Accuracy of genomic prediction using whole-genome sequence data in white egg layer chickens

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Acknowledgements

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Introduction

Why sequence data?

- **Causative mutation** are assumed to be in data
- Expectation: **Higher accuracy** of genomic prediction
- Understand **biology**

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Why imputation?

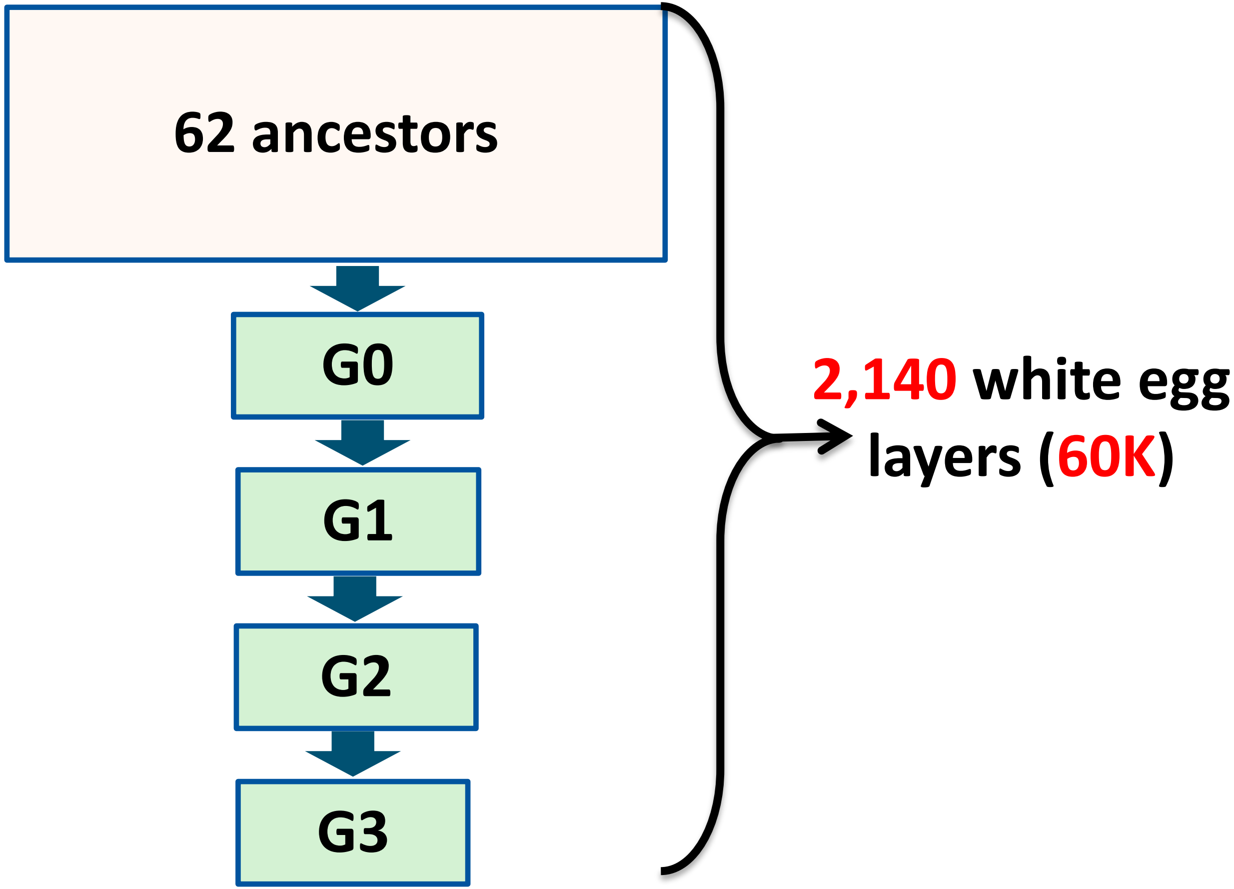
- Sequencing is still expensive!
- To get a large population of sequenced animals:
  - Sequence **key ancestors**
  - **Imputation** of genotyped animals

Objectives

- Can **accuracy** of genomic prediction be **improved** by:
  - Sequencing **key ancestors** of population and imputation of genotyped animals?
  - **Pre-selecting SNPs** that are more likely to affect the phenotype?

Material and methods

Data



62 ancestors

G0

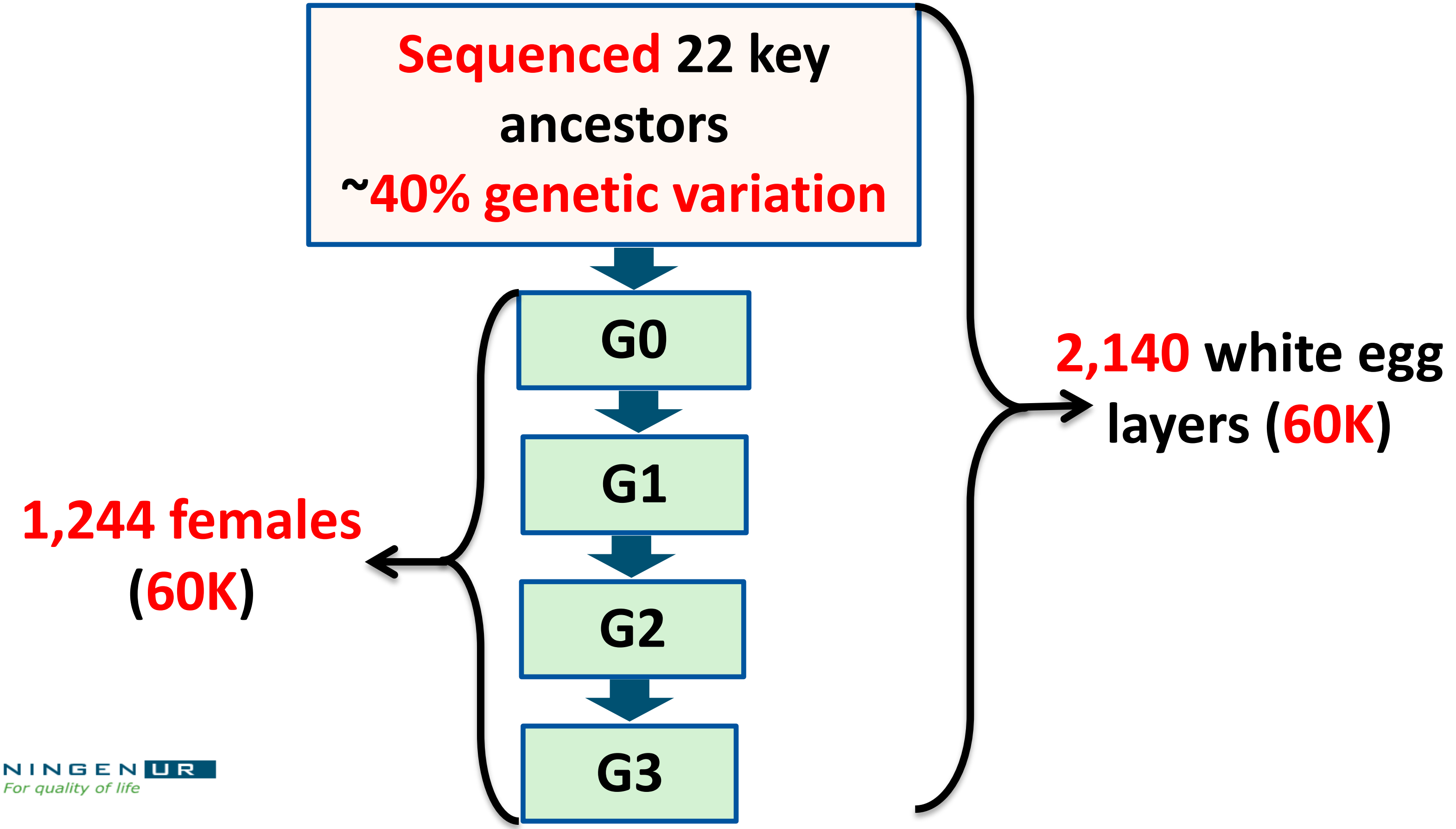
G1

G2

G3

2,140 white egg layers (60K)

Data



Sequenced 22 key ancestors

~40% genetic variation

G0

G1

G2

G3

1,244 females (60K)

2,140 white egg layers (60K)

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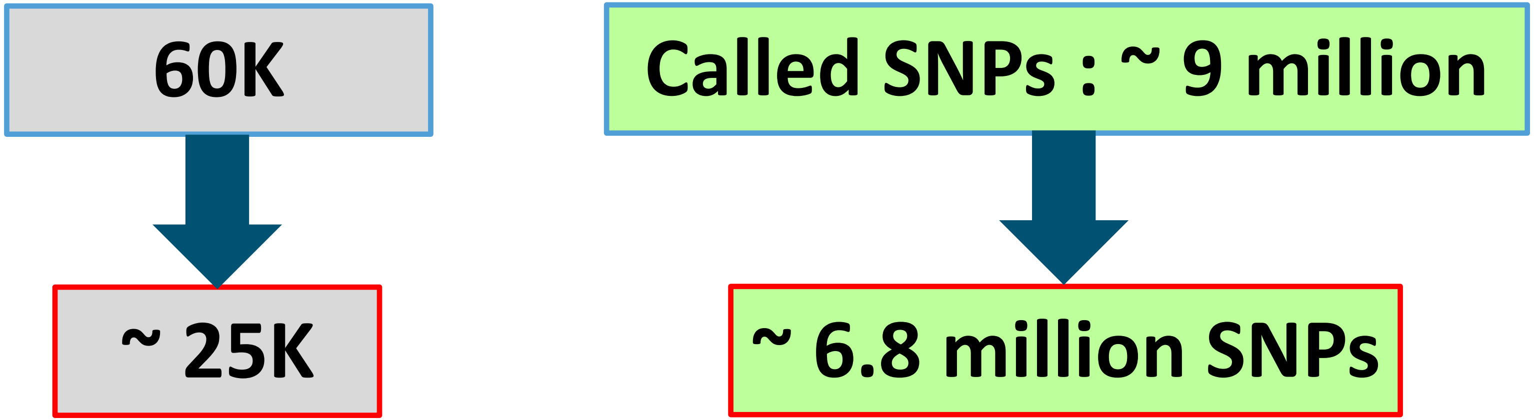
Quality control



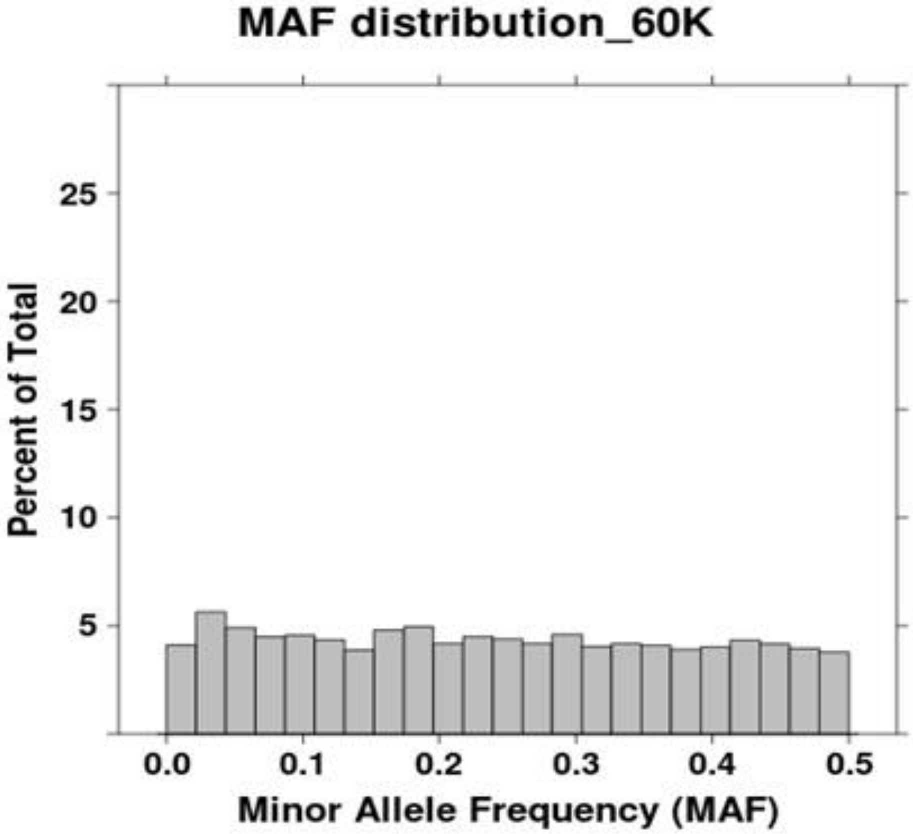
60K

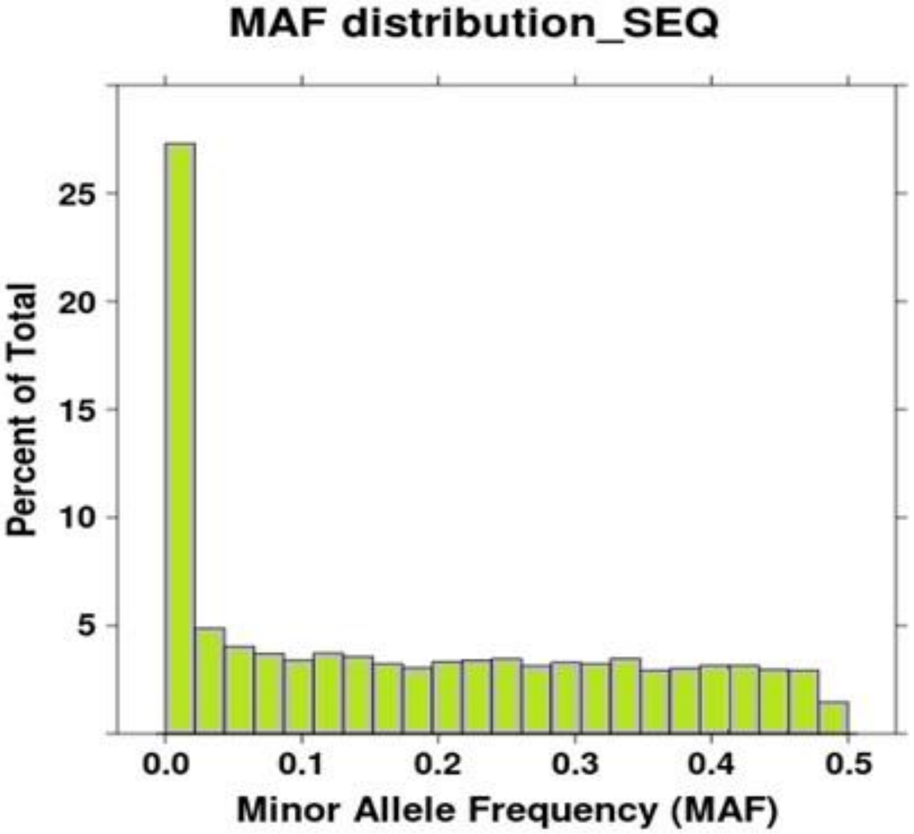
~ 25K

Called SNPs : ~ 9 million

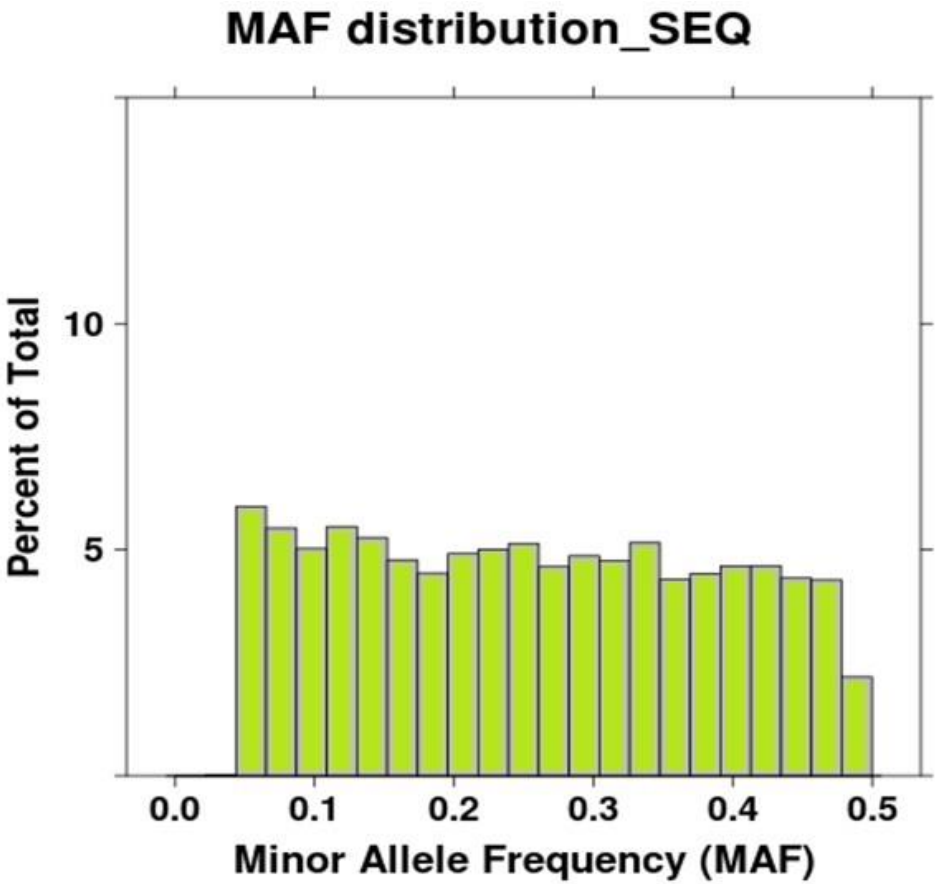
~ 6.8 million SNPs

MAF distribution



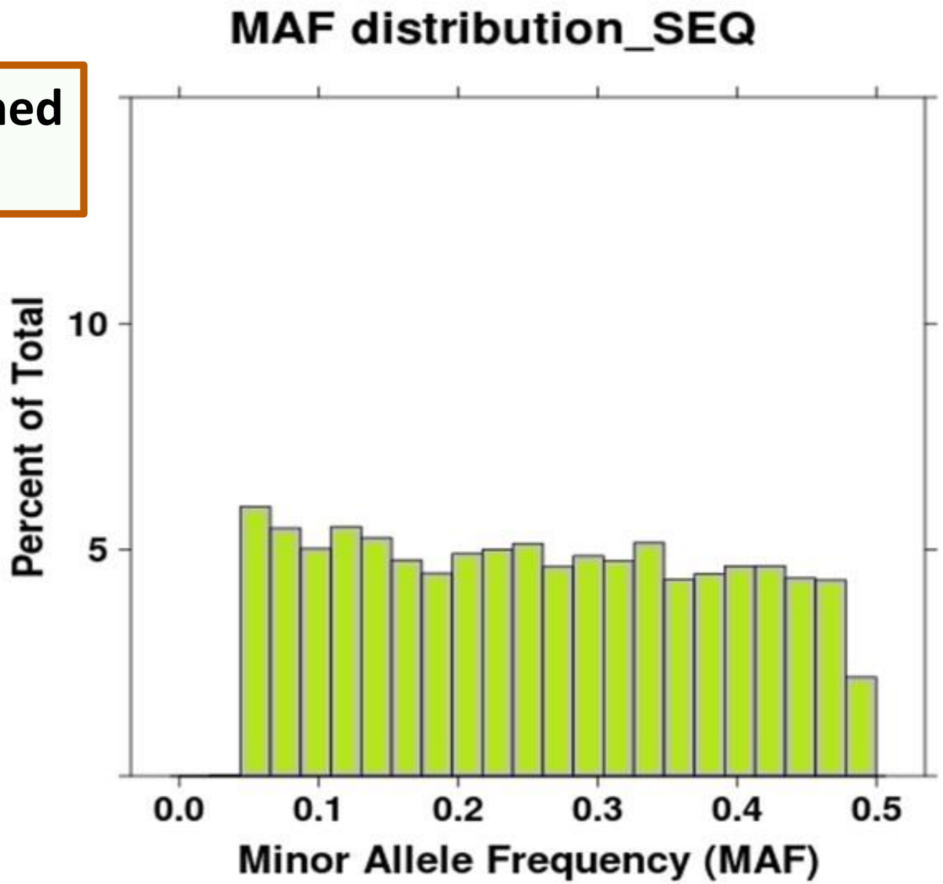


MAF Distribution after MAF filtration (< 0.025)



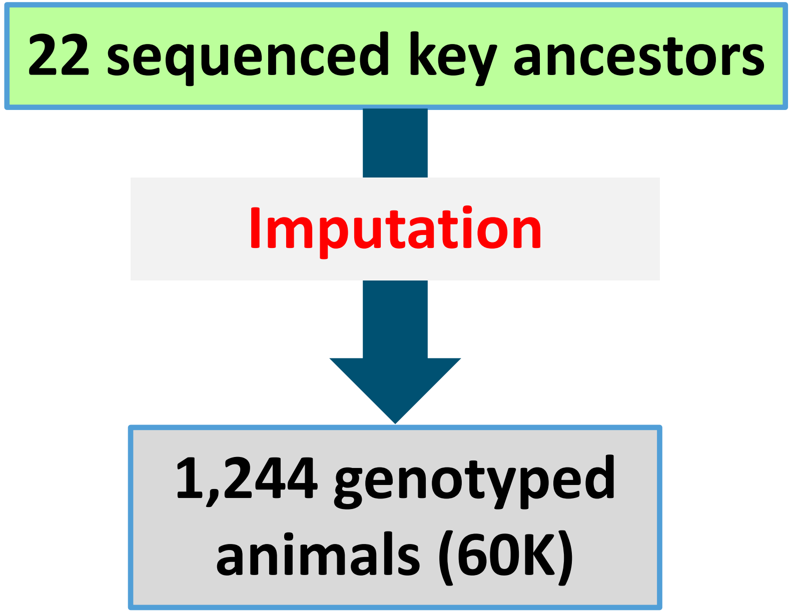
MAF Distribution after MAF filtration (< 0.025)

~ 4.6 million SNPs remained for further analyses



Imputation to whole-genome sequence

- **Beagle V4**



22 sequenced key ancestors

Imputation

1,244 genotyped animals (60K)

Genomic prediction

Trait: Number of eggs in the first production period

1,244 females

Reference: 1,004 animals

Hatched **Apr,2009-June,2011**

Validation: 240 animals

Hatched **Oct-Nov,2011**

$$Accuracy = \frac{r_{BV,Phen}}{\sqrt{h^2}}$$

Prediction models

- **BLUP** (pedigree-based model)
- **GBLUP**
  - **Assumption:** equal variances for all SNPs
- **BayesC**
  - Gibbs sampling
  - 60,000 iterations (10,000 burn-in)
  - **Assumption:**
    - 95% of SNPs with zero effect
    - 5% of SNPs with large effect

Genomic prediction using biological information

Annotation	N
Synonymous	41,010
Non-synonymous	15,516
Non-coding	4,539,701
Total	4,596,227

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Coding SNPs

- **Synonymous SNPs:** do not alter amino acid sequence of a protein
- **Non-synonymous SNPs:** alter amino acid sequence of a protein

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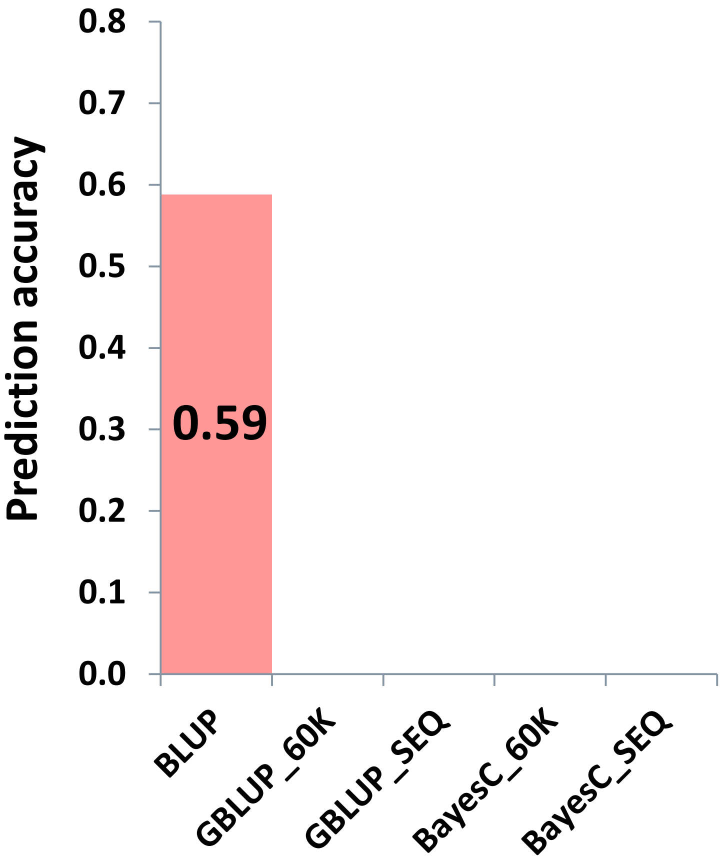
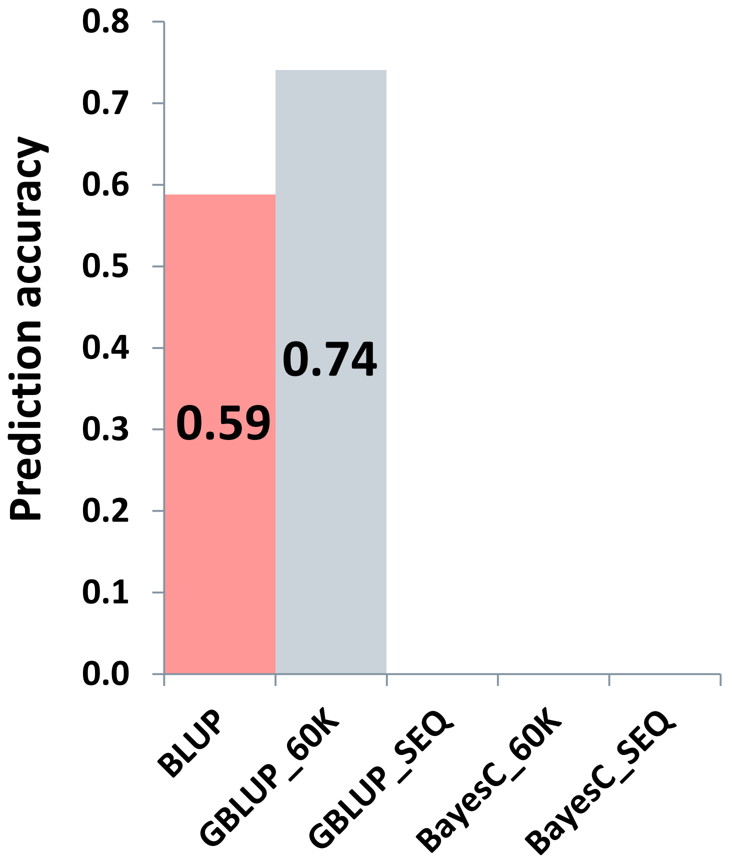
Results

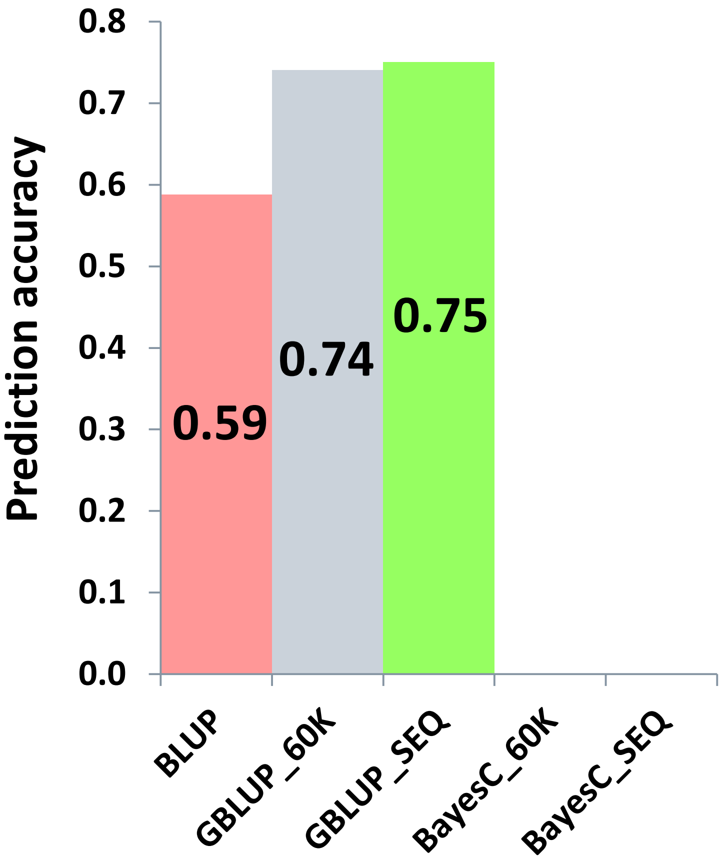
Prediction accuracies



Prediction accuracies



Prediction accuracies



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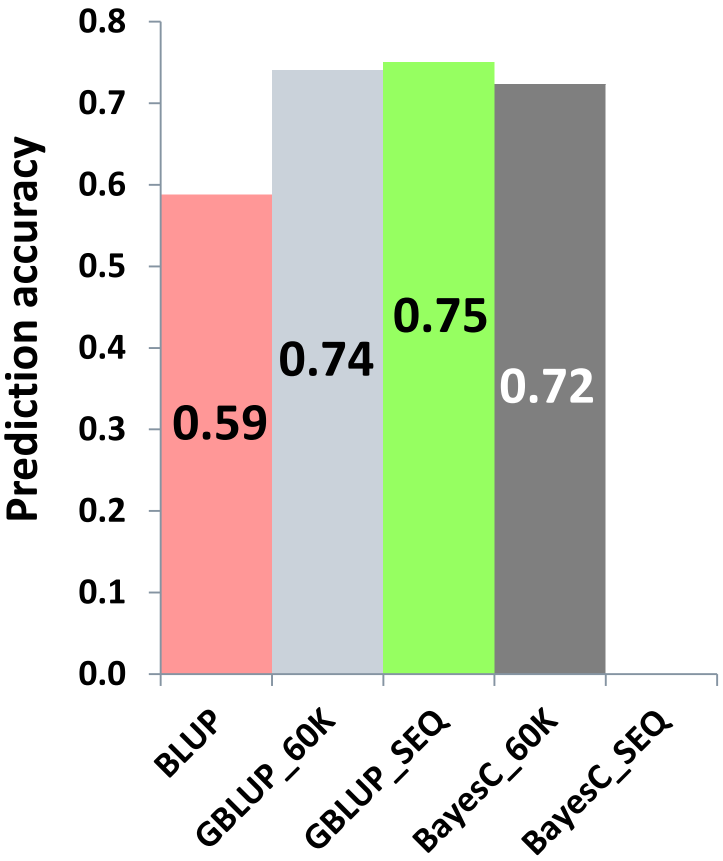
Prediction accuracies



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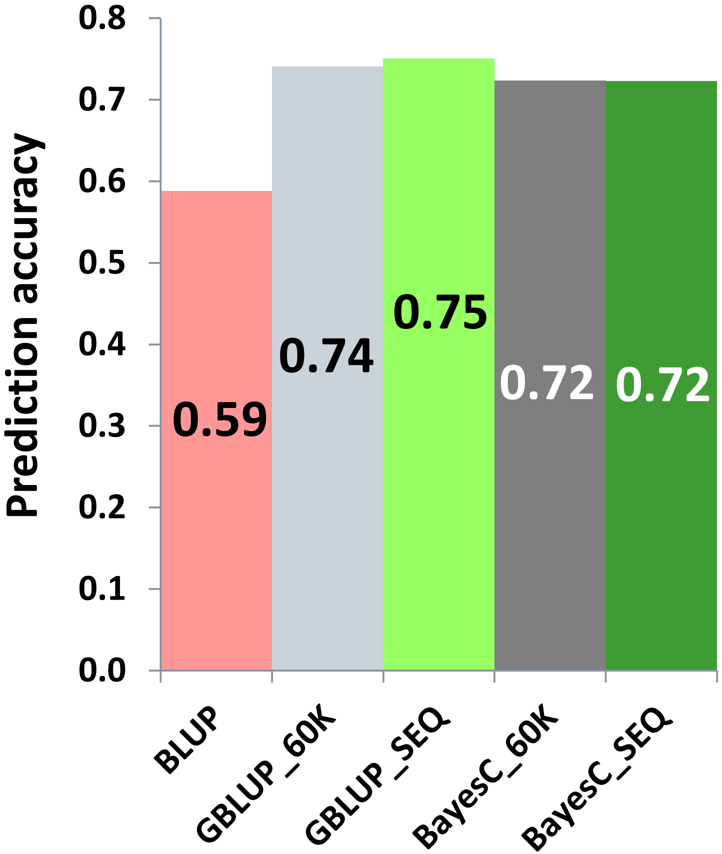
Prediction accuracies



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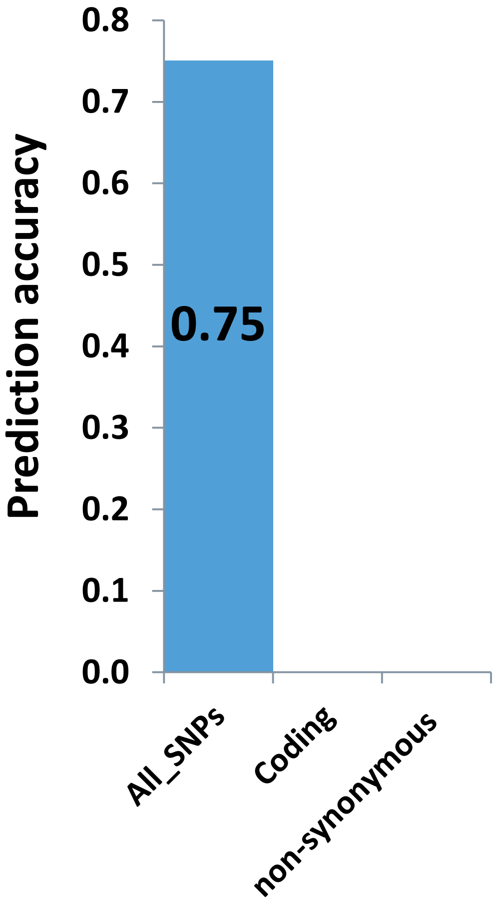
Genomic prediction using biological information



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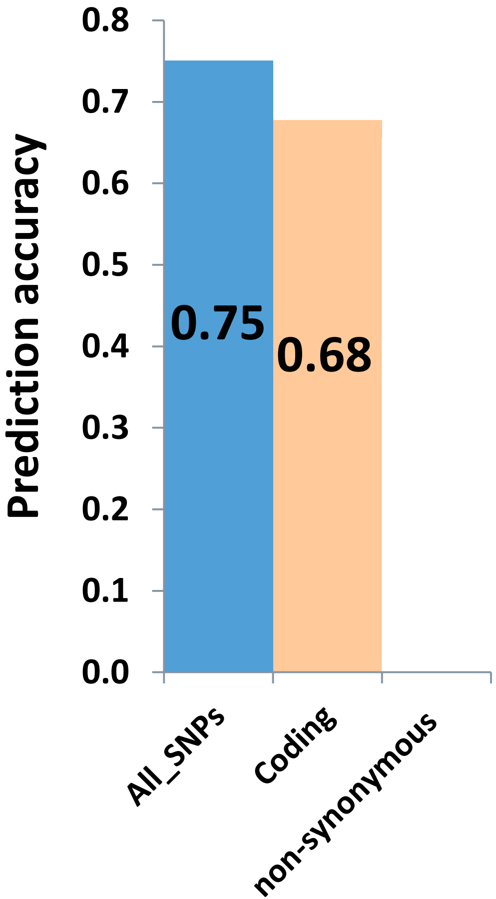

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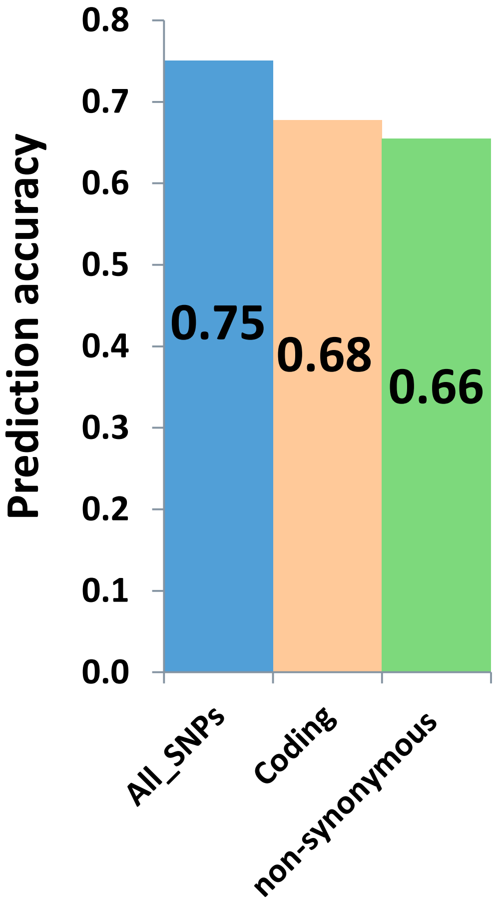
Genomic prediction using biological information



- Non-coding **regulatory regions** have an affect on phenotype (Koufariotis *et al*. 2014)
- **QTL** and **selection signals** were found in non-coding regions (Bird *et al.* 2006; Drake *et al*. 2005)

Conclusions

- **Whole-genome sequence** hardly improved genomic prediction accuracy compared with **60K**
- **GBLUP** and **BayesC** produced **similar** prediction **accuracies**
- Selection of **non-synonymous SNPs** did not improve accuracy of genomic prediction

Thank you

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Which animals to sequence?

Proportion of diversity (Druet et al. 2014)

- **G matrix** for **2,140** genotyped animals

$$P_n = G_n^{-1} c_n$$

- G_n : a subset of G matrix (**62 ancestors**)
- c_n : average genomic relationship of 62 animals with whole population
- P_n : proportion of genetic diversity

Which animals to sequence?

Proportion of diversity (Druet et al. 2014)