Bioanalysis

MACHEREY-NAGEL

Clean-up and size selection for NGS library preps

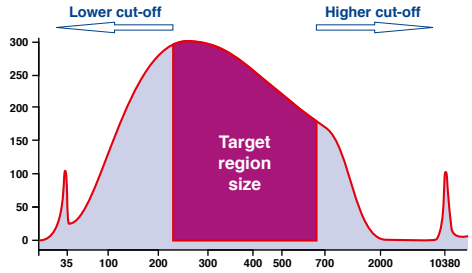
NucleoMag® NGS Clean-up and Size Select

- Efficient clean-up of NGS library preparation reactions
- Tunable size selection
- Scalable magnetic bead technology

NucleoMag® NGS Clean-up and Size Select

High recoveries in NGS library preparation

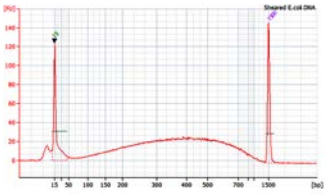
Most sequencing platforms for library preparations require enzymatic reaction clean-up and fragment size selection. NucleoMag® NGS Clean-up and Size Select enables clean-up reactions, as well as a single or double side size selection, to recover the fragment lengths which are needed in your specific application. The magnetic beads in the kit are present in binding buffer and just have to be diluted to tune the required fragment size. The dilution ratio is similar to competitive beads in the market. This allows the NucleoMag® NGS Clean-up and Size Select kit to be used with your current protocols withou the need to make any changes.



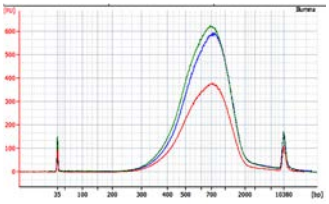
Size selection of fragment mix

For single side size selection (left or right), the sample is mixed with the beads in predetermined ratios for the desired exclusion of smaller or larger sized fragments. For the double sized size selection, two binding steps are performed to exclude larger fragments above the cut-off and smaller fragments below the lower cut-off.

A



B

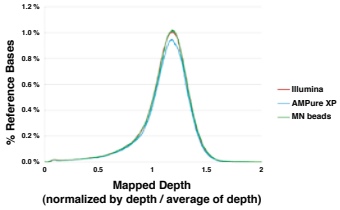


Fragment size analysis of prepared NGS libraries

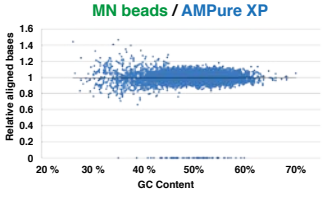
NGS libraries were prepared using Truseq™ DNA PCR Free kit and Illumina (red), AMPure® XP (blue) and NucleoMag® NGS Clean-up and Size Select (green) for clean-up and size selection steps. (A) Input DNA, 1 µg sheared *E. coli* DNA. (B) Size distribution of DNA Fragments after library preparation as input for sequencing, the expected fragment size is 650 bp (insert + adapters).

Data kindly provided by TAKARA BIO INC.

A



B



Sequencing analysis

In order to compare the sequencing performance after library preparation generation with different clean-up and size selection products, the distribution of genome sequence coverage (depth of genome base coverage) and effect on GC content on sequence coverage was tested. (A) No difference in mapped depth of genome base coverage. The depth is constant indicates low bias. (B) Horizontal plot pattern of MN beads against Agencourt beads. After the summary of aligned read bases within a 0.5 kb genome region, the two samples have been normalized / matched resulting in a horizontally pattern showing the similarity of the two samples.

Data kindly provided by TAKARA BIO INC.

Ordering information

Product	Volume	REF
NucleoMag® NGS Clean-up and Size Select Clean-up and size selection in NGS library preparations	5 mL	744970.5
	50 mL	744970.50
	500 mL	744970.500

Trademarks: NucleoMag® (MACHEREY-NAGEL), AmPure® (Agencourt), Truseq™ (illumina)

Your local distributor

www.mn-net.com

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