High Resolution Strain Characterization Using Whole Genome Optical Mapping

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The Optical Mapping Technology developed by OpGen, Inc. USA is unique and powerful, which 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. Optical Mapping is used:

For analyzing and comparing genomes from different strains to better understand gene function and relatedness. Find insertions, deletions, and intragenomic reshuffling of segments of genomic sequences such as inversions, transpositions, duplications and rearrangements. Identify and track mobile genetic elements like phage and transposons.

For accelerating sequence closure by aligning sequence contigs to an Optical Map scaffold to rapidly order and orientate sequences. Misassemblies can be identified, corrected and orientated properly to rapidly locate and close gaps. Complementary to sequencing technologies, Optical Mapping is used to survey genomic architecture prior to sequencing, thereby reducing the number sequence runs required for whole genome analysis

For strain characterizing and monitoring strain stability, determining genetic relatedness between multiple microbial isolates, and differentiating and visualizing genomic differences between the strains. Optical mapping tracks and links outbreak or potential contamination strains to the responsible source.