



Guide to high-molecular-weight DNA extraction and long-read sequencing

Looking for the right high-molecular-weight genomic DNA kit for long-read sequencing?

Long-read sequencing using PacBio® and Oxford Nanopore Technologies® generate extensive reads for complex genomic studies but it is sensitive to DNA quality and integrity, requiring high-quality, contaminant-free genomic DNA (gDNA). Sample preparation challenges include avoiding DNA contamination, degradation, or shearing to ensure accurate sequencing results. To address these, we offer sample preparation kits for high-molecular-weight (HMW) gDNA samples designed to reduce costs and processing times while maintaining DNA quality and integrity.

Follow these 3 steps to find the right kit for you:

1

What's the length of the genomic DNA?


KB

Typical gDNA Size


~100 kb

50–100 kb


10–20 kb




Soil




Stool




Bacteria



Yeast



Cells




Tissue

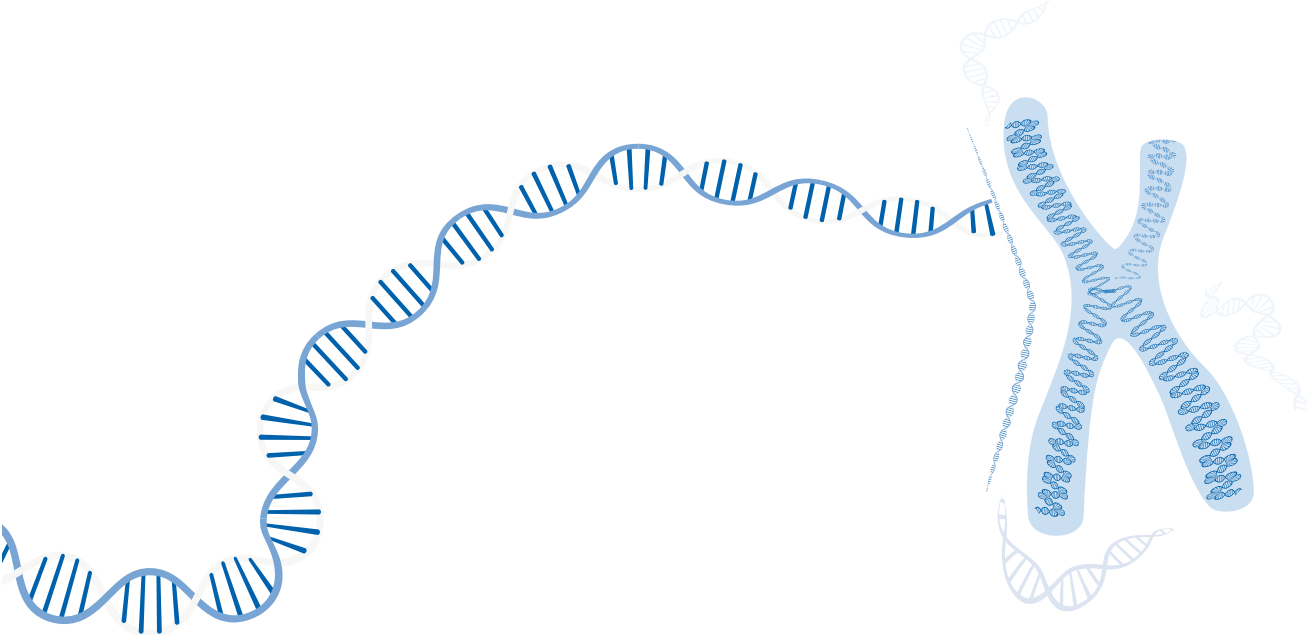
				up to 5×10^7	up to 10^8
	2.2×10^{10} – 1×10^{11}	7×10^9 – 3.5×10^{10}	2×10^7 – 1×10^8	100 – 4×10^6	100 – 4×10^6
	2.2×10^{10} – 1×10^{11}	7×10^9 – 3.5×10^{10}	2×10^7 – 1×10^8	100 – 4×10^6	100 – 4×10^6
	2×10^9			up to 10^6	up to 10^6
				5×10^6	up to 10^6
				up to 5×10^6	up to 10^6
	up to 250 mg				
	up to 250 mg				
	up to 10 g				

2

What's your sample type and input amount?



Scan this QR code to learn more about our HMW gDNA extraction kits



3 Select the kit with your preferred method of purification

Sample Type	Volume	Method
Blood	200 µL – 10 mL	Precipitation
	8.5 mL	Precipitation
Tissue	100 mg	Anion exchange
	100 mg	Anion exchange
Tissue	25 mg	Beads
	200 µL	Spin column
Tissue	25 mg	Spin column
	25 mg	Spin column
Tissue	100 µL	Spin column
		Spin column
Tissue		Spin column
		Spin column

Product
Puregene® Kits
PAXgene® Blood DNA Kit
QIAGEN® Genomic-tips (only Midi & Maxi)
QIAGEN Blood & Cell Culture DNA Kit
MagAttract® HMW DNA Kit
QIAamp® DNA Blood Mini Kit
QIAamp DNA Mini Kit
DNeasy® Blood & Tissue Kits
QIAamp PowerFecal® Pro DNA Kit
DNeasy PowerSoil® Pro Kit
DNeasy PowerMax® Soil Kit

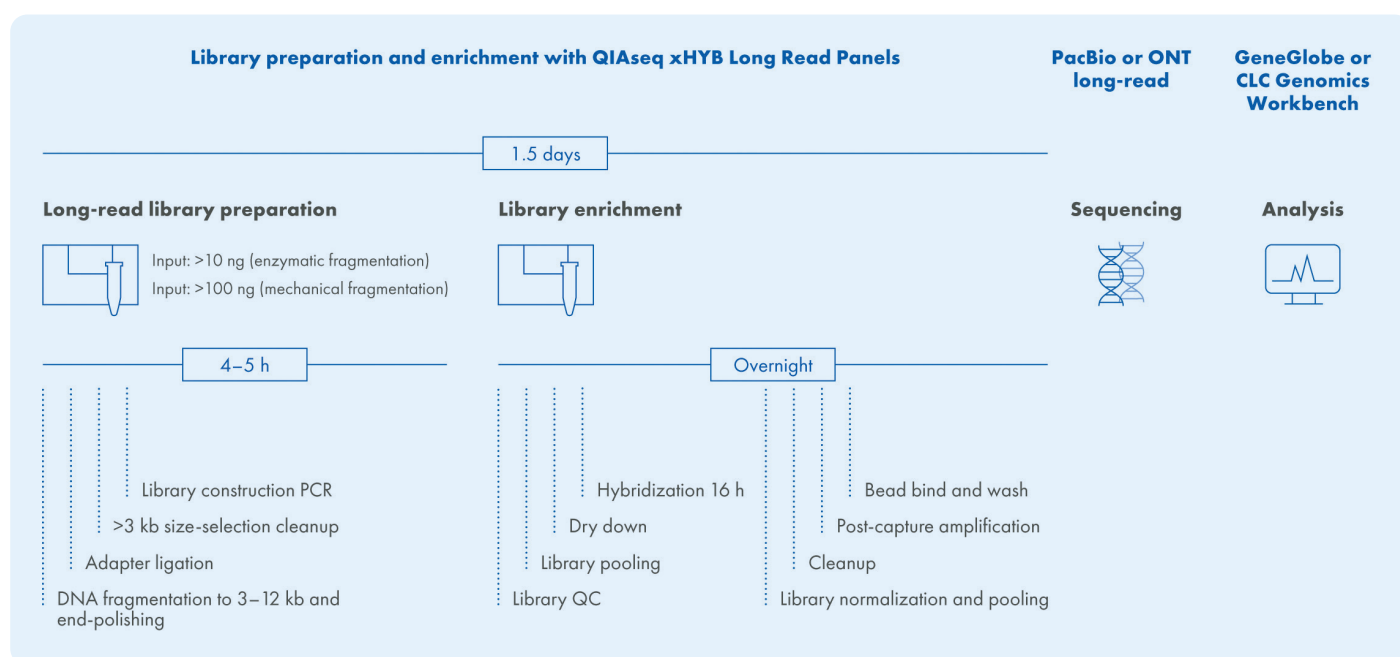
Play the long game in genomics powered by long reads

With high molecular weight DNA in hand, it's crucial to maintain that integrity throughout the library preparation process to fully realize the benefits of long-read sequencing technologies.

QIAseq® xHYB Long Read Panels deliver the resolution you need to tackle the most complex genomic regions using the power of long-read sequencing.

- Complete, uniform coverage with hybrid capture-based target enrichment
- High sensitivity and specificity for accurate variant detection
- Compatible with long-read sequencing for accurate variant calling and phasing
- Flexible and customizable to match diverse research needs and budgets
- Compatible with PacBio (Revio and Vega long-read systems) and ONT long-read systems

Long-read NGS library preparation and target enrichment workflow



HLA Typing Panel

Comprehensive panel design covers all 18 HLA class I and II genes, including introns and UTRs, enabling high-resolution 4-field haplotyping

Hereditary Cancer Panel

Targets over 1000 gross deletions, duplications, insertions and complex rearrangements linked to a wide range of cancer types

Custom Panel

Fully customizable panel design targets your specific regions of interest, enables integration with existing QIAseq xHYB long-read or custom panels and boosts coverage with additional probes – no ROI limits

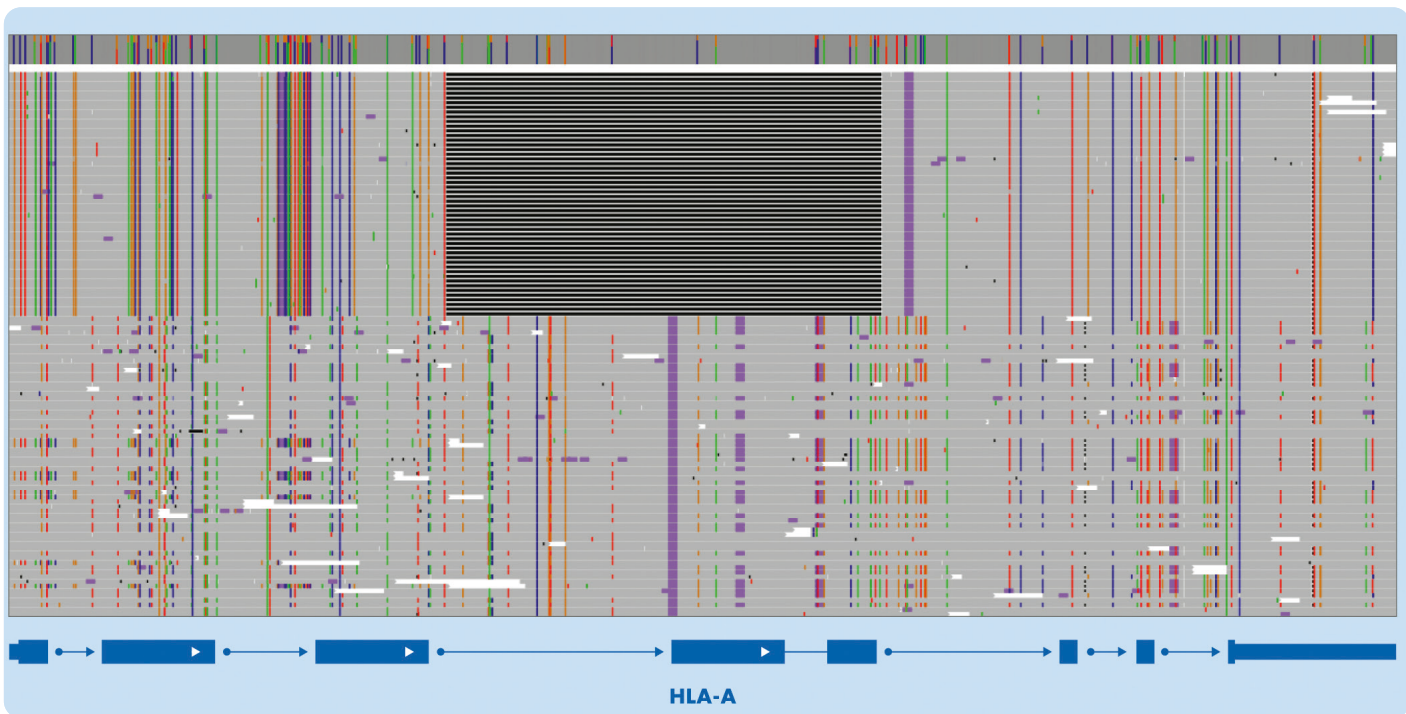


Figure 1: Long reads generated using the QIAseq xHYB Long Read HLA Typing Panel span the HLA-A gene without assembly, simplifying haplotyping. Here, we demonstrate the long reads that span the full length of the HLA-A gene, eliminating the need for complex assembly and simplifying the haplotyping process. Visualized read stacks across the gene clearly show heterozygous polymorphisms, with colored markers indicating roughly equal representation of non-reference bases – consistent with the gene's natural allelic diversity.

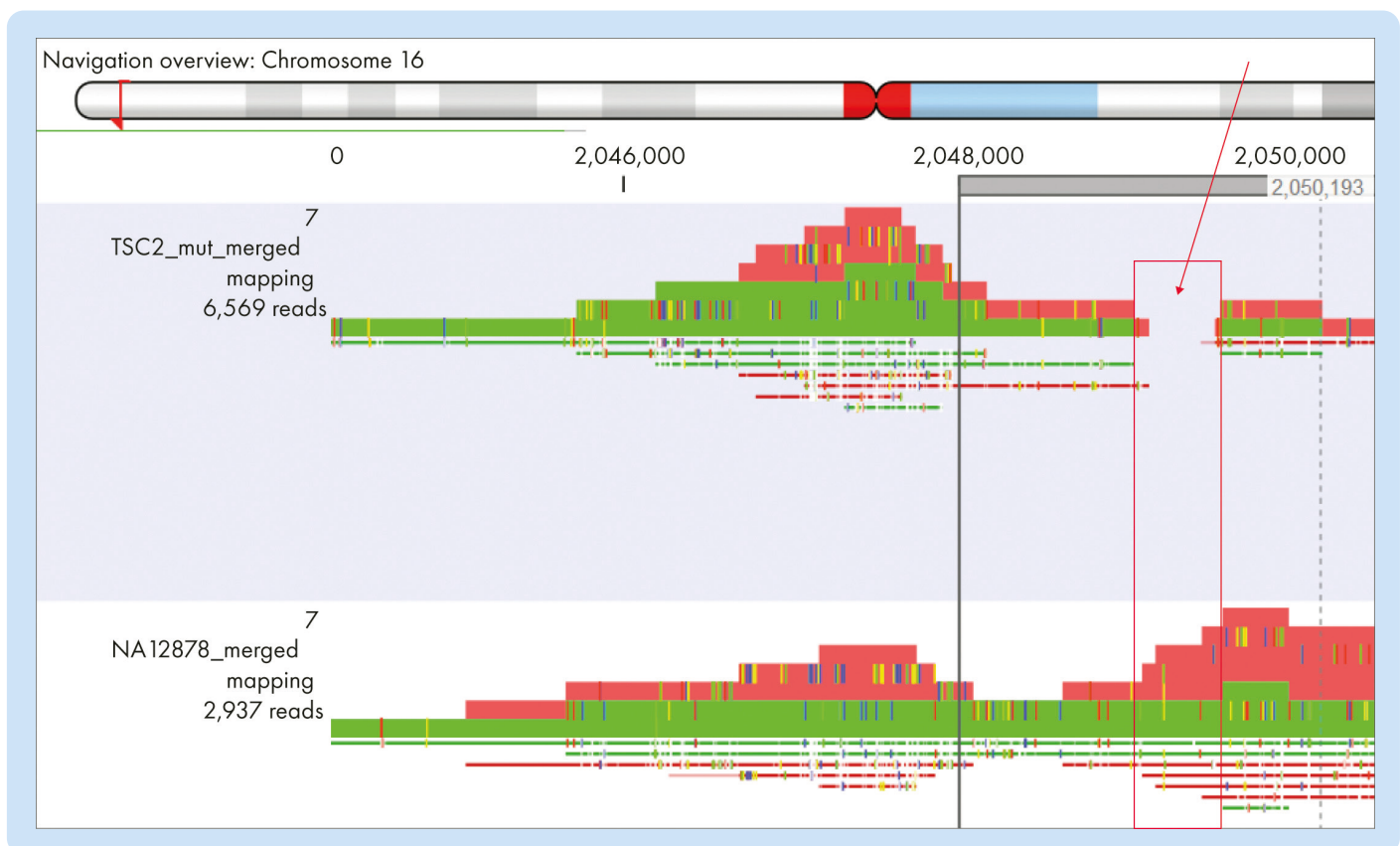


Figure 2: QIAseq xHYB Long Read Hereditary Cancer Panel successfully detects TSC2 deletion after exon 1 through long reads and contiguous mapping. The QIAseq xHYB Long Read Hereditary Cancer Panel accurately identifies a large TSC2 deletion in sample NA04520, a structural variant often challenging for short-read methods. The image displays long-read mapping data generated using CLC Genomics Workbench, comparing Coriell reference DNA NA04520 from an affected individual with benchmark reference DNA NA12878. The zoomed-in view of the 5' end of the TSC2 gene clearly shows a 430 bp deletion in NA04520 (indicated by the red arrow and coverage gap).

Applications



Repeat expansion disorder analysis

Precisely characterize repeat expansions in neurological and genetic disorders



HLA typing

Resolve polymorphic HLA regions for accurate genotyping in immunogenomics and transplantation



Phasing of genetic variants

Determine haplotype structures of genomic variants for critical insights into inheritance patterns and allele-specific expression



Structural variant detection

Accurately detect large-scale genomic alterations for cancer, genetic disease and evolutionary research

Data analysis

The GeneGlobe® Data Analysis portal offers simplified downstream data analysis for HLA haplotyping. The QIAGEN® CLC Genomics Workbench is used to detect large structural variants in hereditary cancers.



To learn more about the long-read sequencing panel, visit <https://www.qiagen.com/qiaseq-long-read-seq>



Visit our **Genomic DNA Resource Center for High-Molecular-Weight DNA** and advance your exploration of long-read sequencing.



The products mentioned here are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

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