Lucilia cuprina

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

Assembly: GCA 022045245.1 ASM2204524v1 genomic

Luc_cup1 | CM039060.1:53856943-53857479 (-) | 537 nt | IncRNA:noe consensus e-value: 9.9e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

Luc_cup3 | CM039060.1:58225287-58225529 (+) | 243 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.85

Luc_cup5 | CM039060.1:58210788-58211021 (+) | 234 nt | IncRNA:noe consensus e-value: 9.9e-01

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

	Luc_cup1	Luc_cup3	Luc_cup5
Luc_cup1	-	36	28
Luc_cup3		-	75
Luc_cup5			-

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.