**Supplementary 1**

1. Cutadapt parameters: --times 1 -e (maximum allowed error rate) 0.1 -O (overlap) 3 --quality-cutoff 25 -m (minimum length) 45

Cutadapt key code: cutadapt -a XXXXXXXXX -A XXXXXXXX --times 1 -e 0.1 -O 3 -m 45 --quality-cutoff 25 --pair-filter=both -o E1\_1\_trimmed.fastq.gz -p E2\_2\_trimmed.fastq.gz E1\_1.fastq.gz E2\_2.fastq.gz

1. Trimmomatic parameters: LEADING (cut bases off the start of a read, if below a threshold quality):28 TRAILING (cut bases off the end of a read, if below a threshold quality):28 SLIDINGWINDOW (perform a sliding window trimming, cutting once the average quality within the window falls below a threshold):5:15 MINLEN (drop the read if it is below a specified length):50

Trimmomatic key code: java -jar /home/wangyihui/miniconda3/share/trimmomatic-0.39-2/trimmomatic.jar PE -threads 2 -phred33 E1\_1\_trimmed.fq E2\_2\_trimmed.fq Elaeocarpus\_1\_trimmed\_clean.fq Elaeocarpus\_2\_trimmed\_clean.fq ILLUMINACLIP:/home/wangyihui/miniconda3/share/trimmomatic-0.39-2/adapters/TruSeq3-PE.fa:2:30:10 LEADING:28 TRAILING:28 SLIDINGWINDOW:5:15 MINLEN:50

1. Getorganelle parameters：-w (the value word size) 0.6 -R (maxium extension rounds) 15 -k (SPAdes kmer settings) 45,65,85,105,125 -F (target organelle genome type) embplant\_pt.

Getorganelle key code: get\_organelle\_from\_reads.py -1 Elaeocarpus\_1\_trimmed\_clean.1.fq.gz -2 Elaeocarpus\_2\_trimmed\_clean.2.fq.gz -w 0.6 -t 1 -o Elaeocarpus\_simulated.plastome -F embplant\_pt -R 15 -k 45,65,85,105,125