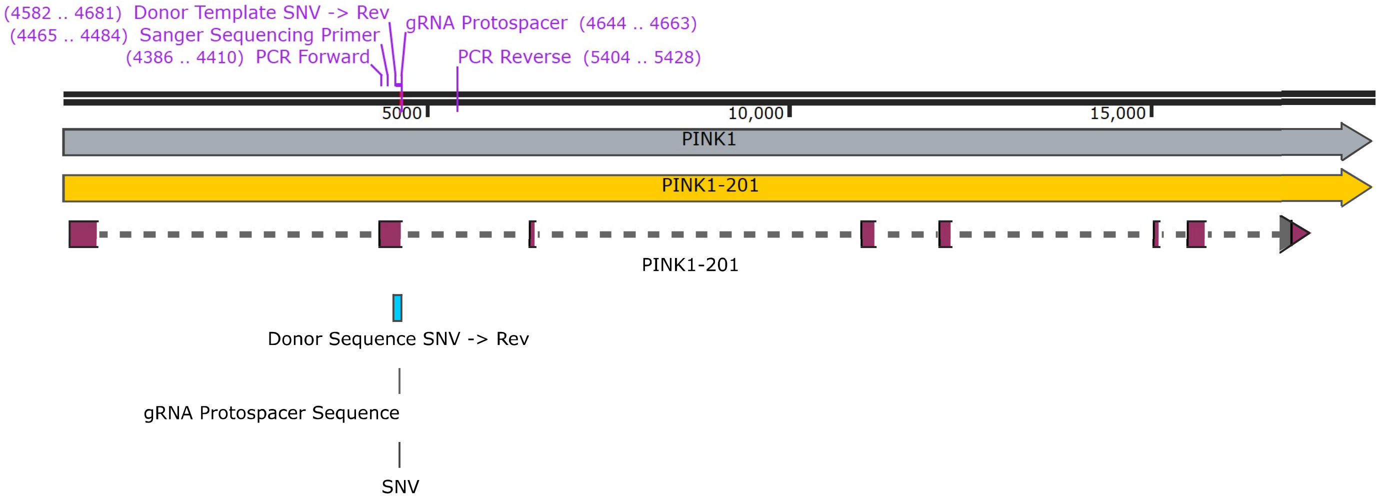

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PINK1-201

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PINK1-201

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PINK1-201

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PINK1

PINK1-201

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PINK1

PINK1-201

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PINK1-201

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PINK1-201

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PINK1-201

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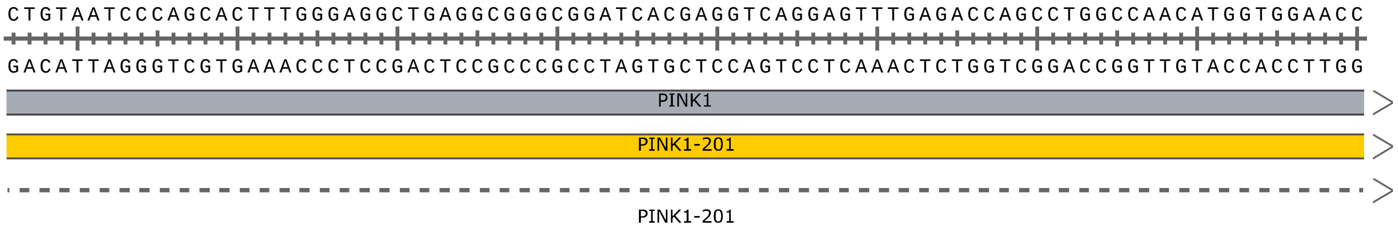
PINK1-201



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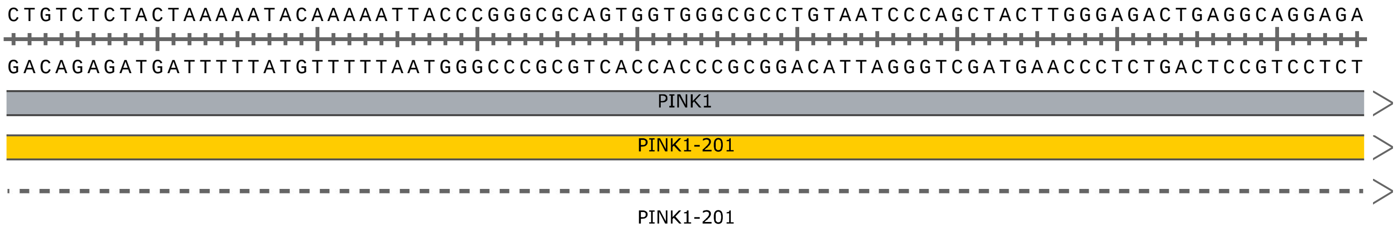

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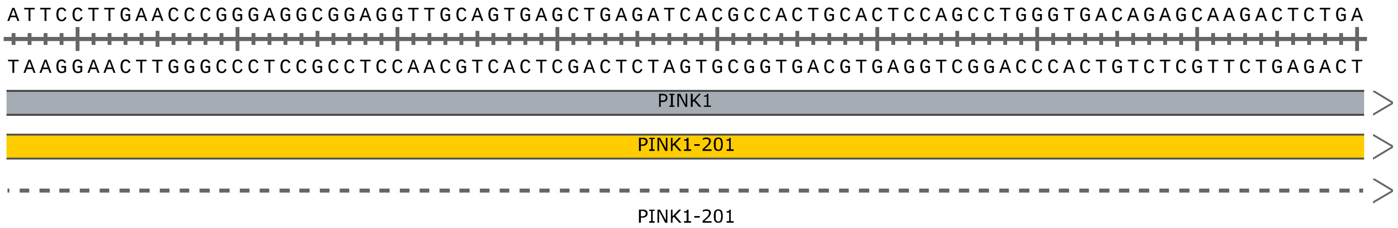

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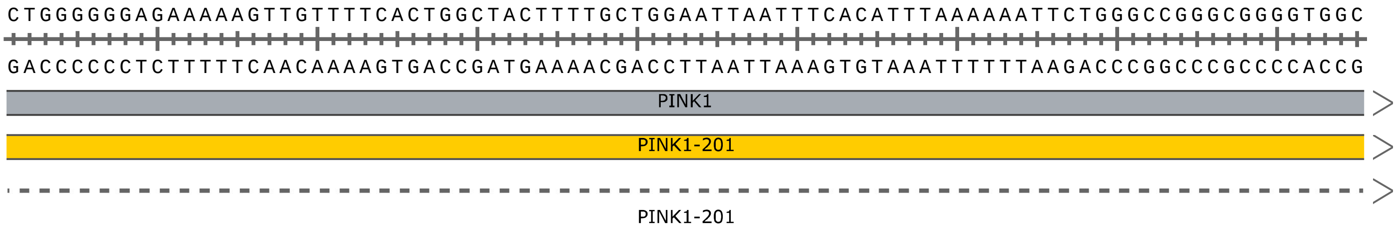

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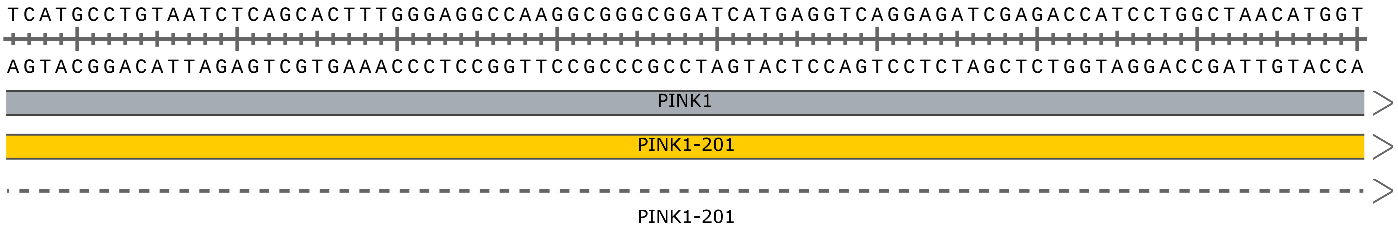

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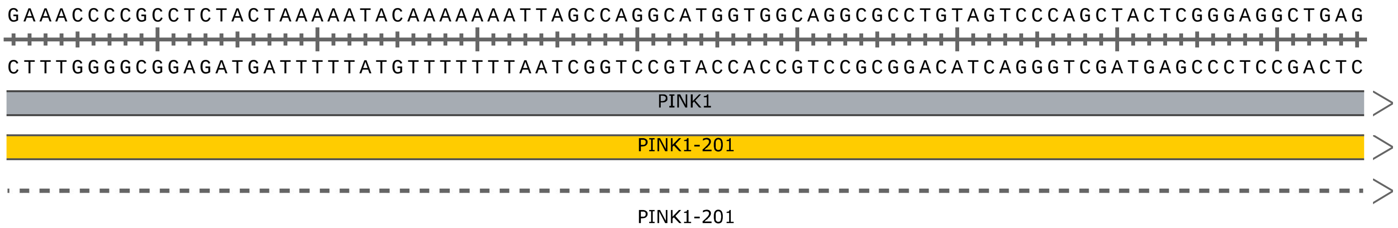

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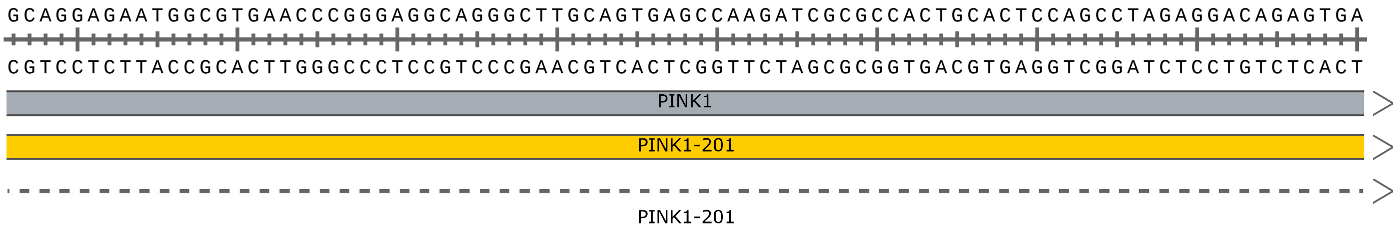

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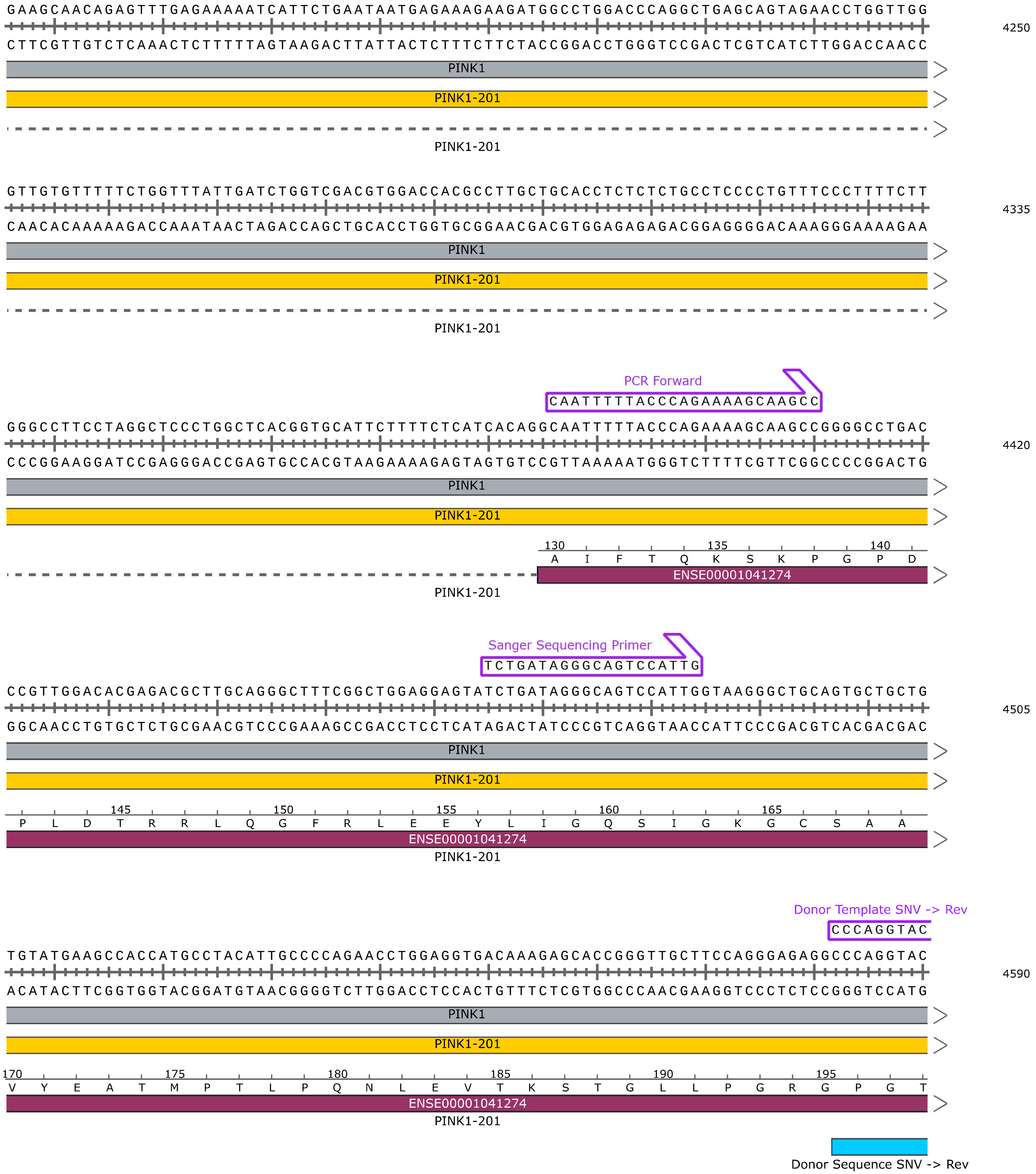

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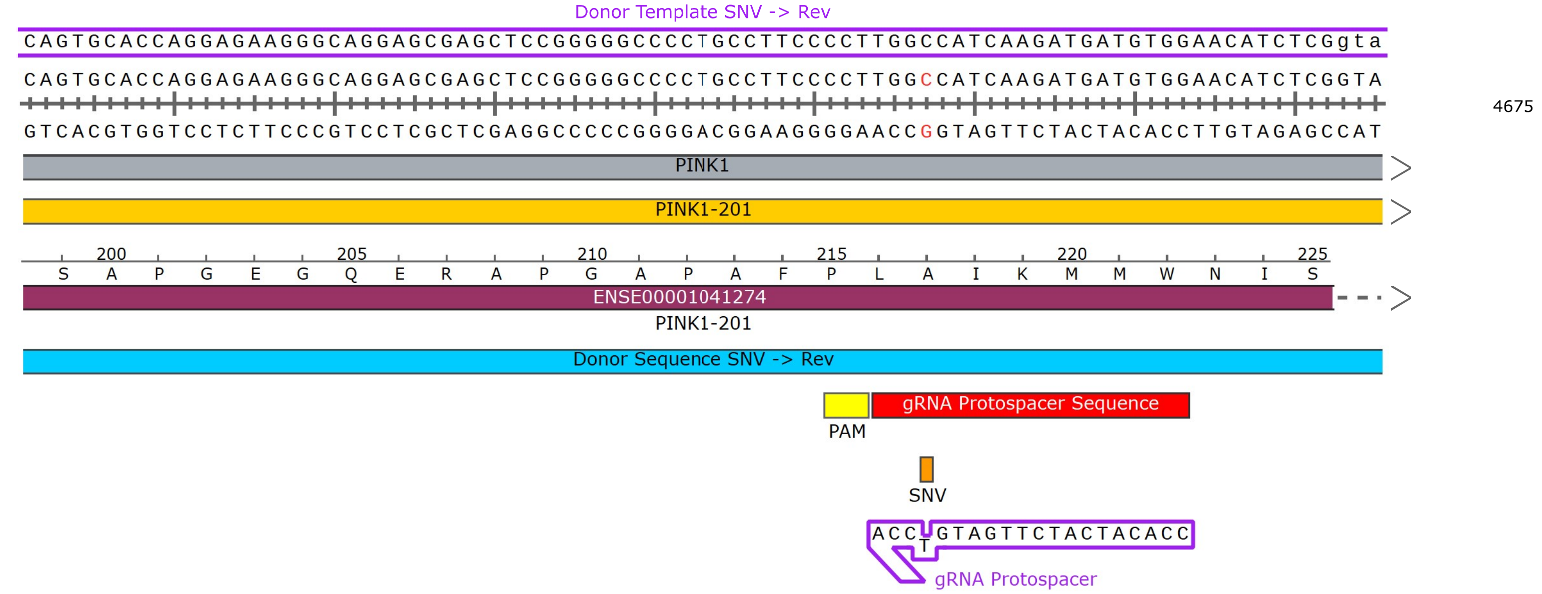
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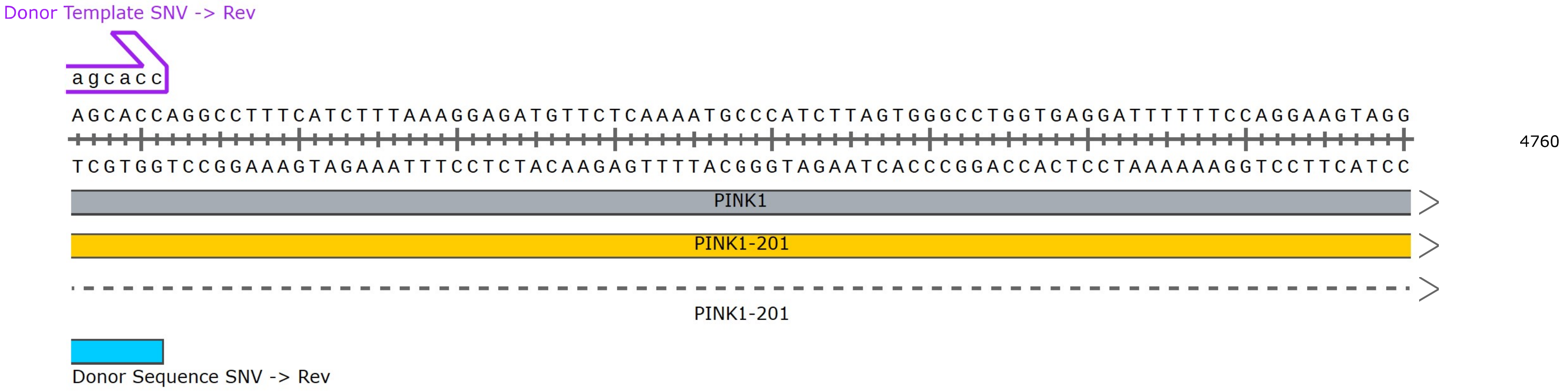
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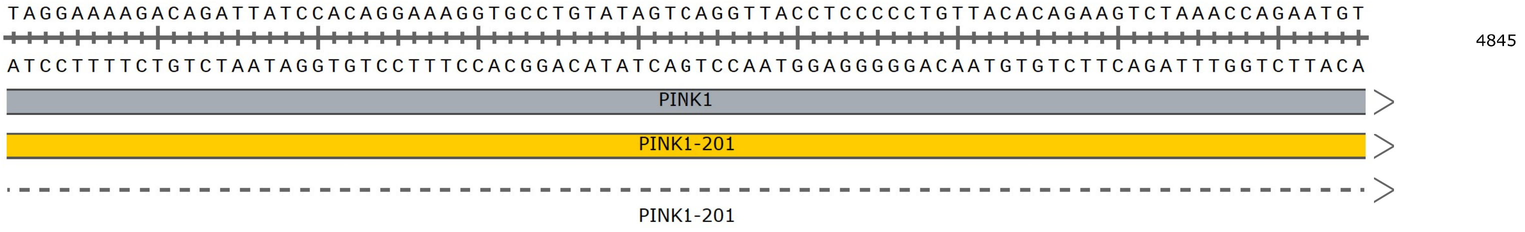
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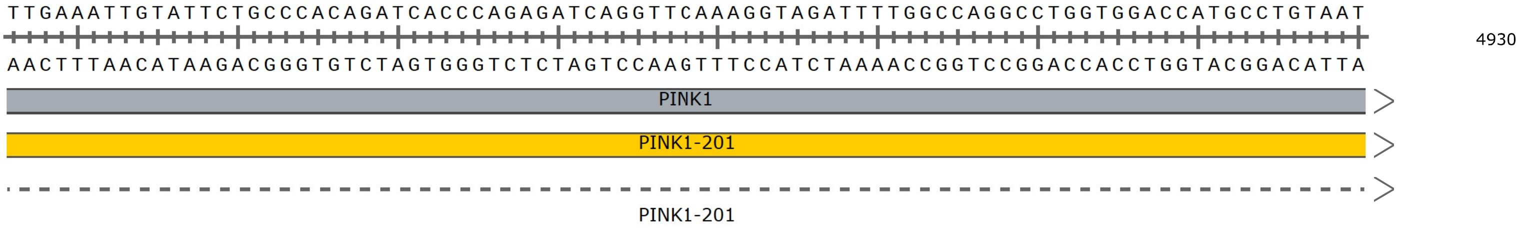
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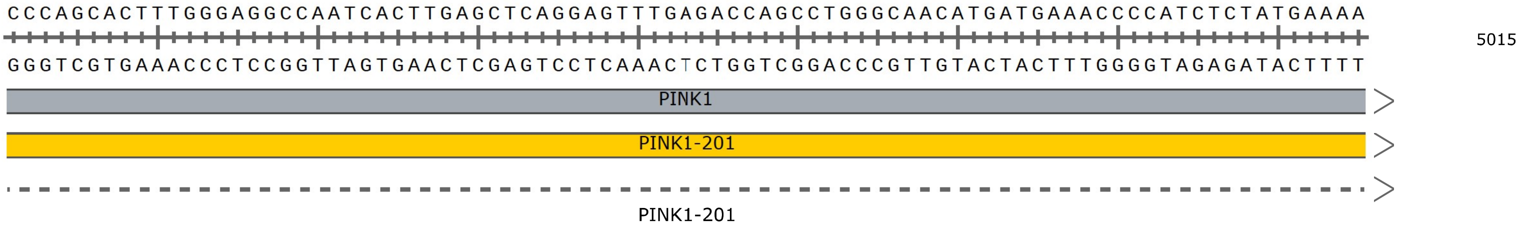
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PINK1

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PINK1-201

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```

PINK1

PINK1-201

PINK1-201

```
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```

PINK1

PINK1-201

PINK1-201

```
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```

PCR Reverse

```
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```

PINK1

PINK1-201

PINK1-201

```
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```

PINK1

PINK1-201

PINK1-201

```
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```

PINK1

PINK1-201

PINK1-201

```
GAGGATGCAGTTTCTTGTTCTGATTTGGGGAATGAAGGTTATTAGACTGTTGCACTCCAAGCTGGGTTAATAGCTAACAAGTAGC   5780
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```

PINK1

PINK1-201

PINK1-201

```
CAAATCCTTTGCCTGTGAAACATCCAGTCTTAGCATCAAAACATGCCCTGGTTGGGGCATGACAGCTGTTGCATTCACAGCAGCT   5865
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PINK1

PINK1-201

PINK1-201

```
ACAAGATTGTTGATTCTTACCAGATCTTCTTGATACAGGTTTCATATGTCCTGAGAGCCCTTCCCAATACAATGAGGACAATAAG   5950
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PINK1

PINK1-201

PINK1-201

```
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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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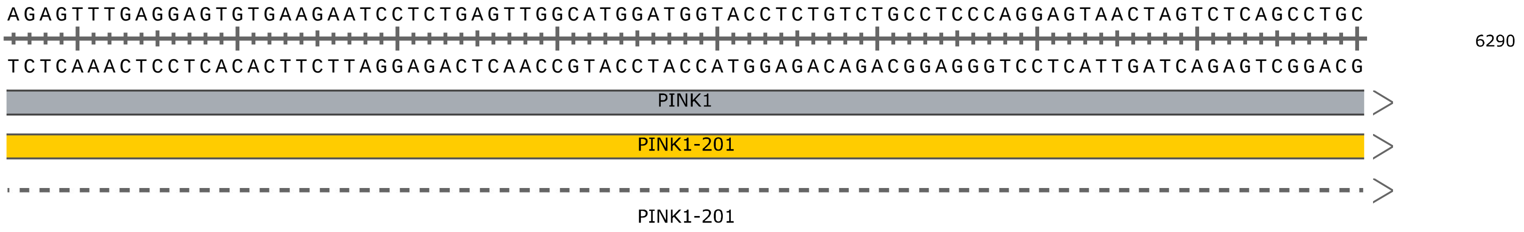
PINK1

PINK1-201

PINK1-201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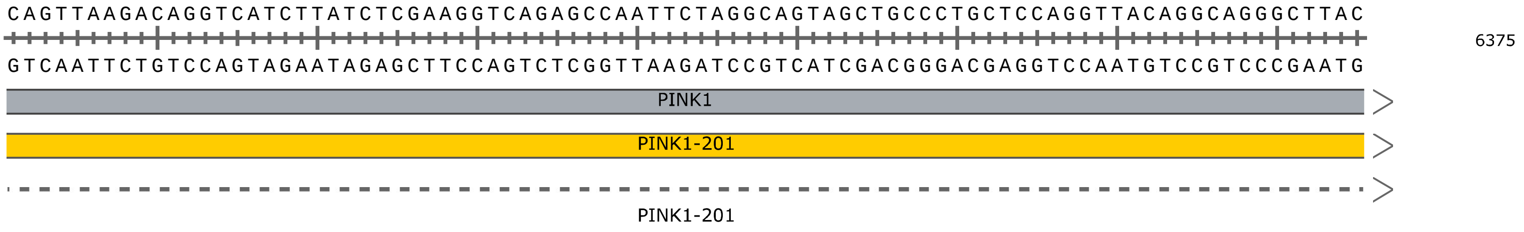
PINK1-201
PINK1-201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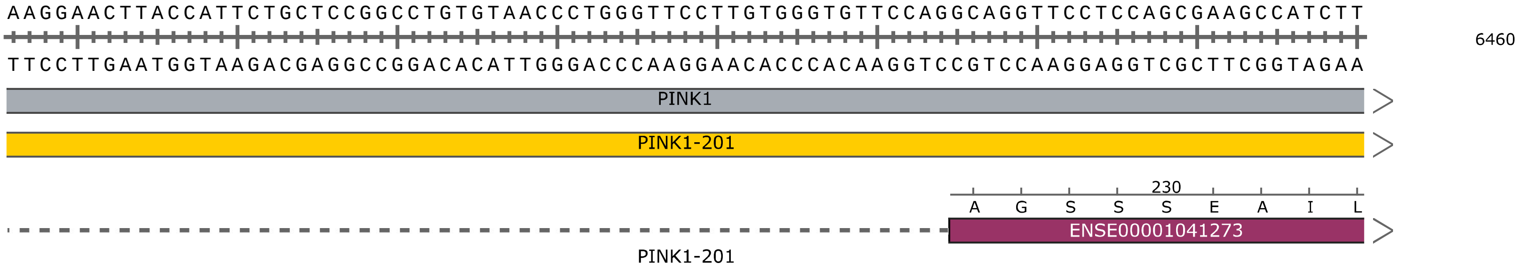
PINK1-201
PINK1-201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PINK1-201
230
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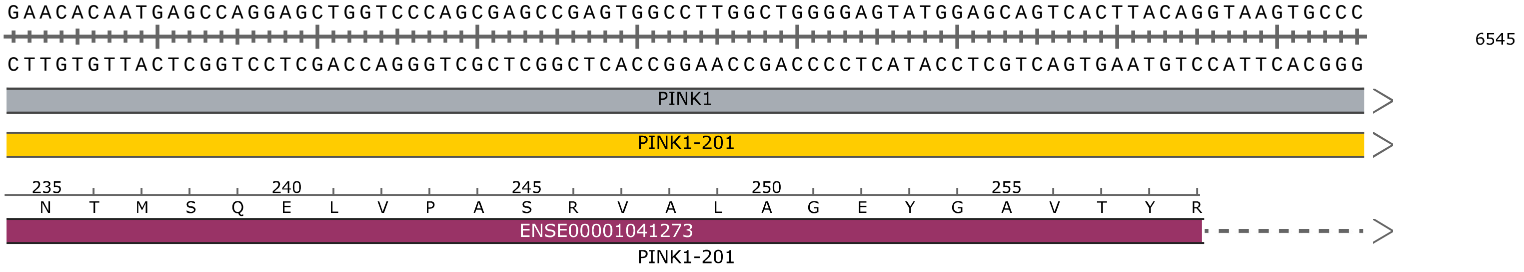
PINK1-201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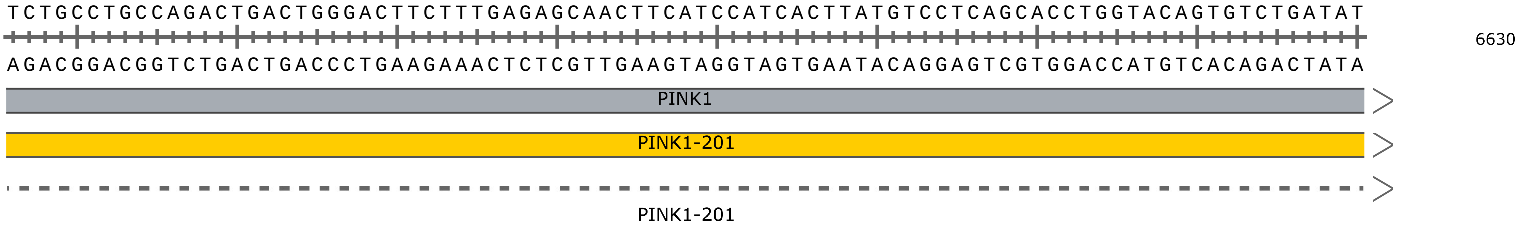
ENSE00001041273
PINK1-201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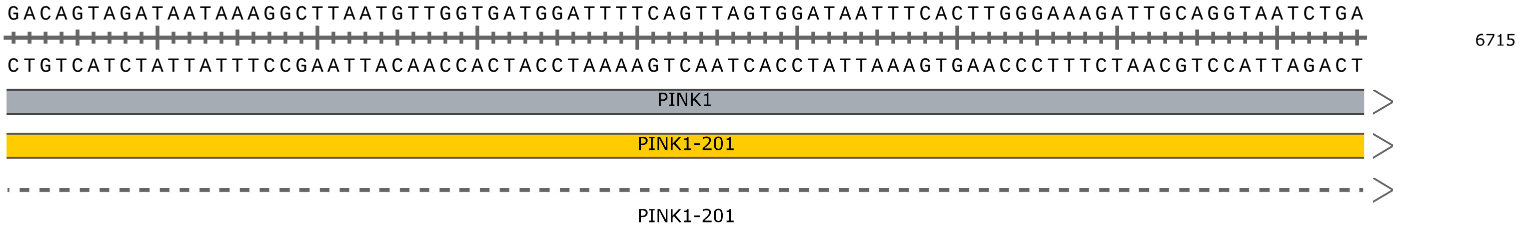
PINK1-201
PINK1-201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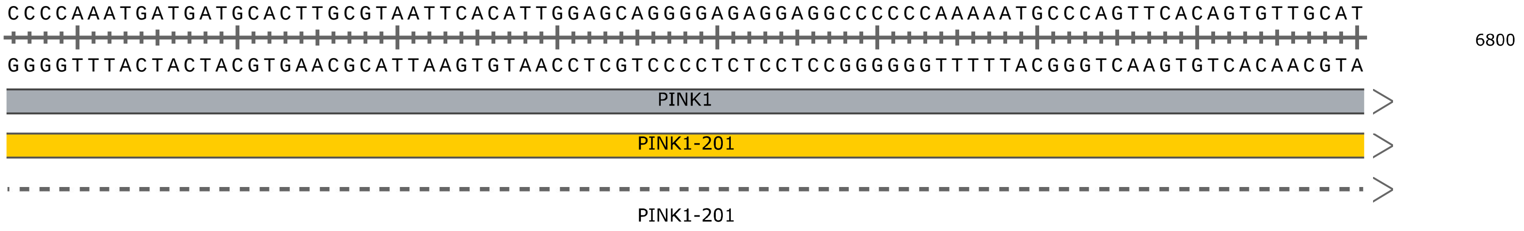
PINK1-201
PINK1-201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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1-201
PINK1-201

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PINK1-201
PINK1-201

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PINK1-201
PINK1-201

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PINK1-201
PINK1-201

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PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
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PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201

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PINK1
PINK1-201
PINK1-201
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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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10,455
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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201


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PINK1-201
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K S K R G P
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PINK1
PINK1-201
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290
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PINK1-201

PINK1-201

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PINK1-201

PINK1-201

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PINK1-201

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PINK1

PINK1-201

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PINK1-201

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PINK1-201

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PINK1-201

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PINK1-201

PINK1-201

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PINK1-201

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PINK1-201

PINK1-201

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PINK1-201

PINK1-201

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PINK1-201

PINK1-201

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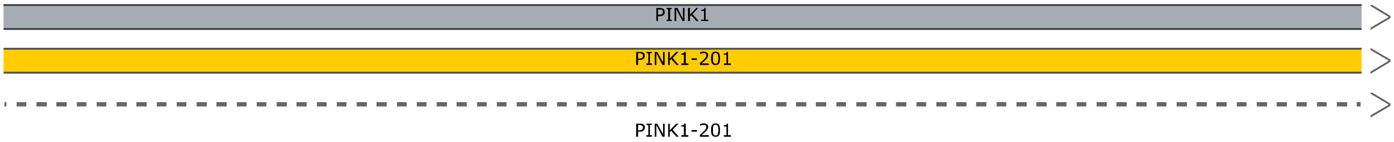

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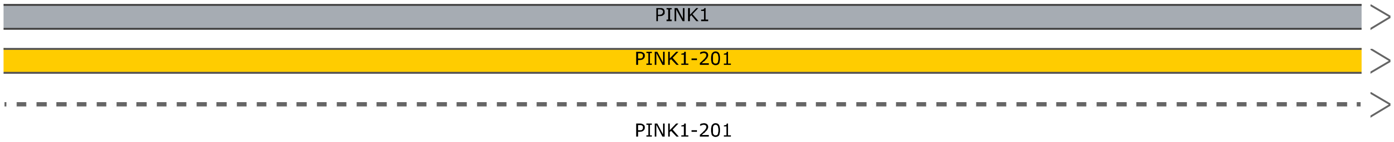

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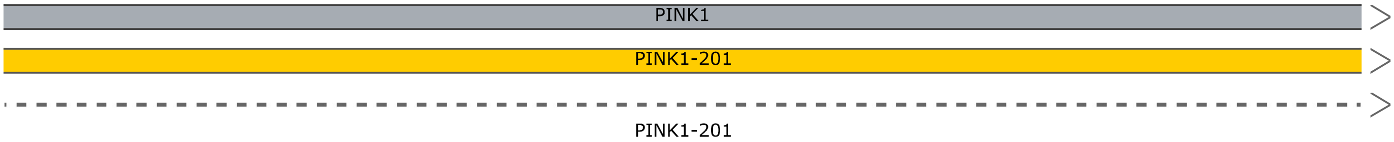

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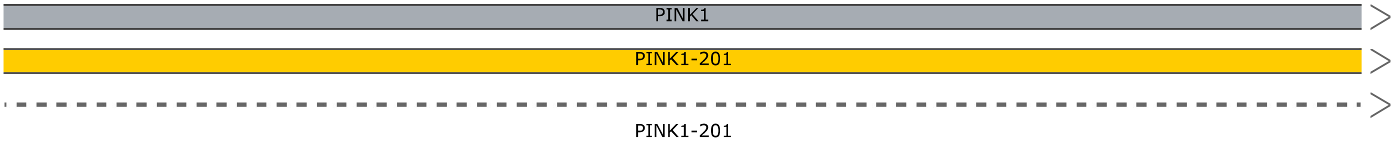

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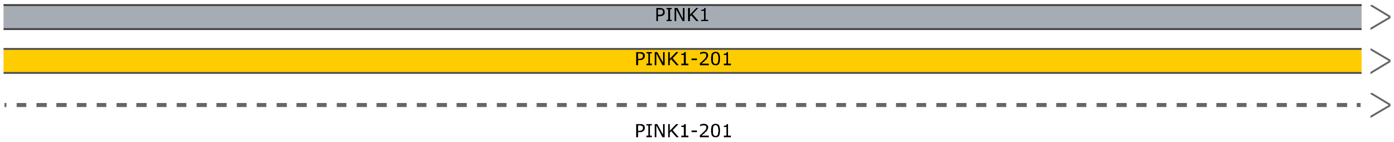

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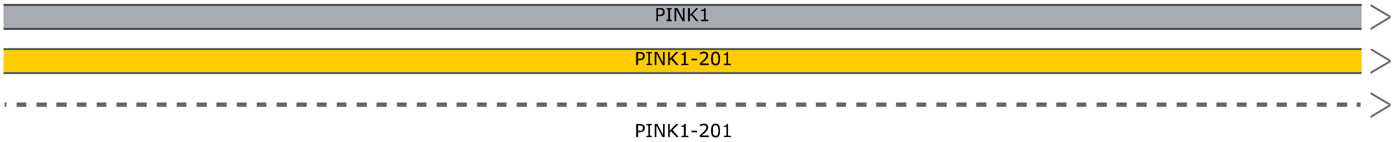

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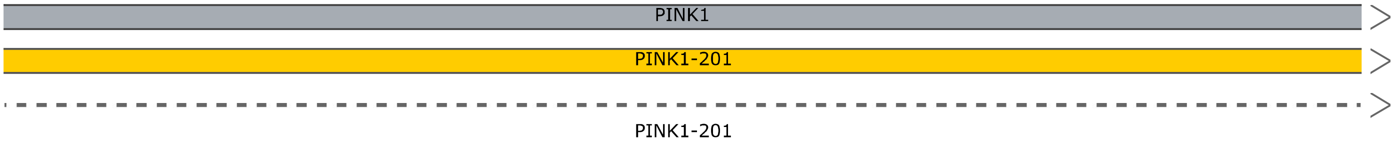

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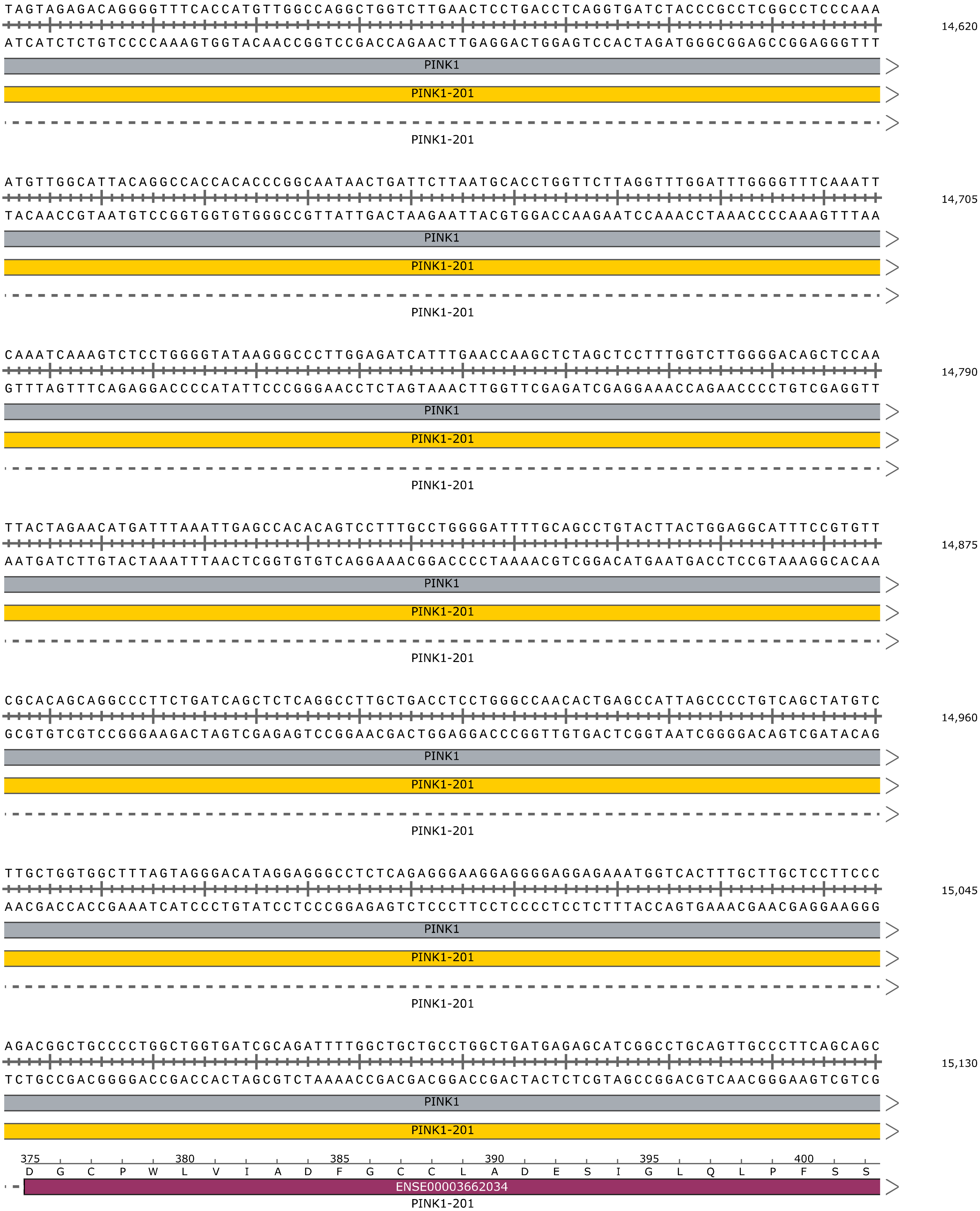

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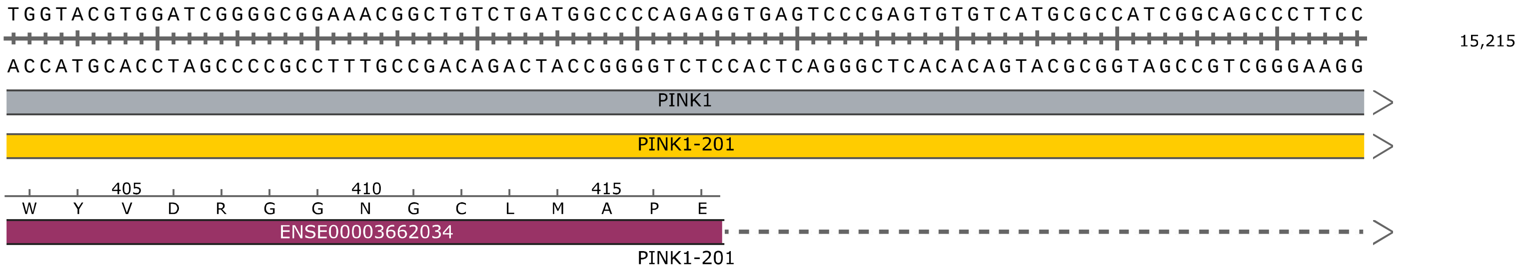
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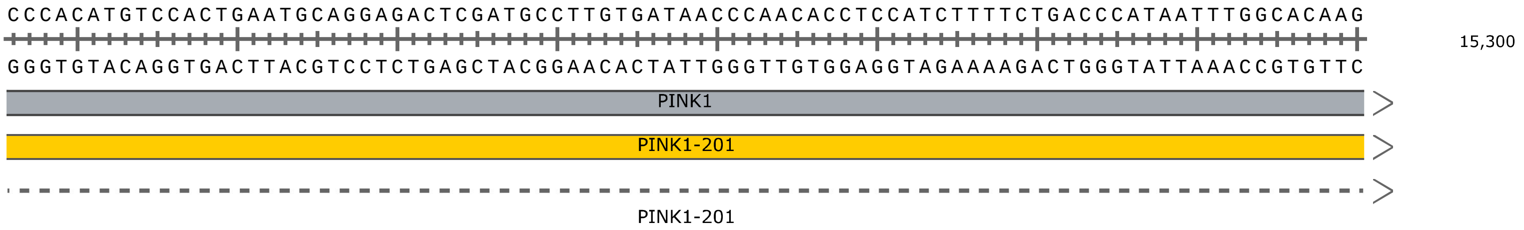
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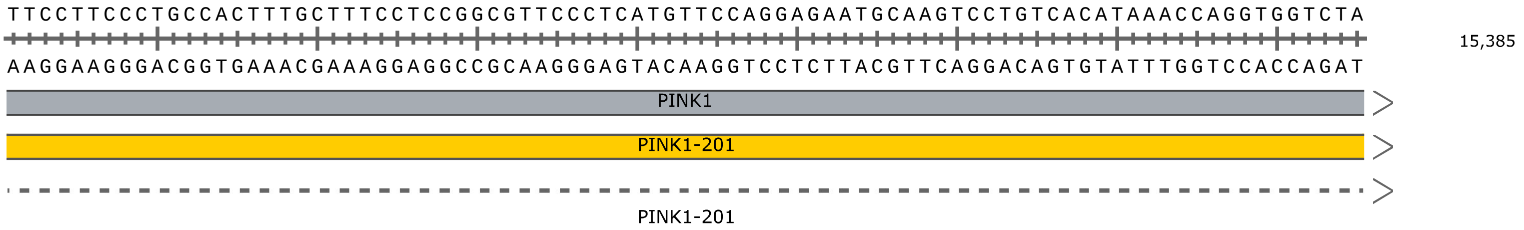
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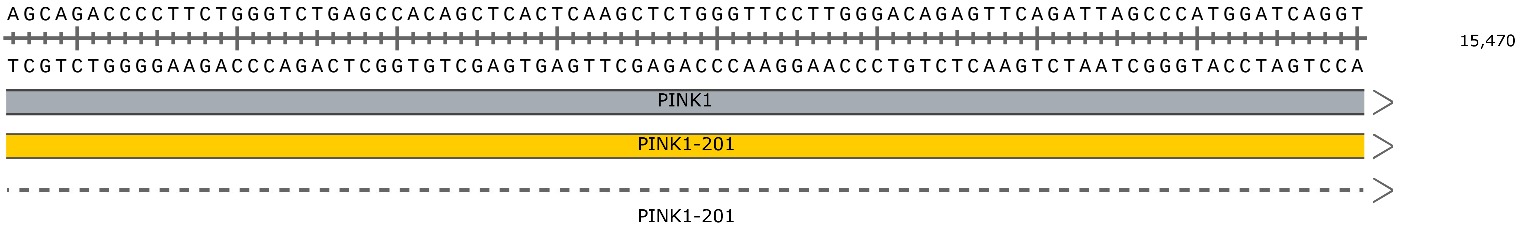
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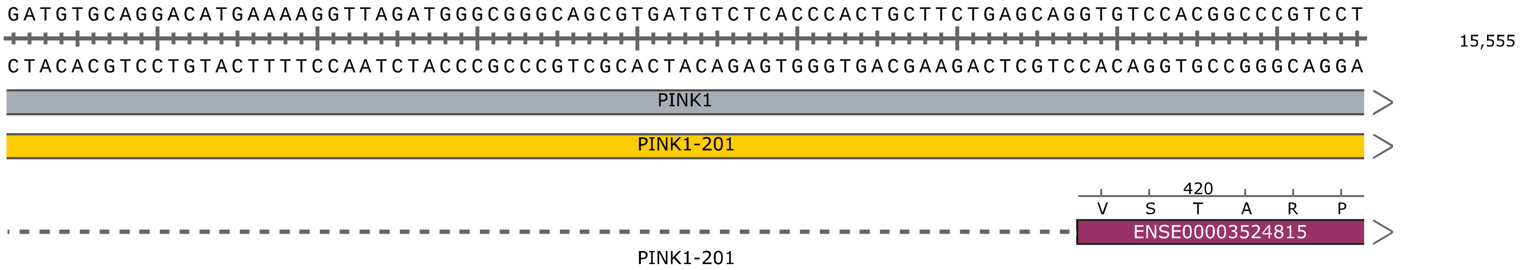
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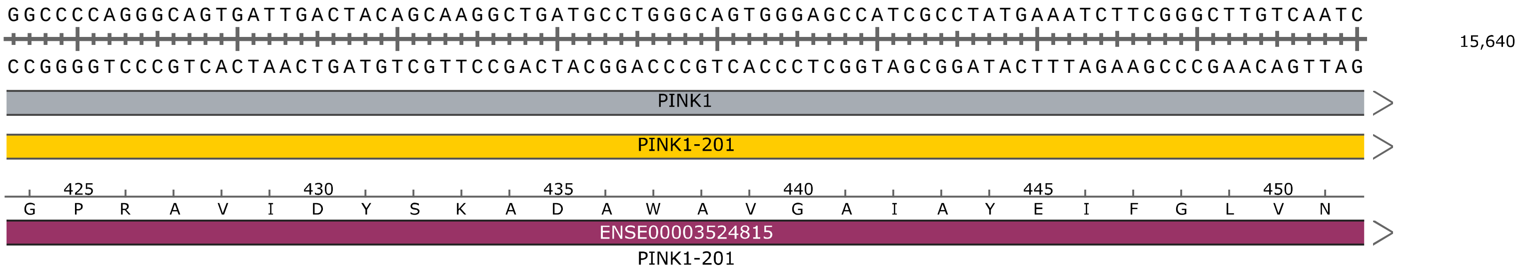
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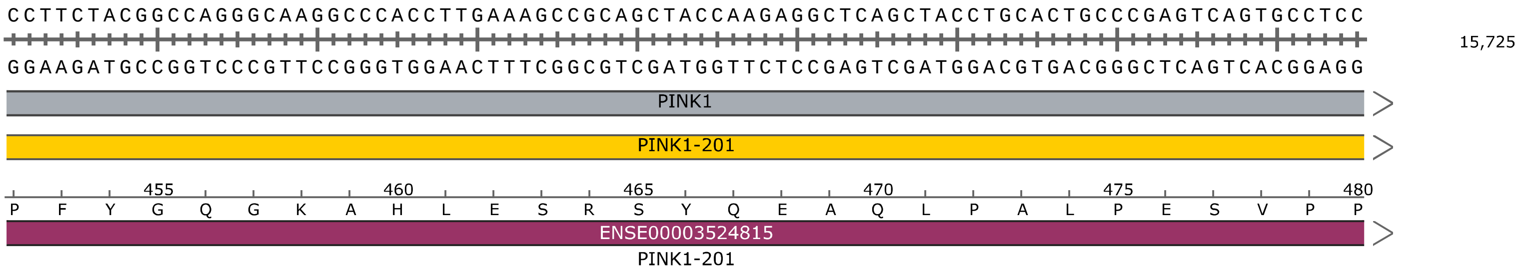
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PINK1-201

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D V R Q L V R A L L Q R E A S K

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PINK1-201

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PINK1-201

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PINK1-201

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PINK1-201

PINK1-201

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PINK1-201

PINK1-201

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PINK1-201

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PINK1

PINK1-201

PINK1-201

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16,575
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PINK1

PINK1-201

PINK1-201

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16,660
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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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PINK1

PINK1-201

PINK1-201

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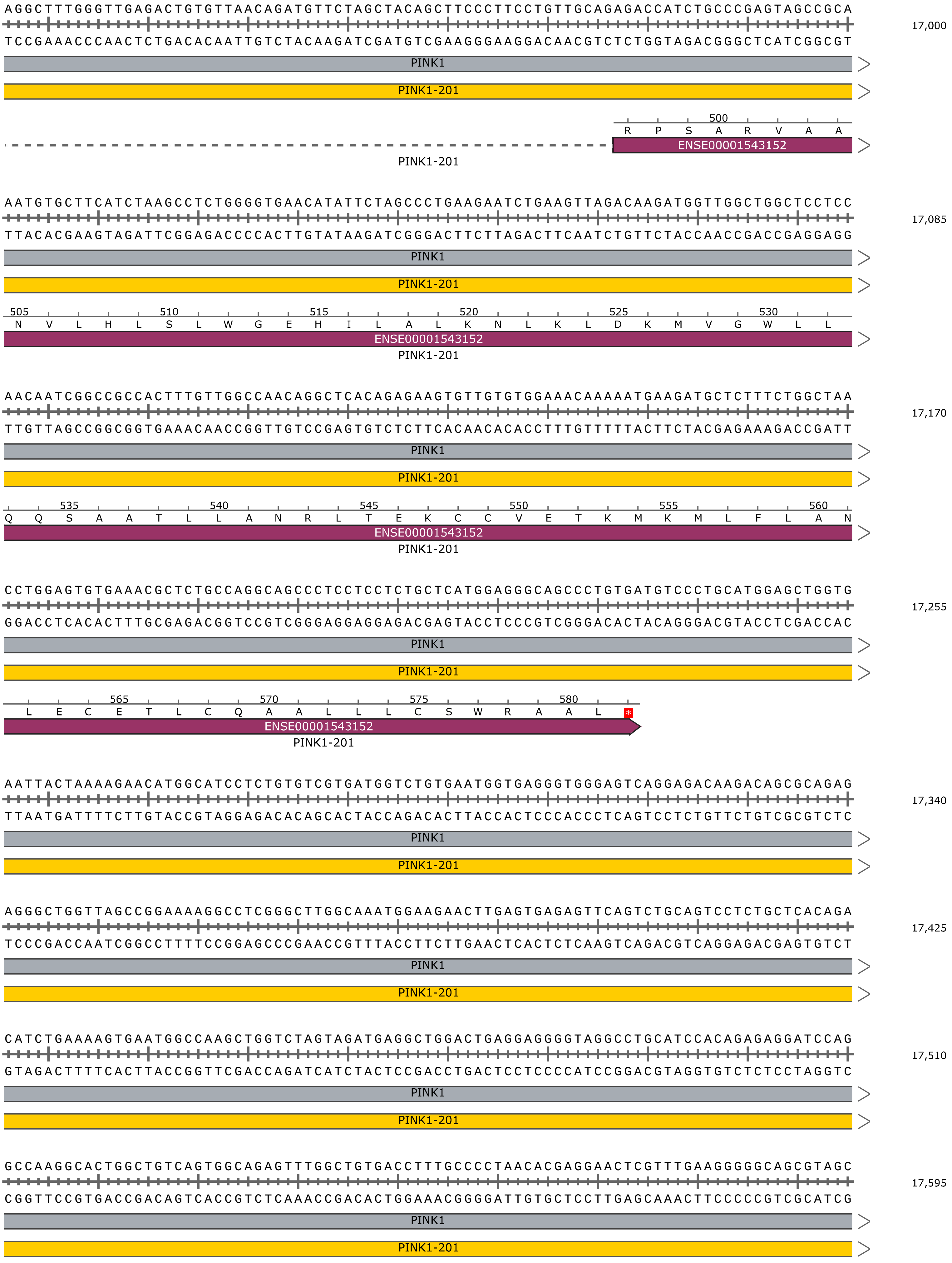
PINK1

PINK1-201

PINK1-201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PINK1-201
500
R P S A R V A A
ENSE00001543152
PINK1-201
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PINK1
PINK1-201
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PINK1-201
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17,170
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PINK1
PINK1-201
535 540 545 550 555 560
Q Q S A A T L L A N R L T E K C C V E T K M K M L F L A N
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PINK1-201
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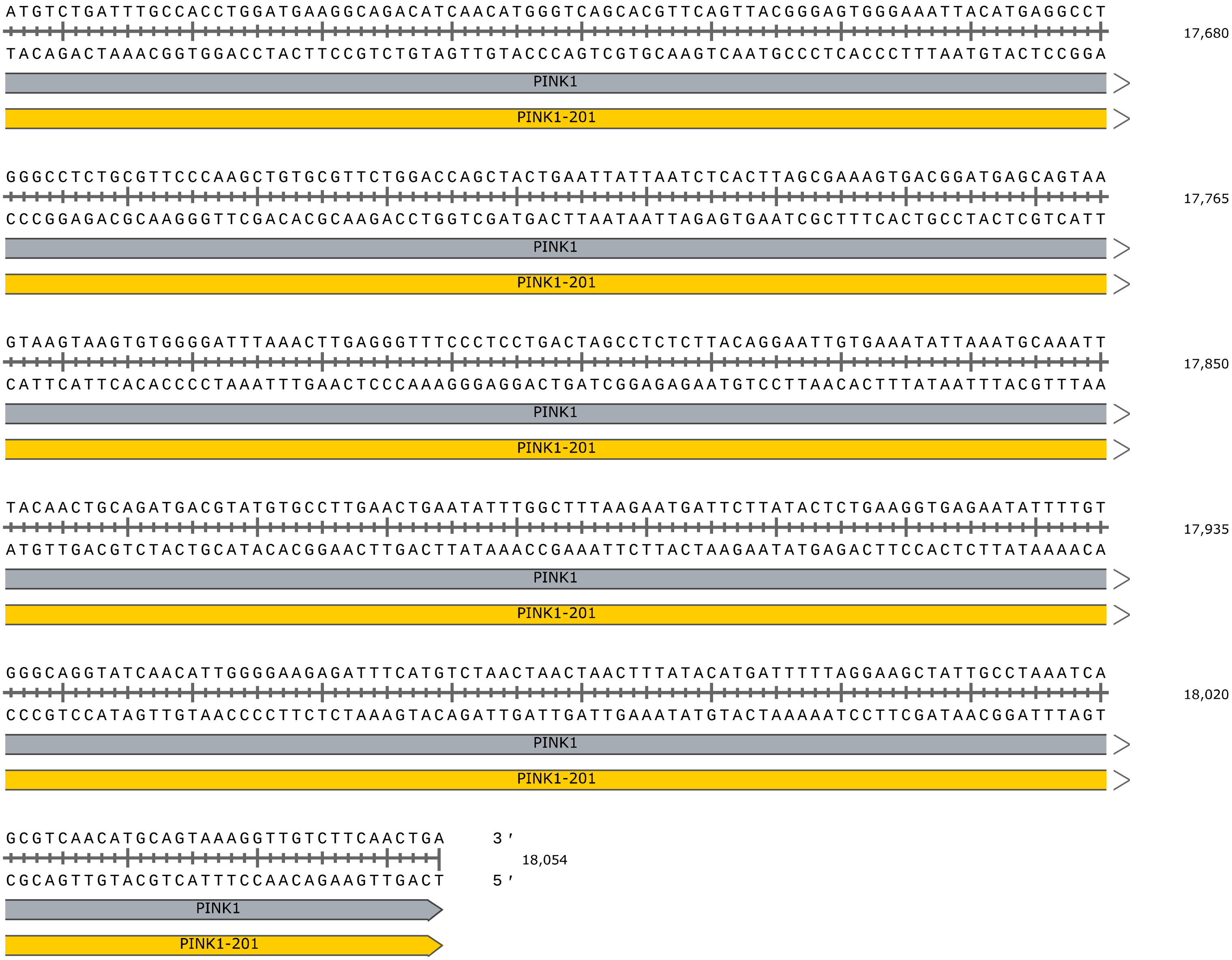
PINK1
PINK1-201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18,020
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PINK1
PINK1-201
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3′
18,054
CGCAGTTGTACGTCATTTCCAACAGAAGTTGACT
5′
PINK1
PINK1-201

	Feature	Location	Size			Type
✓	**PINK1**	1 .. 18,054	18,054 bp	▨	→	gene
	/note = gene ENSG00000158828 Protein coding					
✓	**PINK1-201**	1 .. 18,054	18,054 bp	🟨	→	prim_transcript
	/note = primary transcript ENST00000321556					
✓	**PINK1-201**	92 .. 17,234	17,143 bp	🟪	→	CDS
	▸ 8 segments = 1746 bp					
	/note = coding sequence ENSP00000364204					
	/translation = MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEPRRVGLGLPNRLRFFRQSVAGLAARLQRQFVVRAWGCAGPCGRAVFLAFGLGLGLIEEKQAESRRAVSACQEIQ,,AIFTQKSKPGPDPLDTRRLQGFRLEEYLIGQSIGKGCSAAVYEATMPTLPQNLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNIS,,AGSSSEAILNTMSQELVPASRVALAGEYGAVTYR,,KSKRGPKQLAPHPNIIRVLRAFTSSVPLLPGALVDYPDVLPSRLHPEGLGHGRTLFLVMKN,,YPCTLRQYLCVNTPSPRLAAMMLLQLLEGVDHLVQQGIAHRDLKSDNILVELDP,,DGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPE,,VSTARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFYGQGKAHLESRSYQEAQLPALPESVPPDVRQLVRALLQREASK,,RPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQSAATLLANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL* 581 amino acids = 62.8 kDa					
	MIR6084	222 .. 331	110 bp	▨	→	gene
	/note = gene ENSG00000284005 miRNA					
	MIR6084-201	222 .. 331	110 bp	▨	→	prim_transcript
	/note = primary transcript ENST00000622012 miRNA					
✓	**Donor Sequence SNV -> Rev**	4582 .. 4681	100 bp	🟦	↔	misc_feature
✓	**PAM**	4641 .. 4643	3 bp	🟨	↔	misc_feature
✓	**gRNA Protospacer Sequence**	4644 .. 4663	20 bp	🟥	↔	misc_feature
✓	**SNV**	4647 .. 4647	1 bp	🟧	↔	misc_feature
	/note = SNV = A Rev = C					
	PINK1-203	4672 .. 17,859	13,188 bp	▨	→	prim_transcript
	/note = primary transcript ENST00000492302 protein_coding_CDS_not_defined					
	PINK1-AS	9200 .. 18,736	9537 bp	▨	←	gene
	/note = gene ENSG00000117242 lncRNA					
	PINK1-AS-201	9200 .. 18,736	9537 bp	▨	←	prim_transcript
	/note = primary transcript ENST00000451424 lncRNA					
	PINK1-202	12,051 .. 18,053	6003 bp	▨	→	prim_transcript
	/note = primary transcript ENST00000400490 protein_coding_CDS_not_defined					

	Primer	Length	●	Binding Sites	⇄	Tm	Date Added
✓	**PCR Forward**	25-mer		4386 .. 4410	→	57°C	May 5, 2023
	/sequence = CAATTTTTACCCAGAAAAGCAAGCC 40% GC / 7603.0 Da						
✓	**Sanger Sequencing Primer**	20-mer		4465 .. 4484	→	56°C	May 5, 2023
	/sequence = TCTGATAGGGCAGTCCATTG 50% GC / 6148.1 Da						
✓	**Donor Template SNV -> Rev**	100-mer		4582 .. 4681	→	83°C	May 5, 2023
	/sequence = CCCAGGTACCAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCCGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAAC ATCTGGgtaagcacc 63% GC / 30,850.9 Da						
✓	**gRNA Protospacer**	20-mer		4644 .. 4663	←	46°C	May 5, 2023
	/sequence = CCACATCATCTTGATGTCCA 45% GC / 6012.0 Da						
✓	**PCR Reverse**	25-mer		5404 .. 5428	←	58°C	May 5, 2023
	/sequence = ttaaaggaaagagatccagttcccc 44% GC / 7659.1 Da						