Sample requirements

Library type	Material	Library prep kit	Quantity	Volume approx.	Quality evaluation - user
Whole-genome seq	Genomic DNA	KAPA Hyperprep	250 ng/ul*	20 µl	DNA needs to be run on a 1% agarose gel to confirm integrity.
ChIP-Seq	DNA ChIP-enriched	KAPA Hyperprep	all	20 µl	qPCR analysis is recommended to confirm enrichment.
Cut&Run	DNA Cut&RUN	KAPA Hyperprep	all		
librairie sh/CRISPR	PCR amplicon	Nextera	5-50 ng/µl	10 µl	Migrate on gel.
PCR-Seq	PCR amplicon	Nextera	5-50 ng/µl	10 µl	Migrate on gel.
mRNA-Seq	Total RNA	KAPA Hyperprep RNA	250 ng/ul*	20 µl	Bioanalyzer will be run at the platform.
rRNA-deplété RNA-Seq	Total RNA	FAST select + KAPA hyperprep RNA	250 ng/ul*	15 µl	Bioanalyzer will be run at the platform.
Small RNA seq	Total RNA	Qiaseq small RNA	250 ng/ul*	15 µl	Use purification columns that retain small fragments. Ex: MirVana

* This is the ideal concentration. We can make libraries with less material, contact us for details.

Resuspend samples in H2O. Samples can be in 1.5ml tubes clearly identified.

Samples Quality Requirements

For RNA, RIN>8 is strongly suggested to assess proper RNA quality (for plants and FFPE tissues, RIN can be lower). Librairies for slightly degraded RNA samples should be prepared using ribo-depletion protocol to avoid 3' biaises with a polyA enrichment. Nanodrop 260/280 ratio should be around 1,8-2,1 and 260/230 ratio should be higher than 1,5. Values outside of these ranges indicate contamination.

For DNA, gel must reflect a high DNA quality. Nanodrop 260/280 ratio should be close to 1,8-2,0 and the 260/230 ratio should be higher than 2,0.

Note that the Nanodrop frequently over-estimates RNA/DNA concentration.

We will QC your samples and libraries using a combination of Nanodrop, Qubit and Bioanalyzer. Librairies are quantified by QuBit, run on a BioAnalyzer, diluted to 10nM and normalized with qPCR quantification.

Lanes 1, 3, 4 show high quality gDNA. Lane 2 shows degraded gDNA.