

At San Diego Zoo Wildlife Alliance, the southern white rhinoceros (SWR) is used as a reproductive model for the functionally extinct northern white rhino (NWR) to aid in developing assisted reproductive technologies and in vitro culture systems for oocytes and embryos in this species. Granulosa cells (GC) surround the oocyte and provide insight into follicle growth and oocyte maturation status. Our recent studies focused on transcriptomic changes in GC from different stages of follicle development and identified biomarkers for oocyte competence. As SWR and NWR are taxonomically closely related, we used the NWR genome (more thoroughly sequenced) as the reference genome. The data generated by three sequencing projects using GC collected from SWR was used to greatly improve the current NWR genome annotation. The current NWR genome available (in preprint) has 12,252 genes annotated, 14,274 transcripts, and numerous miscalled genes, including 47% of the transcripts labeled with protein symbols. Therefore, it is challenging to work on transcriptomics with the current annotation. Overall, we improved gene identification by 67%, increased transcript calling by 119%, corrected the assignment of 70% of genes to their proper sequence, and corrected 13% of genes that were assigned to multiple scaffolds. Our data helped determine possible biomarkers for oocyte maturation success while learning about follicle dynamics in this species and improving the annotation of the NWR genome. We hope to use this information and sequencing technology to improve assisted reproductive technologies in rhino species that are facing threats and extinction.