Calliphora vomitoria

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

Assembly: GCA 942486065.2 idCalVomi1.2 genomic

Cal_vom1 | OW818029.2:80624543-80624964 (+) | 422 nt | IncRNA:noe consensus e-value: 2.4e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.95

Cal_vom7 | OW818031.2:55743690-55743915 (+) | 226 nt | IncRNA:noe consensus e-value: 1.4e-03

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.97

Cal_vom8 | OW818031.2:55746707-55746932 (-) | 226 nt | IncRNA:noe consensus e-value: 2.2e-01

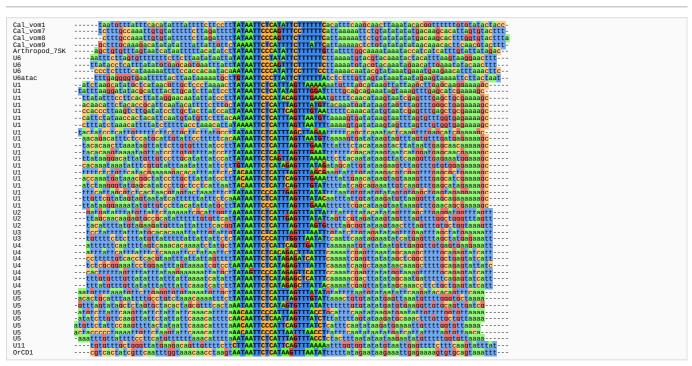
5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98

Cal_vom9 | OW818031.2:55747489-55747716 (-) | 228 nt | IncRNA:noe consensus e-value: 7.9e-05

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

	Cal_vom1	Cal_vom7	Cal_vom8	Cal_vom9
Cal_vom1	-	39	35	39
Cal_vom7		-	94	95
Cal_vom8			-	94
Cal_vom9				-

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.