

# Phaonia tiefii

**Taxonomic lineage:** Brachycera > Muscomorpha > Muscoidea > Muscidae > Phaonia

**Assembly:** GCA\_963931995.1\_idPhaTief1.1\_genomic

<p><b>Pha_tie1   OZ008367.1:20366551-203666086 (+)   536 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 3nt    Trailing-T: 5nt    PSE: 0.93</p> <p>GGCBBTCTGAAAGGCTCTTCATTGAAAGGGTGGATGBCATCCCCCTTCAAAATGCGACAAAATTCACAATGGGAAGTATGGAACGCCAATTCGAATTACCCCTCTCTATCTCTCTCTCAATCATTCAATCTCACTCTCGCTCTCTCCCTATTCACATTTCAGACACACTCATACACATATGAACCTCAAAAACACACACACACACTCACTCAAAAGGGCTTTAACGACACACAAAAGTCCCTCGTCAAAATCAAAACACCAAAATATAACCAAAATCTTTCACACTCTCAAAATCAGACACTCTCAAAATCTCACTCTCAACCTACACACACTCCAGAAAACGCBAAAATTCGTAATCCCTTTCACATAGAAAATTCACACTTTCGCTCTCTCGTCAAGAAATTAACACAACTTCAAAAGATTCAAAATCTCTCAAAAAATTTGTCGCTTAAATTTGAAAACCTTGAAGAGGTTAAAGCAAAATCCAATTCGAAACAAAATGTAAAGGCGCGGAAAATGTAAATCGCCACCTTTTTT</p>
<p><b>Pha_tie2   OZ008369.1:141124304-141124821 (+)   518 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 3nt    Trailing-T: 6nt    PSE: 0.93</p> <p>GGCBBTCTGATGTTCCACTTTGGCATTGGGTTGCTACACATCCCCATCAGAAATGTGTGTTATACAAATGACCTTTTAACTTTTCGTTAAAAACATGAAAACATATAACAAATAAACAAACCAACAACTCCCTCGATGAAAAATATATGCAACCAACATATATACATATATAATGGAAAAACACACCCAAATACCAATGGAAAAATCTCAATTTAAAAATGTCCCGGCTTTTGATATGGAAAAAACACCAAAAAAABCGTTAAATTTTCACATCTCTCAGGATGTTGTAGTATAGACCAGAAATGCTATAACTTGGATACATAACGCTGGAGAGAGCGAACTCACACAGTTGAAAAATGGTCGAATCAAAAACATATAAAATCTCTAAAAACAAACCATAGACATTTTGGCAAAAAATATATAAAATATGAAAAATAGCAATAAAAATGGCGGGTCAAAATATCAAAATCAAAATGCTGGAAACATAACCGGATCGCCCTTTTTTT</p>
<p><b>Pha_tie3   OZ008367.1:146863143-146863428 (-)   286 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 4nt    PSE: 0.83</p> <p>GGCBBTCTGTACTCTCTGGAGAAAAGGTTGTTTCGCATCCCTAAATTCGCGAACAACAAAATTTGACAACTTCTCTTGTCTACTTTGGCAAAAGTACTAAGAAATGTGTACGCTAAGAGACGAAATTTAAAAATGTGTAATGATTAAAAATATACATATGGATTTATGATCCGTGAAAAATGAATCAATTTTCATACCTGAGACCGGTTCCACCTTTCAGGTTTCTGTACTAGGTTAGGTTTCATTTATAAAGCATGAGGAGGAGTACCAATTTGGTGTGCTATTTTT</p>
<p><b>Pha_tie4   OZ008367.1:147367799-147368082 (-)   284 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 6nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGGAGAAAAGGTTGTTTCGCATCCCTAAATTCGCGAACAACAAAATGTTGACGACTTCTCTTGTCTACTTTGGCAAAAGTACTAAGAAATGTGTACGCTAAGAGACGAAATTTAAAAATGTAGAAATGATTAAAAATATATATATGGATTTATGATCCGTGAAAAATGAATCAATTTTCATACCGAGACCGATTCCAGTGGGGCTCCAGGTTTCTGTAGGTTCCATTTCATAAATAAAGCCTGAAAGGGAATACAAATTTGTGATCGCTTTTTTT</p>
<p><b>Pha_tie5   OZ008367.1:146817091-146817372 (-)   282 nt   lncRNA: noe consensus e-value: 9.2e-01</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 6nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGGAGAAAAGGTTGTTTCGCATCCCTAAATTCGCGAACAACAAAATGTTGATGACTTCTCTTGTCTACTTTGGCAAAAGTACTAAGAAATGTGTACGCTAAGAGACGAAATTTAAAAATGTAGAAATGATTAAAAATATATATGGAATTTTATGATCCGTGAAAAATGAATCAATTTTCATACCGAGACCGATTCCAGGCTCTAGGTTTCTGTAGGTTAAGAGAGGTTCAATTCCTAACGAAATGAAGGGGAGGAGTACAATTTGTGATCGCTTTTTTT</p>
<p><b>Pha_tie6   OZ008367.1:147054929-147055206 (+)   278 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 6nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGGAGAAAAGGTTGTTTCGCATCCCTAAATTCGCGAACAACAAAATTTTGACGACTTCTCTTGTCTACTTTGGCAAAAGTACTAAGAAATGTGTACGCTAAGAGACGAAATTTAAAAATGTGTAATGATTAAAAATATATATGGATTTTATGATCCGTGAAAAATTAATCTAATTTTCATACCGAGACCGAATTCGCGTGGGGCCCTCCAGCTTTTCTGTAGGTTTCATTTCATAAGGCTTGAAGGGAGTACAATTTGTGATCGCTTTTTTT</p>
<p><b>Pha_tie7   OZ008367.1:146111674-146111911 (-)   238 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGAT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 6nt    PSE: 0.85</p> <p>GGCBAATCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATCCCTAAATTCGCGAACAACAAAATGTTGATTACTGCTCTACTTGTGGAAATCCCGAGTGAACAAATATAAAAAATAGAAATGATTGTATACGGATTATCCGTGAAAAATGAATCTAAATTTTCATACAGATACCGATTTCAGGTTTTCAGGCTCTGTAGTGGTTTCATAAGGCTTTAAGAGGGAGTACAATTTGTGATCGCTTTTTTT</p>
<p><b>Pha_tie8   OZ008367.1:146939247-146939503 (-)   257 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 6nt    PSE: 0.88</p> <p>GGCBBTCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATCCCTAGTTTCGCGAACAACAAAATGACAAATGGGTGCTACTTTGGAAAAATGTACTACGAAATGGGTACTCTGAGAGACAAAATTTAAATGTAGAAATGATTGTATACGGATTATCCGTGAAAAATGAATCTAAATTTTCATACATTTGCCBATTTCAGGTTTCAGGCTTTCTGTAGTGGTTTCATAAAGCTTGTAAAGGAGTATAATTTGTGATCGCTTTTTTT</p>
<p><b>Pha_tie9   OZ008368.1:26610793-26611049 (+)   257 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 6nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATTCCTTAATTCGCGAATCACAATGACTAATGGGTGCTACTTTGGAAAAATGTACTAACAAATGAGTACTCTGAGAGACAAAATTTAAATGTAGAAATGATTGTATACGGATTATGATCCGTGAAAAATGAATCTAAATTTTCATACAGTTGCCBATTTCAGGTTTCAGGCTTTCTGTAGTGGTTTCATAAAGCTTGTAAAGGAGTACGATTGTGATCGCTTTTTTT</p>
<p><b>Pha_tie10   OZ008368.1:26628611-26628867 (-)   257 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGT    Internal max. Poly-T: 4nt    Trailing-T: 7nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATCCCTTAATTCGCGAACAACAAAATGACTAATGGGTGCTACTTTGGAAAAATGTACTAAGAAATGAGTATACTGAGAGACAAAATTTAAATGTAGAAATGATTGTATACGGATTATGATCCGTGAAAAATGAATCTAAATTTTCATACAGTTGCCBATTTCAGGTTTCAGGCTTTCTGTAGTGGTTTCATAAAGCTTGTAAAGGAGTACAATTTGTGATCGTTTTTTTT</p>
<p><b>Pha_tie11   OZ008368.1:26633188-26633444 (+)   257 nt   lncRNA: noe consensus e-value: 2.6e+00</b></p> <p>5' motif: GCGGT    3' motif: ATCGT    Internal max. Poly-T: 4nt    Trailing-T: 7nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATCCCTTAATTCGCGAACAACAAAATGACTAATGGGTGCTACTTTGGAAAAATGTACTAAGAAATGAGTATACTGAGAGACAAAATTTAAATGTAGAAATGATTGTATACGGATTATGATCCGTGAAAAATGAATCTAAATTTTCATACAGTTGCCBATTTCAGGTTTCAGGCTTTCTGTAGTGGTTTCATAAAGCTTGTAAAGGAGTACAATTTGTGATCGTTTTTTTT</p>
<p><b>Pha_tie12   OZ008368.1:26652898-26653154 (+)   257 nt   lncRNA: noe consensus e-value: NA</b></p> <p>5' motif: GCGGT    3' motif: ATCGT    Internal max. Poly-T: 4nt    Trailing-T: 7nt    PSE: 0.83</p> <p>GGCBBTCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATCCCTTAATTCGCGAACAACAAAATGACTAATGGGTGCTACTTTGGAAAAATGTACTAAGAAATGAGTACTCTGAGAGACAAAATTTAAATGTAGAAATGATTGTATACGGATTATGATCCGTGAAAAATGAATCTAAATTTTCATACAGTTGCCBATTTCAGGTTTCAGGCTTTCTGTAGTGGTTTCATAAAGCTTGTAAAGGAGTACAATTTGTGATCGTTTTTTTT</p>
<p><b>Pha_tie13   OZ008367.1:203221909-203222158 (+)   250 nt   lncRNA: noe consensus e-value: 6.2e-01</b></p> <p>5' motif: GCGGT    3' motif: ATCGC    Internal max. Poly-T: 4nt    Trailing-T: 9nt    PSE: 0.95</p> <p>GGCBBTCTTGTACTCTCTGCTGAAAGGTTGTTTCGCATCCCTTAATTCGCGAACAACAAAATGACTAATGGGTGCTACTTTGGAAAAATGTACTAAGAAATGAGTATACTGAGAGACAAAATTTAAATGTAGAAATGATTGTATACGGATTATGATCCGTGAAAAATGAATCTAAATTTTCATACAGTTGCCBATTTCAGGTTTCAGGCTTTCTGTAGTGGTTTCATAAAGCTTGTAAAGGAGTACAATTTGTGATCGTTTTTTTT</p>

## Pairwise Identity Summary

<p>Sequences: 13</p> <p>Comparisons: 78</p> <p>Identity range: 31.8% - 98.4% (avg: 64.5%)</p>
---

**Distribution:** Low (<30%): 0 | Medium (30-60%): 33 | High (≥60%): 45

[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.