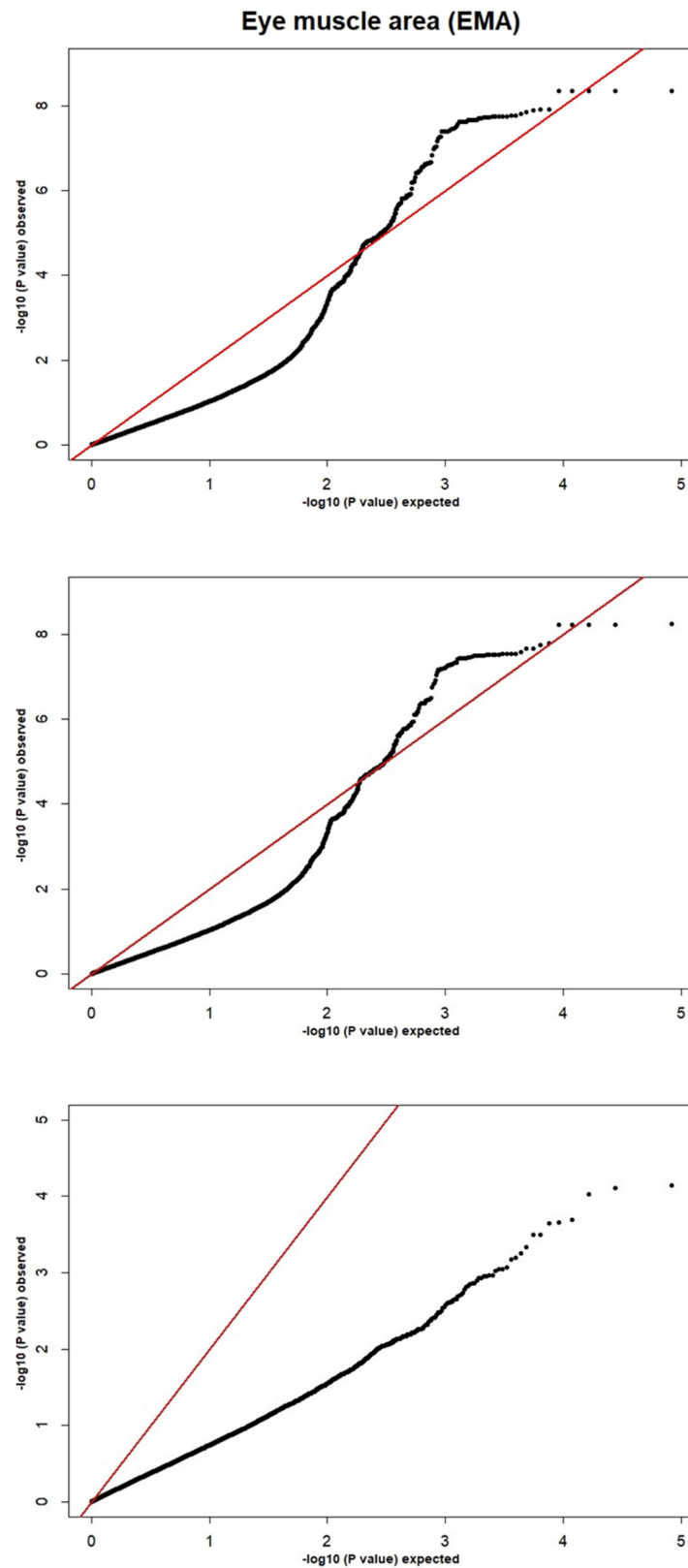
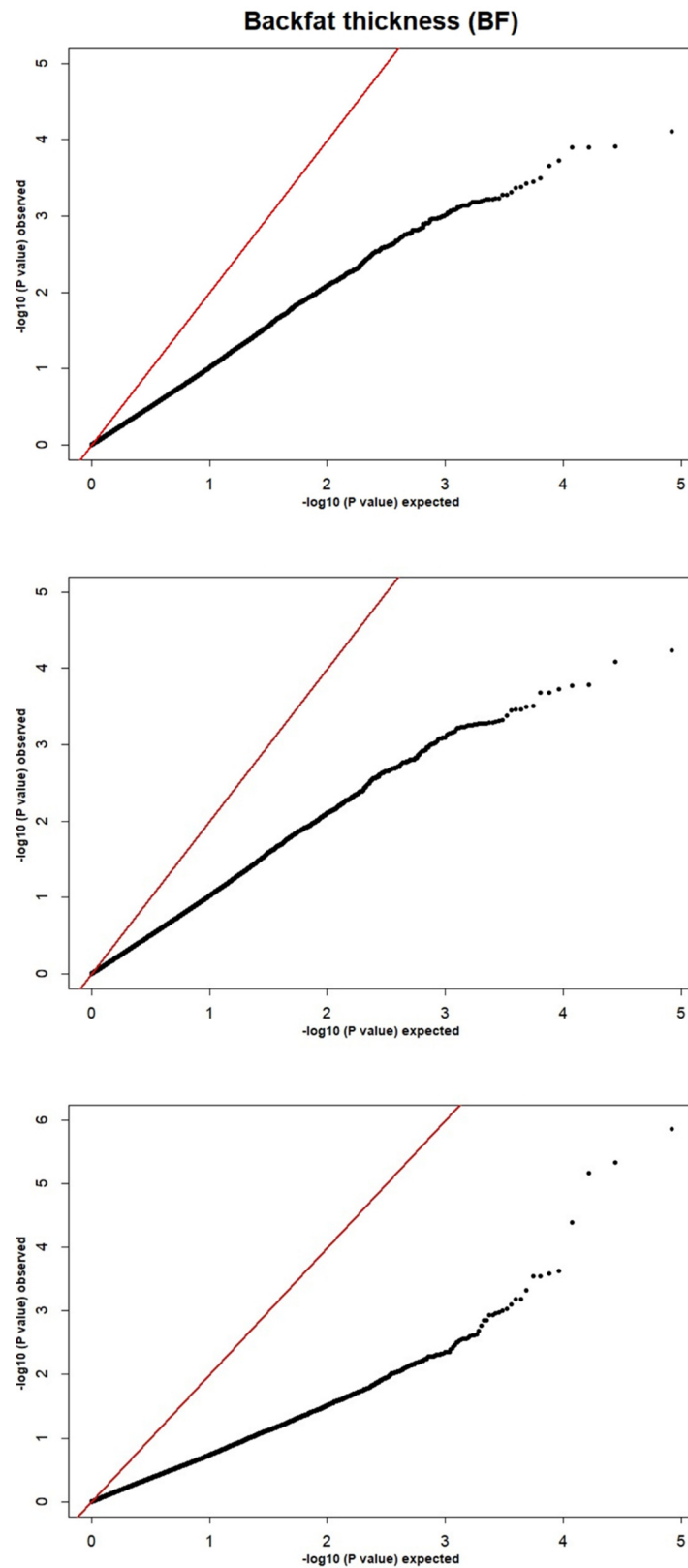


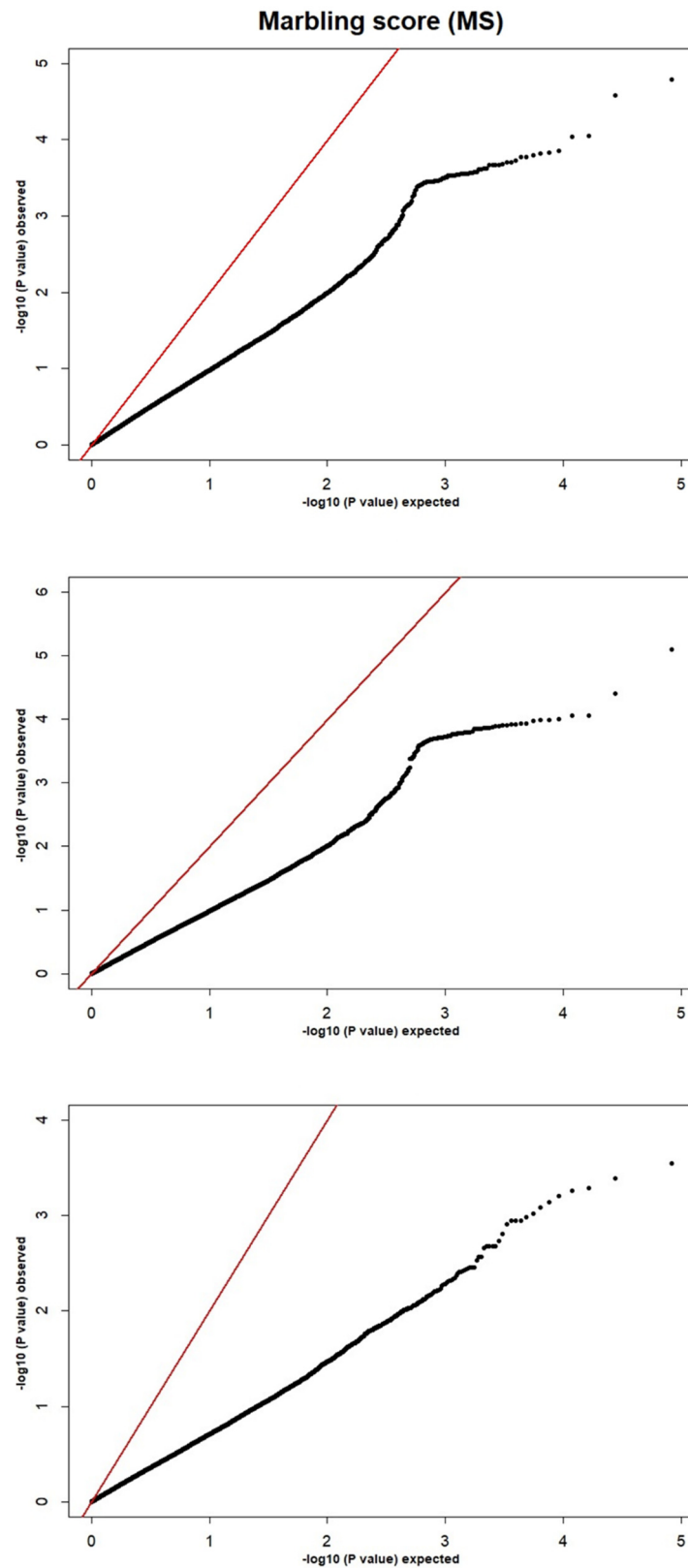
**Figure S1.** Quantile-quantile (Q-Q) plots for carcass weight in Hanwoo cattle using DGEV (upper panel), GEV (middle panel), and residual (lower panel) as predictors in the GBLUP method. Q-Q plot showing the late separation between observed and expected  $p$ -values ( $-\log_{10}P$ ). The red line represents the 95% concentration band under the null hypothesis of no association.



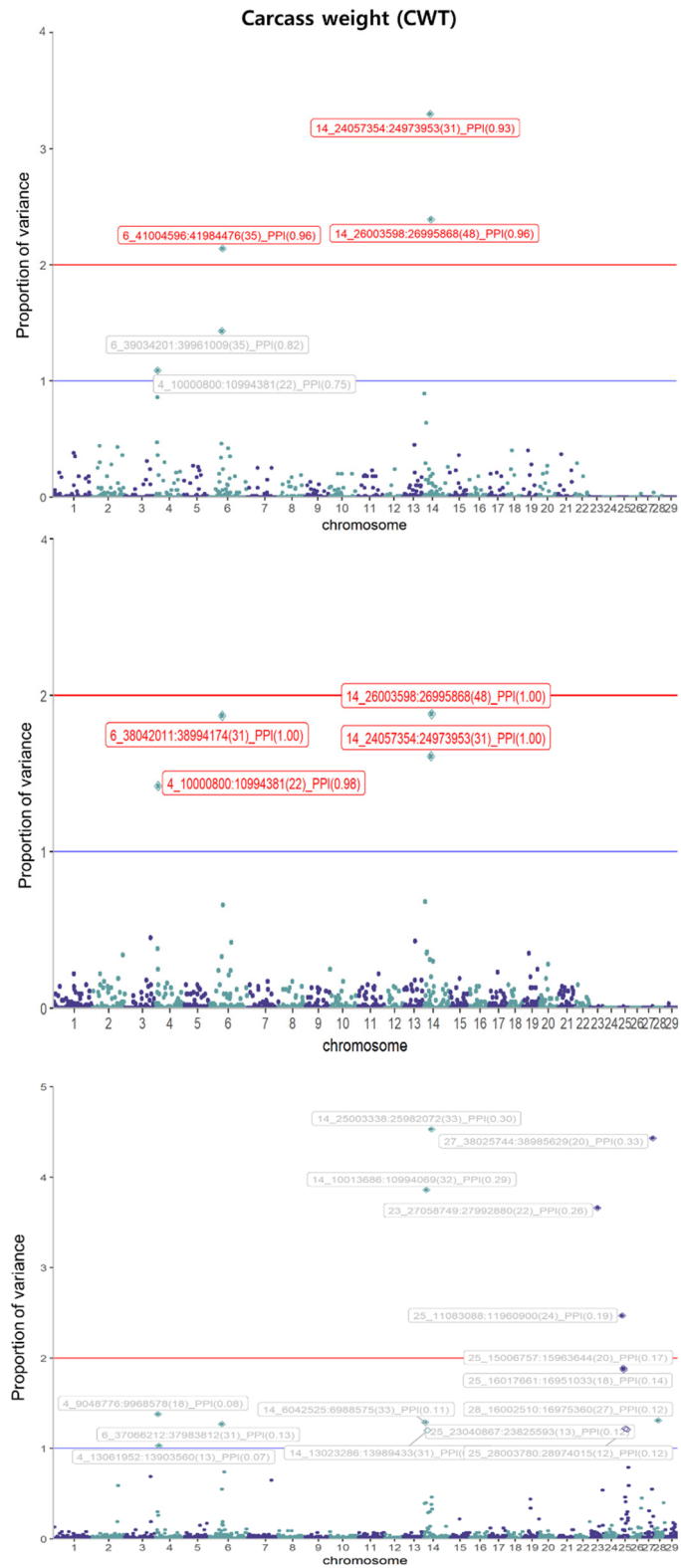
**Figure S2.** Quantile-quantile (Q-Q) plots for eye muscle area in Hanwoo cattle using DGEV (upper panel), GBEV (middle panel), and residual (lower panel) as predictors in the GBLUP method. Q-Q plot showing the late separation between observed and expected  $p$ -values ( $-\log_{10}P$ ). The red line represents the 95% concentration band under the null hypothesis of no association.



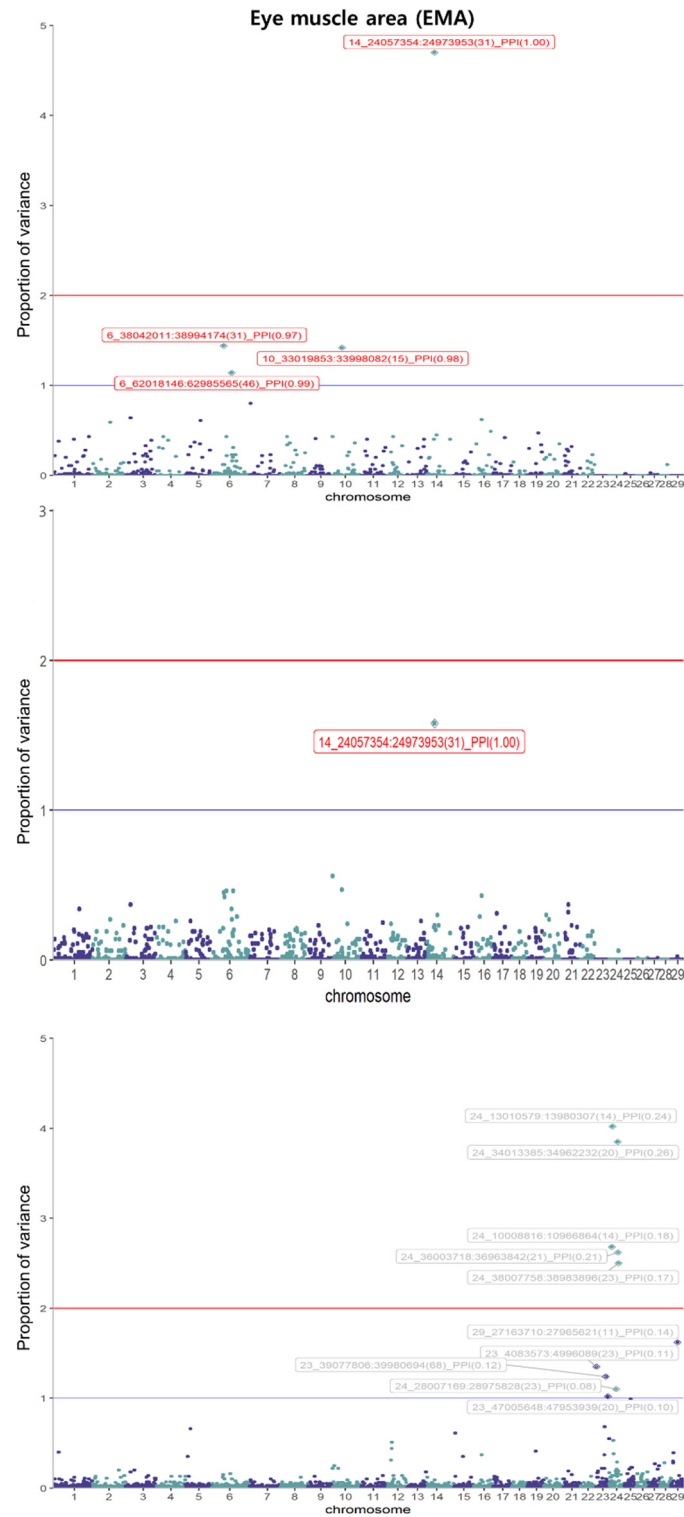
**Figure S3.** Quantile-quantile (Q-Q) plots for backfat thickness in Hanwoo cattle using DGEV (upper panel), GEV (middle panel), and residual (lower panel) as predictors in the GBLUP method. Q-Q plot showing the late separation between observed and expected  $p$ -values ( $-\log_{10}P$ ). The red line represents the 95% concentration band under the null hypothesis of no association.



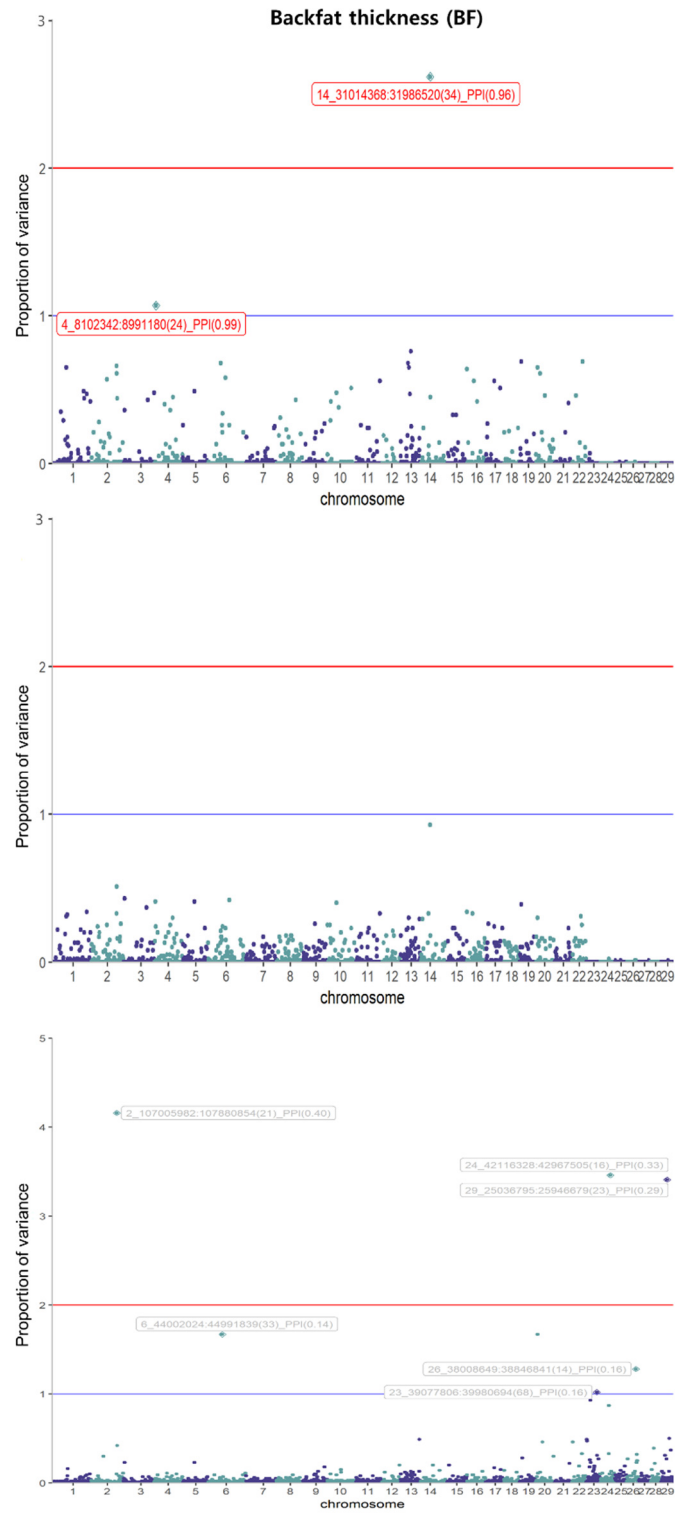
**Figure S4.** Quantile-quantile (Q-Q) plots for marbling score in Hanwoo cattle using DGEV (upper panel), GEV (middle panel), and residual (lower panel) as predictors in the GBLUP method. Q-Q plot showing the late separation between observed and expected  $p$ -values ( $-\log_{10}P$ ). The red line represents the 95% concentration band under the null hypothesis of no association.



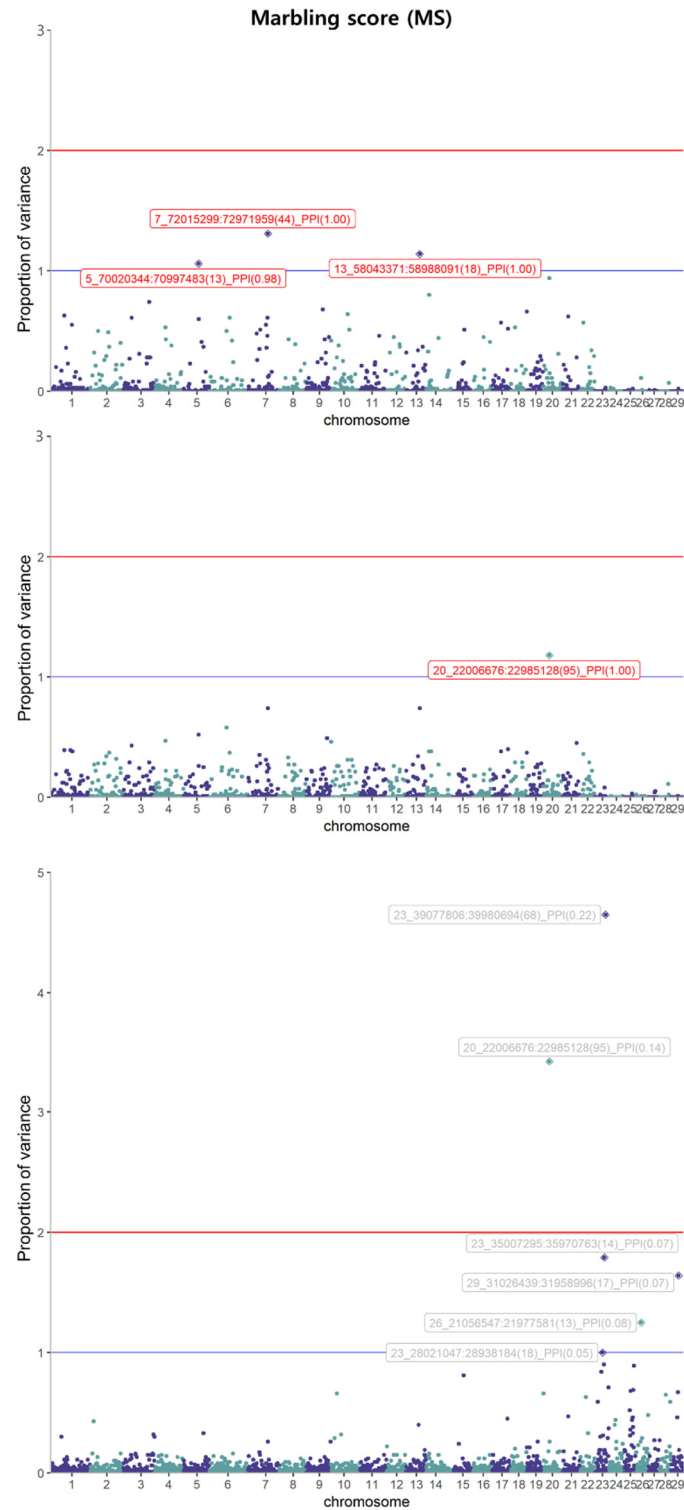
**Figure S5.** Genome-wide proportion of variance for carcass weight in Hanwoo cattle using DGEV (upper panel), GEV (middle panel), and residual (lower panel) as predictors in the Bayes B method. The X-axis represents the 29 *Bos taurus* autosomes, and the Y-axis represents the proportion of variance. The horizontal red line is the threshold 2.0 for significantly of windows.



**Figure S6.** Genome-wide proportion of variance for eye muscle area in Hanwoo cattle using DGEV (upper panel), GEV (middle panel), and residual (lower panel) as predictors in the Bayes B method. The X-axis represents the 29 *Bos taurus* autosomes, and the Y-axis represents the proportion of variance. The horizontal red line is the threshold 2.0 for significantly of windows.



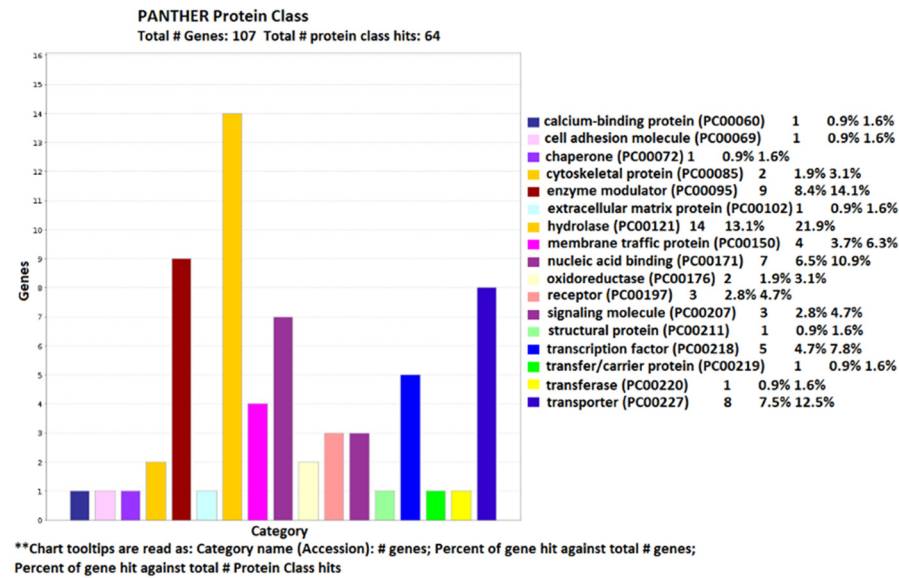
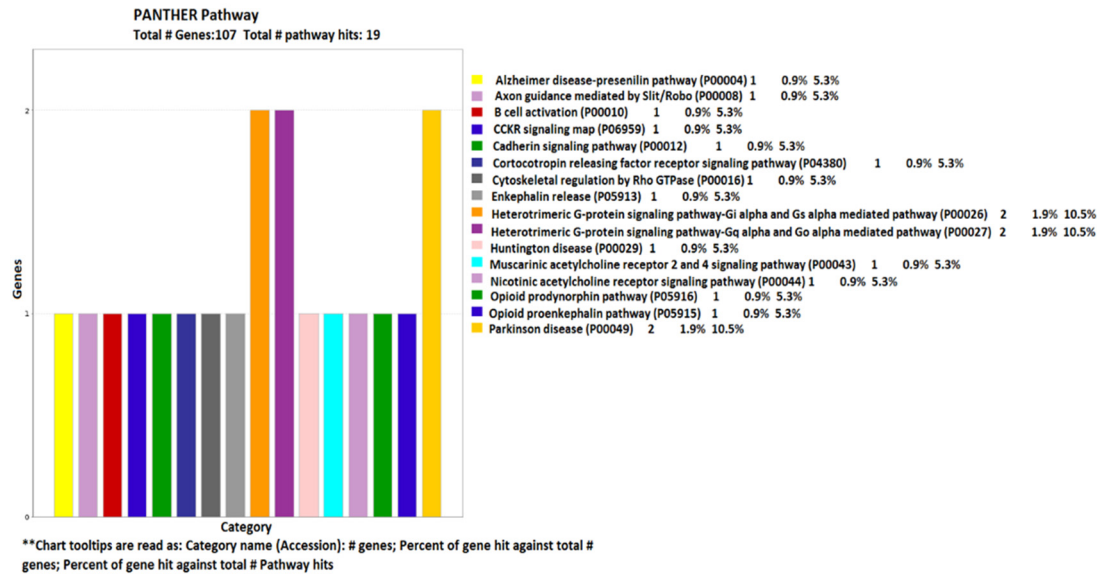
**Figure S7.** Genome-wide proportion of variance for backfat thickness in Hanwoo cattle using DGEV (upper panel), GEV (middle panel), and residual (lower panel) as predictors in the Bayes B method. The X-axis represents the 29 *Bos taurus* autosomes, and the Y-axis represents the proportion of variance. The horizontal red line is the threshold 2.0 for significantly of windows.



**Figure S8.** Genome-wide proportion of variance for marbling score in Hanwoo cattle using DGEV (upper panel), GEBV (middle panel), and residual (lower panel) as predictors in the Bayes B method. The X-axis represents the 29 *Bos taurus* autosomes, and the Y-axis represents the proportion of variance. The horizontal red line is the threshold 2.0 for significantly of windows.







**Figure S10.** The PANTHER pathway (top) and protein class (down) based on 107 selected genes from GWAS study, showing the percent of gene hit against total process hits.

**Table S1.** Estimates of genetic variance, residual variance, phenotypic variance, and heritability for four carcass traits in Hanwoo using 5-fold cross validation.

Method	Traits	$\sigma_a^2$	$\sigma_e^2$	$\sigma_p^2$	$h^2$
GBLUP	CWT	703.18	919.18	1622.36	0.43
	EMA	43.05	73.81	116.86	0.37
	BF	7.89	13.97	21.86	0.36
	MS	1.21	1.34	2.55	0.47
Bayes B	CWT	820.18	1746.92	926.73	0.47
	EMA	43.19	118.34	75.15	0.36
	BF	8.08	22.01	13.93	0.37
	MS	1.06	2.48	1.42	0.43

$\sigma_a^2$ , genetic variance;  $\sigma_e^2$ , residual variance;  $\sigma_p^2$ , phenotypic variance;  $h^2$ , heritability; GBLUP, genomic best linear unbiased prediction.

**Table S2.** Genome-wide significant common SNPs identified by GBLUP and Bayes B method, underlying CWT, EMA, BF, and MS traits in Hanwoo using de-regressed genomic estimated breeding values.

SNP	BTA: Position (bp)	Estimate ±SE	-log <sub>10</sub> P	Nearest gene	Consequence Type
<b>Carcass weight</b>					
rs380287756	6:41182962	4.465±0.136	8.534	<i>LOC782905, SLIT2</i>	IntGV
rs720848149	6:41262050	4.440±0.136	8.462	<i>SLIT2</i>	IV
rs470479052	6:41292118	4.120±0.122	9.024	<i>SLIT2</i>	IV
rs382125547	6:41311528	3.539±0.114	7.778	<i>SLIT2</i>	IV
rs384536472	6:41356212	3.562±0.114	7.784	<i>SLIT2</i>	IV
rs384017132	6:41438938	4.442±0.137	8.414	<i>SLIT2</i>	IV

rs719168867	6:41463763	4.467±0.137	8.508	SLIT2	IV
rs717602666	6:41526051	4.470±0.137	8.514	SLIT2	IV
rs721927483	6:41662240	4.458±0.136	8.516	SLIT2, PACRGL	IntGV
6:41957455	6:41957455	4.359±0.136	8.241	-	-
rs472474214	6:41984476	4.439±0.138	8.292	KCNIP4	IV
rs208411640	14:24141910	3.550±0.100	9.910	RP1, XKR4	IntGV
rs207487600	14:24266976	3.553±0.100	9.936	RP1, XKR4	IntGV
rs211204541	14:24332803	3.533±0.100	9.85	-	-
rs210090325	14:24343693	3.535±0.101	9.682	XKR4	IV
rs380287756	14:24391802	2.484±0.086	6.786	XKR4	IV
rs720848149	14:24432331	1.754±0.073	4.935	XKR4	IV
rs470479052	14:24437778	1.852±0.072	5.555	-	-
rs382125547	14:24462537	2.296±0.077	7.124	XKR4	IV
rs719168867	14:24891324	1.602±0.073	4.211	LYN	IV
rs717602666	14:24954981	1.862±0.078	4.885	RPS20	DGV
6:41957455	14:26023215	1.523±0.071	4.009	LOC107133115	IV
rs472474214	14:26083558	1.845±0.074	5.270	FAM110B	IV
rs208411640	14:26162492	3.603±0.089	12.366	FAM110B, LOC101902490	IntGV
rs207487600	14:26173037	3.607±0.089	12.230	FAM110B, LOC101902490	IntGV
rs211204541	14:26196375	3.433±0.088	11.785	LOC101902490, UBXN2B	IntGV
rs210090325	14:26223753	3.510±0.089	12.173	LOC101902490, UBXN2B	IntGV
rs42648867	14:26264142	3.509±0.089	12.408	LOC101902490, UBXN2B	IntGV
rs42649775	14:26351959	3.396±0.087	11.819	TRNAG-CCC	DGV
rs42649781	14:26395314	2.585±0.083	7.840	CYP7A1, SDCBP	IntGV
rs210258477	14:26399671	2.249±0.080	6.444	CYP7A1, SDCBP	IntGV
rs137279489	6:41182962	4.465±0.136	8.534	LOC782905, SLIT2	IntGV
rs108949025	6:41262050	4.440±0.136	8.462	SLIT2	IV
rs110092040	6:41292118	4.120±0.122	9.024	SLIT2	IV
rs42306838	6:41311528	3.539±0.114	7.778	SLIT2	IV
rs42305732	6:41356212	3.562±0.114	7.784	SLIT2	IV
rs42304778	6:41438938	4.442±0.137	8.414	SLIT2	IV
rs42304792	6:41463763	4.467±0.137	8.508	SLIT2	IV
rs42304759	6:41526051	4.470±0.137	8.514	SLIT2	IV
rs110634307	6:41662240	4.458±0.136	8.516	SLIT2, PACRGL	IntGV
rs42303720	6:41957455	4.359±0.136	8.241	-	-
rs43083563	6:41984476	4.439±0.138	8.292	KCNIP4	IV
rs41614868	14:24141910	3.550±0.100	9.910	RP1, XKR4	IntGV
rs210731567	14:24266976	3.553±0.100	9.936	RP1, XKR4	IntGV
rs41720580	14:24332803	3.533±0.100	9.850	-	-
rs209439851	14:24343693	3.535±0.101	9.682	XKR4	IV
rs41720533	14:26457030	2.237±0.080	6.357	-	-
rs41726059	14:26473490	2.141±0.080	5.984	LOC101902713	DGV
rs41725705	14:26570145	3.583±0.088	12.167	NSMAF, LOC107133116	IntGV
rs109374728	14:26656398	3.524±0.088	12.171	TOX	IV
rs41724548	14:26743126	3.595±0.088	12.181	TOX	IV
rs41724547	14:26746062	3.593±0.088	12.307	TOX	IV
rs41724536	14:26766010	3.607±0.089	12.324	-	-
rs41724028	14:26776546	3.592±0.088	12.335	TOX	IV
rs41627959	14:26804892	3.595±0.088	12.347	TOX	IV
rs208481177	14:26995868	3.184±0.085	10.979	-	-
<b>Eye muscle area</b>					
rs110578126	6:38373128	3.334±0.124	6.000	IBSP, LOC104972726	IntGV
rs110668054	6:38464203	0.534±0.023	4.917		
rs110983998	6:38477781	0.535±0.023	4.927	LOC104972726, TRNAA-CGC	IntGV
rs383197792	6:38509720	0.531±0.023	4.864	LOC104972726, TRNAA-CGC	IntGV
rs110857755	6:38632439	3.351±0.122	6.229	-	-
rs109438687	6:38648218	0.596±0.024	5.517	FAM184B	IV
rs110766531	6:38670165	0.597±0.024	5.562	-	-
rs136600360	6:38698689	0.570±0.023	5.324	-	-
rs110242144	6:38733885	0.600±0.024	5.587	FAM184B	IV
rs110175987	6:38783305	0.597±0.024	5.559	NCAPG	IV
rs379449143	6:38815034	0.597±0.024	5.559	-	-
rs109315734	6:38960730	0.598±0.024	5.579	LCORL	IV

rs109092727	6:38994174	0.456±0.022	4.032	LCORL	UGV
rs382379503	6:62615288	0.527±0.021	5.580	SLC30A9, BEND4	IV
rs208411640	14:24141910	0.449±0.020	4.637	RP1, XKR4	IV
rs207487600	14:24266976	0.447±0.020	4.602	RP1, XKR4	IV
rs211204541	14:24332803	0.449±0.020	4.633	-	-
rs210090325	14:24343693	0.445±0.020	4.514	XKR4	IV
rs42648867	14:24391802	0.350±0.017	4.054	XKR4	IV
rs134315607	14:24432331	1.754±0.073	4.935	XKR4	IV
rs42649775	14:24437778	1.852±0.072	5.555	-	-
rs42649781	14:24462537	0.352±0.015	4.942	XKR4	IV
rs137279489	14:24891324	1.602±0.073	4.211	LYN	IV
rs133832329	14:24920882	0.324±0.014	4.789	LYN	DGV
rs108949025	14:24954981	0.337±0.015	4.724	RPS20	DGV
rs110092040	14:24973953	0.499±0.017	7.019	MOS	DGV
rs42304778	14:26162492	0.506±0.018	7.062	FAM110B, LOC101902490	IntGV
rs42304792	14:26173037	0.507±0.018	7.076	FAM110B, LOC101902490	IntGV
rs42304759	14:26196375	0.495±0.017	6.976	LOC101902490, UBXN2B	IntGV
rs110634307	14:26223753	0.491±0.017	6.759	LOC101902490, UBXN2B	IntGV
rs42303720	14:26264142	0.491±0.017	6.759	LOC101902490, UBXN2B	IntGV
rs43083563	14:26311106	0.495±0.017	6.843	UBXN2B	DGV
rs41614868	14:26351959	0.483±0.017	6.807	TRNAG-CCC	DGV
rs210731567	14:26395314	0.346±0.016	4.192	CYP7A1, SDCBP	IntGV
rs41725705	14:26570145	0.504±0.017	7.083	NSMAF, LOC107133116	IntGV
rs41725159	14:26619895	0.503±0.017	7.076	LOC107133116	DGV
rs41725162	14:26621673	0.503±0.017	7.070	LOC107133116	DGV
rs109374728	14:26656398	0.495±0.017	6.898	TOX	IV
rs41724536	14:26766010	0.505±0.018	7.077	TOX	IV
rs41627960	14:26800529	0.292±0.014	4.015	TOX	IV
rs41627959	14:26804892	0.504±0.017	7.077	TOX	IV
rs42406063	14:26836013	0.293±0.014	4.037	TOX	IV
rs42406058	14:26848418	0.503±0.018	7.052	TOX	IV
rs42406039	14:26859737	0.504±0.017	7.077	TOX	IV
rs42404941	14:26967218	0.373±0.016	5.101	TOX, CA8	IntGV
rs208481177	14:26995868	0.431±0.017	5.778	-	-
<b>Backfat thickness</b>					
rs29021868	14:31014368	0.391±0.015	5.504	CYP7B1	IV
rs109003517	14:31144539	2.684±0.108	5.185	-	-
rs41613423	14:31197593	1.839±0.074	5.206	LOC104974032, ARMC1	IntGV
rs110811917	14:31447238	0.540±0.022	5.075	-	-
rs110684835	14:31616256	0.539±0.022	5.065	LOC104974032, ARMC1	IntGV
rs109048288	14:31646002	0.538±0.022	5.046	LOC104974032, ARMC1	IntGV
rs109858509	14:31684076	0.521±0.020	5.609	LOC104974032, ARMC1	IntGV
rs109658462	14:31795024	0.523±0.020	5.520	-	-
rs110141788	14:31820412	0.518±0.020	5.585	PDE7A	IV
rs109864374	14:31851268	0.518±0.020	5.585	PDE7A	IV
rs110055514	14:31986520	1.713±0.075	4.423	PDE7A, LOC100299601	IntGV
<b>Marbling score</b>					
rs110025998	13:58140449	-0.055±0.003	4.064	LOC783163, C13H20orf85	IV

SNP, single nucleotide polymorphism; BTA, *Bos taurus* autosome; bp, base pair (kb); SE, standard error; IntGV, intergenic variant; IV, intron variant; UGV, upstream gene variant; DGV, downstream gene variant.

**Table S3.** Genome-wide significant common SNPs identified by GBLUP and Bayes B method, underlying CWT, EMA, BF, and MS traits in Hanwoo using genomic estimated breeding values.

SNP	BTA: Position (bp)	Estimate±SE	-log <sub>10</sub> P	Nearest gene	Consequence Type
<b>Carcass weight</b>					
rs110578126	6:38373128	17.200±0.634	6.079	IBSP, LOC104972726	IntGV
rs110668054	6:38464203	19.780±0.597	8.738	-	-
rs110983998	6:38477781	19.780±0.597	8.731	LOC104972726, TRNAA-CGC	IntGV
rs383197792	6:38509720	19.350±0.600	8.318	LOC104972726, TRNAA-CGC	IntGV

rs467005433	6:38530564	22.670±0.701	8.374	-	-
rs798880362	6:38580679	22.710±0.700	8.398	LAP3	IV
rs432843769	6:38581067	20.820±0.680	7.560	LAP3	IV
rs110857755	6:38632439	17.220±0.624	6.266	-	-
rs109438687	6:38648218	22.010±0.622	9.858	FAM184B	IV
rs110766531	6:38670165	22.060±0.621	9.952	-	-
rs136600360	6:38698689	20.930±0.608	9.372	-	-
rs110242144	6:38733885	22.110±0.621	9.976	FAM184B	IV
rs110175987	6:38783305	22.120±0.621	10.006	NCAPG	IV
rs379449143	6:38815034	22.120±0.621	10.006	-	-
rs110834363	6:38939012	17.360±0.571	7.474	LCORL	IV
rs109315734	6:38960730	22.120±0.621	10.004	LCORL	IV
rs109092727	6:38994174	17.530±0.573	7.559	LCORL	IV
rs208411640	14:24141910	18.720±0.510	10.539	RP1, XKR4	IntGV
rs209201458	14:24183559	8.962±0.411	4.118	RP1, XKR4	IntGV
rs210355704	14:24221973	8.981±0.411	4.131	-	-
rs207487600	14:24266976	18.730±0.511	10.549	RP1, XKR4	IntGV
rs211204541	14:24332803	18.650±0.510	10.505	-	-
rs210090325	14:24343693	18.660±0.515	10.325	XKR4	IV
rs42648867	14:24391802	13.040±0.440	7.128	XKR4	IV
rs134315607	14:24432331	9.221±0.371	5.185	XKR4	IV
rs42649775	14:24437778	9.700±0.367	5.799	-	-
rs42649781	14:24462537	12.170±0.395	7.633	XKR4	IV
rs210258477	14:24497726	18.540±0.446	13.277	-	-
rs42646659	14:24524210	18.570±0.447	13.328	XKR4	IV
rs137279489	14:24891324	8.467±0.371	4.460	LYN	IV
rs133832329	14:24920882	8.254±0.382	4.052	LYN	DGV
rs108949025	14:24954981	9.897±0.396	5.239	RPS20	DGV
rs42306838	14:26023215	8.177±0.363	4.371	LOC107133115	IV
rs42305732	14:26083558	9.806±0.376	5.657	FAM110B	IV
rs210731567	14:26395314	13.770±0.422	8.502	CYP7A1, SDCBP	IntGV
rs41720580	14:26399671	12.130±0.409	7.146	CYP7A1, SDCBP	IntGV
rs41720533	14:26457030	12.070±0.409	7.054	-	-
rs41726059	14:26473490	11.520±0.406	6.592	LOC101902713	DGV
rs41725159	14:26619895	18.980±0.449	13.724	LOC107133116	DGV
rs41725162	14:26621673	18.980±0.449	13.712	LOC107133116	DGV
rs109374728	14:26656398	18.670±0.449	13.287	TOX	IV
rs41724548	14:26743126	19.070±0.450	13.277	TOX	IV
rs41724547	14:26746062	19.060±0.449	13.254	TOX	IV
rs41724536	14:26766010	19.100±0.450	13.194	TOX	IV
rs41724028	14:26776546	19.050±0.449	13.188	TOX	IV
rs41627960	14:26800529	8.278±0.378	4.149	TOX	IV
rs41627959	14:26804892	19.070±0.449	13.161	TOX	IV
rs42406063	14:26836013	8.325±0.378	4.197	TOX	IV
rs42406058	14:26848418	19.060±0.450	13.159	TOX	IV
rs42406039	14:26859737	19.070±0.449	12.763	TOX	IV
rs42404949	14:26949215	8.156±0.370	4.197	TOX, CA8	IntGV
rs42404941	14:26967218	16.280±0.396	12.690	TOX, CA8	IntGV
rs208481177	14:26995868	16.910±0.432	11.896	-	-
<b>Eye muscle area</b>					
rs110668054	6:38464203	3.252±0.135	5.108	-	-
rs110983998	6:38477781	3.254±0.135	5.113	LOC104972726, TRNAA-CGC	IntGV
rs383197792	6:38509720	3.226±0.135	5.030	LOC104972726, TRNAA-CGC	IntGV
rs109438687	6:38648218	3.642±0.141	5.765	FAM184B	IV
rs110766531	6:38670165	3.647±0.141	5.809	-	-
rs136600360	6:38698689	3.462±0.137	5.508	-	-
rs110242144	6:38733885	3.660±0.141	5.831	FAM184B	IV
rs110175987	6:38783305	3.647±0.141	5.806	NCAPG	IV
rs379449143	6:38815034	3.647±0.141	5.806	-	-
rs110834363	6:38939012	2.754±0.129	4.125	LCORL	IV
rs109315734	6:38960730	3.651±0.140	5.823	LCORL	IV
rs109092727	6:38994174	2.776±0.129	4.175	LCORL	UGV
rs208411640	14:24141910	2.758±0.117	4.893	RP1, XKR4	IV
rs209201458	14:24183559	8.962±0.411	4.118	RP1, XKR4	IntGV

rs210355704	14:24221973	8.981±0.411	4.131	-	-
rs207487600	14:24266976	2.750±0.117	4.862	<i>RP1, XKR4</i>	IV
rs211204541	14:24332803	2.760±0.117	4.904	-	-
rs210090325	14:24343693	2.740±0.118	4.781	<i>XKR4</i>	IV
rs42648867	14:24391802	2.134±0.098	4.208	<i>XKR4</i>	IV
rs134315607	14:24432331	9.221±0.371	5.185	<i>XKR4</i>	IV
rs42649775	14:24437778	9.700±0.367	5.799	-	-
rs42649781	14:24462537	2.165±0.088	5.245	<i>XKR4</i>	IV
rs137279489	14:24891324	8.467±0.371	4.460	<i>LYN</i>	IV
rs133832329	14:24920882	1.993±0.083	5.055	<i>LYN</i>	DGV
rs108949025	14:24954981	2.063±0.087	4.954	<i>RPS20</i>	DGV
rs110092040	14:24973953	3.069±0.103	7.469	<i>MOS</i>	DGV
rs42305732	14:26083558	1.820±0.083	4.287	<i>FAM110B</i>	IV
rs42304759	14:26196375	3.053±0.102	7.452	<i>LOC101902490, UBXN2B</i>	IntGV
rs110634307	14:26223753	3.023±0.103	7.190	<i>LOC101902490, UBXN2B</i>	IntGV
rs42303720	14:26264142	3.023±0.103	7.200	<i>LOC101902490, UBXN2B</i>	IntGV
rs43083563	14:26311106	3.047±0.103	7.292	<i>UBXN2B</i>	DGV
rs41614868	14:26351959	2.973±0.101	7.240	<i>TRNAG-CCC</i>	DGV
rs210731567	14:26395314	2.140±0.095	4.482	<i>CYP7A1, SDCBP</i>	IntGV
rs41720580	14:26399671	1.948±0.092	4.068	<i>CYP7A1, SDCBP</i>	IntGV
rs41720533	14:26457030	1.941±0.092	4.038	-	-
rs41725162	14:26621673	3.096±0.103	7.526	<i>LOC107133116</i>	DGV
rs109374728	14:26656398	3.039±0.103	7.308	<i>TOX</i>	IV
rs41724536	14:26766010	3.108±0.104	7.523	<i>TOX</i>	IV
rs41627960	14:26800529	1.794±0.083	4.220	<i>TOX</i>	IV
rs41627959	14:26804892	3.101±0.103	7.533	<i>TOX</i>	IV
rs42406063	14:26836013	1.798±0.082	4.247	<i>TOX</i>	IV
rs42406058	14:26848418	3.099±0.103	7.507	<i>TOX</i>	IV
rs42406039	14:26859737	3.101±0.103	7.533	<i>TOX</i>	IV
rs42404941	14:26967218	2.290±0.092	5.371	<i>TOX, CA8</i>	IntGV
rs208481177	14:26995868	2.652±0.099	6.132	-	-

SNP, single nucleotide polymorphism; BTA, *Bos taurus* autosome; bp, base pair (kb); SE, standard error; IntGV, intergenic variant; IV, intron variant; DGV, downstream gene variant.

**Table S4.** Functional cluster enrichment analysis of gene via DAVID database for the carcass traits in Hanwoo.

Term	Genes count	%	<i>p</i> -value	FDR
<b>Annotation Cluster 1</b>	<b>Enrichment Score: 1.6400</b>			
IPR000408:Regulator of chromosome condensation, RCC1	3	3.16	0.004	4.70
IPR009091:Regulator of chromosome condensation	3	3.16	0.005	5.70

1/beta-lactamase-inhibitor protein II

SM00119:HECTc	3	3.16	0.006	5.56
IPR000569:HECT	3	3.16	0.007	7.96
Cell division and chromosome partitioning / Cytoskeleton	3	3.16	0.008	3.87
GO:0016874~ligase activity	4	4.21	0.011	12.53
Ubl conjugation pathway	5	5.26	0.040	36.99
GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	3	3.16	0.116	82.14
GO:0004842~ubiquitin-protein transferase activity	3	3.16	0.239	95.96
Transferase	6	6.32	0.619	100.00
<b>Annotation Cluster 2</b>		<b>Enrichment Score: 0.6602</b>		
GO:0003924~GTPase activity	4	4.21	0.055	48.71
GO:0005525~GTP binding	4	4.21	0.245	96.28
IPR027417:P-loop containing nucleoside triphosphate hydrolase	4	4.21	0.771	100.00
<b>Annotation Cluster 3</b>		<b>Enrichment Score: 0.5895</b>		
Mitochondrion	6	6.32	0.23	94.67
Transit peptide	4	4.21	0.23	95.00
transit peptide:Mitochondrion	4	4.21	0.32	98.84
<b>Annotation Cluster 4</b>		<b>Enrichment Score: 0.5081</b>		
GO:0007268~chemical synaptic transmission	4	4.21	0.02	24.40
GO:0007218~neuropeptide signaling pathway	3	3.16	0.05	51.24
Glycoprotein	11	11.58	0.06	51.99
topological domain:Extracellular	5	5.26	0.42	99.79
topological domain:Cytoplasmic	6	6.32	0.50	99.96
glycosylation site:N-linked (GlcNAc...)	7	7.37	0.57	99.99
transmembrane region	8	8.42	0.67	100.00
disulfide bond	5	5.26	0.76	100.00
Cell membrane	7	7.37	0.81	100.00
GO:0005887~integral component of plasma membrane	3	3.16	0.91	100.00
Disulfide bond	6	6.32	0.92	100.00
<b>Annotation Cluster 5</b>		<b>Enrichment Score: 0.2575</b>		



GO:0005615~extracellular space	7	7.37	0.31	98.5
Secreted	6	6.32	0.44	99.9
Signal	13	13.68	0.77	100.0
signal peptide	5	5.26	0.88	
<b>Annotation Cluster 6</b>		<b>Enrichment Score: 0.1981</b>		
Nucleotide-binding	7	7.37	0.49	99.96
IPR017441:Protein kinase, ATP binding site	3	3.16	0.51	99.99
ATP-binding	5	5.26	0.62	100.00
Transferase	6	6.32	0.62	100.00
IPR000719:Protein kinase, catalytic domain	3	3.16	0.66	100.00
Kinase	3	3.16	0.66	100.00
IPR011009:Protein kinase-like domain	3	3.16	0.71	100.00
GO:0005524~ATP binding	5	5.26	0.87	100.00
<b>Annotation Cluster 7</b>		<b>Enrichment Score: 0.0606</b>		
transmembrane region	8	8.42	0.67	100.00
Membrane	25	26.32	0.86	100.00
GO:0016021~integral component of membrane	17	17.89	0.90	100.00
Transmembrane helix	18	18.95	0.98	100.00
Transmembrane	18	18.95	0.98	100.00