

# A whole genome association study to detect additive and dominant single nucleotide polymorphisms for growth and carcass traits in Korean native cattle, Hanwoo

Yi Li<sup>1</sup>, Yuxuan Gao<sup>1</sup>, You-Sam Kim<sup>2</sup>, Asif Iqbal<sup>2</sup>, and Jong-Joo Kim<sup>2,\*</sup>

\* **Corresponding Author:** Jong-Joo Kim  
**Tel:** +82-53-810-3027, **Fax:** +82-53-810-4769,  
**E-mail:** kimjj@ynu.ac.kr

<sup>1</sup> School of Statistics, Shanxi University of Finance & Economics, Taiyuan 030006, China

<sup>2</sup> School of Biotechnology, Yeungnam University, Gyeongsan 712-749, Korea

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**Objective:** A whole genome association study was conducted to identify single nucleotide polymorphisms (SNPs) with additive and dominant effects for growth and carcass traits in Korean native cattle, Hanwoo.

**Methods:** The data set comprised 61 sires and their 486 Hanwoo steers that were born between spring of 2005 and fall of 2007. The steers were genotyped with the 35,968 SNPs that were embedded in the Illumina bovine SNP 50K beadchip and six growth and carcass quality traits were measured for the steers. A series of lack-of-fit tests between the models was applied to classify gene expression pattern as additive or dominant.

**Results:** A total of 18 (0), 15 (3), 12 (8), 15 (18), 11 (7), and 21 (1) SNPs were detected at the 5% chromosome (genome) - wise level for weaning weight (WWT), yearling weight (YWT), carcass weight (CWT), backfat thickness (BFT), *longissimus dorsi* muscle area (LMA) and marbling score, respectively. Among the significant 129 SNPs, 56 SNPs had additive effects, 20 SNPs dominance effects, and 53 SNPs both additive and dominance effects, suggesting that dominance inheritance mode be considered in genetic improvement for growth and carcass quality in Hanwoo. The significant SNPs were located at 33 quantitative trait locus (QTL) regions on 18 *Bos Taurus* chromosomes (i.e. BTA 3, 4, 5, 6, 7, 9, 11, 12, 13, 14, 16, 17, 18, 20, 23, 26, 28, and 29) were detected. There is strong evidence that BTA14 is the key chromosome affecting CWT. Also, BTA20 is the key chromosome for almost all traits measured (WWT, YWT, LMA).

**Conclusion:** The application of various additive and dominance SNP models enabled better characterization of SNP inheritance mode for growth and carcass quality traits in Hanwoo, and many of the detected SNPs or QTL had dominance effects, suggesting that dominance be considered for the whole-genome SNPs data and implementation of successive molecular breeding schemes in Hanwoo.

**Keywords:** Hanwoo, Single Nucleotide Polymorphism, Whole Genome Association, Carcass Traits, Growth Traits

## INTRODUCTION

In recent years, whole genome association study (WGAS) or genomic selection (GS) has been a main focus on livestock breeding due to the expectation of increased accuracy of selection and reduced generation interval, compared to traditional breeding approaches such as progeny testing. WGAS or GS has been enabled by high-density single nucleotide polymorphism (SNP) chips, which allows identification of causative SNPs for economic traits and improves reliability of breeding value prediction.

Single-marker association analysis with density SNP array has similar or greater power to

detect quantitative trait loci (QTLs) and provides more precise QTL locations than haplotype-based or identity-by-descent based models [1]. Further, the method offers a greater flexibility of including dominance or epistatic effects in the model, enabling better characterization of the QTL in terms of inheritance mode of gene action. Indeed, some WGAS approaches have been routinely practiced in dairy and beef cattle to detect SNPs for milk production, or meat and carcass, respectively [2-4].

A Korean native cattle, Hanwoo (*Bos taurus coreanae*), was used as draft animals and suppliers of organic fertilizer. However, as agricultural technologies became improved and beef consumption increased, Hanwoo became more important as beef cattle. The Korean cattle had low meat production efficiency because of low milk production and slow growth rate, while having a relatively high reproductive rate and high marbling, e.g. 15% to 23% of intramuscular fat at final slaughter [5]. It has been about 30 years since Hanwoo improvement program was implemented, in order to increase meat production and quality to meet the growing demand for beef in Korea [6].

Interactions between genes at the same locus are called dominance. Dominance effect has often been ignored or treated as a nuisance parameter in genetic evaluations of livestock and quantification of variance components [7]. However, quantification of dominance effects underlying complex traits is needed due to increasing evidence of the major effects of dominant QTL on human disease and agricultural traits of economic importance [8,9]. Recently, a number of studies showing that accounting for dominance effects increased the accuracy and reduced the bias of genomically-predicted breeding values in comparison to an additive model. Su et al [10] reported that in a purebred Duroc population the dominance variance accounted for 6% of the total phenotypic variance in daily gain, emphasizing the relevance of dominance [10]. Therefore, an increasing need for WGAS methodology to routinely investigate the non-additive effects such as dominance. Herein, we performed a WGAS to identify SNPs with dominance and/or additive effects that were associated with growth and carcass traits, specifically to investigate the importance of dominance in Korean beef cattle, Hanwoo.

## MATERIALS AND METHODS

### Animals, phenotypes and SNPs

The Hanwoo data were collected from 486 steers that were used for progeny testing in Hanwoo Improvement Center of National Agricultural Cooperative Federation in Seosan, Korea. The steers were born between spring of 2005 and fall of 2007, sired by 61 Hanwoo bulls (paternal halfsibs). The number of steers for each sire ranged from two to 13 with the average of eight steers.

The steers were weaned at 5 or 6 months of age, and each group of 10 steers were raised in a pen. The feeding program was divided into early, middle, and late stage, each with a six

months interval. In the early and middle stages, the steers were fed with concentrates with the amount of 1.8% of the body weight and *ad libitum* in the late stage. The concentrates were composed of 15%, 13%, and 11% of crude protein, and 71%, 72%, and 73% total digestible nutrients (TDN), in the respective feeding stages. Roughages with 4.5% crude protein and 37.5 TDN were offered *ad libitum* with other additives such as vitamin and minerals. All steers were slaughtered at approximately 24 months of age. Traits measured were weaning weight (WWT) at approximately six months of age, 365-d yearling weight (YWT) and carcass weight (CWT) at 24 hours after slaughter. The carcasses were dissected at the last rib and the first lumber vertebra according to the Animal Product Grading System of Korea to measure backfat thickness (BFT), *longissimus dorsi* muscle area (LMA), and marbling score (Marb). The Marb score was numbered as 1 through 9 according to the Korean Beef Marbling Standard (1 = trace, 9 = very abundant). Details about measurement of the traits and management practices were described in Lee et al [2]. The statistics for phenotypic data used in this study are summarized in Table 1.

DNA of the sires and their steers were quantified and genotyped using the Illumina bovine SNP50K beadchip. Details on the SNP genotyping procedure were described in Lee et al [2]. Between the sires and their sons (steers), Mendelian consistency was checked, i.e. any discordance of SNP genotypes between them. If more than 1,000 SNPs were discordant, then the steer was removed. Also, the individual with more than 10% missing genotypes was discarded.

The Illumina bovine SNP50 beadchip assay contained 54,001 SNPs with an average distance interval of 51.5 kb. Criteria for SNP removal were: i) more than 5% pedigree discordant (e.g. cases where a sire was homozygous for one allele and progeny were homozygous for the other allele), ii) less than 90% call rate, iii) monomorphic SNPs or when the minor allele frequency was smaller than 0.05, iv) proportion of individuals with genotype completeness was smaller than 90%, v) markers with significant departure from Hardy-Weinberg equilibrium ( $p < 0.00001$ ), vi) assigned to X chromosome or not assigned to any chromosome on Bovine Genome Build 4.0.

Missing genotypes were imputed using Druet method [11].

**Table 1.** Summary statistics for 486 observations on growth and carcass traits in a Hanwoo steer population

Trait	Average	SD	Minimum	Maximum	CV
Weaning weight (kg)	170	30.7	84.5	271	18.0
Yearling weight (kg)	312	34.2	220	414	11.0
Carcass weight (kg)	357	40.0	158	481	11.2
Backfat thickness (cm)	1.01	0.41	0.30	3.50	40.9
<i>Longissimus dorsi</i> muscle area (cm <sup>2</sup> )	78.9	9.54	22	109	12.1
Marbling score (1-9)	3.38	1.77	1	9	52.5

SD, standard deviation; CV, coefficient of variation (%).

Haplotypes were first partially reconstructed based on genotypes of relatives, i.e. halfsib steers and their sires (based on Mendelian segregation rules and linkage information) with the program, LinkPHASE (Liège, Belgium). Then, DAGPHASE (Liège, Belgium) and Beagle (Seattle, WA, USA) with scale and shift parameter set equal to 2.0 and 0.1, respectively, were iteratively used to estimate the parameters of a directed acyclic graph. The programs were run first with genotypes from animals genotyped for all markers for 10 iterations and then with genotypes from all animals for 10 more iterations. The accuracy of imputing genotypes was ranged from 0.81 to 0.96 [11].

**Whole genome association analysis**

A mixed-inheritance animal model was used to detect SNP with additive or dominance effects for growth and carcass quality of Hanwoo. The ‘snp\_a’, ‘snp\_d’, and ‘snp\_ad’ options of Qxpak software (Barcelona, Spain) were applied for each SNP. For each trait, appropriate fixed factors or covariates were fitted in the models (p<0.05) using a general linear model procedure in SAS (SAS 9.1, SAS Institute Inc., Cary, NC, USA).

Firstly, the additive and dominance expression model (Add+Dom) was chosen as a base model:

$$y_i = \mu + \sum_j \beta_j c_{ij} + SNP_{ad\_i} + u_i + e_i$$

Where  $y_i$  is the phenotypic record of animal  $i$ ,  $\mu$  is the average phenotypic performance,  $c_{ij}$  is the value of the  $j$ th covariate or fixed effect for the animal  $i$ ,  $\beta_j$  is an estimate of the  $j$ th fixed effect or covariate,  $SNP_{ad\_i}$  is the additive and dominance effect of SNP for animal  $i$  (e.g. individuals with marker genotypes ‘11’, ‘12’, and ‘22’ are assumed to have genetic values  $\mu_{kAA}$ ,  $\mu_{kAB}$ , and  $\mu_{kBB}$ ),  $u_i$  is the infinitesimal genetic effect of animal  $i$ , which is distributed as  $N(0, A\sigma_u^2)$  (the numerator relationship matrix  $A$  and the additive genetic variance  $\sigma_u^2$ ) and  $e_i$  is a random

residual for animal  $i$ , which is distributed as  $N(0, I\sigma_e^2)$  (identity matrix  $I$  and residual variance  $\sigma_e^2$ ). Two fixed effects were fitted in the models: year and season of birth (5 levels) for all the traits and region where the steers were born (41 levels) for WWT, YWT, and Marb, and a covariate was fitted; weaning age for WWT, yearling age for YWT, slaughter age for CWT, BFT, and LMA, was also fitted. Pedigrees of the base population animals were traced back for two generations to form the numerator relationship matrix, and 1,033 animals were included in the pedigree analysis.

The next models are the additive (Add) and dominance (Dom) expression models, and the null model:

Additive expression model: 
$$y_i = \mu + \sum_j \beta_j c_{ij} + SNP_{a\_i} + u_i + e_i$$

Dominance expression model: 
$$y_i = \mu + \sum_j \beta_j c_{ij} + SNP_{d\_i} + u_i + e_i$$

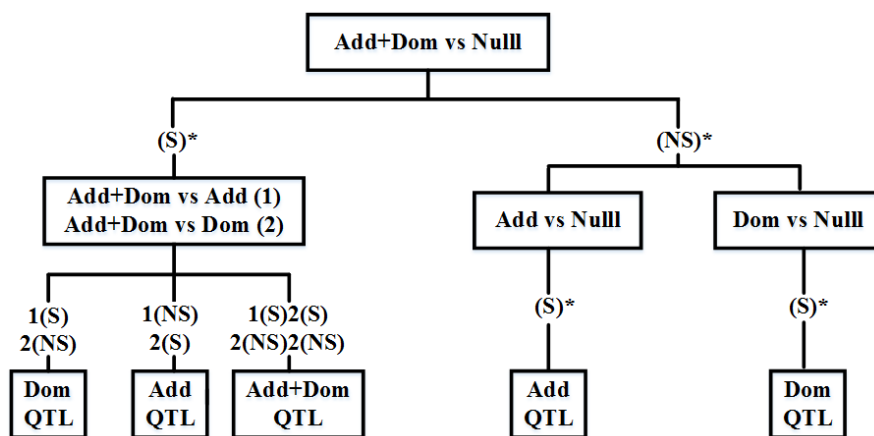
Null model: 
$$y_i = \mu + \sum_j \beta_j c_{ij} + u_i + e_i$$

Where  $y_i$ ,  $\mu$ ,  $c_{ij}$ ,  $\beta_j$ ,  $u_i$  as described above,  $SNP_{a\_i}$  is the additive-(a) effect of the SNP genotype values for animal  $i$  (e.g. individuals with marker genotypes ‘11’, ‘12’, and ‘22’ are assumed to have genetic values  $\mu_{kAA}$ , 0, and  $\mu_{kBB}$ ), and  $SNP_{d\_i}$  is the dominance effect of the SNP for animal  $i$  (e.g. individuals with marker genotypes ‘11’, ‘12’, and ‘22’ are assumed to have genetic values 0,  $\mu_{kAB}$  and 0).

A series of tests was applied to classify gene expression pattern; additive or dominant, following the decision trees (Figure 1):

If the Add+Dom Model vs the Null model was significant at the 5% chromosome-wise (ChW) level:

- i) If the Add+Dom model vs the Add model was significant



**Figure 1.** Decision trees to determine classification of QTL type using Add+Dom, Add and Dom models. S\*, significant at a chromosome-wise level; NS\*, non-significant at a chromosome-wise level; S, significant (p<0.05); NS, non-significant (p<0.05).

and the Add+Dom model vs the Dom model was not significant at the 5% comparison wise level, then the SNP was defined to have dominance inheritance mode of gene action.

ii) If the Add+Dom model vs the Add model was not significant and the Add+Dom model vs the Dom model was significant at the 5% comparison wise level, then the SNP was defined to have additive inheritance mode of gene action.

iii) If the Add+Dom model vs the Add model and the Add+Dom model vs the Dom model were both significant or both not significant at the 5% comparison wise level, then the SNP was defined to have additive and dominance expressed.

If the Add+Dom model vs the Null model was not significant at the 5% ChW level:

i) If the Add model vs the Null model was significant at the 5% ChW level, then the SNP was classified as additive expressed SNP.

ii) If the Dom model vs the Null model was significant at the 5% ChW level, then the SNP was classified as dominance expressed SNP.

All the models were fitted for each of the available SNPs. The log likelihood ratio tests (LRT) statistic was applied by comparing the log likelihoods between the full model and the reduced model:

$$LRT = -2(\text{LogLikelihood}_{\text{reduced\_model}} - \text{LogLikelihood}_{\text{full\_model}})$$

The LRT test statistics approximately followed chi-squared distributions with degree of freedom equal to the number of extra parameters (one or two) estimated in the full model compared with the reduced model.

False discovery rate (FDR) was used to set significant thresholds to account for multiple testing, by calculating q-value based on nominal p-value from LRT test statistic for each trait using the R packages 'qvalue'. The FDR threshold was set at 5% genome-wise (GW) or a 5% ChW level.

### Marking the quantitative trait loci region

Generally, clusters of significant SNPs are expected to locate in the vicinity of a QTL, because there is linkage disequilibrium between adjacent markers that are closely located or clusters of transcription factor binding sites potentially indicating groups of co-regulated genes. In this study, the ChromoScan software (Ann Arbor, USA) was used to get statistical evidence of both a clustering of the SNP locations and a clustering of P-values from the above three mixed-inheritance animal model [12]. In the QTL region, one or more SNPs must be detected, and the variance that was explained by the QTL was estimated with the most significant SNP. The genetic variance was obtained from the estimated genotype effects from the corresponding

model and the observed genotype frequencies. The percentage of the total genetic variance explained by the significant SNP was also obtained.

## RESULTS AND DISCUSSION

### Available single nucleotide polymorphisms

Among the 54,001 SNPs in the Illumina bovine beadchip array, 35,968 SNPs were available for GWA tests. The SNPs covered 2543.6 Mb of the bovine genome with  $70.6 \pm 69.0$  kb average adjacent marker interval (Table 2). The largest gap between adjacent SNPs (2,081.5 kb) was located on BTA 10. Average observed heterozygosity for SNPs was  $0.37 \pm 0.12$ , and average minor allele frequencies (MAF) of all SNPs before (after) editing was 0.20 (0.27). The SNPs genotyped showed an almost uniform distribution across the common frequency classes.

### Whole genome association study

A total of 92 (37) significant SNPs were detected at 5% ChW (GW) level; 18 (0), 15 (3), 12 (8), 15 (18), 11 (7), and 21 (1)

**Table 2.** SNP distributions after quality control and average distances between adjacent SNPs on *Bos taurus* autosomal chromosomes

BTA	No. SNPs	Average intervals (kb)
1	2,376	67.75
2	1,930	72.91
3	1,832	69.40
4	1,736	71.37
5	1,472	85.52
6	1,818	67.38
7	1,577	70.87
8	1,673	69.93
9	1,399	77.21
10	1,487	71.03
11	1,567	70.27
12	1,145	74.47
13	1,228	68.52
14	1,219	66.71
15	1,160	72.96
16	1,101	70.62
17	1,092	69.95
18	930	71.08
19	993	65.59
20	1,114	67.75
21	997	69.42
22	872	70.75
23	792	67.37
24	918	70.81
25	699	61.98
26	764	67.18
27	694	70.28
28	652	70.62
29	731	70.82
Total	35,968	

SNP, single nucleotide polymorphism; BTA, *Bos taurus* autosome.

**Table 3.** Number of significant SNPs with additive and/or dominance effects that were detected for growth and carcass quality traits in Hanwoo<sup>1)</sup>

Trait	Additive	Dominance	Partial	Total
Weaning weight (kg)	9(0)	2(0)	7(0)	18(0)
Yearling weight (kg)	5(1)	6(1)	4(1)	15(3)
Carcass weight (kg)	6(4)	1(0)	5(4)	12(8)
Backfat thickness (cm)	10(6)	1(0)	4(12)	15(18)
<i>Longissimus dorsi</i> muscle area (cm <sup>2</sup> )	7(0)	2(0)	2(7)	11(7)
Marbling score (1-9)	8(0)	6(1)	7(0)	21(1)
Total	45(11)	18(2)	29(24)	92(37)

SNPs, single nucleotide polymorphism; QTL, quantitative trait loci.

<sup>1)</sup> The numbers were for the QTL that were detected at the 5% chromosome-wise level (genome-wise level).

SNPs for WWT, YWT, CWT, BFT, LMA, and Marb respectively (Table 3). Among the significant SNPs, 45 (11) SNPs had additive mode of gene action, 18 (2) SNPs dominance, and 29 (24) had both additive and dominance mode of gene action. The detail description of the significant SNPs for the six growth and carcass quality traits, including their positions in the genome, additive and dominance effects, the estimated proportion of the phenotypic variance and known genes near the SNPs, are in Table 4 through 9.

**Weaning weight (WWT):** Eighteen SNPs were detected at 5% ChW level (Table 4). Of the SNPs, nine, two and seven SNPs were declared to be additive, dominant and both additive and dominant, respectively. Two, five and four SNPs were detected

in BTA1, 5 and 12, respectively. Six SNPs were located within the QTL regions for WWT identified in Angus cattle (McClure et al [13]), *i.e.* BTB-01747944, BTB-02105769, ARS-BFGL-NGS-35164, ARS-BFGL-NGS-5482, ARS-BFGL-BAC-11115, and ARS-BFGL-NGS-39382. Among the 18 SNPs, three SNPs on BTAs 5, 16 and 20 were located within the regions of known genes, *i.e.* LOC505861, PLCH2, and ADAMTS12 (Table 4).

**Yearling weight (YWT):** A total of 18 significant SNP were detected for YWT, of which three SNPs at the 5% GW level (Table 5). Of the SNPs, six, seven, and five were declared as additive, dominant and both additive and dominant SNP, respectively. Five SNPs were located within the QTL regions for YWT in Angus cattle [13], *i.e.* ARS-BFGL-NGS-105590, ARS-BFGL-NGS-17747, ARS-BFGL-NGS-38840, Hapmap50009-BTA-50200, ARS-BFGL-NGS-42226. Among the 18 significant SNPs, seven SNPs were harbored within the regions of known genes (Table 5).

**Carcass weight (CWT):** A total of 20 significant SNPs were detected, of which eight SNPs at 5% GW level. Of the significant SNPs for CWT, ten, one and nine SNPs had additive, dominance and both additive and dominance effects, respectively (Table 6). Fourteen SNPs for CWT were located within a 17.55 Mb (between 18.65 Mb and 36.10 Mb) on BTA14. Fifteen significant SNPs were located within the chromosomal regions where QTL for CWT were reported in previous studies of beef cattle [13-17], and five SNPs for CWT were harbored within the regions of known genes (Table 6). McClure et al [13]

**Table 4.** Position, SNP alleles, estimated effects of SNPs for weaning weight (kg) that were detected at 5% chromosome-wise level

SNP <sup>1)</sup>	Chr	Position (bp) <sup>2)</sup>	Allele <sup>3)</sup>	MAF	Estimates of SNPs effects <sup>4)</sup>		Significance (-log <sub>10</sub> P <sup>5)</sup>	Nearest gene <sup>6)</sup>	
					Additive	Dominance		Name	Distance (bp)
BTB-01747944	1	4,070,974	T/G	G(0.19)	12.1±2.91	-15.2±3.33	4.68	LOC785105	40,376
BTB-02105769	1	4,149,602	T/C	C(0.26)	8.74±2.29	-12.3±2.67	4.73	LOC785105	119,004
ARS-BFGL-NGS-35164	3	55,278,469	G/A	G(0.46)	-	8.86±2.02	4.78	CDC7	14,260
ARS-BFGL-NGS-5482	4	61,908,479	G/A	G(0.26)	-7.65±1.74	-	4.79	THAP5	17,976
BTA-29483-no-rs	5	4,963,140	C/A	C(0.17)	-8.92±2.04	-	5.02	CAPS2	85,827
Hapmap52787-rs29024515	5	33,277,668	T/C	C(0.21)	11.6±2.36	-8.63±2.9	4.8	LOC505861	within
BTA-73718-no-rs	5	66,075,729	T/G	G(0.07)	-12.0±3.01	-	4.06	NEDD1	249,756
ARS-BFGL-NGS-73495	5	90,096,456	G/A	G(0.31)	-6.46±1.64	-	4.01	SSPN	53,061
ARS-BFGL-NGS-34063	5	125,275,403	G/A	G(0.35)	-	-9.06±2.03	5	FAM19A5	324,968
BTB-00317489	7	64,536,896	G/A	G(0.27)	-8.10±1.71	-	5.45	GRIA1	40,884
ARS-BFGL-BAC-11115	11	82,938,260	T/C	T(0.28)	-6.87±1.60	-	4.92	MSGN1	11,224
ARS-BFGL-NGS-103169	12	39,576,130	T/C	T(0.14)	-18.6±4.29	-21.0±4.71	4.05	PCDH9	313,077
Hapmap26937-BTA-127685	12	54,656,928	G/A	G(0.34)	6.49±1.56	-	4.64	RBM26	194,009
BTB-00497582	12	54,690,096	T/G	T(0.37)	6.31±1.51	-	4.65	RBM26	160,841
Hapmap57428-rs29016058	12	78,783,490	T/C	C(0.11)	-21.9±4.99	22.7±5.44	3.81	LOC787750	583,453
ARS-BFGL-NGS-39382	16	47,648,555	G/A	A(0.30)	8.45±1.83	-5.86±2.38	4.63	PLCH2	within
ARS-BFGL-BAC-33668	20	42,739,808	T/G	G(0.16)	3.58±1.56	6.93±2.05	4.4	ADAMTS12	within
Hapmap40017-BTA-65421	29	33,632,380	T/C	T(0.05)	-14.2±3.53	-	4.27	ETS1	86,263

SNP, single nucleotide polymorphism; MAF, minor allele frequency; QTL, quantitative trait loci.

<sup>1,2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Nucleotides of substitution.

<sup>4)</sup> Estimates of additive and dominance effects with standard errors.

<sup>5)</sup> Negative logarithm of the comparison-wise p-value of the test-statistic against the null hypothesis of no QTL at the most likely position for the inferred QTL model.

<sup>6)</sup> The nearest known gene to the significant SNP.

**Table 5.** Position, SNP alleles, estimated effects of SNPs for yearling weight (kg) that were detected at 5% chromosome-wise level

SNP <sup>1)</sup>	Chr	Position (bp) <sup>2)</sup>	Allele <sup>3)</sup>	MAF	Estimates of SNPs effects <sup>4)</sup>		Significance (-log <sub>10</sub> P <sup>5)</sup> )	Nearest gene <sup>6)</sup>	
					Additive	Dominance		Name	Distance (bp)
ARS-BFGL-NGS-98401	2	41,281,224	G/A	G(0.39)	-	-9.54 ± 2.47	4.14	<i>GPDM</i>	63,447
Hapmap36520-SCAFFOLD290052_3670	2	41,325,780	T/C	T(0.42)	-	-10.1 ± 2.45	4.60	<i>NR4A2</i>	4,484
BTA-21857-no-rs	2	72,889,807	T/G	T(0.46)	-	12.4 ± 2.44	6.56*	<i>LOC523484</i>	within
ARS-BFGL-NGS-105590	7	62,525,451	G/A	A(0.28)	-8.19 ± 2.00	-	4.66	<i>FAT2</i>	within
BFGL-NGS-118165	11	60,747,467	T/C	T(0.39)	-9.56 ± 2.06	6.09 ± 2.58	4.90	<i>LRRTM4</i>	489,704
ARS-BFGL-BAC-11115	11	82,938,260	T/C	C(0.28)	-8.77 ± 1.98	-	5.17	<i>MSGN1</i>	11,224
ARS-BFGL-BAC-23724	14	72,289,416	G/A	G(0.35)	-8.69 ± 1.97	9.00 ± 2.70	5.30*	<i>CALB1</i>	24,824
ARS-BFGL-NGS-17747	15	13,517,697	T/C	C(0.35)	7.74 ± 1.84	-	4.82	<i>SES3</i>	21,628
ARS-BFGL-NGS-38840	15	31,874,189	T/A	T(0.48)	8.98 ± 1.81	-	6.43*	<i>UBASH3B</i>	86,347
ARS-BFGL-NGS-39866	18	18,183,364	G/A	G(0.39)	-	-11.0 ± 2.5	5.29	<i>CYLD</i>	within
Hapmap50009-BTA-50200	20	29,598,818	G/A	G(0.09)	35.3 ± 9.40	-26.3 ± 9.77	4.41	<i>LOC100138060</i>	42,816
ARS-BFGL-BAC-33668	20	42,739,808	T/G	T(0.46)	3.26 ± 1.92	9.70 ± 2.51	4.49	<i>ADAMTS12</i>	within
ARS-BFGL-BAC-28936	23	1,664,787	G/A	G(0.26)	-	-10.2 ± 2.61	4.28	<i>HMGCL1</i>	within
ARS-BFGL-BAC-30072	23	1,694,992	T/C	T(0.33)	-	-9.68 ± 2.53	4.15	<i>HMGCL1</i>	within
Hapmap48951-BTA-94291	26	14,828,964	T/C	C(0.25)	-8.86 ± 2.21	-	4.28	<i>EXOC6</i>	within
ARS-BFGL-NGS-42226	26	31,316,453	G/A	G(0.19)	-9.23 ± 2.37	-	4.23	<i>DUSP5</i>	18,449
BTA-98192-no-rs	27	32,786,807	G/A	G(0.28)	8.38 ± 2.29	-12.3 ± 2.99	4.73	<i>LOC783570</i>	184,156
Hapmap36817-SCAFFOLD245829_8774	29	22,927,228	G/A	A(0.21)	-	-11.9 ± 2.60	5.59	<i>LOC100139055</i>	185,099

SNP, single nucleotide polymorphism; MAF, minor allele frequency; QTL, quantitative trait loci.

<sup>1,2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Nucleotides of substitution.

<sup>4)</sup> Estimates of additive and dominance effects with standard errors.

<sup>5)</sup> Negative logarithm of the comparison-wise p-value of the test-statistic against the null hypothesis of no QTL at the most likely position for the inferred QTL model.

<sup>6)</sup> The nearest known gene to the significant SNP.

\* Significant at the 5% genome-wise level.

**Table 6.** Position, SNP alleles, estimated effects of SNPs for carcass weight (kg) that were detected at 5% chromosome-wise level

SNP <sup>1)</sup>	Chr	Position (bp) <sup>2)</sup>	Allele <sup>3)</sup>	MAF	Estimates of SNPs effects <sup>4)</sup>		Significance (-log <sub>10</sub> P <sup>5)</sup> )	Nearest gene <sup>6)</sup>	
					Additive	Dominance		Name	Distance (bp)
ARS-BFGL-NGS-36803	2	63,623,562	G/A	G(0.07)	97.8 ± 17.6	101 ± 18.0	5.45*	<i>LOC100140701</i>	330,224
BFGL-NGS-110568	8	56,596,924	G/A	A(0.06)	-97.8 ± 17.6	100 ± 18.0	5.43*	<i>CEP78</i>	14,027
ARS-BFGL-NGS-59989	10	84,166,596	T/C	C(0.46)	-	16.1 ± 3.17	4.90	<i>SLC8A3</i>	within
ARS-BFGL-NGS-54787	14	18,653,617	G/A	G(0.09)	-14.3 ± 4.14	-	3.32	<i>LOC529047</i>	within
Hapmap41993-BTA-86407	14	19,815,951	T/C	C(0.23)	10.3 ± 2.70	-	3.76	<i>LOC100140381</i>	40,312
BTB-01143619	14	24,315,258	T/C	C(0.06)	22.9 ± 5.02	-	5.17	<i>FAM110B</i>	79,759
BTB-01143580	14	24,383,627	G/A	A(0.06)	27.5 ± 5.02	-	7.20*	<i>UBXN2B</i>	32,070
Hapmap30932-BTC-011225	14	24,898,781	T/C	T(0.06)	-24.7 ± 5.08	-	5.81*	<i>TOX</i>	within
BTB-01280026	14	25,170,557	T/C	C(0.07)	24.0 ± 4.51	-	6.75*	<i>TOX</i>	96,111
Hapmap27934-BTC-065223	14	25,288,714	G/A	G(0.05)	-25.2 ± 5.12	-	5.89*	<i>LOC100140360</i>	144,727
UA-IFASA-9679	14	26,428,822	G/A	G(0.49)	-9.17 ± 2.39	7.08 ± 3.20	4.18	<i>CHD7</i>	101,474
Hapmap49130-BTA-34437	14	28,483,105	T/C	C(0.07)	34.0 ± 10.2	-22.30 ± 11.00	3.40	<i>YTHDF3</i>	422,759
BTB-00562658	14	28,536,444	G/A	A(0.07)	34.3 ± 10.2	-20.80 ± 11.00	3.75	<i>YTHDF3</i>	476,098
ARS-BFGL-BAC-8496	14	30,543,605	G/A	G(0.06)	-18.9 ± 4.82	-	4.09	<i>RRS1</i>	35,258
BTB-00564066	14	30,695,187	G/A	G(0.21)	-5.80 ± 3.97	7.74 ± 4.79	3.19	<i>MYBL1</i>	24,450
ARS-BFGL-NGS-6936	14	33,171,241	G/A	A(0.05)	18.7 ± 5.11	-	3.56	<i>PREX2</i>	within
BTB-01640837	14	36,095,273	T/G	G(0.43)	8.28 ± 2.33	-	3.30	<i>LOC509345</i>	443,377
ARS-BFGL-NGS-39866	18	18,183,364	G/A	A(0.39)	-7.96 ± 2.50	-8.52 ± 3.32	5.23*	<i>CYLD</i>	within
BTB-00752386	19	41,676,085	T/G	T(0.13)	-26.78 ± 6.40	-32.3 ± 7.19	4.41*	<i>MSL1</i>	7,676
BTB-01392802	21	54,287,321	G/A	A(0.11)	-67.0 ± 13.1	62.9 ± 13.3	4.35	<i>LOC787825</i>	125,238

SNP, single nucleotide polymorphism; MAF, minor allele frequency; QTL, quantitative trait loci.

<sup>1,2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Nucleotides of substitution.

<sup>4)</sup> Estimates of additive and dominance effects with standard errors.

<sup>5)</sup> Negative logarithm of the comparison-wise p-value of the test-statistic against the null hypothesis of no QTL at the most likely position for the inferred QTL model.

<sup>6)</sup> The nearest known gene to the significant SNP.

\* Significant at the 5% genome-wise level.

reported a CWT QTL at 46 cM of BTA8 (95% confidence interval (CI) 41.6 to 66.0 cM) in Angus cattle, near which the SNP, BFGL-NGS-110568, was detected at 56.6 Mb in this study [13]. McClure et al [13] also found another CWT QTL at 84 cM of BTA10 (95% CI 79.0-100.0 cM), while we detected one CWT SNP, ARS-BFGL-NGS-54787, at 84.17 Mb of the same chromosome (Table 6) [13]. In the BTA14 region (18.7 to 36.1 Mb) where clusters of CWT SNP were detected, 13 SNPs that were associated with CWT were previously reported in Japanese black (Wagyu) cattle [4,15] as well as in Hanwoo [16]. Casas et al [14] reported one CWT QTL on BTA18 in a halfsib family sired by Brahman×Hereford cross, near which a GW significant SNP, ARS-BFGL-NGS-39866, was detected at 18.18 Mb

(Table 6) [14].

**Backfat thickness (BFT):** Thirty three SNPs for BFT were detected at 5% ChW level, of which 18 SNPs at 5% GW level. Of the significant SNPs for BFT, 16, one and 16 SNPs had additive, dominance and both additive and dominance effects, respectively (Table 7). There were three SNP clusters for BFT, *i.e.* four, five and three SNPs that were located within a 16.4 Mb segment (between 21.0 Mb and 37.4 Mb) on BTA14, a 44.1 Mb segment (between 28.3 Mb and 72.4 Mb) on BTA 16, and a 10.2 Mb segment (between 26.4 and 36.6 Mb) on BTA29, respectively. Eleven SNPs were harbored within the regions of known genes (Table 7), and in the chromosomal regions where twelve SNPs that were detected in this study, BFT QTL also reported in

**Table 7.** Position, SNP alleles, estimated effects of SNPs for backfat thickness (cm) that were detected at 5% chromosome-wise level

SNP <sup>1)</sup>	Chr	Position(bp) <sup>2)</sup>	Allele <sup>3)</sup>	MAF	Estimates of SNPs effects <sup>4)</sup>		Significance (-log <sub>10</sub> P <sup>5)</sup> )	Nearest gene <sup>6)</sup>	
					Additive	Dominance		Name	Distance (bp)
Hapmap24136-BTA-124014	1	55,673,837	T/G	G(0.18)	0.09±0.05	0.10±0.06	5.05*	CD47	19,151
Hapmap51248-BTA-51337	1	128,511,629	G/A	G(0.09)	-0.18±0.04	-	4.57	PLSI	within
Hapmap27170-BTA-142780	5	6,666,948	T/C	T(0.07)	-1.11±0.18	-1.20±0.19	8.47*	ZDHHC17	within
BFGL-NGS-119673	5	38,109,780	T/C	T(0.47)	-0.10±0.03	-	4.29	ANO6	within
ARS-BFGL-NGS-8401	5	76,428,730	T/G	T(0.28)	0.13±0.03	-	5.00*	SYN3	within
BTB-00236217	5	110,984,106	T/C	T(0.41)	0.11±0.03	-	4.13	CD9	2,776
BTB-01384704	6	959,692	A/G	G(0.48)	-0.12±0.03	-	5.57*	LOC100139637	63,038
BTB-01744782	6	1,452,847	T/G	G(0.07)	0.61±0.13	-0.56±0.14	4.74*	1-Mar	77,282
BTA-28590-no-rs	9	10,295,707	G/A	G(0.24)	-0.14±0.03	-	5.61*	bta-mir-30a	406,847
BTB-01374666	11	25,076,270	T/G	G(0.32)	0.12±0.03	-	4.55	U4	570,076
BTB-00467701	11	31,206,484	T/C	T(0.06)	-0.21±0.05	-	4.14	MSH6	54,643
Hapmap34906-BES11_Contig369_1053	11	79,443,335	G/A	A(0.37)	0.11±0.03	-	4.26	LOC513245	431,096
BTB-01493007	13	52,723,213	T/C	T(0.05)	-0.56±0.13	-0.36±0.14	5.57*	PTPRA	within
ARS-BFGL-NGS-34390	14	20,953,071	G/A	G(0.12)	-0.29±0.07	-0.21±0.08	3.87	ST18	within
Hapmap49130-BTA-34437	14	28,483,105	T/C	C(0.07)	0.59±0.11	-0.56±0.11	6.4*	YTHDF3	422,759
BTB-00562658	14	28,536,444	G/A	A(0.07)	0.59±0.11	-0.56±0.11	6.37*	YTHDF3	476,098
BTB-00566332	14	37,352,866	T/C	T(0.13)	-	-0.21±0.04	5.63	PEX2	266,891
ARS-BFGL-NGS-4138	15	39,970,876	T/C	T(0.06)	-1.13±0.19	-1.10±0.19	7.79*	GALNTL4	27,421
BTB-00634483	16	28,329,540	G/A	G(0.14)	-0.44±0.09	-0.43±0.10	4.76*	SMYD3	within
Hapmap42533-BTA-38667	16	31,436,094	G/A	A(0.38)	-0.11±0.03	-	4.68	CEP170	94,723
BTB-00640968	16	40,694,131	G/C	G(0.26)	0.15±0.03	-	6.31*	CTNBP1	12,174
ARS-BFGL-NGS-17466	16	53,804,655	T/A	T(0.26)	0.15±0.04	0.11±0.04	3.81	MRPS14	10,788
ARS-BFGL-NGS-85980	16	72,398,010	T/G	G(0.08)	0.54±0.13	-0.57±0.14	3.76	LOC100139930	46,502
ARS-BFGL-NGS-41599	17	74,420,464	G/A	A(0.07)	0.49±0.11	-0.54±0.12	4.82*	LOC616727	3,592
BTA-54022-no-rs	22	3,844,964	C/A	C(0.10)	-0.41±0.09	-0.41±0.09	4.81*	RBMS3	within
ARS-BFGL-NGS-18665	22	7,042,486	G/A	A(0.07)	0.91±0.14	-0.87±0.14	9.25*	DYNC1L1	1,080
BFGL-NGS-116395	23	11,896,040	C/A	C(0.40)	0.10±0.03	-	4.15	MDGA1	within
ARS-BFGL-BAC-30052	23	11,964,461	G/T	T(0.45)	0.12±0.03	-	5.53*	ZFAND3	24,327
BFGL-NGS-114371	26	51,572,874	G/A	G(0.08)	0.19±0.05	-	4.2	bta-mir-202	6,161
ARS-BFGL-NGS-28346	26	42,712,420	G/A	A(0.13)	0.37±0.08	-0.41±0.09	4.56*	TACC2	within
ARS-BFGL-NGS-39535	29	26,364,496	G/A	G(0.26)	0.13±0.03	-	4.66	NAV2	88,899
BTB-01020342	29	33,014,346	G/A	A(0.49)	-0.12±0.03	-	5.40*	ETS1	459,952
ARS-BFGL-NGS-23717	29	36,574,648	T/C	C(0.19)	0.22±0.05	-0.17±0.06	3.95	NTM	within

SNP, single nucleotide polymorphism; MAF, minor allele frequency; QTL, quantitative trait loci.

<sup>1),2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Nucleotides of substitution.

<sup>4)</sup> Estimates of additive and dominance effects with standard errors.

<sup>5)</sup> Negative logarithm of the comparison-wise p-value of the test-statistic against the null hypothesis of no QTL at the most likely position for the inferred QTL model.

<sup>6)</sup> The nearest known gene to the significant SNP.

\* Significant at the 5% genome-wise level.

Hanwoo, Angus or composite breeds [13,14,18,19]; Hapmap-51248-BTA-51337 on BTA1; BFGL-NGS-119673, ARS-BFGL-NGS-8401, and BTB-00236217 on BTA5; BTB-00236217 and BTB-01744782 on BTA6; Hapmap34906-BES11\_Contig369\_1053 on BTA11; BTB-01493007 on BTA13; BTB-00566332 on BTA14; BTB-00634483 and Hapmap42533-BTA38667 on BTA16; ARS-BFGL-NGS-39535 on BTA29 (Table 7).

**Longissimus dorsi muscle area (LMA):** A total of 18 SNPs were detected, of which seven SNPs at 5% GW level. Seven, two and nine SNPs were declared to be additive, dominance and both additive and dominance SNP, respectively (Table 8). Six LMA SNPs (BTA-99819-no-rs on BTA3; BTB-01321253 on BTA7; BFGL-NGS-110568 on BTA8; BFGL-NGS-112221 and BFGL-NGS-113227 on BTA20; ARS-BFGL-NGS-35298 on BTA24) were located within the QTL regions for LMA that were reported in a WGAS of Angus cattle [13].

**Marbling score (Marb):** A total of 22 SNPs were detected of which, eight, seven and seven had additive, dominance and both additive and dominance effects, respectively (Table 9). One SNP, BTB-00137937, was detected at 5% GW level. Of the significant SNPs for Marb, five SNPs were detected within a 19.2 Mb segment (between 61.5 Mb and 80.7 Mb) on BTA7. Twelve SNPs were located within the Marb QTL regions that were reported in previous studies [13,18,20]. Nine SNPs were harbored within the regions of known genes (Table 9). In particular, one SNP,

Hapmap39048-BTA-99764 was located within *EDG1* gene on BTA3, which was reported to be a positional function candidate gene responsible for marbling [20].

### Characterization of single nucleotide polymorphism for growth and carcass quality

Many SNPs influencing growth and carcass quality in Hanwoo had dominance effects. Of the 129 significant SNPs, 45 (11) SNPs had additive expression, 18 (2) dominance expression, and 29 (24) SNPs had both additive and dominant expression at 5% ChW (GW) level, of which 27 SNPs had overdominance effects, *i.e.* five for WWT, three for YWT, five for CWT, five for BFT, six for LMA, three for Marb, respectively (Tables 4 to 9). Using additive plus dominance effects, rather than additive effects only, led to more significant SNPs. These results indicated that the goodness of fit was improved by including dominance. Estimates of dominance effects have not been widely used in livestock breeding because it is difficult to estimate these effects accurately based on pedigree. The development of dense SNP panels offered new opportunities for detection and use of dominance at individual loci. Boysen et al [21] reported that significant dominance effects on milk production traits in cattle were identified in a WGAS [21].

The effectiveness of selection procedures that are based on genomic information can be increased by correctly characterization of inheritance mode of desired variants [7]. Heterosis

**Table 8.** Position, SNP alleles, estimated effects of SNPs for longissimus dorsi muscle area (cm<sup>2</sup>) that were detected at 5% chromosome-wise level

SNP <sup>1)</sup>	Chr	Position (bp) <sup>2)</sup>	Allele <sup>3)</sup>	MAF	Estimates of SNPs effects <sup>4)</sup>		Significance (-log <sub>10</sub> P <sup>5)</sup>	Nearest gene <sup>6)</sup>	
					Additive	Dominance		Name	Distance (bp)
ARS-BFGL-NGS-96411	1	99,002,229	G/A	A(0.08)	15.8±3.06	15.9±3.20	5.68*	<i>LOC100140324</i>	3,400
ARS-BFGL-NGS-36803	2	63,623,562	G/A	A(0.07)	26.4±4.29	27.3±4.40	8.13*	<i>LOC100140701</i>	330,224
BTA-99819-no-rs	3	84,880,188	T/C	T(0.07)	-9.60±2.23	11.3±2.42	4.69	<i>PDE4B</i>	within
Hapmap43716-BTA-87799	4	25,686,934	G/A	A(0.16)	8.32±1.78	9.79±1.92	5.54*	<i>LOC100139029</i>	144,805
ARS-BFGL-NGS-11156	6	31,210,287	T/C	C(0.06)	15.5±3.07	16.8±3.22	5.84*	<i>UNC5C</i>	within
BTB-01321253	7	83,625,072	G/A	G(0.17)	-	3.88±0.90	4.72	<i>XRCC4</i>	321,087
BFGL-NGS-110568	8	56,596,924	G/A	G(0.06)	-26.6±4.29	26.4±4.40	8.01*	<i>CEP78</i>	14,027
ARS-BFGL-NGS-77091	15	76,834,507	T/C	C(0.22)	-	3.49±0.84	4.47	<i>AMBRA1</i>	within
ARS-BFGL-NGS-25982	20	4,493,745	G/A	A(0.40)	2.49±0.64	-	4.00	<i>NEURL1B</i>	9,980
Hapmap53674-rs29025319	20	8,676,696	T/C	C(0.12)	4.69±0.96	-	5.84	<i>LOC783819</i>	132,888
ARS-BFGL-NGS-38482	20	37,708,167	T/C	C(0.10)	7.25±1.69	6.50±1.90	3.95	<i>RICTOR</i>	within
BFGL-NGS-112221	20	75,476,187	T/C	T(0.27)	-2.80±0.70	-	4.21	<i>ZDHHC11</i>	15,990
BFGL-NGS-113227	20	75,530,515	T/C	T(0.24)	-2.82±0.72	-	4.02	<i>CEP72</i>	within
BTB-01392802	21	54,287,321	G/A	G(0.11)	-16.5±3.21	14.8±3.28	5.95*	<i>LOC787825</i>	125,238
ARS-BFGL-NGS-35298	24	13,445,705	T/C	T(0.27)	-2.57±0.66	-	3.94	<i>LOC781724</i>	3,783
BTA-100770-no-rs	24	40,446,177	T/C	C(0.46)	-2.45±0.60	-	4.25	<i>EPB41L3</i>	within
ARS-BFGL-NGS-16328	26	18,231,319	G/A	A(0.13)	-3.94±0.91	-	4.78	<i>TLL2</i>	within
ARS-BFGL-NGS-94161	28	35,084,332	G/A	G(0.14)	-10.8±2.17	11.0±2.27	5.38*	<i>SFTPD</i>	3,977

SNP, single nucleotide polymorphism; MAF, minor allele frequency; QTL, quantitative trait loci.

<sup>1,2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Nucleotides of substitution.

<sup>4)</sup> Estimates of additive and dominance effects with standard errors.

<sup>5)</sup> Negative logarithm of the comparison-wise p-value of the test-statistic against the null hypothesis of no QTL at the most likely position for the inferred QTL model.

<sup>6)</sup> The nearest known gene to the significant SNP.

\* Significant at the 5% genome-wise level.



**Table 9.** Position, SNP alleles, estimated effects of SNPs for marbling score (1-9) that were detected at 5% chromosome-wise level

SNP <sup>1)</sup>	Chr	Position (bp) <sup>2)</sup>	Allele <sup>3)</sup>	MAF	Estimates of SNPs effects <sup>4)</sup>		Significance (-log <sub>10</sub> P <sup>5)</sup> )	Nearest gene <sup>6)</sup>	
					Additive	Dominance		Name	Distance (bp)
BTB-00126406	3	35,420,885	T/C	T(0.08)	2.04±0.41	-1.55±0.44	5.78	<i>KCNA3</i>	6,892
Hapmap39048-BTA-99764	3	44,502,770	T/G	T(0.30)	0.53±0.12	-	4.81	<i>EDG1</i>	within
BTB-00137937	3	87,445,557	G/A	A(0.15)	-	0.91±0.18	6.32*	<i>ROR1</i>	within
Hapmap3063-BTA-15439	5	109,235,854	C/A	C(0.16)	-	-0.72±0.17	4.57	<i>LOC751811</i>	2,138
UA-IFASA-5392	7	61,523,523	T/C	C(0.17)	-0.68±0.16	-	4.89	<i>LOC100138980</i>	11,789
BTB-00317097	7	65,652,720	T/C	C(0.25)	-0.59±0.13	-	4.88	<i>LOC784642</i>	39,676
BFGL-NGS-114649	7	69,609,512	T/G	T(0.37)	-0.36±0.13	-0.32±0.16	3.91	<i>EPN4</i>	409,625
ARS-BFGL-NGS-63249	7	71,629,520	T/C	C(0.47)	0.36±0.11	0.49±0.15	4.06	<i>FABP6</i>	6,896
Hapmap40812-BTA-80049	7	80,713,755	T/C	T(0.11)	1.39±0.35	-0.90±0.38	3.97	<i>ODZ2</i>	within
Hapmap25504-BTA-125586	10	53,007,997	G/A	G(0.24)	0.90±0.18	-0.77±0.21	5.17	<i>GRINL1A</i>	113,126
ARS-BFGL-NGS-73404	13	54,520,958	T/C	C(0.10)	0.84±0.20	*	4.73	<i>PRPF6</i>	within
BTB-00633720	16	27,646,807	T/G	T(0.12)	0.73±0.18	-	4.06	<i>EPB41L3</i>	within
Hapmap26379-BTA-130999	16	51,370,098	T/C	T(0.37)	0.50±0.12	-	4.71	<i>PDPN</i>	12,031
Hapmap60996-rs29015760	17	25,742,715	C/A	C(0.15)	-	0.75±0.18	4.45	<i>LOC539187</i>	72,892
BTB-00689316	17	73,276,535	T/C	C(0.43)	-	-0.62±0.15	4.26	<i>MORC2</i>	within
ARS-BFGL-NGS-107813	18	33,279,345	C/A	A(0.32)	-	-0.64±0.15	4.60	<i>TK2</i>	within
ARS-BFGL-NGS-55014	18	39,198,464	G/A	A(0.49)	0.31±0.11	-0.53±0.15	4.37	<i>HYDIN</i>	within
Hapmap40994-BTA-46361	19	62,959,153	T/C	T(0.35)	0.50±0.12	-	4.18	<i>MAP2K6</i>	78,574
ARS-BFGL-NGS-36359	19	63,936,266	T/C	C(0.13)	-0.68±0.17	-	4.25	<i>RG59</i>	38,731
ARS-BFGL-NGS-16187	25	8,839,364	G/A	A(0.45)	-0.33±0.12	-0.59±0.15	4.62	<i>LOC538487</i>	37,048
BTB-111681-no-rs	26	10,857,884	G/A	G(0.13)	-	-0.75±0.19	4.12	<i>LIPK</i>	within
BTB-00978135	28	12,940,047	T/G	T(0.37)	-	-0.61±0.15	4.15	<i>BICC1</i>	21,033

SNP, single nucleotide polymorphism; MAF, minor allele frequency; QTL, quantitative trait loci.

<sup>1,2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Nucleotides of substitution.

<sup>4)</sup> Estimates of additive and dominance effects with standard errors.

<sup>5)</sup> Negative logarithm of the comparison-wise p-value of the test-statistic against the null hypothesis of no QTL at the most likely position for the inferred QTL model.

<sup>6)</sup> The nearest known gene to the significant SNP.

\* Significant at the 5% genome-wise level.

that is caused by heterozygosity in single loci is responsible for survival rate by increasing reproductive fitness [22]. Hayes and Miller (2000) showed that dominance effect was needed in mate selection to exploit previously untapped genetic variation [23], while Dekkers and Chakraborty (2004) stressed maximization of crossbred performance by incorporating information from overdominant QTL [24]. Kim et al [8] found that many QTL for growth and carcass quality had a (over) dominant mode of gene action in a cross between Angus and Brahman cattle [8]. The use of dominance effects in a scenario of genomic selection increases the accuracy of estimated breeding values and still offers the opportunity of applying mate-allocation.

These result has important implication that dominance could be routinely included the whole-genome SNPs data in Hanwoo and implementation of successive molecular breeding schemes.

### Quantitative trait locus region

Thirty three QTL regions were identified on 18 BTAs for the significant SNPs for growth and carcass quality (Table 10). Of the QTL, 20, one, and 12 QTL had additive, dominance, and both additive and dominance expression modes, respectively. All the QTL explained small to moderate proportions (2.2%

to 10.9%) of the phenotypic variance with an average of 4.5%±-1.6%. However, the estimates may be overestimated, especially when the SNP effect was small, partly due to so called Beavis effect [25].

Some significant SNPs were located in close proximity, e.g. the two SNPs BTB-01747944 and BTB-02105769 for WWT at 4.07 Mb and 4.15 Mb on BTA1, and ARS-BFGL-BAC-28936 and ARS-BFGL-BAC-30072 for YWT at 1.66 Mb and 1.69 on BTA23, respectively (Tables 4 and 5). These SNPs might not be causal mutation, but so close to the causal SNP as to form high LD with the causal mutation for the trait, and the effect of a single QTL could be spread over multiple SNPs.

A QTL for CWT was detected at 24.1 to 25.7 Mb of BTA14 with a significant evidence (-log<sub>10</sub>P = 10.7). Also, four QTL for CWT were clustered between 19.7 and 36.1 Mb of BTA14 (Table 10). In the region, several QTL were reported that were associated with milk production, growth and carcass traits in cattle [8,15,26]. Especially in beef cattle, a majority of the QTL were located at 18 to 36 Mb of the chromosome [27]. The QTL region corresponded to a human chromosome *homo sapiens* (HSA) region in which genes responsible for growth characteristics reside. Mizoshita et al [15] reported a CWT-QTL in Wagyu

**Table 10.** QTL regions associated with growth and carcass traits and the percentage of the total genetic variance explained

Chr	Region type	Region start (bp) <sup>1)</sup>	Region end (bp) <sup>2)</sup>	Region size (bp)	Marker count	Region -log <sub>10</sub> P	Most significant SNP	
							SNP	%σ <sup>2</sup> <sub>p</sub> <sup>3)</sup>
Weaning weight (kg)								
4	add	61,386,842	61,908,479	521,637	12	2.98	ARS-BFGL-NGS-5482	4.75
5	add	4,528,722	4,963,140	434,418	11	2.70	BTA-29483-no-rs	4.70
11	add	82,506,706	82,998,032	491,326	11	2.21	ARS-BFGL-BAC-11115	4.07
12	add	54,600,867	54,690,096	89,229	4	2.17	Hapmap26937-BTA-127685	4.00
20	add+dom	42,739,808	42,872,996	133,188	4	2.94	ARS-BFGL-NGS-39382	4.33
Yearling weight (kg)								
11	add+dom	60,503,780	60,747,467	243,687	5	2.25	BFGL-NGS-118165	5.67
11	add	82,715,271	82,998,032	282,761	7	2.07	ARS-BFGL-BAC-11115	4.39
20	add+dom	42,739,808	42,819,855	80,047	3	2.17	ARS-BFGL-BAC-33668	4.41
26	add	14,341,149	14,828,964	487,815	9	2.07	Hapmap48951-BTA-94291	4.16
Carcass weight (kg)								
14	add	19,654,754	19,910,197	255,443	5	2.12	Hapmap41993-BTA-86407	2.96
14	add	24,100,495	25,707,512	1,607,017	36	10.65	BTB-01143580	6.25
14	add+dom	28,090,849	28,604,028	513,179	11	2.07	BTB-00562658	3.42
14	add	36,023,989	36,095,273	71,284	3	2.25	BTB-01640837	2.61
Backfat thickness (cm)								
5	add	37,930,354	38,268,770	338,416	6	2.09	BFGL-NGS-119673	3.25
5	add	75,805,133	76,714,910	909,777	14	4.73	ARS-BFGL-NGS-8401	4.45
6	add+dom	454,623	1,496,086	1,041,463	21	5	BTB-01744782	5.34
9	add	10,080,000	11,411,851	1,331,851	13	3.31	BTA-28590-no-rs	4.70
14	add+dom	28,344,924	28,938,888	593,694	12	2.61	Hapmap49130-BTA-34437	4.91
16	add	31,108,917	36,611,548	502,631	11	2.19	Hapmap42533-BTA-38667	3.78
16	add	39,293,150	40,694,131	1,324,364	18	5.83	BTB-00640968	5.76
16	add+dom	53,663,332	53,952,476	289,144	6	2.05	ARS-BFGL-NGS-17466	3.49
17	add+dom	74,292,265	74,738,486	446,221	6	2.34	ARS-BFGL-NGS-41599	3.13
23	add	11,627,828	12,207,677	579,849	9	2.23	ARS-BFGL-BAC-30052	4.71
29	add+dom	35,829,053	36,646,213	817,160	12	3.38	ARS-BFGL-NGS-23717	4
<i>Longissimus dorsi</i> muscle area(cm <sup>2</sup> )								
3	add+dom	84,750,518	85,176,770	426,252	11	2.71	BTA-99819-no-rs	2.97
7	add+dom	107,689,830	107,950,229	260,399	7	2.10	Hapmap48901-BTA-80577	2.19
20	add	4,040,334	4,745,147	704,813	17	3.92	ARS-BFGL-NGS-25982	3.65
20	add	8,115,195	8,810,833	695,638	13	3.12	Hapmap53674-rs29025319	5.52
20	add	75,346,433	75,530,515	184,082	4	2.54	BFGL-NGS-112221	3.82
28	add+dom	34,473,261	35,155,406	649,145	11	2.13	ARS-BFGL-NGS-94161	10.94
Marbling score (1-9)								
13	add	54,474,756	54,548,692	73,936	3	2.24	ARS-BFGL-NGS-73404	4.65
16	add	51,370,098	51,470,017	99,919	5	2.03	Hapmap26379-BTA-130999	4.24
18	dom	32,990,778	33,279,345	288,567	9	2.05	ARS-BFGL-NGS-107813	3.65

QTL, quantitative trait locus; SNP, single nucleotide polymorphism.

<sup>1),2)</sup> SNP marker annotations and their positions were based on the bovine reference genome (btau4.0).

<sup>3)</sup> Proportion of phenotypic variance due to the SNPs.

within a 1.1 Mb chromosomal segment flanked by DIK7012 and DIK7020 on BTA14, in which four genes, including CA8 and RAB2 resided in the corresponding HSA region or six bovine expressed sequence tag (EST) assemblies, which may be a source of additive genetic variation for carcass weight [15]. Pausch et al [3] recently reported a QTL at 24.1 to 25.4 Mb of BTA14 that was associated with polymorphisms for a polyadenylation signal of the gene encoding for ribosomal protein S20 (*RPS20*), explaining major genetic variation of growth-related traits in a sample of 1,800 bulls of the German Fleckvieh breed

[3]. In the similar region, Karim et al [28] identified causative variations influencing bovine stature in the *PLAG1-CHCHD7* inter-genic region in a Holstein-Friesian×Jersey F2 population [28]. At the same region, a QTL for carcass weight was identified in a population of 1,156 Japanese Black steers [4]. In conclusion, the evidence of CWT QTL around 25 Mb of BTA14 in this study supports the QTL or causal mutation for growth, carcass, or stature on the proximal region of BTA14 in cattle.

On BTA20, several QTL for WWT, YWT, and LMA were

identified (Table 10). The QTL for WWT and YWT were located at 42.74 to 42.87 Mb, near which a gene, GHR (33.90 to 34.07 Mb) was located. Growth hormone receptor (GHR) has been proposed as a candidate gene for growth and fat metabolism [29]. Another three QTL for LMA were located at 4.04 to 4.75 Mb, 8.12 to 8.81 Mb and 75.35 to 75.53 Mb, respectively. At the 8 Mb, a QTL for LMA was reported by Garcia et al [30] in F1 crossbred steers of *Bos taurus* breeds (Angus, Hereford, Gelbvieh, Simmental, Charolais, Limousin, and Red Angus) comprising Cycle 7 of the Germplasm Evaluation project [30]. Also, at 75 Mb, a LMA QTL was reported in a commercial Angus population [13].

Some QTL that affected two traits were located in close distance, e.g. the QTL for WWT and YWT at 82.5 and 83.0 Mb of BTA11, or the QTL for CWT and BFT at 28.1 and 28.9 Mb of BTA14 (Table 10), suggesting the nature of gene characteristics, *i.e.* pleiotropy or clustering of multi-genes.

## IMPLICATIONS

This study described a novel approach to model additive and dominance genetic effect using information of genome-wide SNP markers. Implementation of various additive and dominance SNP models enabled characterization of inheritance mode for QTL, and we found significant evidence of additive and/or dominance QTL for growth and carcass quality in a Hanwoo steer population. The QTL regions can be fine-mapped to find causal mutations, which would provide valuable information for subsequent quantitative trait loci analyses and genomic selection schemes. Many dominant QTL influencing growth and carcass traits in Hanwoo were detected in this study. This has the important implication that dominant expression for growth and carcass composition in beef cattle is not rare and thus dominance effect needs to be considered in marker-assisted breeding schemes in Hanwoo. Validation tests for the detected SNPs (QTL) are in progress and the QTLs that are confirmed in commercial Hanwoo populations can be applied to better improve Hanwoo production.

## CONFLICT OF INTEREST

We certify that there is no conflict of interest with any financial organization regarding the material discussed in the manuscript.

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