

BYO DNA guidelines

We welcome UMR-seq workshop attendees to bring their own samples of interest. However, we ask that participants check the quality of their purified genomic DNA:



- Agarose gel electrophoresis to confirm presence of a single, crisp, high-molecular weight band (see lane 2 in example).
- NanoDrop to confirm purity: $260/230 = 2$; $260/280 = 1.8$
- DNA quantification via Qubit with dsDNA broad-range reagents (e.g. ThermoFisher # Q32850). If you only have access to a Nanodrop, please use this to confirm DNA is present and we will have (limited) Qubit reagents to quantify and normalize samples during Workshop Session 1.

We routinely perform UMR-seq in the following plant species

Species	Genome (Gbp)	DNA input (ng)	UMR isolation time
Maize	~2.4	500	3 hours
Barley	~4.2	500	3 hours
Wheat	~15	500	3 hours
<i>N. benthamiana</i>	~3	500	3 hours
Sorghum	~0.73	250	3 hours
Spinach	~1	250 or 500	3 hours

UMR-seq in other species, although possible, will require optimization but here are some starting guidelines

Genome (Gbp)	DNA input (ng)	UMR isolation time
0.5-3	500	3 hours
> 3	1000	3 hours

We typically use 500 ng DNA as input (**20 ng/ μ L**) for relatively large-genome plants (>1 Gb), and 250 ng DNA (**10 ng/ μ L**) for plants with genome sizes <1 Gb.

For untested species, we recommend initial testing with 1000 ng DNA input (**40 ng/ μ L**) for genomes >3 Gb. If DNA quantity is limited, a minimum of 500 ng is required. For genome sizes between 500 Mb and 3 Gb, 500 ng is recommended for initial testing.

Please feel free to discuss the recommended DNA input amount for your BYO samples with us prior to the workshop (see contact details on webpage).