CLARETBIO

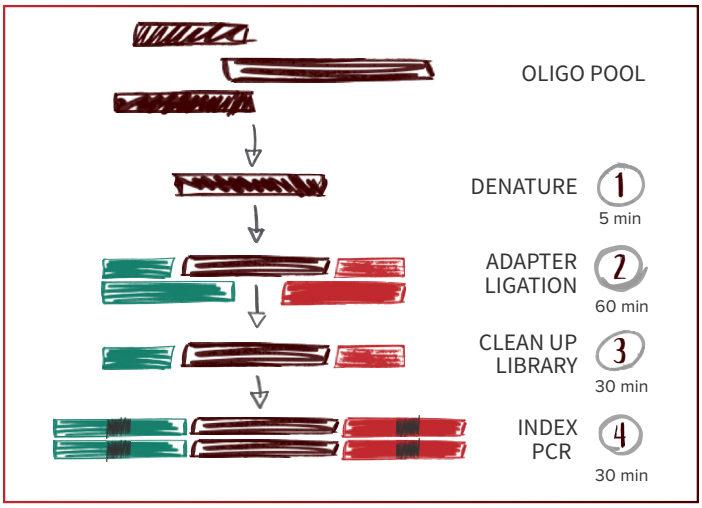
# SRSLY®

## FOR SUPERIOR NGS-BASED OLIGO QC

- Single stranded preparation enables direct NGS of synthesized oligos
- Superior recovery of short fragments (20-100 nt)
- Low input requirements
- Single reaction reduces bench time, and is amenable to automation
- No downstream data trimming necessary; assures compatibility with your pipeline

## SIMPLIFIED WORKFLOW

SRSLY® works in a one-step combined phosphorylation/ ligation step that simultaneously prepares template DNA molecules for ligation without end-polishing and ligates Illumina adapters by utilizing proprietary splint adapters.




## PRODUCT SPECIFICATIONS

Quantify probe sets, enrichment panels, & oligo pools for abundance and quality using **SRSLY PicoPlus**

- From DNA oligo to sequence-ready Illumina® library in under 3 hours
- Optimized for 5 ng of input oligo
- Optimized master mixes and minimal pipetting steps ensures nominal hands-on time

## CLARETBIO PRODUCT INFORMATION

To order the SRSLY kits email at orders@claretbio.com

| Kit | Reactions | Catalog Number |
|---|---|---|
| SRSLY PicoPlus (Input < 10 ng) | 24 or 96 reactions | CBS-K250B-24, CBS-K250B-96 |
| Unique Dual Index Primers | 24 or 96 reactions | CBS-UD-24, CBS-UD-96 |
| Clarefy Beads | 24 or 96 reactions | CBS-BD-24 or CBS-BD-96 |

# SRSLY QC OF SINGLE-STRANDED OLIGOS OF VARIOUS LENGTHS

SRSLY can assay single-stranded DNA oligo pools for abundance and purity as well as quantify incomplete fragments with a level of precision only achievable by NGS. Here, SRSLY is used to analyze a pool containing 11 oligos of varying lengths. Figure A shows the abundance of each oligo in the sequencing library. Figure B shows the percent of oligo product as a function of oligo length. Figure C shows the effect that various purification methods have on oligo purity for an 60 nucleotide oligo.

Figure A. Raw Insert Length Distribution

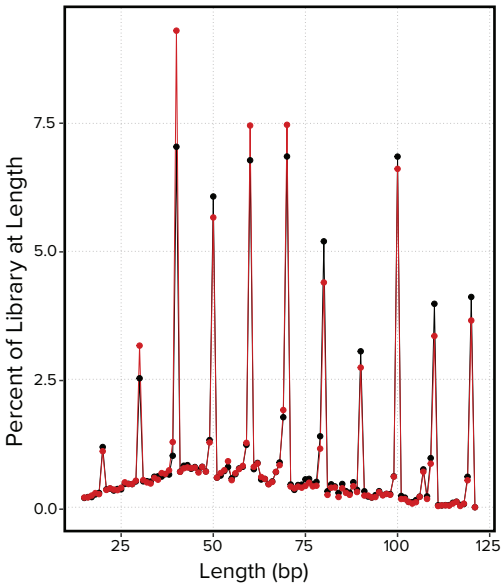



Figure B. Mapped Length Distribution

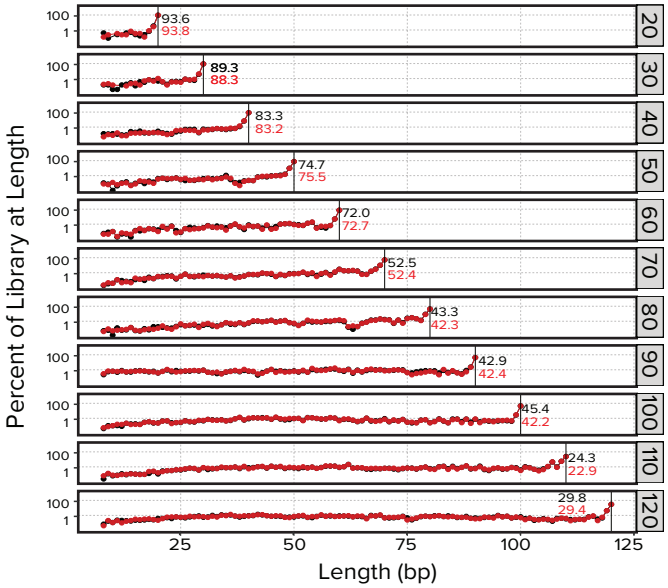



Figure C. Mapped Length Distribution by Oligo Purification Method

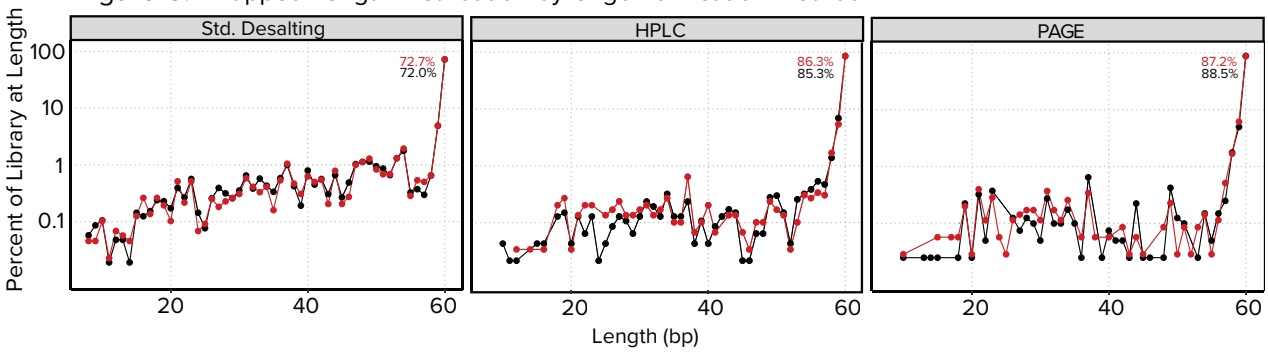



***Figure A:*** *Single-stranded DNA oligos with known sequences were synthesized from lengths 20-120 bp at 10 bp intervals using standard desalting purification methods. The oligos were pooled and used as template for SRSLY library preparation. DNA insert length distributions were calculated from Illumina sequencing data.*

***Figure B:*** *Oligos were mapped to a fasta containing the reference oligo sequences (BWA aln). The library was sequenced to a depth of ~260,000 read pairs (20,000 read pairs per oligo) and fragment lengths mapped to each oligo were plotted as a function of percentage of total reads log10.*

***Figure C:*** *Single-stranded DNA oligo of length 60 bp with known sequence was synthesized using either standard desalting, HPLC, or PAGE purification and analyzed as in Figure B.*

## INTERESTED IN LEARNING MORE ABOUT SRSLY?

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**CLARET BIOSCIENCE** | P.O. Box 3052 | Santa Cruz, CA 95063 | +1.707.412.8484
**FOR MORE INFORMATION** | visit www.ClaretBio.com or write to info@ClaretBio.com