

Assembly: GCA_030504385.2 *Musca domestica*.polishedcontigs.V.1.1 genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.91

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.89

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 26nt PSE: 0.87

	Mus_dom1	Mus_dom2	Mus_dom3	Mus_dom4
Mus_dom1	-	96	47	36
Mus_dom2		-	48	36
Mus_dom3			-	36
Mus_dom4				-

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.