Title: Developing informative microsatellite makers for non-model species using reference mapping against a model species' genome

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Supplementary materials:

Supplementary Figure S1

Supplementary Table S2

Supplementary Figure S1. Map Viewer results of *Mus musculus* (the upper part) and BLASTX results, which comparing *Apodemus semotus* DNA sequences against *M. musculus* protein sequences (the lower part). In the Map Viewer results, digits along the X-axis indicate the locations in the corresponding *M. musculus* chromosomes, horizontal green lines indicate introns and short, vertical green lines indicate exons. Gene names are shown next to the green lines. Purple lines indicate predicted or uncharacterized genes (labeled as "Gm", "LOC" or "Rik") or microRNA (labeled as "Mir"). Long, vertical red lines indicate the locations of the microstatellite loci, and the names of the loci are shown above the red lines. Rectangles indicate 10 kbp segments along *A. semotus* chromosomes anchored on the microstatellie loci. Empty rectangles indicate no BLASTX coding regions found in that 10 kbp segments, whereas blue or black ones (used alternatively for distinguishing different blasted genes) indicate positive BLASTX coding regions located in that 10 kbp segments with gene names shown next to them.

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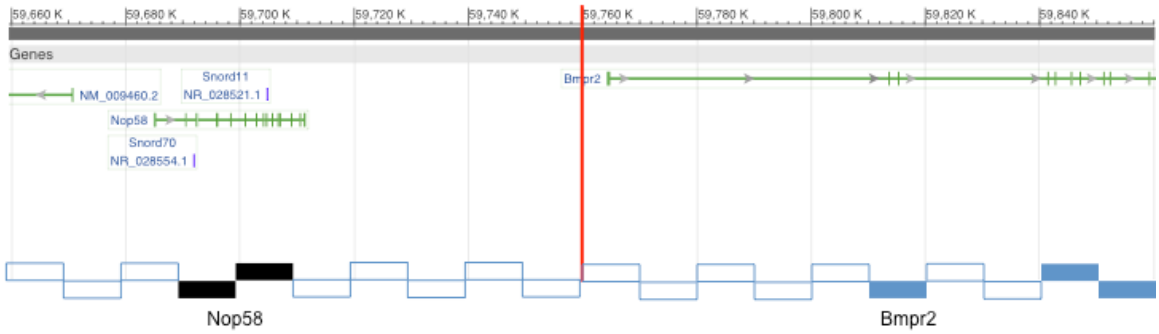

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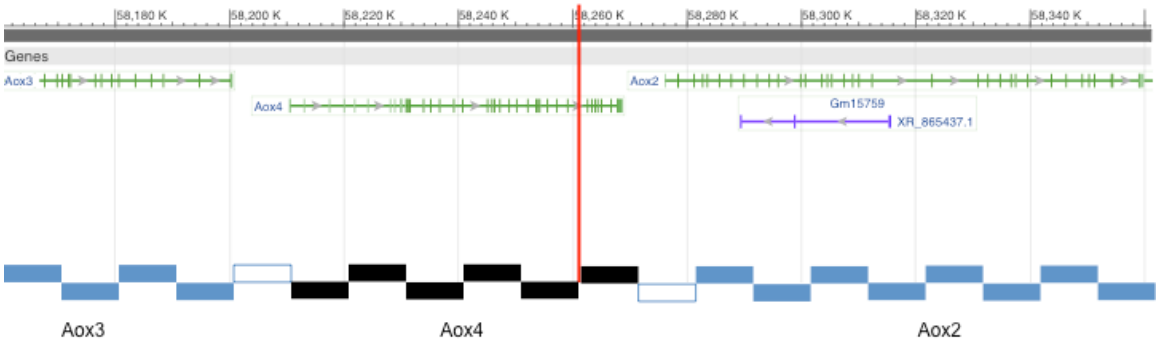

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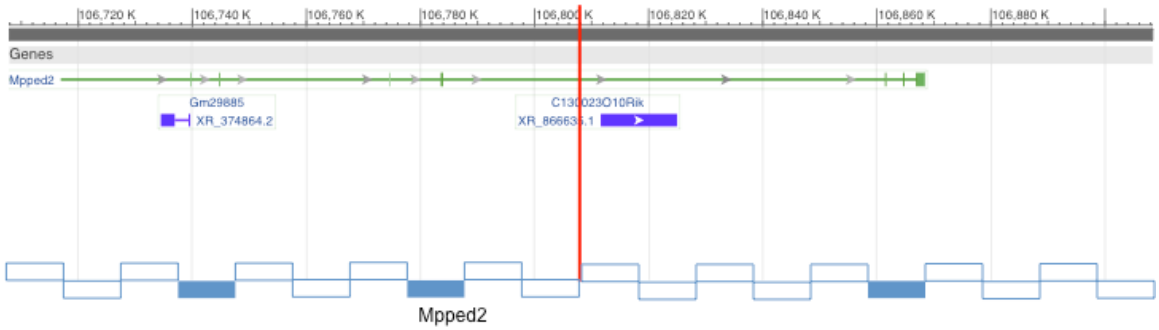

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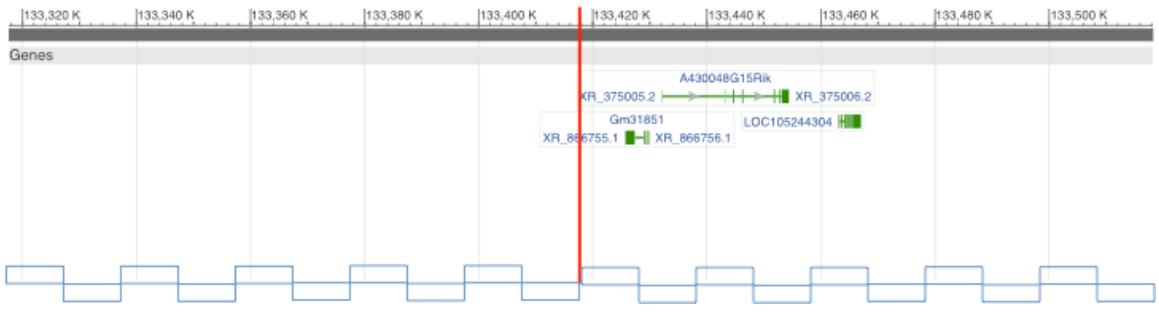

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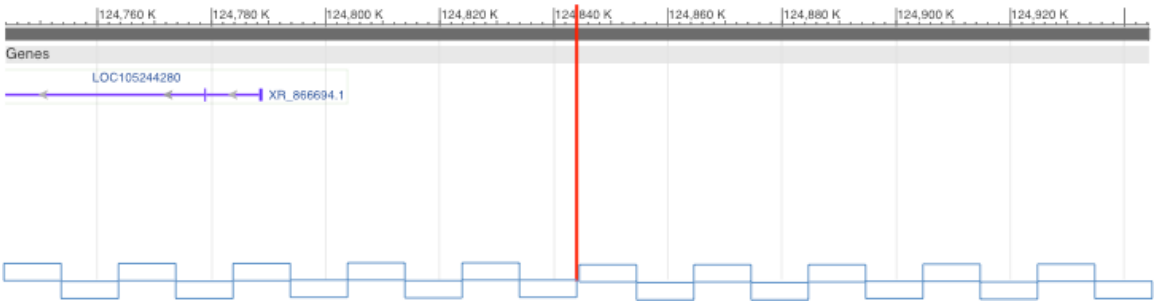

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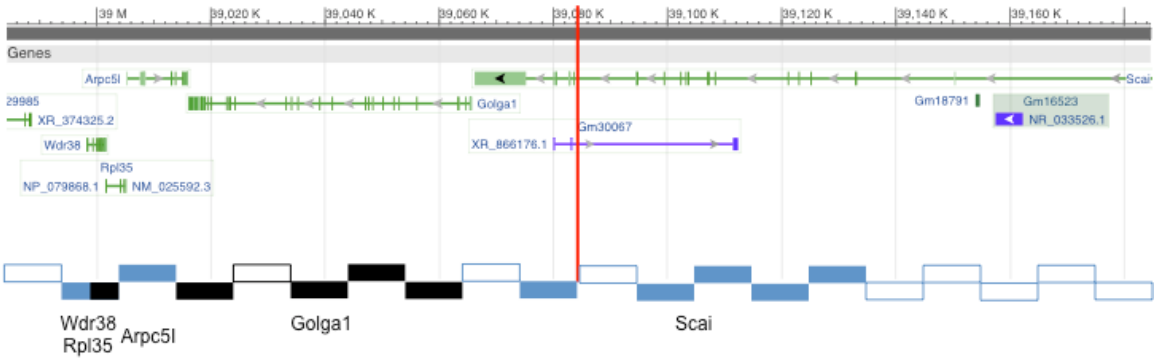

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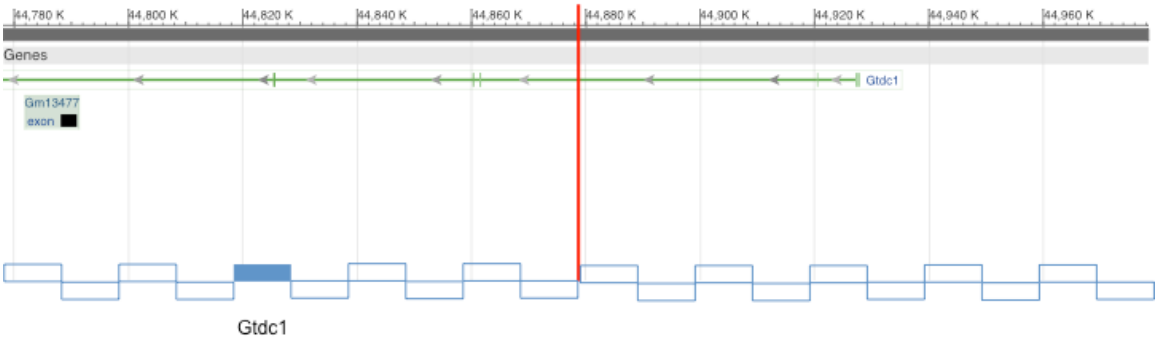

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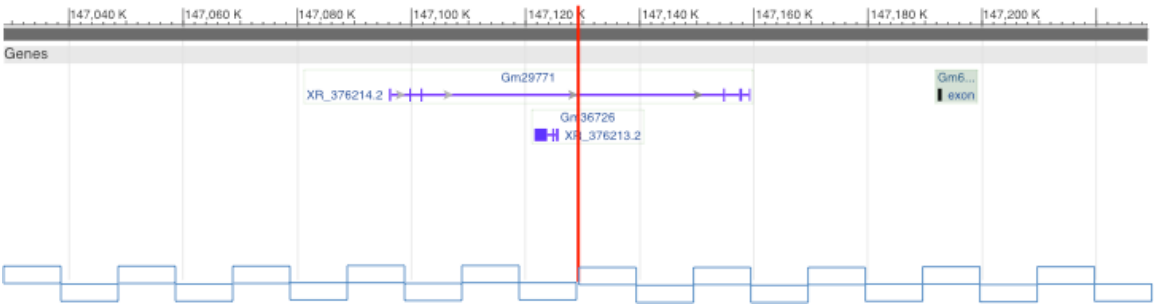

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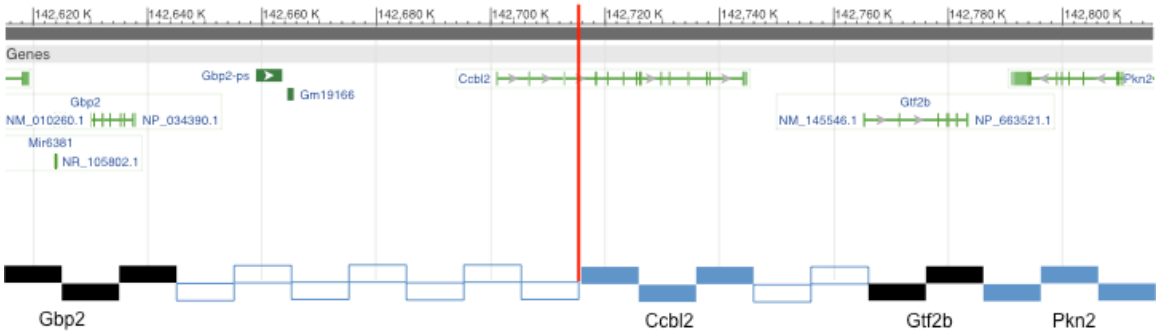

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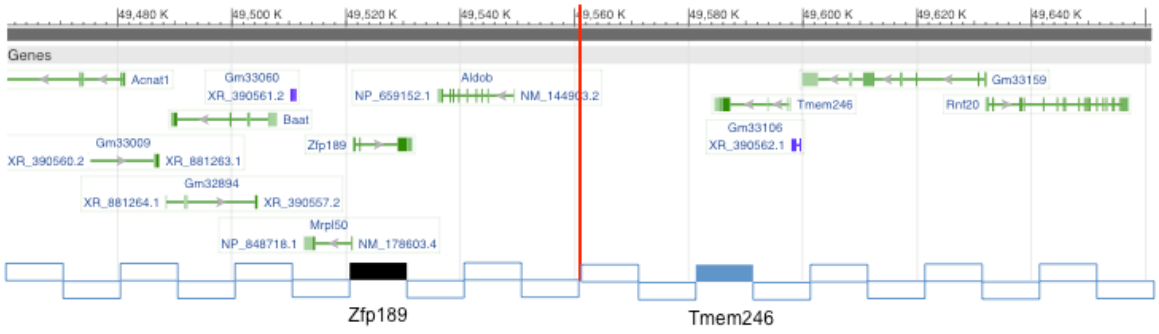

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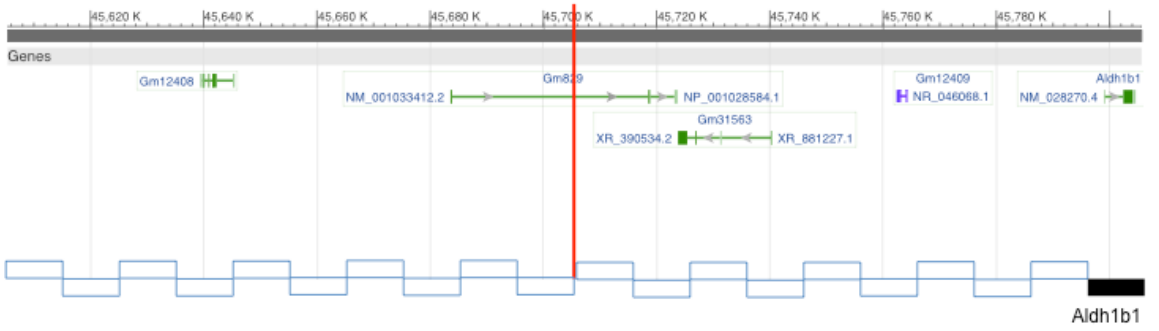

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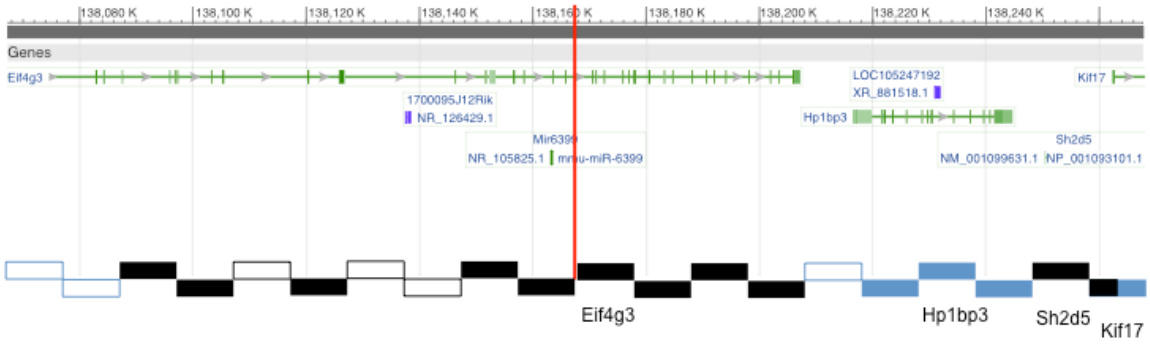

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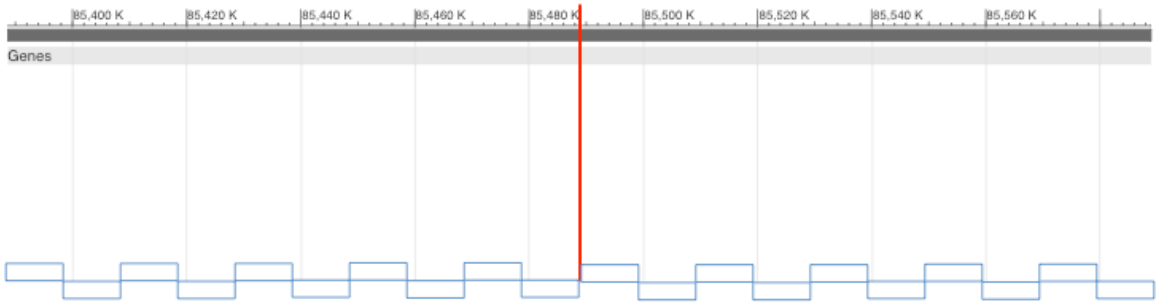

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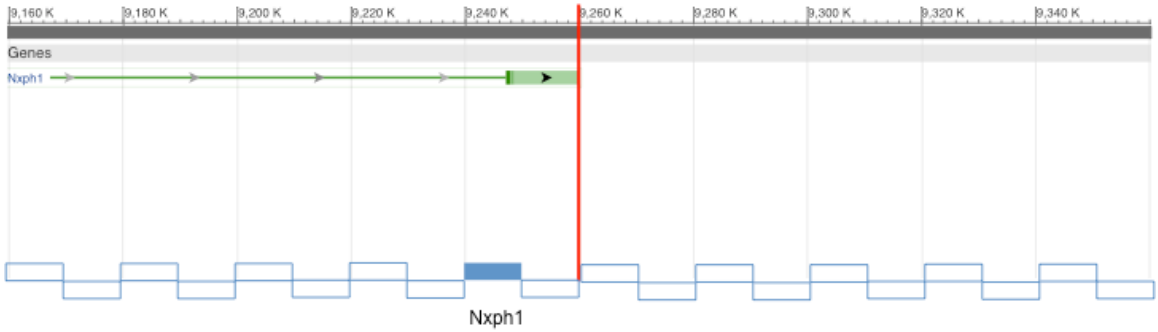

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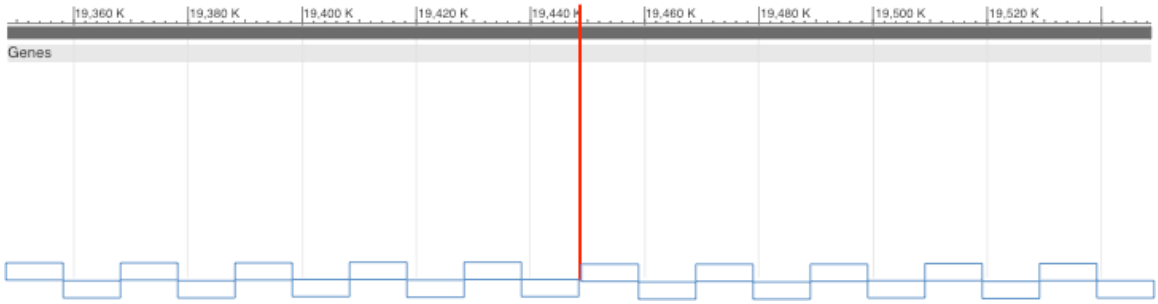

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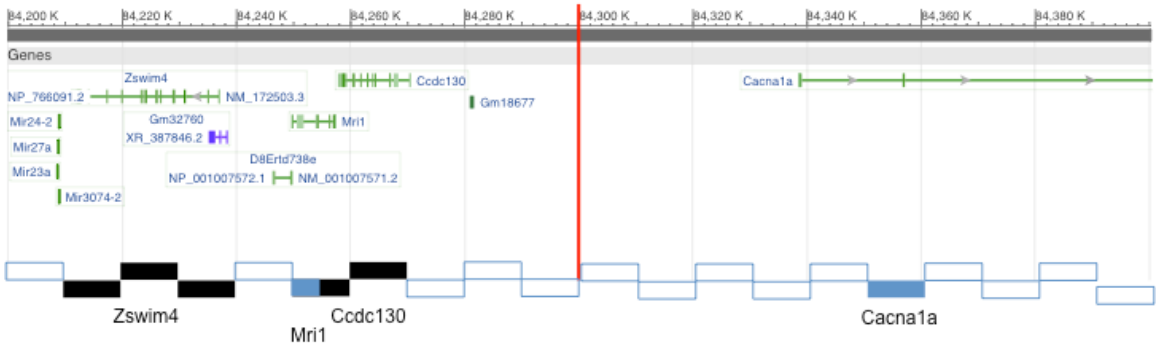

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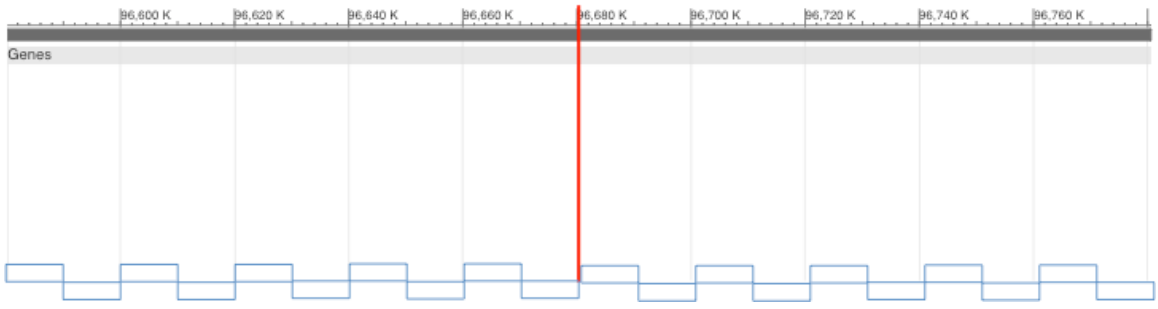

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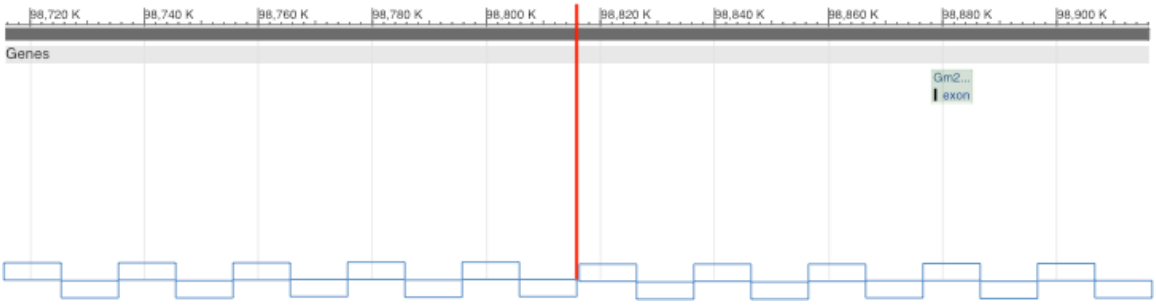

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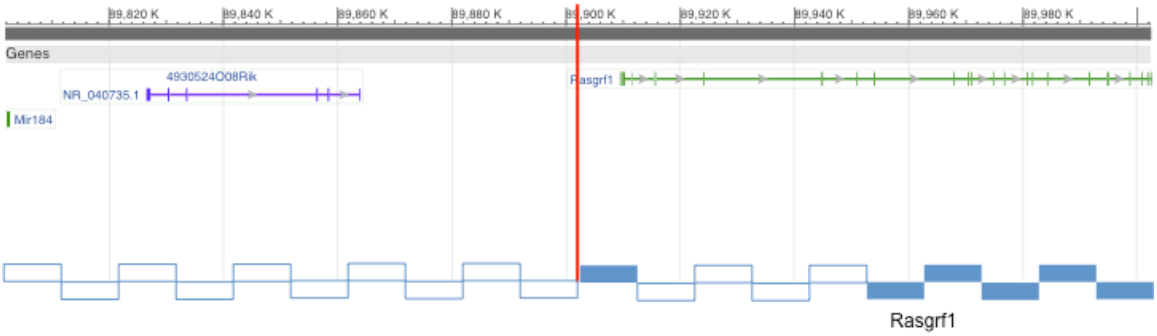

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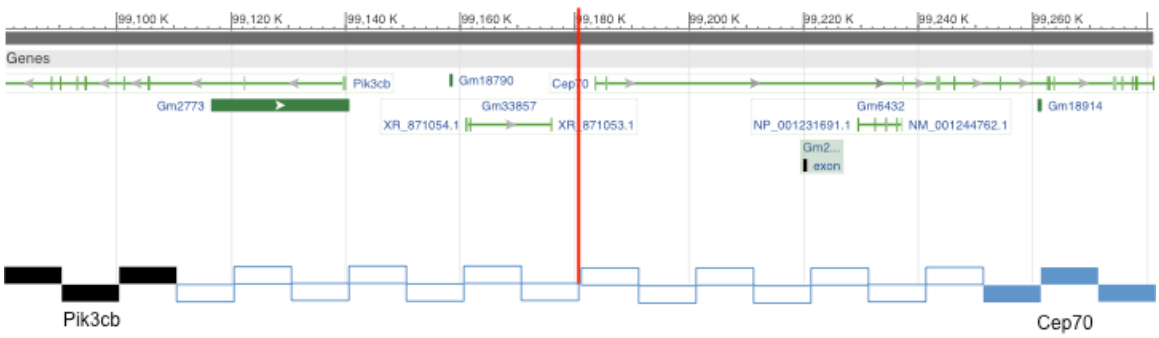

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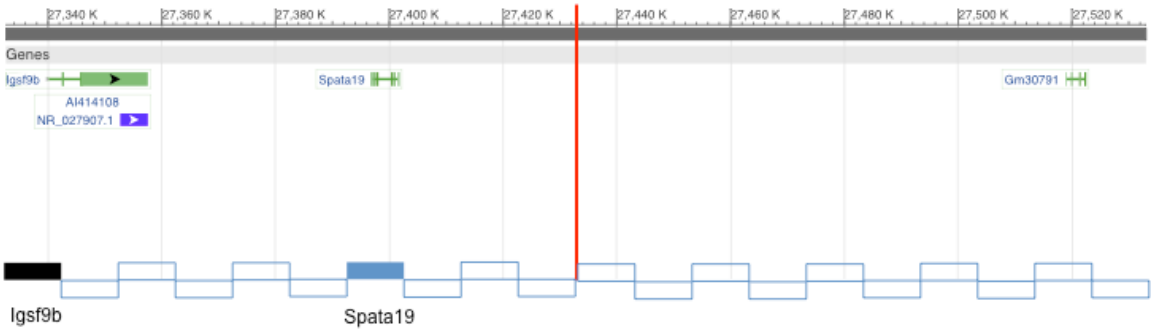

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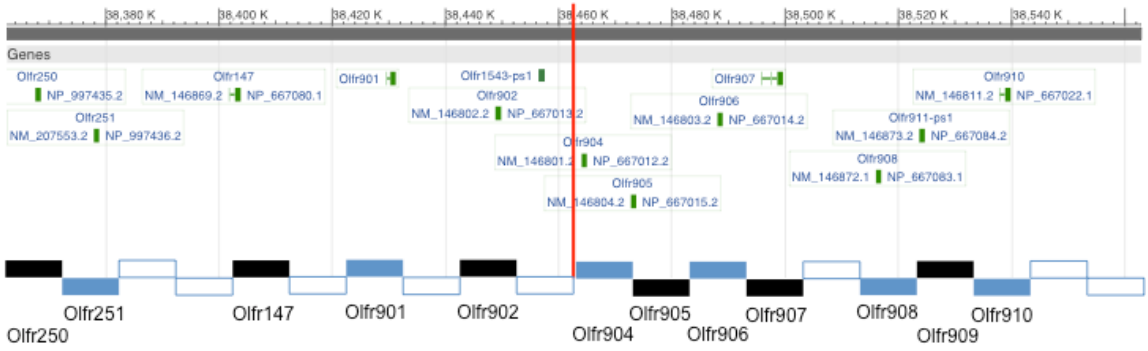

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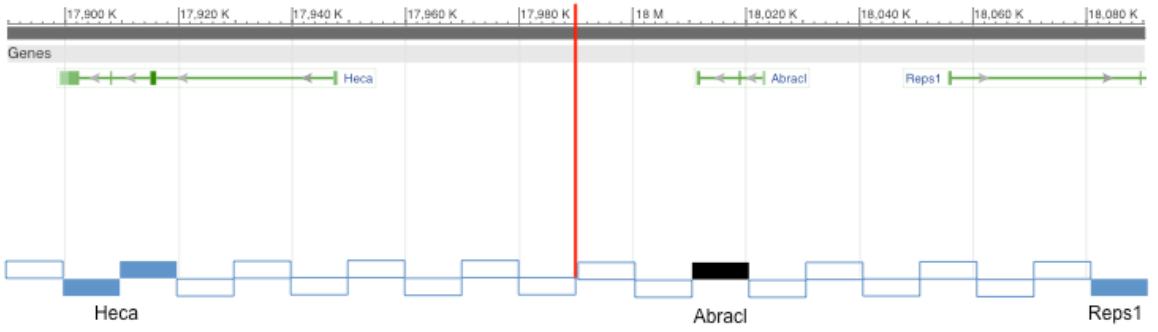

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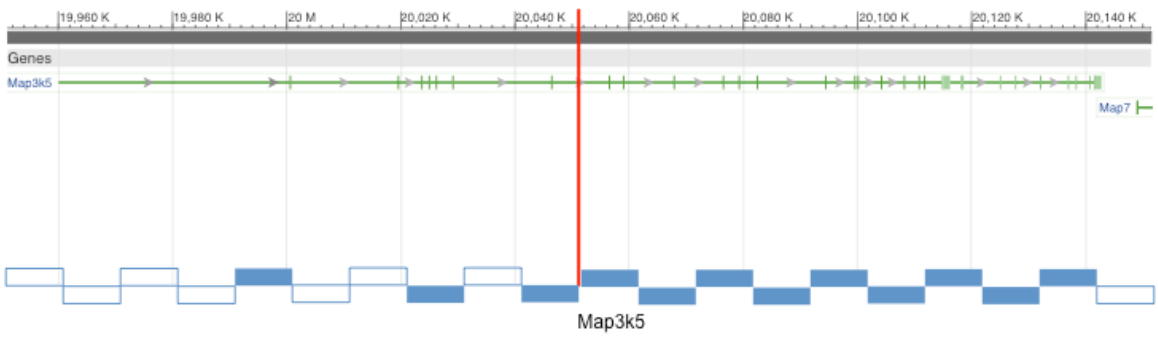

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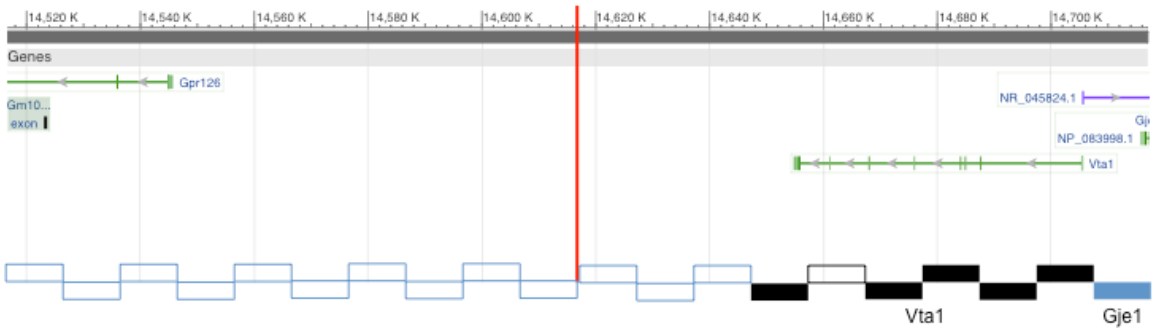

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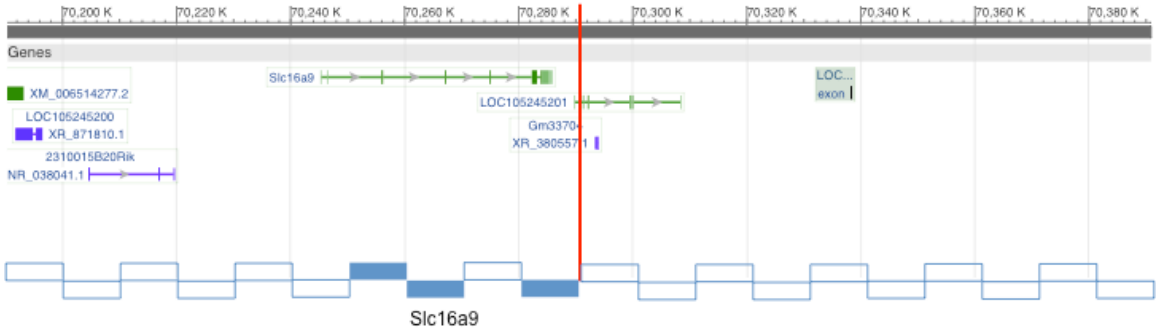

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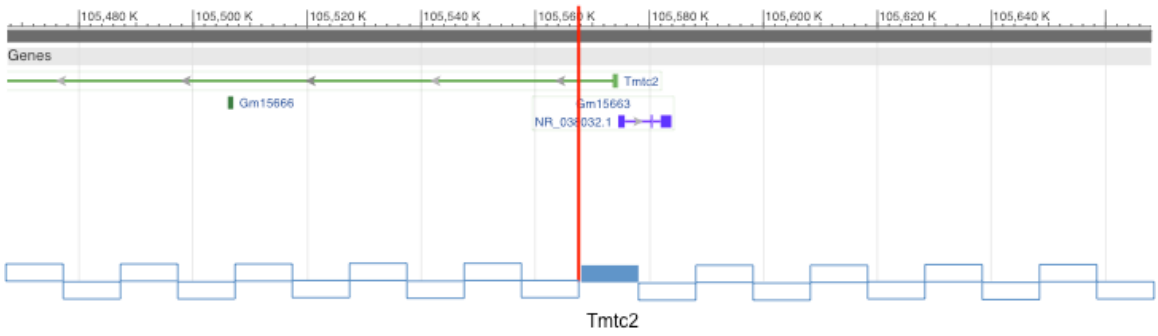

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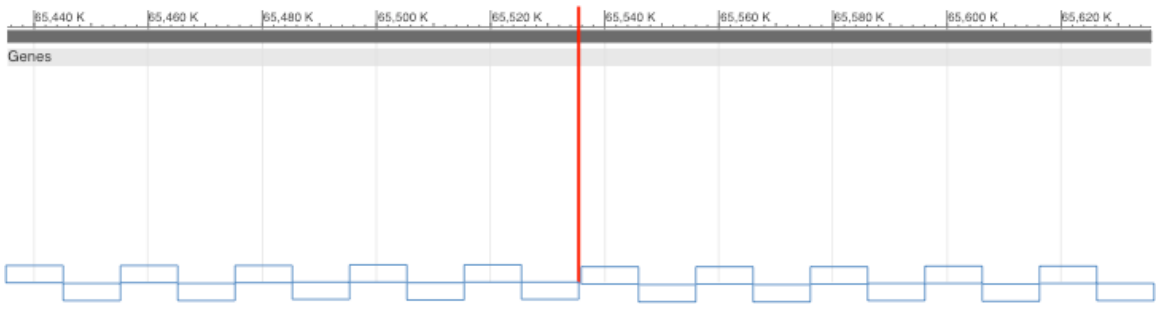

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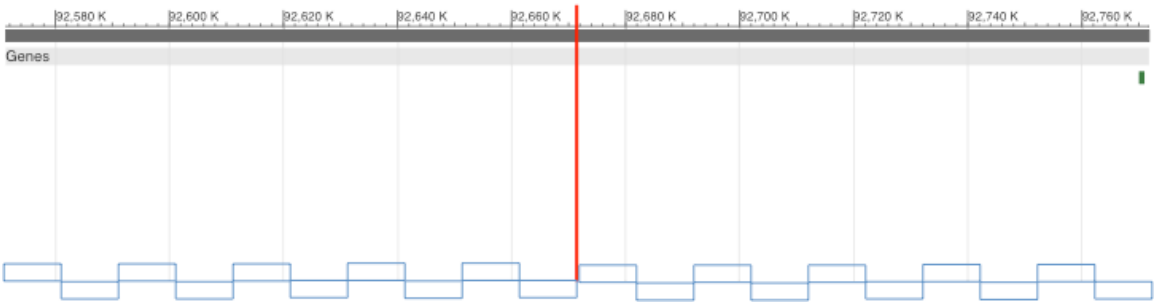

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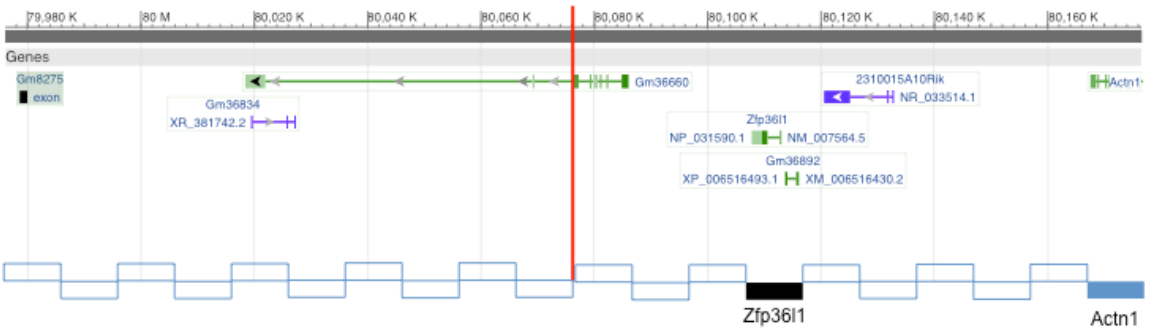

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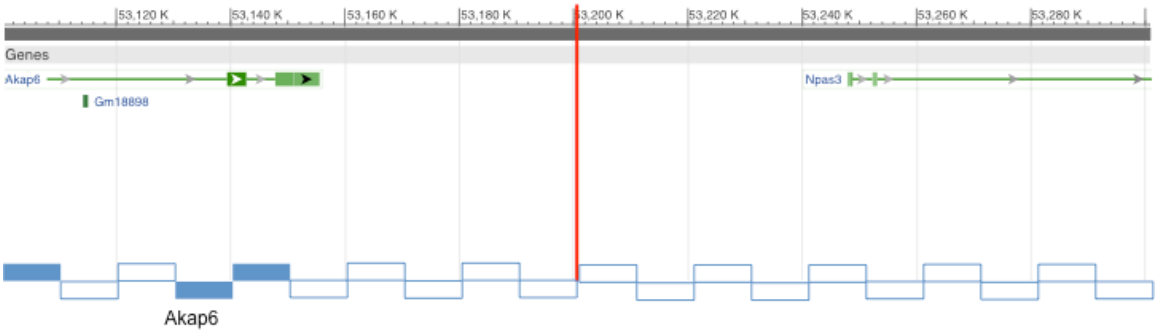

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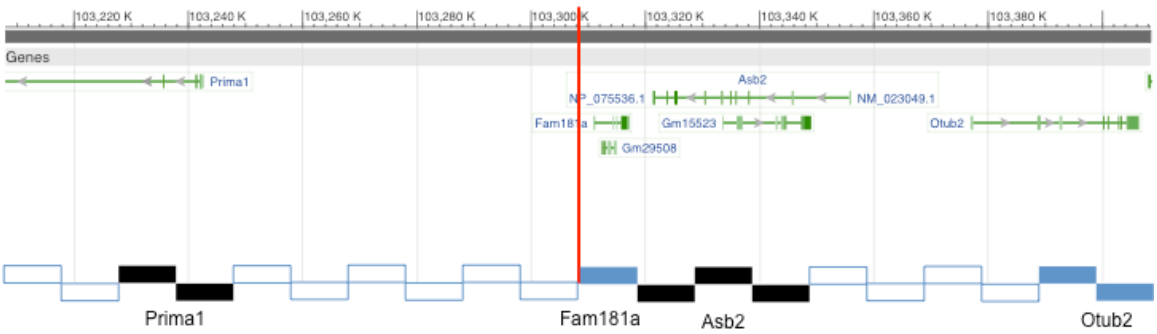

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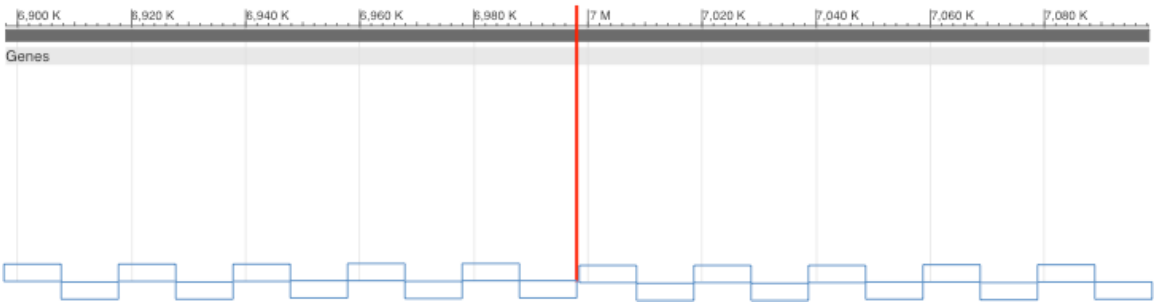

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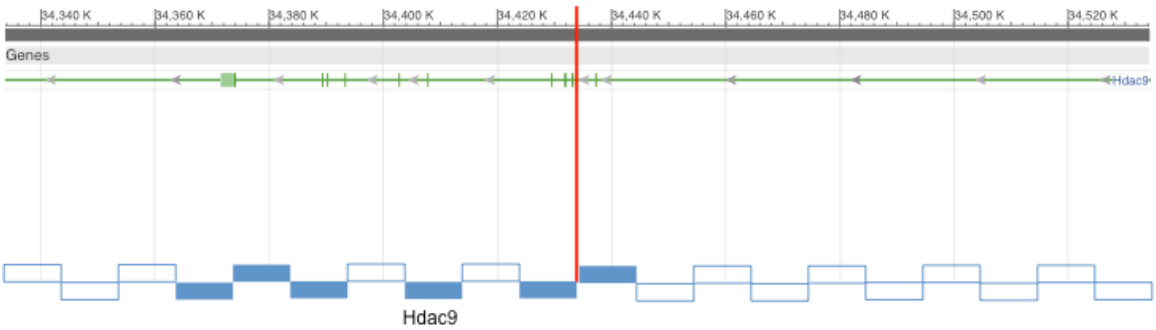

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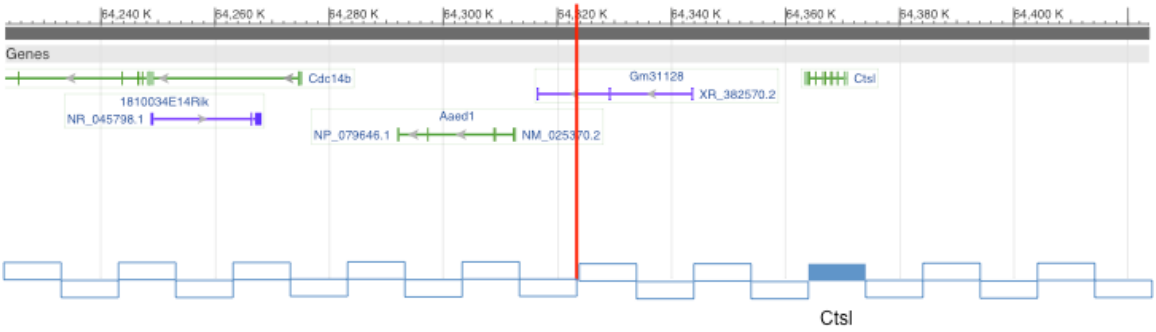

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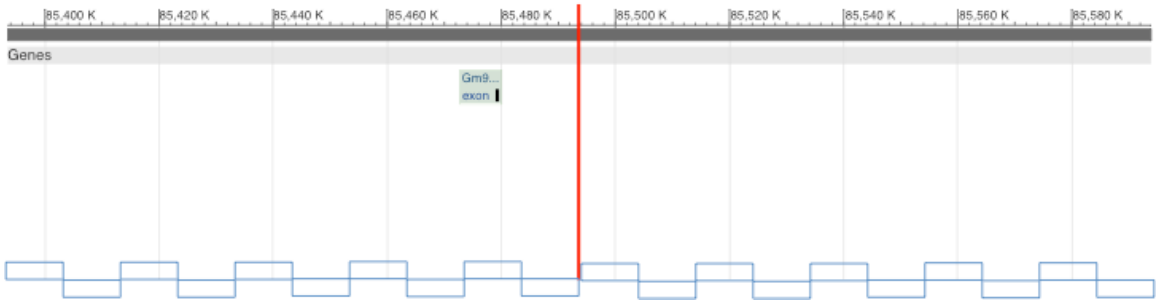

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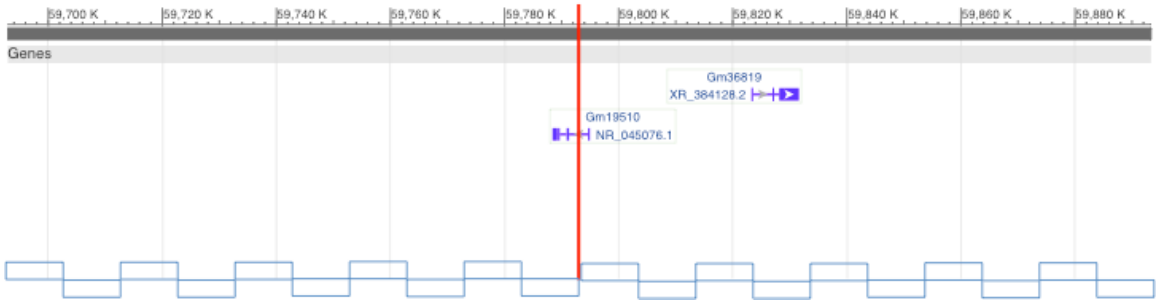

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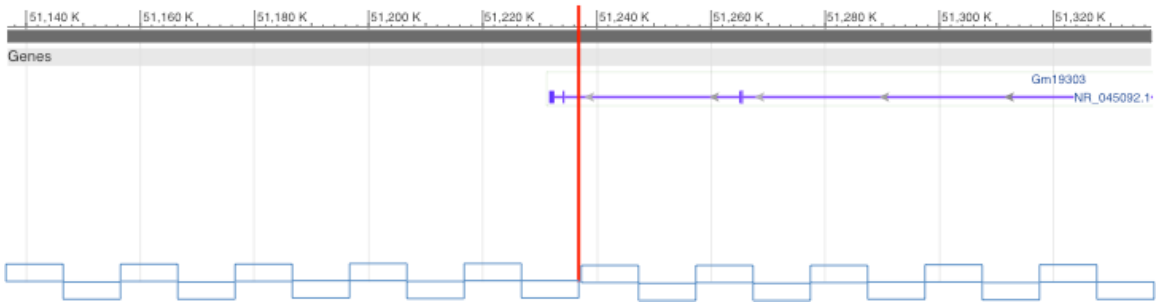

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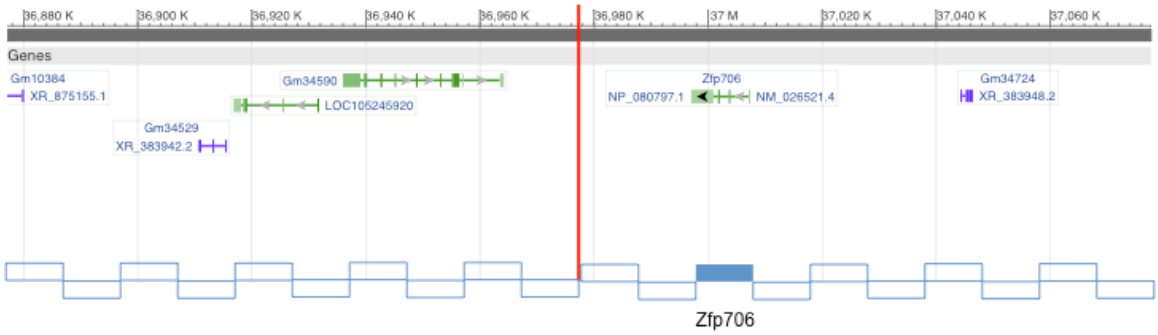

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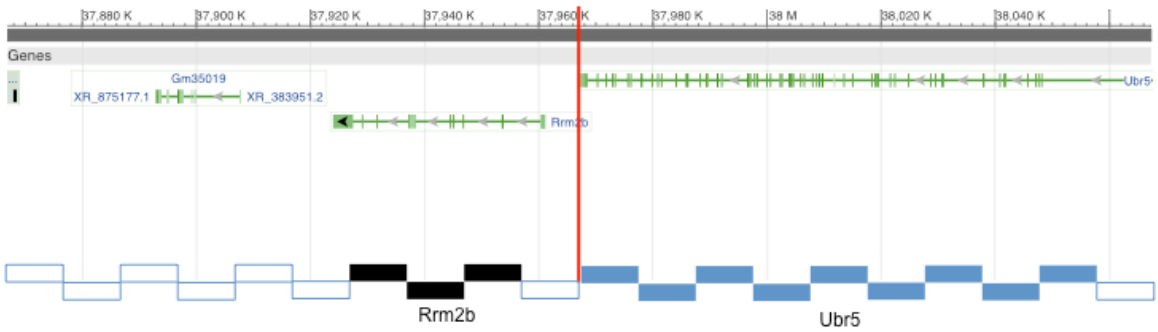

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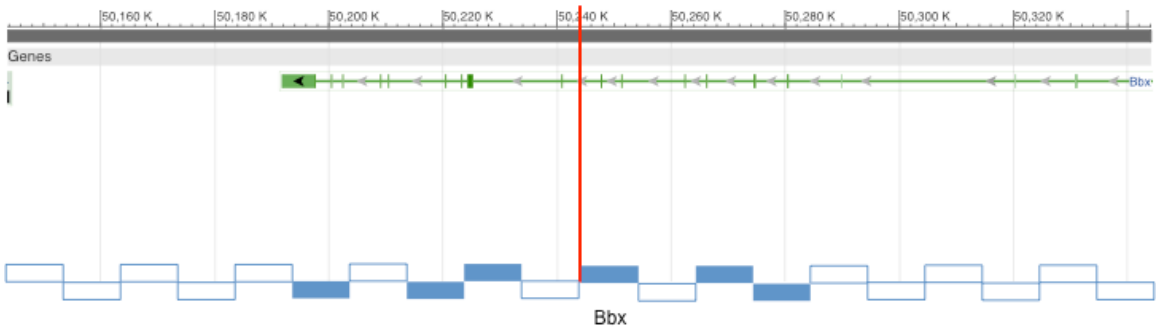

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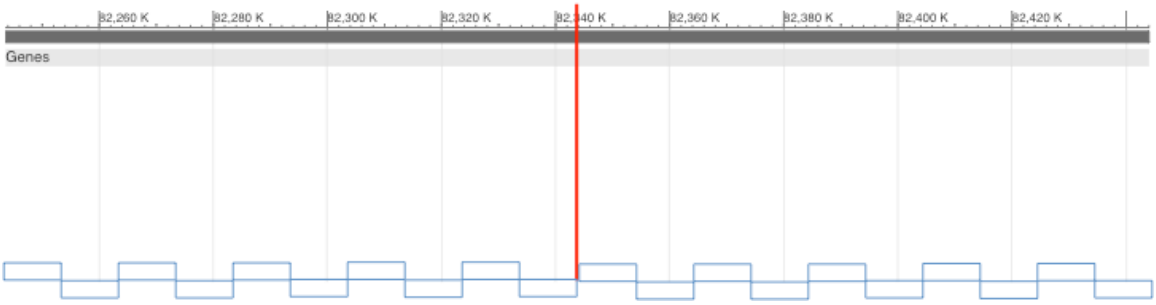

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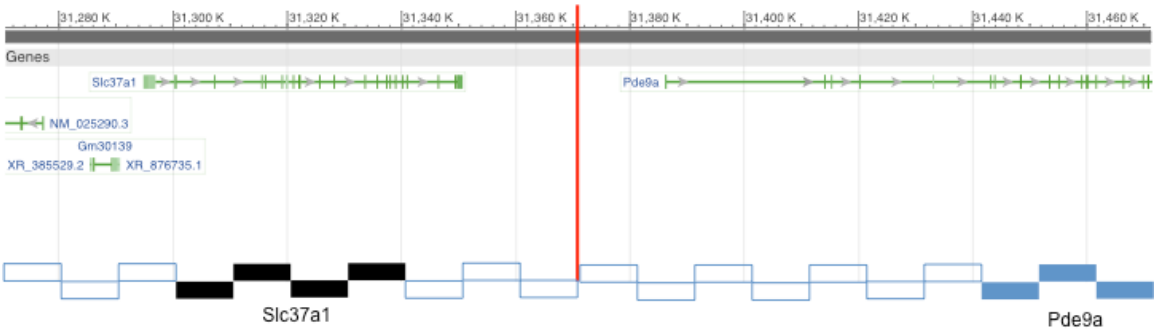

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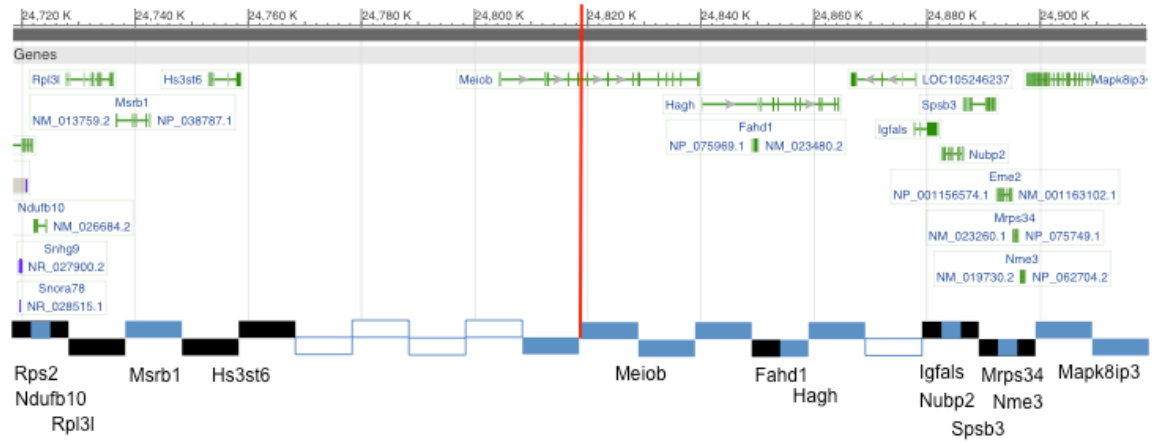

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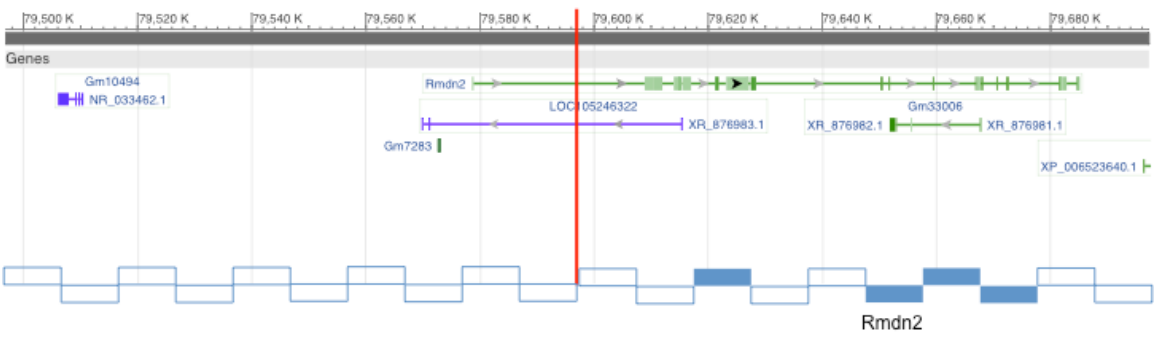

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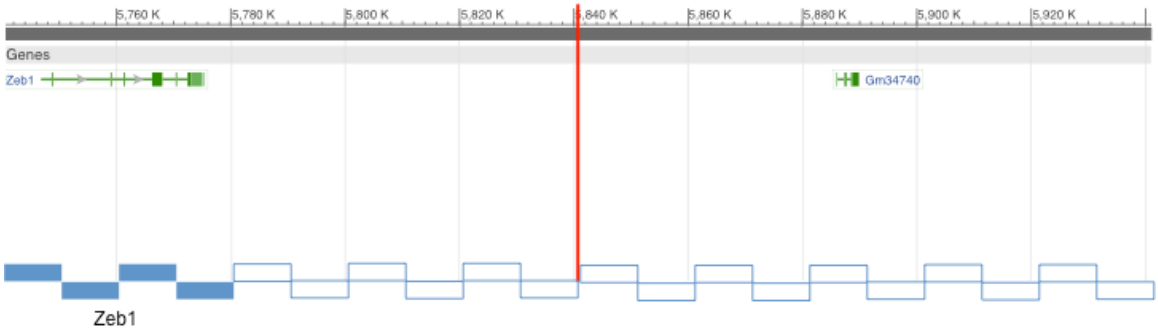

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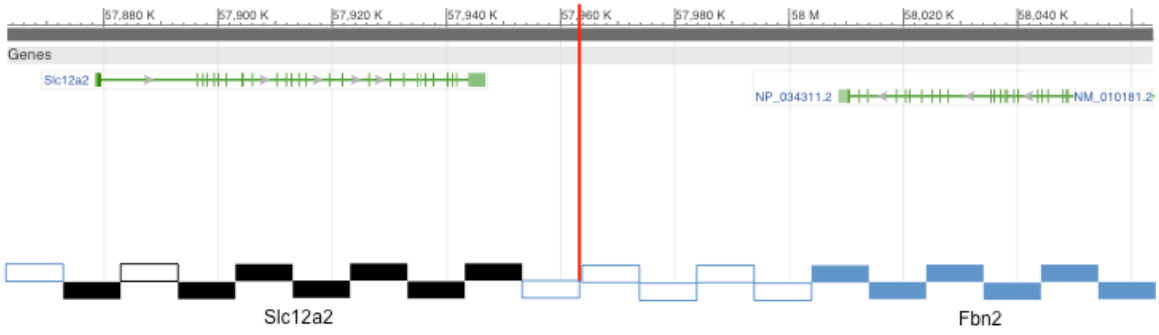

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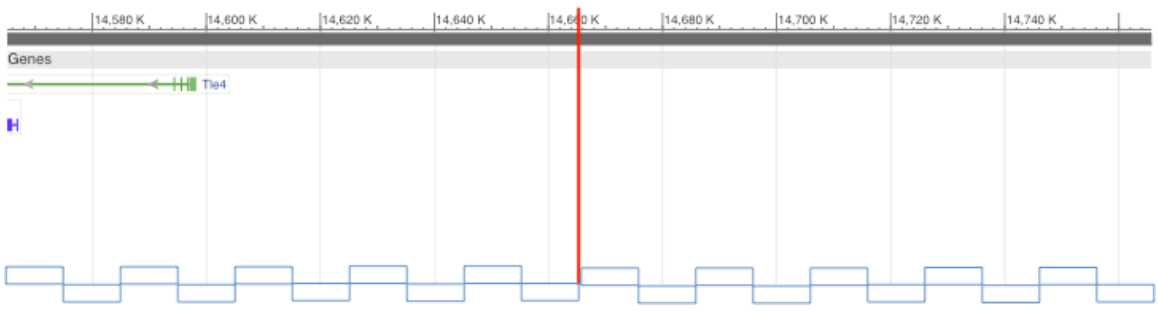

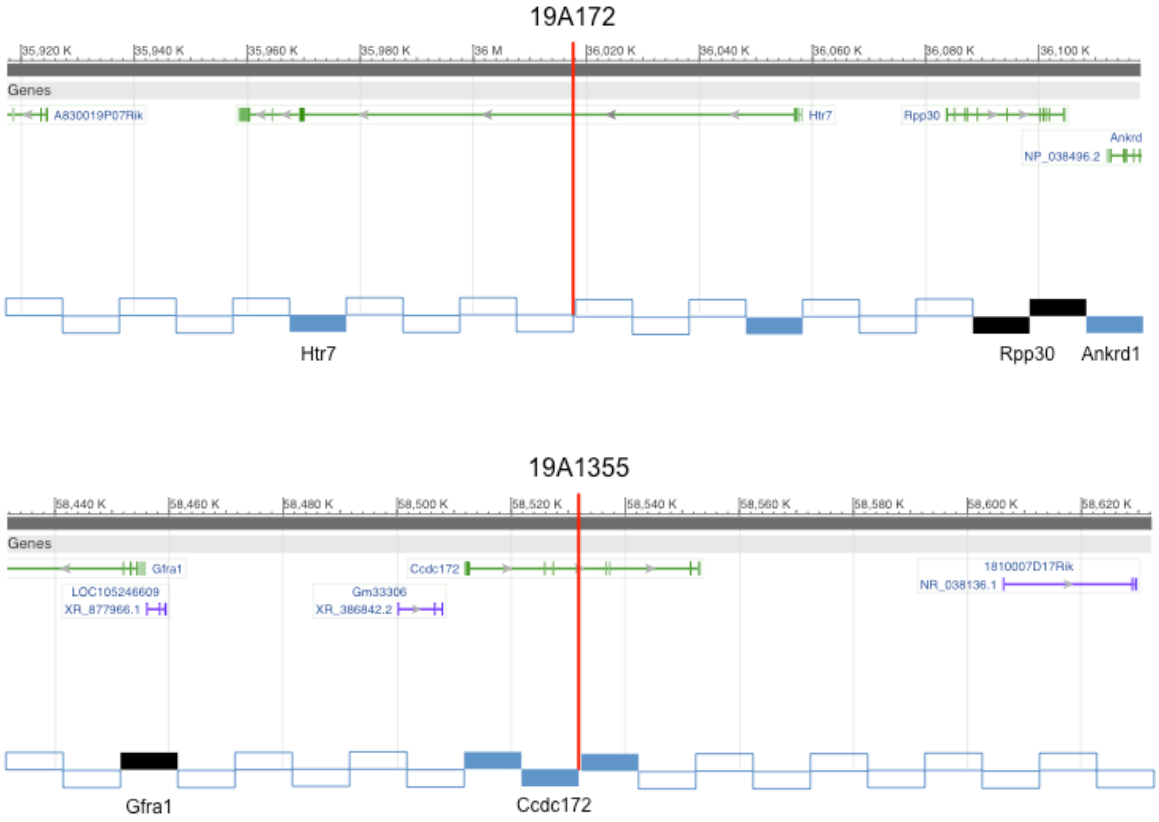

Supplementary Table 2. Laboratory cost, time and yield compared between the traditional approaches of microsatellite isolation based on cloning and Sanger sequence[36,37] and our approach based reference genome mapping.

	Traditional approaches (Cloning + Sanger sequencing)	Our approach (Shotgun sequencing + reference genome mapping)
Time for bench work	1 - 4 weeks	1 - 2 days
Cost (USD)	1,100 – 4,400	3,000
Yield (loci)	100	1,456
Cost / locus	11 - 44	2.1