

## Supplementary Data

### Comparative Analysis of Nuclear tRNA Genes of *Nasonia vitripennis* with *Apis mellifera* and Other Sequenced Arthropods

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Supplementary Table 1a. List of Nasonia tRNA genes.

Gene ID	Position Scaffold	sequence
Ala( agc) -1	11:8988 42-898914 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -2	37:6475 44-647472 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -3	12:3038 187-3038262 Scaffold	taggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcg cctcaa
Ala( agc) -4	11:8974 47-897519 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgtgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -5	11:9106 64-910592 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgtgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -6	11:9083 44-908272 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -7	11:9111 00-911172 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -8	11:9197 60-919832 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -9	12:3037 408-3037480 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -10	12:3045 987-3046059 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -11	12:3046 797-3046869 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc) -12	3:18982 97-1898369 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca
Ala( agc)	37:6224 Scaffold	gggggcgtagctcagatggtagagcgctcgcttagcatgcgagaggtaccgggatcgataaccggcgcc tcca

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Ala(t gc)- 1	2:25953 34- 2595405 Scaffold	ggggatgtagctcagtggttagagcggttcgctttgcatgtgaaagggtcccgggttcgatccccggcatctcca
Ala(t gc)- 2	7:38095 92- 3809521 Scaffold	ggggatgtagctcagtggttagagcggttcgctttgcatgtgaaagggtcccgggttcgatccccggcatctcca
Ala(t gc)- 3	7:38100 39- 3810110 Scaffold	ggggatgtagctcagtggttagagcggttcgctttgcatgtgaaagggtcccgggttcgatccccggcatctcca
Arg( acg) -1	127:662 28- 66302 Scaffold	cggtcctgtggcgcaacggataacgcgtctgactacggatcagaagattccaggttcgaatcctggcagg atcga
Arg( acg) -2	46:2906 34- 290708 Scaffold	cggtcctgtggcgcaacggataacgcgtctgactacggatcagaagattccaggttcgaatcctggcagg atcga
Arg( acg) -3	37:8738 78- 873950 Scaffold	ggtcctgtggcgcaacggataacgcgtctgactacggatcagaagattccaggttcgaatcctggcagga tcg
Arg( acg) -4	9:89213- 89141 Scaffold	ggtcctgtggcgcaacggataacgcgtctgactacggatcagaagattccaggttcgaatcctggcagga tcg
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Arg( tcg)- 2	5:39705 35- 3970612 Scaffold	tgaccgtgtggcctaataaggataaggcgtcggactcggatccgaagattgcaggttcgagtcctgtcacggt cgacca
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-3	1379459	ccacttctgaca
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cag)	6-	gtcaggatggccgagtggtctaaggcgctgcgttcaggctgcagtcaccacttctgtgggcgtgggttcgaatc
-4	550443	ccacttctgaca
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taa)-	55-	gccaggttgcccgagcgggtctaaggcgcggttaagctcctgttccctctgggagcgtgggttcgaatc
1	4954938	ccacacctggca
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3	924392	ccacaccttagca
	Scaffold	
Leu(	16:9485	
tag)-	3-94774	ggcagcgtggccgagcgggtctaaggcgctggttttaggcaccagtccgaaagggcgtgggttcgaatccc
1	3-94774	accgctgtca
	Scaffold	
Leu(	7:38121	
tag)-	91-	ggcagcgtggccgagcgggtctaaggcgctggttttaggcaccagtccgaaagggcgtgggttcgaatccc
2	3812112	accgctgtca
	Scaffold	
Leu.	62:2305	GTCAGGATGGCCGAGCGGTctAAGGCGCCAGACTCAAGgtattaccttctcggtc
I.CA	27-	gaacaccgagtttctgggcaTTCTGGTCTCTCTGAGGGCGTGGGTTCGAATCCC
A-1	230408	ACTTCTGACA
	Scaffold	
Leu.	2:68563	GTCAGGATGGCCGAGCGGTctAAGGCGCCAGACTCAAGgttcatttcttctcggtc
I.CA	57-	taaacaccgagtttctgggcaTTCTGGTCTCTCTGAGGGCGTGGGTTCGAATCCC
A-2	6856237	ACTTCTGACA
	Scaffold	
Leu.	2:68552	GTCAGGATGGCCGAGCGGTctAAGGCGCCAGACTCAAGgattatataataccttct
I.CA	2:68552	cgattagacatcgagtttctgggcaTTCTGGTCTCTCTGAGGGCGTGGGTTCGAA
A-3	76-	TCCCATTCTGACA

6855150  
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9 2676014 cgc  
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Scaffold

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Scaffold

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Scaffold

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Scaffold

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	Scaffold	
	76:1885	
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	Scaffold	
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	Scaffold	
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	Scaffold	
	9:23097	
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	Scaffold	
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	Scaffold	
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	Scaffold	
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	Scaffold	
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	Scaffold	
Phe(	18:2018	
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	Scaffold	
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	Scaffold	
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agg)	93-	
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agg)	576-	
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	Scaffold	
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	Scaffold	
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cgg)	331-	
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 4 2375254 ggctcagtggtctaggggatgattctcgcttgggtgagagaggccccgggtcaaatccccggctgagccc  
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Thr( agt)- 2	37:8379 11- 837984 Scaffold	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatccctccgggg cct
Thr( agt)- 3	127:331 821- 331894 Scaffold	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatcccccggg gcct
Thr( agt)- 4	19:2361 065- 2361138 Scaffold	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatcccccggg gcct
Thr( agt)- 5	38:1706 428- 1706355 Scaffold	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatcccccggg gcct
Thr( cgt)- 1	127:230 914- 230843 Scaffold	gcctcttagctcagtggtagagcactggtctcgtaaaccaggggtcgtgagttcaaacctcacaggaggc a
Thr( cgt)- 2	136:173 645- 173716 Scaffold	gcctcttagctcagtggtagagcactggtctcgtaaaccaggggtcgtgagttcaaacctcacaggaggc a
Thr( cgt)- 3	43:4165 02- 416431 Scaffold	gcctcttagctcagtggtagagcactggtctcgtaaaccaggggtcgtgagttcaaacctcacaggaggc a
Thr(t gt)-1	116:687 501- 687573 Scaffold	gcctccatagctcaggggttagagcactggtctgtaaaccaggggtcgtgagttcaaacctctctggggg ca
Thr(t gt)-2	2:34292 57- 3429185 Scaffold	gcctccatagctcaggggttagagcactggtctgtaaaccaggggtcgtgagttcaaacctctctggggg ca
Trp( cca) -1	24:6670 87- 667159 Scaffold	gacttcgtggcgcaacggtagcgcgtctgactccagatcagaaggttcggtgtcaaatacagtcggggtc ac
Trp( cca) -2	24:6701 50- 670222 Scaffold	gacttcgtggcgcaacggtagcgcgtctgactccagatcagaaggttcggtgtcaaatacagtcgaggtc ac
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Scaffold

Trp( 5:35823  
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A-1 3971824 aaATCCATAGGtCGCTGGTTCAAATCCGGCTCGAAGGA  
Scaffold

Tyr.l 17:6493  
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Scaffold

Tyr.l 17:6530  
.GT 25- CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGTtggcttacaacaaaa  
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Scaffold

Tyr.l 17:6489  
.GT 88- CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGTtgggtttaacaaaaatc  
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Scaffold

Tyr.l 7:34036  
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Scaffold

Tyr.l 17:6504  
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Scaffold

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Scaffold

Tyr.l 19:1460  
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aac) 20:1854 ca



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Supplementary Table 1b. List of honey bee tRNA genes.

Gene id	Position	Sequence
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Ala(aggc)-2	Group4.1 1:26137-26065	gggggcgtagctcagatggtagagcgctcgcttagcatgagaggtaccgggatcgatgcccggcgcctcca
Ala(aggc)-3	Group4.1 1:45143-45071	gggggcgtagctcagatggtagagcgctcgcttagcatgagaggtaccgggatcgatgcccggcgcctcca
Ala(aggc)-4	Group4.8: 58903-58975	gggggcgtagctcagatggtagagcgctcgcttagcatgagaggtaccgggatcgatgcccggcgcctcca
Ala(aggc)-5	Group7.3 7:202242-202170	gggggcgtagctcagatggtagagcgctcgcttagcatgagaggtaccgggatcgatgcccggcgcctcca
Ala(aggc)-6	Group7.3 7:203068-202996	gggggcgtagctcagatggtagagcgctcgcttagcatgagaggtaccgggatcgatgcccggcgcctcca
Ala(aggc)-7	Group7.3 7:203376-203304	gggggcgtagctcagatggtagagcgctcgcttagcatgagaggtaccgggatcgatgcccggcgcctcca
Ala(cgc)-1	Group15. 29:72798-6-728059	tgggggtgtaactcagtggttagagtgtctgcttcgatgctgaaagtctgggttcaaataccagctacctccaa
Ala(cgc)-2	Group15. 34:204620-204691	gggggtgtaactcagtggttagagtgtctgcttcgatgctgaaagtctgggttcaaataccagctacctccaa
Ala(ggc)-1	Group6.3 8:125920-125849	ccctggatagcttaatggttaaagcagtcgcctggcaagcgaagatccgggttcgattcccgggtccaggca
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Met(cat)-3	Group15. 13:15532 -15458	agcagagtggcgcagtggaagcgtgctgggcccataaccagaggtccgtggatcgaaccacgctc tgcta
Met(cat)-4	Group8.2 0:870084 -870155	agcagagtggcgcagtggaagcgtgctgggcccataaccagaggtccgtggatcgaaccacgctc tgcta
Met(cat)-5	Group8.2 0:870432 -870361	agcagagtggcgcagtggaagcgtgctgggcccataaccagaggtccgtggatcgaaccacgctc tgcta
Met(cat)-6	Group8.2 0:870860 -870931	agcaggggtggcgcagtggaagcgtgctgggcccataaccagaggtccgtggatcgaaccacgctc tgcta
Met(cat)-7	GroupUn. 357:5089 -5160	tgctcggtagcgcagtaggcagcgcgtaagtctcataatctaaggtcgtgattcgatcctcaccggg gcaa
Phe(gaa)-1	Group1.7 3:71156- 71084	gccgaaatagctcagttgggagagcgtagactgaagatctaaatgtcccgggtcagatcccgggttcg ca
Phe(gaa)-2	Group11. 4:135005 -134933	gccgaaatagctcagttgggagagcgtagactgaagatctaaatgtcccgggtcaatcccgggttcg gca
Phe(gaa)-3	Group4.5: 9454- 9526	gccgaaatagctcagttgggagagcgtagactgaagatctaaatgtcccgggtcaatcccgggttcg gca
Phe(gaa)-4	Group6.3 8:168377 -168449	gccgaaatagctcagttgggagagcgtagactgaagatctaaatgtcccgggtcaatcccgggttcg gca
Phe(gaa)-5	GroupUn. 81:2865- 2793	gccgaaatagctcagttgggagagcgtagactgaagatctaaatgtcccgggtcagatcccgggttcg gca
Phe(gaa)-6	GroupUn. 81:3185- 3113	gccgaaatagctcagttgggagagcgtagactgaagatctaaagggtcccgggtcaatcccgggttcg gca
Pro(agg)-1	Group16. 19:74288 6-742815	ggctcgttggtctaggggtatgattctcgcttaggggtcgcgagaggtcccgggtcaaatcccggacgagcc c
Pro(agg)-2	Group16. 20:3409- 3338	ggctcgttggtctaggggtatgattctcgcttaggggtcgcgagaggtcccgggtcaaatcccggacgagcc c
Pro(agg)	Group4.2 3:678509	ggctcgttggtctaggggtatgattctcgcttaggggtcgcgagaggtcccgggtcaaatcccggacgagcc c

-3	-678438	
Pro(agg)	GroupUn. 7179:188	ggctcgttggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggacgagcc
-4	-117	c
Pro(cgg)	Group10. 9:108282	ggctcgttggtctaggggatgatttctcgcttaggggtgcgagaggtcccgggtcaaatacccggacgagcc
-1	-108211	c
Pro(cgg)	Group16. 19:74354	ggctcgttggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggacgagcc
-2	8-743619	c
Pro(cgg)	GroupUn. 9233:306	ggctcgttggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggacgagcc
-3	-235	c
Pro(cgg)	GroupUn. 9236:708	ggctcgttggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggacgagcc
-4	2-7153	c
Pro(tgg)	Group10. 19:33560	ggctcagtggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggctgagcc
1	5-335534	c
Pro(tgg)	Group2.3 6:438407	ggctcagtggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggctgagcc
2	-438336	c
Pro(tgg)	Group7.2 8:51137-	ggctcagtggtctaggggatgattctcgcttaggggtgcgagaggtcccgggtcaaatacccggctgagcc
3	51208	c
Pro(tgg)	Group7.2 8:51557-	ggcctcttggtctaggggatgattcctgcttaggggtgcaggaggtcccgggtcaaatacccggagggggcc
4	51628	c
Ser(aga)	Group15. 28:19831	gcagtcgtggccgagtggttaaggcgtctgactagaaatcagattccctctgggagcgtaggttcgagtc
-1	4-198395	ctaccgactgcg
Ser(aga)	Group4.1 2:309507	gcagtcgtggccgagtggttaaggcgtctgactagaaatcagattccctctgggagcgtaggttcgagtc
-2	-309588	ctaccgactgcg
Ser(aga)	Group4.1 7:328828	gcagtcgtggccgagtggttaaggcgtctgactagaaatcagattccctctgggagcgtaggttcgagtc
-3	-328747	ctaccgactgcg
Ser(aga)	Group4.9: 215905-	gcagtcgtggccgagtggttaaggcgtctgactagaaatcagattccctctgggagcgtaggttcgagtc
-4	215824	ctaccgactgcg
Ser(aga)	Group8.1 6:83736-	gcagtcgtggccgagtggttaaggcgtctgactagaaatcagattccctctgggagcgtaggttcgagtc
-5	83655	ctaccgactgcg
Ser(cga)	Group1.2: 279388-	gcagccgtggccgagtggttaaggcgtctgactcgaatcagattccctctgggagcgtaggttcgaatc
-1	279469	ctaccgctgcg
Ser(cga)	Group5.6: 116273-	gctgtggtgtccgagtggttaaggagtcagactcgaatctgatgggctatgcccgcacaggttcgaatc
-2	116354	ctgtccgagcg
Ser(cga)	GroupUn. 101:5407	gctgcggtgtccgagtggttaaggagttggactcgaatccaatgggttttcccgcataaggttcgaatcct
-3	7-53996	atccgtagcg
Ser(gct)	Group10. 37:20168	tgacgaggtggccgagtggttaaggcgttaggactgctaataccaatgtgctctgcacgcgtgggttcgaatc
1	4-201765	ccatcctcgtcga
Ser	Group11. gacgaggtggccgagtggttaaggcgttaggactgctaataccaatgtgctctgcacgcgtgggttcgaatc	

gct)- 2	3:50135- 50216	ccatcctcgtcg
Ser( gct)- 3	Group12. 14:27441 -27522	gacgaggtggccgagtggttaaggcgttgactgctaataccaatgtgctctgcacgcgtgggttcgaat ccatcctcgtcg
Ser( gct)- 4	Group8.2 0:752405 -752488	gacgaggtggccgagtggttaaggcgttgactgctaataccaatgtgctctgcacgcgtgggttcgaat ccatcctcgtcg
Ser(t ga)- 1	Group11. 31:59545 8-595385	aatctttagcgcacgatcgagcgctacaactcttgaaaaggttatcactcgatccttcgagtcacgatc t
Ser(t ga)- 2	Group12. 30:13845 96- 1384678	gctgcggtgtccgagcggtaaggagatggactgaaatccattgggtgtaacccgcacaggttcgaat cctgtccgcagcg
Ser(t ga)- 3	GroupUn. 130:3284 3-32926	tgctgcggtgtccgagcggtaaggagatggactgaaatccattgggttctaccgcgcaggttcgaatc ctgtccgcagcgg
Thr( agt)- 1	Group15. 28:19865 2-198725	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatccctccggg gcct
Thr( agt)- 2	Group16. 19:72892 1-728994	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatccctccggg gcct
Thr( agt)- 3	Group16. 19:74127 2-741197	ggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatccctccggg gcct
Thr( agt)- 4	Group4.2 3:679171 -679244	ggcgccgtggcttagctggtaagcgcctgtctagtaaacaggagatcgaggggttcgaatcccccg ggcct
Thr( agt)- 5	Group6.5 5:648436 -648509	aggcgccgtggcttagttggttaaagcgcctgtctagtaaacaggagatcgaggggttcgaatccctccg gagcctt
Thr( cgt)- 1	Group10. 28:97838 -97909	gcctcttagctcagtggttagagcactggtctcgtaaaccaggggtcgtgagtcaatcctcacaggaggc a
Thr( cgt)- 2	Group6.1 6:30470- 30399	gcctcttagctcagtggcagagcactggtctcgtaaaccaggggtcgtgagtcaaacctcacaggagg ca
Thr(t gt)-1	Group14. 11:22675 9-226687	gcctccatagctcaggggtagagcactggtctgtaaaccaggggtcgagagttcaaatctctctgggg gca
Thr(t gt)-2	Group3.2 7:176965 -176893	gcctccatagctcaggggtagagcactggtctgtaaaccaggggtcgagagttcaaatctctctgggg gca
Thr(t gt)-3	Group3.2 7:182246 -182174	gcctccatagctcaggggtagagcactggtctgtaaaccaggggtcgagagttcaaatctctctggag gca
Trp( cca) -1	Group15. 28:19441 7-194488	gactccgtggcgcaacggtagcgcgtctgactccagatcagaaggttcggtgtcaaatcacgtcggggg ca
Trp( cca) -2	Group15. 28:19779 3-197864	gactccgtggcgcaacggtagcgcgtctgactccagatcagaaggttcggtgtcaaatcacgtcggggg ca
Trp( cca)	Group3.2 5:936255	gactccgtggcgcaacggtagcgcgtctgactccagatcagaaggttcggtgtcaaatcacgtcggggg ca

-3	-936184	
Trp(	Group8.4	
cca)	6:248383	gactccgtggcgcaacggtagcgcgtctgactccagatcagaaggtgctgttcaaatcacgtcgggggt
-4	-248454	ca
	Group11.	
Tyr.l	31:19963	
.GT	84-	CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGttggaagttaaaaat
A-1	1996282	atacggacATCCATAGGtCGCTGGTTCGAATCCGGCTCGAAGGA
Tyr.l	Group2.3	
.GT	3:720608	CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGttggaagttaaaaat
A-2	-720512	atacggacATCCATAGGtCGCTGGTTCGAATCCGGCTCGAAGGA
Tyr.l	Group2.3	
.GT	3:726740	CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGttggtccgagtaatcttt
A-3	-726644	aaaagagagacATCCATAGGtCGCTGGTTCGAATCCGGCTCGAAGGA
Tyr.l	Group3.1	
.GT	3:47543-	CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGttggcttcttaaaaatt
A-4	47449	gacagatATCCATAGGtCGCTGGTTCGAATCCGGCTCGAATGA
Tyr.l	Group5.2	
.GT	7:210227	CCTTCGATAGCTCAGTTGGTAGAGCGGTGGACTGTAGttggtgattctggaga
A-5	-210318	cATCCATAGGtCGCTGGTTCGAATCCGGCTCGAAGGA
Val(	Group3.2	
aac)	5:62723-	gttccgtgggtagtagggtatcacatccgcctaacacgcggaaggtccccggttcgatccccgggcggaa
-1	62651	aca
Val(	Group3.2	
aac)	5:63218-	gttccgtgggtagtagggtatcacatccgcctaacacgcggaaggtccccggttcgatccccgggcggaa
-2	63146	aca
Val(	Group3.4:	
aac)	119167-	gttccgtgggtagtagggtatcacatccgcctaacacgcggaaggtccccggttcgatccccgggcggaa
-3	119239	aca
Val(	Group3.5:	
aac)	76455-	gttccgtgggtagtagggtatcacatccgcctaacacgcggaaggtccccggttcgatccccgggcggaa
-4	76383	aca
Val(	Group4.1	
aac)	5:89921-	gttccgtgggtagtagggtatcacatccgcctaacacgcggaaggtccccagttcgatccccgggcggaa
-5	89849	aca
Val(	Group11.	
cac)	28:93339	gttccgtagtagtagggtatcacgtgtgcttcacacgcacaaggtccccggttcgatccccgggcggaaa
-1	-93267	ca
Val(	Group8.3	
cac)	5:133764	gttccgtagtagtagggtatcacgtgtgcttcacacgcacaaggtccccggttcgatccccgggcggaaa
-2	-133836	ca
Val(	Group9.2	
cac)	1:76362-	gttccgtagtagtagggtatcacgtgtgcttcacacgcacaaggtccccggttcgatccccgggcggaaa
-3	76290	ca
Val(t	Group12.	
ac)-	22:12384	ggtccgtgggtagtagggtatcacatctgctttacacgcagaagatcaccggttcgattccggtcggaaacc
1	3-123768	a
Val(t	Group12.	
ac)-	30:67324	ggtccgtgggtagtagggtatcacgtgtgctttacacgcagaaggtcggcgggttcgatccccggtcggaaac
2	9-673321	cacca
Val(t	Group3.3	
ac)-	8:389054	ggtccgtgggtagtagggtatcacgtgtgctttacacgcagaaggtcggcgggttcgatccccggccggaaac
3	-389126	ca

Supplementary Table 2a. Clusters of tRNAs in the *Nasonia* genome. Different clusters are shown by alternate colors.

tRNA	scaffold	start	end
Arg(cct)-1	Scaffold1	1329943	1329870
Arg(cct)-2	Scaffold1	1337257	1337184
Lys(ctt)-8	Scaffold1	2938137	2938064
Ser(gct)-1	Scaffold1	2939538	2939457
Ala(agg)-4	Scaffold11	897447	897519
Ala(agg)-1	Scaffold11	898842	898914
Ala(agg)-6	Scaffold11	908344	908272
Ala(agg)-5	Scaffold11	910664	910592
Ala(agg)-7	Scaffold11	911100	911172
Ala(agg)-8	Scaffold11	919760	919832
Ala(agg)-9	Scaffold12	3037408	3037480
Ala(agg)-3	Scaffold12	3038187	3038262
Ala(agg)-10	Scaffold12	3045987	3046059
Ala(agg)-11	Scaffold12	3046797	3046869
Gln(ttg)-2	Scaffold127	320220	320291
Gln(ctg)-3	Scaffold127	326382	326311
Thr(agt)-3	Scaffold127	331821	331894
Phe(gaa)-1	Scaffold136	145649	145721
Phe(gaa)-2	Scaffold136	150403	150475
Met(cat)-2	Scaffold139	161051	160980
Met(cat)-3	Scaffold139	162351	162280
Ile(aat)-1	Scaffold14	1817766	1817692
Ile(aat)-2	Scaffold14	1817929	1817855
Gly(tcc)-1	Scaffold1516	8071	7999
Gly(tcc)-6	Scaffold1516	10250	10178
Pro(tgg)-3	Scaffold16	2364362	2364433
Pro(agg)-3	Scaffold16	2373506	2373577
Pro(cgg)-2	Scaffold16	2374331	2374259
Pro(tgg)-4	Scaffold16	2375325	2375254
Pro(tgg)-5	Scaffold16	2375921	2375850
Pro(tgg)-6	Scaffold16	2380219	2380290
Pro(cgg)-1	Scaffold16	2915911	2915982
His(gtg)-1	Scaffold16	2920720	2920649
His(gtg)-2	Scaffold16	2920918	2920847
Tyr.I.GTA-4	Scaffold17	648988	648894
Tyr.I.GTA-2	Scaffold17	649381	649279
Tyr.I.GTA-6	Scaffold17	650468	650562
Tyr.I.GTA-3	Scaffold17	653025	652930
Tyr.I.GTA-7	Scaffold17	653374	653280
Ser(aga)-1	Scaffold174	121495	121414
Ser(aga)-2	Scaffold174	124276	124357
Phe(gaa)-6	Scaffold18	2018736	2018808
Phe(gaa)-7	Scaffold18	2018911	2018983
Tyr.I.GTA-9	Scaffold19	1460475	1460381
Tyr.I.GTA-8	Scaffold19	1460941	1460843
Pro(agg)-6	Scaffold19	2360576	2360504

Thr(agt)-4	Scaffold19	2361065	2361138
Lys(ttt)-5	Scaffold19	2702418	2702346
Lys(ttt)-2	Scaffold19	2702606	2702534
Val(aac)-6	Scaffold2	2586994	2586922
Leu(aag)-2	Scaffold2	2591564	2591645
Ala(tgc)-1	Scaffold2	2595334	2595405
Glu(ttc)-3	Scaffold2	6854218	6854147
Leu.I.CAA-3	Scaffold2	6855276	6855150
Leu.I.CAA-2	Scaffold2	6856357	6856237
Val(cac)-2	Scaffold20	542425	542353
Val(cac)-3	Scaffold20	543802	543730
Val(aac)-1	Scaffold20	1852080	1852154
Val(aac)-3	Scaffold20	1853127	1853199
Val(aac)-4	Scaffold20	1854222	1854294
Gly(gcc)-1	Scaffold21	2766610	2766680
Asp(gtc)-3	Scaffold21	2767278	2767349
Trp(cca)-1	Scaffold24	667087	667159
Trp(cca)-2	Scaffold24	670150	670222
Trp(cca)-3	Scaffold3	42692	42763
Asn(gtt)-1	Scaffold3	43229	43156
Pro(agg)-2	Scaffold3	1897733	1897804
Ala(agc)-12	Scaffold3	1898297	1898369
Cys(gca)-5	Scaffold3	1902611	1902683
Cys(gca)-2	Scaffold3	1902804	1902876
Thr(agt)-1	Scaffold3	1905870	1905797
Gly(gcc)-5	Scaffold36	1181244	1181314
Gly(gcc)-6	Scaffold36	1181887	1181817
Gly(gcc)-2	Scaffold36	1189016	1188943
Asp(gtc)-10	Scaffold36	1190204	1190133
Glu(ttc)-4	Scaffold37	867980	868051
Glu(ttc)-5	Scaffold37	870139	870068
Arg(acg)-3	Scaffold37	873878	873950
Glu(ttc)-6	Scaffold37	879334	879263
Ser(gct)-2	Scaffold38	1705742	1705823
Thr(agt)-5	Scaffold38	1706428	1706355
Asp(gtc)-2	Scaffold38	1707122	1707051
Ile(aat)-5	Scaffold40	467329	467255
Ile(aat)-9	Scaffold40	468070	468143
Pro(tgg)-1	Scaffold40	926365	926294
Pro(tgg)-2	Scaffold40	926922	926851
Arg(tcg)-2	Scaffold5	3970535	3970612
Tyr.I.GTA-1	Scaffold5	3971916	3971824
Val(aac)-7	Scaffold5	4009123	4009051
Val(aac)-2	Scaffold5	4009689	4009617
Pro(agg)-4	Scaffold6	3402691	3402620
Pro(agg)-5	Scaffold6	3402893	3402822
Ile.I.TAT-1	Scaffold62	68579	68670
Ile.I.TAT-3	Scaffold62	69860	69952
Gly(gcc)-8	Scaffold62	858922	858992
Asp(gtc)-5	Scaffold62	862933	863004

Asp(gtc)-6	Scaffold62	863186	863257
Asp(gtc)-7	Scaffold62	863329	863400
Asp(gtc)-8	Scaffold62	872362	872433
Lys(ctt)-11	Scaffold62	876189	876262
Lys(ctt)-6	Scaffold62	878625	878698
Lys(ctt)-3	Scaffold62	879074	879147
Gln(ttg)-3	Scaffold7	3395653	3395724
Tyr.l.GTA-5	Scaffold7	3403698	3403791
Leu(taa)-2	Scaffold7	3802519	3802602
Ala(tgc)-2	Scaffold7	3809592	3809521
Ala(tgc)-3	Scaffold7	3810039	3810110
Gln(ctg)-5	Scaffold7	3811076	3811151
Leu(tag)-2	Scaffold7	3812191	3812112
Glu(ctc)-7	Scaffold8	3271512	3271583
Glu(ttc)-7	Scaffold8	3273877	3273948
Glu(ctc)-5	Scaffold8	3274486	3274415
Arg(acg)-4	Scaffold9	89213	89141
Ile(aat)-6	Scaffold9	95529	95455
His(gtg)-5	Scaffold9	338317	338388
His(gtg)-6	Scaffold9	338960	339031
His(gtg)-7	Scaffold9	342615	342686
His(gtg)-8	Scaffold9	343938	344009
Met(cat)-7	Scaffold9	345769	345843

Supplementary Table 2b. Clusters of tRNAs in the honey bee genome. Different clusters are shown by alternate colors.

tRNA	linkage_group	start	end
Ser(gct)-1	Group10.37	201684	201765
Asp(gtc)-1	Group10.37	202350	202277
Lys(ctt)-2	Group10.37	203884	203956
Asn(gtt)-1	Group10.37	204383	204310
Ile(aat)-2	Group11.38	5049	5122
Arg(acg)-1	Group11.38	7858	7930
Gly(tcc)-1	Group14.23	489378	489450
Gly(ccc)-1	Group14.23	492651	492581
Met(cat)-3	Group15.13	15532	15458
Arg(cct)-2	Group15.13	16134	16206
His(gtg)-2	Group15.13	16856	16785
Leu(aag)-2	Group15.28	193033	193114
Trp(cca)-1	Group15.28	194417	194488
Trp(cca)-2	Group15.28	197793	197864
Ser(aga)-1	Group15.28	198314	198395
Thr(agt)-1	Group15.28	198652	198725
Lys(ttt)-3	Group15.34	202681	202608
Ala(cgc)-2	Group15.34	204620	204691
Thr(agt)-2	Group16.19	728921	728994
Cys(gca)-1	Group16.19	732607	732536
Thr(agt)-3	Group16.19	741272	741197
Ala(agc)-1	Group16.19	741802	741730
Pro(agg)-1	Group16.19	742886	742815
Pro(cgg)-2	Group16.19	743548	743619
Gly(tcc)-2	Group2.33	312541	312468
Gly(tcc)-3	Group2.33	312897	312824
Gly(tcc)-4	Group2.33	313063	312990
Gly(tcc)-5	Group2.33	313229	313156
Ala(tgc)-2	Group2.33	338066	338139
Leu(tag)-1	Group2.33	345629	345708
Gln(ctg)-3	Group2.33	346324	346251
Ala(tgc)-3	Group2.33	346764	346835
Leu(taa)-2	Group2.33	352854	352770
Gln(ttg)-1	Group2.33	718762	718833
Gln(ctg)-4	Group2.33	718918	718991
Gln(ttg)-2	Group2.33	719546	719619
Gln(ttg)-3	Group2.33	719709	719782
Gln(ctg)-5	Group2.33	719873	719944
Tyr.I.GTA-2	Group2.33	720608	720512
Gln(ttg)-4	Group2.33	724582	724653
Gln(ttg)-5	Group2.33	724738	724809
Gln(ttg)-6	Group2.33	724903	724974
Gln(ctg)-6	Group2.33	725060	725133
Gln(ttg)-7	Group2.33	725679	725752



Gln(ttg)-8	Group2.33	725842	725915
Gln(ctg)-7	Group2.33	726006	726077
Tyr.I.GTA-3	Group2.33	726740	726644
Gln(ttg)-9	Group2.33	733442	733371
Arg(tcg)-3	Group3.13	46968	47042
Tyr.I.GTA-4	Group3.13	47543	47449
Val(aac)-1	Group3.25	62723	62651
Val(aac)-2	Group3.25	63218	63146
Asn(gtt)-3	Group3.25	935588	935663
Trp(cca)-3	Group3.25	936255	936184
Thr(tgt)-2	Group3.27	176965	176893
Thr(tgt)-3	Group3.27	182246	182174
Arg(tct)-1	Group3.38	382894	382966
Val(tac)-3	Group3.38	389054	389126
Glu(ttc)-1	Group4.12	263659	263730
Ile(aat)-5	Group4.12	264576	264501
Asp(gtc)-3	Group4.12	270915	270842
Arg(acg)-2	Group4.12	289393	289465
Ile(aat)-6	Group4.12	289961	289888
Glu(ttc)-2	Group4.13	1007031	1006960
Glu(ttc)-3	Group4.13	1007259	1007188
Glu(ctc)-3	Group4.13	1009428	1009357
Glu(ctc)-4	Group4.13	1041564	1041493
Glu(ttc)-4	Group4.13	1042079	1042008
Glu(ttc)-5	Group4.13	1044256	1044185
Glu(ttc)-6	Group4.13	1047522	1047451
Pro(agg)-3	Group4.23	678509	678438
Thr(agt)-4	Group4.23	679171	679244
Lys(ttt)-4	Group4.8	85527	85453
Lys(ttt)-5	Group4.8	85692	85618
Lys(ctt)-4	Group4.8	93619	93691
Gly(gcc)-2	Group4.9	275293	275363
Gly(gcc)-3	Group4.9	275669	275739
Gly(gcc)-4	Group4.9	277549	277619
Asn(gtt)-5	Group6.55	647432	647505
Thr(agt)-5	Group6.55	648436	648509
Pro(tgg)-3	Group7.28	51137	51208
Pro(tgg)-4	Group7.28	51557	51628
Ala(agc)-5	Group7.37	202242	202170
Ala(agc)-6	Group7.37	203068	202996
Ala(agc)-7	Group7.37	203376	203304
Met(cat)-4	Group8.20	870084	870155
Met(cat)-5	Group8.20	870432	870361
Met(cat)-6	Group8.20	870860	870931
Gly(gcc)-7	Group8.27	21318	21248
Gly(gcc)-8	Group8.27	21936	21866
Asp(gtc)-5	Group8.27	23288	23217
Asp(gtc)-6	Group8.27	24089	24018

Glu(ctc)-5	Group9.21	75307	75236
Leu.I.CAA-2	Group9.21	75914	75792
Val(cac)-3	Group9.21	76362	76290
Met(cat)-7	GroupUn.357	5089	5160
Lys(ctt)-6	GroupUn.357	5521	5449
Phe(gaa)-5	GroupUn.81	2865	2793
Phe(gaa)-6	GroupUn.81	3185	3113

Supplementary Table 2c. Selected tRNA gene clusters in the silk worm genome.  
Different clusters are shown by alternate colors.

Bmor tRNA Scaffold		start	end
Tyr	nscaf1898	6657861	6657949
Tyr	nscaf1898	6747169	6747257
Tyr	nscaf1898	6748377	6748465
Tyr	nscaf1898	6750640	6750731
Tyr	nscaf1898	6753351	6753439
Tyr	nscaf1898	6759467	6759555
Asp	nscaf2210	3006094	3006165
Asp	nscaf2210	3007925	3007997
Asp	nscaf2210	3008835	3008907
Asp	nscaf2210	3010143	3010215
Asp	nscaf2210	3013055	3013127
Asp	nscaf2210	3014215	3014287
Asp	nscaf2210	4392827	4392898
Asp	nscaf2210	4397857	4397928
Asp	nscaf2210	4402487	4402558
Asp	nscaf2210	4406195	4406266
Gly	nscaf2853	220297	220367
Gly	nscaf2853	222380	222450
Gly	nscaf2853	223490	223560
Gly	nscaf2853	227808	227878
Gly	nscaf2853	228377	228447
Gly	nscaf2853	234606	234676
Gly	nscaf2853	244621	244691
Gly	nscaf2853	246199	246269
Gly	nscaf2853	261690	261760
Gly	nscaf2853	262230	262300
Gly	nscaf2853	279533	279603
Gly	nscaf2853	283768	283838
Gly	nscaf2853	287478	287548
Ser	nscaf2882	9723	9804
Ser	nscaf2882	10520	10601
Ser	nscaf2882	11322	11403
Ser	nscaf2882	12619	12700
Ser	nscaf2882	15348	15429
Met	nscaf2902	5012141	5012212
Met	nscaf2902	5012306	5012377
Met	nscaf2902	5012471	5012542
Met	nscaf2902	5012641	5012712
Met	nscaf2902	5016401	5016472
Met	nscaf2902	5016566	5016637
Met	nscaf2902	5016731	5016802
Asn	nscaf2964	2675990	2676063

Asn	nscaf2964	2676173	2676246
Asn	nscaf2964	2676356	2676429
Asn	nscaf2964	2715549	2715622
Asn	nscaf2964	2715732	2715805
Asn	nscaf2964	2715915	2715988
Asn	nscaf2964	2716103	2716176
Asn	nscaf2964	2732571	2732644
Asn	nscaf2964	2732754	2732826
Asn	nscaf2964	2732936	2733009
Asn	nscaf2964	2733119	2733192
Ala	nscaf3066	897797	897875
Ala	nscaf3066	900476	900554
Ala	nscaf3066	901865	901943
Ala	nscaf3066	902808	902886
Ala	nscaf3066	904522	904600
Ala	nscaf3066	905284	905362
Ala	nscaf3066	906009	906087
Ala	nscaf3066	906739	906817
Ala	nscaf3066	908416	908494
Ala	scaffold11343	146	218
Ala	scaffold11343	297	369
Ala	scaffold11343	448	520
Ala	scaffold11343	599	671
Ala	scaffold14128	96	168
Ala	scaffold14128	246	318
Ala	scaffold14128	398	470
Ala	scaffold14128	549	621
Met	scaffold15441	154	225
Met	scaffold15441	319	390
Met	scaffold15441	484	555
Asn	scaffold17259	54	127
Asn	scaffold17259	237	310
Asn	scaffold17259	420	493
Asn	scaffold17259	603	676
Ala	scaffold23280	153	225
Ala	scaffold23280	304	376
Ala	scaffold23280	455	527
Asp	scaffold864	3341	3412
Asp	scaffold864	4999	5070
Asp	scaffold864	9953	10024

Supplementary Table 2d. Selected tRNA gene clusters in the *Drosophila melanogaster* genome. Different clusters are shown by alternate colors.

Dmel tRNA	Chromosome	start	end
Arg	chr2R	1668923	1668995
Asn	chr2R	1669411	1669484
Asn	chr2R	1669585	1669658
Asn	chr2R	1669907	1669980
Lys	chr2R	1670069	1670141
Lys	chr2R	1672264	1672336
Lys	chr2R	1673372	1673444
Ile	chr2R	1673539	1673612
Arg	chr2R	1676995	1677067
Lys	chr2R	1678884	1678956
Arg	chr2R	1679075	1679147
Ile	chr2R	8946189	8946262
Leu	chr2R	8946602	8946722
Ile	chr2R	8946891	8946964
Ile	chr2R	8947192	8947265
Ile	chr2R	8947684	8947757
Ile	chr2R	8948000	8948073
Glu	chr2R	15241005	15241076
Glu	chr2R	15242323	15242394
Glu	chr2R	15242844	15242915
Glu	chr2R	15243051	15243122
Glu	chr2R	15243750	15243821
Glu	chr3L	1363466	1363537
Glu	chr3L	1363770	1363841
Glu	chr3L	1364061	1364132
Glu	chr3L	1381227	1381298
Glu	chr3L	1381464	1381535
Glu	chr3L	1381701	1381772
Glu	chr3L	1381938	1382009
Glu	chr3L	1384972	1385043
Glu	chr3L	1385313	1385384
Cys	chr3L	3079269	3079340
Cys	chr3L	3079523	3079594
Cys	chr3L	3079901	3079972
Leu	chr3L	8034161	8034243
Leu	chr3L	8034398	8034480
Leu	chr3L	8034621	8034703
Leu	chr3L	8039590	8039672
Leu	chr3L	8039941	8040023
Asn	chr3R	3965255	3965328
Arg	chr3R	3965673	3965745
Arg	chr3R	3965945	3966017

Arg	chr3R	3966198	3966270
Arg	chr3R	3966449	3966521
Val	chr3R	13443483	13443555
Pro	chr3R	13443832	13443903
Ala	chr3R	13445460	13445532
Pro	chr3R	13445683	13445754
Ala	chr3R	13445866	13445938
Ala	chr3R	13448268	13448340
Thr	chr3R	13450287	13450360
Thr	chr3R	13450528	13450601
Val	chr3R	13454808	13454880
Ala	chr3R	13456764	13456836
Pro	chr3R	13457401	13457472
Ala	chr3R	13471029	13471101
Pro	chr3R	13471332	13471403
Ala	chr3R	13472090	13472162
Ala	chr3R	13472405	13472477
Ala	chr3R	13482867	13482939
Ala	chr3R	13484103	13484175
Ser	chr3R	18222250	18222331
Ser	chr3R	18222521	18222602
Ser	chr3R	18222902	18222983
Arg	chrX	13848751	13848823
Ser	chrX	13848982	13849063
Ser	chrX	13849382	13849463
Arg	chrX	13850140	13850212
Arg	chrX	13850745	13850817
Arg	chrX	13850947	13851019