

## Accepted Manuscript

The role of alternative polyadenylation in cancer progression

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PII: S2452-0144(18)30050-5  
DOI: doi:[10.1016/j.genrep.2018.05.003](https://doi.org/10.1016/j.genrep.2018.05.003)  
Reference: GENREP 256  
To appear in: *Gene Reports*  
Received date: 22 February 2018  
Revised date: 24 April 2018  
Accepted date: 8 May 2018

Please cite this article as: Buddhi Prakash Jain , The role of alternative polyadenylation in cancer progression. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Genrep(2017), doi:[10.1016/j.genrep.2018.05.003](https://doi.org/10.1016/j.genrep.2018.05.003)

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**The role of Alternative polyadenylation in Cancer Progression.**Buddhi Prakash Jain<sup>1\*</sup>

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**Abstract:** Regulation of gene expression is attributed at multiple levels as transcriptional, post-transcriptional and post-translational events. Under various modes of post-transcriptional regulation, alternative polyadenylation (APA) is one of the means to generate transcriptome diversity. In alternative polyadenylation, multiple transcripts are generated from a single gene by the use of the different polyadenylation site in the 3'UTR and other regions. It is a highly regulated process as deregulation in this is associated with the pathogenesis of various diseases. Cancer-associated genes can avoid the miRNA mediated negative regulation by using the proximal polyadenylation signal (PAS) and shorten the length of 3'UTR. Highly proliferative or cancer cells express the transcripts with short 3'UTR which lacks binding sites for many miRNA and regulatory RNA binding proteins (RBPs). Shortening of the 3'UTR associated with tumor aggressiveness and poor survival of cancer patients. Global analysis of APA is now a focused area of study in context to cancer progression. In this review, we will comprehensively discuss the alternative polyadenylation process and their implication in cancer.

**Keywords:** Post-transcriptional regulation; Alternative polyadenylation; Cancer; Intronic polyadenylation; Metastasis.

**1. Alternative Polyadenylation:**

In eukaryotic cells, a diverse array of proteins is generated by the regulation of gene expression at various levels including transcription, alternative splicing, mRNA stability-decay, RNA editing, alternative polyadenylation, proteasomal degradation and post-

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