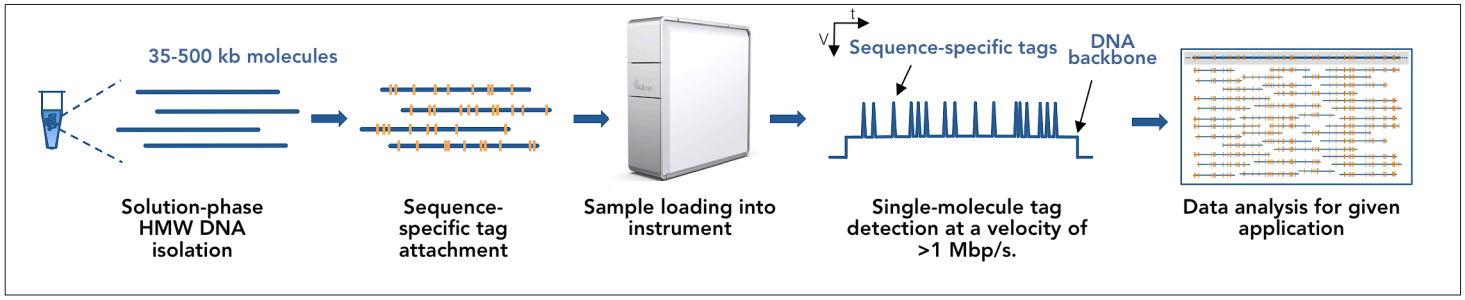
Whole Genome Mapping Using Electronic Detection

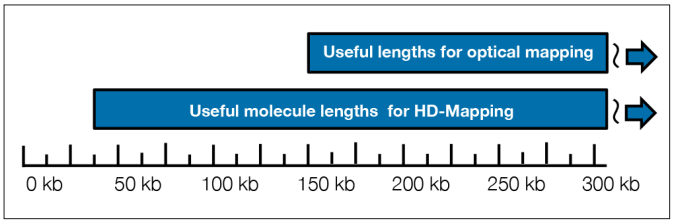
Whole Genome Mapping…Now in High Definition

Why HD-Mapping

Nabsys has developed its HD-Mapping™ platform to construct whole genome maps to provide routine, accurate, cost-effective analysis of genomic structural information. Nabsys employs electronic detection to accomplish higher resolution and accuracy than is possible with optical detection. These features result in higher information content per single-molecule read and the ability to construct high density maps with long-range information that can be used in combination with next-generation sequencing data.

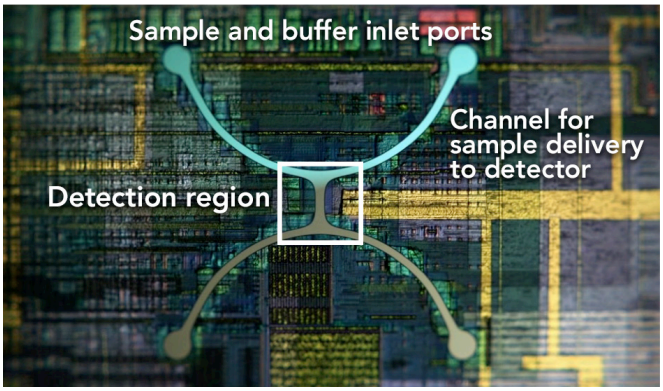


Step 1: Sample Preparation



In order to construct whole genome maps, high molecular weight DNA is isolated using a kit-based DNA isolation protocol. An advantage of the high information content attainable by HD-Mapping is a reduction in the required length of DNA for unique placement of single-molecule reads in a genome in comparison to optical methods. Following isolation, DNA is nicked in a sequence-specific manner and a proprietary marker is attached to the DNA at each nick site to serve as a tag. The tagged DNA is coated with a protein that increases both the persistence length of the molecules and the signal intensity in the detector. DNA isolation and sample prep protocols are straightforward and require minimal hands-on time.

Step 2: Electronic Detection

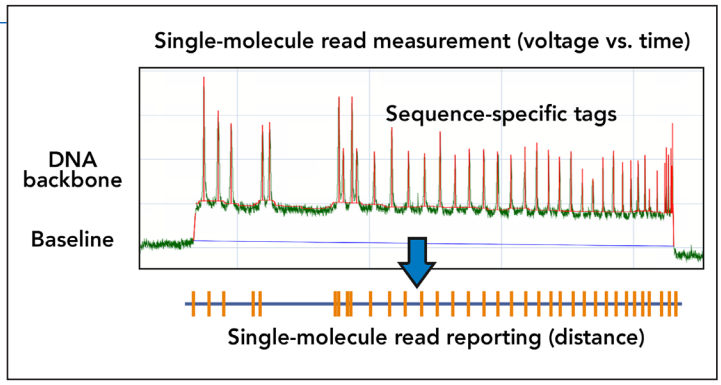


The semiconductor-based nanodetector chip is placed in the instrument and samples are introduced by pipette. Molecules are delivered to the detector at a velocity of 1Mb/s with a combination of electrophoresis and pressure driven flow. System operation including running the sample, detection, and resolution of clogs and cleaning of the chip post-run is completely automated enabling unattended data collection. Detectors are fabricated at wafer-scale at semiconductor foundries and the area on a single chip can accommodate thousands of detectors, enabling nearly unlimited scalability.

Continued (Step 3 and Step 4) >>

Step 3: Data Processing

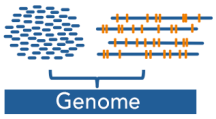
As single molecules pass through the detector, the presence of the DNA backbone and the attached tags are sensed as changes in the resistance of the detector. The resulting data indicate the time between tagged sites on each DNA backbone. The temporal events are converted to distance-based events where the distance between tags is reported in base-pairs. Signal processing of data is completed on-the-fly during data collection with minimal data storage required.



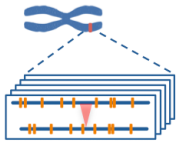
Step 4: Software Analysis and Applications

HD mapping supports a wide variety of genomics applications and software tools tailored for each application are provided. Comparative analysis software enables users to rapidly compare assembled HD maps to ongoing sequence assembly efforts.

***De Novo* Map Assembly**

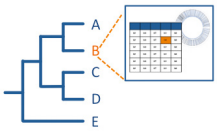


Hybrid Assembly

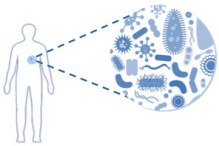


Variant Verification

SV Discovery



Strain Identification



Metagenomics

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