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Genetic Variation and Splicing from Single Cell RNA-Sequencing

Guest Editor:

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Deadline for manuscript submissions:
closed (30 April 2020)

Message from the Guest Editor

Dear colleagues,

Single cell RNA-sequencing (scRNA-seq) provides a unique opportunity to study inter-molecular relationships. Besides, scRNA-seq provides the opportunity to study allele-specific expression at an unprecedented resolution.

We invite submissions of both methodological and original research papers assessing genetic variation, splicing and post-transcriptional modifications from scRNA-seq, and, where possible, their integration with gene and transcript expression. Topics may include, but are not limited to, studies of expressed genetic variation, including single nucleotide variants (SNVs), splicing and posttranscriptional modifications such as RNA-editing. The overarching aim of this issue is to stimulate the emerging and promising research on single cell transcriptomics, pursuing at the same time new exploratory and collaborative venues to address its challenges.

Dr. Anelia Horvath
Guest Editor

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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