High resolution copy number variation analysis using two cattle genome assemblies

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100years
1918 — 2018

Acknowledgement

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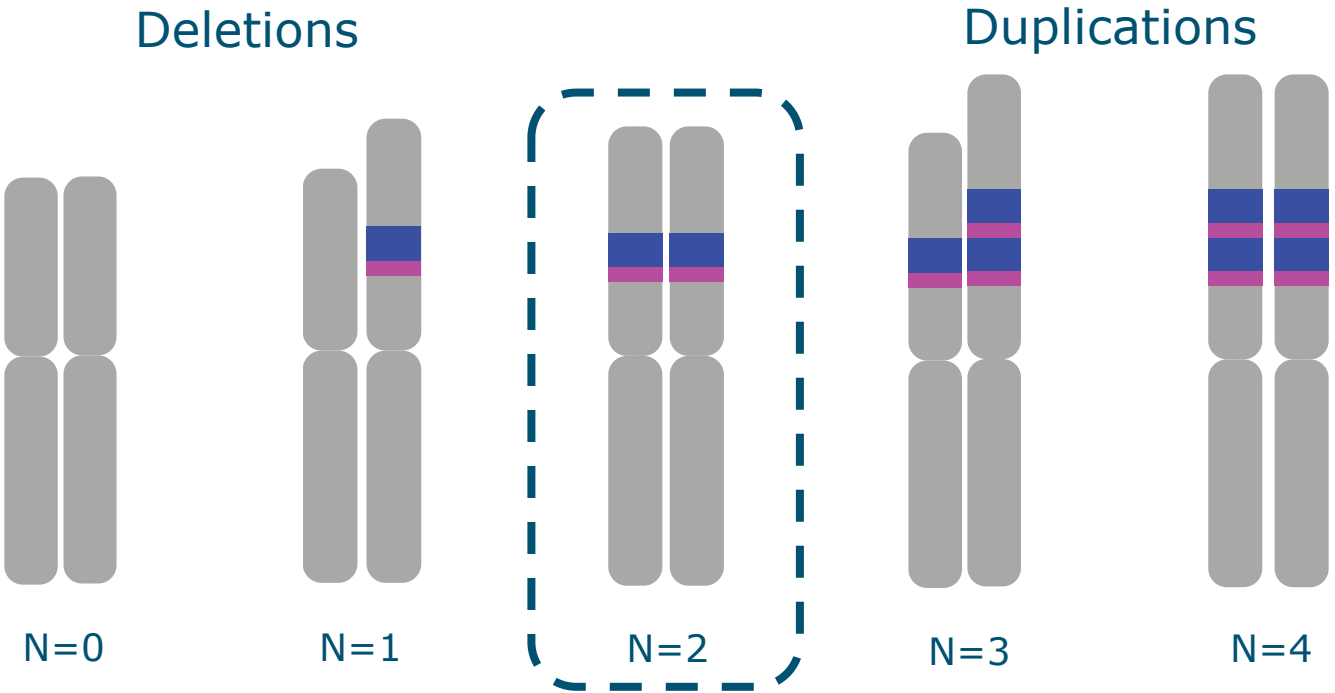
Copy number variations

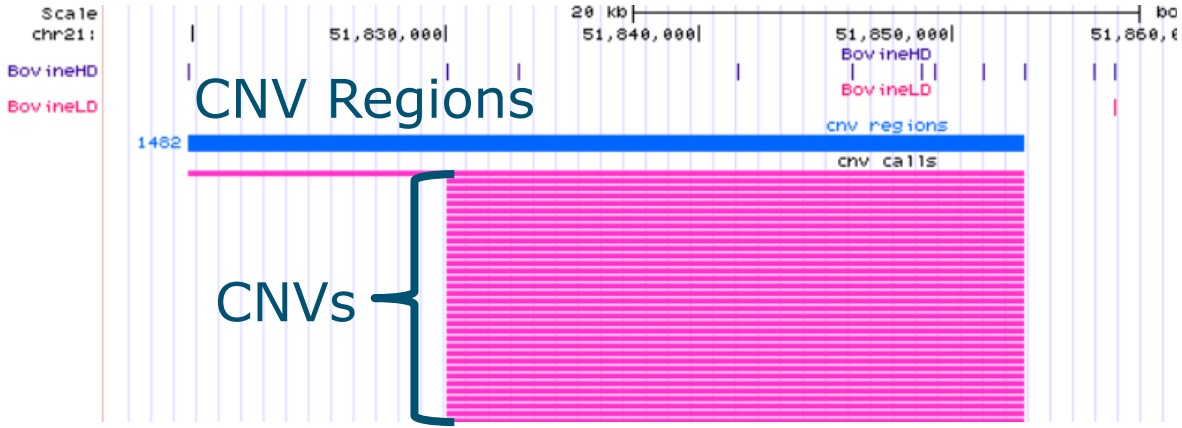


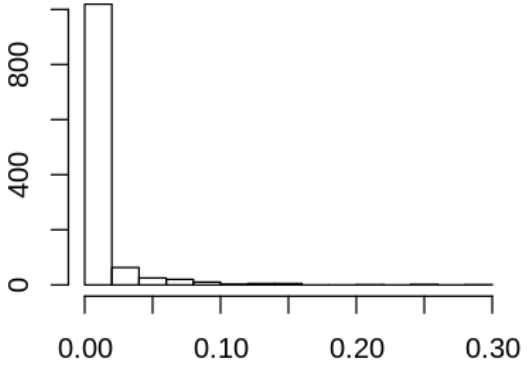
Materials & Methods

- Data
  - Illumina BovineHD data (770K, n=315)
  - WGS data (~10X, n=50)
- Methods
  - Genome assembly ARS-UCD1.2
  - PennCNV software, Smoove, and FreeBayes
  - Shapeit & PLINK software

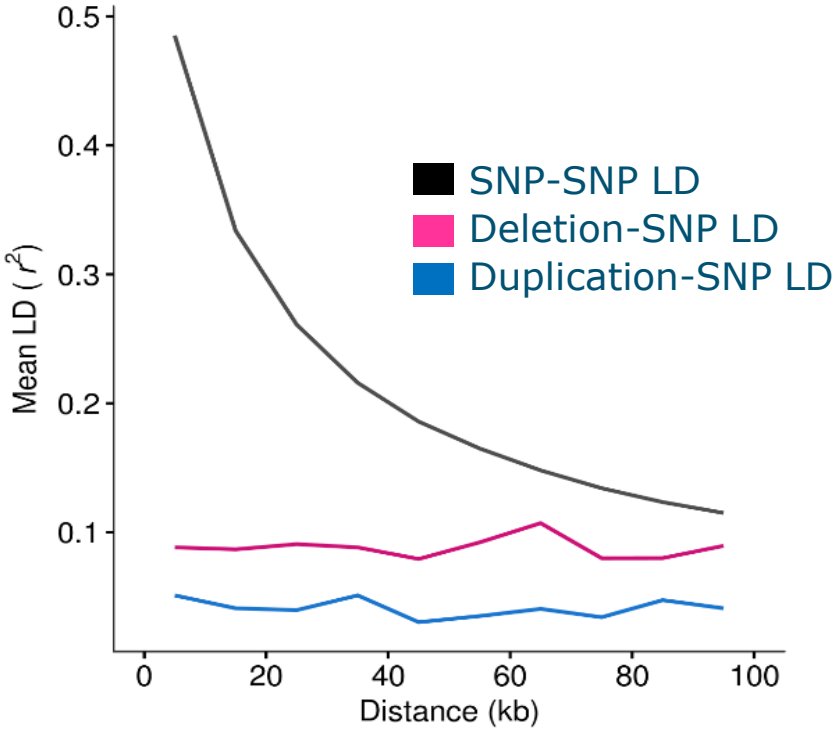
CNV discovery

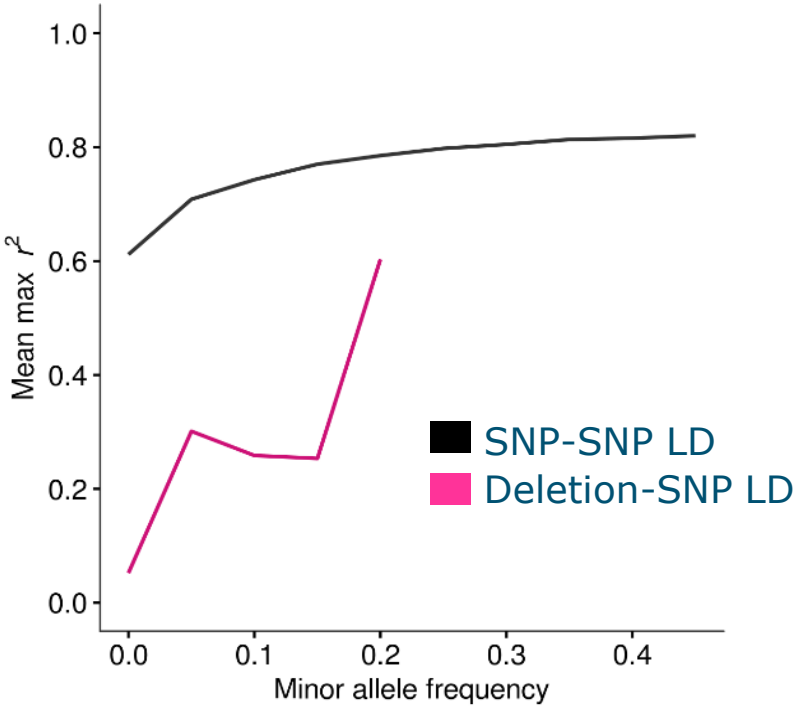
- 8,881 CNVs
- 1,154 CNV regions (CNVRs)





CNV Linkage Disequilibrium (LD)





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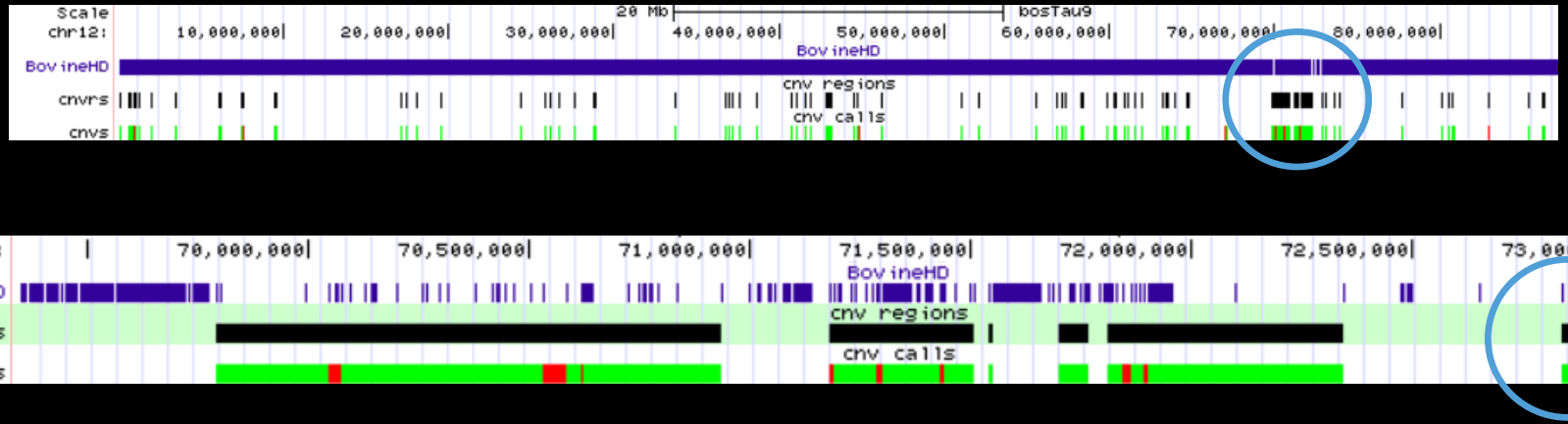
The dark side of CNV discovery in commercial arrays

Two folds bias in commercial SNP arrays

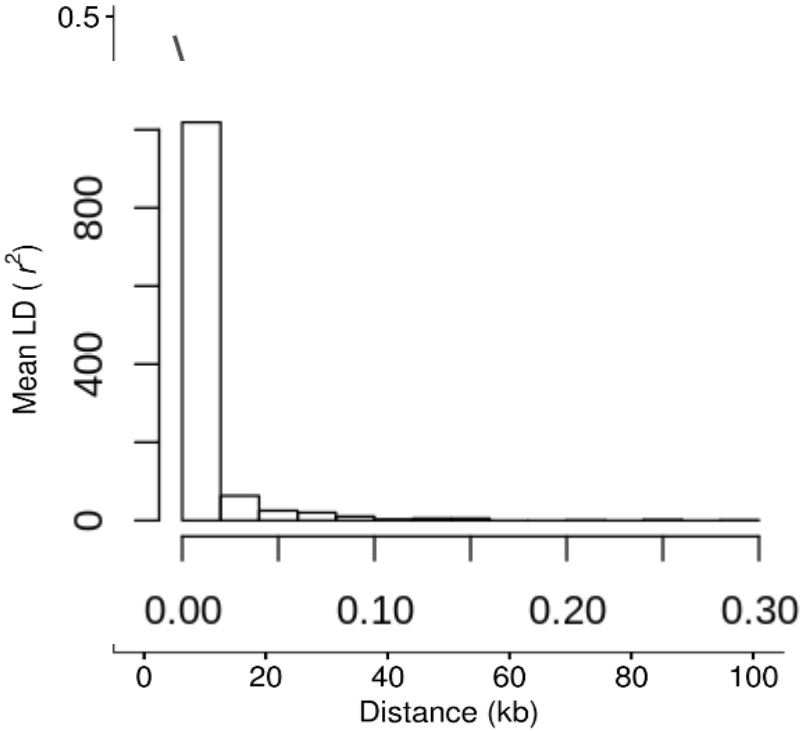
1. SNP density determines size of the detectable CNVs

2. Ascertainment bias determines CNV “detectable” regions



Follow-up on CNV LD

- Why low CNV LD ?
  - Deletions vs. Duplications
  - Low CNV MAF
  - Low local SNP density (ascertainment bias)



Low density (50K)

High density (770K)

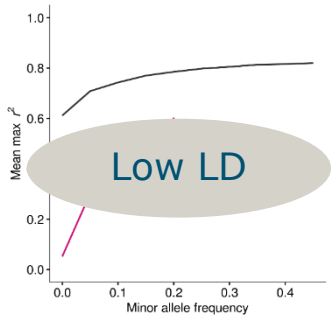
770K+ additional SNPs

Local SNP density

Rare

Minor Allele Frequency

Common



Low LD

High LD

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CNV LD using WGS data

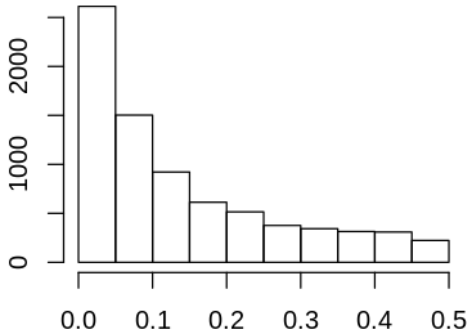
WGS data (n=50)

Calling deletions

7,483 deletions
Uniform MAF

Calling SNPs (15M)

- Bovine 50K
- Bovine 770K
- Bovine 770K+2M



Low density (50K)

High density (770K)

770K+ **additional 2.1M**

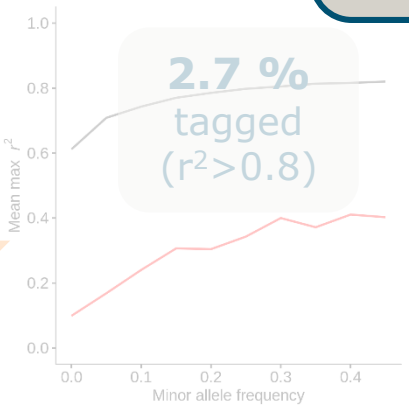
Local SNP density

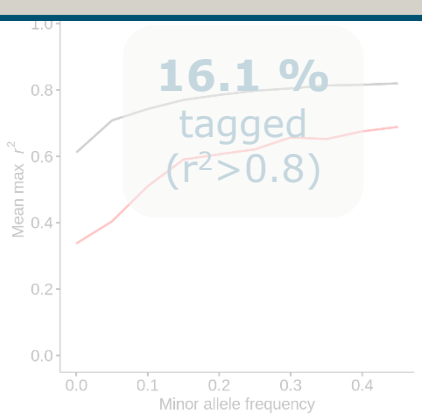
Minor Allele Freq

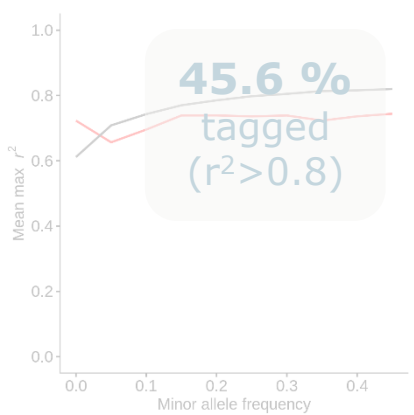
Rare

Common

~47K SNPs from WGS variants tag deletions







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Future plan & Take home messages

Validating **~47K deletion tagging SNPs** in genomic prediction

1. Commercial SNP arrays do not effectively tag CNVs
2. Deletions can be tagged using dense SNP set