

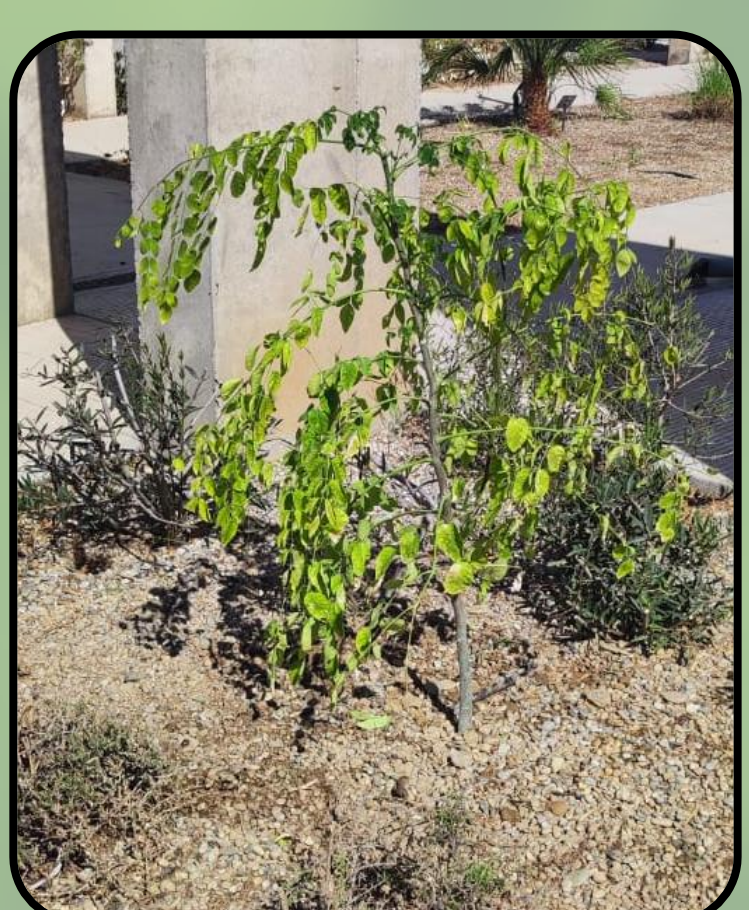
CHARACTERISATION OF MORINGASTENOPETALA ORGANELLAR GENOMES

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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.



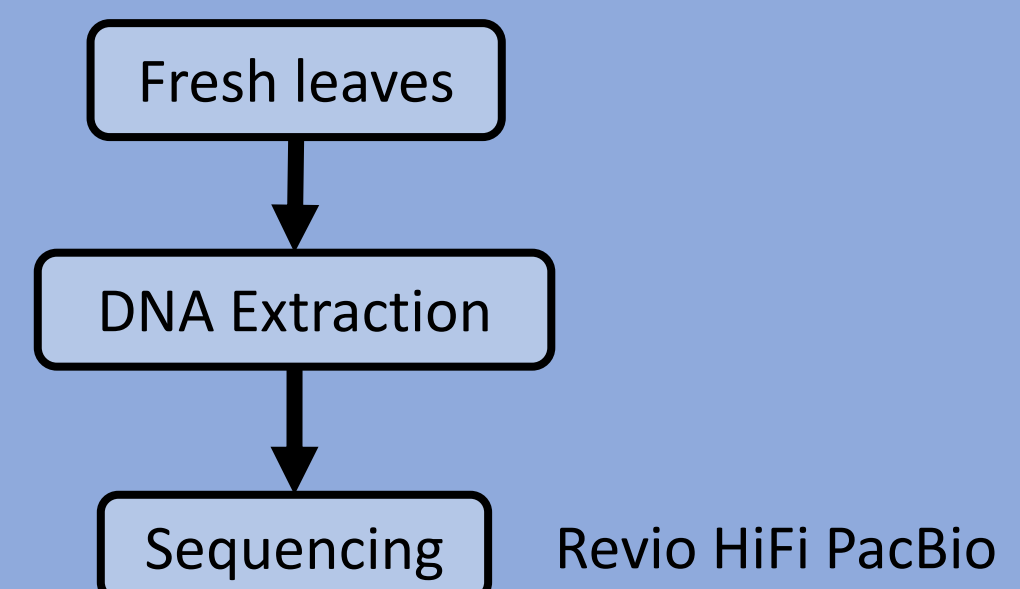
Sequenced *M. stenopetala*



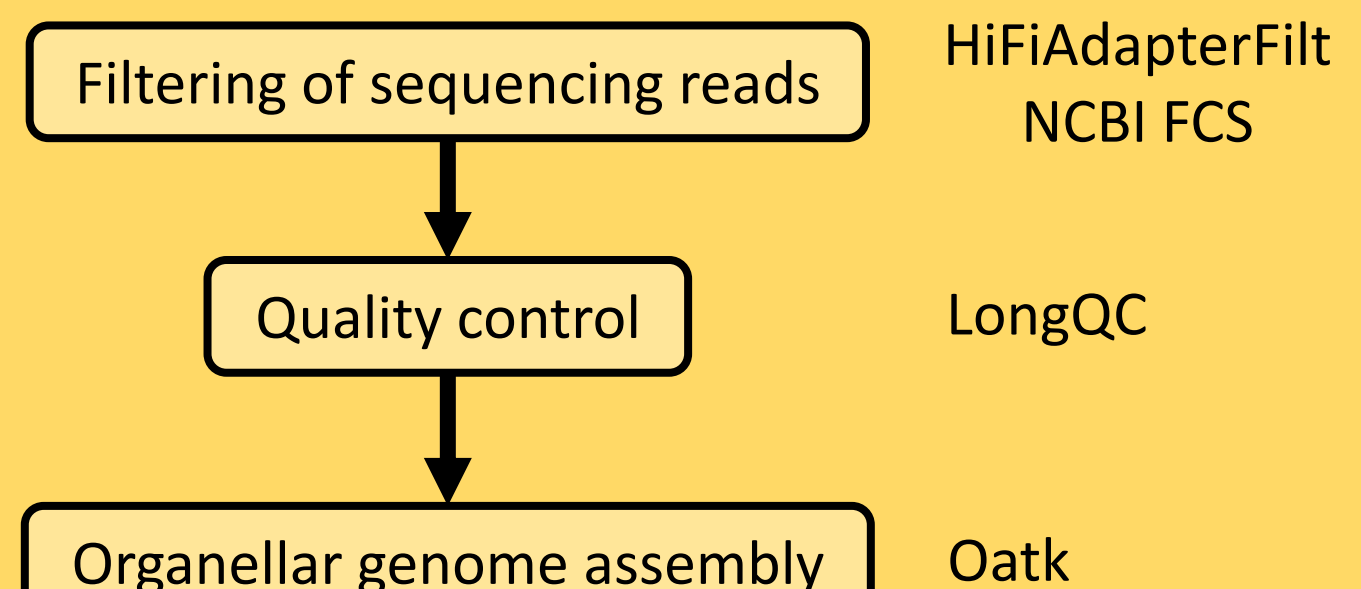
M. stenopetala seeds

Workflow for organelle genome assembly

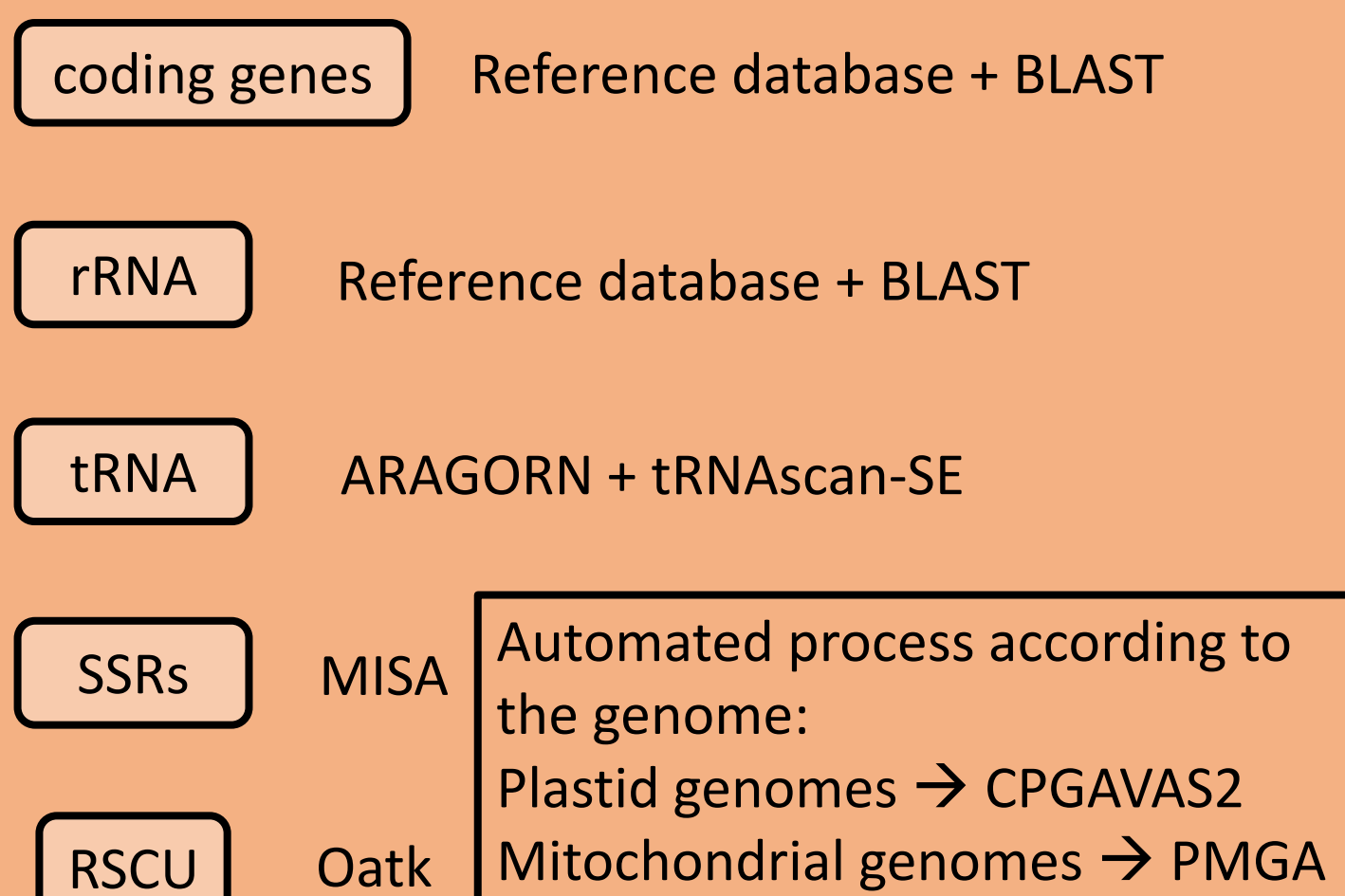
Extraction and sequencing



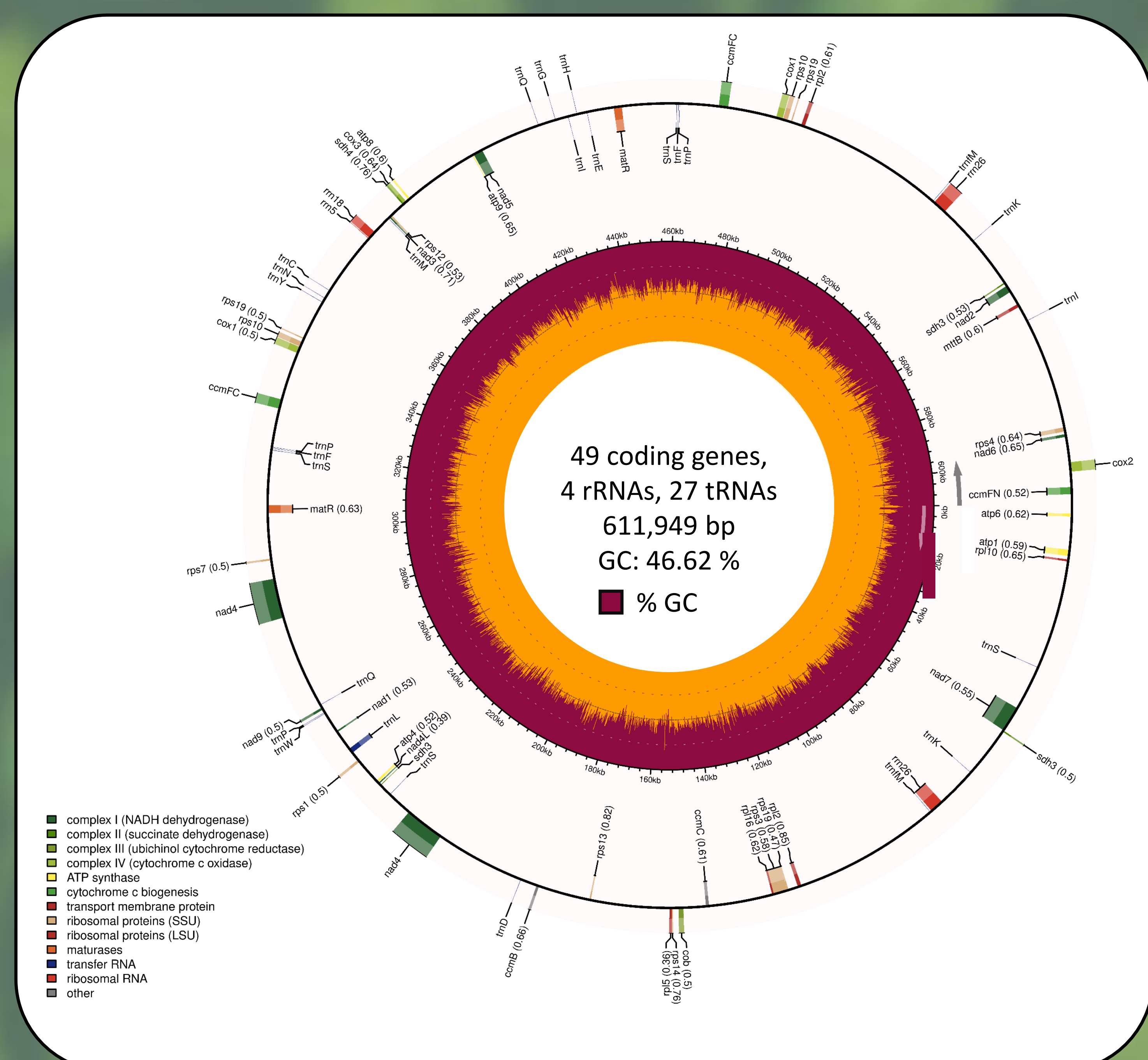
Raw data preprocessing and assembly



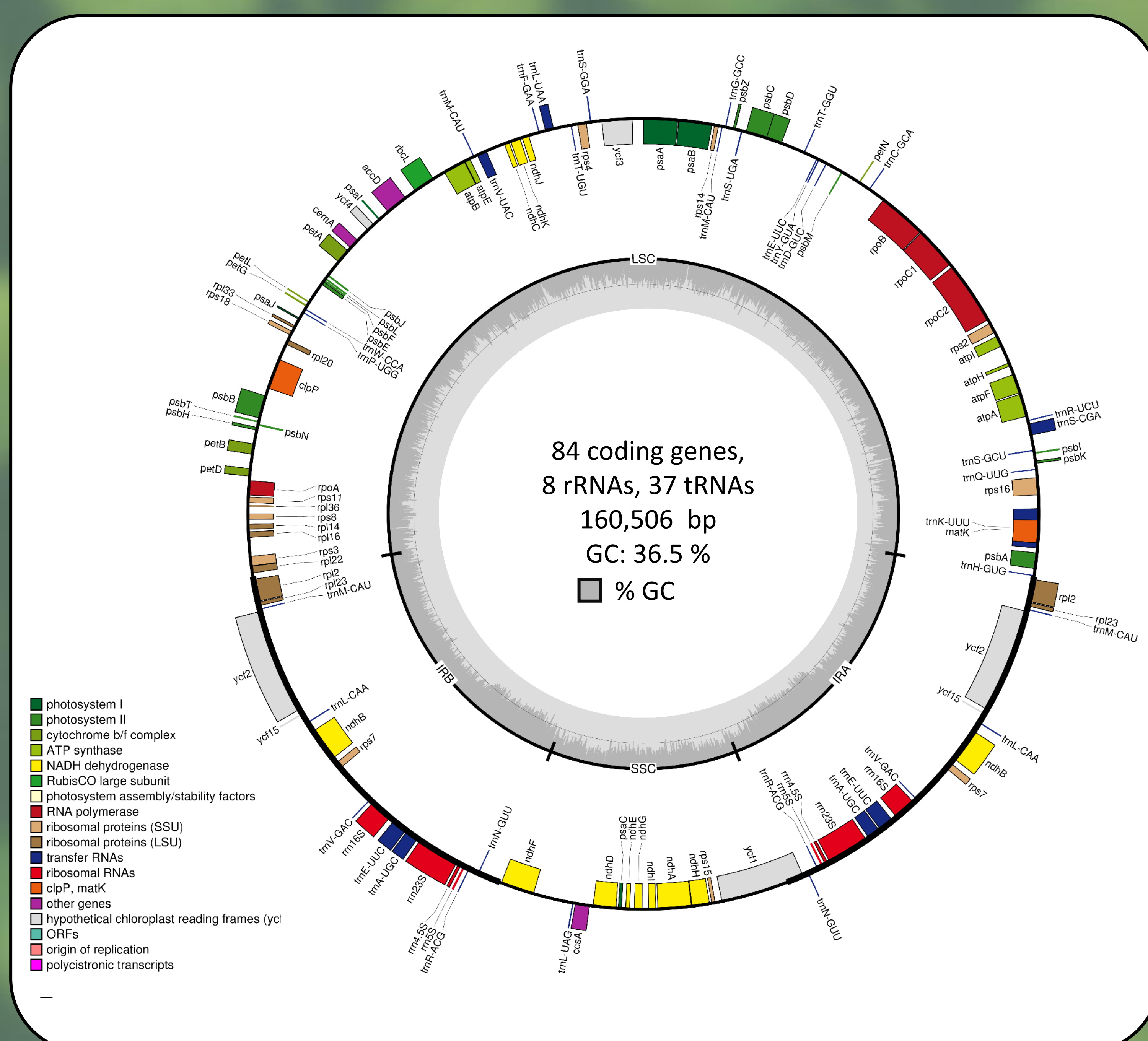
Functional analysis and annotation



Mitochondrial genome



Chloroplast genome



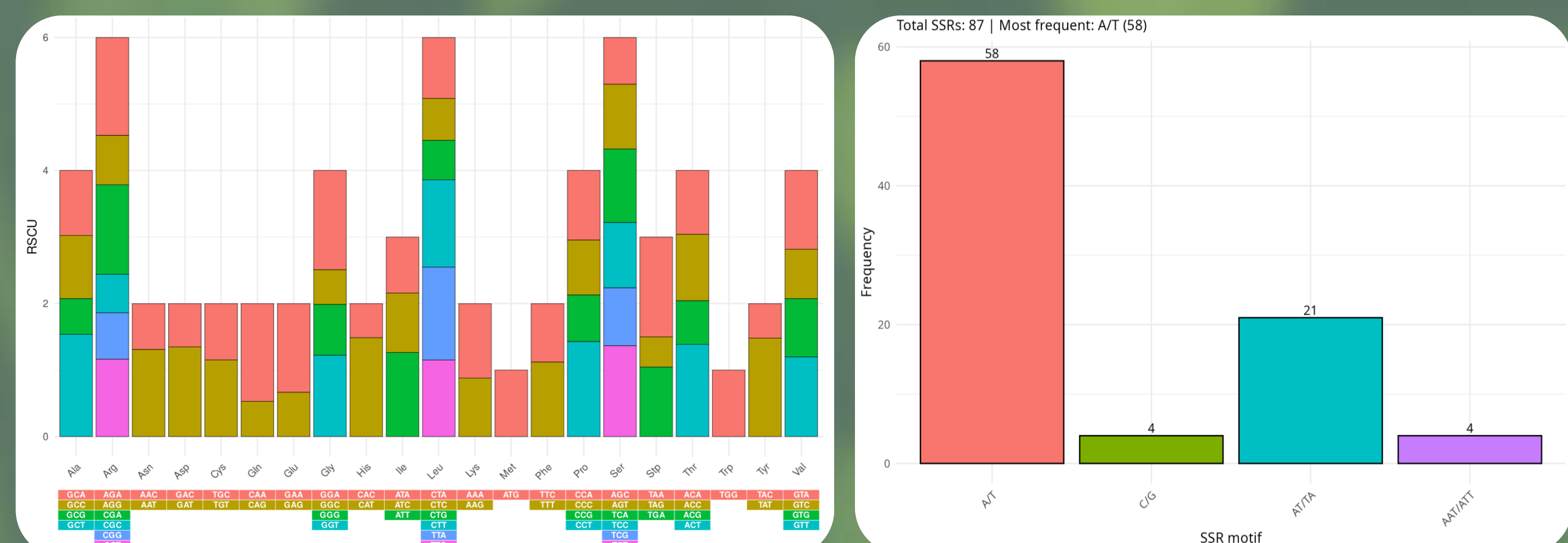
Gene profile and organization

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 c 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>
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>

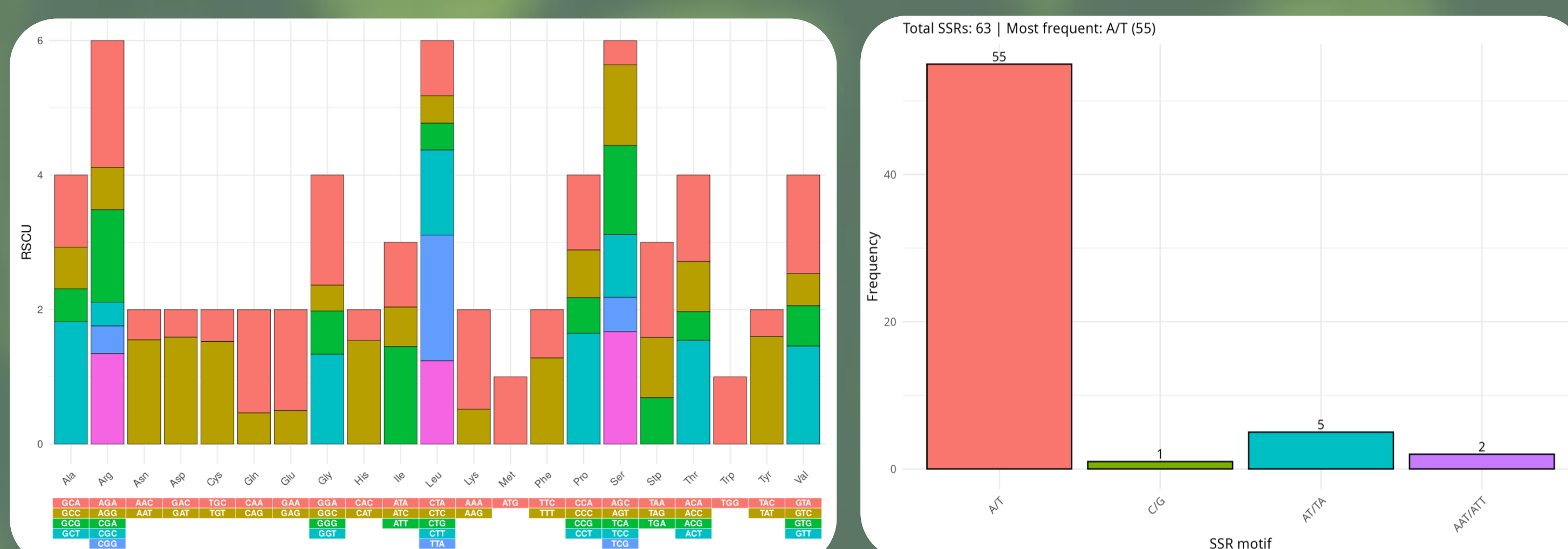
Gene profile and organization

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, rbcL</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>
rRNA genes	Small subunit of ribosome	<i>rps11, rps12 (x2), rps14, rps15, rps16, rps18, rps19, rps2, rps3, rps4, rps7 (x2), rps8</i>
	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



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Acknowledgements

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