

myReads® NGS Service Packages

Flexible, customizable options for different sample and project types

Pick a package that fits your project needs or mix and match!

Don't see anything you like?
We offer à la carte services to meet your needs.

STANDARD DNA

Appropriate for freshly-extracted, good quality DNA

- Includes QC, fragmentation, library preparation, 8-12-plex captures, 1Gbp of PE150 sequencing per sample
- All samples must be high-molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>1 µg DNA)
- Library preparation performance commitment* for samples meeting our guidelines
- Complimentary QC report allowing you to make decisions about which samples to keep, drop, or supplement

DEGRADED DNA

Appropriate for older specimens, herbarium, material, or samples of unknown quality

- Includes extended QC, fragmentation (where necessary), library preparation with specialized chemistry (where necessary), 4-6-plex captures, 1Gbp of PE150 sequencing per sample
- Samples may have a range of molecular weights, UV 260:280 values, and mass (>10 ng DNA)
- Performance is not guaranteed for degraded samples
- Complimentary QC report allowing you to make decisions about which samples to keep, drop, or supplement

ANCIENT DNA – DOUBLE-STRANDED

Appropriate for museum, historical, or ancient DNA

- Includes QC, double-stranded library preparation with specialized chemistry (the “gold standard” for ancient DNA), 2-4-plex dual-round captures, 1Gbp of PE150 sequencing per sample
- All samples must be low-molecular weight (<1kbp modal length)
- Performance is not guaranteed for ancient samples
- Complimentary QC report allowing you to make decisions about which samples to keep, drop, or supplement

ANCIENT DNA – SINGLE-STRANDED

Appropriate for museum, historical, or ancient DNA, cfDNA, single-stranded cDNA

- Includes QC, single-stranded library preparation with specialized chemistry, 2-4-plex dual-round captures, 1Gbp of PE150 sequencing per sample
- All samples must be low-molecular weight (<1kbp modal length)
- Performance is not guaranteed for ancient samples
- Complimentary QC report allowing you to make decisions about which samples to keep, drop, or supplement

LONG-INSERT DNA

Appropriate for DNA or cDNA intended for PacBio sequencing

- Includes QC, long-insert precursor library preparation, 3-plex captures, 24 samples per SMRTbell preparation & Sequel II cell
- All samples must be high-molecular weight (>10kbp modal length), high quality (UV 260:280 1.7-1.9), and high mass (>5 µg DNA)
- Library preparation performance commitment* for samples meeting our guidelines
- Complimentary QC report allowing you to make decisions about which samples to keep, drop, or supplement

STANDARD RNA

Appropriate for high-quality RNA or mRNA

- Includes QC, DNAase treatment, purification, 8-12-plex captures, 1 Gbp of PE150 sequencing per sample
- All samples must be high quality (UV 260:280 1.9-2.1), and high mass (\geq 250 ng RNA)
- Additional options for mRNA capture & rRNA depletion from human/mouse/rat samples
- Library preparation performance commitment* for samples meeting our guidelines
- Complimentary QC report allowing you to make decisions about which samples to keep, drop, or supplement

A LA CARTE SERVICES

Your project, your way

Need fewer samples per capture? DNA extraction? More sequencing? We've got you covered.

Talk to our dedicated team of scientists about the best custom options for your project today.

* See myReads Services Policies document for details.

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