

Assembly: GCA_028554725.2_idZeuCucr1.2_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

Zeus_cuc2 | CM053020.1:8836947-8837405 (-) | 459 nt | lncRNA: noe consensus e-value: 6.6e-03

GCGCATATATATGGCCGATGCGTTGAAAGGGGTGACATGCATTTCCGCCGCCCAATTCAGCAAAAGTAAAGACAGAAAGCAATACAAATTTCCACCATCTATGATCATTTCTGCGATGGCTTCGATGATGACGAAAGCTTTCTATACCCAGAAAT
 CACACGACGATGTGGAGCCGCGCATCTGCGGATCCGCGCATCTGCTTATCAATCAATTTCCCTTAGGCATAGCAAAATAAAGTAAATGATGATCTTCTACACGACGCTCTCAAGTATGAAGTGGCAACAAACAGAAAGAA
 ATTGATATAGAAATTAATTAATAAAAAATACTCTATACAAATTTCAAGAAATTCAGAAAAATAGCAAAAGGACAAATTTGAAACAAAGTTAAATTCGCCGTAAAGCCCTCATCATAGGAGCGGTGCGCCATTGGGACCAACACAAATGGGTGA
 TCGTCTTTT

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

