## Sphaerophoria rueppellii

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

Assembly: GCA 920937365.1 SPRU Genome genomic

## Sph\_rue1 | CAKKXW010000001.1:113469386-113469708 (-) | 323 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 6nt PSE: 0.82

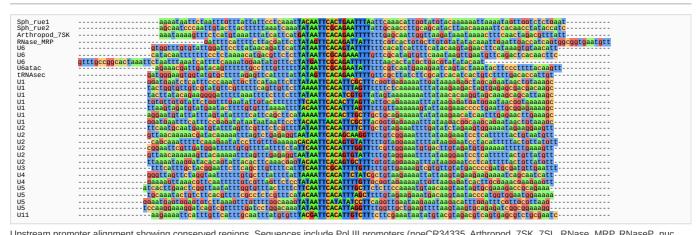
## Sph\_rue2 | CAKKXW010000001.1:36042256-36042572 (-) | 317 nt | IncRNA:noe consensus e-value: 1.5e-08

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

SGCCGTTCAGTGCCTCACAGTTGATACGGTTGCCTACAGTCCGTTTCCAAAATTGTAGCATCTAAATCGTATGCTTTGATAAACATCCAAAACACAAAAACGAACAAAAAATATCATCTAAAAGAACAACAAAAAATTTGTGTGTTTGA SAAATAAACTAAAATTAAGTTTCACCAAAAAAAACAAGCAAAAAACATTCTCCCTCTATCGTATAAGATATAAATATAAGATTAAGCCAATTCAATAAAATTGAGATAAAAATCTATCAAAAAATGATATCTGCTGAGGTA SATGTGATCGCCTTTTT

	Sph_rue1	Sph_rue2
Sph_rue1	-	47
Sph_rue2		-

Pairwise sequence identity matrix (%) showing similarity between IncRNA 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.