Biology-driven genomic predictions for dry matter intake within and across breeds using WGS data

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BovReg Understanding cattle genomes

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Biology-driven genomic predictions

- WGS: millions of variants → pinpoint **causal variants** affecting traits of interest
- Key traits: **biological efficiency**, e.g. **feed efficiency**
- BovReg: catalogue of functionally active **genomic features (GF)** in cattle
- genomics (QTL), transcriptomics (eQTL), epigenomics (mQTL), chromatin accessibility (ATAC-seq/ChIP-seq) → **"multi-omics"** data
- **Functional GF** → SNP prioritization → **Biology-driven genomic predictions**

Aim of the study

Validation of **biology-driven genomic predictions**

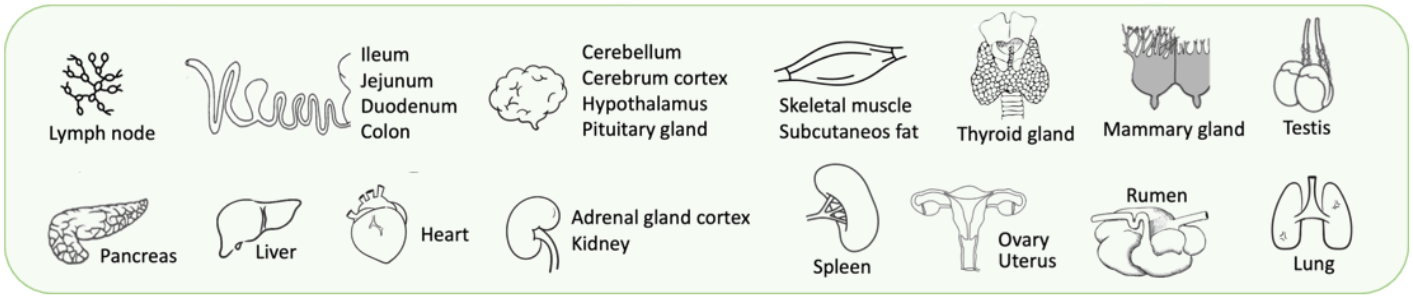
using **genomic features** for **dry matter intake**

Data available for genomic predictions

	NLD	CAN
Breed	Holstein	Beef crosses
Herds	6	14
Dependent variable	DRP on DMI	Pre-corrected DMI
n. animals DMI & geno (training - validation)	~3k (2.2k and 850)	~5.5k (4k and 1.5k)

- **forward-in-time validation** (SE via bootstrapping)
- 50k to imputed WGS (*Beagle*) → prioritize variants based on **GF**

Genomic features used

GF	Traits / Tissues
QTL	Meat quality, Growth, Milk production, Morphology, Fertility, Health, Feed efficiency, Methane
eQTL	(Gene, Transcript, Splice) Jejunum, Blood, Liver, Mammary Gland, Adipose, Muscle, Milk, Rumen
ATAC-seq	

From GC Moreira et al., EAAP #939

ATAC-seq

Genome-wide mapping of **chromatin accessibility → accessible DNA**

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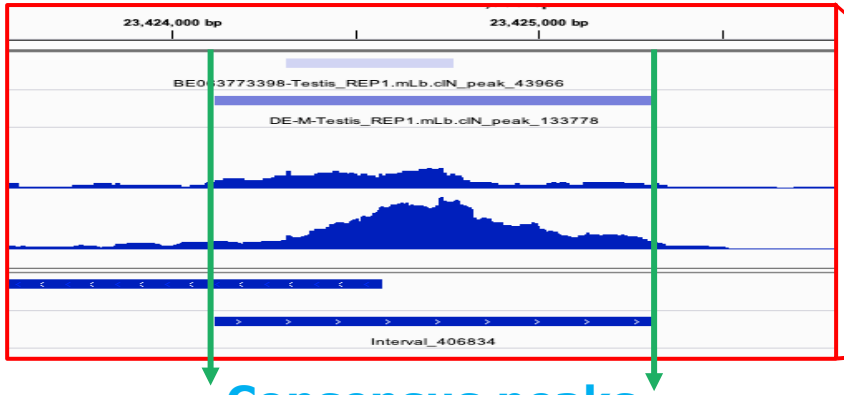
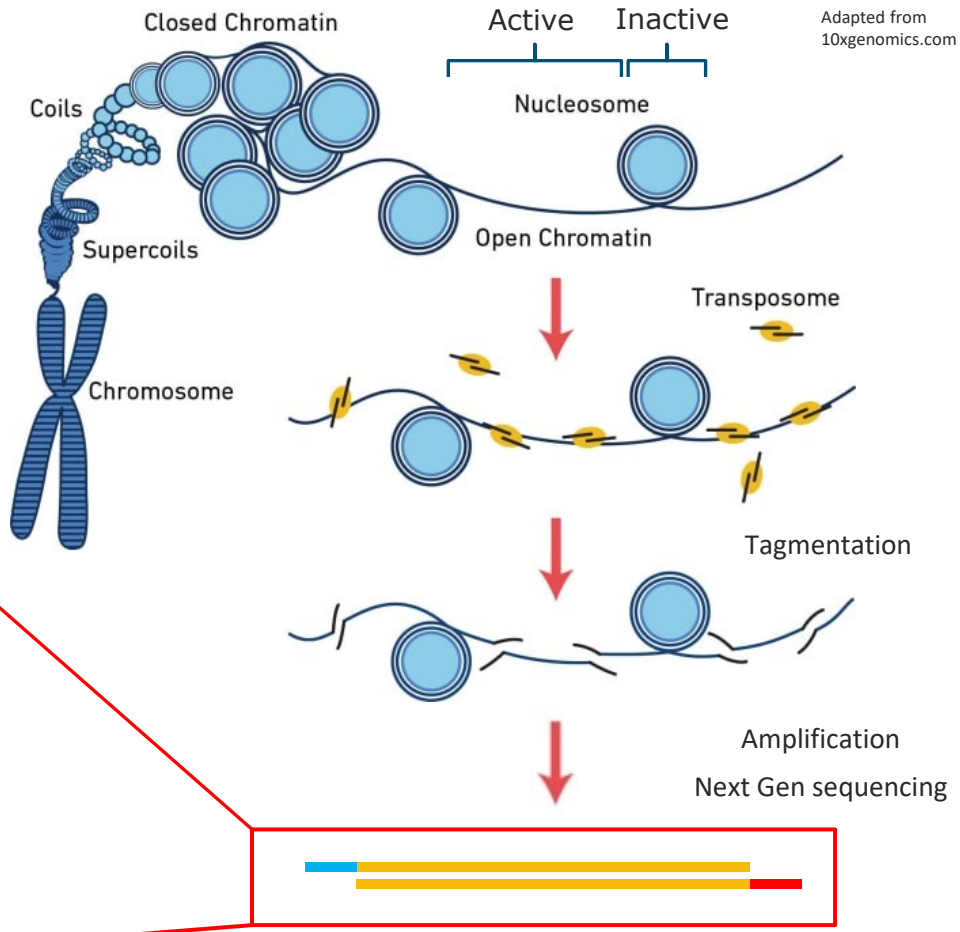
Promotor regions
Enhancers
Regulatory elements

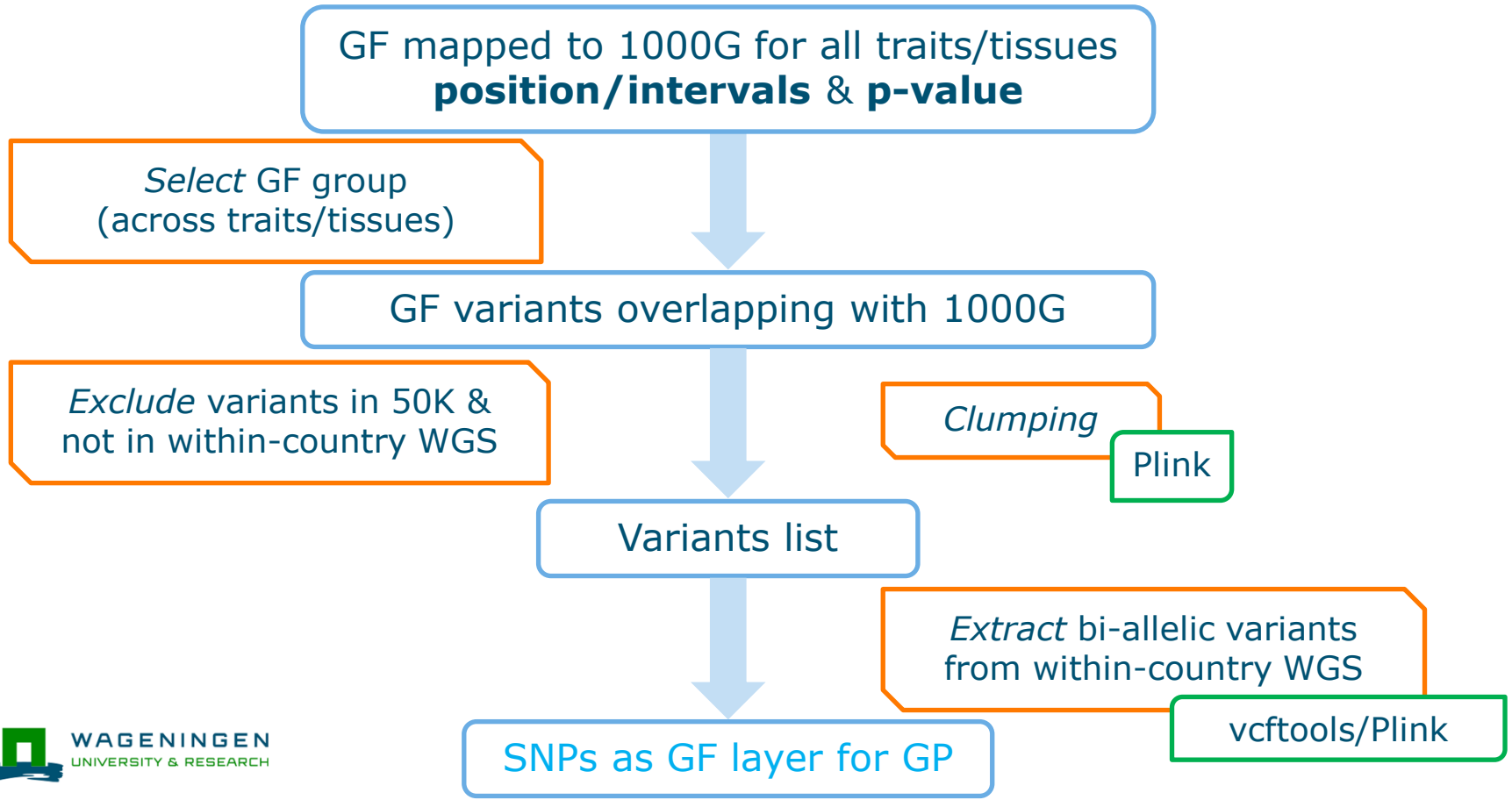


Consensus peaks
across samples



GC Moreira et al., EAAP #939

Selection of genomic features



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Scenarios and software

Scenario	NLD	CAN
50K	48K	46K
50K + **QTL**	48K + 5,416	46K + 4,222
50K + **eQTL**	48K + 12,401	46K + 11,884
50K + **(QTL, eQTL, ATAC)**	48K + 17,796	46K + 16,089

- *NextGP.jl* [1]
- Base 50K: SNPBLUP (BayesC$_0$) common variance across SNPs
- Additional GF layer: SNPBLUP or Bayesian (2 mixture model – no advantage)
- QTL, eQTL, ATAC → Multi-GF → overlapping GF

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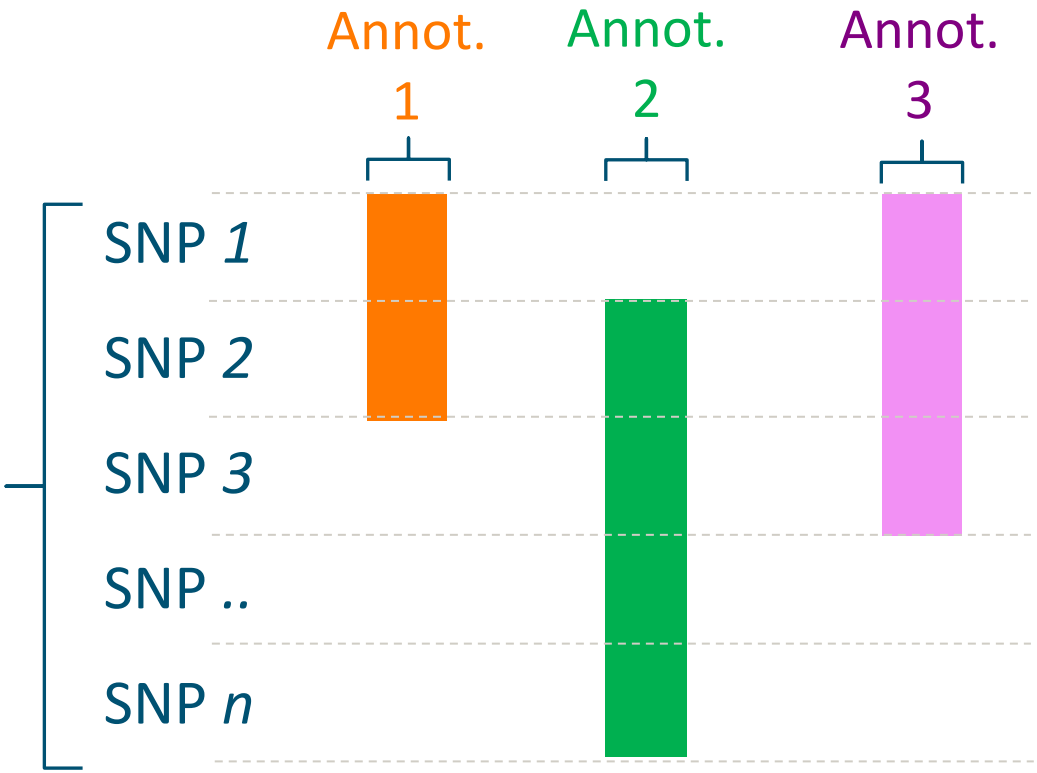
[1] https://github.com/datasciencetoolkit/NextGP.jl

Overlapping genomic features



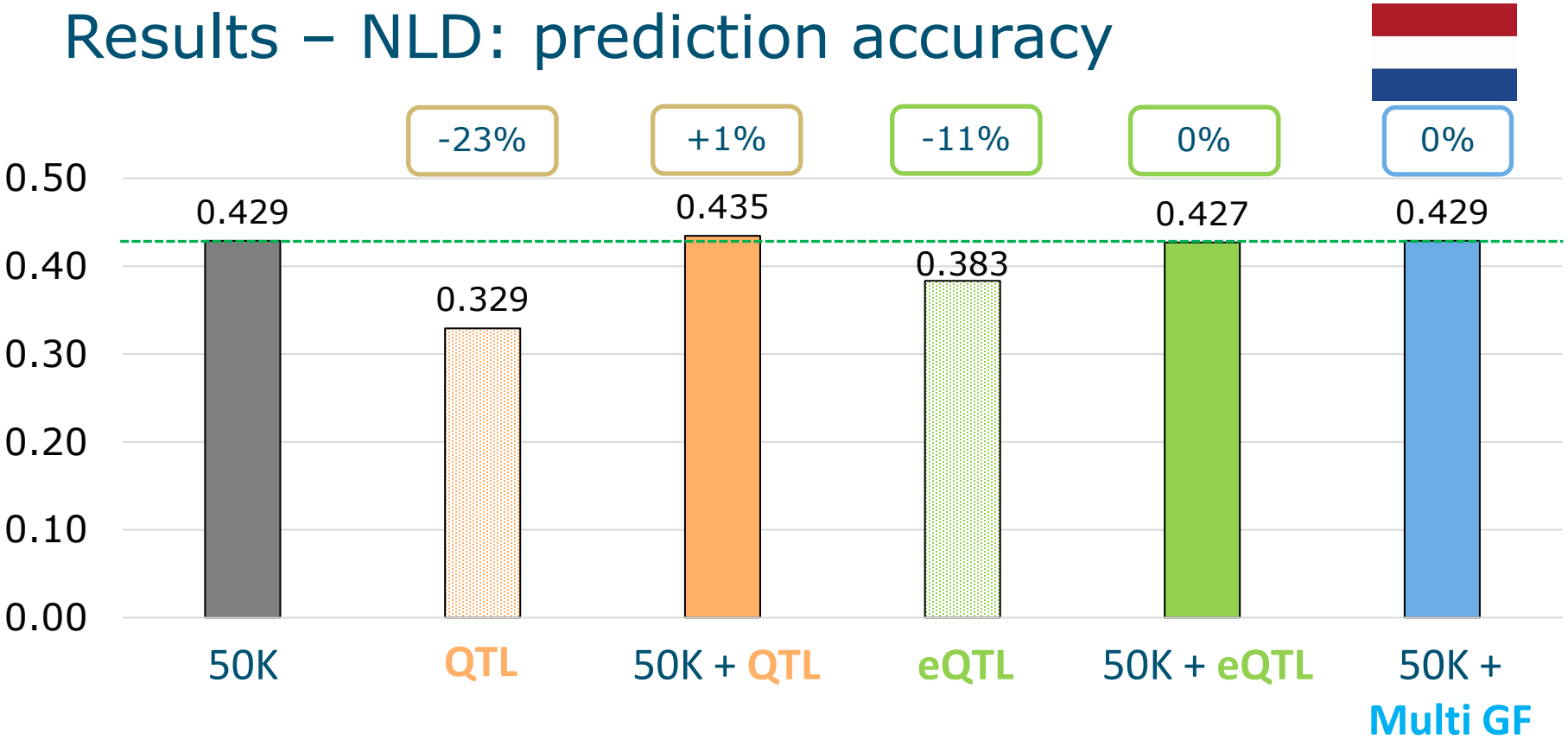
Overlapping genomic features

QTL	eQTL	ATAC	Variants	%
1	1	0	5	0
1	1	1	16	0
1	0	0	2,576	14
1	0	1	2,819	16
0	1	0	5,051	28
0	1	1	7,329	41
			17,796	100

BayesRCπ (2 classes)

Mollandin et al. 2022, BMC bioinformatics

Results – NLD: prediction accuracy



- SE: ±0.03
- No impact on dispersion (slope = 0.68 for 50k)

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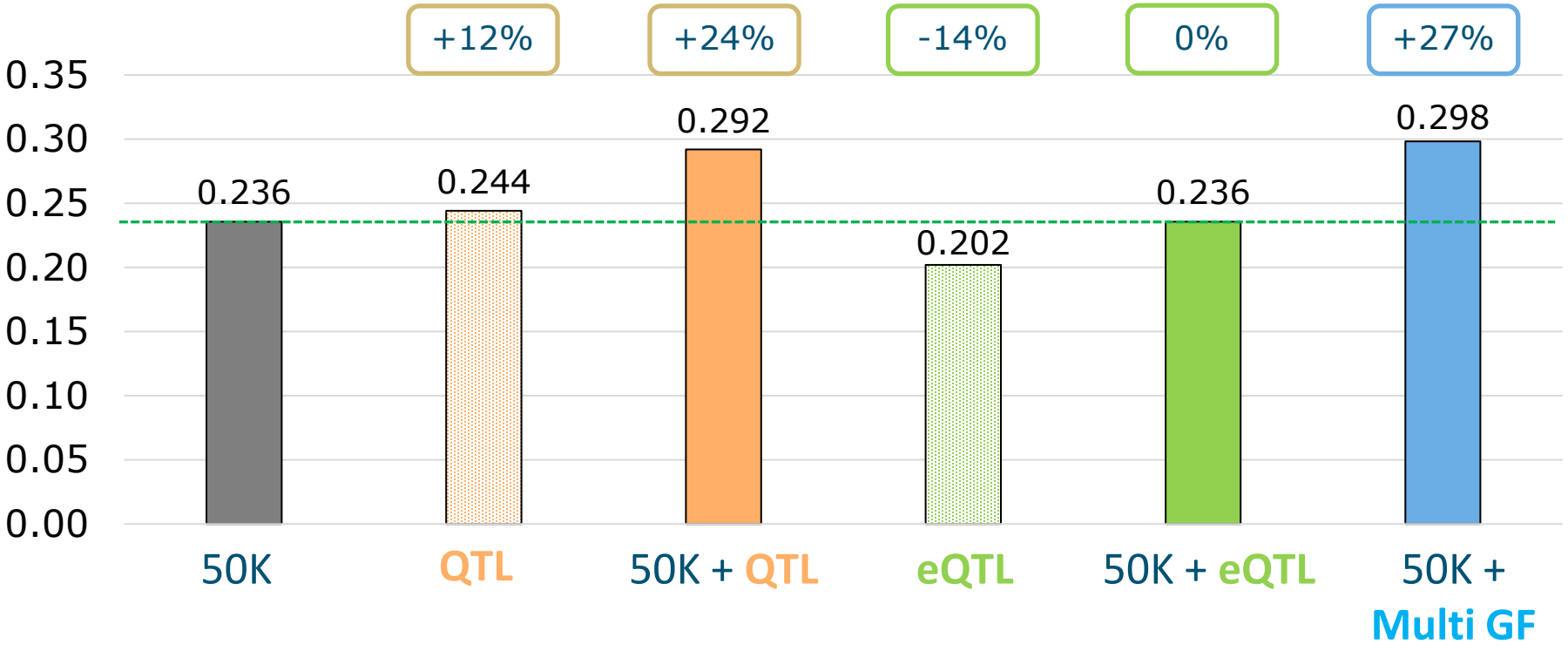
Results – CAN: prediction accuracy



- SE between ±0.02 and ±0.03
- Similar pattern for dispersion (slope = 0.56 for 50k)

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Conclusions and next steps

- Inclusion of **Genomic Features** could increase **genomic prediction accuracies** for **Dry Matter Intake**
- Results may vary across breeds/datasets → find causal variants (complex traits)
- No advantage using (2 mixture) Bayesian approach over SNPBLUP for GF

Next steps

- focus trait/tissues-specific variants, more detailed annotation modelling (BayesLV), across-/multi-breed NLD-CAN

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Thanks for your attention

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Take-home messages

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- Inclusion of Genomic Features could increase genomic prediction accuracies for Dry Matter Intake
- Results vary across breeds/datasets
- No advantage using Bayesian (2 mix model) over SNPBLUP for GF

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