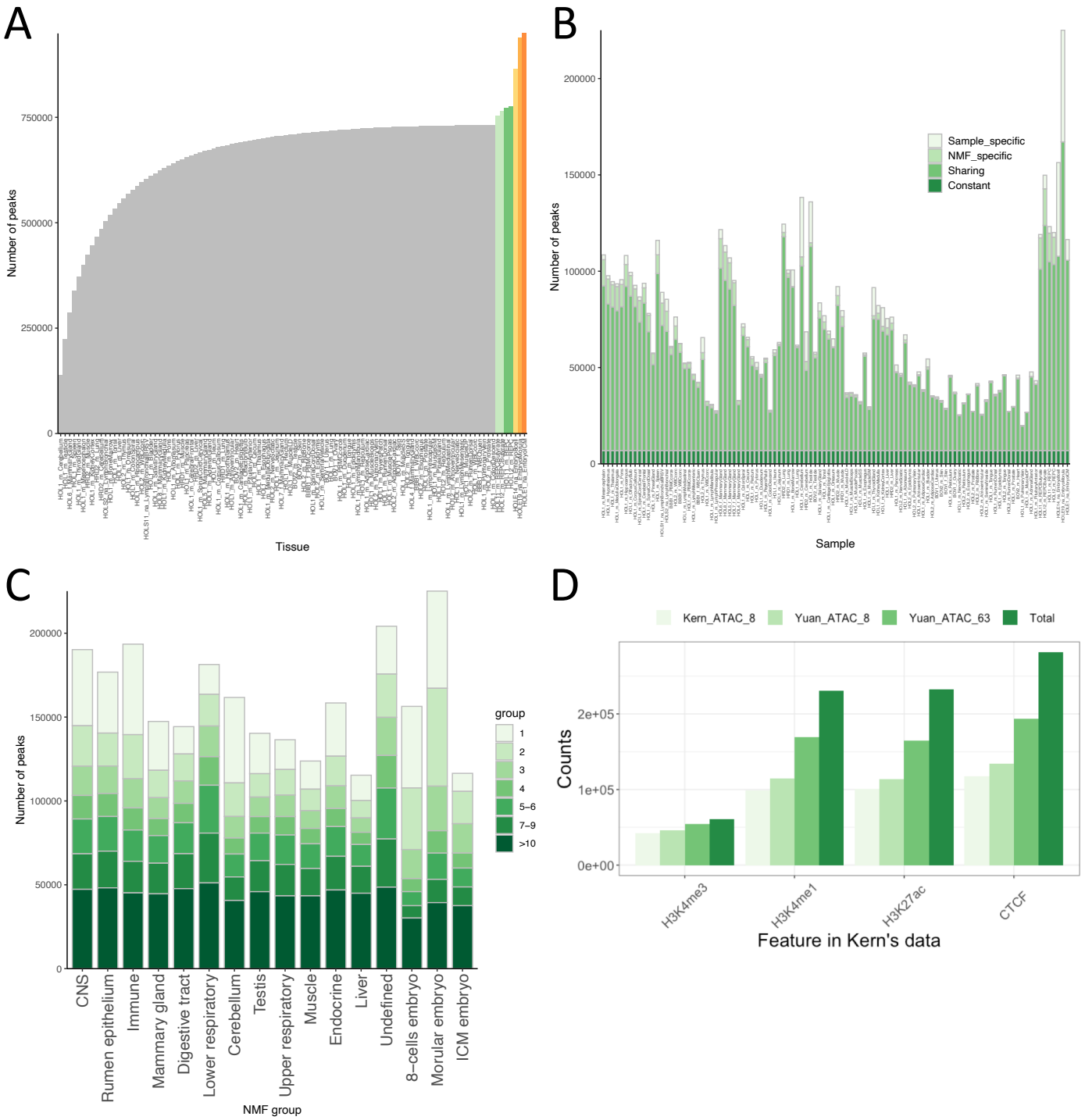

Supplemental Figure S8: (A) Number of additional ATAC-seq peaks that are uncovered when adding new samples. The first 97 samples are the post-natal tissue samples, ordered by decreasing number of new peaks detected. Primary cultured cells (green gradients) and embryonic samples (orange gradient) are added at the end. **(B)** Number of peaks detected in each sample colored by degree of sharing with other samples (Constant: shared with all other samples, Sharing: shared with at least one sample from other NMF component(s), NMF_specific: shared only with samples from the same NMF component, Sample_specific: not shared with any other sample). **(C)** Number of peaks sorted by NMF component (dominant component) and colored by the number of NMF components with whom it is shared. **(D)** Overlap between ATAC-seq and ChIP-seq epigenetic marks in the dataset of Kern *et al.* (2021) studying eight tissue types in cattle. H3K4me3: active promotors, H3K4me1: active and primed enhancers, H3K27ac: active promotors and enhancers, CTCF: boundary elements and regulators of transcription and chromatin architecture. H3K27me3, corresponding to silenced chromatin, was not included (although studied in Kern *et al.*) because they do not correspond to regulatory elements *sensu stricto* but rather reflect the local outcome of gene repression. Kern_ATAC_8: ATAC-seq peaks reported in Kern *et al.* from the analyses of eight tissue types. Yuan_ATAC_8: ATAC-seq peaks detected in this study from the analyses of eight tissue-types matching the Kern *et al.* samples. Yuan_ATAC_63: full ATAC-seq peak catalogue produced in this study.