# Chromosomal localization of the zinc finger protein 15, *Zfp15*, on Mouse Chromosome 4

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***Species:*** Mouse
***Locus name:*** Zinc finger protein 15
***Locus symbol:*** *Zfp15*
***Map position:*** *Zfp15* is localized on mouse Chromosome (Chr) 4: centromere–*D4Bir11*–7.4 ± 2.7–***Zfp15***–1.1 ± 1.1–*D4Mit4*–17.0 ± 3.9–*D4Bir16*–7.4 ± 2.7–(*D4Mit9, D4Bir20*)–4.3 ± 2.1–*D4Bir21*–10.6 ± 3.2–*D4Mit11*–5.4 ± 2.4–*D4Bir23*–3.2 ± 1.8–*D4Bir24*–8.5 ± 2.9–(*D4Mit13, Pnd, D4Bir25, D4Mit14*)–1.1 ± 1.1–*D4Mit42*–6.4 ± 2.5–(*Dvl, Rnr4*)–telomere.
***Method of mapping:*** *Zfp15* was localized by haplotype analysis of 94 progeny from an interspecific backcross, (C57BL/6J × *M. spretus*)$F_1$ × C57BL/6J [1].
***Molecular reagents used for mapping:*** The *Zfp15* probe was obtained by polymerase chain reaction amplification of a 552-bp fragment from mouse pituitary cDNA with primers designed on the basis of the rat *Zfp15* cDNA sequence [2]. The primers amplify 465 bp of coding sequence, outside of the conserved zinc finger regions, corresponding to the last 154 amino acids, and 87 bp of the 3′ untranslated region. The RT-PCR product was cloned into the pGEM4Z vector and sequenced to confirm its correspondence with the rat *Zfp15* cDNA.
***Allele detection:*** A *Bgl*I polymorphism was detected in mouse genomic DNA with the *Zfp15* probe, resulting in an *M. spretus*-specific restriction fragment of 15 kb and a common restriction fragment of 24 kb. The mapping was confirmed with a *Bam*HI polymorphism, resulting in two *M. spretus*-specific restriction fragments of 8.9 and 6.6 kb and two common fragments of 18 and 5.5 kb.

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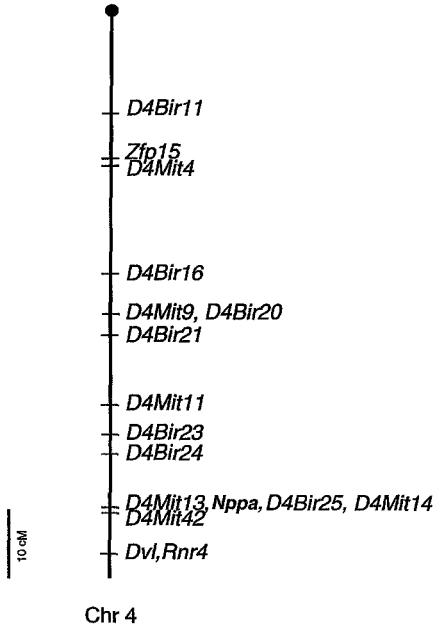


**Fig. 1.** *Zfp15* maps on mouse Chr 4 proximal to *D4Mit4*.

***Discussion:*** Zfp15, formerly called Zn-15, is a transcription factor that binds to a highly conserved DNA-binding site within the GH promoter between the proximal and distal Pit-1 binding sites. Its unique DNA-binding domain consists of three $CysX_{2-4}CysX_{11-16}HisX_{3-6}His$ zinc fingers in the context of 15 highly conserved zinc fingers. It has been shown that Zfp15 acts synergistically with Pit-1 to activate the GH promoter. In contrast to Pit-1, Zfp15 shows no tissue specificity; it has been found in many tissues including pituitary, spleen, and heart [2]. There are no endocrine defects known in the region of Chr 4 where *Zfp15* is localized.

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***References***

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# Localization of sequences related to the human RAD6 DNA repair gene on mouse Chromosomes 11 and 13

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***Species:*** Mouse
***Locus name:*** Ubiquitin conjugation enzyme E2B-related sequences 1 and 2
***Locus symbol:*** *Ube2b-rs1, Ube2b-rs2*
***Map position:*** *Ube2b-rs1* is localized on mouse Chromosome (Chr) 13: centromere–*D13Bir2*–8.7 ± 2.9–*D13Bir4*–3.2 ± 1.8–*D13Mit4*–11.8 ± 3.3–*D13Bir12*–2.1 ± 1.5–*D13Mit10*–5.3 ± 2.3–*D13Bir13*–3.2 ± 1.8–*D13Bir14*–7.4 ± 2.7–*D13Mit8*–1.1 ± 1.1–*D13Mit9*–4.4 ± 2.1–*D13Bir18*–5.5 ± 2.4–*D13Bir19*–9.9 ± 3.1–(*D13Mit31,* ***Ube2b-rs1***)–1.1 ± 1.1–*Rnr13*–telomere. *Ube2b-rs2* is localized on mouse Chr 11: centromere–*Erbb*–12.3 ± 3.7–(*Adra1, Pad1*)–3.2 ± 1.8–(*Csfgm, Sparc*)–1.0 ± 1.0–(*Myhs, D11Mit5*)–2.0 ± 1.4–(*Rpo2-1, Asgr1*)–5.6 ± 2.4–*Tcf2*–3.9 ± 2.2–***Ube2b-rs2***–15.9 ± 4.0–*Erba*–5.4 ± 2.4–*Gh*–telomere.
***Method of mapping:*** *Ube2b-rs1* was localized by haplotype analysis of 91 progeny from an interspecific backcross, (C57BL/6J × *M. spretus*)$F_1$ × C57BL/6J [1]. *Ube2b-rs2* was assigned by haplotype analysis of 96 progeny from an intraspecific backcross (DF/B-*dfldf* × CASA/Rk)$F_1$ × DF/B-*dfldf* [2].
***Molecular reagents used for mapping:*** The mouse brain cDNA clone, MBL 12-900, is homologous to the human RAD6B gene (HHR6B). A 900-kb *Eco*RI fragment containing the complete open reading frame was used for mapping. This is referred to as the Hhr6b probe [3].
***Allele detection:*** In mapping *Ube2b-rs1*, a *Bam*HI polymorphism was detected in mouse genomic DNA hybridized with the Hhr6b

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