Inadequate oocyte competence is a potential explanation for reduced pregnancy rates and(or) increased late embryonic mortality when small dominant follicles are induced to ovulate with gonadotropin releasing hormone (GnRH) following estrous synchronization in beef cows. The current study measured if the size and physiological status (estrous expression) of the pre-ovulatory follicle affects the oocyte transcriptome. Follicular waves were synchronized in 250 beef cows. Cumulus-oocytes complexes were collected from cows of the following follicle classifications: Small (<11.7mm, no estrus), Large (>12.5 mm, no estrus), and Spontaneous (11.6-13.9 mm; estrus expressed). RNA was extracted from pools of 4 oocytes and submitted for sequencing on an Illumina HiSeq 2000. After alignment to the bovine transcriptome or genome, differences in transcript abundance between oocyte pools from large and small follicle classifications, small and spontaneous follicle classifications, and large and spontaneous follicle classifications were determined. Transcripts associated with the ubiquitin/proteasome pathway and mitochondrial function were higher in abundance in oocytes from follicles from the large and spontaneous classifications. Both of the above pathways are essential for proper oocyte maturation. Further investigation of the above mentioned pathways may allow further insight regarding the decreased oocyte competence observed following the GnRH-induced ovulation of small dominant follicles.