

**Table S1. Repeat elements classified de novo by RepeatModeler.** The overall repeat content of the gerbil assembly (33.82%) is somewhat less than initially reported for the mouse genome (38.6%) [105]; this apparent difference may be due to filtering or assembly artifacts and will require alternative approaches such as long read sequencing to resolve.

	# of elements	Length occupied	Percentage of sequence
SINEs	9289	801,082 bp	0.03%
LINEs	656,548	340,218,809 bp	13.48%
LINE1	656,548	340,218,809 bp	13.48%
LINE2	0	0	0
L3/CR1	0	0	0
LTR elements	124,571	38,784,942 bp	1.54%
ERVL	76,924	18,475,837 bp	0.73%
ERVL-MaLRs	0	0	0
ERV classI	15,618	8,397,247 bp	0.33%
ERV-classII	26,542	10,925,795 bp	0.43%
DNA elements	30,507	6,158,874 bp	0.24%
hAT-Charlie	30,507	6,158,874 bp	0.24%
TcMar-Tigger	0	0	0
Unclassified	2,182,352	398,059,747 bp	15.78%
Total bases masked	3,809,406	853,387,920 bp	33.82%