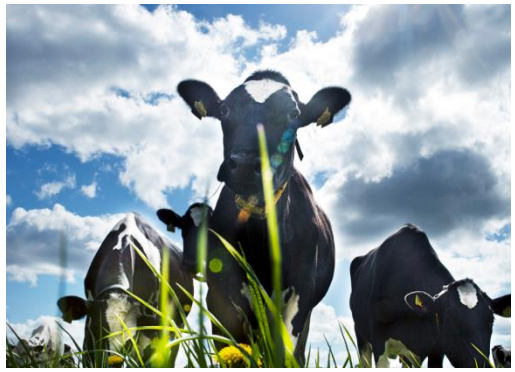
Dissecting H^2 using genomic annotation in ryegrass

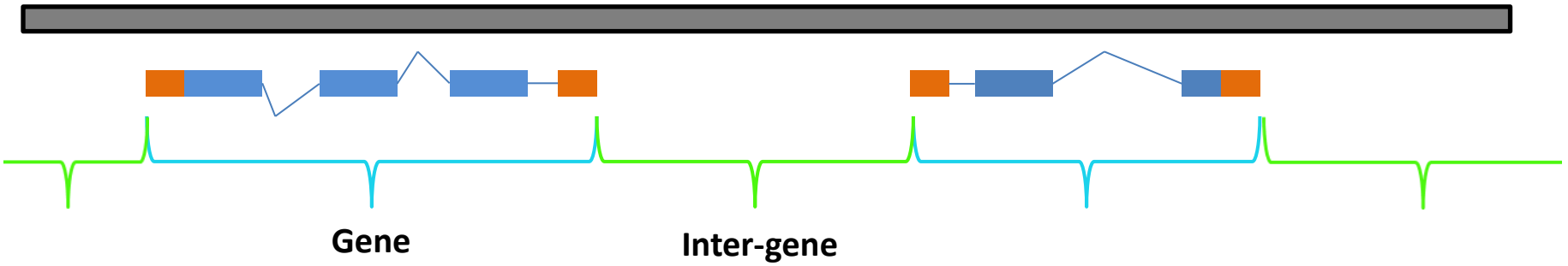
Fabio Cericola - Gen SAP annual meeting - Nov 2014

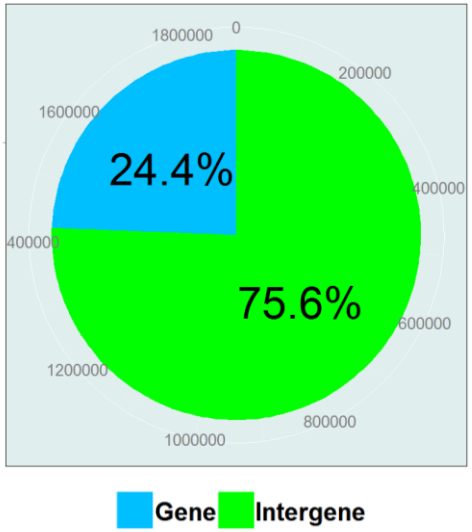

Ryegrass genotype

- GBS as genotyping strategy
- ~ 1.8 M SNPs markers
- By anchoring the sequence on the genome draft we can divide the SNPs according with different genomic feature

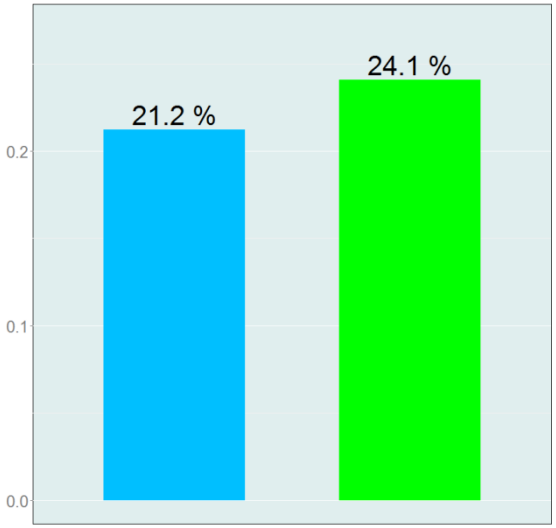
Genomic annotation



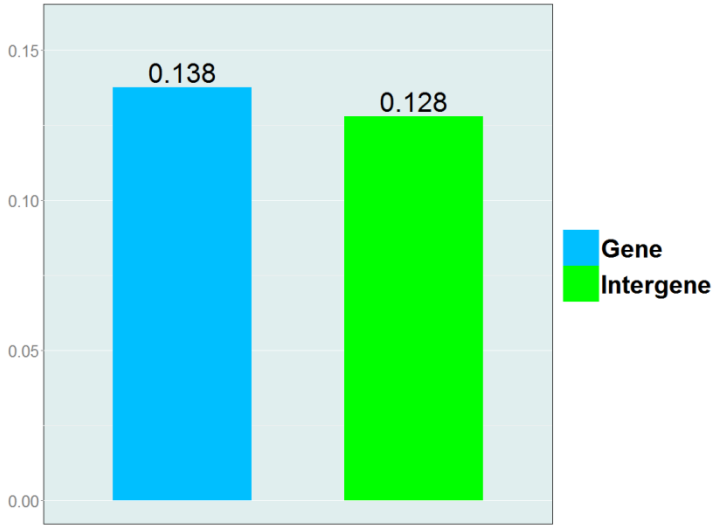
SNPs Number



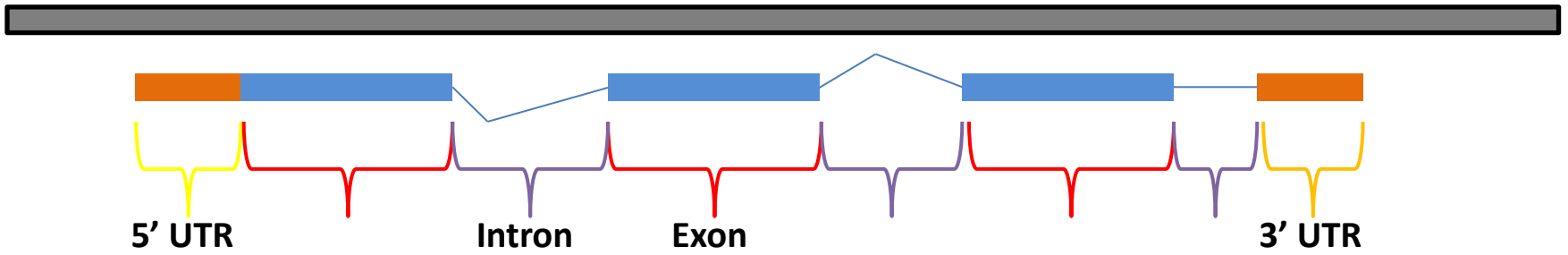
Missing value



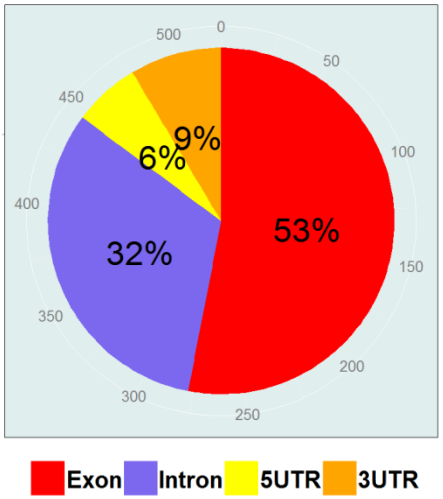
MAF



Genomic annotation



SNPs Number



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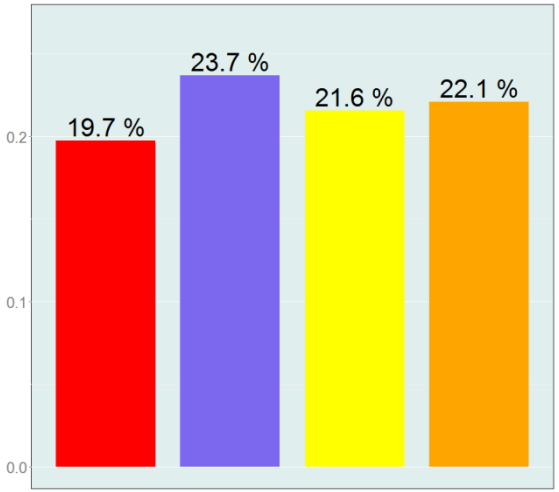

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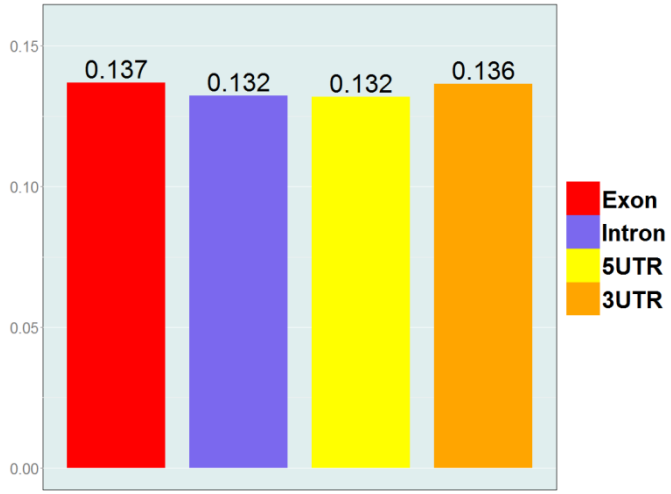


Crown rust resistance score

$$Rust = L + G_{gene} + G_{intergene} + G + EXP + e$$

- Proportion of explained genomic variance by each SNPs set:

$$H^2_{\text{set } i} = \frac{\sigma^2_{\text{set } i}}{\sum_i^n \sigma^2_{\text{set } i} + \sigma^2_{rem.gen.}}$$

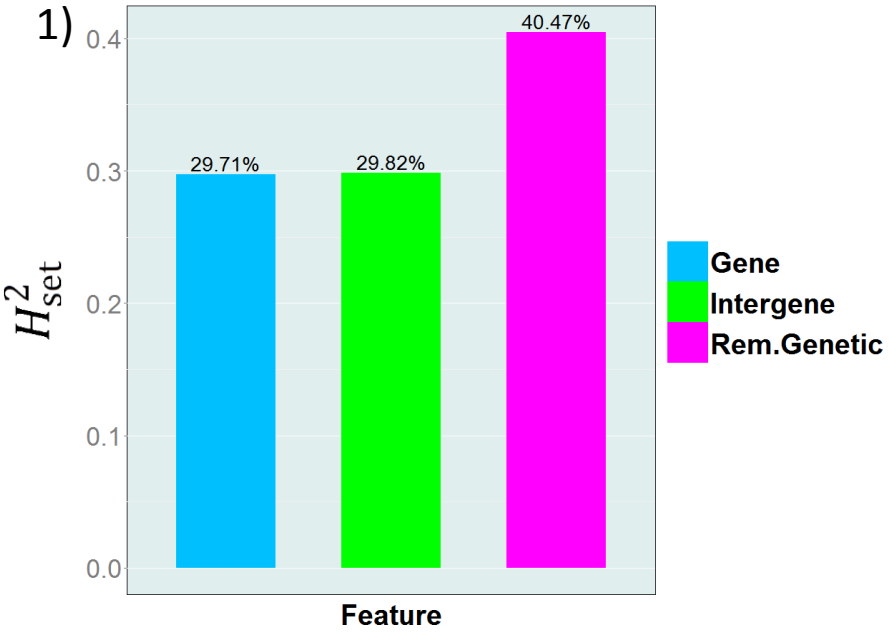
$$n = number\ of\ sets$$

Rust resistance score

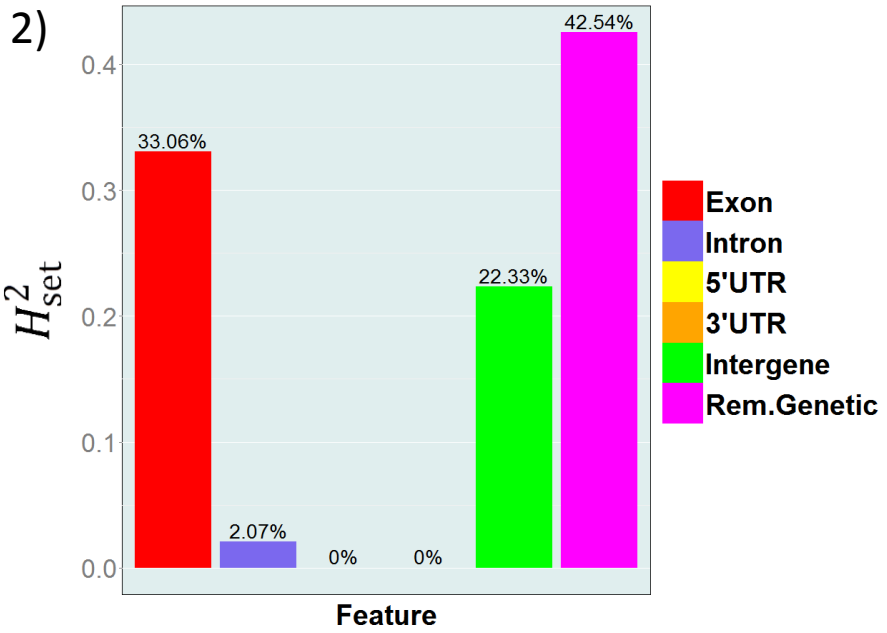
1) $Rust = L + G_{gene} + G_{intergene} + G + EXP + e$

2) $Rust = L + G_{exon} + G_{intron} + G_{5'UTR} + G_{3'UTR} + G_{intergene} + G + EXP + e$

1)



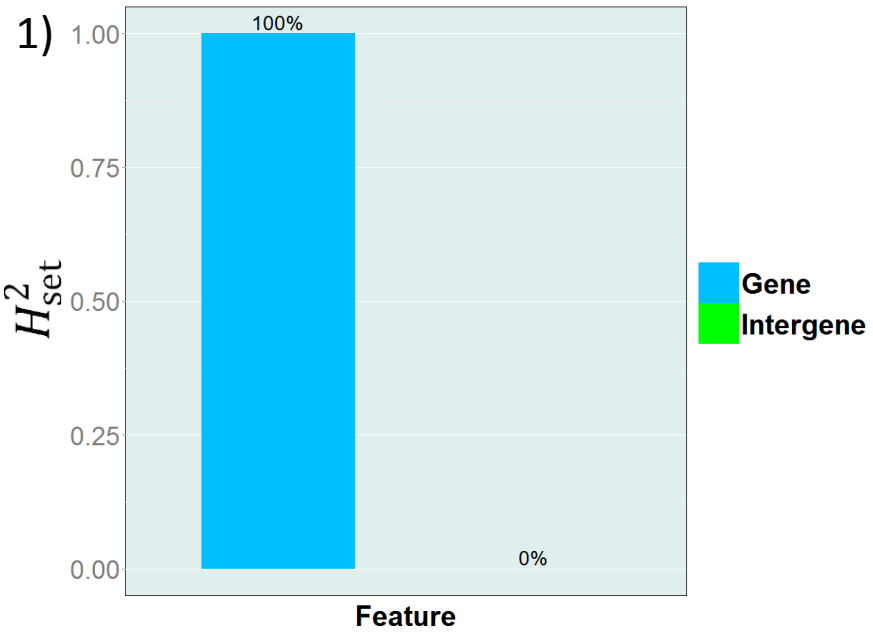
2)

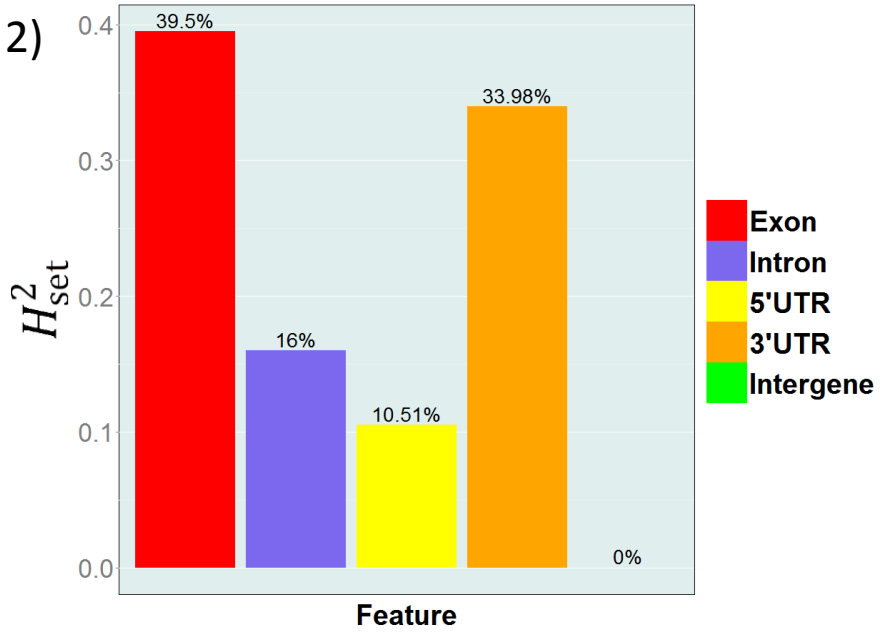


Heading date

1) Heading = L + G_{gene} + $G_{intergne}$ + P1 + P2 + Cross + GxL + EXP + e

2) Heading = L + G_{exon} + G_{intron} + $G_{5'UTR}$ + $G_{3'UTR}$ + $G_{intergne}$ +
P1 + P2 + Cross + GxL + EXP + e



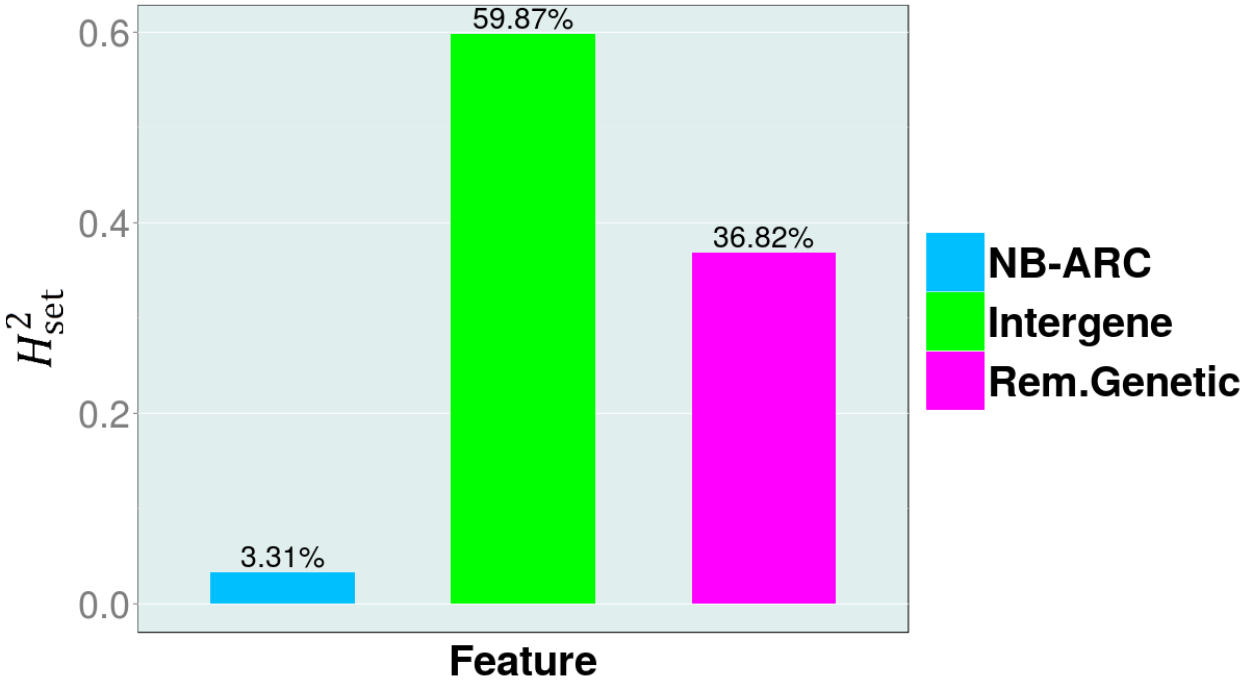


Rust resistance score

SNPs located in NB-ARC domain: 9024 (0.48%)

Common domain in all NB-LRR resistance gene.

$$Rust = L + G_{NB\text{-}ARC} + G_{Intergene} + G + EXP + e$$



Conclusion and perspectives

- SNPs sets in the genetic regions can explain a large proportion of the genomic variance
- Promising for complex trait (e.g. yield related)
- Test the cross validation performance of different SNP sets

Thank you for your attention