

CWseq Universal DirectFast DNA Library Prep Kit (Illumina & MGI) – Enzymatic Library Construction

Advantage

- **Strong compatibility:** Animals, plants, microorganisms, FFPE, etc.
- **Simple operation:** DNA fragmentation/end repair/A-tailing can be finished in one step, with a sample input of 100 pg- 1 µg.
- **Short double selection time:** The two-step selection process is consolidated into a single step.
- **Background microbial quality control:** Optimized background microbial control, strict quality assurance, suitable for pathogenic microorganism detection.

Product Performance

Uniformity

Using templates with different GC contents for library preparation, analyzing the data.

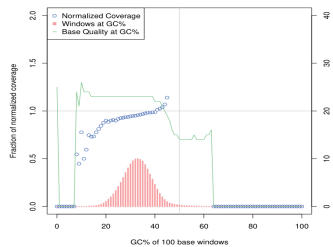


Figure 1a: low GC content templates

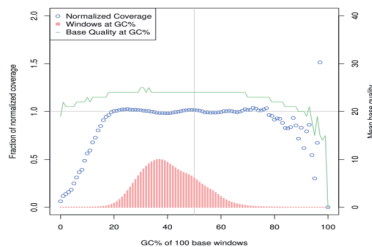


Figure 1b: medium GC content templates

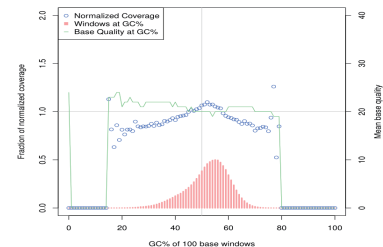


Figure 1c: high GC content templates

Conclusion: Cowin's CWseq Universal DirectFast DNA Library Prep Kit achieves uniform amplification for templates with varying GC contents.

Compatibility

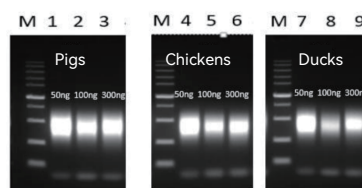


Figure 2a

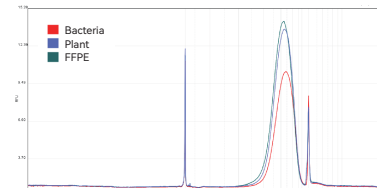


Figure 2b

Conclusion: Cowin's CWseq Universal DirectFast DNA Library Prep Kit is applicable to various sample types, including tumor tissues, blood, FFPE, pathogenic microorganisms, breeding samples (pigs, chickens, ducks), etc., exhibiting consistent fragmentations for samples from different species.

Simple operation

Conclusion: gDNA fragmentation/end repair/A-tailing can be finished in one step, and fragment size can be adjusted by fragmentation time without the influence of input amount.

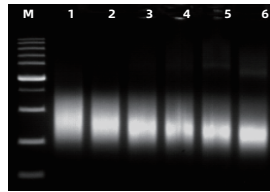


Figure 3a

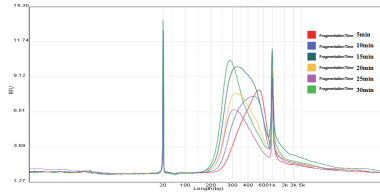


Figure 3b

Short double selection time

In the library preparation process, to obtain the desired fragment size, magnetic bead double selection is typically performed, a process that requires two optimization steps. The upgraded CWseq Universal DirectFast DNA Library Prep Kit streamlines this operation, combining the two steps into one, significantly saving operational time.

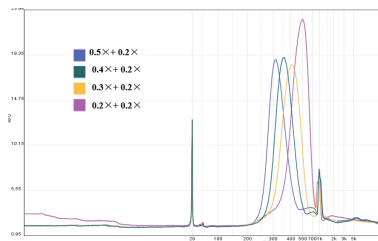
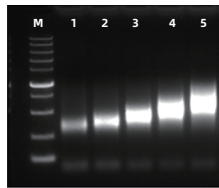


Figure 4a & 4b: Selection result of different bead ratio

Background microbial quality control

Fecal samples were subjected to library construction using this kit, and the data analysis depicted the fecal microbiota as shown in Figure 5. Genomic DNA was employed for next-generation library preparation and sequencing, each sample was examined with 20M reads. The verification of residual background bacteria is detailed in Table 1.

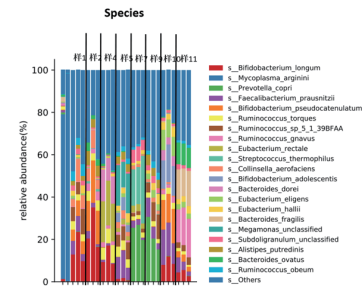


Figure 5a

Background bacteria residue	Reads
Escherichia coli	2 reads

Table 1

Product Information

Cat. No.	Name	Specification	Keyword
CW3048S	CWseq Universal DirectFast DNA	24 rxns	Enzymatic method
CW3048M	Library Prep Kit (Illumina & MGI)	96 rxns	library preparation

Matching adapter & index kits and purification kits are available.