

JIPSC1040_SnapgeneDNA_INK2J00085_HNRNPA1_D262N_SNVWT
 6896 bp

AAAGCTAGGACAAACTCCCGCCAACACGACGAGCGCCGTAGGTTCACTGCTTACTCTGCCCAGCATTTCACGTGTTCTCAGAGGCGGAACCTTCTTAATGCGCCTGCGCAAAACTCGCCATTTTACTACACG
TTTCGATCCTGTTTGAAGGCGGTTGTCGCTCCGCGGCATCCAAGTGACGGATGAGGACGGCGGTAAGTGACACAAGAGTCTCCGTCCACCTTGAAGAAATACGCGGACGCGTTTGAAGCGGTAATAATGATGTGC

135

HNRNPA1

TGCGGTCAACAAGAGTTCATTGCAAAAAATTTGTTACCTCTGGCTGCTTGTCTAATACATAGTGTAAATCATGCTTTGCAAGCGACTTGACTGTAATATTTGCGCGTGAAGATTAAAAAGATGTTAAACACC
ACGCCAGTTGTTCTCAAGTAACGTTTTTTTAACAATGAGGACCGACGAACAGATTATGTATCACAATAGTACGAAACGGTTCGCTGAACTGACATTATAAACCGCGCACCTTCTAATTTTTCTACAATTTGTGG

270

HNRNPA1

CAAGGTAGATTCAAATGTGAATGATTGGTCGGTTGGCCAATCAGACTGGTTAAACAATAACATTACTCGGGAACCAATGGACTCCAAGGGTGGAGACGGCGTAGAACGACCGAAGGAATGACGTTACACAGCAAT
GTTCCATCTAAGTTTACACTTACTAACCGCAACCGGTTAGTCTGACCAATTGTTATTGTAATGAGCCCTGGTTACCTGAGGTTCCCAACCTCTGCGGCATCTTCTGCTGCTTCTACTGCAATGTCGTTA

405

HNRNPA1

GTGGCACCACAGGCCAATAGCAGGGGGAAGCGATTTCAAGTATCCAATCAGAGCTGTTCCAGGGCGGAGTCTACCAATGCCGAAAGCGAGGAGCGGGTAAAAAGAGAGGGCGAAGGTAGGCTGGCAGATACG
CACCGTGGTTCGCGTTATCGTCCCGCTTCGCTAAAGTTCATAGTTAGTCTCGACAAGTCCCGCTCAGATGTTACGGCTTCGCTCCTCGCGCCATTCTCTCCGCTTCCATCCGACCGTCTATGC

540

HNRNPA1

HNRNPA1-202

TTGTCAGCTTGTCTCTTTCTGCCCGTGGACGCGCGCAAGAAGCATCGTTAAAGTCTCTTTCACCTGCCGTCATGTCTAAGTCAGAGGTGAGTTAGGCGCGCTTCCCACTTGAATTTTTCTCTCCCTTT
AAGCAGTCGACAGGAAAGACGGGACCTGCGGCGGCTTCTTCGTAGCAATTCAGAGAGAAGTGGGACGGCAGTACAGATTCAAGTCTCCACTCAATCCGCGGAAAGGGTGAACCTAAAAAGGAGAGGGAAA

675

HNRNPA1

HNRNPA1-202

1 5
M S K S E
ENSE00002375624

HNRNPA1-202

CCTGAATCGGTAAGATGCTGCTGGGTTTCGTTCCCTTGCCACGACCCATTCTACAGTTCCTTCGGTCGCTGCCACGGCTACCCCTCCCAAAGTTCAGTTCGCGCATTTTGTCTCTTGTATGCCATGAGGCGGCTC
GGACTTAGCCATTCTACGACACCCAAAGCAAGGAACGTGGTCCGGTAAGATGTCAGGAAGCCAGCGAGGTCGCGGATGGGAGGGTTTCAAGTTCAGCGGTAAACACAGGAGAAGTACGGTACTCCGGCGAG

810

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TCCGCCAACCATGAGTTATCATGCGGGACTCGTTACTCGTAGCAAAATTCCTTAGGCACACAGGATCTTTGCTTTTTTAAACCTTGCCCTTGGTGAGCGAGTTTTCTAAAGAGCGATTAGTCCATTGTGGAGAT
AGGCGGTTGGTACTCAATAGTACGCCCTGAGCAATGAGCATCGTTTTAAGAAATCCGTGTCTTAGAAACAGAAAAAATTTGGAACGGAACCACTCGCTCAAAAGATTCTCGCTAATCAGGGTAACACCTCTA

945

HNRNPA1

HNRNPA1-202

HNRNPA1-202

GCACCCCTACCGCCAAAGCCTTTGTTGCGGTGCGTCCGAAAGCGACTAGGGACGCATGCGCTTTCGATTTCCTAGCACTCCCAACTCCAGCATACGGCTCCCTTGATAGGCGAAGCACGTGCTTGTGCGA
CGTGGGGATGGCGGTTCCGAAACAACGCGCACGACGCTTCCGCTGATCCCTGCGTACGCGAAACCTAAAGGATCGTGAGGGTTGAGGTCGTATGCCGGAGGGAACATCCGCTCTCTGTCACAGAAACAACGCT

1080

HNRNPA1

HNRNPA1-202

HNRNPA1-202

CCTGAACGAACAATAAGTCTAGGTACACAGTTGGTGTCTAGTTTTCTTTCTCGATGGAATTTGTTGTTGTAGCCATTTAACACTTCCCTCCCTCCCTCCTAGTCTCTAAAGAGCCCGAACACG
GGACTTGCTTGTATTACGATCCATGTGTCAACCACAGATCAAAAAGAAAAGGAGCTACCTTTAACAAAGCACAACTCGGGTAAATTTGGAAGGGGAGGGGGTGAAGTACAGAGGATTTCTCGGCTTGTCTG

1215

HNRNPA1

HNRNPA1-202

10
S P K E P E Q
ENSE00003542256

HNRNPA1-202

TGAGGAAGCTCTTCATTGGAGGTTGAGCTTTGAAACAACGATGAGAGCCTGAGGAGCCATTTGAGCAATGGGAAACGCTCACGACTGTGTGTAAGATTGGAAGGGACAAAGCAGTAAACAGCCGATTT
ACTCCTTCGAGAAGTAACCTCCAACTCGAAACTTTGTTGACTACTCTCGGACTCCTCGGTAACACTCGTTACCCCTTGCAGTGCCTGACACACCATTCTAAACCTTCCCTGTTTCGTCATTTTGTGCGCTAAA

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

CCCTGGCTTATCTTGGTGCAGTCTTCCGAATGCTTATGAAAGTAGTTAATAGCAATTAAGTTAGAGCTTTGTTGGCAAAGGAAAGCTCCTGCTTTGATTTAAAAAGCTACCTCTTAAATCTAGGGTAGTGGAA
GGAACCGAATAGAACCGTGCAGAAGGGCTTACGAATACTTTCATCAATATCGTAATATCAATCTCGAAACAACCGTTTCTTGCAGGACGAAACTAAATTTTCGATGGAGAAATTTAGATCCCATCACCTT

1485

HNRNPA1

HNRNPA1-202

HNRNPA1-202

ACTGGACGACTTTTTAAAAAGGCTGGTGAAGTTTCTATTGCCCTATTCAAAGTTAAAATGACAAAAGCTTTTGGGTCAGACTTTGTTTACATAAATTAACACTGTTCTCAGGTAATGAGAGATCCAAAC
TGACCTGCTGAAAAATATTTTCCGACCACTTCAAGAGATAACGGGATAAGTTTCAATTTTACTGTTTTGAAAAACGCGACTGAAACACAATGATTTAATTTGACAAAGAGTCCATTACTCTCAGGTTTGG

1620

HNRNPA1

HNRNPA1-202

45 50
V M R D P N
ENSE00003638233

HNRNPA1-202

ACCAAGCGCTCCAGGGGCTTTGGGTTTGTACACATATGCCACTGTGGAGGAGGTGGATGCGAGCTGAAGTTCGAAGGCCACACAAGTGGATGGAAAGAGTTGGAAACCAAAGAGAGCTCCAGAGAAAGTGAAGT
TGGTTCGCGAGGTCCCGAAACCAACAGTGTATACGGTGACACCTCTCCACCTACGTGATACCTTACGTTCCGGTGTGTCCACCTACCTTCTCAACACCTTGGTTTCTCTCGACAGAGGTCTCTCACTCA

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

GGGTTTTTTTTCTTCTTCTTAACTTACTTGGATATGTGCTGCTATGGACTTAAGATTCGGGAGTTTTCTAACTTACCAAATTTTTATTTCGAGTATAGGCTTGTCTAACTTAAACCTATGGTTTTTCTC
CCCCAAAAAAGAAAGAAAGAAATTTGAATGAACCTATACACGACGATACCTGAATTTAAGCCCTCAAAGATTTGAATGGTTTTAAAAATAAGCTCATATCCGAAACGATTAGATTTGGATACCAAAAAAGAG

1890

HNRNPA1

HNRNPA1-202

HNRNPA1-202

CTATTAGGATTCTCAAAGACCAGGTGCCCACTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATTATTTTGAACAGTATGGAAAAATGAAGTATTGAAAT
GATAATCCTAAGAGTTTCTGGTCCACGGGTGAATGACACTTTTTCTATAAACACACCAGTAATTTCTCTGTGACTTCTGTAGTGGATTCTCTAATAAACTTGTATACCTTTTTAACTTCACTAACTTTA

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 L R D Y F E Q Y G K I E V I E I
ENSE00003578192

HNRNPA1-202

CATGACTGACCGAGGCGAGTGGCAAGAAAAGGGGCTTTGCCTTGTAACTTTGACGACCATGACTCCGTGGATAAGATTGTGAGTAAGTATCAGATAGTGGCATTAGTAAGGGTCCACAATCTGTATGGCATT
GTACTGACTGGCTCCGTCACGGTCTTTCCCGGAAACGAAACATTGGAACTGCTGGTACTGAGGCACCTATTCTAACAGTATTCTATAGTCTATCACCGTAAATCATTCCCAAGGTGTAGACATACCGTAA

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

CTAAACCTGATACCATGTTGTATCTATGTTTTTTTTAGTTCAGAAATACCATACTGTGAATGGCCCAACTGTGAAGTTAGAAAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGG
GATTTGGACTATGGTACAACATAGATACAAAAAAAATCAAGTCTTTATGGTATGACACTTACCGGTGTTGACACTTCAATCTTTCCGGACAGTTTCGTTCTTCTACCGATCACGAAGTAGGTGGTTTTCTCC

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

TATGCTTGTGCTTAATTAACCTTAAAGGTAACCTTTGAGTTACTCCAGTATGAATGATTAATGCTTAACTTTCATGTCTTAAAGTTCGAAGTGGTCTTGGAACTTTGGTGGTGGTGGTGGGTTTCGGT
ATACGAACAACGAATTAATTTGGAATTTCCATGAAACTCAATGAGGTCACTTACTATAATACGAATTTGAAGTACAGAATTCAGCTTCAACAAGACCTTTGAAACCACCAAGCACCCTCCACCAAAAGCCA

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
CCCTTACTGTTGAAGCCAGCACCTCCTTTGAAGTACCAGCACCATAACCAATAGATGTACATCAAGACTGAAGAGTGGTGAAGACGATCTTCTAAAATGTCATGCCCTTGACGTAAGTCTTACAGTGAA

2565

HNRNPA1

HNRNPA1-202

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

HNRNPA1-202

TAAGTCCAAGTCATACTTAAACTTGAACCTTTTTCTTACAGGTGGCTTTGGTGGCAGCCGTTGGTGGTGGATATGGTGGCAGTGGGGATGGCTATAATGGATTTGGTAAATGATGGTAAATTTTTAGGAATA
ATTACAGGTTGAGTATGAATTTTGAACCTTTGAAAAAGAAATGTCACCGAAACACCGTGGGACCCACCCACCTATACCACCGTACCCTTACCGATATTACCTAAACCTTACTACCATTTCAAAAAATCCTTAT

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

AGTAGAAAAAATTCCTGGCAACCTGGATCTTTAGAATAGGTTAGTAGAGACTAAAATTCGGTGCATGTCAAACCTCAACTTTGCCATAACACGCATGCTGTGAGCAGGCCTTACGCCGTTACACTTGACAAG
TCATCTCTTTTAAAGGACCGTTGGACCTAGAAATCTTATCCAATCATCTCTGATTTTAAAGACCAGTACAGTTTGAAGTGAAGCGGGTATTGTGCGTACGACACTCGTCCGGAAGTCGGCAATGTGAAGTGTTC

2835

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TTTTATTGTCAAACTTTTTGTCTTATTGAGAAGAAATGATTCTTGTAGGTGGTTATGGAGGAGGGCCCTGGTTACTCTGGAGGAAGCAGAGGCTATGGAAGTGGTGGACAGGGTTATGGAACCAAGGGCA
AAAAGTAAACAGTTTATGAAACAGAAATAACTCTTCTTAACATAAAGAACATCCACCAATACCTCTCGCGGGACCAATGAGACCTCTCTGCTCCGATACCTTACCACCTGTCCCAATACCTTTGGTCCCGT

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

GTGGCTATGGCGGAGTGGCAGCTATGACAGCTATAACAACGGAGGCGGAGCGGCTTTGGCGGTGGTAGTGGTAGGTTCCAGTGATCCAAGTACTTGGTGTGACAGCTAGCTTTAGCCTTTTAGAGCTTTGGGTT
CACCGATACCGCCCTCACCGTCGATACTGTCGATATTGTTGCCCTCCGCTCCGCGAAACCGCCACCATCACCATCCATAGGTCACTAGGTTTCATGAACCACACTGTCGATCTAATCGGAAAACTCTGAACCCAA

3105

HNRNPA1

HNRNPA1-202

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

HNRNPA1-202

CTGGTCTGTTGAAGCATTGTGGGTACACTGCATGGTATATTAACAAACAATGGGCTTGGCTACCTCCTCTAGCTTTAAGCTGGGGCCGCTCACTCCCAAAATAGTAGAGATAAGTGGATAGTGTGTC
GACCACGACAACCTCGTAACACACCATGTGACGTACCATATAATTTTGTGTTACCCGAACGATACGATGGAGGAGGATCGAAATTCGACCCCGCGGAGTGAGGGTTTATCATCTCTATTACACATACAAACAG

3240

HNRNPA1

HNRNPA1-202

HNRNPA1-202

PCR Forward
CTTTGGGACCTTAGGCGCTTAGTTG

TTTGGATTAGATTAGTATCATAGAAGGATTTAGTATTTTAACTCCTTTGGGACCTTAGGCGCTTAGTTGATGATCCAAGATACTTCTGCTTGTGTGGCCCTGGATCCGTTGAAGGCCCTCAAGGCTGAAGGGTA
AAACTCAATCTAATCATAGTATCTTCCATAAATGAGGAAACCTTGGAAATCCGCGAATCACTACATAGGTTCTATGAGACGACACACCAGGACCTAGGCACTCCGGAAGTCCGACTTCCCAT

3375

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TGCTTGTGCCACTCTGAAAATCTCTTTATTTATGTCATGGTGGTGGTAGGCCAGTTTTCTTTGATTACTGGATTATCCAAGTAAAGGCTTTCCAGAGAAATGAAATGCAAAAGATTGGAGTCCACATAGTTTGG
ACGAAACCGGTGAGACTTTAGAGAAAATAAATACAGTACCACTCAATCCGGTCAAAGAAACAT AATGACCTAATAAGTTGACTTACGGAAAGGGTCTCTTACTTTACGTTTCTAACCTCAGTGGTATCAAACC

3510

HNRNPA1

HNRNPA1-202

HNRNPA1-202

gRNA Protospacer

GTGGAAGC

GAGAAAGGAAGGCTGATAACTCAACCTTATTTTATCTGACTGCTAAACAGAAATTTGAAAACATAACATCCTCAGGTAACAGATAAAGGCCCTCTTTCCATTTCATAGGAAGCAATTTTGGAGGTGGTGGAAAGC
CTCTTTCCTCCGACTATTGAGTTGGAATAAAATAAGACTGACGATTTGCTTAACTTTGATTGTAGTAGGAGTCCATTGTCTATTTCCGGGAGAAAGGGTAAGTATCCTTCGTTAAAACCTCCACCACCTTCG

3645

HNRNPA1

HNRNPA1-202

305 310
G S N F G G G S
ENSE0001532273

HNRNPA1-202

Donor Template WT -> SNV

Protospacer Sequence

CTTCGTTAAAACCTCCACCCTTCG
Donor Template WT -> SNV

gRNA Protospacer
TACAATGATTTT

TACAATGATTTTGGGAATTACAACAATCAGTCTTCAAAATTTGGACCCATGAAGGGAGGAAATTTGGAGGCAGAAGCTCTGGCCCTATGGCGGTGGAGGCCAATACTTTGCAAAAACACGAAACCAAGGTATG
ATGTTACTAAAACCTTAATGTTGTTAGTCAGAAGTTTAAAACCTGGGTACTTCCCTCCTTTAAAACCTCCGTCCTCGAGACCGGGATACCGCCACCTCCGGTTATGAAACGTTTGGTGCCTTGGTTCCATAC

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 P M K G N F G G R S S G P Y G G G G Q Y F A K P R N Q
ENSE0001532273

HNRNPA1-202

Donor Template WT -> SNV

Protospacer Sequence
PAM
SNV

ATGTTAATAAACCTTAATGTTGTTAGTCAGAAGTTTAAAACCTGGGTACTTCCCTCCTTAAAACCTCCGTC
Donor Template WT -> SNV

GTTTTGGTGCCTTGGTTCCA
Sanger Sequencing Primer

GTATCTATGTAATTTTGGATAATGTCAAAAGAGTGTCTGTAGTACTGCTGGGAAGAAAGCCCTTTAACTGCTATGCTGGGCAGCAAAAAGCTTTATAGTTTAGAACCCTTCAGAAAGTGATAATTTGATCACAAA
CATAGATACATTAACCTTATTACAGTTTTCTCACAGACATCGATGACGACCTTCTTTGGGAAATTTGACGATACAGACCCGTCGTTTTGCAAAATCAAACTTTGGAAGTCTTTCACTATTAACCTAGTGT

3915

HNRNPA1

HNRNPA1-202

HNRNPA1-202

TTAGAAAATCATGGGACCTCTTACCACCTCCCTTGTAGTAGGGCCATTTTAAATGGCCAGACACTTGAATTTAACTTTTATATCCCAATATGAAAACATTACTGTTGGCACCTTGAACCTTTAAAAGAAA
AATCTTTTGTAGTACCCTGGAGAAATGGTGGAGGAAACATCATCCCGTAAAAATTTACCGGTCGTGAACTTAAATGAAAATATAGGGTTTATACTTTGTAATGACAACCGTGAACCTTTGAAATTTCTTT

4050

HNRNPA1

HNRNPA1-202

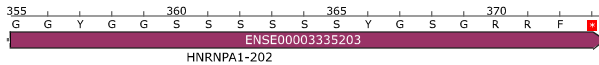
HNRNPA1-202

AATTGTA...TAA

4185

HNRNPA1

HNRNPA1-202



CCCTAAT...TAC

4320

HNRNPA1

HNRNPA1-202

GGGATTACATCGACTCGTCACGTTG PCR Reverse

TTTAGAT...CCG

4455

HNRNPA1

HNRNPA1-202

CTAGCTG...GTT

4590

HNRNPA1

HNRNPA1-202

CAAAGGG...TGA

4725

HNRNPA1

HNRNPA1-202

TGGTAA...CAA

4860

HNRNPA1

HNRNPA1-202

ACTGTT...ACC

4995

HNRNPA1

HNRNPA1-202

GAATGA...CAA

5130

HNRNPA1

HNRNPA1-202

GAATGCT...GTA

5265

HNRNPA1

HNRNPA1-202

TTTAAT...TTG

5400

HNRNPA1

HNRNPA1-202

TAAATTT...AAT

5535

HNRNPA1

HNRNPA1-202

TTTGAC...CTC

5670

HNRNPA1

HNRNPA1-202

GAGGAG...TAA

5805

HNRNPA1

HNRNPA1-202

CGTGACA...TTC

5940

HNRNPA1

HNRNPA1-202

CCAGGGGCGAGGCCACGGCACGCTCCATGAAAGCTAGGAGGGAGTGAATATCAGTGATCATCGCAAGGAAAGGAGGCAGACAAGAGTAAGGCACACCTGACTCTTAGGACTAGCAGTCAAGAACAGGAGGAAAGGT
GGTCCCCGTCCGGTCCCGTGCAGGACTTTTCGATCCTCCCTCACTTTATAGTCACTAGTAGCGTTCCTTCTCCGCTCTGTTCTCATTCCGTTGGACTGAGAATCCTGATCGTCAGTCTTGGTCCCTCTTCCA

6075

HNRNPA1

HNRNPA1-202

TTTATTGCTATGCGGGTAGGTAAGAACAGATTTTACTTACATCCATATAGTTACTTAAAGTCCAGTTTCTGTTAAACATTTTCTTAATATATTGAGCCAAAAGTCCAGTTAAGCTGAACTGGTTTTTCT
AAATAACGATACGCCCATCCATTCTTGTCTAAAAATGAATGTAGGTATATCAATGAATTTGAGTCAAAGACAATTTGTAAGAAAGAAATTATATAACTCGGTTTTGATCAGGTCAAATTCGACTTGAAACAAAAAGA

6210

HNRNPA1

HNRNPA1-202

GGAGATGAATTGTTTTAAATTGACACCCTATTGATGGCTCCCAGTTGAAGGAAGTGAGCACATTTTGTACTGTGAATATAAATTTTTGCCCTTTTATTTATCTTCCCTTGACCCATTTCTTTAAATAATGGC
CCTCTACTTAACAAAATTTAACTGTGGGATAACTACCGAGGGTCAACTTCCCTCACTCGTGAATAAACATGACACTTATATTTAAAAACGGGAAAATAAATAGAAGGAACTGGGTAAAGGAATTTATTACCG

6345

HNRNPA1

HNRNPA1-202

TCAAAGTAATAGACTTCCCCAAATGGTGGGGGGATGGGTGGGTATTAAATGGGAGGTATGGGGGGTTTAGCTTGAGATGGGACTTGGTCTTAGAGCTAGTCTTAAAGTTGTTTACTTTTCTAGGGAGGAGTCTG
AGTTTCATTATCTGAAGGGGTTTACCACCCCTACCCACCCAATAATTACCCTCCATACCCCCCAAATCGAAGTCTACCTGAAACAGAAATCTCGATCAAGATTTCCAACAAAATGAAAAGATCCCTCCTCAGAC

6480

HNRNPA1

HNRNPA1-202

CTACTAGTCTTATCAGCTCTTAAAAACAGAAACTCATCTGTCCAAGTTCGTGGCAGAAAGTAAAGTTTTTACAAAATAGTGCTCAGCAAAAAGAAATGCCCTGCGTTCCCAAAGTAAAAGAAATGACAAGCTGTACCT
GATGATCAGAAATAGTCGAGAAATTTTGTCTTTGAGTAGACAGGTTCAAGCACCGTCTTCCATTCAAAAATGTTTAAATCACGAGTCGTTTTCTTACGGGACGCAAGGGTTTCATTTTCTTACTGTTTCGACATGGA

6615

HNRNPA1

HNRNPA1-202

TAAACAAAACACTTCGTAATCTCATCCAATTGCAAAAAGAGTTATTAGCCAACCAGGTATTCACAGTAGTGACAGTGGATATAACTGTGTAGTCATTACCTCTGCTTATATGAATACTTTACAACCTCTTTTG
ATTTGGTTTTGTGAAGCATTAGAGTAGGTTAACGTTTTTCTCAATAATCGGTTGGTCCATAAGGGTCATCACTGTCACCTATATTGACACATCAGTAAGTGGAGACGAATATACTTATGAAATGTTGGAGAAAAC

6750

HNRNPA1

HNRNPA1-202

CCTTTTGCAAGAACGTCCTTGTGAAGACCTTTATCTGAGCCACTGTACTTCGTTATCACTGCCATGCAAGTTTACATGAGCTGTTCTGCAGCTCAAAATCCATTTTGTGAATGGGTTTTTTTTTAAATAAAGTGT
GGAAAACGTCCTTGCAGGAACACTTCTGAAAATAGACTCGGTGACATGAAGCAATAGTGACGGTACGTCAAATGTAAGTACTGACAAGACGTCGAGTTTAAAGGTAACAACTTACCCAAAAAAAATTTATTGACA

6885

HNRNPA1

HNRNPA1-202

ATTTAACTTAG 3'
6896
TAAATTGAATC 5'

HNRNPA1

HNRNPA1-202

Feature	Location	Size	Type
HNRNPA1	1 .. 6896	6896 bp	gene
/note	= gene ENSG00000135486 Protein coding		
HNRNPA1-203	1 .. 6895	6895 bp	prim_transcript
/note	= primary transcript ENST00000546500		
HNRNPA1-238	471 .. 5651	5181 bp	prim_transcript
/note	= primary transcript ENST00000677385		
HNRNPA1-231	471 .. 5650	5180 bp	prim_transcript
/note	= primary transcript ENST00000677210		
HNRNPA1-237	471 .. 5037	4567 bp	prim_transcript
/note	= primary transcript ENST00000677375		
HNRNPA1-234	499 .. 5553	5055 bp	prim_transcript
/note	= primary transcript ENST00000677249		
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/note	= primary transcript ENST00000676725 Retained intron		
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/note	= primary transcript ENST00000678418 Retained intron		
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/note	= primary transcript ENST00000550482		
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/note	= primary transcript ENST00000340913		
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/note	= primary transcript ENST00000679101		
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/note	= primary transcript ENST00000547566 Nonsense mediated decay		
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/note	= primary transcript ENST00000547708		
HNRNPA1-280	557 .. 5553	4997 bp	prim_transcript
/note	= primary transcript ENST00000679228 Retained intron		
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/note	= primary transcript ENST00000547870 Retained intron		
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/note	= primary transcript ENST00000551702		
HNRNPA1-257	583 .. 6540	5958 bp	prim_transcript
/note	= primary transcript ENST00000678365		
HNRNPA1-201	583 .. 4689	4107 bp	prim_transcript
/note	= primary transcript ENST00000330752		
HNRNPA1-221	583 .. 4125	3543 bp	prim_transcript
/note	= primary transcript ENST00000676794		
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/note	= primary transcript ENST00000547276		
HNRNPA1-272	588 .. 2108	1521 bp	prim_transcript
/note	= primary transcript ENST00000678919		
HNRNPA1-268	588 .. 1749	1162 bp	prim_transcript
/note	= primary transcript ENST00000678690		
HNRNPA1-232	616 .. 6895	6280 bp	prim_transcript
/note	= primary transcript ENST00000677220 Nonsense mediated decay		
HNRNPA1-201	616 .. 4121	3506 bp	CDS
▶ 9 segments = 924 bp			
/note	= coding sequence ENSP00000333504		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDELSRSHFEQWGTLTDCV,,VMRDPNTRKSRGFGFVYATVVEEVDAAMNARPHKVDGRVVEPKRAVSR,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFSGRI,,GDGYNGFGND,,GSNFGGGGSYNDFGYNNQSSNFGPMKGGNFGGRSSGPGYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF*		
HNRNPA1-202	616 .. 4121	3506 bp	CDS
▶ 10 segments = 1119 bp			
/note	= coding sequence ENSP00000341826		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDELSRSHFEQWGTLTDCV,,VMRDPNTRKSRGFGFVYATVVEEVDAAMNARPHKVDGRVVEPKRAVSR,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFSGRI,,GGFGGSRGGGGYGGSDGYNGFGND,,GGYGGGGPGYGGSRGYGSGGQGYGNQSSYGGSGSYDSYNNGGGGGFGGGS,,GSNFGGGGSYNDFGYNNQSSNFGPMKGGNFGGRSSGPGYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 372 amino acids = 38.7 kDa		
HNRNPA1-203	616 .. 4121	3506 bp	CDS
▶ 9 segments = 963 bp			
/note	= coding sequence ENSP00000448617		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDELSRSHFEQWGTLTDCV,,VMRDPNTRKSRGFGFVYATVVEEVDAAMNARPHKVDGRVVEPKRAVSR,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFSGRI,,GGFGGSRGGGGYGGSDGYNGFGND,,GSNFGGGGSYNDFGYNNQSSNFGPMKGGNFGGRSSGPGYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF*		

















Feature	Location	Size	Type
HNRNPA1-204	616 .. 4121	3506 bp	CDS
▶ 8 segments = 804 bp			
/note	= coding sequence ENSP00000447260		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGR,,GGFGSRGGGGYGGSDGYNGFGND,,GSNFGGGSYNDFGNYNQSSNFGPMKGGNFGGSGPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 267 amino acids = 29.4 kDa		
HNRNPA1-209	616 .. 4121	3506 bp	CDS
▶ 9 segments = 963 bp			
/note	= coding sequence ENSP00000446486		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGR,,GGFGSRGGGGYGGSDGYNGFGND,,GSNFGGGSYNDFGNYNQSSNFGPMKGGNFGGSGPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 346 amino acids = 39.5 kDa		
HNRNPA1-231	616 .. 4121	3506 bp	CDS
▶ 10 segments = 1119 bp			
/note	= coding sequence ENSP00000503610		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGR,,GGFGSRGGGGYGGSDGYNGFGND,,GGYGGGGPYGGSRGYGGGGQYGNQSSGYGGSSYDSYNNGGGFGGGGS,,GSNFGGGSYNDFGNYNQSSNFGPMKGGNFGGSRSSPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 372 amino acids = 38.7 kDa		
HNRNPA1-234	616 .. 4121	3506 bp	CDS
▶ 9 segments = 960 bp			
/note	= coding sequence ENSP00000503649		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGR,,RGFGSRGGGGYGGSDGYNGFGND,,GSNFGGGSYNDFGNYNQSSNFGPMKGGNFGGSGPYGGGQYFAKPRNQ,,GGYGGSSSSSYGSGRRF* 349 amino acids = 39.6 kDa		
HNRNPA1-237	616 .. 4121	3506 bp	CDS
▶ 9 segments = 981 bp			
/note	= coding sequence ENSP00000503651		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGR,,GGFGSRGGGGYGGSDGYNGFGND,,GSNFGGGSYNDFGNYNQSSNFGPMKGGNFGGSGPYGGGQYFAKPRNQ,,EKLYFSGGYGGSSSSSYGSGRRF* 349 amino acids = 39.6 kDa		
HNRNPA1-206	616 .. 3686	3071 bp	CDS
▶ 6 segments = 470 bp			
/note	= coding sequence ENSP00000448229		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFV,,GGFGSRGGGGYGGSDGYNGFGND,,GSNFGGGSYNDFGNYNQSSNFGPMKGGNFGGSGPYGGGQYFAKPRNQ,,EKLKLYFSGGYGGSSSSSYGSGRRF* 349 amino acids = 39.6 kDa		
HNRNPA1-238	616 .. 2526	1911 bp	CDS
▶ 6 segments = 729 bp			
/note	= coding sequence ENSP00000502985		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGRGMYLSTCSSDFSPSLL* 242 amino acids = 26.7 kDa		
HNRNPA1-213	616 .. 2294	1679 bp	CDS
▶ 4 segments = 436 bp			
/note	= coding sequence ENSP00000448117		
/translation	= MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGRGMYLSTCSSDFSPSLL* 242 amino acids = 26.7 kDa		
HNRNPA1-272	616 .. 2108	1493 bp	CDS
▶ 2 segments = 226 bp			
/note	= coding sequence ENSP00000504604		
/translation	= MSKSE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV 75 amino acids = 8.6 kDa		
HNRNPA1-268	616 .. 1749	1134 bp	CDS
▶ 2 segments = 162 bp			
/note	= coding sequence ENSP00000503229		
/translation	= MSKSE,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE 54 amino acids = 6.1 kDa		
HNRNPA1-250	680 .. 5047	4368 bp	prim_transcript
/note	= primary transcript ENST00000678077		
HNRNPA1-208	814 .. 2434	1621 bp	prim_transcript
/note	= primary transcript ENST00000548688		
HNRNPA1-208	831 .. 2434	1604 bp	CDS
▶ 6 segments = 694 bp			
/note	= coding sequence ENSP00000447782		
/translation	= MRD SLLVAKFLGTQDLCLFLNLAL,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGGFVYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYVKIEVIEIMTDRGSGKRRGFVFTDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSQR,,GRSGSGNFGGGRGGGFGGNDNFRGGNFGSGRGMYLSTCSSDFSPSLL* 231 amino acids = 25.7 kDa		
HNRNPA1-261	1603 .. 4125	2523 bp	prim_transcript
/note	= primary transcript ENST00000678448 Nonsense mediated decay		
HNRNPA1-282	1603 .. 4125	2523 bp	prim_transcript
/note	= primary transcript ENST00000679273 Nonsense mediated decay		
HNRNPA1-210	1603 .. 2294	692 bp	prim_transcript
/note	= primary transcript ENST00000550994 Nonsense mediated decay		
HNRNPA1-222	1603 .. 2294	692 bp	prim_transcript
/note	= primary transcript ENST00000676842 Nonsense mediated decay		

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

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

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

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

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

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	3285 .. 3309	61°C	Jun 14, 2022
/sequence = CTTGGGACCTTAGGCGCTTAGTTG 52% GC / 7695.0 Da				
✓ Donor Template WT -> SNV	100-mer	3620 .. 3719	73°C	Jun 14, 2022
/sequence = CTGCCTCCAAAATTCCTCCCTTCATGGGTCCAAAATTTGAAGACTGATTGTTGTAATTCCTCCAAAATTTGTAGCTTCCACCACCTCCAAAATTGCTTC 40% GC / 30,480.9 Da				
✓ gRNA Protospacer	20-mer	3638 .. 3657	50°C	Jun 14, 2022
/sequence = GTGGAAGCTACAATGATTTT 35% GC / 6171.1 Da				
✓ Sanger Sequencing Primer	20-mer	3758 .. 3777	56°C	Jun 14, 2022
/sequence = ACCTTGGTTTCGTGGTTTTG 45% GC / 6136.1 Da				
✓ PCR Reverse	25-mer	4186 .. 4210	63°C	Jun 14, 2022
/sequence = GTTGCACTGCTCAGCTACATTAGGG 52% GC / 7673.0 Da				