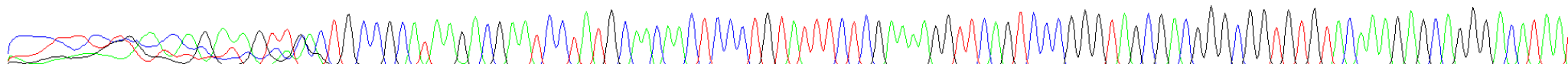
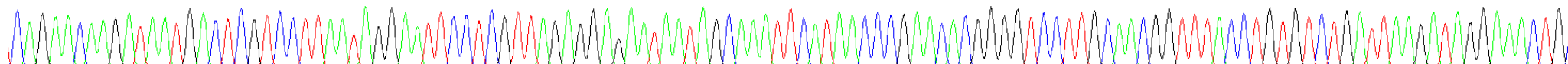


File: F3\_2646R\_premixed.ab1 Run Ended: 2022/6/9 16:39:58 Signal G:1636 A:3047 C:4108 T:3920  
Sample: F3\_2646R\_premixed Lane: 84 Base spacing: 16.04645 1238 bases in 14422 scans Page 1 of 2

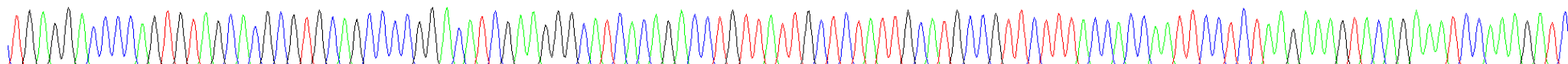
10 20 30 40 50 60 70 80 90 100 110 120  
CCCCGT TCGATGGATCA G ATCGT TGA CTG CCGCATAAGACGAATCCTATGCAACAAC TCCCTGTATTTCTCGAAAAAGTT CAGTCCC GGGTAGCGACGGGCGGTGTGTACAAAGAGCAGGGACATAAT



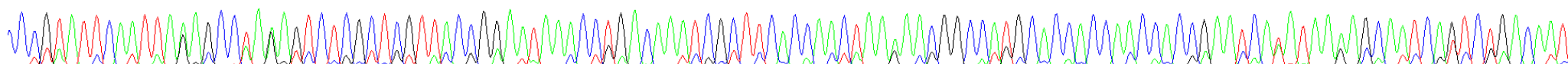
130 140 150 160 170 180 190 200 210 220 230 240 250  
CAGAACAAAGATAATGACTCGTTCCTTAATAGGAATTCCTCGTTAGAGGAGAAATAAGCAAAATTCATAACCCGAACACGGGGTCTTGGCAACGGTTTACCTGTGTCTGATTAAGATAGGAAACTGC



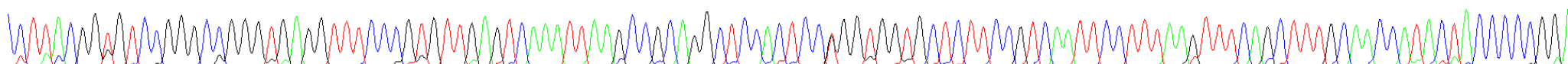
260 270 280 290 300 310 320 330 340 350 360 370  
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380 390 400 410 420 430 440 450 460 470 480 490 500  
CCCGTATTCAATTAAAGCCTAAAGTCTCGCTCGTTACCGGAATAAACCTGACAAATCGCTTCACCAACTAAAAACGGCCATGCACCACCAACCAACCAATCATATAAAGCAATCAGTCTGACAAT



510 520 530 540 550 560 570 580 590 600 610 620 630  
CCTTACGGTGTCCGGGCCGGGTGAGGTTTCCCCTGTTGAGTCAAATTAAAGCCGCAGGCTCCACTCCTGGTGGTGCTCTTCCGTCAATTCTTTTAAAGTTTCAGCTTTGCAACCATACTACCCCGGA



File: F3\_2646R\_premixed.ab1

Run Ended: 2022/6/9 16:39:58

Signal G:1636 A:3047 C:4108 T:3920

Sample: F3\_2646R\_premixed

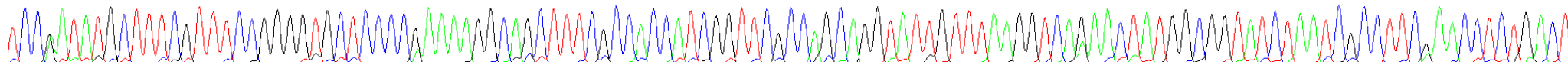
Lane: 84

Base spacing: 16.04645

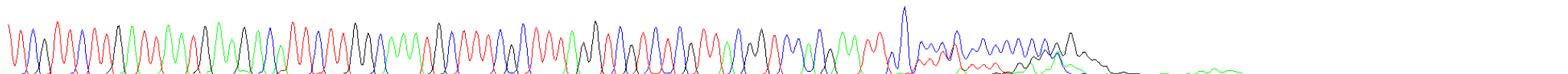
1238 bases in 14422 scans

Page 2 of 2

640 650 660 670 680 690 700 710 720 730 740 750  
TCCGATATGCTTTTCGTTTCCGGGGTGTCTCCCG AAAAGGCAGCTTTCGCCACCATCGGTTCCGAGCAGGTATTGTTTAAGGT CAGAACTATGGCGGTATCTAATCG CCTTCGAACCTCTGACT



760 770 780 790 800 810 820 830 840 850 860 870 880  
TTCGTTCTTGATTAAATGAAGACATTCTTGGCAAATGCTTTCGCTTTAGGTCGTCTCGTTACGGTCCACGAATTCC CCCC CCCCCCGGGGGGGG AAA AAA AACCCT ATAGAA ATAA AA ACAA CAT



890 900 910 920 930 940 950 960 970 980 990 1000  
AATTA AGTCA GGG AAA GAGGACCGAAA TAAGATAAAGTGT AT G GGG A TGACAGAGTAGGA AACTAGACG GAA TAAT AAG AGA AGTATG AAGA TTTCAGAGGAGCG A GGA GAGC AAAA

1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140  
GATA G AG GAAC GAGGATGAGATTGAGGGGAGAGAA GAGATA G GGG AA GTAATA GTCTGTG TGGC GCA CG TATGAGTAAAGT AA TAA GGTCA AGGGTTGTTTGG AAGCCA GTGTGGAAGATGGAGAGGAAGGAGC

1150 1160 1170 1180 1190 1200 1210 1220 1230  
CAGCGAAGAGGTATATGCGGTGATATGTTGATATGCCAGAG ACACAGGAGAGATATGAAGTG GGCCTGCGGTATG GGTGAGTAC G