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Novel deletion alleles of a *C. elegans* gene Y48E1C.1, named as *tm5468*, *tm5625* and *tm5626*

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Description:

We report *tm5468*, *tm5625* and *tm5626* as novel deletion alleles of the gene Y48E1C.1 that is the only ortholog of human calmodulin-lysine N-methyltransferase (CAMKMT)[1]. CAMKMT encodes an evolutionarily conserved enzyme class I protein methyltransferase that acts in the formation of trimethyllysine in calmodulin for calcium-dependent signaling[2]. CAMKMT mutation is associated with Hypotonia-cystinuria syndrome in human[2,3]. The alleles were isolated from the comprehensive screening of gene deletions generated by TMP/UV[4]. In the screening, all the alleles were detected by nested PCR using the following primer sets, 5'- TCAAGCCACGCCCACACTTA-3' and 5'-GAAGGCATACAGTGGGGGTA-3' for the first round PCR and 5'- CGCCCACACTTAATGGTTAT-3' and 5'-GGGCAGTGTAGGGATACTGT-3' for the second round PCR. By Sanger sequencing, the 30 bp flanking sequences of the alleles *tm5468*, *tm5625* and *tm5626* were identified as AATCCTTCACACACCACAACAGAAATCCTA - [384 bp deletion] -CGAGGTCACGCCCACACATTGGGCGGAGTT, CCGATGCTCCGTGCTGCTCCAAGTGCTCCG - [627 bp deletion + 9 bp insertion (TAATCTTGT)] - AGTACTCCTACAGTATCCCTACACTGCCCC, and AAAAAAGGATGACGTCACAGTTGCTCCGAT - [256 bp deletion] - ACGCCGATTCGGCAGCCGAATGATCTACAG, respectively. Based on the information about the splicing isoforms of *Y48E1C.1* (WormBase, http://www.wormbase.org, WS259), the forth exon of *Y48E1C.1a*, *Y48E1C.1b* (annotated as non cording RNA) and the second exon of *Y48E1C.1d* transcripts are deleted in *tm5468*, *tm5625* and *tm5626* (Fig. 1). Presumably, all of the alleles do not affect *Y48E1C.1c*. According to information of protein in Wormbase, this exon contains a predicted some motif, suggesting hypothetical functional deficiency of *Y48E1C.1a Y48E1C.1b*, and *Y48E1C.1d* in the deletion mutants. In addition, these alleles are expected to be usable for comparing functions among the isoform c and the other isoforms. However, no visually obvious phenotypes (Let, Unc, and Dpy) were observed in *tm5468*, *tm5625* and *tm5626*.

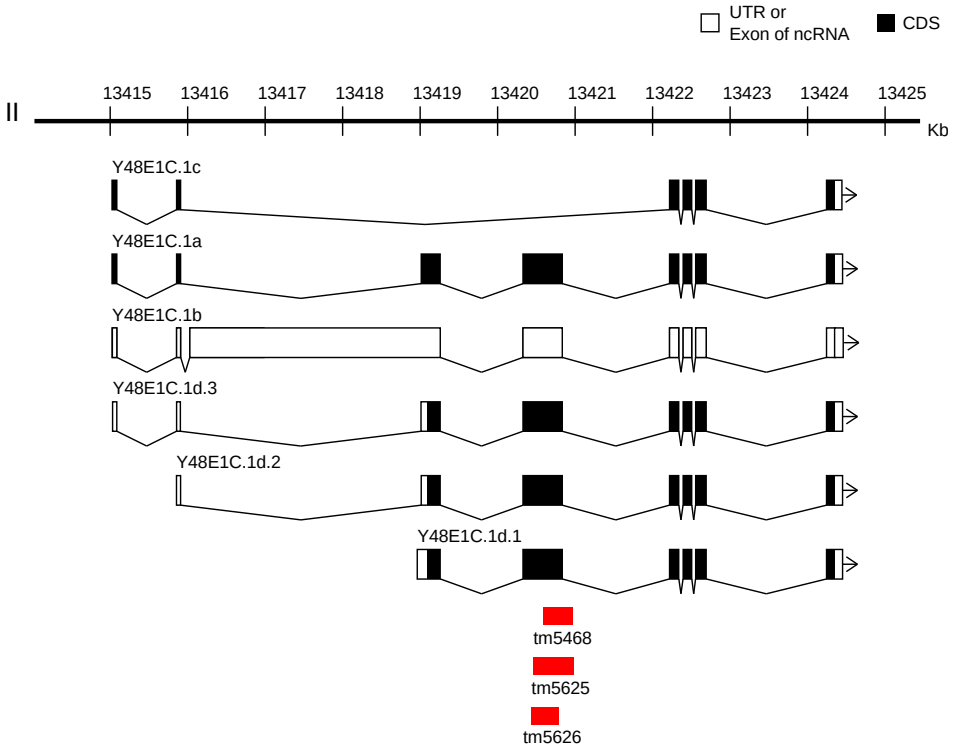

Fig. 1 Location of the novel alleles

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Reagents

FX05468 *Y48E1C.1 (tm5468)* II (Not outcrossed)
FX05625 *Y48E1C.1 (tm5625)* II (Not outcrossed)
FX05626 *Y48E1C.1 (tm5626)* II (Not outcrossed)

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