A

Normalization
TRINITY

Raw reads

Trimming
TRIMMOMATIC

Mapping
GSNAP

Select uniquely mapped reads
SAMTOOLS

Assembly
STRINGTIE

Quantify read counts
KALLISTO

Differential expression
DESEQ2

B

Raw reads

First mapping

Reads that mapped to
Dmrt gene regions

Exon-junction combinations reference

Second mapping

Reads mapped to exon junctions

Analysis

Dmrt gene region sequences from C. picta genome