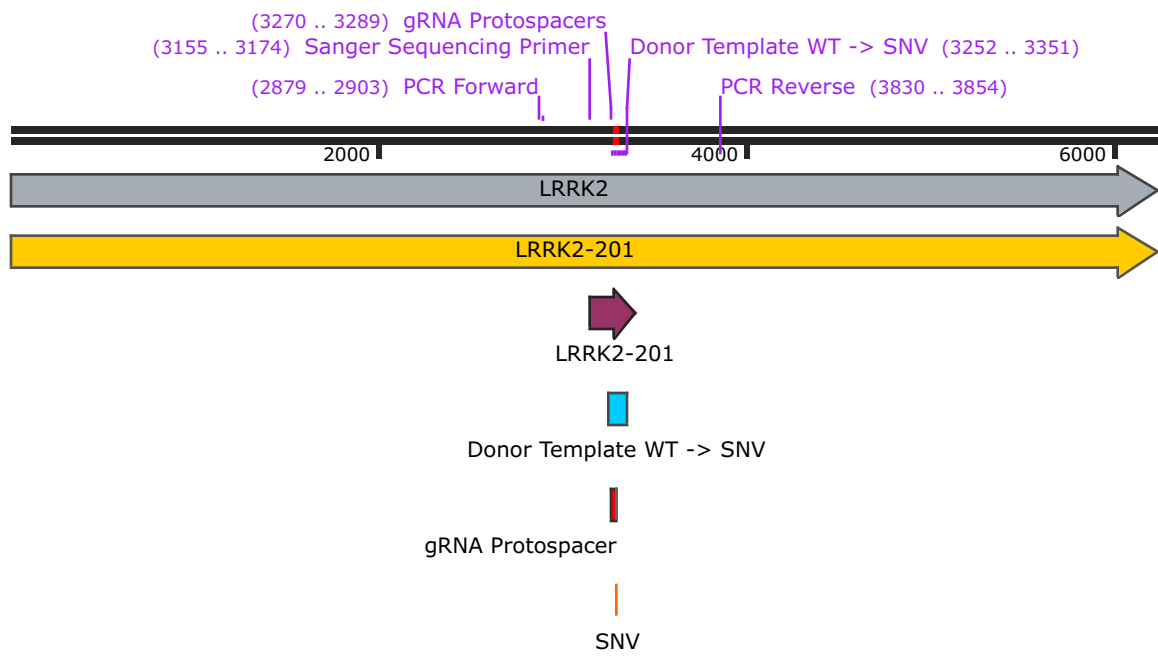
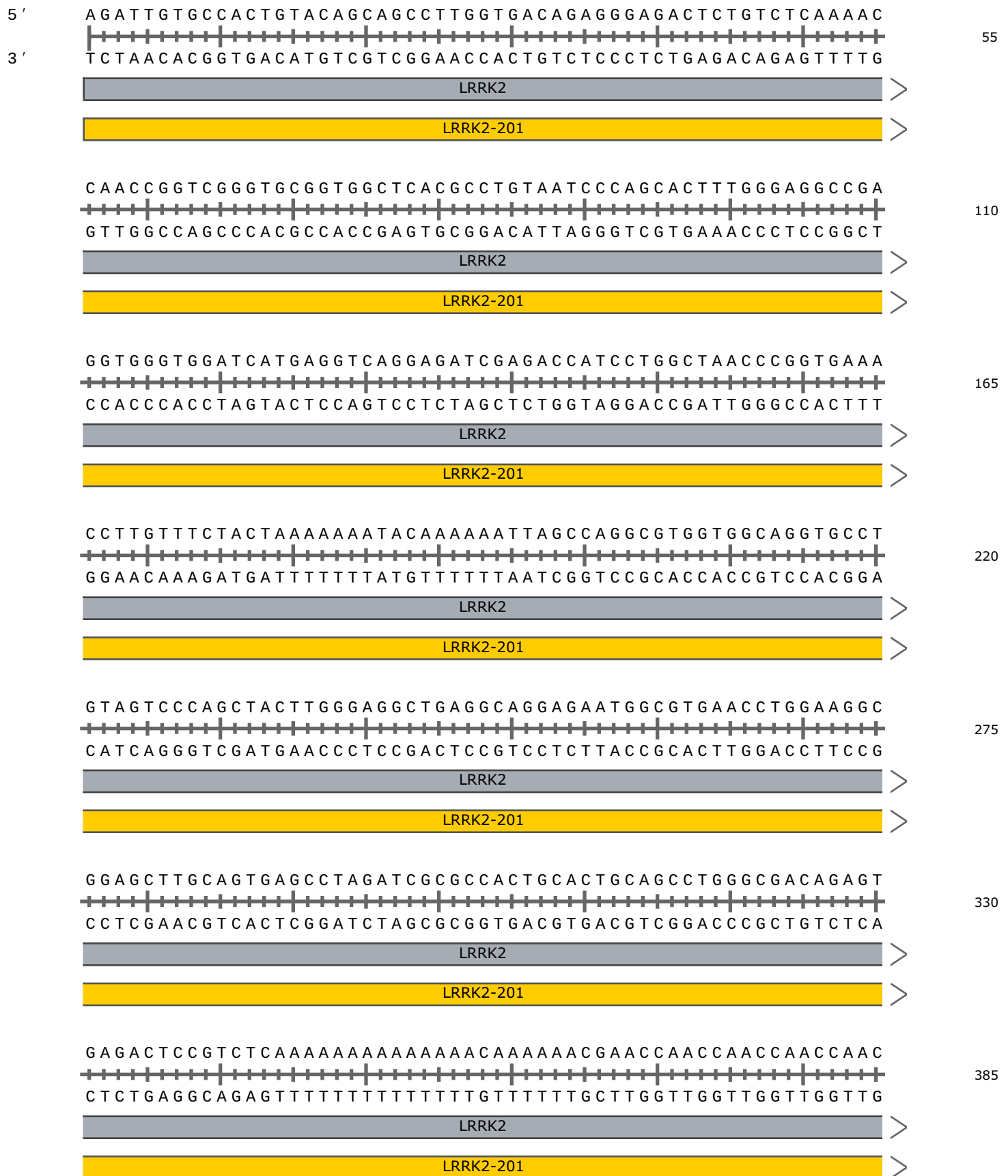


leucine rich repeat kinase 2 [Source:HGNC Symbol;Acc:HGNC:18618]



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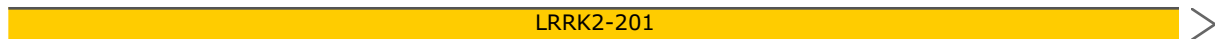
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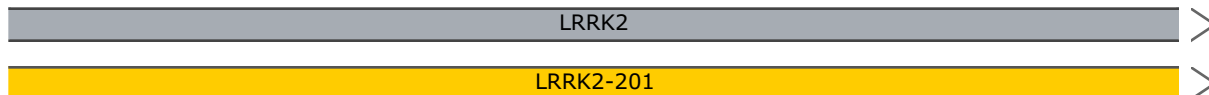


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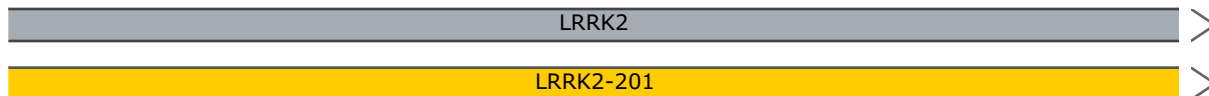
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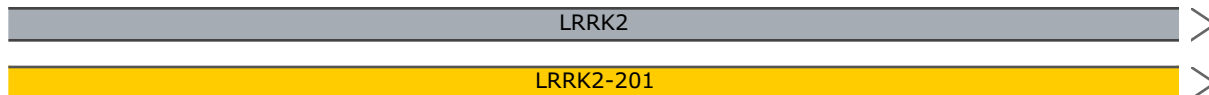
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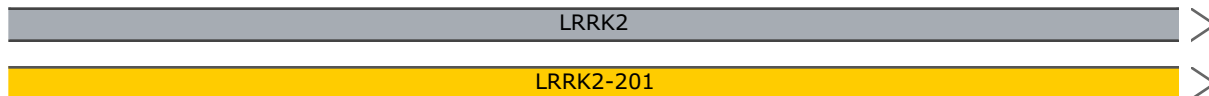
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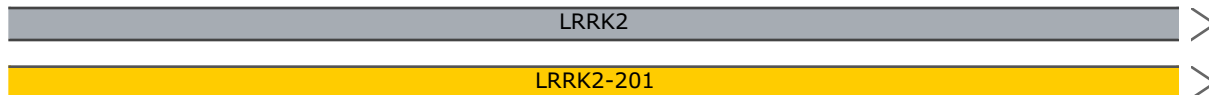
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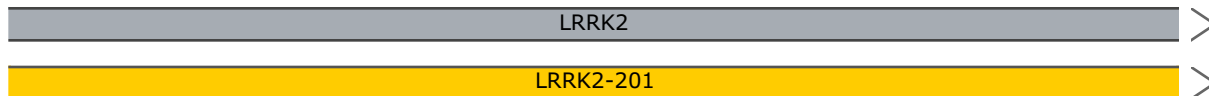
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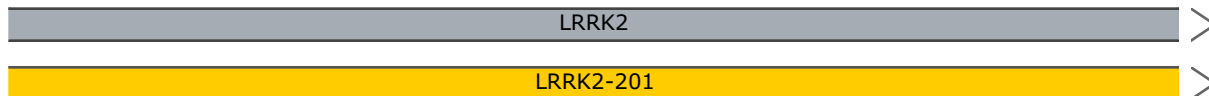
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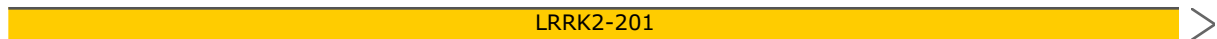
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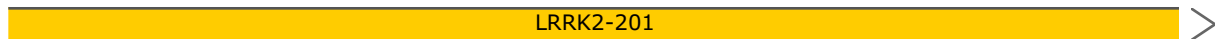
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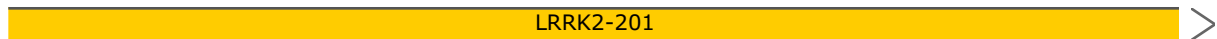
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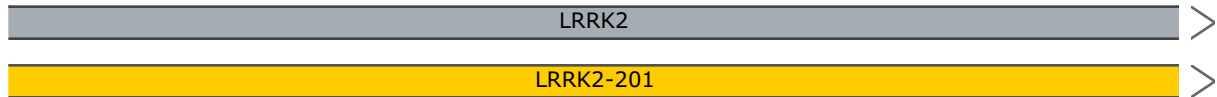


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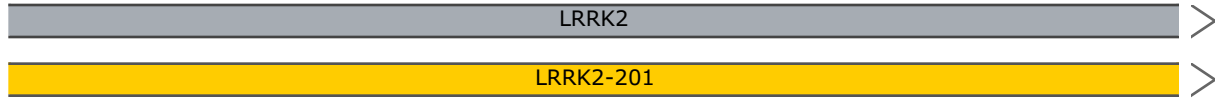
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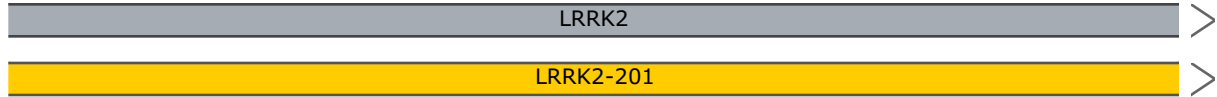
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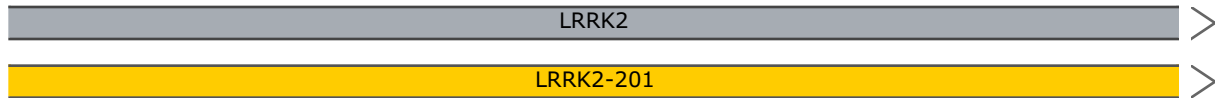


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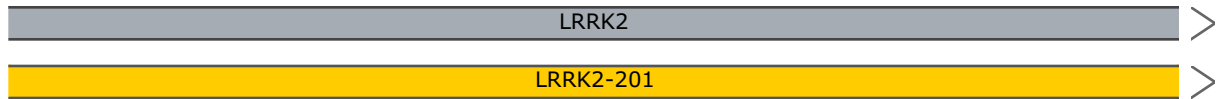


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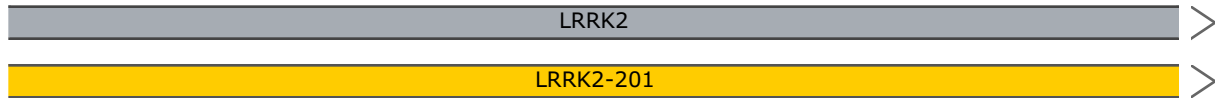
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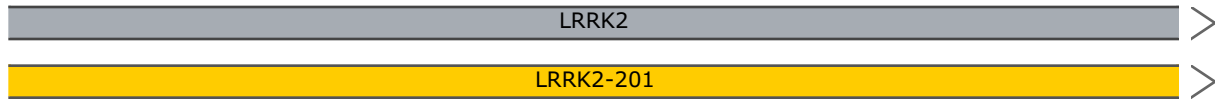
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LRRK2-201

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3190

LRRK2

LRRK2-201

V C E K E S S P K L V E L

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ENSE00001365419

LRRK2-201

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LRRK2

LRRK2-201

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LRRK2-201

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3300

LRRK2

LRRK2-201

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ENSE00001365419

LRRK2-201

Donor Template WT -> SNV

gRNA Protospacer PAM

SNV

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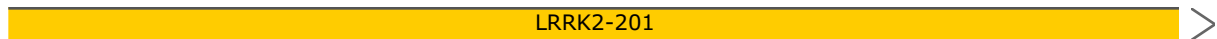
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 ENSE00001365419
 LRRK2-201

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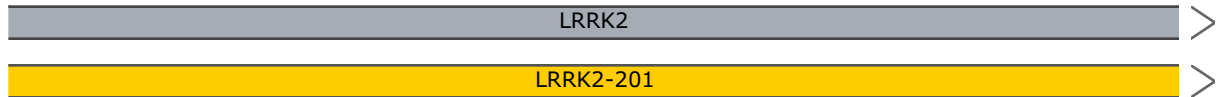
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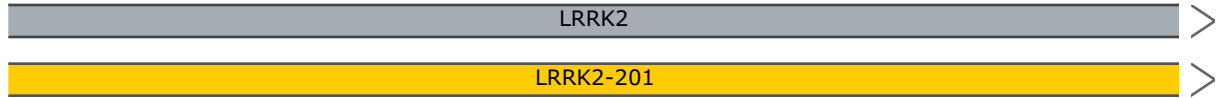
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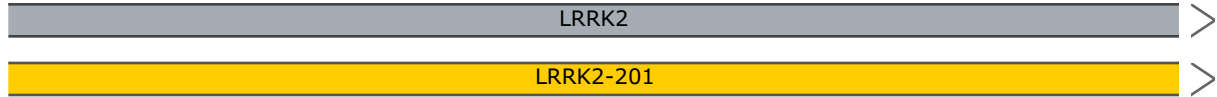
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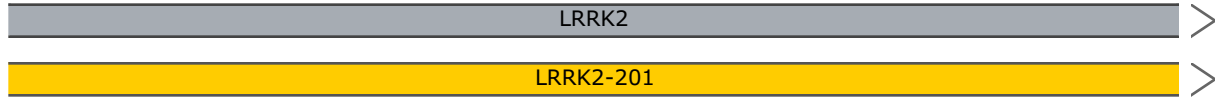
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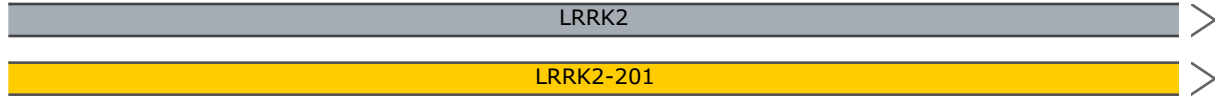
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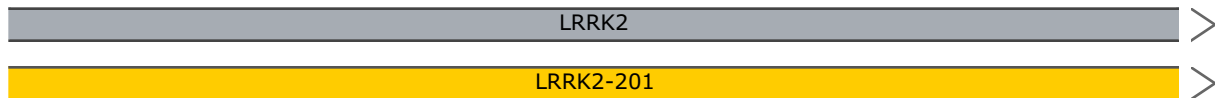


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CGTA

PCR Reverse

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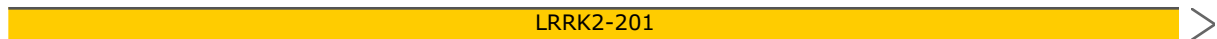
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5115



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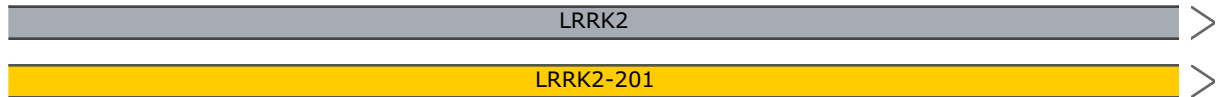
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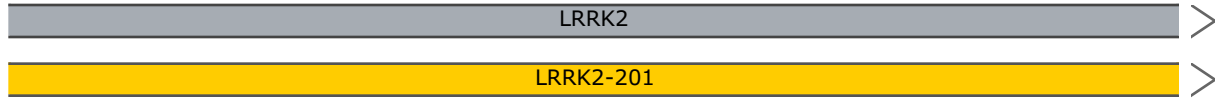
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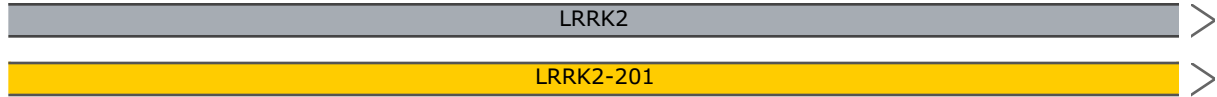
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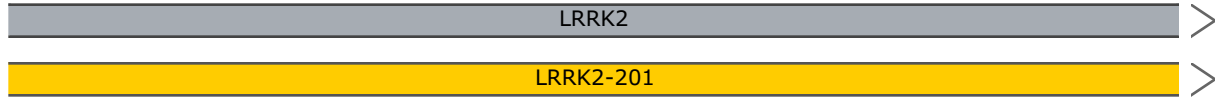
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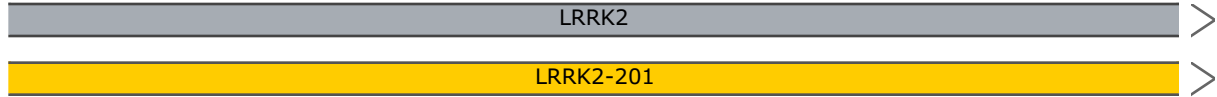
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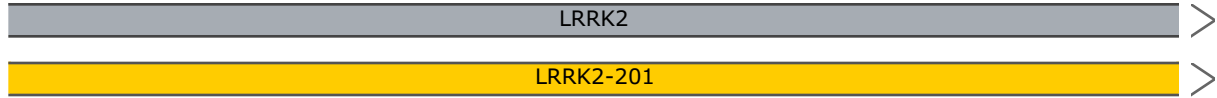
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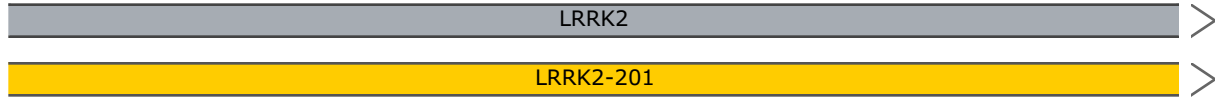
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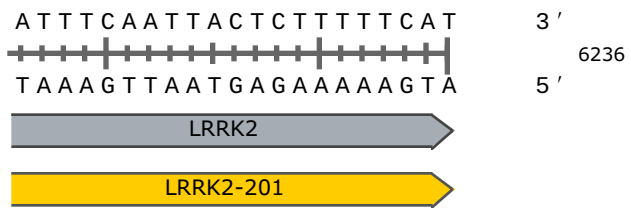


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CTTTATTTAGCAGTTTATGTGTTCTATGCATTGTGCTAAACATTTTATATGCATC 6215
 GAAATAAATCGTCAAATACACAAGATACGTAACACGATTTGTAAAATATACGTAG





Feature	Location	Size	Start	End	Type
LINC02471	1 .. 6236	6236 bp	■	→	gene
/note	= gene ENSG00000223914 lncRNA				
✓ LRRK2	1 .. 6236	6236 bp	■	→	gene
/note	= gene ENSG00000188906 Protein coding				
LINC02471-202	1 .. 6236	6236 bp	■	→	prim_transcript
/note	= primary transcript ENST00000641941 lncRNA				
✓ LRRK2-201	1 .. 6236	6236 bp	■	→	prim_transcript
/note	= primary transcript ENST00000298910				
LRRK2-202	1 .. 6236	6236 bp	■	→	prim_transcript
/note	= primary transcript ENST00000343742				
LRRK2-210	1 .. 6236	6236 bp	■	→	prim_transcript
/note	= primary transcript ENST00000679360 Nonsense mediated decay				
LRRK2-218	1 .. 6236	6236 bp	■	→	prim_transcript
/note	= primary transcript ENST00000680790				
LRRK2-203	1 .. 3228	3228 bp	■	→	prim_transcript
/note	= primary transcript ENST00000416796				
✓ LRRK2-201	3151 .. 3409	259 bp	■	→	CDS
/note	= coding sequence ENSP00000298910				
/translation	= VCEKESP K LV L LLNSGSRE Q DVRKAL T ISIGK G DSQIIS L LLRRLALDVANNSICLGGFCIGKVEPSWLGPLFPDKTSNLRKQT 86 amino acids = 9.4 kDa				
LRRK2-202	3151 .. 3409	259 bp	■	→	CDS
/note	= coding sequence ENSP00000341930				
/translation	= VCEKESP K LV L LLNSGSRE Q DVRKAL T ISIGK G DSQIIS L LLRRLALDVANNSICLGGFCIGKVEPSWLGPLFPDKTSNLRKQT 86 amino acids = 9.4 kDa				
LRRK2-218	3151 .. 3409	259 bp	■	→	CDS
/note	= coding sequence ENSP00000505335				
/translation	= VCEKESP K LV L LLNSGSRE Q DVRKAL T ISIGK G DSQIIS L LLRRLALDVANNSICLGGFCIGKVEPSWLGPLFPDKTSNLRKQT 86 amino acids = 9.4 kDa				
LRRK2-203	3151 .. 3228	78 bp	■	→	CDS
/note	= coding sequence ENSP00000398726				
/translation	= VCEKESP K LV L LLNSGSRE Q DVRK 26 amino acids = 2.9 kDa				
✓ Donor Template WT -> SNV	3252 .. 3351	100 bp	■		misc_feature
✓ gRNA Protospacer	3270 .. 3289	20 bp	■		misc_feature
✓ SNV	3287 .. 3287	1 bp	■		misc_feature
/note	= WT = G SNV = T				

Feature	Location	Size	Color	Icon	Type
✓ PAM	3290 .. 3292	3 bp	Yellow	⏏	misc_feature
	5565 .. 5938	374 bp	Grey	⏏	gene
/note = gene ENSG00000229899 processed_pseudogene					
	5565 .. 5938	374 bp	Grey	⏏	prim_transcript
/note = primary transcript ENST00000434995 processed_pseudogene					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	2879 .. 2903	65°C	Dec 8, 2023
/sequence = TGCCAAGCCTGTGGAGCTTTGTCTC 56% GC / 7640.0 Da				
✓ Sanger Sequencing Primer	20-mer	3155 .. 3174	57°C	Dec 8, 2023
/sequence = GTGAGAAAGAGAGCAGTCCC 55% GC / 6200.1 Da				
✓ Donor Template WT -> SNV	100-mer	3252 .. 3351	76°C	Dec 8, 2023
/sequence = TTCAACTTTTCCTATACAAAATCCTCCAAGGCAAATGCTATTGTTGGCCACATCCAGGGCCAGCATCCTTAAGAGCAAGCTGATGATCTGGCTGTACCT 46% GC / 30,630.9 Da				
✓ gRNA Protospacers	20-mer	3270 .. 3289	58°C	Dec 8, 2023
/sequence = CAGCTTGCTCTTAAGGAGGC 55% GC / 6133.0 Da				
✓ PCR Reverse	25-mer	3830 .. 3854	55°C	Dec 8, 2023
/sequence = ATGCCAAATAAATATGTGTGTATGC 32% GC / 7704.1 Da				