

Assembly: GCA_018904355.1_ASM1890435v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_spr2 | JAEIFY010000119.1:4928429-4928927 (-) | 499 nt | lncRNA: noe consensus e-value: 1.1e-13

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

| | | |
|----------|----------|----------|
| | Dro_spr1 | Dro_spr2 |
| Dro_spr1 | - | 31 |
| Dro_spr2 | | - |

[illegible]

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.