



Comparison of our amphioxus *Hox* cluster assembly and the assembly Brafl1 of the *Branchiostoma floridae* genome (<http://genome.jgi-psf.org/Brafl1/Brafl1.home.html>). Sequences are compared using `blastn`, hits are shown color-coded by their *E*-value (black 0, violet 10^{-70} , magenta 10^{-50} , red 10^{-30} , orange 10^{-20} , green 10^{-10} , cyan 1, blue 10). Black diagonals correspond to nearly identical stretches in the assembly, large colored squares located on the diagonal indicated repeat-rich regions (see main text for more details). The nearly regular grid of off-diagonal hits is generated mostly by the homeoboxes, which are similar enough to be easily recognized across paralog groups. Most of the *Hox* locus matches two separate scaffolds corresponding to two distinct haplotypes. The assembly contains a large number of gaps, small local translocations, as well as major problematic regions. For instance, the first 120 kb are duplicated in scaffold 260 and another region of about 30kb is split into two interleaved blocks.