

Assembly: GCA_040802685.1_UNIL_Dlut_1.0_genomic

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

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

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

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.90

	Dro_lut1	Dro_lut2	Dro_lut3	Dro_lut4
Dro_lut1	-	30	13	15
Dro_lut2		-	36	34
Dro_lut3			-	61
Dro_lut4				-

[illegible]

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.