Drosophila orena

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > melanogaster subgroup

Assembly: GCA_005876975.1_DoreRS1_genomic

Dro_ore1 | VCKV01000009.1:5747463-5748541 (-) | 1079 nt | IncRNA:noe consensus e-value: 2e-198

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

Dro_ore2 | VCKV01000288.1:2050084-2050548 (-) | 465 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 1.00

Dro_ore3 | VCKV01000288.1:1554897-1555214 (+) | 318 nt | IncRNA:noe consensus e-value: 2.1e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 17nt PSE: 1.00

	Dro_ore1	Dro_ore2	Dro_ore3
Dro_ore1	-	23	15
Dro_ore2		-	49
Dro_ore3			-

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.