DNA Normalization Magnetic Beads (NGS, PCR, gDNA)

Catalog No.	40071S	40071L	40072S**	40072L**
Runs*	48	96	48	96

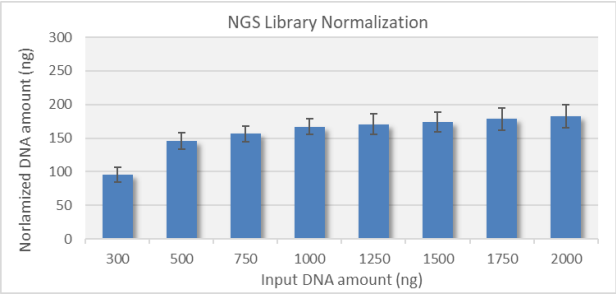
*Based on 50 µl of sample volume
** With Recovery Beads

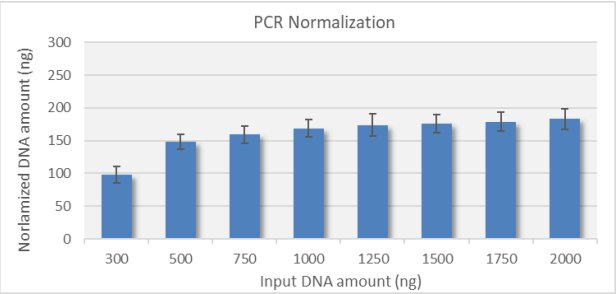
Description

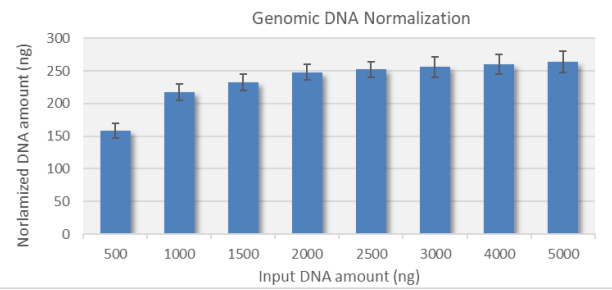
The **DNA Normalization Magnetic Beads (NGS, PCR, gDNA)** was developed for normalization of NGS libraries, PCR fragments, sheared genomic DNA, and genomic DNA based on our magnetic bead technology. Magnetic beads has DNA-binding capacity. With the limitation of the DNA-binding capacity, normalized amount of DNA is recovered, and excess unbound DNA is separated.

The normalized DNA concentration can be obtained from DNA samples of various concentrations. Traditional fluorescent methods of DNA quantification require the setup of a standard curve from known DNA concentrations, compare with DNA samples from various sources, which would need extensive efforts and operating reagents. The protocol is simple, fast, centrifugation free, and filtration free. Additional DNA quantification and dilution is not necessary after DNA normalization with magnetic beads. Labor, time, and reagent are saved with the normalization beads.

The kit (Cat.# 40072) also includes unbound DNA recovery beads, which can be used for the recovery of unbound excess DNA during DNA normalization.







Specification

	NGS Library	PCR Fragment	Genomic DNA
DNA Input	> 300 ng	> 300 ng	> 500 ng
Normalized Range	100-200 ng	100-200 ng	200-300 ng
Elution Volume	> 20 µl	> 20 µl	> 20 µl
Unbound DNA Recovery	Yes (Cat# 40072)	Yes (Cat# 40072)	Yes (Cat# 40072)

Features

- Consistent normalization of various sources: NGS libraries, PCR fragments, and genomic DNA
- Recovery of excess unbound DNA (Cat.# 40072S and 40072L)
- Excellent dynamic range
  - NGS library, PCR, sheared genomic DNA: 7-fold difference in input DNA
  - Genomic DNA: 10-fold difference in input DNA
- Simple and fast protocol with double-stranded DNA output
- No fluorescent quantification needed
- No centrifugation, no filtration

Applications

- NGS library normalization
- Targeted enrichment
- PCR normalization
- Genomic DNA and sheared genomic DNA normalization

Component

Catalog No.	40071S	40071L	40072S	40072L
Normalization Beads	2.4 mL	4.8 mL	2.4 mL	4.8 mL
Recovery Beads	-	-	2.4 mL	4.8 mL
Elution Buffer	4.8 mL	9.6 mL	4.8 mL	9.6 mL

Storage Condition

- Store at 4°C, stable up to 12 months.

Reagent & Equipment Needed (not provided in this reagent)

- Magnetic particle concentrator
- 96-well plates
- 80% ethanol (prepare before use)

Protocol

DNA normalization

Note: Store both DNA and the Normalization beads at 4°C before use.
Invert or shake the Normalization beads bottle thoroughly to resuspend the beads.
DNA samples without buffer is preferred. PCR buffer may be fine depending on the specific buffer composition.

1) Put the 96-well plate containing 50 µl of samples on ice and add 50 µl of the Normalization Beads. Slow pipetting of the viscous beads is needed for precise aliquot. Mix by pipetting gently and thoroughly with a multichannel pipettor. Remove the plate from the ice, put the plate on the bench, and incubate for 10 min.
2) Load the sample on a magnet, incubate for 5 min, and **slowly** transfer the supernatant to a new 96-well plate without disturbing the pellet. The supernatant can be used for recovery of unbound DNA. If unbound DNA is not needed, the supernatant can be discarded.
3) **Slowly** add 200 µl of 80% ethanol without disturbing the beads. Incubate for 2 min and remove the supernatant **slowly and carefully** with a multichannel pipettor. Remove residual ethanol **carefully** with fine tips.
4) Remove the plate from the magnet and resuspend the beads in at least 20 µl of Elution Buffer (10 mM Tris-HCl). Make sure all beads are suspended in the Elution Buffer. DNA can also be eluted in water, low TE buffer, or TE Buffer. **Note**: Resuspension of the beads in less than 20 µl may reduce the yield and generate more yield variation.
5) Load the plate on the magnet, incubate for 1 min, and transfer the supernatant (containing normalized DNA sample) to a new plate or tubes without disturbing the beads.

Recovery of unbound DNA (with Cat.# 40072): The new 96-well plate with supernatant (previous step 2)

Note: Invert or shake the Recovery Beads bottle thoroughly to resuspend the beads.

1) Add 50 µl of the Recovery Beads to the supernatants from previous step 2 (DNA normalization). Slow pipetting of the viscous beads is needed for precise aliquot. Mix by pipetting gently and thoroughly. Incubate for 5 min at room temperature.
2) Load the sample plate on a magnet, incubate for 5 min, and remove the supernatant carefully with a multichannel pipettor.
3) Add 200 µl of 80% ethanol without disturbing the beads. Incubate for 2 min and discard the supernatant carefully. Remove all residual ethanol without disturbing the beads.
4) Air-dry the beads on the magnet for 1 min.
5) Remove the plate from the magnet and resuspend the beads in at least 20 µl of Elution Buffer (10 mM Tris-HCl). Make sure all beads are suspended in the Elution Buffer. DNA can also be eluted in water, low TE buffer, or TE Buffer. **Note**: Resuspension of the beads in less than 20 µl may reduce the yield.
6) Load the plate on the magnet, incubate for 1 min, and transfer the supernatant (containing unbound DNA sample) to a new plate or tubes without disturbing the beads.

Quality Control

Kit components passed stringent functional quality test.

Product Use Limitation

This product is developed and sold for research purposes and *in vitro* use only. Please refer to biodynami.com for Material Safety Data Sheet of the product.

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