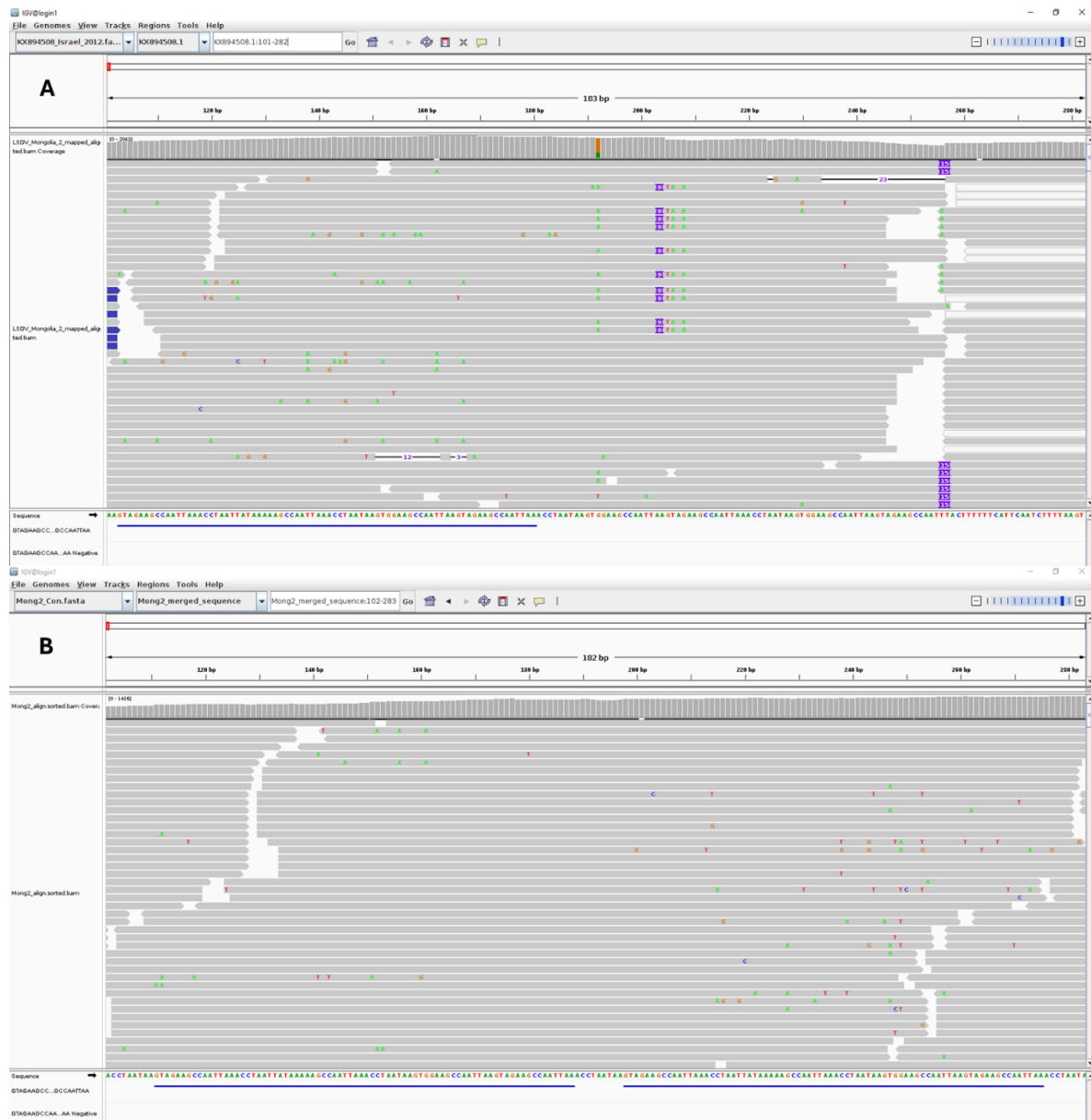
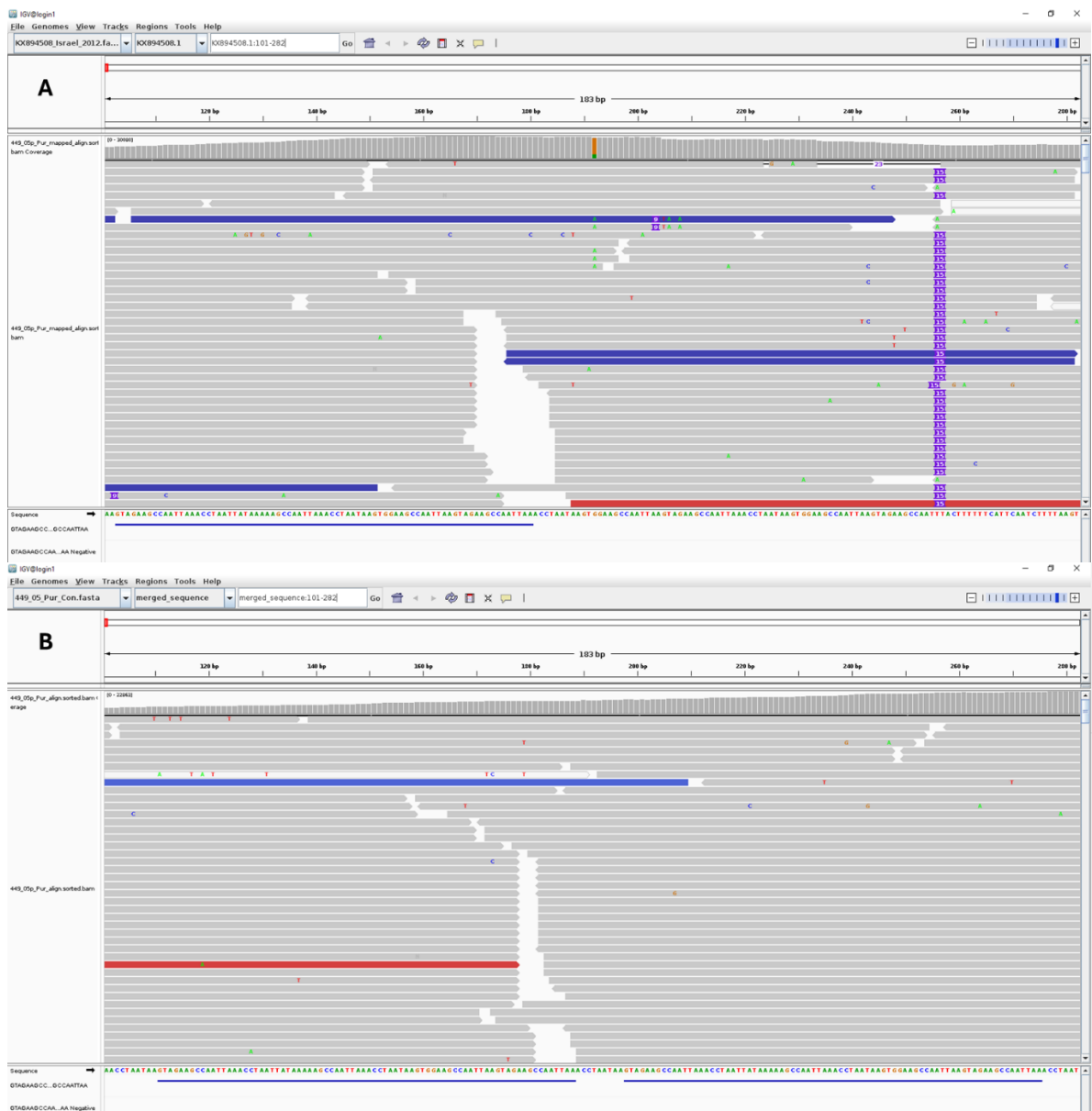
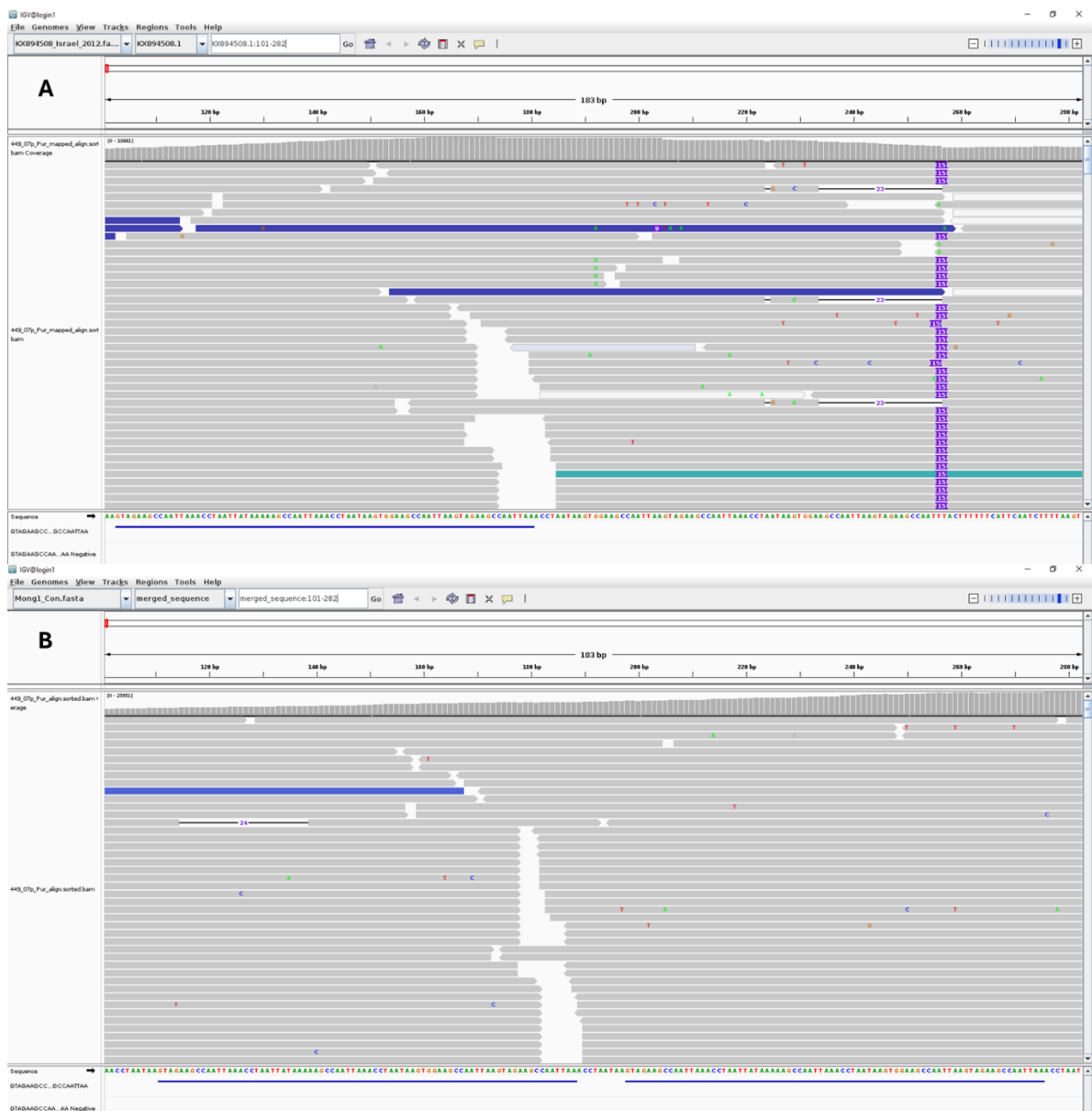


## Supplementary data 1

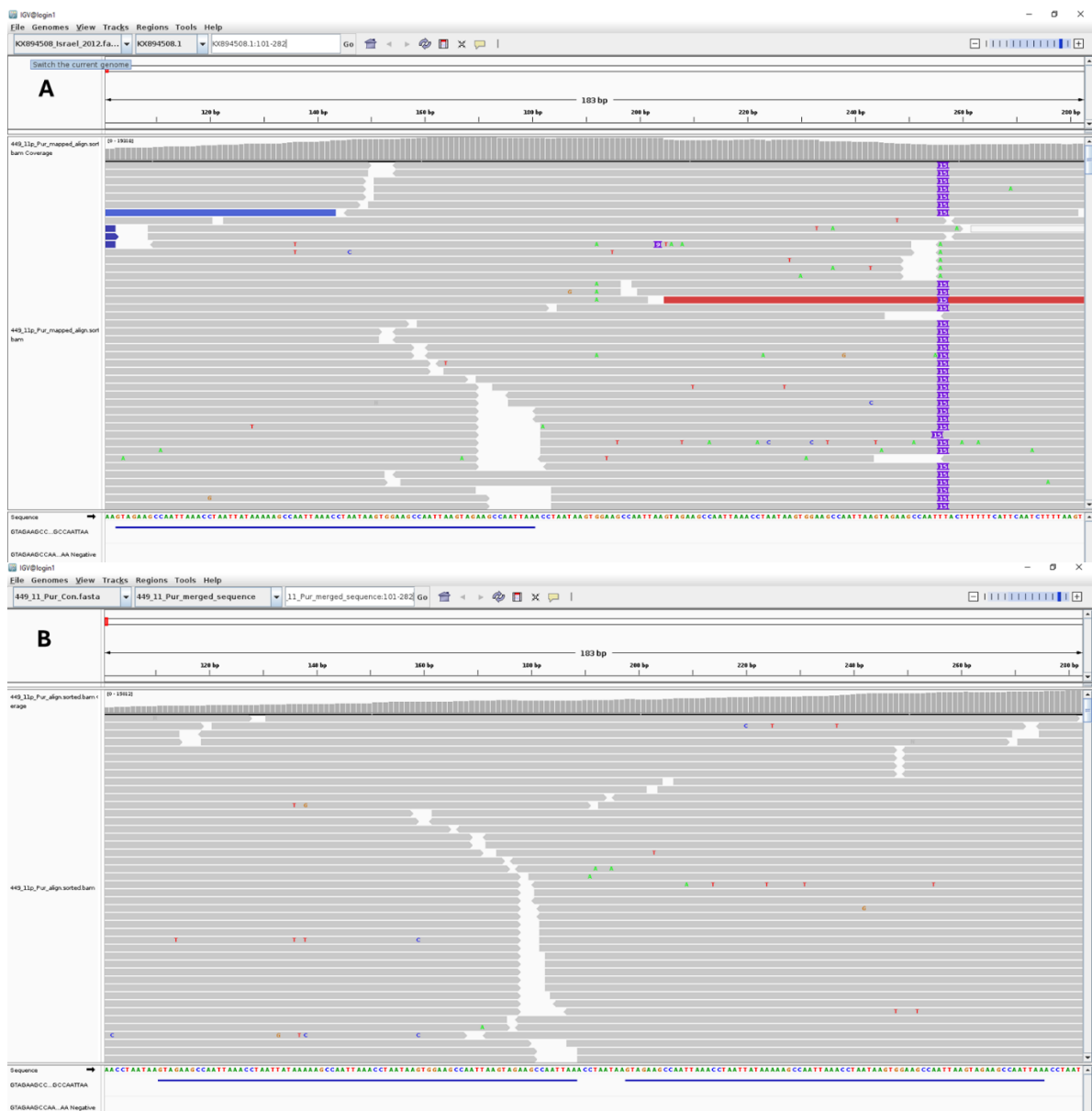


**Figure S1i:** IGV screenshot of LSDV\_Mongolia\_2\_2021 QC filtered paired-end reads mapped to the KX894508.1 reference sequence (A), and the hybrid consensus generated for the LSDV\_Mongolia\_2\_2021 dataset during this project (B).



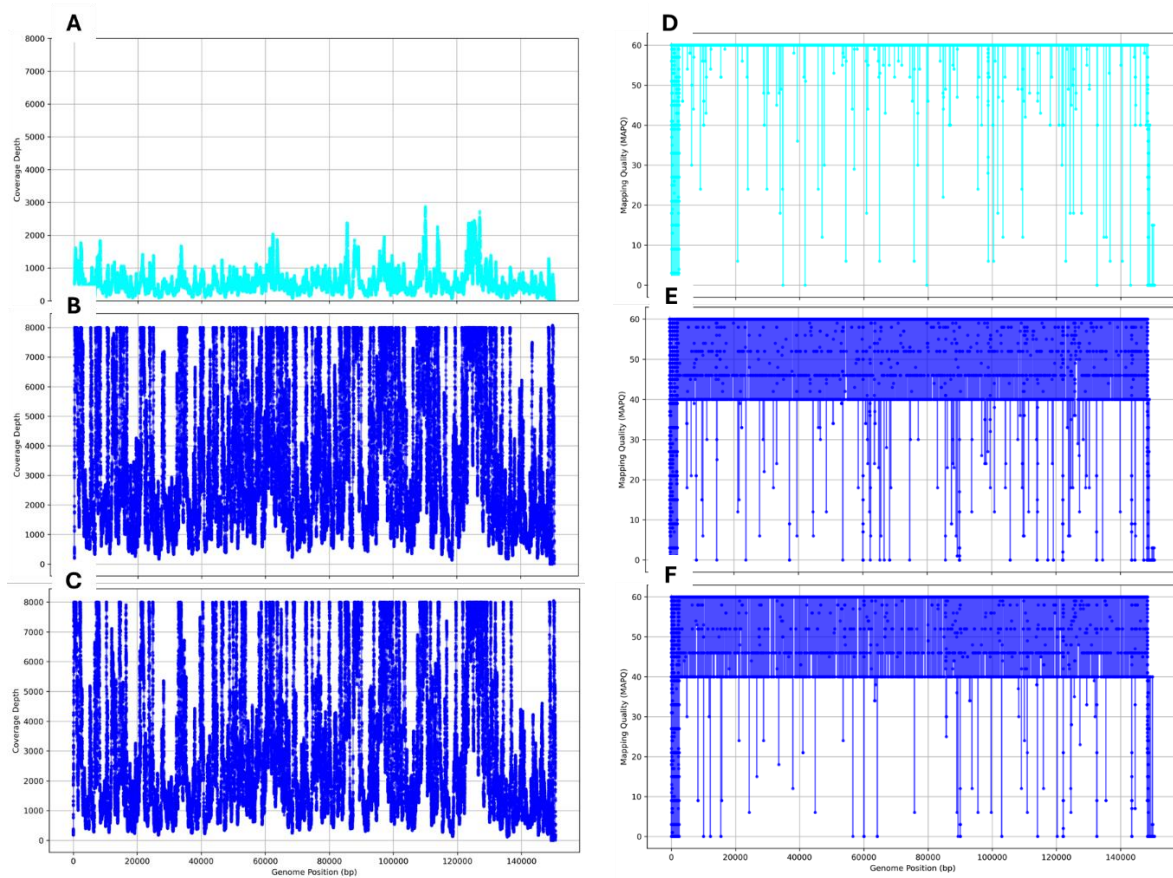


**Figure S1iii:** IGV screenshot of 449\_07\_Sukhbaatar\_2022 QC filtered paired-end reads mapped to the KX894508.1 reference sequence (A), and the hybrid consensus generated for the 449\_07\_Sukhbaatar\_2022 dataset during this project (B).



**Figure S1iv:** IGV screenshot of 449\_11\_Dornod\_2022 QC filtered paired-end reads mapped to the KX894508.1 reference sequence (A), and the hybrid consensus generated for the 449\_11\_Dornod\_2022 dataset during this project (B).

## Supplementary data 2



**Figure S2:** Per base coverage plots (A-C) and per base read mapping quality (D-F) of QC filtered paired-end reads mapped back onto the hybrid consensus sequence generated for that dataset, across genome position, for LSDV\_Mongolia\_2\_2021(A&D), 449\_07\_Sukhbaatar\_2022 (B&E) and 449\_11\_Dornod\_2022 (C&F).