

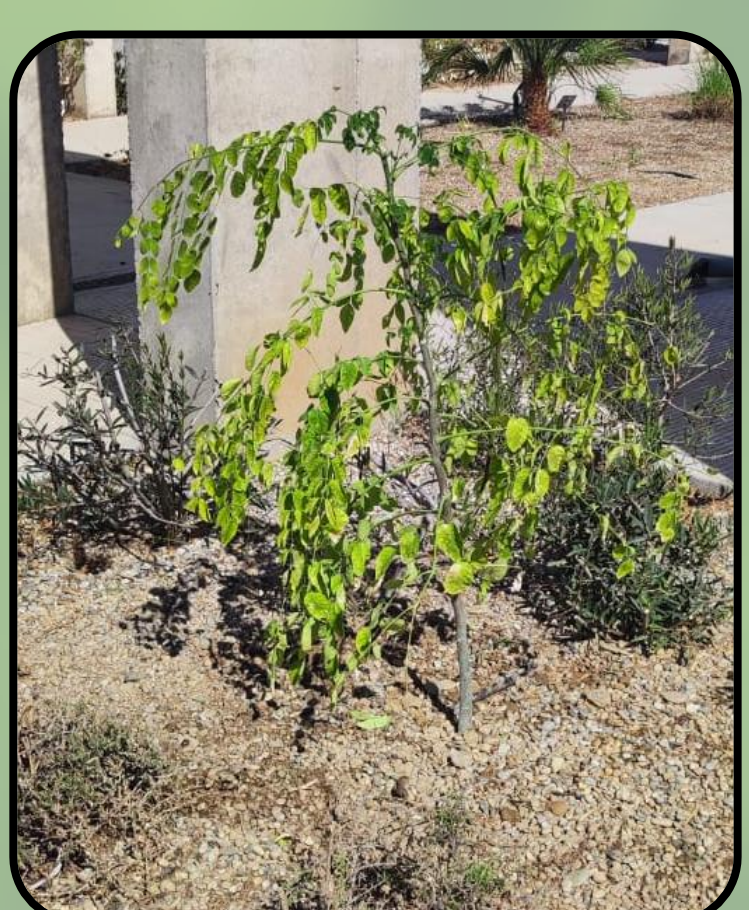
CHARACTERISATION OF MORINGASTENOPETALA ORGANELLAR GENOMES

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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.



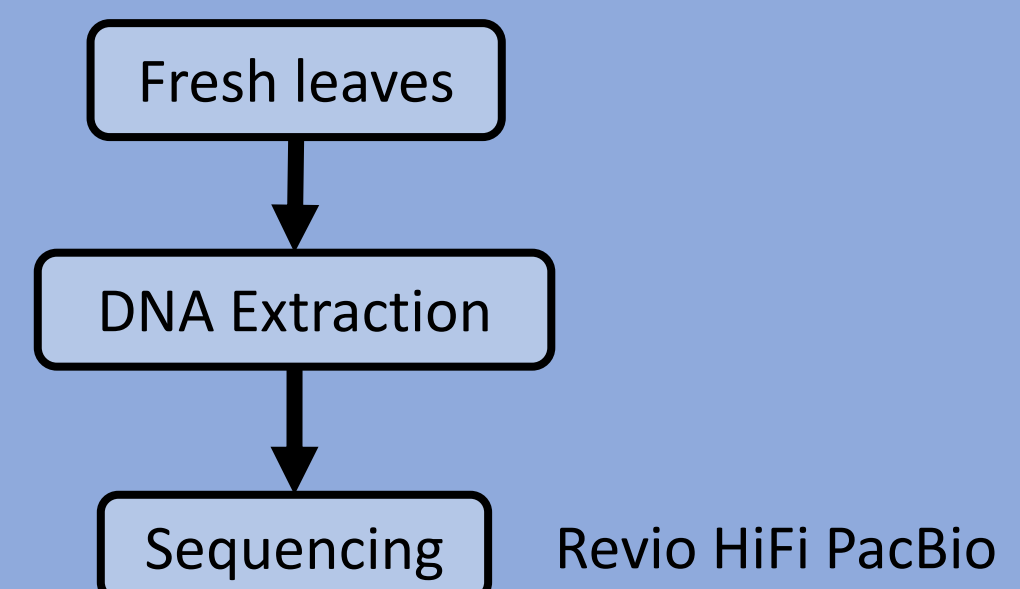
Sequenced *M. stenopetala*



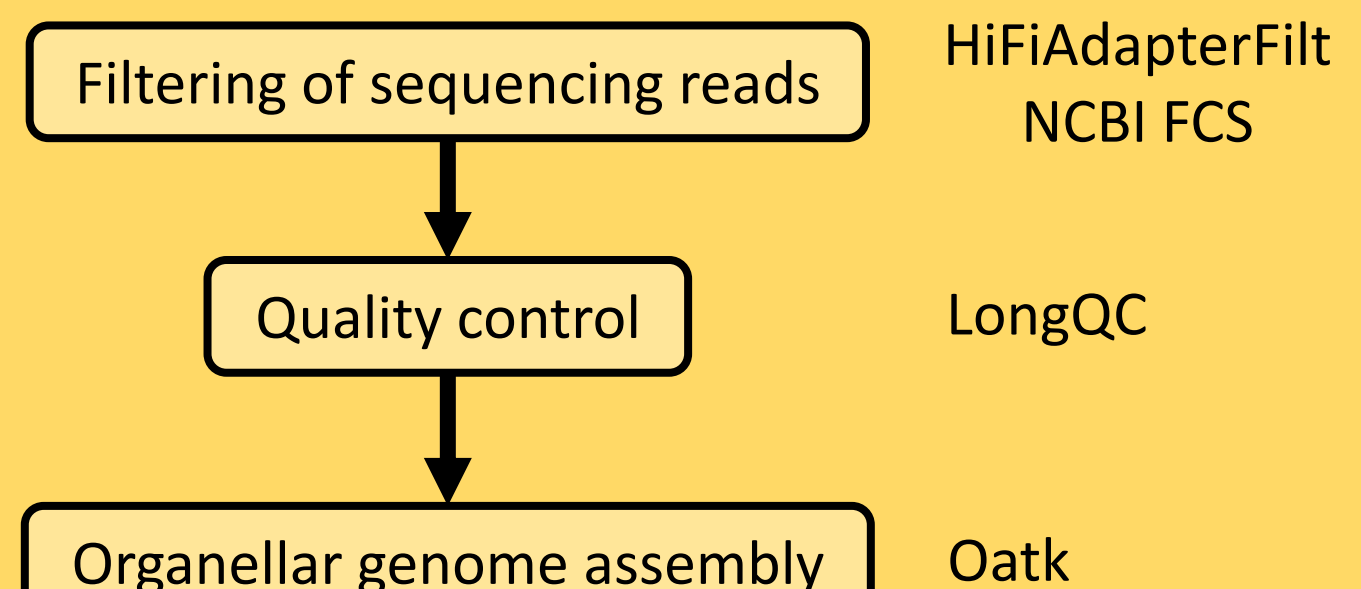
M. stenopetala seeds

Workflow for organelle genome assembly

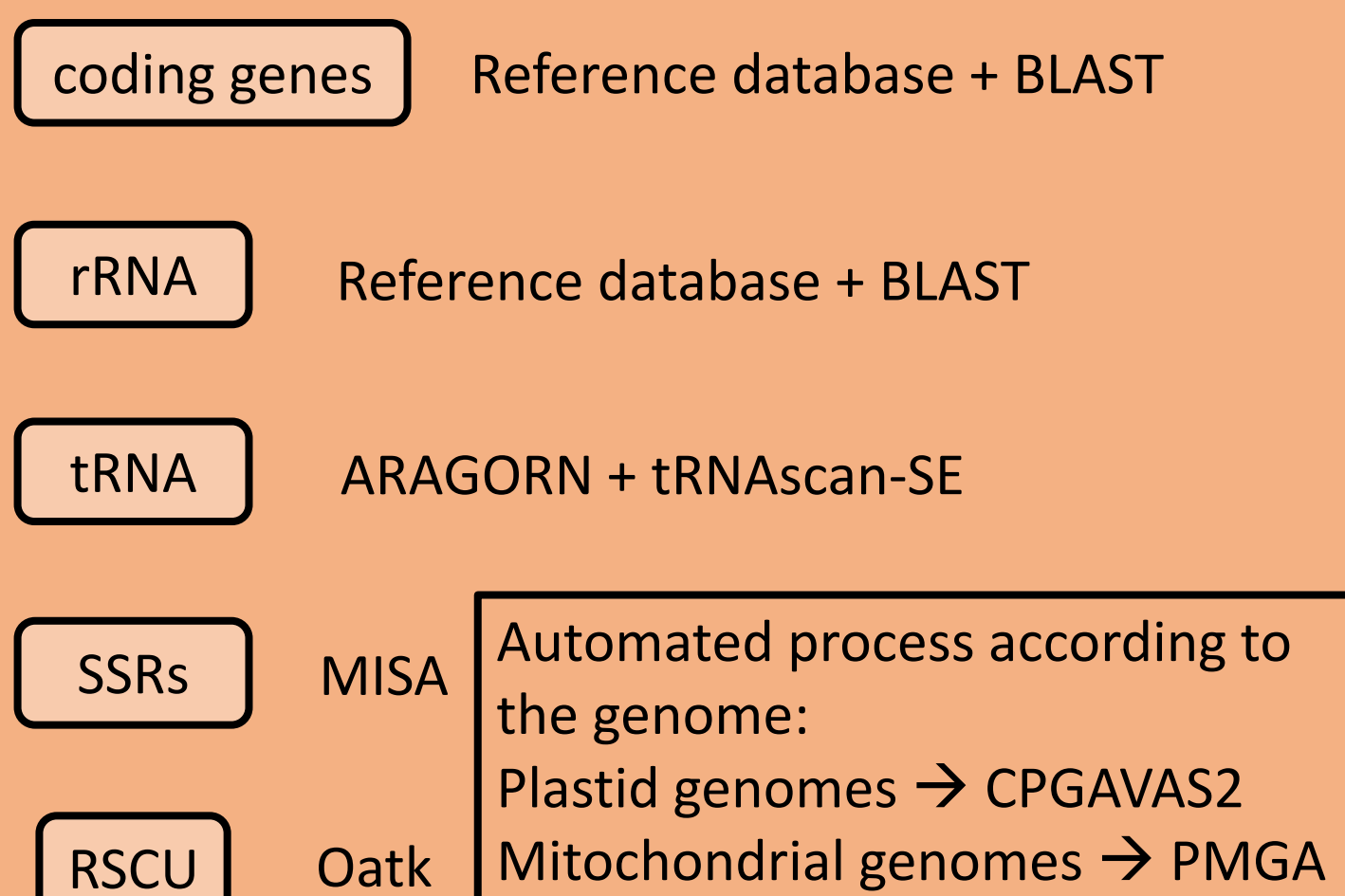
Extraction and sequencing



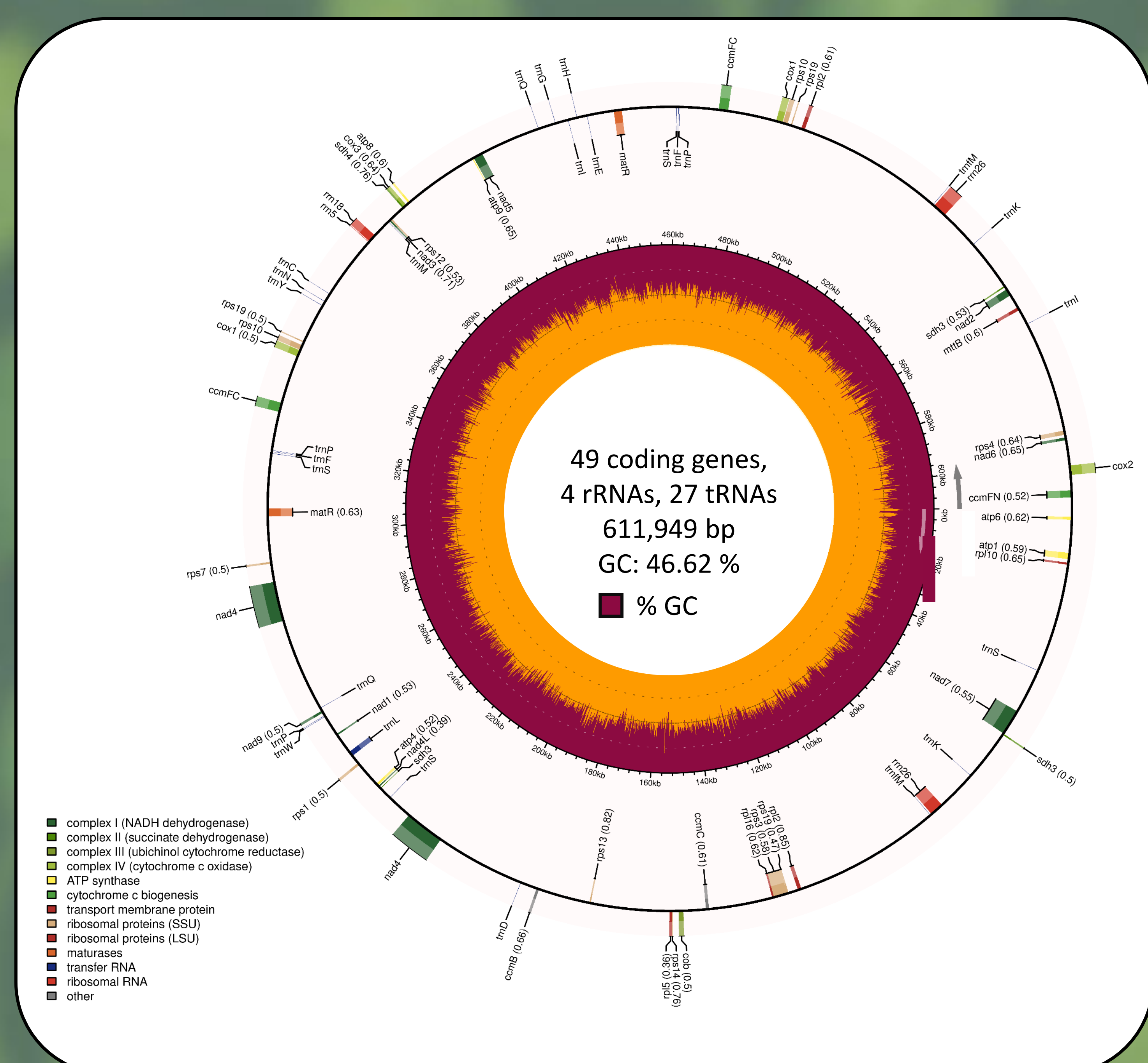
Raw data preprocessing and assembly



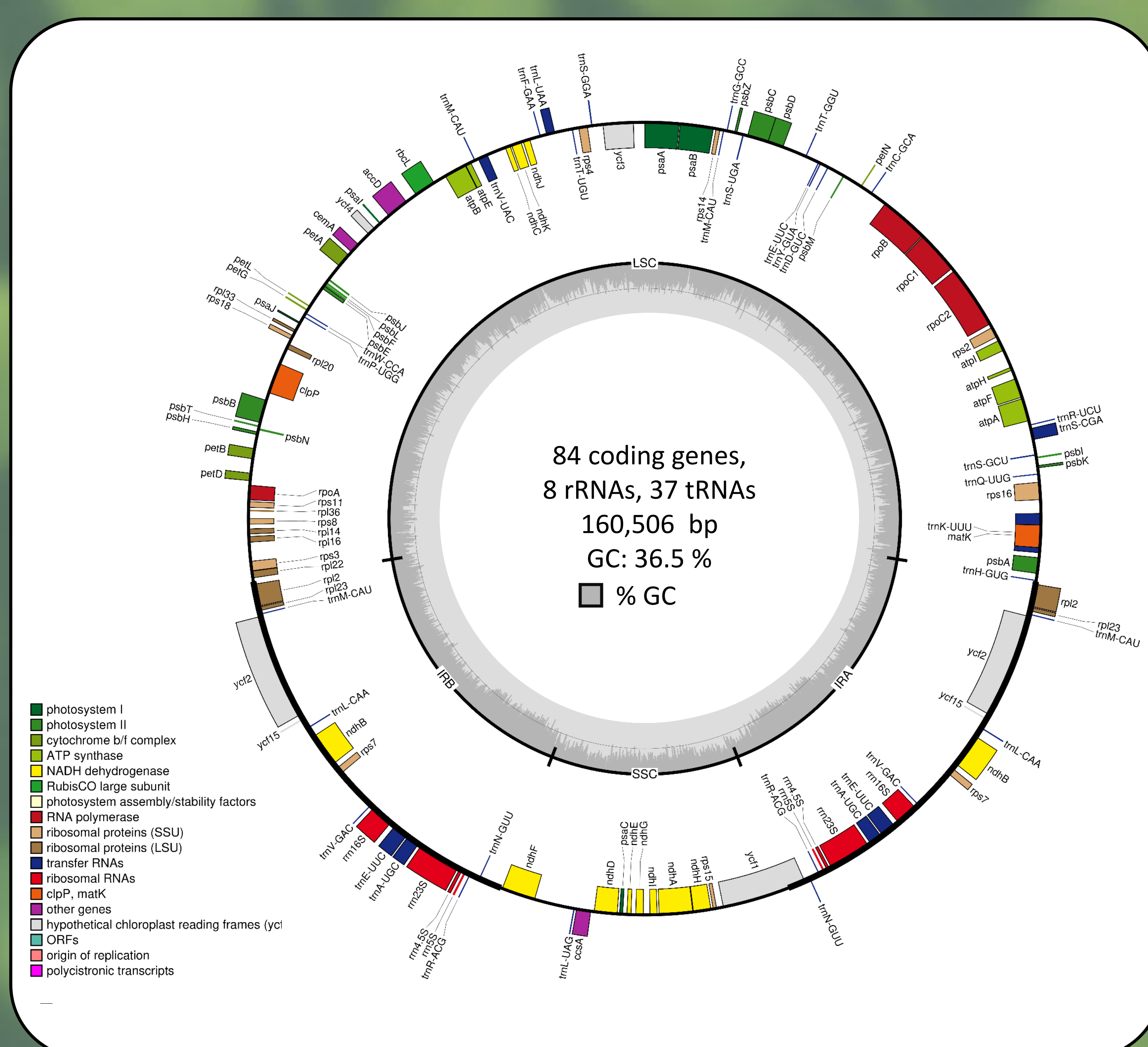
Functional analysis and annotation



Mitochondrial genome



Chloroplast genome



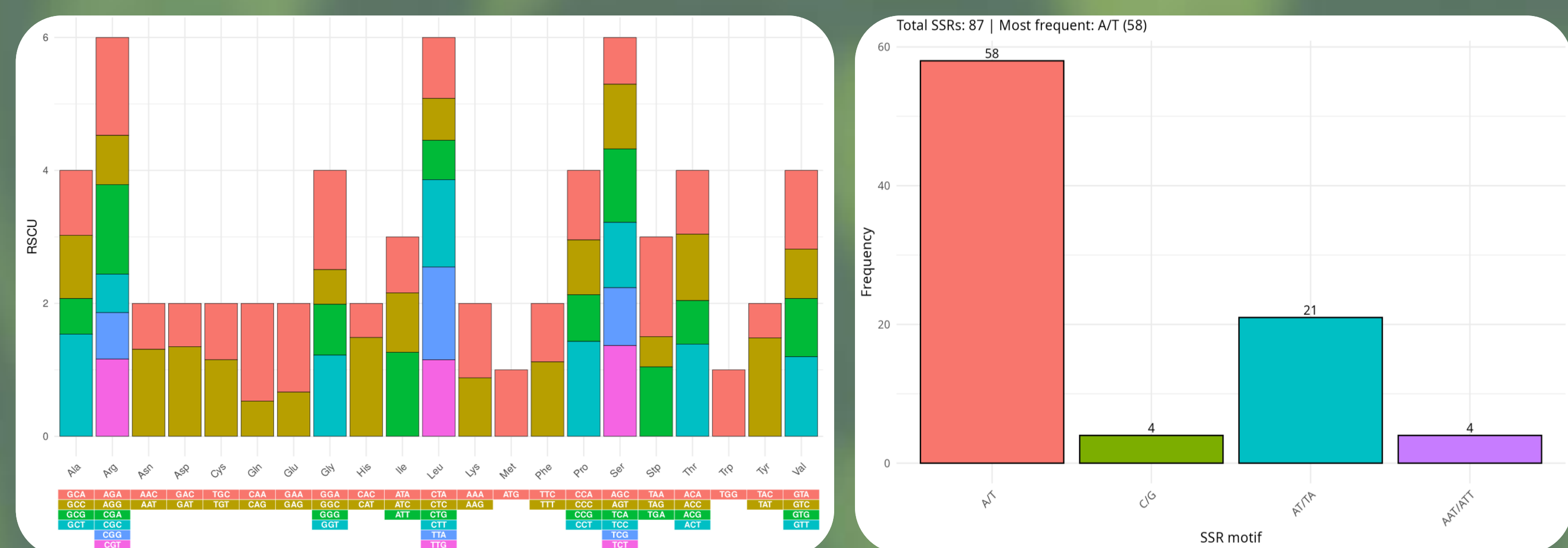
Gene profile and organization

| 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> |
| | 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 | |

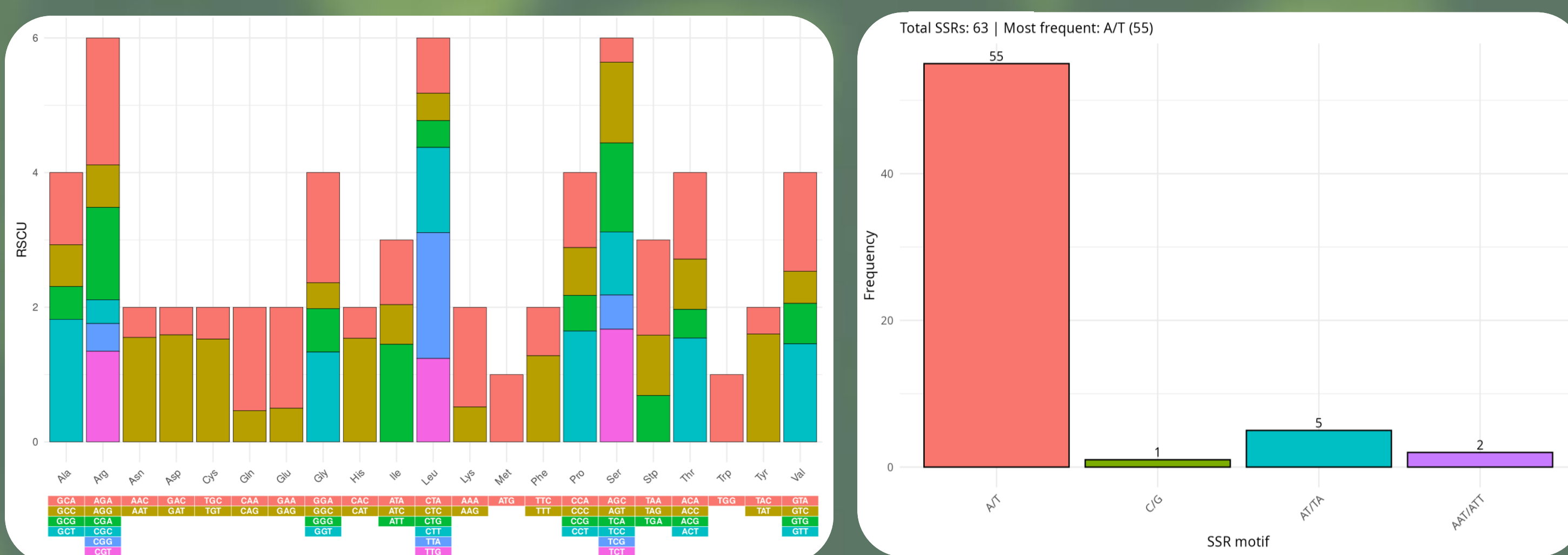
Gene profile and organization

| Category of genes | Group of genes | Name of genes |
|--------------------------|------------------------------------|--|
| Genes for photosynthesis | Subunits of ATP synthase | <i>atpA, atpB, atpE, atpF, atpH, atpI, atpJ, atpK, atpL, atpM, atpN, atpO, atpP, atpQ, atpR, atpS, atpT, atpU, atpV, atpW, atpX, atpY, atpZ</i> |
| | Subunits of photosystem II | <i>psbA, psbB, psbC, psbD, psbE, psbF, psbI, psbJ, psbK, psbL, psbM, psbN, psbO, psbP, psbQ, psbR, psbS, psbT, psbU, psbV, psbW, psbX, psbY, psbZ</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, petN, petP, petQ, petR, petS, petT, petU, petV, petW, petX, petY, petZ</i> |
| | Subunits of photosystem I | <i>psaA, psaB, psaC, psaD, psaE, psaF, psaG, psaH, psaI, psaJ, psaK, psaL, psaM, psaN, psaO, psaP, psaQ, psaR, psaS, psaT, psaU, psaV, psaW, psaX, psaY, psaZ</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), 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> |
| 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



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Acknowledgements

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