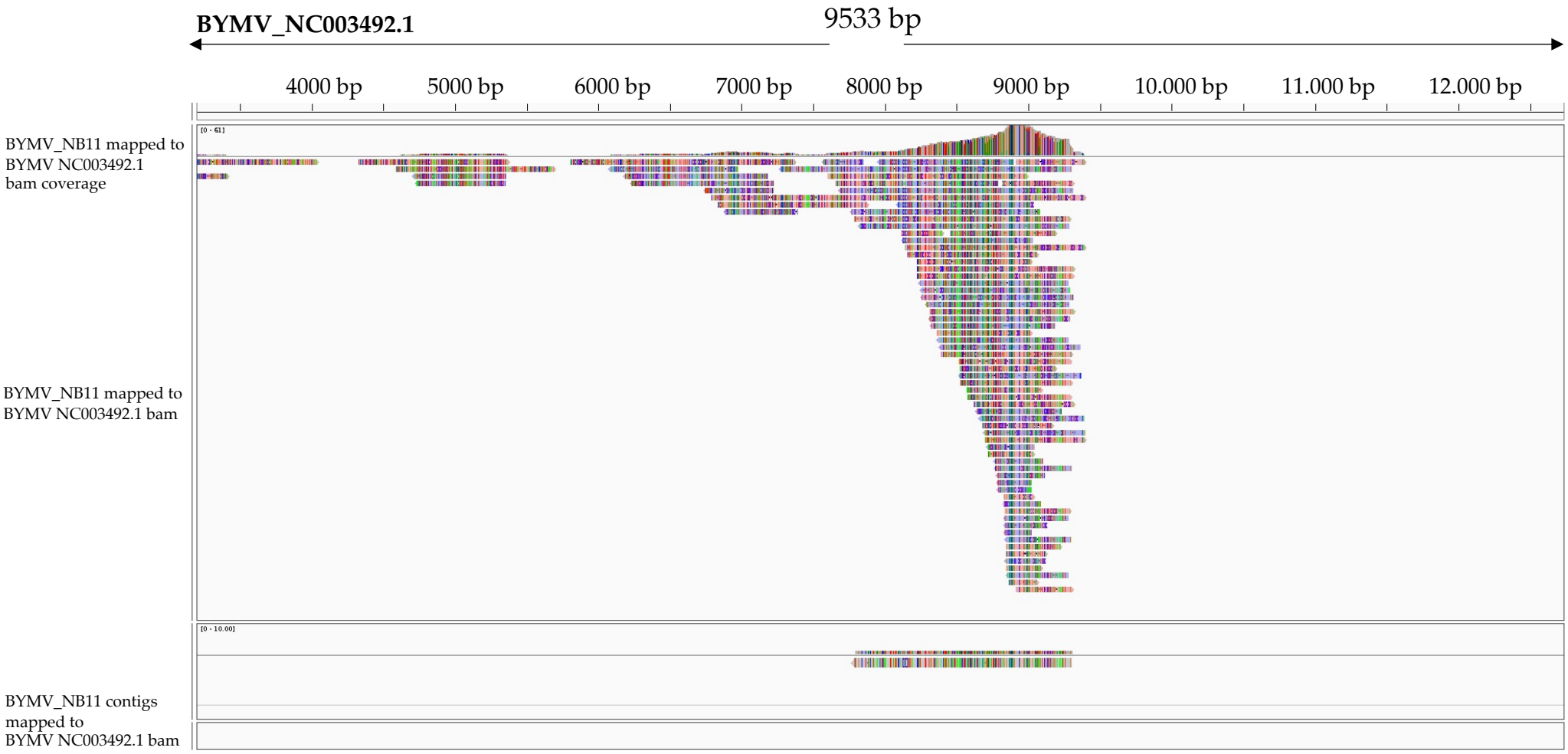

Figure S1 – Reads from sample NB11 assigned to BYMV and resulting contig. Reads from sample NB11 assigned to BYMV are aligned back to BYMV_NC003492.1 genome and visualized in IGV genome browser. A contig obtained assembling such reads is also aligned back to BYMV_NC003492.1 genome. The alignments of both reads and contig show a high number of systematic differences, suggesting biological differences between the sequenced strain and the strain available in the database, rather than sequencing errors.

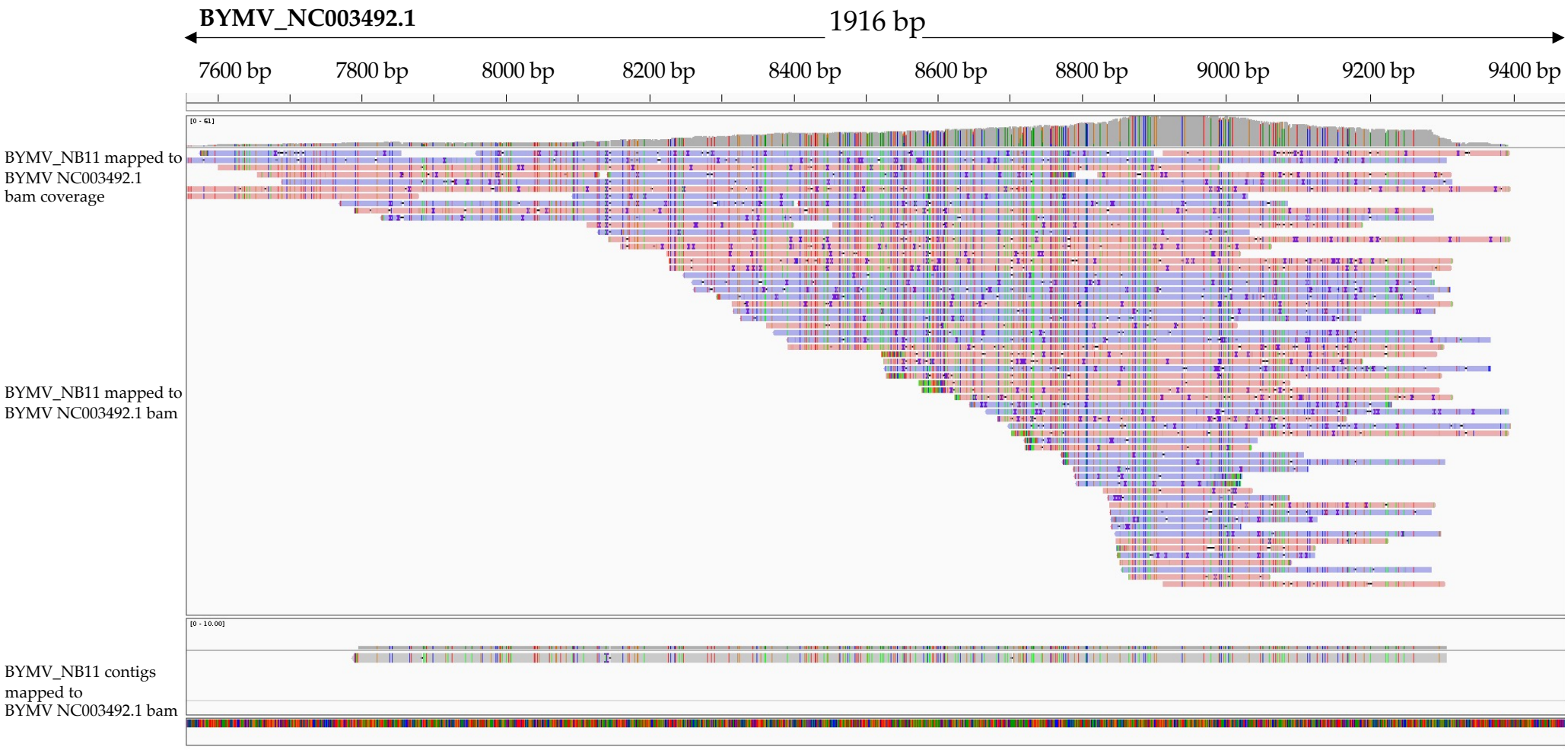

Figure S2 – Reads from sample NB11 assigned to BYMV and resulting contig, magnification.