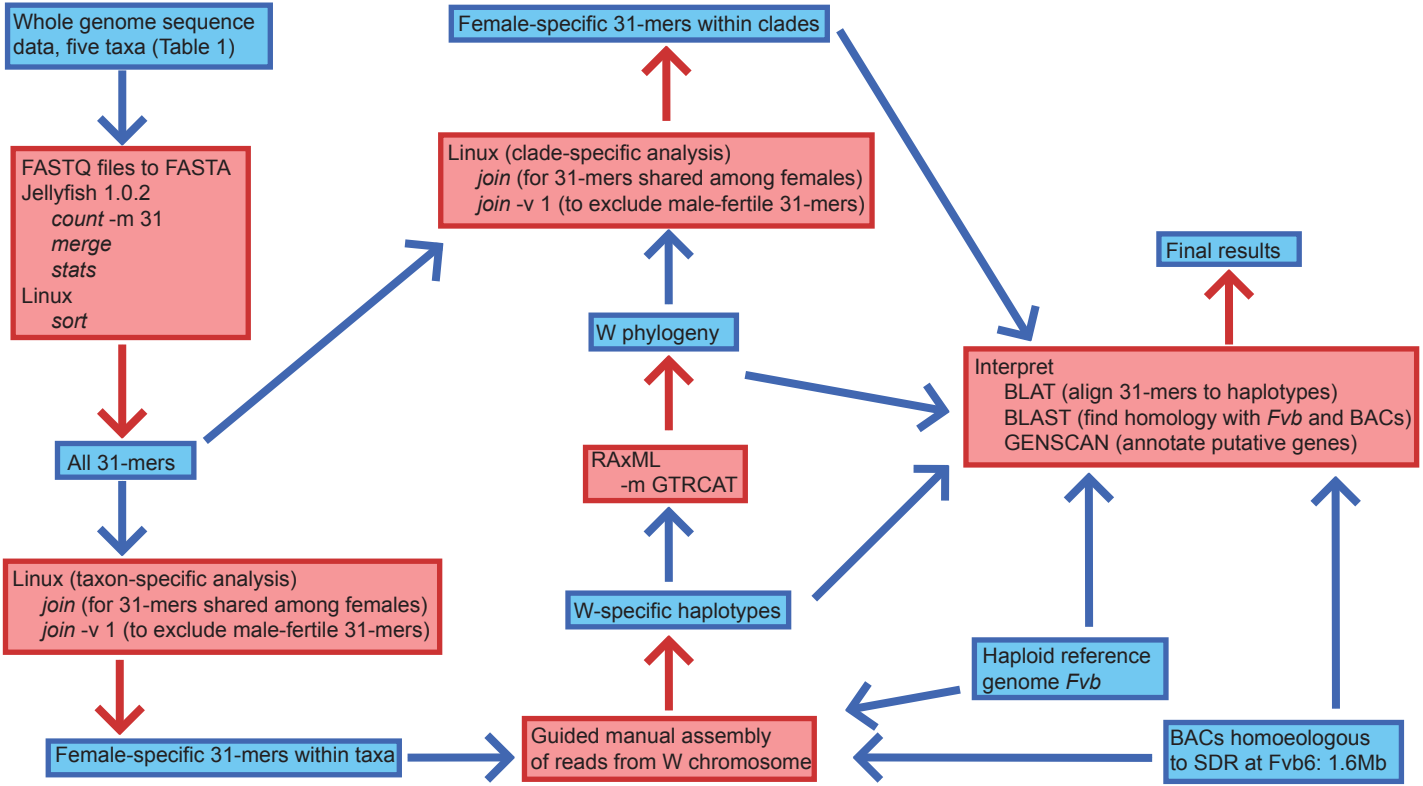
Whole genome sequence data, five taxa (Table 1)
FASTQ files to FASTA
Jellyfish 1.0.2
count -m 31
merge
stats
Linux
sort
All 31-mers
Linux (taxon-specific analysis)
join (for 31-mers shared among females)
join -v 1 (to exclude male-fertile 31-mers)
Female-specific 31-mers within taxa
Guided manual assembly of reads from W chromosome
W-specific haplotypes
RAxML
-m GTRCAT
W phylogeny
Linux (clade-specific analysis)
join (for 31-mers shared among females)
join -v 1 (to exclude male-fertile 31-mers)
Female-specific 31-mers within clades
Haploid reference genome Fvb
BACs homoeologous to SDR at Fvb6: 1.6Mb
Interpret
BLAT (align 31-mers to haplotypes)
BLAST (find homology with Fvb and BACs)
GENSCAN (annotate putative genes)
Final results