Sequence: INK2T00138_MAPT_R406W_C01_BB.dna (Linear / 1074 bp)
Features: 45 total
Primers: 5 total

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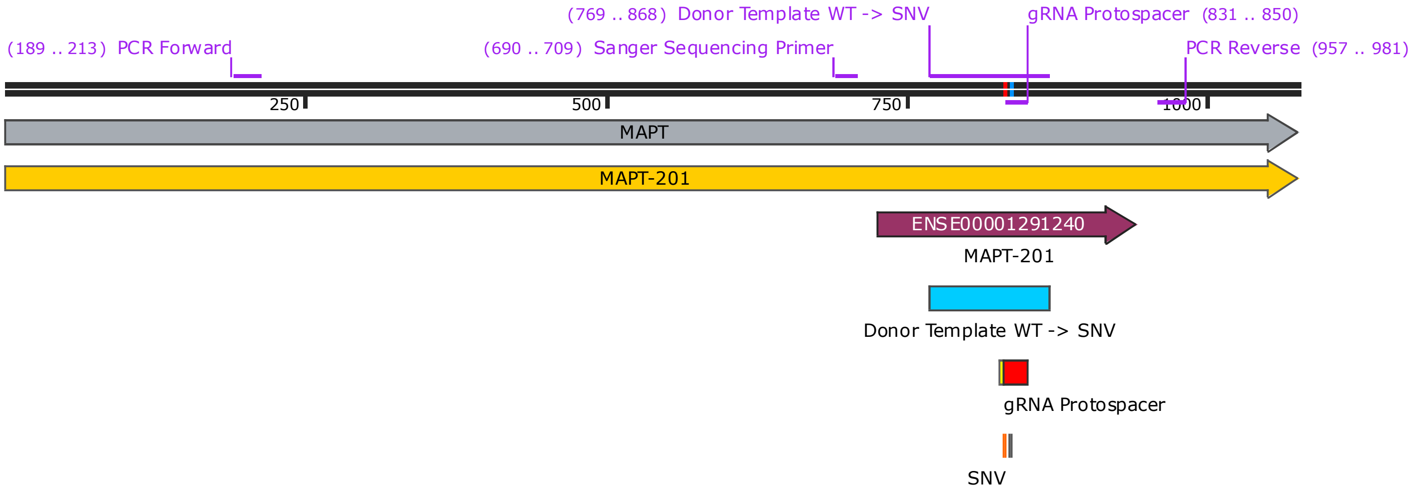
microtubule associated protein tau [Source:HGNC Symbol;Acc:HGNC:6893]



INK2T00138_MAPT_R406W_C01_BB
1074 bp

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5'  TGTGACATGATGTTCATACGGGTTTATTTATCTGAGGTTGTTCATACACACCATTGCCTGTAATCACTAAAGGCGGGAGCAGCCT
                                                                                             85
3'  ACACTGTACTACAAGTATGCCCAAATAAATAGACTCCAACAAGTATGTGTGGTAACGGACATTAGTGATTTCCGCCCTCGTCGGA
    MAPT >
    MAPT-201 >

    ACACATCCATCCACAGAGGAGTAGATGCCTTTTGGTACATCCGTGGCGACGGAATACTAAGCAGCCTGTGTATCTATACACTCAC
                                                                                             170
    TGTGTAGGTAGGTGTCTCCTCATCTACGGAAAACCATGTAGGCACCGCTGCCTTATGATTCGTCGGACACATAGATATGTGAGTG
    MAPT >
    MAPT-201 >

                      PCR Forward
                      ggaatatctctggagggtacacaag
    ACGTGTTTGTTTATGTGTGGAATATCTCTGGAGGGTACACAAGAAACTTAAAATGATCACTGTCTCTGGGGAGGGTACCTGGGTG
                                                                                             255
    TGCACAAACAAATACACACCTTATAGAGACCTCCCATGTGTTCTTTGAATTTTACTAGTGACAGAGACCCCTCCCATGGACCCAC
    MAPT >
    MAPT-201 >

    CCTGGGAGGCAGGTCAGGGAAGGAGTGGGCACAGGTATTACCAATTGGAAGACAATAAAAACAACAGCTCCTGGCCAGGCGCAGT
                                                                                             340
    GGACCCTCCGTCCAGTCCCTTCCTCACCCGTGTCCATAATGGTTAACCTTCTGTTATTTTTGTTGTCGAGGACCGGTCCGCGTCA
    MAPT >
    MAPT-201 >

    GGCTCACGCCTGTAATGGCAGCACTCTGAGAGGCTGAGGCGGGCAGATTGCTTGCGTCCAGGAGTTCAAGACCAGCCTGGGCAAC
                                                                                             425
    CCGAGTGCGGACATTACCGTCGTGAGACTCTCCGACTCCGCCCGTCTAACGAACGCAGGTCCTCAAGTTCTGGTCGGACCCGTTG
    MAPT >
    MAPT-201 >

    ATAGCAAAACCCCGTTTCTATTAAAAATACAAAAAATTAGCCAGGTGTGGTGGCATGCACCTGTAATCCCAGCTACTCGGGAGGC
                                                                                             510
    TATCGTTTTGGGGCAAAGATAATTTTTATGTTTTTTAATCGGTCCACACCACCGTACGTGGACATTAGGGTCGATGAGCCCTCCG
    MAPT >
    MAPT-201 >

    TGAGGTGGGAGAATCACCTGAGCCTGGGAGGTCAAGGCTGCAGTGAGGTGAGATTGTGCCACCGCACTCTAGCCTGGGCGATAGA
                                                                                             595
    ACTCCACCCTCTTAGTGGACTCGGACCCTCCAGTTCCGACGTCACTCCACTCTAACACGGTGGCGTGAGATCGGACCCGCTATCT
    MAPT >
    MAPT-201 >

    GCAAGACCCTGTCTCAAAAACAAACAAAAAACAGTCCCTGGCACTCTGGGCCAGGCCTGGCAGGGCAGTTGGCAGGGCTGGTCTT
                                                                                             680
    CGTTCTGGGACAGAGTTTTTGTTTGTTTTTTGTCAGGGACCGTGAGACCCGGTCCGGACCGTCCCGTCAACCGTCCCGACCAGAA
    MAPT >
    MAPT-201 >
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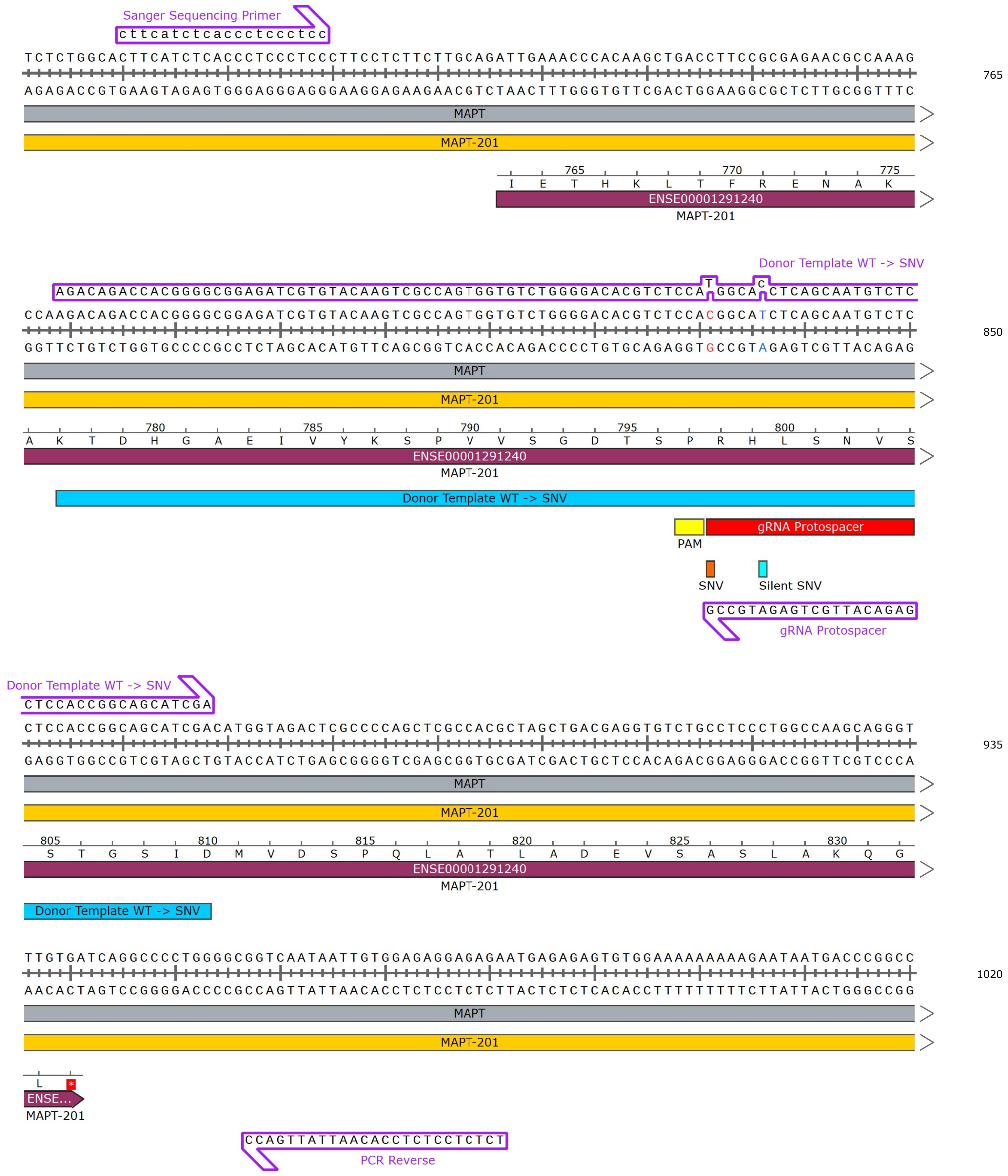
Sanger Sequencing Primer
cttcatctcaccctccctcc
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AGAGACCGTGAAGTAGAGTGGGAGGGAGGGAAGGAGAAGAACGTCTAACTTTGGGTGTTCGACTGGAAGGCGCTCTTGCGGTTTC
765
MAPT
MAPT-201
765
770
775
I E T H K L T F R E N A K
ENSE00001291240
MAPT-201
Donor Template WT -> SNV
AGACAGACCACGGGGCGGAGATCGTGTACAAGTCGCCAGTGGTGTCTGGGGACACGTCTCCA T GGCA C CTCAGCAATGTCTC
CCAAGACAGACCACGGGGCGGAGATCGTGTACAAGTCGCCAGTGGTGTCTGGGGACACGTCTCCACGGCATCTCAGCAATGTCTC
GGTTCTGTCTGGTGCCCCGCCTCTAGCACATGTTCAGCGGTCACCACAGACCCCTGTGCAGAGGTGCCGTAGAGTCGTTACAGAG
850
MAPT
MAPT-201
780
785
790
795
800
A K T D H G A E I V Y K S P V V S G D T S P R H L S N V S
ENSE00001291240
MAPT-201
Donor Template WT -> SNV
gRNA Protospacer
PAM
SNV
Silent SNV
GCCGTAGAGTCGTTACAGAG
gRNA Protospacer
Donor Template WT -> SNV
CTCCACCGGCAGCATCGA
CTCCACCGGCAGCATCGACATGGTAGACTCGCCCCAGCTCGCCACGCTAGCTGACGAGGTGTCTGCCTCCCTGGCCAAGCAGGGT
GAGGTGGCCGTCGTAGCTGTACCATCTGAGCGGGGTCGAGCGGTGCGATCGACTGCTCCACAGACGGAGGGACCGGTTCGTCCCA
935
MAPT
MAPT-201
805
810
815
820
825
830
S T G S I D M V D S P Q L A T L A D E V S A S L A K Q G
ENSE00001291240
MAPT-201
Donor Template WT -> SNV
TTGTGATCAGGCCCCTGGGGCGGTCAATAATTGTGGAGAGGAGAGAATGAGAGAGTGTGGAAAAAAAAAGAATAATGACCCGGCC
AACACTAGTCCGGGGACCCCGCCAGTTATTAACACCTCTCCTCTCTTACTCTCTCACACCTTTTTTTTTCTTATTACTGGGCCGG
1020
MAPT
MAPT-201
L *
ENSE...
MAPT-201
CCAGTTATTAACACCTCTCCTCTCT
PCR Reverse

```
CCCGCCCTCTGCCCCCAGCTGCTCCTCGCAGTTCGGTTAATTGGTTAATCACTT      3′
                                                                  1074
GGGCGGGAGACGGGGGTCGACGAGGAGCGTCAAGCCAATTAACCAATTAGTGAA      5′
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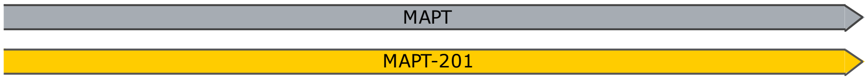

	Feature			Location	Size		⇄	Type
✓	**MAPT**			1 .. 1074	1074 bp	■	→	gene
	/note	=	gene ENSG00000186868 Protein coding					
	MAPT-AS1			1 .. 1074	1074 bp	■	←	gene
	/note	=	gene ENSG00000264589 lncRNA					
✓	**MAPT-201**			1 .. 1074	1074 bp	🟨	→	prim_transcript
	/note	=	primary transcript ENST00000262410					
	MAPT-203			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000344290					
	MAPT-204			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000351559					
	MAPT-206			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000420682					
	MAPT-208			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000446361					
	MAPT-215			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000576518 Retained intron					
	MAPT-217			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000680542 Nonsense mediated decay					
	MAPT-218			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000680674					
	MAPT-219			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703922 Nonsense mediated decay					
	MAPT-220			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703923 Nonsense mediated decay					
	MAPT-221			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703924 Nonsense mediated decay					
	MAPT-226			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703978 Nonsense mediated decay					
	MAPT-228			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703980 protein_coding_CDS_not_defined					
	MAPT-229			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703981 protein_coding_CDS_not_defined					
	MAPT-230			1 .. 1074	1074 bp	■	→	prim_transcript
	/note	=	primary transcript ENST00000703982 Retained intron					
	MAPT-AS1-201			1 .. 1074	1074 bp	■	←	prim_transcript
	/note	=	primary transcript ENST00000579244 lncRNA					
	MAPT-AS1-202			1 .. 1074	1074 bp	■	←	prim_transcript
	/note	=	primary transcript ENST00000579599 lncRNA					
	MAPT-AS1-204			1 .. 1074	1074 bp	■	←	prim_transcript
	/note	=	primary transcript ENST00000634876 lncRNA					

	Feature	Location	Size		⇄	Type
	MAPT-AS1-205	1 .. 1074	1074 bp	■	←	prim_transcript
	/note = primary transcript ENST00000649665 lncRNA					
	MAPT-AS1-206	1 .. 1074	1074 bp	■	←	prim_transcript
	/note = primary transcript ENST00000653949 lncRNA					
	MAPT-209	1 .. 995	995 bp	■	→	prim_transcript
	/note = primary transcript ENST00000535772					
	MAPT-202	1 .. 953	953 bp	■	→	prim_transcript
	/note = primary transcript ENST00000334239					
	MAPT-205	1 .. 941	941 bp	■	→	prim_transcript
	/note = primary transcript ENST00000415613					
	MAPT-207	1 .. 941	941 bp	■	→	prim_transcript
	/note = primary transcript ENST00000431008					
	MAPT-212	1 .. 941	941 bp	■	→	prim_transcript
	/note = primary transcript ENST00000571987					
	MAPT-214	1 .. 941	941 bp	■	→	prim_transcript
	/note = primary transcript ENST00000574436					
✓	**MAPT-201**	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000262410 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-202	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000334886 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-203	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000340820 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-204	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000303214 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-205	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000410838 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-206	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000413056 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-207	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000389250 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-208	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000408975 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-209	726 .. 941	216 bp	■	→	CDS
	/note = coding sequence ENSP00000443028 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					

	Feature	Location	Size		⇄	Type
	MAPT-212	726 .. 941	216 bp	🟪	→	CDS
	/note = coding sequence ENSP00000458742 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-214	726 .. 941	216 bp	🟪	→	CDS
	/note = coding sequence ENSP00000460965 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
	MAPT-218	726 .. 941	216 bp	🟪	→	CDS
	/note = coding sequence ENSP00000505478 /translation = IETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL* 71 amino acids = 7.5 kDa					
✓	**Donor Template WT -> SNV**	769 .. 868	100 bp	🟦	⊢⊣	misc_feature
✓	**PAM**	828 .. 830	3 bp	🟨	⊢⊣	misc_feature
✓	**gRNA Protospacer**	831 .. 850	20 bp	🟥	⊢⊣	misc_feature
✓	**SNV**	831 .. 831	1 bp	🟧	⊢⊣	misc_feature
	/note = WT = C SNV = T					
✓	**Silent SNV**	836 .. 836	1 bp	🟦	⊢⊣	misc_feature
	/note = WT = T Silent SNV = C					

	Primer	Length	●	Binding Sites	⇄	Tm	Date Added
✓	**PCR Forward**	25-mer		189 .. 213	→	59°C	Mar 15, 2024
	/sequence = ggaatatctctggagggtacacaag 48% GC / 7755.1 Da						
✓	**Sanger Sequencing Primer**	20-mer		690 .. 709	→	57°C	Mar 15, 2024
	/sequence = cttcatctcaccctccctcc 60% GC / 5859.8 Da						
✓	**Donor Template WT -> SNV**	100-mer		769 .. 868	→	81°C	Mar 15, 2024
	/sequence = AGACAGACCACGGGGCGGAGATCGTGTACAAGTCGCCAGTGGTGTCTGGGGACACGTCTCCATGGCAcCTCAGCAATGTCTCCTCCACCGGCAGCATCGA 61% GC / 30,840.9 Da						
✓	**gRNA Protospacer**	20-mer		831 .. 850	←	58°C	Mar 15, 2024
	/sequence = GAGACATTGCTGAGATGCCG 55% GC / 6182.1 Da						
✓	**PCR Reverse**	25-mer		957 .. 981	←	57°C	Mar 15, 2024
	/sequence = TCTCTCCTCTCCACAATTATTGACC 44% GC / 7462.9 Da						