Supplementary materials

Cultivated tomato (*Solanum lycopersicum* L.) suffered a severe cytoplasmic bottleneck during domestication: implications from chloroplast genomes

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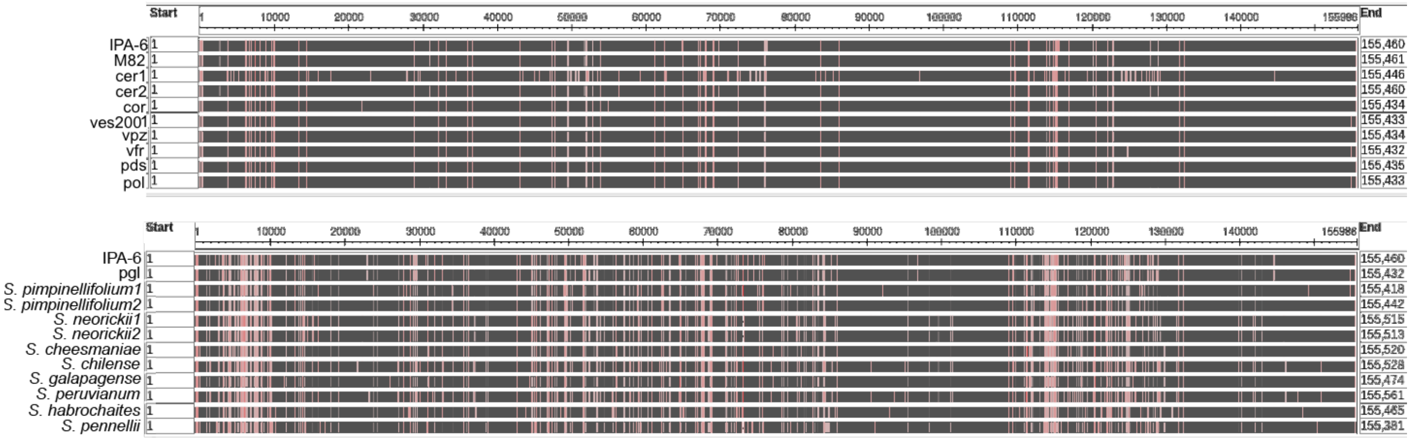


Figure S1. Overview of the nucleotide variability in nine plastomes sequenced in this study and in eleven species available in GenBank. The accession number AM087200 (cv. IPA-6) was used as reference. Red lines represent variable regions.

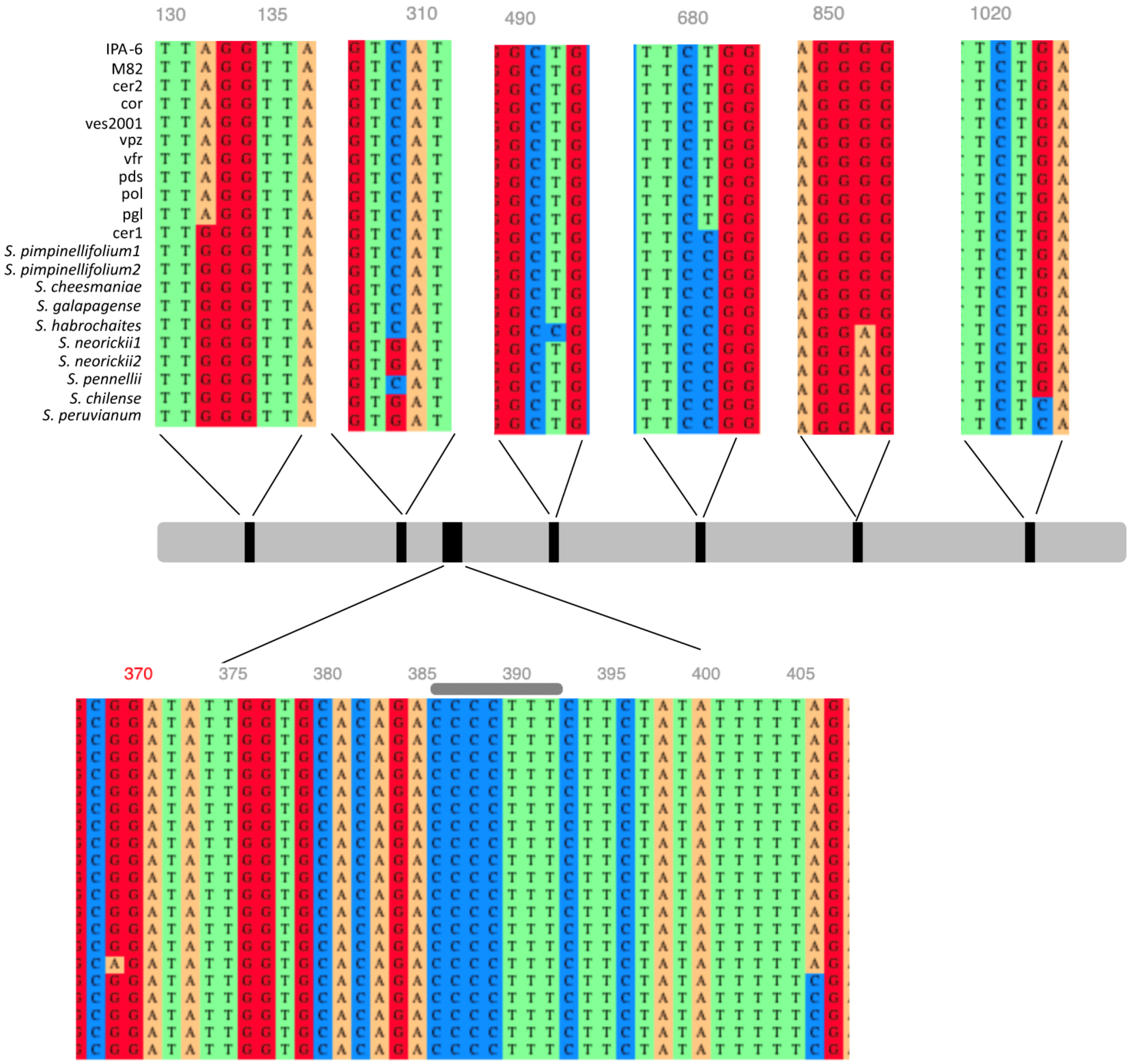
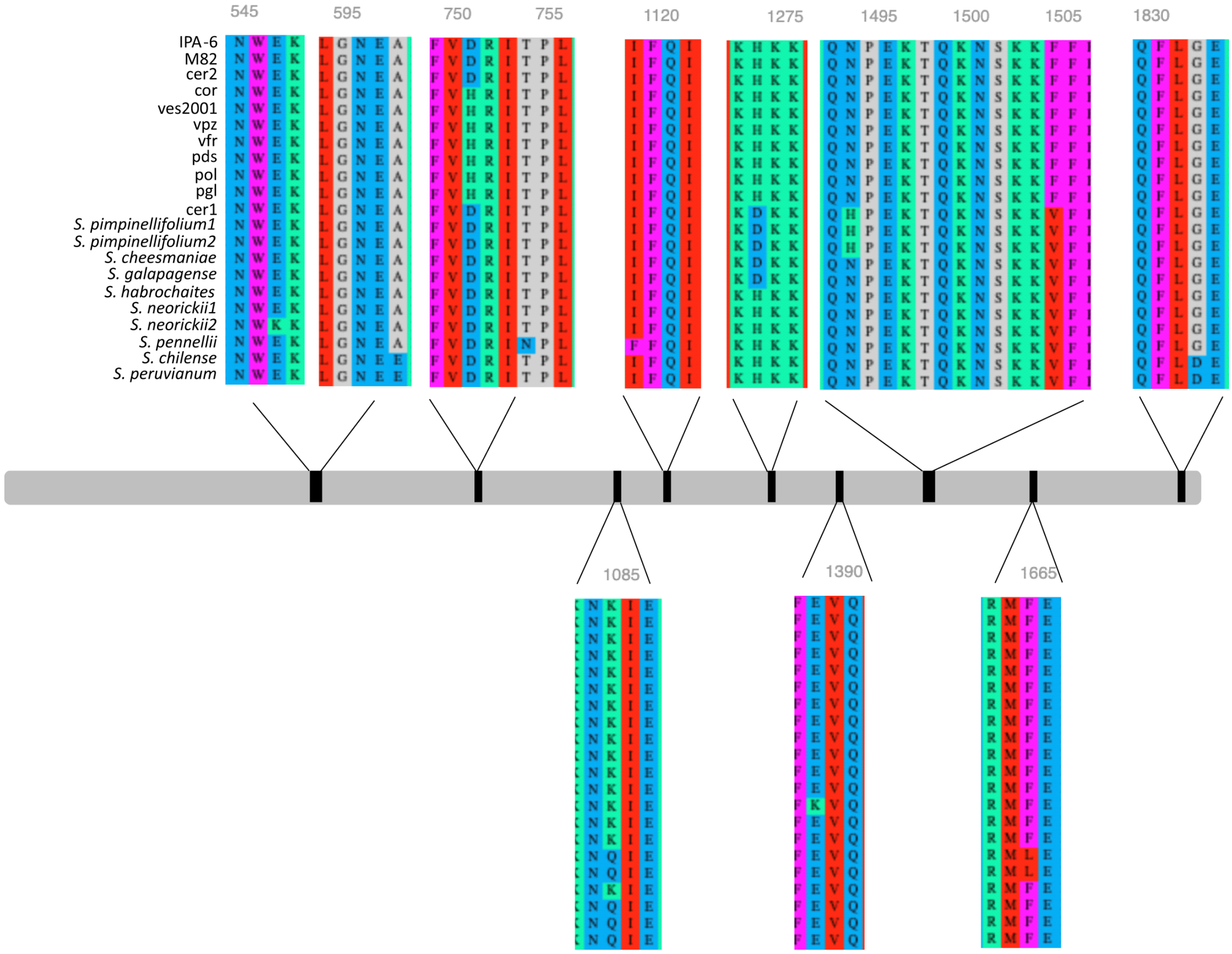


Figure S2. Schematic representation of the nucleotide variability observed in the *ndhH* gene for the plastomes under investigation. Grey bar represents the nucleotide multiple-sequence alignment (MSA) and it is scaled according to the MSA length. Black boxes indicate variable regions in the MSA. Above and below each box, a snapshot of the MSA along with alignment positions is reported.



	545	595	750 755	1120	1275	1495 1500 1505	1830	1085	1390	1665
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M82	NWEK	LGNEA	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
cer2	NWEK	LGNEA	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
cor	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
ves2001	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
vpz	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
vfr	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
pds	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
pol	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
pgl	NWEK	LGNEA	FVHRITPL	IFQI	KHKK	QNPEKTQKNSKKFFI	QFLGE	NKIE	FEVQ	RMFE
cer1	NWEK	LGNEA	FVDRITPL	IFQI	KDKK	QHPEKTQKNSKKVFI	QFLGE	NKIE	FEVQ	RMFE
S. pimpinellifolium1	NWEK	LGNEA	FVDRITPL	IFQI	KDKK	QHPEKTQKNSKKVFI	QFLGE	NKIE	FEVQ	RMFE
S. pimpinellifolium2	NWEK	LGNEA	FVDRITPL	IFQI	KDKK	QHPEKTQKNSKKVFI	QFLGE	NKIE	FKVQ	RMFE
S. cheesmaniae	NWEK	LGNEA	FVDRITPL	IFQI	KDKK	QNPEKTQKNSKKVFI	QFLGE	NKIE	FEVQ	RMFE
S. galapagense	NWEK	LGNEA	FVDRITPL	IFQI	KDKK	QNPEKTQKNSKKVFI	QFLGE	NKIE	FEVQ	RMFE
S. habrochaites	NWEK	LGNEA	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKVFI	QFLGE	NQIE	FEVQ	RMLE
S. neorickii1	NWEK	LGNEA	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKVFI	QFLGE	NQIE	FEVQ	RMLE
S. neorickii2	NWKK	LGNEA	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKVFI	QFLGE	NKIE	FEVQ	RMFE
S. pennellii	NWEK	LGNEA	FVDRINPL	FFQI	KHKK	QNPEKTQKNSKKVFI	QFLGE	NQIE	FEVQ	RMFE
S. chilense	NWEK	LGNEE	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKVFI	QFLDE	NQIE	FEVQ	RMFE
S. peruvianum	NWEK	LGNEE	FVDRITPL	IFQI	KHKK	QNPEKTQKNSKKVFI	QFLDE	NQIE	FEVQ	RMFE

Figure S3. Schematic representation of the amino acid variability observed in the Ycf1 protein for the plastomes under investigation. Grey bar represents the amino acid multiple-sequence alignment (MSA) and it is scaled according to the MSA length. Black boxes indicate variable regions in the MSA. Above and below each box, a snapshot of the MSA along with alignment positions is reported.

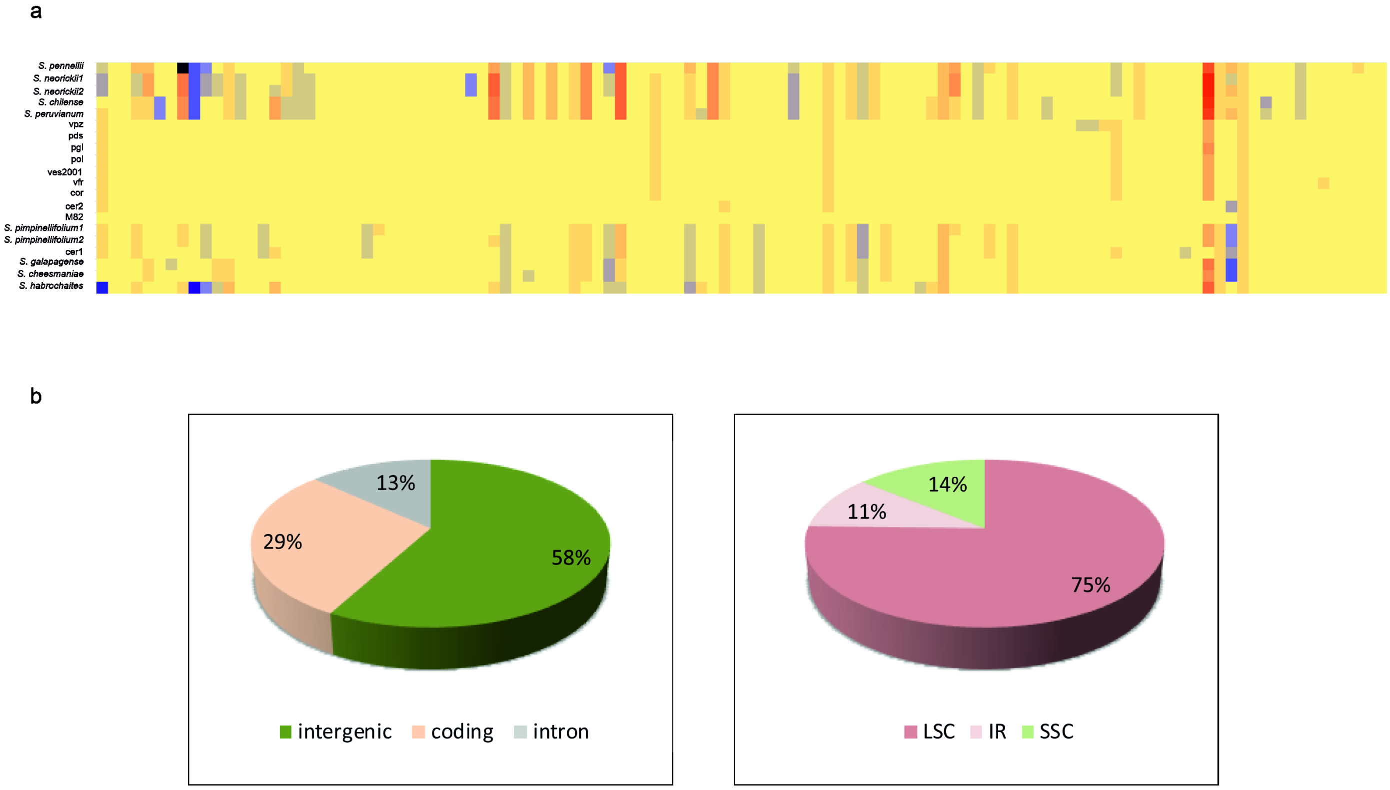
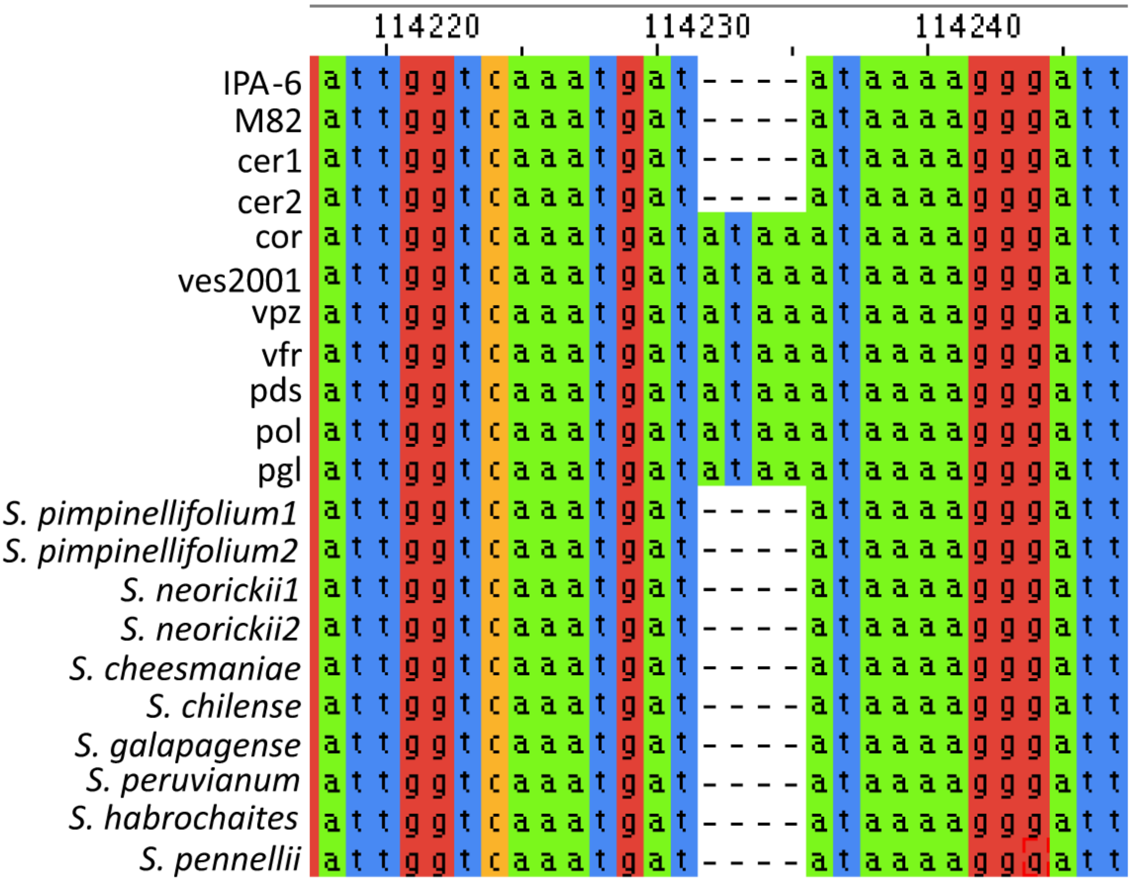


Figure S4. Simple sequence repeats (SSRs) in nine plastomes sequenced in this study and in eleven species available in GenBank. The plastome of IPA-6 (AM087200) was used as reference a) Heatmap representing differences in SSR size; colours range from red (SSR size larger than the reference) through yellow to blue (SSR size smaller than the reference). Black is for missing SSRs. b) Pie chart describing the percentage of SSRs located in coding sequences of genes, introns and intergenic regions as well as in the large single copy (LSC), small single copy (SSC) and inverted repeat b (IR) regions.



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IPA-6                  attggtcaaatgat----ataaaagggatt
M82                    attggtcaaatgat----ataaaagggatt
cer1                   attggtcaaatgat----ataaaagggatt
cer2                   attggtcaaatgat----ataaaagggatt
cor                    attggtcaaatgatataaataaaagggatt
ves2001                attggtcaaatgatataaataaaagggatt
vpz                    attggtcaaatgatataaataaaagggatt
vfr                    attggtcaaatgatataaataaaagggatt
pds                    attggtcaaatgatataaataaaagggatt
pol                    attggtcaaatgatataaataaaagggatt
pgl                    attggtcaaatgatataaataaaagggatt
S. pimpinellifolium1   attggtcaaatgat----ataaaagggatt
S. pimpinellifolium2   attggtcaaatgat----ataaaagggatt
S. neorickii1          attggtcaaatgat----ataaaagggatt
S. neorickii2          attggtcaaatgat----ataaaagggatt
S. cheesmaniae         attggtcaaatgat----ataaaagggatt
S. chilense            attggtcaaatgat----ataaaagggatt
S. galapagense         attggtcaaatgat----ataaaagggatt
S. peruvianum          attggtcaaatgat----ataaaagggatt
S. habrochaites        attggtcaaatgat----ataaaagggatt
S. pennellii           attggtcaaatgat----ataaaagggatt
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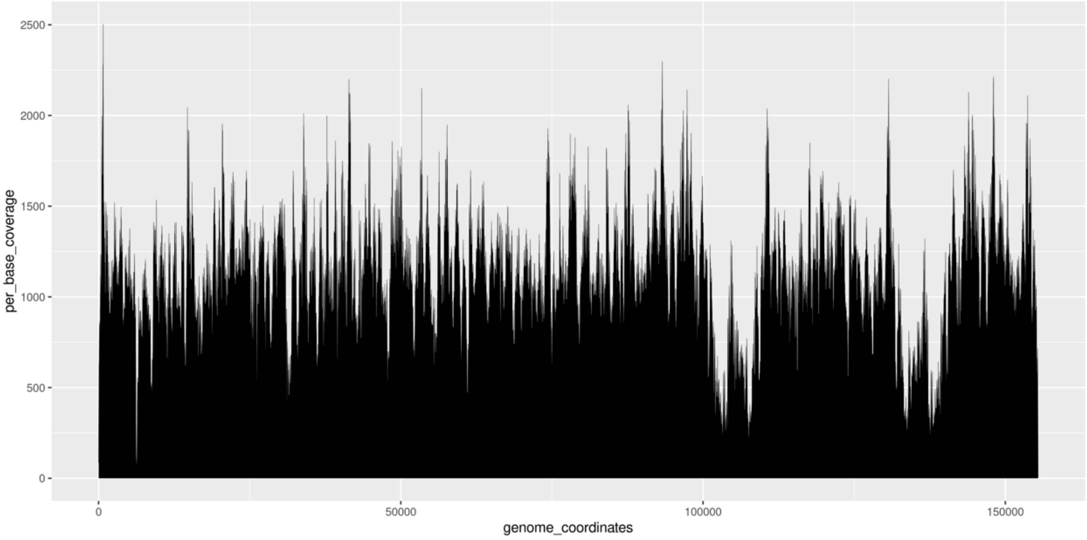
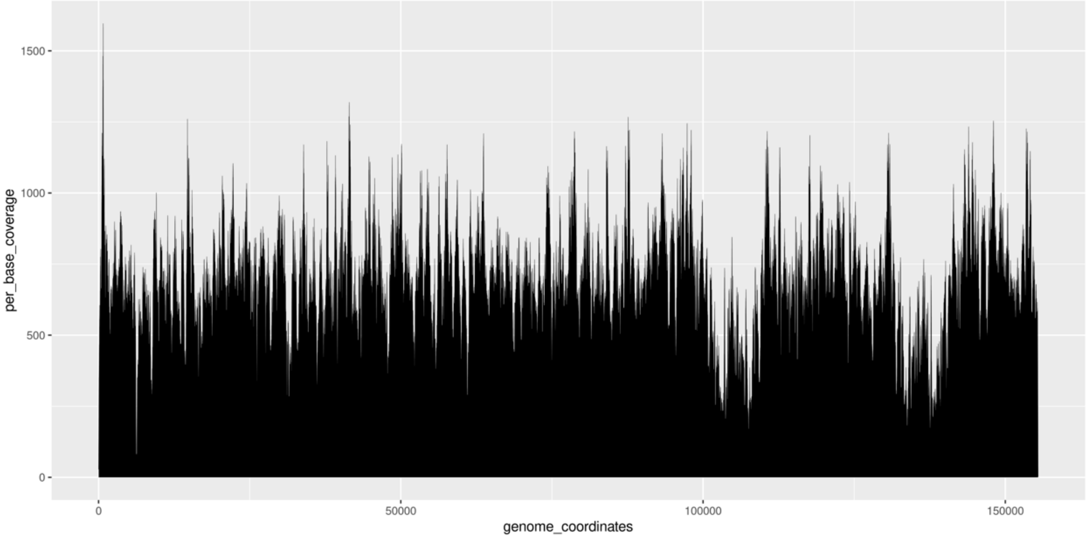
Figure S5. Multiple-sequence alignment (MSA) of the region harbouring the duplicated sequence $(ATAA)_2$ scored only in local landraces.

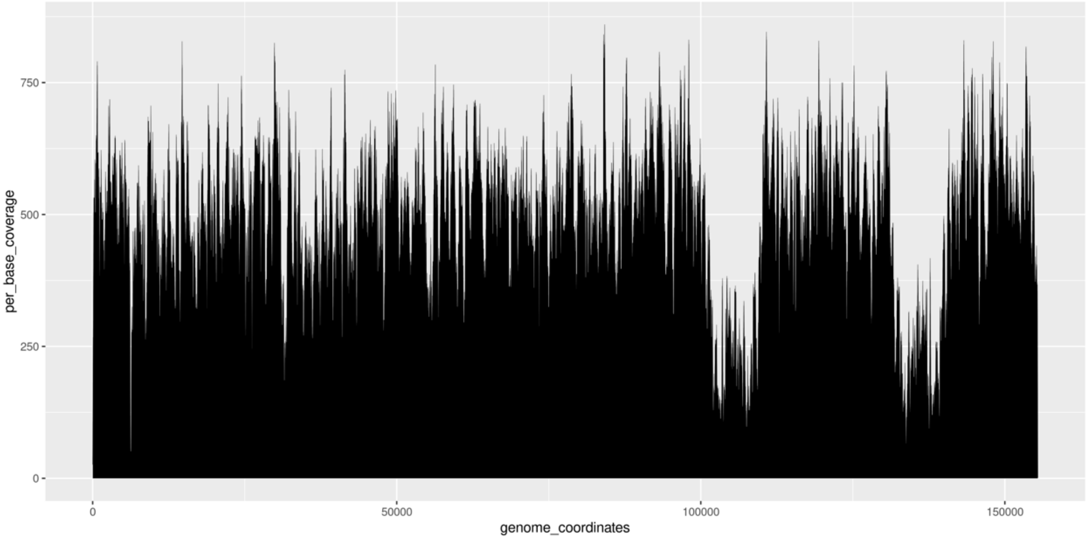
Corbarino (average read depth/nucleotide: 1072.84)



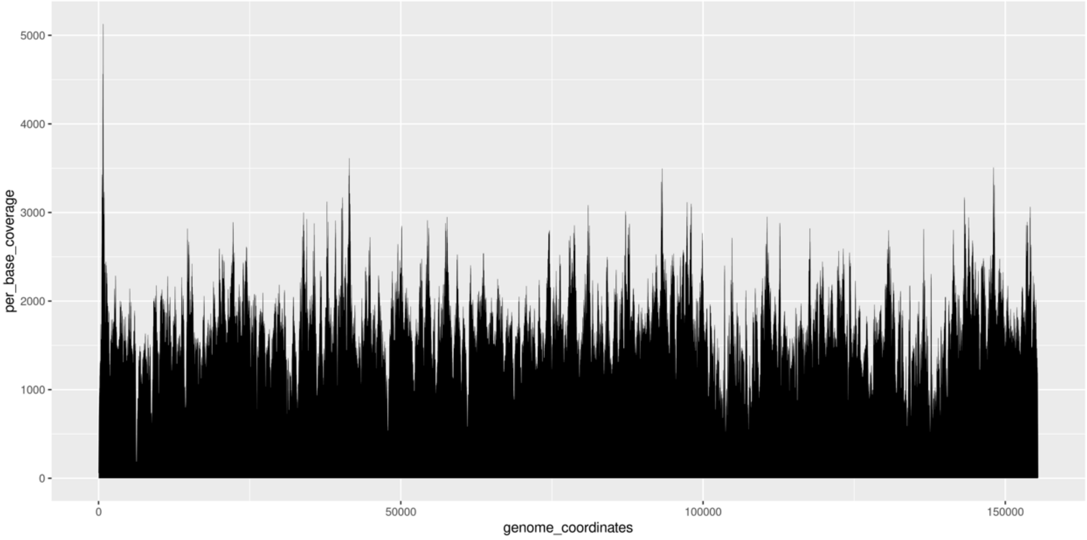
PDS (average read depth/nucleotide: 668.65)



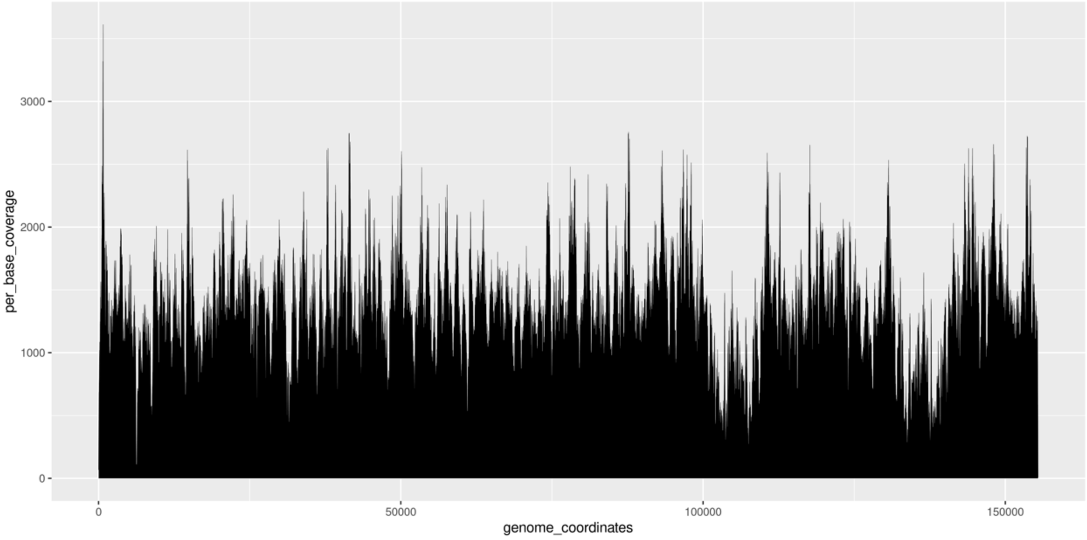
Piennolo giallo (average read depth/nucleotide: 476.94)



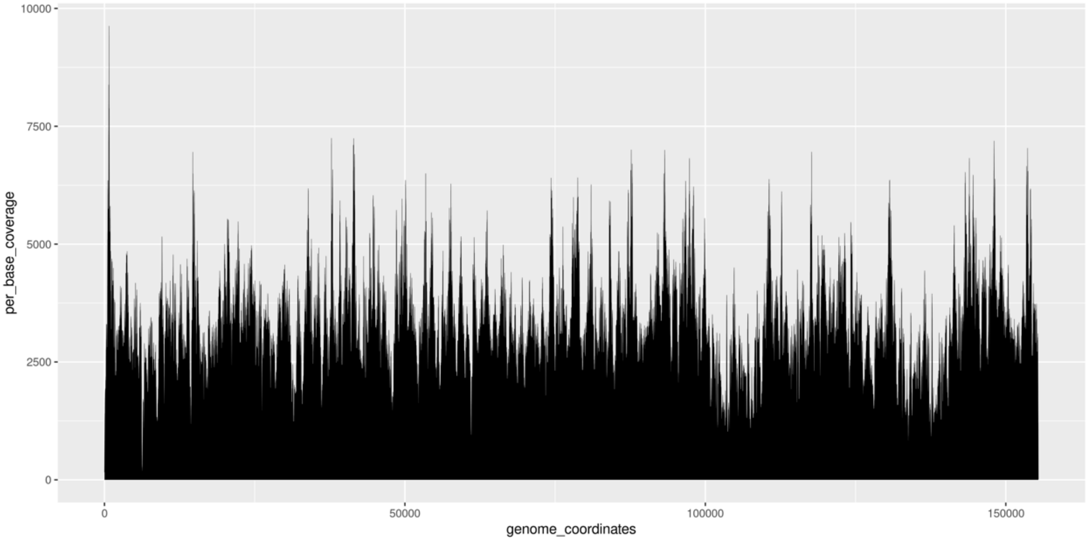
Pollena (average read depth/nucleotide: 1649.77)



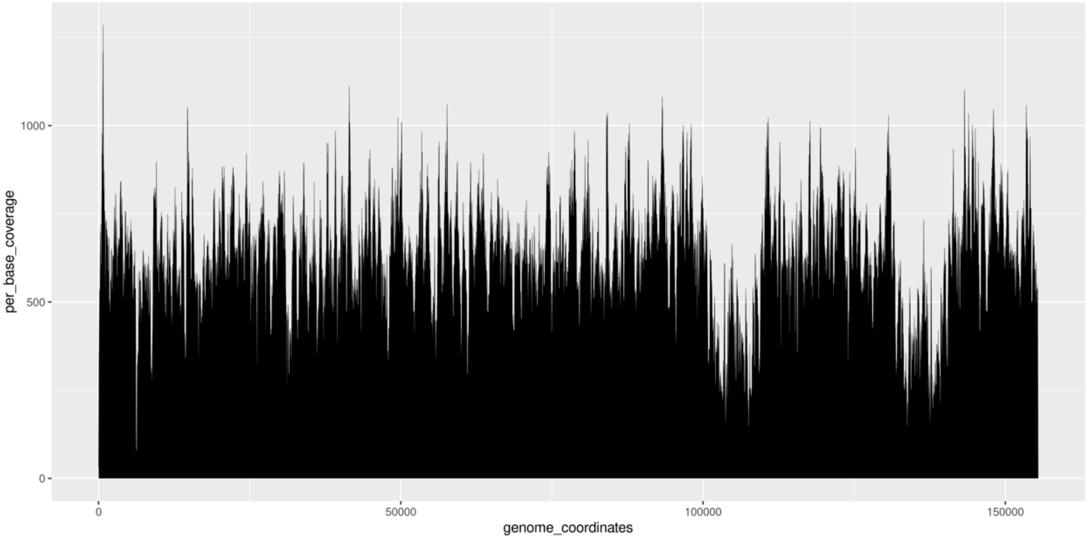
Vesuvio 2001 (average read depth/nucleotide: 1314.46



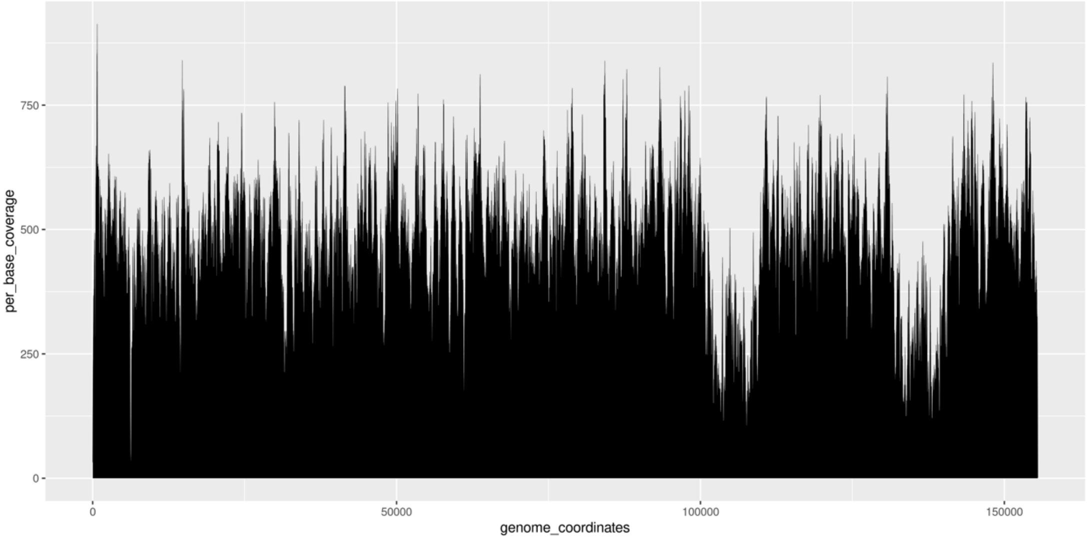
Vesuvio foglia riccia (average read depth/nucleotide: 3147.07)



Vesuviano pizzo (average read depth/nucleotide: 600.02)



S. neorickii 1 (average read depth/nucleotide: 456.53)



S. pimpinellifolium 1 (average read depth/nucleotide: 975.50)

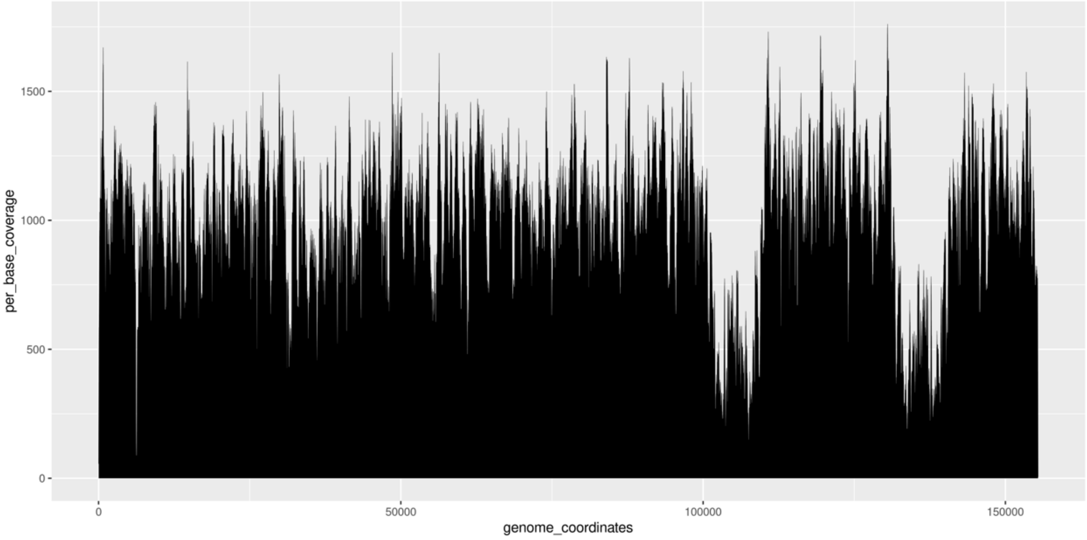


Figure S6. Distribution of *per*-base sequencing depth for each chloroplast genome sequenced in this work. The average coverage *per*-base is also reported.

Table S1. Tomato cpSSR primers developed in this study.

		LOCUS	Repeat	Sequence (5'-3')	Size (bp)	Fluorescent dye	Tm (°C)
LSC	intron	*tRNA-Lys (UUU)*	(T)12	GGTTATCAAATGATACATAGTGC GGAGATGTGTGTAGAAGAAACAG	222	HEX	55
LSC	intron	*tRNA-Gly (UCC)*	(T)13	CTAGAAGGATCATCTACAAAG CGTTAGCTTGGAAGGCTAGG	239	FAM	51
LSC	intergenic	*psbM - tRNA-Asp (GUC)*	(T)16	CGCCTTTCTAAGAGGAGTAGGA CCGATGCATGTAATGGAATCG	314	ATTO550	59
LSC	intergenic	*atpB -rbcL*	(A)13	CATAGATTCATAGAGGAATTCCA GCTTTAGTCTCTGTTTGTGG	389	FAM	55
LSC	intron	*clpP*	(T)17	CCAAACCGCGATGGTATTTTCTT CAATTGGATTGGTAAGATATCTATG	288	ATTO565	58
LSC	intergenic	*rpl14 – rpl16*	(A)10	TGAGCATATCGACGATTGCT CCAAAATGCCTATACGAACTC	262	HEX	55
SSC	intergenic	*ndhF – rpl32*	(A)16-(A)19	TCATTTCTACAGAACAGCCGAT TTCGAGCTAATAGTGTCCTCC	258-261	ATTO550	59
SSC	intergenic	*rpl32 - tRNA-Leu (UAG)*	(A)15	AGACCGCCATGTATATCTTGC CTGAGTCTTTCCTATATTTTCTG	292	ATTO565	58

Table S2. Simple Sequence Repeats (SSRs) in the twenty-one tomato chloroplast genomes using IPA-6 (AM087200) as reference genome. SSRs size, location and distribution among different regions, namely coding, intron, intergenic are reported. The *unit_size/min_repeats* parameters were as follows: 1/8, 2/6, 3/5, 4/5, 5/5, 6/5. SSRs located in IRa were not counted. SSRs were identified using MISA - MIcroSAtellite identification tool (http://pgrc.ipk-gatersleben.de/misa/).

		location	microsatellite	IPA-6	M82	cor	pds	pgl	pol	vpz	ves2001	vfr	cer1	cer2	*S. pimpinellifolium 1*	*S. pimpinellifolium 2*	*S. neorickii 1*	*S. neorickii 2*	*S. habrocaites*	*S. peruvianum*	*S. cheesmaniae*	*S. galapagense*	*S. pennellii*	*S. chilense*
LSC	intergenic	*tRNA-His(GUG) -psbA*	(A)n	13	13	12	12	12	12	12	12	12	12	12	12	12	15	15	18	12	13	13	14	13
LSC	coding	*matK*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	coding	*matK*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
LSC	intron	*tRNA-Lys (UUU)*	(T)n	12	12	12	12	12	12	12	12	12	11	12	11	11	13	13	11	11	12	12	10	11
LSC	intergenic	*tRNA-Lys (UUU) – rps16*	(A)n	11	11	11	11	11	11	11	11	11	11	11	11	11	8	8	11	10	10	10	9	10
LSC	intergenic	*tRNA-Lys (UUU) – rps16*	(AT)n	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	7	4	4	4	7
LSC	intergenic	*rps16 - tRNA-Gln (UUG)*	(T)n	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7
LSC	intergenic	*rps16 - tRNA-Gln (UUG)*	(T)n	16	16	16	16	16	16	16	16	16	16	16	15	15	11	11	15	12	16	16	-	12
LSC	intergenic	*rps16 - tRNA-Gln (UUG)*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	13	13	16	13	9	9	13	13
LSC	intergenic	*rps16 - tRNA-Gln (UUG)*	(A)n	11	11	11	11	11	11	11	11	11	12	11	12	12	13	13	14	11	11	11	14	11
LSC	intergenic	*psbK - psbI*	(T)n	11	11	11	11	11	11	11	11	11	11	11	11	11	12	12	12	11	10	10	11	11
LSC	intergenic	*psbI – tRNA-Ser (GCU)*	(A)n	11	11	11	11	11	11	11	11	11	11	11	11	11	10	10	9	10	10	10	10	10
LSC	intergenic	*tRNA-Ser (GCU) - tRNA-Gly (UCC)*	(T)n	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	7	8	7	7	7	8
LSC	intergenic	*tRNA-Ser (GCU) - tRNA-Gly (UCC)*	(A)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
LSC	intergenic	*tRNA-Ser (GCU) - tRNA-Gly (UCC)*	(A)n	8	8	8	8	8	8	8	8	8	9	8	9	9	8	8	8	8	8	8	8	8
LSC	intron	*tRNA-Gly (UCC)*	(T)n	13	13	13	13	13	13	13	13	13	12	13	13	13	13	14	11	10	13	13	13	10
LSC	intergenic	*tRNA-Gly (UCC) - tRNA-Arg (UCU)*	(T)n	12	12	12	12	12	12	12	12	12	12	12	12	12	11	11	12	13	12	12	11	13
LSC	intergenic	*tRNA-Gly (UCC) - tRNA-Arg (UCU)*	(A)n	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	7	8	7	7	8	8
LSC	intergenic	*tRNA-Arg (UCU) – atpA*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	10	10	9	10	9	9	9	10
LSC	intergenic	*atpA -atpF*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intron	*atpF*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
LSC	coding	*atpF*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*atpH – atpI*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*atpH – atpI*	(T)n	8	8	8	8	8	8	8	8	8	9	8	9	9	8	8	8	8	8	8	8	8
LSC	intergenic	*rps2 - rpoC2*	(A)n	11	11	11	11	11	11	11	11	11	11	11	10	11	11	11	11	11	11	11	11	11
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LSC	coding	*rpoC2*	(C)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	coding	*rpoC2*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
LSC	coding	*rpoC2*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	coding	*rpoC1*	(T)n	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
LSC	coding	*rpoC1*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	coding	*rpoB*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*tRNA-Cys (GCA) - petN*	(TA)n	3	3	3	3	3	3	3	3	3	3	3	3	3	6	6	3	3	3	3	3	3
LSC	intergenic	*petN – psbM*	(A)n	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
LSC	intergenic	*psbM - tRNA-Asp (GUC)*	(T)n	16	16	16	16	16	16	16	16	16	16	16	16	15	10	10	15	11	16	16	13	11
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LSC	intergenic	*psbC - tRNA-Ser (UGA)*	(T)n	12	12	12	12	12	12	12	12	12	12	12	12	12	10	10	12	10	13	12	10	10
LSC	intron	*ycf3*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intron	*ycf3*	(A)n	11	11	11	11	11	11	11	11	11	11	11	11	11	9	9	11	9	11	11	9	9
LSC	intergenic	*ycf3 - tRNA-Ser (GGA)*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*ycf3 - tRNA-Ser (GGA)*	(A)n	8	8	8	8	8	8	8	8	8	7	8	7	7	7	7	7	7	7	7	7	7
LSC	intergenic	*rps4 - tRNA-Thr (UGU)*	(T)n	10	10	10	10	10	10	10	10	10	9	10	9	9	6	6	10	6	9	9	6	6
LSC	intergenic	*rps4 - tRNA-Thr (UGU)*	(TA)n	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
LSC	intergenic	*rps4 - tRNA-Thr (UGU)*	(A)n	10	10	10	10	10	10	10	10	10	11	10	11	11	11	11	11	10	12	12	13	10
LSC	intergenic	*tRNA-Thr (UGU) - tRNA-Leu (UAA)*	(T)n	11	11	11	11	11	11	11	11	11	9	11	9	9	5	5	12	5	10	10	5	5
LSC	intergenic	*tRNA-Leu (UAA) - tRNA-Phe (GAA)*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	coding	*ndhC*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*ndhC – tRNA-Val (UAC)*	(T)n	10	10	9	9	9	9	9	9	9	10	10	10	10	9	9	10	9	10	10	10	9
LSC	intron	*tRNA-Val (UAC)*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intron	*tRNA-Val (UAC)*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*tRNA-Met (CAU) – atpE*	(T)n	12	12	12	12	12	12	12	12	12	13	12	13	13	11	11	14	11	13	13	10	11
LSC	coding	*atpB*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	9	11	10	10	10	10
LSC	intergenic	*atpB -rbcL*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	4	4	8	4	8	8	4	4
LSC	intergenic	*atpB -rbcL*	(A)n	13	13	13	13	13	13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12
LSC	intergenic	*rbcL – accD*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*accD – psaI*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*psaI - ycf4*	(T)n	10	10	10	10	10	10	10	10	10	11	10	11	11	10	10	11	10	11	11	10	10
LSC	coding	*ycf4*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*ycf4 – ycf10*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*ycf4 – ycf10*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	12	12	10	12	10	10	11	12
LSC	intergenic	*petA – psbJ*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
LSC	coding	*psbF*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*psbE – petL*	(T)n	9	9	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*psbE – petL*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*petL – petG*	(T)n	10	10	10	10	10	10	10	10	10	9	10	9	9	9	9	10	9	9	9	9	9
LSC	intergenic	*petL – petG*	(A)n	8	8	8	8	8	8	8	8	8	10	8	10	10	9	9	9	9	9	9	9	9
LSC	intergenic	*tRNA-Pro (UGG) – psaJ*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	9	9	10	9	10	10	9	9
LSC	intergenic	*rpl20 – rps12*	(T)n	9	9	9	9	9	9	9	9	9	8	9	8	8	9	9	9	9	8	8	9	9
LSC	intergenic	*rpl20 – rps12*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
LSC	intron	*clpP*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intron	*clpP*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	10	9	9	9	9	9
LSC	intron	*clpP*	(A)n	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	10	10	11	11	11	10
LSC	intron	*clpP*	(T)n	8	8	8	8	8	8	8	8	8	6	8	6	6	6	6	6	6	6	6	6	6
LSC	intron	*clpP*	(T)n	17	17	17	17	17	17	17	17	17	17	17	16	17	13	13	17	16	17	17	14	16
LSC	intergenic	*clpP -psbB*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intergenic	*psbB -psbT*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	9	9	8	9	8	8	9	9
LSC	intergenic	*psbT – psbN*	(T)n	9	9	9	9	9	9	9	9	9	8	9	8	8	9	9	9	9	9	9	8	9
LSC	coding	*rpoA*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
LSC	intergenic	*rpl14 – rpl16*	(A)n	10	10	10	10	10	10	10	10	10	9	10	9	9	9	9	9	9	9	9	9	9
LSC	intergenic	*rpl14 – rpl16*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LSC	intron	*rpl16*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8

LSC	intron	*rpl16*	(T)n	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	8
LSC	intergenic	*rpl16 – rps3*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
LSC	coding	*rpl22*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
LSC	coding	*rpl22*	(T)n	8	8	8	8	8	8	9	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Irb	coding	*rps19*	(T)n	8	8	8	8	8	8	9	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Irb	coding	*rps19*	(T)n	9	9	9	9	9	9	8	9	9	9	9	9	9	9	9	9	9	9	9	9	9
Irb	intergenic	*rps19 – rpl2*	(T)n	10	10	9	9	9	9	9	9	9	9	10	10	10	11	11	10	10	10	10	11	10
Irb	coding	*ycf2*	(A)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
Irb	intergenic	*ndhB – rps7*	(A)n	10	10	10	10	10	10	10	10	10	10	10	10	10	9	9	10	9	10	10	9	9
Irb	coding	*rps7*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
Irb	intergenic	*rps12 - tRNA-Val (GAC)*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Irb	intergenic	*rrn16 - tRNA-Ile (GAU)*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Irb	intergenic	*rrn5 - tRNA-Arg (ACG)*	(A)n	10	10	10	10	10	10	10	10	10	11	10	10	10	10	10	10	10	10	10	10	10
Irb	coding	*ORF380 truncated ycf1*	(A)n	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	-	-	-	-
Irb	coding	*ORF380 truncated ycf1*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Irb	coding	*ORF380 truncated ycf1*	(A)n	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	-	-	-
SSC	intergenic	*ndhF – rpl32*	(A)n	19	19	16	16	15	16	16	16	16	19	19	16	16	6	6	13	11	15	14	12	10
SSC	intergenic	*rpl32 - tRNA-Leu (UAG)*	(A)n	8	8	8	8	8	8	8	8	8	7	8	7	7	7	7	7	7	7	7	7	7
SSC	intergenic	*rpl32 - tRNA-Leu (UAG)*	(A)n	15	15	15	15	15	15	15	15	15	17	17	18	18	16	13	15	13	19	19	13	14
SSC	intergenic	*rpl32 - tRNA-Leu (UAG)*	(A)n	9	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
SSC	coding	*ccsA*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
SSC	intergenic	*ccsA -ndhD*	(A)n	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	9
SSC	coding	*ndhD*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
SSC	coding	*ndhD*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
SSC	intron	*ndhA*	(A)n	8	8	8	8	8	8	8	8	8	8	8	8	8	9	9	8	9	8	8	9	9
SSC	coding	*ndhA*	(A)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
SSC	coding	*rps15*	(T)n	9	9	9	9	9	9	9	9	8	9	9	9	9	9	9	9	9	9	9	9	9
SSC	intergenic	*rps15 – ycf1*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
SSC	coding	*ycf1*	(T)n	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
SSC	coding	*ycf1*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	7	8
SSC	coding	*ycf1*	(T)n	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
SSC	coding	*ycf1*	(T)n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9

Table S3. Tandem Repeats (TRs) in the twenty-one tomato chloroplast genomes using IPA-6 (AM087200) as reference genome. TRs copy number and location are reported. TRs were identified using the tool available at https://tandem.bu.edu/trf/trf.basic.submit.html.

		Copy Number																							
Sequence	**Period Size**	**IPA-6**	**M82**	**cor**	**pds**	**pgl**	**pol**	**vpz**	**ves2001**	**vfr**	**cer1**	**cer2**	***S. pimpinellifolium 1***	***S. pimpinellifolium 2***	***S. neorickii 1***	***S. neorickii 2***	***S. habrocaites***	***S. peruvianum***	***S. cheesmaniae***	***S. galapagense***	***S. pennellii***	***S. chilense***	**location**		
GTTCAATGATATTATTATT	19	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.0	-	-	-	2.0	LSC	*tRNA-His (GUG) – psbA*	intergenic
ATCATGAATAAAT	13	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	-	-	2.0	-	2.0	2.0	-	-	LSC	*tRNA-His (GUG) – psbA*	intergenic
TATTTCCTTAATT	13	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	LSC	*rps16*	genic
TAATACTATAGAT	13	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	LSC	*rps16 - tRNA-Gln (UUG)*	intergenic
ACTTACTTTCCTTTTCCTTATA	22	2.0	2.0	-	-	-	-	-	-	-	2.0	2.0	-	2.0	3.0	3.0	2.0	2.0	2.0	2.0	2.0	2.0	LSC	*tRNA-Gln (UUG) – psbK*	intergenic
GGTTTAAGTCTGA	13	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	LSC	*rps4*	genic
ACGTAATACATATTAGAAAG	20	-	-	-	-	-	-	-	-	-	-	-	-	-	2.0	2.0	-	2.0	-	-	2.0	2.0	LSC	*tRNA-Phe (GAA) – ndhJ*	intergenic
AGTTTAATAGTTTACCC	17	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.1	-	LSC	*PsbE – petL*	intergenic
TTTTTTCATTCTAGTTA	17	-	-	-	-	-	-	-	-	-	-	-	-	-	2.1	2.1	-	2.1	-	-	-	2.1	LSC	*psaJ – rpl33*	intergenic
GAATCTAGATTTGAGT	16	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	LSC	*rps18 – rpl20*	intergenic
CATAGATATCTTA	13	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	LSC	*clpP*	intronic
AGAATTAAGAATTAGAA	17	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	-	-	2.1	-	2.1	2.1	-	-	LSC	*rpl16 -rps3*	intergenic
AATCAATGCAATTTAGGAGG	20	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	Irb	*tRNA-Ile – ycf2*	intergenic
ACTTAGTGAGTCCTTTCTTC	20	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	Irb	*rps12 - tRNA-Val (GAC)*	intergenic
GTCATTAATATCTTTG	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.0	-	-	-	2.0	Irb	*tRNA-Arg (ACG) - tRNA-Asn (GUU)*	intergenic
AGAAGAACGTATATAAAA	18	-	-	-	-	-	-	-	-	-	-	-	-	-	2.1	2.1	-	-	-	-	-	-	SSC	*rpl32 - tRNA-Leu (UAG)*	intergenic
TTGTTTTAGATCCGAACTAAGCCTTC	26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.0	2.0	-	-	SSC	*ndhG – ndhI*	intergenic