

CAGE™ Library Preparation Kit

CAGE™ – Transcriptome Profiling using NGS

Extensively used within the FANTOM research projects at RIKEN, ENCODE project at NIH, and the National project on “Transcription Network Analysis” in Japan

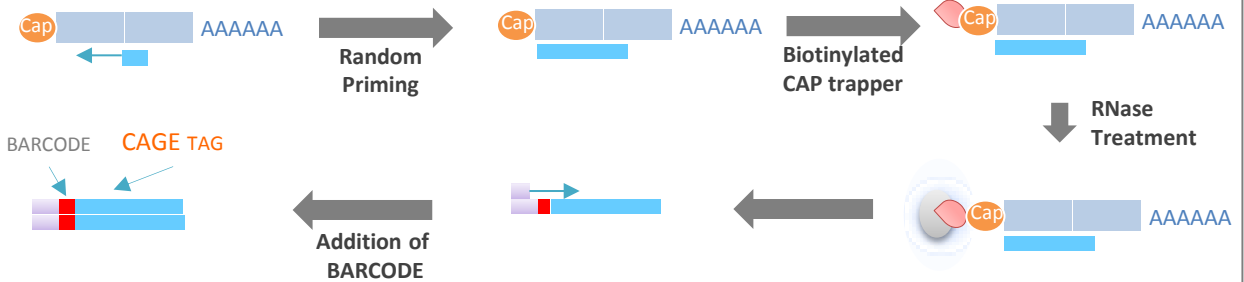
This kit enables large-scale analysis of **T**ranscription **S**tart **S**ite (TSS) and expression profile using Illumina HiSeq Series Sequencers.

This kit is based on an improved technology called **n**on **A**mplified **n**on **T**agging **I**llumina (nAnT-iCAGE) which doesn't involve PCR or tagging.

CAGE (Cap Analysis of Gene Expression) is an analysis technology developed at RIKEN institute.

1

Generation of CAGE™ Library



RNA pool → Capture

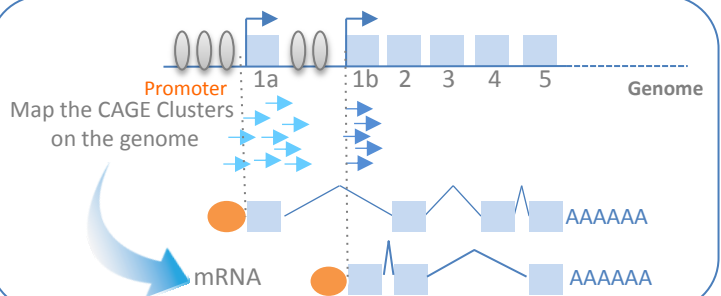
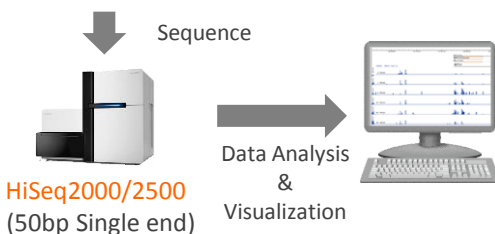
Cap AAAAAA	Full-Length mRNA	○
Cap	Non coding/Non-poly(A) mRNA	○
AAAAAA	Partial mRNA	×
	rRNA	×

- Illumina Sequence Primer
- Biotin
- Streptavidin
- CAP structure at the 5'-end

2

Sequence , Data Analysis and Visualization

CAGE™ Library



How it works

- Cap-Trapper method enables selective capture of fully matured 5'-end and remove rRNA.
- Both coding and non-coding RNA can be captured as CAGE employs random primers.
- Barcode sequence designed on 5'-linker allows you to mix up to 8 samples as 1 library for sequencing.
- Library prepared can be sequenced by NGS from Illumina.
- Free-software is available for data analysis, provided by National Institute of Genetics.

URL : http://cell-innovation.nig.ac.jp/index_en.html

* This kit does not comprise several components such as enzymes required to prepare library.

The kit



Price

Product	Cat. No.	Price
CAGE™ Library preparation kit 8sample version	5201	¥200,000
CAGE™ Library preparation kit 48sample version	5202	¥1,200,000
CAGE™ Library preparation kit 96sample version	5203	¥2,400,000



230-0046, Leading Venture Plaza-2, 75-1,
Ono-cho, Tsurumi-ku, Yokohama City,
Kanagawa Pref., Japan
Tel: 045-510-0607 / Fax:045-510-0608
E-mail: order@dnaform.jp
URL: <http://www.dnaform.jp>

Distributed by: