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

- 1 CAAAGGACAC GGACACGCAT CCTGGCATTG TTTTCAATTC ATTTACGCGT CGACTCAAGT
  9.6 11.8
- 61 CGCTCGCCCA CACATATGTT GGGAAAATAA TCGAAAAACG GTTTGTCCCT TGGCATGAGG
  12.0
- 121 TCCTTTTTGC TGCGCAGCTA GATTTGCAGT CCCTTGGCGC ATAGCACATG CCATTGATTA
  9.2
  10.0
- 181 CCATGTGTGG GAATTAGCCT TGCGAAAAAA GAAGTTAGTT AAAATCACAC ATAAAGAGGC
- 241 AATGCCAATG GCTGTAGGTC CCTGATCCTC CGTCCTGGCA GAGAGCTCAC ACGTCCTGCA
- 301 GCGATCCTTC CACCCTCTGC ACGTTCTAAA TTTAGCCGCT GGATTTATGA CCCCTGTCAT 7.3
- 361 TTGAGCCGCT CTTCCAGTAC TTCTTAAAAA ACCCCTGGAA TTACATGCAG TCGAAGAAGG
- 421 AAGAGAGTGG AGGAGTCCAA TGAGTCGAAG GAGCCCAATG AGTCGAATGA GTCGGAGA ${\it GG}$
- 481 GGGCGTTGAC AGT

>DroMel seq1396\_2R\_19526211\_19526451 2R 19526211 19526451

- 1 CAGAGGCCAT CGTGTCATCC AAGATTATGA TTTTGACAGG CATCACGACG ATATGACATA
- 61 TGCACGAATG TCTCTTCGAT CTATTTTTAT AGGAGAGATA TCTGTCAGCA CATGTTTGTA
- 121 ACCCTACACT CGTGCCCTGC CTATAAATAA AAAAGTTAAG ATCACAATTT TAAGGAGATC
- 181 TTTGTTATAA TATATTGATT AATTTATCTC GAAATACCTA CAATTCTTAT CCCCATTAGC
- 241 C

>DroMel seq1397\_2R\_19526657\_19527033 2R 19526657 19527033

- 1 TTTGTCAAGA GAGTTCGGGC TAAAAAAAAA AAGAAAAACA AGAATAAGAA TAAGAATAAG
- 61 GACAACGAAA AAACAAGGAA ATACAGTTGT AAAACCGGCG ACTCGAGCCA CAGAAAAGCA
- 121 GAAACAAATG CGGATACACA TGCTCGCCGG CTCGTAATCT TAATCCTTCA CACAATAAAC

- 361 CGCCATCATC TGTCCGT

## >DroMel seq2300\_3R\_10415381\_10415780 3R 10415381 10415780

- 1 TTGTTAATAT CTTAACTTTT CAGGATATAA CATGCTAAGT GTTATATTAT ATAACATTAA
- 61 AGTTATTTCT GCCAGTGTAA CGTTGCAGAG TCACTTGCTC CGCAGAGAGC CGCCACTCAA 7.3
- 121 AGATCAACCC TCGATGGCAG ACTCTCGCCT TTATGGACTA CGAAATGTGC AATTTCTGCT 7.9
- 181 CGGGTACCGA GTTTTACGAT TTTTCCATAG GTCCCAATAT GCC*GGGCATC TGT*GTGGTAG

  10.6
- 241 GGGTTATTTG GTTGTTGGCC CAGTATCGAT GGCAGGCCCG ATTTTAGACC CAGTCCACTT
- 301 AGGAATTCCA CGGA*CAGACC ACAT*G*GACTC TCTAG*CATTT TGCCACTTCA GTTGTTGCTT

  11.0 7.9
- 361 CAGTTTCAGT TTTTTTTTC CTAGTTGCAC TGGGGAAAAA

## >DroMel seq257\_2R\_5025930\_5026695 2R 5025930 5026695

- 1 AAGTCCACGA CAATCAACAT GCATCGGAGC ACAATAAAAA GGCAAAAGTG GAAAGGAAGA
- 61 CTAGGCAAGA CCGAGAAGAG TGACAAAGAG CGAGGGCGGA AGTGCGGCGA GGACAAGGCT
- 121 GATCTGCGAT GAACACCAGG TAGAAGGTAA GTGTATCCAC CGCACAGATT TAGCCAAAAC
- 181 AGTCCAAAAC ATATGTATGA AAGCAACTAA AAGAAACGGC GATCAAAACA AACAAATGTT
- 241 TGGTACCAGT GTACCACAGA TGTAGAAACC AGACGCTTTC CAGACTATGG CAGCACCCCA
- 301 AGAAACTCTT GGAAATACTA CTCATTGCTA CACCGCACAT ATGACGTACA CTTGGAGAAA
- 361 CAAGCACATT CCAAACAATG CGTATGTACC TAGTTATTTC ATTACAAGGA ATTGAATTTA

- 421 ATGTACCCAA AGTTAAGCAG TAGCATTTAG TATTTATGTT TTCTGGATAT ATTAACTGAA
  481 TGAATAGGAA ACTTGTACCT AAATCCATTT CAGATCCGTG CCATTTCTTC CAGTGCACGA
  541 GCGGCTTTCC CATGTGTGT TGCTGCGTGG TAGCCACTCA CACAGCGGCA AAACACGACG
  601 CCTTCGCATT TAAAATTGAT TAAAACTAAA AACACTCGAT GCCGACGCCG TGCCTTGTTT
  661 CGTTTTCAGT GCGATCGCAG ACATTGTGCA AAACGGTTCA CAGTTCTCTC CTCGCGACTG
  721 CAGGTGATCG AGTTTTTTC GTTTGAGTGC ACTAAAAAAA AACAGA
- >DroMel seq2820\_3R\_17227574\_17227958 3R 17227574 17227958
- 1 CCTTGTCGCC CGTCGCTCCC GACCAGACAG GACACTCTTG AGGATGTCGG CAGGAGGATG
  10.2 9.7

- 361 NNNNNNNNN NNNGCAAAGA ACGAT
- >DroMel seq2821\_3R\_17228198\_17228402 3R 17228198 17228402
- 1 TGTGGCATAT GTGTATATTT TCCATATGTT AAAGTACATT ATTTTACGCA TTTACTGAAG 8.0
- 61 AAACTTCGTC TAAGTTAATA TATTTTCAGA CAGTTCTTAT GGAAATTATA AATATCATTA
- 121 ATGCCTCGAT CTCTATTTGT TGTTTACAGT ACAGAAACGA TTTTTGGC $^{\text{CC}}$  TGTATCCCAC
- 181 CACTCGACTA GTGCATTTAG TGCTG
- >DroMel seq2837\_3R\_17392100\_17392639 3R 17392100 17392639

- 1 TGCAGTGAAT GCAACTTGTA AATCTGTCAC GCGTCCCAGT AAATCATCCT GCATAAGTAA
- 61 TGTGCAGTTT AGCCCGGAGA ACACACCCAG AATTCGAAAA CGATACTCCC CTCGAACCAC
  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 TGCGGCGACT GAAGGCGGTC CGCGGCTAAT CTATGACAGA AAACATGTAA
  10.7 12.5
- 301 TCGGAGCGAA ATGCCGAAAA TAACTCGTCG TCGGGGACCT TTGACTTCAT TTGCAGCTCT
- 361 TTACTTGGCC ATGTTCCCAA AGGCCTGGCC CCTGGCACTA AAGTTGCTCT GGGTGGCGAT
- 421 TCGGCGGCCA ATTAAAATCC CAATCAGGGC TCTACTGTAA TACATTGTGC GTCGAATTTA
- 481 GTTGTTCAAA TTAATTATGG TACACGGGAA ATAAAAATGA GTTCGTAGAG CGTAGAAAAA

## >DroMel seq6531\_2L\_21853080\_21853669 2L 21853080 21853669

- 1 GAACGAACCG TCGAAAAAGA AAGAGCCTCA GAGAAAATCT CATGGACTGA AAACCATAAA
- 61 TTTGATAATT GACTTTCCAC CAAAGGAAAA GAAGCCAAAG GAACCGAAAA ATTTCTATTG
- 121 GCTTACACAA TCGATGAAAC ACATAAATCT TAAGTGAGGG AATTTAGAAA ATCCAGCCAC
- 181 CTTAAATAGA CAACTGCAAA ACGGAAATGT ACATCATAAA AATATTAAAA ATTCTCTGTC
- 241 ATTCTTCTAA TATGGTCTTT TTGGACATTC TTGGAAAGAT AAAAGTCGAT GCCGGTTGGC
- 301 CGCCGTTCCA GTGCATTAGA GATCGCGTTT AAAATGGTAC CCCGATGGGC TGTCAAGGCC
- 361 GTAAATCTAG AATAGGGGCA CTCTTTGCTG CCCTCTCGTG CAGCTCATGT ATTTTCATAA
- 421 TTTTCATATT TCTCCGTGGC TCAGCAGCTG CGCGCCTGCG CTAAAGTGTC TGACGGATGC
- 481 GGCGCATTCG ATTTCGTTCT GCCAAATTAG CCGGGCCCCG TGATTTATGT CGTCCTTCTG
  - 8.4
- 541 GCTCTTTGGC CGTTTGTCCC TTTTAGCCAG TCCGCGTGAC TCGAGCGTTG