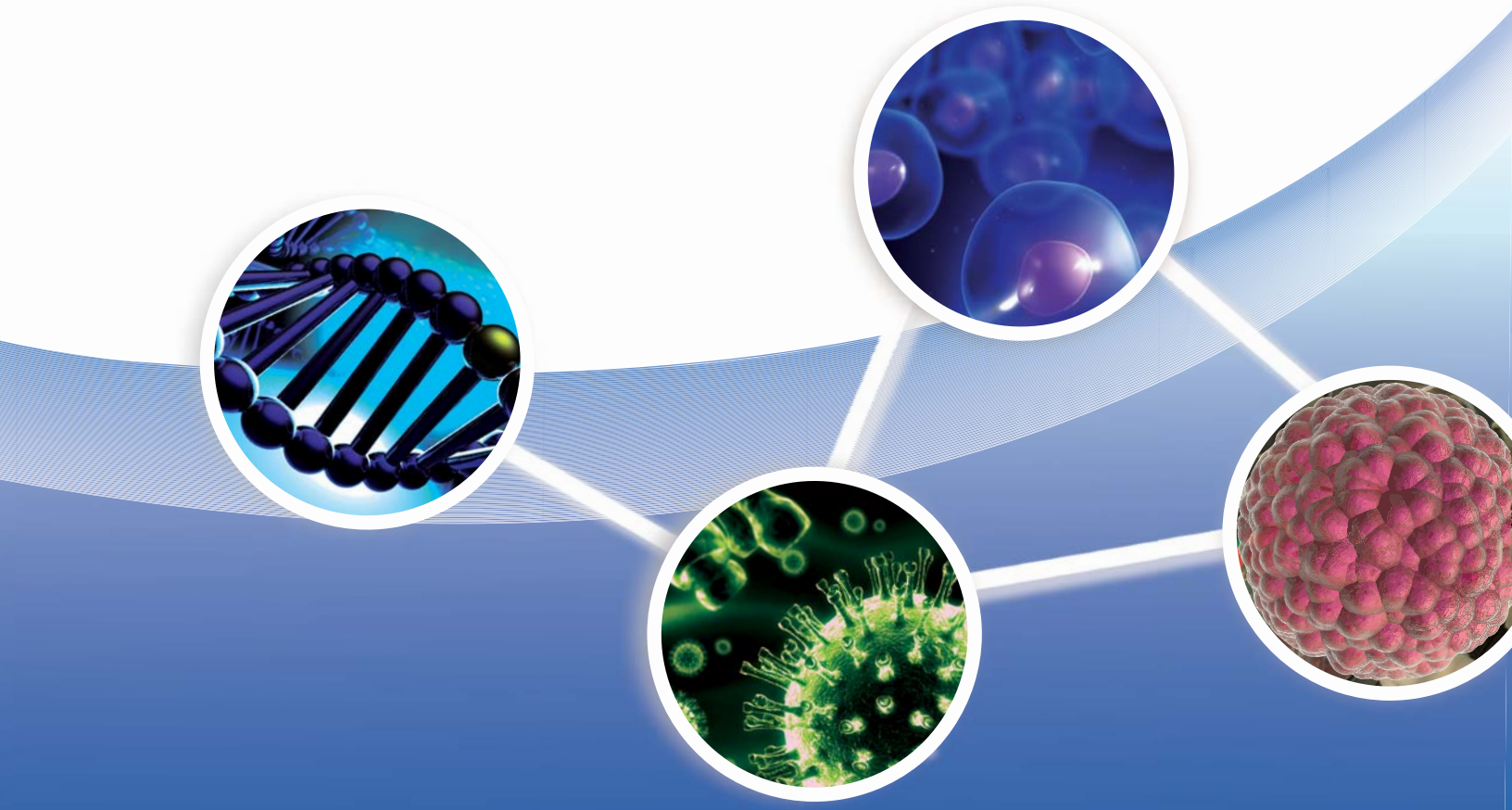
SBI
System Biosciences
Accelerating discoveries through innovations

MicroRNA Research

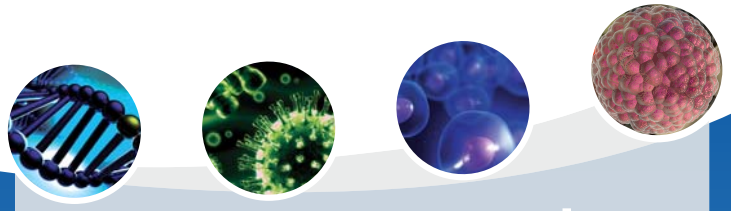
Expression Profiling • Overexpression • Knockdown • Libraries • Target Sensors



Spend less time making tools, and more time making discoveries

Essential Tools for MicroRNA and LncRNA Research

MicroRNAs are a class of naturally-occurring, small non-coding RNAs that control gene expression by translational repression or mRNA degradation. They are widely expressed throughout the plant and animal kingdoms and may comprise 1-5% of animal genes. Like protein-coding genes, microRNAs are transcribed in the nucleus as long primary transcripts (pri-microRNAs). However, distinct from protein-coding genes, they are subsequently cleaved by the nuclear RNase III enzyme Drosha to produce structured, stem-loop precursor molecules (pre-microRNAs) of 70-100 nucleotides (nt) in length. The pre-microRNAs are then exported to the cytoplasm in a process involving exportin-5, where the RNase III enzyme Dicer further processes them into mature microRNAs (~22 nt). One strand of the microRNA duplex is subsequently incorporated into the RNA-induced silencing complex (RISC) that regulates target gene expression. SBI has integrated solutions for microRNA analysis from expression profiling with QuantiMir™ & RNA-Quant™ kits, to overexpression of microRNAs using constitutive LentiMir™ and inducible iMIR™ precursor clones, as well as miRZip™ microRNA knockdown constructs and the microRNA target identification system miR-Selection™. SBI has also developed new technologies to quantify long noncoding RNAs (LncRNAs) by qPCR as well as track their cellular movement using the Spinach RNA fluorophore tag technology.



Index

Contact us today

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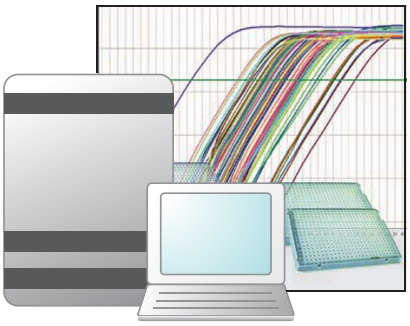
Accurate and Sensitive MicroRNA Profiling

Measure microRNAs by qPCR with QuantiMir™

MicroRNA and siRNA expression analysis is made easy with the QuantiMir™ small RNA quantitation system. Generate qPCR-ready cDNA from total RNA for accurate and sensitive expression measurements. QuantiMir rapidly tags and converts all small RNAs into detectable cDNAs for qPCR —one cDNA synthesis required to quantitate any microRNA.

Capture more expression data with genome-wide miRNome qPCR Profilers

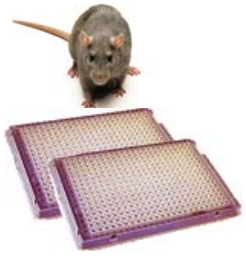
Complete Human, Mouse and Rat qPCR Arrays - 100% miRBase compatible. Characterize microRNA signatures in stem cells, cancer cell lines and FFPE samples. Custom qPCR arrays are also available.



Human complete set

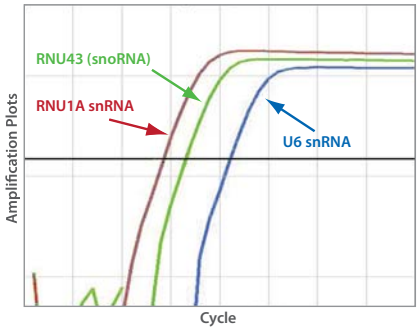
Mouse complete set

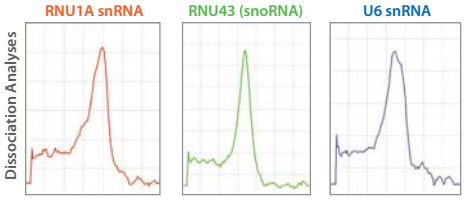
Rat complete set



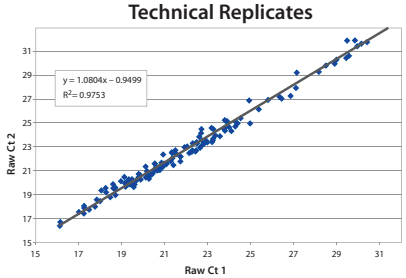
All miR major and minor miR* forms

miRNome Array Controls





Technical Replicates



Cancer and Stem Cell Focused qPCR Arrays

OncoMir microRNA qPCR Array

Detect microRNAs most commonly found in Cancer

	1	2	3	4	5	6	7	8	9	10	11	12
A	let-7 family	miR-7	miR-92	miR-93	miR-9-1	miR-101	miR-103	miR-106a	miR-106b	miR-107	miR-10b	miR-1
B	miR-122a	miR-125a	miR-125b	miR-126	miR-128b	miR-132	miR-133a	miR-134	miR-135b	miR-136	miR-137	miR-140
C	miR-141	miR-142-3p	miR-143	miR-145	miR-146a	miR-149	miR-150	miR-151	miR-153	miR-154	miR-155	miR-15a
D	miR-15b	miR-16	miR-17-3p	miR-17-5p	miR-181a	miR-181b	miR-181c	miR-181d	miR-183	miR-185	miR-186	miR-188
E	miR-18a	miR-190	miR-191	miR-192	miR-194	miR-195	miR-196a	miR-197	miR-198	miR-199ab	miR-30b	miR-19ab
F	miR-95	miR-20a	miR-200a	miR-200b	miR-200c	miR-202	miR-203	miR-204	miR-205	miR-206	miR-21	miR-210
G	miR-214	miR-215	miR-372	miR-373	miR-218	miR-219	miR-22	miR-488	miR-221	miR-222	miR-223	miR-224
H	miR-23a	miR-24	miR-25	miR-26a	miR-26b	miR-27ab	miR-30c	miR-29abc	miR-30a-3p	miR-30a-5p	miR-296	U6 snRNA

Stem Cell microRNA qPCR Array

Profile microRNAs in Pluripotency and Differentiation

	1	2	3	4	5	6	7	8	9	10	11	12
A	miR-18a	miR-19a	miR-19b	miR-24	miR-25	miR-17-5p	miR-30c	miR-34a	miR-106a	miR-106b	miR-130b	miR-141
B	miR-150	miR-199a	miR-200b	miR-200c	miR-301	miR-302a	miR-302b	miR-302c	miR-302d	miR-367	miR-368	miR-369-5p
C	miR-369-3p	miR-370	miR-371	miR-372	miR-373	let-7a	let-7b	miR-10a	miR-10b	miR-16	miR-17-3p	miR-20a
D	miR-20b	miR-23a	miR-23b	miR-26a	miR-26b	miR-30b	miR-30d	miR-32	miR-33	miR-92	miR-93	miR-99a
E	miR-101	miR-107	miR-126	miR-130a	miR-142-5p	miR-142-3p	miR-146a	miR-146b	miR-155	miR-181a	miR-181b	miR-181c
F	miR-181d	miR-191	miR-193a	miR-193b	miR-197	miR-221	miR-223	miR-339	miR-9	miR-103	miR-124a	miR-125a
G	miR-125b	miR-127	miR-128a	miR-128b	miR-132	miR-134	miR-135a	miR-135b	miR-136	miR-138	miR-149	miR-153
H	miR-154	miR-183	miR-218	miR-219	miR-222	miR-1	miR-122a	miR-133a	miR-133b	miR-195	miR-206	U6 snRNA

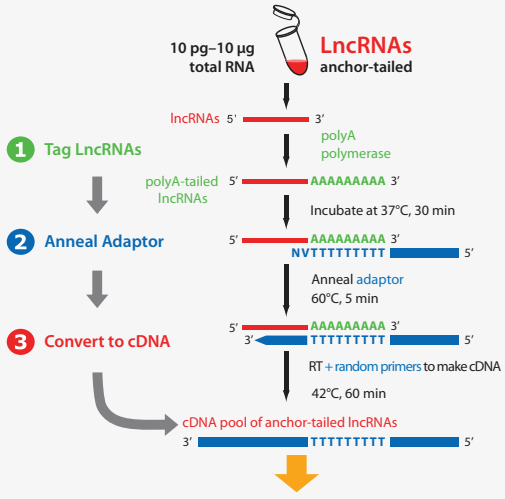
For more information: **www.systembio.com/mirnome**

Quantitate Long Non-coding RNAs by qPCR

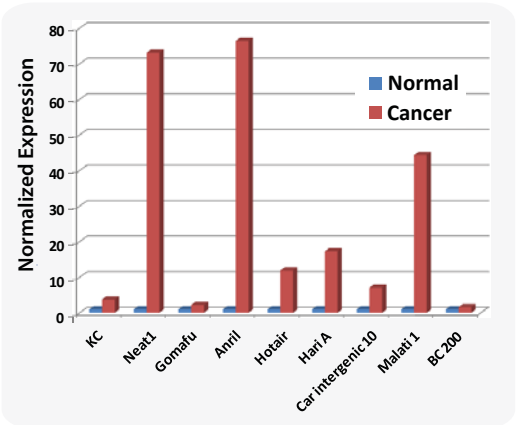
Long non-coding RNAs (LncRNAs) and large intergenic non-coding RNAs (lincRNAs) are emerging as master regulators of embryonic pluripotency, differentiation, patterning of the body axis and promoting developmental transitions. LncRNAs are larger than 200 nucleotides in length and are pervasively expressed across the genome. LncRNAs maintain the commitment to specific cellular fates through modification and remodeling of chromatin at the epigenetic level.

Dysregulated expression of lncRNAs has been shown to be associated with a broad range of diseases such as Alzheimer's, psoriasis and many cancers. Studying the expression patterns of lncRNAs will be a crucial method to understanding the roles they play in many model systems. SBI has built a sensitive, accurate and robust qPCR array that is strand-specific to enable researchers to closely profile the expression changes in the top lncRNAs known to date. All of the lncRNAs on the qPCR array have validated primer sets for well-annotated lncRNAs that are registered in the lncRNA database created by Dr. John Mattick (www.lncrnadb.org).

How the lncRNA cDNA is made



Profile LncRNAs in Skin Cancer



Human Stem Cell and Cancer LncProfiler qPCR Array

	1	2	3	4	5	6	7	8	9	10	11	12
A	21A	7SK	7SL	Air	AK023948	Alpha 280	Alpha 250	ANRIL	anti-NOS2A	antiPeg11	BACE1AS	BC200
B	CAR Intergenic	DHFR upstream	Dio3os	DISC2	DLG2AS	E2F4 antisense	EgoA	EGOB	Emx2os	Evf1 and EVF2	GAS5	Gomafu
C	H19	H19 antisense	H19 upstream	HAR1A	HAR1B	HOTAIR	HOTAIRM1	HOTTIP	Hoxa11as	HOXA3as	HOXA6as	HULC
D	IGF2AS	IPW	Jpx	Kcnq1ot1	KRASP1	L1PA16	p21	RoR	SFMBT2	VLDLR	LOC 285194	LUST
E	Malat1	mascRNA	MEG3	MEG9	MER11C	ncR-uPAR	NDM29	NEAT1	Nespas	NRON	NTT	p53 mRNA
F	PCGEM1	PR antisense	PRINS	PSF inhibiting	PTENP1	RNCR3	SAF	SCA8	snaR	SNHG1	SNHG3	SNHG4
G	SNHG5	SNHG6	Sox2ot	SRA	ST7OT	TEA ncRNAs	Tmevpg1	TncRNA	Tsix	TUG1	UCA1	UM9-5
H	WT1-AS	Xist	Y RNA-1	Zeb2NAT	Zfas1	Zfhx2as	18S rRNA	RNU43	GAPDH	LAMIN A/C	U6	No assay control

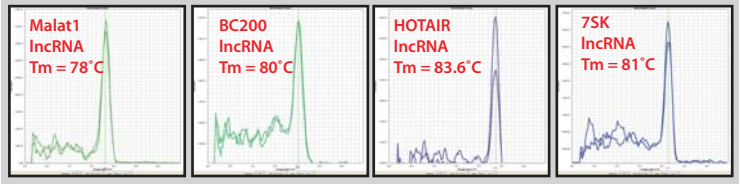
Mouse LncProfiler qPCR Array

	1	2	3	4	5	6	7	8	9	10	11	12
A	Adapt33	Air	AK007836-upstream of	AK141205-Nanog	AK028326-Oct4	AK082072	ATIA	antiPeg11	B2 SINE RNA	BACE1AS	BC1	BGn-As
B	BORG	CDR1-antisense	Dio3os	Dlx1as	Emx2os	Evf2	Foxn2-as	GAS5	Gomafu	Gtl2-as	H19	H19 antisense
C	m HOTAIR	HOTTIP	Hoxa11as	IGF2AS	Jpx	Kcnq1ot1	linc1242 LINC-Enah	LINC1331	linc1368	Linc1612	linc1547	linc1582
D	linc1609-long	linc1609-short	linc1610-long	linc1610-medium	linc1610-short	Linc 1623	Linc1633	lincENC1	lincRNA-Cox2	lincRNA-p21	lincRNA-Sox2	LINC -MD1
E	LXRBSV	Malat1	mascRNA	MEG3	MEG9	MSUR1	Msx1as	Neat1 v1/ MEN	Neat1 v2/ Men beta	Nespas	Nkx2.2AS	NRON
F	Otx2os	PINC	PINC 1Kb isoform	Pldi	Recombination hot spot	RepA transcript	Rian	Rmst	Rmst	SCA8 (KLHL1-AS)	Six3os	Six3os-clone9
G	SNHG1	SNHG3	SNHG4	SNHG5	SNHG6	Sox2ot	SRA	Tsix	TUG1-	Vax2os1	VL30 RNAs	WT1-AS
H	Xist	Y RNAs	Zeb2NAT	Zfas1	Zfhx2as	Mistral	18S rRNA	RNU43 (snoRNA)	GAPDH	Beta Actin	U6 snRNA	No assay control

Human Disease-related qPCR Array

	1	2	3	4	5	6	7	8	9	10	11	12
A	21A	AAA1	aHIF	AK023948	ANRIL	anti-NOS2A	BACE1AS	BC017743	BC043430	BC200	BCMS	BIC
B	CCND1 ANCR	CMPD	DD3	DGCR5	DISC2	DLG2AS	EGO	GAS5	GOMAFU	H19	H19-AS	HAR1A
C	HAR1B	HOTAIR	HOTAIRM1	HOTTIP	HOXA1AS AA489505	HOXA3AS BI823151	HOXA3AS BE873349	HOXA6AS AK092154	HOXA11AS	HULC	IPW	IGF2AS
D	KRASP1	L1PA16	LIT	LOC285194	LUST	LincRNA VLDLR	LincRNA SFMBT2	MALAT1	MEG3	MER11C	NEAT1	NCRMS
E	NDM29	PANDA	PAR5	PCAT1	PCAT14	PCAT29	PCAT32	PCAT43	PCGEM1	PR-AT2	PRINS	PSF inhibiting RNA
F	PTENP1	RMRP	ROR	SAF	SCA8	Sox2OT	SRA	ST7OT1	ST7OT2	ST7OT3	ST7OT4	Telomerase RNA
G	TMEVPG1	TU_001762 9	TUG1	UCA1	WT1-AS	Y1	Y3	Y4	Y5	ZEB2NAT	7SK	Negative control
H	7SLscRNA	5.8SrRNA	U87 scaRNA	U6 smRNA	ACTB	B2M	PGK1	GAPDH	HPRT1	RPL1A	RPL13A	GDC

Human Cancer and Stem Cell qPCR Assay Specificty Tests

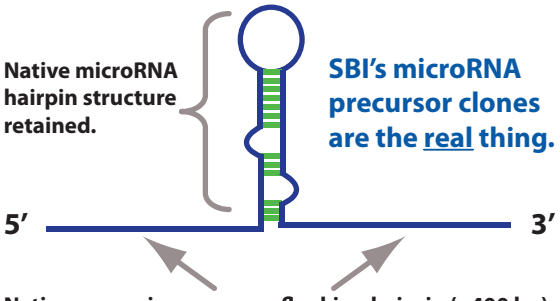


www.systembio.com/LncRNA

Overexpress Human and Mouse MicroRNAs

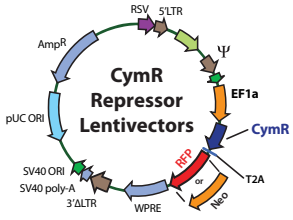
There are expected to be over 2,000 different microRNAs encoded in the human and mouse genomes and they function by either blocking translation of, or degrading, mRNA species corresponding to specific genes. While the number of verified human and mouse microRNAs are expanding, there is an increasing need for effective functional testing. SBI offers an extensive collection of microRNA precursors in lentiviral vectors that can be used to modulate the expression of their targeted mRNAs to study microRNA function. The lentiviral vector constructs can be packaged into pseudoviral particles and delivered to primary cells, stem cells, or other hard-to-transfect cell lines and can be used *in vivo*. SBI can package any construct into high titer lentivirus as a custom service for your studies.

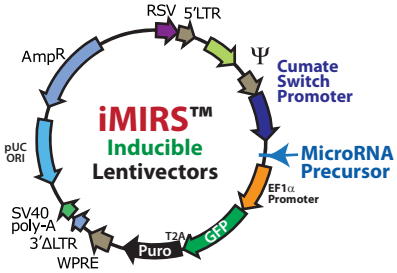
Each construct in SBI's collection consists of the native stem loop structure and 200-400 base pairs of upstream and downstream flanking genomic sequence. This unique feature ensures that the microRNAs expressed from SBI's constructs will be correctly processed in the cell into mature microRNA.



Inducible Human iMIRS

The dual promoter vector configuration enables the inducible expression of the microRNA precursor. The downstream EF1α promoter will constitutively express the GFP+Puro dual markers independent of the cumate switch activation. This system is expressing the microRNA by default and you choose whether or not to add the CymR repressor into the system for inducible regulation.



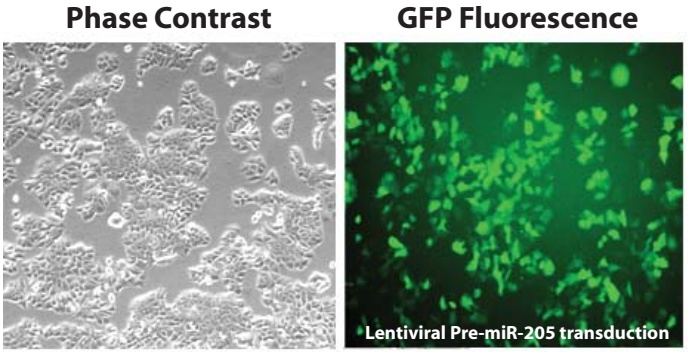


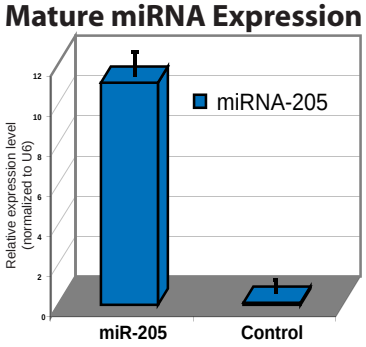
iMIRS
Cumate Inducible Human Lenti-miRs

Constitutive Human and Mouse Lenti-miRs

The advantage of SBI's constructs is that they can be used in transient transfection experiments as well as stably expressed in a wide variety of cell types, as opposed to synthetic microRNAs that can only be transiently expressed in cells.

MCF-7 cells transduced with Lenti-miR-205





MCF-7 Cells infected (MOI 5:1) with Lentivirus made from PMIRH205PA-1 (pre-miR-205) construct. Images taken after 48 hours. Expression of mature miR-205 was validated and quantitated using ABI TaqMan assays.

For more information: **www.systembio.com/lentimir**

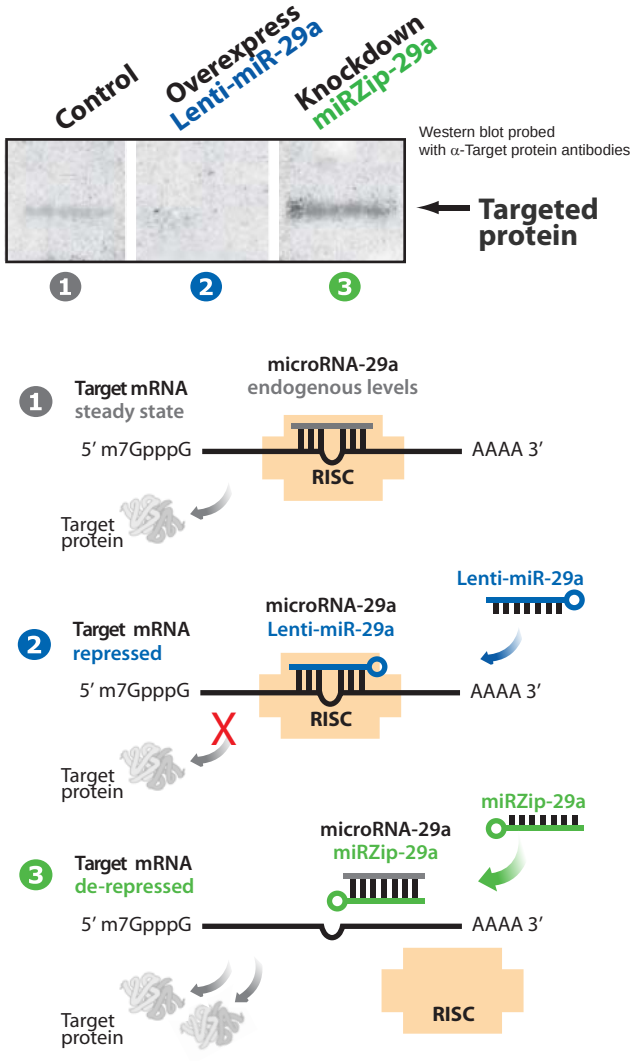
Block MicroRNA Functions with miRZips™

miRZip anti-sense microRNAs are stably expressed RNAi hairpins that have anti-microRNA activity. These miRZip shRNAs produce short, single-stranded anti-microRNAs that competitively bind their endogenous microRNA target and inhibit its function. The result is the derepression and elevation of the protein levels of the transcripts targeted by the microRNA being "zipped".

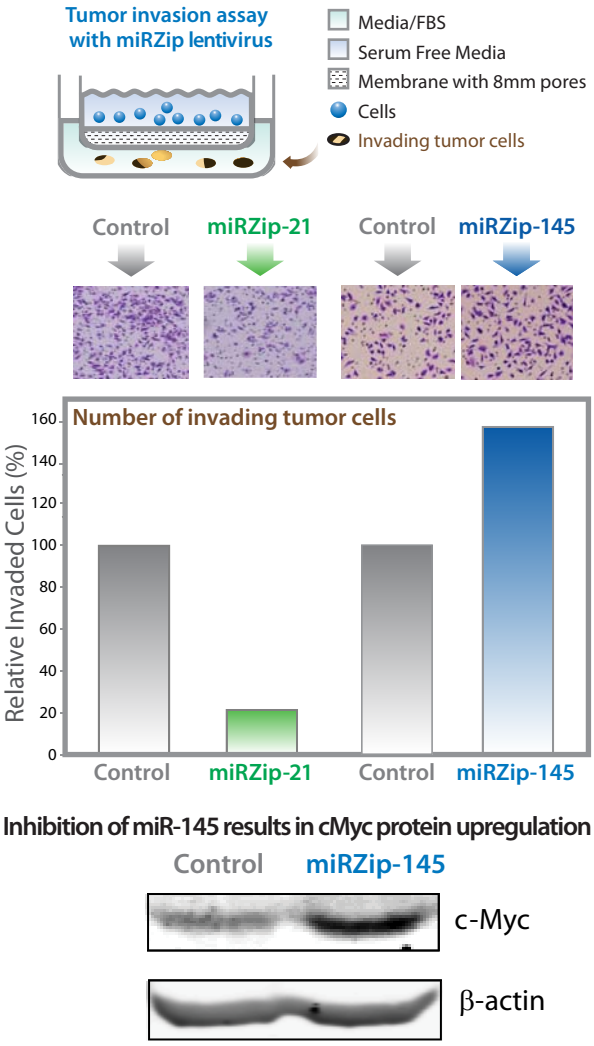
Permanent MicroRNA Knockdown

The miRZip short hairpin RNAs are cloned into SBI's pGreenPuro™ shRNA expression lentivector. The miRZip hairpins are designed for asymmetry such that the lower strand is preferred for producing anti-sense microRNAs that are fully complementary to a specific microRNA target, forming a stable duplex that keeps the zipped microRNA from binding target UTR sequences. Custom constructs, including multiple miRZips in a single vector, are also available.

How miRZips Work



Discover MicroRNA Phenotypes



Inhibition of miR-145 results in cMyc protein upregulation

For more information: **www.systembio.com/mirzips**

MicroRNA Lentivirus Screening Libraries

The Lenti-miR™, OncoMir and miRZip™ pooled virus libraries are tools that enable the study of phenotypic effects associated with the overexpression or suppression of individual microRNAs. The lentivirus preparation is pseudotyped with VSV-G that allows for broad cellular tropism. Use these libraries with hard-to-transfect mammalian cell lines, primary cells, non-dividing cells and even whole animal studies. Transduced cells exhibiting the phenotypes of interest are isolated by selection or sorting. The microRNA or microRNAs responsible for generating the phenotypes of interest may be recovered through simple genomic PCR using lentivector-specific primers followed by direct sequencing of microRNA precursor or miRZip anti-miR shRNA hairpin clones.

Perform one transduction and easily identify the microRNAs involved in your phenotypic screen

SBI's pooled lentiviral libraries allow you to perform high-throughput screening studies on a genome-wide or cancer-focused basis. Pooled lentiviral libraries enable simultaneous identification of multiple genes that alter a specific cellular phenotype in a single experiment. Lentiviral libraries are available as prepackaged virus, so you can begin transducing cells the day you receive the library.

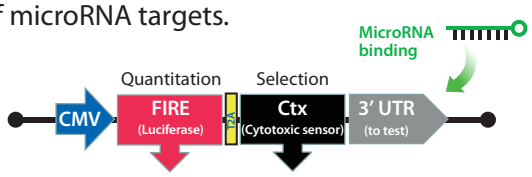
Use microRNA libraries to find targets

Target Selection System

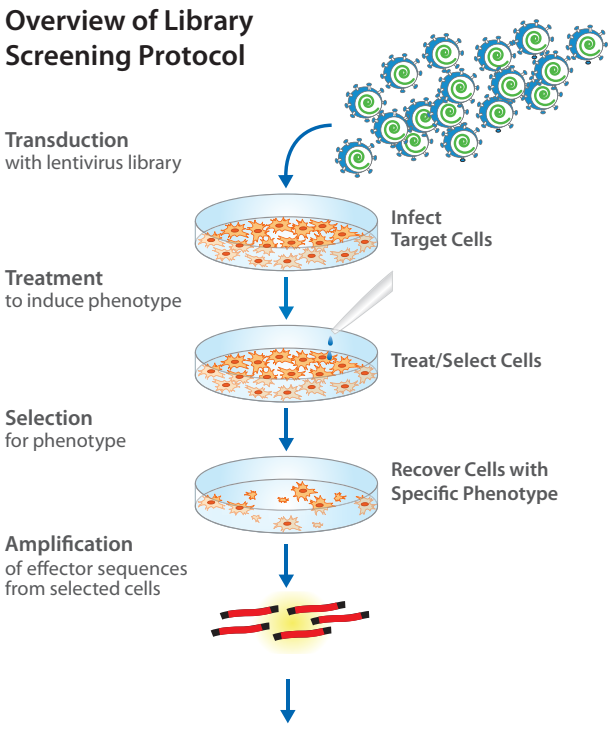
Identify Binding Sites through Cellular Selection and Quantitate Target Interactions

Novel cellular method to detect microRNA binding to its target mRNA using a dual reporter system featuring Luciferase (Fire) and a Cytotoxic Sensor (Ctx). The miR-Select platform captures the 3′ UTR to microRNA binding event using a survival screen by modulating the reduction of the cytotoxic sensor. Validation is made simple using the built-in Luciferase reporter. This powerful and elegant technology finally enables the accurate identification of microRNA targets.

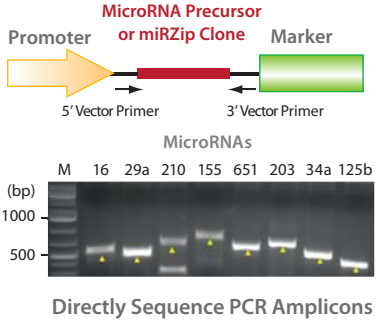
The miR-Select Fire-Ctx-UTR Lentivector



How to use Pooled Lentiviral Libraries



Simple Genomic PCR to Identify microRNA Effectors



Directly Sequence PCR Amplicons

MicroRNAs Affecting Phenotype Identified

For more information: **www.systembio.com/microrna**

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