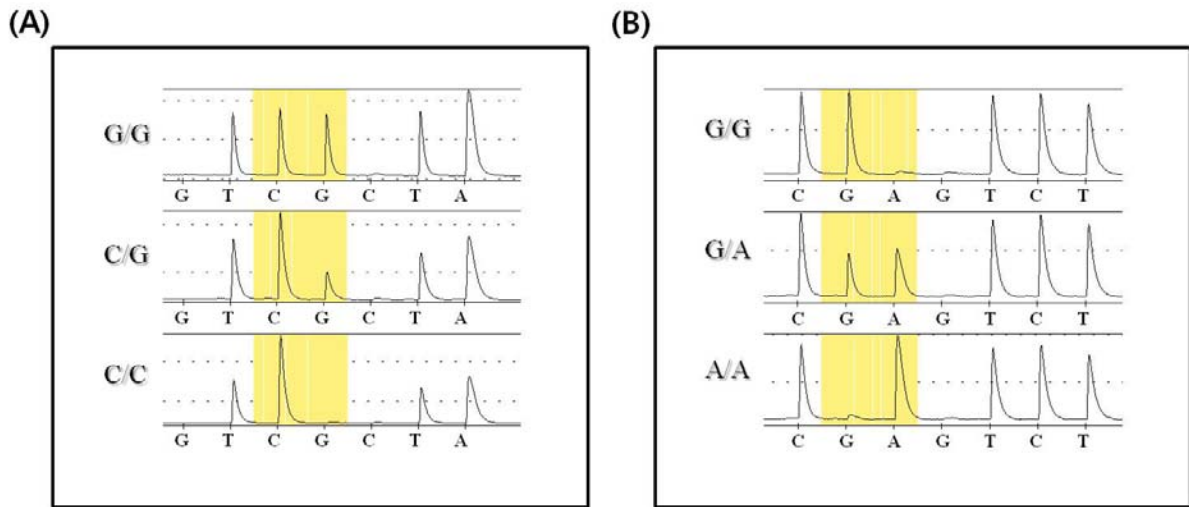


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4 **Supplementary Figure S1.** Pyrosequencing and genotype of the *GRIP1* gene. (A) The

5 presumed functional SNP at nucleotide 3,316 which correspond to codon 1,106 marked by

6 yellow color. (B) Pyrosequencing of exon nucleotide c.2442 C>T.

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1 **Supplementary Table S1.** Pyrosequencing primer sets for putative exonic sequence variants
 2 in the *GRIP1* gene

SNP No.	Region	Sequences	Product size	Annealing Temp.
1 c.3316C>G (R1106G)	exon25	5'-CCCTGTGCTTGCAGTTAATG-3' 5'-biotin-GACTTCGACTGCTGCCTTGTT-3' †Seq:5'-CTATAATGTATTAGTGGGTTC-3'	331	66 °C
*2 c.2442 T>C	Exon20	5'-CCCCAATGACAAATTTCTTG-3' 5'-biotin-AAGCCCAGTCAGCATCAAGT-3'	239	63 °C
*3 c.2421 G>A	Exon20	†Seq:5'-ACCTTGATTCCCATAGCTGG-3'		
4 c.1884 A>C	exon17	5'-TCACACTGCTGGAGGATCTG-3' 5'-biotin-ACTGGCAAACAAGGGATTTG-3' †Seq:5'-CATGGAGCAATTGTCCAGC-3'	258	63 °C
5 c.1686 G>A	exon15	5'-CTGGCTCCACATCTCCGTAT-3' 5'-biotin-TGACTGATGCTCCATTCTTCC-3' †Seq:5'-CACTGCTCGGGATGACAG-3'	285	63 °C
6 c.1581 T>C	exon14	5'-CTGTTGTTCTCCCCATC-3' 5'-biotin-CAACCTGTAACATGTGGTTCTAAA-3' †Seq:5'-GACAGAGTGCTGGCCATTA-3'	271	63 °C
7 c.744 C>T	exon8	5'-TTGCGAAAAGAAGGCACTTT-3' 5'-biotin-AGACCGACATCAGGCTGAAC-3' †Seq:5'-ACTTCCACTAGGAGTGGCC-3'	273	63 °C
8 c.342 C>T	exon4	5'-biotin-GGCAAAAATACGGTGCATCT-3' 5'-CCTGGGCTTGTATGCTCATC-3' †Seq:5'-AACCTGGCCAAATTCCGCC-3'	295	63 °C

3 †Internal sequencing primer

4 *SNP 2 and SNP3 were screened using the single internal sequencing primer.

1 **Supplementary Table S2.** Allele and genotype frequencies for the *GRIP1* polymorphisms in
 2 F₀ parental breeds

SNP	KNP					Landrace				
	Allele frequency		Genotype frequency			Allele frequency		Genotype frequency		
c.3316 C>G (R1106G)	G	C	GG	GC	CC	G	C	GG	GC	CC
	0.32	0.68	0.11	0.42	0.47	0.91	0.09	0.88	0.06	0.06
c.2442 C>T	G	A	GG	GA	AA	G	A	GG	GA	AA
	0.32	0.68	0.11	0.42	0.47	0.03	0.97	0	0.06	0.94
c.2421 G>A	C	T	CC	CT	TT	C	T	CC	CT	TT
	1	0	1	0	0	0.85	0.15	0.71	0.29	0
c.1884 A>C	T	G	TT	TG	GG	T	G	TT	TG	GG
	0.895	0.105	0.84	0.11	0.05	0.85	0.15	0.71	0.29	0
c.1686 G>A	C	T	CC	CT	TT	C	T	CC	CT	TT
	0.32	0.68	0.11	0.42	0.47	0.97	0.03	0.94	0.06	0
c.1581 T>C	A	G	AA	AG	GG	A	G	AA	AG	GG
	0.32	0.68	0.11	0.42	0.47	0.97	0.03	0.94	0.06	0
c.744 C>T	G	A	GG	GA	AA	G	A	GG	GA	AA
	0.47	0.53	0.05	0.84	0.11	0.44	0.56	0	0.88	0.12
c.342 C>T	C	T	CC	CT	TT	C	T	CC	CT	TT
	0.05	0.95	0.05	0.05	0.90	0	1	0	0	1