

**JIPSC1042\_SnappeneDNA\_INK2J00085R\_HNRNPA1\_D262N\_REVWT**  
6896 bp

AAAGCTAGGACAAACTCCCGCCAACACGACGAGCGCCGTAGGTTCACTGCTTACTCTCCGCCCGCATTTACAGTGTTCCTCAGAGGCGGAACCTTCTTAATGCGCCTGCGCAAAACTCGCCATTTTACTACACG  
TTTCGATCCTGTTTGAAGGCGGTTGTCGCTCCGCGGCATCCAAGTGACGGATGAGGACGGGCGGTAAGTGACACAAGAGTCTCCGTCCACCTTGAAGAAATACGCGGACGCGTTTGAAGCGGTAATAATGATGTGC

135

HNRNPA1

TGCGGTCAACAAGAGTTCATTGCAAAAAATTTGTACCTCTGGCTGCTTGTCTAATACATAGTGTAAATCATGCTTTGCAAGCGACTTGACTGTAATATTTGCGCGTGAAGATTAAAAAGATGTTAAACACC  
ACGCCAGTTGTTCTCAAGTAACGTTTTTTTAAACAATGAGGACCGACGAACAGATTATGTATCACAATAGTACGAAACGGTTCGCTGAACTGACATTATAAACCGCGCACCTTCTAATTTTTCTACAATTTGTGG

270

HNRNPA1

CAAGGTAGATTCAAATGTGAATGATTGGTCGGTTGGCCAATCAGACTGGTTAAACAATAACATTACTCGGGAACCAATGGACTCCAAGGGTGGAGACGGCGTAGAACGACCGAAGGAATGACGTTACACAGCAAT  
GTTCCATCTAAGTTTACACTTACTAACCGCAACCGGTTAGTCTGACCAATTGTTATTGTAATGAGCCCTGGTTACCTGAGGTTCCCCACCTCTGCGGCATCTTCTGCTGCTTCTACTGCAATGTCGTTA

405

HNRNPA1

GTGGCACCACAGGCCAATAGCAGGGGGAAGCGATTTCAAGTATCCAATCAGAGCTGTTCCAGGGCGGAGTCTACCAATGCCGAAAGCGAGGAGCGGGTAAAAAGAGAGGGCGAAGGTAGGCTGGCAGATACG  
CACCGTGGTTCGCGTTATCGTCCCGCTTCGCTAAAGTTCATAGTTAGTCTCGACAAGTCCCGCTCAGATGTTACGGCTTCGCTCCTCGCGCCATTCTCTCCGCTTCCATCCGACCGTCTATGC

540

HNRNPA1

HNRNPA1-202

TTGTCAGCTTGTCTCTTTCTGCCCGTGGACGCGCGCAAGAAGCATCGTTAAAGTCTCTTTCACCTGCCGTCATGTCTAAGTCAGAGGTGAGTTAGGCGCGCTTCCCACTTGAATTTTTCTCTCCCTTT  
AAGCAGTCGACAGGAAAGACGGGACCTGCGGCGGCTTCTTCGTAGCAATTTAGAGAGAAGTGGGACGGCAGTACAGATTCAAGTCTCCACTCAATCCGCGGAAAGGGTGAACCTAAAAAGGAGAGGGAAA

675

HNRNPA1

HNRNPA1-202

1 5  
M S K S E  
ENSE00002375624

HNRNPA1-202

CCTGAATCGGTAAGATGCTGCTGGGTTTCGTTCCCTTGCCAGCCCATTTCTACAGTTCCTTCGGTCGCTGCCACGGCTACCCCTCCCAAAGTTCAGTTCGCGCATTTTGTCTCTTGTATGCCATGAGGCGGCTC  
GGACTTAGCCATTTACGACGACCCAAAGCAAGGAACGTGGTCCGGTAAGATGTCAGGAAGCCAGCGAGGTCGCGGATGGGAGGGTTTCAAGTTCAGCGGTAAACACAGGAGAAGTACGGTACTCCGGCGAG

810

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TCCGCCAACCATGAGTTATCATGCGGGACTCGTTACTCGTAGCAAAATTTAGGCACACAGGATCTTTGCTTTTTTAAACCTTGCCCTTGGTGAGCGAGTTTTCTAAAGAGCGATTAGTCCATTGTGGAGAT  
AGGCGGTTGGTACTCAATAGTACGCCCTGAGCAATGAGCATCGTTTTAAGAAATCCGTGTCTTAGAAACAGAAAAAATTTGGAACGGAACCACTCGCTCAAAAGATTCTCGCTAATCAGGGTAACACCTCTA

945

HNRNPA1

HNRNPA1-202

HNRNPA1-202

GCACCCCTACCGCCAAAGCCTTTGTTGCGGTGCGTCCGAAAGCGACTAGGGACGCATGCGCTTTCGATTTCCTAGCACTCCCAACTCCAGCATACGGCTCCCTTGATAGGCAGAAAGCACGTGCTTGTGCGA  
CGTGGGGATGGCGGTTCCGAAACAACGCGCACGACGCTTCCGCTGATCCCTGCGTACGCGAAACGCTAAAGGATCGTGAGGGTTGAGGTCGTATGCCGAGGGAACATCCGCTCTCTGTCACAGAAACAACGCT

1080

HNRNPA1

HNRNPA1-202

HNRNPA1-202

CCTGAACGAACAATAAGTCTAGGTACACAGTTGGTGTCTAGTTTTCTTTCTCGATGGAATTTGTTGTTGTAGCCATTTAACACTTCCCTCCCTCCCTCCTAGTCTCTAAAGAGCCCGAACACG  
GGACTTGCTTGTATTACGATCCATGTGTCAACCACAGATCAAAAAGAAAAGGAGCTACCTTTAACAAAGCACAACTCGGGTAAATTTGGAAGGGGAGGGGGTGAAGTACAGAGGATTTCTCGGCTTGTCTG

1215

HNRNPA1

HNRNPA1-202

10  
S P K E P E Q  
ENSE00003542256

HNRNPA1-202

TGAGGAAGCTCTTCATTGGAGGTTGAGCTTTGAAACAACGATGAGAGCCTGAGGAGCCATTTGAGCAATGGGAAACGCTCACGACTGTGTGTAAGATTGGAAGGGACAAAGCAGTAAACAGCCGATTT  
ACTCCTTCGAGAAGTAACCTCCAACTCGAAACTTTGTTGACTACTCTCGGACTCCTCGGTAACACTCGTTACCCCTTGCAGTGCCTGACACACCAATTTAAACCTTCCCTGTTTCGTCATTTTGTGCGCTAAA

1350

HNRNPA1

HNRNPA1-202

15 20 25 30 35 40  
L R K L F I G G L S F E T T D E S L R S H F E Q W G T L T D C V  
ENSE00003542256

HNRNPA1-202

CCCTGGCTTATCTTGGTGCAGTCTTCCGAATGCTTATGAAAGTAGTTAATAGCAATTAAGTTAGAGCTTTGTTGGCAAAGGAAAGCTCCTGCTTTGATTTAAAAAGCTACCTCTTAAATCTAGGGTAGTGGGAA  
GGAACCGAATAGAACCGTGCAGAAGGGCTTACGAATACTTTCATCAATATCGTAATATCAATCTCGAAACAACCGTTTCTTGCAGGACGAAACTAAATTTTCGATGGAGAAATTTAGATCCCATCACCTT

1485

HNRNPA1

HNRNPA1-202

HNRNPA1-202

ACTGGACGACTTTTTAAAAAGGCTGGTGAAGTTTCTATTGCCCTATTCAAAGTTAAAATGACAAAAGCTTTTGGGTCAGACTTTGTTTACATAAATTAACACTGTTCTCAGGTAATGAGAGATCCAAAC  
TGACCTGCTGAAAAATATTTCCGACCACTTTCAAAGGATAACGGGATAAGTTTCAATTTTACTGTTTTGAAAACGCGAGTCTGAAACACAATGATTTAATTTGACAAAGAGTCCATTACTCTCAGGTTTGG

1620

HNRNPA1

HNRNPA1-202

45 50  
V M R D P N  
ENSE00003638233

HNRNPA1-202

ACCAAGCGCTCCAGGGGCTTTGGGTTTGTACACATATGCCACTGTGGAGGAGGTGGATGCGACTGAATGCAAGGCCACACAAGTGGATGGAAAGAGTTGTGGAAACCAAAGAGAGCTCCAGAGAAAGTGAAT  
TGGTTCGCGAGGTCCCGAAACCAACAGTGTATACGGTGACACCTCTCCACCTACGTGACTACTACGTTCCGGTGTGTCCACCTACCTTCTCAACACCTTGGTTTCTCTCGACAGAGGTCTCTCACTCA

1755

HNRNPA1

HNRNPA1-202

T K R S R G F G F V T Y A T V E E V D A A M N A R P H K V D G R V V E P K R A V S R E  
ENSE00003638233

HNRNPA1-202

GGGTTTTTTTTCTTCTTCTTAACTTACTTGGATATGTGCTGCTATGGACTTAAGATTCGGGAGT TTTCTAACTTACCAAATTTTTATTTCGAGTATAGGCTTGTCTAACTTAACTATGGTTTTTCTC  
CCCCAAAAAAGAAAGAAAGAAATTTGAATGAACCTATACACGACGATACCTGAATTTAAGCCCTCAAAGATTTGAATGGTTTTAAAAAATAAGCTCATATCCGAAACGATTAGATTTGGATACCAAAAAAGAG

1890

HNRNPA1

HNRNPA1-202

HNRNPA1-202

CTATTAGGATTCTCAAAGACCAGGTGCCCACTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATTATTTTGAACAGTATGGAAAAATTTGAAGTATTGAAAT  
GATAATCCTAAGAGTTTCTGGTCCACGGGTGAATGACACTTTTTCTATAAACACACCAGTAATTTCTTCTGTGACTTCTTGTAGTGGATTCTCTAATAAACTTGTCTACCTTTTTAACTTCACTAACTTTA

2025

HNRNPA1

HNRNPA1-202

D S Q R P G A H L T V K K I F V G I K E D T E E H H L R D Y F E Q Y G K I E V I E I  
ENSE00003578192

HNRNPA1-202

CATGACTGACCGAGGCGAGTGGCAAGAAAAGGGGCTTTGCCTTTGTAACTTTGACGACCATGACTCCGTGGATAAGATTGTGAGTAAGTATCAGATAGTGGCATTAGTAAGGGTCCACAATCTGTATGGCATT  
GTACTGACTGGCTCCGTCACGGTCTTTTCCCGGAAACGAAACATTGGAACTGCTGGTACTGAGGCACCTATTCTAACAGTCAATCATAGTCTATCACCGTAAATCATTCCCAAGGTGTAGACATACCGTAA

2160

HNRNPA1

HNRNPA1-202

M T D R G S G K K R G F A F V T F D D H D S V D K I V  
ENSE00003578192

HNRNPA1-202

CTAAACCTGATACCATGTTGTATCTATGTTTTTTTTAGTTCAGAAATACCATACTGTGAATGGCCCAACTGTGAAGTTAGAAAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAAGAGG  
GATTTGGACTATGGTACAACATAGATACAAAAAAAATCAAGTCTTTATGGTATGACACTTACCGGTGTTGACACTTCAATCTTTTCGGGACAGTTTCGTTCTTCTACCGATCACGAAGTAGGTGGTTTTCTCC

2295

HNRNPA1

HNRNPA1-202

I Q K Y H T V N G H N C E V R K A L S K Q E M A S A S S S Q R  
ENSE00003790955

HNRNPA1-202

TATGCTTGTGCTTAATTAACCTTAAAGGTAACCTTTGAGTTACTCCAGTATGAATGATTAATGCTTAACTTTCATGTCTTAAAGTTCGAAGTGGTTCTGAAACCTTTGGTGGTGGTGGTGGGTTTCGGT  
ATACGAACAACGAATTAATTTGGAATTTCCATGAAACTCAATGAGGTCACTTACTATAATACGAATTTGAAGTACAGAATTCAGCTTCACCAAGACCTTTGAAACCAACCAAGCACCCTCCACCAAAAGCCA

2430

HNRNPA1

HNRNPA1-202

G R S G S G N F G G G R G G G F G  
ENSE00000920032

HNRNPA1-202

GGGAATGACAACCTCCGTCGTGGAGAACTTCAAGTGGTGGTATGATGGTTTATCTACATGATGTTCTGACTTCTACCATCTTTGCTATGAAGATTTTACAGTACGGAACTGCATTCAGAATGCACTT  
CCCTTACTGTTGAAGCCAGCACCTCCTTTGAAGTACCAGCACCATACACAAATAGATGTACATCAAGACTGAAGAGTGGTAGAAACGATCTTCTAAAATGTCATGCCCTTGACGTAAGTCTTACAGTGAA

2565

HNRNPA1

HNRNPA1-202

G N D N F G R G G N F S G R  
ENSE00000920032

HNRNPA1-202

TAAGTCCAAGTCATACTTAAACTTGAACCTTTTTCTTACAGGTGGCTTTGGTGGCAGCCGTTGGTGGTGGATATGGTGGCAGTGGGGATGGCTATAATGGATTTGGTAAATGATGGTAAGTTTTTGAAGAATA  
ATTACAGGTTCAAGTATGAATTTTGAACCTTTGAAAAAGAAATGTCACCGAAACCAACCGTGGGACCCACCCACCTATACCACCGTACCCTTACCGATATTACCTAAACCTTACTACCATTCAAAAAATCCTTAT

2700

HNRNPA1

HNRNPA1-202

G G F G G S R G G G G Y G G S G D G Y N G F G N D  
ENSE00000920033

HNRNPA1-202

AGTAGAAAAAATTCCTGGCAACCTGGATCTTTAGAATAGGTTAGTAGAGACTAAAATTCCTGGTGCATGTCAAACCTCAACTTTGCCATAACACGCATGCTGTGAGCAGGCCTTACGCCGTTACACTTGACAAG  
TCATCTCTTTTAAAGGACCGTTGGACCTAGAAAATCTTATCCAATCATCTCTGATTTTAAAGACCAGTACAGTTTGAAGTGAAGCGGGTATTGTGCGTACGACACTCGTCCGGAAGTCGGCAATGTGAAGCGTGTTC

2835

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TTTTATTGTCAAACTTTTTGTCTTATTGAGAAGAAATGATTCTTGTAGGTGGTTATGGAGGAGGGCCCTGGTTACTCTGGAGGAAGCAGAGGCTATGGAAGTGGTGGACAGGGTTATGGAACCAAGGGCA  
AAAAGTAAACAGTTTATGAAAACAGAAATACTCTTCTTAAACATAAAGAACATCCACCAATACCTCTCGCCGGGACCAATGAGACCTCTCTGCTCCGATACCTTACCACCTGTCCCAATACCTTTGGTCCCGT

2970

HNRNPA1

HNRNPA1-202

G G Y G G G G P G Y S G G S R G Y G S G G Q G Y G N Q G  
ENSE00001690592

HNRNPA1-202

G TGGCTATGGCGGAGTGGCAGCTATGACAGCTATAACAACGGAGGCGGAGGCGGCTTTGGCGGTGGTAGTGGTAGGTTCCAGTGATCCAAGTACTTGGTGTGACAGCTAGATTAGCCTTTTAGAGCTTTGGGTT  
CACCAGTACCGCCCTCACCGTCGATACTGTCGATATTGTTGCCCTCCGCCCTCCGCGAAACCGCCACCATCACCATCCATAGGTCAGTGGTTCATGAACCACACTGTCGATCTAATCGGAAAACTCTCGAACCCAA

3105

HNRNPA1

HNRNPA1-202

280 285 290 295 300  
S G Y G G S Y D S Y N N G G G F G G S  
ENSE0001690592

HNRNPA1-202

CTGGTCTGTTGAAGCATTGTGGGTACACTGCATGGTATATTAACAAACAATGGGCTTGGCTACCTCCTAGCTTTAAGCTGGGGCCGCCTCACTCCCAATAGTAGAGATAAGTGGATAGTGTGTC  
GACCACGACAACCTTCGTAACACACCATGTGACGTACCATATAATTTTGTGTTACCCGAACGATACGATGGAGGAGGATCGAAATTCGACCCCGCGGAGTGAGGGTTTATCATCTCTATTACACATCAACAACG

3240

HNRNPA1

HNRNPA1-202

HNRNPA1-202

PCR Forward  
C T T T G G G A C C T T A G G C G C T T A G T T G

TTT GAGTTAGATTAGTATCATAGAAGGATTTAGTATTTAACTCCTTTGGGACCTTAGGCGCTTAGTTGATGTATCCAAGATACTTCTGCTTGTGTGGCCCTGGATCCGTGAAGGCCCTCAAGGCTGAAGGGTA  
AAACTCAATCTAATCATAGTATCTTCCATAAATATAAAATGAGGAAACCCGGAATCCGCGAATCACTACATAGGTTCTATGAGACGACACCCGGGACCTAGGCACTCCGGAAGTCCGACTTCCCAT

3375

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TGCTTGTGCCACTCTGAAAATCTCTTTATTTATGTCATGGTGGAGTTAGGCCAGTTTTCTTTGATTACTGGATTATCCAAGTAAAGGCTTTCCAGAGAAATGAAATGCAAAGATTGGAGTCCACATAGTTTGG  
ACGAAACCGGTGAGACTTTAGAGAAAATAAATACAGTACCACTCAATCCGGTCAAAGAAACAT AATGACCTAATAAGTTGACTTACGGAAAGGGTCTCTTACTTTACGTTTCTAACCTCAGTGGTATCAAAC

3510

HNRNPA1

HNRNPA1-202

HNRNPA1-202

gRNA Protospacer

G T G G A A G C

GAGAAAGGAAGGCTGATAACTCAACCTTATTTTATCTGACTGCTAAACAGAAATTTGAAACTAATCATCTCAGGTAACAGATAAAGGCCCTCTTTCCATTTCATAGGAAGCAATTTTGGAGGTGGTGGAAAGC  
CTCTTTCCTCCGACTATTGAGTTGGAATAAAATAAGACTGACGATTTGCTTAACTTTGATTGTAGTAGGAGTCCATTGTCTATTTCCGGGAGAAAGGGTAAGTATCCTTCGTTAAAACCTCCACCACCTTCG

3645

HNRNPA1

HNRNPA1-202

305 310  
G S N F G G G S  
ENSE0001532273

HNRNPA1-202

Donor Template SNV -> REV

Protospacer Sequence

C T C G T T A A A A C C T C C A C C C T T C G  
Donor Template SNV -> REV

gRNA Protospacer

T A C A A T A T T T T

TACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTGGACCCATGAAGGGAGGAAATTTGGAGGCAGAAAGCTCTGGCCCTATGGCGGTGGAGGCCAATACTTTGCAAAACCACGAAACCAAGGTATG  
ATGTTACTAAAACCTTAATGTTGTTAGTCAGAAGTTTAAAACCTGGGTACTTCCCTCTTTAAAACCTCCGTCTCGAGACCGGGATACCGCCACCTCCGGTATGAAACGTTTGGTCTTTGGTCCATAC

3780

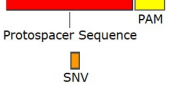
HNRNPA1

HNRNPA1-202

315 320 325 330 335 340 345 350  
Y N D F G N Y N N Q S S N F G G R S S G P Y G G G Q Y F A K P R N Q  
ENSE0001532273  
HNRNPA1-202

HNRNPA1-202

Donor Template SNV -> REV



A T G T T A C T A A A A C C T T A A T G T T A G T C A G A A G T T T A A A A C C T G G G T A C T T C C T C C T T A A A A C C T C C G T C  
Donor Template SNV -> REV

G T T T T G G T G C T T T G G T T C C A  
Sanger Sequencing Primer

GTATCTATGTAATTTTGGATAATGTCAAAGAGTGTCTGTAGCTACTGCTGGGAAGAAAGCCCTTTAACTGCTATGCTGGGCAGCAAAACGTTTATAGTTTAGAACCCTTCAGAAAGTGATAATTTGATCACAAA  
CATAGATACATTAACCTATTACAGTTTCTCACAGACATCGATGACGACCTTCTTTGGGAAATTTGACGATACAGACCCGTCGTTTTGCAAAATCAAACTTTGGAAGTCTTTCACTATTAACCTAGTGT

3915

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TTAGAAAAATCATGGGACCTCTTTACCACCTCCCTTGTAGTAGGGCCATTTTAAATGGCCAGACACTTGAATTTAACTTTTATTATCCCAATATGAAAACATTACTGTTGGCACCTTTGAAACTTTAAAAGAAA  
AATCTTTTGTAGTACCCTGGGAGAAATGGTGGAGGGAACATCATCCCGGTAAAAATTTACCGGTCTGTGAACTTAAATGAAAATATAGGGTTTATACTTTGTAATGACAACCGTGAAACTTTGAAATTTCTTT

4050

HNRNPA1

HNRNPA1-202

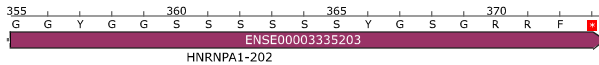
HNRNPA1-202

AATTGTA...TAAACATGAAAGTCCACCGATACCGCAAGGTCGTCGTCGTCATCGATACCGTCACCGCTCTTCAAATTAATCCATTCATTCGTGGAAAAACACACA...TAAACACTGTATAAAAAATTTAACGACTACTTGGGTTATT

4185

HNRNPA1

HNRNPA1-202



CCCTAATGTAGCTGAGCAGTGCACACATGTTAACATTATAAATGTCAGTAATTTGGATATAAAGTTAATATTCAGATCAGCAAAATTTGTGGAAACAAACTTGATATTGGATTGTAGCCTTGAGTCTTAATATG...GGGATTACATCGACTCGTCACGTTGATCAATTGTAATATAACGTCATTAACACCTATATTTCAATATAAGTCTAGTCGTTTTAAACACCCCTTGTGTTGAACATAACCTAACATCGGAACCTCAGAATTATACT

4320

HNRNPA1

HNRNPA1-202

GGGATTACATCGACTCGTCACGTTG PCR Reverse

TTTAGATTAACAACCTTTATTCATATTGTTCAACAGGAAACAAAGCTTAGCAGGAGAGGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACCTCAGCAAGCACAGTGGTGGCAGGGC...AAATCTAATTTGTTGAAATAAGGTATAACAAGTTGTCCTTTGTTTCGAATCGTCCTCTCCTCTCGGTCCTTCACTGTCCTTCGATGTCCAATGTTGTCTAAACACTTGAGTCGGTTCGTGTCAACCGTCCCG

4455

HNRNPA1

HNRNPA1-202

CTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAACCTCGAGGACTGTATTTGTGACTAATTTGTATAACAGGTTATTTTAGTTCTGTCTGTGGAAAGTGTAAAGCATTCCAA...GATCGCAGTATGTTCTTCTGTACAAAATCTGTTTATGAGTACACATACCCGTTTTTGGAGCTCTGACATAAACACTGATTAACATATTGTCCAATAAAATCAAAGACAAGACACCTTTCACATTTCTGTAAGGTT

4590

HNRNPA1

HNRNPA1-202

CAAAGGGTTTTAATGTAGATTTTTTTTTTTCACCCCATGCTGTTGATTGCTAAATGTAACAGTCTGATCGTGACGCTGAATAAATGCTTTTTTAAATGTGCTGTGTAAGTTAGTCTACTCTTAAGCCATCT...GTTTCCAAAATTTACATCTAAAAAATAAAGCTGGGTACGACAACCTAACGATTTACATTGTACAGCTAGCACTGCGACTTATTACAGAAAAAATAACAGACACATTTCAATCAGATGAGAATTCGGTAGA

4725

HNRNPA1

HNRNPA1-202

TGGTAAATTTCCCAACAGTGTGAAGTTAGAATTCCTTCAGGGTGTGTCAGGTTCTATTTGGAATTTATATAACAACCTGCTTGGGTGGAGAAGCCATTGTCTTCGAAACCTTGGTGTAGTTGAACGTATAGTT...ACCTTTAAAGGGTTGTACACCTTCAATCTTAAGGAAGTCCCACTACGGTCCAAGATAAACCTTAAATATATGTTGGACGAACCCACCTCTCGGTAACAGAAGCCTTGGAAACCATCAACTTGACTATCAA

4860

HNRNPA1

HNRNPA1-202

ACTGTTGTGACCTGAAGTTCACCATTAAAAGGGATTACCAAGCAAAATCATGGAATGGTTATAAAAGTGATTGTTGGCACATCCTATGCAATATATCTAAATGAATAATGGTACCAGATAAAAATATAGATGG...TGACAACACTGGACTTCAAGTGGTAATTTCCCTAATGGGTGCTTTTAGTACCTTACCAATATTTTCACTAACAAACCGTGTAGGATACGTTATATAGATTTAACTTATTACCATGGTCTATTTAATATCTACC

4995

HNRNPA1

HNRNPA1-202

GAATGAAGCTTGTATCCATTATCATGTGTAATCAATAAACGATTTAATCTCTTGAATGAAATGACAACCTGTATGGATTTGGGACTGGCAGAGATTTGGACTTTCCCTACCCACTCCCCTGATAAATGTT...CTTACTTCGAACACATAGGTAATAGTACACATTAGTTATTTGCTAAATTAAGGAACTTACTTTACTGTTGACATACCTAAACCTGACCGTCTCTAAACCTGAAAGGGATGGGTGAGGGGACTATTATTACAA

5130

HNRNPA1

HNRNPA1-202

GAATGCTTCTATCACAAATCAAGTTCAAAGCTCTGCCAGGGAATAGAACTAGCTGCTGGCTAATGCCGCTCCATAAATCCGAGATTTGAAGTGTCTGGGAGGCCCTTTAAAAATAACTAATATCGAAAGCAT...CTTACGAAGATAGTGTAAAGTTCAAGTTTCGAGACGGTCCCTTATCTTTGATCGACGACCGATTACGGCAGGATTTAGGCGTCTAAACTTCACAGACCCTCCGGAAAATTTTTATTGATTATAGTCTTTCTGTA

5265

HNRNPA1

HNRNPA1-202

TTTAATGAACGTAAGATAGGCTTACATTAAAGGAAACCTGCACTTTGACTGGGTTCTGGTGGGTGGCCCTCAGAGGTTCTATCAGTTAACTATACTAATTAATTTGGAGATTCAAACCATACCAATAGAAC...AAATTACTTGCATTTCTATCCGAATGTAATTTCTTTTGACGTCAAACCTGACCAAGCAACCCACCGGAAAGTCTCCAAGATAGTCAATTGATATGATTAATTAACCTCTAAGTTGGTATGTTATCTTTG

5400

HNRNPA1

HNRNPA1-202

TAAATTTTCTACATAATTTTCAATGTTAACTGCAGTTTCCCTTATGGCACAAGGGTCCACACAACCTACCTAAAATGTTAATTTGTATAGAAAATGATTTCTAAACCTTTAACAGTTAATATCCAATAATGTGTTA...ATTTAAAAAGATGATTAAGTACAATTTGACGTCAAAGGGAATACCGTGTTCCCAGTGTGTTGGAATGGATTTACAATTAACATATCTTTTACTAAAGATTTGGAAATTTGCAATTTATAGTTATTACACAAT

5535

HNRNPA1

HNRNPA1-202

TTTGACATAGATCTTTTGGGCTTACCTTTGGTGTCTCTCAATTTCAAGTGTATTTGACCTAGTAGCATAGAGATTTGTCTATCAATAGGACTGTATTTCCATCCCATGGGTTGTTGGAAGTTTGGGGAG...AAACATGTATCTAAGAAAACCTCGAATGGAACCCAGAGAGAGTTAAAGTACGATAACATGGATCATCGTATCTTAAACAGATAGTTATCTGACATATAAGGTAGGGTACCCACACAACCTTCAAACCCCTC

5670

HNRNPA1

HNRNPA1-202

GAGGAGGGTGGTGGGAGGTGGTGGGAGGTGGTGGTGGTGGGAAAGCATGGGTGATAGTTCCATGATACTGGCTGAGTTTGCATAGCAGGTGGAACCTTAACTATTGAGGGAGTTTGCAGATACCTCAGGATT...CTCCTCCACCACCCTCCACCACCCTCCACCACCACCACCCTTTCGTACCCACTATCAAGTACTATGACCGACTCAAACGTTATCGTCCACCTTGGGATTGATAACTCCCTCAAACGTTCTATGGAGTCTCTAA

5805

HNRNPA1

HNRNPA1-202

CGTGACAATGCCTTTAAAGATCCAGGAGAGATGTTACGCTACTAGGAACTGCTAGCAAGTATAGCGCGAATGGCTCCGAGCTCAGACACTCTACAGCTGAGAGTAGACACTTGTGGTATGTGGAGTACAGATAAG...GCACGTGTACGAAATTTCTAGGTCCTCTCAAGTTCGATGATCCTTGACGATCGTTTCATATCGCGCTTACCAGGCTCGAGTCTGTGAGATGTCGACTCTCATCTGTGAACCCATACACCTCATGTCTATTCT

5940

HNRNPA1

HNRNPA1-202

CCAGGGGCGAGGCCACGGCACGCTCCATGAAAGCTAGGAGGGAGTGAATATCAGTGATCATCGCAAGGAAAGGAGGCAGACAAGAGTAAGGCACACCTGACTCTTAGGACTAGCAGTACGAAACAGGAGGAAAGGT  
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6075

HNRNPA1

HNRNPA1-202

TTTATTGCTATGCGGGTAGGTAAGAACAGATTTTACTTACATCCATATAGTTACTTAAAGTCCAGTTTCTGTAAACATTTTCTTAATATATTGAGCCAAAAGTCCAGTTAAGCTGAACTGGTTTTTCT  
AAATAACGATACGCCCATCCATTCTTGTCTAAAATGAATGTAGGTATATCAATGAATTTGAGTCAAAGACAATTTGTAAGAAAGAAATTATATAACTCGGTTTTGATCAGGTCAAATTCGACTTGAAACAAAAAGA

6210

HNRNPA1

HNRNPA1-202

GGAGATGAATTGTTTTAAATTGACACCCTATTGATGGCTCCCAGTTGAAGGAAGTGAGCACATTTTGTACTGTGAATATAAATTTTTGCCCTTTTATTTATCTTCCCTTGACCCATTTCTTAAAATAATGGC  
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6345

HNRNPA1

HNRNPA1-202

TCAAAGTAATAGACTTCCCCAAATGGTGGGGGGATGGGTGGGTATTAAATGGGAGGTATGGGGGGTTTAGCTTGAGATGGGACTTGGTCTTAGAGCTAGTCTAAAAGTTGTTTACTTTTCTAGGGAGGAGTCTG  
AGTTTCATTATCTGAAGGGGTTTACCACCCCTACCCACCAATAATTACCCTCCATACCCCCCAAATCGAAGTCTACCTGAAACAGAAATCTCGATCAAGATTTCCAACAAATGAAAAGATCCCTCCTCAGAC

6480

HNRNPA1

HNRNPA1-202

CTACTAGTCTTATCAGCTCTTAAAAACAGAAACTCATCTGTCCAAGTTCGTGGCAGAAAGTAAAGTTTTTACAAATTAGTGCTCAGCAAAAAGAAATGCCCTGCGTTCCCAAAGTAAAAGAAATGACAAGCTGTACCT  
GATGATCAGAAATAGTCGAGAAATTTTGTCTTTGAGTAGACAGGTTCAAGCACCGTCTTCCATTCAAAAATGTTTAAATCACGAGTCGTTTTCTTACGGGACGCAAGGGTTTCATTTTCTTACTGTTTCGACATGGA

6615

HNRNPA1

HNRNPA1-202

TAAACAAAACACTTCGTAATCTCATCCAATTGCAAAAAGAGTTATTAGCCAACCAAGGATTCCCAAGTAGTGACAGTGGATATAACTGTGTAGTCATTACCTCTGCTTATATGAATACTTTACAACCTCTTTTG  
ATTTGGTTTTGTGAAGCATTAGAGTAGGTTAACGTTTTTCTCAATAATCGGTTGGTCCATAAGGGTCATCACTGTCACCTATATTGACACATCAGTAAGTGGAGACGAATATACTTATGAAATGTTGGAGAAAAC

6750

HNRNPA1

HNRNPA1-202

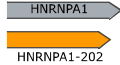
CCTTTTGCAAGAACGTCCTTGTGAAGACCTTTATCTGAGCCACTGTACTTCGTTATCACTGCCATGCAAGTTTACATGAGCTGTTCTGCAGCTCAAAATCCATTTTGTGAATGGGTTTTTTTTTAAATAAAGTGT  
GGAAAACGTCCTTGCAGGAACACTTCTGAAAATAGACTCGGTGACATGAAGCAATAGTGACGGTACGTCAAATGTAAGTACTGACAAGACGTCGAGTTTAAAGGTAACAACTTACCCAAAAAAAATTTATTGACA

6885

HNRNPA1

HNRNPA1-202

ATTTAACTTAG 3'  
6896  
TAAATTGAATC 5'



Feature	Location	Size	Type
<b>HNRNPA1</b>	1 .. 6896	6896 bp	gene
/note	= gene <a href="#">ENSG00000135486</a> Protein coding		
<b>HNRNPA1-203</b>	1 .. 6895	6895 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000546500</a>		
<b>HNRNPA1-238</b>	471 .. 5651	5181 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677385</a>		
<b>HNRNPA1-231</b>	471 .. 5650	5180 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677210</a>		
<b>HNRNPA1-237</b>	471 .. 5037	4567 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677375</a>		
<b>HNRNPA1-234</b>	499 .. 5553	5055 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677249</a>		
<b>HNRNPA1-220</b>	506 .. 5046	4541 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676725</a> Retained intron		
<b>HNRNPA1-259</b>	506 .. 5045	4540 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678418</a> Retained intron		
<b>HNRNPA1-209</b>	512 .. 5650	5139 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000550482</a>		
<b>HNRNPA1-202</b>	534 .. 6895	6362 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000340913</a>		
<b>HNRNPA1-279</b>	534 .. 1749	1216 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679101</a>		
<b>HNRNPA1-205</b>	556 .. 6896	6341 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000547566</a> Nonsense mediated decay		
<b>HNRNPA1-206</b>	556 .. 3686	3131 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000547708</a>		
<b>HNRNPA1-280</b>	557 .. 5553	4997 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679228</a> Retained intron		
<b>HNRNPA1-207</b>	564 .. 2414	1851 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000547870</a> Retained intron		
<b>HNRNPA1-213</b>	571 .. 2294	1724 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000551702</a>		
<b>HNRNPA1-257</b>	583 .. 6540	5958 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678365</a>		
<b>HNRNPA1-201</b>	583 .. 4689	4107 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000330752</a>		
<b>HNRNPA1-221</b>	583 .. 4125	3543 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676794</a>		
<b>HNRNPA1-204</b>	588 .. 5059	4472 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000547276</a>		
<b>HNRNPA1-272</b>	588 .. 2108	1521 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678919</a>		
<b>HNRNPA1-268</b>	588 .. 1749	1162 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678690</a>		
<b>HNRNPA1-232</b>	616 .. 6895	6280 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677220</a> Nonsense mediated decay		
<b>HNRNPA1-201</b>	616 .. 4121	3506 bp	CDS
▶ 9 segments = 924 bp			
/note	= coding sequence <a href="#">ENSP00000333504</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTRKSRGFGFVYATVVEEVDAAMNARPHKVDGRVVEPKRAVSR,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFSGSRGGGGYGGSDGYNGFGND,,GSNFGGGGSYDFGNYNQSSNFGPMKGGNFGGRSSGPGYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF*		
<b>HNRNPA1-202</b>	616 .. 4121	3506 bp	CDS
▶ 10 segments = 1119 bp			
/note	= coding sequence <a href="#">ENSP00000341826</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTRKSRGFGFVYATVVEEVDAAMNARPHKVDGRVVEPKRAVSR,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFSGSRGGGGYGGSDGYNGFGND,,GGYGGGGPGYGGSRGYGSGGQGYGNQSSYGGSGSYDSYNNGGGGGFGGGS,,GSNFGGGGSYDFGNYNQSSNFGPMKGGNFGGRSSGPGYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 372 amino acids = 38.7 kDa		
<b>HNRNPA1-203</b>	616 .. 4121	3506 bp	CDS
▶ 9 segments = 963 bp			
/note	= coding sequence <a href="#">ENSP00000448617</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTRKSRGFGFVYATVVEEVDAAMNARPHKVDGRVVEPKRAVSR,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFSGSRGGGGYGGSDGYNGFGND,,GSNFGGGGSYDFGNYNQSSNFGPMKGGNFGGRSSGPGYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF*		

Feature	Location	Size	Type
<b>HNRNPA1-204</b>	616 .. 4121	3506 bp	CDS
▶ 8 segments = 804 bp			
/note	= coding sequence <a href="#">ENSP00000447260</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 267 amino acids = 29.4 kDa		
<b>HNRNPA1-209</b>	616 .. 4121	3506 bp	CDS
▶ 9 segments = 963 bp			
/note	= coding sequence <a href="#">ENSP00000446486</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 346 amino acids = 39.1 kDa		
<b>HNRNPA1-231</b>	616 .. 4121	3506 bp	CDS
▶ 10 segments = 1119 bp			
/note	= coding sequence <a href="#">ENSP00000503610</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 372 amino acids = 38.7 kDa		
<b>HNRNPA1-234</b>	616 .. 4121	3506 bp	CDS
▶ 9 segments = 960 bp			
/note	= coding sequence <a href="#">ENSP00000503649</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 349 amino acids = 39.4 kDa		
<b>HNRNPA1-237</b>	616 .. 4121	3506 bp	CDS
▶ 9 segments = 981 bp			
/note	= coding sequence <a href="#">ENSP00000503651</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,EKLKLYFSGGYGGSSSSSYGSGRRF* 346 amino acids = 39.1 kDa		
<b>HNRNPA1-206</b>	616 .. 3686	3071 bp	CDS
▶ 6 segments = 470 bp			
/note	= coding sequence <a href="#">ENSP00000448229</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFV,,GGFGSRGGGGYGGSGDGYNGFGND,,GSNFGGGGSYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,EKLKLYFSGGYGGSSSSSYGSGRRF* 346 amino acids = 39.1 kDa		
<b>HNRNPA1-238</b>	616 .. 2526	1911 bp	CDS
▶ 6 segments = 729 bp			
/note	= coding sequence <a href="#">ENSP00000502985</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,EKLKLYFSGGYGGSSSSSYGSGRRF* 242 amino acids = 26.7 kDa		
<b>HNRNPA1-213</b>	616 .. 2294	1679 bp	CDS
▶ 4 segments = 436 bp			
/note	= coding sequence <a href="#">ENSP00000448117</a>		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,EKLKLYFSGGYGGSSSSSYGSGRRF* 242 amino acids = 26.7 kDa		
<b>HNRNPA1-272</b>	616 .. 2108	1493 bp	CDS
▶ 2 segments = 226 bp			
/note	= coding sequence <a href="#">ENSP00000504604</a>		
/translation	= MSKSE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV 75 amino acids = 8.6 kDa		
<b>HNRNPA1-268</b>	616 .. 1749	1134 bp	CDS
▶ 2 segments = 162 bp			
/note	= coding sequence <a href="#">ENSP00000503229</a>		
/translation	= MSKSE,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE 54 amino acids = 6.1 kDa		
<b>HNRNPA1-250</b>	680 .. 5047	4368 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678077</a>		
<b>HNRNPA1-208</b>	814 .. 2434	1621 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000548688</a>		
<b>HNRNPA1-208</b>	831 .. 2434	1604 bp	CDS
▶ 6 segments = 694 bp			
/note	= coding sequence <a href="#">ENSP00000447782</a>		
/translation	= MRD SLLVA KFLGTQ DLCLFLNLAL,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNF,GGGSGYDNFGYNNQSSNFPGMKGGNFGGRSSPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 231 amino acids = 25.7 kDa		
<b>HNRNPA1-261</b>	1603 .. 4125	2523 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678448</a> Nonsense mediated decay		
<b>HNRNPA1-282</b>	1603 .. 4125	2523 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679273</a> Nonsense mediated decay		
<b>HNRNPA1-210</b>	1603 .. 2294	692 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000550994</a> Nonsense mediated decay		
<b>HNRNPA1-222</b>	1603 .. 2294	692 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676842</a> Nonsense mediated decay		



















Feature	Location	Size	Start	End	Type
<b>HNRNPA1-250</b>	1606 .. 4121	2516 bp	■	→	CDS
▶ 7 segments = 828 bp					
/note	= coding sequence <a href="#">ENSP00000504814</a>				
/translation	= MRDPNTKRSRGFGVITYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYKGKIEVIEIMTKDRGSGKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCVVRKALSKQE MASASSSR,,GRSGSGNFGGGGGGGGNDNFRGGNFSGR,,GGFGGSRGGGGYGGSDGYNGFGND,,GSNFGGGGSYNDGNYNNQSSNFGPMKGGNFGGRSSGYPYGGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF 275 amino acids = 29.1 kDa				
<b>HNRNPA1-279</b>	1606 .. 1749	144 bp	■	→	CDS
/note	= coding sequence <a href="#">ENSP00000503166</a>				
/translation	= MRDPNTKRSRGFGVITYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE 48 amino acids = 5.4 kDa				
<b>HNRNPA1-242</b>	2202 .. 3775	1574 bp	■	→	CDS
▶ 2 segments = 249 bp					
/note	= coding sequence <a href="#">ENSP00000503254</a>				
/translation	= FRNTIL*MATTVKLEKPCQSKRWLVLHPAKE,,EAILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 83 codons (2 internal stop codons)				
<b>HNRNPA1-242</b>	2202 .. 3775	1574 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000677636</a>				
<b>HNRNPA1-243</b>	2202 .. 3042	841 bp	■	→	CDS
▶ 2 segments = 249 bp					
/note	= coding sequence <a href="#">ENSP00000504753</a>				
/translation	= FRNTIL*MATTVKLEKPCQSKRWLVLHPAKE,,VVMEEALVTLLEEAEAMEVVDVDRVMETRAVAMAGVAAMTAITTEAEALAVVV 83 codons (1 internal stop codon)				
<b>HNRNPA1-243</b>	2202 .. 3042	841 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000677645</a>				
<b>HNRNPA1-236</b>	2202 .. 2682	481 bp	■	→	CDS
▶ 2 segments = 168 bp					
/note	= coding sequence <a href="#">ENSP00000504458</a>				
/translation	= FRNTIL*MATTVKLEKPCQSKRWLVLHPAKE,,VALVAAVVVVDMVAVGMAIMDLVMM 56 codons (1 internal stop codon)				
<b>HNRNPA1-236</b>	2202 .. 2682	481 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000677291</a>				
<b>HNRNPA1-249</b>	2381 .. 3775	1395 bp	■	→	CDS
▶ 2 segments = 234 bp					
/note	= coding sequence <a href="#">ENSP00000503056</a>				
/translation	= VEVVLETLVVVVEVSVGMTTSSVVEETSVVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 78 codons (1 internal stop codon)				
<b>HNRNPA1-265</b>	2381 .. 3775	1395 bp	■	→	CDS
▶ 2 segments = 180 bp					
/note	= coding sequence <a href="#">ENSP00000504089</a>				
/translation	= VEVVLETLVVVVEVSVGMTTSSVVEETSVVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 60 codons (1 internal stop codon)				
<b>HNRNPA1-269</b>	2381 .. 3775	1395 bp	■	→	CDS
▶ 2 segments = 231 bp					
/note	= coding sequence <a href="#">ENSP00000503516</a>				
/translation	= VEVVLETLVVVVEVSVGMTTSSVVEETSVVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 77 codons (1 internal stop codon)				
<b>HNRNPA1-270</b>	2381 .. 3775	1395 bp	■	→	CDS
▶ 2 segments = 249 bp					
/note	= coding sequence <a href="#">ENSP00000503756</a>				
/translation	= VEVVLETLVVVVEVSVGMTTSSVVEETSVVV,,EAILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 83 codons (1 internal stop codon)				
<b>HNRNPA1-273</b>	2381 .. 3775	1395 bp	■	→	CDS
▶ 2 segments = 210 bp					
/note	= coding sequence <a href="#">ENSP00000504850</a>				
/translation	= VEVVLETLVVVVEVSVGMTTSSVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 70 codons (1 internal stop codon)				
<b>HNRNPA1-249</b>	2381 .. 3775	1395 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000677945</a>				
<b>HNRNPA1-265</b>	2381 .. 3775	1395 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000678597</a>				
<b>HNRNPA1-269</b>	2381 .. 3775	1395 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000678873</a>				
<b>HNRNPA1-270</b>	2381 .. 3775	1395 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000678876</a>				
<b>HNRNPA1-273</b>	2381 .. 3775	1395 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000678934</a>				
<b>HNRNPA1-256</b>	2381 .. 3042	662 bp	■	→	CDS
▶ 2 segments = 249 bp					
/note	= coding sequence <a href="#">ENSP00000504511</a>				
/translation	= VEVVLETLVVVVEVSVGMTTSSVVEETSVVV,,VVMEEALVTLLEEAEAMEVVDVDRVMETRAVAMAGVAAMTAITTEAEALAVVV 83 amino acids = 8.6 kDa				
<b>HNRNPA1-256</b>	2381 .. 3042	662 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000678347</a>				
<b>HNRNPA1-245</b>	2608 .. 6895	4288 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000677778</a>				

Feature	Location	Size	Type
<b>HNRNPA1-245</b>	2608 .. 6859	4252 bp	CDS
▶ 3 segments = 245 bp			
/note	= coding sequence <a href="#">ENSP00000504642</a>		
/translation	= VALVAAVVVDMVAVGMAIMDLVMM,,GGVCY*SYQLKTETHLSKFAER,,NVLVKTFI*ATVLRyhCHAVYMSCSAAQIPFC 81 codons (2 internal stop codons)		
<b>HNRNPA1-217</b>	2608 .. 4125	1518 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676572</a> Nonsense mediated decay		
<b>HNRNPA1-230</b>	2608 .. 4125	1518 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677191</a> Nonsense mediated decay		
<b>HNRNPA1-254</b>	2608 .. 4125	1518 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678212</a> Nonsense mediated decay		
<b>HNRNPA1-262</b>	2608 .. 4125	1518 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678456</a>		
<b>HNRNPA1-284</b>	2608 .. 4125	1518 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679344</a> Nonsense mediated decay		
<b>HNRNPA1-262</b>	2608 .. 4121	1514 bp	CDS
▶ 2 segments = 131 bp			
/note	= coding sequence <a href="#">ENSP00000504368</a>		
/translation	= VALVAAVVVDMVAVGMAIMDLVMM,,VAMAVPAAAVAMAVAEFD 43 amino acids = 4.3 kDa		
<b>HNRNPA1-219</b>	2608 .. 3775	1168 bp	CDS
▶ 2 segments = 210 bp			
/note	= coding sequence <a href="#">ENSP00000504696</a>		
/translation	= VALVAAVVVDMVAVGMAIMDLVMMV,,TTMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 70 codons (1 internal stop codon)		
<b>HNRNPA1-233</b>	2608 .. 3775	1168 bp	CDS
▶ 2 segments = 165 bp			
/note	= coding sequence <a href="#">ENSP00000502876</a>		
/translation	= VALVAAVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 55 codons (1 internal stop codon)		
<b>HNRNPA1-235</b>	2608 .. 3775	1168 bp	CDS
▶ 2 segments = 162 bp			
/note	= coding sequence <a href="#">ENSP00000503602</a>		
/translation	= VALVAAV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 54 codons (1 internal stop codon)		
<b>HNRNPA1-263</b>	2608 .. 3775	1168 bp	CDS
▶ 2 segments = 183 bp			
/note	= coding sequence <a href="#">ENSP00000503162</a>		
/translation	= VALVAAVVVDMVA,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 61 codons (1 internal stop codon)		
<b>HNRNPA1-277</b>	2608 .. 3775	1168 bp	CDS
▶ 2 segments = 231 bp			
/note	= coding sequence <a href="#">ENSP00000504683</a>		
/translation	= VALVAAVVVDMVAVGMAIMDLVMMV,,TILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK 77 codons (1 internal stop codon)		
<b>HNRNPA1-219</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676707</a>		
<b>HNRNPA1-233</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677224</a>		
<b>HNRNPA1-235</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677279</a>		
<b>HNRNPA1-241</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677539</a> Nonsense mediated decay		
<b>HNRNPA1-255</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678279</a>		
<b>HNRNPA1-263</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678513</a>		
<b>HNRNPA1-277</b>	2608 .. 3775	1168 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679063</a>		
<b>HNRNPA1-283</b>	2608 .. 3503	896 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679319</a>		
<b>HNRNPA1-278</b>	2887 .. 4477	1591 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679079</a>		
<b>HNRNPA1-278</b>	2887 .. 4370	1484 bp	CDS
▶ 2 segments = 170 bp			
/note	= coding sequence <a href="#">ENSP00000504545</a>		
/translation	= VMEEAALVTLLEEAEAMEVVDVRVME TRAVAMGVAAMTAITTEAEALAVVV,,ETKL 56 amino acids = 5.8 kDa		
<b>HNRNPA1-225</b>	2887 .. 4125	1239 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676886</a>		

Feature	Location	Size	Type
<b>HNRNPA1-258</b>	2887 .. 4125	1239 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678412</a>		
<b>HNRNPA1-275</b>	2887 .. 4125	1239 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678970</a>		
<b>HNRNPA1-225</b>	2887 .. 4121	1235 bp	CDS
▶ 2 segments = 140 bp			
/note	= coding sequence <a href="#">ENSP00000503468</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRA,,VAMAVPAAAVAMAVAEDF 46 amino acids = 4.8 kDa		
<b>HNRNPA1-258</b>	2887 .. 4121	1235 bp	CDS
▶ 2 segments = 212 bp			
/note	= coding sequence <a href="#">ENSP00000503562</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALAVVV,,VAMAVPAAAVAMAVAEDF 70 amino acids = 7.1 kDa		
<b>HNRNPA1-275</b>	2887 .. 4096	1210 bp	CDS
▶ 3 segments = 263 bp			
/note	= coding sequence <a href="#">ENSP00000503825</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALAVVV,,GGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSS 87 amino acids = 8.7 kDa		
<b>HNRNPA1-215</b>	2887 .. 3775	889 bp	CDS
▶ 2 segments = 195 bp			
/note	= coding sequence <a href="#">ENSP00000503977</a>		
/translation	= VVMEEAALVTLEEAEAME,,VVEATMILGITTISLQILD*REEILEAEALPMAVEANTLQNHETK 65 codons (1 internal stop codon)		
<b>HNRNPA1-223</b>	2887 .. 3775	889 bp	CDS
▶ 2 segments = 291 bp			
/note	= coding sequence <a href="#">ENSP00000503749</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALAVVV,,ATMILGITTISLQILD*REEILEAEALPMAVEANTLQNHETK 97 codons (1 internal stop codon)		
<b>HNRNPA1-227</b>	2887 .. 3775	889 bp	CDS
▶ 2 segments = 312 bp			
/note	= coding sequence <a href="#">ENSP00000502981</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALAVVV,,AILEVVEATMILGITTISLQILD*REEILEAEALPMAVEANTLQNHETK 104 codons (1 internal stop codon)		
<b>HNRNPA1-260</b>	2887 .. 3775	889 bp	CDS
▶ 2 segments = 288 bp			
/note	= coding sequence <a href="#">ENSP00000503030</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALA,,VVEATMILGITTISLQILD*REEILEAEALPMAVEANTLQNHETK 96 codons (1 internal stop codon)		
<b>HNRNPA1-264</b>	2887 .. 3775	889 bp	CDS
▶ 2 segments = 291 bp			
/note	= coding sequence <a href="#">ENSP00000504251</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALAV,,VVEATMILGITTISLQILD*REEILEAEALPMAVEANTLQNHETK 97 codons (1 internal stop codon)		
<b>HNRNPA1-266</b>	2887 .. 3775	889 bp	CDS
▶ 2 segments = 297 bp			
/note	= coding sequence <a href="#">ENSP00000504004</a>		
/translation	= VVMEEAALVTLEEAEAMEVVDVDRVMETRAVAMGVAAMTAITTEAEALAVVV,,VVEATMILGITTISLQILD*REEILEAEALPMAVEANTLQNHETK 99 codons (1 internal stop codon)		
<b>HNRNPA1-215</b>	2887 .. 3775	889 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676472</a>		
<b>HNRNPA1-223</b>	2887 .. 3775	889 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676853</a>		
<b>HNRNPA1-227</b>	2887 .. 3775	889 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676951</a>		
<b>HNRNPA1-260</b>	2887 .. 3775	889 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678424</a>		
<b>HNRNPA1-264</b>	2887 .. 3775	889 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678581</a>		
<b>HNRNPA1-266</b>	2887 .. 3775	889 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678611</a>		
<b>HNRNPA1-239</b>	2887 .. 3042	156 bp	CDS
▶ 2 segments = 36 bp			
/note	= coding sequence <a href="#">ENSP00000504431</a>		
/translation	= VVMEE,,AALAVVV 12 amino acids = 1.2 kDa		
<b>HNRNPA1-274</b>	2887 .. 3042	156 bp	CDS
▶ 2 segments = 42 bp			
/note	= coding sequence <a href="#">ENSP00000503733</a>		
/translation	= VVMEE,,AEALAVVV 14 amino acids = 1.4 kDa		
<b>HNRNPA1-239</b>	2887 .. 3042	156 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677488</a>		
<b>HNRNPA1-274</b>	2887 .. 3042	156 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678947</a>		

Feature	Location	Size	Type
<b>HNRNPA1-212</b>	3531 .. 4179	649 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000551679</a> Retained intron		
	3561 .. 64,891	61,331 bp	gene
/note	= gene <a href="#">ENSG00000258344</a> lncRNA		
	3561 .. 64,891	61,331 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000553061</a> lncRNA		
<b>HNRNPA1-247</b>	3620 .. 6895	3276 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677840</a>		
<b>HNRNPA1-247</b>	3620 .. 6859	3240 bp	CDS
▶ 3 segments = 326 bp			
/note	= coding sequence <a href="#">ENSP00000503273</a>		
/translation	= EAILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK,,GGVCY*SYQLKTEHLSKFVAER,,NVLVKTFI*ATVLRHCHAVYMSCSAAQIPFC 108 codons (3 internal stop codons)		
<b>HNRNPA1-276</b>	3620 .. 4477	858 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679026</a>		
<b>HNRNPA1-276</b>	3620 .. 4370	751 bp	CDS
▶ 2 segments = 170 bp			
/note	= coding sequence <a href="#">ENSP00000504539</a>		
/translation	= EAILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK,,ETKL 56 codons (1 internal stop codon)		
<b>HNRNPA1-240</b>	3620 .. 3775	156 bp	CDS
▶ 2 segments = 126 bp			
/note	= coding sequence <a href="#">ENSP00000503537</a>		
/translation	= EAILEVVEATMILGITTISLQILDP*REEILE,,ANTLQNHETK 42 codons (1 internal stop codon)		
<b>HNRNPA1-248</b>	3620 .. 3775	156 bp	CDS
▶ 2 segments = 96 bp			
/note	= coding sequence <a href="#">ENSP00000503848</a>		
/translation	= EAILEVVE,,EILEAEALAPMAVEANTLQNHETK 32 amino acids = 3.5 kDa		
<b>HNRNPA1-240</b>	3620 .. 3775	156 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677518</a>		
<b>HNRNPA1-248</b>	3620 .. 3775	156 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677847</a>		
<b>Donor Template SNV -&gt; REV</b>	3620 .. 3719	100 bp	misc_feature
<b>Protospacer Sequence</b>	3638 .. 3657	20 bp	misc_feature
<b>SNV</b>	3652 .. 3652	1 bp	misc_feature
/note	= REV=G SNV=A		
<b>PAM</b>	3658 .. 3660	3 bp	misc_feature
<b>HNRNPA1-221</b>	3694 .. 4121	428 bp	CDS
▶ 2 segments = 138 bp			
/note	= coding sequence <a href="#">ENSP00000504819</a>		
/translation	= MKGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 45 amino acids = 4.5 kDa		
<b>HNRNPA1-218</b>	4066 .. 6896	2831 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676661</a> Nonsense mediated decay		
<b>HNRNPA1-228</b>	4066 .. 6896	2831 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677061</a> Nonsense mediated decay		
<b>HNRNPA1-229</b>	4066 .. 6896	2831 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677072</a> Nonsense mediated decay		
<b>HNRNPA1-244</b>	4066 .. 6896	2831 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677666</a>		
<b>HNRNPA1-226</b>	4066 .. 6540	2475 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000676925</a> Nonsense mediated decay		
<b>HNRNPA1-246</b>	4066 .. 6540	2475 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000677832</a> Nonsense mediated decay		
<b>HNRNPA1-253</b>	4066 .. 6540	2475 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678199</a> Nonsense mediated decay		
<b>HNRNPA1-281</b>	4066 .. 6540	2475 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000679251</a> Nonsense mediated decay		
<b>HNRNPA1-251</b>	4066 .. 4773	708 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000678093</a>		
<b>HNRNPA1-244</b>	4066 .. 4121	56 bp	CDS
/note	= coding sequence <a href="#">ENSP00000504664</a>		
/translation	= VAMAVPAAAVAMAVAEDF 18 amino acids = 1.7 kDa		

Feature	Location	Size			Type
<b>HNRNPA1-267</b>	4517 .. 6540	2024 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000678687</a>				
<b>HNRNPA1-216</b>	5616 .. 6540	925 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000676528</a>				
<b>HNRNPA1-211</b>	5715 .. 6859	1145 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000551665</a> Retained intron				
<b>HNRNPA1-214</b>	5755 .. 6895	1141 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000551803</a>				
<b>HNRNPA1-252</b>	6055 .. 6895	841 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000678103</a>				
<b>HNRNPA1-224</b>	6055 .. 6540	486 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000676855</a>				
<b>HNRNPA1-271</b>	6645 .. 6895	251 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000678900</a>				

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	25-mer	3285 .. 3309	61°C	Jun 14, 2022
/sequence = CTTGGGACCTTAGGCGCTTAGTTG 52% GC / 7695.0 Da				
✓ <b>Donor Template SNV -&gt; REV</b>	100-mer	3620 .. 3719	74°C	Jun 14, 2022
/sequence = CTGCCTCCAAAATTCCTCCCTTCATGGGTCCAAAATTTGAAGACTGATTGTTGTAATTCCTCCAAAATCATTGTAGCTTCCACCACCTCCAAAATTGCTTC 41% GC / 30,465.8 Da				
✓ <b>gRNA Protospacer</b>	20-mer	3638 .. 3657	40°C	Jun 14, 2022
/sequence = GTGGAAGCTACAATAATTTT 30% GC / 6155.1 Da				
✓ <b>Sanger Sequencing Primer</b>	20-mer	3758 .. 3777	56°C	Jun 14, 2022
/sequence = ACCTTGGTTTCGTGGTTTTG 45% GC / 6136.1 Da				
✓ <b>PCR Reverse</b>	25-mer	4186 .. 4210	63°C	Jun 14, 2022
/sequence = GTTGCACTGCTCAGCTACATTAGGG 52% GC / 7673.0 Da				