Extract
React
select

sageHLS™

HMW DNA Library System

sage science

One-Stop Sample Prep
for Long-Range Genomics

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HMW DNA Library System

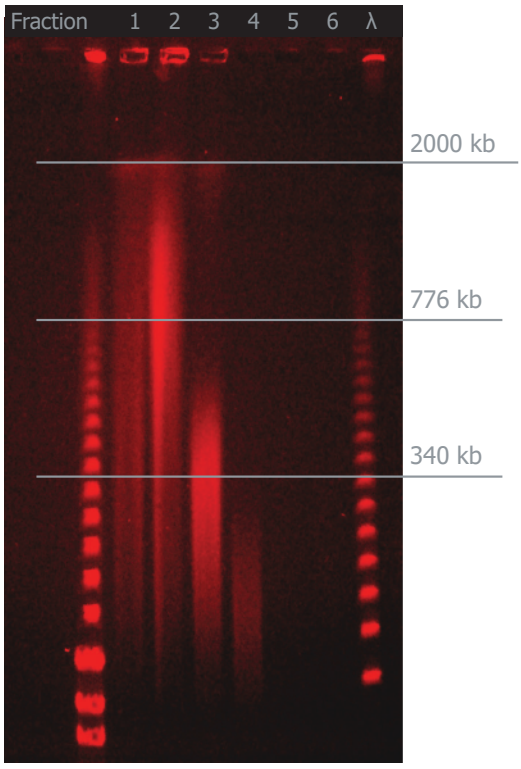
One-Stop Sample Prep for Long-Range Genomics

Extract Ultra-HMW DNA from Cells

Study DNA Fragments as Long as 2MB

Treat Genomic DNA with a Random Cleavase

Pulsed-field Gel Analysis



Input DNA: 8µg DNA Equivalents

Fraction	DNA (ng)	% yield
1	428	5.3%
2	1581	19.8%
3	1691	21.1%
4	314	3.9%
5	24	0.3%
6	26	0.3%
Total	**4064**	**51%**

DNA Recovery per Collection Well

White blood cells were prepared from whole blood using standard centrifugation techniques. The cells (~6.6 x 10^4) we re resuspended in 70µl and loaded onto a SageHLS gel cassette. The purification and cleaving processes include several pipetting, electrophoresis, and incubation steps requiring about 90 minutes. Size selection required 3.5 hours. Total hands-on time was about 15 minutes.

Genome Structure

- Rearrangements
- Copy Number Variation
- Haplotype Phasing

Specifications at a Glance

Run Times	Sample	Instrument
Extraction 1 hr	DNA Load* 10µg	Power Req. 100-240 VAC
Treatment 30 min	Volume 70µl	Incubation Temp. 15-50°C
Collection 1-6 hr	Capacity 1-4/run	Certifications: CE

**recommended DNA equivalency per cell suspension*

Stay Tuned for More...

The SageHLS platform lends itself to new development as needs arise. New suspension kits and protocols are planned for numerous cell types, organisms, and tissues. The system is not limited to endonuclease treatment either: ligases, nickases, or polymerases could be used to modify genomic DNA into labeled or tagged libraries.

Critical Research

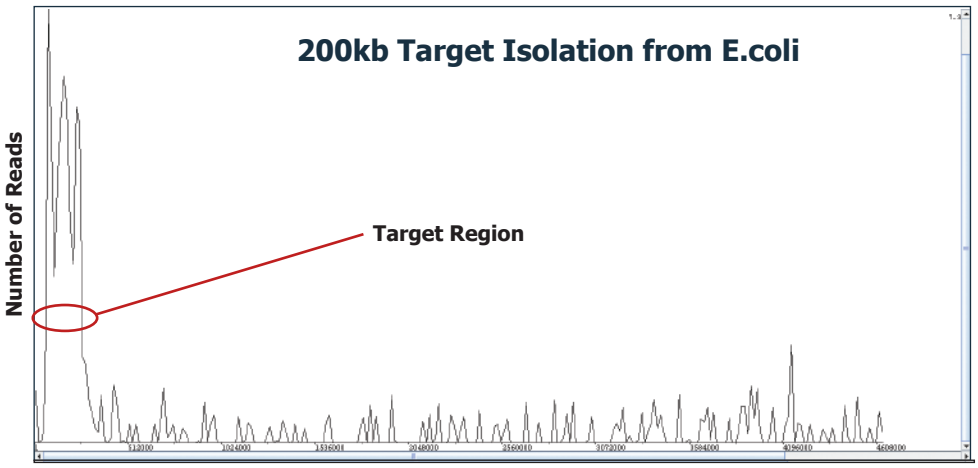
- Cancer Genomics
- Inheritable Disease
- Plant Genomics

Target Large Genomic Regions with Cas9

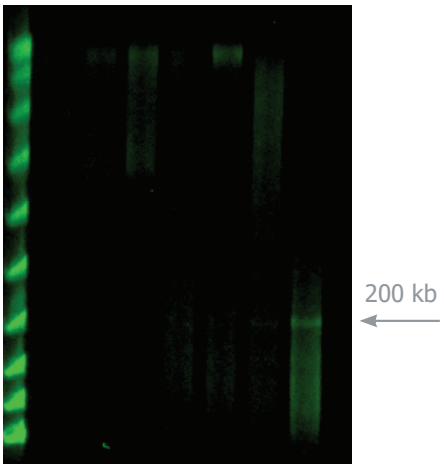
HLS-CATCH*: CRISPR/Cas9, *In Vitro*

You Supply the Guide RNAs, We Supply the Rest

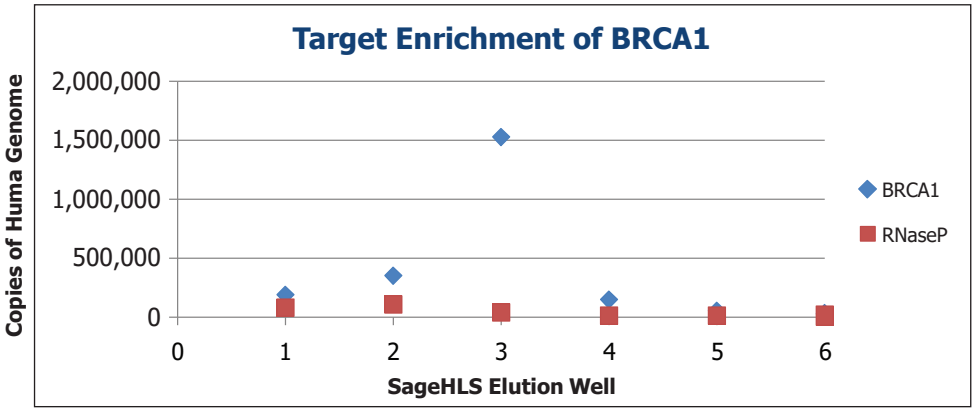
MinION Coverage Plot



Pulsed-field Gel Analysis



A 200 Kb region was isolated from the E. coli genome using HLS-CATCH. A spheroplast suspension was prepared in a SageHLS-compatible buffer using a Sage Science kit. The suspension was lysed under electrophoretic conditions, purifying the genomic DNA, and immobilizing it within the agarose on the sample well wall. The DNA was then treated with wild type spCas9 (New England Biolabs) that had been assembled with guide RNAs (IDT, Alt-R™) bordering a 198 Kb region of interest (4.2% of the genome). DNA released by the Cas9 digestion was electro-eluted with the SageHLS cassette and sequenced with an Oxford Nanopore MinION™ sequencer.



A pool of five effective gRNAs were used in an HLS-CATCH experiment to excise the BRCA1 fragment from 1.5e06 Raji cells (input gDNA content about 10µg). The elution products from each elution well were evaluated by qPCR (ABI Taqman® kits, RNaseP gene as control).

**Cas9-assisted targeting of chromosome segments Jiang et. al., 2015, Nature Communications, doi:10.1038/ncomm9101*

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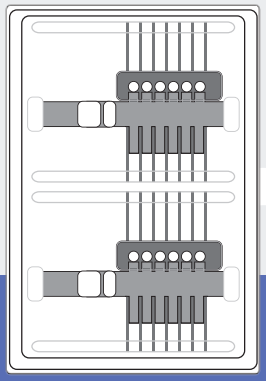
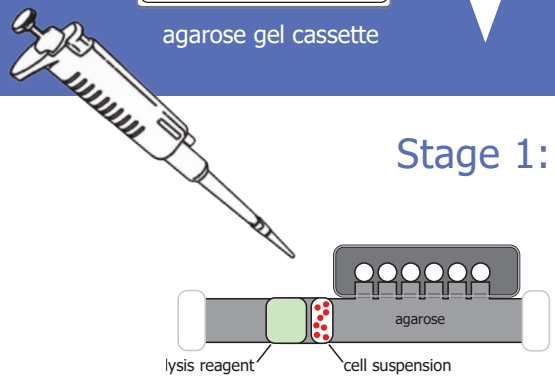
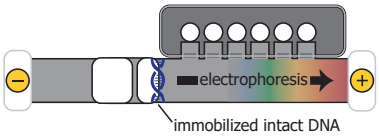


agarose gel cassette

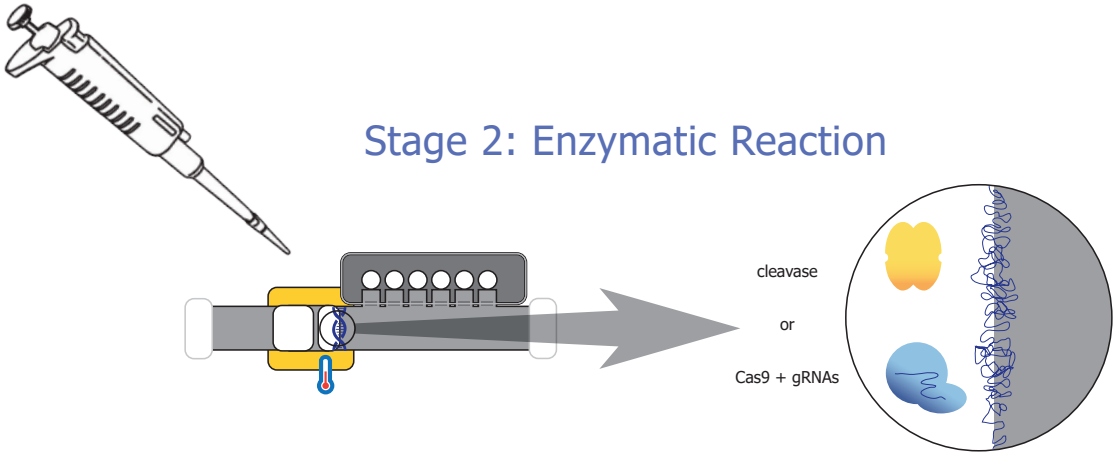
SageHLS Workflow

Stage 1: DNA Extraction

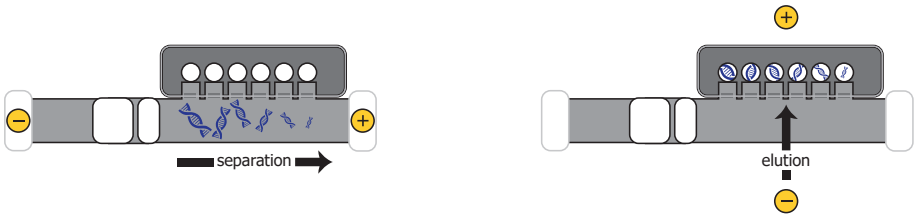




Stage 2: Enzymatic Reaction



Stage 3: DNA Size Selection



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