

# HIFI SEQUENCING WITH TWIST BIOSCIENCE TARGET ENRICHMENT

## Targeted HiFi sequencing at scale with ready-made Twist Alliance Panels or custom designs

Combine **Twist Bioscience** target enrichment with **PacBio**® long and accurate HiFi reads to efficiently sequence your priority genomic regions at scale. Sequence enriched regions with a protocol optimized for HiFi reads to get comprehensive detection of single nucleotide variants, structural variants, and indels with haplotype resolution. HiFi target enrichment can deliver accurate alleles for complex gene families such as immune genes (e.g., *HLA*) and pharmacogenes (e.g., *CYP2D6*).



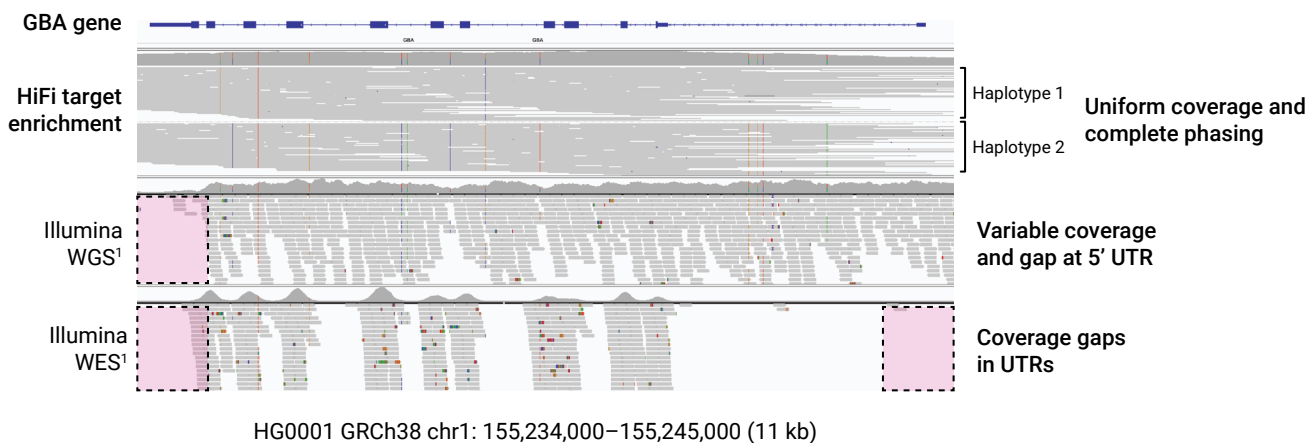
### Why choose HiFi sequencing with Twist target enrichment?

- End-to-end workflow optimized for HiFi reads
- Custom design for any panel size
- Small and large cohorts on a single SMRT® Cell
- High-accuracy variant calls, including SVs
- Direct phasing, unambiguous haplotypes, ancestry-agnostic discovery

### Pool multiple samples per SMRT Cell

Panel example	Large panel	Medium panel	Small panel
Panel size	20 Mb	2 Mb	100 kb
Estimated number of genes	400	50	2
Samples per Sequel® IIe SMRT Cell 8M	4	24	96
Samples per Revio™ SMRT Cell	12	72	288

### Full gene coverage of medically relevant genes

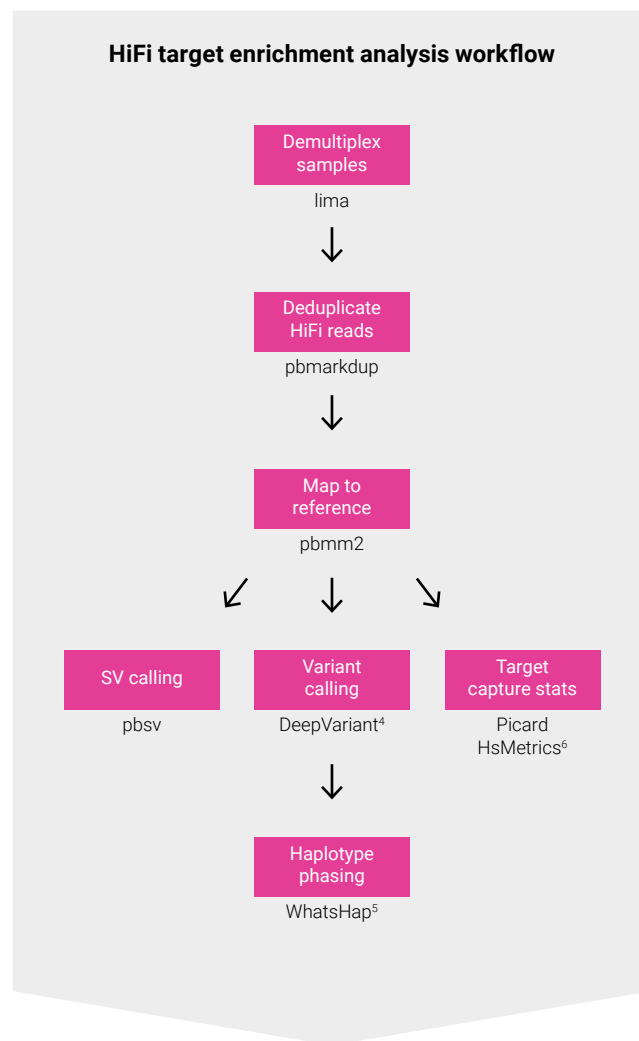
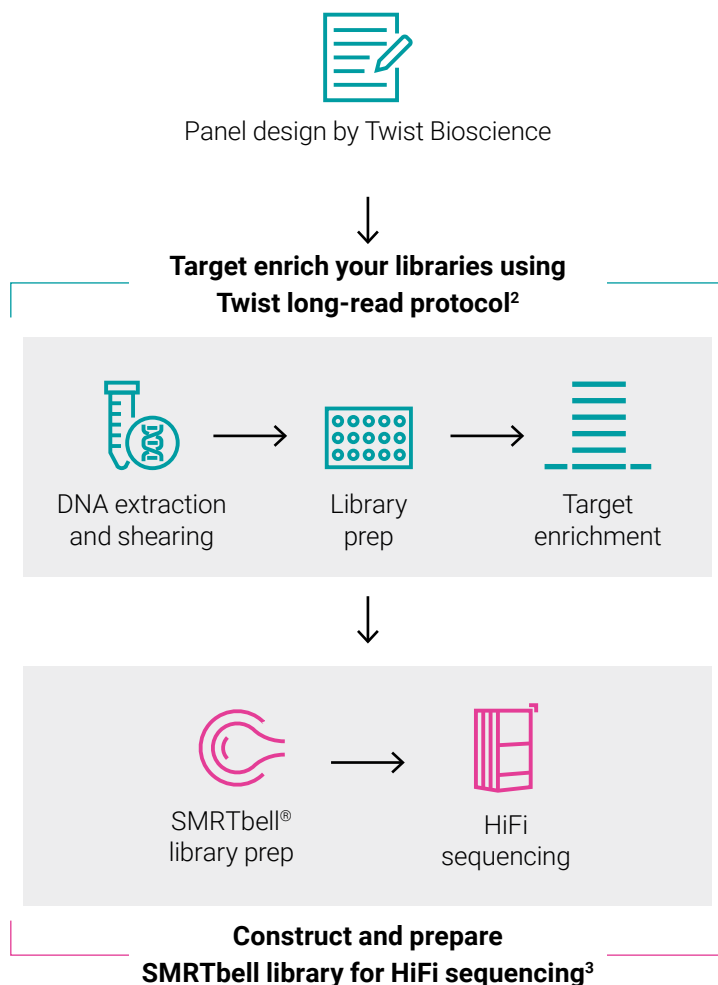


### Performance for Twist Alliance Panels

Twist Alliance Panel	Panel Size (Mb)	Number of genes	PacBio system	Samples per SMRT Cell	Mean target coverage	Fold enrichment	Target bases ≥10-fold read depth	Mean HiFi read length	Duplicate rate
Dark Genes	22	389	Revio	12	75-fold	65-fold	93%	5.5 kb	3%
Dark Genes	22	389	Sequel IIe	4	75-fold	54-fold	93%	5.2 kb	3%
Long Read PGx	2	49	Sequel IIe	24	190-fold	784-fold	99%	5.3 kb	2%

## From targets to HiFi reads

## Supported Analysis in SMRT® Link v13



### REQUIRED REAGENTS

Vendor	Quantity	Description	PN	Quantity supported
Twist Bioscience	1	Twist Library Prep MF Kit 1 & 2	101281	96 samples
	1	Twist Universal Adapter System Plate A	101308	96 samples
	2	Twist Library Prep Kit 2 (AMPure beads)	100573	96 samples
	1	Twist Universal Blockers, 12 reactions	100578	12 captures
	1	Twist Standard Hyb and Wash Kit v2	104446	12 captures
	1	Custom Probe Panel, 12 reactions	101001	12 captures
PacBio	1	SMRTbell prep kit 3.0	102-182-700	24 SMRTbell libraries
	1	Binding kit 3.2 and cleanup beads	102-333-300	24 binding reactions
	1	SMRT Cell 8M tray	101-389-001	4 SMRT Cells
	1	Sequel® II sequencing kit 2.0	101-820-200	4 SMRT Cells
Invitrogen	1	Dynabeads M-270 (2 mL vol)	65305	20 captures
Merck/Millipore/Sigma	1	KOD Hot Start DNA Polymerase (200 units)	71975	44 samples

### KEY REFERENCES

- <https://www.biorxiv.org/content/10.1101/2020.12.11.422022v1.full> (HG002.novaseq.wes-agilent.50X)
- <https://www.twistbioscience.com/resources/protocol/long-read-library-preparation-and-standard-hyb-v2-enrichment>
- Procedure & checklist – Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0** PacBio documentation.
- <https://github.com/google/deepvariant>
- <https://whatshap.readthedocs.io/en/latest/>
- <https://snakemake-wrappers.readthedocs.io/en/stable/wrappers/picard/collecthsmetrics.html>

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