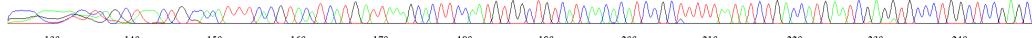
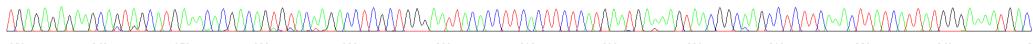


File: CYT19_CYT_R.ab1 Run Ended: 2025/5/10 3:56:54 Signal G:2368 A:2925 C:3513 T:3264

Sample: CYT19_Plate1_G12_CYT_R Lane: 84 Base spacing: 15.4425535 1198 bases in 14275 scans Page 1 of 2

10 20 30 40 50 60 70 80 90 100 110 120 C CC GAA ATCATCA G C TA A CTG CCACATTTTCAC GTACATCAT G ATTAAAGCACTTCCAATGTG GC TGTCATCAACACATC C GC TTTTTAATAT CT GACCATG AATC GAGGT GC CCTG GC TC C GAG







380 390 400 410 420 430 440 450 460 470 480 CTGGTGTAATA CTAGCCGT ACG TA CT AGGA GCT C AG GGT CTATGT CTA CCCCTT TATAGTTCC A AA TTTTTATTTGTC AT A GTTGCGC GTCAA C TTTGT TTGGA CAC A GCCT C GC

490 500 510 520 530 540 550 560 570 580 590 600 61
GGGGCGCCGT AGTAG AGCCGTACACCGTGACTCCATCTCA GACTGTATT ACTCTT AAAAG ACACCTTCAT TTCTGTCCTATACGAACTGCCGGTATTGTAGGCTGTTCTAACGCATCATGTCATGTCATGA

File: CYT19_CYT_R.ab1

Run Ended: 2025/5/10 3:56:54

Signal G:2368 A:2925 C:3513 T:3264

Sample: CYT19 Plate1 G12 CYT R

Lane: 84

Base spacing: 15.4425535

1198 bases in 14275 scans

Page 2 of 2

620 630 640 650 660 670 680 690 700 710 720 730
TAGCGT CGT ATGGCTTTA CGCAC CCTACT GT C G TCCCACTTC G CCGT GTGGTGGCT GTG TC TAAGATTGC G G CA TGGTTAT CTCGGGAAATCATG TTGGTACTC TCACGACATTC GACTC C CTCCTT

740 750 760 770 780 790 800 810 820 830 840 850 860
TTGGTTAA CGAGAGCTGTAGT CTCTTT CCTTTCCAACACTC CGC GTAA TAT CAGAGT CCTCTCCCTTC CCA CTCTAA T GCGCAA AACC GC TATAT CATGG TTTCAAT CATCT CAAACC T GGAAG AT GT

870 880 890 900 910 920 930 940 950 960 970 980 990
GC AC A CCATC CATGCA CAAT CGAGE CT GTAT CAGGCT AG AC CC TTGA AC GAT CTA GT GATGAG AAATTA TTCCGC GAA T ACCTTGTT TAT TA ATT CATGA GCT CACG ATG ACT CGGA C A ATATA CT GTTAC

1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 C GA AAATACACTC ATCCACTCTCATAG CCATAG GATAT CTA GAGGTG T C A A G GAGTG ACC TTCATTCGCC AATT T CGACTGAGAACTATTGT A T AAG C GCCCAC CT T C GCT A ATACT CGCCATTCCT ACCGCGT AGAC