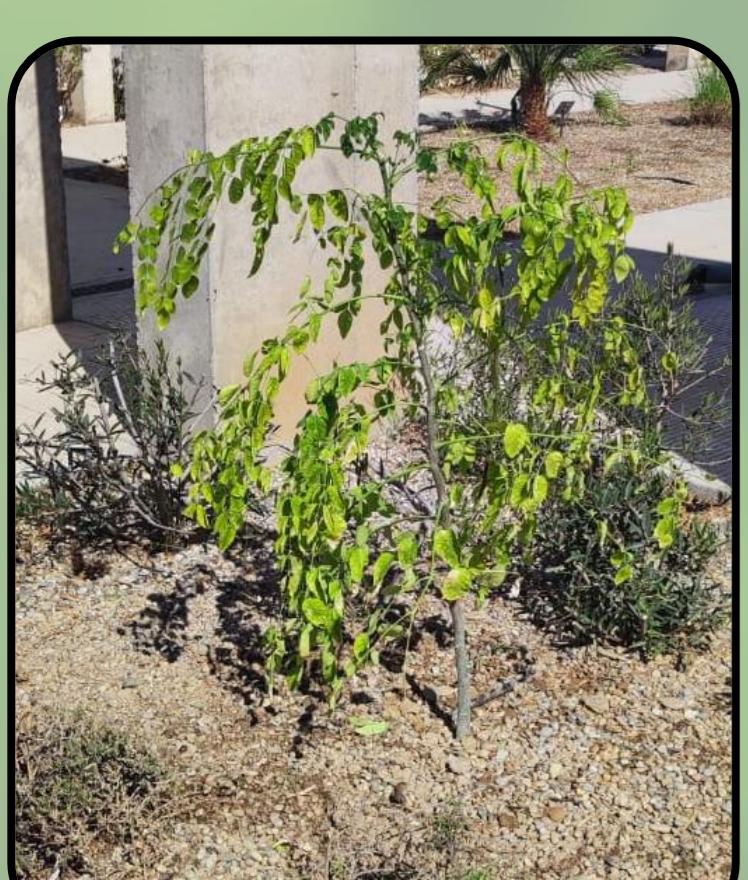


CHARACTERISATION OF *MORINGA STENOPIETALA* ORGANELLAR GENOMES

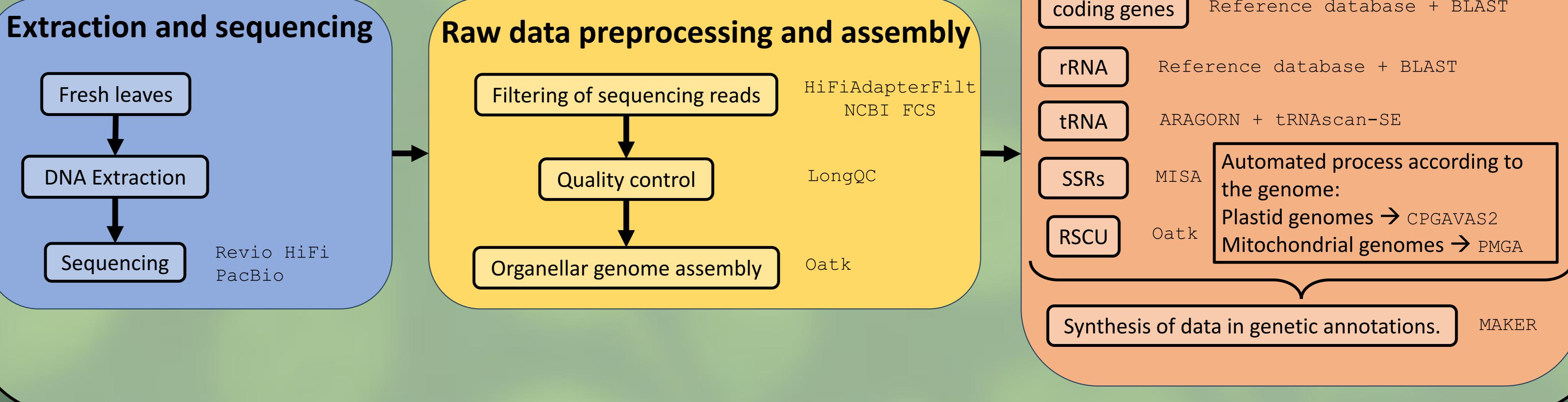
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Introduction

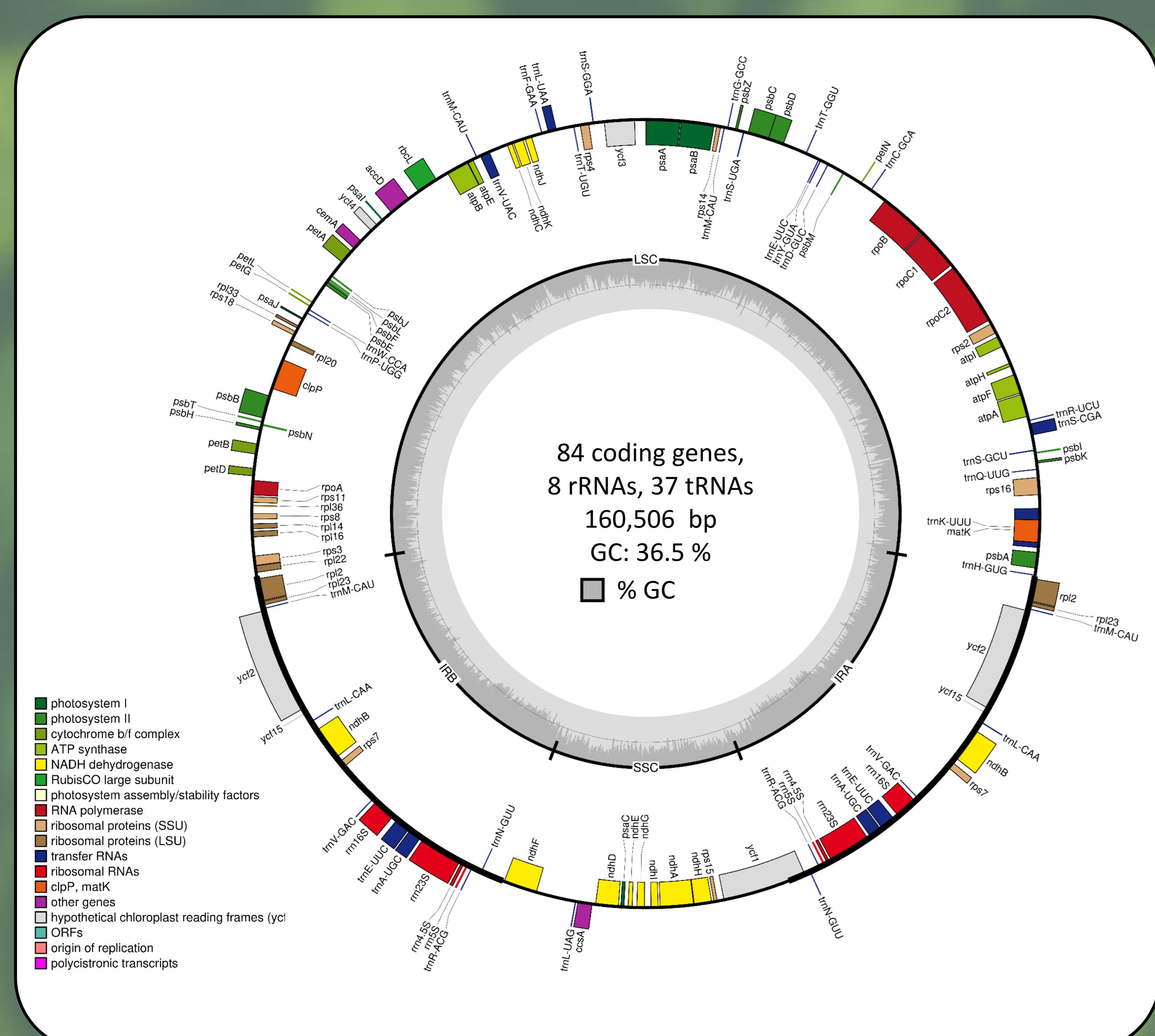


The monogeneric family *Moringaceae* comprises 13 species that are widely used for food, fodder, medicine, and various industrial applications. One notable species is *Moringa stenopetala*, which is native to southern Ethiopia and northern Kenya. It has a high nutritional value, making it a key crop for combating malnutrition in vulnerable populations. Unlike many staple crops, *M. stenopetala* is recognized for its remarkable tolerance to drought and heat-stresses that are expected to worsen under climate change. Despite its significant agronomic, pharmacological, and nutritional potential, *M. stenopetala* is considered an orphan crop and has received minimal attention from scientists and breeders.

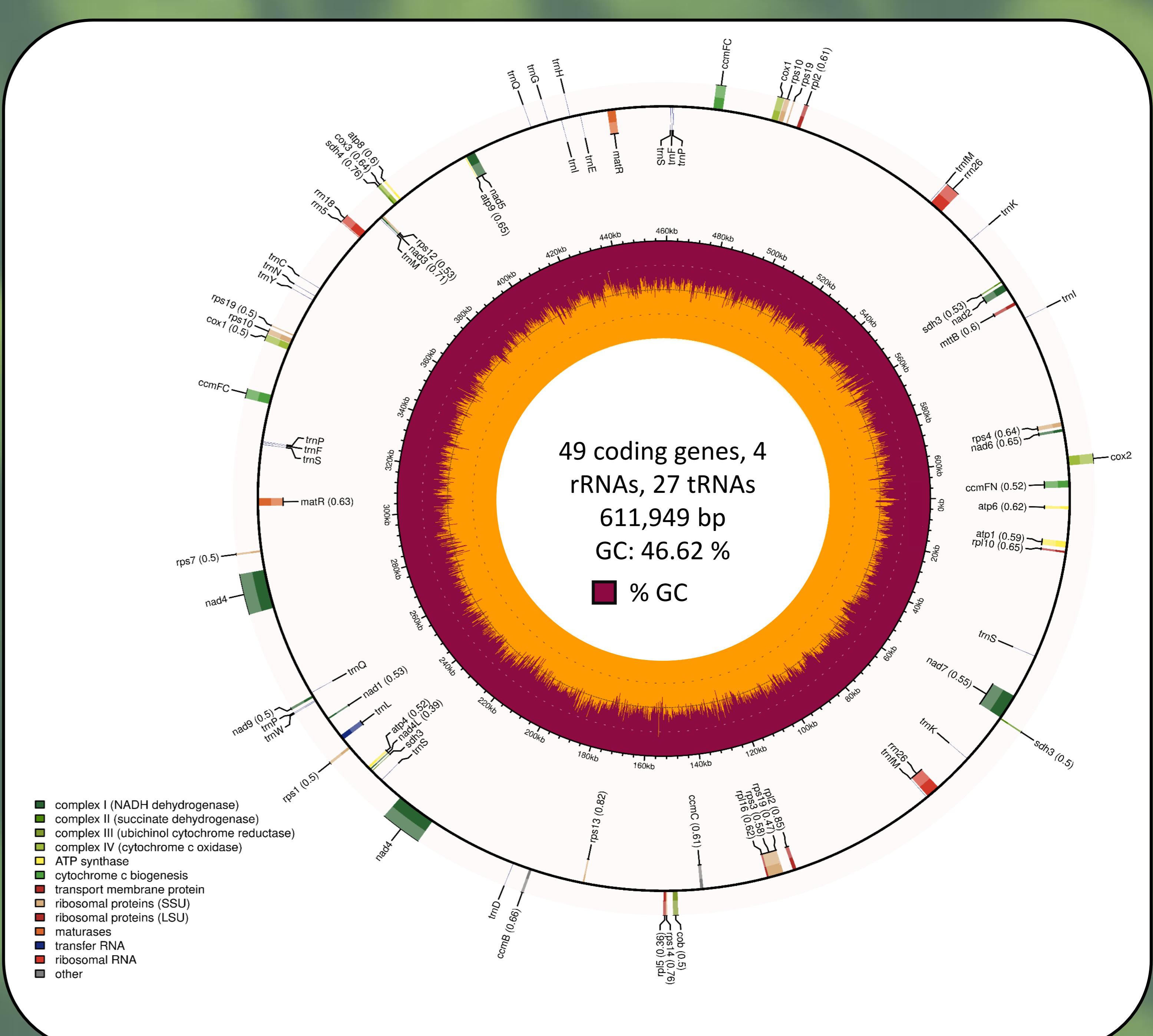
Workflow for organelle genome assembly



Chloroplast genome



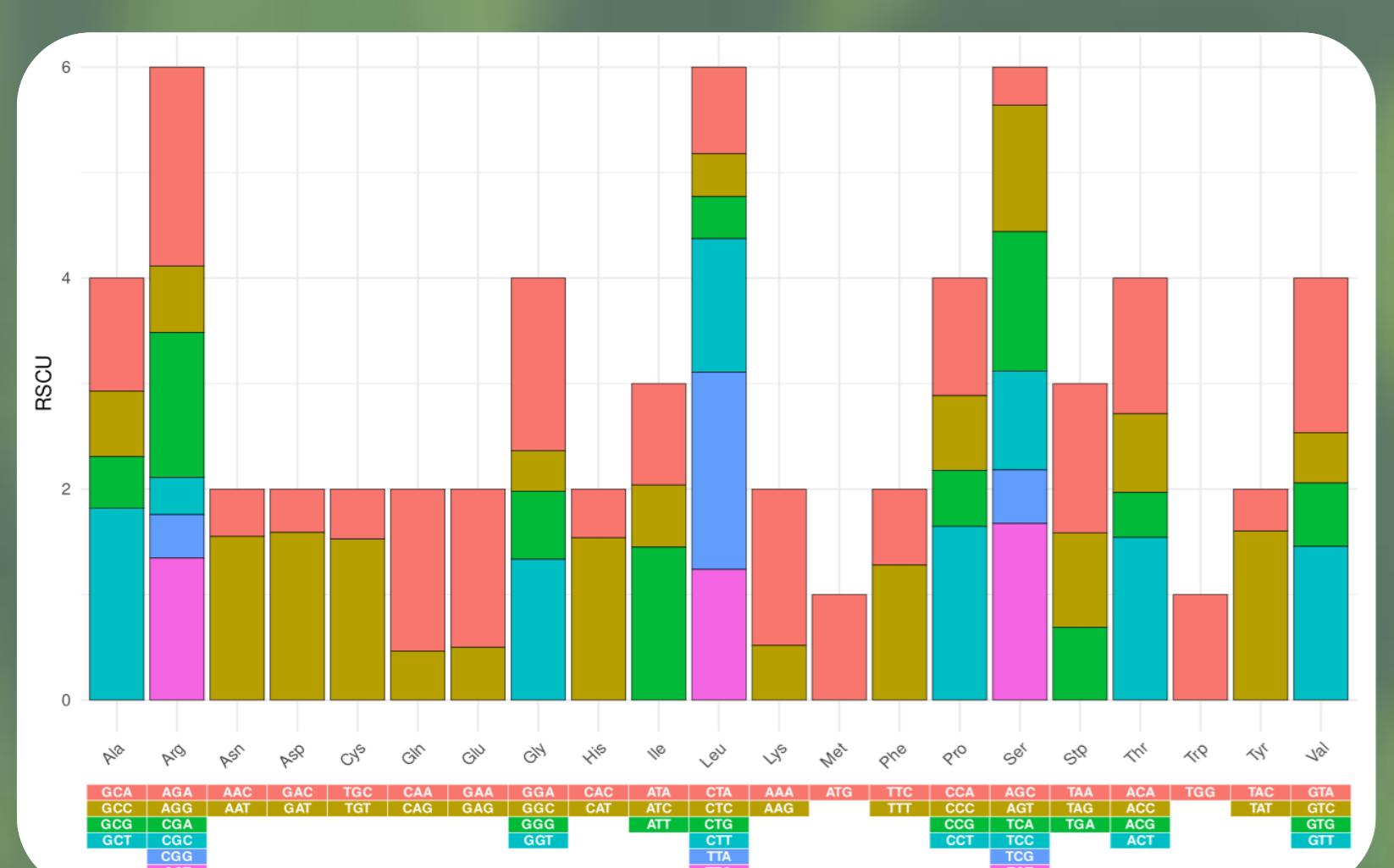
Mitochondrial genome



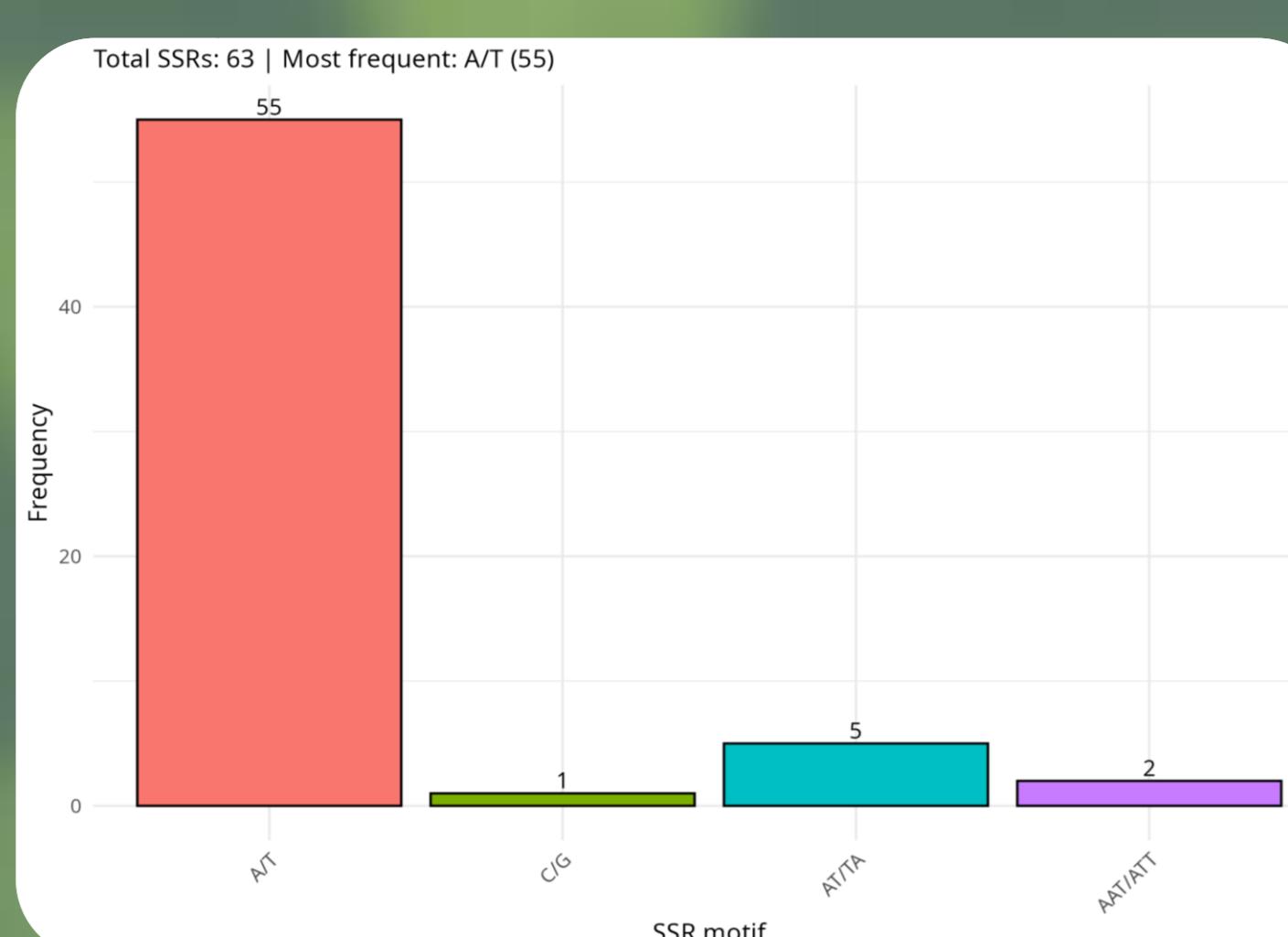
Annotation

Category of genes	Group of genes	Name of genes
Genes for photosynthesis	Subunits of ATP synthase	<i>atpA, atpB, atpE, atpF, atpH, atpI</i>
	Subunits of <i>photosystem II</i>	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ, ycf3</i>
	Subunits of NADH-dehydrogenase	<i>ndhA, ndhB</i> (x2), <i>ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK</i>
	Subunits of cytochrome b/f complex	<i>petA, petB, petD, petG, petL, petN</i>
	Subunits of photosystem I	<i>psaA, psaB, psaC, psaI, psaJ</i>
	Subunit of rubisco	<i>rbcL</i>
Self replication	Large subunit of ribosome	<i>rpl14, rpl16, rpl2</i> (x2), <i>rpl20, rpl22, rpl23</i> (x2), <i>rpl32, rpl33, rpl36</i>
	DNA dependent RNA polymerase	<i>rpoA, rpoB, rpoC1, rpoC2</i>
	Transfer RNAs	<i>trnK-UUU, trnQ-UUG, trnS-GCU, trnS-CGA, trnR-UCU, trnC-GCA, trnD-GUC, trnY-GUA, trnT-GGU, trnS-UGA, trnG-GCC, trnS-GGA, trnT-UGU, trnL-UAA, trnF-GAA, trnV-UAC, trnW-CCA, trnP-UGG, trnL-CAA, trnV-GAC, trnE-UUC</i> (x3), <i>trnA-UGC</i> (x2), <i>trnR-ACG</i> (x2), <i>trnN-GUU</i> (x2), <i>trnL-UAG, trnV-GAC, trnL-CAA, trnM-CAU</i> (x4), <i>trnH-GUG</i>
	Small subunit of ribosome	<i>rps11, rps12</i> (x2), <i>rps14, rps15, rps16, rps18, rps19, rps2, rps3, rps4, rps7</i> (x2), <i>rps8</i>
rRNA genes	Ribosomal RNA	<i>rrn16</i> (x2), <i>rrn23</i> (x2), <i>rrn5</i> (x2), <i>rrn4.5</i> (x2)
Other genes	Subunit of Acetyl-CoA-carboxylase	<i>accD</i>
	c-type cytochrom synthesis gene	<i>ccsA</i>
	Envelop membrane protein	<i>cemA</i>
	Protease	<i>clpP</i>
	Maturase	<i>matK</i>
Unkown	Conserved open reading frames	<i>ycf1</i> (x2), <i>ycf15</i> (x2), <i>ycf2</i> (x2), <i>ycf4</i>

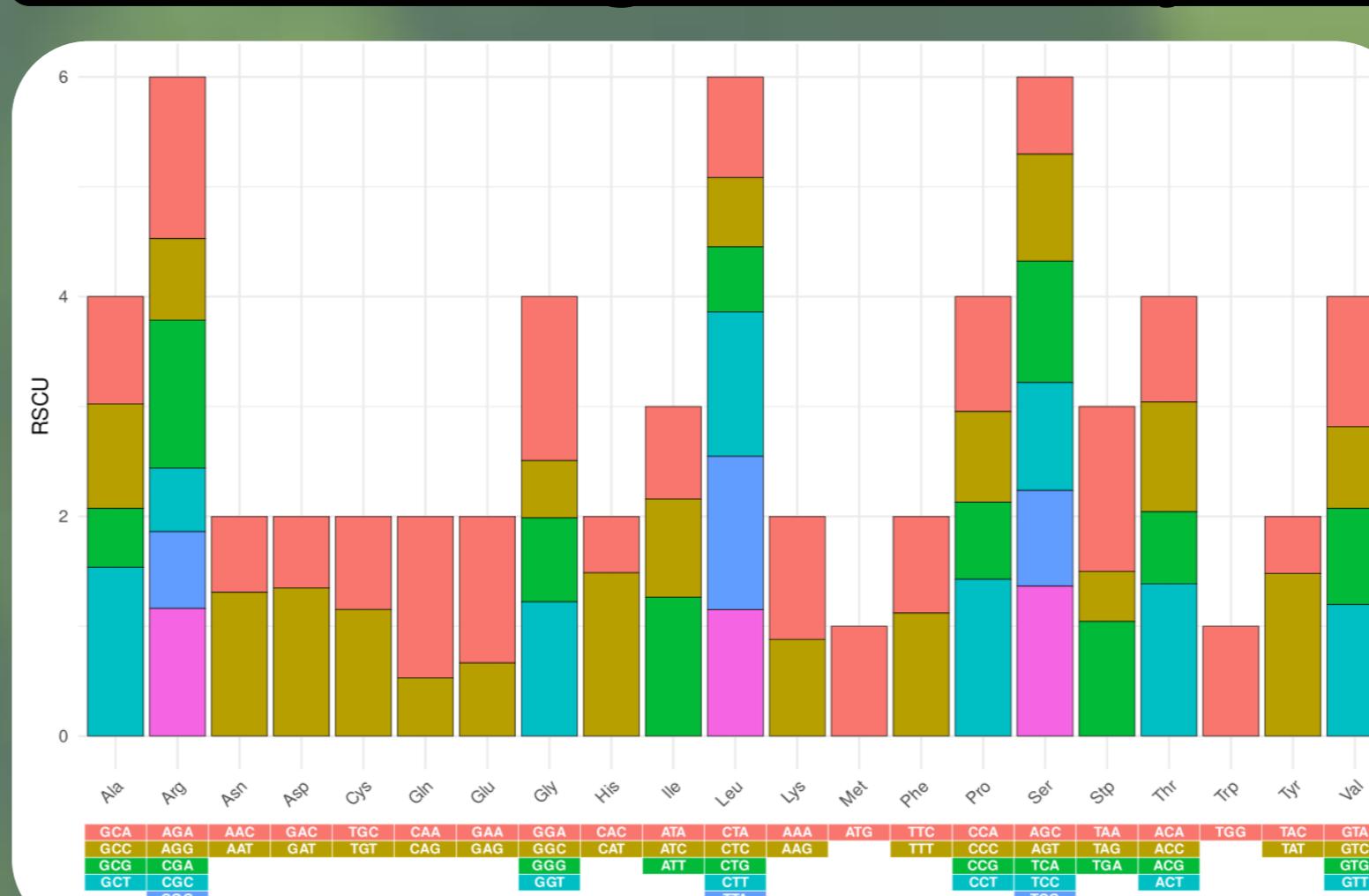
Codon usage bias analysis



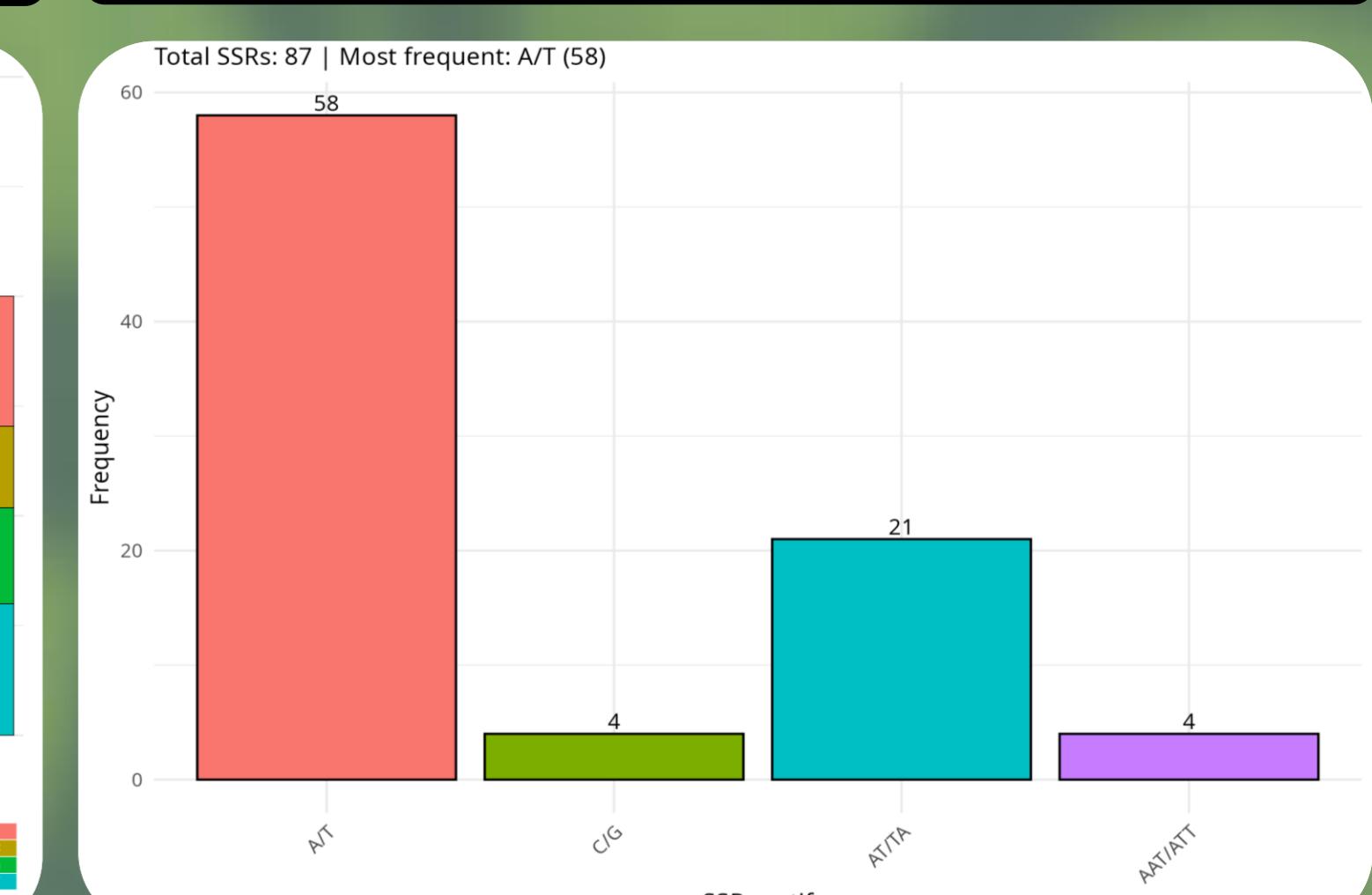
Characterization of SSRs



Codon usage bias analysis



Characterization of SSRs



Conclusions

These genomic resources provide **valuable tools for future breeding programs** of this orphan crop, enabling the development of improved varieties. They also offer a foundation for **comparative studies** within the morphologically diverse ***Moringaceae* family**, enhancing our understanding of **adaptive evolution** at the genome level. Altogether, these resources will support the expansion of *M. stenopetala* cultivation to dryland regions increasingly affected by **desertification and climate change**, including Almería in southeastern Spain.

Acknowledgements

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