IRIC
Université de Montréal

Sample requirements

Type de librairies	Matériel	Kit utilisé	Quantité de matériel	Volume approx.	Évaluation de la qualité par l'usager
Whole-genome seq	gADN	KAPA Hyperprep	100 ng- 1 µg*	20 µl	DNA needs to be run on a 1% agarose gel to confirm integrity.
ChIP-Seq	ADN ChIP-enrichi	KAPA Hyperprep	1-5 ng*	20 µl	qPCR analysis is recommended to confirm enrichment.
librairie sh/CRISPR	amplicon de PCR	Nextera	5-50 ng/µl	10 µl	Migrate on gel.
PCR-Seq	amplicon de PCR	Nextera	5-50 ng/µl	10 µl	Migrate on gel.
mRNA-Seq	ARN total	KAPA Hyperprep RNA	500 ng-4 µg*	20 µl	Bioanalyzer will be run at the platform.
rRNA-deplété RNA-Seq	ARN total	FAST select + KAPA hyperprep RNA	100ng- 1 ug	15 µl	Bioanalyzer will be run at the platform.
miRNA/smallRNA-Seq	ARN total	Qiaseq small RNA	10-100 ng ARN total	15 µl	Use purification columns that retain small fragments. Ex: MirVana

* Quantity may be lower but the complexity will be impaired. Also, no backup will be kept in case of library or sequencing failure. However, succesful mRNA-seq librairies have been made with 10ng of total RNA. Sucessful ChIP-seq libraries have been made with 250 pg of ChIPed DNA. High quality gDNA can be used at 1-10ng.

ARN samples must be resuspended in nuclease-free water. DNA samples must be resuspended in Tris-HCl pH8. Samples should be submitted in a 1.5ml tube clearly marked with your sample name and DSP number. Samples should be shipped on dry ice with the DSP number.

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.