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## Supplemental Information

# LincRNA-p21 Suppresses Target mRNA Translation

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### INVENTORY of SUPPLEMENTAL INFORMATION

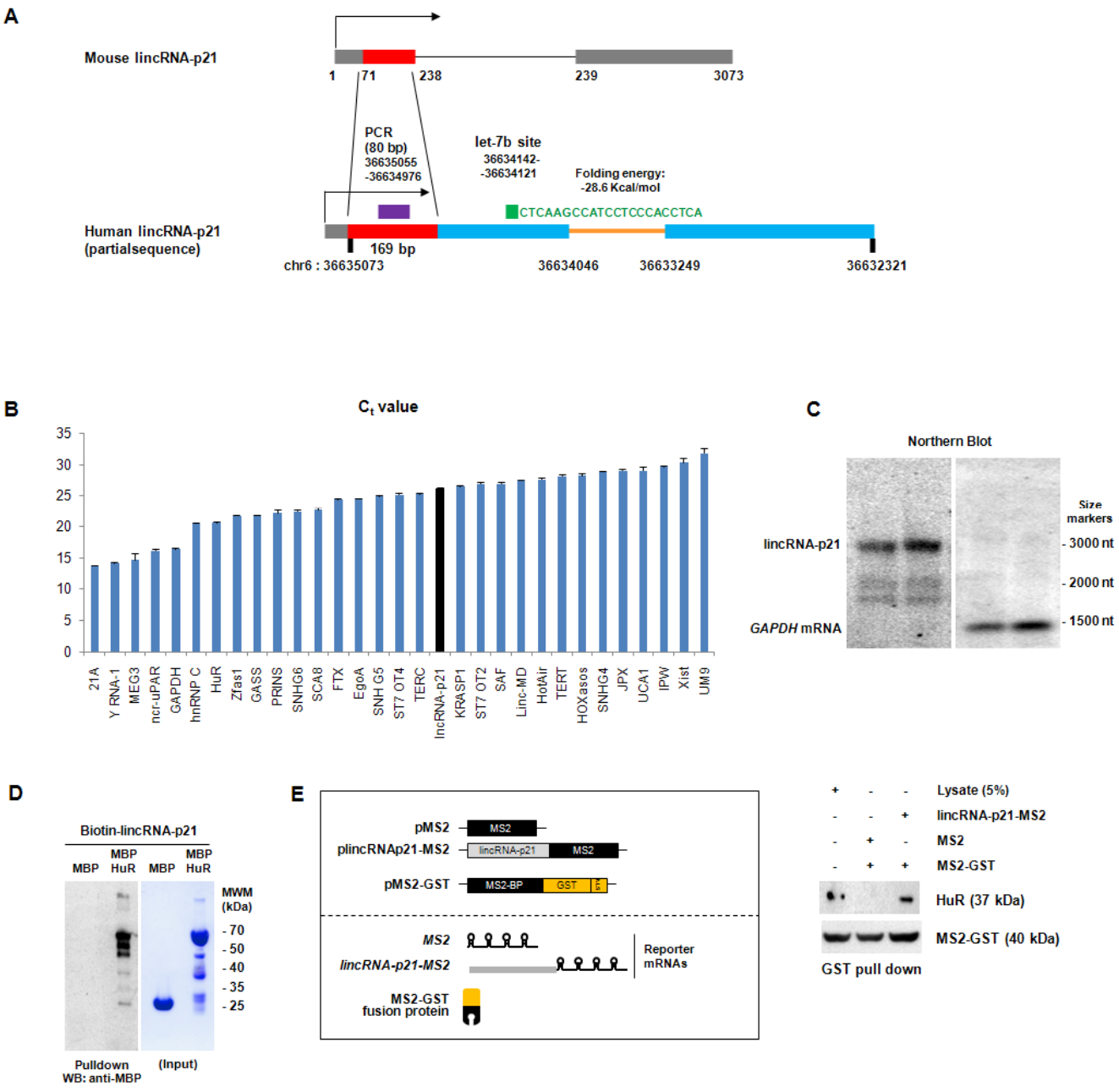
## Supplemental text

### Human lincRNA-p21 partial sequence (1956 nt)

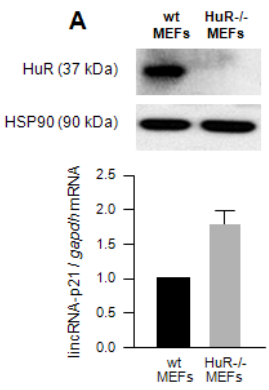
**Exon 1**: Human lincRNA-p21: hg19_dna range=chr6:36635073-36634046'pad=0 3'pad=0 strand=-
Intron 1: Human lincRNA-p21: hg19_dna range=chr6:36634045-36633250'pad=0 3'pad=0 strand=-
**Exon 2**: Human lincRNA-p21: hg19_dna range=chr6:36633249-36632321'pad=0 3'pad=0 strand=-

**GGCCGGCAGAGCTCCCGCTGGCCTTGCCCGGGCTTGTCTTTTGTTGCATTGTTGCATCATCATGCGGCCTTGCAGGGTGCCAG**
**AAGAGTGAGCCACCCACTCACCACTGGAAGAAAACAGCTAATTATATCACCAAGAGACCCAGGGCATATGGTCACTCTCAGCT**
**GGCCCAGCCTGTTTCTACTTGCTTTGCATGATTGTTCTGGATTTTTCAAAATAATAATAACTACCAACCAGGAAAAAAAAAAA**
**TCACCCCTGACTGTGGAGCGTGCTGCTGAAGTAGGAGCTTTAGTCTACCTGCTGCTCTAGGAGAGACCTACACAGCCCCCTGA**
**GCTCAGAAAACAAAAAGCCAGACTCCCAGACTAGGGTTCAATAGACAAGTGGCTCTGAGAACAGGATACACTGGAATCAGCAG**
**AATCCAAAAGACAAGCATTGCTTTGACAGCATCACAGTAATTTATTTTTTCCAAAATCTTTAAAATTCTATTTGTAGTTTAGT**
**CAAAAGTGCAGAGCGTTTTGTTTGTCCATAGTTTCCTGTATTTATTTTTTCAGTAGATAATACATTCACATGGTCCACAGTCA**
**AAAGATGCAAAAGGCTATTCAGTGAAAACTCTCCCTCCTACCCCTACCCTCCAGCTACCCATTTTCTTCCCAGAGGCTGTGGC**
**TGGTGGCTTGTGTCCCCTTCCCACAGATAGTCTAAGAACATCCAGGTCCTTCAGCTGAAACCCTTGGGCACAGATGGGTTGCA**
**GAATCTAGAACTTTTCCCATTTTAGACAGGTAATAAAGTGCATACAGCCTGTATTCCACAACACCAGCGGGCTCCGCCCAGGG**
**TGAGCAGTCAGCCAGTTTGCCCCAGACTGTTCCAGTTCCATGTCCAGGGAACCCCTTCAATCCCAGGCAAACCAAGACAGTAG**
**GTCCTGCTAGCTGTG**ggctgtaatgtattcacactaacagggacaattaaaaactgcaaatggcttcacatccttttagctct
ggttttgctaccaaataaatttgccacaaaccaaagaaaaaagttttggtttccagagccttttggatttgggaattgtggat
gaggggctggggacctatacacaatatacatatatatttttaatctgcttgaatggaaacacagtgttgggcacattgttttt
gcactcaatttatcttagtggctttccacatcagtacatagaaatcctgccctttccttttttactgctgcattggacttcaac
acacgggtgaacatttaggatgtctctagttttctgttattacaaacacacatagttttacaagcagctaacaacatggggag
ggggcagaggaggaatggaatcattctttttttttttttattggagatggagtctcactctgttgctcaggctggagtgtagt
ggtgcgaacttggctcactgcagcctccacctcccaggctcaagcaattctcctgcctcagcctcccgagtagctgggattac
aggtgtctgctatcacacccagctaaagtttttatatttttagtagaaatggagtttcaccatgttggacaggctggtctcga
actcctgacctcaggtgatccacccgcctcagcctcccaaagtgctgggattacaggcatgagccactgtacccagccaggga
tcttcattcctaatgtttgtttatgactgaaagtttatgtccaagcctgctcagaagttgcgggg**CAGAAACAAGACCTACTG**
**AGGTCTCCCAGACCAGCTGCCCCGCCCATCCACCTACATCACGAAGAGTCACTCCCATTCAGAATGATTTTTCCAAACAAGAA**
**GACAACTTACATTCAGACCTACTGTATTAGTCGGGGTTCTCCAGAGAAACAGAACCAATACAAGAATATATTCAGATAGATAT**
**AGACATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAATGTTCCTCAATTTTATGATA**
**AAGTAAAAAAATTATAAGCTGAACCATCATAAGTCAGAGACTATCTATATATCTATATACAGGCTCATGTGGGCAAAAAATAC**
**CACCCAGGGTGGGTCTCTGGTGACCAGATCCAGTTAATGAAAGGGGCTAGATTTCAGCTGATGGGGCCGTGGAAATCTGAATT**
**GGGAGCCCCCTTCCTAAAACCAAGAGAAGATCCATCCATGTGTGGTGGGGCTGAAGTTTATGCAATGATAGAGGCCTTCTTCA**
**CGATAAAGAAGGCAATTATAATACTAGGCACCCCTATGCAAATGAGAGTCCTAGAAGCCTCCTTTCATCGGTTTCACCATCAA**
**CCCACCTGTGTGTGTGGCTGAATAAAGATCAGGGAAGTAGCGGTCTCTGGGGGGCAGATGTGACACCTGGGGGGCCACAGTTC**
**TAAAACTTGAAGGACCAGAATAACCCGAGCTGAAGGAGGACACAGGAGAGGCAAGATAGAGAGAGAATGGGGCCATCCTGCAG**
**TGCCCACCACAACCGTCTATGCATCCTGGACCCCAGGCTGGCACTATACAGGGTGCTGTGTGATTCCTCACCCTCATTCTCTG**
**CCTCCACCAAGAGTAATAGGCTGGGCGTGGTGGCTCACGCCTGTAATCCCACCACTTTGGGAGGCCGAGGCAGGCGGATCACT**
**TGAGGTCAGGAGTCCAAGACCAGCCTGGCCAACAAGGCGAAACCCTGTCTCTACTAAAAATACAAAAACTAGCTGGGCGTAGT**
**GGTGGGCACCTGTA**

Rapid Amplification of cDNA Ends (RACE) was performed according to manufacturer`s protocol (Invitrogen) using total RNA from HeLa cells.


A
Mouse lincRNA-p21
1
71
238
239
3073
PCR
(80 bp)
36635055
-36634976
let-7b site
36634142-
-36634121
Folding energy:
-28.6 Kcal/mol
CTCAAGCCATCCTCCCACCTCA
Human lincRNA-p21
(partialsequence)
169 bp
chr6 : 36635073
36634046
36633249
36632321
B
Ct value
35
30
25
20
15
10
5
0
21A
Y RNA-1
MEG3
ncr-uPAR
GAPDH
hnRNP C
HuR
Zfas1
GASS
PRINS
SNHG6
SCA8
FTX
EgoA
SNH G5
ST7 OT4
TERC
lncRNA-p21
KRASP1
ST7 OT2
SAF
Linc-MD
HotAir
TERT
HOXasos
SNHG4
JPX
UCA1
IPW
Xist
UM9
C
Northern Blot
lincRNA-p21
GAPDH mRNA
Size markers
3000 nt
2000 nt
1500 nt
D
Biotin-lincRNA-p21
MBP
MBP HuR
MBP
MBP HuR
MWM (kDa)
70
50
40
35
25
Pulldown WB: anti-MBP
(Input)
E
pMS2
MS2
plincRNAp21-MS2
lincRNA-p21
MS2
pMS2-GST
MS2-BP
GST
MS2
lincRNA-p21-MS2
Reporter mRNAs
MS2-GST fusion protein
Lysate (5%)
lincRNA-p21-MS2
MS2
MS2-GST
HuR (37 kDa)
MS2-GST (40 kDa)
GST pull down

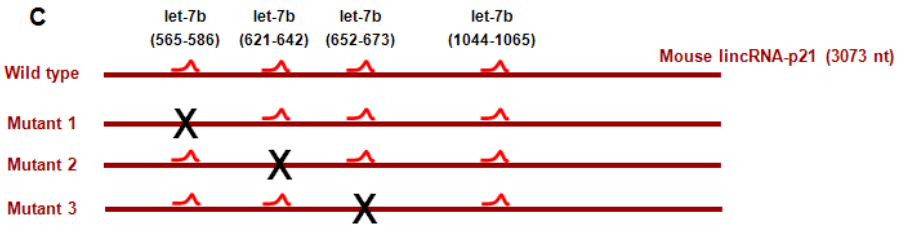
**Yoon et al. Supplementary Fig. S2**

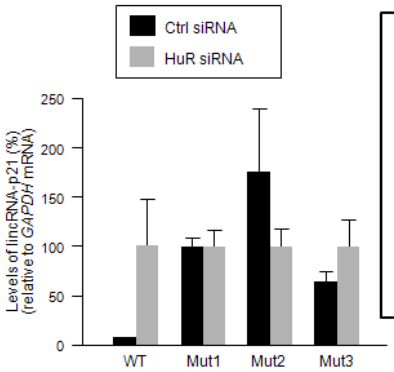



B

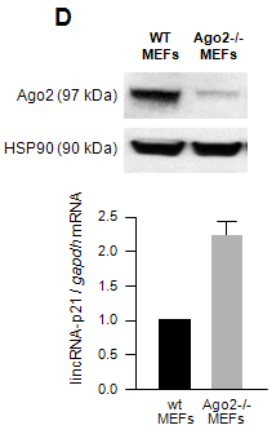
Putative miRNA targets of mouse lincRNA-p21 (3073 nt)

| miRNA | start | end |
|---|---|---|
| let-7a-1/b/c/i | 652 | 673 |
| let-7a-1/b/c/i | 565 | 586 |
| let-7b | 621 | 642 |
| let-7b | 1044 | 1065 |
| let-7c | 618 | 639 |
| let-7d | 643 | 664 |
| let-7d | 2922 | 2943 |
| let-7d | 1462 | 1483 |
| let-7d | 2033 | 2054 |
| let-7d | 1418 | 1439 |
| let-7d | 2184 | 2205 |
| let-7d | 1407 | 1428 |
| mir130b | 1042 | 1063 |
| mir143 | 88 | 107 |
| mir206 | 728 | 748 |
| mir22 | 92 | 113 |
| mir22 | 641 | 662 |
| mir221 | 2020 | 2042 |
| mir320a | 94 | 115 |
| mir660 | 634 | 655 |

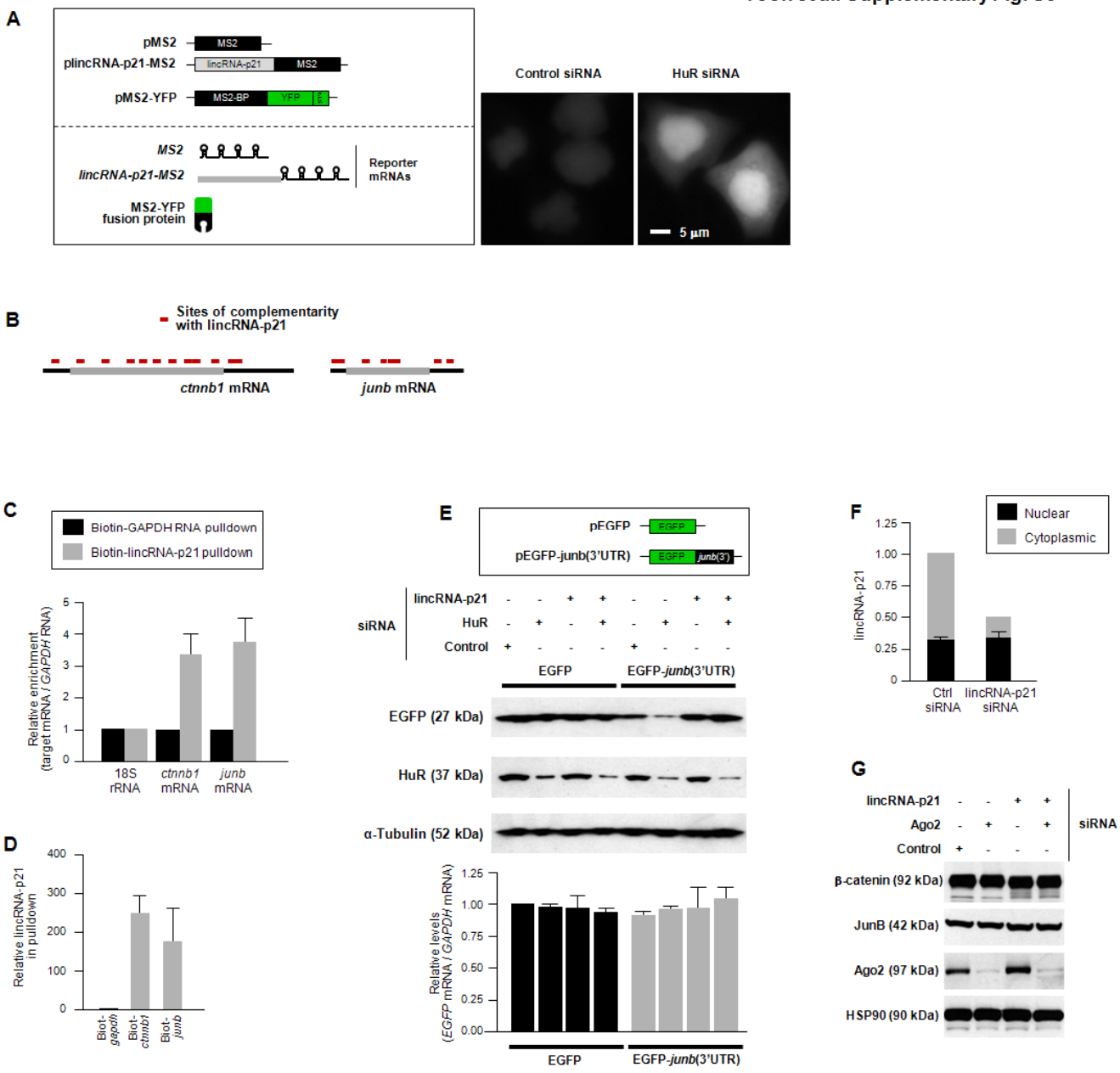


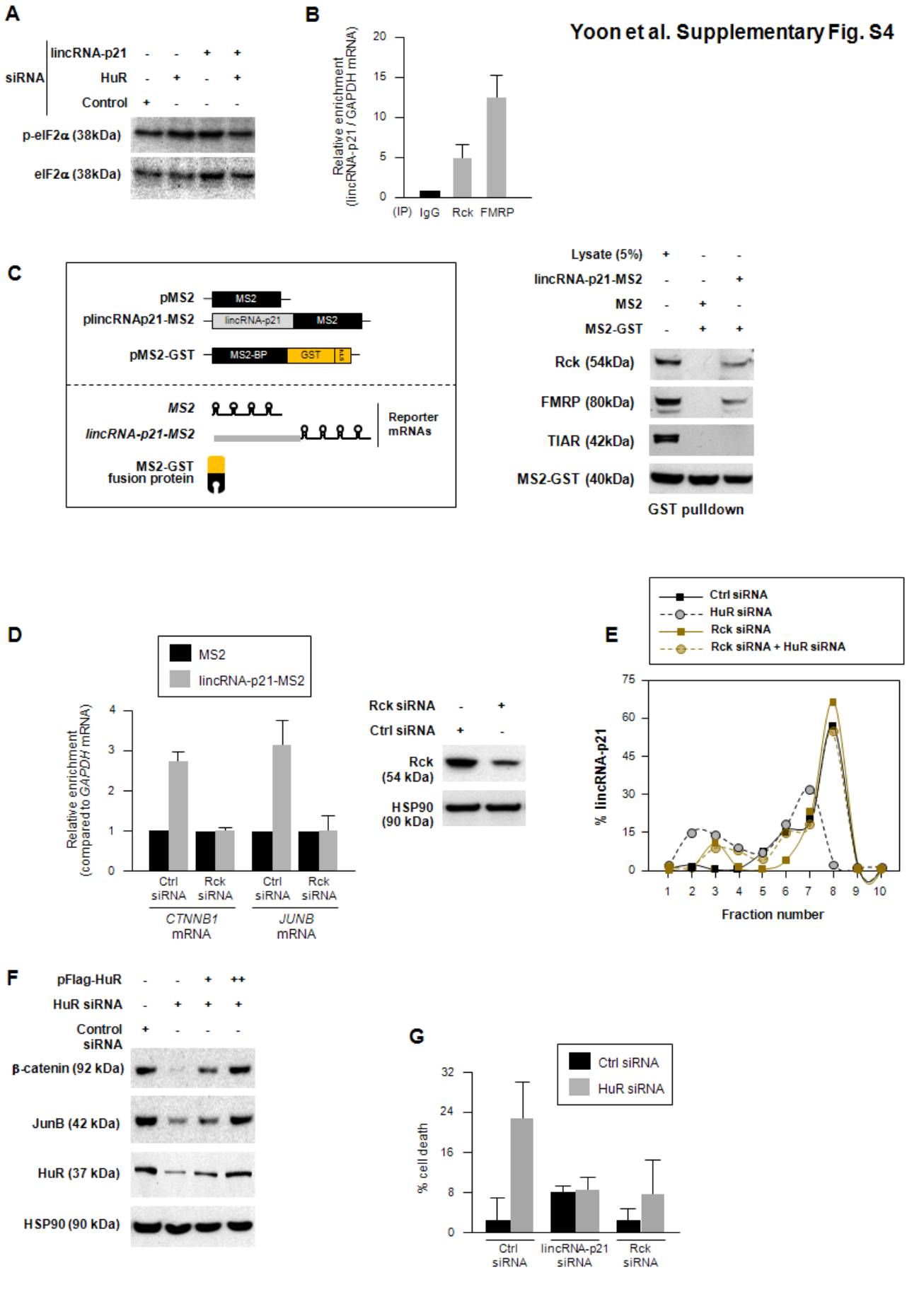




```
Mutant 1
Query  563  CTCATGCAGCCCAGACCAATCTCAAATTGACTAGGTAAACTG  604
             ||||||||||||||||||  ||||||||||||||||||
Sbjct  1    CTCATGCAGCCCAGACCAAGGAGAAATTGACTAGGTAAACTG  42

Mutant 2
Query  620  CAGTCCCTCCTGCCTCTATCTCCTGAGAGCTGGGTAACAG  659
             ||||||||||||||||||  ||||||||||||||||||
Sbjct  1    CAGTCCCTCCTGCCTCTAGGAGCTGAGAGCTGGGTAACAG  40

Mutant 3
Query  652  GGTAACAGCTTCTGGAGCCTCACCCAGCTTCGCTTTC  688
             ||||||||||||||||  ||||||||||||||||
Sbjct  1    GGTAACAGCTTCTGGAGGGAGACCCAGCTTCGCTTTC  37
```



Yoon et al. Supplementary Fig. S3




Yoon et al. Supplementary Fig. S4
A
siRNA
lincRNA-p21 - - + +
HuR - + - +
Control + - - -
p-eIF2α (38kDa)
eIF2α (38kDa)
B
Relative enrichment (lincRNA-p21 / GAPDH mRNA)
20
15
10
5
0
(IP) IgG Rck FMRP
C
pMS2
MS2
plincRNAp21-MS2
lincRNA-p21
MS2
pMS2-GST
MS2-BP
GST
MS2
lincRNA-p21-MS2
Reporter mRNAs
MS2-GST fusion protein
Lysate (5%) + - -
lincRNA-p21-MS2 - - +
MS2 - + -
MS2-GST - + +
Rck (54kDa)
FMRP (80kDa)
TIAR (42kDa)
MS2-GST (40kDa)
GST pulldown
D
MS2
lincRNA-p21-MS2
Relative enrichment (compared to GAPDH mRNA)
4
3
2
1
0
Ctrl siRNA
Rck siRNA
Ctrl siRNA
Rck siRNA
CTNNB1 mRNA
JUNB mRNA
Rck siRNA - +
Ctrl siRNA + -
Rck (54 kDa)
HSP90 (90 kDa)
E
Ctrl siRNA
HuR siRNA
Rck siRNA
Rck siRNA + HuR siRNA
% lincRNA-p21
75
60
45
30
15
0
1 2 3 4 5 6 7 8 9 10
Fraction number
F
pFlag-HuR - - + ++
HuR siRNA - + + +
Control siRNA + - - -
β-catenin (92 kDa)
JunB (42 kDa)
HuR (37 kDa)
HSP90 (90 kDa)
G
Ctrl siRNA
HuR siRNA
% cell death
32
24
16
8
0
Ctrl siRNA
lincRNA-p21 siRNA
Rck siRNA

## Legends of Supplemental Figures

**Figure S1 (complements Fig. 1). Additional characterization of mouse and human lincRNA-p21 and their interaction with HuR.**
**(A)** Genomic localization of mouse (*top*) and human (*bottom*) lincRNA-p21. The human lincRNA-p21 was sequenced partially by RACE (Rapid Amplification of cDNA Ends; Invitrogen) using total RNA from HeLa cells (supplemental text). *Red*, region of homology between mouse and human lincRNA-p21. *Purple*, region used to detect human lincRNA-p21 by qPCR. *Green*, let-7b site, with the interaction sequence indicated in green text. **(B)** Relative abundance of lincRNA-p21 (black) as determined by calculating $C_t$ values among a subset of mRNAs (those encoding hnRNPC and HuR) and lincRNAs, as measured in HeLa cells. **(C)** Northern blot analysis of lincRNA-p21 expression in HeLa cells. Duplicate samples (20 and 30 μg of total RNA) were run in agarose/formaldehyde gels; after transfer to nylon membranes, lincRNA-p21 and *GAPDH* mRNA were detected using antisense oligomers (GGGTGGCTCACTCTTCTGGC and GCCCAATACGACCAAATCC respectively) that were end-labeled with $^{32}P$ and used as probes. Bands were visualized using a Typhoon scanner (GE Healthcare). **(D)** *In vitro* interaction of maltose-binding protein (MBP) or MBP-HuR (2 μg each) with biotinylated lincRNA-p21 was assessed by pulldown using streptavidin-coated beads and Western blotting (WB) detection using anti-MBP antibody. Input, 2 μg recombinant protein. As shown, MBP-HuR selectively interacted with biotinylated mouse lincRNA-p21, while MBP did not. MWM, protein molecular weight markers. **(E)** HeLa cells were transfected with the plasmids shown in the schematic (*left*). Forty-eight h later, lysates were used in IP reactions employing GSH-agarose beads. The presence of HuR in IP reactions from each transfection group (cells expressing MS2 RNA compared with cells expressing lincRNA-p21 RNA) was assessed by Western blot analysis using an anti-HuR antibody.

**Figure S2 (complements Fig. 1). Influence of HuR and let-7 on lincRNA-p21 levels.**
**(A)** In wild-type (wt) and HuR-null (HuR-/-) MEFs, HuR levels were assessed by WB, and lincRNA-p21 by RT-qPCR. **(B)** Putative microRNAs interacting with mouse lincRNA-p21, as predicted using TargetScan. **(C)** Predicted let-7 sites on mouse lincRNA-p21. Using a plasmid vector that expressed the wild-type mouse lincRNA-p21 expressed from a CMV promoter (Huarte et al., 2010), site-directed mutagenesis (box) was used to generate the mutants indicated (Mut1, Mut2, Mut3). After transfection of each plasmid into MEFs expressing normal or silenced HuR, the levels of lincRNA-p21 (WT, Mut1, Mut2, Mut3) were quantified by RT-qPCR. Site-directed mutagenesis of mouse lincRNA-p21 was performed with the QuikChange® Site-Directed Mutagenesis Kit (Stratagene). **(D)** In wild-type (wt) and Ago2-null (Ago2-/-) MEFs, Ago2 levels were assessed by WB (*top*), and lincRNA-p21 by RT-qPCR (*graph*). Data in (A,C,D) represent the means and S.D. (error bars) from 3 independent experiments.

**Figure S3 (complements Fig. 2). Translational repression of β-catenin and JunB translation by lincRNA-p21 in mouse cells.**
**(A)** HeLa cells were transfected with the plasmids shown in the schematic. Forty-eight hours later, the localization of the MS2-tagged lincRNA-p21 was assessed by fluorescence microscopy. **(B)** Regions of predicted interaction between mouse lincRNA-p21 and mouse *ctnnb1* and *junb* mRNAs. **(C)** Following incubation of mouse biotin-lincRNA-p21 (or control biotin-*GAPDH* RNA) with MEF lysates, RNA was extracted and *ctnnb1* and *junb* mRNAs, as well as normalization control 18S rRNA were assessed by RT-qPCR and represented as fold difference relative to mRNA levels in biotin-*GAPDH* pulldown samples. **(D)** Biotinylated *GAPDH* mRNA, *ctnnb1* RNA (NM_007614.3, nucleotides 288-2633), and *junb* RNA (NM_008416.3, nucleotides 320-1354) were incubated with MEF lysates; after pulldown, the levels of lincRNA-p21 in beads were assessed by RT-qPCR. **(E)** MEFs were transfected with the plasmids indicated: pEGFP-*junb*(3'UTR), containing the entire mouse *junb* 3'UTR (amplified from mouse total RNA and cloned into pEGFP-C1), and control plasmid pEGFP, together with the siRNAs shown. Forty-eight h later, the levels of the reporter protein EGFP were detected by Western blot analysis and the levels of *EGFP* or *EGFP*-

*junb(3'UTR)* mRNAs by RT-qPCR analysis. **(F)** Forty-eight hours after siRNA transfection in HeLa cells, lincRNA-p21 levels were assessed by RT-qPCR in nuclear and cytoplasmic fractions as explained in main Fig. 2A. **(G)** Forty-eight hours after transfection with the siRNAs shown, the levels of Ago2, β-catenin, JunB and loading control HSP90 were assessed by Western blot analysis. Data in (C-F) represent the means and S.D. (error bars) from 3 independent experiments. Oligomer sequences are in Table 2.

Microscopy: forty-eight h after transfection of pMS2-YFP together with either pMS2 or pMS2-lincRNA-p21, HeLa cells were fixed and images were acquired with Axio Observer microscope (ZEISS) with Axio Vision 4.7 Zeiss image-processing software or with LSM 510 Meta (ZEISS).

**Figure S4 (complements Figs. 3 and 4). Translational inhibition by mouse lincRNA-p21 associated to the recruitment of translational repressor Rck.**

**(A)** HeLa cells were transfected with the siRNAs shown and 48 h later, the levels of eIF2α and phospho-eIF2α were assessed by Western blot analysis. **(B)** RIP analysis of lincRNA-p21 interaction with Rck and FMRP in MEFs. **(C)** *Left*, plasmids used to study the *in vitro* interaction of lincRNA-p21 with Rck, FMRP, and TIAR present in HeLa cell lysates, as detected by WB analysis in GST pulldown assays (*right*). **(D)** Mouse lincRNA-p21-MS2 and MS2-GST were expressed in HeLa cells using the plasmids shown in panel (C) in cells expressing normal Rck levels or cells in which Rck was silenced (*right*). RIP analysis was carried out to study if silencing Rck affected the interaction of lincRNA-p21 with endogenous *CTNNB1* and *JUNB* mRNAs. **(E)** 48 h after transfecting HeLa cells with the siRNAs shown, polysomes were prepared as shown in the main Fig. 4E; the relative distribution of lincRNA-p21 is indicated. **(F)** In order to establish whether the effects of lincRNA-p21 were directly attributed to HuR, a rescue experiment was devised in which HeLa cells were transfected with siRNA directed to the 3'UTR of HuR or with a plasmid (1 and 2 μg) to express only the coding region of HuR (pFlag-HuR). Forty-eight h later, the levels of β-catenin and JunB were assessed by Western blot analysis. **(G)** Percentages of HeLa cell death (as assessed by trypan blue exclusion) 48 h after transfection of the siRNAs shown; cell number and viability were quantified using a TC10 automated cell counter (BioRad). Data in (B,D,G) represent the means and S.D. (error bars) from 3 independent experiments.

**Table S1. Putative Regions of interaction of lincRNA-p21 with human *CTNNB1* mRNA, *JUNB* mRNA, and (control) *GAPDH* mRNA.**

I. Putative interaction regions of the *CTNNB* mRNA (query) with lincRNA-p21 (subject).

| Matched sequence | Identity (%) | Mach Size (bp) | E-value |
|---|---|---|---|
| Query 3295 TTTTTAA--GTCTCTCGTAGTGTTAA 3318<br>Sbjct 966 TTTTTAATTGTCCCTGTTAGTGTGAA 941 (intron) | 76.92 | 26 | 54 |
| Query 3441 TTTTGTATAAAATAGACAAATAGAA 3465<br>Sbjct 503 TTTTGACTAAACTA--CAAATAGAA 481 | 80 | 25 | 4.4 |
| Query 879 ATACAAATGATGTAGAAACAG 899<br>Sbjct 195 ATGCAAAGCAAGTAGAAACAG 175 | 80.95 | 21 | 4.4 |
| Query 3511 TGGATCTATTTCATGTTTTT 3530<br>Sbjct 2192 TGGATCT-TCTCTTGGTTTT 2174 | 80 | 20 | 189 |
| Query 1353 GAATGCAAGCTT-TAGGACT 1371<br>Sbjct 2307 GAAAGGAGGCTTCTAGGACT 2288 | 80 | 20 | 189 |
| Query 3339 AGCAATTTCTAATTTTTAA 3357<br>Sbjct 978 AGCCATTTGCAGTTTTTAA 960 (intron) | 78.95 | 19 | 54 |
| Query 297 TGGACATGGCCATGGAAC 314<br>Sbjct 876 TGGACATGGAACTGGAAC 859 | 83.33 | 18 | 15 |
| Query 1509 TAAATGTGGTCACCTGTG 1526<br>Sbjct 1262 TAAATGT--TCACCCGTG 1247 (intron) | 83.33 | 18 | 54 |
| Query 1350 GTGGAATGCAAGCTTTA 1366<br>Sbjct 806 GTGGAATACAGGCTGTA 790 | 82.35 | 17 | 54 |
| Query 3060 AAACTTTTTGTTCTGGT 3076<br>Sbjct 1042 AAACTTTTTTCTTTGGT 1026 (intron) | 82.35 | 17 | 54 |
| Query 2885 CATTTGCTGTTTTTAAA 2900<br>Sbjct 975 CATTTGCAGTTTTTAA 960 (intron) | 87.5 | 16 | 4.4 |
| Query 2173 AGCCACAGCTCCTCTG 2188<br>Sbjct 665 AGCCACAG--CCTCTG 652 | 87.5 | 16 | 54 |
| Query 247 TTTTGAAAA-TCCAG 260<br>Sbjct 217 TTTTGAAAAATCCAG 203 | 93.33 | 15 | 15 |
| Query 110 GGGAGGCGGAGACGG 124<br>Sbjct 1615 GGGAGGCTGAGGCGG 1601 (intron) | 86.67 | 15 | 15 |
| Query 1812 GAAATCTTGCCCTTT 1826<br>Sbjct 2130 GAAATCTAGCCCCTT 2116 | 86.67 | 15 | 15 |
| Query 2913 CCTTTCTCTCTTTAT 2927<br>Sbjct 2477 CCATTCTCTCTCTAT 2463 | 86.67 | 15 | 15 |
| Query 1409 TGTCTT-TGGACTCT 1422<br>Sbjct 428 TGTCTTTTGGATTCT 414 | 86.67 | 15 | 189 |
| Query 383 GCCACTA-CCACAGC 396<br>Sbjct 671 GCCACCAGCCACAGC 657 | 86.67 | 15 | 189 |
| Query 214 CCCTGAG-GGTATTT 227<br>Sbjct 2084 CCCTGGGTGGTATTT 2070 | 86.67 | 15 | 189 |
| Query 1096 TGGTGGG--CTGCAG 1108<br>Sbjct 2499 TGGTGGGCACTGCAG 2485 | 86.67 | 15 | 189 |
| Query 384 CCACTAC-CACAGCT 397<br>Sbjct 2741 CCACTACGCCCAGCT 2727 | 86.67 | 15 | 189 |

II. Putative interaction regions of the *JUNB* mRNA (query) with lincRNA-p21 (subject).

| Matched Regions | Identity (%) | Mach Size (bp) | E-value |
|---|---|---|---|
| Query 770 CCCCGGCTGGGCCCGGGGGCGTCTACGCCGGCC 802<br>Sbjct 32 CCCGGGCAAGGCCAGCGGGAG-CTCTGCCGGCC 1 | 72.73 | 33 | 93 |
| Query 1654 TGGGAAGGGGAcccccgccccctgcc 1679<br>Sbjct 687 TGGGAAGGGGACACAAGCCACCAGCC 662 | 80.77 | 26 | 0.18 |
| Query 1559 AATATA-ATATAT-TTGTGTAT 1578<br>Sbjct 1117 AATATATATGTATATTGTGTAT 1096 (intron) | 86.36 | 22 | 7.6 |
| Query 956 CGGCGCAGCTGGGCTTGG 973<br>Sbjct 1767 CGGGGCAGCTGGTCTGGG 1750 | 83.33 | 18 | 7.6 |
| Query 1653 TTGGGAAGGGGAccccc 1669<br>Sbjct 2175 TTAGGAAGGGGGCTCCC 2159 | 82.35 | 17 | 27 |
| Query 11 GCCAGCCTCGGAGCCAG 27<br>Sbjct 2532 GCCAGCCTGGGGTCCAG 2516 | 82.35 | 17 | 27 |
| Query 1564 AATATATTTGTGTATT 1579<br>Sbjct 1117 AATATATATGTATATT 1102 (intron) | 87.5 | 16 | 2.2 |
| Query 1564 AATATATTTGTGTATT 1579<br>Sbjct 1898 AATATATTCTTGTATT 1883 | 87.5 | 16 | 2.2 |
| Query 1053 CCCCATCA-ACATGGA 1067<br>Sbjct 2208 CCCCACCACACATGGA 2193 | 87.5 | 16 | 27 |
| Query 1443 TGGACTCCGGCCCTC 1457<br>Sbjct 2672 TGGACTCCTGACCTC 2658 | 86.67 | 15 | 7.6 |

III. Putative interaction regions of the *GAPDH* mRNA (query) with lincRNA-p21 (subject).

| Matched Regions | Identity (%) | Mach Size (bp) | E-value |
|---|---|---|---|
| Query 431 CTCATTTGCAGGGGGGAGCC 450<br>Sbjct 2287 CTCATTTGCATAGGGGTGCC 2268 | 85.00 | 20 | 0.44 |
| Query 98 ACACCATGGGGAAGG 112<br>Sbjct 1316 ACAACATGGGGAGGG 1330 (intron) | 86.67 | 15 | 5.4 |
| Query 506 TGAACCATGAGAAGT 520<br>Sbjct 2012 TGAACCATCATAAGT 2026 | 86.67 | 15 | 5.4 |

**Table S2. Primers used in qPCR reactions.** Bold text indicates T7 RNA polymerase promoter sequence.

| Name | Species | Sequence | Reference |
|---|---|---|---|
| lincRNA-p21-F | human | GGGTGGCTCACTCTTCTGGC | Huarte et al., 2010 |
| lincRNA-p21-R | human | TGGCCTTGCCCGGGCTTGTC | Huarte et al., 2010 |
| GAPDH-F | human | AGCCACATCGCTCAGACAC | Huarte et al., 2010 |
| GAPDH-R | human | GCCCAATACGACCAAATCC | Huarte et al., 2010 |
| mLincRNA-p21-1 (F) | mouse | CCTGTCCACTCGCTTTC | Huarte et al., 2010 |
| mLincRNA-p21-1 (R) | mouse | GGAACTGGAGACGGAATGTC | Huarte et al., 2010 |
| mGapdh (F) | mouse | GGGAAATTCAACGGCACAGT | Huarte et al., 2010 |
| mGapdh (R) | mouse | AGATGGTGATGGGCTTCCC | Huarte et al., 2010 |
| JUNB human (F) | human | AGGCTCGGTTTCAGGAGTTT | |
| JUNB human (R) | human | GAACAGCCCTTCTACCACGA | |
| junb mouse (F) | mouse | CGATAGGGATCCGCCAGG | |
| junb mouse (R) | mouse | CGGGATACGGTCGGAGC | |
| b catenin human (F) | human | ATTGTCCACGCTGGATTTTC | |
| b catenin human (R) | human | TCGAGGACGGTCGGACT | |
| b catenin mouse (F) | mouse | ATGGAGCCGGACAGAAAAGC | |
| b catenin mouse (R) | mouse | GAATCCAAGTAAGACTGCTGCT | |
| 18S rRNA (F) | human | CGAACGTCTGCCCTATCAACTT | |
| 18S rRNA (R) | human | ACCCGTGGTCACCATGGTA | |
| T7 beta catenin (F) | mouse | **CCAAGCTTCTAATACGACTCACTATAGGGAGA**ATGGCTACTCAAGCTGACCTG | |
| T7 beta catenin (R) | mouse | TTACAGGTCAGTATCAAACCAGGC | |
| T7 JunB (F) | mouse | **CCAAGCTTCTAATACGACTCACTATAGGGAGA**ATGTGCACGAAAATGGAACA | |
| T7 JunB (R) | mouse | TCAGAAGGCGTGTCCCTT | |
| T7 HO1 (F) | mouse | **CCAAGCTTCTAATACGACTCACTATAGGGAGA**ATGGAGCGTCCACAGCCC | |
| T7 HO1 (R) | mouse | TTACATGGCATAAATTCCCACTG | |
| T7 GAPDH ORF (F) | mouse | **CCAAGCTTCTAATACGACTCACTATAGGGAGA**ATGGTGAAGGTCGGTGTGA | |
| T7 GAPDH ORF (R) | mouse | TTACTCCTTGGAGGCCATGT | |
| Mut 2073-2094 (F) | mouse | ACTTCTCAACATCTCTTGTGCTGTGTGTGTGTGTCACACACACACACACACACGC | |
| Mut 2073-2094 (R) | mouse | GCTGGTGTGTGTGTGTGTGTGACACACACACACAGCACAAGAGATGTTGAGAGGT | |
| Mut 2457-2496 (F) | mouse | AAACAGCTGTGGTGCAGGCCTAGGGGCCCGGCGCCCGAAGCTGGACACTGGCAGAGGCCG | |
| Mut2457-2496 (R) | mouse | GCGGCCTCTGCCAGTGTCCAGCTTCGGGCGCCGGGCCCCTAGGCCTGCACCACAGCTGTTT | |
| B-Catenin 5UTR Xho1 (F) | mouse | AAAACTCGAG GCGCGGCGGAACGCTCCGCGC | |
| B-Catenin 5UTR EcoR1 (R) | mouse | AAAAGAATTCTGTCCACGCAGCGGTGTCACA | |
| JunB 3UTR Kpn1 (F) | mouse | AAAAGGTACCTAAGAGCCTCCCTTGCCCCATACG | |
| JunB 3UTR BamH1 (R) | mouse | AAAAGGATCC ATTAATAAAGACAATTTTTTT | |
| EGFP (F) | | TAAACGGCCACAAGTTCAGCGT | |
| EGFP (R) | | AAGTCGTGCTGCTTCATGTGGT | |
| lincRNA-p21 mutant 1(F) | mouse | GCAGCCCAGACCAAGGAGAAATTGACTAGGTAAAC | |
| lincRNA-p21 mutant 1(R) | mouse | GTTTACCTAGTCAATTTCTCCTTGGTCTGGGCTGC | |
| lincRNA-p21 mutant 2(F) | mouse | CCTCCTGCCTCTAGGAGCTGAGAGCTG | |
| lincRNA-p21 mutant 2(R) | mouse | CAGCTCTCAGCTCCTAGAGGCAGGAGG | |
| lincRNA-p21 mutant 3(F) | mouse | GTAACAGCTTCTGGAGGGAGACCCAGCTTCGCTTTCAC | |
| lincRNA-p21 mutant 3(R) | mouse | GTGAAAGCGAAGCTGGGTCTCCCTCCAGAAGCTGTTAC | |
| 5'biotinylated sense (for pulldown) | human | GGGTGGCTCACTCTTCTGGC | |
| 5'biotinylated antisense (for pulldown) | human | GCCAGAAGAGTGAGCCACCC | |