

Lucilia caesar

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Calliphoridae > Lucilia

Assembly: GCA_965655125.1_idLucCaes4.1_genomic

Luc_cae1 | OZ296612.1:78836291-78836728 (+) | 438 nt | lncRNA: noe consensus e-value: 5.9e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 1.00

GGCGGTTCTAATCCCTGCAATGAAAGGGTTGTTACAGTTCCCTAACCAAAATGTTGAAATTCGTTAAAAATTCATTTCTCTAAAGCCGCCGTTAAATTAACGACGGACATTTCCAAAACATAAATAAAAAAATAAAAAATTTCTTCTCTAACAAAATCAAATACAAATTAATTTCTCTCAAACTTACACAAATGTTCTCTCTCTCGCATATTCAAAGCAATGTTTAAAAACACGATGACAAACCGCGCAATTCCTGAAAGATCAAATCTACAAATCCAAACAAAATAAAAAATATCTCAAAACAAATTCCAAAACACTTCTCTCTCAAAATGAAGCTTAAGATTAATGAAAAATTCGAGCCAAATTTGAAACAAAAAACATACAAATTCAAATGCCAAGAGGTTACGAAAAAGGTTGATCGCCATTTTTTTTTTT

Luc_cae2 | OZ296615.1:64197279-64197524 (-) | 246 nt | lncRNA: noe consensus e-value: 6.0e-01

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

GGCGATCTTGGTCTCTCAAGTGACAAAGGTTGTTCTCAAGCCCTTAATTTGTAGAAACTTTGAAAAATTTGCAAACTATCTATGAAAAATGATAAAATAGAGTTTAAAGTAAATCCAGGAATGTTTATAATGTTTTCAAAACAAATGAAATTTTCAAACACACTGCTGAGATTTCATGCTTTGGTAAGTGGTTGTATATAATGCAAAAGCTTTAAAGAGAGATAATGTCATGAAAAATGATCGCTACTTTTTT

Luc_cae3 | OZ296615.1:64203695-64203939 (-) | 245 nt | lncRNA: noe consensus e-value: 9.4e-01

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.86

GGCGATCTGAGTCTCTCAAGTGACAAAGGTTGTTCTCAAGCCCTGAATTTGTAAAACTTTGAAAAATTTGTCAAACTATCTATGAAAAATGATAAAATAGAGTTTAAATAAATCCAGGATGATGTTTAAATGATTGTTTCAAAACACTCAATTTTCAAAACACACTGCTGAGATTTCATGCTTTGGTAAGCGATTGTATATAATCTAAAGCTTTCAAGAGACTGAAAAAGTATCGCTACTATTTT

Luc_cae4 | OZ296615.1:64194284-64194521 (-) | 238 nt | lncRNA: noe consensus e-value: 1.4e-02

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.91

GGCGATCTTGGTCTCTCAAGTGATAAGGTTGTTCTCAAGCCCTTAATTTGTAGAAACTTTGAAAAATTTGCAAACTACTATCTGCGAAAAATGTTGAGTATGTAGTTTAAAAAATTCCTGGTTAAATGTTGTTCCAATATAATCGACTTTTCAAACACACTGCTGAGATTTCATGCTTTGGTAAGTGGTCGTGTATAAAAATAAGCTTTTAAGGGAGATGAAAAAGTATCGCTACTTTTTT

Luc_cae5 | OZ296615.1:64195584-64195813 (-) | 230 nt | lncRNA: noe consensus e-value: NA

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

GGCGATCTGGGTTCTCAAGTGACAAAGGTTGTTCTCAAGCCCTTAATTTGTAAAACTTTGAAAAATTTGTAAGCTATCTATGATAAAATAGAGTTTAAATAAAATCCAGGAATGATGATTGTTTCAAAACAAATCGATTTTCAAACACACTGCTGAGATTTCATGCTTTGGTAAGTGGTTGTATATAATCTAAAGCTTTAAAAAGAGACTTAAAAAGTATCGCTACTTTTTT

Luc_cae6 | OZ296615.1:64203012-64203247 (-) | 236 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.86

GGCGATCTTAGTCTCTCAAGTGATAAGGTTGTTCTCAAGCCCTTAATTTGTAAAACTTTGAAAAATTTGCAAACTATCTATGAAAAATGATAAAATAGAGTTTAAATAAAATCCAGGATGATGATTGTTTCAAAACAAATCGATTTTCAAACACACTGCTAAGATTTCATGCTTTGGTAAGTGGTTGTATATAATATAAGCTTTAAAGGGAGATAAAAATGTCATCGCTACTTTTTT

Luc_cae7 | OZ296615.1:64204844-64205079 (-) | 236 nt | lncRNA: noe consensus e-value: 1.2e+00

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.92

GGCGATCTTGGTCTATCATGAGAAAAAGTTGTTCCACATTCCTTAATTTGTATACCTTTGAAAAATTTGCAAACTATCTATGAAAAATTAATATAGTAAAGTTTAAATATACCCAGATAATGATGTTTGTGTCAAAACAAATATAATTAATAACACTCCGCTAAGATTTCAGGCTTTGGTAAGTGGTTGTATATAATACAAAGCTTAAAGGGAGACTGTAAAGTATCGCTACTTTTTT

Luc_cae8 | OZ296615.1:64190670-64190902 (-) | 233 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 6nt PSE: 0.90

GGCGATCTCGGTCCTCTAGCGACTAGGTTATTCACAGCCCTTAATTTGTAGAAACTTTGAAAAATTTGCAAACTACAAATGATGAAAAATGTTTGTAGTTTAAATAAAATCCTGGTTAAATGTTTTTCCAATACAAATCGACTTTTCAAACACACTGCTGAGATTTCATGCTTTGGTAAGTGGTCGTGTTCAAATAAATAAGCATTAAAGGGAGATAAAAAATGTCATCGCTACTTTTTT

	Luc_cae1	Luc_cae2	Luc_cae3	Luc_cae4	Luc_cae5	Luc_cae6	Luc_cae7	Luc_cae8
Luc_cae1	-	39	41	41	39	38	36	40
Luc_cae2		-	84	81	84	88	79	78
Luc_cae3			-	81	88	89	78	76
Luc_cae4				-	80	86	75	88
Luc_cae5					-	90	80	79
Luc_cae6						-	84	81
Luc_cae7							-	73
Luc_cae8								-

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

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Luc_cae1  -----caggatcttctgctgattttacattttacccctTATAATCCCATATTCCTTTTTcttagttttgaaacttaaatgatcatctttacccctgtacc--
Luc_cae2  -----tccattctttacaatctcaaaattattttttTATAATCCCATATTCCTTTTTCCactcataattttotataaatatcacgatcattataaadtattc--
Luc_cae3  -----aaatcagattcttataaaattataaaccctTATAATCCCATATTCCTTTTTactaaaaacctgtataaatatcacgatcattataaagaatttc--
Luc_cae4  -----ctctgcaaaaacttttacaataaacagtcctTATAATCCCATATTCCTTTTTctttagaacctctgtataaatatcttgatcattataaagcatctc--
Luc_cae5  -----tcttttcaaacatttactttttatttcttactTATAATCCCATATTCCTTTTTccaataaaaactttotataaataaacaacattataaadcattctc--
Luc_cae6  -----tctctttccaaattattctattttatttggctctTATAATCCCATATTCCTTTTTctttagaaacctctgtataaatgccatgatcaccctgaagcattcc--
Luc_cae7  -----aagtattttttatgtattctaaatactacacctTATAATCCCATATTCCTTTTTtggaaaaactctgtataaatataaaaaacttttaacttatttc--
Luc_cae8  -----aaatatctttgaacctctdcaaacattttttctTATAATCCCATATTCCTTTTTCCattfaaacctttotataaatatcacaaacatatcaadtatttc--
Arthropod_7SK -----catcacaagaacgtgttttagttaacattattttTATAATCCCATATTCCTTTTTcttatttggtaaaaaataataccacccaatttggataaccgac--
U6       -----ttaaactttctagcaataacactctcaccTATAATCCCATATTCCTTTTTcttaaaaaaacctgtataaatagcagagataacatttgaactctc--
U6       -----ttctaaacaattattttctctacatatctttTATAATCCCATATTCCTTTTTcttaaaaaactctgtataaatatcttcttaaatgaaccaccttc--
U6       -----aaatctataaaatttttacttgaatcgtttttctTACAATCCCATATTCCTTTTTctttaaactgtacgtataaaatagctctttaaagttagaaccttc--
U6       -----atctttttaaatagttttgtgtacagattttttTATAATCCCATATTCCTTTTTcttaaaaaactgtatacaaaatagtagatttaagttagataacctc--
U6       -----tttcaaatataattttgaacctcdaattttctTATAATCCCATATTCCTTTTTctttaaactgtacatacaaaatattttttaaantagccaacttc--
U6       -----ttttactatttatactcccaacatatcttctTATAATCCCATATTCCTTTTTcttaaaaaactgtacatacaaaatattttttaaagcagtaacttc--
U6       -----ttttactatttatactcccaacatatcttctTATAATCCCATATTCCTTTTTctttaaactgtacatacaaaatattttttaaagcagtaacttc--
U6       -----cccatatgtatataatttacttataaaaaaataTACAATCCCATATTCCTTTTTcttccctcttataataaatacaaaaataaattacttaaaaaa--
Luc_atac  -----aggatgttttctgtgatttacttttatttaagTACAATCCCATATTCCTTTTTtatttaaagtgttaaatataaacatcgccctcaatagtttttgtt--
tRNAsec  -----caatttcagttttacaatttttctgtctattttcattTATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----actttttdcttctotatataatttctctctTATAATCCCATATTCCTTTTTAGTTGATGtttaattttotataaadtcttcaactttaaocnaadaaaoc--
U1       -----tggaaaaacaataacatttcaaacactgtttattctTATAATCCCATATTCCTTTTTAGTTGATGtttaatttttaacatttttaacatttttaaggttagcaaaagc--
U1       -----caatttcagttttacaatttttctgtttattctTATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----ttctcaaacacataattataaacacatatatactTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
U1       -----tataatcaaaaataatgtttatctcagtcagtcagtcctTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
U1       -----accctagtttttttataattttttctcacaacaaacTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
U1       -----taaacacactaaadtaaacacacatatotatatctTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
U1       -----attctctcttatactacacacacataatattctTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
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U1       -----aaaatctactttttatcataattttaattattttaTCAATTCCTCAATAGTTTACAAAatctccttataaataaatttaatttttaaaadnaaaagac--
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U1       -----tctctgtgtatcttctgtgtgtgtctctcgaTATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----catatgtgtctcactaacgtcttctacaaaactcttTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
U1       -----cctaaadnaaaacataataaacacactcttcttatcTACAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----tctgtattttatctctgacattatttttttattctTATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----acatttttttctagtttttttctacttctttctTATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----taaacacactaaadtaaacacacatatotatatctTATAATCCCATATTCCTTTTTAGTTGATGttttaaacttttaacataaataaacaacttttaacacacaaagc--
U1       -----caggaaacgataaacacaaatttttataaaattctTGAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U1       -----ttcttaacaatttctgagaattcttctcttcttctTATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U2       -----aaccaacattttaaatattcttccaacatttaacTACAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
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U3       -----tcaatctctcttcaacataaaaataaattctctTATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
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U4       -----tatgccatgagttctgtttttattctatttactctTAATAATCCCATATTCCTTTTTAGTTTAAAAatattcatcataaagtagtcaaggttagcagcataaagc--
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U4atac    ttttatatacaaaaacgcaaaattttgtttattttttttTATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U5       -----aaacaaatttttcaacattctctcttcttaattctTATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U5       -----tattatagcttagctctcaacacgttacacattataTATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U5       -----aatcgaatttttaactagaaataagttctcattctctTCAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U5       -----atagctccacataatttctattttcacattatatctTGAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U5       -----atgactccacataatttctattttcacattatatctTGAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U5       -----atttcaaatattatcagcaaaccttctctgatttaagtaATAAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U11      -----tatttataatttttcaaaaacaaatgttttttctctTATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
U12      -----ttcaaaaacaaataaaatttgaataaaccttttgcTATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--
OrCD1    ---taaacaccacttagttctcacactaagaacactagctAATAATTCCTCAATAGTTTACAAAatattcatcataaagtagtcaaggttagcagcataaagc--

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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.