

# Long-Read Insight. Short-Read Accuracy. Lower Cost.

## Full-Length Transcriptome Analysis

Powered by Proprietary cDNA library and CoolIMPS™ Technology

Short-read sequencing offers high throughput and low cost but limited resolution of complex transcript isoforms. Long-read sequencing improves resolution, often at higher cost and lower throughput.

The DNBSEQ Complete Transcriptome Set (CTx) reconstructs 1–8 kb full-length transcripts using a proprietary co-barcoding workflow and accurate 600 bp reads from CoolIMPS™ 600. With the DNBSEQ Complete Transcriptome Analysis Pipeline, a single flow cell can generate approximately 50–60 million full-length transcripts at 10× read coverage, enabling cost-effective transcriptome analysis without a dedicated long-read platform.



### Flexible

Independent flowcell based operation and WGS scale output



### Accurate

Enhance breakthroughs with Q40 accuracy and novel read lengths



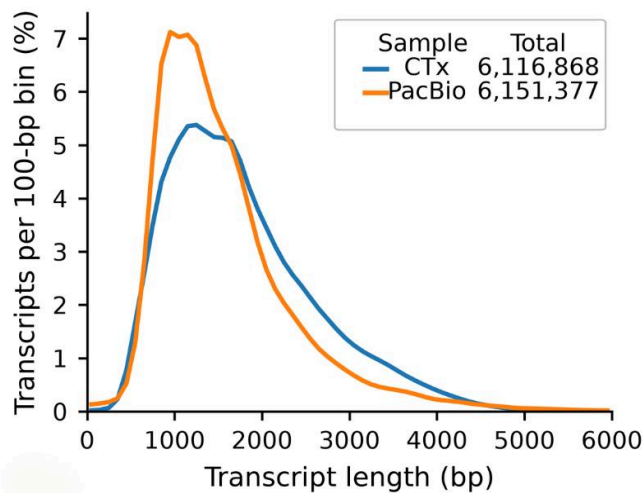
### Versatile

Comprehensive genomics with novel WGS and full transcriptomics

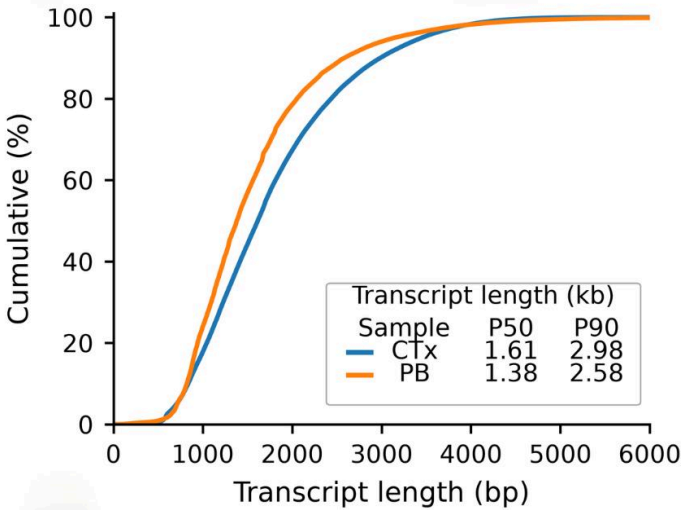
## Accurate Full-Length Transcript Reconstruction

CTx and PacBio showed similar transcript-length distributions (A) and cumulative profiles (B), with CTx modestly shifted toward longer transcripts (median: 1.61 kb vs. 1.38 kb). Approximately 6 million de novo assembled CTx transcripts from Universal Human Reference RNA, generated using CoolIMPS™ SE600 reads, were compared with approximately 6 million publicly available PacBio Revio/Kinnex full-length non-concatemer reads, analyzed directly using the same SQANTI3 workflow (Pardo-Palacios et al., 2024).

(A)



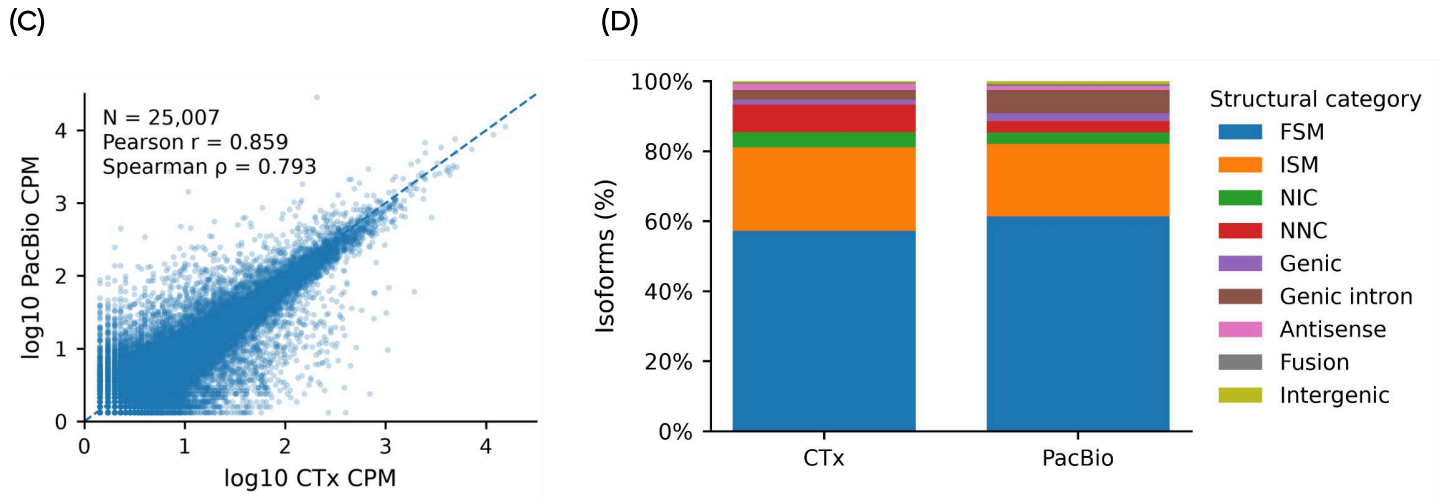
(B)



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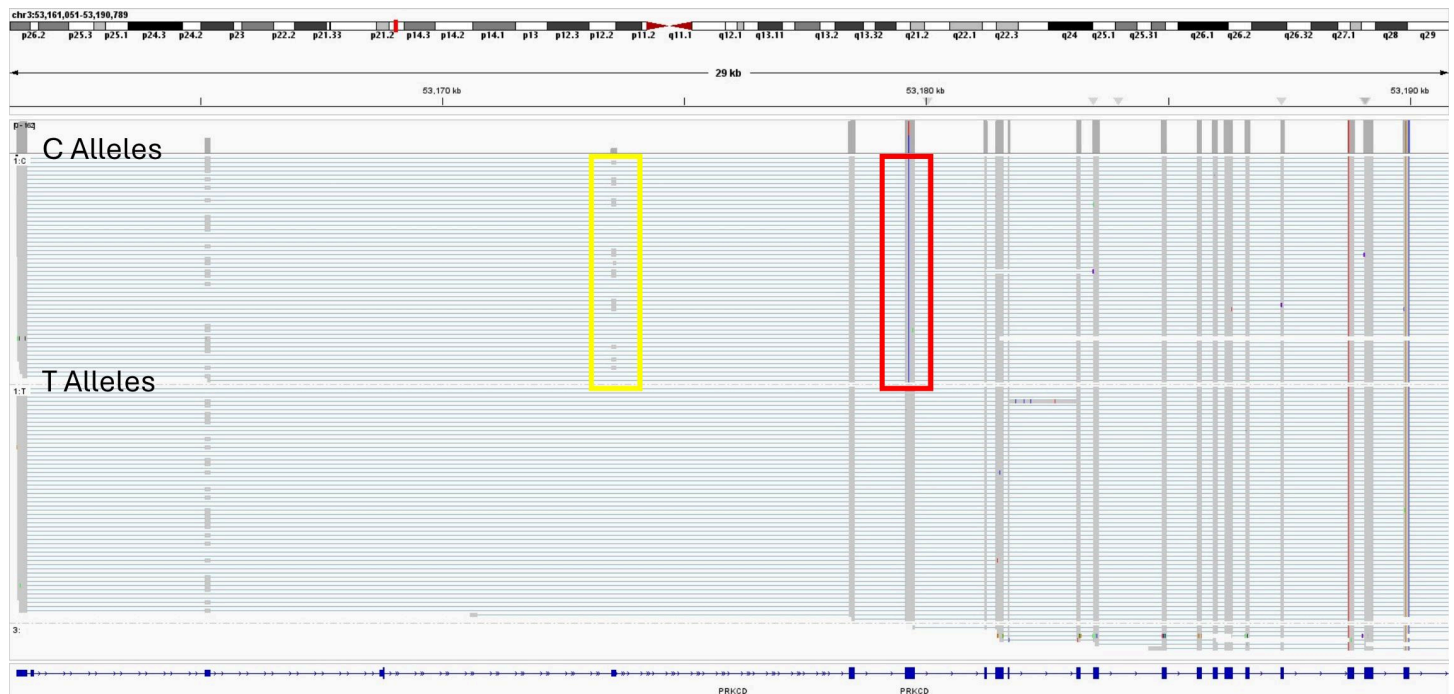
## Consistent Transcript Quantification and Splice Structure

Transcript abundance correlated between CTx and PacBio across 25,007 transcripts (C; Spearman's  $\rho = 0.793$ ), supporting quantitative profiling with CTx. Structural-category profiles were also similar (D), with approximately 60% of transcripts in both datasets classified as full-splice matches (FSM), whose splice junctions correspond to an annotated transcript isoform.



## Resolving Allele-Specific Alternative Splicing

CTx distinguishes allele-specific splicing patterns by linking sequence variants to transcript isoforms. The C allele of SNP rs2230493 (red box) is found in approximately 10% of individuals. In HG002 (GM24385), an alternatively spliced exon (yellow box) was observed in transcripts carrying the C allele, but not in those carrying the T allele.



To learn more, visit [completegenomics.com](https://completegenomics.com)

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