Sequence-based genetic map reveals similar recombination patterns on macro- and microchromosomes in chicken

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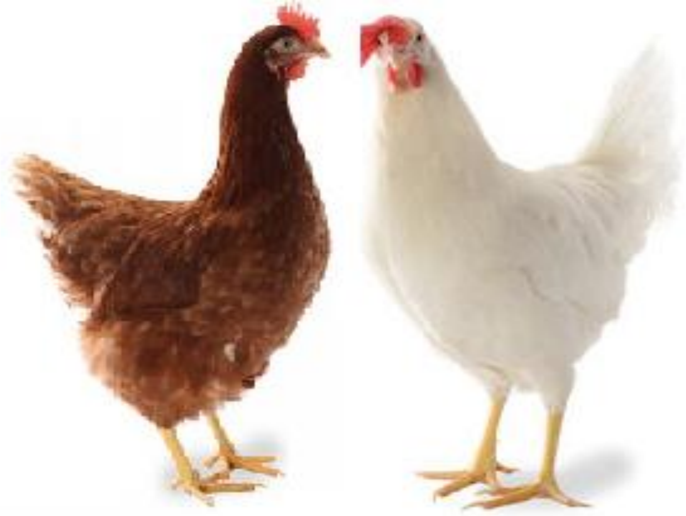
Outline

Sequence-based analysis of two chicken populations

1. Linkage disequilibrium
2. Ancestral demography
3. Recombination landscape

Remarks and conclusions



Background

- High-resolution genetic maps are key elements of
  - successful fine mapping programs.
  - assemblies of whole-genome sequences
  - comparative genome analysis
- The available pedigree-based maps of the chicken genome have poor resolution

Motivation:

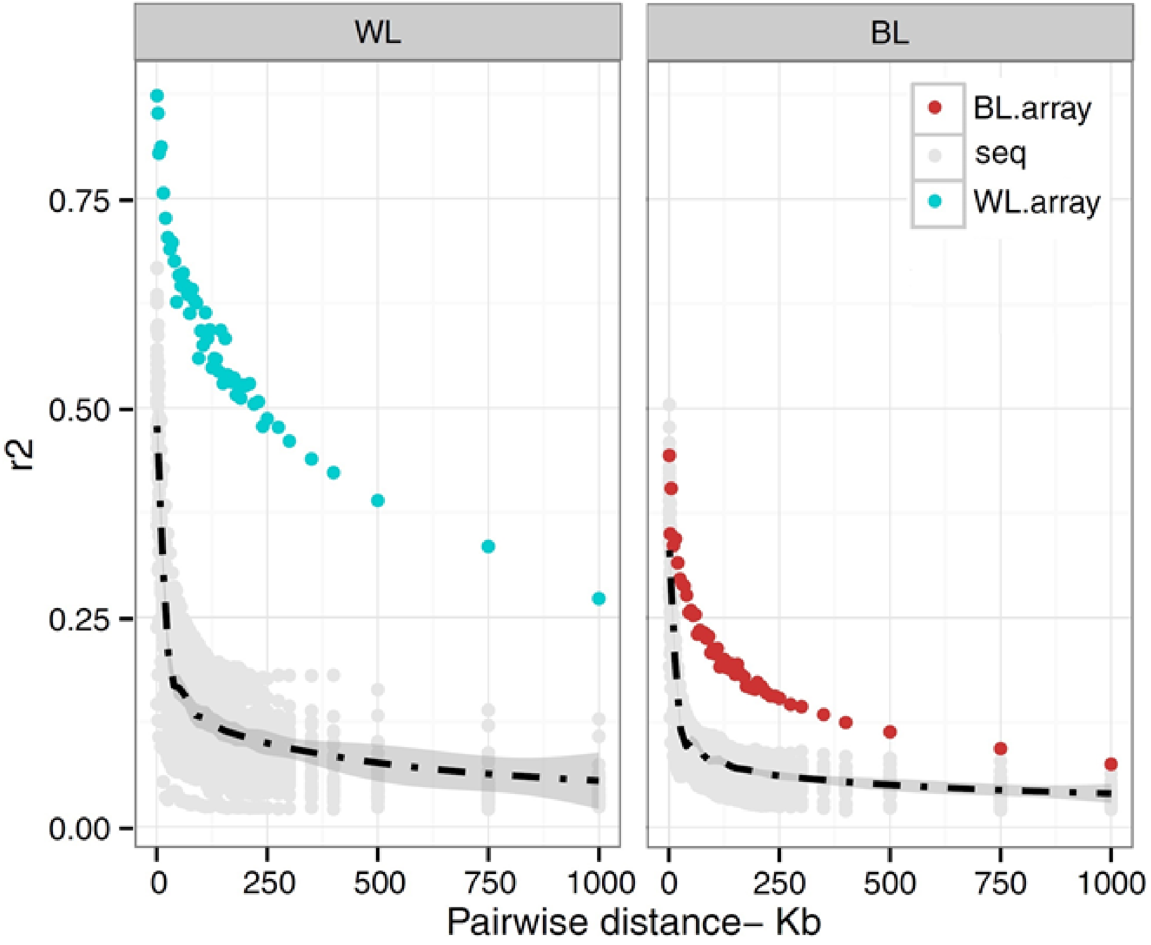
Constructing the first sequence-based linkage map of chicken.

Genetic material:

- Two pops of White (WL) and Brown (BL) egg layers.
- 2 x 25 DNA (hens) were sequenced (coverage ≈ 10 folds)
- Final panel of SNPs involved > 9.3 mio
- Mean inter-marker space = 107 bp
- + 4 Red Jungle Fowls (RJF) sequenced

  (coverage ≈ 10 folds)

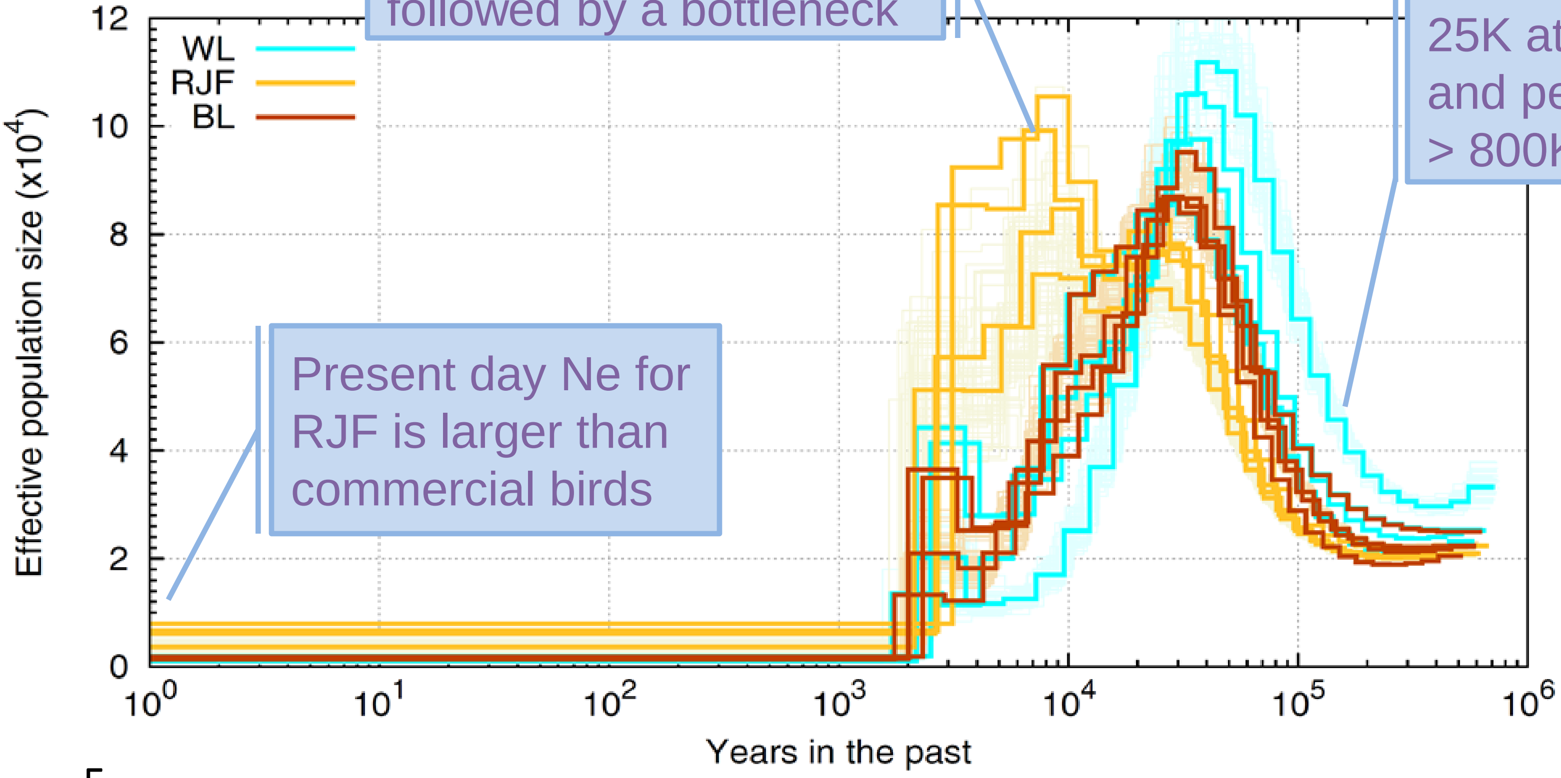
1. Linkage Disequilibrium (LD)



- ✓ LD in WL is stronger than BL
- ✓ [sequence based] LD decays at a much faster rate than previously thought.
- ✓ 3. level of LD is ~comparable to cattle or human

2. Ancestral demography

- ✓ Historical Ne was estimated in PSMC framework (Li and Durbin 2011).



Ne was largest at the time of domestication followed by a bottleneck

Historical Ne ≈ 25K at 1 mya and persisted for > 800K years

Present day Ne for RJF is larger than commercial birds

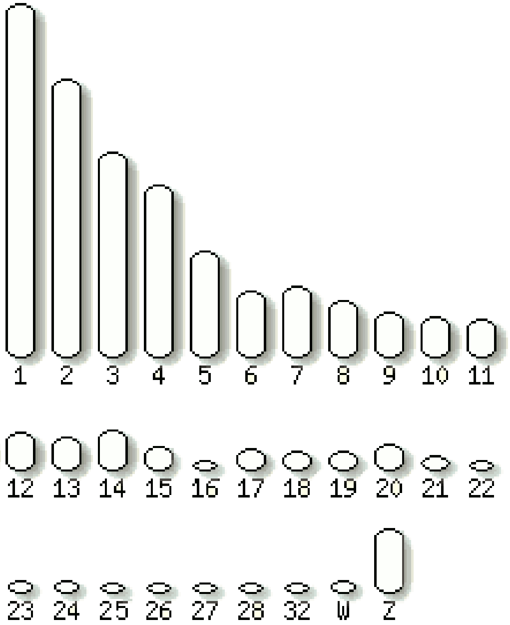
3.1. Recombination rates (ρ)

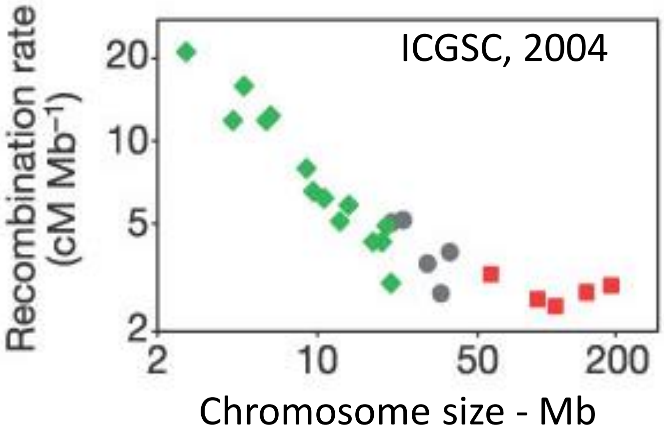
- LDhat 2.2 (McVean & Auton 2011) used to estimate rec- rates $\rho = 4Ner$
- The map length ≈ 3.39 cM Mbp^{-1}, consistent with pedigree based maps.

Table 1. A summary of recombination rates estimated along GGA1-28.

Chr	Mb		White layer			Brown layer			Mean
			cM	cM Mb^{-1}		cM	cM Mb^{-1}		
1	195.3		723.17	3.70		626.59	3.2		3.45
2	148.8		626.57	4.21		439.36	3.0		3.61
3	110.4		209.63	1.90		300.17	2.7		2.30
9	23.4		39.41	1.68		27.54	1.2		1.44
10	19.9		65.17	3.27		36.83	1.8		2.54
26	5.3		9.96	1.87		12.91	2.4		2.14
27	5.2		29.66	5.69		12.91	2.5		4.10
28	4.7		13.28	2.80		19.52	4.1		3.45
Autosomes	**923.3**		**2560.28**	**3.17**		**2732.18**	**3.6**		**3.39**

3.2. Genome heterogeneity

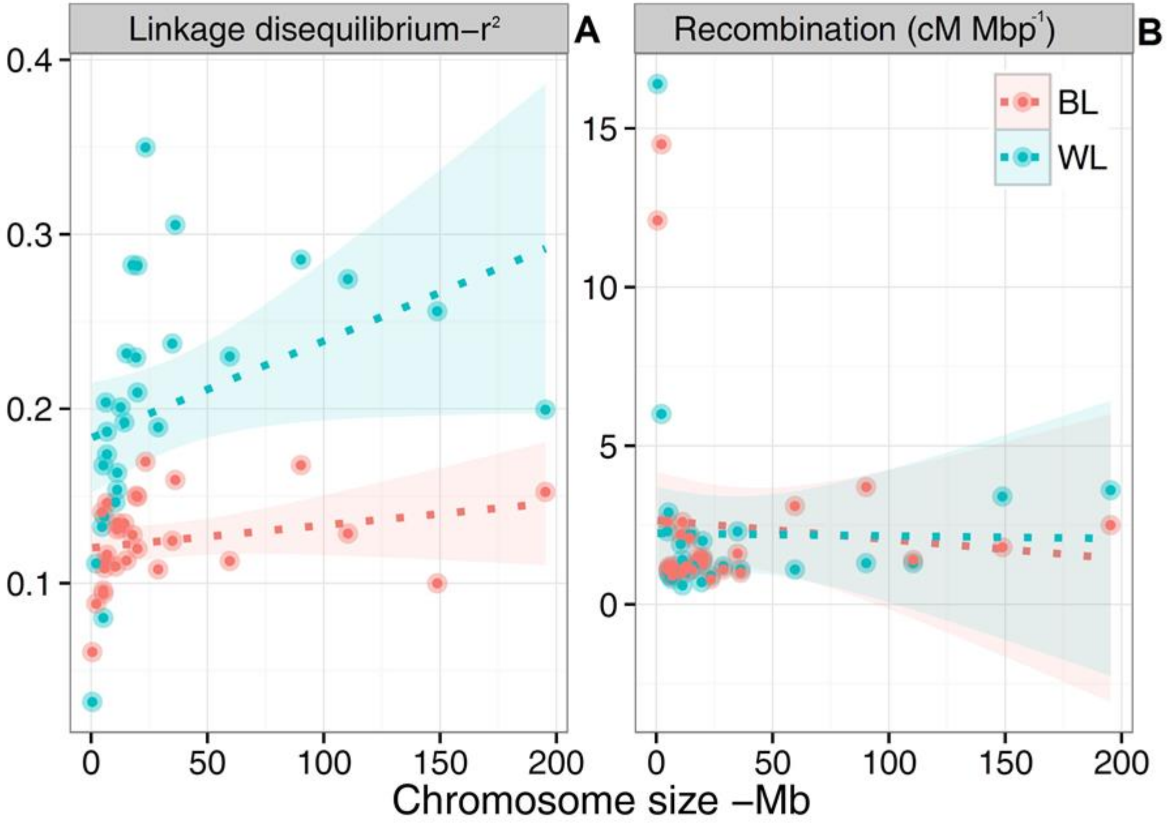




ICGSC, 2004

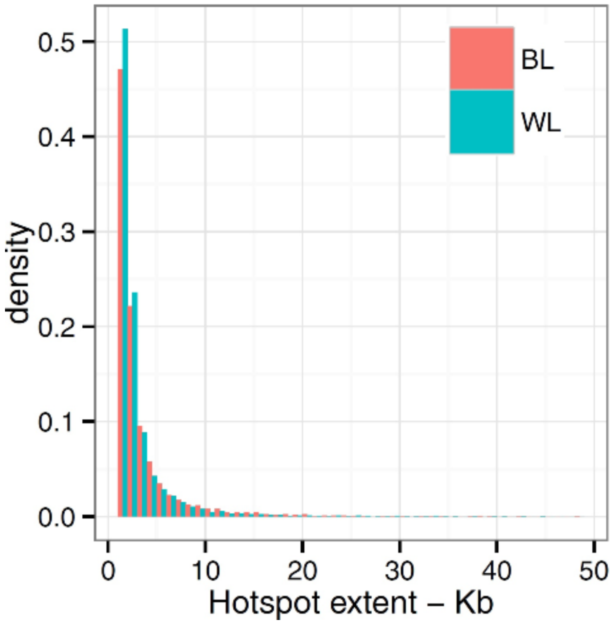
(*P* = 0.07)

(*P* = 0.68)



3.3. Analysis of hotspots

- In average 75% of recombination emerges from 12% of genome.
- We defined a hotspot as recombination rate > $5\bar{\rho}$.
- Hotspots had a density of one every 100Kb >>> ~8000 hotspots
- The median length of the identified hotspots was 2 kb
- Only 27.4% of hotspot overlapped in two pops.

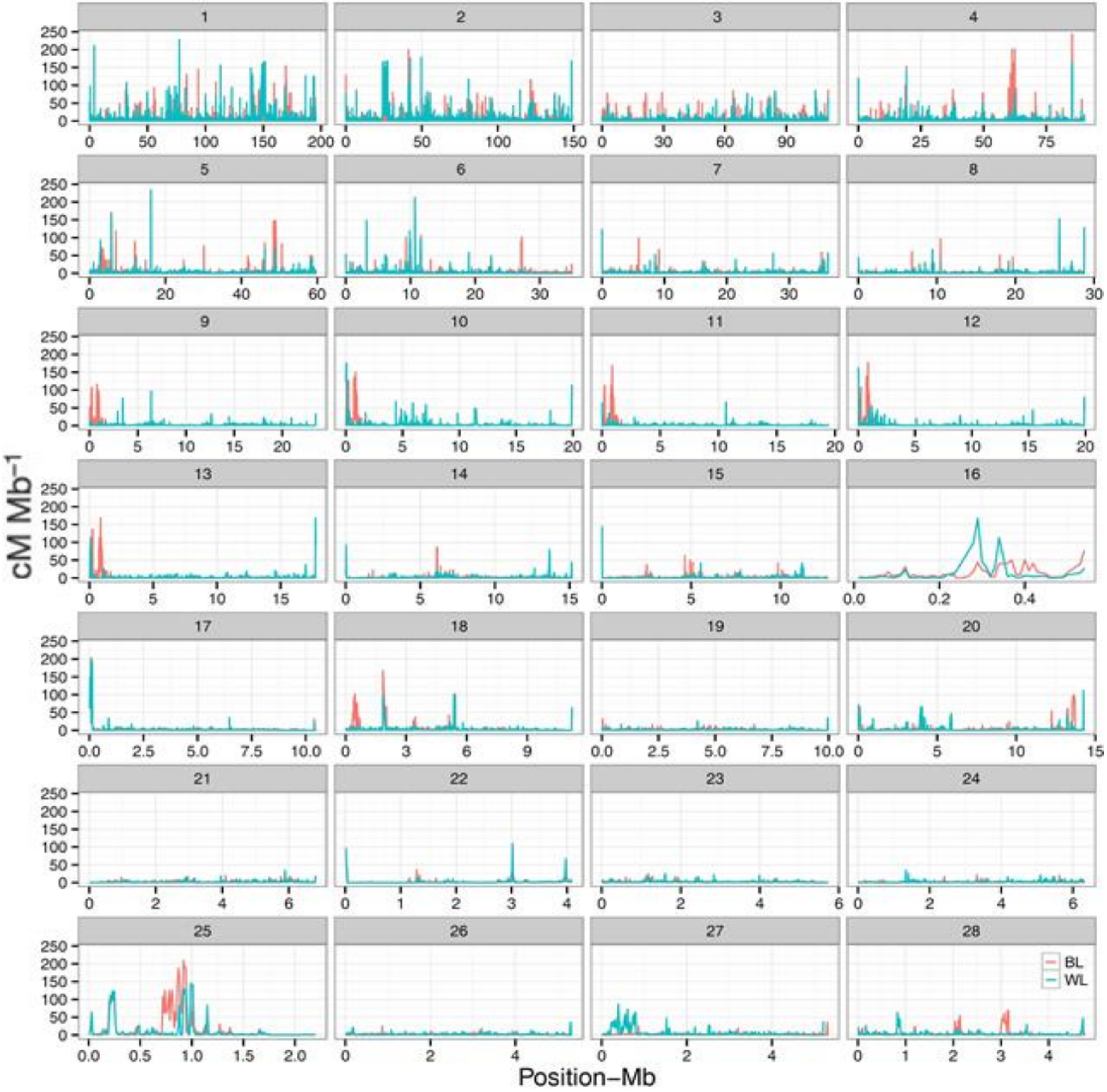


- **Frequency of hotspots/Mb was similar on micro vs., macr-chromosomoes (*P* = 0.52)**

Remarks and conclusion

- The first ultra-dense recombination map of the chicken genome
- LD in chicken decays at a much faster rate than previously thought.
- Importantly, through three lines of evidence derived by examining LD ($P = 0.07$), ρ ($P = 0.68$) and hotspot density ($P = 0.52$) we show **insignificant difference** between macro vs., microchromosomes !

THANK YOU FOR ATTENTION ☺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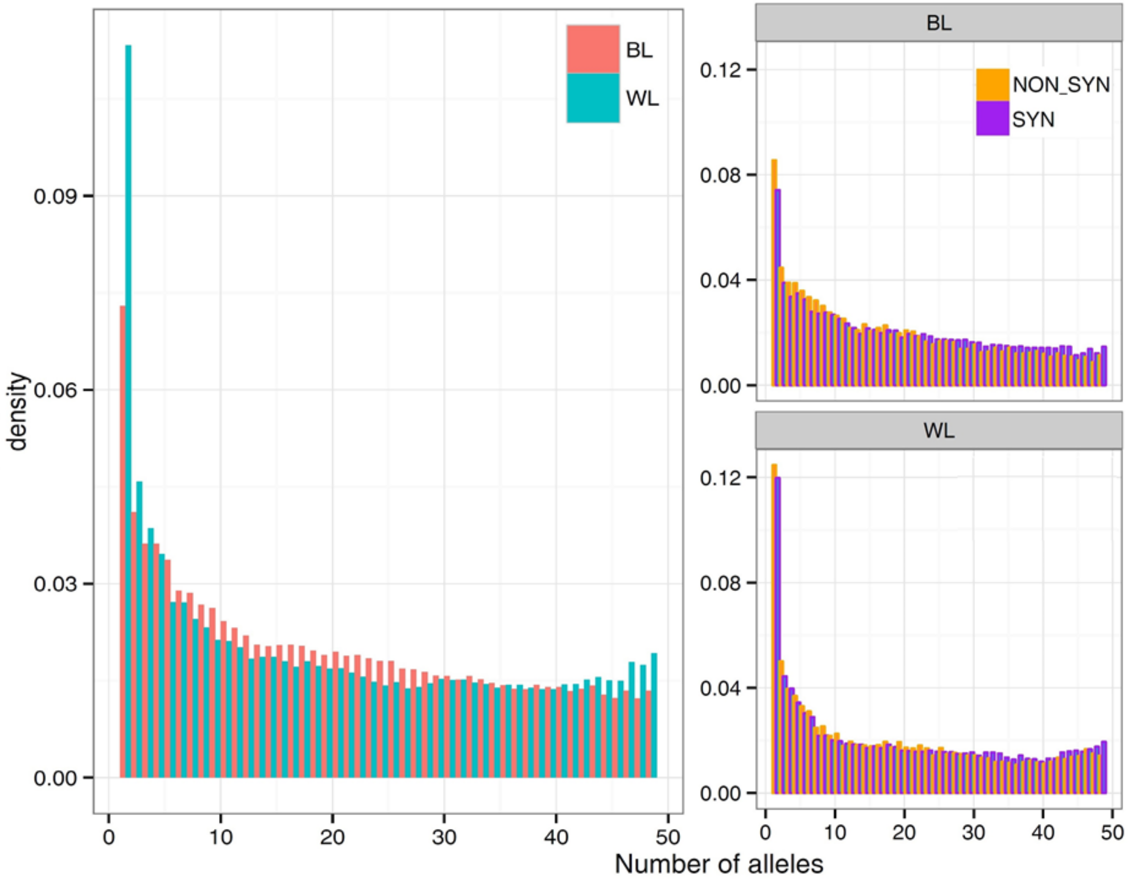
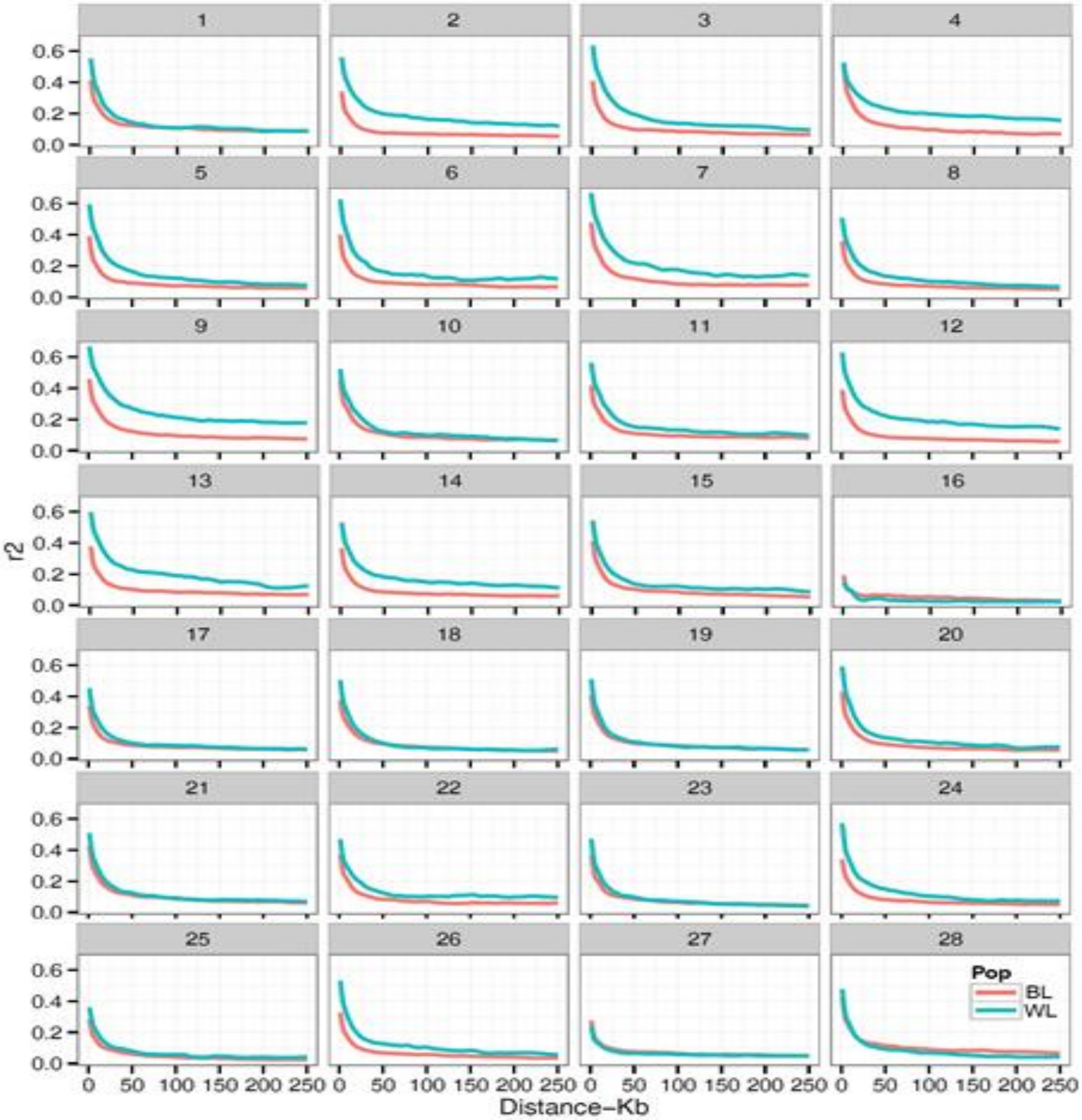
cM Mb⁻¹
Position–Mb
BL
WL

Allele frequency distribution

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Distance-Kb
Pop
BL
WL

Recombination and sequence features