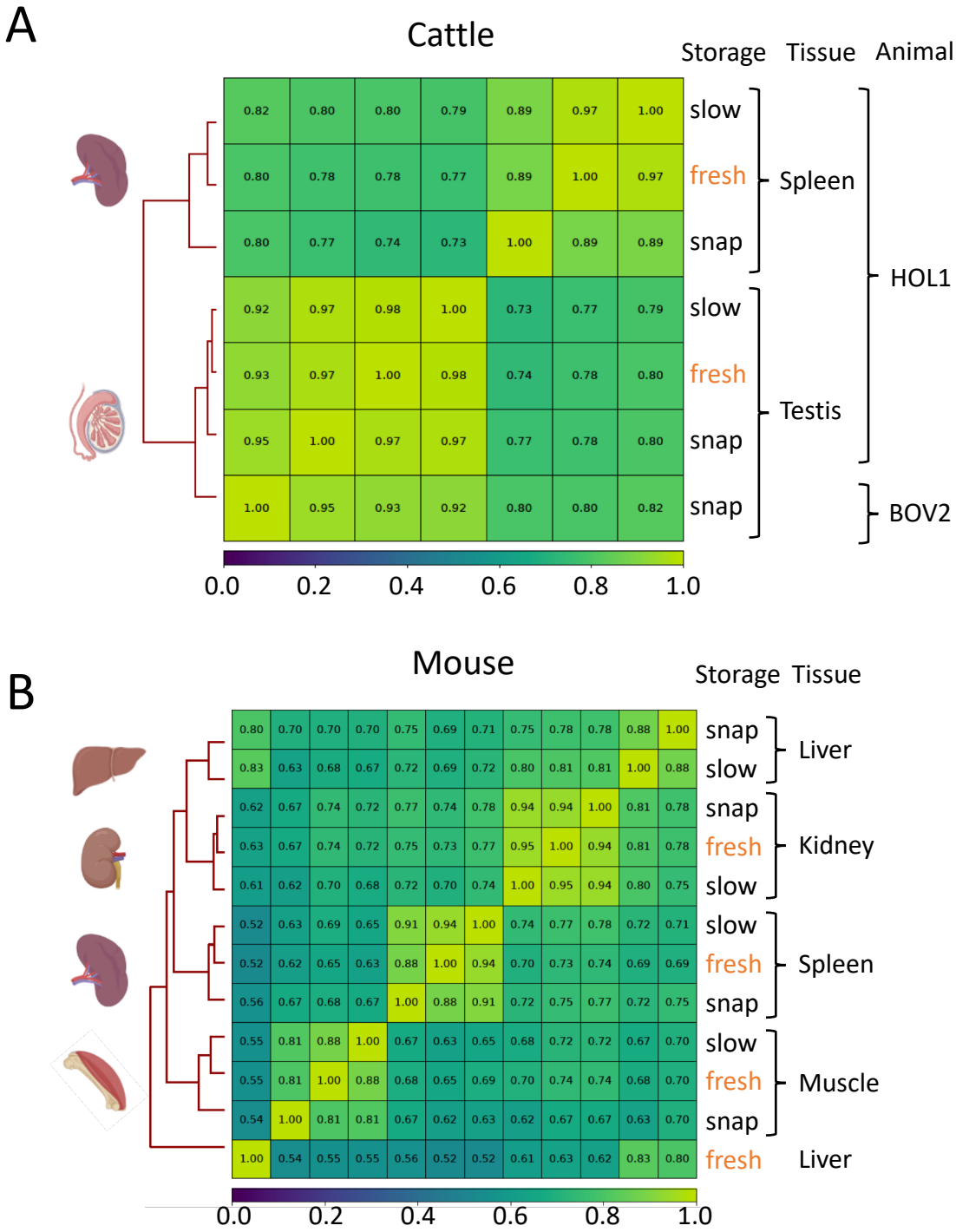

Supplemental Figure S1: Impacts of sample storage conditions on genome-wide ATAC-seq signals were examined using cattle **(A)** and mouse **(B)** tissues. Pearson's correlation was calculated using normalized read coverage in 500-bp windows spanning the entire genome. Pairwise correlation coefficients are shown in color code between hierarchically clustered samples. Tissues were collected in the UW cold storage solution on ice and further processed in three ways: (i) fresh: Tissues were directly subjected to library construction on the day of sampling, (ii) slow: Tissues cut into ~ 3 mm cubes were soaked in STEM-CELLBANKER DMSO-free cell freezing medium for ~ 10 minutes on ice and stored at -80°C until use, and (iii) snap: Tissues cut into ~ 3 mm cubes were snap-frozen in liquid nitrogen and stored at -80°C until use. Correlations between fresh and slow-frozen samples are slightly higher than between fresh and snap-frozen samples. This suggests that cell freezing medium better preserves nuclear structure of cryopreserved tissues. It is noteworthy that, for tissues that are difficult to homogenize (e.g., stomach, nerve, vein), pulverizing snap-frozen tissues using mortar and pestle in liquid nitrogen achieved better results (see also Supplemental Table S3).