# Supplement

## Methods

The AS-IC region was amplified and sequenced as described before (Zogel et al. 2006). The newly identified oocyte-specific promotor region (Lewis et al. 2014) not completely included in the region investigated by Zogel et al. was amplified using standard protocols with primers AS-SRO_F_kurz 5'-ACAGTCCATGATTTGTCTGGTG-3' and AS-SRO_R_k_u_l 5'-AGGCCAAGGGCTGATCATA-3'. In newer cases the whole region was amplified using primers IC16 5'-GCTCAAGCCGTGTTCATTTT-3' (Zogel et al. 2006) and AS-SRO_R_k_u_l with additional primers for sequencing (usage depending on the presence of the 4bp InDel SNP rs36061418: AS-SRO_Seq_F 5'-GGTCAGCTGCTGTTAAAGGTT-3', AS-SRO_Seq_R 5'-CAGCAGCTGACCTAAAACACA-3', AS-SRO_Seq_F2 5'-GCTGGGGAGTAAGGGAGAAC-3' and AS-SRO_Seq_R2 5'-AGCCTGTCAGAAGAGCCTTG-3').

Sequencing of the PCR products was conducted on the ABI3130XL capillary sequencer (Applied Biosystems) with subsequent analysis using the Sequencing Analysis (Applied Biosystems) and the Geneious software (Biomatters, Auckland, New Zealand).

## Transmission disequilibrium test (TDT)

The AS-IC haplotypes were determined as described previously (Zogel et al. 2006). Since the disease locus is subject to genomic imprinting, we determined the transmitted and non-transmitted haplotypes separately for each parent. Parents homozygous for a haplotype, or trios where the transmitting parent could not be determined (e.g. because all three family members shared the same two haplotypes), were excluded. TDT was calculated as described

by Spielman et al. 1996: $(b-c)^2/(b+c)$, where b is the number of times a given haplotype was not transmitted while c is the number of times the haplotype was transmitted. This was calculated separately for each haplotype and each parent. Significance of overtransmission was determined by chi square.

## Investigated common variants

| rs No. | Alleles | MAF | Genomic position (GRCh37.p13) |
|---|---|---|---|
| rs2075814 | A/G | 0.09922 | NC_000015.9:g.25165776A>G |
| rs2736711 | G/A | 0.1649 | NC_000015.9:g.25165844G>A |
| rs36061418 | TATG/Del* | 0.09835 | NC_000015.9:g.25165936_25165939del |
| rs35207533 | C/G | 0.09915 | NC_000015.9:g.25166089C>G |
| rs17114852 | G/T | 0.04958 | NC_000015.9:g.25166183G>T |
| rs17785249 | C/T | 0.1684 | NC_000015.9:g.25166455C>T |

**Haplotypes**

| | | | | | | |
|---|---|---|---|---|---|---|
| H-AS1 | A | G | TATG | C | G | C |
| H-AS2 | A | A | TATG | C | G | T |
| H-AS3 | G | G | Del | C | G | C |
| H-AS4 | A | G | TATG | C | T | C |
| H-AS5 | A | G | TATG | G | G | C |

Haplotypes as given by Zogel et al. 2006. The order of the benign variants is the same as described above.

**MAF – minor allele frequency**

MAF data taken from GnomAD (the Genome Aggregation Database, https://gnomad.broadinstitute.org/ August 2019). The MAF data given in the table above correspond to all investigated samples given in GnomAD for the respective variants without differentiation of the investigated populations.

Variant identifiers (rs No.) and the genomic position according to GRCh37.p13 are taken from NCBI dbSNP version 153 (https://www.ncbi.nlm.nih.gov/snp/ August 2019).

* This variant was called TATG/Del up to dbSNP151. Afterwards it was changed to ATGT. For reasons of continuity, we stayed with TATG/Del.