Lordiphosa magnipectinata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Lordiphosa > miki group

Assembly: GCA 037044535.1 ASM3704453v1 genomic

Lor_mag1 | JBAMBO010001043.1:220603-221541 (+) | 939 nt | IncRNA:noe consensus e-value: 5e-187

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

Lor_mag2 | JBAMBO010001581.1:209314-209590 (-) | 277 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.77

Lor_mag3 | JBAMBO010004433.1:473056-473335 (+) | 280 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 17nt PSE: 0.75

Lor_mag4 | JBAMBO010004433.1:456471-456709 (+) | 239 nt | IncRNA:noe consensus e-value: 5.3e-04

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.85

Lor_mag5 | JBAMBO010004433.1:459883-460136 (+) | 254 nt | IncRNA:noe consensus e-value: 1.5e-03

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 2nt Trailing-T: 8nt PSE: 0.80

| | Lor_mag1 | Lor_mag2 | Lor_mag3 | Lor_mag4 | Lor_mag5 |
|----------|----------|----------|----------|----------|----------|
| Lor_mag1 | - | 17 | 16 | 17 | 18 |
| Lor_mag2 | | - | 55 | 57 | 60 |
| Lor_mag3 | | | - | 51 | 49 |
| Lor_mag4 | | | | - | 72 |
| Lor_mag5 | | | | | - |

Pairwise sequence identity matrix (%) showing similarity between IncRNA sequences.

| Lor_mag1 | tt <mark>q</mark> ctt <mark>q</mark> aaaaaa <mark>u</mark> cttt <mark>qcatttcctu</mark> ct <mark>qcactTGTAATTCACAAGTTT<u>TTATTCqq</u>cqactcqtcutttaaatac<mark>c</mark>aaata<mark>qccaqq</mark>ctcttttqqtt</mark> |
|------------------|--|
| Lor_mag2 | <mark>acqttcactcqctttttqttqttcactcaacttctTGGAATTCTCAAATACGAATTCcaqcaaatqqaaatataaataqcqcaactttatattccctqtc</mark> |
| Lor mag3 | |
| Lor_mag4 | <mark>cctqaccttcataatttttctattcttqcq</mark> ttatt TATGATTCTCAACTGCAAATTC qqccaaatqaqaatataaataqcqcaacqttttttcqtcagcc |
| Lor_mag5 | ctqqccttcaacatttttcattcttqcqttattTATGATTCTTAACTACGAATTCqqccaaatqaqaatataaataqcqcaacqttttqtcatcaqcc |
| Arthropod 7SK | ugcaatagcgacgcgtggcattatttcgttgcgtTACAGTTCCCAACTCTTTATTCggcttcagcatttaaatacaacctacgttcgcttgtafctc |
| RNase_MRP | ccaccaactaccataattttgtcttccTAAAATTCTCAACTCGTTTTTCgqccactgaggcatataaatagcqqccgttcgttttgcttcagcagccgctt |
| U6 | ctaatugaactacaacautctucttuctttuctttucttTATAATTCTCAAGTGTTTATTCcccaucattuacatttaaatagucctttutctuucttuaacttc |
| U6 | ttmgaatguttagtaaaaatcaacccttutgtctTATAATTCCCAAGTGCTTATTCgcctgctgttgtacatataaatagcgcagttttgcgttagaattctc |
| Ü6 | aaaacagatggcgccaccacaaaatgctcgttttAAAATTCTCAAGTGCTTATTCtccaataggttcatttatatagaggaatttaagtacaacactc |
| U6atac | ttgaacgaacttcagtggcagtcattttgcgctca TGCAATTCCTAAG TTTT TATTC gccgattcgagcatataaaaagggagtaggccagcgcgcgc |
| tRNAsec | craaatctqqaaatcataattttqcttactttTATAATTCTCAAGTTCTTTTTCqccacattcttcqtttaaataaqactacttcaqcctcatactacc |
| snoRNAMe18SA1806 | aatcatcctaaaaqtatqctacaaatatqtaqcct TATAATTCCCAACTGCTTATTC qccqtqttqqtcatttaaatactcaaattqcqtatqaaacaaa |
| U1 | cataggttcagctgtctatttttcacaactacttcct TACAATTCCCAACTGCTTCTCA cactttttggcatggaaacccatgcgctgagcagtggaaagc |
| U1 | ctactttgaggtatccaattttactgccggtctactTGCAATCCCAACCAGTTTTCGaagtgcaaggcatggaagccccagtctgagggttgagggaaagc |
| Ŭ1 | a <mark>cctactttttcqttccaattttttqacaatttatctTAAAATTCCCAACTGGTCTTGGcaacttaqqcatcqataccccttqactqaqqaqaqqc</mark> |
| U1 | cctactttuaugtatccaattttactgcccttctactTGCAATTCCCAACCAGTTTTCGaagtgcatggcatggaagaccaagtctgggggttgagggaaggc |
| U1 | tgatacaaaaautcattttucatacttttuugututtTGAAATTCCCAACTGGTTTTGGcacttcaugcauggaaaaccctactggtgagctgagggaaagut |
| Ŭ1 | tacttctaggcctgcaatttgactagcccacaacttAGCAATTCCCAAGCGCTTTTGGtagtcattgaaaacccagtcagtgggtctgaacaaaac |
| U1 | tacttttaggcctgcaatttactagcccacacttAGCAATTCCCAASCGCTTTTGGtagtgccggtcatggaacccaatcagtggggctgaacaaaac |
| U1 | |
| U1 | gctactgtgatgacgaataattgcaaaaggtgacctTATAATTCCCAACTGTTCCAAGcagttcaggcatggaaaccccttggttaagcagaggaagc |
| U1 | |
| U1 | cataggttcagctgtctatttttcacaactacttcct7ACAATTCCCAACTGATTCTCAcacttttggcatggaagcccatgcgctgagcagtggaaaagc |
| U1 | Cataguit Cancil Catattiticaca actactic (TaCAATTCCCAACTGCTTTCCAactitium catumanacccat month and an ange |
| U1 | ttgtatgaagcaatgtatttttcactgtgtgcgcacTAAAATTCCCAAATGGTTCTGGcaacgctggcatggaaagcctctcgttgtgctgggggaaagc |
| U1 | ctacttacoctotacaattttcatcocottgattTAGAATTCCCAACTGGTCCTAGcaottcogocatogaagccccttoctdgctgacagaggaaagc |
| U1 | Ctatcatoucatactatttatttactactattattatta |
| U2 | ataaaaatgtctgacaaggcaaaccctttgtcatttTACAATTCCCAACTATTATTAGcaatgttgtcattgattagttagtttgtcatcaagttt |
| U2 | taccttttaucacatatutcatcccataccataCcatataccatatataccatatatat |
| U2 | |
| U2 U2 | |
| U2 | ataaaaatoctaacaagocaaacctttotcatttTACAATTCCCAACTGGTTCTAGcactttactcatogaatocaotcaotttoccaaccaactt |
| U2 U2 | atacacat vertigacaagecaacecttigicatti Accattectatiga attacat in tota at garagacagitgattigacateaget |
| U2 U2 | |
| U2 | ataaaaat utdaggaaaaacaattccatactagact TATAATTCTCAACTBACTTAGGtaactcgctcatgagaggctgtaaattgcctcattcaagtt |
| U2 U2 | atabadatututudadatatutatatatatatatatatatatat |
| U2 U2 | at argant and canadical (canadical lackar lac |
| U2 U2 | acataaatittudaaatitutatattittutatti TACAATTCCCAACTGTTTCTA Gaatticacttatudadagtuttattituttittataatti |
| U2 U2 | getaadatitetudadatadatetettettatetti aanta teena tii tina aatteetta tugatuutaataatta tutaataa taatti aanta |
| U2 U3 | taattctaagcattcttttcatcticattogcctTACAATTCCAACTGCTTTGGcaottagctcattogagagacccttottogcctotoattctt |
| U3 | |
| | |
| U4 U4 | |
| U4 U4 | |
| | |
| U4atac U5 | |
| | <mark>cagcaataatgggaatttcttgtactgactgacagcctTACAATTCCCAAACGGTTCTCG</mark> cattgcagcatggaaagggctctgaattgcattggaaag |
| U5 | <mark>tgccgccttgcttagtttagtttagtttcgcctTACAATTCACAACCAGTTAAGGtagtttatatatggagtgacgtgtgtctgttc<mark>g</mark>tag</mark> |
| U5 U5 | ucctactitcoudtutctuntutcaaaattittutitTAAAATtCCAACACTITAAGGcaucaccancatudaaaaactutctuttuutuutuccaau |
| U5 U5 | <mark>ucctactttcqqqtqttctqqtqtcaqacqqqtttqttT6AAATTCTCAACTGTTTAAGG</mark> caqcaccaqcatqqaqaqactqcctqttqqtqccaaq |
| | <mark>qtcaqqtaqaaaqqtatqaatttqtacatqttqtqactTACGATTCCCAACTGGTTAAAGcatt<mark>qcctq</mark>catqqaaaq<mark>qc</mark>cttqtqttqqtqttttat</mark> |
| U5 U5 | |
| | glcaggtaggatagtatgatagtaggactiAcAeiicutaAciegiiAAAgcattgcctgcatggaaaggctttgagttggttggttgaaa |
| U5 | |
| U5 | tcattfcaacttacctmaatttttatactttttcamct TATAATTCCCAACTGGTTAAGG cttmacatmaaammaccttmtmttmatmattmttat |
| U7 | tqtqtqtqctqaattttacacaqtttcatqctA CAAATTCCCAACTCGTTTCAG taacatttqcatqaatqtqtttqtttqcaaqcacaaatcaga |
| U11 | acacacauattttcttttttucccactctaaccct <mark>ACGAATTCCCAACTGGTTTTAG</mark> ccctcuucutaacttaccttcauttuctcuttutuattc |
| U12 0rCD1 | <mark>cadccadcaaaadctttttacactttacccaccctTaGABTTCCCAACTGETTTCAG</mark> ttdtdcctddatdaadtdctdcdacaatttttdccatcaacaattc |
| OLCDI | ttcttatctaca <mark>gc</mark> atttttatactctgttgccaaA <mark>GCAATTCCCAAACAGTTATAT</mark> cactt <mark>ccagag</mark> tgacatacacactgattggtagggaaaatttg |
| | |

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.