

Regulatory landscape of the vertebrate *six2/six3* locus

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ABSTRACT

Six3 and *Six2* are transcription factors from the SIX family of homeoproteins. The *Six* genes play important roles during development controlling patterning, cell proliferation and migration. Across bilaterian evolution, *Six3* and *Six2* genes have been maintained in very close proximity in the genome despite displaying largely different expression patterns. This suggests that these genes are exposed to different regulatory environments. Using zebrafish as a model, we are trying to precisely define the regulatory landscape for each gene and determine how and why synteny is maintained and differential expression patterns is generated. For this goal, we have used our zebrafish histone epigenomic data to select and test putative enhancers for both genes. We also use circular chromatin conformation capture (4C) derived technologies to elucidate the global chromatin architecture of each promoter. In addition, BAC recombineering will allow us to test the influence of regulatory elements and potential insulators on gene expression and chromatin architecture of the locus.