

# Drosophila bocki

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

**Assembly:** GCA\_008042715.1\_UCB\_Dboc\_1.0\_genomic

**Dro\_boc1 | VNJY01007854.1:5692-6927 (-) | 1236 nt | lncRNA: noe consensus e-value: 2e-190**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

866CGGTCCGCAATTCGCGAACAACGCGTTGGACACATCCCGTCTCATCCCGCACTCTCTGAAATGTTGTCCGTGGTACGCGAAGTTACGATTGCAAAACTTTGTCATCCTCTCTCACTCTCTGAAACAAAAACAAAGCCAGGAG  
CACAGGAGCAACTAAAGCAAAATAAAACABAAAAAGBACAGAAAAAGAAAAATCAACAACACCAAAAGTCTAAACAATATAAATACGAAAAACACBAATCGAAAAAGATAAATGACAAAAAGAGAACAAAAATATCAGACCAAAAGTATA  
TCAATGCAAAACAAAAAATCTAAAAATACACATAAAAAACACTACAAAAABABABACATAAATGATGACCTAGATAGATAAATCATCATCTGTTTATCABGACGACCTAAAAAATCTCTGAAAAATCGCAAAAAAATATTAAA  
ACCGCAAAATGCAATTTGGTGTGTGTCTCCCGTTGCTTAATGCTGGCGCGCACGCCCCCAGCCCTTACATCCGCAACCTCATCCGGAATCCAGGATGCGCCGCCACCACTCCGCCCCCGGAGCAAAAGCCGAGAACCATCTC  
CCTCTCACCCCGCTGAGGACCTACCATCTCCTCTCTCACCGGGTGTCAACAGTGTCCGTCCAGTTTTCGGGGGACAGAAAGGCGAATCGTTGGGCGGCGGCGAGGACTACTCACAGGACATCCAGTAAAAATAAATCGTCGCCGTAACTG  
AATAACAACAATTAAGAAATGAACTCTGCCCGCCGCGGGCGCCCTCTGCAAAAGAGTACGCGATTGGGGCGGGGCTGGACCGGACCGGCGGAGAGTATGACGGAATGGAATCGGGAAGCGGAATTAAGAACGGAACACGGGAC  
CGGCAAAACGGAACAGGAAATGCGGGTGGCTGCGGTGTGGTGGGGACACGCGGCGCTCCACAAAAATAACCATAGAGAGCTTTAAGGCAATTTCTAAATGAACAAAAATATAAAACAAAAACAATTGTAACGAGAAACAAACGA  
ATTCAAAATGAGCAATATGAGAACAAACAACTAATATGGCAAAAAAGCAAAAAACGACAACTGCAAAATTCGACACAAACCTTCGAAAAACCTCGAATAATAATAAGTAAAAACACCAACACAAAAACAGTGAATGCTTGGTGG  
CTGCAAGGGAATGCTTGTGTATCGCCCTTTT

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Dro_boc1      -----TggatgactgaatgctgtgtgacactgttgacactTGCBAATCCCAAGTGCCTGTTCCgcttagcgttgcaataatagccgcatcgccaggaccttagtc-----
Arthropod_7SK -----ggtaacctgaccggcgcatggaattggtgtgtgctctGTGATTCCCAAGTACAGATTCCgcccagatgtataaataccggtcaaaacttcttcttcc-----
RNase_MRP     -----taatctattttatccacacacacactATGATTCCCAAGTGTGTTTTACcacaacttctctataaataagcctccnccctaaacacataacgcccgtt-----
U6            -----cccgaaactcaggcagaaagcaaatgcaaggcttctAATAAATCTCAAGTCCATTTTCgcgctgaagtatatataatagagaattttcactgaacttt-----
U6            -----caattggcatatttcacacatcgagacaaatccttTATGATTCCAAGTGCCTTTTCgcgctgaagtcatataaataagggaataatcctcgtaacttt-----
U6            -----cgcacaaadccccttctcactcaccacactctcttTATAATTCTCAAGTCCGTTTTCCccttctctatataaataagagaattttcccttttaacttc-----
U6atac        -----TacaacatacaaatctatttttagctctgtgcttTACAATTCCCAAGTCAITATTCgtgtagcgtgcataaaacggcgagcgagccacgaactt-----
tRNAsec       -----gataaaaaaccaagattctcactgtcgagcgtctTATAATTCCCAAGTCTTATTTCTcagagtggcatttaaataggagaacctgtttgctctatgtt-----
snoRNAme18SA1806 -----caaatgtatggdaactattttcttttaactcactTACGATTCCCAAGTGTCTGATTTcttattatcttgaatttaaatgaadgaacttccctcaaaacaa-----
U1            -----atattttacggggtgttttcttgccaccaccagcgacatACGATTCCCAAGTGGTTCTGGcgttgctggcatggaacccctgcccgagcagaggaagac-----
U1            -----ccaacccatagaggagcctatttttcagagcccgctctTGAATTCCCAAGTGGTTCTGGcgttgctggcatggaacccctgcccgagcagaggaagac-----
U1            -----tcatatcttcaadgaacattttdaacacatttcttTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U1            -----gttgtgttaagagaatattttcactcttctgtgctTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U1            -----taactttaggggttaagttttaccgacaccccttgcgtTATGATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U1            -----taacttccgggaatcacttccactcacttccgaactTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U2            -----gatttgttatatacaaatcttctgctttcacatcAATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U2            -----aaaccgaggtttgaacgaccccttcgctttttgttttTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U2            -----acacttccaaatttgaatttcttcttcccttttcaadgaacAATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U2            -----acggggcgatatactgtttgcccgcgtgtgtgacTACGAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U2            -----ccatttcgaagtgaactcttatttcttgggtacattTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U2            -----ccaacttccgttaaatatttttcccccttcccaactTATGATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U3            -----accgcgctgtgttctatttttccacgcggtttgctTGAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U4            -----tcgtttgcttgacttatttttccatcgctgtgtgcgaTACAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U4            -----acagtttctatttacctatttcccaacactgaacttTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U4            -----atcttttcaatcatactcaggcagagcattTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U4atac        TgagatctcagaattgcaatttctgctctcttctgctgcacatATAAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U5            -----tatctcaodttacaaaaaadaaaacaaatatttgaactTATGATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U5            -----ctacctttaggggtgcttttttttacccttctgtgttcaTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U5            -----ctacttttaggtgtcttttttttacccttattgtcacatTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U5            -----tttaagdttttaodacatttttccactcacttttgcacTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U5            -----cgacagcttttgtttgttttcccttgcagcagggctgctTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U7            -----tatgggggttaaatttttcccttttttcttcttTATAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U11           -----cccccttgcatttcagcgataacgagctgcgtgccatATAAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
U12           -----tcttttcacaaacttttataccccaccagcctccctTACGAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
OrCD1        gctgctatcacaataaaacaaacccagcagcgttctTACGAATTCCCAAGTGTCTGAAAGcaattttcccaadgaacccctgcccgagcagaggaagac-----
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Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod\_7SK, 7SL, RNase\_MRP, RNaseP\_nuc, U6, U6atac, tRNAsec, snoRNAme18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.