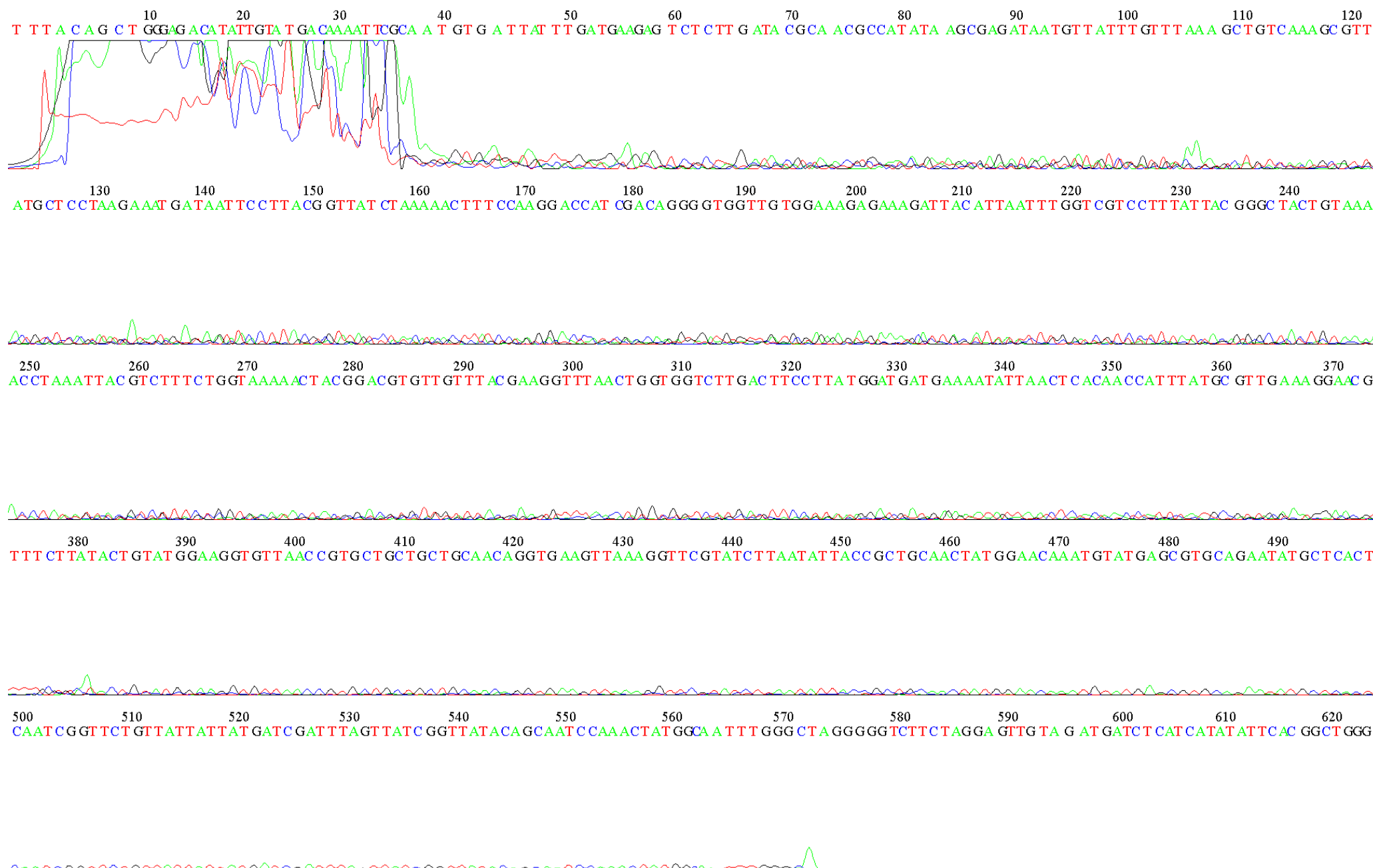


File: smA\_rbcLF.ab1 Run Ended: 2023-05-31 19:51:33 Signal G:598 A:634 C:691 T:577  
Sample: smA\_rbcLF Lane: 31 Base spacing: 14.82727 1048 bases in 16302 scans Page 1 of 2



File: smA\_rbcLF.ab1 Run Ended: 2023-05-31 19:51:33 Signal G:598 A:634 C:691 T:577

Sample: smA\_rbcLF Lane: 31 Base spacing: 14.82727 1048 bases in 16302 scans Page 2 of 2

630 640 650 660 670 680 690 700 710 720 730 740 750  
A TAGAC GT TGAAT A CGG GCTTAT T TCAC TTCT GCCACAATAATC AT TGC AC TCCC GACT GGAA TTAAAA TT GT CAGTTTGAC CTGCCA CCC GT CACGGGACCTAATT AAC TTACA GCCCAGCTTTT GATAT

760 770 780 790 800 810 820 830 840 850 860 870 880  
GAGTT CC TGGGTTC GTAT GCCGAATCA CCAT CGGT GG ATTAAG T GGAGTTGCAA TAG CATC TCCTCAATCGTAT ATAATCTAACA C GATACTCTTCTTGTA GTTGCTCACT CCC ACT ACCACTT GCATA G

890 900 910 920 930 940 950 960 970 980 990 1000 1010  
GACGATATCTGCTCT GTACCCGGATTCAATCCGTG A ACC TT GATTCCACATGATAAC T TAA GTC T AAA GGATTGTAAATCTATTACAG TAT GTCT GCTGACCACTTT CAC ATCTCCCTCAAC CT

1020 1030 1040  
TCT A GGGTAG C ACG AAGC CCGAC AATCT CAAATAC C