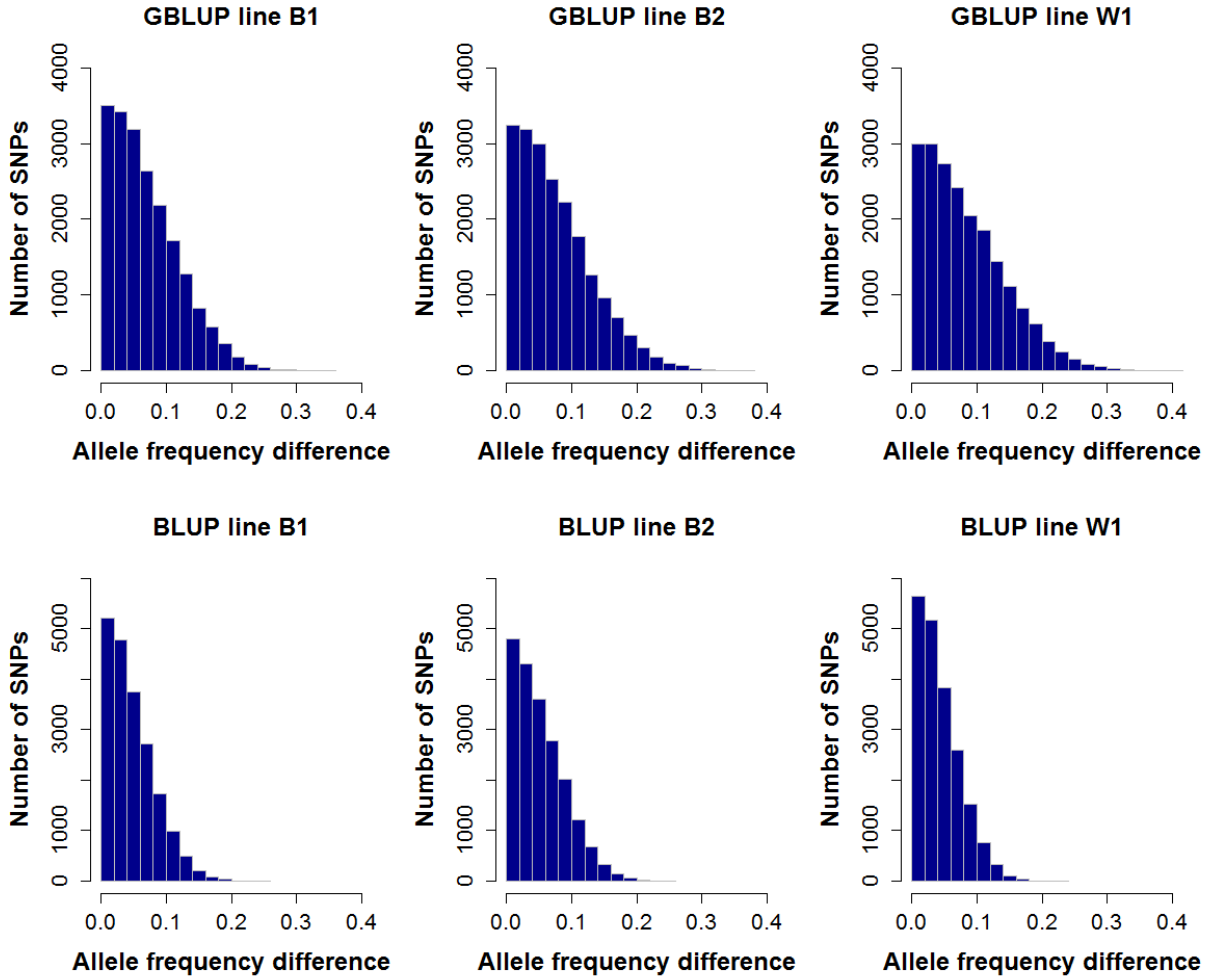
Supplementary Materials

Supplementary Material 1. The distribution of allele frequency difference values obtained from gene dropping method. The distribution is under pure drift.



Supplementary Material 2. Chromosomal regions with evidence of selection and their size by GBLUP in Line B1.

Number	Chr	Start Region (b)	End Region (b)	Size (Kb)	# SNPs within Window
1	1	4720681	4758257	38	2
2	1	166584824	167901966	1317	13
3	2	28920690	29217563	297	9
4	2	45508551	46132452	624	20
5	2	132208978	136448286	4239	23
6	2	146308646	147213733	905	12
7	2	154650591	154773773	123	3
8	3	102824077	103300601	477	32
9	4	16886356	17041365	155	5
10	5	33373065	33943902	571	11
11	6	28570859	28596240	25	2
12	6	36668647	36694690	26	2
13	8	15164327	15386078	222	6
14	12	7691443	8072782	381	16
15	12	16254872	16348587	94	5
16	17	566109	576200	10	3

17	18	588543	679660	91	6
18	20	9264214	9358727	95	10
19	21	4640996	4915810	275	5
20	27	1523159	1582373	59	7
21	Z	43150739	43389428	239	8
22	Z	45979603	46522178	543	14
23	Z	49611037	49734015	123	4
24	Z	55076530	56159359	1083	22

Abbreviations: Chr, chromosome; SNP, Single Nucleotide Polymorphism.

Supplementary Material 3. Chromosomal regions with evidence of selection and their size by GBLUP in Line B2.

Number	Chr	Start Region (b)	End Region (b)	Size (Kb)	# SNPs within Window
1	1	8401914	8781041	379	15
2	1	95898565	96327303	429	9
3	1	152635633	152738843	103	3
4	2	118893774	119623629	730	24
5	2	152274434	153504517	1230	16
6	3	54888621	55308850	420	11
7	4	21568436	22527061	959	29
8	4	37930765	38125680	195	5
9	5	19083517	19462239	379	2
10	5	22063274	22221157	158	5
11	5	36054328	36593177	539	13
12	5	50458849	52048861	1590	5
13	6	26140788	26220466	80	5
14	6	28570859	28740314	169	6
15	7	26777669	27014569	237	7
16	8	15164327	15874082	710	23
17	9	21512582	21543999	31	2
18	10	14728444	14774628	46	3
19	12	7744495	7799424	55	4
20	14	5753769	5803989	50	4
21	15	1737293	2020018	283	16
22	17	9247986	9321117	73	3
23	20	4048348	4069974	22	2
24	20	6458146	6508290	50	5
25	21	4766473	4871368	105	6
26	21	5319394	5849715	530	25
27	27	81812	128044	46	6
28	Z	63443182	64159026	716	14
29	Z	67845625	68188297	343	11
30	Z	71016792	71170715	154	4

Abbreviations: Chr, chromosome; SNP, Single Nucleotide Polymorphism.

Supplementary Material 4. Chromosomal regions with evidence of selection and their size by GBLUP in Line W1.

Number	Chr	Start Region (b)	End Region (b)	Size (Kb)	# SNPs within Window
1	1	167395216	169276943	1882	17
2	2	30519034	30760143	241	8
3	2	41196442	41500199	304	6
4	2	91379231	91630576	251	9
5	3	70491928	70718748	227	10
6	3	106157684	106493357	336	14
7	4	41342661	44852911	3510	45

8	6	22109324	22197788	88	4
9	7	13973139	14071039	98	3
10	8	27274382	27607198	333	6
11	14	1299671	2112686	813	20
12	14	7530640	7807504	277	8
13	15	897724	1308491	411	13
14	24	539599	959127	420	18
15	24	5055555	5141562	86	8
16	Z	22188375	23226854	1038	15

Abbreviations: Chr, chromosome; SNP, Single Nucleotide Polymorphism.

Supplementary Material 5. Chromosomal regions with evidence of selection and their size by BLUP in Line B1.

Number	Chr	Start Region (b)	End Region (b)	Size (Kb)	# SNPs within Window
1	5	5259614	5548921	289	6
2	5	41614429	42813979	1200	11
3	6	24613780	24734193	120	3
4	7	6096647	6177766	81	6
5	7	9781078	11908872	2128	9
6	10	6230374	6652251	422	6
7	21	6780205	6930673	150	15
8	Z	33473589	33832610	359	10
9	Z	40001342	41155850	1155	11
10	Z	52247377	52772760	525	11

Abbreviations: Chr, chromosome; SNP, Single Nucleotide Polymorphism.

Supplementary Material 6. Chromosomal regions with evidence of selection and their size by BLUP in Line B2.

Number	Chr	Start Region (b)	End Region (b)	Size (Kb)	# SNPs within Window
1	2	50530766	50893951	363	4
2	3	36796454	37001278	205	6
3	3	60672286	60784548	112	4
4	4	71538605	71706644	168	4
5	4	80768115	80890011	122	5
6	6	36698845	37029368	331	12
7	10	11684478	11742160	58	3
8	12	18001140	18109181	108	6
9	13	1291424	1533552	242	10
10	19	5953716	5979279	26	2
11	Z	5909968	8728268	2818	43
12	Z	21650099	21704940	55	3

Abbreviations: Chr, chromosome; SNP, Single Nucleotide Polymorphism.

Supplementary Material 7. Chromosomal regions with evidence of selection and their size by BLUP in Line W1.

Number	Chr	Start Region (b)	End Region (b)	Size (Kb)	# SNPs within Window
1	1	161339470	161795934	456	5
2	3	80155629	80821745	666	14
3	4	45516115	46697542	1181	26
4	4	55775170	55991394	216	5
5	5	46490989	49086660	2596	52
6	8	15134962	15266419	131	5
7	9	23496401	23683979	188	3
8	11	5445683	6203062	757	25

9	11	16558599	16927919	369	9
10	17	872685	995536	123	9
11	18	592250	633908	42	3
12	19	4807455	4840810	33	4
13	21	3887935	3982657	95	2

Abbreviations: Chr, chromosome; SNP, Single Nucleotide Polymorphism.

Supplementary Material 8. Initial allele frequency, selection coefficients, selection intensities and additive effect for the alleles at peak of allele frequency changes in lines B1, B2, and W1.

Region Name: line(chr #)*	Initial minor allele frequency at peak (p_0)	Selection coefficient (s)	Selection intensity (i)	Additive effect (a)	Additive effect (standardized unit)	Variance explained (%)
B1(3)	0.302	0.757	1.66	50.5	0.23	2.19
B1(8)	0.337	0.974	1.66	65	0.29	3.85
B1(12)	0.567	0.820	1.66	54.7	0.25	3
B1(20)	0.364	0.684	1.66	45.7	0.21	1.97
B1(21)	0.467	0.877	1.66	58.5	0.26	3.48
B2(2)	0.191	1.244	1.70	106.1	0.37	4.14
B2(3)	0.131	0.791	1.70	67.5	0.23	1.23
B2(4)	0.016	1.904	1.70	162	0.56	0.98
B2(8)	0.059	1.700	1.70	145	0.50	2.78
B2(21)	0.137	0.806	1.70	69	0.24	1.34
W1(2)	0.369	0.909	1.85	61.1	0.25	2.81
W1(3)	0.259	0.660	1.85	44.3	0.18	1.22
W1(4)	0.332	0.872	1.85	58.6	0.24	2.46
W1(14)	0.389	0.626	1.85	42.1	0.17	1.36
W1(Z)	0.377	0.844	1.85	56.7	0.23	2.44
Average	0.29	0.96	1.74	72.4	0.28	2.3

* Additive effects were calculated for the 5 largest peaks of each line.

Supplementary Material 9. Selected regions overlapping with selected regions detected in other studies.

Number	Chr	Line	Selected regions detected by our study		Selected regions detected by other studies		Line type used in other studies
			Start Region (b)	End Region (b)	Start Region (b)	End Region (b) Reference	
8	2	**B1**	132208978	136504544	132620000	132660000[b]	commercial white leghorn layer
9	2	**B1**	146242439	147240186	146980000	147020000[b]	domestic line
10	5	**B1**	33373065	35793825	33752931	33833740[a]	broiler sire line
					34026477	34289307[a]	broiler sire line, broiler
					34635714	34879253[a]	commercial, broiler, broiler sire line
11	18	**B1**	588543	679660	578906	615438[a]	broiler, broiler sire line
1	1	**B2**	152635633	152738843	152516746	153003586[a]	domesticated line, commercial, broiler, layer, broiler sire line, broiler dam line, dutch new breeds
					152660000	152700000[b]	commercial white leghorn layer
2	2	**B2**	118893774	119623629	118647414	118747803[a]	commercial line,

							broiler, layer
					119340000	119380000[b]	domestic line
3	2	**B2**	152274434	153504517	152674603	152903909[a]	domesticated line, commercial, non-commercial, broiler, broiler ire line, dutch new breed
					152720000	152860000[b]	commercial white leghorn layer
					152880000	152900000[b]	commercial white leghorn layer
4	3	**B2**	54888621	55308850	54910306	55009153[a]	chinese breed
5	4	**B2**	21568436	22527061	22274031	22470419[a]	chinese breed
6	5	**B2**	22063274	22221157	22085297	22155963[a]	broiler, broiler dam line
7	7	**B2**	26777669	27014569	26760000	26820000[b]	commercial white leghorn layer
12	1	**W1**	167395216	169276943	168540000	168580000[b]	commercial white leghorn layer
13	4	**W1**	41342661	44852911	43160000	43200000[b]	domestic line
14	7	**W1**	13973139	14093954	13973139	14057861[a]	non-commercial, dutch
15	14	**W1**	1281294	1876724	1500000	2000000[c]	commercial white layer
16	15	**W1**	897724	1385483	1201531	1274715[a]	layer, dam broiler line

Abbreviations: Chr, chromosome.

[a] (Elferink *et al.*, 2012).

[b] (Rubin *et al*, 2010).

[c] (Amaral, 2010).

Supplementary notes

Calculation of selection coefficient (s) and selection intensity (*i*)

Selection coefficient (s) was calculated using the following formula as:

$$s = -\ln \frac{\left(\left(\frac{1}{p_t} - 1\right) \Big/ \left(\frac{1-p_0}{p_0}\right)\right)}{t} \quad (1)$$

The above formula was derived from the general formula for the change in gene frequency due to selection at an additive gene which is: $\Delta p = sp(1-p)$. With the assumption that the allele frequency is a continuous process in time, changes in allele frequency can be written as: $dp/dt = sp(1-p)$ (Goddard, 2009). The integrated form of this formula becomes $p_t = p_0 e^{st}/(1 - p_0 + p_0 e^{st})$, where p_0 is the starting allele frequency at the peak, t is the number of generations of selection, p_t is the allele frequency after t generations of selection.

Finally, the selection coefficient against the unfavourable homozygote for a given SNP was estimated from the formula (1).

Selection intensities (i) were retrieved from proportion of selection candidates selected (p) using the tables on pp. 379-380 in Falconer and Mackay (Falconer and Mackay, 1996). p was calculated separately for males and females by dividing the number of selected parents by the total number of selection candidates in each generation of GBLUP and BLUP. Since the number of males and females selected in each generation were not equal, i was different for males and females (Table 1 and Table 3).

Calculation of effective population size (N_e)

N_e was estimated as: $N_e = \frac{p_0 * (1 - p_0)}{2 * \mathrm{var}(d_{02})}$

, where p_0 and $1 - p_0$ were the allele frequencies from gene dropping, $\mathrm{var}(d_{02})$ was the variance of allele frequency difference from gene dropping.

Calculation of Fst

Fst was calculated as: $Fst = \frac{H_t - H_s}{H_t}$

,where $H_s = ((2 * p_i * (1 - p_i) + (2 * p_j * (1 - p_j))/2$ and $H_t = 2 * p_{ij} * (1 - p_{ij})$.

$p_{ij} = (p_i + p_j)/2$.

, where p_i was the allele frequency in line i, p_j was the allele frequency in line j, p_{ij} was the average between the allele frequencies of the two lines. H_s was the mean expected heterozygosity between lines, and H_t was the total heterozygosity in total population.