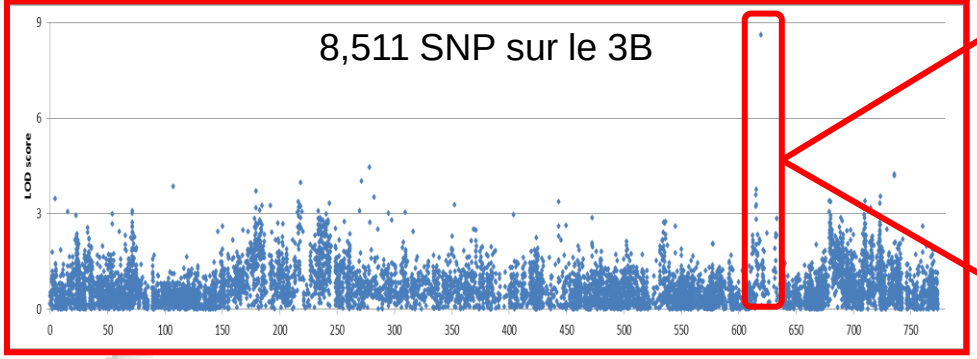
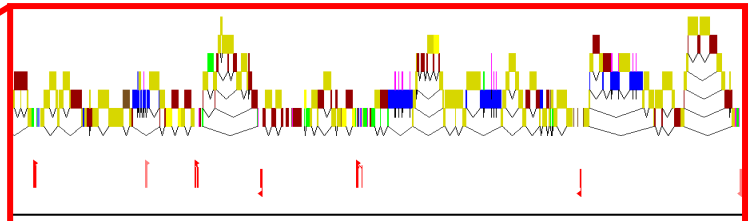


8,511 SNP sur le 3B





Région de 1 Mb
Sept gènes
Cluster de cinq gènes candidats

Conclusion

- ✓ La puce Illumina donne de bons résultats …
- ✓ … mais nécessite une curation manuelle des clusters

- ✓ Environ 2/3 des SNP sont convertis sur la puce Axiom
- ✓ 50% de ces SNP convertis sont dans un contexte diploïde

- ✓ Les résultats obtenus grâce à la puce Axiom permettent des analyses puissantes (cartographie, association, diversité, …)

Remerciements