

**Assembly:** GCA\_037044535.1\_ASM3704453v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

Lor\_mag2 | JBAMBO010001581.1:209314-209590 (-) | 277 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.77

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 17nt PSE: 0.75

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.85

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 2nt Trailing-T: 8nt PSE: 0.80

	Lor_mag1	Lor_mag2	Lor_mag3	Lor_mag4	Lor_mag5
Lor_mag1	-	17	16	17	18
Lor_mag2		-	55	57	60
Lor_mag3			-	51	49
Lor_mag4				-	72
Lor_mag5					-

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



Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod\_7SK, 7SL, RNase\_MRP, RNaseP\_nuc, U6, U6atac, tRNAsec, snoRNAM18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in

the alignment.