Simple And Gentle Method To Extract 10Kb Dna From Agarose Gels

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BACKGROUND

As opposed to short-read sequencing which requires extensive fragmentation and amplification, long-read sequencing allows researchers to sequence transcripts that span a few thousand to tens of thousands of nucleotides in length. Long-read sequencing provides several advantages over short-read sequencing due to its increased context. These benefits include enhanced confidence in mapping highly repetitive regions, the ability to determine isoform-specific expression, identification of structural variants, and characterization of epigenetic modifications.

While commercial long-read technologies like PacBio and ONT require long DNA as input, currently there is no simple way to separate long and short DNA strands in a mixed pool. Standard methods are either proprietary, unreliable, low yield, highly labor intensive, or a combination of these concerns. Because of this, there is a need to develop a generalized and efficient way of isolating long DNA strands for subsequent sequencing.

TECHNOLOGY DESCRIPTION

This work presents a method to prepare high molecular weight nucleic acids using selective gel excision paired with SPRI bead isolation. Briefly, nucleic acids migrate through a polymeric matrix, high molecular weight nucleic acids are excised from this matrix, immobilized on particulate solid supports, and eluted from these particulates. This gentle and straightforward isolation yields highly pure, long DNA with minimal degradation. This method may further require sequence analysis of high molecular weight nucleic acids using a sequencing device.

APPLICATIONS

- High molecular weight DNA isolation
- Long read sequencing preparation

ADVANTAGES

- Higher yield of high molecular weight DNA
- Cheaper than other commercially available technologies

INTELLECTUAL PROPERTY INFORMATION

Country	Type	Number	Dated	Case
United States Of America	Published Application	20210123099	04/29/2021	2019-513

RELATED MATERIALS

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- TMI-seq: Tn5 Transposase Mediated Production of Complex Libraries for Short Read Sequencing
- Simplified Workflow For Hybridoma Antibody Sequencing

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OTHER INFORMATION

KEYWORDS

long read sequencing, long nucleic acid isolation, gel isolation, SPRI bead, nanopore sequencing

CATEGORIZED AS

- **Research Tools**
  - Nucleic Acids/DNA/RNA

RELATED CASES

2019-513-0

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