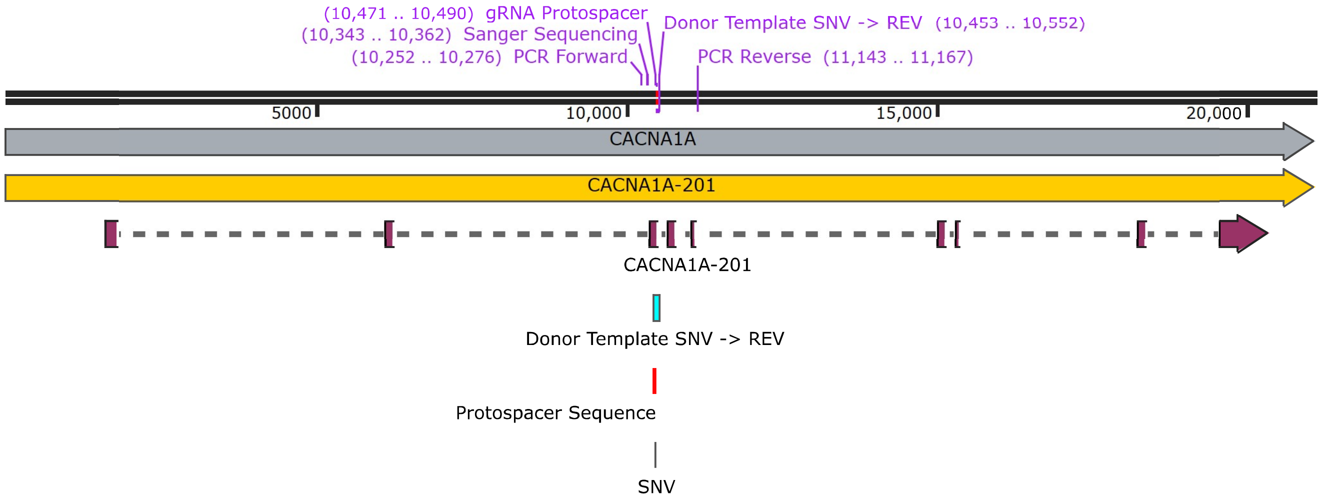

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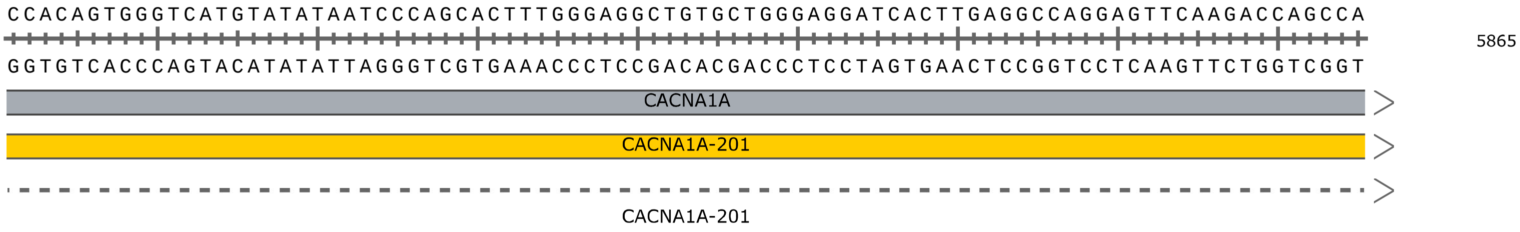
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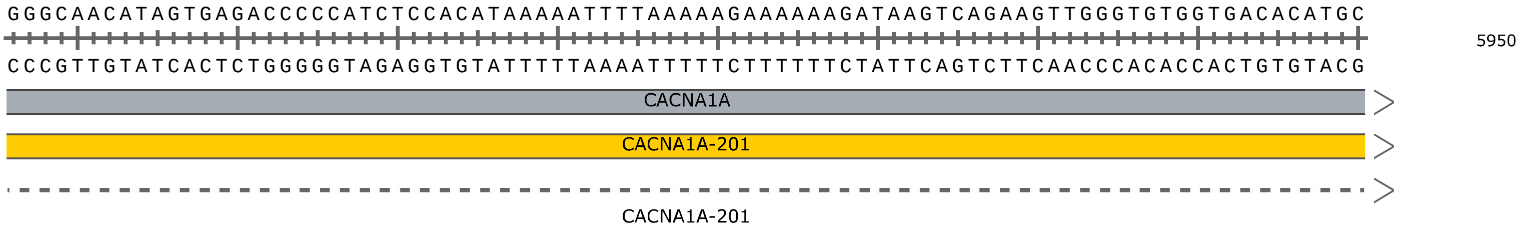
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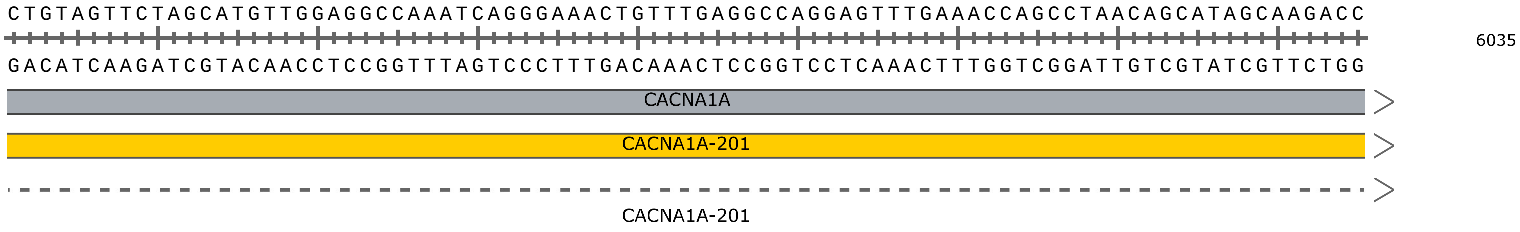
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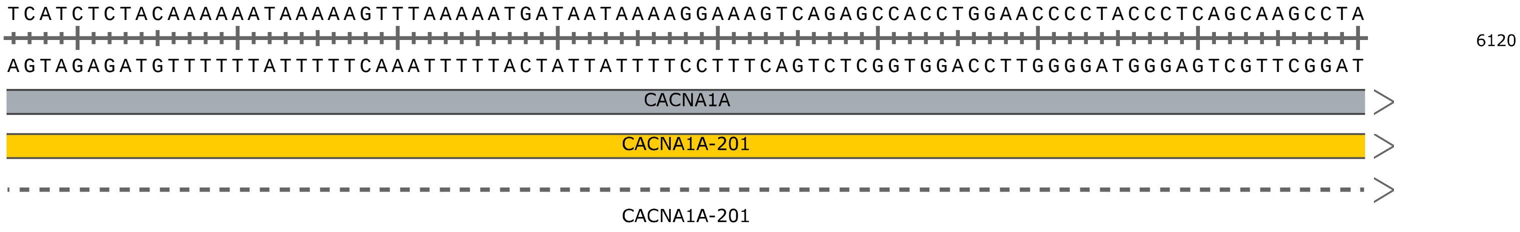
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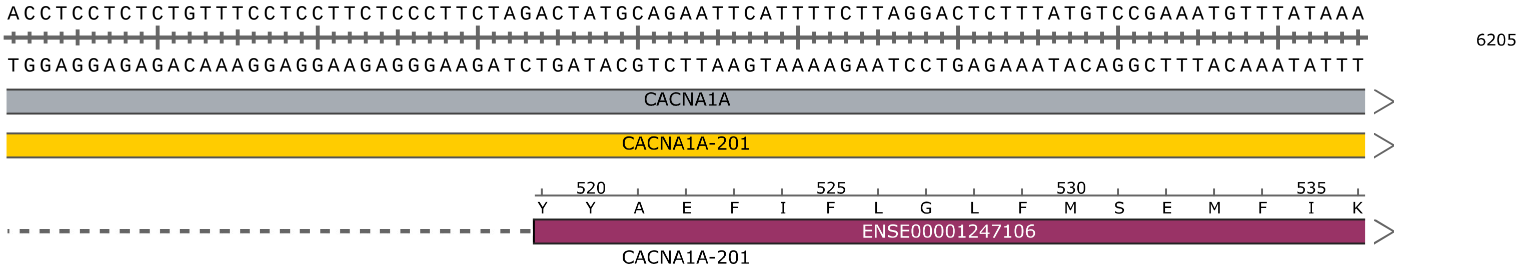
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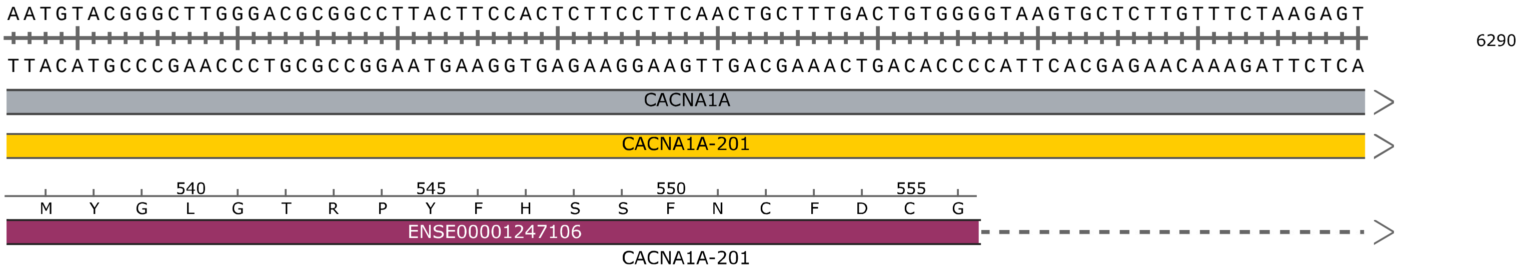
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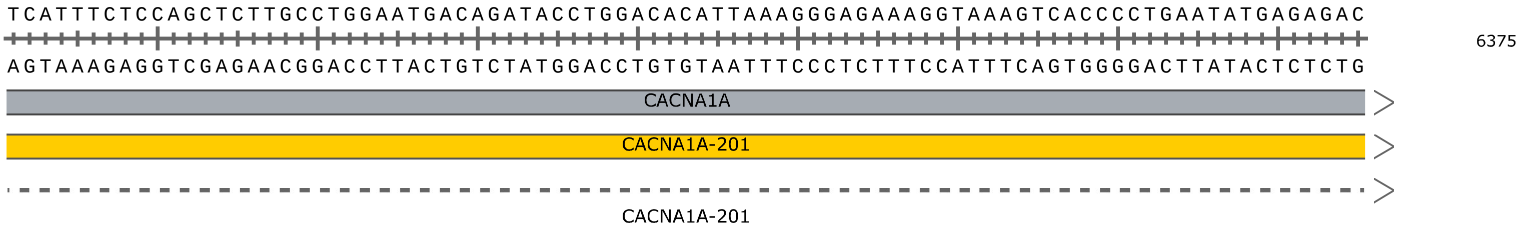
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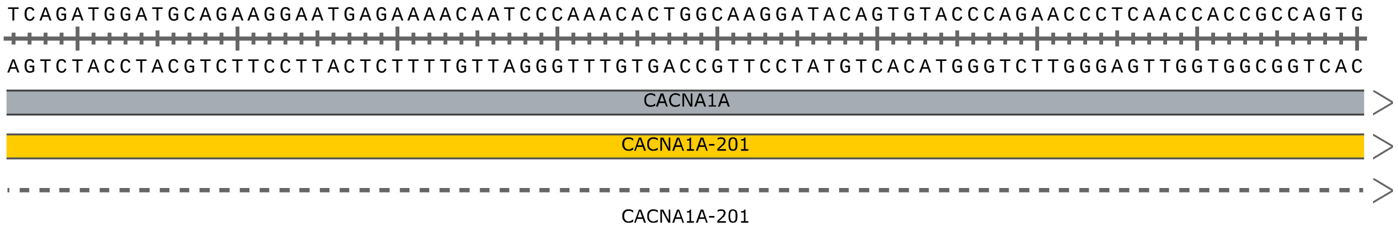

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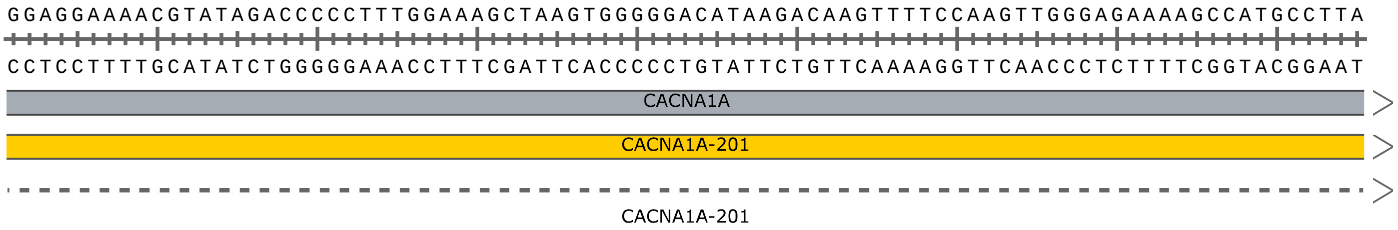

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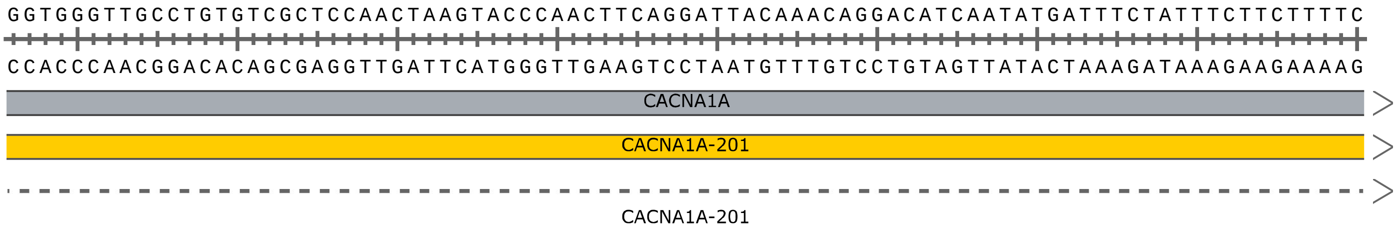

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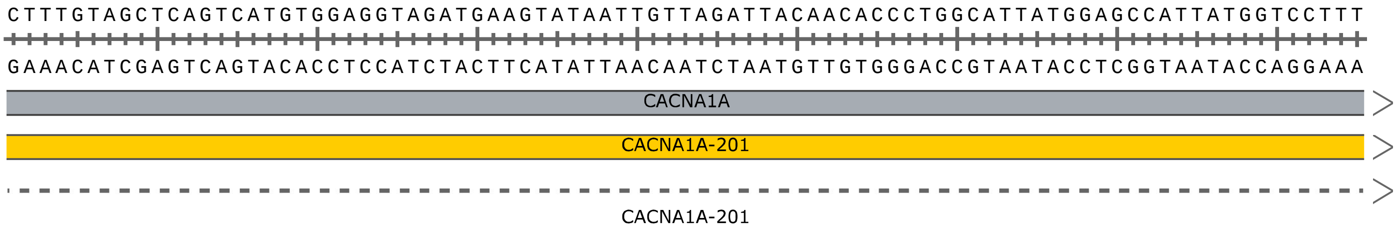

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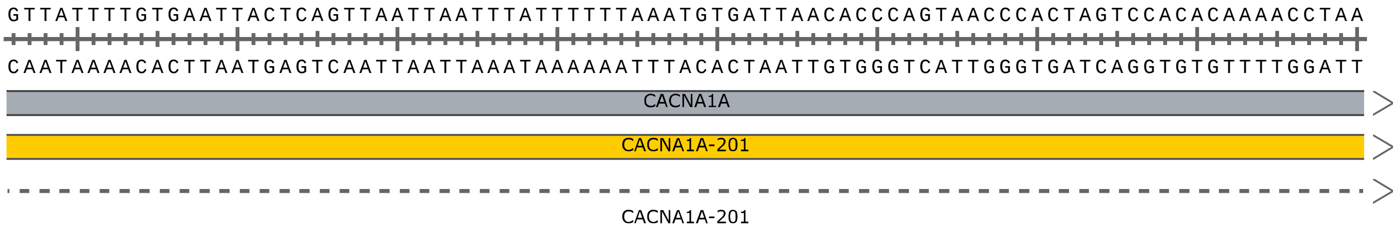

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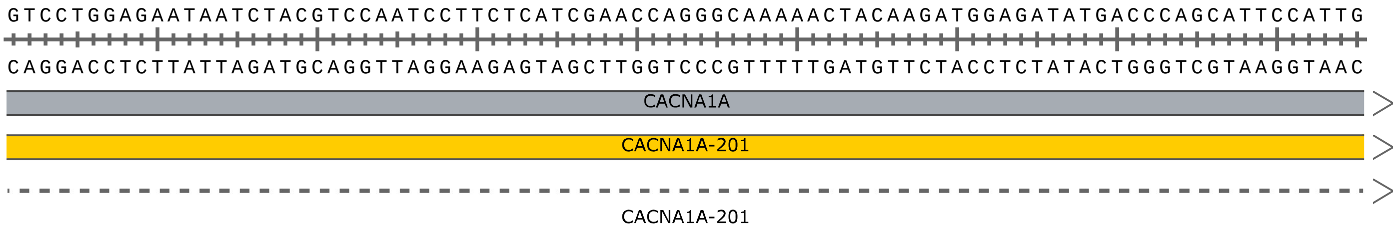

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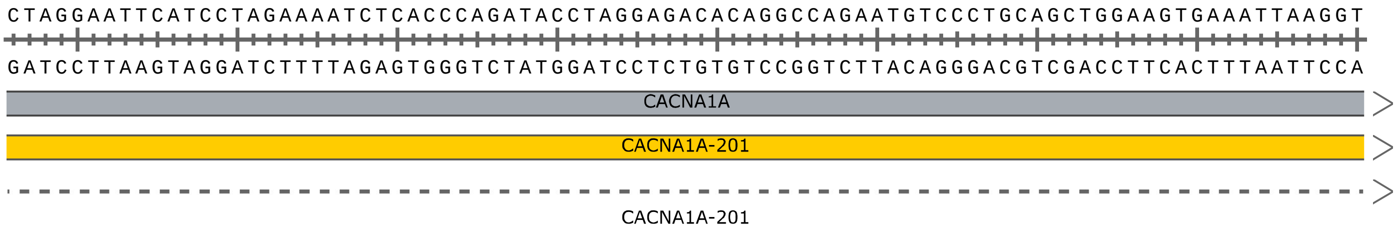

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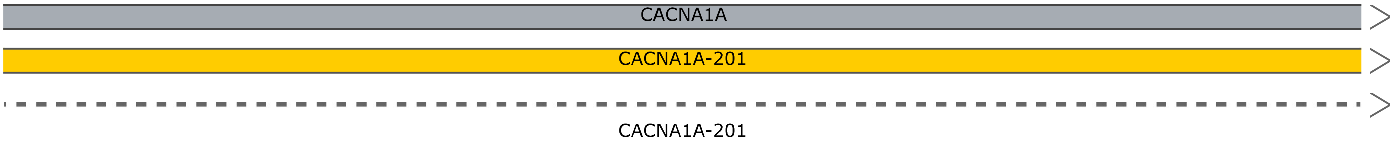

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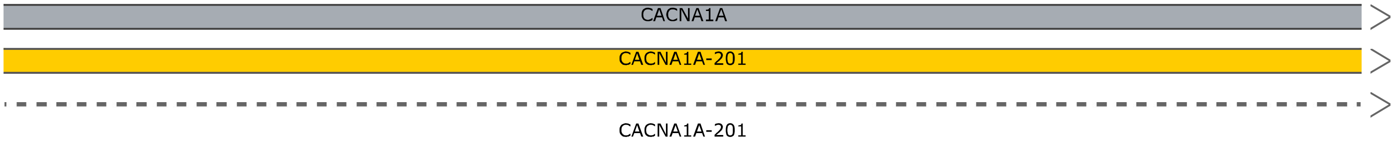

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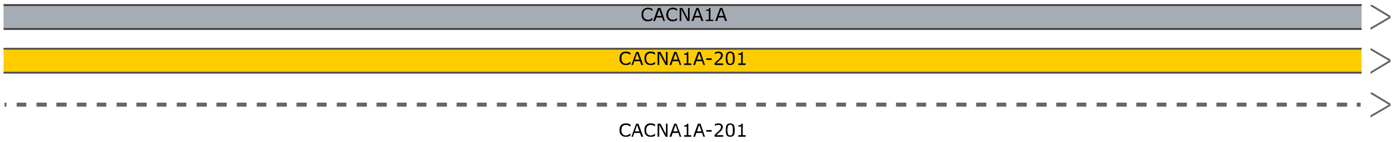

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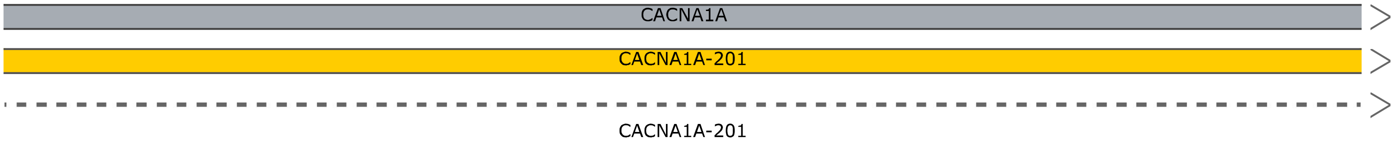

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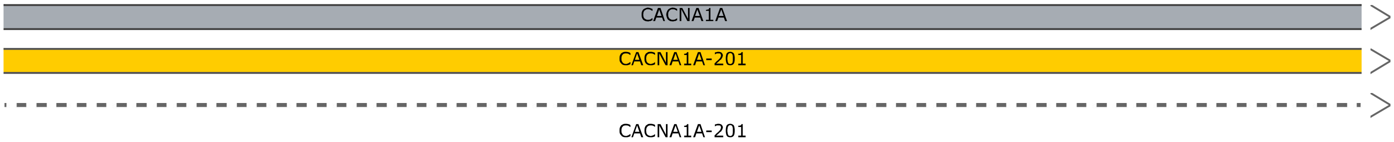

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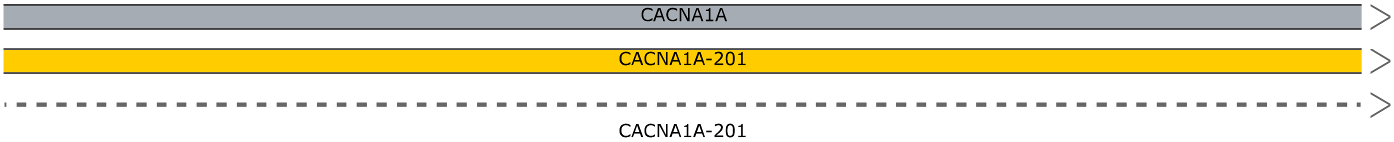

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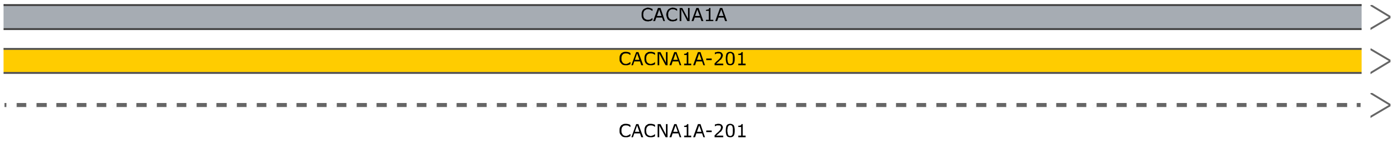

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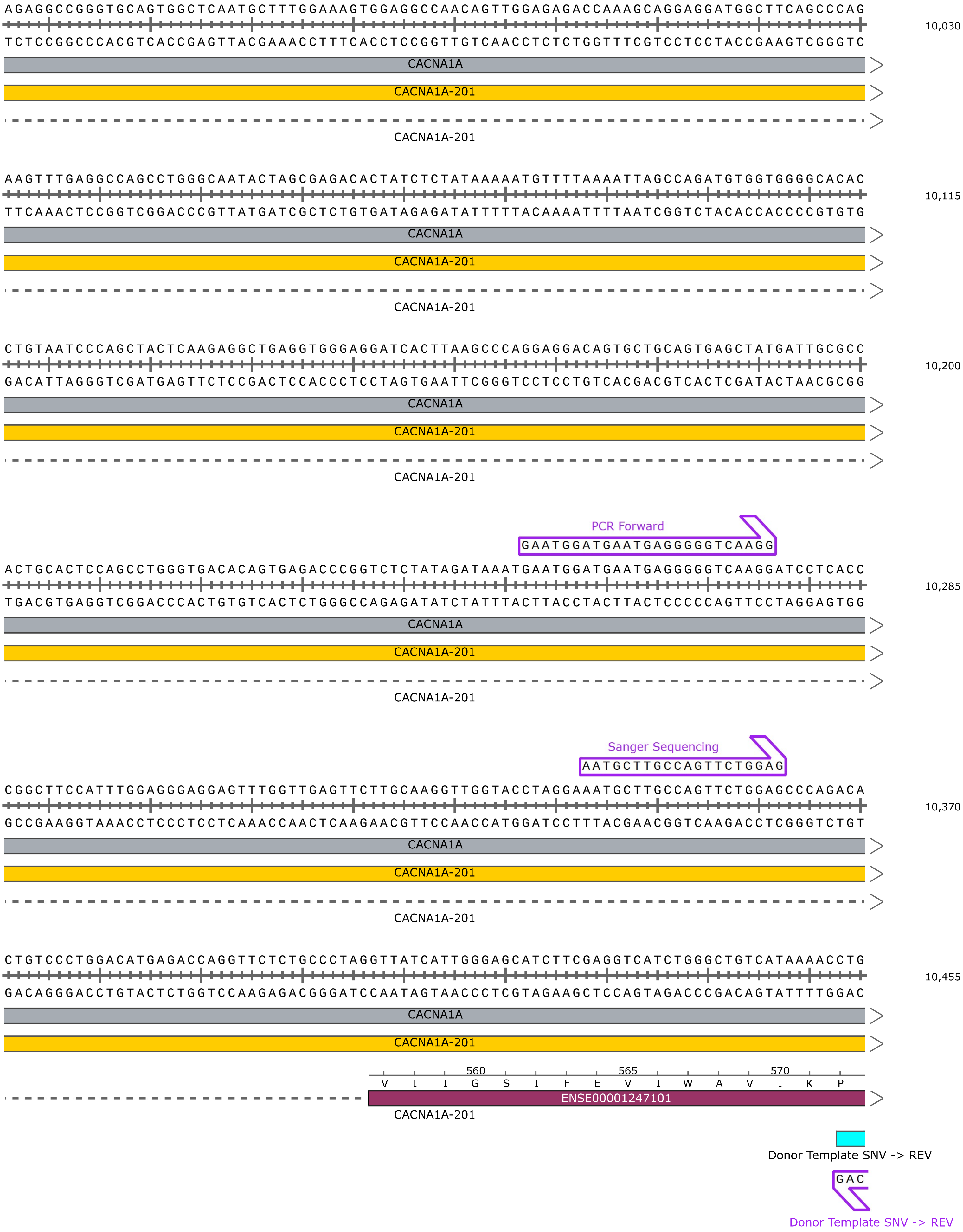
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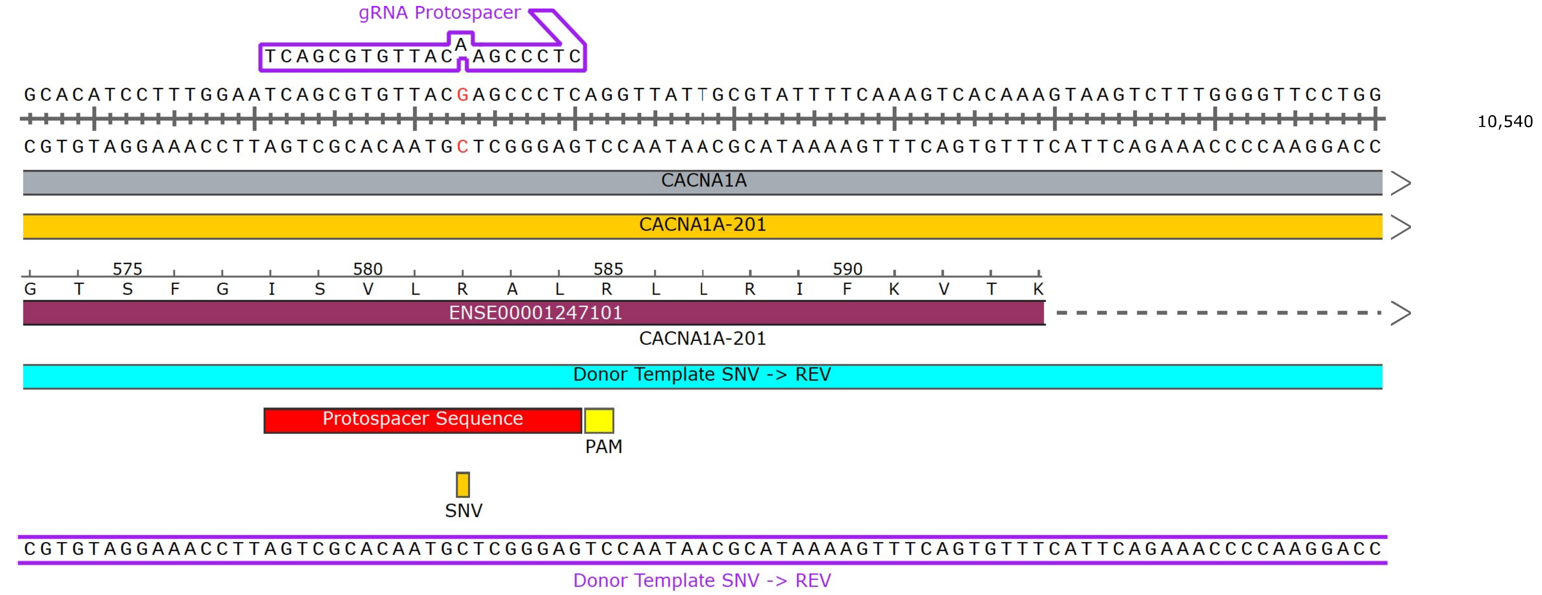
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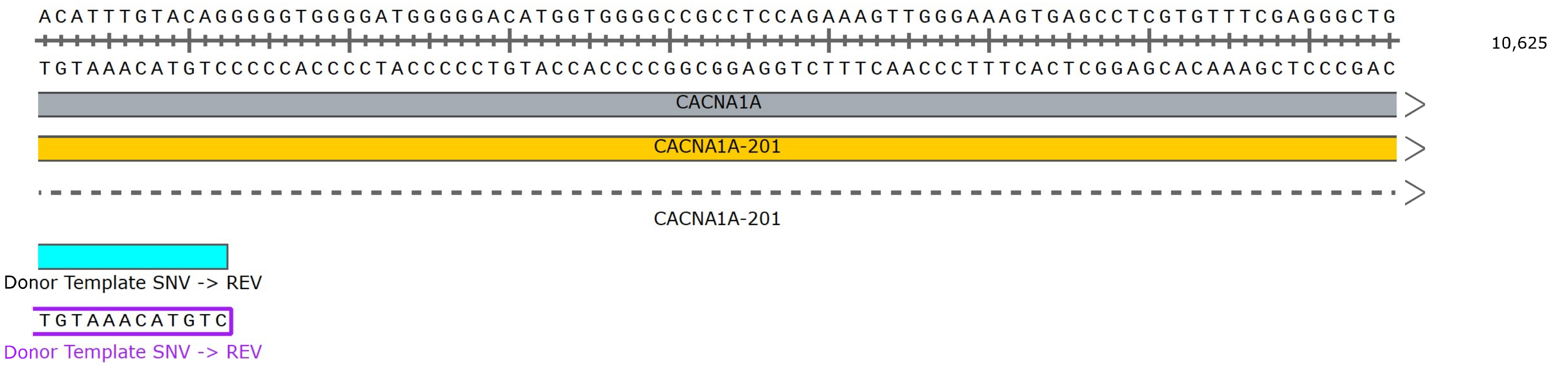
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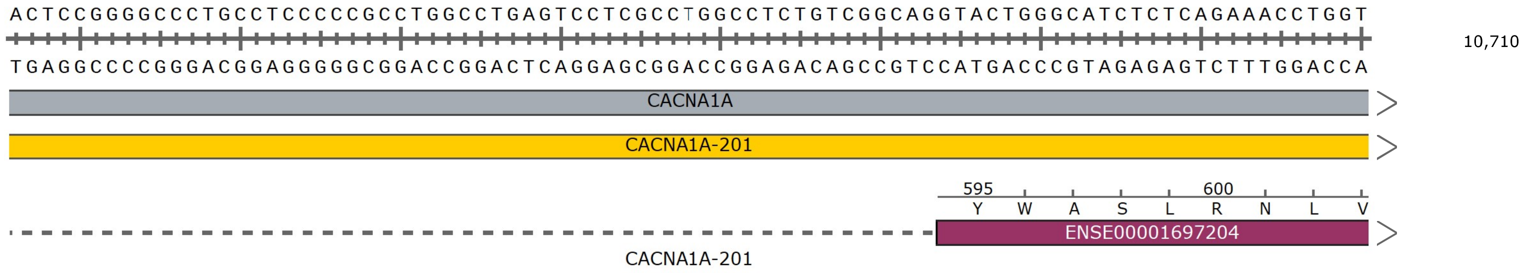
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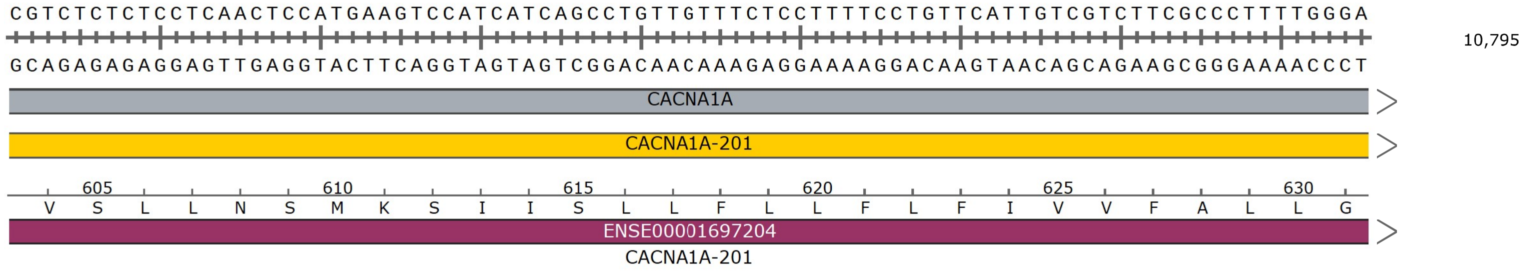
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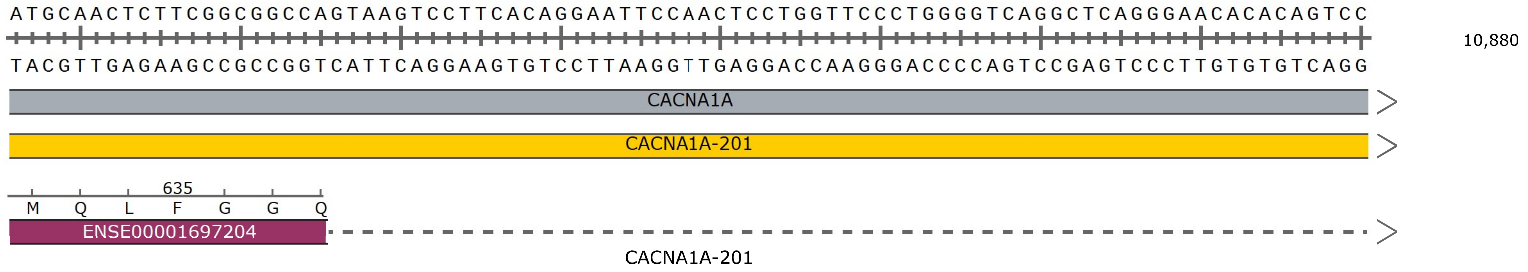
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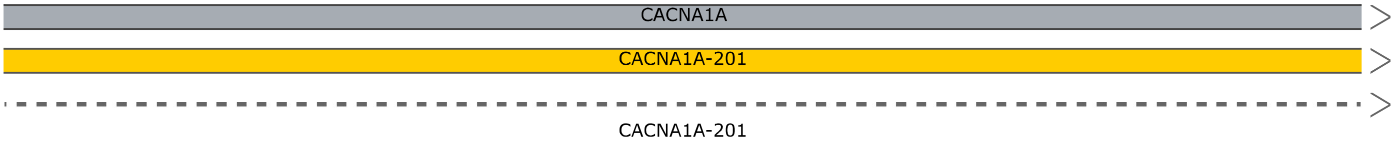

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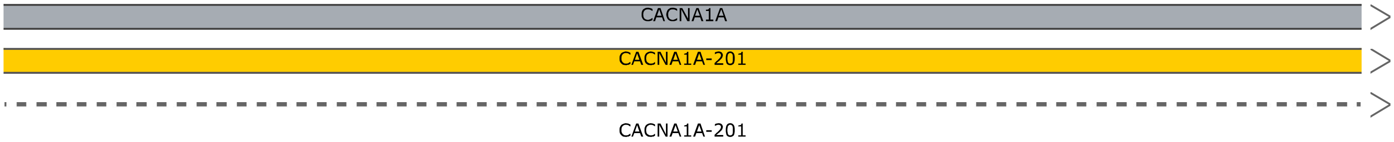

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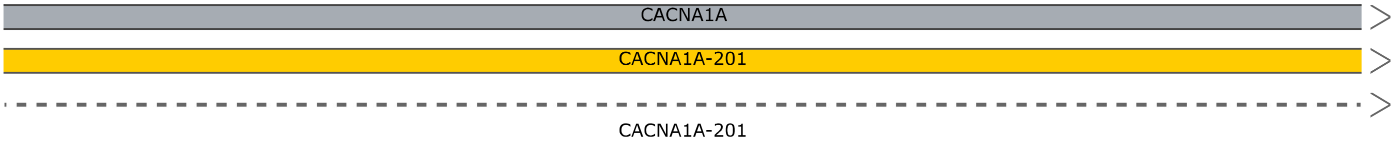

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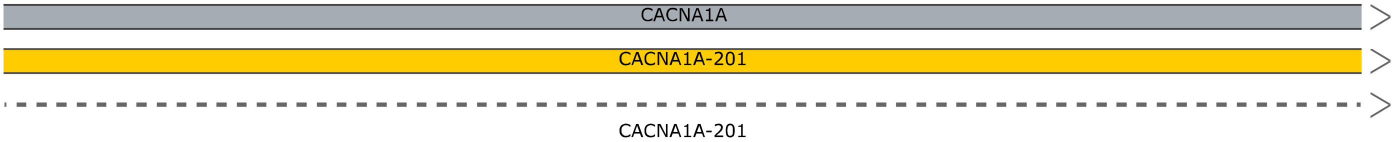

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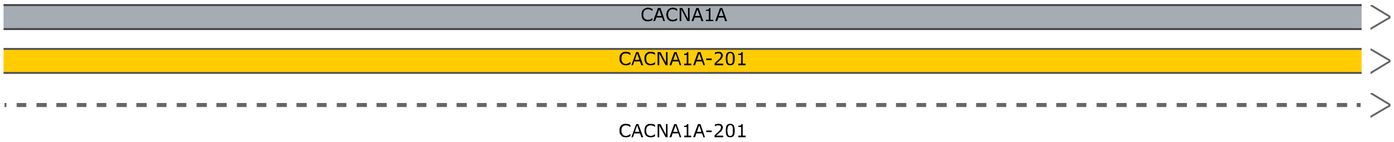

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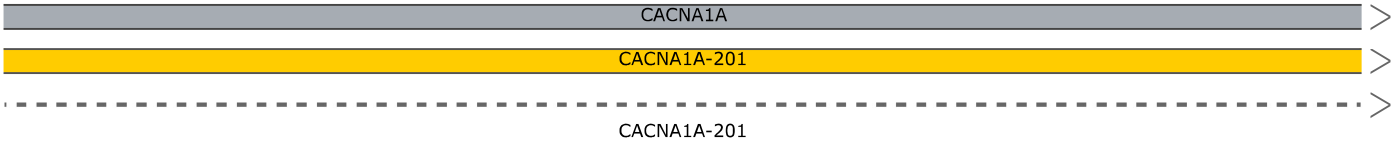

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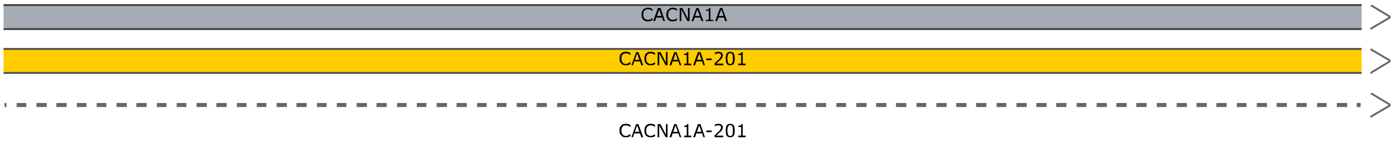

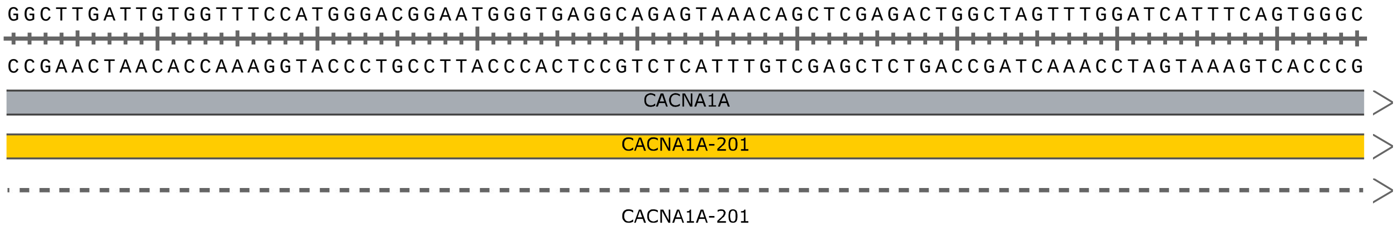

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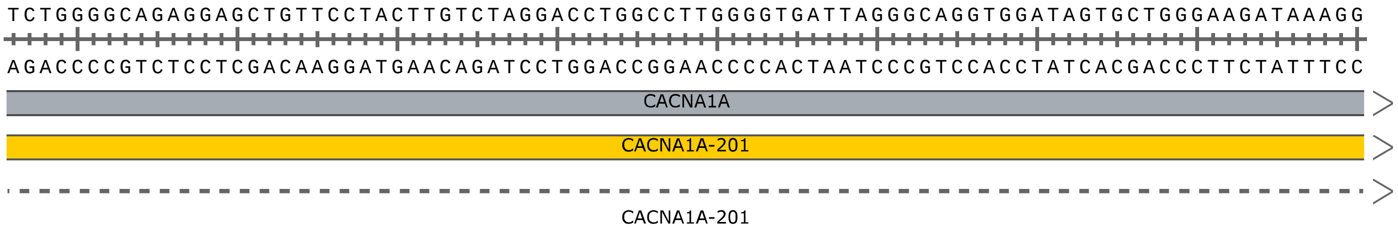

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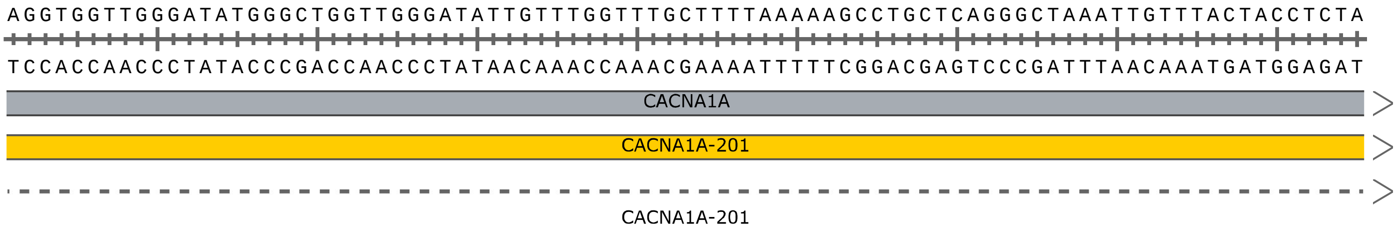

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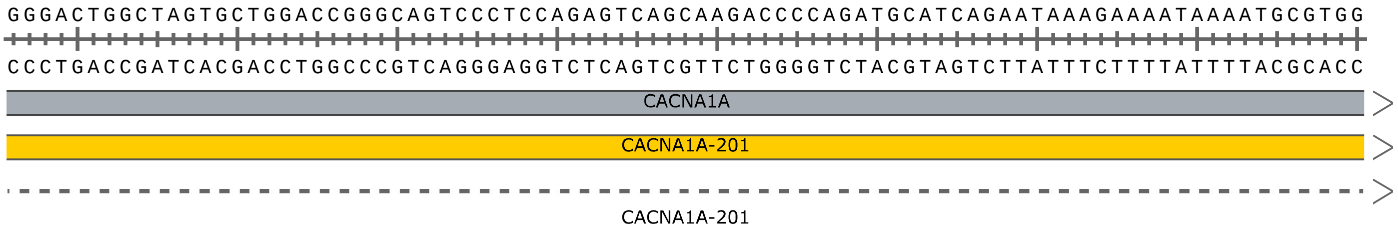

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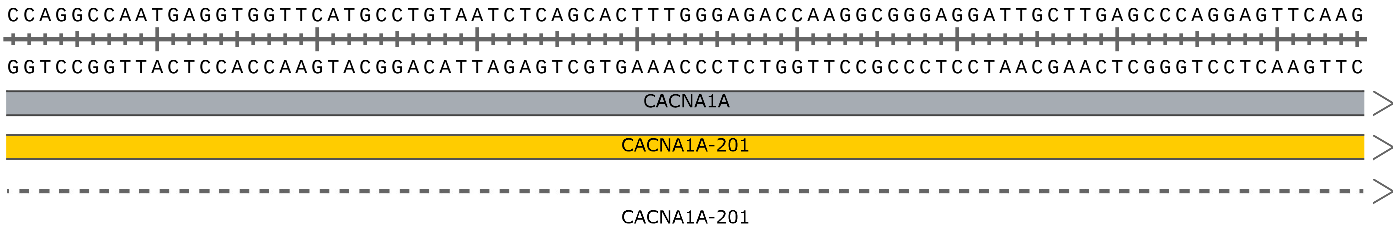

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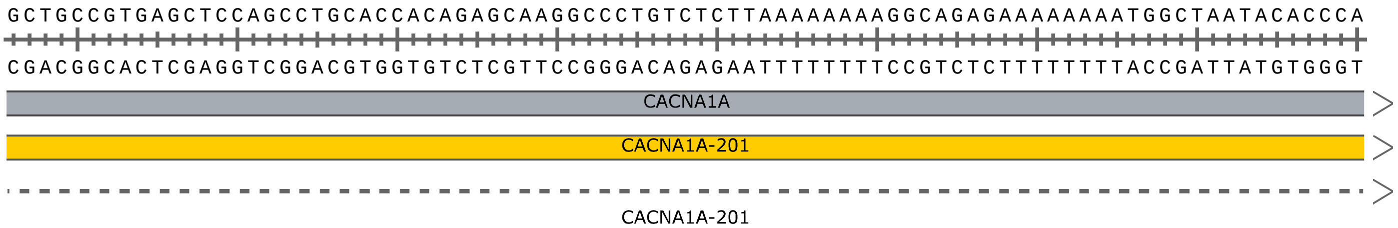

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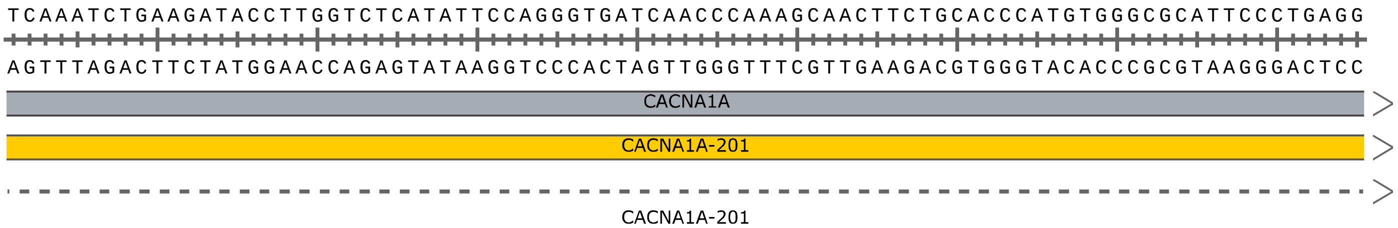

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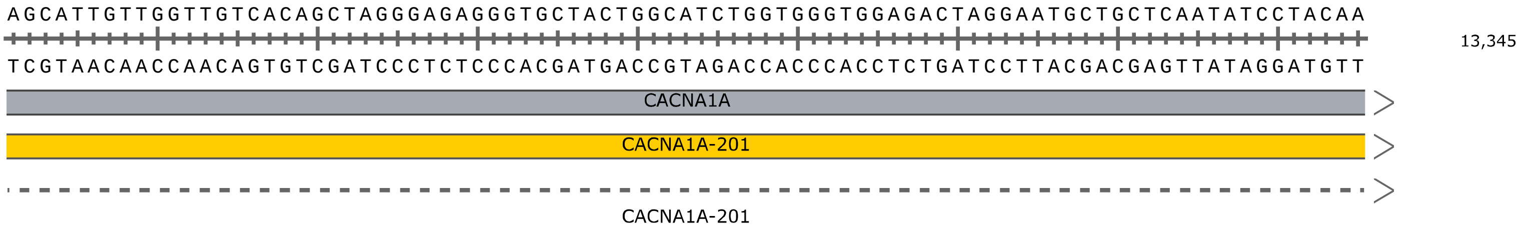
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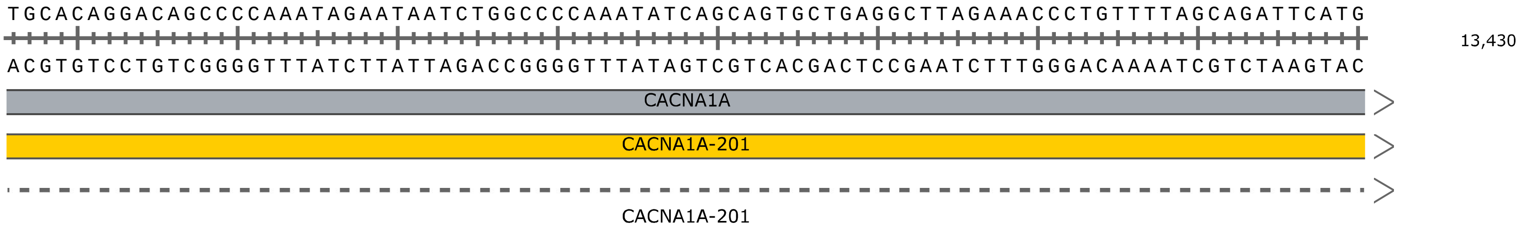
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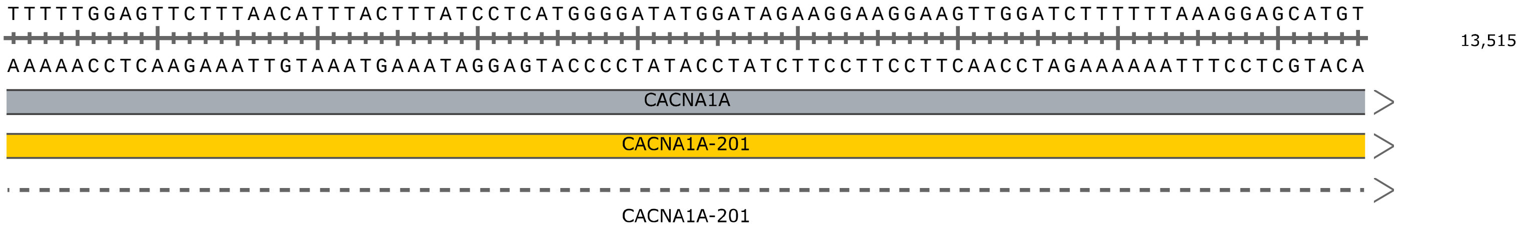
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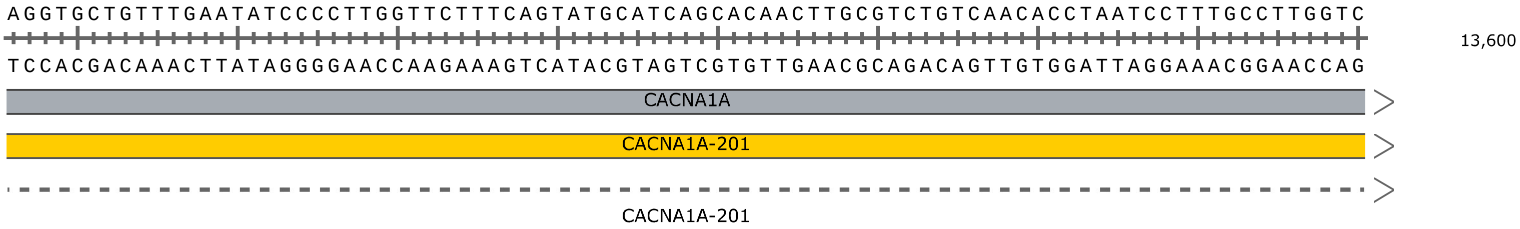
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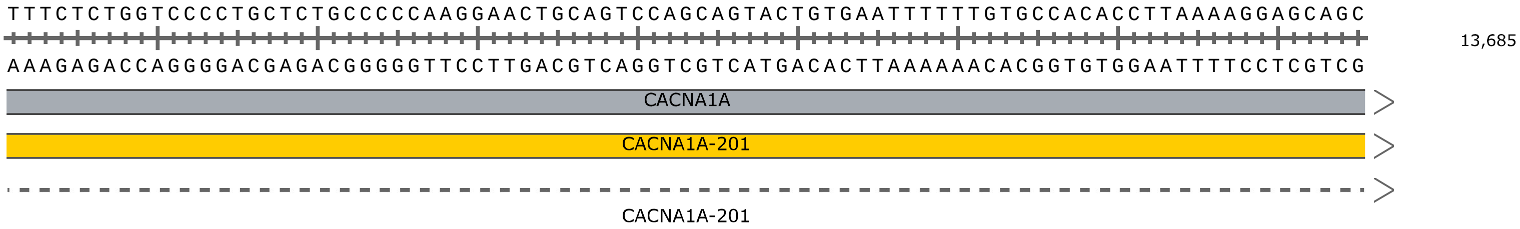
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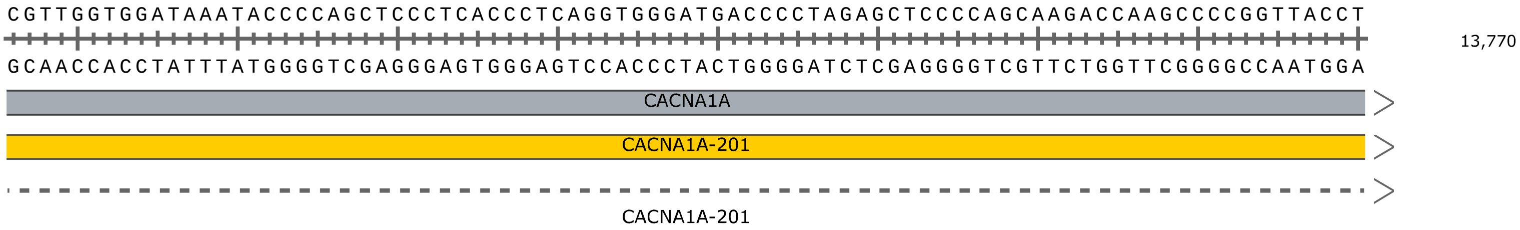
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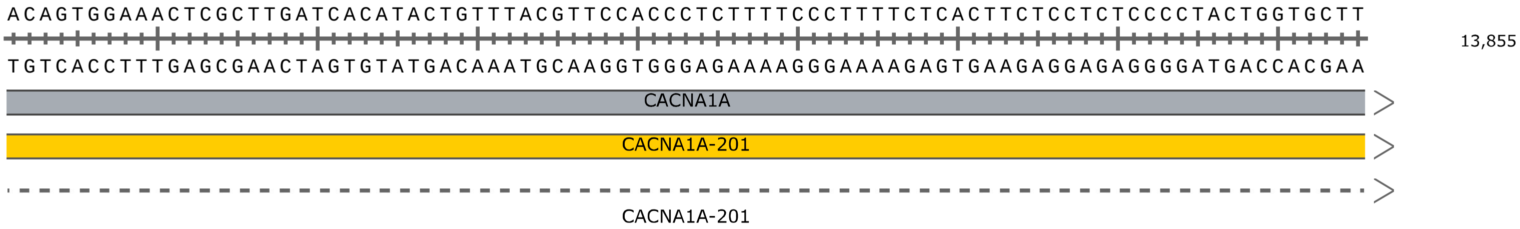
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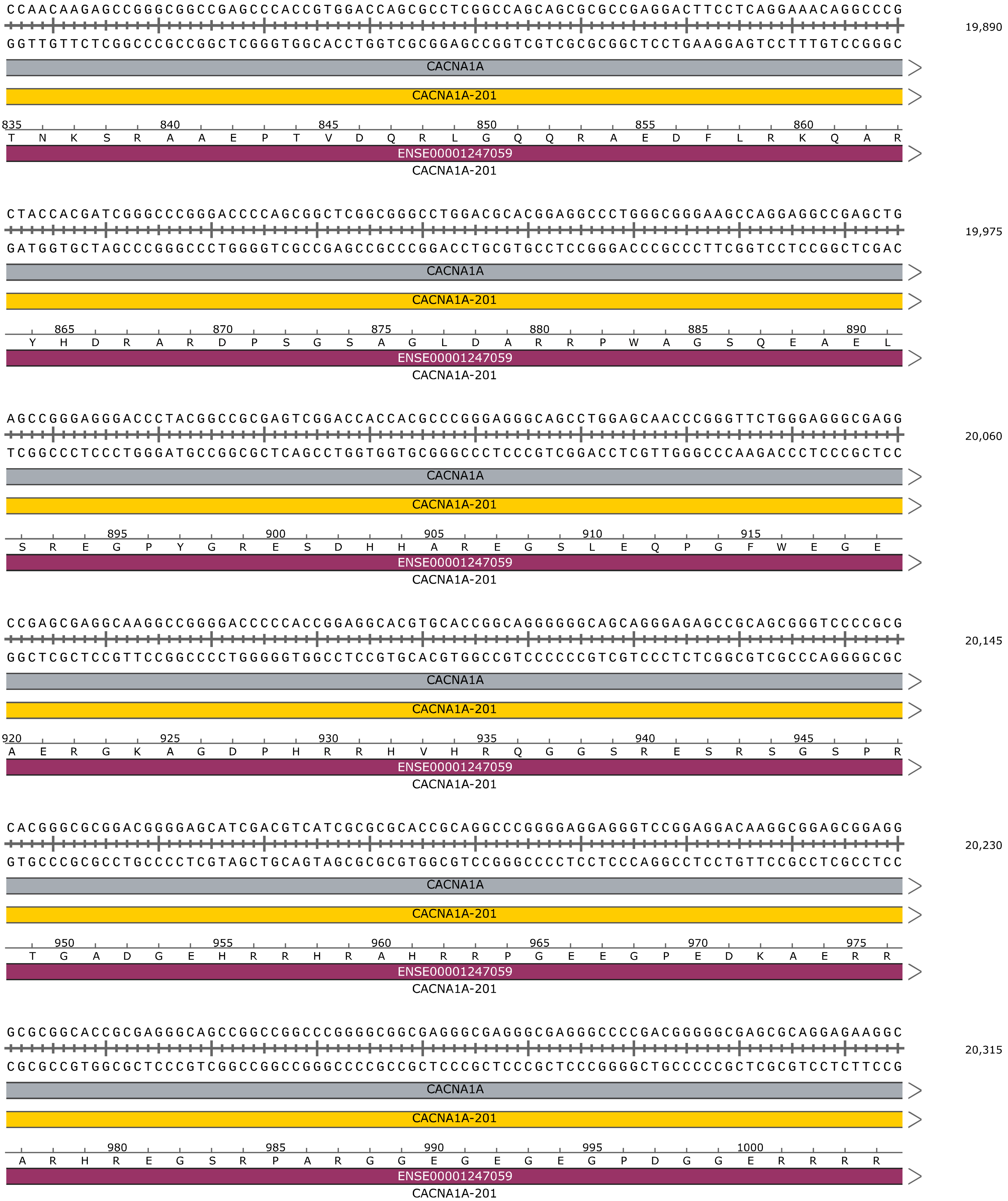

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CACNA1A-201

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CACNA1A-201

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CACNA1A

CACNA1A-201

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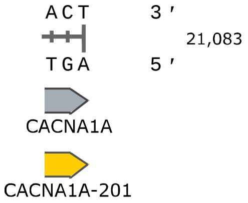
21,080

CACNA1A

CACNA1A-201


ACT
3′
21,083
TGA
5′
CACNA1A
CACNA1A-201

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   Feature                                              Location         Size        🟨   ⇄    Type
✓  CACNA1A                                             1  ..  21,083   21,083 bp    ■   →    gene

   /note          =  gene ENSG00000141837
                     Protein coding
✓  CACNA1A-201                                         1  ..  21,083   21,083 bp    🟨   →    prim_transcript

   /note          =  primary transcript ENST00000360228
   CACNA1A-202                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000573710
   CACNA1A-214                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000635727
   CACNA1A-217                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000635895
   CACNA1A-220                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000636012
   CACNA1A-224                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000636389
   CACNA1A-226                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000636549
   CACNA1A-237                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000637276
   CACNA1A-239                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000637432
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   /note          =  primary transcript ENST00000637736
   CACNA1A-246                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000637769
   CACNA1A-252                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000637927
   CACNA1A-256                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000638009
   CACNA1A-257                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000638029
   CACNA1A-259                                         1  ..  21,083   21,083 bp    ■   →    prim_transcript

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   CACNA1A-254                                         1  ..  12,371   12,371 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000637966
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   CACNA1A-232                                         1  ..  11,588   11,588 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000636974
                     Retained intron
   CACNA1A-221                                         1  ..    6283     6283 bp    ■   →    prim_transcript

   /note          =  primary transcript ENST00000636022
                     Retained intron
✓  CACNA1A-201                                      1614  ..  20,391   18,778 bp    🟥   →    CDS

   ▸ 9 segments  =  1744 bp

   /codon_start   =  1
   /note          =  coding sequence ENSP00000353362
   /translation   =  SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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                     FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
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                     VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
                     FWEGEAERGKAGDPHRRHVHRQGGSRESRSGPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
                     HGAPATYEGDARREDKERRHRRR
                     581 amino acids  =  66.4 kDa
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Feature Location Size Type

CACNA1A-202 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000460092
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-214 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000490001
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-217 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000490323
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVVFALLGMQLFGGQ,,FN
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-220 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000490223
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-224 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000489992
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-226 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000490578
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

Feature Location Size ⇄ Type

CACNA1A-237 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000489777
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-239 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1753 bp

/codon_start = 1
/note = coding sequence ENSP00000490617
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTKVEA,,DEQEE
EEAANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLD
RPLVVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLE
QPGFWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERR
RRHRHGAPATYEGDARREDKERRHRRR
584 amino acids = 66.7 kDa

CACNA1A-245 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000489861
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-246 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000489778
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-252 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

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/note = coding sequence ENSP00000489715
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

CACNA1A-256 1614 .. 20,391 18,778 bp ■ → CDS

9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000489913
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP
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FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEA
ANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL
VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPG
FWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR
HGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

	Feature	Location	Size	🟨	⇄	Type
	CACNA1A-257	1614 .. 20,391	18,778 bp	🟪	→	CDS

▸ 9 segments = 1753 bp

/codon_start = 1
/note = coding sequence ENSP00000489829
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVVFALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTKVEA,,DEQEEEEAANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHRHGAPATYEGDARREDKERRHRRR
584 amino acids = 66.7 kDa

	Feature	Location	Size	🟨	⇄	Type
	CACNA1A-259	1614 .. 20,391	18,778 bp	🟪	→	CDS

▸ 9 segments = 1744 bp

/codon_start = 1
/note = coding sequence ENSP00000499449
/translation = SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVVFALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEAANQKLALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDHHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGSRESRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHRHGAPATYEGDARREDKERRHRRR
581 amino acids = 66.4 kDa

	Feature	Location	Size	🟨	⇄	Type
	CACNA1A-243	1808 .. 3697	1890 bp	⬜	→	prim_transcript

/note = primary transcript ENST00000637625
Retained intron

	Feature	Location	Size	🟨	⇄	Type
	CACNA1A-235	10,104 .. 11,656	1553 bp	⬜	→	prim_transcript

/note = primary transcript ENST00000637117
Retained intron

	Feature	Location	Size	🟨	⇄	Type
✓	**Donor Template SNV -> REV**	10,453 .. 10,552	100 bp	🟦	↦	misc_feature
✓	**Protospacer Sequence**	10,471 .. 10,490	20 bp	🟥	↦	misc_feature
✓	**SNV**	10,483 .. 10,483	1 bp	🟨	↦	misc_feature

/note = REV = G
SNV = A

	Feature	Location	Size	🟨	⇄	Type
✓	**PAM**	10,491 .. 10,492	2 bp	🟨	↦	misc_feature

	Primer	Length	●	Binding Sites	⇄	Tm	Date Added
✓	**PCR Forward**	25-mer		10,252 .. 10,276	→	62°C	Jan 18, 2023
	/sequence = GAATGGATGAATGAGGGGGTCAAGG 52% GC / 7900.2 Da						
✓	**Sanger Sequencing**	20-mer		10,343 .. 10,362	→	58°C	Jan 18, 2023
	/sequence = AATGCTTGCCAGTTCTGGAG 50% GC / 6148.1 Da						
✓	**Donor Template SNV -> REV**	100-mer		10,453 .. 10,552	←	75°C	Jan 18, 2023
	/sequence = CTGTACAAATGTCCAGGAACCCCAAAGACTTACTTTGTGACTTTGAAAATACGCAATAACCTGAGGGCTCGTAACACGCTGATTCCAAA GGATGCTGCAG 45% GC / 30,611.1 Da						
✓	**gRNA Protospacer**	20-mer		10,471 .. 10,490	→	52°C	Jan 18, 2023
	/sequence = TCAGCGTGTTACAAGCCCTC 55% GC / 6053.0 Da						
✓	**PCR Reverse**	25-mer		11,143 .. 11,167	←	64°C	Jan 18, 2023
	/sequence = GGTGGAGGCTGTACCTGAAACACCG 60% GC / 7732.1 Da						