

Supplementary Data

Features of transcriptome in trioecious papaya revealed by a large-scale sequencing of ESTs and comparative analysis in higher plants

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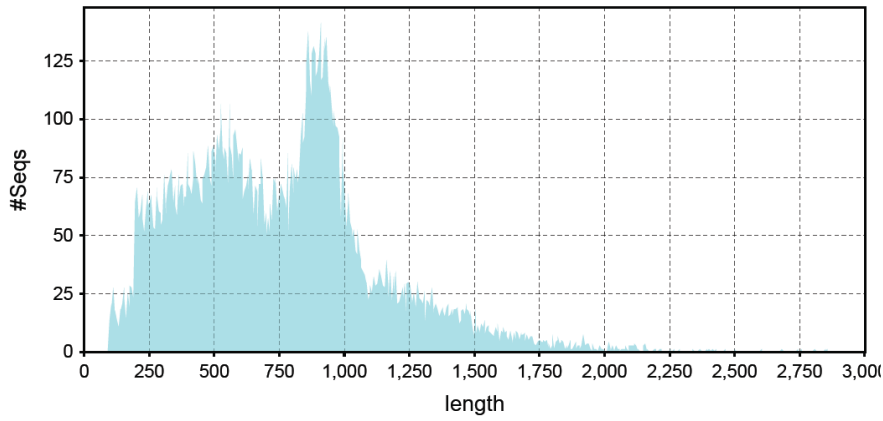
Supplementary Table 1. KEGG pathway annotation of papaya transcriptome unique ESTs. (Excel)

Supplementary Table 2. Annotated GO terms of papaya transcriptome unique ESTs. (Excel)

Supplementary Table 3. Multiple tissues used for cDNA library construction and ESTs sequencing.

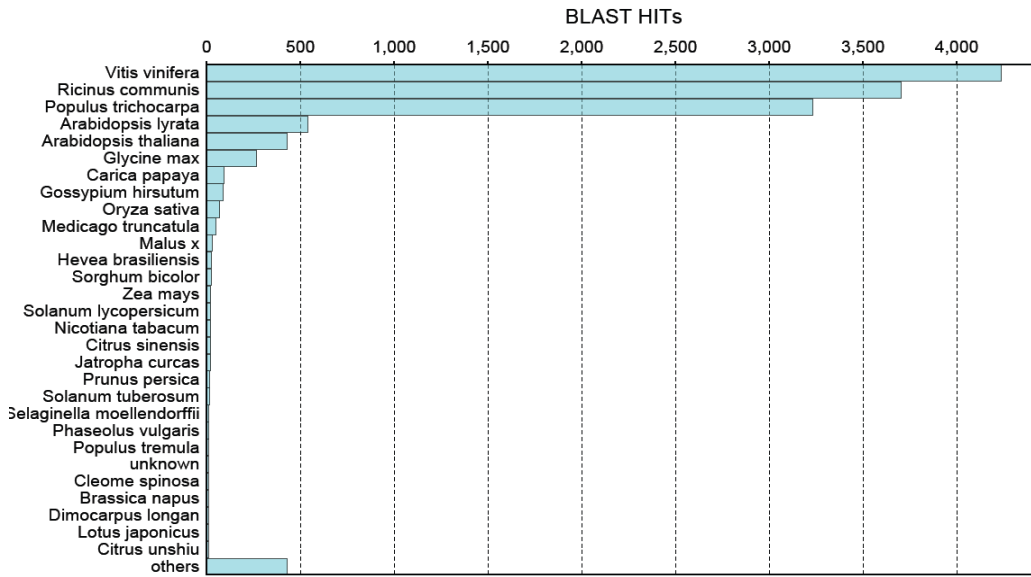
Tissues	Female flower	Hermaphrodite flower	Male flower	Leaf	Root	Stem	Fruit	Seed
Stages	Before & after meiosis	Before & after meiosis	Before meiosis	Young seedlings & mature trees	Young seedlings	Young seedlings	10 different stages from 7 days after pollination to 100% ripe fruits	10 different stages from 7 days after pollination to 100% ripe fruits

Number of sequences with length(x)

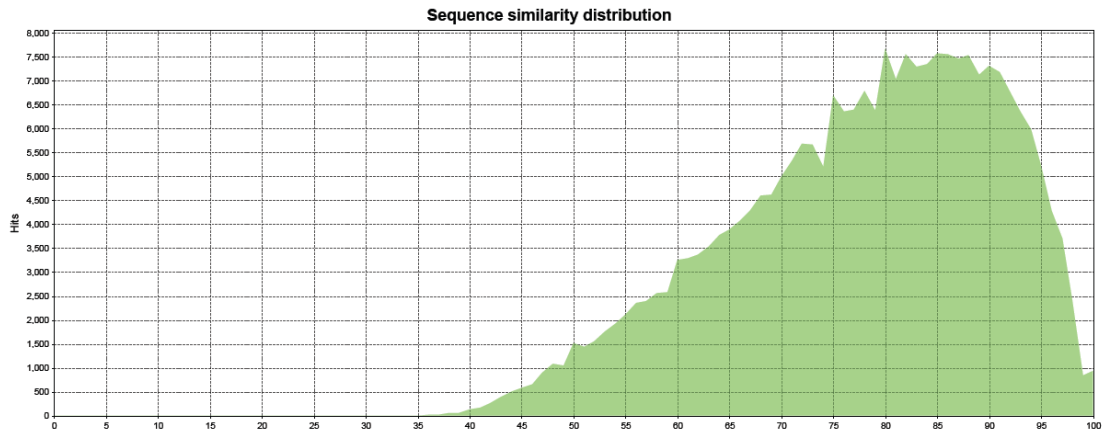


Supplementary Fig 1. Sequence length statistics for genome wide whole ESTs collection in papaya.

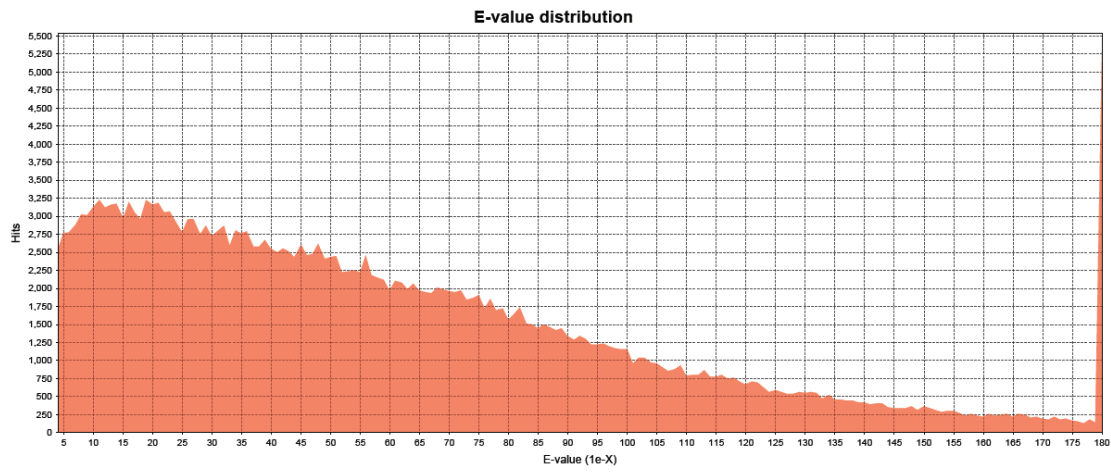
Top-Hit species distribution



Supplementary Fig 2. Top-Hit species distribution for whole ESTs collection in papaya transcriptome.

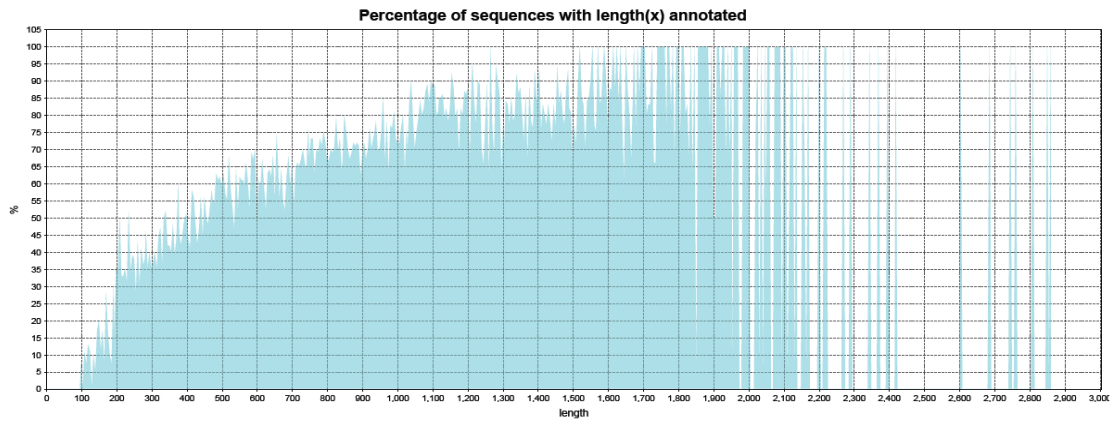


Supplementary Fig 3. Sequence similarity distribution for whole unique ESTs collection in papaya transcriptome.

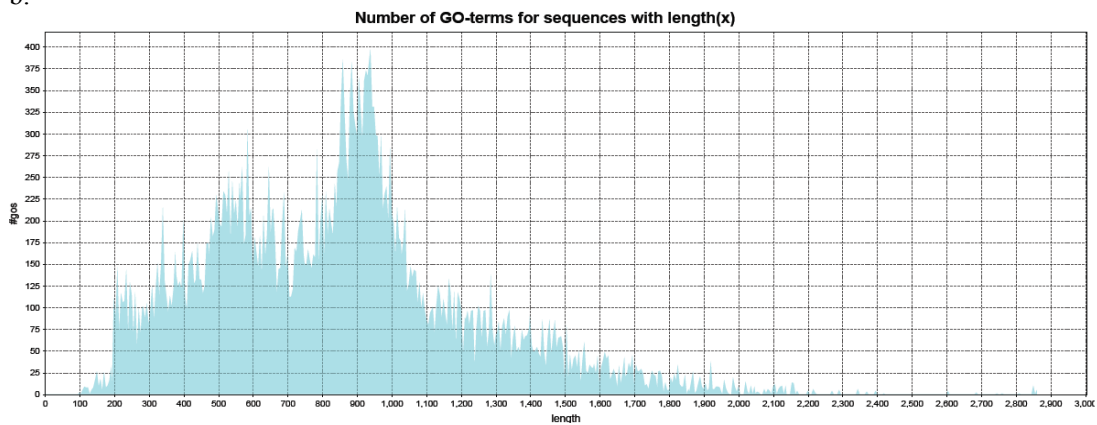


Supplementary Fig 4. Sequence E-value distribution for whole unique ESTs collection in papaya transcriptome.

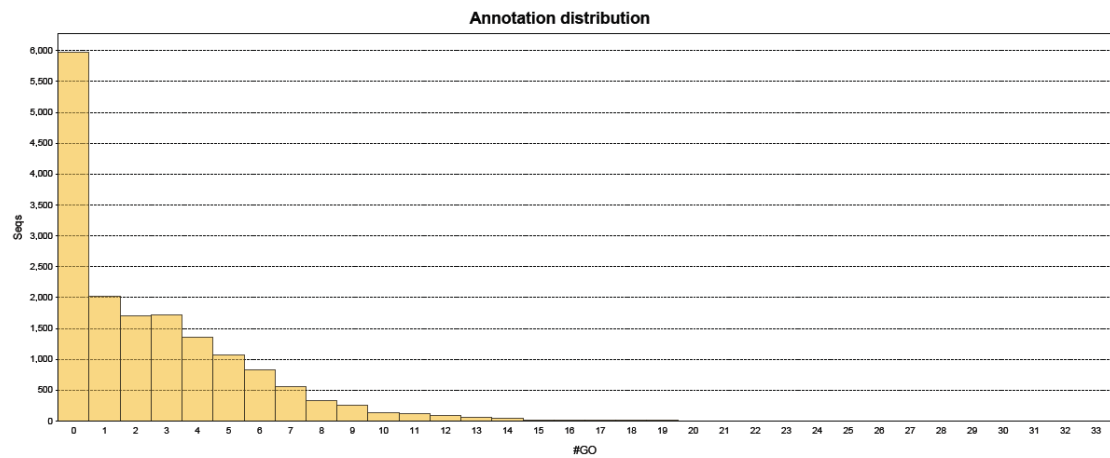
a.



b.



Supplementary Fig 5. GO-terms annotation statistics for sequences with length(x) for whole unique ESTs collection in papaya transcriptome.



Supplementary Fig 6. GO annotation distribution for sequences with length(x) for whole unique ESTs collection in papaya transcriptome.