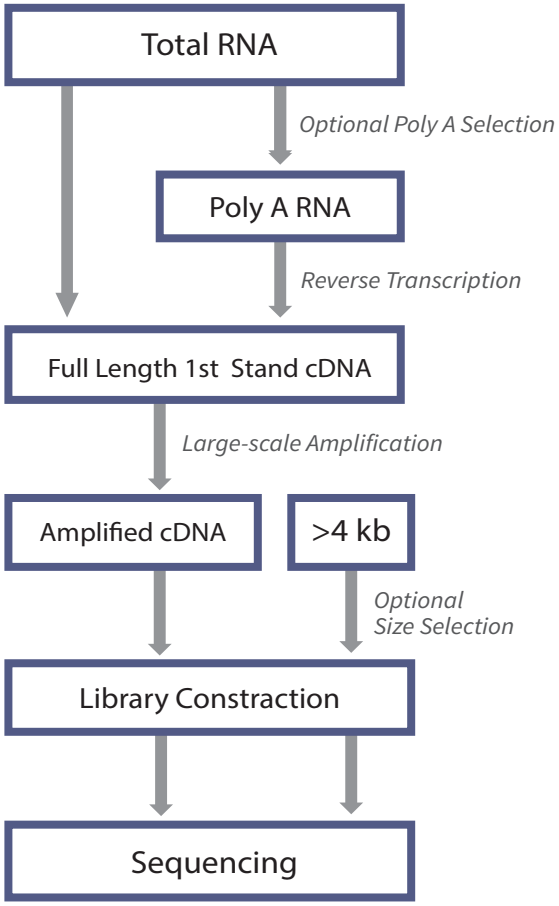
Full-Length Transcriptome Sequencing

The complete transcript consists of the sequence from the 5' end to the 3' end of the poly(A) tail, with a concentrated length of 1-6 kb. CD Genomics full-length transcriptome sequencing service (PacBio SMRT and Nanopore Sequencing) overcomes the problem of assembly and incomplete information, and obtains higher quality transcripts, which is beneficial for RNA structural studies, such as alternative splicing, fusion genes, allelic expression, *etc*. It can also obtain more comprehensive annotation information with the help of next-generation sequencing data.

Advantages

- Obtain more uniform coverage of the genome
- Direct access to full-length transcript sequences
- Gene expression quantification
- Discover more splice sites and alternative splicing
- Discover new functional genes that complement genome annotation
- Analyze fusion genes, homologous genes, superfamily genes or alleles



Applications

Basic Research

- Suitable for large reference genome-free species and reference genome imperfect reference species
- Complete genomic/transcriptomic information: complex gene structure, transcript structure and functional analysis

Agriculture

- Differential/dynamic transcriptomes: stress treatment or transcriptomic changes at different timescales, mechanisms of plant and animal domestication
- Comparative transcriptome: affinity between closely related species, mRNA sequence differences

Medicine

- Complex Disease Research: the pathogenesis of cancer with fusion genes
- Complex transcriptome study: complex alternative splicing in disease or cancer
- Quantitative transcriptome: gene/transcript level quantification, mining condition-specific genes/transcripts

CD Genomics aims at providing the research community with Illumina, PacBio SMRT and Nanopore platforms, and bioinformatics services. How to choose a suitable approach? Use the table below to learn the differences between PacBio SMRT and Nanopore platforms.

	PacBio SMRT	Nanopore
Principle of sequencing	Sequencing by synthesis/DNA polymerase	Electronic signals sequencing/exonuclease
Read length	10-15 kb, up to 20 kb	10-100 kb, up to 4 Mb
Read accuracy (%)	88–90/99.9 (CCS)	96–99
Bases per sample	20-30 Gb	6 Gb
Runtime (h)	10–30	72
Advantages	Long average read length; No amplification of sequencing Fragments; More accurate in isoform discovery	Ultra-long read; Electronic sequencing; Portable; No amplification of sequencing fragments; Powerful in expression level quantification