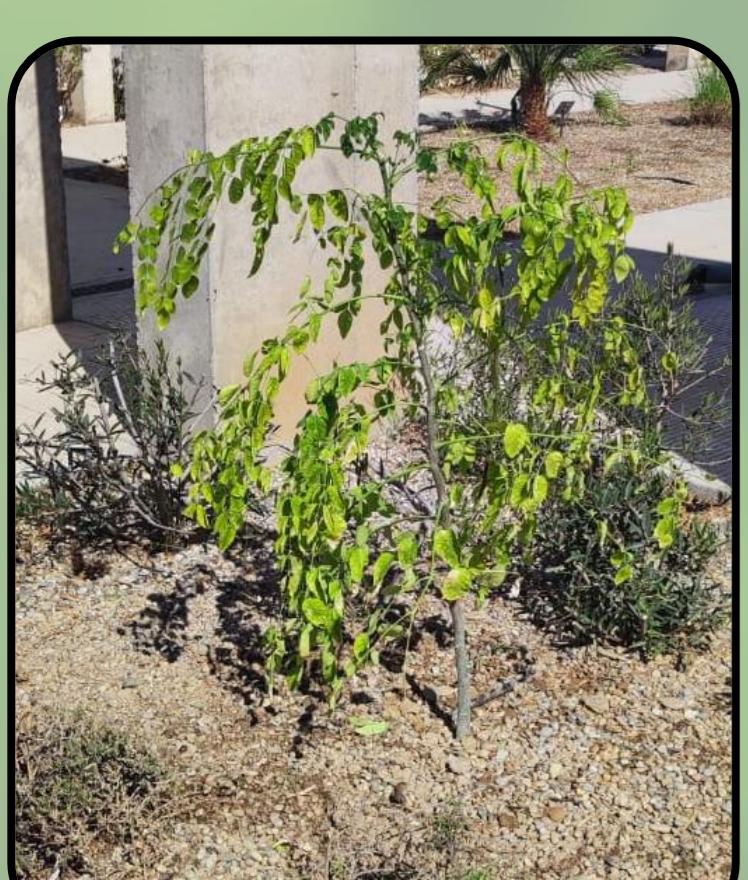


# CHARACTERISATION OF MORINGA STENOPIETALA ORGANELLAR GENOMES

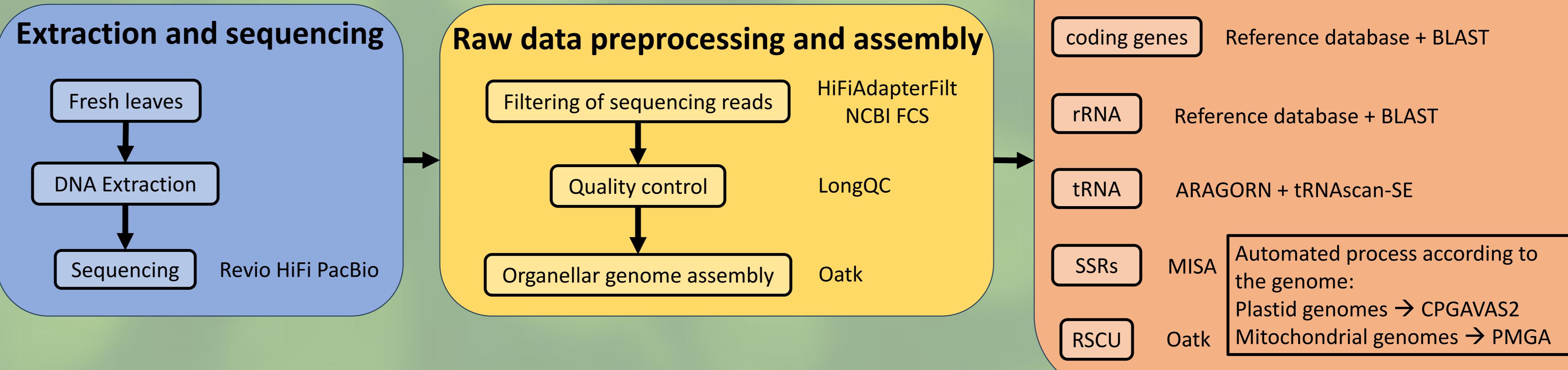
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# Introduction

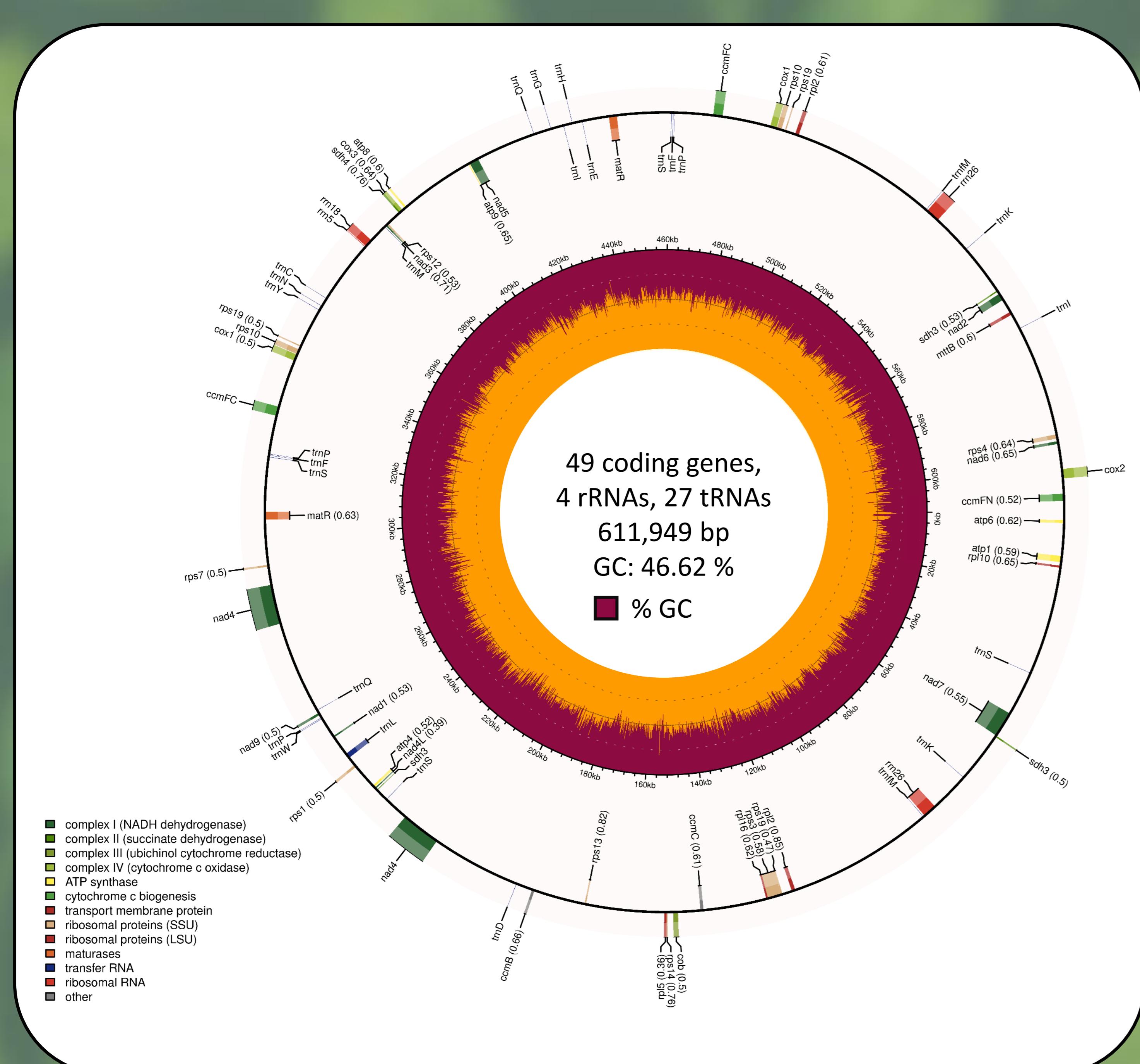


The monogeneric family *Moringaceae* comprises 13 species that are widely used for food, fodder, medicine, and various industrial applications. One notable species is *Moringa stenopetala*, which is native to southern Ethiopia and northern Kenya. It has a high nutritional value, making it a key crop 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.

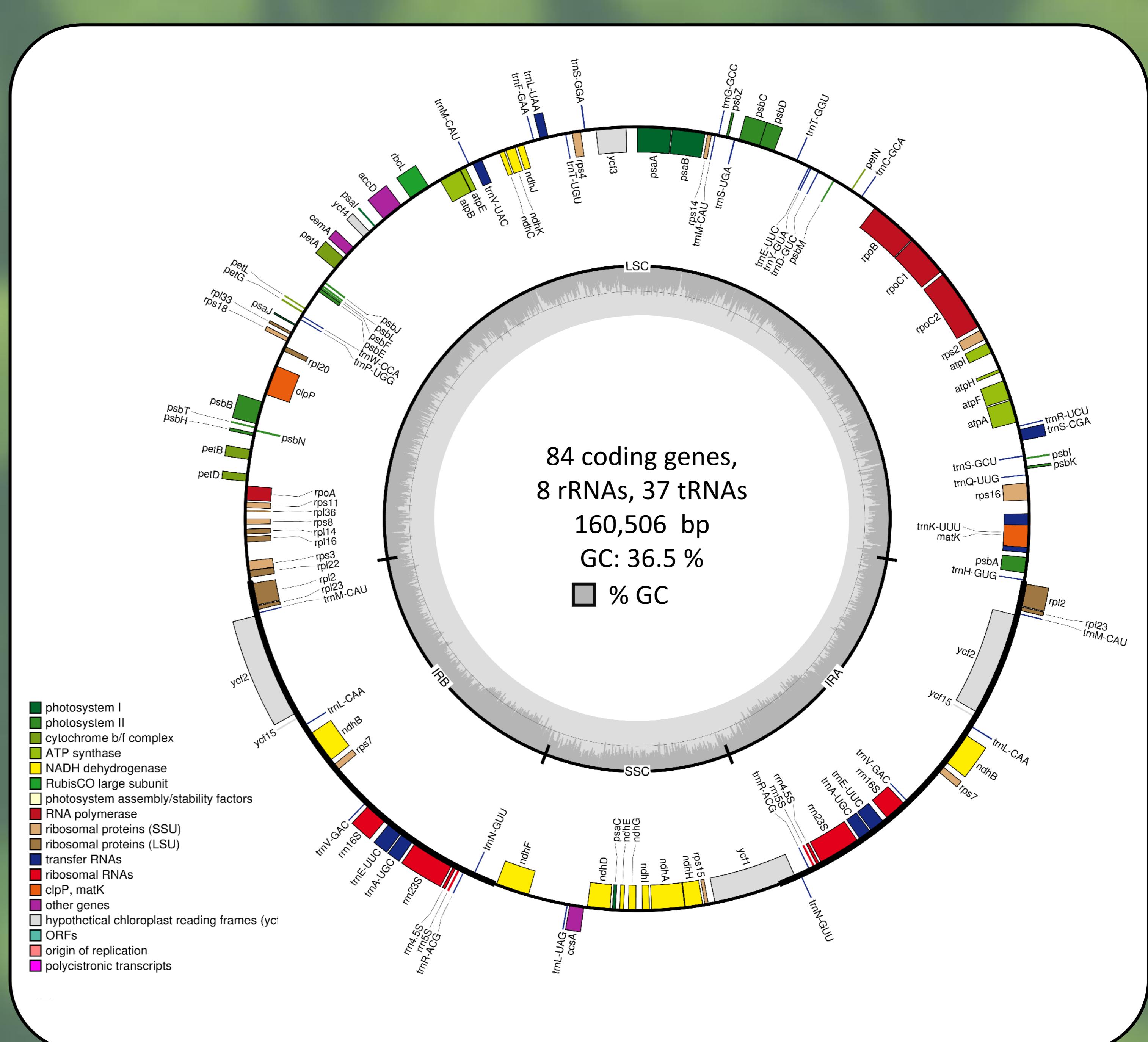
# Workflow for organelle genome assembly



# Mitochondrial genome



# Chloroplast genome



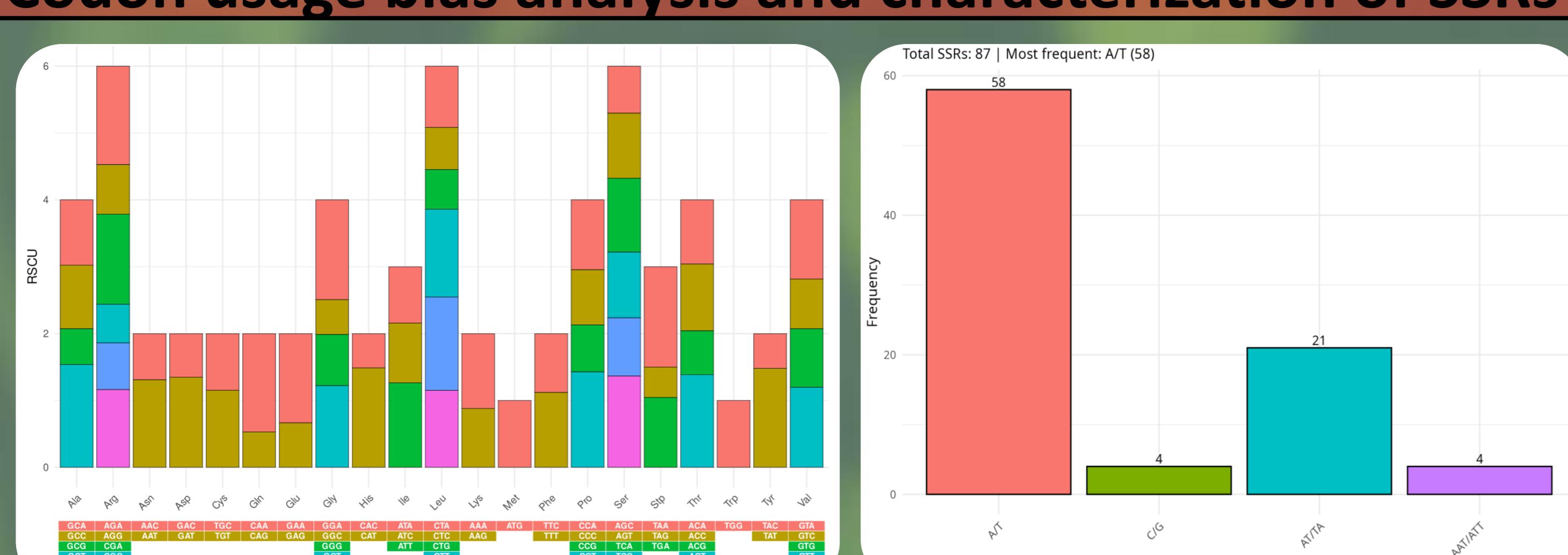
# Gene profile and organization

Category of genes	Group of genes	Name of genes
Core genes	Complex I (NADH dehydrogenase)	<i>nad1, nad2, nad3, nad4</i> (x2), <i>nad4L, nad5, nad6, nad7, nad9</i>
	Complex II (succinate dehydrogenase)	<i>sdh3</i> (x3), <i>sdh4</i>
	Complex III (ubiquinol cytochrome c reductase)	<i>cob</i>
	Complex IV (cytochrome c 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</i> (x2), <i>ccmFN</i>
	Maturases	<i>matR</i> (x2)
	Transport membrane protein	<i>mttB</i>
Variable genes	Large subunit of ribosome	<i>rpl10, rpl16, rpl2</i> (x2), <i>rpl5</i>
	Small subunit of ribosome	<i>rps1, rps10</i> (x2), <i>rps12, rps13, rps14, rps19</i> (x3), <i>rps3, rps4, rps7</i>
rRNA genes	Ribosomal RNA	<i>rrn18, rrn26</i> (x2), <i>rrn5</i>
tRNAs	Transfer RNA	<i>trnL-CAA, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA</i> (x2), <i>trnG-GCC, trnH-GUG, trnK-UUU</i> (x2), <i>trnM-CAU, trnfM-CAU</i> (x2), <i>trnI-CAU</i> (x2), <i>trnN-GUU, trnP-UGG</i> (x3), <i>trnQ-UUG</i> (x2), <i>trnS-GCU, trnS-GGA</i> , <i>trnS-IUGA, trnW-GCA, trnY-GUA</i>

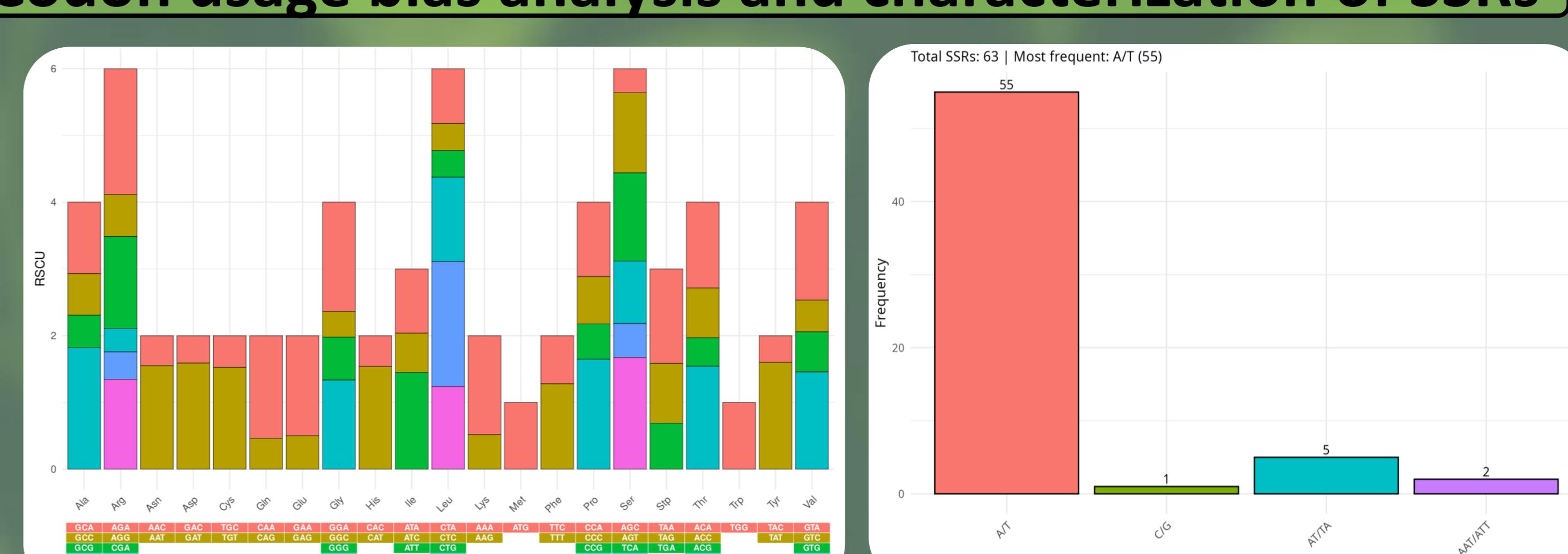
**Category of genes**      **Group of genes**      **Name of gene**

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 <i>photosystem II</i>	<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>
<b>Self replication</b>	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-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>
<b>rRNA genes</b>	Ribosomal RNA	<i>rrn16 (x2), rrn23 (x2), rrn5 (x2), rrn4.5 (x2)</i>
<b>Other genes</b>	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>
<b>Unknown</b>	Conserved open reading frames	<i>ycf1 (x2), ycf15 (x2), ycf2 (x2), ycf4</i>

## Coden usage bias analysis and characterization of SSPs



## Codon usage bias analysis and characterization of SSRs



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