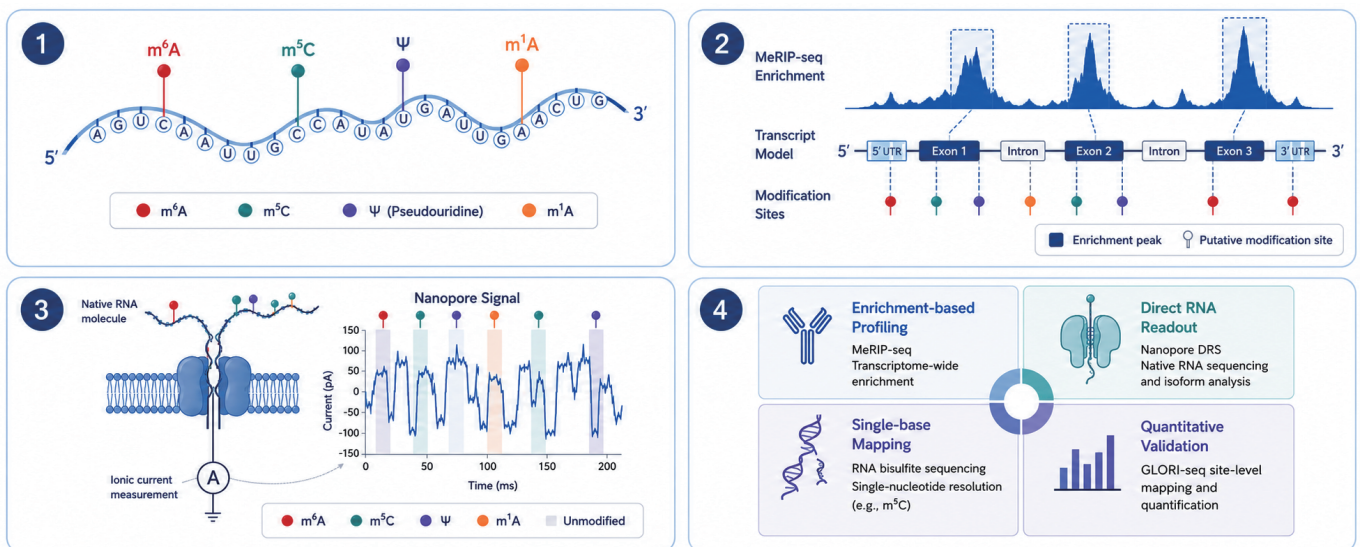


CD Genomics supports RNA methylation and modification studies through enrichment-based, direct RNA, single-base, and quantitative workflows tailored to diverse epitranscriptomics research goals.

Service Advantages

- Multi-technology RNA modification support covering enrichment-based, direct RNA, chemical mapping, and quantitative workflows
- Flexible strategy selection for transcriptome-wide profiling, isoform-aware interpretation, single-base analysis, or global quantification
- Coverage of diverse RNA modification needs, including m⁶A, m⁵C, m¹A, m⁷G, and pseudouridine (Ψ) modification studies
- Integrated bioinformatics support for peak calling, differential modification analysis, enrichment, and visualization
- Research-focused deliverables supporting project planning, data interpretation, and follow-up validation

Representative RNA Modification Analysis



From Question to Workflow

- Start with transcriptome-wide, isoform-level, site-specific, or quantitative goals
- Align RNA modification targets with suitable sequencing or validation strategies
- Adapt workflows to sample type, RNA quality, and downstream analysis needs
- Support study planning from exploratory profiling to candidate site follow-up

Application Flexibility

- Profiling RNA modification landscapes across mRNA, lncRNA, and other RNA species
- Comparing condition-specific modification patterns and transcriptome-wide changes
- Supporting isoform-aware interpretation through direct RNA sequencing
- Enabling both site-level investigation and global quantification depending on project goals

Bioinformatics Deliverables

- Peak calling and differential modification analysis
- Functional interpretation and pathway-level insights
- Standardized bioinformatics outputs for downstream epitranscriptomics research
- Visualization-ready results for project discussion, reporting, and follow-up studies

Technology Portfolio

Method	Best Fit	Key Strength
MeRIP-seq	m ⁶ A enrichment profiling	Established transcriptome-wide workflow
Nanopore DRS	Native RNA analysis	Isoform-aware direct readout
RNA-BS-seq	m ⁵ C site mapping	Single-base resolution for RNA m ⁵ C
GLORI-seq	Site-specific m ⁶ A studies	Single-base stoichiometry
LC-MS/MS	Global m ⁶ A quantification	Quantitative validation