



A genome-wide association study to identify novel genomic regions associated for aviary with winter garden usage by laying hens

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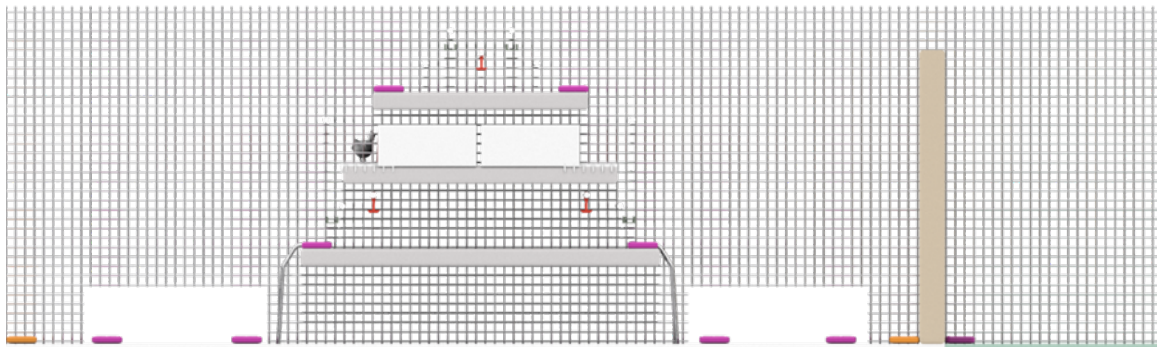
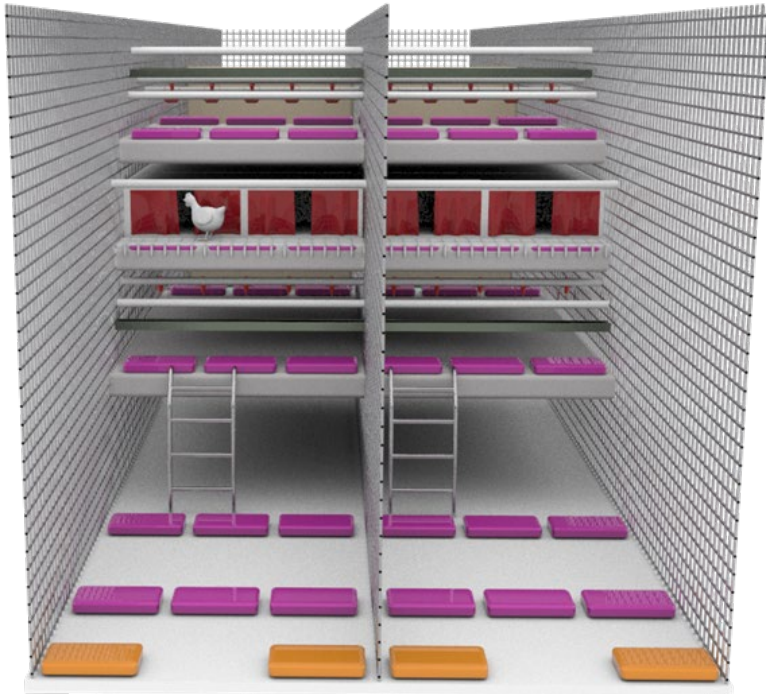
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Background

- Commercial egg production has transitioned away from cages and towards free run systems
 - One common cage-free housing system is an aviary
- Selection has not kept up with this transition in industry



Background – movement behaviour



Zone 5: Highest Tier
Feed, water, perches
Nighttime roosting

Zone 4: Middle Tier
Nestboxes, perches

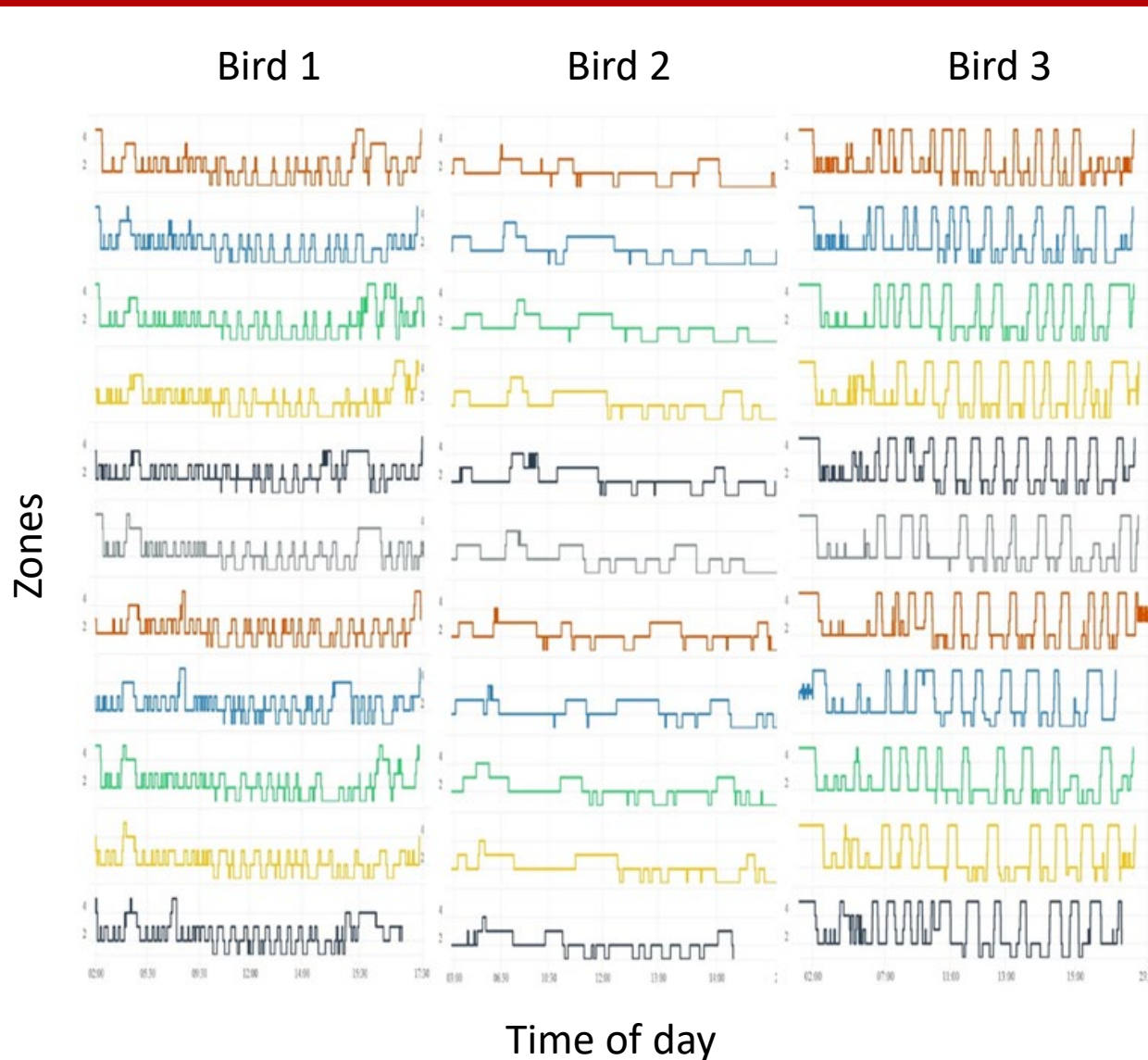
Zone 3: Lowest Tier
Feed, water, perches

Zone 2: Floor
Litter

Zone 1: Wintergarden
Water, perches



Background – movement behaviour



Zone 5: Highest Tier
Feed, water, perches
Nighttime roosting

Zone 4: Middle Tier
Nestboxes, perches

Zone 3: Lowest Tier
Feed, water, perches

Zone 2: Floor
Litter

Zone 1: Wintergarden
Water, perches



Background – duration phenotypes

Table 2. Estimates of residual variances (σ_e^2), additive genetic variances (σ_a^2), permanent environment variances (σ_{pe}^2), heritability (h^2), and repeatability (re) (standard errors are in parentheses).

Zones ¹	σ_e^2	σ_a^2	σ_{pe}^2	h^2 (%)	re (%)
TLT	40,901.30	5,779.55	13,867.10	9.55 (1.73)	32.45 (1.04)
NBT	292.82	42.50	36.43	11.43 (1.49)	21.23 (0.92)
LLT	29,034.00	1,919.53	5,308.19	5.29 (1.06)	19.93 (0.76)
LIT	5,805.73	3,402.53	3,151.02	27.53 (3.21)	53.03 (1.33)
WG	722.39	103.15	235.37	9.72 (1.81)	31.91 (1.06)

¹Top level tier (TLT), nest box tier (NBT), lower level tier (LLT), floor littered area (LIT), winter garden (WG).

(Makanjuola et al., 2024)

Objective

Further investigate traits for duration in different zones of an aviary and identify genomic regions associated with zone usage

Material and methods

- 1,098 white laying hens investigated in study
 - Dekalb parental lines
 - Housed in 5 pens
- Records from ~ 18 – 59 weeks of age
 - Monitored for 15 hours a day
- Hens genotyped using 60K SNP panel (Illumina Inc. 60K)



Univariate linear mixed model

$$\mathbf{y} = \mathbf{W}\boldsymbol{\alpha} + \mathbf{x}\boldsymbol{\beta} + \mathbf{u} + \mathbf{e},$$

$\mathbf{y}$: vector of phenotype for average duration in zone over weeks 18 - 59 of age, as well as in 50-day segments

$\mathbf{W}$: matrix of fixed effects of the top 2 PCs, number of visits to the zone, and pen number

$\boldsymbol{\alpha}$: vector of coefficients of fixed effects

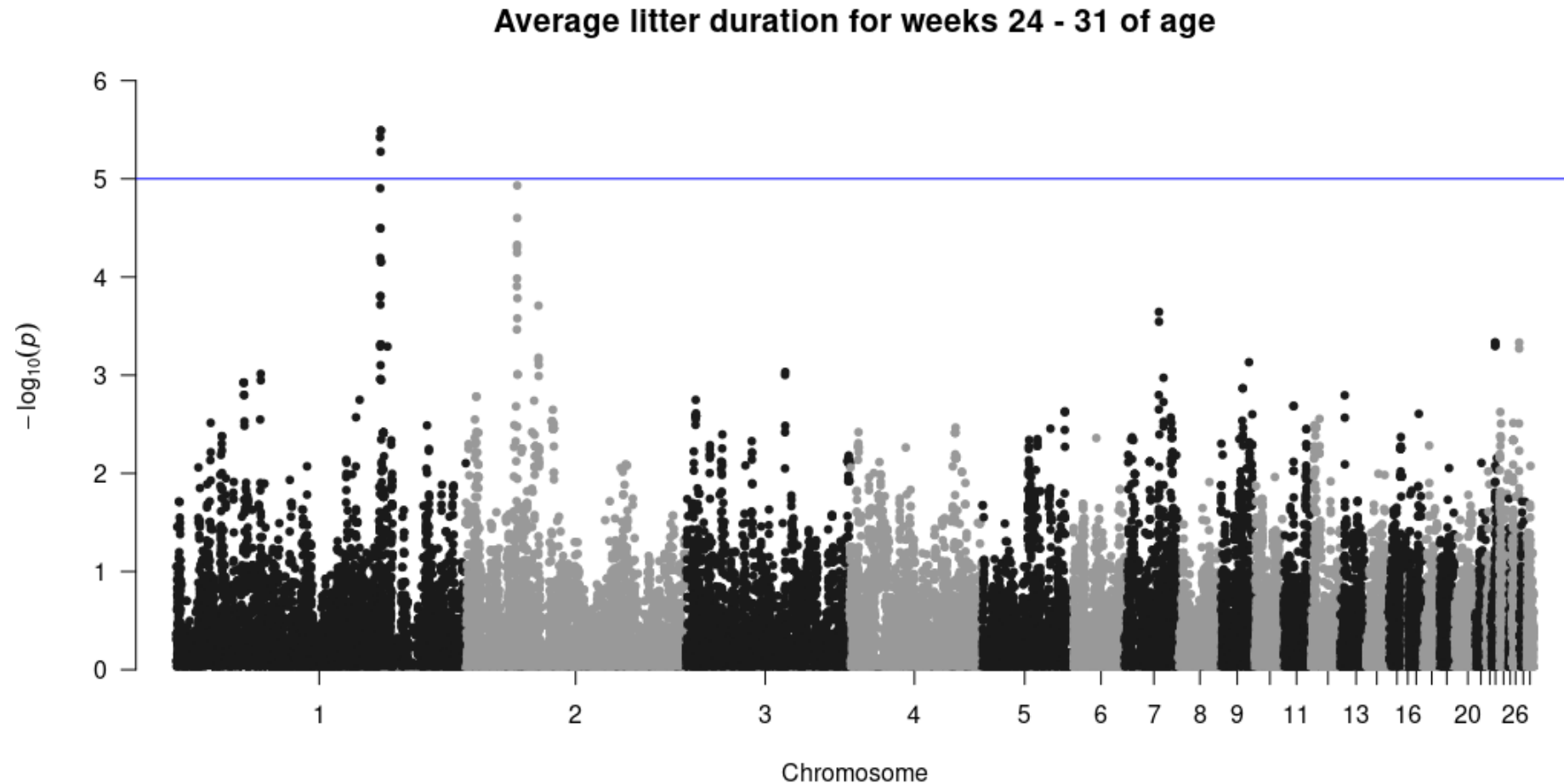
$\mathbf{x}$: vector of marker genotypes

$\boldsymbol{\beta}$: effect size of the marker

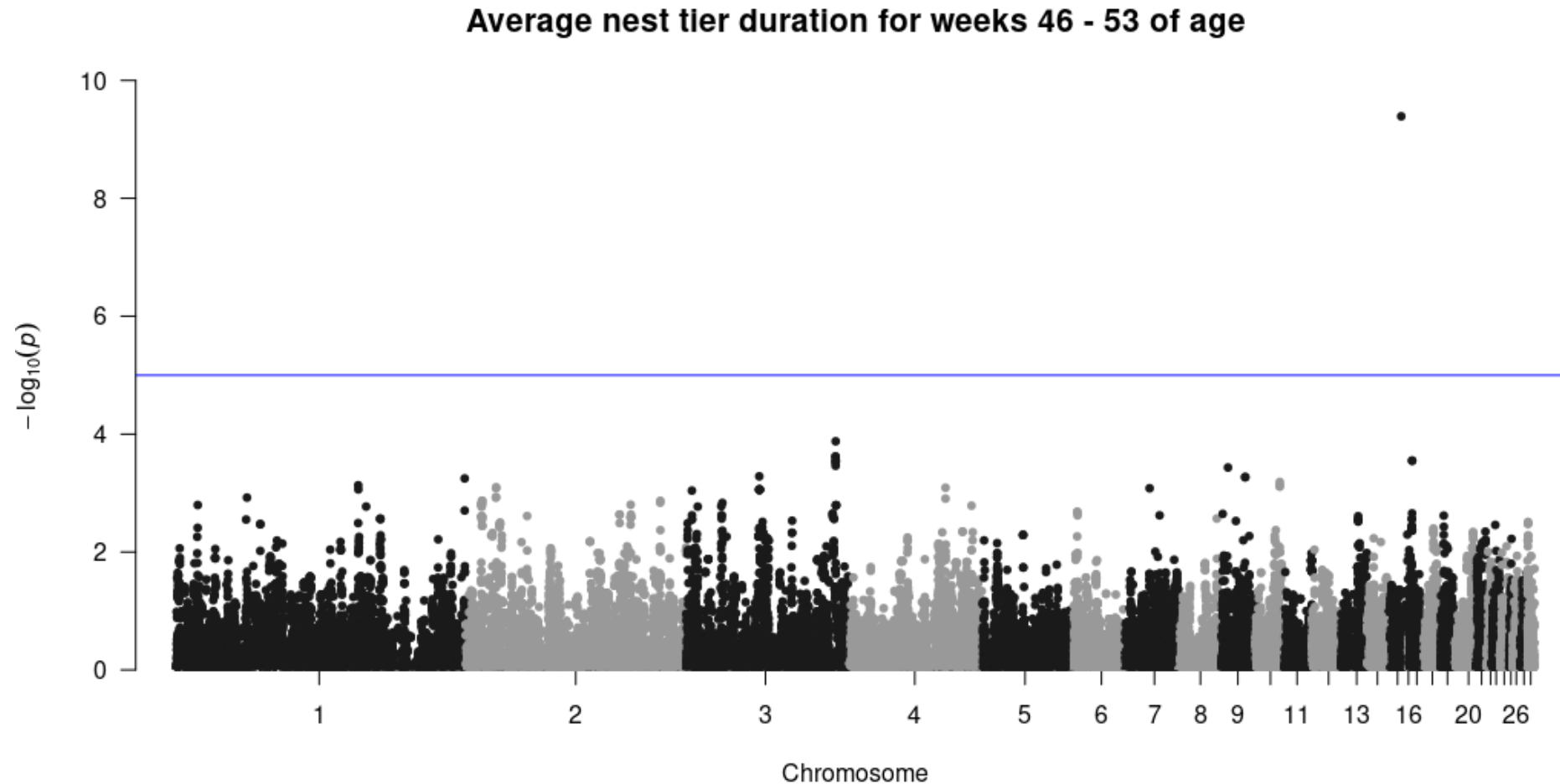
$\mathbf{u}$: vector of random polygenic effects

$\mathbf{e}$: vector of random residuals

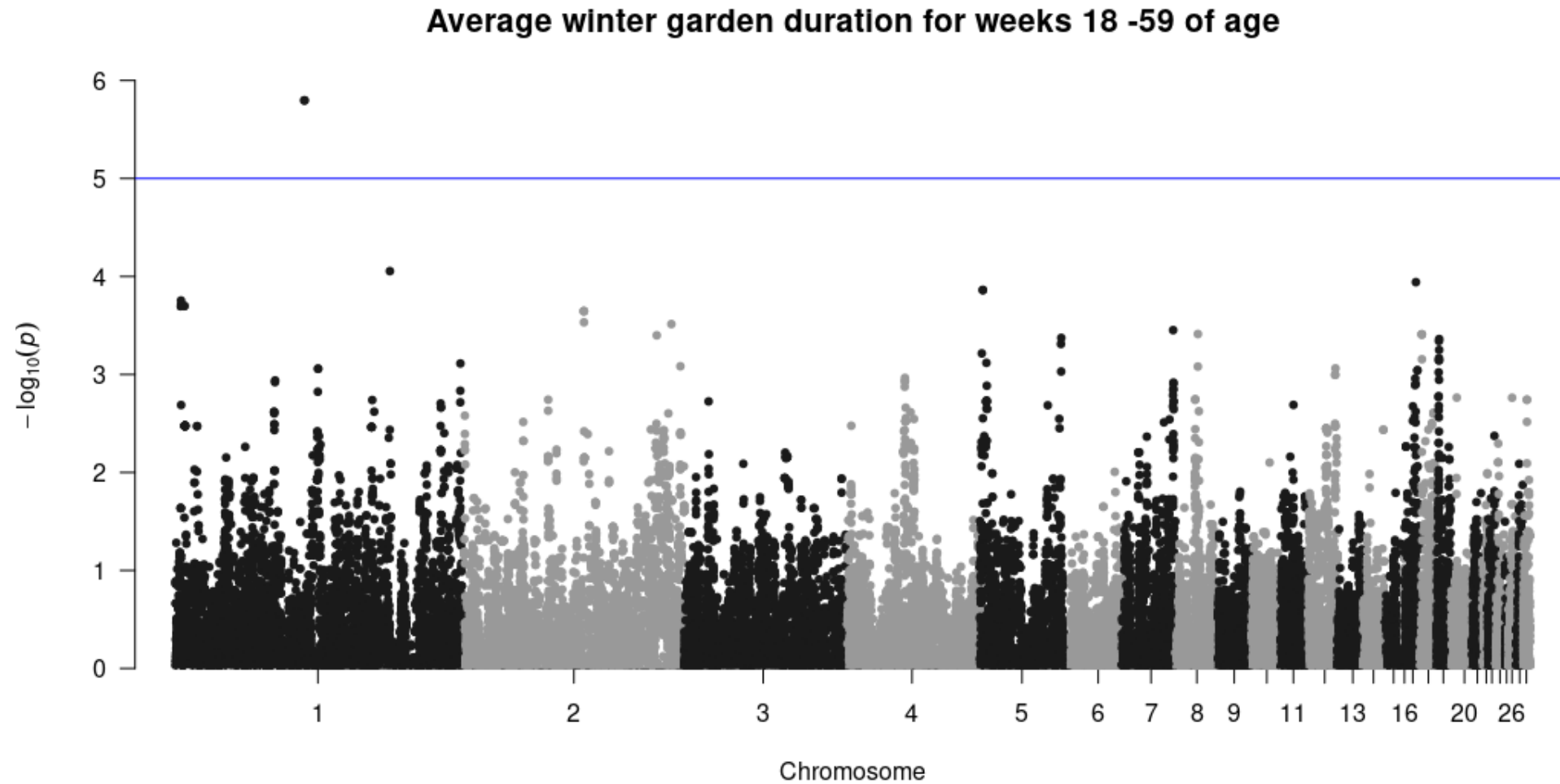
Manhattan plot for duration in litter



Manhattan plot for duration in nestbox tier



Manhattan plot for duration in winter garden



Results from GWAS

Zone	Chromosome	SNP	SNP location	Effect	P value	Gene name	Gene distance
Litter	1	HGC005373	137,872,259	1,714.28	3.12E-06	ATP11A -ATPase phospholipid transporting 11A	Within
						TUBGCP3 -tubulin gamma complex associated protein 3	60,317 bp downstream
	1	HGC005374	137,889,452	1,714.28	3.12E-06	ATP11A -ATPase phospholipid transporting 11A	Within
						TUBGCP3 -tubulin gamma complex associated protein 3	43,124 bp downstream

Results from GWAS



Zone	Chromosome	SNP	SNP location	Effect	P value	Gene name	Gene distance
Nest	15	HGC035687	7,939,433	-12,615.9	3.86E-10	CA15L -carbonic anhydrase 15-like	2,052 bp downstream
						IGLL1 - immunoglobulin lambda-like polypeptide 1	4,122 bp upstream
						DGCR2 -DiGeorge syndrome critical region gene 2	9,461 bp downstream
						VPS29L -VPS29 retromer complex component like	30,458 bp upstream

Results from GWAS

Zone	Chromosome	SNP	SNP location	Effect	P value	Gene name	Gene distance
Winter garden	1	HGC003381	86,895,002	-2,710.15	1.60E-06	LOC112530378 - uncharacterized	Within
	1	HGC003401	87,374,392	-2,710.15	1.60E-06	ALCAM -activated leukocyte cell adhesion molecule	Within
						CBLB -Cbl proto-oncogene B	46,227 bp downstream

Final thoughts

- Results from this study show that there are genetic components influencing aviary usage by hens
- Genomic regions that influence these traits were identified
- Further investigation into the function of identified genes and how they are related to movement within the aviary is needed

Thank you for listening

Acknowledgements

