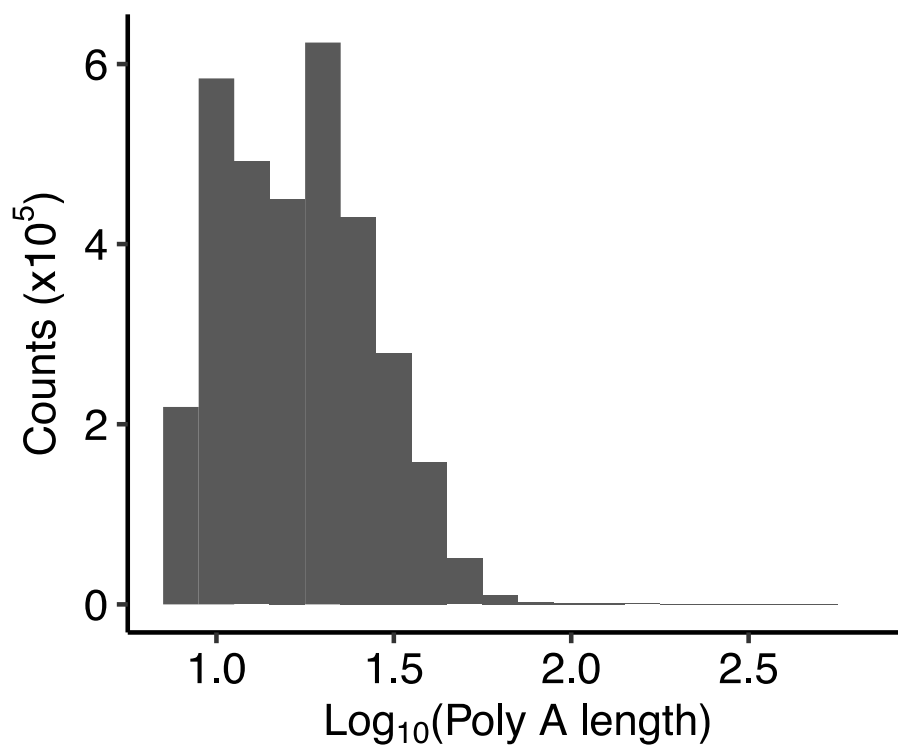
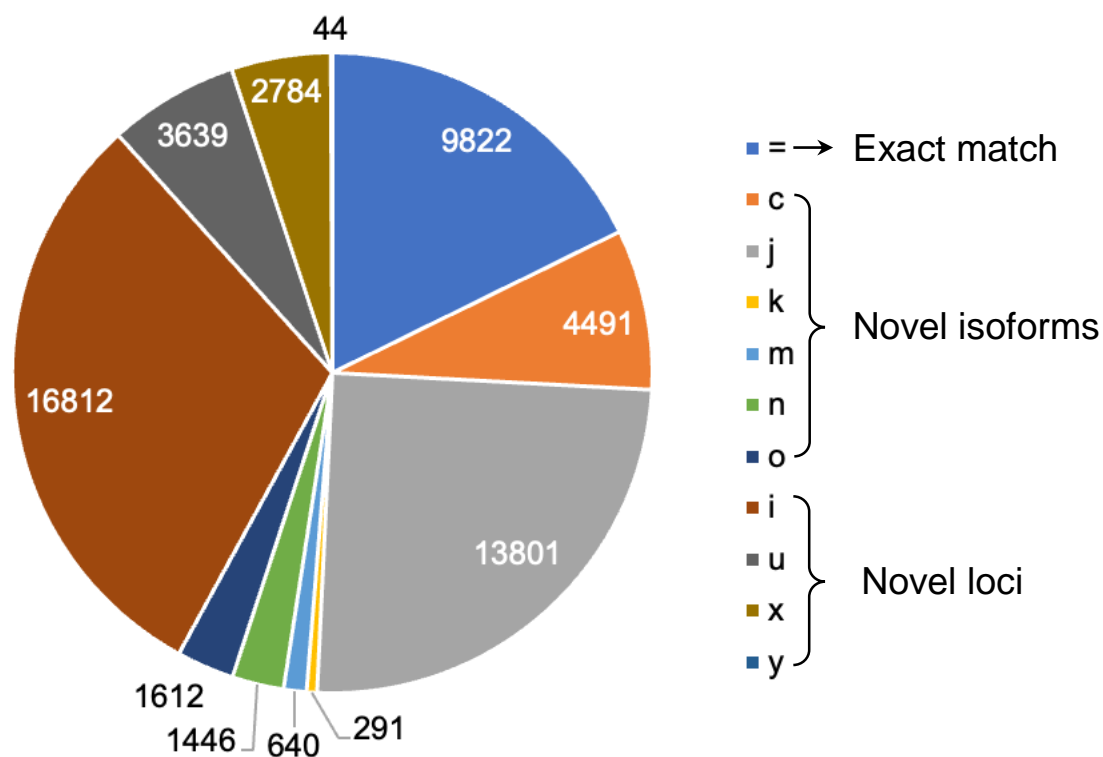


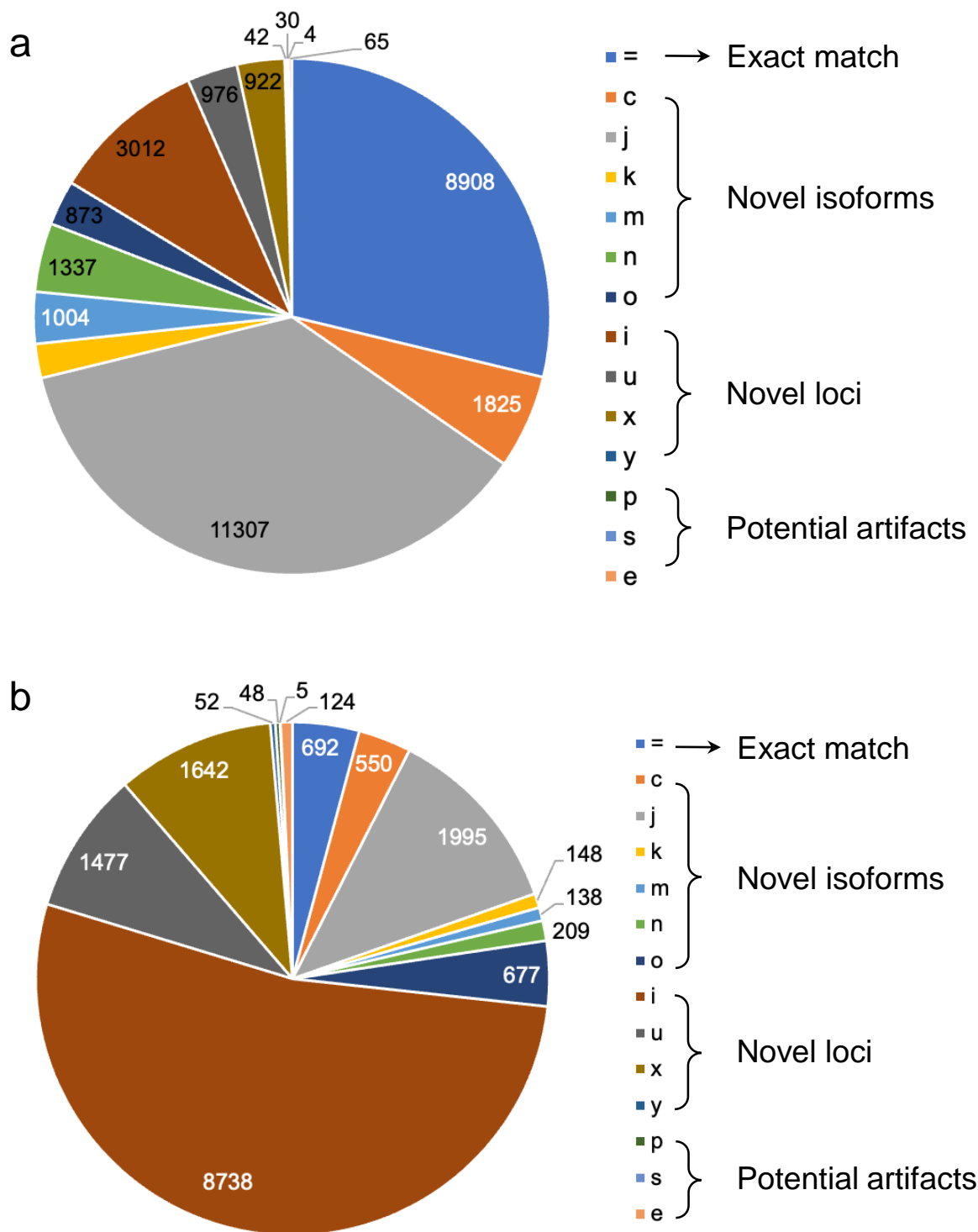
**Supplementary Figure 1.** Principal component analysis of 68 chicken Nanopore long-read transcriptomes. The red arrow indicated the sample, Cecum\_CA, which was not clustered with other samples from the cecum tissue. The corresponding eigenvalues are shown in Supplementary Table 3.



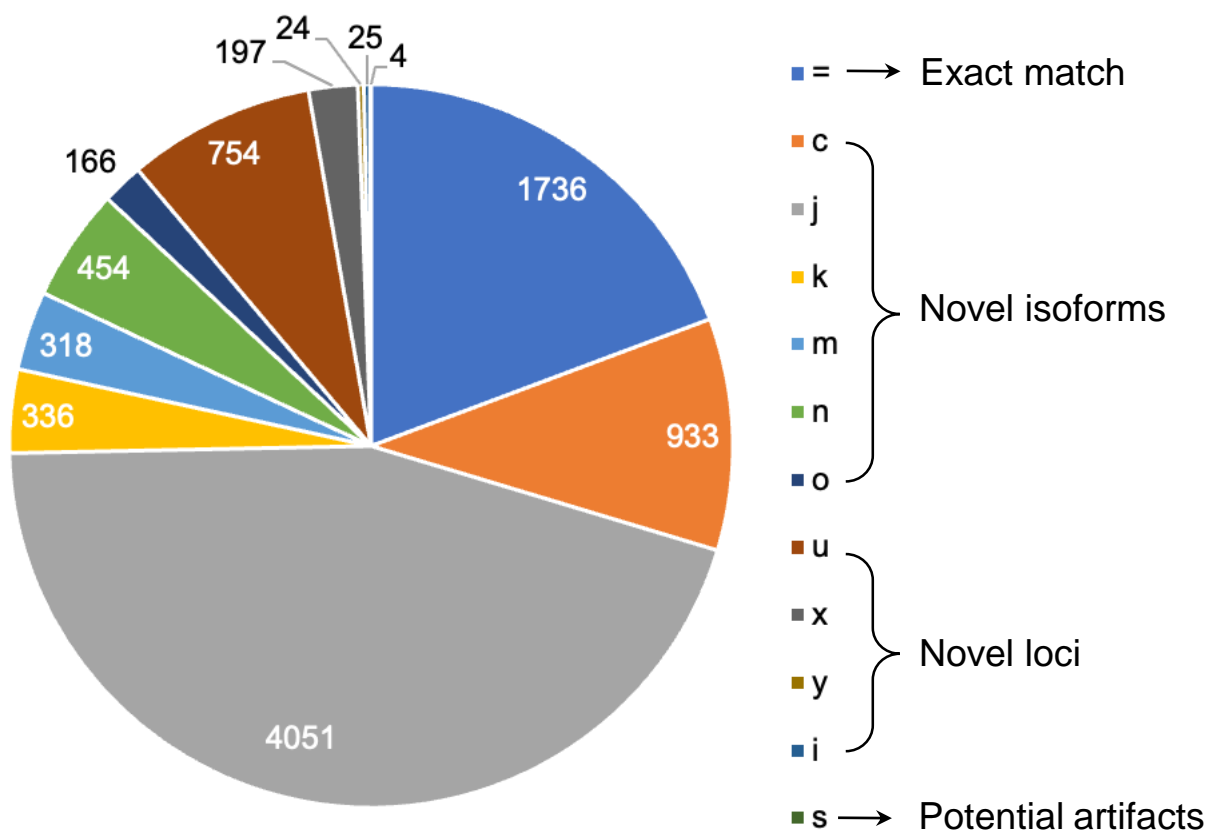
**Supplementary Figure 2.** Histogram depicting the distribution of poly(A) tail length (bp) predicted by the PolyAtailor software tool (Liu et al., 2022).



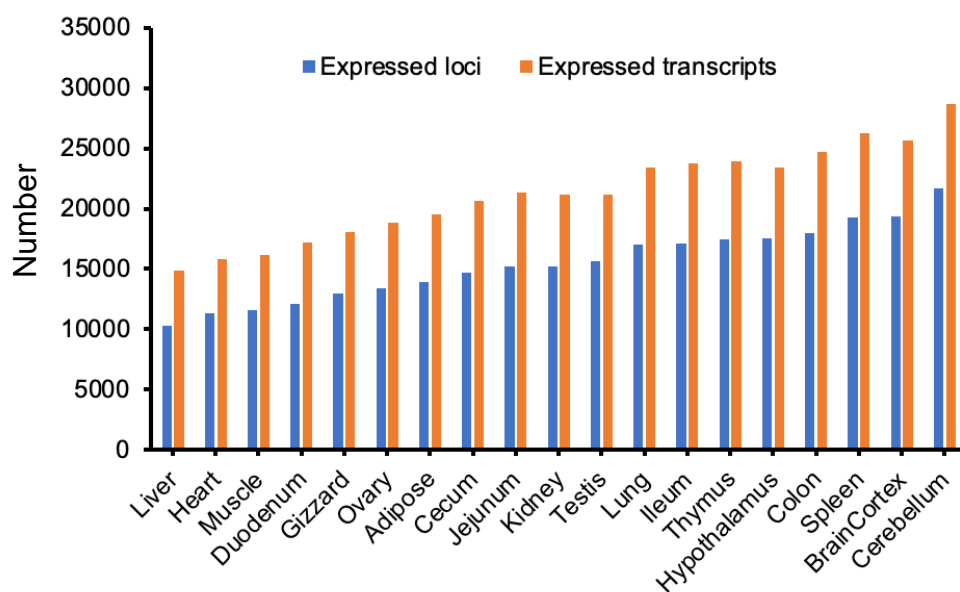
**Supplementary Figure 3.** GffCompare types when comparing our predicted transcripts to NCBI annotation (V105). Transcripts were classified into: 1) Exact match: GffCompare code "=", which means the intron chains of our annotated transcripts can exactly match to reference annotations; 2) Novel isoform: GffCompare codes 'c,' 'k,' 'j,' 'm,' 'n,' or 'o', which means predicted transcript cannot match a reference transcript but can match a reference gene; 3) Novel loci: GffCompare codes 'i,' 'u,' 'y,' or 'x', which means predicted transcript cannot match either a reference transcript or a reference locus.



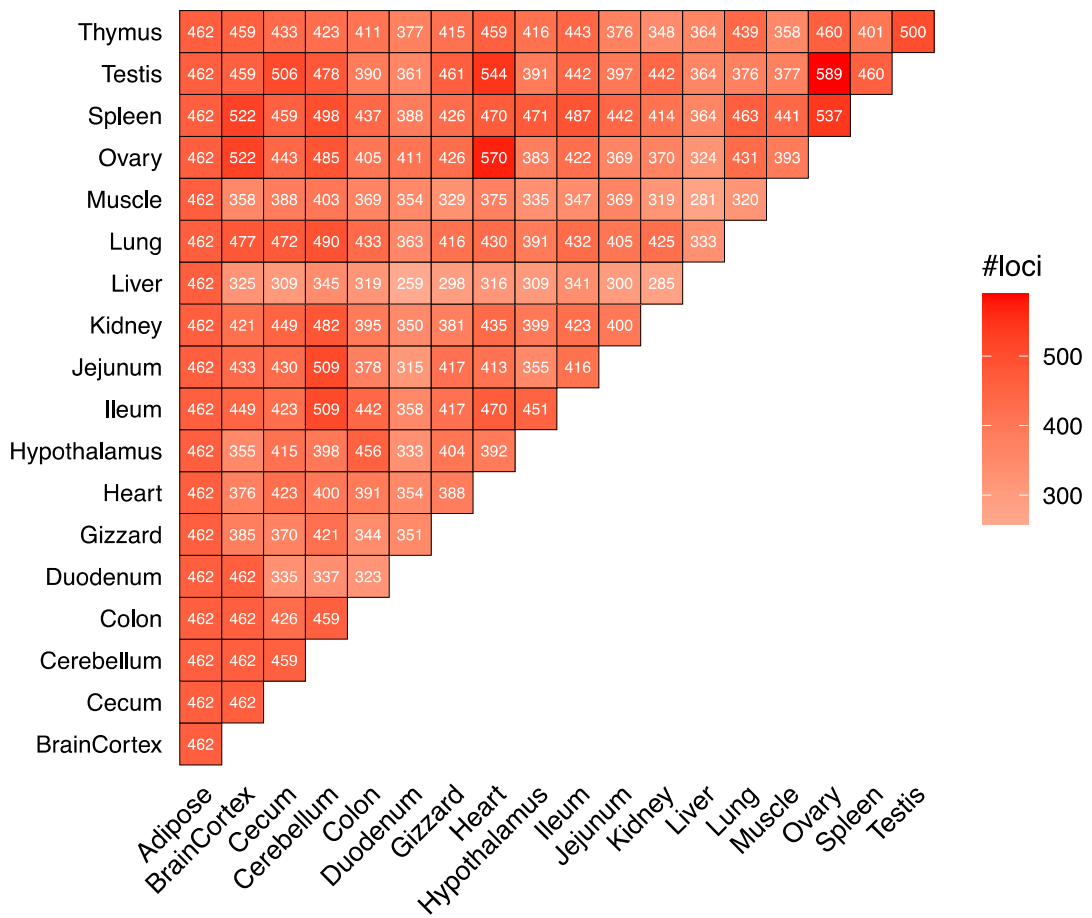
**Supplementary Figure 4.** GffCompare types when comparing protein-coding (a) and lncRNA loci (b) predicted in this study with those predicted in Jehl et al. (2020). Transcripts were classified into: 1) Exact match: GffCompare code "=", which means the intron chains of our annotated transcripts can exactly match to reference annotations; 2) Novel isoform: GffCompare codes 'c,' 'k,' 'j,' 'm,' 'n,' or 'o', which means predicted transcript cannot match a reference transcript but can match a reference gene; 3) Novel loci: GffCompare codes 'i,' 'u,' 'y,' or 'x', which means predicted transcript cannot match either a reference transcript or a reference locus.



**Supplementary Figure 5.** GffCompare types when comparing novel transcripts reported by Thomas et al. (2014) to our annotation. Transcripts were classified into: 1) Exact match: GffCompare code "=", which means the intron chains of our annotated transcripts can exactly match to reference annotations; 2) Novel isoform: GffCompare codes 'c,' 'k,' 'j,' 'm,' 'n,' or 'o', which means predicted transcript cannot match a reference transcript but can match a reference gene; 3) Novel loci: GffCompare codes 'i,' 'u,' 'y,' or 'x', which means predicted transcript cannot match either a reference transcript or a reference locus.



**Supplementary Figure 6.** Number of expression loci and transcripts (TPM > 0.1) across tissues



**Supplementary Figure 7.** Number of loci showing differential alternative splicing between tissues