Supplemental Data Legends

Data S1: Gmr1-like matches to various genomes.
The results of profile searches for retrotransposon protein domains in the genomes of various species. After each species a number of elements are listed, with matches to various retroelement domains present in a Gmr1-like order.

Data S2: Genomic BLAST matches to pfam SCAN and gypsy-SCAN domain profiles.
BLAST hits for both the canonical SCAN domain as defined by pfam and a gypsy-SCAN domain profile are given for several species.

Data S3: *Anolis carolinensis* predicted SCAN-ZF genes.
The results of our prediction of SCAN-ZF and SCAN-KRAB-ZF genes in Anolis lizard. Each putative gene has listed the genomic position of its zinc finger exon (e.g. acar_scaffold_371_209727-211364), the number of zinc finger domains predicted (e.g. acar_scaffold_371_209727-211364_**13**), and a unique identifier (PSZ# for **P**utative **S**CAN-**Z**F, PSKZ# for **P**utative **S**CAN-**K**RAB-**Z**F). Following each name line is genomic sequence.

Data S4: Anolis SCAN-ZF predicted binding profiles.
The results of our binding predictions for all Anolis SCAN-ZF genes is given herein. Each name line is similar to Data S3 with the addition of a new field at the end denoting ZF array (a predicted protein with two or more sets of non-contiguous ZF domains was given an independent binding prediction for each). The best predicted binding site is given next, along with its associated SVM score. Next is the SVM score of all 1-nucleotide mutations of the best binding site, arranged as per a PSSM. Finally a PSSM is given, calculated as described in Methods.

Data S5: *Anolis carolinensis* predicted Gmr1-like elements.
Similar to Data S3, this file gives the genomic location and sequence of all predicted Gmr1-like elements in Anolis, which were used as queries against the predicted binding profiles given in Data S4.

Data S6: *Anolis carolinensis* predicted SCAN-ZF/Gmr1-like binding relationships.
This file gives all significant predicted binding relationships between Anolis SCAN-ZF proteins and Anolis Gmr1-like elements. Results are arranged first by Gmr1-like element (location given first on each name-like, then the results of an LTRFinder search on the sequence, then retroelement protein domain matches in the sequence), with individual SCAN-ZF matches to each element inset on subsequent lines. The order of fields for each match is as follows: p-value ; PSSM score ; [FW/RV] for forward or reverse complement ; internal location information [IGNORE] ; name of matching SCAN-ZF protein ; BONF ; p-value (Bonferroni corrected for length of the Gmr1-like element) ; POSITION ; position of the match in the Gmr1-like element.