



PureTarget™

Shine a light on dark regions of the genome

Comprehensive and scalable characterization of challenging regions with PureTarget

The PureTarget technology enables scalable HiFi sequencing of native DNA libraries that maintain methylation and are free of PCR artifacts, errors, and bias. With off-the-shelf panels of targets for repeat expansion neurological disease and carrier screening, labs can retire their cumbersome legacy genotyping assays and consolidate all the challenging genes on a modern long-read panel.

Off-the-shelf panels

PureTarget repeat expansion panel 2.0

The updated repeat expansion panel features 38 targets covering a variety of commonly screened tandem repeats associated with neurological disorders. New targets not on the 20 gene panel are **highlighted**.

Disease	Targets
Spinocerebellar ataxia (SCA)	ATN1, ATXN1, ATXN2, ATXN3, ATXN7, ATXN8, ATXN10, CACNA1A, PPP2R2B, TBP BEAN1, DAB1, FGF14, NOP56, ZFHX3
Fragile-X disease (FXS)	FMR1
Fragile X syndrome, FRAXE type	AFF2
Intellectual disability associated with fragile site FRA2A	AFF3
Frontotemporal dementia (FTD), amyotrophic lateral sclerosis (ALS)	C9orf72
Friedreich ataxia (FRDA)	FXN
Cerebellar ataxia, neuropathy, and vestibular areflexia syndrome (CANVAS)	RFC1
Neuronal intranuclear inclusion disease, Alzheimer disease and parkinsonism phenotype (NIID)	NOTCH2NLC
Myotonic dystrophy (DM)	DMPK, CNBP
Huntington disease (HD)	HTT
Huntington's disease-like type2 (HDL2)	JPH3
Fuchs endothelial corneal dystrophy 3 (FECD3)	TCF4
Kennedy Disease, Spinal and bulbar muscular atrophy, (SBMA)	AR
Oculopharyngeal muscular dystrophy (OPMD)	PABPN1
Oculopharyngodistal myopathy (OPDM)	ABCD3, GIPC1, LRP12, RILPL1
Syndactyly (SD5)	HOXD13
Congenital central hypoventilation syndrome (CCHS)	PHOX2B
Creutzfeldt-Jakob disease (CJD)	PRNP
Progressive Myoclonic Epilepsy Type 1 (EPM1) Unverricht-Lundborg Disease (ULD)	CSTB
Familial adult myoclonic epilepsy type 1 (FAME)	SAMD12

PureTarget carrier panel 1.0

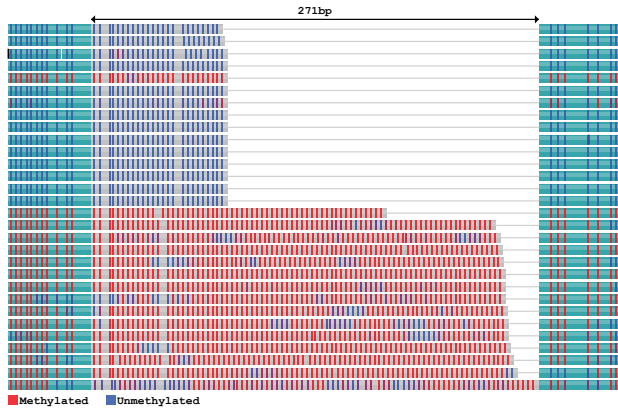
The carrier screening panel enables the consolidation of 12 genes which are commonly genotyped with legacy non-NGS assays (e.g. triplet-primed PCR, long-range PCR, qPCR, MLPA, or Sanger sequencing)¹. PureTarget is an attractive and streamlined assay that can be run alongside routine short read panels to capture all expanded carrier screening targets.

Disease	Targets
Hemophilia	F8
Friedreich ataxia (FRDA)	FXN
Fragile-X disease (FXS)	FMR1
Congenital adrenal hyperplasia	CYP21A2
Classical-like Ehlers-Danlos syndrome	TNXB
Alpha thalassemia	HBA1/2
Gaucher disease	GBA
Spinal muscular atrophy	SMN1/2
Early-infantile epileptic encephalopathy (EIEE1) and Partington syndrome (PRTS)	ARX
Beta thalassemia	HBB
X-linked retinitis pigmentosa	RPGR
Fragile X syndrome, FRAXE type	AFF2

What can PureTarget do?

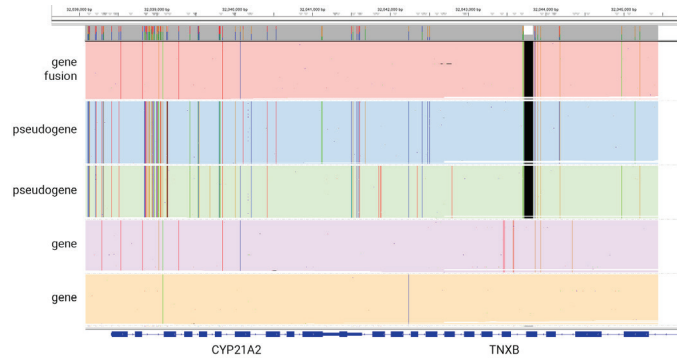
Powered by the *Tandem Repeat Genotyping Tool* (TRGT)² and *paraphase*³, analysis of PureTarget data enables methylation detection, accurate sizing and motif analysis of repeat expansions, copy number and fusion allele detection at challenging genes like *SMN1/2* and *CYP21A2*, and capture of large structural variants in *HBA1/2*.

Allele-specific methylation in *FMR1* for carrier female



Carrier female (Coriell sample NA06905) with hypermethylated premutation. Expected genotype is 23 and 70 CGG copies based on Southern and PCR analysis. Sample was prepared with PureTarget repeat expansion panel using 1 µg of DNA and sequenced on the Vega® system. Spanning read count for allele 1 is 121 and for allele 2 is 139. Observed genotype from trgt 2.0.0² is 23 and 79 CGG motifs with 1 AGG interruption motif observed on each allele (not shown). Discrepancy between observed and expected long allele length may be attributable to mosaicism in length as observe in the waterfall plot.

Copy number variation in *CYP21A2*



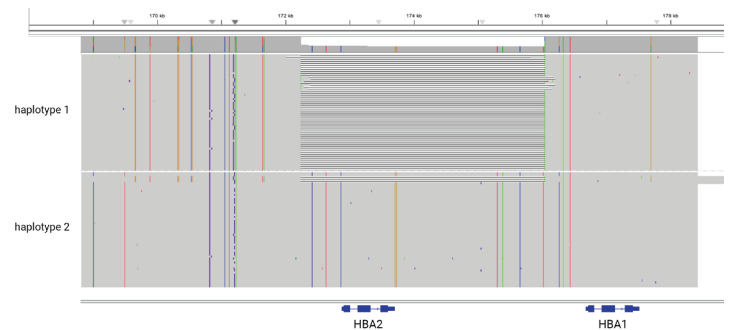
HG03540 reference sample with copy number variation in *CYP21A2*. A pair of gRNAs capture ~7.4 kb spanning the full *CYP21A2* gene and 13 exons of *TNXB* on the 3' end. The gRNAs also cut the segmental duplication containing *CYP21A1P* and *TNXA*. Sample was sequenced on the Revio® system + SPRQ™ chemistry, reads for gene and pseudogene are mapped to the gene and analyzed with paraphase v3.3.1 in the PureTarget Carrier Pipeline (PTCP). Five haplotypes are captured showing 2 gene copies, 2 pseudogene copies, and a fusion allele.

Heterozygous expansion in *FGF14* (SCA27B)



Sample with pathogenic heterozygous expansion in *FGF14* associated with SCA27B. DNA (2 µg) extracted from blood with QIAasympyphony, was manually prepared with PureTarget repeat expansion panel 2.0, sequenced on Revio + SPRQ in an 8plex, and analyzed with TRGT v3.0.0. Expected genotype from rpPCR is 10 +/- 2 and approximately 350 repeats and is concordant with observed genotype: 8 and 390 repeats. HiFi sequencing reveals that the long allele has with 66 AGG and 307 AAG motifs with consensus length 1155 bp.

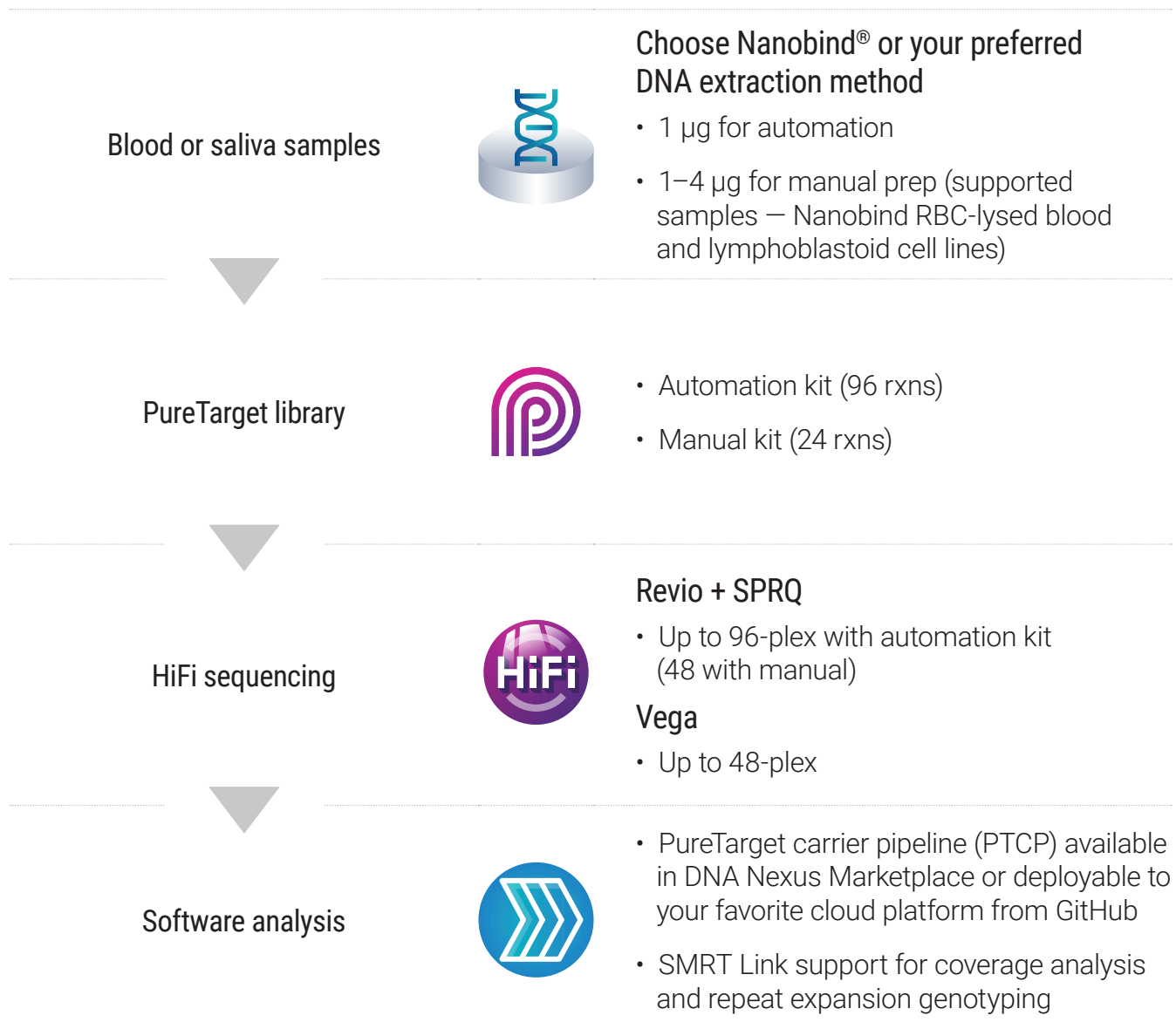
Large deletion spanning *HBA2*



Sample was sequenced on Revio + SPRQ and analyzed with paraphase v3.3.1 in the PureTarget Carrier Pipeline (PTCP). A pair of gRNAs capture ~9.5 kb spanning *HBA1* and *HBA2*. The 3p7 deletion is neatly captured showing one copy of *HBA2* and 2 copies of *HBA1*.

Stay on target

Pair your favorite off-the-shelf panel with manual or automated library prep. New automation kit enables easy and scalable prep of 96 samples on Hamilton NGS STAR MOA. Updated SMRT® Link repeat expansion genotyping deploys the latest TRGT software. Best practice variant calling with PureTarget carrier pipeline available in DNA Nexus Marketplace or deployable to your preferred cloud platform from GitHub.



New products available in second half of 2025

KEY REFERENCES

1. Guha S, et al. (2024). **Laboratory testing for preconception/prenatal carrier screening: A technical standard of the American College of Medical Genetics and Genomics (ACMG).** *Genet Med.* 2024 Jul;26(7):101137. doi: 10.1016/j.jgim.2024.101137.
2. Dolzhenko E, English A, Dashnow H, et al., (2024). **Characterization and visualization of tandem repeats at genome scale.** *Nature Biotechnology*, 1–9.
3. Chen X, Baker D, Dolzhenko E, et al. **Genome-wide profiling of highly similar paralogous genes using HiFi sequencing.** *Nature Communications*. 2025. doi:10.1038/s41467-025-57505-2



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