

(A) 565-635 bp in *CpMYC2a* coding sequence

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                                10         20         30         40         50         60         70
MW775565      GCCCCATCCATATCTGCACTCGAGCTCATTTGGCCAAGATGGCCGG--CATTAGACAATTGTTTGTGTTCC
GWHTAMMO011051 GCCCCATCCATATCTGCACTCGAGCTCATTTGGCCAAGGTTTTCTTGTCCTCGAGACAATTGTTTGTGTTCC
Clustal Consensus *****.*      *      *.*****

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(B) 555-624 bp in *CpMYC2b* coding sequence containing 352 bp intron

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          10          20          30          40          50          60          70          80
MW775566      GCTAGAACAAGCCGACAAGGCCTCTAATCAAGTCTGCACACGAGCTAATTTAGCGAAG-----
GWH TAMMO007338 GCTAGAACAAGCCGACAAGGCCTCTAATCAAGTCTGCACACGAGCTAATTTAGCGAAG-----
Genome sequence GCTAGAACAAGCCGACAAGGCCTCTAATCAAGTCTGCACACGAGCTAATTTAGCGAAGGTGAGATTCATGGATTACTCT
Clustal Consensus *****

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[illegible]

		170 180 190 200 210 220 230 240
MW775566	-----	
GWH TAMMO007338	-----	
Genome sequence	TGAAACATTACATTGTTCCTTTGAAGCCCGTGCTGAGT GAGTAGAGTAACGCATTCACATGTTTAGATTTTCTTTAGT	
Clustal Consensus		

MW775566
GWH TAMMO007338
Genome sequence
Clustal Consensus

TTATGGTGGATTATGCAGATTATTTCTCTGATAGGAGTTTTAAAGGATTGGAGATTGTGATTTTTGGTCGTAACGGTATGGG

3'-End of annotated intron

[illegible]

Putative branchpoint

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                                410          420
                                ....|....|....|....|....
MW775566                      -----ATGGCCGGAATT
GWHTAMMO007338                CCCAAGAACAGATGGCCGGAATT
Genome sequence                CCCAAGAACAGATGGCCGGAATT
Clustal Consensus              *****

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3'-End of actual intron

Supplementary Figure 4. Differences between cloned CpMYC2s sequences and annotated sequences in the genome database.

(A) Differences between cloned *CpMYC2a* and annotated sequences in the genome database. MW775565 is cloned sequence in this study. GWHTAMMO011051 is annotated transcript sequence.

(B) Differences between cloned *CpMYC2b* and annotated sequences in the genome database. MW775566 is cloned sequence in this study. GWHTAMMO007338 is annotated transcript sequence. Consensus

sequences of 3'-end of intron (5' -AG- 3') are highlighted by black. Putative branchpoint is indicated by a box. Nucleotide sequences were aligned by CLUSTALW in GenomeNet

(<https://www.genome.jp/tools-bin/clustalw>). Sequence alignments were drawn using BioEdit software version 7.2.5.respectively.