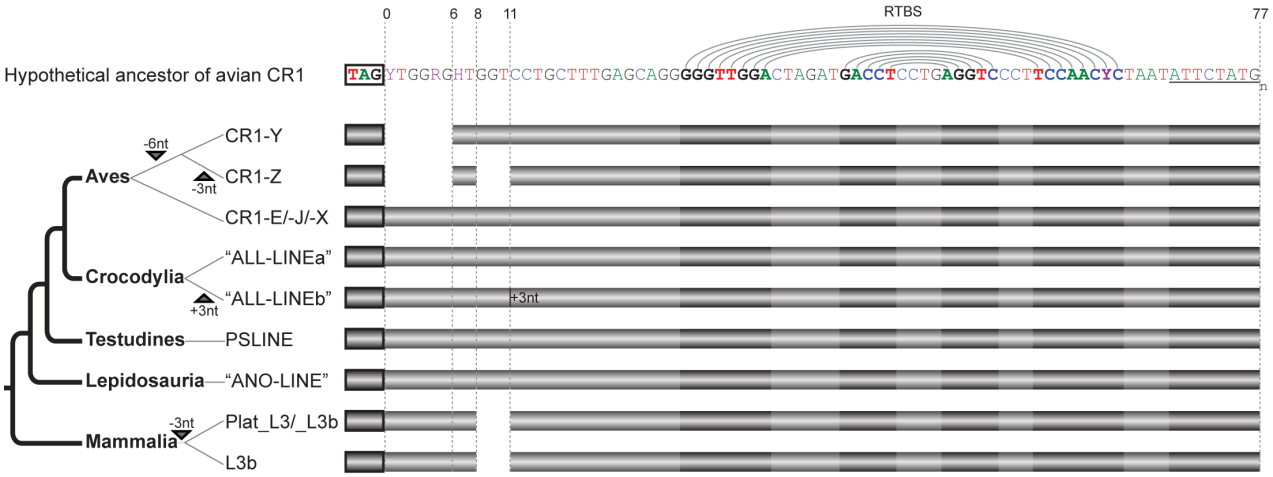
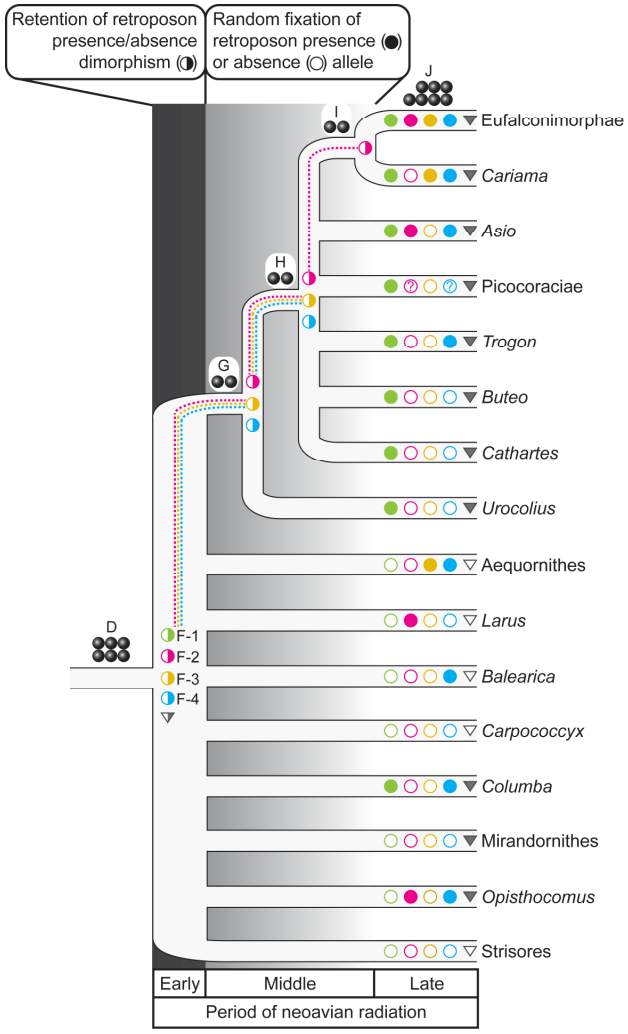
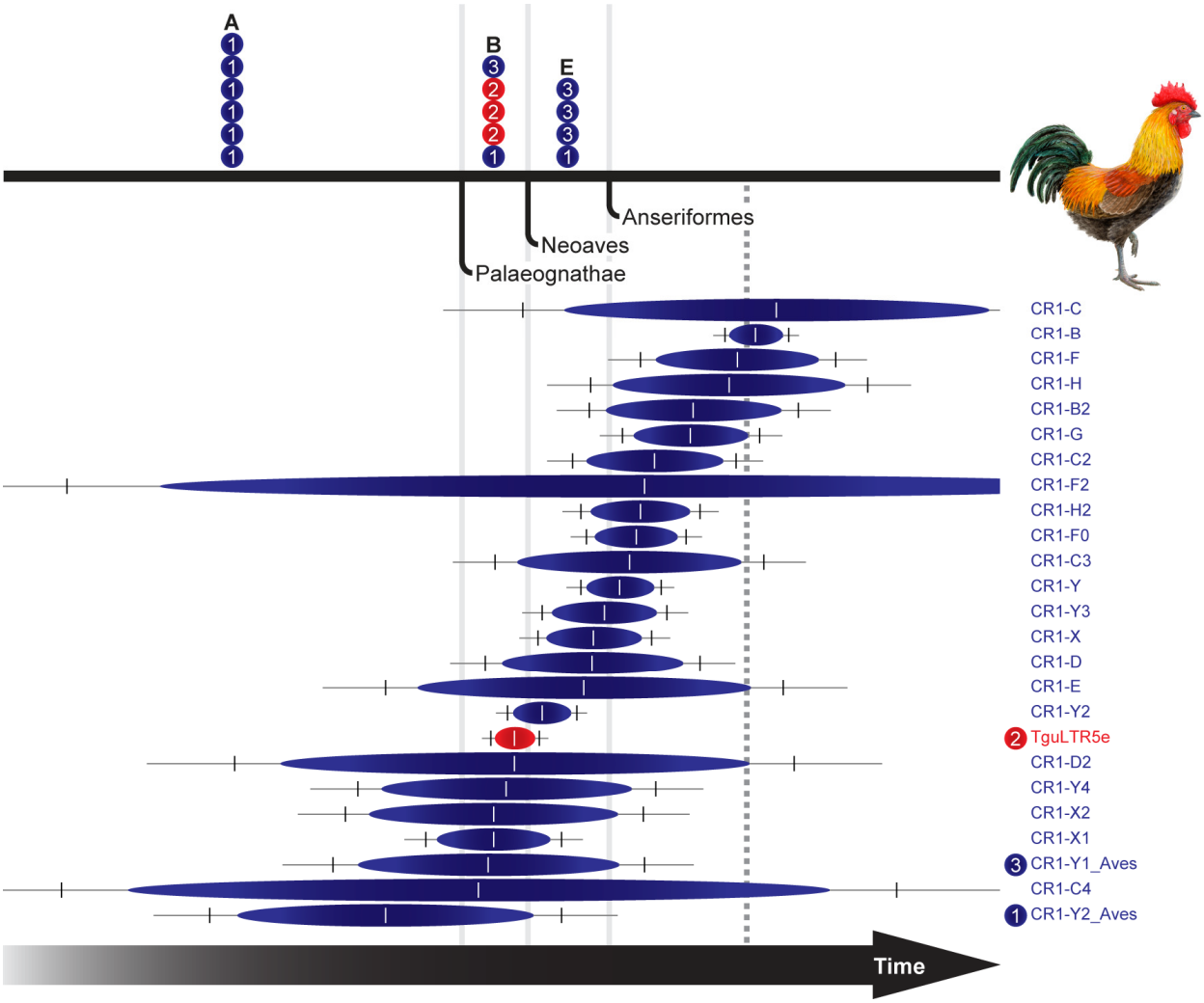


Supplementary Figure S1 | Structural comparison of 3' untranslated regions (3' UTR) in amniote-specific CR1 LINE retroposons. The topology of the amniote species tree (black lines) corresponds to the current understanding of amniote phylogeny[51]. Grey straight lines indicate putative relationships among lineage-specific CR1s based on the shown diagnostic random indels (triangles) larger than two nucleotides (nt). To facilitate comprehension, the 3' UTR nucleotide sequence of the putative ancestor of all bird CR1 elements was reconstructed by comparison of bird and reptile CR1s and all extant CR1 sequences were depicted as grey gradient bars. Bold nucleotides or dark grey bars depict highly conserved regions, i.e., the putative binding site for the reverse transcriptase or other CR1-encoded proteins[52] (RTBS, grey curves indicate a potential hairpin structure in RNA) and the typical octamer microsatellite[47] (underlined, n = tandem repeats) at the 3' terminus. The first three nucleotides (black box) correspond to the stop codon of the second open reading frame (ORF2), marking the 5' boundary of the 3' UTR. Name suggestions for previously unrecognized CR1 subtypes (in the crocodylian *Alligator mississippiensis* and the lepidosaurian *Anolis carolinensis*) are highlighted by quotation marks.



Supplementary Figure S2 | Incongruent retroposon presence/absence patterns within the neoavian radiation. The topology and the branch labels correspond to those of Fig. 1. Dark grey balls are retroposon markers that (when the four incongruent markers F-1 to F-4 are not considered) yield a topology without conflicts. The presence/absence pattern (filled circle: presence; empty circle: absence; question mark in empty circle: missing data) of each of the four incongruent markers and of an 82-nt random deletion (grey triangle, in the flanking sequences of marker J-5) is shown in corresponding colours on the terminal branches. This complex phenomenon is presumably caused by incomplete lineage sorting[26] of retroposon presence/absence dimorphisms (semi-filled circles). Our data suggest that these retroposons inserted during an early period of the neoavian radiation (dark grey shade) and did not have enough time for fixation in the whole population of the ancestral species. In combination with the extensive and accelerated speciation events of the neoavian radiation, these retroposon dimorphisms seemingly persisted (coloured dashed lines) during most of the radiation (light grey gradient) and, subsequently, one of the two alleles was randomly fixed in each of the descendant lineages, leading to incongruence with some of our otherwise congruent markers (branches G, H and I). Notably, the four incongruent markers are not in any conflict with the late period of the neoavian radiation, i.e., the new taxa Eufalconimorphae (branch J) and Psittacopasserae (branch K in Fig. 1). In summary, our results indicate that the neoavian radiation can be divided into an early (occurrence of retroposon presence/absence dimorphisms), a middle (random fixation of dimorphisms leading to incongruent retroposon presence/absence patterns, occurrence of congruent presence/absence patterns) and a late period (occurrence of congruent presence/absence patterns).



Supplementary Figure S3 | Chronology of Mesozoic retroposon activity in the chicken genome. Computational estimates of activity periods (normal distributions displayed as ovals[29]) of selected retroposon subtypes were calculated via the TinT model[25,29] and plotted on a simplified chronogram[30] (black lines) by using the experimentally verified retroposon insertion events (numbered blue or red balls, numbers indicate the respective retroposon subtype) of Fig. 1 as temporal landmarks. Single capital letters correspond to the branch labels of Fig. 1 (A, Aves; B, Neognathae; E, Galloanserae). CR1 retroposons are highlighted in blue and LTR retroposons are shown in red. The grey dashed vertical line indicates the estimated end of the Mesozoic Era at the Cretaceous/Tertiary boundary[30]. Note that during their shared TinT activity range in the ancestor of Aves and Neognathae (see also Fig. 3), several CR1 subfamilies (chicken CR1-C/D/E and zebra finch CR1-E; chicken CR1-F2 and zebra finch CR1-J2_Pass; chicken CR1-X and zebra finch CR1-X; chicken CR1-Y and zebra finch CR1-Y) appear to be identical, which also corresponds to the highly similar nucleotide sequences of their consensus sequences in Repbase (http://www.girinst.org/repbase/index.html).

Supplementary Table S1 | Presence/absence table of all retroposon markers including genomic positions, retroposon subtype, and strategies (see Methods for details).

Marker	*Taeniopygia*	*Acanthisitta*	*Nestor*	*Falco*	*Cariama*	*Asio*	*Alcedo*	*Picus*	*Trogon*	*Buteo/Gyps*	*Cathartes/Gymnogyps*	*Urocolius*	*Ciconia*	*Larus*	*Balearica*	*Carpococcyx/Cuculus*	*Columba*	*Tachybaptus/Podiceps*	*Phoenicopterus*	*Opisthocomus*	*Apus*	*Chrysolampis*	*Gallus*	*Alectura*	*Anas*	*Dendrocygna*	*Dromaius*	*Eudromia*	*Pterocnemia*	*Struthio*
A-1	+										+						+						+				+			
A-2	+																						+				+			
A-3	+										+		+				+						d				+			
A-4	+																						d				+			+
A-5	+																						+				+			
A-6	+										+		+										+				+			
B-1	+			+							+		+	+			+	+					+		+	+		-		-
B-2	+																+						+		+			-		-
B-3	+												+										+		+					-
B-4	+												+										+			+		-		-
B-5	+												+										+		?		-			?
C-1	-																						-				+	+	+	+
C-2	-																						-				+	+	+	+
C-3	-												-										-		-		+	?	?	+
C-4	-												-										-				+	+	+	+
D-1	+					+	+		+	+	+	+	+	+	+	+	+	+		+		+	-		-	-				
D-2	+					+		+	+	+	+		+	+	+	+	?	+		+		+	-	-	d	-				-
D-3	+					+	+		+	+	+	+	+	+	+	+	+	+		+		+	-		-					
D-4	+					+	+		+	+	+	+	+	+	+	+	+	+		+	+		-		-					
D-5	+			+		+		?	?	+	+	+	+	+	+	+	+		+	+	+		-		?					
D-6	+			+		+	+		+	+	+	d	+	+	+	+	+	+		+		+	-			-		-		-
E-1	-																-						+		+			-		-
E-2	-												-										+	?	+	+	-	-		
E-3	-												-				-					-	+	+	+	+	-	-		
E-4	-												-										+	+	+	?	?			
F-1	+	+	+	+	+	+	?	+	+	+	+	+	-	-	-	-	+	-	-	-	-	-	-							
F-2	+		+	+	-	+		?	-	-	-	-	-	+	-	-	-	-		+		-	-				-	-		
F-3	+		+	+	+	-		-	-	-	-	-	+	-	-	-	-	-		-	-		-							
F-4	+		+	+	+	+		?	+	-	-	-	+	-	+	-	+	-		+		-	-				-			
G-1	+		+	+	+	+		+	+	+	+	+	-	-	d	-	d	-		-		-	-							
G-2	+		+	+	+	+	+		+	+	+	+	-	-	-	-	-	-		-		-	-		-		-			
H-1	+		+	+	+	+	+	+	+	+	+		-	-	-	-	-	-		-		-	-							
H-2	+		+	+	+	+	+	d	+	+	+	-	-	-	-	-	-		-	-		-	-							
I-1	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
I-2	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
J-1	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
J-2	+	+	+	+	-	-	d	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	d							
J-3	+	+	+	+	-	-	-	d	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
J-4	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
J-5	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
J-6	+	+	+	+	-	-	?	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
J-7	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	?	-	-							
K-1	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	?	-	-							
K-2	+	+	+	-	-	-	-	-	-	-	-	d	-	-	-	-	-	-	-	-	-	-	-							
K-3	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
L-1	+	+	-	-			-	-			-		-			-							-							
L-2	+	+	-	-			-	-			-		-			-							-							
L-3	+	+	-	-			-			-	-		-			-	-						-							
L-4	+	+	-	-			-	-			-		-			-							-							
L-5	+	+	-	-			d	-			-		-			-							-							
L-6	+	+	-	-			-	-			-		-			-							-							

Character states are presence (+) or absence (-) of a retroposon insertion at a given genomic locus. Unspecific deletions are marked by 'd' and missing experimental data is indicated by '?'. For each marker, the taxon sampling was optimized to all phylogenetically essential taxa (blank cells: not analysed).

Supplementary Table S1 | (continued).

Marker	RE subtype	RE orientation	Chromosome (taeGut1)	Start and end (taeGut1)	Strategy
A-1	CR1-Y2_Aves	+	2	26059437-26060242	I
A-2	CR1-Y2_Aves	+	2	24760332-24761039	I
A-3	CR1-Y2_Aves	+	2	25303447-25304574	I
A-4	CR1-Y2_Aves	+	2	18685609-18686573	I
A-5	CR1-Y2_Aves	+	1A	20376757-20377989	I
A-6	CR1-Y2_Aves	+	1A	20375110-20375988	I
B-1	CR1-Y2_Aves	+	Z	24736112-24736753	I
B-2	TguLTR5e	+	Z	24741461-24742589	I
B-3	TguLTR5e	-	1	29915747-29916601	II
B-4	TguLTR5e	-	5	14985700-14986976	II
B-5	CR1-Y1_Aves	-	2	25167690-25168178	I
C-1	CR1-Y2_Aves	-	4	64193638-64194132	III
C-2	CR1-Y2_Aves	+	2	54424564-54425428	III
C-3	CR1-Y1_Aves	+	17	8094466-8094952	I
C-4	CR1-Y1_Aves	+	3	108853900-108854584	I
D-1	TguLTR5e	-	1A	13493804-13495145	II
D-2	CR1-E_Pass	+	23	2210820-2211801	I
D-3	TguLTR5d	+	2	43944384-43945448	II
D-4	TguLTR5d	+	3	77815159-77816217	II
D-5	TguLTR5a	+	1A	53818237-53819230	II
D-6	CR1-J2_Pass	-	Z	42095413-42096259	I
E-1	CR1-Y2_Aves	-	Z	24741461-24742589	I
E-2	CR1-Y1_Aves	-	3	108854577-108854902	I
E-3	CR1-Y1_Aves	-	3	108828593-108829533	I
E-4	CR1-Y1_Aves	-	Z	4905862-4906760	II
F-1	CR1-J2_Pass	-	1	38803625-38804919	II
F-2	CR1-J2_Pass	+	3	108756503-108757505	I
F-3	CR1-J2_Pass	-	2	143483216-143484373	II
F-4	CR1-J2_Pass	+	2	25246211-25246841	I
G-1	CR1-X3_Pass	+	3	108701927-108703291	II
G-2	TguLTR5a	+	1A	20294073-20295316	I
H-1	TguLTR5d	+	3	85253635-85255015	II
H-2	TguLTR5a	+	4	58849092-58850972	II
I-1	TguLTR5d	+	5	34776063-34777405	II
I-2	TguLTR5d	-	7	23352566-23354134	II
J-1	TguLTR5d	+	1A	59391304-59392588	II
J-2	TguLTR5d	+	Z	29203733-29205351	II
J-3	TguLTR5d	-	15	8418945-8419797	II
J-4	TguLTR5d	-	5	30767928-30769035	II
J-5	TguLTR5a	+	1A	32879518-32880652	II
J-6	TguLTR5a	+	1	38803625-38804919	II
J-7	TguLTR5a	+	9	21782642-21784130	II
K-1	TguLTR5d	-	1A	43914270-43915689	II
K-2	TguLTR5d	-	4	32753338-32754835	II
K-3	TguLTR5d	-	1	86620295-86621332	II
L-1	TguLTR5d	-	7	10143600-10144882	II
L-2	TguLTR5d	-	3	31049664-31051072	II
L-3	TguLTR5a	+	20	7141389-7142483	II
L-4	TguLTR5a	+	2	108771408-108772227	II
L-5	TguLTR5a	+	1	56216733-56218030	II
L-6	TguLTR5a	+	14	13779122-13780263	II

Supplementary Table S2 | **Oligonucleotide primer sequences.**

Marker	forward primer (5'-3')	reverse primer (5'-3')
A-1	CATACCTGACACAGTTGGTGAC	GAGAGTGCCTGGGTCAGTAG
A-2	CTTAATCCTGCTGCAAATACAC	GGAAGAGCTACAAGAACGTCTC
A-3	CTACACTGAATGTAATAAGGCTTG	CTCTCCAACCTAAGTCACAGATC
A-4	GAAGGTGTGAAACTGTCTGGAC	GAGAGATCCACCTGAAGAAAGTAG
A-5	TTACCCTGGCATGTGCTG	CTGTTCTTTTGTTCTCATTCTCTG
A-6	ATCCAAGCAGAAACAAATGTC	CTAGACTTCTTGTGCTGGGAG
B-1	GTCCTGATTTTCTCACAGATGG[21]	ATGATCCAGTGCTTGTTTCC[21]
B-2	CAGCAGAAATCAATCCAAGAC[21]	CAGCCCATTTAACTGATAATCTC[21]
B-3	GGTGGAAACTGGACACTTGG	CATGAAATAGACTTGACTGCTTC
B-4	CCTAAAGGAATGTACCTGAACC	GCCTCCCATTAACACAGTAGC
B-5	AGGTCTGATWCCTAAGAAAACTAAG	CGCTCCTCTGAGTTCCATC
C-1	TAGTTTACAACCAGAACTGAAGG	GGATTAACCAGAGTAACCTGATTG AACCTGATTGATCTCTGTGTGAG
C-2	AACAGCAAGTCTTCAGTCAGC GAGTAGGTGAGGGTGAGAAGG	GAATCTTTTCACCTTCAGTACAC AAAATCCCAGCCACTTCAG
C-3	TGGAGGTGAAATTCTGCC	TTCTCTTGCTGTTTGGGAC
C-4	CTCAGTTTCCCTTGATGAATG	TAAAATCCCACCAACCTCC AACCTCCGCTGCCTGTC
D-1	CTCTGTCAAATGAAACCATAGG TCTTCAAACATGGAGATGACC	AGAGGTCCAAGGATTCTGC GGTCCAAGGATTCTGCTTC
D-2	CGCAGCATGGGAGATTC ACCACTGAAGAACTCATTTGG CATTTGGGCCAGTTCTCAG	AAGAGCAACAGCAAGTAAAGAG AAAGCAGACACCTCCTCCTC ACCTCCTCCTCACAGGACAG AACAGAGGGAAGAGGAAAGC
D-3	GAATGGCTGGGTGCTGTC GCTGGGTGCTGTCTTGAATC	GCTCCAATAACTGAATAATCTTCTC
D-4	TCTCTATGGTGGCAGAAAGG ATGGTGGCAGAAAGGTCTG	AGTTCAGCACTTGGCAGTTC GAAGGCTCTGGACAAAACC
D-5	CCAAAGACATGCTTCAAGATTC AAGAAGATCAATGTCCTTGTGTC	AGTCCTTCATTTCAAGTAACAGTG ACAGTGCTTCTGTAGTGAAAGG
D-6	TTGTCAGAGTTGCTGGAGATAC[21]	AATTTGATGGCACATAACTGTAG[21]
E-1	see B-2	see B-2
E-2	GTAAGGCAGGGATGTAGGAG	AAACKGRGKCTTTCTAACTC
E-3	AGYACAGAATAATGGGTCAAC	AAATCAGGCATCTAGTCTAAACTC
E-4	ATTTCCTCCTTATCTTCTCTGC	CGATTATCTGGCTGTTCATCC
F-1	TTCATTCAGAACAGTGTGCTTC	GCTTTGTGGAAGAACTGGATAG CTGGATAGATTTACAACCTTTCC
F-2	CATTGCCAGTTTCTYTCCAC CTGAAAAAATGGTCTAGGATGAC	TTCCTGTTCTTTTCTTKATTCC CATGCTCCAGAAAGAGTTACAC
F-3	TGGTACTCCAGTGTCTCAGATG GGTACTCCAGTGTCTCAGATGATAC CAGATGTAGGCACTGCTGAAG	AGTTGCTGAAACCTCCTGC ACAGAAATTAAATCCAGAGAAGC CAAGAATGCACACCACGTAAG
F-4	ATAATGGTGCTCTGTCAAAGG GGAGACTTCTGGCTTTAACAG	TGTTGTGCTTGCTAATACTGG AAGCAAAACACAGATCACTGAG GGTGATAGCGATGTGAAATG
G-1	CTCCTCTCTCCAGTTTCAGTG GTGGTTATTCCCCTGCTATG	AACACACAGTGTATCACACATGG CTGTCCAGACTGATAAATTGTTAG
G-2	CATTGAGGASAAGGGGATG TGTAATCCATTTGTGCTAAAGAC TTGTCAGTCTGTCCTTTCCTC	TAMGGTTATTTGATTGCTGWC GGCTGACTGTACTTTAGGTTGC TGTTTAGCCTAGTACCTGAAGC
H-1	GGTTGGTAATCCTGGAGACC ATCCTGGAGACCCTGGTTC	CAAACCTGCTTAATGTGCTG ATCACTTGGTTCTTTTCCCTAG
H-2	CAGAAGAATCTGCCCAACAC GCTCACCTGGGACTCTCAG CCGCATAGAAGGAGTGGTC CACTGTTCACAACAATCATCTG CACTGCATATTCCTGAGAACC	CCAGCATTCACAGTCACTTG TCTGAGTTATTGTCTGGTGAGC GACTGCTTTAGAGTTTTCCAGC TTTTCCAGCATTCACAGTCAC
I-1	GGTCACACGCTGTTAGAGTTAC	GTGTCTCAAGATGATGTGGATG CGCACCAGATACTACAATACAG
I-2	CTGAAAATAAAGAATGGCACAC CTGGAATTACTTGTAGGTTGATG ATAAAGAATGGCACACCTCC	AGGCAGAATCTGATTGAACAG CAAGCAAGTGACGCTCCTG
J-1	TTGGAGCAGAGGAATGAGC	CACAAAGAAACGGACAAAGG

Supplementary Table S2 | **(continued).**

Marker	forward primer (5'-3')	reverse primer (5'-3')
J-2	CATCCATTGACCCTAAAACTG	ACTAACACTCCACTGATATGCTTC
	TATCAATGCTGATGACCTTCC	TTTAATAAGCCGTGTCTGTCC
J-3	ATCTGAGGATTGGCTGTGC	TCAAAGGAGATGAGGGAGC
	CAGTTCCATCACCGACACAG	TGCCTCTCAACACAGAATCC
J-4	GCGTAAATTCAACAGAAACCAG	CGAAAATCAGCATGATAACAGAG
		CAGCATGATAACAGAGTATGAGTTG
J-5	TCTGTACTGGCATCCTGGTC	CTAAACAAAATCATTAGGCTGG
	CACTGTATGGGCTGTCACTG	GCTGGAGATGACTATTGGTAAG
J-6	see F-1	see F-1
J-7	CCCTCTAGTTTGACTGCTGTG	GGCTATGAAAATGGTAACAAGG
	ATGTCATTAGCATCTGTCTTGG	CTGAGCAGTCTCATCCCTTC
K-1	AAGTGAGCAACATCTCCAGG	CATGGGCTTTCTGTAAGTCTG
	CAACATCTCCAGGGAAAGC	GTGCTGACAAAATAGACTGCTG
K-2	CATTCATGTTAAGTGGTTTCG	ATTCTTACCAGGTTCAGTTGC
K-3	CAAGTCCAGACCATGATATGTG	TCTCTAGGCAAATCTGTGTAAAC
L-1	AACTGTGCTGCCTGATGC	GCCTATTAGCTTCCTTCTGTG
	GCGGATGTATTTGGATGC	TTAGCTTCCTTCTGTGTGGTC
L-2	GGAAGTTGGTGATTGAAGATG	ATAGGGGTTAGACCTTGTTCG
	TGGTGATTGAAGATGAAACAGAG	GCATTTCTTCTCCATCCAGC
L-3	TGTGAGCCTTGTGTAAGTTGAG	CCTTTGAGTTTAGCCCAGAC
L-4	ATGTACTACCACCAAGTTATCCAC	GCTTTACGTTCTCTATTTGAGG
L-5	TCCAGCATCAACATCTCCTG	TGGTTACAATGCCTTTCCTG
L-6	CTCCAATGACAGTTGTTACAGC	ATGGAAAGTCTGTGGATGATG
L5216 + H6313	GGCCCATACCCCGRAAATG	ACTCTTRTTTAAGGCTTTGAAGGC