

RNA sequencing of kidney and liver transcriptome obtained from wild cynomolgus macaque (*Macaca fascicularis*) originating from Peninsular Malaysia

ABSTRACT

Objective: Using high-throughput RNA sequencing technology, this study aimed to sequence the transcriptome of kidney and liver tissues harvested from Peninsular Malaysia cynomolgus macaque (*Macaca fascicularis*). *M. fascicularis* are significant nonhuman primate models in the biomedical field, owing to the macaque's biological similarities with humans. The additional transcriptomic dataset will supplement the previously described Peninsular Malaysia *M. fascicularis* transcriptomes obtained in a past endeavour. Results: A total of 75,350,240 sequence reads were obtained via Hi-seq 2500 sequencing technology. A total of 5473 significant differentially expressed genes were called. Gene ontology functional categorisation showed that cellular process, catalytic activity, and cell part categories had the highest number of expressed genes, while the metabolic pathways category possessed the highest number of expressed genes in the KEGG pathway analysis. The additional sequence dataset will further enrich existing *M. fascicularis* transcriptome assemblies, and provide a dataset for further downstream studies.

Keyword: *Macaca fascicularis*; *Cynomolgus macaque*; RNA sequencing; Transcriptome; Biomedical science; Kidney; Liver