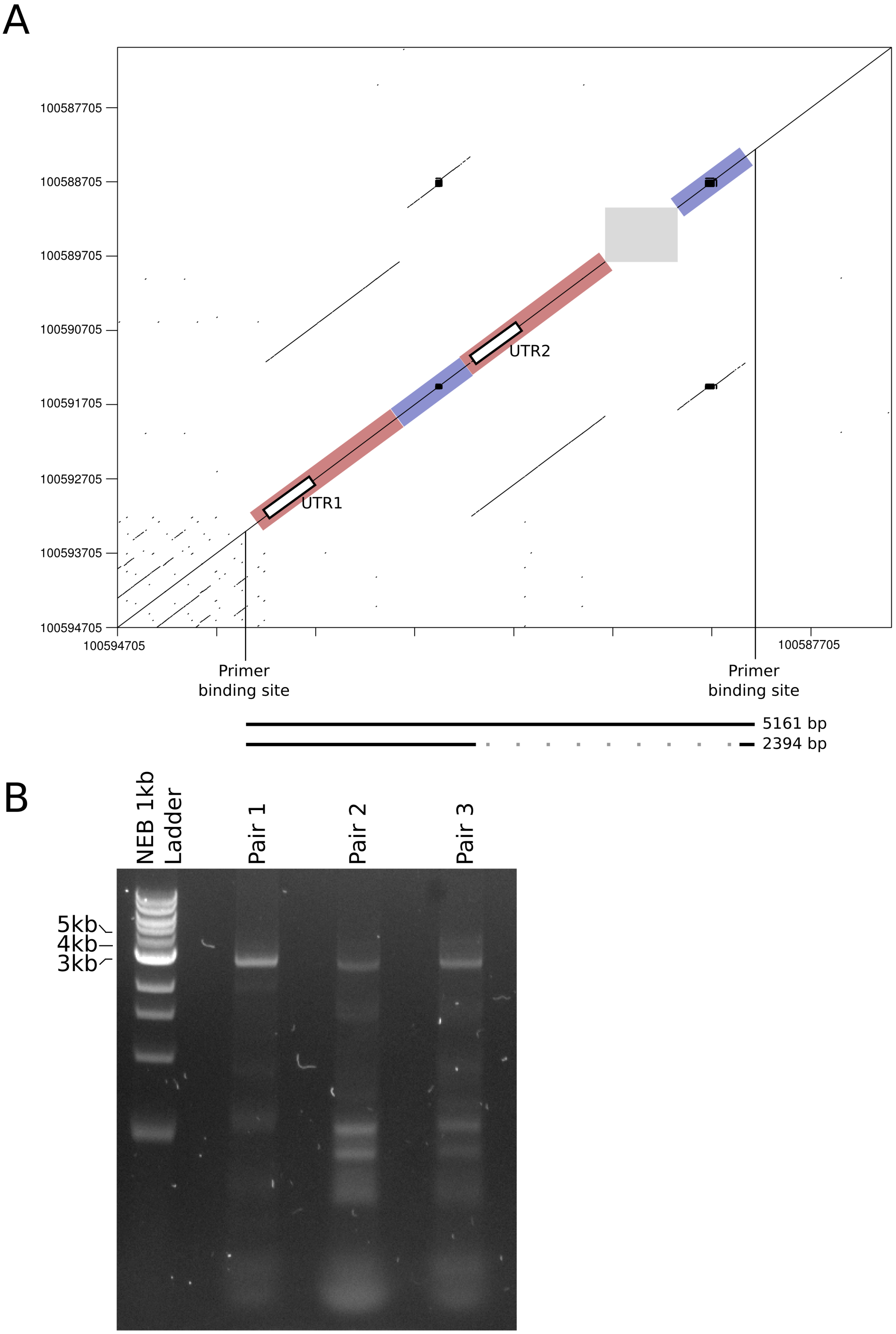
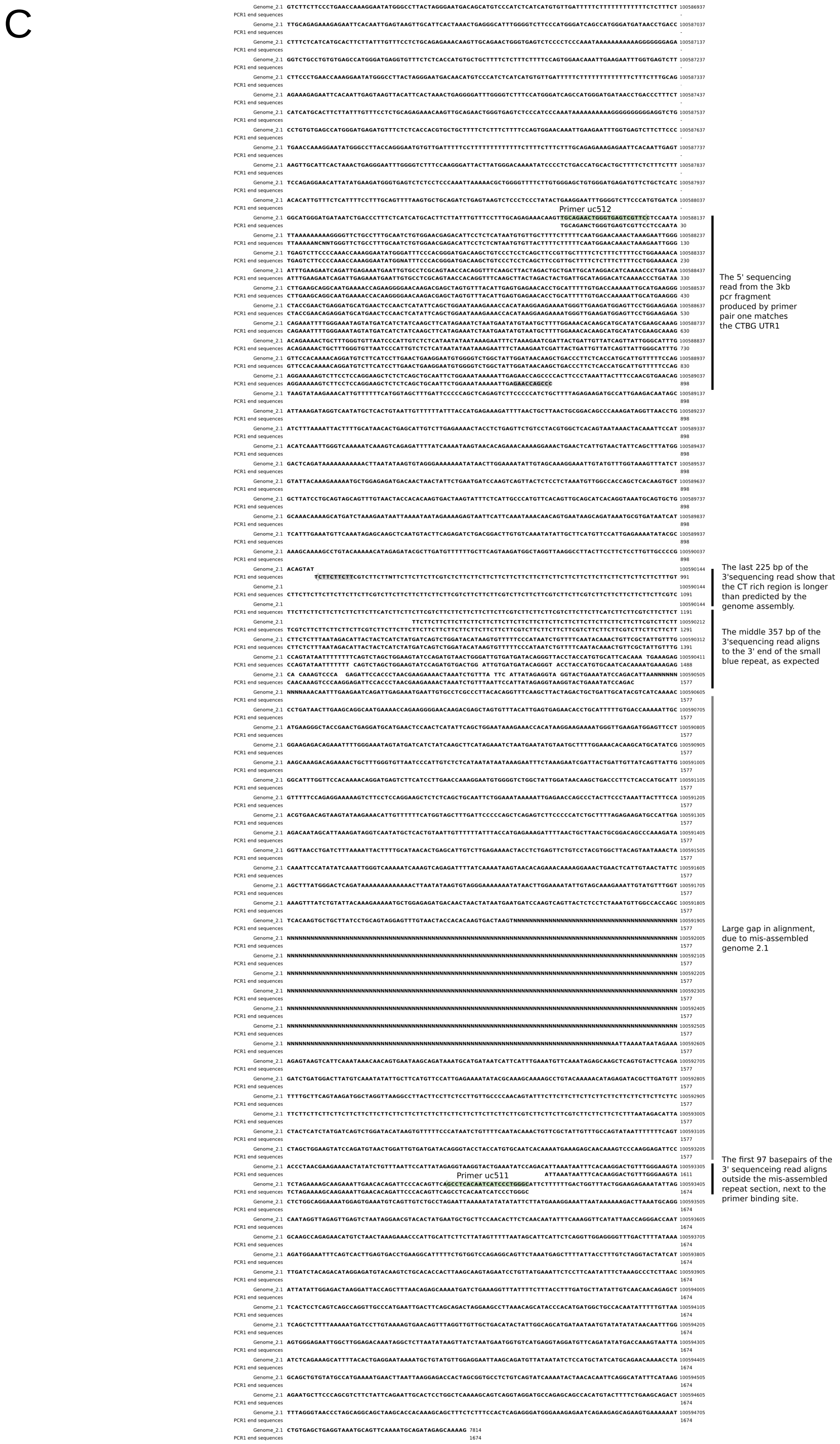

A
100587705
100588705
100589705
100590705
100591705
100592705
100593705
100594705
100594705
100587705
UTR1
UTR2
Primer binding site
Primer binding site
5161 bp
2394 bp
B
NEB 1kb Ladder
Pair 1
Pair 2
Pair 3
5kb
4kb
3kb



The 5' sequencing read from the 3kb pcr fragment produced by primer pair one matches the CTBG UTR1

The last 225 bp of the 3'sequencing read show that the CT rich region is longer than predicted by the genome assembly.

The middle 357 bp of the 3'sequencing read aligns to the 3' end of the small blue repeat, as expected

Large gap in alignment, due to mis-assembled genome 2.1

The first 97 basepairs of the 3' sequenceing read aligns outside the mis-assembled repeat section, next to the primer binding site.