

Sondovac script, part a

Raw paired-end genome data

removing reads of plastid and mitochondrial origin
Bowtie2, SAMtools

combining the paired-end reads
FLASH

combined reads without plastids and mitochondrial reads

Transcriptome

removing transcripts that share $\geq 90\%$ similarity
BLAT

Unique Transcripts

matching the combined genome skim reads and unique transcripts sharing $\geq 85\%$ similarity
BLAT

Matched sequences

Filtering BLAT output

choosing either transcript or genome skim sequences as basic sequences
UNIX commands

removing sequences with > 1000 BLAT hits
UNIX commands

removing sequences with masked nucleotides
UNIX commands

Filtered sequences

Geneious

de novo assembly of BLAT hits into larger contigs
Geneious

Assembled sequences of filtered BLAT hits