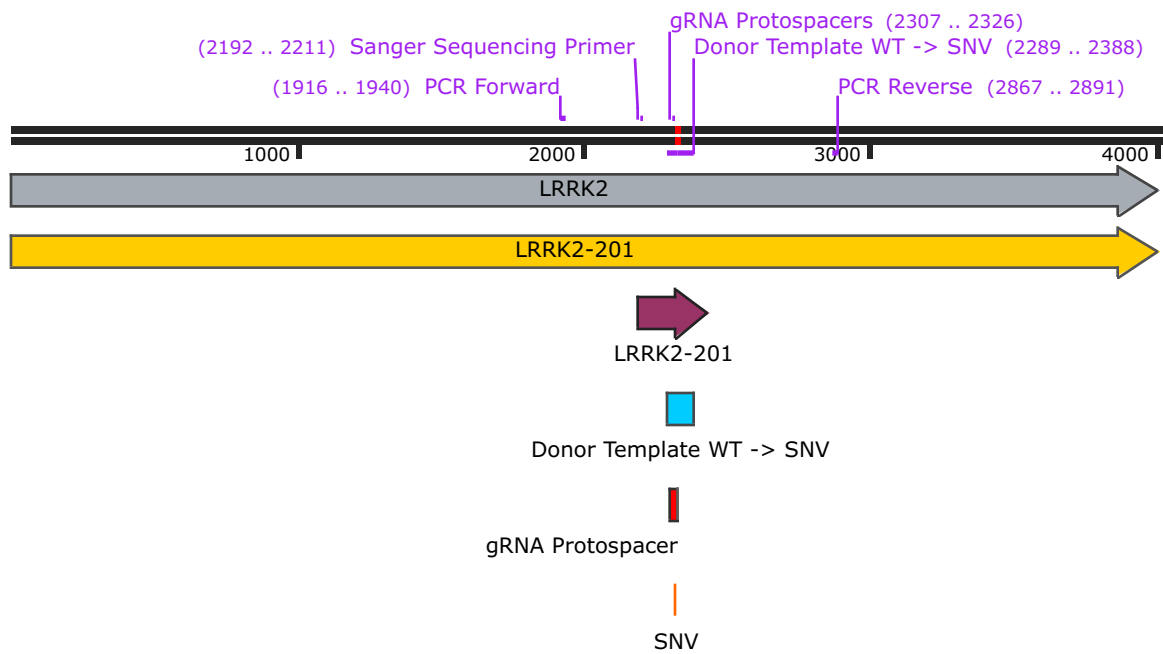
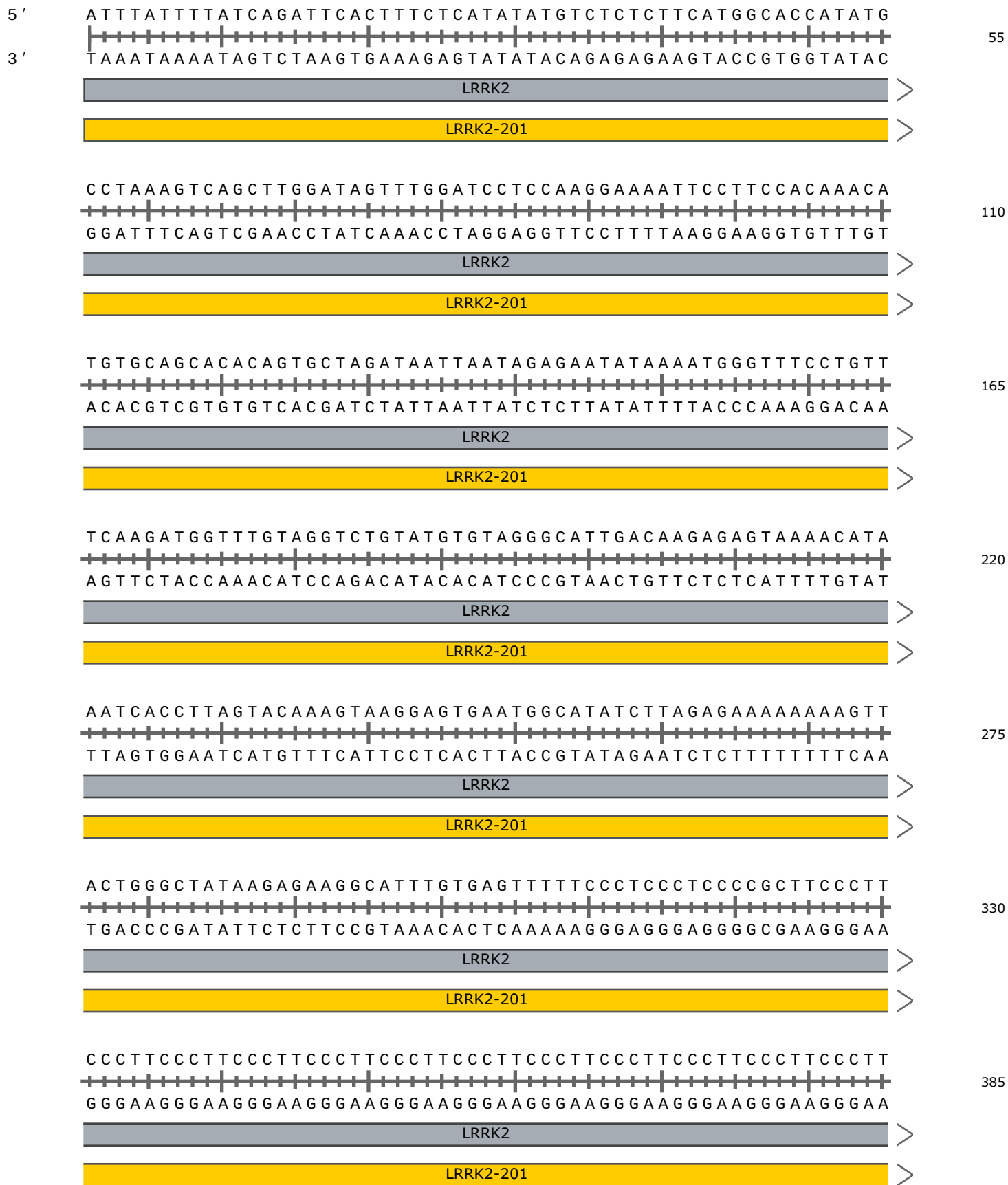


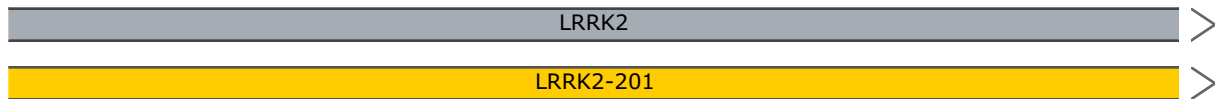
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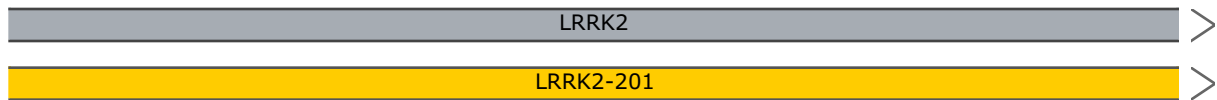
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4007 bp



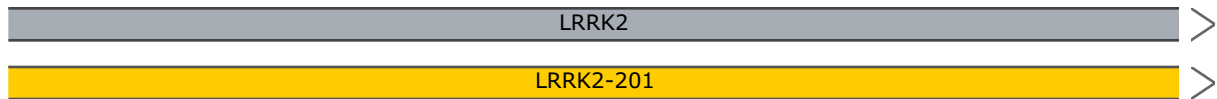
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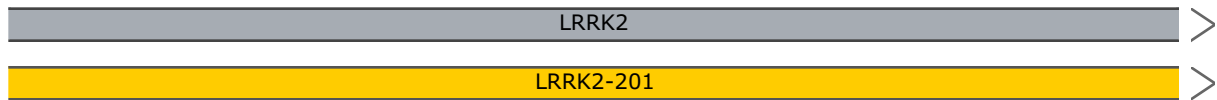
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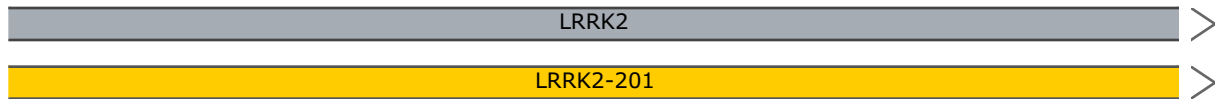
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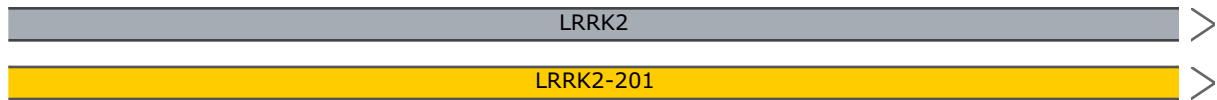
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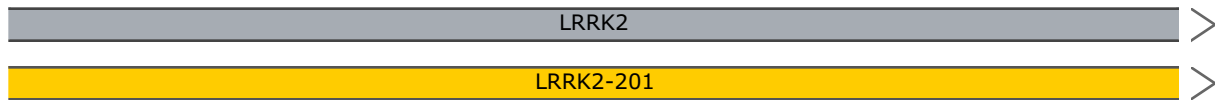
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825



CACCTTTTTGCTGGGTGAAAAGTAGAGGAAGGCATTTGGGGTAATAGAAATAGCA  
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880



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935



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990



AGTGCTTTGAGGATGGGTTGAAGGTGGGCGTACTTGGAGACTGGTGGGCATTTAA  
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1045



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1100

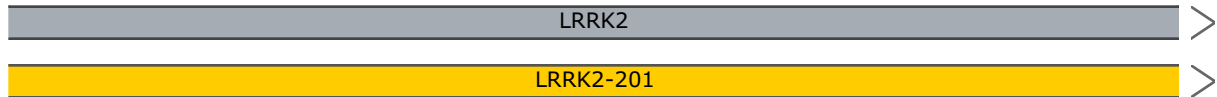


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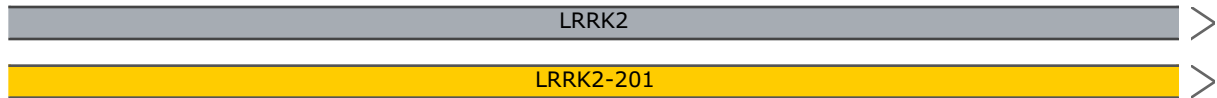
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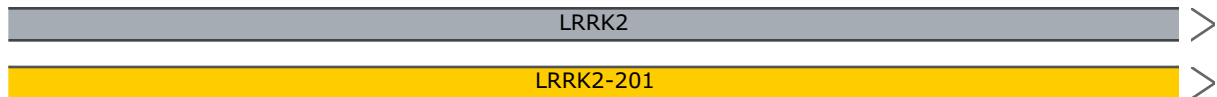
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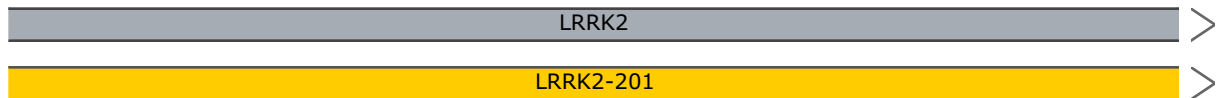
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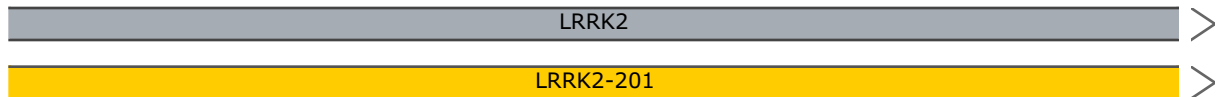
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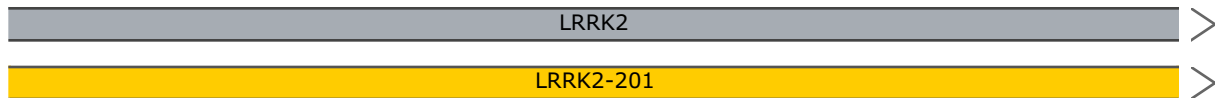
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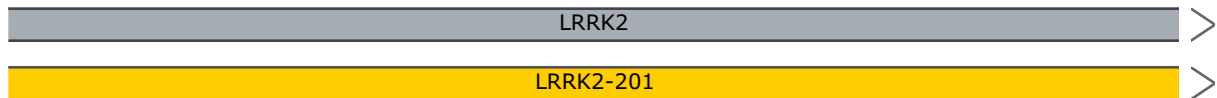
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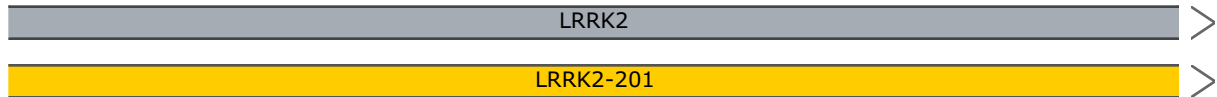
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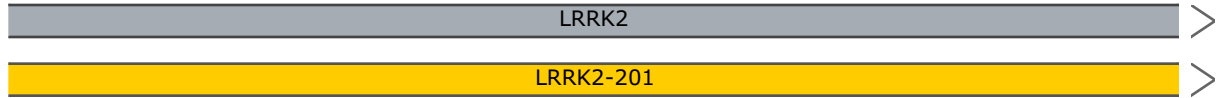
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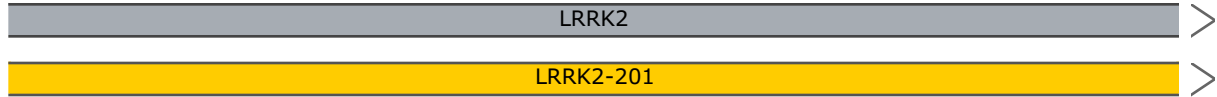
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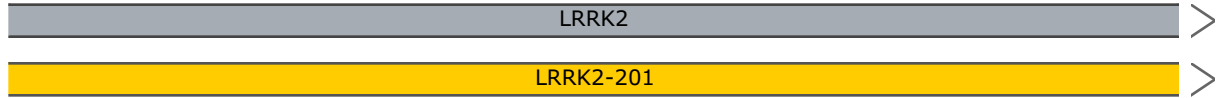
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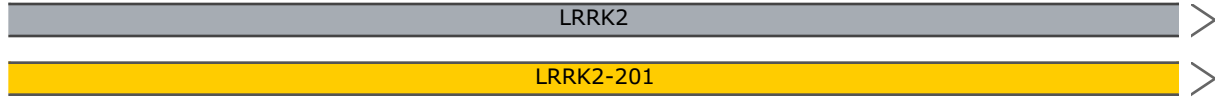
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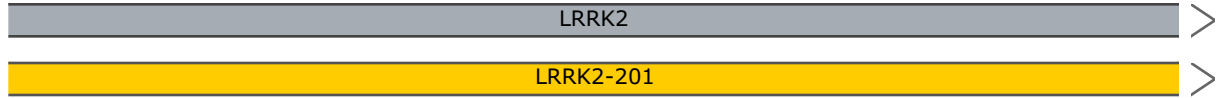
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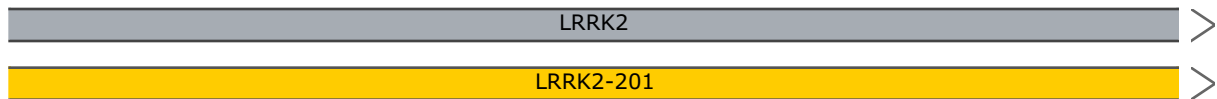
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PCR Forward

TGCCAAGCCT

CAATGTGCATATTTGGTGGAGTCTGGATGTAAACAGAGATCTTGATGCCAAGCCT  
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PCR Forward

GTGGAGCTTTGTCTC

GTGGAGCTTTGTCTCCATATAATGTTGTCTCTTTCATAAATACTGACTGTCATGT  
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1980



GGCAGATTATTCATGCTATTCTGACATTGATGGCATTAAATATCATCTTATTTTCC  
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2035



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2090



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2145

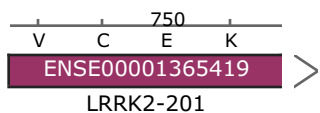


Sanger Sequencing Primer

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2200

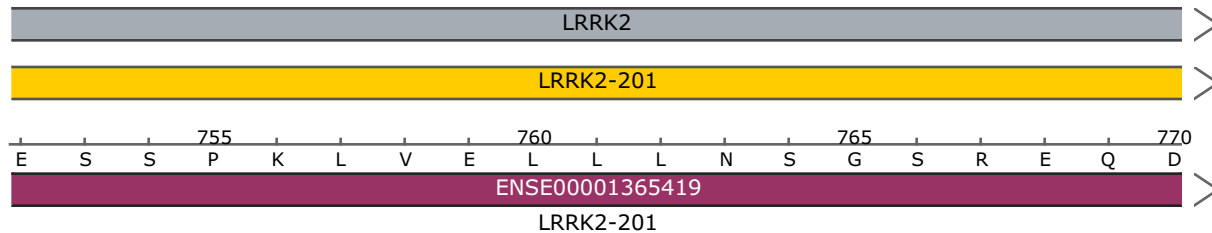


Sanger Sequencing Primer

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2255

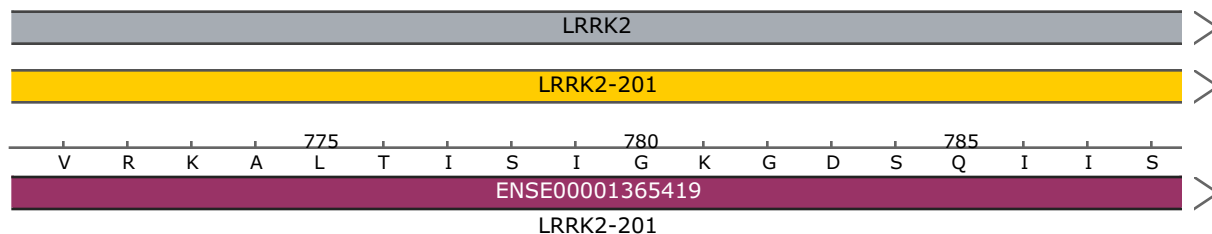


gRNA Protospacers

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2310

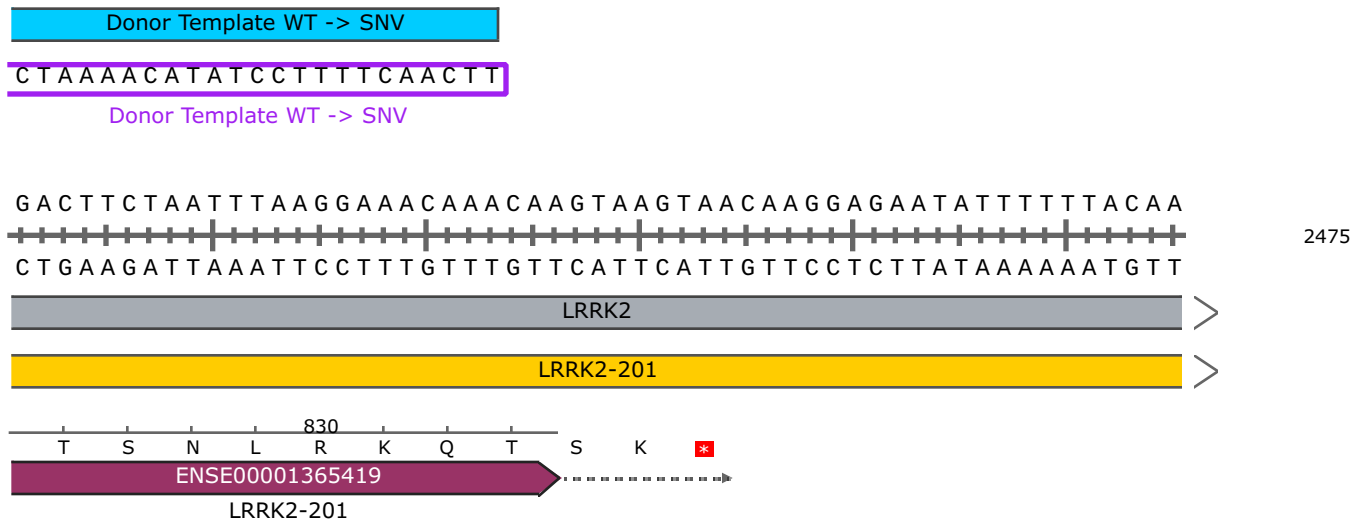
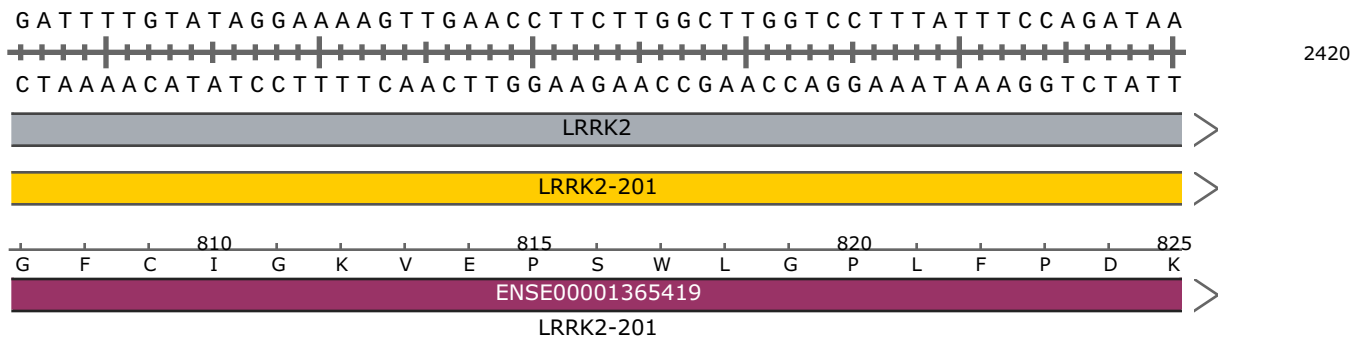
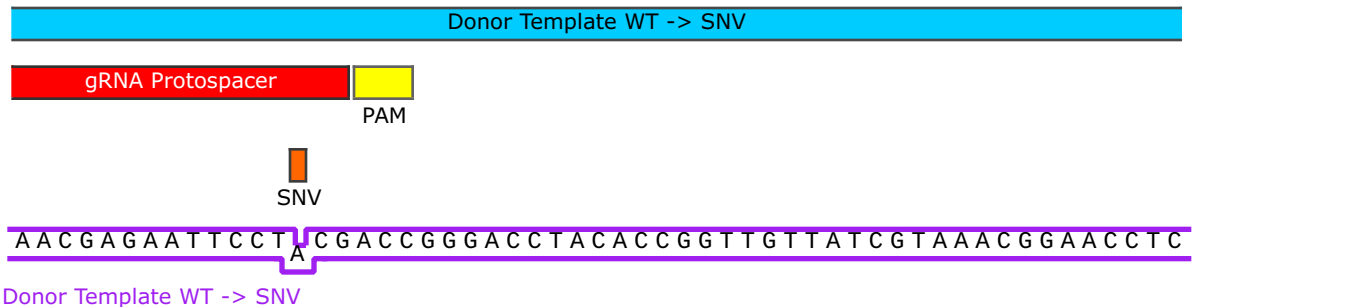
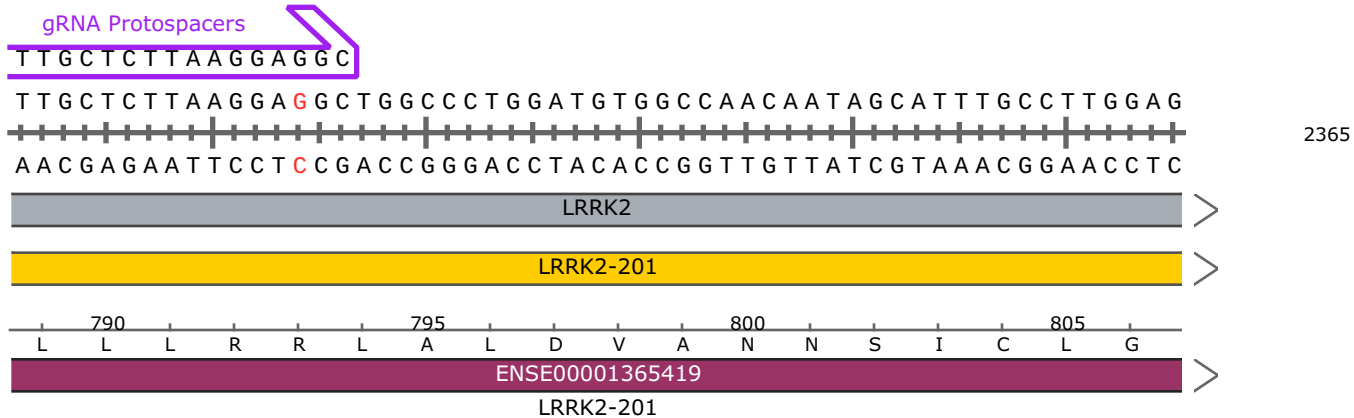


Donor Template WT -> SNV

**gRNA Protospacer**

**TCCACTGTCGGTCTAGTAGTCG**  
 Donor Template WT -> SNV





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2530



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2585



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2640



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2695



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2750



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2805



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2860



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2915



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 PCR Reverse

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2970



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3025



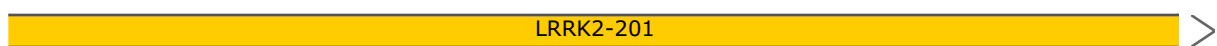
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3080



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3135



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3190

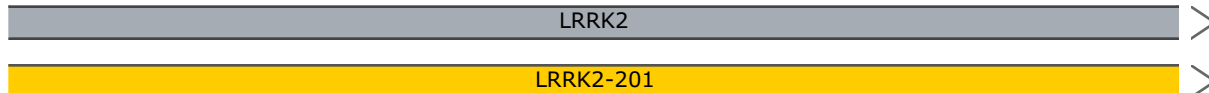


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3245



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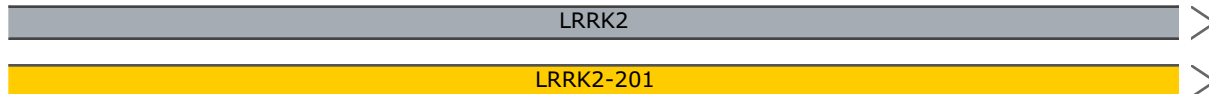
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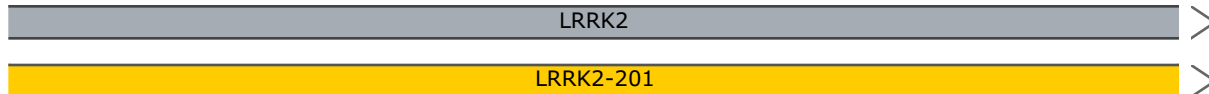
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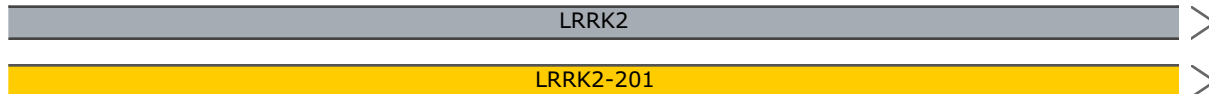
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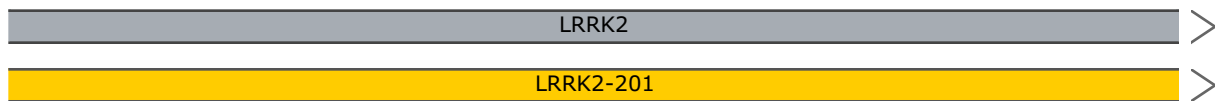


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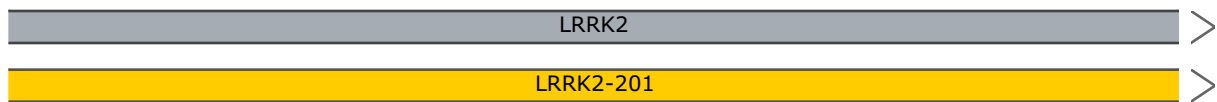
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3685



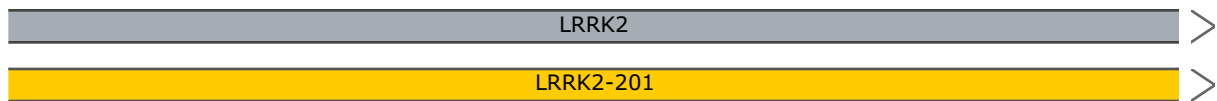
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3740



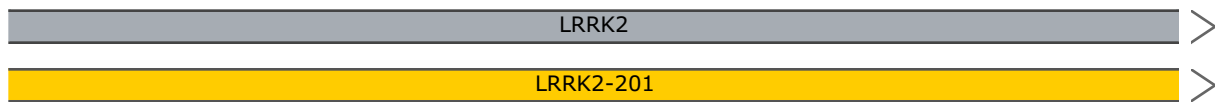
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3795



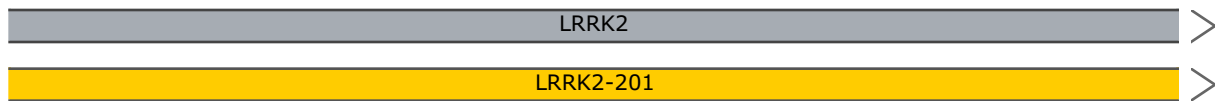
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3850



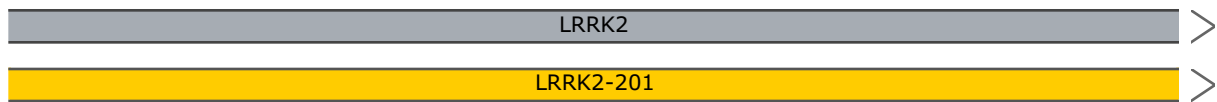
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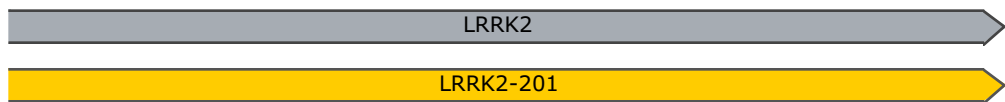
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3960



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4007



Feature	Location	Size	Start	End	Type
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✓ <b>LRRK2</b>	1 .. 4007	4007 bp	■	→	gene
/note	= gene <a href="#">ENSG00000188906</a> Protein coding				
<b>LINC02471-202</b>	1 .. 4007	4007 bp	■	→	prim_transcript
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<b>LRRK2-210</b>	1 .. 4007	4007 bp	■	→	prim_transcript
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<b>LRRK2-218</b>	1 .. 4007	4007 bp	■	→	prim_transcript
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<b>LRRK2-203</b>	1 .. 2265	2265 bp	■	→	prim_transcript
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<b>LRRK2-218</b>	2188 .. 2446	259 bp	■	→	CDS
/note	= coding sequence <a href="#">ENSP00000505335</a>				
/translation	= VCEKESP <del>K</del> LV <del>L</del> LLNSGSRE <del>Q</del> DVRKAL <del>T</del> ISIGK <del>G</del> DSQIIS <del>L</del> LLRRLALDVANNSICLGGFCIGKVEPSWLGPLFPDKTSNLRKQT 86 amino acids = 9.4 kDa				
<b>LRRK2-203</b>	2188 .. 2265	78 bp	■	→	CDS
/note	= coding sequence <a href="#">ENSP00000398726</a>				
/translation	= VCEKESP <del>K</del> LV <del>L</del> LLNSGSRE <del>Q</del> DVRK 26 amino acids = 2.9 kDa				
✓ <b>Donor Template WT -&gt; SNV</b>	2289 .. 2388	100 bp	■		misc_feature
✓ <b>gRNA Protospacer</b>	2307 .. 2326	20 bp	■		misc_feature
✓ <b>SNV</b>	2324 .. 2324	1 bp	■		misc_feature
/note	= WT = G SNV = T				

	Feature	Location	Size			Type
✓	<b>PAM</b>	2327 .. 2329	3 bp	■	H	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	25-mer	1916 .. 1940	65°C	Dec 8, 2023
/sequence = TGCCAAGCCTGTGGAGCTTTGTCTC 56% GC / 7640.0 Da				
✓ <b>Sanger Sequencing Primer</b>	20-mer	2192 .. 2211	57°C	Dec 8, 2023
/sequence = GTGAGAAAGAGAGCAGTCCC 55% GC / 6200.1 Da				
✓ <b>Donor Template WT -&gt; SNV</b>	100-mer	2289 .. 2388	76°C	Dec 8, 2023
/sequence = TTCAACTTTTCCTATACAAAATCCTCCAAGGCAAATGCTATTGTTGGCCACATCCAGGGCCAGCATCCTTAAGAGCAAGCTGATGATCTGGCTGTCACCT 46% GC / 30,630.9 Da				
✓ <b>gRNA Protospacers</b>	20-mer	2307 .. 2326	58°C	Dec 8, 2023
/sequence = CAGCTTGCTCTTAAGGAGGC 55% GC / 6133.0 Da				
✓ <b>PCR Reverse</b>	25-mer	2867 .. 2891	55°C	Dec 8, 2023
/sequence = ATGCCAAATAAATATGTGTGTATGC 32% GC / 7704.1 Da				