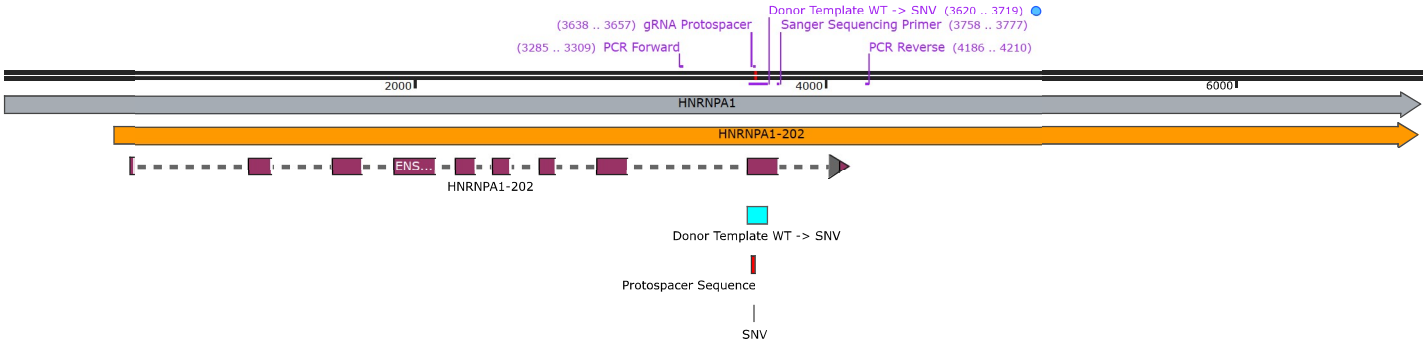

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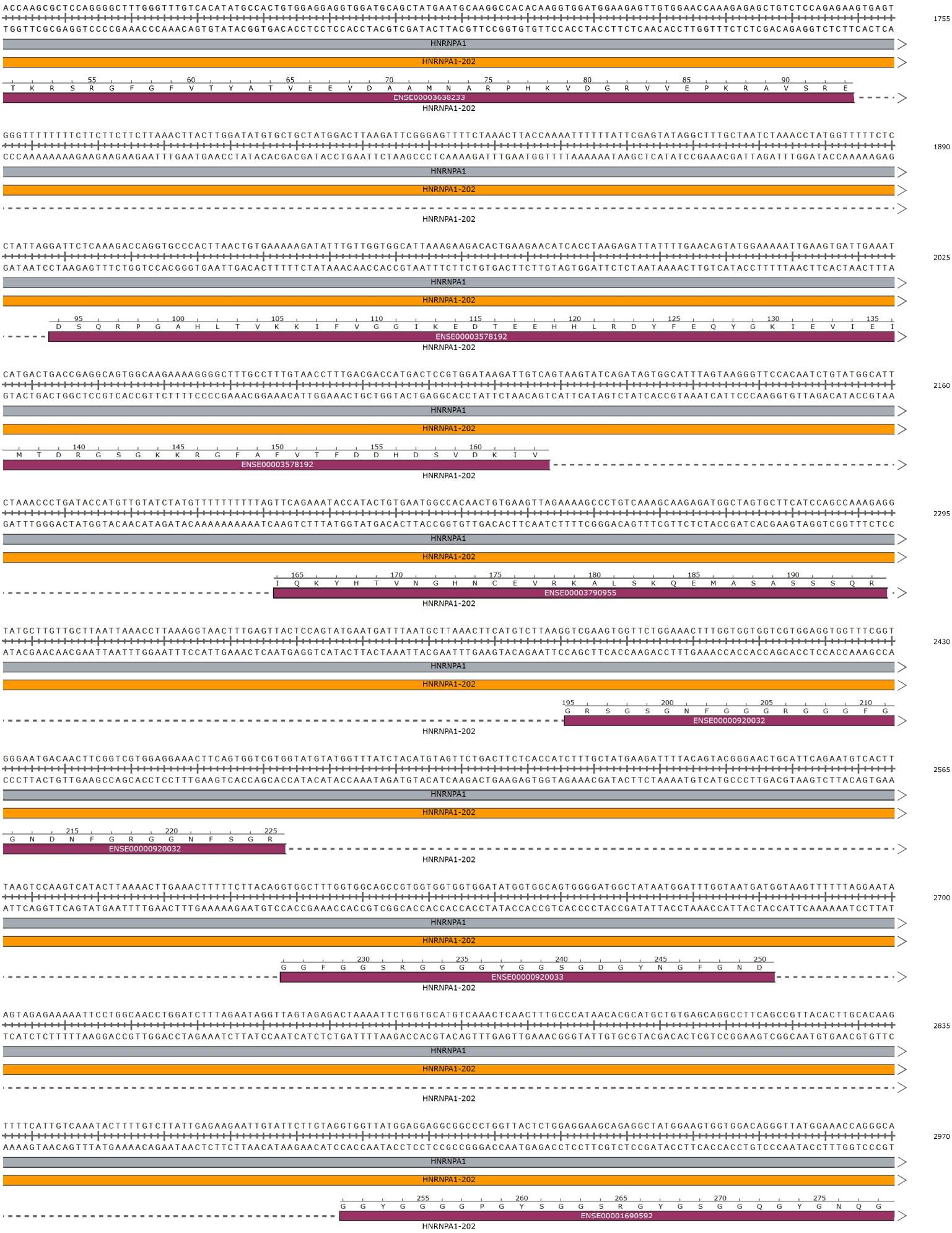
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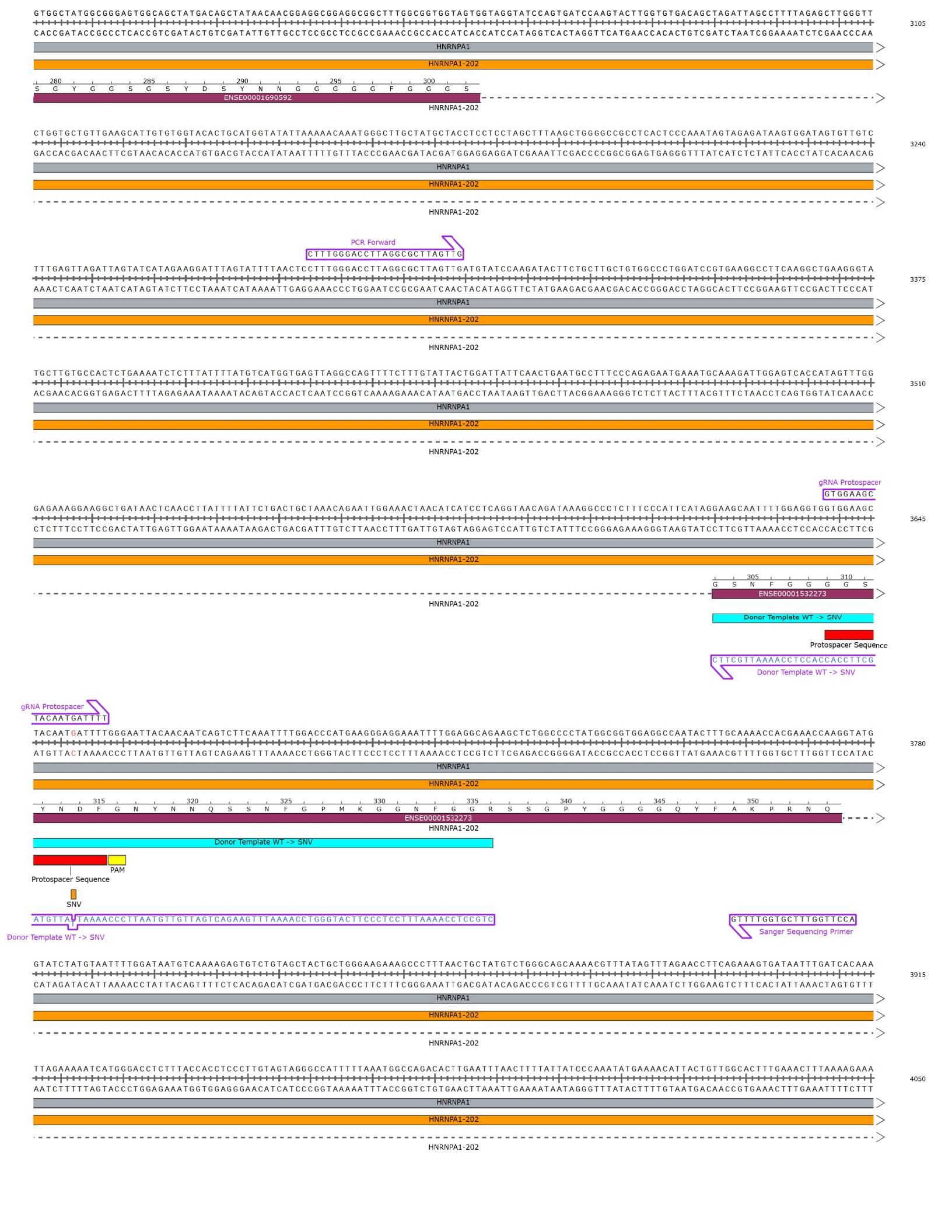
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HNRNPA1

HNRNPA1-202

GGAGATGAATTGTTTTAAATTGACACCCTATTGATGGCTCCCAGTTGAAGGAAGTGAGCACATTATTTGTACTGTGAATATAAATTTTTGCCCTTTTATTTATCTTCCTTTGACCCATTTCCTTAAAATAATGGC 6345
CCTCTACTTAACAAAATTTAACTGTGGGATAACTACCGAGGGTCAACTTCCTTCACTCGTGTAATAAACATGACACTTATATTTAAAAACGGGAAAATAAATAGAAGGAAACTGGGTAAAGGAATTTTATTACCG

HNRNPA1

HNRNPA1-202

TCAAAGTAATAGACTTCCCCAAATGGTGGGGGGATGGGTGGGTTATTAATGGGAGGTATGGGGGGTTTAGCTTGAGATGGGACTTGGTCTTAGAGCTAGTTCTAAAGGTTGTTTACTTTTCTAGGGAGGAGTCTG 6480
AGTTTCATTATCTGAAGGGGTTTACCACCCCCCTACCCACCCAATAATTACCCTCCATACCCCCCAAATCGAACTCTACCCTGAACCAGAATCTCGATCAAGATTTCCAACAAATGAAAAGATCCCTCCTCAGAC

HNRNPA1

HNRNPA1-202

CTACTAGTCTTATCAGCTCTTAAAAACAGAAACTCATCTGTCCAAGTTCGTGGCAGAAAGGTAAGTTTTTACAAATTAGTGCTCAGCAAAAGAATGCCCTGCGTTCCCAAAGTAAAAGAATGACAAGCTGTACCT 6615
GATGATCAGAATAGTCGAGAATTTTTGTCTTTGAGTAGACAGGTTCAAGCACCGTCTTTCCATTCAAAAATGTTTAATCACGAGTCGTTTTCTTACGGGACGCAAGGGTTTCATTTTCTTACTGTTCGACATGGA

HNRNPA1

HNRNPA1-202

TAAACCAAAACACTTCGTAATCTCATCCAATTGCAAAAAGAGTTATTAGCCAACCAGGTATTCCCAGTAGTGACAGTGGATATAACTGTGTAGTCATTCACCTCTGCTTATATGAATACTTTACAACCTCTTTTG 6750
ATTTGGTTTTGTGAAGCATTAGAGTAGGTTAACGTTTTTCTCAATAATCGGTTGGTCCATAAGGGTCATCACTGTCACCTATATTGACACATCAGTAAGTGGAGACGAATATACTTATGAAATGTTGGAGAAAAC

HNRNPA1

HNRNPA1-202

CCTTTTGCAGGAACGTCCTTGTGAAGACCTTTATCTGAGCCACTGTACTTCGTTATCACTGCCATGCAGTTTACATGAGCTGTTCTGCAGCTCAAATTCCATTTTGTGAATGGGTTTTTTTTTTTAATAAACTGT 6885
GGAAAACGTCCTTGCAGGAACACTTCTGGAAATAGACTCGGTGACATGAAGCAATAGTGACGGTACGTCAAATGTACTCGACAAGACGTCGAGTTTAAGGTAAAACACTTACCCAAAAAAAAAAATTATTTGACA

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			
HNRNPA1-220	506 .. 5046	4541 bp	prim_transcript
/note = primary transcript ENST00000676725 Retained intron			
HNRNPA1-259	506 .. 5045	4540 bp	prim_transcript
/note = primary transcript ENST00000678418 Retained intron			
HNRNPA1-209	512 .. 5650	5139 bp	prim_transcript
/note = primary transcript ENST00000550482			
✓ **HNRNPA1-202**	534 .. 6895	6362 bp	prim_transcript
/note = primary transcript ENST00000340913			
HNRNPA1-279	534 .. 1749	1216 bp	prim_transcript
/note = primary transcript ENST00000679101			
HNRNPA1-205	556 .. 6896	6341 bp	prim_transcript
/note = primary transcript ENST00000547566 Nonsense mediated decay			
HNRNPA1-206	556 .. 3686	3131 bp	prim_transcript
/note = primary transcript ENST00000547708			
HNRNPA1-280	557 .. 5553	4997 bp	prim_transcript
/note = primary transcript ENST00000679228 Retained intron			
HNRNPA1-207	564 .. 2414	1851 bp	prim_transcript
/note = primary transcript ENST00000547870 Retained intron			
HNRNPA1-213	571 .. 2294	1724 bp	prim_transcript
/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			
HNRNPA1-204	588 .. 5059	4472 bp	prim_transcript
/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,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGRGI,,GDGYNGFGND,,GSNFGGGGSYNDFGNYNNQSSNFGPMKGGNFGGRSSGPYG GGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF* 307 amino acids = 33.2 kDa			
✓ **HNRNPA1-202**	616 .. 4121	3506 bp	CDS
▸ 10 segments = 1119 bp			
/note = coding sequence ENSP00000341826			
/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFGGSRGGGGYGGSGDGYNGFGND,,GGYGGGGPGYSGGSRGYGSGGQGYGN QGSGYGGSGSYDSYNNGGGGGFGGGS,,GSNFGGGGSYNDFGNYNNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF* 372 amino acids = 38.7 kDa			
HNRNPA1-203	616 .. 4121	3506 bp	CDS
▸ 9 segments = 963 bp			
/note = coding sequence ENSP00000448617			
/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFGGSRGGGGYGGSGDGYNGFGND,,GSNFGGGGSYNDFGNYNNQSSNFGPM KGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF* 326 amino acids = 34.2 kDa			

Feature	Location	Size			Type
HNRNPA1-204	616 .. 4121	3506 bp	■	→	CDS

▸ 8 segments = 804 bp

/note = coding sequence ENSP00000447260

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG
SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNF,,GGGSYNDFGNYNNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF*
267 amino acids = 29.4 kDa

HNRNPA1-209	616 .. 4121	3506 bp	■	→	CDS

▸ 9 segments = 963 bp

/note = coding sequence ENSP00000446486

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG
SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFGGSRGGGGYGGSGDGYNGFGND,,GSNFGGGGSYNDFGNYNNQSSNFGPM
KGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF*
526 amino acids = 54.1 kDa

HNRNPA1-231	616 .. 4121	3506 bp	■	→	CDS

▸ 10 segments = 1119 bp

/note = coding sequence ENSP00000503610

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG
SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFGGSRGGGGYGGSGDGYNGFGND,,GGYGGGGPGYSGGSRGYGSGGQGYGN
QGSGYGGSGSYDSYNNGGGGGFGGGS,,GSNFGGGGSYNDFGNYNNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF*
372 amino acids = 38.7 kDa

HNRNPA1-234	616 .. 4121	3506 bp	■	→	CDS

▸ 9 segments = 960 bp

/note = coding sequence ENSP00000503649

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG
SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSG,,RGFGGSRGGGGYGGSGDGYNGFGND,,GSNFGGGGSYNDFGNYNNQSSNFGPMK
GGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF*
519 amino acids = 54.1 kDa

HNRNPA1-237	616 .. 4121	3506 bp	■	→	CDS

▸ 9 segments = 981 bp

/note = coding sequence ENSP00000503651

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG
SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFGGSRGGGGYGGSGDGYNGFGND,,GSNFGGGGSYNDFGNYNNQSSNFGPM
KGGNFGGRSSGPYGGGGQYFAKPRNQ,,EKLYFSGGYGGSSSSSSYGSGRRF*
526 amino acids = 55.0 kDa

HNRNPA1-206	616 .. 3686	3071 bp	■	→	CDS

▸ 6 segments = 470 bp

/note = coding sequence ENSP00000448229

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFV,,GGFGGSRGGGGYGGSGDGYNGFGND,,GSNF
GGGGSYNDFGNYNNQSSN
356 amino acids = 36.8 kDa

HNRNPA1-238	616 .. 2526	1911 bp	■	→	CDS

▸ 6 segments = 729 bp

/note = coding sequence ENSP00000502985

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRG
SGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGRGMYGLSTCSSDFSPSLL*
242 amino acids = 26.7 kDa

HNRNPA1-213	616 .. 2294	1679 bp	■	→	CDS

▸ 4 segments = 436 bp

/note = coding sequence ENSP00000448117

/translation = MSKSE,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASS
SQR
425 amino acids = 16.5 kDa

HNRNPA1-272	616 .. 2108	1493 bp	■	→	CDS

▸ 2 segments = 226 bp

/note = coding sequence ENSP00000504604

/translation = MSKSE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIV
75 amino acids = 8.6 kDa

HNRNPA1-268	616 .. 1749	1134 bp	■	→	CDS

▸ 2 segments = 162 bp

/note = coding sequence ENSP00000503229

/translation = MSKSE,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE
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 = MRDSLLVAKFLGTQDLCLFLNLAL,,SPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCV,,VMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLR
DYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQEMASASSSQR,,GRSGSGNFGGGRGGGFGG
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	Type
HNRNPA1-250	1606 .. 4121	2516 bp	CDS

▸ 7 segments = 828 bp

/note = coding sequence ENSP00000504814
/translation = MRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE,,DSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIV,,IQKYHTVNGHNCEVRKALSKQE
MASASSSQR,,GRSGSGNFGGGRGGGFGGNDNFGRGGNFSGR,,GGFGGSRGGGGYGGSGDGYNGFGND,,GSNFGGGGSYNDFGNYNNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSSSYGSGRRF
275 amino acids = 29.1 kDa

HNRNPA1-279	1606 .. 1749	144 bp	CDS

/note = coding sequence ENSP00000503166
/translation = MRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE
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,,VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVV
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 = VEVVLETLVVVVEVVSVGMTTSVVEETSVVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
78 codons (1 internal stop codon)

HNRNPA1-265	2381 .. 3775	1395 bp	CDS

▸ 2 segments = 180 bp

/note = coding sequence ENSP00000504089
/translation = VEVVLETLVVVVE,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
60 codons (1 internal stop codon)

HNRNPA1-269	2381 .. 3775	1395 bp	CDS

▸ 2 segments = 231 bp

/note = coding sequence ENSP00000503516
/translation = VEVVLETLVVVVEVVSVGMTTSVVEETSVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
77 codons (1 internal stop codon)

HNRNPA1-270	2381 .. 3775	1395 bp	CDS

▸ 2 segments = 249 bp

/note = coding sequence ENSP00000503756
/translation = VEVVLETLVVVVEVVSVGMTTSVVEETSVVV,,EAILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
83 codons (1 internal stop codon)

HNRNPA1-273	2381 .. 3775	1395 bp	CDS

▸ 2 segments = 210 bp

/note = coding sequence ENSP00000504850
/translation = VEVVLETLVVVVEVVSVGMTTSV,,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 = VEVVLETLVVVVEVVSVGMTTSVVEETSVVV,,VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVV
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*SYQLLKTETHLSKFVAER,,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,,VAMAVPAAAVAMAVAEDF
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 = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVV,,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 = VVMEEAALVTLEEAEAMEVVDRVMETRA,,VAMAVPAAAVAMAVAEDF
46 amino acids = 4.8 kDa

HNRNPA1-258	2887 .. 4121	1235 bp		→	CDS

▸ 2 segments = 212 bp

/note = coding sequence ENSP00000503562
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVV,,VAMAVPAAAVAMAVAEDF
70 amino acids = 7.1 kDa

HNRNPA1-275	2887 .. 4096	1210 bp		→	CDS

▸ 3 segments = 263 bp

/note = coding sequence ENSP00000503825
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVV,,GGNFGGRSSGPYGGGGQYFAKPRNQ,,GGYGGSSSSS
87 amino acids = 8.7 kDa

HNRNPA1-215	2887 .. 3775	889 bp		→	CDS

▸ 2 segments = 195 bp

/note = coding sequence ENSP00000503977
/translation = VVMEEAALVTLEEAEAME,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
65 codons (1 internal stop codon)

HNRNPA1-223	2887 .. 3775	889 bp		→	CDS

▸ 2 segments = 291 bp

/note = coding sequence ENSP00000503749
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVVV,,ATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
97 codons (1 internal stop codon)

HNRNPA1-227	2887 .. 3775	889 bp		→	CDS

▸ 2 segments = 312 bp

/note = coding sequence ENSP00000502981
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVVV,,AILEVVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
104 codons (1 internal stop codon)

HNRNPA1-260	2887 .. 3775	889 bp		→	CDS

▸ 2 segments = 288 bp

/note = coding sequence ENSP00000503030
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALA,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
96 codons (1 internal stop codon)

HNRNPA1-264	2887 .. 3775	889 bp		→	CDS

▸ 2 segments = 291 bp

/note = coding sequence ENSP00000504251
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
97 codons (1 internal stop codon)

HNRNPA1-266	2887 .. 3775	889 bp		→	CDS

▸ 2 segments = 297 bp

/note = coding sequence ENSP00000504004
/translation = VVMEEAALVTLEEAEAMEVVDRVMETRAVAMAGVAAMTAITTEAEAALAVVV,,VVEATMILGITTISLQILDP*REEILEAEALAPMAVEANTLQNHETK
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,,AEAALAVVV
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*SYQLLKTETHLSKFVAER,,NVLVKTFI*ATVLRYHCHAVYMSCSAAQIPFC 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,,GGYGGSSSSSSYGSGRRF* 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 = CTTTGGGACCTTAGGCGCTTAGTTG 52% GC / 7695.0 Da					
✓	**Donor Template WT -> SNV**	100-mer	3620 .. 3719	←	73°C	Jun 14, 2022
	/sequence = CTGCCTCCAAAATTTCCTCCCTTCATGGGTCCAAAATTTGAAGACTGATTGTTGTAATTCCCAAAATTATTGTAGCTTCCACCACCTCCAAAATTGCTTC 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					