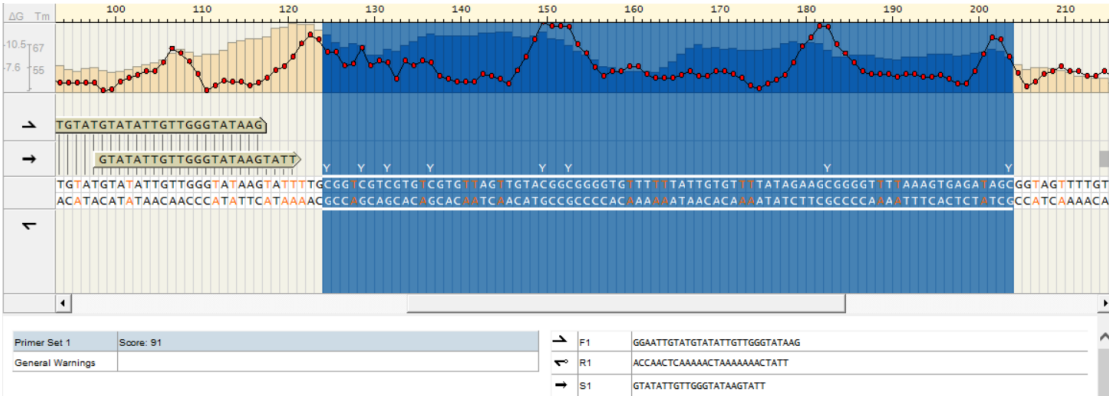


>ncbi\_106033926

<--up2k--AACAACATTGTTACTTAAAAAAAAAAGGCAATTTTATTGCACTTTT  
TTGTTATTTAAAATTCTAAAAATAGAAAAAAGATCCCTTTATTTTTGTATATT  
TGTAATGTCCTGATGAAATTTCAAACCAAAGCACTTAGCATACATAATTA  
ACATACACATTTATGCCCTTTCTCTTTATCCATTGCAACAGTTTGAATAAGTT  
TGAGTAAGATAAACCAATAGTGCTGGTTTCATCATGCAGCTTCAGCAGAGC  
TTTCTGAAGCTACCAAATCAAACCAAACcgTTGCTAAGATACACACTTATCTT  
CATGTTCAAGAGCAGCTAGTTTTCTTTAATTAGTAGTAGTTATCTGACTTTCT  
GGAGGTAGCCTTCTGTAGGAAGCATCAGTTCTAAAACCTTCAGTGAAAAGT  
TTCACACCTACATTGGGTCTGGCTCTGACTTGCcgTGTCAAGGCAGCTTGAT  
AAGAGGAAGGGTCTGGTTTGCAGTGCTCCTCAGTTTTCCCTAAGCTCTGCA  
TGTCAGTGCCATTGGCCACATTCAGATTTTTTCAATCTTcgTCCTGCAGAATA  
TcgACTcgGAACCCATAGGCTATAAATcgATGGTTTCAGACTGTTGGTGTGTGT  
CTGTAGACCCAGCTAGACTGCAGTTTGCCTTGCAGGGTGATCCCTAAATGG  
GTTTTCAGGAGCCCAATTTAAGAACCAAAGTTTGCAAACcgCTGGGTGAGTC  
TTATTTGTTTCCTCAGCTCTGCTTATGTTTCCTTGTACAGTTGGAAGTGAAC  
AAAGCTCAGAATCCAGATTTTTTCCAACCTTGAAATGTTTGCACATGGAACG  
GGTTGTACTTCcgTCAGCAACATGCCATCCTCTTGATGCACAAATGAGGAGA  
GTAATTCAGGCATTTATTTTAAAAATACTGCCTTAGAAATAGACGCGCAA  
AATTGCACAGGGTATATATTTTTCTTATTTAAGTTGAAAAATAAATATAGCTG  
TAATCTAAGTGTGTATTTATCAGCATTGATGCCCTTTGGTCTTGCTCCTGTGG  
ACTTCTCTCACTGACATCAGTGGGAAAAAGATGGGTTCTGCACAGTAAATC  
TGAATATTTTTTTCATCTTTATCCATCCATCTATTTTGGGATGTGCTAAATGCT  
TGCTCTCTGTTGTAACATTAACATCAGTATGTGGAAACTTGGGTGCTAAAA  
TAAATCACTGAAATGCAATATACATGACTTCAcgTGGAAGTGCATGTACATTG  
TTGGGCACAAGCACCTGcgGCGcgTcgTGCcgTGCCAGCTGTACGcgGcgGGGTGC  
TTCCTATTGTGTCCTATAGAAGcgGGGTCTCAAAGTGAGACAGcgGCAGCTT  
TGTGCTGCCAGTTTATATAAATAGTCTTTTTAGTCCCTGAGCTGGCAAAGT  
ATTTCTTGGTTGCCATTATcgTGATTGTGAATTTGAATCCATGATGCTTTTACC  
AGGCTcgGAGTACAAAGAcgACAAGGTcgTGGTATTTCTCACAAGCATTTTTT

TCATTGTGcgCCTGTTTGTTTGCTGGAGGCAATGAAATAGTTATAATTTATAT  
GTGAAGTACTGATTTGTGGGGCTCTAGCAGTGTTTCTTTAGTTTTTTGAGTT  
AAAGGTAGTGGCTTTGATCAAAATAGCATGGGGCATTTTTCTCAcgTTAGCA  
GAGGCACTCCTGATTCATGACAGTATGAATGAGCACACCcgCAAGTTCATTT  
CCTTTTTATATTTAAGGGAAAAAATGAAGGTAAATAAGAGGGGGGAAAAGGG  
GTAAGCTCAGCACTTACAACCTGGACTGTTTTCTGCCACAGCAAAGTCAA  
TGTGACACCTTTACAAAGCTGGAcgTTGATGAAGGTGTAGAGGGGACAGCC  
CTGCCTCAGAGTCCCCTCcgATCTGcgCAGTGGTCCcgTGCCTCAGAGCACCA  
GTTTGTTCATCCACCATGGTCACCACACACAATGAGGGAGCTGATGAGCTGT  
TCCCTTCTTACTTTGTCCTGCT--up2k-->--

1S



Primer Set 1	Score: 91	F1	GGAATTGTATGTATATTGTTGGGTATAAG
General Warnings		R1	ACCAACTCAAAACTAAAAAACTATT
		S1	GTATATTGTTGGGTATAAGTATT

	PCR Product	Forward PCR Primer, F1	Reverse PCR Primer, R1	Sequencing Primer, S1
Length, nt	170	29	27	23
Position, 5'- 3'		88 - 116	257 - 231	98 - 120
Warnings				
Tm, °C		59.2	57.9	44.9
%GC	30.0	31.0	22.2	26.1
Sequence to Analyze	TTGYGGTYGT YGTGYGTGT TAGTTGTAYG GYGGGGTGT TTTTATTGTG TTTTATAGAA GYGGGGTTTT AAAGTGAGAT AGYGGTAGTT TTGTGTTGTT AGTTTATA			

Name: **Mispriming Analysis**

Description: Identifies alternate annealing sites for the sequencing primer on the amplicon.

Mispriming 1

5'- GTATATTGTTGGGTATAAGTATT -3'

3'- CCTTAACATACATATAACAACCCATATTTCATAAAAAGCCAGCAGCAGCACACAAATCAACA... -5'

Mispriming 3' Position: 104

Penalty: 20

Mispriming 2

5'- GTATATTGTTGGGTATAAGTATT -3'

3'- CCTTAACATACATATAACAACCCATATTTCATAAAAAGCCAGCAGCAGCACACAAATCAACA... -5'

Mispriming 3' Position: 104

Penalty: 20

Mispriming 3

5'- GTATATTGTTGGGTATAAGTATT -3'

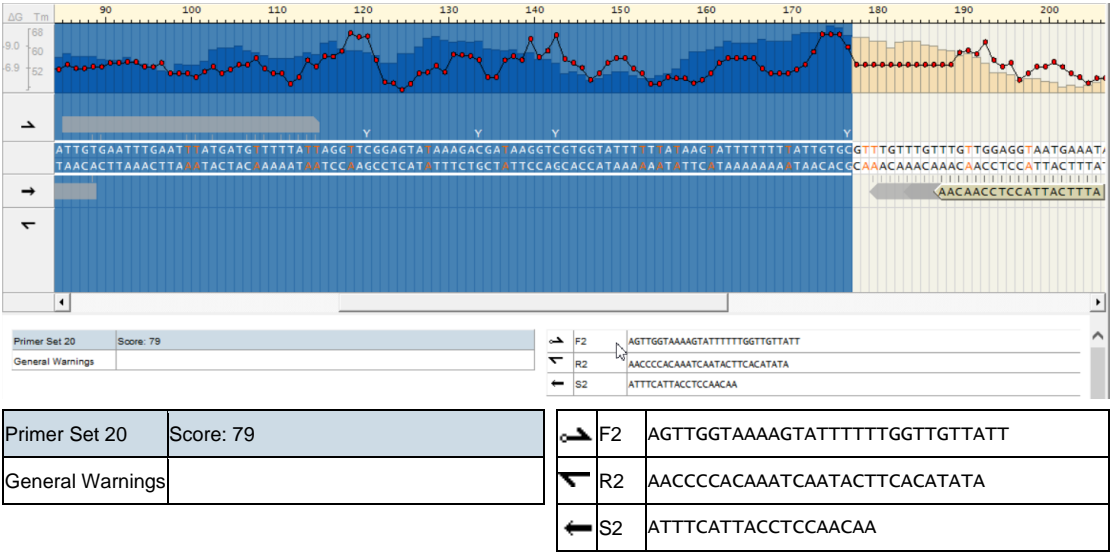
3'- ...CACTCTATCGCCATCAAAACACAAATCAATCAATATATTTATCAAAAAATCAAAAAC... -5'

Mispriming 3' Position: 236

Penalty: 15

Penalty: 20

2S



	PCR Product	Forward PCR Primer, F2	Reverse PCR Primer, R2	Sequencing Primer, S2
Length, nt	196	30	28	19
Position, 5'- 3'		48 - 77	243 - 216	205 - 187
Warnings				
Tm, °C		59.9	61.7	45.2
%GC	24.5	23.3	32.1	31.6
Sequence to Analyze	ACAAACAAAC RCACAATAAA AAAAATACTT ATAAAAAATA CCACRACCTT ATCRTCTTTA TACTCCRAAC CTAATAAAAA CATCATAAAT TCAATTAC AATCACRATA ATAACAACCA AAAAATACTT TT			