

pcDNA4/HisMax-tFoxP2



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			tFoxP2																																	
			PvuII																																	
+3	Glu	Val	Ser	Thr	Val	Glu	Leu	Leu	His	Leu	Gln	Gln	Gln	Gln	Ala	Leu	Gln	Ala	Ala	Arg	Gln	Leu	Leu	Gln	Gln	Gln	Thr	Ser	Gly	Leu	Lys	Ser	Pro			
1101	GAAGTAAGCA	CAGTAGAACT	GCTGCATCTG	CAACAACAGC	AGGCACTCCA	GGCAGCAAGG	CAGCTGCTTT	TACAGCAACA	GACAAGTGGA	CTGAAATCTC																										
			tFoxP2																																	
			PstI																																	
+3	Pro	Lys	Gly	Ser	Glu	Lys	Gln	Arg	Pro	Leu	Gln	Val	Pro	Val	Ser	Val	Ala	Met	Met	Thr	Pro	Gln	Val	Ile	Thr	Pro	Gln	Gln	Met	Gln	Gln	Ile	Leu	Gln		
1201	CTAAGGGCAG	TGAGAAACAG	AGACCGCTGC	AGGTGCCTGT	GTCAGTGGCC	ATGATGACTC	CCCAGGTGAT	CACCCCTCAG	CAAATGCAGC	AGATTCTCCA																										
			tFoxP2																																	
+3	Gln	Gln	Gln	Val	Leu	Ser	Pro	Gln	Gln	Leu	Gln	Ala	Leu	Leu	Gln	Gln	Gln	Gln	Ala	Val	Met	Leu	Gln	Gln	Gln	Gln	Gln	Leu	Gln	Glu	Phe	Tyr	Lys	Lys	Gln	
1301	GCAGCAAGTG	TTGTCTCCGC	AGCAGCTTCA	AGCACTTCTC	CAGCAGCAGC	AAGCAGTTAT	GTTGCAGCAG	CAACAACACTAC	AAGAGTTTTTA	CAAGAAACAG																										
			tFoxP2																																	
+3	Gln	Glu	Gln	Leu	His	Leu	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
1401	CAAGAGCAGT	TACATCTTCA	GCTTTTGCAG	CAGCAGCAGC	AACAGCAGCA	GCAACAGCAA	CAACAGCAGC	AACAACAGCA	ACAACAGCAG	CAGCAGCAAC																										
			tFoxP2																																	
+3	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His	Pro	Gly	Lys	Gln	Ala	Lys	Glu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Leu	Ala	Ala	Gln
1501	AACAACAACA	GCAGCAGCAG	CAACAGCAAC	AGCAGCAACA	GCATCCAGGA	AAGCAAGCAA	AAGAGCAACA	GCAGCAGCAG	CAGCAGCAGT	TGGCAGCCCA																										
			tFoxP2																																	
			MscI																																	
+3	Gln	Gln	Leu	Val	Phe	Gln	Gln	Gln	Leu	Leu	Gln	Met	Gln	Gln	Leu	Gln	Gln	Gln	Gln	His	Leu	Leu	Asn	Leu	Gln	Arg	Gln	Gly	Leu	Ile	Ser	Ile	Pro	Pro		
1601	GCAGCTTGTC	TTCCAGCAGC	AGCTCCTCCA	GATGCAACAA	CTTCAGCAGC	AGCAACATCT	GCTGAACCTT	CAGCGTCAGG	GACTCATTTT	CATCCCACCT																										
			tFoxP2																																	
			MscI																																	
+3	Gly	Gln	Ser	Ala	Leu	Pro	Val	Gln	Ser	Leu	Pro	Gln	Ala	Gly	Leu	Ser	Pro	Ala	Glu	Ile	Gln	Gln	Leu	Trp	Lys	Glu	Val	Thr	Gly	Val	His	Ser	Met	Glu		
1701	GGCCAATCTG	CTCTTCCTGT	CCAGTCTCTG	CCACAAGCTG	GCTTAAGTCC	TGCTGAGATT	CAGCAGTTAT	GGAAAGAAGT	GACTGGAGTT	CACAGTATGG																										
			tFoxP2																																	
+3	Glu	Asp	Asn	Gly	Ile	Lys	His	Gly	Gly	Leu	Asp	Leu	Thr	Thr	Asn	Asn	Ser	Ser	Ser	Thr	Thr	Ser	Ser	Thr	Thr	Ser	Lys	Ala	Ser	Pro	Pro	Ile	Thr	His		
1801	AAGACAATGG	CATTAAACAT	GGAGGGCTAG	ACCTCACTAC	TAACAATTCC	TCCTCTACTA	CCTCCTCCAC	CACTTCCAAA	GCATCACCAC	CAATAACTCA																										
			tFoxP2																																	
+3	His	His	Ser	Ile	Val	Asn	Gly	Gln	Ser	Ser	Val	Leu	Asn	Ala	Arg	Arg	Asp	Ser	Ser	Ser	His	Glu	Glu	Thr	Gly	Ala	Ser	His	Thr	Leu	Tyr	Gly	His	Gly		
1901	TCATTCCATA	GTGAATGGAC	AGTCTTCAGT	TCTAAATGCA	AGGCGAGACA	GCTCGTCACA	TGAGGAGACT	GGGGCCTCCC	ATACTCTCTA	TGGTCATGGA																										

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		tFoxP2																																
+3	Val	Cys	Lys	Trp	Pro	Gly	Cys	Glu	Ser	Val	Cys	Glu	Asp	Phe	Gly	Gln	Phe	Leu	Lys	His	Leu	Asn	Asn	Glu	His	Ala	Leu	Asp	Asp	Arg	Ser	Thr	Ala	Gln
2001	GTTTGCAAAT	GGCCTGGCTG	TGAAAGCGTT	TGTGAAGATT	TTGGACAATT	TTTAAAGCAC	CTTAACAATG	AACATGCATT	GGATGACAGA	AGCACTGCTC																								
		tFoxP2																																
+3	Gln	Cys	Arg	Val	Gln	Met	Gln	Val	Val	Gln	Gln	Leu	Glu	Ile	Gln	Leu	Ser	Lys	Glu	Arg	Glu	Arg	Leu	Gln	Ala	Met	Met	Thr	His	Leu	His	Met	Arg	Pro
2101	AGTGTCGGGT	GCAAATGCAA	GTGGTTCAGC	AGTTAGAAAT	ACAGCTTTCT	AAAGAACGCG	AACGTCTTCA	AGCAATGATG	ACCACTTGC	ACATGCGACC																								
		tFoxP2																																
+3	Pro	Ser	Glu	Pro	Lys	Pro	Ser	Pro	Lys	Pro	Val	Ser	Ala	Tyr	Cys	Phe	Ile	Asn	Ser	Lys	***													
2201	CTCGGAGCCC	AAGCCATCTC	CAAAACCTGT	AAGTGCATAT	TGCTTTATAA	ACAGTAAATA	GGTCTACGAA	GGGCTGTAC	CTAGGATCCA	GTGTGGTGGA																								
		3'-T overhang																																
2301	ATTCTGCAGA	TATCCAGCAC	AGTGGCGGCC	GCTCGAGTCT	AGAGGGCCCG	TTTAAACCCG	CTGATCAGCC	TCGACTGTGC	CTTCTAGTTG	CCAGCCATCT																								
2401	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA																								
2501	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGC																								
2601	TTCTGAGGCG	GAAAGAACCA	GCTGGGGGCTC	TAGGGGGTAT	CCCCACGCGC	CCTGTAGCGG	CGCATTAAGC	GCGGCGGGTG	TGGTGGTTAC	GCGCAGCGTG																								
2701	ACCGCTACAC	TTGCCAGCGC	CCTAGCGCCC	GCTCCTTTTCG	CTTTCTTTCC	TTCTTTTCTC	GCCACGTTTCG	CCGGCTTTCC	CCGTCAAGCT	CTAAATCGGG																								
2801	GGCTCCCTTT	AGGGTTCCGA	TTTAGTGCTT	TACGGCACCT	CGACCCCAA	AACTTGATT	AGGGTGATGG	TTACGTAAGT	GGGCCATCGC	CCTGATAGAC																								
2901	GGTTTTTCGC	CCTTTGACGT	TGGAGTCCAC	GTTCTTTAAT	AGTGGACTCT	TGTTCCAAAC	TGGAACAACA	CTCAACCCTA	TCTCGGTCTA	TTCTTTTGAT																								
3001	TTATAAGGGA	TTTTGCCGAT	TTCGGCCTAT	TGGTTAAAAA	ATGAGCTGAT	TTAACAAAAA	TTTAACGCGA	ATTAATTCTG	TGGAATGTGT	GTCAGTTAGG																								
		SV40 early promoter																																
3101	GTGTGGAAG	TCCCCAGGCT	CCCAGCAGG	CAGAAGTATG	CAAAGCATGC	ATCTCAATTA	GTCAGCAACC	AGGTGTGGAA	AGTCCCCAGG	CTCCCCAGCA																								
		SV40 early promoter																																
3201	GGCAGAAGTA	TGCAAAGCAT	GCATCTCAAT	TAGTCAGCAA	CCATAGTCCC	GCCCCTAACT	CCGCCCCATCC	CGCCCCCTAAC	TCCGCCCCAGT	TCCGCCCCATT																								
		SV40 early promoter																																
3301	CTCCGCCCCA	TGGCTGACTA	ATTTTTTTTTA	TTTATGCAGA	GGCCGAGGCC	GCCTCTGCCT	CTGAGCTATT	CCAGAAGTAG	TGAGGAGGCT	TTTTTGGAGG																								

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ApaI

4801 TAGCTCACGC TGTAGGTATC TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC CCGACCGCTG CGCCTTATCC

4901 GGTAAC TATC GTCTT GAGTC CAACCC GGT AAGACAC GACT TATCG CCACT GGCAG CAGCC ACTGG TAAAC GGATT AGCAG AGCGAG GTAT GTAGGC GGTG

5001 CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGAACA GTATTTGGTA TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT

5101 TGGTAGCTCT TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA AAGGATCTCA AGAAGATCCT

5201 TTGATCTTTT CTACGGGGTC TGACGCTCAG TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG GATCTTCACC TAGATCCTTT

5301 TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT

 $\text{Amp}(R)$

5401 CTGTCTATTT CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG

 $\text{Amp}(R)$

5501 CGAGACCCAC GCTCACCGGC TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC

 $\text{Amp}(R)$

5601 AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC

 $\text{Amp}(R)$

5701 GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG CGGTTAGCTC CTTCGGTCTT

 $\text{Amp}(R)$

Pvul

5801 CCGATCGTTG TCAGAAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT

 $\text{Amp}(R)$

Scal

5901 CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC GGCGTCAATA CGGGATAATA CCGCGCCACA

 $\text{Amp}(R)$

6001 TAGCAGAACT TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT CCAGTTCGAT GTAACCCACT

 $\text{Amp}(R)$

ApaLI

6101 CGTGCACCCA ACTGATCTTC AGCATCTTTT ACTTTTACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA

 $\text{Amp}(R)$

6201 CACGGAATG TTGAATACTC ATACTCTTCC TTTTTC AATA TTATTGAAGC ATTTATCAGG GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA

 $\text{Amp}(R)$

Sall

ApaLI

6301 GAAAAATAAA CAAATAGGGG TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCGA CGGATCGGGA GATCTCCCGA TCCCCTATGG TGCACCTCTCA

pcDNA4/HisMax-tFoxP2

6401	GTACAACTCTG	CTCTGATGCC	GCATAGTTAA	GCCAGTATCT	GCTCCCTGCT	TGTGTGTTGG	AGGTCGCTGA	GTAGTGCGCG	AGCAAAATTT	AAGCTACAAC
6501	AAGGCAAGGC	TTGACCGACA	ATTGCATGAA	GAATCTGCTT	AGGGTTAGGC	GTTTTGCGCT	GCTTCGCG			

Page 1

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780
c a a t g t a g c t t g a c c t a g a g t t g t c g c c a t t c t a g g a a c t c t c a a a a g c g g g g c t t c t t g c a a a a
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Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
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 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln
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 90 95 100 105
 Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr
 AMP

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155 160 165 170

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro

AMP

1105

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 175 180 185 190
 Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala Met Thr Thr Leu Arg Lys Leu Leu Thr Gly
 AMP

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 Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly
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2860

175 170 165 160
 * Thr Ala Thr Ser Pro Asp Ile Asp Phe His Met Val Glu Glu Arg Ile Gly Leu Lys
 Gentamicin

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2925

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 Gentamicin

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2990

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 Gentamicin

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3055

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 Gentamicin

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3120

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 Gentamicin

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 70 65 60 55
 Arg Leu Leu Asn Gly Leu Tyr Asp Ser Asp Pro Gln His Gln Ser Tyr Thr Ala Val Asp Gly Phe
 Gentamicin

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 Gentamicin

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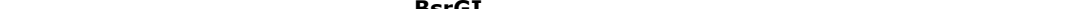
< Gentamicin

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< Gentamicin

3380



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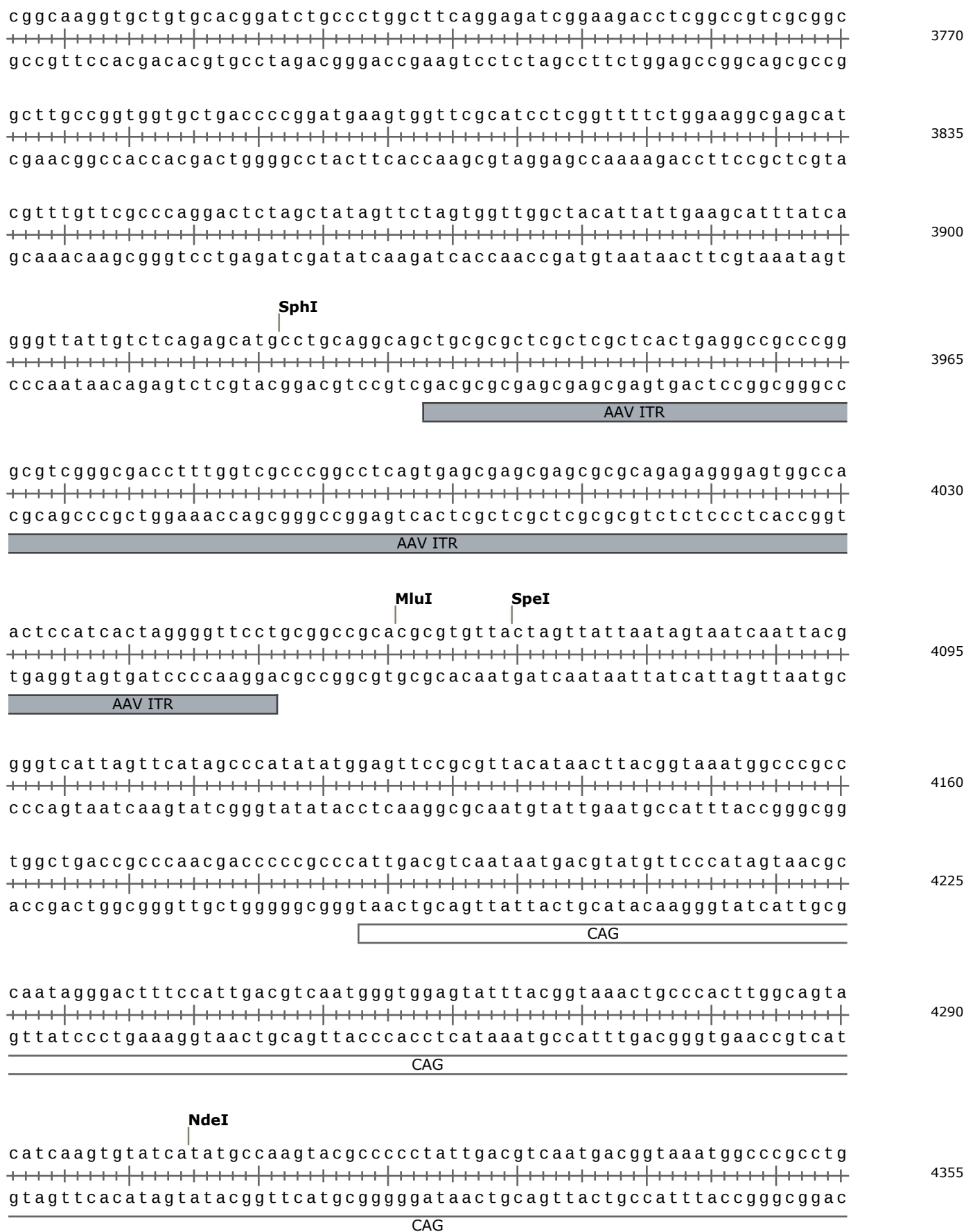
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 1472-correct-G-to-A-PCR-R

Page 10

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5850

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7930

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