Contents:

Dot\_Plots

* Min\_block\_size(s)\_X
  + Dot plots for each of the 19 species based on a minimum block size (s) of 3/5.
* MCScanX\_collinearity\_files
  + Raw MCScanX output for each species.

DupPupe\_final\_Ks

* Raw DupPipe output. Please find a description of the file type on the git repo: <https://gitlab.com/barker-lab/EvoPipes>

Ks\_Plots\_Duppipe\_Mixture

* Ks plots with red dotted ablines for the median Ks of each mixture model component (k). These were generated using the Mix\_Plot.R script.

Fig\_3\_Updated.pdf

* Updated figure 3 with added mixture model k components.
* Please note there was a mistake in the prior draft’s labeling; *T. urticae* and *N. clavipes.* This has been fixed and the requested mixture models added. I decided to use the median Ks rather than the full distribution to make viewing easier. The R script can be changed to add the entire K component distributions, please let me know if you would prefer this format.

Mix\_Plot.R

* Script used to plot the Ks plots and fit mixture components.

SLEDGE\_Results

* Tables summarizing the SLEDGe results. Please refer to the notes therein for the columns. I removed the spurious columns, thanks for sending along the supplemental files.

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* Update draft from Gregg with my replies to the comments and minor edits.