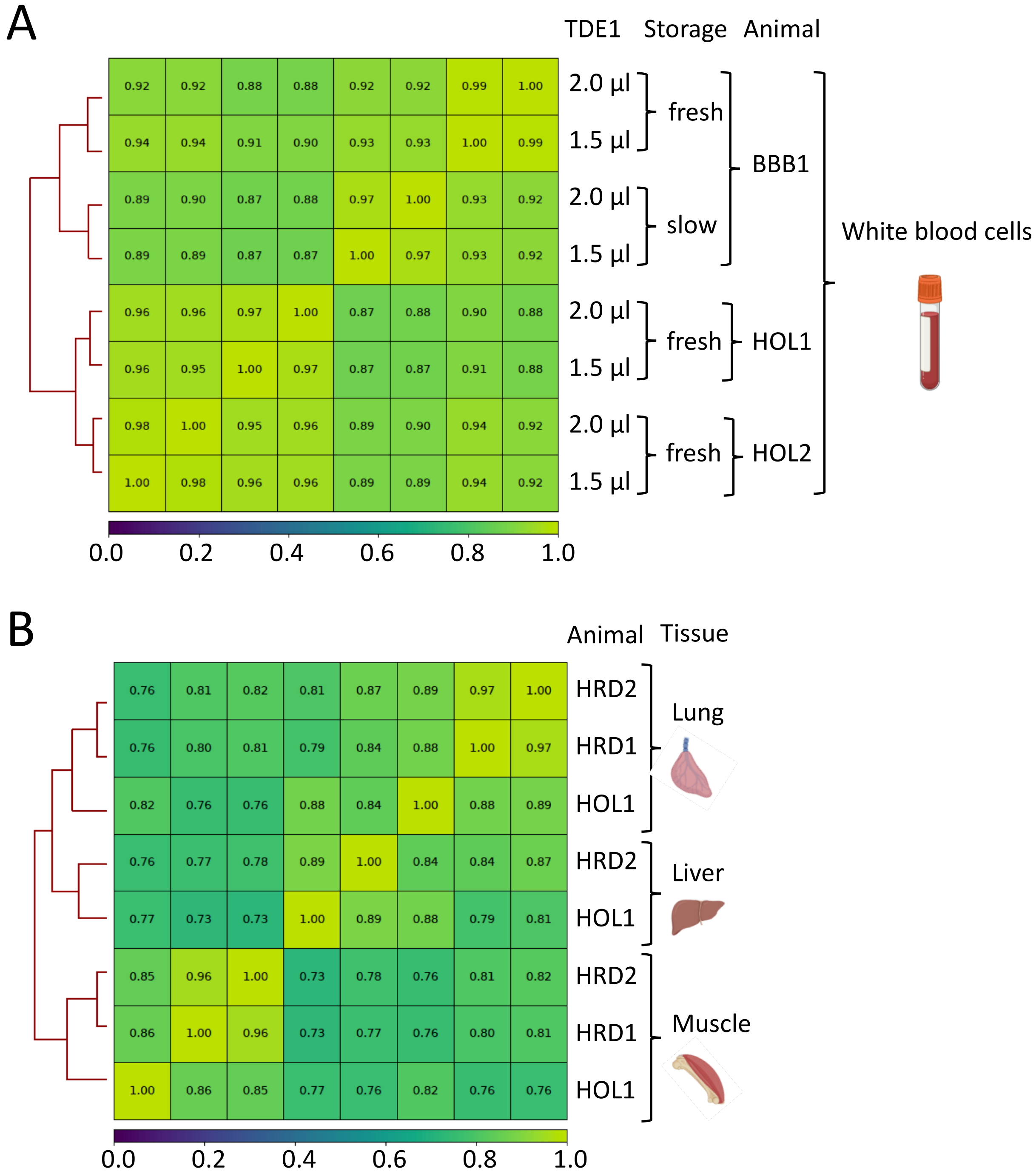

								TDE1	Storage	Animal	
0.92	0.92	0.88	0.88	0.92	0.92	0.99	1.00	2.0 µl	fresh	BBB1	White blood cells
0.94	0.94	0.91	0.90	0.93	0.93	1.00	0.99	1.5 µl			
0.89	0.90	0.87	0.88	0.97	1.00	0.93	0.92	2.0 µl	slow		
0.89	0.89	0.87	0.87	1.00	0.97	0.93	0.92	1.5 µl			
0.96	0.96	0.97	1.00	0.87	0.88	0.90	0.88	2.0 µl	fresh	HOL1	
0.96	0.95	1.00	0.97	0.87	0.87	0.91	0.88	1.5 µl			
0.98	1.00	0.95	0.96	0.89	0.90	0.94	0.92	2.0 µl	fresh	HOL2	
1.00	0.98	0.96	0.96	0.89	0.89	0.94	0.92	1.5 µl			

								Animal	Tissue
0.76	0.81	0.82	0.81	0.87	0.89	0.97	1.00	HRD2	Lung
0.76	0.80	0.81	0.79	0.84	0.88	1.00	0.97	HRD1	
0.82	0.76	0.76	0.88	0.84	1.00	0.88	0.89	HOL1	
0.76	0.77	0.78	0.89	1.00	0.84	0.84	0.87	HRD2	Liver
0.77	0.73	0.73	1.00	0.89	0.88	0.79	0.81	HOL1	
0.85	0.96	1.00	0.73	0.78	0.76	0.81	0.82	HRD2	Muscle
0.86	1.00	0.96	0.73	0.77	0.76	0.80	0.81	HRD1	
1.00	0.86	0.85	0.77	0.76	0.82	0.76	0.76	HOL1	

Supplemental Figure S2: Reproducibility of ATAC-seq data. Pairwise correlation coefficients calculated using normalized read coverage in 500-bp windows are shown in color code for hierarchically clustered samples. **(A)** Comparisons between in-house ATAC-seq data using white blood cells (WBC) isolated from one Belgium Blue adult female (BBB1) and two Holstein juvenile male (HOL1 and HOL2). Samples were either directly subjected to library construction (fresh) or stored in the Stem-Cellbanker freezing media until use (slow). Tagmentation reactions were performed using two different amounts of TDE1 transposase enzyme (1.5 µl or 2.0 µl) per 50,000 nuclei. **(B)** Correlation between in-house (HOL1) and publicly available ATAC-Seq data (HRD1 and HRD2, two adult Hereford cattle, Halstead *et al.*, 2020). Genome-wide ATAC-Seq signal was highly reproducible between technical (0.92 – 0.99) as well as biological replicates (0.85 – 0.97).