ResolveSEQ LongRead
Early Access Program

BioSkryb GENOMICS

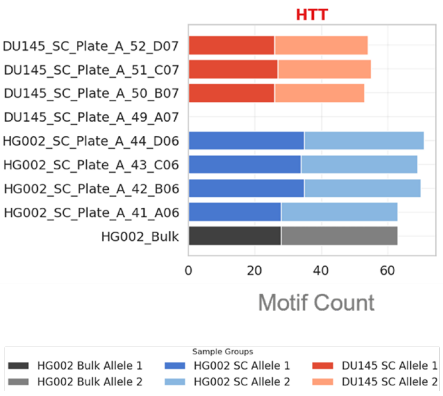
The benefits of long-read sequencing, now available at single-cell resolution

PTA Tuned for Long-Read Sequencing	
Characteristic	**Observed Value**
Fragment Length (N 50)	3.9–4.4 kb
Genome Coverage	83% (75–92%)
F-score	83%
Sensitivity (Recall)	70–80%
Precision (PPV)	95% (91–99%)
Duplicate Frequency	4–7%
Chimera Frequency	7–8%

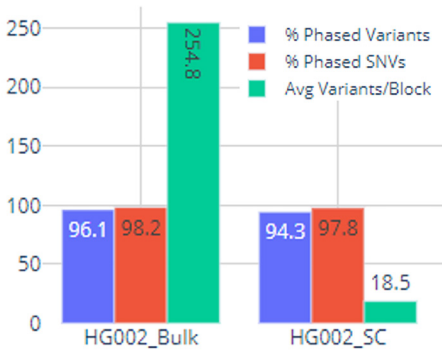
Introducing ResolveSEQ LongRead, an early access service offering from BioSkryb Genomics

ResolveServices℠ is proud to announce early access to ResolveSEQ LongRead, which leverages our tuned whole genome amplification chemistry, primary template-directed amplification (PTA), to generate longer fragments suitable for long read sequencing. These longer fragments, coupled with long read whole genome sequencing, enable researchers to study repeat expansions, phase single nucleotide variants (SNV) or gene edits, and characterize structural variants (SV) within individual cells.

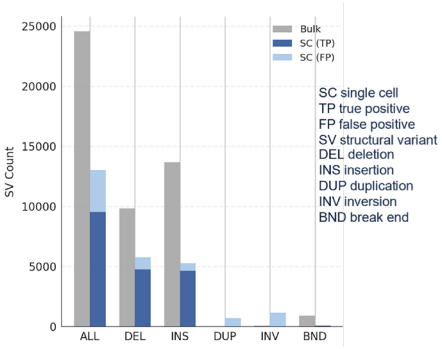
Assess Repeat Expansions



Phase SNV



Define SV



Contact us at info@bioskryb.com if you would like additional information about the ResolveSEQ LongRead Early Access Program

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