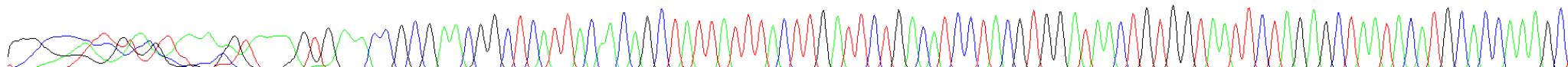
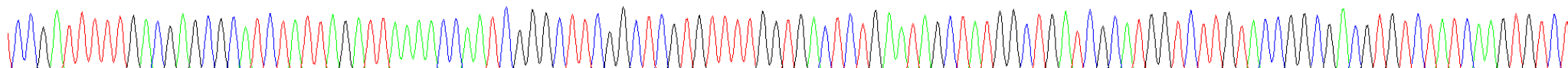


File: A3_988F_premixed.ab1 Run Ended: 2022/6/9 16:39:58 Signal G:617 A:982 C:1063 T:1240
Sample: A3_988F_premixed Lane: 5 Base spacing: 15.75621 1546 bases in 19453 scans Page 1 of 2

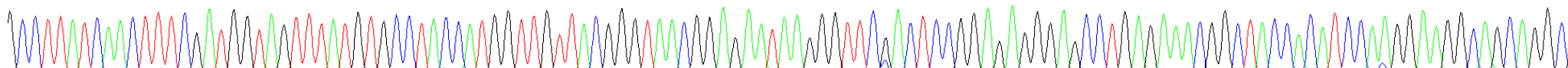
10 20 30 40 50 60 70 80 90 100 110 120
G GGA C GCG C CCG TGG T AGGT GA ACC GCG AACGGCTCAT TACAACAGCTATTATTTACTTTG AT TCTGACATCCTACGTGG ATAACTGTGGTAATTCTAGAGCTAATACATGCACCAAAGCT



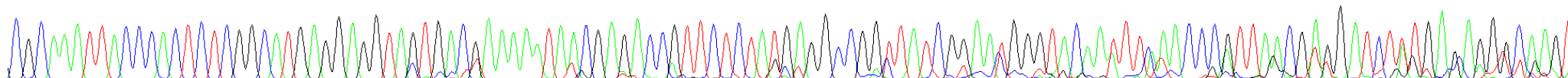
130 140 150 160 170 180 190 200 210 220 230 240
CCGATTTTTGACGAGCGCATCTATTAGATTAAACCAATCGGGCTTCGGCTCGTGTGTTTGGT GACTCTGAATAGCTATGGCTGATCGCATGGTCTTGTACCGGCGACGTGTCTATCAAGTGTCT



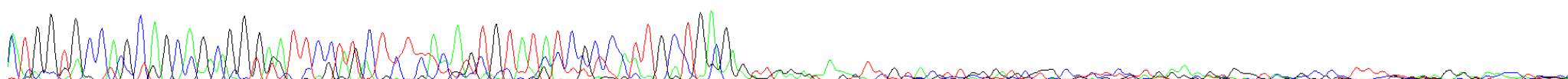
250 260 270 280 290 300 310 320 330 340 350 360 370
GCCTTATCAACTTT CGATGGTAGTTTATGT GCCTACCATGGTTGTTACGGGTAAACGGAGAATAAGGGTTCGACTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG



380 390 400 410 420 430 440 450 460 470 480 490
CGCAAATTACCACTCTCGGCATGAGGAGGTAGTGACGAAAAATAACGAGACCGTTCTCTATGAGGCCGGTTATCGGAATGGGTACAATTTCAACCCGTTAACGAGGATCTTTGAGAGGGCAAGT



500 510 520 530 540 550 560 570 580 590 600 610
CTGGTGCCA GC AGCAGCGG GAATTCATCTCTCACA GTGTATATCGC CATTGC TGA G GTTAGATAGCTT GTACTTTGGG TC GGCGTTCC TGAACGTGGTAAGC CCTTTTGAAGGTA CCTG CT



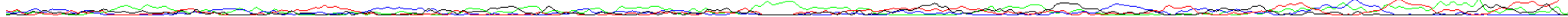
620 630 640 650 660 670 680 690 700 710 720 730 740
CGGGG GT CAAAC CAT TATCT AG TTTT CCCTTG A ATG CACGTG GGTGGGGC T GAGAGAA CG GTGCGAAA TTT A TTTA GGATGAG ACT CTTGT AGAAAGCG CTTT C ACCGGGG AA G TACAA GG



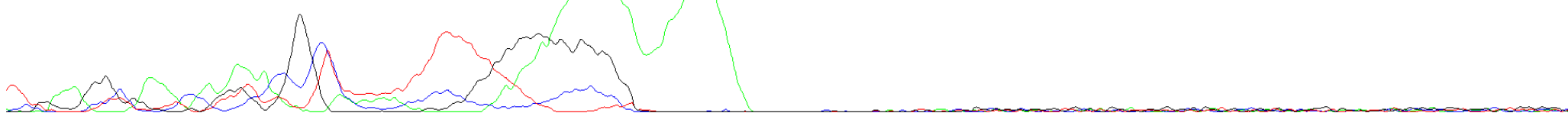
750 760 770 780 790 800 810 820 830 840 850 860
CG ATA TC GT C CT GCCG TTTT AGC AAAGC GACCA AA AAACC CGGCG G AA AACC G GTG GGGGT TTTTAAAT AAAAG AAAA C CG CTCAG AA AAACAC CGACAG TGT TGC GTT G AAGGT A TT



870 880 890 900 910 920 930 940 950 960 970 980
T CGCT GG AA GAA GTACCA A CT T TTTT CCCCCGT AAGGGAA GTT CAC AAGAAC AAGG TAAAA AAAA GAGT T GGGG A GAA AA CGG C CCGGT TT CC C G ATTT CC ACACAT A TAAAA G T T GAT



990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
TT G AAAGGGCG AAC CAGGAT ACC GCC ATTT TT TT T TTGT GGA GGA AAA AAAAAA AAAAAA C GTGT TCGCG GCC TTT T G GTTCGCTGC AGGA G GGA GT CCGC CCA TGC TC GCGACGTGAC TGTGGC



1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230
CGCA CATGTACGCACA T GAGGGGTTC AGC GGAC GAT TCT ATGG TGACGACGGGTGTGCGC TT TGT AGTATAGGCTC GGA GATAATGGA AAGG A CAC TGTGT GCA C GG AGA CT CGCTGCTGGCGT

