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A Molecular Phylogeny of Planthoppers (Hemiptera: Fulgoroidea) Inferred from Mitochondrial 16S rDNA Sequences

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Wen-Bin Yeh, Chung-Tu Yang, and Cho-Fat Hui (2005) A molecular phylogeny of planthoppers (Hemiptera: Fulgoroidea) inferred from mitochondrial 16S rDNA sequences. *Zoological Studies* **44**(4): 519-535. Phylogenetic reconstruction of family relationships within the superfamily Fulgoroidea was conducted based on DNA sequences of the mitochondrial 16S rDNA gene. Sequences of 569 bases of the 3' end of the gene from 59 populations representing 53 species within 15 families were analyzed. Ranges of the 16S rDNA nucleotide divergences within species were 0%-0.6%, those among species of a given genus were 1.7%-7.8%, and those among genera of the same tribe or subfamily were 8.1%-19.5%. Scatterplots of total substitutions (Tvs) against transversions (Tv), or transitions (Ts) of the 16S rDNA gene revealed that the mutation rate of Tv was 3 times higher than Ts, and substitutional saturation has not yet been reached. Phylogenetic reconstruction and bootstrap confidence analysis revealed several basal lineages and 1 advanced group. The basal lineages included 5 families, where the Cixiidae exhibited close affinity to the Delphacidae, while the phylogenetic positions of the Achilidae, Meenoplidae, and Lophopidae were ambiguous. Monophyly of the remaining 10 advanced families showed several subdivided family groups with close affinities of the Derbidae to the Tropiduchidae, Dictyopharidae to the Fulgoridae, and Ricaniidae to the Eurybrachidae. The ancestral lineage of the Tettigometridae which exhibits many ancestral morphological characters was not supported by the 16S rDNA sequence data analysis, and the relationship of the families Flatidae and Nogodinidae was poorly resolved. In addition, the Issidae was not shown to be monophyletic, although issid members at the subfamily level were well supported. http://zoolstud.sinica.edu.tw/Journals/44.4/519.pdf

Key words: Molecular phylogeny, Mitochondrial 16S rDNA, Hemiptera, Fulgoroidea.

Planthoppers constitute a large group of phytophagous insects in the order Hemiptera and family Fulgoroidea including more than 9000 described species with division into 19 families distributed worldwide (O'Brien and Wilson 1985). These insects occupy extensive ranges of habitats (Denno and Roderick 1990), and some major agricultural pests are included (Wilson and O'Brien 1987). The Fulgoroidea consists of common herbivores in both agricultural and natural systems, often causing severe damage to their host plants. Attention has focused on a number of planthopper species because of large damage incurred by the crops of maize, rice, wheat, and forage grasses. Several species of delphacids exhibit high reproductive potentials and dispersal capabilities which allow them to track changes in favorable resources and therefore predispose them to be agricultural pests (Denno and Roderick 1990). *Nilaparvata lugens* (Stål), for example, a delphacid, caused more than US$1.23 billion in losses to rice in South and Southeast Asia annually (Herdt 1987).

The first phylogenetic hypothesis concerning

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the Fulgoroidea was proposed by Muir (1923). Thereafter, several such hypotheses were proposed based on adult or nymphal morphological characters (Asche 1988, Emeljanov 1991, Chen and Yang 1995). The Tettigometridae is usually considered the most-ancestral family in the Fulgoroidea since it exhibits many ancestral characters pertaining to the Cicadoidea (Muir 1923). Other popular relationships of the remaining fulgoroids are those proposed by Asche (1988) and Emeljanov (1991). Figure 1A shows a cladistic analysis based on 30 adult morphological characters. It suggests that the Cixiidae is a sister group to the Delphacidae, and both are more ancestral than the others which form several aligned lineages including 1 major group, but the affinity among these lineages is ambiguous (Asche 1988, Wilson et al. 1994). Asche's hypothesis was criticized by Emeljanov (1991) based on 50 morphological characters (Fig. 1B), and the Delphacidae has been suggested as being the next-most ancestral and not a sister group of the Cixiidae. Each of the following lineages in Asche's hypothesis is further divided in an unequal succession of dichotomies. Both hypotheses suggest that the Meenoplidae is a sister group to the Kinnaridae, and the Fulgoridae is a sister group to the Dictyopharidae. These commonly cited fulgoroid phylogenies have frequently been challenged. The ancestral taxon of the Tettigometridae is questionable, and the primitive characters in tettigometrids are the result of convergence (Fig. 1C) (Bourgoin 1993). Further molecular evidence using 18S rDNA sequences confirms this controversial point (Bourgoin et al. 1997). Also, based on the ontogeny of metatarsal characters, Cheng and Yang (1995) suggested that the Delphacidae and Cixiidae constitute the most-advanced lineage of fulgoroids (Fig. 1D). Thus, the only conclusion generally accepted in fulgoroid systematics is that the Fulgoridae and Dictyopharidae are sister groups. Obviously, more studies of fulgoroid phylogeny using different characters are needed.

The 3' end sequences of the mitochondrial

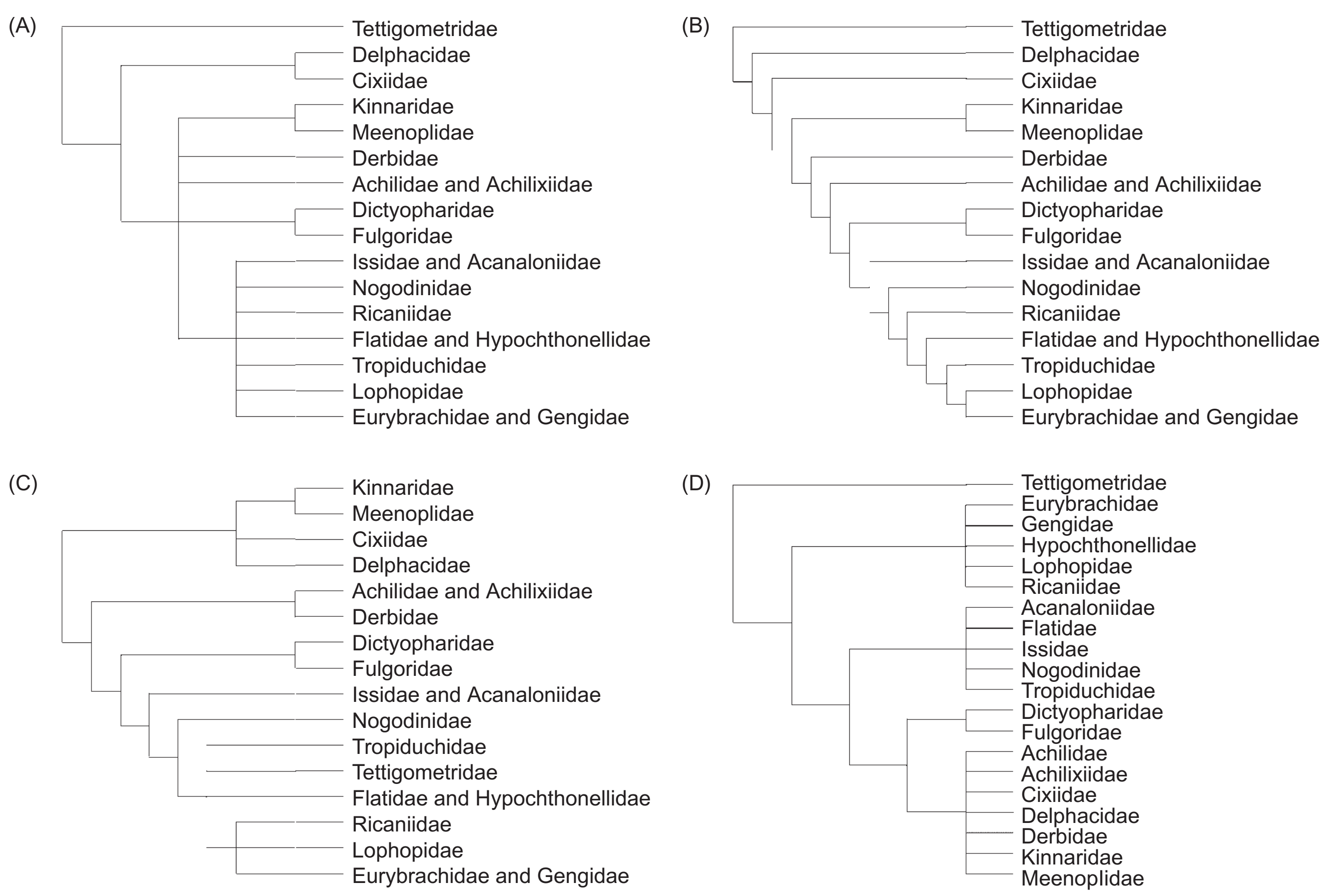

Fig. 1. Hypotheses of phylogenetic relationships of fulgoroid families. (A) Phylogenies proposed by Asche (1988) , (B) Emelyanov (1991) , (C) Bourgoin et al. (1993 1997), and (D) Cheng and Yang (1995) .

Table 1. Taxonomic status of fulgoroid taxa examined in this study with accession nos

Family	Subfamily or Tribe	Abbrev.	Species name	Accession no.
Achilidae	Plectoderini	Ach1	*Betatropis formosana* Matsumura	AF158028
	Rhotalini	Ach2	*Rhotala formosana*	AF158029
Cixiidae	Cixiinae	Cix2	*Pentastiridius pachyceps* (Matsumura)	AF158030
	Cixiinae	Cix3	*Cixius circulus* Tsaur et Hsu	AF158031
	Cixiinae	Cix4	*Cixius inflatus* Tsaur et Hsu	AF158032
	Cixiinae	Cix6	*Betacixius ocellatus*	AF158033
Delphacidae	Delphacinae	Del2	*Nilaparvata lugens* Stål	AF158034
	Delphacinae	Del3	*Purohita taiwanensis* Muir	AF158035
	Asiracinae	Del4	*Ugyops tripunctatus* (Kato)	AF158036
	Asiracinae	Del6	*Ugyops vittatus* (Matsumura)[a]	AF158037
	Delphacinae	Del7	*Nilaparvata lugens* Stål	AF158038
	Dlephacinae	Del8	Delphacinae sp.	AF158039
Derbidae	Zoraidini	Der1	*Zoraida kotoshoensis* Matsumura	AF158040
	Zoraidini	Der2	*Diostrombus politus* Uhler	AF158041
	Otiocerini	Der3	*Kamendaka aculeata* Yang et Wu	AF158042
	Rhotanini	Der4	*Rhotana obaerata* Yang et Wu	AF158043
	Otiocerini	Der9	*Kamendaka aculeata* Yang et Wu	AF158044
Dictyopharidae	Dictyopharinae	Dic1	*Orthopagus splendens* (Germar)	AF158045
	Dictyopharinae	Dic2	*Raivuna* sp.	AF158046
	Dictyopharinae	Dic3	*Saigona gibbosa* Matsumura	AF158047
	Dictyopharinae	Dic4	*Orthopagus* sp.[a]	AF158048
Eurybrachidae	Platybrachinae	Eur1	*Platybrachys decemmacula* Walker	AF158049
Flatidae	Flatini	Fla1	*Phylliana alba* (Jacobi)	AF158050
	Flatini	Fla2	*Mimophantia maritina* Matsumura	AF158051
	Nephesini	Fla3	*Geisha distinetissima* (Walker)	AF158052
	Flatini	Fla4	*Mimophantia maritina* Matsumura	AF158053
	Flatoidinae	Fla5	*Atracis* sp.	AF158054
Fulgoridae	Aphaeninae	Ful2	*Lycorma meliae* Kato	AF158055
	Aphaeninae	Ful3	*Lycorma olivacea* Kato	AF158056
	Fulgorinae	Ful4	*Fulgora laternaria* Linne’	AF158057
	Aphaeninae	Ful5	*Lycorma delicatula* White[a]	AF158058
Issidae	Hemisphaerinae	Iss1	*Epyhemisphaerius tappanus* (Matsumura)	AF158059
	Tonginae	Iss2	*Tonga botelensis* Kato	AF158060
	Issinae	Iss3	*Eusarima astuta* Chan et Yang	AF158061
	Caliscelinae	Iss4	*Mushya faciata* Kato	AF158062
	Hemisphaerinae	Iss5	*Hemisphaerius formosus* Melichar	AF158063
	Caliscelinae	Iss6	*Bruchomorpha oculata* Newman	AF158064
	Caliscelinae	Iss7	*Bruchomorpha jocosa* Stål	AF158065
	Caliscelinae	Iss8	*Aphelonema histrionica* Stål	AF158066
	Hemisphaerinae	Iss9	*Gergithus rotundus* Chan et Yang	AF158067
	Hemisphaerinae	Iss10	*Gergithus yayeyamensis* Hori	AF158068
	Tonginae	Iss11	*Tonga westwoodi* (Signoret)[a]	AF158069
	Tonginae	Iss12	*Tonga westwoodi* (Signoret)[a]	AF158070
	Issinae	Iss14	*Eusarima condensa*	AF158071
Lophopidae	Lophopinae	Lop1	*Lophops carinata* (Kirby)	AF158072
Meenoplidae	Kermesiinae	Mee2	*Nisia serrata* Tsaur	AF158073
	Kermesiinae	Mee3	*Nisia lansunensis* Yang	AF158074
	Kermesiinae	Mee6	*Nisia serrata* Tsaur	AF158075
Nogodinidae	Varciini	Nog1	*Mindura subfasciata kotoshonis* Matsumura	AF158076
	Pisachini	Nog2	*Pisacha naga* Distant	AF158077
Ricaniidae		Ric1	*Ricania fumosa* (Walker)	AF158078
		Ric3	*Ricanula pulverosa* Stål	AF158079
		Ric4	*Ricania simulans* (Walker)	AF158080
		Ric5	*Euricania ocella* (Walker)	AF158081
Tettigometridae	Tettigometrinae	Tet2	*Tettigometra* sp.	AF158082
Tropiduchidae	Tambiniini	Tro1	*Kallitaxila sinica* (Walker)	AF158083
	Tambiniini	Tro2	*Ossoides lineatus* Bierman	AF158084
	Catulliini	Tro3	*Catullia subtestacea* Stål	AF158085
	Tambiniini	Tro4	*Ossoides lineatus* Bierman	AF158086

[a]Nymph material.

16S rDNA gene have been shown to be useful for examining insect relationships from the genus level to the family level (Han and McPheron 1997, Yeh et al. 1998, Marini and Mantovani 2002, Hypša et al. 2002, Whitfield et al. 2002, Ribera et al. 2003). Mitochondrial 16S rDNA sequences have been used to infer relationships of 6 fulgoroid families of the Tropiduchidae group, and the results indicated that the 3'end sequences of the 16S rDNA are suitable for studying family relationships within the Fulgoroidea since nucleotide divergence increases with increasing taxonomic distance (Yeh et al. 1998). Nuclear 18S rDNA sequences have been used to evaluate 5 fulgoroid families and the affiliation of the Tettigometridae (Campbell et al. 1995, Bourgoin et al. 1997). Nucleotide sequences of the 18S rDNA gene may be too conserved for analysis of closely related families since nucleotide divergences between fulgoroid families are in the range of 1.5% to 6.3% (Campbell et al. 1995, Bourgoin et al. 1997). Also, too few families have been studied so far to obtain a general picture of fulgoroid phylogeny (Campbell et al. 1995, Bourgoin et al. 1997, Yeh et al. 1998).

In this work, sequences of the 16S rDNA gene of 59 populations within 53 species representing 15 families of fulgoroids were analyzed. The primary aims of this study were to use molecular characters to infer phylogenetic relationships within the Fulgoroidea as well as to address 2 issues that are still being debated: the phylogenetic position of the Tettigometridae, and whether Cixiidae and Delphacidae are ancestral taxa. Results from fulgoroid 16S rDNA sequences revealed that transversion substitutions are accumulating 3 times faster than transition substitutions. Phylogenetic analysis showed that members of the same family are grouped together with high bootstrap values, and that the Tettigometridae is not an ancestral taxon. Finally, the Achilidae, Cixiidae, Delphacidae, Lophopidae, and Meenoplidae were found to constitute the basal lineages, with the remaining 10 families comprising advanced lineages.

MATERIALS AND METHODS

Taxa examined

In total, 59 populations representing 53 species of 15 families of fulgoroids were included in this study (Table 1). Specimens of *Bruchomorpha oculata*, *B. jocosa*, and *Aphelonema histrionica* of the Issidae were provided by M. R. Wilson (International Institute of Entomology, London). Six species selected for outgroup comparisons were *Mogannia* sp. (Cicadidae, Cica, GenBank accession no.: AF158087), *Cosmoscarta kotoensis* (Cercopidae, Cerc, accession no.: AF158088), and 4 species of the Cicadellidae: *Macrosteles fascifrons* (Cic1), *Exitianus exitiosus* (Cic2), *Mocuellus caprillus* (Cic3), and *Amblysellus grex* (Cic4) (Fang et al. 1993).

DNA extraction, amplification, and sequencing

Live insects were collected and preserved in 95% ethanol at -20°C. The entire insect body or the leg of a large specimen was homogenized in a glass homogenizer in 500 μl digestion buffer that contained 100 mM Tris-Cl (pH 8.0), 10 mM EDTA, 100 mM NaCl, 0.5% SDS, 50 mM dithiothreitol, and 0.5 mg/ml proteinase K. The mixture was incubated at 50°C overnight, then extracted with phenol-chloroform (modified from Yeh et al. 1998). Extracted crude DNA was dissolved in 50 μl TE buffer, and an aliquot of 10 μl crude DNA was diluted 10-fold and used as the DNA template in the following amplification reaction.

The polymerase chain reaction (PCR) was employed to amplify a partial sequence of the mitochondrial 16S rDNA gene. The primers used to amplify the region were 5'-GCCTGTTTATCAAAAACAT-3' and 5'-CCGGTCTGAACTCAGATCA-3' that correspond to nucleotides 13416-13396 and 12866-12884, respectively, of the 16S rDNA gene of *Drosophila yakuba* (Clary and Wolstenholme 1985). Amplification was carried out for 39 cycles in a final volume of 100 μl containing 10 mM Tris-Cl (pH 9.0), 50 mM KCl, 1.5 mM $MgCl_2$, 0.01% gelatin, 0.1% Triton-X100, 2 units of SuperTaq polymerase (HT Biotechnology, Taiwan), 0.2 mM of each dNTP, 20 pmoles of each primer, and 2 μl DNA template with the following temperature profile: denaturation for 50 s at 95°C, annealing for 1 min at 50°C, and extension for 1 min at 72°C. Amplified DNA fragments were separated by agarose gel electrophoresis and extracted from the gel using the Nucleotrap Kit (Macherey-Nagel, Germany). The resulting DNA product was directly sequenced using the Cycling PCR Sequencing Kit (Perkin Elmer, USA), and 29 cycles were carried out with the following temperature profile: 40 s for denaturation at 95℃, annealing at 50°C, and extension at 72°C (modified from Yeh et al. 1998).

DNA analysis

Initial alignment of the mitochondrial sequences was conducted using the Pileup program of the GCG software package (available at http://bioinfo.nhri.org.tw), then manually refined based on the secondary structures of the 16S rRNA sequences (Davis et al. 1994, Fang et al. 1993, Kambhampati et al. 1996). The proportion of the nucleotide composition of each taxon was calculated using the MEGA version 3 program (Kumar et al. 2004) with a variety of genetic distances. To correct for AT-richness of the mtDNA sequences and different substitution patterns of transition (Ts) and transversion (Tv), the parameters of nucleotide composition and substitution types were used in the sequence divergence estimation. The pair-wise distance estimates were based on models that included the proportional, Kimura 2-parameter, and Tamura 3-parameter distance measures. A statistical analysis system (SAS Institute 2001) was used to test for significant correlations between nucleotide base compositions and substitution patterns of Ts and Tv.

Following the sequence variation estimation, neighbor-joining (NJ) and minimum evolution (ME) implemented in MEGA3 (Kumar et al. 2004) were used for the phylogenetic reconstruction. Different values of the parameter of α in the gamma distribution were used to determine the effect of heterogeneity in substitution rates among sites. Sites 40-45, 69-74, 185-186, 279-280, 290-291, 375-377, and 496-497 of the mitochondrial sequence data were excluded from the phylogenetic analysis because they could not be aligned unambiguously. Bootstrap analyses of 1000 replications were carried out on the trees inferred from the NJ and ME methods.

RESULTS

Sequence variation

When gaps were added to the alignment, 569 bases (Appendix I) were analyzed. Length variations of the partial 16S rDNA sequences among taxa ranged from 534 to 548 bases. Of the 569 bases examined, 375 bases (66%) were variable. The average nucleotide composition proportions (± SD) for the fulgoroid sequences were: G, 16.7 (± 1.2); A, 30.6 (± 2.5); T, 43.1 (± 1.7); and C, 9.6 (± 0.5). A bias towards adenine and thymine is consistent with the base composition of the corresponding 16S rDNA region of other insects (Fang et al. 1993, Dowton and Austin 1994, Kambhampati 1995, Vogler and Pearson 1996, Han and McPheron 1997). Variable sites were not randomly distributed over the examined 16S rDNA region, and nucleotide divergence patterns in the 3' region of this gene showed that there are 3 highly variable regions (positions 40-74, 279-291, and 372-393; Appendix I). This result suggests that substitution patterns might be constrained by the function of the gene. The pattern of substitutions showed the greatest bias with A↔T (11.5%), which was larger than changes of A↔G (3.2%), T ↔C (1.8%), and T↔G (2.3%), while changes of A ↔C (0.5%) and G↔C (0.1%) were rare. However, correlation analysis of the base composition and substitution patterns using Kendall's tau (τ) (Kendall 1938) showed no significant relationship between base composition and substitution patterns (τ = 0.6; τ*= 0.6, α = 0.1).

The uncorrected nucleotide divergences within species were 0%-0.6%, those among species of a given genus were 1.7%-7.8%, and those among genera of the same tribe or subfamily of fulgorids were 8.1%-19.5%. Regression analysis of total substitutions (Tvs) versus transversions (Tv) and transitions (Ts) revealed that the mutation rate of Tv (with a slope of 0.74; R^2 = 0.94) was 3 times higher than that of Ts (with a slope of 0.26; R^2 = 0.71), and substitutional saturation due to multiple hits was not yet observed in fulgoroids (Fig. 2). This information indicates that both Tv and Ts may provide phylogenetic information.

Phylogenetic analysis

Information on the differentiated nucleotide composition and Tv and Ts substitution patterns

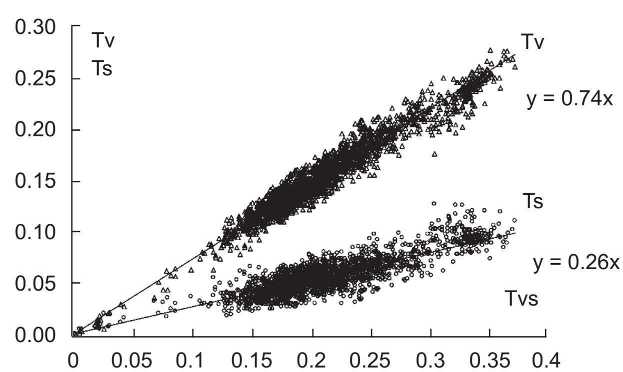

Fig. 2. Regression analysis of total substitutions (Tvs) versus transitions (Ts, ○) and transversions (Tv, △) in the 16S rDNA sequences of fulgoroids.

allowed us to use the 3-parameter estimated distance model (Tamura 1992) in the NJ analysis, and the results are shown in figure 3A, for which the results of 1000 bootstrap replications are shown in the phylogenetic tree. Members of the same family were generally grouped together and received significant bootstrap possibilities of from 88% to 99%. The phylogenetic tree reveals the presence of 2 patterns of lineages. The basal lineages include 5 families of the Cixiidae, Delphacidae, Meenoplidae, Lophopidae, and Achilidae, and a close relationship is evident in the lineages of the Cixiidae and Delphacidae, although members Del4 and Del6 of the Delphacidae are cohesive to the Cixiidae lineage. After excluding the 5 basal families, the derived lineages can be divided into many groups and several independently aligned families: (i) Derbidae-Tropiduchidae; (ii) Fulgoridae-Dictyopharidae; (iii) Eurybrachidae-Ricaniidae, and the Flatidae, Nogodinidae, Tettigometridae, and Issidae. Bootstrap values suggest a robust relationship for each lineage of these groups. Furthermore, similar phylogenetic topologies were obtained when the data matrix was analyzed under other distance estimation models (Kimura 2-parameter with different values of α in the gamma distribution, Fig. 4a-d). These trees use family names since members of the same family consistently grouped together (Fig. 3). The trees support the 2 patterns of lineages but lack resolution among family groups in the advanced lineages.

The minimum evolution result constructed from the 3-parameter estimated distances exhibits the grouping pattern shown in figure 3B and is mostly consistent with that from the NJ analysis. The basal lineages include 5 families, and the relationship between the Delphacidae and Cixiidae is close, but it is necessary to further elucidate the paraphyletic resolution in the Delphacidae. Relationships among the Meenoplidae, Delphacidae-Cixiidae, Lophopidae, and Achilidae cannot be clearly resolved (Fig. 3B). Several groups among families in the derived lineages are revealed, including Derbidae-Tropiduchidae, Dictyopharidae-Fulgoridae, and Eurybrachidae-Ricaniidae, but relationships among the remaining families were poorly resolved. Furthermore, similar phylogenetic topologies were inferred in the minimum evolution analyses when using different values of α in the gamma distribution under the Kimura 2-parameter distance estimate model (Fig. 4e-h).

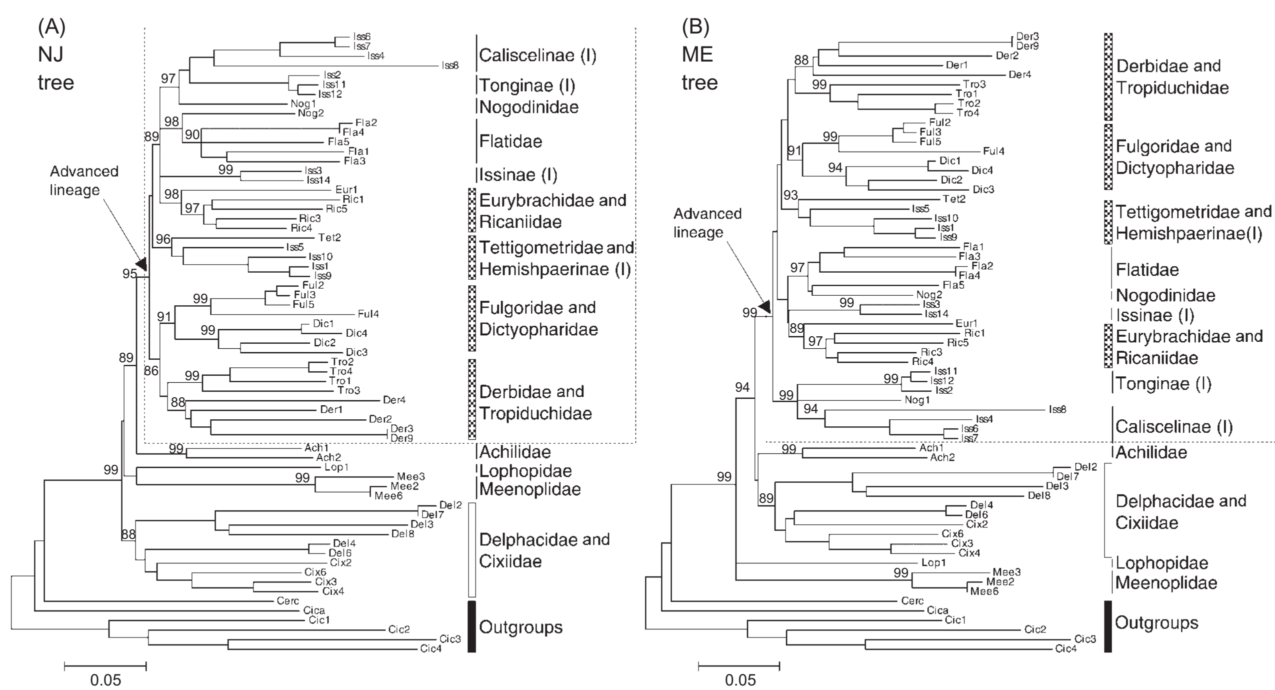

Fig. 3. Phylogeny of fulgoroids based on the partial mitochondrial 16S rDNA sequences by neighbor-joining (A) and minimum evolution (B) reconstructions based on the 3-parameter Tamura model. Bootstrap scores exceeding 80% from 1000 replications are given beneath the branches (not shown for branches below the family level). The black, white, and hatched rectangular boxes indicate clusters of the outgroups and two defined subdivided groups, respectively. The black lines indicate families whose phylogenetic relationships are ambiguous according to these analyses. The dotted-line box indicates advanced lineages. Taxa of the Issidae (I) are labeled in the subfamily category.

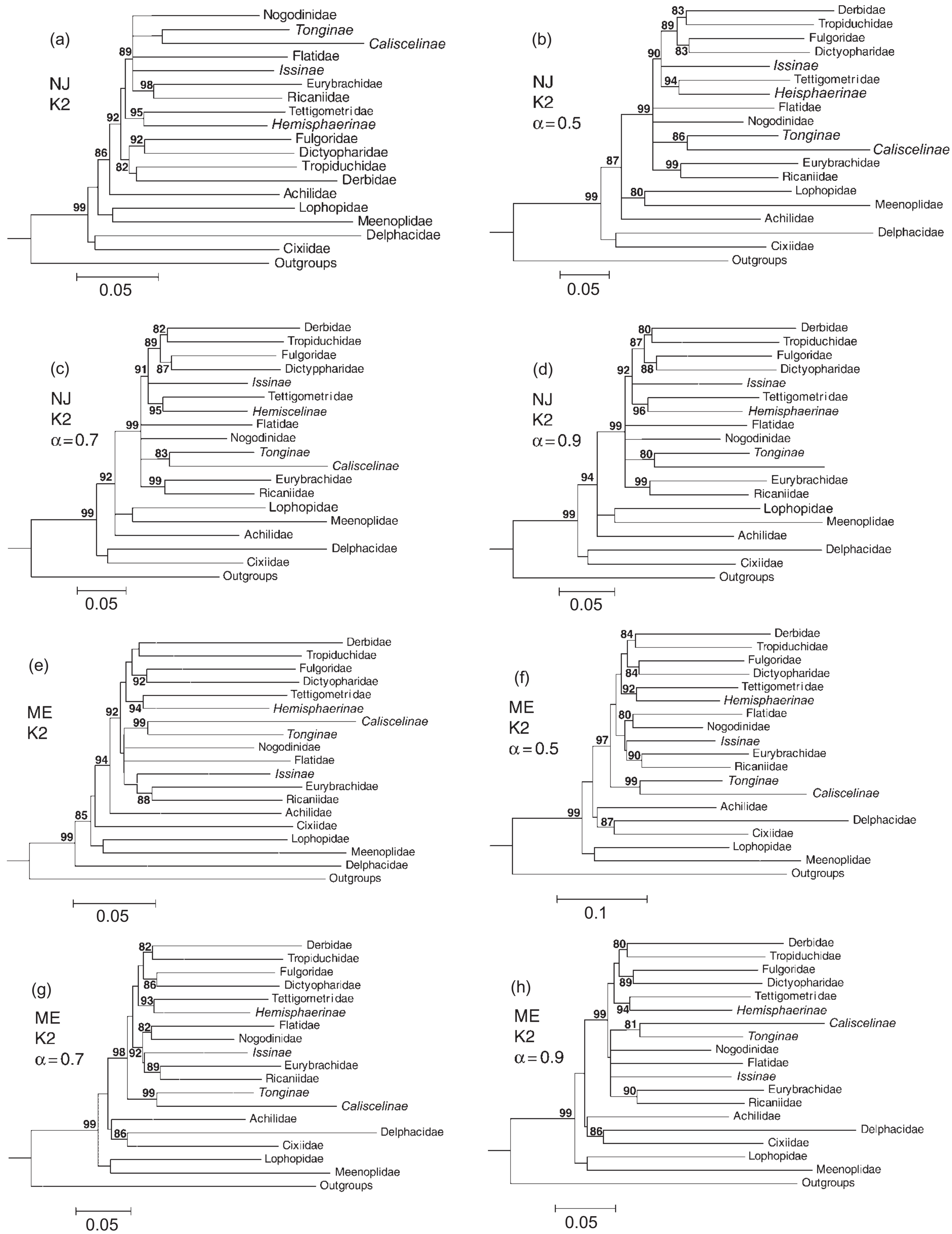

Fig. 4. Phylogenetic tree inferred from the partial mitochondrial 16S rDNA sequences by neighbor-joining (a-d) and minimum evolution (e-h) analyses based on the Kimura-2-parameter distance model. Correction for rate heterogeneity among sites with different values for the parameter α in the gamma distribution are shown, and bootstrap scores exceeding 80% from 1000 replications are given beneath the branches (not shown for branches below the family level). The trees use family names since members of the same family grouped together in figure 3.

However, monophyly of the Nogodinidae was not recovered by phylogenetic analysis, with Varciini (Nog1) and Pisachini (Nog2) falling into the Issidae and Flatidae, respectively. In addition, a non-monophyletic composition was seen in the family Issidae, particularly the subfamily Hemisphaerinae which formed a well-supported cluster with the family Tettigometridae.

DISCUSSION

The popular view among fulgoroid systematists that the Tettigometridae is the most-ancestral lineage among fulgoroids (Muir 1923, Asche 1988, Emeljanov 1991, Cheng and Yang 1995) was not supported by the 16S rDNA sequence data analyses. Average nucleotide sequence divergence between the tettigometrid and other fulgoroid families (19.3%) was small when compared to the 2 most-divergent families, i.e., the Meenoplidae (24.5%) and Delphacidae (23.8%). Also, phylogenetic analyses indicated that the Tettigometridae belongs to a more-advanced lineage of the Fulgoroidea and is grouped with the subfamily Hemisphaerinae of the Issidae. Based on the 18S rDNA sequence data, Bourgoin et al. (1997) indicated that the Tettigometridae is not a basal family in the Fulgoroidea, and they depicted it as a sister group of the Tropiduchidae. However, Bourgoin et al. also suggested that the sister taxon of tettigometrids still needed to be rigorously determined partly due to the weak sequence information in the 5' terminal region of 18S rDNA of the Tropiduchidae. Obviously, the sister group of Tettigometridae can be further clarified when additional numbers of related sequences are included.

Molecular phylogenies of planthoppers inferred from the 16S rDNA sequences indicate that fulgoroids are monophyletic. The relationships among families in these analyses are nearly identical: (i) The basal lineages are constituted by the Achilidae, Cixiidae-Delphacidae, Lophopidae, and Meenoplidae; (ii) Robust family groups of the Derbidae-Tropiduchidae, Dictyopharidae-Fulgoridae, and Eurybrachidae-Ricaniidae are aligned with other families in the advanced lineage; and (iii) The Issidae is a non-monophyletic group. It has been generally accepted that cixiids, delphacids, and meenoplids are relatively ancient families, but the relationships among these 3 families have not been resolved. For example, it was proposed that cixiids and delphacids are sister groups and are more ancestral than meenoplids based on a cladistic analysis (Asche 1988) with delphacids being more ancestral than cixiids, and cixiids more ancestral than meenoplids (Emeljanov 1991); furthermore, 18S rDNA sequence analysis showed that cixiids and delphacids are sister groups and are more ancestral than the other 5 fulgoroid families (Bourgoin et al. 1997). However, more-recent relationship reconstruction using cytochrome b (COB) sequences suggested that meenoplids are the most-ancestral family within the fulgoroids (Yeh et al. 1998). Phylogenetic inferences in these analyses indicated that the Cixiidae has a close affinity to the Delphacidae and constitutes one of the ancestral lineages within the fulgoroids.

Additional evidence from fossil records supports these basal lineages. The first fossil known of an extant member of the Fulgoroidea is of the Cixiidae, which appears at the beginning of the Jurassic period (210 Ma) (Shcherbakov 1996), and the next-oldest fossil is of the Achilidae (135 Ma) (Hamilton 1990). Most of the other fulgoroid families radiated out in the Cenozoic period (Shcherbakov 1993). However, sequence analyses revealed an unexpected phylogenetic position of the Lophopidae, which had been considered to be in the advanced lineage based on morphological characters (Asche 1988, Emeljanov 1991, Chen and Yang 1995). Soulier et al. (1996) pointed out that the Lophopidae is a paraphyletic family. Molecular results may have been biased from the sample size or the poor alignment of the AT-rich 16S rDNA. More than 1 taxon of lophopids or an additional sequence, such as 18S rDNA, must necessarily be included to help clarify the evolutionary relationship of the lophopids.

Excluding the 5 families (Achilidae, Cixiidae, Delphacidae, Lophopidae, and Meenoplidae), phylogenetic relationships confirm 1 major derived lineage although several phylogenetic relationships within it are poorly resolved. This polytomous result was possibly caused by the poor alignment of the 16S rDNA AT-rich regions or by the rapid radiation of fulgoroid families in the Cenozoic period (Shcherbakov 1993). However, some reliable conclusions can be drawn from the phylogenetic analyses. Molecular data confirm a close relationship between the Dictyopharidae and Fulgoridae, and depict the Derbidae as a sister group of the Tropiduchidae, and the Ricaniidae as a sister group to the Eubrybrachidae. Characters of female genitalia suggest that the family Achilidae has a close affinity to the Derbidae (Fig. 1C). However, according to the adult and nymphal morphological characters (Asche 1988, Chen and

Yang 1995), the phylogenetic affinity is ambiguous between the Achilidae and Derbidae. Asche (1988) proposed a polytomous relationship for the following 7 families: Eurybrachidae, Flatidae, Issidae, Lophopidae, Nogodinidae, Ricaniidae, and Tropiduchidae. Nymphal characters also reveal a polytomous relationship of the Eurybrachidae, Gengidae, Hypothonellidae, Lophopidae, and Ricaniidae (Chen and Yang 1995). Sequence data in this study further confirm the relationship of the Eurybrachidae and Ricaniidae, although the positions of the remaining Flatidae, Issidae, and Nogodinidae cannot be precisely defined. The non-monophyletic resolution of the Issidae and Nogodinidae highlights the difficulty in defining their phylogenetic position. It has been proposed that the Issidae is a nonhomogenous group (Yeh et al. 1998, Emeljanov 1999, Gnezdilov 2003), although many key morphological characters such as the tegmina, wing length, clavus, corium, and aedeagus shape in issids can effectively define the subfamily classification (Chan and Yang 1994). A revision of the Caliscelidae was described by Emeljanov (1999), whereas efficient molecular sequence is needed to delimitate the category of issid subfamilies. Furthermore, according to the characters of the tegmina, more than 10 species of issids were revised into the Nogodinidae (Fennah 1984). Analyses of 16S rDNA sequences elucidate many phylogenetic relationships within the Fulgoroidea, although many questions remain unresolved and more research effort is needed.

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APPENDIX I: Alignment of the fulgoroid 16S rDNA sequences. Secondary structure domains in the last line are based on previous models (see text)

```
                                                                                    81
Ful2  CGCC TGTTT ATCAA AAACA TGT CCTT TTGGAATTTATTT------ AAGG TT T-GGCC T GCTCAATGA- ---T-- -TTAAAT
Ful3  CGCC TGTTT ATCAA AAACA TGT CCTT TTGGAATTTATTT------ AAGG TT TGGGCC T GCTCAATGA- ---T-- -TTAAAT
Ful4  CGCC TGTTT ATCAA AAACA TGT CTTC CAGGGTTTAATTG------ GAGG TT T-GGCC T GCTCAATGCA ---T-- AGTAAAT
Ful5  CGCC TGTTT ATCAA AAACA TGT CCTT TTGTAATTTATTT------ AAGG TT T-GACC T GCTCAATGA- ---T-- -TTAAAT
Dic1  CGCC TGTTT AACAA AAACA TCT TCTT -TAGTGTTTATTA------ AAGA TA T-AACC T GCTCAATGAT ---T-- TTTAAAT
Dic2  CGCC TGTTT ATCAA AAACA TCT CTTT -TTGGTTTTATTT------ ---- -- A-AACC T GCTCAATGAA ---A-- TTTAAAT
Dic3  ???? ????? ????? ????? ??? ???? ??????????????????? ???? ?? ?????? ? ?????????? ?????? ???????
Dic4  CGCC TGTTT ATCAA AAACA TCT TCTT -TAGTGTTTATTA------ AAGA TA T-AACC T GCTCAATGAT ---T-- TTTAAAT
Fla1  TGCC TGTTT AACAA AAACA TGT CTTT -TAGTTTTTATTT------ AAAG TC T-AACC T GCTCAATGAT -TTA-- TTTAAAT
Fla2  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGAATTTGTTA------ AAAG TT G-ATTC T GCTCAATGAT --AA-- TTTAAAT
Fla3  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGGTTTTATTT------ AAAG TC T-AACC T GCTCAATGAA ---G-- TTTAAAT
Fla4  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGAATTTGTTA------ AAAG TT G-ATTC T GCTCAATGAT --AA-- TTTAAAT
Del8  CGCC TGTTT ATCAA AAACA TTT CTTT -TAGTTTTAATCTTA---- AAGG TT G-GGCC T GCTCAATGAA ---T-- ATTAAAT
Nog1  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGTTTATGTTA------ AAAG TC T-ATCC T GCTCAATGAT -TA--- TTTAAAT
Nog2  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGGTTTT-TTA------ AAAG TC T-GGCC T GCTCAATGAA -TAT-- TTTAAAT
Ach1  CGCC TTGTT ATCAA AAACA TGT TTTT -TTGTTTATTTATTT---- AAGA TT G-GCCC T GCTCAATGAT --A--- TTTAAAT
Ach2  CGCC TTGTT ATCAA AAACA TGG TTTT -TAGTTTATATTA------ AAGA TC A-GACC T GCTCAATGAA -TAT-- TTTAAAT
Der1  CGCC TGTTT ATCAA AAACA TGT CTTT -TTGATTTTATTT------ AAGG TT T-TACC T GCTCAATGAT -----T TTTAAAT
Der2  CGCC TGTTT ATCAA AAACA TGT TATT -TTGATTTTATATT----- TAAT AT TTAACC T GCTCAATGAT ---AA- TTTAAAT
Der3  CGCC TGTTT ATCAA AAACA TGT TTTT -TTGTTTTTTTAA------ AAAG AT TAAATC T GCTCAATGAA A-TAAT ATTAAAT
Der4  CGCC TGTTT ATCAA AAACA TGG TTTT -TAGTTTTTAATTT----- AAAA AT T-TGGC T GCCCAATGA- --T--T -CTAAAT
Der9  CGCC TGTTT ATCAA AAACA TGT TTTT -TTGTTTTTTTAA------ AAAG AT TAAATC T GCTCAATGAA ATTAAT ATTAAAT
Tro1  CGCC TGTTT ATCAA AAACA TGT CGTC -TTGATTTTATAT------ GATG TT T-AACC T GCTCAATGAT --TA-- TTTAAAT
Tro2  CGCC TGTTT ATCAA AAACA TGT CTTC -TTGATTTTATTT------ GAAG TC T-GGCC T GCTCAATGAT --TA-- ATTAAAT
Tro3  CGCC TGTTT ATCAA AAACA TCT CTTC -ATGAATTTATTT------ GAAG TC A-GGCC T GCTCAATGAG --T--- TTTAAAT
Tro4  CGCC TGTTT ATCAA AAACA T-T CTTA ---GGTTTTATTT------ GAAG TC T-A-CC T GCTCAATGAT --TA-- ATTAAAT
Ric1  ???? ????? ????? ????? ??? ???? ??????????????????? ???? ?? ?????? ? ?????????? ?????? ???????
Ric3  CGCC TGTTT ATCAA AAACA TGT CTTT -AAGTTTATATTT------ AAAG TC T-GACC T GCTCAATGAT ---TA- TTTAAAT
Ric4  CGCC TGTTT ATCAA AAACA TGT CTTT -AAGTTTTTTTTT------ AAAG TC T-GGCC T GCTCAATGAG -AAT-- TTTAAAT
Ric5  CGCC TGTTT ATCAA AAACA TGT CCTT -GAGAGTTTATTT------ AAGG TC T-GTCC T GCTCAATGAA TTTTTT TTTAAAT
Eur1  CGCC TGTTT ATCAA AAACA TGT CTTT -GAGAGTTTATTT------ AAAG TT T-GTCC T GCTCAATGAA -TTTA- TTTAAAT
Lop1  CACC TGTTT ATCAA AAACA TGT CTTT -AAGATTTATATTT----- AAAG TC T-AACC T GCTCAATGAA ---T-- TTTAAAT
Tet2  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGAGTTTATTA------ AAAG TC A-AACC T GCTCAATGAT -AATT- TTTAAAT
Iss1  CGCC TGTTT ATCAA AAACA TGT CTTT -GAGAGTTTATTT------ AAGG TC T-GACC T GCTCAGTGAT TTT--- ATTAAAT
Iss5  CGCC TGTTT ATCAA AAACA TGT CTTT -AAGAGTTTATTT------ AAAG TC T-GGCC T GCTCAATGAA TT---- TTTAAAT
Iss9  CGCC TGTTT ATCAA AAACA TGT CTTT -GAGGGTTTATTT------ AAAG TC T-GACC T GCTCAGTGAT -TAA-- ATTAAAT
Iss10 CGCC TGTTT ATCAA AAACA TGT CTTT -AAGTTGTTTATTT----- AAAG TC T-GGCC T GCTCAGTGAT TTTA-- ATTAAAT
Iss2  CGCC TGTTT AACAA AAACA TGT CTTG -TAGATTTTTTTA------ TAAG TC T-GTCC T GCTCAGTGAT ---T-- TTTAAAT
Iss11 CGCC TGTTT ATCAA AAACA TGT CTTG -TAGTTTTTTTTA------ TAAG TC T-ATCC T GCTCAGTGAT ---T-- TTTAAAT
Iss12 CGCC TGTTT ATCAA AAACA TGT CTTG -TAGTTTTTTTTA------ TAAG TC T-ATCC T GCTCAGTGAT ---T-- TTTAAAT
Iss3  CGCC TGTTT AACAA AAACA TGT CTTT -TAGTTTTTATTT------ AAGG TC A-AGCC T GCTCAATGAT ATATT- TTTAAAT
Iss14 CGCC TGTTT AACAA AAACA TGT CCTT -TAGTTTTTTTTT------ AAGG TC T-AGCC T GCTCAATGAT GTTAA- TTTAAAT
Iss4  CACC TGTTT ATCAA AAACA TGT CTTA -AAAAAATTTATTT----- TAAG TT T-AACC T GCTCAATGAA TTAT-- TTTAAAT
Iss6  CGCC TGTTT ATCAA AAACA TGT CTTA -ATGTTATTTATTT----- TAAG TC T-AGCC T GCTCAATGAA TTGT-- TTTAAAT
Iss7  CGCC TGTTT ATCAA AAACA TGT CTTA -ATGTTATTTATTT----- TAGG TC T-AGCC T GCTCAATGAA TTAT-- TTTAAAT
Iss8  CGCC TGTTT ATCAA AAACA TGT CTTG -TAGTTTTTTTTA------ TAAG TC T-ATCC T GCTCAATGAA GTGATT TTTAAAT
Cix2  CGCC TGTTT ATCAA AAACA TGT TCTT -TAGATTTATTA------- AAGA TT T-AGCC T GCTCTATGAT -TTAA- ATTAAAT
Cix3  CGCC TGTTT ATCAA AAACA TGT TCTT -TAGATTTTTTA------- AAGG TT T-AACC A GCTCTATGAT --GA-- TTTAAAT
Cix4  CGCC TGTTT ATCAA AAACA TGT TCTT -TAGATTTTTTTA------ AAGG TT T-AACC T GCTCTATGAT --TA-- TTTAAAT
Cix6  CGCC TGTTT ATCAA AAACA TGT CTTT -TAGATTTTTTTA------ AAGG TT T-AACC T GCTCTATGAA --TA-- TTTAAAT
Del2  CGCC TGTTT ATCAA AAACA TTT CTTT -CAGGTATTATATTTATTG AAAG TT T-AACC T GCTCAATGAA -TT-T- TTTAAAT
Del3  TGAC TGTTT ATCAA AAACA TTT TCTT -TTGAT-TTATTTAA---- AAGG TA A-AACC T GCTCACTGAA -TTTT- TTTAAAT
Del4  TGCC TGTTT ATCAA AAACA TGT TCTT -TAGGTTTTATTT------ AAGG TC T-CGCC T GCTCAATGAT -TGAT- TTTAAAT
Del6  TGCC TGTTT ATCAA AAACA TGT TCTT -TAGGTTTTATTT------ AAGG TT T-CGCC T GCTCAATGAT -TAAT- TTTAAAT
Del7  CGCC TGTTT ATCAA AAACA TTT CTTT -CAGGTATTATATTTATTG AAAG TT T-AACC T GCTCAATGAA -TT-T- TTTAAAT
Fla5  CGCC TGTTT ATCAA AAACA TGT CTTT -TTGTTTATATTT------ AAAG TC T-GACC T GCTCAATGAA -TTA-- TTTAAAT
Mcc2  TGAA TGTTT ATCAA AAACA TTT CTTC -ATGGGTTTTTTT------ GAAG TA T-TCCC T GCCCTATGAA -TTA-T TTTAAAT
Mee3  TGAA TGTTT ATCAA AAACA TTT CTTC -ATGTTTTTTTTT------ GAAG TA T-TCCC T GCTCTATGAA -TTAGT TTTAAAT
Mee6  TGAA TGTTT ATCAA AAACA TTT CTTC -ATGGGTTTTTTT------ GAAG TA T-TCCC T GCCCTATGAA -TTA-T TTTAAAT
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Cic2  CGCC TGTTT AACAA AAACA TTT CTTT -TTGCTTTTATA------- AAAG GT G-AGTC T GCCCTATGGG --AT-- ACTAAAT
Cic3  CGCC TGTTT AACAA AAACA TTT CTTT -TTGTGTGTTTA------- AAAG GT ATCTTC T GCCCTATGAT -TATT- ATTAAAT
Cic4  CGCC TGTTT AACAA AAACA TTT CTTT -TTAGTTTTTTTTA----- AAAG TA C-TTTC T GCCCTATGGT -TTGT- TCTAAAT
           <65a> <---> <65b> <-> <66a><-----------------> <66b><> <67a-> - <---68a--> <----> <--68b-
```

APPENDIX I : (Cont.)

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                                                                                                   158
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Ful3  AGC CGCAGT ATTTTG ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTT GA CG
Ful4  AGC CGCAGT ATTTTG ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GGGGTC TAGGATGAAG GGTTA GA CG
Ful5  AGC CGCAGT ATTTTG ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTT GA CG
Dic1  AGC CGCAGT AATTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG GA CG
Dic2  AGC CGCGGT AAATTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG AA CG
Dic3  ?GC CGCGGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG AA CG
Dic4  AGC CGCAGT AATTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG GA CG
Fla1  AGC CGCAGT ATATTG ACTGTG CGA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGTATGAAT GGTTG GA CA
Fla2  AGC CGCAGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GATTT GA CG
Fla3  AGC CGCAGT ATATTG ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGTATGAAT GGTTA GA CG
Fla4  AGC CGCAGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GATTT GA CG
Del8  AGC TGCAGT ATTTTA ACTGTA CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTT GA CA
Nog1  AGC CGCGGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG GA CG
Nog2  AGC CGCAGT ATTTTG ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGTATGAAT GGTTA AA CG
Ach1  AGC CGCGGT AATTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGGTT GA CA
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Der2  AGC CGCGGT ATTTTG ACCGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAA GGTTG GA CG
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Der9  AGC CGCGGT ATATTG ACCGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TTGAATGAAT GATTT GA CG
Tro1  AGC CGCGGT AATTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG GA CG
Tro2  AGC CGCGGT AATTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TAGAATGAAT GGTTG GA CG
Tro3  AGC CGCGGT AATTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GGGGTC TTGAATGAAT GGTTA GA CG
Tro4  AGC CGCGGT AATTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TAGAATGAAT GGTTG GG CG
Ric1  ??? ?????? ?????? ?????G CAA AGG TAGCATAGTA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTA GA CG
Ric3  AGC CGCAGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGTATGAAT GGTTG GA CG
Ric4  AGC CGCGGT ATTTTG ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTA GA CG
Ric5  AGC CGCGGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGTATGAAT GGTTA GA CG
Eur1  AGC CGCAGT ATTTTG ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAA GGTTA GA CG
Lop1  AGC CGCAGT ATTTTA ACTGTG TAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTG AA TG
Tet2  AGC CGCAGT ATTTTA ACTATA CAA AGG TAGCATAATC  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTA AA CG
Iss1  AGC CGCGGT ATATTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TAGAATGAAT GGTTG AA CG
Iss5  AGC CGCGGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGGATGAAT GGTTG AA CG
Iss9  AGC CGCGGT ATATTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GGGGTC TAGAATGAAT GGTTA AA CG
Iss10 AGC CGCGGT ATATTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGTATGAAT GGTTA AA CG
Iss2  AGC CGCAGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGATT CA CG
Iss11 AGC CGCAGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGATT CA CG
Iss12 AGC CGCAGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGATT CA CG
Iss3  AGC CGCGGT AAATTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGGATGAAT GGTTA GA CG
Iss14 AGC CGCGGT ATTTTG ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTA AA CG
Iss4  AGC CGCAGT AAATTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT AAGGTC TTGAATGAAT GGTTG GA TG
Iss6  AGC CGCAGT AATTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAAGTC TTGAATGAAA GGTTG GA TG
Iss7  AGC CGCAGT AATTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAAGTC TTGAATGAAA GGTTG GA TG
Iss8  AGC CGCAGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT AAAGTC TTGAATGAAT GGTTG GG TG
Cix2  GGC CGCAGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTTTCT TAATT AGGATC TGGAATGAAT GGTTG GA CA
Cix3  GGC CGCGGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTCT TAATT AGGGTC TTGAATGAAT GGTTG GA CG
Cix4  GGC CGCGGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTCT TAATT GGGGTC TTGAATGAAT GGTTG AA CG
Cix6  GGC CGCGGT ATTTTA ACTGTG CTA AGG TAGCATAATA  ATT  A GTCTCT TAATT AGGGTC TTGAATGAAT GGTTG GA CG
Del2  AGC TGCAGT AATTTA ACTGTA CAA AGG TAGCATAGTA  ATT  A GTCTTT TAATT GAGGTC TAGAATGAAT GGTTT AA CA
Del3  AGC CGCAGT ATTTTA ACTGTA CTA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TGGAATGAAT GGTTT AA CA
Del4  GGC CGCGGT AATTTA ACTGTG CTA AGG TAGCGTGATA  ATT  A GTCTTT TAATT GAGGTC TTGTATGAAT GGTTG GA CA
Del6  AGC CGCGGT AATTTA ACTGTG CTA AGG TAGCGTAATA  ATT  A GTCTTT TAATT GGGGTC TTGTATGAAT GGTTG GA CA
Del7  AGC TGCAGT AATTTA ACTGTA CAA AGG TAGCATAGTA  ATT  A GTCTTT TAATT GAGGTC TAGAATGAAT GGTTT AA CA
Fla5  AGC CGCAGT ATATTG ACTGTG CGA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TTGAATGAAT GGTTA AA CG
Mee2  GGC CGCGGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TTGAATGAAT GGGTT AA CA
Mee3  GGC CGCGGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TTGAATGAAT GGGTT AA CA
Mee6  GGC CGCGGT ATTTTA ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAGGTC TTGAATGAAT GGGTT AA CA
Cerc  GGC CGCAGT AATTTG ACTGTG CAA AGG TAGCATAATA  ATT  A GTCTTT TAATT AAAGTC TTGTATGAAT GATTG GA TG
Cica  GGC CGCGGT AAACTG ACCGTG CGA AGG TAGCATAATA  ATT  A GTCTTT TAATT GAAGGC TTGAATGAAT GATTG GA TG
Cic1  GGC CGCAGT ATACTA ACTGTG CAA AGG TAGCAAAATA  ATT  A GTTTCT TAATT AGAAGC TAGAATGAAT GGATA TA TG
Cic2  GGC TGCAGT ATTTTG ACTGTG CAA AGG TAGCATAGTA  ATT  A GTTTCT TAATT AGAAGC TGGTATGAAT GAATT AA TG
Cic3  GGC TGCAGT ATATTG ACTGTG CAA AGG TAGCATAGTA  ATT  A GTTTCT TAATT GGAAGC TTGTATGAAT GGATG TA TG
Cic4  GGC TGCAGT AGCTTG ACTGTG CAA AGG TAGCATAATA  ATT  A GTTTTT TAATT GAAGGC TGGTATGAAT GGAAA TT TG
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APPENDIX I：(Cont.)

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Ful3   AAAATTAT AC TTTATTTTTTTAATTTAA TTTGAATTTTATTT TTAAG TTAAAAAG CTTAA ATTTA GGAGAGGGACGA TAAGA CC
Ful4   AGAAGTAA AC TTTATTATCTTAATTTTA TTTGAATTTTATTT TTTAG TAAAAAAG CTAAA TTGTT GAAGAGGGACGA TAAGA CC
Ful5   AAAATTAT AC TTTATTTTTGTAATTTAA TTTGAATTTTATTT TTAAG TTAAAAAG CTTGA ATTTT GAAGAGGGACGA TAAGA CC
Dic1   AGAAATAT AC TTTATTTAATTGATTTT- TTTGAATTTTATTT TTTAG TTAAAAAG CTAAA ATTTT GAAGAGGGACGA TAAGA CC
Dic2   AAAAATTT AC TTTATTTTTTTTATTGT- TTTGAATTTTATTT TTTAG TCAAAAAG CTTAA ATATT AAAGAGGGACGA TAAGA CC
Dic3   AGAAATTT AC TTTATTTCATTTATTTT- TTTGAATTTTATAT TTTGG TTAAAAAG CTTAA ATGTT GAAGAGGGACGA AAAGA CC
Dic4   AGAAATAT AC TTTATTTAATTGATTTT- ATTGAATTTTATTT TTTAG TTAAAAAG CTAAA ATTTT GAAGAGGGACGA TAAGA CC
Fla1   AGGAAATT AC TTTATTTTTTTAATTTTT GTTGAATTTTAGAT TTTGG TTAAAATT CCAAA ATTTT TAAAAGGGACGA TAAGA CC
Fla2   AGGAATTA AC TTTATTTAAATTATTTT- TTTTAATTTTTGTT TTTGG TTAAAATA CCAAA ATTTT TATAAGGGACGA TAAGA CC
Fla3   AGGGAATT TC TTTATTTGGGGGAAGTTA ATTTAATTTATGTT TTTGG TTAAAATA CCAGG ATTTT TAAAAGGGACGA TAAGA CC
Fla4   AGGAATTA AC TTTATTTAAATTATTTT- TTTTAATTTTTGTT TTTGG TTAAAATA CCAAA ATTTT TATAAGGGACGA TAAGA CC
Del8   AGAAAATA AC TTTATTAATTAATCTTT- TTTCAATTTTATTT TTTAG TTAAAAAG CTAAA ATTTT TAAATGGGACGA TAAGA CC
Nog1   AGAAATTT TC TTTATTTTTTTTATTTTA TTTGAATTTTTATT TTTGG TTAAAATT CCAAA ATTTT TAAGAGGGACGA TAAGA CC
Nog2   AAAAATTT AC TTTATTTATTTTATTTT- TTTTAACTTTTATT TTTGG TTAAAATA CCAAA GTTTA TAAGAGGGACGA TAAGA CC
Ach1   AGGAAATA AC TTTATTTATTAA?????? ?????????????? ????? ???????? ????? ????? ???????????? ????? ??
Ach2   AGAAAATA AC TTTATTAATTTAAATTT- TTTGAATTTAATTT TTAAG TAAAAAAG CTTAA GTATT GAAGAGGGACGA TAAGA CC
Der1   AGGAGACA AC TTTATTAATTTTTAT--- ATTTAATTTAATTT TTTAG TTAAAAAG CTAAA ATTTT TAAGAGGGACGA TAAGA CC
Der2   AGAAAATA GC TTTATTTTTTGTAATTT- TTTGAATTTAATTA TCAAG TTAAAAAG CTTGA ATTTA TTAAAGGGACGA TAAGA CC
Dcr3   AAAAATAA TC TATTTTAATTTTATTTTT TTTGAATTTAAATT TTTTG TTAAAATG CTAAA ATTTA ATAGAGGGACGA TAAGA CC
Der4   AAAAATAA TC TTTATTTTTTTTTT---- TTTTAATTTTAATT TTGTG TTAAAATG CATAA ATTTT TAAGAGGGACGA TAAGA CC
Der9   AAAAATAA TC TATTTTAATTTTATTTTT TTTGAATTTAAATT TTTTG TTAAAATG CTAAA ATTTA ATAGAGGGACGA TAAGA CC
Tro1   AGAAAAAT AC TTTATTTTTTAAAATTT- ATTTAATTTAATTT TATTG TTAAAACG CAATA ATTAT TTGAAGTGACGA TAAGA CC
Tro2   AAAAAAAT GC TTTATTTGATTTATTT-- ATTTAATTTAACTT CATTG TTAAAATG CAATG ATTTT TTAAAGTGACGA TAAGA CC
Tro3   AGAAATAA AC TTTATTTTTTTAAATA-- ATTAAATTTAATTT TTTTG TTAAAAAG CTTAA ATTTA TTGAAGTGACGA TAAGA CC
Tro4   AAAAAAAT GC TTTATTTGATTTATTT-- ATTTAATTTAACTT CATTG TTAAAATG CAATG ATTTT TTAAAGTGACGA TAAGA CC
Ric1   AGAAACAA AC TTTATTGAAATAAATTT- TTTTAATTTTGATT TTGAG TTAGAATA CTTAA ATTTT AAAGGGGGACGA TAAGA CC
Ric3   AAAAACAT AC TTTATTAATTTTTAAT-- TTTTAATTTTTACT TTAAG TTAAAATA CTTAA ATATT AAAGTGGGACGA TAAGA CC
Ric4   AGAAATAA CC TTTATTTATTTTATTAA- ATTTAATTTTTTTT TTAAG TTAAAATA CTTAA ATTTT TAAGAGGGACGA TAAGA CC
Ric5   AGAAATAT AC TTTATTTGAAAAATTTT- TTTGAATTTTAAAT TTAAG TTAAAATT CTTAA ATTTT TAAGAGGGACGA TAAGA CC
Eur1   AAGAATAA AC TTTATTAATTTGATTAA- TTTGAATTTTAATT TCAAG TAAAAAT- CTT?A ATTTT AATAAGGGACGA TAAGA CC
Lop1   AGAAACTT GT TTTATTAAATAAATTTT- TTTGAATTTAAGTT TCTAG TTAAAATT CTAGA ATAAT TAAGAGGGACGA TAAGA CC
Tet2   AGAAATAA AC TTTATTTTTTAAATTAT- TTTGAATTTTTTTT TATAG TAAAAAAA CTATA ATTTG TAAGTGGGACGA TAAGA CC
Iss1   AGAAATTT AC TTTATTGTTTTTATTTTT TTTGAATTTTATTT ATTGG TTAAAAAG CCATT ATGTT TAAGAGGGACGA TAAGA CC
Iss5   AGAAATTT TC TTTATTAATTTAATTCA- ATTGAATTTTATTT TTTTG TTAAAAAG CTTAA ATTTA AAAGAGGGACGA TAAGA CC
Iss9   AGAAATTT AC TTTATTGTTTTTATTTTT TTTGAATTTTATTT ATTGG TTAAAAAG CCATT ATGTT TAAGAGGGACGA TAAGA CC
Iss10  AGAAAATT AC TTTATTTTATTTATTTTT TTTGAACTTTACTT TTTGG TTAAAAGG CCAAT ATTTT AAAGAGGGACGA TAAGA CC
Iss2   AGGAATAT AC TTTATTAATTTAATTTTT TTTGAATTTTATAT TTTTG TTAAAAAG CTTAA GTTAA AAAGAGTGACGA TAAGA CC
Iss11  AGGAATAT AC TTTATTAATTTAATTTTT TTTGAATTTTATAT TTTTG TTAAAAAG CTTAA GTTAT AAAGAGTGACGA TAAGA CC
Iss12  AGGAATAT AC TTTATTAATTTAATTTTT TTTGAATTTTATAT TTTTG TTAAAAAG CTTAA GTTAT AAAGAGTGACGA TAAGA CC
Iss3   AGAAATAA AC TTTATTTAATTTATTTTT TTTGAATTTGTTTT TTTAG TTAAAATT CTAAA ATGTT TTAGAGGGACGA CAAGA CC
Iss14  AGATATGA AC TTTATTTAATTTATTTT- TTTGAATTTGTTTT TTTAG TTAAAATT CTAAA ATGTT TAAGTGGGACGA CAAGA CC
Iss4   AAAAAAAA AC TTTATTAATTTTTTTTGT ATTGAATTTTATTT TTAAT TTAAAAAG ATTAA ATTTT TGAAGGGGACGA TAAGA CC
Iss6   AAAAATCT AC TTTATTAATATTTTTTT- ATTGAATTTTATTT TTAAT TTAAAAAG ATTAA ATTTA TTTAGGGGACGA TAAGA CC
Iss7   AAAAAACT AC TTTATTAATATTTTTTT- ATTGAATTTTATTT TTGAT TTAAAAAG ATTAA ATTTA TTTAGGGGACGA TAAGA CC
Iss8   AAAAAATT TC TTTATTAGTTTTATTAAT TGAAATTTATTTTT AATTT AAAAAGAT TAATT GTTTA AAAGGGGCACGA TAAGA CC
Cix2   GGAGGTAA AC TTTATTATTTTTTTT--- TTTGAATTTAATTT TTTAG TTAAAAAG CTTAA ATTTT TAATTGTGACGA TAAGA CC
Cix3   AGAAAATA AC TTTATTAAAATAAATTTT TCTTAATTTAATAT TTTTG TTAAAAAG CTAAA ATGAT TAAGTGGGACGA TAAGA CC
Cix4   AGAAAATA AC TTTATTAAAATGATTTTT TTTTAATTTAATAT TTTTG TTAAAAAG CTTAA ATAAT TAAGTGGGACGA TAAGA CC
Cix6   AGAAAACA AC TTTATTAATAAAATTTTT TTTTAATTTAATTT TTTAG TTAAAAAG CTTAA ATAAT TAAGTGGGACGA TAAGA CC
Del2   AGAAGTAA GC TTTATTAATTCAATTA-- AGTGAAATTTATTT TTTAG TTAAAAAG CTAAA ATTTA AAAATGGGACGA TAAGA CC
Del3   AGGTGAAA AC TTTCTTATTTAAATTAC- TTTGAATTTAATTT TTTAG TTAAAAAG CTAAA ATTTT TAAATGGGACGA TAAGA CC
Del4   AGAAGATT TC TTTATTTAATTTATTT-- TTTTAATTTAATTT TGTAG TTAAAAAG CTTCA ATTTT TAATTGGGACGA TAAGA CC
Del6   AGAAGATT TC TTTATTTAATTTATTT-- TTTTAATTTAATTT TTTAG TTAAAAAG CTTTA ATTAT TAATTGGGACGA TAAGA CC
Del7   AGAAGTAA GC TTTATTAATTCAATTA-- AGTGAAATTTATTT TTTAG TTAAAAAG CTAAA ATTTA AAAATGGGACGA TAAGA CC
Fla5   AAGAATAA AC TTTATTTAATTAATTTT- TTTTAATTTTTGTT TTTGG TTAAAATA CCAGA ATATT TAAAAGGGACGA TAAGA CC
Mee2   AAAAAATA TC TTTATTAAATTAAATTT- TTTTAAGTTAATTT TAAAG TTAAAATT CTTTA ATAAT TAAGGGGGACGA TAAGA CC
Mee3   AAATAATA GC TTTATTAAATTAAATTT- TTTGAAATTAATTT TAAAG TTAAAATT CTTTA ATTAT TAAGGGGGACGA TAAGA CC
Mee6   AAAAAATA TC TTTATTAAATTAAATTT- TTTTAAGTTAATTT TAAAG TTAAAATT CTTTA ATAAT TAAGGGGGACGA TAAGA CC
Cerc   AGAAATTA TC TTTCTTTATTATTTTA-- ACTGAATTTGATAT TTAGG TGAAAAAG CTTAA ATTTT TCTGTGGGACGA TAAGA CC
Cica   AAAAGCTA TC TTTATTAATATAAAAA-- TTTTAATTTAACAT TTAAG TAAAAAGG CTTAA ATATT TTAGTGGGACGA GAAGA CC
Cic1   TGATATAT AT TTTATTAGGTTTAAAA-- TTAAAATTTTAATT TTGGG TTAAAATG CTCAA TTTCT TTTTAGGGACGA TAAGA CC
Cic2   AGAAATAT AT TTTATTAATTTTAATA-- TTGAAATTTAAATT TTAAG TGAAAATG CTTAA AGGTT TTCTTGGGACGA TAAGA CC
Cic3   AGAAATAT GT TTTATTAATTTTACTA-- TTAAAAATTAAATT TTAAG TCAAAATG CTTAA TTATT TTTCTGGGACGA TCAGA CC
Cic4   AGATACAT GT TTTATTTGATTTAAATT- TATAAATTTAAACT TTAAG TTAAAATG CTTAA GTGAA TTCTTGGGACGA TAAGA CC
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APPENDIX I：(Cont.)

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Ful3  CTATAGATCTT T ATTTTATTTTTGATTTTTTTTTTT-- TAGTTTATT --TTTAAAATTTTTATTAATTAAAT TT TGTTG GGG TGAC
Ful4  CTATAGATCTT T ATTTTTTTCCATTTTTTTTTTATTT-- TAGTTTATT --TTAGATTTTTTTTGGTTATAAAT TT TGCTG GGG TGGT
Ful5  CTATAGATCTT T ATTTTATTTTTGATTTTTTTTTTT-- TAGTTTATT --TTTAAAATTTTTATGAATTAAAT TT TGTTG GGG TGAC
Dic1  CTATAGATCTT A ATTTAATTTATTTAAGTTTTTTTT-- TTGTTGTCT --TTTTTAATTTATTTAATTTAAAT TT GGTTG GGG CGAC
Dic2  CTATAGATCTT G AATTTATTAAATTAATTTATTTTT-- TTGTTGTTT --TTATTAATTTATTTTAATTAATT TT AGTTG GGG CGAT
Dic3  CTATAGATCTT A AATTTTTTATTATAATTTATTTTT-- TTGTGGTTT --TTTTTAATTTGAAGTAATCAATT TT GGTTG GGG CGAT
Dic4  CTATAGATCTT A ATTTAATTTATTTAAGATAAAAT--- TTGTTGTAT --TTTTTAATTTATTTATTTTAAAT TT GGTTG GGG CGAC
Fla1  CTATAGATCTT T ATAATTCTTATTTTTTTGTTTTTT-- TTGTTGTTT -TAAGATTATTTATTTATGATTTAT TT AGTTG GGG TGAT
Fla2  CTATAGATCTT T AAAAAAAATATTTATTTTTCTTTT-- TTGTTGTAT --TTTAAAATTAAGATATTTTTTTT TT TGTTG GGG TGAC
Fla3  CTATAGATCTT T ATAATATTTTATTATTTAGGTTTT-- TTGTTGTAT --TTTTTATTTAGTATTTTTTTAT TT AGTTG GGG TGAT
Fla4  CTATAGATCTT T AAAAAAAATATTTATTTTTCTTTT-- TTGTTGTAT --TTTAAAATTAAGATATTTTTTTT TT TGTTG GGG TGAC
Del8  CTATAGATCTT A AAATTTTTTATATTTGAAATAATTT- TATGGGTTA ATTTAAATTTTGTTTGGGAAAATTT TT TGTTG GGG TGAC
Nog1  CTATAGATCTT T AAAATAATTTATTTATTATTTTTTT- TTGTTGTAT --TTATTTTTATTTATATATTTTTT TT TGTTG GGG TGAT
Nog2  CTATAGATCTT T AAAATTGTTTTTTTTTCTTTTTTT-- TTGATGTGT -TTTTAGGAGAATTATTTCATTTTT TT TGTTG GGG TGAT
Ach1  ??????????? ? ?????????????????????????? ????????? ??????TTTTTTAGGAAGTAAAAAT TT TGTTG GGG TGAC
Ach2  CTATAGATCTT T ATTATTAATTTTTATAAGATGTTTAG TAGATTTTT -----TTTTTTGTGAAAATTATTAA TT TGCTG GGG TGGC
Der1  CTATAGATCTT T ATTATTGATTTTTTATTTTTG----- TTAATTTTT -----TATTTAATTTAATTAATAAT TT TATTG GGG TGAT
Der2  CTATAGATCTT T ATTATTTAGGTTTTATATTATTA--- TTATTGTTT --TTGATTTTTATAATTTAAATAAT TT TATTG GGG TGAT
Der3  CTATAGATCTT T ATTATATTTATAATATTTATTTTTT- TTATTGTTT ---TTTATTATATTATAAATTTAAT TT TATTG GGG TGAT
Der4  CTAAAGATCTT T ATTTAATAATTATTTTAATTTTT--- TTTAA---- --TTTTTTTATTTTAATTTTTAAAT TT GGTTG GGG TGAT
Der9  CTATAGATCTT T ATTATATTTATAATATTTATTTTTT- TTATTGTTT ---TTTATTATATTATAAATTTAAT TT TATTG GGG TGAT
Tro1  CTATAGATCTT T ATTTTATTTTTTTTTTTTTTCTTT-- TTGATGGTT -TTTATTTAAATTTAATTATAAAAT TT TGTTG GGG TGAC
Tro2  CTATAGATCTT T ATTTTTTTTATATTTTTTTTTTTT-- TTGTTGATT -TTATATAATTTTAGTTTAAAAAAT TT TGTTG GGG TGAT
Tro3  CTATAGATCTT A ATTAATTTTTAATATTTTTTTTTT-- TTGTTGTAT ----TTTATTGTTATTAAATTTAAT TT TGTTG GGG TGAT
Tro4  CTATAGATCTT T ATTTTTTT-CTATTTTTTTTTTTT--- TTGTTGATT -TTATGTATTTTTAGTTTAAAAAAT TT TGTTG GGG TGAT
Ric1  CTATAGATCTT A AAAATATTTACTTTTTATTTTTTTT- TTGTTGTTT --TTTATTTAAATATTATTTATTTT TT AGTTG GGG TGAT
Ric3  CTATAGATCTT A ATAATTTTATTATTTATTTTTTTT-- TTGTTGTTT -TATTAATTTATTTATTAATTTTTT TT AGTTG GGG TGAT
Ric4  CTATAGATCTT G AGAATTTTTTTTTTTTTTTTTTTT-- TTGTTGTTT --TTTATTTGGAATTTTAATTTTCT TT AGTTG GGG TGAT
Ric5  CTATAGATCTT A ATAATTATTTTTTTTTGTTTTTTT-- TTGTTGTGA --TTTAATATATTTAAAATTTTTTT TT TGTTG GGG TGAT
Eur1  CTATAGATCTT - ATAATAATTTTTTTTTTAAAATTT-- TAGTTGTTT -ATAAATTTAAAATAAAAATTTTAA TT TGTTG GGG TGAT
Lop1  CTATAGATCTT A ATAATATAAATAATTAATAAAATTT- TAGATTATA ---TATTGGTAATTTTTTTTTTTAT TT TGTTG GGG TGAT
Tet2  CTATAGATCTT T ATAAATTAAAAGTTTATTTTTTTT-- TTGAATTAT -TTTTATATTAAATTTTTAATTTAT TT TGTTG GGG TGAT
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Iss10 CTGTAGATCTT T ATAATTTAAACTATTTTTATTTTT-- TTGTTTGTC --TTTTTGTAATTTTTTATTTTAT TT TGTTG GGG TGAT
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Iss11 CTATAGATCTT T AAAATTTTTTTTTTTTTAATTTTTT-- TTGTTGTTT --ATTGTTTATTTAAATTAATTTTT TT TGTTG GGG AGAT
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Iss14 CTATAGATCTT T AAATAGGTTTATTTTATTTTTTTT-- TTGTTGTTT ---TTTAATTAATATTAATCTTTTT TT TGTTG GGG TGAT
Iss4  CTATAGATCTT A AAAATATTATATTTATATATATTT-- TTGTTGTTT ATATTTATAAAAATTATATTATTTT TT TGTTG GGG TGAC
Iss6  CTATAGATCTT A AAAATATTTTTTTTTTATTAATTT-- TTGTTGTTA AATTTTTTGTAAA-AATATTATTTT TT TGTTG GGG TGAC
Iss7  CTATAGATCTT A AAAATATTTTTTTTTTATTAATTT-- TTGTTGTTA AATTTTTTGAAATTAATATTATTTT TT TGTTG GGG TGAC
Iss8  CTATAGATCTT T AAAATTTTTTATATATTTATTTTT-- TTGTTGTTT -TTAATAAATTTTTAAATAGATTTT TT TATTG GGG TGAT
Cix2  CTATAGATCTT A AAAATATTTTTATATAAATTTTT--- TTGTGGTAT -TCTTTTTTTTGTAGGAATTATTTT TT AGTTG GGG TGAT
Cix3  CTGTAGATCTT T ATAATTAATTAATATAAAATTTT--- TGGTTGTAT --TATTTTTTTTTTTAGTTAATTAT TT TGTTG GGG TGAC
Cix4  CTGTAGATCTT T ATAATTAATTAAAATAATTTTTT--- TGGTTGATA --TTTTTTTTTTTTTAATTAATTTT TT TGTTG GGG TGCC
Cix6  CTGTAGATCTT A AAATATTTAATAAGTTCATTTTT--- TTGTTGTTA TTATGTGTTTCTTATTTAAACTTTT TT TATTG GGG TGAT
Del2  CTTTAGATCTG T AAATTTTAATTGAATAATAATATTA- ATGTGGATT ---TAATTTTTATTAAATAAAATTT TT TGTTG GGG TGAC
Del3  CTATAGATCTT A AATTTTTTTTTATCTTAATTTCT--- TGGTTAATA AAATGTTAAAATTTTAAAAAAAATT TT TGTTG GGG TGAC
Del4  CTGTAGATCTT T AAAATTGGTTTTTTTAATTTTTT--- TTGTTTATT --TAATTTTTATTTTTATTAATTTT TT GGTTG GGG TGAT
Del6  CTGTAGATCTT T AAAATTGATTTTAATAATTTTTT--- TTGTTTATT --TAGTTTTTATTTTTATTAATTTT TT GGTTG GGG TGAT
Del7  CTTTAGATCTT T AAATTTTAATTGAATAATAATATTA- ATGTGGATT ---TAATTTTTATTAAATAAAATTT TT TGTTG GGG TGAC
Fla5  CTATAGATCTT A AAAATATTTTTTTATTTTTTTTTT-- TTGTTGTTT -TTTAAAAAAATTTATCTTTTATTTT TT TGTTG GGG TGAT
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Mee3  CTATAGATCTT A AAAAATAAATTTTTATATT------- TAGTTTTTT ---TTATTTTTTAAAATTTATTTTT TT AATTG GGG AGAT
Mee6  CTATAGATCTT A AAAAAATAAATTTCTTATT------- TGGTTTTTT --TATTTATAAATTAATTTATTTAT TT AGTTG GGG AGAT
Cerc  CTATAGATCTT T AAAATTATTTTTTTTTAATATTTTT- AGAATTTAT -ATTTCTTATTAAATTATTAATTTT TT TGTTG GGG TGAT
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Cic1  CTATAGAACTT T ACTAAATATAATTTAGTTGGTTTT-- TTTTTTATA ----TAAATTTATTAAATTTTATTT TT AGTTG GGG TGAC
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Cic3  CTATAGAACTT T ATATTACCTAGTTATAGTTTATTT-- TTGATTATA -ATACTATCTTAATATTACAGTACT TT TGCTG GGG TGGT
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APPENDIX I：(Cont.)

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Ful3   A AATAAA -ATTTTAATC TTTATT TT TT  TTTTACATTTTTTTAT- GA  --ATATTTGATC CTTA TT- TTTG ATTAAAAGATT
Ful4   A GATAAA -ATTTTAATC TTTATT TT TT  TTTTACATTTCTTTAT- GT  --GATTTTGATC CTTT TT- TTTG ATTATAAGATT
Ful5   A AATAAA -ATTTTAATC TTTATT TT TT  TTTTACATTTTTTTAT- GT  --CTGTTTGATC CTTT AT- TTTG ATTAAAAGATT
Dic1   A AATAAA -TTTTTAATC TTT-TT TT TT  TTTTACAATTATTTTTG GT  ----TTTTGATC TTTT TT- ATTG ATTATAAGATG
Dic2   G AATAAA -ATTTTAATC TTTTTT TT TT  TTTTACA-TTATATTTG GA  ---TATTTGATC CTTT TTT TTTG ATTAAAAGATA
Dic3   A ATTAAA -CATTTAAAC CTTTTT TT TT  TTTTACATTTATTTTT- GA  --TTTATTGATC TTTA TT- TTTG ATTAAAAGATT
Dic4   A AATAAA -TTTTTAAAC CTTTTT TT TT  TTTTACAATTATTTTTG GT  ----TTTTGATC TTTT TT- ATTG ATTATAAGATG
Fla1   T AATAAA -AATTTTATC TTTATT TA TT  TTTTACATTTTTTTTTG GT  ---TATTTGATC TTAA ATT TTGG ATTATAAGAAA
Fla2   G TTTAAA -ATTTTTGAC TTTAAA TT TT  TTTTACA-TTTTTTTT- GT  -TTAATTTGATC TTGA ATT TTTG ATTATATGATT
Fla3   T AATAAA -ATTTTAAAC TTTATT TC TT  TTTTACAATTATTTTTG GT  ---TTTTTGATC CTTA AAT TTAG ATTATAAGATT
Fla4   G TTTAAA -ATTTTTGAC TTTAAA TT TT  TTTTACA-TTTTTTTT- GT  -TTAATTTGATC TTGA ATT TTTG ATTATATGATT
Del8   A TATAAA TTTTTAAAAC TTTAAA AT TT  TTTTACATTTATAGAT- GT  --ATAAATGATC CAAA CTT TTTG ATTATTAAAAT
Nog1   A GATAAA -AACTTAAAC TTTTTT TT AT  TATTACATTTATTTATG GT  --TTTTTTGATC CTTA ATT TTTG ATTTCAAGATT
Nog2   A TATAAA -ATTTTAAAC TTTATA TT TT  TTTTACATTTATTTTTG GT  --TATATTGATC CTTT TTT TTTG ATTTTAAGATT
Ach1   A TATAAA -ATTTTAAAC TTTATT TT TT  CTTTGCTTTTATTTTTG GT  --TTATTTGATC CTTA AT- TTTG GATTTTAGATT
Ach2   A GGTAAA -ATATTTATC TTTATT TT TT  TTTTACATTTATTTATG TT  --TAGTTTGATC CAGA ATT TTTG ATTGAAAGATT
Der1   A ATTAAA -TTTTTTTAC TTTTTT TT TT  TAGAACAATTTTTTATG GG  ---AATTTGATC TTTT AT- TTTG ATTTTAAGAAA
Der2   A ATTAAA -AATTTAAAC TTTTTT TT TT  ATTAACATTTATTT--- GT  --GAATTAAGTA TTTT TTT TAAG AGAATAAGATA
Der3   A ATTAAA -ATTTTTATC TTTTTT AT TT  TATTACAATAGTTTTTG GT  -TAAATGATCCT AAAT AAT TTAG ATTAATAGATA
Der4   A AATAAA -TATTTAATC TTTTTT TT TT  TTTTACATTTTTTTATG GT  ---TATTTGAGT ---T TTT A--- AATTAAAAGAA
Der9   A ATTAAA -ATTTTTATC TTTTTT AT TT  TATTACAATAGTTTTTG GT  -TAAATGATCCT AAAT AAT TTAG ATTAATAGATA
Tro1   A TTTAAA -ATTTTAATC TTTATT TA TT  TTTTACATTTTTTTTT- GT  --GTTTTTGAAC CATA ATT TTTG TTTATTAGAAA
Tro2   A ATTAAA -AATTTTATC TTTAAT TT TT  TTTTACATTTATTTAT- GT  -TTAGTTTGAAC CTTA ATT TTTG TTTAAAAGAAT
Tro3   T GCTAAA -ATTTTAATC TTTAGT TT TT  TATTACATTTATTTTTG GT  --TAGTTTGAAC TTAT AT- TTTG TTTGTAAGATA
Tro4   A ATTAAA -AATTTTATC TTTAAT TT TT  TTTTACATTTATTTAT- GT  -TTAGTTTGAAC CTTA ATT TTTG TTTAAAAGAAC
Ric1   T ATTAAA -ATTTTAAAC TTTGAT TT AT  TTTTACATTTAATTTTG GC  TTATTTTTGATC CTTC TTT TTTG ATTATAAGATA
Ric3   T ACTAAA -ATTTTAAAC TTTAGT TT AT  TTTTACATTTGTTATT- GT  -TTTTTTTGATC TTTT TT- TTTG ATTATAAGATA
Ric4   T ACTAAA -AATTTAAAC TTTAGT TT AT  TTTTACATTTATTATT- GT  -ATTTATTGATC CTTT TT- TTTG ATTATAAGATA
Ric5   T ACCAAA -AATTTAAAC TTTGGT TT AT  TTTTACATAAAATTTAT GT  -ATTTTTTGATC CTTT TT- TTTG ATTATAAGAAA
Eur1   A ACTAAA -ATTTTAAAC TTTAGT TT TT  TTTTACATAAATAAAT- GT  -ATAAATTGATC TTTA TT- ATTG ATTATAAGATT
Lop1   A GCTAAA -ATTTTAAAC TTTAGT TT TT  TTTAACAATAATTTTT- GT  -GTAATTTGATC TTTT AT- TTTG ATTATAAGATA
Tet2   A AATAAA -ATTTTAAAC TTTTTT TT TT  TTTTACATTTATAAAT- GA  -TTAATTTGATC CTTT AAT ATTG AAAATAAGATC
Iss1   A GTTAAA -ATTTTAAAC TTTAGT TT TT  TTTTACATATATTTATG GT  --TTGTTAGATC TTTA ATT TTTG ATATCAAGATC
Iss5   A GCTAAA -ATATTAAAC TTTAGT TT AT  TTTTACAATTTTTTTTG GT  --TTTTTTGATC CTTT -TT ATTG ATATAAAGAAG
Iss9   A GTTAAA -ATTTTAAAC TTTAGT TT TT  TTTTACATACATTTATG GT  --TTACTAGATC TTTA ATT TTTG ATATTAAGATT
Iss10  A ACTAAA -ATTTTAAAC TTTAGT TT TT  TTTTACATACATAGATG GT  --TTTTTTGATC TTTA ATT TTGG ATATTAAGATT
Iss2   A GATAAA -ATTTTAAAC TTTATT TT TT  TTTTACTTTTTTT-AT- GA  --ATTTTTGATC CTTA ATT TTGG ATTATAAGAAT
Iss11  A GATAAA -AATTTTAAC TTTATT TT TT  TTTTACTTTTTTTG-TG GT  ---TTTTTGATC CTTA ATT TTGG ATTATAAGAAT
Iss12  A GATAAA -AATTTTAAC TTTATT TT TT  TTTTACTTTTTTTG-TG GT  ---TTTTTGATC CTTA ATT TTGG ATTATAAGAAT
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Iss14  A GTTAAA -ATTTTTAAC TTTAAT TT TT  TTTTTCATTTATTTAT- GA  --ATTTTTGATC TTTT TTT GATG ATTAAAAGATA
Iss4   A AATAAA -AATTTAAAC TTTATT TT TT  TTTTACATTTGTTTAT- GA  -AATTTTTGATC CTTT -T- TTGG ATAAAAAGAAA
Iss6   A AATAAA -AATTTAAAC TTTATT TA TT  TTTTACATTTATAGTT- GA  --TTTTTTGATC CTAA GTT TTGG ATAGTAAGATA
Iss7   A AATAAA -AATTTAAAC TTTATT TA TT  TTTTACATTTATAGAT- GA  --TTTTTTGATC CTAG -TT TTGG ATAATAAGATA
Iss8   A ATCAAA -AATTTTAAC TTTAAT TT AT  TTTAACATTAATTTAT- GA  -TTTTTTTGATC CTTA TTT TTGG AGAAAAAGAAC
Cix2   T AAAGAA -ATTTTAAAC TTTTTT TT TT  TTTTACATTGATATAT- GT  --TTTTTTGATC TTTA AT- TTTG ATTAAAAGAGT
Cix3   A AATAAA -TTTTTTAAC TTTTTT TA TT  ATATACATTATTTTTTG GT  ---TTTTTGATC CTTA AT- TTTG ATTAAAAGAAA
Cix4   A GTAAAA -TTTTTTAAC CTTTTT TT TT  TAGGACAATAATTTTTT TT  GGGTTTTTGATC CTTT CAT TTTG ATTAAAAGAAA
Cix6   A AATAAA TTTTTTAAAC TTTTTT TT AT  ATTTACATTTATTTATG AA  --AAATTTGATC CTTT TAT TTTG ATTAAAAGAAA
Del2   A GCTAAA ATCTTAAATC TTTAGT AT TT  TACACCATTTATTTAT- GT  --ATATTTGAAC CTTA ATT TAAG GTTATTAAAAT
Del3   A TTAAAA TTTTTAAATC TTTTAA TC AT  TTTTACATAAATAAAT- GT  --ATATTTGATC TTAA CAT TTAG ATTAAAAAATT
Dcl4   T TTTAAA TTTTTATTAC TTTATT TT TT  TTTTACATTTATTTAT- GT  --TTAATTGATC TTTA ATT TTTG ATTTTTAGATT
Del6   T TTTAAA TTTTTATTAC TTTATT TT TT  TTTTACATTTATTTAT- GT  --TTAATTGATC TTTA ATT TTTG ATTTTTAGATT
Del7   A GCTAAA ATCTTAAATC TTTAGT AT TT  TACACCATTTATTTAT- GT  --ATATTTGAAC CTTA ATT TAGG GTTATTAAAAT
Fla5   A AATAAA ATTTTTGACC TTTATT TT TT  TTTTACATTTATTTTT- GG  -TTTTATTGATC CTTT ATT TTGG ATTATAAGATA
Mee2   T TTTAAA -AATTTAAAC TTTATT TT TT  TTTTACATCAATTTAT- GT  -TTATATTGATC CAGT ATT TCTG ATTATAAGATA
Mee3   T TATAAA -AAATTAAAC TTTATA TT TT  TTTTACATTAATTGTT- GT  TTTATATTGATC CATT TTT AGTG ATTTAAAGATA
Mee6   T TTTAAA -AATTTAAAC TTTATT TT TT  TTTTACATCAATTTAT- GT  -TTATATTGATC CAGT ATT TCTG ATTATAAGATA
Cerc   A AATTAA -TTAATATAA CTTTTT TA TG  TTTTTTCATTAATTTAT GT  --TTTTATGATC TTTT ATT AATG ATTAATAGATT
Cica   A TTAAAA TATTAATAAC TTTTAA TT AA  ATTTTCATAGATAAAT- GA  --TTATTAGATC CAAT TTT TTTG ATTTTAAGACT
Cic1   A GTTAAA -TTTT-AA-C TTTAAT TT TG  ATAATCATTATTTTAT- GT  -AGTTTTTGATC CATA TA- TATG ATAATAAGATA
Cic2   G GATAAA -TTT-AAA-C TTTATT AT TT  TATATCAATTATTTTT- GT  -TTGTTTAGATC CTTT TGG AATC -----AAGAAT
Cic3   G GATAAA -TTT-AAA-C TTTATA TA AT  AATATCAATTATTAAT- GA  -ATGTTAAGATC TTAC AAC TTAG ATTAAAAGATA
Cic4   G AATAAA -TTT-AAA-C TTTATT AA TA  AAAATCA-TTATAAAT- GT  -TTGTGTTGATC TGTT ATT AAGA ATT--AAGAAT
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APPENDIX I： (Cont.)

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                                                                                                  495
Ful2   AAGATACCTTAGGG ATAACAG CGTTATAAATCTGGAGA GTTC-TTA TTGAT-AGATTTGTTTGCG ACCTCGATG TTGGATTAAAA GT
Ful3   AAGATACCTTAGGG ATAACAG CGTTATAAATCTGGAGA GTTC-TTA TTGAT-AGATTTGTTTGCG ACCTCGATG TTGGATTAAAA GT
Ful4   AAGATACCTTAGGG ATAACAG CGTGATAATTCTGGAGA GTTC-ATA TTGAT-AGAGTTGTTTGCG ACCTCGATG TTGGATTAAAA AT
Ful5   AAGATACCTTAGGG ATAACAG CGTTATAAATCTGGAGA GTTC-TTA TTGAT-AGATTTGTTTGCG ACCTCGATG TTGGATTAAAA GT
Dic1   AAGATACCTTAGGG ATAACAG CGTTATTTAGTTGGATA GTTC-ATA TTGAT-AACTAAGATTGCG ACCTCGATG TTGGATTAAAA TT
Dic2   AAGATACCTTAGGG ATAACAG CGTTATTTAGTTGGAGA GTTC-TTA TTGAT-AATTAAGTTTGCG ACCTCGATG TTGGATTAATA AT
Dic3   TAGATACCTTAGGG ATAACAG CGTTATTTAATTGGAGA GTTC-TAA TCAAT-AATTAAGATTGCG ACCTCGATG TTGGATTAAAA TT
Dic4   AAGATACCTTAGGG ATAACAG CGTTATTTAGTTGGATA GTTC-ATA TTGAT-AGCTAAGATTGCG ACCTCGATG TTGAATTAAAA TT
Fla1   AAGATACCTTAGGG ATAACAG CATAATAATTCTGGAGA GTTC-TAA TCGAT-AGACTTGTTTGTG ACCTCGATG TTGGATTAAAA TT
Fla2   AAGATACCTTAGGG ATAACAG CATAATTTATTTGGAGA GTTC-AAA TCGAT-AATTAAGTTTGTG ACCTCGATG TTGGATTAAAA TT
Fla3   AAGATACCTTAGGG ATAACAG CATAATTTACCTGGAGA GTTC-TTA TTGAT-AGGTTTGTTTGTG ACCTCGATG TTGGATTAAAA TT
Fla4   AAGATACCTTAGGG ATAACAG CATAATTTATTTGGAGA GTTC-AAA TCGAT-AATTAAGTTTGTG ACCTCGATG TTGAATTAAAA TT
Del8   AAGATACCTTAGGG ATAACAG CGTAATAAATTTGTATA GTAC-ACA TAAAT-AAGTTTGTTTACG ACCTCGATG TTGAATTAATA TT
Nog1   AAGATACCTTAGGG ATAACAG CGTTATATATCTGGAGA GTTC-TAA TTGAT-AGATATGTTTGCG ACCTCGATG TTGGATTAATT TA
Nog2   AAGATACCTTAGGG ATAACAG CGTTATATGTTTGGAGA GTTC-TTA TCGAT-AAATATGTTTGCG ACCTCGATG TTGGATTAAAA TT
Ach1   AAGATACCTTAGGG ATAACAG CGTTATATATTTGGAGA GTTC-AAA TTGAT-AAATATGTTTGCG ACCTCGATG TTGGATTAAAT TT
Ach2   AAGATACCTTAGGG ATAACAG CGTAATATATTTGGAGA GTTC-TTA TTGAT-AAATATGTTTGCG ACCTCGATG TTGGATTAAAA TT
Der1   AAGATACCTTAGGG ATAACAG CGTTATTTAATTGGAGA GTTC-ATA TTGAT-AATTAAGATTGCG ACCTCGATG TTGGATTAATA AT
Der2   AAGATACCTTAGGG ATAACAG CGTTATATAACTGGAGA GTTC-TTA TTGAT-AGTTATGTTTGCG ACCTCGATG TTGGATTAAAA TT
Der3   TAGATACCTTAGGG ATAACAG CGTTATATAATTGGAAA GTTC-TTA TTGAT-AATTATGATTGCG ACCTCGATG TTGGATTAAAG TT
Der4   AAGATACCTTAGGG ATAACAG CGTTATAAAATTGGATA GTTC-AAA TTGAT-AATTTTGTTTGCG ACCTCGATG TTGGATTAATA AA
Der9   TAGATACCTTAGGG ATAACAG CGTTATATAATTGGAAA GTTC-TTA TTGAT-AATTATGATTGCG ACCTCGATG TTGGATTAAAG TT
Tro1   AAGATACCTTAGGG ATAACAG CGTAATATATTTGGATA GTTC-TTA TTGAT-AAATATTTTTGCG ACCTCGATG TTGGATTAAAA TT
Tro2   AAGATACCTTAGGG ATAACAG CGTAATTTATTTGGATA GTTC-ATA TTGAT-AAATATATTTGCG ACCTCGATG TTGGATTAATA TT
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Tro4   AAGATACCTTAGGG ATAACAG CGTAATTTATTTGGATA GTTC-ATA TTGAT-AAATATAATTGCG ACCTCGATG TTGGATTAAAA TT
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Ric4   AAGATACCTTAGGG ATAACAG CGTAATTTATTTGGAGA GTTC-TTA TTGAT-AAATAAGTTTGCG ACCTCGATG TTGGATTAAGT TT
Ric5   TAGATACCTTAGGG ATAACAG CGTTATTTAATTGGAGA GTTC-TTA TCTAT-AATTAAGTTTGCG ACCTCGATG TTGGATTAAAT TT
Eur1   AAGATACCTTAGGG ATAACAG CGTTATATATTTGGAGA GTTC-TAA TTGAT-AAATATGATTGCG ACCTCGATG TTGGATTAAAA TT
Lop1   AAGATACCTTAGGG ATAACAG CGTTATTCATTTGAAGA GTCC-ATA TCTGT-AAATGAGTTTGCG ACCTCGATG TTGGATTAAAA TA
Tet2   CAGATACCTTAGGG ATAACAG CGTTATATATTTGGAGA GTTC-AAA TTGAT-AAATATGTTTGCG ACCTCGATG TTGGATTAAAA TT
Iss1   AAGATACCTCAGGG ATAACAG CGTTATAGATTTGGAGA GTTC-TTA TTGAT-AAATTTGTTTGCG ACCTCGATG TTGGATTAAAG TT
Iss5   AAGATACCTTAGGG ATAACAG CGTTATATAGTTGGAGA GTTC-AAA TTGAT-AATTATGTTTGCG ACCTCGATG TTGGATTAAAG TT
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Iss10  AAGATACCTCAGGG ATAACAG CGTTATAAATTTGGAGA GTTC-TTA TTGAT-AAATTTGTTTGCG ACCTCGATG TTGGATTAAAA TT
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Cix3   AAGATACCTCAGGG ATAACAG CGTTATACATTTGGAAA GTTC-ATA TTGAT-AAATGTGTTTGCG ACCTCGATG TTGAATTAAGT TT
Cix4   AAGATACCTCAGGG ATAACAG CGTTATACATTTGGAAA GTTCTATA TTGAT-AAATGTGTTTGCG ACCTCGATG TTGAATTAAAG TT
Cix6   AAGATACCTCAGGG ATAACAG CGTTATATATTTGGAGA GTTC-TTA TTAAT-AAATATGTTTGCG ACCTCGATG TTGGATTAAAA TT
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Del6   AAGATACCTCAGGG ATAACAG CGTTTATTTTTTGGAAA GTTC-TTA TTGAT-AAATTAAATTGCG ACCTCGATG TTGGATTAATA TA
Del7   AAGATACCTTAGGG ATAACAG CATAATAAATTTGCAAA GTTC-ATA TATAT-AAATTTGATTGTG ACCTCGATG TTGAATTAATC TA
Fla5   AAGATACCTTAGGG ATAACAG CATAATATAGTTGGAGA GTTC-AAA TCGAT-AATTATGTTTGTG ACCTCGATG TTGGATTAAGA ??
Mee2   AAGATACCTTAGGG ATAACAG CGTAATAAATTTGGGGA GTTC-ATA TTTAT-AAATTTGTTTGCG ACCTCGATG TTGAATTAAAA TT
Mee3   AAGATACCTTAGGG ATAACAG CGTAATAAATTTGGGGA GTTC-ATA TTTAT-AAATTTGTTTGCG ACCACGATG TTGAATTAAAA TT
Mee6   AAGATACCTTAGGG ATAACAG CGTAATAAATTTGGGGA GTTC-ATA TTTAT-AAATTTGTTTGCG ACCTCGATG TTGAATTAAAA TT
Cerc   AAGTTACCTTAGGG ATAACAG CGTGATTTATTTGGAAA GTTC-ATA TTTAT-AAATAAGTTTGCG ACCTCGATG TTGGATTAAGA TT
Cica   AAATTACCTTAGGG ATAACAG CGTTATTATTTTAAAAA GTTC-TTA TTGATAAAATTAGATTGCG ACCTCGATG ??????????? ??
Cic1   AAGTTACCTTAGGG ATAACAG CGTAATTTTAGTGGGGA GTTC-ACA TCTAT-ACTAAATTTTGCG ACCTCGATG TTGAATTAAGA TA
Cic2   TAGTTACCTTAGGG ATAACAG CGTAATTTTATTGGCGA GTTC-ATA TCTAT-A-TTAATTTTGCG ACCTCGATG TTGAATTAAGG AA
Cic3   AAGTTACCTTAGGG ATAACAG CGTAATTATTATGGGAA GGTTATAA TTTAT-A-TAAGTTTTGCG ACCTGAATG TTGAATTAAGG AA
Cic4   AAGTTACCTTAGGG ATAACAG CGTAATTACAATGGAAA GTTC-ATA TTTAT-ATTGATTTTTGCG ACCTCGATG TTGAATTAAGG TA
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APPENDIX I : (Cont.)

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                                                                                   569
Ful2   -- TTCTGTGGG GTAGGT TTTACAATA CT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Ful3   -- TTCTGTGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Ful4   -- TTCTGTGAG GCAGGT TTTACAGTT TA GGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Ful5   -- TTCTGTGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Dic1   -- TTCTGTGGG GTAGGT TTTACAGTT AA GGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Dic2   -- TTCTGTGGG GTAGGT TTCACAGTT TA AGGTC TGTTC GACTT ATAAA TTTTACATGATCTGA GTTCA GACCGG
Dic3   -- TTCTGTGGG GTAGGT TTTACAGTT TA AGGTC TGTTC GACTT ATAAA TTTTACATGATCTGA GTTCA GACCGG
Dic4   -- TTCTGTGGA GTAGG? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Fla1   T- ATTTGTGGG GTAGTT TTTACAATT TT AGGTC TGTTC ????? ????? ??????????????? ????? ??????
Fla2   TA AATTGTGGG GTAGGT TTTACAATT TT AGGTC TGTTC GACC? ????? ??????????????? ????? ??????
Fla3   T- ATTTGTGGG GTAGTT TTTACAATT CT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Fla4   TA AATTGTGGG GTAGGT TTTACAATT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Del8   A- ATTTTTGGA GCAGAA GCTAGAATT TT AGGTC TATAC GACTT TTTAA TATTACATGATCTGA GTTCA GACCGG
Nog1   A- AGCTGTGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Nog2   T- TGCTATGGG GTAGGT TTTATAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Ach1   -- AATTGTGGG GTAGG? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Ach2   T- GTTTGTGGG GTAGGT TTTACAAAT CT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Der1   -- AATTGTAAG GTAGGT TTTACAATG TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Der2   T- ATTTATGGG GTAGGT TTCATAATA TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Der3   -- AATTGTGAG GTAGGT TTCACAATG TT AAGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Der4   -- ATGTATGAG GTAGGT TTCATATTA TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Der9   -- AATTGTGAG GTAGGT TTCACAATG TT AAGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Tro1   T- TTTTGTGGG GTAGGT TTCACAATA TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Tro2   T- TTTTGTGGG GAAGGT TTCTCAATA AT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Tro3   T- GTTTATGGG GTAGGT TTCATAATT CT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Tro4   T- TTTTGTGGG GTAGGT TTCACAATA AT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Ric1   T- GTTTGAGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Ric3   T- GTTTGTGGG GTAGGT TTTACAATT CT AGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Ric4   T- GTTTGTGGG GTAGGT TTCACAATT CT AGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Ric5   T- GTTTGTGGG GTAGGT TTTACAAAA CT AGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Eur1   T- GGTTGTGGG GTAGGT TTTACAATT CT AGGTC TGT?? ????? ????? ??????????????? ????? ??????
Lop1   A- ATTTGTGGG GTAGGT TCTACAATT TT AGGTC TGTTC GACC? ????? ??????????????? ????? ??????
Tct2   T- AATTGTGGG GTAGGT TTTACAAGT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Iss1   T- TACTGTGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Iss5   T- TACTGTGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Iss9   T- TACTGTGGG GTAGGT TTTACAGTT TT AGGTC TGTTC GACTT TAAAA CTTTACATGATCTGA GTTCA GACCGG
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Iss2   T- TACTGTGGG GTAGGT TTTACAGTT GT GGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Iss11  A- TTTTGTGGG GTAAGT TTTACAATT TT AGGTC TGTTC GACTT TAAAT AGTTACATGATCTGA GTTCA GACCGG
Iss12  T- TACTGTGGG GTAGGT TTTACAGTT GT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Iss3   T- ATTTGTGGG GCAGTT TTTACAATC TT AGGTC TGTTC GACTT TAAAA GTTTACATGATCTGA GTTCA GACCGG
Iss14  T- ATTTGTGGG GCAGTT TTTACAATT TT AGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Iss4   A- ATTTGTGGG GTAGAT TTTACAGTT TT AGGTC TGTTC GAC?? ????? ??????????????? ????? ??????
Iss6   A- ATTTGTGGG GTAGAT TTTACAATT TT AGGTC TGTTC GACTT TAAAA AATTACATGATCTGA GTTCA GACCGG
Iss7   A- ATTTGTGGG GTAGAT TTTACAATT TT AGGTC TGTTC GACTT TAAAA AATTACATGATCTGA GTTCA GACCGG
Iss8   A- TTTTGTGGG GTAGG? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Cix2   A- ATAATTGGG GCAGAA GATTATTTA TT AGGTC TGTTC GACTT TAAAA TCTTACATGATCTGA GTTCA GACCGG
Cix3   T- AATTGTGGA GCAGAA TATACAATA TT AGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Cix4   T- AATTGTGGA GCAGAA TATACAATG TT AGGTC TGTTC GACTT TAAAA ATTTACATGATCTGA GTTCA GACCGG
Cix6   T- AATTGTGGA GCAGAA TATTCAAAG TT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Del2   G- AATTCTGGA GCAAAA AA??????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Del3   A- AATTTTAGA GCAGAA ACTTAAAGT TT AGGTC TGTTC GACTT TAAAT ATTTACATGATCTGA GTTCG AGCCGG
Del4   A- GTTTTTGGT GTAGAT GATAATTAA CT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Del6   A- GTTTTTGGT GTAGAT GATAATTAA CT AGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Del7   G- AATTCTGG- ?????? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Fla5   ?? ????????? ?????? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Mee2   T- TGGGAGGGG GAAGGT TTTTTCTAT AT TGG?? ????? ????? ????? ??????????????? ????? ??????
Mee3   T- TAGGAAGGG GAAGGT TTTTTCTAT AT TGGTC TG??? ????? ????? ??????????????? ????? ??????
Mee6   T- TGGGAGGGG GAAGGT TTTTTCTAT AT TGGTC TGTTC GACTT TAAAA TTTTACATGATCTGA GTTCA GACCGG
Cerc   A- GAATAAGGG GTAGGT TTTTTA??? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Cica   ?? ????????? ?????? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Cic1   A- AAAAAAGAA GCAG?? ????????? ?? ????? ????? ????? ????? ??????????????? ????? ??????
Cic2   A- GATTAAGAA GCAGAA TTCTTAAGT CT AACTT TTAAA TCCT? ????? ??????????????? ????? ??????
Cic3   -- TAGTTTGAG TCTGTT CGACTTTTA AA TTCTT ACTTG ATCT? ????? ??????????????? ????? ??????
Cic4   AA TTTTTAGAG TCTGTT CGACTTTTA AA TCCCT ACTTG ATCT? ????? ??????????????? ????? ??????
       -> <--91a--> <----> <--91b--> <> <92a> <---> <92b> <---> <-----90b-----> <---> <93a->
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