Large offspring syndrome (LOS) is a loss-of-imprinting fetal overgrowth disorder in ruminants. Genomic imprinting is an epigenetic mechanism that regulates parental-allele specific expression of a subset of genes in mammals. Maternally expressed gene 3 (*MEG3*) is an imprinted long noncoding RNA associated with birthweight regulation. We hypothesized that there is loss-of- imprinting of *Meg3* in bovine LOS. To test this, we designed genomic DNA primers for all seven exons of *MEG3* (ARS-UCD1.2, 21:65,724,243–65,746,033) in order to identify polymorphisms between *Bos taurus indicus* and *Bos taurus taurus* to determine the allele specificity of *MEG3* in F1 hybrid fetuses. We performed polymerase chain reactions (PCR) using the DNA from the F1's sire (i.e. *indicus* bull) and a pool of genomic DNA from 123 F1 hybrid fetuses (both control and LOS). The PCR products were resolved by agarose gel electrophoresis, purified, and genotyped by Sanger sequencing. We identified three single nucleotide polymorphisms (SNP) in *MEG3*. Sequencing results show that the bull is heterozygous for all three SNPs while the DNA pool of fetuses contains both alleles at the three positions. The SNPs were a C/G in exon 3 at position 21:65,727,762, a C/A in exon 4 at position 21:65,729,889 and a G/A in exon 6 at position 21:65,744,366. Therefore, we are unable to ascribe allele specificity of the *MEG3* transcript in F1 hybrid fetuses. However, biallelic expression may still be identifiable if the F1s inherit different alleles, at least at one of these SNPs. To determine if biallelic expression is detected in individual LOS fetuses when compared to control fetuses, we have designed cDNA primers that will produce an amplicon that includes all three SNPs. We are currently processing the RNA from these fetuses for further analyses. Results will be shown.