**Assembly**

* dmel\_scaffold2\_V5.fasta
  + Title: Dmel.Iso1\_V5.fasta
  + Description: The final assembly from the merging of heterochromatin-enriched assemblies and whole genome assemblies.
* dmel\_scaffold2\_merge\_V5.gtf
  + Title: Dmel.Iso1\_V5.gtf
  + Description: The gene annotation of our assembly from combining Flybase annotation and transcriptome data from males and testes.

**Alignment**

* SuSte\_mel.faTitle:cry-stellate.fasta

Description: All sequences from the blast output file

* Ste\_align\_all.fasta
  + Title: cry-stellate\_aligned.fasta
  + Description: Aligned sequences from the blast output file with manual curation
* Ste\_alignment\_for\_tree.fasta
  + Title: cry-stellate\_aligned\_for\_tree.fasta
  + Description: Aligned sequences from the blast output file with manual curation and selected long sequences for phylogeny construction
* PCKR\_Yonly.fasta
  + Title: PCKR\_aligned.fasta
  + Description: Aligned sequences for PCKR for calculating Y-linked gene conversion rate
* ste\_Yonly.fasta
  + Title: Suste\_aligned.fasta
  + Description: Aligned sequences for Su(Ste) for calculating Y-linked gene conversion rate

**Scripts**

* basic\_blast\_grep.pl
  + Title: basic\_blast\_grep.pl
  + Description: Perl script to grep the sequences from genome file using blast output (–outfmt 6)
* merged\_del\_copy.pl
  + Title: merged\_del\_copy.pl
  + Description: Perl script to merge transcripts or degenerated copies with large indels.
* frame\_depth\_new.pl
  + Title: frame\_depth\_new.pl
  + Description: Perl script to calculate sum of depth, average and median F/M for each 10kb window.
* generate\_scaffold.pl
  + Title: generate\_scaffold.pl
  + Description: This code is from Xue et al. 2013 L\_RNA\_scaffolder: scaffolding genomes with transcripts. Please see the example of input file in final.path
* pilon\_mel.sh
  + Title: pilon\_mel.sh
  + Description: A bash script to run Pilon iteratively to polish the assembly
* Heterochromatin.contigs.list.txt
  + Title: Heterochromatin.contigs.list.txt
  + Description: The list of contigs from heterochromatic region of R6. We used the list to extract heterochromatin enriched region.
* final.path
  + Title: final.path
  + Description: The example input for generating scaffold using generate\_scaffold.pl