Smartlife Biosciences

How to prepare your samples

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Proper sample preparation is essential to ensure high-quality sequencing data. To help you get the most out of your Long Read and Sanger runs, we've compiled a clear set of recommendations for preparing DNA and cDNA samples. Whether you're submitting purified DNA, PCR products, plasmids, or double-stranded cDNA, these guidelines will help you avoid failed runs, optimize your results, and ensure a smooth experience from submission to analysis.
Follow the steps below to make sure your samples meet our quality requirements and are ready for reliable, high-performance sequencing.

General Sample Handling

Use the right tubes

All samples must be prepared in 1.5 mL LoBind microtubes to minimize DNA loss and ensure optimal recovery.

Label correctly

Please label each tube clearly with:

- either dedicated labels
- or floating labels

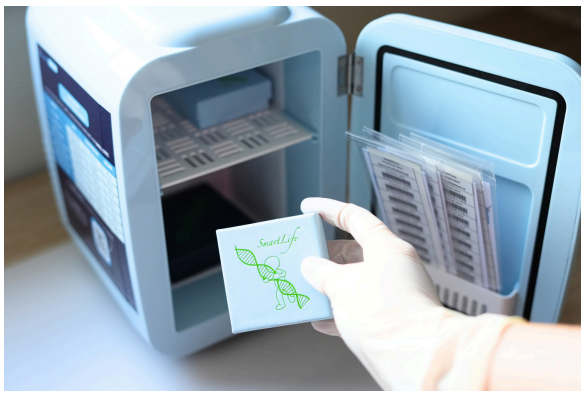
Clear and consistent labeling helps prevent delays and ensures accurate processing. Please make sure to place the labels exactly as shown in the reference photo.

Transport your samples safely

After ordering online, place your prepared tubes in a SmartLife transport box.
On the back label of the box, please write:

- The sample names
- The corresponding order number

Then drop the box into the SMART Box at your institute's reception.



How to prepare your samples

Recommendations

Required Quantities & Recommended Volumes

Each service has specific requirements for DNA amount, concentration, and volume.

Please refer to the tables below for:

- Minimum DNA concentrations
- Required volumes

Providing samples within these recommended ranges ensures maximum data quality and coverage.

Long Read

PLASMIDS

CATEGORY	SIZE	CONCENTRATION	MINIMUM VOLUME
SMALL	2,5 to 25 kb	30 ng/µL	30 µL
BIG	25 to 125 kb	50 ng/µL	30 µL
HUGE	125 to 300 kb	50 ng/µL	30 µL

AMPLICONS

CATEGORY	SIZE	CONCENTRATION	MINIMUM VOLUME
SMALL	450 bp to 25 kb	30 ng/µL	30 µL
BIG	25 to 75 kb	50 ng/µL	30 µL
HUGE	75 to 125 kb	50 ng/µL	30 µL

BACTERIAL & YEAST GENOME

CATEGORY	SIZE	CONCENTRATION	MINIMUM VOLUME
SMALL	Up to 7 Mb	100 ng/µL	30 µL
BIG	7 Mb to 10 Mb	100 ng/µL	30 µL
HUGE	10 Mb to 12Mb	110 ng/µL	30 µL
EXTRA	12 Mb to 15Mb	110 ng/µL	30 µL

VIRAL GENOME

CATEGORY	SIZE	CONCENTRATION	MINIMUM VOLUME
SMALL	2,5 to 25 kb	30 ng/µL	30 µL
BIG	25 to 125 kb	50 ng/µL	30 µL
HUGE	125 to 300 kb	50 ng/µL	30 µL

METAGENOMICS

CATEGORY	CONCENTRATION	MINIMUM VOLUME
16S Total (V1-V9)	10 ng/µL	20 µL
Whole Metagenomics	100 ng/µL	30 µL

RNA SEQ

CATEGORY	CONCENTRATION	MINIMUM VOLUME
RNA	100 ng/µL	20 µL
cDNA	100 ng/µL	20 µL

DNA POOL

	READS	CONCENTRATION	VOLUME
FOR ONE ALIQUOT	up to 5000	40 ng/µL	30 µL

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Sanger

SANGER PREMIX

	PCR PRODUCT	PLASMID
DNA CONCENTRATION	20 ng/µL	100 ng/µL
DNA VOLUME	12 µL	12 µL
PRIMER CONCENTRATION	4 pmol/µL	4 pmol/µL
PRIMER VOLUME	3 µL	3 µL

SANGER PREMIUM

	CONCENTRATION	VOLUME
PURIFIED PCR PRODUCT	20 ng/µL	12 µL
PLASMID	100 ng/µL	12 µL
PRIMER	10 pmol/µL	3 µL

Quantification

To avoid failed runs and insufficient input during library preparation, accurate quantification is critical.

We strongly recommend measuring DNA concentration with a Qubit fluorometer.

- Nanodrop overestimates DNA concentration
- It is not reliable for low-concentration samples
- It cannot distinguish DNA from RNA, free nucleotides, or contaminants
- Qubit provides precise, dsDNA-specific values

Using Qubit ensures your samples meet the true requirements for the sequencing workflow.

Specific Note for cDNA sequencing

We sequence double-stranded cDNA only.

Single-stranded cDNA cannot be processed and will result in failed library prep.

If you are sending cDNA, please ensure:

- It is double-stranded
- It has been cleaned and quantified accurately
- A minimum amount (as indicated in the tables) is provided

How to generate double-stranded cDNA ?

You may use a second-strand synthesis method such as:

- Klenow fragment (exo–)
- Any validated ds-cDNA synthesis kit
- A combination of reverse transcription followed by second-strand amplification

Make sure the final product is purified and free of primers, enzymes, and buffer contaminants.

Final Checklist Before Submission

- ☐ DNA/cDNA prepared in 1.5 mL LoBind tubes
- ☐ Clear and complete tube labels
- ☐ DNA quantified with Qubit
- ☐ Concentration and volume meet table recommendations
- ☐ Samples placed in SmartLife transport box
- ☐ Order Online Submitted
- ☐ Your name + order number written on the box
- ☐ Box deposited in your institute's SMART Box or Fridge Box

We warmly thank you for the trust you place in our scientific expertise, for your loyalty to our services, as well as for your intelligent contribution to reducing the carbon footprint by outsourcing routine sequencing to our local SMART laboratory established in your city.

With our most distinguished regards,
SMARTLife Biosciences

Please do not hesitate to contact us by email for any questions or additional information — our team will be happy to respond to you as quickly as possible.

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