LncRNA of interest: ENST00000453837.1 (RP11-84A19.2)

TFO: lncRNA **TTS: site on the gene promoter where lncRNA forms triplex**

1. **Gene: KIAA1324**

Promoter region (1kb upstream): chr1:109655584-109656584

Potential Triplex Site (PTS):

```
chr1     109656055        109656090
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656053        109656090
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656051        109656090
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656049        109656091
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGttG -5'
         |||||||||||||||||||||||||||||||||||**|
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC -5'
chr1     109656047        109656086
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'
chr1     109656045        109656084
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656043        109656082
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656041        109656080
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656037        109656078
TFO: 3'- AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |*|||||||||||||||||||||||||||||||||
TTS: 5'- AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'
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chr1     109656038        109656076
TFO: 3'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||||||||||
TTS: 5'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656035        109656074
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||*|||||||||||||||||||||||||||||||||||||
TTS: 5'- GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656033        109656072
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||*||||||||||||||||||||||||||||||||||
TTS: 5'- GAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656031        109656070
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||*|||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656029        109656068
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||*||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656027        109656066
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||||*|||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656025        109656064
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||||||*||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656023        109656062
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||||||||*||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656021        109656060
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||||||||||*|||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656019        109656058
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||*||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTCTC -5'

chr1     109656017        109656056
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||||||||||||||*||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAAAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTC -5'
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chr1     109656015         109656054
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||*|||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAAAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTC -5
chr1     109656014         109656052
TFO: 3'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||||||||||||||||||*|||||||||||||||
TTS: 5'- AGAGAGAGAGAGAGAGAGAGAGAAAGAGAGAGAGAGAG -3'
     3'- TCTCTCTCTCTCTCTCTCTCTCTTTCTCTCTCTCTCTC -5'

chr1     109656014         109656050
TFO: 3'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||*||||||||||||
TTS: 5'- AGAGAGAGAGAGAGAGAGAGAGAAAGAGAGAGAGAG -3'
     3'- TCTCTCTCTCTCTCTCTCTCTCTTTCTCTCTCTCTC -5'
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2. Gene Symbol: PROX1

Promoter region (1kb upstream): chr1:214160843-214161843

Potential Triplex Site (PTS):

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chr1     214161764         214161799
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||*||||||||||||||||||||||||||||||||
TTS: 5'- GAGAtAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     214161762         214161799
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||*||||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAtAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     214161760         214161799
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||*||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAtAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'


chr1     214161758         214161800
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGttG -5'
         ||||||||||*||||||||||||||||||||||||||**|
TTS: 5'- GAGAGAGAGAtAGAGAGAGAGAGAGAGAGAGAGAGAGAGG -3'
     3'- CTCTCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCC -5'

chr1     214161756         214161795
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||*||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAtAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     214161752         214161793
TFO: 3'- AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |*||||||||||||||||*||||||||||||||||||||
TTS: 5'- AAGAGAGAGAGAGAGAtAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- TTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTCTC -5'

chr1     214161750         214161791
TFO: 3'- AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |**||||||||||||||||*||||||||||||||||||||
TTS: 5'- AAAAGAGAGAGAGAGAGAtAGAGAGAGAGAGAGAGAGAG -3'
     3'- TTTTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTC -5'
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chr1     214161748        214161789
TFO: 3'- AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |**|*|||||||||||||||*||||||||||||||||||||
TTS: 5'- AAAAAAGAGAGAGAGAGAGAtAGAGAGAGAGAGAGAGAGAG -3'
     3'- TTTTTTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTC -5'

chr1     214161749        214161787
TFO: 3'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |*|*|||||||||||||||*||||||||||||||||||
TTS: 5'- AAAAAGAGAGAGAGAGAGAtAGAGAGAGAGAGAGAGAG -3'
     3'- TTTTTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTC -5'

chr1     214161749        214161785
TFO: 3'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |*|*|||||||||||||||*|||||||||||||||||
TTS: 5'- AAAAAGAGAGAGAGAGAGAtAGAGAGAGAGAGAGAGAG -3'
     3'- TTTTTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTC -5'
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3. **Gene: BCL9**

Promoter region (1kb upstream): chr1:147012270-147013270

Potential Triplex Sites (PTS):

```
chr1     147012921        147012956
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||*|*|*|
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGtGtGtG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACACAC -5'

chr1     147012919        147012956
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||*|*|*|
TTS: 5'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGtGtGtG -3'
     3'- CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACACAC -5'

chr1     147012918        147012956
TFO: 3'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||||||||||*|*|*|
TTS: 5'- AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGtGtGtG -3'
     3'- TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACACAC -5'

chr1     147012915        147012954
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||*|||||||||||||||||||||||||||||||*|*|
TTS: 5'- GAcAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGtGtG -3'
     3'- CTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACAC -5'

chr1     147012913        147012952
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||*|||||||||||||||||||||||||||||||*|
TTS: 5'- GAGAcAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGtG -3'
     3'- CTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAC -5'

chr1     147012911        147012950
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||*|||||||||||||||||||||||||||||||
TTS: 5'- GAGAGAcAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     147012909        147012948
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         ||||||||*||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAcAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'
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chr1     147012907        147012946
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||*|||||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAcAGAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     147012905        147012944
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||*|||||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAcAGAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     147012903        147012942
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||*|||||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAcAGAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     147012901        147012940
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||*|||||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAcAGAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTGTCTCTCTCTCTCTCTCTCTCTC -5'

chr1     147012899        147012938
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||*|||||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAcAGAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTGTCTCTCTCTCTCTCTCTCTC -5'

chr1     147012897        147012936
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||*|||||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAcAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTGTCTCTCTCTCTCTCTCTC -5'

chr1     147012897        147012934
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||*|||||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAcAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTGTCTCTCTCTCTCTCTCTC -5'

chr1     147012897        147012932
TFO: 3'- GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG -5'
         |||||||||||||||||||||||*||||||||||||||
TTS: 5'- GAGAGAGAGAGAGAGAGAGAcAGAGAGAGAGAGAGAGAG -3'
     3'- CTCTCTCTCTCTCTCTCTCTGTCTCTCTCTCTCTCTCTC -5'
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