

NEVER PHASE SEPARATE AGAIN!

RNA *Directly* from TRIzol® with Direct-zol™ RNA Kits

The Direct-zol™ RNA Kits are designed for the purification of RNA from samples in TRIzol®, TRI Reagent®, or similar reagents. Samples are loaded directly into a spin column bypassing the need for conventional phase separation and precipitation steps.



High-quality RNA

A) [kb]

B) [nt]

A) High-quality small and large RNA are effectively recovered using the Direct-zol™ kit. RNA is **DNA-free**.

B) High RNA integrity numbers (RIN > 9; Bioanalyzer) indicate high-quality RNA was purified from human epithelial cells using the Direct-zol™-96 MagBead RNA on a Freedom EVO® (Tecan liquid handler).

High quality RNA & miRNA for:
RNA-Seq, miRNA-Seq, Microarray, qRT-PCR, Hybridization, and more!

Efficient & Non-biased miRNA Recovery

Cells

Tissue (liver)

miRNA-Seq

nCounter

The Direct-zol™ RNA MiniPrep recovers ~4-fold more miRNA (<40 nt) than the conventional phase-separation method. Micro-RNAs purified from cells and tissue were quantified using a Bioanalyzer® with small RNA chip.

Micro-RNA isolation using Direct-zol™ RNA kits is non-biased. The data show RNA purified from TRIzol® samples using the Direct-zol™ RNA MiniPrep compared to an unbiased method (mirVana™, Ambion).

Micro-RNA analysis was performed using miRNA-Seq (MiSeq®, Illumina) and a direct hybridization assay (nCounter®, Nanostring).



Samples are available!
www.zymoresearch.com/Direct-zol

Product	Cat. No.	Size
Direct-zol™ RNA MiniPrep	R2050, R2051* R2052, R2053*	50 Preps. 200 Preps.
Direct-zol™-96 RNA	R2054, R2055* R2056, R2057*	2 x 96 Preps. 4 x 96 Preps.
Direct-zol™-96 MagBead RNA (For automation)	R2100, R2101* R2102, R2103* R2104, R2105*	2 x 96 Preps. 4 x 96 Preps. 8 x 96 Preps.

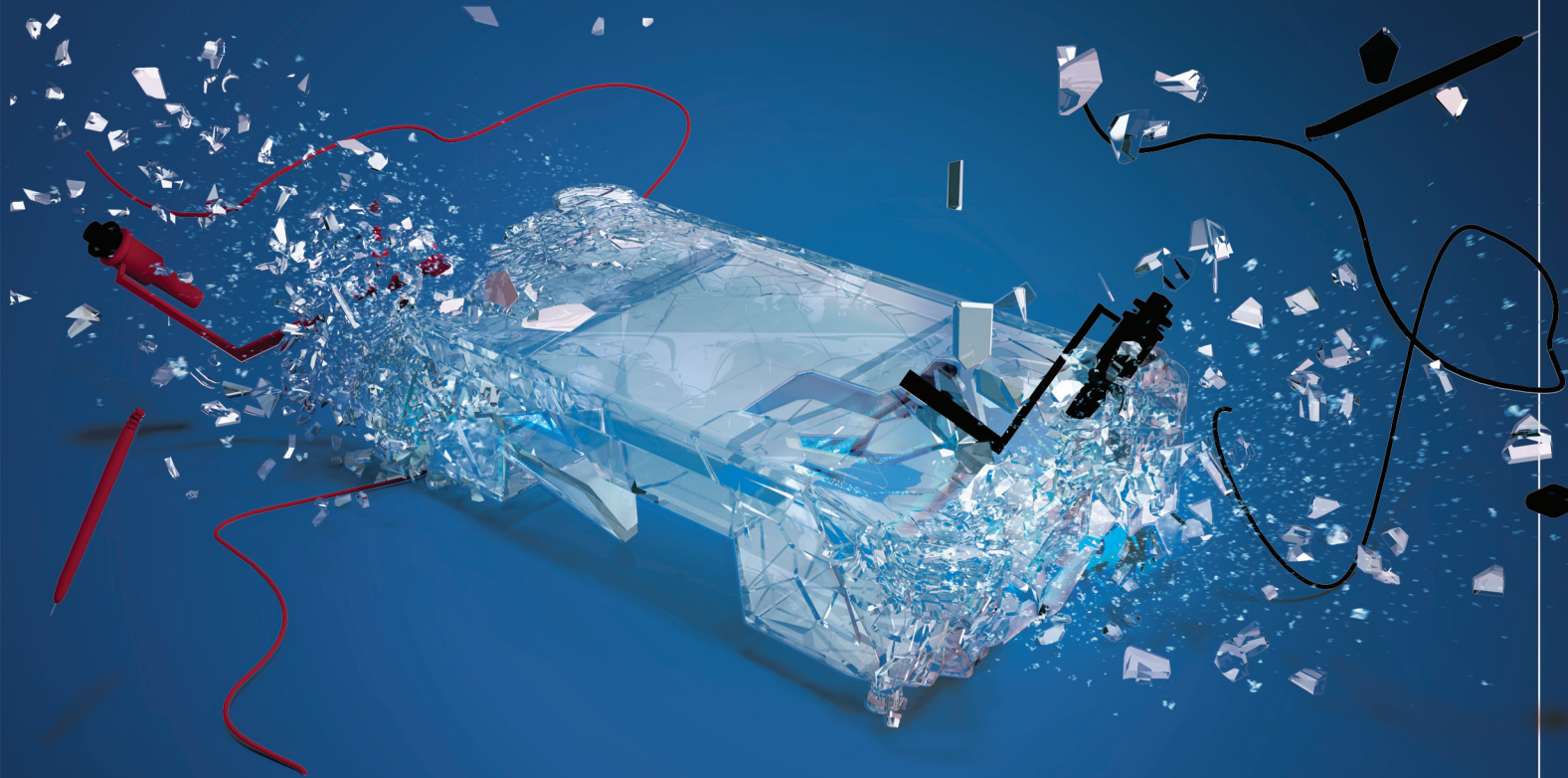


* Supplied with TRI Reagent®

ZYMO RESEARCH
The Beauty of Science is to Make Things Simple

THE
Epigenetics
COMPANY™

TRI-Reagent® and TRIzol® are registered trademarks of Molecular Research Center, Inc. Freedom EVO® is a registered trademark of Tecan Group AG. mirVana™ is a trademark of Ambion, Inc. MiSeq® is a registered trademark of Illumina, Inc. nCounter® is a registered trademark of Nanostring Technologies Inc. Bioanalyzer® is a registered trademark of Agilent Technologies, Inc. Some technologies included in this product are patent pending.



BLOW UP YOUR GENOMICS WORKFLOW.

Automate nucleic acid QC and get on with your life sciences.

If sample QC takes you more than two minutes, it's too manual. Fragment Analyzer™ takes the job off your hands—streamlining lab operations and wiping out errors. Just pipette once and it delivers truly reliable results via automated capillary electrophoresis.

No chips. No tapes. No compromises.

- Setup in seconds
- Get resolution down to 2 base pairs
- Detection starts at 5 pg/μL

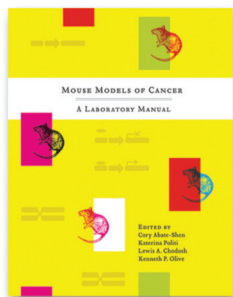
DITCH YOUR TIRED OLD WORKFLOW AT FRAGMENTANALYZER.COM.





MOUSE MODELS OF CANCER

A LABORATORY MANUAL



Edited by Cory Abate-Shen, *Herbert Irving Comprehensive Cancer Center, Columbia University College of Physicians and Surgeons, Columbia University Medical Center*, Katerina Politi, *Yale Cancer Center, Yale University School of Medicine*, Lewis Chodosh, *Abramson Cancer Center, Perelman School of Medicine, University of Pennsylvania*, and Kenneth P. Olive, *Herbert Irving Comprehensive Cancer Center, Columbia University Medical Center*

The laboratory mouse is an important model for studying cancer and its treatment. This book includes both background information and step-by-step protocols for generating mouse models that accurately recapitulate many features of human cancer. It covers genetic models, including transgenic germline models, gene knockouts and knockins, and conditional and inducible systems, as well as models derived using chemical carcinogens, RNA interference, tissue recombination, and other strategies. Techniques to characterize tumor development, progression, and metastasis in these mice

using state-of-the-art imaging, histopathological, surgical, and other approaches are described. The uses of these models in preclinical and translational research are also discussed.

2014, 536 pp., illus., index

Hardcover \$240 £150

Paperback \$165 £104

ISBN 978-1-621820-04-8

ISBN 978-1-621820-03-1

Contents

Preface

INTRODUCTION

Of Model Pets and Cancer Models: An Introduction to Mouse Models of Cancer
Andrea Lunardi, Caterina Nardella, John G. Clobessy, and Pier Paolo Pandolfi

PART 1: ORIGINS AND HISTORY OF MOUSE MODELS OF CANCER

CHAPTER 1

Transgenic Mouse Models—A Seminal Breakthrough in Oncogene Research
Harvey W. Smith and William J. Muller

CHAPTER 2

Analyses of Tumor-Suppressor Genes in Germline Mouse Models of Cancer
Jingqiang Wang and Cory Abate-Shen

CHAPTER 3

Conditional Knockout Mouse Models of Cancer
Chu-Xia Deng

CHAPTER 4

Animal Models of Chemical Carcinogenesis: Driving Breakthroughs in Cancer Research for 100 Years
Christopher J. Kemp

CHAPTER 5

The Effects of Genetic Background of Mouse Models of Cancer: Friend or Foe?
Karlyne M. Reilly

PART 2: RECENT APPROACHES TO MODELING CANCER IN MICE

CHAPTER 6

Genetically Engineered Knock-In and Conditional Knock-In Mouse Models of Cancer
Amy Rappaport and Leisa Johnson

CHAPTER 7

Strategies to Achieve Conditional Gene Mutation in Mice
Jessica J. Gierut, Tyler E. Jacks, and Kevin M. Haigis

CHAPTER 8

Tetracycline-Regulated Mouse Models of Cancer
Elizabeth S. Yeh, Ann Vernon-Grey, Heather Martin, and Lewis A. Chodosh

CHAPTER 9

The Estrogen Receptor Fusion System in Mouse Models: A Reversible Switch
Jonathan Whitfield, Trevor Littlewood, Gerard I. Evan, and Laura Soucek

CHAPTER 10

Using the RCAS-TVA System to Model Human Cancer in Mice
Leanne G. Ahronian and Brian C. Lewis

CHAPTER 11

Transposon Insertional Mutagenesis Models of Cancer
Karen M. Mann, Nancy A. Jenkins, Neal G. Copeland, and Michael B. Mann

CHAPTER 12

Accelerating Cancer Modeling with RNAi and Nongerm-line Genetically Engineered Mouse Models
Geulah Livshits and Scott W. Lowe

CHAPTER 13

Chimeric Tumor and Organ Transplantation Models
Michael Hemann

CHAPTER 14

Tissue Recombination Models for the Study of Epithelial Cancer
Yang Zong, Andrew S. Goldstein, and Owen N. Witte

CHAPTER 15

Human Cancer Growth and Therapy in Immunodeficient Mouse Models
Leonard D. Shultz, Neal Goodwin, Fumihiko Ishikawa, Vishnu Hosur, Bonnie L. Lyons, and Dale L. Greiner

PART 3: ANALYZING MOUSE CANCER PHENOTYPES

CHAPTER 16

Analysis of Mouse Model Pathology: A Primer for Studying the Anatomic Pathology of Genetically Engineered Mice
Robert D. Cardiff, Claramae H. Miller, and Robert J. Munn

CHAPTER 17

Imaging Mouse Cancer Models In Vivo Using Reporter Transgenes
Scott K. Lyons, P. Stephen Patrick, and Kevin M. Brindle

CHAPTER 18

Noninvasive Imaging of Tumor Burden and Molecular Pathways in Mouse Models of Cancer
Yuchuan Wang, Jen-Chieh Tseng, Yanping Sun, Andrew H. Beck, and Andrew L. Kung

CHAPTER 19

Methods to Study Metastasis in Genetically Modified Mice
Farhia Kabeer, Levi J. Beverly, Guillaume Darrasse-Jeze, and Katrina Podsypanina

CHAPTER 20

Methods for Analysis of the Immune System in Mouse Cancer Models
Lauren J. Bayne and Robert H. Vonderheide

CHAPTER 21

Culturing Mouse Tumor Cells
Andrew D. Rhim, Martin Jechlinger, and Anil K. Rustgi

CHAPTER 22

Translational Therapeutics in Genetically Engineered Mouse Models of Cancer
Kenneth P. Olive and Katerina Politi

APPENDICES

A. APPLICATIONS FOR GEMMs IN CLINICAL RESEARCH

APPENDIX A1

Effective Utilization and Appropriate Selection of Genetically Engineered Mouse Models for Translational Integration of Mouse and Human Trials
Cory Abate-Shen and Pier Paolo Pandolfi

APPENDIX A2

Infrastructure Needs for Translational Integration of Mouse and Human Trials
John G. Clobessy and Elisa de Stanchina

APPENDIX A3

Structured Reporting in Anatomic Pathology for Coclinical Trials: The caELMIR Model
Robert D. Cardiff, Claramae H. Miller, Robert J. Munn, and Jose J. Galvez

APPENDIX A4

Mouse to Human Blood-Based Cancer Biomarker Discovery Strategies
Samir M. Hanash and Ayumu Taguchi

APPENDIX A5

Evaluation of Cancer Immunity in Mice
Mary L. Disis and Karolina Palucka

APPENDIX A6

Cross-Species Analysis of Mouse and Human Cancer Genomes
Carla Daniela Robles-Espinoza and David J. Adams

B. GENERAL SAFETY AND HAZARDOUS MATERIAL INFORMATION

APPENDIX B

General Safety and Hazardous Material Information
Index

www.cshlpress.org



Live cell RNA detection of cancer biomarkers enables sorting of mixed cell populations

Introduction

Cancer biomarkers have been used to identify transformed cells within heterogeneous tissues and cell lysates but currently only provide retrospective confirmation of disease state. Identifying RNA biomarkers in live cells provides the unique opportunity to understand the impact of tumor heterogeneity on the behavior of transformed cells and to enrich for cells based on RNA markers using fluorescent activated cell sorting.

Live cell sorting has traditionally been accomplished by detecting the presence of cell surface proteins using fluorescently labeled antibodies. However, the cell recovery rate is poor after irreversible antibody labeling. Furthermore, live cells cannot be sorted based on endogenous intracellular protein markers, because of the need for fixation. Sometimes cells can be sorted on the basis of transfected reporter constructs; however, this treatment also compromises cell integrity and may perturb cellular pathways, confounding downstream analyses.

On the other hand, identifying cell types and sorting cells based on expression of specific RNA markers, without any transfection reagents or intrusive sample preparation, can drastically improve live cell sorting efficiency, physiological relevance, and post-sorting survival rate. Using novel SmartFlare™ RNA detection probes, which are capable of detecting levels of RNA inside living cells, we have demonstrated the ability to sort and further propagate live cell populations purely based on gene expression levels or in combination with surface markers detected with antibodies. This technology eliminates the need for permeabilization or transfection reagents to interrogate the cytoplasmic content of cells, leaving the cells intact and viable after sorting. More importantly, because the particles are

inert and leave the cells unharmed, the cells are available for use in downstream assays, enabling the measurement of additional biomarkers or collection of functional data.

In our study, we sorted breast cancer cells on the basis of RNA biomarkers. First, we isolated ErbB2 mRNA high- and low-expressing cells from a mixed cell population and characterized the sorted cells using downstream immunocytochemistry (ICC) and quantitative RT-PCR. Then, we sorted two cell lines based on expression of miR-221 and miR-222 and further characterized the sort products with respect to expression of epithelial-mesenchymal transition (EMT) markers, collagen invasion potential and formation of invadopodia.

Methods

RNA detection and sorting using SmartFlare™ probes. Cells were mixed in a 1:1 ratio prior to detection of RNA. SmartFlare™ detection reagent was then added to the culture media at a final concentration of 100 pM and incubated at 37 °C overnight. The following morning, the mixed cell population was sorted by fluorescence-activated cell sorting. Cells were washed using Hanks' Balanced Salt Solution, adherent cells detached using Accutase® reagent, collected, centrifuged and resuspended in culture medium. Sorting was performed using a MoFlo™ XDP cell sorter (Beckman Coulter). Sorted populations were then returned to cell culture.

Visualization of RNAs in live cells. After incubation with SmartFlare™ probes, signals were visualized using a Nikon C2 confocal laser scanning microscope.

Invasion assay. Collagen invasion assays were performed using the QCM™ High Sensitivity Non-cross-linked Collagen Invasion Assay, Colorimetric (EMD Millipore, Cat. No. ECM1401). Each sort product was serum-starved, applied to the collagen-coated inserts and incubated overnight. Invading cells were visualized by cell staining, and the stain was extracted to measure optical density at 560 nm.

Invadopodia assay. Invadopodia formation was assessed using the QCM™ Gelatin Invadopodia Assay (EMD Millipore, Cat. No. ECM671). Each sort product was applied onto the Cy-3-gelatin-coated well and incubated for 48 hours. Cells were counterstained with phalloidin and nuclear stain. Percent degradation area of total cell area was analyzed using NIH ImageJ software.

Results

Live cancer cell sorting based on RNA expression and post-sort ICC and qRT-PCR analysis.

A mixed population of MCF10A and BT474 cells was sorted based on ERBB2 RNA SmartFlare™ signal intensity (Figure 1A). Each sort product was then analyzed by antibody staining for ERBB2 protein, which was expressed exclusively in BT474 cells. As expected, protein expression was detected only in ERBB2 SmartFlare™-high sort products but not in low intensity populations (Figure 1B). qRT-PCR confirmed the purity of those sort populations (Figure 1C).

Sorting live cells based on miRNA cancer biomarkers.

Next, we used two miRNA biomarkers to sort T47D and MDA-MB-231 breast cancer cell lines. T47D is epithelial (expressing E-cadherin) and MDA-MB-231 is mesenchymal (expressing vimentin). The two lines are distinguishable based on two miRNA expression levels; MDA-MB-231 shows higher expression of both miR-221 and miR-222².

Cell sorting based on miR-221 expression

and post-sort invasion assay. A mixed population of T47D and MDA-MB-231 cells was sorted based on miR-221 expression using SmartFlare™ probes recognizing miR-221 (Figure 2A). The sort products were then analyzed using a transwell collagen invasion assay. The miR-221-high population displayed significant invasion but the low population displayed minimal invasion (Figure 2B and 2C). Staining for EMT markers showed that miR-221-low cells expressed E-cadherin but not vimentin and displayed epithelial morphology (phalloidin, green), while miR-221-high cells expressed vimentin but not E-cadherin and displayed mesenchymal morphology (Figure 2D).

Cell sorting based on miR-222 expression

and post-sort invadopodia assay. One hallmark of metastatic cancers is matrix degradation associated with the formation of protrusions



EMD Millipore is a division of Merck KGaA, Darmstadt, Germany

of localized protease activity, termed invadopodia or podosomes. An effective method for visualizing subcellular invadopodia formation involves the plating of cells onto a thin layer of fluorescently-labeled matrix. To analyze the correlation between miR-222 expression and invadopodia formation, we sorted cells based on miR-222 SmartFlare™ probe intensity and then seeded sort products onto Cy3-gelatin substrates. The miR-222-high population displayed strong degradation patterns after 48 hours that may have been due to invadopodia formation shown in dark areas as devoid of Cy3 fluorescence. The miR-222-low population did not display gelatin degradation (Figure 3B and 3C). Staining for EMT markers showed that miR-222-low cells expressed E-cadherin but not vimentin and displayed epithelial morphology (phalloidin, green), while miR-222-high cells expressed vimentin but not E-cadherin and displayed mesenchymal morphology (Figure 3D).

Conclusions

We have demonstrated the ability to sort live cells based on intracellular cancer biomarker expression using SmartFlare™ RNA detection technology. The sorted products were then returned to culture, where they remain viable and unchanged following detection, enabling downstream analyses, such as antibody staining, functional assays and RT-PCR.

Sorting cells using any miRNA or mRNA of interest followed by the ability to use those same cells for additional experiments makes SmartFlare™ technology an extremely powerful research tool. SmartFlare™ probes enable the simultaneous detection of multiple RNAs, as well as measurement of nucleic acids, proteins, and functional characteristics in the same live cells, providing a link between the transcriptome, the proteome and their functions that was missing until now. The ability to sort cells and obtain a highly enriched cell population based on gene expression also greatly increases the sensitivity of cell analysis—analyzing the molecular roles of rare events and labile species is now possible.

References

1. Stinson et al. TRPS1 targeting by miR-221/222 promotes the epithelial-to-mesenchymal transition in breast cancer. *Sci Signal*. 2011 Jun 14;4(177):ra41.
2. Zhang N et al. MicroRNA-30a suppresses breast tumor growth and metastasis by targeting metadherin. *Oncogene* 2013, Jul 15; 1-10

For more information, please visit:
www.emdmillipore.com/SmartFlare

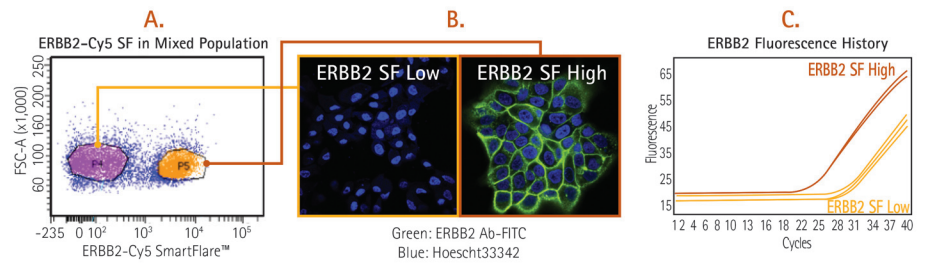


Figure 1.

A mixed population of cells was sorted into subpopulations based on ERBB2 SmartFlare™ probe intensity (A). When the sort products were stained with anti-ERBB2 antibody (B, green), the ERBB2 SmartFlare™-high cells (corresponding to BT474 cells) were positive. The qRT-PCR analysis confirmed the difference in ERBB2 mRNA levels.

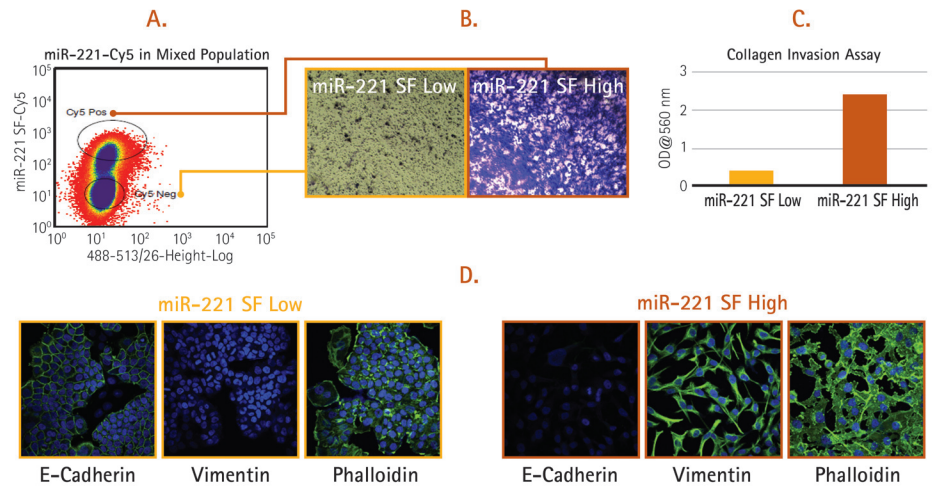


Figure 2.

Cy5 positive cells ("miR-221-high") and Cy5 negative cells ("miR-221-low") were sorted (A) and analyzed using a transwell collagen invasion assay. Cells that invaded through to the underside of the transwell membrane were stained and either visualized (B) or the stain was extracted and absorbance measured (C). ICC using the antibodies listed was used for EMT characterization of the sort products (D).

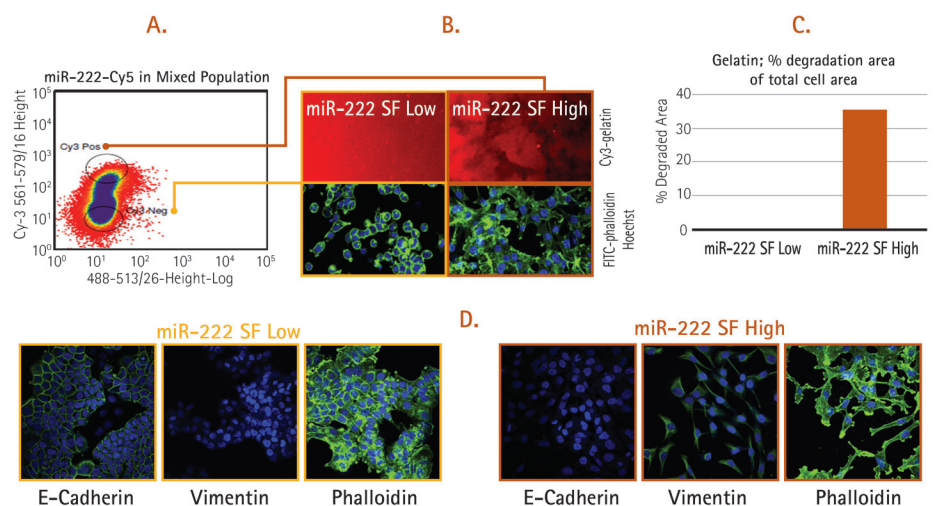
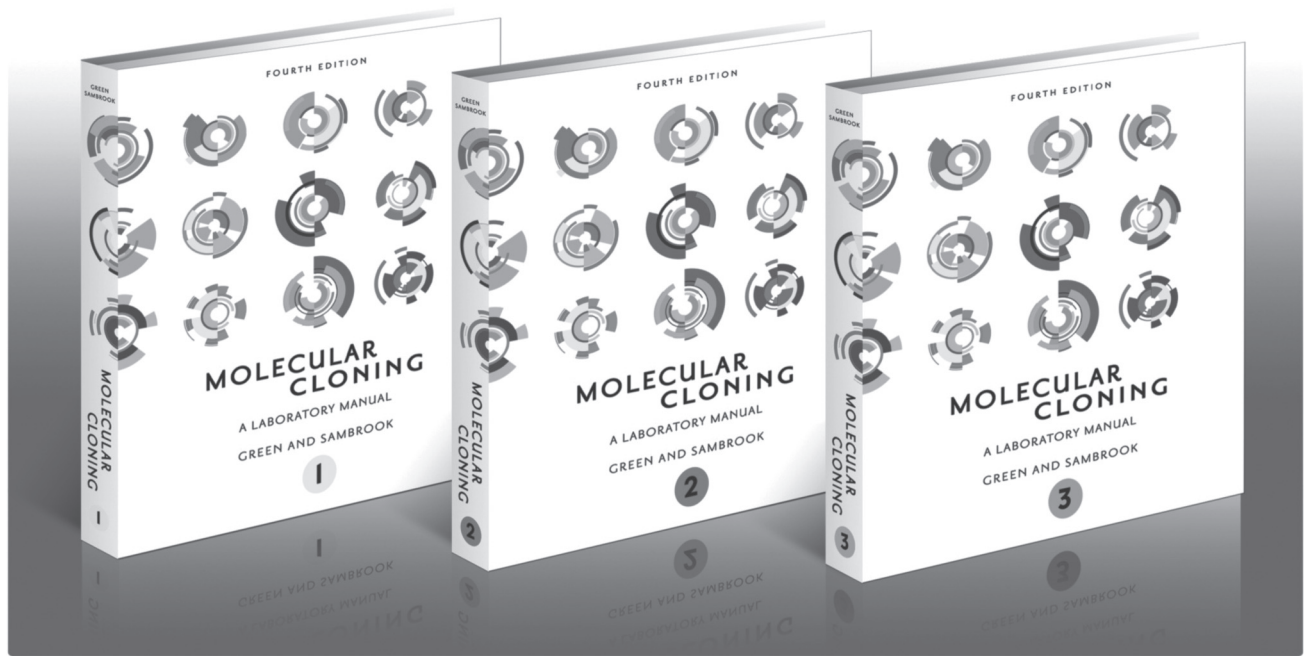


Figure 3.

Cy3 positive cells ("miR-222-high") and Cy3 negative cells ("miR-222-low") were sorted (A) and analyzed using an invadopodia formation assay. Invadopodia that degraded the gelatin matrix could be seen as dark areas on the red gelatin substrate and quantified using ImageJ software (B and C). ICC using the antibodies listed was used for EMT characterization of the sort products (D).



MOLECULAR CLONING 4



By Michael R. Green, *Howard Hughes Medical Institute, University of Massachusetts Medical School* and Joseph Sambrook, *Peter MacCallum Cancer Institute, Melbourne, Australia*

Molecular Cloning: A Laboratory Manual has always been the **M**one indispensable molecular biology laboratory manual for protocols and techniques. The fourth edition of this classic manual preserves the detail and clarity of previous editions as well as the theoretical and historical underpinnings of the techniques presented. Ten original core chapters reflect developments and innovation in standard techniques and introduce new cutting-edge protocols. Twelve entirely new chapters are devoted to the most exciting current research strategies, including epigenetic analysis, RNA interference, genome sequencing, and bioinformatics. This manual is essential for both the inexperienced and the advanced user.

2012, 2,028 pp., illus., appendices, index

Cloth (three-volume set)

\$395

ISBN 978-1-936113-41-5

Paperback (three-volume set)

\$365

ISBN 978-1-936113-42-2

Contents

VOLUME 1

Part 1 Essentials

1. Isolation and Quantification of DNA
2. Analysis of DNA
3. Cloning and Transformation with Plasmid Vectors
4. Gateway Recombinational Cloning
5. Working with Bacterial Artificial Chromosomes and Other High-Capacity Vectors
6. Extraction, Purification, and Analysis of RNA from Eukaryotic Cells
7. Polymerase Chain Reaction
8. Bioinformatics

VOLUME 2

Part 2 Analysis and Manipulation of DNA and RNA

9. Quantification of DNA and RNA by Real-Time Polymerase Chain Reaction
10. Nucleic Acid Platform Technologies
11. DNA Sequencing
12. Analysis of DNA Methylation in Mammalian Cells
13. Preparation of Labeled DNA, RNA, and Oligonucleotide Probes
14. Methods for In Vitro Mutagenesis

Part 3 Introducing Genes into Cells

15. Introducing Genes into Cultured Mammalian Cells
16. Introducing Genes into Mammalian Cells: Viral Vectors

VOLUME 3

Part 4 Gene Expression

17. Analysis of Gene Regulation Using Reporter Systems
18. RNA Interference and Small RNA Analysis
19. Expressing Cloned Genes for Protein Production, Purification, and Analysis

Part 5 Interaction Analysis

20. Cross-Linking Technologies for Analysis of Chromatin Structure and Function
21. Mapping of In Vivo RNA-Binding Sites by UV-Cross-Linking Immunoprecipitation (CLIP)
22. Gateway-Compatible Yeast One-Hybrid and Two-Hybrid Assays

Appendices

1. Reagents and Buffers
2. Commonly Used Techniques
3. Detection Systems
4. General Safety and Hazardous Material

Index



WWW.CSHLPRESS.ORG



Manipulating the Mouse Embryo

A Laboratory Manual, Fourth Edition

By Richard Behringer, *University of Texas, M.D. Anderson Cancer Center*, Marina Gertsenstein, *Toronto Centre for Phenogenomics, Transgenic Core*, Kristina Vintersten Nagy, *Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto*, and Andras Nagy, *Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto*

This fourth edition of “The Mouse Manual” is once again the definitive reference source on mouse development, transgenesis techniques, and molecular biology. Its preeminent authors Richard Behringer, Marina Gertsenstein, Kristina Nagy, and Andras Nagy have reorganized and updated this edition to include new information and protocols on:

- generation of induced pluripotent stem cells
- RNA microinjections
- lentiviral microinjections and infection
- assisted reproduction techniques for sperm and embryo cryopreservation
- isolation, generation, and transplantation of spermatogonial stem cell lines
- in utero electroporation of gene constructs into postimplantation embryos
- vibratome sectioning of live and fixed tissues for imaging thick tissue sections
- whole-mount fluorescent staining methods for three-dimensional visualization

Recombinant DNA techniques and methods for studies of mouse embryonic development have been updated from previous editions, as has the wealth of information on mouse laboratory strains, mouse housing and breeding, surgical procedures, assisted reproduction, handling of embryos, and micromanipulation setups. The first edition of this classic work appeared more than 20 years ago, with authors that included Brigid Hogan, Rosa Beddington, Frank Costantini, and Elizabeth Lacy. The field's technological sophistication has grown exponentially but the manual remains the essential practical and theoretical guide for all students, lab technicians, and investigators who work with mice.

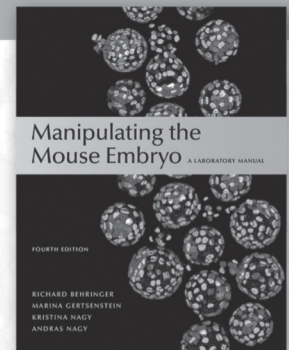
2013, 814 pp., illus. (42 4C, 134 BW), index

Hardcover \$240

Paperback \$165

ISBN 978-1-936113-00-2

ISBN 978-1-936113-01-9



Contents

Preface	Chapter 10 Vector Designs for Pluripotent Stem Cell–Based Transgenesis and Genome Alterations	Chapter 16 Cryopreservation, Rederivation, and Transport of Mouse Strains
Chapter 1 Genetics and Embryology of the Mouse: Past, Present, and Future	Chapter 11 Introduction of Foreign DNA into Embryonic Stem Cells	Chapter 17 Techniques for Visualizing Gene Products, Cells, Tissues, and Organ Systems
Chapter 2 Summary of Mouse Development	Chapter 12 Production of Chimeras	Chapter 18 Setting Up a Micromanipulation Laboratory
Chapter 3 A Mouse Colony for the Production of Transgenic and Chimeric Animals	Chapter 13 Genotyping	Appendices:
Chapter 4 Recovery and In Vitro Culture of Preimplantation Embryos	Chapter 14 Parthenogenesis, Pronuclear Transfer, and Mouse Cloning	Buffers and Solutions
Chapter 5 Isolation, Culture, and Manipulation of Postimplantation Embryos	Chapter 15 Assisted Reproduction: Ovary Transplantation, In Vitro Fertilization, Artificial Insemination, and Intracytoplasmic Sperm Injection	WWW Resources
Chapter 6 Surgical Procedures		General Safety and Hazardous Material Information
Chapter 7 Production of Transgenic Mice by Pronuclear Microinjection		Index
Chapter 8 Embryo-Derived Stem Cell Lines		
Chapter 9 Germline–Competent Stem Cells Derived from Adult Mice		



www.cshlpress.org



RNA interference

SKILLED AND ACCOMPLISHED siRNA CAPABILITIES

Specializing in the design and synthesis of siRNA, miRNA, siRNA-Aptamer and RNA oligos with challenging combinations of modifications

SmartBase™ siRNA modifications to specifically increase duplex stability, nuclease resistance and cell permeation.

SmartSeed™ siRNA modifications that assist to minimize the off-target effects induced by seed region complementarity.

Guaranteed RNAi Explorer™ Simply give us the accession number or sequence and Gene Link designs, synthesizes and supplies 3 siRNA. Gene Link guarantees a minimum of 70% silencing of your gene with at least one of the siRNA supplied*.

Gene Link. Results you can rely on.

*Not every siRNA can effectively down regulate a gene. The process of RNA interference varies by individual siRNA while some do not exhibit any interference at all.



toll free: **1-800-GENE LINK**

www.genelink.com



Gene Link™

190 Saw Mill River Road
Hawthorne, NY 10532
tel: 914-769-1192
email: support@genelink.com



Exo-Glow™

Fluorescently label exosome RNA and protein cargo to monitor cellular delivery

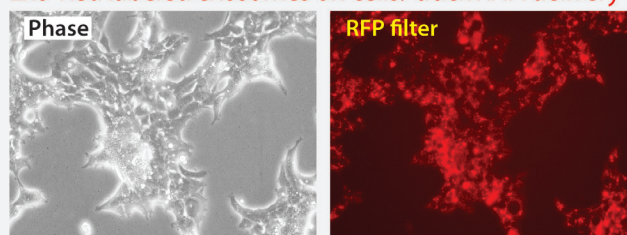
LEARN MORE



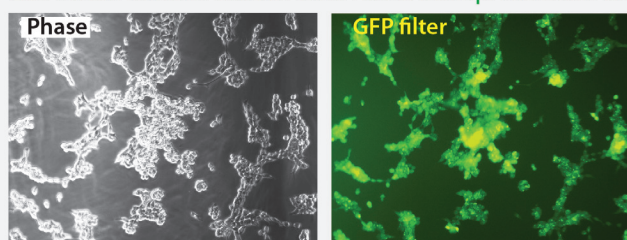
www.systembio.com/RedRNA

Exosomes are nano-sized membrane signaling vesicles secreted by most cell types in vivo and in vitro and are shuttles that transport signaling RNAs and proteins to other cells. The Exo-Glow kits allow you to fluorescently-label isolated exosomes to track cellular interaction and uptake. You can fluorescently label endogenous exosome RNAs red or internal exosome proteins green for tracking. These red exoRNAs and green exosome proteins can then be monitored for delivery into target cells using fluorescent microscopy. Visit www.systembio.com/exosomes to view the entire Exosome research toolbox.

Exo-Red labeled exosomes on cells: track RNA delivery



Exo-Green labeled exosomes on cells: track protein delivery



ExoQuick

Rapid exosome isolation

Antibodies

Exosome Abs and ELISAs

Exo-FBS

Exosome depleted media supplement

Exo-Flow

Immunopurify specific exosomes

Exo-NGS

Sequence exoRNA for biomarkers