

# Profiling of Long Non-coding RNA by Quantitative PCR www.systembio.com/LncRNA

265 North Whisman Rd. Mountain View, CA 94043

Nandita Sarkar\* and Travis Antes

### LncRNA Overview

Long non-coding RNAs (LncRNAs) 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 function as molecular scaffolds regulating histone modifications and influence the epigenetic programs of the transcriptome. Dysregulated expression of IncRNAs has been shown to be associated with a broad range of defects in development and diseases. Studying the expression patterns of IncRNAs will be a crucial method to understanding the roles they play in many model systems.

# LncProfiler qPCR Arrays

SBI's LncProfilers comes as complete cDNA synthesis kits combined with a 96-well based qPCR assay set for either Human or Mouse IncRNAs. The qPCR assays have been validated across numerous cell types for robust and specific performance. Some IncRNAs have endogenouse polyA tails, while other IncRNAs do not. To enhance qPCR assay performance, the cDNA synthesis kit includes reagents to polyadenylate all IncRNAs before cDNA conversion using the tagged oligo dT adaptor and random primers. This combined RNA tailing and oligo dT plus random primers boosts cDNA yield significantly and enables strand-specific IncRNA qPCR profiling.

## Screen Cancer Phenotypes

Comparison of IncRNA expression in Human normal Fibroblasts and Fibrosarcoma cells.

Total RNA was isolated from approximately 2x10^6 cells using standard Trizol/Ethanol precipitation methods. Two micrograms of the RNA samples were used as input into the lncRNA cDNA synthesis kit. The entire cDNA synthesized was then profiled across the 90 lncRNAs and 5 reference controls on the Human LncProfiler qPCR array. LncRNAs known to be upregulated in cancer, such as Neat1, Anril, Hotair and Malat1 were all detected at highly elevated levels in the fibrosarcoma cells (HT1080) when compared to the normal fibroblast cells (HFF). The data are plotted as normalized expression levels. Selected data are shown in the bar graph.

To date, IncRNAs have been found to exhibit a wide range of functions ranging from signaling, serving as molecular decoys, guiding ribonulceoprotein complexes to specific chromatin sites and also participating as scaffolds in the formation of complexes.



### How the IncRNA cDNA is made





II. Guides



III. Scaffolds



#### Human 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
В	CAR Intergenic	DHFR upstream	Dio3os	DISC2	DLG2AS	E2F4 antisense	EgoA	EGO B	Emx2os	Evf1 and EVF2	GAS5	Gomafu
c	H19	H19 antisense	H19 upstream	HAR1A	HAR1B	HOTAIR	HOTAIRM1	HOTTIP	Hoxa11as	HOXA3as	<b>HOXA6as</b>	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 mRN
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
н	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
	Adapt33	Air	AK007836- upstream of	AK141205- Nanog	AK028326- Oct4	AK082072	ΑΤΙΑ	antiPeg11	<b>B2 SINE RNA</b>	BACE1AS	BC1	BGn-As
	BORG	CDR1- antisense	Dio3os	Dlx1as	Emx2os	Evf2	Foxn2-as	GAS5	Gomafu	Gtl2-as	H19	H19 antisense
;	m HOTAIR	ΗΟΤΤΙΡ	Hoxa11as	IGF2AS	Jpx	Kcnq1ot1	linc1242 LINC-Enah	LINC1331	linc1368	Linc1612	linc1547	linc1582
1	linc1609- long	linc1609- short	linc1610- long	linc1610- medium	linc1610- short	Linc 1623	Linc1633	lincENC1	lincRNA- Cox2	lincRNA- p21	lincRNA- Sox2	LINC -MD1
	LXRBSV	Malat1	mascRNA	MEG3	MEG9	MSUR1	Msx1as	Neat1 v1/ MEN	Neat1 v2/ Men beta	Nespas	Nkx2.2AS	NRON
	Otx2os	PINC	PINC 1Kb isoform	Pldi	Recombinat ion hot spot	RepA transcript	Rian	Rmst	Rmst	SCA8 (KLHL1-AS)	Six3os	Six3os- clone9
	church .	church -			chulc c		6D.4					

### **COMING SOON!**

With the emergence of RNA as one of the master regulators of cellular functions, it has become important to have tools that can track RNAs directly and understand their functions. Spinach is an RNA mimic of GFP developed by Dr. Jeremy Paige at the Weill Cornell Medical College. SBI will be releasing new vectors for tagging RNAs with Spinach and show applications of tagging LncRNAs.







#### G ISNHG1 ISNHG3 ISNHG4 ISNHG5 ISNHG6 ISOX200 ISRA IISIX IIUG1- IVax2001 IVL30 RNAS IWI1-AS



#### RNA mimics of green fluorescent protein. Paige JS, Wu KY, Jaffrey SR. Science. 2011 Jul 29;333(6042):642-6

