

Dasysyrphus tricinctus

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Dasysyrphus

Assembly: GCA_963921185.1_idDasTrii1.1_genomic

Das_tri1 | OY992532.1:48355042-48355338 (+) | 297 nt | lncRNA: noe consensus e-value: 1.7e-09

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

GGGCGGTTGGATGCTCACAGTTGATACGGTTGGTACATTCCGTTCCCAAAATGTAGTATCTAAATCGTATGCTTTGACAACATCCATACAAAAACGAAAAACAAAAACAAAAACAACTGC AAAATTTGTGTTTGAGAAATAAAATATAAGTTTTACCAAAAAAACACGCAAAACAAAAACTCTCCCTATCGTATAAGGATATCTATAATATAGAAATTAAGCCAAATCAATACAAATTGAGAAAAATATCTATCAAAAATGATATCTGCTGAGGTAGATGTGATCCCTTTTT

Das_tri1	-----	aaactttt	oattot	acotaa	ttatda	tcaaa	TATAAT	TCACAGAA	TTTT	attt	catcaat	daat	cattc	ataaa	aaatt	daa	tact	catacc	atc	-----	
Arthropod_7SK	-----	agatttact	attct	ctcat	attta	attta	aacact	cg	TATAGT	TCACAGAT	TTTT	tttt	ctgt	gttga	gttt	catat	agaact	cc	attact	atacca	ac
RNAse_MRP	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
U6	---	aaaa	taaaaa	aaat	ccct	gaat	tttt	gcac	ctca	TTTAAAT	TCACAGAT	TTTT	tttt	aaat	gaat	tt	caaat	gaat	taact	ctca	aaat
U6	---	aaaa	ataca	attaa	caat	gga	atttt	agc	attct	taTATAGT	TCACAGAT	TTTT	tttt	ccact	actt	gaaat	aaat	taaac	atttt	accca	ataac
U6	-----	taaa	ataat	ata	atg	attc	aaat	ttgt	tttaaaa	gTATAAT	TCACAGAT	TTTT	tttt	ccac	attaa	agtt	ctata	agt	gcatt	tttaaa	ttacat
U6atac	-----	aaaa	aaac	ccct	acaaa	tc	aaat	ccct	cttt	ctTTATAGT	TCACAGAT	TTTT	tttt	ccct	ctca	ta	caaat	tact	acaaa	atcc	tttccatt
tRNAsec	-----	aga	atg	ggag	ttgt	gtg	caag	attt	aaat	ctatc	ggTATAGT	TCACAGT	TTTT	tttt	ctga	attt	gttat	ctgt	tacat	caat	gtcttt
U1	---	ttct	caattt	ttc	atatt	tatt	gtatt	gtt	gattt	aaATAAT	TCACAT	TCAGTT	ttgt	gtag	aaaa	tt	aaat	gaaat	caag	cat	gataac
U1	---	ata	aat	ccca	aaat	ga	atc	attt	tttt	ttTATAGT	TCACAT	TTTAC	tttt	tacc	ataa	agtt	ac	taaa	atg	taaa	acatt
U1	---	ca	ct	cat	gtt	atc	acga	agga	gatt	tttt	gtatt	TTTTAAT	TCACAGT	TTGG	tttt	cca	atag	taaga	agac	gca	aaagat
U1	---	tt	cat	gat	cat	gat	att	tttt	gtct	tttaatt	ttAAATAAT	TCACAT	TTAG	TTgt	gtg	tag	aaat	tt	aaat	gaaat	caag
U1	---	tt	cat	gtt	cat	gat	att	tttt	gtct	tttaatt	ttAAATAAT	TCACAT	TTAG	TTgt	gtg	tag	aaat	tt	aaat	gaaat	caag
U2	---	aa	aa	at	a	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at
U2	---	ta	tg	caaaa	atg	ac	ttg	attt	tttt	ccct	cttt	taaa	TATAAT	TCACAGT	GTATG	ttg	tg	ag	cat	ta	taac
U3	---	ga	at	ac	caaaa	atg	att	tt	taatt	ttct	cttca	TATAAT	TTACAGT	TAC	TTatt	gc	caaa	gt	taac	ttgt	aga
U3	---	cc	at	at	acaaa	taaa	ta	at	at	at	at	at	at	at	at	at	at	at	at	at	at
U4	---	cg	ta	at	gtt	ga	attt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt
U4atac	---	tt	tt	ct	ac	cc	tt	ta	at	ac	taaa	TACAAT	TCACAT	TTTAC	TTc	ag	tag	att	gtt	ta	aa
U4atac	---	ag	o	tt	ct	ac	tt	ta	at	ac	taaa	TATTAT	TCACAT	TTTAC	TTc	ag	tag	att	gtt	ta	aa
U5	---	ta	cg	tc	ac	ac	at	g	at	ct	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt	tttt
U5	---	ta	ta	cat	ac	aa	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at
U5	---	tt	tt	att	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at
U5	---	tt	tt	ta	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at	at
U12	---	aa	t	caaa	atg	tc	att	gtt	gatt	ttta	attt	taac	at	tc	gatt	ttat	ctt	at	gatt	gc	ataa

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.