



NxSeq[®] 40 kb Mate-Pair Cloning Kit

True long-span, mate-pair libraries for Next Gen Sequencing!

- Complete your genome with 40kb, long-span, mate-pair NGS libraries
- Skip the adapters: pNGS vector contains built-in Illumina, Roche 454, or Ion Torrent* primer sites
- Ideal for de novo, whole genome sequencing projects

The pNGS FOS vector (right, Fig. 1) represents the combination of Lucigen's patented transcription free vectors with a first-of-its-kind feature: built-in Roche 454 and Illumina primer binding sites – no adapter ligation necessary! Using a 40 kb paired-end library, you can now build the critical scaffold that enables a truly complete genome assembly. Get exceptionally stable clones due to our transcription-free vector, reduce time and uncertainty by skipping adapter ligation, and get more sequence coverage with less bias than ever before.

Unique Workflow:

Let Lucigen make the process of generating long-span, mate-pair libraries easier than ever before.

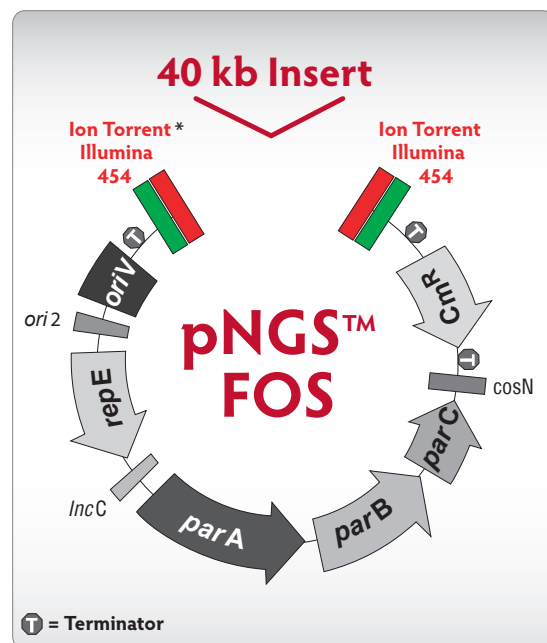
- Shear and size select for 40 kb fragments, ligate to the pNGS FOS vector and perform lambda packaging.
- Cut with a 4bp restriction enzyme (RsaI, CviQI, BfaI, or FspBI).
- Reconstitute the restriction site to create a known mate-pair junction.
- Amplify with either Roche 454 or Illumina primers and proceed to sequencing (next page, Fig. 2).

Products	Size	Cat. No.	Price
NxSeq [™] 40kb Mate-Pair Cloning Kit	5 rxns	42028-1	\$499
	10 rxns	42028-2	\$949
	20 rxns	42028-3	\$1799

ORDER INFORMATION

Each NxSeq[®] 40 kb Mate-Pair Cloning Kit contains: pre-cut, dephosphorylated pNGS FOS vector, CloneSmart[®] DNA Ligase, CloneDirect[™] 10X Ligation Buffer (includes ATP), DNATerminator End Repair Enzyme Mix and End Repair Buffer, Replicator FOS strain (glycerol stock), 20% Maltose Solution, 1M MgSO₄, SM Buffer, Arabinose Induction Solution, Sequencing Primers, and complete protocols

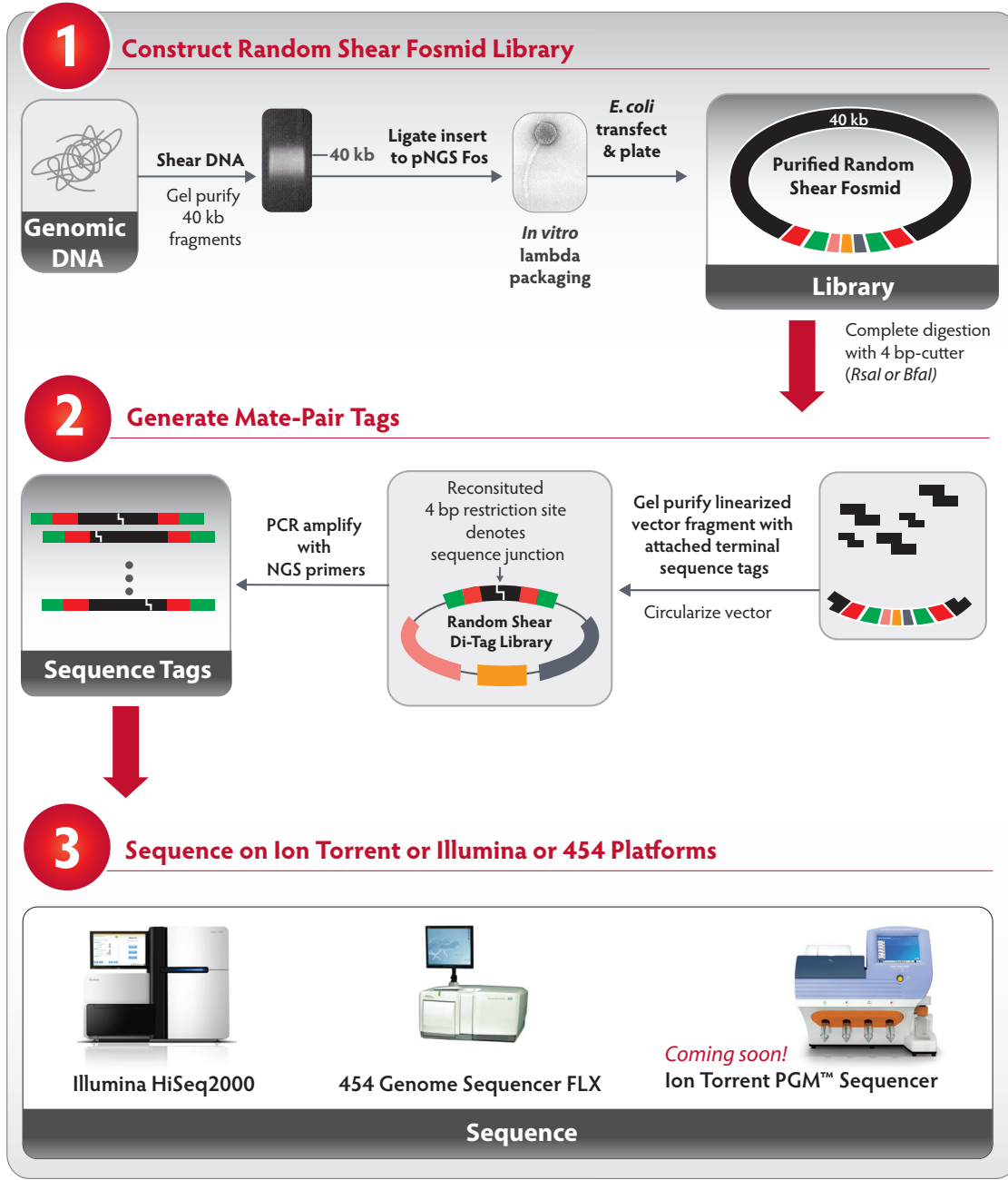
Replicator FOS Strain: F⁻ mcrA Δ(mrr-hsdRMS-mcrBC) endA1 recA1 Φ80dlacZΔM15 ΔlacX74 araΔ139 Δara,leu)7697 galU galK rpsL nupG (attL araC-PBAD-trfA250 bla attR) λ-.



*Ion Torrent Compatible version available late 2012. Patent Pending.



NxSeq 40 kb Mate-Pair Sequencing



High Efficiency 40 kb Paired-end Sequencing for Next Generation Platforms

To demonstrate the efficiency of cloning and sequencing using the pNGS FOS vector, large-scale, long-span, mate-pair sequencing of a human cell line (GM15510, Coriell) using Illumina technology resulted in 64% of filtered reads accurately mapping to the genome (Table 1). This represents many-fold higher efficiency than existing systems and will allow the accurate assembly of genomes for the first time using next gen sequencing platforms.

Table 1. Summary of Illumina long-span, mate-pair sequencing of a human cell line

Stage	No. of Reads	%
Pipeline	8,683,854	
Filtered reads	6,506,126	
Reads mapped	5,173,778	79.2
Reads with pair-sequences	4,685,996	90.6
Long-span, mate pairs*	3,018,576	64.4

*Mapped on same chromosome, ~40 kb apart, uniquely mapped.

