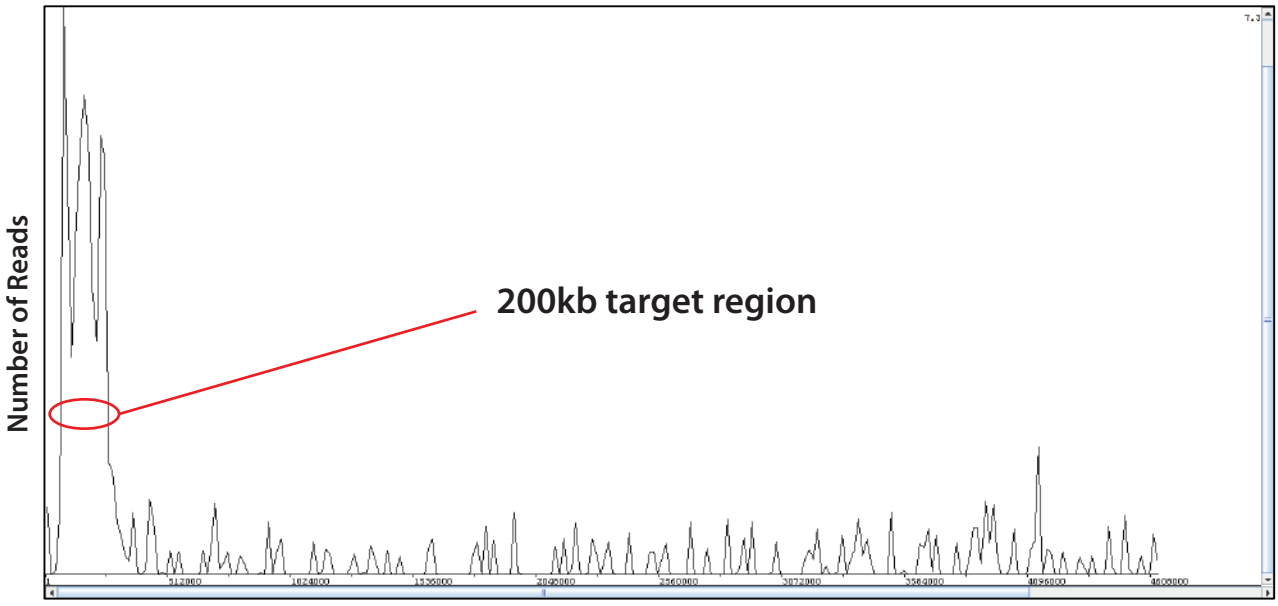
sageHLS™
HMW Library System

Extract.
React.
Select.

sage science

HLS-CATCH*: Purify genomic regions of interest using CRISPR/Cas9



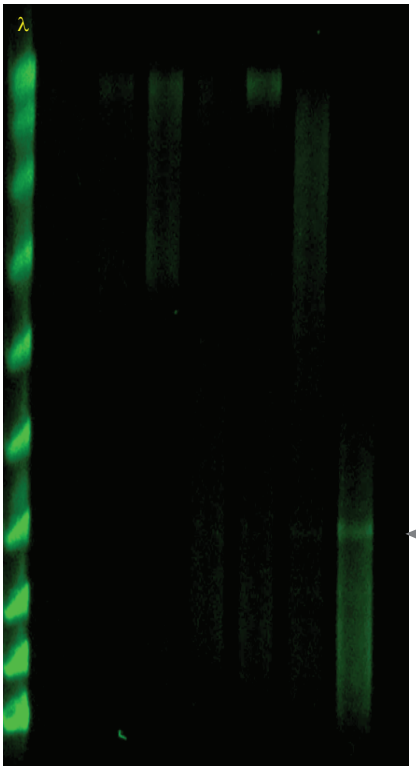
*Cas9-assisted targeting of chromosome segments
Jiang et. al., 2015, Nature Communications, doi:10.1038/ncomm9101

About SageHLS

The SageHLS instrument is a new automated platform from Sage Science designed to help scientists work with high molecular weight (HMW) DNA for applications ranging from long-read sequencing to optical mapping. The instrument uses electrophoresis to quiescently purify DNA from cell suspensions, causing intact DNA to become immobilized on an agarose gel surface. DNA is then re-mobilized through enzymatic cleaving, and collected in six size-fractions using automated preparative electrophoresis. The maximum fragment sizes that can be collected are 2 Mb.

CATCH with *E. coli*

The 200 kb region on the previous page was purified on the SageHLS platform. *E. coli* spheroplasts were lysed under electrophoretic conditions, extracting and immobilizing the genomic DNA. The DNA was then digested, in the cassette, with wild type spCas9 (New England Biolabs) and assembled with guide RNAs (IDT, Alt-R™) bordering a198 kb region of interest (4.2% of the genome). DNA released by the Cas9 digestion was electro-eluted with the SageHLS cassette and analyzed using Oxford Nanopore sequencing and pulsed-field gel electrophoresis.



A target region purified from *E. coli* spheroplasts using a CRISPR/Cas9 nuclease.

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