Exploring different strategies to implement a weighted single-step GBLUP in Belgian Blue beef cattle

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Introduction

- Genomic evaluation in Belgian Blue Beef (BBB) cattle:
  - Single-step GBLUP (males and females genotyped)
  - ssGBLUP assumes same variance for all SNP effects
  - Presence of QTL with large effects
  - Some methods (BayesB, BayesR, BSLMM) have higher prediction accuracy

Objectives

Optimize SNP weighting in the genomic relationship matrix (GRM) to increase prediction accuracy

- Use GBLUP to compare weighting strategies
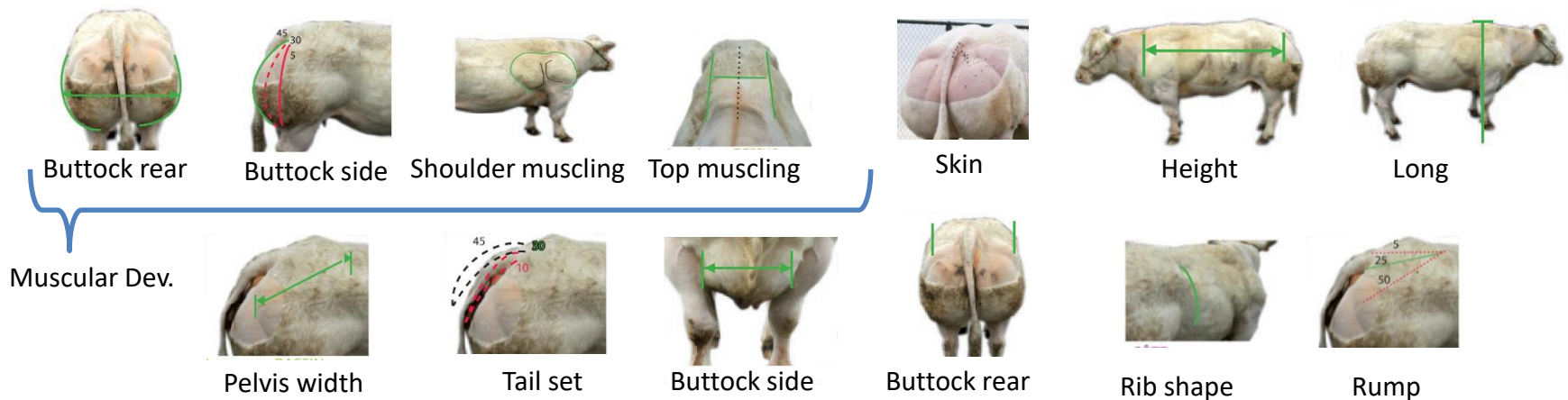
- (Use optimal weighted GRM in ssGBLUP)

Materials and methods

- **Data**

- 10.000 animal, 36K (including 1000 specific variants) , 14 traits

Buttock rear   Buttock side   Shoulder muscling   Top muscling   Skin   Height   Long

Muscular Dev.

Pelvis width   Tail set   Buttock side   Buttock rear   Rib shape   Rump

- **Accuracy evaluation by cross validation**

- Birthday (threshold) : Reference panel 87% / Target panel 13%
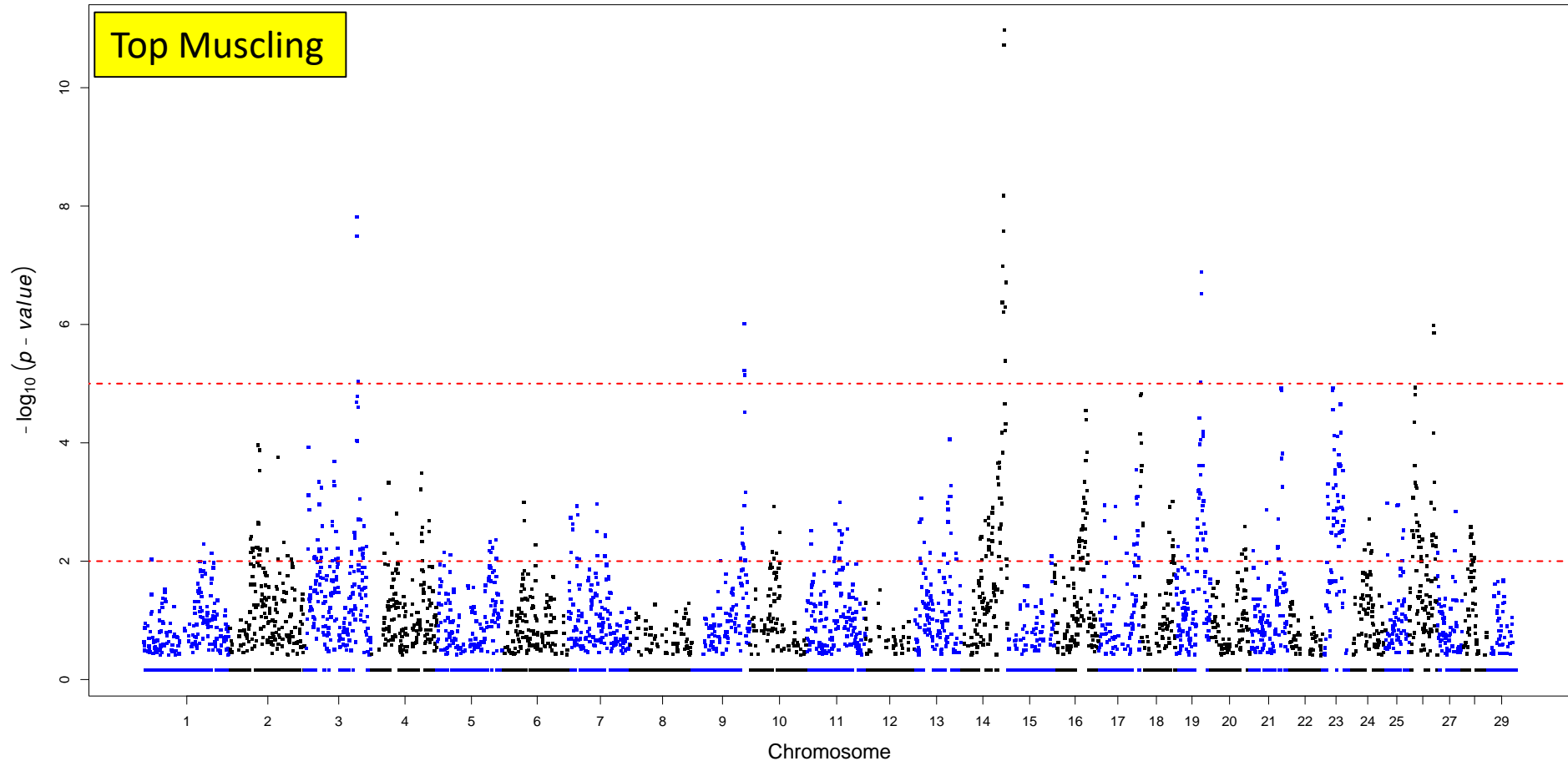
- Test using *Reliability* (target panel)

Genomic prediction methods

- Traditional methods

Model	Formula	Methods
Normal	$b_i \square N(0, S_a^2)$	**GBLUP**
Normal - Mixture	$b_i \square \rho N(0, S_a^2 + S_b^2) + (1 - \rho)N(0, S_a^2)$	**BSLMM**
Point Normal Mixture	$b_i \square \rho_1 N(0, S_a^2) + \rho_2 N(0, 0.1 S_a^2)$ $+ \rho_3 N(0, 0.01 S_a^2) + (1 - \rho_1 - \rho_2 - \rho_3)d_0$	**Bayes-R**

Gemomic prediction with MultiBLUP

Top Muscling
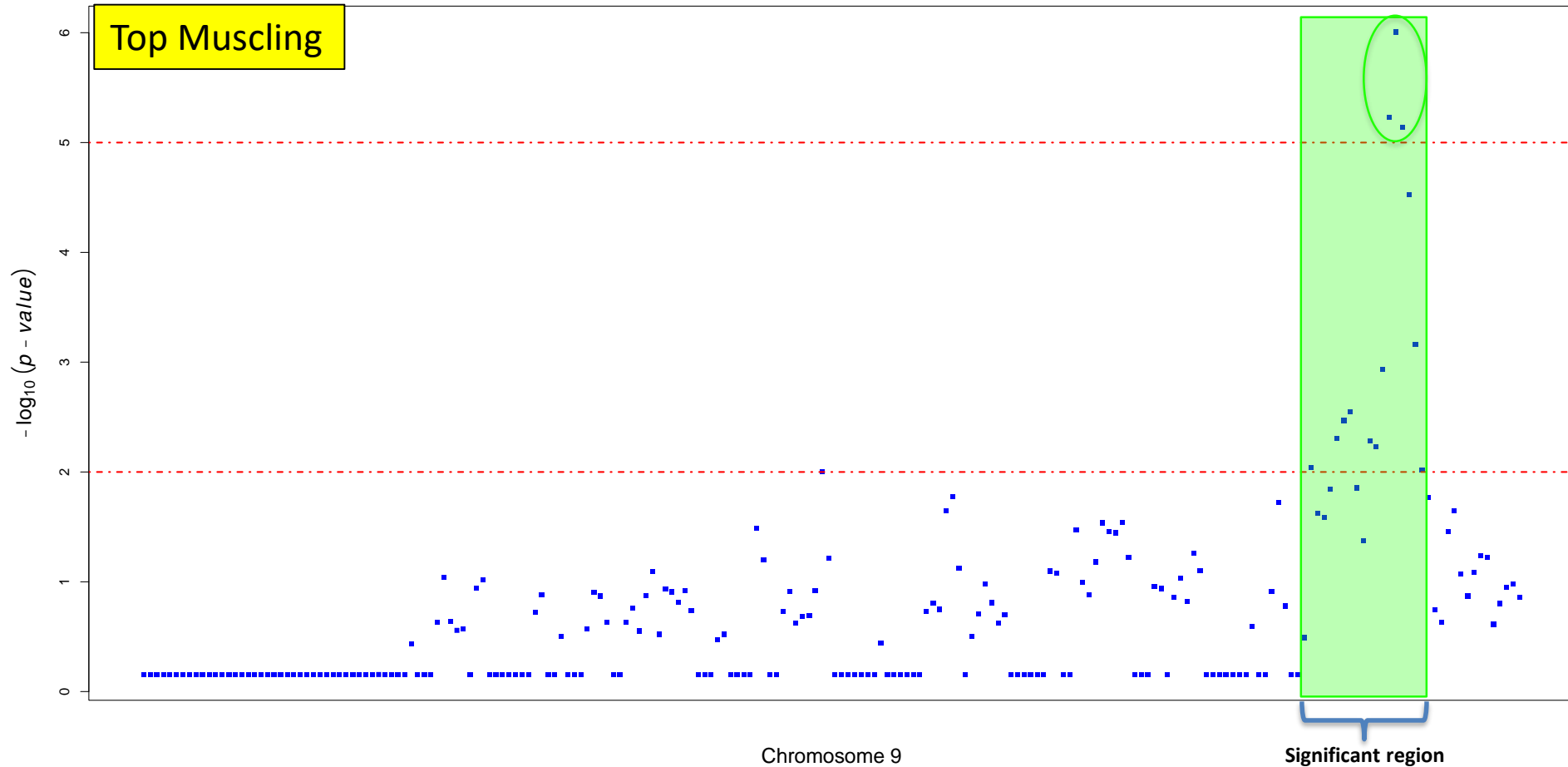
1) Cut the genome in non-overlapping 1 Mb windows
2) For each window, construct the GRM
3) Use the GRM to test whether the region is associated to the trait

'Genome Scan'

Gemomic prediction with MultiBLUP

Chromosome 9

Significant region

1) Windows with a p-value < 10^{-5} are selected.
2) Define the selected region as all the surrounding windows with a p-value < 10^{-2}
3) Run a model with one GRM per significant region (with its own variance / weight)

Adaptative MultiBLUP

EAAP 2019 - Ghent, Belgium

GRM weighting strategies

- Weight SNPs based on their solution
  - Iterative GBLUP approach postGSf90 (select 5th iteration)

- Weight SNPs based on their variance
  - Posterior variance (p_i) from BayesR

- Select SNPs or windows of 25 SNPs :
  - with posterior inclusion probabilities (PIP) from BSLMM
  - Estimate individual variance for each selected SNP / window

RESULTS

Regions identified by MultiBLUP

| TRAIT	h^2	% h^2	Regions	Average Mb	All region Mb	Chr < $10e^{-6}$	Chr < $10e^{-8}$
Length	0.28	0.28	11	7.4	81.0	6	4
Chest width	0.22	0.08	3	6.2	18.5	4	0
Rib shape	0.19	0.03	1	2.0	2.0	1	1
Rump	0.24	0.13	3	13.2	39.5	1	1
Tail set	0.20	0.04	1	7.5	7.5	1	0
Height	0.42	0.30	11	12.8	140.5	8	6
Pelvis length	0.22	0.23	7	8.0	56.0	3	1
Buttock side	0.35	0.08	4	13.2	53.0	4	1
Buttock rear	0.28	0.18	6	13.2	79.0	4	1
Skin	0.15	0.14	2	11.7	23.5	2	1
Pelvis width	0.22	0.10	3	12.2	36.5	3	1
Shoulder muscling	0.30	0.08	3	11.5	34.5	2	1
Top muscling	0.32	0.12	5	7.6	38.0	4	2
Muscular Develop.	0.39	0.17	9	10.3	92.5	4	1

Reliability comparisons
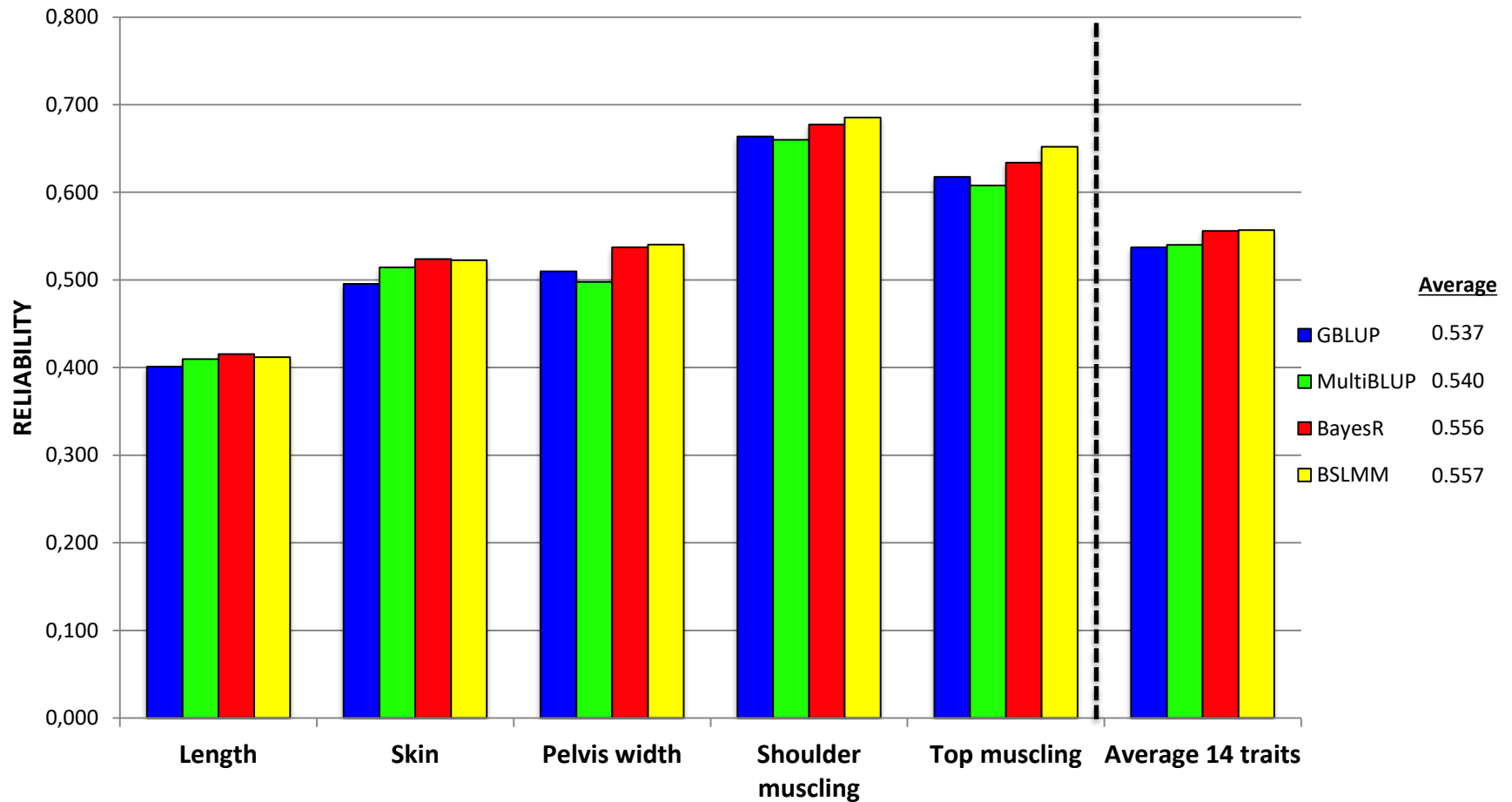
Individual SNP weighting
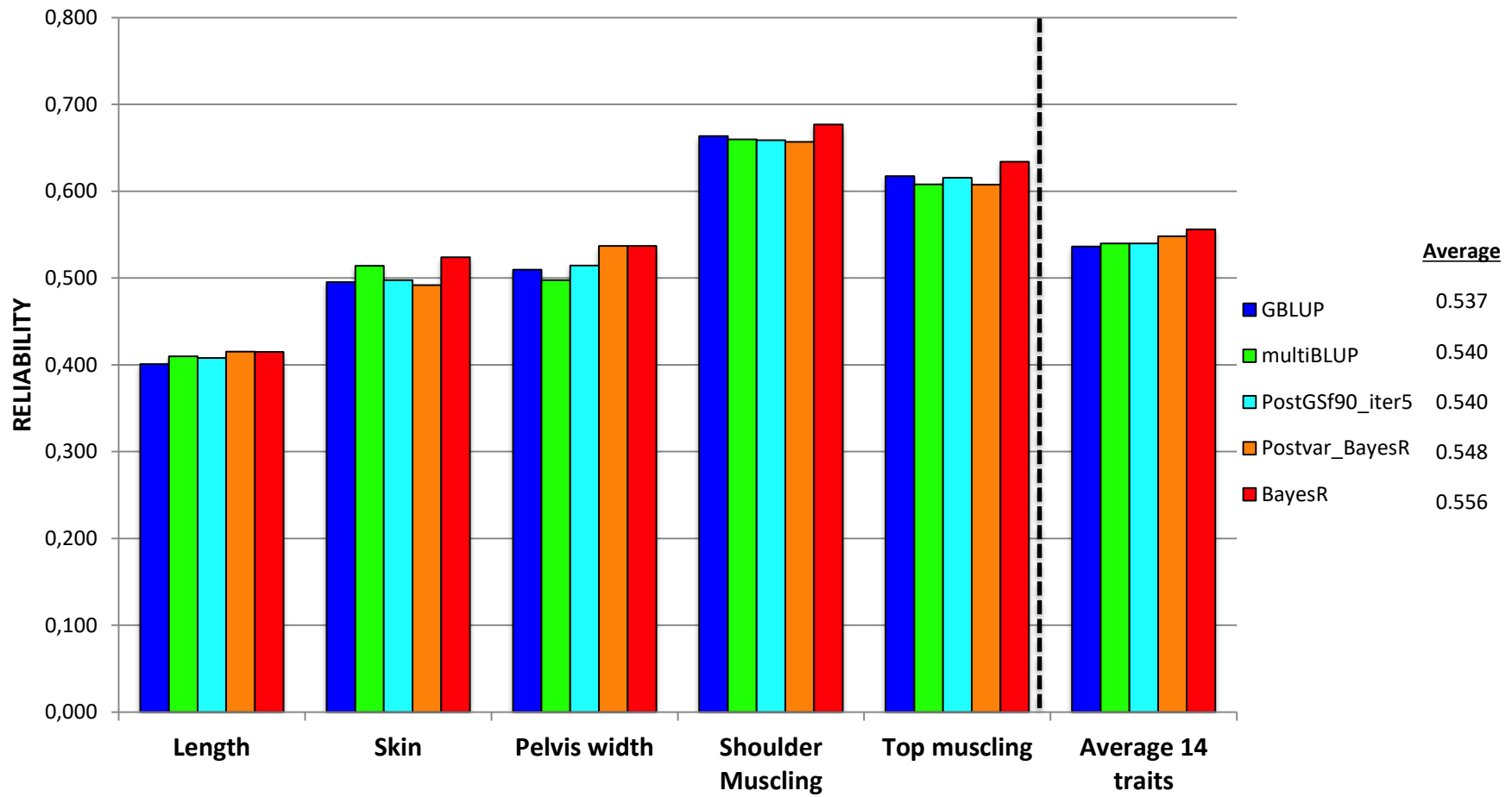
SNP selection based on PIP

TRAIT	# SNPs with PIP > 0.5	RNF11	WWP1	MRC2	ATPA2A1	KITLG	Count
Length	6		X	X			2/6
Chest width	4		X				1/4
Rib shape	1			X			1/1
Rump	2			X		X	2/2
Tail set	0						0/0
Height	9	X	X	X			3/9
Pelvis length	4		X				1/4
Buttock side	0						0/0
Buttock rear	1		X				1/1
Skin	1				X		1/1
Pelvis width	2		X				1/2
Shoulder Musc.	1		X				1/1
Top muscling	4	X	X	X			3/4
Muscular Devel.	4	X	X	X			3/4

RNF11 = Dwarfism , *WWP1* = selection against homozygotes, *MRC2* = Crooked tail syndrome (CTS) , *ATPA2A1* = Congenital muscular dystonia 1 (CMD1) , *KITLG* = roan locus (coat color) and white heifer disease.

SNP selection based on PIP
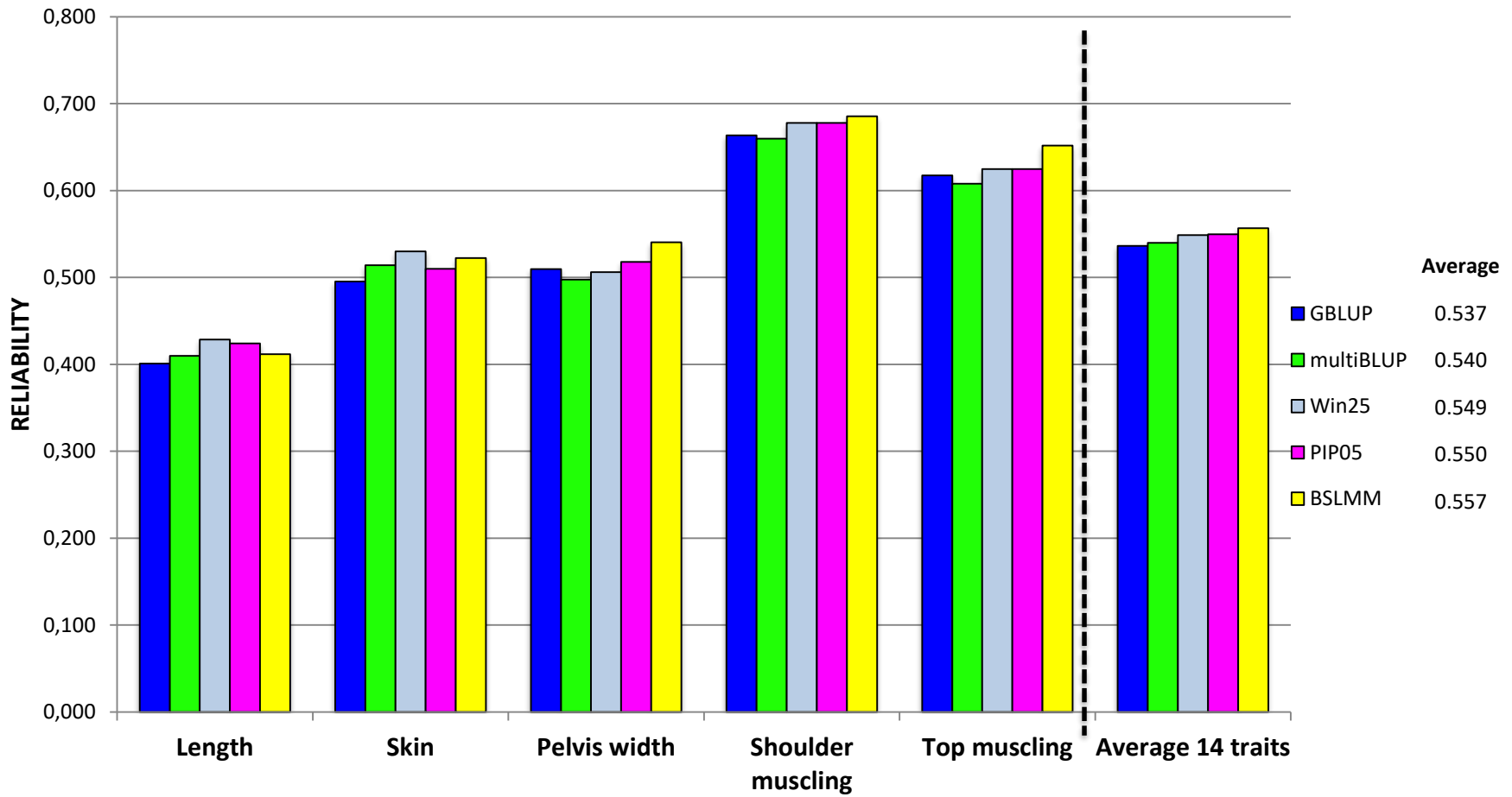
PIP05 = Select SNPs wit PIP ≥ 0.5, Win25 = sum PIP for windows of 25 SNP

Conclusions

- BSLMM and BayesR were the most accurate
  - Modest gain
  - Polygenic traits?
- Limited number of SNPs with PIP > 0.5
  - Recessive deleterious variants presenting heterozygous advantage
- Including specific weights for these few variants performed better than Adaptive MutiBLUP
  - Benefit of identifying and genotyping more causative variants
  - Adaptive MultiBLUP less efficient than in human

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