Supplementary Data *Mismatch-PCR-RFLP for detection of AHSP haplotype*

**Genbank accession number:** AC106730.2

**Location:** AHSP gene chromosome 16 11.1-11.2

**Polymorphism:** G/A dinucleotide polymorphism (coordinate number 12390)

**Genotyping technique:** Mismatched PCR-RFLP

Forward primer; AHSP-GF (12179-12200) 5'- TGCACAGAGAGATTCACGCACC–3'

Reverse primer; AHSP-R7 (12392-12418) 5'- CCTGGGTAGAGAAAGGGTAGAA G TTA -3'

- Complementary sequence 5'- CCTGGGTAGAGAAAGGGTAGAA T TTA -3'
- Sense strand sequence 5'- GGACCCATCTCTTTTCCCATCTTT A AATG-3'

Mismatched-nucleotide (G) in the reverse primer creates a Mae III restriction site in normal allele (CAATG).

**Condition:** 1.5 mM MgCl$_2$, 16.6 mM (NH$_4$)$_2$SO$_4$, Tris-HCl pH 8.8, 200 µM of each dNTP, 25 pmol of each forward and reverse primer and 2.5 U of Taq polymerase (Roche Diagnostic, Mannheim, Germany)

**Cycles:**
- 95°C for 15 minutes
- 95°C for 1 minute
- 56°C for 1 minute
- 72°C for 1.30 minute; all for total 35 cycles

**Digestion:** Mae III (A abolish this site) for 2 hours at 55°C and run on 3% agarose gel with ethidium bromide

**Result:**
- PCR product before digestion 240 bp
  - G/G digested to 124 bp and 88 bp and 28 bp
  - A/A digested to 152 bp and 88 bp
  - G/A digested to 152bp, 124 bp, 88 bp and 28 bp