

Automating Microbial Sequencing Applications

Cost-Effective Solutions for Microbiology



Beckman Coulter Genomics has been simplifying microbial sequencing applications for over 10 years. Using automated sample preparation including library construction, next generation sequencing technologies and automated annotation pipelines, timely and affordable solutions with unprecedented sensitivity and discriminative power are delivered.

Whether surveying the unique properties of a strain collection, engineering new strains, analyzing emerging pathogens, testing the stability of production strains or sampling the environment for novel microbes and genetic content, Beckman Coulter Genomics offers proven solutions that will enhance any research program. Services range from small pilot-scale analysis to whole genome sequencing including finishing and annotation.

Fully Automated Pipeline

Next generation sequencing technologies have enabled scientists to generate vastly increased data sets from their sequencing experiments. The increase in throughput, however, is supported by workflows that are relatively complicated and labor intensive and require significant hands-on time to prepare samples.

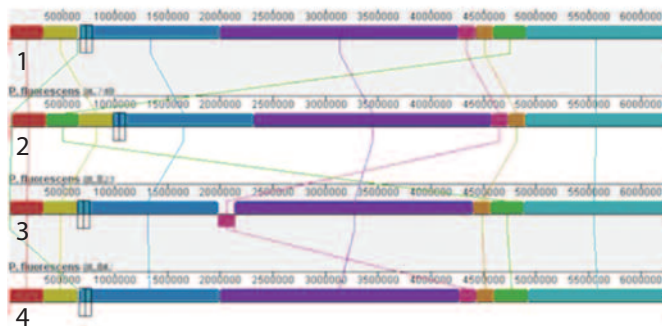
Beckman Coulter Genomics has implemented an automated workflow that uses Solid Phase Reversible Immobilization (SPRI) paramagnetic bead technology. Use of this technology combined with laboratory automation allows us to create four times as many fragment libraries as a manual process in the same time frame.

By combining the short run time of the 454 FLX instrument and proprietary automated data assembly, the annotation pipeline provides meaningful high quality data in a timely fashion.



Sequencing of Bacterial Strains with Existing Expected Sequence

For many bacterial species of interest, a type strain as well as other widely available laboratory strains have been sequenced. These reference strains are attractive genetic engineering subjects since derived strains can easily be compared at the genome level against the parental strain by using today's next generation sequencing techniques. Because of its high throughput and long read lengths, the GS-FLX Titanium technology provides the best price/performance ratio. With 400 Mb of nominal run yield, resequencing ten 4 Mb bacterial genomes whilst resolving most of the repeated elements with the average 450 bp read length can be achieved. Repeated elements are increasingly recognized as important genetic variability generators. Thanks to the direct parental relationship, the downstream processing maps quickly read to the reference genomes while documenting local differences and their eventual change to the protein encoding genes.



De novo sequencing of four 7 Mb Pseudomonas fluorescens strains using 3 kb paired end combined with fragment libraries. The paired end information has made it possible to document genome rearrangements between the parental strain (1) and the mutant strains. Genomes were annotated with a proprietary automated annotation pipeline.

Beckman Coulter Genomics successfully uses a combination of *de novo* and re-sequencing approaches on the 454 FLX platform as well as other next generation and Sanger techniques to achieve the most effective solution.

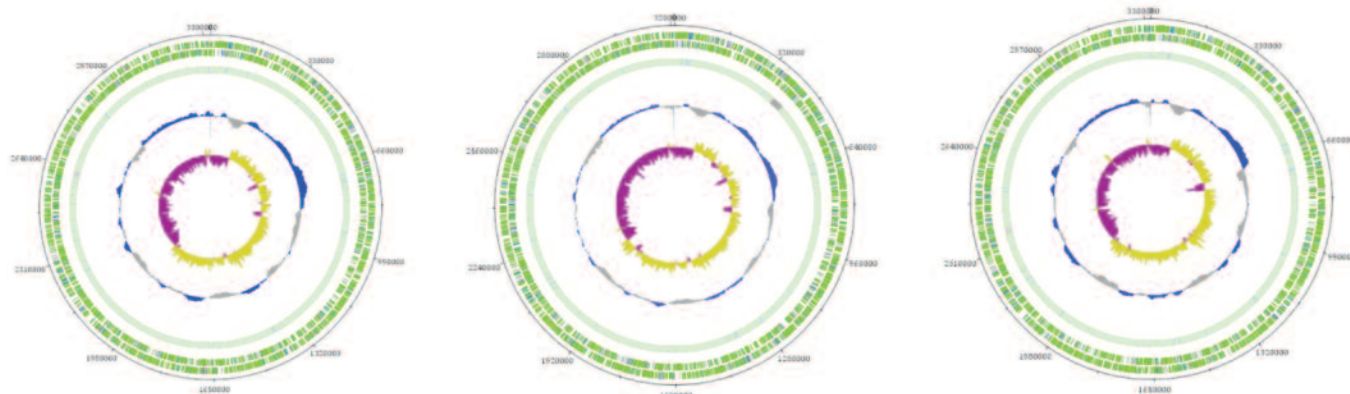
I need a sequencing provider to understand the science and who understands the science and can deliver.

We Get It.

Microbial *de novo* Sequencing

Certain species of interest call for a *de novo* sequencing approach because no parental strains are available or because acquisition of genetic material or rearrangements may have important consequences on the properties of the experimental strains. If the species has a relatively conserved overall genome organization, such as *S. aureus*, a cost-

effective fragment library approach may still be used. For genomes known for high plasticity such as the human pathogens *L. pneumophila* and *V. vulnificus* using a 3 kb mate-pair library instead is recommended. High GC organisms call for a combined fragment/mate-pair sequencing approach.



De novo sequencing of three strains of a 3 Mb human pathogen. There are no whole genome sequences available for this species. We have built 3 separate 3 kb mate-pair libraries. These were sequenced using a single GS-FLX Titanium run. Contig ordering and orientation was performed with Consed. Scaffold ordering and orientation was performed with Mauve using a genome available from another species belonging to the same genus. CDSs were predicted using the Prokov program, using a learning step. Annotations were obtained by BlastP against Uniprot. The image was obtained with the Artemis genome browser. Outer- to inner tracks show predicted genes on forward and reverse strands, BlastX annotations at the genome level, GC content and GC skew. The origin of replication is situated at 160 k bp.

Proven Expertise

Beckman Coulter Genomics has a proven services track record with over 10 years experience successfully sequencing viruses, bacteria and fungi for academic, commercial and government institutions as well as the food, chemical and pharmaceutical industries. By responding to a wide range of analysis needs in the field of Microbiology, Beckman Coulter Genomics provides landmark genomes, comparative genome analysis at the structural and SNP level, as well as markers and DNA arrays suitable for downstream typing. Additionally, routine analyses such as viral quasispecies sequencing and master cellbank survey sequencing address the need for recurring and reproducible DNA analysis. In-house studies range from small scale pilot analysis projects to whole genome sequencing of strain collections, providing automated annotation and optional finishing.

Collaborative Culture

Beckman Coulter Genomics' scientists have a strong culture of collaboration. By working together, they are able to figure out the optimal way to respond to the needs of the customer, taking into account cost and timing constraints. During project execution customers are always involved, with optional go/no-go points, conference calls and intermediate study reports. Final reports are comprised of material and method documentation and any data generated is transferred using the appropriate media and the confidentiality measures. At the completion of the project, to ensure that the customer fully understands the data, optional result presentations and training on the use of downstream analysis tools can be proposed.

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† The PCR process is covered by patents owned by Roche Molecular Systems, Inc., and F. Hoffman-La Roche, Ltd. Beckman Coulter, the stylized logo and SPRI are registered trademarks of Beckman Coulter, Inc.

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