

Table S1. Annotation of significant SNPs associated with 7 lines.

Lines	rs	GGA ^a	Position ^b	β^c	P value	Gene	Gap, kb ^d
Y1	rs14404973	3	101,343,319	2.61	2.56E-06	<i>ENSGALG00000016475</i>	intron
Y1	rs314600081	10	18,394,068	2.34	4.70E-06	<i>IGDCC4</i>	intron
Y1	rs312892904	10	19,796,467	-2.24	1.44E-05	<i>KIF23</i>	D 3.76
Y1	rs315407734	10	19,803,842	2.34	4.74E-06	<i>KIF23</i>	D 10.96
Y1	rs314663731	10	19,804,829	2.34	5.39E-06	<i>KIF23</i>	D 11.92
Y2	rs318061712	2	107,771,809	-3.18	1.41E-05	<i>SPIDR</i>	intron
Y2	rs317654235	4	32,260,081	-2.79	2.08E-05	<i>NR3C2</i>	intron
Y2	rs312789477	7	21,897,882	-2.86	1.34E-05	<i>LY75</i>	intron
Y3	rs315622159	1	14,368,997	-5.77	3.12E-05	<i>NAMPTP1</i>	intron
W1	rs317899003	1	63,942,199	6.87	6.23E-05	<i>ENSGALG00000053831</i>	intron
W1	rs316040498	2	62,981,592	-5.42	1.02E-04	<i>TMEM170B</i>	D 9.04
W1	rs317557970	2	62,983,613	-5.42	1.02E-04	<i>TMEM170B</i>	D 11.02
W1	rs16018073	2	62,989,847	-5.42	1.02E-04	<i>TMEM170B</i>	D 17.11
W1	rs314293804	3	42,424,680	-9.18	8.82E-06	<i>ENSGALG00000051089</i>	D 3.93
W1	rs315274567	3	57,379,107	7.54	4.07E-05	<i>MED23</i>	intron
W1	rs314851312	11	16,190,275	-8.14	4.76E-05	<i>CDH13</i>	intron
W1	rs14027438	11	16,197,749	-8.14	4.76E-05	<i>CDH13</i>	intron
W1	rs317528345	20	8,604,396	-9.83	9.90E-05	<i>ENSGALG00000046924</i>	intron
W2	rs14747990	6	20,750,628	-3.4	1.88E-06	<i>ENSGALG00000050084</i>	exon
W2	rs166 77209	9	20,459,639	-3.35	5.19E-05	<i>MECOM</i>	D 22.31
W2	rs316948110	12	9,191,205	2.75	8.60E-05	<i>SLMAP</i>	intron
W3	rs316386348	1	62,183,595	10.53	7.27E-05	<i>BPGM</i>	3 prime UTR
W3	rs315825336	6	17,092,252	-5.77	1.40E-05	<i>ENSGALG00000051819</i>	intron
W3	rs15855668	7	18,602,932	-8.16	4.09E-05	<i>ENSGALG00000044224</i>	U 0.85
W3	rs313721223	7	18,647,907	7.12	1.18E-05	<i>FASTKD1</i>	intron
W3	rs312667371	12	2,151,697	-5.97	1.46E-05	<i>ENSGALG00000048708</i>	U 0.52
W3	rs315486653	17	3,121,708	5.78	4.25E-05	<i>TNC</i>	U 22.98
W3	rs431881571	19	6,736,363	-5.65	7.15E-05	<i>ENSGALG0000004509</i>	U 1.68
W4	rs13897687	1	87,509,580	4.35	1.80E-05	<i>ENSGALG00000048148</i>	intron
W4	chr5:35782438	5	35,782,438	-16.99	7.39E-05	<i>NPAS3</i>	intron
W4	rs312322983	5	52,560,002	3.82	2.96E-05	<i>ENSGALG00000048544</i>	D 9.63
W4	rs313726052	10	19,251,303	-5.15	1.55E-05	<i>AAGAB/SMAD3</i>	intron
W4	rs733550169	10	19,456,463	-4.87	7.32E-05	<i>MAP2K5</i>	intron
W4	rs10721736	10	19,575,366	-4.92	4.52E-05	<i>CALML4</i>	3 prime UTR
W4	rs312625498	15	8,440,067	-3.84	6.08E-05	<i>CABIN1</i>	intron

a: Gallus gallus chromosome

b: Gallus_gallus-6.0 source

c: Allele substitution effect was the additive effect estimated by GEMMA

d: U and D indicate that the SNP is upstream and downstream of a gene, respectively