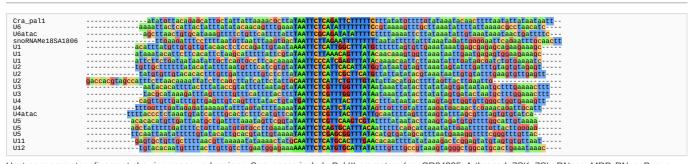# *Crataerina pallida*

Taxonomic lineage: Brachycera > Muscomorpha > Hippoboscoidea > Hippoboscidae > Crataerina

Assembly: GCA_949710015.1_idCraPall2.1_genomic

Cra_pal1 | OX453291.1:8591759-8592026 (+) | 268 nt | lncRNA:noe consensus e-value: 6.8e-08

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 9nt   PSE: 0.95

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GGGCGGTTTGTTCCTCATTGTTGAAAAGGTTGGCTACATCCCTGGCAAGATAATTGTGGCAACAAAATGTTGAAAAGATAGAATACGATATATATTATAAATAAATAAAAGATCTGTAATCGCGAAAAAATCATTTCTTCTAAATACAAC
ACGAAACGAAGTTTGTGTCCGGTTTCGCTCTGGAGAGAGGGAATTTCAGACAATCGAAAAAAACAAATTAACTCAAACTGGCATAGAGAGGAACGCCTGTGATCGCCTATTTTTTTTT
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Cra_pal1        ---------------atatattacagadcattдctattattaaaacдcttaTAATTCTCAGATTCTTTTTCtttatatдtttдtataaatacaacttttaatattataataatt--
U6              ---------------aaaattactcattactatttatatacaacagtttgaaaTAATTCTCATATTTTTTTCcgtaaaagtttgcttaaatattttattaaaacgcctaacatc----
U6atac          ---------------agcttaactgtgcataaagttttctgttcattttattTAATTCGCAGATATATTTTCttttaaaattccttataaatattдtaaataaataactдattttc---
snoRNAMe18SA1806 ----------------ttgaддatttccttttaatдtttaattaagtдacTAATTCTTAGAATTTTTTTTtaatattttatttaaatagattдддgdaattcaдaatttдcaactt
U1              ---------------acatttatдtдtдtдtacaactctccagattgtaataAAATTCTCATTGGCTTTATGttttttagtgttдaaataaatgagcgagagcagaagaaagc-----
U1              ---------------ataaatacattcttcacattctaagcattttttattcgtaTAATTCTTAAACAGTTTATAcaacaaagtggttaaataattgaatgagagtggaagaaagc-----
U1              ---------------attcttctдataataatatatдctcaдtдccttcacaaaaTAATTCCCATCGAGTTTATAcaaaacaattccttaaatatttgataдcgatctctдtдaaaatc----
U2              ---------------tgttgctctttttatacatatttttaatgtttcatcgtgtaTAATTCTCATTCACATTATGgtataataдtaagtaaaaagtatttgatttgtagtgtagagt----
U2              ---------------tatgtдttgtacacactttgttgattttttcgtctcttaTAATTCTCATTCGCTTCATGtgtattatatacgtaaataagtatgtgtatttgaagtgtgagtt--
U2              gaccacgtagccattтcttaacaaaatatcttcaдcttatcattctattдcaAATTCTCATTCTGTTTGTATattacatдactтttaдttacttдaattд----------------
U3              ---------------aatacacatttttactttataccдtattтttaatagtaTAATTCTCGTTTGGTTTATAataaattatactttatatagtggataataatgдctttgaaaacttt---
U3              ---------------tacgcataaagatttagtttttgtttcattttacttttTAATTCTCGTTTGGTTTATAataaattatactttatatagtgatactaatgctttддaaactttt--
U4              ---------------cagttgttgatttgttgagttgtcagtttatactgtatGATTCTCATTTACTTTATActtttataataсttaagtagttggtgtggдctggtgaaaдtt-----
U4              ---------------ttдogttдataдagдataaaaatatttaдtattttaaaaTAATTCTCTATTTACTTTAtAдttдttttдtatttaaдatдacaactcдaaacaдattдcatt----
U4atac          ----------tttttaccctctaaatgtatcatttgcactctttcatgttcaTAATTCTCGTTTACTTTATTgcaattttagtttaagtatttagcgtttagtgtgtcatca------
U5              ----------acacacatдttgattaatgctgattttaaatagttcggtaTAATTCTCGTTCAAGTCGTAtttttataatacttaagtaaatgtggtttддcattgtaaaa-----
U5              ----------aдctattttttдattttctattттaatatattgacctтgaaataTAATTCTCAGTGCATTACAattttcaдcattaaatattдaatttttдttacttоддaд------
U5              ----------ttcaattaatattтttтgtatacattgcacgtattдtaaaaTAATTCTCGAGCGGTTTACAcatдtgatagcatttaatgaaaggttttcдggtttgttac------
U11             ----------gagtgctgttgctttaacдttaaaaatataaaactatgCAATTCTCATGCACTTTGAAcacaatttтtatataaagactcggagtgatgtagtgtgttaat-----
U12             ----------tgtacacaatgtttttacttgttgtcttgaatgдaaaagaaaAAATTCTCATGTGCATTATAtttgtttgccgtaaagtagggctggcatgcactgaaataaac----
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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.