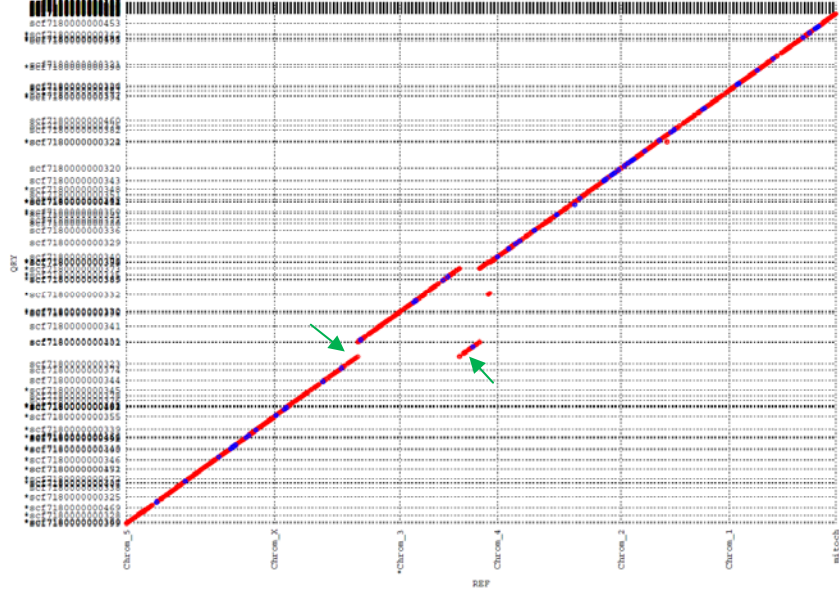
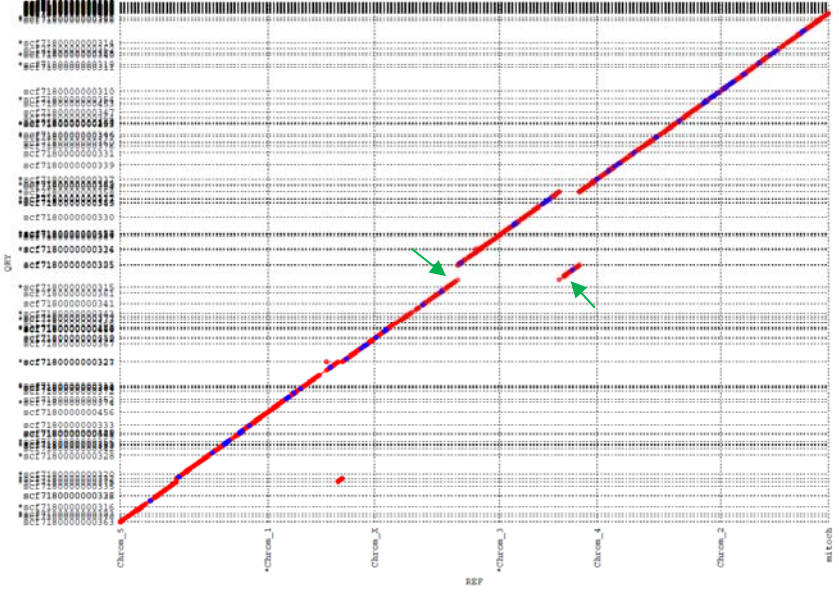


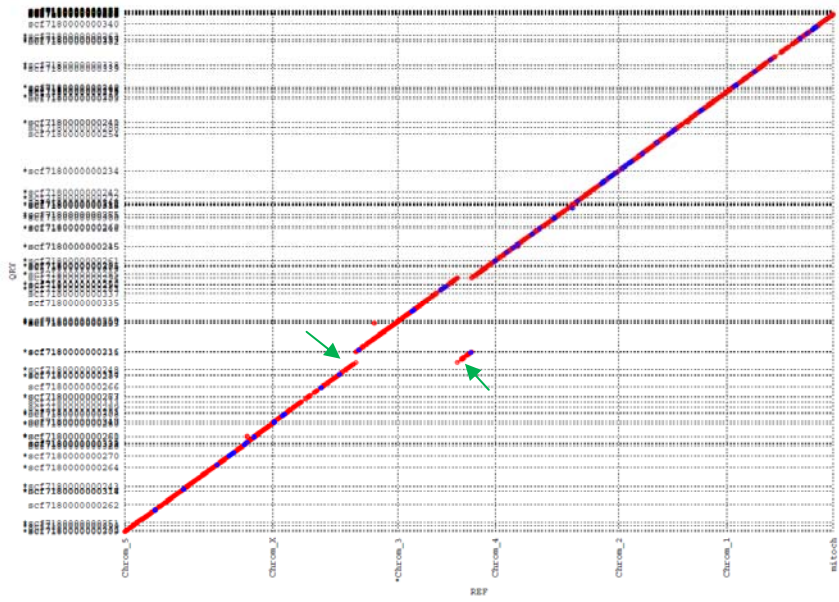
*C. elegans* M



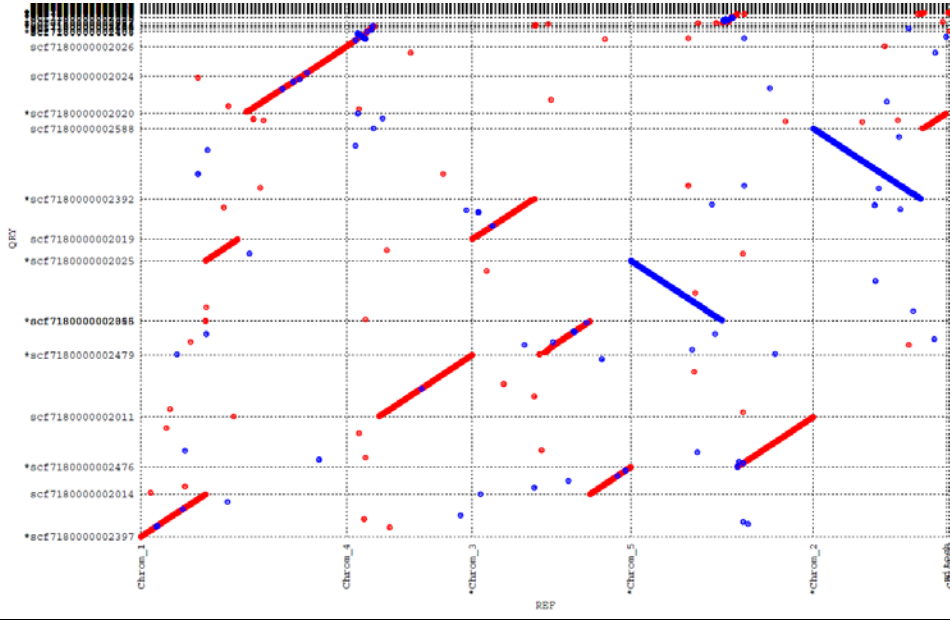
*C. elegans* L



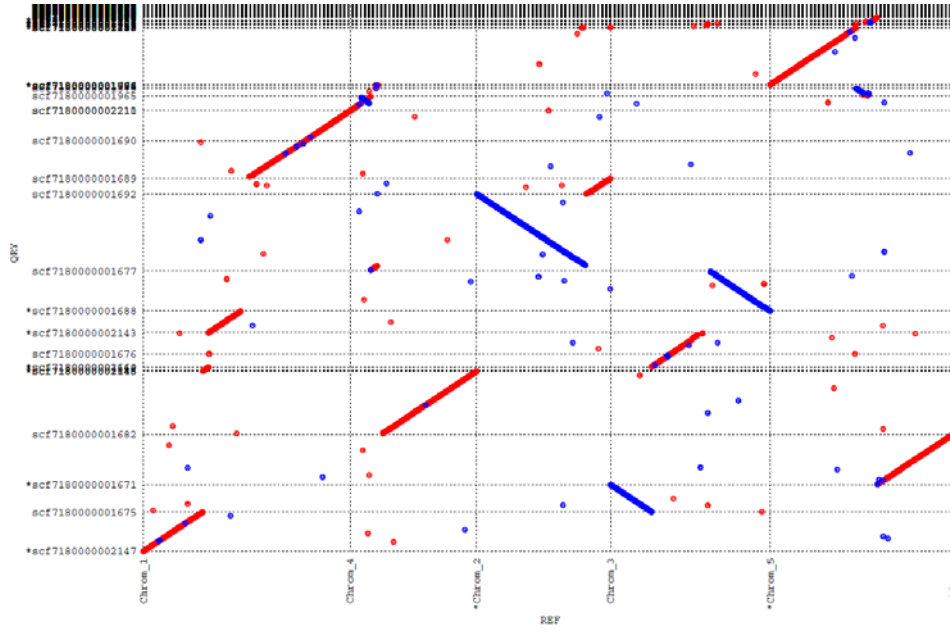
*C. elegans* LH



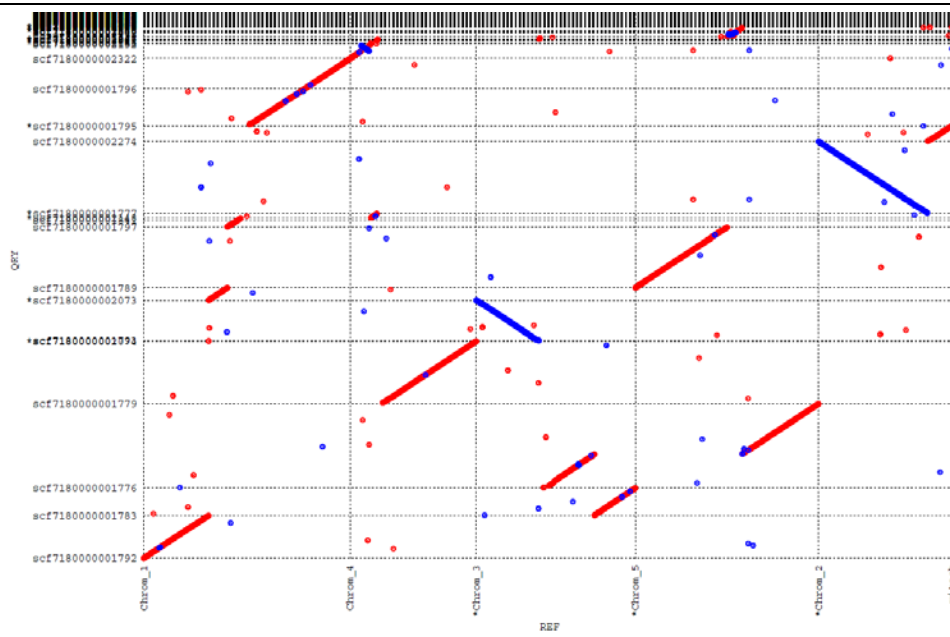
*A. thaliana* M



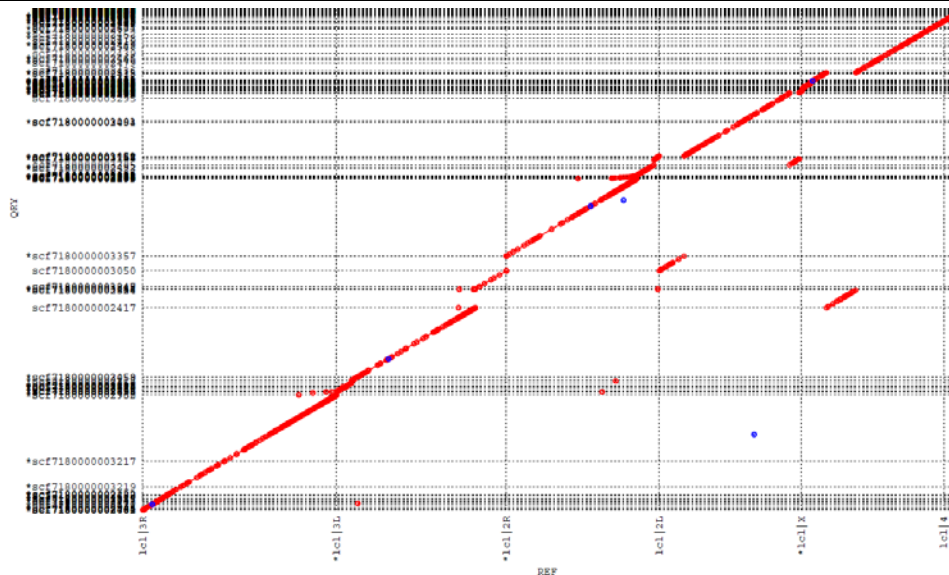
*A. thaliana* L



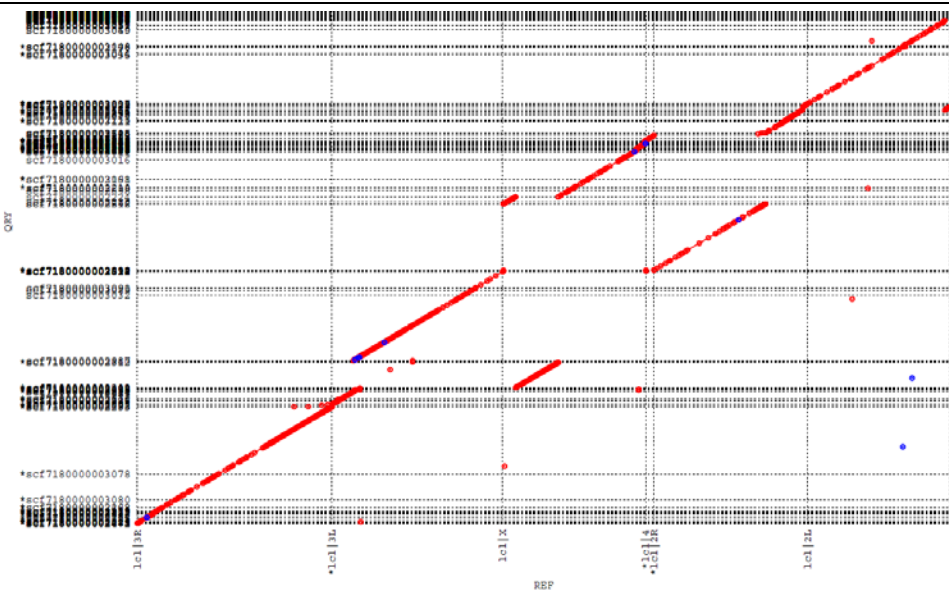
*A. thaliana* LH



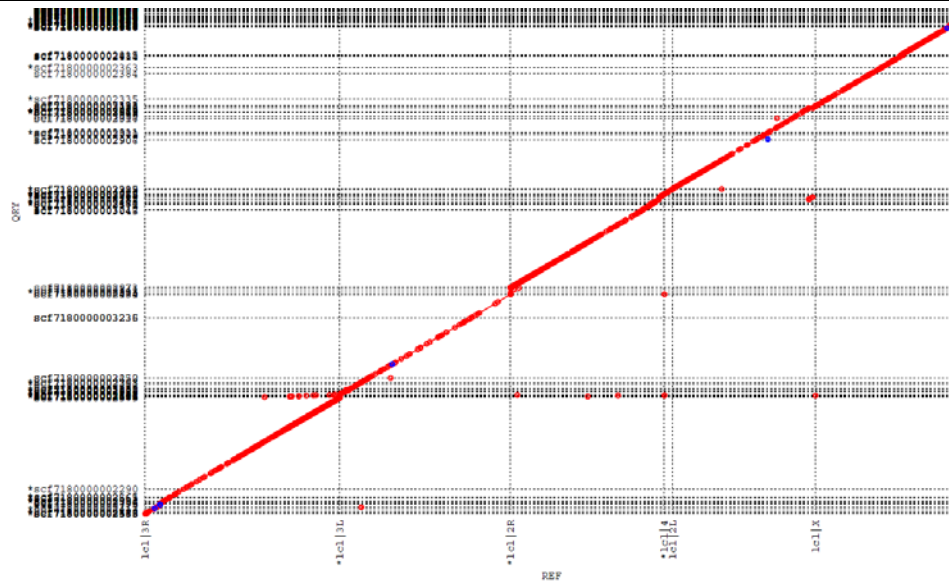
*D. melanogaster* M



*D. melanogaster* L



*D. melanogaster* LH



Supplemental Figure S14. Search for misassemblies that might inflate contiguity statistics. All assemblies of *C. elegans*, *A. thaliana* and *D. melanogaster* were checked for the presence of gross misassemblies (e.g., contigs with spurious junctions between different chromosomes) that might inflate the NG50 of LH over MHAP assemblies, using *mummerplot* (Kurtz et al. 2004) and the reference genomes. In all assemblies we set the *ovlMemory* parameter of the PBcR pipeline to 96Gb because we found that *Arabidopsis* assemblies with a smaller value (56 Gb) have a gross misassembly (Supplemental Figure S7). Using *ovlMemory*=96Gb we found only one visible misassembly: in all *C. elegans* there is a contig that contains sequences from chromosomes X and 3 (green arrows). As the same misassembly is present in the three *C. elegans* assemblies (M, L, and LH), and the misassembled contig is actually smaller in the LH assembly (M: scf7180000000323, 4.3 Mbp; L: scf7180000000315, 4.4 Mbp; LH: scf7180000000248, 3.5 Mbp), it is not inflating the NG50. *Arabidopsis* assemblies seem to contain many more misassemblies, but this probably is an artifact: in this species the reference assembly came from a different strain, so all polymorphisms. For the sake of clarity we removed the small contigs from the figures.