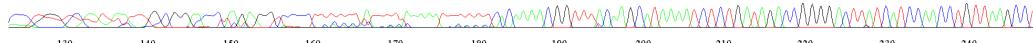
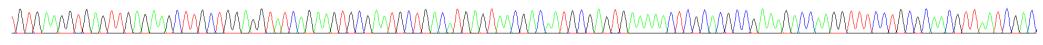


File: 22CCRAA000_C07_premix.ab1 Run Ended: 2023/4/4 0:17:12 Signal G:2198 A:3144 C:3308 T:3187

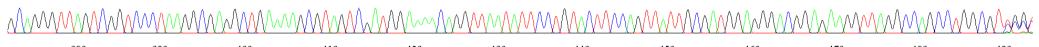
Sample: 22CCRAA000_C07_premix Lane: 59 Base spacing: 14.945197 1637 bases in 20857 scans Page 1 of 2

10 20 30 40 50 60 70 80 90 100 110 120 AA TG TC A T TAT T TG C G GAAC C TA GA G G C CCCT T T TT TATT T AAAAATTTT T TT CA CAA AAC G G T TT ACAA G CAT AAAAT CT C T G ATA G AC C G G G G ACTTTAT CAT CCAAC C T G T T AGAC C





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



380 390 400 410 420 430 440 450 460 470 480 490
TGT CCAGGTCT AGT CTG C CAAAA CTTA GG CAAAT CCGGG ATTT CAA GG CCG AG AGCTG AT GAC GAG TGACCTT CA C G AGA GT GGT TGAT ACCAT GCTT CC AAG AAA AGCT CC



500 510 520 530 540 550 560 570 580 590 600 610 TAAGCTT CAGAT AAGAGGGGAACCGT ACC CC CACCGACAC AGGT GGTT AGGT AG AGAAT ACCAAGGC GCTT GTA A GAACT CC GGTG AAG GAACT AC GCC GCAT GGCG CCGT A ACT T CCGG

File: 22CCRAA000_C07_premix.ab1 Signal G:2198 A:3144 C:3308 T:3187 Run Ended: 2023/4/4 0:17:12 Sample: 22CCRAA000 C07 premix Page 2 of 2 Lane: 59 Base spacing: 14.945197 1637 bases in 20857 scans 620 650 670 710 C AGA A GGTGCGC C GGC GAG GATG AAAG A CTTGCTC C CT AAT AA CATGC C GGT CGA AGA T A CC ACGC CGC T G C TGC GGTT GTTTATC AAC ACACA GT CTG CTC AC AC C AAC G AA GGA C 740 750 760 770 780 790 800 810 820 830 840 850 GTA CAT GGT GA GA CT GC C GCT CCC TGAC C GGAAA GTT CAATT GGCT GAGGT G GC GC AAGCAAAA GCT CT C GGAT CG A C GC C A C A GTT A A C GGC T G C C GAT AA CT A TT A GGG AA C M

