Random Shear BAC Library Services

Got Gaps?

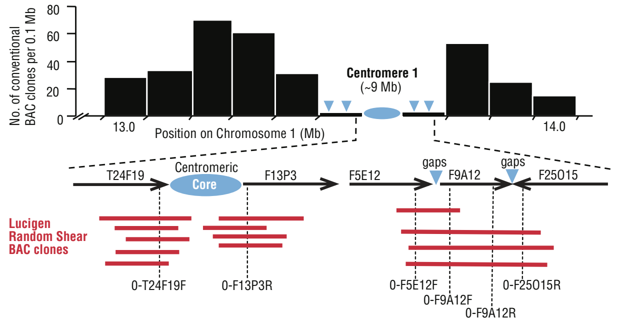
Eliminate gaps in genomic libraries with Lucigen's exclusive Random Shear BAC Library technical expertise.

Resulting in:

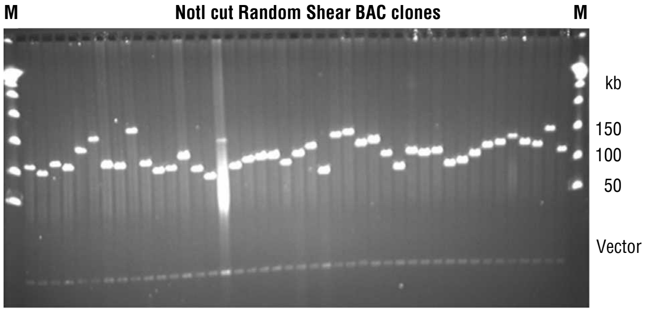
- **Complete genome sequence** with as low as 5x coverage
- **Elimination of restriction site bias** found in conventional libraries by utilizing random shearing of DNA into BAC-size fragments
- **Vast reduction of deleted and rearranged sequences** by cloning in our Transcription-Free BAC vectors
- **Greatly reduced finishing costs.**

Detailed information on the benefits of Random Shear BAC Libraries for genome projects is available on-line: **www.lucigen.com/BAC.pdf**

Closing centromeric gaps with a Random Shear BAC Library



An *Arabidopsis* Random Shear BAC Library (5X coverage) closed several existing centromeric gaps in the published "finished" physical and sequencing map (arrows, known sequences; bars, Random Shear clones).



Potato genomic DNA was randomly sheared, size-selected to >100 kb, and cloned into pSMART® BAC vector. DNA from minipreps was digested with NotI to excise inserts. The vector band is at 7 kb.

Contact Lucigen for a free quote on a Random Shear BAC Library.

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Jeremy Schmutz
Investigator

Greg Barsh, M.D., Ph.D.
Visiting Investigator

For descriptions of research areas see hudsonalpha.org/pages/sr-researchareas.html

Please send resume and cover letter to:
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Director of Research Affairs
HudsonAlpha Institute for Biotechnology
601 Genome Way
Huntsville, AL 35806
cgunter@hudsonalpha.org

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From spirit to physical design, the institute's primary facility embodies and nurtures the sharing of ideas and information. Researchers employed by the not-for-profit HudsonAlpha Institute reside in one wing of the 270,000 square-ft. facility, while a separate wing houses 12 for-profit businesses. The wings are physically bridged with walkways spanning a soaring atrium that features inviting common areas. Proximity to the University of Alabama in Huntsville, the University of Alabama at Birmingham, Auburn University and Vanderbilt University adds to a rich intellectual environment for collaboration, discovery and innovation.

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🅁 = Recombinant

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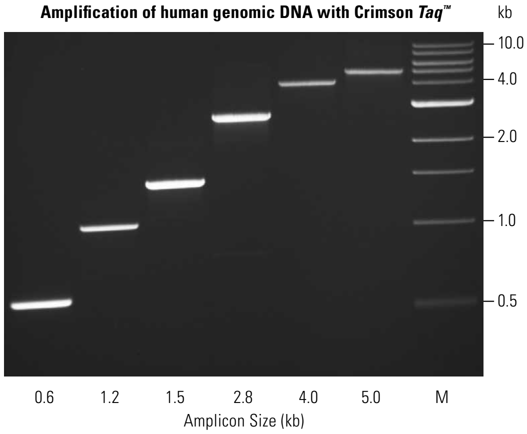

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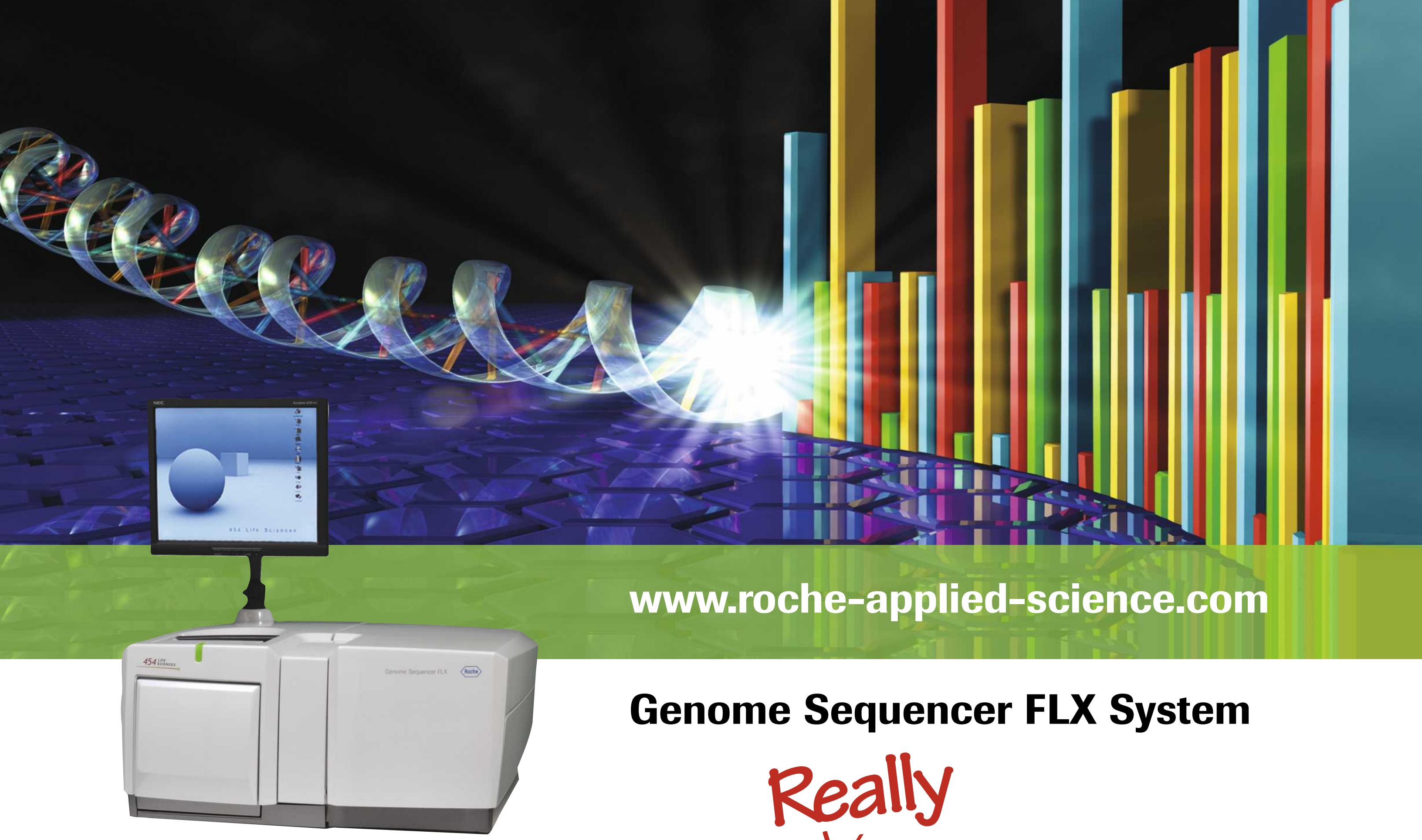

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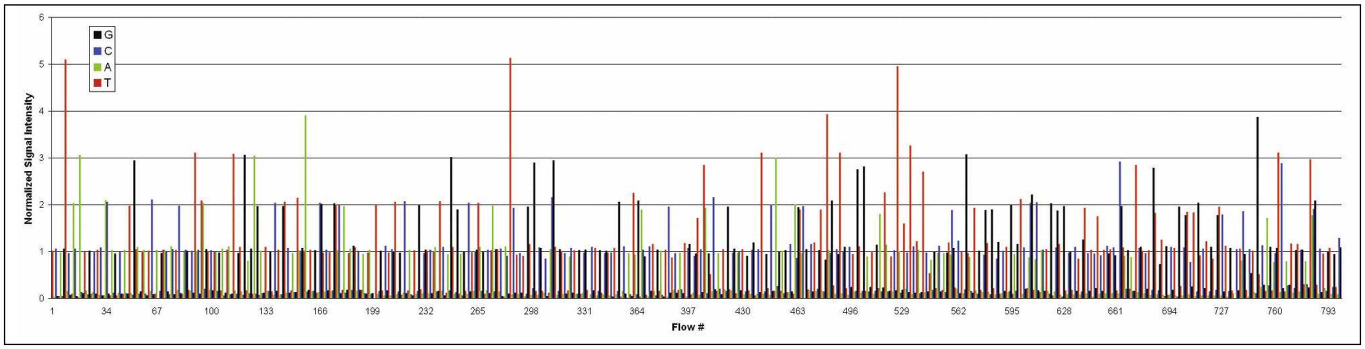

DNA Sequencing Flowgram: Each bar within the flowgram represents a discrete nucleotide (A, T, C, or G) and the height of the bar corresponds to the number of nucleotides detected. The flowgram above represents a 458-base-pair sequencing read from *E. coli* K-12.

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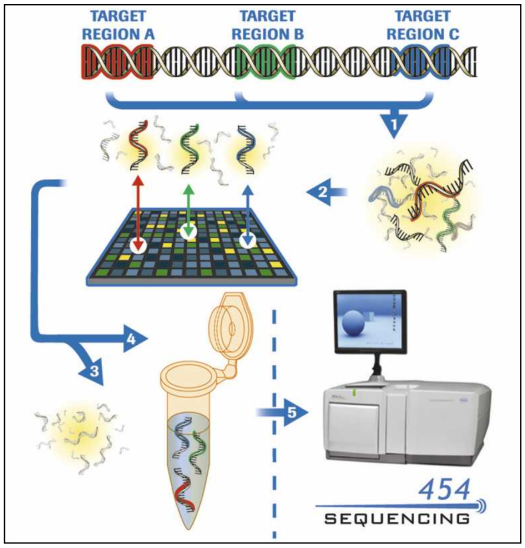

Figure 1: NimbleGen Sequence Capture Protocol
1. The genomic DNA sample is fragmented. 2. The sample is hybridized to a custom NimbleGen Sequence Capture array. 3. Unbound fragments are removed. 4. The target-enriched pool is eluted and amplified. 5. The enriched sample is ready for processing in the GS FLX sample processing workflow.

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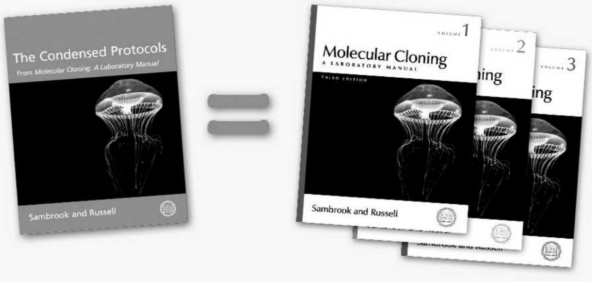

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