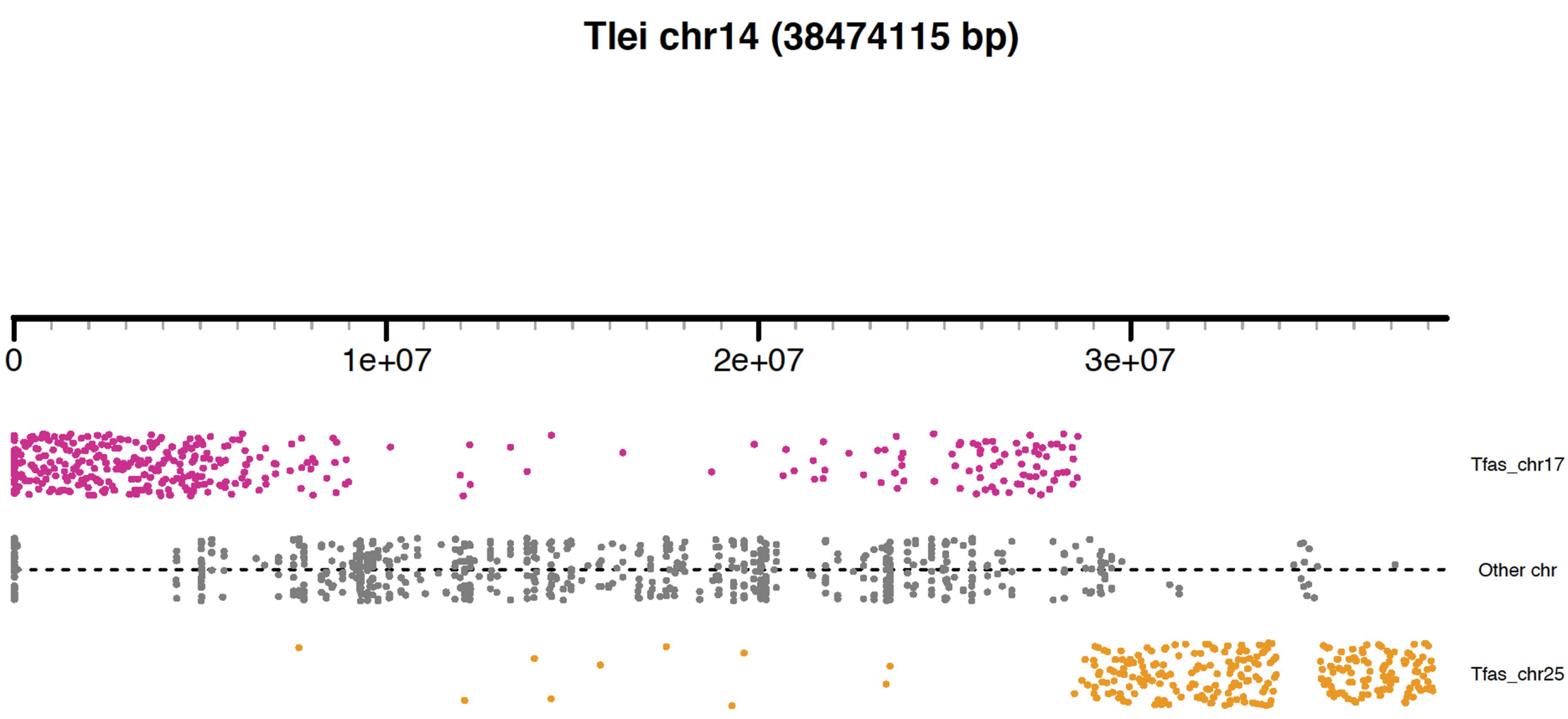
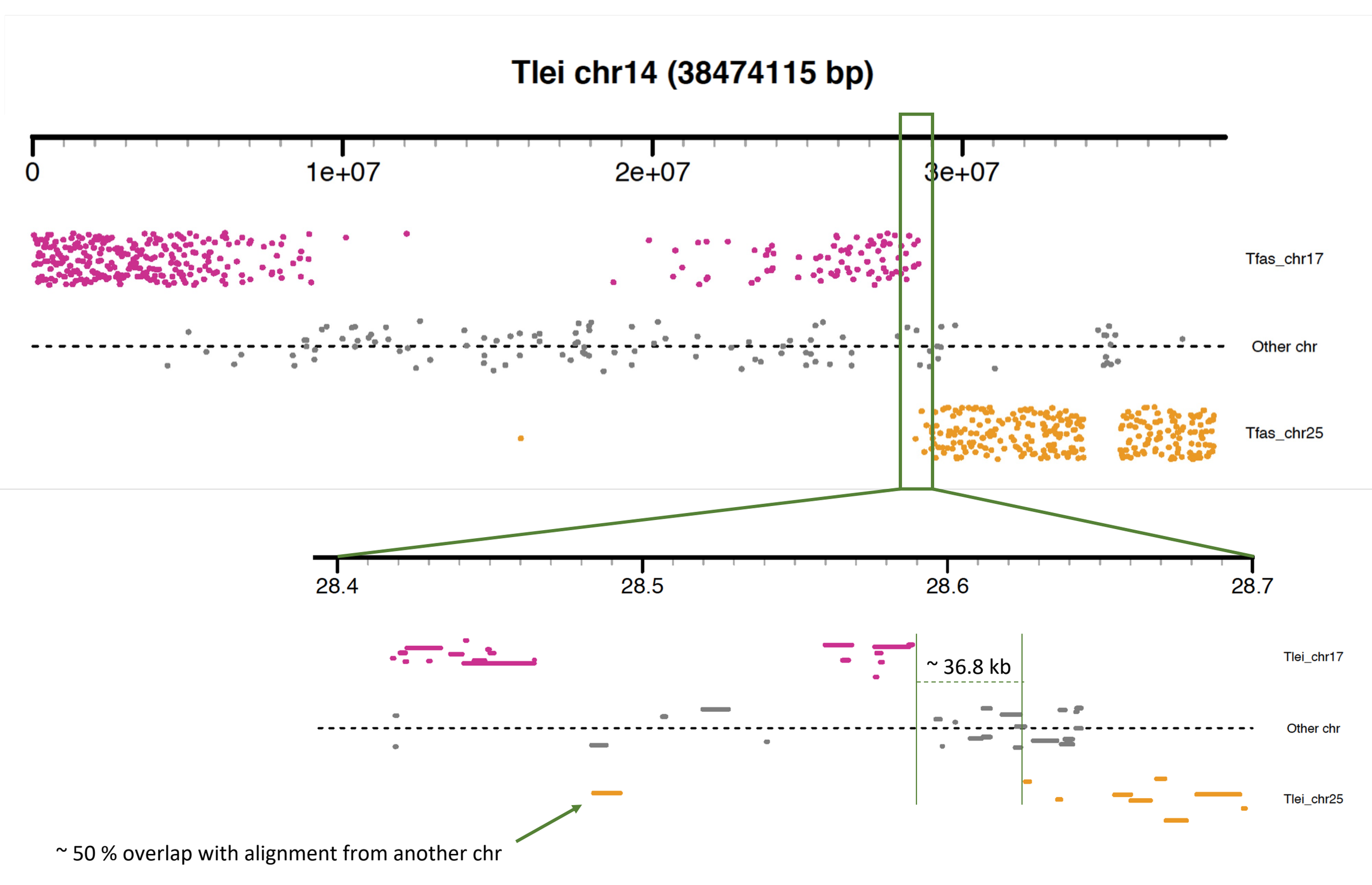
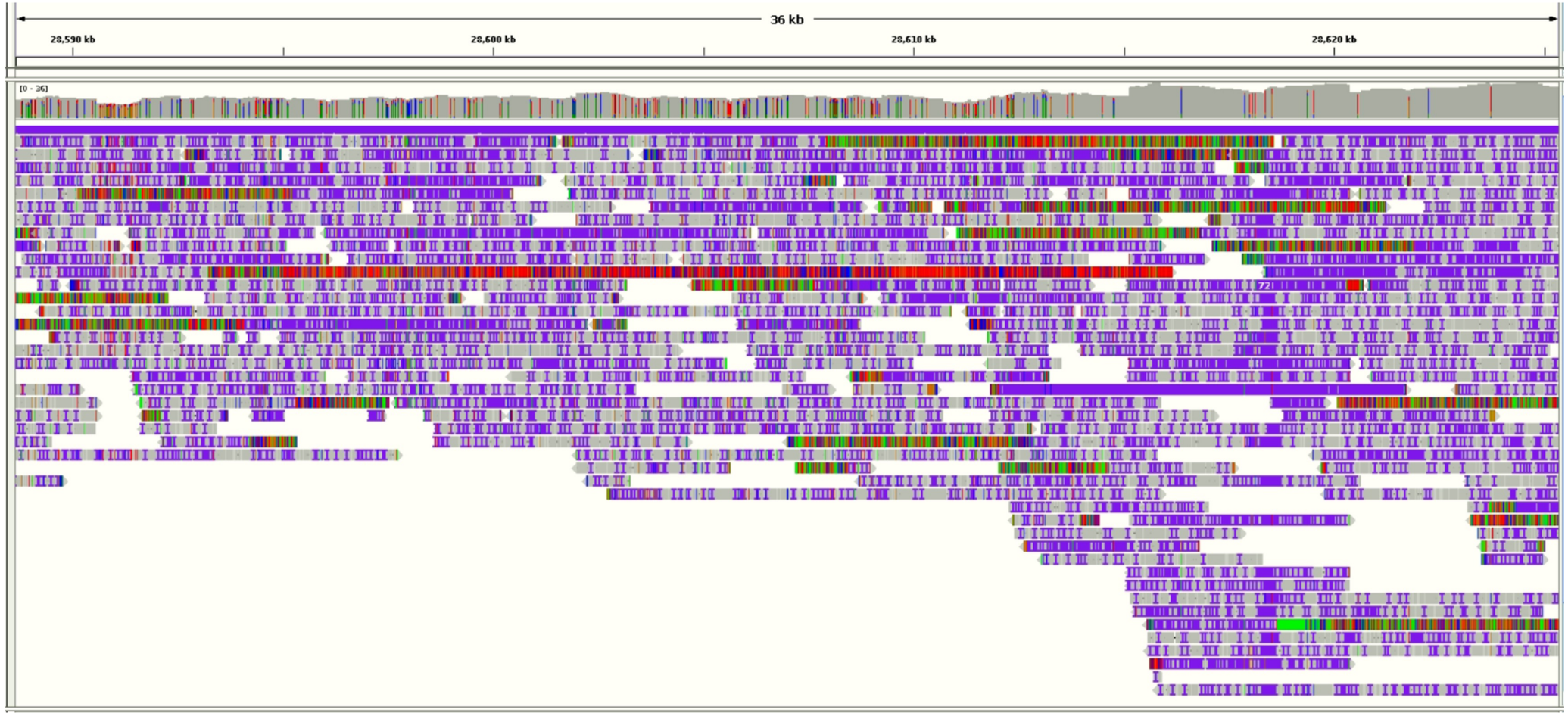
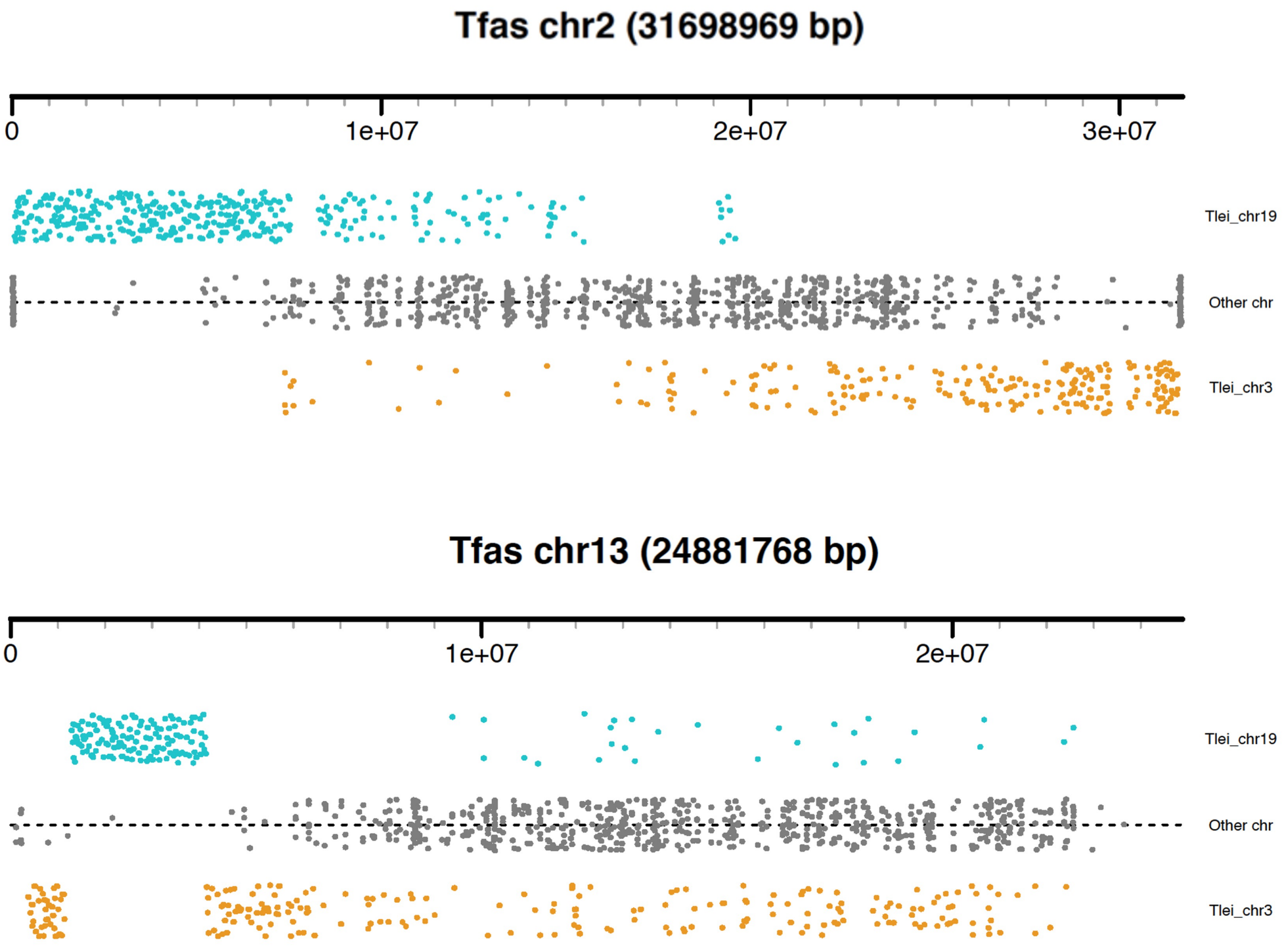
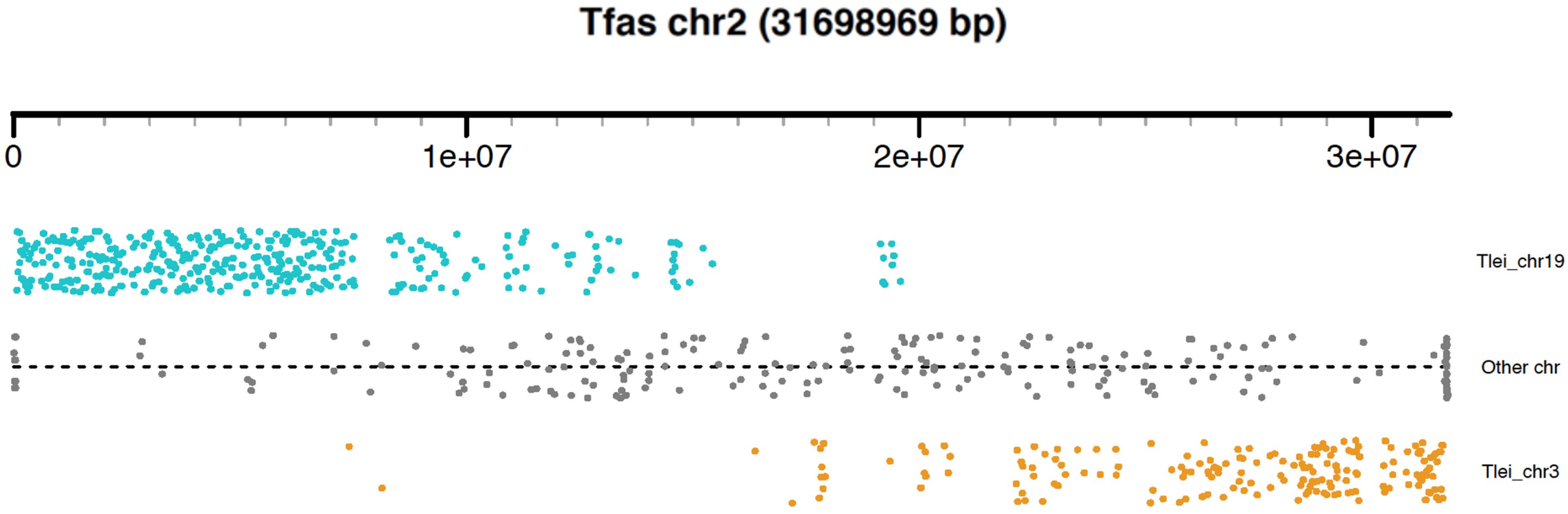

Tlei chr14 (38474115 bp)
0
1e+07
2e+07
3e+07
Tfas_chr17
Other chr
Tfas_chr25


Tlei chr14 (38474115 bp)
0
1e+07
2e+07
3e+07
Tfas_chr17
Other chr
Tfas_chr25
28.4
28.5
28.6
28.7
~ 36.8 kb
Tlei_chr17
Other chr
Tlei_chr25
~ 50 % overlap with alignment from another chr

Raw pacbio data seems to span the region continuously

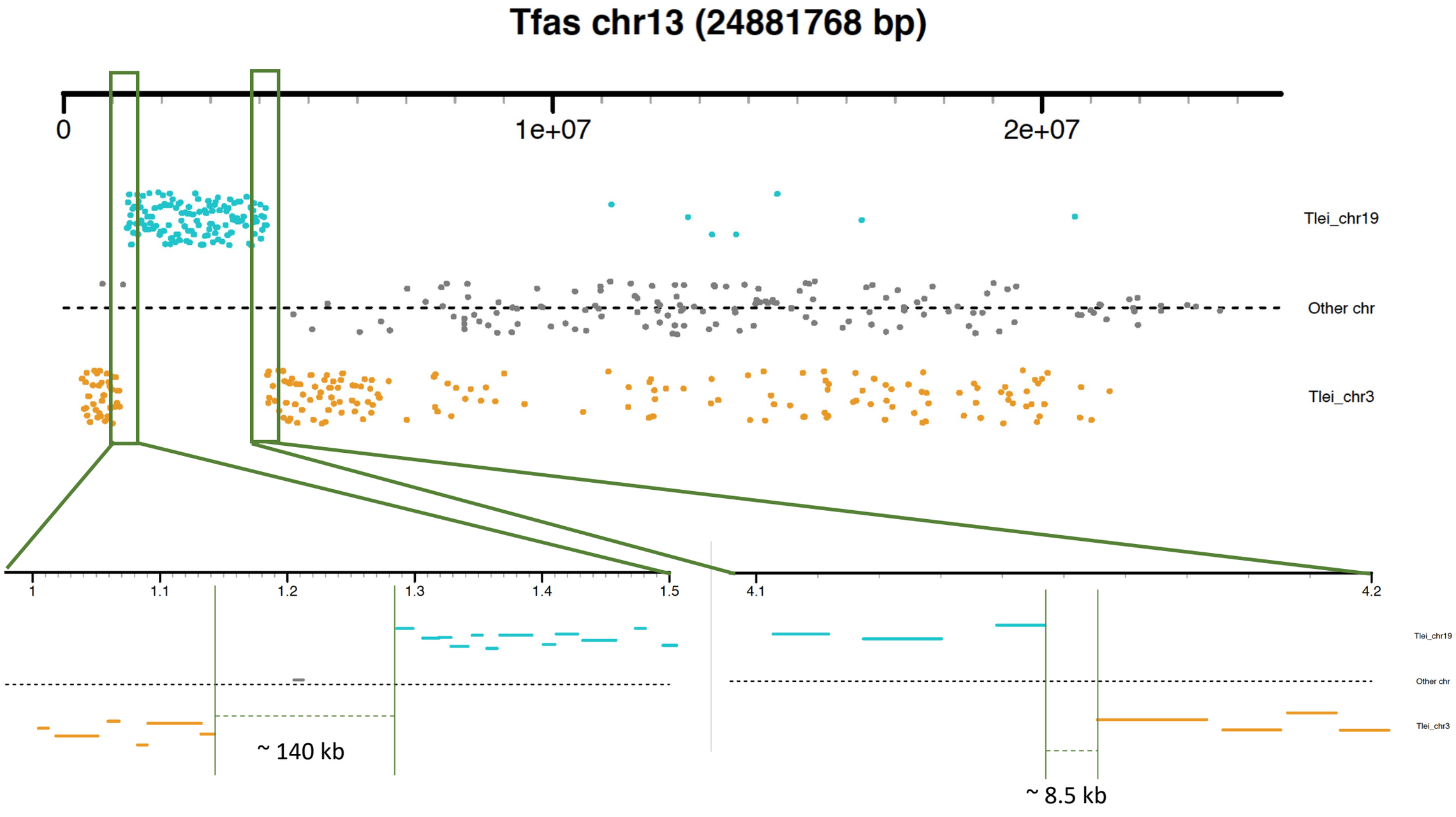



Tfas chr2 (31698969 bp)
0
1e+07
2e+07
3e+07
Tlei_chr19
Other chr
Tlei_chr3
Tfas chr13 (24881768 bp)
0
1e+07
2e+07
Tlei_chr19
Other chr
Tlei_chr3

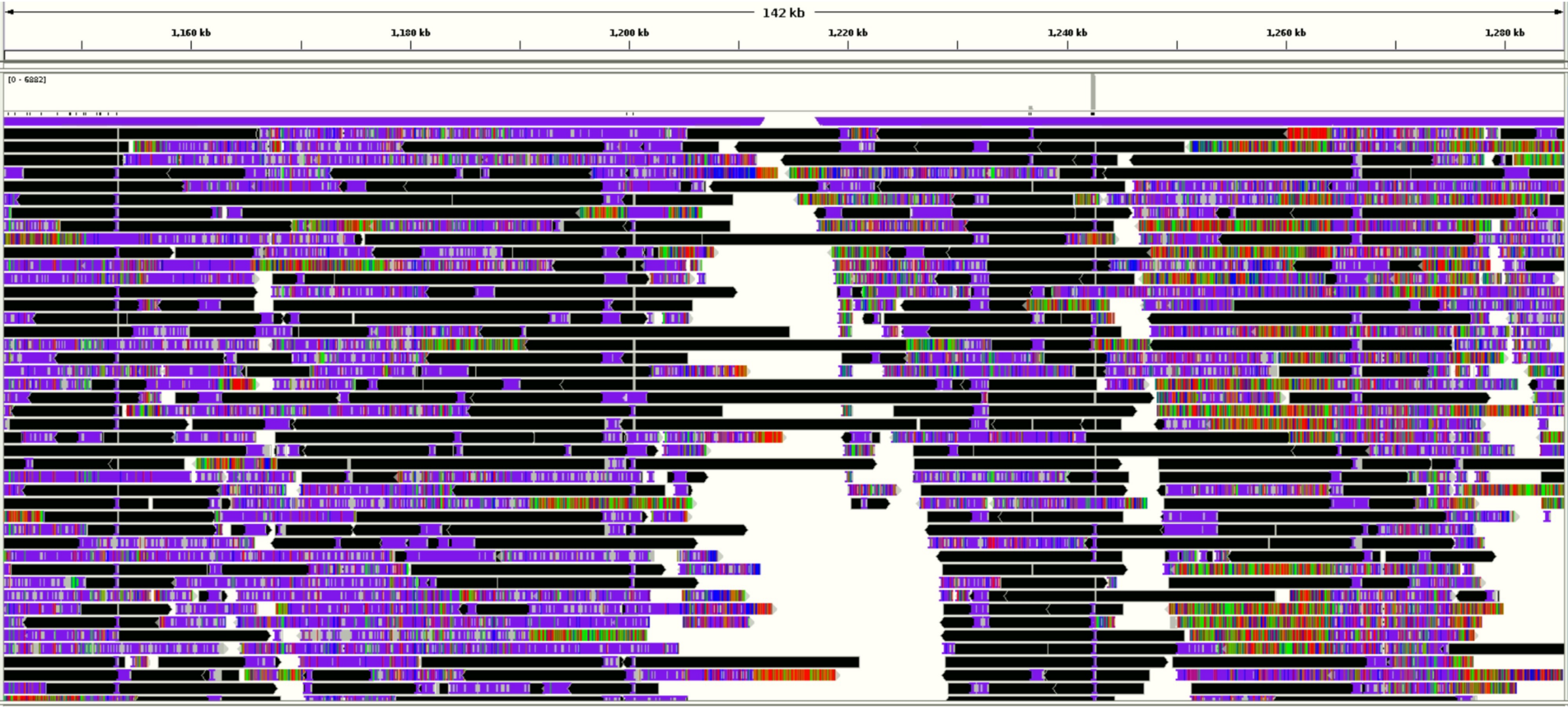


After removing non-unique alignments, it looks even more like each arm of chromosome 2 is syntenic with chromosomes 19 and 3 in Tlei.

However the resolution of alignment is too low to determine a breakpoint.

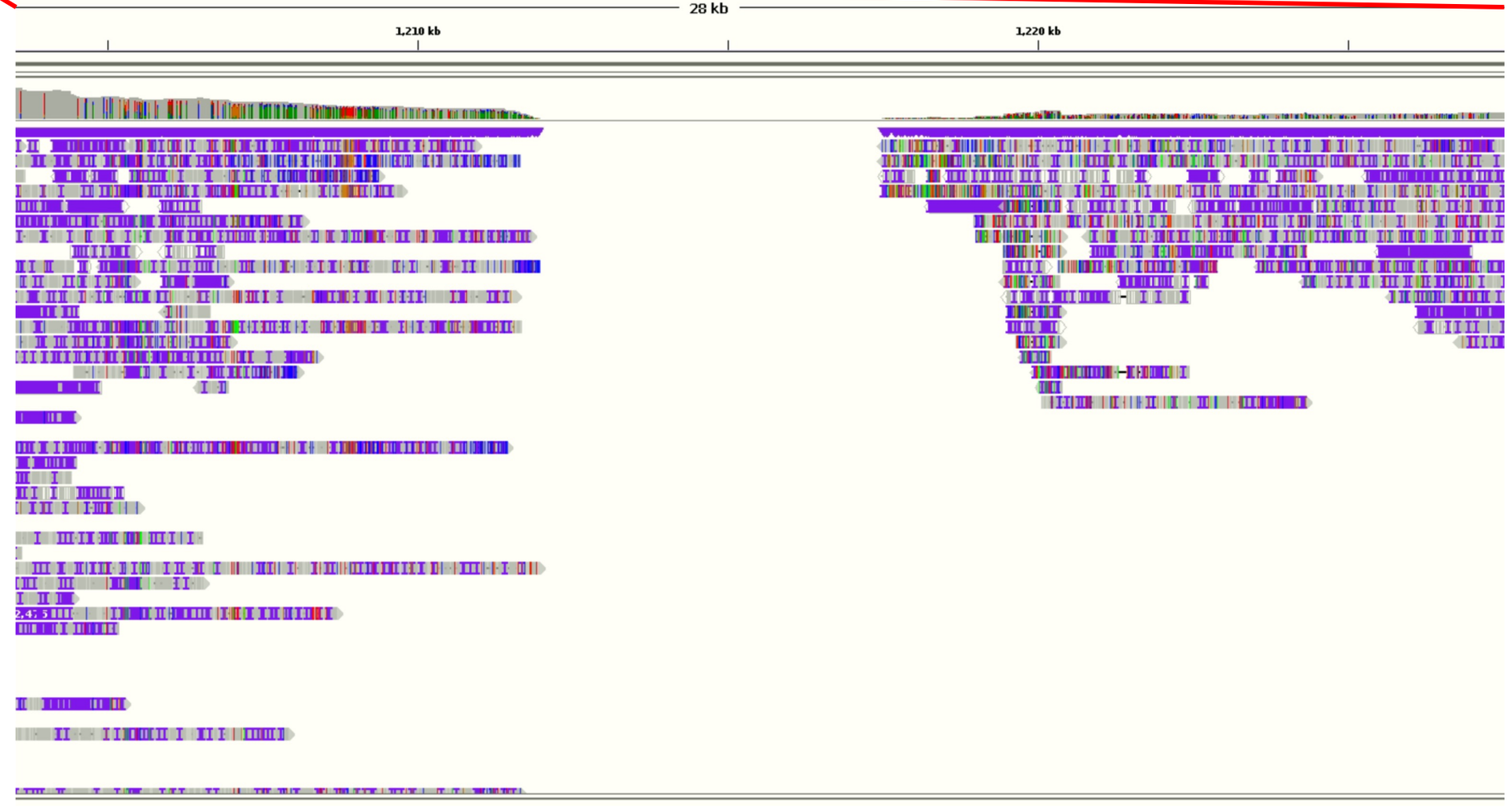

Tfas chr13 (24881768 bp)
0
1e+07
2e+07
Tlei_chr19
Other chr
Tlei_chr3
1
1.1
1.2
1.3
1.4
1.5
4.1
4.2
~ 140 kb
~ 8.5 kb

Breakpoint 1 – black are softclipped bases. There seems to be a gap in the alignment.

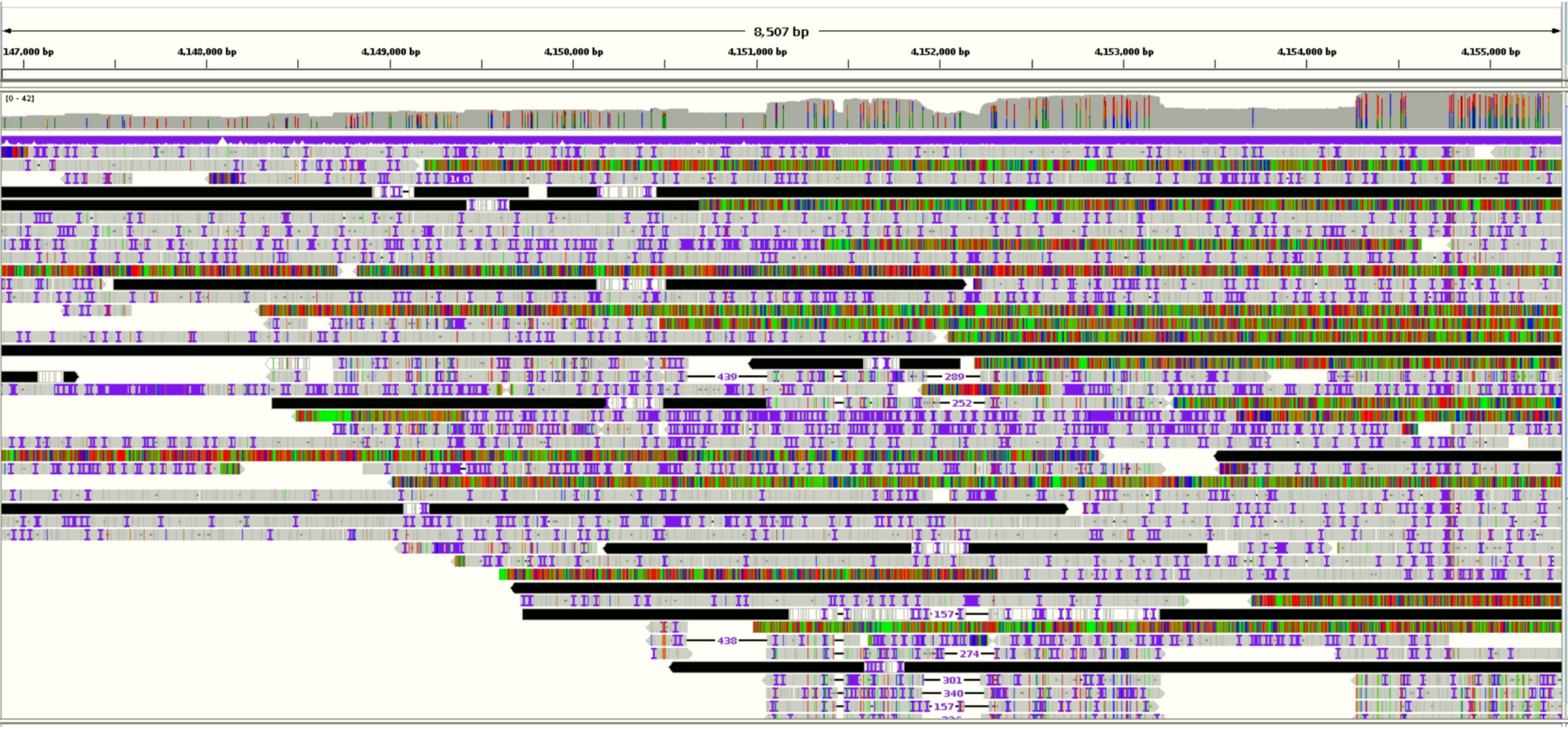


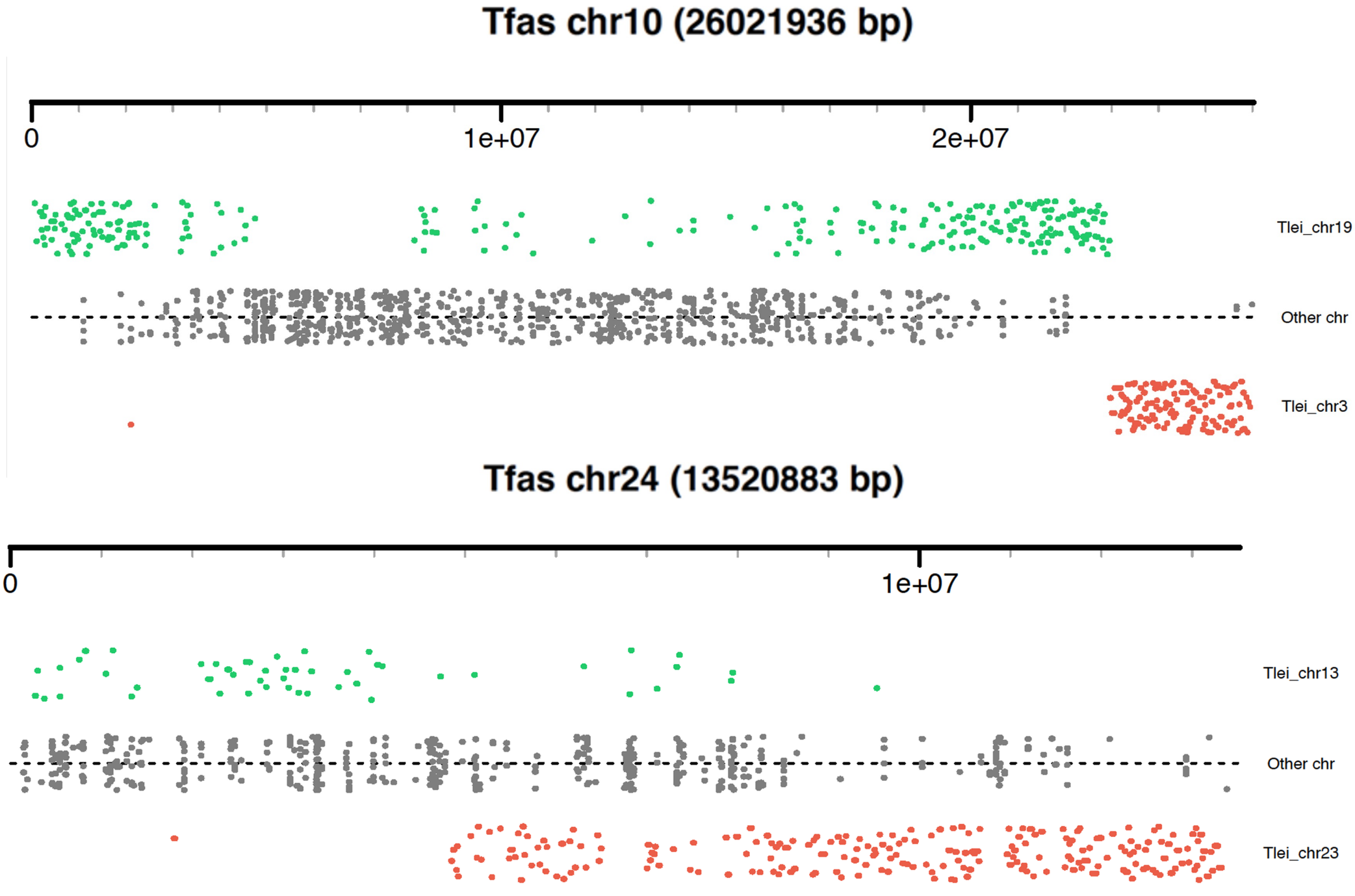
Breakpoint 1 – black are softclipped bases. There seems to be a gap in the alignment.

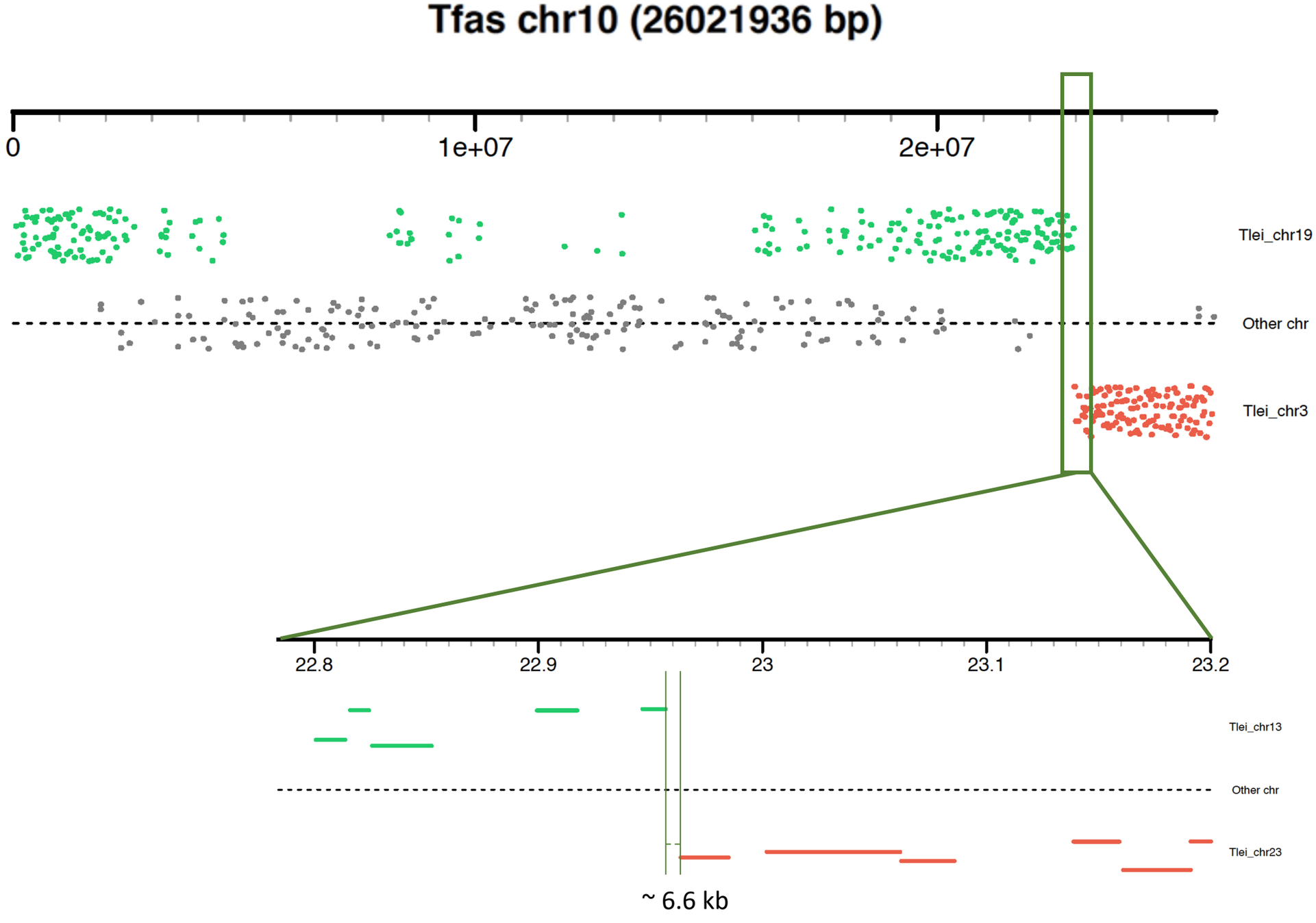
Importantly, the sequence is not a gap of Ns here

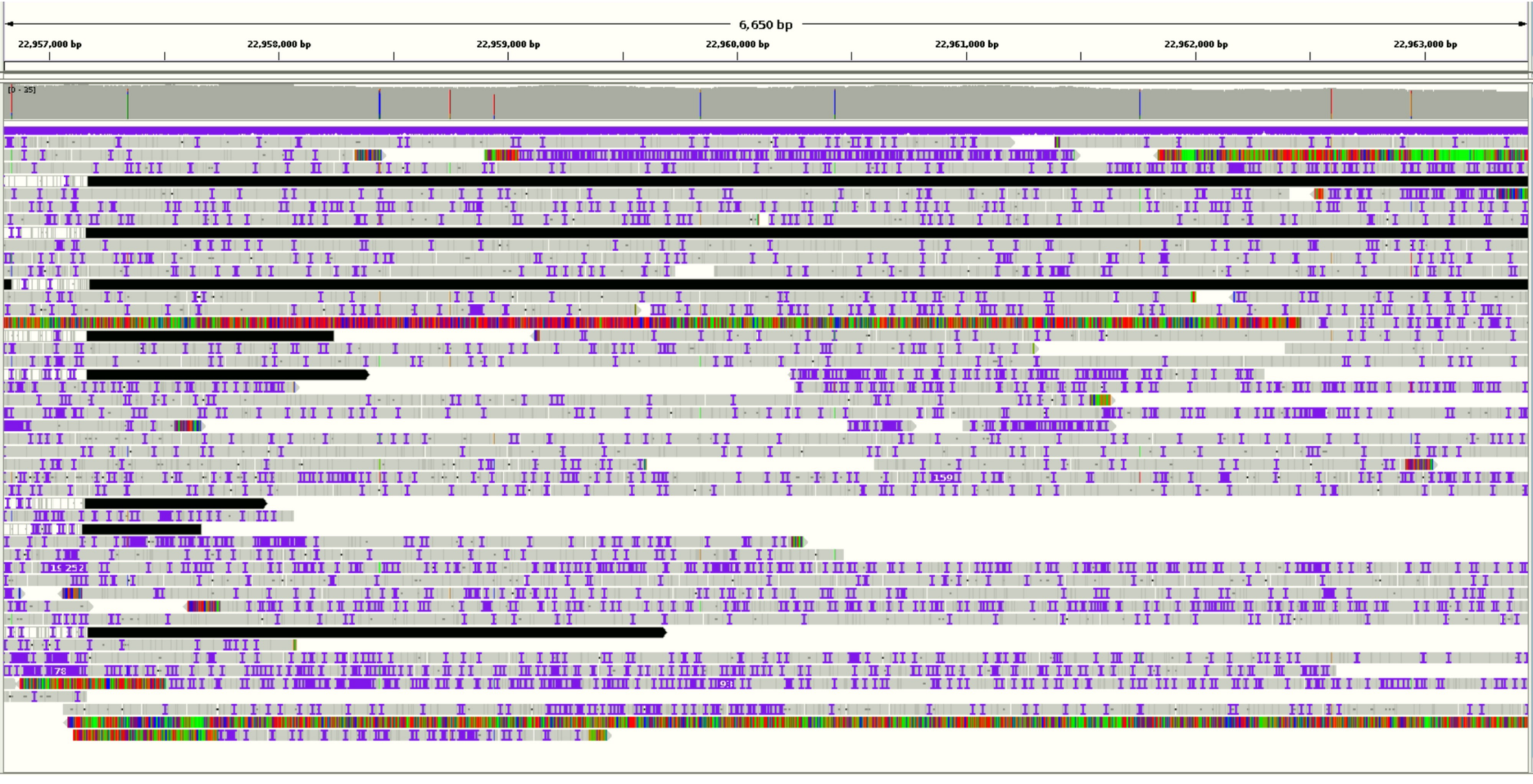


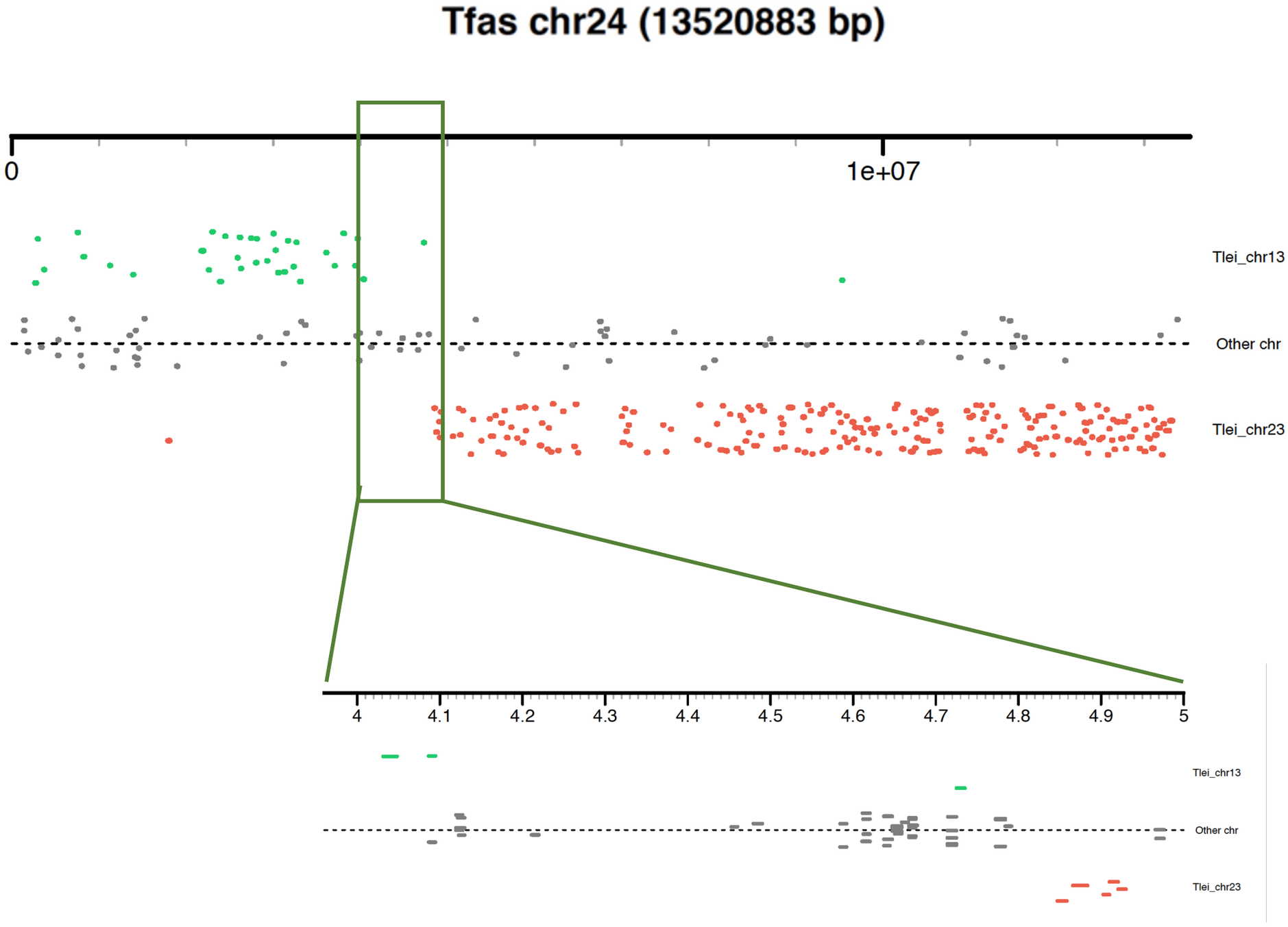
Breakpoint 2.

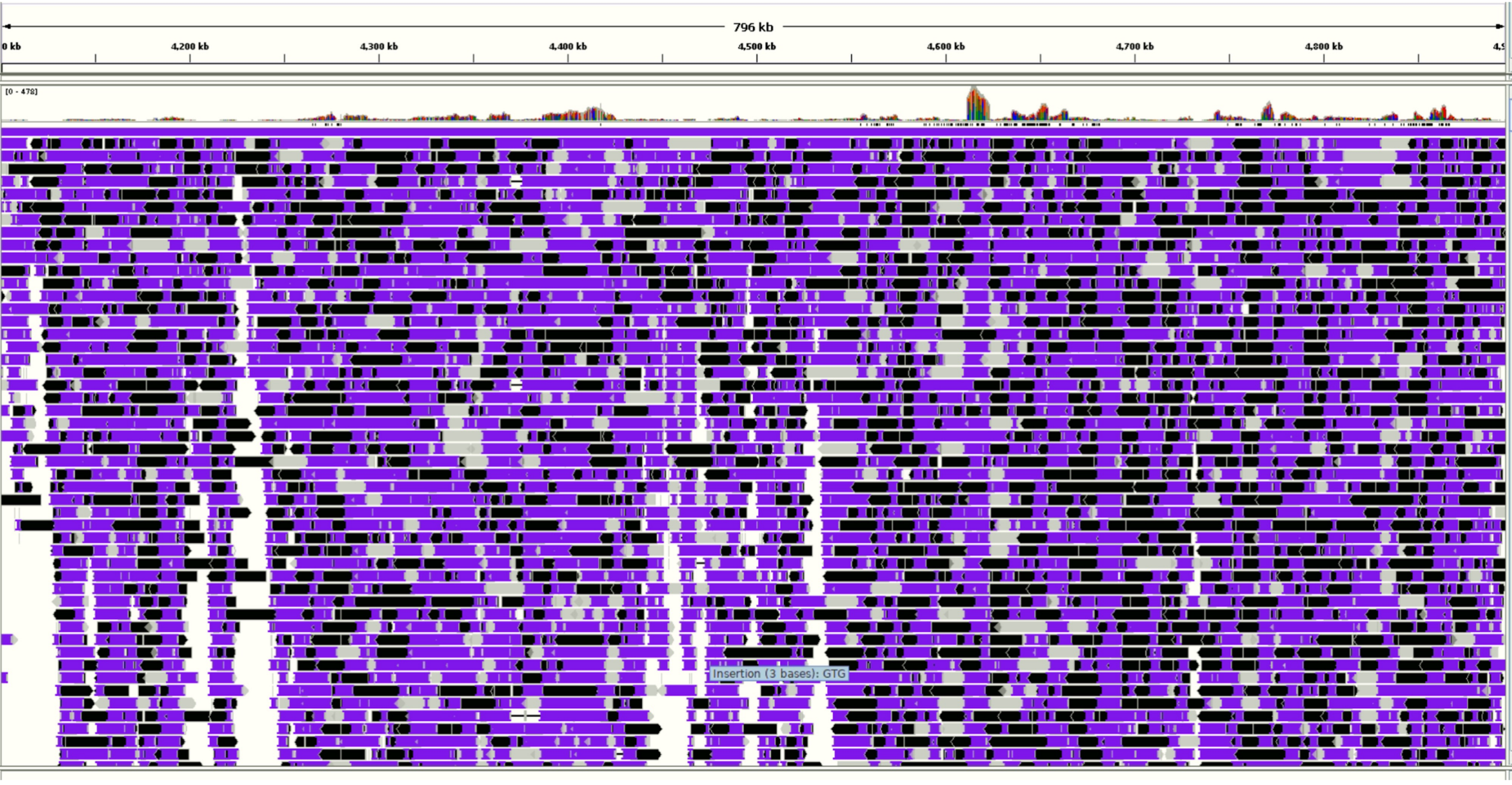



Tfas chr10 (26021936 bp)
0
1e+07
2e+07
Tlei_chr19
Other chr
Tlei_chr3
Tfas chr24 (13520883 bp)
0
1e+07
Tlei_chr13
Other chr
Tlei_chr23


Tfas chr10 (26021936 bp)
0
1e+07
2e+07
Tlei_chr19
Other chr
Tlei_chr3
22.8
22.9
23
23.1
23.2
Tlei_chr13
Other chr
Tlei_chr23
~ 6.6 kb


6,650 bp
22,957,000 bp
22,958,000 bp
22,959,000 bp
22,960,000 bp
22,961,000 bp
22,962,000 bp
22,963,000 bp
[0 - 35]


Tfas chr24 (13520883 bp)
0
1e+07
Tlei_chr13
Other chr
Tlei_chr23
4
4.1
4.2
4.3
4.4
4.5
4.6
4.7
4.8
4.9
5
Tlei_chr13
Other chr
Tlei_chr23


796 kb
0 kb
4,200 kb
4,300 kb
4,400 kb
4,500 kb
4,600 kb
4,700 kb
4,800 kb
[0 - 478]
Insertion (3 bases): GTG