

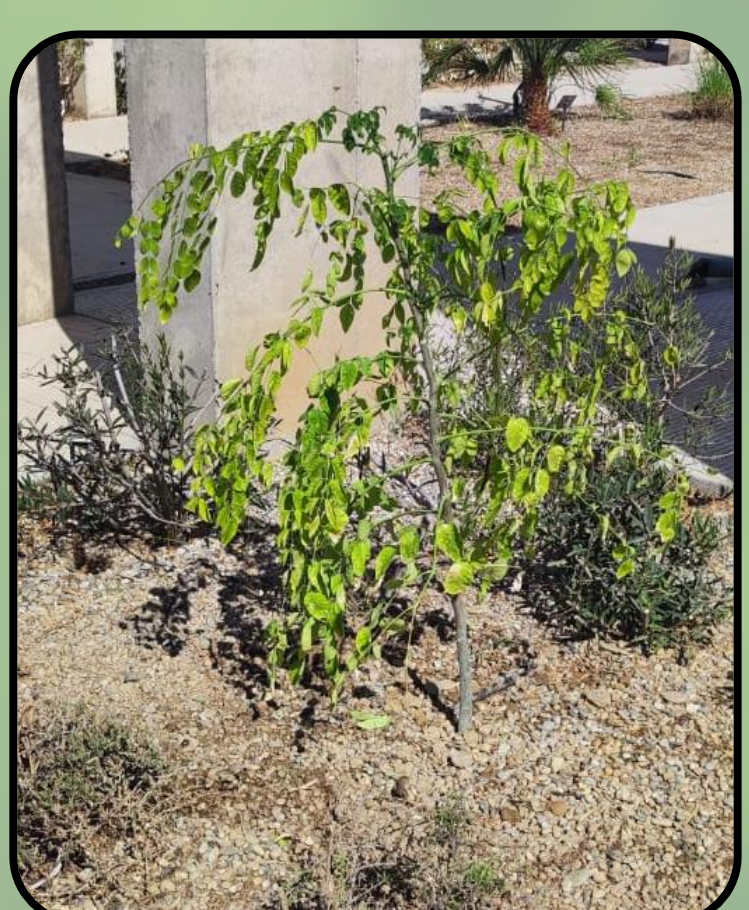
CHARACTERISATION OF MORINGASTENOPETALA ORGANELLAR GENOMES

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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.



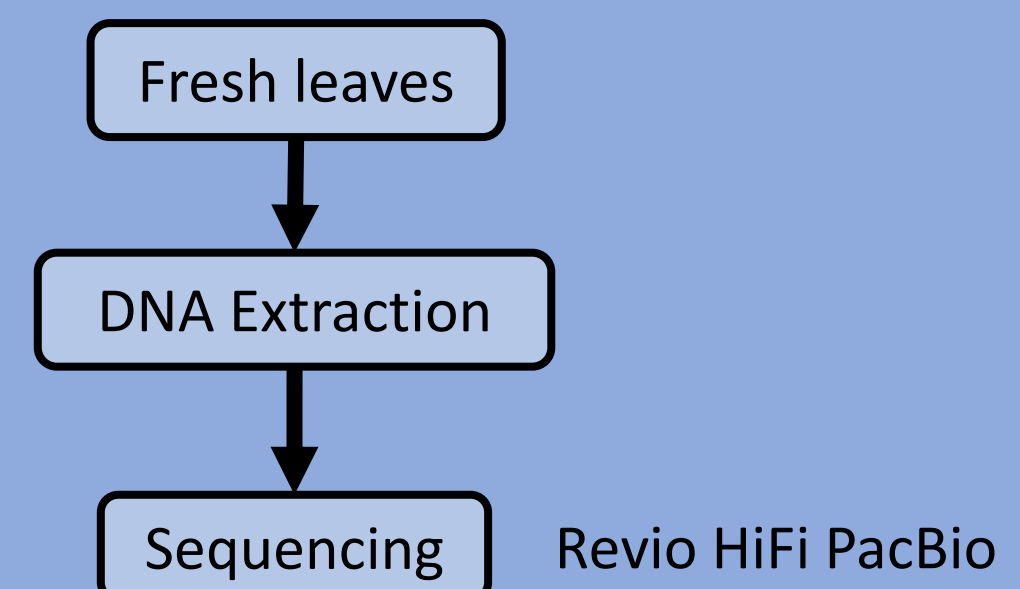
Sequenced *M. stenopetala*



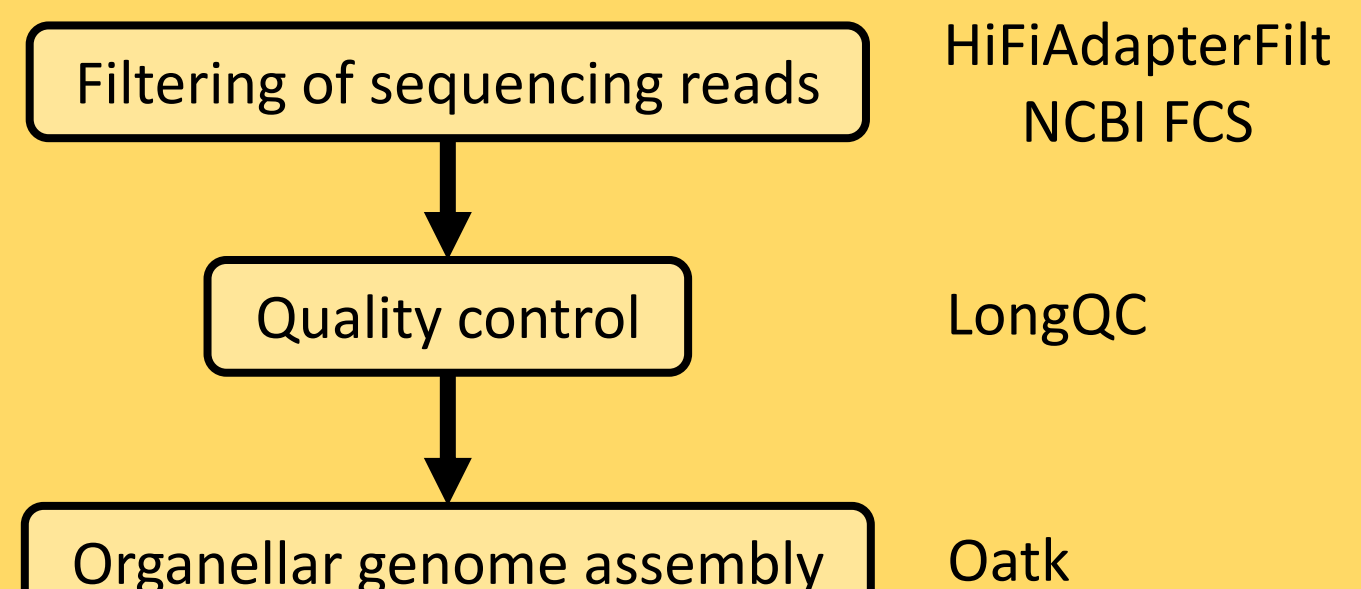
M. stenopetala seeds

Workflow for organelle genome assembly

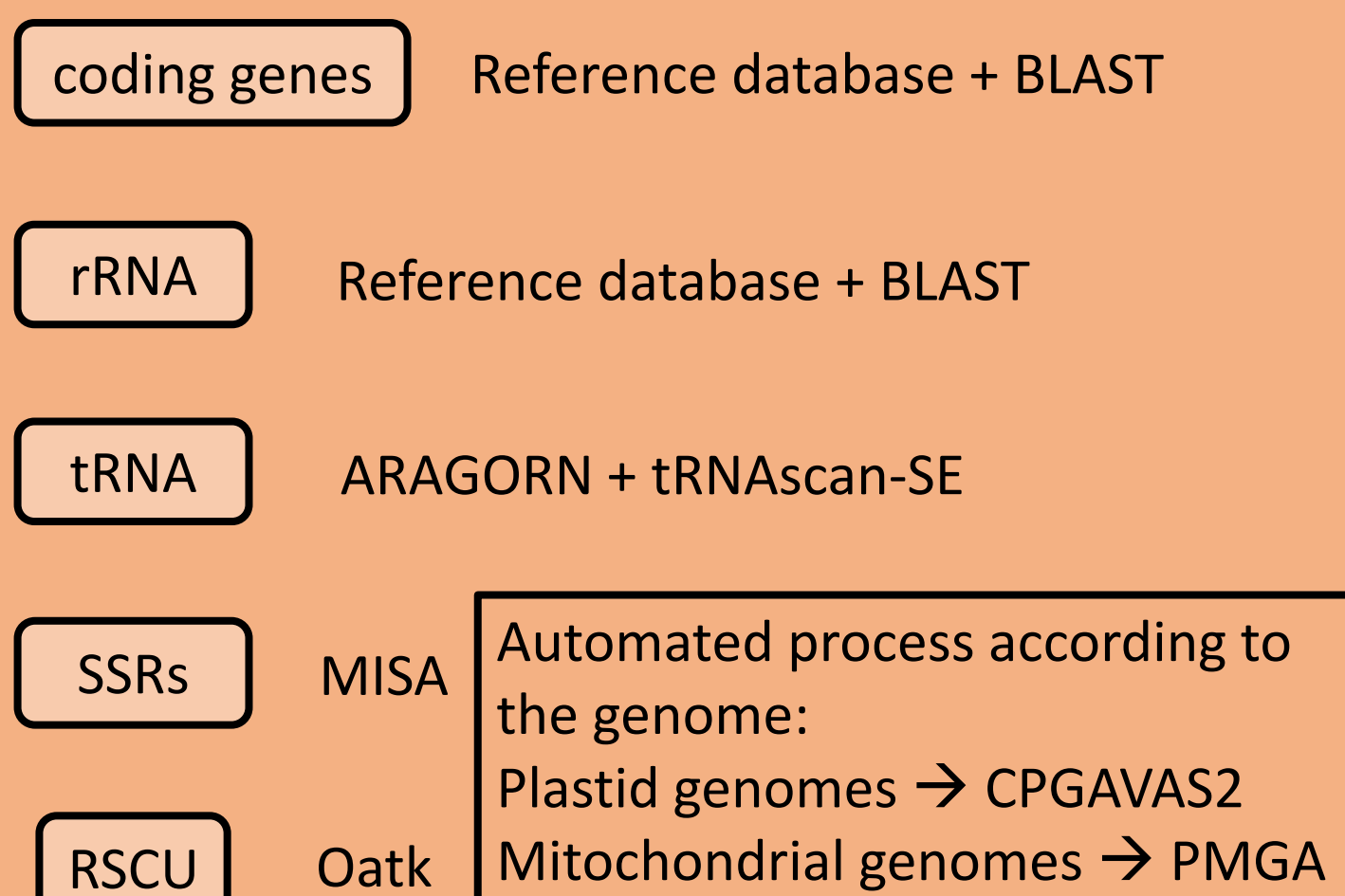
Extraction and sequencing



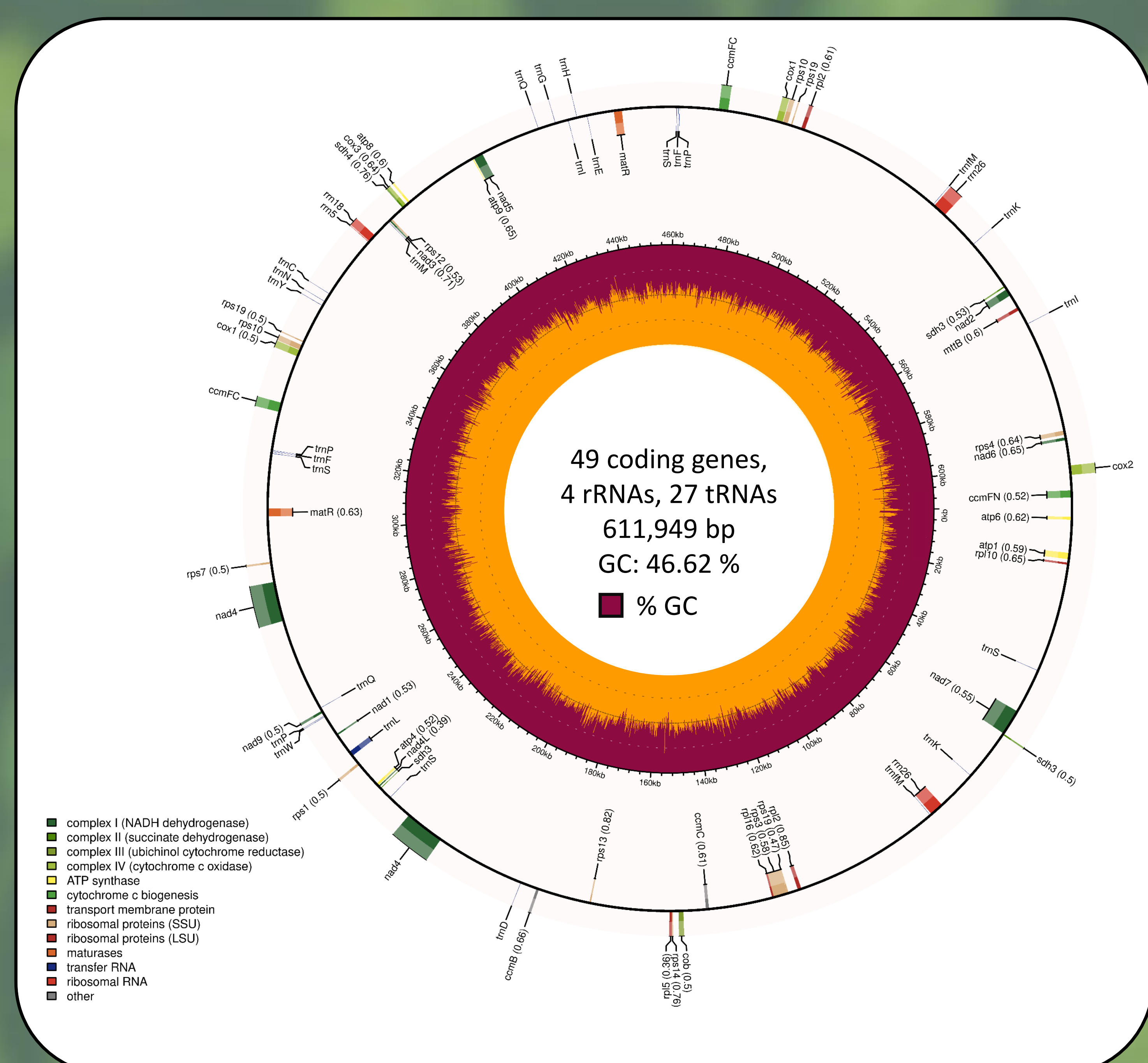
Raw data preprocessing and assembly



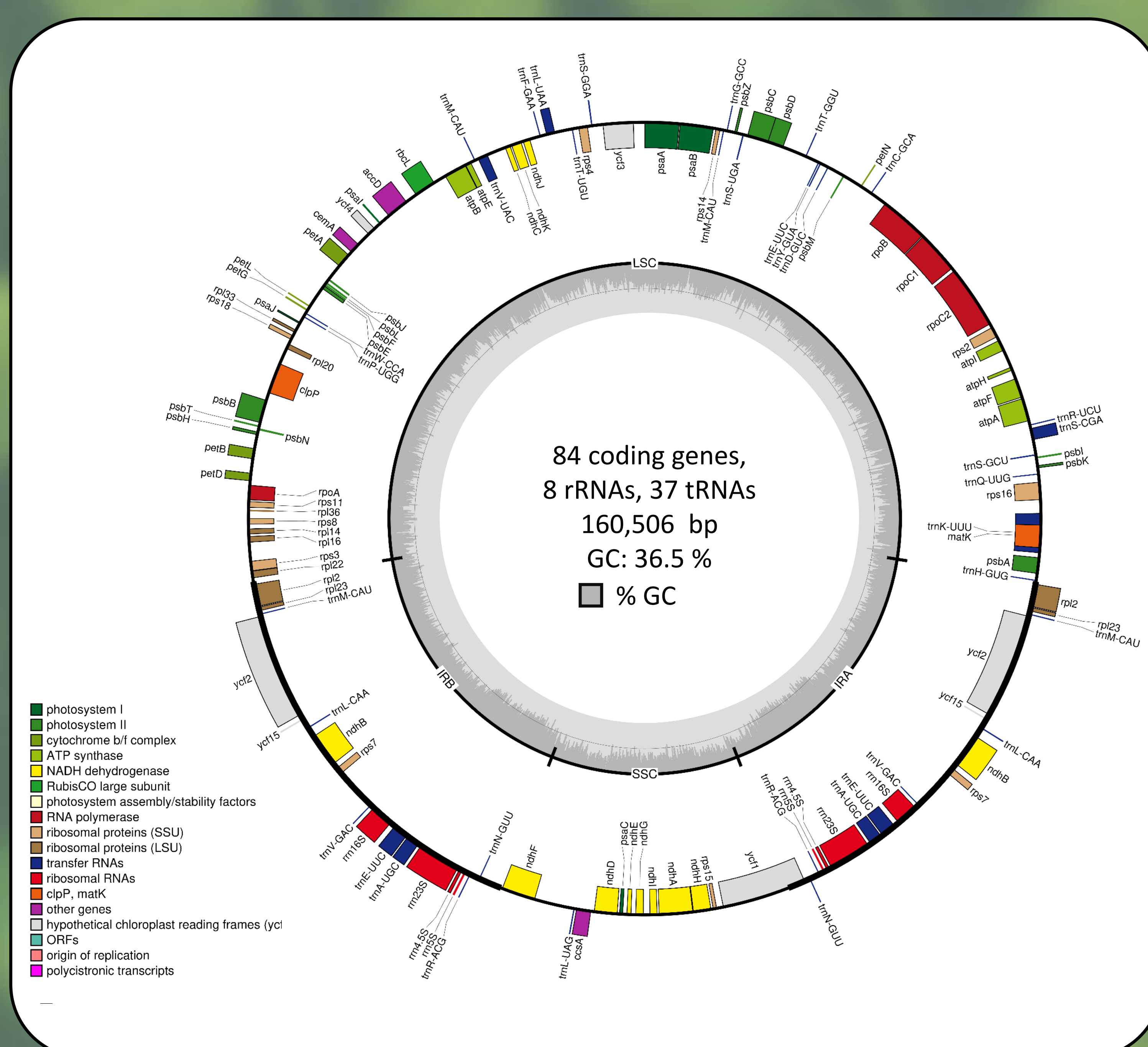
Functional analysis and annotation



Mitochondrial genome



Chloroplast genome



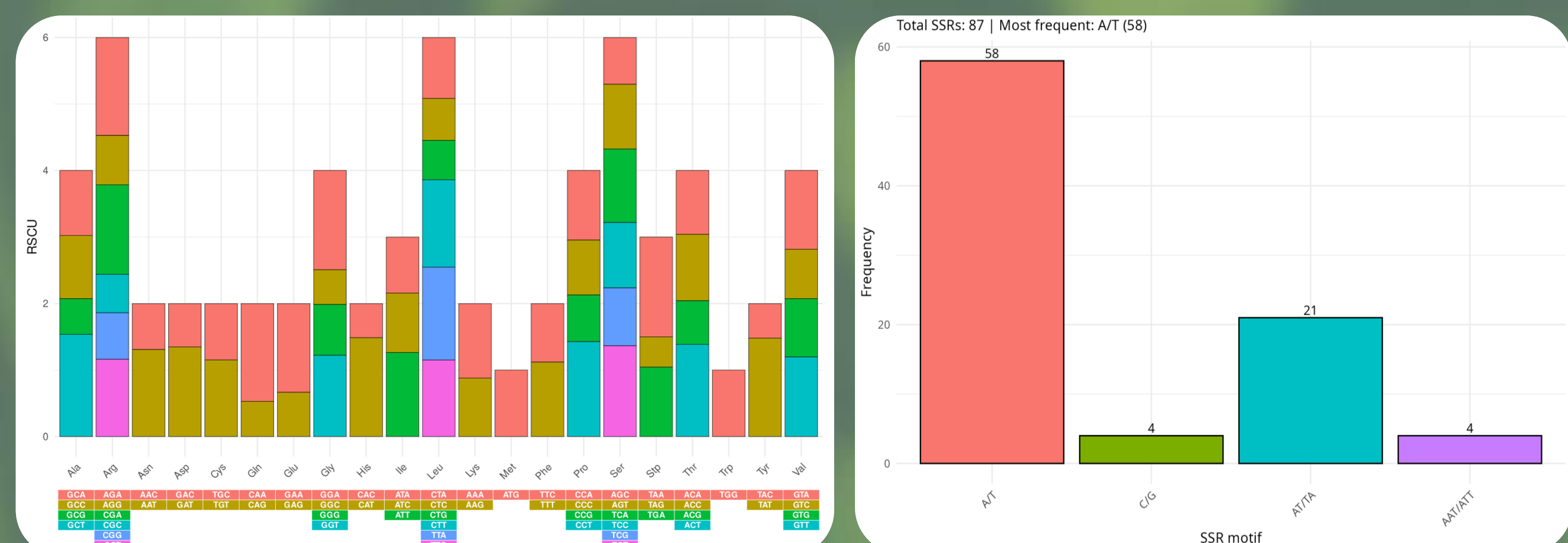
Gene profile and organization

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>
Variable genes		<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>
rRNA genes	Ribosomal RNA	
tRNAs	Transfer RNA	

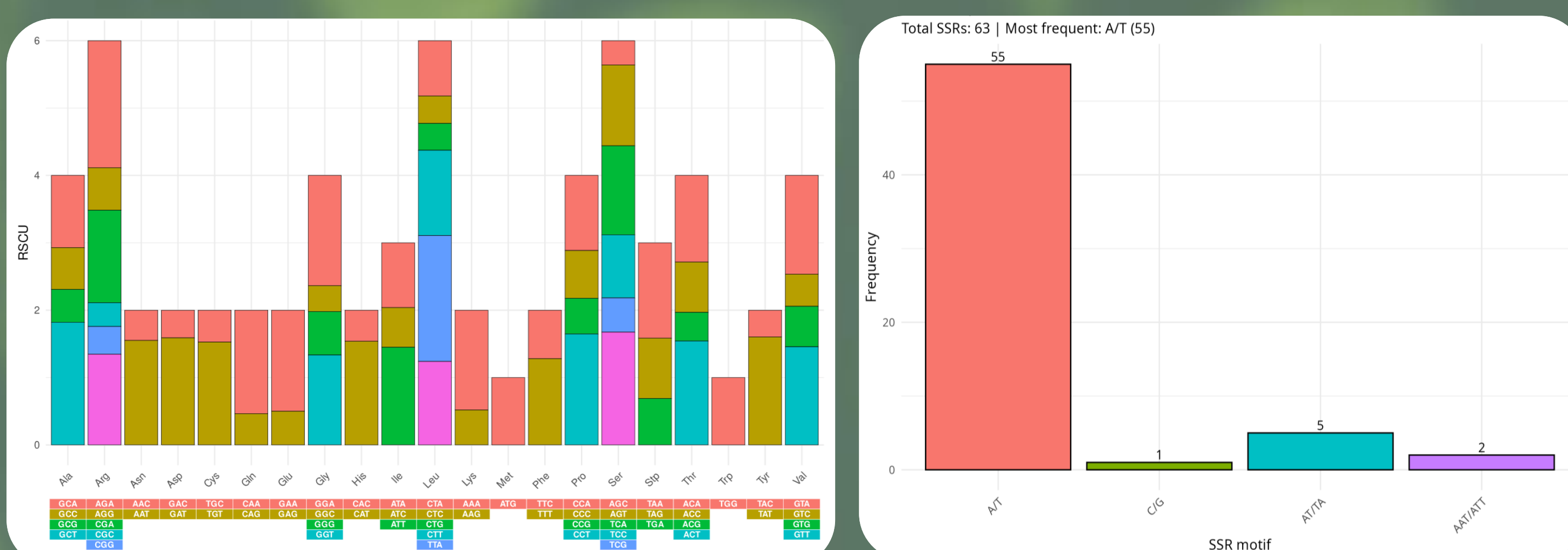
Gene profile and organization

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, rbcL</i>
	Subunit of rubisco	<i>rpl14, rpl16, rpl2(x2), rpl20, rpl22, rpl23(x2), rpl32, rpl33, rpl36</i>
	Large subunit of ribosome	<i>rpoA, rpoB, rpoC1, rpoC2</i>
	DNA dependent RNA polymerase	<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), trnL-UAG, trnV-GAC, trnL-CAA, trnM-CAU (x4), trnH-GUG</i>
	Transfer RNAs	<i>rps11, rps12 (x2), rps14, rps15, rps16, rps18, rps19, rps2, rps3, rps4, rps7 (x2), rps8</i>
	Small subunit of ribosome	<i>rrn16 (x2), rrn23 (x2), rrn5 (x2), rrn4.5 (x2)</i>
rRNA genes	Ribosomal RNA	
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>
	Conserved open reading frames	<i>ycf1 (x2), ycf15 (x2), ycf2 (x2), ycf4</i>
Unknown		

Codon usage bias analysis and characterization of SSRs



Codon usage bias analysis and characterization of SSRs



Acknowledgements

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