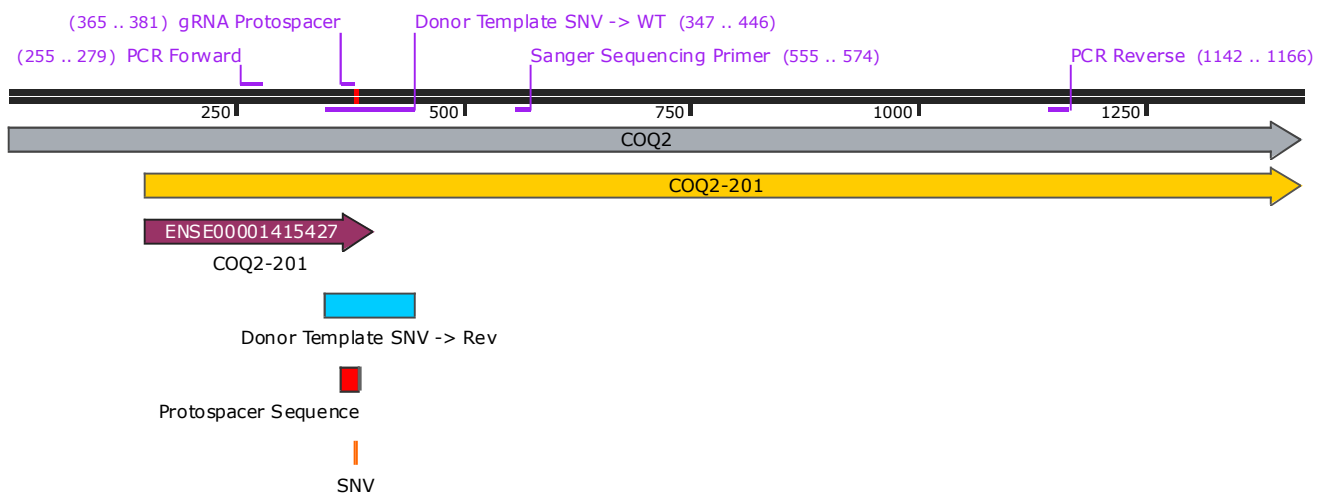


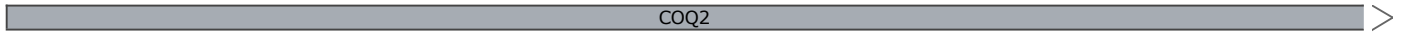
coenzyme Q2, polyprenyltransferase [Source:HGNC Symbol;Acc:HGNC:25223]



INK2J00046R_COQ2_M128V_E02_AA
1419 bp

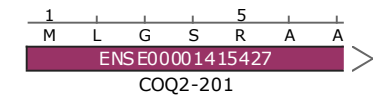
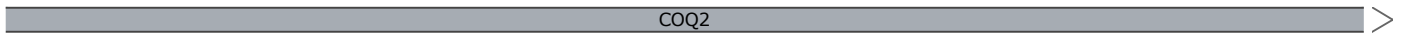
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 3' TACTGGGGTTAAAGTGTTTCATTCCTACTCCTTTCCAAGACGGGTGTGGCGGCGGGTCTGGACCGTCTGATCCTAACGTAGGACGCC

85



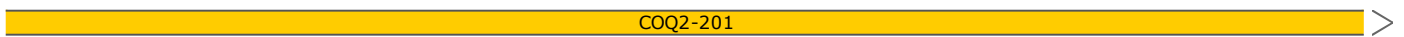
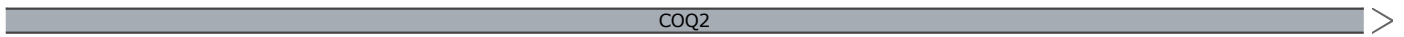
GTGCCACTGCGCATGCCTGCCGGGGAATGACGTCAATCCGAGCTCGTCCCGGCCTCACCAGCGCCATGCTGGGCTCGCGAGCCGC
 CACGGTGACGCGTACGGACGGCCCTTACTGCAGTTAGGCTCGAGCAGGGCCGGAGTGGTTCGCGGTACGACCCGAGCGCTCGGCG

170



GGGGTTCGCGCGGGGCTGCCGGGCTGTGGCACTGGCGTGGCTGCCGGGCTGGCGGGGCCGCTCCTTCGCCCTGGCGCGTGGCGCA
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255



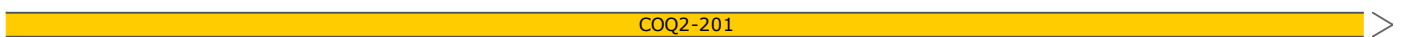
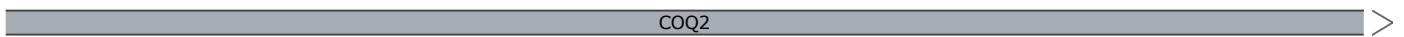
G F A R G L R A V A L A W L P G W R G R S F A L A R A A
 ENSE00001415427
 COQ2-201

PCR Forward

A

GGCGCGCCCCACGGTGGTGACTTG
 GGCGCGCCCCACGGTGGTGACTTGCAGCCCCCGCCTGTCCCGAGCCGCGGGGCGCCAGCTCAGTTTGTCCGCGGGCGGGTGG
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340

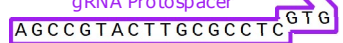


G A P H G G D L Q P P A C P E P R G R Q L S L S A A A V
 ENSE00001415427
 COQ2-201

PCR Forward

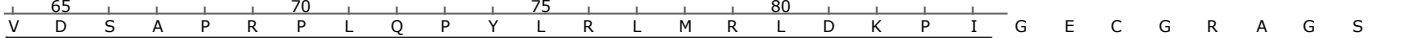
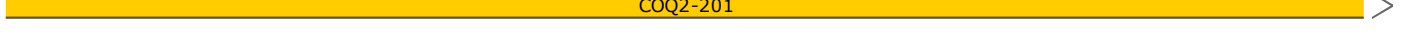


gRNA Protospacer



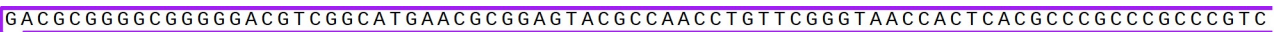
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 ACCTGAGACGCGGGGCGGGGACGTGGCATGAACGCGGAGTACGCCAACCTGTTTCGGGTAACCACTCACGCCCGCCCCGCCCGT

425



V D S A P R P L Q P Y L R L M R L D K P I G E C G R A G S
 ENSE00001415427
 COQ2-201

(in frame with COQ2-201)



Donor Template SNV -> WT

C C C G G G A A T T T G C A A G T A G C A G C C T C C G A G T C G G G T C C G C G G A G C T G T C C G C G G C G G C C G G C C G G G G C G T G A T G G A A A T G A G A A C
 510
 G G G C C C T T A A A C G T T C A T C G T C G G A G G C T C A G C C G A G G C G C C T C G A C A G G C G C C G C C G G C C G G C C C C G C A C T A C T T T A C T C T T G
 COQ2
 COQ2-201

P G I C K *
 - (in frame with COQ2-201) ▶

Donor Template SNV -> Rev
 G G G C C C T T A A A C G T T C A T C G T
 Donor Template SNV -> WT

C T G A A A G C T T G G G C T T G G C T G C C G G G T G C C G T G C G C C C T G G G G C G A A T C A C C T C G G G A C A C T T T G A A A T G A G A G C C T G A A A G C T T
 595
 G A C T T T C G A A C C C G A A C C G A C G G C C C A C G G C A C G C G G G A C C C C G C T T A G T G G A G C C C T G T G A A A C T T T A C T C T C G G A C T T T C G A A
 COQ2
 COQ2-201

CTTAGTGGAGCCCTGTGAAA
 Sanger Sequencing Primer

G A G C T T G G C T G C C G G C T G C C G T G C G C C C T G G G G C G A G T C A C C T C A G G A C A C G C A G T C G G G A C A G T C T C C T A A A G G A C C C G C C A G T
 680
 C T C G A A C C G A C G G C C G A C G G C A C G C G G G A C C C C G C T C A G T G G A G T C C T G T G C G T C A G C C C T G T C A G A G G A T T T C C T G G G C G G T C A
 COQ2
 COQ2-201

T T C A C G T C T G T C T G C A T C C T G A G C A C C T G A A G C G G G C A A G A T A A T T C T C A T T C C A C A A A C A C T T G T T T A A A T G G T G A C T C A A G C G
 765
 A A G T G C A G A C A G A C G T A G G A C T C G T G G A C T T C G C C C G T T C A T T A A G A G T A A G G T G T T T G T G A A C A A A T T T A C C A C T G A G T T C G C
 COQ2
 COQ2-201

G A A G G T T C C G T T C T C G T G G C C C T C T T C A T T T A T T A G A A T G T T T G A T C C T C C C C G C A A T C T T G T A A G G C C C A C A A A G A C A A T C C T
 850
 C T T C C A A G G C A A G A G C A C C G G G A G G A A G T A A A T A A T C T T A C A A A C T A G G A G G G G C G T T A G A A C A T T C C G G G T G T T T C T G T T A G G A
 COQ2
 COQ2-201

T A A G A C A G T T A A G A C G C T G A G G A A A C T A A G G C T C C T C G T C A G A G C C A G A C C A G A A G A A C T C T G T G T T T T G A T G C T G A G T C G G A G C
 935
 A T T C T G T C A A T T C T G C G A C T C C T T T G A T T C C G A G G A G C A G T C T C G G T C T G G T C T T C T T G A G A C A C A A A A C T A C G A C T C A G C C T C G
 COQ2
 COQ2-201

T C T T T T A C C T G C A T C A C C C A T A A G G C A A A G A T T T A A T T C A T T T G A A C G C A G C A G G G A C A G C G C T T A C G G A C T G C C T G T C A G C T T A
 1020
 A G A A A T G G A C G T A G T G G G T A T T C C G T T T C T A A A T T A A G T A A A C T T G C G T C G T C C C T G T C G C G A A T G C C T G A C G G A C A G T C G A A T
 COQ2
 COQ2-201

C A A T C G C C C C C G A C A G A A A G A T T T T C C T G A C C T T C C T A T C T T A A T T A A C A C C T A C C A A C C T C A C T T T C T A T C G C T T T A T C C G C A A
 1105
 G T T A G C G G G G C T G T C T T T C T A A A A G G A C T G G A A G G A T A G A A T T A A T T G T G G A T G G T T G G A G T G A A A G A T A G C G A A A T A G G C G T T
 COQ2
 COQ2-201

TTTTTCTTAATAGCACTCACCCTAACTAACCTTATGCGCTTGTTGATTGATTGGCTTCTCCAGTAGTGTTAAGTGAATTAATAA 1190
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 AAAAAAGAATTATCGTGAGTGGTGATTGATTGGAATACGCGAACAACCTAACTAACC GAAGAGGTCATCACAATTCACTTAATTATT
 COQ2 >
 COQ2-201 >

CGCGAACAACCTAACTAACC GAAGAG
 PCR Reverse

GTTCC TACTACGTTGTCCGGCCATAGAGATAGAAAAAGCTATGGAAACCTTTGCTTTCAAGGAACTCTGGTCTAGTTGAAAAAG 1275
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 CAAGGATGATGCAACAGGCCGGTATCTCTATCTTTTTCGATACCTTTGGGAAACGAAAGTTCTTGAGACCAGATCAACTTTTTTC
 COQ2 >
 COQ2-201 >

ACTATTTGGTGAGCTAGGAAAATATGGATCAAATATGAGTGATACAAAAGCAAGTGCTACAGGAAAAAGAGAAATTACTGTGGAT 1360
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TGATAAACCACTCGATCCTTTTATACCTAGTTTATACTCACTATGTTTTCGTTACAGATGTCCTTTTTCTCTTTAATGACACCTA
 COQ2 >
 COQ2-201 >

CCCTTGCTGGAAAGTTTCGAGAAGAAATTATACTCAAAGGACAAGTTGATTTTGCAGA 3'
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1419
 GGGAACGACCTTTCAAAGCTCTTCTTTAATATGAGGTTTCCTGTTCAACTAAAACGTCT 5'
 COQ2 >
 COQ2-201 >

Feature	Location	Size	Start	End	Type
✓ COQ2	1 .. 1419	1419 bp	■	➔	gene
/note = gene ENSG00000173085 Protein coding					
COQ2-202	1 .. 1419	1419 bp	■	➔	prim_transcript
/note = primary transcript ENST00000311469					
COQ2-202	1 .. 403	403 bp	■	➔	CDS
/note = coding sequence ENSP00000310873 /translation = MTPISQVRMRKGSHTAAQPGRGLGLHPAGATAHACRGMTSIRARPGLTSAAMLGSRAGFARGLRAVALAWLPGWRGRSFALARAAGAPHGGDLQPPACPEPRGRQLSLSAAAV VDSAPRPLQPYLRLMRDKPI 134 amino acids = 14.0 kDa					
COQ2-206	117 .. 1419	1303 bp	■	➔	prim_transcript
/note = primary transcript ENST00000647002					
COQ2-203	120 .. 1419	1300 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503391 Nonsense mediated decay					
✓ COQ2-201	150 .. 1419	1270 bp	■	➔	prim_transcript
/note = primary transcript ENST00000311461					
✓ COQ2-201	151 .. 403	253 bp	■	➔	CDS
/note = coding sequence ENSP00000311835 /translation = MLGSRAAGFARGLRAVALAWLPGWRGRSFALARAAGAPHGGDLQPPACPEPRGRQLSLSAAAVVDSAPRPLQPYLRLMRDKPI 84 amino acids = 8.9 kDa					
COQ2-206	151 .. 403	253 bp	■	➔	CDS
/note = coding sequence ENSP00000495761 /translation = MLGSRAAGFARGLRAVALAWLPGWRGRSFALARAAGAPHGGDLQPPACPEPRGRQLSLSAAAVVDSAPRPLQPYLRLMRDKPI 84 amino acids = 8.9 kDa					
✓ Donor Template SNV -> Rev	347 .. 446	100 bp	■	⌊	misc_feature
✓ Protospacer Sequence	365 .. 384	20 bp	■	⌊	misc_feature
✓ SNV	382 .. 382	1 bp	■	⌊	misc_feature
/note = SNV = G REV = A					
✓ PAM	385 .. 387	3 bp	■	⌊	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = AGGCGCGCCCCACGGTGGTACTTG 72% GC / 7700.0 Da	25-mer	255 .. 279	73°C	Feb 27, 2024
✓ Donor Template SNV -> WT /sequence = TGCTACTTGCAAATTCCTGGGCTGCCCGCCCGCCGCACTCACCAATGGGCTTGTCCAACCGCATGAGGCGCAAGTACGGCTGCAGGGGGCGGGGCGCAG 68% GC / 30,810.8 Da	100-mer	347 .. 446	87°C	Feb 27, 2024
✓ gRNA Protospacer /sequence = AGCCGTACTTGCGCCTCGTG 65% GC / 6085.0 Da	20-mer	365 .. 381	60°C	Feb 27, 2024
✓ Sanger Sequencing Primer /sequence = AAAGTGTCCTCCGAGGTGATTC 50% GC / 6157.1 Da	20-mer	555 .. 574	56°C	Feb 27, 2024
✓ PCR Reverse /sequence = GAGAAGCCAATCAATCAACAAGCGC 48% GC / 7662.1 Da	25-mer	1142 .. 1166	61°C	Feb 27, 2024