

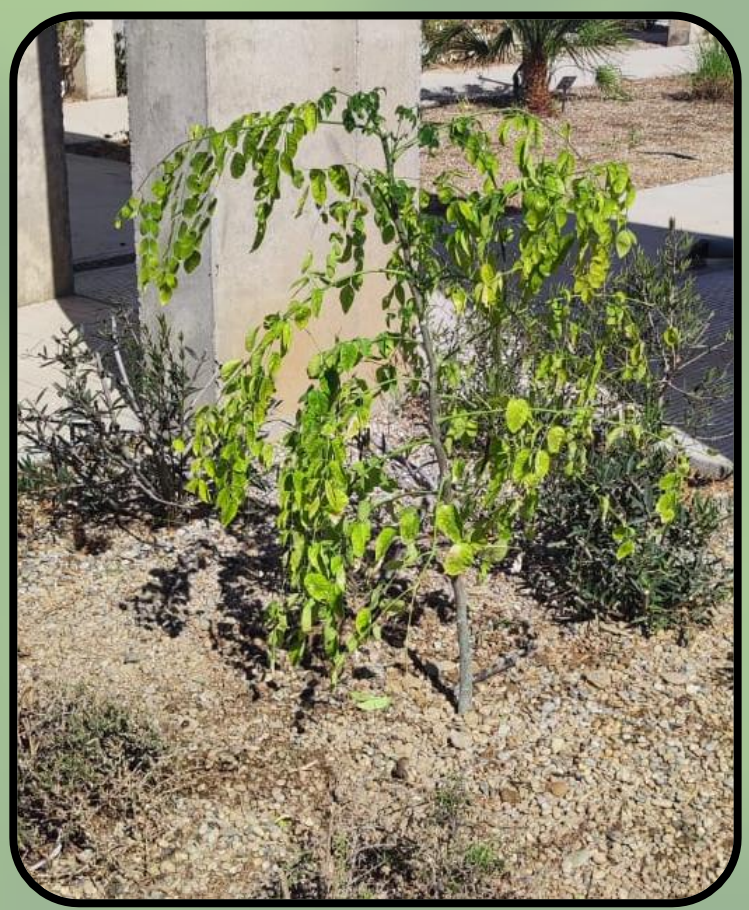
# CHARACTERISATION OF *MORINGASTENOPETALA* ORGANELLAR GENOMES

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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.



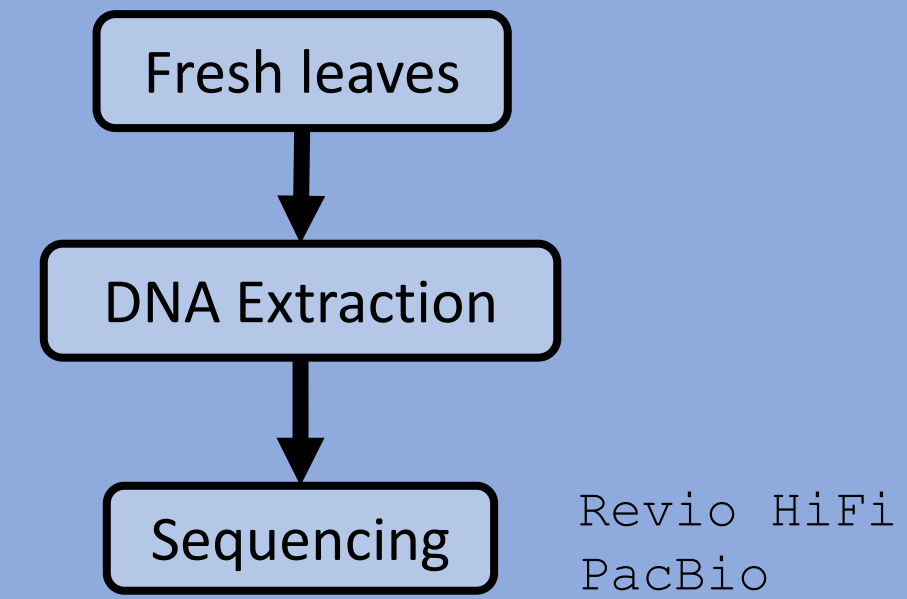
Sequenced *M. stenopetala*



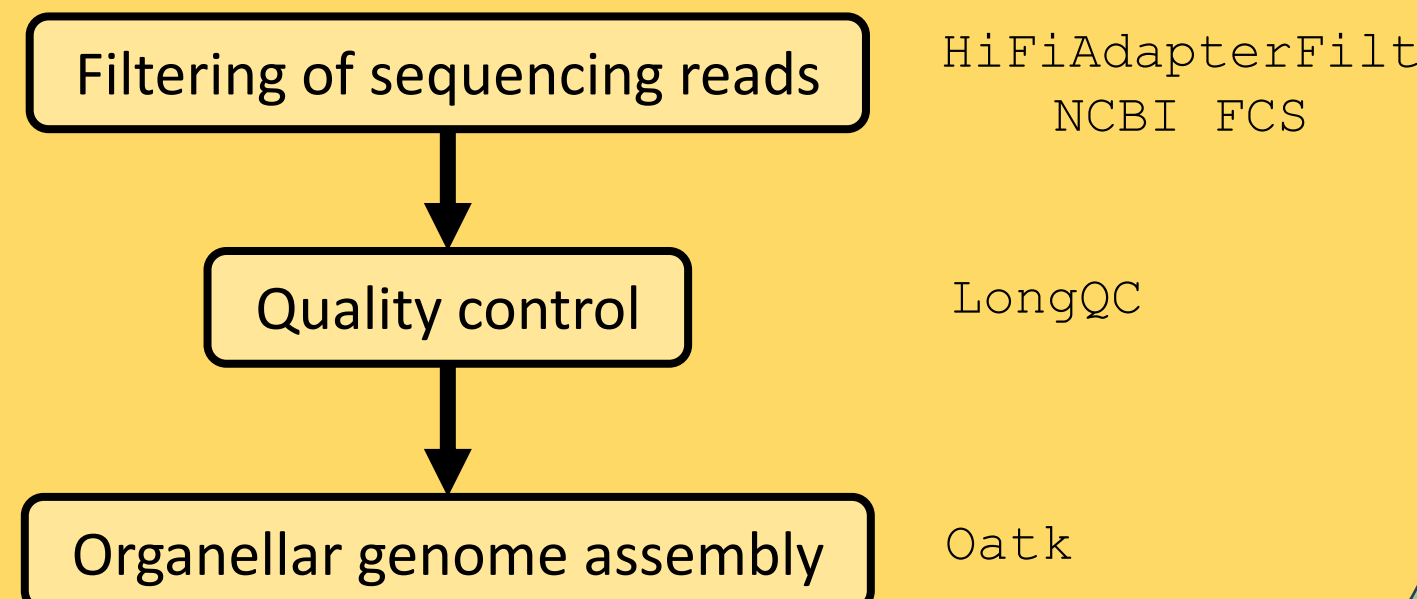
*M. stenopetala* seeds

## Workflow for organelle genome assembly

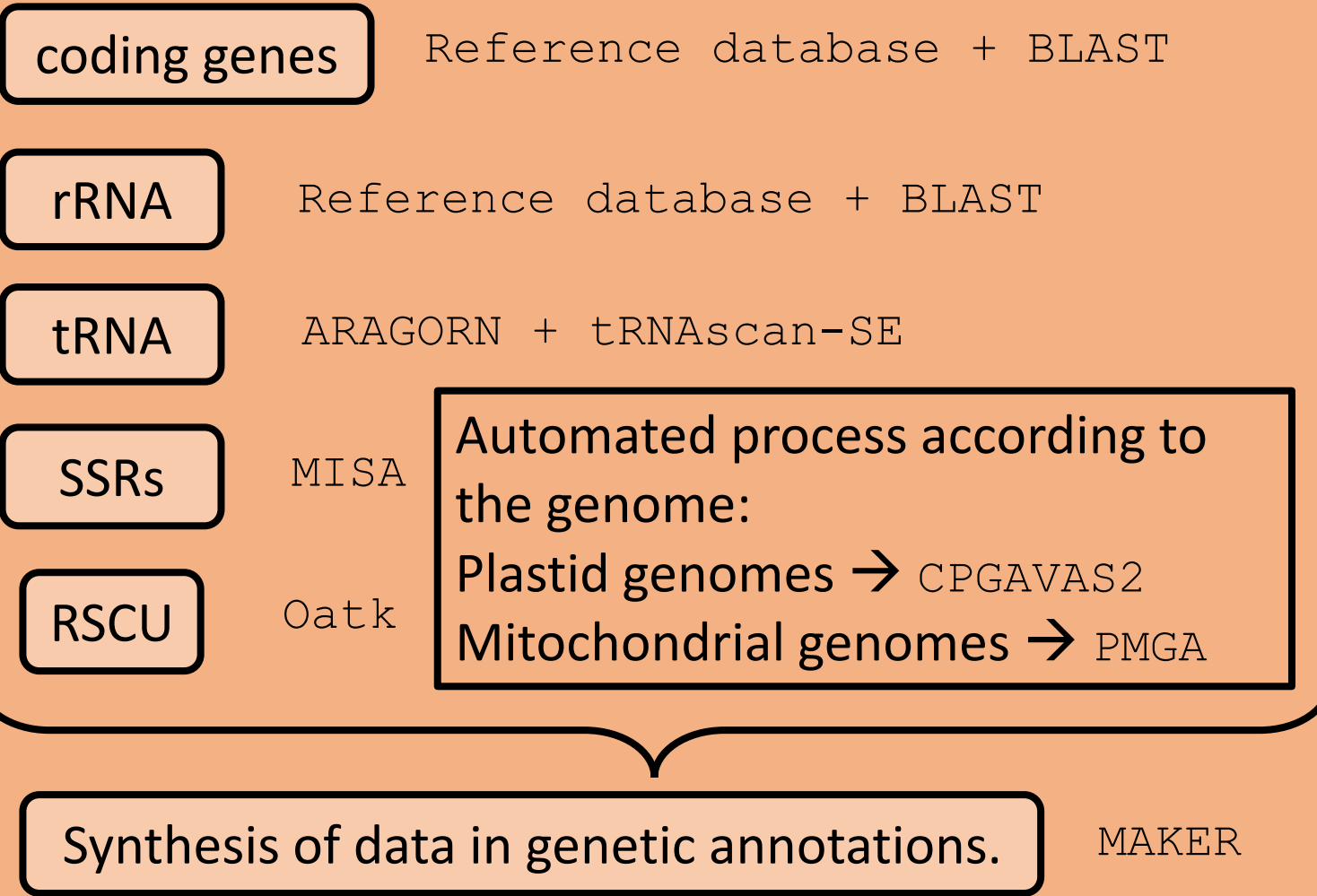
### Extraction and sequencing



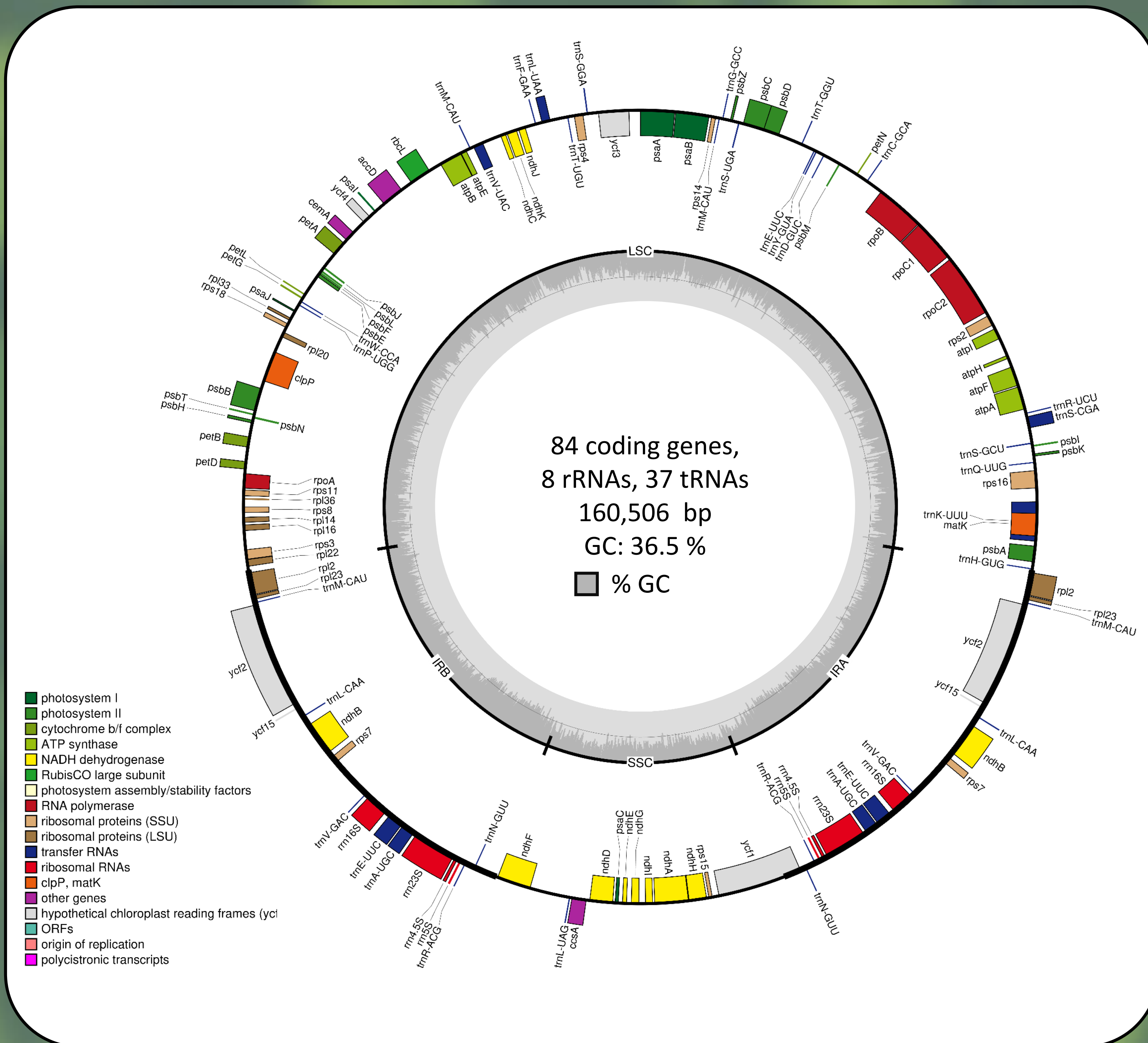
### Raw data preprocessing and assembly



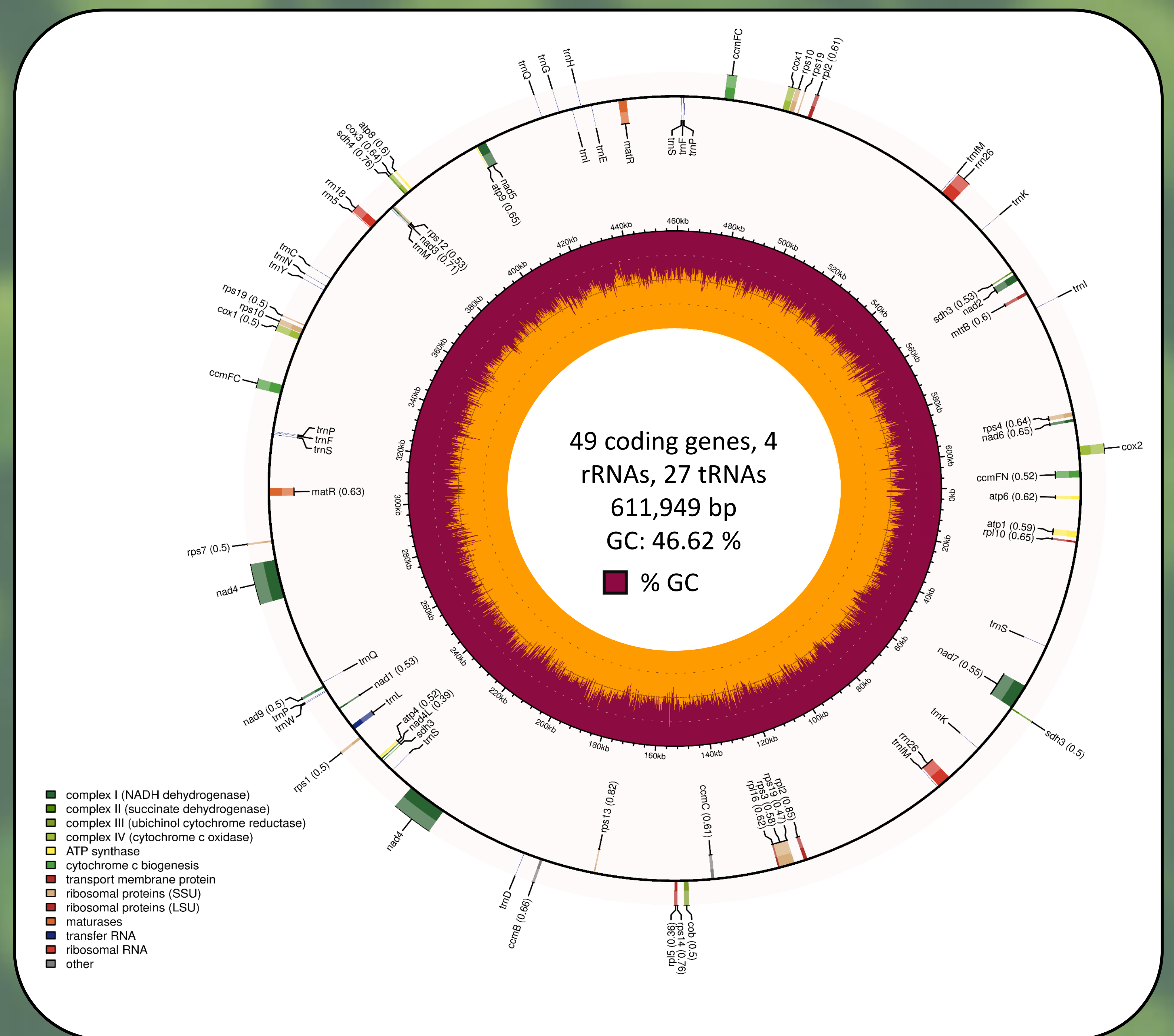
### Functional analysis and annotation



## Chloroplast genome



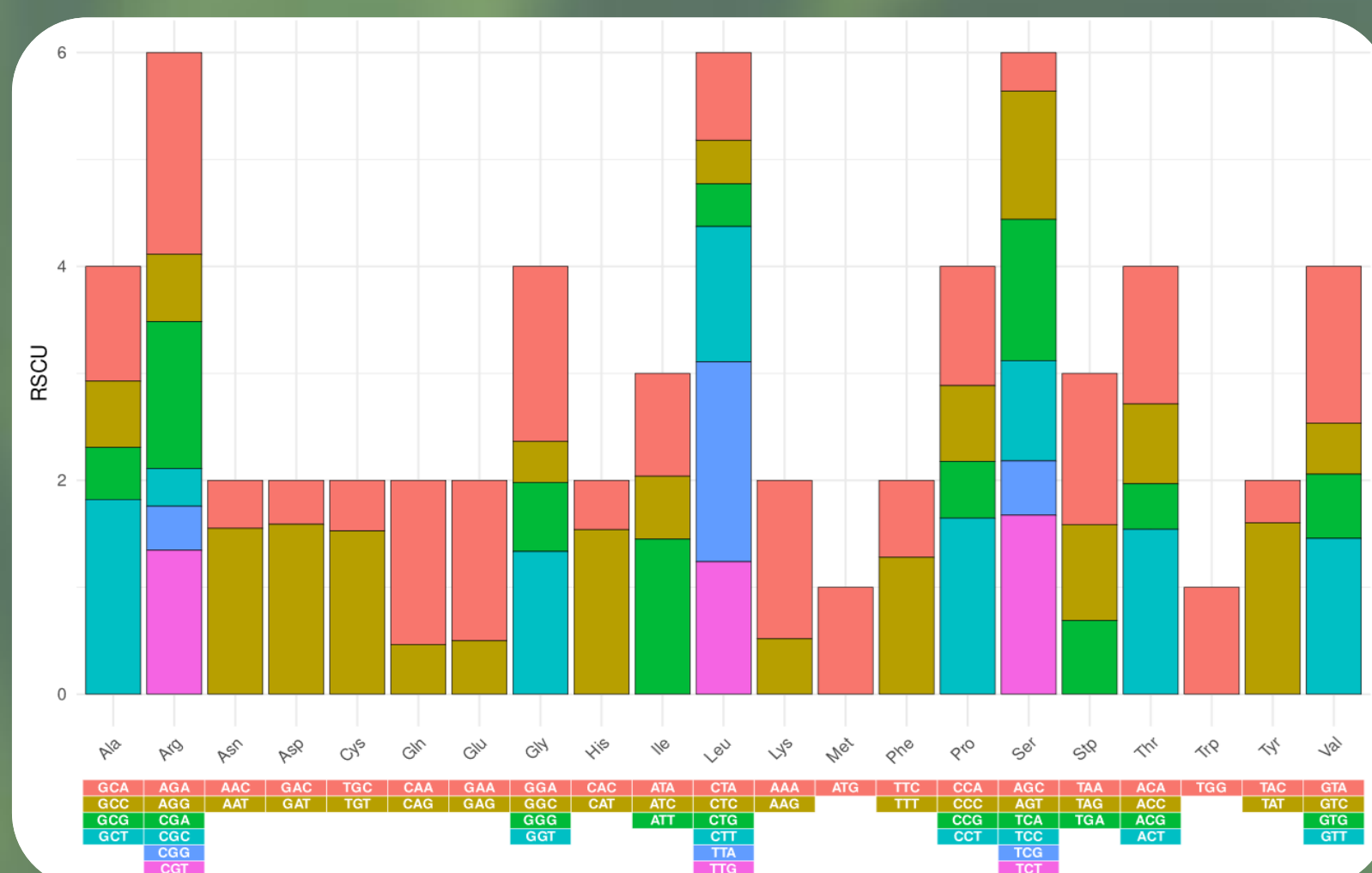
## Mitochondrial genome



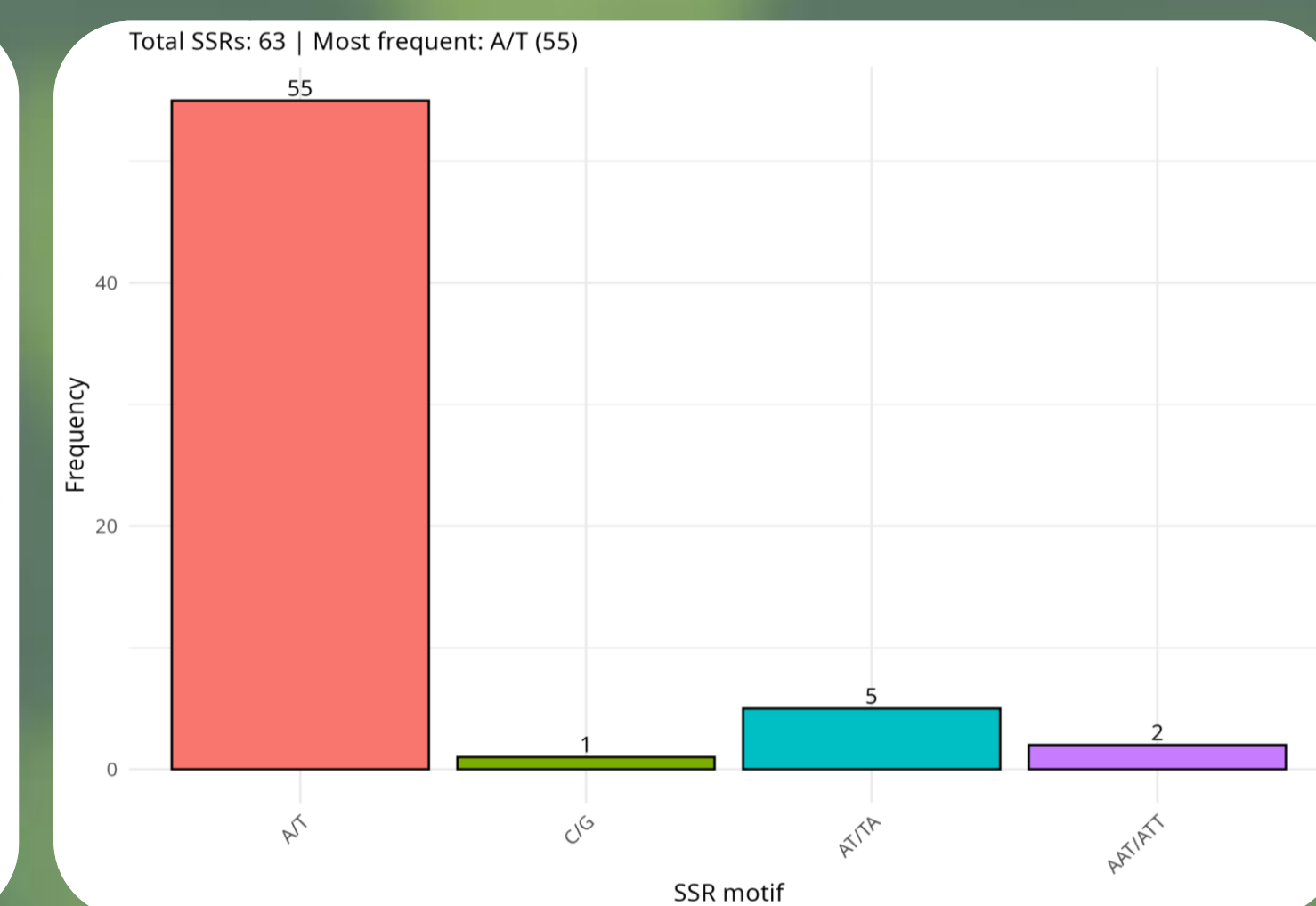
## Annotation

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, psbM, psbN, psbT, psbZ, ycf3</i>
	Subunits of NADH-dehydrogenase	<i>ndhA, ndhB (x2), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, 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>
rRNA genes	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 (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>
Other genes	Ribosomal RNA	<i>rrn16 (x2), rrn23 (x2), rrn5 (x2), rrn44.5 (x2)</i>
	Subunit of Acetyl-CoA-carboxylase	<i>accD</i>
Unknown	c-type cytochrom synthesis gene	<i>ccsA</i>
	Envelop membrane protein	<i>cemA</i>
	Protease	<i>clpP</i>
	Maturase	<i>matK</i>
Unknown	Conserved open reading frames	<i>ycf1 (x2), ycf15 (x2), ycf2 (x2), ycf4</i>

## Codon usage bias analysis



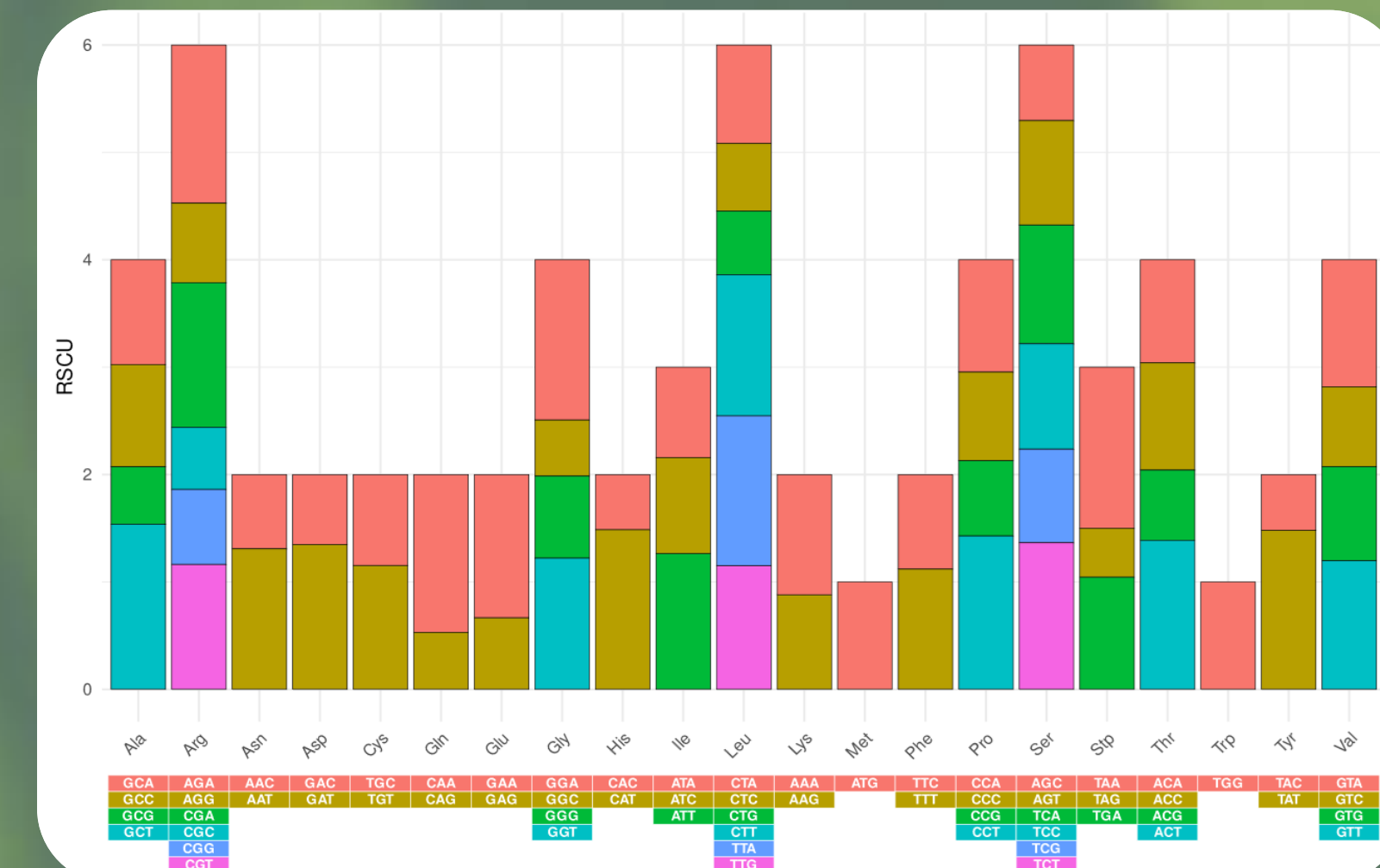
## Characterization of SSRs



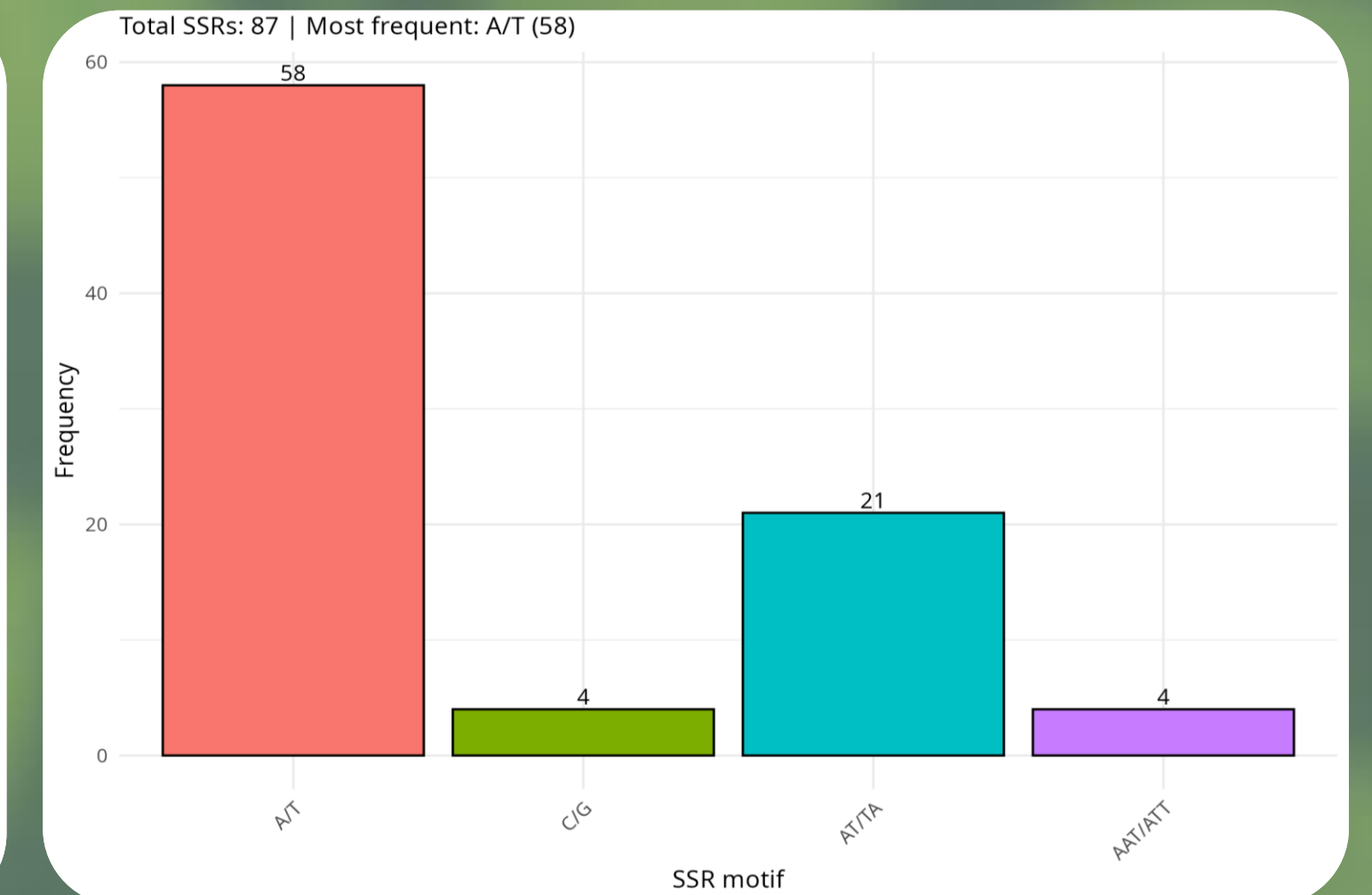
## Annotation

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, 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	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>
rRNA genes	Ribosomal RNA	<i>rrn18, rrn26 (x2), rrn5</i>
tRNAs	Transfer RNA	<i>trnL-CAA, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA (x2), trnG-GCC, trnH-GUG, trnK-UUU (x2), trnM-CAU, trnM-CAU (x2), trnL-CAU (x2), trnN-GUU, trnP-UGG (x3), trnQ-UUG (x2), trnS-GCU, trnS-GGA, trnS-UGA, trnW-CCA, trnY-GUA</i>

## 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

This research was supported by the projects: "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 "Puesta en valor del cultivo huérfano etíope *Moringa stenopetala* mediante la secuenciación y anotación funcional de su genoma (shiferawgenome)" (UAL2024\_1) funded by the 2024 Plan Propio for International Cooperation (Program I) of the University of Almería, granted to Dr. Lorenzo Carretero Paulet.

