

# ANNOTATION OF PUTATIVELY CONSERVED NON-CODING REGIONS IN AMPHIOXUS, BRANCHIOSTOMA FLORIDAE

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Evolution explains the progressive development in genomic complexity across widely diverse organisms. Understanding crucial changes in genomic structure that correlate with significant branch points in the evolutionary tree is of great importance in increasing our knowledge of the mechanisms behind evolutionary change. At the heart of this research is the exploration into the uncharted waters of *Branchiostoma floridae's* genome. *B. floridae* as a member of the cephalochordates is of particular interest because of its location on the evolutionary tree. Previously published non-coding regions from humans were mapped onto a multiple-genome alignment including *B. floridae*, *P. marinus* (lamprey), *G. gallus* (chicken), *M. musculus* (mouse) and *H. sapiens sapiens* (human) to reveal those regions that were conserved across the various species. The commonalities between the non-coding regions of these organisms will help with discerning the remnant vestiges of the common ancestor present in currently extant organisms. Prior research has established a set of 123 sequences in *B. floridae's* genome that are potentially conserved in non-coding regions of *H. sapiens sapiens*. However, further analysis of these sequences is necessary to quantify the level of conservancy between organisms as well as to determine the functional affects of this conservancy. The goal is to characterize putatively conserved non-coding regions in amphioxus through to humans. This is done through the assessment of pairwise similarities between *H. sapiens*, *M. musculus*, *G. gallus*, *P. marinus* and *B. floridae*. Non-coding regions that are found to be conserved between various combinations of these organisms are likely to be important because they have been retained through the course of evolution. This research hopes to discover the evolutionary significance of the conservation of various non-coding regions from the cephalochordates through to the vertebrates and to further annotate regions of *B. floridae's* genome that are at present not fully understood.