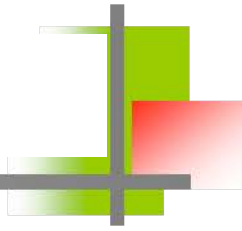# A new Marker-Assisted BLUP genomic evaluation for French dairy breeds

Pascal Croiseau, Aurélia Baur, David Jonas, Chris Hoze, Julie Promp, Didier Boichard, Sébastien Fritz, Vincent Ducrocq[*]

Genomic evaluation in France : 2009-2014

❖ Holstein, Normande, Montbéliarde then Brown Swiss

❖ A Marker-Assisted BLUP model with pre-detected QTL (via an LDLA approach) traced using haplotypes of 3 to 5 SNP

❖ 300 to 700 QTL per trait

❖ a residual polygenic effect (explaining 30-50% of total genetic variance) using pedigree information

❖ imputation LD ➜ 50k, with DagPhase (*Druet & George, 2010*)

❖ phases needed, created using DagPhase
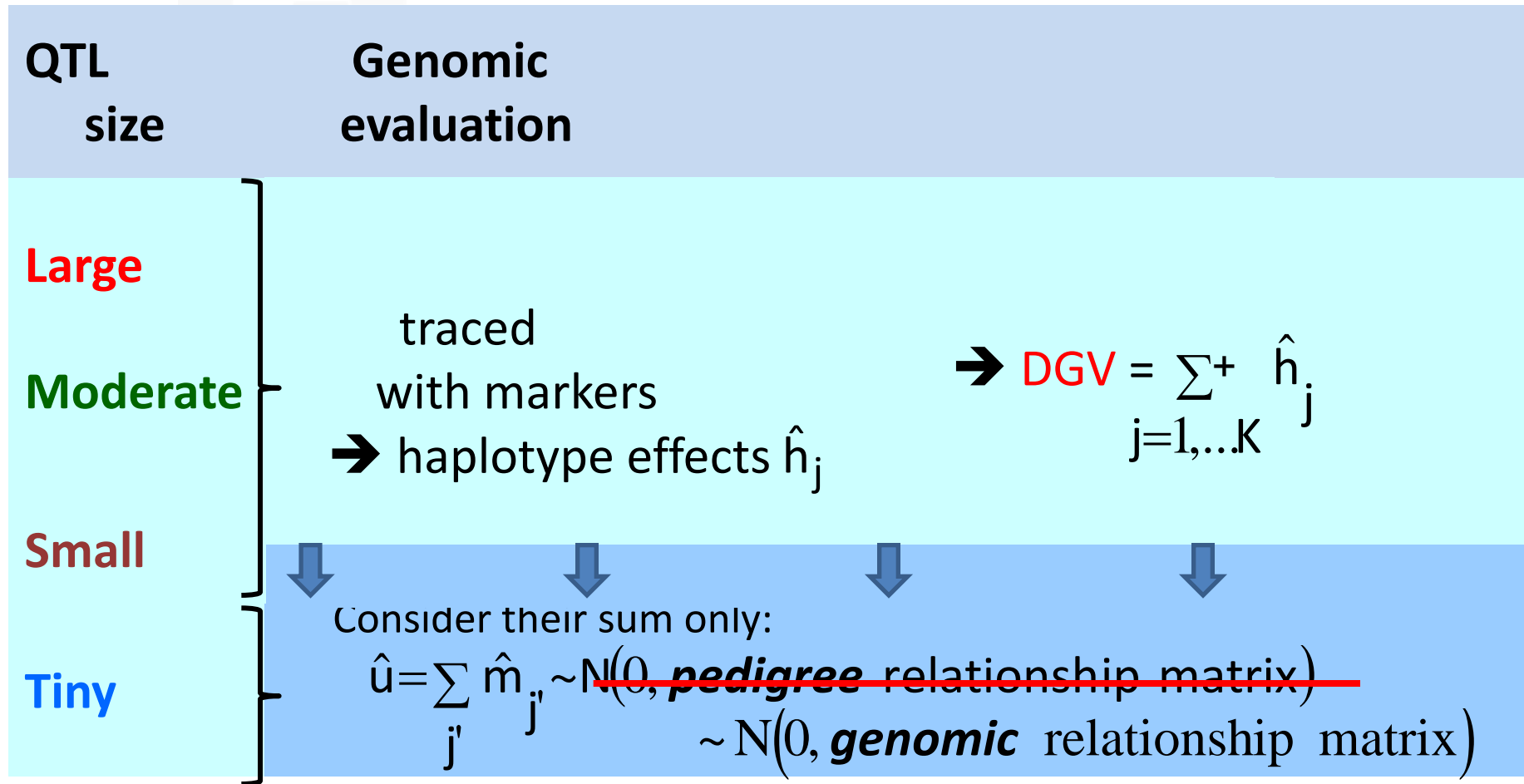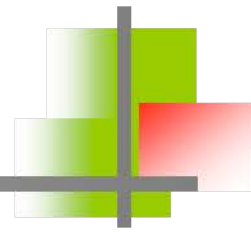
❖ Reference populations consisting of bulls only

Previous model: limits

❖Imputation could be improved:

      DagPhase seemed less efficient than initially

❖ Our research projects showed that 500 QTL did not give

      maximal accuracy

❖Large residual polygenic variance penalized sons /

      daughters of bulls with no progeny test information

❖ No use of female information, therefore loss of accuracy

      in medium size reference populations

❖Time consuming computations (old software)

Imputation

❖ Software comparison

❖ FImpute (*Sargolzaei et al*, 2011) is as accurate as Beagle in populations with a dense pedigree information

❖ Accuracy increased from 98.0 % to 99.2%

❖ Fimpute is at least 3 times faster

❖ Can impute the whole population in one run

=> **Switch to Fimpute** (with commercial licence)

A new genomic model

QTL size	Genomic evaluation

Large

Moderate

Small

traced
with markers
➜ haplotype effects $\hat{h}_j$

➜ DGV $= \sum_{j=1,..K}^{+} \hat{h}_j$

Tiny

Consider their sum only:
$$\hat{u} = \sum_{j'} \hat{m}_{j'} \sim N\left(0, \textbf{\textit{pedigree}} \text{ relationship matrix}\right)$$
$$\sim N\left(0, \textbf{\textit{genomic}} \text{ relationship matrix}\right)$$

In practice…

$$g_i = \sum_{j=1}^{n}(h_{ij1} + h_{ij2}) \quad + \quad u_i$$

Trait dependent **Trait independent**

$$g_i = \sum_{j=1}^{n^+}(h_{ij1} + h_{ij2}) + \sum_{j=1}^{k}(SNP_{ij1} + SNP_{ij2})$$

❖ Genomic relationships via EuroG10K chip: System size = constant

❖New software

to cope with very large increase in number of genotyped animals

strategy: read genotypes and store in memory

preconditioned conjugate gradient with iteration on data in memory

Haplotype construction

❖ first steps: QTL (SNP) detection with ~~GWAS~~ Bayes Cπ,

K (=1000 | 3000 | 6000) largest SNP selected

❖ For each SNP selected, choose « best » combination of

3, 4, 5 SNP in a window of 10 SNP *(David Jonas, submitted)*

allele	1	2	3	4	5	6	Total
Haplotype A	300	300	200	200	-	-	1000
Haplotype B	350	350	100	100	100		1000
Haplotype C	220	220	200	180	180	-	1000
Haplotype D	600	200	100	50	30	20	1000

= a compromise between allele # and "a priori predictability"

Reference populations

	Genomic evaluation	
	2010	**2015**
Holstein	**16000** bulls	**30700** bulls
Montbéliarde	**1500** bulls	**2650** bulls + **22000** cows
Normande	**1250** bulls	**2330** bulls + **11800** cows
Brown Swiss	-	**6015** bulls

➢ females included in Normande and Montbéliarde

➢ x2 in Holstein, x3 in Normande, x4 in Montbéliarde
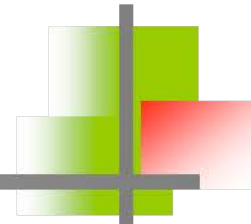
➢ post-blending for Holstein and Brown Swiss cows

Validation studies
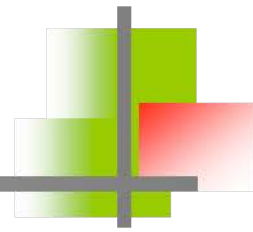
Comparison criteria : correlation ($GEBV_{t-4}$, DYD_t), regression slope

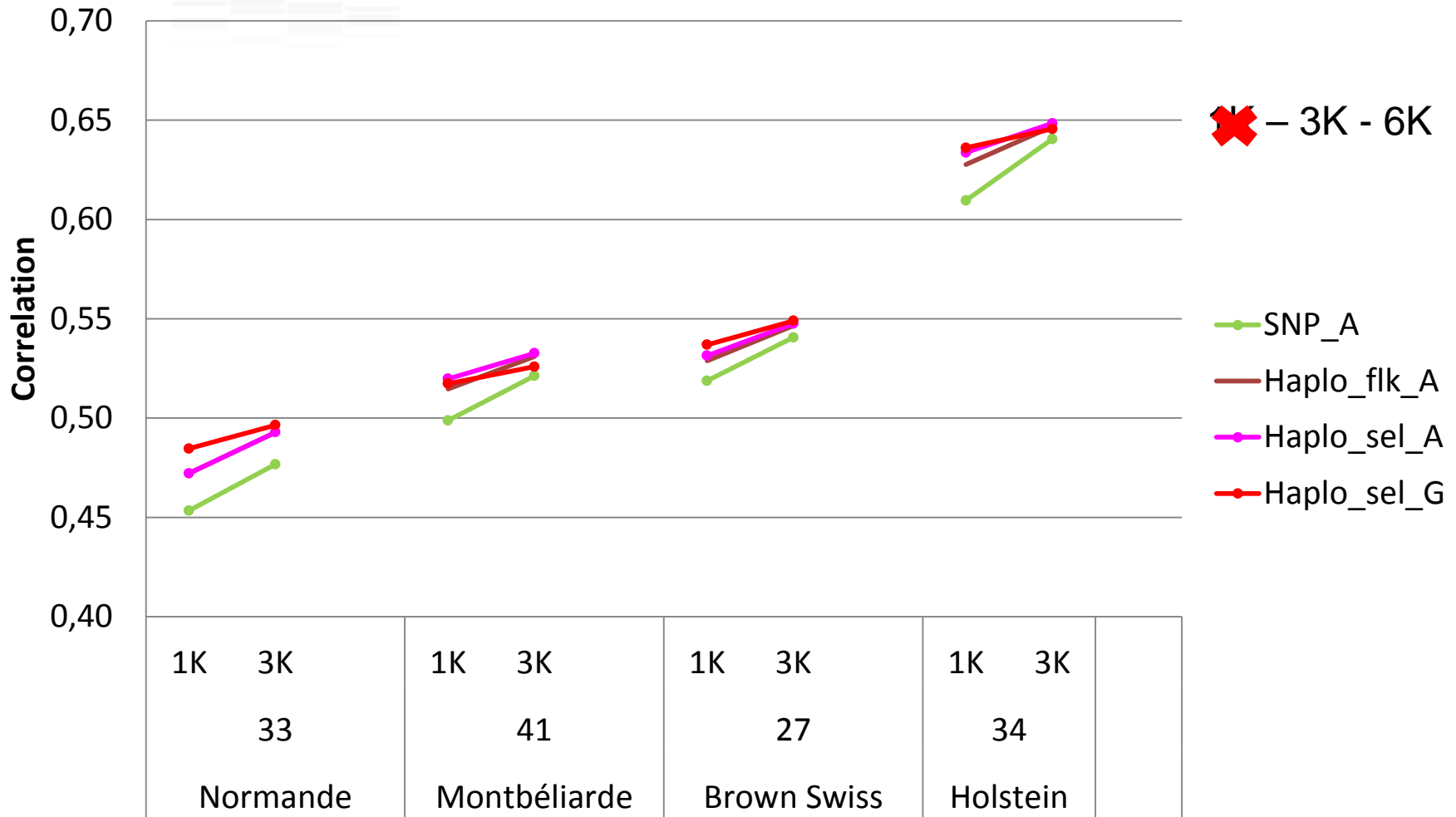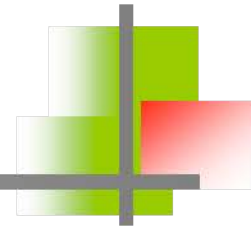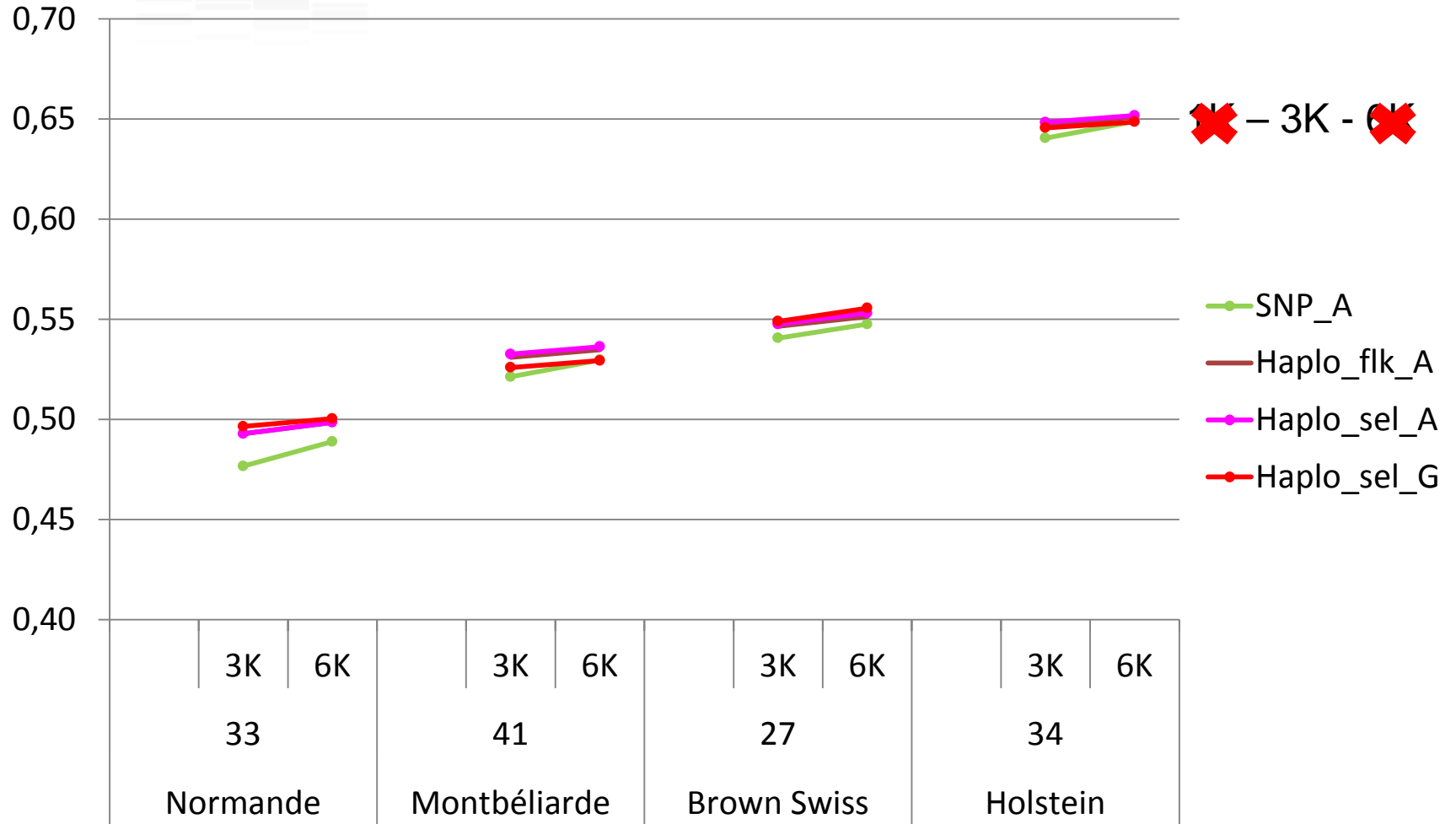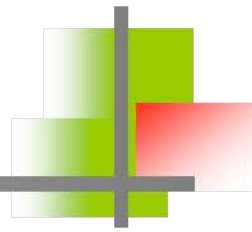|	Validation population	
	Number	**years**
Holstein	**3391** bulls	**2006-2009**
Montbéliarde	**535** bulls	**2005-2008**
Normande	**385** bulls	**2006-2008**
Brown Swiss	**458** bulls	**2005-2008**

Validation results: all breeds
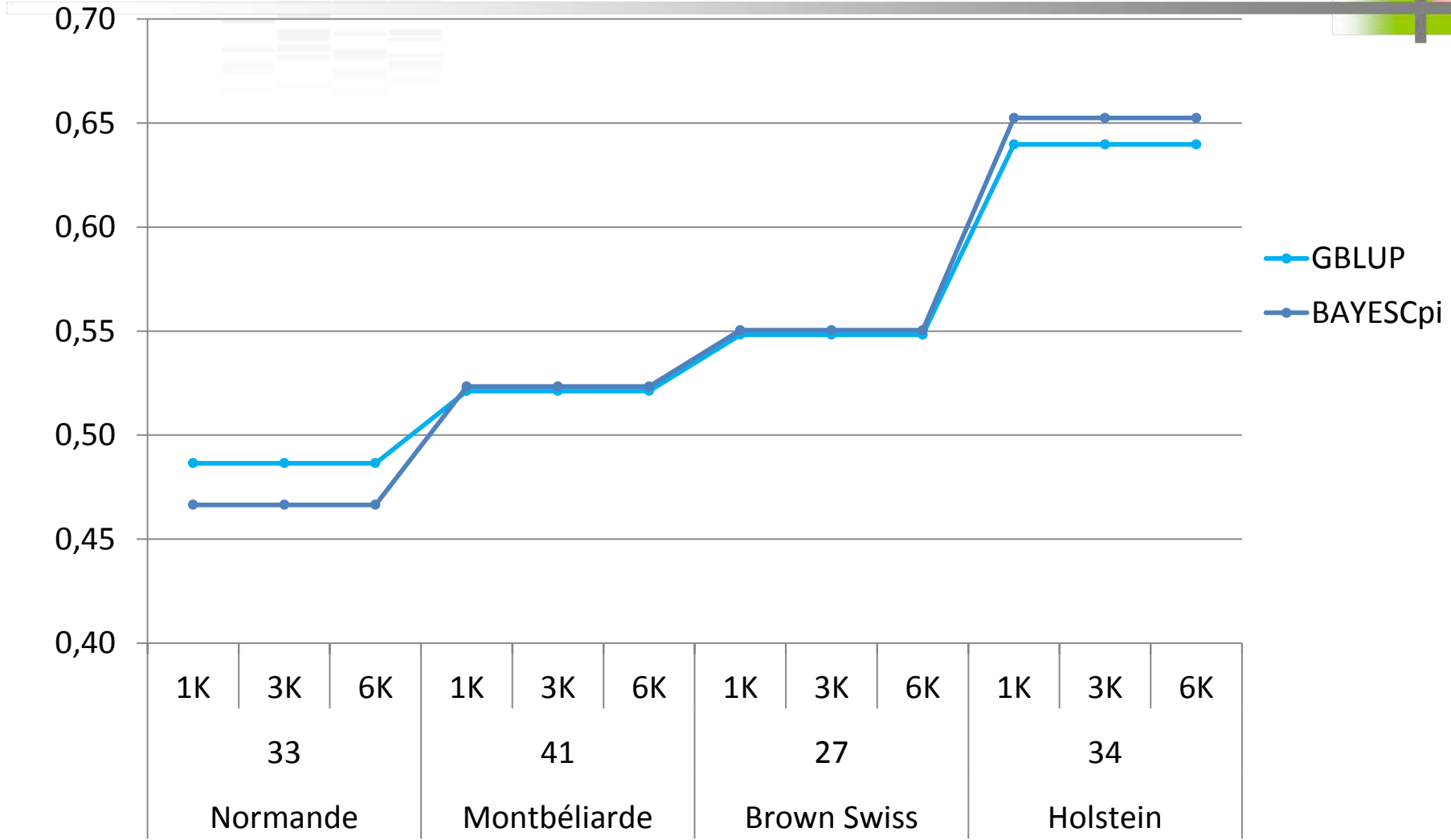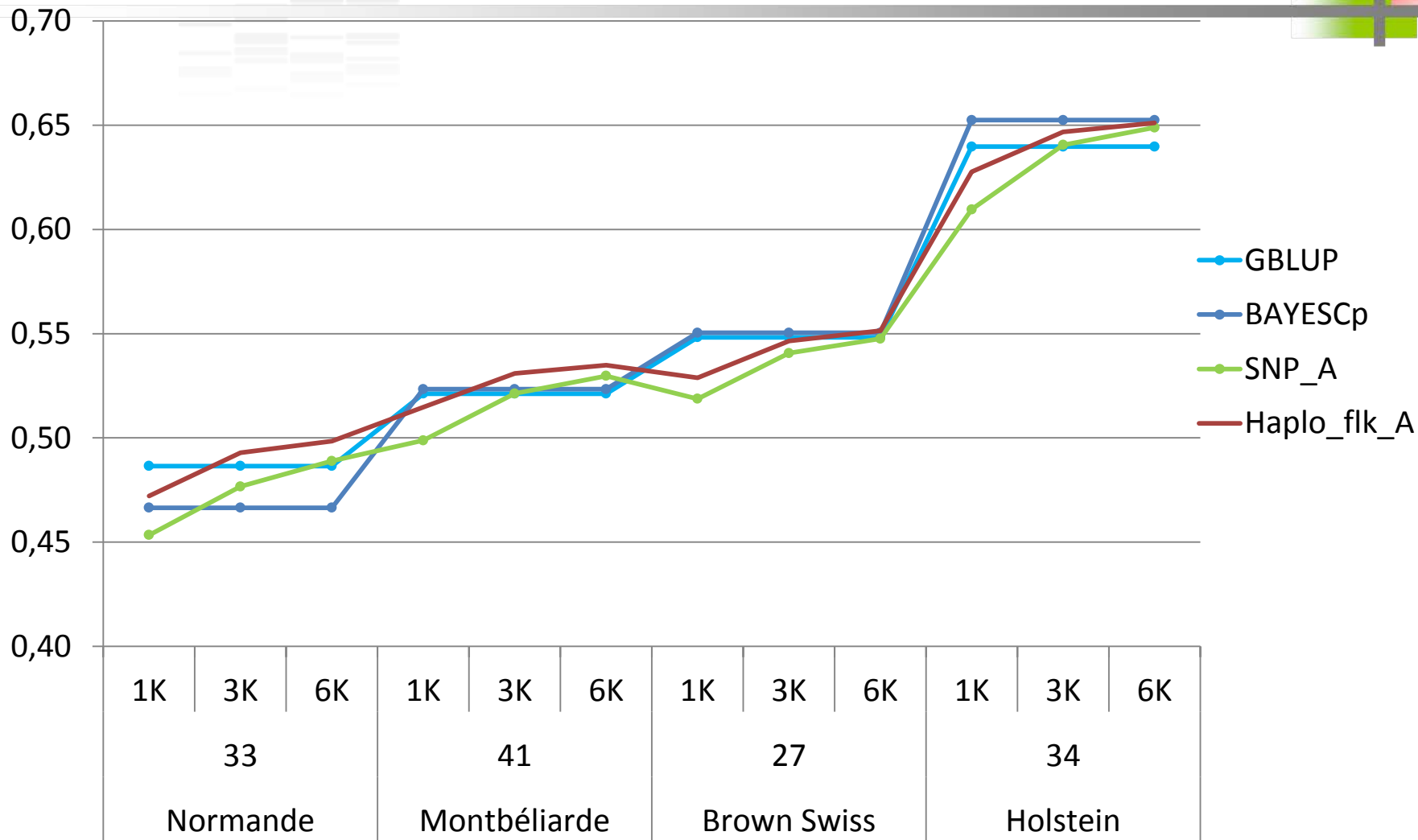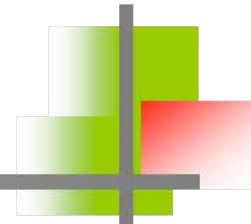
Validation results: all breeds

Legend: GBLUP, BAYESCp, SNP_A, Haplo_flk_A

	1K	3K	6K	1K	3K	6K	1K	3K	6K	1K	3K	6K
	33			41			27			34		
	Normande			Montbéliarde			Brown Swiss			Holstein		

Validation results: all breeds

Legend:
- GBLUP
- BAYESCp
- SNP_A
- Haplo_flk_A
- Haplo_sel_A
- Haplo_sel_G

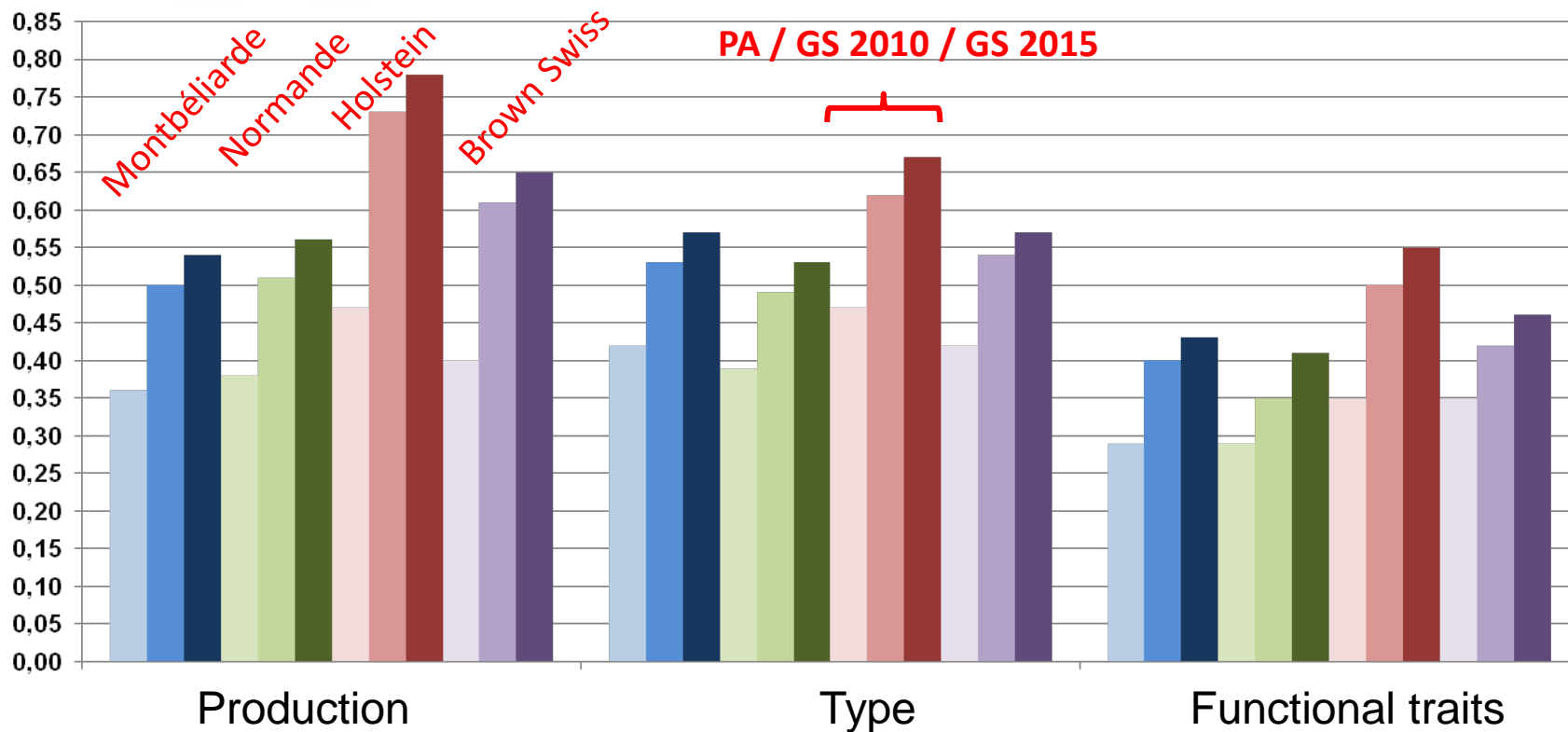|	1K	3K	6K	1K	3K	6K	1K	3K	6K	1K	3K	6K
	33			41			27			34		
	Normande			Montbéliarde			Brown Swiss			Holstein		
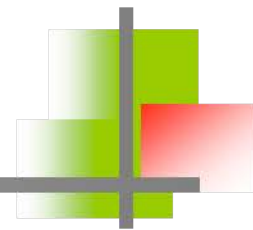
Validation results: all breeds

Validation results: all breeds

Validation results: overview
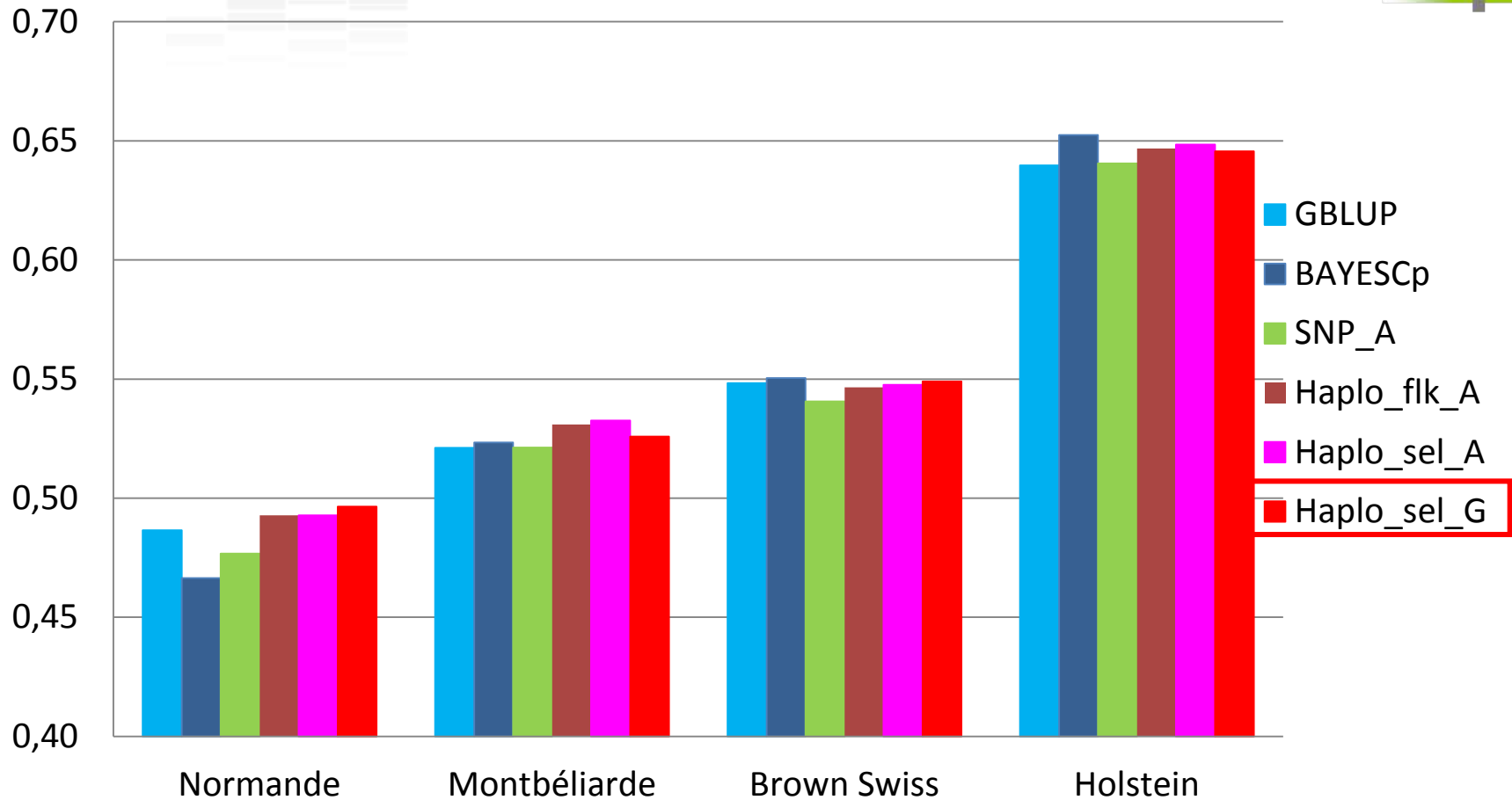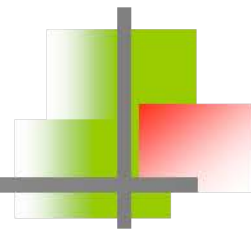
New evaluation: overall impact
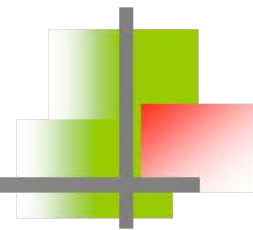
Correlations PA/GEBV at year t-4 and DYD at year t

> Increase in reliability: Normande: +0.11   Montbéliarde : +0.10
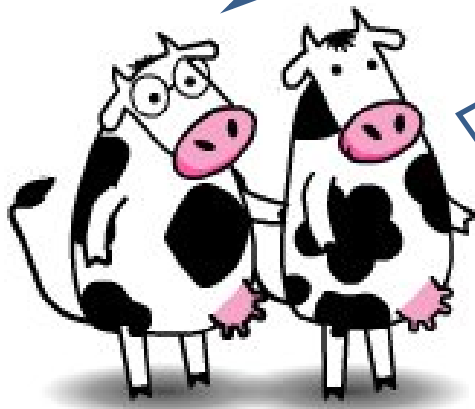> Holstein :   +0.08   Brown Swiss :   +0.11

A new genomic evaluation in Spring 2015

❖ Substantial gain in reliability

❖ Much faster, system size = constant

❖ much less sensitive to missing pedigree information, to absence of phenotypes of sires, to absence of foreign information

❖ easy to extend to include causal mutations

❖ also being developed for other French minor breeds
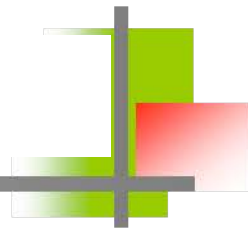
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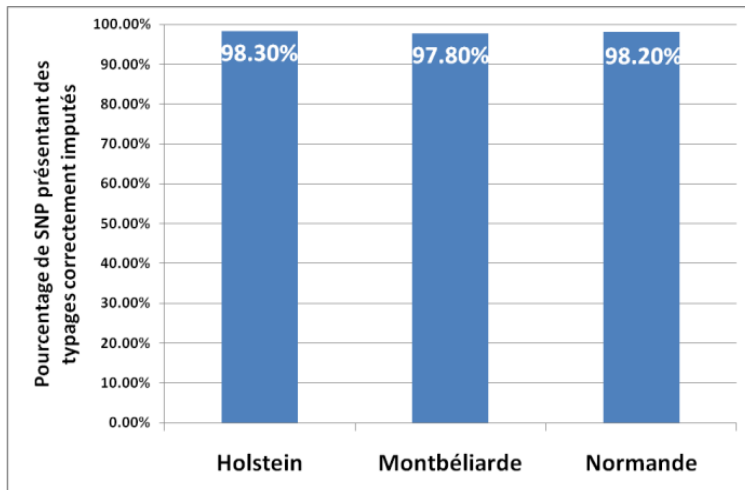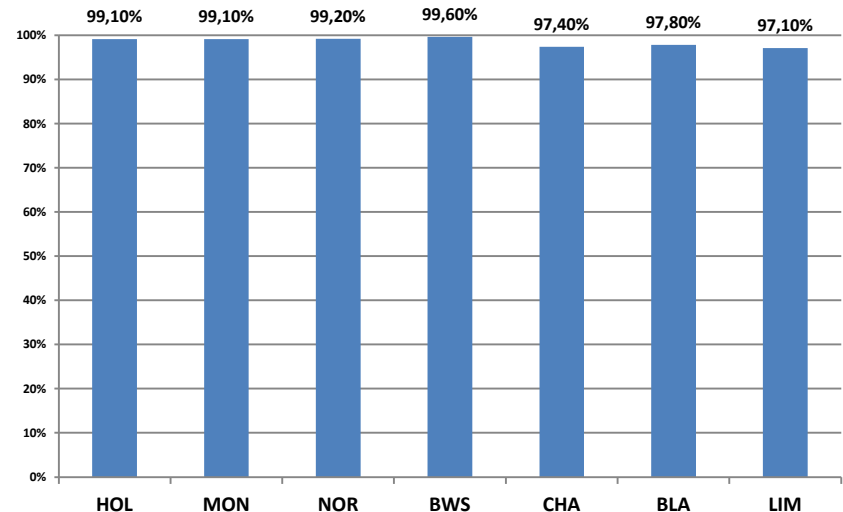
Imputation

Old situation

(Dassonneville et al., 2011)

with Fimpute

(Saintilan et al., 2014)

Computation time divided by 3 – 200-300 SNP/animal corrected