

Genome-wide profiling reveals cancer-related genes with switched alternative polyadenylation sites in colorectal cancer

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Background: Alternative polyadenylation (APA) is an important post-transcriptional regulation in eukaryotic cells. It plays considerable roles in many biological processes and diseases, such as cell differentiation, proliferation and cancer. Colorectal cancer (CRC) is one of the most common malignancies worldwide, which is among the top five in incidence and mortality of all cancers in China. Although there have been some studies on the APA of CRC, the normal and carcinoma samples used for genome-wide profiling were not matched. The purpose of this study was to obtain genes with switched 3'-untranslated region (UTR) that may be associated with intracellular regulation of CRC by analyzing APA patterns of strict control groups from clinical patients.

Materials and methods: CRC and matched normal tissues were acquired from surgical specimens from three CRC patients. Their libraries of 3'-terminal fragments of mRNA with poly(A) tails were constructed by 3T-seq technology and sequenced by Illumina HiSeq X Ten. APA patterns of cancer and matched normal tissues were analyzed by bioinformatics analysis, and a representative gene, *GPI*, was verified by quantitative reverse transcription PCR.

Results: Overall, we identified 35,076 poly(A) sites in total. Compared to the matched normal tissues, we detected 350, 405 and 375 genes with significantly APA-mediated 3'-UTR alteration in cancer tissues of three patients, respectively. Forty-seven genes with switched 3'-UTR were shared in all three patients. In addition, most of these genes have shortened 3'-UTRs, some of which were associated with cancers, such as *GPI*.

Conclusion: Our studies found several genes with switched 3'-UTR in CRC patients, which may provide some important clues for more in-depth study of the cellular regulation in CRC from the perspective of post-transcriptional regulation. It may also help in the search for new biomarkers of CRC.

Keywords: alternative polyadenylation, CRC, 3T-seq, 3'-UTR

Introduction

Almost all eukaryotic pre-messenger RNAs (pre-mRNAs) and a portion of noncoding transcripts have poly(A) sites (PAS) and are polyadenylated.¹⁻³ Recent discoveries have found that more than two-thirds of all genes have multiple PAS,¹ which means that alternative polyadenylation (APA) can take place. APA can be typically divided into the following two categories: untranslated region (UTR)-APA and coding region (CR)-APA.⁴ APA is extensively used to regulate gene expression by producing transcript isoforms with diverse 3'-UTRs. Alternative 3'-UTR may affect stability, cellular localization and translation efficiency of transcript isoforms, even if the encoded proteins have the same sequences.^{5,6} Recent studies have shown that APA alterations

are displayed in a series of biological processes, such as development, cell differentiation, proliferation, neuron activity and cancer.⁷

A study has shown that ~70% of protein-coding genes have conserved microRNA (miRNA) target sites within their 3'-UTRs.¹ During transformation, the cell starts using the PAS most proximal to the open reading frame (ORF) to generate a short 3'-UTR, which makes the mRNA resistant to miRNA by eliminating miRNA-binding sites.⁸ A recent study reported a widespread preferential usage of proximal PAS in cancers, such as breast, lung, liver and colorectal cancers (CRCs),² even if the role of APA in transformation and cancer is still not very clear.

CRC, which is one of the most common malignancies worldwide, remains among the top five in incidence and mortality of all cancers in China, even though it is not a high prevalence area in comparison with Western Europe and North America.⁹ Although Morris et al¹⁰ have studied APA in CRC patients, their normal and carcinoma samples in the high-throughput sequencing data used for analysis were not matched. The establishment of the control group in that study was not sufficiently rigorous, which may influence the accuracy of APA sites obtained through high-throughput sequencing.

In this study, we used a previous published method, the 3T-seq technology, to profile genome-wide APA sites in CRC patients to analyze the effects of this kind of post-transcriptional modification on CRC. Comparisons between cancer samples and the matched normal samples help to understand the role of APA in clinical patients.

Materials and methods

Collection of human tissue samples

Fresh tissue samples from three CRC patients were collected at the Anhui Medical University, First Affiliated Hospital, Anhui, China. This study plan was approved by the institutional review boards of Anhui Medical University and was carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki). All patients had signed an informed consent form. All samples were examined by one experienced pathologist, and clinical

information of all individuals are listed in Table 1. After being collected, the samples were put in liquid nitrogen quickly and preserved in low temperature environment. TRIzol (Thermo Fisher Scientific, Waltham, MA, USA) was used to isolate total RNA from tissue samples following the manufacturer's protocol. Total RNA quantity was determined with Nanodrop 2000 (Thermo Fisher Scientific), and quality was assessed by running a 1% agarose gel electrophoresis, stained with 4S Red Plus Nucleic Acid Stain (Sango, Shanghai, China).

3T-seq library preparation

The libraries were prepared following the previous published method.¹¹ In general, after being extracted, ~50 µg of total RNA was incubated with Dynabeads™ M-280 streptavidin (Thermo Fisher Scientific) with biotin-modified reverse transcription GsuI-Oligo (dT)₂₀ primers. Catalyzed by Super Script III (Thermo Fisher Scientific), the first strand was synthesized, in which 5-methylated-dCTP had replaced dCTP to prevent GsuI from cutting the new synthetic chain. When the second strand of cDNA chain was synthesized, dNTP mixture contained dUTP instead of dTTP. Then, cDNA was randomly fragmented to ~200–400 bp with Fragmentase (NEB, Ipswich, MA, USA). After that 3'-terminal fragments were released from beads by GsuI (Fermentas, Waltham, MA, USA) digestion. Next, Illumina p5/p7 adaptors were ligated to the released cDNA. Before PCR amplification, the second strand of cDNA which had dUTP was digested by USER (NEB) to achieve chain specificity sequencing. Finally, a series of 3T-seq libraries were sequenced by Illumina Hiseq X Ten. Raw sequence data have been submitted to the EMBL-EBI ArrayExpress (accession number: E-MTAB-6403).

Data analysis

The data analysis process is similar to our previous study.¹¹ Briefly, raw reads were filtered with custom C++ scripts to obtain usable and valid reads. The selected reads were then mapped to the UCSC human reference genome (hg19) with bowtie2.¹² The PAS were identified through iteratively clustering the neighbor sites. The linear trend test was employed to identify the genes with significantly switched 3'-UTR.

Table 1 Pathology information of clinical samples

Number	Gender	Age	Location	Histopathological type	Size	Stage	Differentiation degree
1	Female	82	Right hemicolon	Adenocarcinoma	6×5×1.2	T4N2M0	Poorly differentiated
2	Female	56	Rectum	Adenocarcinoma	5×4×4.5	T4N2M0	Moderately to poorly differentiated
3	Female	73	Rectum	Adenocarcinoma	5×4.5×1.5	T4N1M0	Well differentiated

Table 2 Primer sequence of qRT-PCR

Name	Primer sequence
ACTB forward primer	5'-GGACTTCGAGCAAGAGATGG-3'
ACTB reverse primer	5'-AGCACTGTGTTGGCGTACAG-3'
GPI common forward primer	5'-GATCCTCCTGGCCAATTCT-3'
GPI common reverse primer	5'-GTTGGTTGGGCGATTTCCTT-3'
GPI distal forward primer	5'-CGGGTCTAGAGTGGAGCAAG-3'
GPI distal reverse primer	5'-TCTTGGGATTGTTGACACA-3'

Abbreviation: qRT-PCR, quantitative reverse transcription PCR.

The function annotation was performed with the online tool DAVID (<https://david.ncicrf.gov>).

Quantitative reverse transcription PCR validation

One microgram of total RNA was reverse transcribed by using PrimeScript™ RT reagent kit (TAKARA, Kyoto, Japan). RT primer mixture used in reverse transcription was a mixture of oligo dT and random hexamer primers. qRT-PCR was performed with PowerUp SYBR Green Master Mix (Thermo Fisher Scientific). Reactions were run in triplicate and normalized against *ACTB*. Primers design and data analysis were based on those in a previous study.¹³ Primer sequences are shown in Table 2.

Results

Identification of polyadenylation sites

After total RNA was extracted, we constructed libraries for sequencing by using the 3T-seq technology.¹¹ The 3'-terminal fragments were subjected to deep sequencing by Illumina Hiseq X Ten. Data from high-throughput sequencing were exhibited on Integrative Genomics Viewer (IGV) software (Figure 1). Totally, we generated ~107 million reads, of which ~52% are uniquely mappable (Table 3). Possible polyadenylation sites, whose downstream 20 nt bases included continuous 8 or 12 or more adenine ribonucleic acids, were identified as internal priming and filtered out.¹⁴ Approximately 43 million reads passed internal priming filter, and most of them were concentrated near the annotated transcription termination sites (TTSs) (Figure 2A). Identification method of PAS was based on that in a previous study;¹⁵ totally, we identified 34,982 PAS in patient 1, 34,187 PAS in patient 2 and 35,303 PAS in patient 3. We examined the presence of a hexamer motif such as AAUAAA within 20–30 nt upstream of the identified sites and reported that motifs could be found in this interval (Figure 2B). For example, among the 34,982 identified PAS in patient 1, 13.7% were mapped to UCSC TTS and 42.1%

to 3'-UTR regions (Figure 2C). Among expressed genes detected in this study, an average of 64.9% genes had three or more PAS in three patients (Figure 2D).

Variation analysis of APA between clinical samples

To facilitate comparison between samples, the cancer 3'-UTR length index (CULI) was adopted to quantitatively characterize the 3'-UTR alteration in CRC patients.¹⁵ A positive CULI means that a gene harbors lengthened 3'-UTR in cancer tissues compared with their corresponding normal tissues, and a negative CULI suggests the shortened one (Table S1). With this standard, the number of genes was identified with a significant difference in 3'-UTR length between cancer tissues and their corresponding normal tissues. In patient 1, the number was 350, and in patients 2 and 3, the numbers were 405 and 375, respectively (Figure 3A). In patient 1, 79.1% genes in cancer tissues had shortened 3'-UTR, while in other patients, the percentage became 88.1% (in patient 2) and 50.4% (in patient 3). To obtain the relationship between APA alteration and gene expression, we compared the APA change with mRNA abundance, and the result showed that there was no linear correlation on transcriptome scale (Figure 3B–D).

Functional enrichment of genes with switched APA sites

To understand the biological consequences of altered patterns in clinical CRC patients, genes with shortened 3'-UTR were analyzed by DAVID (<https://david.ncicrf.gov>). Analysis of 277 genes with 3'-UTR shortening in patient 1 yielded proliferation-related biological processes that were statistically overrepresented, including metabolic process, mRNA processing and RNA splicing (Figure 4A and Table S2). Similar results were also observed in other two patients (Figure 4B and C and Table S2).

Genes associated with cancer preferentially use proximal APA in cancer samples

Because shortened 3'-UTR increased the stability of the mRNA and meanwhile reduced cis elements that can interact with the transcription regulation of trans function factor (such as RNA binding protein) or miRNA interaction, these genes were more likely to escape gene silencing induced by miRNA, which then leads to higher expression level.⁵ Based on this, genes that had switched APA patterns between cancer tissues and their corresponding normal tissues in three

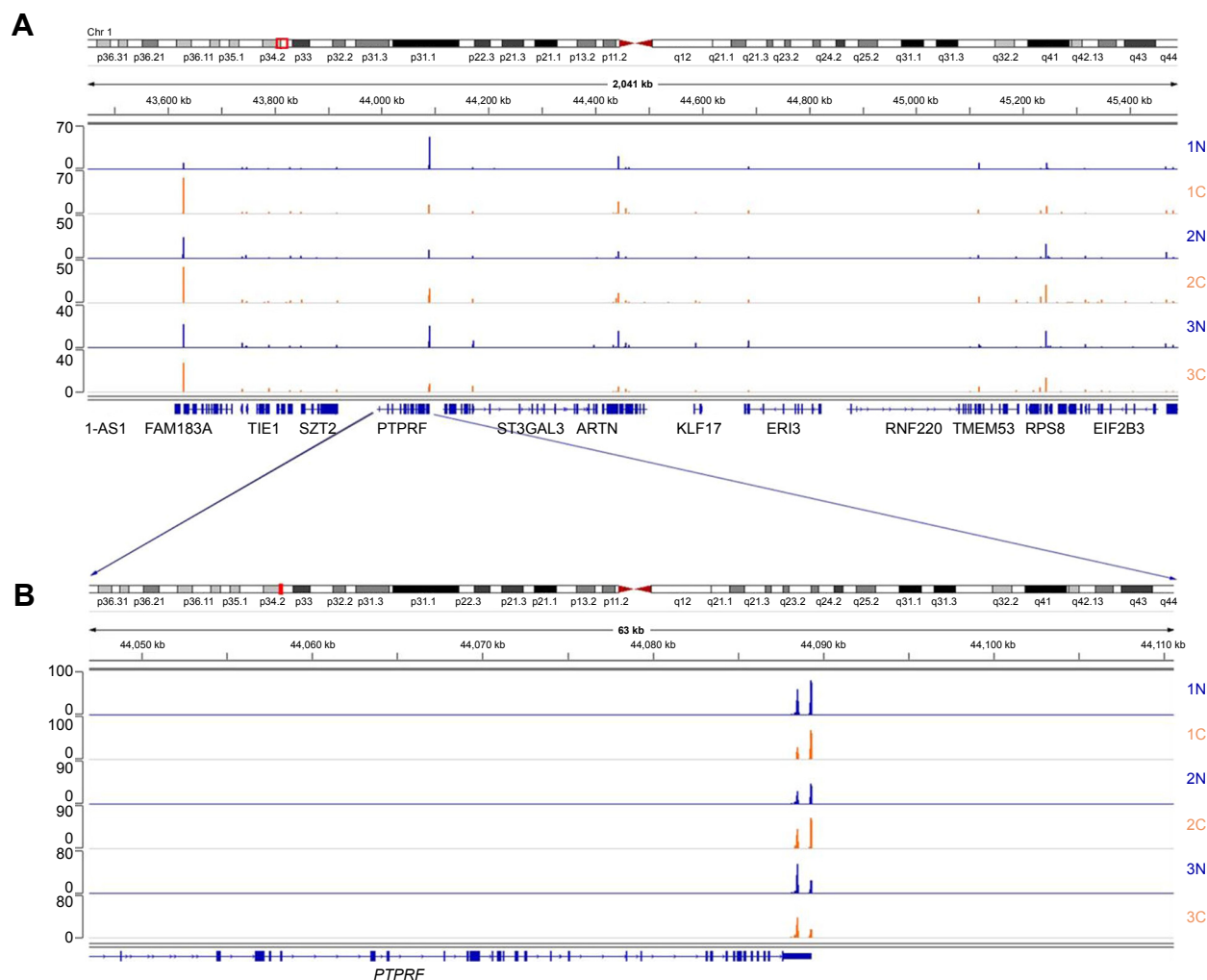


Figure 1 A genomic view of APA sites defined by 3T-seq in IGV genome browser.

Notes: (A) A genomic view of APA sites defined by 3T-seq on chromosome 1 in IGV genome browser. (B) *PTPRF* transcript isoforms with alternative poly(A) sites. (Blue track: normal tissues; orange track: cancer tissues.)

Abbreviations: APA, alternative polyadenylation; IGV, Integrative Genomics Viewer.

patients were further analyzed. Especially, some of them had a tendency to preferentially use proximal APA and higher expression level in cancer tissues.

There were 35 genes with shortened 3'-UTR present in all three patients. Gene ontology analysis showed that most of them are related to the metabolic process (Table S3). *GPI*, which was one of them, showed increased expression in cancer tissues in all three patients (Figure 5A). qRT-PCR was

used to prove the shortening of 3'-UTR. The design of primers was based on a previous research, common primers targeted the ORF, and distal primers were located just before the distal PAS (Figure 5B).¹³ The relative use of the distal PAS was calculated, and genes preferentially used proximal APA in cancer tissues when the value was negative. Taking *GPI* as an example, qRT-PCR results showed that it tended to use proximal PAS in the cancer tissues of three patients (Figure 5C).

Table 3 Summary statistics of sequencing data from Illumina Hiseq X Ten

	1C	1N	2C	2N	3C	3N
Total reads after trimming	15,187,751	16,284,726	7,806,383	19,701,651	32,642,442	15,390,604
Reads uniquely mapped to genome	8,571,073	9,116,362	4,233,853	9,744,901	15,792,660	8,201,900
Reads passed internal priming filter	6,782,560	7,097,533	3,233,879	7,668,647	12,019,614	6,083,447
Identified poly(A) sites (merged)		34,982		34,187		35,303
Genes hit by poly(A) sites (merged)		10,237		9,885		9,217

Notes: N means normal tissue; C means cancer tissue; number means the patient number.

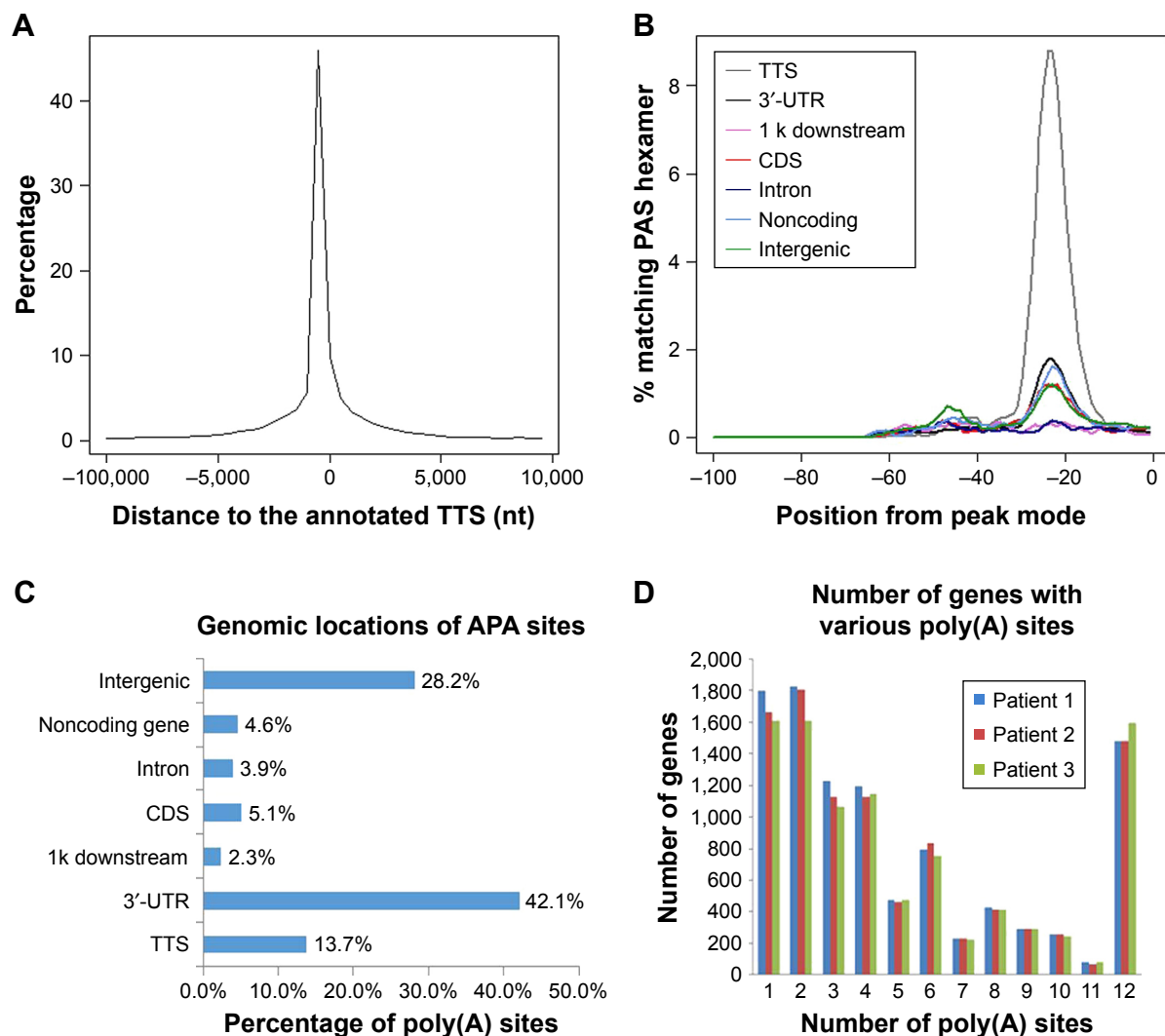


Figure 2 Characterizations and comparative analyses of APA sites in these clinical samples.

Notes: (A) Distribution of 3T-seq reads across the gene body in patient 1. (B) Position-specific distribution of PAS signal hexamer for PAS in patient 1. (C) Genomic locations of PAS in patient 1. (D) Statistics of genes with various numbers of detected PAS (12 means greater than or equal to 12 PAS).

Abbreviations: APA, alternative polyadenylation; CUL1, cancer 3'-UTR length index; PAS, poly(A) sites; TTS, transcription termination sites.

Discussion

With an increasing number of studies reported, APA events are involved in various biological processes.⁷ APA can affect mRNA stability, translation and localization. The shortening of the 3'-UTR can eliminate miRNA-binding sites, which can be found in longer 3'-UTR and usually result in the escape of miRNA-regulated programmed cell death.²² The APA events in the whole genome, which may have a major impact on mechanisms of tumorigenesis and antitumor, can be investigated by means of genome-wide analyses. Through comparison of cancer tissue samples and their corresponding normal tissue samples, APA events in cancer tissue samples were found to have significant differences with APA patterns of normal tissue samples. There were 350 genes that have changed 3'-UTR in a cancer tissue sample of patient 1, and 79.1% of them had

shortened 3'-UTR. The number of genes in the other two patients was 405 and 375, respectively, and 3'-UTR shortened genes accounted for 88.1% and 50.4%, respectively (Figure 2B). It was interesting to note that the proportion of genes with shortened 3'-UTR seemed to be consistent with the disease stage. However, cases were too few to draw from this conclusion.

3'-UTR shortening could increase gene expression level by eliminating miRNA-binding sites.²² However, in our data, genes with shortened 3'-UTR did not always have higher expression level. In patient 1, 180 of 277 genes had shortened 3'-UTR and higher level of expression in the cancer tissue. In patient 2, the number became 168 of 357, and it became 83 of 189 in patient 3. This suggested that the length and expression of 3'-UTR were not simply negatively correlated. In addition, similar phenomenon has

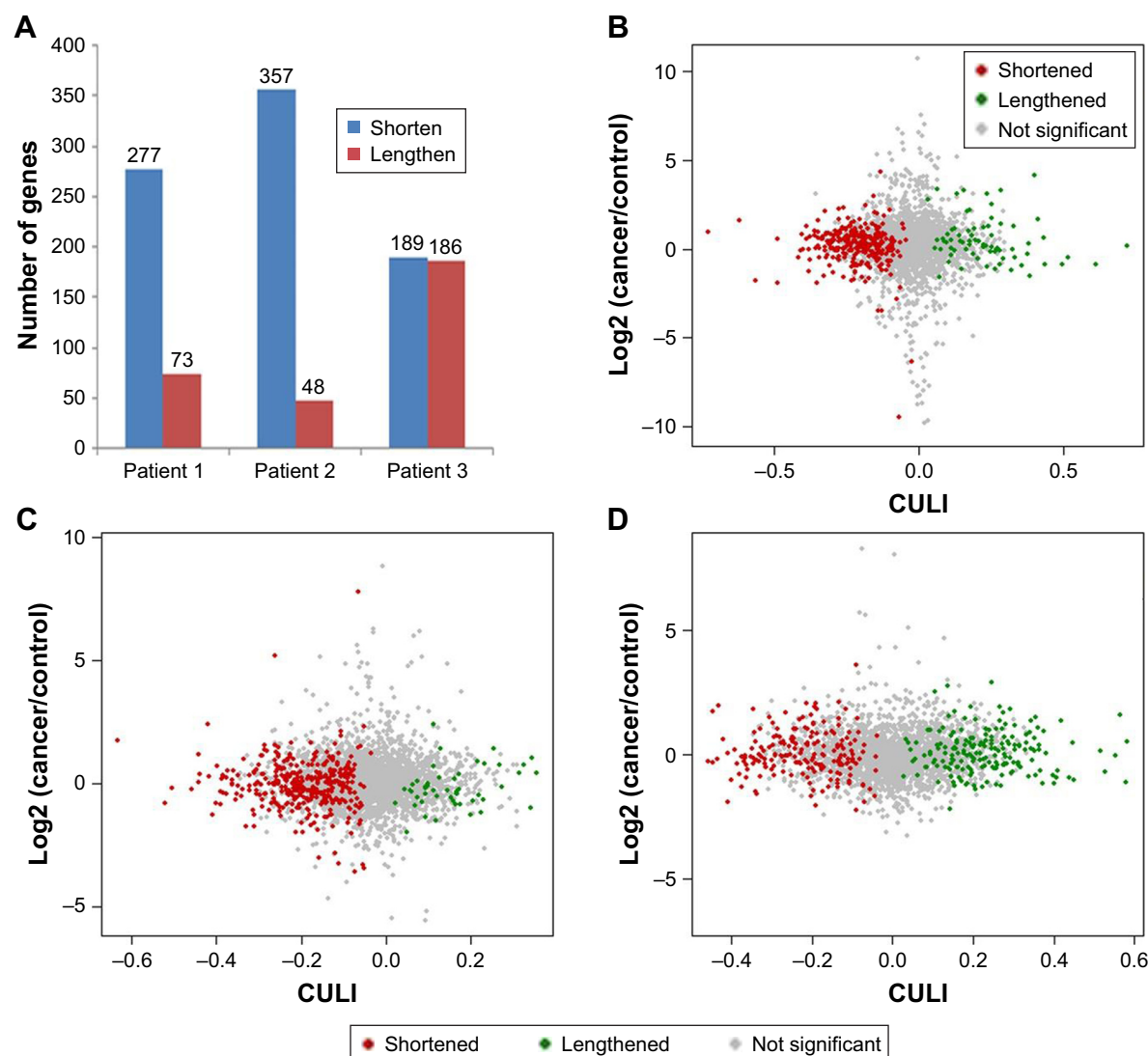


Figure 3 APA-mediated 3'-UTR alteration and the transcriptional activity of the affected genes in CRC patients compared with normal counterparts.

Notes: (A) Statistics on the number of genes with switched 3'-UTR in three patients. (B–D) Scatter diagrams of genes with differential APA defined by CULI, which was used for the quantitative measurement of 3'-UTR alteration in cancer tissues compared with matched normal tissues (FDR < 0.05). (B) Patient 1; (C) patient 2; (D) patient 3.

Abbreviations: APA, alternative polyadenylation; CRC, colorectal cancer; CULI, cancer 3'-UTR length index; FDR, false discovery rate; UTR, untranslated region.

been found in a previous study.¹⁵ The mechanism of the reduction of 3'-UTR to the expression level has not been fully understood.

Cancer tissues in three patients all preferentially used proximal APA of *GPI*. GPI, alternatively known as PGI or PHI, has been identified as the autocrine motility factor (AMF), which can regulate tumor cell growth and stimulate metastasis.^{16–18} Overexpression of AMF has been shown to induce epithelial-to-mesenchymal transition (EMT) in some cancers.^{19,20} Elevated serum GPI levels have been used as a prognostic biomarker for various cancers, including CRC.²¹ Nevertheless, 3'-UTR-shortened genes only partially overlapped in three patients. This may be due to the heterogeneity of individuals. When the number of samples increases,

the heterogeneity may be more obvious. In recent studies, Morris et al¹⁰ also found a series of genes with changed PAS in CRC, some of which were overlapped with our results. However, 3T-seq was more focused on 3'-UTR PAS, and relative to 3'seq when paired-end sequencing was used; this method largely avoided sequencing desynchronization. More importantly, the normal control that Morris et al¹⁰ used in high-throughput sequencing was not sufficiently rigorous.

Conclusion

Briefly, in this study we used a robust approach, 3T-seq, to profile global APA sites in three patients and observed that hundreds of genes exhibit shortened 3'-UTR, and some

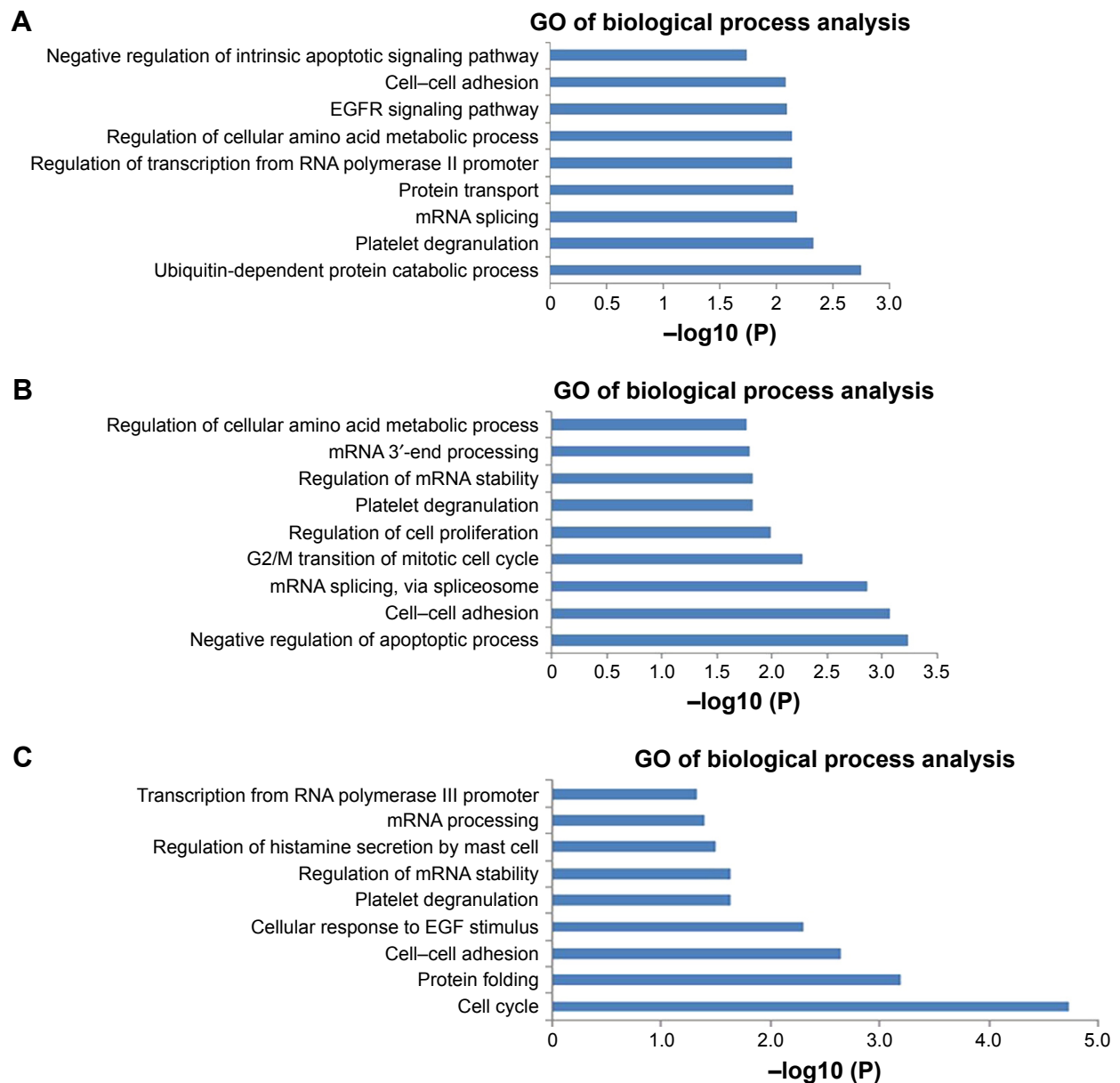


Figure 4 GO analysis using DAVID of genes with shortened 3'-UTR in three patients.

Notes: (A) Patient 1; (B) patient 2; (C) patient 3.

Abbreviations: GO, gene ontology; UTR, untranslated region.



Figure 5 (Continued)

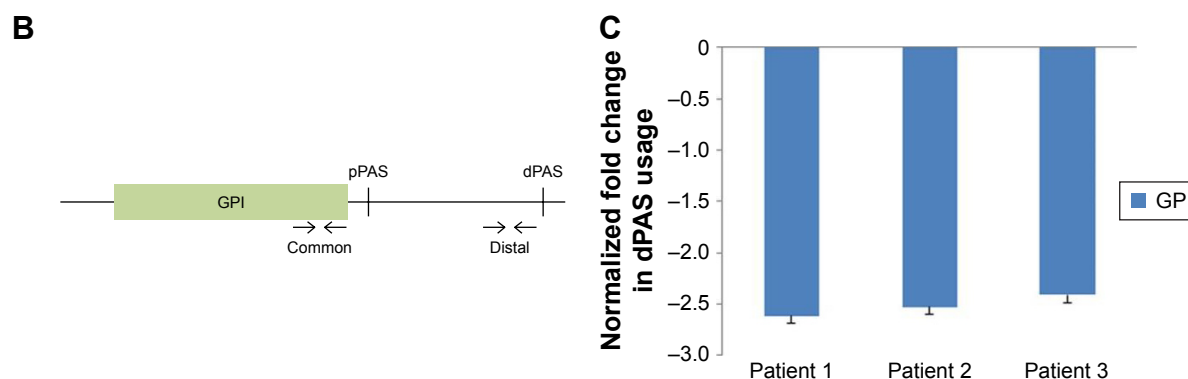


Figure 5 GPI preferentially use proximal APA in cancer samples.

Notes: (A) A genomic view of GPI transcript isoforms with alternative poly(A) sites in CRC tissues (orange) and normal counterparts (blue). (B) The schematic diagram represented the relative location of the common and distal primer annealing sites in a test gene and the approximate locations of the labeled proximal and distal PAS, depicted as pPAS and dPAS, respectively. (C) Shortened 3'-UTR of GPI mRNA was verified by qRT-PCR.

Abbreviations: APA, alternative polyadenylation; CRC, colorectal cancer; GPI, glucose-6-phosphate isomerase; PAS, poly(A) sites; UTR, untranslated region.

of them have been reported to play a key role in cancer. Comparative results provide some clues for more in-depth study of the cell regulation mechanism of CRC from post-transcriptional regulation.

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Disclosure

The authors report no conflicts of interest in this work.

References

- Derti A, Garrett-Engle P, Macisaac KD, et al. A quantitative atlas of polyadenylation in five mammals. *Genome Res.* 2012;22(6):1173–1183.
- Lin Y, Li Z, Ozsolak F, et al. An in-depth map of polyadenylation sites in cancer. *Nucleic Acids Res.* 2012;40(17):8460–8471.
- Shepard PJ, Choi EA, Lu J, Flanagan LA, Hertel KJ, Shi Y. Complex and dynamic landscape of RNA polyadenylation revealed by PAS-Seq. *RNA.* 2011;17(4):761–772.
- Rehfeld A, Plass M, Krogh A, Friis-Hansen L. Alterations in polyadenylation and its implications for endocrine disease. *Front Endocrinol.* 2013;4:53.
- Sandberg R, Neilson JR, Samra A, Sharp PA, Burge CB. Proliferating cells express mRNAs with shortened 3' untranslated regions and fewer microRNA target sites. *Science (New York, N. Y.).* 2008;320(5883):1643–1647.
- Ji Z, Lee JY, Pan Z, Jiang B, Tian B. Progressive lengthening of 3' untranslated regions of mRNAs by alternative polyadenylation during mouse embryonic development. *Proc Natl Acad Sci U S A.* 2009;106(17):7028–7033.
- Elkon R, Ugalde AP, Agami R. Alternative cleavage and polyadenylation: extent, regulation and function. *Nat Rev Genet.* 2013;14(7):496–506.
- Masamha CP, Wagner EJ. The contribution of alternative polyadenylation to the cancer phenotype. *Carcinogenesis.* 2017;39(1):2–10.
- Chen W, Zheng R, Baade PD, et al. Cancer statistics in China, 2015. *CA: a cancer journal for clinicians.* Mar. 2016;66(2):115–132.
- Morris AR, Bos A, Diosdado B, et al. Alternative cleavage and polyadenylation during colorectal cancer development. *Clin Cancer Res.* 2012;18(19):5256–5266.
- Lai DP, Tan S, Kang YN, et al. Genome-wide profiling of polyadenylation sites reveals a link between selective polyadenylation and cancer metastasis. *Hum Mol Genet.* 2015;24(12):3410–3417.
- Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol.* 2009;10(3):R25.
- Masamha CP, Xia Z, Yang J, et al. CFIm25 links alternative polyadenylation to glioblastoma tumour suppression. *Nature.* 2014;510(7505):412–416.
- Beaudoing E, Freier S, Wyatt JR, Claverie JM, Gautheret D. Patterns of variant polyadenylation signal usage in human genes. *Genome Res.* 2000;10(7):1001–1010.
- Fu Y, Sun Y, Li Y, et al. Differential genome-wide profiling of tandem 3' UTRs among human breast cancer and normal cells by high-throughput sequencing. *Genome Res.* 2011;21(5):741–747.
- Stoker M, Gherardi E, Perryman M, Gray J. Scatter factor is a fibroblast-derived modulator of epithelial cell mobility. *Nature.* 1987;327(6119):239–242.
- Watanabe H, Takehana K, Date M, Shinozaki T, Raz A. Tumor cell autocrine motility factor is the neuroleukin/phosphohexose isomerase polypeptide. *Cancer Res.* 1996;56(13):2960–2963.
- Silletti S, Raz A. Autocrine motility factor is a growth factor. *Biochem Biophys Res Commun.* 1993;194(1):446–457.
- Tsutsumi S, Hogan V, Nabi IR, Raz A. Overexpression of the autocrine motility factor/phosphoglucose isomerase induces transformation and survival of NIH-3T3 fibroblasts. *Cancer Res.* 2003;63(1):242–249.
- Li Y, Che Q, Bian Y, et al. Autocrine motility factor promotes epithelial-mesenchymal transition in endometrial cancer via MAPK signaling pathway. *Int J Oncol.* 2015;47(3):1017–1024.
- Baumann M, Brand K, Matthias Baumann KB. Purification and characterization of phosphohexose isomerase from human gastrointestinal carcinoma and its potential relationship to neuroleukin. *Cancer Res.* 1988;48(24 Pt 1):7018–7021.
- Mayr C, Bartel DP. Widespread shortening of 3'UTRs by alternative cleavage and polyadenylation activates oncogenes in cancer cells. *Cell.* 2009;138(4):673–684.

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