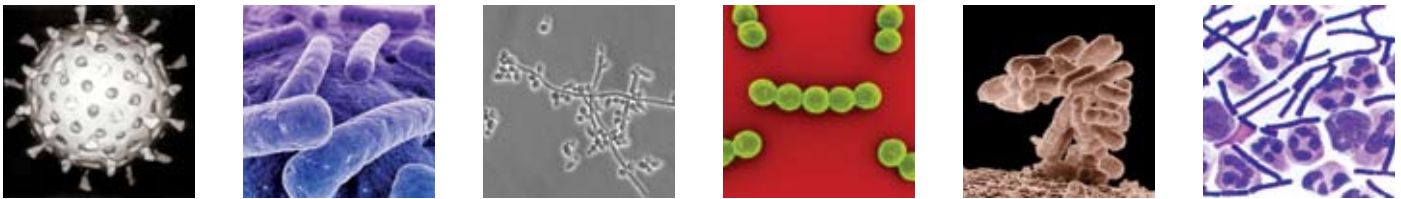


De Novo Sequencing of Small Genomes

Near finished quality assemblies from a single sequencing run



Take your bacterial, fungal, viral and other small genome *de novo* sequencing projects to new lengths with the GS FLX Titanium Series. Combine 400-500 base shotgun and multi-span paired end reads (3 Kb, 8 Kb, 20 Kb) with advanced assembly tools to rapidly generate high quality draft assemblies.

You can achieve...

Multiple High Quality Draft Genome Assemblies of...
 One Large Scaffold per Chromosome *from just...*
 One Sequencing Run *in as little as...*
 One Week.

Faster, Easier, More Complete *de novo* sequencing and high quality assembly.

- **One genome → One scaffold:** Generate near finished quality assemblies of multiple small genomes in a single 10-hour sequencing run.
- **Streamlined *de novo* sequencing processes:** Combine multiple shotgun and paired end libraries in the same run for faster time to results.
- **Reduce project costs:** Trim overall time and labor with more efficient sequencing processes and included suite of assembly and mapping software.

Microbial Genome Assembly				
Organism	<i>S. pneumoniae</i>	<i>E. coli</i>	<i>T. thermophilus</i>	<i>C. jejuni</i>
Number of Chromosomes	1	1	2	1
Large Scaffolds	1	1	2	1
Genome Size	2.2 Mb	4.6 Mb	2.1 Mb	1.6 Mb
N50 Scaffold Size	2.2 Mb	4.6 Mb	1.9 Mb	1.6 Mb
N50 Contig Size	26.1 Kb	57.1 Kb	10.5 Kb	153.8 Kb
Genome Coverage	99.6%	100%	100%	99.3%
Oversampling	25x	15x	33x	33x
Number of Runs	¼	¼	¼	¼

▲ **Table 1: Four microbial genomes. One run. One week.** The assemblies above were generated using one 8 Kb library per genome.

Fungal & Other Small Genome Assembly	
Organism	<i>S. cerevisiae</i>
Number of Chromosomes	17
Large Scaffolds	17
Genome Size	12.1 Mb
N50 Scaffold Size	79 - 1,523 Kb
Chromosome Size	86 - 1,532 Kb
N50 Contig Size	53.1 Kb
Genome Coverage	99.5%
Oversampling	23x
Number of Runs	1

◀ **Table 2: One fungal genome. One run.** This assembly was generated using one of each 3 Kb, 8 Kb and 20 Kb paired end libraries and one shotgun library, all sequenced simultaneously in a single run.

Complete Coverage. Longest Contigs. Rapid Results.

GS FLX Titanium Series Multi Span Paired End Library Adaptors

Paired end reads (also known as “mate pair” reads) supplement shotgun reads to significantly improve *de novo* assemblies by completely or partially spanning highly repetitive genomic regions.

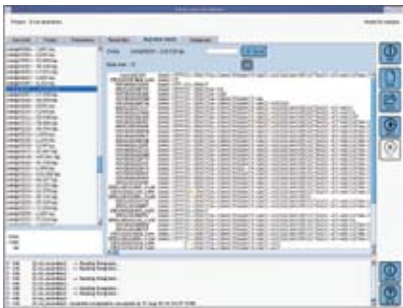
Paired end reads aid in:

- Ordering contigs into large scaffolds
- Determining the sequence within larger repeat regions
- Identifying structural variations
- Providing the complete genomic landscape, including gene order and operons



Beyond Data to Insight

Easy-to-use software for quick and affordable assemblies



- The GS *De Novo* Assembler is a straightforward tool for automated *de novo* assembly of small to mid-size genomes (<1 Gb).
- Biologist or Bioinformatician - Benefit from an easy-to-use graphical user interface, as well as a powerful, scriptable command line interface.
- Modest system and expertise requirements eliminate the need for a high performance computing infrastructure and a dedicated bioinformatics team to produce results.
- Generate assemblies from a variety of shotgun and paired end reads - GS FLX Titanium series, GS FLX Standard series, GS 20 System, and Sanger reads.

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Roche Applied Science
68298 Mannheim
Germany

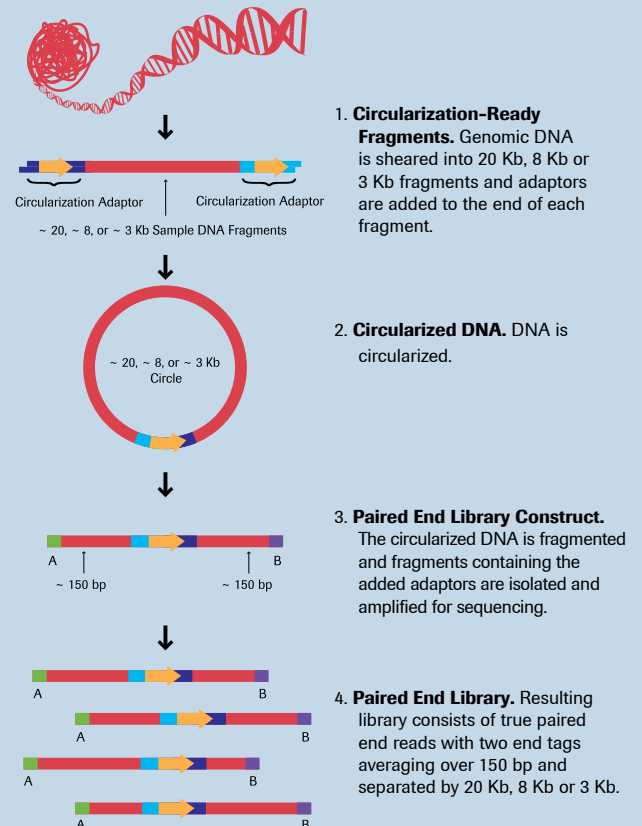
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The system's unique features include:

- **Long reads:** Extra long 400-500 base pair shotgun reads can sequence through many genomic repeat features directly without the need for paired ends.
- **Long tags:** Paired end reads with long tags, averaging 150+ bases, can be aligned uniquely with higher confidence.
- **Long spans:** Long 20 Kb paired end reads can span most repeat regions in nearly any size genome.
- **Span variety:** The broad selection of insert lengths enables optimization of project design according to the unique characteristics of any genome for the best possible results.

The GS FLX Titanium Series Paired End Protocol



Selected References:

Zehr JP et al. (2008) Globally distributed uncultivated oceanic N₂-fixing cyanobacteria lack oxygenic photosystem II. *Science* 322(5904):1110-2.

Tauch A et al. (2008) Ultrafast pyrosequencing of *Corynebacterium kropenstedtii* DSM44385 revealed insights into the physiology of a lipophilic corynebacterium that lacks mycolic acids. *J Biotechnol.* 136(1-2):22-30.

Review the complete list of publications at www.454.com.