

Volucella bombylans

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Volucella

Assembly: GCA_949129095.1_idVolBomb1.1_genomic

Vol_bom1 | OX422143.1:113851371-113851652 (+) | 282 nt | lncRNA: noe consensus e-value: 2.8e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.97

GGGCGGTTGATGCTCACAGTGTGCGGTGGCTACATCCGTTCCCCCAATTGTAGCTTCTAAATCGTCTATGCTTTGACATCCATACTATAAAATAAAGAACTACTATAAAAAAGTGTGTTGAAAAAGTTTACCCAAAAACA

ACGCAAAACAAAAATAATCTTTCTCTCTATCATAGATACATAAAAATATAGAAATTAAGCAATTCATCGAATCGAGAAAAAAGTTTGTCCAAACGGTTTCTGCTGGGGTAGATCGCATCGCCTTTTT

Vol_bom2 | OX422143.1:113850727-113850951 (+) | 225 nt | lncRNA: noe consensus e-value: 3.6e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.97

GGGCGGTTGATGCTCACAGTGTGCGGTGGCTACATCCGTTCCCCCAATTGTAGCTTCTAAATCGTCTATGCTTTGACATCCATACTATAAAATAAAGAACTACTATAAAAAAGTGTGTTGAAAAAGTTTACCCAAAAACA

AGCAAAATTCATCGAATCGAGAAAAAAGTTTGTCCAAACGGTTACTGTGGGGTCGTGGTGCATCGCCTTTTT

	Vol_bom1	Vol_bom2
Vol_bom1	-	72
Vol_bom2		-

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

Vol_bom1	-----gtgttacctaagcagttacctaactttttgcgacgtttTATACTTCACAGTATTTtattctccagtgcaatctataagcaaaattcaaaacgctaccgtc-----
Vol_bom2	-----ttgtaccgaagcagttacctaactttttgcgacgtttTATACTTCACAGTATTTtattctccctgtgcggtctataagcaaaattcaaaacgctaccgtc-----
RNase_MRP	-----tatadadaaataattatttttaccatttTATAATTCACAGAAATTTtttddaaatottttactaataccotttddataotttttddatodgaggtgt
U6	-----caccaattagtgcccatatttttttgcataatTATAATTCACAGAAATTTtttcccttccgtgttatcacaaaaacagttctctttaaacacatttc-----
U6	-----cacagatcgacgaacacagtttttccattcgtTATACTTCACAGTATTTtattagctccttaagttgtatagatgacgtcaggaagtaacgttattt-----
U6atac	-----ttataaacaatttadaaadaaaattttaatccctTGTAAATTCACAGAAATTTtttccacatttadaattattatattadtaadadaaadaaatttddatt-----
tRNAsec	-----tcctattttcatgtaatttccaaatttcgttgcgaatAGAAATTCACAGAAATTTtttccgtattccctttggatgggtatattctgtctttttaaacacatgat-----
U1	-----tgtacatctgaatctggcgaatttttagtccttactTATAATTCACATCCTCTTgtaccgaaaagcataaagagaagtcacctcccatgaaaggc-----
U1	-----ttotacatctotatctddcaattatttttaotccttactTATAATTCACATCCTCTTttacadaaaaaaacaataaadaadaotccactcacataaaaac-----
U1	-----aaaaacaacacagcttagagatttttcaltcccttttTACAGTTACATTTGGTTgggtcagaagaagaataaagaagatattcgatagcggagaaaaagc-----
U1	-----acaaacaaaattgacggcgatattttcattcaattgtTATAGTTACATCTTGGTTcagcaaaatttaattaaagaagtaaacctgtttgcggtgaaagc-----
U2	-----corttcactccacactaaataatttttattccctttTATAATTCACATCCACTTgaaccaaotatcttctataaadaaattccatttttcccttddaaaatt-----
U2	-----aaaaacaaagcacacagattatttttctgtgattTATGATTCACATTCGACTagatgcaacgaatacagttatgtagggttaataaacgacgcaaaatt-----
U2	-----aaacaacaacaaaattgtgtgtgaaatttcatttatcaTCTAATTCACATACTCTTttggtagagaattcctaaagttagagcagtgaaatggacaacgtt-----
U2	-----aatotaccctdaatttcataaadaatttttcactccatTATAATTCACATCCAGTTdaotdaagcattcttadaaotatttattatgtataaaotacaact-----
U2	-----gaagggcatalaatalacatagatttaccacccatTATATTCACATCCAAATTgcttgaagattccttagaagatttccattatgtdaadaaaglacattt-----
U3	-----caccaagttcacacacaaaagttccacttccctttTACAAATTCACAGTCACCTTcaagcagtagtatccataagaatagtcgctatttcggaagtaacgtt-----
U3	-----cctaataaataacadaaaatttttcactcaatattTATAATTCACAGTTGCTTgaaccaaaaadaaacctatttaataccadaaotcttadaaottttaattt-----
U4	-----ccttagagattgtatccttttatttatttttcactctttTATAATTCACAGTCTCTTcagggtagatatctttaaactgtagtagaadaaattaaagatcgtt-----
U4	-----tgcaatagatattgtttgttttttttcaatcgtttctTATAATTCACATCCACTTcgtgtaaaaagatttactaaacccgttttacagagtttaagttcgtt-----
U4	-----notadadaaatacttddctccttttttcaatcattTATAATTCACABTTACTTTdaaccaaaaaataatcataadacaadotdaaadaadadaadattgttt-----
U4atac	-----gttaataacttttttaactattttgaaaattgcattcacTATAATTCACABTTACTTTcaagcataaagatttcaaaagtaacaaaaagatttaccctt-----
U5	-----tttatctatttttattatgttttttttcaatcgtttcaatTATAATTCACATCCACTTgaacagagaagaattataaaggagttgaacataccaccacatcg-----
U5	-----tatttttattacgaataacttttttttcaatccttcacaTATAATTCGATCCACTTgaacadaadaaattataaadaaotttaacataccaccaatcg-----
U5	-----tactaaaattttaaaggccgttaatttttttttgatcaTATAATTCACATCCACTTgaagcaaaaataattagtaaggtttgaagcaatcgtttgtagaaa-----
U5	-----gcagtcgttactcctaccctgtgattttgttcacatcctTATACTTCACACCTAGTTTctggcacaattcacatgaattcttcacaaaaacaatgaaaaaa-----
U11	-----tddcatcacaaattaccatttaataatttcattcctttTATAATTCACACATGGTTtttgcacaaaaataaataaotactgaatttddaatccoccttcadaatt-----
U12	-----ccttatgtgcatttaggaagccttttcatttgattTACAAATTCACABTTACTTataacatgctactactgttaacgattttaaatttagcaggaaacctc-----

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.