Lucilia sericata

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Calliphoridae > Lucilia

Assembly: GCA 015586225.1 ASM1558622v1 genomic

Luc_ser1 | JADFTR010003896.1:164054-164471 (+) | 418 nt | IncRNA:noe consensus e-value: 8.9e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.99

Luc_ser2 | JADFTR010002762.1:1774-2190 (+) | 417 nt | IncRNA:noe consensus e-value: 9.2e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.99

Luc_ser3 | JADFTR010002089.1:192356-192608 (-) | 253 nt | IncRNA:noe consensus e-value: NA

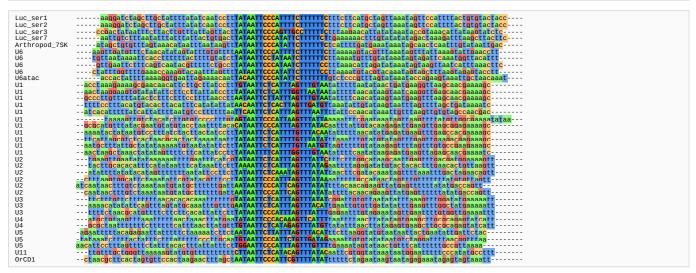
5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.85

Luc_ser7 | JADFTR010002089.1:204385-204622 (-) | 238 nt | IncRNA:noe consensus e-value: 2.7e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.99

	Luc_ser1	Luc_ser2	Luc_ser3	Luc_ser7
Luc_ser1	-	100	43	38
Luc_ser2		-	43	38
Luc_ser3			-	74
Luc_ser7				-

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.