

Supplemental information

Table S1 Details of genotyping assays

Polymorphism (Reference)	Position on chromo-some 18	Assay type
Ins227bp (Hill et al. 2010)	66495327 [Ins227bp] 66495326	qPCR
g.66493737C/T (GenBank: AY840554.2)	66493737	Dye-based ARMS-qPCR
BIEC2-417495 (Binns et al. 2010; Hill et al. 2010), BLAT)c	67186093	Probe-based ARMS-qPCR

Tabel S1 (cont)

Polymorphism	Sequence of oligonucleotide (5' to 3')	T _m (°C) ^a	Length (bp)	Amplicon length (bp)	Amplicon T _m (°C) ^b
Ins227bp	F: TGACAGCGAGATTCATTGTGG	58.3	21	174 and	77.8 and
	R: CTTTTGAGCAATGCCAAGCA	58.6	20	401	83.9
g.66493737C/ T	F: CTTTATCTACTTTAAACAGGACACAACA	55.6	28	78	76.4 to 77.3
	R(T): TGATAGCAGAGTCATAAAGGAAAATgA <u>I</u>	58.8	28		
	R(C): TGATAGCAGAGTCATAAAGGAAAATaA <u>C</u>	56.7	28		
BIEC2- 417495	F(C): AATACCTTGATTGATTGGTTTTAcA <u>C</u>	55.7	26	160	not applicable
	F(T): AATACCTTGATTGATTGGTTTTAcA <u>I</u>	55.4	26		
	R: AGATGATGGTTAGACTTTGTGTCTGAT	57.5	27		
	Probe: FAM- CCTTCTTCAATCTCTGTTCCCTGGCCT-BHQ1	67.3	27		

Underlined and small letters in the sequence of a SNP-specific primer designate the targeted nucleotide and the artificial mismatch introduced to increase specificity, respectively.

F(C), F(T), R(C), R(T): forward or reverse primer specific for C or T allele, respectively

T_m: melting temperature

^apredicted by Primer Express 2.0 software (Life Technologies); in case of SNP-specific primers, T_m was predicted for the completely matching sequence

^bdetermined by dissociating products of fluorogenic dye-based qPCR

^camplicon spans positions 67,186,068 to 67,186,227 in the alignment tool BLAT (BLAST-Ilike Alignment Tool)