A protocol for epitranscriptome analysis from m6A-seq data

		MarkDown		Yes	Yes	Yes	Yes	Yes	Yes
Software	**Function**		M0. Checking Existing Databases	M1. Data Preprocessing	M2. Differential Expression	M3. Site Detection - Host	M4. Site Detection - Virus	M5. Differential Methylation	M6. Reference based analysis
m6A-Atlas	m6A database		R			O		O	
RMDisease	SNP disease database		R			O		O	
Whistle Server	Site prediction	Less Reliable	O			O		O	
SRA toolkit	Obtaining GEO data			O					
FASTQC	Quality evaluation			O					
Trim Galore	Reads trimming			O					
Hisat2	Reads alignment			R					
Ballgown	Differential expression				R				
exomePeak2	m6A-seq data analysis					R	R	R	R
Homer	Motif finding	Strand Specific				R		N	
MetaTX	Distribution of m6A sites	Isoform ambiguity				R		O	
IGV	Visualization of reads					R	R	N	
DAVID	GO enrichment analysis	hyper/hypo vs both				N		R	
RNAmod	Annotation web server					O		O	
		Key Points			Input control samples of m6A-seq data	Strand-specificity GC correction	Strand-specificity GC correction M level problem	GC correction Absolute vs relative DM	Differential analysis M level quantification (reasonable)

Note
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Abbreviation: Required (R), Optional (O) and Not Recommended (N)
Expectation: a GitHub MarkDown file with the source codes for all the analysis & a research paper of top quality
Additional information: Jingxian Zhou will help check everything by reproducing the results with your source codes.
MarkDown example: https://github.com/scottzijiezhang/m6A-seq_analysis_workflow
Paper example: https://www.sciencedirect.com/science/article/abs/pii/S1046202314002308