

## **Transcriptome Annotation of 17 Porcine Tissues Using Nanopore Sequencing Technology**

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### **ABSTRACT**

The annotation of animal genomes plays an important role in elucidating molecular mechanisms behind the genetic control of economically important traits. Here, we employed the long-read sequencing technology, Oxford Nanopore Technology (ONT), to annotate the pig transcriptome across 17 tissues from two Yorkshire littermate pigs. More than 9.8 million reads were obtained from a single ONT flow cell, and 69,781 unique transcripts at 50,108 loci were identified. Of these transcripts, 16,255 were found to be novel isoforms, and 22,344 were found at novel loci compared to the Ensembl (release 102) and NCBI (release 106) references. Novel transcripts were mostly found from cerebellum, followed by lung, liver, spleen, and hypothalamus. By comparing the transcripts found at novel loci to existing databases, we found that 21,285 (95.3%) transcripts were matched to the NT database (v5) and 13,676 (61.2%) were matched to the NR database (v5). Moreover, there were 4,324 (19.4%) transcripts matched to the SwissProt database (v5), corresponding to 11,356 proteins. Tissue-specificity gene expression analyses showed that 9,749 transcripts were highly tissue-specific, and cerebellum contained the most tissue-specific transcripts. As the same samples were used for cis-regulatory elements annotation in pig genome, the transcriptome annotation generated by this study provides an additional and complementary annotation resource for the Functional Annotation of Animal Genomes (FAANG) effort to comprehensively annotate the pig genome.

**Key words** transcriptome annotation, pig tissues, long-read sequencing, Nanopore sequencing