

Motif(s) : Mot_1, Mot_2, Mot_3, Mot_4, Mot_5, Mot_6, Mot_7, Mot_8, Mot_9, Mot_10

>DroMel seq1357_2R_18937351_18937843 2R 18937351 18937843

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1   CAAAGGACAC GGACACGCAT CCTGGCATTG TTTTCAATTC ATTTACGCGT CGACTCAAGT
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61  CGCTCGCCCA CACATATGTT GGGAAAATAA TCGAAAAACG GTTGTCCCT TGGCATGAGG
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121 TCCTTTTTGC TGCGCAGCTA GATTGCACT CCCTTGGCGC ATAGCACATG CCATTGATTA
                               9.2                               10.0
181 CCATGTGTGG GAATTAGCCT TCGGAAAAAA GAAGTTAGTT AAAATCACAC ATAAAGAGGC

241 AATGCCAATG GCTGTAGGTC CCTGATCCTC CGTCCTGGCA GAGAGCTCAC ACGTCCTGCA
    7.7
301 GCGATCCTTC CACCCTCTGC ACGTTCTAAA TTTAGCCGCT GGATTTATGA CCCCTGTCAT
                               7.3
361 TTGAGCCGCT CTTCCAGTAC TTCTTAAAAA ACCCCTGGAA TTACATGCAG TCGAAGAAGG

421 AAGAGAGTGG AGGAGTCCAA TGAGTCGAAG GAGCCCAATG AGTCGAATGA GTCGGAGAGG
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481 GGGCGTTGAC AGT
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>DroMel seq1396_2R_19526211_19526451 2R 19526211 19526451

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121 ACCCTACACT CGTGCCCTGC CTATAAATAA AAAAGTTAAG ATCACAATTT TAAGGAGATC

181 TTTGTTATAA TATATTGATT AATTTATCTC GAAATACCTA CAATTCTTAT CCCCATTAGC

241 C
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>DroMel seq1397_2R_19526657_19527033 2R 19526657 19527033

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121 GAAACAAATG CGGATACACA TGCTCGCCGG CTCGTAATCT TAATCCTTCA CACAATAAAC
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421 ATGTACCCAA AGTTAAGCAG TAGCATTTAG TATTTATGTT TTCTGGATAT ATTAAGTGAA
 481 TGAATAGGAA ACTTGTACCT AAATCCATTT CAGATCCGTG CCATTTCTTC CAGTGCACGA
 541 GCGGCTTTCC CATGTGTGTG TGCTGCGTGG TAGCCACTCA CACAGCGGCA AAACACGACG
 601 CCTTCGCATT TAAAATTGAT TAAAACTAAA AACACTCGAT GCCGACGCCG TGCCTTGTTT
 661 CGTTTTTCAGT GCGATCGCAG ACATTGTGCA AAACGGTTCA CAGTTCTCTC CTCGCGACTG
 721 CAGGTGATCG AGTTTTTTTTC GTTTGAGTGC ACTAAAAAAA AACAGA

>DroMel seq2820_3R_17227574_17227958 3R 17227574 17227958

1 CCTTGTGCGC *C***GTGCTCCC** *G*ACCAGACAG *G***ACACTCTTG** AGGATGTCGG CAGGAGGATG
 10.2 9.7
 61 AAATNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
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>DroMel seq2821_3R_17228198_17228402 3R 17228198 17228402

1 TG**TGGCATAT** *G***T**GTATATTT TCCATATGTT AAAGTACATT ATTTTACGCA TTTACTGAAG
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 61 AA**ACTTCGTC** TAAGTTAATA TATTTTCAGA CAGTTCTTAT GGAAATTATA AATATCATT
 121 ATGCCTCGAT CTCTATTTGT TGTTTACAGT ACAGAAACGA TTTTGGC**CG** *T***GTATCCCAC**
 7.7
 181 CACTCGACTA GTGCATTTAG TGCTG

>DroMel seq2837_3R_17392100_17392639 3R 17392100 17392639

1 TGCAGTGAAT GCAACTTGTA AATCTGTCAC GCGTCCCAGT AAATCATCCT GCATAAGTAA
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 9.2 9.0
 121 TTTGTCACTC GAGATACTCG AAATACCCGA GGAGACACTG CGGGATACTC CGGAATACTC
 7.8 11.9
 181 AAAGATACTC CTCTGACTGC AACAGATGCC GGAATATAAT AAAGTCGGGG GAGTGTGAAA
 8.8 10.9
 241 TTGTGTGCTC TCGGCGACT GAAGGCGGTC CGCGGCTAAT CTATGACAGA AAACATGTAA
 10.7 12.5
 301 TCGGAGCGAA ATGCCGAAAA TAACTCGTCG TCGGGGACCT TTGACTTCAT TTGCAGCTCT
 361 TTAATTGGCC ATGTTCCCAA AGGCCTGGCC CCTGGCACTA AAGTTGCTCT GGGTGGCGAT
 421 TCGGCGGCCA ATTAATAATCC CAATCAGGGC TCTACTGTAA TACATTGTGC GTCGAATTTA
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 481 GTTGTTCAAA TTAATTATGG TACACGGGAA ATAAAAATGA GTTCGTAGAG CGTAGAAAAA

>DroMel seq6531_2L_21853080_21853669 2L 21853080 21853669

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 121 GCTTACACAA TCGATGAAAC ACATAAATCT TAAGTGAGGG AATTTAGAAA ATCCAGCCAC
 181 CTTAAATAGA CAACTGCAAA ACGGAAATGT ACATCATAAA AATATTAAAA ATTCTCTGTC
 241 ATTCTTCTAA TATGGTCTTT TTGGACATTC TTGGAAAGAT AAAAGTCGAT GCCGGTTGGC
 7.5
 301 CGCCGTTCCA GTGCATTAGA GATCGCGTTT AAAATGGTAC CCCGATGGGC TGTCAAGGCC
 361 GTAAATCTAG AATAGGGGCA CTCTTTGCTG CCCTCTCGTG CAGCTCATGT ATTTTCATAA
 421 TTTTCATATT TCTCCGTGGC TCAGCAGCTG CGCGCCTGCG CTAAAGTGTC TGACGGATGC
 481 GGCGCATTCG ATTTCTGTTCT GCCAATTAG CCGGGCCCCG TGATTTATGT CGTCCTTCTG
 8.4
 541 GCTCTTTGGC CGTTTGTCCT TTTTAGCCAG TCCGCGTGAC TCGAGCGTTG
 7.9