



# GemCode Library Services

## ACCESS LONG-RANGE DATA FROM SHORT-READ ILLUMINA SEQUENCING!!!

- **We start with very long gDNA, make GemCode Illumina Library and use the Illumina short read NGS sequencing (HiSeq2500) to get LONG RANGE DATA!**
- **Linked Reads enable** haplotyping, structural variation detection and >12 Mbp haplotype blocks!
- **Low gDNA inputs** allow accurate human chromosome phasing from ~1ng of gDNA.
- **Powerful Software Tools – Analysis Pipeline and Visualization Package** from 10X Genomics.



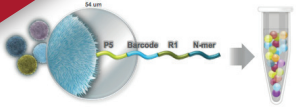
**Amplicon Express**  
makes very long gDNA for  
maximum results!



**DNA EXPERTS FOCUSING ON YOUR RESEARCH**

## HMW gDNA Extraction\*

\*Amplicon Express performing the gDNA extraction maximizes the length and usefulness of the Linked Reads data.



The GemCode Instrument uses a network of microfluidic channels and pressures to create >100,000 GEMs gel bead-containing emulsions in minutes!

## GemCode Library Prep

## Library Quantification

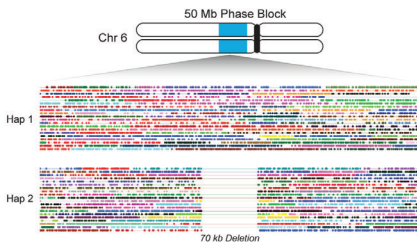
The DNA is delivered "ready to run" on any Illumina HiSeq2500.

## Illumina Sequencing

## Linked Reads Data Analysis

The GemCode Technology partions gDNA into more than 100,000 fractions, each containing about 0.3 percent of the genome, and has 750,000 different barcodes available.

## Linked Reads find the IMPORTANT mutation(s) in your sample!



A 50 Mb phase block from NA12878 within the q arm of Chr 6 is shown.

Phased Linked-Reads from within the phase block are shown. Haplotype 2 contains a 70 kb deletion as seen by the haplotype-specific loss of coverage.



**GemCodes technology is  
now compatible with  
Polyploid Genomes!!!!**

For orders and enquiries, please contact us:

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