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Statistical examination of the dynamics of mouse lung tissue promoterome during development

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Digital gene expression technologies have improved the resolution of genome-wide transcriptional activity to the single nucleotide level. Cap analysis of gene expression (CAGE) in particular is a 5' focused technology applicable for determination of transcription starting sites (TSS). Due to the high resolution of such sequence-based expression profiling, tissue specific transcriptional activity can be mapped with high accuracy. The present work uses CAGE data, to clarify molecular mechanisms of the mouse lung tissue during development based on the transcriptome. Differential usage of transcription start sites is examined and mapping of transcription factor binding is further applied to verify up-regulation and down-regulation. Stratified expression patterns and candidate mechanisms driving embryonic development are identified. Statistical analyses shows differential preference of transcription start sites among the different developmental stages and most notably gene-specific disparate utilization of transcription start sites were observed.

Biography

Nelson Kibinge is currently a Ph.D. student at Nara Institute of Science and Technology.

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