

Nemotelus nigrinus

Taxonomic lineage: Brachycera > Stratiomyomorpha > Stratiomyidae > Nemotelus

Assembly: GCA_947369275.1_idNemNigr1.1_genomic

Nem_nig1 | OX376373.1:20752753-20752934 (+) | 182 nt | lncRNA: noe consensus e-value: 7.1e-02
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.92

CGGGTCCAA

6TTCTATTGGTTAGCATGGGTTTGTCTATACATCCCTAA

TTGTGACAGTTTATACCTAA

TTGTAGACTTAAC

TTATAATTAGATATTAATTTAAAAACCCG

CTACGACGGTACCATAG

TTGGCGAATCAACCTTACGGT

AAACAACCAATAGGACGTTCTGATCGCTTTTT

Nem_nig1	-----	caatac	atattt	tottca	aaattt	tottct	adag	aTATGATTCGGGATGACAAT	tt	aa	aaact	oot	ag	tata	aaac	aa	ottt	o	aaac	cacc	ca	-----
Arthropod_7SK	-----	tgctt	caaccatt	gctgc	acagatt	ttccgc	gga	TATACTTCGCA	TTGTCAAT	tt	ca	ga	ag	gata	aa	gc	gattt	ga	at	gtac	gg	-----
RNase_MRP	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
U6	---	gtt	cttggc	taaa	tttt	ccg	ttga	TATAATTCGCA	ATCACA	AAAT	ctt	tg	tata	aa	gt	tata	aa	gc	gtg	acc	tc	ca
U6	---	gt	ctttaa	aaatac	ctataa	attt	tottct	gcacaa	TATCGCGAGT	TGTACA	AAAT	to	aaat	ta	att	to	aa	at	ct	tc	ccatt	taatt
U6atac	-----	ca	ctttt	gac	tttt	gtat	gga	attt	gtgtt	gtgc	TATAACTTCGCA	ATGTGAAT	ct	aa	aa	aa	gc	ttt	aa	at	ca	at
U1	---	aa	ggt	ag	gtgc	gc	tc	gc	at	gc	ctt	cc	gt	aga	TATACTTCGCG	ATGTCAAA	at	ga	at	ct	aa	gt
U1	---	at	ttt	ct	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	
U1	---	ag	act	g	cc	gg	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
U2	---	tt	ct	gt	at	ga	at	gc	ac	ata	aa	gt	tt	gc	ac	ac	ac	ac	ac	ac	ac	
U2	---	tt	cg	ac	ag	cc	g	ac	ct	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	
U2	---	tt	cg	ac	ag	cc	g	ac	ct	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	
U2	---	cg	at	gg	c	ag	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
U2	---	tg	at	g	tt	c	ga	at	g	ct	tc	cc	aa	TATACCTATGG	CTATGT	GA	gt	gt	gt	gt	gt	
U3	---	tc	ac	ca	ad	at	act	ca	cc	ata	aa	ct	aa	at	gc	ac	ac	ac	ac	ac	ac	
U3	---	ga	gt	ttt	ga	at	ttt	gc	ct	g	aa	tt	at	tt	gc	ct	g	aa	tt	at	tt	
U4	---	aa	ta	ag	ct	tt	gt	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	
U4atac	---	gt	at	ttt	at	tt	o	g	aa	ad	at	ct	ct	ct	cc	ac	ca	TATAACTCGCA	ACCCAG	aa	tt	
U5	---	aa	at	g	aa	cc	g	at	g	at	g	at	g	at	g	at	g	at	g	at	g	
U5	---	aa	at	g	aa	cc	g	at	g	at	g	at	g	at	g	at	g	at	g	at	g	
U11	---	tt	cc	ca	aa	g	at	at	g	at	g	at	g	at	g	at	g	at	g	at	g	
U12	---	tc	aa	gg	act	tc	gt	tt	ag	tt	gt	gg	at	ta	ac	ct	ca	aa	TATACCTAG	CAGTCA	TGTTG	

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.