EPIPLEX RNA REAGENT KIT

Sample#	Reagents for 8 samples (includes 8 enrichment and 8 solution reactions)
Price	$2,800; early access discount available
RNA modifications	m6A, inosine
Binding reagents	engineered small protein scaffolds
RNA species	poly-A(+) RNA, total RNA (rRNA depletion at cDNA step recommended)
RNA amount	>= 20 ng polyA+ RNA >= 250 ng total RNA
Library type	stranded RNA library
Quantification	fold-enrichment relative to spike-in controls
Sample definition	an enrichment reaction with a paired solution reaction
Sequencing depth	>= 20 - 50M reads per sample*, 200 cycles
Analysis	Alida Bio's analysis pipeline
Supported genomes	human, mouse – others per request
Turnaround time	Library prep using reagent kit: 7 hours

* Sequencing depth depends on sensitivity expectation. Prominent modification sites are accessible at lower coverage.

DATA ANALYSIS OUTPUT

PEAK LOCATIONS	**BED FILES**
Transcript regions ("peaks") with RNA modifications for visualization in any genome viewer.	
COVERAGE TRACKS	**BIGWIG FILES**
Read coverage corrected for the non-enriched input coverage and normalized to spike-in controls for visualization in any genome viewer. One file per RNA modification.	
GENOME ALIGNMENT	**BAM FILES**
Aligned and deduplicated reads for visualization in any genome viewer. One file per RNA modification.	
RAW SEQUENCING DATA	**FASTQ**
Unprocessed sequencing reads, demultiplexed per sample for publication and data storage.	
SUMMARY OUTPUTS	**HTML, TSV, CSV, PNG**
RNA-seq TPM values *Peaks table with peak location, annotated gene features, #reads per peak, fold-enrichment, q-values, and more* *Fold-enrichment correlation plots of user-defined conditions* *Modification distribution along the transcript* *DRACH motif enrichment (m6A) and A-to-G (inosine) mutations under peaks*	

Contact us
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