

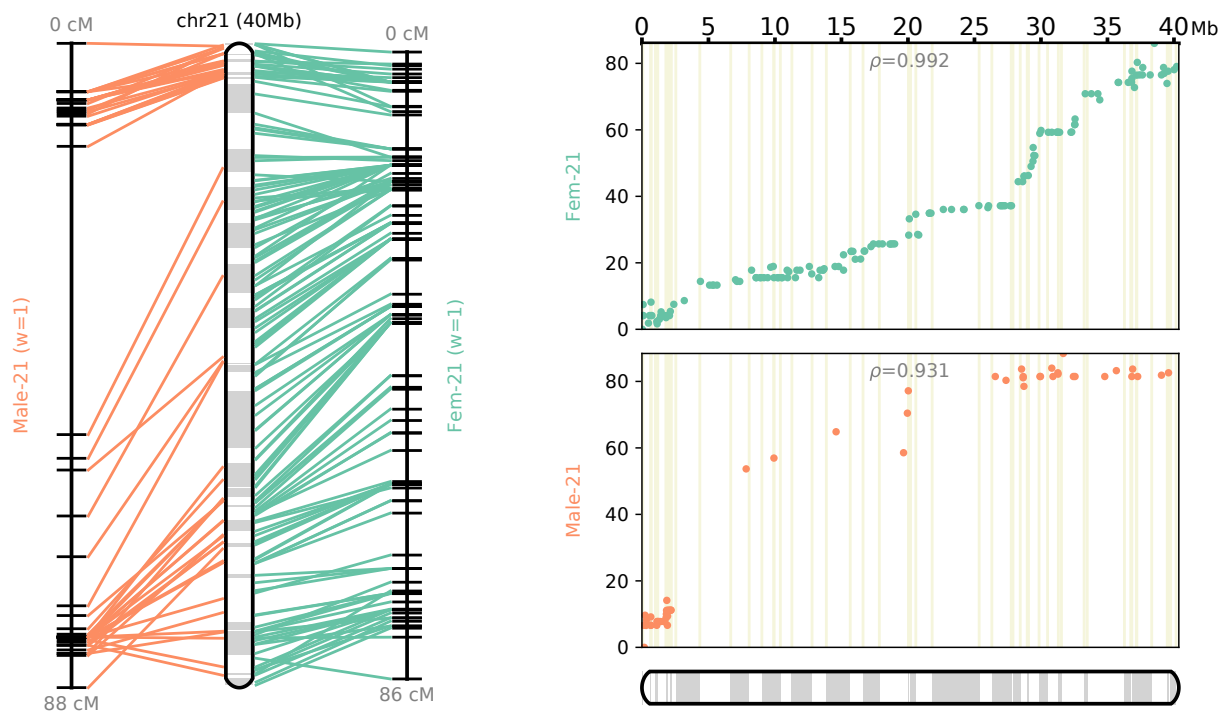
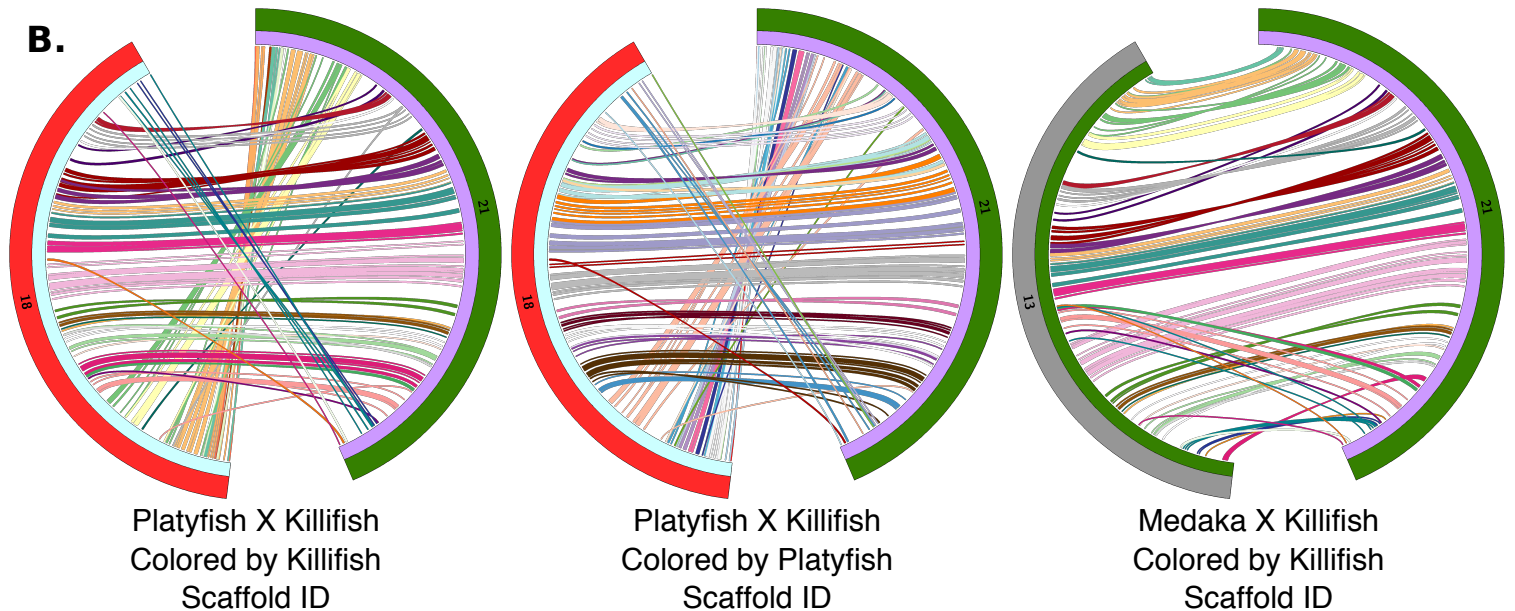
**A.****B.**

Figure S3. LGs that differed between the two sex-specific maps and the order and orientation of the consensus map (ALLMAPs) scaffolds in closely related platyfish and medaka. A) Markers informative for recombination in the male are in orange and blue-green for female markers. Left figures indicate the placement of markers in each sex specific map with the resulting consensus map in the center to indicate the final genome scaffold placement (alternating in white and grey along the chromosome). Plots on the right correlate the original centi-morgan (cM) position for markers (y-axis) with the resulting position in the consensus map. The female map included markers along the entire chromosome (left, blue-green) that highly correlated with cM position in the consensus map (right, top), while the male map did not have mappable markers in the middle of the chromosome but did have markers at both ends and resulted in a similar total cM length. B) Circos plots indicate that the resulting consensus sequence order of scaffolds is supported by synteny in platyfish and medaka, but might indicate an inversion in platyfish, but not in medaka. Killifish LG21 is green in each Circos plot, the homologous chromosome in platyfish colored red, and medaka colored grey. One-to-one orthologs from the same scaffold are coded the same color, and connect to their position in the comparison species chromosome.