DNA Nanoball Sequencing

Workflow:

1. Isolate DNA

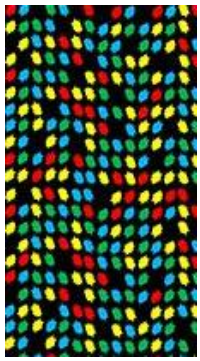
2. Fragment DNA (400-500 bp)

3. Attach adapters & circularize fragments

An iteration of the sequencing-by-ligation next-generation approach, developed by **Complete Genomics** as a human genome sequencing service.

Pros
- *Highly accurate*
- *Low cost*- can generate ~45-87 fold coverage at a consumables cost of $4400/genome
- Nanoballs loaded in an organized array- *high # of reads per flow cell*

Cons
- Chemistry is complex and proprietary
- *Short reads* (35 base paired end)- complex data analysis, challenges with highly repetitive DNA
- Not optimized for a wide range of organisms

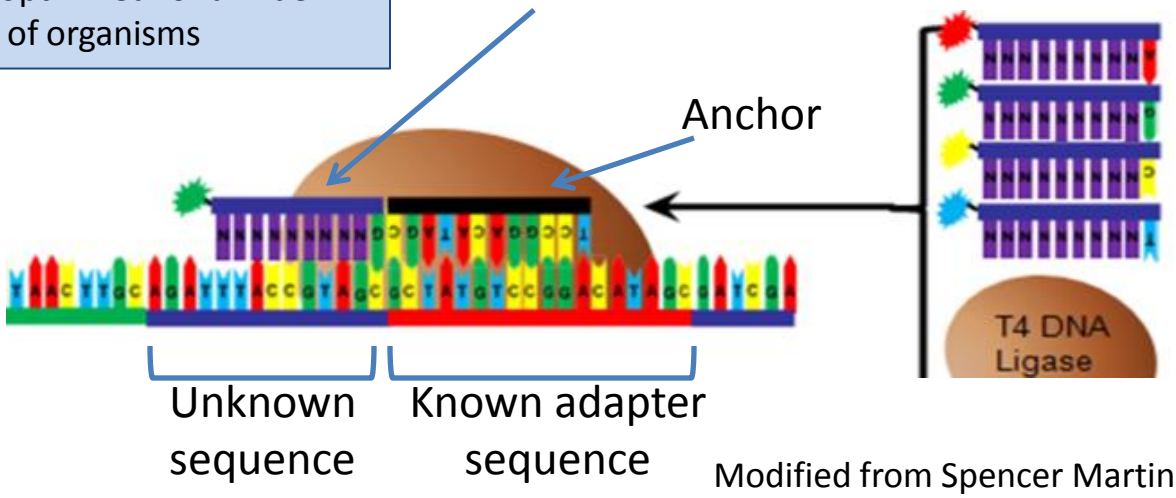


4. *Rolling circle replication*
- amplifies coils of ssDNA to form a chain of copies of the fragment
- the chain is compacted into a *DNA nanoball*- folds on itself due to hybridizing palindromic sequences in adapters

5. *Adsorption onto a silicon flow cell*- a highly ordered microarray

6. *Sequencing using cPAL technology*
-Combinatorial probe-anchor unchained ligation
- Flourescent detection of each hybridization & ligation reaction

Probe for position 1- Subsequent probes will interrogate other positions adjacent to the adapter



Modified from Spencer Martin