Certain regions of the genome are more difficult to study than others due to intrinsic characteristics of the region. The mitochondrial genome is small with high copy number and therefore easy to sequence. The challenge comes from transmission mechanisms that actually allow certain individuals to have more than one mitochondrial genome—mitochondrial heteroplasmy. This phenomenon has potential implications for many fields including evolutionary, forensic, and disease studies. In this thesis we determined the frequency of mitochondrial heteroplasmy to be about 5% in canines by analyzing whole-genome sequence data. This level is likely higher, but we employed a very strict definition of heteroplasmy in order to increase confidence. Most importantly, there is potential for heteroplasmy to complicate studies resting on the tenet that organisms have a single mitochondrial genome inherited from their mother. The challenge with the Y chromosome exists as a result of its history of degeneration. This chromosome is gene poor, repetitive, and palindromic thereby making it difficult to sequence. This reduced ability to sequence has led to fewer investigations into Y chromosome variation and diversity. In this thesis we determined the number of Y chromosome haplotypes within the Angus breed. Furthermore, we also identified single nucleotide polymorphisms specific to cattle haplogroups Y1, Y2, and Y3. It was determined between 5 and 8 haplotypes exist and the Angus breed exhibits very little within breed diversity a likely result of the use of popular bulls and their sons in the population today.