



# **De novo assembly and characterization of farmed blue fox (*Alopex lagopus*) global transcriptome using Illumina paired-end sequencing**

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Genet. Mol. Res. 15 (1): gmr.15017603

Received September 9, 2015

Accepted November 27, 2015

Published March 24, 2016

DOI <http://dx.doi.org/10.4238/gmr.15017603>

**ABSTRACT.** The blue fox (*Alopex lagopus*), a coat-color variant of the Arctic fox, is a domesticated fur-bearing mammal. In the present study, transcriptome data generated from a pool of nine different tissues were obtained with Illumina HiSeq2500 paired-end sequencing technology. After filtering from raw reads, 32,358,290 clean reads were assembled into 161,269 transcripts and 97,252 unigenes by the Trinity fragment assembly software. Of the assembled unigenes, 37,967 were annotated in the National Center for Biotechnology Information (NCBI) Non-Redundant (NR) protein database and 26,264 in the Swiss-Prot database. Among the annotated unigenes, 24,839 and 24,267 were assigned using the Gene Ontology (GO) and euKaryotic Orthologous Groups (KOG) databases, respectively. Altogether, 17,057 unigenes were mapped onto 227 pathways using the Kyoto Encyclopedia of Genes and Genomes database. In addition, 6394 simple sequence repeats were identified by examining

12,965 unigenes (>1 kb), which could contribute to the development of molecular markers. This study generated transcriptome data for the blue fox that will promote further progress in expression profiling studies, and provide a good annotation basis for genomic studies.

**Key words:** Blue fox; Transcriptome; Assembly