

Shasta™ Whole-Genome Amplification Reagents

Catalog No.

640287 (Not sold separately)

Sold as part of 640286

Amount

2 chips

Lot Number

Specified on product label.

Description

Shasta Whole-Genome Amplification Reagents, sold as part of Shasta Whole-Genome Amplification Kit - 2 Chip (Cat. No. 640286), contains the reagents to analyze single-cell DNA sequences with whole-genome coverage using the ICELL8® cx Single-Cell System (Cat. No. 640188 or 640189).

Package Contents

- 2 x 25 µl Second Diluent (100X)
- 2 x 240 µl DNA Extraction Buffer
- 2 x 10 µl DNA Extraction Enzyme
- 2 x 240 µl PreAmp Buffer
- 2 x 10 µl PreAmp Enzyme
- 2 x 177.5 µl Amplification Buffer
- 2 x 10 µl Amplification Enzyme
- 2 x 500 µl Nuclease-Free Water
- 2 x 350 µl Elution Buffer
- 2 x 12 ml 1X TE Buffer

Storage Conditions

- Store all reagents at -20°C.

Expiration Date

- Specified on product label.

Shipping Conditions

- Dry ice

Product Documents

Documents for our products are available for download at takarabio.com/manuals

The following documents apply to this product:

- Shasta Whole-Genome Amplification Kit - 2 Chip User Manual for the ICELL8 cx Single-Cell System

Takara Bio USA, Inc.

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Certificate of Analysis

Cat. No. 640287

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Quality Control Data

A sample kit from each lot was tested on the ICELL8 cx Single-Cell System using the following procedure to ensure that it produces an appropriate library in terms of yield, size, and sequencing metrics.

15 pg of human gDNA (Coriell NA12878) was dispensed into 216 nanowells and subjected to DNA extraction, preamplification, and amplification with P5 and P7 indexes as described in the user manual. The final reaction product was extracted from the chip. Half of the product was purified with NucleoMag NGS Clean-up and Size Select (Cat. No. 744970.50) following a double-sided purification protocol and eluted in 20 µl of Elution Buffer to get the Illumina®-sequencing ready library.

The yield of the library was ≥ 200 ng, determined using a Qubit 1X dsDNA HS Assay Kit (Life Technologies, Cat. No. Q33231) on a Qubit 2.0 Fluorometer (Thermo Fisher Scientific, Cat. No. Q32866). The average size of the library was ~500–900 bp, measured using a High Sensitivity DNA Analysis Kit (Agilent Technologies, Cat. No. 5067-4626) on an Agilent Bioanalyzer 2100.

The library was quantified by qPCR with a Library Quantification Kit (Takara Bio, Cat. No. 638324), denatured, and sequenced on a NextSeq® 550 sequencer using the NextSeq 500/550 Mid-Output Kit v2.5 150 Cycles (Illumina, Cat. No. 20024904) as follows: Read 1 = 76 cycles, Read 2 = 76 cycles, Forward index (i5) = 8 cycles, and Reverse index (i7) = 8 cycles. PhiX spike-in was 15%.

Sequencing data analysis, including demultiplexing, alignment, and statistical analysis of the sequencing metrics, was performed using a Linux command-based QC pipeline with the same packages and structures as Cogent™ NGS Analysis Pipeline v3.1 (Takara Bio). Results were as follows:

Measured value	Passing result
Average reads per sample	>500,000
Percentage of total barcoded reads in the negative control	<1%
Median percentage of GC content	$\geq 40\%$
Median insert size	≥ 200 bp
Percentage of uniquely mapped reads (hg38)	>80%
Mean of normalized reads per chromosome	0.9–1.1
Mean of the Pearson correlation across the samples	≥ 0.7

It is certified that this product meets the above specifications, as reviewed and approved by the Quality Department.

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NOTICE TO PURCHASER:

Our products are to be used for **Research Use Only**. They may not be used for any other purpose, including, but not limited to, use in humans, therapeutic or diagnostic use, or commercial use of any kind. Our products may not be transferred to third parties, resold, modified for resale, or used to manufacture commercial products or to provide a service to third parties without our prior written approval.

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