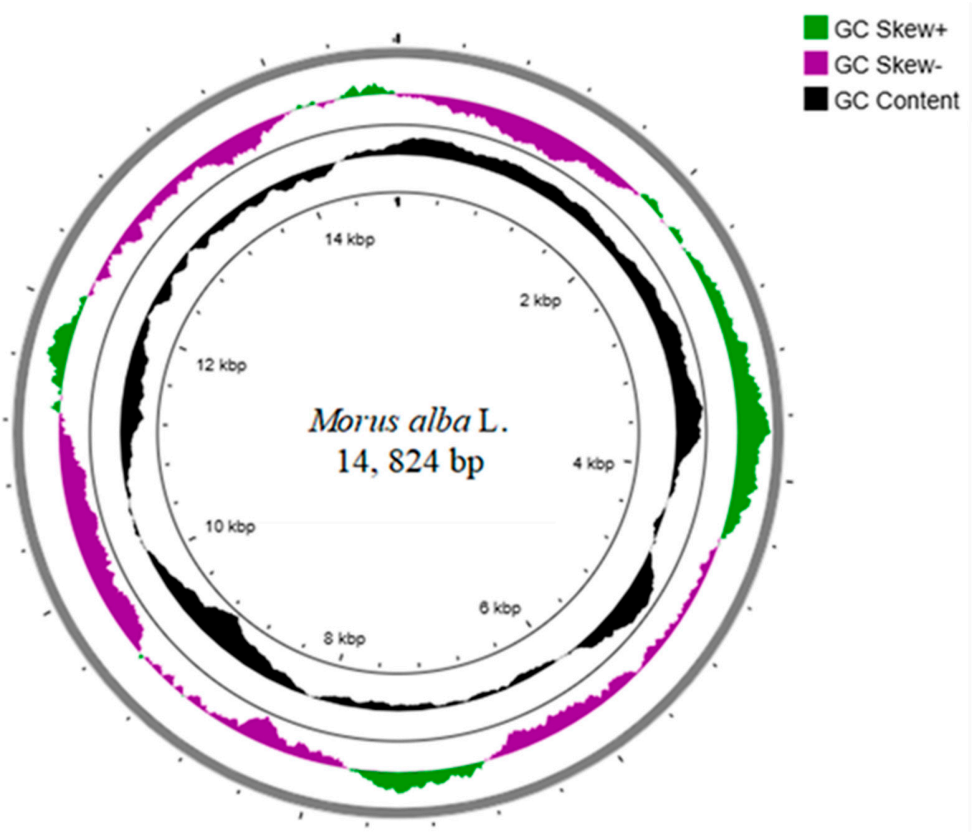
Supplementary Information

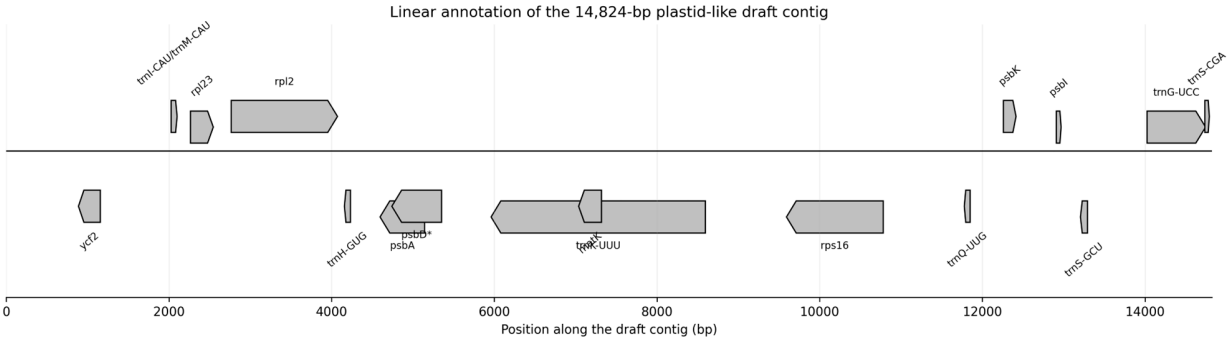
Interpretive note. The visualisations and annotations below are retained to document the exploratory Oxford Nanopore workflow. The 14,824-bp sequence is incomplete, unpolished, non-collinear, and lacks retained depth, assembly-graph, polishing, and boundary-support diagnostics. It must not be interpreted as a complete plastome, a physically circular DNA molecule, a structurally validated plastome segment, or evidence of biological gene-order rearrangement.

Supplementary Figure S1



Supplementary Figure S1. GC content and GC skew plotted around the 14,824-bp candidate plastid-associated contig recovered from Oxford Nanopore reads. The circular plotting format is retained as a compositional visualisation only and does not demonstrate physical circularisation, complete plastome recovery, native gene order, or structural integrity of the assembled sequence.

Supplementary Figure S2



Supplementary Figure S2. Linear representation of annotations reported on the 14,824-bp candidate plastid-associated contig. Coordinates refer only to the assembled sequence. The map does not establish native plastome collinearity, continuity across proposed joins, or a biologically rearranged chloroplast genome.

Supplementary Table S1

Complete list of features reported by GeSeq on the 14,824-bp candidate plastid-associated contig. Partial, overlapping, HMM-only, and boundary annotations are retained for transparency and should be interpreted cautiously.

Element	Coordinates (bp)	Strand	Type	Annotation note
ycf2	888-1157	-	CDS	Partial fragment of a protein-coding gene
trnI-CAU / trnM-CAU	2028-2101	+	tRNA	Short tRNA region; annotation merged
rpl23	2265-2546	+	CDS	Ribosomal protein gene L23
rpl2	2766-4073	+	CDS	Intron-containing gene; two exons and one intron
trnH-GUG	4158-4232	-	tRNA	tRNA-His annotation
psbA	4596-5144	-	CDS	Photosystem II D1 protein annotation
psbD*	4741-5352	-	CDS	Detected by HMMER only; likely partial/overlapping annotation
trnK-UUU	5961-8595	-	tRNA	Large intron-containing annotation
matK	7037-7318	-	CDS	Located within the trnK-UUU intron
rps16	9592-10781	-	CDS	Intron-containing annotation; two exons and one intron
trnQ-UUG	11778-11850	-	tRNA	tRNA-Gln annotation
psbK	12259-12414	+	CDS	Photosystem II short-gene annotation
psbI	12909-12968	+	CDS	Photosystem II short-gene annotation
trnS-GCU	13206-13293	-	tRNA	tRNA-Ser annotation
trnG-UCC	14025-14744	+	tRNA	Intron-containing annotation; extends near the contig boundary
trnS-CGA	14735-14790	+	tRNA	Boundary annotation; probably incomplete

Technical interpretation. The local placement of *matK* within the *trnK-UUU* intron and the presence of plastid ribosomal, photosystem, and tRNA annotations support the recovery of plastid-derived sequence. However, the overall non-collinear order, incomplete and overlapping features, and contig-boundary annotations are more consistent with low coverage, sequencing error, nuclear plastid-derived reads, or chimeric/repeat-mediated misassembly than with a biological rearrangement.