Align all known mature miRNAs against entire *C.intestinalis* genome
3229 mature miRs X 2501 scaffolds

Align all known mature miRNAs against entire *C.savignyi* genome
3229 mature miRs X 446 scaffolds

Retain only the 10-mer seed matches to both *C.intestinalis* and *C.savignyi*.

Retain only the mature matches to *C.elegans* and/or *H.sapiens*.
Extend matches 10nts downstream to create 20-mers.

Align *C.int* X *C.sav* 20-mers. Keep matches >= 90% identity.
Extend 20-mers by +/- 100 nts to create 220-mers.

Mfold 220-mers to find hairpins in *C.int* and *C.sav*

14 microRNA families appear in both *C.intestinalis* and *C.savignyi*