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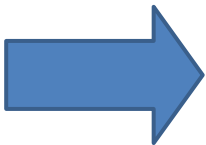
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Design of a low-density SNP chip for genomic selection in layer chickens

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Introduction – Context & Objective

- ▶ Since 2013, a commercial high-density SNP chip of 600 000 SNP for chicken is available
 - ▶ Enables implementation of genomic selection in layers production
 - ▶ But genotyping costs still remain high on a large number of selection candidates
 - ▶ Combining genotyping on low-density SNP chip and imputation should be considered
-  Main objective : To choose the best strategy for low density genotyping of laying hens to optimize selection scheme

Introduction – What is imputation ?

- ▶ Imputation « is t_e_rt_fg_es__ng_e_te__ » (Dassonneville, 2012)

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- ▶ Imputation « is **the art of guessing letters** » (Dassonneville, 2012)

Introduction – What is imputation ?

- ▶ Imputation « is the art of guessing letters » (Dassonneville, 2012)
- ▶ In our case, it is deduction of HD genotyping of selection candidates from their LD genotyping and HD genotyping of reference population (Dassonneville, 2012)

	SNP i SNP j SNP k																	
Individual 1	A	C	G	G	G	A	G	C	T	C	A	T	C	G	C	A	T	C
	T	G	A	C	A	G	C	T	C	G	A	G	T	C	T	G	C	T

- ▶ Imputation relies on the rules of Mendelian transmission of the traits and on linkage disequilibrium in the population.

Material & Methods – Study populations

- ▶ 2 different lines of Rhode Island (RI) and Leghorn (L).
- ▶ Both genotyped on HD SNP Chip.
- ▶ Respectively 300 351 and 245 667 SNP retained and distributed on the genome for RI and L.

Line	Rhode Island	Leghorn
Number	1027	1474
Sires	1027 ♂	561 ♂
Dams	0 ♀	913 ♀
Generation 0 (G0)	447	711
Generation 1 (G1)	580	763

Material & Methods – Low-density SNP chips

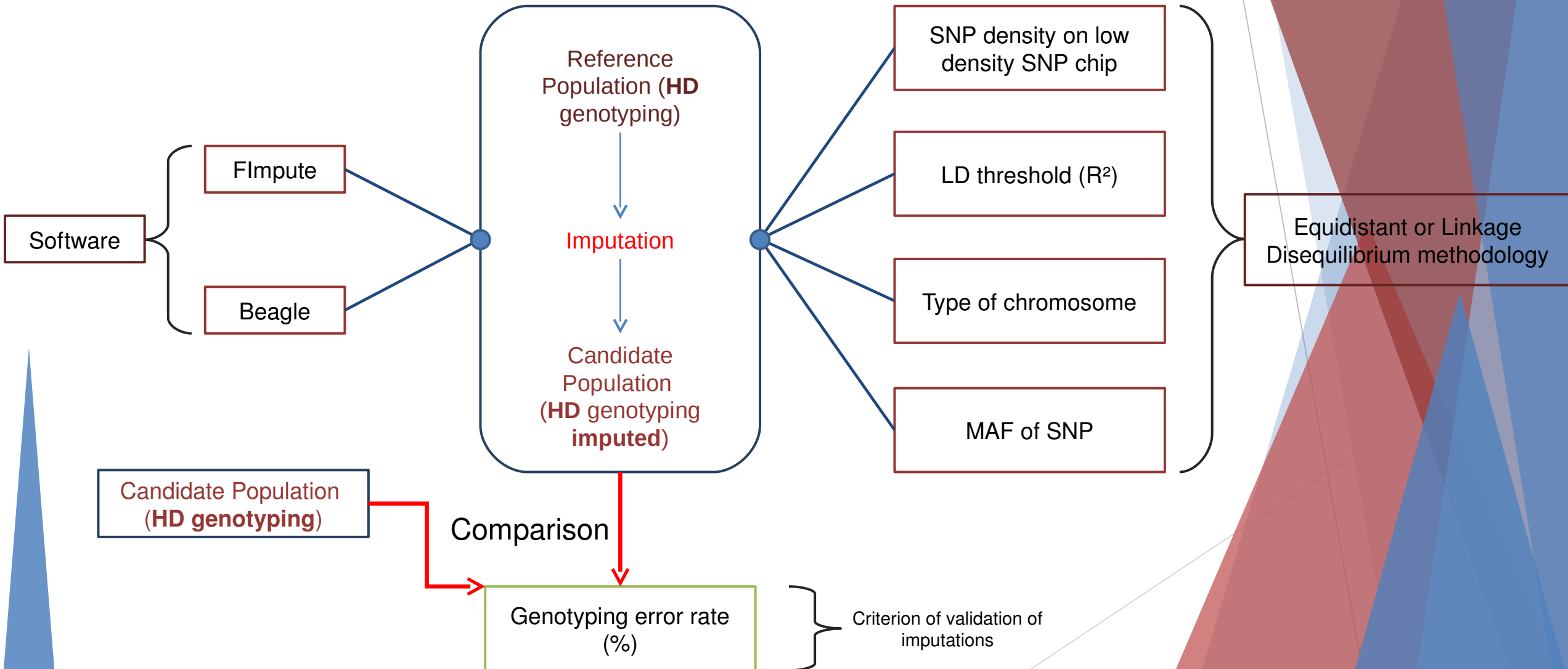
- ▶ Simulation of low-density SNP chip according to 2 different intra-chromosomes methodologies:
 - ▶ « Equidistant » methodology: Selection of SNP at regular intervals, taking into account MAF of SNP
 - ▶ 11 low-density SNP chips are designed from 50K to 2K SNP
 - ▶ « Linkage disequilibrium » methodology: Selection of SNP according to the LD between SNP, by hierarchical clustering
 - ▶ Select SNP 4 Imputation
(https://forge-dga.jouy.inra.fr/projects/select_snp_4_imputation)
 - ▶ 7 low-density SNP chips are designed for a LD threshold (R^2) ranging from 0.2 to 0.8

Methodology	SNP Chip	Number of SNP	
		Rhode Island	Leghorn
Equidistant	50Kequi	49636	50307
	40Kequi	40160	39838
	30Kequi	29970	30075
	20Kequi	19910	19948
	15Kequi	14963	14955
	10Kequi	10001	9966
	7.5Kequi	7527	7496
	5Kequi	4991	4996
	4Kequi	4023	4000
	3Kequi	2992	3003
	2Kequi	2013	2004
Linkage Disequilibrium	DL0.8	21717	18052
	DL0.7	16615	13696
	DL0.6	13214	10736
	DL0.5	10711	8626
	DL0.4	8521	6944
	DL0.3	6875	5578
	DL0.2	5371	4330

Material & Methods – Imputation software

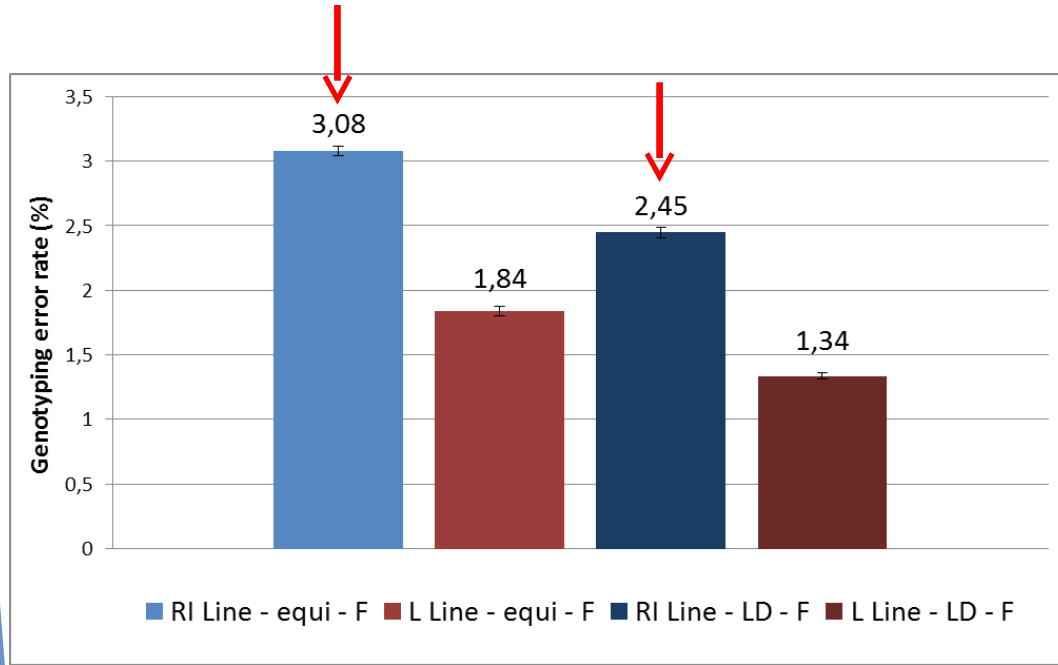
- ▶ Use of two software :
 - ▶ FImpute (Sargolzaei et al., 2014)
 - ▶ Beagle (Browning and Browning, 2009)

Material & Methods – Imputation strategies

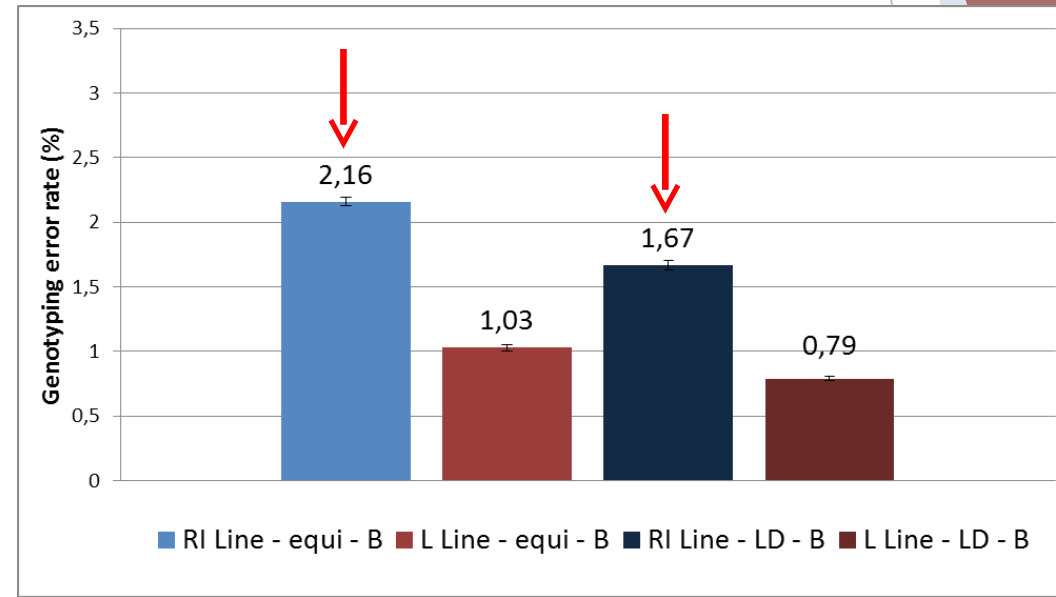


Results & Discussion – Comparison of software

Comparison between Fimpute (F) and Beagle (B) for both lines, at equivalent SNP density



Fimpute



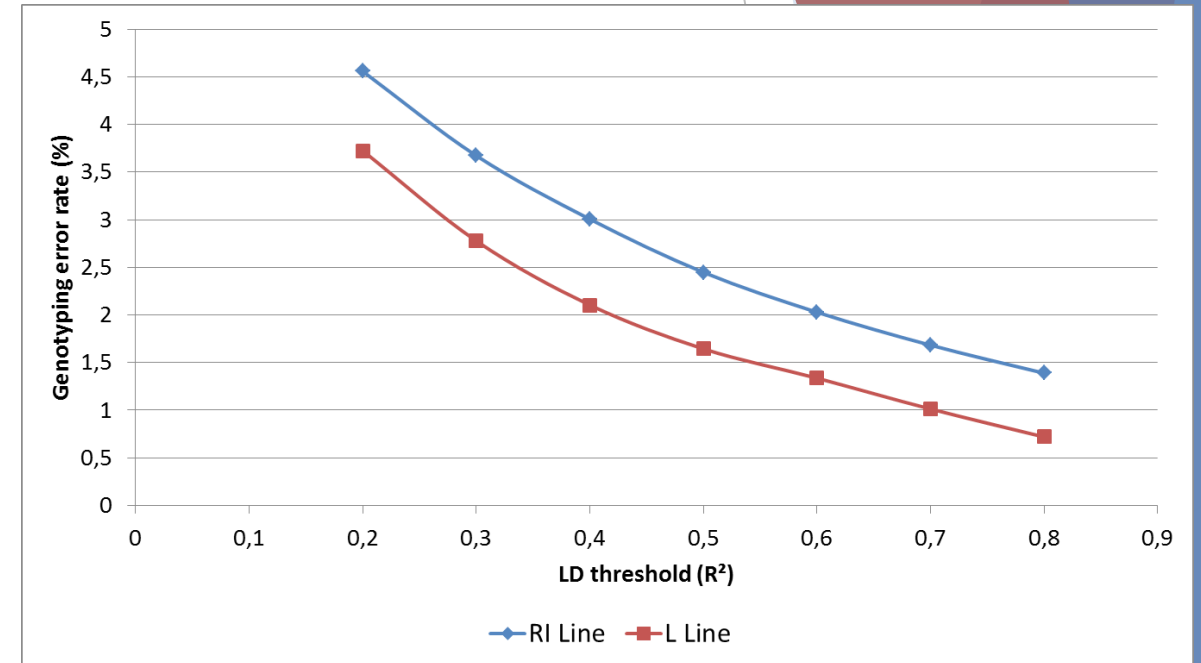
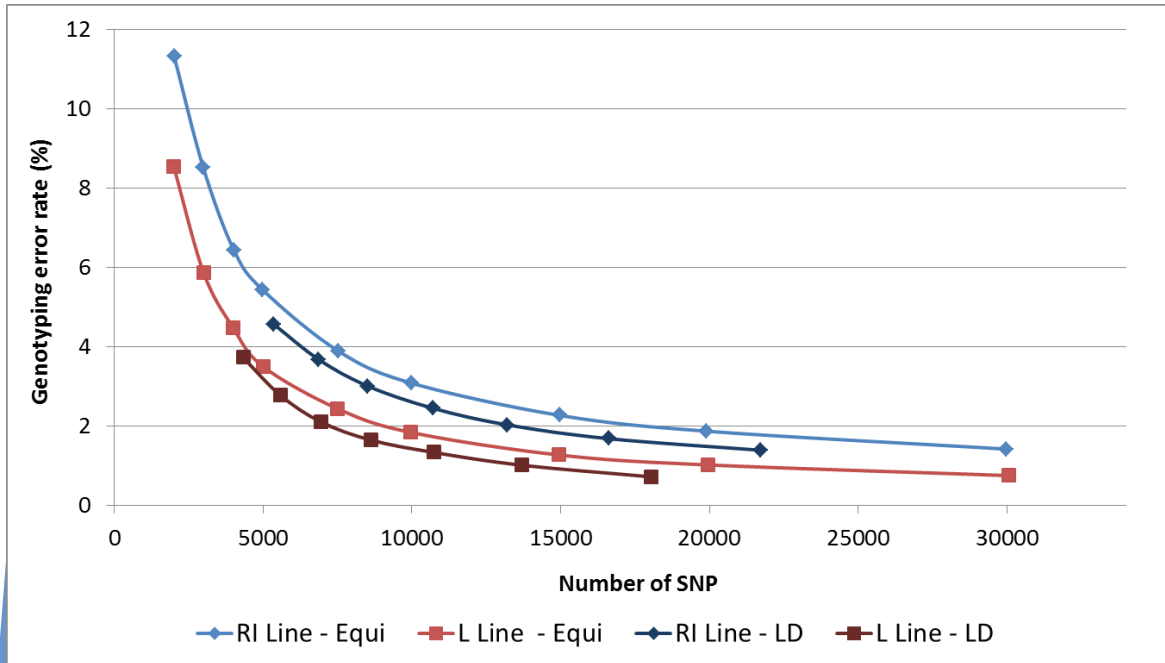
Beagle

- ▶ Beagle > Fimpute
- ▶ But Fimpute is far much faster than Beagle...

	Fimpute	Beagle
Execution Time (average)	5 minutes	12 hours



Results & Discussion – What kind of chip for imputations ?



- ▶ Decrease of genotyping error rate with an increase in the number of SNP
- ▶ Decrease of genotyping error rate with an increase in LD threshold (R^2)

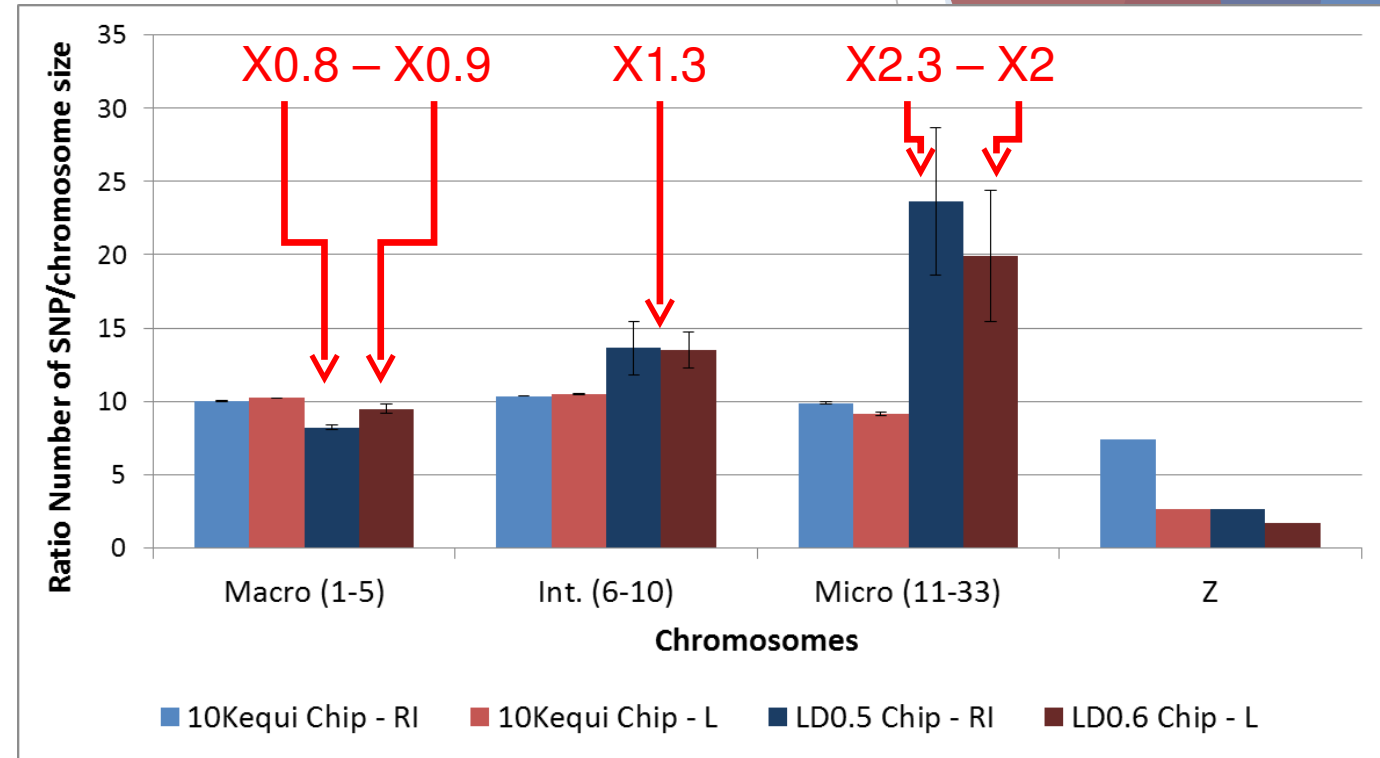


« LD » methodology seems to be better than « equidistant » methodology to get good imputations.

Results & Discussion – What kind of chip for imputations ?

- ▶ Structure of the poultry genome:

- ▶ Macro: High extent of LD few SNP to cover the chromosome
- ▶ Micro: Low extent of LD more SNP to cover the chromosome

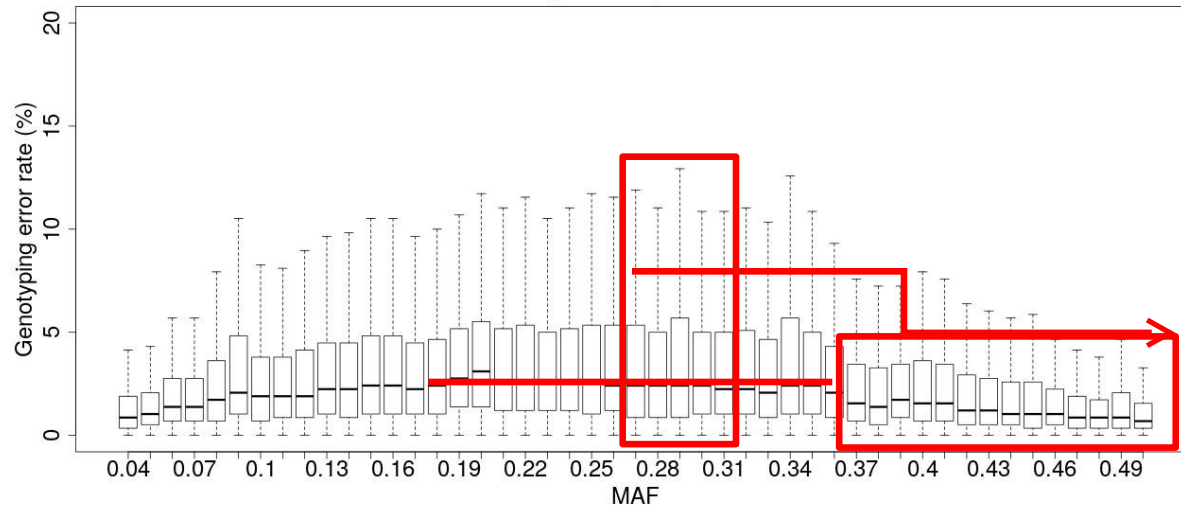


- ▶ With « LD » methodology:

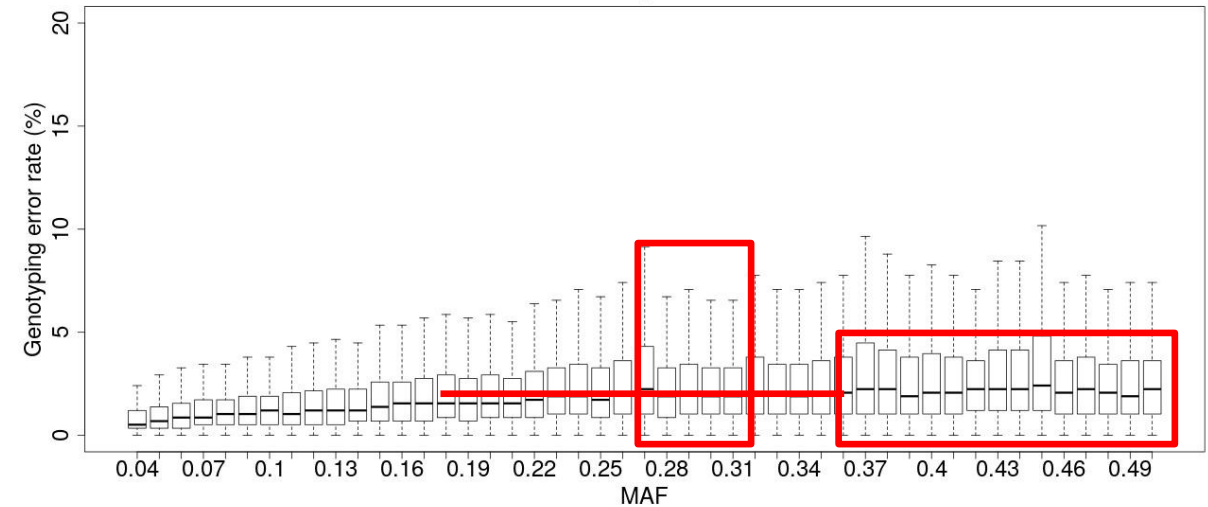
- ▶ Optimization of the number of SNP on macro-chromosomes
- ▶ Densification of the number of SNP on micro-chromosomes

Results & Discussion – Influence of MAF

10Kequi Chip - RI Line



LD0.5 Chip - RI Line



- ▶ Higher variability of genotyping error rate with equidistant methodology.
- ▶ Lower genotyping error rates with LD methodology.
- ▶ Decrease of genotyping error rates of SNP with high MAF with equidistant methodology.
- ▶ Valid for both lines.

Conclusion

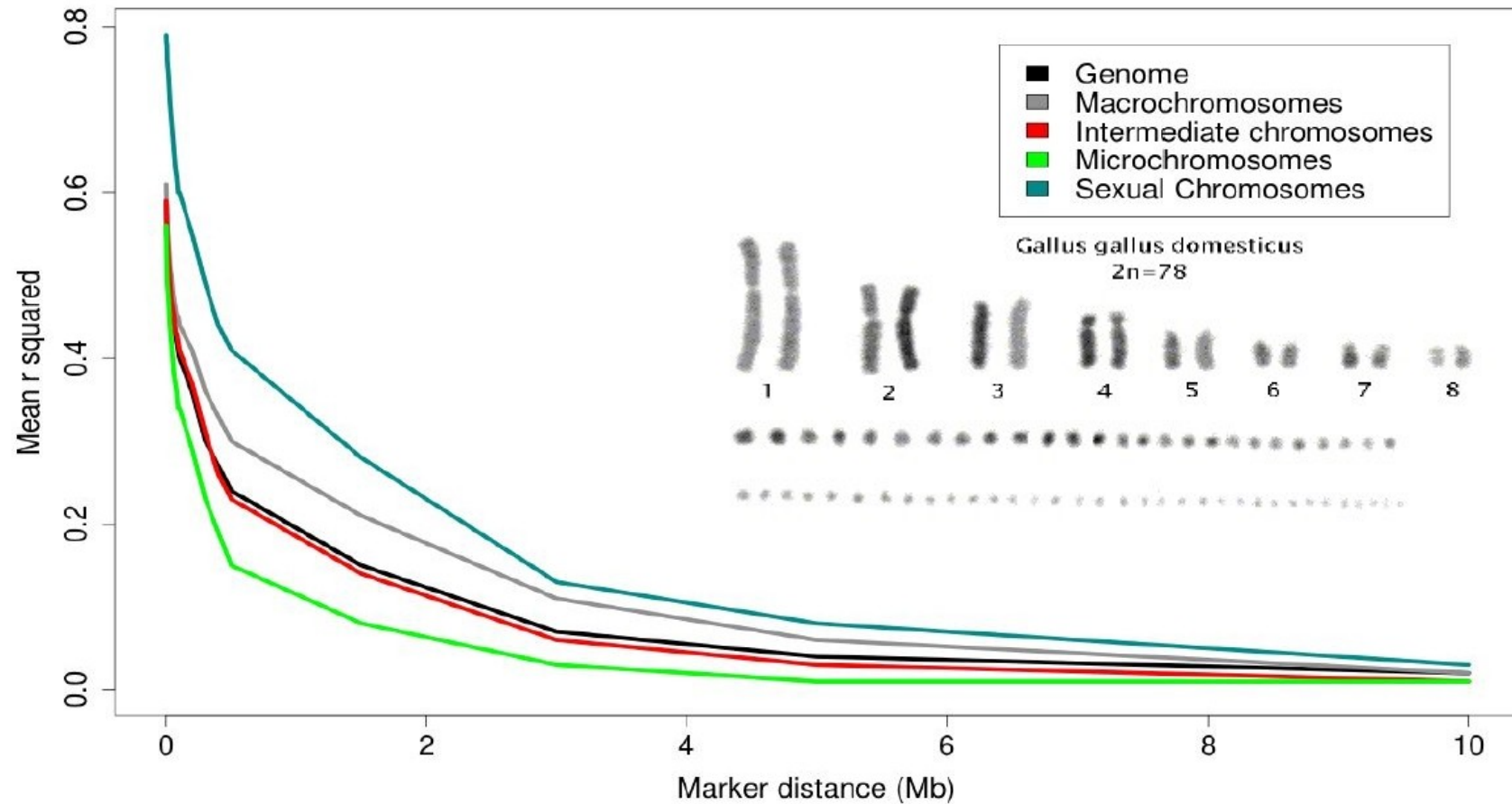
- ▶ Consideration of the particular structure of chicken species' LD with LD methodology.
- ▶ Better results of imputation with low-density SNP chip based on LD.
- ▶ According to the MAF, lower genotyping error rates with LD methodology, excepted for SNP with high MAF.
- ▶ Soon :
 - ▶ Creation of a multi-line chicken low-density SNP chip
 - ▶ Study of its imputation accuracy
 - ▶ Study of the impact on genomic evaluations

Thanks for your attention !



Particular extent of LD

Extent of LD across genome



Robert et al., 2015

Distribution of SNP on sexual chromosome Z

