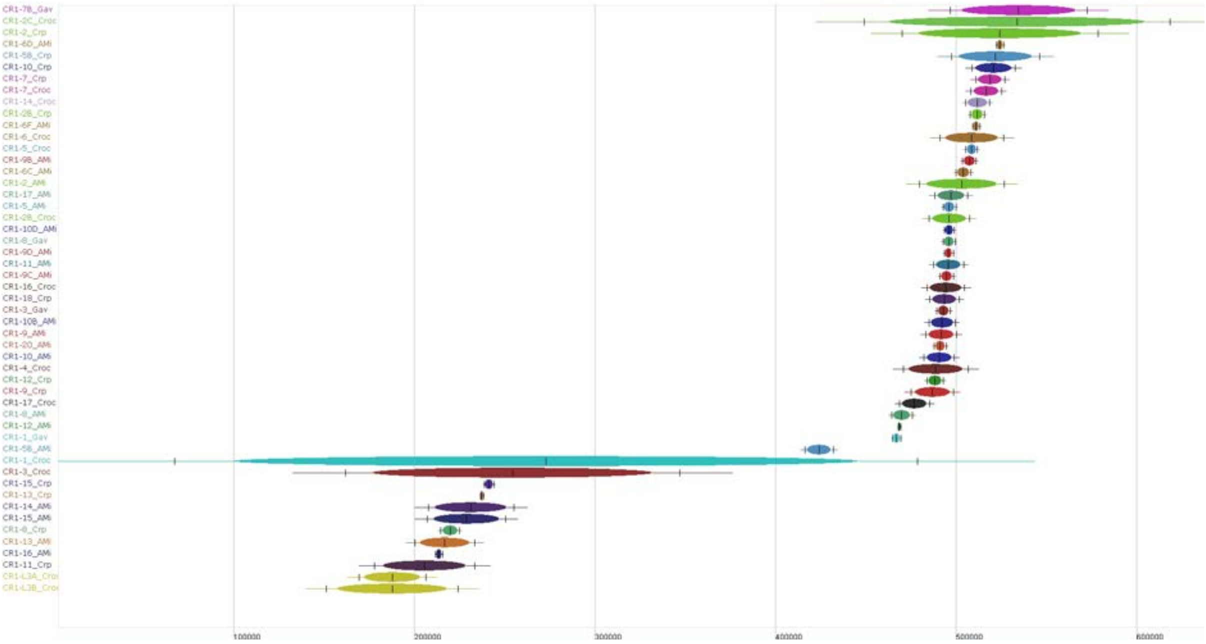
Supplementary Information

A



B

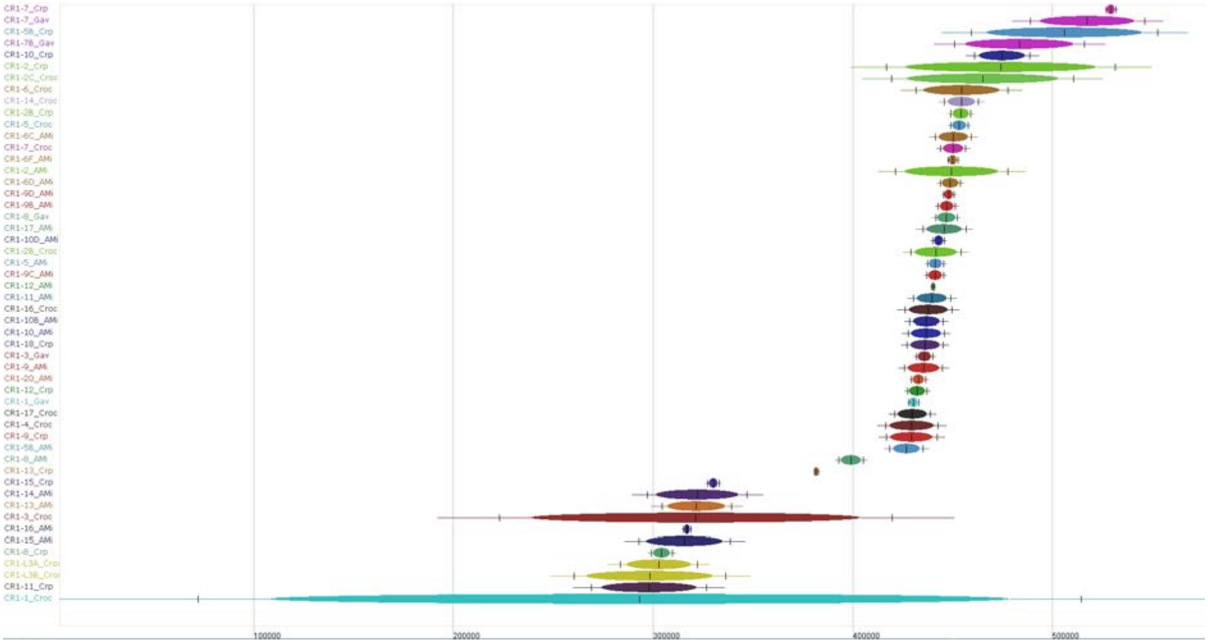


Fig. S1. TinT patterns of unmerged CR1 subfamilies within four crocodilian genomes. The transposition in transposition graphs from (*A*) saltwater crocodile, (*B*) gharial, (*C*) Chinese alligator, and (*D*) American alligator correspond to the computational estimates of CR1 activity in fig. 2A, but comprise all unmerged CR1 subfamily sequences from fig. 3.

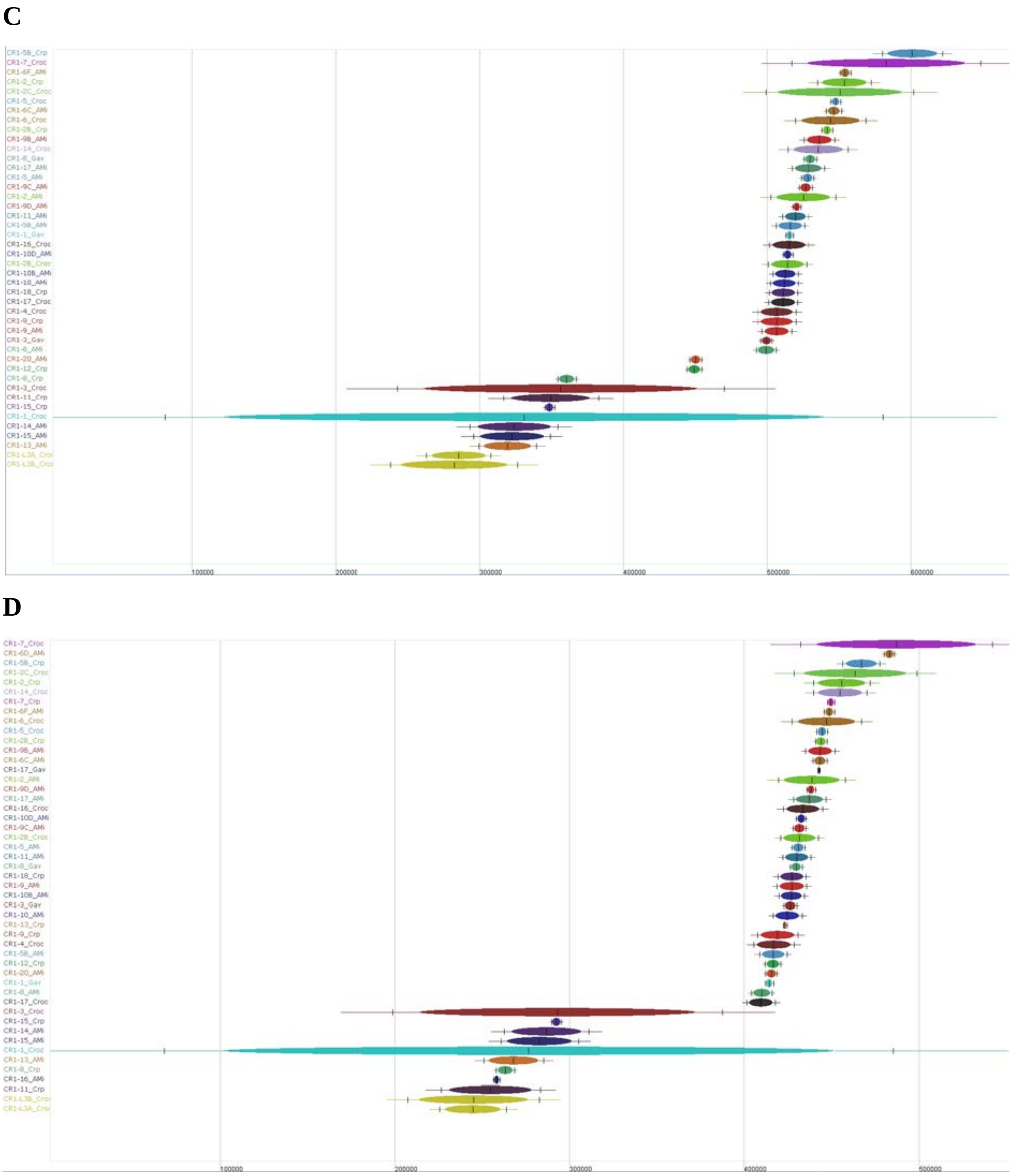


Fig. S1. Continued.

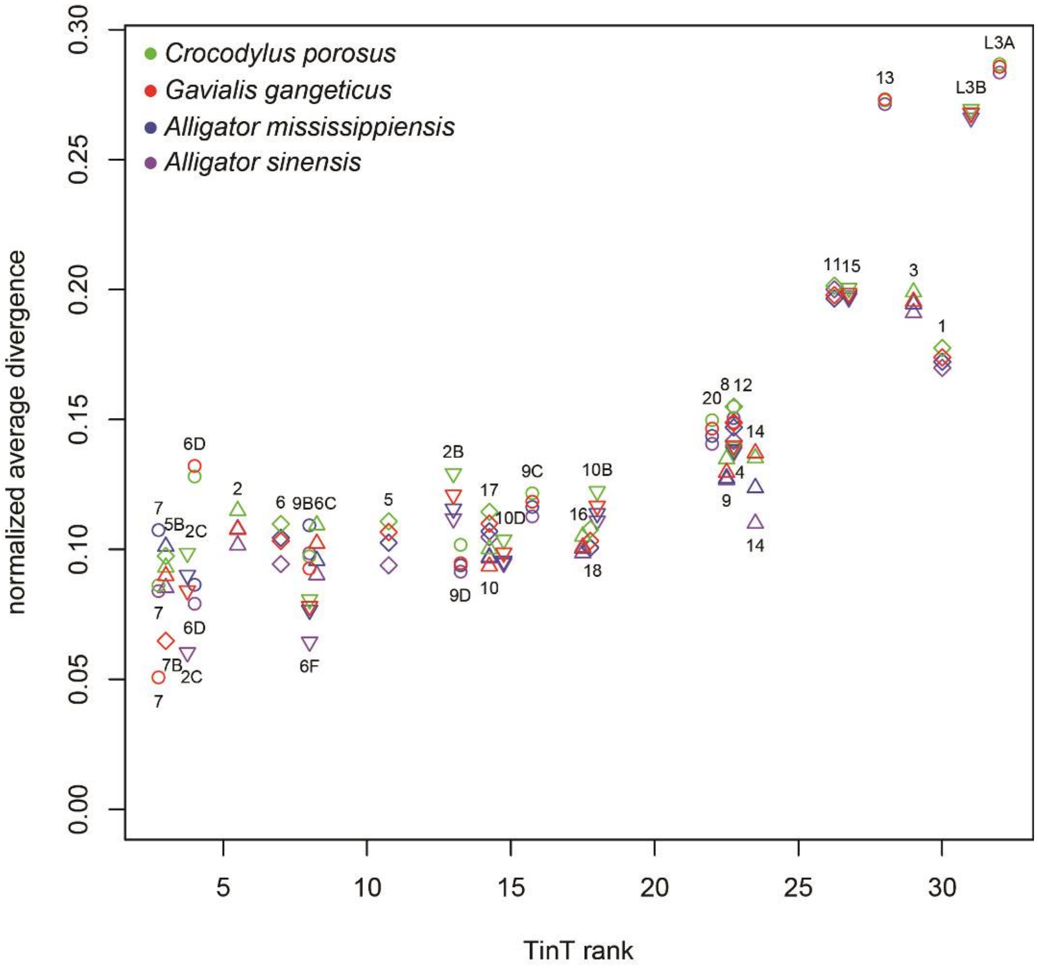


Fig. S2. Average divergence among CR1 subfamilies within four crocodilian genomes. While most CR1 subfamilies exhibit similar average divergences, a few (e.g., CR1-7) show variation between the Saltwater crocodile, gharial, American alligator, and Chinese alligator, suggesting lineage-specific differences in activity as also indicated by fig. 2. Note that the divergence value of each CR1 insertion was normalized for the length of the insertion. The TinT rank is derived from the computational estimation of activity successions of CR1 subfamilies in the transposition in transposition model, wherein recent retropositional activity is reflected by a low TinT rank.

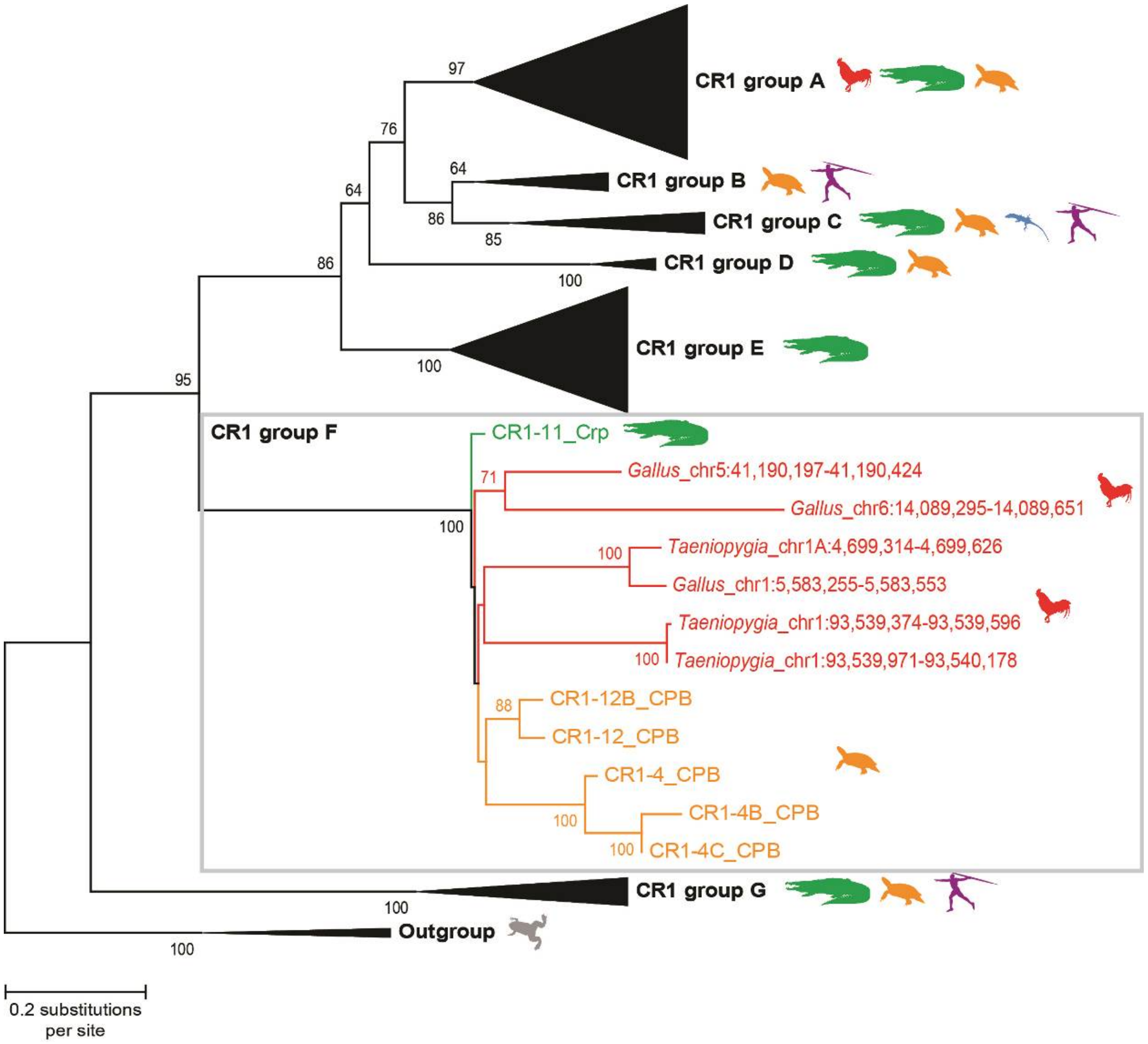


Fig. S3. Low copy number of CR1 group F-like elements in bird genomes. Maximum likelihood nucleotide sequence analysis of the same data set as in fig. 3, but including all BLASTn hits (representatives from crocodilian/turtle CR1 groups B–G as queries, no cutoff e-value, hits >200 bp) from chicken and zebra finch genomes. Unlabeled nodes received a bootstrap support of <50%.

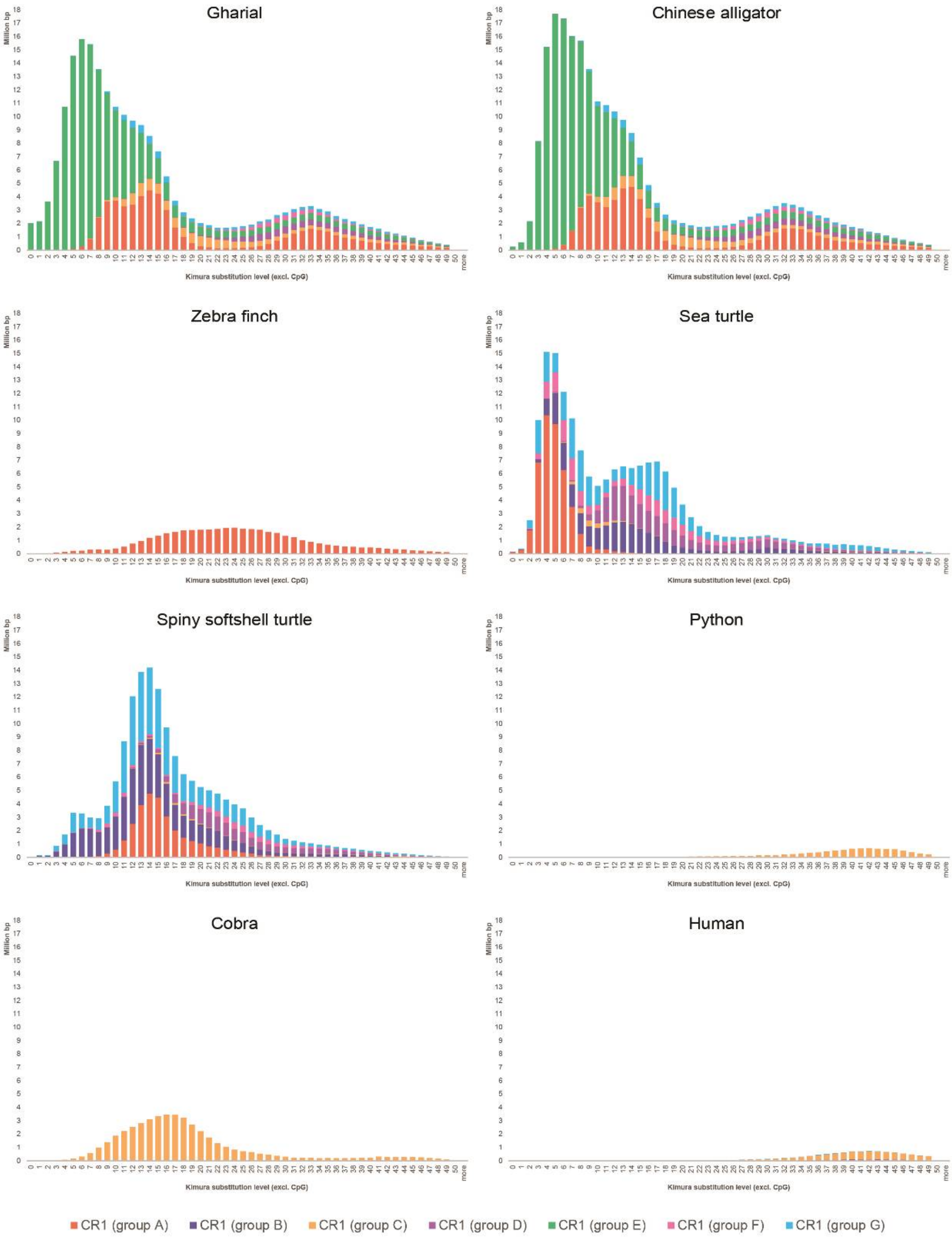


Fig. S4. CR1 divergence landscape plots of amniote genomes not shown in fig. 4. Definitions of CR1 groups A–G correspond to fig. 3 and divergences of CR1 copies to their respective consensus sequences were calculated excluding CpG dinucleotide sites.

Table S1. Presence/absence of RE markers among orthologous loci in crocodilian genomes.

marker	*Cr. porosus*	*Cr. palustris*	*Cr. niloticus*	*Cr. mindoensis*	*Cr. novaeguineae*	*Cr. johnstoni*	*Os. tetraspis*	*Me. cataphractus*	*To. schlegelii*	*Ga. gangeticus*	*Ca. yacare*	*Me. niger*	*Pa. palpebrosus*	*Al. sinensis*	*Al. mississippiensis*	RE subfamily	target site duplication	comments
AM02	-								?	-	+	+	+	+	+	Penelope-1_Crp	TTTCAG	*
AM05	-								-	-	-	-	-	+	+	Penelope-1_Crp	TGCATCAGTG	
AM06	-								-	-	+	+	+	+	+	CR1-7_Croc	GTT	
AM07	-								-	-	-	-	-	+	+	CR1-7_Croc	AACTT	
AM09	-									-				-	+	CR1-7_Croc	TT	**
AM15	-									-	-		-	-	+	CR1-2C_Croc	GAAAT	
AM21	-								-	-	+	+	+	+	+	CR1-2_Crp	GACT	***
AM22	-								-	-	+	+	+	+	+	CR1-2_Crp	A	
AM24	-								-	-	+	?	+	+	+	CR1-14_Croc	AAA	
AM25	-								-	-	+	+	+	+	+	CR1-2_Crp	AC	
CP01	+		+		+	+	-	-	-	-	-			-	-	CR1-2C_Croc	GAC	
CP06	+		+		+	+	-	-	-	-	-			-	-	CR1-2C_Croc	ATATC	
CP07	+		+		+	+	-	-	-	-	-			-	-	CR1-2C_Croc	TG	
CP08	+				+		+	+	-	-	-			-	-	CR1-4_Croc	T	
CP10	+				+		+	+	-	-	-			-	-	CR1-7B_Gav	AAC	
CP13	+				+		+	+	?	-	-			-	-	CR1-2C_Croc	CTTAT	
CP14	+				+		+	+	-	-	-			-	-	CR1-7B_Gav	AAT	
CP15	+	-		-						-				-	-	CR1-7_Crp	G	
CP18	+				+		+	+	-	-	-			-	-	CR1-2C_Croc	GTTT	
CP19	+				+		+	+	-	-	-			-	-	CR1-7B_Gav	TGTAAT	
GC01	+						+	+	+	+	-			-	-	CR1-2_Crp	AACC	****
GC03	+						+	+	+	+	-			-	-	CR1-2_Crp	CATGT	
GC04	+						+	+	+	+	-			-	-	CR1-7B_Gav	TATTTC	
GC08	+						+	+	+	+	-			-	-	CR1-2_Crp	AACC	
GC09	+						+	+	+	+	-			-	-	CR1-7B_Gav	AAA	
GC12	+						+	+	+	+	-			-	-	ERV1-4_Crp-LTR	GTTG	
GG01	-						-	-	+	+	-			-	-	CR1-7B_Gav	ATGAAT	
GG03	-								-	+				-	-	CR1-5B_Crp	ATTTCA	
GG10	-								-	+				-	-	CR1-7_Gav	AGAGG	
GG12	-						?	-	+	+				-	-	CR1-5B_Crp	TCTTG	
GG13	-						-	-	+	+				-	-	CR1-5B_Crp	AATATA	
GG14	-								-	+				-	-	CR1-5B_Crp	AGCTTC	
CG_0062	+									+				+	+	CR1-2_AMi	?	
CG_0066	+									+				+	+	CR1-9B_AMi	CCA	
CG_0077	+									+				+	+	CR1-17_AMi	?	
CG_0087	+									+				+	+	CR1-6C_AMi	?	

Character states are '**+**' for RE presence, '**-**' for absence, and '**?**' for missing data. Blank cells: not analyzed.

*****: 17 nt insertion in Caimaninae and 17 nt deletion in *Caiman* + *Melanosuchus* . ******: TE most similar to CR1-derived insertion within Gypsy-38_AMi-I-int consensus.
*******: 267 nt deletion in Caimaninae and 7 nt deletion in *Caiman* + *Melanosuchus* . ********: 9 nt deletion in Crocodylidae and 197 nt deletion in Gavialidae.

Table S1. Continued.

marker	locus scaffold in allMis1	locus orientation in allMis1	locus start in allMis1	locus end in allMis1
AM02	JH739241	+	386608	387618
AM05	JH734058	+	123912	124245
AM06	JH733477	+	407117	407956
AM07	JH734288	+	182819	183242
AM09	JH732763	+	178094	178907
AM15	JH733358	+	947797	948668
AM21	JH734499	+	399867	400499
AM22	JH734753	+	766093	767197
AM24	JH734874	+	172032	172987
AM25	JH735357	+	331471	332118
CP01	JH734442	+	536671	537582
CP06	JH732326	-	1186970	1187967
CP07	JH735857	-	551518	552142
CP08	JH737363	+	3079328	3079611
CP10	JH739179	+	157198	157874
CP13	JH738577	+	133118	133833
CP14	JH731454	-	464555	465406
CP15	JH731391	+	1188298	1189162
CP18	JH734773	+	889393	889951
CP19	JH739451	+	243914	244427
GC01	JH737872	+	271884	272456
GC03	JH737792	-	6210	6986
GC04	JH737792	-	146993	147574
GC08	JH732327	+	620975	621602
GC09	JH733358	-	462882	463085
GC12	JH736113	-	1205940	1206409
GG01	JH732121	-	128337	128746
GG03	JH731430	+	399807	400518
GG10	JH733284	+	84786	84936
GG12	JH738572	+	46606	46823
GG13	JH736752	+	50716	51014
GG14	JH737086	-	985458	985734
CG_0062	JH731248	-	267734	269121
CG_0066	JH731145	-	355472	356412
CG_0077	JH731451	+	5082	6528
CG_0087	JH734874	+	258990	260122

allMis1: American alligator assembly in UCSC Genome Browser (http://genome.ucsc.edu/cgi-bin/hgBlat?command=start).

Table S2. Oligonucleotide primer sequences.

Marker	forward primer (5'-3')	reverse primer (5'-3')
AM02	AGGTGGGATGGAAAACAAC	TGGTCAACGTAACAGAACTGG
AM05	TTGTGCGTCCAGAACAGC	GGTTGCCTGGGATCAGAG
	CAGAACAGCCCTCAGGAAG	
AM06	GTTGGAGATTCTCATCTTGGAG	TCATTATCGTAGATGGTGTAGTAGC
AM07	ACACAGGAACAACCCATCG	ACCTGGCAAAGCTGGATG
		TGGCAAAGCTGGATGACA
AM09	ATGGACCAAGATGAGGAGG	CAAAGAGAATCAGTCCCAAAG
AM15	TCATCTCTGGTGACAATGCTG	CTCTCCTCAGGGGTGAAGTC
	ATCTCTGGTGACAATGCTGAG	CTGTGACTGCCGTGGAAG
AM21	TTCAAGTCCAAGAAGAAGGTG	GCTCAGCTTGTGGCACAC
	CCAACAACTCCTTCAGGTG	
AM22	TTCGGACAGGCTATCAAGG	AATGCCCTCTGAGTTTCCTC
	CCCTCAAAGCCTCTTCTACC	GACCATCACCTCTCCTGTCTC
AM24	AAGTTTCCATGATTGGCTACAG	CCCACCAGAACCTAGTGACAG
AM25	TGCCAGAGCACTTAACAGTTG	CAGATCCCCACCTTCCAAG
CP01	TTTGCCCTCTCCAACTCC	CTACTACTCCATCCATCAGATAGG
CP06	ATAATCTTGCTGGGCTATGC	TCTGGAGATGTGACACTGTTATG
CP07	AACATCCCCAACATCATCC	GAGGCGATTCTCCTGTCAC
	CCCCAACATCATCCTTACAG	TCCTGTCACTGGAATCAAGAG
CP08	AAGATTATGAGCAAGTAGCAGG	GTTCAATGTGCTTTAGGAAGG
CP10	GACTGCTGAAGAGAGAGACTGC	ATGAGCTTTGGCTTCTTGG
CP13	CATGGGCAGATATTGGAGC	TGGATTCCGAACAGGTGC
CP14	GCTTGTCCTGTTTTGTTACTCC	TCTGAATGTATGGTGAAGGTCTG
CP15	GGAGGAAGTTGGTGTTGAAC	CCACTGTTGTGTCCTTAATATCTC
CP18	AGCACATGCCAACAAACC	CTGCTGAATTGACGAATGC
CP19	ACAGATGAAGCCCTGGTAAG	GCACAGCAGCTACAGTGAAAG
GC01	ACATCAGGGCTTGCTTCTC	CGTGAAGATGCTCAAGTGTG
GC03	GCCTACAGCAGTGACACACC	AATCAGTTTGTTCAGTGGTTCC
GC04	GAGACCCTCAGACCTTCAATC	AGGAAGACAGAGAAGATCACAAG
GC08	CATCACAGTGCGATCTCCAG	ACATTGCTTTCTTCTCCACTAAC
GC09	AGTAGGGTTCATGGAACATAGC	ACAGCATTCAAAGCCTTTTC
GC12	CTTTCCAGCCGTGTGAGAG	GGTGTTCCATCGCTTGAAG
GG01	GCATCATCAAAAGCTGTAATG	GGTAGTGAAGAGGTTGCCTG
		CAGATATGTGAACCTACTGAAAAG
GG03	CATCCTCACTGAAATCTCACAG	TCTTGTCAATGATCTCCATCTC
GG10	TCACACTGAACTCTGGACAGG	CTCTGTGGGCTCCTCATTC
GG12	GCTTGGGATACACAGGAGG	GGAGGGTTGTCTTCTGTTCTG
GG13	CTTGTTTTACAGCAAGGAAGG	GAGATATTAAGAAGGAGACCAGG
GG14	CCCTAATTTCTTTGCCTAGATAG	TGATGAAGCCTTACTGGTGC

Table S3. CR1 group classification of all analyzed amniote CR1 subfamilies.

CR1 group A	CR1 group B	CR1 group C	CR1 group D	CR1 group E	CR1 group F	CR1 group G
CR1-B	CR1-9_CPB	CR1-3_Croc	CR1-L3A_Croc	CR1-1_Gav	CR1-11_Crp	CR1-13_AMi
CR1-B2	CR1-10_CPB	CR1-5_CPB	CR1-L3B_Croc	CR1-10_AMi	CR1-12_CPB	CR1-14_AMi
CR1-C	CR1-10B_CPB	CR1-1_ACo	CR1-7_CPB	CR1-10_Crp	CR1-12B_CPB	CR1-15_AMi
CR1-C2	L3b	CR1-1_PMo	CR1-8_CPB	CR1-10B_AMi	CR1-4_CPB	CR1-1_CPB
CR1-C3	Plat_L3	CR1_AC_1		CR1-10D_AMi	CR1-4B_CPB	CR1-1B_CPB
CR1-C4	Plat_L3b	L3		CR1-11_AMi	CR1-4C_CPB	CR1_Mam
CR1-D		L3_ME		CR1-12_AMi		PlatCR1
CR1-D2				CR1-12_Crp		PlatCR1_old1
CR1-E_Pass				CR1-13_Crp		PlatCR1_old2
CR1-F				CR1-14_Croc		
CR1-F2				CR1-15_Crp		
CR1-G				CR1-16_AMi		
CR1-H				CR1-16_Croc		
CR1-H2				CR1-16_Crp		
CR1-I_Tgu				CR1-17_AMi		
CR1-J1_Pass				CR1-17_Croc		
CR1-J2_Pass				CR1-17_Crp		
CR1-J3_Pass				CR1-17_Gav		
CR1-K1_Tgu				CR1-18_Crp		
CR1-K2_Tgu				CR1-2_AMi		
CR1-K3_Tgu				CR1-2_Crp		
CR1-K4_Tgu				CR1-20_AMi		
CR1-L1_Tgu				CR1-2B_Croc		
CR1-L2_Tgu				CR1-2B_Crp		
CR1-X1				CR1-2C_Croc		
CR1-X1_Pass				CR1-3_Gav		
CR1-X2				CR1-4_Croc		
CR1-X2_Pass				CR1-5_AMi		
CR1-X3_Pass				CR1-5_Croc		
CR1-Y				CR1-5B_AMi		
CR1-Y_Pass				CR1-5B_Crp		
CR1-Y1_Aves				CR1-6_Croc		
CR1-Y2				CR1-6C_AMi		
CR1-Y2_Aves				CR1-6D_AMi		
CR1-Y3				CR1-6F_AMi		
CR1-Y4				CR1-7_Croc		
CR1-YB1_Tgu				CR1-7_Crp		
CR1-YB2_Pass				CR1-7_Gav		
CR1-Z1_Pass				CR1-7B_Gav		
CR1-Z2_Pass				CR1-8_AMi		
CR1-1_Croc				CR1-8_Crp		
PSLINE				CR1-8_Gav		
CR1-2_CPB				CR1-9_AMi		
CR1-2B_CPB				CR1-9_Crp		
				CR1-9B_AMi		
				CR1-9C_AMi		
				CR1-9D_AMi		

Note that font colors correspond to the taxon designations of fig. 3.

Supplementary data S1

36 loci of crocodilian retroposon markers in FASTA format. Consensus sequences of retroposed elements represent the first sequence. The second sequence indicates exonic regions (Exons; if available). Experimentally derived sequences are labeled in a 3-letter code for species names (e.g., Cya for *Caiman yacare*). Other sequences were extracted from genomic scaffolds or from the NCBI GenBank (GB). Intronic sequences and inserted retroposons (and target site duplications) are separated by 3-dashes. Ns denote uncharacterized nucleotides. The loci are sorted by names of genomes that were used for primer design (*Alligator mississippiensis* (AM), *Crocodylus porosus* (CP), *Gavialis* plus *Crocodylus* (GC), *Gavialis gangeticus* (GG) and electronic search for monophyly markers (CG)).

AM02

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>Penelope-1
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AM09

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CP08

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CP10

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