



CELLECTA

Gene functional analysis. Simplified.



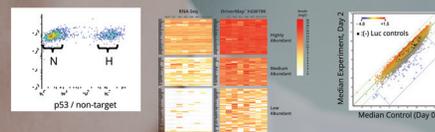
CELLECTA

YOUR BRIDGE TO DISCOVERY

- **CRISPR / RNAi** Libraries & Genetic Screens
- **DriverMap™** Targeted RNA Expression Profiling
- **CloneTracker™** Barcode Libraries

YOUR RESULTS

**Functionally Important Genes
& Biomarkers**



YOUR INPUT

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Biological Samples



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Who we are

Cellecta is a leading provider of genomic products and services. Our functional genomics portfolio includes gene knockout and knockdown screens, custom and genome-wide CRISPR and RNAi libraries, construct services, cell engineering, NGS kits and targeted expression profiling products and services.

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www.cellecta.com info@cellecta.com +1 877-938-3910 or +1 650-938-3910



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New to single-cell sequencing?

that's
GOOD
science!

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- **SMART-Seq[®] HT kit**—streamlined full-length cDNA library prep
- **SMART-Seq Stranded kit**—complete RNA library prep that captures coding and noncoding RNAs
- **SMARTer[®] PicoPLEX[®] Gold kit**—accurate detection of SNVs and CNVs from single cells
- **SMARTer[™] ICELL8[®] system**—automated high-throughput single-cell isolation, selection, and processing

SMARTer NGS



To learn more:
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Takara Bio USA, Inc.

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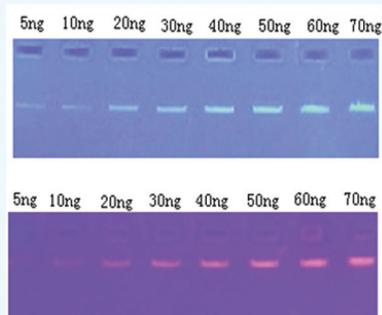
Clontech Takara cellartis

GoodView™ Nucleic Acid Stain

—An alternative to EB

GoodView™ is a safer nucleic acid stain, an alternative to the traditional ethidium bromide (EB) stain for detecting nucleic acid in agarose gels. It emits green fluorescence when bound to DNA or RNA. This new stain has two fluorescence excitation maxima when bound to nucleic acid, one centered at 268 nm and another at 294 nm. In addition, it has one visible excitation at 491 nm. The Fluorescence emission of GoodView™ bound to DNA is centered at 530 nm.

Comparative sensitivity test of GV and EB



Sensitivity test result of
GV at UV 300nm.

Sensitivity test result of
EB at UV 300nm.

The result of electrophoresis demonstrates GV is almost as sensitive as EB.

The Test Report from Institute for Environmental Health and Related Product Safety of Chinese Center for Disease Control and Prevention concludes that:

- ◆ Acute Oral Toxicity Test: GoodView™ Nucleic Acid Stain belongs to nontoxic.
- ◆ Mouse Marrow Chromophilous Erythrocyte Micronucleus Test: Negative. There is no significant difference in the incidence of micronuclei between test and control groups.
- ◆ Ames Test: Negative. No mutagenicity was observed.
- ◆ In Vitro Mammalian Cell Chromosome Aberration Test: Negative. No increasing aberration rate was observed.

The test report is available upon request.

Beijing SBS Genetech Co., Ltd.

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Design Engineer Innovate

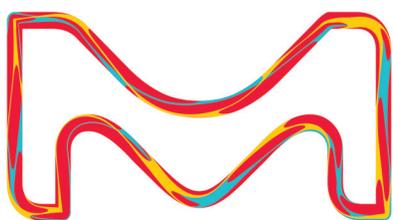
with MISSION™ CRISPR

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The SygRNA® synthetic, crRNA:tracrRNA and one-part sgRNA systems accelerate genome editing. Pair with Cas9 protein, mRNA, or established Cas9 expressing cell lines. Deliver by a variety of methods including microinjection, electroporation, and lipofection.

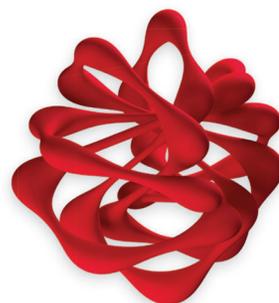
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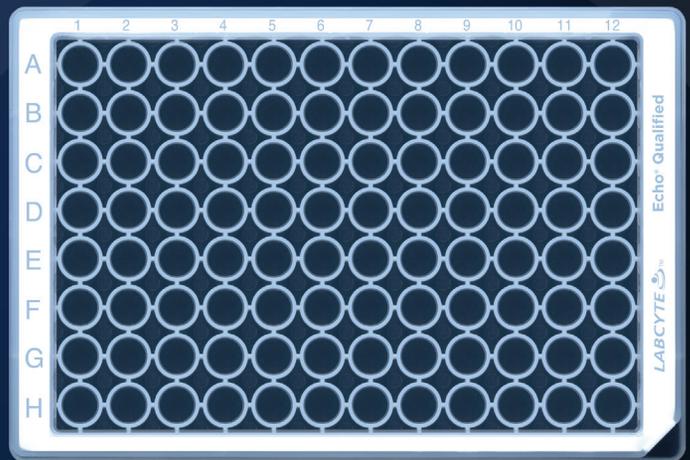
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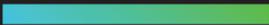
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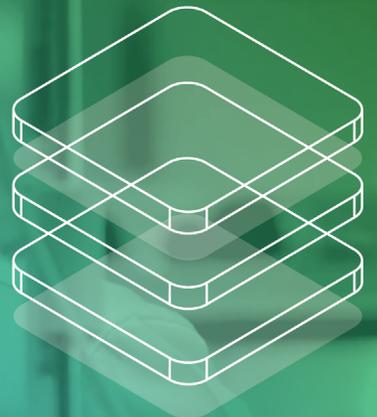
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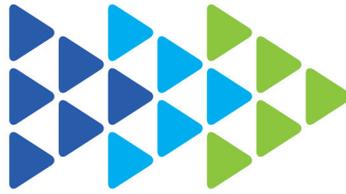
INTEGRATIVE CANCER SCIENCE
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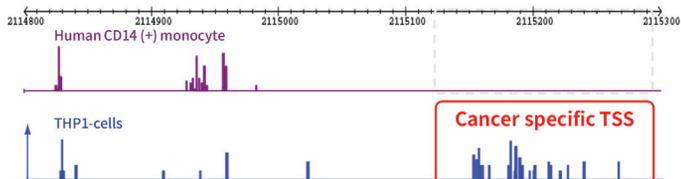
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Promoter / Enhancer Annotation in the NGS era

Cap Analysis of Gene Expression (CAGE) is a new NGS library preparation method using “cap-trapping” technology which enables you to detect and quantify **transcription start site (TSS)** of RNA pol II transcripts including **mRNAs**, **lincRNAs** and **enhancer RNAs**.

- **Accurate promoter annotation**—reliable estimation of promoter positions and their activities based on precise TSS information
- **Estimation of transcription factor binding sites**—genome-wide motif search around TSS which have different expression profiles among samples
- **Detection of active enhancers**—identify active enhancers by detection of bidirectional enhancer RNAs
- **Development of new biomarkers**—TSS variants are valuable candidate of biomarkers even in the case that there are no difference at the gene expression level
- **Accurate quantification of gene expression**—PCR-free library preparation process without fragmentation allow for more reliable quantification of gene expression than RNA-seq



CAGE expression pattern of a histone H3 methyltransferase gene of human CD14(+) monocytes and THP-1 leukemia monocytic cells.

CAGE library preparation & analysis services

Library preparation for Illumina sequencers	500 USD/sample
Sequencing (Illumina HiSeq/ NextSeq)	250 USD/sample
Bioinformatics analysis	250 USD/sample

CAGE library preparation kit

8 samples (Cat. 52003-8)	2,000 USD
48 samples (Cat. 52003-48)	10,000 USD

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