

Table S1. Organization of the *Myrmeleon immanis* mt genome.

Gene	Strand	position	size	start codon	stop codon	anticodon	Intergenic nucleotides
<i>rnI</i>	J	1-64	64			GAT	
<i>s1</i>		65-134	70				0
<i>trnQ</i>	N	135-203	69			TTG	0
<i>trnM</i>	J	213-280	68			CAT	9
<i>nad2</i>	J	281-1294	1014	ATT	TAA		0
<i>trnC</i>	N	1293-1356	64			GCA	-2
<i>trnW</i>	J	1361-1426	66			TCA	4
<i>trnY</i>	N	1430-1495	66			GTA	3
<i>cox1</i>	J	1499-3032	1534	ACG	T-tRNA		3
<i>trnL1(UUR)</i>	J	3033-3097	65			TAA	0
<i>cox2</i>	J	3099-3780	682	ATG	T-tRNA		1
<i>trnK</i>	J	3781-3851	71			CTT	0
<i>trnD</i>	J	3855-3922	68			GTC	3
<i>atp8</i>	J	3923-4081	159	ATT	TAA		0
<i>atp6</i>	J	4075-4752	678	ATG	TAA		-7
<i>cox3</i>	J	4753-5541	789	ATG	TAA		0
<i>trnG</i>	J	5542-5606	65			TCC	0
<i>nad3</i>	J	5607-5960	354	ATA	TAA		0
<i>trnA</i>	J	5963-6027	65			TGC	2
<i>trnR</i>	J	6028-6091	64			TCG	0
<i>trnN</i>	J	6091-6158	68			GTT	-1
<i>trnS1(AGN)</i>	J	6158-6226	69			GCT	-1
<i>trnE</i>	J	6226-6291	66			TTC	-1
<i>trnF</i>	N	6290-6354	65			GAA	-2
<i>nad5</i>	N	6354-8087	1734	ATA	TAA		-1
<i>trnH</i>	N	8085-8149	65			GTG	-3
<i>nad4</i>	N	8149-9489	1341	ATG	TAA		-1
<i>nad4l</i>	N	9483-9779	297	ATG	TAA		-7
<i>trnT</i>	J	9782-9846	65			TGT	2
<i>trnP</i>	N	9847-9913	67			TGG	0
<i>nad6</i>	J	9916-10431	516	ATT	TAA		2
<i>Cytb</i>	J	10431-11567	1137	ATG	TAA		-1
<i>trnS2(UCN)</i>	J	11566-11635	70			TGA	-2
<i>s2</i>		11636-11656	21				0
<i>nad1</i>	N	11657-12610	954	ATA	TAG		0
<i>trnL2(CUN)</i>	N	12611-12675	65			TAG	0
<i>rrnL</i>	N	12676-13979	1304				0
<i>trnV</i>	N	13980-14051	72			TAC	0
<i>rrnS</i>	N	14052-14828	777				0
<i>A+T-rich region</i>		14829-15799	971				0
whole genome		1-15799	15799				

Negative numbers indicate that adjacent genes overlap.

Table S2. Organization of the *Nymphes myrmeleonoides* mt genome.

Gene	Strand	position	size	start codon	stop codon	anticodon	Intergenic nucleotides
<i>trnI</i>	J	1-66	66			GAT	0
<i>s1</i>		67-124	58				0
<i>trnQ</i>	N	125-193	69			TTG	0
<i>trnM</i>	J	223-291	69			CAT	29
<i>nad2</i>	J	292-1302	1011	ATT	TAA		0
<i>trnC</i>	N	1301-1367	67			GCA	-2
<i>trnW</i>	J	1368-1433	66			TCA	0
<i>trnY</i>	N	1442-1509	68			GTA	8
<i>cox1</i>	J	1512-3045	1533	TCG	T-tRNA		2
<i>trnL1(UUR)</i>	J	3046-3111	66			TAA	1
<i>cox2</i>	J	3115-3799	685	ATG	T-tRNA		3
<i>trnK</i>	J	3800-3870	71			CTT	0
<i>trnD</i>	J	3870-3935	66			GTC	-1
<i>atp8</i>	J	3936-4097	162	ATT	TAA		0
<i>atp6</i>	J	4091-4768	678	ATG	TAA		7
<i>cox3</i>	J	4772-5560	789	ATG	TAA		3
<i>trnG</i>	J	5567-5631	65			TCC	6
<i>nad3</i>	J	5632-5985	354	ATT	TAA		0
<i>trnA</i>	J	5998-6064	67			TGC	12
<i>trnR</i>	J	6079-6143	65			TCG	14
<i>trnN</i>	J	6146-6211	66			GTT	2
<i>trnS1(AGN)</i>	J	6211-6280	70			GCT	-1
<i>trnE</i>	J	6281-6347	67			TTC	0
<i>trnF</i>	N	6351-6416	66			GAA	3
<i>nad5</i>	N	6418-8151	1734	ATT	TAA		1
<i>trnH</i>	N	8149-8213	65			GTG	-3
<i>nad4</i>	N	8214-9551	1338	ATG	TAA		0
<i>nad4l</i>	N	9545-9838	294	ATG	TAA		-7
<i>trnT</i>	J	9841-9907	67			TGT	2
<i>trnP</i>	N	9908-9972	65			TGG	0
<i>nad6</i>	J	9974-10489	516	ATT	TAA		1
<i>Cytb</i>	J	10493-11629	1137	ATG	TAA		3
<i>trnS2(UCN)</i>	J	11628-11694	67			TGA	-2
<i>s2</i>		11695-11710	16				0
<i>nad1</i>	N	11711-12661	951	ATA	TAG		0
<i>trnL2(CUN)</i>	N	12659-12722	64			TAG	-3
<i>rrnL</i>	N	12723-14042	1320				0
<i>trnV</i>	N	14043-14114	72			TAC	0
<i>rrnS</i>	N	14115-14900	786				0
<i>A+T-rich region</i>		14901-15712	812				0
whole genome		1-15712	15713				

Negative numbers indicate that adjacent genes overlap.

Table S3. Start/Stop codons in Neuropterida mitochondrial genes.

Taxon	<i>nad2</i>		<i>cox1</i>		<i>cox2</i>		<i>atp8</i>		<i>atp6</i>		<i>cox3</i>		<i>nad3</i>	
	ST	EN	ST	EN	ST	EN	ST	EN	ST	EN	ST	EN	ST	EN
<i>Myrmeleon immanis</i>	ATT	TAA	ACG	Taa	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAA	ATA	TAA
<i>Nymphes myrmeleonoides</i>	ATT	TAA	TCG	Taa	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAA	ATT	TAA
<i>Libelloides macaronius</i>	TTG	TAA	ACG	Taa	ATG	Taa	ATT	TAA	ATG	TAa	ATG	TAA	ATA	TAA
<i>Ascaloptynx appendiculatus</i>	ATT	TAA	TTA	Taa	ATG	Taa	ATT	TAA	ATG	TAa	ATG	TAA	ATA	TAA
<i>Chrysoperla nipponensis</i>	ATT	TAA	TCG	Taa	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAA	ATT	TAG
<i>Chrysopa pallens</i>	ATT	TAA	ATT	Taa	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAA	ATT	TAG
<i>Apochrysa matsumurae</i>	ATT	TAA	TCG	Taa	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAA	ATC	TAG
<i>Ditaxis biseriata</i>	ATT	TAA	ATT	Taa	ATG	Taa	ATT	TAA	ATG	TAa	ATG	TAA	ATT	TAA
<i>Polystoechotes punctatus</i>	ATT	TAA	TCG	Taa	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAa	ATT	TAA
<i>Thyridosmylus langii</i>	ATG	TAA	TCG	TAA	ATG	Taa	ATT	TAA	ATG	TAA	ATG	TAA	ATT	TAG
<i>Corydalus cornutus</i>	ATT	TAA	ATT	TAa	ATG	Taa	ATT	TAA	ATG	TAa	ATG	Taa	ATT	Taa
<i>Neochauliodes punctatolus</i>	ATT	TAA	ATC	Taa	ATG	TAA	ATC	TAA	ATG	TAA	ATG	TAA	ATT	TAG
<i>Sialis hamata</i>	ATT	TAA	ATT	Taa	ATG	Taa	ATC	TAA	ATG	TAa	ATG	TAA	ATT	TAA
<i>Mongoloraphidia harmandi</i>	ATT	TAa	CTG	Taa	ATA	Taa	ATC	Taa	ATG	TAa	ATG	TAa	ATC	Taa

Taxon	<i>nad5</i>		<i>nad4</i>		<i>nad4L</i>		<i>nad6</i>		<i>cytb</i>		<i>nad1</i>	
	ST	EN	ST	EN	ST	EN	ST	EN	ST	EN	ST	EN
<i>Myrmeleon immanis</i>	ATA	TAA	ATG	TAA	ATG	TAA	ATT	TAA	ATG	TAA	ATA	TAG
<i>Nymphes myrmeleonoides</i>	ATT	TAA	ATG	TAA	ATG	TAA	ATT	TAA	ATG	TAA	ATA	TAG
<i>Libelloides macaronius</i>	ATT	Taa	ATG	TAA	ATG	TAA	ATA	TAa	ATG	Taa	ATA	TAG
<i>Ascaloptynx appendiculatus</i>	ATA	Taa	ATG	TAa	ATG	TAA	ATC	TAA	ATG	Taa	ATA	TAG
<i>Chrysoperla nipponensis</i>	ATA	Taa	ATG	Taa	ATG	TAA	ATT	TAA	ATG	TAA	ATG	TAA
<i>Chrysopa pallens</i>	ATT	Taa	ATG	Taa	ATG	TAA	ATT	TAA	ATG	TAA	ATA	TAA
<i>Apochrysa matsumurae</i>	ATA	Taa	ATG	Taa	ATG	TAA	ATT	TAA	ATG	TAA	ATA	TAA
<i>Ditaxis biseriata</i>	ATT	Taa	ATG	Taa	ATG	TAA	ATT	TAA	ATG	Taa	TTG	TAA
<i>Polystoechotes punctatus</i>	ATT	Taa	ATG	Taa	ATG	TAA	ATC	TAa	ATG	Taa	TTG	TAG
<i>Thyridosmylus langii</i>	ATC	Taa	ATG	Taa	ATG	TAA	ATT	TAA	ATG	Taa	ATT	TAG
<i>Corydalus cornutus</i>	ATT	Taa	ATG	Taa	ATG	TAA	ATT	TAa	ATG	Taa	TTG	TAA
<i>Neochauliodes punctatolus</i>	ATA	Taa	ATG	TAa	ATG	TAA	ATA	TAA	ATG	TAA	TTG	TAA
<i>Sialis hamata</i>	ATT	Taa	ATG	Taa	ATG	TAA	ATT	TAa	ATG	Taa	ATG	TAA
<i>Mongoloraphidia harmandi</i>	ATA	TAA	ATG	Taa	ATT	TAA	ATA	TAa	ATG	TAA	TTG	TAA

ST: start codon; EN: stop codon; TAa and Taa: incomplete stop codon.

Table S4. The tRNA feature of the *Myrmeleon immanis* mt genome.

	AA arm	DHU arm	AC arm	AC loop	TΨC arm	mismatch	Position
Ala(A)	7	4	5	7	4	G-U	AA arm
Arg(R)	7	3	5	7	4		
Asn(N)	7	3	5	7	4		
Asp(D)	7	4	5	7	5	2 G-U	AC arm, TΨC arm
Cys(C)	7	3	5	7	3		
Gln(Q)	7	4	5	7	5	3 G-U	2 DHU arm, 1 AC arm
Glu(E)	7	4	5	7	4		
Gly(G)	7	4	5	7	5	2 G-U	2 DHU arm
His(H)	7	4	5	7	4	2 G-U	DHU arm, AC arm
Ile(I)	6	3	5	7	5	G-U	TΨC arm
Leu1(L1,UUR)	7	3	5	7	5		
Leu2(L2,CUN)	7	3	5	7	5		
Lys(K)	7	3	4	7	5	G-U	AA arm
Met(M)	7	4	4	7	5	G-U	AA arm
Phe(F)	7	4	5	7	4	G-U	DHU arm
Pro(P)	7	4	5	7	4	G-U	DHU arm
Ser1(S1,AGN)	7	loop	5	7	5	G-U	TΨC arm
Ser2(S2,UCN)	7	4	5	7	5	G-U	TΨC arm
Thr(T)	7	4	5	7	4		
Trp(W)	7	4	5	7	3	<u>U-U</u>	TΨC arm
Tyr(Y)	7	3	5	7	4	3 G-U	DHU arm, AC arm, TΨC arm
Val(V)	7	4	4	7	5		
total							20 G-U mismatch : AA arm (3); AC arm (4); TΨC arm (5); DHU arm (8)

Number exhibits the base pair on the arm and the base on the loop. The U-U mismatch underlined.

Table S5. The tRNA feature of the *Nymphes myrmeleonoides* mt genome.

	AA arm	DHU arm	AC arm	AC loop	TΨC arm	mismatch	Position
Ala(A)	7	4	5	7	5	G-U	AA arm
Arg(R)	7	4	5	7	4	G-U	DHU arm
Asn(N)	7	3	5	7	3		
Asp(D)	7	4	5	7	5		
Cys(C)	7	4	5	7	4		
Gln(Q)	7	4	5	7	5	G-U	DHU arm
Glu(E)	7	4	5	7	5		
Gly(G)	7	4	5	7	5	2 G-U	2 DHU arm
His(H)	7	4	5	7	4	2 G-U	DHU arm, AC arm
Ile(I)	7	3	5	7	4	G-U	AC arm
Leu1(L1,UUR)	7	3	5	7	5		
Leu2(L2,CUN)	7	3	5	7	3	G-U	DHU arm
Lys(K)	7	3	4	7	5		
Met(M)	7	4	4	7	5		
Phe(F)	7	4	5	7	4	G-U	DHU arm
Pro(P)	7	4	5	7	5	G-U	DHU arm
Ser1(S1,AGN)	7	loop	4	7	5	G-U,A-C	TΨC arm, AC arm
Ser2(S2,UCN)	7	4	5	7	5		
Thr(T)	7	4	5	7	5		
Trp(W)	7	4	4	7	4	<u>U-U</u>	AC arm
Tyr(Y)	7	3	5	7	4	2 G-U	AA arm, DHU arm
Val(V)	7	4	5	7	4	G-U	AA arm
total							15 G-U mismatch AA arm (3); AC arm (2); TΨC arm (1); DHU arm (9)

Number exhibits the base pair on the arm and the base on the loop. The U-U mismatch underlined.

Table S6. AT-, GC-Skew and A+T% in whole mt genomes within Neuropterida.

Number	Name	A+T%	AT-Skew	GC-Skew
1	<i>Libelloides macaronius</i>	<u>74.5</u>	<u>0.0711</u>	-0.1765
2	<i>Ascaloptynx appendiculatus</i>	75.5	0.0675	-0.2049
3	<i>Chrysoperla nipponensis</i>	78.9	-0.0063	<u>-0.1374</u>
4	<i>Chrysopa pallens</i>	79.5	0.0038	-0.1471
5	<i>Apochrysa matsumurae</i>	79.1	<u>-0.0367</u>	-0.1810
6	<i>Ditaxis biseriata</i>	79.8	0.0150	-0.1782
7	<i>Polystoechotes punctatus</i>	78.9	-0.0292	-0.1619
8	<i>Thyridosmylus langii</i>	76.7	-0.0143	-0.2103
9	<i>Corydalis cornutus</i>	74.9	0.0147	<u>-0.2590</u>
10	<i>Neochauliodes punctatolus</i>	76.3	0.0170	-0.2489
11	<i>Sialis hamata</i>	78.3	0.0140	-0.1705
12	<i>Mongoloraphidia harmandi</i>	80.3	0.0237	-0.2284
13	<i>Nymphes myrmeleonoides</i>	<u>80.5</u>	-0.0112	-0.1385
14	<i>Myrmeleon immanis</i>	75.6	0.0238	-0.1755
	average	77.8	0.0109	-0.1870

The maximum and minimum values marked by underline.

Table S7. Taxa and accession numbers used in the present phylogenetic analysis.

Superorder	Order	Family/Subfamily	Name	Length	NCBI	
Neuropteroidae	Neuroptera	Ascalaphidae	<i>Libelloides macaronius</i>	15,890	NC_015609	
			<i>Ascaloptynx appendiculatus</i>	15,877	NC_011277	
			<i>Myrmeleon immanis</i>	15799	KJ461323	
		Myrmeleontidae	Nymphidae	<i>Nymphes myrmeleonoides</i>	15713	KJ461322
			Chrysopidae	<i>Chrysoperla nipponensis</i>	16,057	NC_015093
		<i>Chrysopa pallens</i>		16,723	NC_019618	
		<i>Apochrysa matsumurae</i>		16,214	NC_015095	
		Mantispidae	<i>Ditaxis biseriata</i>	16,416	NC_013257	
			Ithonidae	<i>Polystoechotes punctatus</i>	16,036	NC_011278
				Osmylidae	<i>Thyridosmylus langii</i>	16,221
		Megaloptera	Corydalinae	<i>Corydalus cornutus</i>	15,687	NC_011276
			Chauliodinae	<i>Neochauliodes punctatolus</i>	15,734	NC_018772
			Sialidae	<i>Sialis hamata</i>	15,608	NC_013256
		Raphidioptera	Raphidiidae	<i>Mongoloraphidia harmandi</i>	16,006	NC_013251

Table S8. Primer sequences of *Myrmeleon immanis* mt genome used in this study.

Number	Primer ID	Nucleotide sequence (5'-3')	Reference
1	F20(SPB-586)	CCATTCCATTTYTGATTTC	Simon <i>et al.</i> , 2006
	R20(SPB-1738)	TTTATTCGTGGAAATGCTATGTC	Simon <i>et al.</i> , 2006
2	F21(SPB-1709)	AATTGGTGGTTTTGGAAATTG	Simon <i>et al.</i> , 2006
	R21(SPB-2776)	GGTAATCAGAGTATCGACG	Simon <i>et al.</i> , 2006
3	F01(SPA-2756)	ACATTTTTCTCAACATT	Simon <i>et al.</i> , 2006
	R01(SPA-3665)	CCACAAATTTCTGAACACTG	Simon <i>et al.</i> , 2006
4	F02(SPA-3399)	TCTATTGGTCATCAATGGTACTG	Simon <i>et al.</i> , 2006
	R02(SPA-4061)	GAAAATAAATTTGTTATCATTTTTCA	Simon <i>et al.</i> , 2006
5	F03(SPA-3790)	CATTAAGTACTGAAAGCAAGTA	Simon <i>et al.</i> , 2006
	R03(SPA-4552)	ATGACCTGCAATTATATTAGC	Simon <i>et al.</i> , 2006
6	TF4463	TTTGCCCATCTWGTWCNCAAGG	Simon <i>et al.</i> , 2006
	TR4908	CGAGTTAYATCTCGTCATCATTG	Simon <i>et al.</i> , 2006
7	YY12F4391	GTCACCTAGCAATAACACTAGCCTT	Present study
	YY12R6406	TAGTGATATTTGTGTCATGAGTTGG	Present study
8	F08(SPA-7077)	TTAAATCCTTTGAGTAAAATCC	Simon <i>et al.</i> , 2006
	R08(SPA-7793)	TTAGGTTGAGATGGTTTAGG	Simon <i>et al.</i> , 2006
9	TF-J7572	AAAGGGAATTTGAGCTCTTTWGT	Simon <i>et al.</i> , 2006
	TR-N8487	TATCAGSTAATATRGCWGCTCC	Simon <i>et al.</i> , 2006
10	F10(SPA-8641)	CCAGAAGAACATAGCCCATG	Simon <i>et al.</i> , 2006
	R10(SPA-9629)	GTTTGTGAAGGTGTGTTGGG	Simon <i>et al.</i> , 2006
11	F11(SPA-9648)	TCCCAACACACCTTCACAAAC	Simon <i>et al.</i> , 2006
	R11(SPA-11010)	TATCAACAGCAAATCCTCCTCA	Simon <i>et al.</i> , 2006
12	F23(SPC-10621)	CTCATACTGATGAAATTTGGTTC	Simon <i>et al.</i> , 2006
	R23(SPC-11526)	TTCTACTGGTCGTGCTCCAATTCA	Simon <i>et al.</i> , 2006
13	F12(SPB-11335)	CATATTC AACAGAATGATA	Simon <i>et al.</i> , 2006
	R12(SPB-12067)	AATCGTTCTCCATTTGATTTTGC	Simon <i>et al.</i> , 2006
14	F13(SPB-11876)	CGAGGTAAGTACCACGTACTCA	Simon <i>et al.</i> , 2006
	R13(SPB-12595)	GTTGGATTTCTAACTTTATTRGARCG	Simon <i>et al.</i> , 2006
15	F14(SPB-12261)	TACCTCATAAGAAATAGTTTGAGC	Simon <i>et al.</i> , 2006
	R14(SPB-13000)	TTACCTTAGGGATAACAGCGTAA	Simon <i>et al.</i> , 2006
16	F15(SPB-12888)	CCGGTCTGAACTCAGATCATGTA	Simon <i>et al.</i> , 2006
	R15(SPB-13889)	ATTTATTGTACCTTTGTATCAG	Simon <i>et al.</i> , 2006
17	F16(SPB-13342)	CCTTTCACAGTCAAATACTGC	Simon <i>et al.</i> , 2006
	R16(SPB-14220)	TTATGCACACATCGCCCGTC	Simon <i>et al.</i> , 2006
18	F17(SPB-14197)	GTAAAYCTACTTTGTTACGACTT	Simon <i>et al.</i> , 2006
	R17(SPB-14745)	GTGCCAGCAAYCGCGTTATAC	Simon <i>et al.</i> , 2006
19	YY16F14490	CTTTTAGGTTTCAAGATCAT	Present study
	YY16R759	CCAATAAAA ACTGATAGGAT	Present study

Table S9. Primer sequences of *Nymphes myrmeleonoides* mt genome used in this study.

Number	Primer ID	Nucleotide sequence (5'-3')	Reference
1	FL-34	GCCTGAAAAAGGGTTACTTTGATA	Simon <i>et al.</i> , 2006
	TR1284	ACARCTTTGAAGGYTAWTAGTTT	Simon <i>et al.</i> , 2006
2	F20(SPB-586)	CCATTCCATTTYTGATTTCC	Simon <i>et al.</i> , 2006
	R20(SPB-1738)	TTTATTCGTGGAAATGCTATGTC	Simon <i>et al.</i> , 2006
3	F21(SPB-1709)	AATTGGTGGTTTTGGAAATTG	Simon <i>et al.</i> , 2006
	R21(SPB-2776)	GGTAATCAGAGTATCGACG	Simon <i>et al.</i> , 2006
4	F22(SPB-2756)	ACATTTTTTTCCTCAACATTT	Simon <i>et al.</i> , 2006
	R22(SPB-3389)	TATTCATATCTTCAATATCATTGATG	Simon <i>et al.</i> , 2006
5	F02(SPA-3399)	TCTATTGGTCATCAATGGTACTG	Simon <i>et al.</i> , 2006
	R02(SPA-4061)	GAAAATAAATTTGTTATCATTTTCA	Simon <i>et al.</i> , 2006
6	F03(SPA-3790)	CATTAAGTGACTGAAAGCAAGTA	Simon <i>et al.</i> , 2006
	R03(SPA-4552)	ATGACCTGCAATTATATTAGC	Simon <i>et al.</i> , 2006
7	YY113F4462	CATTATCTTTAGCATTACCA	Present study
	YY113R4665	CAACTAAATGATAAGGATGA	Present study
8	TF4463	TTTGCCCATCTWGTWCCNCAAGG	Simon <i>et al.</i> , 2006
	TR5460	TCAACAAAATGTCARTAYCA	Simon <i>et al.</i> , 2006
9	TF4792	GTTGATTATAGACCWTGRCC	Simon <i>et al.</i> , 2006
	TR5731	TTAGGGTCAAATCCRCAYTC	Simon <i>et al.</i> , 2006
10	TF5470	GCAGCTGCYTGATAYTGRCA	Simon <i>et al.</i> , 2006
	TR6384	TATATTTAGAGYATRAYAYTGAAG	Simon <i>et al.</i> , 2006
11	YY114F6205	AATTGAAACCAAATAGAGG	Present study
	YY114R6530	AAGTGAATATATAGGGGGTC	Present study
12	TF6400	TAACATCTTCAATRYATRCTCT	Simon <i>et al.</i> , 2006
	TR7211	TTAAGGCTTTAYTATTTATRTGYGC	Simon <i>et al.</i> , 2006
13	F08(SPA-7077)	TTAAATCCTTTGAGTAAAATCC	Simon <i>et al.</i> , 2006
	R08(SPA-7793)	TTAGGTTGAGATGGTTTAGG	Simon <i>et al.</i> , 2006
14	TF-J7572	AAAGGGAATTTGAGCTCTTTTWTG	Simon <i>et al.</i> , 2006
	TR-N8487	TATCAGSTAATATRGWCWCTCC	Simon <i>et al.</i> , 2006
15	TF-J7806	GAMACAARACCTAACCCATCYCA	Simon <i>et al.</i> , 2006
	TR-N8727	AAATCTTTRATTGCTTATTCWTC	Simon <i>et al.</i> , 2006
16	F10(SPA-8641)	CCAGAAGAACATAGCCCATG	Simon <i>et al.</i> , 2006
	R10(SPA-9629)	GTTTGTGAAGGTGTGTTGGG	Simon <i>et al.</i> , 2006
17	YY117F9560	TGAACCAATCAATATCTA	Present study
	YY117R9726	TTGTGGTAGTATATCATTTG	Present study
18	TF-J9648	ACCTAAAGCTCCCTCACAWAC	Simon <i>et al.</i> , 2006
	TR-N10608	CCAAGTARTGAWCCAAARTTTCA	Simon <i>et al.</i> , 2006
19	F11(SPA-9648)	TCCAACACACCTTCACAAAC	Simon <i>et al.</i> , 2006
	R11(SPA-11010)	TATCAACAGCAAATCCTCCTCA	Simon <i>et al.</i> , 2006
20	YY118F10921	TATTTACATATTGGACGAGG	Present study
	YY118R11247	CTAAAGGATTGCTGGGATA	Present study
21	F12(SPB-11335)	CATATTCAACCAGAATGATA	Simon <i>et al.</i> , 2006
	R12(SPB-12067)	AATCGTTCTCCATTTGATTTTGC	Simon <i>et al.</i> , 2006

22	F13(SPB-11876)	CGAGGTAAAGTACCACGTACTCA	Simon <i>et al.</i> , 2006
	R13(SPB-12595)	GTTGGATTTCTAACTTTATTRGARCG	Simon <i>et al.</i> , 2006
23	F14(SPB-12261)	TACCTCATAAGAAATAGTTTGAGC	Simon <i>et al.</i> , 2006
	R14(SPB-13000)	TTACCTTAGGGATAACAGCGTAA	Simon <i>et al.</i> , 2006
24	F15(SPB-12888)	CCGGTCTGAACTCAGATCATGTA	Simon <i>et al.</i> , 2006
	R15(SPB-13889)	ATTTATTGTACCTTTTGTATCAG	Simon <i>et al.</i> , 2006
25	F16(SPB-13342)	CCTTTGCACAGTCAAAATACTGC	Simon <i>et al.</i> , 2006
	R16(SPB-14220)	TTATGCACACATCGCCCGTC	Simon <i>et al.</i> , 2006
26	F17(SPB-14197)	GTAAAYCTACTTTGTTACGACTT	Simon <i>et al.</i> , 2006
	R17(SPB-14745)	GTGCCAGCAAAYCGCGTTATAC	Simon <i>et al.</i> , 2006
27	YY132F14733	CAGGTTCTCTAAATAGACT	Present study
	YY132R210	GGGTATGAACCCAGTAGCTT	Present study
