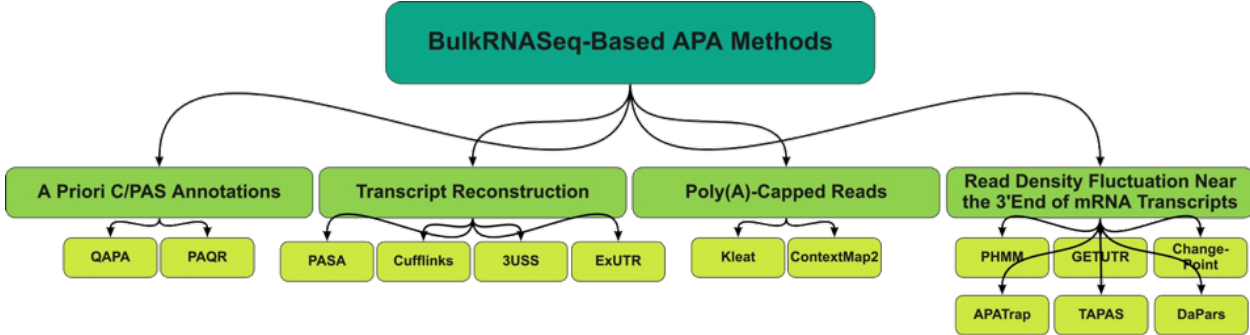
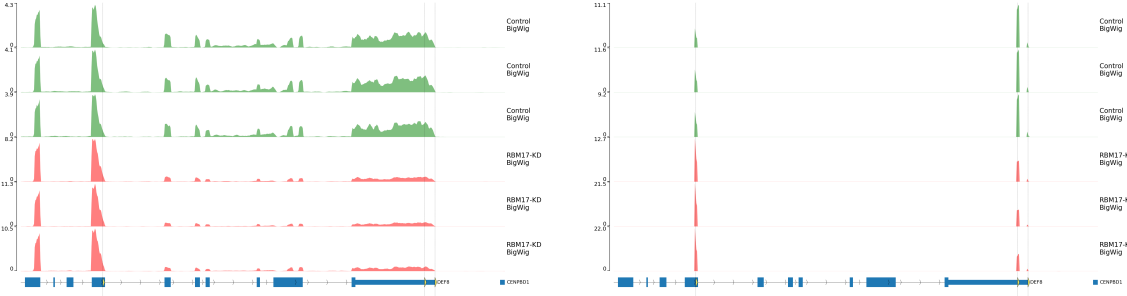


SUPPLEMENTARY FIGURE S1



**SUPPLEMENTARY FIGURE S2**

**DEF8 = Representative Differential APA Gene (DAG)**



**Bulk RNA-Seq Read Density Visualization**

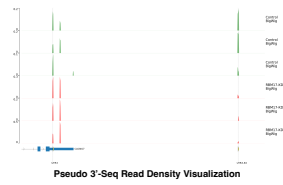
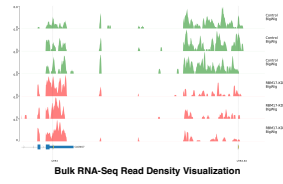
**Pseudo 3'-Seq Read Density Visualization**

	CR_1	CR_2	CR_3	KD_1	KD_2	KD_3
C/PAS_1	0.23	0.26	0.27	0.55	0.61	0.62
C/PAS_2	0.64	0.64	0.62	0.37	0.33	0.31
C/PAS_3	0.12	0.1	0.11	0.079	0.055	0.066

**Read Density Heatmap**

# SUPPLEMENTARY FIGURE S3

**A** CACNG7 = DAG that is identified by PolyAMiner-Bulk but not APAnalyzer or DaPars



	CR_1	CR_2	CR_3	KD_1	KD_2	KD_3
CPAS_1	0.22	0.12	0.26	0.77	0.46	0.46
CPAS_2	0.70	0.88	0.74	0.23	0.54	0.52

Read Density Heatmap

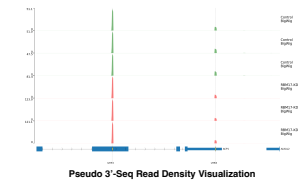
**B** ANK1 = DAG that is identified by APAnalyzer but not PolyAMiner-Bulk



	CR_1	CR_2	CR_3	KD_1	KD_2	KD_3
CPAS_1	0.26	0.25	0.23	0.18	0.24	0.23
CPAS_2	0.31	0.27	0.45	0.42	0.42	0.38
CPAS_3	0.38	0.4	0.29	0.35	0.3	0.34
CPAS_4	0.055	0.07	0.028	0.056	0.043	0.052

Read Density Heatmap

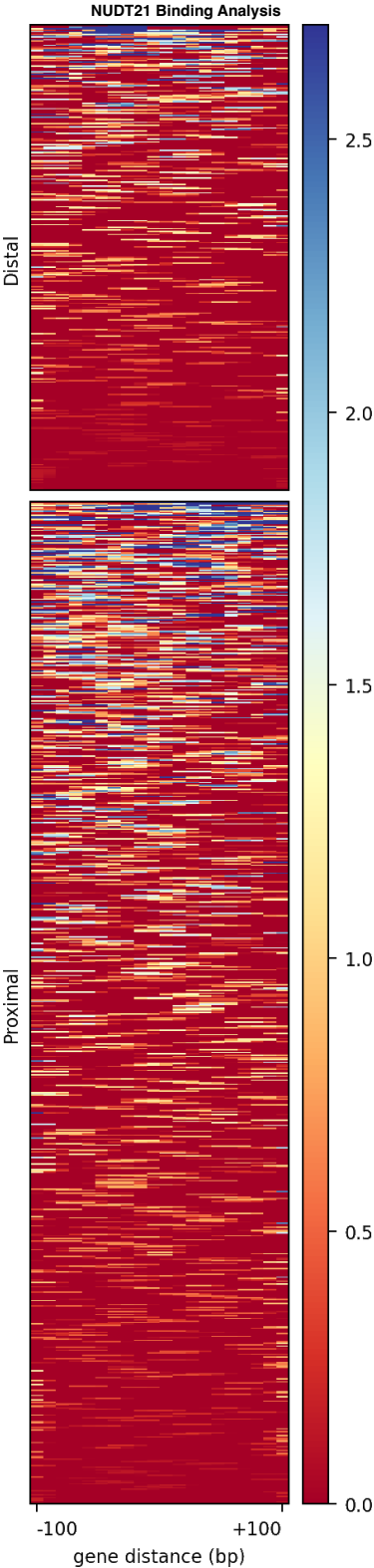
**C** ACP1 = DAG that is identified by DaPars but not PolyAMiner-Bulk



	CR_1	CR_2	CR_3	KD_1	KD_2	KD_3
CPAS_1	0.85	0.83	0.82	0.86	0.88	0.87
CPAS_2	0.15	0.17	0.18	0.14	0.12	0.13

Read Density Heatmap

SUPPLEMENTARY FIGURE S4



## Supplementary Table S1

Feature	PolyAMiner-Bulk	APalyzer	APAtrap	DaPars	QAPA	Roar	TAPAS
<i>De novo</i> C/PAS identification	YES	NO	YES	YES	NO	NO	YES
Reference Database	PolyASite & PolyA_DB	PolyA_DB only	N/A	N/A	PolyASite/GENCODE	PolyA_DB & APASdb	N/A
Deep Learning Model	YES	NO	NO	NO	NO	NO	NO
Intral-distal and intra-proximal APA quantification	YES	NO	NO	NO	NO	NO	NO
3'UTR APA	YES	YES	YES	YES	YES	YES	YES
IPA	YES	YES	NO	NO	NO	NO	NO
Visualization (Volcano Plot)	YES	YES	NO	NO	NO	NO	NO
Visualization (IGV Read Density)	YES	NO	NO	NO	NO	NO	NO
Visualization (Heatmap)	YES	NO	NO	NO	NO	NO	NO
Reference	This study	(Wang, et al., 2020)	(Ye, et al., 2018)	(Xia, et al., 2014)	(Ha, et al., 2018)	(Grassi, et al., 2016)	(Arefeen, et al., 2018)

### Program download site:

PolyAMiner-Bulk: <https://github.com/venkatajonnakuti/PolyAMiner-Bulk>

APalyzer: <https://bioconductor.org/packages/release/bioc/html/APalyzer.html>

APAtrap: <https://sourceforge.net/projects/apatrap/>

DaPars: <https://github.com/ZhengXia/dapars>

QAPA: <https://github.com/morrislab/qapa>

ROAR: <https://bioconductor.org/packages/release/bioc/html/roar.html>

TAPAS: <https://github.com/arefeen/TAPAS>

### References:

Wang, R., et al. APalyzer: a bioinformatics package for analysis of alternative poladenylation isoforms. *Bioinformatics* 2020; 36(12):3907-3309

Arefeen, A., et al. TAPAS: tool for alternative polyadenylation site analysis. *Bioinformatics* 2018;34(15):2521-2529.

Grassi, E., et al. Roar: detecting alternative polyadenylation with standard mRNA sequencing libraries. *BMC bioinformatics* 2016;17(1):423.

Ha, K.C., Blencowe, B.J. and Morris, Q. QAPA: a new method for the systematic analysis of alternative polyadenylation from RNA-seq data. *Genome biology* 2018;19(1):45.

Xia, Z., et al. Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3'-UTR landscape across seven tumour types. *Nature communications* 2014;5(1):1-13.

Ye, C., et al. APAtrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. *Bioinformatics* 2018;34(11):1841-1849.