

1 Supplementary Material

2 Appendix A Descriptive statistics of all traits in the yellow-feathered chicken population.

Category	Traits	N-obs ¹⁾	N-gen ²⁾	Min	Max	Median	Mean	SD
Growth traits	ADG (g/d)	1,338	895	4.660	44.650	27.535	27.668	4.547
	BW45 (kg)	1,326	884	0.341	1.508	0.778	0.775	0.122
	BW49 (kg)	1,276	849	0.570	1.332	0.900	0.902	0.134
	BW56 (kg)	1,291	862	0.669	1.607	1.105	1.104	0.156
	BW63 (kg)	1,301	865	0.831	1.831	1.285	1.288	0.171
	BW70 (kg)	1,286	859	1.021	2.114	1.494	1.498	0.181
	BW77 (kg)	1,304	872	1.148	2.326	1.691	1.695	0.202
	BW84 (kg)	1,264	848	1.247	2.591	1.841	1.846	0.219
	BW91 (kg)	1,163	802	1.038	2.477	1.761	1.761	0.216
Carcass traits	AFP (%)	1,174	824	0.000	0.148	0.048	0.049	0.020
	AFW (kg)	1,193	824	0.003	0.191	0.057	0.059	0.025
	BMW (kg)	1,191	825	0.051	0.190	0.102	0.102	0.016
	CW (kg)	1,192	809	0.909	2.230	1.566	1.564	0.199
	DW (kg)	1,193	825	0.102	0.328	0.201	0.204	0.036
	EW (kg)	1,192	824	0.711	1.704	1.190	1.193	0.157
	EWG (kg)	1,192	825	0.008	0.061	0.031	0.031	0.006
	GW (kg)	1,179	814	0.070	0.226	0.164	0.164	0.016
Feeding traits	IL (cm)	1,173	811	60.300	155.920	0.105	0.105	0.016
	ADFI (kg)	1,174	895	0.844	2.055	1.434	1.432	0.185
	FCR	1,193	895	2.222	20.959	3.799	3.867	0.811
	MBW (kg)	1,191	895	0.795	1.854	1.332	1.330	0.169
	MMBW (kg)	1,192	895	0.150	0.283	0.221	0.220	0.021
	RFI	1,193	895	-41.904	40.616	-0.641	0.000	11.094

3 ADG = average daily gain; BW* = body weight, e.g. body weight at 45d (BW45); AFP = abdominal fat percentage; AFW =
4 abdominal fat weight; BMW = breast muscle weight; CW = carcass weight; DW = drumstick weight; EW = eviscerated
5 weight; EWG = eviscerated weight with giblets; GW = gizzard weight; IL = intestine length; ADFI = average daily feed
6 intake; FCR = feed conversion ratio; MBW = mid-term body weight; MMBW = mid-term metabolic body weight; RFI =
7 residual feed intake.

8 ¹ Numbers of individuals with phenotypic records.

9 ² Numbers of genotyped individuals.

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12 **Appendix B** Runtime (minutes) of building genomic relationship matrices in different
 13 prediction models.

Genomic region ¹⁾	SNP-based G ²⁾	Haplotype-based G ³⁾	
		Chromosome 2	Mean±SD across all chromosomes
WGS	1.58	179.6	-
Genes	1.05	39.95	-
Exons	0.15	2.41	0.92±0.83

14 ¹⁾ Genomic regions extracted based on different annotation information.
 15 ²⁾ SNP-based genomic relationship matrix used in ssGBLUP, ssGBLUPgene and ssGBLUPexon models.
 16 ³⁾ Haplotype-based genomic relationship matrix used in ssGHBLUP, ssGHBLUPgene and ssGHBLUPexon models.
 17 - represents no record.

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29 **Appendix C** Unbiasedness \pm standard error of all models using whole-genome sequence
30 data in the yellow-feathered chicken population.

Category	Traits	BLUP	GBLUP	ssGBLUP	ssGBLUP _{gene}	ssGBLUP _{exon}	ssG _H BLUP	ssG _H BLUP _{gene}	ssG _H BLUP _{exon}
Growth	ADG	1.24 \pm 0.05	1.11 \pm 0.05	1.16 \pm 0.04	1.16 \pm 0.04	1.16 \pm 0.04	1.15 \pm 0.04	1.15 \pm 0.04	1.16 \pm 0.04
traits	BW45	1.21 \pm 0.03	0.96 \pm 0.03	1.15 \pm 0.03	1.16 \pm 0.03	1.16 \pm 0.03	1.14 \pm 0.03	1.16 \pm 0.03	1.16 \pm 0.03
	BW49	1.17 \pm 0.03	0.98 \pm 0.03	1.13 \pm 0.03	1.14 \pm 0.03	1.13 \pm 0.03	1.12 \pm 0.03	1.14 \pm 0.03	1.13 \pm 0.03
	BW56	1.09 \pm 0.04	0.93 \pm 0.03	1.05 \pm 0.03	1.07 \pm 0.03	1.07 \pm 0.03	1.04 \pm 0.03	1.07 \pm 0.03	1.08 \pm 0.03
	BW63	1.04 \pm 0.04	0.92 \pm 0.03	1.01 \pm 0.03	1.03 \pm 0.03	1.05 \pm 0.03	1.00 \pm 0.03	1.03 \pm 0.03	1.05 \pm 0.03
	BW70	1.05 \pm 0.04	0.92 \pm 0.03	1.02 \pm 0.03	1.04 \pm 0.03	1.06 \pm 0.03	1.01 \pm 0.03	1.04 \pm 0.03	1.05 \pm 0.03
	BW77	1.10 \pm 0.04	0.95 \pm 0.04	1.06 \pm 0.03	1.07 \pm 0.03	1.09 \pm 0.03	1.05 \pm 0.03	1.08 \pm 0.03	1.09 \pm 0.03
	BW84	1.06 \pm 0.04	0.96 \pm 0.04	1.03 \pm 0.04	1.05 \pm 0.04	1.06 \pm 0.04	1.03 \pm 0.04	1.05 \pm 0.04	1.06 \pm 0.04
	BW91	1.02 \pm 0.04	0.90 \pm 0.04	0.98 \pm 0.04	0.99 \pm 0.04	1.00 \pm 0.04	0.98 \pm 0.04	1.00 \pm 0.04	1.00 \pm 0.04
	Carcass	AFP	1.01 \pm 0.03	1.08 \pm 0.04	0.98 \pm 0.03	0.97 \pm 0.03	0.98 \pm 0.03	0.98 \pm 0.03	0.97 \pm 0.03
AFW		1.06 \pm 0.04	1.08 \pm 0.04	1.02 \pm 0.04	1.01 \pm 0.04	1.02 \pm 0.04	1.01 \pm 0.04	1.01 \pm 0.04	1.02 \pm 0.04
BMW		1.05 \pm 0.04	1.11 \pm 0.05	1.02 \pm 0.04	1.02 \pm 0.04	1.03 \pm 0.04	1.01 \pm 0.04	1.02 \pm 0.04	1.03 \pm 0.04
CW		1.01 \pm 0.04	0.95 \pm 0.04	1.00 \pm 0.04	1.01 \pm 0.04	1.02 \pm 0.04	0.99 \pm 0.04	1.02 \pm 0.04	1.02 \pm 0.04
DW		1.16 \pm 0.05	1.13 \pm 0.05	1.09 \pm 0.04	1.10 \pm 0.04	1.10 \pm 0.04	1.10 \pm 0.04	1.10 \pm 0.04	1.11 \pm 0.04
EW		1.00 \pm 0.04	0.94 \pm 0.04	0.98 \pm 0.04	1.00 \pm 0.04	1.01 \pm 0.04	0.98 \pm 0.04	1.00 \pm 0.04	1.01 \pm 0.04
EWG		1.01 \pm 0.04	0.93 \pm 0.03	1.00 \pm 0.04	1.01 \pm 0.04	1.02 \pm 0.04	1.00 \pm 0.04	1.02 \pm 0.04	1.02 \pm 0.04
GW		0.99 \pm 0.03	1.12 \pm 0.04	0.96 \pm 0.03	0.96 \pm 0.03	0.96 \pm 0.03	0.96 \pm 0.03	0.96 \pm 0.03	0.96 \pm 0.03
IL		1.00 \pm 0.03	1.14 \pm 0.03	0.98 \pm 0.03	0.99 \pm 0.03	0.98 \pm 0.03	0.99 \pm 0.03	0.98 \pm 0.03	0.98 \pm 0.03
Feeding	ADFI	1.08 \pm 0.03	1.10 \pm 0.03	1.03 \pm 0.03	1.04 \pm 0.03	1.04 \pm 0.03	1.03 \pm 0.03	1.04 \pm 0.03	1.04 \pm 0.03
	FCR	1.44 \pm 0.09	1.22 \pm 0.07	1.33 \pm 0.08	1.32 \pm 0.08	1.34 \pm 0.08	1.31 \pm 0.08	1.31 \pm 0.08	1.33 \pm 0.08
	MBW	1.08 \pm 0.03	0.96 \pm 0.03	1.05 \pm 0.03	1.07 \pm 0.03	1.08 \pm 0.03	1.05 \pm 0.03	1.08 \pm 0.03	1.08 \pm 0.03
	MMBW	1.13 \pm 0.04	1.09 \pm 0.04	1.08 \pm 0.04	1.09 \pm 0.03	1.09 \pm 0.03	1.08 \pm 0.04	1.09 \pm 0.03	1.09 \pm 0.03
	RFI	1.10 \pm 0.03	1.10 \pm 0.03	1.05 \pm 0.03	1.05 \pm 0.03	1.06 \pm 0.03	1.05 \pm 0.03	1.05 \pm 0.03	1.05 \pm 0.03

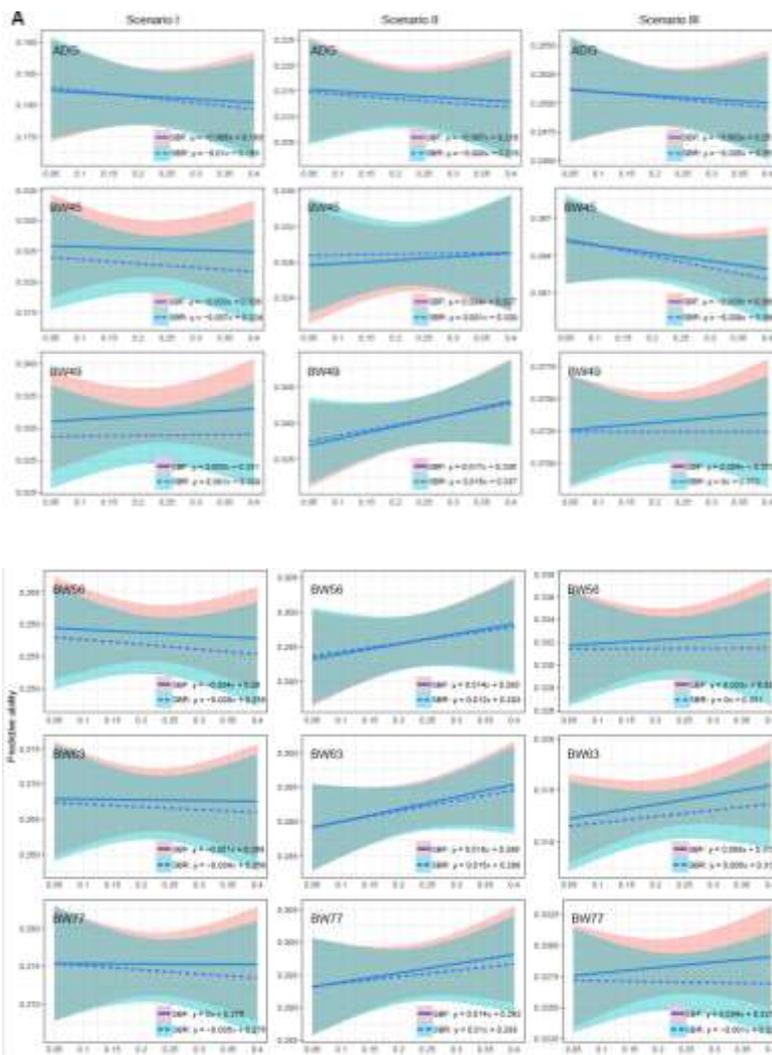
31 ADG = average daily gain; BW* = body weight, e.g. body weight at 45d (BW45); AFP = abdominal fat percentage; AFW =
32 abdominal fat weight; BMW = breast muscle weight; CW = carcass weight; DW = drumstick weight; EW = eviscerated
33 weight; EWG = eviscerated weight with giblets; GW = gizzard weight; IL = intestine length; ADFI = average daily feed
34 intake; FCR = feed conversion ratio; MBW = mid-term body weight; MMBW = mid-term metabolic body weight; RFI =
35 residual feed intake; BLUP = conventional best linear unbiased prediction; GBLUP = genomic best linear unbiased prediction;
36 ssGBLUP = single-step genomic best linear unbiased prediction.

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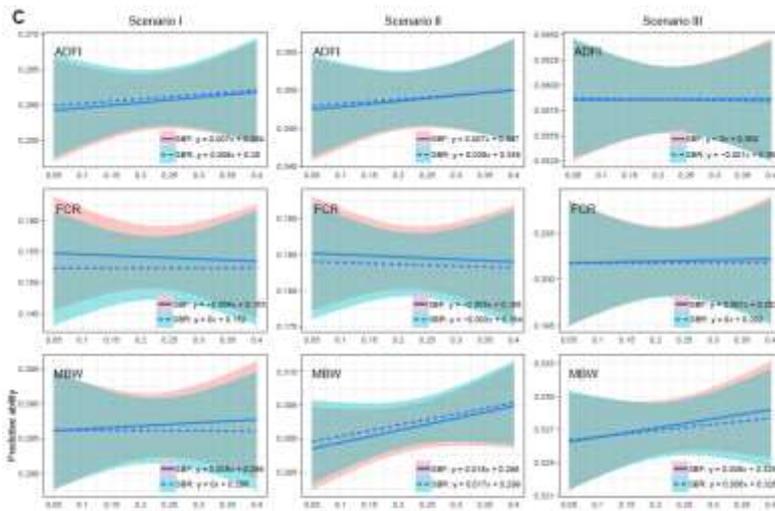
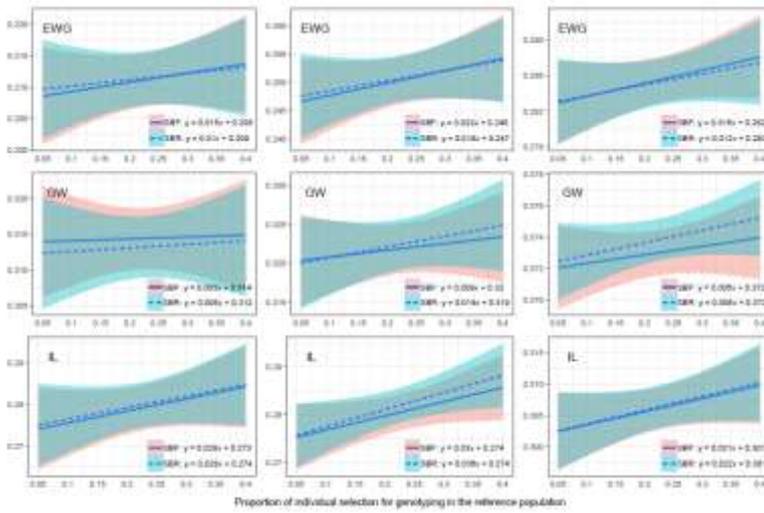
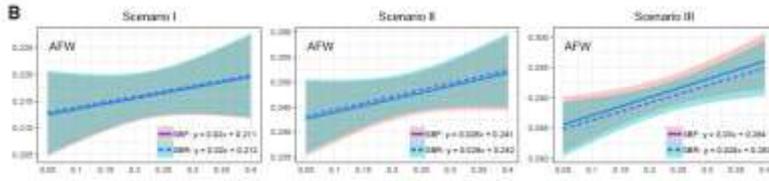
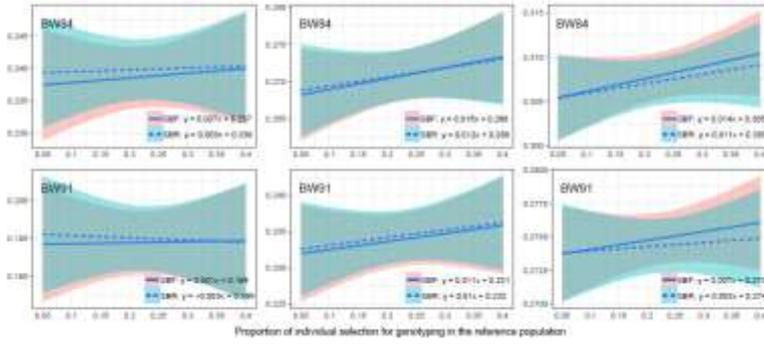
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39 **Appexdix D** Predictive ability of single-step genomic best linear unbiased prediction using
40 whole-genome sequence data in three different genetic relationships between the reference
41 and candidate population in the yellow-feathered chicken population.

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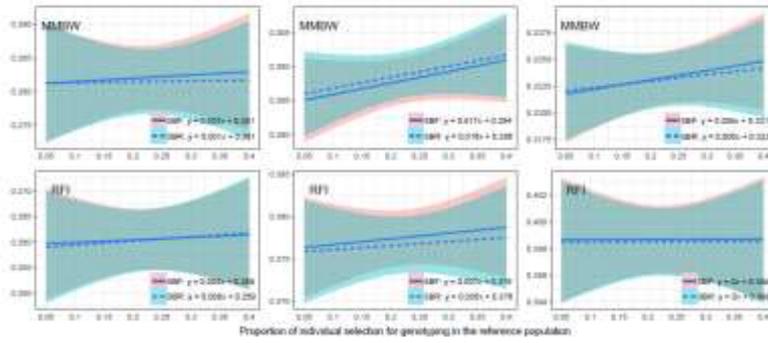
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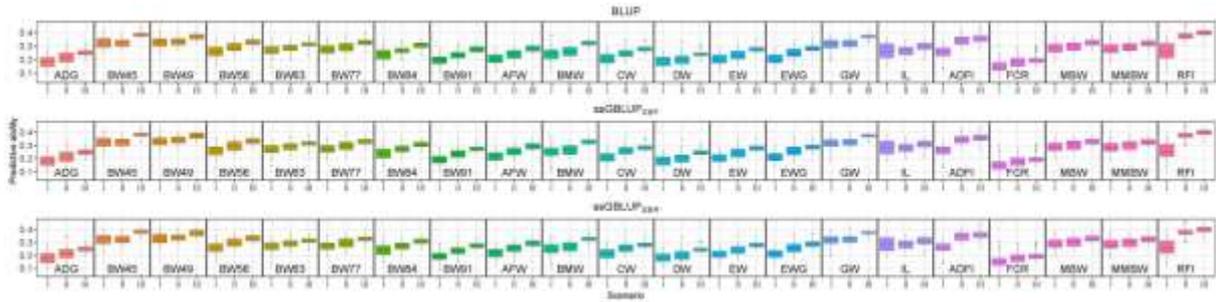
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48 **Appendix E** Predictive ability of single-step genomic best linear unbiased prediction using
 49 whole-genome sequence data under different genotyped individual selection strategies for **A)**
 50 **growth, B) carcass, and C) feeding traits** in the yellow-feathered chicken population.



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