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Construction of mouse immune lncRNA atlas from various mouse cell types

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Long non-coding RNAs (lncRNAs) are RNA molecules of ≥200nt, which are known to play their major regulatory roles at epigenetic and transcriptional levels. Although their cancer-related functions have been reported at the tumor immune microenvironment (TIME) level, the landscape of TIME lncRNAs remains unexplored yet. Because lncRNAs show a strong cell type-specific expression, we believe that many have been overlooked in rare immune cell types. To fill this gap, our study attempted to identify novel immune cell-expressing lncRNAs using 173 RNA-seq data of 25 mouse immune cell types, resulting in the identification of 3204 novel lncRNA transcripts (1706 of genes). To improve and evaluate the structural accuracy, we used an alignment score, transcript-end signal refinement, and expression level. Our research would be extended to build the database and web-based analysis tool to analyze the annotated and novel lncRNAs in both bulk and single cell datasets, which will facilitate further exploration and research by the community.