









Figure S7. Conserved synteny of *Kryptolebias marmoratus*/*K. hermaphroditus* linkage groups (Kma LGs) to either platyfish (*Xiphophorus maculatus*, Xma) or medaka (*Oryzias latipes*, Ola) chromosomes, suggesting basically one to one relationship (24 orthologous chromosome pairs). Dotted lines indicate homology of mapped Kma markers to either Xma or Ola mapped genome sequences identified by the blastn program with default parameters. For platyfish, blast hits with a cut-off e-value of 1.0E-9 are shown. Many Kma LGs show intrachromosomal rearrangements probably due to recurrent inversions after divergence from common ancestors between either Xma or Ola. Some Kma markers show homology to sequences on non-orthologous chromosomes (indicated by red letters in parenthesis). For example, a marker at 8.2 cM on Kma LG1 (Kma1) has a homology to a sequence on Xma chromosome 20 at 7.8 Mb. Two such markers, 5064 (represented by 1948 on Kma LG1) and 34956 (represented by 1052 on Kma LG2), had homologous sequences on another orthologous chromosomes (Ola23-Kma18-Xma17 and Ola19-Kma17-Xma10, respectively), indicating translocations happened after the *K. marmoratus*/*K. hermaphroditus* lineage diverged from platyfish. Similarly, markers 18609 (represented by 5464 on Kma LG2) and 38898 (represented by 2302 on Kma LG8), had homologous sequences on orthologous platy chromosomes (Xma18 and Xma1, respectively) but on non-orthologous medaka chromosomes (Ola22 and Ola19, respectively), indicating translocations happened after the medaka lineage diverged from cyprinodontiformes.