

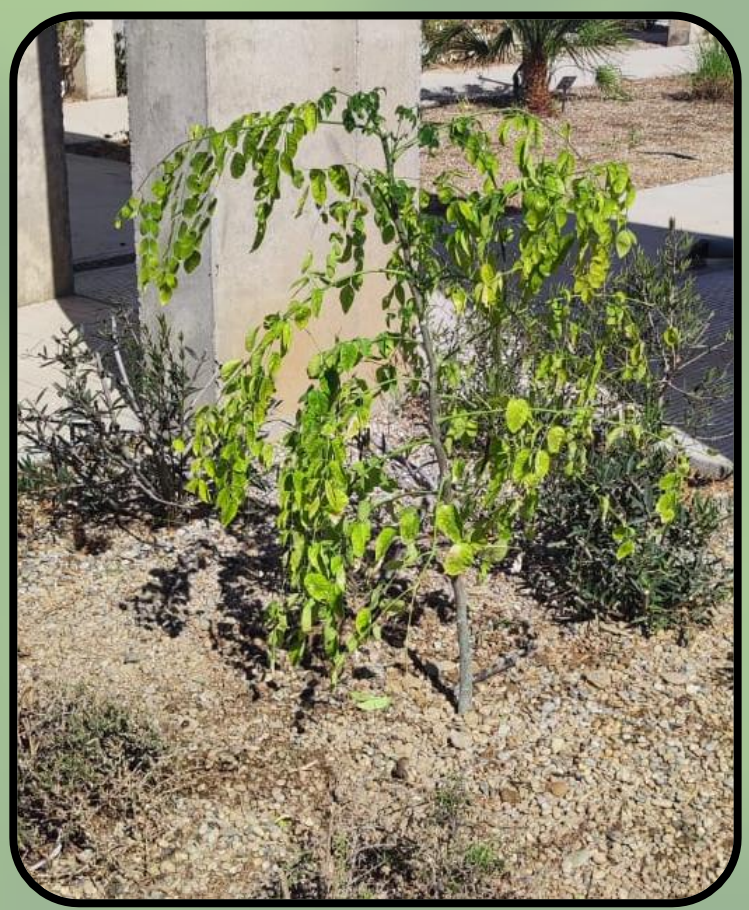
CHARACTERISATION OF MORINGASTENOPETALA ORGANELLAR GENOMES

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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.



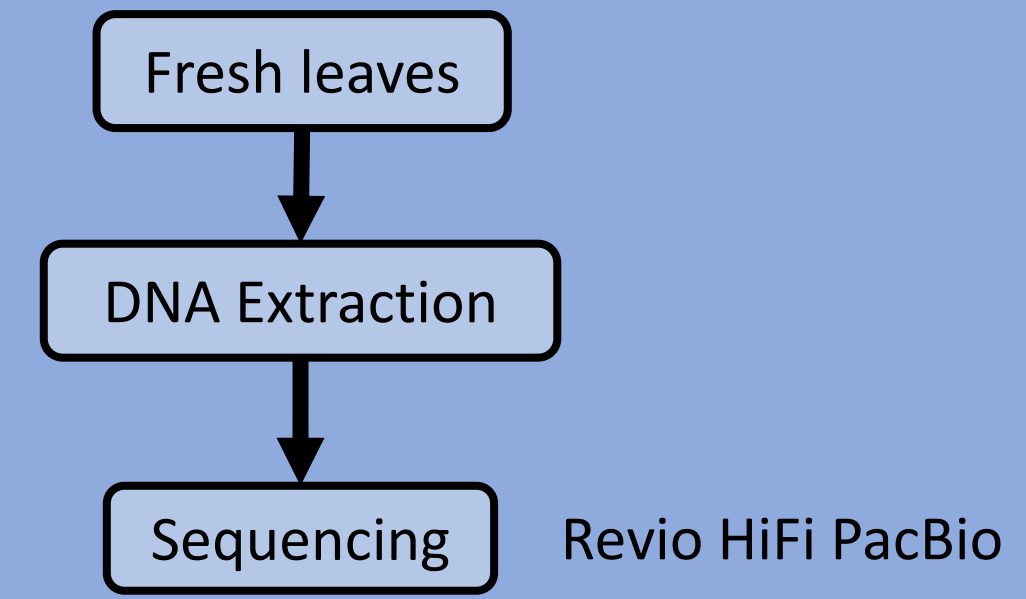
Sequenced *M. stenopetala*



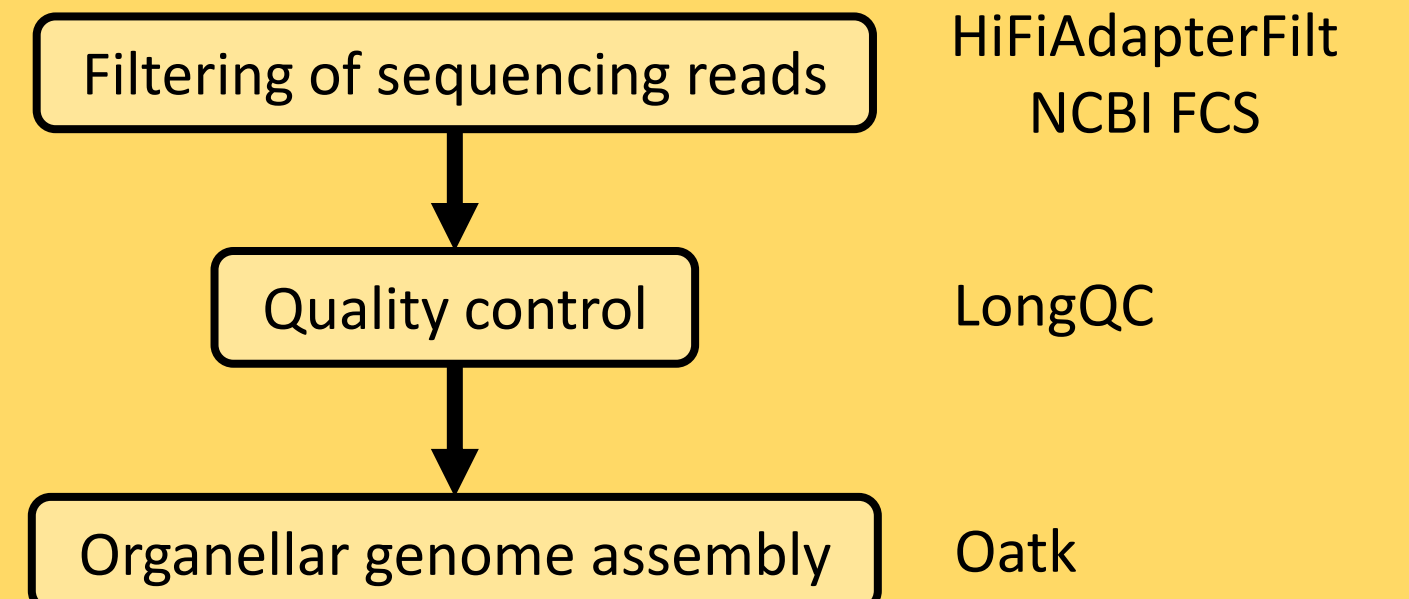
M. stenopetala seeds

Workflow for organelle genome assembly

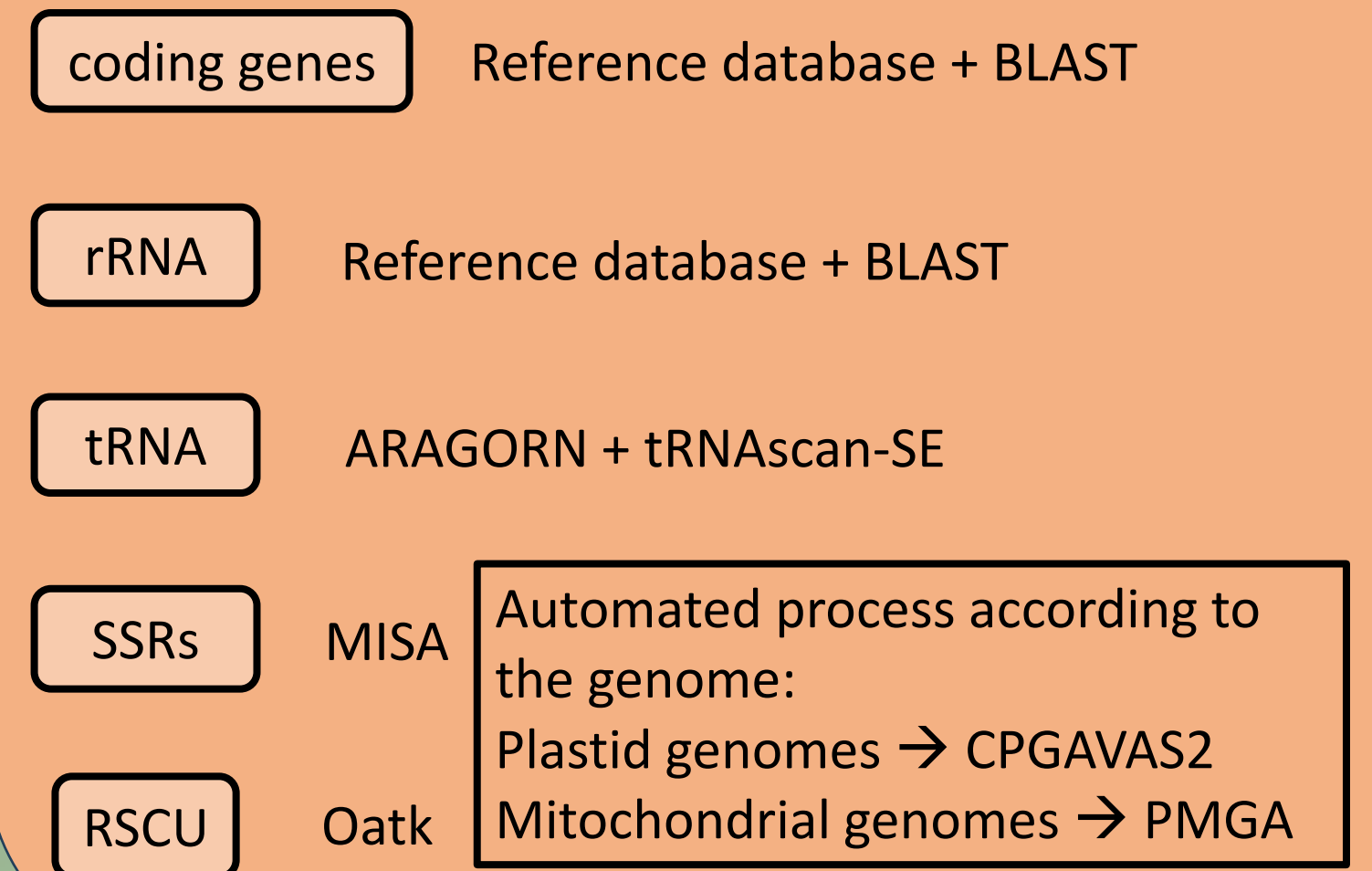
Extraction and sequencing



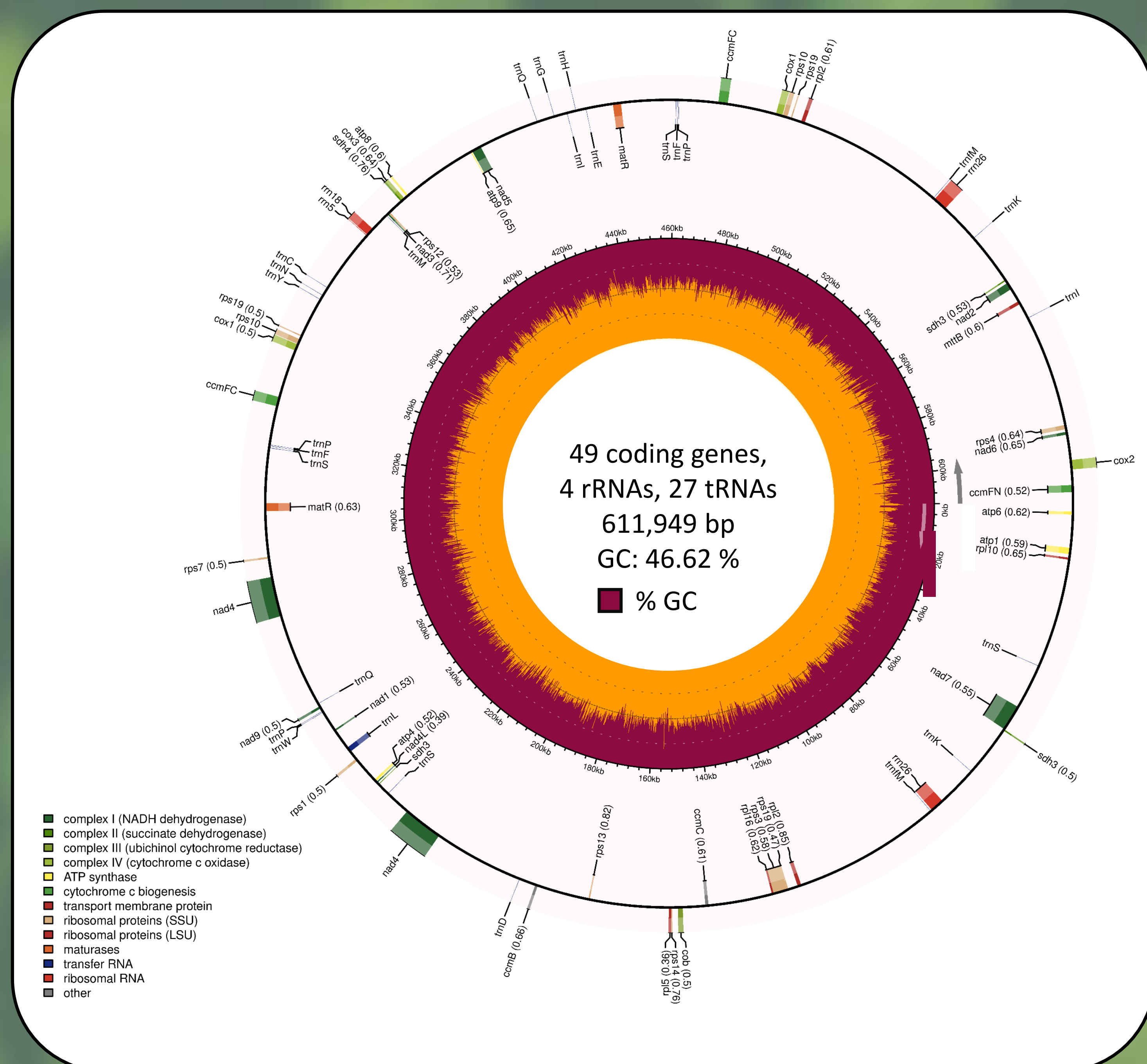
Raw data preprocessing and assembly



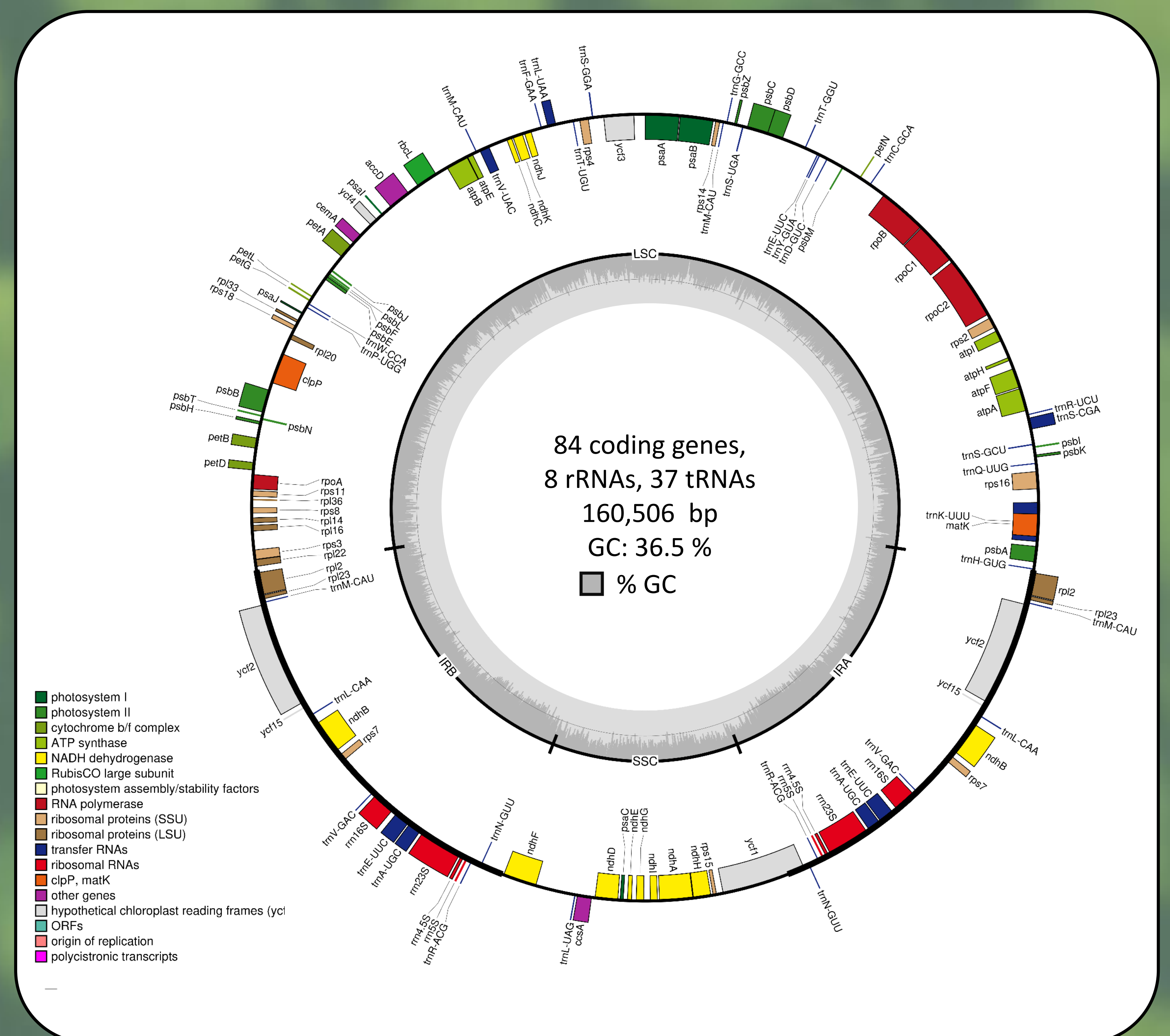
Functional analysis and annotation



Mitochondrial genome



Chloroplast genome



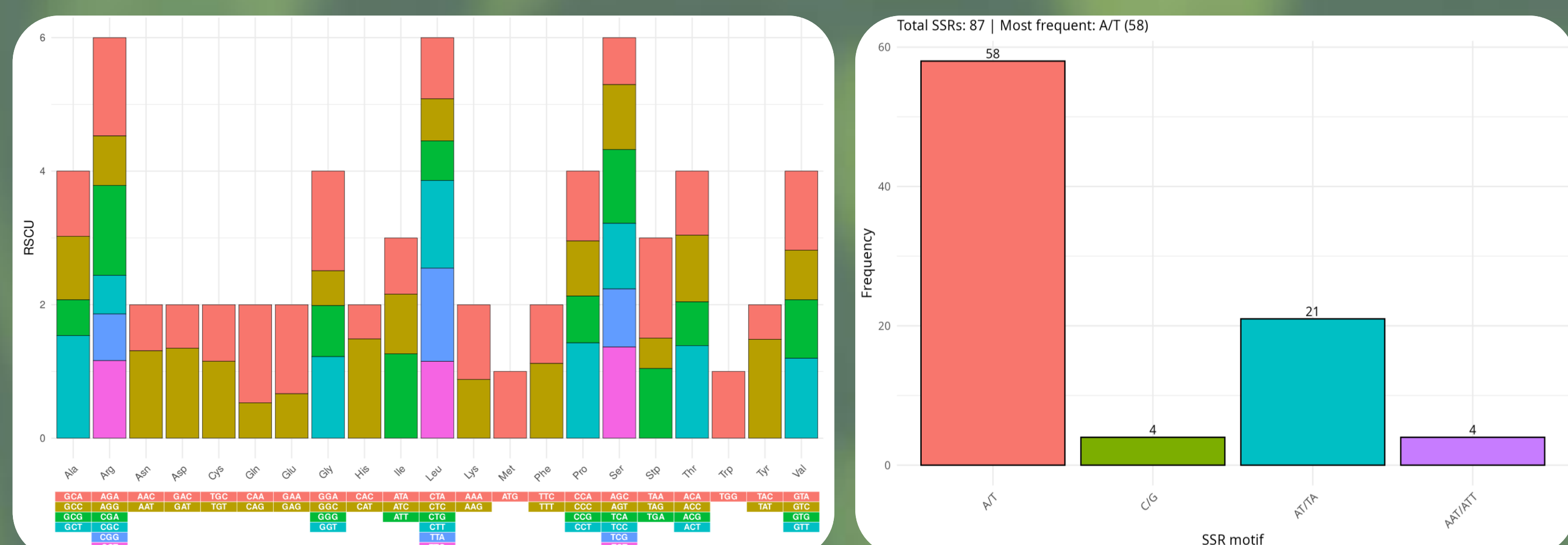
Gene profile and organization

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>cox1, cox12, cox2, cox3</i>
	Complex IV (cytochrome oxidase)	<i>atp1, atp4, atp6, atp8, atp9</i>
	Complex V (ATP synthase)	<i>ccmB, ccmC, ccmFC (x2), ccmFM</i>
	Cytochrome c biogenesis	<i>matR (x2)</i>
	Maturases	<i>mttB</i>
	Transport membrane protein	<i>rpl10, rpl16, rpl2 (x2), rpl5</i>
	Large subunit of ribosome	<i>rps1, rps10 (x2), rps12, rps13, rps14, rps19 (x3), rps3, rps4, rps7</i>
	Small subunit of ribosome	<i>rrn18, rrn26 (x2), rrn5</i>
rRNA genes	Ribosomal 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), trnI-CAU (x2), trnN-GUU, trnP-UGG (x3), trnQ-UUG (x2), trnS-GCU, trnS-GGA, trnS-UGA, trnW-CCA, trnY-GUA</i>
tRNAs	Transfer RNA	

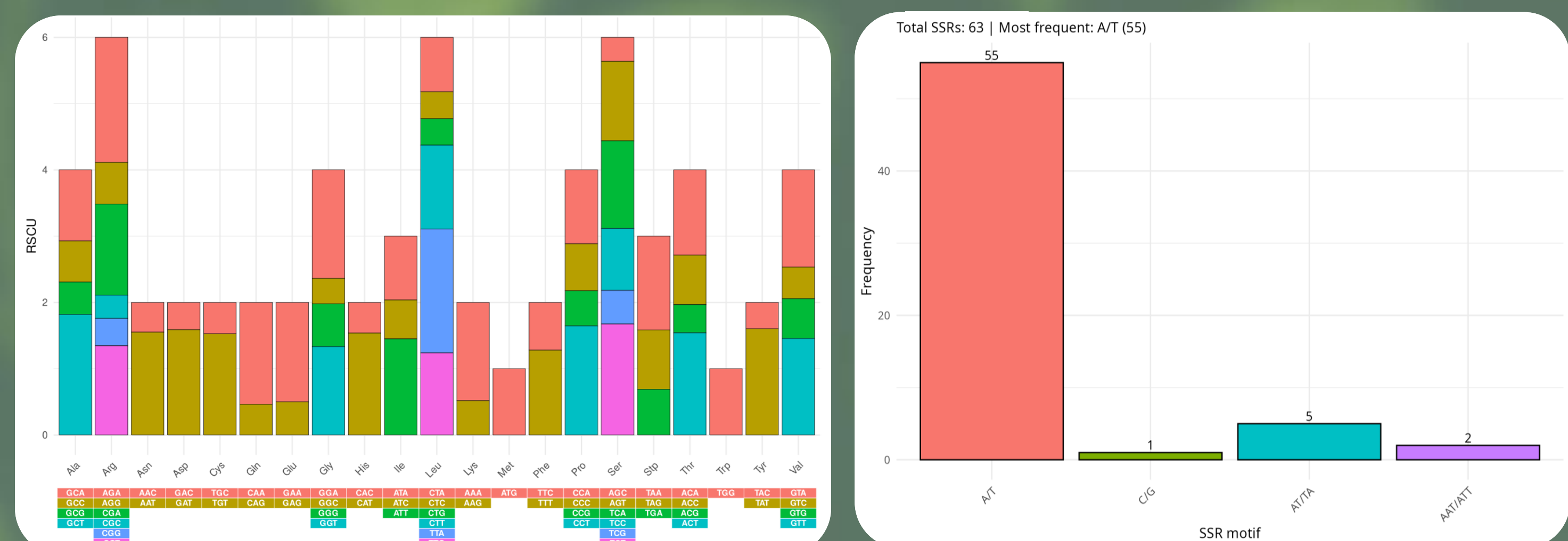
Gene profile and organization

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, petM</i>
	Subunits of photosystem I	<i>psaA, psaB, psaC, psaI, psaJ</i>
	Subunit of rubisco	<i>rbcl</i>
	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-UUC, 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), trnI-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>
Unknown	Conserved open reading frames	<i>ycf1 (x2), ycf15 (x2), ycf2 (x2), ycf4</i>

Codon usage bias analysis and characterization of SSRs



Codon usage bias analysis and characterization of SSRs



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. The Principal Investigator and supervisor is Dr. Lorenzo Carretero Paulet, Professor in Genetics at the University of Almería and head of the Plant Evolutionary Genomics research group (SICA id BIO359). Additional support was provided by the project UAL2024_1, "Puesta en valor del cultivo huérfano etíope *Moringa stenopetala* mediante la secuenciación y anotación funcional de su genoma (shiferaawgenome)" (Modality 1), funded by the 2024 Plan Propio for International Cooperation (Program I) of the University of Almería, granted to Dr. Lorenzo Carretero Paulet.