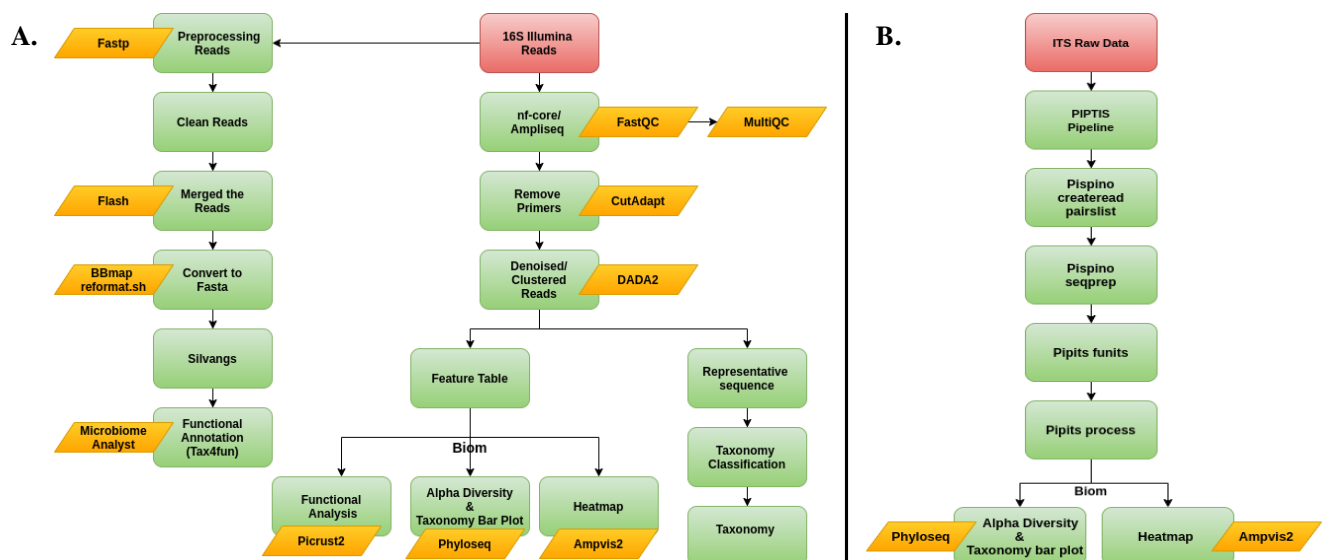
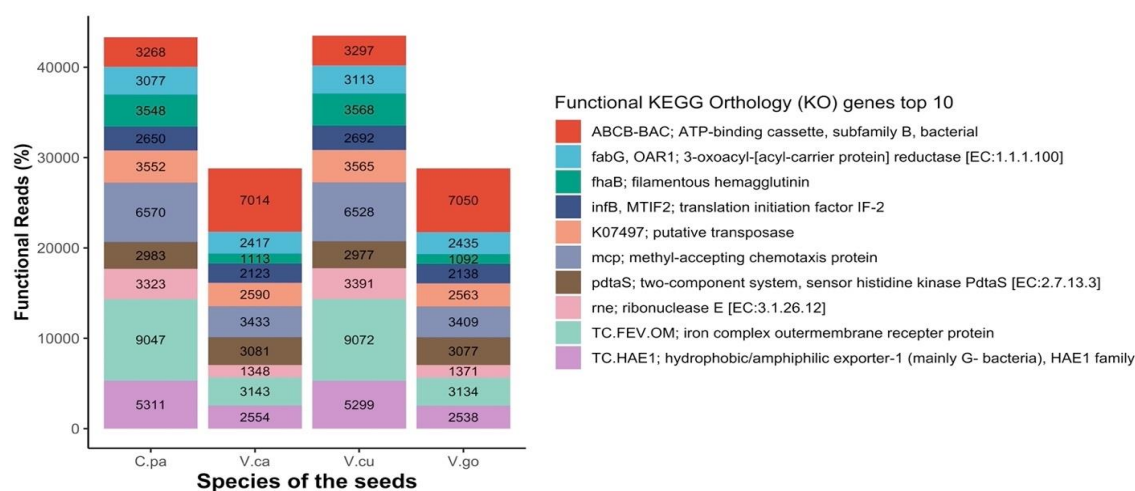


**Figure S1.** Collection sites of papaya and their wild relatives namely, *Carica papaya* Va. *Arka prabhath*; *Vasconcellea cauliflora*; *Vasconcellea cundinamarcensis*; and *Vasconcellea goudotiana* from Southern India. The map of India in this figure is a copyright product of 3 Biotech, Springer.



**Figure S2.** Pipelines of next generation sequencing for (A) 16S rRNA amplicons from endophytic bacteria and (B) ITS amplicons from endophytic fungi.



**Figure S3.** Top 10 functional orthologues genes across the samples. The sample species are represented as 1. *Carica papaya* (C.pa); 2. *Vasconcellea cauliflora* (V.ca); 3. *Vasconcellea cundinamarcensis* (V.cu); and 4. *Vasconcellea goudotiana* (V.go).

**Table S1.** Primers used in this study for the PCR amplifications of bacterial 16S rRNA and the fungal ITS sequences from the DNA extracts of the seed pulps.

Primer Name.	Primer Sequence (5'–3')
16S rRNA F	GCCTACGGGNGGCWGCAG
16S rRNA R	ACTACHVGGGTATCTAATCC
ITS-F	GCATCGATGAAGAACGCAGC
ITS-R	TCCTCCGCTTATTGATATGC