

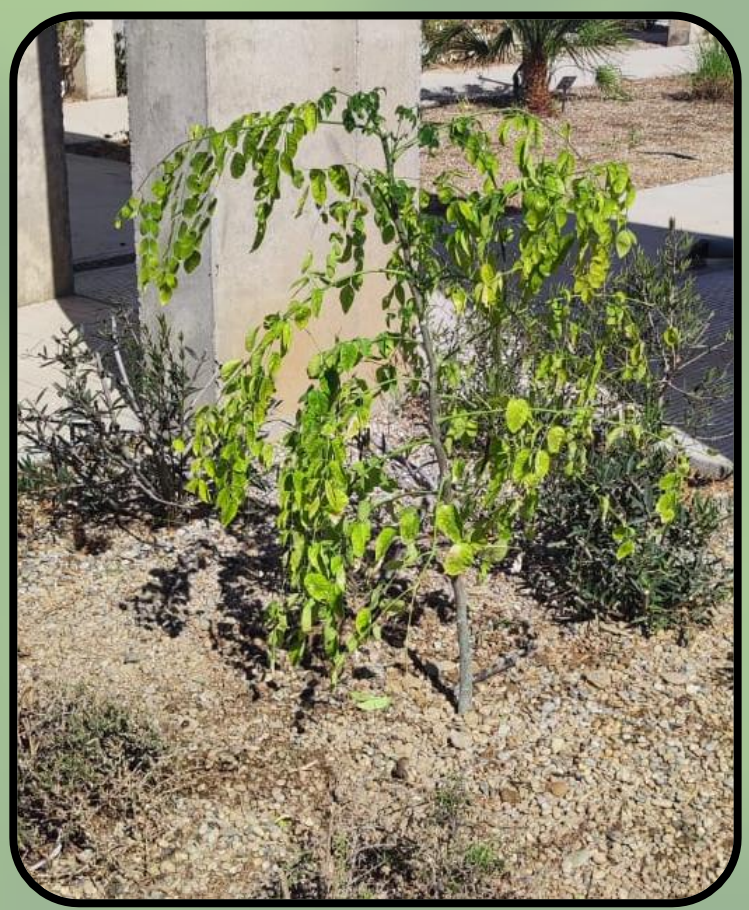
CHARACTERISATION OF *MORINGASTENOPETALA* ORGANELLAR GENOMES

A. Gálvez-Salido, P. Contreras Saavedra, C. Martínez Padilla, A. Ríos Bravo, J.J. Regalado-González, and L. Carretero-Paulet*

Department of Biology and Geology, "Pabellón de Historia Natural-Centro de Investigación de Colecciones Científicas de la Universidad de Almería" (PHN-CECOUAL), University of Almería, E04120 Almería (Spain), ags408@ual.es (presenting author); lpaulet@ual.es (*corresponding author)

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.



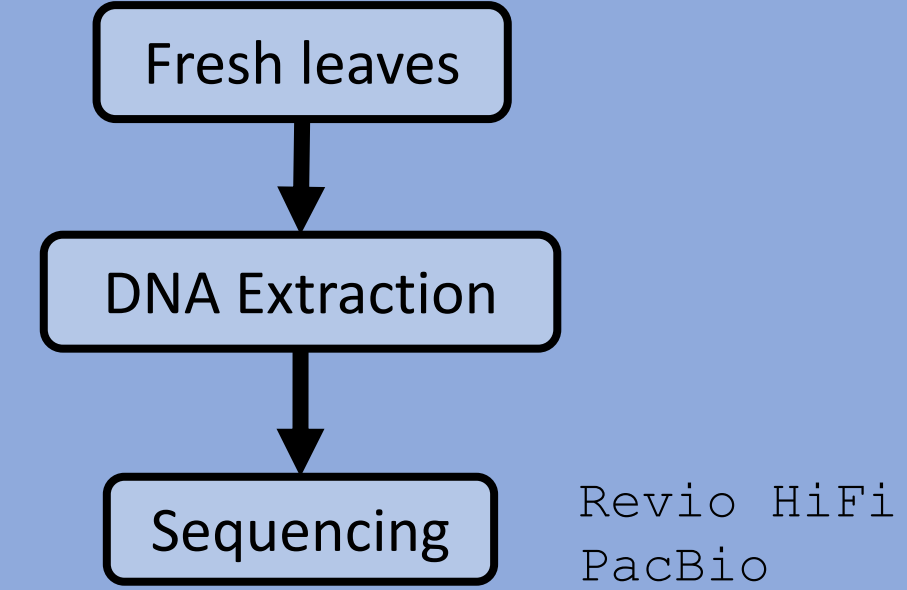
Sequenced *M. stenopetala*



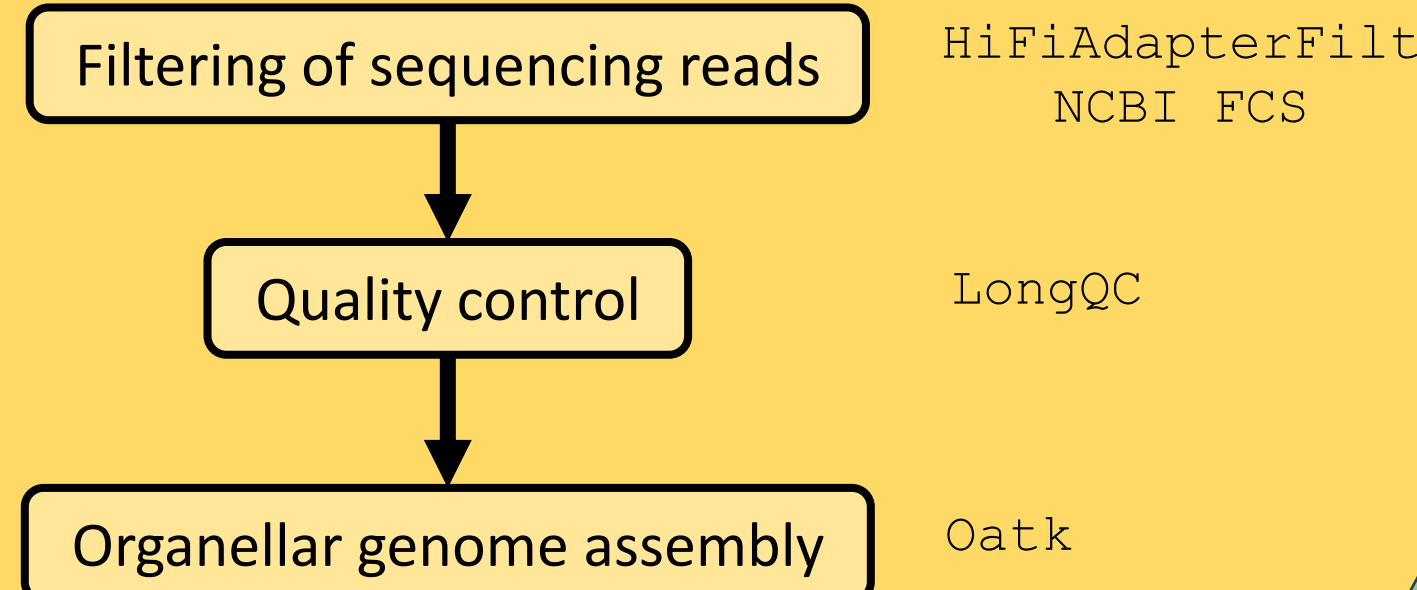
M. stenopetala seeds

Workflow for organelle genome assembly

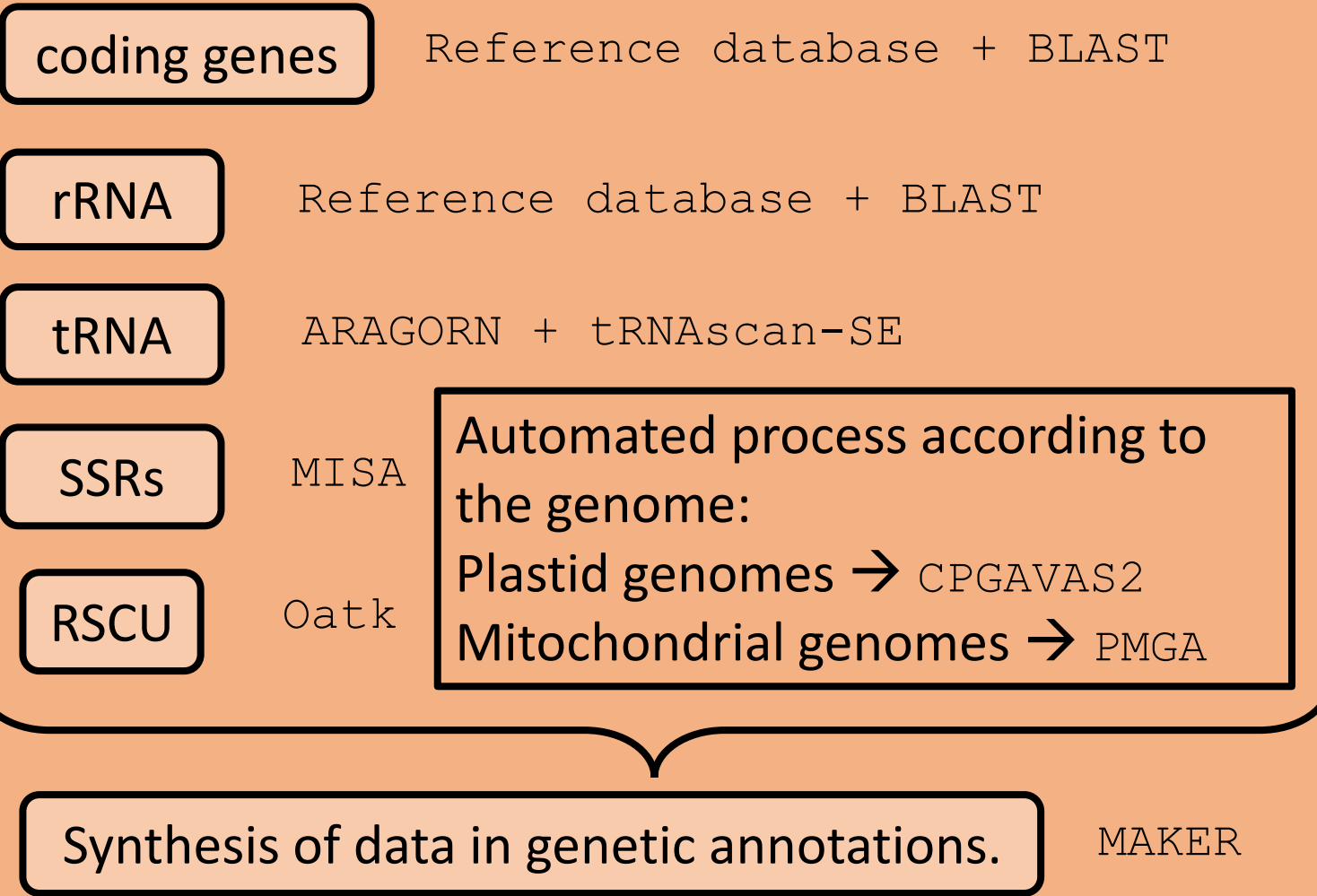
Extraction and sequencing



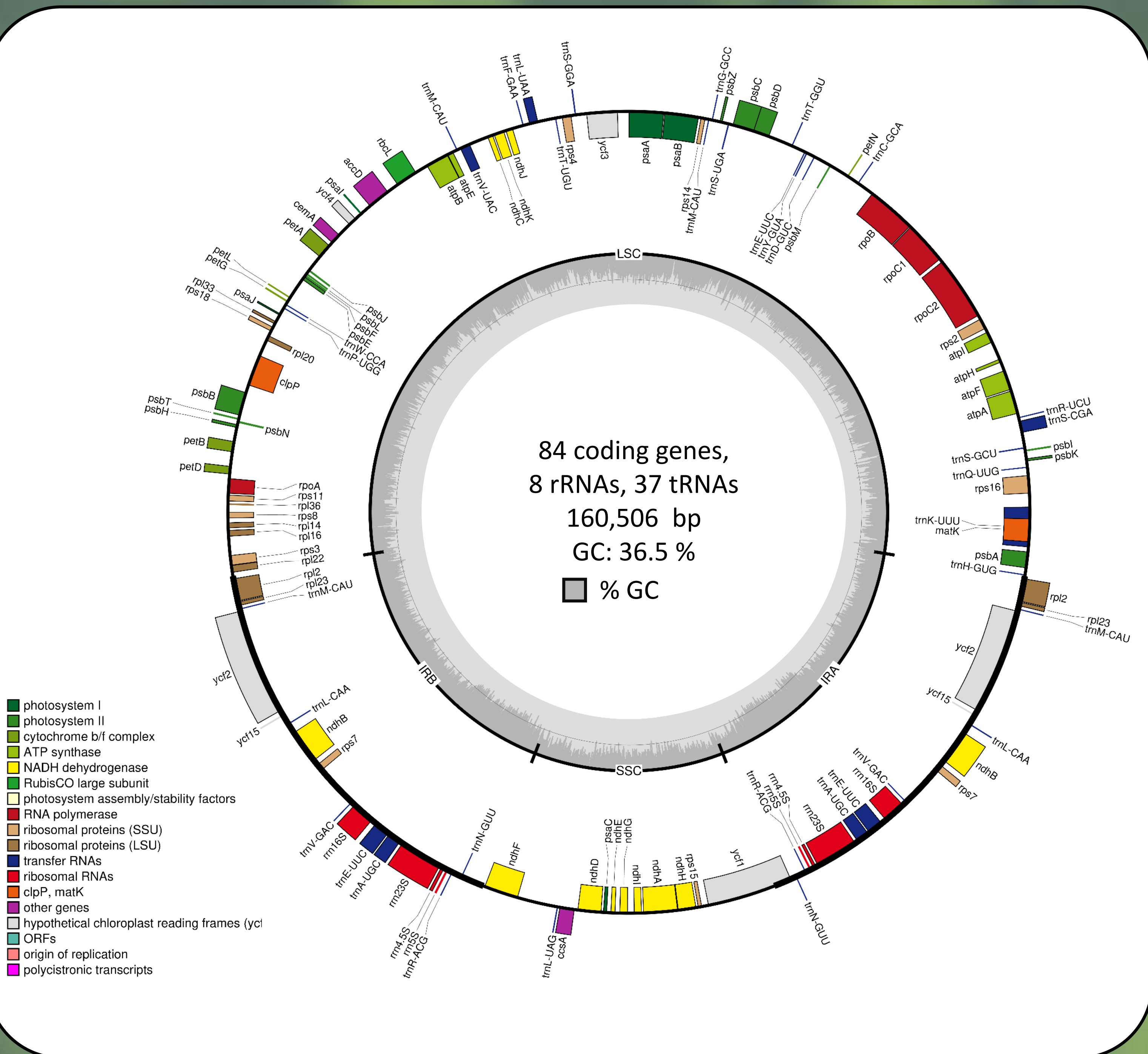
Raw data preprocessing and assembly



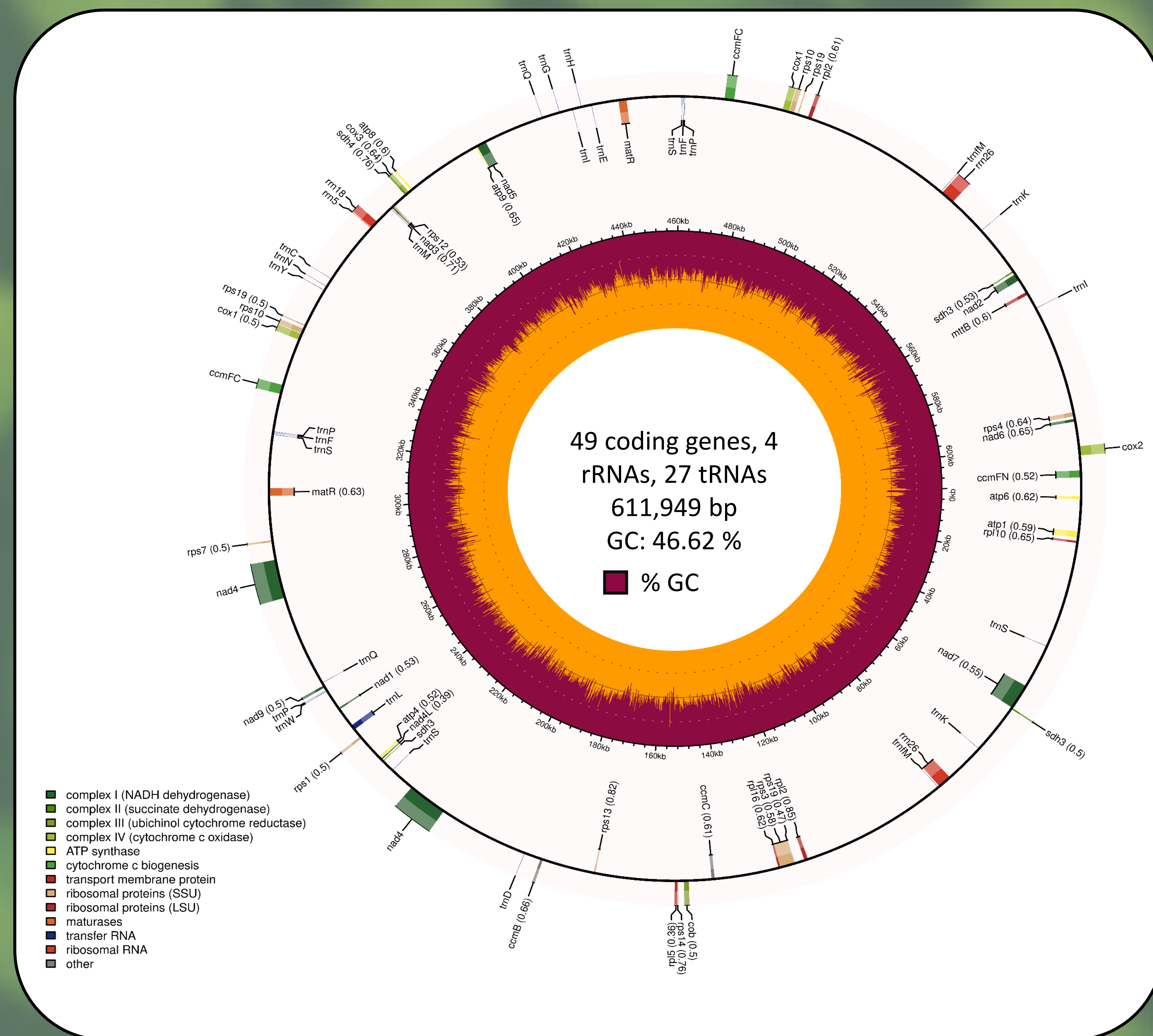
Functional analysis and annotation



Chloroplast genome



Mitochondrial genome



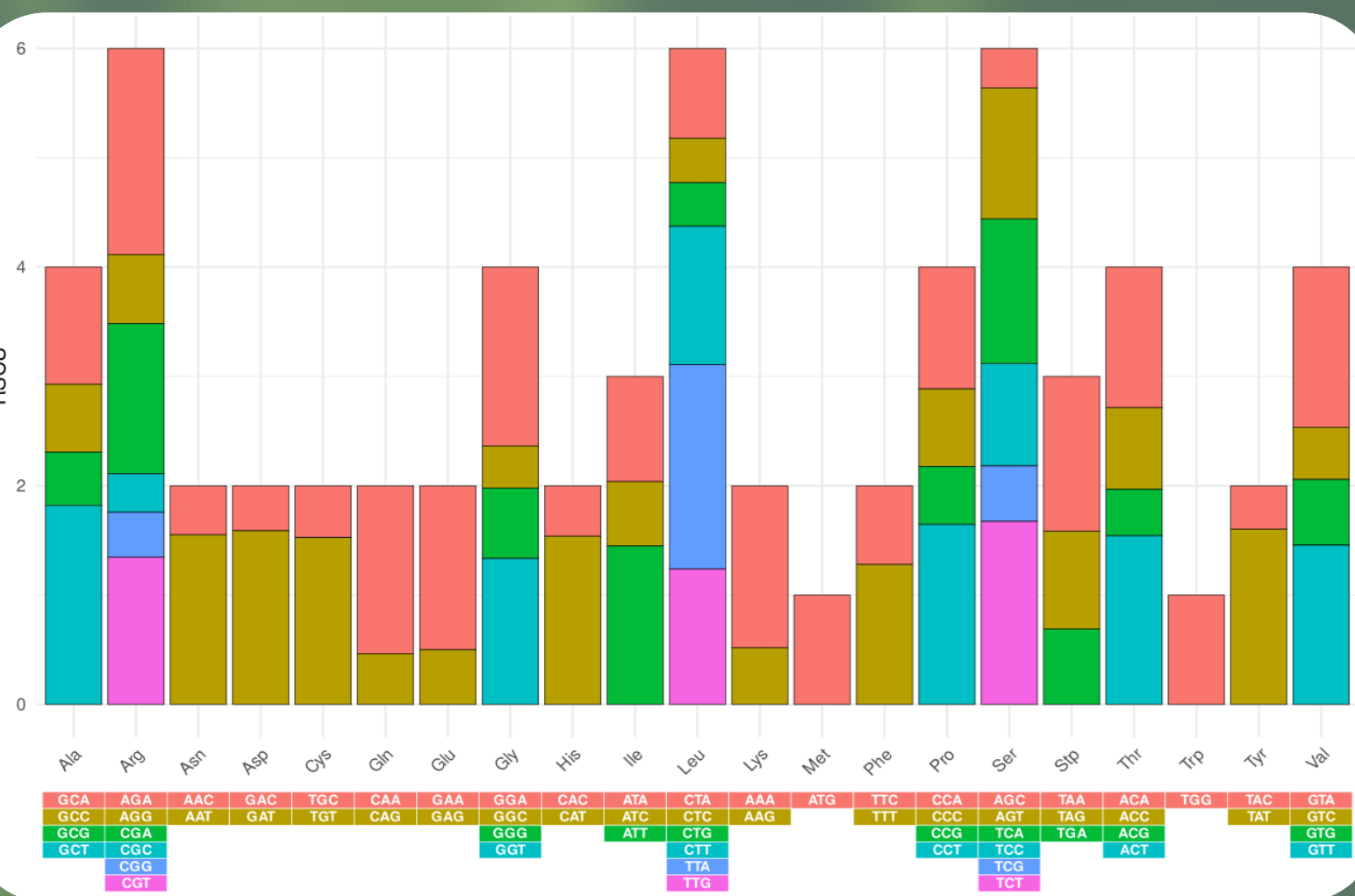
Annotation

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 photosystem II	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ, ycf3</i>
	Subunits of NADH-dehydrogenase	<i>ndhA, ndhB (x2), 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(x2), rpl20, rpl22, rpl23(x2), rpl32, rpl33, rpl36</i>
	DNA dependent RNA polymerase	<i>rpoA, rpoB, rpoC1, rpoC2</i>
Transfer RNAs		<i>trnK-UUU, trnQ-UUG, trnS-GCU, trnS-GGA, 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 (x3), trnA-UGC (x2), trnR-ACG (x2), trnN-GUU (x2), trnL-UAG, trnV-GAC, trnL-CAA, trnM-CAU (x4), trnH-GUG</i>
	Small subunit of ribosome	<i>rps11, rps12 (x2), rps14, rps15, rps16, rps18, rps19, rps2, rps3, rps4, rps7 (x2), rps8</i>
rRNA genes	Ribosomal RNA	<i>rrn16 (x2), rrn23 (x2), rrn5 (x2), rrn4.5 (x2)</i>
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 (x2), ycf15 (x2), ycf2 (x2), ycf4</i>

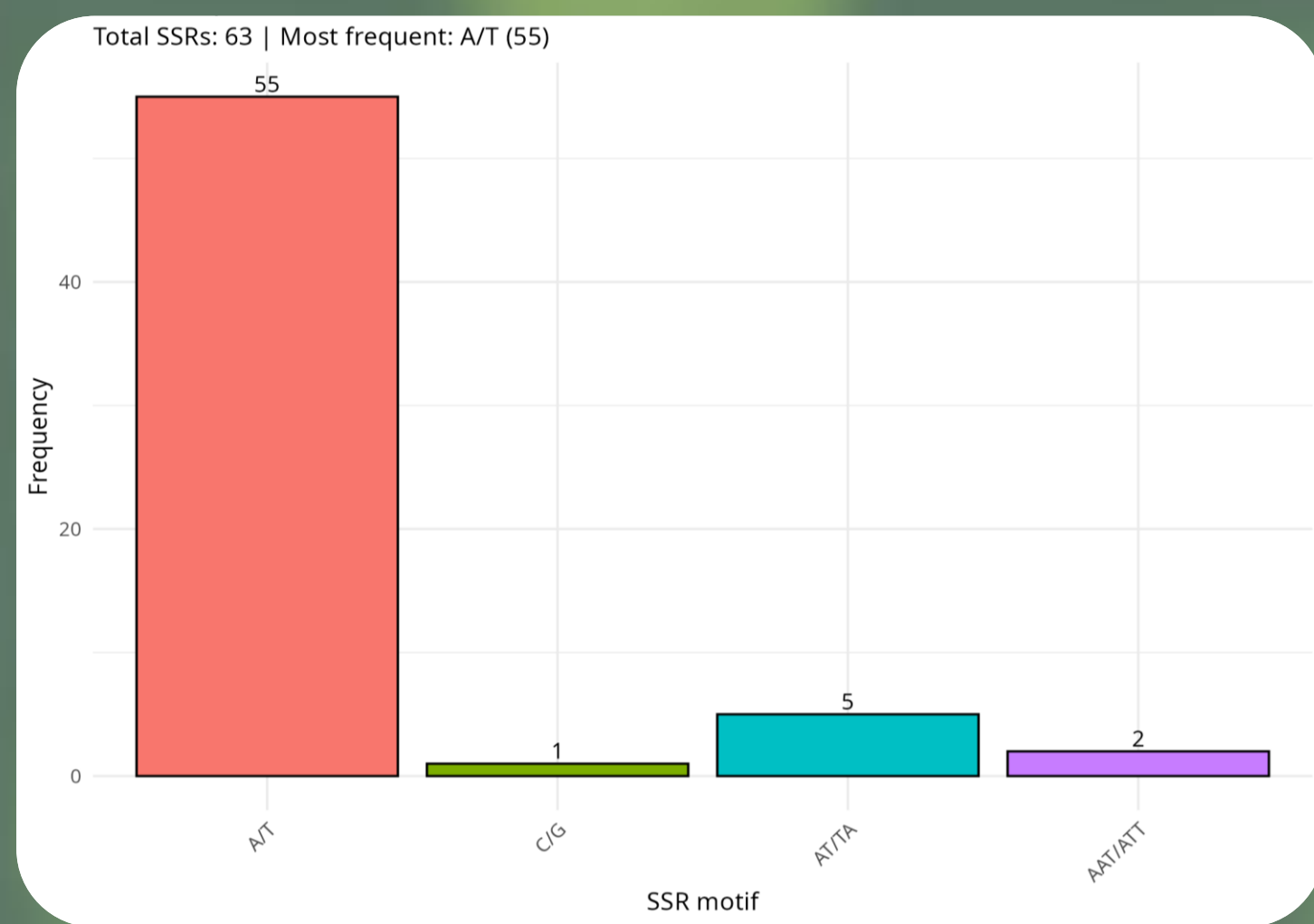
Annotation

Category of genes	Group of genes	Name of genes
Core genes	Complex I (NADH dehydrogenase)	<i>nad1, nad2, nad3, nad4 (x2), nad4L, nad5, nad6, nad7, nad9</i>
	Complex II (succinate dehydrogenase)	<i>sdh3 (x3), sdh4</i>
	Complex III (ubiquinol cytochrome c reductase)	<i>cob</i>
	Complex IV (cytochrome oxidase)	<i>cox1, cox12, cox2, cox3</i>
	Complex V (ATP synthase)	<i>atp1, atp4, atp6, atp8, atp9</i>
	Cytochrome c biogenesis	<i>ccmB, ccmC, ccmFC (x2), ccmFN</i>
Variable genes	Maturases	<i>matR (x2)</i>
	Transport membrane protein	<i>mttB</i>
rRNA genes	Large subunit of ribosome	<i>rpl10, rpl16, rpl2 (x2), rpl5</i>
	Small subunit of ribosome	<i>rps1, rps10 (x2), rps12, rps13, rps14, rps19 (x3), rps3, rps4, rps7</i>
tRNAs	Transfer RNA	<i>trn18, trn26 (x2), trn5</i>

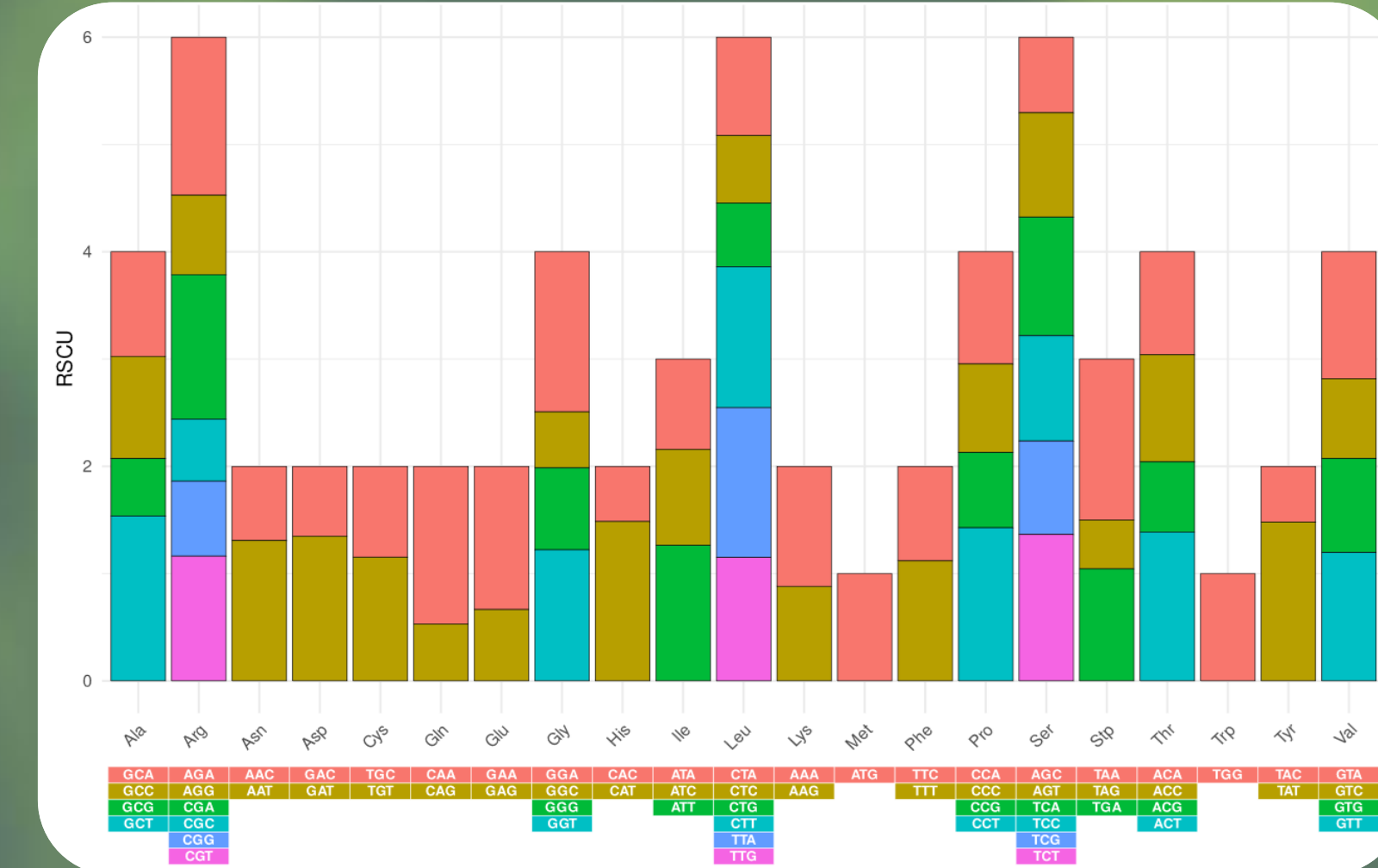
Codon usage bias analysis



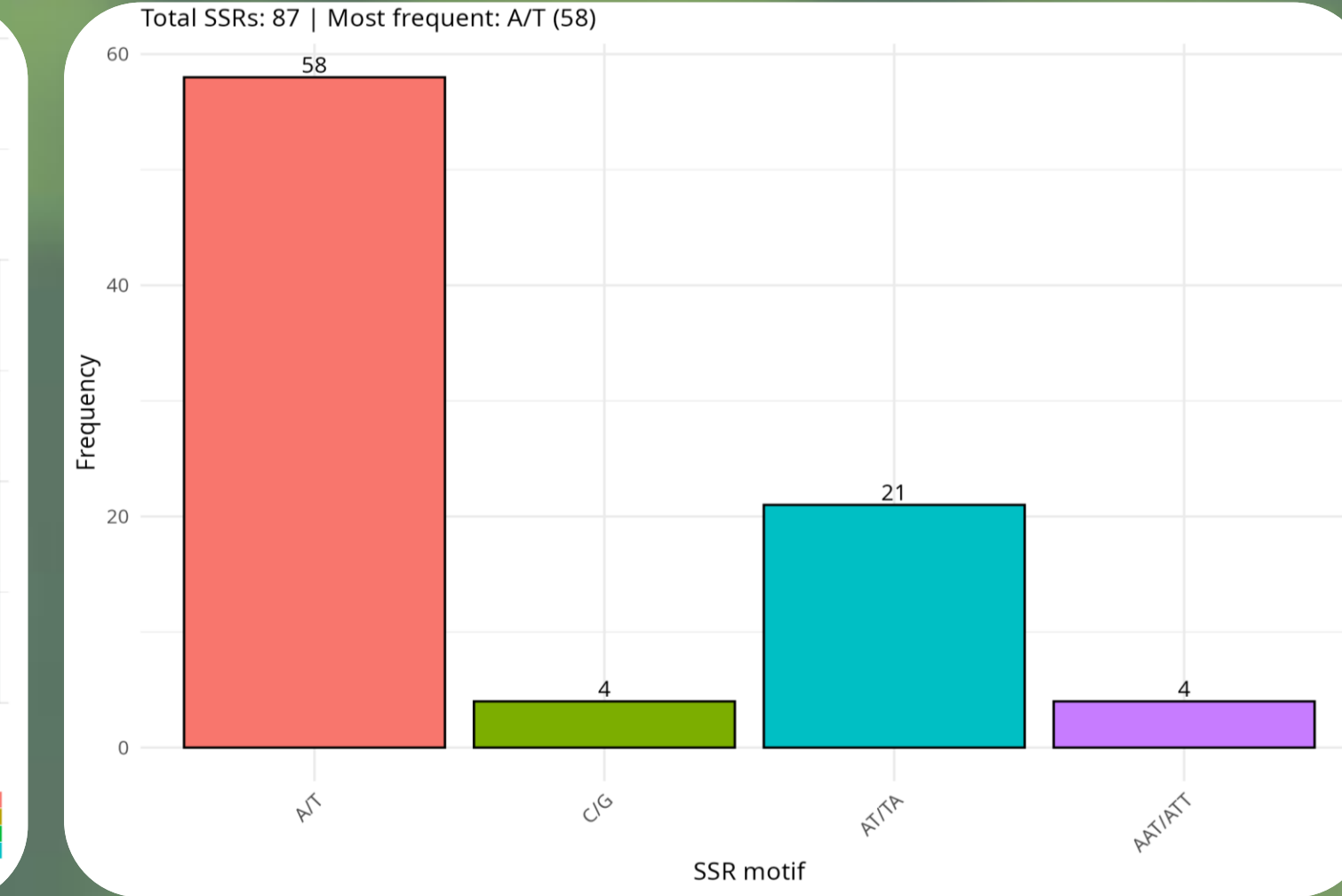
Characterization of SSRs



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 varieties with **improved stress tolerance and productivity**. They also offer a foundation for **comparative studies within Moringaceae**, enhancing our understanding of adaptive evolution. 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

This research was supported by the project "El modelo agrícola de Almería ante el cambio global. Propuestas desde la genómica de la agrobiodiversidad (OrphanEvolGen)" (PID2023-146207OB-I00), funded by the 2023 Call for Knowledge Generation Projects and associated predoctoral training actions of the Spanish Ministry of Science and Innovation and the project UAL2024_1, "Puesta en valor del cultivo huérfano etíope *Moringa stenopetala* mediante la secuenciación y anotación funcional de su genoma (shiferawgenome)" (Modality 1), funded by the 2024 Plan Propio for International Cooperation (Program I) of the University of Almería, granted to Dr. Lorenzo Carretero Paulet.