

# Within and across population genomic predictions incorporating functional genomic annotations

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## Aim

Validate biology-driven genomic predictions (GP) incorporating functional genomic annotations (FGA) for cattle feed efficiency within and across populations

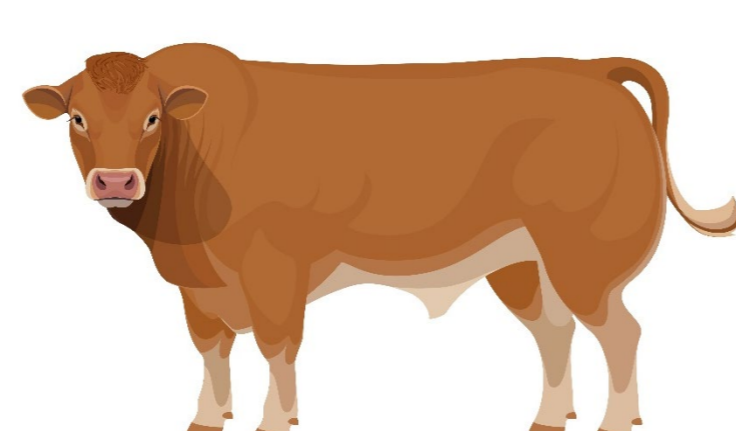
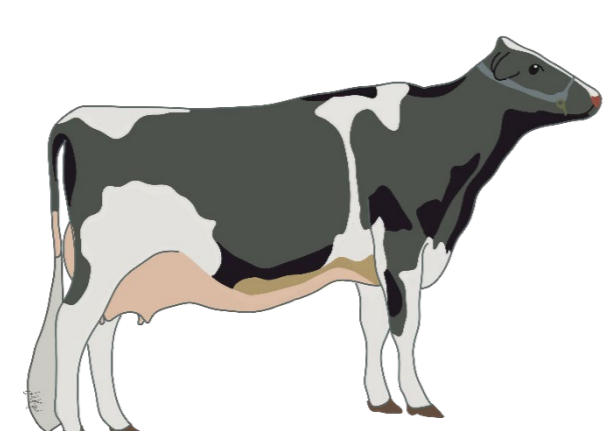
## Take-home messages

- Biology-driven GP can improve accuracy for complex traits like feed efficiency
- Across populations GP using SNP effects not accurate → Next: multi-trait approach
- FGA databases → efficient pre-selection of SNPs

Population



Breeds



Dependent variable  
(Dry Matter Intake)


De-regressed DMI

Pre-corrected DMI

Phenotyped & genotyped animals

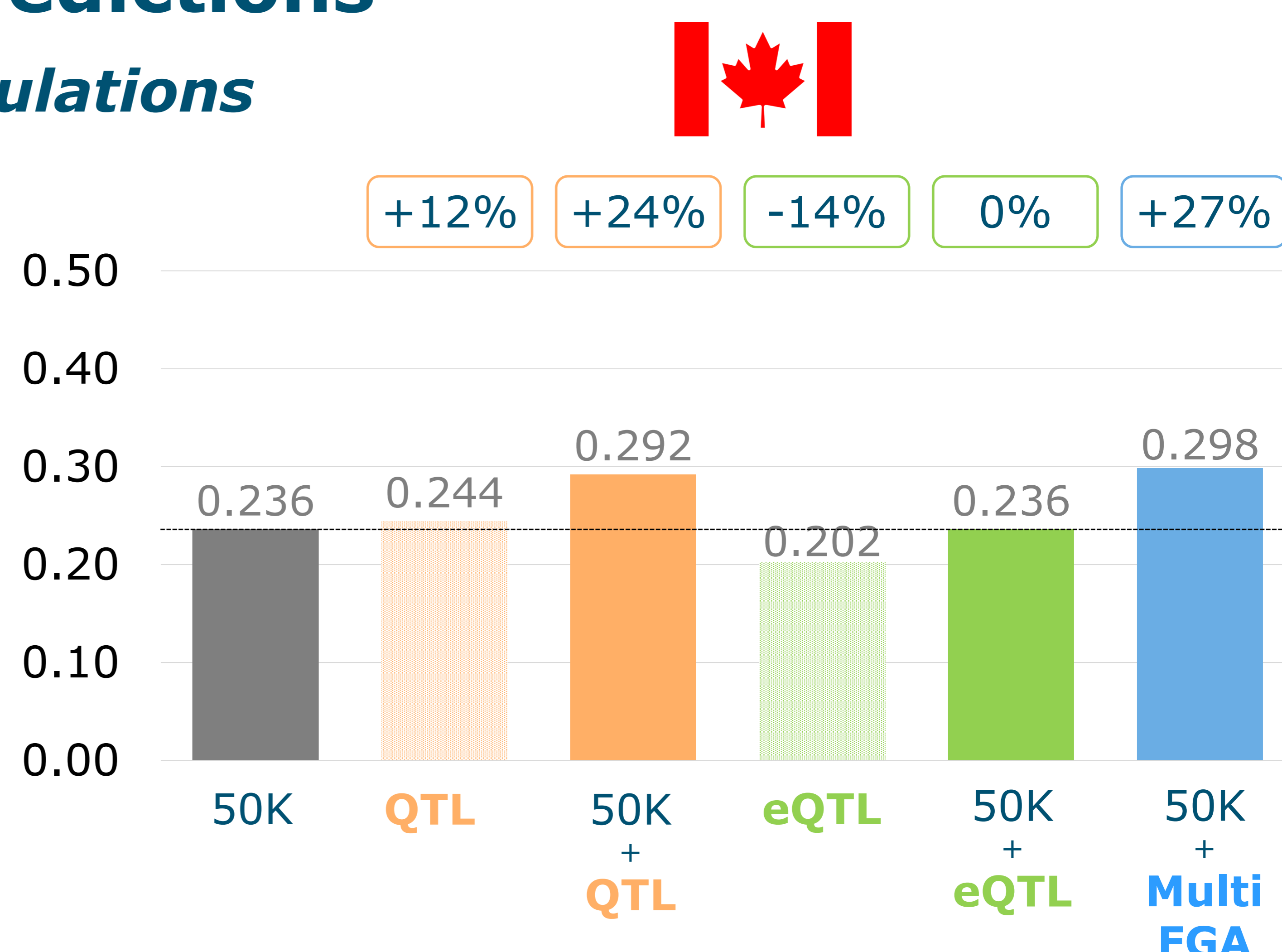
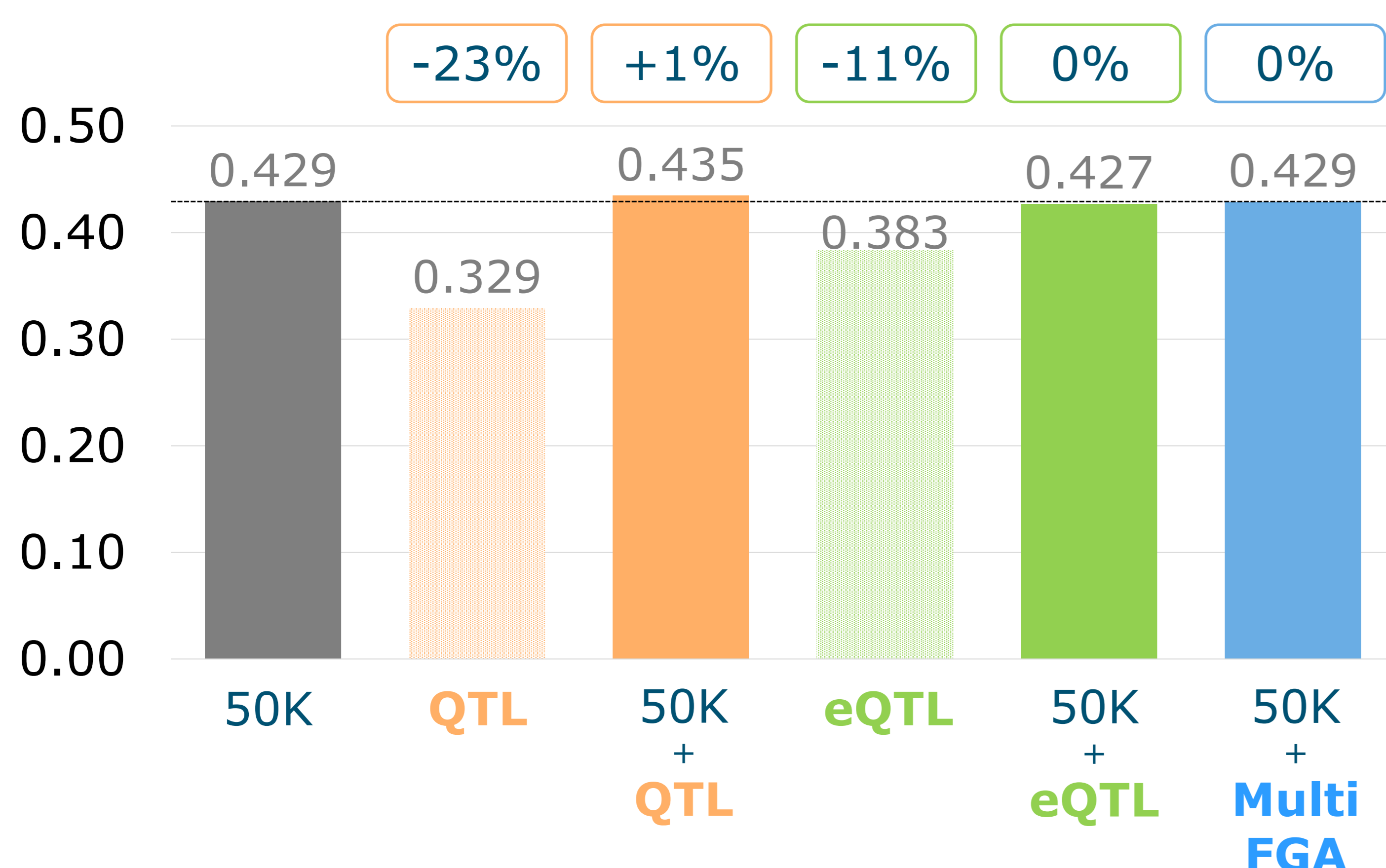
~3.6k

~5.5k

- FGA on several traits & tissues  NEW
- Developed pipeline prioritizing WGS SNPs NEW from FGA (QTL, eQTL, ATAC-seq)
- Bayesian modelling in *NextGP.jl*
- SNPs overlapping with multiple FGA: NEW  
0/1 or continuous (e.g. *p*-values)
- Forward-in-time validation

## Genomic predictions

### Within populations



### Across populations

No prediction accuracy using SNP effects from the other population

**Next:** implement multi-trait approach



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