



RNA sequencing (RNA-Seq) of lymph node, spleen, and thymus transcriptome from wild Peninsular Malaysian cynomolgus macaque (*Macaca fascicularis*)

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ABSTRACT

The cynomolgus macaque (*Macaca fascicularis*) is an extensively utilised nonhuman primate model for biomedical research due to its biological, behavioural, and genetic similarities to humans. Genomic information of cynomolgus macaque is vital for research in various fields; however, there is presently a shortage of genomic information on the Malaysian cynomolgus macaque. This study aimed to sequence, assemble, annotate, and profile the Peninsular Malaysian cynomolgus macaque transcriptome derived from three tissues (lymph node, spleen, and thymus) using RNA sequencing (RNA-Seq) technology. A total of 174,208,078 paired end 70 base pair sequencing reads were obtained from the Illumina Hi-Seq 2500 sequencer. The overall mapping percentage of the sequencing reads to the *M. fascicularis* reference genome ranged from 53–63%. Categorisation of expressed genes to Gene Ontology (GO) and KEGG pathway categories revealed that GO terms with the highest number of associated expressed genes include Cellular process, Catalytic activity, and Cell part, while for pathway categorisation, the majority of expressed genes in lymph node, spleen, and thymus fall under the Global overview and maps pathway category, while 266, 221, and 138 genes from lymph node, spleen, and thymus were respectively enriched in the Immune system category. Enriched Immune system pathways include Platelet activation pathway, Antigen processing and presentation, B cell receptor signalling pathway, and Intestinal immune network for IgA production. Differential gene expression analysis among the three tissues revealed 574 differentially expressed genes (DEG) between lymph and spleen, 5402 DEGs between lymph and thymus, and 7008 DEGs between spleen and thymus. Venn diagram analysis of expressed genes revealed a total of 2,630, 253, and 279 tissue-specific genes respectively for lymph node, spleen, and thymus tissues. This is the first time the lymph node, spleen, and thymus transcriptome of the Peninsular Malaysian cynomolgus macaque have been sequenced via RNA-Seq. Novel transcriptomic data will further enrich the present *M. fascicularis* genomic database and provide future research potentials, including novel transcript discovery, comparative studies, and molecular markers development.

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Additional Information and
Declarations can be found on
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