seqWell and Gencove partner to offer a low-pass whole genome sequencing end-to-end solution

Companies Bring Together plexWell™ Multiplexed Library Preparation Technology and Powerful Imputation Software to Accelerate Large-scale, Sequencing-based Genomic Projects

NEWS PROVIDED BY
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Jan 31, 2019, 11:31 ET

BEVERLY, Mass. and NEW YORK, Jan. 31, 2019 /PRNewswire/ -- seqWell and Gencove today announced a partnership to bring together seqWell's plexWell™ library preparation technology and Gencove's imputation and analysis software to provide genomic researchers a powerful and scalable end-to-end solution for low-pass whole genome sequencing and genotype imputation.

Gencove is the industry pioneer in low-pass sequencing technologies. This technology offers a high-throughput, cost-efficient and accurate solution for large-scale genomic projects that historically have relied on genotyping microarrays. Gencove's cloud-based imputation software calls variants with high accuracy across the whole genome resulting in more data, greater statistical power, and enhanced variant discovery capabilities than genotyping arrays.

The adoption of this approach has been driven partly by lower costs of raw sequencing data, but also requires robust, reliable and scalable methods of multiplexed library preparation. plexWell technology from seqWell overcomes challenges of library preparation workflow scalability through massively paralleled multiplexing of samples. Well-balanced libraries containing hundreds to thousands of samples can be prepared and sequenced in a single day using low-pass, next generation sequencing (NGS).

"Our experience with plexWell technology is that it makes library prep both more scalable and user-friendly," according to Joe Pickrell, Chief Executive Officer and co-founder of Gencove. "This partnership will enable anyone with an Illumina sequencer to efficiently replace genotyping arrays with low-pass whole genome sequencing across applications, including genomic selection, marker assisted selection, QTL mapping and genome-wide association studies."

"The combined throughput, quality and power of plexWell technology and Gencove software create a uniquely enabling, complete solution that allows researcher to harness the full potential of NGS for genotyping human, animal and plant genomes," says Joseph Mellor, Chief Executive Officer and Founder of seqWell, Inc. "We are excited about making cost-effective, large-scale, low-pass whole genome sequencing a reality for the genomics community"

About seqWell:

seqWell, Inc. (www.seqwell.com) is a global provider of innovative NGS library preparation products and solutions, based in Beverly, Massachusetts. The company's multiplexed library preparation technology, plexWell, vastly improves the ease and scale by which multiple samples can be prepared and for standard sequencing instruments. seqWell's mission is to develop and provide library preparation products and application workflows that redefine the standards for throughput, quality, and utility of any DNA sequencer.

About Gencove:

Gencove is a spin-out of the New York Genome Center dedicated to making genomic data more accessible and interpretable through the development of molecular and computational tools. Gencove's flagship product is its low-pass genome sequencing platform; the company

operates a laboratory in New York and offers both low-pass sequencing and analytics software as a service, with customers that include top academic institutions, biotechnology and pharmaceutical companies. More information is available at www.gencove.com.

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