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Fertility is a major economic factor in cow-calf operations. Productive, profitable cows are ones which conceive and calve early in the season, year after year. The age at which heifers reach reproductive maturity determines their ability to do this. Therefore, it is important to accurately identify and predict puberty onset to improve reproductive efficiency. Genetic variation plays a large role in the variation of reproductive development, but currently, tools for reproductive genetic progress are limited. Our aim is to create a more accurate genomic prediction of fertility to allow prepubertal and infertile heifers to be culled prior to breeding, minimizing losses for farmers. First, information-rich, highly variable fertility indicators need to be identified. Age, weight, body condition score (BCS), pelvic area, hip height, uterine horn diameter, largest follicle diameter, antral follicle count, days open (days to conception), and reproductive tract score (RTS), which is made up of separate ovarian and uterine scores, were assessed as possible indicator traits. To identify overall trends in the data and determine which traits are the major sources of variance, R programming was used to conduct principal component analyses (PCA) on these traits. Most variation within the dataset is assigned to the first principal component (PC) which consistently included traits accounting for differences in growth, size, and maturity, suggesting these traits are highly correlated and vary together. Although ovarian score and uterine score were measured separately, they often agreed and represent a continuum of development. Days open was often assigned to its own PC except when immature heifers were analyzed separately. In this case, RTS was added to the same PC suggesting that RTS has a bigger influence on determination of days open in prepubertal heifers than in mature heifers. Future work will identify which genes control the variation in these reproductive phenotypes substrate.