



Figure S6: RCM maps of FLS2 generated using different FLS2 ortholog sets. Input was derived amino acid sequences from: A) Seven Brassicaceae species, similar to print Figure 8. B) One representative each from Brassicaceae lineages I, II and III as in Couvreur et al. 2010 (*Camelina laxa*, *Eruca vesicaria* and *Chorispora tenella*). C) Two highly similar FLS2 isolates, both from *Brassica rapa*. D), E) and F) Two FLS2 isolates are compared, from: D) lineages I and II *Camelina laxa* and *Eruca vesicaria*; E) lineages I and III *Camelina laxa* and *Chorispora tenella*; F) lineages II and III *Eruca vesicaria* and *Chorispora tenella*. Maps are described in print Figure 2.