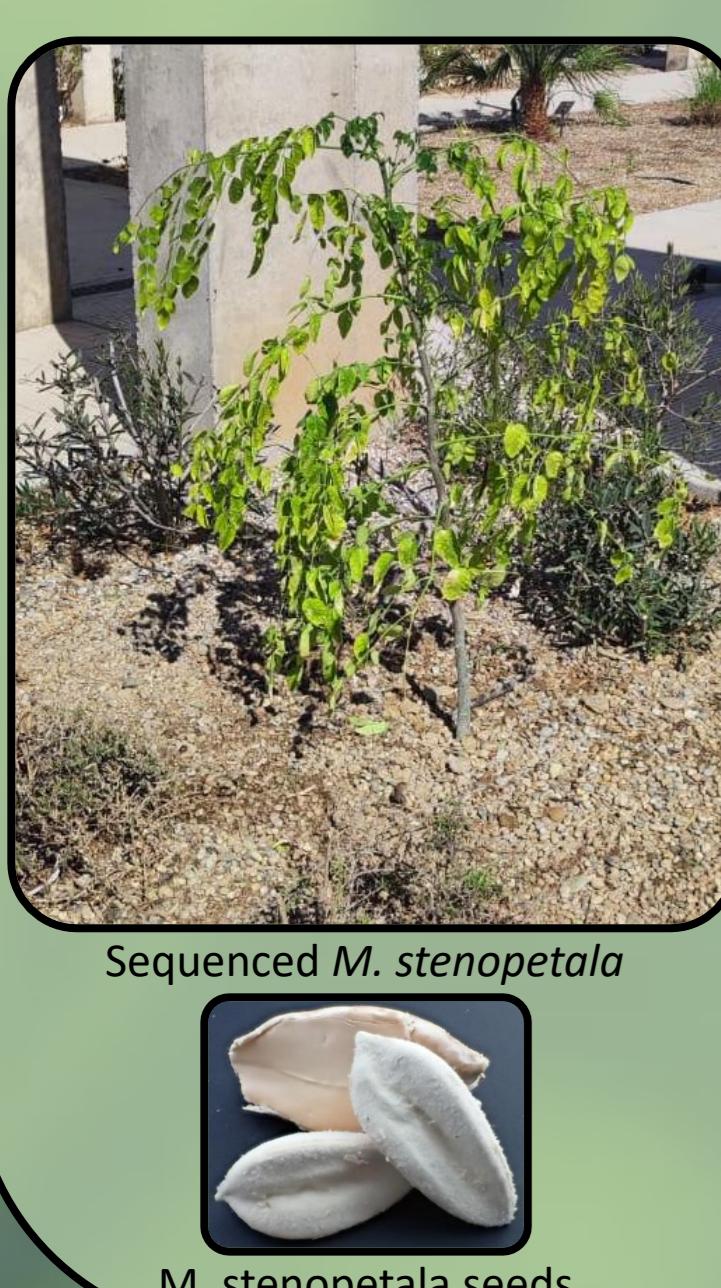


CHARACTERISATION OF MORINGA STENOPETALA ORGANELLAR GENOMES

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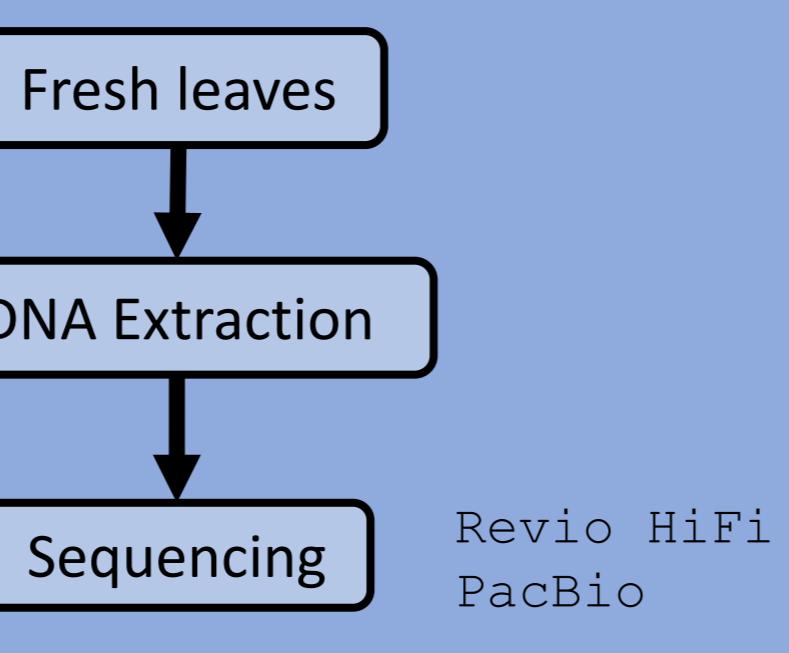
Introduction



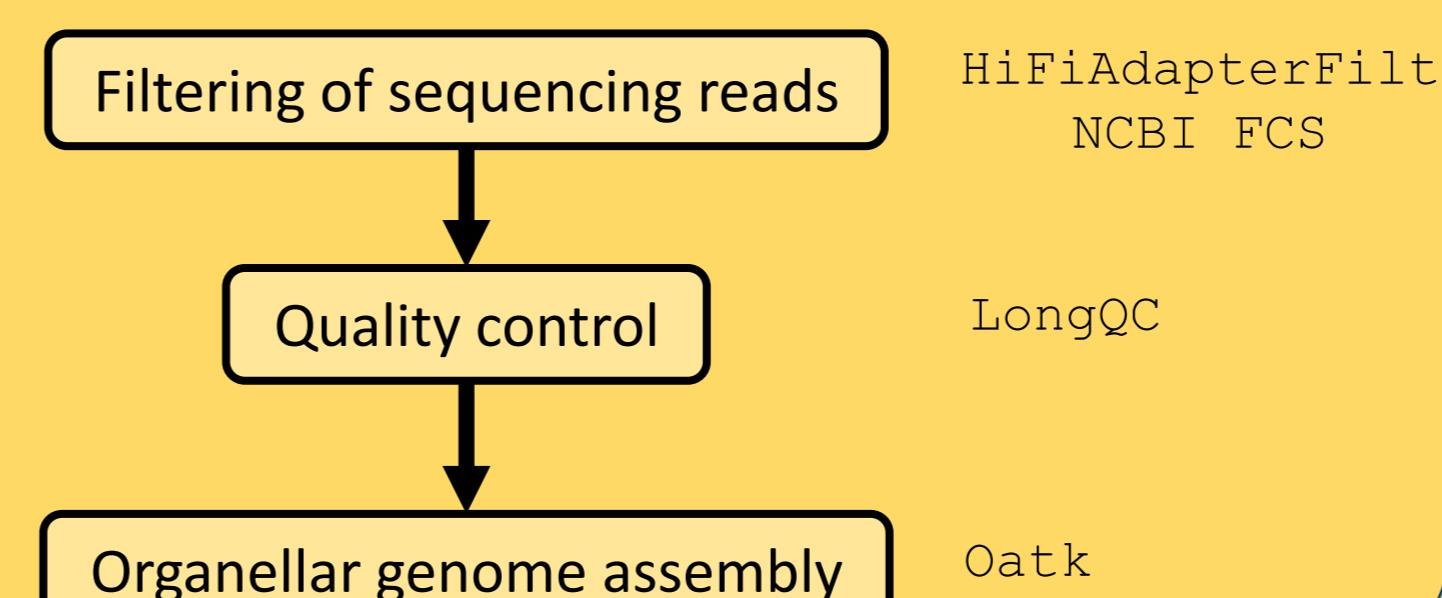
The monogeneric family *Moringaceae* comprises 13 species that are widely used for food, fodder, medicine, and various industrial applications. One notable species is *Moringa stenopetala*, which is native to southern Ethiopia and northern Kenya. It has a high nutritional value, making it a key crop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

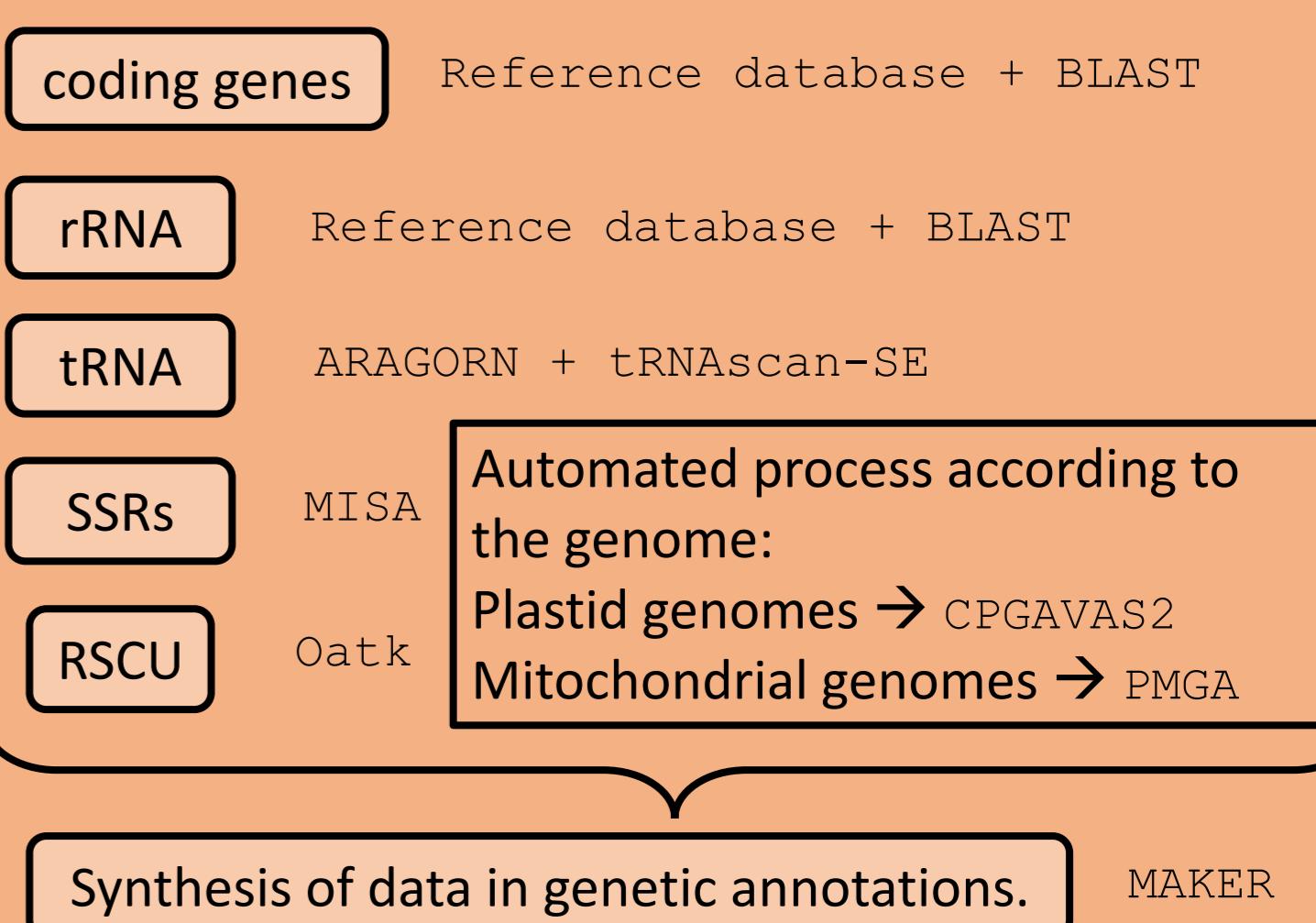
Extraction and sequencing



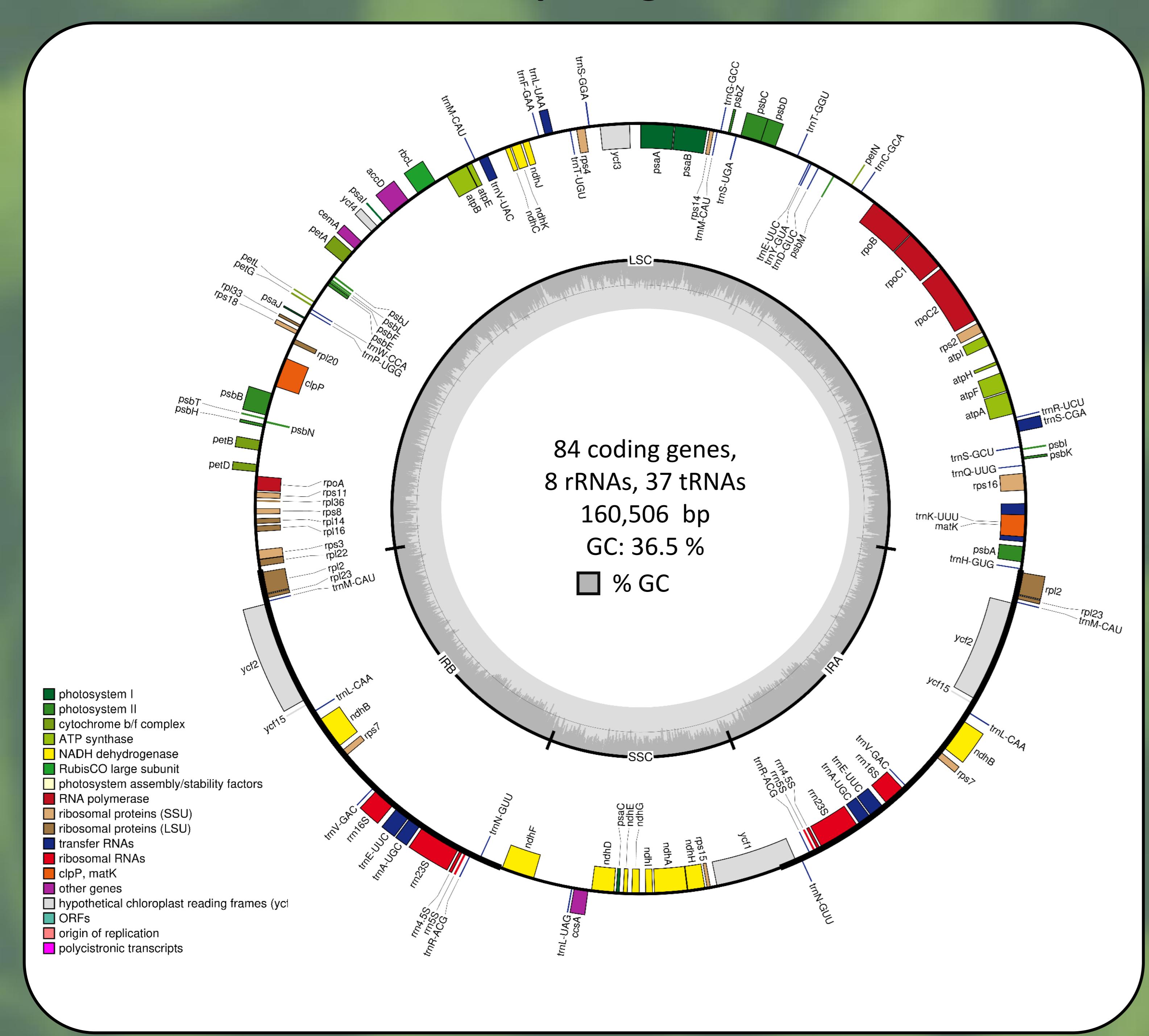
Raw data preprocessing and assembly



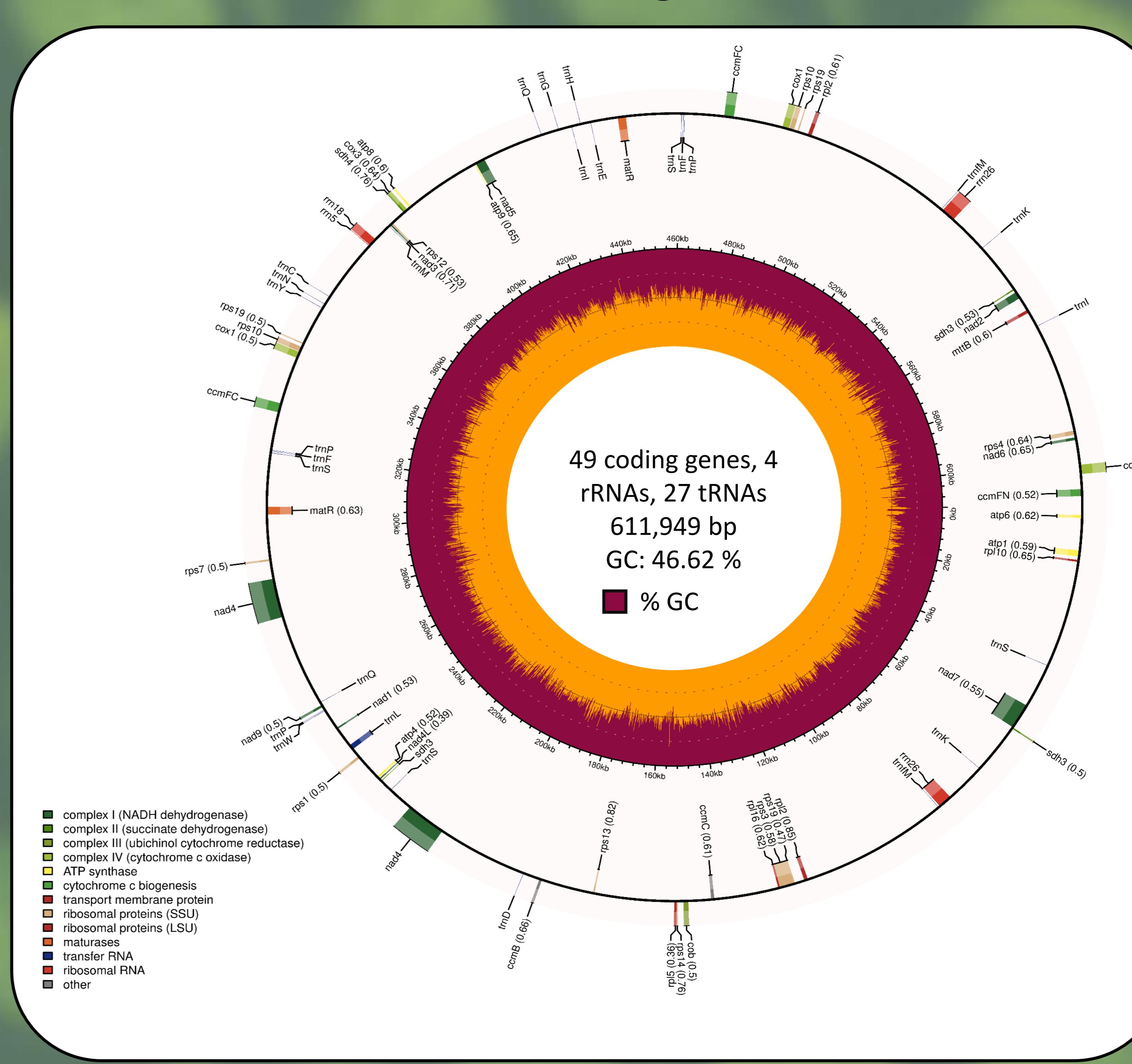
Functional analysis and annotation



Chloroplast genome



Mitochondrial genome

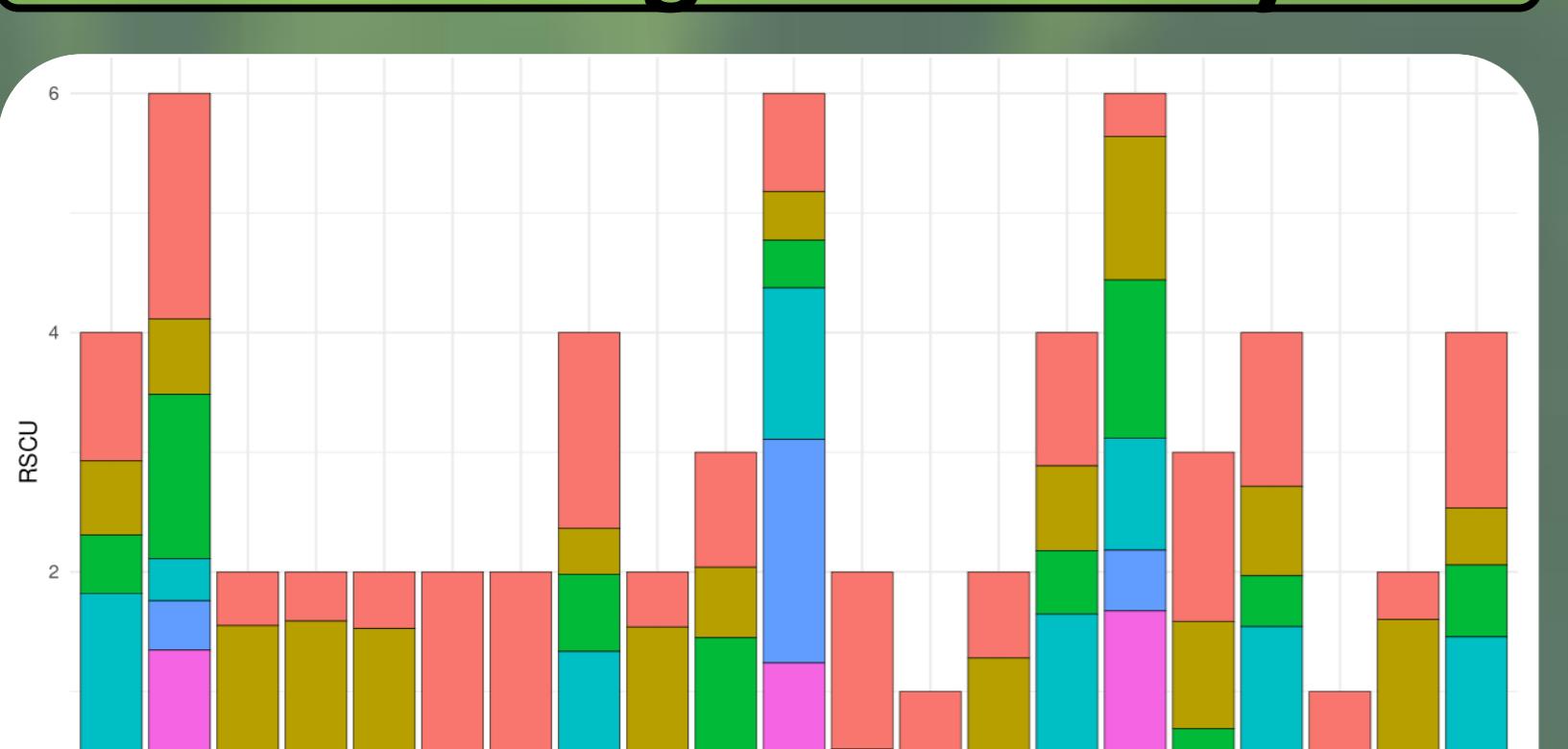


Annotation

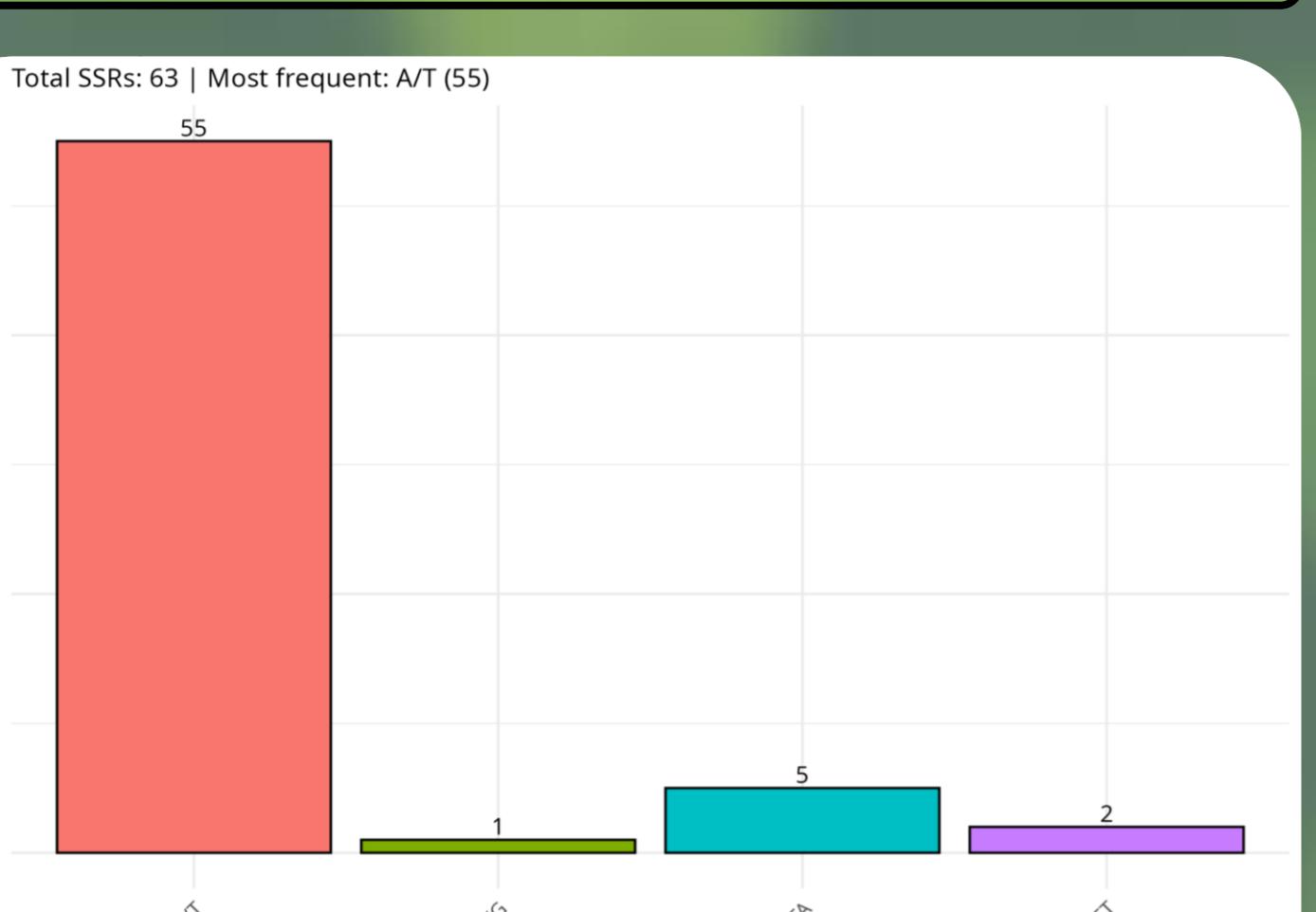
Category of genes	Group of genes	Name of genes
Genes for photosynthesis	Subunits of ATP synthase	atpA, atpB, atpE, atpH, atpI
	Subunits of photosystem II	psbA, psbB, psbC, psbD, psbE, psbF, psbI, psbK, psbM, psbN, psbT, psbZ, ycf3
	Subunits of NADH-dehydrogenase	ndhA, ndhB (x2), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK
	Subunits of cytochrome b/f complex	petA, petB, petD, petG, petI, petN
	Subunits of photosystem I	psaA, psaB, psaC, psaI, psaJ
	Subunit of rubisco	rbcL
Self replication	Large subunit of ribosome	rpl14, rpl16, rpl2(x2), rpl20, rpl22, rpl23(x2), rpl32, rpl33, rpl36
	DNA dependent RNA polymerase	rpoA, rpoB, rpoC1, rpoC2
	Transfer RNAs	trnK-UUU, trnQ-UUG, trnS-GCU, trnS-CGA, trnR-UCU, trnC-GCA, trnD-GUC, trnY-GUA, trnT-GGU, trnS-GUA, trnG-GCC, trnS-GGA, trnU-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
	Small subunit of ribosome	rps11, rps12 (x2), rps14, rps15, rps16, rps18, rps2, rps3, rps4, rps7 (x2), rps8
rRNA genes	Ribosomal RNA	rrn16 (x2), rrn23 (x2), rrn5 (x2), rrn4.5 (x2)
Other genes	Subunit of Acetyl-CoA-carboxylase	accD
	c-type cytochrome synthesis gene	ccsA
	Envelop membrane protein	cemA
	Protease	clpP
	Maturase	matK
Unknown	Conserved open reading frames	ycf1 (x2), ycf15 (x2), ycf2 (x2), ycf4

Category of genes	Group of genes	Name of genes
Core genes	Complex I (NADH dehydrogenase)	nad1, nad2, nad3, nad4 (x2), nad4L, nad5, nad6, nad7, nad9
	Complex II (succinate dehydrogenase)	sdh3 (x3), sdh4
	Complex III (ubiquinol cytochrome c reductase)	cox1, cox12, cox2, cox3
	Complex IV (cytochrome c oxidase)	atp1, atp4, atp6, atp8, atp9
	Complex V (ATP synthase)	ccmB, ccmC, ccmFC (x2), ccmFN
	Cytochrome c biogenesis	matR (x2)
	Maturases	mttB
Variable genes	Large subunit of ribosome	rpl10, rpl16, rpl2 (x2), rpl5
	Small subunit of ribosome	rps1, rps10 (x2), rps12, rps13, rps14, rps19 (x3), rps3, rps4, rps7
rRNA genes	Ribosomal RNA	rnr18, rnr26 (x2), rnr5
tRNAs	Transfer RNA	trnL-CAA, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA (x2), trnG-GCC, trnH-GUG, trnK-UUU (x2), trnM-CAU (x2), trnL-CAU (x2), trnN-GUU, trnP-UGG (x3), trnQ-UUG (x2), trnS-GCU, trnS-GGA, trnW-CCA, trnY-GUA

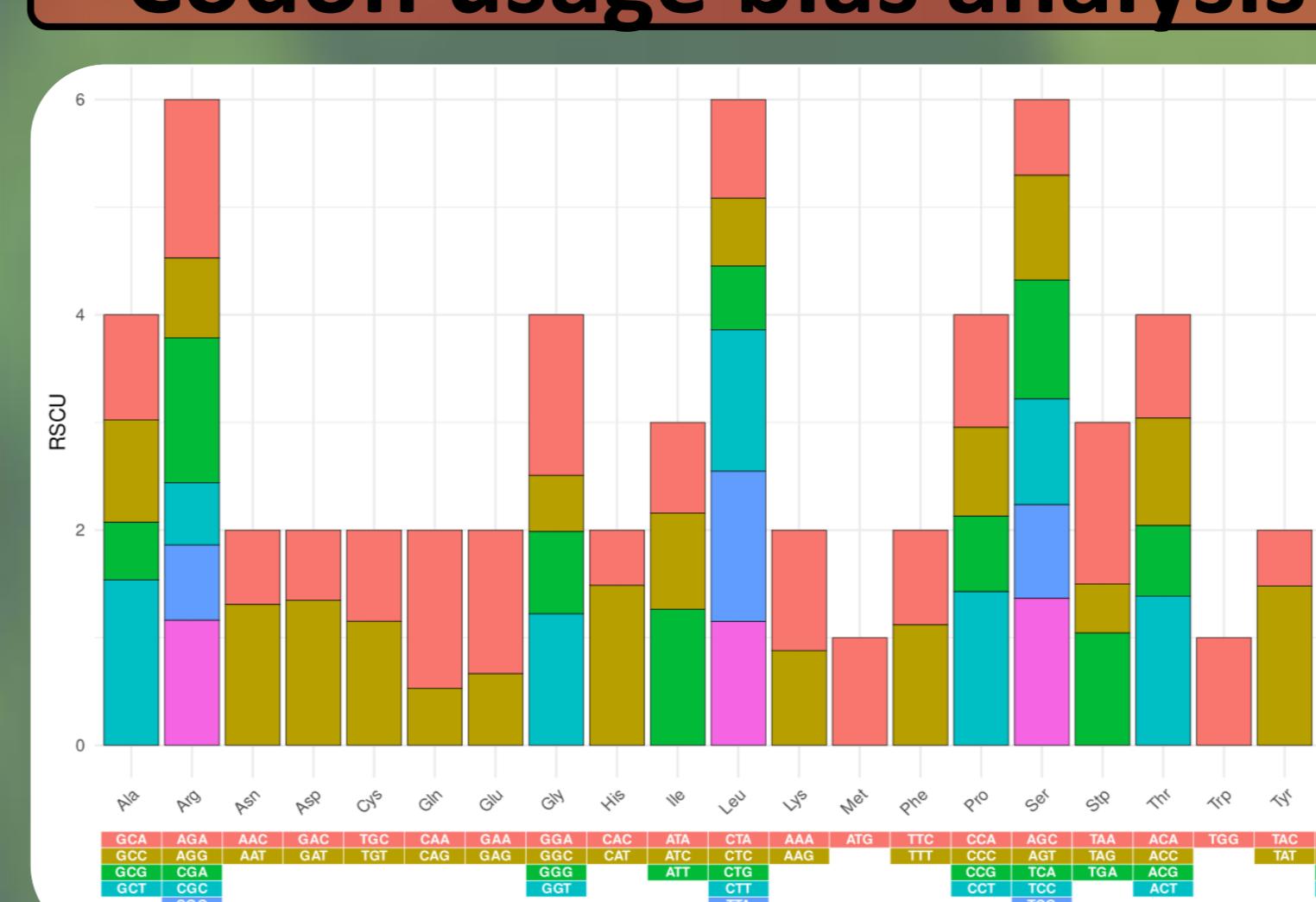
Codon usage bias analysis



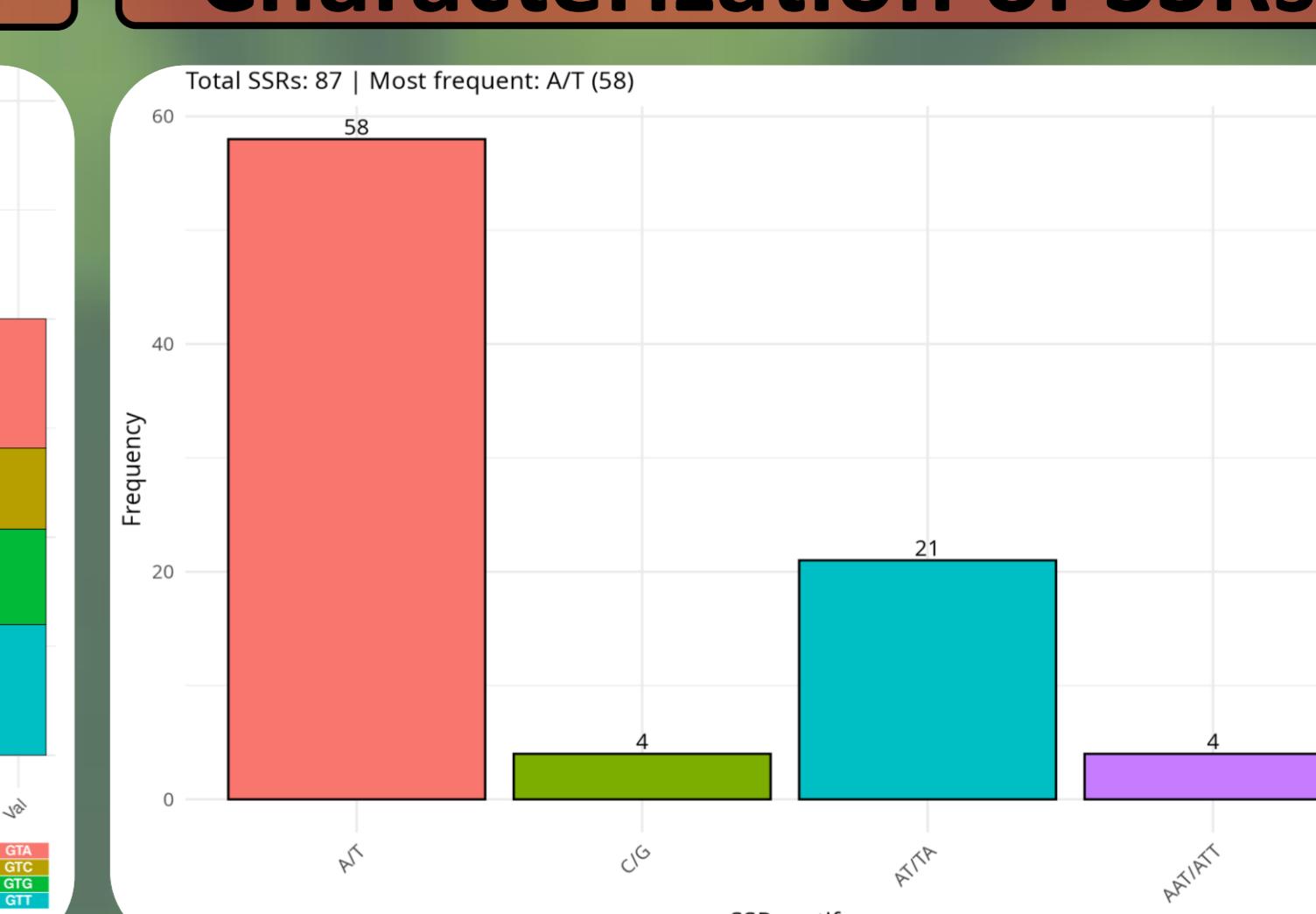
Characterization of SSRs



Codon usage bias analysis



Characterization of SSRs



Conclusions

These genomic resources provide valuable tools for future breeding programs of this orphan crop, enabling the development of varieties with improved stress tolerance and productivity. They also offer a foundation for comparative studies within *Moringaceae*, enhancing our understanding of adaptive evolution. Altogether, these resources will support the expansion of *M. stenopetala* cultivation to dryland regions increasingly affected by desertification and climate change, including Almería in southeastern Spain.

Acknowledgements

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