Sequence: SEQ10013054_A1_F09_0

Samples:	17450
Bases:	445
Average spacing:	40.0
Average quality >=	10: 13, 20: 29, 30: 393

Quality:
- 0 - 9
- 10 - 19
- 20 - 29
- >= 30


```
10        20        30        40        50        60        70        80
T T T K S C Y T T T C R R G G G T T A A C C T T C A T C A T T T C T G A T G G A G A A T A C G T T A G C T G C A C C A C A T T G A T C T T G T A A A T C G T A A C C G T A S A A
```

```
90       100       110       120       130       140       150       160       170
T C C T A A T C T G G A A T G T T G T T C T T T G T G T A A G T A C A T A G C T A A G T A C C A T G C G C T T A A A C C A G T T T G A G C A T T A C C A G T A G C G A
```

```
180       190       200       210       220       230       240       250
A T G C A G T A G A T G C A C C A G C T G C T G C G G A A A T T A C G G A A G C T C T T T G A G A T C C A C C G A A G T G A G T T T C A A G T A A T G C T G G G T A T T
```

```
260       270       280       290       300       310       320       330
C T T C G T A T T G T T C T A A T G C G T A G A A T G C A A C T T C A G A A C C T A C A T C A A G A A C A G T G T C C A T G T T G T T A G G T G C T T C A G T T A A T
```

```
340       350       360       370       380       390       400       410       420
C C A C C A T A T T T G T C T T C T A C A T A G T C T T T A C C A T A G T A A G T A A A G T C A T C T A A T A C A T C A T C A G T A T A T G C T G C A G T A G C A T A
```

```
430       440
Y T G H G T R A H C C A A C H C C D C C A A
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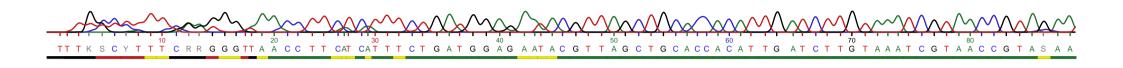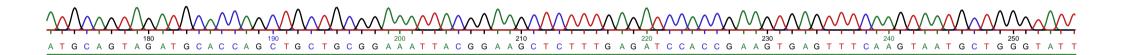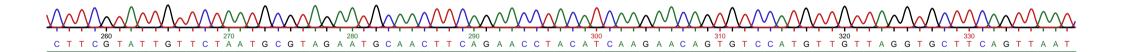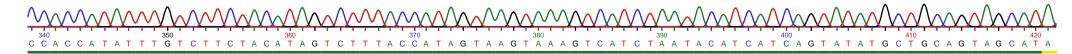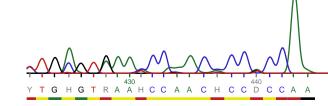
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16.09.2022