**Final Alignment (doesn’t need to be in Appendix):** CladeMAFFTWCdone.fasta

**Clade by clade alignment in MAFFT**: RAxML\_bipartitions.CladeMAFTWCdone.rax.out (this is the tree used in the figure in the main paper

**MAFFT alignment of all taxa simultaneously:** RAxML\_bipartitions.PlastidGenomesNoIRaMAFFT.rax.out