

Additional file 4. Dot plot pairwise comparison (window size of 11) of the reverse complement of BACs 62d19 and contig 63n5-43b24, and the corresponding region of the amphioxus genome (last 350 kb of scaffold_295 [native orientation] and the first 300 kb [reverse complement] of scaffold_82). Dot plot comparisons indicate that the contig formed by BACs 63n5 and 43b24 corresponds to the scaffold_82 allele and BAC 62d19 corresponds to the scaffold_295 allele. Repetitive elements [(a) – (c)] are polymorphic (length variable) across haplotypes. Note length of repeat (b) in panel 5 and 7 varies in size and reflects assembly artifacts across the repeat. Banding patterns that span panel 1, 4, 13, and 16 represent breaks (i.e., unresolved sequence) in scaffold assemblies.

