

**Assembly:** GCA\_035045005.1\_ASM3504500v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.82

Lio\_aer2 | JAWNNL010000728.1:39901-40403 (+) | 503 nt | lncRNA: noe consensus e-value: 9.6e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.86

|          |          |          |
|----------|----------|----------|
|          | Lio_aer1 | Lio_aer2 |
| Lio_aer1 | -        | 30       |
| Lio_aer2 |          | -        |

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.