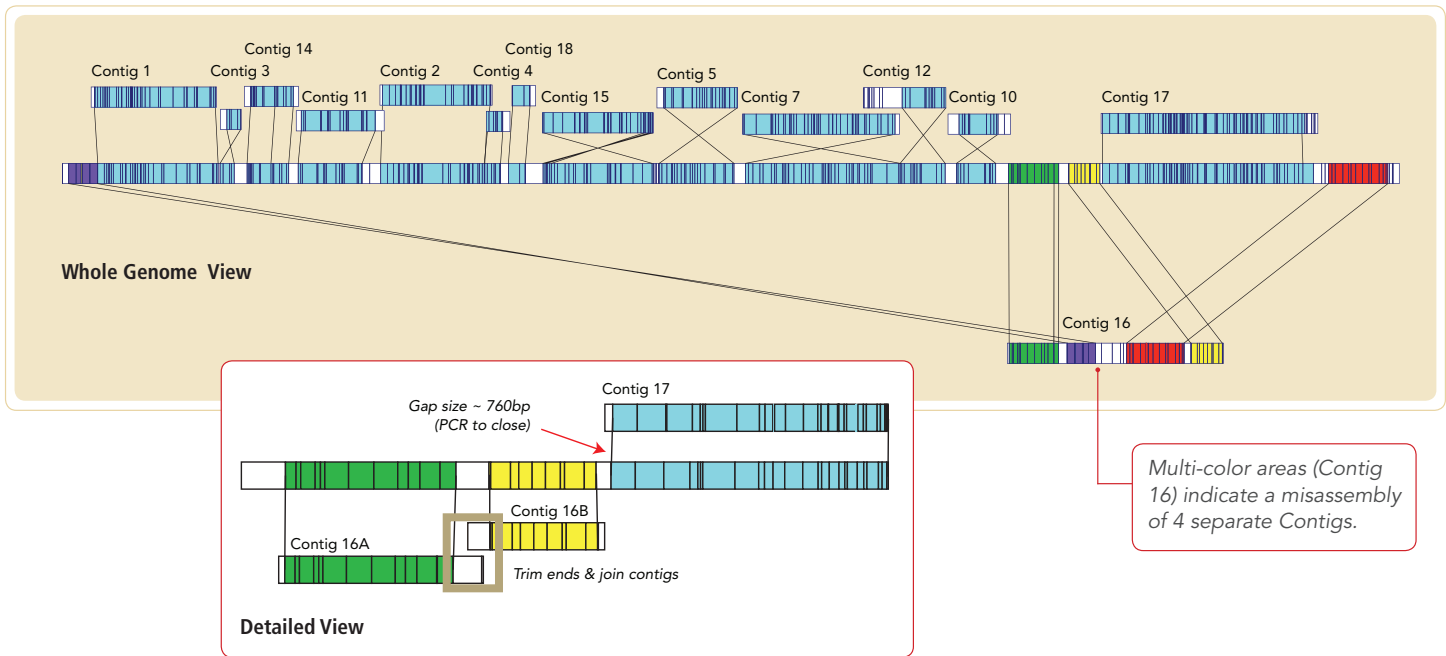


### Rapidly Orders Contigs Against a Whole Genome Optical Map Scaffold

The MapSolver™ software tool correctly and rapidly aligns unordered sequence contigs to matching regions on the Optical Map. Alignment lines are drawn between compared Optical Maps to show placement. Crossing alignment lines indicate reverse orientation. Multi-color areas indicate a misassembly. Gap size and location are visualized and enable further targeted analysis for whole genome closure.

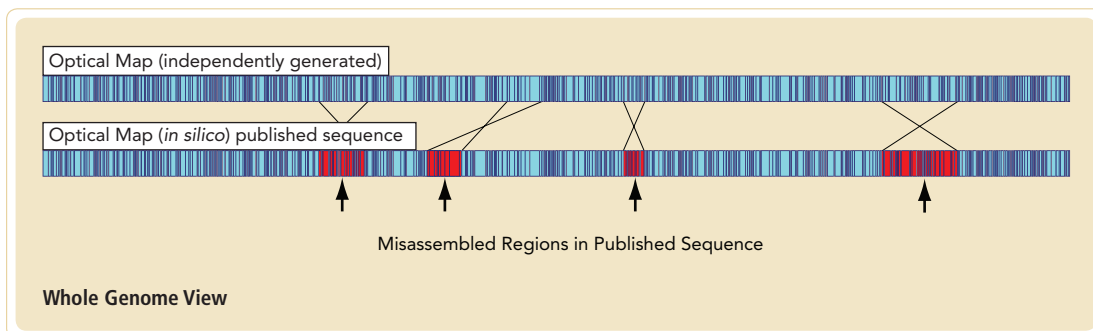
Contig 1, Contig 2, Contig 3, Contig 4, Contig 5, Contig 7, Contig 10, Contig 11, Contig 12, Contig 14, Contig 15, Contig 16, Contig 17, Contig 18

An unordered group of contigs from a sequencing project are converted to Optical Map data in preparation for alignment to the Optical Map scaffold below.



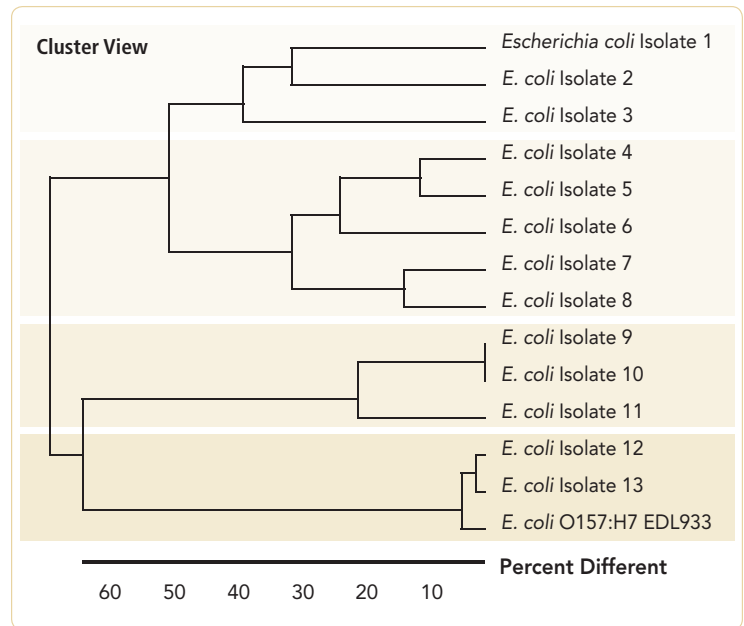
### Provides Independent Confirmation of Assembled Sequence

An *in silico* whole genome Optical Map generated from a published sequence assembly is compared to an independently generated Optical Map of the same isolate. Crossed-over alignment lines drawn between compared Optical Maps reveal multiple inverted misassemblies (red) in the published sequence.



## Identifies Best Sequencing Target

Optical Map similarity clustering describes the percent difference of the genomes between 13 *E. coli* isolates relative to the published sequence of *E. coli* O157. Optical Map similarity clustering can be used to identify the best sequencing targets. These sequencing targets can then be compared at the whole genome level to discover differences and similarities in the whole genome architecture.



## Capabilities and Advantages

- Preview genomic architecture to identify the best sequencing targets
- Rapidly order and align contigs correctly against an Optical Map scaffold
- Identify and correct misassemblies
- Resolve sequence challenges due to repetitive sequences
- Determine gap size and location
- Confirm the accuracy of assembly with a non-sequencing method before publishing
- Generate *in silico* Optical Maps from published sequences using the MapSolver software tool

## References

- Nagarajan, N., et al. "Scaffolding and validation of bacterial genome assemblies using optical restriction maps." *Bioinformatics*. 2008 Mar24 [Epub ahead of print].
- Latreille P, Norton S, Goldman BS, Henkhaus J, Miller N, Barbazuk B, Bode HB, Darby C, Du Z, Forst S, Gaudriault S, Goodner B, Goodrich-Blair H, Slater S. Optical mapping as a routine tool in bacterial genome sequencing. *BMC Genomics*. 2007 Sept 14;4(1):321.
- Nierman WC, et al. "Genomic sequence of the pathogenic and allergenic filamentous fungus *Aspergillus fumigatus*." *Nature*. 2005 Dec; 438: 1151-1156.
- Chen Q, Savarino S, Venkatesan M. Subtractive hybridization and optical mapping of the enterotoxigenic *Escherichia coli* H10407 chromosome: isolation of unique sequences and demonstration of significant similarity to the chromosome of *E. coli* K-12. *Microbiology* 152 (2006), 1041-1054.
- All bibliography articles may be found at [www.OpGen.com](http://www.OpGen.com), or by contacting OpGen, Inc.

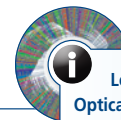


## MapIt™ Optical Mapping Services

Comparative Genomics • Sequence Assembly • Strain Typing

To place an Order, contact Customer Support, or find OpGen Global Distribution Partners please visit [www.OpGen.com](http://www.OpGen.com).

US toll free 888.856.2748 Corporate 301.869.9683 Fax 301.869.9684



Learn more about  
Optical Mapping Solutions.  
[www.OpGen.com](http://www.OpGen.com)