

## DNA Normalization Magnetic Beads (5-30 ng Input)

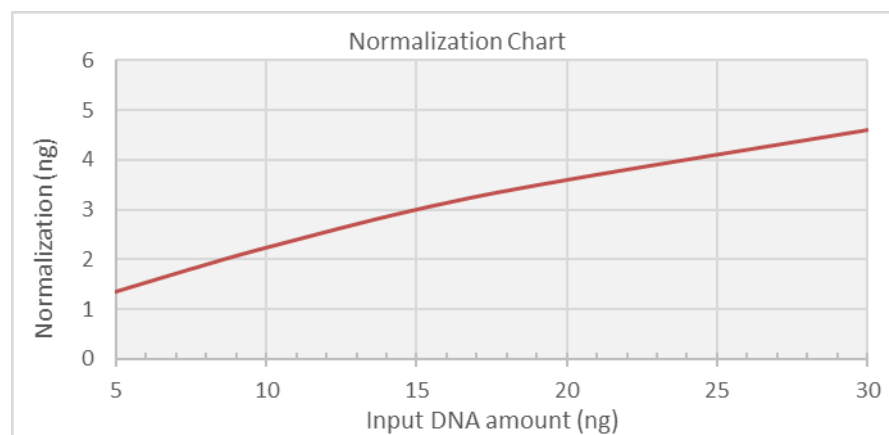
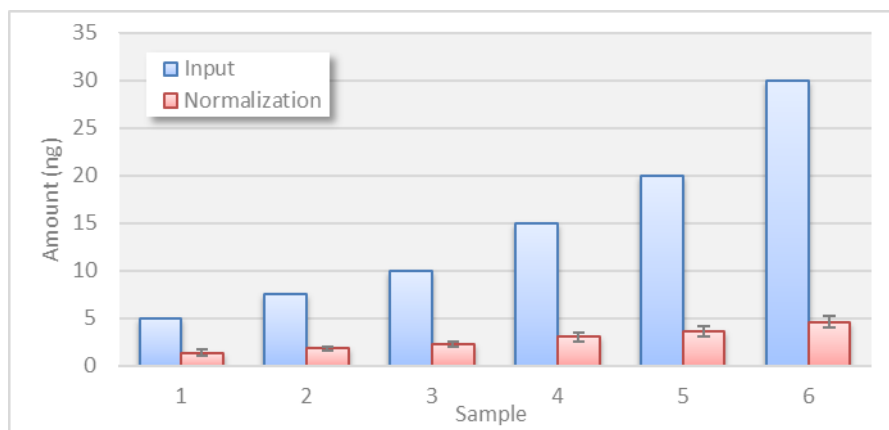
Catalog No.	40079S	40079L
Rxns*	48	96

\*Based on 15 µl of sample volume

### Description

The **DNA Normalization Magnetic Beads (5-30 ng Input)** was developed for normalization of NGS libraries, PCR fragments, and sheared 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.



## Specification

Specification	
DNA input range	5-30 ng
DNA input type	NGS library, PCR fragment, sheared genomic DNA
Normalized range	1.5-4.5 ng
Elution volume	> 10 µl
Technology	Magnetic beads

## Features

- Consistent normalization of various sources
  - NGS libraries
  - PCR fragments
  - Sheared genomic DNA
- Excellent dynamic input range: 6 folds from 5 ng to 30 ng
- Magnetic beads technology
  - No centrifugation
  - No column
  - No filtration
- Elution: as low as 10 µl without yield loss
- Removal of unwanted components and impurities

## Component

Catalog No.	40079S	40079L
PG8 Buffer	500 µl	1000 µl
MK2 Buffer	72 µl	144 µl
B3M Buffer	72 µl	144 µl
SS60 Beads	72 µl	144 µl
Elution Buffer	960 µl	1920 µl

## Storage Condition

- Store at 4°C, stable up to 6 months.

## Reagent & Equipment Needed (not provided in this reagent)

- Magnetic particle concentrator
- 96-well plates
- 100% ethanol and 80% ethanol (prepare before use)
- Thermal cycler

## Protocol

### Note:

- Store DNA samples at 4°C before use.
  - DNA samples without buffer are preferred. PCR buffer may be fine depending on the specific buffer composition.
- 1) Prepare **Normalization Beads** (15 µl per sample) by adding the following to a tube/bottle, and mix by vortexing the Normalization Beads thoroughly. **Attention:** vortex or shake the **SS60 Beads** tube to resuspend the beads thoroughly just before use.

PG8 Buffer	10.5 µl
MK2 Buffer	1.5 µl
B3M Buffer	1.5 µl
<u>SS60 Beads</u>	<u>1.5 µl</u>
Total	15 µl

- 2) Transfer 15 µl of the Normalization Beads to the wells of a 96-well plate, incubate the plate on ice for 3 min. Slow pipetting of the viscous Normalization Beads is needed for precise aliquot.
- 3) Add 15 µl of DNA samples, mix by pipetting gently and thoroughly with a multichannel pipettor. Remove the plate from the ice, load the plate on a thermal cycler, and incubate at 22°C for 10 min.
- 4) Load the sample on a magnet, incubate for 5 min.
- 5) Add 150 µl of **100% ethanol**, incubate for 2 min, and **slowly** remove the supernatant without disturbing the pellet.
- 6) **Slowly** add 200 µl of **80% ethanol** without disturbing the beads. Incubate for 1 min and remove the supernatant **slowly and carefully** with a multichannel pipettor. Remove residual ethanol **carefully** with fine tips.
- 7) Remove the plate from the magnet and resuspend the beads in at least 10 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 (pH>6.0), low TE buffer, or TE Buffer. Resuspension of the beads in less than 10 µl may reduce the yield and generate more yield variation.
- 8) Load the plate on the magnet, incubate for 1 min, and transfer the supernatant (containing normalized DNA samples) to a new plate or tubes without disturbing the beads.

### Quality Control

Kit components passed stringent functional quality test.

### Product Use Limitation




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