

Assembly: GCA_051014185.1_ASM5101418v1_genomic

Mus_sta1 | CM117225.1:133927982-133928502 (-) | 521 nt | lncRNA: noe consensus e-value: 1.2e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

[illegible]

Mus_sta2 | CM117227.1:78543873-78544138 (-) | 266 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

GGGCGGTCTGTCTCCTCTCAGTTGAATGGTTGGCCACATCTCCATTAAATTGTGGCAAAATATACTTTGATATAAGCAAAACCATATATCTACTAAAGAAATATTTCCTCCACACAAAAAAATTCAAAAATATTACAAATATCAAAACGAT
CACTATCTATATAACTTAGATTGAGATTAAATAAAAAACAACCTTTCAAATTCCTCTCTTCATCGAGGGGTGTTTAAAGTAGAAAGTGACAGAGGGGTGTGTGATCGCCTTCTTTTTT

	Mus_sta1	Mus_sta2
Mus_sta1	-	38
Mus_sta2		-

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

[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.