

Figure 1: The genomic location of TSS uni-directional clusters shared across 24 tissue types (55,139 TSS and 2,543 TSS-Enhancer regions were identified in total)

In summary for this project, we have:

- Generated a high-resolution analysis of TSS complexity across tissues, including drivers of transcription using Cap Analysis Gene Expression (CAGE) (Figure 1)
- Captured diverse transcriptomes from 3 populations of cattle (Holstein, Charolais x Holstein and Kinsella beef composite [KC])
- Provided information about breed, tissue and population-specific promoter complexity that is valuable for cattle genomic breeding programmes
- Performed a comparative analysis of TSS across species (7 mammalian and 1 avian) to identify TSS and TSS-Enhancers that are specific to cattle (Figure 2)

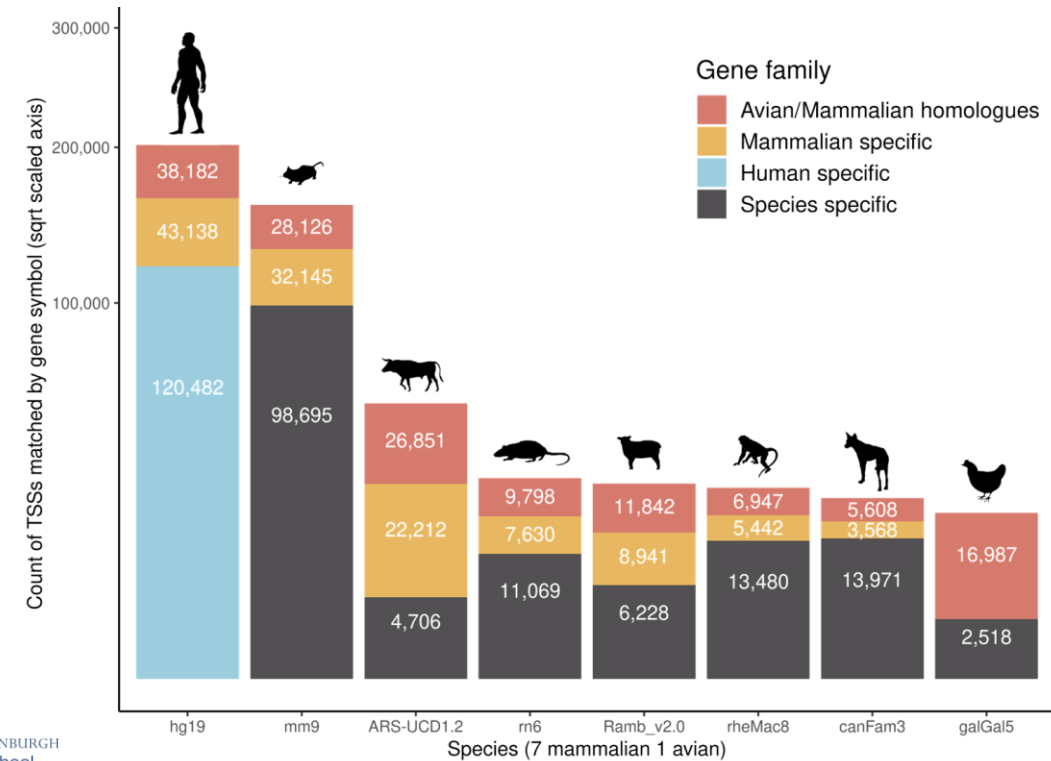


Figure 2: Comparative analysis of TSS across species