

STAR BEADS Genomic DNA Extraction kit

Rapid isolation of genomic DNA from various biological samples

Overview

STAR BEADS Genomic DNA Extraction Kit provides a fast and efficient purification method to isolate high-quality genomic DNA (gDNA) from a set of biological samples such as whole blood, saliva, cultured cells and FFPE.

The extracted nucleic acids are highly pure ready for downstream reactions, including real time PCR, qRT-PCR, Sanger Sequencing, NGS, and other enzymatic reactions.

For automated scripts and protocols visit the document section or email to technical.support@cyanagen.com



Features

- **Magnetic bead-based technology:** 50% reduction in plastic use
- **Rapid:** protocol for manual extraction, automatic extraction time about 50 minutes for 96 and 32 samples
- **Easy storage:** room temperature
- **Easy to use:** available as both bottled and pre-filled plate format ready-to-use by manual procedure or on automatic extractors
- **Automatable:** compatible with
 - ✓ Thermo Scientific KingFisher™ Flex
 - ✓ Allsheng Auto-Pure96/Auto-Pure32A/Mini
 - ✓ Accuris IsoPure™ Mini/96
 - ✓ Procomcure Phoenix-Pure96/32
 - ✓ MOLGEN PurePrep 96/32
 - ✓ BIOER GenePure Pro NPA-32P
 - ✓ MGI SP-NE32
 - ✓ BIGFISH BFEX-32
 - ✓ 3DMED ANDIS350
 ...and many other systems

Order information

PRODUCT	ORDER-NO.	FORMAT	UNIT SIZE
STAR BEADS Genomic DNA Extraction kit	SBK265,1x96	bottles	96 preps
	SBK287,1X96PFI	pre-filled plates for 96 extractors	96 preps
	SBK261,2X32PFI	pre-filled plates for 16/32 extractors	64 preps

Recommended sample input and expected yields from different sample types

Sample type	Input amount	Typical yield (µg)	Typical A ₂₆₀ /A ₂₈₀
Whole blood §	200 µL	2-8	> 1,8
Saliva*§	200 µL	2-8	> 1,8
Cultured mammalian cells	From 10 ⁵ to 10 ⁶ cells	2-30	> 1,8
Formalin-Fixed Paraffin-Embedded	3-8 paraffin sample sections (≥ 4 µm)	1.5-3	> 1,8

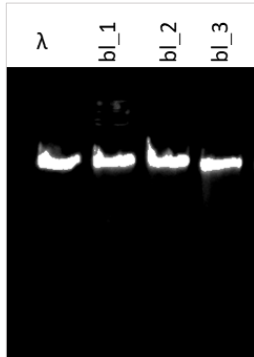
Average yield, A₂₆₀/A₂₈₀ and A₂₆₀/A₂₃₀ were measured using Implen™ NanoPhotometer™ NP80 or Nanodrop2000.

* Saliva stored in Oragene™ collection kit (DNA Genotek).

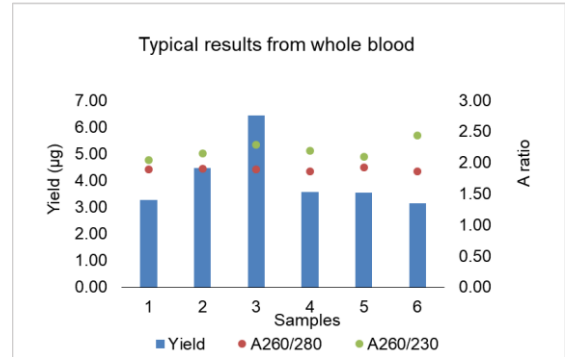
§ CE-IVD certified for whole blood and saliva.

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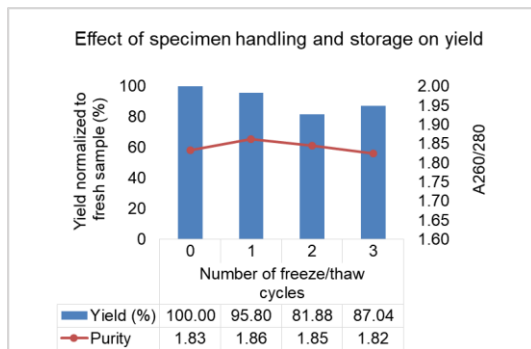
Isolation of high quality genomic DNA from whole blood



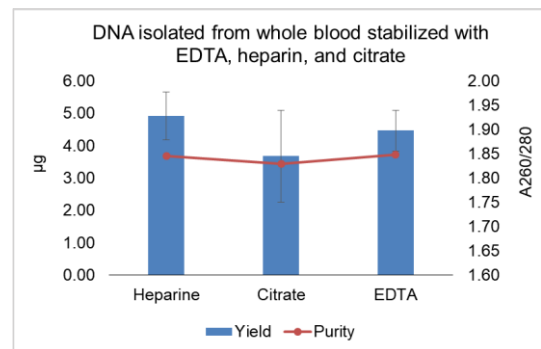
High quality and purity of extracted genomic DNA. gDNA is un-sheared and >48 kb in length. RNA contamination is absent.



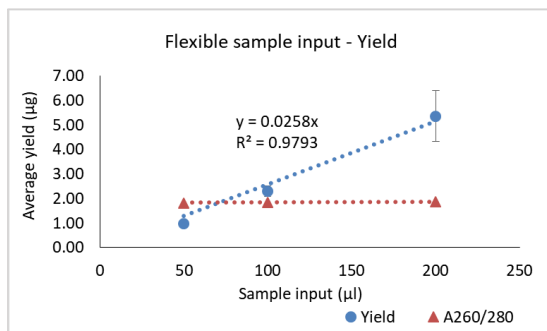
Yield and purity of genomic DNA from 200 µL of whole blood. Automated extraction of six blood samples (200 µL).



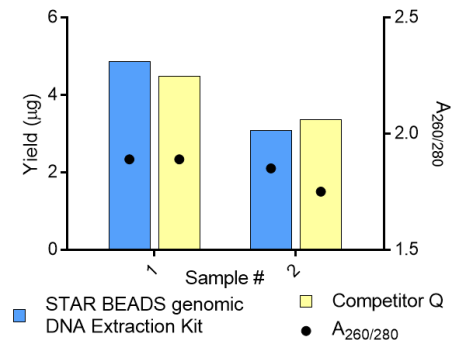
Effects of freezing and thawing blood samples. EDTA-treated blood was frozen and thawed up to 3 times. Data are represented as mean ±SD (n=16).



Yield and purity of genomic DNA extracted from 200 µL of whole blood collected on citrate, EDTA and heparin tubes. Data are represented as mean ±SD (n=16).



Yield and purity of genomic DNA extracted from different input volumes of whole blood. Graph shows average values from two readings. Data are represented as mean ±SD (n=3).



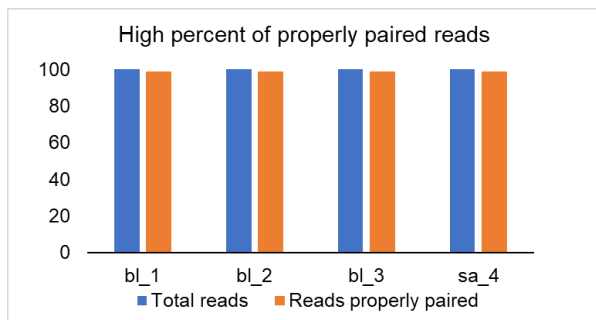
Performance comparison between STAR BEADS Genomic Kit and kit from Competitor Q. DNA was purified from 200 µL of whole blood. Graph shows average values.

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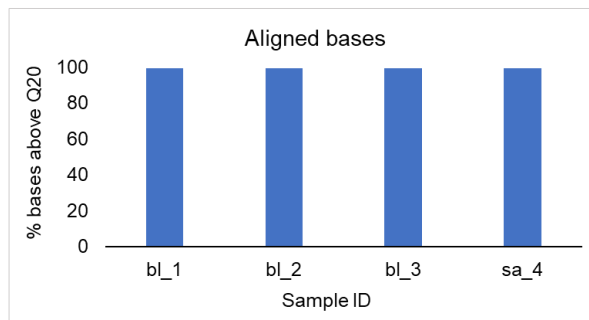
High quality DNA for Next Generation Sequencing

Sample ID	Total reads	Reads properly paired	% bases above Q20	Mean coverage
bl_1	565800	556010	99.4	411,39
bl_2	441106	433152	99.4	323,09
bl_3	399148	391934	99.4	290,12
sa_4	420652	413438	99.4	300,29

NGS of a custom target gene library starting from genomic DNA isolated with the STAR BEADS Genomic DNA Extraction Kit. DNA was isolated from 200 µL aliquots of frozen whole blood (bl-1,2,3) and saliva (sa_4) using an automated protocol on Allsheng AutoPure 32A. Dual-index paired-end libraries were generated from 150 ng of extracted genomic DNA with the Lotus DNA library prep kit (Integrated DNA Technologies IDT). Target panel hybridisation was performed using the custom xGen Lockdown probe pool (IDT, 224318852, 26 genes) and xGen hybridisation capture of DNA libraries kit (IDT). NGS was performed on the MiSeq™ Sequencing System according to the manufacturer’s instructions on a Nano v.2 flow cell, 300 cycles paired-ends. Reads were properly paired and mapped to unique positions on the human reference genome (hg19) according to a dedicated pipeline (Bonora et al, 2021).

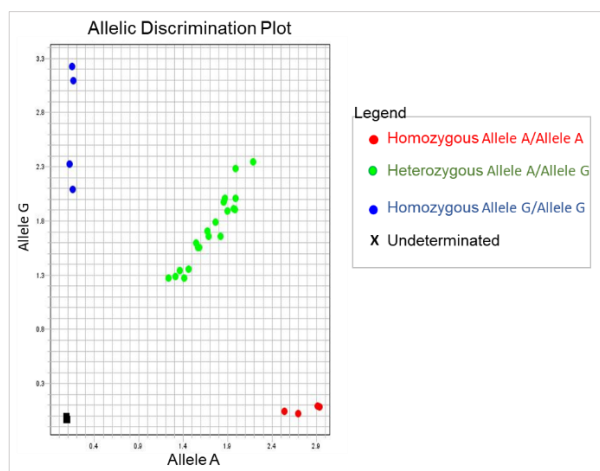


High percent of properly paired reads. Average percentage of properly paired reads is 98,86.



High percent of bases above Q20. Average percentage of bases in which the phred score is above 20 is 99,4%.

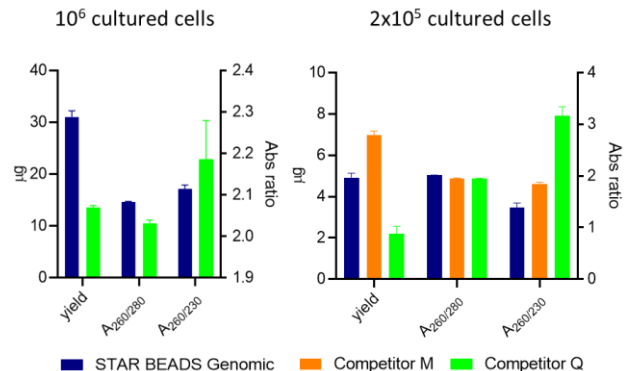
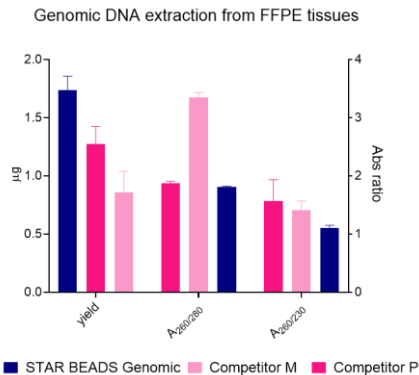
High quality DNA for SNP genotyping



SNP genotyping on gDNA isolated with the STAR BEADS Genomic DNA Extraction Kit. Allelic discrimination plots obtained for BCL11A rs1123573 using Taqman SNP Genotyping Method. Red and blue dots represent the homozygous genotypes, green circles represent heterozygous genotypes and squares on the bottom left of the plot are no-template control. No sample gave undetermined result.

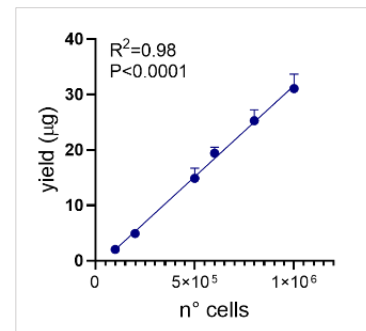
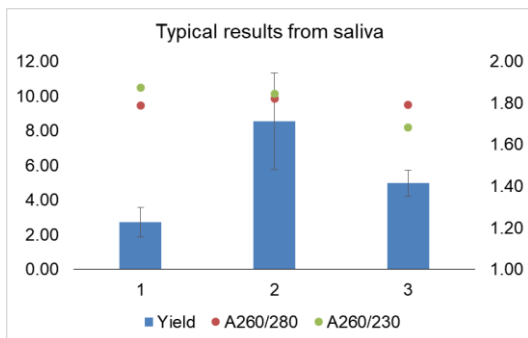
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Genomic DNA purification from a variety of sample types



Performance comparison between STAR BEADS Genomic Kit and kits from Competitors for genomic DNA extraction from FFPE tissues. Three slices of the same FFPE tissue were considered as sample. Data are represented as mean ±SD (n≥8).

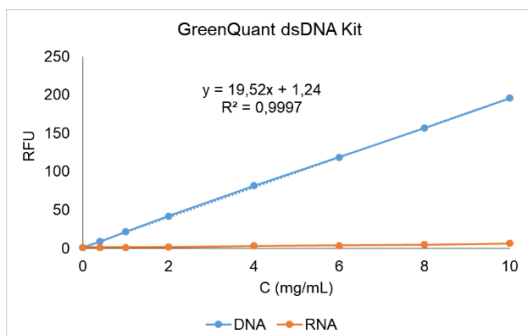
Performance comparison between STAR BEADS Genomic Kit and kits from Competitors for genomic DNA extraction from cultured cells. DNA was purified with at least 2 independent extractions. Data are represented as mean ±SD (n≥2).



Yield and purity of genomic DNA from 200 µL of saliva. Three specimens stored in Oragene™ collection kit (DNA Genotek) were extracted with automated protocol. Data are represented as mean ±SD (n=16)

Linear recovery of gDNA from cultured cells. DNA was isolated from 1x10⁵ to 1x10⁶ cells. Data are represented as mean of two independent experiments. Simple linear regression analysis performed with GraphPad 8.

Order in combination with GreenQuant dsDNA kit, cod. NAGS299 for DNA quantification



dsDNA selectivity and sensitivity of GreenQuant dsDNA kit. Triplicate 10 µL samples of λDNA and yeast RNA were assayed with GreenQuant dsDNA kit. Graph was plotted as fluorescence versus the RNA or DNA concentration. Background fluorescence was not subtracted and the y-intercept was set at the RFU of the blank.