

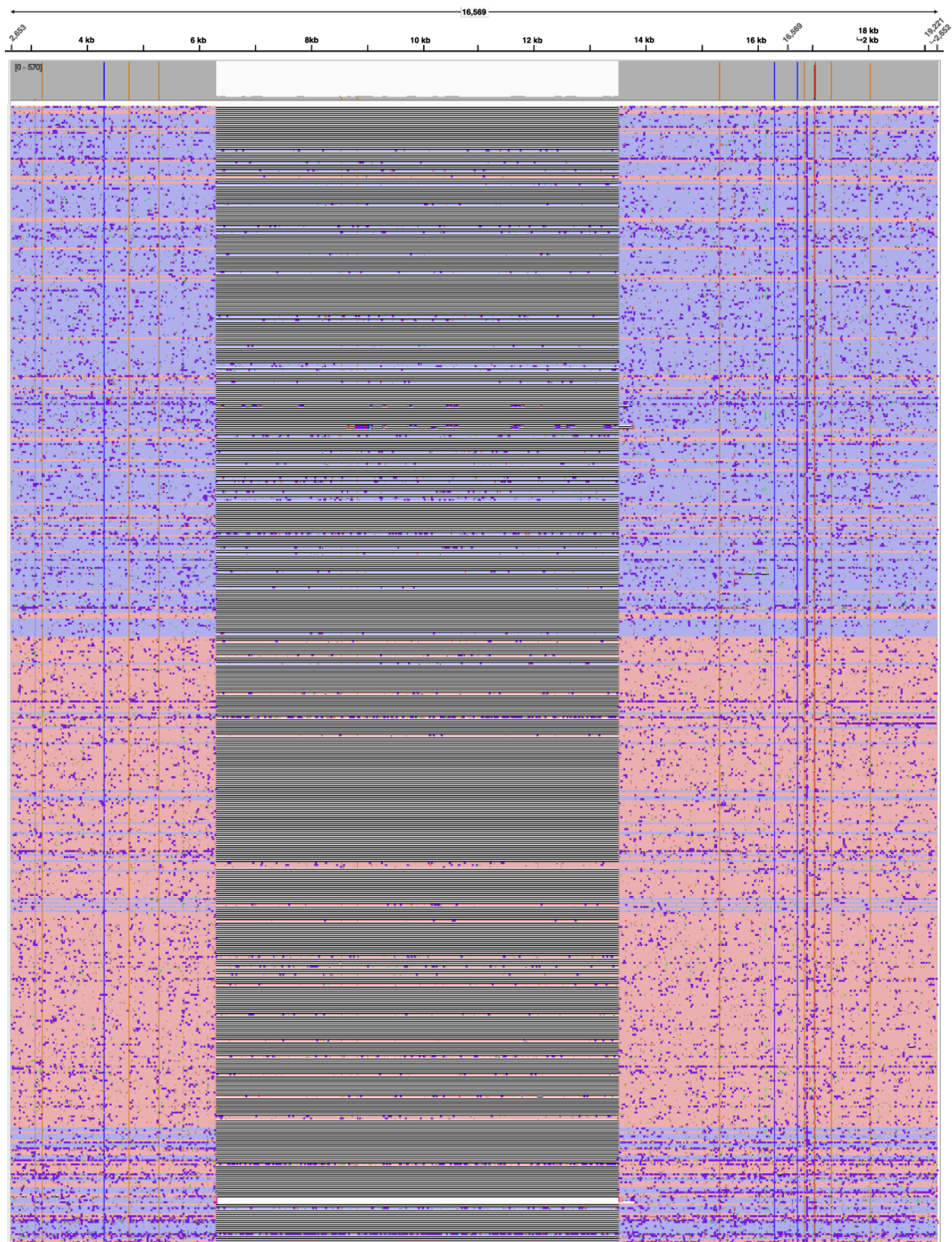
Nanomito enables amplification-free full-length analysis of mitochondrial DNA variants and deletions

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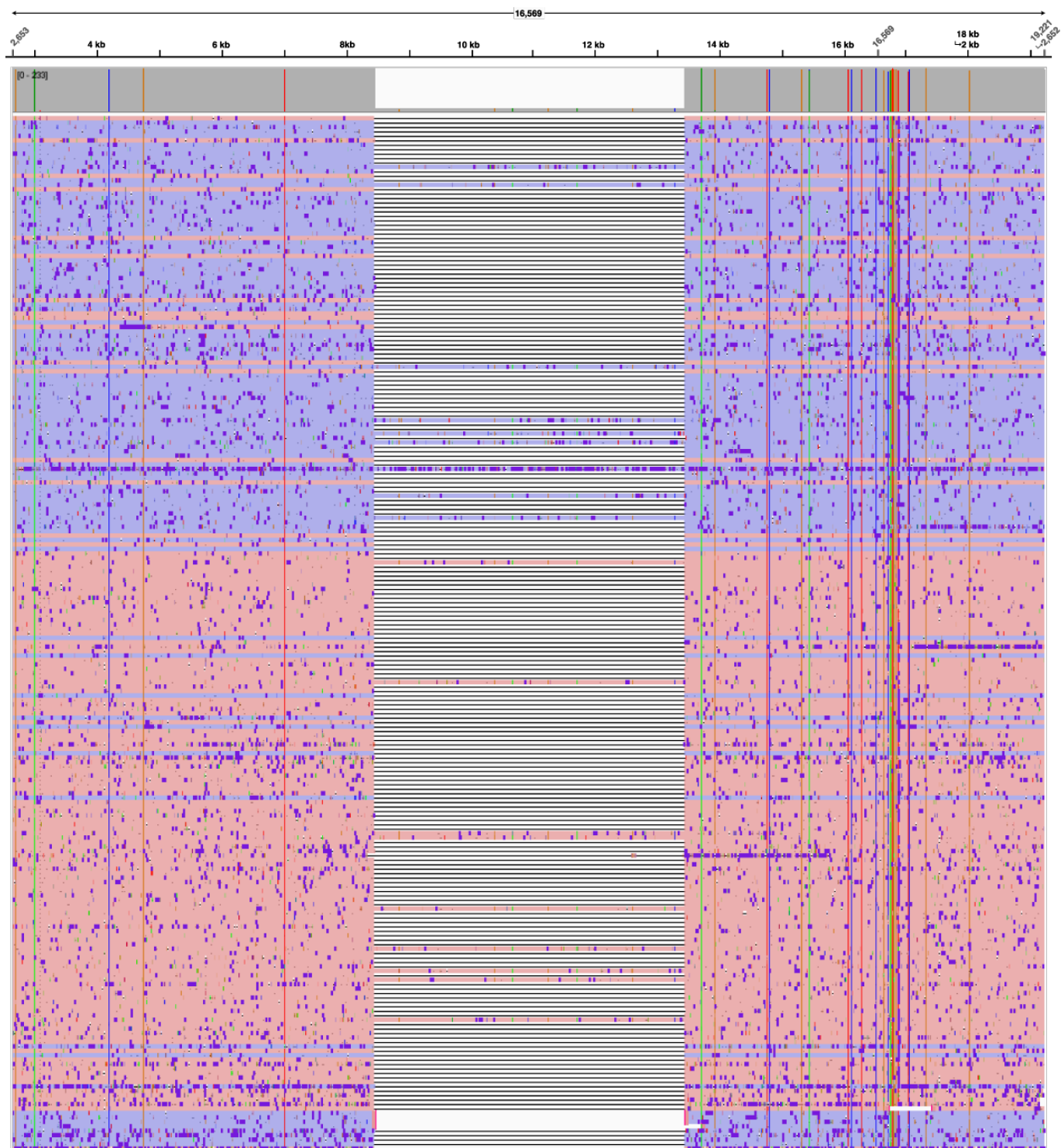
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Supplementary Fig. S1. Integrative Genomics Viewer (IGV) visualization of reads from sample DEL-1 obtained by amplification-free long-read sequencing, showing a primary large-scale mtDNA deletion, m.6332_13516del, spanning 7,185 bp and detected at 90.1% heteroplasmy based on 570 complete mtDNA molecules. Alignments are displayed in squished mode with strand-specific coloring. The coverage track and coordinates, shown above the alignments, are displayed both as linear positions on the tandem reference and as circular genome coordinates (modulo 16,569). Full-length mtDNA molecules appear as continuous alignments, whereas deleted molecules show gaps corresponding to the missing segment, visible as thin black lines on a white background.



Supplementary Fig. S2. IGV visualization of reads from sample DEL-2 obtained by amplification-free long-read sequencing, showing a primary large-scale mtDNA deletion, m.8470_13446del, spanning 4,977 bp and detected at 92.2% heteroplasmy based on 233 complete mtDNA molecules. Alignments are displayed in squished mode with strand-specific coloring. The coverage track and coordinates, shown above the alignments, are displayed both as linear positions on the tandem reference and as circular genome coordinates (modulo 16,569). Full-length mtDNA molecules appear as continuous alignments, whereas deleted molecules show gaps corresponding to the missing segment, visible as thin black lines on a white background.