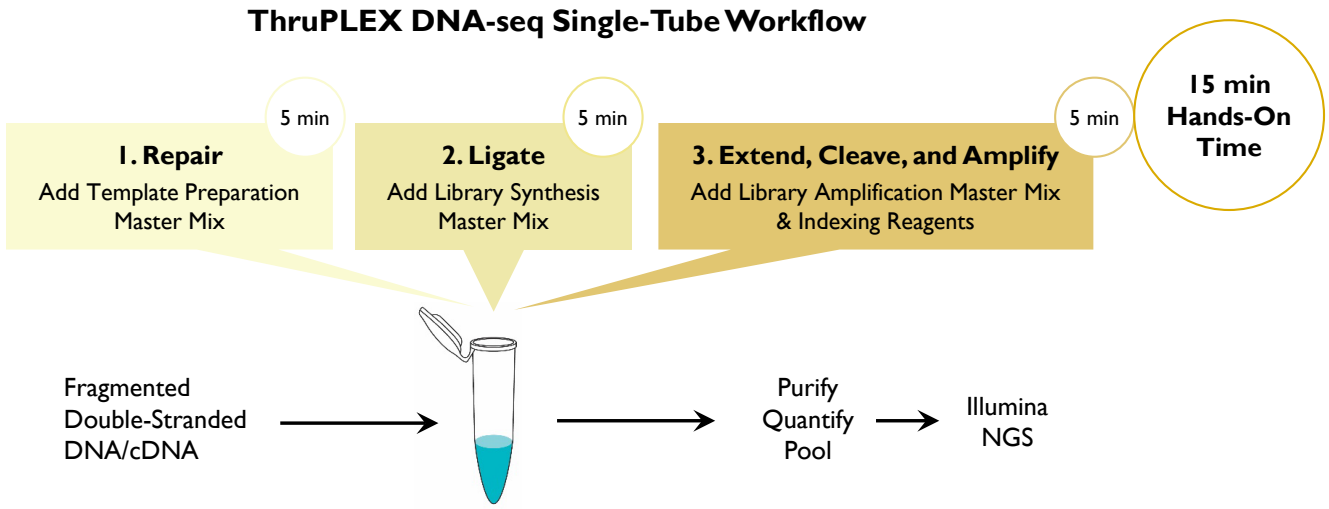
ThruPLEX® DNA-seq Kit

High Performance Libraries for Illumina® NGS Platforms for General Purpose Use

- High performance from lowest input – 50 pg to 50 ng
- Fast and simple workflow – 3 steps in a single tube or well in about 2 hours, no transfers necessary
- Compatible with major target enrichment platforms – Agilent SureSelect®, Roche NimbleGen® SeqCap® EZ, and IDT xGen® Lockdown® probes

ThruPLEX DNA-seq builds on the innovative ThruPLEX chemistry to generate DNA libraries with expanded multiplexing capability and higher diversity with lower duplication rates. Kits are available with up to 96 dual or single read Illumina-compatible indexes in either a pre-dispensed barcoded microplate or tubes. Starting with a low input amount, ThruPLEX DNA-seq produces uniform GC coverage and improves molecular complexity yielding reproducible sequencing results. ThruPLEX DNA-seq can be used in any DNA-seq application, including ChIP-seq as well as RNA-seq applications, and offers robust target enrichment performance with all of the leading platforms.

Simple Workflow: Single Tube or Well, 2 Hours, No Transfers

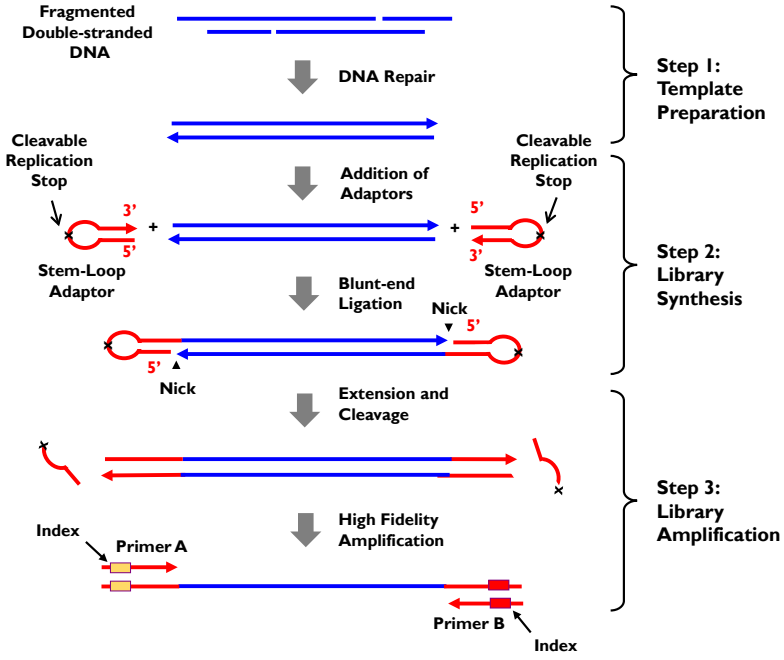


Starting with as little as 50 pg of fragmented double-stranded DNA or cDNA, ThruPLEX DNA-seq creates indexed libraries in 3 simple steps: end repair, adapter ligation, and high-fidelity library amplification. The streamlined workflow is performed in about 2 hours in a single tube or well preventing sample loss and enhancing positive sample identification.

WE ARE VERY HAPPY WITH THE RESULTS AND WE PLAN TO START USING THRUPLEX DNA-SEQ AS A PART OF OUR CAPTURE WORKFLOWS. VARIANTS ARE CALLED WITH VERY EQUAL DISTRIBUTION (ONLY A SMALL FRACTION OF LOW/HIGH COVERAGE EXTREMES). IN OUR CLASSIC SAMPLE PREPS, THE COVERAGE IS NOT THIS HOMOGENOUS, AND LOW TAIL IS MUCH LONGER. OUR LAB STAFF WAS PLEASED WITH THE CONVENIENCE OF THE THRUPLEX WORKFLOW (LESS MANUAL STEPS).

—PEKKA ELLONEN, HEAD OF DNA SEQUENCING LABORATORY, INSTITUTE FOR MOLECULAR MEDICINE FINLAND FIMM

ThruPLEX DNA-seq Technology

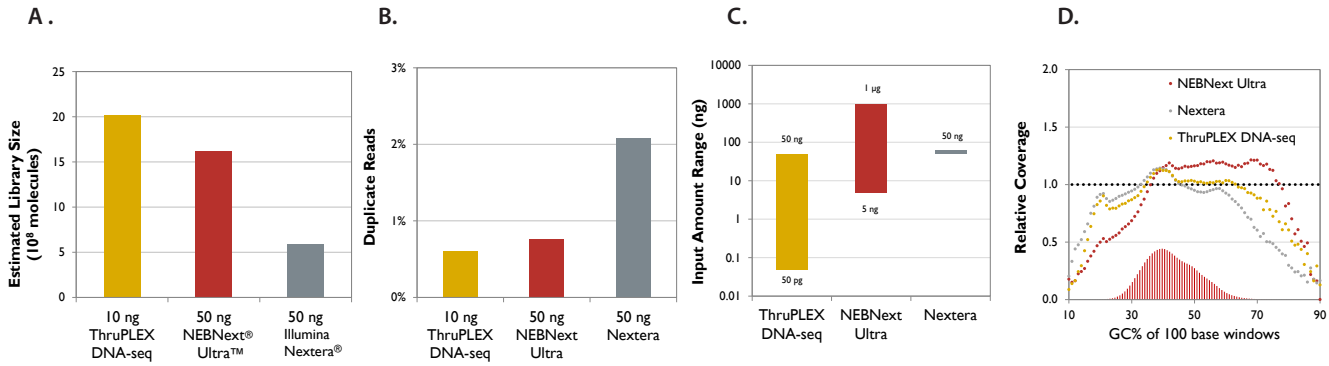


Step 1. Fragmented double-stranded DNA (0.05 ng to 50 ng) is repaired in a highly efficient process.

Step 2. Blunt-end ligation occurs with high-efficiency. Primer dimer formation and subsequent background is reduced since the hairpin adapters have blocked 5′ ends and no single-stranded tails are present.

Step 3. Background is reduced by destroying unused adaptors after ligation. High fidelity amplification reduces errors introduced through amplification.

ThruPLEX DNA-seq Outperforms Other NGS Library Preparation Kits



NGS libraries were prepared with the indicated amount of reference gDNA using the library preparation kits indicated and sequenced on a MiSeq®, v3 flow cell. ThruPLEX DNA-seq yielded more diverse libraries (A) with less input DNA and generated fewer duplicates (B) than other kits (25M read pairs). It also has a lower and broader recommended input range than the other kits (C). ThruPLEX DNA-seq has excellent GC coverage over the entire genome (D). Note that the optimal coverage should be equal to 1 in these graphs. GC composition distribution of the human genome is represented by the red bars.

Ordering Information

ThruPLEX® DNA-seq Kit contains everything required to create Illumina NGS ready libraries including indexes.

CAT. NO.	Product	Rxns	Indexes	CAT. NO.	Product	Rxns	Indexes
R400523	ThruPLEX DNA-seq 6S (12) Kit	12	6 single in tubes	R400427	ThruPLEX DNA-seq 48S Kit	48	48 single in a plate
R400428	ThruPLEX DNA-seq 12S (48) Kit	48	12 single in tubes	R400406	ThruPLEX DNA-seq 48D Kit	48	48 dual in a plate
R400429	ThruPLEX DNA-seq 12S Kit	12	12 single in tubes	R400407	ThruPLEX DNA-seq 96D Kit	96	96 dual in a plate

Order on-line at www.rubicongenomics.com. For custom orders contact busdev@rubicongenomics.com.

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