COMPREHENSIVE CHARACTERIZATION OF REPEAT EXPANSIONS WITH PURETARGET

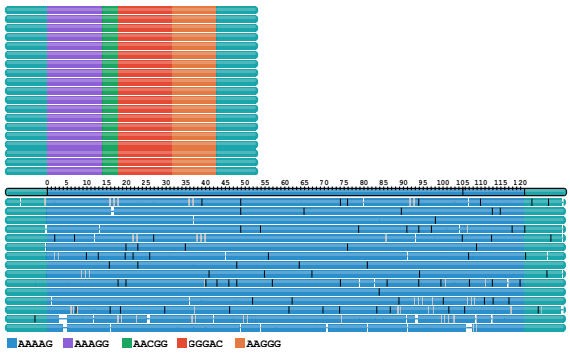
PureTarget™

Shine a light on dark regions of the genome

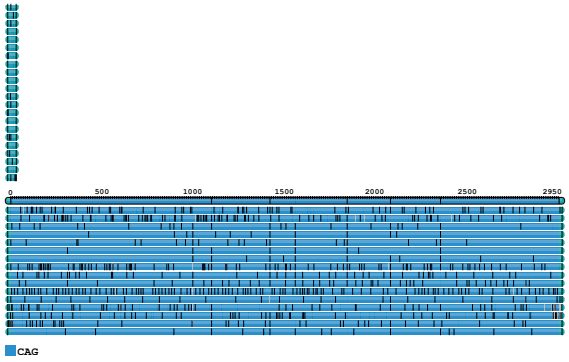
Expansions of repetitive DNA sequences have been linked to over 50 monogenic disorders and cancers where the repeat length, sequence context and methylation can be factors in disease severity and/or age of onset. Once notoriously difficult to characterize, these regions can now be comprehensively genotyped at scale with the PacBio® PureTarget™ repeat expansion panel. Offering a gene panel for 20 of the most important repeat expansions for human health, PureTarget now grants a clear view of these once-dark regions of the genome.

What can PureTarget do?

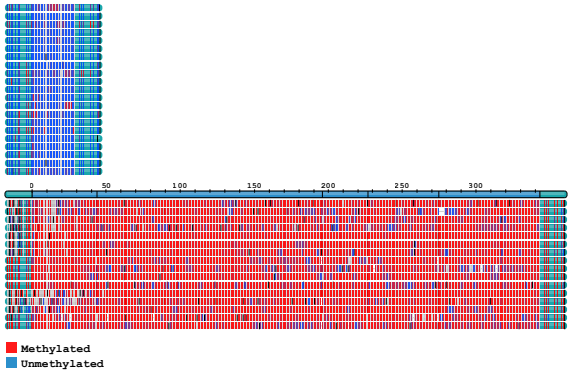
Powered by the *Tandem Repeat Genotyping Tool* (TRGT)[1] and deep coverage of long and accurate HiFi reads, the PureTarget panel provides A. single-base resolution of repeats, B. precise sizing of long repeats, C. methylation profiles, and D. deep coverage to characterize mosaicism.



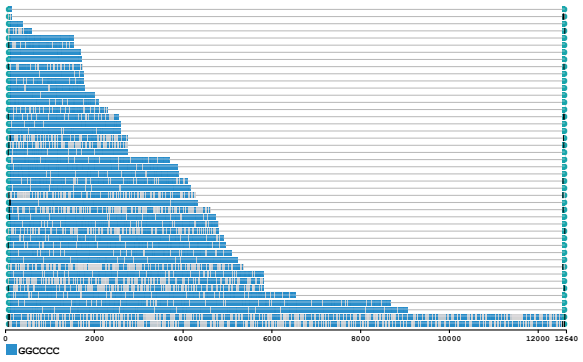
A. Single-base resolution shows diverse repeat motifs at *RFC1*.



B. Accurate sizing of expanded *DMPK* allele with 2950 repeat motifs (8,850 bp).



C. Profile at *FMR1* shows consistent methylation of expanded allele in female carrier (NA07537).



D. Deep coverage captures distribution of repeat lengths within a sample at *C9orf72*.

PacBio

Stay on target

PureTarget offers an easy and scalable workflow to capture repeat expansions and brings you from sample to answer in three days. Compatible with the Revio™ and Sequel® II systems, PureTarget libraries can be multiplexed with up to 48 samples, generating deep coverage across the 20-gene target panel.

Nanobind® DNA extraction		**2 hours**
PureTarget library		**8 hours**
HiFi sequencing		**1 hour prep** **24 hour movie**
SMRT™ Analysis		**15 minutes**

Spec	Metric
DNA input[1]	2 µg/sample
DNA quality[2]	GQN at 30 kb >5
Mean target coverage[3]	>200-fold
Minimum target coverage	50-fold
Sample multiplexing[4]	48 —Revio system 24 —Sequel II systems
Library size[5]	4–5 kb
Methylation[6]	Detected

1. 1–4 µg supported
2. 50% of mass of DNA molecules longer than 30 kb as measured on Femto Pulse (Agilent). Official product support for Nanobind-extracted DNA from human blood and cell line.
3. Mean and minimum target coverage is for 2 ug of input DNA from supported samples types (Nanobind-extracted human blood and cell line) for unexpanded alleles.
4. Kit supports smaller batches in multiples of 8 samples.
5. Inserts with expanded alleles will be longer.
6. Methylation probabilities for CpG sites encoded in BAM.

Gene list	Disease
ATN1, ATXN1, ATXN2, ATXN3, ATXN7, ATXN8, ATXN10, CACNA1A, PPP2R2B, TBP	Spinocerebellar ataxia
FMR1	Fragile X-associated disorders
C9ORF72	Amyotrophic lateral sclerosis (ALS) and Frontotemporal dementia (FTD)
DMPK, CNBP	Myotonic dystrophy (DM1, DM2)
FXN	Friedreich's ataxia
RFC1	RFC1 CANVAS / spectrum disorder
HTT	Huntington's disease
AR	Spinal-bulbar muscular atrophy
PABPN1	Oculopharyngeal muscular dystrophy
TCF4	Fuchs endothelial corneal dystrophy

KEY REFERENCES

1. Dolzhenko E, English A, Dashnow H, et al., (2024). Characterization and visualization of tandem repeats at genome scale. *Nature Biotechnology*, 1–9.

Learn more: pacb.com/target

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