Sample's Quantity Requirements

Library type	Input	Kit used	Input quantity	Approx. Volume	Quality assessment at user's site
Whole-genome seq	gDNA	KAPA Library preparation	100 ng- 1 µg*	55 µl	gDNA must be run a 1% agarose gel to assess integrity. A picture of the gel must be sent. See below for an example of high quality gDNA
PCR-free	gDNA	Illumina PCR-free	1 µg for 350 bp insert size; 2 µg for 550 bp insert size	55 µl	
Exome capture	gDNA	KAPA Library preparation; NimbleGen exome capture	100 ng- 1 µg*	55 µl	gDNA must be run a 1% agarose gel to assess integrity. A picture of the gel must be sent. See below for an example of high quality gDNA
Methyl-Seq	gDNA	Agilent SureSelectXT Human Methyl-Seq	2-4 µg	55 µl	gDNA must be run a 1% agarose gel to assess integrity. A picture of the gel must be sent. See below for an example of high quality gDNA
ChIP-Seq	ChIP enriched DNA	KAPA Library preparation	1-5 ng*	~55 µl	qPCR is strongly recommended to make sure an enrichement is seen before starting the library preparation. A picture of the ChIP/input DNA on a 1% agarose gel must be sent to assess good fragmentation (200-600 bp)
CRISPR library screen	PCR amplicons	PCR amplicons with custom primers	5-50 ng/µl	10 µl	You can run your PCR amplicons on an agarose gel to ensure expected PCR products length.
PCR-Seq	PCR amplicons	Nextera, Miseq only	5-50 ng/µl; > 300 bp	10 µl	You can run your PCR amplicons on an agarose gel to ensure expected PCR products length.
mRNA-Seq	total RNA	KAPA stranded RNA-seq Library preparation	500 ng-4 µg*	55 µl	
rRNA-depleted RNA-Seq	total RNA	Ribo-Zero; KAPA Library prep	1-5 µg	55 µl	
miRNA/smallRNA-Seq	total RNA	SeqMatic	10-100 ng total RNA or isolated miRNA	15 µl	It is critical not to use commun purification columns that removes fragments <100 nt. Make sure your RNA isolation retains micro and small RNAs (e.g MirVana)
smallRNA-Seq	total RNA	Illumina TruSeq SmallRNA	1 µg total RNA or 10-50 ng isolated smallRNA	15 µl	It is critical not to use commun purification columns that removes fragments <100 nt. Make sure your RNA isolation retains micro and small RNAs (e.g MirVana)
LncRNA capture	total RNA	KAPA stranded RNA-seq; NimbleGen lncRNA capture	100ng- 1ug	55 µl	

* Quantity may be much 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 ChIP DNA. High quality gDNA can be used at 1-10ng.

All samples must be resuspended in nuclease-free water. 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.

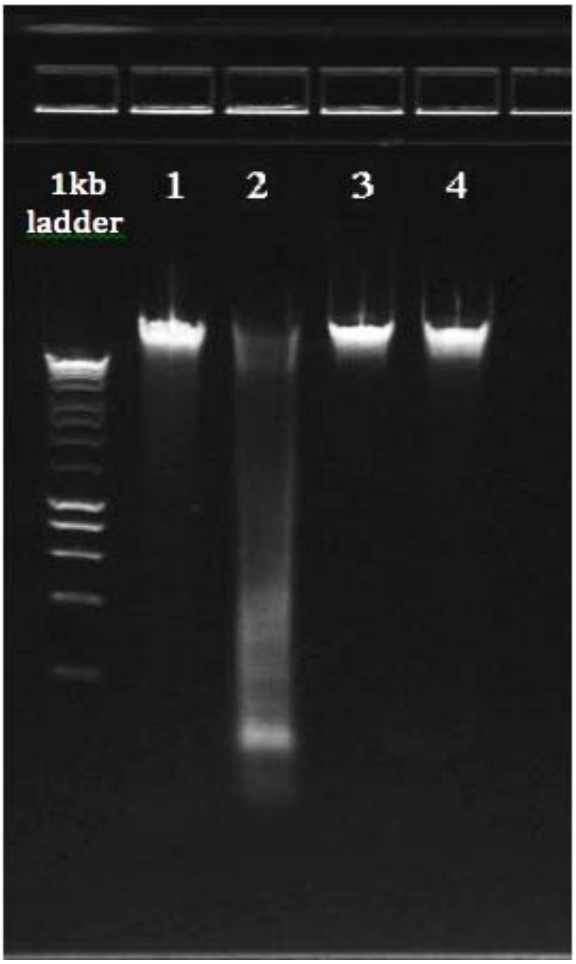
Sample's Quality Requirements

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 KAPA qPCR quantification.



Les colonnes 1, 3 et 4 présentent de l'ADNg de haute qualité.
La colonne 2 montre des signes de dégradation

Lane 1, 3, 4 shows high quality gDNA.
Lane 2 shows signs of degradation.