

***Mycobacterium tuberculosis* resistance prediction and lineage classification
from genome sequencing: comparison of automated analysis tools**

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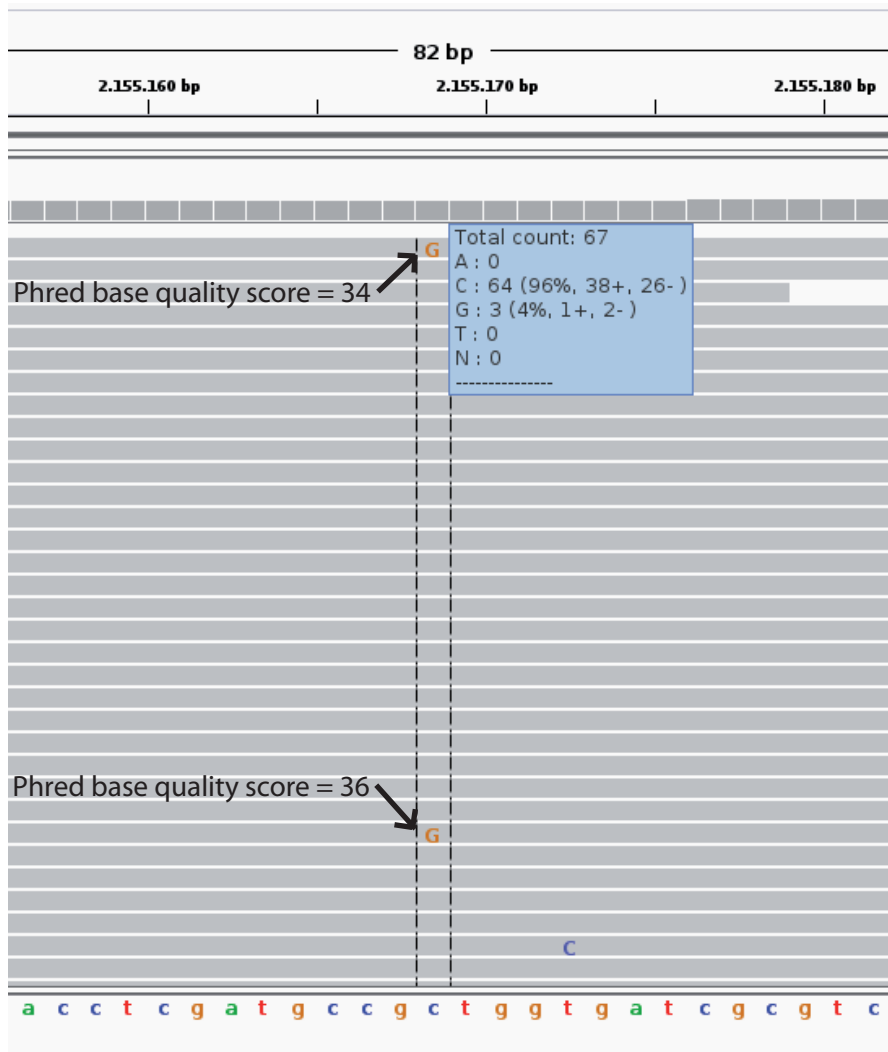
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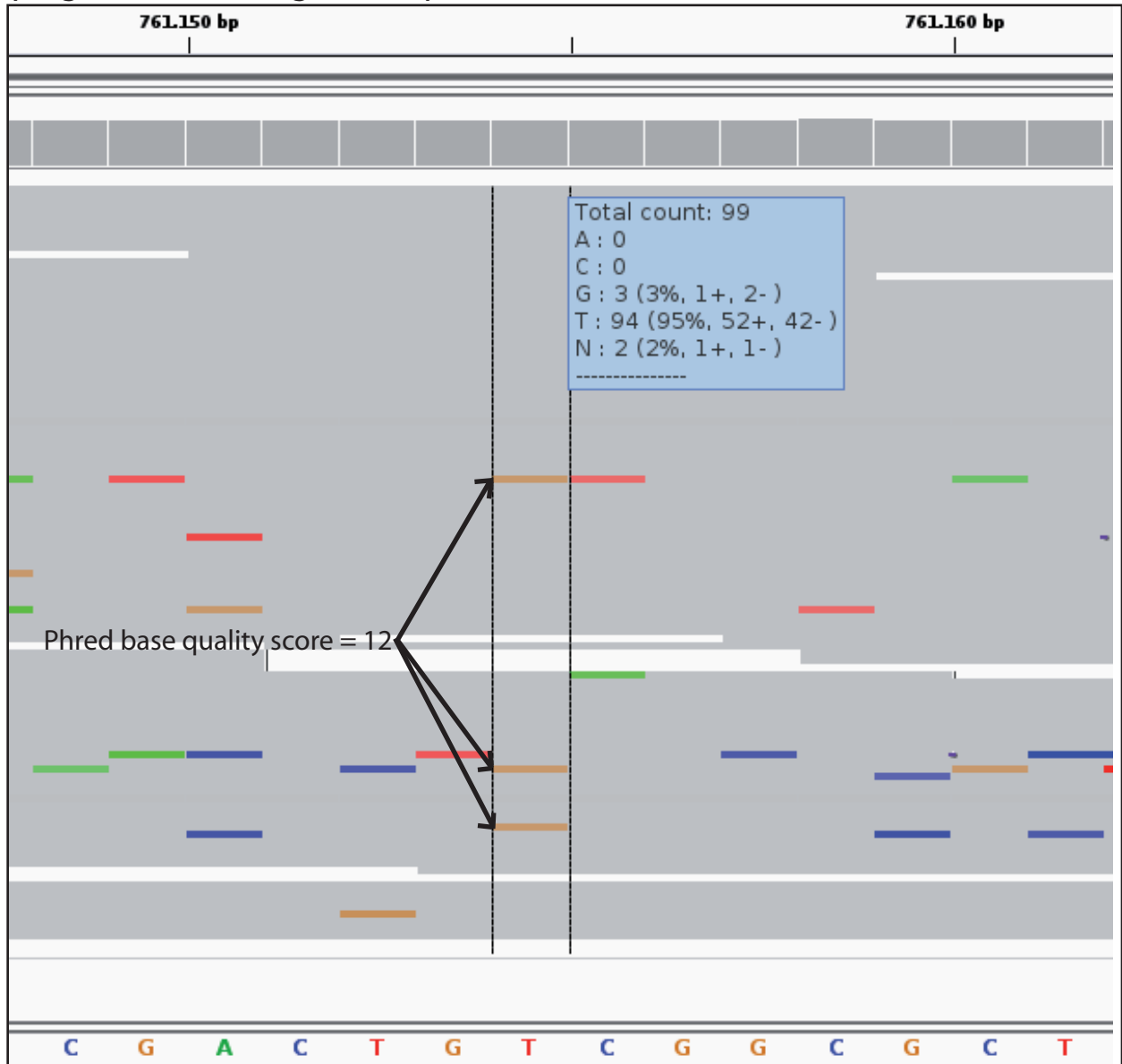
Supplementary Figure S1.

Mapping results (stampy) for Mykrobe Predictor TB's low-frequency variants in *rpoB* (n=7) and *katG* (n=1)

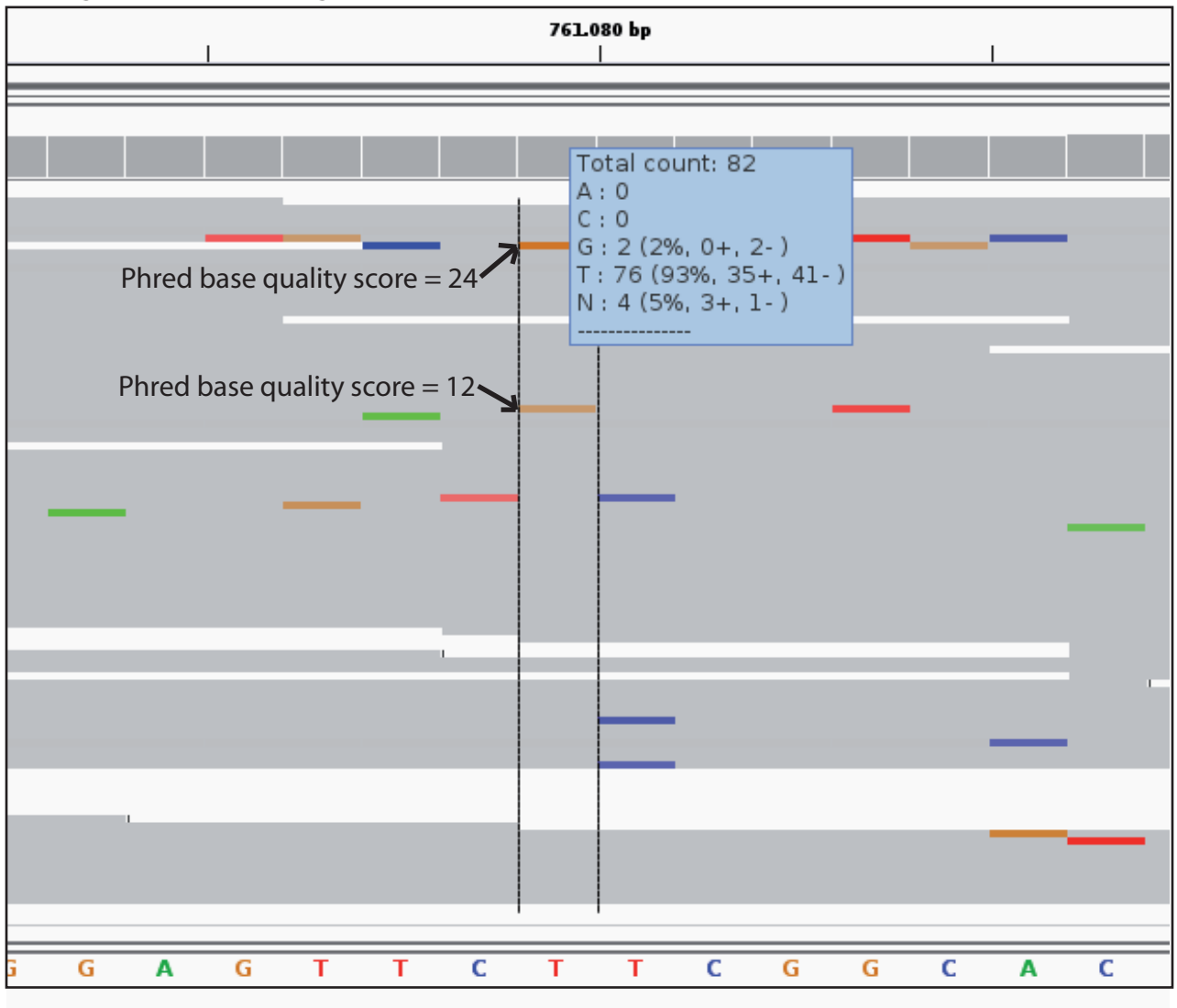
IGV mapping of 1327-04 at genome position 2155168



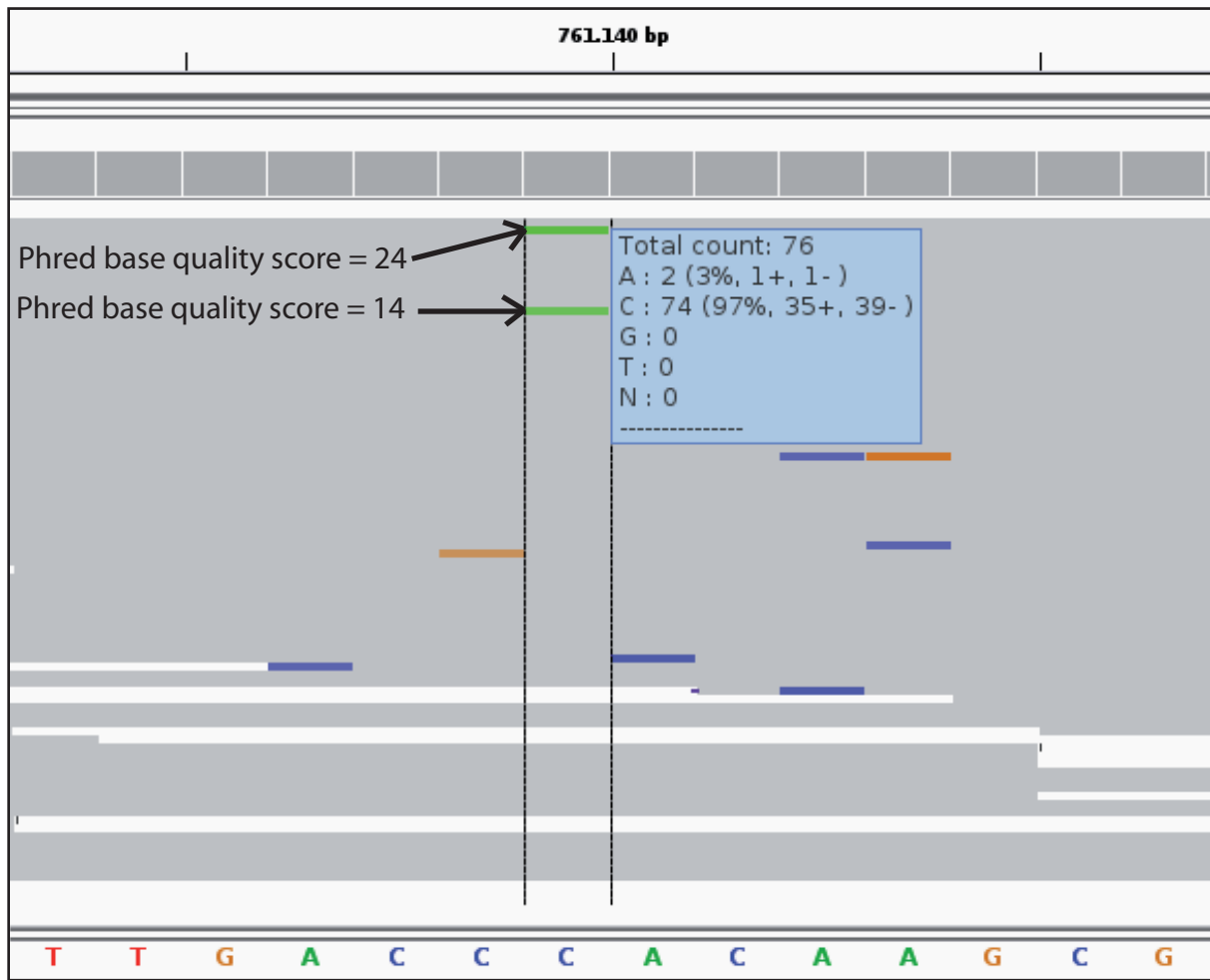
IGV mapping of 3158-04 at genome position 761154



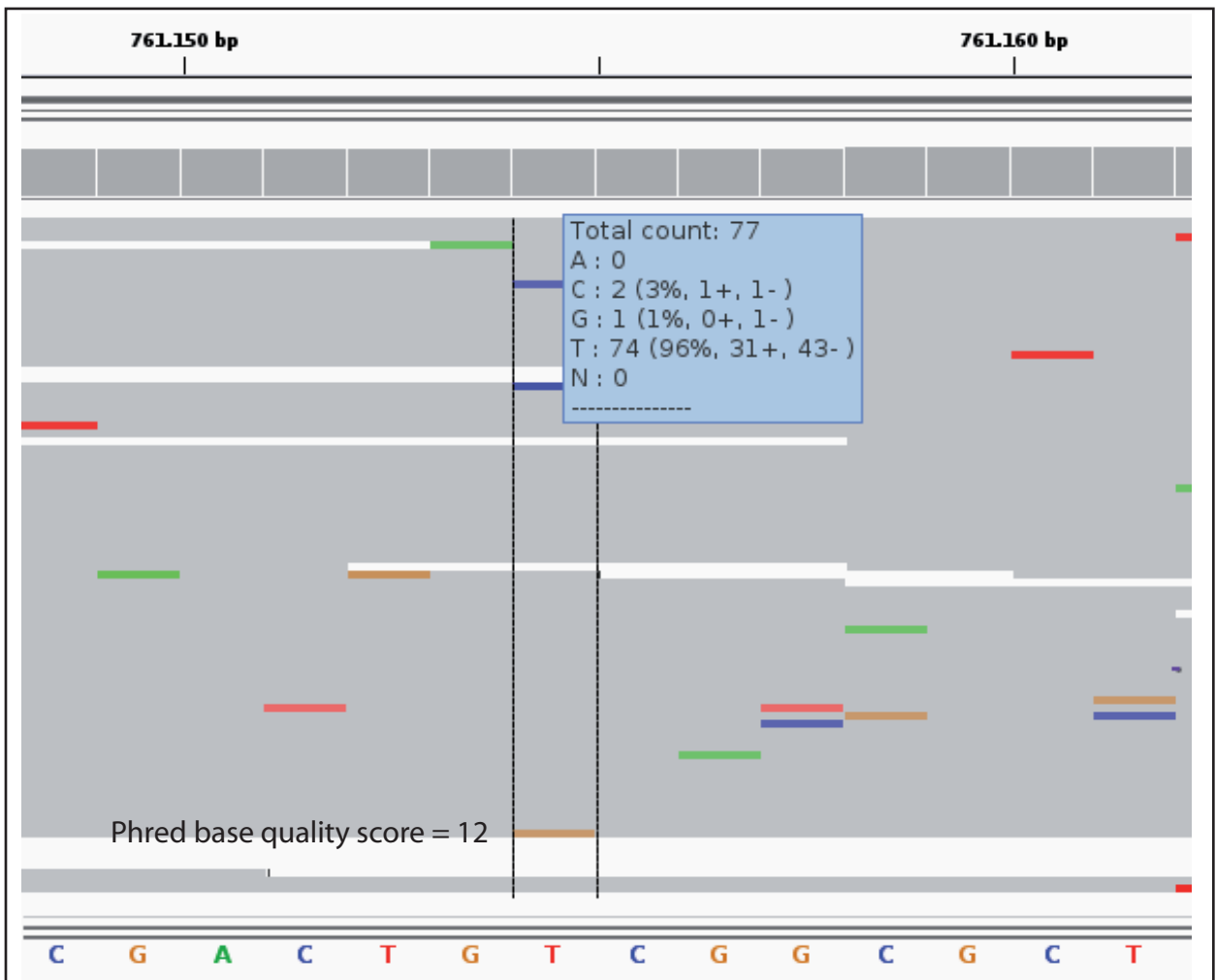
IGV mapping of 4712-04 at genome position 761079



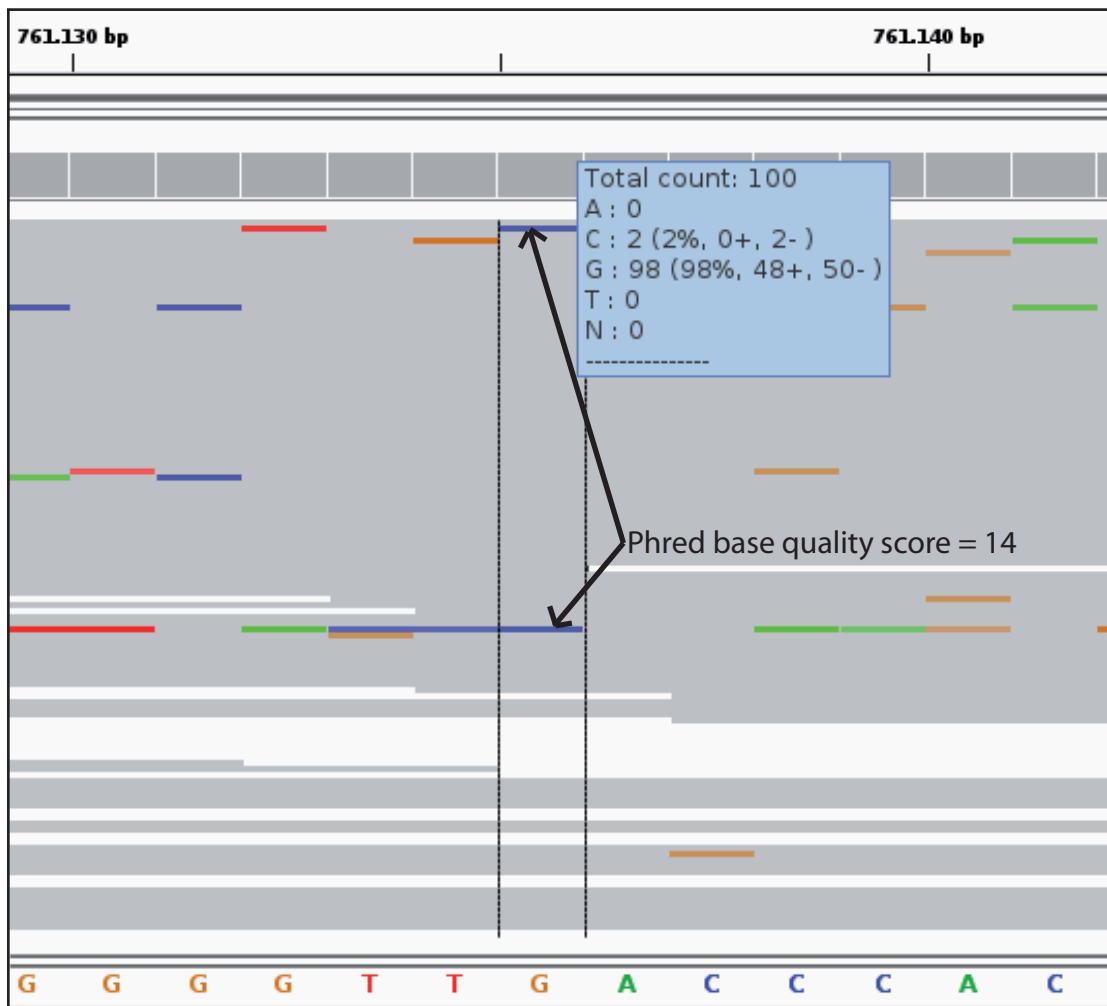
IGV mapping of 4717-04 at genome position 761139



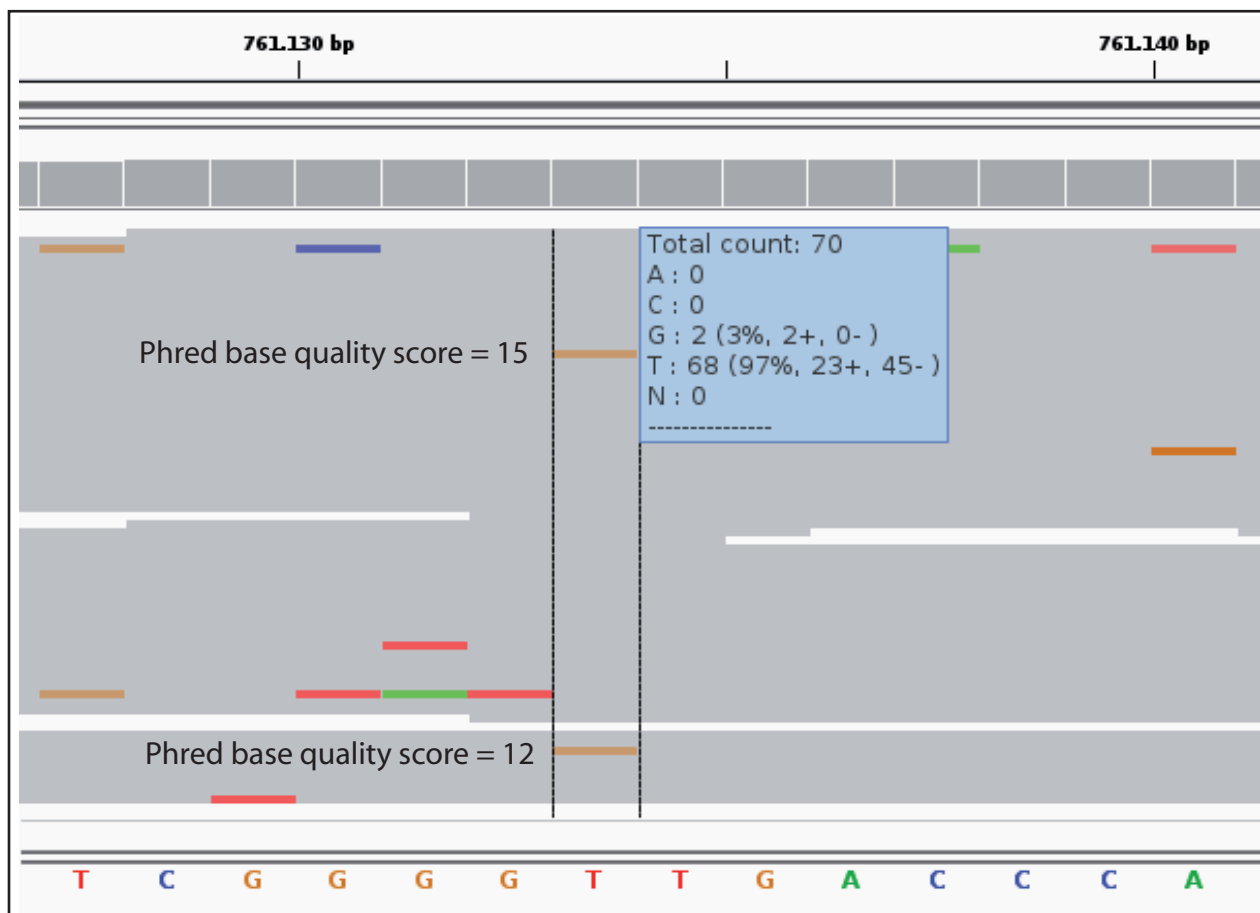
IGV mapping of 6640-04 at genome position 761154



IGV mapping of 8082-03 at genome position 761133



IGV mapping of 10205-03 at genome position 761133



IGV mapping of 11818-03 at genome position 761108

