Lucilia caesar

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

Assembly: GCA 965655125.1 idLucCaes4.1 genomic

Luc_cae1 | OZ296612.1:78836291-78836728 (+) | 438 nt | IncRNA:noe consensus e-value: 5.9e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 1.00

Luc_cae2 | OZ296615.1:64197279-64197524 (-) | 246 nt | IncRNA:noe consensus e-value: 6.0e-01

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.95

Luc_cae3 | OZ296615.1:64203695-64203939 (-) | 245 nt | IncRNA:noe consensus e-value: 9.4e-01

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.86

Luc_cae4 | OZ296615.1:64194284-64194521 (-) | 238 nt | IncRNA:noe consensus e-value: 1.4e-02

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

GGCGATCTTGGTCTCTCAAGTGATAAGGTTGTTCACAGCCCTTAATTGTAGAAAATTTCAAAAATGTCAAACTATCTGCGAAAATGTTGAGTATGTAGTTTAAAAAAATTCCTGGTTAAATGTTGTTCCAATATAATCGACTTTCAA ACACACTGCTGAGATTTCATGCTTTGGTAAGTGGTCGTGTATAAAAATAAAGCTTTAAGGGAGATGAAAAACGTGATCGCTACTTTTT

Luc_cae5 | OZ296615.1:64195584-64195813 (-) | 230 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.95

Luc_cae6 | OZ296615.1:64203012-64203247 (-) | 236 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.86

Luc_cae7 | OZ296615.1:64204844-64205079 (-) | 236 nt | IncRNA:noe consensus e-value: 1.2e+00

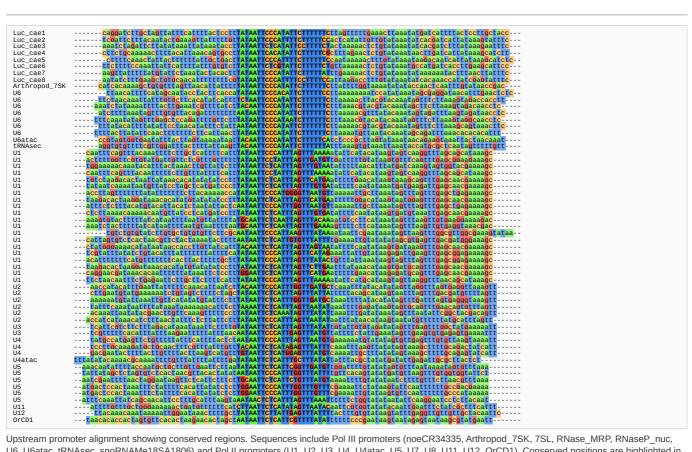
5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.92

Luc_cae8 | OZ296615.1:64190670-64190902 (-) | 233 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 6nt PSE: 0.90

	Luc_cae1	Luc_cae2	Luc_cae3	Luc_cae4	Luc_cae5	Luc_cae6	Luc_cae7	Luc_cae8
Luc_cae1	-	39	41	41	39	38	36	40
Luc_cae2		-	84	81	84	88	79	78
Luc_cae3			-	81	88	89	78	76
Luc_cae4				-	80	86	75	88
Luc_cae5					-	90	80	79
Luc_cae6						-	84	81
Luc_cae7							-	73
Luc_cae8								-

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, snoRNAMe18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.