sRNA: raw data

Filter: low quality sequences and adapter

↓

18-25 nt sRNA database

Filter: small non-coding RNAs

↓

sRNA filtered

Bowtie, match=0 with Viridiplantae miRNAs

↓

Matched sequences

SOAP, match=0 with L1-L2-L3 transcript library

↓

Plant known miRNAs

Matched sequences

↓

Conserved and novel pre-miRNAs

RNAfold

↓

Non-predicted pre-miRNA structure

Figure S1. Flow chart of the methodology adopted to identify J. curcas miRNAs.