Date: 08-05-2025
Version: 2.0

Sample Requirements Library Sequencing

Libraries with Illumina Sequencing Adapters

Method 1: Quantification by *Molarity*
This is the preferred method for libraries with an average insert size between 300-600 bp. Calculate the molarity of the library as follows:
fmol/µL = (3030 x concentration in ng/µL) / (average length in bp x 2)

Sequencing type	Sequencer Type	Sample concentration	Minimum Amount	Average Library Length
Whole flow cell sequencing	MGI G99RS MGI G400RS	>10 fmol/uL	>200 fmol	300-600

Method 2: Quantification by *Weight*
This method is generally applicable to convert any linear dsDNA library to a single stranded circular (ssCirc) DNA library compatible with MGI sequencing.

Sequencing type	Sequencer Type	Sample concentration	Minimum Amount	Average Library Length
Whole flow cell sequencing	MGI G99RS MGI G400RS	>3 ng/uL	>60 ng	200-900
	MGI T7RS		>180 ng	200-700

We can also work with libraries that do not meet the above specifications (eg. low concentration samples, libraries outside of the recommended length range). In these cases, please contact us with your library QC results and we will discuss a customized solution.

Libraries with MGI Adapters & Converted Libraries

When submitting single stranded circular (ssCirc) DNA library for MGI sequencing, users need to make sure that ssCirc DNA has been prepared with the appropriate kit from MGI (Article numbers 1000004155/940-000915-00/940-001919-00).

Sequencing type	Sequencer Type	Sample concentration	Minimum Amount
Whole flow cell sequencing	MGI G99RS	>5 fmol/uL	>50 fmol
	MGI G400RS		>100 fmol
	MGI T7RS		>400 fmol

For all submissions to XG, please fill out our library submission sheet!