

Assembly: GCA_035042145.1_ASM3504214v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.97

	Dro_kok1	Dro_kok2
Dro_kok1	-	20
Dro_kok2		-

Dro_koki
Dro_kok2
Arthropod_75K
Arthropod_75K
Rnase_MRP
U6
U6atc
U6atc
U6atc
tRNAsec
snRNAME18SA1806
U1
U1
U1
U1
U2
U2
U2
U3
U4
U4
U4atc
U5
U5
U5
U11
U12
ORC21

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.