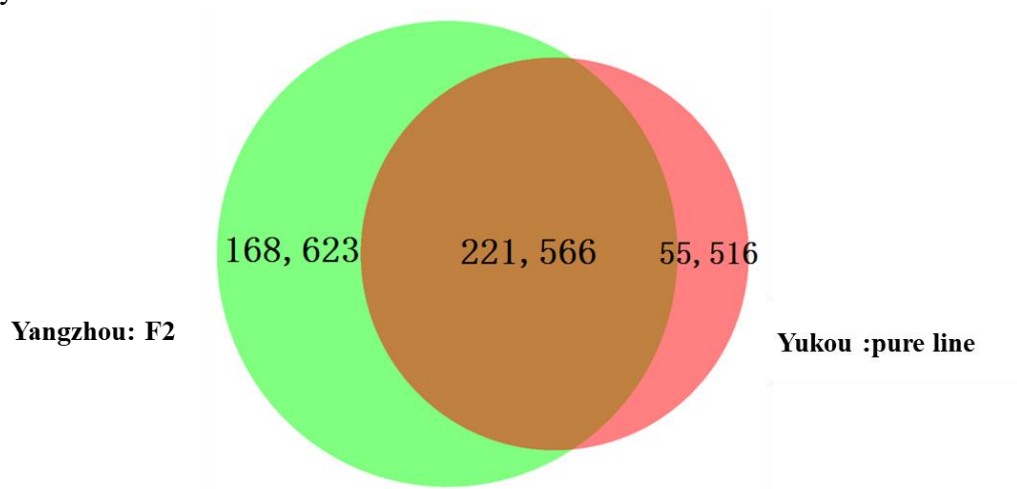


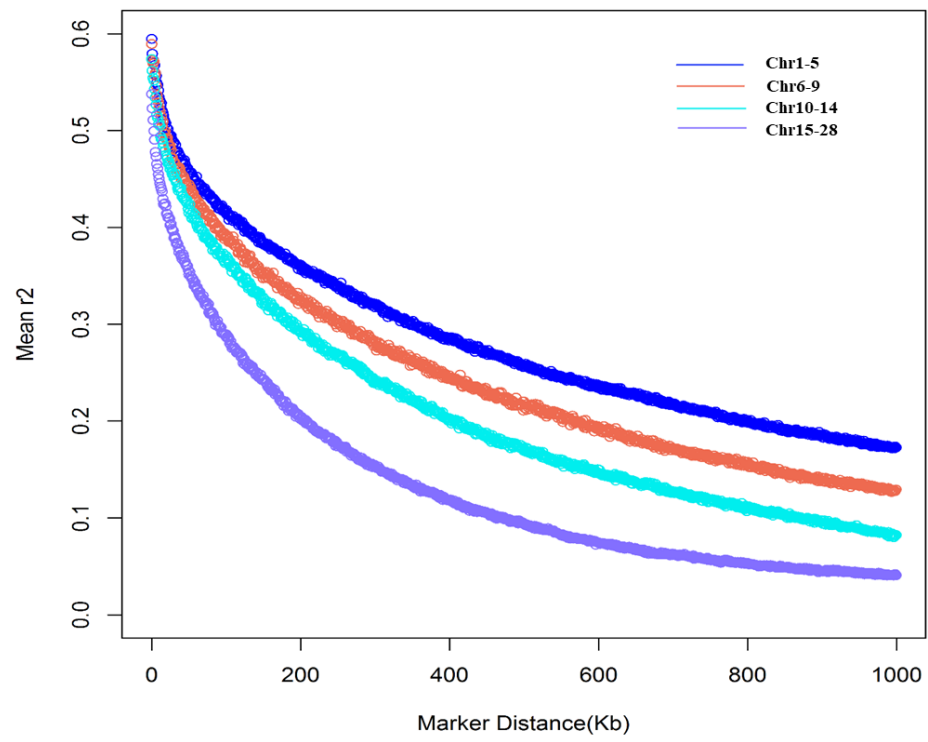
**Figure S1** Overlapped SNPs between Yangzhou (F2) and Yukou (Pure line) after quality control.



**Table S1** Distribution and parameter of space setting between SNPs on the custom 50K SNP array (Based on Gallus-gallus6.0).

CHROM	Length(bp)	NO.SNPs	Space settings(bp)	Actual Space(bp)	Max(bp)	Min(bp)
chr1	197,677,740	7,683	20,000	25,676.52	704,460	552
chr2	149,682,049	5,839	20,000	25,552.15	1,130,114	62
chr3	110,854,228	4,523	20,000	24,404.47	684,165	40
chr4	91,315,245	3,909	20,000	23,136.59	522,262	94
chr5	59,809,098	2,537	20,000	23,379.82	653,705	28
chr6	36,428,957	1,809	15,000	19,284.12	930,620	73
chr7	36,742,308	1,956	15,000	18,399.28	526,588	150
chr8	30,219,446	1,394	15,000	21,188.97	555,602	425
chr9	24,181,049	1,243	15,000	18,978.08	521,893	140
chr10	21,119,840	1,354	12,000	14,615.46	516,979	457
chr11	20,200,042	1,280	12,000	15,583.60	536,886	484
chr12	20,387,278	1,375	12,000	14,057.78	306,511	148
chr13	19,168,871	1,092	12,000	15,188.01	1,594,123	101
chr14	16,220,073	990	12,000	14,174.40	52,287	32
chr15	13,064,218	1,193	9,000	10,242.42	80,489	153
chr16	2,994,104	54	9,000	15,390.57	263,840	24
chr17	10,762,512	828	9,000	11,261.19	243,961	131
chr18	11,373,140	914	9,000	11,889.74	97,515	1,100
chr19	10,324,343	854	9,000	11,737.33	173,683	929
chr20	13,897,287	1,061	9,000	12,543.49	173,589	855
chr21	6,844,979	604	9,000	11,173.89	69,785	26
chr22	5,460,380	342	9,000	14,777.48	731,461	1,628
chr23	6,202,910	373	9,000	16,006.10	1,242,629	1,980
chr24	6,491,222	490	9,000	11,829.76	62,570	1,482
chr25	3,982,494	148	9,000	26,114.44	783,966	2,389
chr26	6,055,710	758	6,000	6,714.04	49,694	151
chr27	8,080,432	522	6,000	9,127.74	204,149	121
chr28	5,118,401	650	6,000	7,004.24	71,261	32
chr30	1,818,525	1	--	--	--	--
chr31	6,185,160	141	6,000	6,283.31	101,762	387
chr32	725,831	13	6,000	7,853.00	44,545	1,394
chr33	7,821,848	258	6,000	17,839.93	1,729,648	134
chrZ	82,545,508	3,639	20,000	22,465.72	2,342,602	217

**Figure S2** The decay of linkage disequilibrium in different chromosomes.



**Figure S3** Manhattan plot of genome-wide association study for EW36. The horizontal red line and black line indicated the genome-wide significant threshold ( $8.1e-06$ ) and genome-wide suggestive significant threshold ( $1.62e-04$ ), respectively. The Manhattan plot indicates  $-\log_{10}$  (observed P-values) for genome-wide SNP (y-axis) against their corresponding position on each chromosome (x-axis).

