Calliphora vicina

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

Assembly: GCA 958450345.1 idCalVici1.1 genomic

Cal_vic10 | OY288232.1:102506798-102507219 (-) | 422 nt | IncRNA:noe consensus e-value: 2.7e+00

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

Cal_vic2 | OY288234.1:45712663-45712892 (+) | 230 nt | IncRNA:noe consensus e-value: 1.1e-01

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.93

Cal_vic3 | OY288234.1:45716990-45717217 (-) | 228 nt | IncRNA:noe consensus e-value: 2.3e-01

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

Cal_vic4 | OY288234.1:45709138-45709363 (+) | 226 nt | IncRNA:noe consensus e-value: 4.4e-04

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

Cal_vic5 | OY288234.1:45711210-45711431 (+) | 222 nt | IncRNA:noe consensus e-value: 6.5e-04

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

Cal_vic6 | OY288234.1:45719261-45719488 (-) | 228 nt | IncRNA:noe consensus e-value: 2.6e-04

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

Cal_vic7 | OY288234.1:45708388-45708614 (+) | 227 nt | IncRNA:noe consensus e-value: 3.2e-01

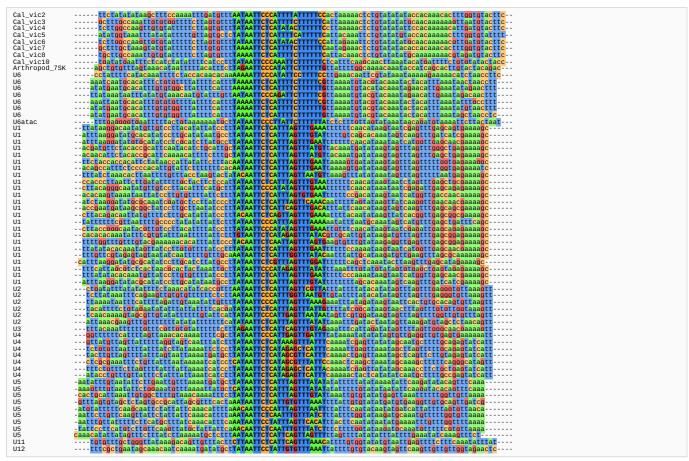
5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.99

Cal_vic8 | OY288234.1:45714864-45715090 (+) | 227 nt | IncRNA:noe consensus e-value: 1.3e-04

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.99

	Cal_vic10	Cal_vic2	Cal_vic3	Cal_vic4	Cal_vic5	Cal_vic6	Cal_vic7	Cal_vic8
Cal_vic10	-	40	38	32	38	39	39	39
Cal_vic2		-	92	88	88	91	92	90
Cal_vic3			-	90	88	88	91	90
Cal_vic4				-	86	92	91	89
Cal_vic5					-	86	90	87
Cal_vic6						-	93	89
Cal_vic7							-	90
Cal_vic8								-

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.