

Drosophila melanogaster chromosome 2L, complete sequence

NCBI Reference Sequence: NT_033779.4

[GenBank Graphics](#)

>gi|116010444:4955509-4958292 Drosophila melanogaster chromosome 2L, complete sequence

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GAAAATCAAA AACGTCTGCA ACAGGTGCGA GCCAACATGC GAATAATGGA AAATCAAATC
CCAATCAACC GCAGGCCAAA TCCCCATTGA ATTTCTACCG ATCACCGACG GGGGAGCAGA
AGAAGATCAA CAGGAGCGGT CCCACGCCCG GTGACAACAA GAGCTCATCC TTTCTGAACG
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ACCAGCGGCC AAATGGAGGG AACGAAAGAA ACAAGCCCAC TCTTTCCTG AGTTCGGATA
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CGAAAGTGGA GGTGCTGCCT CAACTCGCTG AGAAGAACC GGTGGTGTGTT CACATTGTTG
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TCAACTATTC CAGCTAAAGA GCCGCCTGAG CAAAATAATA ATACAGAAAT GACCAAAGTA
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Drosophila melanogaster Marcal1 (Marcal1), mRNA

NCBI Reference Sequence: NM_135039.1

>gi|24581779|ref|NM_135039.1| Drosophila melanogaster Marcal1 (Marcal1), mRNA

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CAGCATGTCC ACTTGCAGTT CATCCGAGAT AGCGGAGAAG AAGCGCATTG CGCTGGCCAA
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GCAGGCCAAA TCCCATTGA ATTTCTACCG ATCACCACG GGGGAGCAGA AGAAGATCAA
CAGGAGCGGT CCCACGCCCG GTGACAACAA GAGCTCATCC TTTCTGAACG CTCTGAAAGC
AATCAAACAG ACATCCAACC GGAATTGTG CCGCGGAGCA GCACATCCTT ACCAGCGGCC
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GGTGGCTGTG CTA CTACTCGGAA ACTCCATCAC GTGTAATCTC TACTTGATCA GCACACATCG
GTTTGCTGCC CAAACCTCAG GATATCACGA ACAGCTCGTG ACCGTGTTCA AGAACATGCC
CACCAAGTGC TACGATGGCC AAACCCGTAT CTGGAGTTTC GATCTGTCGG ACTACCAATC
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CCTTGAACCG GAAAGGAATA GCATAAAACA ATATTTTTTCA ACTATTCCAG CTAAAGAGCC
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T
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EXON

INTRON

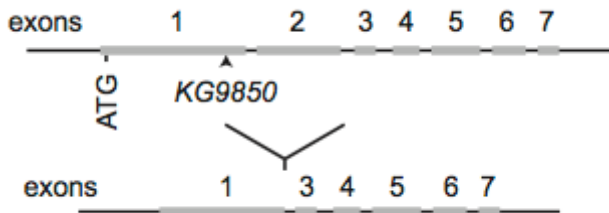
5' or 3' UTR

DELETED

INSERTED: ATGATGAAATAACATCATTATATCGATTAACACAG

**NM_135039.1: c.673_1258delinsATGATGAAATAACATCATTATATCGATTAACACAG
p.G225MfsX3**

The loss-of-function mutant was obtained by imprecise P element excision (67); this deleted **679 bp** nucleotides extending from the middle of the first exon into the second intron.



586 bp **deletion** of coding DNA (i.e., residues 673 to 1258)
35 bp **insertion** (i.e., ATGATGAAATAACATCATTATATCGATTAACACAG) in that region

679 bp **deletion** of genomic DNA
35 bp **insertion** of genomic DNA

Wild type

M S T C S S S E I A E K K R I A L A K L Q A K K S Q L L A S
A P A T N G K S T T S A T G A T Q H A N N G K S N P N Q P Q
A K S P L N F Y R S P T G E Q K K I N R S G P T P G D N K S
S S F L N A L K A I K Q T S N R E L S R G A A H P Y Q R P N
G G N E R N K P T L S L S S D K E K P V A V L L G N S I T C
N L Y L I S T H R F A A Q T S G Y H E Q L V T V F K N M P T
K C Y D G Q T R I W S F D L S D Y Q S L K T H A A D L K P Y
V H M N G I P K K V L D L C **G** Q P P V V P E R S V L A etc.

Marcal1^{del}

M S T C S S S E I A E K K R I A L A K L Q A K K S Q L L A S
A P A T N G K S T T S A T G A T Q H A N N G K S N P N Q P Q
A K S P L N F Y R S P T G E Q K K I N R S G P T P G D N K S
S S F L N A L K A I K Q T S N R E L S R G A A H P Y Q R P N
G G N E R N K P T L S L S S D K E K P V A V L L G N S I T C
N L Y L I S T H R F A A Q T S G Y H E Q L V T V F K N M P T
K C Y D G Q T R I W S F D L S D Y Q S L K T H A A D L K P Y
V H M N G I P K K V L D L C **M M K Stop**

Coordinates of the deletion in Release 5 genome coordinates

Coordinates in the *Drosophila melanogaster* Genome

http://petrov.stanford.edu/cgi-bin/Dmel_Coordinates_FBr4_FBr5.pdf

FlyBase release 4.3

<http://rice.bio.indiana.edu:7082/>

A Tool for Coordinates Conversion

http://flybase.org/static_pages/downloads/COORD.html

- Go to BLAST on FlyBase release 4.3 to get initial coordinates for conversion

- BLAST the deletion

- Go to the highest hit

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species=dmel
      Length = 22407834
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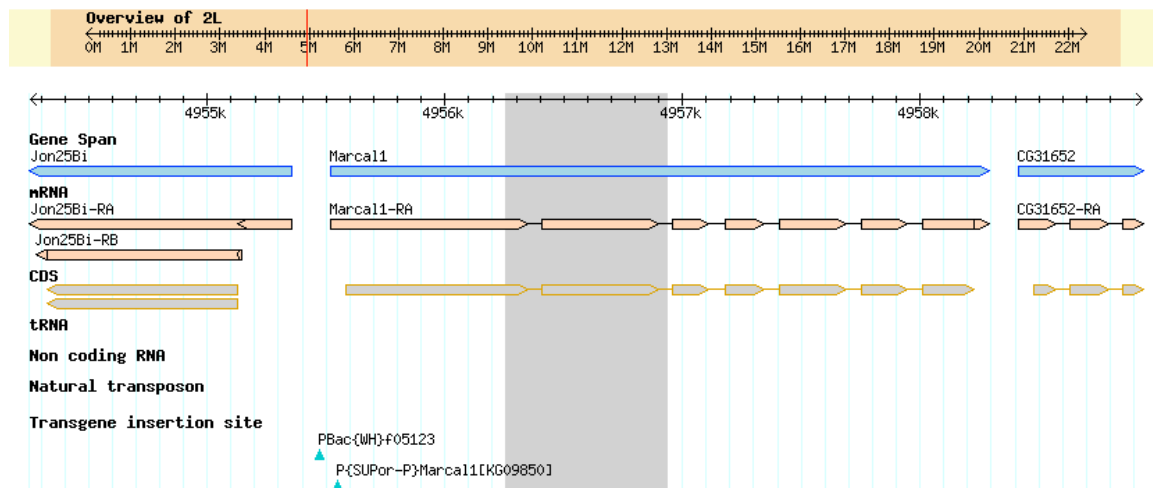
Score = 1346 bits (679), Expect = 0.0 [BLAST HIT on Genome Map](#)

Identities = 679/679 (100%)

Strand = Plus / Plus

- Click on 'BLAST HIT on Genome Map'

- Go to Landmark or Region for Coordinates (e.g., 2L:4956255..4956933)



- Enter FlyBase release 4.3 coordinates in the Coordinate Conversion tool

(Species: *D. melanogaster*, Input Assembly: 4, Output Assembly: 5)

- Note the FlyBase release 5 coordinates (e.g., 2L:4956255..4956933)