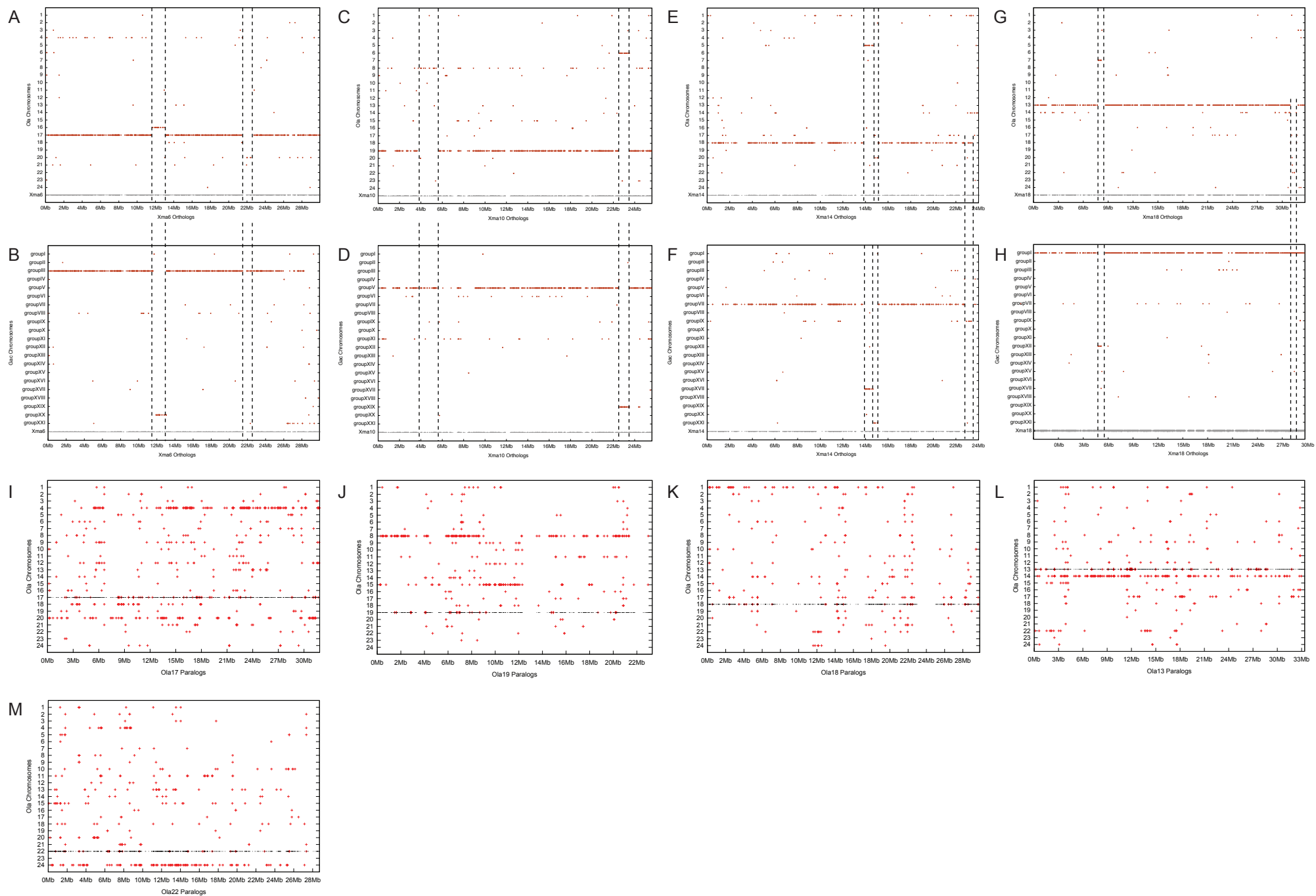


Fig. S5



**Figure S5** Differences in conserved syntenies comparing platyfish and medaka.

A. Xma6 is mostly orthologous to Ola17 but has about a 2Mb region that is orthologous to a part of Ola16 at about 12Mb and a 1Mb region at about 22Mb that does not seem to be shared with the medaka genome. The 'ghost' of Ola4 represents paralogs rather than orthologs because Ola4 is the ohnolog of Ola17 (see Supporting Figure S5I).

B. A comparison of Xma6 to stickleback chromosomes shows that it is mostly orthologous to GacIII and that, as in medaka, the region at 12Mb is also anomalous, suggesting that this region is either a transposition in the platyfish lineage or an assembly error in platyfish. The short region at 22Mb that was missing from medaka is present in stickleback, showing that this is either a medaka-lineage deletion or a misassembly in the medaka genome.

C. Xma10 is mostly orthologous to Ola19 but has about a 2Mb region at 5Mb that finds best hits on Ola8, the ohnolog of Ola19, rather than Ola19 itself, suggesting that the medaka genome assembly may be missing the orthologs of Xma10 genes located around 5Mb. In addition, a 1Mb segment on Xma10 at about 23Mb is orthologous to a part of Ola6 in the medaka genome. The 'ghost' of Ola8 represents paralogs rather than orthologs because Ola8 is the ohnolog of Ola19 (see Figure S5J).

D. A comparison of Xma6 to stickleback chromosomes shows orthology mostly to GacV but that, in contrast to medaka, the 2Mb region at 5Mb of Xma10 is contiguous with the rest of GacV, suggesting that this region is missing from the medaka genome assembly. The short region at 23Mb on Xma10 that appeared to be a translocation in platyfish based on medaka is confirmed to be a translocation (or assembly error) in the platyfish genome by comparison to stickleback as outgroup.

E. Xma14 is mostly orthologous to Ola18 but has two short sections at 15Mb that are orthologous to Ola5 and Ola20, suggesting translocations or assembly errors. The 'ghost' of Ola1 represents paralogs rather than orthologs because Ola1 appears to be the ohnolog of Ola18, although the data are not real clear on this point (see Figure S5K).

F. A comparison of Xma14 to stickleback chromosomes shows orthology mostly to GacVII and that the regions about 15Mb are also anomalous in stickleback as they are in medaka, consistent with a translocation or assembly error in the platyfish lineage. In addition, a 1Mb region at 23Mb on Xma14 that did not appear to be a translocation when comparing platyfish to medaka does appear to be a translocation (or assembly error) comparing stickleback and platyfish suggesting that this is a translocation that appeared in the stickleback lineage or in the common ancestor of medaka and platyfish, or is an assembly error in stickleback.

G. Xma18 is mostly orthologous to Ola13 but has about a 1Mb region at 8Mb that is orthologous to a small portion of Ola7. In addition, a 1Mb segment on Xma18 at about 31Mb appears to be missing from the medaka genome assembly. The 'ghost' of Ola14 represents paralogs rather than orthologs because Ola14 is the ohnolog of Ola13 (see Supporting Figure S5L).

H. A comparison of Xma18 to stickleback chromosomes shows orthology mostly to GacI and that, as in medaka, the 1Mb region at 5Mb of Xma18 is not with the rest of Xma18 orthologs, but is on GacXII, suggesting that this region is a translocation in the platyfish lineage or is a misassembly. The short region at 31Mb on Xma18 that appeared to be missing from medaka is present in stickleback, suggesting a deletion or assembly error in medaka.

I. A paralogy plot of Ola17 vs. the medaka genome shows that Ola4 is largely ohnologous to Ola17.

J. A paralogy plot of Ola19 vs. the medaka genome shows that Ola8 and Ola15 are largely ohnologous to Ola19.

K. A paralogy plot of Ola18 vs. the medaka genome shows that Ola1 is largely ohnologous to Ola18, although the plot has substantial noise.

L. A paralogy plot of Ola13 vs. the medaka genome shows that Ola14 is largely ohnologous to Ola13.

M. A paralogy plot of Ola22 vs. the medaka genome shows that Ola24 is largely ohnologous to Ola22.