

# Genomic analyses on the Meis2 transcription regulation

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Meis2 gene, one of Hox cofactors, occupies large chromosomal region spanning around 200 kb in mammals. Transgenic analysis using sequences around transcription start site yielded no specific pattern of expression. These results and the large genomic structure suggest that the transcription regulatory sequences (enhancers) dispersed across long distance of chromosome. To study the mechanisms of interaction between DNA sequences locating in a long distance, we are analyzing Meis2 regulatory sequences. By conventional transgenic studies using evolutionary conserved sequences exhibited several enhancer candidates remote from the promoter. We identified two of these sequences physically interacting with the promoter by 3C (chromosomal conformation capture), one of which locates 300 kb in distance from the promoter and in an intron of neighboring gene. We are currently analyzing functional significance of these remote enhancers on Meis2 promoter.

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