



# NxSeq<sup>®</sup> Long Mate Pair Library Kit

Close your microbial genome with two libraries

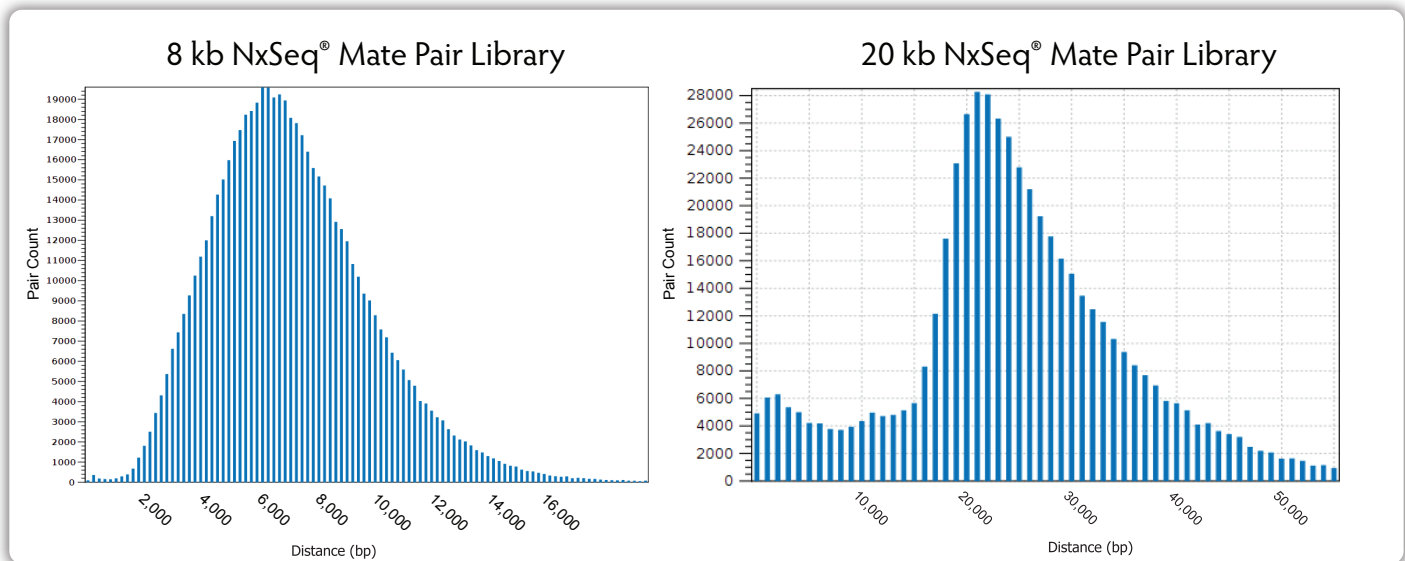
- Flexible insert sizes: gel-based 20 kb and gel-free < 8 kb
- Enable microbial genome closure using 20 kb protocol with your existing Illumina sequencer
- Ideal for NGS de novo genome assembly, closure and finishing, chromosomal rearrangement detection, haplotyping, and BAC sequencing
- Increased N50's and larger scaffolds from your assembly in Next Gen Sequencing

**CLOSE & FINISH  
Microbial Genomes  
with Two Libraries!**

See reverse for example genomes.

## The Longest Insert Mate Pair Libraries Available

The NxSeq Long Mate Pair Library Kit can accommodate a wide range of insert sizes to fit your needs. Bead-based, gel-free fragment sizing protocols enable libraries up to 8 kb insert size, while gel-based sizing protocols will accommodate 10-20 kb insert size. The result is tight sizing of your mate pairs, enabling accurate and complete bioinformatic assembly.



An 8 kb NxSeq Long Mate Pair library was constructed using bead-based, gel-free methods, and a 20 kb mate pair library was constructed using gel isolation. Resulting true mate pairs were mapped against the respective reference genome to determine the resulting mate pair distances.



FM 598408

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**Lucigen<sup>®</sup>**  
Simplifying Genomics



# Close your genome with Lucigen Mate Pair Libraries

## De Novo Assembly and Closing of Four Microbial Genomes Using 10-20 kb Mate Pair Library + Fragment Library

Genome	Size	GC Content	Scaffolds	Gaps
<i>Thermus aquaticus</i>	2.3 Mb	68%	1	0
<i>Staphylococcus aureus</i>	2.8 Mb	32%	1	0
<i>Streptomyces spp.</i>	8.6 Mb	71%	1	0
<i>Nonomurea spp.</i>	10.3 Mb	70%	1	3

A fragment library (paired end, mean insert size ~500 bases) and a 10-20 kb mate pair library were constructed for four bacterial strains. Assembly of the first two (*T. aquaticus* and *S. aureus*) was performed with CLC Genomics Workbench 7.5, and the second two (*Streptomyces* and *Nonomurea*) were assembled with SPAdes 3.5.0 (spades.bioinf.spbau.ru).

In all four cases, the assembler was able to create single scaffolds, and the remaining gaps were readily filled and closed. Completely finished genomes were generated within 1-4 days.

Products	Size	Cat. No.
NxSeq® Long Mate Pair Library Kit	10 libraries	13000-1
NxSeq® Long Mate Pair Library Kit and Index Kit	10 libraries + 12 indices (5 rxns each)	13100-1
NxSeq® Long Mate Pair Index Kit	12 indices (5 rxns each)	13200-1
NxSeq® Long Mate Pair Library Kit, Box 1	10 rxns	13300-1
NxSeq® Long Mate Pair Library Kit, Box 2	10 rxns	13400-1

### ORDER INFORMATION

For a full list of reagents and components included in this product, refer to the user manual. The NxSeq Long Mate Pair Library kit includes two boxes, each of which can be ordered separately. Box 1 contains all reagents necessary for end repair and tailing of fragmented DNA, ligase, and an internal adapter sequence. Box 2 contains reagents for ligation to the coupler and Junction Code™ sequence, exonuclease digestion, biotin capture, and amplification.

The NxSeq Long Mate Pair Library Index kit contains 5 reactions each of 12 separate index primer sets, for a total of 60 index reactions. The kit may be ordered in combination with the library kit or as a separate item.

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