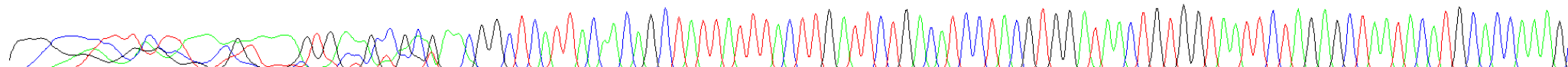
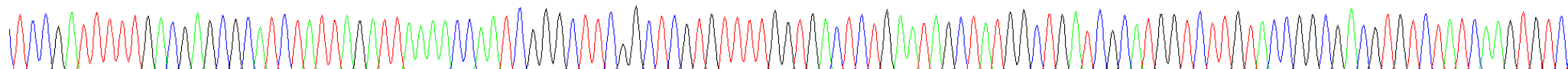


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Sample: A2_988F_premixed Lane: 3 Base spacing: 15.952547 2296 bases in 26507 scans Page 1 of 2

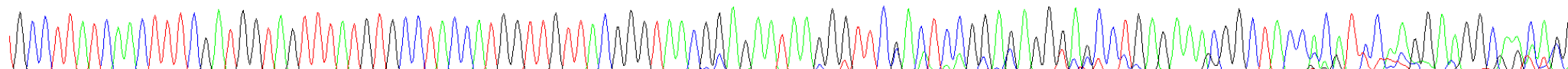
10 20 30 40 50 60 70 80 90 100 110 120
T T GAGGA GAG CCC CTGCC TTGTT GCTACCAGCG AACGGCTCATTACAACAGCTATTATTTACTTG ATTCTGACATCCTACGTGGATAACTGTGGTAATTCTAGAGCTAATACATGCACCAAAGC



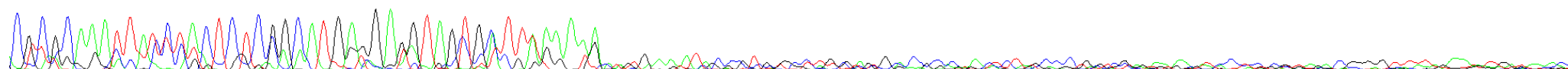
130 140 150 160 170 180 190 200 210 220 230 240
TCCGATTTTTGACGAGCGCATCTATTAGATTAAAACCAATCGGGCTTCGGCTCGTGTGTTTGGTGACTCTGAATAGCTATGGCTGATCGCATGGTCTTGTACCGGCGACGTGTCTATCAAGTGTCT



250 260 270 280 290 300 310 320 330 340 350 360 370
GCCTTATCAACTTTTCGATGGTAGTTTATGTGCCTACCATGTTTGTTCACGGGTAAACGGAGAATAAGGGTTCGACTCCGGAGAGGGAGCCTGAGAAACGGCTACCAATCCAAGGAAGGCAACAGG



380 390 400 410 420 430 440 450 460 470 480 490
CGCGCAAAATTATCTACTCTCCGCATGACGAGGTAGTGA TTAATAAAAAATGAAATACCGTGTCTTGATGACGCCTA TCTTCCC GGCGAATAATACTC CGTACG GGT TTA AA GTG GAACC



500 510 520 530 540 550 560 570 580 590 600 610
AAT TA CAAAT AAACG GGCCAT ATTGG AGAACGGT TT CGTT GTTTTT TCC GTCAAT A CCCTCCCTCA AGGT CGGAAA G GGGGT AAA GATGGGCC GGGCC GCGCA G CCTT CCG TTGGAAAGAG



File: A2_988F_premixed.ab1 Run Ended: 2022/6/9 16:39:58 Signal G:433 A:728 C:805 T:941

Sample: A2_988F_premixed Lane: 3 Base spacing: 15.952547 2296 bases in 26507 scans Page 2 of 2

620 630 640 650 660 670 680 690 700 710 720 730
GG TA A GGC CG TTT GC GT ATT G GG CCC AA AA AC CC GG GA G AG TTC AG AC ACCC CAT ATG TTT TGA GC C TTT A AT C TTT TGG T A CT GG CG T CT G GGG GG TA AG G GCC GGC T GC AA GAT AA GC GG ATT



740 750 760 770 780 790 800 810 820 830 840 850 860
GG CG AAA AG TGT T GG AT TTA AG GGT GCT A AAA CA AC ATT GGT GAA AAA AC TT G ACCT TCT CC A CGG G GGGG AC AAT AT AAA AC TTT GG G G AAAA TT AA AT CGC C TTTT T TG C GT TGG GAT



870 880 890 900 910 920 930 940 950 960 970 980 990
ATC CAA AAAAAA G CT CC AA CCC A GAA AA A AC CC ACCC CC GGGGGT CCCCC AA AAAA C CCCC GAC GA ATT GT TGGGGT TT TTTT TTT TTAGT GAA AAT T CCG AT AAAAAA G AGT GA A AAA GGGGC



1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140
C GGG C GGT C GT ACC A A TAA C AAAAAA G G GAAAA AAA AC CG CA GGGG GAA AC AG GGGC GT GG G TTGGG GGGGGT T T TGG CAC CA AT AT GTT GTAT GTAT ATTAT CT ATAA GCGCC CCCTTC CCTCC



1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280
TTG AAG AAAAG AAAAAA TTATT GTT GG C ACCA CCA CAAA C ATT T TTT TTTT GTT GTT G GAC CC CAAC AC ACCC G G GA ATG A GG G GTG AAGT AAGT GGCC A CACCC GGC CCA CC AC AATC AC CGC AC

