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Asian Australas. J. Anim. Sci.

Vol. 27, No. 3 : 303-309 March 2014

<http://dx.doi.org/10.5713/ajas.2013.13385>

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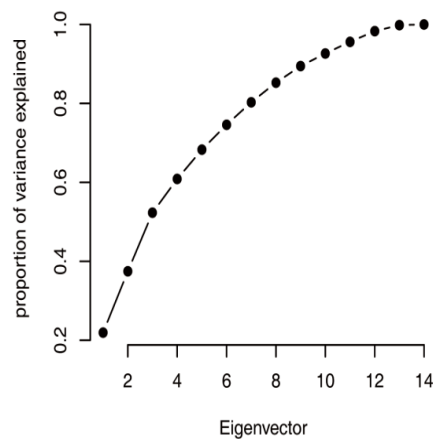
pISSN 1011-2367 eISSN 1976-5517

## Genome-wide Association Study of Integrated Meat Quality-related Traits of the Duroc Pig Breed

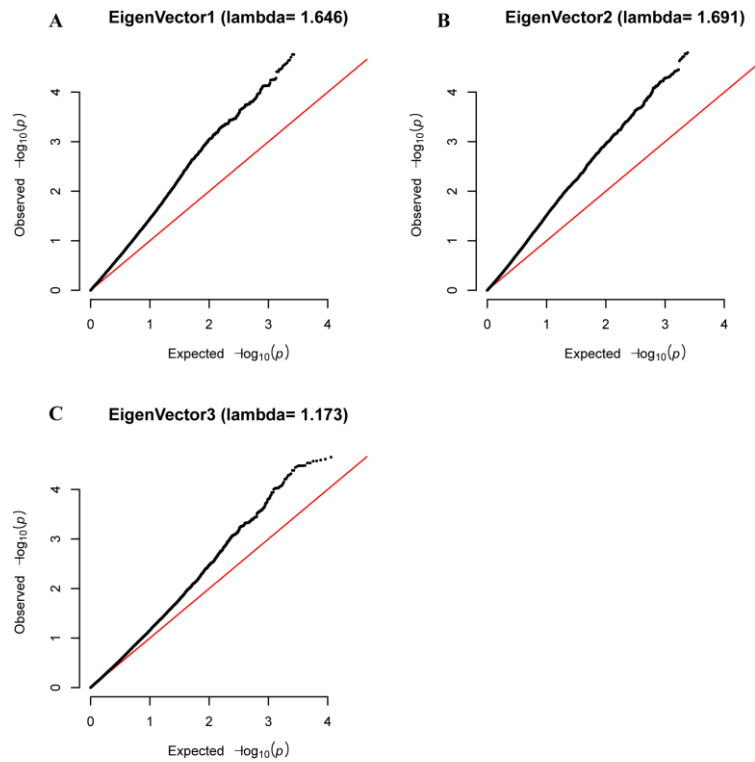
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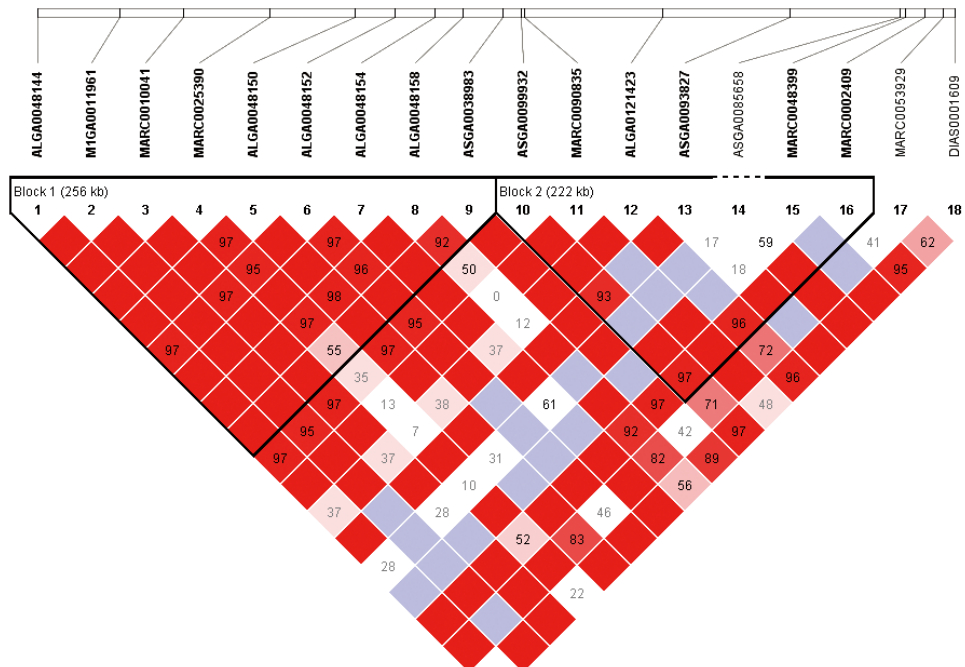
### - Supplementary Data -



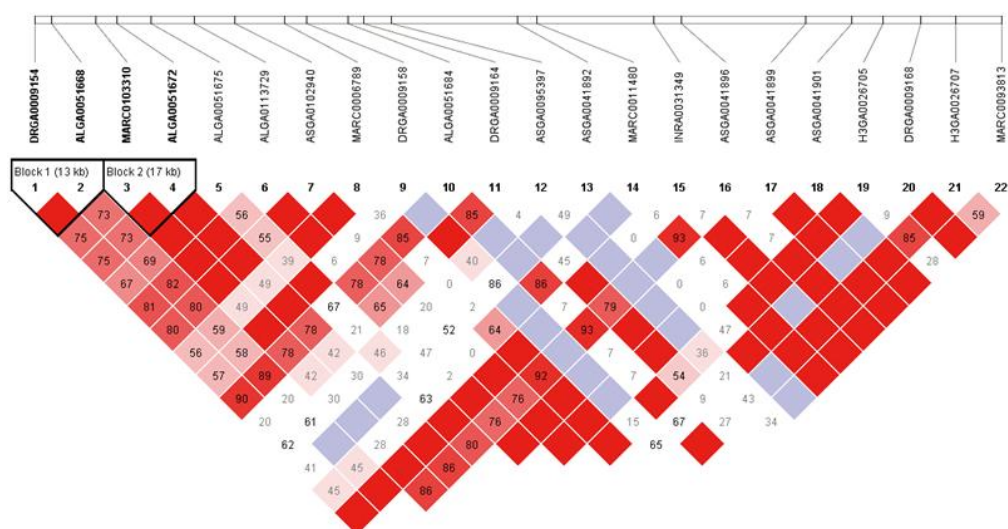
**Supplementary Figure S1.** Principal component analysis of meat-quality-related phenotypes. The x-axis represents the eigenvector and the y-axis represents the proportion of variance explained. The top three PCs jointly accounted for 52.3% of the total variability of meat quality-related phenotypes.



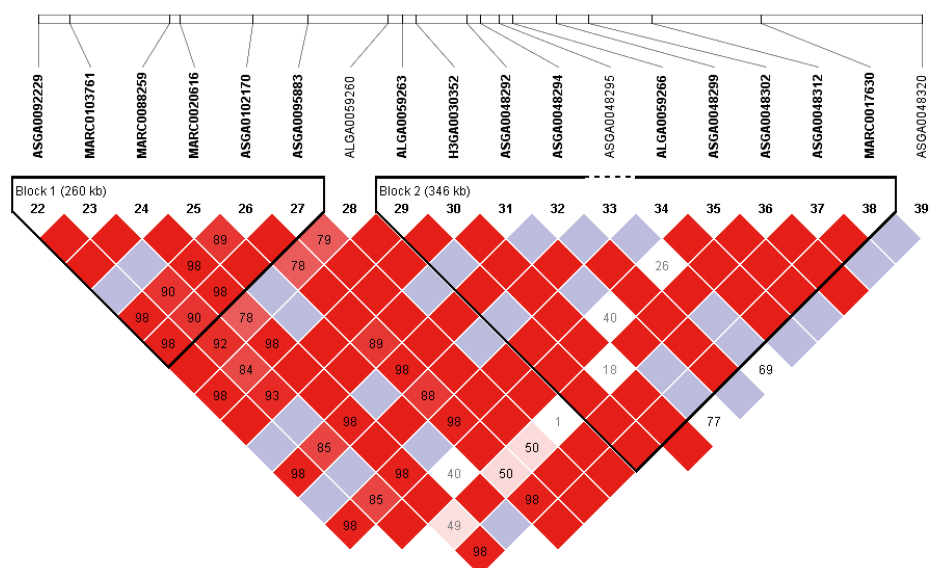
Supplementary Figure S2. QQ-plots of GWAS results.



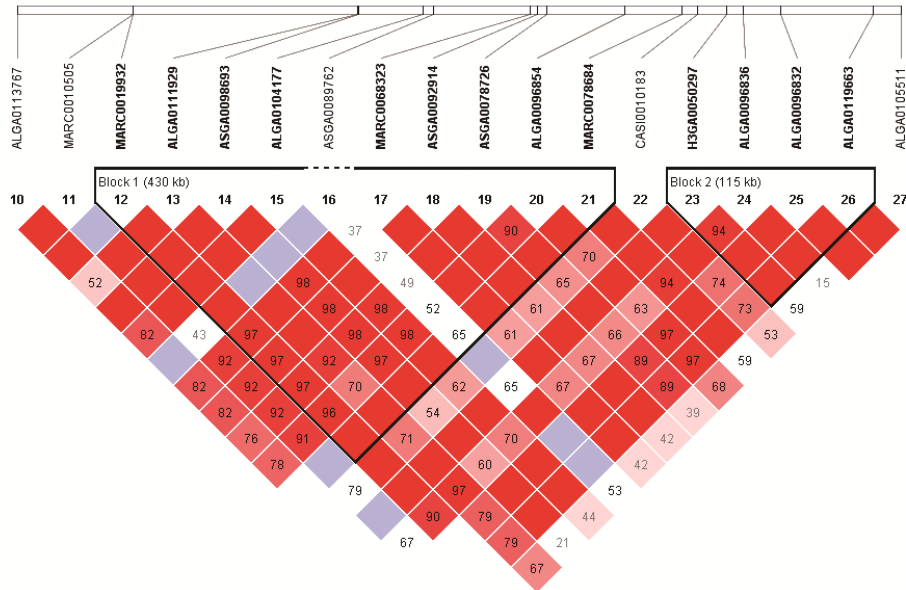
**Supplementary Figure S3.** Linkage disequilibrium around the significant SNPs of eigenvector 2 PCA results on chromosome 8. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $\cdot 100$ ) are indicated; blue blocks indicate  $D' = 0$ .



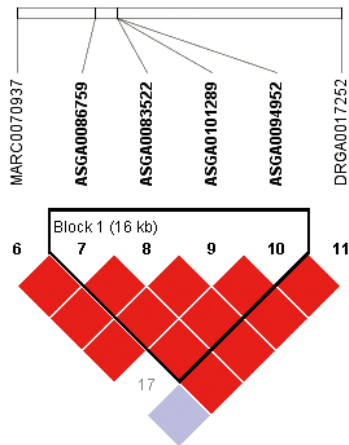
**Supplementary Figure S4.** Linkage disequilibrium around the significant SNPs of eigenvector 2 PCA results on chromosome 9. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $'/100$ ) are indicated; blue blocks indicate  $D' = 0$ .



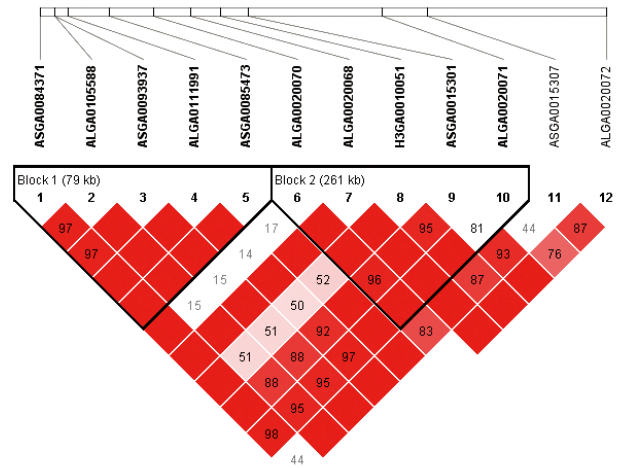
**Supplementary Figure S5.** Linkage disequilibrium around the significant SNPs of eigenvector 2 PCA results on chromosome 10. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $'/100$ ) are indicated; blue blocks indicate  $D' = 0$ .



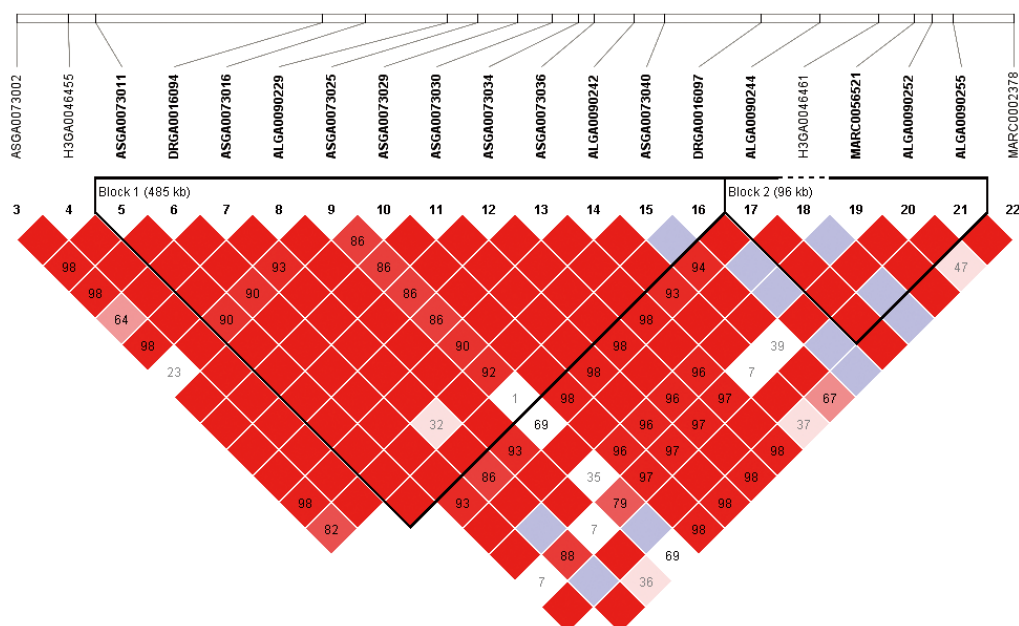
**Supplementary Figure S6.** Linkage disequilibrium around the significant SNPs of eigenvector 2 PCA results on chromosome 18. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $\times 100$ ) are indicated; blue blocks indicate  $D' = 0$ .



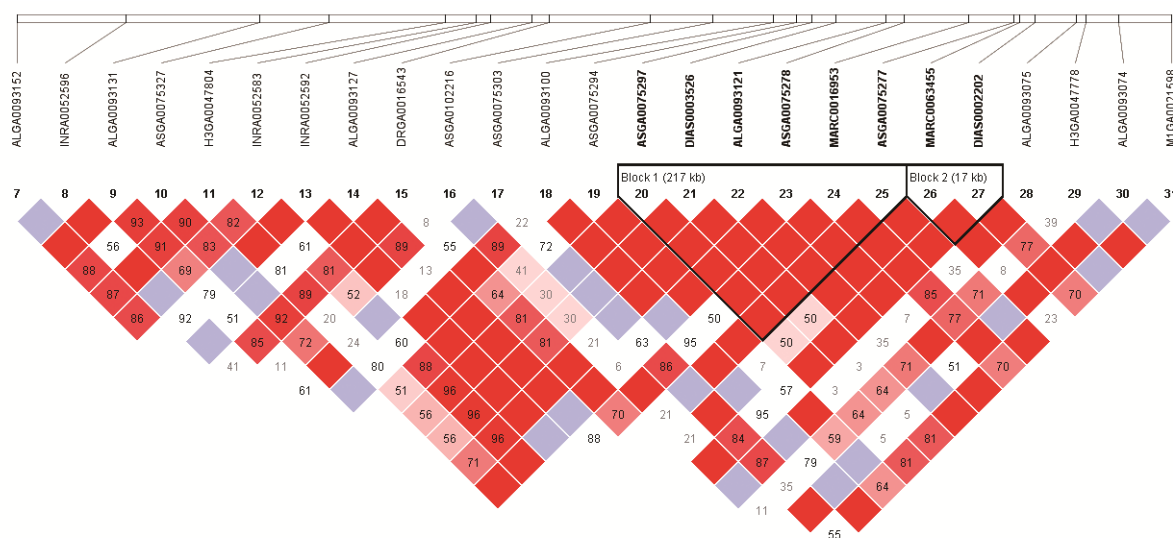
**Supplementary Figure S7.** Linkage disequilibrium around the significant SNPs of eigenvector 2 PCA results on chromosome X. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $\times 100$ ) are indicated; blue blocks indicate  $D' = 0$ .



**Supplementary Figure S8.** Linkage disequilibrium around the significant SNPs of eigenvector 3 PCA results on chromosome 3. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $\times 100$ ) are indicated; blue blocks indicate  $D' = 0$ .



**Supplementary Figure S9.** Linkage disequilibrium around the significant SNPs of eigenvector 3 PCA results on chromosome 16. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $\times 100$ ) are indicated; blue blocks indicate  $D' = 0$ .



**Supplementary Figure S10.** Linkage disequilibrium around the significant SNPs of eigenvector 1 PCA results on chromosome 17. Linkage disequilibrium (LD) was determined using Haploview, and LD blocks were defined using the Gabriel rule. Darker boxes represent higher LD percentages. Pairwise  $D'$  values ( $\times 100$ ) are indicated; blue blocks indicate  $D' = 0$ .

**Supplementary Table S1.** Summary description of phenotypes measurement

Trait	Method
pH24	Meat pH24 was measured at twenty-four hours after slaughtering at 20°C.
CIE-L*, CIE-a*, CIE-b*	Meat color was measured with as three coordinates according to Hunter L, a, b systems, where L is a general indication of lightness, a represents the degree of green-redness and b represents the degree of blue-yellowness.
Shear force (SF)	Shear force was determined using the Warner-Bratzler shear force meter (G-R Elec. Mfg. Co., USA).
Drip loss	Drip loss during vacuum storage was determined at one day postmortem by weighing the samples before and after storage.
Heat loss	Heat loss was measured difference between sample weight before and after incubating of sample at 75°C for 10 min.
water-holding capacity (WHC)	Water holding capacity (WHC) % = Moisture % – expressible water (EW) %
Back-fat thickness (BF)	measured in between 10th and 11th rib
Fat (intramuscular fat content)	Intramuscular fat (IMF) content was measured using a chemical fat extraction procedures.
Protein	The protein content was measured using the Macro-Kjeldahl method.
Cholesterol	Total cholesterol content was measured using a colorimetric procedure.
Moisture	The moisture content was analysed by drying a 2.5 g sample at 100°C for a period of 24 h.
Ash	Ashing was done at 500°C for a period of 5 h.

**Supplementary Table S2.** Summary table (average, SD) of meat quality phenotypes and integrated phenotypes (PC1, PC2, and PC3)

Trait	Average	SD
PC1	-6.63E-11	0.07
PC2	4.59E-05	0.07
PC3	1.02E-05	0.07
BF	20.69	5.60
Moisture	73.06	1.13
Protein	22.79	0.80
Fat	3.04	1.02
ASH	1.09	0.27
WHC	58.65	4.17
pH	5.73	0.16
Drip loss	3.77	1.27
Heat loss	28.21	3.27
SF	1,511.33	342.84
CIE-L*	55.81	2.79
CIE-a*	4.88	1.00
CIE-b*	8.28	0.96
Cholesterol	93.64	42.60

**Supplementary Table S3.** Previously reported QTL regions related with significant SNPs

	CHR	QTL name (animal QTLdb ID)	p-value	References	
PC1	2	Muscle moisture percentage QTL (2975)	0.00014	Rohrer et al., 2006	
	2	pH for <i>Longissimus Dorsi</i> QTL (2976)	0.00079	Rohrer et al., 2006	
	2	Drip loss QTL (3780)	<0.05	Thomsen et al., 2004	
	2	CIE-b* QTL (3982)	0.07	Harmegnies et al., 2006	
	2	Backfat at mid-back QTL (5208, 5242)	<0.05	Guo et al., 2008	
	2	pH for Semimembranosus QTL (5682)	<0.05	Liu et al., 2007	
	2	Shear force QTL (5684)	<0.05	Liu et al., 2007	
	2	Backfat at last rib QTL (5685)	<0.05	Liu et al., 2007	
	2	Fat to meat ratio QTL (5689)	<0.05	Liu et al., 2007	
	2	Muscle fat content QTL (5754)	<0.01	Kim et al., 2005a	
	2	Cooking loss QTL (12103, 12104)	0.03, 0.04	Wimmers et al., 2007	
	2	Intramuscular fat content QTL (12105)	0.05	Wimmers et al., 2007	
	2	Shear force QTL (12106)	0.03	Wimmers et al., 2007	
	2	Backfat weight QTL (12746)	<0.01	Geldermann et al., 2010	
	2	Fat to meat ratio QTL (12748)	<0.05	Geldermann et al., 2010	
	PC2	17	Average backfat thickness QTL (7531)	0.014	Gilbert et al., 2008
		17	Meat color-a QTL (12069)	0.05	Wimmers et al., 2007
17		Cooking loss QTL (12071)	0.03	Wimmers et al., 2007	
17		Drip loss QTL (12072)	0.03	Wimmers et al., 2007	
17		Intramuscular fat content QTL (12074)	0.04	Wimmers et al., 2007	
17		Shear force QTL (12075)	0.01	Wimmers et al., 2007	
7		Backfat (average) thickness - ultra sound QTL (3760)	0.05	Nagamine et al., 2003	
7		Backfat at last rib QTL (3762)	0.006	Nagamine et al., 2003	
PC3	7	Backfat at tenth rib QTL (3860)	0.021	Paszek et al., 2001	
	7	Backfat at first rib QTL (3956)	0.39	Harmegnies et al., 2006	
	8	CIE-b* QTL (2993)	0.00067	Rohrer et al., 2006	
	8	Backfat at tenth rib QTL (10600)	<0.04	Houston et al., 2006	
	9	Backfat above muscle dorsi QTL (5205)	<0.05	Guo et al., 2008	
	9	Backfat at mid-back QTL (5213, 5246)	<0.05	Guo et al., 2008	
	10	Backfat at last rib QTL (2952)	0.045	Kim et al., 2005b	
	10	Backfat at mid-back QTL (5247)	<0.05	Guo et al., 2008	
	10	Shear force QTL (6011)	<0.05	Kim et al., 2005b	
	3	Fat androstenone level (140 days) QTL (597)	<0.001	Kim et al., 2000	
3	Ham fat thickness QTL (3935)	<0.001	Harmegnies et al., 2006		
3	Blood pH QTL (6320)	<0.05	Reiner et al., 2009		
16	Backfat above muscle dorsi QTL (5994)	<0.05	Liu et al., 2008		
16	Shoulder subcutaneous fat thickness QTL (5995)	<0.05	Liu et al., 2008		
16	Fat area QTL (5999)	<0.05	Liu et al., 2008		
16	Cooking loss QTL (6014)	<0.05	Liu et al., 2008		
16	Shear force QTL (6015)	<0.01	Liu et al., 2008		

## REFERENCES

- Geldermann, H., S. Cepica, A. Stratil, H. Bartenschlager, and S. Preuss. 2010. Genome-wide mapping of quantitative trait loci for fatness, fat cell characteristics and fat metabolism in three porcine F<sub>2</sub> crosses. *Genet. Sel. Evol.* 42:31.
- Gilbert, J. R., M.-J. Ronan Gueblez, J.-P. B. Mercat, D. Milan, and P. Le Roy. 2008. Detection of quantitative trait loci for reproduction and production traits in Large White and French Landrace pig populations. *Genet. Sel. Evol.* 40:61-78.
- Guo, Y.-M., G. Lee, A. Archibald, and C. Haley. 2008. Quantitative trait loci for production traits in pigs: a combined analysis of two Meishan×Large White populations. *Anim. Genet.* 39:486-495.
- Harmegnies, N., F. Davin, S. De Smet, N. Buys, M. Georges, and W. Coppieters. 2006. Results of a whole-genome quantitative trait locus scan for growth, carcass composition and meat quality in a porcine four-way cross. *Anim. Genet.* 37:543-553.
- Houston, R. D., C. S. Haley, A. L. Archibald, N. D. Cameron, G. S. Plastow, and K. A. Rance. 2006. A polymorphism in the 5'-untranslated region of the porcine cholecystokinin type a receptor gene affects feed intake and growth. *Genetics* 174:1555-1563.
- Kim, J.-J., M. Rothschild, J. Beever, S. Rodriguez-Zas, and J. Dekkers. 2005a. Joint analysis of two breed cross populations in pigs to improve detection and characterization of quantitative trait loci. *J. Anim. Sci.* 83:1229-1240.
- Kim, J.-J., H. Zhao, H. Thomsen, M. F. Rothschild, and J. C. Dekkers. 2005b. Combined line-cross and half-sib QTL analysis of crosses between outbred lines. *Genet. Res.* 85:235-248.
- Kim, K. S., N. Larsen, T. Short, G. Plastow, and M. F. Rothschild. 2000. A missense variant of the porcine melanocortin-4 receptor (*MC4R*) gene is associated with fatness, growth, and feed intake traits. *Mamm. Genome* 11:131-135.
- Liu, G., D. Jennen, E. Tholen, H. Juengst, T. Kleinwächter, M. Hölker, D. Tesfaye, G. Ün, H. J. Schreinemachers, and E. Murani. 2007. A genome scan reveals QTL for growth, fatness, leanness and meat quality in a Duroc-Pietrain resource population. *Anim. Genet.* 38:241-252.
- Liu, G., J. J. Kim, E. Jonas, K. Wimmers, S. Ponsuksili, E. Murani, C. Phatsara, E. Tholen, H. Juengst, and D. Tesfaye. 2008. Combined line-cross and half-sib QTL analysis in Duroc-Pietrain population. *Mamm. Genome* 19:429-438.
- Nagamine, Y., C. S. Haley, A. Sewalem, and P. M. Visscher. 2003. Quantitative trait loci variation for growth and obesity between and within lines of pigs (*Sus scrofa*). *Genetics* 164:629-635.
- Paszek, A., P. Wilkie, G. Flickinger, L. Miller, C. Louis, G. Rohrer, L. Alexander, C. Beattie, and L. Schook. 2001. Interval mapping of carcass and meat quality traits in a divergent swine cross. *Anim. Biotechnol.* 12:155-165.
- Reiner, G., R. Fischer, F. Köhler, T. Berge, S. Hepp, and H. Willems. 2009. Heritabilities and quantitative trait loci for blood gases and blood pH in swine. *Anim. Genet.* 40:142-148.
- Rohrer, G., R. Thallman, S. Shackelford, T. Wheeler, and M. Koohmaraie. 2006. A genome scan for loci affecting pork quality in a Duroc-Landrace F<sub>2</sub> population. *Anim. Genet.* 37:17-27.
- Thomsen, H., H. Lee, M. Rothschild, M. Malek, and J. Dekkers. 2004. Characterization of quantitative trait loci for growth and meat quality in a cross between commercial breeds of swine. *J. Anim. Sci.* 82:2213-2228.
- Wimmers, K., E. Murani, M. Te Pas, K. Chang, R. Davoli, J. Merks, H. Henne, M. Muraniová, N. Da Costa, and B. Harlizius. 2007. Associations of functional candidate genes derived from gene-expression profiles of prenatal porcine muscle tissue with meat quality and muscle deposition. *Anim. Genet.* 38:474-484.