

What is Optical Mapping?

OpGen, Inc. has developed a unique and powerful OPTICAL MAPPING TECHNOLOGY that rapidly generates high-resolution, ordered, whole genome restriction maps from single DNA molecules. Optical Maps are generated *de novo*, independent of sequence information, and provide a comprehensive view of genomic architecture. An Optical Map is displayed in the pattern below where the vertical lines indicate the locations of restriction sites, and the distance between the lines represent the fragment size.



Whole Genome Restriction Map – vertical lines represent restriction sites

Step 1. Extract

High molecular weight (HMW) DNA is recovered from microbial cells.

- Microbial cells are embedded in low melting agarose plugs and treated with lysing solutions.
- Samples are washed thoroughly, melted at 70°C, and treated with β -agarase to release the HMW DNA.
- Sample prep procedure varies with the specific microbial sample.

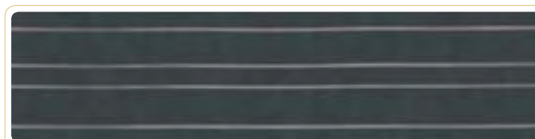


E. coli microbial cells

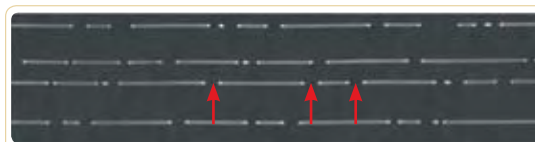
Step 2. Capture & Digest

Genomic DNA is captured and immobilized as single molecules on a charged optical substrate, then digested with a restriction endonuclease.

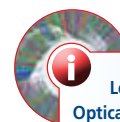
- Prepared HMW DNA is loaded into the channels of a microfluidics Optical Chip device.
- Genomic DNA is captured in parallel arrays as long, single DNA molecules. Immobilized molecules are retained electrostatically.
- Genomic DNA is interrogated with a restriction endonuclease. The restriction fragment order is maintained for each molecule.



Genomic DNA, captured as single DNA molecules produced by random breakage of intact chromosomes



Digestion reveals cleavage sites as "gaps"



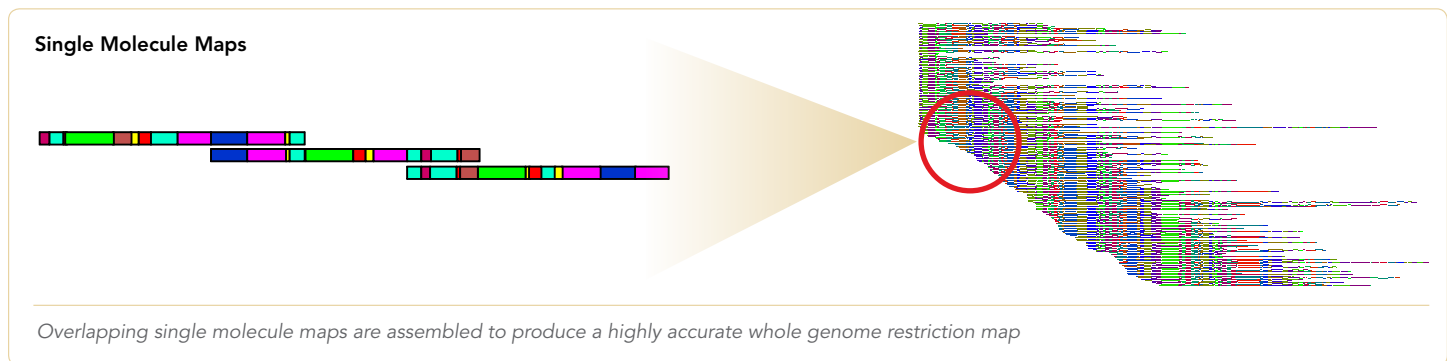
Step 3. Stain & Assemble

Genomic DNA is stained, scanned, measured, and assembled into a whole genome ordered restriction map.

- Digested genomic DNA is stained with a fluorescent dye and then positioned onto an automated fluorescent microscopy system for data acquisition.
- Image analysis software measures the size and order of restriction fragments for each molecule. This process converts optical data into digital data resulting in defined single molecule restriction maps.
- Collections of single molecule maps are then assembled by overlapping fragment patterns to produce a whole genome ordered restriction map, an Optical Map.
- **Single Molecule Maps** (below) are assembled to produce a high resolution consensus map covering the entire genome.



Fluorescent intensity is measured to determine fragment sizes while fragment order is maintained

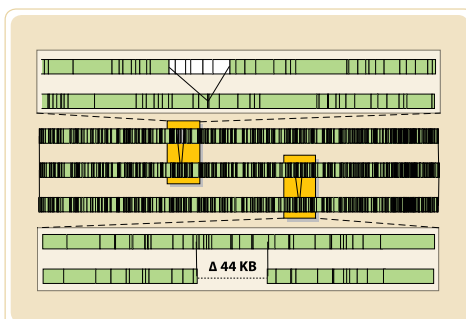


Overlapping single molecule maps are assembled to produce a highly accurate whole genome restriction map

Step 4. Analyze

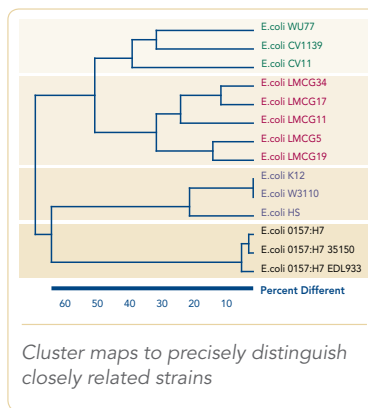
Using MapSolver Optical Map Analysis Tool, whole genome maps may be compared to discover genetic variation, to perform high resolution epidemiology, or to accelerate whole genome sequencing finishing.

Comparative Genomics



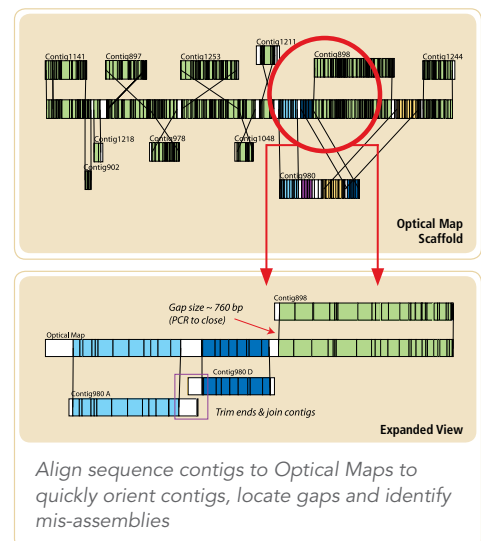
Directly compare maps to discover novel differences other technologies miss: insertions, deletions, and other genetic elements

Strain Typing



Cluster maps to precisely distinguish closely related strains

Sequence Finishing



Align sequence contigs to Optical Maps to quickly orient contigs, locate gaps and identify mis-assemblies



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