

# Drosophila atripex

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

**Assembly:** GCA\_035045925.1\_ASM3504592v1\_genomic

## Dro\_atr1 | JAWNOP010000012.1:15567013-15568078 (+) | 1066 nt | lncRNA: noe consensus e-value: 1e-183

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

GGGCGGTCGTCGATTCGCGACCAACGAGGGTGGACACATCCCGTCCCATCCCGCACTCTCTGAATTGTGTCCGTTGGTAGCCGAAGTTACGATTCGCAAAACTTTCGTCATCTCTCTCTCACTCTCTGAAGCAAAACAAAGGCGTAG  
CAGGACAGGCGCCACTGCCAAAGCGCACACAGCAAGAGCACAAAAACAAATGCTGTAGGTGGCTGAGAGCATTAAGCAAAATGCAATGCAATGGCTGAAGCACAGGACCAAACTACTAATATACAAAGTAAACAAAAACA  
AACAAACAGCAAAAGTCTAAACACACATATATATGAATCAGCAATCGAAAGATATATGACAAAAATGAAAAAATATCAGAACCAAAAGTATATCAATGCAAAACAAAAATCTAAAAACGTACATAAAAACACATAAAAAAAGA  
GAAGACATAACATAATGTACCTTAGATATATGATCATCTGTGTATATCGAGACCGCACAAAACTCGAAAAAATGTACAAAAAATATTTAAAAACCAAAATGCAATTGGTGTGTGTCTCCCTTTCGTATATCGTGGCG  
CGCCACGCCCCCAGCGCCACCCGCCAACCAACTAAACAAATTTCTAAATAGTAAAGAAATGGCAACGGAAATACGCTACCGGGCCAAAGACACBGACACGGTATCGGGAACCGACAGAGAAAGAACCCCGGGCG  
GGTTCAAAATCGGGTGGGTGGTGGGGCGCTCCACAAAAATTAACCATAGAGACGTTTAAAGCAATTCATAATGAACAAAAATTAACCAAAACAAATTTGATACGAGAAATTAAGCATTCAAAAATGAGCAATATGAGCA  
ACAACTAATAATGGCAAAAAAGCAAAACGCAACTGCAAAATACGACACAAACCTTCGAAAAAGACCTCAGTAATTAATACGAAAAAAGATGAAAAACCAACAAAAACACGTAAATGCTTGGTGGCTGCAAGGAAATGCTTTCGT  
TGATCGCCCTTTTTT

## Dro\_atr2 | JAWNOP010000063.1:8676018-8676482 (-) | 465 nt | lncRNA: noe consensus e-value: 9.5e-05

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

GGGCGTCGAGCGCTCAGAGTTATCAAGGGTTGTCACGTTCCCGACTTAATCGTGGAAACCAAAACAAATTAAGTGTGTGATCTCTCTCATCGGAGTGTCAAACTGCTAATAGCGCGCTAATGATTTCGCCGAAAAGCTAAATCGAGGA  
TTCAAAATTTGATGATCCTTCACTACTTTCBAAAACGCAATTTGAAAGAAAAAGATAATTTACGGGTGGGGGAAACTTAGCCAACTTCTCCCTCTCCACAAAGAAAAATTTATGATTGGAGCATTTGGCBATGCTGCTGCTATGAAAAATGC  
AAATGGCBATTTGACTAAATCCACCCGCTAGCGTGAAGTGTGTTAATCCATCCCTGGTAAATGAGTGGGGATTAATCAAAACAGCAAAATTCAAAAAACAACAAAAACACGTAAATGCTTGGTGGCTGCAAGGAAATGCTTTCGT  
TGATCGCTACTTTTT

	Dro_atr1	Dro_atr2
Dro_atr1	-	24
Dro_atr2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

Dro_atr1	-----c t t t t g c c g t t c a c t t t c a c c g c a t t t c g g c a t t t t g t g a t t c c c a a a t c g a a t t c a g g a c g a a c t g c a t a a g t a c a g g a t c g a a g g a c c t c c g t c-----
Dro_atr2	-----c t c t c t c a g a t t c g c t c g c t t g c c t a g t t a t a a t t c c a a g t g c a t a t t c g g a a g g t c a g a a t a a t a g c g t t g a t t g t a a t t t t c-----
Arthropod_7SK	-----a a a g g c a a a a c c a c c c c t d t t t t t t c t c t c t a t a a t t c t c a a c t g c a a t t t c d a a a t t t o o t c o t a t a t a t o o d a a a o t t t o a c o o t a o a t-----
RNAse_MRP	-----g c t a t t c t a t c g t t t g c c g c c c t t a t a a t t c c c a a c c g a a t t c a t c c a c t g g t a g c t a t a a a t a a c t c t g a g c c g a a d t c t c g t g c g t t-----
U6	-----h a t t g a c c c t a g a g g c c g c t c g c c g a g g t g c c t a t a a t t c c c a a g t a c t t t t t c a g c a t c g c t t c c t t t a a t a c a a c c t c t t c g a a c t a a c t t t-----
U6	-----h a a a d c c a c c t a t c d a a a t c c t t c t c t t t t a t a a t t c t c a a g t g t g a a t t c a a a a a d t g c a a t a a t a g o o d a t a t c t t a o d a c a a c t t c-----
U6atac	-----t t a a t a a a g t c a a a t a t t t t t a t c g t t g g c t a t a a t t c c c a a c t c g t a t t a t t c a g c g a g c a g c g t a t a a a t g c g c t g t a c c c g t a c c t-----
tRNAsec	-----h a t t t a t g t c t c t t t t a c t a c t t a g a a a t t c t a a t a a t t c t c a a g t g c t t t t t c a c a a a c c c t t t a t t a a t g g g a a t c a t g a a c a t t a g a a t-----
snoRNAme18SA1806	-----h a a a c a a t a c t o t o a a d t t c t t t t t o a d t c a a c t a t a a t t c c c a a g t g c t t t t t c o t t c d a a d t o a t t a t a t a a a t c a t t a c c a a c a a c c-----
U1	-----a a t t t t c a a t t g a t t c t t a a t c a t a a t t a t t g a c t a a a t t c c c a a c t g g t t c t g a c a t t g t c c t c a a c g a a a c c c t a c c t g g a c t g g a t a a g c-----
U1	-----c t g g t t t c c t c a c t c c a c g c t t g a a t a t g a a g t g g c t a a a a t t c t c a a c t g g t t c a g a a a t g t c c t c a t g g a a c c c t c t a c c g a g c c g a g a a a g c-----
U1	-----g a t t t t c a a c c c t a a g g t t a a a t t c g t t t g a g g a a t a a a a t t c t c a a c t a g t t t t a g a a t t g g t c t t c c g a a a t c c t t t a c c t g a g a g a a g a a g c-----
U1	-----h t c t a t t t t t a c t t a t t a a t t o t c g a a c t t g t a a t t c c c a a c t a g t t c a g c a t t g c c t t a a g a a a c c c t a c c t g a g c c g a a a a g c-----
U1	-----t c g g a a t t t c a a a a c a t t t c a a a c a a g c a a a c g a a a a a t t c c a a c t g g t t c t g t c t a a g a t a c a g a a a a c c c t t g a g g a g t c g g a a a a g c-----
U1	-----a c t a g g g g g t g g c t g c a t t g c a g c g a g t t c c a c t a t a a t t c t c a a c t g g t t c a g a c c a c g g g c t g a g a a c c c c t a g a g a g t g a g a a a g c-----
U1	-----h c c a t o t a c a c a a c o t t a t a a t t c a c t d a c c o t t a t a a t t c c c a a c t g g t t c t a g c a c c a t t c t a a t o a a a c c t a t t o t t o a c d a a a a a c-----
U1	-----t t t t g a a g a t t a a t t t t t a c a c c c g g a t t c g a g t a a a a t t c c c a a c a g t t c a g a c a g t c t c c t a t g g a a c c c t a c c t g a g c c g a g a a a g c-----
U1	-----t a t a t g t c t c a c a g c a c t t t c t t t c c c g t t c a t a a a a t t c c c a a c t a g t t c t g g c t a c a g c a t c a t g g a a t c c c c t a t a g a g a d c t g g g a a a g c-----
U2	-----t c a a a c a c a c c t c a c a t a d c a a d t t t t a c a t t g t a a t t c c c a a t c g g t t c a g a a g a t a t a t c a t t a a t t o o t t a c t t c a c c a t c t a a g t-----
U2	-----t g c t a c a g a a t a g a a c t t t c g t t c a c a g g a a t t g t a a t t c b c a a c c g t t t a g t c g c g t g c a t g a a g t g g c t a c t c t c g c t g g t t c a g u t-----
U2	-----c a t t t t c a c a g g t g a a a t t t t t c c a c t t t t a t c t a g a a t t c c c a a t c g g t t t t g g c a a t t c t c c g t c g a g a c a a c t t t t t g c t a a c c t a g t t-----
U2	-----c c a a c a a a c a c t c t a t a t a d a c a d a t t t c a d c t t c g a a t t c c c a a t c g g t t c a a g a a t a a d t o c a t t a a t o o t t a c c t t c c a d c c t c a a o t-----
U2	-----c c c t t a g g t a t g c t a c a a g a a t t a g t a c t c c c t c c c t g t a a t t c c t a a c c g g t t a a g a c a c a a a t g c a t t a c g g g g t a a a c g a t t c c a c c t t c a g g t-----
U2	-----a t a g a t t t t a c c t g a a a t t t t c g t c c g a c a t t t c t g t a a t t c t c a a c t g g t t c a a g t c g a a c a t t c a t a a g g t g g c t a t c t g t a c c a g g c t c a g g t-----
U2	-----c c c a t c t c a c t t t t t t t t t t t t o t a a a t o t c c t t g t a a t t c t a a c t g g t t t a a g a c a a a t a c a t a c a d o o d a a a c c t c c a t c t c a a o t-----
U2	-----g a c t c a t a a a a c g a a a t a g g t t t t g g a t a t c g a a t a a t t c c c a a c t a t t c t a g c t g t t c g c a t t a g a t c t g g g c t t c t a t a g g c a g g t t-----
U3	-----a a c a t t g c c t g g t t t t t t t t t t t t c t t t c t t t c t g t t a t g a t t c b c a a g t g g t t c t g g c a c a c c g c t c a g c a a c t c g g c a g g c t t g a a g t g t a t c t t t-----
U3	-----a c a t t o t t c o t o d d t t t t t c t t t t c t t o t t t a t g a t t c b c a a g t g g t t c t g g c c a c c c t c a a c a a c t c o d a a c c o t t o a d t o t a t c t t t-----
U4	-----t t t t g t g g t t g c t t g c t g t a c g t t a t g c g c c c t a t a a t t c b c a a c c g a t t c t g g c c a c t g g a a t g g a t a a g c a g g c t a c c g c a t t t g t t-----
U4atac	-----a a a a g t a t g t c a c t a t t g c a a a t a a a c c c c t a t a a t t c c c a a c a g t t c t g c a g c c c c a c t g t a a g c g g t t a g t t c c a a t g a a a g t t-----
U5	-----t t t g c c t a t c a a g g g t t g t a t a c c t g g a g t t t c g a t a t a a t t c c c a a c t a g t t a t a c t a c a g a a c c t a g g a g t t g a a g t t t t g a t g c a-----
U5	-----t t t a a g t a c a c t c c c c a t t a t-----
U5	-----t a t c t a c c d t t t t c c c a a c a t t c t t t t c a a g g t c t a t a a t t c c c a a c t g c t t c t a g c a n n c c a t t a a t t c t a c c c n a n a n c t a d c a a a-----
U5	-----a g g g c t a g g o d t a c g a c a a d a t d c c c c t a d t c c t a t a a t t c c a a c t t g t t t t a a g c a d c a a t d a c a d a a t a a a c t a t t q d d t t a d a d-----
U7	-----t t-----
U11	-----t a t a t a c c o t t o a a a t t c a c a a c a a a a a a t t a a a t t c c c a a c c g g t t t a g t-----
U12	-----t a a a a g c t t t t o d c g a a a c t a c c t t t c c c c c a c c a a t t c b c a a c t g g t t c t g g c a c c c t c a c a c t c c a c t c c c a c t o t a c a a c t c-----
OrCD1	-----a a c g t a c t a t a c c a g a t a t a c a a c c c a t g c c t t a t a a t t c t c a a c t g g t t g t a g c g c t g t c g t a a t a t g a a a g c a g a a a g t a c t t c t g g t t g-----

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod\_7SK, 7SL, RNAse\_MRP, RNAse\_P\_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.