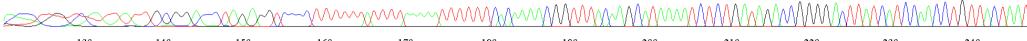


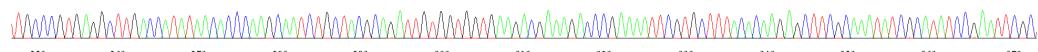
File: 22CCRAA000\_E01\_premix.ab1 Run Ended: 2023/4/4 0:17:12 Signal G:1335 A:2284 C:3021 T:2545

Sample: 22CCRAA000\_E01\_premix Lane: 7 Base spacing: 15.180631 1197 bases in 16301 scans Page 1 of 2

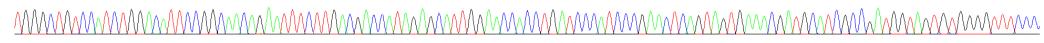
10 20 30 40 50 60 70 80 90 100 110 120 CAC TT TOTAGTATT GOGGGAC CTAGAGGTCCCCTTTTTTATTTTAAAAATTTTTTCACAAAACGGTTTACAAGCGATAAAATCTCTGATAGACCGGGGACTTATCATCCAACCTGTTACTAAT



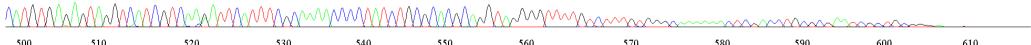
130 140 150 160 170 180 190 200 210 220 230 240
TGC CC GTG AGGCTTG ACCATATAACAC CCAAGCAAT CTGC TAC GCAGATTGTG GT GGT GAAGAC CGAAAGTTC GT GCT TTACACAA GAGCTTC GCAAATATC GCATAT CC GAATT C GC



 $\frac{250}{\text{TGGGCTGTCCAT}} \underbrace{\frac{260}{270}} \underbrace{\frac{280}{290}} \underbrace{\frac{290}{300}} \underbrace{\frac{310}{310}} \underbrace{\frac{320}{320}} \underbrace{\frac{330}{340}} \underbrace{\frac{340}{350}} \underbrace{\frac{350}{360}} \underbrace{\frac{360}{370}} \underbrace{\frac{370}{370}} \underbrace{\frac{370}{3$ 



380 390 400 410 420 430 440 450 460 470 480 490 CATGT GAGAGT CGT CAAGAT TCATTT CGCAAAACC CCTATC T GC GCAC GC AGGT AG G GTTTT GT CTTT GT GGCAAAAACT C GACCT GC GC GAAT C GC T GC G G GAGC G G GCAA GGA



File: 22CCRAA000\_E01\_premix.ab1

Run Ended: 2023/4/4 0:17:12

Signal G:1335 A:2284 C:3021 T:2545

Sample: 22CCRAA000\_E01\_premix

Lane: 7

Base spacing: 15.180631

1197 bases in 16301 scans

Page 2 of 2

740 750 760 770 780 790 800 810 820 830 840 850 860 GCC G TTAGGCTGG CGGCTG TA CATGCC GGA C GC A GCATGAT CAA TAGCA GGTGA C G A TGACC G CCCAG CAG C CAGGGT G AAG TG ATC CGG AGC CAT TA T T A GA C GGGGAC GC A A AG CGAA C T GG CC

870 880 890 900 910 920 930 940 950 960 970 980 990 AGG C GATTGATT GAAAA CG C GAAAC G AGTAT GACG TA GCAGA CGAT T CCTT AG CG G AAAC T TCC GC C A CGC T T ATAAGT G CT C G G G GAAA C T T T T

1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120
AGT TACATC CGT AG AGGAGA GGT T TG GEA AC CT GTA ACAT T T T T AGGC A AT CT T G GAGAGGC CTATAT GTGTCTC C AGC ATGGA A GGPCT G AGA GGG T T C T T FGAGG CC GGGG G A A T G C C C T

1130 1140 1150 1160 1170 1180 1190 1190 TG TG TG TG GGAGGGG C G GT CTA A A G GC CTTCTC GC C A A A GGAGGT CA A T T CTCTT TG GCA C C