



Title	A dual enhancer-silencer element, DES-K16, in mouse spermatocyte-derived GC-2spd(ts) cells
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18 : 40307886 to 40308445

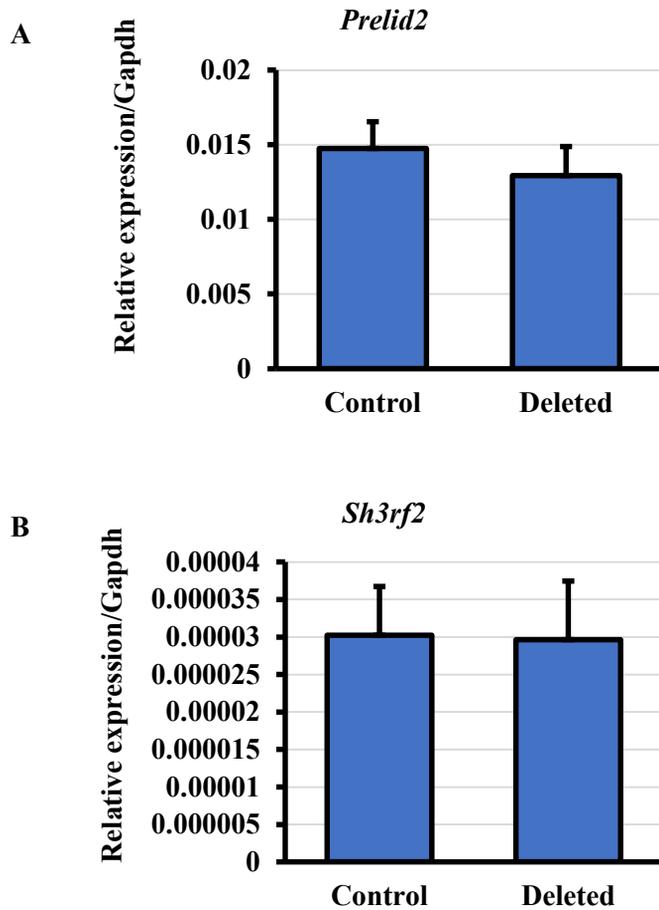
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Chr 18: 40308000 to 40308357

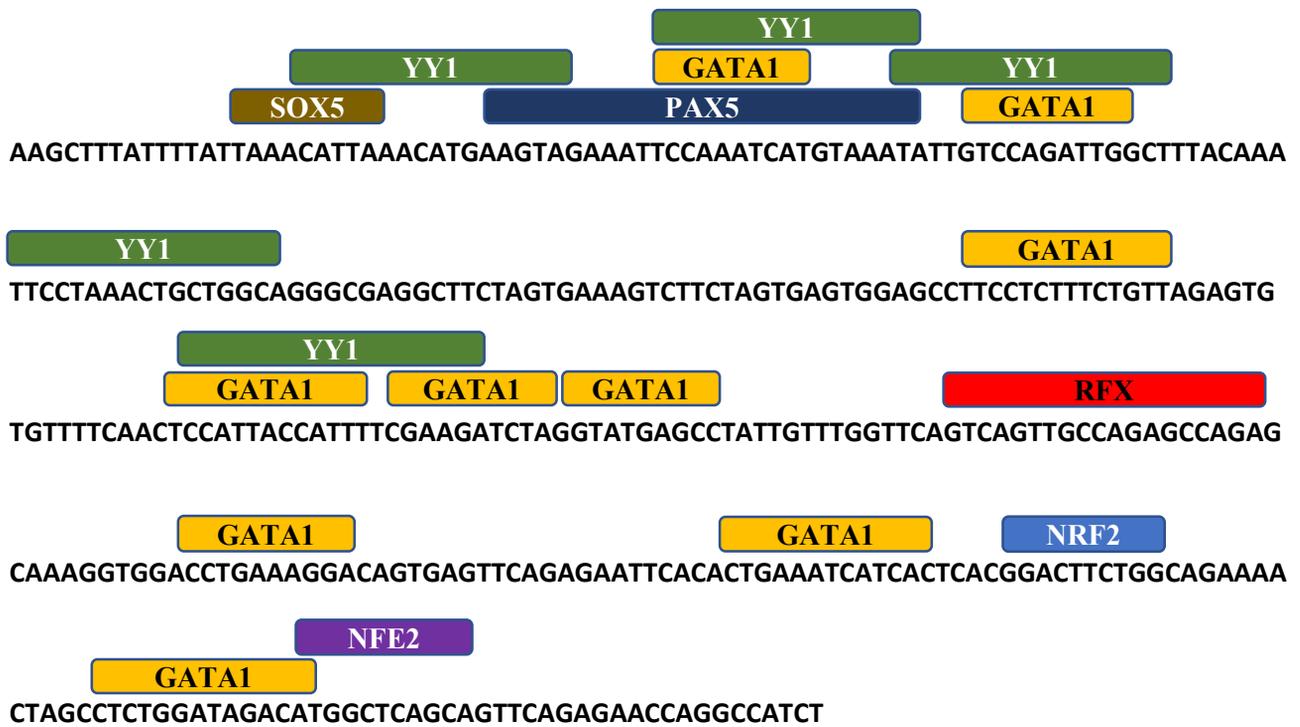
Yellow – reporter assayed region

Yellow & red – Deleted region

Supplemental Fig. 1. The DES-K16 sequence and a deleted region. A genome sequence including DES-K16 is shown. A genomic region used for reporter gene analysis is marked with yellow, and the region deleted by the CRISPR/Cas9 system is the sequence marked with yellow and red.



Supplemental Fig. 2. Effect of a deletion of DES-K16 on expression of *Prelid2* and *Sh3rf2* genes in GC-2spd(ts) cells. qRT-PCR was performed with total RNAs from GC-2spd(ts) cells with or without a deletion of DES-K16. *Gapdh* was amplified as an internal control and used to normalize the expression level. Data are presented as means \pm S.D. from six to eight independent experiments, and statistical significance was analyzed by Student t test. No significant differences were detected for the expression levels of any of these genes.



Supplemental Fig. 3. Potential binding sequences of transcription factors associated with enhancer and silencer in DES-K16. Potential transcription factor binding sites in DES-K16 were searched by the TRANSFAC software and are indicated in boxes at the upper side of each sequence. Purportedly, PAX5 and SOX5 are associated with enhancer and other factors are associated with silencer. GATA1 has a potential binding ability to both enhancer and silencer regions. All of these transcription factors are expressed in mouse spermatocytes.