

**Assembly:** GCA\_018150405.1\_ASM1815040v1\_genomic

Assembly: C:\\_010100 Tool: \_010100 Rev: \_ygeninfo

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.87

GGGCGGTCGTGCATTCGCGACGAAGGACGGTGGACACATCCCGTCTCATCCCCACTCTCTCBAATTTGTGTCGGTTGGTAGCCGAAGTTACBATTGCAAAAACTTTGTCATCTCTCTCACTCTCTGAAGCAAAAAACGCGCAGGACGAGGACGAGGACGGGCGCCACACCGCCGCGTCTACACAGCAAAAGCCCTGAAACGGGAGATGTCATTTTG6GTAAAGGCGAAGCAATGCAATTCATGAGGCGCAAAAGCAGCAGGACGAAACCACTTAATAAAGCAAAAAACAGCAAGCAAAAAACCAACACGACAAAAAATCTAAAAACAAATATAATGAATCCAAATCAAGAAAGATAATGACAAAAAATATCAGACCAAAAGATATGCAATGCAAAAAAATAAAATCTAAAAAACTACACATAAAATCACTAAAAAAGAAAAAGAAAGTAAACTTAAATGTGACCCCTAATGATGAATGATCATCATGCTGTTATGACAGGACCGCAGCAAAATCTGAAAAAATATGACAAAAAATAATATAAAACGCAAAATGACCTGGTGTTGTGTTCCGGTCTGGTGAATCTGGCGCGCGCTCGCCGCCCAACGCCCCACACGCCGCCGCCCAACCACTTACAATTTTAAATGACAAACCGGAACCGGAACCAACCGGCCGCAAAACGAGTAGAGACAAACGACCAACACCCGCGCGGAGTAAGATAGCGGCGCTGCGGCGCGGCGGACCTCTCCCAAAAAAATACCATAGAGACTTTAAGGACAACTCTAAATGAAACAAAAATATAAAACCAAAAAAATATGTAACGCAAGCAACCAAGTTCAAAATGAGCAATAGACCAACATAATAGGCAAAAAACCAAAAAACGATACCAATGCAAAATAGACCAACCACTTGAAAGAAAGCTTAGTAAATATGAAAAAATAATGAAAAAACCAAAAAACCAACCAACCAACACCTGATGCTGTGTGTGCTGCGCTTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.93

GCGGGTCTGAGCGGATTCAGATTCATCAAGGGTTTCTCCACTTCCGCGACTAATTG1696AAAAAAAAACTATAAACGGCGCGCTCCCAAAGAGAGAGGGCTCCAAATTCGTCGATAGCAGCAAGCTTATATATGGGAAGATTCATTGCAAGAAC  
 CAATTTTCAGACGGCAATCAGGATCATATCTATCATCTATGATAAAAAATCATATGGGTG864AAAAATCTCTCCBGCATTGCAAAAAAAGCCATATATAGCAAGATTTTAAATGTGTGTTATGAAAAACCCCATATCGAAAAAC  
 GCCCACTCCCCG6AAAAATGGGGGGATATGGGTGAAAAAATCATACCGGCTAAAAAATATACCCATATATCCCCAGATATCCCGAGGAGGGCGGGGGGCGCTATATAAAGAACCAAGCAAGAGAGAAAAAAACCCAAAAAATAAACCAACCAAGATATAAGT  
 CAAAGATGAAAAATAATAAATAAGCTGAGAGAGCGCCGATTAATCGCTATTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.85

GGCGGTGAGAGCCTCACAATCATCAAGGGTGACCACTGTCGACAAATGTGGTAAAAATTTGAAGATGGTATGTGATTGCGAAGAATTGTGTTTAAAGTTTAATGAGAAATCTGTAATTTGTGAAAAAGAAAGTTTCCGAGTCCCTTACGATTACATGTCAGAGAGACATGTTTGGAAATCCGGTAATTTCTGCTCTCTCTCCCTCTGAGGGGCGAATGTGAGTGAAGAAATCTGAAGTGAAGTTGGGAGGGTGTGTTTGCCCTATAGAAAAATACCTCCCCCATAAAAATGACGAGATTTGGAAATTTCCCTCAATAGCAACCAATTTGAAACCCATGACGACAAAAATTTCAAAAAAAAATAAAAAGAAATAAAAAGAAATCACTGTGAGTGCATCTGATGCCATTATTT

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

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.

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