

# myReads<sup>®</sup> 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? Bioinformatics? 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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